Description

Toxoplasma gondii ME49 genome Release 7.0 available at http://www.toxodb.org

Note

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

-- information not available --

See ?BSgenomeForge and the BSgenomeForge vignette (vignette("BSgenomeForge")) in the
BSgenome software package for how to make a BSgenome data package.

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See Also

BSgenome-class, DNAString-class, available.genomes, BSgenomeForge

Examples

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

## 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:

```r
options(verbose=TRUE)
for (seqname in seqnames(Tgondii)) {
  cat("Checking sequence", seqname, "...")
  seq <- Tgondii[[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:

```r
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```
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