Package 'geneLenDataBase'

October 4, 2014

Version 1.0.0

Date 2010/03/30

Title Lengths of mRNA transcripts for a number of genomes

Author Matthew Young

Maintainer

Matthew Young <myoung@wehi.edu.au>, Nadia Davidson <nadia.davidson@mcri.edu.au>

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 HighThroughputSequencingData, ExperimentData, Transcription,RNAseq

License LGPL (>= 2)

R topics documented:

anoCar1.ensGene.LENGTH	
anoCar1.genscan.LENGTH	
anoCar1.xenoRefGene.LENGTH	0
anoGam1.ensGene.LENGTH	0
anoGam1.geneid.LENGTH	1
anoGam1.genscan.LENGTH	1
apiMel1.genscan.LENGTH	2
apiMel2.ensGene.LENGTH	2
apiMel2.geneid.LENGTH	
apiMel2.genscan.LENGTH	
aplCal1.xenoRefGene.LENGTH	
bosTau2.geneid.LENGTH 1	4
bosTau2.geneSymbol.LENGTH 1	5

bosTau2.genscan.LENGTH	
bosTau2.refGene.LENGTH	
bosTau2.sgpGene.LENGTH	
bosTau3.ensGene.LENGTH	
bosTau3.geneid.LENGTH	
bosTau3.geneSymbol.LENGTH	
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	
ce2.geneid.LENGTH	
ce2.geneSymbol.LENGTH	
ce2.refGene.LENGTH	
ce4.geneSymbol.LENGTH	
ce4.refGene.LENGTH	
ce6.ensGene.LENGTH	

