Package ‘geneLenDataBase’

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Title Lengths of mRNA transcripts for a number of genomes
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Depends R (>= 2.11.0)
Imports utils, rtracklayer, GenomicFeatures (>= 1.3.15)
LazyLoad yes
Description Length of mRNA transcripts for a number of genomes and gene ID formats, largely based on UCSC table browser
biocViews ExperimentData, Genome
License LGPL (>= 2)
NeedsCompilation no

R topics documented:

anoCar1.ensGene.LENGTH ........................................ 8
anoCar1.genscan.LENGTH ....................................... 8
anoCar1.xenoRefGene.LENGTH ................................... 9
anoGam1.ensGene.LENGTH ....................................... 9
anoGam1.geneid.LENGTH ......................................... 10
anoGam1.genscan.LENGTH ...................................... 10
apiMel1.genscan.LENGTH ....................................... 11
apiMel2.ensGene.LENGTH ....................................... 11
apiMel2.geneid.LENGTH ......................................... 12
apiMel2.genscan.LENGTH ...................................... 12
aplCal1.xenoRefGene.LENGTH .................................. 13
bosTau2.geneid.LENGTH ....................................... 13
bosTau2.geneSymbol.LENGTH .................................. 14
bosTau2.genscan.LENGTH ...................................... 14
bosTau2.refGene.LENGTH ....................................... 15
bosTau2.sgpGene.LENGTH ...................................... 15
bosTau3.ensGene.LENGTH ....................................... 16
bosTau3.geneid.LENGTH ......................................... 16
bosTau3.geneSymbol.LENGTH .................................. 17
topics documented:

- bosTau3.genscan.LENGTH
- bosTau3.refGene.LENGTH
- bosTau3.sgpGene.LENGTH
- bosTau4.ensGene.LENGTH
- bosTau4.geneSymbol.LENGTH
- bosTau4.genscan.LENGTH
- bosTau4.nscanGene.LENGTH
- bosTau4.refGene.LENGTH
- braFlo1.xenoRefGene.LENGTH
- caeJap1.xenoRefGene.LENGTH
- caePb1.xenoRefGene.LENGTH
- caePb2.xenoRefGene.LENGTH
- caeRem2.xenoRefGene.LENGTH
- caeRem3.xenoRefGene.LENGTH
- calJac1.genscan.LENGTH
- calJac1.nscanGene.LENGTH
- calJac1.xenoRefGene.LENGTH
- canFam1.ensGene.LENGTH
- canFam1.geneSymbol.LENGTH
- canFam1.genscan.LENGTH
- canFam1.nscanGene.LENGTH
- canFam1.refGene.LENGTH
- canFam1.xenoRefGene.LENGTH
- canFam2.ensGene.LENGTH
- canFam2.geneSymbol.LENGTH
- canFam2.genscan.LENGTH
- canFam2.nscanGene.LENGTH
- canFam2.refGene.LENGTH
- canFam2.xenoRefGene.LENGTH
- cavPor3.ensGene.LENGTH
- cavPor3.genscan.LENGTH
- cavPor3.nscanGene.LENGTH
- cavPor3.xenoRefGene.LENGTH
- cb1.xenoRefGene.LENGTH
- cb3.xenoRefGene.LENGTH
- ce2.geneid.LENGTH
- ce2.geneSymbol.LENGTH
- ce2.refGene.LENGTH
- ce4.geneSymbol.LENGTH
- ce4.refGene.LENGTH
- ce4.xenoRefGene.LENGTH
- ce6.ensGene.LENGTH
- ce6.geneSymbol.LENGTH
- ce6.refGene.LENGTH
- ce6.xenoRefGene.LENGTH
- ci1.geneSymbol.LENGTH
- ci1.refGene.LENGTH
- ci1.xenoRefGene.LENGTH
- ci2.ensGene.LENGTH
- ci2.geneSymbol.LENGTH
- ci2.refGene.LENGTH
- ci2.xenoRefGene.LENGTH
topics documented:

