

# Package ‘geneLenDataBase’

December 12, 2024

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

**Version** 1.43.0

**Date** 2024-06-08

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

**Depends** R (>= 2.11.0)

**Imports** utils, rtracklayer, GenomicFeatures, txdbmaker

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

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

**License** LGPL (>= 2)

**biocViews** ExperimentData, Genome

**RoxygenNote** 7.3.1

**Encoding** UTF-8

**git\_url** <https://git.bioconductor.org/packages/geneLenDataBase>

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## Contents

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

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

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

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

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

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

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



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

**Index****182**

anoCar1.ensGene.LENGTH

*Transcript length data for the organism anoCar***Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

anoCar1.genscan.LENGTH

*Transcript length data for the organism anoCar***Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
anoCar1.xenoRefGene.LENGTH
```

*Transcript length data for the organism anoCar*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
anoGam1.ensGene.LENGTH
```

*Transcript length data for the organism anoGam*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

apiMe11.genscan.LENGTH

*Transcript length data for the organism apiMel*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

apiMe12.ensGene.LENGTH

*Transcript length data for the organism apiMel*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

`aplCa11.xenoRefGene.LENGTH`*Transcript length data for the organism aplCa1*

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
bosTau3.geneSymbol.LENGTH
```

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
bosTau3.genscan.LENGTH
```

*Transcript length data for the organism bosTau*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
caeJap1.xenoRefGene.LENGTH
```

*Transcript length data for the organism caeJap*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
caePb1.xenoRefGene.LENGTH
```

*Transcript length data for the organism caePb*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
caePb2.xenoRefGene.LENGTH
```

*Transcript length data for the organism caePb*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
caeRem2.xenoRefGene.LENGTH
```

*Transcript length data for the organism caeRem*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

```
danRer4.ensGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer4.geneSymbol.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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



---

```
danRer5.geneSymbol.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer5.refGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer5.vegaGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer5.vegaPseudoGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer6.ensGene.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

```
danRer6.geneSymbol.LENGTH
```

*Transcript length data for the organism danRer*

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

**Description**

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

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

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

downloadLengthFromUCSC  
*Download Transcript Length Data*

---

### Description

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

### Usage

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

### Arguments

genome	A string identifying the genome that genes refer to. For a list of supported organisms see <a href="#">supportedGenomes</a> .
id	A string identifying the gene identifier used by genes. For a list of supported gene identifiers see <a href="#">supportedGeneIDs</a> .

## Details

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

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

## Value

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

## Note

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

## Author(s)

Matthew D. Young <[myoung@wehi.edu.au](mailto:myoung@wehi.edu.au)>

## See Also

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

## Examples

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

## End(Not run)
```

---

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)
```

---

geneLenDatabase-pkg    *geneLenDatabase:*

---

### Description

Lengths of mRNA transcripts for a number of genomes

### Details

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

### Author(s)

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Authors:

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### See Also

Useful links:

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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

---

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

---

### Description

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

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

### See Also

[downloadLengthFromUCSC](#)

### Examples

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



---

hg16.geneid.LENGTH      *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	<i>Supported Gene IDs</i>
------------------	---------------------------

---

**Description**

Lists supported gene ID formats

**Usage**

supportedGeneIDs()

**Details**

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

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

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

**Value**

A data.frame containing supported gene ID formats.

**Author(s)**

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

**Examples**

```
supportedGeneIDs()
```

---

supportedGenomes	<i>Supported Genomes</i>
------------------	--------------------------

---

**Description**

Lists supported genomes

**Usage**

supportedGenomes()

**Details**

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

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

**Value**

A data.frame containing supported genomes.

**Author(s)**

Matthew D. Young <[myoung@wehi.edu.au](mailto:myoung@wehi.edu.au)>

**Examples**

```
supportedGenomes()
```

---

`taeGut1.ensGene.LENGTH`

*Transcript length data for the organism taeGut*

---

**Description**

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

The data file was made by calling `downloadLengthFromUCSC(taeGut1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)
```

---

```
taeGut1.geneSymbol.LENGTH
```

*Transcript length data for the organism taeGut*

---

### Description

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

The data file was made by calling `downloadLengthFromUCSC(taeGut1, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)
```

---

```
taeGut1.genscan.LENGTH
```

*Transcript length data for the organism taeGut*

---

### Description

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

The data file was made by calling `downloadLengthFromUCSC(taeGut1, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)
```

---

```
taeGut1.nscanGene.LENGTH
```

*Transcript length data for the organism taeGut*

---

### Description

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

The data file was made by calling `downloadLengthFromUCSC(taeGut1, nscanGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)
```

