mouseCHRLOC

April 16, 2025

`mouseCHRLOC` *Bioconductor annotation data package*

Description

The annotation package was built using a downloadable R package - AnnBuilder (download and build your own) from www.bioconductor.org using the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Thu Aug 30 09:55:54 2007

mouseCHRLOC

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The function mouseCHRLOC() provides information about the binary data files

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`mouseCHRLOC10END` *An annotation data file for transciption ending location of genes on chromosome 10*

Description

mouseCHRLOC10END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 10 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

http://www.genome.ucsc.edu/goldenPath/hg16/database/

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC10END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC10START` *An annotation data file for transciption starting locations of genes on chromosome 10*

Description

mouseCHRLOC10START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 10 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

http://www.genome.ucsc.edu/goldenPath/hg16/database/

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC10START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC11END` *An annotation data file for transciption ending location of genes on chromosome 11*

Description

mouseCHRLOC11END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 11 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

http://www.genome.ucsc.edu/goldenPath/hg16/database/

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC11END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC11START` *An annotation data file for transciption starting locations of genes on chromosome 11*

Description

mouseCHRLOC11START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 11 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

http://www.genome.ucsc.edu/goldenPath/hg16/database/

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC11START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC12END` *An annotation data file for transciption ending location of genes on chromosome 12*

Description

mouseCHRLOC12END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 12 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC12END)
if(length(xx) > 0){
 # Get the value of the first key
```

```
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC12START` *An annotation data file for transciption starting locations of genes on chromosome 12*

Description

mouseCHRLOC12START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 12 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC12START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC13END` *An annotation data file for transciption ending location of genes on chromosome 13*

Description

mouseCHRLOC13END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 13 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC13END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC13START` *An annotation data file for transciption starting locations of genes on chromosome 13*

Description

mouseCHRLOC13START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 13 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC13START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC14END` *An annotation data file for transciption ending location of genes on chromosome 14*

Description

mouseCHRLOC14END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 14 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC14END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC14START` *An annotation data file for transciption starting locations of genes on chromosome 14*

Description

mouseCHRLOC14START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 14 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC14START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC15END` *An annotation data file for transciption ending location of genes on chromosome 15*

Description

mouseCHRLOC15END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 15 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC15END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC15START` *An annotation data file for transciption starting locations of genes on chromosome 15*

Description

mouseCHRLOC15START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 15 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC15START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC16END` *An annotation data file for transciption ending location of genes on chromosome 16*

Description

mouseCHRLOC16END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 16 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC16END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC16START` *An annotation data file for transciption starting locations of genes on chromosome 16*

Description

mouseCHRLOC16START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 16 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

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Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC16START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC17END` *An annotation data file for transciption ending location of genes on chromosome 17*

Description

mouseCHRLOC17END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 17 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC17END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC17START` *An annotation data file for transciption starting locations of genes on chromosome 17*

Description

mouseCHRLOC17START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 17 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC17START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC18END` *An annotation data file for transciption ending location of genes on chromosome 18*

Description

mouseCHRLOC18END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 18 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC18END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC18START` *An annotation data file for transciption starting locations of genes on chromosome 18*

Description

mouseCHRLOC18START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 18 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC18START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC19END` *An annotation data file for transciption ending location of genes on chromosome 19*

Description

mouseCHRLOC19END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 19 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC19END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC19START` *An annotation data file for transciption starting locations of genes on chromosome 19*

Description

mouseCHRLOC19START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 19 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC19START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC1END` *An annotation data file for transciption ending location of genes on chromosome 1*

Description

mouseCHRLOC1END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 1 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC1END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC1START` *An annotation data file for transciption starting locations of genes on chromosome 1*

Description

mouseCHRLOC1START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 1 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC1START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC2END` *An annotation data file for transciption ending location of genes on chromosome 2*

Description

mouseCHRLOC2END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 2 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC2END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC2START` *An annotation data file for transciption starting locations of genes on chromosome 2*

Description

mouseCHRLOC2START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 2 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC2START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC3END` *An annotation data file for transciption ending location of genes on chromosome 3*

Description

mouseCHRLOC3END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 3 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC3END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC3START` *An annotation data file for transciption starting locations of genes on chromosome 3*

Description

mouseCHRLOC3START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 3 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC3START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC4END` *An annotation data file for transciption ending location of genes on chromosome 4*

Description

mouseCHRLOC4END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 4 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC4END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC4START` *An annotation data file for transciption starting locations of genes on chromosome 4*

Description

mouseCHRLOC4START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 4 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC4START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC5END` *An annotation data file for transciption ending location of genes on chromosome 5*

Description

mouseCHRLOC5END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 5 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC5END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC5START` *An annotation data file for transciption starting locations of genes on chromosome 5*

Description

mouseCHRLOC5START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 5 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC5START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC6END` *An annotation data file for transciption ending location of genes on chromosome 6*

Description

mouseCHRLOC6END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 6 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC6END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC6START` *An annotation data file for transciption starting locations of genes on chromosome 6*

