

# mirbase.db

July 24, 2024

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mirbase.db

*Bioconductor Custom Annotation Data Package*

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## Description

Welcome to the mirbase.db custom annotation package. This package contains multiple organisms. The purpose is to provide detailed information about the miRBase 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](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](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](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")
```

---

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]
}
```

---

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]
}
```

---

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 beyond 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 containing 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 overlapping transcripts.

### Details

Each microRNA identifier maps to a `mirnaContext` object that has 6 slots: `contextTranscriptID`: Transcript identifier `contextOverlapSense`: Strand of transcript `contextOverlapType`: Type of overlap (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)
```

---

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]
}
```

---

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	<i>MicroRNA IDs to Sequence</i>
-----------------	---------------------------------

---

**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])
```

---

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 <a href="#">cat</a> 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()
```

---

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, contextOverlapType, contextNumber, contextTranscriptSource, contextTranscriptName)`.

### Slots

**contextTranscriptID:** Object of class "character" A character string for Transcript identifier 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, matureTo, matureEvidence, matureExperiment, matureSimilarity)`.

**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 sequence of a mature microRNA.

**matureTo:** Object of class "character" A character string for the End position in precursor sequence 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 description 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 matureAccession.

**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 matureEvidence.

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

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

**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, pmidOrderAdded)`.

**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](#)

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