

Package ‘geneLenDataBase’

October 7, 2015

Version 1.4.0

Date 2010/03/30

Title Lengths of mRNA transcripts for a number of genomes

Author Matthew Young

Maintainer Nadia Davidson <nadia.davidson@mcri.edu.au>

Depends R (>= 2.11.0)

Imports utils, rtracklayer, GenomicFeatures (>= 1.3.15)

LazyLoad yes

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

biocViews ExperimentData, Genome

License LGPL (>= 2)

NeedsCompilation no

R topics documented:

anoCar1.ensGene.LENGTH	8
anoCar1.genscan.LENGTH	9
anoCar1.xenoRefGene.LENGTH	10
anoGam1.ensGene.LENGTH	10
anoGam1.geneid.LENGTH	11
anoGam1.genscan.LENGTH	11
apiMel1.genscan.LENGTH	12
apiMel2.ensGene.LENGTH	12
apiMel2.geneid.LENGTH	13
apiMel2.genscan.LENGTH	13
aplCal1.xenoRefGene.LENGTH	14
bosTau2.geneid.LENGTH	14
bosTau2.geneSymbol.LENGTH	15
bosTau2.genscan.LENGTH	15
bosTau2.refGene.LENGTH	16
bosTau2.sgpGene.LENGTH	16

bosTau3.ensGene.LENGTH	17
bosTau3.geneid.LENGTH	17
bosTau3.geneSymbol.LENGTH	18
bosTau3.genscan.LENGTH	18
bosTau3.refGene.LENGTH	19
bosTau3.sgpGene.LENGTH	19
bosTau4.ensGene.LENGTH	20
bosTau4.geneSymbol.LENGTH	20
bosTau4.genscan.LENGTH	21
bosTau4.nscanGene.LENGTH	21
bosTau4.refGene.LENGTH	22
braFlo1.xenoRefGene.LENGTH	22
caeJap1.xenoRefGene.LENGTH	23
caePb1.xenoRefGene.LENGTH	23
caePb2.xenoRefGene.LENGTH	24
caeRem2.xenoRefGene.LENGTH	24
caeRem3.xenoRefGene.LENGTH	25
calJac1.genscan.LENGTH	25
calJac1.nscanGene.LENGTH	26
calJac1.xenoRefGene.LENGTH	26
canFam1.ensGene.LENGTH	27
canFam1.geneSymbol.LENGTH	27
canFam1.genscan.LENGTH	28
canFam1.nscanGene.LENGTH	28
canFam1.refGene.LENGTH	29
canFam1.xenoRefGene.LENGTH	29
canFam2.ensGene.LENGTH	30
canFam2.geneSymbol.LENGTH	30
canFam2.genscan.LENGTH	31
canFam2.nscanGene.LENGTH	31
canFam2.refGene.LENGTH	32
canFam2.xenoRefGene.LENGTH	32
cavPor3.ensGene.LENGTH	33
cavPor3.genscan.LENGTH	33
cavPor3.nscanGene.LENGTH	34
cavPor3.xenoRefGene.LENGTH	34
cb1.xenoRefGene.LENGTH	35
cb3.xenoRefGene.LENGTH	35
ce2.geneid.LENGTH	36
ce2.geneSymbol.LENGTH	36
ce2.refGene.LENGTH	37
ce4.geneSymbol.LENGTH	37
ce4.refGene.LENGTH	38
ce4.xenoRefGene.LENGTH	38
ce6.ensGene.LENGTH	39
ce6.geneSymbol.LENGTH	39
ce6.refGene.LENGTH	40
ce6.xenoRefGene.LENGTH	40

ci1.geneSymbol.LENGTH	41
ci1.refGene.LENGTH	41
ci1.xenoRefGene.LENGTH	42
ci2.ensGene.LENGTH	42
ci2.geneSymbol.LENGTH	43
ci2.refGene.LENGTH	43
ci2.xenoRefGene.LENGTH	44
danRer3.ensGene.LENGTH	44
danRer3.geneSymbol.LENGTH	45
danRer3.refGene.LENGTH	45
danRer4.ensGene.LENGTH	46
danRer4.geneSymbol.LENGTH	46
danRer4.genscan.LENGTH	47
danRer4.nscanGene.LENGTH	47
danRer4.refGene.LENGTH	48
danRer5.ensGene.LENGTH	48
danRer5.geneSymbol.LENGTH	49
danRer5.refGene.LENGTH	49
danRer5.vegaGene.LENGTH	50
danRer5.vegaPseudoGene.LENGTH	50
danRer6.ensGene.LENGTH	51
danRer6.geneSymbol.LENGTH	51
danRer6.refGene.LENGTH	52
danRer6.xenoRefGene.LENGTH	52
dm1.geneSymbol.LENGTH	53
dm1.genscan.LENGTH	53
dm1.refGene.LENGTH	54
dm2.geneid.LENGTH	54
dm2.geneSymbol.LENGTH	55
dm2.genscan.LENGTH	55
dm2.nscanGene.LENGTH	56
dm2.refGene.LENGTH	56
dm3.geneSymbol.LENGTH	57
dm3.nscanPasaGene.LENGTH	57
dm3.refGene.LENGTH	58
dp2.genscan.LENGTH	58
dp2.xenoRefGene.LENGTH	59
dp3.geneid.LENGTH	59
dp3.genscan.LENGTH	60
dp3.xenoRefGene.LENGTH	60
droAna1.geneid.LENGTH	61
droAna1.genscan.LENGTH	61
droAna1.xenoRefGene.LENGTH	62
droAna2.genscan.LENGTH	62
droAna2.xenoRefGene.LENGTH	63
droEre1.genscan.LENGTH	63
droEre1.xenoRefGene.LENGTH	64
droGri1.genscan.LENGTH	64

droGri1.xenoRefGene.LENGTH	65
droMoj1.geneid.LENGTH	65
droMoj1.genscan.LENGTH	66
droMoj1.xenoRefGene.LENGTH	66
droMoj2.genscan.LENGTH	67
droMoj2.xenoRefGene.LENGTH	67
droPer1.genscan.LENGTH	68
droPer1.xenoRefGene.LENGTH	68
droSec1.genscan.LENGTH	69
droSec1.xenoRefGene.LENGTH	69
droSim1.geneid.LENGTH	70
droSim1.genscan.LENGTH	70
droSim1.xenoRefGene.LENGTH	71
droVir1.geneid.LENGTH	71
droVir1.genscan.LENGTH	72
droVir1.xenoRefGene.LENGTH	72
droVir2.genscan.LENGTH	73
droVir2.xenoRefGene.LENGTH	73
droYak1.geneid.LENGTH	74
droYak1.genscan.LENGTH	74
droYak1.xenoRefGene.LENGTH	75
droYak2.genscan.LENGTH	75
droYak2.xenoRefGene.LENGTH	76
equCab1.geneid.LENGTH	76
equCab1.geneSymbol.LENGTH	77
equCab1.nscanGene.LENGTH	77
equCab1.refGene.LENGTH	78
equCab1.sgpGene.LENGTH	78
equCab2.ensGene.LENGTH	79
equCab2.geneSymbol.LENGTH	79
equCab2.nscanGene.LENGTH	80
equCab2.refGene.LENGTH	80
equCab2.xenoRefGene.LENGTH	81
felCat3.ensGene.LENGTH	81
felCat3.geneid.LENGTH	82
felCat3.geneSymbol.LENGTH	82
felCat3.genscan.LENGTH	83
felCat3.nscanGene.LENGTH	83
felCat3.refGene.LENGTH	84
felCat3.sgpGene.LENGTH	84
felCat3.xenoRefGene.LENGTH	85
fr1.ensGene.LENGTH	85
fr1.genscan.LENGTH	86
fr2.ensGene.LENGTH	86
galGal2.ensGene.LENGTH	87
galGal2.geneid.LENGTH	87
galGal2.geneSymbol.LENGTH	88
galGal2.genscan.LENGTH	88

