BSgenome.Amellifera.NCBI.AmelHAV3.1

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BSgenome.Amellifera.NCBI.AmelHAV3.1

Full genome sequences for Apis mellifera (Amel_HAv3.1)

Description

Full genome sequences for Apis mellifera as provided by NCBI (assembly Amel_HAv3.1, assembly accession GCF_003254395.2) 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)

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.NCBI.AmelHAv3.1
genome <- BSgenome.Amellifera.NCBI.AmelHAv3.1
head(seqlengths(genome))
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")
Index

* data
  BSgenome.Amellifera.NCBI.AmelHAv3.1,
  |
* package
  BSgenome.Amellifera.NCBI.AmelHAv3.1,
  |
  Amellifera
  (BSgenome.Amellifera.NCBI.AmelHAv3.1),
  |
  available.genomes, /

  BSgenome, /
  BSgenome.Amellifera.NCBI.AmelHAv3.1, |
  BSgenome.Amellifera.NCBI.AmelHAv3.1-package
  (BSgenome.Amellifera.NCBI.AmelHAv3.1), |
  BSgenomeForge, /

  DNAString, /