# Package 'geneLenDataBase'

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**Version** 0.99.10

**Date** 2010/03/30

**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** HighThroughputSequencingData, ExperimentData, Transcription,RNAseq

**License** LGPL (>= 2)

## 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](#)

### Examples

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

anoCar1.genscan.LENGTH

*Transcript length data for the organism anoCar*

### Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

anoCar1.xenoRefGene.LENGTH
*Transcript length data for the organism anoCar*

---

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

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

---

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

anoGam1.geneid.LENGTH

*Transcript length data for the organism anoGam*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

anoGam1.genscan.LENGTH

*Transcript length data for the organism anoGam*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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

### 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

### 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](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](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

### Examples

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

bosTau2.genscan.LENGTH

*Transcript length data for the organism bosTau*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

bosTau2.refGene.LENGTH

*Transcript length data for the organism bosTau*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

bosTau2.sgpGene.LENGTH

*Transcript length data for the organism bosTau*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

bosTau3.ensGene.LENGTH

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

bosTau3.geneid.LENGTH

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

bosTau3.geneSymbol.LENGTH

*Transcript length data for the organism bosTau*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

bosTau3.genscan.LENGTH

*Transcript length data for the organism bosTau*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

bosTau3.refGene.LENGTH

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

bosTau3.sgpGene.LENGTH

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

bosTau4.ensGene.LENGTH

*Transcript length data for the organism bosTau*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

bosTau4.geneSymbol.LENGTH

*Transcript length data for the organism bosTau*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

bosTau4.genscan.LENGTH

*Transcript length data for the organism bosTau*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

bosTau4.nscanGene.LENGTH

*Transcript length data for the organism bosTau*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

bosTau4.refGene.LENGTH

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

braFlo1.xenoRefGene.LENGTH

*Transcript length data for the organism braFlo*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

caeJap1.xenoRefGene.LENGTH

*Transcript length data for the organism caeJap*

### Description

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

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

### See Also

[downloadLengthFromUCSC](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

### Examples

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

caeRem2.xenoRefGene.LENGTH

*Transcript length data for the organism caeRem*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

caeRem3.xenoRefGene.LENGTH

*Transcript length data for the organism caeRem*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

calJac1.genscan.LENGTH

*Transcript length data for the organism calJac*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

calJac1.nscanGene.LENGTH

*Transcript length data for the organism calJac*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

calJac1.xenoRefGene.LENGTH

*Transcript length data for the organism calJac*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

canFam1.ensGene.LENGTH

*Transcript length data for the organism canFam*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

canFam1.geneSymbol.LENGTH

*Transcript length data for the organism canFam*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

canFam1.genscan.LENGTH

*Transcript length data for the organism canFam*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

canFam1.nscanGene.LENGTH

*Transcript length data for the organism canFam*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

canFam1.refGene.LENGTH

*Transcript length data for the organism canFam*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

canFam1.xenoRefGene.LENGTH

*Transcript length data for the organism canFam*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

## canFam2.ensGene.LENGTH

*Transcript length data for the organism canFam*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

## canFam2.geneSymbol.LENGTH

*Transcript length data for the organism canFam*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

canFam2.genscan.LENGTH

*Transcript length data for the organism canFam*

---

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

canFam2.nscanGene.LENGTH

*Transcript length data for the organism canFam*

---

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

canFam2.refGene.LENGTH

*Transcript length data for the organism canFam*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

canFam2.xenoRefGene.LENGTH

*Transcript length data for the organism canFam*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

cavPor3.ensGene.LENGTH

*Transcript length data for the organism cavPor*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

cavPor3.genscan.LENGTH

*Transcript length data for the organism cavPor*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

cavPor3.nscanGene.LENGTH

*Transcript length data for the organism cavPor*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

cavPor3.xenoRefGene.LENGTH

*Transcript length data for the organism cavPor*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

cb1.xenoRefGene.LENGTH

*Transcript length data for the organism cb*

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

cb3.xenoRefGene.LENGTH

*Transcript length data for the organism cb*

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

ce2.geneSymbol.LENGTH

*Transcript length data for the organism ce*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

| ce4.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

### 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](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](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

### Examples

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

ce6.xenoRefGene.LENGTH

*Transcript length data for the organism ce*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

ci1.geneSymbol.LENGTH

*Transcript length data for the organism ci*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](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](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](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

