**BSgenome.Btaurus.UCSC.bosTau4**

February 28, 2017

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**Description**

Full genome sequences for Bos taurus (Cow) as provided by UCSC (bosTau4, Oct. 2007) 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/bosTau4/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.bosTau4
genome <- BSgenome.Btaurus.UCSC.bosTau4
seqlengths(genome)
genome$chr1 # same as genome[['chr1']]
```

```r
## Upstream sequences
##
## Upstream sequences
```
library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("bosTau4", "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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