Full genome sequences for Bos taurus (Cow) as provided by UCSC (bosTau6, Nov. 2009) and stored in Biostrings objects.

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


See ?BSgenomeForge and the BSgenomeForge vignette (vignette("BSgenomeForge")) in the BSgenome software package for how to make a BSgenome data package.

The Bioconductor Dev Team

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.

```
BSgenome.Btaurus.UCSC.bosTau6
genome <- BSgenome.Btaurus.UCSC.bosTau6
seqlengths(genome)
genome$chr1 # same as genome["chr1"]
```

---

Upstream sequences

## Upstream sequences

```
## Starting with BioC 3.0, the \texttt{upstream1000}, \texttt{upstream2000}, and \texttt{upstream5000} sequences for \texttt{bosTau6} are not included in the BSgenome data package anymore. However they can easily be extracted from the full genome sequences with something like:

```r
library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("bosTau6", "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 \texttt{getSeq()}. Note that you can make your own custom TranscriptDb object from various annotation resources. See the \texttt{makeTranscriptDbFromUCSC()}, \texttt{makeTranscriptDbFromBiomart()}, \texttt{makeTranscriptDbFromGFF()} functions in the GenomicFeatures package.

## Genome-wide motif searching

See the \texttt{GenomeSearching} vignette in the BSgenome software package for some examples of genome-wide motif searching using Biostrings and the BSgenome data packages:

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