- danRer3.ensGene.LENGTH
- danRer3.geneSymbol.LENGTH
- danRer3.refGene.LENGTH
- danRer4.ensGene.LENGTH
- danRer4.geneSymbol.LENGTH
- danRer4.genscan.LENGTH
- danRer4.nscanGene.LENGTH
- danRer4.refGene.LENGTH
- danRer5.ensGene.LENGTH
- danRer5.geneSymbol.LENGTH
- danRer5.refGene.LENGTH
- danRer5.vegaGene.LENGTH
- danRer5.vegaPseudoGene.LENGTH
- danRer6.ensGene.LENGTH
- danRer6.geneSymbol.LENGTH
- danRer6.refGene.LENGTH
- dm1.geneSymbol.LENGTH
- dm1.genscan.LENGTH
- dm1.refGene.LENGTH
- dm2.geneid.LENGTH
- dm2.geneSymbol.LENGTH
- dm2.genscan.LENGTH
- dm2.nscanGene.LENGTH
- dm2.refGene.LENGTH
- dm3.geneSymbol.LENGTH
- dm3.nscanPasaGene.LENGTH
- dm3.refGene.LENGTH
- dp2.genscan.LENGTH
- dp2.xenoRefGene.LENGTH
- dp3.geneid.LENGTH
- dp3.genscan.LENGTH
- dp3.xenoRefGene.LENGTH
- droAna1.geneid.LENGTH
- droAna1.genscan.LENGTH
- droAna1.xenoRefGene.LENGTH
- droAna2.genscan.LENGTH
- droAna2.xenoRefGene.LENGTH
- droEre1.genscan.LENGTH
- droEre1.xenoRefGene.LENGTH
- droGri1.genscan.LENGTH
- droGri1.xenoRefGene.LENGTH
- droMoj1.geneid.LENGTH
- droMoj1.genscan.LENGTH
- droMoj1.xenoRefGene.LENGTH
- droMoj2.genscan.LENGTH
- droMoj2.xenoRefGene.LENGTH
- droPer1.genscan.LENGTH
- droPer1.xenoRefGene.LENGTH
- droSec1.genscan.LENGTH
- droSec1.xenoRefGene.LENGTH
- droSim1.geneid.LENGTH
R topics documented:
droSim1.genscan.LENGTH .............................................. 69
droSim1.xenoRefGene.LENGTH ........................................ 70
droVir1.geneid.LENGTH ............................................... 70
droVir1.genscan.LENGTH .............................................. 71
droVir1.xenoRefGene.LENGTH ........................................ 71
droVir2.genscan.LENGTH .............................................. 72
droVir2.xenoRefGene.LENGTH ........................................ 72
droYak1.geneid.LENGTH ............................................... 73
droYak1.genscan.LENGTH .............................................. 73
droYak1.xenoRefGene.LENGTH ........................................ 74
droYak2.genscan.LENGTH .............................................. 74
droYak2.xenoRefGene.LENGTH ........................................ 75
equCab1.geneid.LENGTH ............................................... 75
equCab1.geneSymbol.LENGTH ......................................... 76
equCab1.nscanGene.LENGTH ........................................... 76
equCab1.refGene.LENGTH ............................................. 77
equCab1.sgpGene.LENGTH ............................................. 77
equCab2.ensGene.LENGTH ............................................. 78
equCab2.geneSymbol.LENGTH ......................................... 78
equCab2.nscanGene.LENGTH ........................................... 79
equCab2.refGene.LENGTH ............................................. 79
equCab2.xenoRefGene.LENGTH ........................................ 80
felCat3.ensGene.LENGTH ............................................. 80
felCat3.geneid.LENGTH ............................................... 81
felCat3.geneSymbol.LENGTH ......................................... 81
felCat3.genscan.LENGTH .............................................. 82
felCat3.nscanGene.LENGTH ........................................... 82
felCat3.refGene.LENGTH ............................................. 83
felCat3.sgpGene.LENGTH ............................................. 83
felCat3.xenoRefGene.LENGTH ........................................ 84
fr1.ensGene.LENGTH ................................................ 84
fr1.genscan.LENGTH ................................................ 85
fr2.ensGene.LENGTH ................................................ 85
galGal2.ensGene.LENGTH ............................................ 86
galGal2.geneid.LENGTH .............................................. 86
galGal2.geneSymbol.LENGTH ......................................... 87
galGal2.genscan.LENGTH .............................................. 87
galGal2.refGene.LENGTH ............................................. 88
