humanCHRLOC

November 11, 2026

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humanCHRLOC *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//Homo_sapiens/database/. Built: No build info available.

Thu Aug 30 09:54:07 2007

humanCHRLOC

Y

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

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humanCHRLOC10END *An annotation data file for transciption ending location of genes on chromosome 10*

Description

humanCHRLOC10END 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:

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Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC10END)
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]
 }
}
```

---

humanCHRLOC10START *An annotation data file for transciption starting locations of genes on chromosome 10*

Description

humanCHRLOC10START 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:

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Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC10START)
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]
 }
}
```

---

humanCHRLOC11END *An annotation data file for transciption ending location of genes on chromosome 11*

Description

humanCHRLOC11END 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:

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Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC11END)
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]
 }
}
```

---

humanCHRLOC11START *An annotation data file for transciption starting locations of genes on chromosome 11*

Description

humanCHRLOC11START 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:

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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC11START)
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]
 }
}
```

---

humanCHRLOC12END *An annotation data file for transciption ending location of genes on chromosome 12*

Description

humanCHRLOC12END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC12END)
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]
 }
}
```

---

humanCHRLOC12START *An annotation data file for transciption starting locations of genes on chromosome 12*

Description

humanCHRLOC12START 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:

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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC12START)
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]
 }
}
```

humanCHRLOC13END *An annotation data file for transciption ending location of genes on chromosome 13*

Description

humanCHRLOC13END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC13END)
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]
 }
}
```

humanCHRLOC13START *An annotation data file for transciption starting locations of genes on chromosome 13*

Description

humanCHRLOC13START 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:

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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC13START)
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]
 }
}
```

humanCHRLOC14END *An annotation data file for transciption ending location of genes on chromosome 14*

Description

humanCHRLOC14END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC14END)
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]
 }
}
```

humanCHRLOC14START *An annotation data file for transciption starting locations of genes on chromosome 14*

Description

humanCHRLOC14START 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:

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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC14START)
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]
 }
}
```

humanCHRLOC15END *An annotation data file for transciption ending location of genes on chromosome 15*

Description

humanCHRLOC15END 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:

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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC15END)
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]
 }
}
```

humanCHRLOC15START *An annotation data file for transciption starting locations of genes on chromosome 15*

Description

humanCHRLOC15START 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:

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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC15START)
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]
 }
}
```

humanCHRLOC16END *An annotation data file for transciption ending location of genes on chromosome 16*

Description

humanCHRLOC16END 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:

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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC16END)
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]
 }
}
```

humanCHRLOC16START *An annotation data file for transciption starting locations of genes on chromosome 16*

Description

humanCHRLOC16START 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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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC16START)
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]
 }
}
```

humanCHRLOC17END *An annotation data file for transciption ending location of genes on chromosome 17*

Description

humanCHRLOC17END 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:

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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC17END)
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]
 }
}
```

humanCHRLOC17START *An annotation data file for transciption starting locations of genes on chromosome 17*

Description

humanCHRLOC17START 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:

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Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC17START)
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]
 }
}
```

humanCHRLOC18END *An annotation data file for transciption ending location of genes on chromosome 18*

Description

humanCHRLOC18END 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:

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Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC18END)
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]
 }
}
```

humanCHRLOC18START *An annotation data file for transciption starting locations of genes on chromosome 18*

Description

humanCHRLOC18START 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:

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References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC18START)
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]
 }
}
```

humanCHRLOC19END *An annotation data file for transciption ending location of genes on chromosome 19*

Description

humanCHRLOC19END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC19END)
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]
 }
}
```

humanCHRLOC19START *An annotation data file for transciption starting locations of genes on chromosome 19*

Description

humanCHRLOC19START 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC19START)
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]
 }
}
```

humanCHRLOC1END *An annotation data file for transciption ending location of genes on chromosome 1*

Description

humanCHRLOC1END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC1END)
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]
 }
}
```

humanCHRLOC1START *An annotation data file for transciption starting locations of genes on chromosome 1*

Description

humanCHRLOC1START 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC1START)
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]
 }
}
```

humanCHRLOC20END *An annotation data file for transciption ending location of genes on chromosome 20*

Description

humanCHRLOC20END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 20 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC20END)
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]
 }
}
```

humanCHRLOC20START *An annotation data file for transciption starting locations of genes on chromosome 20*

Description

humanCHRLOC20START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 20 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC20START)
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]
 }
}
```

humanCHRLOC21END *An annotation data file for transciption ending location of genes on chromosome 21*

