BSgenome.Athaliana.TAIR.TAIR9

November 11, 2026

`BSgenome.Athaliana.TAIR.TAIR9`
Full genome sequences for Arabidopsis thaliana (TAIR9)

Description

Full genome sequences for Arabidopsis thaliana as provided by TAIR (TAIR9 Genome Release) and stored in Biostrings objects. Note that TAIR10 is an "annotation release" based on the same genome assembly as TAIR9.

Note

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

`ftp://ftp.arabidopsis.org/home/tair/Genes/TAIR9_genome_release/TAIR9_chr_all.fas`

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.Athaliana.TAIR.TAIR9
genome <- BSgenome.Athaliana.TAIR.TAIR9
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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