cc6.refGene.LENGTH 40 cc6.xenoRefGene.LENGTH 41 cil.geneSymbol.LENGTH 41 cil.geneSymbol.LENGTH 42 ci2.ensGene.LENGTH 42 ci2.ensGene.LENGTH 42 ci2.ensGene.LENGTH 43 ci2.refGene.LENGTH 43 ci2.refGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer3.ensGene.LENGTH 45 danRer4.ensGene.LENGTH 45 danRer4.ensGene.LENGTH 46 danRer4.genscan.LENGTH 47 danRer4.genscan.LENGTH 47 danRer4.genscan.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 49 danRer5.refGene.LENGTH 49 danRer5.refGene.LENGTH 49 danRer5.refGene.LENGTH 50 danRer5.regensymbol.LENGTH 50 danRer5.regenesymbol.LENGTH 51 danRer5.regenesymbol.LENGTH 52 danRer5.regenesymbol.LENGTH 52 <th>ce6.geneSymbol.LENGTH</th> <th></th> <th></th> <th></th>	ce6.geneSymbol.LENGTH			
cil.geneSymbol.LENGTH 41 cil.renoRefGene.LENGTH 42 ci2.ensGene.LENGTH 42 ci2.ensGene.LENGTH 43 ci2.refGene.LENGTH 43 ci2.refGene.LENGTH 43 ci2.enoRefGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer4.ensGene.LENGTH 45 danRer4.ensGene.LENGTH 46 danRer4.ensGene.LENGTH 46 danRer4.ensGene.LENGTH 47 danRer4.enscan.LENGTH 47 danRer4.enscan.LENGTH 47 danRer4.genesan.LENGTH 47 danRer4.genesan.LENGTH 48 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 49 danRer5.refGene.LENGTH 49 danRer5.refGene.LENGTH 49 danRer5.regaesupmobl.LENGTH 49 danRer5.regenes.LENGTH 50 danRer5.regenes.LENGTH 50 danRer5.regenes.LENGTH 50 danRer5.regenes.LENGTH 50 danRer5.regene.LENGTH 50 danRer				
cil.refGene.LENGTH 41 cil.xenoRefGene.LENGTH 42 ci2.ensGene LENGTH 43 ci2.refGene.LENGTH 43 ci2.xenoRefGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer3.refGene.LENGTH 45 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 48 danRer5.ensGene.LENGTH 48 danRer5.geneSymbol.LENGTH 48 danRer5.geneSymbol.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer5.vegaBscudoGene.LENGTH 50 danRer5.vegaBscudoGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 52 danRer6.venoRefGene.LENGTH 52 danRer6.venoRefGene.LENGTH <td>ce6.xenoRefGene.LENGTH</td> <td> </td> <td> </td> <td> 40</td>	ce6.xenoRefGene.LENGTH	 	 	 40
cil.refGene.LENGTH 41 cil.xenoRefGene.LENGTH 42 ci2.ensGene LENGTH 43 ci2.refGene.LENGTH 43 ci2.xenoRefGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer3.refGene.LENGTH 45 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 48 danRer5.ensGene.LENGTH 48 danRer5.geneSymbol.LENGTH 48 danRer5.geneSymbol.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer5.vegaBscudoGene.LENGTH 50 danRer5.vegaBscudoGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 52 danRer6.venoRefGene.LENGTH 52 danRer6.venoRefGene.LENGTH <td>ci1.geneSymbol.LENGTH</td> <td> </td> <td> </td> <td> 41</td>	ci1.geneSymbol.LENGTH	 	 	 41
ci2.ensGene.LENGTH 42 ci2.retGene.LENGTH 43 ci2.retGene.LENGTH 43 ci2.xenoRetGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer3.ensGene.LENGTH 45 danRer4.ensGene.LENGTH 45 danRer4.ensGene.LENGTH 46 danRer4.ensGene.LENGTH 46 danRer4.ensGene.LENGTH 47 danRer4.ensGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 49 danRer5.retGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer5.vegaGene.LENGTH 50 danRer5.vegaGene.LENGTH 50 danRer6.geneSymbol.LENGTH 51 danRer6.retGene.LENGTH 51 danRer6.geneSymbol.LENGTH 51 danRer6.geneSymbol.LENGTH 52 danRer6.geneSymbol.LENGTH 53 danRer6.sensGene.LENGTH 53 danRer6.sensGene.LENGTH 53 danl.genSymbol.LENGTH 53	ci1.refGene.LENGTH	 	 	 41
ci2.geneSymbol.LENGTH 43 ci2.renGene.LENGTH 43 ci2.xenoRefGene.LENGTH 44 danRer3.geneSymbol.LENGTH 45 danRer3.refGene.LENGTH 45 danRer4.ensGene.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 48 danRer5.geneSymbol.LENGTH 49 danRer5.geneSymbol.LENGTH 49 danRer5.geneSymbol.LENGTH 49 danRer5.geneSymbol.LENGTH 49 danRer5.geneSymbol.LENGTH 50 danRer5.vegaGene.LENGTH 50 danRer6.geneSymbol.LENGTH 50 danRer6.geneSymbol.LENGTH 51 danRer6.geneSymbol.LENGTH 52 danRer6.geneSymbol.LENGTH 52 danRer6.geneSymbol.LENGTH 53 dm1.genseSymbol.LENGTH 53 dm1.genseSymbol.LENGTH 53 dm1.genseSymbol.LENGTH 53 dm1.geneSymbol.LEN	ci1.xenoRefGene.LENGTH	 	 	 42
ci2.geneSymbol.LENGTH 43 ci2.renGene.LENGTH 43 ci2.xenoRefGene.LENGTH 44 danRer3.geneSymbol.LENGTH 45 danRer3.refGene.LENGTH 45 danRer4.ensGene.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 48 danRer5.geneSymbol.LENGTH 49 danRer5.geneSymbol.LENGTH 49 danRer5.geneSymbol.LENGTH 49 danRer5.geneSymbol.LENGTH 49 danRer5.geneSymbol.LENGTH 50 danRer5.vegaGene.LENGTH 50 danRer6.geneSymbol.LENGTH 50 danRer6.geneSymbol.LENGTH 51 danRer6.geneSymbol.LENGTH 52 danRer6.geneSymbol.LENGTH 52 danRer6.geneSymbol.LENGTH 53 dm1.genseSymbol.LENGTH 53 dm1.genseSymbol.LENGTH 53 dm1.genseSymbol.LENGTH 53 dm1.geneSymbol.LEN	ci2.ensGene.LENGTH	 	 	 42
ci2.xenoRefGene.LENGTH 44 danRer3.ensGene.LENGTH 44 danRer3.refGene.LENGTH 45 danRer4.ensGene.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 47 danRer5.ensGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 48 danRer5.geneSymbol.LENGTH 49 danRer5.geneSymbol.LENGTH 49 danRer5.ensGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.seneSeneb.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 52 danRer6.ensOffle.LENGTH 52 danRer6.ensOffle.LENGTH 52 danLenGene.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 54 dm2.geneSymbol.LENGTH 54 <td>ci2.geneSymbol.LENGTH</td> <td> </td> <td> </td> <td> 43</td>	ci2.geneSymbol.LENGTH	 	 	 43
danRer3.ensGene.LENGTH 44 danRer4.geneSymbol.LENGTH 45 danRer4.ensGene.LENGTH 46 danRer4.ensGene.LENGTH 46 danRer4.geneSymbol.LENGTH 46 danRer4.geneSymbol.LENGTH 47 danRer4.genscan.LENGTH 47 danRer5.ensGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer5.vegaPseudoGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 52 danRer6.sensGene.LENGTH 53 dm1.gensSymbol.LENGTH 53 dm1.gensSymbol.LENGTH 53 dm1.genscan.LENGTH 53 dm1.genscan.LENGTH 54 dm2.genescan.LENGTH 55 dm3.genes.lensGTH 56 dm3.segnes.lensGTH 56 dm3.segnes.lensGTH 56 <	ci2.refGene.LENGTH	 	 	 43
danRer3.geneSymbol.LENGTH 45 danRer4.ensGene.LENGTH 45 danRer4.ensGene.LENGTH 46 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 47 danRer4.refGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 48 danRer5.geneSymbol.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer5.vegaGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensOrdene.LENGTH 52 danRer6.ensOrdene.LENGTH 52 danRer6.ensOrdene.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSunbl.LENGTH 53 dm1.genescan.LENGTH 53 dm2.genescan.LENGTH 54 dm2.genescan.LENGTH 54 dm2.genescan.LENGTH 55 dm3.nerefGene.LENGTH 56 <	ci2.xenoRefGene.LENGTH	 	 	 44
danRer3.refGene.LENGTH 45 danRer4.ensGene.LENGTH 46 danRer4.geneSymbol.LENGTH 47 danRer4.geneSymbol.LENGTH 47 danRer4.refGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 52 danRer6.ensGene.LENGTH 52 danRer6.zenoRefGene.LENGTH 52 dm1.genscan.LENGTH 53 dm1.genscan.LENGTH 53 dm1.genscan.LENGTH 53 dm2.geneid.LENGTH 55 dm2.geneid.LENGTH 55 dm2.geneid.LENGTH 56 dm2.geneid.LENGTH 56 dm3.genes.LENGTH 56 dm3.geneid.LENGT	danRer3.ensGene.LENGTH	 	 	 44
danRer4.ensGene.LENGTH 46 danRer4.gencSymbol.LENGTH 46 danRer4.genscan.LENGTH 47 danRer4.refGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.gencSymbol.LENGTH 48 danRer5.refGene.LENGTH 49 danRer5.vegaPseudoGene.LENGTH 49 danRer5.vegaPseudoGene.LENGTH 50 danRer5.vegaPseudoGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.refGene.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.refGene.LENGTH 52 danRer6.refGene.LENGTH 52 danLenesymbol.LENGTH 53 dm1.gencsan.LENGTH 53 dm1.gencsan.LENGTH 53 dm2.gencsymbol.LENGTH 55 dm2.gencsymbol.LENGTH 55 dm2.gencsymbol.LENGTH 56 dm3.gencsymbol.LENGTH 56 dm3.gencsymbol.LENGTH 57 dm1.refGene.LENGTH 56 dm3.genesymbol.LENGTH 57	danRer3.geneSymbol.LENGTH	 	 	 45
danRer4.ensGene.LENGTH 46 danRer4.gencSymbol.LENGTH 46 danRer4.genscan.LENGTH 47 danRer4.refGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.gencSymbol.LENGTH 48 danRer5.refGene.LENGTH 49 danRer5.vegaPseudoGene.LENGTH 49 danRer5.vegaPseudoGene.LENGTH 50 danRer5.vegaPseudoGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.refGene.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.refGene.LENGTH 52 danRer6.refGene.LENGTH 52 danLenesymbol.LENGTH 53 dm1.gencsan.LENGTH 53 dm1.gencsan.LENGTH 53 dm2.gencsymbol.LENGTH 55 dm2.gencsymbol.LENGTH 55 dm2.gencsymbol.LENGTH 56 dm3.gencsymbol.LENGTH 56 dm3.gencsymbol.LENGTH 57 dm1.refGene.LENGTH 56 dm3.genesymbol.LENGTH 57	danRer3.refGene.LENGTH	 	 	 45
danRer4.genscan.LENGTH 47 danRer4.nscanGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.geneSymbol.LENGTH 49 danRer5.refGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.geneSymbol.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.senoReffeene.LENGTH 52 danRer6.xenoReffeene.LENGTH 52 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.genescan.LENGTH 53 dm1.genescan.LENGTH 53 dm2.genescan.LENGTH 55 dm2.nscanGene.LENGTH 56 dm2.genescan.LENGTH 56 dm2.refGene.LENGTH 57 dm3.geneSymbol.LENGTH 57 dm3.geneSymbol.LENGTH 57 dm3.geneSymbol.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 59	danRer4.ensGene.LENGTH	 	 	 46
danRer4.nscanGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 49 danRer5.refGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.geneSymbol.LENGTH 51 danRer6.geneSymbol.LENGTH 51 danRer6.ensGene.LENGTH 52 danRer6.senoRefGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.genescan.LENGTH 53 dm2.genescan.LENGTH 55 dm2.genescan.LENGTH 55 dm2.nscanGene.LENGTH 56 dm2.refGene.LENGTH 56 dm2.refGene.LENGTH 57 dm3.sendPasaGene.LENGTH 57 dm3.sendPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genscan.LENGTH 59 dp3				
danRer4.nscanGene.LENGTH 47 danRer5.ensGene.LENGTH 48 danRer5.ensGene.LENGTH 49 danRer5.refGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.geneSymbol.LENGTH 51 danRer6.geneSymbol.LENGTH 51 danRer6.ensGene.LENGTH 52 danRer6.senoRefGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.genescan.LENGTH 53 dm2.genescan.LENGTH 55 dm2.genescan.LENGTH 55 dm2.nscanGene.LENGTH 56 dm2.refGene.LENGTH 56 dm2.refGene.LENGTH 57 dm3.sendPasaGene.LENGTH 57 dm3.sendPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genscan.LENGTH 59 dp3	danRer4.genscan.LENGTH	 	 	 47
danRer5.ensGene.LENGTH 48 danRer5.geneSymbol.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.eneSymbol.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm2.geneid.LENGTH 54 dm2.geneid.LENGTH 55 dm2.genesymbol.LENGTH 55 dm2.negGene.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.necanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genscan.LENGTH 59 dp3.genesul.ENGTH 59 dp3.genesul.	danRer4.nscanGene.LENGTH	 	 	 47
danRer5.ensGene.LENGTH 48 danRer5.geneSymbol.LENGTH 49 danRer5.vegaGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer6.ensGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.ensGene.LENGTH 51 danRer6.eneSymbol.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm2.geneid.LENGTH 54 dm2.geneid.LENGTH 55 dm2.genesymbol.LENGTH 55 dm2.negGene.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.necanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genscan.LENGTH 59 dp3.genesul.ENGTH 59 dp3.genesul.	danRer4.refGene.LENGTH	 	 	 48
danRer5.refGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer5.vegaPseudoGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.geneSymbol.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 53 dm1.genscan.LENGTH 53 dm1.genscan.LENGTH 53 dm1.genscan.LENGTH 54 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 56 dm2.geneSymbol.LENGTH 56 dm3.nscanGene.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 59 dp3.geneid.LENGTH 59 dp3.genscan.LENGTH 60 dp3.geneid.LENGTH 61 droAnal.geneid				
danRer5.refGene.LENGTH 49 danRer5.vegaGene.LENGTH 50 danRer5.vegaPseudoGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.geneSymbol.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 53 dm1.genscan.LENGTH 53 dm1.genscan.LENGTH 53 dm1.genscan.LENGTH 54 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 56 dm2.geneSymbol.LENGTH 56 dm3.nscanGene.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 59 dp3.geneid.LENGTH 59 dp3.genscan.LENGTH 60 dp3.geneid.LENGTH 61 droAnal.geneid	danRer5.geneSymbol.LENGTH	 	 	 49
danRer5.vegaPseudoGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.geneSymbol.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.refGene.LENGTH 53 dm2.geneid.LENGTH 54 dm2.geneid.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 56 dm2.refGene.LENGTH 56 dm3.nscanGene.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 59 dp3.geneid.LENGTH 59 dp3.geneid.LENGTH 60 dp3.ageneid.LENGTH 60 dp3.geneid.LENGTH 60 dp3.geneid.LENGTH 60 dp3.geneid.LENGTH 61 dp0Anal.geneid.LENGTH <				
danRer5.vegaPseudoGene.LENGTH 50 danRer6.ensGene.LENGTH 51 danRer6.geneSymbol.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.refGene.LENGTH 53 dm2.geneid.LENGTH 54 dm2.geneid.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 56 dm2.refGene.LENGTH 56 dm3.nscanGene.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 59 dp3.geneid.LENGTH 59 dp3.geneid.LENGTH 60 dp3.ageneid.LENGTH 60 dp3.geneid.LENGTH 60 dp3.geneid.LENGTH 60 dp3.geneid.LENGTH 61 dp0Anal.geneid.LENGTH <	danRer5.vegaGene.LENGTH	 	 	 50
danRer6.geneSymbol.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm2.geneid.LENGTH 54 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 56 dm2.refGene.LENGTH 56 dm3.geneSymbol.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.xenoRefGene.LENGTH 59 dp3.geneid.LENGTH 59 dp3.geneid.LENGTH 60 droAnal.genscan.LENGTH 61 droAnal.genscan.LENGTH 61 droAnal.genscan.LENGTH 61 droAnal.genscan.LENGTH 61	danRer5.vegaPseudoGene.LENGTH .	 	 	 50
danRer6.geneSymbol.LENGTH 51 danRer6.refGene.LENGTH 52 danRer6.xenoRefGene.LENGTH 52 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm1.geneSymbol.LENGTH 53 dm2.geneid.LENGTH 54 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 56 dm2.refGene.LENGTH 56 dm3.geneSymbol.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.xenoRefGene.LENGTH 59 dp3.geneid.LENGTH 59 dp3.geneid.LENGTH 60 droAnal.genscan.LENGTH 61 droAnal.genscan.LENGTH 61 droAnal.genscan.LENGTH 61 droAnal.genscan.LENGTH 61	danRer6.ensGene.LENGTH	 	 	 51
danRer6.xenoRefGene.LENGTH 52 dm1.geneSymbol.LENGTH 53 dm1.genscan.LENGTH 53 dm1.refGene.LENGTH 54 dm2.geneid.LENGTH 54 dm2.geneSymbol.LENGTH 54 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm3.geneSymbol.LENGTH 56 dm3.geneSymbol.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.geneSymbol.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.nscanPasaGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genescan.LENGTH 59 dp3.geneid.LENGTH 59 dp3.geneid.LENGTH 60 droAna1.geneid.LENGTH 60 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 62 droAna1.geneid.LENGTH 62				
danRer6.xenoRefGene.LENGTH 52 dm1.geneSymbol.LENGTH 53 dm1.genscan.LENGTH 53 dm1.refGene.LENGTH 54 dm2.geneid.LENGTH 54 dm2.geneSymbol.LENGTH 54 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm3.geneSymbol.LENGTH 56 dm3.geneSymbol.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.geneSymbol.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.nscanPasaGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genescan.LENGTH 59 dp3.geneid.LENGTH 59 dp3.geneid.LENGTH 60 droAna1.geneid.LENGTH 60 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 62 droAna1.geneid.LENGTH 62				
dm1.genscan.LENGTH 53 dm1.refGene.LENGTH 54 dm2.geneid.LENGTH 54 dm2.geneSymbol.LENGTH 55 dm2.geneSymbol.LENGTH 55 dm2.genescan.LENGTH 55 dm2.genescan.LENGTH 55 dm2.genescan.LENGTH 55 dm2.genescan.LENGTH 56 dm2.refGene.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.refGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genscan.LENGTH 58 dp3.geneid.LENGTH 59 dp3.geneid.LENGTH 60 dp3.xenoRefGene.LENGTH 60 dp3.xenoRefGene.LENGTH 60 droAnal.geneid.LENGTH 61 droAnal.geneid.LENGTH 61 droAnal.geneid.LENGTH 61 droAnal.geneid.LENGTH 61 droAnal.geneid.LENGTH 61 droAnal.genscan.LENGTH 61 droAnal.genscan.LENGTH 62 droAnal.genscan.LENGTH 61	danRer6.xenoRefGene.LENGTH	 	 	 52
dm1.refGene.LENGTH54dm2.geneid.LENGTH54dm2.geneSymbol.LENGTH55dm2.genescan.LENGTH55dm2.refGene.LENGTH56dm3.geneSymbol.LENGTH56dm3.geneSymbol.LENGTH57dm3.nscanPasaGene.LENGTH57dm3.refGene.LENGTH58dp2.genscan.LENGTH58dp2.genscan.LENGTH59dp3.geneid.LENGTH59dp3.geneid.LENGTH60droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61droAna1.geneid.LENGTH61	dm1.geneSymbol.LENGTH	 	 	 53
dm2.geneid.LENGTH 54 dm2.geneSymbol.LENGTH 55 dm2.genscan.LENGTH 55 dm2.nscanGene.LENGTH 56 dm2.refGene.LENGTH 56 dm3.geneSymbol.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genscan.LENGTH 59 dp3.geneid.LENGTH 59 dp3.geneid.LENGTH 60 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61	dm1.genscan.LENGTH	 	 	 53
dm2.geneid.LENGTH 54 dm2.geneSymbol.LENGTH 55 dm2.genscan.LENGTH 55 dm2.nscanGene.LENGTH 56 dm2.refGene.LENGTH 56 dm3.geneSymbol.LENGTH 56 dm3.geneSymbol.LENGTH 57 dm3.nscanPasaGene.LENGTH 57 dm3.refGene.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genscan.LENGTH 58 dp2.genscan.LENGTH 59 dp3.geneid.LENGTH 59 dp3.geneid.LENGTH 60 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61 droAna1.geneid.LENGTH 61	dm1.refGene.LENGTH	 	 	 54
dm2.genscan.LENGTH55dm2.nscanGene.LENGTH56dm2.refGene.LENGTH56dm3.geneSymbol.LENGTH57dm3.nscanPasaGene.LENGTH57dm3.refGene.LENGTH58dp2.genscan.LENGTH58dp2.genscan.LENGTH59dp3.geneid.LENGTH59dp3.geneid.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH62droAna2.genscan.LENGTH62				
dm2.nscanGene.LENGTH56dm2.refGene.LENGTH56dm3.geneSymbol.LENGTH57dm3.nscanPasaGene.LENGTH57dm3.refGene.LENGTH58dp2.genscan.LENGTH58dp2.xenoRefGene.LENGTH59dp3.geneid.LENGTH59dp3.genscan.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH62droAna2.genscan.LENGTH62	dm2.geneSymbol.LENGTH	 	 	 55
dm2.nscanGene.LENGTH56dm2.refGene.LENGTH56dm3.geneSymbol.LENGTH57dm3.nscanPasaGene.LENGTH57dm3.refGene.LENGTH58dp2.genscan.LENGTH58dp2.xenoRefGene.LENGTH59dp3.geneid.LENGTH59dp3.genscan.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH62droAna2.genscan.LENGTH62	dm2.genscan.LENGTH	 	 	 55
dm3.geneSymbol.LENGTH57dm3.nscanPasaGene.LENGTH57dm3.refGene.LENGTH58dp2.genscan.LENGTH58dp2.xenoRefGene.LENGTH59dp3.geneid.LENGTH59dp3.genscan.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH62droAna2.genscan.LENGTH62	dm2.nscanGene.LENGTH	 	 	 56
dm3.nscanPasaGene.LENGTH57dm3.refGene.LENGTH58dp2.genscan.LENGTH58dp2.xenoRefGene.LENGTH59dp3.geneid.LENGTH59dp3.genscan.LENGTH60dp3.xenoRefGene.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH62droAna2.genscan.LENGTH62	dm2.refGene.LENGTH	 	 	 56
dm3.refGene.LENGTH58dp2.genscan.LENGTH58dp2.xenoRefGene.LENGTH59dp3.geneid.LENGTH59dp3.genscan.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH62droAna1.genscan.LENGTH62droAna1.genscan.LENGTH62	dm3.geneSymbol.LENGTH	 	 	 57
dp2.genscan.LENGTH58dp2.xenoRefGene.LENGTH59dp3.geneid.LENGTH59dp3.genscan.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genescan.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH62droAna2.genscan.LENGTH62	dm3.nscanPasaGene.LENGTH	 	 	 57
dp2.xenoRefGene.LENGTH59dp3.geneid.LENGTH59dp3.genscan.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH61droAna1.genscan.LENGTH62droAna2.genscan.LENGTH62	dm3.refGene.LENGTH	 	 	 58
dp3.geneid.LENGTH59dp3.genscan.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.xenoRefGene.LENGTH62droAna2.genscan.LENGTH62	dp2.genscan.LENGTH	 	 	 58
dp3.genscan.LENGTH60dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.xenoRefGene.LENGTH62droAna2.genscan.LENGTH62	dp2.xenoRefGene.LENGTH	 	 	 59
dp3.xenoRefGene.LENGTH60droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.xenoRefGene.LENGTH62droAna2.genscan.LENGTH62	dp3.geneid.LENGTH	 	 	 59
droAna1.geneid.LENGTH61droAna1.genscan.LENGTH61droAna1.xenoRefGene.LENGTH62droAna2.genscan.LENGTH62	dp3.genscan.LENGTH	 	 	 60
droAna1.genscan.LENGTH61droAna1.xenoRefGene.LENGTH62droAna2.genscan.LENGTH62	dp3.xenoRefGene.LENGTH	 	 	 60
droAna1.genscan.LENGTH61droAna1.xenoRefGene.LENGTH62droAna2.genscan.LENGTH62	droAna1.geneid.LENGTH	 	 	 61
droAna1.xenoRefGene.LENGTH 62 droAna2.genscan.LENGTH 62	•	 	 	 61
droAna2.genscan.LENGTH	e			
e		 	 	 62
	droAna2.xenoRefGene.LENGTH	 	 	 63

