# BSgenome.Amellifera.UCSC.apiMel2

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BSgenome.Amellifera.UCSC.apiMel2

*Full genome sequences for Apis mellifera (UCSC version apiMel2)*

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### Description

Full genome sequences for Apis mellifera (Honey Bee) as provided by UCSC (apiMel2, Jan. 2005) and stored in Biostrings objects.

### Note

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

```
GroupFa.zip from http://hgdownload.cse.ucsc.edu/goldenPath/apiMel2/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.Amellifera.UCSC.apiMel2
genome <- BSgenome.Amellifera.UCSC.apiMel2
seqlengths(genome)
genome$Group1  # same as genome[["Group1"]]


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