BSgenome.Rnorvegicus.UCSC.rn6

January 3, 2024

Description

Full genome sequences for Rattus norvegicus (Rat) as provided by UCSC (rn6, Jul. 2014) and stored in Biostrings objects.

Note

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

rn6.2bit from http://hgdownload.cse.ucsc.edu/goldenPath/rn6/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.Rnorvegicus.UCSC.rn6

genoeme <- BSgenome.Rnorvegicus.UCSC.rn6
genoeme$chr1 # same as genome[["chr1"]]

## Extract the upstream sequences
## The upstream sequences can easily be extracted from the full genome

library(GenomicFeatures)

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