

Package ‘geneLenDataBase’

November 18, 2025

Title Lengths of mRNA transcripts for a number of genomes

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

Depends R (>= 2.11.0)

Imports utils, rtracklayer, GenomicFeatures, txdbmaker

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

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

License LGPL (>= 2)

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Contents

anoCar1.ensGene.LENGTH	9
anoCar1.genscan.LENGTH	9
anoCar1.xenoRefGene.LENGTH	10
anoGam1.ensGene.LENGTH	10
anoGam1.geneid.LENGTH	11
anoGam1.genscan.LENGTH	11
apiMel1.genscan.LENGTH	12
apiMel2.ensGene.LENGTH	12
apiMel2.geneid.LENGTH	13
apiMel2.genscan.LENGTH	13
aplCal1.xenoRefGene.LENGTH	14
bosTau2.geneid.LENGTH	14
bosTau2.geneSymbol.LENGTH	15
bosTau2.genscan.LENGTH	15
bosTau2.refGene.LENGTH	16
bosTau2.sgpGene.LENGTH	16
bosTau3.ensGene.LENGTH	17
bosTau3.geneid.LENGTH	17
bosTau3.geneSymbol.LENGTH	18
bosTau3.genscan.LENGTH	18
bosTau3.refGene.LENGTH	19
bosTau3.sgpGene.LENGTH	19
bosTau4.ensGene.LENGTH	20
bosTau4.geneSymbol.LENGTH	20
bosTau4.genscan.LENGTH	21
bosTau4.nscanGene.LENGTH	21
bosTau4.refGene.LENGTH	22
braFlo1.xenoRefGene.LENGTH	22
caeJap1.xenoRefGene.LENGTH	23
caePb1.xenoRefGene.LENGTH	23
caePb2.xenoRefGene.LENGTH	24
caeRem2.xenoRefGene.LENGTH	24
caeRem3.xenoRefGene.LENGTH	25
calJac1.genscan.LENGTH	25
calJac1.nscanGene.LENGTH	26
calJac1.xenoRefGene.LENGTH	26
canFam1.ensGene.LENGTH	27
canFam1.geneSymbol.LENGTH	27
canFam1.genscan.LENGTH	28
canFam1.nscanGene.LENGTH	28
canFam1.refGene.LENGTH	29
canFam1.xenoRefGene.LENGTH	29
canFam2.ensGene.LENGTH	30
canFam2.geneSymbol.LENGTH	30
canFam2.genscan.LENGTH	31
canFam2.nscanGene.LENGTH	31

canFam2.refGene.LENGTH	32
canFam2.xenoRefGene.LENGTH	32
cavPor3.ensGene.LENGTH	33
cavPor3.genscan.LENGTH	33
cavPor3.nscanGene.LENGTH	34
cavPor3.xenoRefGene.LENGTH	34
cb1.xenoRefGene.LENGTH	35
cb3.xenoRefGene.LENGTH	35
ce2.geneid.LENGTH	36
ce2.geneSymbol.LENGTH	36
ce2.refGene.LENGTH	37
ce4.geneSymbol.LENGTH	37
ce4.refGene.LENGTH	38
ce4.xenoRefGene.LENGTH	38
ce6.ensGene.LENGTH	39
ce6.geneSymbol.LENGTH	39
ce6.refGene.LENGTH	40
ce6.xenoRefGene.LENGTH	40
ci1.geneSymbol.LENGTH	41
ci1.refGene.LENGTH	41
ci1.xenoRefGene.LENGTH	42
ci2.ensGene.LENGTH	42
ci2.geneSymbol.LENGTH	43
ci2.refGene.LENGTH	43
ci2.xenoRefGene.LENGTH	44
danRer3.ensGene.LENGTH	44
danRer3.geneSymbol.LENGTH	45
danRer3.refGene.LENGTH	45
danRer4.ensGene.LENGTH	46
danRer4.geneSymbol.LENGTH	46
danRer4.genscan.LENGTH	47
danRer4.nscanGene.LENGTH	47
danRer4.refGene.LENGTH	48
danRer5.ensGene.LENGTH	48
danRer5.geneSymbol.LENGTH	49
danRer5.refGene.LENGTH	49
danRer5.vegaGene.LENGTH	50
danRer5.vegaPseudoGene.LENGTH	50
danRer6.ensGene.LENGTH	51
danRer6.geneSymbol.LENGTH	51
danRer6.refGene.LENGTH	52
danRer6.xenoRefGene.LENGTH	52
dm1.geneSymbol.LENGTH	53
dm1.genscan.LENGTH	53
dm1.refGene.LENGTH	54
dm2.geneid.LENGTH	54
dm2.geneSymbol.LENGTH	55
dm2.genscan.LENGTH	55

dm2.nscanGene.LENGTH	56
dm2.refGene.LENGTH	56
dm3.geneSymbol.LENGTH	57
dm3.nscanPasaGene.LENGTH	57
dm3.refGene.LENGTH	58
downloadLengthFromUCSC	58
dp2.genscan.LENGTH	59
dp2.xenoRefGene.LENGTH	60
dp3.geneid.LENGTH	60
dp3.genscan.LENGTH	61
dp3.xenoRefGene.LENGTH	61
droAna1.geneid.LENGTH	62
droAna1.genscan.LENGTH	62
droAna1.xenoRefGene.LENGTH	63
droAna2.genscan.LENGTH	63
droAna2.xenoRefGene.LENGTH	64
droEre1.genscan.LENGTH	64
droEre1.xenoRefGene.LENGTH	65
droGri1.genscan.LENGTH	65
droGri1.xenoRefGene.LENGTH	66
droMoj1.geneid.LENGTH	66
droMoj1.genscan.LENGTH	67
droMoj1.xenoRefGene.LENGTH	67
droMoj2.genscan.LENGTH	68
droMoj2.xenoRefGene.LENGTH	68
droPer1.genscan.LENGTH	69
droPer1.xenoRefGene.LENGTH	69
droSec1.genscan.LENGTH	70
droSec1.xenoRefGene.LENGTH	70
droSim1.geneid.LENGTH	71
droSim1.genscan.LENGTH	71
droSim1.xenoRefGene.LENGTH	72
droVir1.geneid.LENGTH	72
droVir1.genscan.LENGTH	73
droVir1.xenoRefGene.LENGTH	73
droVir2.genscan.LENGTH	74
droVir2.xenoRefGene.LENGTH	74
droYak1.geneid.LENGTH	75
droYak1.genscan.LENGTH	75
droYak1.xenoRefGene.LENGTH	76
droYak2.genscan.LENGTH	76
droYak2.xenoRefGene.LENGTH	77
equCab1.geneid.LENGTH	77
equCab1.geneSymbol.LENGTH	78
equCab1.nscanGene.LENGTH	78
equCab1.refGene.LENGTH	79
equCab1.sgpGene.LENGTH	79
equCab2.ensGene.LENGTH	80

equCab2.geneSymbol.LENGTH	80
equCab2.nscanGene.LENGTH	81
equCab2.refGene.LENGTH	81
equCab2.xenoRefGene.LENGTH	82
felCat3.ensGene.LENGTH	82
felCat3.geneid.LENGTH	83
felCat3.geneSymbol.LENGTH	83
felCat3.genscan.LENGTH	84
felCat3.nscanGene.LENGTH	84
felCat3.refGene.LENGTH	85
felCat3.sgpGene.LENGTH	85
felCat3.xenoRefGene.LENGTH	86
fr1.ensGene.LENGTH	86
fr1.genscan.LENGTH	87
fr2.ensGene.LENGTH	87
galGal2.ensGene.LENGTH	88
galGal2.geneid.LENGTH	88
galGal2.geneSymbol.LENGTH	89
galGal2.genscan.LENGTH	89
galGal2.refGene.LENGTH	90
galGal2.sgpGene.LENGTH	90
galGal3.ensGene.LENGTH	91
galGal3.geneSymbol.LENGTH	91
galGal3.genscan.LENGTH	92
galGal3.nscanGene.LENGTH	92
galGal3.refGene.LENGTH	93
galGal3.xenoRefGene.LENGTH	93
gasAcu1.ensGene.LENGTH	94
gasAcu1.nscanGene.LENGTH	94
geneLenDatabase-pkg	95
hg16.acembly.LENGTH	95
hg16.ensGene.LENGTH	96
hg16.exoniphy.LENGTH	96
hg16.geneid.LENGTH	97
hg16.geneSymbol.LENGTH	97
hg16.genscan.LENGTH	98
hg16.knownGene.LENGTH	98
hg16.refGene.LENGTH	99
hg16.sgpGene.LENGTH	99
hg17.acembly.LENGTH	100
hg17.acescan.LENGTH	100
hg17.ccdsGene.LENGTH	101
hg17.ensGene.LENGTH	101
hg17.exoniphy.LENGTH	102
hg17.geneid.LENGTH	102
hg17.geneSymbol.LENGTH	103
hg17.genscan.LENGTH	103
hg17.knownGene.LENGTH	104

