Package 'geneLenDataBase'

May 15, 2025

```
    Title Lengths of mRNA transcripts for a number of genomes
    Version 1.44.0
    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
```

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

git_branch RELEASE_3_21

git_last_commit ad5f383

git_last_commit_date 2025-04-15

Repository Bioconductor 3.21

Date/Publication 2025-05-15

Author Matthew Young [aut],

Nadia Davidson [aut],

Federico Marini [ctb, cre] (ORCID:

<https://orcid.org/0000-0003-3252-7758>)

Maintainer Federico Marini <marinif@uni-mainz.de>

canFam2.refGene.LENGTH	
canFam2.xenoRefGene.LENGTH	
cavPor3.ensGene.LENGTH	 . 33
cavPor3.genscan.LENGTH	 . 33
cavPor3.nscanGene.LENGTH	 . 34
cavPor3.xenoRefGene.LENGTH	 . 34
cb1.xenoRefGene.LENGTH	
cb3.xenoRefGene.LENGTH	 . 35
ce2.geneid.LENGTH	 . 36
ce2.geneSymbol.LENGTH	 . 36
ce2.refGene.LENGTH	 . 37
ce4.geneSymbol.LENGTH	
ce4.refGene.LENGTH	
ce4.xenoRefGene.LENGTH	 . 38
ce6.ensGene.LENGTH	 . 39
ce6.geneSymbol.LENGTH	
ce6.refGene.LENGTH	
ce6.xenoRefGene.LENGTH	
cil.geneSymbol.LENGTH	
cil.refGene.LENGTH	 . 41
ci1.xenoRefGene.LENGTH	 . 42
ci2.ensGene.LENGTH	 . 42
ci2.geneSymbol.LENGTH	. 43
ci2.refGene.LENGTH	. 43
ci2.xenoRefGene.LENGTH	
danRer3.ensGene.LENGTH	
danRer3.geneSymbol.LENGTH	
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	
danRer5.geneSymbol.LENGTH	
danRer5.refGene.LENGTH	
danRer5.vegaGene.LENGTH	
danRer5.vegaPseudoGene.LENGTH	
danRer6.ensGene.LENGTH	
danRer6.geneSymbol.LENGTH	
danRer6.refGene.LENGTH	
danRer6.xenoRefGene.LENGTH	
dm1.geneSymbol.LENGTH	
dm1.genscan.LENGTH	
dm1.refGene.LENGTH	
dm2.geneid.LENGTH	
dm2.geneSymbol.LENGTH	
dm2.genscan.LENGTH	 . 55

Contents Contents

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	
droMoj1.xenoRefGene.LENGTH	
droMoj2.genscan.LENGTH	 68
droMoj2.xenoRefGene.LENGTH	
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	
droVir1.xenoRefGene.LENGTH	
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
equCab? ensGene L FNGTH	 80

	80
1	81
1	81
	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
frl.ensGene.LENGTH	86
	87
	87
	88
	88
	89
	89
	90
•	90
	91
	91
galGal3.genscan.LENGTH	92
	92
	93
	93
	94
	94
	95
	95
<i>E</i> ,	96
	96
	90
\mathcal{C}	97 97
6 6	98
ϵ	98
ϵ	99
hg16.sgpGene.LENGTH	99
hg17.acembly.LENGTH	
hg17.acescan.LENGTH	
hg17.ccdsGene.LENGTH	
hg17.ensGene.LENGTH	
hg17.exoniphy.LENGTH	
hg17.geneid.LENGTH	
hg17.geneSymbol.LENGTH	
hg17.genscan.LENGTH	
hg17.knownGene.LENGTH	04

hg17.refGene.LENGTH	
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	
hg18.ensGene.LENGTH	
hg18.exoniphy.LENGTH	. 109
hg18.geneid.LENGTH	. 109
hg18.geneSymbol.LENGTH	. 110
hg18.genscan.LENGTH	
hg18.knownGene.LENGTH	. 111
hg18.knownGeneOld3.LENGTH	. 111
hg18.refGene.LENGTH	. 112
hg18.sgpGene.LENGTH	
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	
mm7.ensGene.LENGTH	. 118
mm7.geneid.LENGTH	
mm7.geneSymbol.LENGTH	
mm7.genscan.LENGTH	
mm7.knownGene.LENGTH	
mm7.refGene.LENGTH	
mm7.sgpGene.LENGTH	
mm7.xenoRefGene.LENGTH	. 122
mm8.ccdsGene.LENGTH	. 122
mm8.ensGene.LENGTH	
mm8.geneid.LENGTH	. 123
mm8.geneSymbol.LENGTH	
mm8.genscan.LENGTH	
mm8.knownGene.LENGTH	
mm8.nscanGene.LENGTH	
mm8.refGene.LENGTH	
mm8.sgpGene.LENGTH	
mm8.sibGene.LENGTH	
mm8.xenoRefGene.LENGTH	. 127
mm9.acembly.LENGTH	