galGal2.sgpGene.LENGTH ............................................. 88
galGal3.ensGene.LENGTH ............................................ 89
galGal3.geneSymbol.LENGTH ......................................... 89
galGal3.genscan.LENGTH .............................................. 89
galGal3.nscanGene.LENGTH ........................................... 90
galGal3.refGene.LENGTH ............................................. 90
galGal3.xenoRefGene.LENGTH ........................................ 91
gasAcu1.ensGene.LENGTH ............................................ 91
gasAcu1.geneSymbol.LENGTH ......................................... 92
hg16.acembly.LENGTH ............................................... 93
hg16.exoniphy.LENGTH ............................................... 93
hg16.geneid.LENGTH ................................................ 94
hg16.geneSymbol.LENGTH ........................................... 95
<table>
<thead>
<tr>
<th>Topics Documented</th>
<th>Length</th>
</tr>
</thead>
<tbody>
<tr>
<td>hg16.genscan.LENGTH</td>
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<td>hg16.refGene.LENGTH</td>
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<tr>
<td>hg16.sgpGene.LENGTH</td>
<td>97</td>
</tr>
<tr>
<td>hg17.acembly.LENGTH</td>
<td>97</td>
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<tr>
<td>hg17.acescan.LENGTH</td>
<td>98</td>
</tr>
<tr>
<td>hg17.ccdsGene.LENGTH</td>
<td>98</td>
</tr>
<tr>
<td>hg17.ensGene.LENGTH</td>
<td>99</td>
</tr>
<tr>
<td>hg17.exoniphy.LENGTH</td>
<td>99</td>
</tr>
<tr>
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<tr>
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<td>101</td>
</tr>
<tr>
<td>hg17.refGene.LENGTH</td>
<td>102</td>
</tr>
<tr>
<td>hg17.sgpGene.LENGTH</td>
<td>102</td>
</tr>
<tr>
<td>hg17.vegaGene.LENGTH</td>
<td>103</td>
</tr>
<tr>
<td>hg17.vegaPseudoGene.LENGTH</td>
<td>103</td>
</tr>
<tr>
<td>hg17.xenoRefGene.LENGTH</td>
<td>104</td>
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<tr>
<td>hg18.acsembly.LENGTH</td>
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<tr>
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<td>105</td>
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<tr>
<td>hg18.ccdsGene.LENGTH</td>
<td>105</td>
</tr>
<tr>
<td>hg18.ensGene.LENGTH</td>
<td>106</td>
</tr>
<tr>
<td>hg18.exoniphy.LENGTH</td>
<td>106</td>
</tr>
<tr>
<td>hg18.geneid.LENGTH</td>
<td>107</td>
</tr>
<tr>
<td>hg18.geneSymbol.LENGTH</td>
<td>107</td>
</tr>
<tr>
<td>hg18.genscan.LENGTH</td>
<td>108</td>
</tr>
<tr>
<td>hg18.knownGene.LENGTH</td>
<td>108</td>
</tr>
<tr>
<td>hg18.knownGeneOld3.LENGTH</td>
<td>109</td>
</tr>
<tr>
<td>hg18.refGene.LENGTH</td>
<td>109</td>
</tr>
<tr>
<td>hg18.sgpGene.LENGTH</td>
<td>110</td>
</tr>
<tr>
<td>hg18.sibGene.LENGTH</td>
<td>110</td>
</tr>
<tr>
<td>hg18.xenoRefGene.LENGTH</td>
<td>111</td>
</tr>
<tr>
<td>hg19.ccdsGene.LENGTH</td>
<td>111</td>
</tr>
<tr>
<td>hg19.ensGene.LENGTH</td>
<td>112</td>
</tr>
<tr>
<td>hg19.exoniphy.LENGTH</td>
<td>112</td>
</tr>
<tr>
<td>hg19.geneSymbol.LENGTH</td>
<td>113</td>
</tr>
<tr>
<td>hg19.knownGene.LENGTH</td>
<td>113</td>
</tr>
<tr>
<td>hg19.nscanGene.LENGTH</td>
<td>114</td>
</tr>
<tr>
<td>hg19.refGene.LENGTH</td>
<td>114</td>
</tr>
<tr>
<td>hg19.xenoRefGene.LENGTH</td>
<td>115</td>
</tr>
<tr>
<td>loxAfr3.xenoRefGene.LENGTH</td>
<td>115</td>
</tr>
<tr>
<td>mm7.ensGene.LENGTH</td>
<td>116</td>
</tr>
<tr>
<td>mm7.geneid.LENGTH</td>
<td>116</td>
</tr>
<tr>
<td>mm7.geneSymbol.LENGTH</td>
<td>117</td>
</tr>
<tr>
<td>mm7.genscan.LENGTH</td>
<td>117</td>
</tr>
<tr>
<td>mm7.knownGene.LENGTH</td>
<td>118</td>
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<td>mm7.refGene.LENGTH</td>
<td>118</td>
</tr>
<tr>
<td>mm7.sgpGene.LENGTH</td>
<td>119</td>
</tr>
<tr>
<td>mm7.xenoRefGene.LENGTH</td>
<td>119</td>
</tr>
<tr>
<td>mm8.ccdsGene.LENGTH</td>
<td>120</td>
</tr>
<tr>
<td>mm8.ensGene.LENGTH</td>
<td>120</td>
</tr>
<tr>
<td>mm8.geneid.LENGTH</td>
<td>121</td>
</tr>
</tbody>
</table>
topics documented:

