geneLenDataBase

October 5, 2010

anoCarl.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

downloadLengthFromUCSC

Examples

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data(anoCarl.ensGene.LENGTH)
head(anoCarl.ensGene.LENGTH)
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anoCarl.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(anoCarl.genscan.LENGTH)
head(anoCarl.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(anoCarl.xenoRefGene.LENGTH)
head(anoCarl.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)

2

anoGaml.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

Examples

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

apiMell.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/cgibin/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(apiMell.genscan.LENGTH)
head(apiMell.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

Examples

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

apiMel2.geneid.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

apiMel2.genscan.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

aplCall.xenoRefGene.LENGTH

Transcript length data for the organism aplCal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

```
data(aplCall.xenoRefGene.LENGTH)
head(aplCall.xenoRefGene.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.geneid.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau2.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/cgibin/hgTables) using the genscan table.

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau2.refGene.LENGTH

Transcript length data for the organism bosTau

Description

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

Examples

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

bosTau3.ensGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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bosTau3.geneid.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau3.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/cgibin/hgTables) using the genscan table.

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau3.refGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau4.ensGene.LENGTH

Transcript length data for the organism bosTau

Description

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

Examples

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

bosTau4.genscan.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau4.nscanGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau4.refGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

caeJap1.xenoRefGene.LENGTH

Transcript length data for the organism caeJap

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

caePb2.xenoRefGene.LENGTH

Transcript length data for the organism caePb

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

caeRem3.xenoRefGene.LENGTH

Transcript length data for the organism caeRem

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

calJac1.genscan.LENGTH

Transcript length data for the organism calJac

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

calJac1.nscanGene.LENGTH

Transcript length data for the organism calJac

Description

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

Examples

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

canFam1.ensGene.LENGTH

Transcript length data for the organism canFam

Description

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

Examples

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

canFam1.genscan.LENGTH

Transcript length data for the organism canFam

Description

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

canFaml.nscanGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam1.refGene.LENGTH

Transcript length data for the organism canFam

Description

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

 ${\tt downloadLengthFromUCSC}$

Examples

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

canFam2.ensGene.LENGTH

Transcript length data for the organism canFam

Description

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

Examples

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

canFam2.genscan.LENGTH

Transcript length data for the organism canFam

Description

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

Examples

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

canFam2.refGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

cavPor3.ensGene.LENGTH

Transcript length data for the organism cavPor

Description

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

Examples

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

cavPor3.nscanGene.LENGTH

Transcript length data for the organism cavPor

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

cb1.xenoRefGene.LENGTH

Transcript length data for the organism cb

Description

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

Examples

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

downloadLengthFromUCSC

Examples

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

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ce4.xenoRefGene.LENGTH

Transcript length data for the organism ce

Description

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

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ce6.geneSymbol.LENGTH

Transcript length data for the organism ce

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ce6.xenoRefGene.LENGTH

Transcript length data for the organism ce

Description

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

Examples

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

cil.geneSymbol.LENGTH

Transcript length data for the organism ci

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

cil.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

downloadLengthFromUCSC

Examples

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

cil.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

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ci2.geneSymbol.LENGTH

Transcript length data for the organism ci

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ci2.xenoRefGene.LENGTH

Transcript length data for the organism ci

Description

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

Examples

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

danRer3.geneSymbol.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer3.refGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer4.ensGene.LENGTH

Transcript length data for the organism danRer

Description

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

Examples

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

danRer4.genscan.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer4.nscanGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer4.refGene.LENGTH

Transcript length data for the organism danRer

Description

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

Examples

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

danRer5.geneSymbol.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer5.refGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer5.vegaGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer6.ensGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer6.geneSymbol.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer6.refGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

dm1.geneSymbol.LENGTH

Transcript length data for the organism dm

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

dm2.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/cgibin/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.geneid.LENGTH Transcript length data for the organism dm

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

dm2.nscanGene.LENGTH

Transcript length data for the organism dm

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

dm3.geneSymbol.LENGTH

Transcript length data for the organism dm

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

downloadLengthFromUCSC

Download Transcript Length Data

Description

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

Usage

downloadLengthFromUCSC(genome, id)

Arguments

genome	A string identifying the genome that genes refer to. For a list of supported
	organisms see 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.

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See Also

supportedGenomes, supportedGeneIDs

Examples

```
flat_length <- downloadLengthFromUCSC('hg19', 'ensGene')</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/cgibin/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/cgi-bin/hgTables) using the geneid table.

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

dp3.xenoRefGene.LENGTH

Transcript length data for the organism dp

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droAnal.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(droAnal.geneid.LENGTH)
head(droAnal.geneid.LENGTH)

droAnal.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

Examples

data(droAnal.genscan.LENGTH)
head(droAnal.genscan.LENGTH)

droAnal.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(droAnal.xenoRefGene.LENGTH)
head(droAnal.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/cgibin/hgTables) using the genscan table.

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

See Also

downloadLengthFromUCSC

Examples

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

droAna2.xenoRefGene.LENGTH

Transcript length data for the organism droAna

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droErel.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

Examples

data(droErel.genscan.LENGTH)
head(droErel.genscan.LENGTH)

droErel.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(droErel.xenoRefGene.LENGTH)
head(droErel.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/cgibin/hgTables) using the genscan table.

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

See Also

downloadLengthFromUCSC

Examples

data(droGril.genscan.LENGTH)
head(droGril.genscan.LENGTH)

droGri1.xenoRefGene.LENGTH

Transcript length data for the organism droGri

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droMoj1.geneid.LENGTH

Transcript length data for the organism droMoj

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droMoj1.genscan.LENGTH

Transcript length data for the organism droMoj

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(droMojl.genscan.LENGTH)
head(droMojl.genscan.LENGTH)

droMoj1.xenoRefGene.LENGTH

Transcript length data for the organism droMoj

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(droMojl.xenoRefGene.LENGTH)
head(droMojl.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

Examples

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

droPer1.genscan.LENGTH

Transcript length data for the organism droPer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droSecl.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/cgi-bin/hgTables) using the xenoRefGene table.

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

See Also

downloadLengthFromUCSC

Examples

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

droSiml.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

Examples

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

droSim1.xenoRefGene.LENGTH

Transcript length data for the organism droSim

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droVir1.geneid.LENGTH

Transcript length data for the organism droVir

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droVir1.genscan.LENGTH

Transcript length data for the organism droVir

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droVir2.genscan.LENGTH

Transcript length data for the organism droVir

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droYak1.geneid.LENGTH

Transcript length data for the organism droYak

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droYak1.genscan.LENGTH

Transcript length data for the organism droYak

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droYak1.xenoRefGene.LENGTH

Transcript length data for the organism droYak

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droYak2.genscan.LENGTH

Transcript length data for the organism droYak

Description

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

Examples

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

droYak2.xenoRefGene.LENGTH

Transcript length data for the organism droYak

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab1.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.geneid.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab1.nscanGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(equCabl.nscanGene.LENGTH)
head(equCabl.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/cgibin/hgTables) using the refGene table.