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

galGal2.geneid.LENGTH	87
galGal2.geneSymbol.LENGTH	88
galGal2.genscan.LENGTH	88
galGal2.refGene.LENGTH	89
galGal2.sgpGene.LENGTH	
galGal3.ensGene.LENGTH	
galGal3.geneSymbol.LENGTH	90
galGal3.genscan.LENGTH	91
galGal3.nscanGene.LENGTH	91
galGal3.refGene.LENGTH	92
galGal3.xenoRefGene.LENGTH	92
gasAcu1.ensGene.LENGTH	
gasAcu1.nscanGene.LENGTH	
hg16.acembly.LENGTH	
hg16.ensGene.LENGTH	
hg16.exoniphy.LENGTH	
hg16.geneid.LENGTH	
hg16.geneSymbol.LENGTH	
hg16.genscan.LENGTH	
hg16.knownGene.LENGTH	
hg16.refGene.LENGTH	
hg16.sgpGene.LENGTH	
hg17.acembly.LENGTH	
hg17.acescan.LENGTH	
hg17.ccdsGene.LENGTH	
hg17.ensGene.LENGTH	
hg17.exoniphy.LENGTH	
hg17.geneid.LENGTH	
hg17.geneSymbol.LENGTH	
hg17.genscan.LENGTH	
hg17.knownGene.LENGTH	
hg17.refGene.LENGTH	
hg17.sgpGene.LENGTH	
hg17.vegaGene.LENGTH	
hg17.vegaPseudoGene.LENGTH	
hg17.xenoRefGene.LENGTH	
hg18.acembly.LENGTH	
hg18.acescan.LENGTH	
hg18.ccdsGene.LENGTH	
hg18.ensGene.LENGTH	
hg18.exoniphy.LENGTH	
hg18.geneid.LENGTH	
hg18.geneSymbol.LENGTH	
hg18.genscan.LENGTH	
hg18.knownGene.LENGTH	
hg18.knownGeneOld3.LENGTH	
hg18.refGene.LENGTH	
hg18.sgpGene.LENGTH	
ngro.spoenc.Deno111	111

hg18.sibGene.LENGTH	. 111
hg18.xenoRefGene.LENGTH	. 112
hg19.ccdsGene.LENGTH	
hg19.ensGene.LENGTH	
hg19.exoniphy.LENGTH	
hg19.geneSymbol.LENGTH	
hg19.knownGene.LENGTH	
hg19.nscanGene.LENGTH	. 115
hg19.refGene.LENGTH	
hg19.xenoRefGene.LENGTH	
loxAfr3.xenoRefGene.LENGTH	
mm7.ensGene.LENGTH	
mm7.geneid.LENGTH	
mm7.geneSymbol.LENGTH	
mm7.genesymbol.LENGTH	
mm7.genscan.LENGTH	
mm7.refGene.LENGTH	
mm7.sgpGene.LENGTH	
mm7.xenoRefGene.LENGTH	
mm8.ccdsGene.LENGTH	
mm8.ensGene.LENGTH	
mm8.geneid.LENGTH	
mm8.geneSymbol.LENGTH	
mm8.genscan.LENGTH	
mm8.knownGene.LENGTH	. 123
mm8.nscanGene.LENGTH	. 124
mm8.refGene.LENGTH	. 124
mm8.sgpGene.LENGTH	
mm8.sibGene.LENGTH	
mm8.xenoRefGene.LENGTH	
mm9.acembly.LENGTH	. 126
mm9.ccdsGene.LENGTH	127
mm9.ensGene.LENGTH	
mm9.exoniphy.LENGTH	
mm9.geneid.LENGTH	128
mm9.geneSymbol.LENGTH	120
mm9.gencsymbol.LENGTH	
mm9.genscan.eleNGTH	
mm9.nscanGene.LENGTH	
mm9.refGene.LENGTH	
mm9.sgpGene.LENGTH	
mm9.xenoRefGene.LENGTH	
monDom1.genscan.LENGTH	
monDom4.ensGene.LENGTH	
monDom4.geneSymbol.LENGTH	
monDom4.genscan.LENGTH	
monDom4.nscanGene.LENGTH	
monDom4.refGene.LENGTH	. 135

monDom4.xenoRefGene.LENGTH						
monDom5.ensGene.LENGTH						
monDom5.geneSymbol.LENGTH .	 	 				 . 136
monDom5.genscan.LENGTH	 	 				 . 137
monDom5.nscanGene.LENGTH	 	 				 . 137
monDom5.refGene.LENGTH	 	 				 . 138
monDom5.xenoRefGene.LENGTH	 	 				 . 138
ornAnal.ensGene.LENGTH						
ornAna1.geneSymbol.LENGTH						
ornAna1.refGene.LENGTH						
ornAna1.xenoRefGene.LENGTH .						
oryLat2.ensGene.LENGTH						
oryLat2.geneSymbol.LENGTH						
oryLat2.refGene.LENGTH	 	 				 142
oryLat2.xenoRefGene.LENGTH	 	 ••••	•••		•••	 142
panTro1.ensGene.LENGTH						
panTro1.geneid.LENGTH						
panTro1.genscan.LENGTH						
panTro1.xenoRefGene.LENGTH						
panTro2.ensGene.LENGTH						
panTro2.geneSymbol.LENGTH						
panTro2.genscan.LENGTH						
panTro2.nscanGene.LENGTH						
panTro2.refGene.LENGTH						
panTro2.xenoRefGene.LENGTH						
$petMar1.xenoRefGene.LENGTH\ .\ .$						
ponAbe2.ensGene.LENGTH						
$ponAbe 2. gene Symbol. LENGTH \ . \ .$						
ponAbe2.genscan.LENGTH	 	 				 . 149
ponAbe2.nscanGene.LENGTH						
ponAbe2.refGene.LENGTH	 	 				 . 150
ponAbe2.xenoRefGene.LENGTH .	 	 				 . 151
priPac1.xenoRefGene.LENGTH						
rheMac2.ensGene.LENGTH	 	 				 . 152
rheMac2.geneid.LENGTH	 	 				 . 152
rheMac2.geneSymbol.LENGTH						
rheMac2.nscanGene.LENGTH						
rheMac2.refGene.LENGTH						
rheMac2.sgpGene.LENGTH						
rheMac2.xenoRefGene.LENGTH .						
rn3.ensGene.LENGTH						
rn3.geneid.LENGTH						
rn3.geneSymbol.LENGTH						
rn3.genscan.LENGTH						
rn3.knownGene.LENGTH						
rn3.nscanGene.LENGTH						
rn3.refGene.LENGTH						
rn3.sgpGene.LENGTH	 	 • • •	• • •	• • •		 . 139

rn3.xenoRefGene.LENGTH
rn4.ensGene.LENGTH
rn4.geneid.LENGTH
rn4.geneSymbol.LENGTH
rn4.genscan.LENGTH
rn4.knownGene.LENGTH162
rn4.nscanGene.LENGTH
rn4.refGene.LENGTH
rn4.sgpGene.LENGTH
rn4.xenoRefGene.LENGTH164
sacCer1.ensGene.LENGTH
sacCer2.ensGene.LENGTH
strPur1.geneSymbol.LENGTH
strPur1.genscan.LENGTH
strPur1.refGene.LENGTH
strPur1.xenoRefGene.LENGTH
strPur2.geneSymbol.LENGTH
strPur2.genscan.LENGTH
strPur2.refGene.LENGTH
strPur2.xenoRefGene.LENGTH
supportedGeneIDs
supportedGenomes
taeGut1.ensGene.LENGTH
taeGut1.geneSymbol.LENGTH
taeGut1.genscan.LENGTH
taeGut1.nscanGene.LENGTH
taeGut1.refGene.LENGTH
taeGut1.xenoRefGene.LENGTH
tetNig1.ensGene.LENGTH
tetNig1.geneid.LENGTH
tetNig1.genscan.LENGTH
tetNig1.nscanGene.LENGTH
tetNig2.ensGene.LENGTH
unfactor
xenTro1.genscan.LENGTH
xenTro2.ensGene.LENGTH
xenTro2.geneSymbol.LENGTH
xenTro2.genscan.LENGTH
xenTro2.refGene.LENGTH

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/cgibin/hgTables) using the ensGene table.

