

Package ‘RISmed’

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Type Package

Title Download Content from NCBI Databases

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Description

A set of tools to extract bibliographic content from the National Center for Biotechnology Information (NCBI) databases, including PubMed. The name RISmed is a portmanteau of RIS (for Research Information Systems, a common tag format for bibliographic data) and PubMed.

License GPL (>= 2)

NeedsCompilation no

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RISmed-package

Download content from NCBI databases.

Description

Download content from NCBI databases. This package is intended to facilitate analyses of NCBI database content. This package is not intended for reference management.

Details

Package:	RISmed
Type:	Package
Version:	2.1.3
Date:	2014-7-20
License:	GPL (>=2)
LazyLoad:	yes

Note on usage:

In order not to overload the E-utility servers, NCBI recommends that users post no more than three URL requests per second and limit large jobs to either weekends or between 9:00 PM and 5:00 AM Eastern time during weekdays. Failure to comply with this policy may result in an IP address being blocked from accessing NCBI.

Author(s)

Maintainer: Stephanie Kovalchik <s.a.kovalchik@gmail.com>

AbstractText

Extracts AbstractText from Medline object.

Description

Extractor for the AbstractText of a Medline object.

Usage

```
AbstractText(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
AbstractText(myeloma)
```

AbstractText-methods

*~~ Methods for Function AbstractText in Package **RISmed** ~~*

Description

*~~ Methods for function AbstractText in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

Acronym	<i>Extracts Acronym from Medline object.</i>
---------	--

Description

Extractor for the Acronym of a Medline object.

Usage

```
Acronym(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
Acronym(myeloma)
```

Description

*~~ Methods for function Acronym in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

Affiliation	<i>Extracts Affiliation from Medline object.</i>
-------------	--

Description

Extractor for the Affiliation of a Medline object.

Usage

```
Affiliation(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
Affiliation(myeloma)
```

Affiliation-methods	<i>~ Methods for Function Affiliation in Package RISmed ~</i>
---------------------	--

Description

*~~ Methods for function Affiliation in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

Agency	<i>Extracts Agency from Medline object.</i>
--------	---

Description

Extractor for the Agency of a Medline object.

Usage

`Agency(object)`

Arguments

`object` instance of class `Medline`

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
Agency(myeloma)
```

Agency-methods	<i>~~ Methods for Function Agency in Package RISmed ~~</i>
----------------	---

Description

*~~ Methods for function Agency in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

ArticleId	<i>Extracts ArticleId from Medline object.</i>
-----------	--

Description

Extractor for the ArticleId of a Medline object.

Usage

ArticleId(object)

Arguments

object instance of class Medline

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
ArticleId(myeloma)
```

ArticleId-methods	<i>~~ Methods for Function ArticleId in Package RISmed ~~</i>
-------------------	--

Description

*~~ Methods for function ArticleId in package **RISmed** ~~*

Methods

signature(object = "Medline")

ArticleTitle	<i>Extracts ArticleTitle from Medline object.</i>
--------------	---

Description

Extractor for the ArticleTitle of a Medline object.

Usage

```
ArticleTitle(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
ArticleTitle(myeloma)
```

ArticleTitle-methods	<i>~~ Methods for Function ArticleTitle in Package RISmed ~~</i>
----------------------	---

Description

*~~ Methods for function ArticleTitle in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

Author	<i>Extracts Author from Medline object.</i>
--------	---

Description

Extractor for the Author of a Medline object.

Usage

`Author(object)`

Arguments

`object` instance of class `Medline`

Value

List by Pubmed article. Each list contains a data frame with `LastName`, `ForeName`, `Initials`, and order of article authors.

See Also

[Medline](#)

Examples

```
data(myeloma)
Author(myeloma)
```

Author-methods	<i>~~ Methods for Function Author in Package RISmed ~~</i>
----------------	---

Description

*~~ Methods for function Author in package **RISmed** ~~*

Methods

`signature(object = "Medline")` List by Pubmed article. Each list contains a data frame with `LastName`, `ForeName`, `Initials`, and order of article authors.

Cited	<i>Number of citations</i>
-------	----------------------------

Description

Retrieves the number of citations in PubMed Central for the articles contained in the EUtilsSummary or Medline object.

Usage

```
Cited(object)
```

Arguments

object	instance of class Medline or EUtilsSummary
--------	--

Value

vector	
--------	--

See Also

[Medline](#), [EUtilsSummary](#)

Examples

```
res <- EUtilsSummary("myeloma[ti]", mindate = "2002/01/01", maxdate = "2002/02/01", retmax = 5)
Cited(res)
```

Cited-methods	<i>~~ Methods for Function Cited in Package RISmed ~~</i>
---------------	---

Description

~~ Methods for function Cited in package **RISmed** ~~

Methods

```
signature(object = "Medline")
```

CollectiveName	<i>Extracts CollectiveName from Medline object.</i>
----------------	---

Description

Extractor for the CollectiveName of a Medline object.

Usage

```
CollectiveName(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

CollectiveName-methods

*~~ Methods for Function CollectiveName in Package **RISmed** ~~*

Description

*~~ Methods for function CollectiveName in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

CopyrightInformation *Extracts CopyrightInformation from Medline object.*

Description

Extractor for the CopyrightInformation of a Medline object.

Usage

`CopyrightInformation(object)`

Arguments

`object` instance of class `Medline`

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
CopyrightInformation(myeloma)
```

CopyrightInformation-methods

~~ Methods for Function `CopyrightInformation` in Package
RISmed ~~

Description

~~ Methods for function `CopyrightInformation` in package **RISmed** ~~

Methods

`signature(object = "Medline")`

Country	<i>Extracts Country from Medline object.</i>
---------	--

Description

Extractor for the Country of a Medline object.

