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/

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"]

# Upstream sequences
# Upstream sequences
library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("bosTau4", "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")
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