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

See Also

downloadLengthFromUCSC

Examples

data(equCabl.refGene.LENGTH)
head(equCabl.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

Examples

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

equCab2.ensGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab2.geneSymbol.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab2.nscanGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab2.refGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab2.xenoRefGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

felCat3.ensGene.LENGTH

Transcript length data for the organism felCat

Description

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

Examples

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

felCat3.geneSymbol.LENGTH

Transcript length data for the organism felCat

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

felCat3.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.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

Examples

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

felCat3.refGene.LENGTH

Transcript length data for the organism felCat

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

felCat3.sgpGene.LENGTH

Transcript length data for the organism felCat

Description

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

Examples

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

felCat3.xenoRefGene.LENGTH

Transcript length data for the organism felCat

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

```
galGal2.ensGene.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal2.geneSymbol.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal2.geneid.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal2.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/cgibin/hgTables) using the genscan table.

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

See Also

downloadLengthFromUCSC

Examples

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

```
galGal2.refGene.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.ensGene.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.geneSymbol.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

```
galGal3.genscan.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.refGene.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.xenoRefGene.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

gasAcul.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

downloadLengthFromUCSC

Examples

data(gasAcul.ensGene.LENGTH)
head(gasAcul.ensGene.LENGTH)

gasAcu1.nscanGene.LENGTH

Transcript length data for the organism gasAcu

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg16.acembly.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg16.ensGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg16.exoniphy.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg16.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/cgibin/hgTables) using the geneSymbol table.

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

See Also

downloadLengthFromUCSC

Examples

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

hg16.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.genscan.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg16.knownGene.LENGTH

Transcript length data for the organism hg

Description

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

downloadLengthFromUCSC

Examples

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

hg16.refGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg16.sgpGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.acembly.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.acescan.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.ccdsGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.ensGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.exoniphy.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.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

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.genscan.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.knownGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.refGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.sgpGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.vegaGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.vegaPseudoGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.xenoRefGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.acembly.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.acescan.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.ccdsGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.ensGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.exoniphy.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.genscan.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.knownGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.knownGeneOld3.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.refGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(hg18.refGene.LENGTH)
head(hg18.refGene.LENGTH)

hg18.sgpGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.sibGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(hg18.sibGene.LENGTH)
head(hg18.sibGene.LENGTH)

hg18.xenoRefGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(hg18.xenoRefGene.LENGTH)
head(hg18.xenoRefGene.LENGTH)

hg19.ccdsGene.LENGTH

Transcript length data for the organism hg

Description

hg19.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, ccdsGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(hg19.ccdsGene.LENGTH)
head(hg19.ccdsGene.LENGTH)

hg19.ensGene.LENGTH

Transcript length data for the organism hg

Description

hg19.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

hg19.exoniphy.LENGTH

Transcript length data for the organism hg

Description

hg19.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the exoniphy table.

The data file was made by calling downloadLengthFromUCSC(hg19, exoniphy) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(hg19.exoniphy.LENGTH)
head(hg19.exoniphy.LENGTH)

hg19.geneSymbol.LENGTH

Transcript length data for the organism hg

Description

hg19.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(hg19, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(hg19.geneSymbol.LENGTH)
head(hg19.geneSymbol.LENGTH)

hg19.knownGene.LENGTH

Transcript length data for the organism hg

Description

hg19.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(hg19.nscanGene.LENGTH)
head(hg19.nscanGene.LENGTH)

hg19.refGene.LENGTH

Transcript length data for the organism hg

Description

hg19.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(hg19.refGene.LENGTH)
head(hg19.refGene.LENGTH)

hg19.xenoRefGene.LENGTH

Transcript length data for the organism hg

Description

hg19.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(hg19, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

loxAfr3.xenoRefGene.LENGTH Transcript length data for the organism loxAfr

Description

loxAfr3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(loxAfr3, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(loxAfr3.xenoRefGene.LENGTH)
head(loxAfr3.xenoRefGene.LENGTH)

mm7.ensGene.LENGTH Transcript length data for the organism mm

Description

mm7.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm7.ensGene.LENGTH)
head(mm7.ensGene.LENGTH)

mm7.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/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(mm7, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm7.geneSymbol.LENGTH)
head(mm7.geneSymbol.LENGTH)

mm7.geneid.LENGTH Transcript length data for the organism mm

Description

mm7.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(mm7, geneid) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm7.genscan.LENGTH Transcript length data for the organism mm

Description

mm7.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(mm7, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm7.knownGene.LENGTH

Transcript length data for the organism mm

Description

mm7.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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

downloadLengthFromUCSC

Examples

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

mm7.refGene.LENGTH Transcript length data for the organism mm

Description

mm7.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm7.refGene.LENGTH)
head(mm7.refGene.LENGTH)

mm7.sgpGene.LENGTH Transcript length data for the organism mm

Description

mm7.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(mm7, sgpGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm7.sgpGene.LENGTH)
head(mm7.sgpGene.LENGTH)

mm7.xenoRefGene.LENGTH

Transcript length data for the organism mm

Description

mm7.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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

downloadLengthFromUCSC

Examples

data(mm7.xenoRefGene.LENGTH)
head(mm7.xenoRefGene.LENGTH)

mm8.ccdsGene.LENGTH

Transcript length data for the organism mm

Description

mm8.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, ccdsGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm8.ensGene.LENGTH Transcript length data for the organism mm

Description

mm8.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm8.ensGene.LENGTH)
head(mm8.ensGene.LENGTH)

mm8.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/cgibin/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.geneid.LENGTH Transcript length data for the organism mm

Description

mm8.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(mm8, geneid) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm8.genscan.LENGTH Transcript length data for the organism mm

Description

mm8.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(mm8, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm8.knownGene.LENGTH

Transcript length data for the organism mm

Description

mm8.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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

downloadLengthFromUCSC

Examples

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

mm8.refGene.LENGTH Transcript length data for the organism mm

Description

mm8.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm8.refGene.LENGTH)
head(mm8.refGene.LENGTH)

mm8.sgpGene.LENGTH Transcript length data for the organism mm

Description

mm8.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, sgpGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm8.sibGene.LENGTH Transcript length data for the organism mm

Description

mm8.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sibGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, sibGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm8.xenoRefGene.LENGTH

Transcript length data for the organism mm

Description

mm8.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(mm8, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm8.xenoRefGene.LENGTH)
head(mm8.xenoRefGene.LENGTH)

mm9.acembly.LENGTH Transcript length data for the organism mm

Description

mm9.acembly.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the acembly table.

The data file was made by calling downloadLengthFromUCSC(mm9, acembly) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm9.acembly.LENGTH)
head(mm9.acembly.LENGTH)

mm9.ccdsGene.LENGTH

Transcript length data for the organism mm

Description

mm9.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ccdsGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, ccdsGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm9.ensGene.LENGTH Transcript length data for the organism mm

Description

mm9.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm9.ensGene.LENGTH)
head(mm9.ensGene.LENGTH)

mm9.exoniphy.LENGTH

Transcript length data for the organism mm

Description

mm9.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the exoniphy table.

The data file was made by calling downloadLengthFromUCSC(mm9, exoniphy) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm9.exoniphy.LENGTH)
head(mm9.exoniphy.LENGTH)

mm9.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/cgibin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(mm9, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm9.geneSymbol.LENGTH)
head(mm9.geneSymbol.LENGTH)

mm9.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.genscan.LENGTH Transcript length data for the organism mm

Description

mm9.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(mm9, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm9.knownGene.LENGTH

Transcript length data for the organism mm

Description

mm9.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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

downloadLengthFromUCSC

Examples

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

mm9.nscanGene.LENGTH

Transcript length data for the organism mm

Description

mm9.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm9.nscanGene.LENGTH)
head(mm9.nscanGene.LENGTH)

mm9.refGene.LENGTH Transcript length data for the organism mm

Description

mm9.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm9.sgpGene.LENGTH Transcript length data for the organism mm

Description

mm9.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, sgpGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

mm9.xenoRefGene.LENGTH

Transcript length data for the organism mm

Description

mm9.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(mm9, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(mm9.xenoRefGene.LENGTH)
head(mm9.xenoRefGene.LENGTH)

monDom1.genscan.LENGTH

Transcript length data for the organism monDom

Description

monDom1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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

Examples

data(monDom4.ensGene.LENGTH)
head(monDom4.ensGene.LENGTH)

monDom4.geneSymbol.LENGTH

Transcript length data for the organism monDom

Description

monDom4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(monDom4, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom4.geneSymbol.LENGTH)
head(monDom4.geneSymbol.LENGTH)

monDom4.genscan.LENGTH

Transcript length data for the organism monDom

Description

monDom4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(monDom4, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom4.genscan.LENGTH)
head(monDom4.genscan.LENGTH)

monDom4.nscanGene.LENGTH

Transcript length data for the organism monDom

Description

monDom4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(monDom4, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom4.nscanGene.LENGTH)
head(monDom4.nscanGene.LENGTH)

monDom4.refGene.LENGTH

Transcript length data for the organism monDom

Description

monDom4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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

Examples

data(monDom4.refGene.LENGTH)
head(monDom4.refGene.LENGTH)

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

Examples

data(monDom5.ensGene.LENGTH)
head(monDom5.ensGene.LENGTH)

monDom5.geneSymbol.LENGTH

Transcript length data for the organism monDom

Description

monDom5.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(monDom5, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom5.geneSymbol.LENGTH)
head(monDom5.geneSymbol.LENGTH)

monDom5.genscan.LENGTH

Transcript length data for the organism monDom

Description

monDom5.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(monDom5, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom5.genscan.LENGTH)
head(monDom5.genscan.LENGTH)

monDom5.nscanGene.LENGTH

Transcript length data for the organism monDom

Description

monDom5.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)

monDom5.refGene.LENGTH

Transcript length data for the organism monDom

Description

monDom5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)

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)

ornAnal.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

Examples

data(ornAnal.ensGene.LENGTH)
head(ornAnal.ensGene.LENGTH)

ornAnal.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(ornAnal.geneSymbol.LENGTH)
head(ornAnal.geneSymbol.LENGTH)

ornAnal.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

Examples

data(ornAnal.refGene.LENGTH)
head(ornAnal.refGene.LENGTH)

ornAnal.xenoRefGene.LENGTH Transcript length data for the organism ornAna

Description

ornAna1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ornAnal.xenoRefGene.LENGTH)
head(ornAnal.xenoRefGene.LENGTH)

oryLat2.ensGene.LENGTH

Transcript length data for the organism oryLat

Description

oryLat2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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

Examples

data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)

oryLat2.geneSymbol.LENGTH

Transcript length data for the organism oryLat

Description

oryLat2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)

oryLat2.refGene.LENGTH

Transcript length data for the organism oryLat

Description

oryLat2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)

oryLat2.xenoRefGene.LENGTH

Transcript length data for the organism oryLat

Description

oryLat2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)

panTrol.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

Examples

data(panTrol.ensGene.LENGTH)
head(panTrol.ensGene.LENGTH)

panTrol.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)

panTrol.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/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(panTro1, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTrol.genscan.LENGTH)
head(panTrol.genscan.LENGTH)

panTrol.xenoRefGene.LENGTH

Transcript length data for the organism panTro

Description

panTro1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(panTro1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTrol.xenoRefGene.LENGTH)
head(panTrol.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/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)

panTro2.geneSymbol.LENGTH

Transcript length data for the organism panTro

Description

panTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(panTro2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)

panTro2.genscan.LENGTH

Transcript length data for the organism panTro

Description

panTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(panTro2, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.genscan.LENGTH)
head(panTro2.genscan.LENGTH)

panTro2.nscanGene.LENGTH

Transcript length data for the organism panTro

Description

panTro2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.nscanGene.LENGTH)
head(panTro2.nscanGene.LENGTH)

panTro2.refGene.LENGTH

Transcript length data for the organism panTro

Description

panTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.refGene.LENGTH)
head(panTro2.refGene.LENGTH)

panTro2.xenoRefGene.LENGTH

Transcript length data for the organism panTro

Description

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.xenoRefGene.LENGTH)
head(panTro2.xenoRefGene.LENGTH)

petMar1.xenoRefGene.LENGTH

Transcript length data for the organism petMar

Description

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(petMar1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