galGal2.refGene.LENGTH	89
galGal2.sgpGene.LENGTH	89
galGal3.ensGene.LENGTH	90
galGal3.geneSymbol.LENGTH	90
galGal3.genscan.LENGTH	91
galGal3.nscanGene.LENGTH	91
galGal3.refGene.LENGTH	92
galGal3.xenoRefGene.LENGTH	92
gasAcu1.ensGene.LENGTH	93
gasAcu1.nscanGene.LENGTH	93
hg16.acembly.LENGTH	94
hg16.ensGene.LENGTH	94
hg16.exoniphy.LENGTH	95
hg16.geneid.LENGTH	95
hg16.geneSymbol.LENGTH	96
hg16.genscan.LENGTH	96
hg16.knownGene.LENGTH	97
hg16.refGene.LENGTH	97
hg16.sgpGene.LENGTH	98
hg17.acembly.LENGTH	98
hg17.acescan.LENGTH	99
hg17.ccdsGene.LENGTH	99
hg17.ensGene.LENGTH	100
hg17.exoniphy.LENGTH	100
hg17.geneid.LENGTH	101
hg17.geneSymbol.LENGTH	101
hg17.genscan.LENGTH	102
hg17.knownGene.LENGTH	102
hg17.refGene.LENGTH	103
hg17.sgpGene.LENGTH	103
hg17.vegaGene.LENGTH	104
hg17.vegaPseudoGene.LENGTH	104
hg17.xenoRefGene.LENGTH	105
hg18.acembly.LENGTH	105
hg18.acescan.LENGTH	106
hg18.ccdsGene.LENGTH	106
hg18.ensGene.LENGTH	107
hg18.exoniphy.LENGTH	107
hg18.geneid.LENGTH	108
hg18.geneSymbol.LENGTH	108
hg18.genscan.LENGTH	109
hg18.knownGene.LENGTH	109
hg18.knownGeneOld3.LENGTH	110
hg18.refGene.LENGTH	110
hg18.sgpGene.LENGTH	111
hg18.sibGene.LENGTH	111
hg18.xenoRefGene.LENGTH	112
hg19.ccdsGene.LENGTH	112

hg19.ensGene.LENGTH	113
hg19.exoniphy.LENGTH	113
hg19.geneSymbol.LENGTH	114
hg19.knownGene.LENGTH	114
hg19.nscanGene.LENGTH	115
hg19.refGene.LENGTH	115
hg19.xenoRefGene.LENGTH	116
loxAfr3.xenoRefGene.LENGTH	116
mm7.ensGene.LENGTH	117
mm7.geneid.LENGTH	117
mm7.geneSymbol.LENGTH	118
mm7.genscan.LENGTH	118
mm7.knownGene.LENGTH	119
mm7.refGene.LENGTH	119
mm7.sgpGene.LENGTH	120
mm7.xenoRefGene.LENGTH	120
mm8.ccdsGene.LENGTH	121
mm8.ensGene.LENGTH	121
mm8.geneid.LENGTH	122
mm8.geneSymbol.LENGTH	122
mm8.genscan.LENGTH	123
mm8.knownGene.LENGTH	123
mm8.nscanGene.LENGTH	124
mm8.refGene.LENGTH	124
mm8.sgpGene.LENGTH	125
mm8.sibGene.LENGTH	125
mm8.xenoRefGene.LENGTH	126
mm9.acembly.LENGTH	126
mm9.ccdsGene.LENGTH	127
mm9.ensGene.LENGTH	127
mm9.exoniphy.LENGTH	128
mm9.geneid.LENGTH	128
mm9.geneSymbol.LENGTH	129
mm9.genscan.LENGTH	129
mm9.knownGene.LENGTH	130
mm9.nscanGene.LENGTH	130
mm9.refGene.LENGTH	131
mm9.sgpGene.LENGTH	131
mm9.xenoRefGene.LENGTH	132
monDom1.genscan.LENGTH	132
monDom4.ensGene.LENGTH	133
monDom4.geneSymbol.LENGTH	133
monDom4.genscan.LENGTH	134
monDom4.nscanGene.LENGTH	134
monDom4.refGene.LENGTH	135
monDom4.xenoRefGene.LENGTH	135
monDom5.ensGene.LENGTH	136
monDom5.geneSymbol.LENGTH	136

monDom5.genscan.LENGTH	137
monDom5.nscanGene.LENGTH	137
monDom5.refGene.LENGTH	138
monDom5.xenoRefGene.LENGTH	138
ornAna1.ensGene.LENGTH	139
ornAna1.geneSymbol.LENGTH	139
ornAna1.refGene.LENGTH	140
ornAna1.xenoRefGene.LENGTH	140
oryLat2.ensGene.LENGTH	141
oryLat2.geneSymbol.LENGTH	141
oryLat2.refGene.LENGTH	142
oryLat2.xenoRefGene.LENGTH	142
panTro1.ensGene.LENGTH	143
panTro1.geneid.LENGTH	143
panTro1.genscan.LENGTH	144
panTro1.xenoRefGene.LENGTH	144
panTro2.ensGene.LENGTH	145
panTro2.geneSymbol.LENGTH	145
panTro2.genscan.LENGTH	146
panTro2.nscanGene.LENGTH	146
panTro2.refGene.LENGTH	147
panTro2.xenoRefGene.LENGTH	147
petMar1.xenoRefGene.LENGTH	148
ponAbe2.ensGene.LENGTH	148
ponAbe2.geneSymbol.LENGTH	149
ponAbe2.genscan.LENGTH	149
ponAbe2.nscanGene.LENGTH	150
ponAbe2.refGene.LENGTH	150
ponAbe2.xenoRefGene.LENGTH	151
priPac1.xenoRefGene.LENGTH	151
rheMac2.ensGene.LENGTH	152
rheMac2.geneid.LENGTH	152
rheMac2.geneSymbol.LENGTH	153
rheMac2.nscanGene.LENGTH	153
rheMac2.refGene.LENGTH	154
rheMac2.sgpGene.LENGTH	154
rheMac2.xenoRefGene.LENGTH	155
rn3.ensGene.LENGTH	155
rn3.geneid.LENGTH	156
rn3.geneSymbol.LENGTH	156
rn3.genscan.LENGTH	157
rn3.knownGene.LENGTH	157
rn3.nscanGene.LENGTH	158
rn3.refGene.LENGTH	158
rn3.sgpGene.LENGTH	159
rn3.xenoRefGene.LENGTH	159
rn4.ensGene.LENGTH	160
rn4.geneid.LENGTH	160

rn4.geneSymbol.LENGTH	161
rn4.genscan.LENGTH	161
rn4.knownGene.LENGTH	162
rn4.nscanGene.LENGTH	162
rn4.refGene.LENGTH	163
rn4.sgpGene.LENGTH	163
rn4.xenoRefGene.LENGTH	164
sacCer1.ensGene.LENGTH	164
sacCer2.ensGene.LENGTH	165
strPur1.geneSymbol.LENGTH	165
strPur1.genscan.LENGTH	166
strPur1.refGene.LENGTH	166
strPur1.xenoRefGene.LENGTH	167
strPur2.geneSymbol.LENGTH	167
strPur2.genscan.LENGTH	168
strPur2.refGene.LENGTH	168
strPur2.xenoRefGene.LENGTH	169
supportedGeneIDs	169
supportedGenomes	170
taeGut1.ensGene.LENGTH	171
taeGut1.geneSymbol.LENGTH	171
taeGut1.genscan.LENGTH	172
taeGut1.nscanGene.LENGTH	172
taeGut1.refGene.LENGTH	173
taeGut1.xenoRefGene.LENGTH	173
tetNig1.ensGene.LENGTH	174
tetNig1.geneid.LENGTH	174
tetNig1.genscan.LENGTH	175
tetNig1.nscanGene.LENGTH	175
tetNig2.ensGene.LENGTH	176
unfactor	176
xenTro1.genscan.LENGTH	177
xenTro2.ensGene.LENGTH	178
xenTro2.geneSymbol.LENGTH	178
xenTro2.genscan.LENGTH	179
xenTro2.refGene.LENGTH	179

Index**180**

anoCar1.ensGene.LENGTH

Transcript length data for the organism anoCar

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

anoCar1.genscan.LENGTH

Transcript length data for the organism anoCar

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
anoCar1.xenoRefGene.LENGTH
```

Transcript length data for the organism anoCar

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
anoGam1.ensGene.LENGTH
```

Transcript length data for the organism anoGam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

apiMe11.genscan.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

apiMe12.ensGene.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
aplCa11.xenoRefGene.LENGTH
```

Transcript length data for the organism aplCa1

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau2.geneid.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.geneSymbol.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.genscan.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.ensGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.geneSymbol.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caeJap1.xenoRefGene.LENGTH
```

Transcript length data for the organism caeJap

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caePb1.xenoRefGene.LENGTH
```

Transcript length data for the organism caePb

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caePb2.xenoRefGene.LENGTH
```

Transcript length data for the organism caePb

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caeRem2.xenoRefGene.LENGTH
```

Transcript length data for the organism caeRem

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer4.ensGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer4.geneSymbol.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer5.vegaGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer5.vegaPseudoGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer6.ensGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer6.geneSymbol.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droEre1.xenoRefGene.LENGTH
```

