

# Package ‘geneLenDataBase’

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

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**Depends** R (>= 2.11.0)

**Imports** utils, rtracklayer, GenomicFeatures (>= 1.3.15)

**LazyLoad** yes

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

**biocViews** HighThroughputSequencingData, ExperimentData, Transcription,RNAseq

**License** LGPL (>= 2)

## R topics documented:

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 . . . . .	58
dp2.xenoRefGene.LENGTH . . . . .	59
dp3.geneid.LENGTH . . . . .	59
dp3.genscan.LENGTH . . . . .	60
dp3.xenoRefGene.LENGTH . . . . .	60
droAna1.geneid.LENGTH . . . . .	61
droAna1.genscan.LENGTH . . . . .	61
droAna1.xenoRefGene.LENGTH . . . . .	62
droAna2.genscan.LENGTH . . . . .	62
droAna2.xenoRefGene.LENGTH . . . . .	63

droEre1.genscan.LENGTH . . . . .	63
droEre1.xenoRefGene.LENGTH . . . . .	64
droGri1.genscan.LENGTH . . . . .	64
droGri1.xenoRefGene.LENGTH . . . . .	65
droMoj1.geneid.LENGTH . . . . .	65
droMoj1.genscan.LENGTH . . . . .	66
droMoj1.xenoRefGene.LENGTH . . . . .	66
droMoj2.genscan.LENGTH . . . . .	67
droMoj2.xenoRefGene.LENGTH . . . . .	67
droPer1.genscan.LENGTH . . . . .	68
droPer1.xenoRefGene.LENGTH . . . . .	68
droSec1.genscan.LENGTH . . . . .	69
droSec1.xenoRefGene.LENGTH . . . . .	69
droSim1.geneid.LENGTH . . . . .	70
droSim1.genscan.LENGTH . . . . .	70
droSim1.xenoRefGene.LENGTH . . . . .	71
droVir1.geneid.LENGTH . . . . .	71
droVir1.genscan.LENGTH . . . . .	72
droVir1.xenoRefGene.LENGTH . . . . .	72
droVir2.genscan.LENGTH . . . . .	73
droVir2.xenoRefGene.LENGTH . . . . .	73
droYak1.geneid.LENGTH . . . . .	74
droYak1.genscan.LENGTH . . . . .	74
droYak1.xenoRefGene.LENGTH . . . . .	75
droYak2.genscan.LENGTH . . . . .	75
droYak2.xenoRefGene.LENGTH . . . . .	76
equCab1.geneid.LENGTH . . . . .	76
equCab1.geneSymbol.LENGTH . . . . .	77
equCab1.nscanGene.LENGTH . . . . .	77
equCab1.refGene.LENGTH . . . . .	78
equCab1.sgpGene.LENGTH . . . . .	78
equCab2.ensGene.LENGTH . . . . .	79
equCab2.geneSymbol.LENGTH . . . . .	79
equCab2.nscanGene.LENGTH . . . . .	80
equCab2.refGene.LENGTH . . . . .	80
equCab2.xenoRefGene.LENGTH . . . . .	81
felCat3.ensGene.LENGTH . . . . .	81
felCat3.geneid.LENGTH . . . . .	82
felCat3.geneSymbol.LENGTH . . . . .	82
felCat3.genscan.LENGTH . . . . .	83
felCat3.nscanGene.LENGTH . . . . .	83
felCat3.refGene.LENGTH . . . . .	84
felCat3.sgpGene.LENGTH . . . . .	84
felCat3.xenoRefGene.LENGTH . . . . .	85
fr1.ensGene.LENGTH . . . . .	85
fr1.genscan.LENGTH . . . . .	86
fr2.ensGene.LENGTH . . . . .	86
galGal2.ensGene.LENGTH . . . . .	87

galGal2.geneid.LENGTH . . . . .	87
galGal2.geneSymbol.LENGTH . . . . .	88
galGal2.genscan.LENGTH . . . . .	88
galGal2.refGene.LENGTH . . . . .	89
galGal2.sgpGene.LENGTH . . . . .	89
galGal3.ensGene.LENGTH . . . . .	90
galGal3.geneSymbol.LENGTH . . . . .	90
galGal3.genscan.LENGTH . . . . .	91
galGal3.nscanGene.LENGTH . . . . .	91
galGal3.refGene.LENGTH . . . . .	92
galGal3.xenoRefGene.LENGTH . . . . .	92
gasAcu1.ensGene.LENGTH . . . . .	93
gasAcu1.nscanGene.LENGTH . . . . .	93
hg16.acembly.LENGTH . . . . .	94
hg16.ensGene.LENGTH . . . . .	94
hg16.exoniphy.LENGTH . . . . .	95
hg16.geneid.LENGTH . . . . .	95
hg16.geneSymbol.LENGTH . . . . .	96
hg16.genscan.LENGTH . . . . .	96
hg16.knownGene.LENGTH . . . . .	97
hg16.refGene.LENGTH . . . . .	97
hg16.sgpGene.LENGTH . . . . .	98
hg17.acembly.LENGTH . . . . .	98
hg17.acescan.LENGTH . . . . .	99
hg17.ccdsGene.LENGTH . . . . .	99
hg17.ensGene.LENGTH . . . . .	100
hg17.exoniphy.LENGTH . . . . .	100
hg17.geneid.LENGTH . . . . .	101
hg17.geneSymbol.LENGTH . . . . .	101
hg17.genscan.LENGTH . . . . .	102
hg17.knownGene.LENGTH . . . . .	102
hg17.refGene.LENGTH . . . . .	103
hg17.sgpGene.LENGTH . . . . .	103
hg17.vegaGene.LENGTH . . . . .	104
hg17.vegaPseudoGene.LENGTH . . . . .	104
hg17.xenoRefGene.LENGTH . . . . .	105
hg18.acembly.LENGTH . . . . .	105
hg18.acescan.LENGTH . . . . .	106
hg18.ccdsGene.LENGTH . . . . .	106
hg18.ensGene.LENGTH . . . . .	107
hg18.exoniphy.LENGTH . . . . .	107
hg18.geneid.LENGTH . . . . .	108
hg18.geneSymbol.LENGTH . . . . .	108
hg18.genscan.LENGTH . . . . .	109
hg18.knownGene.LENGTH . . . . .	109
hg18.knownGeneOld3.LENGTH . . . . .	110
hg18.refGene.LENGTH . . . . .	110
hg18.sgpGene.LENGTH . . . . .	111

hg18.sibGene.LENGTH . . . . .	111
hg18.xenoRefGene.LENGTH . . . . .	112
hg19.ccdsGene.LENGTH . . . . .	112
hg19.ensGene.LENGTH . . . . .	113
hg19.exoniphy.LENGTH . . . . .	113
hg19.geneSymbol.LENGTH . . . . .	114
hg19.knownGene.LENGTH . . . . .	114
hg19.nscanGene.LENGTH . . . . .	115
hg19.refGene.LENGTH . . . . .	115
hg19.xenoRefGene.LENGTH . . . . .	116
loxAfr3.xenoRefGene.LENGTH . . . . .	116
mm7.ensGene.LENGTH . . . . .	117
mm7.geneid.LENGTH . . . . .	117
mm7.geneSymbol.LENGTH . . . . .	118
mm7.genscan.LENGTH . . . . .	118
mm7.knownGene.LENGTH . . . . .	119
mm7.refGene.LENGTH . . . . .	119
mm7.sgpGene.LENGTH . . . . .	120
mm7.xenoRefGene.LENGTH . . . . .	120
mm8.ccdsGene.LENGTH . . . . .	121
mm8.ensGene.LENGTH . . . . .	121
mm8.geneid.LENGTH . . . . .	122
mm8.geneSymbol.LENGTH . . . . .	122
mm8.genscan.LENGTH . . . . .	123
mm8.knownGene.LENGTH . . . . .	123
mm8.nscanGene.LENGTH . . . . .	124
mm8.refGene.LENGTH . . . . .	124
mm8.sgpGene.LENGTH . . . . .	125
mm8.sibGene.LENGTH . . . . .	125
mm8.xenoRefGene.LENGTH . . . . .	126
mm9.acembly.LENGTH . . . . .	126
mm9.ccdsGene.LENGTH . . . . .	127
mm9.ensGene.LENGTH . . . . .	127
mm9.exoniphy.LENGTH . . . . .	128
mm9.geneid.LENGTH . . . . .	128
mm9.geneSymbol.LENGTH . . . . .	129
mm9.genscan.LENGTH . . . . .	129
mm9.knownGene.LENGTH . . . . .	130
mm9.nscanGene.LENGTH . . . . .	130
mm9.refGene.LENGTH . . . . .	131
mm9.sgpGene.LENGTH . . . . .	131
mm9.xenoRefGene.LENGTH . . . . .	132
monDom1.genscan.LENGTH . . . . .	132
monDom4.ensGene.LENGTH . . . . .	133
monDom4.geneSymbol.LENGTH . . . . .	133
monDom4.genscan.LENGTH . . . . .	134
monDom4.nscanGene.LENGTH . . . . .	134
monDom4.refGene.LENGTH . . . . .	135