```
data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)
```

ponAbe2.ensGene.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)

ponAbe2.geneSymbol.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

```
data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)
```

ponAbe2.genscan.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)

ponAbe2.nscanGene.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

```
data(ponAbe2.nscanGene.LENGTH)
head(ponAbe2.nscanGene.LENGTH)
```

ponAbe2.refGene.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.refGene.LENGTH)
head(ponAbe2.refGene.LENGTH)

ponAbe2.xenoRefGene.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)

priPac1.xenoRefGene.LENGTH

Transcript length data for the organism priPac

Description

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(priPac1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)

rheMac2.ensGene.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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

Examples

data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)

rheMac2.geneSymbol.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)

rheMac2.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.nscanGene.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)

rheMac2.refGene.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)

rheMac2.sgpGene.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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

Examples

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

rn3.ensGene.LENGTH Transcript length data for the organism rn

Description

rn3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.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.geneid.LENGTH Transcript length data for the organism rn

Description

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rn3, geneid) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

```
data(rn3.geneid.LENGTH)
head(rn3.geneid.LENGTH)
```

rn3.genscan.LENGTH Transcript length data for the organism rn

Description

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(rn3, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

```
data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)
```

rn3.knownGene.LENGTH

Transcript length data for the organism rn

Description

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/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/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

rn3.refGene.LENGTH Transcript length data for the organism rn

Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

rn3.sgpGene.LENGTH Transcript length data for the organism rn

Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, sgpGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

```
data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)
```

rn3.xenoRefGene.LENGTH

Transcript length data for the organism rn

Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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

downloadLengthFromUCSC

Examples

data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)

rn4.ensGene.LENGTH Transcript length data for the organism rn

Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

rn4.geneSymbol.LENGTH

Transcript length data for the organism rn

Description

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rn4, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)

rn4.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.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

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

rn4.knownGene.LENGTH

Transcript length data for the organism rn

Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, knownGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

rn4.nscanGene.LENGTH

Transcript length data for the organism rn

Description

rn4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)

rn4.refGene.LENGTH Transcript length data for the organism rn

Description

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

rn4.sgpGene.LENGTH Transcript length data for the organism rn

Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, sgpGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

```
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/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn4.xenoRefGene.LENGTH)
head(rn4.xenoRefGene.LENGTH)

sacCer1.ensGene.LENGTH

Transcript length data for the organism sacCer

Description

sacCer1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/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(sacCerl.ensGene.LENGTH)
head(sacCerl.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

Examples

data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)

strPur1.geneSymbol.LENGTH

Transcript length data for the organism strPur

Description

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(strPur1, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)

strPurl.genscan.LENGTH

Transcript length data for the organism strPur

Description

strPur1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(strPur1, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPurl.genscan.LENGTH)
head(strPurl.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

 ${\tt downloadLengthFromUCSC}$

Examples

data(strPurl.refGene.LENGTH)
head(strPurl.refGene.LENGTH)

strPurl.xenoRefGene.LENGTH

Transcript length data for the organism strPur

Description

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(strPur1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

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

strPur2.genscan.LENGTH

Transcript length data for the organism strPur

Description

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(strPur2, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur2.genscan.LENGTH)
head(strPur2.genscan.LENGTH)

strPur2.refGene.LENGTH

Transcript length data for the organism strPur

Description

strPur2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(strPur2, refGene) on the date on which the package was last updated.