mm9.ccdsGene.LENGTH	
mm9.ensGene.LENGTH	
mm9.exoniphy.LENGTH	
mm9.geneid.LENGTH	
mm9.geneSymbol.LENGTH	
mm9.genscan.LENGTH	
mm9.knownGene.LENGTH	
mm9.nscanGene.LENGTH	
mm9.refGene.LENGTH	
mm9.sgpGene.LENGTH	. 133
mm9.xenoRefGene.LENGTH	
monDom1.genscan.LENGTH	
monDom4.ensGene.LENGTH	
monDom4.geneSymbol.LENGTH	
monDom4.genscan.LENGTH	
monDom4.nscanGene.LENGTH	
monDom4.refGene.LENGTH	. 136
monDom4.xenoRefGene.LENGTH	
monDom5.ensGene.LENGTH	. 137
monDom5.geneSymbol.LENGTH	
monDom5.genscan.LENGTH	. 138
monDom5.nscanGene.LENGTH	. 139
monDom5.refGene.LENGTH	
monDom5.xenoRefGene.LENGTH	. 140
ornAna1.ensGene.LENGTH	. 140
ornAna1.geneSymbol.LENGTH	. 141
ornAna1.refGene.LENGTH	
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	
ponAbe2.ensGene.LENGTH	
ponAbe2.geneSymbol.LENGTH	
ponAbe2.genscan.LENGTH	
ponAbe2.nscanGene.LENGTH	
ponAbe2.refGene.LENGTH	

ponAbe2.xenoRefGene.LENGTH .				
priPac1.xenoRefGene.LENGTH				
rheMac2.ensGene.LENGTH				
rheMac2.geneid.LENGTH				
$rhe Mac 2. gene Symbol. LENG TH \ \ . \ \ .$				
rheMac2.nscanGene.LENGTH	 	 	 	. 155
rheMac2.refGene.LENGTH	 	 	 	. 155
rheMac2.sgpGene.LENGTH				
rheMac2.xenoRefGene.LENGTH .				
rn3.ensGene.LENGTH				
rn3.geneid.LENGTH	 	 	 	. 157
rn3.geneSymbol.LENGTH	 	 	 	. 158
rn3.genscan.LENGTH				
rn3.knownGene.LENGTH	 	 	 	. 159
rn3.nscanGene.LENGTH				
rn3.refGene.LENGTH	 	 	 	. 160
rn3.sgpGene.LENGTH				
rn3.xenoRefGene.LENGTH				
rn4.ensGene.LENGTH	 	 	 	. 161
rn4.geneid.LENGTH				
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				
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				
tetNig1.ensGene.LENGTH	 	 	 	. 175
tetNig1.geneid.LENGTH	 	 	 	. 176
tetNig1.genscan.LENGTH				

	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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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/cgibin/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/cgibin/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/cgibin/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

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

apiMel1.genscan.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

apiMel2.ensGene.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

downloadLengthFromUCSC

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

apiMel2.genscan.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

downloadLengthFromUCSC

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

```
aplCal1.xenoRefGene.LENGTH
```

Transcript length data for the organism aplCal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

```
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

```
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/cgibin/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

```
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/cgibin/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

```
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

```
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/cgibin/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

```
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/cgibin/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

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
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

```
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

```
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

```
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/cgibin/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

```
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/cgibin/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

```
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/cgibin/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

```
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

```
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/cgibin/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

```
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/cgibin/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

```
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/cgibin/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

```
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/cgibin/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/cgibin/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

```
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

```
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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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

ce2.refGene.LENGTH 37

ce2.refGene.LENGTH

Transcript length data for the organism ce

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

 ${\tt downloadLengthFromUCSC}$

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

ce4.refGene.LENGTH

Transcript length data for the organism ce

Description

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

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

ce6.ensGene.LENGTH 39

ce6.ensGene.LENGTH

Transcript length data for the organism ce

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

 ${\tt downloadLengthFromUCSC}$

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

ce6.refGene.LENGTH

Transcript length data for the organism ce

Description

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

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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

42 ci2.ensGene.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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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/cgibin/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

```
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

```
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/cgibin/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

```
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

```
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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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

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

56 dm2.refGene.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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

Examples

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

 ${\tt downloadLengthFromUCSC}$

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 supportedGenomes.
id	A string identifying the gene identifier used by genes. For a list of supported gene identifierst see supportedGeneIDs .

Details

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

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

Value

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

Note

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

Author(s)

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

See Also

```
supportedGenomes, supportedGeneIDs
```

Examples

```
## Not run:
    flat_length <- downloadLengthFromUCSC('hg19', 'ensGene')
## End(Not run)</pre>
```

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/cgibin/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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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

```
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/cgibin/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

```
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

```
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/cgibin/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

```
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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

```
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/cgibin/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

```
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/cgibin/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/cgibin/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

```
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/cgibin/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/cgibin/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

```
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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

```
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/cgibin/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/cgibin/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

```
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/cgibin/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

dro Vir2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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

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

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

Description

dro Yak 1. 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

 ${\tt downloadLengthFromUCSC}$

Examples

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

droYak1.genscan.LENGTH

Transcript length data for the organism droYak

Description

dro Yak 1. genscan. LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained 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

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

droYak1.xenoRefGene.LENGTH

Transcript length data for the organism droYak

Description

dro Yak 1. xeno Ref Gene. LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xeno Ref Gene 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

dro Yak2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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

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

droYak2.xenoRefGene.LENGTH

Transcript length data for the organism droYak

Description

dro Yak2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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/cgibin/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

```
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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

