BSgenome.Btaurus.UCSC.bosTau4

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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

Starting with BioC 3.0, the upstream1000, upstream2000, and
upstream5000 sequences for bosTau4 are not included in the BSgenome
data package anymore. However they can easily be extracted from the
full genome sequences with something like:

library(GenomicFeatures)
taxdb <- 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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