mm8.geneSymbol.LENGTH ...................................................... 121
mm8.genscan.LENGTH .......................................................... 122
mm8.knownGene.LENGTH ...................................................... 122
mm8.nscanGene.LENGTH ....................................................... 123
mm8.refGene.LENGTH .......................................................... 123
mm8.sgpGene.LENGTH .......................................................... 124
mm8.sibGene.LENGTH .......................................................... 124
mm8.xenoRefGene.LENGTH ..................................................... 125
mm9.acembly.LENGTH .......................................................... 125
mm9.ccdsGene.LENGTH ........................................................ 126
mm9.ensGene.LENGTH ........................................................ 126
mm9.exoniphy.LENGTH ....................................................... 127
mm9.geneid.LENGTH ............................................................ 127
mm9.geneSymbol.LENGTH ..................................................... 128
mm9.genscan.LENGTH .......................................................... 128
mm9.knownGene.LENGTH ...................................................... 129
mm9.nscanGene.LENGTH ....................................................... 129
mm9.refGene.LENGTH .......................................................... 130
mm9.sgpGene.LENGTH .......................................................... 130
mm9.xenoRefGene.LENGTH ..................................................... 131
monDom1.genscan.LENGTH .................................................... 131
monDom4.ensGene.LENGTH ................................................... 132
monDom4.geneSymbol.LENGTH .............................................. 132
monDom4.genscan.LENGTH .................................................... 133
monDom4.nscanGene.LENGTH ................................................ 133
monDom4.refGene.LENGTH .................................................... 134
monDom4.xenoRefGene.LENGTH ............................................. 134
monDom5.ensGene.LENGTH ................................................... 135
monDom5.geneSymbol.LENGTH .............................................. 135
monDom5.genscan.LENGTH .................................................... 136
monDom5.nscanGene.LENGTH ................................................ 136
monDom5.refGene.LENGTH .................................................... 137
monDom5.xenoRefGene.LENGTH ............................................. 137
ornAna1.ensGene.LENGTH .................................................... 138
ornAna1.geneSymbol.LENGTH .............................................. 138
ornAna1.refGene.LENGTH ..................................................... 139
ornAna1.xenoRefGene.LENGTH ............................................. 139
oryLat2.ensGene.LENGTH ..................................................... 140
oryLat2.geneSymbol.LENGTH .............................................. 140
oryLat2.refGene.LENGTH ..................................................... 141
oryLat2.xenoRefGene.LENGTH ............................................. 141
panTro1.ensGene.LENGTH .................................................... 142
panTro1.geneid.LENGTH ...................................................... 142
panTro1.genscan.LENGTH ..................................................... 143
panTro1.xenoRefGene.LENGTH ............................................. 143
panTro2.ensGene.LENGTH .................................................... 144
panTro2.geneSymbol.LENGTH .............................................. 144
panTro2.genscan.LENGTH ..................................................... 145
panTro2.nscanGene.LENGTH ................................................ 145
panTro2.refGene.LENGTH ..................................................... 146
panTro2.xenoRefGene.LENGTH ............................................. 146
petMar1.xenoRefGene.LENGTH ............................................. 147
R topics documented:

