

# Package ‘geneLenDataBase’

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

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**Depends** R (>= 2.11.0)

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

**LazyLoad** yes

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

**biocViews** ExperimentData, Genome

**License** LGPL (>= 2)

**NeedsCompilation** no

**git\_url** <https://git.bioconductor.org/packages/geneLenDataBase>

**git\_branch** devel

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---

`anoCar1.ensGene.LENGTH`*Transcript length data for the organism anoCar*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

`anoCar1.genscan.LENGTH`*Transcript length data for the organism anoCar*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
anoCar1.xenoRefGene.LENGTH
```

*Transcript length data for the organism anoCar*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
anoGam1.ensGene.LENGTH
```

*Transcript length data for the organism anoGam*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

`apiMe11.genscan.LENGTH`*Transcript length data for the organism apiMel*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

`apiMe12.ensGene.LENGTH`*Transcript length data for the organism apiMel*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
bosTau3.geneSymbol.LENGTH
```

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
bosTau3.genscan.LENGTH
```

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
caeJap1.xenoRefGene.LENGTH
```

*Transcript length data for the organism caeJap*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
caePb1.xenoRefGene.LENGTH
```

*Transcript length data for the organism caePb*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
caePb2.xenoRefGene.LENGTH
```

*Transcript length data for the organism caePb*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
caeRem2.xenoRefGene.LENGTH
```

*Transcript length data for the organism caeRem*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

`caeRem3.xenoRefGene.LENGTH`*Transcript length data for the organism caeRem*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

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

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
danRer4.ensGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer4.geneSymbol.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
danRer5.vegaGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer5.vegaPseudoGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer6.ensGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer6.geneSymbol.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

`dp2.xenoRefGene.LENGTH`*Transcript length data for the organism dp*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

`droGri1.genscan.LENGTH`*Transcript length data for the organism droGri*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

```
droGri1.xenoRefGene.LENGTH
```

*Transcript length data for the organism droGri*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
droMoj1.geneid.LENGTH
```

*Transcript length data for the organism droMoj*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
droVir1.genscan.LENGTH
```

*Transcript length data for the organism droVir*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
droVir1.xenoRefGene.LENGTH
```

*Transcript length data for the organism droVir*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

`droVir2.genscan.LENGTH`*Transcript length data for the organism droVir*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

`droVir2.xenoRefGene.LENGTH`*Transcript length data for the organism droVir*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

hg18.sibGene.LENGTH    *Transcript length data for the organism hg*

---

### Description

hg18.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sibGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, sibGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg18.sibGene.LENGTH)
head(hg18.sibGene.LENGTH)
```

---

hg18.xenoRefGene.LENGTH

*Transcript length data for the organism hg*

---

### Description

hg18.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg18.xenoRefGene.LENGTH)
head(hg18.xenoRefGene.LENGTH)
```

---

hg19.ccdsGene.LENGTH *Transcript length data for the organism hg*

---

### Description

hg19.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ccdsGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.ccdsGene.LENGTH)
head(hg19.ccdsGene.LENGTH)
```



---

hg19.ensGene.LENGTH *Transcript length data for the organism hg*

---

### Description

hg19.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.ensGene.LENGTH)
head(hg19.ensGene.LENGTH)
```

---

hg19.exoniphy.LENGTH *Transcript length data for the organism hg*

---

### Description

hg19.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg19, exoniphy)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.exoniphy.LENGTH)
head(hg19.exoniphy.LENGTH)
```

---

```
hg19.geneSymbol.LENGTH
```

*Transcript length data for the organism hg*

---

### Description

hg19.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg19, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.geneSymbol.LENGTH)
head(hg19.geneSymbol.LENGTH)
```

---

```
hg19.knownGene.LENGTH
```

*Transcript length data for the organism hg*

---

### Description

hg19.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.knownGene.LENGTH)
head(hg19.knownGene.LENGTH)
```

---

hg19.nscanGene.LENGTH *Transcript length data for the organism hg*

---

### Description

hg19.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.nscanGene.LENGTH)
head(hg19.nscanGene.LENGTH)
```

---

hg19.refGene.LENGTH *Transcript length data for the organism hg*

---

### Description

hg19.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.refGene.LENGTH)
head(hg19.refGene.LENGTH)
```

---

```
hg19.xenoRefGene.LENGTH
```

*Transcript length data for the organism hg*

---

### Description

hg19.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.xenoRefGene.LENGTH)
head(hg19.xenoRefGene.LENGTH)
```

---

