

Package ‘geneLenDataBase’

March 17, 2026

Title Lengths of mRNA transcripts for a number of genomes

Version 1.46.0

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

Depends R (>= 2.11.0)

Imports utils, rtracklayer, GenomicFeatures, txdbmaker

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

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

License LGPL (>= 2)

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Contents

| | |
|--------------------------------------|---|
| anoCar1.ensGene.LENGTH | 8 |
| anoCar1.genscan.LENGTH | 9 |
| anoCar1.xenoRefGene.LENGTH | 9 |

| | |
|--------------------------------------|----|
| anoGam1.ensGene.LENGTH | 10 |
| anoGam1.geneid.LENGTH | 10 |
| anoGam1.genscan.LENGTH | 11 |
| apiMel1.genscan.LENGTH | 11 |
| apiMel2.ensGene.LENGTH | 12 |
| apiMel2.geneid.LENGTH | 12 |
| apiMel2.genscan.LENGTH | 13 |
| aplCal1.xenoRefGene.LENGTH | 13 |
| bosTau2.geneid.LENGTH | 14 |
| bosTau2.geneSymbol.LENGTH | 14 |
| bosTau2.genscan.LENGTH | 15 |
| bosTau2.refGene.LENGTH | 15 |
| bosTau2.sgpGene.LENGTH | 16 |
| bosTau3.ensGene.LENGTH | 16 |
| bosTau3.geneid.LENGTH | 17 |
| bosTau3.geneSymbol.LENGTH | 17 |
| bosTau3.genscan.LENGTH | 18 |
| bosTau3.refGene.LENGTH | 18 |
| bosTau3.sgpGene.LENGTH | 19 |
| bosTau4.ensGene.LENGTH | 19 |
| bosTau4.geneSymbol.LENGTH | 20 |
| bosTau4.genscan.LENGTH | 20 |
| bosTau4.nscanGene.LENGTH | 21 |
| bosTau4.refGene.LENGTH | 21 |
| braFlo1.xenoRefGene.LENGTH | 22 |
| caeJap1.xenoRefGene.LENGTH | 22 |
| caePb1.xenoRefGene.LENGTH | 23 |
| caePb2.xenoRefGene.LENGTH | 23 |
| caeRem2.xenoRefGene.LENGTH | 24 |
| caeRem3.xenoRefGene.LENGTH | 24 |
| calJac1.genscan.LENGTH | 25 |
| calJac1.nscanGene.LENGTH | 25 |
| calJac1.xenoRefGene.LENGTH | 26 |
| canFam1.ensGene.LENGTH | 26 |
| canFam1.geneSymbol.LENGTH | 27 |
| canFam1.genscan.LENGTH | 27 |
| canFam1.nscanGene.LENGTH | 28 |
| canFam1.refGene.LENGTH | 28 |
| canFam1.xenoRefGene.LENGTH | 29 |
| canFam2.ensGene.LENGTH | 29 |
| canFam2.geneSymbol.LENGTH | 30 |
| canFam2.genscan.LENGTH | 30 |
| canFam2.nscanGene.LENGTH | 31 |
| canFam2.refGene.LENGTH | 31 |
| canFam2.xenoRefGene.LENGTH | 32 |
| cavPor3.ensGene.LENGTH | 32 |
| cavPor3.genscan.LENGTH | 33 |
| cavPor3.nscanGene.LENGTH | 33 |
| cavPor3.xenoRefGene.LENGTH | 34 |
| cb1.xenoRefGene.LENGTH | 34 |
| cb3.xenoRefGene.LENGTH | 35 |
| ce2.geneid.LENGTH | 35 |

| | |
|---|----|
| ce2.geneSymbol.LENGTH | 36 |
| ce2.refGene.LENGTH | 36 |
| ce4.geneSymbol.LENGTH | 37 |
| ce4.refGene.LENGTH | 37 |
| ce4.xenoRefGene.LENGTH | 38 |
| ce6.ensGene.LENGTH | 38 |
| ce6.geneSymbol.LENGTH | 39 |
| ce6.refGene.LENGTH | 39 |
| ce6.xenoRefGene.LENGTH | 40 |
| ci1.geneSymbol.LENGTH | 40 |
| ci1.refGene.LENGTH | 41 |
| ci1.xenoRefGene.LENGTH | 41 |
| ci2.ensGene.LENGTH | 42 |
| ci2.geneSymbol.LENGTH | 42 |
| ci2.refGene.LENGTH | 43 |
| ci2.xenoRefGene.LENGTH | 43 |
| danRer3.ensGene.LENGTH | 44 |
| danRer3.geneSymbol.LENGTH | 44 |
| danRer3.refGene.LENGTH | 45 |
| danRer4.ensGene.LENGTH | 45 |
| danRer4.geneSymbol.LENGTH | 46 |
| danRer4.genscan.LENGTH | 46 |
| danRer4.nscanGene.LENGTH | 47 |
| danRer4.refGene.LENGTH | 47 |
| danRer5.ensGene.LENGTH | 48 |
| danRer5.geneSymbol.LENGTH | 48 |
| danRer5.refGene.LENGTH | 49 |
| danRer5.vegaGene.LENGTH | 49 |
| danRer5.vegaPseudoGene.LENGTH | 50 |
| danRer6.ensGene.LENGTH | 50 |
| danRer6.geneSymbol.LENGTH | 51 |
| danRer6.refGene.LENGTH | 51 |
| danRer6.xenoRefGene.LENGTH | 52 |
| dm1.geneSymbol.LENGTH | 52 |
| dm1.genscan.LENGTH | 53 |
| dm1.refGene.LENGTH | 53 |
| dm2.geneid.LENGTH | 54 |
| dm2.geneSymbol.LENGTH | 54 |
| dm2.genscan.LENGTH | 55 |
| dm2.nscanGene.LENGTH | 55 |
| dm2.refGene.LENGTH | 56 |
| dm3.geneSymbol.LENGTH | 56 |
| dm3.nscanPasaGene.LENGTH | 57 |
| dm3.refGene.LENGTH | 57 |
| downloadLengthFromUCSC | 58 |
| dp2.genscan.LENGTH | 59 |
| dp2.xenoRefGene.LENGTH | 59 |
| dp3.geneid.LENGTH | 60 |
| dp3.genscan.LENGTH | 60 |
| dp3.xenoRefGene.LENGTH | 61 |
| droAna1.geneid.LENGTH | 61 |
| droAna1.genscan.LENGTH | 62 |

| | |
|--------------------------------------|----|
| droAna1.xenoRefGene.LENGTH | 62 |
| droAna2.genscan.LENGTH | 63 |
| droAna2.xenoRefGene.LENGTH | 63 |
| droEre1.genscan.LENGTH | 64 |
| droEre1.xenoRefGene.LENGTH | 64 |
| droGri1.genscan.LENGTH | 65 |
| droGri1.xenoRefGene.LENGTH | 65 |
| droMoj1.geneid.LENGTH | 66 |
| droMoj1.genscan.LENGTH | 66 |
| droMoj1.xenoRefGene.LENGTH | 67 |
| droMoj2.genscan.LENGTH | 67 |
| droMoj2.xenoRefGene.LENGTH | 68 |
| droPer1.genscan.LENGTH | 68 |
| droPer1.xenoRefGene.LENGTH | 69 |
| droSec1.genscan.LENGTH | 69 |
| droSec1.xenoRefGene.LENGTH | 70 |
| droSim1.geneid.LENGTH | 70 |
| droSim1.genscan.LENGTH | 71 |
| droSim1.xenoRefGene.LENGTH | 71 |
| droVir1.geneid.LENGTH | 72 |
| droVir1.genscan.LENGTH | 72 |
| droVir1.xenoRefGene.LENGTH | 73 |
| droVir2.genscan.LENGTH | 73 |
| droVir2.xenoRefGene.LENGTH | 74 |
| droYak1.geneid.LENGTH | 74 |
| droYak1.genscan.LENGTH | 75 |
| droYak1.xenoRefGene.LENGTH | 75 |
| droYak2.genscan.LENGTH | 76 |
| droYak2.xenoRefGene.LENGTH | 76 |
| equCab1.geneid.LENGTH | 77 |
| equCab1.geneSymbol.LENGTH | 77 |
| equCab1.nscanGene.LENGTH | 78 |
| equCab1.refGene.LENGTH | 78 |
| equCab1.sgpGene.LENGTH | 79 |
| equCab2.ensGene.LENGTH | 79 |
| equCab2.geneSymbol.LENGTH | 80 |
| equCab2.nscanGene.LENGTH | 80 |
| equCab2.refGene.LENGTH | 81 |
| equCab2.xenoRefGene.LENGTH | 81 |
| felCat3.ensGene.LENGTH | 82 |
| felCat3.geneid.LENGTH | 82 |
| felCat3.geneSymbol.LENGTH | 83 |
| felCat3.genscan.LENGTH | 83 |
| felCat3.nscanGene.LENGTH | 84 |
| felCat3.refGene.LENGTH | 84 |
| felCat3.sgpGene.LENGTH | 85 |
| felCat3.xenoRefGene.LENGTH | 85 |
| fr1.ensGene.LENGTH | 86 |
| fr1.genscan.LENGTH | 86 |
| fr2.ensGene.LENGTH | 87 |
| galGal2.ensGene.LENGTH | 87 |
| galGal2.geneid.LENGTH | 88 |

