BSgenome.Hsapiens.UCSC.hg19

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BSgenome.Hsapiens.UCSC.hg19

*Full genome sequences for Homo sapiens (UCSC version hg19, based on GRCh37.p13)*

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**Description**

Full genome sequences for Homo sapiens (Human) as provided by UCSC (hg19, based on GRCh37.p13) and stored in Biostrings objects.

**Note**

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


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

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