ponAbe2.ensGene.LENGTH .................................................. 147
ponAbe2.geneSymbol.LENGTH ............................................. 148
ponAbe2.genscan.LENGTH .................................................. 148
ponAbe2.nscanGene.LENGTH .............................................. 149
ponAbe2.refGene.LENGTH .................................................. 149
ponAbe2.xenoRefGene.LENGTH ........................................... 150
priPac1.xenoRefGene.LENGTH ............................................ 150
rheMac2.ensGene.LENGTH .................................................. 151
rheMac2.geneid.LENGTH .................................................... 151
rheMac2.geneSymbol.LENGTH ............................................. 152
rheMac2.nscanGene.LENGTH .............................................. 152
rheMac2.refGene.LENGTH .................................................. 153
rheMac2.sgpGene.LENGTH .................................................. 153
rheMac2.xenoRefGene.LENGTH ......................................... 154
rn3.ensGene.LENGTH ........................................................ 154
rn3.geneid.LENGTH .......................................................... 155
rn3.geneSymbol.LENGTH ................................................... 155
rn3.genscan.LENGTH ........................................................ 156
rn3.knownGene.LENGTH ..................................................... 156
rn3.nscanGene.LENGTH ..................................................... 157
rn3.refGene.LENGTH ........................................................ 157
rn3.sgpGene.LENGTH ........................................................ 158
rn3.xenoRefGene.LENGTH ............................................... 158
rn4.ensGene.LENGTH ........................................................ 159
rn4.geneid.LENGTH .......................................................... 159
rn4.geneSymbol.LENGTH ................................................... 160
rn4.genscan.LENGTH ........................................................ 160
rn4.knownGene.LENGTH ..................................................... 161
rn4.nscanGene.LENGTH ..................................................... 161
rn4.refGene.LENGTH ........................................................ 162
rn4.sgpGene.LENGTH ........................................................ 162
rn4.xenoRefGene.LENGTH ............................................... 162
sacCer1.ensGene.LENGTH .................................................. 163
sacCer2.ensGene.LENGTH .................................................. 163
strPur1.geneSymbol.LENGTH .............................................. 164
strPur1.genscan.LENGTH .................................................... 164
strPur1.refGene.LENGTH ................................................... 165
strPur1.xenoRefGene.LENGTH .......................................... 165
strPur2.geneSymbol.LENGTH .............................................. 166
strPur2.genscan.LENGTH .................................................... 166
strPur2.refGene.LENGTH ................................................... 167
strPur2.xenoRefGene.LENGTH .......................................... 168
supportedGeneIDs .......................................................... 168
supportedGenomes .......................................................... 169
taeGut1.ensGene.LENGTH .................................................. 169
taeGut1.geneSymbol.LENGTH ............................................. 170
taeGut1.genscan.LENGTH .................................................. 170
taeGut1.nscanGene.LENGTH .............................................. 171
taeGut1.refGene.LENGTH .................................................. 171
taeGut1.xenoRefGene.LENGTH .......................................... 172
tetNig1.ensGene.LENGTH .................................................. 172
tetNig1.geneid.LENGTH ..................................................... 173
tetNig1.genscan.LENGTH                       173
tetNig1.nscanGene.LENGTH                   174
tetNig2.ensGene.LENGTH                   174
unfactor                                   175
xenTro1.genscan.LENGTH                     176
xenTro2.ensGene.LENGTH                     176
xenTro2.geneSymbol.LENGTH                 177
xenTro2.genscan.LENGTH                     177
xenTro2.refGene.LENGTH                    178

Index

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)
anoGaml.geneid.LENGTH  Transcript length data for the organism anoGaml

Description

anoGaml.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(anoGaml, geneid) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(anoGaml.geneid.LENGTH)
head(anoGaml.geneid.LENGTH)

anoGaml.genscan.LENGTH  Transcript length data for the organism anoGaml

Description

anoGaml.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a 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(anoGaml, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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

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

See Also
downloadLengthFromUCSC

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

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

Description

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

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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**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)
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)

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)
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)

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**

```r
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**

```r
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)

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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)
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)
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

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/cgibin/hgTables) using the ensGene table.