---

```
taeGut1.refGene.LENGTH
```

*Transcript length data for the organism taeGut*

---

### Description

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

The data file was made by calling `downloadLengthFromUCSC(taeGut1, refGene)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

---

`taeGut1.xenoRefGene.LENGTH`*Transcript length data for the organism taeGut*

---

**Description**

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

The data file was made by calling `downloadLengthFromUCSC(taeGut1, xenoRefGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

---

`tetNig1.ensGene.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

`tetNig1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

---

tetNig1.geneid.LENGTH *Transcript length data for the organism tetNig*

---

### Description

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, geneid)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

---

tetNig1.genscan.LENGTH  
*Transcript length data for the organism tetNig*

---

### Description

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```



---

`tetNig1.nscanGene.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

`tetNig1.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, nscanGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

---

`tetNig2.ensGene.LENGTH`*Transcript length data for the organism tetNig*

---

**Description**

`tetNig2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(tetNig2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

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

---

`unfactor`*Purge factors*

---

**Description**

Removes all factors from a variable in a sensible way.

**Usage**

```
unfactor(var)
```

**Arguments**

`var`                    The variable from which you want the factors removed.

**Details**

As factors are their own type, to remove factors we must convert each level into another type. This is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be done without inducing NAs, otherwise it is coerced using `as.character`. Currently supported types are: `factor`, `data.frame` and `list`.

**Value**

The variable with all factors converted to characters or numbers (see details).

**Author(s)**

Matthew D. Young <[myoung@wehi.edu.au](mailto:myoung@wehi.edu.au)>

**Examples**

```
# A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep='.')
x
unfactor(x)

# A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"),
                score <- factor(c(9, 7, 8, 9)), stringsAsFactors=TRUE)
x$player
x$score
y <- unfactor(x)
y$player
y$score
```

---

`xenTro1.genscan.LENGTH`*Transcript length data for the organism xenTro*

---

**Description**

`xenTro1.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro1, genscan)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(xenTro1.genscan.LENGTH)
head(xenTro1.genscan.LENGTH)
```

---

`xenTro2.ensGene.LENGTH`*Transcript length data for the organism xenTro*

---

**Description**

`xenTro2.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, ensGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(xenTro2.ensGene.LENGTH)
head(xenTro2.ensGene.LENGTH)
```

---

```
xenTro2.geneSymbol.LENGTH
```

*Transcript length data for the organism xenTro*

---

### Description

xenTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, geneSymbol)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(xenTro2.geneSymbol.LENGTH)
head(xenTro2.geneSymbol.LENGTH)
```

---

```
xenTro2.genscan.LENGTH
```

*Transcript length data for the organism xenTro*

---

### Description

xenTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, genscan)` on the date on which the package was last updated.

### See Also

[downloadLengthFromUCSC](#)

### Examples

```
data(xenTro2.genscan.LENGTH)
head(xenTro2.genscan.LENGTH)
```

---

`xenTro2.refGene.LENGTH`*Transcript length data for the organism xenTro*

---

**Description**

`xenTro2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, refGene)` on the date on which the package was last updated.

**See Also**

[downloadLengthFromUCSC](#)

**Examples**