```
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

```
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

```
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/cgibin/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

```
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

```
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/cgibin/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

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

felCat3.refGene.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/cgibin/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

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

86 fr1.ensGene.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/cgibin/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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
galGal2.ensGene.LENGTH
```

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

 ${\tt downloadLengthFromUCSC}$

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

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

```
galGal2.geneSymbol.LENGTH
```

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

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

```
galGal2.refGene.LENGTH
```

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

```
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

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

```
galGal3.genscan.LENGTH
```

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

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

```
galGal3.refGene.LENGTH
```

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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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

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

geneLenDatabase-pkg 95

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)

Maintainer: Federico Marini <marinif@uni-mainz.de> (ORCID) [contributor] Authors:

- Matthew Young <my4@sanger.ac.uk>
- Nadia Davidson <nadia.davidson@mcri.edu.au>

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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

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

 ${\tt downloadLengthFromUCSC}$

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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

```
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

 ${\tt downloadLengthFromUCSC}$

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

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

 ${\tt downloadLengthFromUCSC}$

```
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/cgibin/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

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

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

 ${\tt downloadLengthFromUCSC}$

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

```
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

```
data(hg19.xenoRefGene.LENGTH)
head(hg19.xenoRefGene.LENGTH)
```

mm7.ensGene.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/cgibin/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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$

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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
data(mm7.knownGene.LENGTH)
head(mm7.knownGene.LENGTH)
```

mm7.refGene.LENGTH 121

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

 ${\tt downloadLengthFromUCSC}$

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

```
data(mm8.ccdsGene.LENGTH)
head(mm8.ccdsGene.LENGTH)
```

mm8.ensGene.LENGTH 123

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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
data(mm8.sgpGene.LENGTH)
head(mm8.sgpGene.LENGTH)
```

mm8.sibGene.LENGTH 127

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

```
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

 ${\tt downloadLengthFromUCSC}$

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

 ${\tt downloadLengthFromUCSC}$

```
data(mm9.ccdsGene.LENGTH)
head(mm9.ccdsGene.LENGTH)
```

mm9.ensGene.LENGTH 129

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
data(mm9.knownGene.LENGTH)
head(mm9.knownGene.LENGTH)
```

132 mm9.refGene.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

 ${\tt downloadLengthFromUCSC}$

```
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

```
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/cgibin/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

```
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

```
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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
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

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

```
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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$

Examples

```
data(ornAna1.xenoRefGene.LENGTH)
head(ornAna1.xenoRefGene.LENGTH)
```

orvLat2.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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
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

```
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

```
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

```
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

```
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

```
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/cgibin/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

```
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/cgibin/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

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
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/cgibin/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

```
data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)
```

rn3.ensGene.LENGTH 157

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

 ${\tt downloadLengthFromUCSC}$

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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

```
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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

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/cgibin/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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
data(rn4.knownGene.LENGTH)
head(rn4.knownGene.LENGTH)
```

164 rn4.refGene.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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

```
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

```
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/cgibin/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/cgibin/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

```
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

```
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

```
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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)
```

supportedGeneIDs 171

supportedGeneIDs

Supported Gene IDs

Description

Lists supported gene ID formats

Usage

supportedGeneIDs()

Details

Uses the supportedUCSCtables function from the GenomicFeatures package to obtain a list of gene ID formats available from the UCSC genome browser. The db column gives the gene ID formats which are provided to the id arguement 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 avaible 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

Supported Genomes

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 arguement of various functions.

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

Value

A data.frame containing supported genomes.

Author(s)

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

Examples

supportedGenomes()

taeGut1.ensGene.LENGTH

Transcript length data for the organism taeGut

Description

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

```
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/cgibin/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

```
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/cgibin/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/cgibin/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

```
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

 ${\tt downloadLengthFromUCSC}$

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

```
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

```
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/cgibin/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

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

178 unfactor

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>

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/cgibin/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/cgibin/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