| | |
|--------------------------------------|-----|
| galGal2.geneSymbol.LENGTH | 88 |
| galGal2.genscan.LENGTH | 89 |
| galGal2.refGene.LENGTH | 89 |
| galGal2.sgpGene.LENGTH | 90 |
| galGal3.ensGene.LENGTH | 90 |
| galGal3.geneSymbol.LENGTH | 91 |
| galGal3.genscan.LENGTH | 91 |
| galGal3.nscanGene.LENGTH | 92 |
| galGal3.refGene.LENGTH | 92 |
| galGal3.xenoRefGene.LENGTH | 93 |
| gasAcu1.ensGene.LENGTH | 93 |
| gasAcu1.nscanGene.LENGTH | 94 |
| geneLenDatabase-pkg | 94 |
| hg16.acembly.LENGTH | 95 |
| hg16.ensGene.LENGTH | 95 |
| hg16.exoniphy.LENGTH | 96 |
| hg16.geneid.LENGTH | 96 |
| hg16.geneSymbol.LENGTH | 97 |
| hg16.genscan.LENGTH | 97 |
| hg16.knownGene.LENGTH | 98 |
| hg16.refGene.LENGTH | 98 |
| hg16.sgpGene.LENGTH | 99 |
| hg17.acembly.LENGTH | 99 |
| hg17.acescan.LENGTH | 100 |
| hg17.ccdsGene.LENGTH | 100 |
| hg17.ensGene.LENGTH | 101 |
| hg17.exoniphy.LENGTH | 101 |
| hg17.geneid.LENGTH | 102 |
| hg17.geneSymbol.LENGTH | 102 |
| hg17.genscan.LENGTH | 103 |
| hg17.knownGene.LENGTH | 103 |
| hg17.refGene.LENGTH | 104 |
| hg17.sgpGene.LENGTH | 104 |
| hg17.vegaGene.LENGTH | 105 |
| hg17.vegaPseudoGene.LENGTH | 105 |
| hg17.xenoRefGene.LENGTH | 106 |
| hg18.acembly.LENGTH | 106 |
| hg18.acescan.LENGTH | 107 |
| hg18.ccdsGene.LENGTH | 107 |
| hg18.ensGene.LENGTH | 108 |
| hg18.exoniphy.LENGTH | 108 |
| hg18.geneid.LENGTH | 109 |
| hg18.geneSymbol.LENGTH | 109 |
| hg18.genscan.LENGTH | 110 |
| hg18.knownGene.LENGTH | 110 |
| hg18.knownGeneOld3.LENGTH | 111 |
| hg18.refGene.LENGTH | 111 |
| hg18.sgpGene.LENGTH | 112 |
| hg18.sibGene.LENGTH | 112 |
| hg18.xenoRefGene.LENGTH | 113 |
| hg19.ccdsGene.LENGTH | 113 |
| hg19.ensGene.LENGTH | 114 |

| | |
|--------------------------------------|-----|
| hg19.exoniphy.LENGTH | 114 |
| hg19.geneSymbol.LENGTH | 115 |
| hg19.knownGene.LENGTH | 115 |
| hg19.nscanGene.LENGTH | 116 |
| hg19.refGene.LENGTH | 116 |
| hg19.xenoRefGene.LENGTH | 117 |
| loxAfr3.xenoRefGene.LENGTH | 117 |
| mm7.ensGene.LENGTH | 118 |
| mm7.geneid.LENGTH | 118 |
| mm7.geneSymbol.LENGTH | 119 |
| mm7.genscan.LENGTH | 119 |
| mm7.knownGene.LENGTH | 120 |
| mm7.refGene.LENGTH | 120 |
| mm7.sgpGene.LENGTH | 121 |
| mm7.xenoRefGene.LENGTH | 121 |
| mm8.ccdsGene.LENGTH | 122 |
| mm8.ensGene.LENGTH | 122 |
| mm8.geneid.LENGTH | 123 |
| mm8.geneSymbol.LENGTH | 123 |
| mm8.genscan.LENGTH | 124 |
| mm8.knownGene.LENGTH | 124 |
| mm8.nscanGene.LENGTH | 125 |
| mm8.refGene.LENGTH | 125 |
| mm8.sgpGene.LENGTH | 126 |
| mm8.sibGene.LENGTH | 126 |
| mm8.xenoRefGene.LENGTH | 127 |
| mm9.acembly.LENGTH | 127 |
| mm9.ccdsGene.LENGTH | 128 |
| mm9.ensGene.LENGTH | 128 |
| mm9.exoniphy.LENGTH | 129 |
| mm9.geneid.LENGTH | 129 |
| mm9.geneSymbol.LENGTH | 130 |
| mm9.genscan.LENGTH | 130 |
| mm9.knownGene.LENGTH | 131 |
| mm9.nscanGene.LENGTH | 131 |
| mm9.refGene.LENGTH | 132 |
| mm9.sgpGene.LENGTH | 132 |
| mm9.xenoRefGene.LENGTH | 133 |
| monDom1.genscan.LENGTH | 133 |
| monDom4.ensGene.LENGTH | 134 |
| monDom4.geneSymbol.LENGTH | 134 |
| monDom4.genscan.LENGTH | 135 |
| monDom4.nscanGene.LENGTH | 135 |
| monDom4.refGene.LENGTH | 136 |
| monDom4.xenoRefGene.LENGTH | 136 |
| monDom5.ensGene.LENGTH | 137 |
| monDom5.geneSymbol.LENGTH | 137 |
| monDom5.genscan.LENGTH | 138 |
| monDom5.nscanGene.LENGTH | 138 |
| monDom5.refGene.LENGTH | 139 |
| monDom5.xenoRefGene.LENGTH | 139 |
| ornAna1.ensGene.LENGTH | 140 |

| | |
|--------------------------------------|-----|
| ornAna1.geneSymbol.LENGTH | 140 |
| ornAna1.refGene.LENGTH | 141 |
| ornAna1.xenoRefGene.LENGTH | 141 |
| oryLat2.ensGene.LENGTH | 142 |
| oryLat2.geneSymbol.LENGTH | 142 |
| oryLat2.refGene.LENGTH | 143 |
| oryLat2.xenoRefGene.LENGTH | 143 |
| panTro1.ensGene.LENGTH | 144 |
| panTro1.geneid.LENGTH | 144 |
| panTro1.genscan.LENGTH | 145 |
| panTro1.xenoRefGene.LENGTH | 145 |
| panTro2.ensGene.LENGTH | 146 |
| panTro2.geneSymbol.LENGTH | 146 |
| panTro2.genscan.LENGTH | 147 |
| panTro2.nscanGene.LENGTH | 147 |
| panTro2.refGene.LENGTH | 148 |
| panTro2.xenoRefGene.LENGTH | 148 |
| petMar1.xenoRefGene.LENGTH | 149 |
| ponAbe2.ensGene.LENGTH | 149 |
| ponAbe2.geneSymbol.LENGTH | 150 |
| ponAbe2.genscan.LENGTH | 150 |
| ponAbe2.nscanGene.LENGTH | 151 |
| ponAbe2.refGene.LENGTH | 151 |
| ponAbe2.xenoRefGene.LENGTH | 152 |
| priPac1.xenoRefGene.LENGTH | 152 |
| rheMac2.ensGene.LENGTH | 153 |
| rheMac2.geneid.LENGTH | 153 |
| rheMac2.geneSymbol.LENGTH | 154 |
| rheMac2.nscanGene.LENGTH | 154 |
| rheMac2.refGene.LENGTH | 155 |
| rheMac2.sgpGene.LENGTH | 155 |
| rheMac2.xenoRefGene.LENGTH | 156 |
| rn3.ensGene.LENGTH | 156 |
| rn3.geneid.LENGTH | 157 |
| rn3.geneSymbol.LENGTH | 157 |
| rn3.genscan.LENGTH | 158 |
| rn3.knownGene.LENGTH | 158 |
| rn3.nscanGene.LENGTH | 159 |
| rn3.refGene.LENGTH | 159 |
| rn3.sgpGene.LENGTH | 160 |
| rn3.xenoRefGene.LENGTH | 160 |
| rn4.ensGene.LENGTH | 161 |
| rn4.geneid.LENGTH | 161 |
| rn4.geneSymbol.LENGTH | 162 |
| rn4.genscan.LENGTH | 162 |
| rn4.knownGene.LENGTH | 163 |
| rn4.nscanGene.LENGTH | 163 |
| rn4.refGene.LENGTH | 164 |
| rn4.sgpGene.LENGTH | 164 |
| rn4.xenoRefGene.LENGTH | 165 |
| sacCer1.ensGene.LENGTH | 165 |
| sacCer2.ensGene.LENGTH | 166 |

| | |
|--------------------------------------|-----|
| strPur1.geneSymbol.LENGTH | 166 |
| strPur1.genscan.LENGTH | 167 |
| strPur1.refGene.LENGTH | 167 |
| strPur1.xenoRefGene.LENGTH | 168 |
| strPur2.geneSymbol.LENGTH | 168 |
| strPur2.genscan.LENGTH | 169 |
| strPur2.refGene.LENGTH | 169 |
| strPur2.xenoRefGene.LENGTH | 170 |
| supportedGeneIDs | 170 |
| supportedGenomes | 171 |
| taeGut1.ensGene.LENGTH | 171 |
| taeGut1.geneSymbol.LENGTH | 172 |
| taeGut1.genscan.LENGTH | 172 |
| taeGut1.nscanGene.LENGTH | 173 |
| taeGut1.refGene.LENGTH | 173 |
| taeGut1.xenoRefGene.LENGTH | 174 |
| tetNig1.ensGene.LENGTH | 174 |
| tetNig1.geneid.LENGTH | 175 |
| tetNig1.genscan.LENGTH | 175 |
| tetNig1.nscanGene.LENGTH | 176 |
| tetNig2.ensGene.LENGTH | 176 |
| unfactor | 177 |
| xenTro1.genscan.LENGTH | 178 |
| xenTro2.ensGene.LENGTH | 178 |
| xenTro2.geneSymbol.LENGTH | 179 |
| xenTro2.genscan.LENGTH | 179 |
| xenTro2.refGene.LENGTH | 180 |

Index 181

anoCar1.ensGene.LENGTH

Transcript length data for the organism anoCar

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
anoCar1.genscan.LENGTH
```

Transcript length data for the organism anoCar

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
anoCar1.xenoRefGene.LENGTH
```

Transcript length data for the organism anoCar

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
anoGam1.ensGene.LENGTH
```

Transcript length data for the organism anoGam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
anoGam1.geneid.LENGTH
```

Transcript length data for the organism anoGam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
anoGam1.genscan.LENGTH
```

Transcript length data for the organism anoGam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
apiMel1.genscan.LENGTH
```

