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

```r
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:

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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