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

See Also

downloadLengthFromUCSC

Examples

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

anoCar1.genscan.LENGTH

Transcript length data for the organism anoCar

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

anoCar1.xenoRefGene.LENGTH

Transcript length data for the organism anoCar

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

anoGam1.ensGene.LENGTH

Transcript length data for the organism anoGam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

anoGam1.genscan.LENGTH

Transcript length data for the organism anoGam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

apiMel1.genscan.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

apiMel2.ensGene.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

apiMel2.genscan.LENGTH

Transcript length data for the organism apiMel

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

aplCal1.xenoRefGene.LENGTH

Transcript length data for the organism aplCal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau2.geneSymbol.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau2.genscan.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau2.refGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau2.sgpGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau3.ensGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau3.geneSymbol.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau3.genscan.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau3.refGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau3.sgpGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau4.ensGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau4.geneSymbol.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau4.genscan.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau4.nscanGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

bosTau4.refGene.LENGTH

Transcript length data for the organism bosTau

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

braFlo1.xenoRefGene.LENGTH

Transcript length data for the organism braFlo

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

caeJap1.xenoRefGene.LENGTH

Transcript length data for the organism caeJap

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

caePb1.xenoRefGene.LENGTH

Transcript length data for the organism caePb

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

caePb2.xenoRefGene.LENGTH

Transcript length data for the organism caePb

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

caeRem2.xenoRefGene.LENGTH

Transcript length data for the organism caeRem

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

caeRem3.xenoRefGene.LENGTH

Transcript length data for the organism caeRem

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

calJac1.genscan.LENGTH

Transcript length data for the organism calJac

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

calJac1.nscanGene.LENGTH

Transcript length data for the organism calJac

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

calJac1.xenoRefGene.LENGTH

Transcript length data for the organism calJac

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam1.ensGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam1.geneSymbol.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam1.genscan.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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/cgibin/hgTables) using the refGene table.

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

See Also

downloadLengthFromUCSC

Examples

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

canFam1.xenoRefGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam2.ensGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam2.geneSymbol.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam2.genscan.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam2.nscanGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam2.refGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

canFam2.xenoRefGene.LENGTH

Transcript length data for the organism canFam

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

cavPor3.ensGene.LENGTH

Transcript length data for the organism cavPor

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

cavPor3.genscan.LENGTH

Transcript length data for the organism cavPor

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

cavPor3.nscanGene.LENGTH

Transcript length data for the organism cavPor

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

cavPor3.xenoRefGene.LENGTH

Transcript length data for the organism cavPor

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

cb1.xenoRefGene.LENGTH

Transcript length data for the organism cb

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

cb3.xenoRefGene.LENGTH

Transcript length data for the organism cb

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ce2.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 Transcript length data for the organism ce

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ce4.xenoRefGene.LENGTH

Transcript length data for the organism ce

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ce6.xenoRefGene.LENGTH

Transcript length data for the organism ce

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ci1.xenoRefGene.LENGTH

Transcript length data for the organism ci

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

ci2.xenoRefGene.LENGTH

Transcript length data for the organism ci

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer3.ensGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer3.geneSymbol.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer3.refGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer4.ensGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer4.geneSymbol.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer4.genscan.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer4.nscanGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer4.refGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer5.ensGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer5.geneSymbol.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer5.refGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer5.vegaGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer5.vegaPseudoGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer6.ensGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer6.geneSymbol.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer6.refGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

danRer6.xenoRefGene.LENGTH

Transcript length data for the organism danRer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

dm3.nscanPasaGene.LENGTH

Transcript length data for the organism dm

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

dp2.xenoRefGene.LENGTH

Transcript length data for the organism dp

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

dp3.xenoRefGene.LENGTH

Transcript length data for the organism dp

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droAna1.geneid.LENGTH Transcript length data for the organism droAna

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droAna1.genscan.LENGTH

Transcript length data for the organism droAna

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droAna1.xenoRefGene.LENGTH

Transcript length data for the organism droAna

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droAna2.genscan.LENGTH

Transcript length data for the organism droAna

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droAna2.xenoRefGene.LENGTH

Transcript length data for the organism droAna

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droEre1.genscan.LENGTH

Transcript length data for the organism droEre

Description

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

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

See Also

downloadLengthFromUCSC

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/cgibin/hgTables) using the genscan table.

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

See Also

downloadLengthFromUCSC

Examples

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

droGri1.xenoRefGene.LENGTH

Transcript length data for the organism droGri

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droMoj1.genscan.LENGTH

Transcript length data for the organism droMoj

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(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/cgibin/hgTables) using the genscan table.

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

See Also

downloadLengthFromUCSC

Examples

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

droMoj2.xenoRefGene.LENGTH

Transcript length data for the organism droMoj

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droPer1.genscan.LENGTH

Transcript length data for the organism droPer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droPer1.xenoRefGene.LENGTH

Transcript length data for the organism droPer

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droSec1.genscan.LENGTH

Transcript length data for the organism droSec

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droSec1.xenoRefGene.LENGTH

Transcript length data for the organism droSec

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droSim1.xenoRefGene.LENGTH

Transcript length data for the organism droSim

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droVir1.genscan.LENGTH

Transcript length data for the organism droVir

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droVir1.xenoRefGene.LENGTH

Transcript length data for the organism droVir

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droVir2.genscan.LENGTH

Transcript length data for the organism droVir

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droVir2.xenoRefGene.LENGTH

Transcript length data for the organism droVir

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droYak1.genscan.LENGTH

Transcript length data for the organism droYak

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droYak1.xenoRefGene.LENGTH

Transcript length data for the organism droYak

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droYak2.genscan.LENGTH

Transcript length data for the organism droYak

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

droYak2.xenoRefGene.LENGTH

Transcript length data for the organism droYak

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab1.geneSymbol.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab1.nscanGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab1.refGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab1.sgpGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab2.ensGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab2.geneSymbol.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab2.nscanGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab2.refGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

equCab2.xenoRefGene.LENGTH

Transcript length data for the organism equCab

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

felCat3.ensGene.LENGTH

Transcript length data for the organism felCat

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

felCat3.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/cgibin/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/cgibin/hgTables) using the nscanGene table.

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

See Also

downloadLengthFromUCSC

Examples

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

felCat3.refGene.LENGTH

Transcript length data for the organism felCat

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

felCat3.sgpGene.LENGTH

Transcript length data for the organism felCat

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

felCat3.xenoRefGene.LENGTH

Transcript length data for the organism felCat

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal2.geneSymbol.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal2.genscan.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal2.refGene.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal2.sgpGene.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.ensGene.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.geneSymbol.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.genscan.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.nscanGene.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.refGene.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

galGal3.xenoRefGene.LENGTH

Transcript length data for the organism galGal

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

gasAcu1.ensGene.LENGTH

Transcript length data for the organism gasAcu

Description

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

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

See Also

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)

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

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

hg16.geneSymbol.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg16.genscan.LENGTH Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

```
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

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

```
downloadLengthFromUCSC
```

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.vegaPseudoGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg17.xenoRefGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

