mirbase.db

April 2, 2013

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mirbase.db   *Bioconductor Custom Annotation Data Package*

Description

Welcome to the mirbase.db custom annotation package. This package contains multiple organisms. The purpose is to provide detailed information about the mirRBase microRNA database (http://www.mirbase.org/). In particular, it covers the searchable database of published microRNA sequences and annotation and not the miRBase Registry and Targets database. As requested by the providers of this resource, the references below should be cited when making use of the data. Ambros et al. 2003 provides guidelines on microRNA annotation.

The current version and release date are: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012. This information is also available by using the mirbase() function.

This package is updated biannually.

You can learn what objects this package supports with the following command: ls("package:mirbase.db")

Each of these objects has their own manual page detailing where relevant data was obtained along with examples of how to use it. Many of these objects also have a reverse map available. When this is true, expect to usually find relevant information on the same manual page as the forward map.

References

Griffiths-Jones S, Saini HK, van Dongen S, Enright AJ. miRBase: tools for microRNA genomics. NAR 2008 36(Database Issue):D154-D158 http://nar.oxfordjournals.org/cgi/content/full/36/suppl_1/D154

Griffiths-Jones S, Grocock RJ, van Dongen S, Bateman A, Enright AJ. miRBase: microRNA sequences, targets and gene nomenclature. NAR 2006 34(Database Issue):D140-D144 http://nar.oxfordjournals.org/cgi/content/full/34/suppl_1/D140

Griffiths-Jones S. The microRNA Registry. NAR 2004 32(Database Issue):D109-D111 http://nar.oupjournals.org/cgi/content/full/32/suppl_1/D109

Ambros V, Bartel B, Bartel DP, Burge CB, Carrington JC, Chen X, Dreyfuss G, Eddy SR, Griffiths-Jones S, Marshall M, Matzke M, Ruvkun G, Tuschl T. A uniform system for microRNA annotation. RNA 2003 9(3):277-279 http://www.rnajournal.org/cgi/content/full/9/3/277

Examples

ls("package:mirbase.db")

---

mirbaseCHRLOC   *MicroRNA IDs to Chromosomal Location*

Description

mirbaseCHRLOC is an R object that maps microRNA identifiers to the starting position of the microRNA. The position of a microRNA is measured as the number of base pairs.

The CHRLOCEND mapping is the same as the CHRLOC mapping except that it specifies the ending base of a microRNA instead of the start.

Details

Each microRNA identifier maps to a named vector of chromosomal locations, where the name indicates the chromosome.

Chromosomal locations on both the sense and antisense strands are measured as the number of base pairs from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Chromosomal locations on the antisense strand have a leading "-" sign (e. g. -1234567).

Since some microRNAs have multiple start sites, this field can map to multiple locations.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

Examples

```
x <- mirbaseCHRLOC
# Get the microRNA identifiers that are mapped to chromosome locations
mapped_keys <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_keys])
if(length(xx) > 0) {
    # Get the CHRLOC for the first five entries
    xx[1:5]
}
```

---

mirbaseCHR   *MicroRNA IDs to Chromosomes*

Description

mirbaseCHR is an R object that provides mappings between microRNA identifiers and the chromosome that contains the microRNA of interest.

Details

Each microRNA identifier maps to a vector of character strings representing possibly multiple chromosomes.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

Examples

```
x <- mirbaseCHR
# Get the microRNA identifiers that are mapped to a chromosome
mapped_keys <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_keys])
if(length(xx) > 0) {
    # Get the CHR for the first five entries
    xx[1:5]
}
```

---

mirbaseCLUSTER   *MicroRNA IDs to Clusters*

Description

mirbaseCLUSTER is an R object that provides mappings between microRNA identifiers and other microRNA identifiers within a 10kb window ('genomic cluster').

Details

Each microRNA identifier maps to a vector of a microRNA identifiers belonging to a cluster (if any beyound itself). This information was computed ad-hoc as it is not included in the original data tables provided by mirbase.org.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

Examples

```
x <- mirbaseCLUSTER
# Get the first cluster containg more than one element
clL <- eapply(x, length)
id <- names(clL[clL > 1])[1]
get(id, x)
```

---

mirbaseCOMMENT   *MicroRNA IDs to Comments*

Description

mirbaseCOMMENTS is an R object that provides mappings between microRNA identifiers and comments related to their description.

