# Package 'geneLenDataBase'

May 1, 2025

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Title Lengths of mRNA transcripts for a number of genomes
<b>Version</b> 1.45.0
<b>Date</b> 2024-06-08
<b>Description</b> 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.
<b>Depends</b> R (>= 2.11.0)
Imports utils, rtracklayer, GenomicFeatures, txdbmaker
<pre>URL https://github.com/federicomarini/geneLenDataBase</pre>
BugReports https://github.com/federicomarini/geneLenDataBase/issues
License LGPL (>= 2)
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Contents
anoCar1.ensGene.LENGTH

anoGam1.ensGene.LENGTH	10
anoGam1.geneid.LENGTH	10
anoGam1.genscan.LENGTH	11
apiMel1.genscan.LENGTH	11
apiMel2.ensGene.LENGTH	12
apiMel2.geneid.LENGTH	12
apiMel2.genscan.LENGTH	13
aplCal1.xenoRefGene.LENGTH	13
bosTau2.geneid.LENGTH	14
bosTau2.geneSymbol.LENGTH	14
bosTau2.genscan.LENGTH	15
bosTau2.refGene.LENGTH	15
bosTau2.sgpGene.LENGTH	16
bosTau3.ensGene.LENGTH	16
bosTau3.geneid.LENGTH	17
bosTau3.geneSymbol.LENGTH	17
bosTau3.genscan.LENGTH	18
bosTau3.refGene.LENGTH	18
bosTau3.sgpGene.LENGTH	19
bosTau4.ensGene.LENGTH	19
bosTau4.geneSymbol.LENGTH	20
bosTau4.genscan.LENGTH	20
bosTau4.nscanGene.LENGTH	21
bosTau4.refGene.LENGTH	21
braFlo1.xenoRefGene.LENGTH	22
caeJap1.xenoRefGene.LENGTH	
caePb1.xenoRefGene.LENGTH	
caePb2.xenoRefGene.LENGTH	23
caeRem2.xenoRefGene.LENGTH	24
caeRem3.xenoRefGene.LENGTH	24
calJac1.genscan.LENGTH	25
calJac1.nscanGene.LENGTH	
calJac1.xenoRefGene.LENGTH	
canFam1.ensGene.LENGTH	
canFam1.geneSymbol.LENGTH	
canFam1.genscan.LENGTH	
canFam1.nscanGene.LENGTH	28
canFam1.refGene.LENGTH	28
canFam1.xenoRefGene.LENGTH	29
canFam2.ensGene.LENGTH	29
canFam2.geneSymbol.LENGTH	30
canFam2.genscan.LENGTH	30
canFam2.nscanGene.LENGTH	31
canFam2.refGene.LENGTH	31
canFam2.xenoRefGene.LENGTH	32
cavPor3.ensGene.LENGTH	32
cavPor3.genscan.LENGTH	33
cavPor3.nscanGene.LENGTH	33
cavPor3.xenoRefGene.LENGTH	34
cb1.xenoRefGene.LENGTH	34
cb3.xenoRefGene.LENGTH	35
ce2.geneid.LENGTH	

ce2.geneSymbol.LENGTH
ce2.refGene.LENGTH
ce4.geneSymbol.LENGTH
ce4.refGene.LENGTH
ce4.xenoRefGene.LENGTH
ce6.ensGene.LENGTH
ce6.geneSymbol.LENGTH
ce6.refGene.LENGTH
ce6.xenoRefGene.LENGTH
cil.geneSymbol.LENGTH
cil.refGene.LENGTH
ci1.xenoRefGene.LENGTH
ci2.ensGene.LENGTH
ci2.geneSymbol.LENGTH
ci2.refGene.LENGTH
ci2.xenoRefGene.LENGTH
danRer3.ensGene.LENGTH
danRer3.geneSymbol.LENGTH
danRer3.refGene.LENGTH
danRer4.ensGene.LENGTH
danRer4.geneSymbol.LENGTH
danRer4.genscan.LENGTH
danRer4.nscanGene.LENGTH
danRer4.refGene.LENGTH
danRer5.ensGene.LENGTH
danRer5.geneSymbol.LENGTH
danRer5.refGene.LENGTH
danRer5.vegaGene.LENGTH
danRer5.vegaPseudoGene.LENGTH
danRer6.ensGene.LENGTH
danRer6.geneSymbol.LENGTH
danRer6.refGene.LENGTH
danRer6.xenoRefGene.LENGTH
dm1.geneSymbol.LENGTH
dm1.genscan.LENGTH
dm1.refGene.LENGTH
dm2.geneid.LENGTH
dm2.geneSymbol.LENGTH
dm2.gencay.LENGTH
dm2.nscanGene.LENGTH
dm2.refGene.LENGTH
dm3.geneSymbol.LENGTH
dm3.nscanPasaGene.LENGTH
dm3.refGene.LENGTH
dp2.genscan.LENGTH
dp2.xenoRefGene.LENGTH
dp3.geneid.LENGTH
dp3.genscan.LENGTH
dp3.xenoRefGene.LENGTH
droAnal.geneid.LENGTH
droAna1.genscan.LENGTH

	52
$\epsilon$	53
	53
	54
	54
	55
	55
	66
	66
J	57
<i>j C</i>	57
J	58
C	58
	59
	59
	70
$\epsilon$	70
	71
	71
$\boldsymbol{\varepsilon}$	72
	72
	73
droVir2.genscan.LENGTH	73
droVir2.xenoRefGene.LENGTH	14
$\mathcal{C}$	74
	75
	75
	76
	76
	77
	77
1	78
1	78
	79
1	79
	30
equCab2.nscanGene.LENGTH	
1	31
1	31
	32
$\epsilon$	32
<i>5</i> ,	33
C	33
	34
	34
Ci	35
	35
	36
6	36
	37
	37
galGal2.geneid.LENGTH	38

	88
galGal2.genscan.LENGTH	89
galGal2.refGene.LENGTH	89
	90
	90
	91
galGal3.genscan.LENGTH	91
	92
galGal3.refGene.LENGTH	92
	93
gasAcu1.ensGene.LENGTH	93
gasAcu1.nscanGene.LENGTH	94
	94
hg16.acembly.LENGTH	95
	95
	96
hg16.geneid.LENGTH	96
hg16.geneSymbol.LENGTH	97
	97
	98
hg16.refGene.LENGTH	98
hg16.sgpGene.LENGTH	99
hg17.acembly.LENGTH	99
hg17.acescan.LENGTH	00
hg17.ccdsGene.LENGTH	
hg17.ensGene.LENGTH	
hg17.exoniphy.LENGTH	
hg17.geneid.LENGTH	02
hg17.geneSymbol.LENGTH	.02
hg17.genscan.LENGTH	.03
hg17.knownGene.LENGTH	
hg17.refGene.LENGTH	04
hg17.sgpGene.LENGTH	04
hg17.vegaGene.LENGTH	05
hg17.vegaPseudoGene.LENGTH	.05
hg17.xenoRefGene.LENGTH	06
hg18.acembly.LENGTH	06
hg18.acescan.LENGTH	07
hg18.ccdsGene.LENGTH	07
hg18.ensGene.LENGTH	.08
hg18.exoniphy.LENGTH	.08
hg18.geneid.LENGTH	
hg18.geneSymbol.LENGTH	.09
hg18.genscan.LENGTH	10
hg18.knownGene.LENGTH	10
hg18.knownGeneOld3.LENGTH	
hg18.refGene.LENGTH	
hg18.sgpGene.LENGTH	
hg18.sibGene.LENGTH	12
hg18.xenoRefGene.LENGTH	
hg19.ccdsGene.LENGTH	
hg19.ensGene.LENGTH	