```
data(xenTro2.refGene.LENGTH)
head(xenTro2.refGene.LENGTH)
```

# Index

## \* datasets

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

canFam1.genscan.LENGTH, 28  
canFam1.nscanGene.LENGTH, 28  
canFam1.refGene.LENGTH, 29  
canFam1.xenoRefGene.LENGTH, 29  
canFam2.ensGene.LENGTH, 30  
canFam2.geneSymbol.LENGTH, 30  
canFam2.genscan.LENGTH, 31  
canFam2.nscanGene.LENGTH, 31  
canFam2.refGene.LENGTH, 32  
canFam2.xenoRefGene.LENGTH, 32  
cavPor3.ensGene.LENGTH, 33  
cavPor3.genscan.LENGTH, 33  
cavPor3.nscanGene.LENGTH, 34  
cavPor3.xenoRefGene.LENGTH, 34  
cb1.xenoRefGene.LENGTH, 35  
cb3.xenoRefGene.LENGTH, 35  
ce2.geneid.LENGTH, 36  
ce2.geneSymbol.LENGTH, 36  
ce2.refGene.LENGTH, 37  
ce4.geneSymbol.LENGTH, 37  
ce4.refGene.LENGTH, 38  
ce4.xenoRefGene.LENGTH, 38  
ce6.ensGene.LENGTH, 39  
ce6.geneSymbol.LENGTH, 39  
ce6.refGene.LENGTH, 40  
ce6.xenoRefGene.LENGTH, 40  
ci1.geneSymbol.LENGTH, 41  
ci1.refGene.LENGTH, 41  
ci1.xenoRefGene.LENGTH, 42  
ci2.ensGene.LENGTH, 42  
ci2.geneSymbol.LENGTH, 43  
ci2.refGene.LENGTH, 43  
ci2.xenoRefGene.LENGTH, 44  
danRer3.ensGene.LENGTH, 44  
danRer3.geneSymbol.LENGTH, 45  
danRer3.refGene.LENGTH, 45  
danRer4.ensGene.LENGTH, 46  
danRer4.geneSymbol.LENGTH, 46  
danRer4.genscan.LENGTH, 47

- danRer4.nscanGene.LENGTH, 47  
danRer4.refGene.LENGTH, 48  
danRer5.ensGene.LENGTH, 48  
danRer5.geneSymbol.LENGTH, 49  
danRer5.refGene.LENGTH, 49  
danRer5.vegaGene.LENGTH, 50  
danRer5.vegaPseudoGene.LENGTH, 50  
danRer6.ensGene.LENGTH, 51  
danRer6.geneSymbol.LENGTH, 51  
danRer6.refGene.LENGTH, 52  
danRer6.xenoRefGene.LENGTH, 52  
dm1.geneSymbol.LENGTH, 53  
dm1.genscan.LENGTH, 53  
dm1.refGene.LENGTH, 54  
dm2.geneid.LENGTH, 54  
dm2.geneSymbol.LENGTH, 55  
dm2.genscan.LENGTH, 55  
dm2.nscanGene.LENGTH, 56  
dm2.refGene.LENGTH, 56  
dm3.geneSymbol.LENGTH, 57  
dm3.nscanPasaGene.LENGTH, 57  
dm3.refGene.LENGTH, 58  
dp2.genscan.LENGTH, 59  
dp2.xenoRefGene.LENGTH, 60  
dp3.geneid.LENGTH, 60  
dp3.genscan.LENGTH, 61  
dp3.xenoRefGene.LENGTH, 61  
droAna1.geneid.LENGTH, 62  
droAna1.genscan.LENGTH, 62  
droAna1.xenoRefGene.LENGTH, 63  
droAna2.genscan.LENGTH, 63  
droAna2.xenoRefGene.LENGTH, 64  
droEre1.genscan.LENGTH, 64  
droEre1.xenoRefGene.LENGTH, 65  
droGri1.genscan.LENGTH, 65  
droGri1.xenoRefGene.LENGTH, 66  
droMoj1.geneid.LENGTH, 66  
droMoj1.genscan.LENGTH, 67  
droMoj1.xenoRefGene.LENGTH, 67  
droMoj2.genscan.LENGTH, 68  
droMoj2.xenoRefGene.LENGTH, 68  
droPer1.genscan.LENGTH, 69  
droPer1.xenoRefGene.LENGTH, 69  
droSec1.genscan.LENGTH, 70  
droSec1.xenoRefGene.LENGTH, 70  
droSim1.geneid.LENGTH, 71  
droSim1.genscan.LENGTH, 71  
droSim1.xenoRefGene.LENGTH, 72  
droVir1.geneid.LENGTH, 72  
droVir1.genscan.LENGTH, 73  
droVir1.xenoRefGene.LENGTH, 73  
