# Package 'geneLenDataBase'

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**Version** 1.32.0

**Date** 2019/04/26

**Title** Lengths of mRNA transcripts for a number of genomes

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**Depends** R (>= 2.11.0)

**Imports** utils, rtracklayer, GenomicFeatures (>= 1.3.15)

**LazyLoad** yes

**Description** Length of mRNA transcripts for a number of genomes and gene ID formats, largely based on UCSC table browser

**biocViews** ExperimentData, Genome

**License** LGPL (>= 2)

**NeedsCompilation** no

**git_url** https://git.bioconductor.org/packages/geneLenDataBase

**git_branch** RELEASE_3_15

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## R topics documented:

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](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](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](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](downloadLengthFromUCSC)

### Examples

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

apiMel1.genscan.LENGTH

*Transcript length data for the organism apiMel*

**Description**

apiMel1.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(apiMel1, genscan) on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](downloadLengthFromUCSC)

**Examples**

```
data(apiMel1.genscan.LENGTH)
head(apiMel1.genscan.LENGTH)
```

apiMel2.ensGene.LENGTH

*Transcript length data for the organism apiMel*

**Description**

apiMel2.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(apiMel2, ensGene) on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](downloadLengthFromUCSC)

**Examples**

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

---

aplCal1.xenoRefGene.LENGTH

*Transcript length data for the organism aplCal*

---

### Description

aplCal1.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(aplCal1, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(aplCal1.xenoRefGene.LENGTH)
head(aplCal1.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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](downloadLengthFromUCSC)

### Examples

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

---

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

---

### Description

ce4.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(ce4, geneSymbol) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](downloadLengthFromUCSC)

### Examples

```
data(ce4.geneSymbol.LENGTH)
head(ce4.geneSymbol.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.geneSymbol.LENGTH *Transcript length data for the organism ce*

---

### Description

ce6.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(ce6, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(ce6.geneSymbol.LENGTH)
head(ce6.geneSymbol.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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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)
```

---

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](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](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 as-
sociated 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](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 ma-
ture mRNA transcripts. Where available, it will also provide the mapping between a 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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](downloadLengthFromUCSC)

### Examples

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

---

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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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 as-
sociated 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 ma-
ture mRNA transcripts. Where available, it will also provide the mapping between a 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](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](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](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](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 as-
sociated 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](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 as-
sociated 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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](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](downloadLengthFromUCSC)

### Examples

```
data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)
```

---

supportedGeneIDs            *Supported Gene IDs*

---

### 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` arguement 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 avaible 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            *Supported Genomes*

---

**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 arguement of various functions.

The final column, headed `AvailableGeneIDs` lists the gene ID formats for which there is a local copy of the length information avaible 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](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](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](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](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](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: /codefactor, /codedata.frame and /codelist.

## 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](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](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](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](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](downloadLengthFromUCSC)

### Examples

```
data(xenTro2.refGene.LENGTH)
head(xenTro2.refGene.LENGTH)
```

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