hg19.exoniphy.LENGTH
hg19.geneSymbol.LENGTH
hg19.knownGene.LENGTH
hg19.nscanGene.LENGTH
hg19.refGene.LENGTH
hg19.xenoRefGene.LENGTH
loxAfr3.xenoRefGene.LENGTH
mm7.ensGene.LENGTH
mm7.geneid.LENGTH
mm7.geneSymbol.LENGTH
mm7.genscan.LENGTH
mm7.knownGene.LENGTH
mm7.refGene.LENGTH
mm7.sgpGene.LENGTH
mm7.xenoRefGene.LENGTH
mm8.ccdsGene.LENGTH
mm8.ensGene.LENGTH
mm8.geneid.LENGTH
mm8.geneSymbol.LENGTH
mm8.genscan.LENGTH
mm8.knownGene.LENGTH
mm8.nscanGene.LENGTH
mm8.refGene.LENGTH
mm8.sgpGene.LENGTH
mm8.sibGene.LENGTH
mm8.xenoRefGene.LENGTH
mm9.acembly.LENGTH
mm9.ccdsGene.LENGTH
mm9.ensGene.LENGTH
mm9.exoniphy.LENGTH
mm9.geneid.LENGTH
mm9.geneSymbol.LENGTH
mm9.genscan.LENGTH
mm9.knownGene.LENGTH
mm9.nscanGene.LENGTH
mm9.refGene.LENGTH
mm9.sgpGene.LENGTH
mm9.xenoRefGene.LENGTH
monDom1.genscan.LENGTH
monDom4.ensGene.LENGTH
monDom4.geneSymbol.LENGTH
monDom4.genscan.LENGTH
monDom4.nscanGene.LENGTH
monDom4.refGene.LENGTH
monDom4.xenoRefGene.LENGTH
monDom5.ensGene.LENGTH
monDom5.geneSymbol.LENGTH
monDom5.genscan.LENGTH
monDom5.nscanGene.LENGTH
monDom5.refGene.LENGTH
monDom5.xenoRefGene.LENGTH
orn Ana 1 ens Gene I ENGTH

ornAna1.geneSymbol.LENGTH .	 	 	 	 	140
ornAna1.refGene.LENGTH					
ornAna1.xenoRefGene.LENGTH					
oryLat2.ensGene.LENGTH					
oryLat2.geneSymbol.LENGTH					
oryLat2.refGene.LENGTH					
oryLat2.xenoRefGene.LENGTH .					
panTro1.ensGene.LENGTH					
panTro1.geneid.LENGTH					
panTro1.genscan.LENGTH					
panTro1.xenoRefGene.LENGTH.					
panTro2.ensGene.LENGTH					
panTro2.geneSymbol.LENGTH .					
panTro2.genscan.LENGTH					
panTro2.nscanGene.LENGTH					
panTro2.refGene.LENGTH					
panTro2.xenoRefGene.LENGTH.					
petMar1.xenoRefGene.LENGTH.					
ponAbe2.ensGene.LENGTH					
ponAbe2.geneSymbol.LENGTH .					
ponAbe2.genscan.LENGTH					
ponAbe2.nscanGene.LENGTH					
ponAbe2.refGene.LENGTH					
ponAbe2.xenoRefGene.LENGTH					
priPac1.xenoRefGene.LENGTH .					
rheMac2.ensGene.LENGTH					
rheMac2.geneid.LENGTH	 	 	 	 	153
rheMac2.geneSymbol.LENGTH .	 	 	 	 	154
rheMac2.nscanGene.LENGTH	 	 	 	 	154
rheMac2.refGene.LENGTH	 	 	 	 	155
rheMac2.sgpGene.LENGTH	 	 	 	 	155
rheMac2.xenoRefGene.LENGTH					
rn3.ensGene.LENGTH	 	 	 	 	156
rn3.geneid.LENGTH	 	 	 	 	157
rn3.geneSymbol.LENGTH					
rn3.genscan.LENGTH					
rn3.knownGene.LENGTH	 	 	 	 	158
rn3.nscanGene.LENGTH	 	 	 	 	159
rn3.refGene.LENGTH	 	 	 	 	159
rn3.sgpGene.LENGTH					
rn3.xenoRefGene.LENGTH					
rn4.ensGene.LENGTH	 	 	 	 	161
rn4.geneid.LENGTH	 	 	 	 	161
rn4.geneSymbol.LENGTH	 	 	 	 	162
rn4.genscan.LENGTH					
rn4.knownGene.LENGTH					
rn4.nscanGene.LENGTH					
rn4.refGene.LENGTH	 	 	 	 	164
rn4.sgpGene.LENGTH					
rn4.xenoRefGene.LENGTH					
sacCer1.ensGene.LENGTH	 	 	 	 	165
sacCer2 ensGene LENGTH					166

181

strPur1.geneSymbol.LENGTH	6
strPur1.genscan.LENGTH	
strPur1.refGene.LENGTH	
strPur1.xenoRefGene.LENGTH	8
strPur2.geneSymbol.LENGTH	8
strPur2.genscan.LENGTH	
strPur2.refGene.LENGTH	
strPur2.xenoRefGene.LENGTH	0
supportedGeneIDs	0
supportedGenomes	1
taeGut1.ensGene.LENGTH	1
taeGut1.geneSymbol.LENGTH	2
taeGut1.genscan.LENGTH	2
taeGut1.nscanGene.LENGTH	
taeGut1.refGene.LENGTH	3
taeGut1.xenoRefGene.LENGTH	4
tetNig1.ensGene.LENGTH	4
tetNig1.geneid.LENGTH	5
tetNig1.genscan.LENGTH	5
tetNig1.nscanGene.LENGTH	6
tetNig2.ensGene.LENGTH	
unfactor	7
xenTro1.genscan.LENGTH	8
xenTro2.ensGene.LENGTH	8
xenTro2.geneSymbol.LENGTH	
xenTro2.genscan.LENGTH	9
xenTro2.refGene.LENGTH	0

anoCar1.ensGene.LENGTH

Transcript length data for the organism anoCar

# Description

Index

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

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

anoCar1.genscan.LENGTH

Transcript length data for the organism anoCar

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

#### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

# **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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

```
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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/hgTables) using the xenoRefGene table.

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

#### See Also

downloadLengthFromUCSC

## **Examples**

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

ce2.geneid.LENGTH

Transcript length data for the organism ce

# Description

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

 ${\tt downloadLengthFromUCSC}$ 

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

36 ce2.refGene.LENGTH

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

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

ce2.refGene.LENGTH

Transcript length data for the organism ce

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

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

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

ce4.refGene.LENGTH

Transcript length data for the organism ce

# Description

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

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

### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

38 ce6.ensGene.LENGTH