Transcript length data for the organism droEre

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droGri1.genscan.LENGTH
```

Transcript length data for the organism droGri

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droGri1.xenoRefGene.LENGTH
```

Transcript length data for the organism droGri

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droMoj1.geneid.LENGTH
```

Transcript length data for the organism droMoj

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droMoj1.genscan.LENGTH
```

Transcript length data for the organism droMoj

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droMoj1.xenoRefGene.LENGTH
```

Transcript length data for the organism droMoj

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droVir2.genscan.LENGTH
```

Transcript length data for the organism droVir

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droVir2.xenoRefGene.LENGTH
```

Transcript length data for the organism droVir

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

felCat3.refGene.LENGTH

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

felCat3.sgpGene.LENGTH

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg18.knownGeneOld3.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg18.refGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg18.xenoRefGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg19.ccdsGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.ccdsGene.LENGTH)
head(hg19.ccdsGene.LENGTH)
```

hg19.ensGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.ensGene.LENGTH)
head(hg19.ensGene.LENGTH)
```

hg19.exoniphy.LENGTH *Transcript length data for the organism hg*

Description

hg19.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg19, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.exoniphy.LENGTH)
head(hg19.exoniphy.LENGTH)
```

```
hg19.geneSymbol.LENGTH
```

Transcript length data for the organism hg

Description

hg19.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg19, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.geneSymbol.LENGTH)
head(hg19.geneSymbol.LENGTH)
```

```
hg19.knownGene.LENGTH
```

Transcript length data for the organism hg

Description

hg19.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.knownGene.LENGTH)
head(hg19.knownGene.LENGTH)
```

hg19.nscanGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.nscanGene.LENGTH)
head(hg19.nscanGene.LENGTH)
```

hg19.refGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.refGene.LENGTH)
head(hg19.refGene.LENGTH)
```

```
hg19.xenoRefGene.LENGTH
```

Transcript length data for the organism hg

Description

hg19.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.xenoRefGene.LENGTH)
head(hg19.xenoRefGene.LENGTH)
```

```
loxAfr3.xenoRefGene.LENGTH
```

Transcript length data for the organism loxAfr

Description

loxAfr3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(loxAfr3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(loxAfr3.xenoRefGene.LENGTH)
head(loxAfr3.xenoRefGene.LENGTH)
```

mm7.ensGene.LENGTH *Transcript length data for the organism mm*

Description

mm7.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.ensGene.LENGTH)
head(mm7.ensGene.LENGTH)
```

mm7.geneid.LENGTH *Transcript length data for the organism mm*

Description

mm7.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.geneid.LENGTH)
head(mm7.geneid.LENGTH)
```

mm7.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

mm7.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.geneSymbol.LENGTH)
head(mm7.geneSymbol.LENGTH)
```

mm7.genscan.LENGTH *Transcript length data for the organism mm*

Description

mm7.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm7, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.genscan.LENGTH)
head(mm7.genscan.LENGTH)
```

mm7.knownGene.LENGTH *Transcript length data for the organism mm*

Description

mm7.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.knownGene.LENGTH)
head(mm7.knownGene.LENGTH)
```

mm7.refGene.LENGTH *Transcript length data for the organism mm*

Description

mm7.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.refGene.LENGTH)
head(mm7.refGene.LENGTH)
```

mm7.sgpGene.LENGTH *Transcript length data for the organism mm*

Description

mm7.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.sgpGene.LENGTH)
head(mm7.sgpGene.LENGTH)
```

mm7.xenoRefGene.LENGTH *Transcript length data for the organism mm*

Description

mm7.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.xenoRefGene.LENGTH)
head(mm7.xenoRefGene.LENGTH)
```

mm8.ccdsGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.ccdsGene.LENGTH)
head(mm8.ccdsGene.LENGTH)
```

mm8.ensGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.ensGene.LENGTH)
head(mm8.ensGene.LENGTH)
```

mm8.geneid.LENGTH *Transcript length data for the organism mm*

Description

mm8.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.geneid.LENGTH)
head(mm8.geneid.LENGTH)
```

mm8.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

mm8.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.geneSymbol.LENGTH)
head(mm8.geneSymbol.LENGTH)
```

mm8.genscan.LENGTH *Transcript length data for the organism mm*

Description

mm8.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm8, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.genscan.LENGTH)
head(mm8.genscan.LENGTH)
```

mm8.knownGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.knownGene.LENGTH)
head(mm8.knownGene.LENGTH)
```

mm8.nscanGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.nscanGene.LENGTH)
head(mm8.nscanGene.LENGTH)
```

mm8.refGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.refGene.LENGTH)
head(mm8.refGene.LENGTH)
```

mm8.sgpGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.sgpGene.LENGTH)
head(mm8.sgpGene.LENGTH)
```

mm8.sibGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sibGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sibGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.sibGene.LENGTH)
head(mm8.sibGene.LENGTH)
```

`mm8.xenoRefGene.LENGTH`*Transcript length data for the organism mm*

Description

`mm8.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm8, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.xenoRefGene.LENGTH)
head(mm8.xenoRefGene.LENGTH)
```

`mm9.acembly.LENGTH`*Transcript length data for the organism mm*

Description

`mm9.acembly.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `acembly` table.

The data file was made by calling `downloadLengthFromUCSC(mm9, acembly)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.acembly.LENGTH)
head(mm9.acembly.LENGTH)
```

mm9.ccdsGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.ccdsGene.LENGTH)
head(mm9.ccdsGene.LENGTH)
```

mm9.ensGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.ensGene.LENGTH)
head(mm9.ensGene.LENGTH)
```

mm9.exoniphy.LENGTH *Transcript length data for the organism mm*

Description

mm9.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(mm9, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.exoniphy.LENGTH)
head(mm9.exoniphy.LENGTH)
```

mm9.geneid.LENGTH *Transcript length data for the organism mm*

Description

mm9.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.geneid.LENGTH)
head(mm9.geneid.LENGTH)
```

mm9.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

mm9.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.geneSymbol.LENGTH)
head(mm9.geneSymbol.LENGTH)
```

mm9.genscan.LENGTH *Transcript length data for the organism mm*

Description

mm9.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm9, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.genscan.LENGTH)
head(mm9.genscan.LENGTH)
```

mm9.knownGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.knownGene.LENGTH)
head(mm9.knownGene.LENGTH)
```

mm9.nscanGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.nscanGene.LENGTH)
head(mm9.nscanGene.LENGTH)
```

mm9.refGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.refGene.LENGTH)
head(mm9.refGene.LENGTH)
```

mm9.sgpGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.sgpGene.LENGTH)
head(mm9.sgpGene.LENGTH)
```

`mm9.xenoRefGene.LENGTH`*Transcript length data for the organism mm*

Description

`mm9.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm9, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.xenoRefGene.LENGTH)
head(mm9.xenoRefGene.LENGTH)
```

`monDom1.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom1.genscan.LENGTH)
head(monDom1.genscan.LENGTH)
```

`monDom4.ensGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.ensGene.LENGTH)
head(monDom4.ensGene.LENGTH)
```

`monDom4.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.geneSymbol.LENGTH)
head(monDom4.geneSymbol.LENGTH)
```

`monDom4.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.genscan.LENGTH)
head(monDom4.genscan.LENGTH)
```

`monDom4.nscanGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.nscanGene.LENGTH)
head(monDom4.nscanGene.LENGTH)
```

`monDom4.refGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.refGene.LENGTH)
head(monDom4.refGene.LENGTH)
```

`monDom4.xenoRefGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.xenoRefGene.LENGTH)
head(monDom4.xenoRefGene.LENGTH)
```

`monDom5.ensGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.ensGene.LENGTH)
head(monDom5.ensGene.LENGTH)
```

`monDom5.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.geneSymbol.LENGTH)
head(monDom5.geneSymbol.LENGTH)
```

`monDom5.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.genscan.LENGTH)
head(monDom5.genscan.LENGTH)
```

`monDom5.nscanGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)
```

```
monDom5.refGene.LENGTH
```

Transcript length data for the organism monDom

Description

monDom5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)
```

```
monDom5.xenoRefGene.LENGTH
```

Transcript length data for the organism monDom

Description

monDom5.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.xenoRefGene.LENGTH)
head(monDom5.xenoRefGene.LENGTH)
```

`ornAna1.ensGene.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.ensGene.LENGTH)
head(ornAna1.ensGene.LENGTH)
```

`ornAna1.geneSymbol.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.geneSymbol.LENGTH)
head(ornAna1.geneSymbol.LENGTH)
```

`ornAna1.refGene.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.refGene.LENGTH)
head(ornAna1.refGene.LENGTH)
```

`ornAna1.xenoRefGene.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.xenoRefGene.LENGTH)
head(ornAna1.xenoRefGene.LENGTH)
```

