

ratCHRLOC

October 13, 2016

ratCHRLOC

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//Rattus_norvegicus/database/. Built: No build info available.

Thu Aug 30 09:57:40 2007

ratCHRLOC

Y

The function `ratCHRLOC()` provides information about the binary data files

ratCHRLOC10END

An annotation data file for transcription ending location of genes on chromosome 10

Description

ratCHRLOC10END maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC10END)
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]
  }
}
```

ratCHRLOC10START	<i>An annotation data file for transcription starting locations of genes on chromosome 10</i>
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Description

ratCHRLOC10START maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC10START)
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]
  }
}
```

ratCHRLOC11END

An annotation data file for transcription ending location of genes on chromosome 11

Description

ratCHRLOC11END maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC11END)
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]
  }
}
```

ratCHRLOC11START	<i>An annotation data file for transcription starting locations of genes on chromosome 11</i>
------------------	---

Description

ratCHRLOC11START maps Entrez Gene identifiers to the transcription 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 transcription 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(ratCHRLOC11START)
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]
  }
}
```

ratCHRLOC12END

An annotation data file for transcription ending location of genes on chromosome 12

Description

ratCHRLOC12END maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC12END)
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]
  }
}
```

ratCHRLOC12START	<i>An annotation data file for transcription starting locations of genes on chromosome 12</i>
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Description

ratCHRLOC12START maps Entrez Gene identifiers to the transcription 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 transcription 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(ratCHRLOC12START)
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]
  }
}
```

ratCHRLOC13END

An annotation data file for transcription ending location of genes on chromosome 13

Description

ratCHRLOC13END maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC13END)
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]
  }
}
```

ratCHRLOC13START	<i>An annotation data file for transcription starting locations of genes on chromosome 13</i>
------------------	---

Description

ratCHRLOC13START maps Entrez Gene identifiers to the transcription 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 transcription 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(ratCHRLOC13START)
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]
  }
}
```

ratCHRLOC14END

An annotation data file for transcription ending location of genes on chromosome 14

Description

ratCHRLOC14END maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC14END)
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]
  }
}
```

ratCHRLOC14START	<i>An annotation data file for transcription starting locations of genes on chromosome 14</i>
------------------	---

Description

ratCHRLOC14START maps Entrez Gene identifiers to the transcription 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 transcription 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(ratCHRLOC14START)
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]
  }
}
```

ratCHRLOC15END

An annotation data file for transcription ending location of genes on chromosome 15

Description

ratCHRLOC15END maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC15END)
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]
  }
}
```

ratCHRLOC15START	<i>An annotation data file for transcription starting locations of genes on chromosome 15</i>
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Description

ratCHRLOC15START maps Entrez Gene identifiers to the transcription 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 transcription 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(ratCHRLOC15START)
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]
  }
}
```

ratCHRLOC16END

An annotation data file for transcription ending location of genes on chromosome 16

Description

ratCHRLOC16END maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC16END)
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]
  }
}
```

ratCHRLOC16START	<i>An annotation data file for transcription starting locations of genes on chromosome 16</i>
------------------	---

Description

ratCHRLOC16START maps Entrez Gene identifiers to the transcription 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 transcription 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(ratCHRLOC16START)
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]
  }
}
```

ratCHRLOC17END

An annotation data file for transcription ending location of genes on chromosome 17

Description

ratCHRLOC17END maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC17END)
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]
  }
}
```

ratCHRLOC17START	<i>An annotation data file for transcription starting locations of genes on chromosome 17</i>
------------------	---

Description

ratCHRLOC17START maps Entrez Gene identifiers to the transcription 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 transcription 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 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC17START)
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]
  }
}
```

ratCHRLOC18END

An annotation data file for transcription ending location of genes on chromosome 18

Description

ratCHRLOC18END maps Entrez Gene identifiers to the transcription 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 transcription 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(ratCHRLOC18END)
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]
  }
}
```

ratCHRLOC18START	<i>An annotation data file for transcription starting locations of genes on chromosome 18</i>
------------------	---

Description

ratCHRLOC18START maps Entrez Gene identifiers to the transcription 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 transcription 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(ratCHRLOC18START)
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]
  }
}
```

ratCHRLOC19END

An annotation data file for transcription ending location of genes on chromosome 19

Description

ratCHRLOC19END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC19END)
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]
  }
}
```

ratCHRLOC19START

An annotation data file for transcription starting locations of genes on chromosome 19

Description

ratCHRLOC19START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC19START)
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]
  }
}
```

ratCHRLOC1END

An annotation data file for transcription ending location of genes on chromosome 1