See Also

 ${\tt downloadLengthFromUCSC}$

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

Examples

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

supportedGeneIDs Supported Gene IDs

Description

Lists supported gene ID formats

Usage

supportedGeneIDs()

Details

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

Value

A data.frame containing supported gene ID formats.

Author(s)

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

supportedGenomes

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 available for the genome listed in the geneLenDataBase package.

Value

A data.frame containing supported genomes.

Author(s)

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

Examples

supportedGenomes()

taeGut1.ensGene.LENGTH

Transcript length data for the organism taeGut

Description

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

Examples

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

taeGut1.geneSymbol.LENGTH

Transcript length data for the organism taeGut

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

taeGut1.genscan.LENGTH

Transcript length data for the organism taeGut

Description

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

Examples

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

164

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

Examples

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

taeGut1.xenoRefGene.LENGTH

Transcript length data for the organism taeGut

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

tetNig1.ensGene.LENGTH

Transcript length data for the organism tetNig

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(tetNigl.ensGene.LENGTH)
head(tetNigl.ensGene.LENGTH)

tetNigl.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(tetNigl.geneid.LENGTH)
head(tetNigl.geneid.LENGTH)

tetNig1.genscan.LENGTH

Transcript length data for the organism tetNig

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(tetNigl.genscan.LENGTH)
head(tetNigl.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/cgibin/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(tetNigl.nscanGene.LENGTH)
head(tetNigl.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

Examples

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

unfactor

Description

Removes all factors from a variable in a sensible way.

Usage

unfactor(var)

Arguments

var

The variable from which you want the factors removed.

Details

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

Value

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

Author(s)

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

```
#A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep='.')
x
unfactor(x)
#A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"), score <- factor(c(9, 7, 8, 9)
x$player
x$score
y <- unfactor(x)
y$player
y$score
```

```
xenTrol.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(xenTrol.genscan.LENGTH)
head(xenTrol.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

Examples

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

xenTro2.geneSymbol.LENGTH

Transcript length data for the organism xenTro

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

xenTro2.genscan.LENGTH

Transcript length data for the organism xenTro

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

xenTro2.refGene.LENGTH

Transcript length data for the organism xenTro

Description

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

downloadLengthFromUCSC

Examples

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

Index

*Topic datasets

anoCarl.ensGene.LENGTH, 1 anoCarl.genscan.LENGTH, 1 anoCarl.xenoRefGene.LENGTH, 2 anoGam1.ensGene.LENGTH, 2 anoGam1.geneid.LENGTH, 3 anoGam1.genscan.LENGTH,3 apiMel1.genscan.LENGTH,4 apiMel2.ensGene.LENGTH, 4 apiMel2.geneid.LENGTH, 5 apiMel2.genscan.LENGTH, 5 aplCall.xenoRefGene.LENGTH, 6 bosTau2.geneid.LENGTH,7 bosTau2.geneSymbol.LENGTH, 6 bosTau2.genscan.LENGTH, 7 bosTau2.refGene.LENGTH,8 bosTau2.sgpGene.LENGTH, 8 bosTau3.ensGene.LENGTH, 9 bosTau3.geneid.LENGTH, 10 bosTau3.geneSymbol.LENGTH,9 bosTau3.genscan.LENGTH, 10 bosTau3.refGene.LENGTH, 11 bosTau3.sqpGene.LENGTH, 11 bosTau4.ensGene.LENGTH, 12 bosTau4.geneSymbol.LENGTH, 12 bosTau4.genscan.LENGTH, 13 bosTau4.nscanGene.LENGTH, 13 bosTau4.refGene.LENGTH, 14 braFlo1.xenoRefGene.LENGTH, 14 caeJap1.xenoRefGene.LENGTH, 15 caePb1.xenoRefGene.LENGTH, 15 caePb2.xenoRefGene.LENGTH, 16 caeRem2.xenoRefGene.LENGTH, 16 caeRem3.xenoRefGene.LENGTH, 17 calJac1.genscan.LENGTH, 17 calJac1.nscanGene.LENGTH, 18 calJac1.xenoRefGene.LENGTH, 18 canFam1.ensGene.LENGTH, 19

canFam1.geneSymbol.LENGTH, 19 canFam1.genscan.LENGTH, 20 canFam1.nscanGene.LENGTH, 20 canFam1.refGene.LENGTH, 21 canFam1.xenoRefGene.LENGTH, 21 canFam2.ensGene.LENGTH, 22 canFam2.geneSymbol.LENGTH, 22 canFam2.genscan.LENGTH, 23 canFam2.nscanGene.LENGTH, 23 canFam2.refGene.LENGTH, 24 canFam2.xenoRefGene.LENGTH, 24 cavPor3.ensGene.LENGTH, 25 cavPor3.genscan.LENGTH, 25 cavPor3.nscanGene.LENGTH, 26 cavPor3.xenoRefGene.LENGTH, 26 cbl.xenoRefGene.LENGTH, 27 cb3.xenoRefGene.LENGTH, 27 ce2.geneid.LENGTH, 28 ce2.geneSymbol.LENGTH, 28 ce2.refGene.LENGTH, 29 ce4.geneSymbol.LENGTH, 29 ce4.refGene.LENGTH, 30 ce4.xenoRefGene.LENGTH, 30 ce6.ensGene.LENGTH, 31 ce6.geneSymbol.LENGTH, 31 ce6.refGene.LENGTH, 32 ce6.xenoRefGene.LENGTH, 32 cil.geneSymbol.LENGTH, 33 cil.refGene.LENGTH, 33 cil.xenoRefGene.LENGTH, 34 ci2.ensGene.LENGTH, 34 ci2.geneSymbol.LENGTH, 35 ci2.refGene.LENGTH, 35 ci2.xenoRefGene.LENGTH, 36 danRer3.ensGene.LENGTH, 36 danRer3.geneSymbol.LENGTH, 37 danRer3.refGene.LENGTH, 37 danRer4.ensGene.LENGTH, 38 danRer4.geneSymbol.LENGTH, 38 danRer4.genscan.LENGTH, 39