`oryLat2.ensGene.LENGTH`*Transcript length data for the organism oryLat*

Description

`oryLat2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)
```

`oryLat2.geneSymbol.LENGTH`*Transcript length data for the organism oryLat*

Description

`oryLat2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)
```

oryLat2.refGene.LENGTH

Transcript length data for the organism oryLat

Description

oryLat2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)
```

oryLat2.xenoRefGene.LENGTH

Transcript length data for the organism oryLat

Description

oryLat2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)
```

`panTro1.ensGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.ensGene.LENGTH)
head(panTro1.ensGene.LENGTH)
```

`panTro1.geneid.LENGTH` *Transcript length data for the organism panTro*

Description

panTro1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.geneid.LENGTH)
head(panTro1.geneid.LENGTH)
```

`panTro1.genscan.LENGTH`*Transcript length data for the organism panTro*

Description

panTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.genscan.LENGTH)
head(panTro1.genscan.LENGTH)
```

`panTro1.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.xenoRefGene.LENGTH)
head(panTro1.xenoRefGene.LENGTH)
```

`panTro2.ensGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)
```

`panTro2.geneSymbol.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)
```

`panTro2.genscan.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.genscan.LENGTH)
head(panTro2.genscan.LENGTH)
```

`panTro2.nscanGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.nscanGene.LENGTH)
head(panTro2.nscanGene.LENGTH)
```

`panTro2.refGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.refGene.LENGTH)
head(panTro2.refGene.LENGTH)
```

`panTro2.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.xenoRefGene.LENGTH)
head(panTro2.xenoRefGene.LENGTH)
```

```
petMar1.xenoRefGene.LENGTH
```

Transcript length data for the organism petMar

Description

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(petMar1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)
```

```
ponAbe2.ensGene.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)
```

`ponAbe2.geneSymbol.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)
```

`ponAbe2.genscan.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)
```

`ponAbe2.nscanGene.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.nscanGene.LENGTH)
head(ponAbe2.nscanGene.LENGTH)
```

`ponAbe2.refGene.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.refGene.LENGTH)
head(ponAbe2.refGene.LENGTH)
```

```
ponAbe2.xenoRefGene.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)
```

```
priPac1.xenoRefGene.LENGTH
```

Transcript length data for the organism priPac

Description

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(priPac1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)
```

```
rheMac2.ensGene.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)
```

```
rheMac2.geneid.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.geneid.LENGTH)
head(rheMac2.geneid.LENGTH)
```

```
rheMac2.geneSymbol.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)
```

```
rheMac2.nscanGene.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)
```

`rheMac2.refGene.LENGTH`*Transcript length data for the organism rheMac*

Description

rheMac2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)
```

`rheMac2.sgpGene.LENGTH`*Transcript length data for the organism rheMac*

Description

rheMac2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.sgpGene.LENGTH)
head(rheMac2.sgpGene.LENGTH)
```

`rheMac2.xenoRefGene.LENGTH`*Transcript length data for the organism rheMac*

Description

`rheMac2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)
```

`rn3.ensGene.LENGTH`*Transcript length data for the organism rn*

Description

`rn3.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(rn3, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.LENGTH)
```

rn3.geneid.LENGTH *Transcript length data for the organism rn*

Description

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.geneid.LENGTH)
head(rn3.geneid.LENGTH)
```

rn3.geneSymbol.LENGTH *Transcript length data for the organism rn*

Description

rn3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.geneSymbol.LENGTH)
head(rn3.geneSymbol.LENGTH)
```

rn3.genscan.LENGTH *Transcript length data for the organism rn*

Description

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn3, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)
```

rn3.knownGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

rn3.nscanGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

rn3.refGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

rn3.sgpGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)
```

rn3.xenoRefGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)
```

rn4.ensGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)
```

rn4.geneid.LENGTH *Transcript length data for the organism rn*

Description

rn4.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```

rn4.geneSymbol.LENGTH *Transcript length data for the organism rn*

Description

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

rn4.genscan.LENGTH *Transcript length data for the organism rn*

Description

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn4, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

rn4.knownGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.knownGene.LENGTH)
head(rn4.knownGene.LENGTH)
```

rn4.nscanGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)
```

rn4.refGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)
```

rn4.sgpGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

```
rn4.xenoRefGene.LENGTH
```

Transcript length data for the organism rn

Description

rn4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.xenoRefGene.LENGTH)
head(rn4.xenoRefGene.LENGTH)
```

```
sacCer1.ensGene.LENGTH
```

Transcript length data for the organism sacCer

Description

sacCer1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(sacCer1.ensGene.LENGTH)
head(sacCer1.ensGene.LENGTH)
```

`sacCer2.ensGene.LENGTH`*Transcript length data for the organism sacCer*

Description

sacCer2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)
```

`strPur1.geneSymbol.LENGTH`*Transcript length data for the organism strPur*

Description

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)
```

```
strPur1.genscan.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.genscan.LENGTH)
head(strPur1.genscan.LENGTH)
```

```
strPur1.refGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.refGene.LENGTH)
head(strPur1.refGene.LENGTH)
```

```
strPur1.xenoRefGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.xenoRefGene.LENGTH)
head(strPur1.xenoRefGene.LENGTH)
```

```
strPur2.geneSymbol.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.geneSymbol.LENGTH)
head(strPur2.geneSymbol.LENGTH)
```

```
strPur2.genscan.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.genscan.LENGTH)
head(strPur2.genscan.LENGTH)
```

```
strPur2.refGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.refGene.LENGTH)
head(strPur2.refGene.LENGTH)
```

```
strPur2.xenoRefGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)
```

```
supportedGeneIDs
```

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` argument of various functions. The `track` and `subtrack` columns are the names of the UCSC track/subtrack from which information is fetched.

The `GeneID` column lists the "full name" of the gene ID format where available.

The final column, headed `AvailableGenomes` lists the genomes for which there is a local copy of the length information available for the gene ID format listed in the `geneLenDataBase` package.

Value

A data.frame containing supported gene ID formats.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
supportedGeneIDs()
```

supportedGenomes	<i>Supported Genomes</i>
------------------	--------------------------

Description

Lists supported genomes

Usage

```
supportedGenomes()
```

Details

Uses the `ucscGenomes()` function from the `rtracklayer` package to obtain a list of genomes available from the UCSC genome browser. The `db` column lists genomes as they are provided to the genome argument of various functions.

The final column, headed `AvailableGeneIDs` lists the gene ID formats for which there is a local copy of the length information available for the genome listed in the `geneLenDataBase` package.

Value

A data.frame containing supported genomes.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
supportedGenomes()
```

`taeGut1.ensGene.LENGTH`*Transcript length data for the organism taeGut*

Description

taeGut1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)
```

`taeGut1.geneSymbol.LENGTH`*Transcript length data for the organism taeGut*

Description

taeGut1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)
```

```
taeGut1.genscan.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)
```

```
taeGut1.nscanGene.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)
```

`taeGut1.refGene.LENGTH`*Transcript length data for the organism taeGut*

Description

`taeGut1.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

`taeGut1.xenoRefGene.LENGTH`*Transcript length data for the organism taeGut*

Description

`taeGut1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

```
tetNig1.ensGene.LENGTH
```

Transcript length data for the organism tetNig

Description

tetNig1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

```
tetNig1.geneid.LENGTH
```

Transcript length data for the organism tetNig

Description

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

`tetNig1.genscan.LENGTH`*Transcript length data for the organism tetNig*

Description

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```

`tetNig1.nscanGene.LENGTH`*Transcript length data for the organism tetNig*

Description

tetNig1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

```
tetNig2.ensGene.LENGTH
```

Transcript length data for the organism tetNig

Description

tetNig2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig2.ensGene.LENGTH)
head(tetNig2.ensGene.LENGTH)
```

```
unfactor
```

Purge factors

Description

Removes all factors from a variable in a sensible way.

Usage

```
unfactor(var)
```

Arguments

var The variable from which you want the factors removed.

Details

As factors are their own type, to remove factors we must convert each level into another type. This is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be done without inducing NAs, otherwise it is coerced using `as.character`. Currently supported types are: `/codefactor`, `/codedata.frame` and `/codelist`.

Value

The variable with all factors converted to characters or numbers (see details).

