

# BSgenome.Alyrata.JGI.v1

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Alyrata

*Arabidopsis lyrata* full genome (JGI version V1.0)

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## Description

Arabidopsis lyrata 8x Release [project ID 4002920] as provided by JGI ( snapshot from March 24, 2011) and stored in Biostrings objects.

## Note

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

all the chr\*.fa file from <http://genome.jgi-psf.org/Araly1/Araly1.download.ftp.html>  
Chloroplast and mitochondrion genomes are presented as scaffolds, see JGI websites for INFO.  
WARNING: This is where things are today (March 24, 2011) but is probably NOT aimed to be the permanent URL for the V1.0 snapshot of the genome.  
JGI might update the content of this folder in the future with a new snapshot and move the V1.0 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-class](#), [DNAString-class](#), [available.genomes](#), [BSgenomeForge](#)

**Examples**

```
Alyrata
seqlengths(Alyrata)
Alyrata$chr1 # same as Alyrata[["chr1"]]

if ("AGAPS" %in% masknames(Alyrata)) {

  ## Check that the assembly gaps contain only Ns:
  checkOnlyNsInGaps <- function(seq)
  {
    ## Replace all masks by the inverted AGAPS mask
    masks(seq) <- gaps(masks(seq)["AGAPS"])
    unique_letters <- uniqueLetters(seq)
    if (any(unique_letters != "N"))
      stop("assembly gaps contain more than just Ns")
  }

  ## A message will be printed each time a sequence is removed
  ## from the cache:
  options(verbose=TRUE)

  for (seqname in seqnames(Alyrata)) {
    cat("Checking sequence", seqname, "... ")
    seq <- Alyrata[[seqname]]
    checkOnlyNsInGaps(seq)
    cat("OK\n")
  }
}

## 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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