droVir2.genscan.LENGTH, 74  
droVir2.xenoRefGene.LENGTH, 74  
droYak1.geneid.LENGTH, 75  
droYak1.genscan.LENGTH, 75  
droYak1.xenoRefGene.LENGTH, 76  
droYak2.genscan.LENGTH, 76  
droYak2.xenoRefGene.LENGTH, 77  
equCab1.geneid.LENGTH, 77  
equCab1.geneSymbol.LENGTH, 78  
equCab1.nscanGene.LENGTH, 78  
equCab1.refGene.LENGTH, 79  
equCab1.sgpGene.LENGTH, 79  
equCab2.ensGene.LENGTH, 80  
equCab2.geneSymbol.LENGTH, 80  
equCab2.nscanGene.LENGTH, 81  
equCab2.refGene.LENGTH, 81  
equCab2.xenoRefGene.LENGTH, 82  
felCat3.ensGene.LENGTH, 82  
felCat3.geneid.LENGTH, 83  
felCat3.geneSymbol.LENGTH, 83  
felCat3.genscan.LENGTH, 84  
felCat3.nscanGene.LENGTH, 84  
felCat3.refGene.LENGTH, 85  
felCat3.sgpGene.LENGTH, 85  
felCat3.xenoRefGene.LENGTH, 86  
fr1.ensGene.LENGTH, 86  
fr1.genscan.LENGTH, 87  
fr2.ensGene.LENGTH, 87  
galGal2.ensGene.LENGTH, 88  
galGal2.geneid.LENGTH, 88  
galGal2.geneSymbol.LENGTH, 89  
galGal2.genscan.LENGTH, 89  
galGal2.refGene.LENGTH, 90  
galGal2.sgpGene.LENGTH, 90  
galGal3.ensGene.LENGTH, 91  
galGal3.geneSymbol.LENGTH, 91  
galGal3.genscan.LENGTH, 92  
galGal3.nscanGene.LENGTH, 92  
galGal3.refGene.LENGTH, 93  
galGal3.xenoRefGene.LENGTH, 93  
gasAcu1.ensGene.LENGTH, 94  
gasAcu1.nscanGene.LENGTH, 94  
hg16.acembly.LENGTH, 95  
hg16.ensGene.LENGTH, 96  
hg16.exoniphy.LENGTH, 96

hg16.geneid.LENGTH, 97  
hg16.geneSymbol.LENGTH, 97  
hg16.genscan.LENGTH, 98  
hg16.knownGene.LENGTH, 98  
hg16.refGene.LENGTH, 99  
hg16.sgpGene.LENGTH, 99  
hg17.acembly.LENGTH, 100  
hg17.acescan.LENGTH, 100  
hg17.ccdsGene.LENGTH, 101  
hg17.ensGene.LENGTH, 101  
hg17.exoniphy.LENGTH, 102  
hg17.geneid.LENGTH, 102  
hg17.geneSymbol.LENGTH, 103  
hg17.genscan.LENGTH, 103  
hg17.knownGene.LENGTH, 104  
hg17.refGene.LENGTH, 104  
hg17.sgpGene.LENGTH, 105  
hg17.vegaGene.LENGTH, 105  
hg17.vegaPseudoGene.LENGTH, 106  
hg17.xenoRefGene.LENGTH, 106  
hg18.acembly.LENGTH, 107  
hg18.acescan.LENGTH, 107  
hg18.ccdsGene.LENGTH, 108  
hg18.ensGene.LENGTH, 108  
hg18.exoniphy.LENGTH, 109  
hg18.geneid.LENGTH, 109  
hg18.geneSymbol.LENGTH, 110  
hg18.genscan.LENGTH, 110  
hg18.knownGene.LENGTH, 111  
hg18.knownGeneOld3.LENGTH, 111  
hg18.refGene.LENGTH, 112  
hg18.sgpGene.LENGTH, 112  
hg18.sibGene.LENGTH, 113  
hg18.xenoRefGene.LENGTH, 113  
hg19.ccdsGene.LENGTH, 114  
hg19.ensGene.LENGTH, 114  
hg19.exoniphy.LENGTH, 115  
hg19.geneSymbol.LENGTH, 115  
hg19.knownGene.LENGTH, 116  
hg19.nscanGene.LENGTH, 116  
hg19.refGene.LENGTH, 117  
hg19.xenoRefGene.LENGTH, 117  
loxAfr3.xenoRefGene.LENGTH, 118  
mm7.ensGene.LENGTH, 118  
mm7.geneid.LENGTH, 119  
mm7.geneSymbol.LENGTH, 119  
mm7.genscan.LENGTH, 120  
mm7.knownGene.LENGTH, 120  
mm7.refGene.LENGTH, 121  
mm7.sgpGene.LENGTH, 121  
mm7.xenoRefGene.LENGTH, 122  
mm8.ccdsGene.LENGTH, 122  