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
#A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep='.')
x
unfactor(x)
```

```
#A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"), score <- factor(c(9, 7, 8, 9)), stringsAsFactors=TRUE)
x$player
x$score
y <- unfactor(x)
y$player
y$score
```

xenTro1.genscan.LENGTH

Transcript length data for the organism xenTro

Description

xenTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(xenTro1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro1.genscan.LENGTH)
head(xenTro1.genscan.LENGTH)
```

`xenTro2.ensGene.LENGTH`*Transcript length data for the organism xenTro*

Description

`xenTro2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.ensGene.LENGTH)
head(xenTro2.ensGene.LENGTH)
```

`xenTro2.geneSymbol.LENGTH`*Transcript length data for the organism xenTro*

Description

`xenTro2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.geneSymbol.LENGTH)
head(xenTro2.geneSymbol.LENGTH)
```

`xenTro2.genscan.LENGTH`*Transcript length data for the organism xenTro*

Description

`xenTro2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.genscan.LENGTH)
head(xenTro2.genscan.LENGTH)
```

`xenTro2.refGene.LENGTH`*Transcript length data for the organism xenTro*

Description

`xenTro2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.refGene.LENGTH)
head(xenTro2.refGene.LENGTH)
```

Index

*Topic **datasets**

anoCar1.ensGene.LENGTH, 8
anoCar1.genscan.LENGTH, 9
anoCar1.xenoRefGene.LENGTH, 10
anoGam1.ensGene.LENGTH, 10
anoGam1.geneid.LENGTH, 11
anoGam1.genscan.LENGTH, 11
apiMel1.genscan.LENGTH, 12
apiMel2.ensGene.LENGTH, 12
apiMel2.geneid.LENGTH, 13
apiMel2.genscan.LENGTH, 13
aplCal1.xenoRefGene.LENGTH, 14
bosTau2.geneid.LENGTH, 14
bosTau2.geneSymbol.LENGTH, 15
bosTau2.genscan.LENGTH, 15
bosTau2.refGene.LENGTH, 16
bosTau2.sgpGene.LENGTH, 16
bosTau3.ensGene.LENGTH, 17
bosTau3.geneid.LENGTH, 17
bosTau3.geneSymbol.LENGTH, 18
bosTau3.genscan.LENGTH, 18
bosTau3.refGene.LENGTH, 19
bosTau3.sgpGene.LENGTH, 19
bosTau4.ensGene.LENGTH, 20
bosTau4.geneSymbol.LENGTH, 20
bosTau4.genscan.LENGTH, 21
bosTau4.nscanGene.LENGTH, 21
bosTau4.refGene.LENGTH, 22
braFlo1.xenoRefGene.LENGTH, 22
caeJap1.xenoRefGene.LENGTH, 23
caePb1.xenoRefGene.LENGTH, 23
caePb2.xenoRefGene.LENGTH, 24
caeRem2.xenoRefGene.LENGTH, 24
caeRem3.xenoRefGene.LENGTH, 25
calJac1.genscan.LENGTH, 25
calJac1.nscanGene.LENGTH, 26
calJac1.xenoRefGene.LENGTH, 26
canFam1.ensGene.LENGTH, 27
canFam1.geneSymbol.LENGTH, 27

canFam1.genscan.LENGTH, 28
canFam1.nscanGene.LENGTH, 28
canFam1.refGene.LENGTH, 29
canFam1.xenoRefGene.LENGTH, 29
canFam2.ensGene.LENGTH, 30
canFam2.geneSymbol.LENGTH, 30
canFam2.genscan.LENGTH, 31
canFam2.nscanGene.LENGTH, 31
canFam2.refGene.LENGTH, 32
canFam2.xenoRefGene.LENGTH, 32
cavPor3.ensGene.LENGTH, 33
cavPor3.genscan.LENGTH, 33
cavPor3.nscanGene.LENGTH, 34
cavPor3.xenoRefGene.LENGTH, 34
cb1.xenoRefGene.LENGTH, 35
cb3.xenoRefGene.LENGTH, 35
ce2.geneid.LENGTH, 36
ce2.geneSymbol.LENGTH, 36
ce2.refGene.LENGTH, 37
ce4.geneSymbol.LENGTH, 37
ce4.refGene.LENGTH, 38
ce4.xenoRefGene.LENGTH, 38
ce6.ensGene.LENGTH, 39
ce6.geneSymbol.LENGTH, 39
ce6.refGene.LENGTH, 40
ce6.xenoRefGene.LENGTH, 40
ci1.geneSymbol.LENGTH, 41
ci1.refGene.LENGTH, 41
ci1.xenoRefGene.LENGTH, 42
ci2.ensGene.LENGTH, 42
ci2.geneSymbol.LENGTH, 43
ci2.refGene.LENGTH, 43
ci2.xenoRefGene.LENGTH, 44
danRer3.ensGene.LENGTH, 44
danRer3.geneSymbol.LENGTH, 45
danRer3.refGene.LENGTH, 45
danRer4.ensGene.LENGTH, 46
danRer4.geneSymbol.LENGTH, 46
danRer4.genscan.LENGTH, 47

danRer4.nscanGene.LENGTH, 47
danRer4.refGene.LENGTH, 48
danRer5.ensGene.LENGTH, 48
danRer5.geneSymbol.LENGTH, 49
danRer5.refGene.LENGTH, 49
danRer5.vegaGene.LENGTH, 50
danRer5.vegaPseudoGene.LENGTH, 50
danRer6.ensGene.LENGTH, 51
danRer6.geneSymbol.LENGTH, 51
danRer6.refGene.LENGTH, 52
danRer6.xenoRefGene.LENGTH, 52
dm1.geneSymbol.LENGTH, 53
dm1.genscan.LENGTH, 53
dm1.refGene.LENGTH, 54
dm2.geneid.LENGTH, 54
dm2.geneSymbol.LENGTH, 55
dm2.genscan.LENGTH, 55
dm2.nscanGene.LENGTH, 56
dm2.refGene.LENGTH, 56
dm3.geneSymbol.LENGTH, 57
dm3.nscanPasaGene.LENGTH, 57
dm3.refGene.LENGTH, 58
dp2.genscan.LENGTH, 58
dp2.xenoRefGene.LENGTH, 59
dp3.geneid.LENGTH, 59
dp3.genscan.LENGTH, 60
dp3.xenoRefGene.LENGTH, 60
droAna1.geneid.LENGTH, 61
droAna1.genscan.LENGTH, 61
droAna1.xenoRefGene.LENGTH, 62
droAna2.genscan.LENGTH, 62
droAna2.xenoRefGene.LENGTH, 63
droEre1.genscan.LENGTH, 63
droEre1.xenoRefGene.LENGTH, 64
droGri1.genscan.LENGTH, 64
droGri1.xenoRefGene.LENGTH, 65
droMoj1.geneid.LENGTH, 65
droMoj1.genscan.LENGTH, 66
droMoj1.xenoRefGene.LENGTH, 66
droMoj2.genscan.LENGTH, 67
droMoj2.xenoRefGene.LENGTH, 67
droPer1.genscan.LENGTH, 68
droPer1.xenoRefGene.LENGTH, 68
droSec1.genscan.LENGTH, 69
droSec1.xenoRefGene.LENGTH, 69
droSim1.geneid.LENGTH, 70
droSim1.genscan.LENGTH, 70
droSim1.xenoRefGene.LENGTH, 71
droVir1.geneid.LENGTH, 71
droVir1.genscan.LENGTH, 72
droVir1.xenoRefGene.LENGTH, 72
droVir2.genscan.LENGTH, 73
droVir2.xenoRefGene.LENGTH, 73
droYak1.geneid.LENGTH, 74
droYak1.genscan.LENGTH, 74
droYak1.xenoRefGene.LENGTH, 75
droYak2.genscan.LENGTH, 75
droYak2.xenoRefGene.LENGTH, 76
equCab1.geneid.LENGTH, 76
equCab1.geneSymbol.LENGTH, 77
equCab1.nscanGene.LENGTH, 77
equCab1.refGene.LENGTH, 78
equCab1.sgpGene.LENGTH, 78
equCab2.ensGene.LENGTH, 79
equCab2.geneSymbol.LENGTH, 79
equCab2.nscanGene.LENGTH, 80
equCab2.refGene.LENGTH, 80
equCab2.xenoRefGene.LENGTH, 81
felCat3.ensGene.LENGTH, 81
felCat3.geneid.LENGTH, 82
felCat3.geneSymbol.LENGTH, 82
felCat3.genscan.LENGTH, 83
felCat3.nscanGene.LENGTH, 83
felCat3.refGene.LENGTH, 84
felCat3.sgpGene.LENGTH, 84
felCat3.xenoRefGene.LENGTH, 85
fr1.ensGene.LENGTH, 85
fr1.genscan.LENGTH, 86
fr2.ensGene.LENGTH, 86
galGal2.ensGene.LENGTH, 87
galGal2.geneid.LENGTH, 87
galGal2.geneSymbol.LENGTH, 88
galGal2.genscan.LENGTH, 88
galGal2.refGene.LENGTH, 89
galGal2.sgpGene.LENGTH, 89
galGal3.ensGene.LENGTH, 90
galGal3.geneSymbol.LENGTH, 90
galGal3.genscan.LENGTH, 91
galGal3.nscanGene.LENGTH, 91
galGal3.refGene.LENGTH, 92
galGal3.xenoRefGene.LENGTH, 92
gasAcu1.ensGene.LENGTH, 93
gasAcu1.nscanGene.LENGTH, 93
hg16.acembly.LENGTH, 94
hg16.ensGene.LENGTH, 94
hg16.exoniphy.LENGTH, 95

