# 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

```
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:

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")
```

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