Usage

`Country(object)`

Arguments

`object` instance of class `Medline`

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
Country(myeloma)
```

Country-methods	<i>~~ Methods for Function Country in Package RISmed ~~</i>
-----------------	--

Description

*~~ Methods for function Country in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

<code>DayAccepted</code>	<i>Extracts DayAccepted from Medline object.</i>
--------------------------	--

Description

Extractor for the DayAccepted of a Medline object. This date corresponds to the date the article was accepted.

Usage

```
DayAccepted(object)
```

Arguments

<code>object</code>	instance of class <code>Medline</code>
---------------------	--

Value

<code>vector</code>	
---------------------	--

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
DayAccepted(myeloma)
```

<code>DayAccepted-methods</code>	<i>~~ Methods for Function <code>DayAccepted</code> in Package RISmed ~~</i>
----------------------------------	---

Description

*~~ Methods for function `DayAccepted` in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

DayEpublish	<i>Extracts DayEpublish from Medline object.</i>
-------------	--

Description

Extractor for the DayEpublish of a Medline object. This date corresponds to the date the article was published online.

Usage

```
DayEpublish(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
DayEpublish(myeloma)
```

DayEpublish-methods	<i>~~ Methods for Function DayEpublish in Package RISmed ~~</i>
---------------------	--

Description

*~~ Methods for function DayEpublish in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

DayPmc	<i>Extracts DayPmc from Medline object.</i>
--------	---

Description

Extractor for the DayPmc of a Medline object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

```
DayPmc(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
DayPmc(myeloma)
```

Description

*~~ Methods for function DayPmc in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

DayPpublish	<i>Extracts DayPpublish from Medline object.</i>
-------------	--

Description

Extractor for the DayPpublish of a Medline object. This date corresponds to the date the article was published in print.

Usage

```
DayPpublish(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
DayPpublish(myeloma)
```

DayPpublish-methods	<i>~~ Methods for Function DayPpublish in Package RISmed ~~</i>
---------------------	--

Description

*~~ Methods for function DayPpublish in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

DayPubmed

*Extracts DayPubmed from Medline object.***Description**

Extractor for the DayPubmed of a Medline object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

```
DayPubmed(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
DayPubmed(myeloma)
```

DayPubmed-methods

*~~ Methods for Function DayPubmed in Package **RISmed** ~~***Description**

~~ Methods for function DayPubmed in package **RISmed** ~~

Methods

```
signature(object = "Medline")
```

DayReceived	<i>Extracts DayReceived from Medline object.</i>
-------------	--

Description

Extractor for the DayReceived of a Medline object. This date corresponds to the date the article was received.

Usage

```
DayReceived(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
DayReceived(myeloma)
```

DayReceived-methods	<i>~~ Methods for Function DayReceived in Package RISmed ~~</i>
---------------------	--

Description

*~~ Methods for function DayReceived in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

ElocationID *Extracts ElocationID from Medline object.*

Description

Extractor for the ElocationID of a Medline object.

Usage

`ElocationID(object)`

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
ElocationID(myeloma)
```

ElocationID-methods *~ Methods for Function ElocationID in Package **RISmed** ~*

Description

~~ Methods for function ElocationID in package **RISmed** ~~

Methods

`signature(object = "Medline")`

EUtilsGet*Results of an NCBI EUtils query*

Description

Download results of a query for any database of the National Center for Biotechnology Information (NCBI).

Usage

```
EUtilsGet(x, type="efetch", db="pubmed")
```

Arguments

x	Either vector of NCBI records ids, i.e. returned ids from EUtilsSummary, or the EUtilsSummary object itself
type	string indicating type of NCBI Utility, efetch, esummary, etc.
db	string indicating the NCBI database used in query

Details

Possible E-utilities to supply to type are efetch, esummary, and elink.

The database name supplied to db can be any valid Entrez database, such as pubmed, protein, nlm, etc.

For further details on available E-utilities and databases visit <http://www.ncbi.nlm.nih.gov/books/NBK25499/>.

Note on usage:

In order not to overload the E-utility servers, NCBI recommends that users post no more than three URL requests per second and limit large jobs to either weekends or between 9:00 PM and 5:00 AM Eastern time during weekdays. Failure to comply with this policy may result in an IP address being blocked from accessing NCBI.

Value

For queries to PubMed, a list by article, with named vectors for each field of the article result.

For all other database, a vector with each element name the field returned from XML output.

Author(s)

Stephanie Kovalchik <s.a.kovalchik@gmail.com>

References

Summary help:

<http://www.ncbi.nlm.nih.gov/books/NBK3827/>

MEDLINE/PubMed Field Descriptions

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html>

See Also

[EUtilsSummary](#)

Examples

```
# PUBMED QUERY FOR MYELOMA ARTICLES FOR LAST YEAR
res <- EUtilsSummary("myeloma[ti]",retmax=2,reldate=365)

summary(res)

fetch <- EUtilsGet(res)

# PUBMED RETURNS A MEDLINE OBJECT
fetch

PMID(fetch)

