

BSgenome.Tguttata.UCSC.taeGut2

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Full genome sequences for Taeniopygia guttata (UCSC version taeGut2)

Description

Full genome sequences for *Taeniopygia guttata* (Zebra finch) as provided by UCSC (taeGut2, Feb. 2013) and stored in Biostrings objects.

Note

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

taeGut2.2bit from <http://hgdownload.soe.ucsc.edu/goldenPath/taeGut2/bigZips/>

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

Author(s)

The Bioconductor Dev Team

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.Tguttata.UCSC.taeGut2
genome <- BSgenome.Tguttata.UCSC.taeGut2
head(seqlengths(genome))
genome$chr1 # same as genome[["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")
```

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