```
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

```
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/cgibin/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

 ${\tt downloadLengthFromUCSC}$

Examples

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

Index

* datasets	canFam1.genscan.LENGTH, 28
anoCar1.ensGene.LENGTH, 9	canFam1.nscanGene.LENGTH, 28
anoCar1.genscan.LENGTH, 9	canFam1.refGene.LENGTH, 29
anoCar1.xenoRefGene.LENGTH, 10	canFam1.xenoRefGene.LENGTH, 29
anoGam1.ensGene.LENGTH, 10	canFam2.ensGene.LENGTH, 30
anoGam1.geneid.LENGTH, 11	canFam2.geneSymbol.LENGTH, 30
anoGam1.genscan.LENGTH, 11	canFam2.genscan.LENGTH, 31
apiMel1.genscan.LENGTH, 12	canFam2.nscanGene.LENGTH, 31
apiMel2.ensGene.LENGTH, 12	canFam2.refGene.LENGTH, 32
apiMel2.geneid.LENGTH, 13	canFam2.xenoRefGene.LENGTH, 32
apiMel2.genscan.LENGTH, 13	cavPor3.ensGene.LENGTH, 33
aplCal1.xenoRefGene.LENGTH, 14	cavPor3.genscan.LENGTH, 33
bosTau2.geneid.LENGTH, 14	cavPor3.nscanGene.LENGTH, 34
bosTau2.geneSymbol.LENGTH, 15	cavPor3.xenoRefGene.LENGTH, 34
bosTau2.genscan.LENGTH, 15	cb1.xenoRefGene.LENGTH, 35
bosTau2.refGene.LENGTH, 16	cb3.xenoRefGene.LENGTH, 35
bosTau2.sgpGene.LENGTH, 16	ce2.geneid.LENGTH, 36
bosTau3.ensGene.LENGTH, 17	ce2.geneSymbol.LENGTH, 36
bosTau3.geneid.LENGTH, 17	ce2.refGene.LENGTH,37
bosTau3.geneSymbol.LENGTH, 18	ce4.geneSymbol.LENGTH, 37
bosTau3.genscan.LENGTH, 18	ce4.refGene.LENGTH,38
bosTau3.refGene.LENGTH, 19	ce4.xenoRefGene.LENGTH, 38
bosTau3.sgpGene.LENGTH, 19	ce6.ensGene.LENGTH, 39
bosTau4.ensGene.LENGTH, 20	ce6.geneSymbol.LENGTH, 39
bosTau4.geneSymbol.LENGTH, 20	ce6.refGene.LENGTH,40
bosTau4.genscan.LENGTH, 21	${\sf ce6.xenoRefGene.LENGTH}, 40$
bosTau4.nscanGene.LENGTH, 21	ci1.geneSymbol.LENGTH,41
bosTau4.refGene.LENGTH, 22	ci1.refGene.LENGTH,41
braFlo1.xenoRefGene.LENGTH, 22	ci1.xenoRefGene.LENGTH, 42
caeJap1.xenoRefGene.LENGTH, 23	ci2.ensGene.LENGTH, 42
caePb1.xenoRefGene.LENGTH, 23	ci2.geneSymbol.LENGTH, 43
caePb2.xenoRefGene.LENGTH, 24	ci2.refGene.LENGTH,43
caeRem2.xenoRefGene.LENGTH, 24	ci2.xenoRefGene.LENGTH,44
caeRem3.xenoRefGene.LENGTH, 25	danRer3.ensGene.LENGTH, 44
calJac1.genscan.LENGTH, 25	danRer3.geneSymbol.LENGTH,45
calJac1.nscanGene.LENGTH, 26	danRer3.refGene.LENGTH, 45
calJac1.xenoRefGene.LENGTH, 26	danRer4.ensGene.LENGTH, 46
canFam1.ensGene.LENGTH, 27	danRer4.geneSymbol.LENGTH, 46
canFam1.geneSymbol.LENGTH, 27	danRer4.genscan.LENGTH,47

danRer4.nscanGene.LENGTH, 47	droVir1.geneid.LENGTH, 72
danRer4.refGene.LENGTH, 48	droVir1.genscan.LENGTH, 73
danRer5.ensGene.LENGTH, 48	droVir1.xenoRefGene.LENGTH, 73
danRer5.geneSymbol.LENGTH,49	droVir2.genscan.LENGTH,74
danRer5.refGene.LENGTH, 49	droVir2.xenoRefGene.LENGTH, 74
danRer5.vegaGene.LENGTH, 50	droYak1.geneid.LENGTH, 75
danRer5.vegaPseudoGene.LENGTH, 50	droYak1.genscan.LENGTH, 75
danRer6.ensGene.LENGTH, 51	droYak1.xenoRefGene.LENGTH, 76
danRer6.geneSymbol.LENGTH, 51	droYak2.genscan.LENGTH, 76
danRer6.refGene.LENGTH, 52	droYak2.xenoRefGene.LENGTH, 77
danRer6.xenoRefGene.LENGTH, 52	equCab1.geneid.LENGTH, 77
dm1.geneSymbol.LENGTH, 53	equCab1.geneSymbol.LENGTH, 78
dm1.genscan.LENGTH, 53	equCab1.nscanGene.LENGTH, 78
