

Package ‘geneLenDataBase’

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Title Lengths of mRNA transcripts for a number of genomes

Author Matthew Young

Maintainer Matthew Young <myoung@wehi.edu.au>, Nadia Davidson
<nadia.davidson@mcri.edu.au>

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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

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R topics documented:

anoCar1.ensGene.LENGTH	8
anoCar1.genscan.LENGTH	8
anoCar1.xenoRefGene.LENGTH	9
anoGam1.ensGene.LENGTH	9
anoGam1.geneid.LENGTH	10
anoGam1.genscan.LENGTH	10
apiMel1.genscan.LENGTH	11
apiMel2.ensGene.LENGTH	11
apiMel2.geneid.LENGTH	12
apiMel2.genscan.LENGTH	12
aplCal1.xenoRefGene.LENGTH	13
bosTau2.geneid.LENGTH	13
bosTau2.geneSymbol.LENGTH	14
bosTau2.genscan.LENGTH	14
bosTau2.refGene.LENGTH	15
bosTau2.sgpGene.LENGTH	15
bosTau3.ensGene.LENGTH	16

bosTau3.geneid.LENGTH	16
bosTau3.geneSymbol.LENGTH	17
bosTau3.genscan.LENGTH	17
bosTau3.refGene.LENGTH	18
bosTau3.sgpGene.LENGTH	18
bosTau4.ensGene.LENGTH	19
bosTau4.geneSymbol.LENGTH	19
bosTau4.genscan.LENGTH	20
bosTau4.nscanGene.LENGTH	20
bosTau4.refGene.LENGTH	21
braFlo1.xenoRefGene.LENGTH	21
caeJap1.xenoRefGene.LENGTH	22
caePb1.xenoRefGene.LENGTH	22
caePb2.xenoRefGene.LENGTH	23
caeRem2.xenoRefGene.LENGTH	23
caeRem3.xenoRefGene.LENGTH	24
calJac1.genscan.LENGTH	24
calJac1.nscanGene.LENGTH	25
calJac1.xenoRefGene.LENGTH	25
canFam1.ensGene.LENGTH	26
canFam1.geneSymbol.LENGTH	26
canFam1.genscan.LENGTH	27
canFam1.nscanGene.LENGTH	27
canFam1.refGene.LENGTH	28
canFam1.xenoRefGene.LENGTH	28
canFam2.ensGene.LENGTH	29
canFam2.geneSymbol.LENGTH	29
canFam2.genscan.LENGTH	30
canFam2.nscanGene.LENGTH	30
canFam2.refGene.LENGTH	31
canFam2.xenoRefGene.LENGTH	31
cavPor3.ensGene.LENGTH	32
cavPor3.genscan.LENGTH	32
cavPor3.nscanGene.LENGTH	33
cavPor3.xenoRefGene.LENGTH	33
cb1.xenoRefGene.LENGTH	34
cb3.xenoRefGene.LENGTH	34
ce2.geneid.LENGTH	35
ce2.geneSymbol.LENGTH	35
ce2.refGene.LENGTH	36
ce4.geneSymbol.LENGTH	36
ce4.refGene.LENGTH	37
ce4.xenoRefGene.LENGTH	37
ce6.ensGene.LENGTH	38
ce6.geneSymbol.LENGTH	38
ce6.refGene.LENGTH	39
ce6.xenoRefGene.LENGTH	39
ci1.geneSymbol.LENGTH	40
ci1.refGene.LENGTH	40
ci1.xenoRefGene.LENGTH	41
ci2.ensGene.LENGTH	41
ci2.geneSymbol.LENGTH	42

ci2.refGene.LENGTH	42
ci2.xenoRefGene.LENGTH	43
danRer3.ensGene.LENGTH	43
danRer3.geneSymbol.LENGTH	44
danRer3.refGene.LENGTH	44
danRer4.ensGene.LENGTH	45
danRer4.geneSymbol.LENGTH	45
danRer4.genscan.LENGTH	46
danRer4.nscanGene.LENGTH	46
danRer4.refGene.LENGTH	47
danRer5.ensGene.LENGTH	47
danRer5.geneSymbol.LENGTH	48
danRer5.refGene.LENGTH	48
danRer5.vegaGene.LENGTH	49
danRer5.vegaPseudoGene.LENGTH	49
danRer6.ensGene.LENGTH	50
danRer6.geneSymbol.LENGTH	50
danRer6.refGene.LENGTH	51
danRer6.xenoRefGene.LENGTH	51
dm1.geneSymbol.LENGTH	52
dm1.genscan.LENGTH	52
dm1.refGene.LENGTH	53
dm2.geneid.LENGTH	53
dm2.geneSymbol.LENGTH	54
dm2.genscan.LENGTH	54
dm2.nscanGene.LENGTH	55
dm2.refGene.LENGTH	55
dm3.geneSymbol.LENGTH	56
dm3.nscanPasaGene.LENGTH	56
dm3.refGene.LENGTH	57
dp2.genscan.LENGTH	57
dp2.xenoRefGene.LENGTH	58
dp3.geneid.LENGTH	58
dp3.genscan.LENGTH	59
dp3.xenoRefGene.LENGTH	59
droAna1.geneid.LENGTH	60
droAna1.genscan.LENGTH	60
droAna1.xenoRefGene.LENGTH	61
droAna2.genscan.LENGTH	61
droAna2.xenoRefGene.LENGTH	62
droEre1.genscan.LENGTH	62
droEre1.xenoRefGene.LENGTH	63
droGri1.genscan.LENGTH	63
droGri1.xenoRefGene.LENGTH	64
droMoj1.geneid.LENGTH	64
droMoj1.genscan.LENGTH	65
droMoj1.xenoRefGene.LENGTH	65
droMoj2.genscan.LENGTH	66
droMoj2.xenoRefGene.LENGTH	66
droPer1.genscan.LENGTH	67
droPer1.xenoRefGene.LENGTH	67
droSec1.genscan.LENGTH	68