Transcript length data for the organism apiMel

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
apiMel2.ensGene.LENGTH
```

Transcript length data for the organism apiMel

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
apiMel2.geneid.LENGTH
```

Transcript length data for the organism apiMel

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
apiMel2.genscan.LENGTH
```

Transcript length data for the organism apiMel

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
aplCal1.xenoRefGene.LENGTH
```

Transcript length data for the organism aplCal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau2.sgpGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.ensGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.genscan.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau3.refGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.geneSymbol.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.genscan.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.nscanGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
bosTau4.refGene.LENGTH
```

Transcript length data for the organism bosTau

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
braFlo1.xenoRefGene.LENGTH
```

Transcript length data for the organism braFlo

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caeJap1.xenoRefGene.LENGTH
```

Transcript length data for the organism caeJap

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caePb1.xenoRefGene.LENGTH
```

Transcript length data for the organism caePb

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caePb2.xenoRefGene.LENGTH
```

Transcript length data for the organism caePb

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caeRem2.xenoRefGene.LENGTH
```

Transcript length data for the organism caeRem

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
caeRem3.xenoRefGene.LENGTH
```

Transcript length data for the organism caeRem

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

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

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

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

Description

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

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

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

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

```
calJac1.xenoRefGene.LENGTH
```

Transcript length data for the organism calJac

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
canFam1.ensGene.LENGTH
```

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

canFam1.nscanGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

canFam1.refGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
canFam1.xenoRefGene.LENGTH
```

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
canFam2.ensGene.LENGTH
```

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
canFam2.geneSymbol.LENGTH
```

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
canFam2.genscan.LENGTH
```

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
canFam2.nscanGene.LENGTH
```

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
canFam2.refGene.LENGTH
```

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
canFam2.xenoRefGene.LENGTH
```

Transcript length data for the organism canFam

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
cavPor3.ensGene.LENGTH
```

Transcript length data for the organism cavPor

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
cavPor3.genscan.LENGTH
```

Transcript length data for the organism cavPor

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
cavPor3.nscanGene.LENGTH
```

Transcript length data for the organism cavPor

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
cavPor3.xenoRefGene.LENGTH
```

Transcript length data for the organism cavPor

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
cb1.xenoRefGene.LENGTH
```

Transcript length data for the organism cb

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

`ce2.geneid.LENGTH`*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.geneSymbol1.LENGTH *Transcript length data for the organism ce*

Description

ce2.geneSymbol1.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

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

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ce2.geneSymbol1.LENGTH)
head(ce2.geneSymbol1.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/cgi-bin/hgTables>) using the geneSymbol table.

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
ce4.xenoRefGene.LENGTH
```

Transcript length data for the organism ce

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
ce6.ensGene.LENGTH
```

Transcript length data for the organism ce

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[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/cgi-bin/hgTables>) using the xenoRefGene table.

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer3.ensGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer3.geneSymbol.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer3.refGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer4.ensGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer4.geneSymbol.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer4.genscan.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

danRer5.ensGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

danRer5.geneSymbol.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer5.refGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer5.vegaGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer5.vegaPseudoGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer6.ensGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer6.geneSymbol.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer6.refGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
danRer6.xenoRefGene.LENGTH
```

Transcript length data for the organism danRer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
dm1.geneSymbol.LENGTH
```

Transcript length data for the organism dm

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

`downloadLengthFromUCSC`*Download Transcript Length Data*

Description

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

Usage

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

Arguments

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

Details

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

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

Value

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

Note

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

Author(s)

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See Also

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

Examples

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

## End(Not run)
```

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
dp3.xenoRefGene.LENGTH
```

Transcript length data for the organism dp

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droAna1.geneid.LENGTH
```

Transcript length data for the organism droAna

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

droAna1.genscan.LENGTH

Transcript length data for the organism droAna

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

droAna1.xenoRefGene.LENGTH

Transcript length data for the organism droAna

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droEre1.genscan.LENGTH
```

Transcript length data for the organism droEre

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droEre1.xenoRefGene.LENGTH
```

Transcript length data for the organism droEre

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droGri1.genscan.LENGTH
```

Transcript length data for the organism droGri

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droGri1.xenoRefGene.LENGTH
```

Transcript length data for the organism droGri

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droMoj1.xenoRefGene.LENGTH
```

Transcript length data for the organism droMoj

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droMoj2.genscan.LENGTH
```

Transcript length data for the organism droMoj

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droMoj2.xenoRefGene.LENGTH
```

Transcript length data for the organism droMoj

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droPer1.genscan.LENGTH
```

Transcript length data for the organism droPer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droPer1.xenoRefGene.LENGTH
```

Transcript length data for the organism droPer

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droSec1.genscan.LENGTH
```

Transcript length data for the organism droSec

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droSec1.xenoRefGene.LENGTH
```

Transcript length data for the organism droSec

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droSim1.geneid.LENGTH
```

Transcript length data for the organism droSim

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droSim1.genscan.LENGTH
```

Transcript length data for the organism droSim

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droSim1.xenoRefGene.LENGTH
```

Transcript length data for the organism droSim

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droYak1.genscan.LENGTH
```

Transcript length data for the organism droYak

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droYak1.xenoRefGene.LENGTH
```

Transcript length data for the organism droYak

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droYak2.genscan.LENGTH
```

Transcript length data for the organism droYak

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
droYak2.xenoRefGene.LENGTH
```

Transcript length data for the organism droYak

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

equCab1.nscanGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

equCab1.refGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
equCab1 . sgpGene . LENGTH
```

Transcript length data for the organism equCab

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
equCab2 . ensGene . LENGTH
```

Transcript length data for the organism equCab

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
equCab2.geneSymbol.LENGTH
```

Transcript length data for the organism equCab

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
equCab2.nscanGene.LENGTH
```

Transcript length data for the organism equCab

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
equCab2.refGene.LENGTH
```

Transcript length data for the organism equCab

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
equCab2.xenoRefGene.LENGTH
```

Transcript length data for the organism equCab

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
felCat3.ensGene.LENGTH
```

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
felCat3.geneid.LENGTH
```

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
felCat3.geneSymbol.LENGTH
```

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
felCat3.genscan.LENGTH
```

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
felCat3.nscanGene.LENGTH
```

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
felCat3.refGene.LENGTH
```

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
felCat3.sgpGene.LENGTH
```

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
felCat3.xenoRefGene.LENGTH
```

Transcript length data for the organism felCat

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
galGal2.genscan.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
galGal2.refGene.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
galGal2.sgpGene.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
galGal3.ensGene.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
galGal3.geneSymbol.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
galGal3.genscan.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
galGal3.nscanGene.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
galGal3.refGene.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
galGal3.xenoRefGene.LENGTH
```

Transcript length data for the organism galGal

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
gasAcu1.ensGene.LENGTH
```

Transcript length data for the organism gasAcu

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

gasAcu1.nscanGene.LENGTH

Transcript length data for the organism gasAcu

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

geneLenDatabase-pkg *geneLenDatabase:*

Description

Lengths of mRNA transcripts for a number of genomes

Details

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

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See Also

Useful links:

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
hg16.geneSymbol.LENGTH
```

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
hg16.genscan.LENGTH
```

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg17.xenoRefGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
hg18.xenoRefGene.LENGTH
```

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
hg19.ccdsGene.LENGTH
```

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg19.ensGene.LENGTH *Transcript length data for the organism hg*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg19.exoniphy.LENGTH *Transcript length data for the organism hg*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
hg19.geneSymbol.LENGTH
```

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

```
hg19.knownGene.LENGTH
```

Transcript length data for the organism hg

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg19.nscanGene.LENGTH *Transcript length data for the organism hg*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

hg19.refGene.LENGTH *Transcript length data for the organism hg*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

`hg19.xenoRefGene.LENGTH`*Transcript length data for the organism hg*

Description

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

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

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

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

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

Description

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

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

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

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

mm7.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

mm7.knownGene.LENGTH *Transcript length data for the organism mm*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

mm7.xenoRefGene.LENGTH *Transcript length data for the organism mm*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

mm8.ccdsGene.LENGTH *Transcript length data for the organism mm*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

mm8.geneid.LENGTH *Transcript length data for the organism mm*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

mm8.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

mm8.knownGene.LENGTH *Transcript length data for the organism mm*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

mm8.nscanGene.LENGTH *Transcript length data for the organism mm*

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

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

See Also

[downloadLengthFromUCSC](#)

Examples

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

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

Description

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

The data file was made by calling `downloadLengthFromUCSC(mm8, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.sgpGene.LENGTH)
head(mm8.sgpGene.LENGTH)
```

mm8.sibGene.LENGTH *Transcript length data for the organism mm*

Description

mm8.sibGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sibGene table.

The data file was made by calling `downloadLengthFromUCSC(mm8, sibGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.sibGene.LENGTH)
head(mm8.sibGene.LENGTH)
```

`mm8.xenoRefGene.LENGTH`*Transcript length data for the organism mm*

Description

`mm8.xenoRefGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `xenoRefGene` table.

The data file was made by calling `downloadLengthFromUCSC(mm8, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm8.xenoRefGene.LENGTH)
head(mm8.xenoRefGene.LENGTH)
```

`mm9.acembly.LENGTH`*Transcript length data for the organism mm*

Description

`mm9.acembly.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `acembly` table.

The data file was made by calling `downloadLengthFromUCSC(mm9, acembly)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.acembly.LENGTH)
head(mm9.acembly.LENGTH)
```

mm9.ccdsGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.ccdsGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ccdsGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ccdsGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.ccdsGene.LENGTH)
head(mm9.ccdsGene.LENGTH)
```

mm9.ensGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.ensGene.LENGTH)
head(mm9.ensGene.LENGTH)
```

mm9.exoniphy.LENGTH *Transcript length data for the organism mm*

Description

mm9.exoniphy.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the exoniphy table.