```
danRer4.nscanGene.LENGTH, 39
danRer4.refGene.LENGTH.40
danRer5.ensGene.LENGTH, 40
danRer5.geneSymbol.LENGTH, 41
danRer5.refGene.LENGTH, 41
danRer5.vegaGene.LENGTH, 42
danRer5.vegaPseudoGene.LENGTH,
   42
danRer6.ensGene.LENGTH, 43
danRer6.geneSymbol.LENGTH, 43
danRer6.refGene.LENGTH.44
danRer6.xenoRefGene.LENGTH,
   44
dm1.geneSymbol.LENGTH, 45
dm1.genscan.LENGTH,45
dm1.refGene.LENGTH, 46
dm2.geneid.LENGTH, 47
dm2.geneSymbol.LENGTH, 46
dm2.genscan.LENGTH, 47
dm2.nscanGene.LENGTH, 48
dm2.refGene.LENGTH, 48
dm3.geneSymbol.LENGTH, 49
dm3.nscanPasaGene.LENGTH, 49
dm3.refGene.LENGTH, 50
dp2.genscan.LENGTH, 51
dp2.xenoRefGene.LENGTH, 52
dp3.geneid.LENGTH, 52
dp3.genscan.LENGTH, 53
dp3.xenoRefGene.LENGTH, 53
droAnal.geneid.LENGTH, 54
droAnal.genscan.LENGTH, 54
droAnal.xenoRefGene.LENGTH,
   55
droAna2.genscan.LENGTH, 55
droAna2.xenoRefGene.LENGTH,
   56
droErel.genscan.LENGTH, 56
droErel.xenoRefGene.LENGTH,
   57
droGril.genscan.LENGTH, 57
droGri1.xenoRefGene.LENGTH,
   58
droMojl.geneid.LENGTH, 58
droMojl.genscan.LENGTH, 59
droMoj1.xenoRefGene.LENGTH,
   59
droMoj2.genscan.LENGTH, 60
droMoj2.xenoRefGene.LENGTH,
   60
droPer1.genscan.LENGTH, 61
droPer1.xenoRefGene.LENGTH,
   61
```

droSec1.genscan.LENGTH, 62 droSec1.xenoRefGene.LENGTH. 62 droSim1.geneid.LENGTH, 63 droSim1.genscan.LENGTH, 63 droSim1.xenoRefGene.LENGTH, 64 droVir1.geneid.LENGTH, 64 droVir1.genscan.LENGTH, 65 droVir1.xenoRefGene.LENGTH, 65 droVir2.genscan.LENGTH, 66 droVir2.xenoRefGene.LENGTH, 66 droYak1.geneid.LENGTH, 67 droYak1.genscan.LENGTH, 67 droYak1.xenoRefGene.LENGTH, 68 droYak2.genscan.LENGTH, 68 droYak2.xenoRefGene.LENGTH, 69 equCab1.geneid.LENGTH, 70 equCab1.geneSymbol.LENGTH, 69 equCab1.nscanGene.LENGTH, 70 equCab1.refGene.LENGTH, 71 equCab1.sqpGene.LENGTH, 71 equCab2.ensGene.LENGTH, 72 equCab2.geneSymbol.LENGTH, 72 equCab2.nscanGene.LENGTH, 73 equCab2.refGene.LENGTH, 73 equCab2.xenoRefGene.LENGTH, 74 felCat3.ensGene.LENGTH,74 felCat3.geneid.LENGTH,75 felCat3.geneSymbol.LENGTH, 75 felCat3.genscan.LENGTH, 76 felCat3.nscanGene.LENGTH, 76 felCat3.refGene.LENGTH,77 felCat3.sqpGene.LENGTH,77 felCat3.xenoRefGene.LENGTH, 78 fr1.ensGene.LENGTH, 78 fr1.genscan.LENGTH, 79 fr2.ensGene.LENGTH, 79 galGal2.ensGene.LENGTH, 80 galGal2.geneid.LENGTH,81 galGal2.geneSymbol.LENGTH, 80 galGal2.genscan.LENGTH,81 galGal2.refGene.LENGTH,82 galGal2.sgpGene.LENGTH,82 galGal3.ensGene.LENGTH,83 galGal3.geneSymbol.LENGTH,83

174

galGal3.genscan.LENGTH,84 galGal3.nscanGene.LENGTH,84 galGal3.refGene.LENGTH,85 galGal3.xenoRefGene.LENGTH, 85 gasAcul.ensGene.LENGTH,86 gasAcul.nscanGene.LENGTH,86 hg16.acembly.LENGTH, 87 hg16.ensGene.LENGTH, 87 hq16.exoniphy.LENGTH, 88 hq16.geneid.LENGTH, 89 hg16.geneSymbol.LENGTH, 88 hg16.genscan.LENGTH, 89 hg16.knownGene.LENGTH, 90 hq16.refGene.LENGTH, 90 hg16.sgpGene.LENGTH, 91 hg17.acembly.LENGTH,91 hg17.acescan.LENGTH, 92 hg17.ccdsGene.LENGTH, 92 hq17.ensGene.LENGTH,93 hg17.exoniphy.LENGTH, 93 hg17.geneid.LENGTH,94 hg17.geneSymbol.LENGTH, 94 hg17.genscan.LENGTH,95 hg17.knownGene.LENGTH, 95 hg17.refGene.LENGTH,96 hq17.sqpGene.LENGTH,96 hg17.vegaGene.LENGTH, 97 hg17.vegaPseudoGene.LENGTH, 97 hg17.xenoRefGene.LENGTH,98 hq18.acembly.LENGTH, 98 hg18.acescan.LENGTH, 99 hg18.ccdsGene.LENGTH, 99 hg18.ensGene.LENGTH, 100 hg18.exoniphy.LENGTH, 100 hq18.geneid.LENGTH, 101 hg18.geneSymbol.LENGTH, 101 hg18.genscan.LENGTH, 102 hg18.knownGene.LENGTH, 102 hg18.knownGeneOld3.LENGTH, 103 hg18.refGene.LENGTH, 103 hg18.sgpGene.LENGTH, 104 hq18.sibGene.LENGTH, 104 hg18.xenoRefGene.LENGTH, 105 hq19.ccdsGene.LENGTH, 105 hg19.ensGene.LENGTH, 106 hg19.exoniphy.LENGTH, 106 hg19.geneSymbol.LENGTH, 107 hg19.knownGene.LENGTH, 107 hg19.nscanGene.LENGTH, 108

hq19.refGene.LENGTH, 108 hq19.xenoRefGene.LENGTH, 109 loxAfr3.xenoRefGene.LENGTH, 109 mm7.ensGene.LENGTH, 110 mm7.geneid.LENGTH, 111 mm7.geneSymbol.LENGTH, 110 mm7.genscan.LENGTH, 111 mm7.knownGene.LENGTH, 112 mm7.refGene.LENGTH, 112 mm7.sqpGene.LENGTH, 113 mm7.xenoRefGene.LENGTH, 113 mm8.ccdsGene.LENGTH, 114 mm8.ensGene.LENGTH, 114 mm8.geneid.LENGTH, 115 mm8.geneSymbol.LENGTH, 115 mm8.genscan.LENGTH, 116 mm8.knownGene.LENGTH, 116 mm8.nscanGene.LENGTH, 117 mm8.refGene.LENGTH, 117 mm8.sqpGene.LENGTH, 118 mm8.sibGene.LENGTH, 118 mm8.xenoRefGene.LENGTH, 119 mm9.acembly.LENGTH, 119 mm9.ccdsGene.LENGTH, 120 mm9.ensGene.LENGTH, 120 mm9.exoniphy.LENGTH, 121 mm9.geneid.LENGTH, 122 mm9.geneSymbol.LENGTH, 121 mm9.genscan.LENGTH, 122 mm9.knownGene.LENGTH, 123 mm9.nscanGene.LENGTH, 123 mm9.refGene.LENGTH, 124 mm9.sqpGene.LENGTH, 124 mm9.xenoRefGene.LENGTH, 125 monDom1.genscan.LENGTH, 125 monDom4.ensGene.LENGTH, 126 monDom4.geneSymbol.LENGTH, 126 monDom4.genscan.LENGTH, 127 monDom4.nscanGene.LENGTH, 127 monDom4.refGene.LENGTH, 128 monDom4.xenoRefGene.LENGTH, 128 monDom5.ensGene.LENGTH, 129 monDom5.geneSymbol.LENGTH, 129 monDom5.genscan.LENGTH, 130 monDom5.nscanGene.LENGTH, 130 monDom5.refGene.LENGTH, 131 monDom5.xenoRefGene.LENGTH, 131