hg17.refGene.LENGTH	104
hg17.sgpGene.LENGTH	105
hg17.vegaGene.LENGTH	105
hg17.vegaPseudoGene.LENGTH	106
hg17.xenoRefGene.LENGTH	106
hg18.acembly.LENGTH	107
hg18.acescan.LENGTH	107
hg18.ccdsGene.LENGTH	108
hg18.ensGene.LENGTH	108
hg18.exoniphy.LENGTH	109
hg18.geneid.LENGTH	109
hg18.geneSymbol.LENGTH	110
hg18.genscan.LENGTH	110
hg18.knownGene.LENGTH	111
hg18.knownGeneOld3.LENGTH	111
hg18.refGene.LENGTH	112
hg18.sgpGene.LENGTH	112
hg18.sibGene.LENGTH	113
hg18.xenoRefGene.LENGTH	113
hg19.ccdsGene.LENGTH	114
hg19.ensGene.LENGTH	114
hg19.exoniphy.LENGTH	115
hg19.geneSymbol.LENGTH	115
hg19.knownGene.LENGTH	116
hg19.nscanGene.LENGTH	116
hg19.refGene.LENGTH	117
hg19.xenoRefGene.LENGTH	117
loxAfr3.xenoRefGene.LENGTH	118
mm7.ensGene.LENGTH	118
mm7.geneid.LENGTH	119
mm7.geneSymbol.LENGTH	119
mm7.genscan.LENGTH	120
mm7.knownGene.LENGTH	120
mm7.refGene.LENGTH	121
mm7.sgpGene.LENGTH	121
mm7.xenoRefGene.LENGTH	122
mm8.ccdsGene.LENGTH	122
mm8.ensGene.LENGTH	123
mm8.geneid.LENGTH	123
mm8.geneSymbol.LENGTH	124
mm8.genscan.LENGTH	124
mm8.knownGene.LENGTH	125
mm8.nscanGene.LENGTH	125
mm8.refGene.LENGTH	126
mm8.sgpGene.LENGTH	126
mm8.sibGene.LENGTH	127
mm8.xenoRefGene.LENGTH	127
mm9.acembly.LENGTH	128

mm9.ccdsGene.LENGTH	128
mm9.ensGene.LENGTH	129
mm9.exoniphy.LENGTH	129
mm9.geneid.LENGTH	130
mm9.geneSymbol.LENGTH	130
mm9.genscan.LENGTH	131
mm9.knownGene.LENGTH	131
mm9.nscanGene.LENGTH	132
mm9.refGene.LENGTH	132
mm9.sgpGene.LENGTH	133
mm9.xenoRefGene.LENGTH	133
monDom1.genscan.LENGTH	134
monDom4.ensGene.LENGTH	134
monDom4.geneSymbol.LENGTH	135
monDom4.genscan.LENGTH	135
monDom4.nscanGene.LENGTH	136
monDom4.refGene.LENGTH	136
monDom4.xenoRefGene.LENGTH	137
monDom5.ensGene.LENGTH	137
monDom5.geneSymbol.LENGTH	138
monDom5.genscan.LENGTH	138
monDom5.nscanGene.LENGTH	139
monDom5.refGene.LENGTH	139
monDom5.xenoRefGene.LENGTH	140
ornAna1.ensGene.LENGTH	140
ornAna1.geneSymbol.LENGTH	141
ornAna1.refGene.LENGTH	141
ornAna1.xenoRefGene.LENGTH	142
oryLat2.ensGene.LENGTH	142
oryLat2.geneSymbol.LENGTH	143
oryLat2.refGene.LENGTH	143
oryLat2.xenoRefGene.LENGTH	144
panTro1.ensGene.LENGTH	144
panTro1.geneid.LENGTH	145
panTro1.genscan.LENGTH	145
panTro1.xenoRefGene.LENGTH	146
panTro2.ensGene.LENGTH	146
panTro2.geneSymbol.LENGTH	147
panTro2.genscan.LENGTH	147
panTro2.nscanGene.LENGTH	148
panTro2.refGene.LENGTH	148
panTro2.xenoRefGene.LENGTH	149
petMar1.xenoRefGene.LENGTH	149
ponAbe2.ensGene.LENGTH	150
ponAbe2.geneSymbol.LENGTH	150
ponAbe2.genscan.LENGTH	151
ponAbe2.nscanGene.LENGTH	151
ponAbe2.refGene.LENGTH	152

ponAbe2.xenoRefGene.LENGTH	152
priPac1.xenoRefGene.LENGTH	153
rheMac2.ensGene.LENGTH	153
rheMac2.geneid.LENGTH	154
rheMac2.geneSymbol.LENGTH	154
rheMac2.nscanGene.LENGTH	155
rheMac2.refGene.LENGTH	155
rheMac2.sgpGene.LENGTH	156
rheMac2.xenoRefGene.LENGTH	156
rn3.ensGene.LENGTH	157
rn3.geneid.LENGTH	157
rn3.geneSymbol.LENGTH	158
rn3.genscan.LENGTH	158
rn3.knownGene.LENGTH	159
rn3.nscanGene.LENGTH	159
rn3.refGene.LENGTH	160
rn3.sgpGene.LENGTH	160
rn3.xenoRefGene.LENGTH	161
rn4.ensGene.LENGTH	161
rn4.geneid.LENGTH	162
rn4.geneSymbol.LENGTH	162
rn4.genscan.LENGTH	163
rn4.knownGene.LENGTH	163
rn4.nscanGene.LENGTH	164
rn4.refGene.LENGTH	164
rn4.sgpGene.LENGTH	165
rn4.xenoRefGene.LENGTH	165
sacCer1.ensGene.LENGTH	166
sacCer2.ensGene.LENGTH	166
strPur1.geneSymbol.LENGTH	167
strPur1.genscan.LENGTH	167
strPur1.refGene.LENGTH	168
strPur1.xenoRefGene.LENGTH	168
strPur2.geneSymbol.LENGTH	169
strPur2.genscan.LENGTH	169
strPur2.refGene.LENGTH	170
strPur2.xenoRefGene.LENGTH	170
supportedGeneIDs	171
supportedGenomes	171
taeGut1.ensGene.LENGTH	172
taeGut1.geneSymbol.LENGTH	173
taeGut1.genscan.LENGTH	173
taeGut1.nscanGene.LENGTH	174
taeGut1.refGene.LENGTH	174
taeGut1.xenoRefGene.LENGTH	175
tetNig1.ensGene.LENGTH	175
tetNig1.geneid.LENGTH	176
tetNig1.genscan.LENGTH	176

tetNig1.nscanGene.LENGTH	177
tetNig2.ensGene.LENGTH	177
unfactor	178
xenTro1.genscan.LENGTH	179
xenTro2.ensGene.LENGTH	179
xenTro2.geneSymbol.LENGTH	180
xenTro2.genscan.LENGTH	180
xenTro2.refGene.LENGTH	181

Index	182
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anoCar1.ensGene.LENGTH
<i>Transcript length data for the organism anoCar</i>

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

anoCar1.genscan.LENGTH
<i>Transcript length data for the organism anoCar</i>

Description

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

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

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

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

```
anoCar1.xenoRefGene.LENGTH
```

Transcript length data for the organism anoCar

Description

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

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

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

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

```
anoGam1.ensGene.LENGTH
```

Transcript length data for the organism anoGam

Description

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

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

See Also[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

`caeJap1.xenoRefGene.LENGTH`*Transcript length data for the organism caeJap*

Description

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

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

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

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

`caePb1.xenoRefGene.LENGTH`*Transcript length data for the organism caePb*

Description

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

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

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

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

`caePb2.xenoRefGene.LENGTH`*Transcript length data for the organism caePb*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

`caeRem2.xenoRefGene.LENGTH`*Transcript length data for the organism caeRem*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

ce2.geneid.LENGTH	<i>Transcript length data for the organism ce</i>
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Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

ce2.geneSymbol.LENGTH	<i>Transcript length data for the organism ce</i>
-----------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

ce2.refGene.LENGTH	<i>Transcript length data for the organism ce</i>
--------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

dm1.refGene.LENGTH	<i>Transcript length data for the organism dm</i>
--------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

dm2.geneid.LENGTH	<i>Transcript length data for the organism dm</i>
-------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

dm3.refGene.LENGTH	<i>Transcript length data for the organism dm</i>
--------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

downloadLengthFromUCSC	<i>Download Transcript Length Data</i>
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Description

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

Usage

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

Arguments

genome	A string identifying the genome that genes refer to. For a list of supported organisms see supportedGenomes .
id	A string identifying the gene identifier used by genes. For a list of supported gene identifiers see supportedGeneIDs .

Details

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

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

Value

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

Note

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

Author(s)

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See Also

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

Examples

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

## End(Not run)
```

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
dp2.xenoRefGene.LENGTH
```

Transcript length data for the organism dp

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
dp3.geneid.LENGTH
```

Transcript length data for the organism dp

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

dp3.genscan.LENGTH	<i>Transcript length data for the organism dp</i>
--------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

dp3.xenoRefGene.LENGTH	<i>Transcript length data for the organism dp</i>
------------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

fr1.genscan.LENGTH	<i>Transcript length data for the organism fr</i>
--------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

fr2.ensGene.LENGTH	<i>Transcript length data for the organism fr</i>
--------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

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

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

geneLenDatabase-pkg *geneLenDatabase:*

Description

Lengths of mRNA transcripts for a number of genomes

Details

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

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See Also

Useful links:

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg17.acembly.LENGTH	<i>Transcript length data for the organism hg</i>
---------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg17.acescan.LENGTH	<i>Transcript length data for the organism hg</i>
---------------------	---

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

hg17.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.ccdsGene.LENGTH)
head(hg17.ccdsGene.LENGTH)
```

hg17.ensGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.ensGene.LENGTH)
head(hg17.ensGene.LENGTH)
```

hg17.exoniphy.LENGTH *Transcript length data for the organism hg*

Description

hg17.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg17, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.exoniphy.LENGTH)
head(hg17.exoniphy.LENGTH)
```

hg17.geneid.LENGTH *Transcript length data for the organism hg*

Description

hg17.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(hg17, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.geneid.LENGTH)
head(hg17.geneid.LENGTH)
```

`hg17.geneSymbol.LENGTH`*Transcript length data for the organism hg*

Description

hg17.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg17, geneSymbol)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(hg17.geneSymbol.LENGTH)
head(hg17.geneSymbol.LENGTH)
```