Author(fetch)[[1]]
```

EUtilsQuery

Construct URL to make NCBI EUtils query

Description

Construct a URL query for any database of the National Center for Biotechnology Information (NCBI).

Usage

`EUtilsQuery(query,type="esearch",db="pubmed",...)`

Arguments

query	string query as given in NCBI search box
type	string indicating type of NCBI Utility
db	string indicating the NCBI database used in query
...	additional limits added to query

Details

Possible E-utilities to supply to type are einfo, esearch, epost, esummary, elink, egquery, espell.

The database name supplied to db can be any valid Entrez database, such as pubmed, protein, nlm, etc.

For further details on available E-utilities and databases visit <http://www.ncbi.nlm.nih.gov/books/NBK25499/>.

Limits that can be supplied to . . . to refine the query include:

reldate	Limits search results to be within the specified number of days from current date.
mindate	Minimum of date range for search results (examples: 2002; 2002/01/01); must be supplied with maxdate.
maxdate	Maximum of date range for search results; must be supplied with mindate.
datatype	Which date field to use in setting date limits. Possible choices are edat, Entrez date, which is the date article was
restart	Where in the sequence of returned results to begin retrieving, default is 0.
retmax	Maximum number of records to retrieve, default is 1000.

Value

String URL to access NCBI E-utility.

Author(s)

Stephanie Kovalchik <s.a.ovalchik@gmail.com>

References

Query help:

<http://www.ncbi.nlm.nih.gov/books/NBK3827/>

MEDLINE/PubMed Field Descriptions

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html>

Examples

```
# PUBMED QUERY
EUtilsQuery("myeloma[ti] jones[au]")

# RESTRICT TO RECORDS WITHIN LAST 30 days
EUtilsQuery("myeloma[ti] jones[au]",reldat=30)
```

EUtilsSummary*Get summary of NCBI EUtils query*

Description

Get summary information on the results of a query for any database of the National Center for Biotechnology Information (NCBI).

Usage

```
EUtilsSummary(query, type="esearch", db="pubmed", url=NULL, encoding="unknown", ...)
```

Arguments

query	string query as given in NCBI search box
type	string indicating type of NCBI Utility
db	string indicating the NCBI database used in query
url	string of url to bypass query construction
encoding	encoding to be assumed for input strings, see readLines
...	additional limits added to query

Details

Possible E-utilities to supply to type are einfo, esearch, epost, esummary, elink, egquery, espell.

The database name supplied to db can be any valid Entrez database, such as pubmed, protein, nlm, etc.

For further details on available E-utilities and databases visit <http://www.ncbi.nlm.nih.gov/books/NBK25499/>.

Limits that can be supplied to ... to refine the query include:

reldate	Limits search results to be within the specified number of days from current date.
mindate	Minimum of date range for search results (examples: 2002; 2002/01/01); must be supplied with maxdate.
maxdate	Maximum of date range for search results; must be supplied with mindate.
datatype	Which date field to use in setting date limits. Possible choices are edat, Entrez date, which is the date article was
restart	Where in the sequence of returned results to begin retrieving, default is 0.
retmax	Maximum number of records to retrieve, default is 1000.

Value

Returns an EUtilsSummary object.

Author(s)

Stephanie Kovalchik <s.a.kovalchik@gmail.com>

References

Summary help:
<http://www.ncbi.nlm.nih.gov/books/NBK3827/>
 MEDLINE/PubMed Field Descriptions
<http://www.nlm.nih.gov/bsd/mms/medlineelements.html>

See Also

[EUtilsQuery](#)

Examples

```
# PUBMED QUERY
res <- EUtilsSummary("myeloma[ti] jones[au]", retmax = 10)

res

summary(res)
QueryCount(res)
QueryId(res)
QueryTranslation(res)

# PROTEIN QUERY
res <- EUtilsSummary("C-reactive[ti]", db="protein", retmax = 10)
summary(res)
```

EUtilsSummary-class *Class "EUtilsSummary"*

Description

Summary of query of an NCBI E-utility

Objects from the Class

Objects can be created by calls of the form `new("EUtilsSummary", ...)`.

Slots

db: Name of database
count: total ids
retmax: limit on number of records to return
retstart: numeric indicating where return records start
PMID: character vector of matching ids
querytranslation: character of NCBI translation of query

Methods

```
QueryCount signature(object = "EUtilsSummary"): ...
QueryId signature(object = "EUtilsSummary"): ...
print signature(x = "EUtilsSummary"): ...
show signature(object = "EUtilsSummary"): ...
summary signature(object = "EUtilsSummary"): ...
QueryTranslation signature(object = "EUtilsSummary"): ...
```

Author(s)

Stephanie Kovalchik

GrantID

Extracts GrantID from Medline object.

Description

Extractor for the GrantID of a Medline object.

Usage

`GrantID(object)`

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
GrantID(myeloma)
```

GrantID-methods

*~~ Methods for Function GrantID in Package **RISmed** ~~*

Description

~~ Methods for function GrantID in package **RISmed** ~~

Methods

`signature(object = "Medline")`

HourAccepted

Extracts HourAccepted from Medline object.

Description

Extractor for the HourAccepted of a Medline object. This date corresponds to the date the article was accepted.