```
ornAnal.ensGene.LENGTH, 132
ornAnal.geneSymbol.LENGTH,
   132
ornAnal.refGene.LENGTH, 133
ornAnal.xenoRefGene.LENGTH,
   133
oryLat2.ensGene.LENGTH, 134
oryLat2.geneSymbol.LENGTH,
   134
oryLat2.refGene.LENGTH, 135
oryLat2.xenoRefGene.LENGTH,
   135
panTrol.ensGene.LENGTH, 136
panTrol.geneid.LENGTH, 136
panTrol.genscan.LENGTH, 137
panTrol.xenoRefGene.LENGTH,
   137
panTro2.ensGene.LENGTH, 138
panTro2.geneSymbol.LENGTH,
   138
panTro2.genscan.LENGTH, 139
panTro2.nscanGene.LENGTH, 139
panTro2.refGene.LENGTH, 140
panTro2.xenoRefGene.LENGTH,
   140
petMar1.xenoRefGene.LENGTH,
   141
ponAbe2.ensGene.LENGTH, 141
ponAbe2.geneSymbol.LENGTH,
   142
ponAbe2.genscan.LENGTH, 142
ponAbe2.nscanGene.LENGTH, 143
ponAbe2.refGene.LENGTH, 143
ponAbe2.xenoRefGene.LENGTH,
   144
priPac1.xenoRefGene.LENGTH,
   144
rheMac2.ensGene.LENGTH, 145
rheMac2.geneid.LENGTH, 146
rheMac2.geneSymbol.LENGTH,
   145
rheMac2.nscanGene.LENGTH, 146
rheMac2.refGene.LENGTH, 147
rheMac2.sqpGene.LENGTH, 147
rheMac2.xenoRefGene.LENGTH,
   148
rn3.ensGene.LENGTH, 148
rn3.geneid.LENGTH, 149
rn3.geneSymbol.LENGTH, 149
rn3.genscan.LENGTH, 150
rn3.knownGene.LENGTH, 150
rn3.nscanGene.LENGTH, 151
```

```
rn3.refGene.LENGTH, 151
   rn3.sqpGene.LENGTH, 152
   rn3.xenoRefGene.LENGTH, 152
   rn4.ensGene.LENGTH, 153
   rn4.geneid.LENGTH, 154
   rn4.geneSymbol.LENGTH, 153
   rn4.genscan.LENGTH, 154
   rn4.knownGene.LENGTH, 155
   rn4.nscanGene.LENGTH, 155
   rn4.refGene.LENGTH, 156
   rn4.sqpGene.LENGTH, 156
   rn4.xenoRefGene.LENGTH, 157
   sacCerl.ensGene.LENGTH, 157
   sacCer2.ensGene.LENGTH, 158
   strPur1.geneSymbol.LENGTH,
       158
   strPur1.genscan.LENGTH, 159
   strPur1.refGene.LENGTH, 159
   strPur1.xenoRefGene.LENGTH,
       160
   strPur2.geneSymbol.LENGTH,
       160
   strPur2.genscan.LENGTH, 161
   strPur2.refGene.LENGTH, 161
   strPur2.xenoRefGene.LENGTH,
       162
   taeGut1.ensGene.LENGTH, 163
   taeGut1.geneSymbol.LENGTH,
       164
   taeGut1.genscan.LENGTH, 164
   taeGut1.nscanGene.LENGTH, 165
   taeGut1.refGene.LENGTH, 165
   taeGut1.xenoRefGene.LENGTH,
       166
   tetNig1.ensGene.LENGTH, 166
   tetNig1.geneid.LENGTH, 167
   tetNig1.genscan.LENGTH, 167
   tetNig1.nscanGene.LENGTH, 168
   tetNig2.ensGene.LENGTH, 168
   xenTrol.genscan.LENGTH, 170
   xenTro2.ensGene.LENGTH, 170
   xenTro2.geneSymbol.LENGTH,
       171
   xenTro2.genscan.LENGTH, 171
   xenTro2.refGene.LENGTH, 172
anoCarl.ensGene.LENGTH, 1
anoCarl.genscan.LENGTH, 1
anoCarl.xenoRefGene.LENGTH, 2
anoGam1.ensGene.LENGTH, 2
anoGam1.geneid.LENGTH, 3
anoGam1.genscan.LENGTH, 3
apiMel1.genscan.LENGTH,4
```

apiMel2.ensGene.LENGTH,4 apiMel2.geneid.LENGTH, 5 apiMel2.genscan.LENGTH,5 aplCall.xenoRefGene.LENGTH, 6 bosTau2.geneid.LENGTH,7 bosTau2.geneSymbol.LENGTH, 6 bosTau2.genscan.LENGTH,7 bosTau2.refGene.LENGTH, 8 bosTau2.sgpGene.LENGTH,8 bosTau3.ensGene.LENGTH,9 bosTau3.geneid.LENGTH, 10 bosTau3.geneSymbol.LENGTH,9 bosTau3.genscan.LENGTH, 10 bosTau3.refGene.LENGTH, 11 bosTau3.sqpGene.LENGTH, 11 bosTau4.ensGene.LENGTH, 12 bosTau4.geneSymbol.LENGTH, 12 bosTau4.genscan.LENGTH, 13 bosTau4.nscanGene.LENGTH, 13 bosTau4.refGene.LENGTH, 14 braFlo1.xenoRefGene.LENGTH, 14 caeJap1.xenoRefGene.LENGTH, 15 caePb1.xenoRefGene.LENGTH.15 caePb2.xenoRefGene.LENGTH, 16 caeRem2.xenoRefGene.LENGTH, 16 caeRem3.xenoRefGene.LENGTH, 17 calJac1.genscan.LENGTH, 17 calJac1.nscanGene.LENGTH, 18 calJac1.xenoRefGene.LENGTH, 18 canFam1.ensGene.LENGTH, 19 canFam1.geneSymbol.LENGTH, 19 canFam1.genscan.LENGTH, 20 canFam1.nscanGene.LENGTH, 20 canFam1.refGene.LENGTH.21 canFam1.xenoRefGene.LENGTH, 21 canFam2.ensGene.LENGTH, 22 canFam2.geneSymbol.LENGTH, 22 canFam2.genscan.LENGTH, 23 canFam2.nscanGene.LENGTH, 23 canFam2.refGene.LENGTH, 24 canFam2.xenoRefGene.LENGTH, 24 cavPor3.ensGene.LENGTH, 25 cavPor3.genscan.LENGTH, 25 cavPor3.nscanGene.LENGTH, 26 cavPor3.xenoRefGene.LENGTH, 26 cb1.xenoRefGene.LENGTH, 27 cb3.xenoRefGene.LENGTH, 27 ce2.geneid.LENGTH, 28 ce2.geneSymbol.LENGTH, 28 ce2.refGene.LENGTH, 29 ce4.geneSymbol.LENGTH, 29

ce4.refGene.LENGTH, 30 ce4.xenoRefGene.LENGTH.30 ce6.ensGene.LENGTH, 31 ce6.geneSymbol.LENGTH, 31 ce6.refGene.LENGTH, 32 ce6.xenoRefGene.LENGTH, 32 cil.geneSymbol.LENGTH, 33 cil.refGene.LENGTH, 33 cil.xenoRefGene.LENGTH, 34 ci2.ensGene.LENGTH, 34 ci2.geneSymbol.LENGTH, 35 ci2.refGene.LENGTH, 35 ci2.xenoRefGene.LENGTH, 36 danRer3.ensGene.LENGTH, 36 danRer3.geneSymbol.LENGTH, 37 danRer3.refGene.LENGTH, 37 danRer4.ensGene.LENGTH, 38 danRer4.geneSymbol.LENGTH, 38 danRer4.genscan.LENGTH, 39 danRer4.nscanGene.LENGTH, 39 danRer4.refGene.LENGTH, 40 danRer5.ensGene.LENGTH, 40 danRer5.geneSymbol.LENGTH, 41 danRer5.refGene.LENGTH, 41 danRer5.vegaGene.LENGTH, 42 danRer5.vegaPseudoGene.LENGTH, 42 danRer6.ensGene.LENGTH, 43 danRer6.geneSymbol.LENGTH, 43 danRer6.refGene.LENGTH, 44 danRer6.xenoRefGene.LENGTH, 44 dm1.geneSymbol.LENGTH, 45 dm1.genscan.LENGTH,45 dm1.refGene.LENGTH, 46 dm2.geneid.LENGTH,47 dm2.geneSymbol.LENGTH, 46 dm2.genscan.LENGTH, 47 dm2.nscanGene.LENGTH, 48 dm2.refGene.LENGTH, 48 dm3.geneSymbol.LENGTH, 49 dm3.nscanPasaGene.LENGTH, 49 dm3.refGene.LENGTH, 50 downloadLengthFromUCSC, 1-49, 50, 50-168, 170-172 dp2.genscan.LENGTH, 51 dp2.xenoRefGene.LENGTH, 52 dp3.geneid.LENGTH, 52 dp3.genscan.LENGTH, 53 dp3.xenoRefGene.LENGTH, 53 droAnal.geneid.LENGTH, 54 droAnal.genscan.LENGTH, 54 droAnal.xenoRefGene.LENGTH, 55 droAna2.genscan.LENGTH, 55

