# BSgenome.Rnorvegicus.UCSC.rn6

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`BSgenome.Rnorvegicus.UCSC.rn6`

*Full genome sequences for Rattus norvegicus (UCSC version rn6)*

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## 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)

The Bioconductor Dev Team

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

## ---------------------------------------------------------------------
## Extract the upstream sequences
## ---------------------------------------------------------------------
## The upstream sequences can easily be extracted from the full genome
## sequences with something like:

library(GenomicFeatures)
txdb <- makeTxDbFromUCSC("rn6", tablename="refGene")
up1000seqs <- extractUpstreamSeqs(genome, txdb, width=1000)

## IMPORTANT: Make sure you use a TxDb package (or TxDb object) that
## contains a gene model based on rn6 or on a compatible genome (i.e.
## a genome with sequences identical to the sequences in rn6). 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.

## ---------------------------------------------------------------------
## 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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