

BSgenome.Btaurus.UCSC.bosTau4

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BSgenome.Btaurus.UCSC.bosTau4

Full genome sequences for Bos taurus (UCSC version bosTau4)

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/>
+ the upstream*.fa.gz files from <http://hgdownload.cse.ucsc.edu/goldenPath/bosTau4/bigZips/>

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

Author(s)

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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.bosTau4
genome <- BSgenome.Btaurus.UCSC.bosTau4
seqlengths(genome)
genome$chr1 # same as genome[["chr1"]]

## 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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