Usage

`HourAccepted(object)`

Arguments

`object` instance of class `Medline`

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
HourAccepted(myeloma)
```

HourAccepted-methods ~~ *Methods for Function HourAccepted in Package **RISmed*** ~~

Description

~ Methods for function HourAccepted in package **RISmed** ~

Methods

```
signature(object = "Medline")
```

HourEpublish *Extracts HourEpublish from Medline object.*

Description

Extractor for the HourEpublish of a Medline object. This date corresponds to the date the article was published online.

Usage

HourEpublish(object)

Arguments

object instance of class Medline

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

Medline

Examples

```
data(myeloma)  
HourEpublish(myeloma)
```

HourEpublish-methods *~~ Methods for Function HourEpublish in Package **RISmed** ~~*

Description

~~ Methods for function HourEpublish in package **RISmed** ~~

Methods

`signature(object = "Medline")`

HourPmc *Extracts HourPmc from Medline object.*

Description

Extractor for the HourPmc of a Medline object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

`HourPmc(object)`

Arguments

`object` instance of class `Medline`

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
HourPmc(myeloma)
```

HourPmc-methods

*~~ Methods for Function HourPmc in Package **RISmed** ~~***Description***~~ Methods for function HourPmc in package **RISmed** ~~***Methods**`signature(object = "Medline")`

HourPpublish

*Extracts HourPpublish from Medline object.***Description**

Extractor for the HourPpublish of a Medline object. This date corresponds to the date the article was published in print.

Usage`HourPpublish(object)`**Arguments**object instance of class `Medline`**Value**

vector

References<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>**See Also**[Medline](#)**Examples**

```
data(myeloma)
HourPpublish(myeloma)
```

HourPpublish-methods *~~ Methods for Function HourPpublish in Package **RISmed** ~~*

Description

~~ Methods for function HourPpublish in package **RISmed** ~~

Methods

`signature(object = "Medline")`

HourPubmed *Extracts HourPubmed from Medline object.*

Description

Extractor for the HourPubmed of a Medline object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

`HourPubmed(object)`

Arguments

`object` instance of class `Medline`

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
HourPubmed(myeloma)
```

HourPubmed-methods

*~~ Methods for Function HourPubmed in Package **RISmed** ~~***Description***~~ Methods for function HourPubmed in package **RISmed** ~~***Methods**`signature(object = "Medline")`

HourReceived

*Extracts HourReceived from Medline object.***Description**

Extractor for the HourReceived of a Medline object. This date corresponds to the date the article was received.

Usage`HourReceived(object)`**Arguments**

object instance of class Medline

Value

vector

References<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>**See Also**[Medline](#)**Examples**

```
data(myeloma)
HourReceived(myeloma)
```

HourReceived-methods *~~ Methods for Function HourReceived in Package **RISmed** ~~*

Description

*~~ Methods for function HourReceived in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

ISOAbbreviation *Extracts ISOAbbreviation from Medline object.*

Description

Extractor for the ISOAbbreviation of a Medline object.

Usage

`ISOAbbreviation(object)`

Arguments

object instance of class Medline

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
ISOAbbreviation(myeloma)
```

ISOAbbreviation-methods

*~~ Methods for Function ISOAbbreviation in Package **RISmed** ~~*

Description

*~~ Methods for function ISOAbbreviation in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

ISSN

Extracts ISSN from Medline object.

Description

Extractor for the ISSN of a Medline object.

Usage

`ISSN(object)`

Arguments

`object` instance of class `Medline`

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
ISSN(myeloma)
```

ISSN-methods

*~~ Methods for Function ISSN in Package **RISmed** ~~*

Description

*~~ Methods for function ISSN in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

ISSNLinking

Extracts ISSNLinking from Medline object.

Description

Extractor for the ISSNLinking of a Medline object.

Usage

`ISSNLinking(object)`

Arguments

`object` instance of class `Medline`

Value

`vector`

See Also

[Medline](#)

Examples

```
data(myeloma)
ISSNLinking(myeloma)
```

ISSNLinking-methods *~~ Methods for Function ISSNLinking in Package **RISmed** ~~*

Description

*~~ Methods for function ISSNLinking in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

Issue *Extracts Issue from Medline object.*

Description

Extractor for the Issue of a Medline object.

Usage

`Issue(object)`

Arguments

`object` instance of class `Medline`

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
Issue(myeloma)
```

Issue-methods

~~ Methods for Function Issue in Package **RISmed** ~~

Description

~~ Methods for function Issue in package **RISmed** ~~

Methods

`signature(object = "Medline")`

Language

Extracts Language from Medline object.

Description

Extractor for the Language of a Medline object.

Usage

`Language(object)`

Arguments

object instance of class `Medline`

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
Language(myeloma)
```

Language-methods

*~~ Methods for Function Language in Package **RISmed** ~~*

Description

*~~ Methods for function Language in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

Medline-class

Class "Medline"

Description

Class for Medline citation of query to PubMed.

Objects from the Class

Objects can be created by calls of the form `new("Medline", ...)`.

Slots

Unless stated otherwise, each of the components is a vector of the given field where each element corresponds to a PubMed article.

Query:

PMID:

YearAccepted:

MonthAccepted:

DayAccepted:

HourAccepted:

MinuteAccepted:

YearReceived:

MonthReceived:

DayReceived:

HourReceived:

MinuteReceived:

YearEpublish:

MonthEpublish:

DayEpublish:

HourEpublish:
MinuteEpublish:
YearPpublish:
MonthPpublish:
DayPpublish:
HourPpublish:
MinutePpublish:
YearPmc:
MonthPmc:
DayPmc:
HourPmc:
MinutePmc:
YearPubmed:
MonthPubmed:
DayPubmed:
HourPubmed:
MinutePubmed:
Author: list of data frames giving LastName, ForeName, Initials, and order of authors by PubMed article.
ISSN:
Title:
ArticleTitle:
ELocationID:
AbstractText:
Affiliation:
Language:
PublicationType:
MedlineTA:
NlmUniqueID:
ISSNLinking:
PublicationStatus:
ArticleId:
Volume:
Issue:
ISOAbbreviation:
MedlinePgn:
CopyrightInformation:

Country:
GrantID:
Acronym:
Agency:
RegistryNumber:
RefSource:
CollectiveName:
Mesh: list of data frames giving Heading and Type of MeSH term or NA if no terms are in MEDLINE record

Methods

In addition to `print` and `show` methods, each slot of the `Medline` class has a corresponding extractor of the same name.