`hg17.genscan.LENGTH`*Transcript length data for the organism hg*

Description

hg17.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(hg17, genscan)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(hg17.genscan.LENGTH)
head(hg17.genscan.LENGTH)
```

hg17.knownGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.knownGene.LENGTH)
head(hg17.knownGene.LENGTH)
```

hg17.refGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.refGene.LENGTH)
head(hg17.refGene.LENGTH)
```

hg17.sgpGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.sgpGene.LENGTH)
head(hg17.sgpGene.LENGTH)
```

hg17.vegaGene.LENGTH *Transcript length data for the organism hg*

Description

hg17.vegaGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the vegaGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, vegaGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.vegaGene.LENGTH)
head(hg17.vegaGene.LENGTH)
```

`hg17.vegaPseudoGene.LENGTH`*Transcript length data for the organism hg*

Description

hg17.vegaPseudoGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the vegaPseudoGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, vegaPseudoGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.vegaPseudoGene.LENGTH)
head(hg17.vegaPseudoGene.LENGTH)
```

`hg17.xenoRefGene.LENGTH`*Transcript length data for the organism hg*

Description

hg17.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg17, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg17.xenoRefGene.LENGTH)
head(hg17.xenoRefGene.LENGTH)
```

hg18.acembly.LENGTH	<i>Transcript length data for the organism hg</i>
---------------------	---

Description

hg18.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the acembly table.

The data file was made by calling `downloadLengthFromUCSC(hg18, acembly)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.acembly.LENGTH)
head(hg18.acembly.LENGTH)
```

hg18.acescan.LENGTH	<i>Transcript length data for the organism hg</i>
---------------------	---

Description

hg18.acescan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the acescan table.

The data file was made by calling `downloadLengthFromUCSC(hg18, acescan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.acescan.LENGTH)
head(hg18.acescan.LENGTH)
```

hg18.ccdsGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.ccdsGene.LENGTH)
head(hg18.ccdsGene.LENGTH)
```

hg18.ensGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.ensGene.LENGTH)
head(hg18.ensGene.LENGTH)
```

hg18.exoniphy.LENGTH *Transcript length data for the organism hg*

Description

hg18.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg18, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.exoniphy.LENGTH)
head(hg18.exoniphy.LENGTH)
```

hg18.geneid.LENGTH *Transcript length data for the organism hg*

Description

hg18.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(hg18, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.geneid.LENGTH)
head(hg18.geneid.LENGTH)
```

`hg18.geneSymbol.LENGTH`*Transcript length data for the organism hg*

Description

hg18.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg18, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.geneSymbol.LENGTH)
head(hg18.geneSymbol.LENGTH)
```

`hg18.genscan.LENGTH`*Transcript length data for the organism hg*

Description

hg18.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(hg18, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.genscan.LENGTH)
head(hg18.genscan.LENGTH)
```

hg18.knownGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.knownGene.LENGTH)
head(hg18.knownGene.LENGTH)
```

hg18.knownGeneOld3.LENGTH
Transcript length data for the organism hg

Description

hg18.knownGeneOld3.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGeneOld3 table.

The data file was made by calling `downloadLengthFromUCSC(hg18, knownGeneOld3)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.knownGeneOld3.LENGTH)
head(hg18.knownGeneOld3.LENGTH)
```

hg18.refGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.refGene.LENGTH)
head(hg18.refGene.LENGTH)
```

hg18.sgpGene.LENGTH *Transcript length data for the organism hg*

Description

hg18.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.sgpGene.LENGTH)
head(hg18.sgpGene.LENGTH)
```

hg18.sibGene.LENGTH	<i>Transcript length data for the organism hg</i>
---------------------	---

Description

hg18.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sibGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, sibGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.sibGene.LENGTH)
head(hg18.sibGene.LENGTH)
```

hg18.xenoRefGene.LENGTH	<i>Transcript length data for the organism hg</i>
-------------------------	---

Description

hg18.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg18, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg18.xenoRefGene.LENGTH)
head(hg18.xenoRefGene.LENGTH)
```

hg19.ccdsGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.ccdsGene.LENGTH)
head(hg19.ccdsGene.LENGTH)
```

hg19.ensGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.ensGene.LENGTH)
head(hg19.ensGene.LENGTH)
```

hg19.exoniphy.LENGTH *Transcript length data for the organism hg*

Description

hg19.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg19, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.exoniphy.LENGTH)
head(hg19.exoniphy.LENGTH)
```

hg19.geneSymbol.LENGTH *Transcript length data for the organism hg*

Description

hg19.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg19, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.geneSymbol.LENGTH)
head(hg19.geneSymbol.LENGTH)
```

hg19.knownGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.knownGene.LENGTH)
head(hg19.knownGene.LENGTH)
```

hg19.nscanGene.LENGTH *Transcript length data for the organism hg*

Description

hg19.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.nscanGene.LENGTH)
head(hg19.nscanGene.LENGTH)
```

hg19.refGene.LENGTH	<i>Transcript length data for the organism hg</i>
---------------------	---

Description

hg19.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.refGene.LENGTH)
head(hg19.refGene.LENGTH)
```

hg19.xenoRefGene.LENGTH	<i>Transcript length data for the organism hg</i>
-------------------------	---

Description

hg19.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(hg19.xenoRefGene.LENGTH)
head(hg19.xenoRefGene.LENGTH)
```

`loxAfr3.xenoRefGene.LENGTH`*Transcript length data for the organism loxAfr*

Description

`loxAfr3.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(loxAfr3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(loxAfr3.xenoRefGene.LENGTH)
head(loxAfr3.xenoRefGene.LENGTH)
```

`mm7.ensGene.LENGTH`*Transcript length data for the organism mm*

Description

`mm7.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm7, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.ensGene.LENGTH)
head(mm7.ensGene.LENGTH)
```

mm7.geneid.LENGTH	<i>Transcript length data for the organism mm</i>
-------------------	---

Description

mm7.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.geneid.LENGTH)
head(mm7.geneid.LENGTH)
```

mm7.geneSymbol.LENGTH	<i>Transcript length data for the organism mm</i>
-----------------------	---

Description

mm7.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.geneSymbol.LENGTH)
head(mm7.geneSymbol.LENGTH)
```

mm7.genscan.LENGTH	<i>Transcript length data for the organism mm</i>
--------------------	---

Description

mm7.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm7, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.genscan.LENGTH)
head(mm7.genscan.LENGTH)
```

mm7.knownGene.LENGTH	<i>Transcript length data for the organism mm</i>
----------------------	---

Description

mm7.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.knownGene.LENGTH)
head(mm7.knownGene.LENGTH)
```

mm7.refGene.LENGTH	<i>Transcript length data for the organism mm</i>
--------------------	---

Description

mm7.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.refGene.LENGTH)
head(mm7.refGene.LENGTH)
```

mm7.sgpGene.LENGTH	<i>Transcript length data for the organism mm</i>
--------------------	---

Description

mm7.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm7.sgpGene.LENGTH)
head(mm7.sgpGene.LENGTH)
```

`mm7.xenoRefGene.LENGTH`*Transcript length data for the organism mm*

Description

`mm7.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm7, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(mm7.xenoRefGene.LENGTH)
head(mm7.xenoRefGene.LENGTH)
```

`mm8.ccdsGene.LENGTH`*Transcript length data for the organism mm*

Description

`mm8.ccdsGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ccdsGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ccdsGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(mm8.ccdsGene.LENGTH)
head(mm8.ccdsGene.LENGTH)
```

mm8.ensGene.LENGTH	<i>Transcript length data for the organism mm</i>
--------------------	---

Description

mm8.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.ensGene.LENGTH)
head(mm8.ensGene.LENGTH)
```

mm8.geneid.LENGTH	<i>Transcript length data for the organism mm</i>
-------------------	---

Description

mm8.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.geneid.LENGTH)
head(mm8.geneid.LENGTH)
```

mm8.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

mm8.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.geneSymbol.LENGTH)
head(mm8.geneSymbol.LENGTH)
```

mm8.genscan.LENGTH *Transcript length data for the organism mm*

Description

mm8.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm8, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.genscan.LENGTH)
head(mm8.genscan.LENGTH)
```

mm8.knownGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.knownGene.LENGTH)
head(mm8.knownGene.LENGTH)
```

mm8.nscanGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.nscanGene.LENGTH)
head(mm8.nscanGene.LENGTH)
```

mm8.refGene.LENGTH	<i>Transcript length data for the organism mm</i>
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Description

mm8.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.refGene.LENGTH)
head(mm8.refGene.LENGTH)
```

mm8.sgpGene.LENGTH	<i>Transcript length data for the organism mm</i>
--------------------	---

Description

mm8.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.sgpGene.LENGTH)
head(mm8.sgpGene.LENGTH)
```

mm8.sibGene.LENGTH	<i>Transcript length data for the organism mm</i>
--------------------	---

Description

mm8.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sibGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sibGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.sibGene.LENGTH)
head(mm8.sibGene.LENGTH)
```

mm8.xenoRefGene.LENGTH	<i>Transcript length data for the organism mm</i>
------------------------	---

Description

mm8.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.xenoRefGene.LENGTH)
head(mm8.xenoRefGene.LENGTH)
```

mm9.acembly.LENGTH	<i>Transcript length data for the organism mm</i>
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Description

mm9.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the acembly table.

The data file was made by calling `downloadLengthFromUCSC(mm9, acembly)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.acembly.LENGTH)
head(mm9.acembly.LENGTH)
```

mm9.ccdsGene.LENGTH	<i>Transcript length data for the organism mm</i>
---------------------	---

Description

mm9.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.ccdsGene.LENGTH)
head(mm9.ccdsGene.LENGTH)
```

mm9.ensGene.LENGTH	<i>Transcript length data for the organism mm</i>
--------------------	---

Description

mm9.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.ensGene.LENGTH)
head(mm9.ensGene.LENGTH)
```

mm9.exoniphy.LENGTH	<i>Transcript length data for the organism mm</i>
---------------------	---