```
downloadLengthFromUCSC
```

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.geneSymbol.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.knownGeneOld3.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg18.xenoRefGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg19.ccdsGene.LENGTH Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg19.geneSymbol.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg19.knownGene.LENGTH Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

hg19.xenoRefGene.LENGTH

Transcript length data for the organism hg

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

loxAfr3.xenoRefGene.LENGTH

Transcript length data for the organism loxAfr

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

mm7.xenoRefGene.LENGTH

Transcript length data for the organism mm

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

mm8.geneid.LENGTH

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(mm8.geneSymbol.LENGTH)
head(mm8.geneSymbol.LENGTH)

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(mm8.knownGene.LENGTH)
head(mm8.knownGene.LENGTH)

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

mm8.xenoRefGene.LENGTH

Transcript length data for the organism mm

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(mm9.geneid.LENGTH)
head(mm9.geneid.LENGTH)

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

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

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

mm9.xenoRefGene.LENGTH

Transcript length data for the organism mm

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

monDom1.genscan.LENGTH

Transcript length data for the organism monDom

Description

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

The data file was made by calling downloadLengthFromUCSC(monDom1, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom1.genscan.LENGTH)
head(monDom1.genscan.LENGTH)

monDom4.ensGene.LENGTH

Transcript length data for the organism monDom

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

monDom4.geneSymbol.LENGTH

Transcript length data for the organism monDom

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

monDom4.genscan.LENGTH

Transcript length data for the organism monDom

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

monDom4.nscanGene.LENGTH

Transcript length data for the organism monDom

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

monDom4.refGene.LENGTH

Transcript length data for the organism monDom

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

monDom4.xenoRefGene.LENGTH

Transcript length data for the organism monDom

Description

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

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

See Also

downloadLengthFromUCSC

Examples

data(monDom4.xenoRefGene.LENGTH)
head(monDom4.xenoRefGene.LENGTH)

monDom5.ensGene.LENGTH

Transcript length data for the organism monDom

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

monDom5.geneSymbol.LENGTH

Transcript length data for the organism monDom

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

monDom5.genscan.LENGTH

Transcript length data for the organism monDom

Description

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

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

See Also

downloadLengthFromUCSC

Examples

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

monDom5.nscanGene.LENGTH

Transcript length data for the organism monDom

Description

monDom5.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom5.nscanGene.LENGTH)
head(monDom5.nscanGene.LENGTH)

monDom5.refGene.LENGTH

Transcript length data for the organism monDom

Description

monDom5.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom5.refGene.LENGTH)
head(monDom5.refGene.LENGTH)

monDom5.xenoRefGene.LENGTH

Transcript length data for the organism monDom

Description

monDom5.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(monDom5, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(monDom5.xenoRefGene.LENGTH)
head(monDom5.xenoRefGene.LENGTH)

ornAna1.ensGene.LENGTH

Transcript length data for the organism ornAna

Description

ornAna1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ornAna1.ensGene.LENGTH)
head(ornAna1.ensGene.LENGTH)

ornAna1.geneSymbol.LENGTH

Transcript length data for the organism ornAna

Description

ornAna1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ornAna1.geneSymbol.LENGTH)
head(ornAna1.geneSymbol.LENGTH)

ornAna1.refGene.LENGTH

Transcript length data for the organism ornAna

Description

ornAna1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ornAna1, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

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/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(oryLat2.ensGene.LENGTH)
head(oryLat2.ensGene.LENGTH)

oryLat2.geneSymbol.LENGTH

Transcript length data for the organism oryLat

Description

oryLat2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(oryLat2.geneSymbol.LENGTH)
head(oryLat2.geneSymbol.LENGTH)

oryLat2.refGene.LENGTH

Transcript length data for the organism oryLat

Description

oryLat2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(oryLat2.refGene.LENGTH)
head(oryLat2.refGene.LENGTH)

oryLat2.xenoRefGene.LENGTH

Transcript length data for the organism oryLat

Description

oryLat2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(oryLat2, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(oryLat2.xenoRefGene.LENGTH)
head(oryLat2.xenoRefGene.LENGTH)

panTro1.ensGene.LENGTH

Transcript length data for the organism panTro

Description

panTro1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(panTro1, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

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/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(panTro1, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro1.genscan.LENGTH)
head(panTro1.genscan.LENGTH)

panTro1.xenoRefGene.LENGTH

Transcript length data for the organism panTro

Description

panTro1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(panTro1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro1.xenoRefGene.LENGTH)
head(panTro1.xenoRefGene.LENGTH)

panTro2.ensGene.LENGTH

Transcript length data for the organism panTro

Description

panTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.ensGene.LENGTH)
head(panTro2.ensGene.LENGTH)

panTro2.geneSymbol.LENGTH

Transcript length data for the organism panTro

Description

panTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(panTro2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.geneSymbol.LENGTH)
head(panTro2.geneSymbol.LENGTH)

panTro2.genscan.LENGTH

Transcript length data for the organism panTro

Description

panTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(panTro2, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.genscan.LENGTH)
head(panTro2.genscan.LENGTH)

panTro2.nscanGene.LENGTH

Transcript length data for the organism panTro

Description

panTro2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.nscanGene.LENGTH)
head(panTro2.nscanGene.LENGTH)

panTro2.refGene.LENGTH

Transcript length data for the organism panTro

Description

panTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.refGene.LENGTH)
head(panTro2.refGene.LENGTH)

panTro2.xenoRefGene.LENGTH

Transcript length data for the organism panTro

Description

panTro2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(panTro2, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(panTro2.xenoRefGene.LENGTH)
head(panTro2.xenoRefGene.LENGTH)

petMar1.xenoRefGene.LENGTH

Transcript length data for the organism petMar

Description

petMar1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(petMar1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(petMar1.xenoRefGene.LENGTH)
head(petMar1.xenoRefGene.LENGTH)

ponAbe2.ensGene.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.ensGene.LENGTH)
head(ponAbe2.ensGene.LENGTH)

ponAbe2.geneSymbol.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.geneSymbol.LENGTH)
head(ponAbe2.geneSymbol.LENGTH)

ponAbe2.genscan.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.genscan.LENGTH)
head(ponAbe2.genscan.LENGTH)

ponAbe2.nscanGene.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.nscanGene.LENGTH)
head(ponAbe2.nscanGene.LENGTH)

ponAbe2.refGene.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.refGene.LENGTH)
head(ponAbe2.refGene.LENGTH)

ponAbe2.xenoRefGene.LENGTH

Transcript length data for the organism ponAbe

Description

ponAbe2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(ponAbe2, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(ponAbe2.xenoRefGene.LENGTH)
head(ponAbe2.xenoRefGene.LENGTH)

priPac1.xenoRefGene.LENGTH

Transcript length data for the organism priPac

Description

priPac1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(priPac1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(priPac1.xenoRefGene.LENGTH)
head(priPac1.xenoRefGene.LENGTH)

rheMac2.ensGene.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.ensGene.LENGTH)
head(rheMac2.ensGene.LENGTH)

rheMac2.geneid.LENGTH Transcript length data for the organism rheMac

Description

rheMac2.geneid.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneid table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, geneid) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.geneid.LENGTH)
head(rheMac2.geneid.LENGTH)

rheMac2.geneSymbol.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.geneSymbol.LENGTH)
head(rheMac2.geneSymbol.LENGTH)

rheMac2.nscanGene.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.nscanGene.LENGTH)
head(rheMac2.nscanGene.LENGTH)

rheMac2.refGene.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.refGene.LENGTH)
head(rheMac2.refGene.LENGTH)

rheMac2.sgpGene.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, sgpGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.sgpGene.LENGTH)
head(rheMac2.sgpGene.LENGTH)

rheMac2.xenoRefGene.LENGTH

Transcript length data for the organism rheMac

Description

rheMac2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rheMac2, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rheMac2.xenoRefGene.LENGTH)
head(rheMac2.xenoRefGene.LENGTH)

rn3.ensGene.LENGTH Transcript length data for the organism rn

Description

rn3.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

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 Transcript length data for the organism rn

Description

rn3.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rn3, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn3.geneSymbol.LENGTH)
head(rn3.geneSymbol.LENGTH)

rn3.genscan.LENGTH Transcript length data for the organism rn

Description

rn3.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(rn3, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn3.genscan.LENGTH)
head(rn3.genscan.LENGTH)

rn3.knownGene.LENGTH Transcript length data for the organism rn

Description

rn3.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, knownGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

```
data(rn3.knownGene.LENGTH)
head(rn3.knownGene.LENGTH)
```

rn3.nscanGene.LENGTH Transcript length data for the organism rn

Description

rn3.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn3.nscanGene.LENGTH)
head(rn3.nscanGene.LENGTH)

rn3.refGene.LENGTH Transcript length data for the organism rn

Description

rn3.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

```
data(rn3.refGene.LENGTH)
head(rn3.refGene.LENGTH)
```

rn3.sgpGene.LENGTH Transcript length data for the organism rn

Description

rn3.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, sgpGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn3.sgpGene.LENGTH)
head(rn3.sgpGene.LENGTH)

rn3.xenoRefGene.LENGTH

Transcript length data for the organism rn

Description

rn3.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rn3, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn3.xenoRefGene.LENGTH)
head(rn3.xenoRefGene.LENGTH)

rn4.ensGene.LENGTH Transcript length data for the organism rn

Description

rn4.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn4.ensGene.LENGTH)
head(rn4.ensGene.LENGTH)

rn4.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

```
data(rn4.geneid.LENGTH)
head(rn4.geneid.LENGTH)
```

rn4.geneSymbol.LENGTH Transcript length data for the organism rn

Description

rn4.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(rn4, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

```
data(rn4.geneSymbol.LENGTH)
head(rn4.geneSymbol.LENGTH)
```

rn4.genscan.LENGTH Transcript length data for the organism rn

Description

rn4.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(rn4, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

```
data(rn4.genscan.LENGTH)
head(rn4.genscan.LENGTH)
```

rn4.knownGene.LENGTH Transcript length data for the organism rn

Description

rn4.knownGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the knownGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, knownGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn4.knownGene.LENGTH)
head(rn4.knownGene.LENGTH)

rn4.nscanGene.LENGTH Transcript length data for the organism rn

Description

rn4.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

```
data(rn4.nscanGene.LENGTH)
head(rn4.nscanGene.LENGTH)
```

rn4.refGene.LENGTH Transcript length data for the organism rn

Description

rn4.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn4.refGene.LENGTH)
head(rn4.refGene.LENGTH)

rn4.sgpGene.LENGTH Transcript length data for the organism rn

Description

rn4.sgpGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the sgpGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, sgpGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

```
data(rn4.sgpGene.LENGTH)
head(rn4.sgpGene.LENGTH)
```

rn4.xenoRefGene.LENGTH

Transcript length data for the organism rn

Description

rn4.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(rn4, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(rn4.xenoRefGene.LENGTH)
head(rn4.xenoRefGene.LENGTH)

sacCer1.ensGene.LENGTH

Transcript length data for the organism sacCer

Description

sacCer1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(sacCer1, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(sacCer1.ensGene.LENGTH)
head(sacCer1.ensGene.LENGTH)

sacCer2.ensGene.LENGTH

Transcript length data for the organism sacCer

Description

sacCer2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(sacCer2, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(sacCer2.ensGene.LENGTH)
head(sacCer2.ensGene.LENGTH)

strPur1.geneSymbol.LENGTH

Transcript length data for the organism strPur

Description

strPur1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(strPur1, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur1.geneSymbol.LENGTH)
head(strPur1.geneSymbol.LENGTH)

strPur1.genscan.LENGTH

Transcript length data for the organism strPur

Description

strPur1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(strPur1, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur1.genscan.LENGTH)
head(strPur1.genscan.LENGTH)

strPur1.refGene.LENGTH

Transcript length data for the organism strPur

Description

strPur1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(strPur1, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur1.refGene.LENGTH)
head(strPur1.refGene.LENGTH)

strPur1.xenoRefGene.LENGTH

Transcript length data for the organism strPur

Description

strPur1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(strPur1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur1.xenoRefGene.LENGTH)
head(strPur1.xenoRefGene.LENGTH)

strPur2.geneSymbol.LENGTH

Transcript length data for the organism strPur

Description

strPur2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(strPur2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur2.geneSymbol.LENGTH)
head(strPur2.geneSymbol.LENGTH)

strPur2.genscan.LENGTH

Transcript length data for the organism strPur

Description

strPur2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(strPur2, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur2.genscan.LENGTH)
head(strPur2.genscan.LENGTH)

strPur2.refGene.LENGTH

Transcript length data for the organism strPur

Description

strPur2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(strPur2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur2.refGene.LENGTH)
head(strPur2.refGene.LENGTH)

strPur2.xenoRefGene.LENGTH

Transcript length data for the organism strPur

Description

strPur2.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(strPur2, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(strPur2.xenoRefGene.LENGTH)
head(strPur2.xenoRefGene.LENGTH)

supportedGeneIDs Supported Gene IDs

Description

Lists supported gene ID formats

Usage

supportedGeneIDs()

Details

Uses the supportedUCSCtables function from the GenomicFeatures package to obtain a list of gene ID formats available from the UCSC genome browser. The db column gives the gene ID formats which are provided to the id argument of various functions. The track and subtrack columns are the names of the UCSC track/subtrack from which information is fetched.

The GeneID column lists the "full name" of the gene ID format where available.

The final column, headed AvailableGenomes lists the genomes for which there is a local copy of the length information available for the gene ID format listed in the geneLenDataBase package.

Value

A data.frame containing supported gene ID formats.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

supportedGeneIDs()

supportedGenomes Supported Genomes

Description

Lists supported genomes

Usage

supportedGenomes()

Details

Uses the ucscGenomes() function from the rtracklayer package to obtain a list of genomes available from the UCSC genome browser. The db column lists genomes as they are provided to the genome arguement of various functions.

The final column, headed AvailableGeneIDs lists the gene ID formats for which there is a local copy of the length information available for the genome listed in the geneLenDataBase package.

Value

A data.frame containing supported genomes.

Author(s)

Matthew D. Young <myoung@wehi.edu.au>

Examples

supportedGenomes()

taeGut1.ensGene.LENGTH

Transcript length data for the organism taeGut

Description

taeGut1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(taeGut1.ensGene.LENGTH)
head(taeGut1.ensGene.LENGTH)

taeGut1.geneSymbol.LENGTH

Transcript length data for the organism taeGut

Description

taeGut1.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(taeGut1.geneSymbol.LENGTH)
head(taeGut1.geneSymbol.LENGTH)

taeGut1.genscan.LENGTH

Transcript length data for the organism taeGut

Description

taeGut1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(taeGut1.genscan.LENGTH)
head(taeGut1.genscan.LENGTH)

taeGut1.nscanGene.LENGTH

Transcript length data for the organism taeGut

Description

taeGut1.nscanGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the nscanGene table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, nscanGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(taeGut1.nscanGene.LENGTH)
head(taeGut1.nscanGene.LENGTH)

taeGut1.refGene.LENGTH

Transcript length data for the organism taeGut

Description

taeGut1.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(taeGut1.refGene.LENGTH)
head(taeGut1.refGene.LENGTH)

taeGut1.xenoRefGene.LENGTH

Transcript length data for the organism taeGut

Description

taeGut1.xenoRefGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the xenoRefGene table.

The data file was made by calling downloadLengthFromUCSC(taeGut1, xenoRefGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(taeGut1.xenoRefGene.LENGTH)
head(taeGut1.xenoRefGene.LENGTH)

tetNig1.ensGene.LENGTH

Transcript length data for the organism tetNig

Description

tetNig1.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(tetNig1, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(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/cgibin/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)

Matthew D. Young <myoung@wehi.edu.au>

Examples

