BSgenome.Dvirilis.Ensembl.dvircaf1

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`BSgenome.Dvirilis.Ensembl.dvircaf1` *Full genome sequences for Drosophila virilis (assembly dvir_caf1)*

Description

Full genome sequences for Drosophila virilis (assembly dvir_caf1, GenBank assembly accession GCA_000005245.1) as provided by Ensembl and stored in Biostrings objects.

Note

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

`Drosophila_virilis.dvir_caf1.dna.toplevel.fa.gz, downloaded from ftp://ftp.ensemblgenomes.org/pub/re`

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.Dvirilis.Ensembl.dvircaf1
genome <- BSgenome.Dvirilis.Ensembl.dvircaf1
head(seqlengths(genome))
genome$scaffold_13049  # same as genome[["scaffold_13049"]]

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