Details

Each microRNA identifier maps to a character string. The references cited in the comment can be found by using mirbasePMID.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

See Also

mirbasePMID

Examples

```
# first microRNA with a comment that includes a citation.
mir1 <- intersect(mappedkeys(mirbaseCOMMENT),
              mappedkeys(mirbasePMID))[1]
get(mir1, mirbaseCOMMENT)
get(mir1, mirbasePMID)
```

---

mirbaseCONTEXT   *MicroRNA IDs to Genomic Context*

Description

mirbaseCONTEXT is an R object that maps microRNA identifiers to information related to over-lapping transcripts.

Details

Each microRNA identifier maps to a mirnaContext object that has 6 slots: contextTranscriptID: Transcript identifer contextOverlapSense: Strand of transcript contextOverlapType: Type of over-lap (exon, intron, 3' or 5' UTR) contextNumber: Type of overlap number (eg exon 3) contextTranscriptSource: Transcript database contextTranscriptName: Transcript Name

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

See Also

mirnaContext

Examples

```
x <- mirbaseCONTEXT
# Get the CONTEXT for the first element mapped
get(mappedkeys(x)[1], x)
```

---

mirbase_dbconn   *Collect information about the package annotation DB*

Description

Some convenience functions for getting a connection object to (or collecting information about) the package annotation DB.

Usage

```
mirbase_dbconn()
mirbase_dbfile()
mirbase_dbschema(file="", show.indices=FALSE)
mirbase_dbInfo()
```

Arguments

file	A connection, or a character string naming the file to print to (see the file argument of the cat function for the details).
show.indices	The CREATE INDEX statements are not shown by default. Use show.indices=TRUE to get them.

Details

mirbase_dbconn returns a connection object to the package annotation DB. IMPORTANT: Don't call dbDisconnect on the connection object returned by mirbase_dbconn or you will break all the AnnDbObj objects defined in this package!

mirbase_dbfile returns the path (character string) to the package annotation DB (this is an SQLite file).

mirbase_dbschema prints the schema definition of the package annotation DB.

mirbase_dbInfo prints other information about the package annotation DB.

Value

mirbase_dbconn: a DBIConnection object representing an open connection to the package annotation DB.

mirbase_dbfile: a character string with the path to the package annotation DB.

mirbase_dbschema: none (invisible NULL).

mirbase_dbInfo: none (invisible NULL).

See Also

dbGetQuery, dbConnect, dbconn, dbfile, dbschema, dbInfo

Examples

```
## Count the number of rows in the "ID2ACC" table:
dbGetQuery(mirbase_dbconn(), "SELECT COUNT(*) FROM mirna")

## The connection object returned by mirbase_dbconn() was
## created with:
dbConnect(SQLite(), dbname=mirbase_dbfile(), cache_size=64000,
synchronous=0)

mirbase_dbschema()

mirbase_dbInfo()
```

---

mirbaseDESCRIPTION   *MicroRNA IDs to Descriptions*

Description

mirbaseDESCRIPTION is an R object that provides mappings between microRNA identifiers and their full names.

Details

Each microRNA identifier maps to a character string.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

Examples

```
x <- mirbaseDESCRIPTION
# first 3 entries with a description.
mget(mappedkeys(x)[1:3], x)
```

---

mirbaseFAMILY   *MicroRNA IDs to Family*

Description

mirbaseFAMILY is an R object that provides mappings between microRNA identifiers and their family.

Details

Each microRNA identifier maps to a character string which is the miRNA gene family ID. The name of the returned value is the family name.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

Examples

```
x <- mirbaseFAMILY
# first 3 microRNA with a family.
mget(mappedkeys(x)[1:3], x)
```

---

mirbaseHAIRPIN	*MicroRNA IDs to Hairpin*

Description

mirbaseHAIRPIN is an R object that provides mappings between microRNA identifiers and an ASCII representation of the the folded precursor (stem-loop sequence).

Details

Each microRNA identifier maps to a character string. The mature microRNA(s) sequence are highlighted in capital letters.