```
#A named factor
x <- factor(sample(1:6, 100, replace=TRUE))
names(x) <- paste("Roll.No", 1:100, sep=.)
x
unfactor(x)
#A data.frame
x <- data.frame(player <- c("Alice", "Bob", "Mary", "Fred"), score <- factor(c(9, 7, 8, 9)), stringsAsFactors=TRUE)
x$player
x$score
y <- unfactor(x)
y$player
y$score</pre>
```

```
xenTro1.genscan.LENGTH
```

Transcript length data for the organism xenTro

Description

xenTro1.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(xenTro1, genscan) on the date on which the package was last updated.

See Also

```
downloadLengthFromUCSC
```

Examples

data(xenTro1.genscan.LENGTH)
head(xenTro1.genscan.LENGTH)

xenTro2.ensGene.LENGTH

Transcript length data for the organism xenTro

Description

xenTro2.ensGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the ensGene table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, ensGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(xenTro2.ensGene.LENGTH)
head(xenTro2.ensGene.LENGTH)

xenTro2.geneSymbol.LENGTH

Transcript length data for the organism xenTro

Description

xenTro2.geneSymbol.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgi-bin/hgTables) using the geneSymbol table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, geneSymbol) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(xenTro2.geneSymbol.LENGTH)
head(xenTro2.geneSymbol.LENGTH)

xenTro2.genscan.LENGTH

Transcript length data for the organism xenTro

Description

xenTro2.genscan.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the genscan table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, genscan) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(xenTro2.genscan.LENGTH)
head(xenTro2.genscan.LENGTH)

xenTro2.refGene.LENGTH

Transcript length data for the organism xenTro

Description

xenTro2.refGene.LENGTH is an R object which maps transcripts to the length (in bp) of their mature mRNA transcripts. Where available, it will also provide the mapping between a gene ID and its associated transcripts. The data is obtained from the UCSC table browser (http://genome.ucsc.edu/cgibin/hgTables) using the refGene table.

The data file was made by calling downloadLengthFromUCSC(xenTro2, refGene) on the date on which the package was last updated.

See Also

downloadLengthFromUCSC

Examples

data(xenTro2.refGene.LENGTH)
head(xenTro2.refGene.LENGTH)

Index

*Topic **datasets** anoCar1.ensGene.LENGTH, 9 anoCar1.genscan.LENGTH, 9 anoCar1.xenoRefGene.LENGTH, 10 anoGam1.ensGene.LENGTH, 10 anoGam1.geneid.LENGTH, 11 anoGam1.genscan.LENGTH, 11 apiMel1.genscan.LENGTH, 12 apiMel2.ensGene.LENGTH, 12 apiMel2.geneid.LENGTH, 13 apiMel2.genscan.LENGTH, 13 aplCal1.xenoRefGene.LENGTH, 14 bosTau2.geneid.LENGTH, 14 bosTau2.geneSymbol.LENGTH, 15 bosTau2.genscan.LENGTH, 15 bosTau2.refGene.LENGTH, 16 bosTau2.sgpGene.LENGTH, 16 bosTau3.ensGene.LENGTH, 17 bosTau3.geneid.LENGTH, 17 bosTau3.geneSymbol.LENGTH, 18 bosTau3.genscan.LENGTH, 18 bosTau3.refGene.LENGTH, 19 bosTau3.sgpGene.LENGTH, 19 bosTau4.ensGene.LENGTH, 20 bosTau4.geneSymbol.LENGTH, 20 bosTau4.genscan.LENGTH, 21 bosTau4.nscanGene.LENGTH, 21 bosTau4.refGene.LENGTH, 22 braFlo1.xenoRefGene.LENGTH, 22 caeJap1.xenoRefGene.LENGTH, 23 caePb1.xenoRefGene.LENGTH, 23 caePb2.xenoRefGene.LENGTH. 24 caeRem2.xenoRefGene.LENGTH, 24 caeRem3.xenoRefGene.LENGTH, 25 calJac1.genscan.LENGTH, 25 calJac1.nscanGene.LENGTH, 26 calJac1.xenoRefGene.LENGTH, 26 canFam1.ensGene.LENGTH, 27 canFam1.geneSymbol.LENGTH, 27

canFam1.genscan.LENGTH, 28 canFam1.nscanGene.LENGTH, 28 canFam1.refGene.LENGTH, 29 canFam1.xenoRefGene.LENGTH, 29 canFam2.ensGene.LENGTH, 30 canFam2.geneSymbol.LENGTH, 30 canFam2.genscan.LENGTH, 31 canFam2.nscanGene.LENGTH, 31 canFam2.refGene.LENGTH, 32 canFam2.xenoRefGene.LENGTH. 32 cavPor3.ensGene.LENGTH, 33 cavPor3.genscan.LENGTH, 33 cavPor3.nscanGene.LENGTH, 34 cavPor3.xenoRefGene.LENGTH, 34 cb1.xenoRefGene.LENGTH, 35 cb3.xenoRefGene.LENGTH, 35 ce2.geneid.LENGTH, 36 ce2.geneSymbol.LENGTH, 36 ce2.refGene.LENGTH, 37 ce4.geneSymbol.LENGTH, 37 ce4.refGene.LENGTH, 38 ce4.xenoRefGene.LENGTH. 38 ce6.ensGene.LENGTH, 39 ce6.geneSymbol.LENGTH, 39 ce6.refGene.LENGTH, 40 ce6.xenoRefGene.LENGTH, 40 ci1.geneSymbol.LENGTH, 41 ci1.refGene.LENGTH, 41 ci1.xenoRefGene.LENGTH, 42 ci2.ensGene.LENGTH, 42 ci2.geneSymbol.LENGTH, 43 ci2.refGene.LENGTH, 43 ci2.xenoRefGene.LENGTH, 44 danRer3.ensGene.LENGTH, 44 danRer3.geneSymbol.LENGTH, 45 danRer3.refGene.LENGTH, 45 danRer4.ensGene.LENGTH, 46 danRer4.geneSymbol.LENGTH, 46 danRer4.genscan.LENGTH, 47

danRer4.nscanGene.LENGTH, 47 danRer4.refGene.LENGTH, 48 danRer5.ensGene.LENGTH, 48 danRer5.geneSymbol.LENGTH, 49 danRer5.refGene.LENGTH, 49 danRer5.vegaGene.LENGTH, 50 danRer5.vegaPseudoGene.LENGTH, 50 danRer6.ensGene.LENGTH, 51 danRer6.geneSymbol.LENGTH, 51 danRer6.refGene.LENGTH, 52 danRer6.xenoRefGene.LENGTH, 52 dm1.geneSymbol.LENGTH, 53 dm1.genscan.LENGTH, 53 dm1.refGene.LENGTH, 54 dm2.geneid.LENGTH, 54 dm2.geneSvmbol.LENGTH.55 dm2.genscan.LENGTH, 55 dm2.nscanGene.LENGTH, 56 dm2.refGene.LENGTH, 56 dm3.geneSymbol.LENGTH, 57 dm3.nscanPasaGene.LENGTH. 57 dm3.refGene.LENGTH, 58 dp2.genscan.LENGTH, 58 dp2.xenoRefGene.LENGTH, 59 dp3.geneid.LENGTH, 59 dp3.genscan.LENGTH, 60 dp3.xenoRefGene.LENGTH, 60 droAna1.geneid.LENGTH, 61 droAna1.genscan.LENGTH, 61 droAna1.xenoRefGene.LENGTH, 62 droAna2.genscan.LENGTH, 62 droAna2.xenoRefGene.LENGTH, 63 droEre1.genscan.LENGTH, 63 droEre1.xenoRefGene.LENGTH, 64 droGri1.genscan.LENGTH, 64 droGri1.xenoRefGene.LENGTH, 65 droMoj1.geneid.LENGTH, 65 droMoj1.genscan.LENGTH, 66 droMoj1.xenoRefGene.LENGTH, 66 droMoj2.genscan.LENGTH, 67 droMoj2.xenoRefGene.LENGTH, 67 droPer1.genscan.LENGTH, 68 droPer1.xenoRefGene.LENGTH, 68 droSec1.genscan.LENGTH, 69 droSec1.xenoRefGene.LENGTH, 69 droSim1.geneid.LENGTH, 70 droSim1.genscan.LENGTH, 70 droSim1.xenoRefGene.LENGTH, 71

droVir1.geneid.LENGTH, 71 droVir1.genscan.LENGTH, 72 droVir1.xenoRefGene.LENGTH, 72 droVir2.genscan.LENGTH, 73 droVir2.xenoRefGene.LENGTH, 73 droYak1.geneid.LENGTH, 74 droYak1.genscan.LENGTH, 74 droYak1.xenoRefGene.LENGTH, 75 droYak2.genscan.LENGTH, 75 droYak2.xenoRefGene.LENGTH, 76 equCab1.geneid.LENGTH, 76 equCab1.geneSymbol.LENGTH, 77 equCab1.nscanGene.LENGTH, 77 equCab1.refGene.LENGTH, 78 equCab1.sgpGene.LENGTH, 78 equCab2.ensGene.LENGTH, 79 equCab2.geneSymbol.LENGTH, 79 equCab2.nscanGene.LENGTH, 80 equCab2.refGene.LENGTH, 80 equCab2.xenoRefGene.LENGTH, 81 felCat3.ensGene.LENGTH.81 felCat3.geneid.LENGTH, 82 felCat3.geneSymbol.LENGTH, 82 felCat3.genscan.LENGTH, 83 felCat3.nscanGene.LENGTH, 83 felCat3.refGene.LENGTH, 84 felCat3.sgpGene.LENGTH, 84 felCat3.xenoRefGene.LENGTH, 85 fr1.ensGene.LENGTH, 85 fr1.genscan.LENGTH, 86 fr2.ensGene.LENGTH, 86 galGal2.ensGene.LENGTH, 87 galGal2.geneid.LENGTH, 87 galGal2.geneSymbol.LENGTH, 88 galGal2.genscan.LENGTH, 88 galGal2.refGene.LENGTH, 89 galGal2.sgpGene.LENGTH, 89 galGal3.ensGene.LENGTH, 90 galGal3.geneSymbol.LENGTH, 90 galGal3.genscan.LENGTH, 91 galGal3.nscanGene.LENGTH, 91 galGal3.refGene.LENGTH, 92 galGal3.xenoRefGene.LENGTH, 92 gasAcu1.ensGene.LENGTH, 93 gasAcu1.nscanGene.LENGTH, 93 hg16.acembly.LENGTH, 94 hg16.ensGene.LENGTH, 94 hg16.exoniphy.LENGTH, 95