mm8.ensGene.LENGTH, 123  
mm8.geneid.LENGTH, 123  
mm8.geneSymbol.LENGTH, 124  
mm8.genscan.LENGTH, 124  
mm8.knownGene.LENGTH, 125  
mm8.nscanGene.LENGTH, 125  
mm8.refGene.LENGTH, 126  
mm8.sgpGene.LENGTH, 126  
mm8.sibGene.LENGTH, 127  
mm8.xenoRefGene.LENGTH, 127  
mm9.acembly.LENGTH, 128  
mm9.ccdsGene.LENGTH, 128  
mm9.ensGene.LENGTH, 129  
mm9.exoniphy.LENGTH, 129  
mm9.geneid.LENGTH, 130  
mm9.geneSymbol.LENGTH, 130  
mm9.genscan.LENGTH, 131  
mm9.knownGene.LENGTH, 131  
mm9.nscanGene.LENGTH, 132  
mm9.refGene.LENGTH, 132  
mm9.sgpGene.LENGTH, 133  
mm9.xenoRefGene.LENGTH, 133  
monDom1.genscan.LENGTH, 134  
monDom4.ensGene.LENGTH, 134  
monDom4.geneSymbol.LENGTH, 135  
monDom4.genscan.LENGTH, 135  
monDom4.nscanGene.LENGTH, 136  
monDom4.refGene.LENGTH, 136  
monDom4.xenoRefGene.LENGTH, 137  
monDom5.ensGene.LENGTH, 137  
monDom5.geneSymbol.LENGTH, 138  
monDom5.genscan.LENGTH, 138  
monDom5.nscanGene.LENGTH, 139  
monDom5.refGene.LENGTH, 139  
monDom5.xenoRefGene.LENGTH, 140  
ornAna1.ensGene.LENGTH, 140  
ornAna1.geneSymbol.LENGTH, 141  
ornAna1.refGene.LENGTH, 141  
ornAna1.xenoRefGene.LENGTH, 142  
oryLat2.ensGene.LENGTH, 142  
oryLat2.geneSymbol.LENGTH, 143  
oryLat2.refGene.LENGTH, 143  
oryLat2.xenoRefGene.LENGTH, 144  
panTro1.ensGene.LENGTH, 144



- panTro1.geneid.LENGTH, 145  
 panTro1.genscan.LENGTH, 145  
 panTro1.xenoRefGene.LENGTH, 146  
 panTro2.ensGene.LENGTH, 146  
 panTro2.geneSymbol.LENGTH, 147  
 panTro2.genscan.LENGTH, 147  
 panTro2.nscanGene.LENGTH, 148  
 panTro2.refGene.LENGTH, 148  
 panTro2.xenoRefGene.LENGTH, 149  
 petMar1.xenoRefGene.LENGTH, 149  
 ponAbe2.ensGene.LENGTH, 150  
 ponAbe2.geneSymbol.LENGTH, 150  
 ponAbe2.genscan.LENGTH, 151  
 ponAbe2.nscanGene.LENGTH, 151  
 ponAbe2.refGene.LENGTH, 152  
 ponAbe2.xenoRefGene.LENGTH, 152  
 priPac1.xenoRefGene.LENGTH, 153  
 rheMac2.ensGene.LENGTH, 153  
 rheMac2.geneid.LENGTH, 154  
 rheMac2.geneSymbol.LENGTH, 154  
 rheMac2.nscanGene.LENGTH, 155  
 rheMac2.refGene.LENGTH, 155  
 rheMac2.sgpGene.LENGTH, 156  
 rheMac2.xenoRefGene.LENGTH, 156  
 rn3.ensGene.LENGTH, 157  
 rn3.geneid.LENGTH, 157  
 rn3.geneSymbol.LENGTH, 158  
 rn3.genscan.LENGTH, 158  
 rn3.knownGene.LENGTH, 159  
 rn3.nscanGene.LENGTH, 159  
 rn3.refGene.LENGTH, 160  
 rn3.sgpGene.LENGTH, 160  
 rn3.xenoRefGene.LENGTH, 161  
 rn4.ensGene.LENGTH, 161  
 rn4.geneid.LENGTH, 162  
 rn4.geneSymbol.LENGTH, 162  
 rn4.genscan.LENGTH, 163  
 rn4.knownGene.LENGTH, 163  
 rn4.nscanGene.LENGTH, 164  
 rn4.refGene.LENGTH, 164  
 rn4.sgpGene.LENGTH, 165  
 rn4.xenoRefGene.LENGTH, 165  
 sacCer1.ensGene.LENGTH, 166  
 sacCer2.ensGene.LENGTH, 166  
 strPur1.geneSymbol.LENGTH, 167  
 strPur1.genscan.LENGTH, 167  
 strPur1.refGene.LENGTH, 168  
 strPur1.xenoRefGene.LENGTH, 168  