monDom4.xenoRefGene.LENGTH . . . . .	135
monDom5.ensGene.LENGTH . . . . .	136
monDom5.geneSymbol.LENGTH . . . . .	136
monDom5.genscan.LENGTH . . . . .	137
monDom5.nscanGene.LENGTH . . . . .	137
monDom5.refGene.LENGTH . . . . .	138
monDom5.xenoRefGene.LENGTH . . . . .	138
ornAna1.ensGene.LENGTH . . . . .	139
ornAna1.geneSymbol.LENGTH . . . . .	139
ornAna1.refGene.LENGTH . . . . .	140
ornAna1.xenoRefGene.LENGTH . . . . .	140
oryLat2.ensGene.LENGTH . . . . .	141
oryLat2.geneSymbol.LENGTH . . . . .	141
oryLat2.refGene.LENGTH . . . . .	142
oryLat2.xenoRefGene.LENGTH . . . . .	142
panTro1.ensGene.LENGTH . . . . .	143
panTro1.geneid.LENGTH . . . . .	143
panTro1.genscan.LENGTH . . . . .	144
panTro1.xenoRefGene.LENGTH . . . . .	144
panTro2.ensGene.LENGTH . . . . .	145
panTro2.geneSymbol.LENGTH . . . . .	145
panTro2.genscan.LENGTH . . . . .	146
panTro2.nscanGene.LENGTH . . . . .	146
panTro2.refGene.LENGTH . . . . .	147
panTro2.xenoRefGene.LENGTH . . . . .	147
petMar1.xenoRefGene.LENGTH . . . . .	148
ponAbe2.ensGene.LENGTH . . . . .	148
ponAbe2.geneSymbol.LENGTH . . . . .	149
ponAbe2.genscan.LENGTH . . . . .	149
ponAbe2.nscanGene.LENGTH . . . . .	150
ponAbe2.refGene.LENGTH . . . . .	150
ponAbe2.xenoRefGene.LENGTH . . . . .	151
priPac1.xenoRefGene.LENGTH . . . . .	151
rheMac2.ensGene.LENGTH . . . . .	152
rheMac2.geneid.LENGTH . . . . .	152
rheMac2.geneSymbol.LENGTH . . . . .	153
rheMac2.nscanGene.LENGTH . . . . .	153
rheMac2.refGene.LENGTH . . . . .	154
rheMac2.sgpGene.LENGTH . . . . .	154
rheMac2.xenoRefGene.LENGTH . . . . .	155
rn3.ensGene.LENGTH . . . . .	155
rn3.geneid.LENGTH . . . . .	156
rn3.geneSymbol.LENGTH . . . . .	156
rn3.genscan.LENGTH . . . . .	157
rn3.knownGene.LENGTH . . . . .	157
rn3.nscanGene.LENGTH . . . . .	158
rn3.refGene.LENGTH . . . . .	158
rn3.sgpGene.LENGTH . . . . .	159

rn3.xenoRefGene.LENGTH . . . . .	159
rn4.ensGene.LENGTH . . . . .	160
rn4.geneid.LENGTH . . . . .	160
rn4.geneSymbol.LENGTH . . . . .	161
rn4.genscan.LENGTH . . . . .	161
rn4.knownGene.LENGTH . . . . .	162
rn4.nscanGene.LENGTH . . . . .	162
rn4.refGene.LENGTH . . . . .	163
rn4.sgpGene.LENGTH . . . . .	163
rn4.xenoRefGene.LENGTH . . . . .	164
sacCer1.ensGene.LENGTH . . . . .	164
sacCer2.ensGene.LENGTH . . . . .	165
strPur1.geneSymbol.LENGTH . . . . .	165
strPur1.genscan.LENGTH . . . . .	166
strPur1.refGene.LENGTH . . . . .	166
strPur1.xenoRefGene.LENGTH . . . . .	167
strPur2.geneSymbol.LENGTH . . . . .	167
strPur2.genscan.LENGTH . . . . .	168
strPur2.refGene.LENGTH . . . . .	168
strPur2.xenoRefGene.LENGTH . . . . .	169
supportedGeneIDs . . . . .	169
supportedGenomes . . . . .	170
taeGut1.ensGene.LENGTH . . . . .	171
taeGut1.geneSymbol.LENGTH . . . . .	171
taeGut1.genscan.LENGTH . . . . .	172
taeGut1.nscanGene.LENGTH . . . . .	172
taeGut1.refGene.LENGTH . . . . .	173
taeGut1.xenoRefGene.LENGTH . . . . .	173
tetNig1.ensGene.LENGTH . . . . .	174
tetNig1.geneid.LENGTH . . . . .	174
tetNig1.genscan.LENGTH . . . . .	175
tetNig1.nscanGene.LENGTH . . . . .	175
tetNig2.ensGene.LENGTH . . . . .	176
unfactor . . . . .	176
xenTro1.genscan.LENGTH . . . . .	177
xenTro2.ensGene.LENGTH . . . . .	178
xenTro2.geneSymbol.LENGTH . . . . .	178
xenTro2.genscan.LENGTH . . . . .	179
xenTro2.refGene.LENGTH . . . . .	179



---

`anoCar1.ensGene.LENGTH`*Transcript length data for the organism anoCar*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

`anoCar1.genscan.LENGTH`*Transcript length data for the organism anoCar*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
anoCar1.xenoRefGene.LENGTH
```

*Transcript length data for the organism anoCar*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
anoGam1.ensGene.LENGTH
```

*Transcript length data for the organism anoGam*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

apiMe11.genscan.LENGTH

*Transcript length data for the organism apiMel*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

apiMe12.ensGene.LENGTH

*Transcript length data for the organism apiMel*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
bosTau3.geneSymbol.LENGTH
```

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
bosTau3.genscan.LENGTH
```

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
caeJap1.xenoRefGene.LENGTH
```

*Transcript length data for the organism caeJap*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
caePb1.xenoRefGene.LENGTH
```

*Transcript length data for the organism caePb*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
caePb2.xenoRefGene.LENGTH
```

*Transcript length data for the organism caePb*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
caeRem2.xenoRefGene.LENGTH
```

*Transcript length data for the organism caeRem*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
canFam2.refGene.LENGTH
```

*Transcript length data for the organism canFam*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
canFam2.xenoRefGene.LENGTH
```

*Transcript length data for the organism canFam*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
danRer4.ensGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer4.geneSymbol.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
danRer5.vegaGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer5.vegaPseudoGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer6.ensGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer6.geneSymbol.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
droEre1.xenoRefGene.LENGTH
```

*Transcript length data for the organism droEre*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
droGri1.genscan.LENGTH
```

*Transcript length data for the organism droGri*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
droMoj1.genscan.LENGTH
```

*Transcript length data for the organism droMoj*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
droMoj1.xenoRefGene.LENGTH
```

*Transcript length data for the organism droMoj*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
equCab2.ensGene.LENGTH
```

*Transcript length data for the organism equCab*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
equCab2.geneSymbol.LENGTH
```

*Transcript length data for the organism equCab*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
equCab2.nscanGene.LENGTH
```

*Transcript length data for the organism equCab*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
equCab2.refGene.LENGTH
```

*Transcript length data for the organism equCab*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

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

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

---

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

---

**Description**

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

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

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

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

---

felCat3.refGene.LENGTH

*Transcript length data for the organism felCat*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

felCat3.sgpGene.LENGTH

*Transcript length data for the organism felCat*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

`hg18.knownGeneOld3.LENGTH`*Transcript length data for the organism hg*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

`hg18.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(hg18, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(hg18.xenoRefGene.LENGTH)
head(hg18.xenoRefGene.LENGTH)
```

---

`hg19.ccdsGene.LENGTH` *Transcript length data for the organism hg*

---

**Description**

`hg19.ccdsGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ccdsGene` table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ccdsGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(hg19.ccdsGene.LENGTH)
head(hg19.ccdsGene.LENGTH)
```