```
hg16.geneid.LENGTH, 95
hg16.geneSymbol.LENGTH, 96
hg16.genscan.LENGTH, 96
hg16.knownGene.LENGTH, 97
hg16.refGene.LENGTH, 97
hg16.sgpGene.LENGTH, 98
hg17.acembly.LENGTH, 98
hg17.acescan.LENGTH, 99
hg17.ccdsGene.LENGTH, 99
hg17.ensGene.LENGTH, 100
hg17.exoniphy.LENGTH, 100
hg17.geneid.LENGTH, 101
hg17.geneSymbol.LENGTH, 101
hg17.genscan.LENGTH, 102
hg17.knownGene.LENGTH, 102
hg17.refGene.LENGTH. 103
hg17.sgpGene.LENGTH, 103
hg17.vegaGene.LENGTH, 104
hg17.vegaPseudoGene.LENGTH, 104
hg17.xenoRefGene.LENGTH, 105
hg18.acembly.LENGTH, 105
hg18.acescan.LENGTH, 106
hg18.ccdsGene.LENGTH, 106
hg18.ensGene.LENGTH, 107
hg18.exoniphy.LENGTH, 107
hg18.geneid.LENGTH, 108
hg18.geneSymbol.LENGTH, 108
hg18.genscan.LENGTH, 109
hg18.knownGene.LENGTH, 109
hg18.knownGeneOld3.LENGTH, 110
hg18.refGene.LENGTH, 110
hg18.sgpGene.LENGTH, 111
hg18.sibGene.LENGTH, 111
hg18.xenoRefGene.LENGTH, 112
hg19.ccdsGene.LENGTH, 112
hg19.ensGene.LENGTH, 113
hg19.exoniphy.LENGTH, 113
hg19.geneSymbol.LENGTH, 114
hg19.knownGene.LENGTH, 114
hg19.nscanGene.LENGTH, 115
hg19.refGene.LENGTH, 115
hg19.xenoRefGene.LENGTH, 116
loxAfr3.xenoRefGene.LENGTH, 116
mm7.ensGene.LENGTH, 117
mm7.geneid.LENGTH, 117
mm7.geneSymbol.LENGTH, 118
mm7.genscan.LENGTH, 118
mm7.knownGene.LENGTH, 119
```

mm7.refGene.LENGTH, 119 mm7.sgpGene.LENGTH, 120 mm7.xenoRefGene.LENGTH.120 mm8.ccdsGene.LENGTH, 121 mm8.ensGene.LENGTH, 121 mm8.geneid.LENGTH, 122 mm8.geneSymbol.LENGTH, 122 mm8.genscan.LENGTH, 123 mm8.knownGene.LENGTH, 123 mm8.nscanGene.LENGTH, 124 mm8.refGene.LENGTH, 124 mm8.sgpGene.LENGTH, 125 mm8.sibGene.LENGTH, 125 mm8.xenoRefGene.LENGTH, 126 mm9.acembly.LENGTH, 126 mm9.ccdsGene.LENGTH. 127 mm9.ensGene.LENGTH, 127 mm9.exoniphy.LENGTH, 128 mm9.geneid.LENGTH, 128 mm9.geneSymbol.LENGTH, 129 mm9.genscan.LENGTH, 129 mm9.knownGene.LENGTH, 130 mm9.nscanGene.LENGTH, 130 mm9.refGene.LENGTH, 131 mm9.sgpGene.LENGTH, 131 mm9.xenoRefGene.LENGTH, 132 monDom1.genscan.LENGTH, 132 monDom4.ensGene.LENGTH, 133 monDom4.geneSymbol.LENGTH, 133 monDom4.genscan.LENGTH, 134 monDom4.nscanGene.LENGTH, 134 monDom4.refGene.LENGTH, 135 monDom4.xenoRefGene.LENGTH, 135 monDom5.ensGene.LENGTH, 136 monDom5.geneSymbol.LENGTH, 136 monDom5.genscan.LENGTH, 137 monDom5.nscanGene.LENGTH, 137 monDom5.refGene.LENGTH, 138 monDom5.xenoRefGene.LENGTH, 138 ornAna1.ensGene.LENGTH, 139 ornAna1.geneSymbol.LENGTH, 139 ornAna1.refGene.LENGTH, 140 ornAna1.xenoRefGene.LENGTH, 140 oryLat2.ensGene.LENGTH, 141 oryLat2.geneSymbol.LENGTH, 141 oryLat2.refGene.LENGTH, 142 oryLat2.xenoRefGene.LENGTH, 142 panTro1.ensGene.LENGTH, 143

182

panTro1.geneid.LENGTH, 143 panTro1.genscan.LENGTH, 144 panTro1.xenoRefGene.LENGTH, 144 panTro2.ensGene.LENGTH, 145 panTro2.geneSymbol.LENGTH, 145 panTro2.genscan.LENGTH, 146 panTro2.nscanGene.LENGTH, 146 panTro2.refGene.LENGTH, 147 panTro2.xenoRefGene.LENGTH, 147 petMar1.xenoRefGene.LENGTH, 148 ponAbe2.ensGene.LENGTH, 148 ponAbe2.geneSymbol.LENGTH, 149 ponAbe2.genscan.LENGTH, 149 ponAbe2.nscanGene.LENGTH, 150 ponAbe2.refGene.LENGTH, 150 ponAbe2.xenoRefGene.LENGTH, 151 priPac1.xenoRefGene.LENGTH, 151 rheMac2.ensGene.LENGTH, 152 rheMac2.geneid.LENGTH, 152 rheMac2.geneSymbol.LENGTH, 153 rheMac2.nscanGene.LENGTH. 153 rheMac2.refGene.LENGTH, 154 rheMac2.sgpGene.LENGTH, 154 rheMac2.xenoRefGene.LENGTH, 155 rn3.ensGene.LENGTH, 155 rn3.geneid.LENGTH, 156 rn3.geneSymbol.LENGTH, 156 rn3.genscan.LENGTH, 157 rn3.knownGene.LENGTH, 157 rn3.nscanGene.LENGTH, 158 rn3.refGene.LENGTH, 158 rn3.sgpGene.LENGTH, 159 rn3.xenoRefGene.LENGTH, 159 rn4.ensGene.LENGTH, 160 rn4.geneid.LENGTH, 160 rn4.geneSymbol.LENGTH, 161 rn4.genscan.LENGTH, 161 rn4.knownGene.LENGTH, 162 rn4.nscanGene.LENGTH, 162 rn4.refGene.LENGTH, 163 rn4.sgpGene.LENGTH, 163 rn4.xenoRefGene.LENGTH, 164 sacCer1.ensGene.LENGTH, 164 sacCer2.ensGene.LENGTH, 165 strPur1.geneSymbol.LENGTH, 165 strPur1.genscan.LENGTH, 166 strPur1.refGene.LENGTH, 166 strPur1.xenoRefGene.LENGTH, 167

strPur2.geneSymbol.LENGTH, 167 strPur2.genscan.LENGTH, 168 strPur2.refGene.LENGTH, 168 strPur2.xenoRefGene.LENGTH, 169 taeGut1.ensGene.LENGTH, 171 taeGut1.geneSymbol.LENGTH, 171 taeGut1.genscan.LENGTH, 172 taeGut1.nscanGene.LENGTH, 172 taeGut1.refGene.LENGTH.173 taeGut1.xenoRefGene.LENGTH, 173 tetNig1.ensGene.LENGTH, 174 tetNig1.geneid.LENGTH, 174 tetNig1.genscan.LENGTH, 175 tetNig1.nscanGene.LENGTH, 175 tetNig2.ensGene.LENGTH, 176 xenTro1.genscan.LENGTH, 177 xenTro2.ensGene.LENGTH, 178 xenTro2.geneSymbol.LENGTH, 178 xenTro2.genscan.LENGTH, 179 xenTro2.refGene.LENGTH, 179 anoCar1.ensGene.LENGTH, 9 anoCar1.genscan.LENGTH, 9 anoCar1.xenoRefGene.LENGTH, 10 anoGam1.ensGene.LENGTH, 10 anoGam1.geneid.LENGTH, 11 anoGam1.genscan.LENGTH, 11 apiMel1.genscan.LENGTH, 12 apiMel2.ensGene.LENGTH, 12 apiMel2.geneid.LENGTH, 13 apiMel2.genscan.LENGTH, 13 aplCal1.xenoRefGene.LENGTH, 14 bosTau2.geneid.LENGTH, 14 bosTau2.geneSymbol.LENGTH, 15 bosTau2.genscan.LENGTH, 15 bosTau2.refGene.LENGTH, 16 bosTau2.sgpGene.LENGTH, 16 bosTau3.ensGene.LENGTH, 17 bosTau3.geneid.LENGTH, 17 bosTau3.geneSymbol.LENGTH, 18 bosTau3.genscan.LENGTH, 18 bosTau3.refGene.LENGTH, 19 bosTau3.sgpGene.LENGTH, 19 bosTau4.ensGene.LENGTH, 20 bosTau4.geneSymbol.LENGTH, 20 bosTau4.genscan.LENGTH, 21 bosTau4.nscanGene.LENGTH, 21 bosTau4.refGene.LENGTH, 22

184