dm1.refGene.LENGTH, 54	equCab1.refGene.LENGTH, 79
dm2.geneid.LENGTH, 54	equCab1.sgpGene.LENGTH, 79
dm2.geneSymbol.LENGTH, 55	equCab2.ensGene.LENGTH, 80
dm2.genscan.LENGTH, 55	equCab2.geneSymbol.LENGTH, 80
dm2.nscanGene.LENGTH, 56	eguCab2.nscanGene.LENGTH, 81
dm2.refGene.LENGTH, 56	equCab2.refGene.LENGTH, 81
dm3.geneSymbol.LENGTH, 57	equCab2.xenoRefGene.LENGTH, 82
dm3.nscanPasaGene.LENGTH, 57	felCat3.ensGene.LENGTH, 82
dm3.refGene.LENGTH, 58	felCat3.geneid.LENGTH, 83
dp2.genscan.LENGTH, 59	felCat3.geneSymbol.LENGTH, 83
dp2.xenoRefGene.LENGTH, 60	felCat3.genscan.LENGTH, 84
dp3.geneid.LENGTH, 60	felCat3.nscanGene.LENGTH, 84
dp3.genscan.LENGTH, 61	felCat3.refGene.LENGTH, 85
dp3.xenoRefGene.LENGTH, 61	felCat3.sgpGene.LENGTH, 85
droAna1.geneid.LENGTH, 62	felCat3.xenoRefGene.LENGTH, 86
droAna1.genscan.LENGTH, 62	fr1.ensGene.LENGTH, 86
droAna1.xenoRefGene.LENGTH, 63	fr1.genscan.LENGTH, 87
droAna2.genscan.LENGTH, 63	fr2.ensGene.LENGTH, 87
droAna2.xenoRefGene.LENGTH, 64	galGal2.ensGene.LENGTH, 88
droEre1.genscan.LENGTH, 64	galGal2.geneid.LENGTH, 88
droEre1.xenoRefGene.LENGTH, 65	galGal2.geneSymbol.LENGTH, 89
droGri1.genscan.LENGTH, 65	galGal2.genscan.LENGTH, 89
droGri1.xenoRefGene.LENGTH,66	galGal2.refGene.LENGTH, 90
droMoj1.geneid.LENGTH,66	galGal2.sgpGene.LENGTH, 90
droMoj1.genscan.LENGTH, 67	galGal3.ensGene.LENGTH, 91
droMoj1.xenoRefGene.LENGTH, 67	galGal3.geneSymbol.LENGTH, 91
droMoj2.genscan.LENGTH, 68	galGal3.genscan.LENGTH, 92
droMoj2.xenoRefGene.LENGTH, 68	galGal3.nscanGene.LENGTH, 92
droPer1.genscan.LENGTH, 69	galGal3.refGene.LENGTH,93
droPer1.xenoRefGene.LENGTH, 69	galGal3.xenoRefGene.LENGTH, 93
droSec1.genscan.LENGTH, 70	gasAcu1.ensGene.LENGTH, 94
droSec1.xenoRefGene.LENGTH, 70	gasAcu1.nscanGene.LENGTH, 94
droSim1.geneid.LENGTH,71	hg16.acembly.LENGTH, 95
droSim1.genscan.LENGTH, 71	hg16.ensGene.LENGTH, 96
droSim1.xenoRefGene.LENGTH, 72	hg16.exoniphy.LENGTH, 96
•	- · · ·

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

panTro1.geneid.LENGTH, 145	strPur2.geneSymbol.LENGTH, 169
panTro1.genscan.LENGTH, 145	strPur2.genscan.LENGTH, 169
panTro1.xenoRefGene.LENGTH, 146	strPur2.refGene.LENGTH, 170
panTro2.ensGene.LENGTH, 146	strPur2.xenoRefGene.LENGTH, 170
panTro2.geneSymbol.LENGTH, 147	taeGut1.ensGene.LENGTH, 172
panTro2.genscan.LENGTH, 147	taeGut1.geneSymbol.LENGTH, 173
panTro2.nscanGene.LENGTH, 148	taeGut1.genscan.LENGTH, 173
panTro2.refGene.LENGTH, 148	taeGut1.nscanGene.LENGTH, 174
panTro2.xenoRefGene.LENGTH, 149	taeGut1.refGene.LENGTH, 174
petMar1.xenoRefGene.LENGTH, 149	taeGut1.xenoRefGene.LENGTH, 175
ponAbe2.ensGene.LENGTH, 150	tetNig1.ensGene.LENGTH, 175
ponAbe2.geneSymbol.LENGTH, 150	tetNig1.geneid.LENGTH, 176
ponAbe2.genscan.LENGTH, 151	tetNig1.genscan.LENGTH, 176
ponAbe2.nscanGene.LENGTH, 151	tetNig1.nscanGene.LENGTH, 177
ponAbe2.refGene.LENGTH, 152	tetNig2.ensGene.LENGTH, 177
ponAbe2.xenoRefGene.LENGTH, 152	xenTro1.genscan.LENGTH, 179
priPac1.xenoRefGene.LENGTH, 153	xenTro2.ensGene.LENGTH, 179
rheMac2.ensGene.LENGTH, 153	xenTro2.geneSymbol.LENGTH, 180
, ·	xenTro2.genscan.LENGTH, 180
rheMac2.geneid.LENGTH, 154	xenTro2.refGene.LENGTH, 181
rheMac2.geneSymbol.LENGTH, 154	* internal
rheMac2.nscanGene.LENGTH, 155	geneLenDatabase-pkg, 95