### Examples

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

---

danRer3.refGene.LENGTH

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

danRer4.ensGene.LENGTH

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

danRer4.geneSymbol.LENGTH

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

danRer4.genscan.LENGTH

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

danRer4.nscanGene.LENGTH

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

danRer4.refGene.LENGTH

*Transcript length data for the organism danRer*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

danRer5.ensGene.LENGTH

*Transcript length data for the organism danRer*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

danRer5.geneSymbol.LENGTH

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

danRer5.refGene.LENGTH

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

danRer5.vegaGene.LENGTH

*Transcript length data for the organism danRer*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

danRer5.vegaPseudoGene.LENGTH

*Transcript length data for the organism danRer*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

danRer6.ensGene.LENGTH

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

danRer6.geneSymbol.LENGTH

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

danRer6.refGene.LENGTH

*Transcript length data for the organism danRer*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

danRer6.xenoRefGene.LENGTH

*Transcript length data for the organism danRer*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

dm1.geneSymbol.LENGTH

*Transcript length data for the organism dm*

---

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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

### Description

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

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

### See Also

[downloadLengthFromUCSC](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](#)

### Examples

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

dm3.nscanPasaGene.LENGTH

*Transcript length data for the organism dm*

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

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

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

dp2.xenoRefGene.LENGTH

*Transcript length data for the organism dp*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

dp3.geneid.LENGTH          *Transcript length data for the organism dp*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

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

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

droAna1.geneid.LENGTH

*Transcript length data for the organism droAna*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

droAna1.genscan.LENGTH

*Transcript length data for the organism droAna*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

droAna1.xenoRefGene.LENGTH

*Transcript length data for the organism droAna*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

droAna2.genscan.LENGTH

*Transcript length data for the organism droAna*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

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

### Description

droEre1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their 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 genscan table.

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

droEre1.xenoRefGene.LENGTH

*Transcript length data for the organism droEre*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

droGri1.genscan.LENGTH

*Transcript length data for the organism droGri*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

droGri1.xenoRefGene.LENGTH

*Transcript length data for the organism droGri*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

droMoj1.geneid.LENGTH

*Transcript length data for the organism droMoj*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

## droMoj1.genscan.LENGTH

*Transcript length data for the organism droMoj*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

## droMoj1.xenoRefGene.LENGTH

*Transcript length data for the organism droMoj*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

droMoj2.genscan.LENGTH

*Transcript length data for the organism droMoj*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

droMoj2.xenoRefGene.LENGTH

*Transcript length data for the organism droMoj*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

droPer1.genscan.LENGTH

*Transcript length data for the organism droPer*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

droPer1.xenoRefGene.LENGTH

*Transcript length data for the organism droPer*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

droSec1.genscan.LENGTH

*Transcript length data for the organism droSec*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

droSec1.xenoRefGene.LENGTH

*Transcript length data for the organism droSec*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

droSim1.geneid.LENGTH

*Transcript length data for the organism droSim*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

droSim1.genscan.LENGTH

*Transcript length data for the organism droSim*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

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

#### Description

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

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

#### See Also

downloadLengthFromUCSC

#### Examples

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

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

#### Description

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

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

#### See Also

downloadLengthFromUCSC

#### Examples

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

---

droVir1.genscan.LENGTH

*Transcript length data for the organism droVir*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](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](#)

### Examples

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

---

droVir2.xenoRefGene.LENGTH

*Transcript length data for the organism droVir*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

droYak1.geneid.LENGTH

*Transcript length data for the organism droYak*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

droYak1.genscan.LENGTH

*Transcript length data for the organism droYak*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

droYak1.xenoRefGene.LENGTH

*Transcript length data for the organism droYak*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

droYak2.genscan.LENGTH

*Transcript length data for the organism droYak*

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

## droYak2.xenoRefGene.LENGTH

*Transcript length data for the organism droYak*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

