BSgenome.Gaculeatus.UCSC.gasAcu1

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Full genome sequences for Gasterosteus aculeatus (UCSC version gasAcu1)

Description

Full genome sequences for Gasterosteus aculeatus (Stickleback) as provided by UCSC (gasAcu1, Feb. 2006) and stored in Biostrings objects.

Note

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

chromFa.tar.gz from http://hgdownload.cse.ucsc.edu/goldenPath/gasAcu1/bigZips/

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

```r
BSgenome.Gaculeatus.UCSC_gasAcuI
genome <- BSgenome.Gaculeatus.UCSC_gasAcuI
seqlengths(genome)
genome$chrI # same as genome[["chrI"]]
```

### Upstream sequences
```
library(GenomicFeatures)
taxdb <- makeTranscriptDbFromUCSC("gasAcuI", "refGene")
bn <- sort(genes(txdb))
up1000 <- flank(bn, width=1000)
up1000seqs <- getSeq(genome, up1000)
```

### Genome-wide motif searching
```
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
```
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