rheMac2.refGene.LENGTH, 155	80.1020.154040400 p.16, 30
rheMac2.sgpGene.LENGTH, 156	anoCar1.ensGene.LENGTH, 9
rheMac2.xenoRefGene.LENGTH, 156	anoCar1.genscan.LENGTH, 9
rn3.ensGene.LENGTH, 157	anoCar1.xenoRefGene.LENGTH, 10
rn3.geneid.LENGTH, 157	anoGam1.ensGene.LENGTH, 10
rn3.geneSymbol.LENGTH, 158	anoGam1.geneid.LENGTH, 11
rn3.genscan.LENGTH, 158	anoGam1.genscan.LENGTH, 11
rn3.knownGene.LENGTH, 159	apiMel1.genscan.LENGTH, 12
rn3.nscanGene.LENGTH, 159	apiMel2.ensGene.LENGTH, 12
rn3.refGene.LENGTH, 160	apiMel2.geneid.LENGTH, 13
rn3.sgpGene.LENGTH, 160	apiMel2.genscan.LENGTH, 13
rn3.xenoRefGene.LENGTH, 161	aplCal1.xenoRefGene.LENGTH, 14
rn4.ensGene.LENGTH, 161	,
rn4.geneid.LENGTH, 162	bosTau2.geneid.LENGTH, 14
rn4.geneSymbol.LENGTH, 162	bosTau2.geneSymbol.LENGTH, 15
rn4.genscan.LENGTH, 163	bosTau2.genscan.LENGTH, 15
rn4.knownGene.LENGTH, 163	bosTau2.refGene.LENGTH, 16
rn4.nscanGene.LENGTH, 164	bosTau2.sgpGene.LENGTH, 16
rn4.refGene.LENGTH, 164	bosTau3.ensGene.LENGTH, 17
rn4.sgpGene.LENGTH, 165	bosTau3.geneid.LENGTH, 17
rn4.xenoRefGene.LENGTH, 165	bosTau3.geneSymbol.LENGTH, 18
sacCer1.ensGene.LENGTH, 166	bosTau3.genscan.LENGTH, 18
sacCer2.ensGene.LENGTH, 166	bosTau3.refGene.LENGTH, 19
strPur1.geneSymbol.LENGTH, 167	bosTau3.sgpGene.LENGTH, 19
strPur1.genscan.LENGTH, 167	bosTau4.ensGene.LENGTH, 20
strPur1.refGene.LENGTH, 168	bosTau4.geneSymbol.LENGTH, 20
strPur1.xenoRefGene.LENGTH, 168	bosTau4.genscan.LENGTH, 21
· · · · · · · · · · · · · · · · · · ·	-

bosTau4.nscanGene.LENGTH, 21	danRer3.geneSymbol.LENGTH,45
bosTau4.refGene.LENGTH, 22	danRer3.refGene.LENGTH, 45
braFlo1.xenoRefGene.LENGTH, 22	danRer4.ensGene.LENGTH, 46
	danRer4.geneSymbol.LENGTH, 46
caeJap1.xenoRefGene.LENGTH, 23	danRer4.genscan.LENGTH, 47
caePb1.xenoRefGene.LENGTH, 23	danRer4.nscanGene.LENGTH, 47
caePb2.xenoRefGene.LENGTH, 24	danRer4.refGene.LENGTH, 48
caeRem2.xenoRefGene.LENGTH, 24	danRer5.ensGene.LENGTH, 48
caeRem3.xenoRefGene.LENGTH, 25	danRer5.geneSymbol.LENGTH, 49
calJac1.genscan.LENGTH, 25	danRer5.refGene.LENGTH, 49
calJac1.nscanGene.LENGTH, 26	danRer5.vegaGene.LENGTH, 50
calJac1.xenoRefGene.LENGTH, 26	danRer5.vegaPseudoGene.LENGTH, 50
canFam1.ensGene.LENGTH, 27	danRer6.ensGene.LENGTH, 51
canFam1.geneSymbol.LENGTH, 27	danRer6.geneSymbol.LENGTH, 51
canFam1.genscan.LENGTH, 28	danRer6.refGene.LENGTH, 52
canFam1.nscanGene.LENGTH, 28	danRer6.xenoRefGene.LENGTH, 52
canFam1.refGene.LENGTH, 29	dm1.geneSymbol.LENGTH, 53
canFam1.xenoRefGene.LENGTH, 29	dm1.genscan.LENGTH, 53
canFam2.ensGene.LENGTH, 30	dm1.refGene.LENGTH, 54
canFam2.geneSymbol.LENGTH, 30	dm2.geneid.LENGTH, 54
canFam2.genscan.LENGTH, 31	dm2.geneSymbol.LENGTH, 55
canFam2.nscanGene.LENGTH, 31	dm2.genscan.LENGTH, 55
canFam2.refGene.LENGTH, 32	dm2.nscanGene.LENGTH, 56
canFam2.xenoRefGene.LENGTH, 32	dm2.refGene.LENGTH, 56
cavPor3.ensGene.LENGTH, 33	dm3.geneSymbol.LENGTH, 57
cavPor3.genscan.LENGTH, 33	dm3.nscanPasaGene.LENGTH, 57
cavPor3.nscanGene.LENGTH, 34	dm3.refGene.LENGTH, 58
cavPor3.xenoRefGene.LENGTH, 34	downloadLengthFromUCSC, <i>9–58</i> , 58, <i>60–170</i> ,
cb1.xenoRefGene.LENGTH, 35	172–177, 179–181
cb3.xenoRefGene.LENGTH, 35	dp2.genscan.LENGTH, 59