```
loxAfr3.xenoRefGene.LENGTH
```

*Transcript length data for the organism loxAfr*

---

### Description

loxAfr3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(loxAfr3, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(loxAfr3.xenoRefGene.LENGTH)
head(loxAfr3.xenoRefGene.LENGTH)
```

---

mm7.ensGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm7.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.ensGene.LENGTH)
head(mm7.ensGene.LENGTH)
```

---

mm7.geneid.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm7.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.geneid.LENGTH)
head(mm7.geneid.LENGTH)
```

---

mm7.geneSymbol.LENGTH *Transcript length data for the organism mm*

---

### Description

mm7.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.geneSymbol.LENGTH)
head(mm7.geneSymbol.LENGTH)
```

---

mm7.genscan.LENGTH *Transcript length data for the organism mm*

---

### Description

mm7.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm7, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.genscan.LENGTH)
head(mm7.genscan.LENGTH)
```

---

mm7.knownGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm7.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.knownGene.LENGTH)
head(mm7.knownGene.LENGTH)
```

---

mm7.refGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm7.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.refGene.LENGTH)
head(mm7.refGene.LENGTH)
```

---

mm7.sgpGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm7.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.sgpGene.LENGTH)
head(mm7.sgpGene.LENGTH)
```

---

mm7.xenoRefGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm7.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.xenoRefGene.LENGTH)
head(mm7.xenoRefGene.LENGTH)
```



---

mm8.ccdsGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm8.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ccdsGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.ccdsGene.LENGTH)
head(mm8.ccdsGene.LENGTH)
```

---

mm8.ensGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm8.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.ensGene.LENGTH)
head(mm8.ensGene.LENGTH)
```

---

mm8.geneid.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm8.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.geneid.LENGTH)
head(mm8.geneid.LENGTH)
```

---

mm8.geneSymbol.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm8.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.geneSymbol.LENGTH)
head(mm8.geneSymbol.LENGTH)
```

---

mm8.genscan.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm8.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm8, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.genscan.LENGTH)
head(mm8.genscan.LENGTH)
```

---

mm8.knownGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm8.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.knownGene.LENGTH)
head(mm8.knownGene.LENGTH)
```

---

mm8.nscanGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm8.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.nscanGene.LENGTH)
head(mm8.nscanGene.LENGTH)
```

---

mm8.refGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm8.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.refGene.LENGTH)
head(mm8.refGene.LENGTH)
```

---

mm8.sgpGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm8.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.sgpGene.LENGTH)
head(mm8.sgpGene.LENGTH)
```

---

mm8.sibGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm8.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sibGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sibGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.sibGene.LENGTH)
head(mm8.sibGene.LENGTH)
```

---

`mm8.xenoRefGene.LENGTH`*Transcript length data for the organism mm*

---

**Description**

`mm8.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm8, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(mm8.xenoRefGene.LENGTH)
head(mm8.xenoRefGene.LENGTH)
```

---

`mm9.acembly.LENGTH`*Transcript length data for the organism mm*

---

**Description**

`mm9.acembly.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `acembly` table.

The data file was made by calling `downloadLengthFromUCSC(mm9, acembly)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(mm9.acembly.LENGTH)
head(mm9.acembly.LENGTH)
```

---

mm9.ccdsGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm9.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ccdsGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.ccdsGene.LENGTH)
head(mm9.ccdsGene.LENGTH)
```

---

mm9.ensGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm9.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.ensGene.LENGTH)
head(mm9.ensGene.LENGTH)
```

---

mm9.exoniphy.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm9.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(mm9, exoniphy)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.exoniphy.LENGTH)
head(mm9.exoniphy.LENGTH)
```

---

mm9.geneid.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm9.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.geneid.LENGTH)
head(mm9.geneid.LENGTH)
```



---

mm9.geneSymbol.LENGTH *Transcript length data for the organism mm*

---

### Description

mm9.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.geneSymbol.LENGTH)
head(mm9.geneSymbol.LENGTH)
```

---

mm9.genscan.LENGTH *Transcript length data for the organism mm*

---

### Description

mm9.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm9, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.genscan.LENGTH)
head(mm9.genscan.LENGTH)
```

---

mm9.knownGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm9.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.knownGene.LENGTH)
head(mm9.knownGene.LENGTH)
```

---

mm9.nscanGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm9.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.nscanGene.LENGTH)
head(mm9.nscanGene.LENGTH)
```

---

mm9.refGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm9.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.refGene.LENGTH)
head(mm9.refGene.LENGTH)
```

---

mm9.sgpGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm9.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.sgpGene.LENGTH)
head(mm9.sgpGene.LENGTH)
```