The data file was made by calling `downloadLengthFromUCSC(mm9, exoniphy)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.exoniphy.LENGTH)
head(mm9.exoniphy.LENGTH)
```

mm9.geneid.LENGTH *Transcript length data for the organism mm*

Description

mm9.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.geneid.LENGTH)
head(mm9.geneid.LENGTH)
```

mm9.geneSymbol.LENGTH *Transcript length data for the organism mm*

Description

mm9.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(mm9, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.geneSymbol.LENGTH)
head(mm9.geneSymbol.LENGTH)
```

mm9.genscan.LENGTH *Transcript length data for the organism mm*

Description

mm9.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(mm9, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.genscan.LENGTH)
head(mm9.genscan.LENGTH)
```

mm9.knownGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.knownGene.LENGTH)
head(mm9.knownGene.LENGTH)
```

mm9.nscanGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.nscanGene.LENGTH)
head(mm9.nscanGene.LENGTH)
```

mm9.refGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.refGene.LENGTH)
head(mm9.refGene.LENGTH)
```

mm9.sgpGene.LENGTH *Transcript length data for the organism mm*

Description

mm9.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.sgpGene.LENGTH)
head(mm9.sgpGene.LENGTH)
```

```
mm9.xenoRefGene.LENGTH
```

Transcript length data for the organism mm

Description

mm9.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(mm9, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(mm9.xenoRefGene.LENGTH)
head(mm9.xenoRefGene.LENGTH)
```

```
monDom1.genscan.LENGTH
```

Transcript length data for the organism monDom

Description

monDom1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(monDom1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom1.genscan.LENGTH)
head(monDom1.genscan.LENGTH)
```

```
monDom4.ensGene.LENGTH
```

Transcript length data for the organism monDom

Description

monDom4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.ensGene.LENGTH)
head(monDom4.ensGene.LENGTH)
```

```
monDom4.geneSymbol.LENGTH
```

Transcript length data for the organism monDom

Description

monDom4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.geneSymbol.LENGTH)
head(monDom4.geneSymbol.LENGTH)
```

`monDom4.genscan.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.genscan.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `genscan` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.genscan.LENGTH)
head(monDom4.genscan.LENGTH)
```

`monDom4.nscanGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom4.nscanGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `nscanGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.nscanGene.LENGTH)
head(monDom4.nscanGene.LENGTH)
```

```
monDom4.refGene.LENGTH
```

Transcript length data for the organism monDom

Description

monDom4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.refGene.LENGTH)
head(monDom4.refGene.LENGTH)
```

```
monDom4.xenoRefGene.LENGTH
```

Transcript length data for the organism monDom

Description

monDom4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom4, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom4.xenoRefGene.LENGTH)
head(monDom4.xenoRefGene.LENGTH)
```

`monDom5.ensGene.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.ensGene.LENGTH)
head(monDom5.ensGene.LENGTH)
```

`monDom5.geneSymbol.LENGTH`*Transcript length data for the organism monDom*

Description

`monDom5.geneSymbol.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `geneSymbol` table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.geneSymbol.LENGTH)
head(monDom5.geneSymbol.LENGTH)
```

monDom5.genscan.LENGTH

Transcript length data for the organism monDom

Description

monDom5.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.genscan.LENGTH)
head(monDom5.genscan.LENGTH)
```

monDom5.nscanGene.LENGTH

Transcript length data for the organism monDom

Description

monDom5.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)
```

```
monDom5.refGene.LENGTH
```

Transcript length data for the organism monDom

Description

monDom5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)
```

```
monDom5.xenoRefGene.LENGTH
```

Transcript length data for the organism monDom

Description

monDom5.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(monDom5, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(monDom5.xenoRefGene.LENGTH)
head(monDom5.xenoRefGene.LENGTH)
```

```
ornAna1.ensGene.LENGTH
```

Transcript length data for the organism ornAna

Description

ornAna1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.ensGene.LENGTH)
head(ornAna1.ensGene.LENGTH)
```

```
ornAna1.geneSymbol.LENGTH
```

Transcript length data for the organism ornAna

Description

ornAna1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.geneSymbol.LENGTH)
head(ornAna1.geneSymbol.LENGTH)
```

```
ornAna1.refGene.LENGTH
```

Transcript length data for the organism ornAna

Description

ornAna1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.refGene.LENGTH)
head(ornAna1.refGene.LENGTH)
```

```
ornAna1.xenoRefGene.LENGTH
```

Transcript length data for the organism ornAna

Description

ornAna1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(ornAna1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ornAna1.xenoRefGene.LENGTH)
head(ornAna1.xenoRefGene.LENGTH)
```

```
oryLat2.ensGene.LENGTH
```

Transcript length data for the organism oryLat

Description

oryLat2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)
```

```
oryLat2.geneSymbol.LENGTH
```

Transcript length data for the organism oryLat

Description

oryLat2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)
```

```
oryLat2.refGene.LENGTH
```

Transcript length data for the organism oryLat

Description

oryLat2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)
```

```
oryLat2.xenoRefGene.LENGTH
```

Transcript length data for the organism oryLat

Description

oryLat2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(oryLat2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)
```

```
panTro1.ensGene.LENGTH
```

Transcript length data for the organism panTro

Description

panTro1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.ensGene.LENGTH)
head(panTro1.ensGene.LENGTH)
```

```
panTro1.geneid.LENGTH
```

Transcript length data for the organism panTro

Description

panTro1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.geneid.LENGTH)
head(panTro1.geneid.LENGTH)
```

```
panTro1.genscan.LENGTH
```

Transcript length data for the organism panTro

Description

panTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.genscan.LENGTH)
head(panTro1.genscan.LENGTH)
```

```
panTro1.xenoRefGene.LENGTH
```

Transcript length data for the organism panTro

Description

panTro1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro1.xenoRefGene.LENGTH)
head(panTro1.xenoRefGene.LENGTH)
```

```
panTro2.ensGene.LENGTH
```

Transcript length data for the organism panTro

Description

panTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)
```

```
panTro2.geneSymbol.LENGTH
```

Transcript length data for the organism panTro

Description

panTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)
```

```
panTro2.genscan.LENGTH
```

Transcript length data for the organism panTro

Description

panTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.genscan.LENGTH)
head(panTro2.genscan.LENGTH)
```

```
panTro2.nscanGene.LENGTH
```

Transcript length data for the organism panTro

Description

panTro2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.nscanGene.LENGTH)
head(panTro2.nscanGene.LENGTH)
```

```
panTro2.refGene.LENGTH
```

Transcript length data for the organism panTro

Description

panTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.refGene.LENGTH)
head(panTro2.refGene.LENGTH)
```

```
panTro2.xenoRefGene.LENGTH
```

Transcript length data for the organism panTro

Description

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(panTro2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(panTro2.xenoRefGene.LENGTH)
head(panTro2.xenoRefGene.LENGTH)
```

```
petMar1.xenoRefGene.LENGTH
```

Transcript length data for the organism petMar

Description

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(petMar1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)
```

```
ponAbe2.ensGene.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)
```

```
ponAbe2.geneSymbol.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)
```

```
ponAbe2.genscan.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)
```

```
ponAbe2.nscanGene.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.nscanGene.LENGTH)
head(ponAbe2.nscanGene.LENGTH)
```

```
ponAbe2.refGene.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.refGene.LENGTH)
head(ponAbe2.refGene.LENGTH)
```

```
ponAbe2.xenoRefGene.LENGTH
```

Transcript length data for the organism ponAbe

Description

ponAbe2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(ponAbe2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)
```

```
priPac1.xenoRefGene.LENGTH
```

Transcript length data for the organism priPac

Description

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(priPac1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)
```

```
rheMac2.ensGene.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)
```

```
rheMac2.geneid.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.geneid.LENGTH)
head(rheMac2.geneid.LENGTH)
```

```
rheMac2.geneSymbol.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)
```

```
rheMac2.nscanGene.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)
```

`rheMac2.refGene.LENGTH`*Transcript length data for the organism rheMac*

Description

rheMac2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)
```

`rheMac2.sgpGene.LENGTH`*Transcript length data for the organism rheMac*

Description

rheMac2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.sgpGene.LENGTH)
head(rheMac2.sgpGene.LENGTH)
```

```
rheMac2.xenoRefGene.LENGTH
```

Transcript length data for the organism rheMac

Description

rheMac2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rheMac2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)
```

```
rn3.ensGene.LENGTH
```

Transcript length data for the organism rn

Description

rn3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.ensGene.LENGTH)
head(rn3.ensGene.LENGTH)
```

rn3.geneid.LENGTH *Transcript length data for the organism rn*

Description

rn3.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.geneid.LENGTH)
head(rn3.geneid.LENGTH)
```

rn3.geneSymbol.LENGTH *Transcript length data for the organism rn*

Description

rn3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn3, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.geneSymbol.LENGTH)
head(rn3.geneSymbol.LENGTH)
```

rn3.genscan.LENGTH *Transcript length data for the organism rn*

Description

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn3, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)
```

rn3.knownGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

rn3.nscanGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)
```

rn3.refGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

rn3.sgpGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)
```

rn3.xenoRefGene.LENGTH *Transcript length data for the organism rn*

Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn3, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)
```

rn4.ensGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)
```

rn4.geneid.LENGTH *Transcript length data for the organism rn*

Description

rn4.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```

rn4.geneSymbol.LENGTH *Transcript length data for the organism rn*

Description

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(rn4, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

rn4.genscan.LENGTH *Transcript length data for the organism rn*

Description

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(rn4, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

rn4.knownGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the knownGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, knownGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.knownGene.LENGTH)
head(rn4.knownGene.LENGTH)
```

rn4.nscanGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)
```

rn4.refGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)
```

rn4.sgpGene.LENGTH *Transcript length data for the organism rn*

Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the sgpGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, sgpGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

`rn4.xenoRefGene.LENGTH`*Transcript length data for the organism rn*

Description

rn4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(rn4, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(rn4.xenoRefGene.LENGTH)
head(rn4.xenoRefGene.LENGTH)
```

`sacCer1.ensGene.LENGTH`*Transcript length data for the organism sacCer*

Description

sacCer1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(sacCer1.ensGene.LENGTH)
head(sacCer1.ensGene.LENGTH)
```

sacCer2.ensGene.LENGTH

Transcript length data for the organism sacCer

Description

sacCer2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(sacCer2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)
```

strPur1.geneSymbol.LENGTH

Transcript length data for the organism strPur

Description

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)
```

```
strPur1.genscan.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.genscan.LENGTH)
head(strPur1.genscan.LENGTH)
```

```
strPur1.refGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.refGene.LENGTH)
head(strPur1.refGene.LENGTH)
```

```
strPur1.xenoRefGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur1.xenoRefGene.LENGTH)
head(strPur1.xenoRefGene.LENGTH)
```

```
strPur2.geneSymbol.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.geneSymbol.LENGTH)
head(strPur2.geneSymbol.LENGTH)
```

```
strPur2.genscan.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.genscan.LENGTH)
head(strPur2.genscan.LENGTH)
```

```
strPur2.refGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.refGene.LENGTH)
head(strPur2.refGene.LENGTH)
```

```
strPur2.xenoRefGene.LENGTH
```

Transcript length data for the organism strPur

Description

strPur2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(strPur2, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)
```

```
supportedGeneIDs
```

Supported Gene IDs

Description

Lists supported gene ID formats

Usage

```
supportedGeneIDs()
```

Details

Uses the `supportedUCSCTables` function from the `GenomicFeatures` package to obtain a list of gene ID formats available from the UCSC genome browser. The `db` column gives the gene ID formats which are provided to the `id` argument of various functions. The `track` and `subtrack` columns are the names of the UCSC track/subtrack from which information is fetched.