ce2.geneid.LENGTH, 36	dp2.xenoRefGene.LENGTH, 60
ce2.geneSymbol.LENGTH, 36	dp3.geneid.LENGTH, 60
ce2.refGene.LENGTH, 37	dp3.genscan.LENGTH, 61
ce4.geneSymbol.LENGTH, 37	dp3.xenoRefGene.LENGTH, 61
ce4.refGene.LENGTH, 38	droAna1.geneid.LENGTH, 62
ce4.xenoRefGene.LENGTH, 38	droAna1.genscan.LENGTH, 62
ce6.ensGene.LENGTH, 39	droAna1.xenoRefGene.LENGTH, 63
ce6.geneSymbol.LENGTH, 39	droAna2.genscan.LENGTH, 63
ce6.refGene.LENGTH, 40	droAna2.xenoRefGene.LENGTH, 64
ce6.xenoRefGene.LENGTH, 40	droEre1.genscan.LENGTH, 64
ci1.geneSymbol.LENGTH, 41	droEre1.xenoRefGene.LENGTH, 65
ci1.refGene.LENGTH,41	•
ci1.xenoRefGene.LENGTH, 42	droGri1.genscan.LENGTH, 65
ci2.ensGene.LENGTH, 42	droGri1.xenoRefGene.LENGTH, 66
ci2.geneSymbol.LENGTH, 43	droMoj1.geneid.LENGTH, 66
ci2.refGene.LENGTH, 43	droMoj1.genscan.LENGTH, 67
ci2.xenoRefGene.LENGTH, 44	droMoj1.xenoRefGene.LENGTH, 67
der De 22 ann a Compa de FNCTU 44	droMoj2.genscan.LENGTH, 68
danRer3.ensGene.LENGTH, 44	droMoj2.xenoRefGene.LENGTH,68

	7 - 7
droPer1.genscan.LENGTH, 69	galGal3.genscan.LENGTH, 92
droPer1.xenoRefGene.LENGTH, 69	galGal3.nscanGene.LENGTH, 92
droSec1.genscan.LENGTH, 70	galGal3.refGene.LENGTH, 93
droSec1.xenoRefGene.LENGTH, 70	galGal3.xenoRefGene.LENGTH, 93
droSim1.geneid.LENGTH, 71	gasAcu1.ensGene.LENGTH, 94
droSim1.genscan.LENGTH, 71	gasAcu1.nscanGene.LENGTH, 94
droSim1.xenoRefGene.LENGTH, 72	<pre>geneLenDataBase (geneLenDatabase-pkg),</pre>
droVir1.geneid.LENGTH, 72	95
droVir1.genscan.LENGTH, 73	geneLenDataBase-package
droVir1.xenoRefGene.LENGTH,73	(geneLenDatabase-pkg), 95
droVir2.genscan.LENGTH,74	geneLenDatabase-pkg, 95
droVir2.xenoRefGene.LENGTH, 74	
droYak1.geneid.LENGTH, 75	hg16.acembly.LENGTH, 95
droYak1.genscan.LENGTH, 75	hg16.ensGene.LENGTH, 96
droYak1.xenoRefGene.LENGTH, 76	hg16.exoniphy.LENGTH, 96
droYak2.genscan.LENGTH, 76	hg16.geneid.LENGTH, 97
droYak2.xenoRefGene.LENGTH, 77	hg16.geneSymbol.LENGTH, 97
,	hg16.genscan.LENGTH, 98
equCab1.geneid.LENGTH, 77	hg16.knownGene.LENGTH, 98
equCab1.geneSymbol.LENGTH, 78	hg16.refGene.LENGTH,99
equCab1.nscanGene.LENGTH, 78	hg16.sgpGene.LENGTH, 99
equCab1.refGene.LENGTH, 79	hg17.acembly.LENGTH, 100
equCab1.sgpGene.LENGTH, 79	hg17.acescan.LENGTH, 100
equCab2.ensGene.LENGTH, 80	hg17.ccdsGene.LENGTH, 101
equCab2.geneSymbol.LENGTH, 80	hg17.ensGene.LENGTH, 101
equCab2.nscanGene.LENGTH, 81	hg17.exoniphy.LENGTH, 102
equCab2.refGene.LENGTH, 81	hg17.geneid.LENGTH, 102
equCab2.xenoRefGene.LENGTH, 82	hg17.geneSymbol.LENGTH, 103
5445451776.15116.1516.1517.1517.	hg17.genscan.LENGTH, 103
felCat3.ensGene.LENGTH, 82	hg17.knownGene.LENGTH, 104
felCat3.geneid.LENGTH, 83	hg17.refGene.LENGTH, 104
felCat3.geneSymbol.LENGTH, 83	hg17.sgpGene.LENGTH, 105
felCat3.genscan.LENGTH, 84	hg17.vegaGene.LENGTH, 105
felCat3.nscanGene.LENGTH, 84	hg17.vegaPseudoGene.LENGTH, 106
felCat3.refGene.LENGTH, 85	hg17.xenoRefGene.LENGTH, 106
felCat3.sgpGene.LENGTH, 85	hg18.acembly.LENGTH, 107
felCat3.xenoRefGene.LENGTH, 86	hg18.acescan.LENGTH, 107
fr1.ensGene.LENGTH, 86	hg18.ccdsGene.LENGTH, 108
fr1.genscan.LENGTH, 87	hg18.ensGene.LENGTH, 108
fr2.ensGene.LENGTH, 87	hg18.exoniphy.LENGTH, 109
11 2. ensdene. Lendin, 67	hg18.geneid.LENGTH, 109
galGal2.ensGene.LENGTH, 88	hg18.geneSymbol.LENGTH, 110