droSec1.xenoRefGene.LENGTH	68
droSim1.geneid.LENGTH	69
droSim1.genscan.LENGTH	69
droSim1.xenoRefGene.LENGTH	70
droVir1.geneid.LENGTH	70
droVir1.genscan.LENGTH	71
droVir1.xenoRefGene.LENGTH	71
droVir2.genscan.LENGTH	72
droVir2.xenoRefGene.LENGTH	72
droYak1.geneid.LENGTH	73
droYak1.genscan.LENGTH	73
droYak1.xenoRefGene.LENGTH	74
droYak2.genscan.LENGTH	74
droYak2.xenoRefGene.LENGTH	75
equCab1.geneid.LENGTH	75
equCab1.geneSymbol.LENGTH	76
equCab1.nscanGene.LENGTH	76
equCab1.refGene.LENGTH	77
equCab1.sgpGene.LENGTH	77
equCab2.ensGene.LENGTH	78
equCab2.geneSymbol.LENGTH	78
equCab2.nscanGene.LENGTH	79
equCab2.refGene.LENGTH	79
equCab2.xenoRefGene.LENGTH	80
felCat3.ensGene.LENGTH	80
felCat3.geneid.LENGTH	81
felCat3.geneSymbol.LENGTH	81
felCat3.genscan.LENGTH	82
felCat3.nscanGene.LENGTH	82
felCat3.refGene.LENGTH	83
felCat3.sgpGene.LENGTH	83
felCat3.xenoRefGene.LENGTH	84
fr1.ensGene.LENGTH	84
fr1.genscan.LENGTH	85
fr2.ensGene.LENGTH	85
galGal2.ensGene.LENGTH	86
galGal2.geneid.LENGTH	86
galGal2.geneSymbol.LENGTH	87
galGal2.genscan.LENGTH	87
galGal2.refGene.LENGTH	88
galGal2.sgpGene.LENGTH	88
galGal3.ensGene.LENGTH	89
galGal3.geneSymbol.LENGTH	89
galGal3.genscan.LENGTH	90
galGal3.nscanGene.LENGTH	90
galGal3.refGene.LENGTH	91
galGal3.xenoRefGene.LENGTH	91
gasAcu1.ensGene.LENGTH	92
gasAcu1.nscanGene.LENGTH	92
hg16.acembly.LENGTH	93
hg16.ensGene.LENGTH	93
hg16.exoniphy.LENGTH	94

hg16.geneid.LENGTH	94
hg16.geneSymbol.LENGTH	95
hg16.genscan.LENGTH	95
hg16.knownGene.LENGTH	96
hg16.refGene.LENGTH	96
hg16.sgpGene.LENGTH	97
hg17.acembly.LENGTH	97
hg17.acescan.LENGTH	98
hg17.ccdsGene.LENGTH	98
hg17.ensGene.LENGTH	99
hg17.exoniphy.LENGTH	99
hg17.geneid.LENGTH	100
hg17.geneSymbol.LENGTH	100
hg17.genscan.LENGTH	101
hg17.knownGene.LENGTH	101
hg17.refGene.LENGTH	102
hg17.sgpGene.LENGTH	102
hg17.vegaGene.LENGTH	103
hg17.vegaPseudoGene.LENGTH	103
hg17.xenoRefGene.LENGTH	104
hg18.acembly.LENGTH	104
hg18.acescan.LENGTH	105
hg18.ccdsGene.LENGTH	105
hg18.ensGene.LENGTH	106
hg18.exoniphy.LENGTH	106
hg18.geneid.LENGTH	107
hg18.geneSymbol.LENGTH	107
hg18.genscan.LENGTH	108
hg18.knownGene.LENGTH	108
hg18.knownGeneOld3.LENGTH	109
hg18.refGene.LENGTH	109
hg18.sgpGene.LENGTH	110
hg18.sibGene.LENGTH	110
hg18.xenoRefGene.LENGTH	111
hg19.ccdsGene.LENGTH	111
hg19.ensGene.LENGTH	112
hg19.exoniphy.LENGTH	112
hg19.geneSymbol.LENGTH	113
hg19.knownGene.LENGTH	113
hg19.nscanGene.LENGTH	114
hg19.refGene.LENGTH	114
hg19.xenoRefGene.LENGTH	115
loxAfr3.xenoRefGene.LENGTH	115
mm7.ensGene.LENGTH	116
mm7.geneid.LENGTH	116
mm7.geneSymbol.LENGTH	117
mm7.genscan.LENGTH	117
mm7.knownGene.LENGTH	118
mm7.refGene.LENGTH	118
mm7.sgpGene.LENGTH	119
mm7.xenoRefGene.LENGTH	119
mm8.ccdsGene.LENGTH	120

mm8.ensGene.LENGTH	120
mm8.geneid.LENGTH	121
mm8.geneSymbol.LENGTH	121
mm8.genscan.LENGTH	122
mm8.knownGene.LENGTH	122
mm8.nscanGene.LENGTH	123
mm8.refGene.LENGTH	123
mm8.sgpGene.LENGTH	124
mm8.sibGene.LENGTH	124
mm8.xenoRefGene.LENGTH	125
mm9.acembly.LENGTH	125
mm9.ccdsGene.LENGTH	126
mm9.ensGene.LENGTH	126
mm9.exoniphy.LENGTH	127
mm9.geneid.LENGTH	127
mm9.geneSymbol.LENGTH	128
mm9.genscan.LENGTH	128
mm9.knownGene.LENGTH	129
mm9.nscanGene.LENGTH	129
mm9.refGene.LENGTH	130
mm9.sgpGene.LENGTH	130
mm9.xenoRefGene.LENGTH	131
monDom1.genscan.LENGTH	131
monDom4.ensGene.LENGTH	132
monDom4.geneSymbol.LENGTH	132
monDom4.genscan.LENGTH	133
monDom4.nscanGene.LENGTH	133
monDom4.refGene.LENGTH	134
monDom4.xenoRefGene.LENGTH	134
monDom5.ensGene.LENGTH	135
monDom5.geneSymbol.LENGTH	135
monDom5.genscan.LENGTH	136
monDom5.nscanGene.LENGTH	136
monDom5.refGene.LENGTH	137
monDom5.xenoRefGene.LENGTH	137
ornAna1.ensGene.LENGTH	138
ornAna1.geneSymbol.LENGTH	138
ornAna1.refGene.LENGTH	139
ornAna1.xenoRefGene.LENGTH	139
oryLat2.ensGene.LENGTH	140
oryLat2.geneSymbol.LENGTH	140
oryLat2.refGene.LENGTH	141
oryLat2.xenoRefGene.LENGTH	141
panTro1.ensGene.LENGTH	142
panTro1.geneid.LENGTH	142
panTro1.genscan.LENGTH	143
panTro1.xenoRefGene.LENGTH	143
panTro2.ensGene.LENGTH	144
panTro2.geneSymbol.LENGTH	144
panTro2.genscan.LENGTH	145
panTro2.nscanGene.LENGTH	145
panTro2.refGene.LENGTH	146