The `GeneID` column lists the "full name" of the gene ID format where available.

The final column, headed `AvailableGenomes` lists the genomes for which there is a local copy of the length information available for the gene ID format listed in the `geneLenDataBase` package.

Value

A data.frame containing supported gene ID formats.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
supportedGeneIDs()
```

| | |
|------------------|--------------------------|
| supportedGenomes | <i>Supported Genomes</i> |
|------------------|--------------------------|

Description

Lists supported genomes

Usage

```
supportedGenomes()
```

Details

Uses the `ucscGenomes()` function from the `rtracklayer` package to obtain a list of genomes available from the UCSC genome browser. The `db` column lists genomes as they are provided to the genome argument of various functions.

The final column, headed `AvailableGeneIDs` lists the gene ID formats for which there is a local copy of the length information available for the genome listed in the `geneLenDataBase` package.

Value

A data.frame containing supported genomes.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
supportedGenomes()
```

| | |
|-------------------------------------|---|
| <code>taeGut1.ensGene.LENGTH</code> | <i>Transcript length data for the organism taeGut</i> |
|-------------------------------------|---|

Description

`taeGut1.ensGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `ensGene` table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)
```

```
taeGut1.geneSymbol.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)
```

```
taeGut1.genscan.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)
```

```
taeGut1.nscanGene.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)
```

```
taeGut1.refGene.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the refGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)
```

```
taeGut1.xenoRefGene.LENGTH
```

Transcript length data for the organism taeGut

Description

taeGut1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the xenoRefGene table.

The data file was made by calling `downloadLengthFromUCSC(taeGut1, xenoRefGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)
```

```
tetNig1.ensGene.LENGTH
```

Transcript length data for the organism tetNig

Description

tetNig1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.ensGene.LENGTH)
head(tetNig1.ensGene.LENGTH)
```

tetNig1.geneid.LENGTH *Transcript length data for the organism tetNig*

Description

tetNig1.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneid table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, geneid)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.geneid.LENGTH)
head(tetNig1.geneid.LENGTH)
```

tetNig1.genscan.LENGTH
Transcript length data for the organism tetNig

Description

tetNig1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.genscan.LENGTH)
head(tetNig1.genscan.LENGTH)
```

```
tetNig1.nscanGene.LENGTH
```

Transcript length data for the organism tetNig

Description

tetNig1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the nscanGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig1, nscanGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig1.nscanGene.LENGTH)
head(tetNig1.nscanGene.LENGTH)
```

```
tetNig2.ensGene.LENGTH
```

Transcript length data for the organism tetNig

Description

tetNig2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(tetNig2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(tetNig2.ensGene.LENGTH)
head(tetNig2.ensGene.LENGTH)
```

`unfactor`*Purge factors*

Description

Removes all factors from a variable in a sensible way.

Usage

```
unfactor(var)
```

Arguments

`var` The variable from which you want the factors removed.

Details

As factors are their own type, to remove factors we must convert each level into another type. This is currently done using "typeless" behaviour: a factor is converted to a numeric vector if this can be done without inducing NAs, otherwise it is coerced using `as.character`. Currently supported types are: `factor`, `data.frame` and `list`.

Value

The variable with all factors converted to characters or numbers (see details).

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
# A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep='.')
x
unfactor(x)

# A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"),
                score <- factor(c(9, 7, 8, 9)), stringsAsFactors=TRUE)
x$player
x$score
y <- unfactor(x)
y$player
y$score
```

```
xenTro1.genscan.LENGTH
```

Transcript length data for the organism xenTro

Description

xenTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(xenTro1, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro1.genscan.LENGTH)
head(xenTro1.genscan.LENGTH)
```

```
xenTro2.ensGene.LENGTH
```

Transcript length data for the organism xenTro

Description

xenTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the ensGene table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, ensGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.ensGene.LENGTH)
head(xenTro2.ensGene.LENGTH)
```

```
xenTro2.geneSymbol.LENGTH
```

Transcript length data for the organism xenTro

Description

xenTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the geneSymbol table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, geneSymbol)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.geneSymbol.LENGTH)
head(xenTro2.geneSymbol.LENGTH)
```

```
xenTro2.genscan.LENGTH
```

Transcript length data for the organism xenTro

Description

xenTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the genscan table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, genscan)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.genscan.LENGTH)
head(xenTro2.genscan.LENGTH)
```

`xenTro2.refGene.LENGTH`*Transcript length data for the organism xenTro*

Description

`xenTro2.refGene.LENGTH` is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (<http://genome.ucsc.edu/cgi-bin/hgTables>) using the `refGene` table.

The data file was made by calling `downloadLengthFromUCSC(xenTro2, refGene)` on the date on which the package was last updated.

See Also

[downloadLengthFromUCSC](#)

Examples

```
data(xenTro2.refGene.LENGTH)
head(xenTro2.refGene.LENGTH)
```

Index

* datasets

anoCar1.ensGene.LENGTH, 8
anoCar1.genscan.LENGTH, 9
anoCar1.xenoRefGene.LENGTH, 9
anoGam1.ensGene.LENGTH, 10
anoGam1.geneid.LENGTH, 10
anoGam1.genscan.LENGTH, 11
apiMe11.genscan.LENGTH, 11
apiMe12.ensGene.LENGTH, 12
apiMe12.geneid.LENGTH, 12
apiMe12.genscan.LENGTH, 13
aplCa11.xenoRefGene.LENGTH, 13
bosTau2.geneid.LENGTH, 14
bosTau2.geneSymbol.LENGTH, 14
bosTau2.genscan.LENGTH, 15
bosTau2.refGene.LENGTH, 15
bosTau2.sgpGene.LENGTH, 16
bosTau3.ensGene.LENGTH, 16
bosTau3.geneid.LENGTH, 17
bosTau3.geneSymbol.LENGTH, 17
bosTau3.genscan.LENGTH, 18
bosTau3.refGene.LENGTH, 18
bosTau3.sgpGene.LENGTH, 19
bosTau4.ensGene.LENGTH, 19
bosTau4.geneSymbol.LENGTH, 20
bosTau4.genscan.LENGTH, 20
bosTau4.nscanGene.LENGTH, 21
bosTau4.refGene.LENGTH, 21
braFlo1.xenoRefGene.LENGTH, 22
caeJap1.xenoRefGene.LENGTH, 22
caePb1.xenoRefGene.LENGTH, 23
caePb2.xenoRefGene.LENGTH, 23
caeRem2.xenoRefGene.LENGTH, 24
caeRem3.xenoRefGene.LENGTH, 24
calJac1.genscan.LENGTH, 25
calJac1.nscanGene.LENGTH, 25
calJac1.xenoRefGene.LENGTH, 26
canFam1.ensGene.LENGTH, 26
canFam1.geneSymbol.LENGTH, 27
canFam1.genscan.LENGTH, 27
canFam1.nscanGene.LENGTH, 28
canFam1.refGene.LENGTH, 28
canFam1.xenoRefGene.LENGTH, 29
canFam2.ensGene.LENGTH, 29
canFam2.geneSymbol.LENGTH, 30
canFam2.genscan.LENGTH, 30
canFam2.nscanGene.LENGTH, 31
canFam2.refGene.LENGTH, 31
canFam2.xenoRefGene.LENGTH, 32
cavPor3.ensGene.LENGTH, 32
cavPor3.genscan.LENGTH, 33
cavPor3.nscanGene.LENGTH, 33
cavPor3.xenoRefGene.LENGTH, 34
cb1.xenoRefGene.LENGTH, 34
cb3.xenoRefGene.LENGTH, 35
ce2.geneid.LENGTH, 35
ce2.geneSymbol.LENGTH, 36
ce2.refGene.LENGTH, 36
ce4.geneSymbol.LENGTH, 37
ce4.refGene.LENGTH, 37
ce4.xenoRefGene.LENGTH, 38
ce6.ensGene.LENGTH, 38
ce6.geneSymbol.LENGTH, 39
ce6.refGene.LENGTH, 39
ce6.xenoRefGene.LENGTH, 40
ci1.geneSymbol.LENGTH, 40
ci1.refGene.LENGTH, 41
ci1.xenoRefGene.LENGTH, 41
ci2.ensGene.LENGTH, 42
ci2.geneSymbol.LENGTH, 42
ci2.refGene.LENGTH, 43
ci2.xenoRefGene.LENGTH, 43
danRer3.ensGene.LENGTH, 44
danRer3.geneSymbol.LENGTH, 44
danRer3.refGene.LENGTH, 45
danRer4.ensGene.LENGTH, 45
danRer4.geneSymbol.LENGTH, 46
danRer4.genscan.LENGTH, 46
danRer4.nscanGene.LENGTH, 47
danRer4.refGene.LENGTH, 47
danRer5.ensGene.LENGTH, 48
danRer5.geneSymbol.LENGTH, 48
danRer5.refGene.LENGTH, 49
danRer5.vegaGene.LENGTH, 49
danRer5.vegaPseudoGene.LENGTH, 50
danRer6.ensGene.LENGTH, 50

