BSgenome.Gaculeatus.UCSC.gasAcu1

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**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.gasAcu1
genome <- BSgenome.Gaculeatus.UCSC.gasAcu1
seqlengths(genome)
genome$chrI # same as genome[['chrI']]
```

## Upstream sequences

## Starting with BioC 3.0, the upstream1000, upstream2000, and upstream5000 sequences for gasAcu1 are not included in the BSgenome data package anymore. However they can easily be extracted from the full genome sequences with something like:

library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("gasAcu1", "refGene")
gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)

## 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:

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

* data
  BSgenome.Gaculeatus.UCSC.gasAcu1,
* package
  BSgenome.Gaculeatus.UCSC.gasAcu1,
available.genomes,

BSgenome,
BSgenome.Gaculeatus.UCSC.gasAcu1,
BSgenome.Gaculeatus.UCSC.gasAcu1-package
  (BSgenome.Gaculeatus.UCSC.gasAcu1),
BSgenomeForge,
DNAString,
Gaculeatus
  (BSgenome.Gaculeatus.UCSC.gasAcu1),