Full genome sequences for Arabidopsis thaliana (TAIR version from April 23, 2008)

Description

Full genome sequences for Arabidopsis thaliana as provided by TAIR (snapshot from April 23, 2008) and stored in Biostrings objects.

Note

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

call the chr*.fas file from ftp://ftp.arabidopsis.org/home/tair/Sequences/whole_chromosomes/

WARNING: This is where things are today (Oct 1st, 2008) but is probably NOT aimed to be the permanent URL for the 04232008 snapshot of the genome. TAIR might update the content of this folder in the future with a new snapshot and move the 04232008 snapshot to the OLD/ subfolder.

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.04232008
geno <- BSgenome.Athaliana.TAIR.04232008
seqlengths(geno)
geno$chr1 # same as geno["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")
Index

*Topic data
  BSgenome.Athaliana.TAIR.04232008,
*Topic package
  BSgenome.Athaliana.TAIR.04232008,

Athaliana
  (BSgenome.Athaliana.TAIR.04232008),
  available.genomes,/  

BSgenome,/  
BSgenome.Athaliana.TAIR.04232008,/  
BSgenome.Athaliana.TAIR.04232008-package
  (BSgenome.Athaliana.TAIR.04232008),
  BSgenomeForge,/  

DNAString,/  