## equCab1.geneid.LENGTH

*Transcript length data for the organism equCab*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

equCab1.geneSymbol.LENGTH
*Transcript length data for the organism equCab*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

equCab1.nscanGene.LENGTH
*Transcript length data for the organism equCab*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

equCab1.refGene.LENGTH

*Transcript length data for the organism equCab*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

equCab1.sgpGene.LENGTH

*Transcript length data for the organism equCab*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

equCab2.ensGene.LENGTH

*Transcript length data for the organism equCab*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

equCab2.geneSymbol.LENGTH

*Transcript length data for the organism equCab*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

equCab2.nscanGene.LENGTH

*Transcript length data for the organism equCab*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

equCab2.refGene.LENGTH

*Transcript length data for the organism equCab*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

equCab2.xenoRefGene.LENGTH

*Transcript length data for the organism equCab*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

felCat3.ensGene.LENGTH

*Transcript length data for the organism felCat*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

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

---

## Description

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

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

## See Also

[downloadLengthFromUCSC](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](#)

### Examples

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

---

felCat3.nscanGene.LENGTH

*Transcript length data for the organism felCat*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

felCat3.refGene.LENGTH

*Transcript length data for the organism felCat*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

felCat3.sgpGene.LENGTH

*Transcript length data for the organism felCat*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

felCat3.xenoRefGene.LENGTH
### *Transcript length data for the organism felCat*

---

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

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

---

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

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

### Description

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

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

### See Also

[downloadLengthFromUCSC](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](downloadLengthFromUCSC)

### Examples

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

galGal2.ensGene.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal2.geneid.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal2.geneSymbol.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal2.genscan.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal2.refGene.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal2.sgpGene.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal3.ensGene.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal3.geneSymbol.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal3.genscan.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal3.nscanGene.LENGTH

*Transcript length data for the organism galGal*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

galGal3.refGene.LENGTH

*Transcript length data for the organism galGal*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

galGal3.xenoRefGene.LENGTH

*Transcript length data for the organism galGal*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

gasAcu1.ensGene.LENGTH

*Transcript length data for the organism gasAcu*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

gasAcu1.nscanGene.LENGTH

*Transcript length data for the organism gasAcu*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

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

---

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

hg16.geneSymbol.LENGTH

*Transcript length data for the organism hg*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

hg16.knownGene.LENGTH

*Transcript length data for the organism hg*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

hg17.ccdsGene.LENGTH

*Transcript length data for the organism hg*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

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

---

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

---

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

---

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

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

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

hg17.geneSymbol.LENGTH

*Transcript length data for the organism hg*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

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

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

hg17.knownGene.LENGTH

*Transcript length data for the organism hg*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

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

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

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

hg17.vegaGene.LENGTH

*Transcript length data for the organism hg*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

hg17.vegaPseudoGene.LENGTH

*Transcript length data for the organism hg*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

hg17.xenoRefGene.LENGTH

*Transcript length data for the organism hg*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

hg18.ccdsGene.LENGTH

*Transcript length data for the organism hg*

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

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

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

hg18.geneSymbol.LENGTH

*Transcript length data for the organism hg*

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

hg18.knownGene.LENGTH

*Transcript length data for the organism hg*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

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

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

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

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

---

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

---

### Description

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

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

### See Also

downloadLengthFromUCSC

### Examples

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

hg18.xenoRefGene.LENGTH

*Transcript length data for the organism hg*

## Description

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

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

## See Also

downloadLengthFromUCSC

## Examples

    data(hg18.xenoRefGene.LENGTH)
    head(hg18.xenoRefGene.LENGTH)

hg19.ccdsGene.LENGTH

*Transcript length data for the organism hg*

## Description

hg19.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, ccdsGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

    data(hg19.ccdsGene.LENGTH)
    head(hg19.ccdsGene.LENGTH)

hg19.ensGene.LENGTH  *Transcript length data for the organism hg*

---

### Description

hg19.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(hg19.ensGene.LENGTH)
head(hg19.ensGene.LENGTH)
```

---

hg19.exoniphy.LENGTH  *Transcript length data for the organism hg*

---

### Description

hg19.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the exoniphy table.

The data file was made by calling downloadLengthFromUCSC(hg19, exoniphy) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(hg19.exoniphy.LENGTH)
head(hg19.exoniphy.LENGTH)
```

---

hg19.geneSymbol.LENGTH

*Transcript length data for the organism hg*

---

## Description

hg19.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(hg19, geneSymbol) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

    data(hg19.geneSymbol.LENGTH)
    head(hg19.geneSymbol.LENGTH)

