

# BSgenome.Btaurus.UCSC.bosTau3

January 15, 2025

---

BSgenome.Btaurus.UCSC.bosTau3

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

---

## 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")
```

# Index

\* **data**

BSgenome.Btaurus.UCSC.bosTau3, [1](#)

\* **package**

BSgenome.Btaurus.UCSC.bosTau3, [1](#)

available.genomes, [1](#)

BSgenome, [1](#)

BSgenome.Btaurus.UCSC.bosTau3, [1](#)

BSgenome.Btaurus.UCSC.bosTau3-package  
(BSgenome.Btaurus.UCSC.bosTau3),  
[1](#)

BSgenomeForge, [1](#)

Btaurus  
(BSgenome.Btaurus.UCSC.bosTau3),  
[1](#)

DNAStrng, [1](#)