```
droAna2.xenoRefGene.LENGTH, 56
droErel.genscan.LENGTH, 56
droErel.xenoRefGene.LENGTH, 57
droGril.genscan.LENGTH, 57
droGril.xenoRefGene.LENGTH, 58
droMoj1.geneid.LENGTH, 58
droMojl.genscan.LENGTH, 59
droMoj1.xenoRefGene.LENGTH, 59
droMoj2.genscan.LENGTH, 60
droMoj2.xenoRefGene.LENGTH, 60
droPer1.genscan.LENGTH, 61
droPer1.xenoRefGene.LENGTH, 61
droSec1.genscan.LENGTH, 62
droSec1.xenoRefGene.LENGTH, 62
droSim1.geneid.LENGTH, 63
droSim1.genscan.LENGTH, 63
droSim1.xenoRefGene.LENGTH, 64
droVir1.geneid.LENGTH, 64
droVir1.genscan.LENGTH, 65
droVir1.xenoRefGene.LENGTH, 65
droVir2.genscan.LENGTH, 66
droVir2.xenoRefGene.LENGTH, 66
droYak1.geneid.LENGTH, 67
droYak1.genscan.LENGTH, 67
droYak1.xenoRefGene.LENGTH, 68
droYak2.genscan.LENGTH, 68
droYak2.xenoRefGene.LENGTH, 69
```

```
equCab1.geneid.LENGTH,70
equCab1.geneSymbol.LENGTH,69
equCab1.nscanGene.LENGTH,70
equCab1.refGene.LENGTH,71
equCab1.sgpGene.LENGTH,71
equCab2.ensGene.LENGTH,72
equCab2.geneSymbol.LENGTH,72
equCab2.nscanGene.LENGTH,73
equCab2.refGene.LENGTH,73
```

```
felCat3.ensGene.LENGTH, 74
felCat3.geneid.LENGTH, 75
felCat3.geneSymbol.LENGTH, 75
felCat3.genscan.LENGTH, 76
felCat3.nscanGene.LENGTH, 76
felCat3.refGene.LENGTH, 77
felCat3.sgpGene.LENGTH, 77
felCat3.xenoRefGene.LENGTH, 78
fr1.ensGene.LENGTH, 78
fr1.genscan.LENGTH, 79
fr2.ensGene.LENGTH, 79
```