---

hg19.ensGene.LENGTH *Transcript length data for the organism hg*

---

### Description

hg19.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.ensGene.LENGTH)
head(hg19.ensGene.LENGTH)
```

---

hg19.exoniphy.LENGTH *Transcript length data for the organism hg*

---

### Description

hg19.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(hg19, exoniphy)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.exoniphy.LENGTH)
head(hg19.exoniphy.LENGTH)
```

---

`hg19.geneSymbol.LENGTH`*Transcript length data for the organism hg*

---

**Description**

hg19.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(hg19, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(hg19.geneSymbol.LENGTH)
head(hg19.geneSymbol.LENGTH)
```

---

`hg19.knownGene.LENGTH` *Transcript length data for the organism hg*

---

**Description**

hg19.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, knownGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(hg19.knownGene.LENGTH)
head(hg19.knownGene.LENGTH)
```

---

hg19.nscanGene.LENGTH *Transcript length data for the organism hg*

---

### Description

hg19.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.nscanGene.LENGTH)
head(hg19.nscanGene.LENGTH)
```

---

hg19.refGene.LENGTH *Transcript length data for the organism hg*

---

### Description

hg19.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.refGene.LENGTH)
head(hg19.refGene.LENGTH)
```

---

```
hg19.xenoRefGene.LENGTH
```

*Transcript length data for the organism hg*

---

### Description

hg19.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(hg19, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(hg19.xenoRefGene.LENGTH)
head(hg19.xenoRefGene.LENGTH)
```

---

```
loxAfr3.xenoRefGene.LENGTH
```

*Transcript length data for the organism loxAfr*

---

### Description

loxAfr3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(loxAfr3, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(loxAfr3.xenoRefGene.LENGTH)
head(loxAfr3.xenoRefGene.LENGTH)
```

---

mm7.ensGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm7.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.ensGene.LENGTH)
head(mm7.ensGene.LENGTH)
```

---

mm7.geneid.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm7.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.geneid.LENGTH)
head(mm7.geneid.LENGTH)
```

---

mm7.geneSymbol.LENGTH *Transcript length data for the organism mm*

---

### Description

mm7.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm7, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.geneSymbol.LENGTH)
head(mm7.geneSymbol.LENGTH)
```

---

mm7.genscan.LENGTH *Transcript length data for the organism mm*

---

### Description

mm7.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm7, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.genscan.LENGTH)
head(mm7.genscan.LENGTH)
```

---

mm7.knownGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm7.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.knownGene.LENGTH)
head(mm7.knownGene.LENGTH)
```

---

mm7.refGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm7.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.refGene.LENGTH)
head(mm7.refGene.LENGTH)
```

---

mm7.sgpGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm7.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.sgpGene.LENGTH)
head(mm7.sgpGene.LENGTH)
```

---

mm7.xenoRefGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm7.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(mm7, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm7.xenoRefGene.LENGTH)
head(mm7.xenoRefGene.LENGTH)
```



---

mm8.ccdsGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm8.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ccdsGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.ccdsGene.LENGTH)
head(mm8.ccdsGene.LENGTH)
```

---

mm8.ensGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm8.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.ensGene.LENGTH)
head(mm8.ensGene.LENGTH)
```

---

mm8.geneid.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm8.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.geneid.LENGTH)
head(mm8.geneid.LENGTH)
```

---

mm8.geneSymbol.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm8.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm8, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.geneSymbol.LENGTH)
head(mm8.geneSymbol.LENGTH)
```

---

mm8.genscan.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm8.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm8, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.genscan.LENGTH)
head(mm8.genscan.LENGTH)
```

---

mm8.knownGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm8.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.knownGene.LENGTH)
head(mm8.knownGene.LENGTH)
```

---

mm8.nscanGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm8.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.nscanGene.LENGTH)
head(mm8.nscanGene.LENGTH)
```

---

mm8.refGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm8.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.refGene.LENGTH)
head(mm8.refGene.LENGTH)
```

---

mm8.sgpGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm8.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.sgpGene.LENGTH)
head(mm8.sgpGene.LENGTH)
```

---

mm8.sibGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm8.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sibGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sibGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm8.sibGene.LENGTH)
head(mm8.sibGene.LENGTH)
```

---

`mm8.xenoRefGene.LENGTH`*Transcript length data for the organism mm*

---

**Description**

`mm8.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm8, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(mm8.xenoRefGene.LENGTH)
head(mm8.xenoRefGene.LENGTH)
```

---

`mm9.acembly.LENGTH`*Transcript length data for the organism mm*

---

**Description**

`mm9.acembly.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `acembly` table.

The data file was made by calling `downloadLengthFromUCSC(mm9, acembly)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(mm9.acembly.LENGTH)
head(mm9.acembly.LENGTH)
```

---

mm9.ccdsGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm9.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ccdsGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.ccdsGene.LENGTH)
head(mm9.ccdsGene.LENGTH)
```

---

mm9.ensGene.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm9.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.ensGene.LENGTH)
head(mm9.ensGene.LENGTH)
```

---

mm9.exoniphy.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm9.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(mm9, exoniphy)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.exoniphy.LENGTH)
head(mm9.exoniphy.LENGTH)
```

---

mm9.geneid.LENGTH     *Transcript length data for the organism mm*

---

### Description

mm9.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.geneid.LENGTH)
head(mm9.geneid.LENGTH)
```



---

mm9.geneSymbol.LENGTH *Transcript length data for the organism mm*

---

### Description

mm9.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.geneSymbol.LENGTH)
head(mm9.geneSymbol.LENGTH)
```

---

mm9.genscan.LENGTH *Transcript length data for the organism mm*

---

### Description

mm9.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm9, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.genscan.LENGTH)
head(mm9.genscan.LENGTH)
```

---

mm9.knownGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm9.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.knownGene.LENGTH)
head(mm9.knownGene.LENGTH)
```

---

mm9.nscanGene.LENGTH *Transcript length data for the organism mm*

---

### Description

mm9.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.nscanGene.LENGTH)
head(mm9.nscanGene.LENGTH)
```

---

mm9.refGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm9.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.refGene.LENGTH)
head(mm9.refGene.LENGTH)
```

---

mm9.sgpGene.LENGTH      *Transcript length data for the organism mm*

---

### Description

mm9.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(mm9.sgpGene.LENGTH)
head(mm9.sgpGene.LENGTH)
```

---

`mm9.xenoRefGene.LENGTH`*Transcript length data for the organism mm*

---

**Description**

`mm9.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm9, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(mm9.xenoRefGene.LENGTH)
head(mm9.xenoRefGene.LENGTH)
```

---

`monDom1.genscan.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom1.genscan.LENGTH)
head(monDom1.genscan.LENGTH)
```

---

`monDom4.ensGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.ensGene.LENGTH)
head(monDom4.ensGene.LENGTH)
```

---

`monDom4.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.geneSymbol.LENGTH)
head(monDom4.geneSymbol.LENGTH)
```

---

`monDom4.genscan.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.genscan.LENGTH)
head(monDom4.genscan.LENGTH)
```

---

`monDom4.nscanGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.nscanGene.LENGTH)
head(monDom4.nscanGene.LENGTH)
```

---

`monDom4.refGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.refGene.LENGTH)
head(monDom4.refGene.LENGTH)
```

---

`monDom4.xenoRefGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom4.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom4.xenoRefGene.LENGTH)
head(monDom4.xenoRefGene.LENGTH)
```

---

`monDom5.ensGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom5.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.ensGene.LENGTH)
head(monDom5.ensGene.LENGTH)
```

---

`monDom5.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom5.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.geneSymbol.LENGTH)
head(monDom5.geneSymbol.LENGTH)
```



---

`monDom5.genscan.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom5.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.genscan.LENGTH)
head(monDom5.genscan.LENGTH)
```

---

`monDom5.nscanGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

`monDom5.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)
```

---

`monDom5.refGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

monDom5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)
```

---

`monDom5.xenoRefGene.LENGTH`*Transcript length data for the organism monDom*

---

**Description**

monDom5.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(monDom5.xenoRefGene.LENGTH)
head(monDom5.xenoRefGene.LENGTH)
```

---

`ornAna1.ensGene.LENGTH`*Transcript length data for the organism ornAna*

---

**Description**

`ornAna1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ornAna1.ensGene.LENGTH)
head(ornAna1.ensGene.LENGTH)
```

---

`ornAna1.geneSymbol.LENGTH`*Transcript length data for the organism ornAna*

---

**Description**

`ornAna1.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ornAna1.geneSymbol.LENGTH)
head(ornAna1.geneSymbol.LENGTH)
```