panTro2.xenoRefGene.LENGTH	146
petMar1.xenoRefGene.LENGTH	147
ponAbe2.ensGene.LENGTH	147
ponAbe2.geneSymbol.LENGTH	148
ponAbe2.genscan.LENGTH	148
ponAbe2.nscanGene.LENGTH	149
ponAbe2.refGene.LENGTH	149
ponAbe2.xenoRefGene.LENGTH	150
priPac1.xenoRefGene.LENGTH	150
rheMac2.ensGene.LENGTH	151
rheMac2.geneid.LENGTH	151
rheMac2.geneSymbol.LENGTH	152
rheMac2.nscanGene.LENGTH	152
rheMac2.refGene.LENGTH	153
rheMac2.sgpGene.LENGTH	153
rheMac2.xenoRefGene.LENGTH	154
rn3.ensGene.LENGTH	154
rn3.geneid.LENGTH	155
rn3.geneSymbol.LENGTH	155
rn3.genscan.LENGTH	156
rn3.knownGene.LENGTH	156
rn3.nscanGene.LENGTH	157
rn3.refGene.LENGTH	157
rn3.sgpGene.LENGTH	158
rn3.xenoRefGene.LENGTH	158
rn4.ensGene.LENGTH	159
rn4.geneid.LENGTH	159
rn4.geneSymbol.LENGTH	160
rn4.genscan.LENGTH	160
rn4.knownGene.LENGTH	161
rn4.nscanGene.LENGTH	161
rn4.refGene.LENGTH	162
rn4.sgpGene.LENGTH	162
rn4.xenoRefGene.LENGTH	163
sacCer1.ensGene.LENGTH	163
sacCer2.ensGene.LENGTH	164
strPur1.geneSymbol.LENGTH	164
strPur1.genscan.LENGTH	165
strPur1.refGene.LENGTH	165
strPur1.xenoRefGene.LENGTH	166
strPur2.geneSymbol.LENGTH	166
strPur2.genscan.LENGTH	167
strPur2.refGene.LENGTH	167
strPur2.xenoRefGene.LENGTH	168
supportedGeneIDs	168
supportedGenomes	169
taeGut1.ensGene.LENGTH	169
taeGut1.geneSymbol.LENGTH	170
taeGut1.genscan.LENGTH	170
taeGut1.nscanGene.LENGTH	171
taeGut1.refGene.LENGTH	171
taeGut1.xenoRefGene.LENGTH	172

tetNig1.ensGene.LENGTH	172
tetNig1.geneid.LENGTH	173
tetNig1.genscan.LENGTH	173
tetNig1.nscanGene.LENGTH	174
tetNig2.ensGene.LENGTH	174
unfactor	175
xenTro1.genscan.LENGTH	176
xenTro2.ensGene.LENGTH	176
xenTro2.geneSymbol.LENGTH	177
xenTro2.genscan.LENGTH	177
xenTro2.refGene.LENGTH	178

Index	179
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anoCar1.ensGene.LENGTH

Transcript length data for the organism anoCar

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

anoCar1.genscan.LENGTH

Transcript length data for the organism anoCar

Description

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

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

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

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

```
anoCar1.xenoRefGene.LENGTH
```

Transcript length data for the organism anoCar

Description

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

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

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

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

```
anoGam1.ensGene.LENGTH
```

Transcript length data for the organism anoGam

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
apiMel1.genscan.LENGTH
```

Transcript length data for the organism apiMel

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
apiMel2.ensGene.LENGTH
```

Transcript length data for the organism apiMel

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
aplCal1.xenoRefGene.LENGTH
```

Transcript length data for the organism aplCal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau2.geneid.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau2.geneSymbol.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau2.genscan.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.ensGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.geneid.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.geneSymbol.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.genscan.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.refGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.sgpGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.ensGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.geneSymbol.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.genscan.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.nscanGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caeJap1.xenoRefGene.LENGTH
```

Transcript length data for the organism caeJap

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caePb1.xenoRefGene.LENGTH
```

Transcript length data for the organism caePb

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caePb2.xenoRefGene.LENGTH
```

Transcript length data for the organism caePb

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caeRem2.xenoRefGene.LENGTH
```

Transcript length data for the organism caeRem

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caeRem3.xenoRefGene.LENGTH
```

Transcript length data for the organism caeRem

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
calJac1.genscan.LENGTH
```

Transcript length data for the organism calJac

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
calJac1.nscanGene.LENGTH
```

Transcript length data for the organism calJac

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
calJac1.xenoRefGene.LENGTH
```

Transcript length data for the organism calJac

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

canFam1.refGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

canFam1.xenoRefGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
cavPor3.ensGene.LENGTH
```

Transcript length data for the organism cavPor

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
cavPor3.genscan.LENGTH
```

Transcript length data for the organism cavPor

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
cavPor3.nscanGene.LENGTH
```

Transcript length data for the organism cavPor

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
cavPor3.xenoRefGene.LENGTH
```

Transcript length data for the organism cavPor

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

cb1.xenoRefGene.LENGTH

Transcript length data for the organism cb

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

cb3.xenoRefGene.LENGTH

Transcript length data for the organism cb

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

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()
```

<code>taeGut1.ensGene.LENGTH</code>	<i>Transcript length data for the organism taeGut</i>
-------------------------------------	---