 strPur2.geneSymbol.LENGTH, 169  
 strPur2.genscan.LENGTH, 169  
 strPur2.refGene.LENGTH, 170  
 strPur2.xenoRefGene.LENGTH, 170  
 taeGut1.ensGene.LENGTH, 172  
 taeGut1.geneSymbol.LENGTH, 173  
 taeGut1.genscan.LENGTH, 173  
 taeGut1.nscanGene.LENGTH, 174  
 taeGut1.refGene.LENGTH, 174  
 taeGut1.xenoRefGene.LENGTH, 175  
 tetNig1.ensGene.LENGTH, 175  
 tetNig1.geneid.LENGTH, 176  
 tetNig1.genscan.LENGTH, 176  
 tetNig1.nscanGene.LENGTH, 177  
 tetNig2.ensGene.LENGTH, 177  
 xenTro1.genscan.LENGTH, 179  
 xenTro2.ensGene.LENGTH, 179  
 xenTro2.geneSymbol.LENGTH, 180  
 xenTro2.genscan.LENGTH, 180  
 xenTro2.refGene.LENGTH, 181
- \* internal**  
 geneLenDatabase-pkg, 95
- anoCar1.ensGene.LENGTH, 9  
 anoCar1.genscan.LENGTH, 9  
 anoCar1.xenoRefGene.LENGTH, 10  
 anoGam1.ensGene.LENGTH, 10  
 anoGam1.geneid.LENGTH, 11  
 anoGam1.genscan.LENGTH, 11  
 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, 9–58, 58, 60–170,  
     172–177, 179–181  
 dp2.genscan.LENGTH, 59  
 dp2.xenoRefGene.LENGTH, 60  
 dp3.geneid.LENGTH, 60  
 dp3.genscan.LENGTH, 61  
 dp3.xenoRefGene.LENGTH, 61  
 droAna1.geneid.LENGTH, 62  
 droAna1.genscan.LENGTH, 62  
 droAna1.xenoRefGene.LENGTH, 63  
 droAna2.genscan.LENGTH, 63  
 droAna2.xenoRefGene.LENGTH, 64  
 droEre1.genscan.LENGTH, 64  
 droEre1.xenoRefGene.LENGTH, 65  
 droGri1.genscan.LENGTH, 65  
 droGri1.xenoRefGene.LENGTH, 66  
 droMoj1.geneid.LENGTH, 66  
 droMoj1.genscan.LENGTH, 67  
 droMoj1.xenoRefGene.LENGTH, 67  
 droMoj2.genscan.LENGTH, 68  
 droMoj2.xenoRefGene.LENGTH, 68

- droPer1.genscan.LENGTH, 69
- droPer1.xenoRefGene.LENGTH, 69
- droSec1.genscan.LENGTH, 70
- droSec1.xenoRefGene.LENGTH, 70
- droSim1.geneid.LENGTH, 71
- droSim1.genscan.LENGTH, 71
- droSim1.xenoRefGene.LENGTH, 72
- droVir1.geneid.LENGTH, 72
- droVir1.genscan.LENGTH, 73
- droVir1.xenoRefGene.LENGTH, 73
- droVir2.genscan.LENGTH, 74
- droVir2.xenoRefGene.LENGTH, 74
- droYak1.geneid.LENGTH, 75
- droYak1.genscan.LENGTH, 75
- droYak1.xenoRefGene.LENGTH, 76
- droYak2.genscan.LENGTH, 76
- droYak2.xenoRefGene.LENGTH, 77
  
- equCab1.geneid.LENGTH, 77
- equCab1.geneSymbol.LENGTH, 78
- equCab1.nscanGene.LENGTH, 78
- equCab1.refGene.LENGTH, 79
- equCab1.sgpGene.LENGTH, 79
- equCab2.ensGene.LENGTH, 80
- equCab2.geneSymbol.LENGTH, 80
- equCab2.nscanGene.LENGTH, 81
- equCab2.refGene.LENGTH, 81
- equCab2.xenoRefGene.LENGTH, 82
  
- felCat3.ensGene.LENGTH, 82
- felCat3.geneid.LENGTH, 83
- felCat3.geneSymbol.LENGTH, 83
- felCat3.genscan.LENGTH, 84
- felCat3.nscanGene.LENGTH, 84
- felCat3.refGene.LENGTH, 85
- felCat3.sgpGene.LENGTH, 85
- felCat3.xenoRefGene.LENGTH, 86
- fr1.ensGene.LENGTH, 86
- fr1.genscan.LENGTH, 87
- fr2.ensGene.LENGTH, 87
  
- galGal2.ensGene.LENGTH, 88
- galGal2.geneid.LENGTH, 88