---

hg19.knownGene.LENGTH

*Transcript length data for the organism hg*

---

## Description

hg19.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, knownGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

    data(hg19.knownGene.LENGTH)
    head(hg19.knownGene.LENGTH)

## hg19.nscanGene.LENGTH

*Transcript length data for the organism hg*

### Description

hg19.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, nscanGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(hg19.nscanGene.LENGTH)
head(hg19.nscanGene.LENGTH)
```

## hg19.refGene.LENGTH    *Transcript length data for the organism hg*

### Description

hg19.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, refGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(hg19.refGene.LENGTH)
head(hg19.refGene.LENGTH)
```

---

hg19.xenoRefGene.LENGTH

*Transcript length data for the organism hg*

---

## Description

hg19.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, xenoRefGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

```
data(hg19.xenoRefGene.LENGTH)
head(hg19.xenoRefGene.LENGTH)
```

---

loxAfr3.xenoRefGene.LENGTH

*Transcript length data for the organism loxAfr*

---

## Description

loxAfr3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(loxAfr3, xenoRefGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

```
data(loxAfr3.xenoRefGene.LENGTH)
head(loxAfr3.xenoRefGene.LENGTH)
```

---

mm7.ensGene.LENGTH    *Transcript length data for the organism mm*

---

**Description**

mm7.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature
mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its 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(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 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(mm7, geneid) on the date on which
the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

    data(mm7.geneid.LENGTH)
    head(mm7.geneid.LENGTH)

mm7.geneSymbol.LENGTH

*Transcript length data for the organism mm*

### Description

mm7.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(mm7, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm7.geneSymbol.LENGTH)
head(mm7.geneSymbol.LENGTH)
```

mm7.genscan.LENGTH *Transcript length data for the organism mm*

### Description

mm7.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(mm7, genscan) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm7.genscan.LENGTH)
head(mm7.genscan.LENGTH)
```

---

mm7.knownGene.LENGTH

*Transcript length data for the organism mm*

---

**Description**

mm7.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, knownGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(mm7.knownGene.LENGTH)
head(mm7.knownGene.LENGTH)
```

---

mm7.refGene.LENGTH     *Transcript length data for the organism mm*

---

**Description**

mm7.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, refGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(mm7.refGene.LENGTH)
head(mm7.refGene.LENGTH)
```

mm7.sgpGene.LENGTH  *Transcript length data for the organism mm*

### Description

mm7.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, sgpGene) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](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](downloadLengthFromUCSC)

### Examples

```
data(mm7.xenoRefGene.LENGTH)
head(mm7.xenoRefGene.LENGTH)
```

---

mm8.ccdsGene.LENGTH

*Transcript length data for the organism mm*

---

### Description

mm8.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, ccdsGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm8.ccdsGene.LENGTH)
head(mm8.ccdsGene.LENGTH)
```

---

mm8.ensGene.LENGTH  *Transcript length data for the organism mm*

---

### Description

mm8.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm8.ensGene.LENGTH)
head(mm8.ensGene.LENGTH)
```

mm8.geneid.LENGTH *Transcript length data for the organism mm*

### Description

mm8.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(mm8, geneid) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm8.geneid.LENGTH)
head(mm8.geneid.LENGTH)
```

mm8.geneSymbol.LENGTH

*Transcript length data for the organism mm*

### Description

mm8.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(mm8, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm8.geneSymbol.LENGTH)
head(mm8.geneSymbol.LENGTH)
```

mm8.genscan.LENGTH    *Transcript length data for the organism mm*

**Description**

mm8.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(mm8, genscan) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(mm8.genscan.LENGTH)
head(mm8.genscan.LENGTH)
```

mm8.knownGene.LENGTH

*Transcript length data for the organism mm*

**Description**

mm8.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, knownGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(mm8.knownGene.LENGTH)
head(mm8.knownGene.LENGTH)
```

mm8.nscanGene.LENGTH

*Transcript length data for the organism mm*

## Description

mm8.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, nscanGene) on the date on which the package was last updated.

## See Also

[downloadLengthFromUCSC](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

### Examples

```
data(mm8.xenoRefGene.LENGTH)
head(mm8.xenoRefGene.LENGTH)
```

mm9.acembly.LENGTH  *Transcript length data for the organism mm*

### Description

mm9.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the acembly table.