The representation was created the RNAfold program from the ViennaRNA suite http://www.tbi.univie.ac.at/~ivo/RNA/. Extra information include the minimum free energy ('MFE') which can be found by using mirbaseMFE and the position on the sequence of mature mirna(s) which can be found by using mirbaseMATURE.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

References

Hofacker IL, Stadler PF. Memory efficient folding algorithms for circular RNA secondary structures. Bioinformatics. 2006 May 15; 22(10):1172-6. http://www.ncbi.nlm.nih.gov/pubmed/16452114

Examples

```
x <- mirbaseHAIRPIN
# hairpin representation sequences of all microRNAs
mirnaHairpin <- mget(mappedkeys(x), x)
# print first one
cat(mirnaHairpin[[1]], "\n")
```

---

mirbaseID2ACC	*MicroRNA IDs to Accessions*

Description

mirbaseID2ACC is an R object that provides mappings between microRNA identifiers and their Accession numbers.

Details

Each microRNA identifier maps to a unique Accession number.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

Examples

```
x <- mirbaseID2ACC
# Get the microRNA identifiers that are mapped to an Accession
mapped_keys <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_keys])
if(length(xx) > 0) {
  # Get the ID2ACC for the first five entries
  xx[1:5]
}
```

---

mirbaseID2SPECIES   *MicroRNA IDs to Species*

Description

mirbaseID2SPECIES is an R object that provides mappings between microRNA identifiers and the species they belong to.

Details

Each microRNA identifier maps to a unique character string which is an abbreviated name of the species. Further information concerning the species can be found by using the name with mirbaseSPECIES.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

Examples

```
x <- mirbaseID2SPECIES
# Get the microRNA identifiers that are mapped to a species
mapped_keys <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_keys])
if(length(xx) > 0) {
  # Get the ID2SPECIES for the first five entries
  xx[1:5]
}
```

---

mirbaseLINKS   *MicroRNA IDs to External Database Links*

Description

mirbaseLINKS is an R object that maps microRNA identifiers to a set external database identifiers.

Details

Each microRNA identifier maps to a mirnaLinks object that has 3 slots: linksDbLink: Accession number linksDbId: Database linksDbSecondary: Second accession number (or name)

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

See Also

mirnaLinks

Examples

```
x <- mirbaseLINKS
mapped_keys <- mappedkeys(x)
# Get the LINKS for the first element of xx
get(mapped_keys[1], x)
```

---

mirbaseMAPCOUNTS   *Number of mapped keys for the maps in package mirbase.db*

Description

mirbaseMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package mirbase.db.

Details

This "map count" information is precalculated and stored in the package annotation DB. This allows some quality control and is used by the checkMAPCOUNTS function defined in AnnotationDbi to compare and validate different methods (like count.mappedkeys(x) or sum(!is.na(as.list(x)))) for getting the "map count" of a given map.

See Also

mappedkeys, count.mappedkeys, checkMAPCOUNTS

Examples

```
mirbaseMAPCOUNTS
mapnames <- names(mirbaseMAPCOUNTS)
mirbaseMAPCOUNTS[mapnames[1]]
x <- get(mapnames[1])
sum(!is.na(as.list(x)))
count.mappedkeys(x)   # much faster!

## Check the "map count" of all the maps in package mirbase.db
checkMAPCOUNTS("mirbase.db")
```

---

mirbaseMATURE   *MicroRNA IDs to Mature MicroRNAs*

Description

mirbaseMATURE is an R object that maps microRNA identifiers to information related to their corresponding mature microRNA(s).

Details

Each microRNA identifier maps to a mirnaMATURE object that has 7 slots: matureAccession: Accession number matureName: ID (or name) matureFrom: Start position in precursor sequence matureTo: End position in precursor sequence matureEvidence: Experimental evidence matureExperiment: Experiment description and citation matureSimilarity: Accession number of similar precursor microRNA

The citations in the Experiment description can be retrieved by using mirbasePMID.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

Examples

```
x <- mirbaseMATURE
mapped_keys <- mappedkeys(x)
# Get the MATURE for the first element of xx
get(mapped_keys[1], x)
```

---

mirbaseMFE   *MicroRNA IDs to Minimum Fold Energy*

Description

mirbaseMFE is an R object that provides mappings between microRNA identifiers and the Minimum Fold Energy of the folded precursor (stem-loop sequence).