```

print signature(x = "Medline", ...): ...
show signature(object = "Medline"): ...
Query signature(object = "Medline"): ...
PMID signature(object = "Medline"): ...
YearAccepted signature(object = "Medline"): ...
MonthAccepted signature(object = "Medline"): ...
DayAccepted signature(object = "Medline"): ...
HourAccepted signature(object = "Medline"): ...
MinuteAccepted signature(object = "Medline"): ...
YearReceived signature(object = "Medline"): ...
MonthReceived signature(object = "Medline"): ...
DayReceived signature(object = "Medline"): ...
HourReceived signature(object = "Medline"): ...
MinuteReceived signature(object = "Medline"): ...
YearEpublish signature(object = "Medline"): ...
MonthEpublish signature(object = "Medline"): ...
DayEpublish signature(object = "Medline"): ...
HourEpublish signature(object = "Medline"): ...
MinuteEpublish signature(object = "Medline"): ...
YearPpublish signature(object = "Medline"): ...
MonthPpublish signature(object = "Medline"): ...
DayPpublish signature(object = "Medline"): ...
HourPpublish signature(object = "Medline"): ...
MinutePpublish signature(object = "Medline"): ...
  
```

```
YearPmc signature(object = "Medline"): ...
MonthPmc signature(object = "Medline"): ...
DayPmc signature(object = "Medline"): ...
HourPmc signature(object = "Medline"): ...
MinutePmc signature(object = "Medline"): ...
YearPubmed signature(object = "Medline"): ...
MonthPubmed signature(object = "Medline"): ...
DayPubmed signature(object = "Medline"): ...
HourPubmed signature(object = "Medline"): ...
MinutePubmed signature(object = "Medline"): ...
Author signature(object = "Medline"): ...
ISSN signature(object = "Medline"): ...
Title signature(object = "Medline"): ...
ArticleTitle signature(object = "Medline"): ...
ElocationID signature(object = "Medline"): ...
AbstractText signature(object = "Medline"): ...
Affiliation signature(object = "Medline"): ...
Language signature(object = "Medline"): ...
PublicationType signature(object = "Medline"): ...
MedlineTA signature(object = "Medline"): ...
NlmUniqueID signature(object = "Medline"): ...
ISSNLinking signature(object = "Medline"): ...
PublicationStatus signature(object = "Medline"): ...
ArticleId signature(object = "Medline"): ...
Volume signature(object = "Medline"): ...
Issue signature(object = "Medline"): ...
ISOAbbreviation signature(object = "Medline"): ...
MedlinePgn signature(object = "Medline"): ...
CopyrightInformation signature(object = "Medline"): ...
Country signature(object = "Medline"): ...
GrantID signature(object = "Medline"): ...
Acronym signature(object = "Medline"): ...
Agency signature(object = "Medline"): ...
RegistryNumber signature(object = "Medline"): ...
RefSource signature(object = "Medline"): ...
CollectiveName signature(object = "Medline"): ...
Mesh signature(object = "Medline"): ...
```

Author(s)

Stephanie Kovalchik

MedlinePgn*Extracts MedlinePgn from Medline object.***Description**

Extractor for the MedlinePgn of a Medline object.

Usage

```
MedlinePgn(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
MedlinePgn(myeloma)
```

MedlinePgn-methods*~~ Methods for Function MedlinePgn in Package **RISmed** ~~***Description**

~~ Methods for function MedlinePgn in package **RISmed** ~~

Methods

```
signature(object = "Medline")
```

MedlineTA*Extracts MedlineTA from Medline object.*

Description

Extractor for the MedlineTA of a Medline object.

Usage

```
MedlineTA(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
MedlineTA(myeloma)
```

MedlineTA-methods*~~ Methods for Function MedlineTA in Package **RISmed** ~~*

Description

~~ Methods for function MedlineTA in package **RISmed** ~~

Methods

```
signature(object = "Medline")
```

Mesh	<i>Extracts Mesh headings from Medline object.</i>
------	--

Description

Extractor for the Mesh headings of a Medline object.

Usage

`Mesh(object)`

Arguments

`object` instance of class `Medline`

Details

In Process and publisher-supplied records lack MeSH terms. See the MeSH Fact Sheet <http://www.nlm.nih.gov/pubs/factsheets/mesh.html> or the MeSH home page <http://www.nlm.nih.gov/mesh/meshhome.html> for additional information about MeSH. Note that more recent records may lack MeSH headings.

Value

List by Pubmed article. Each list contains a data frame with `Heading` and `Type`. The `Heading` is a MeSH Term and `Type` is either a Descriptor or a Qualifier of a Descriptor term. Qualifiers of a Descriptor immediately follow the Descriptor term in the data frame. When MeSH headings have not been included with a MEDLINE record, the list will contain NAs (see details).

See Also

[Medline](#)

Examples