hg16.geneid.LENGTH, 95
 hg16.geneSymbol.LENGTH, 96
 hg16.genscan.LENGTH, 96
 hg16.knownGene.LENGTH, 97
 hg16.refGene.LENGTH, 97
 hg16.sgpGene.LENGTH, 98
 hg17.acembly.LENGTH, 98
 hg17.acescan.LENGTH, 99
 hg17.ccdsGene.LENGTH, 99
 hg17.ensGene.LENGTH, 100
 hg17.exoniphy.LENGTH, 100
 hg17.geneid.LENGTH, 101
 hg17.geneSymbol.LENGTH, 101
 hg17.genscan.LENGTH, 102
 hg17.knownGene.LENGTH, 102
 hg17.refGene.LENGTH, 103
 hg17.sgpGene.LENGTH, 103
 hg17.vegaGene.LENGTH, 104
 hg17.vegaPseudoGene.LENGTH, 104
 hg17.xenoRefGene.LENGTH, 105
 hg18.acembly.LENGTH, 105
 hg18.acescan.LENGTH, 106
 hg18.ccdsGene.LENGTH, 106
 hg18.ensGene.LENGTH, 107
 hg18.exoniphy.LENGTH, 107
 hg18.geneid.LENGTH, 108
 hg18.geneSymbol.LENGTH, 108
 hg18.genscan.LENGTH, 109
 hg18.knownGene.LENGTH, 109
 hg18.knownGeneOld3.LENGTH, 110
 hg18.refGene.LENGTH, 110
 hg18.sgpGene.LENGTH, 111
 hg18.sibGene.LENGTH, 111
 hg18.xenoRefGene.LENGTH, 112
 hg19.ccdsGene.LENGTH, 112
 hg19.ensGene.LENGTH, 113
 hg19.exoniphy.LENGTH, 113
 hg19.geneSymbol.LENGTH, 114
 hg19.knownGene.LENGTH, 114
 hg19.nscanGene.LENGTH, 115
 hg19.refGene.LENGTH, 115
 hg19.xenoRefGene.LENGTH, 116
 loxAfr3.xenoRefGene.LENGTH, 116
 mm7.ensGene.LENGTH, 117
 mm7.geneid.LENGTH, 117
 mm7.geneSymbol.LENGTH, 118
 mm7.genscan.LENGTH, 118
 mm7.knownGene.LENGTH, 119
 mm7.refGene.LENGTH, 119
 mm7.sgpGene.LENGTH, 120
 mm7.xenoRefGene.LENGTH, 120
 mm8.ccdsGene.LENGTH, 121
 mm8.ensGene.LENGTH, 121
 mm8.geneid.LENGTH, 122
 mm8.geneSymbol.LENGTH, 122
 mm8.genscan.LENGTH, 123
 mm8.knownGene.LENGTH, 123
 mm8.nscanGene.LENGTH, 124
 mm8.refGene.LENGTH, 124
 mm8.sgpGene.LENGTH, 125
 mm8.sibGene.LENGTH, 125
 mm8.xenoRefGene.LENGTH, 126
 mm9.acembly.LENGTH, 126
 mm9.ccdsGene.LENGTH, 127
 mm9.ensGene.LENGTH, 127
 mm9.exoniphy.LENGTH, 128
 mm9.geneid.LENGTH, 128
 mm9.geneSymbol.LENGTH, 129
 mm9.genscan.LENGTH, 129
 mm9.knownGene.LENGTH, 130
 mm9.nscanGene.LENGTH, 130
 mm9.refGene.LENGTH, 131
 mm9.sgpGene.LENGTH, 131
 mm9.xenoRefGene.LENGTH, 132
 monDom1.genscan.LENGTH, 132
 monDom4.ensGene.LENGTH, 133
 monDom4.geneSymbol.LENGTH, 133
 monDom4.genscan.LENGTH, 134
 monDom4.nscanGene.LENGTH, 134
 monDom4.refGene.LENGTH, 135
 monDom4.xenoRefGene.LENGTH, 135
 monDom5.ensGene.LENGTH, 136
 monDom5.geneSymbol.LENGTH, 136
 monDom5.genscan.LENGTH, 137
 monDom5.nscanGene.LENGTH, 137
 monDom5.refGene.LENGTH, 138
 monDom5.xenoRefGene.LENGTH, 138
 ornAna1.ensGene.LENGTH, 139
 ornAna1.geneSymbol.LENGTH, 139
 ornAna1.refGene.LENGTH, 140
 ornAna1.xenoRefGene.LENGTH, 140
 oryLat2.ensGene.LENGTH, 141
 oryLat2.geneSymbol.LENGTH, 141
 oryLat2.refGene.LENGTH, 142
 oryLat2.xenoRefGene.LENGTH, 142
 panTro1.ensGene.LENGTH, 143

- panTro1.geneid.LENGTH, 143
panTro1.genscan.LENGTH, 144
panTro1.xenoRefGene.LENGTH, 144
panTro2.ensGene.LENGTH, 145
panTro2.geneSymbol.LENGTH, 145
panTro2.genscan.LENGTH, 146
panTro2.nscanGene.LENGTH, 146
panTro2.refGene.LENGTH, 147
panTro2.xenoRefGene.LENGTH, 147
petMar1.xenoRefGene.LENGTH, 148
ponAbe2.ensGene.LENGTH, 148
ponAbe2.geneSymbol.LENGTH, 149
ponAbe2.genscan.LENGTH, 149
ponAbe2.nscanGene.LENGTH, 150
ponAbe2.refGene.LENGTH, 150
ponAbe2.xenoRefGene.LENGTH, 151
priPac1.xenoRefGene.LENGTH, 151
rheMac2.ensGene.LENGTH, 152
rheMac2.geneid.LENGTH, 152
rheMac2.geneSymbol.LENGTH, 153
rheMac2.nscanGene.LENGTH, 153
rheMac2.refGene.LENGTH, 154
rheMac2.sgpGene.LENGTH, 154
rheMac2.xenoRefGene.LENGTH, 155
rn3.ensGene.LENGTH, 155
rn3.geneid.LENGTH, 156
rn3.geneSymbol.LENGTH, 156
rn3.genscan.LENGTH, 157
rn3.knownGene.LENGTH, 157
rn3.nscanGene.LENGTH, 158
rn3.refGene.LENGTH, 158
rn3.sgpGene.LENGTH, 159
rn3.xenoRefGene.LENGTH, 159
rn4.ensGene.LENGTH, 160
rn4.geneid.LENGTH, 160
rn4.geneSymbol.LENGTH, 161
rn4.genscan.LENGTH, 161
rn4.knownGene.LENGTH, 162
rn4.nscanGene.LENGTH, 162
rn4.refGene.LENGTH, 163
rn4.sgpGene.LENGTH, 163
rn4.xenoRefGene.LENGTH, 164
sacCer1.ensGene.LENGTH, 164
sacCer2.ensGene.LENGTH, 165
strPur1.geneSymbol.LENGTH, 165
strPur1.genscan.LENGTH, 166
strPur1.refGene.LENGTH, 166
strPur1.xenoRefGene.LENGTH, 167
strPur2.geneSymbol.LENGTH, 167
strPur2.genscan.LENGTH, 168
strPur2.refGene.LENGTH, 168
strPur2.xenoRefGene.LENGTH, 169
taeGut1.ensGene.LENGTH, 171
taeGut1.geneSymbol.LENGTH, 171
taeGut1.genscan.LENGTH, 172
taeGut1.nscanGene.LENGTH, 172
taeGut1.refGene.LENGTH, 173
taeGut1.xenoRefGene.LENGTH, 173
tetNig1.ensGene.LENGTH, 174
tetNig1.geneid.LENGTH, 174
tetNig1.genscan.LENGTH, 175
tetNig1.nscanGene.LENGTH, 175
tetNig2.ensGene.LENGTH, 176
xenTro1.genscan.LENGTH, 177
xenTro2.ensGene.LENGTH, 178
xenTro2.geneSymbol.LENGTH, 178
xenTro2.genscan.LENGTH, 179
xenTro2.refGene.LENGTH, 179
anoCar1.ensGene.LENGTH, 8
anoCar1.genscan.LENGTH, 9
anoCar1.xenoRefGene.LENGTH, 10
anoGam1.ensGene.LENGTH, 10
anoGam1.geneid.LENGTH, 11
anoGam1.genscan.LENGTH, 11
apiMe11.genscan.LENGTH, 12
apiMe12.ensGene.LENGTH, 12
apiMe12.geneid.LENGTH, 13
apiMe12.genscan.LENGTH, 13
aplCa11.xenoRefGene.LENGTH, 14
bosTau2.geneid.LENGTH, 14
bosTau2.geneSymbol.LENGTH, 15
bosTau2.genscan.LENGTH, 15
bosTau2.refGene.LENGTH, 16
bosTau2.sgpGene.LENGTH, 16
bosTau3.ensGene.LENGTH, 17
bosTau3.geneid.LENGTH, 17
bosTau3.geneSymbol.LENGTH, 18
bosTau3.genscan.LENGTH, 18
bosTau3.refGene.LENGTH, 19
bosTau3.sgpGene.LENGTH, 19
bosTau4.ensGene.LENGTH, 20
bosTau4.geneSymbol.LENGTH, 20
bosTau4.genscan.LENGTH, 21
bosTau4.nscanGene.LENGTH, 21
bosTau4.refGene.LENGTH, 22