```
ce4.xenoRefGene.LENGTH
```

Transcript length data for the organism ce

## **Description**

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

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

### See Also

downloadLengthFromUCSC

## **Examples**

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

ce6.ensGene.LENGTH

Transcript length data for the organism ce

# Description

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

 ${\tt downloadLengthFromUCSC}$ 

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

ce6.geneSymbol.LENGTH Transcript length data for the organism ce

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

ce6.refGene.LENGTH

Transcript length data for the organism ce

# Description

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

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

### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

ce6.xenoRefGene.LENGTH

Transcript length data for the organism ce

# Description

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

 ${\tt downloadLengthFromUCSC}$ 

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

ci1.refGene.LENGTH 41

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

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **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

 ${\tt downloadLengthFromUCSC}$ 

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

ci2.refGene.LENGTH 43

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

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

dm1.refGene.LENGTH

Transcript length data for the organism dm

# Description

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

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

### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

dm2.geneid.LENGTH

Transcript length data for the organism dm

## **Description**

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

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

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

dm3.refGene.LENGTH

Transcript length data for the organism dm

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

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

downloadLengthFromUCSC

Download Transcript Length Data

## **Description**

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

## Usage

downloadLengthFromUCSC(genome, id)

### **Arguments**

genome A string identifying the genome that genes refer to. For a list of supported

organisms see supportedGenomes.

id A string identifying the gene identifier used by genes. For a list of supported

gene identifierst see supportedGeneIDs.

#### **Details**

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

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

### Value

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

#### Note

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

### Author(s)

Matthew D. Young <myoung@wehi.edu.au>

### See Also

supportedGenomes, supportedGeneIDs

### **Examples**

```
## Not run:
    flat_length <- downloadLengthFromUCSC('hg19', 'ensGene')
## End(Not run)</pre>
```

dp2.genscan.LENGTH

Transcript length data for the organism dp

### **Description**

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

dp3.genscan.LENGTH

Transcript length data for the organism dp

# Description

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

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

### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

```
dp3.xenoRefGene.LENGTH
```

Transcript length data for the organism dp

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

dro Yak 1. 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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

# **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

 ${\tt downloadLengthFromUCSC}$ 

### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

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

fr1.genscan.LENGTH

Transcript length data for the organism fr

# Description

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

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

### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

fr2.ensGene.LENGTH 87

fr2.ensGene.LENGTH

Transcript length data for the organism fr

#### **Description**

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

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

```
galGal2.sgpGene.LENGTH
```

# **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

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

```
galGal3.geneSymbol.LENGTH
```

### **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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

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

```
galGal3.nscanGene.LENGTH
```

# **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

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

```
galGal3.xenoRefGene.LENGTH
```

#### **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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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/cgibin/hgTables) using the nscanGene table.

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

#### See Also

downloadLengthFromUCSC

# **Examples**

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

geneLenDatabase-pkg

geneLenDatabase:

#### **Description**

Lengths of mRNA transcripts for a number of genomes

### **Details**

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

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# See Also

Useful links:

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

hg16.acembly.LENGTH

Transcript length data for the organism hg

# **Description**

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

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

# See Also

downloadLengthFromUCSC

# **Examples**

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

hg16.ensGene.LENGTH

Transcript length data for the organism hg

# Description

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

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

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

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

hg16.geneid.LENGTH

Transcript length data for the organism hg

# Description

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

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

### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

hg16.geneSymbol.LENGTH

Transcript length data for the organism hg

# **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

# **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/hgTables) using the knownGene table.

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

#### See Also

downloadLengthFromUCSC

# **Examples**

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

hg16.refGene.LENGTH

Transcript length data for the organism hg

# Description

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

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

### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

hg16.sgpGene.LENGTH

Transcript length data for the organism hg

# **Description**

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

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

# See Also

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

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

hg17.acembly.LENGTH

Transcript length data for the organism hg

# Description

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

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

### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

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

# **Description**

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

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

# See Also

 ${\tt downloadLengthFromUCSC}$ 

# **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

 ${\tt downloadLengthFromUCSC}$ 

### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

# **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

# **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

# **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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

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

```
hg17.xenoRefGene.LENGTH
```

# **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/cgibin/hgTables) using the xenoRefGene table.

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

#### See Also

downloadLengthFromUCSC

# **Examples**

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

hg18.acembly.LENGTH

Transcript length data for the organism hg

# Description

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

 ${\tt downloadLengthFromUCSC}$ 

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

hg18.acescan.LENGTH

Transcript length data for the organism hg

# **Description**

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

hg18.sibGene.LENGTH

Transcript length data for the organism hg

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

hg18.xenoRefGene.LENGTH

Transcript length data for the organism hg

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

hg19.refGene.LENGTH

Transcript length data for the organism hg

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

hg19.xenoRefGene.LENGTH

Transcript length data for the organism hg

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

#### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

mm7.geneid.LENGTH

Transcript length data for the organism mm

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

mm7.geneSymbol.LENGTH Transcript length data for the organism mm

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

mm7.genscan.LENGTH

Transcript length data for the organism mm

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

120 mm7.refGene.LENGTH

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

mm7.refGene.LENGTH

Transcript length data for the organism mm

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

mm7.sgpGene.LENGTH

Transcript length data for the organism mm

### **Description**

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

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

#### See Also

downloadLengthFromUCSC

## **Examples**

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

mm7.xenoRefGene.LENGTH

Transcript length data for the organism mm

# Description

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

 ${\tt downloadLengthFromUCSC}$ 

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

122 mm8.ensGene.LENGTH

mm8.ccdsGene.LENGTH

Transcript length data for the organism mm

## **Description**

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

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

## See Also

downloadLengthFromUCSC

## **Examples**

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

mm8.ensGene.LENGTH

Transcript length data for the organism mm

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

mm8.geneid.LENGTH

mm8.geneid.LENGTH

Transcript length data for the organism mm

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

## **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

mm8.refGene.LENGTH

Transcript length data for the organism mm

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

126 mm8.sibGene.LENGTH

mm8.sgpGene.LENGTH

Transcript length data for the organism mm

# Description

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

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

## See Also

downloadLengthFromUCSC

## **Examples**

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

mm8.sibGene.LENGTH

Transcript length data for the organism mm

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

mm8.xenoRefGene.LENGTH

Transcript length data for the organism mm

## **Description**

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

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

#### See Also

downloadLengthFromUCSC

## **Examples**

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

mm9.acembly.LENGTH

Transcript length data for the organism mm

# Description

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

 ${\tt downloadLengthFromUCSC}$ 

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

128 mm9.ensGene.LENGTH

mm9.ccdsGene.LENGTH

Transcript length data for the organism mm

# Description

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

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

## See Also

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

mm9.ensGene.LENGTH

Transcript length data for the organism mm

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

mm9.exoniphy.LENGTH

Transcript length data for the organism mm

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

mm9.geneid.LENGTH

Transcript length data for the organism mm

# Description

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

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

## See Also

 ${\tt downloadLengthFromUCSC}$ 

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

mm9.geneSymbol.LENGTH Transcript length data for the organism mm

## **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

mm9.genscan.LENGTH

Transcript length data for the organism mm

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

## **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/cgibin/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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

## **Examples**

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

mm9.sgpGene.LENGTH

Transcript length data for the organism mm

# Description

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

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

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

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

mm9.xenoRefGene.LENGTH

Transcript length data for the organism mm

#### **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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)
```

 ${\tt monDom5.nscanGene.LENGTH}$ 

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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

#### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

# **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

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

156 rn3.ensGene.LENGTH

rheMac2.xenoRefGene.LENGTH

Transcript length data for the organism rheMac

# **Description**

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

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

### See Also

downloadLengthFromUCSC

# **Examples**

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

rn3.ensGene.LENGTH

Transcript length data for the organism rn

# Description

rn3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.LENGTH)
```

rn3.geneid.LENGTH 157

rn3.geneid.LENGTH

Transcript length data for the organism rn

# **Description**

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rn3, geneid) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

# **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

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

rn3.nscanGene.LENGTH 159

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

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

rn3.refGene.LENGTH

Transcript length data for the organism rn

# Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, refGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

rn3.sgpGene.LENGTH

Transcript length data for the organism rn

# Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, sgpGene) on the date on which the package was last updated.

#### See Also

 ${\tt downloadLengthFromUCSC}$ 

# **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)
```

rn4.ensGene.LENGTH 161

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

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)
```

rn4.geneid.LENGTH

Transcript length data for the organism rn

# Description

rn4.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rn4, geneid) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```

rn4.geneSymbol.LENGTH Transcript length data for the organism rn

# **Description**

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

rn4.genscan.LENGTH

Transcript length data for the organism rn

# Description

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(rn4, genscan) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

rn4.knownGene.LENGTH

163

rn4.knownGene.LENGTH Transcript length data for the organism rn

# **Description**

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

```
data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)
```

rn4.sgpGene.LENGTH

Transcript length data for the organism rn

# Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, sgpGene) on the date on which the package was last updated.

### See Also

 ${\tt downloadLengthFromUCSC}$ 

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

rn4.xenoRefGene.LENGTH

Transcript length data for the organism rn

### **Description**

rn4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **Examples**

```
data(strPur1.xenoRefGene.LENGTH)
head(strPur1.xenoRefGene.LENGTH)
```

 ${\tt strPur2.geneSymbol.LENGTH}$ 

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

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

170 supportedGeneIDs

```
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

 ${\tt downloadLengthFromUCSC}$ 

# **Examples**

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

supportedGeneIDs

Supported Gene IDs

### **Description**

Lists supported gene ID formats

#### **Usage**

supportedGeneIDs()

# **Details**

Uses the supportedUCSCtables function from the GenomicFeatures package to obtain a list of gene ID formats available from the UCSC genome browser. The db column gives the gene ID formats which are provided to the id arguement of various functions. The track and subtrack columns are the names of the UCSC track/subtrack from which information is fetched.

The GeneID column lists the "full name" of the gene ID format where available.

The final column, headed AvailableGenomes lists the genomes for which there is a local copy of the length information avaible for the gene ID format listed in the geneLenDataBase package.

### Value

A data.frame containing supported gene ID formats.

### Author(s)

Matthew D. Young <myoung@wehi.edu.au>

supportedGenomes 171

#### **Examples**

supportedGeneIDs()

supportedGenomes

Supported Genomes

# **Description**

Lists supported genomes

### Usage

supportedGenomes()

#### **Details**

Uses the ucscGenomes() function from the rtracklayer package to obtain a list of genomes available from the UCSC genome browser. The db column lists genomes as they are provided to the genome arguement of various functions.

The final column, headed AvailableGeneIDs lists the gene ID formats for which there is a local copy of the length information avaible for the genome listed in the geneLenDataBase package.

### Value

A data.frame containing supported genomes.

### Author(s)

Matthew D. Young <myoung@wehi.edu.au>

#### **Examples**

supportedGenomes()

taeGut1.ensGene.LENGTH

Transcript length data for the organism taeGut

### **Description**

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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

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

unfactor 177

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>

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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