Details

Each microRNA identifier maps to a unique numeric value representing the Minimum Fold Energy of the folded precursor (stem-loop sequence) computed by the RNAfold program from the ViennaRNA suite http://www.tbi.univie.ac.at/~ivo/RNA/.

A graphical representation of the folded sequence can be found by using mirbaseHAIRPIN.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

References

Hofacker IL, Stadler PF. Memory efficient folding algorithms for circular RNA secondary structures. Bioinformatics. 2006 May 15; 22(10):1172-6. http://www.ncbi.nlm.nih.gov/pubmed/16452114

See Also

mirbaseHAIRPIN

Examples

```
x <- mirbaseMFE
# Get the microRNA identifiers that are mapped to a MFE
mapped_keys <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_keys])
if(length(xx) > 0) {
    # Get the MFE for the first five entries
    xx[1:5]
}
```

---

mirnaContext-class   *Class "mirnaContext"*

Description

A class to represent the genomic context of a microRNA

Objects from the Class

Objects can be created by calls of the form new("mirnaContext", contextTranscriptID, contextOverlapSense, cont

Slots

contextTranscriptID**:** Object of class "character" A character string for Transcript identifer overlapping a microRNA.

contextOverlapSense**:** Object of class "character" A character string for the Strand of transcript.

contextOverlapType**:** Object of class "character" A character string for the of Type of overlap (exon, intron, 3' or 5' UTR).

contextNumber**:** Object of class "numeric" A numeric vector for the Type of overlap number (eg exon 3).

contextTranscriptSource**:** Object of class "character" A character string for the Transcript database.

contextTranscriptName**:** Object of class "character" A character string for the Transcript Name.

Methods

contextTranscriptID signature(object = "mirnaContext"): The get method for slot contextTranscriptID.

contextOverlapSense signature(object = "mirnaContext"): The get method for slot contextOverlapSense.

contextOverlapType signature(object = "mirnaContext"): The get method for slot contextOverlapType.

contextNumber signature(object = "mirnaContext"): The get method for slot contextNumber.

contextTranscriptSource signature(object = "mirnaContext"): The get method for slot contextTranscriptSource.

contextTranscriptName signature(object = "mirnaContext"): The get method for slot contextTranscriptName.

show signature(x = "mirnaContext"): The method for pretty print.

See Also

mirbaseCONTEXT

---

mirnaLinks-class   *Class "mirnaLinks"*

Description

A class to represent microRNA external database links

Objects from the Class

Objects can be created by calls of the form new("mirnaLinks", linksDbLink, linksDbId, linksDbSecondary).

Slots

linksDbLink: Object of class "character" A character string for the Accession number of a microRNA.

linksDbId: Object of class "character" A character string for the Database of a microRNA.

linksDbSecondary: Object of class "character" A character string for the Second accession number (or name) of a mature microRNA.

Methods

linksDbLink signature(object = "mirnaLinks"): The get method for slot linksDbLink.

linksDbId signature(object = "mirnaLinks"): The get method for slot linksDbId.

linksDbSecondary signature(object = "mirnaLinks"): The get method for slot linksDbSecondary.

show signature(x = "mirnaLinks"): The method for pretty print.

See Also

mirbaseLINKS

---

mirnaMature-class *Class "mirnaMature"*

Description

A class to represent mature microRNAs

Objects from the Class

Objects can be created by calls of the form new("mirnaMature", matureAccession, matureName, matureFrom,   ma

Slots

matureAccession: Object of class "character" A character string for the Accession number of a
mature microRNA.

matureName: Object of class "character" A character string for the ID (or name) of a mature
microRNA.

matureFrom: Object of class "character" A character string for Start position in precursor se-
quence of a mature microRNA.

matureTo: Object of class "character" A character string for the End position in precursor se-
quence of a mature microRNA.

matureEvidence: Object of class "character" A character string for the Experimental evidence
of a mature microRNA.

matureExperiment: Object of class "character" A character string for the Experiment descrip-
tion and citation of a mature microRNA.

matureSimilarity: Object of class "character" A character string for the Accession number of
similar precursor microRNA of a mature microRNA.