galGal2.geneid.LENGTH, 88	hg18.genscan.LENGTH, 110
galGal2.geneSymbol.LENGTH, 89	hg18.knownGene.LENGTH, 111
galGal2.genscan.LENGTH, 89	hg18.knownGeneOld3.LENGTH, 111
galGal2.refGene.LENGTH, 90	<u> </u>
galGal2.rerGene.LENGTH, 90 galGal2.sgpGene.LENGTH, 90	hg18.refGene.LENGTH, 112
	hg18.sgpGene.LENGTH, 112
galGal3.ensGene.LENGTH, 91	hg18.sibGene.LENGTH, 113
galGal3.geneSymbol.LENGTH, 91	hg18.xenoRefGene.LENGTH, 113

ng19.ccasGene.LENG1H, 114	monDom5.ensGene.LENGIH, 13/
hg19.ensGene.LENGTH, 114	monDom5.geneSymbol.LENGTH, 138
hg19.exoniphy.LENGTH, 115	monDom5.genscan.LENGTH, 138
hg19.geneSymbol.LENGTH, 115	monDom5.nscanGene.LENGTH, 139
hg19.knownGene.LENGTH, 116	monDom5.refGene.LENGTH, 139
hg19.nscanGene.LENGTH, 116	monDom5.xenoRefGene.LENGTH, 140
hg19.refGene.LENGTH, 117	
hg19.xenoRefGene.LENGTH, 117	ornAna1.ensGene.LENGTH, 140
	ornAna1.geneSymbol.LENGTH, 141
loxAfr3.xenoRefGene.LENGTH, 118	ornAna1.refGene.LENGTH, 141
	ornAna1.xenoRefGene.LENGTH, 142
mm7.ensGene.LENGTH, 118	oryLat2.ensGene.LENGTH, 142
mm7.geneid.LENGTH, 119	oryLat2.geneSymbol.LENGTH, 143
mm7.geneSymbol.LENGTH, 119	oryLat2.refGene.LENGTH, 143
mm7.genscan.LENGTH, 120	oryLat2.xenoRefGene.LENGTH, 144
mm7.knownGene.LENGTH, 120	,
mm7.refGene.LENGTH, 121	panTro1.ensGene.LENGTH, 144
mm7.sgpGene.LENGTH, 121	panTro1.geneid.LENGTH, 145
mm7.xenoRefGene.LENGTH, 122	panTro1.genscan.LENGTH, 145
mm8.ccdsGene.LENGTH, 122	panTro1.xenoRefGene.LENGTH, 146
mm8.ensGene.LENGTH, 123	panTro2.ensGene.LENGTH, 146
mm8.geneid.LENGTH, 123	panTro2.geneSymbol.LENGTH, 147
mm8.geneSymbol.LENGTH, 124	panTro2.genscan.LENGTH, 147
mm8.genscan.LENGTH, 124	panTro2.nscanGene.LENGTH, 148
mm8.knownGene.LENGTH, 125	panTro2.refGene.LENGTH, 148
mm8.nscanGene.LENGTH, 125	panTro2.xenoRefGene.LENGTH, 149
mm8.refGene.LENGTH, 126	petMar1.xenoRefGene.LENGTH, 149
mm8.sgpGene.LENGTH, 126	ponAbe2.ensGene.LENGTH, 150
mm8.sibGene.LENGTH, 127	ponAbe2.geneSymbol.LENGTH, 150
mm8.xenoRefGene.LENGTH, 127	ponAbe2.genscan.LENGTH, 151
mm9.acembly.LENGTH, 128	ponAbe2.nscanGene.LENGTH, 151
mm9.ccdsGene.LENGTH, 128	ponAbe2.refGene.LENGTH, 152
mm9.ensGene.LENGTH, 129	ponAbe2.xenoRefGene.LENGTH, 152
mm9.exoniphy.LENGTH, 129	priPac1.xenoRefGene.LENGTH, 153
mm9.geneid.LENGTH, 130	printer .xenoner dene. ELNorm, 155
mm9.geneSymbol.LENGTH, 130	rheMac2.ensGene.LENGTH, 153
mm9.genscan.LENGTH, 131	rheMac2.geneid.LENGTH, 154
mm9.knownGene.LENGTH, 131	rheMac2.geneSymbol.LENGTH, 154
mm9.nscanGene.LENGTH, 132	rheMac2.nscanGene.LENGTH, 155
mm9.refGene.LENGTH, 132	rheMac2.refGene.LENGTH, 155
mm9.sgpGene.LENGTH, 133	rheMac2.sgpGene.LENGTH, 156
mm9.xenoRefGene.LENGTH, 133	rheMac2.xenoRefGene.LENGTH, 156
monDom1.genscan.LENGTH, 134	rn3.ensGene.LENGTH, 157
monDom4.ensGene.LENGTH, 134	rn3.geneid.LENGTH, 157
monDom4.geneSymbol.LENGTH, 135	rn3.geneSymbol.LENGTH, 158
monDom4.genscan.LENGTH, 135	rn3.genscan.LENGTH, 158
monDom4.nscanGene.LENGTH, 136	rn3.knownGene.LENGTH, 159
monDom4.refGene.LENGTH, 136	rn3.nscanGene.LENGTH, 159
monDom4.xenoRefGene.LENGTH, 137	rn3.refGene.LENGTH, 160
monboint. Actioner defic. LLNGTH, 137	i iio. i e i delie. ELito III, 100

```
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
```