Description

mm9.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(mm9, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.exoniphy.LENGTH)
head(mm9.exoniphy.LENGTH)
```

mm9.geneid.LENGTH	<i>Transcript length data for the organism mm</i>
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Description

mm9.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.geneid.LENGTH)
head(mm9.geneid.LENGTH)
```

mm9.geneSymbol.LENGTH	<i>Transcript length data for the organism mm</i>
-----------------------	---

Description

mm9.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.geneSymbol.LENGTH)
head(mm9.geneSymbol.LENGTH)
```

mm9.genscan.LENGTH	<i>Transcript length data for the organism mm</i>
--------------------	---

Description

mm9.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm9, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.genscan.LENGTH)
head(mm9.genscan.LENGTH)
```

mm9.knownGene.LENGTH	<i>Transcript length data for the organism mm</i>
----------------------	---

Description

mm9.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.knownGene.LENGTH)
head(mm9.knownGene.LENGTH)
```

mm9.nscanGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.nscanGene.LENGTH)
head(mm9.nscanGene.LENGTH)
```

mm9.refGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.refGene.LENGTH)
head(mm9.refGene.LENGTH)
```

mm9.sgpGene.LENGTH	<i>Transcript length data for the organism mm</i>
--------------------	---

Description

mm9.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.sgpGene.LENGTH)
head(mm9.sgpGene.LENGTH)
```

mm9.xenoRefGene.LENGTH	<i>Transcript length data for the organism mm</i>
------------------------	---

Description

mm9.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.xenoRefGene.LENGTH)
head(mm9.xenoRefGene.LENGTH)
```

`monDom1.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom1.genscan.LENGTH)
head(monDom1.genscan.LENGTH)
```

`monDom4.ensGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.ensGene.LENGTH)
head(monDom4.ensGene.LENGTH)
```

`monDom4.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

Description

monDom4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, geneSymbol)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(monDom4.geneSymbol.LENGTH)
head(monDom4.geneSymbol.LENGTH)
```

`monDom4.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

monDom4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, genscan)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(monDom4.genscan.LENGTH)
head(monDom4.genscan.LENGTH)
```

`monDom4.nscanGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.nscanGene.LENGTH)
head(monDom4.nscanGene.LENGTH)
```

`monDom4.refGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.refGene.LENGTH)
head(monDom4.refGene.LENGTH)
```

`monDom4.xenoRefGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.xenoRefGene.LENGTH)
head(monDom4.xenoRefGene.LENGTH)
```

`monDom5.ensGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.ensGene.LENGTH)
head(monDom5.ensGene.LENGTH)
```

`monDom5.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, geneSymbol)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(monDom5.geneSymbol.LENGTH)
head(monDom5.geneSymbol.LENGTH)
```

`monDom5.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, genscan)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(monDom5.genscan.LENGTH)
head(monDom5.genscan.LENGTH)
```

`monDom5.nscanGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)
```

`monDom5.refGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)
```

`monDom5.xenoRefGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.xenoRefGene.LENGTH)
head(monDom5.xenoRefGene.LENGTH)
```

`ornAna1.ensGene.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.ensGene.LENGTH)
head(ornAna1.ensGene.LENGTH)
```

`ornAna1.geneSymbol.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.geneSymbol.LENGTH)
head(ornAna1.geneSymbol.LENGTH)
```

`ornAna1.refGene.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.refGene.LENGTH)
head(ornAna1.refGene.LENGTH)
```

`ornAna1.xenoRefGene.LENGTH`*Transcript length data for the organism ornAna*

Description

`ornAna1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.xenoRefGene.LENGTH)
head(ornAna1.xenoRefGene.LENGTH)
```

`oryLat2.ensGene.LENGTH`*Transcript length data for the organism oryLat*

Description

`oryLat2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)
```

`oryLat2.geneSymbol.LENGTH`*Transcript length data for the organism oryLat*

Description

`oryLat2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, geneSymbol)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)
```

`oryLat2.refGene.LENGTH`*Transcript length data for the organism oryLat*

Description

`oryLat2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, refGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)
```

```
oryLat2.xenoRefGene.LENGTH
```

Transcript length data for the organism oryLat

Description

oryLat2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)
```

```
panTro1.ensGene.LENGTH
```

Transcript length data for the organism panTro

Description

panTro1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.ensGene.LENGTH)
head(panTro1.ensGene.LENGTH)
```

panTro1.geneid.LENGTH *Transcript length data for the organism panTro*

Description

panTro1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.geneid.LENGTH)
head(panTro1.geneid.LENGTH)
```

panTro1.genscan.LENGTH
Transcript length data for the organism panTro

Description

panTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.genscan.LENGTH)
head(panTro1.genscan.LENGTH)
```

`panTro1.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(panTro1.xenoRefGene.LENGTH)
head(panTro1.xenoRefGene.LENGTH)
```

`panTro2.ensGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, ensGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)
```

`panTro2.geneSymbol.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, geneSymbol)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)
```

`panTro2.genscan.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, genscan)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(panTro2.genscan.LENGTH)
head(panTro2.genscan.LENGTH)
```

`panTro2.nscanGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, nscanGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(panTro2.nscanGene.LENGTH)
head(panTro2.nscanGene.LENGTH)
```

`panTro2.refGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, refGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(panTro2.refGene.LENGTH)
head(panTro2.refGene.LENGTH)
```

`panTro2.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

Description

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(panTro2.xenoRefGene.LENGTH)
head(panTro2.xenoRefGene.LENGTH)
```

`petMar1.xenoRefGene.LENGTH`*Transcript length data for the organism petMar*

Description

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(petMar1, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)
```

`ponAbe2.ensGene.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, ensGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)
```

`ponAbe2.geneSymbol.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, geneSymbol)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)
```

`ponAbe2.genscan.LENGTH`*Transcript length data for the organism ponAbe*

Description

ponAbe2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, genscan)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)
```

`ponAbe2.nscanGene.LENGTH`*Transcript length data for the organism ponAbe*

Description

ponAbe2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, nscanGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(ponAbe2.nscanGene.LENGTH)
head(ponAbe2.nscanGene.LENGTH)
```

`ponAbe2.refGene.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, refGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(ponAbe2.refGene.LENGTH)
head(ponAbe2.refGene.LENGTH)
```

`ponAbe2.xenoRefGene.LENGTH`*Transcript length data for the organism ponAbe*

Description

`ponAbe2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)
```

`priPac1.xenoRefGene.LENGTH`*Transcript length data for the organism priPac*

Description

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(priPac1, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)
```

`rheMac2.ensGene.LENGTH`*Transcript length data for the organism rheMac*

Description

rheMac2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, ensGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)
```

rheMac2.geneid.LENGTH *Transcript length data for the organism rheMac*

Description

rheMac2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.geneid.LENGTH)
head(rheMac2.geneid.LENGTH)
```

rheMac2.geneSymbol.LENGTH
Transcript length data for the organism rheMac

Description

rheMac2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)
```

`rheMac2.nscanGene.LENGTH`*Transcript length data for the organism rheMac*

Description

rheMac2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, nscanGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)
```

`rheMac2.refGene.LENGTH`*Transcript length data for the organism rheMac*

Description

rheMac2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, refGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)
```

`rheMac2.sgpGene.LENGTH`*Transcript length data for the organism rheMac*

Description

`rheMac2.sgpGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `sgpGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.sgpGene.LENGTH)
head(rheMac2.sgpGene.LENGTH)
```

`rheMac2.xenoRefGene.LENGTH`*Transcript length data for the organism rheMac*

Description

`rheMac2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)
```

rn3.ensGene.LENGTH	<i>Transcript length data for the organism rn</i>
--------------------	---

Description

rn3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.LENGTH)
```

rn3.geneid.LENGTH	<i>Transcript length data for the organism rn</i>
-------------------	---

Description

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.geneid.LENGTH)
head(rn3.geneid.LENGTH)
```

rn3.geneSymbol.LENGTH *Transcript length data for the organism rn*

Description

rn3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.geneSymbol.LENGTH)
head(rn3.geneSymbol.LENGTH)
```

rn3.genscan.LENGTH *Transcript length data for the organism rn*

Description

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn3, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)
```

rn3.knownGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

rn3.nscanGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

rn3.refGene.LENGTH	<i>Transcript length data for the organism rn</i>
--------------------	---

Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

rn3.sgpGene.LENGTH	<i>Transcript length data for the organism rn</i>
--------------------	---

Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)
```

`rn3.xenoRefGene.LENGTH`*Transcript length data for the organism rn*

Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)
```

`rn4.ensGene.LENGTH`*Transcript length data for the organism rn*

Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, ensGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)
```

rn4.geneid.LENGTH	<i>Transcript length data for the organism rn</i>
-------------------	---

Description

rn4.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```

rn4.geneSymbol.LENGTH	<i>Transcript length data for the organism rn</i>
-----------------------	---

Description

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

rn4.genscan.LENGTH	<i>Transcript length data for the organism rn</i>
--------------------	---

Description

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn4, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

rn4.knownGene.LENGTH	<i>Transcript length data for the organism rn</i>
----------------------	---

Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.knownGene.LENGTH)
head(rn4.knownGene.LENGTH)
```

rn4.nscanGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)
```

rn4.refGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)
```

rn4.sgpGene.LENGTH	<i>Transcript length data for the organism rn</i>
--------------------	---

Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

rn4.xenoRefGene.LENGTH	<i>Transcript length data for the organism rn</i>
------------------------	---

Description

rn4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.xenoRefGene.LENGTH)
head(rn4.xenoRefGene.LENGTH)
```

`sacCer1.ensGene.LENGTH`*Transcript length data for the organism sacCer*

Description

sacCer1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer1, ensGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(sacCer1.ensGene.LENGTH)
head(sacCer1.ensGene.LENGTH)
```

`sacCer2.ensGene.LENGTH`*Transcript length data for the organism sacCer*

Description

sacCer2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer2, ensGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)
```