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, 8
anoCar1.xenoRefGene.LENGTH, 9
anoGam1.ensGene.LENGTH, 9
anoGam1.geneid.LENGTH, 10
anoGam1.genscan.LENGTH, 10
apiMe11.genscan.LENGTH, 11
apiMe12.ensGene.LENGTH, 11
apiMe12.geneid.LENGTH, 12
apiMe12.genscan.LENGTH, 12
aplCa11.xenoRefGene.LENGTH, 13
bosTau2.geneid.LENGTH, 13
bosTau2.geneSymbol.LENGTH, 14
bosTau2.genscan.LENGTH, 14
bosTau2.refGene.LENGTH, 15
bosTau2.sgpGene.LENGTH, 15
bosTau3.ensGene.LENGTH, 16
bosTau3.geneid.LENGTH, 16
bosTau3.geneSymbol.LENGTH, 17
bosTau3.genscan.LENGTH, 17
bosTau3.refGene.LENGTH, 18
bosTau3.sgpGene.LENGTH, 18
bosTau4.ensGene.LENGTH, 19
bosTau4.geneSymbol.LENGTH, 19
bosTau4.genscan.LENGTH, 20
bosTau4.nscanGene.LENGTH, 20
bosTau4.refGene.LENGTH, 21
braFlo1.xenoRefGene.LENGTH, 21
caeJap1.xenoRefGene.LENGTH, 22
caePb1.xenoRefGene.LENGTH, 22
caePb2.xenoRefGene.LENGTH, 23
caeRem2.xenoRefGene.LENGTH, 23
caeRem3.xenoRefGene.LENGTH, 24
calJac1.genscan.LENGTH, 24
calJac1.nscanGene.LENGTH, 25
calJac1.xenoRefGene.LENGTH, 25
canFam1.ensGene.LENGTH, 26
canFam1.geneSymbol.LENGTH, 26
canFam1.genscan.LENGTH, 27
canFam1.nscanGene.LENGTH, 27
canFam1.refGene.LENGTH, 28
canFam1.xenoRefGene.LENGTH, 28
canFam2.ensGene.LENGTH, 29
canFam2.geneSymbol.LENGTH, 29
canFam2.genscan.LENGTH, 30
canFam2.nscanGene.LENGTH, 30
canFam2.refGene.LENGTH, 31
canFam2.xenoRefGene.LENGTH, 31
cavPor3.ensGene.LENGTH, 32
cavPor3.genscan.LENGTH, 32
cavPor3.nscanGene.LENGTH, 33
cavPor3.xenoRefGene.LENGTH, 33
cb1.xenoRefGene.LENGTH, 34
cb3.xenoRefGene.LENGTH, 34
ce2.geneid.LENGTH, 35
ce2.geneSymbol.LENGTH, 35
ce2.refGene.LENGTH, 36
ce4.geneSymbol.LENGTH, 36
ce4.refGene.LENGTH, 37
ce4.xenoRefGene.LENGTH, 37
ce6.ensGene.LENGTH, 38
ce6.geneSymbol.LENGTH, 38
ce6.refGene.LENGTH, 39
ce6.xenoRefGene.LENGTH, 39
ci1.geneSymbol.LENGTH, 40
ci1.refGene.LENGTH, 40
ci1.xenoRefGene.LENGTH, 41
ci2.ensGene.LENGTH, 41
ci2.geneSymbol.LENGTH, 42
ci2.refGene.LENGTH, 42
ci2.xenoRefGene.LENGTH, 43
danRer3.ensGene.LENGTH, 43
danRer3.geneSymbol.LENGTH, 44
danRer3.refGene.LENGTH, 44
danRer4.ensGene.LENGTH, 45
danRer4.geneSymbol.LENGTH, 45
danRer4.genscan.LENGTH, 46
danRer4.nscanGene.LENGTH, 46
danRer4.refGene.LENGTH, 47
danRer5.ensGene.LENGTH, 47
danRer5.geneSymbol.LENGTH, 48
danRer5.refGene.LENGTH, 48
danRer5.vegaGene.LENGTH, 49
danRer5.vegaPseudoGene.LENGTH, 49
danRer6.ensGene.LENGTH, 50

- danRer6.geneSymbol.LENGTH, 50
 danRer6.refGene.LENGTH, 51
 danRer6.xenoRefGene.LENGTH, 51
 dm1.geneSymbol.LENGTH, 52
 dm1.genscan.LENGTH, 52
 dm1.refGene.LENGTH, 53
 dm2.geneid.LENGTH, 53
 dm2.geneSymbol.LENGTH, 54
 dm2.genscan.LENGTH, 54
 dm2.nscanGene.LENGTH, 55
 dm2.refGene.LENGTH, 55
 dm3.geneSymbol.LENGTH, 56
 dm3.nscanPasaGene.LENGTH, 56
 dm3.refGene.LENGTH, 57
 dp2.genscan.LENGTH, 57
 dp2.xenoRefGene.LENGTH, 58
 dp3.geneid.LENGTH, 58
 dp3.genscan.LENGTH, 59
 dp3.xenoRefGene.LENGTH, 59
 droAna1.geneid.LENGTH, 60
 droAna1.genscan.LENGTH, 60
 droAna1.xenoRefGene.LENGTH, 61
 droAna2.genscan.LENGTH, 61
 droAna2.xenoRefGene.LENGTH, 62
 droEre1.genscan.LENGTH, 62
 droEre1.xenoRefGene.LENGTH, 63
 droGri1.genscan.LENGTH, 63
 droGri1.xenoRefGene.LENGTH, 64
 droMoj1.geneid.LENGTH, 64
 droMoj1.genscan.LENGTH, 65
 droMoj1.xenoRefGene.LENGTH, 65
 droMoj2.genscan.LENGTH, 66
 droMoj2.xenoRefGene.LENGTH, 66
 droPer1.genscan.LENGTH, 67
 droPer1.xenoRefGene.LENGTH, 67
 droSec1.genscan.LENGTH, 68
 droSec1.xenoRefGene.LENGTH, 68
 droSim1.geneid.LENGTH, 69
 droSim1.genscan.LENGTH, 69
 droSim1.xenoRefGene.LENGTH, 70
 droVir1.geneid.LENGTH, 70
 droVir1.genscan.LENGTH, 71
 droVir1.xenoRefGene.LENGTH, 71
 droVir2.genscan.LENGTH, 72
 droVir2.xenoRefGene.LENGTH, 72
 droYak1.geneid.LENGTH, 73
 droYak1.genscan.LENGTH, 73
 droYak1.xenoRefGene.LENGTH, 74
 droYak2.genscan.LENGTH, 74
 droYak2.xenoRefGene.LENGTH, 75
 equCab1.geneid.LENGTH, 75
 equCab1.geneSymbol.LENGTH, 76
 equCab1.nscanGene.LENGTH, 76
 equCab1.refGene.LENGTH, 77
 equCab1.sgpGene.LENGTH, 77
 equCab2.ensGene.LENGTH, 78
 equCab2.geneSymbol.LENGTH, 78
 equCab2.nscanGene.LENGTH, 79
 equCab2.refGene.LENGTH, 79
 equCab2.xenoRefGene.LENGTH, 80
 felCat3.ensGene.LENGTH, 80
 felCat3.geneid.LENGTH, 81
 felCat3.geneSymbol.LENGTH, 81
 felCat3.genscan.LENGTH, 82
 felCat3.nscanGene.LENGTH, 82
 felCat3.refGene.LENGTH, 83
 felCat3.sgpGene.LENGTH, 83
 felCat3.xenoRefGene.LENGTH, 84
 fr1.ensGene.LENGTH, 84
 fr1.genscan.LENGTH, 85
 fr2.ensGene.LENGTH, 85
 galGal2.ensGene.LENGTH, 86
 galGal2.geneid.LENGTH, 86
 galGal2.geneSymbol.LENGTH, 87
 galGal2.genscan.LENGTH, 87
 galGal2.refGene.LENGTH, 88
 galGal2.sgpGene.LENGTH, 88
 galGal3.ensGene.LENGTH, 89
 galGal3.geneSymbol.LENGTH, 89
 galGal3.genscan.LENGTH, 90
 galGal3.nscanGene.LENGTH, 90
 galGal3.refGene.LENGTH, 91
 galGal3.xenoRefGene.LENGTH, 91
 gasAcu1.ensGene.LENGTH, 92
 gasAcu1.nscanGene.LENGTH, 92
 hg16.acembly.LENGTH, 93
 hg16.ensGene.LENGTH, 93
 hg16.exoniphy.LENGTH, 94
 hg16.geneid.LENGTH, 94
 hg16.geneSymbol.LENGTH, 95
 hg16.genscan.LENGTH, 95
 hg16.knownGene.LENGTH, 96
 hg16.refGene.LENGTH, 96
 hg16.sgpGene.LENGTH, 97
 hg17.acembly.LENGTH, 97
 hg17.acescan.LENGTH, 98
 hg17.ccdsGene.LENGTH, 98
 hg17.ensGene.LENGTH, 99
 hg17.exoniphy.LENGTH, 99
 hg17.geneid.LENGTH, 100
 hg17.geneSymbol.LENGTH, 100
 hg17.genscan.LENGTH, 101
 hg17.knownGene.LENGTH, 101
 hg17.refGene.LENGTH, 102