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

cavPor3.genscan.LENGTH

*Transcript length data for the organism cavPor*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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cavPor3.xenoRefGene.LENGTH

**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)
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)

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  

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ce2.geneSymbol.LENGTH  

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

---

description

description

description

description

description

description

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)
**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**

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

---

**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**

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

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)
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

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

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

```r
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)
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

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)
**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

**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)
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

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)
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)

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)
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/cgibin/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)

Transcript length data for the organism danRer

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

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)
**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)

**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)
**Description**

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

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

**See Also**

downloadLengthFromUCSC

**Examples**

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

---

danRer6.xenoRefGene.LENGTH

*Transcript length data for the organism danRer*

**Description**

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

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

**See Also**

downloadLengthFromUCSC

**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**

```r
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**

```r
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

**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

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

### dp2.genscan.LENGTH

**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

```r
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)
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)
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)
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

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

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

```r
data(droPer1.xenoRefGene.LENGTH)
head(droPer1.xenoRefGene.LENGTH)
```
droSec1.genscan.LENGTH

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

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)
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)
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

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/cgibin/hgTables) using the xenoRefGene table.

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

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)

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**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)
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)

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)
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)

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)
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)

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)
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)

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)
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)

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)
### 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)

---

### 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)
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)

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)
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)

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)
**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)

**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)
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)

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**

```r
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**

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

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)
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)

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)
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)

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)
**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**

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

---

**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**

```r
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**

```r
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**

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

---

**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)
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)

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)
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/hgTable) 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)

---

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/hgTable) 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)
**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**

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

**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**

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

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

---

**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**

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

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)
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)

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)
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)

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**

```r
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**

```r
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)
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)

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**

```r
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**

```r
data(mm7.xenoRefGene.LENGTH)
head(mm7.xenoRefGene.LENGTH)
```
mm8.ccdsGene.LENGTH

**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

**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**

```r
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**

```r
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)
**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**

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

---

**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**

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

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)
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)

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)
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)

---

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)
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

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

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

```r
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**

```r
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**

```r
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)
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)

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)
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)

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 

**See Also**

`downloadLengthFromUCSC`

**Examples**

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

---

**monDom5.xenoRefGene.LENGTH**

*Transcript length data for the organism monDom*

**Description**

`monDom5.xenoRefGene.LENGTH` is an 

**See Also**

`downloadLengthFromUCSC`

**Examples**

```r
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/cgibin/hgTables) using the refGene table.

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

See Also

downloadLengthFromUCSC

Examples

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

oryLat2.xenoRefGene.LENGTH

Transcript length data for the organism oryLat

Description

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

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)
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)

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)
Description

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

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

See Also

\texttt{downloadLengthFromUCSC}

Examples

\begin{verbatim}
data(petMar1.xenoRefGene.LENGTH) head(petMar1.xenoRefGene.LENGTH)
\end{verbatim}

Description

ponAbe\text{2}.\text{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 (\url{http://genome.ucsc.edu/cgi-bin/hgTables}) using the ensGene table.

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

See Also

\texttt{downloadLengthFromUCSC}

Examples

\begin{verbatim}
data(ponAbe2.ensGene.LENGTH) head(ponAbe2.ensGene.LENGTH)
\end{verbatim}
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**

```r
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**

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

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

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)
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)

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

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

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**

```r
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**

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

**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

**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

**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

**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 is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a 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)

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

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

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

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

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

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

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 geneLen DataBase package.

**Value**

A data.frame containing supported gene ID formats.

**Author(s)**

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

Examples

supportedGeneIDs()

---

supportedGenomes  
Supported Genomes

Description

Lists supported genomes

Usage

supportedGenomes()

Details

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

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

Value

A data.frame containing supported genomes.

Author(s)

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

Examples

supportedGenomes()

taeGut1.ensGene.LENGTH  
*Transcript length data for the organism taeGut*

Description

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

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

See Also

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

taeGut1.geneSymbol.LENGTH

Transcript length data for the organism taeGut

Description

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

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

See Also

downloadLengthFromUCSC

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

taeGut1.genscan.LENGTH

Transcript length data for the organism taeGut

Description

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

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

See Also

downloadLengthFromUCSC

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

Transcript length data for the organism taeGut

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

---------------------------------------------------------------------

taeGut1.refGene.LENGTH

Transcript length data for the organism taeGut

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

*Transcript length data for the organism taeGut*

**Description**

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

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

**See Also**

`downloadLengthFromUCSC`

**Examples**

```r
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**

```r
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/cgibin/hgTables) using the nscanGene table.