The data file was made by calling downloadLengthFromUCSC(mm9, acembly) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm9.acembly.LENGTH)
head(mm9.acembly.LENGTH)
```

mm9.ccdsGene.LENGTH

*Transcript length data for the organism mm*

### Description

mm9.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, ccdsGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm9.ccdsGene.LENGTH)
head(mm9.ccdsGene.LENGTH)
```

mm9.ensGene.LENGTH  *Transcript length data for the organism mm*

### Description

mm9.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm9.ensGene.LENGTH)
head(mm9.ensGene.LENGTH)
```

mm9.exoniphy.LENGTH

*Transcript length data for the organism mm*

### Description

mm9.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the exoniphy table.

The data file was made by calling downloadLengthFromUCSC(mm9, exoniphy) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.exoniphy.LENGTH)
head(mm9.exoniphy.LENGTH)
```

mm9.geneid.LENGTH    *Transcript length data for the organism mm*

### Description

mm9.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(mm9, geneid) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.geneid.LENGTH)
head(mm9.geneid.LENGTH)
```

mm9.geneSymbol.LENGTH

*Transcript length data for the organism mm*

#### Description

mm9.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(mm9, geneSymbol) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### Examples

```
data(mm9.geneSymbol.LENGTH)
head(mm9.geneSymbol.LENGTH)
```

mm9.genscan.LENGTH   *Transcript length data for the organism mm*

#### Description

mm9.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(mm9, genscan) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### Examples

```
data(mm9.genscan.LENGTH)
head(mm9.genscan.LENGTH)
```

---

mm9.knownGene.LENGTH

*Transcript length data for the organism mm*

---

**Description**

mm9.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, knownGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

    data(mm9.knownGene.LENGTH)
    head(mm9.knownGene.LENGTH)

---

mm9.nscanGene.LENGTH

*Transcript length data for the organism mm*

---

**Description**

mm9.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, nscanGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

    data(mm9.nscanGene.LENGTH)
    head(mm9.nscanGene.LENGTH)

mm9.refGene.LENGTH    *Transcript length data for the organism mm*

**Description**

mm9.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, refGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

    data(mm9.refGene.LENGTH)
    head(mm9.refGene.LENGTH)

mm9.sgpGene.LENGTH    *Transcript length data for the organism mm*

**Description**

mm9.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, sgpGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

    data(mm9.sgpGene.LENGTH)
    head(mm9.sgpGene.LENGTH)

## mm9.xenoRefGene.LENGTH

*Transcript length data for the organism mm*

### Description

mm9.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(mm9.xenoRefGene.LENGTH)
head(mm9.xenoRefGene.LENGTH)
```

## monDom1.genscan.LENGTH

*Transcript length data for the organism monDom*

### Description

monDom1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(monDom1, genscan) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(monDom1.genscan.LENGTH)
head(monDom1.genscan.LENGTH)
```

monDom4.ensGene.LENGTH
                    *Transcript length data for the organism monDom*

### Description

monDom4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their
mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and
its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-
bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(monDom4, ensGene) on the date
on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(monDom4.ensGene.LENGTH)
head(monDom4.ensGene.LENGTH)
```

monDom4.geneSymbol.LENGTH
                    *Transcript length data for the organism monDom*

### Description

monDom4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their
mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and
its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-
bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(monDom4, geneSymbol) on the
date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(monDom4.geneSymbol.LENGTH)
head(monDom4.geneSymbol.LENGTH)
```

---

monDom4.genscan.LENGTH

*Transcript length data for the organism monDom*

---

### Description

monDom4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(monDom4, genscan) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(monDom4.genscan.LENGTH)
head(monDom4.genscan.LENGTH)
```

---

monDom4.nscanGene.LENGTH

*Transcript length data for the organism monDom*

---

### Description

monDom4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(monDom4, nscanGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(monDom4.nscanGene.LENGTH)
head(monDom4.nscanGene.LENGTH)
```

monDom4.refGene.LENGTH

*Transcript length data for the organism monDom*

### Description

monDom4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(monDom4, refGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(monDom4.refGene.LENGTH)
head(monDom4.refGene.LENGTH)
```