```
galGal2.ensGene.LENGTH, 80 galGal2.geneid.LENGTH, 81
```

galGal2.geneSymbol.LENGTH, 80 galGal2.genscan.LENGTH.81 galGal2.refGene.LENGTH,82 galGal2.sqpGene.LENGTH, 82 galGal3.ensGene.LENGTH, 83 galGal3.geneSymbol.LENGTH, 83 galGal3.genscan.LENGTH,84 galGal3.nscanGene.LENGTH, 84 galGal3.refGene.LENGTH,85 galGal3.xenoRefGene.LENGTH,85 gasAcul.ensGene.LENGTH,86 gasAcul.nscanGene.LENGTH, 86 hg16.acembly.LENGTH,87 hq16.ensGene.LENGTH, 87 hg16.exoniphy.LENGTH, 88 hq16.geneid.LENGTH, 89 hg16.geneSymbol.LENGTH, 88 hg16.genscan.LENGTH, 89 hg16.knownGene.LENGTH, 90 hg16.refGene.LENGTH, 90 hg16.sgpGene.LENGTH,91 hq17.acembly.LENGTH, 91 hq17.acescan.LENGTH, 92 hg17.ccdsGene.LENGTH, 92 hq17.ensGene.LENGTH,93 hq17.exoniphy.LENGTH, 93 hg17.geneid.LENGTH, 94 hg17.geneSymbol.LENGTH, 94 hg17.genscan.LENGTH,95 hg17.knownGene.LENGTH, 95 hg17.refGene.LENGTH,96 hg17.sgpGene.LENGTH,96 hg17.vegaGene.LENGTH,97 hg17.vegaPseudoGene.LENGTH, 97 hg17.xenoRefGene.LENGTH, 98 hq18.acembly.LENGTH, 98 hg18.acescan.LENGTH, 99 hq18.ccdsGene.LENGTH, 99 hg18.ensGene.LENGTH, 100 hg18.exoniphy.LENGTH, 100 hg18.geneid.LENGTH, 101 hg18.geneSymbol.LENGTH, 101 hg18.genscan.LENGTH, 102 hg18.knownGene.LENGTH, 102 hg18.knownGeneOld3.LENGTH, 103 hq18.refGene.LENGTH, 103 hg18.sgpGene.LENGTH, 104 hg18.sibGene.LENGTH, 104 hg18.xenoRefGene.LENGTH, 105 hg19.ccdsGene.LENGTH, 105 hg19.ensGene.LENGTH, 106 hg19.exoniphy.LENGTH, 106

178

hg19.geneSymbol.LENGTH, 107 hg19.knownGene.LENGTH, 107 hg19.nscanGene.LENGTH, 108 hg19.refGene.LENGTH, 108 hg19.xenoRefGene.LENGTH, 109 loxAfr3.xenoRefGene.LENGTH, 109 mm7.ensGene.LENGTH, 110 mm7.geneid.LENGTH, 111 mm7.geneSymbol.LENGTH, 110 mm7.genscan.LENGTH, 111 mm7.knownGene.LENGTH.112 mm7.refGene.LENGTH, 112 mm7.sgpGene.LENGTH, 113 mm7.xenoRefGene.LENGTH, 113 mm8.ccdsGene.LENGTH, 114 mm8.ensGene.LENGTH, 114 mm8.geneid.LENGTH, 115 mm8.geneSymbol.LENGTH, 115 mm8.genscan.LENGTH, 116 mm8.knownGene.LENGTH, 116 mm8.nscanGene.LENGTH, 117 mm8.refGene.LENGTH, 117 mm8.sqpGene.LENGTH, 118 mm8.sibGene.LENGTH, 118 mm8.xenoRefGene.LENGTH, 119 mm9.acembly.LENGTH, 119 mm9.ccdsGene.LENGTH, 120 mm9.ensGene.LENGTH, 120 mm9.exoniphy.LENGTH, 121 mm9.geneid.LENGTH, 122 mm9.geneSymbol.LENGTH, 121 mm9.genscan.LENGTH, 122 mm9.knownGene.LENGTH, 123 mm9.nscanGene.LENGTH, 123 mm9.refGene.LENGTH, 124 mm9.sqpGene.LENGTH, 124 mm9.xenoRefGene.LENGTH, 125 monDom1.genscan.LENGTH, 125 monDom4.ensGene.LENGTH, 126 monDom4.geneSymbol.LENGTH, 126 monDom4.genscan.LENGTH, 127 monDom4.nscanGene.LENGTH, 127 monDom4.refGene.LENGTH, 128 monDom4.xenoRefGene.LENGTH, 128 monDom5.ensGene.LENGTH, 129 monDom5.geneSymbol.LENGTH, 129 monDom5.genscan.LENGTH, 130 monDom5.nscanGene.LENGTH, 130 monDom5.refGene.LENGTH, 131 monDom5.xenoRefGene.LENGTH, 131

ornAnal.ensGene.LENGTH, 132 ornAnal.geneSymbol.LENGTH, 132 ornAnal.refGene.LENGTH, 133 ornAnal.xenoRefGene.LENGTH, 133 oryLat2.ensGene.LENGTH, 134 oryLat2.geneSymbol.LENGTH, 134 oryLat2.refGene.LENGTH, 135 oryLat2.xenoRefGene.LENGTH, 135 panTrol.ensGene.LENGTH, 136 panTrol.geneid.LENGTH, 136 panTrol.genscan.LENGTH, 137 panTrol.xenoRefGene.LENGTH, 137 panTro2.ensGene.LENGTH, 138 panTro2.geneSymbol.LENGTH, 138 panTro2.genscan.LENGTH, 139 panTro2.nscanGene.LENGTH, 139 panTro2.refGene.LENGTH, 140 panTro2.xenoRefGene.LENGTH, 140 petMar1.xenoRefGene.LENGTH, 141 ponAbe2.ensGene.LENGTH, 141 ponAbe2.geneSymbol.LENGTH, 142 ponAbe2.genscan.LENGTH, 142 ponAbe2.nscanGene.LENGTH, 143 ponAbe2.refGene.LENGTH, 143 ponAbe2.xenoRefGene.LENGTH, 144 priPac1.xenoRefGene.LENGTH, 144 rheMac2.ensGene.LENGTH, 145 rheMac2.geneid.LENGTH, 146 rheMac2.geneSymbol.LENGTH, 145 rheMac2.nscanGene.LENGTH, 146 rheMac2.refGene.LENGTH, 147 rheMac2.sqpGene.LENGTH, 147 rheMac2.xenoRefGene.LENGTH, 148 rn3.ensGene.LENGTH.148 rn3.geneid.LENGTH, 149 rn3.geneSymbol.LENGTH, 149 rn3.genscan.LENGTH, 150 rn3.knownGene.LENGTH, 150 rn3.nscanGene.LENGTH, 151 rn3.refGene.LENGTH, 151 rn3.sgpGene.LENGTH, 152 rn3.xenoRefGene.LENGTH, 152 rn4.ensGene.LENGTH, 153 rn4.geneid.LENGTH, 154 rn4.geneSymbol.LENGTH, 153 rn4.genscan.LENGTH, 154 rn4.knownGene.LENGTH, 155 rn4.nscanGene.LENGTH, 155 rn4.refGene.LENGTH, 156 rn4.sgpGene.LENGTH, 156 rn4.xenoRefGene.LENGTH, 157

```
sacCerl.ensGene.LENGTH, 157
sacCer2.ensGene.LENGTH, 158
strPurl.geneSymbol.LENGTH, 158
strPurl.genscan.LENGTH, 159
strPurl.refGene.LENGTH, 159
strPurl.xenoRefGene.LENGTH, 160
strPur2.geneSymbol.LENGTH, 160
strPur2.refGene.LENGTH, 161
strPur2.refGene.LENGTH, 161
strPur2.xenoRefGene.LENGTH, 162
supportedGeneIDs, 50, 51, 162
supportedGenomes, 50, 51, 163
```

```
taeGut1.ensGene.LENGTH, 163
taeGut1.geneSymbol.LENGTH, 164
taeGut1.genscan.LENGTH, 164
taeGut1.nscanGene.LENGTH, 165
taeGut1.refGene.LENGTH, 165
taeGut1.xenoRefGene.LENGTH, 166
tetNig1.ensGene.LENGTH, 166
tetNig1.geneid.LENGTH, 167
tetNig1.genscan.LENGTH, 167
tetNig1.nscanGene.LENGTH, 168
tetNig2.ensGene.LENGTH, 168
```

```
unfactor, 169
```

```
xenTrol.genscan.LENGTH, 170
xenTro2.ensGene.LENGTH, 170
xenTro2.geneSymbol.LENGTH, 171
xenTro2.genscan.LENGTH, 171
xenTro2.refGene.LENGTH, 172
```