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

See Also

downloadLengthFromUCSC

Examples

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

tetNig2.ensGene.LENGTH

Transcript length data for the organism tetNig

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

Purge factors

Description

Removes all factors from a variable in a sensible way.

Usage

unfactor(var)

Arguments

var The variable from which you want the factors removed.

Details

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

Value

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

Author(s)

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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

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

*Topic datasets
  anoCar1.ensGene.LENGTH, 8
  anoCar1.genscan.LENGTH, 8
  anoCar1.xenoRefGene.LENGTH, 9
  anoGam1.ensGene.LENGTH, 9
  anoGam1.geneid.LENGTH, 10
  anoGam1.genscan.LENGTH, 10
  apiMe11.genscan.LENGTH, 11
  apiMe12.ensGene.LENGTH, 11
  apiMe12.geneid.LENGTH, 12
  apiMe12.genscan.LENGTH, 12
  apiCa11.xenoRefGene.LENGTH, 13
  bosTau2.geneid.LENGTH, 13
  bosTau2.geneSymbol.LENGTH, 14
  bosTau2.genscan.LENGTH, 14
  bosTau2.refGene.LENGTH, 15
  bosTau2.sgspGene.LENGTH, 15
  bosTau3.ensGene.LENGTH, 16
  bosTau3.geneid.LENGTH, 16
  bosTau3.geneSymbol.LENGTH, 17
  bosTau3.genscan.LENGTH, 17
  bosTau3.refGene.LENGTH, 18
  bosTau3.sgspGene.LENGTH, 18
  bosTau4.ensGene.LENGTH, 19
  bosTau4.geneSymbol.LENGTH, 19
  bosTau4.genscan.LENGTH, 20
  bosTau4.nscanGene.LENGTH, 20
  bosTau4.refGene.LENGTH, 21
  brafL01.xenoRefGene.LENGTH, 21
  caeJap1.xenoRefGene.LENGTH, 22
  caePb1.xenoRefGene.LENGTH, 22
  caePb2.xenoRefGene.LENGTH, 23
  caeRem2.xenoRefGene.LENGTH, 23
  caeRem3.xenoRefGene.LENGTH, 24
  cal3Ac1.genscan.LENGTH, 24
  cal3Ac1.nscanGene.LENGTH, 25
  canFam1.ensGene.LENGTH, 26
  canFam1.geneSymbol.LENGTH, 26
  canFam1.genscan.LENGTH, 27
  canFam1.nscanGene.LENGTH, 27
  canFam1.refGene.LENGTH, 28
  canFam1.xenoRefGene.LENGTH, 28
  canFam2.ensGene.LENGTH, 29
  canFam2.geneSymbol.LENGTH, 29
  canFam2.genscan.LENGTH, 30
  canFam2.nscanGene.LENGTH, 30
  canFam2.refGene.LENGTH, 31
  canFam2.xenoRefGene.LENGTH, 31
  cavPor3.ensGene.LENGTH, 32
  cavPor3.genscan.LENGTH, 32
  cavPor3.nscanGene.LENGTH, 33
  cavPor3.xenoRefGene.LENGTH, 33
  cb1.xenoRefGene.LENGTH, 34
  cb3.xenoRefGene.LENGTH, 34
  ce2.geneid.LENGTH, 35
  ce2.geneSymbol.LENGTH, 35
  ce2.refGene.LENGTH, 36
  ce4.geneSymbol.LENGTH, 36
  ce4.refGene.LENGTH, 37
  ce4.xenoRefGene.LENGTH, 37
  ce6.ensGene.LENGTH, 38
  ce6.geneSymbol.LENGTH, 38
  ce6.refGene.LENGTH, 39
  ce6.xenoRefGene.LENGTH, 39
  ce11.geneSymbol.LENGTH, 40
  ce11.refGene.LENGTH, 40
  ce11.xenoRefGene.LENGTH, 41
  ci1.ensGene.LENGTH, 41
  ci1.geneSymbol.LENGTH, 42
  ci1.refGene.LENGTH, 42
  ci1.xenoRefGene.LENGTH, 43
  danRer3.ensGene.LENGTH, 43
  danRer3.geneSymbol.LENGTH, 44
  danRer3.refGene.LENGTH, 44
  danRer4.ensGene.LENGTH, 45
  danRer4.geneSymbol.LENGTH, 45
  danRer4.genscan.LENGTH, 46
  danRer4.nscanGene.LENGTH, 46
  danRer4.refGene.LENGTH, 47
  danRer5.ensGene.LENGTH, 47
  danRer5.geneSymbol.LENGTH, 48
  danRer5.refGene.LENGTH, 48
  danRer5.vegaGene.LENGTH, 49
  danRer5.vegaPseudoGene.LENGTH, 49
  danRer6.ensGene.LENGTH, 50
<table>
<thead>
<tr>
<th>Gene Symbol</th>
<th>Length</th>
<th>Position</th>
</tr>
</thead>
<tbody>
<tr>
<td>danRer6</td>
<td>LENGTH</td>
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<tr>
<td>refGene</td>
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</tr>
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<td>LENGTH</td>
<td>51</td>
</tr>
<tr>
<td>dm1</td>
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</tr>
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<td>LENGTH</td>
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</tr>
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<td>geneid</td>
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<td>LENGTH</td>
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</tr>
<tr>
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<td>LENGTH</td>
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</tr>
<tr>
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<td>LENGTH</td>
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</tr>
<tr>
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<td>genscan</td>
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</tr>
<tr>
<td>xenoRefGene</td>
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<td>59</td>
</tr>
<tr>
<td>droAna1</td>
<td>geneid</td>
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<td>genscan</td>
<td>LENGTH</td>
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</tr>
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<td>nscanGene</td>
<td>LENGTH</td>
<td>85</td>
</tr>
<tr>
<td>refGene</td>
<td>LENGTH</td>
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<td>LENGTH</td>
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</tr>
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<td>galGal2</td>
<td>geneid</td>
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</tr>
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</tr>
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<td>hg16</td>
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<td>LENGTH</td>
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<td>LENGTH</td>
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<td>geneid</td>
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<tr>
<td>nscanGene</td>
<td>LENGTH</td>
<td>102</td>
</tr>
<tr>
<td>refGene</td>
<td>LENGTH</td>
<td>102</td>
</tr>
</tbody>
</table>
INDEX