monDom4.xenoRefGene.LENGTH

*Transcript length data for the organism monDom*

### Description

monDom4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(monDom4, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(monDom4.xenoRefGene.LENGTH)
head(monDom4.xenoRefGene.LENGTH)
```

## monDom5.ensGene.LENGTH

*Transcript length data for the organism monDom*

### Description

monDom5.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

    data(monDom5.ensGene.LENGTH)
    head(monDom5.ensGene.LENGTH)

## monDom5.geneSymbol.LENGTH

*Transcript length data for the organism monDom*

### Description

monDom5.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(monDom5, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

    data(monDom5.geneSymbol.LENGTH)
    head(monDom5.geneSymbol.LENGTH)

---

monDom5.genscan.LENGTH

*Transcript length data for the organism monDom*

---

**Description**

monDom5.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(monDom5, genscan) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(monDom5.genscan.LENGTH)
head(monDom5.genscan.LENGTH)
```

---

monDom5.nscanGene.LENGTH

*Transcript length data for the organism monDom*

---

**Description**

monDom5.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, nscanGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)
```

monDom5.refGene.LENGTH

*Transcript length data for the organism monDom*

### Description

monDom5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, refGene) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)
```

monDom5.xenoRefGene.LENGTH

*Transcript length data for the organism monDom*

### Description

monDom5.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, xenoRefGene) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(monDom5.xenoRefGene.LENGTH)
head(monDom5.xenoRefGene.LENGTH)
```

ornAna1.ensGene.LENGTH

*Transcript length data for the organism ornAna*

### Description

ornAna1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(ornAna1.ensGene.LENGTH)
head(ornAna1.ensGene.LENGTH)
```

ornAna1.geneSymbol.LENGTH

*Transcript length data for the organism ornAna*

### Description

ornAna1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(ornAna1.geneSymbol.LENGTH)
head(ornAna1.geneSymbol.LENGTH)
```

## ornAna1.refGene.LENGTH

*Transcript length data for the organism ornAna*

### Description

ornAna1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, refGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(ornAna1.refGene.LENGTH)
head(ornAna1.refGene.LENGTH)
```

## ornAna1.xenoRefGene.LENGTH

*Transcript length data for the organism ornAna*

### Description

ornAna1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(ornAna1.xenoRefGene.LENGTH)
head(ornAna1.xenoRefGene.LENGTH)
```

oryLat2.ensGene.LENGTH

*Transcript length data for the organism oryLat*

### Description

oryLat2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)
```

oryLat2.geneSymbol.LENGTH

*Transcript length data for the organism oryLat*

### Description

oryLat2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)
```

oryLat2.refGene.LENGTH

*Transcript length data for the organism oryLat*

### Description

oryLat2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, refGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)
```

oryLat2.xenoRefGene.LENGTH

*Transcript length data for the organism oryLat*

### Description

oryLat2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)
```

---

panTro1.ensGene.LENGTH

*Transcript length data for the organism panTro*

---

## Description

panTro1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(panTro1, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

```
data(panTro1.ensGene.LENGTH)
head(panTro1.ensGene.LENGTH)
```

---

panTro1.geneid.LENGTH

*Transcript length data for the organism panTro*

---

## Description

panTro1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(panTro1, geneid) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

```
data(panTro1.geneid.LENGTH)
head(panTro1.geneid.LENGTH)
```

panTro1.genscan.LENGTH

*Transcript length data for the organism panTro*

### Description

panTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(panTro1, genscan) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

data(panTro1.genscan.LENGTH)
head(panTro1.genscan.LENGTH)

panTro1.xenoRefGene.LENGTH

*Transcript length data for the organism panTro*

### Description

panTro1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(panTro1, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

data(panTro1.xenoRefGene.LENGTH)
head(panTro1.xenoRefGene.LENGTH)

panTro2.ensGene.LENGTH

*Transcript length data for the organism panTro*

### Description

panTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)
```

panTro2.geneSymbol.LENGTH

*Transcript length data for the organism panTro*

### Description

panTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(panTro2, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)
```

## panTro2.genscan.LENGTH

*Transcript length data for the organism panTro*

### Description

panTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(panTro2, genscan) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](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

**Examples**

    data(panTro2.refGene.LENGTH)
    head(panTro2.refGene.LENGTH)

panTro2.xenoRefGene.LENGTH

*Transcript length data for the organism panTro*

**Description**

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, xenoRefGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

    data(panTro2.xenoRefGene.LENGTH)
    head(panTro2.xenoRefGene.LENGTH)

## petMar1.xenoRefGene.LENGTH

*Transcript length data for the organism petMar*

### Description

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(petMar1, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)
```