- braFlo1.xenoRefGene.LENGTH, 22
- caeJap1.xenoRefGene.LENGTH, 23
- caePb1.xenoRefGene.LENGTH, 23
- caePb2.xenoRefGene.LENGTH, 24
- caeRem2.xenoRefGene.LENGTH, 24
- caeRem3.xenoRefGene.LENGTH, 25
- calJac1.genscan.LENGTH, 25
- calJac1.nscanGene.LENGTH, 26
- calJac1.xenoRefGene.LENGTH, 26
- canFam1.ensGene.LENGTH, 27
- canFam1.geneSymbol.LENGTH, 27
- canFam1.genscan.LENGTH, 28
- canFam1.nscanGene.LENGTH, 28
- canFam1.refGene.LENGTH, 29
- canFam1.xenoRefGene.LENGTH, 29
- canFam2.ensGene.LENGTH, 30
- canFam2.geneSymbol.LENGTH, 30
- canFam2.genscan.LENGTH, 31
- canFam2.nscanGene.LENGTH, 31
- canFam2.refGene.LENGTH, 32
- canFam2.xenoRefGene.LENGTH, 32
- cavPor3.ensGene.LENGTH, 33
- cavPor3.genscan.LENGTH, 33
- cavPor3.nscanGene.LENGTH, 34
- cavPor3.xenoRefGene.LENGTH, 34
- cb1.xenoRefGene.LENGTH, 35
- cb3.xenoRefGene.LENGTH, 35
- ce2.geneid.LENGTH, 36
- ce2.geneSymbol.LENGTH, 36
- ce2.refGene.LENGTH, 37
- ce4.geneSymbol.LENGTH, 37
- ce4.refGene.LENGTH, 38
- ce4.xenoRefGene.LENGTH, 38
- ce6.ensGene.LENGTH, 39
- ce6.geneSymbol.LENGTH, 39
- ce6.refGene.LENGTH, 40
- ce6.xenoRefGene.LENGTH, 40
- ci1.geneSymbol.LENGTH, 41
- ci1.refGene.LENGTH, 41
- ci1.xenoRefGene.LENGTH, 42
- ci2.ensGene.LENGTH, 42
- ci2.geneSymbol.LENGTH, 43
- ci2.refGene.LENGTH, 43
- ci2.xenoRefGene.LENGTH, 44
- danRer3.ensGene.LENGTH, 44
- danRer3.geneSymbol.LENGTH, 45
- danRer3.refGene.LENGTH, 45
- danRer4.ensGene.LENGTH, 46
- danRer4.geneSymbol.LENGTH, 46
- danRer4.genscan.LENGTH, 47
- danRer4.nscanGene.LENGTH, 47
- danRer4.refGene.LENGTH, 48
- danRer5.ensGene.LENGTH, 48
- danRer5.geneSymbol.LENGTH, 49
- danRer5.refGene.LENGTH, 49
- danRer5.vegaGene.LENGTH, 50
- danRer5.vegaPseudoGene.LENGTH, 50
- danRer6.ensGene.LENGTH, 51
- danRer6.geneSymbol.LENGTH, 51
- danRer6.refGene.LENGTH, 52
- danRer6.xenoRefGene.LENGTH, 52
- dm1.geneSymbol.LENGTH, 53
- dm1.genscan.LENGTH, 53
- dm1.refGene.LENGTH, 54
- dm2.geneid.LENGTH, 54
- dm2.geneSymbol.LENGTH, 55
- dm2.genscan.LENGTH, 55
- dm2.nscanGene.LENGTH, 56
- dm2.refGene.LENGTH, 56
- dm3.geneSymbol.LENGTH, 57
- dm3.nscanPasaGene.LENGTH, 57
- dm3.refGene.LENGTH, 58
- downloadLengthFromUCSC, 9–169, 171–179
- dp2.genscan.LENGTH, 58
- dp2.xenoRefGene.LENGTH, 59
- dp3.geneid.LENGTH, 59
- dp3.genscan.LENGTH, 60
- dp3.xenoRefGene.LENGTH, 60
- droAna1.geneid.LENGTH, 61
- droAna1.genscan.LENGTH, 61
- droAna1.xenoRefGene.LENGTH, 62
- droAna2.genscan.LENGTH, 62
- droAna2.xenoRefGene.LENGTH, 63
- droEre1.genscan.LENGTH, 63
- droEre1.xenoRefGene.LENGTH, 64
- droGri1.genscan.LENGTH, 64
- droGri1.xenoRefGene.LENGTH, 65
- droMoj1.geneid.LENGTH, 65
- droMoj1.genscan.LENGTH, 66
- droMoj1.xenoRefGene.LENGTH, 66
- droMoj2.genscan.LENGTH, 67
- droMoj2.xenoRefGene.LENGTH, 67
- droPer1.genscan.LENGTH, 68
- droPer1.xenoRefGene.LENGTH, 68
- droSec1.genscan.LENGTH, 69

- droSec1.xenoRefGene.LENGTH, 69
droSim1.geneid.LENGTH, 70
droSim1.genscan.LENGTH, 70
droSim1.xenoRefGene.LENGTH, 71
droVir1.geneid.LENGTH, 71
droVir1.genscan.LENGTH, 72
droVir1.xenoRefGene.LENGTH, 72
droVir2.genscan.LENGTH, 73
droVir2.xenoRefGene.LENGTH, 73
droYak1.geneid.LENGTH, 74
droYak1.genscan.LENGTH, 74
droYak1.xenoRefGene.LENGTH, 75
droYak2.genscan.LENGTH, 75
droYak2.xenoRefGene.LENGTH, 76
- equCab1.geneid.LENGTH, 76
equCab1.geneSymbol.LENGTH, 77
equCab1.nscanGene.LENGTH, 77
equCab1.refGene.LENGTH, 78
equCab1.sgpGene.LENGTH, 78
equCab2.ensGene.LENGTH, 79
equCab2.geneSymbol.LENGTH, 79
equCab2.nscanGene.LENGTH, 80
equCab2.refGene.LENGTH, 80
equCab2.xenoRefGene.LENGTH, 81
- felCat3.ensGene.LENGTH, 81
felCat3.geneid.LENGTH, 82
felCat3.geneSymbol.LENGTH, 82
felCat3.genscan.LENGTH, 83
felCat3.nscanGene.LENGTH, 83
felCat3.refGene.LENGTH, 84
felCat3.sgpGene.LENGTH, 84
felCat3.xenoRefGene.LENGTH, 85
fr1.ensGene.LENGTH, 85
fr1.genscan.LENGTH, 86
fr2.ensGene.LENGTH, 86
- galGal2.ensGene.LENGTH, 87
galGal2.geneid.LENGTH, 87
galGal2.geneSymbol.LENGTH, 88
galGal2.genscan.LENGTH, 88
galGal2.refGene.LENGTH, 89
galGal2.sgpGene.LENGTH, 89
galGal3.ensGene.LENGTH, 90
galGal3.geneSymbol.LENGTH, 90
galGal3.genscan.LENGTH, 91
galGal3.nscanGene.LENGTH, 91
galGal3.refGene.LENGTH, 92
- galGal3.xenoRefGene.LENGTH, 92
gasAcu1.ensGene.LENGTH, 93
gasAcu1.nscanGene.LENGTH, 93
- hg16.acembly.LENGTH, 94
hg16.ensGene.LENGTH, 94
hg16.exoniphy.LENGTH, 95
hg16.geneid.LENGTH, 95
hg16.geneSymbol.LENGTH, 96
hg16.genscan.LENGTH, 96
hg16.knownGene.LENGTH, 97
hg16.refGene.LENGTH, 97
hg16.sgpGene.LENGTH, 98
hg17.acembly.LENGTH, 98
hg17.acescan.LENGTH, 99
hg17.ccdsGene.LENGTH, 99
hg17.ensGene.LENGTH, 100
hg17.exoniphy.LENGTH, 100
hg17.geneid.LENGTH, 101
hg17.geneSymbol.LENGTH, 101
hg17.genscan.LENGTH, 102
hg17.knownGene.LENGTH, 102
hg17.refGene.LENGTH, 103
hg17.sgpGene.LENGTH, 103
hg17.vegaGene.LENGTH, 104
hg17.vegaPseudoGene.LENGTH, 104
hg17.xenoRefGene.LENGTH, 105
hg18.acembly.LENGTH, 105
hg18.acescan.LENGTH, 106
hg18.ccdsGene.LENGTH, 106
hg18.ensGene.LENGTH, 107
hg18.exoniphy.LENGTH, 107
hg18.geneid.LENGTH, 108
hg18.geneSymbol.LENGTH, 108
hg18.genscan.LENGTH, 109
hg18.knownGene.LENGTH, 109
hg18.knownGeneOld3.LENGTH, 110
hg18.refGene.LENGTH, 110
hg18.sgpGene.LENGTH, 111
hg18.sibGene.LENGTH, 111
hg18.xenoRefGene.LENGTH, 112
hg19.ccdsGene.LENGTH, 112
hg19.ensGene.LENGTH, 113
hg19.exoniphy.LENGTH, 113
hg19.geneSymbol.LENGTH, 114
hg19.knownGene.LENGTH, 114
hg19.nscanGene.LENGTH, 115
hg19.refGene.LENGTH, 115
hg19.xenoRefGene.LENGTH, 116