---

`ornAna1.refGene.LENGTH`*Transcript length data for the organism ornAna*

---

**Description**

`ornAna1.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ornAna1.refGene.LENGTH)
head(ornAna1.refGene.LENGTH)
```

---

`ornAna1.xenoRefGene.LENGTH`*Transcript length data for the organism ornAna*

---

**Description**

`ornAna1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ornAna1.xenoRefGene.LENGTH)
head(ornAna1.xenoRefGene.LENGTH)
```

---

`oryLat2.ensGene.LENGTH`*Transcript length data for the organism oryLat*

---

**Description**

oryLat2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)
```

---

`oryLat2.geneSymbol.LENGTH`*Transcript length data for the organism oryLat*

---

**Description**

oryLat2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)
```

---

`oryLat2.refGene.LENGTH`*Transcript length data for the organism oryLat*

---

**Description**

`oryLat2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)
```

---

`oryLat2.xenoRefGene.LENGTH`*Transcript length data for the organism oryLat*

---

**Description**

`oryLat2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)
```

---

`panTro1.ensGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro1.ensGene.LENGTH)
head(panTro1.ensGene.LENGTH)
```

---

`panTro1.geneid.LENGTH` *Transcript length data for the organism panTro*

---

**Description**

panTro1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, geneid)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro1.geneid.LENGTH)
head(panTro1.geneid.LENGTH)
```

---

`panTro1.genscan.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

`panTro1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro1.genscan.LENGTH)
head(panTro1.genscan.LENGTH)
```

---

`panTro1.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

`panTro1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro1.xenoRefGene.LENGTH)
head(panTro1.xenoRefGene.LENGTH)
```



---

`panTro2.ensGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)
```

---

`panTro2.geneSymbol.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)
```

---

`panTro2.genscan.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.genscan.LENGTH)
head(panTro2.genscan.LENGTH)
```

---

`panTro2.nscanGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.nscanGene.LENGTH)
head(panTro2.nscanGene.LENGTH)
```

---

`panTro2.refGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.refGene.LENGTH)
head(panTro2.refGene.LENGTH)
```

---

`panTro2.xenoRefGene.LENGTH`*Transcript length data for the organism panTro*

---

**Description**

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(panTro2.xenoRefGene.LENGTH)
head(panTro2.xenoRefGene.LENGTH)
```

---

```
petMar1.xenoRefGene.LENGTH
```

*Transcript length data for the organism petMar*

---

### Description

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(petMar1, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)
```

---

```
ponAbe2.ensGene.LENGTH
```

*Transcript length data for the organism ponAbe*

---

### Description

ponAbe2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)
```

---

`ponAbe2.geneSymbol.LENGTH`*Transcript length data for the organism ponAbe*

---

**Description**

`ponAbe2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)
```

---

`ponAbe2.genscan.LENGTH`*Transcript length data for the organism ponAbe*

---

**Description**

`ponAbe2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)
```

---

`ponAbe2.nscanGene.LENGTH`*Transcript length data for the organism ponAbe*

---

**Description**

`ponAbe2.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ponAbe2.nscanGene.LENGTH)
head(ponAbe2.nscanGene.LENGTH)
```

---

`ponAbe2.refGene.LENGTH`*Transcript length data for the organism ponAbe*

---

**Description**

`ponAbe2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(ponAbe2.refGene.LENGTH)
head(ponAbe2.refGene.LENGTH)
```

---

```
ponAbe2.xenoRefGene.LENGTH
```

*Transcript length data for the organism ponAbe*

---

### Description

ponAbe2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)
```

---

```
priPac1.xenoRefGene.LENGTH
```

*Transcript length data for the organism priPac*

---

### Description

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(priPac1, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)
```

---

`rheMac2.ensGene.LENGTH`*Transcript length data for the organism rheMac*

---

**Description**

`rheMac2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)
```

---

`rheMac2.geneid.LENGTH` *Transcript length data for the organism rheMac*

---

**Description**

`rheMac2.geneid.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneid` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneid)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(rheMac2.geneid.LENGTH)
head(rheMac2.geneid.LENGTH)
```



---

```
rheMac2.geneSymbol.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)
```

---

```
rheMac2.nscanGene.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)
```

---

```
rheMac2.refGene.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)
```

---

```
rheMac2.sgpGene.LENGTH
```

*Transcript length data for the organism rheMac*

---

### Description

rheMac2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rheMac2.sgpGene.LENGTH)
head(rheMac2.sgpGene.LENGTH)
```

---

`rheMac2.xenoRefGene.LENGTH`*Transcript length data for the organism rheMac*

---

**Description**

`rheMac2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)
```

---

`rn3.ensGene.LENGTH`*Transcript length data for the organism rn*

---

**Description**

`rn3.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(rn3, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.LENGTH)
```

---

rn3.geneid.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.geneid.LENGTH)
head(rn3.geneid.LENGTH)
```

---

rn3.geneSymbol.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.geneSymbol.LENGTH)
head(rn3.geneSymbol.LENGTH)
```

---

rn3.genscan.LENGTH     *Transcript length data for the organism rn*

---

### Description

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn3, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)
```

---

rn3.knownGene.LENGTH     *Transcript length data for the organism rn*

---

### Description

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

---

rn3.nscanGene.LENGTH *Transcript length data for the organism rn*

---

### Description

rn3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

---

rn3.refGene.LENGTH *Transcript length data for the organism rn*

---

### Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

---

rn3.sgpGene.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)
```

---

rn3.xenoRefGene.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)
```

---

rn4.ensGene.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)
```

---

rn4.geneid.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn4.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```



---

rn4.geneSymbol.LENGTH *Transcript length data for the organism rn*

---

### Description

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

---

rn4.genscan.LENGTH *Transcript length data for the organism rn*

---

### Description

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn4, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

---

rn4.knownGene.LENGTH *Transcript length data for the organism rn*

---

### Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, knownGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.knownGene.LENGTH)
head(rn4.knownGene.LENGTH)
```

---

rn4.nscanGene.LENGTH *Transcript length data for the organism rn*

---

### Description

rn4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)
```

---

rn4.refGene.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)
```

---

rn4.sgpGene.LENGTH      *Transcript length data for the organism rn*

---

### Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, sgpGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

---

```
rn4.xenoRefGene.LENGTH
```

*Transcript length data for the organism rn*

---

### Description

rn4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(rn4.xenoRefGene.LENGTH)
head(rn4.xenoRefGene.LENGTH)
```

---

```
sacCer1.ensGene.LENGTH
```

*Transcript length data for the organism sacCer*

---

### Description

sacCer1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer1, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(sacCer1.ensGene.LENGTH)
head(sacCer1.ensGene.LENGTH)
```

---

`sacCer2.ensGene.LENGTH`*Transcript length data for the organism sacCer*

---

**Description**

sacCer2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)
```

---

`strPur1.geneSymbol.LENGTH`*Transcript length data for the organism strPur*

---

**Description**

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)
```

---

```
strPur1.genscan.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur1.genscan.LENGTH)
head(strPur1.genscan.LENGTH)
```

---

```
strPur1.refGene.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur1.refGene.LENGTH)
head(strPur1.refGene.LENGTH)
```

---

```
strPur1.xenoRefGene.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur1.xenoRefGene.LENGTH)
head(strPur1.xenoRefGene.LENGTH)
```

---

```
strPur2.geneSymbol.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur2.geneSymbol.LENGTH)
head(strPur2.geneSymbol.LENGTH)
```

---

```
strPur2.genscan.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur2.genscan.LENGTH)
head(strPur2.genscan.LENGTH)
```

---

```
strPur2.refGene.LENGTH
```

*Transcript length data for the organism strPur*

---

### Description

strPur2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur2.refGene.LENGTH)
head(strPur2.refGene.LENGTH)
```



---

`strPur2.xenoRefGene.LENGTH`*Transcript length data for the organism strPur*

---

### Description

`strPur2.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, xenoRefGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)
```

---

`supportedGeneIDs`*Supported Gene IDs*

---

### Description

Lists supported gene ID formats

### Usage

```
supportedGeneIDs()
```

### Details

Uses the `supportedUCSCtables` function from the `GenomicFeatures` package to obtain a list of gene ID formats available from the UCSC genome browser. The `db` column gives the gene ID formats which are provided to the `id` argument of various functions. The `track` and `subtrack` columns are the names of the UCSC track/subtrack from which information is fetched.

