

# BSgenome.Tguttata.UCSC.taeGut1

January 15, 2025

---

BSgenome.Tguttata.UCSC.taeGut1

*Full genome sequences for Taeniopygia guttata (UCSC version taeGut1)*

---

## Description

Full genome sequences for *Taeniopygia guttata* (Zebra finch) as provided by UCSC (taeGut1, Jul. 2008) and stored in Biostrings objects.

## Note

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

chromFa.tar.gz from <http://hgdownload.soe.ucsc.edu/goldenPath/taeGut1/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.taeGut1
genome <- BSgenome.Tguttata.UCSC.taeGut1
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")
```

# Index

\* **data**

BSgenome.Tguttata.UCSC.taeGut1, [1](#)

\* **package**

BSgenome.Tguttata.UCSC.taeGut1, [1](#)

available.genomes, [1](#)

BSgenome, [1](#)

BSgenome.Tguttata.UCSC.taeGut1, [1](#)

BSgenome.Tguttata.UCSC.taeGut1-package  
(BSgenome.Tguttata.UCSC.taeGut1),  
[1](#)

BSgenomeForge, [1](#)

DNAStrng, [1](#)

Tguttata

(BSgenome.Tguttata.UCSC.taeGut1),  
[1](#)