```
braFlo1.xenoRefGene.LENGTH, 22
```

caeJap1.xenoRefGene.LENGTH, 23 caePb1.xenoRefGene.LENGTH, 23 caePb2.xenoRefGene.LENGTH, 24 caeRem2.xenoRefGene.LENGTH, 24 caeRem3.xenoRefGene.LENGTH, 25 calJac1.genscan.LENGTH, 25 calJac1.nscanGene.LENGTH, 26 calJac1.xenoRefGene.LENGTH. 26 canFam1.ensGene.LENGTH, 27 canFam1.geneSymbol.LENGTH, 27 canFam1.genscan.LENGTH, 28 canFam1.nscanGene.LENGTH, 28 canFam1.refGene.LENGTH, 29 canFam1.xenoRefGene.LENGTH, 29 canFam2.ensGene.LENGTH, 30 canFam2.geneSymbol.LENGTH, 30 canFam2.genscan.LENGTH, 31 canFam2.nscanGene.LENGTH, 31 canFam2.refGene.LENGTH.32 canFam2.xenoRefGene.LENGTH, 32 cavPor3.ensGene.LENGTH, 33 cavPor3.genscan.LENGTH, 33 cavPor3.nscanGene.LENGTH, 34 cavPor3.xenoRefGene.LENGTH, 34 cb1.xenoRefGene.LENGTH, 35 cb3.xenoRefGene.LENGTH, 35 ce2.geneid.LENGTH, 36 ce2.geneSymbol.LENGTH, 36 ce2.refGene.LENGTH, 37 ce4.geneSymbol.LENGTH, 37 ce4.refGene.LENGTH, 38 ce4.xenoRefGene.LENGTH, 38 ce6.ensGene.LENGTH, 39 ce6.geneSymbol.LENGTH, 39 ce6.refGene.LENGTH, 40ce6.xenoRefGene.LENGTH, 40 ci1.geneSymbol.LENGTH, 41 ci1.refGene.LENGTH, 41 ci1.xenoRefGene.LENGTH, 42 ci2.ensGene.LENGTH, 42 ci2.geneSymbol.LENGTH, 43 ci2.refGene.LENGTH, 43 ci2.xenoRefGene.LENGTH, 44

danRer3.ensGene.LENGTH, 44
danRer3.geneSymbol.LENGTH, 45
danRer3.refGene.LENGTH, 45

danRer4.ensGene.LENGTH, 46 danRer4.geneSymbol.LENGTH, 46 danRer4.genscan.LENGTH, 47 danRer4.nscanGene.LENGTH, 47 danRer4.refGene.LENGTH, 48 danRer5.ensGene.LENGTH, 48 danRer5.geneSymbol.LENGTH, 49 danRer5.refGene.LENGTH, 49 danRer5.vegaGene.LENGTH, 50 danRer5.vegaPseudoGene.LENGTH, 50 danRer6.ensGene.LENGTH, 51 danRer6.geneSymbol.LENGTH, 51 danRer6.refGene.LENGTH, 52 danRer6.xenoRefGene.LENGTH, 52 dm1.geneSymbol.LENGTH, 53 dm1.genscan.LENGTH, 53 dm1.refGene.LENGTH, 54 dm2.geneid.LENGTH, 54 dm2.geneSymbol.LENGTH, 55 dm2.genscan.LENGTH, 55 dm2.nscanGene.LENGTH. 56 dm2.refGene.LENGTH, 56 dm3.geneSymbol.LENGTH, 57 dm3.nscanPasaGene.LENGTH, 57 dm3.refGene.LENGTH, 58 downloadLengthFromUCSC, 9-169, 171-179 dp2.genscan.LENGTH, 58 dp2.xenoRefGene.LENGTH, 59 dp3.geneid.LENGTH, 59 dp3.genscan.LENGTH, 60 dp3.xenoRefGene.LENGTH, 60 droAna1.geneid.LENGTH, 61 droAna1.genscan.LENGTH, 61 droAna1.xenoRefGene.LENGTH, 62 droAna2.genscan.LENGTH, 62 droAna2.xenoRefGene.LENGTH, 63 droEre1.genscan.LENGTH, 63 droEre1.xenoRefGene.LENGTH, 64 droGri1.genscan.LENGTH, 64 droGri1.xenoRefGene.LENGTH, 65 droMoj1.geneid.LENGTH, 65 droMoj1.genscan.LENGTH, 66 droMoj1.xenoRefGene.LENGTH, 66 droMoj2.genscan.LENGTH, 67 droMoj2.xenoRefGene.LENGTH, 67 droPer1.genscan.LENGTH, 68 droPer1.xenoRefGene.LENGTH, 68 droSec1.genscan.LENGTH, 69

INDEX

droSec1.xenoRefGene.LENGTH, 69 droSim1.geneid.LENGTH, 70 droSim1.genscan.LENGTH, 70 droSim1.xenoRefGene.LENGTH, 71 droVir1.geneid.LENGTH, 71 droVir1.genscan.LENGTH, 72 droVir1.xenoRefGene.LENGTH, 72 droVir2.genscan.LENGTH, 73 droVir2.xenoRefGene.LENGTH, 73 droYak1.geneid.LENGTH, 74 droYak1.genscan.LENGTH, 74 droYak1.xenoRefGene.LENGTH, 75 droYak2.genscan.LENGTH, 75 droYak2.xenoRefGene.LENGTH, 76 equCab1.geneid.LENGTH, 76 equCab1.geneSymbol.LENGTH, 77 equCab1.nscanGene.LENGTH, 77 equCab1.refGene.LENGTH, 78 equCab1.sgpGene.LENGTH, 78 equCab2.ensGene.LENGTH, 79 equCab2.geneSymbol.LENGTH, 79 equCab2.nscanGene.LENGTH, 80 equCab2.refGene.LENGTH, 80 equCab2.xenoRefGene.LENGTH, 81 felCat3.ensGene.LENGTH.81 felCat3.geneid.LENGTH, 82

felCat3.geneSymbol.LENGTH, 82
felCat3.genscan.LENGTH, 83
felCat3.nscanGene.LENGTH, 83
felCat3.refGene.LENGTH, 84
felCat3.sgpGene.LENGTH, 84
felCat3.xenoRefGene.LENGTH, 85
fr1.ensGene.LENGTH, 85
fr1.genscan.LENGTH, 86
fr2.ensGene.LENGTH, 86

galGal2.ensGene.LENGTH, 87 galGal2.geneid.LENGTH, 87 galGal2.geneSymbol.LENGTH, 88 galGal2.genscan.LENGTH, 88 galGal2.refGene.LENGTH, 89 galGal3.ensGene.LENGTH, 90 galGal3.geneSymbol.LENGTH, 90 galGal3.genscan.LENGTH, 91 galGal3.nscanGene.LENGTH, 91 galGal3.refGene.LENGTH, 92

galGal3.xenoRefGene.LENGTH, 92 gasAcu1.ensGene.LENGTH, 93 gasAcu1.nscanGene.LENGTH, 93 hg16.acembly.LENGTH, 94 hg16.ensGene.LENGTH, 94 hg16.exoniphy.LENGTH, 95 hg16.geneid.LENGTH, 95 hg16.geneSymbol.LENGTH, 96 hg16.genscan.LENGTH, 96 hg16.knownGene.LENGTH, 97 hg16.refGene.LENGTH, 97 hg16.sgpGene.LENGTH, 98 hg17.acembly.LENGTH, 98 hg17.acescan.LENGTH, 99 hg17.ccdsGene.LENGTH, 99 hg17.ensGene.LENGTH, 100 hg17.exoniphy.LENGTH, 100 hg17.geneid.LENGTH, 101 hg17.geneSymbol.LENGTH, 101 hg17.genscan.LENGTH, 102 hg17.knownGene.LENGTH, 102 hg17.refGene.LENGTH, 103 hg17.sgpGene.LENGTH, 103 hg17.vegaGene.LENGTH, 104 hg17.vegaPseudoGene.LENGTH, 104 hg17.xenoRefGene.LENGTH, 105 hg18.acembly.LENGTH, 105 hg18.acescan.LENGTH, 106 hg18.ccdsGene.LENGTH, 106 hg18.ensGene.LENGTH, 107 hg18.exoniphy.LENGTH, 107 hg18.geneid.LENGTH, 108 hg18.geneSymbol.LENGTH, 108 hg18.genscan.LENGTH, 109 hg18.knownGene.LENGTH, 109 hg18.knownGeneOld3.LENGTH, 110 hg18.refGene.LENGTH, 110 hg18.sgpGene.LENGTH, 111 hg18.sibGene.LENGTH, 111 hg18.xenoRefGene.LENGTH, 112 hg19.ccdsGene.LENGTH, 112 hg19.ensGene.LENGTH, 113 hg19.exoniphy.LENGTH, 113 hg19.geneSymbol.LENGTH, 114 hg19.knownGene.LENGTH, 114 hg19.nscanGene.LENGTH, 115 hg19.refGene.LENGTH, 115 hg19.xenoRefGene.LENGTH, 116

loxAfr3.xenoRefGene.LENGTH, 116

mm7.ensGene.LENGTH, 117 mm7.geneid.LENGTH, 117 mm7.geneSymbol.LENGTH, 118 mm7.genscan.LENGTH, 118 mm7.knownGene.LENGTH, 119 mm7.refGene.LENGTH, 119 mm7.sgpGene.LENGTH, 120 mm7.xenoRefGene.LENGTH.120 mm8.ccdsGene.LENGTH, 121 mm8.ensGene.LENGTH. 121 mm8.geneid.LENGTH, 122 mm8.geneSymbol.LENGTH, 122 mm8.genscan.LENGTH, 123 mm8.knownGene.LENGTH, 123 mm8.nscanGene.LENGTH, 124 mm8.refGene.LENGTH, 124 mm8.sgpGene.LENGTH, 125 mm8.sibGene.LENGTH, 125 mm8.xenoRefGene.LENGTH.126 mm9.acembly.LENGTH, 126 mm9.ccdsGene.LENGTH, 127 mm9.ensGene.LENGTH, 127 mm9.exoniphy.LENGTH, 128 mm9.geneid.LENGTH, 128 mm9.geneSymbol.LENGTH, 129 mm9.genscan.LENGTH, 129 mm9.knownGene.LENGTH, 130 mm9.nscanGene.LENGTH, 130 mm9.refGene.LENGTH, 131 mm9.sgpGene.LENGTH, 131 mm9.xenoRefGene.LENGTH, 132 monDom1.genscan.LENGTH, 132 monDom4.ensGene.LENGTH, 133 monDom4.geneSymbol.LENGTH, 133 monDom4.genscan.LENGTH, 134 monDom4.nscanGene.LENGTH, 134 monDom4.refGene.LENGTH, 135 monDom4.xenoRefGene.LENGTH, 135 monDom5.ensGene.LENGTH, 136 monDom5.geneSymbol.LENGTH, 136 monDom5.genscan.LENGTH, 137 monDom5.nscanGene.LENGTH, 137 monDom5.refGene.LENGTH, 138 monDom5.xenoRefGene.LENGTH, 138

ornAna1.ensGene.LENGTH, 139 ornAna1.geneSymbol.LENGTH, 139

ornAna1.refGene.LENGTH, 140 ornAna1.xenoRefGene.LENGTH, 140 oryLat2.ensGene.LENGTH, 141 oryLat2.geneSymbol.LENGTH, 141 oryLat2.refGene.LENGTH, 142 oryLat2.xenoRefGene.LENGTH, 142 panTro1.ensGene.LENGTH, 143 panTro1.geneid.LENGTH, 143 panTro1.genscan.LENGTH, 144 panTro1.xenoRefGene.LENGTH, 144 panTro2.ensGene.LENGTH, 145 panTro2.geneSymbol.LENGTH, 145 panTro2.genscan.LENGTH, 146 panTro2.nscanGene.LENGTH, 146 panTro2.refGene.LENGTH, 147 panTro2.xenoRefGene.LENGTH, 147 petMar1.xenoRefGene.LENGTH, 148 ponAbe2.ensGene.LENGTH, 148 ponAbe2.geneSymbol.LENGTH, 149 ponAbe2.genscan.LENGTH, 149 ponAbe2.nscanGene.LENGTH, 150 ponAbe2.refGene.LENGTH, 150 ponAbe2.xenoRefGene.LENGTH, 151 priPac1.xenoRefGene.LENGTH, 151 rheMac2.ensGene.LENGTH, 152 rheMac2.geneid.LENGTH, 152 rheMac2.geneSymbol.LENGTH, 153 rheMac2.nscanGene.LENGTH, 153 rheMac2.refGene.LENGTH, 154 rheMac2.sgpGene.LENGTH, 154 rheMac2.xenoRefGene.LENGTH, 155 rn3.ensGene.LENGTH, 155 rn3.geneid.LENGTH, 156 rn3.geneSymbol.LENGTH, 156 rn3.genscan.LENGTH, 157 rn3.knownGene.LENGTH, 157 rn3.nscanGene.LENGTH, 158 rn3.refGene.LENGTH, 158 rn3.sgpGene.LENGTH, 159 rn3.xenoRefGene.LENGTH, 159 rn4.ensGene.LENGTH, 160 rn4.geneid.LENGTH, 160 rn4.geneSymbol.LENGTH, 161 rn4.genscan.LENGTH, 161 rn4.knownGene.LENGTH, 162 rn4.nscanGene.LENGTH, 162 rn4.refGene.LENGTH, 163

INDEX

rn4.sgpGene.LENGTH, 163 rn4.xenoRefGene.LENGTH, 164 sacCer1.ensGene.LENGTH, 164 sacCer2.ensGene.LENGTH, 165 strPur1.geneSymbol.LENGTH, 165 strPur1.genscan.LENGTH, 166 strPur1.refGene.LENGTH, 166 strPur1.xenoRefGene.LENGTH, 167 strPur2.geneSymbol.LENGTH, 167 strPur2.genscan.LENGTH, 168 strPur2.refGene.LENGTH, 168 strPur2.xenoRefGene.LENGTH, 169 supportedGeneIDs, 169 supportedGenomes, 170 taeGut1.ensGene.LENGTH, 171 taeGut1.geneSymbol.LENGTH, 171 taeGut1.genscan.LENGTH, 172 taeGut1.nscanGene.LENGTH, 172 taeGut1.refGene.LENGTH, 173 taeGut1.xenoRefGene.LENGTH, 173

tetNig1.ensGene.LENGTH, 174 tetNig1.geneid.LENGTH, 174 tetNig1.genscan.LENGTH, 175 tetNig1.nscanGene.LENGTH, 175 tetNig2.ensGene.LENGTH, 176

unfactor, 176

xenTro1.genscan.LENGTH, 177 xenTro2.ensGene.LENGTH, 178 xenTro2.geneSymbol.LENGTH, 178 xenTro2.genscan.LENGTH, 179 xenTro2.refGene.LENGTH, 179