```
res <- EUtilsSummary("myeloma[MeSh]",retmax=2,reldate=365)
summary(res)
fetch <- EUtilsGet(res)

Mesh(fetch)
```

Mesh-methods

*~~ Methods for Function Mesh in Package **RISmed** ~~*

Description

*~~ Methods for function Mesh in package **RISmed** ~~*

Methods

`signature(object = "Medline")` List by Pubmed article. Each list contains a data frame with Heading and Type. The Heading is a MeSH Term and Type is either a Descriptor or a Qualifier of a Descriptor term.

MinuteAccepted

Extracts MinuteAccepted from Medline object.

Description

Extractor for the MinuteAccepted of a Medline object. This date corresponds to the date the article was accepted.

Usage

`MinuteAccepted(object)`

Arguments

`object` instance of class `Medline`

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
MinuteAccepted(myeloma)
```

MinuteAccepted-methods

*~~ Methods for Function MinuteAccepted in Package **RISmed** ~~*

Description

*~~ Methods for function MinuteAccepted in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

MinuteEpublish

Extracts MinuteEpublish from Medline object.

Description

Extractor for the MinuteEpublish of a Medline object. This date corresponds to the date the article was published online.

Usage

`MinuteEpublish(object)`

Arguments

`object` instance of class `Medline`

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
MinuteEpublish(myeloma)
```

MinuteEpublish-methods

*~~ Methods for Function MinuteEpublish in Package **RISmed** ~~*

Description

~~ Methods for function **MinuteEpublish** in package **RISmed** ~~

Methods

`signature(object = "Medline")`

MinutePmc

Extracts MinutePmc from Medline object.

Description

Extractor for the **MinutePmc** of a **Medline** object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

`MinutePmc(object)`

Arguments

`object` instance of class **Medline**

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
MinutePmc(myeloma)
```

MinutePmc-methods

*~~ Methods for Function MinutePmc in Package **RISmed** ~~***Description***~~ Methods for function MinutePmc in package **RISmed** ~~***Methods**`signature(object = "Medline")`

MinutePpublish

*Extracts MinutePpublish from Medline object.***Description**

Extractor for the MinutePpublish of a Medline object. This date corresponds to the date the article was published in print.

Usage`MinutePpublish(object)`**Arguments**

object instance of class Medline

Value

vector

References<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>**See Also**[Medline](#)**Examples**

```
data(myeloma)
MinutePpublish(myeloma)
```

MinutePpublish-methods

*~~ Methods for Function MinutePpublish in Package **RISmed** ~~*

Description

~~ Methods for function **MinutePpublish** in package **RISmed** ~~

Methods

`signature(object = "Medline")`

MinutePubmed

Extracts MinutePubmed from Medline object.

Description

Extractor for the **MinutePubmed** of a **Medline** object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

`MinutePubmed(object)`

Arguments

`object` instance of class **Medline**

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
MinutePubmed(myeloma)
```

MinutePubmed-methods *~~ Methods for Function MinutePubmed in Package **RISmed** ~~*

Description

~~ Methods for function MinutePubmed in package **RISmed** ~~

Methods

`signature(object = "Medline")`

MinuteReceived *Extracts MinuteReceived from Medline object.*

Description

Extractor for the MinuteReceived of a Medline object. This date corresponds to the date the article was received.

Usage

`MinuteReceived(object)`

Arguments

`object` instance of class `Medline`

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
MinuteReceived(myeloma)
```

MinuteReceived-methods

*~~ Methods for Function MinuteReceived in Package **RISmed** ~~*

Description

~~ Methods for function MinuteReceived in package **RISmed** ~~

Methods

signature(object = "Medline")

MonthAccepted

Extracts MonthAccepted from Medline object.

Description

Extractor for the MonthAccepted of a Medline object. This date corresponds to the date the article was accepted.

Usage

MonthAccepted(object)

Arguments

object instance of class **Medline**

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
MonthAccepted(myeloma)
```

MonthAccepted-methods ~~ *Methods for Function MonthAccepted in Package **RISmed** ~~*

Description

~~ Methods for function MonthAccepted in package **RISmed** ~~

Methods

`signature(object = "Medline")`

MonthEpublish	<i>Extracts MonthEpublish from Medline object.</i>
----------------------	--

Description

Extractor for the MonthEpublish of a Medline object. This date corresponds to the date the article was published online.

Usage

`MonthEpublish(object)`

Arguments

object	instance of class <code>Medline</code>
--------	--

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
MonthEpublish(myeloma)
```

MonthEpublish-methods ~~ *Methods for Function MonthEpublish in Package **RISmed*** ~~

Description

~~ Methods for function MonthEpublish in package **RISmed** ~~

Methods

```
signature(object = "Medline")
```

MonthPmc

Extracts MonthPmc from Medline object.

Description

Extractor for the MonthPmc of a Medline object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

MonthPmc(object)

Arguments

object instance of class Medline

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

Medline

Examples

```
data(myeloma)  
MonthPmc(myeloma)
```

MonthPmc-methods

*~~ Methods for Function MonthPmc in Package **RISmed** ~~***Description***~~ Methods for function MonthPmc in package **RISmed** ~~***Methods**`signature(object = "Medline")`

MonthPpublish

*Extracts MonthPpublish from Medline object.***Description**

Extractor for the MonthPpublish of a Medline object. This date corresponds to the date the article was published in print.