rn3.ensGene.LENGTH, 154
rn3.geneid.LENGTH, 155
rn3.geneSymbol.LENGTH, 155
rn3.genscan.LENGTH, 156
rn3.knownGene.LENGTH, 156
rn3.nscanGene.LENGTH, 157
rn3.refGene.LENGTH, 157
rn3.sgpGene.LENGTH, 158
rn3.xenoRefGene.LENGTH, 158
rn4.ensGene.LENGTH, 159
rn4.geneid.LENGTH, 160
rn4.geneSymbol.LENGTH, 160
rn4.genscan.LENGTH, 160
rn4.knownGene.LENGTH, 161
rn4.nscanGene.LENGTH, 161
rn4.refGene.LENGTH, 162
rn4.sgpGene.LENGTH, 162
rn4.xenoRefGene.LENGTH, 163
sacCer1.ensGene.LENGTH, 163
sacCer2.ensGene.LENGTH, 164
strPur1.geneSymbol.LENGTH, 164
strPur1.genscan.LENGTH, 165
strPur1.refGene.LENGTH, 165
strPur1.xenoRefGene.LENGTH, 166
strPur2.geneSymbol.LENGTH, 166
strPur2.genscan.LENGTH, 167
strPur2.refGene.LENGTH, 167
strPur2.xenoRefGene.LENGTH, 168
taeGut1.ensGene.LENGTH, 169
taeGut1.geneSymbol.LENGTH, 170
taeGut1.genscan.LENGTH, 170
taeGut1.nscanGene.LENGTH, 171
taeGut1.refGene.LENGTH, 171
taeGut1.xenoRefGene.LENGTH, 172
tetNig1.ensGene.LENGTH, 172
tetNig1.geneid.LENGTH, 173
tetNig1.genscan.LENGTH, 173
tetNig1.nscanGene.LENGTH, 174
tetNig2.ensGene.LENGTH, 174
tetNig2.genscan.LENGTH, 176
tetNig2.refGene.LENGTH, 176
xenTro1.genscan.LENGTH, 176
xenTro1.refGene.LENGTH, 177
xenTro2.genscan.LENGTH, 177
xenTro2.refGene.LENGTH, 178
anoCar1.ensGene.LENGTH, 8
anoCar1.genscan.LENGTH, 8
anoCar1.xenoRefGene.LENGTH, 9
anoGam1.ensGene.LENGTH, 9
anoGam1.geneid.LENGTH, 10
anoGam1.genscan.LENGTH, 10
apiMe11.genscan.LENGTH, 11
apiMe12.ensGene.LENGTH, 11
apiMe12.geneid.LENGTH, 12
apiMe12.genscan.LENGTH, 12
apiCali.xenoRefGene.LENGTH, 13
bosTau2.geneid.LENGTH, 13
bosTau2.geneSymbol.LENGTH, 14
bosTau2.genscan.LENGTH, 14
bosTau2.refGene.LENGTH, 15
bosTau2.sgpGene.LENGTH, 15
bosTau3.ensGene.LENGTH, 16
bosTau3.geneid.LENGTH, 16
bosTau3.geneSymbol.LENGTH, 17
bosTau3.genscan.LENGTH, 17
bosTau3.refGene.LENGTH, 18
bosTau3.xenoRefGene.LENGTH, 18
bosTau4.geneid.LENGTH, 19
bosTau4.geneSymbol.LENGTH, 19
bosTau4.genscan.LENGTH, 20
bosTau4.sgpGene.LENGTH, 20
bosTau4.xenoRefGene.LENGTH, 21
braFlo1.xenoRefGene.LENGTH, 21
caeJap1.xenoRefGene.LENGTH, 22
caePb1.xenoRefGene.LENGTH, 22
caePb2.xenoRefGene.LENGTH, 23
caeRem2.xenoRefGene.LENGTH, 23
caeRem3.xenoRefGene.LENGTH, 24
calJac1.genscan.LENGTH, 24
calJac1.xenoRefGene.LENGTH, 25
canFam1.ensGene.LENGTH, 26
canFam1.geneSymbol.LENGTH, 26
canFam1.genscan.LENGTH, 27
canFam1.nscanGene.LENGTH, 27
canFam1.refGene.LENGTH, 28
canFam1.xenoRefGene.LENGTH, 28
canFam2.ensGene.LENGTH, 29
canFam2.geneSymbol.LENGTH, 29
canFam2.genscan.LENGTH, 30
canFam2.nscanGene.LENGTH, 30
canFam2.refGene.LENGTH, 31
canFam2.xenoRefGene.LENGTH, 31
cavPor3.ensGene.LENGTH, 32
cavPor3.genscan.LENGTH, 32
cavPor3.nscanGene.LENGTH, 33
cavPor3.xenoRefGene.LENGTH, 33
cb1.xenoRefGene.LENGTH, 34
cb3.xenoRefGene.LENGTH, 34
ce2.geneid.LENGTH, 35
ce2.geneSymbol.LENGTH, 35
ce2.refGene.LENGTH, 36
ce4.geneSymbol.LENGTH, 36
ce4.refGene.LENGTH, 37
ornAna1.refGene.LENGTH, 139
ornAna1.xenoRefGene.LENGTH, 139
oryLat2.ensGene.LENGTH, 140
oryLat2.geneSymbol.LENGTH, 141
oryLat2.refGene.LENGTH, 141
oryLat2.xenoRefGene.LENGTH, 141
panTro1.ensGene.LENGTH, 142
panTro1.geneid.LENGTH, 142
panTro1.genscan.LENGTH, 143
panTro1.xenoRefGene.LENGTH, 143
panTro2.geneSymbol.LENGTH, 144
panTro2.genscan.LENGTH, 145
panTro2.refGene.LENGTH, 146
panTro2.xenoRefGene.LENGTH, 146
petMar1.xenoRefGene.LENGTH, 147
ponAbe2.ensGene.LENGTH, 147
ponAbe2.geneSymbol.LENGTH, 148
ponAbe2.genscan.LENGTH, 148
ponAbe2.nscanGene.LENGTH, 149
ponAbe2.refGene.LENGTH, 149
ponAbe2.xenoRefGene.LENGTH, 150
priPac1.xenoRefGene.LENGTH, 150
rheMac2.ensGene.LENGTH, 151
rheMac2.geneid.LENGTH, 151
rheMac2.geneSymbol.LENGTH, 152
rheMac2.nscanGene.LENGTH, 152
rheMac2.refGene.LENGTH, 153
rheMac2.sgpGene.LENGTH, 153
rheMac2.xenoRefGene.LENGTH, 154
rn3.ensGene.LENGTH, 154
rn3.geneid.LENGTH, 155
rn3.geneSymbol.LENGTH, 155
rn3.genscan.LENGTH, 156
rn3.knownGene.LENGTH, 156
rn3.nscanGene.LENGTH, 157
rn3.refGene.LENGTH, 157
rn3.sgpGene.LENGTH, 158
rn3.xenoRefGene.LENGTH, 158
rn4.ensGene.LENGTH, 158
rn4.geneid.LENGTH, 159
rn4.geneSymbol.LENGTH, 160
rn4.genscan.LENGTH, 160
rn4.knownGene.LENGTH, 161
rn4.nscanGene.LENGTH, 161
rn4.refGene.LENGTH, 162
rn4.sgpGene.LENGTH, 162
rn4.xenoRefGene.LENGTH, 163
sacCer1.ensGene.LENGTH, 163
sacCer2.ensGene.LENGTH, 164
strPur1.geneSymbol.LENGTH, 164
strPur1.genscan.LENGTH, 165
strPur1.refGene.LENGTH, 165
strPur1.xenoRefGene.LENGTH, 166
strPur2.geneSymbol.LENGTH, 166
strPur2.genscan.LENGTH, 167
strPur2.refGene.LENGTH, 167
strPur2.xenoRefGene.LENGTH, 168
supportedGeneIDs, 168
supportedGenomes, 169
taeGut1.ensGene.LENGTH, 169
taeGut1.geneSymbol.LENGTH, 170
taeGut1.genscan.LENGTH, 170
taeGut1.nscanGene.LENGTH, 171
taeGut1.refGene.LENGTH, 171
taeGut1.xenoRefGene.LENGTH, 172
tetNig1.ensGene.LENGTH, 172
tetNig1.geneid.LENGTH, 173
tetNig1.genscan.LENGTH, 173
tetNig1.nscanGene.LENGTH, 174
tetNig1.refGene.LENGTH, 174
unfactor, 175
xenTro1.genscan.LENGTH, 176
xenTro1.ensGene.LENGTH, 176
xenTro2.geneSymbol.LENGTH, 177
xenTro2.genscan.LENGTH, 177
xenTro2.refGene.LENGTH, 178