 ${\tt downloadLengthFromUCSC}$ 

### **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/cgibin/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

 ${\tt downloadLengthFromUCSC}$ 

```
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/cgibin/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)

# Index

datasets	canFam2.ensGene.LENGTH, 29
anoCar1.ensGene.LENGTH, 8	canFam2.geneSymbol.LENGTH, 30
anoCar1.genscan.LENGTH, 9	canFam2.genscan.LENGTH, 30
anoCar1.xenoRefGene.LENGTH, 9	canFam2.nscanGene.LENGTH, 31
anoGam1.ensGene.LENGTH, 10	canFam2.refGene.LENGTH, 31
anoGam1.geneid.LENGTH, 10	canFam2.xenoRefGene.LENGTH, 32
anoGam1.genscan.LENGTH, 11	cavPor3.ensGene.LENGTH, 32
apiMel1.genscan.LENGTH, 11	cavPor3.genscan.LENGTH, 33
apiMel2.ensGene.LENGTH, 12	cavPor3.nscanGene.LENGTH, 33
apiMel2.geneid.LENGTH, 12	cavPor3.xenoRefGene.LENGTH, 34
apiMel2.genscan.LENGTH, 13	cb1.xenoRefGene.LENGTH, 34
aplCall.xenoRefGene.LENGTH, 13	cb3.xenoRefGene.LENGTH, 35
bosTau2.geneid.LENGTH, 14	ce2.geneid.LENGTH, 35
bosTau2.geneSymbol.LENGTH, 14	ce2.geneSymbol.LENGTH, 36
bosTau2.genscan.LENGTH, 15	ce2.refGene.LENGTH, 36
bosTau2.refGene.LENGTH, 15	ce4.geneSymbol.LENGTH, 37
bosTau2.sgpGene.LENGTH, 16	ce4.refGene.LENGTH, 37
bosTau3.ensGene.LENGTH, 16	ce4.xenoRefGene.LENGTH, 38
bosTau3.geneid.LENGTH, 17	ce6.ensGene.LENGTH, 38
bosTau3.geneSymbol.LENGTH, 17	ce6.geneSymbol.LENGTH, 39
bosTau3.genscan.LENGTH, 18	ce6.refGene.LENGTH, 39
bosTau3.refGene.LENGTH, 18	ce6.xenoRefGene.LENGTH, 40
bosTau3.sgpGene.LENGTH, 19	ci1.geneSymbol.LENGTH, 40
bosTau4.ensGene.LENGTH, 19	ci1.refGene.LENGTH,41
bosTau4.geneSymbol.LENGTH, 20	ci1.xenoRefGene.LENGTH,41
bosTau4.genscan.LENGTH, 20	ci2.ensGene.LENGTH,42
bosTau4.nscanGene.LENGTH, 21	ci2.geneSymbol.LENGTH,42
bosTau4.refGene.LENGTH, 21	ci2.refGene.LENGTH,43
braFlo1.xenoRefGene.LENGTH, 22	ci2.xenoRefGene.LENGTH, 43
caeJap1.xenoRefGene.LENGTH, 22	danRer3.ensGene.LENGTH, 44
caePb1.xenoRefGene.LENGTH, 23	danRer3.geneSymbol.LENGTH,44
caePb2.xenoRefGene.LENGTH, 23	danRer3.refGene.LENGTH,45
caeRem2.xenoRefGene.LENGTH, 24	danRer4.ensGene.LENGTH, 45
caeRem3.xenoRefGene.LENGTH, 24	danRer4.geneSymbol.LENGTH, $46$
calJac1.genscan.LENGTH, 25	danRer4.genscan.LENGTH,46
calJac1.nscanGene.LENGTH, 25	danRer4.nscanGene.LENGTH, 47
calJac1.xenoRefGene.LENGTH, 26	danRer4.refGene.LENGTH,47
canFam1.ensGene.LENGTH, 26	danRer5.ensGene.LENGTH, 48
canFam1.geneSymbol.LENGTH, 27	${\sf danRer5.geneSymbol.LENGTH,48}$
canFam1.genscan.LENGTH, 27	danRer5.refGene.LENGTH, 49
canFam1.nscanGene.LENGTH, 28	danRer5.vegaGene.LENGTH, 49
canFam1.refGene.LENGTH, $28$	danRer5.vegaPseudoGene.LENGTH, 50
canFam1.xenoRefGene.LENGTH, 29	danRer6.ensGene.LENGTH, 50

danRer6.geneSymbol.LENGTH, 51	equCab1.nscanGene.LENGTH, 78
danRer6.refGene.LENGTH, 51	equCab1.refGene.LENGTH, 78
danRer6.xenoRefGene.LENGTH, 52	equCab1.sgpGene.LENGTH, 79
dm1.geneSymbol.LENGTH, 52	equCab2.ensGene.LENGTH, 79
dm1.genscan.LENGTH, 53	equCab2.geneSymbol.LENGTH, 80
dm1.refGene.LENGTH, 53	equCab2.nscanGene.LENGTH, $80$
dm2.geneid.LENGTH, 54	equCab2.refGene.LENGTH, 81
dm2.geneSymbol.LENGTH, 54	equCab2.xenoRefGene.LENGTH, 81
dm2.genscan.LENGTH, 55	felCat3.ensGene.LENGTH, 82
dm2.nscanGene.LENGTH, 55	felCat3.geneid.LENGTH, 82
dm2.refGene.LENGTH, 56	felCat3.geneSymbol.LENGTH, 83
dm3.geneSymbol.LENGTH, 56	felCat3.genscan.LENGTH, 83
dm3.nscanPasaGene.LENGTH, 57	felCat3.nscanGene.LENGTH, 84
dm3.refGene.LENGTH, 57	felCat3.refGene.LENGTH,84
dp2.genscan.LENGTH, 59	felCat3.sgpGene.LENGTH, 85
dp2.xenoRefGene.LENGTH, 59	felCat3.xenoRefGene.LENGTH, 85
dp3.geneid.LENGTH, 60	fr1.ensGene.LENGTH,86
dp3.genscan.LENGTH, 60	fr1.genscan.LENGTH,86
dp3.xenoRefGene.LENGTH, 61	fr2.ensGene.LENGTH,87
droAna1.geneid.LENGTH, 61	galGal2.ensGene.LENGTH, 87
droAna1.genscan.LENGTH, 62	galGal2.geneid.LENGTH, 88
droAna1.xenoRefGene.LENGTH, 62	galGal2.geneSymbol.LENGTH, 88
droAna2.genscan.LENGTH, 63	galGal2.genscan.LENGTH, 89
droAna2.xenoRefGene.LENGTH, 63	galGal2.refGene.LENGTH, 89
droEre1.genscan.LENGTH, 64	galGal2.sgpGene.LENGTH, 90
droEre1.xenoRefGene.LENGTH,64	galGal3.ensGene.LENGTH, 90
droGri1.genscan.LENGTH, 65	galGal3.geneSymbol.LENGTH, 91
droGri1.xenoRefGene.LENGTH, 65	galGal3.genscan.LENGTH, 91
droMoj1.geneid.LENGTH,66	galGal3.nscanGene.LENGTH, 92
droMoj1.genscan.LENGTH,66	galGal3.refGene.LENGTH, 92
droMoj1.xenoRefGene.LENGTH,67	galGal3.xenoRefGene.LENGTH, 93
droMoj2.genscan.LENGTH, 67	gasAcu1.ensGene.LENGTH, 93
droMoj2.xenoRefGene.LENGTH,68	gasAcu1.nscanGene.LENGTH, 94
droPer1.genscan.LENGTH, 68	hg16.acembly.LENGTH, 95
droPer1.xenoRefGene.LENGTH, 69	hg16.ensGene.LENGTH, 95
droSec1.genscan.LENGTH, 69	hg16.exoniphy.LENGTH,96
droSec1.xenoRefGene.LENGTH, 70	hg16.geneid.LENGTH,96
droSim1.geneid.LENGTH, 70	hg16.geneSymbol.LENGTH, 97
droSim1.genscan.LENGTH, 71	hg16.genscan.LENGTH, 97
droSim1.xenoRefGene.LENGTH,71	hg16.knownGene.LENGTH, 98