`strPur1.geneSymbol.LENGTH`*Transcript length data for the organism strPur*

Description

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, geneSymbol)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)
```

`strPur1.genscan.LENGTH`*Transcript length data for the organism strPur*

Description

strPur1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, genscan)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(strPur1.genscan.LENGTH)
head(strPur1.genscan.LENGTH)
```

`strPur1.refGene.LENGTH`*Transcript length data for the organism strPur*

Description

strPur1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, refGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(strPur1.refGene.LENGTH)
head(strPur1.refGene.LENGTH)
```

`strPur1.xenoRefGene.LENGTH`*Transcript length data for the organism strPur*

Description

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(strPur1.xenoRefGene.LENGTH)
head(strPur1.xenoRefGene.LENGTH)
```

`strPur2.geneSymbol.LENGTH`*Transcript length data for the organism strPur*

Description

strPur2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, geneSymbol)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(strPur2.geneSymbol.LENGTH)
head(strPur2.geneSymbol.LENGTH)
```

`strPur2.genscan.LENGTH`*Transcript length data for the organism strPur*

Description

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, genscan)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(strPur2.genscan.LENGTH)
head(strPur2.genscan.LENGTH)
```

`strPur2.refGene.LENGTH`*Transcript length data for the organism strPur*

Description

strPur2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, refGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(strPur2.refGene.LENGTH)
head(strPur2.refGene.LENGTH)
```

`strPur2.xenoRefGene.LENGTH`*Transcript length data for the organism strPur*

Description

strPur2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)
```

supportedGeneIDs	<i>Supported Gene IDs</i>
------------------	---------------------------

Description

Lists supported gene ID formats

Usage

```
supportedGeneIDs()
```

Details

Uses the supportedUCSCTables function from the GenomicFeatures package to obtain a list of gene ID formats available from the UCSC genome browser. The db column gives the gene ID formats which are provided to the id argument of various functions. The track and subtrack columns are the names of the UCSC track/subtrack from which information is fetched.

The GeneID column lists the "full name" of the gene ID format where available.

The final column, headed AvailableGenomes lists the genomes for which there is a local copy of the length information available for the gene ID format listed in the geneLenDataBase package.

Value

A data.frame containing supported gene ID formats.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
supportedGeneIDs()
```

supportedGenomes	<i>Supported Genomes</i>
------------------	--------------------------

Description

Lists supported genomes

Usage

```
supportedGenomes()
```

Details

Uses the `ucscGenomes()` function from the `rtracklayer` package to obtain a list of genomes available from the UCSC genome browser. The `db` column lists genomes as they are provided to the genome argument of various functions.

The final column, headed `AvailableGeneIDs` lists the gene ID formats for which there is a local copy of the length information available for the genome listed in the `geneLenDataBase` package.

Value

A `data.frame` containing supported genomes.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
supportedGenomes()
```

```
taeGut1.ensGene.LENGTH
```

Transcript length data for the organism taeGut

Description

`taeGut1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)
```

`taeGut1.geneSymbol.LENGTH`*Transcript length data for the organism taeGut*

Description

`taeGut1.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, geneSymbol)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)
```

`taeGut1.genscan.LENGTH`*Transcript length data for the organism taeGut*

Description

`taeGut1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, genscan)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)
```

`taeGut1.nscanGene.LENGTH`*Transcript length data for the organism taeGut*

Description

taeGut1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, nscanGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)
```

`taeGut1.refGene.LENGTH`*Transcript length data for the organism taeGut*

Description

taeGut1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, refGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

`taeGut1.xenoRefGene.LENGTH`*Transcript length data for the organism taeGut*

Description

`taeGut1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, xenoRefGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

`tetNig1.ensGene.LENGTH`*Transcript length data for the organism tetNig*

Description

`tetNig1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, ensGene)` on the date on which the package was last updated.

See Also[downloadLengthFromUCSC](#)**Examples**

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

tetNig1.geneid.LENGTH *Transcript length data for the organism tetNig*

Description

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

tetNig1.genscan.LENGTH
Transcript length data for the organism tetNig

Description

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```

`tetNig1.nscanGene.LENGTH`*Transcript length data for the organism tetNig*

Description

tetNig1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

`tetNig2.ensGene.LENGTH`*Transcript length data for the organism tetNig*

Description

tetNig2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig2.ensGene.LENGTH)
head(tetNig2.ensGene.LENGTH)
```

`unfactor`*Purge factors*

Description

Removes all factors from a variable in a sensible way.

Usage