Usage`MonthPpublish(object)`**Arguments**object instance of class `Medline`**Value**

vector

References<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>**See Also**[Medline](#)**Examples**

```
data(myeloma)
MonthPpublish(myeloma)
```

MonthPpublish-methods ~~ *Methods for Function MonthPpublish in Package **RISmed*** ~~

Description

~~ Methods for function MonthPpublish in package **RISmed** ~~

Methods

`signature(object = "Medline")`

`MonthPubmed` *Extracts MonthPubmed from Medline object.*

Description

Extractor for the MonthPubmed of a Medline object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

`MonthPubmed(object)`

Arguments

`object` instance of class `Medline`

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
MonthPubmed(myeloma)
```

MonthPubmed-methods

*~~ Methods for Function MonthPubmed in Package **RISmed** ~~***Description***~~ Methods for function MonthPubmed in package **RISmed** ~~***Methods**`signature(object = "Medline")`

MonthReceived

*Extracts MonthReceived from Medline object.***Description**

Extractor for the MonthReceived of a Medline object. This date corresponds to the date the article was received.

Usage`MonthReceived(object)`**Arguments**

<code>object</code>	instance of class <code>Medline</code>
---------------------	--

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also[Medline](#)**Examples**

```
data(myeloma)
MonthReceived(myeloma)
```

MonthReceived-methods ~~ *Methods for Function MonthReceived in Package **RISmed*** ~~

Description

~~ Methods for function MonthReceived in package **RISmed** ~~

Methods

`signature(object = "Medline")`

myeloma

Example of results from EUtilsGet

Description

First five records of query of NCBI PubMed for "myeloma[MeSh]" in the past year (at the time of this writing) as a Medline object.

Usage

`myeloma`

Format

A list object with five PubMed article records.

Author(s)

Stephanie Kovalchik <s.a.kovalchik@gmail.com>

Source

PubMed database of the US National Library of Medicine

See Also

[EUtilsGet](#), [Medline](#)

NlmUniqueID *Extracts NlmUniqueID from Medline object.*

Description

Extractor for the NlmUniqueID of a Medline object.

Usage

`NlmUniqueID(object)`

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
NlmUniqueID(myeloma)
```

NlmUniqueID-methods *~ Methods for Function NlmUniqueID in Package **RISmed** ~*

Description

~~ Methods for function NlmUniqueID in package **RISmed** ~~

Methods

`signature(object = "Medline")`

PMID	<i>Extracts PMID from Medline object.</i>
------	---

Description

Extractor for the PMID of a Medline object.

Usage

`PMID(object)`

Arguments

`object` instance of class `Medline`

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
PMID(myeloma)
```

PMID-methods	<i>~~ Methods for Function PMID in Package RISmed ~~</i>
--------------	---

Description

*~~ Methods for function PMID in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

`print-Medline` *Print method for Medline object*

Description

Print object of class Medline

Methods

`signature(object = "Medline")` Query translation (if provided) and total fetched record count for Medline object.

`print-methods` *Print method for EUtilsSummary object*

Description

Print object of class EUtilsSummary

Methods

`signature(object = "EUtilsSummary")` Query translation for EUtilsSummary object.

`PublicationStatus` *Extracts PublicationStatus from Medline object.*

Description

Extractor for the PublicationStatus of a Medline object.

Usage

`PublicationStatus(object)`

Arguments

`object` instance of class Medline

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
PublicationStatus(myeloma)
```

PublicationStatus-methods

*~~ Methods for Function PublicationStatus in Package **RISmed***

~~

Description

*~~ Methods for function PublicationStatus in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

PublicationType	<i>Extracts PublicationType from Medline object.</i>
-----------------	--

Description

Extractor for the PublicationType of a Medline object.

Usage

```
PublicationType(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

list

See Also

[Medline](#)

Examples

```
data(myeloma)
PublicationType(myeloma)
```

PublicationType-methods

*~~ Methods for Function PublicationType in Package **RISmed** ~~*

Description

*~~ Methods for function PublicationType in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

Query

Extract Query from Medline object.

Description

Extractor for the translated Query of a Medline object.

Usage

`Query(object)`

Arguments

`object` instance of class `Medline`

Value

`vector`

See Also

[Medline](#)

Examples

```
data(myeloma)
Query(myeloma)
```

Query-methods

*~~ Methods for Function Query in Package **RISmed** ~~*

Description

*~~ Methods for function Query in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

QueryCount

Count of record results for EUtilsQuery

Description

Returns the number of Ids from a E-utility query

Usage

`QueryCount(object)`

Arguments

`object` object of the `EUtilsSummary` class.

Value

numeric count

Author(s)

Stephanie Kovalchik

See Also

[EUtilsSummary](#)

QueryId	<i>Get ids from EUtilsQuery</i>
---------	---------------------------------

Description

Returns the vector Ids from a E-utility query

Usage

`QueryId(object)`

Arguments

`object` object of the EUtilsSummary class.

Value

character vector of ids

Author(s)

Stephanie Kovalchik

See Also

[EUtilsSummary](#)

QueryTranslation	<i>Get the NCBI query translation from EUtilsQuery</i>
------------------	--

Description

Returns the string translation of a E-utility query

Usage

`QueryTranslation(object)`

Arguments

`object` object of the EUtilsSummary class.

Value

character query translation

Author(s)

Stephanie Kovalchik

See Also

[EUtilsSummary](#)

RefSource

Extracts RefSource from Medline object.

Description

Extractor for the RefSource of a Medline object.

Usage

`RefSource(object)`

Arguments

`object` instance of class `Medline`

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
RefSource(myeloma)
```

RefSource-methods

*~~ Methods for Function RefSource in Package **RISmed** ~~*

Description

*~~ Methods for function RefSource in package **RISmed** ~~*

Methods

`signature(object = "Medline")`

RegistryNumber	<i>Extracts RegistryNumber from Medline object.</i>
----------------	---

Description

Extractor for the RegistryNumber of a Medline object.