hg17.sgpGene.LENGTH, 102
hg17.vegaGene.LENGTH, 103
hg17.vegaPseudoGene.LENGTH, 103
hg17.xenoRefGene.LENGTH, 104
hg18.acembly.LENGTH, 104
hg18.acescan.LENGTH, 105
hg18.ccdsGene.LENGTH, 105
hg18.ensGene.LENGTH, 106
hg18.exoniphy.LENGTH, 106
hg18.geneid.LENGTH, 107
hg18.geneSymbol.LENGTH, 107
hg18.genscan.LENGTH, 108
hg18.knownGene.LENGTH, 108
hg18.knownGeneOld3.LENGTH, 109
hg18.refGene.LENGTH, 109
hg18.sgpGene.LENGTH, 110
hg18.sibGene.LENGTH, 110
hg18.xenoRefGene.LENGTH, 111
hg19.ccdsGene.LENGTH, 111
hg19.ensGene.LENGTH, 112
hg19.exoniphy.LENGTH, 112
hg19.geneSymbol.LENGTH, 113
hg19.knownGene.LENGTH, 113
hg19.nscanGene.LENGTH, 114
hg19.refGene.LENGTH, 114
hg19.xenoRefGene.LENGTH, 115
loxAfr3.xenoRefGene.LENGTH, 115
mm7.ensGene.LENGTH, 116
mm7.geneid.LENGTH, 116
mm7.geneSymbol.LENGTH, 117
mm7.genscan.LENGTH, 117
mm7.knownGene.LENGTH, 118
mm7.refGene.LENGTH, 118
mm7.sgpGene.LENGTH, 119
mm7.xenoRefGene.LENGTH, 119
mm8.ccdsGene.LENGTH, 120
mm8.ensGene.LENGTH, 120
mm8.geneid.LENGTH, 121
mm8.geneSymbol.LENGTH, 121
mm8.genscan.LENGTH, 122
mm8.knownGene.LENGTH, 122
mm8.nscanGene.LENGTH, 123
mm8.refGene.LENGTH, 123
mm8.sgpGene.LENGTH, 124
mm8.sibGene.LENGTH, 124
mm8.xenoRefGene.LENGTH, 125
mm9.acembly.LENGTH, 125
mm9.ccdsGene.LENGTH, 126
mm9.ensGene.LENGTH, 126
mm9.exoniphy.LENGTH, 127
mm9.geneid.LENGTH, 127
mm9.geneSymbol.LENGTH, 128
mm9.genscan.LENGTH, 128
mm9.knownGene.LENGTH, 129
mm9.nscanGene.LENGTH, 129
mm9.refGene.LENGTH, 130
mm9.sgpGene.LENGTH, 130
mm9.xenoRefGene.LENGTH, 131
monDom1.genscan.LENGTH, 131
monDom4.ensGene.LENGTH, 132
monDom4.geneSymbol.LENGTH, 132
monDom4.genscan.LENGTH, 133
monDom4.nscanGene.LENGTH, 133
monDom4.refGene.LENGTH, 134
monDom4.xenoRefGene.LENGTH, 134
monDom5.ensGene.LENGTH, 135
monDom5.geneSymbol.LENGTH, 135
monDom5.genscan.LENGTH, 136
monDom5.nscanGene.LENGTH, 136
monDom5.refGene.LENGTH, 137
monDom5.xenoRefGene.LENGTH, 137
ornAna1.ensGene.LENGTH, 138
ornAna1.geneSymbol.LENGTH, 138
ornAna1.refGene.LENGTH, 139
ornAna1.xenoRefGene.LENGTH, 139
oryLat2.ensGene.LENGTH, 140
oryLat2.geneSymbol.LENGTH, 140
oryLat2.refGene.LENGTH, 141
oryLat2.xenoRefGene.LENGTH, 141
panTro1.ensGene.LENGTH, 142
panTro1.geneid.LENGTH, 142
panTro1.genscan.LENGTH, 143
panTro1.xenoRefGene.LENGTH, 143
panTro2.ensGene.LENGTH, 144
panTro2.geneSymbol.LENGTH, 144
panTro2.genscan.LENGTH, 145
panTro2.nscanGene.LENGTH, 145
panTro2.refGene.LENGTH, 146
panTro2.xenoRefGene.LENGTH, 146
petMar1.xenoRefGene.LENGTH, 147
ponAbe2.ensGene.LENGTH, 147
ponAbe2.geneSymbol.LENGTH, 148
ponAbe2.genscan.LENGTH, 148
ponAbe2.nscanGene.LENGTH, 149
ponAbe2.refGene.LENGTH, 149
ponAbe2.xenoRefGene.LENGTH, 150
priPac1.xenoRefGene.LENGTH, 150
rheMac2.ensGene.LENGTH, 151
rheMac2.geneid.LENGTH, 151
rheMac2.geneSymbol.LENGTH, 152
rheMac2.nscanGene.LENGTH, 152
rheMac2.refGene.LENGTH, 153
rheMac2.sgpGene.LENGTH, 153
rheMac2.xenoRefGene.LENGTH, 154