- danRer6.geneSymbol.LENGTH, 51
 danRer6.refGene.LENGTH, 51
 danRer6.xenoRefGene.LENGTH, 52
 dm1.geneSymbol.LENGTH, 52
 dm1.genscan.LENGTH, 53
 dm1.refGene.LENGTH, 53
 dm2.geneid.LENGTH, 54
 dm2.geneSymbol.LENGTH, 54
 dm2.genscan.LENGTH, 55
 dm2.nscanGene.LENGTH, 55
 dm2.refGene.LENGTH, 56
 dm3.geneSymbol.LENGTH, 56
 dm3.nscanPasaGene.LENGTH, 57
 dm3.refGene.LENGTH, 57
 dp2.genscan.LENGTH, 59
 dp2.xenoRefGene.LENGTH, 59
 dp3.geneid.LENGTH, 60
 dp3.genscan.LENGTH, 60
 dp3.xenoRefGene.LENGTH, 61
 droAna1.geneid.LENGTH, 61
 droAna1.genscan.LENGTH, 62
 droAna1.xenoRefGene.LENGTH, 62
 droAna2.genscan.LENGTH, 63
 droAna2.xenoRefGene.LENGTH, 63
 droEre1.genscan.LENGTH, 64
 droEre1.xenoRefGene.LENGTH, 64
 droGri1.genscan.LENGTH, 65
 droGri1.xenoRefGene.LENGTH, 65
 droMoj1.geneid.LENGTH, 66
 droMoj1.genscan.LENGTH, 66
 droMoj1.xenoRefGene.LENGTH, 67
 droMoj2.genscan.LENGTH, 67
 droMoj2.xenoRefGene.LENGTH, 68
 droPer1.genscan.LENGTH, 68
 droPer1.xenoRefGene.LENGTH, 69
 droSec1.genscan.LENGTH, 69
 droSec1.xenoRefGene.LENGTH, 70
 droSim1.geneid.LENGTH, 70
 droSim1.genscan.LENGTH, 71
 droSim1.xenoRefGene.LENGTH, 71
 droVir1.geneid.LENGTH, 72
 droVir1.genscan.LENGTH, 72
 droVir1.xenoRefGene.LENGTH, 73
 droVir2.genscan.LENGTH, 73
 droVir2.xenoRefGene.LENGTH, 74
 droYak1.geneid.LENGTH, 74
 droYak1.genscan.LENGTH, 75
 droYak1.xenoRefGene.LENGTH, 75
 droYak2.genscan.LENGTH, 76
 droYak2.xenoRefGene.LENGTH, 76
 equCab1.geneid.LENGTH, 77
 equCab1.geneSymbol.LENGTH, 77
 equCab1.nscanGene.LENGTH, 78
 equCab1.refGene.LENGTH, 78
 equCab1.sgpGene.LENGTH, 79
 equCab2.ensGene.LENGTH, 79
 equCab2.geneSymbol.LENGTH, 80
 equCab2.nscanGene.LENGTH, 80
 equCab2.refGene.LENGTH, 81
 equCab2.xenoRefGene.LENGTH, 81
 felCat3.ensGene.LENGTH, 82
 felCat3.geneid.LENGTH, 82
 felCat3.geneSymbol.LENGTH, 83
 felCat3.genscan.LENGTH, 83
 felCat3.nscanGene.LENGTH, 84
 felCat3.refGene.LENGTH, 84
 felCat3.sgpGene.LENGTH, 85
 felCat3.xenoRefGene.LENGTH, 85
 fr1.ensGene.LENGTH, 86
 fr1.genscan.LENGTH, 86
 fr2.ensGene.LENGTH, 87
 galGal2.ensGene.LENGTH, 87
 galGal2.geneid.LENGTH, 88
 galGal2.geneSymbol.LENGTH, 88
 galGal2.genscan.LENGTH, 89
 galGal2.refGene.LENGTH, 89
 galGal2.sgpGene.LENGTH, 90
 galGal3.ensGene.LENGTH, 90
 galGal3.geneSymbol.LENGTH, 91
 galGal3.genscan.LENGTH, 91
 galGal3.nscanGene.LENGTH, 92
 galGal3.refGene.LENGTH, 92
 galGal3.xenoRefGene.LENGTH, 93
 gasAcu1.ensGene.LENGTH, 93
 gasAcu1.nscanGene.LENGTH, 94
 hg16.acembly.LENGTH, 95
 hg16.ensGene.LENGTH, 95
 hg16.exoniphy.LENGTH, 96
 hg16.geneid.LENGTH, 96
 hg16.geneSymbol.LENGTH, 97
 hg16.genscan.LENGTH, 97
 hg16.knownGene.LENGTH, 98
 hg16.refGene.LENGTH, 98
 hg16.sgpGene.LENGTH, 99
 hg17.acembly.LENGTH, 99
 hg17.acescan.LENGTH, 100
 hg17.ccdsGene.LENGTH, 100
 hg17.ensGene.LENGTH, 101
 hg17.exoniphy.LENGTH, 101
 hg17.geneid.LENGTH, 102
 hg17.geneSymbol.LENGTH, 102
 hg17.genscan.LENGTH, 103
 hg17.knownGene.LENGTH, 103
 hg17.refGene.LENGTH, 104

hg17.sgpGene.LENGTH, 104
hg17.vegaGene.LENGTH, 105
hg17.vegaPseudoGene.LENGTH, 105
hg17.xenoRefGene.LENGTH, 106
hg18.acembly.LENGTH, 106
hg18.acescan.LENGTH, 107
hg18.ccdsGene.LENGTH, 107
hg18.ensGene.LENGTH, 108
hg18.exoniphy.LENGTH, 108
hg18.geneid.LENGTH, 109
hg18.geneSymbol.LENGTH, 109
hg18.genscan.LENGTH, 110
hg18.knownGene.LENGTH, 110
hg18.knownGeneOld3.LENGTH, 111
hg18.refGene.LENGTH, 111
hg18.sgpGene.LENGTH, 112
hg18.sibGene.LENGTH, 112
hg18.xenoRefGene.LENGTH, 113
hg19.ccdsGene.LENGTH, 113
hg19.ensGene.LENGTH, 114
hg19.exoniphy.LENGTH, 114
hg19.geneSymbol.LENGTH, 115
hg19.knownGene.LENGTH, 115
hg19.nscanGene.LENGTH, 116
hg19.refGene.LENGTH, 116
hg19.xenoRefGene.LENGTH, 117
loxAfr3.xenoRefGene.LENGTH, 117
mm7.ensGene.LENGTH, 118
mm7.geneid.LENGTH, 118
mm7.geneSymbol.LENGTH, 119
mm7.genscan.LENGTH, 119
mm7.knownGene.LENGTH, 120
mm7.refGene.LENGTH, 120
mm7.sgpGene.LENGTH, 121
mm7.xenoRefGene.LENGTH, 121
mm8.ccdsGene.LENGTH, 122
mm8.ensGene.LENGTH, 122
mm8.geneid.LENGTH, 123
mm8.geneSymbol.LENGTH, 123
mm8.genscan.LENGTH, 124
mm8.knownGene.LENGTH, 124
mm8.nscanGene.LENGTH, 125
mm8.refGene.LENGTH, 125
mm8.sgpGene.LENGTH, 126
mm8.sibGene.LENGTH, 126
mm8.xenoRefGene.LENGTH, 127
mm9.acembly.LENGTH, 127
mm9.ccdsGene.LENGTH, 128
mm9.ensGene.LENGTH, 128
mm9.exoniphy.LENGTH, 129
mm9.geneid.LENGTH, 129
mm9.geneSymbol.LENGTH, 130
mm9.genscan.LENGTH, 130
mm9.knownGene.LENGTH, 131
mm9.nscanGene.LENGTH, 131
mm9.refGene.LENGTH, 132
mm9.sgpGene.LENGTH, 132
mm9.xenoRefGene.LENGTH, 133
monDom1.genscan.LENGTH, 133
monDom4.ensGene.LENGTH, 134
monDom4.geneSymbol.LENGTH, 134
monDom4.genscan.LENGTH, 135
monDom4.nscanGene.LENGTH, 135
monDom4.refGene.LENGTH, 136
monDom4.xenoRefGene.LENGTH, 136
monDom5.ensGene.LENGTH, 137
monDom5.geneSymbol.LENGTH, 137
monDom5.genscan.LENGTH, 138
monDom5.nscanGene.LENGTH, 138
monDom5.refGene.LENGTH, 139
monDom5.xenoRefGene.LENGTH, 139
ornAna1.ensGene.LENGTH, 140
ornAna1.geneSymbol.LENGTH, 140
ornAna1.refGene.LENGTH, 141
ornAna1.xenoRefGene.LENGTH, 141
oryLat2.ensGene.LENGTH, 142
oryLat2.geneSymbol.LENGTH, 142
oryLat2.refGene.LENGTH, 143
oryLat2.xenoRefGene.LENGTH, 143
panTro1.ensGene.LENGTH, 144
panTro1.geneid.LENGTH, 144
panTro1.genscan.LENGTH, 145
panTro1.xenoRefGene.LENGTH, 145
panTro2.ensGene.LENGTH, 146
panTro2.geneSymbol.LENGTH, 146
panTro2.genscan.LENGTH, 147
panTro2.nscanGene.LENGTH, 147
panTro2.refGene.LENGTH, 148
panTro2.xenoRefGene.LENGTH, 148
petMar1.xenoRefGene.LENGTH, 149
ponAbe2.ensGene.LENGTH, 149
ponAbe2.geneSymbol.LENGTH, 150
ponAbe2.genscan.LENGTH, 150
ponAbe2.nscanGene.LENGTH, 151
ponAbe2.refGene.LENGTH, 151
ponAbe2.xenoRefGene.LENGTH, 152
priPac1.xenoRefGene.LENGTH, 152
rheMac2.ensGene.LENGTH, 153
rheMac2.geneid.LENGTH, 153
rheMac2.geneSymbol.LENGTH, 154
rheMac2.nscanGene.LENGTH, 154
rheMac2.refGene.LENGTH, 155
rheMac2.sgpGene.LENGTH, 155
rheMac2.xenoRefGene.LENGTH, 156

