

# mta10transcriptcluster.db

March 12, 2025

---

mta10transcriptclusterACCNUM

*Map Manufacturer identifiers to Accession Numbers*

---

## Description

mta10transcriptclusterACCNUM is an R object that contains mappings between a manufacturer's identifiers and manufacturers accessions.

## Details

For chip packages such as this, the ACCNUM mapping comes directly from the manufacturer. This is different from other mappings which are mapped onto the probes via an Entrez Gene identifier.

Each manufacturer identifier maps to a vector containing a GenBank accession number.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2021-Apr14

## See Also

- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```
## select() interface:  
## Objects in this package can be accessed using the select() interface  
## from the AnnotationDbi package. See ?select for details.
```

```
## Bimap interface:  
x <- mta10transcriptclusterACCNUM  
# Get the probe identifiers that are mapped to an ACCNUM  
mapped_probes <- mappedkeys(x)  
# Convert to a list  
xx <- as.list(x[mapped_probes][1:300])  
if(length(xx) > 0) {  
  # Get the ACCNUM for the first five probes
```

```

xx[1:5]
# Get the first one
xx[[1]]
}

```

---

```
mta10transcriptclusterALIAS2PROBE
```

*Map between Common Gene Symbol Identifiers and Manufacturer Identifiers*

---

## Description

mta10transcriptclusterALIAS is an R object that provides mappings between common gene symbol identifiers and manufacturer identifiers.

## Details

Each gene symbol is mapped to a named vector of manufacturer identifiers. The name represents the gene symbol and the vector contains all manufacturer identifiers that are found for that symbol. An NA is reported for any gene symbol that cannot be mapped to any manufacturer identifiers.

This mapping includes ALL gene symbols including those which are already listed in the SYMBOL map. The SYMBOL map is meant to only list official gene symbols, while the ALIAS maps are meant to store all used symbols.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2021-Apr14

## See Also

- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```

## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
# Convert the object to a list
xx <- as.list(mta10transcriptclusterALIAS2PROBE)
if(length(xx) > 0){
  # Get the probe identifiers for the first two aliases
  xx[1:2]
  # Get the first one
  xx[[1]]
}

```

---

mta10transcriptcluster.db

*Bioconductor annotation data package*

---

## Description

Welcome to the mta10transcriptcluster.db annotation Package. The purpose of this package is to provide detailed information about the mta10transcriptcluster platform. This package is updated biannually.

Objects in this package are accessed using the `select()` interface. See `?select` in the AnnotationDbi package for details.

## See Also

- [AnnotationDb-class](#) for use of `keys()`, `columns()` and `select()`.

## Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.
columns(mta10transcriptcluster.db)

## Bimap interface:
## The 'old style' of interacting with these objects is manipulation as
## bimap. While this approach is still available we strongly encourage the
## use of select().
ls("package:mta10transcriptcluster.db")
```

---

mta10transcriptclusterCHR

*Map Manufacturer IDs to Chromosomes*

---

## Description

mta10transcriptclusterCHR is an R object that provides mappings between a manufacturer identifier and the chromosome that contains the gene of interest.

## Details

Each manufacturer identifier maps to a vector of chromosomes. Due to inconsistencies that may exist at the time the object was built, the vector may contain more than one chromosome (e.g., the identifier may map to more than one chromosome). If the chromosomal location is unknown, the vector will contain an NA.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2021-Apr14

**See Also**

- [AnnotationDb-class](#) for use of the `select()` interface.

**Examples**

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterCHR
# Get the probe identifiers that are mapped to a chromosome
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0) {
  # Get the CHR for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

mta10transcriptclusterCHRENGTHS

*A named vector for the length of each of the chromosomes*

---

**Description**

mta10transcriptclusterCHRENGTHS provides the length measured in base pairs for each of the chromosomes.

**Details**

This is a named vector with chromosome numbers as the names and the corresponding lengths for chromosomes as the values.

Total lengths of chromosomes were derived by calculating the number of base pairs on the sequence string for each chromosome.

**See Also**

- [AnnotationDb-class](#) for use of the `select()` interface.

**Examples**

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.
```

```
## Bimap interface:
tt <- mta10transcriptclusterCHRENGTHS
# Length of chromosome 1
tt["1"]
```

---

```
mta10transcriptclusterCHRLOC
```

*Map Manufacturer IDs to Chromosomal Location*

---

## Description

mta10transcriptclusterCHRLOC is an R object that maps manufacturer identifiers to the starting position of the gene. The position of a gene 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 gene instead of the start.

## Details

Each manufacturer identifier maps to a named vector of chromosomal locations, where the name indicates the chromosome. Due to inconsistencies that may exist at the time the object was built, these vectors may contain more than one chromosome and/or location. If the chromosomal location is unknown, the vector will contain an NA.

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 genes have multiple start sites, this field can map to multiple locations.