The `GeneID` column lists the "full name" of the gene ID format where available.

The final column, headed `AvailableGenomes` lists the genomes for which there is a local copy of the length information available for the gene ID format listed in the `geneLenDataBase` package.

**Value**

A data.frame containing supported gene ID formats.

**Author(s)**

Matthew D. Young <myoung@wehi.edu.au>

**Examples**

```
supportedGeneIDs()
```

---

supportedGenomes	<i>Supported Genomes</i>
------------------	--------------------------

---

**Description**

Lists supported genomes

**Usage**

```
supportedGenomes()
```

**Details**

Uses the `ucscGenomes()` function from the `rtracklayer` package to obtain a list of genomes available from the UCSC genome browser. The `db` column lists genomes as they are provided to the genome argument of various functions.

The final column, headed `AvailableGeneIDs` lists the gene ID formats for which there is a local copy of the length information available for the genome listed in the `geneLenDataBase` package.

**Value**

A data.frame containing supported genomes.

**Author(s)**

Matthew D. Young <myoung@wehi.edu.au>

**Examples**

```
supportedGenomes()
```

---

`taeGut1.ensGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

`taeGut1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)
```

---

`taeGut1.geneSymbol.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

`taeGut1.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)
```

---

```
taeGut1.genscan.LENGTH
```

*Transcript length data for the organism taeGut*

---

### Description

taeGut1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)
```

---

```
taeGut1.nscanGene.LENGTH
```

*Transcript length data for the organism taeGut*

---

### Description

taeGut1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)
```

---

`taeGut1.refGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

`taeGut1.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

---

`taeGut1.xenoRefGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

`taeGut1.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

---

```
tetNig1.ensGene.LENGTH
```

*Transcript length data for the organism tetNig*

---

### Description

tetNig1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

---

```
tetNig1.geneid.LENGTH
```

*Transcript length data for the organism tetNig*

---

### Description

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

---

`tetNig1.genscan.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```

---

`tetNig1.nscanGene.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

tetNig1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

---

```
tetNig2.ensGene.LENGTH
```

*Transcript length data for the organism tetNig*

---

### Description

tetNig2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig2, ensGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig2.ensGene.LENGTH)
head(tetNig2.ensGene.LENGTH)
```

---

```
unfactor
```

*Purge factors*

---

### Description

Removes all factors from a variable in a sensible way.

### Usage

```
unfactor(var)
```

### Arguments

var            The variable from which you want the factors removed.

### Details

As factors are their own type, to remove factors we must convert each level into another type. This is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be done without inducing NAs, otherwise it is coerced using `as.character`. Currently supported types are: `/codefactor`, `/codedata.frame` and `/codelist`.



**Value**

The variable with all factors converted to characters or numbers (see details).

**Author(s)**

Matthew D. Young <myoung@wehi.edu.au>

**Examples**

```
#A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep='.')
x
unfactor(x)

#A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"), score <- factor(c(9, 7, 8, 9)), stringsAsFactors=TRUE)
x$player
x$score
y <- unfactor(x)
y$player
y$score
```

---

xenTro1.genscan.LENGTH

*Transcript length data for the organism xenTro*

---

**Description**

xenTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(xenTro1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(xenTro1.genscan.LENGTH)
head(xenTro1.genscan.LENGTH)
```

---

`xenTro2.ensGene.LENGTH`*Transcript length data for the organism xenTro*

---

**Description**

`xenTro2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(xenTro2.ensGene.LENGTH)
head(xenTro2.ensGene.LENGTH)
```

---

`xenTro2.geneSymbol.LENGTH`*Transcript length data for the organism xenTro*

---

**Description**

`xenTro2.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, geneSymbol)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(xenTro2.geneSymbol.LENGTH)
head(xenTro2.geneSymbol.LENGTH)
```

---

`xenTro2.genscan.LENGTH`*Transcript length data for the organism xenTro*

---

**Description**

`xenTro2.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(xenTro2.genscan.LENGTH)
head(xenTro2.genscan.LENGTH)
```

---

`xenTro2.refGene.LENGTH`*Transcript length data for the organism xenTro*

---

**Description**

`xenTro2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(xenTro2.refGene.LENGTH)
head(xenTro2.refGene.LENGTH)
```

# Index

## \*Topic **datasets**

anoCar1.ensGene.LENGTH, 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, 58  
dp2.xenoRefGene.LENGTH, 59  
dp3.geneid.LENGTH, 59  
dp3.genscan.LENGTH, 60  
dp3.xenoRefGene.LENGTH, 60  
droAna1.geneid.LENGTH, 61  
droAna1.genscan.LENGTH, 61  
droAna1.xenoRefGene.LENGTH, 62  
droAna2.genscan.LENGTH, 62  
droAna2.xenoRefGene.LENGTH, 63  
droEre1.genscan.LENGTH, 63  
droEre1.xenoRefGene.LENGTH, 64  
droGri1.genscan.LENGTH, 64  
droGri1.xenoRefGene.LENGTH, 65  
droMoj1.geneid.LENGTH, 65  
droMoj1.genscan.LENGTH, 66  
droMoj1.xenoRefGene.LENGTH, 66  
droMoj2.genscan.LENGTH, 67  
droMoj2.xenoRefGene.LENGTH, 67  
droPer1.genscan.LENGTH, 68  
droPer1.xenoRefGene.LENGTH, 68  
droSec1.genscan.LENGTH, 69  
droSec1.xenoRefGene.LENGTH, 69  
droSim1.geneid.LENGTH, 70  
droSim1.genscan.LENGTH, 70  
droSim1.xenoRefGene.LENGTH, 71  
droVir1.geneid.LENGTH, 71  
droVir1.genscan.LENGTH, 72  
droVir1.xenoRefGene.LENGTH, 72  
droVir2.genscan.LENGTH, 73  
droVir2.xenoRefGene.LENGTH, 73  
droYak1.geneid.LENGTH, 74  
droYak1.genscan.LENGTH, 74  
droYak1.xenoRefGene.LENGTH, 75  
droYak2.genscan.LENGTH, 75  
droYak2.xenoRefGene.LENGTH, 76  
equCab1.geneid.LENGTH, 76  
equCab1.geneSymbol.LENGTH, 77  
equCab1.nscanGene.LENGTH, 77  
equCab1.refGene.LENGTH, 78  
equCab1.sgpGene.LENGTH, 78  
equCab2.ensGene.LENGTH, 79  
equCab2.geneSymbol.LENGTH, 79  
equCab2.nscanGene.LENGTH, 80  
equCab2.refGene.LENGTH, 80  
equCab2.xenoRefGene.LENGTH, 81  
felCat3.ensGene.LENGTH, 81  
felCat3.geneid.LENGTH, 82  
felCat3.geneSymbol.LENGTH, 82  
felCat3.genscan.LENGTH, 83  
felCat3.nscanGene.LENGTH, 83  
felCat3.refGene.LENGTH, 84  
felCat3.sgpGene.LENGTH, 84  
felCat3.xenoRefGene.LENGTH, 85  
fr1.ensGene.LENGTH, 85  
fr1.genscan.LENGTH, 86  
fr2.ensGene.LENGTH, 86  
galGal2.ensGene.LENGTH, 87  
galGal2.geneid.LENGTH, 87  
galGal2.geneSymbol.LENGTH, 88  
galGal2.genscan.LENGTH, 88  
galGal2.refGene.LENGTH, 89  
galGal2.sgpGene.LENGTH, 89  
galGal3.ensGene.LENGTH, 90  
galGal3.geneSymbol.LENGTH, 90  
galGal3.genscan.LENGTH, 91  
galGal3.nscanGene.LENGTH, 91  
galGal3.refGene.LENGTH, 92  
galGal3.xenoRefGene.LENGTH, 92  
gasAcu1.ensGene.LENGTH, 93  
gasAcu1.nscanGene.LENGTH, 93  
hg16.acembly.LENGTH, 94  
hg16.ensGene.LENGTH, 94  
hg16.exoniphy.LENGTH, 95

