

# BSgenome.Btaurus.UCSC.bosTau9

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BSgenome.Btaurus.UCSC.bosTau9

*Full genome sequences for Bos taurus (UCSC version bosTau9)*

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## Description

Full genome sequences for Bos taurus (Cow) as provided by UCSC (bosTau9, Apr. 2018) and stored in Biostrings objects.

## Note

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

bosTau9.2bit from <http://hgdownload.cse.ucsc.edu/goldenPath/bosTau9/bigZips/>

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.bosTau9
genome <- BSgenome.Btaurus.UCSC.bosTau9
head(seqlengths(genome))
genome$chr1 # same as genome[["chr1"]]
```

```
## -----
## Extract the upstream sequences
```

```
## -----  
## The upstream sequences located in  
## http://hgdownload.cse.ucsc.edu/goldenPath/bosTau9/bigZips/  
## are based on RefSeq genes (RefSeq Genes track in the Genome Browser).  
## These can easily be extracted from the full genome sequences with:  
  
library(GenomicFeatures)  
refGene_txdb <- suppressWarnings(makeTxDbFromUCSC("bosTau9", "refGene"))  
refGene_up1000seqs <- extractUpstreamSeqs(genome, refGene_txdb)  
  
## Note that you can make a TxDb object from various annotation  
## resources. See the makeTxDbFromUCSC(), makeTxDbFromEnsembl(), and  
## makeTxDbFromGFF() functions in the GenomicFeatures package for more  
## information.  
## IMPORTANT: Make sure you use a TxDb package (or TxDb object) that  
## contains a gene model based on bosTau9 or on a compatible genome  
## (i.e. a genome with sequences identical to the sequences in bosTau9).  
## See ?extractUpstreamSeqs in the GenomicFeatures package for more  
## information.  
  
## -----  
## 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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