---

```
mm9.xenoRefGene.LENGTH
```

*Transcript length data for the organism mm*

---

### Description

mm9.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.xenoRefGene.LENGTH)
head(mm9.xenoRefGene.LENGTH)
```

---

```
monDom1.genscan.LENGTH
```

*Transcript length data for the organism monDom*

---

### Description

monDom1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(monDom1, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(monDom1.genscan.LENGTH)
head(monDom1.genscan.LENGTH)
```

---

`monDom4.ensGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.ensGene.LENGTH)
head(monDom4.ensGene.LENGTH)
```

---

`monDom4.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.geneSymbol.LENGTH)
head(monDom4.geneSymbol.LENGTH)
```

---

`monDom4.genscan.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.genscan.LENGTH)
head(monDom4.genscan.LENGTH)
```

---

`monDom4.nscanGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.nscanGene.LENGTH)
head(monDom4.nscanGene.LENGTH)
```

---

`monDom4.refGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.refGene.LENGTH)
head(monDom4.refGene.LENGTH)
```

---

`monDom4.xenoRefGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.xenoRefGene.LENGTH)
head(monDom4.xenoRefGene.LENGTH)
```

---

`monDom5.ensGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom5.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.ensGene.LENGTH)
head(monDom5.ensGene.LENGTH)
```

---

`monDom5.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom5.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.geneSymbol.LENGTH)
head(monDom5.geneSymbol.LENGTH)
```



---

`monDom5.genscan.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom5.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.genscan.LENGTH)
head(monDom5.genscan.LENGTH)
```

---

`monDom5.nscanGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom5.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)
```

---

```
monDom5.refGene.LENGTH
```

*Transcript length data for the organism monDom*

---

### Description

monDom5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)
```

---

```
monDom5.xenoRefGene.LENGTH
```

*Transcript length data for the organism monDom*

---

### Description

monDom5.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(monDom5.xenoRefGene.LENGTH)
head(monDom5.xenoRefGene.LENGTH)
```

---

`ornAna1.ensGene.LENGTH`*Transcript length data for the organism ornAna*

---

**Description**

`ornAna1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ornAna1.ensGene.LENGTH)
head(ornAna1.ensGene.LENGTH)
```

---

`ornAna1.geneSymbol.LENGTH`*Transcript length data for the organism ornAna*

---

**Description**

`ornAna1.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ornAna1.geneSymbol.LENGTH)
head(ornAna1.geneSymbol.LENGTH)
```

---

`ornAna1.refGene.LENGTH`*Transcript length data for the organism ornAna*

---

**Description**

`ornAna1.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ornAna1.refGene.LENGTH)
head(ornAna1.refGene.LENGTH)
```

---

`ornAna1.xenoRefGene.LENGTH`*Transcript length data for the organism ornAna*

---

**Description**

`ornAna1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ornAna1.xenoRefGene.LENGTH)
head(ornAna1.xenoRefGene.LENGTH)
```

---

`oryLat2.ensGene.LENGTH`*Transcript length data for the organism oryLat*

---

**Description**

`oryLat2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)
```

---

`oryLat2.geneSymbol.LENGTH`*Transcript length data for the organism oryLat*

---

**Description**

`oryLat2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)
```

---

`oryLat2.refGene.LENGTH`*Transcript length data for the organism oryLat*

---

**Description**

`oryLat2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)
```

---

`oryLat2.xenoRefGene.LENGTH`*Transcript length data for the organism oryLat*

---

**Description**

`oryLat2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)
```

---

`panTro1.ensGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro1.ensGene.LENGTH)
head(panTro1.ensGene.LENGTH)
```

---

`panTro1.geneid.LENGTH` *Transcript length data for the organism panTro*

---

**Description**

panTro1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, geneid)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro1.geneid.LENGTH)
head(panTro1.geneid.LENGTH)
```

---

`panTro1.genscan.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro1.genscan.LENGTH)
head(panTro1.genscan.LENGTH)
```

---

`panTro1.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro1.xenoRefGene.LENGTH)
head(panTro1.xenoRefGene.LENGTH)
```



---

`panTro2.ensGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)
```

---

`panTro2.geneSymbol.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)
```

---

`panTro2.genscan.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

`panTro2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.genscan.LENGTH)
head(panTro2.genscan.LENGTH)
```

---

`panTro2.nscanGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

`panTro2.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.nscanGene.LENGTH)
head(panTro2.nscanGene.LENGTH)
```

---

`panTro2.refGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.refGene.LENGTH)
head(panTro2.refGene.LENGTH)
```

---

`panTro2.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.xenoRefGene.LENGTH)
head(panTro2.xenoRefGene.LENGTH)
```