- hg16.geneid.LENGTH, 95
- hg16.geneSymbol.LENGTH, 96
- hg16.genscan.LENGTH, 96
- hg16.knownGene.LENGTH, 97
- hg16.refGene.LENGTH, 97
- hg16.sgpGene.LENGTH, 98
- hg17.acembly.LENGTH, 98
- hg17.acescan.LENGTH, 99
- hg17.ccdsGene.LENGTH, 99
- hg17.ensGene.LENGTH, 100
- hg17.exoniphy.LENGTH, 100
- hg17.geneid.LENGTH, 101
- hg17.geneSymbol.LENGTH, 101
- hg17.genscan.LENGTH, 102
- hg17.knownGene.LENGTH, 102
- hg17.refGene.LENGTH, 103
- hg17.sgpGene.LENGTH, 103
- hg17.vegaGene.LENGTH, 104
- hg17.vegaPseudoGene.LENGTH, 104
- hg17.xenoRefGene.LENGTH, 105
- hg18.acembly.LENGTH, 105
- hg18.acescan.LENGTH, 106
- hg18.ccdsGene.LENGTH, 106
- hg18.ensGene.LENGTH, 107
- hg18.exoniphy.LENGTH, 107
- hg18.geneid.LENGTH, 108
- hg18.geneSymbol.LENGTH, 108
- hg18.genscan.LENGTH, 109
- hg18.knownGene.LENGTH, 109
- hg18.knownGeneOld3.LENGTH, 110
- hg18.refGene.LENGTH, 110
- hg18.sgpGene.LENGTH, 111
- hg18.sibGene.LENGTH, 111
- hg18.xenoRefGene.LENGTH, 112
- hg19.ccdsGene.LENGTH, 112
- hg19.ensGene.LENGTH, 113
- hg19.exoniphy.LENGTH, 113
- hg19.geneSymbol.LENGTH, 114
- hg19.knownGene.LENGTH, 114
- hg19.nscanGene.LENGTH, 115
- hg19.refGene.LENGTH, 115
- hg19.xenoRefGene.LENGTH, 116
- loxAfr3.xenoRefGene.LENGTH, 116
- mm7.ensGene.LENGTH, 117
- mm7.geneid.LENGTH, 117
- mm7.geneSymbol.LENGTH, 118
- mm7.genscan.LENGTH, 118
- mm7.knownGene.LENGTH, 119
- mm7.refGene.LENGTH, 119
- mm7.sgpGene.LENGTH, 120
- mm7.xenoRefGene.LENGTH, 120
- mm8.ccdsGene.LENGTH, 121
- mm8.ensGene.LENGTH, 121
- mm8.geneid.LENGTH, 122
- mm8.geneSymbol.LENGTH, 122
- mm8.genscan.LENGTH, 123
- mm8.knownGene.LENGTH, 123
- mm8.nscanGene.LENGTH, 124
- mm8.refGene.LENGTH, 124
- mm8.sgpGene.LENGTH, 125
- mm8.sibGene.LENGTH, 125
- mm8.xenoRefGene.LENGTH, 126
- mm9.acembly.LENGTH, 126
- mm9.ccdsGene.LENGTH, 127
- mm9.ensGene.LENGTH, 127
- mm9.exoniphy.LENGTH, 128
- mm9.geneid.LENGTH, 128
- mm9.geneSymbol.LENGTH, 129
- mm9.genscan.LENGTH, 129
- mm9.knownGene.LENGTH, 130
- mm9.nscanGene.LENGTH, 130
- mm9.refGene.LENGTH, 131
- mm9.sgpGene.LENGTH, 131
- mm9.xenoRefGene.LENGTH, 132
- monDom1.genscan.LENGTH, 132
- monDom4.ensGene.LENGTH, 133
- monDom4.geneSymbol.LENGTH, 133
- monDom4.genscan.LENGTH, 134
- monDom4.nscanGene.LENGTH, 134
- monDom4.refGene.LENGTH, 135
- monDom4.xenoRefGene.LENGTH, 135
- monDom5.ensGene.LENGTH, 136
- monDom5.geneSymbol.LENGTH, 136
- monDom5.genscan.LENGTH, 137
- monDom5.nscanGene.LENGTH, 137
- monDom5.refGene.LENGTH, 138
- monDom5.xenoRefGene.LENGTH, 138
- ornAna1.ensGene.LENGTH, 139
- ornAna1.geneSymbol.LENGTH, 139
- ornAna1.refGene.LENGTH, 140
- ornAna1.xenoRefGene.LENGTH, 140
- oryLat2.ensGene.LENGTH, 141
- oryLat2.geneSymbol.LENGTH, 141
- oryLat2.refGene.LENGTH, 142
- oryLat2.xenoRefGene.LENGTH, 142
- panTro1.ensGene.LENGTH, 143

- panTro1.geneid.LENGTH, 143  
panTro1.genscan.LENGTH, 144  
panTro1.xenoRefGene.LENGTH, 144  
panTro2.ensGene.LENGTH, 145  
panTro2.geneSymbol.LENGTH, 145  
panTro2.genscan.LENGTH, 146  
panTro2.nscanGene.LENGTH, 146  
panTro2.refGene.LENGTH, 147  
panTro2.xenoRefGene.LENGTH, 147  
petMar1.xenoRefGene.LENGTH, 148  
ponAbe2.ensGene.LENGTH, 148  
ponAbe2.geneSymbol.LENGTH, 149  
ponAbe2.genscan.LENGTH, 149  
ponAbe2.nscanGene.LENGTH, 150  
ponAbe2.refGene.LENGTH, 150  
ponAbe2.xenoRefGene.LENGTH, 151  
priPac1.xenoRefGene.LENGTH, 151  
rheMac2.ensGene.LENGTH, 152  
rheMac2.geneid.LENGTH, 152  
rheMac2.geneSymbol.LENGTH, 153  
rheMac2.nscanGene.LENGTH, 153  
rheMac2.refGene.LENGTH, 154  
rheMac2.sgpGene.LENGTH, 154  
rheMac2.xenoRefGene.LENGTH, 155  
rn3.ensGene.LENGTH, 155  
rn3.geneid.LENGTH, 156  
rn3.geneSymbol.LENGTH, 156  
rn3.genscan.LENGTH, 157  
rn3.knownGene.LENGTH, 157  
rn3.nscanGene.LENGTH, 158  
rn3.refGene.LENGTH, 158  
rn3.sgpGene.LENGTH, 159  
rn3.xenoRefGene.LENGTH, 159  
rn4.ensGene.LENGTH, 160  
rn4.geneid.LENGTH, 160  
rn4.geneSymbol.LENGTH, 161  
rn4.genscan.LENGTH, 161  
rn4.knownGene.LENGTH, 162  
rn4.nscanGene.LENGTH, 162  
rn4.refGene.LENGTH, 163  
rn4.sgpGene.LENGTH, 163  
rn4.xenoRefGene.LENGTH, 164  
sacCer1.ensGene.LENGTH, 164  
sacCer2.ensGene.LENGTH, 165  
strPur1.geneSymbol.LENGTH, 165  
strPur1.genscan.LENGTH, 166  
strPur1.refGene.LENGTH, 166  
strPur1.xenoRefGene.LENGTH, 167  
strPur2.geneSymbol.LENGTH, 167  
strPur2.genscan.LENGTH, 168  
strPur2.refGene.LENGTH, 168  
strPur2.xenoRefGene.LENGTH, 169  
taeGut1.ensGene.LENGTH, 171  
taeGut1.geneSymbol.LENGTH, 171  
taeGut1.genscan.LENGTH, 172  
taeGut1.nscanGene.LENGTH, 172  
taeGut1.refGene.LENGTH, 173  
taeGut1.xenoRefGene.LENGTH, 173  
tetNig1.ensGene.LENGTH, 174  
tetNig1.geneid.LENGTH, 174  
tetNig1.genscan.LENGTH, 175  
tetNig1.nscanGene.LENGTH, 175  
tetNig2.ensGene.LENGTH, 176  
xenTro1.genscan.LENGTH, 177  
xenTro2.ensGene.LENGTH, 178  
xenTro2.geneSymbol.LENGTH, 178  
xenTro2.genscan.LENGTH, 179  
xenTro2.refGene.LENGTH, 179  
anoCar1.ensGene.LENGTH, 9  
anoCar1.genscan.LENGTH, 9  
anoCar1.xenoRefGene.LENGTH, 10  
anoGam1.ensGene.LENGTH, 10  
anoGam1.geneid.LENGTH, 11  
anoGam1.genscan.LENGTH, 11  
apiMe11.genscan.LENGTH, 12  
apiMe12.ensGene.LENGTH, 12  
apiMe12.geneid.LENGTH, 13  
apiMe12.genscan.LENGTH, 13  
aplCa11.xenoRefGene.LENGTH, 14  
bosTau2.geneid.LENGTH, 14  
bosTau2.geneSymbol.LENGTH, 15  
bosTau2.genscan.LENGTH, 15  
bosTau2.refGene.LENGTH, 16  
bosTau2.sgpGene.LENGTH, 16  
bosTau3.ensGene.LENGTH, 17  
bosTau3.geneid.LENGTH, 17  
bosTau3.geneSymbol.LENGTH, 18  
bosTau3.genscan.LENGTH, 18  
bosTau3.refGene.LENGTH, 19  
bosTau3.sgpGene.LENGTH, 19  
bosTau4.ensGene.LENGTH, 20  
bosTau4.geneSymbol.LENGTH, 20  
bosTau4.genscan.LENGTH, 21  
bosTau4.nscanGene.LENGTH, 21  
bosTau4.refGene.LENGTH, 22

