BSgenome.Hsapiens.UCSC.hg19

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Full genome sequences for Homo sapiens (UCSC version hg19)

Description

Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg19, Feb. 2009) and stored in Biostrings objects.

Note

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

```
chromFa.zip, upstream1000.zip, upstream2000.zip, upstream5000.zip
from http://hgdownload.cse.ucsc.edu/goldenPath/hg19/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.

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Examples

```
BSgenome.Hsapiens.UCSC.hg19
genome <- BSgenome.Hsapiens.UCSC.hg19
seqlengths(genome)
genome$chr1  # same as genome[["chr1"]]

## 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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