- galGal2.geneSymbol.LENGTH, 89
- galGal2.genscan.LENGTH, 89
- galGal2.refGene.LENGTH, 90
- galGal2.sgpGene.LENGTH, 90
- galGal3.ensGene.LENGTH, 91
- galGal3.geneSymbol.LENGTH, 91
  
- galGal3.genscan.LENGTH, 92
- galGal3.nscanGene.LENGTH, 92
- galGal3.refGene.LENGTH, 93
- galGal3.xenoRefGene.LENGTH, 93
- gasAcu1.ensGene.LENGTH, 94
- gasAcu1.nscanGene.LENGTH, 94
- geneLenDataBase (geneLenDatabase-pkg), 95
- geneLenDataBase-package (geneLenDatabase-pkg), 95
- geneLenDatabase-pkg, 95
  
- hg16.acembly.LENGTH, 95
- hg16.ensGene.LENGTH, 96
- hg16.exoniphy.LENGTH, 96
- hg16.geneid.LENGTH, 97
- hg16.geneSymbol.LENGTH, 97
- hg16.genscan.LENGTH, 98
- hg16.knownGene.LENGTH, 98
- hg16.refGene.LENGTH, 99
- hg16.sgpGene.LENGTH, 99
- hg17.acembly.LENGTH, 100
- hg17.acescan.LENGTH, 100
- hg17.ccdsGene.LENGTH, 101
- hg17.ensGene.LENGTH, 101
- hg17.exoniphy.LENGTH, 102
- hg17.geneid.LENGTH, 102
- hg17.geneSymbol.LENGTH, 103
- hg17.genscan.LENGTH, 103
- hg17.knownGene.LENGTH, 104
- hg17.refGene.LENGTH, 104
- hg17.sgpGene.LENGTH, 105
- hg17.vegaGene.LENGTH, 105
- hg17.vegaPseudoGene.LENGTH, 106
- hg17.xenoRefGene.LENGTH, 106
- hg18.acembly.LENGTH, 107
- hg18.acescan.LENGTH, 107
- hg18.ccdsGene.LENGTH, 108
- hg18.ensGene.LENGTH, 108
- hg18.exoniphy.LENGTH, 109
- hg18.geneid.LENGTH, 109
- hg18.geneSymbol.LENGTH, 110
- hg18.genscan.LENGTH, 110
- hg18.knownGene.LENGTH, 111
- hg18.knownGeneOld3.LENGTH, 111
- hg18.refGene.LENGTH, 112
- hg18.sgpGene.LENGTH, 112
- hg18.sibGene.LENGTH, 113
- hg18.xenoRefGene.LENGTH, 113

- hg19.ccdsGene.LENGTH, 114  
 hg19.ensGene.LENGTH, 114  
 hg19.exoniphy.LENGTH, 115  
 hg19.geneSymbol.LENGTH, 115  
 hg19.knownGene.LENGTH, 116  
 hg19.nscanGene.LENGTH, 116  
 hg19.refGene.LENGTH, 117  
 hg19.xenoRefGene.LENGTH, 117  
  
 loxAfr3.xenoRefGene.LENGTH, 118  
  
 mm7.ensGene.LENGTH, 118  
 mm7.geneid.LENGTH, 119  
 mm7.geneSymbol.LENGTH, 119  
 mm7.genscan.LENGTH, 120  
 mm7.knownGene.LENGTH, 120  
 mm7.refGene.LENGTH, 121  
 mm7.sgpGene.LENGTH, 121  
 mm7.xenoRefGene.LENGTH, 122  
 mm8.ccdsGene.LENGTH, 122  
 mm8.ensGene.LENGTH, 123  
 mm8.geneid.LENGTH, 123  
 mm8.geneSymbol.LENGTH, 124  
 mm8.genscan.LENGTH, 124  
 mm8.knownGene.LENGTH, 125  
 mm8.nscanGene.LENGTH, 125  
 mm8.refGene.LENGTH, 126  
 mm8.sgpGene.LENGTH, 126  
 mm8.sibGene.LENGTH, 127  
 mm8.xenoRefGene.LENGTH, 127  
 mm9.acembly.LENGTH, 128  
 mm9.ccdsGene.LENGTH, 128  
 mm9.ensGene.LENGTH, 129  
 mm9.exoniphy.LENGTH, 129  
 mm9.geneid.LENGTH, 130  
 mm9.geneSymbol.LENGTH, 130  
 mm9.genscan.LENGTH, 131  
 mm9.knownGene.LENGTH, 131  
 mm9.nscanGene.LENGTH, 132  
 mm9.refGene.LENGTH, 132  
 mm9.sgpGene.LENGTH, 133  
 mm9.xenoRefGene.LENGTH, 133  
 monDom1.genscan.LENGTH, 134  
 monDom4.ensGene.LENGTH, 134  
 monDom4.geneSymbol.LENGTH, 135  
 monDom4.genscan.LENGTH, 135  