## ponAbe2.ensGene.LENGTH

*Transcript length data for the organism ponAbe*

### Description

ponAbe2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)
```

---

ponAbe2.geneSymbol.LENGTH

*Transcript length data for the organism ponAbe*

---

### Description

ponAbe2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)
```

---

ponAbe2.genscan.LENGTH

*Transcript length data for the organism ponAbe*

---

### Description

ponAbe2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, genscan) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)
```

ponAbe2.nscanGene.LENGTH

*Transcript length data for the organism ponAbe*

### Description

ponAbe2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, nscanGene) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](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

### Examples

```
data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)
```

---

priPac1.xenoRefGene.LENGTH

*Transcript length data for the organism priPac*

---

### Description

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(priPac1, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)
```

rheMac2.ensGene.LENGTH

*Transcript length data for the organism rheMac*

### Description

rheMac2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)
```

rheMac2.geneid.LENGTH

*Transcript length data for the organism rheMac*

### Description

rheMac2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, geneid) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(rheMac2.geneid.LENGTH)
head(rheMac2.geneid.LENGTH)
```

rheMac2.geneSymbol.LENGTH

*Transcript length data for the organism rheMac*

### Description

rheMac2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)
```

rheMac2.nscanGene.LENGTH

*Transcript length data for the organism rheMac*

### Description

rheMac2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, nscanGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)
```

rheMac2.refGene.LENGTH

*Transcript length data for the organism rheMac*

## Description

rheMac2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, refGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

```
data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)
```

rheMac2.sgpGene.LENGTH

*Transcript length data for the organism rheMac*

## Description

rheMac2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, sgpGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

```
data(rheMac2.sgpGene.LENGTH)
head(rheMac2.sgpGene.LENGTH)
```

rheMac2.xenoRefGene.LENGTH
*Transcript length data for the organism rheMac*

**Description**

rheMac2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, xenoRefGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)
```

rn3.ensGene.LENGTH        *Transcript length data for the organism rn*

**Description**

rn3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, ensGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.LENGTH)
```

---

rn3.geneid.LENGTH *Transcript length data for the organism rn*

---

#### Description

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rn3, geneid) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### Examples

    data(rn3.geneid.LENGTH)
    head(rn3.geneid.LENGTH)

---

rn3.geneSymbol.LENGTH

*Transcript length data for the organism rn*

---

#### Description

rn3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rn3, geneSymbol) on the date on which the package was last updated.

#### See Also

downloadLengthFromUCSC

#### Examples

    data(rn3.geneSymbol.LENGTH)
    head(rn3.geneSymbol.LENGTH)

| rn3.genscan.LENGTH | *Transcript length data for the organism rn* |

**Description**

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(rn3, genscan) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)
```

| rn3.knownGene.LENGTH | |
| *Transcript length data for the organism rn* |

**Description**

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, knownGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

rn3.nscanGene.LENGTH

*Transcript length data for the organism rn*

**Description**

rn3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, nscanGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

rn3.refGene.LENGTH    *Transcript length data for the organism rn*

**Description**

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, refGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

rn3.sgpGene.LENGTH       *Transcript length data for the organism rn*

### Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, sgpGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)
```

rn3.xenoRefGene.LENGTH

*Transcript length data for the organism rn*

### Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)
```

rn4.ensGene.LENGTH *Transcript length data for the organism rn*

### Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)
```

rn4.geneid.LENGTH *Transcript length data for the organism rn*

### Description

rn4.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rn4, geneid) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```

---

rn4.geneSymbol.LENGTH

*Transcript length data for the organism rn*

---

**Description**

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rn4, geneSymbol) on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

---

rn4.genscan.LENGTH     *Transcript length data for the organism rn*

---

**Description**

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(rn4, genscan) on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

rn4.knownGene.LENGTH

*Transcript length data for the organism rn*

### Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, knownGene) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](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](downloadLengthFromUCSC)

### Examples

```
data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)
```

| rn4.refGene.LENGTH | *Transcript length data for the organism rn* |

**Description**

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, refGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)
```

| rn4.sgpGene.LENGTH | *Transcript length data for the organism rn* |

**Description**

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, sgpGene) on the date on which the package was last updated.

**See Also**

downloadLengthFromUCSC

**Examples**

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

---

rn4.xenoRefGene.LENGTH

*Transcript length data for the organism rn*

---

### Description

rn4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, xenoRefGene) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](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

### Examples