- rn3.ensGene.LENGTH, 154
 rn3.geneid.LENGTH, 155
 rn3.geneSymbol.LENGTH, 155
 rn3.genscan.LENGTH, 156
 rn3.knownGene.LENGTH, 156
 rn3.nscanGene.LENGTH, 157
 rn3.refGene.LENGTH, 157
 rn3.sgpGene.LENGTH, 158
 rn3.xenoRefGene.LENGTH, 158
 rn4.ensGene.LENGTH, 159
 rn4.geneid.LENGTH, 159
 rn4.geneSymbol.LENGTH, 160
 rn4.genscan.LENGTH, 160
 rn4.knownGene.LENGTH, 161
 rn4.nscanGene.LENGTH, 161
 rn4.refGene.LENGTH, 162
 rn4.sgpGene.LENGTH, 162
 rn4.xenoRefGene.LENGTH, 163
 sacCer1.ensGene.LENGTH, 163
 sacCer2.ensGene.LENGTH, 164
 strPur1.geneSymbol.LENGTH, 164
 strPur1.genscan.LENGTH, 165
 strPur1.refGene.LENGTH, 165
 strPur1.xenoRefGene.LENGTH, 166
 strPur2.geneSymbol.LENGTH, 166
 strPur2.genscan.LENGTH, 167
 strPur2.refGene.LENGTH, 167
 strPur2.xenoRefGene.LENGTH, 168
 taeGut1.ensGene.LENGTH, 169
 taeGut1.geneSymbol.LENGTH, 170
 taeGut1.genscan.LENGTH, 170
 taeGut1.nscanGene.LENGTH, 171
 taeGut1.refGene.LENGTH, 171
 taeGut1.xenoRefGene.LENGTH, 172
 tetNig1.ensGene.LENGTH, 172
 tetNig1.geneid.LENGTH, 173
 tetNig1.genscan.LENGTH, 173
 tetNig1.nscanGene.LENGTH, 174
 tetNig2.ensGene.LENGTH, 174
 xenTro1.genscan.LENGTH, 176
 xenTro2.ensGene.LENGTH, 176
 xenTro2.geneSymbol.LENGTH, 177
 xenTro2.genscan.LENGTH, 177
 xenTro2.refGene.LENGTH, 178
- anoCar1.ensGene.LENGTH, 8
 anoCar1.genscan.LENGTH, 8
 anoCar1.xenoRefGene.LENGTH, 9
 anoGam1.ensGene.LENGTH, 9
 anoGam1.geneid.LENGTH, 10
 anoGam1.genscan.LENGTH, 10
 apiMel1.genscan.LENGTH, 11
 apiMel2.ensGene.LENGTH, 11
 apiMel2.geneid.LENGTH, 12
 apiMel2.genscan.LENGTH, 12
 aplCa11.xenoRefGene.LENGTH, 13
- bosTau2.geneid.LENGTH, 13
 bosTau2.geneSymbol.LENGTH, 14
 bosTau2.genscan.LENGTH, 14
 bosTau2.refGene.LENGTH, 15
 bosTau2.sgpGene.LENGTH, 15
 bosTau3.ensGene.LENGTH, 16
 bosTau3.geneid.LENGTH, 16
 bosTau3.geneSymbol.LENGTH, 17
 bosTau3.genscan.LENGTH, 17
 bosTau3.refGene.LENGTH, 18
 bosTau3.sgpGene.LENGTH, 18
 bosTau4.ensGene.LENGTH, 19
 bosTau4.geneSymbol.LENGTH, 19
 bosTau4.genscan.LENGTH, 20
 bosTau4.nscanGene.LENGTH, 20
 bosTau4.refGene.LENGTH, 21
 braFlo1.xenoRefGene.LENGTH, 21
- caeJap1.xenoRefGene.LENGTH, 22
 caePb1.xenoRefGene.LENGTH, 22
 caePb2.xenoRefGene.LENGTH, 23
 caeRem2.xenoRefGene.LENGTH, 23
 caeRem3.xenoRefGene.LENGTH, 24
 calJac1.genscan.LENGTH, 24
 calJac1.nscanGene.LENGTH, 25
 calJac1.xenoRefGene.LENGTH, 25
 canFam1.ensGene.LENGTH, 26
 canFam1.geneSymbol.LENGTH, 26
 canFam1.genscan.LENGTH, 27
 canFam1.nscanGene.LENGTH, 27
 canFam1.refGene.LENGTH, 28
 canFam1.xenoRefGene.LENGTH, 28
 canFam2.ensGene.LENGTH, 29
 canFam2.geneSymbol.LENGTH, 29
 canFam2.genscan.LENGTH, 30
 canFam2.nscanGene.LENGTH, 30
 canFam2.refGene.LENGTH, 31
 canFam2.xenoRefGene.LENGTH, 31
 cavPor3.ensGene.LENGTH, 32
 cavPor3.genscan.LENGTH, 32
 cavPor3.nscanGene.LENGTH, 33
 cavPor3.xenoRefGene.LENGTH, 33
 cb1.xenoRefGene.LENGTH, 34
 cb3.xenoRefGene.LENGTH, 34
 ce2.geneid.LENGTH, 35
 ce2.geneSymbol.LENGTH, 35
 ce2.refGene.LENGTH, 36
 ce4.geneSymbol.LENGTH, 36
 ce4.refGene.LENGTH, 37