---

```
petMar1.xenoRefGene.LENGTH
```

*Transcript length data for the organism petMar*

---

### Description

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(petMar1, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)
```

---

```
ponAbe2.ensGene.LENGTH
```

*Transcript length data for the organism ponAbe*

---

### Description

ponAbe2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)
```

---

```
ponAbe2.geneSymbol.LENGTH
```

*Transcript length data for the organism ponAbe*

---

### Description

ponAbe2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)
```

---

```
ponAbe2.genscan.LENGTH
```

*Transcript length data for the organism ponAbe*

---

### Description

ponAbe2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)
```

---

`ponAbe2.nscanGene.LENGTH`*Transcript length data for the organism ponAbe*

---

**Description**

`ponAbe2.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ponAbe2.nscanGene.LENGTH)
head(ponAbe2.nscanGene.LENGTH)
```

---

`ponAbe2.refGene.LENGTH`*Transcript length data for the organism ponAbe*

---

**Description**

`ponAbe2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ponAbe2.refGene.LENGTH)
head(ponAbe2.refGene.LENGTH)
```

---

```
ponAbe2.xenoRefGene.LENGTH
```

*Transcript length data for the organism ponAbe*

---

### Description

ponAbe2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)
```

---

```
priPac1.xenoRefGene.LENGTH
```

*Transcript length data for the organism priPac*

---

### Description

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(priPac1, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)
```

---

```
rheMac2.ensGene.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)
```

---

```
rheMac2.geneid.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.geneid.LENGTH)
head(rheMac2.geneid.LENGTH)
```



---

```
rheMac2.geneSymbol.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)
```

---

```
rheMac2.nscanGene.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)
```

---

```
rheMac2.refGene.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)
```

---

```
rheMac2.sgpGene.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.sgpGene.LENGTH)
head(rheMac2.sgpGene.LENGTH)
```

---

`rheMac2.xenoRefGene.LENGTH`*Transcript length data for the organism rheMac*

---

**Description**

`rheMac2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)
```

---

`rn3.ensGene.LENGTH`*Transcript length data for the organism rn*

---

**Description**

`rn3.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(rn3, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.LENGTH)
```

---

rn3.geneid.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.geneid.LENGTH)
head(rn3.geneid.LENGTH)
```

---

rn3.geneSymbol.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.geneSymbol.LENGTH)
head(rn3.geneSymbol.LENGTH)
```

---

rn3.genscan.LENGTH     *Transcript length data for the organism rn*

---

### Description

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn3, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)
```

---

rn3.knownGene.LENGTH     *Transcript length data for the organism rn*

---

### Description

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

---

rn3.nscanGene.LENGTH *Transcript length data for the organism rn*

---

### Description

rn3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

---

rn3.refGene.LENGTH *Transcript length data for the organism rn*

---

### Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

---

rn3.sgpGene.LENGTH     *Transcript length data for the organism rn*

---

### Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)
```

---

rn3.xenoRefGene.LENGTH     *Transcript length data for the organism rn*

---

### Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)
```

---

rn4.ensGene.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)
```

---

rn4.geneid.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn4.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```



---

rn4.geneSymbol.LENGTH *Transcript length data for the organism rn*

---

### Description

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

---

rn4.genscan.LENGTH *Transcript length data for the organism rn*

---

### Description

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn4, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

---

rn4.knownGene.LENGTH *Transcript length data for the organism rn*

---

### Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.knownGene.LENGTH)
head(rn4.knownGene.LENGTH)
```

---

rn4.nscanGene.LENGTH *Transcript length data for the organism rn*

---

### Description

rn4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)
```

---

rn4.refGene.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)
```

---

rn4.sgpGene.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

---

`rn4.xenoRefGene.LENGTH`*Transcript length data for the organism rn*

---

**Description**

`rn4.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(rn4, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(rn4.xenoRefGene.LENGTH)
head(rn4.xenoRefGene.LENGTH)
```

---

`sacCer1.ensGene.LENGTH`*Transcript length data for the organism sacCer*

---

**Description**

`sacCer1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(sacCer1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(sacCer1.ensGene.LENGTH)
head(sacCer1.ensGene.LENGTH)
```

---

`sacCer2.ensGene.LENGTH`*Transcript length data for the organism sacCer*

---

**Description**

sacCer2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)
```

---

`strPur1.geneSymbol.LENGTH`*Transcript length data for the organism strPur*

---

**Description**

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)
```

---

`strPur1.genscan.LENGTH`*Transcript length data for the organism strPur*

---

**Description**

`strPur1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(strPur1.genscan.LENGTH)
head(strPur1.genscan.LENGTH)
```

