

# BSgenome.Ptroglodytes.UCSC.panTro3

April 2, 2013

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Ptroglodytes

*Pan troglodytes (Chimp) full genome (UCSC version panTro3)*

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## Description

Pan troglodytes (Chimp) full genome 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:

sequences: panTro3.fa.gz, upstream1000.fa.gz, upstream2000.fa.gz, upstream5000.fa.gz  
from <http://hgdownload.cse.ucsc.edu/goldenPath/panTro3/bigZips/>  
AGAPS masks: gap.txt.gz from <ftp://hgdownload.cse.ucsc.edu/goldenPath/panTro3/database/>  
RM masks: <http://hgdownload.cse.ucsc.edu/goldenPath/panTro3/bigZips/panTro3.fa.out.gz>  
TRF masks: <http://hgdownload.cse.ucsc.edu/goldenPath/panTro3/bigZips/panTro3.trf.bed.gz>

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

## Author(s)

The Bioconductor Dev Team

## See Also

[BSgenome-class](#), [DNAString-class](#), [available.genomes](#), [BSgenomeForge](#)

## Examples

```
Ptroglodytes
seqlengths(Ptroglodytes)
Ptroglodytes$chr1 # same as Ptroglodytes[["chr1"]]

if ("AGAPS" %in% masknames(Ptroglodytes)) {

  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
```

```
{
  ## Replace all masks by the inverted AGAPS mask
  masks(seq) <- gaps(masks(seq)["AGAPS"])
  unique_letters <- uniqueLetters(seq)
  if (any(unique_letters != "N"))
    stop("assembly gaps contain more than just Ns")
}

## A message will be printed each time a sequence is removed
## from the cache:
options(verbose=TRUE)

for (seqname in seqnames(Ptroglydites)) {
  cat("Checking sequence", seqname, "... ")
  seq <- Ptroglydites[[seqname]]
  checkOnlyNsInGaps(seq)
  cat("OK\n")
}
}

## 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")
```

# Index

**\*Topic data**

Ptroglydytes, [1](#)

**\*Topic package**

Ptroglydytes, [1](#)

available.genomes, [1](#)

BSgenome-class, [1](#)

BSgenome.Ptroglydytes.UCSC.panTro3  
(Ptroglydytes), [1](#)

BSgenome.Ptroglydytes.UCSC.panTro3-package  
(Ptroglydytes), [1](#)

BSgenomeForge, [1](#)

DNASTring-class, [1](#)

Ptroglydytes, [1](#)