

# Package ‘geneLenDataBase’

September 4, 2025

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

**Version** 1.44.0

**Date** 2024-06-08

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

**Depends** R (>= 2.11.0)

**Imports** utils, rtracklayer, GenomicFeatures, txdbmaker

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

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

**License** LGPL (>= 2)

**biocViews** ExperimentData, Genome

**RoxygenNote** 7.3.1

**Encoding** UTF-8

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

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|                                                       |
|-------------------------------------------------------|
| anoCar1.ensGene.LENGTH                                |
| <i>Transcript length data for the organism anoCar</i> |

---

**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                                |
| <i>Transcript length data for the organism anoCar</i> |

---

**Description**

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

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

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

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

---

```
anoCar1.xenoRefGene.LENGTH
```

*Transcript length data for the organism anoCar*

---

**Description**

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

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

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

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

---

```
anoGam1.ensGene.LENGTH
```

*Transcript length data for the organism anoGam*

---

**Description**

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

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

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

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

`apiMel1.genscan.LENGTH`*Transcript length data for the organism apiMel*

---

**Description**

`apiMel1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(apiMel1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

`apiMel2.ensGene.LENGTH`*Transcript length data for the organism apiMel*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

`aplCal1.xenoRefGene.LENGTH`*Transcript length data for the organism aplCal*

---

**Description**

`aplCal1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(aplCal1, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**[downloadLengthFromUCSC](#)**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 | <i>Transcript length data for the organism ce</i> |
|-------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism ce</i> |
|-----------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism ce</i> |
|--------------------|---------------------------------------------------|

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

|                       |                                                   |
|-----------------------|---------------------------------------------------|
| ce4.geneSymbol.LENGTH | <i>Transcript length data for the organism ce</i> |
|-----------------------|---------------------------------------------------|

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

|                    |                                                   |
|--------------------|---------------------------------------------------|
| ce4.refGene.LENGTH | <i>Transcript length data for the organism ce</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism ce</i> |
|------------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism ce</i> |
|--------------------|---------------------------------------------------|

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

|                       |                                                   |
|-----------------------|---------------------------------------------------|
| ce6.geneSymbol.LENGTH | <i>Transcript length data for the organism ce</i> |
|-----------------------|---------------------------------------------------|

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

|                    |                                                   |
|--------------------|---------------------------------------------------|
| ce6.refGene.LENGTH | <i>Transcript length data for the organism ce</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism ce</i> |
|------------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism dm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism dm</i> |
|-------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism dm</i> |
|--------------------|---------------------------------------------------|

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

|                        |                                        |
|------------------------|----------------------------------------|
| downloadLengthFromUCSC | <i>Download Transcript Length Data</i> |
|------------------------|----------------------------------------|

---

### Description

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

### Usage

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

### Arguments

|        |                                                                                                                                         |
|--------|-----------------------------------------------------------------------------------------------------------------------------------------|
| genome | A string identifying the genome that genes refer to. For a list of supported organisms see <a href="#">supportedGenomes</a> .           |
| id     | A string identifying the gene identifier used by genes. For a list of supported gene identifiers see <a href="#">supportedGeneIDs</a> . |

**Details**

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

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

**Value**

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

**Note**

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

**Author(s)**

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**See Also**

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

**Examples**

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

## End(Not run)
```

---

|                    |                                                   |
|--------------------|---------------------------------------------------|
| dp2.genscan.LENGTH | <i>Transcript length data for the organism dp</i> |
|--------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism dp</i> |
|--------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism dp</i> |
|------------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism fr</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism fr</i> |
|--------------------|---------------------------------------------------|

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

geneLenDatabase-pkg     *geneLenDatabase:*

---

## Description

Lengths of mRNA transcripts for a number of genomes

## Details

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

## Author(s)

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## See Also

Useful links:

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

---

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

---

## Description

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

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

## See Also

[downloadLengthFromUCSC](#)

## Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

|                    |                                                   |
|--------------------|---------------------------------------------------|
| hg16.geneid.LENGTH | <i>Transcript length data for the organism hg</i> |
|--------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism hg</i> |
|------------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism hg</i> |
|---------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism hg</i> |
|---------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism hg</i> |
|---------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism hg</i> |
|---------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism hg</i> |
|---------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism hg</i> |
|---------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism hg</i> |
|---------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism hg</i> |
|-------------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism hg</i> |
|---------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism hg</i> |
|-------------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism mm</i> |
|-------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|-----------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|----------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|-------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|------------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|---------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|---------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|-------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism mm</i> |
|-----------------------|---------------------------------------------------|

---

**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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|----------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism mm</i> |
|------------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|-------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|-------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|-----------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|----------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|--------------------|---------------------------------------------------|

---

### 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 | <i>Transcript length data for the organism rn</i> |
|------------------------|---------------------------------------------------|

---

### 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](mailto:myoung@wehi.edu.au)>

**Examples**

```
supportedGenomes()
```

---

```
taeGut1.ensGene.LENGTH
```

*Transcript length data for the organism taeGut*

---

**Description**

`taeGut1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)
```

---

`taeGut1.geneSymbol.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

`taeGut1.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, geneSymbol)` on the date on which the package was last updated.

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

```
data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)
```

---

`taeGut1.genscan.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

`taeGut1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, genscan)` on the date on which the package was last updated.

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

```
data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)
```

---

`taeGut1.nscanGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

taeGut1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, nscanGene)` on the date on which the package was last updated.

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

```
data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)
```

---

`taeGut1.refGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

taeGut1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, refGene)` on the date on which the package was last updated.

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

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

---

`taeGut1.xenoRefGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

taeGut1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, xenoRefGene)` on the date on which the package was last updated.

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

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

---

`tetNig1.ensGene.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

tetNig1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, ensGene)` on the date on which the package was last updated.

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

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

---

tetNig1.geneid.LENGTH *Transcript length data for the organism tetNig*

---

### Description

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

---

tetNig1.genscan.LENGTH  
*Transcript length data for the organism tetNig*

---

### Description

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```

---

`tetNig1.nscanGene.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

tetNig1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, nscanGene)` on the date on which the package was last updated.

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

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

---

`tetNig2.ensGene.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

tetNig2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig2, ensGene)` on the date on which the package was last updated.

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

```
data(tetNig2.ensGene.LENGTH)
head(tetNig2.ensGene.LENGTH)
```

---

`unfactor`*Purge factors*

---

**Description**

Removes all factors from a variable in a sensible way.

**Usage**

```
unfactor(var)
```

**Arguments**

`var`                      The variable from which you want the factors removed.

**Details**

As factors are their own type, to remove factors we must convert each level into another type. This is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be done without inducing NAs, otherwise it is coerced using `as.character`. Currently supported types are: `factor`, `data.frame` and `list`.

**Value**

The variable with all factors converted to characters or numbers (see details).

**Author(s)**

Matthew D. Young <[myoung@wehi.edu.au](mailto: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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