```
unfactor(var)
```

Arguments

`var` The variable from which you want the factors removed.

Details

As factors are their own type, to remove factors we must convert each level into another type. This is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be done without inducing NAs, otherwise it is coerced using `as.character`. Currently supported types are: `factor`, `data.frame` and `list`.

Value

The variable with all factors converted to characters or numbers (see details).

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

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

* datasets

anoCar1.ensGene.LENGTH, 9
anoCar1.genscan.LENGTH, 9
anoCar1.xenoRefGene.LENGTH, 10
anoGam1.ensGene.LENGTH, 10
anoGam1.geneid.LENGTH, 11
anoGam1.genscan.LENGTH, 11
apiMel1.genscan.LENGTH, 12
apiMel2.ensGene.LENGTH, 12
apiMel2.geneid.LENGTH, 13
apiMel2.genscan.LENGTH, 13
aplCal1.xenoRefGene.LENGTH, 14
bosTau2.geneid.LENGTH, 14
bosTau2.geneSymbol.LENGTH, 15
bosTau2.genscan.LENGTH, 15
bosTau2.refGene.LENGTH, 16
bosTau2.sgpGene.LENGTH, 16
bosTau3.ensGene.LENGTH, 17
bosTau3.geneid.LENGTH, 17
bosTau3.geneSymbol.LENGTH, 18
bosTau3.genscan.LENGTH, 18
bosTau3.refGene.LENGTH, 19
bosTau3.sgpGene.LENGTH, 19
bosTau4.ensGene.LENGTH, 20
bosTau4.geneSymbol.LENGTH, 20
bosTau4.genscan.LENGTH, 21
bosTau4.nscanGene.LENGTH, 21
bosTau4.refGene.LENGTH, 22
braFlo1.xenoRefGene.LENGTH, 22
caeJap1.xenoRefGene.LENGTH, 23
caePb1.xenoRefGene.LENGTH, 23
caePb2.xenoRefGene.LENGTH, 24
caeRem2.xenoRefGene.LENGTH, 24
caeRem3.xenoRefGene.LENGTH, 25
calJac1.genscan.LENGTH, 25
calJac1.nscanGene.LENGTH, 26
calJac1.xenoRefGene.LENGTH, 26
canFam1.ensGene.LENGTH, 27
canFam1.geneSymbol.LENGTH, 27

canFam1.genscan.LENGTH, 28
canFam1.nscanGene.LENGTH, 28
canFam1.refGene.LENGTH, 29
canFam1.xenoRefGene.LENGTH, 29
canFam2.ensGene.LENGTH, 30
canFam2.geneSymbol.LENGTH, 30
canFam2.genscan.LENGTH, 31
canFam2.nscanGene.LENGTH, 31
canFam2.refGene.LENGTH, 32
canFam2.xenoRefGene.LENGTH, 32
cavPor3.ensGene.LENGTH, 33
cavPor3.genscan.LENGTH, 33
cavPor3.nscanGene.LENGTH, 34
cavPor3.xenoRefGene.LENGTH, 34
cb1.xenoRefGene.LENGTH, 35
cb3.xenoRefGene.LENGTH, 35
ce2.geneid.LENGTH, 36
ce2.geneSymbol.LENGTH, 36
ce2.refGene.LENGTH, 37
ce4.geneSymbol.LENGTH, 37
ce4.refGene.LENGTH, 38
ce4.xenoRefGene.LENGTH, 38
ce6.ensGene.LENGTH, 39
ce6.geneSymbol.LENGTH, 39
ce6.refGene.LENGTH, 40
ce6.xenoRefGene.LENGTH, 40
ci1.geneSymbol.LENGTH, 41
ci1.refGene.LENGTH, 41
ci1.xenoRefGene.LENGTH, 42
ci2.ensGene.LENGTH, 42
ci2.geneSymbol.LENGTH, 43
ci2.refGene.LENGTH, 43
ci2.xenoRefGene.LENGTH, 44
danRer3.ensGene.LENGTH, 44
danRer3.geneSymbol.LENGTH, 45
danRer3.refGene.LENGTH, 45
danRer4.ensGene.LENGTH, 46
danRer4.geneSymbol.LENGTH, 46
danRer4.genscan.LENGTH, 47

danRer4.nscanGene.LENGTH, 47
danRer4.refGene.LENGTH, 48
danRer5.ensGene.LENGTH, 48
danRer5.geneSymbol.LENGTH, 49
danRer5.refGene.LENGTH, 49
danRer5.vegaGene.LENGTH, 50
danRer5.vegaPseudoGene.LENGTH, 50
danRer6.ensGene.LENGTH, 51
danRer6.geneSymbol.LENGTH, 51
danRer6.refGene.LENGTH, 52
danRer6.xenoRefGene.LENGTH, 52
dm1.geneSymbol.LENGTH, 53
dm1.genscan.LENGTH, 53
dm1.refGene.LENGTH, 54
dm2.geneid.LENGTH, 54
dm2.geneSymbol.LENGTH, 55
dm2.genscan.LENGTH, 55
dm2.nscanGene.LENGTH, 56
dm2.refGene.LENGTH, 56
dm3.geneSymbol.LENGTH, 57
dm3.nscanPasaGene.LENGTH, 57
dm3.refGene.LENGTH, 58
dp2.genscan.LENGTH, 59
dp2.xenoRefGene.LENGTH, 60
dp3.geneid.LENGTH, 60
dp3.genscan.LENGTH, 61
dp3.xenoRefGene.LENGTH, 61
droAna1.geneid.LENGTH, 62
droAna1.genscan.LENGTH, 62
droAna1.xenoRefGene.LENGTH, 63
droAna2.genscan.LENGTH, 63
droAna2.xenoRefGene.LENGTH, 64
droEre1.genscan.LENGTH, 64
droEre1.xenoRefGene.LENGTH, 65
droGri1.genscan.LENGTH, 65
droGri1.xenoRefGene.LENGTH, 66
droMoj1.geneid.LENGTH, 66
droMoj1.genscan.LENGTH, 67
droMoj1.xenoRefGene.LENGTH, 67
droMoj2.genscan.LENGTH, 68
droMoj2.xenoRefGene.LENGTH, 68
droPer1.genscan.LENGTH, 69
droPer1.xenoRefGene.LENGTH, 69
droSec1.genscan.LENGTH, 70
droSec1.xenoRefGene.LENGTH, 70
droSim1.geneid.LENGTH, 71
droSim1.genscan.LENGTH, 71
droSim1.xenoRefGene.LENGTH, 72
droVir1.geneid.LENGTH, 72
droVir1.genscan.LENGTH, 73
droVir1.xenoRefGene.LENGTH, 73
droVir2.genscan.LENGTH, 74
droVir2.xenoRefGene.LENGTH, 74
droYak1.geneid.LENGTH, 75
droYak1.genscan.LENGTH, 75
droYak1.xenoRefGene.LENGTH, 76
droYak2.genscan.LENGTH, 76
droYak2.xenoRefGene.LENGTH, 77
equCab1.geneid.LENGTH, 77
equCab1.geneSymbol.LENGTH, 78
equCab1.nscanGene.LENGTH, 78
equCab1.refGene.LENGTH, 79
equCab1.sgpGene.LENGTH, 79
equCab2.ensGene.LENGTH, 80
equCab2.geneSymbol.LENGTH, 80
equCab2.nscanGene.LENGTH, 81
equCab2.refGene.LENGTH, 81
equCab2.xenoRefGene.LENGTH, 82
felCat3.ensGene.LENGTH, 82
felCat3.geneid.LENGTH, 83
felCat3.geneSymbol.LENGTH, 83
felCat3.genscan.LENGTH, 84
felCat3.nscanGene.LENGTH, 84
felCat3.refGene.LENGTH, 85
felCat3.sgpGene.LENGTH, 85
felCat3.xenoRefGene.LENGTH, 86
fr1.ensGene.LENGTH, 86
fr1.genscan.LENGTH, 87
fr2.ensGene.LENGTH, 87
galGal2.ensGene.LENGTH, 88
galGal2.geneid.LENGTH, 88
galGal2.geneSymbol.LENGTH, 89
galGal2.genscan.LENGTH, 89
galGal2.refGene.LENGTH, 90
galGal2.sgpGene.LENGTH, 90
galGal3.ensGene.LENGTH, 91
galGal3.geneSymbol.LENGTH, 91
galGal3.genscan.LENGTH, 92
galGal3.nscanGene.LENGTH, 92
galGal3.refGene.LENGTH, 93
galGal3.xenoRefGene.LENGTH, 93
gasAcu1.ensGene.LENGTH, 94
gasAcu1.nscanGene.LENGTH, 94
hg16.acembly.LENGTH, 95
hg16.ensGene.LENGTH, 96
hg16.exoniphy.LENGTH, 96

hg16.geneid.LENGTH, 97
 hg16.geneSymbol.LENGTH, 97
 hg16.genscan.LENGTH, 98
 hg16.knownGene.LENGTH, 98
 hg16.refGene.LENGTH, 99
 hg16.sgpGene.LENGTH, 99
 hg17.acembly.LENGTH, 100
 hg17.acescan.LENGTH, 100
 hg17.ccdsGene.LENGTH, 101
 hg17.ensGene.LENGTH, 101
 hg17.exoniphy.LENGTH, 102
 hg17.geneid.LENGTH, 102
 hg17.geneSymbol.LENGTH, 103
 hg17.genscan.LENGTH, 103
 hg17.knownGene.LENGTH, 104
 hg17.refGene.LENGTH, 104
 hg17.sgpGene.LENGTH, 105
 hg17.vegaGene.LENGTH, 105
 hg17.vegaPseudoGene.LENGTH, 106
 hg17.xenoRefGene.LENGTH, 106
 hg18.acembly.LENGTH, 107
 hg18.acescan.LENGTH, 107
 hg18.ccdsGene.LENGTH, 108
 hg18.ensGene.LENGTH, 108
 hg18.exoniphy.LENGTH, 109
 hg18.geneid.LENGTH, 109
 hg18.geneSymbol.LENGTH, 110
 hg18.genscan.LENGTH, 110
 hg18.knownGene.LENGTH, 111
 hg18.knownGeneOld3.LENGTH, 111
 hg18.refGene.LENGTH, 112
 hg18.sgpGene.LENGTH, 112
 hg18.sibGene.LENGTH, 113
 hg18.xenoRefGene.LENGTH, 113
 hg19.ccdsGene.LENGTH, 114
 hg19.ensGene.LENGTH, 114
 hg19.exoniphy.LENGTH, 115
 hg19.geneSymbol.LENGTH, 115
 hg19.knownGene.LENGTH, 116
 hg19.nscanGene.LENGTH, 116
 hg19.refGene.LENGTH, 117
 hg19.xenoRefGene.LENGTH, 117
 loxAfr3.xenoRefGene.LENGTH, 118
 mm7.ensGene.LENGTH, 118
 mm7.geneid.LENGTH, 119
 mm7.geneSymbol.LENGTH, 119
 mm7.genscan.LENGTH, 120
 mm7.knownGene.LENGTH, 120
 mm7.refGene.LENGTH, 121
 mm7.sgpGene.LENGTH, 121
 mm7.xenoRefGene.LENGTH, 122
