BSgenome.Btaurus.UCSC.bosTau3

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Full genome sequences for Bos taurus (UCSC version bosTau3)

Description

Full genome sequences for Bos taurus (Cow) 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:

all the *.fa.gz files from http://hgdownload.cse.ucsc.edu/goldenPath/bosTau3/chromosomes/

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.Btaurus.UCSC.bosTau3
genome <- BSgenome.Btaurus.UCSC.bosTau3
seqlengths(genome)
genome$chr1 # same as genome["chr1"]
```

## Upstream sequences
The upstream sequences for bosTau3 (i.e. the sequences 1000 bases upstream of annotated transcription starts) can easily be extracted from the full genome sequences with something like:

```r
library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("bosTau3", "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

```r
vignette("GenomeSearching", package="BSgenome")
```
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