- rn3.ensGene.LENGTH, 156
 rn3.geneid.LENGTH, 157
 rn3.geneSymbol.LENGTH, 157
 rn3.genscan.LENGTH, 158
 rn3.knownGene.LENGTH, 158
 rn3.nscanGene.LENGTH, 159
 rn3.refGene.LENGTH, 159
 rn3.sgpGene.LENGTH, 160
 rn3.xenoRefGene.LENGTH, 160
 rn4.ensGene.LENGTH, 161
 rn4.geneid.LENGTH, 161
 rn4.geneSymbol.LENGTH, 162
 rn4.genscan.LENGTH, 162
 rn4.knownGene.LENGTH, 163
 rn4.nscanGene.LENGTH, 163
 rn4.refGene.LENGTH, 164
 rn4.sgpGene.LENGTH, 164
 rn4.xenoRefGene.LENGTH, 165
 sacCer1.ensGene.LENGTH, 165
 sacCer2.ensGene.LENGTH, 166
 strPur1.geneSymbol.LENGTH, 166
 strPur1.genscan.LENGTH, 167
 strPur1.refGene.LENGTH, 167
 strPur1.xenoRefGene.LENGTH, 168
 strPur2.geneSymbol.LENGTH, 168
 strPur2.genscan.LENGTH, 169
 strPur2.refGene.LENGTH, 169
 strPur2.xenoRefGene.LENGTH, 170
 taeGut1.ensGene.LENGTH, 171
 taeGut1.geneSymbol.LENGTH, 172
 taeGut1.genscan.LENGTH, 172
 taeGut1.nscanGene.LENGTH, 173
 taeGut1.refGene.LENGTH, 173
 taeGut1.xenoRefGene.LENGTH, 174
 tetNig1.ensGene.LENGTH, 174
 tetNig1.geneid.LENGTH, 175
 tetNig1.genscan.LENGTH, 175
 tetNig1.nscanGene.LENGTH, 176
 tetNig2.ensGene.LENGTH, 176
 xenTro1.genscan.LENGTH, 178
 xenTro2.ensGene.LENGTH, 178
 xenTro2.geneSymbol.LENGTH, 179
 xenTro2.genscan.LENGTH, 179
 xenTro2.refGene.LENGTH, 180
- * **internal**
 geneLenDatabase-pkg, 94
- anoCar1.ensGene.LENGTH, 8
 anoCar1.genscan.LENGTH, 9
 anoCar1.xenoRefGene.LENGTH, 9
 anoGam1.ensGene.LENGTH, 10
 anoGam1.geneid.LENGTH, 10
 anoGam1.genscan.LENGTH, 11
- apiMe11.genscan.LENGTH, 11
 apiMe12.ensGene.LENGTH, 12
 apiMe12.geneid.LENGTH, 12
 apiMe12.genscan.LENGTH, 13
 ap1Ca11.xenoRefGene.LENGTH, 13
- bosTau2.geneid.LENGTH, 14
 bosTau2.geneSymbol.LENGTH, 14
 bosTau2.genscan.LENGTH, 15
 bosTau2.refGene.LENGTH, 15
 bosTau2.sgpGene.LENGTH, 16
 bosTau3.ensGene.LENGTH, 16
 bosTau3.geneid.LENGTH, 17
 bosTau3.geneSymbol.LENGTH, 17
 bosTau3.genscan.LENGTH, 18
 bosTau3.refGene.LENGTH, 18
 bosTau3.sgpGene.LENGTH, 19
 bosTau4.ensGene.LENGTH, 19
 bosTau4.geneSymbol.LENGTH, 20
 bosTau4.genscan.LENGTH, 20
 bosTau4.nscanGene.LENGTH, 21
 bosTau4.refGene.LENGTH, 21
 braFlo1.xenoRefGene.LENGTH, 22
- caeJap1.xenoRefGene.LENGTH, 22
 caePb1.xenoRefGene.LENGTH, 23
 caePb2.xenoRefGene.LENGTH, 23
 caeRem2.xenoRefGene.LENGTH, 24
 caeRem3.xenoRefGene.LENGTH, 24
 calJac1.genscan.LENGTH, 25
 calJac1.nscanGene.LENGTH, 25
 calJac1.xenoRefGene.LENGTH, 26
 canFam1.ensGene.LENGTH, 26
 canFam1.geneSymbol.LENGTH, 27
 canFam1.genscan.LENGTH, 27
 canFam1.nscanGene.LENGTH, 28
 canFam1.refGene.LENGTH, 28
 canFam1.xenoRefGene.LENGTH, 29
 canFam2.ensGene.LENGTH, 29
 canFam2.geneSymbol.LENGTH, 30
 canFam2.genscan.LENGTH, 30
 canFam2.nscanGene.LENGTH, 31
 canFam2.refGene.LENGTH, 31
 canFam2.xenoRefGene.LENGTH, 32
 cavPor3.ensGene.LENGTH, 32
 cavPor3.genscan.LENGTH, 33
 cavPor3.nscanGene.LENGTH, 33
 cavPor3.xenoRefGene.LENGTH, 34
 cb1.xenoRefGene.LENGTH, 34
 cb3.xenoRefGene.LENGTH, 35
 ce2.geneid.LENGTH, 35
 ce2.geneSymbol.LENGTH, 36
 ce2.refGene.LENGTH, 36

- ce4.geneSymbol.LENGTH, 37
 ce4.refGene.LENGTH, 37
 ce4.xenoRefGene.LENGTH, 38
 ce6.ensGene.LENGTH, 38
 ce6.geneSymbol.LENGTH, 39
 ce6.refGene.LENGTH, 39
 ce6.xenoRefGene.LENGTH, 40
 ci1.geneSymbol.LENGTH, 40
 ci1.refGene.LENGTH, 41
 ci1.xenoRefGene.LENGTH, 41
 ci2.ensGene.LENGTH, 42
 ci2.geneSymbol.LENGTH, 42
 ci2.refGene.LENGTH, 43
 ci2.xenoRefGene.LENGTH, 43

 danRer3.ensGene.LENGTH, 44
 danRer3.geneSymbol.LENGTH, 44
 danRer3.refGene.LENGTH, 45
 danRer4.ensGene.LENGTH, 45
 danRer4.geneSymbol.LENGTH, 46
 danRer4.genscan.LENGTH, 46
 danRer4.nscanGene.LENGTH, 47
 danRer4.refGene.LENGTH, 47
 danRer5.ensGene.LENGTH, 48
 danRer5.geneSymbol.LENGTH, 48
 danRer5.refGene.LENGTH, 49
 danRer5.vegaGene.LENGTH, 49
 danRer5.vegaPseudoGene.LENGTH, 50
 danRer6.ensGene.LENGTH, 50
 danRer6.geneSymbol.LENGTH, 51
 danRer6.refGene.LENGTH, 51
 danRer6.xenoRefGene.LENGTH, 52
 dm1.geneSymbol.LENGTH, 52
 dm1.genscan.LENGTH, 53
 dm1.refGene.LENGTH, 53
 dm2.geneid.LENGTH, 54
 dm2.geneSymbol.LENGTH, 54
 dm2.genscan.LENGTH, 55
 dm2.nscanGene.LENGTH, 55
 dm2.refGene.LENGTH, 56
 dm3.geneSymbol.LENGTH, 56
 dm3.nscanPasaGene.LENGTH, 57
 dm3.refGene.LENGTH, 57
 downloadLengthFromUCSC, 8–57, 58, 59–170,
 172–176, 178–180
 dp2.genscan.LENGTH, 59
 dp2.xenoRefGene.LENGTH, 59
 dp3.geneid.LENGTH, 60
 dp3.genscan.LENGTH, 60
 dp3.xenoRefGene.LENGTH, 61
 droAna1.geneid.LENGTH, 61
 droAna1.genscan.LENGTH, 62
 droAna1.xenoRefGene.LENGTH, 62

 droAna2.genscan.LENGTH, 63
 droAna2.xenoRefGene.LENGTH, 63
 droEre1.genscan.LENGTH, 64
 droEre1.xenoRefGene.LENGTH, 64
 droGri1.genscan.LENGTH, 65
 droGri1.xenoRefGene.LENGTH, 65
 droMoj1.geneid.LENGTH, 66
 droMoj1.genscan.LENGTH, 66
 droMoj1.xenoRefGene.LENGTH, 67
 droMoj2.genscan.LENGTH, 67
 droMoj2.xenoRefGene.LENGTH, 68
 droPer1.genscan.LENGTH, 68
 droPer1.xenoRefGene.LENGTH, 69
 droSec1.genscan.LENGTH, 69
 droSec1.xenoRefGene.LENGTH, 70
 droSim1.geneid.LENGTH, 70
 droSim1.genscan.LENGTH, 71
 droSim1.xenoRefGene.LENGTH, 71
 droVir1.geneid.LENGTH, 72
 droVir1.genscan.LENGTH, 72
 droVir1.xenoRefGene.LENGTH, 73
 droVir2.genscan.LENGTH, 73
 droVir2.xenoRefGene.LENGTH, 74
 droYak1.geneid.LENGTH, 74
 droYak1.genscan.LENGTH, 75
 droYak1.xenoRefGene.LENGTH, 75
 droYak2.genscan.LENGTH, 76
 droYak2.xenoRefGene.LENGTH, 76

