

# GenomicFeatures.Mmusculus.UCSC.mm9

October 25, 2011

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CpG.mm9

*CpG islands for mm9*

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## Description

Locations of the CpG islands in the Mouse genome (build mm9). Coordinates are relative to the mm9 build and are in nucleotides from the 5' end of the positive ("+") strand. They are always \*one-based\*, that is, the coordinate of the first (or leftmost) nucleotide in the strand is 1.

## Usage

CpG.mm9 ()

## Value

A data frame with 16026 observations on the following 4 variables.

1. `chromosome`: Chromosome name as a character vector.
2. `start`: Interval start points.
3. `end`: Interval end points.
4. `ID`: An identifier.

## Source

This table was obtained by downloading the following database file from UCSC (on Sep 28, 2009): <http://hgdownload.cse.ucsc.edu/goldenPath/mm9/database/cpgIslandExt.txt.gz> and by translating the start coordinates found in the file from zero-based to one-based.

The `cpgIslandExt.txt.gz` file is a database dump containing the UCSC track called "CpG Islands" and described here: <http://genome.ucsc.edu/cgi-bin/hgTrackUi?db=mm9&g=cpgIslandExt>

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```
GenomicFeatures.Mmusculus.UCSC.mm9_dbconn
```

*Get the connection to the built-in DB*

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### Description

A convenience function for getting a connection object to the annotation DB included in the `GenomicFeatures.Mmusculus.UCSC.mm9` package.

### Usage

```
GenomicFeatures.Mmusculus.UCSC.mm9_dbconn()
GenomicFeatures.Mmusculus.UCSC.mm9_dbfile()
```

### Details

`GenomicFeatures.Mmusculus.UCSC.mm9_dbconn` returns a connection object that was created at load-time and is aimed to hold a permanent connection. It is used internally by some of the functions defined in this package. Don't call `dbDisconnect` on this connection object or you will break these functions.

### See Also

[dbGetQuery](#), [dbConnect](#), [geneMouse](#)

### Examples

```
library(RSQLite)

## Get Mouse genes in chromosome 1:
chr1_genes <- dbGetQuery(GenomicFeatures.Mmusculus.UCSC.mm9_dbconn(),
                        "SELECT * FROM knownGene WHERE chrom='chr1'")

## Get all the Mouse genes:
genes <- dbReadTable(GenomicFeatures.Mmusculus.UCSC.mm9_dbconn(),
                    "knownGene", row.names=NULL)

## NOTE: The recommended way to get all the Mouse genes is to use geneMouse().
```

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```
geneMouse
```

*UCSC Gene Predictions for mm9*

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### Description

Gene coordinates and annotations for *M. musculus* from UCSC. Coordinates are relative to the mm9 build and are in nucleotides from the 5' end of the positive ("+") strand. They are always *\*one-based\**, that is, the coordinate of the first (or leftmost) nucleotide in the strand is 1. Each "gene", or row in the dataset, corresponds to a unique combination of transcript (TSS, TES and exons) and coding sequence (start and end).

### Usage

```
geneMouse()
```

**Value**

A data frame with 49409 observations on the following 12 variables.

1. `name`: The name of the gene.
2. `chrom`: The name of the chromosome the gene is located on.
3. `strand`: The strand the gene is coded on, "+", or "-".
4. `txStart`: Transcription start site.
5. `txEnd`: Transcription stop site.
6. `cdsStart`: Start position of the coding sequence.
7. `cdsEnd`: End position of the coding sequence.
8. `exonCount`: The number of exons.
9. `exonStarts`: A comma separated list of the exon start positions.
10. `exonEnds`: A comma separated list of exon stop positions.
11. `proteinID`: An ID for the protein produced, missing values are coded as NA.
12. `alignID`: Unique identifier of each gene and RNA alignment pair, apparently redundant with `name`.

**Note**

For genes coded on the negative strand the `txStart` is really the end, and similarly for the coding regions.

**Source**

This table was obtained by downloading the following database file from UCSC (on Sep 28, 2009): <http://hgdownload.cse.ucsc.edu/goldenPath/mm9/database/knownGene.txt.gz> and by translating the start coordinates found in the file from zero-based to one-based.

The `knownGene.txt.gz` file is a database dump containing the UCSC track called "UCSC Genes" and described here: <http://genome.ucsc.edu/cgi-bin/hgTrackUi?db=mm9&g=knownGene>

See <http://genome.ucsc.edu/cgi-bin/hgTables> and Hsu F, Kent WJ, Clawson H, Kuhn RM, Diekhans M, Haussler D. The UCSC Known Genes. *Bioinformatics*. 2006 May 1;22(9):1036-46.

All the annotations in this package are freely available for public use, except for the Swiss-Prot/UniProt data in the `knownGene` table, which has the following terms of use:

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### **Examples**

```
genes <- geneMouse()  
str(genes)  
transcripts_deprecated(genes)
```

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