**BSgenome.Btaurus.UCSC.bosTau8**

**Description**

Full genome sequences for Bos taurus (Cow) as provided by UCSC (bosTau8, Jun. 2014) and stored in Biostrings objects.

**Note**

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

bosTau8.2bit from http://hgdownload.cse.ucsc.edu/goldenPath/bosTau8/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**

```r
BSgenome.Btaurus.UCSC.bosTau8
geno <- BSgenome.Btaurus.UCSC.bosTau8
head(seqlengths(genome))
genome$chr1 # same as genome[["chr1"]]
```

# Extract the upstream sequences
The upstream sequences located in
http://hgdownload.cse.ucsc.edu/goldenPath/bosTau8/bigZips/
are based on RefSeq genes (RefSeq Genes track in the Genome Browser).
These can easily be extracted from the full genome sequences with:

```r
library(GenomicFeatures)
refGene_txdb <- suppressWarnings(makeTxDbFromUCSC("bosTau8", "refGene"))
refGene_up1000seqs <- extractUpstreamSeqs(genome, refGene_txdb)
```

Note that you can make a TxDb object from various annotation
resources. See the makeTxDbFromUCSC(), makeTxDbFromBiomart(), 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 bosTau8 or on a compatible genome
(i.e. a genome with sequences identical to the sequences in bosTau8).
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:

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