---

`strPur1.refGene.LENGTH`*Transcript length data for the organism strPur*

---

**Description**

`strPur1.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(strPur1.refGene.LENGTH)
head(strPur1.refGene.LENGTH)
```

---

```
strPur1.xenoRefGene.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur1.xenoRefGene.LENGTH)
head(strPur1.xenoRefGene.LENGTH)
```

---

```
strPur2.geneSymbol.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur2.geneSymbol.LENGTH)
head(strPur2.geneSymbol.LENGTH)
```

---

```
strPur2.genscan.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur2.genscan.LENGTH)
head(strPur2.genscan.LENGTH)
```

---

```
strPur2.refGene.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur2.refGene.LENGTH)
head(strPur2.refGene.LENGTH)
```



---

```
strPur2.xenoRefGene.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)
```

---

supportedGeneIDs	<i>Supported Gene IDs</i>
------------------	---------------------------

---

### Description

Lists supported gene ID formats

### Usage

```
supportedGeneIDs()
```

### Details

Uses the `supportedUCSCTables` function from the `GenomicFeatures` package to obtain a list of gene ID formats available from the UCSC genome browser. The `db` column gives the gene ID formats which are provided to the `id` argument of various functions. The `track` and `subtrack` columns are the names of the UCSC track/subtrack from which information is fetched.

The `GeneID` column lists the "full name" of the gene ID format where available.

The final column, headed `AvailableGenomes` lists the genomes for which there is a local copy of the length information available for the gene ID format listed in the `geneLenDataBase` package.

### Value

A `data.frame` containing supported gene ID formats.

**Author(s)**

Matthew D. Young <myoung@wehi.edu.au>

**Examples**

```
supportedGeneIDs()
```

---

supportedGenomes	<i>Supported Genomes</i>
------------------	--------------------------

---

**Description**

Lists supported genomes

**Usage**

```
supportedGenomes()
```

**Details**

Uses the `ucscGenomes()` function from the `rtracklayer` package to obtain a list of genomes available from the UCSC genome browser. The `db` column lists genomes as they are provided to the genome argument of various functions.

The final column, headed `AvailableGeneIDs` lists the gene ID formats for which there is a local copy of the length information available for the genome listed in the `geneLenDataBase` package.

**Value**

A `data.frame` containing supported genomes.

**Author(s)**

Matthew D. Young <myoung@wehi.edu.au>

**Examples**

```
supportedGenomes()
```

---

`taeGut1.ensGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

`taeGut1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)
```

---

`taeGut1.geneSymbol.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

`taeGut1.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)
```

---

```
taeGut1.genscan.LENGTH
```

*Transcript length data for the organism taeGut*

---

### Description

taeGut1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)
```

---

```
taeGut1.nscanGene.LENGTH
```

*Transcript length data for the organism taeGut*

---

### Description

taeGut1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)
```

---

`taeGut1.refGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

taeGut1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

---

`taeGut1.xenoRefGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

taeGut1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

---

```
tetNig1.ensGene.LENGTH
```

*Transcript length data for the organism tetNig*

---

### Description

tetNig1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

---

```
tetNig1.geneid.LENGTH
```

*Transcript length data for the organism tetNig*

---

### Description

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

---

`tetNig1.genscan.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```

---

`tetNig1.nscanGene.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

tetNig1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

---

```
tetNig2.ensGene.LENGTH
```

*Transcript length data for the organism tetNig*

---

### Description

tetNig2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig2, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig2.ensGene.LENGTH)
head(tetNig2.ensGene.LENGTH)
```

---

```
unfactor
```

*Purge factors*

---

### Description

Removes all factors from a variable in a sensible way.

### Usage

```
unfactor(var)
```

### Arguments

var                   The variable from which you want the factors removed.

### Details

As factors are their own type, to remove factors we must convert each level into another type. This is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be done without inducing NAs, otherwise it is coerced using `as.character`. Currently supported types are: `/codefactor`, `/codedata.frame` and `/codelist`.



**Value**

The variable with all factors converted to characters or numbers (see details).

**Author(s)**

Matthew D. Young <myoung@wehi.edu.au>

**Examples**

```
#A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep='.')
x
unfactor(x)

#A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"), score <- factor(c(9, 7, 8, 9)), stringsAsFactors=TRUE)
x$player
x$score
y <- unfactor(x)
y$player
y$score
```

---

xenTro1.genscan.LENGTH

*Transcript length data for the organism xenTro*

---

**Description**

xenTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(xenTro1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**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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