- ce4.xenoRefGene.LENGTH, 37
 ce6.ensGene.LENGTH, 38
 ce6.geneSymbol.LENGTH, 38
 ce6.refGene.LENGTH, 39
 ce6.xenoRefGene.LENGTH, 39
 ci1.geneSymbol.LENGTH, 40
 ci1.refGene.LENGTH, 40
 ci1.xenoRefGene.LENGTH, 41
 ci2.ensGene.LENGTH, 41
 ci2.geneSymbol.LENGTH, 42
 ci2.refGene.LENGTH, 42
 ci2.xenoRefGene.LENGTH, 43

 danRer3.ensGene.LENGTH, 43
 danRer3.geneSymbol.LENGTH, 44
 danRer3.refGene.LENGTH, 44
 danRer4.ensGene.LENGTH, 45
 danRer4.geneSymbol.LENGTH, 45
 danRer4.genscan.LENGTH, 46
 danRer4.nscanGene.LENGTH, 46
 danRer4.refGene.LENGTH, 47
 danRer5.ensGene.LENGTH, 47
 danRer5.geneSymbol.LENGTH, 48
 danRer5.refGene.LENGTH, 48
 danRer5.vegaGene.LENGTH, 49
 danRer5.vegaPseudoGene.LENGTH, 49
 danRer6.ensGene.LENGTH, 50
 danRer6.geneSymbol.LENGTH, 50
 danRer6.refGene.LENGTH, 51
 danRer6.xenoRefGene.LENGTH, 51
 dm1.geneSymbol.LENGTH, 52
 dm1.genscan.LENGTH, 52
 dm1.refGene.LENGTH, 53
 dm2.geneid.LENGTH, 53
 dm2.geneSymbol.LENGTH, 54
 dm2.genscan.LENGTH, 54
 dm2.nscanGene.LENGTH, 55
 dm2.refGene.LENGTH, 55
 dm3.geneSymbol.LENGTH, 56
 dm3.nscanPasaGene.LENGTH, 56
 dm3.refGene.LENGTH, 57
 downloadLengthFromUCSC, 8–174, 176–178
 dp2.genscan.LENGTH, 57
 dp2.xenoRefGene.LENGTH, 58
 dp3.geneid.LENGTH, 58
 dp3.genscan.LENGTH, 59
 dp3.xenoRefGene.LENGTH, 59
 droAna1.geneid.LENGTH, 60
 droAna1.genscan.LENGTH, 60
 droAna1.xenoRefGene.LENGTH, 61
 droAna2.genscan.LENGTH, 61
 droAna2.xenoRefGene.LENGTH, 62
 droEre1.genscan.LENGTH, 62

 droEre1.xenoRefGene.LENGTH, 63
 droGri1.genscan.LENGTH, 63
 droGri1.xenoRefGene.LENGTH, 64
 droMoj1.geneid.LENGTH, 64
 droMoj1.genscan.LENGTH, 65
 droMoj1.xenoRefGene.LENGTH, 65
 droMoj2.genscan.LENGTH, 66
 droMoj2.xenoRefGene.LENGTH, 66
 droPer1.genscan.LENGTH, 67
 droPer1.xenoRefGene.LENGTH, 67
 droSec1.genscan.LENGTH, 68
 droSec1.xenoRefGene.LENGTH, 68
 droSim1.geneid.LENGTH, 69
 droSim1.genscan.LENGTH, 69
 droSim1.xenoRefGene.LENGTH, 70
 droVir1.geneid.LENGTH, 70
 droVir1.genscan.LENGTH, 71
 droVir1.xenoRefGene.LENGTH, 71
 droVir2.genscan.LENGTH, 72
 droVir2.xenoRefGene.LENGTH, 72
 droYak1.geneid.LENGTH, 73
 droYak1.genscan.LENGTH, 73
 droYak1.xenoRefGene.LENGTH, 74
 droYak2.genscan.LENGTH, 74
 droYak2.xenoRefGene.LENGTH, 75

 equCab1.geneid.LENGTH, 75
 equCab1.geneSymbol.LENGTH, 76
 equCab1.nscanGene.LENGTH, 76
 equCab1.refGene.LENGTH, 77
 equCab1.sgpGene.LENGTH, 77
 equCab2.ensGene.LENGTH, 78
 equCab2.geneSymbol.LENGTH, 78
 equCab2.nscanGene.LENGTH, 79
 equCab2.refGene.LENGTH, 79
 equCab2.xenoRefGene.LENGTH, 80

 felCat3.ensGene.LENGTH, 80
 felCat3.geneid.LENGTH, 81
 felCat3.geneSymbol.LENGTH, 81
 felCat3.genscan.LENGTH, 82
 felCat3.nscanGene.LENGTH, 82
 felCat3.refGene.LENGTH, 83
 felCat3.sgpGene.LENGTH, 83
 felCat3.xenoRefGene.LENGTH, 84
 fr1.ensGene.LENGTH, 84
 fr1.genscan.LENGTH, 85
 fr2.ensGene.LENGTH, 85

 galGal2.ensGene.LENGTH, 86
 galGal2.geneid.LENGTH, 86
 galGal2.geneSymbol.LENGTH, 87
 galGal2.genscan.LENGTH, 87