 mm8.ccdsGene.LENGTH, 122
 mm8.ensGene.LENGTH, 123
 mm8.geneid.LENGTH, 123
 mm8.geneSymbol.LENGTH, 124
 mm8.genscan.LENGTH, 124
 mm8.knownGene.LENGTH, 125
 mm8.nscanGene.LENGTH, 125
 mm8.refGene.LENGTH, 126
 mm8.sgpGene.LENGTH, 126
 mm8.sibGene.LENGTH, 127
 mm8.xenoRefGene.LENGTH, 127
 mm9.acembly.LENGTH, 128
 mm9.ccdsGene.LENGTH, 128
 mm9.ensGene.LENGTH, 129
 mm9.exoniphy.LENGTH, 129
 mm9.geneid.LENGTH, 130
 mm9.geneSymbol.LENGTH, 130
 mm9.genscan.LENGTH, 131
 mm9.knownGene.LENGTH, 131
 mm9.nscanGene.LENGTH, 132
 mm9.refGene.LENGTH, 132
 mm9.sgpGene.LENGTH, 133
 mm9.xenoRefGene.LENGTH, 133
 monDom1.genscan.LENGTH, 134
 monDom4.ensGene.LENGTH, 134
 monDom4.geneSymbol.LENGTH, 135
 monDom4.genscan.LENGTH, 135
 monDom4.nscanGene.LENGTH, 136
 monDom4.refGene.LENGTH, 136
 monDom4.xenoRefGene.LENGTH, 137
 monDom5.ensGene.LENGTH, 137
 monDom5.geneSymbol.LENGTH, 138
 monDom5.genscan.LENGTH, 138
 monDom5.nscanGene.LENGTH, 139
 monDom5.refGene.LENGTH, 139
 monDom5.xenoRefGene.LENGTH, 140
 ornAna1.ensGene.LENGTH, 140
 ornAna1.geneSymbol.LENGTH, 141
 ornAna1.refGene.LENGTH, 141
 ornAna1.xenoRefGene.LENGTH, 142
 oryLat2.ensGene.LENGTH, 142
 oryLat2.geneSymbol.LENGTH, 143
 oryLat2.refGene.LENGTH, 143
 oryLat2.xenoRefGene.LENGTH, 144
 panTro1.ensGene.LENGTH, 144

panTro1.geneid.LENGTH, 145
 panTro1.genscan.LENGTH, 145
 panTro1.xenoRefGene.LENGTH, 146
 panTro2.ensGene.LENGTH, 146
 panTro2.geneSymbol.LENGTH, 147
 panTro2.genscan.LENGTH, 147
 panTro2.nscanGene.LENGTH, 148
 panTro2.refGene.LENGTH, 148
 panTro2.xenoRefGene.LENGTH, 149
 petMar1.xenoRefGene.LENGTH, 149
 ponAbe2.ensGene.LENGTH, 150
 ponAbe2.geneSymbol.LENGTH, 150
 ponAbe2.genscan.LENGTH, 151
 ponAbe2.nscanGene.LENGTH, 151
 ponAbe2.refGene.LENGTH, 152
 ponAbe2.xenoRefGene.LENGTH, 152
 priPac1.xenoRefGene.LENGTH, 153
 rheMac2.ensGene.LENGTH, 153
 rheMac2.geneid.LENGTH, 154
 rheMac2.geneSymbol.LENGTH, 154
 rheMac2.nscanGene.LENGTH, 155
 rheMac2.refGene.LENGTH, 155
 rheMac2.sgpGene.LENGTH, 156
 rheMac2.xenoRefGene.LENGTH, 156
 rn3.ensGene.LENGTH, 157
 rn3.geneid.LENGTH, 157
 rn3.geneSymbol.LENGTH, 158
 rn3.genscan.LENGTH, 158
 rn3.knownGene.LENGTH, 159
 rn3.nscanGene.LENGTH, 159
 rn3.refGene.LENGTH, 160
 rn3.sgpGene.LENGTH, 160
 rn3.xenoRefGene.LENGTH, 161
 rn4.ensGene.LENGTH, 161
 rn4.geneid.LENGTH, 162
 rn4.geneSymbol.LENGTH, 162
 rn4.genscan.LENGTH, 163
 rn4.knownGene.LENGTH, 163
 rn4.nscanGene.LENGTH, 164
 rn4.refGene.LENGTH, 164
 rn4.sgpGene.LENGTH, 165
 rn4.xenoRefGene.LENGTH, 165
 sacCer1.ensGene.LENGTH, 166
 sacCer2.ensGene.LENGTH, 166
 strPur1.geneSymbol.LENGTH, 167
 strPur1.genscan.LENGTH, 167
 strPur1.refGene.LENGTH, 168
 strPur1.xenoRefGene.LENGTH, 168

strPur2.geneSymbol.LENGTH, 169
 strPur2.genscan.LENGTH, 169
 strPur2.refGene.LENGTH, 170
 strPur2.xenoRefGene.LENGTH, 170
 taeGut1.ensGene.LENGTH, 172
 taeGut1.geneSymbol.LENGTH, 173
 taeGut1.genscan.LENGTH, 173
 taeGut1.nscanGene.LENGTH, 174
 taeGut1.refGene.LENGTH, 174
 taeGut1.xenoRefGene.LENGTH, 175
 tetNig1.ensGene.LENGTH, 175
 tetNig1.geneid.LENGTH, 176
 tetNig1.genscan.LENGTH, 176
 tetNig1.nscanGene.LENGTH, 177
 tetNig2.ensGene.LENGTH, 177
 xenTro1.genscan.LENGTH, 179
 xenTro2.ensGene.LENGTH, 179
 xenTro2.geneSymbol.LENGTH, 180
 xenTro2.genscan.LENGTH, 180
 xenTro2.refGene.LENGTH, 181

*** internal**

geneLenDatabase-pkg, 95

anoCar1.ensGene.LENGTH, 9
 anoCar1.genscan.LENGTH, 9
 anoCar1.xenoRefGene.LENGTH, 10
 anoGam1.ensGene.LENGTH, 10
 anoGam1.geneid.LENGTH, 11
 anoGam1.genscan.LENGTH, 11
 apiMel1.genscan.LENGTH, 12
 apiMel2.ensGene.LENGTH, 12
 apiMel2.geneid.LENGTH, 13
 apiMel2.genscan.LENGTH, 13
 aplCal1.xenoRefGene.LENGTH, 14

bosTau2.geneid.LENGTH, 14
 bosTau2.geneSymbol.LENGTH, 15
 bosTau2.genscan.LENGTH, 15
 bosTau2.refGene.LENGTH, 16
 bosTau2.sgpGene.LENGTH, 16
 bosTau3.ensGene.LENGTH, 17
 bosTau3.geneid.LENGTH, 17
 bosTau3.geneSymbol.LENGTH, 18
 bosTau3.genscan.LENGTH, 18
 bosTau3.refGene.LENGTH, 19
 bosTau3.sgpGene.LENGTH, 19
 bosTau4.ensGene.LENGTH, 20
 bosTau4.geneSymbol.LENGTH, 20
 bosTau4.genscan.LENGTH, 21

- bosTau4.nscanGene.LENGTH, 21
 bosTau4.refGene.LENGTH, 22
 braFlo1.xenoRefGene.LENGTH, 22

 caeJap1.xenoRefGene.LENGTH, 23
 caePb1.xenoRefGene.LENGTH, 23
 caePb2.xenoRefGene.LENGTH, 24
 caeRem2.xenoRefGene.LENGTH, 24
 caeRem3.xenoRefGene.LENGTH, 25
 calJac1.genscan.LENGTH, 25
 calJac1.nscanGene.LENGTH, 26
 calJac1.xenoRefGene.LENGTH, 26
 canFam1.ensGene.LENGTH, 27
 canFam1.geneSymbol.LENGTH, 27
 canFam1.genscan.LENGTH, 28
 canFam1.nscanGene.LENGTH, 28
 canFam1.refGene.LENGTH, 29
 canFam1.xenoRefGene.LENGTH, 29
 canFam2.ensGene.LENGTH, 30
 canFam2.geneSymbol.LENGTH, 30
 canFam2.genscan.LENGTH, 31
 canFam2.nscanGene.LENGTH, 31
 canFam2.refGene.LENGTH, 32
 canFam2.xenoRefGene.LENGTH, 32
 cavPor3.ensGene.LENGTH, 33
 cavPor3.genscan.LENGTH, 33
 cavPor3.nscanGene.LENGTH, 34
 cavPor3.xenoRefGene.LENGTH, 34
 cb1.xenoRefGene.LENGTH, 35
 cb3.xenoRefGene.LENGTH, 35
 ce2.geneid.LENGTH, 36
 ce2.geneSymbol.LENGTH, 36
 ce2.refGene.LENGTH, 37
 ce4.geneSymbol.LENGTH, 37
 ce4.refGene.LENGTH, 38
 ce4.xenoRefGene.LENGTH, 38
 ce6.ensGene.LENGTH, 39
 ce6.geneSymbol.LENGTH, 39
 ce6.refGene.LENGTH, 40
 ce6.xenoRefGene.LENGTH, 40
 ci1.geneSymbol.LENGTH, 41
 ci1.refGene.LENGTH, 41
 ci1.xenoRefGene.LENGTH, 42
 ci2.ensGene.LENGTH, 42
 ci2.geneSymbol.LENGTH, 43
 ci2.refGene.LENGTH, 43
 ci2.xenoRefGene.LENGTH, 44

 danRer3.ensGene.LENGTH, 44
 danRer3.geneSymbol.LENGTH, 45
 danRer3.refGene.LENGTH, 45
 danRer4.ensGene.LENGTH, 46
 danRer4.geneSymbol.LENGTH, 46
 danRer4.genscan.LENGTH, 47
 danRer4.nscanGene.LENGTH, 47
 danRer4.refGene.LENGTH, 48
 danRer5.ensGene.LENGTH, 48
 danRer5.geneSymbol.LENGTH, 49
 danRer5.refGene.LENGTH, 49
 danRer5.vegaGene.LENGTH, 50
 danRer5.vegaPseudoGene.LENGTH, 50
 danRer6.ensGene.LENGTH, 51
 danRer6.geneSymbol.LENGTH, 51
 danRer6.refGene.LENGTH, 52
 danRer6.xenoRefGene.LENGTH, 52
 dm1.geneSymbol.LENGTH, 53
 dm1.genscan.LENGTH, 53
 dm1.refGene.LENGTH, 54
 dm2.geneid.LENGTH, 54
 dm2.geneSymbol.LENGTH, 55
 dm2.genscan.LENGTH, 55
 dm2.nscanGene.LENGTH, 56
 dm2.refGene.LENGTH, 56
 dm3.geneSymbol.LENGTH, 57
 dm3.nscanPasaGene.LENGTH, 57
 dm3.refGene.LENGTH, 58
 downloadLengthFromUCSC, 9–58, 58, 60–170,
 172–177, 179–181
 dp2.genscan.LENGTH, 59
 dp2.xenoRefGene.LENGTH, 60
 dp3.geneid.LENGTH, 60
 dp3.genscan.LENGTH, 61
 dp3.xenoRefGene.LENGTH, 61
 droAna1.geneid.LENGTH, 62
 droAna1.genscan.LENGTH, 62
 droAna1.xenoRefGene.LENGTH, 63
 droAna2.genscan.LENGTH, 63
 droAna2.xenoRefGene.LENGTH, 64
 droEre1.genscan.LENGTH, 64
 droEre1.xenoRefGene.LENGTH, 65
 droGri1.genscan.LENGTH, 65
 droGri1.xenoRefGene.LENGTH, 66
 droMoj1.geneid.LENGTH, 66
 droMoj1.genscan.LENGTH, 67
 droMoj1.xenoRefGene.LENGTH, 67
 droMoj2.genscan.LENGTH, 68
 droMoj2.xenoRefGene.LENGTH, 68

- droPer1.genscan.LENGTH, 69
- droPer1.xenoRefGene.LENGTH, 69