Methods

matureAccession signature(object = "mirnaMature"): The get method for slot matureAcces-
sion.

matureName signature(object = "mirnaMature"): The get method for slot matureName.

matureFrom signature(object = "mirnaMature"): The get method for slot matureFrom.

matureTo signature(object = "mirnaMature"): The get method for slot matureTo.

matureEvidence signature(object = "mirnaMature"): The get method for slot matureEvi-
dence.

matureExperiment signature(object = "mirnaMature"): The get method for slot matureEx-
periment.

matureSimilarity signature(object = "mirnaMature"): The get method for slot matureSimilar-
ity.

show signature(x = "mirnaMature"): The method for pretty print.

See Also

mirbaseMATURE

mirnaPmid-class   *Class "mirnaPmid"*

Description

A class to represent microRNA references

Objects from the Class

Objects can be created by calls of the form new("mirnaPmid", pmidAuthor, pmidTitle, pmidJournal, pmidMedline

Slots

pmidAuthor: Object of class "character" A character string for the authors of a reference.

pmidTitle: Object of class "character" A character string for the title of a reference.

pmidJournal: Object of class "character" A character string for the citation of a reference.

pmidMedline: Object of class "numeric" A numeric vector for the Pubmed identifier of a reference.

pmidOrderAdded: Object of class "numeric" A numeric vector for the order of the reference.

Methods

pmidAuthor signature(object = "mirnaPmid"): The get method for slot pmidAuthor.

pmidTitle signature(object = "mirnaPmid"): The get method for slot pmidTitle.

pmidJournal signature(object = "mirnaPmid"): The get method for slot pmidJournal.

pmidMedline signature(object = "mirnaPmid"): The get method for slot pmidMedline.

pmidOrderAdded signature(object = "mirnaPmid"): The get method for slot pmidOrderAdded.

show signature(x = "mirnaPmid"): The method for pretty print.

See Also

mirbasePMID

mirbasePMID   *MicroRNA IDs to References*

Description

mirbasePMID is an R object that maps microRNA identifiers to a set of references (PubMed IDentifiers).

Details

Each microRNA identifier maps to a mirnaPmid object that has 5 slots: pmidAuthor: List of authors pmidTitle: Title pmidJournal: Citation pmidMedline: Pubmed identifier pmidOrderAdded: Order

The Order is the same as the one used in mirbaseCOMMENT and in mirbaseMATURE.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

See Also

mirnaPmid

Examples

```
x <- mirbasePMID
mapped_keys <- mappedkeys(x)
# Get the PMIDs for the first element of xx
get(mapped_keys[1], x)
```

---

mirbaseSEQUENCE   *MicroRNA IDs to Sequence*

Description

mirbaseSEQUENCE is an R object that provides mappings between microRNA identifiers and their precursor sequence (stem-loop).

Details

Each microRNA identifier maps to a unique character string representing the precursor (stem-loop) sequence of the microRNA. A graphical representation of the folded sequence can be found by using mirbaseHAIRPIN.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

See Also

mirbaseHAIRPIN

Examples

```
x <- mirbaseSEQUENCE
# Get the microRNA identifiers that are mapped to a SEQUENCE
mapped_keys <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_keys])
if(length(xx) > 0) {
    # Get the SEQUENCE for the first five entries
    xx[1:5]
}
```

mirbaseSPECIES   *Organism Acronym to Species*

Description

mirbaseSPECIES is an R object that provides mappings between organism acronyms and the species specifications.

Details

Each organism acronym to a unique character string which is the full name of the species. Further information concerning the species can be found by using the toTable function which reports the 'division', 'taxonomy', 'genome_assembly' and the 'ensembl_db' used.

The organism acronym of a microRNA is returned by using mirbaseID2SPECIES.

Source: miRBase (Version: 19) ftp://mirbase.org/pub/mirbase/CURRENT/ With a date stamp from the source of: 01 Aug 2012

See Also

mirbaseID2SPECIES

Examples

```
x <- mirbaseID2SPECIES
y <- mirbaseSPECIES
# get full species information for the first microRNA
mir1 <- mappedkeys(x)[1]
mir1Species <- get(mir1, x)
get(mir1Species, y)
toTable(y[mir1Species])
```

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