droVir1.geneid.LENGTH,72	hg16.refGene.LENGTH,98
droVir1.genscan.LENGTH, 72	hg16.sgpGene.LENGTH, 99
droVir1.xenoRefGene.LENGTH,73	hg17.acembly.LENGTH, 99
droVir2.genscan.LENGTH, 73	hg17.acescan.LENGTH, 100
droVir2.xenoRefGene.LENGTH,74	hg17.ccdsGene.LENGTH, 100
droYak1.geneid.LENGTH, 74	hg17.ensGene.LENGTH, 101
droYak1.genscan.LENGTH, 75	hg17.exoniphy.LENGTH, 101
droYak1.xenoRefGene.LENGTH, 75	hg17.geneid.LENGTH, 102
droYak2.genscan.LENGTH, 76	hg17.geneSymbol.LENGTH, 102
droYak2.xenoRefGene.LENGTH, 76	hg17.genscan.LENGTH, 103
equCab1.geneid.LENGTH, 77	hg17.knownGene.LENGTH, 103
equCab1.geneSymbol.LENGTH, 77	hg17.refGene.LENGTH, 104

hg17.sgpGene.LENGTH, 104	mm9.genscan.LENGTH, 130
hg17.vegaGene.LENGTH, 105	mm9.knownGene.LENGTH, 131
hg17.vegaPseudoGene.LENGTH, 105	mm9.nscanGene.LENGTH, 131
hg17.xenoRefGene.LENGTH, 106	mm9.refGene.LENGTH, 132
hg18.acembly.LENGTH, 106	mm9.sgpGene.LENGTH, 132
hg18.acescan.LENGTH, 107	mm9.xenoRefGene.LENGTH, 133
hg18.ccdsGene.LENGTH, 107	monDom1.genscan.LENGTH, 133
hg18.ensGene.LENGTH, 108	monDom4.ensGene.LENGTH, 134
hg18.exoniphy.LENGTH, 108	monDom4.geneSymbol.LENGTH, 134
hg18.geneid.LENGTH, 109	monDom4.genscan.LENGTH, 135
hg18.geneSymbol.LENGTH, 109	monDom4.nscanGene.LENGTH, 135
hg18.genscan.LENGTH, 110	monDom4.refGene.LENGTH, 136
hg18.knownGene.LENGTH, 110	monDom4.xenoRefGene.LENGTH, 136
hg18.knownGeneOld3.LENGTH, 111	monDom5.ensGene.LENGTH, 137
hg18.refGene.LENGTH, 111	monDom5.geneSymbol.LENGTH, 137
hg18.sgpGene.LENGTH, 112	monDom5.genscan.LENGTH, 138
hg18.sibGene.LENGTH, 112	monDom5.nscanGene.LENGTH, 138
hg18.xenoRefGene.LENGTH, 113	monDom5.refGene.LENGTH, 139
hg19.ccdsGene.LENGTH, 113	monDom5.xenoRefGene.LENGTH, 139
hg19.ensGene.LENGTH, 114	ornAna1.ensGene.LENGTH, 140
hg19.exoniphy.LENGTH, 114	ornAna1.geneSymbol.LENGTH, 140
hg19.geneSymbol.LENGTH, 115	ornAna1.refGene.LENGTH, 141
hg19.knownGene.LENGTH, 115	ornAna1.xenoRefGene.LENGTH, 141
hg19.nscanGene.LENGTH, 116	oryLat2.ensGene.LENGTH, 142
hg19.refGene.LENGTH, 116	oryLat2.geneSymbol.LENGTH, 142
hg19.xenoRefGene.LENGTH, 117	oryLat2.refGene.LENGTH, 143
loxAfr3.xenoRefGene.LENGTH, 117	oryLat2.xenoRefGene.LENGTH, 143
mm7.ensGene.LENGTH, 118	panTro1.ensGene.LENGTH, 144
mm7.geneid.LENGTH, 118	panTro1.geneid.LENGTH, 144
mm7.geneSymbol.LENGTH, 119	panTro1.genscan.LENGTH, 145
mm7.genscan.LENGTH, 119	panTro1.xenoRefGene.LENGTH, 145
mm7.knownGene.LENGTH, 120	panTro2.ensGene.LENGTH, 146
mm7.refGene.LENGTH, 120	panTro2.geneSymbol.LENGTH, 146
mm7.sgpGene.LENGTH, 121	panTro2.genscan.LENGTH, 147
mm7.xenoRefGene.LENGTH, 121	panTro2.nscanGene.LENGTH, 147
mm8.ccdsGene.LENGTH, 122	panTro2.refGene.LENGTH, 148
mm8.ensGene.LENGTH, 122	panTro2.xenoRefGene.LENGTH, 148
mm8.geneid.LENGTH, 123	petMar1.xenoRefGene.LENGTH, 149
mm8.geneSymbol.LENGTH, 123	ponAbe2.ensGene.LENGTH, 149
mm8.genscan.LENGTH, 124	ponAbe2.geneSymbol.LENGTH, 150
mm8.knownGene.LENGTH, 124	ponAbe2.genesymbo1.EENGTH, 150
mm8.nscanGene.LENGTH, 125	ponAbe2.nscanGene.LENGTH, 151
mm8.refGene.LENGTH, 125	ponAbe2.refGene.LENGTH, 151
mm8.sgpGene.LENGTH, 126	ponAbe2.xenoRefGene.LENGTH, 151
mm8.sibGene.LENGTH, 126	priPac1.xenoRefGene.LENGTH, 152
mm8.xenoRefGene.LENGTH, 127	
•	rheMac2.ensGene.LENGTH, 153
mm9.acembly.LENGTH, 127	rheMac2.geneid.LENGTH, 153
mm9.ccdsGene.LENGTH, 128	rheMac2.geneSymbol.LENGTH, 154
mm9.ensGene.LENGTH, 128	rheMac2.nscanGene.LENGTH, 154
mm9.exoniphy.LENGTH, 129	rheMac2.refGene.LENGTH, 155
mm9.geneid.LENGTH, 129	rheMac2.sgpGene.LENGTH, 155
mm9.geneSymbol.LENGTH, 130	rheMac2.xenoRefGene.LENGTH, 156

rn3.ensGene.LENGTH, 156	apiMel1.genscan.LENGTH, 11
rn3.geneid.LENGTH, 157	apiMel2.ensGene.LENGTH, 12
rn3.geneSymbol.LENGTH, 157	apiMel2.geneid.LENGTH, 12
rn3.genscan.LENGTH, 158	apiMel2.genscan.LENGTH, 13
rn3.knownGene.LENGTH, 158	aplCal1.xenoRefGene.LENGTH, 13
rn3.nscanGene.LENGTH, 159	,
rn3.refGene.LENGTH, 159	bosTau2.geneid.LENGTH, 14
rn3.sgpGene.LENGTH, 160	bosTau2.geneSymbol.LENGTH, 14
rn3.xenoRefGene.LENGTH, 160	bosTau2.genscan.LENGTH, 15
rn4.ensGene.LENGTH, 161	bosTau2.refGene.LENGTH, 15
rn4.geneid.LENGTH, 161	bosTau2.sgpGene.LENGTH, 16
rn4.geneSymbol.LENGTH, 162	bosTau3.ensGene.LENGTH, 16
rn4.genscan.LENGTH, 162	bosTau3.geneid.LENGTH, 17
rn4.knownGene.LENGTH, 163	bosTau3.geneSymbol.LENGTH, 17
rn4.nscanGene.LENGTH, 163	bosTau3.genscan.LENGTH, 18
rn4.refGene.LENGTH, 164	bosTau3.refGene.LENGTH, 18
rn4.sgpGene.LENGTH, 164	bosTau3.sgpGene.LENGTH, 19
rn4.xenoRefGene.LENGTH, 165	bosTau4.ensGene.LENGTH, 19
sacCer1.ensGene.LENGTH, 165	bosTau4.geneSymbol.LENGTH, 20
sacCer2.ensGene.LENGTH, 166	bosTau4.genscan.LENGTH, 20
strPur1.geneSymbol.LENGTH, 166	bosTau4.nscanGene.LENGTH, 21
strPur1.genscan.LENGTH, 167	bosTau4.refGene.LENGTH, 21
strPur1.refGene.LENGTH, 167	braFlo1.xenoRefGene.LENGTH, 22
strPur1.xenoRefGene.LENGTH, 168	ar ar 101. Xerioner cene. 22.Norm, 22
strPur2.geneSymbol.LENGTH, 168	caeJap1.xenoRefGene.LENGTH, 22
strPur2.genscan.LENGTH, 169	caePb1.xenoRefGene.LENGTH, 23