Description

mouseCHRLOC6START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 6 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC6START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC7END` *An annotation data file for transciption ending location of genes on chromosome 7*

Description

mouseCHRLOC7END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 7 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC7END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC7START` *An annotation data file for transciption starting locations of genes on chromosome 7*

Description

mouseCHRLOC7START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 7 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC7START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC8END` *An annotation data file for transciption ending location of genes on chromosome 8*

Description

mouseCHRLOC8END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 8 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC8END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC8START` *An annotation data file for transciption starting locations of genes on chromosome 8*

Description

mouseCHRLOC8START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 8 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC8START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC9END` *An annotation data file for transciption ending location of genes on chromosome 9*

Description

mouseCHRLOC9END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 9 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC9END)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOC9START` *An annotation data file for transciption starting locations of genes on chromosome 9*

Description

mouseCHRLOC9START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 9 corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOC9START)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOCCYTOLOC` *An annotation data file for Cytoband locations on chromosomes*

Description

mouseCHRLOCCYTOLOC maps chromosome numbers and the locations of cytobands on chromosoms

Details

This is an environment object containing key and value pairs. Keys are chromosome numbers and values are the locations of cytobands on correponding chromosoms. The mapped values are lists of named vectors. The names of lists are cytoband identifiers (e. g. qA2, ...). Each list contains a vector of two elements of integers for the starting and ending locations of the band on the chromosome defined by the key the lists mapped to. Names of the vectors indicate whether the value is for the starting or ending location.

Mappings were based on the following source(s):

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

Examples

```
bands <- as.list(mouseCHRLOCCYTOLOC)
# cytobands on chromosome number 1
names(bands[[1]])
# The start and end locations for one band on chromosome number 1
bands[[1]][[1]]
```

`mouseCHRLOCENTREZID2CHR` *An annotation data file that maps Entrez Gene identifiers to chromosome number*

Description

mouseCHRLOCENTREZID2CHR maps Entrez Gene identifiers to the chromosome numbers the genes represented by the Locuslink identifiers reside

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the corresponding chromosome numbers the genes reside. Values are vectors of length 1 or more depending on whether a give Entrez Gene identifier can be mapped to one or more chromosomes.

Mappings were derived from data provided by:

Golden Path:http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

http://www.genome.ucsc.edu/goldenPath/hg16/database/

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOCENTREZID2CHR)
if(length(xx) > 0){
 # Get the value of the first Entrez Gene id
 xx[1]
 # Get the values for a few Entrez Gene identifiers
 if(length(xx) >= 3){
  xx[1:3]
 }
}
```

`mouseCHRLOCQC` *Quality control information for mouseCHRLOC*

Description

mouseCHRLOCQC is an R environment that provides quality control information for mouseCHRLOC

Details

This file contains quality control information that can be displayed by typing mouseCHRLOC() after loading the package using library(mouseCHRLOC). The follow items are included:

Date built: Date when the package was built.

Number of probes: total number of probes included

Probe number missmatch: if the total number of probes of any of the data file is different from a base file used to check the data files the name of the data file will be listed

Probe missmatch: if any of probes in a data file missmatched that of the base file, the name of the data file will be listed

Mappings found for probe based files: number of mappings obtained for the total number of probes

Mappings found for non-probe based files: total number of mappings obtained

---

`mouseCHRLOCXEND` *An annotation data file for transciption ending location of genes on chromosome X*

Description

mouseCHRLOCXEND maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number X corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOCXEND)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOCXSTART` *An annotation data file for transciption starting locations of genes on chromosome X*

Description

mouseCHRLOCXSTART maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number X corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOCXSTART)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOCYEND` *An annotation data file for transciption ending location of genes on chromosome Y*

Description

mouseCHRLOCYEND maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number Y corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption ending location for genes. The ending positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the largest end value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOCYEND)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

`mouseCHRLOCYSTART` *An annotation data file for transciption starting locations of genes on chromosome Y*

Description

mouseCHRLOCYSTART maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number Y corresponding to the Entrez Gene identifiers

Details

This is an environment object containing key and value pairs. Keys are Entrez Gene identifiers and values are the transciption starting location for genes. The starting positions for genes on both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Values for the antisense strand have a leading "-" sign (e. g. -1234567).

Values for keys are named vectors derived from the smallest starting value found for the Entrez Gene identifier. Names of chromosome location values can be "Confident" when the gene can be confidently placed on a chromosome and "Unconfident" otherwise (denoted by "_random" in UCSC data).

Mappings were derived from the following public data sources:

Golden Path:`http://gopher6/compbio/annotationSourceData/hgdownload.cse.ucsc.edu/goldenPath/currentGenomes//Mus_musculus/database/`. Built: No build info available.

Package built: Thu Aug 30 09:55:54 2007

References

`http://www.genome.ucsc.edu/goldenPath/hg16/database/`

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(mouseCHRLOCYSTART)
if(length(xx) > 0){
 # Get the value of the first key
 xx[1]
 # Get the values for a few keys
 if(length(xx) >= 3){
     xx[1:3]
 }
}
```

Index