- braFlo1.xenoRefGene.LENGTH, 22
- caeJap1.xenoRefGene.LENGTH, 23
- caePb1.xenoRefGene.LENGTH, 23
- caePb2.xenoRefGene.LENGTH, 24
- caeRem2.xenoRefGene.LENGTH, 24
- caeRem3.xenoRefGene.LENGTH, 25
- calJac1.genscan.LENGTH, 25
- calJac1.nscanGene.LENGTH, 26
- calJac1.xenoRefGene.LENGTH, 26
- canFam1.ensGene.LENGTH, 27
- canFam1.geneSymbol.LENGTH, 27
- canFam1.genscan.LENGTH, 28
- canFam1.nscanGene.LENGTH, 28
- canFam1.refGene.LENGTH, 29
- canFam1.xenoRefGene.LENGTH, 29
- canFam2.ensGene.LENGTH, 30
- canFam2.geneSymbol.LENGTH, 30
- canFam2.genscan.LENGTH, 31
- canFam2.nscanGene.LENGTH, 31
- canFam2.refGene.LENGTH, 32
- canFam2.xenoRefGene.LENGTH, 32
- cavPor3.ensGene.LENGTH, 33
- cavPor3.genscan.LENGTH, 33
- cavPor3.nscanGene.LENGTH, 34
- cavPor3.xenoRefGene.LENGTH, 34
- cb1.xenoRefGene.LENGTH, 35
- cb3.xenoRefGene.LENGTH, 35
- ce2.geneid.LENGTH, 36
- ce2.geneSymbol.LENGTH, 36
- ce2.refGene.LENGTH, 37
- ce4.geneSymbol.LENGTH, 37
- ce4.refGene.LENGTH, 38
- ce4.xenoRefGene.LENGTH, 38
- ce6.ensGene.LENGTH, 39
- ce6.geneSymbol.LENGTH, 39
- ce6.refGene.LENGTH, 40
- ce6.xenoRefGene.LENGTH, 40
- ci1.geneSymbol.LENGTH, 41
- ci1.refGene.LENGTH, 41
- ci1.xenoRefGene.LENGTH, 42
- ci2.ensGene.LENGTH, 42
- ci2.geneSymbol.LENGTH, 43
- ci2.refGene.LENGTH, 43
- ci2.xenoRefGene.LENGTH, 44
- danRer3.ensGene.LENGTH, 44
- danRer3.geneSymbol.LENGTH, 45
- danRer3.refGene.LENGTH, 45
- danRer4.ensGene.LENGTH, 46
- danRer4.geneSymbol.LENGTH, 46
- danRer4.genscan.LENGTH, 47
- danRer4.nscanGene.LENGTH, 47
- danRer4.refGene.LENGTH, 48
- danRer5.ensGene.LENGTH, 48
- danRer5.geneSymbol.LENGTH, 49
- danRer5.refGene.LENGTH, 49
- danRer5.vegaGene.LENGTH, 50
- danRer5.vegaPseudoGene.LENGTH, 50
- danRer6.ensGene.LENGTH, 51
- danRer6.geneSymbol.LENGTH, 51
- danRer6.refGene.LENGTH, 52
- danRer6.xenoRefGene.LENGTH, 52
- dm1.geneSymbol.LENGTH, 53
- dm1.genscan.LENGTH, 53
- dm1.refGene.LENGTH, 54
- dm2.geneid.LENGTH, 54
- dm2.geneSymbol.LENGTH, 55
- dm2.genscan.LENGTH, 55
- dm2.nscanGene.LENGTH, 56
- dm2.refGene.LENGTH, 56
- dm3.geneSymbol.LENGTH, 57
- dm3.nscanPasaGene.LENGTH, 57
- dm3.refGene.LENGTH, 58
- downloadLengthFromUCSC, 9–169, 171–179
- dp2.genscan.LENGTH, 58
- dp2.xenoRefGene.LENGTH, 59
- dp3.geneid.LENGTH, 59
- dp3.genscan.LENGTH, 60
- dp3.xenoRefGene.LENGTH, 60
- droAna1.geneid.LENGTH, 61
- droAna1.genscan.LENGTH, 61
- droAna1.xenoRefGene.LENGTH, 62
- droAna2.genscan.LENGTH, 62
- droAna2.xenoRefGene.LENGTH, 63
- droEre1.genscan.LENGTH, 63
- droEre1.xenoRefGene.LENGTH, 64
- droGri1.genscan.LENGTH, 64
- droGri1.xenoRefGene.LENGTH, 65
- droMoj1.geneid.LENGTH, 65
- droMoj1.genscan.LENGTH, 66
- droMoj1.xenoRefGene.LENGTH, 66
- droMoj2.genscan.LENGTH, 67
- droMoj2.xenoRefGene.LENGTH, 67
- droPer1.genscan.LENGTH, 68
- droPer1.xenoRefGene.LENGTH, 68
- droSec1.genscan.LENGTH, 69



- droSec1.xenoRefGene.LENGTH, 69  
droSim1.geneid.LENGTH, 70  
droSim1.genscan.LENGTH, 70  
droSim1.xenoRefGene.LENGTH, 71  
droVir1.geneid.LENGTH, 71  
droVir1.genscan.LENGTH, 72  
droVir1.xenoRefGene.LENGTH, 72  
droVir2.genscan.LENGTH, 73  
droVir2.xenoRefGene.LENGTH, 73  
droYak1.geneid.LENGTH, 74  
droYak1.genscan.LENGTH, 74  
droYak1.xenoRefGene.LENGTH, 75  
droYak2.genscan.LENGTH, 75  
droYak2.xenoRefGene.LENGTH, 76
- equCab1.geneid.LENGTH, 76  
equCab1.geneSymbol.LENGTH, 77  
equCab1.nscanGene.LENGTH, 77  
equCab1.refGene.LENGTH, 78  
equCab1.sgpGene.LENGTH, 78  
equCab2.ensGene.LENGTH, 79  
equCab2.geneSymbol.LENGTH, 79  
equCab2.nscanGene.LENGTH, 80  
equCab2.refGene.LENGTH, 80  
equCab2.xenoRefGene.LENGTH, 81
- felCat3.ensGene.LENGTH, 81  
felCat3.geneid.LENGTH, 82  
felCat3.geneSymbol.LENGTH, 82  
felCat3.genscan.LENGTH, 83  
felCat3.nscanGene.LENGTH, 83  
felCat3.refGene.LENGTH, 84  
felCat3.sgpGene.LENGTH, 84  
felCat3.xenoRefGene.LENGTH, 85  
fr1.ensGene.LENGTH, 85  
fr1.genscan.LENGTH, 86  
fr2.ensGene.LENGTH, 86
- galGal2.ensGene.LENGTH, 87  
galGal2.geneid.LENGTH, 87  
galGal2.geneSymbol.LENGTH, 88  
galGal2.genscan.LENGTH, 88  
galGal2.refGene.LENGTH, 89  
galGal2.sgpGene.LENGTH, 89  
galGal3.ensGene.LENGTH, 90  
galGal3.geneSymbol.LENGTH, 90  
galGal3.genscan.LENGTH, 91  
galGal3.nscanGene.LENGTH, 91  
galGal3.refGene.LENGTH, 92
- galGal3.xenoRefGene.LENGTH, 92  
gasAcu1.ensGene.LENGTH, 93  
gasAcu1.nscanGene.LENGTH, 93
- hg16.acembly.LENGTH, 94  
hg16.ensGene.LENGTH, 94  
hg16.exoniphy.LENGTH, 95  
hg16.geneid.LENGTH, 95  
hg16.geneSymbol.LENGTH, 96  
hg16.genscan.LENGTH, 96  
hg16.knownGene.LENGTH, 97  
hg16.refGene.LENGTH, 97  
hg16.sgpGene.LENGTH, 98  
hg17.acembly.LENGTH, 98  
hg17.acescan.LENGTH, 99  
hg17.ccdsGene.LENGTH, 99  
hg17.ensGene.LENGTH, 100  
hg17.exoniphy.LENGTH, 100  
hg17.geneid.LENGTH, 101  
hg17.geneSymbol.LENGTH, 101  
hg17.genscan.LENGTH, 102  
hg17.knownGene.LENGTH, 102  
hg17.refGene.LENGTH, 103  
hg17.sgpGene.LENGTH, 103  
hg17.vegaGene.LENGTH, 104  
hg17.vegaPseudoGene.LENGTH, 104  
hg17.xenoRefGene.LENGTH, 105  
hg18.acembly.LENGTH, 105  
hg18.acescan.LENGTH, 106  
hg18.ccdsGene.LENGTH, 106  
hg18.ensGene.LENGTH, 107  
hg18.exoniphy.LENGTH, 107  
hg18.geneid.LENGTH, 108  
hg18.geneSymbol.LENGTH, 108  
hg18.genscan.LENGTH, 109  
hg18.knownGene.LENGTH, 109  
hg18.knownGeneOld3.LENGTH, 110  
hg18.refGene.LENGTH, 110  
hg18.sgpGene.LENGTH, 111  
hg18.sibGene.LENGTH, 111  
hg18.xenoRefGene.LENGTH, 112  
hg19.ccdsGene.LENGTH, 112  
hg19.ensGene.LENGTH, 113  
hg19.exoniphy.LENGTH, 113  
hg19.geneSymbol.LENGTH, 114  
hg19.knownGene.LENGTH, 114  
hg19.nscanGene.LENGTH, 115  
hg19.refGene.LENGTH, 115  
hg19.xenoRefGene.LENGTH, 116