 equCab1.geneid.LENGTH, 77
 equCab1.geneSymbol.LENGTH, 77
 equCab1.nscanGene.LENGTH, 78
 equCab1.refGene.LENGTH, 78
 equCab1.sgpGene.LENGTH, 79
 equCab2.ensGene.LENGTH, 79
 equCab2.geneSymbol.LENGTH, 80
 equCab2.nscanGene.LENGTH, 80
 equCab2.refGene.LENGTH, 81
 equCab2.xenoRefGene.LENGTH, 81

 felCat3.ensGene.LENGTH, 82
 felCat3.geneid.LENGTH, 82
 felCat3.geneSymbol.LENGTH, 83
 felCat3.genscan.LENGTH, 83
 felCat3.nscanGene.LENGTH, 84
 felCat3.refGene.LENGTH, 84
 felCat3.sgpGene.LENGTH, 85
 felCat3.xenoRefGene.LENGTH, 85
 fr1.ensGene.LENGTH, 86
 fr1.genscan.LENGTH, 86
 fr2.ensGene.LENGTH, 87

 galGal2.ensGene.LENGTH, 87

- galGal2.geneid.LENGTH, 88
- galGal2.geneSymbol.LENGTH, 88
- galGal2.genscan.LENGTH, 89
- galGal2.refGene.LENGTH, 89
- galGal2.sgpGene.LENGTH, 90
- galGal3.geneid.LENGTH, 90
- galGal3.geneSymbol.LENGTH, 91
- galGal3.genscan.LENGTH, 91
- galGal3.nscanGene.LENGTH, 92
- galGal3.refGene.LENGTH, 92
- galGal3.xenoRefGene.LENGTH, 93
- gasAcu1.ensGene.LENGTH, 93
- gasAcu1.nscanGene.LENGTH, 94
- geneLenDataBase (geneLenDatabase-pkg), 94
- geneLenDataBase-package (geneLenDatabase-pkg), 94
- geneLenDatabase-pkg, 94
- hg16.acembly.LENGTH, 95
- hg16.ensGene.LENGTH, 95
- hg16.exoniphy.LENGTH, 96
- hg16.geneid.LENGTH, 96
- hg16.geneSymbol.LENGTH, 97
- hg16.genscan.LENGTH, 97
- hg16.knownGene.LENGTH, 98
- hg16.refGene.LENGTH, 98
- hg16.sgpGene.LENGTH, 99
- hg17.acembly.LENGTH, 99
- hg17.acescan.LENGTH, 100
- hg17.ccdsGene.LENGTH, 100
- hg17.ensGene.LENGTH, 101
- hg17.exoniphy.LENGTH, 101
- hg17.geneid.LENGTH, 102
- hg17.geneSymbol.LENGTH, 102
- hg17.genscan.LENGTH, 103
- hg17.knownGene.LENGTH, 103
- hg17.refGene.LENGTH, 104
- hg17.sgpGene.LENGTH, 104
- hg17.vegaGene.LENGTH, 105
- hg17.vegaPseudoGene.LENGTH, 105
- hg17.xenoRefGene.LENGTH, 106
- hg18.acembly.LENGTH, 106
- hg18.acescan.LENGTH, 107
- hg18.ccdsGene.LENGTH, 107
- hg18.ensGene.LENGTH, 108
- hg18.exoniphy.LENGTH, 108
- hg18.geneid.LENGTH, 109
- hg18.geneSymbol.LENGTH, 109
- hg18.genscan.LENGTH, 110
- hg18.knownGene.LENGTH, 110
- hg18.knownGeneOld3.LENGTH, 111
- hg18.refGene.LENGTH, 111
- hg18.sgpGene.LENGTH, 112
- hg18.sibGene.LENGTH, 112
- hg18.xenoRefGene.LENGTH, 113
- hg19.ccdsGene.LENGTH, 113
- hg19.ensGene.LENGTH, 114
- hg19.exoniphy.LENGTH, 114
- hg19.geneSymbol.LENGTH, 115
- hg19.knownGene.LENGTH, 115
- hg19.nscanGene.LENGTH, 116
- hg19.refGene.LENGTH, 116
- hg19.xenoRefGene.LENGTH, 117
- loxAfr3.xenoRefGene.LENGTH, 117
- mm7.ensGene.LENGTH, 118
- mm7.geneid.LENGTH, 118
- mm7.geneSymbol.LENGTH, 119
- mm7.genscan.LENGTH, 119
- mm7.knownGene.LENGTH, 120
- mm7.refGene.LENGTH, 120
- mm7.sgpGene.LENGTH, 121
- mm7.xenoRefGene.LENGTH, 121
- mm8.ccdsGene.LENGTH, 122
- mm8.ensGene.LENGTH, 122
- mm8.geneid.LENGTH, 123
- mm8.geneSymbol.LENGTH, 123
- mm8.genscan.LENGTH, 124
- mm8.knownGene.LENGTH, 124
- mm8.nscanGene.LENGTH, 125
- mm8.refGene.LENGTH, 125
- mm8.sgpGene.LENGTH, 126
- mm8.sibGene.LENGTH, 126
- mm8.xenoRefGene.LENGTH, 127
- mm9.acembly.LENGTH, 127
- mm9.ccdsGene.LENGTH, 128
- mm9.ensGene.LENGTH, 128
- mm9.exoniphy.LENGTH, 129
- mm9.geneid.LENGTH, 129
- mm9.geneSymbol.LENGTH, 130
- mm9.genscan.LENGTH, 130
- mm9.knownGene.LENGTH, 131
- mm9.nscanGene.LENGTH, 131
- mm9.refGene.LENGTH, 132
- mm9.sgpGene.LENGTH, 132
- mm9.xenoRefGene.LENGTH, 133
- monDom1.genscan.LENGTH, 133
- monDom4.ensGene.LENGTH, 134
- monDom4.geneSymbol.LENGTH, 134
- monDom4.genscan.LENGTH, 135
- monDom4.nscanGene.LENGTH, 135
- monDom4.refGene.LENGTH, 136
- monDom4.xenoRefGene.LENGTH, 136
- monDom5.ensGene.LENGTH, 137

- monDom5.geneSymbol.LENGTH, 137
monDom5.genscan.LENGTH, 138
monDom5.nscanGene.LENGTH, 138
monDom5.refGene.LENGTH, 139
monDom5.xenoRefGene.LENGTH, 139
- ornAna1.ensGene.LENGTH, 140
ornAna1.geneSymbol.LENGTH, 140
ornAna1.refGene.LENGTH, 141
ornAna1.xenoRefGene.LENGTH, 141
oryLat2.ensGene.LENGTH, 142
oryLat2.geneSymbol.LENGTH, 142
oryLat2.refGene.LENGTH, 143
oryLat2.xenoRefGene.LENGTH, 143
- panTro1.ensGene.LENGTH, 144
panTro1.geneid.LENGTH, 144
panTro1.genscan.LENGTH, 145
panTro1.xenoRefGene.LENGTH, 145
panTro2.ensGene.LENGTH, 146
panTro2.geneSymbol.LENGTH, 146
panTro2.genscan.LENGTH, 147
panTro2.nscanGene.LENGTH, 147
panTro2.refGene.LENGTH, 148
panTro2.xenoRefGene.LENGTH, 148
petMar1.xenoRefGene.LENGTH, 149
ponAbe2.ensGene.LENGTH, 149
ponAbe2.geneSymbol.LENGTH, 150
ponAbe2.genscan.LENGTH, 150
ponAbe2.nscanGene.LENGTH, 151
ponAbe2.refGene.LENGTH, 151
ponAbe2.xenoRefGene.LENGTH, 152
priPac1.xenoRefGene.LENGTH, 152
- rheMac2.ensGene.LENGTH, 153
rheMac2.geneid.LENGTH, 153
rheMac2.geneSymbol.LENGTH, 154
rheMac2.nscanGene.LENGTH, 154
rheMac2.refGene.LENGTH, 155
rheMac2.sgpGene.LENGTH, 155
rheMac2.xenoRefGene.LENGTH, 156
- rn3.ensGene.LENGTH, 156
rn3.geneid.LENGTH, 157
rn3.geneSymbol.LENGTH, 157
rn3.genscan.LENGTH, 158
rn3.knownGene.LENGTH, 158
rn3.nscanGene.LENGTH, 159
rn3.refGene.LENGTH, 159
rn3.sgpGene.LENGTH, 160
rn3.xenoRefGene.LENGTH, 160
- rn4.ensGene.LENGTH, 161
rn4.geneid.LENGTH, 161
rn4.geneSymbol.LENGTH, 162
rn4.genscan.LENGTH, 162
rn4.knownGene.LENGTH, 163
rn4.nscanGene.LENGTH, 163
rn4.refGene.LENGTH, 164
rn4.sgpGene.LENGTH, 164
rn4.xenoRefGene.LENGTH, 165
- sacCer1.ensGene.LENGTH, 165
sacCer2.ensGene.LENGTH, 166
strPur1.geneSymbol.LENGTH, 166
strPur1.genscan.LENGTH, 167
strPur1.refGene.LENGTH, 167
strPur1.xenoRefGene.LENGTH, 168
strPur2.geneSymbol.LENGTH, 168
strPur2.genscan.LENGTH, 169
strPur2.refGene.LENGTH, 169
strPur2.xenoRefGene.LENGTH, 170
supportedGeneIDs, 58, 170
supportedGenomes, 58, 171
- taeGut1.ensGene.LENGTH, 171
taeGut1.geneSymbol.LENGTH, 172
taeGut1.genscan.LENGTH, 172
taeGut1.nscanGene.LENGTH, 173
taeGut1.refGene.LENGTH, 173
taeGut1.xenoRefGene.LENGTH, 174
tetNig1.ensGene.LENGTH, 174
tetNig1.geneid.LENGTH, 175
tetNig1.genscan.LENGTH, 175
tetNig1.nscanGene.LENGTH, 176
tetNig2.ensGene.LENGTH, 176
- unfactor, 177
- xenTro1.genscan.LENGTH, 178
xenTro2.ensGene.LENGTH, 178
xenTro2.geneSymbol.LENGTH, 179
xenTro2.genscan.LENGTH, 179
xenTro2.refGene.LENGTH, 180