strPur2.refGene.LENGTH, 169	caePb2.xenoRefGene.LENGTH, 23
strPur2.xenoRefGene.LENGTH, 170	caeRem2.xenoRefGene.LENGTH, 24
taeGut1.ensGene.LENGTH, 171	caeRem3.xenoRefGene.LENGTH, 24
taeGut1.geneSymbol.LENGTH, 172	calJac1.genscan.LENGTH, 25
taeGut1.genscan.LENGTH, 172	calJac1.nscanGene.LENGTH, 25
taeGut1.nscanGene.LENGTH, 173	calJac1.xenoRefGene.LENGTH, 26
taeGut1.refGene.LENGTH, 173	canFam1.ensGene.LENGTH, 26
taeGut1.xenoRefGene.LENGTH, 174	canFam1.geneSymbol.LENGTH, 27
tetNig1.ensGene.LENGTH, 174	canFam1.genscan.LENGTH, 27
tetNig1.geneid.LENGTH, 175	canFam1.nscanGene.LENGTH, 28
tetNig1.genscan.LENGTH, 175	canFam1.refGene.LENGTH, 28
tetNig1.nscanGene.LENGTH, 176	canFam1.xenoRefGene.LENGTH, 29
tetNig2.ensGene.LENGTH, 176	canFam2.ensGene.LENGTH, 29
xenTro1.genscan.LENGTH, 178	canFam2.geneSymbol.LENGTH, 30
xenTro2.ensGene.LENGTH, 178	canFam2.genscan.LENGTH, 30
xenTro2.geneSymbol.LENGTH, 179	canFam2.nscanGene.LENGTH, 31
xenTro2.genecymbo1.LENGTH, 179	canFam2.refGene.LENGTH, 31
xenTro2.refGene.LENGTH, 180	canFam2.xenoRefGene.LENGTH, 32
* internal	cavPor3.ensGene.LENGTH, 32
geneLenDatabase-pkg, 94	cavPor3.genscan.LENGTH, 33
geneLendatabase-pkg, 94	cavPor3.nscanGene.LENGTH, 33
anoCar1.ensGene.LENGTH, 8	cavPor3.xenoRefGene.LENGTH, 34
anoCar1.genscan.LENGTH, 9	cb1.xenoRefGene.LENGTH, 34
anoCar1.xenoRefGene.LENGTH, 9	cb3.xenoRefGene.LENGTH, 35
anoGam1.ensGene.LENGTH, 10	ce2.geneid.LENGTH, 35
anoGam1.geneid.LENGTH, 10	ce2.geneSymbol.LENGTH, 36
anoGam1.genscan.LENGTH, 11	ce2.refGene.LENGTH,36
<del>-</del>	,

ce4.geneSymbol.LENGTH, 37	droAna2.genscan.LENGTH, 63
ce4.refGene.LENGTH, 37	droAna2.xenoRefGene.LENGTH, 63
ce4.xenoRefGene.LENGTH, 38	droEre1.genscan.LENGTH, 64
ce6.ensGene.LENGTH, 38	droEre1.xenoRefGene.LENGTH, 64
ce6.geneSymbol.LENGTH, 39	droGri1.genscan.LENGTH, 65
ce6.refGene.LENGTH, 39	droGri1.xenoRefGene.LENGTH, 65
ce6.xenoRefGene.LENGTH, 40	droMoj1.geneid.LENGTH,66
ci1.geneSymbol.LENGTH, 40	droMoj1.genscan.LENGTH,66
cil.refGene.LENGTH, 41	droMoj1.xenoRefGene.LENGTH, 67
cil.xenoRefGene.LENGTH, 41	droMoj2.genscan.LENGTH, 67
ci2.ensGene.LENGTH, 42	droMoj2.xenoRefGene.LENGTH, 68
ci2.geneSymbol.LENGTH, 42	droPer1.genscan.LENGTH, 68
ci2.refGene.LENGTH, 43	droPer1.xenoRefGene.LENGTH, 69
ci2.xenoRefGene.LENGTH, 43	droSec1.genscan.LENGTH, 69
CIZ:XCHORCI GCHC:ZERCIH, 15	droSec1.xenoRefGene.LENGTH, 70
danRer3.ensGene.LENGTH, 44	droSim1.geneid.LENGTH, 70
danRer3.geneSymbol.LENGTH, 44	droSim1.genera.LENGTH, 70
danRer3.refGene.LENGTH, 45	droSim1.genscan.LENGTH, 71
danRer4.ensGene.LENGTH, 45	•
danRer4.geneSymbol.LENGTH, 46	droVir1.geneid.LENGTH, 72
danRer4.genscan.LENGTH, 46	droVir1.genscan.LENGTH, 72
danRer4.nscanGene.LENGTH, 47	droVir1.xenoRefGene.LENGTH, 73
danRer4.refGene.LENGTH, 47	droVir2.genscan.LENGTH, 73
danRer5.ensGene.LENGTH, 48	droVir2.xenoRefGene.LENGTH, 74
danRer5.geneSymbol.LENGTH, 48	droYak1.geneid.LENGTH,74
danRer5.refGene.LENGTH, 49	droYak1.genscan.LENGTH, 75
danRer5.vegaGene.LENGTH, 49	droYak1.xenoRefGene.LENGTH, 75
danRer5.vegaPseudoGene.LENGTH, 50	droYak2.genscan.LENGTH, 76
danRer6.ensGene.LENGTH, 50	droYak2.xenoRefGene.LENGTH, 76
danRer6.geneSymbol.LENGTH, 51	Cold man did I ENGTH 77
danRer6.refGene.LENGTH, 51	equCab1.geneid.LENGTH, 77
danRer6.xenoRefGene.LENGTH, 52	equCab1.geneSymbol.LENGTH, 77
dm1.geneSymbol.LENGTH, 52	equCab1.nscanGene.LENGTH, 78
· · ·	equCab1.refGene.LENGTH, 78
dm1.genscan.LENGTH, 53	equCab1.sgpGene.LENGTH, 79
dm1.refGene.LENGTH, 53	equCab2.ensGene.LENGTH, 79
dm2.geneid.LENGTH, 54	equCab2.geneSymbol.LENGTH, 80
dm2.geneSymbol.LENGTH, 54	equCab2.nscanGene.LENGTH, 80
dm2.genscan.LENGTH, 55	equCab2.refGene.LENGTH, 81
dm2.nscanGene.LENGTH, 55	equCab2.xenoRefGene.LENGTH, 81
dm2.refGene.LENGTH, 56	
dm3.geneSymbol.LENGTH, 56	felCat3.ensGene.LENGTH, 82
dm3.nscanPasaGene.LENGTH, 57	felCat3.geneid.LENGTH, 82
dm3.refGene.LENGTH, 57	felCat3.geneSymbol.LENGTH, 83
downloadLengthFromUCSC, 8-57, 58, 59-170,	felCat3.genscan.LENGTH, 83
172–176, 178–180	felCat3.nscanGene.LENGTH, 84
dp2.genscan.LENGTH, 59	felCat3.refGene.LENGTH, 84
dp2.xenoRefGene.LENGTH, 59	felCat3.sgpGene.LENGTH, 85
dp3.geneid.LENGTH, 60	felCat3.xenoRefGene.LENGTH, 85
dp3.genscan.LENGTH, 60	fr1.ensGene.LENGTH,86
dp3.xenoRefGene.LENGTH, 61	fr1.genscan.LENGTH,86
droAna1.geneid.LENGTH, 61	fr2.ensGene.LENGTH,87
droAna1.genscan.LENGTH, 62	
droAna1.xenoRefGene.LENGTH, 62	galGal2.ensGene.LENGTH, 87

galGal2.geneid.LENGTH, $88$	hg18.sgpGene.LENGTH, 112
galGal2.geneSymbol.LENGTH, 88	hg18.sibGene.LENGTH, 112
galGal2.genscan.LENGTH, 89	hg18.xenoRefGene.LENGTH, 113
galGal2.refGene.LENGTH, 89	hg19.ccdsGene.LENGTH, 113
galGal2.sgpGene.LENGTH, 90	hg19.ensGene.LENGTH, 114
galGal3.ensGene.LENGTH, 90	hg19.exoniphy.LENGTH, 114
galGal3.geneSymbol.LENGTH, 91	hg19.geneSymbol.LENGTH, 115
galGal3.genscan.LENGTH, 91	hg19.knownGene.LENGTH, 115
galGal3.nscanGene.LENGTH, 92	hg19.nscanGene.LENGTH, 116