- loxAfr3.xenoRefGene.LENGTH, 116  
 mm7.ensGene.LENGTH, 117  
 mm7.geneid.LENGTH, 117  
 mm7.geneSymbol.LENGTH, 118  
 mm7.genscan.LENGTH, 118  
 mm7.knownGene.LENGTH, 119  
 mm7.refGene.LENGTH, 119  
 mm7.sgpGene.LENGTH, 120  
 mm7.xenoRefGene.LENGTH, 120  
 mm8.ccdsGene.LENGTH, 121  
 mm8.ensGene.LENGTH, 121  
 mm8.geneid.LENGTH, 122  
 mm8.geneSymbol.LENGTH, 122  
 mm8.genscan.LENGTH, 123  
 mm8.knownGene.LENGTH, 123  
 mm8.nscanGene.LENGTH, 124  
 mm8.refGene.LENGTH, 124  
 mm8.sgpGene.LENGTH, 125  
 mm8.sibGene.LENGTH, 125  
 mm8.xenoRefGene.LENGTH, 126  
 mm9.acembly.LENGTH, 126  
 mm9.ccdsGene.LENGTH, 127  
 mm9.ensGene.LENGTH, 127  
 mm9.exoniphy.LENGTH, 128  
 mm9.geneid.LENGTH, 128  
 mm9.geneSymbol.LENGTH, 129  
 mm9.genscan.LENGTH, 129  
 mm9.knownGene.LENGTH, 130  
 mm9.nscanGene.LENGTH, 130  
 mm9.refGene.LENGTH, 131  
 mm9.sgpGene.LENGTH, 131  
 mm9.xenoRefGene.LENGTH, 132  
 monDom1.genscan.LENGTH, 132  
 monDom4.ensGene.LENGTH, 133  
 monDom4.geneSymbol.LENGTH, 133  
 monDom4.genscan.LENGTH, 134  
 monDom4.nscanGene.LENGTH, 134  
 monDom4.refGene.LENGTH, 135  
 monDom4.xenoRefGene.LENGTH, 135  
 monDom5.ensGene.LENGTH, 136  
 monDom5.geneSymbol.LENGTH, 136  
 monDom5.genscan.LENGTH, 137  
 monDom5.nscanGene.LENGTH, 137  
 monDom5.refGene.LENGTH, 138  
 monDom5.xenoRefGene.LENGTH, 138  
 ornAna1.ensGene.LENGTH, 139  
 ornAna1.geneSymbol.LENGTH, 139  
 ornAna1.refGene.LENGTH, 140  
 ornAna1.xenoRefGene.LENGTH, 140  
 oryLat2.ensGene.LENGTH, 141  
 oryLat2.geneSymbol.LENGTH, 141  
 oryLat2.refGene.LENGTH, 142  
 oryLat2.xenoRefGene.LENGTH, 142  
 panTro1.ensGene.LENGTH, 143  
 panTro1.geneid.LENGTH, 143  
 panTro1.genscan.LENGTH, 144  
 panTro1.xenoRefGene.LENGTH, 144  
 panTro2.ensGene.LENGTH, 145  
 panTro2.geneSymbol.LENGTH, 145  
 panTro2.genscan.LENGTH, 146  
 panTro2.nscanGene.LENGTH, 146  
 panTro2.refGene.LENGTH, 147  
 panTro2.xenoRefGene.LENGTH, 147  
 petMar1.xenoRefGene.LENGTH, 148  
 ponAbe2.ensGene.LENGTH, 148  
 ponAbe2.geneSymbol.LENGTH, 149  
 ponAbe2.genscan.LENGTH, 149  
 ponAbe2.nscanGene.LENGTH, 150  
 ponAbe2.refGene.LENGTH, 150  
 ponAbe2.xenoRefGene.LENGTH, 151  
 priPac1.xenoRefGene.LENGTH, 151  
 rheMac2.ensGene.LENGTH, 152  
 rheMac2.geneid.LENGTH, 152  
 rheMac2.geneSymbol.LENGTH, 153  
 rheMac2.nscanGene.LENGTH, 153  
 rheMac2.refGene.LENGTH, 154  
 rheMac2.sgpGene.LENGTH, 154  
 rheMac2.xenoRefGene.LENGTH, 155  
 rn3.ensGene.LENGTH, 155  
 rn3.geneid.LENGTH, 156  
 rn3.geneSymbol.LENGTH, 156  
 rn3.genscan.LENGTH, 157  
 rn3.knownGene.LENGTH, 157  
 rn3.nscanGene.LENGTH, 158  
 rn3.refGene.LENGTH, 158  
 rn3.sgpGene.LENGTH, 159  
 rn3.xenoRefGene.LENGTH, 159  
 rn4.ensGene.LENGTH, 160  
 rn4.geneid.LENGTH, 160  
 rn4.geneSymbol.LENGTH, 161  
 rn4.genscan.LENGTH, 161  
 rn4.knownGene.LENGTH, 162  
 rn4.nscanGene.LENGTH, 162  
 rn4.refGene.LENGTH, 163

rn4.sgpGene.LENGTH, [163](#)  
rn4.xenoRefGene.LENGTH, [164](#)

sacCer1.ensGene.LENGTH, [164](#)  
sacCer2.ensGene.LENGTH, [165](#)  
strPur1.geneSymbol.LENGTH, [165](#)  
strPur1.genscan.LENGTH, [166](#)  
strPur1.refGene.LENGTH, [166](#)  
strPur1.xenoRefGene.LENGTH, [167](#)  
strPur2.geneSymbol.LENGTH, [167](#)  
strPur2.genscan.LENGTH, [168](#)  
strPur2.refGene.LENGTH, [168](#)  
strPur2.xenoRefGene.LENGTH, [169](#)  
supportedGeneIDs, [169](#)  
supportedGenomes, [170](#)

taeGut1.ensGene.LENGTH, [171](#)  
taeGut1.geneSymbol.LENGTH, [171](#)  
taeGut1.genscan.LENGTH, [172](#)  
taeGut1.nscanGene.LENGTH, [172](#)  
taeGut1.refGene.LENGTH, [173](#)  
taeGut1.xenoRefGene.LENGTH, [173](#)  
tetNig1.ensGene.LENGTH, [174](#)  
tetNig1.geneid.LENGTH, [174](#)  
tetNig1.genscan.LENGTH, [175](#)  
tetNig1.nscanGene.LENGTH, [175](#)  
tetNig2.ensGene.LENGTH, [176](#)

unfactor, [176](#)

xenTro1.genscan.LENGTH, [177](#)  
xenTro2.ensGene.LENGTH, [178](#)  
xenTro2.geneSymbol.LENGTH, [178](#)  
xenTro2.genscan.LENGTH, [179](#)  
xenTro2.refGene.LENGTH, [179](#)