- galGal2.refGene.LENGTH, 88
galGal2.sgpGene.LENGTH, 88
galGal3.ensGene.LENGTH, 89
galGal3.geneSymbol.LENGTH, 89
galGal3.genscan.LENGTH, 90
galGal3.nscanGene.LENGTH, 90
galGal3.refGene.LENGTH, 91
galGal3.xenoRefGene.LENGTH, 91
gasAcu1.ensGene.LENGTH, 92
gasAcu1.nscanGene.LENGTH, 92
- hg16.acembly.LENGTH, 93
hg16.ensGene.LENGTH, 93
hg16.exoniphy.LENGTH, 94
hg16.geneid.LENGTH, 94
hg16.geneSymbol.LENGTH, 95
hg16.genscan.LENGTH, 95
hg16.knownGene.LENGTH, 96
hg16.refGene.LENGTH, 96
hg16.sgpGene.LENGTH, 97
hg17.acembly.LENGTH, 97
hg17.acescan.LENGTH, 98
hg17.ccdsGene.LENGTH, 98
hg17.ensGene.LENGTH, 99
hg17.exoniphy.LENGTH, 99
hg17.geneid.LENGTH, 100
hg17.geneSymbol.LENGTH, 100
hg17.genscan.LENGTH, 101
hg17.knownGene.LENGTH, 101
hg17.refGene.LENGTH, 102
hg17.sgpGene.LENGTH, 102
hg17.vegaGene.LENGTH, 103
hg17.vegaPseudoGene.LENGTH, 103
hg17.xenoRefGene.LENGTH, 104
hg18.acembly.LENGTH, 104
hg18.acescan.LENGTH, 105
hg18.ccdsGene.LENGTH, 105
hg18.ensGene.LENGTH, 106
hg18.exoniphy.LENGTH, 106
hg18.geneid.LENGTH, 107
hg18.geneSymbol.LENGTH, 107
hg18.genscan.LENGTH, 108
hg18.knownGene.LENGTH, 108
hg18.knownGeneOld3.LENGTH, 109
hg18.refGene.LENGTH, 109
hg18.sgpGene.LENGTH, 110
hg18.sibGene.LENGTH, 110
hg18.xenoRefGene.LENGTH, 111
hg19.ccdsGene.LENGTH, 111
hg19.ensGene.LENGTH, 112
hg19.exoniphy.LENGTH, 112
hg19.geneSymbol.LENGTH, 113
hg19.knownGene.LENGTH, 113
hg19.nscanGene.LENGTH, 114
hg19.refGene.LENGTH, 114
hg19.xenoRefGene.LENGTH, 115
- loxAfr3.xenoRefGene.LENGTH, 115
- mm7.ensGene.LENGTH, 116
mm7.geneid.LENGTH, 116
mm7.geneSymbol.LENGTH, 117
mm7.genscan.LENGTH, 117
mm7.knownGene.LENGTH, 118
mm7.refGene.LENGTH, 118
mm7.sgpGene.LENGTH, 119
mm7.xenoRefGene.LENGTH, 119
mm8.ccdsGene.LENGTH, 120
mm8.ensGene.LENGTH, 120
mm8.geneid.LENGTH, 121
mm8.geneSymbol.LENGTH, 121
mm8.genscan.LENGTH, 122
mm8.knownGene.LENGTH, 122
mm8.nscanGene.LENGTH, 123
mm8.refGene.LENGTH, 123
mm8.sgpGene.LENGTH, 124
mm8.sibGene.LENGTH, 124
mm8.xenoRefGene.LENGTH, 125
mm9.acembly.LENGTH, 125
mm9.ccdsGene.LENGTH, 126
mm9.ensGene.LENGTH, 126
mm9.exoniphy.LENGTH, 127
mm9.geneid.LENGTH, 127
mm9.geneSymbol.LENGTH, 128
mm9.genscan.LENGTH, 128
mm9.knownGene.LENGTH, 129
mm9.nscanGene.LENGTH, 129
mm9.refGene.LENGTH, 130
mm9.sgpGene.LENGTH, 130
mm9.xenoRefGene.LENGTH, 131
monDom1.genscan.LENGTH, 131
monDom4.ensGene.LENGTH, 132
monDom4.geneSymbol.LENGTH, 132
monDom4.genscan.LENGTH, 133
monDom4.nscanGene.LENGTH, 133
monDom4.refGene.LENGTH, 134
monDom4.xenoRefGene.LENGTH, 134
monDom5.ensGene.LENGTH, 135
monDom5.geneSymbol.LENGTH, 135
monDom5.genscan.LENGTH, 136
monDom5.nscanGene.LENGTH, 136
monDom5.refGene.LENGTH, 137
monDom5.xenoRefGene.LENGTH, 137
- ornAna1.ensGene.LENGTH, 138
ornAna1.geneSymbol.LENGTH, 138

- ornAna1.refGene.LENGTH, 139
ornAna1.xenoRefGene.LENGTH, 139
oryLat2.ensGene.LENGTH, 140
oryLat2.geneSymbol.LENGTH, 140
oryLat2.refGene.LENGTH, 141
oryLat2.xenoRefGene.LENGTH, 141
- panTro1.ensGene.LENGTH, 142
panTro1.geneid.LENGTH, 142
panTro1.genscan.LENGTH, 143
panTro1.xenoRefGene.LENGTH, 143
panTro2.ensGene.LENGTH, 144
panTro2.geneSymbol.LENGTH, 144
panTro2.genscan.LENGTH, 145
panTro2.nscanGene.LENGTH, 145
panTro2.refGene.LENGTH, 146
panTro2.xenoRefGene.LENGTH, 146
petMar1.xenoRefGene.LENGTH, 147
ponAbe2.ensGene.LENGTH, 147
ponAbe2.geneSymbol.LENGTH, 148
ponAbe2.genscan.LENGTH, 148
ponAbe2.nscanGene.LENGTH, 149
ponAbe2.refGene.LENGTH, 149
ponAbe2.xenoRefGene.LENGTH, 150
priPac1.xenoRefGene.LENGTH, 150
- rheMac2.ensGene.LENGTH, 151
rheMac2.geneid.LENGTH, 151
rheMac2.geneSymbol.LENGTH, 152
rheMac2.nscanGene.LENGTH, 152
rheMac2.refGene.LENGTH, 153
rheMac2.sgpGene.LENGTH, 153
rheMac2.xenoRefGene.LENGTH, 154
rn3.ensGene.LENGTH, 154
rn3.geneid.LENGTH, 155
rn3.geneSymbol.LENGTH, 155
rn3.genscan.LENGTH, 156
rn3.knownGene.LENGTH, 156
rn3.nscanGene.LENGTH, 157
rn3.refGene.LENGTH, 157
rn3.sgpGene.LENGTH, 158
rn3.xenoRefGene.LENGTH, 158
rn4.ensGene.LENGTH, 159
rn4.geneid.LENGTH, 159
rn4.geneSymbol.LENGTH, 160
rn4.genscan.LENGTH, 160
rn4.knownGene.LENGTH, 161
rn4.nscanGene.LENGTH, 161
rn4.refGene.LENGTH, 162
rn4.sgpGene.LENGTH, 162
rn4.xenoRefGene.LENGTH, 163
- sacCer1.ensGene.LENGTH, 163
sacCer2.ensGene.LENGTH, 164
strPur1.geneSymbol.LENGTH, 164
strPur1.genscan.LENGTH, 165
strPur1.refGene.LENGTH, 165
strPur1.xenoRefGene.LENGTH, 166
strPur2.geneSymbol.LENGTH, 166
strPur2.genscan.LENGTH, 167
strPur2.refGene.LENGTH, 167
strPur2.xenoRefGene.LENGTH, 168
supportedGeneIDs, 168
supportedGenomes, 169
- taeGut1.ensGene.LENGTH, 169
taeGut1.geneSymbol.LENGTH, 170
taeGut1.genscan.LENGTH, 170
taeGut1.nscanGene.LENGTH, 171
taeGut1.refGene.LENGTH, 171
taeGut1.xenoRefGene.LENGTH, 172
tetNig1.ensGene.LENGTH, 172
tetNig1.geneid.LENGTH, 173
tetNig1.genscan.LENGTH, 173
tetNig1.nscanGene.LENGTH, 174
tetNig2.ensGene.LENGTH, 174
- unfactor, 175
- xenTro1.genscan.LENGTH, 176
xenTro2.ensGene.LENGTH, 176
xenTro2.geneSymbol.LENGTH, 177
xenTro2.genscan.LENGTH, 177
xenTro2.refGene.LENGTH, 178