 monDom4.nscanGene.LENGTH, 136  
 monDom4.refGene.LENGTH, 136  
 monDom4.xenoRefGene.LENGTH, 137  
  
 monDom5.ensGene.LENGTH, 137  
 monDom5.geneSymbol.LENGTH, 138  
 monDom5.genscan.LENGTH, 138  
 monDom5.nscanGene.LENGTH, 139  
 monDom5.refGene.LENGTH, 139  
 monDom5.xenoRefGene.LENGTH, 140  
  
 ornAna1.ensGene.LENGTH, 140  
 ornAna1.geneSymbol.LENGTH, 141  
 ornAna1.refGene.LENGTH, 141  
 ornAna1.xenoRefGene.LENGTH, 142  
 oryLat2.ensGene.LENGTH, 142  
 oryLat2.geneSymbol.LENGTH, 143  
 oryLat2.refGene.LENGTH, 143  
 oryLat2.xenoRefGene.LENGTH, 144  
  
 panTro1.ensGene.LENGTH, 144  
 panTro1.geneid.LENGTH, 145  
 panTro1.genscan.LENGTH, 145  
 panTro1.xenoRefGene.LENGTH, 146  
 panTro2.ensGene.LENGTH, 146  
 panTro2.geneSymbol.LENGTH, 147  
 panTro2.genscan.LENGTH, 147  
 panTro2.nscanGene.LENGTH, 148  
 panTro2.refGene.LENGTH, 148  
 panTro2.xenoRefGene.LENGTH, 149  
 petMar1.xenoRefGene.LENGTH, 149  
 ponAbe2.ensGene.LENGTH, 150  
 ponAbe2.geneSymbol.LENGTH, 150  
 ponAbe2.genscan.LENGTH, 151  
 ponAbe2.nscanGene.LENGTH, 151  
 ponAbe2.refGene.LENGTH, 152  
 ponAbe2.xenoRefGene.LENGTH, 152  
 priPac1.xenoRefGene.LENGTH, 153  
  
 rheMac2.ensGene.LENGTH, 153  
 rheMac2.geneid.LENGTH, 154  
 rheMac2.geneSymbol.LENGTH, 154  
 rheMac2.nscanGene.LENGTH, 155  
 rheMac2.refGene.LENGTH, 155  
 rheMac2.sgpGene.LENGTH, 156  
 rheMac2.xenoRefGene.LENGTH, 156  
 rn3.ensGene.LENGTH, 157  
 rn3.geneid.LENGTH, 157  
 rn3.geneSymbol.LENGTH, 158  
 rn3.genscan.LENGTH, 158  
 rn3.knownGene.LENGTH, 159  
 rn3.nscanGene.LENGTH, 159  
 rn3.refGene.LENGTH, 160

rn3.sgpGene.LENGTH, 160  
rn3.xenoRefGene.LENGTH, 161  
rn4.ensGene.LENGTH, 161  
rn4.geneid.LENGTH, 162  
rn4.geneSymbol.LENGTH, 162  
rn4.genscan.LENGTH, 163  
rn4.knownGene.LENGTH, 163  
rn4.nscanGene.LENGTH, 164  
rn4.refGene.LENGTH, 164  
rn4.sgpGene.LENGTH, 165  
rn4.xenoRefGene.LENGTH, 165

sacCer1.ensGene.LENGTH, 166  
sacCer2.ensGene.LENGTH, 166  
strPur1.geneSymbol.LENGTH, 167  
strPur1.genscan.LENGTH, 167  
strPur1.refGene.LENGTH, 168  
strPur1.xenoRefGene.LENGTH, 168  
strPur2.geneSymbol.LENGTH, 169  
strPur2.genscan.LENGTH, 169  
strPur2.refGene.LENGTH, 170  
strPur2.xenoRefGene.LENGTH, 170  
supportedGeneIDs, 58, 59, 171  
supportedGenomes, 58, 59, 171

taeGut1.ensGene.LENGTH, 172  
taeGut1.geneSymbol.LENGTH, 173  
taeGut1.genscan.LENGTH, 173  
taeGut1.nscanGene.LENGTH, 174  
taeGut1.refGene.LENGTH, 174  
taeGut1.xenoRefGene.LENGTH, 175  
tetNig1.ensGene.LENGTH, 175  
tetNig1.geneid.LENGTH, 176  
tetNig1.genscan.LENGTH, 176  
tetNig1.nscanGene.LENGTH, 177  
tetNig2.ensGene.LENGTH, 177

unfactor, 178

xenTro1.genscan.LENGTH, 179  
xenTro2.ensGene.LENGTH, 179  
xenTro2.geneSymbol.LENGTH, 180  
xenTro2.genscan.LENGTH, 180  
xenTro2.refGene.LENGTH, 181