BSgenome.Btaurus.UCSC.bosTau3

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`Btaurus` *Bos taurus (Cow) full genome (UCSC version bosTau3)*

Description

Bos taurus (Cow) full genome as provided by UCSC (bosTau3, Aug. 2006) and stored in Biostrings objects.

Note

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

```
sequences: all the *.fa.gz files from http://hgdownload.cse.ucsc.edu/goldenPath/
AGAPS masks: http://hgdownload.cse.ucsc.edu/goldenPath/bosTau3/database/gap.txt.
RM masks: http://hgdownload.cse.ucsc.edu/goldenPath/bosTau3/bigZips/bosTau3.fa.c
TRF masks: http://hgdownload.cse.ucsc.edu/goldenPath/bosTau3/bigZips/bosTau3.trf
```

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-class, DNAString-class, `available.genomes`, BSgenomeForge

Examples

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

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

  ## 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(Btaurus)) {
    cat("Checking sequence", seqname, "... ")
    seq <- Btaurus[[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