- droSec1.genscan.LENGTH, 70
- droSec1.xenoRefGene.LENGTH, 70
- droSim1.geneid.LENGTH, 71
- droSim1.genscan.LENGTH, 71
- droSim1.xenoRefGene.LENGTH, 72
- droVir1.geneid.LENGTH, 72
- droVir1.genscan.LENGTH, 73
- droVir1.xenoRefGene.LENGTH, 73
- droVir2.genscan.LENGTH, 74
- droVir2.xenoRefGene.LENGTH, 74
- droYak1.geneid.LENGTH, 75
- droYak1.genscan.LENGTH, 75
- droYak1.xenoRefGene.LENGTH, 76
- droYak2.genscan.LENGTH, 76
- droYak2.xenoRefGene.LENGTH, 77

- equCab1.geneid.LENGTH, 77
- equCab1.geneSymbol.LENGTH, 78
- equCab1.nscanGene.LENGTH, 78
- equCab1.refGene.LENGTH, 79
- equCab1.sgpGene.LENGTH, 79
- equCab2.ensGene.LENGTH, 80
- equCab2.geneSymbol.LENGTH, 80
- equCab2.nscanGene.LENGTH, 81
- equCab2.refGene.LENGTH, 81
- equCab2.xenoRefGene.LENGTH, 82

- felCat3.ensGene.LENGTH, 82
- felCat3.geneid.LENGTH, 83
- felCat3.geneSymbol.LENGTH, 83
- felCat3.genscan.LENGTH, 84
- felCat3.nscanGene.LENGTH, 84
- felCat3.refGene.LENGTH, 85
- felCat3.sgpGene.LENGTH, 85
- felCat3.xenoRefGene.LENGTH, 86
- fr1.ensGene.LENGTH, 86
- fr1.genscan.LENGTH, 87
- fr2.ensGene.LENGTH, 87

- galGal2.ensGene.LENGTH, 88
- galGal2.geneid.LENGTH, 88
- galGal2.geneSymbol.LENGTH, 89
- galGal2.genscan.LENGTH, 89
- galGal2.refGene.LENGTH, 90
- galGal2.sgpGene.LENGTH, 90
- galGal3.ensGene.LENGTH, 91
- galGal3.geneSymbol.LENGTH, 91
- galGal3.genscan.LENGTH, 92
- galGal3.nscanGene.LENGTH, 92
- galGal3.refGene.LENGTH, 93
- galGal3.xenoRefGene.LENGTH, 93
- gasAcu1.ensGene.LENGTH, 94
- gasAcu1.nscanGene.LENGTH, 94
- geneLenDataBase (geneLenDatabase-pkg), 95
- geneLenDataBase-package (geneLenDatabase-pkg), 95
- geneLenDatabase-pkg, 95

- hg16.acembly.LENGTH, 95
- hg16.ensGene.LENGTH, 96
- hg16.exoniphy.LENGTH, 96
- hg16.geneid.LENGTH, 97
- hg16.geneSymbol.LENGTH, 97
- hg16.genscan.LENGTH, 98
- hg16.knownGene.LENGTH, 98
- hg16.refGene.LENGTH, 99
- hg16.sgpGene.LENGTH, 99
- hg17.acembly.LENGTH, 100
- hg17.acescan.LENGTH, 100
- hg17.ccdsGene.LENGTH, 101
- hg17.ensGene.LENGTH, 101
- hg17.exoniphy.LENGTH, 102
- hg17.geneid.LENGTH, 102
- hg17.geneSymbol.LENGTH, 103
- hg17.genscan.LENGTH, 103
- hg17.knownGene.LENGTH, 104
- hg17.refGene.LENGTH, 104
- hg17.sgpGene.LENGTH, 105
- hg17.vegaGene.LENGTH, 105
- hg17.vegaPseudoGene.LENGTH, 106
- hg17.xenoRefGene.LENGTH, 106
- hg18.acembly.LENGTH, 107
- hg18.acescan.LENGTH, 107
- hg18.ccdsGene.LENGTH, 108
- hg18.ensGene.LENGTH, 108
- hg18.exoniphy.LENGTH, 109
- hg18.geneid.LENGTH, 109
- hg18.geneSymbol.LENGTH, 110
- hg18.genscan.LENGTH, 110
- hg18.knownGene.LENGTH, 111
- hg18.knownGeneOld3.LENGTH, 111
- hg18.refGene.LENGTH, 112
- hg18.sgpGene.LENGTH, 112
- hg18.sibGene.LENGTH, 113
- hg18.xenoRefGene.LENGTH, 113

- hg19.ccdsGene.LENGTH, 114
- hg19.ensGene.LENGTH, 114
- hg19.exoniphy.LENGTH, 115
- hg19.geneSymbol.LENGTH, 115
- hg19.knownGene.LENGTH, 116
- hg19.nscanGene.LENGTH, 116
- hg19.refGene.LENGTH, 117
- hg19.xenoRefGene.LENGTH, 117

- loxAfr3.xenoRefGene.LENGTH, 118

- mm7.ensGene.LENGTH, 118
- mm7.geneid.LENGTH, 119
- mm7.geneSymbol.LENGTH, 119
- mm7.genscan.LENGTH, 120
- mm7.knownGene.LENGTH, 120
- mm7.refGene.LENGTH, 121
- mm7.sgpGene.LENGTH, 121
- mm7.xenoRefGene.LENGTH, 122
- mm8.ccdsGene.LENGTH, 122
- mm8.ensGene.LENGTH, 123
- mm8.geneid.LENGTH, 123
- mm8.geneSymbol.LENGTH, 124
- mm8.genscan.LENGTH, 124
- mm8.knownGene.LENGTH, 125
- mm8.nscanGene.LENGTH, 125
- mm8.refGene.LENGTH, 126
- mm8.sgpGene.LENGTH, 126
- mm8.sibGene.LENGTH, 127
- mm8.xenoRefGene.LENGTH, 127
- mm9.acembly.LENGTH, 128
- mm9.ccdsGene.LENGTH, 128
- mm9.ensGene.LENGTH, 129
- mm9.exoniphy.LENGTH, 129
- mm9.geneid.LENGTH, 130
- mm9.geneSymbol.LENGTH, 130
- mm9.genscan.LENGTH, 131
- mm9.knownGene.LENGTH, 131
- mm9.nscanGene.LENGTH, 132
- mm9.refGene.LENGTH, 132
- mm9.sgpGene.LENGTH, 133
- mm9.xenoRefGene.LENGTH, 133
- monDom1.genscan.LENGTH, 134
- monDom4.ensGene.LENGTH, 134
- monDom4.geneSymbol.LENGTH, 135
- monDom4.genscan.LENGTH, 135
- monDom4.nscanGene.LENGTH, 136
- monDom4.refGene.LENGTH, 136
- monDom4.xenoRefGene.LENGTH, 137

- monDom5.ensGene.LENGTH, 137
- monDom5.geneSymbol.LENGTH, 138
- monDom5.genscan.LENGTH, 138
- monDom5.nscanGene.LENGTH, 139
- monDom5.refGene.LENGTH, 139
- monDom5.xenoRefGene.LENGTH, 140

- ornAna1.ensGene.LENGTH, 140
- ornAna1.geneSymbol.LENGTH, 141
- ornAna1.refGene.LENGTH, 141
- ornAna1.xenoRefGene.LENGTH, 142
- oryLat2.ensGene.LENGTH, 142
- oryLat2.geneSymbol.LENGTH, 143
- oryLat2.refGene.LENGTH, 143
- oryLat2.xenoRefGene.LENGTH, 144

- panTro1.ensGene.LENGTH, 144
- panTro1.geneid.LENGTH, 145
- panTro1.genscan.LENGTH, 145
- panTro1.xenoRefGene.LENGTH, 146
- panTro2.ensGene.LENGTH, 146
- panTro2.geneSymbol.LENGTH, 147
- panTro2.genscan.LENGTH, 147
- panTro2.nscanGene.LENGTH, 148
- panTro2.refGene.LENGTH, 148
- panTro2.xenoRefGene.LENGTH, 149
- petMar1.xenoRefGene.LENGTH, 149
- ponAbe2.ensGene.LENGTH, 150
- ponAbe2.geneSymbol.LENGTH, 150
- ponAbe2.genscan.LENGTH, 151
- ponAbe2.nscanGene.LENGTH, 151
- ponAbe2.refGene.LENGTH, 152
- ponAbe2.xenoRefGene.LENGTH, 152
- priPac1.xenoRefGene.LENGTH, 153

- rheMac2.ensGene.LENGTH, 153
- rheMac2.geneid.LENGTH, 154
- rheMac2.geneSymbol.LENGTH, 154
- rheMac2.nscanGene.LENGTH, 155
- rheMac2.refGene.LENGTH, 155
- rheMac2.sgpGene.LENGTH, 156
- rheMac2.xenoRefGene.LENGTH, 156
- rn3.ensGene.LENGTH, 157
- rn3.geneid.LENGTH, 157
- rn3.geneSymbol.LENGTH, 158
- rn3.genscan.LENGTH, 158
- rn3.knownGene.LENGTH, 159
- rn3.nscanGene.LENGTH, 159
- rn3.refGene.LENGTH, 160

rn3.sgpGene.LENGTH, [160](#)
rn3.xenoRefGene.LENGTH, [161](#)
rn4.ensGene.LENGTH, [161](#)
rn4.geneid.LENGTH, [162](#)
rn4.geneSymbol.LENGTH, [162](#)
rn4.genscan.LENGTH, [163](#)
rn4.knownGene.LENGTH, [163](#)
rn4.nscanGene.LENGTH, [164](#)
rn4.refGene.LENGTH, [164](#)
rn4.sgpGene.LENGTH, [165](#)
rn4.xenoRefGene.LENGTH, [165](#)

sacCer1.ensGene.LENGTH, [166](#)
sacCer2.ensGene.LENGTH, [166](#)
strPur1.geneSymbol.LENGTH, [167](#)
strPur1.genscan.LENGTH, [167](#)
strPur1.refGene.LENGTH, [168](#)
strPur1.xenoRefGene.LENGTH, [168](#)
strPur2.geneSymbol.LENGTH, [169](#)
strPur2.genscan.LENGTH, [169](#)
strPur2.refGene.LENGTH, [170](#)
strPur2.xenoRefGene.LENGTH, [170](#)
supportedGeneIDs, [58](#), [59](#), [171](#)
supportedGenomes, [58](#), [59](#), [171](#)

taeGut1.ensGene.LENGTH, [172](#)
taeGut1.geneSymbol.LENGTH, [173](#)
taeGut1.genscan.LENGTH, [173](#)
taeGut1.nscanGene.LENGTH, [174](#)
taeGut1.refGene.LENGTH, [174](#)
taeGut1.xenoRefGene.LENGTH, [175](#)
tetNig1.ensGene.LENGTH, [175](#)
tetNig1.geneid.LENGTH, [176](#)
tetNig1.genscan.LENGTH, [176](#)
tetNig1.nscanGene.LENGTH, [177](#)
tetNig2.ensGene.LENGTH, [177](#)

unfactor, [178](#)

xenTro1.genscan.LENGTH, [179](#)
xenTro2.ensGene.LENGTH, [179](#)
xenTro2.geneSymbol.LENGTH, [180](#)
xenTro2.genscan.LENGTH, [180](#)
xenTro2.refGene.LENGTH, [181](#)