Usage

```
RegistryNumber(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
RegistryNumber(myeloma)
```

RegistryNumber-methods

*~~ Methods for Function RegistryNumber in Package **RISmed** ~~*

Description

*~~ Methods for function RegistryNumber in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

show-Medline

Show method for Medline object

Description

Show object of class Medline

Methods

`signature(object = "Medline")` Query translation (if provided) and total fetched record count for Medline object.

show-methods

Show method for EUtilsSummary object

Description

Show object of class EUtilsSummary

Methods

`signature(object = "EUtilsSummary")` Query translation for EUtilsSummary object.

summary-methods

Summary method for EUtilsSummary object

Description

Summary of object of class EUtilsSummary

Methods

`signature(object = "EUtilsSummary", ...)` Returns the number of records and id vector.

Title	<i>Extracts Title from Medline object.</i>
-------	--

Description

Extractor for the Title of a Medline object.

Usage

```
Title(object)
```

Arguments

object instance of class Medline

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
Title(myeloma)
```

Title-methods	<i>~~ Methods for Function Title in Package RISmed ~~</i>
---------------	--

Description

*~~ Methods for function Title in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

Volume	<i>Extracts Volume from Medline object.</i>
--------	---

Description

Extractor for the Volume of a Medline object.

Usage

```
Volume(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

See Also

[Medline](#)

Examples

```
data(myeloma)
Volume(myeloma)
```

Volume-methods	<i>~~ Methods for Function Volume in Package RISmed ~~</i>
----------------	---

Description

*~~ Methods for function Volume in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

<code>YearAccepted</code>	<i>Extracts YearAccepted from Medline object.</i>
---------------------------	---

Description

Extractor for the YearAccepted of a Medline object. This date corresponds to the date the article was accepted.

Usage

```
YearAccepted(object)
```

Arguments

<code>object</code>	instance of class <code>Medline</code>
---------------------	--

Value

<code>vector</code>	
---------------------	--

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
YearAccepted(myeloma)
```

<code>YearAccepted-methods</code>	<i>~~ Methods for Function <code>YearAccepted</code> in Package RISmed ~~</i>
-----------------------------------	--

Description

*~~ Methods for function `YearAccepted` in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

YearEpubish *Extracts YearEpubish from Medline object.*

Description

Extractor for the YearEpubish of a Medline object. This date corresponds to the date the article was published online.

Usage

```
YearEpubish(object)
```

Arguments

object instance of class Medline

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
YearEpubish(myeloma)
```

YearEpubish-methods *~~ Methods for Function YearEpubish in Package **RISmed** ~~*

Description

*~~ Methods for function YearEpubish in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

YearPmc*Extracts YearPmc from Medline object.***Description**

Extractor for the YearPmc of a Medline object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

```
YearPmc(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
YearPmc(myeloma)
```

YearPmc-methods*~~ Methods for Function YearPmc in Package **RISmed** ~~***Description**

~~ Methods for function YearPmc in package **RISmed** ~~

Methods

```
signature(object = "Medline")
```

YearPpublish *Extracts YearPpublish from Medline object.*

Description

Extractor for the YearPpublish of a Medline object. This date corresponds to the date the article was published in print.

Usage

```
YearPpublish(object)
```

Arguments

object instance of class Medline

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
YearPpublish(myeloma)
```

YearPpublish-methods *~~ Methods for Function YearPpublish in Package **RISmed** ~~*

Description

*~~ Methods for function YearPpublish in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

YearPubmed*Extracts YearPubmed from Medline object.***Description**

Extractor for the YearPubmed of a Medline object. This date corresponds to the date the article was made available through Pubmed Central.

Usage

```
YearPubmed(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
YearPubmed(myeloma)
```

YearPubmed-methods*~~ Methods for Function YearPubmed in Package **RISmed** ~~***Description**

~~ Methods for function YearPubmed in package **RISmed** ~~

Methods

```
signature(object = "Medline")
```

YearReceived	<i>Extracts YearReceived from Medline object.</i>
--------------	---

Description

Extractor for the YearReceived of a Medline object. This date corresponds to the date the article was received.

Usage

```
YearReceived(object)
```

Arguments

object	instance of class Medline
--------	---------------------------

Value

vector

References

<http://www.nlm.nih.gov/bsd/mms/medlineelements.html#phst>

See Also

[Medline](#)

Examples

```
data(myeloma)
YearReceived(myeloma)
```

YearReceived-methods	<i>~~ Methods for Function YearReceived in Package RISmed ~~</i>
----------------------	---

Description

*~~ Methods for function YearReceived in package **RISmed** ~~*

Methods

```
signature(object = "Medline")
```

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