BSgenome.Ptroglodytes.UCSC.panTro3

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BSgenome.Ptroglodytes.UCSC.panTro3

Full genome sequences for *Pan troglodytes* (UCSC version panTro3)

Description

Full genome sequences for *Pan troglodytes* (Chimp) as provided by UCSC (panTro3, Oct. 2010) and stored in Biostrings objects.

Note

This BSgenome data package was made from the following source data files:

panTro3.fa.gz from http://hgdownload.cse.ucsc.edu/goldenPath/panTro3/bigZips/

See ?BSgenomeForge and the BSgenomeForge vignette (vignette("BSgenomeForge")) in the BSgenome software package for how to make a BSgenome data package.

Author(s)

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See Also

- BSgenome objects and the available.genomes function in the BSgenome software package.
- DNAString objects in the Biostrings package.
- The BSgenomeForge vignette (vignette("BSgenomeForge")) in the BSgenome software package for how to make a BSgenome data package.
Examples

BSgenome.Ptroglodytes.UCSC.panTro3

genome <- BSgenome.Ptroglodytes.UCSC.panTro3
seqlengths(genome)

genome$chr1 # same as genome[["chr1"]]

## Upstream sequences

## Starting with BioC 3.0, the upstream1000, upstream2000, and
## upstream5000 sequences for panTro3 are not included in the BSgenome
## data package anymore. However they can easily be extracted from the
## full genome sequences with something like:

library(GenomicFeatures)

txdb <- makeTranscriptDbFromUCSC("panTro3", "refGene")

gn <- sort(genes(txdb))

up1000 <- flank(gn, width=1000)

up1000seqs <- getSeq(genome, up1000)

## IMPORTANT: Make sure you use a TxDb package (or TranscriptDb object),
## that contains a gene model based on the exact same reference genome
## as the BSgenome object you pass to getSeq(). Note that you can make
## your own custom TranscriptDb object from various annotation resources.
## See the makeTranscriptDbFromUCSC(), makeTranscriptDbFromBiomart(),
## and makeTranscriptDbFromGFF() functions in the GenomicFeatures
## package.

## Genome-wide motif searching

## See the GenomeSearching vignette in the BSgenome software
## package for some examples of genome-wide motif searching using
## Biostrings and the BSgenome data packages:

if (interactive())
    vignette("GenomeSearching", package="BSgenome")
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