```
data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)
```

strPur1.geneSymbol.LENGTH

*Transcript length data for the organism strPur*

### Description

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(strPur1, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)
```

strPur1.genscan.LENGTH

*Transcript length data for the organism strPur*

## Description

strPur1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(strPur1, genscan) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

```
data(strPur1.genscan.LENGTH)
head(strPur1.genscan.LENGTH)
```

strPur1.refGene.LENGTH

*Transcript length data for the organism strPur*

## Description

strPur1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(strPur1, refGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

```
data(strPur1.refGene.LENGTH)
head(strPur1.refGene.LENGTH)
```

strPur1.xenoRefGene.LENGTH
                    *Transcript length data for the organism strPur*

## Description

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their
mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and
its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-
bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(strPur1, xenoRefGene) on the date
on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

    data(strPur1.xenoRefGene.LENGTH)
    head(strPur1.xenoRefGene.LENGTH)

strPur2.geneSymbol.LENGTH
                    *Transcript length data for the organism strPur*

## Description

strPur2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their
mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and
its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-
bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(strPur2, geneSymbol) on the date
on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

    data(strPur2.geneSymbol.LENGTH)
    head(strPur2.geneSymbol.LENGTH)

strPur2.genscan.LENGTH

*Transcript length data for the organism strPur*

### Description

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(strPur2, genscan) on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](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

### 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

**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](downloadLengthFromUCSC)

### Examples

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

taeGut1.xenoRefGene.LENGTH

*Transcript length data for the organism taeGut*

### Description

taeGut1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, xenoRefGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

tetNig1.ensGene.LENGTH

*Transcript length data for the organism tetNig*

### Description

tetNig1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(tetNig1, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

tetNig1.geneid.LENGTH

*Transcript length data for the organism tetNig*

### Description

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(tetNig1, geneid) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

tetNig1.genscan.LENGTH

*Transcript length data for the organism tetNig*

### Description

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(tetNig1, genscan) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```

tetNig1.nscanGene.LENGTH

*Transcript length data for the organism tetNig*

### Description

tetNig1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(tetNig1, nscanGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

tetNig2.ensGene.LENGTH

*Transcript length data for the organism tetNig*

### Description

tetNig2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(tetNig2, ensGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

```
data(tetNig2.ensGene.LENGTH)
head(tetNig2.ensGene.LENGTH)
```

---

| unfactor | *Purge factors* |
|----------|-----------------|

---

## Description

Removes all factors from a variable in a sensible way.

## Usage

unfactor(var)

## Arguments

var             The variable from which you want the factors removed.

## Details

As factors are their own type, to remove factors we must convert each level into another type. This
is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be
done without inducing NAs, otherwise it is coerced using as.character. Currently supported types
are: /codefactor, /codedata.frame and /codelist.

## Value

The variable with all factors converted to characters or numbers (see details).

## Author(s)

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## Examples

```
#A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep='.')
x
unfactor(x)

#A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"), score <- factor(c(9, 7, 8, 9)), stringsAsFactors=TRUE)
x$player
x$score
y <- unfactor(x)
y$player
y$score
```

xenTro1.genscan.LENGTH

*Transcript length data for the organism xenTro*

## Description

xenTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(xenTro1, genscan) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

```
data(xenTro1.genscan.LENGTH)
head(xenTro1.genscan.LENGTH)
```

xenTro2.ensGene.LENGTH

*Transcript length data for the organism xenTro*

## Description

xenTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, ensGene) on the date on which the package was last updated.

## See Also

downloadLengthFromUCSC

## Examples

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

---

xenTro2.geneSymbol.LENGTH

*Transcript length data for the organism xenTro*

---

### Description

xenTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, geneSymbol) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

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

---

xenTro2.genscan.LENGTH

*Transcript length data for the organism xenTro*

---

### Description

xenTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, genscan) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

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

xenTro2.refGene.LENGTH

*Transcript length data for the organism xenTro*

### Description

xenTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, refGene) on the date on which the package was last updated.

### See Also

downloadLengthFromUCSC

### Examples

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

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