

BSgenome.Mfuro.UCSC.musFur1

February 5, 2025

BSgenome.Mfuro.UCSC.musFur1

Full genome sequences for Mustela putorius furo (UCSC version musFur1)

Description

Full genome sequences for *Mustela putorius furo* (Ferret) as provided by UCSC (musFur1, Apr. 2011) and stored in Biostrings objects.

Note

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

musFur1.2bit from <http://hgdownload.soe.ucsc.edu/goldenPath/musFur1/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.Mfuro.UCSC.musFur1
genome <- BSgenome.Mfuro.UCSC.musFur1
seqlengths(genome)
genome$GL896898 # same as genome[["GL896898"]]

## -----
## 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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