galGal3.refGene.LENGTH, 92	hg19.refGene.LENGTH, 116
galGal3.xenoRefGene.LENGTH, 93	hg19.xenoRefGene.LENGTH, 117
gasAcu1.ensGene.LENGTH, 93	
gasAcu1.nscanGene.LENGTH, 94	loxAfr3.xenoRefGene.LENGTH, 117
<pre>geneLenDataBase (geneLenDatabase-pkg),</pre>	
94	mm7.ensGene.LENGTH, 118
geneLenDataBase-package	mm7.geneid.LENGTH, 118
(geneLenDatabase-pkg), 94	mm7.geneSymbol.LENGTH, 119
geneLenDatabase-pkg, 94	mm7.genscan.LENGTH, 119
	mm7.knownGene.LENGTH, 120
hg16.acembly.LENGTH, 95	mm7.refGene.LENGTH, 120
hg16.ensGene.LENGTH, 95	mm7.sgpGene.LENGTH, 121
hg16.exoniphy.LENGTH, 96	mm7.xenoRefGene.LENGTH, 121
hg16.geneid.LENGTH,96	mm8.ccdsGene.LENGTH, 122
hg16.geneSymbol.LENGTH, 97	mm8.ensGene.LENGTH, 122
hg16.genscan.LENGTH, 97	mm8.geneid.LENGTH, 123
hg16.knownGene.LENGTH, 98	mm8.geneSymbol.LENGTH, 123
hg16.refGene.LENGTH, 98	mm8.genscan.LENGTH, 124
hg16.sgpGene.LENGTH, 99	mm8.knownGene.LENGTH, 124
hg17.acembly.LENGTH, 99	mm8.nscanGene.LENGTH, 125
hg17.acescan.LENGTH, 100	mm8.refGene.LENGTH, 125
hg17.ccdsGene.LENGTH, 100	mm8.sgpGene.LENGTH, 126
hg17.ensGene.LENGTH, 101	mm8.sibGene.LENGTH, 126
hg17.exoniphy.LENGTH, 101	mm8.xenoRefGene.LENGTH, 127
hg17.geneid.LENGTH, 102	mm9.acembly.LENGTH, 127
hg17.geneSymbol.LENGTH, 102	mm9.ccdsGene.LENGTH, 128
hg17.genscan.LENGTH, 103	mm9.ensGene.LENGTH, 128
hg17.knownGene.LENGTH, 103	mm9.exoniphy.LENGTH, 129
hg17.refGene.LENGTH, 104	mm9.geneid.LENGTH, 129
hg17.sgpGene.LENGTH, 104	mm9.geneSymbol.LENGTH, 130
hg17.vegaGene.LENGTH, 105	mm9.genscan.LENGTH, 130
hg17.vegaPseudoGene.LENGTH, 105	mm9.knownGene.LENGTH, 131
hg17.xenoRefGene.LENGTH, 106	mm9.nscanGene.LENGTH, 131
hg18.acembly.LENGTH, 106	mm9.refGene.LENGTH, 132
hg18.acescan.LENGTH, 107	mm9.sgpGene.LENGTH, 132
hg18.ccdsGene.LENGTH, 107	mm9.xenoRefGene.LENGTH, 133
hg18.ensGene.LENGTH, 108	monDom1.genscan.LENGTH, 133
hg18.exoniphy.LENGTH, 108	monDom4.ensGene.LENGTH, 134
hg18.geneid.LENGTH, 109	monDom4.geneSymbol.LENGTH, 134
hg18.geneSymbol.LENGTH, 109	monDom4.genscan.LENGTH, 135
hg18.genscan.LENGTH, 110	monDom4.nscanGene.LENGTH, 135
hg18.knownGene.LENGTH, 110	monDom4.refGene.LENGTH, 136
hg18.knownGeneOld3.LENGTH, 111	monDom4.xenoRefGene.LENGTH, 136
hg18.refGene.LENGTH, 111	monDom5.ensGene.LENGTH, 137
nbrotter ochet Elitotti, 111	monbolio, Chaoche, ELNOTH, 13/

monDom5.geneSymbol.LENGTH, 137	rn4.genscan.LENGTH, 162
monDom5.genscan.LENGTH, 138	rn4.knownGene.LENGTH, 163
monDom5.nscanGene.LENGTH, 138	rn4.nscanGene.LENGTH, 163
monDom5.refGene.LENGTH, 139	rn4.refGene.LENGTH, 164
	rn4.sgpGene.LENGTH, 164
monDom5.xenoRefGene.LENGTH, 139	rn4.xenoRefGene.LENGTH, 165
ornAna1.ensGene.LENGTH, 140	rna. xenoker gene. Length, 103
ornAna1.geneSymbol.LENGTH, 140	sacCer1.ensGene.LENGTH, 165
ornAna1.refGene.LENGTH, 141	sacCer2.ensGene.LENGTH, 166
ornAna1.xenoRefGene.LENGTH, 141	strPur1.geneSymbol.LENGTH, 166
oryLat2.ensGene.LENGTH, 142	strPur1.genscan.LENGTH, 167
oryLat2.geneSymbol.LENGTH, 142	strPur1.refGene.LENGTH, 167
oryLat2.refGene.LENGTH, 143	strPur1.xenoRefGene.LENGTH, 168
oryLat2.xenoRefGene.LENGTH, 143	strPur2.geneSymbol.LENGTH, 168
of years. Actioner defic. Lettorii, 143	strPur2.genscan.LENGTH, 169
panTro1.ensGene.LENGTH, 144	strPur2.refGene.LENGTH, 169
panTro1.geneid.LENGTH, 144	strPur2.xenoRefGene.LENGTH, 170
panTro1.genscan.LENGTH, 145	supportedGeneIDs, 58, 170
panTro1.xenoRefGene.LENGTH, 145	supportedGenomes, 58, 171
panTro2.ensGene.LENGTH, 146	3uppor teaderiomes, 50, 171
panTro2.geneSymbol.LENGTH, 146	taeGut1.ensGene.LENGTH, 171
panTro2.genesymbo1.LENGTH, 147	taeGut1.geneSymbol.LENGTH, 172
panTro2.nscanGene.LENGTH, 147	taeGut1.genscan.LENGTH, 172
panTro2.refGene.LENGTH, 148	taeGut1.nscanGene.LENGTH, 173
	taeGut1.refGene.LENGTH, 173
panTro2.xenoRefGene.LENGTH, 148	taeGut1.xenoRefGene.LENGTH, 174
petMar1.xenoRefGene.LENGTH, 149 ponAbe2.ensGene.LENGTH, 149	tetNig1.ensGene.LENGTH, 174
ponAbe2.geneSymbol.LENGTH, 150	tetNig1.geneid.LENGTH, 175
ponAbe2.genscan.LENGTH, 150	tetNig1.genscan.LENGTH, 175
ponAbe2.nscanGene.LENGTH, 151	tetNig1.nscanGene.LENGTH, 176
ponAbe2.refGene.LENGTH, 151	tetNig2.ensGene.LENGTH, 176
ponAbe2.xenoRefGene.LENGTH, 152	<b>3</b> , ,
priPac1.xenoRefGene.LENGTH, 152	unfactor, 177
priraci. Xenoker Gene. Length, 132	
rheMac2.ensGene.LENGTH, 153	xenTro1.genscan.LENGTH, 178
rheMac2.geneid.LENGTH, 153	xenTro2.ensGene.LENGTH, 178
rheMac2.geneSymbol.LENGTH, 154	xenTro2.geneSymbol.LENGTH, 179
rheMac2.nscanGene.LENGTH, 154	xenTro2.genscan.LENGTH, 179
rheMac2.refGene.LENGTH, 155	xenTro2.refGene.LENGTH, 180
rheMac2.sgpGene.LENGTH, 155	
rheMac2.xenoRefGene.LENGTH, 156	
rn3.ensGene.LENGTH, 156	
rn3.geneid.LENGTH, 157	
rn3.geneSymbol.LENGTH, 157	
rn3.genscan.LENGTH, 158	
rn3.knownGene.LENGTH, 158	
rn3.nscanGene.LENGTH, 159	
rn3.refGene.LENGTH, 159	
rn3.sgpGene.LENGTH, 160	
rn3.xenoRefGene.LENGTH, 160	
rn4.ensGene.LENGTH, 161	
rn4.geneid.LENGTH, 161	
rn4.geneSymbol.LENGTH, 162	