Description

humanCHRLOC21END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 21 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC21END)
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]
 }
}
```

humanCHRLOC21START *An annotation data file for transciption starting locations of genes on chromosome 21*

Description

humanCHRLOC21START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 21 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC21START)
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]
 }
}
```

humanCHRLOC22END *An annotation data file for transciption ending location of genes on chromosome 22*

Description

humanCHRLOC22END maps Entrez Gene identifiers to the transciption ending location of genes on chromosome number 22 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC22END)
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]
 }
}
```

humanCHRLOC22START *An annotation data file for transciption starting locations of genes on chromosome 22*

Description

humanCHRLOC22START maps Entrez Gene identifiers to the transciption starting locations of genes on chromosome number 22 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC22START)
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]
 }
}
```

humanCHRLOC2END *An annotation data file for transciption ending location of genes on chromosome 2*

Description

humanCHRLOC2END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC2END)
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]
 }
}
```

humanCHRLOC2START *An annotation data file for transciption starting locations of genes on chromosome 2*

Description

humanCHRLOC2START 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC2START)
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]
 }
}
```

humanCHRLOC3END *An annotation data file for transciption ending location of genes on chromosome 3*

Description

humanCHRLOC3END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC3END)
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]
 }
}
```

humanCHRLOC3START *An annotation data file for transciption starting locations of genes on chromosome 3*

Description

humanCHRLOC3START 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC3START)
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]
 }
}
```

humanCHRLOC4END *An annotation data file for transciption ending location of genes on chromosome 4*

Description

humanCHRLOC4END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC4END)
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]
 }
}
```

humanCHRLOC4START *An annotation data file for transciption starting locations of genes on chromosome 4*

Description

humanCHRLOC4START 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC4START)
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]
 }
}
```

humanCHRLOC5END *An annotation data file for transciption ending location of genes on chromosome 5*

Description

humanCHRLOC5END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC5END)
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]
 }
}
```

humanCHRLOC5START *An annotation data file for transciption starting locations of genes on chromosome 5*

Description

humanCHRLOC5START 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC5START)
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]
 }
}
```

humanCHRLOC6END *An annotation data file for transciption ending location of genes on chromosome 6*

Description

humanCHRLOC6END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC6END)
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]
 }
}
```

humanCHRLOC6START *An annotation data file for transciption starting locations of genes on chromosome 6*

Description

humanCHRLOC6START 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC6START)
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]
 }
}
```

humanCHRLOC7END *An annotation data file for transciption ending location of genes on chromosome 7*

Description

humanCHRLOC7END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC7END)
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]
 }
}
```

humanCHRLOC7START *An annotation data file for transciption starting locations of genes on chromosome 7*

Description

humanCHRLOC7START 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:

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Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC7START)
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]
 }
}
```

humanCHRLOC8END *An annotation data file for transciption ending location of genes on chromosome 8*

Description

humanCHRLOC8END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC8END)
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]
 }
}
```

humanCHRLOC8START *An annotation data file for transciption starting locations of genes on chromosome 8*

Description

humanCHRLOC8START 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC8START)
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]
 }
}
```

humanCHRLOC9END *An annotation data file for transciption ending location of genes on chromosome 9*

Description

humanCHRLOC9END 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC9END)
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]
 }
}
```

humanCHRLOC9START *An annotation data file for transciption starting locations of genes on chromosome 9*

Description

humanCHRLOC9START 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOC9START)
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]
 }
}
```

humanCHRLOCCYTOLOC *An annotation data file for Cytoband locations on chromosomes*

Description

humanCHRLOCCYTOLOC 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

Examples

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

humanCHRLOCENTREZID2CHR *An annotation data file that maps Entrez Gene identifiers to chromosome number*

Description

humanCHRLOCENTREZID2CHR 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOCENTREZID2CHR)
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]
 }
}
```

---

humanCHRLOCQC *Quality control information for humanCHRLOC*

Description

humanCHRLOCQC is an R environment that provides quality control information for humanCHRLOC

Details

This file contains quality control information that can be displayed by typing humanCHRLOC() after loading the package using library(humanCHRLOC). 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

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

Description

humanCHRLOCXEND 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOCXEND)
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]
 }
}
```

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

Description

humanCHRLOCXSTART 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOCXSTART)
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]
 }
}
```

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

Description

humanCHRLOCYEND 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOCYEND)
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]
 }
}
```

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

Description

humanCHRLOCYSTART 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//Homo_sapiens/database/. Built: No build info available.

Package built: Thu Aug 30 09:54:07 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(humanCHRLOCYSTART)
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]
 }
}
```

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