Description

ratCHRLOC1END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC1END)
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]
  }
}
```

ratCHRLOC1START	<i>An annotation data file for transcription starting locations of genes on chromosome 1</i>
-----------------	--

Description

ratCHRLOC1START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC1START)
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]
  }
}
```

ratCHRLOC20END

An annotation data file for transcription ending location of genes on chromosome 20

Description

ratCHRLOC20END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC20END)
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]
  }
}
```

ratCHRLOC20START

An annotation data file for transcription starting locations of genes on chromosome 20

Description

ratCHRLOC20START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC2START)
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]
  }
}
```

ratCHRLOC2END

An annotation data file for transcription ending location of genes on chromosome 2

Description

ratCHRLOC2END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC2END)
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]
  }
}
```

ratCHRLOC2START

An annotation data file for transcription starting locations of genes on chromosome 2

Description

ratCHRLOC2START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC2START)
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]
  }
}
```

ratCHRLOC3END

An annotation data file for transcription ending location of genes on chromosome 3

Description

ratCHRLOC3END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC3END)
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]
  }
}
```

ratCHRLOC3START	<i>An annotation data file for transcription starting locations of genes on chromosome 3</i>
-----------------	--

Description

ratCHRLOC3START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC3START)
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]
  }
}
```

ratCHRLOC4END

An annotation data file for transcription ending location of genes on chromosome 4

Description

ratCHRLOC4END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC4END)
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]
  }
}
```

ratCHRLOC4START

An annotation data file for transcription starting locations of genes on chromosome 4

Description

ratCHRLOC4START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC4START)
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]
  }
}
```

ratCHRLOC5END

An annotation data file for transcription ending location of genes on chromosome 5

Description

ratCHRLOC5END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC5END)
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]
  }
}
```

ratCHRLOC5START	<i>An annotation data file for transcription starting locations of genes on chromosome 5</i>
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Description

ratCHRLOC5START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC5START)
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]
  }
}
```

ratCHRLOC6END

An annotation data file for transcription ending location of genes on chromosome 6

Description

ratCHRLOC6END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC6END)
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]
  }
}
```

ratCHRLOC6START	<i>An annotation data file for transcription starting locations of genes on chromosome 6</i>
-----------------	--

Description

ratCHRLOC6START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC6START)
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]
  }
}
```

ratCHRLOC7END

An annotation data file for transcription ending location of genes on chromosome 7

Description

ratCHRLOC7END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC7END)
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]
  }
}
```

ratCHRLOC7START

An annotation data file for transcription starting locations of genes on chromosome 7

Description

ratCHRLOC7START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC7START)
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]
  }
}
```

ratCHRLOC8END

An annotation data file for transcription ending location of genes on chromosome 8

Description

ratCHRLOC8END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC8END)
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]
  }
}
```

ratCHRLOC8START	<i>An annotation data file for transcription starting locations of genes on chromosome 8</i>
-----------------	--

Description

ratCHRLOC8START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC8START)
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]
  }
}
```

ratCHRLOC9END

An annotation data file for transcription ending location of genes on chromosome 9

Description

ratCHRLOC9END maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC9END)
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]
  }
}
```

ratCHRLOC9START

An annotation data file for transcription starting locations of genes on chromosome 9

Description

ratCHRLOC9START maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOC9START)
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]
  }
}
```

ratCHRLOCCYTOLOC

An annotation data file for Cytoband locations on chromosomes

Description

ratCHRLOCCYTOLOC maps chromosome numbers and the locations of cytobands on chromosomes

Details

This is an environment object containing key and value pairs. Keys are chromosome numbers and values are the locations of cytobands on corresponding chromosomes. 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

Examples

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

ratCHRLOCENTREZID2CHR *An annotation data file that maps Entrez Gene identifiers to chromosome number*

Description

ratCHRLOCENTREZID2CHR 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOCENTREZID2CHR)
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]
}
}

```

ratCHRLOCQC

Quality control information for ratCHRLOC

Description

ratCHRLOCQC is an R environment that provides quality control information for ratCHRLOC

Details

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

Date built: Date when the package was built.

Number of probes: total number of probes included

Probe number mismatch: 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 mismatch: if any of probes in a data file mismatched 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

ratCHRLOCXEND

An annotation data file for transcription ending location of genes on chromosome X

Description

ratCHRLOCXEND maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

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

ratCHRLOCXSTART	<i>An annotation data file for transcription starting locations of genes on chromosome X</i>
-----------------	--

Description

ratCHRLOCXSTART maps Entrez Gene identifiers to the transcription 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 transcription 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//Rattus_norvegicus/database/. Built: No build info available.

Package built: Thu Aug 30 09:57:40 2007

References

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

Examples

```
require("annotate") || stop("annotate unavailable")
xx <- as.list(ratCHRLOCXSTART)
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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