- loxAfr3.xenoRefGene.LENGTH, 116
 mm7.ensGene.LENGTH, 117
 mm7.geneid.LENGTH, 117
 mm7.geneSymbol.LENGTH, 118
 mm7.genscan.LENGTH, 118
 mm7.knownGene.LENGTH, 119
 mm7.refGene.LENGTH, 119
 mm7.sgpGene.LENGTH, 120
 mm7.xenoRefGene.LENGTH, 120
 mm8.ccdsGene.LENGTH, 121
 mm8.ensGene.LENGTH, 121
 mm8.geneid.LENGTH, 122
 mm8.geneSymbol.LENGTH, 122
 mm8.genscan.LENGTH, 123
 mm8.knownGene.LENGTH, 123
 mm8.nscanGene.LENGTH, 124
 mm8.refGene.LENGTH, 124
 mm8.sgpGene.LENGTH, 125
 mm8.sibGene.LENGTH, 125
 mm8.xenoRefGene.LENGTH, 126
 mm9.acembly.LENGTH, 126
 mm9.ccdsGene.LENGTH, 127
 mm9.ensGene.LENGTH, 127
 mm9.exoniphy.LENGTH, 128
 mm9.geneid.LENGTH, 128
 mm9.geneSymbol.LENGTH, 129
 mm9.genscan.LENGTH, 129
 mm9.knownGene.LENGTH, 130
 mm9.nscanGene.LENGTH, 130
 mm9.refGene.LENGTH, 131
 mm9.sgpGene.LENGTH, 131
 mm9.xenoRefGene.LENGTH, 132
 monDom1.genscan.LENGTH, 132
 monDom4.ensGene.LENGTH, 133
 monDom4.geneSymbol.LENGTH, 133
 monDom4.genscan.LENGTH, 134
 monDom4.nscanGene.LENGTH, 134
 monDom4.refGene.LENGTH, 135
 monDom4.xenoRefGene.LENGTH, 135
 monDom5.ensGene.LENGTH, 136
 monDom5.geneSymbol.LENGTH, 136
 monDom5.genscan.LENGTH, 137
 monDom5.nscanGene.LENGTH, 137
 monDom5.refGene.LENGTH, 138
 monDom5.xenoRefGene.LENGTH, 138
 ornAna1.ensGene.LENGTH, 139
 ornAna1.geneSymbol.LENGTH, 139
 ornAna1.refGene.LENGTH, 140
 ornAna1.xenoRefGene.LENGTH, 140
 oryLat2.ensGene.LENGTH, 141
 oryLat2.geneSymbol.LENGTH, 141
 oryLat2.refGene.LENGTH, 142
 oryLat2.xenoRefGene.LENGTH, 142
 panTro1.ensGene.LENGTH, 143
 panTro1.geneid.LENGTH, 143
 panTro1.genscan.LENGTH, 144
 panTro1.xenoRefGene.LENGTH, 144
 panTro2.ensGene.LENGTH, 145
 panTro2.geneSymbol.LENGTH, 145
 panTro2.genscan.LENGTH, 146
 panTro2.nscanGene.LENGTH, 146
 panTro2.refGene.LENGTH, 147
 panTro2.xenoRefGene.LENGTH, 147
 petMar1.xenoRefGene.LENGTH, 148
 ponAbe2.ensGene.LENGTH, 148
 ponAbe2.geneSymbol.LENGTH, 149
 ponAbe2.genscan.LENGTH, 149
 ponAbe2.nscanGene.LENGTH, 150
 ponAbe2.refGene.LENGTH, 150
 ponAbe2.xenoRefGene.LENGTH, 151
 priPac1.xenoRefGene.LENGTH, 151
 rheMac2.ensGene.LENGTH, 152
 rheMac2.geneid.LENGTH, 152
 rheMac2.geneSymbol.LENGTH, 153
 rheMac2.nscanGene.LENGTH, 153
 rheMac2.refGene.LENGTH, 154
 rheMac2.sgpGene.LENGTH, 154
 rheMac2.xenoRefGene.LENGTH, 155
 rn3.ensGene.LENGTH, 155
 rn3.geneid.LENGTH, 156
 rn3.geneSymbol.LENGTH, 156
 rn3.genscan.LENGTH, 157
 rn3.knownGene.LENGTH, 157
 rn3.nscanGene.LENGTH, 158
 rn3.refGene.LENGTH, 158
 rn3.sgpGene.LENGTH, 159
 rn3.xenoRefGene.LENGTH, 159
 rn4.ensGene.LENGTH, 160
 rn4.geneid.LENGTH, 160
 rn4.geneSymbol.LENGTH, 161
 rn4.genscan.LENGTH, 161
 rn4.knownGene.LENGTH, 162
 rn4.nscanGene.LENGTH, 162
 rn4.refGene.LENGTH, 163

rn4.sgpGene.LENGTH, [163](#)
rn4.xenoRefGene.LENGTH, [164](#)

sacCer1.ensGene.LENGTH, [164](#)
sacCer2.ensGene.LENGTH, [165](#)
strPur1.geneSymbol.LENGTH, [165](#)
strPur1.genscan.LENGTH, [166](#)
strPur1.refGene.LENGTH, [166](#)
strPur1.xenoRefGene.LENGTH, [167](#)
strPur2.geneSymbol.LENGTH, [167](#)
strPur2.genscan.LENGTH, [168](#)
strPur2.refGene.LENGTH, [168](#)
strPur2.xenoRefGene.LENGTH, [169](#)
supportedGeneIDs, [169](#)
supportedGenomes, [170](#)

taeGut1.ensGene.LENGTH, [171](#)
taeGut1.geneSymbol.LENGTH, [171](#)
taeGut1.genscan.LENGTH, [172](#)
taeGut1.nscanGene.LENGTH, [172](#)
taeGut1.refGene.LENGTH, [173](#)
taeGut1.xenoRefGene.LENGTH, [173](#)
tetNig1.ensGene.LENGTH, [174](#)
tetNig1.geneid.LENGTH, [174](#)
tetNig1.genscan.LENGTH, [175](#)
tetNig1.nscanGene.LENGTH, [175](#)
tetNig2.ensGene.LENGTH, [176](#)

unfactor, [176](#)

xenTro1.genscan.LENGTH, [177](#)
xenTro2.ensGene.LENGTH, [178](#)
xenTro2.geneSymbol.LENGTH, [178](#)
xenTro2.genscan.LENGTH, [179](#)
xenTro2.refGene.LENGTH, [179](#)