**BSgenome.Btaurus.UCSC.bosTau3**

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**BSgenome.Btaurus.UCSC.bosTau3**

*Full genome sequences for Bos taurus (UCSC version bosTau3)*

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**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)**

The Bioconductor Dev Team

**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"]
```

```r
## 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
## 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**
    BSgenome.Btaurus.UCSC.bosTau3, 1

*Topic **package**
    BSgenome.Btaurus.UCSC.bosTau3, 1

available.genomes, /

BSgenome, /
BSgenome.Btaurus.UCSC.bosTau3, 1
BSgenome.Btaurus.UCSC.bosTau3-package
    (BSgenome.Btaurus.UCSC.bosTau3), 1
BSgenomeForge, /
Btaurus
    (BSgenome.Btaurus.UCSC.bosTau3), 1

DNAString, /