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

**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**

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

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

```r
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.

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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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