Mappings were based on data provided by: UCSC Genome Bioinformatics (Mus musculus)

With a date stamp from the source of: 2021-Feb16

## See Also

- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterCHRLOC
# Get the probe identifiers that are mapped to chromosome locations
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0) {
  # Get the CHRLOC for the first five probes
```

```

xx[1:5]
# Get the first one
xx[[1]]
}

```

---

mta10transcriptclusterENSEMBL

*Map Ensembl gene accession numbers with Entrez Gene identifiers*

---

## Description

mta10transcriptclusterENSEMBL is an R object that contains mappings between manufacturer identifiers and Ensembl gene accession numbers.

## Details

This object is a simple mapping of manufacturer identifiers to Ensembl gene Accession Numbers.

Mappings were based on data provided by BOTH of these sources: <http://www.ensembl.org/biomart/martview/> <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA>

For most species, this mapping is a combination of manufacturer to ensembl IDs from BOTH NCBI and ensembl. Users who wish to only use mappings from NCBI are encouraged to see the ncbi2ensembl table in the appropriate organism package. Users who wish to only use mappings from ensembl are encouraged to see the ensembl2ncbi table which is also found in the appropriate organism packages. These mappings are based upon the ensembl table which contains data from BOTH of these sources in an effort to maximize the chances that you will find a match.

For worms and flies however, this mapping is based only on sources from ensembl, as these organisms do not have ensembl to entrez gene mapping data at NCBI.

## See Also

- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```

## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterENSEMBL
# Get the entrez gene IDs that are mapped to an Ensembl ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes][1:300])
if(length(xx) > 0) {
  # Get the Ensembl gene IDs for the first five genes
  xx[1:5]
  # Get the first one
}

```

```
  xx[[1]]
}
#For the reverse map ENSEMBL2PROBE:
x <- mta10transcriptclusterENSEMBL2PROBE
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes][1:300])
if(length(xx) > 0){
  # Gets the entrez gene IDs for the first five Ensembl IDs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

mta10transcriptclusterENTREZID

*Map between Manufacturer Identifiers and Entrez Gene*

---

## Description

mta10transcriptclusterENTREZID is an R object that provides mappings between manufacturer identifiers and Entrez Gene identifiers.

## Details

Each manufacturer identifier is mapped to a vector of Entrez Gene identifiers. An NA is assigned to those manufacturer identifiers that can not be mapped to an Entrez Gene identifier at this time.

If a given manufacturer identifier can be mapped to different Entrez Gene identifiers from various sources, we attempt to select the common identifiers. If a concensus cannot be determined, we select the smallest identifier.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2021-Apr14

## References

<https://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene>

## See Also

- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
```

```
x <- mta10transcriptclusterENTREZID
# Get the probe identifiers that are mapped to an ENTREZ Gene ID
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0) {
  # Get the ENTREZID for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

mta10transcriptclusterENZYME

*Maps between Manufacturer IDs and Enzyme Commission (EC) Numbers*

---

## Description

mta10transcriptclusterENZYME is an R object that provides mappings between manufacturer identifiers and EC numbers. mta10transcriptclusterENZYME2PROBE is an R object that maps Enzyme Commission (EC) numbers to manufacturer identifiers.

## Details

When the mta10transcriptclusterENZYME mapping viewed as a list, each manufacturer identifier maps to a named vector containing the EC number that corresponds to the enzyme produced by that gene. The names corresponds to the manufacturer identifiers. If this information is unknown, the vector will contain an NA.

For the mta10transcriptclusterENZYME2PROBE, each EC number maps to a named vector containing all of the manufacturer identifiers that correspond to the gene that produces that enzyme. The name of the vector corresponds to the EC number.

Enzyme Commission numbers are assigned by the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology <http://www.chem.qmw.ac.uk/iubmb/enzyme/> to allow enzymes to be identified.

An Enzyme Commission number is of the format EC x.y.z.w, where x, y, z, and w are numeric numbers. In mta10transcriptclusterENZYME2PROBE, EC is dropped from the Enzyme Commission numbers.

Enzyme Commission numbers have corresponding names that describe the functions of enzymes in such a way that EC x is a more general description than EC x.y that in turn is a more general description than EC x.y.z. The top level EC numbers and names are listed below:

EC 1 oxidoreductases

EC 2 transferases

EC 3 hydrolases

EC 4 lyases



EC 5 isomerases

EC 6 ligases

The EC name for a given EC number can be viewed at <http://www.chem.qmul.ac.uk/iupac/jcbn/index.html#6>

Mappings between probe identifiers and enzyme identifiers were obtained using files provided by: KEGG GENOME <ftp://ftp.genome.jp/pub/kegg/genomes> With a date stamp from the source of: 2011-Mar15

## References

<ftp://ftp.genome.ad.jp/pub/kegg/pathways>

## See Also

- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterENZYME
# Get the probe identifiers that are mapped to an EC number
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:3])
if(length(xx) > 0) {
  # Get the ENZYME for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}

# Now convert mta10transcriptclusterENZYME2PROBE to a list to see inside
x <- mta10transcriptclusterENZYME2PROBE
mapped_probes <- mappedkeys(x)
## convert to a list
xx <- as.list(x[mapped_probes][1:3])
if(length(xx) > 0){
  # Get the probe identifiers for the first five enzyme
  #commission numbers
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

mta10transcriptclusterGENENAME

*Map between Manufacturer IDs and Genes*

---

## Description

mta10transcriptclusterGENENAME is an R object that maps manufacturer identifiers to the corresponding gene name.

## Details

Each manufacturer identifier maps to a named vector containing the gene name. The vector name corresponds to the manufacturer identifier. If the gene name is unknown, the vector will contain an NA.

Gene names currently include both the official (validated by a nomenclature committee) and preferred names (interim selected for display) for genes. Efforts are being made to differentiate the two by adding a name to the vector.

Mappings were based on data provided by: Entrez Gene ftp://ftp.ncbi.nlm.nih.gov/gene/DATA With a date stamp from the source of: 2021-Apr14

## See Also

- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterGENENAME
# Get the probe identifiers that are mapped to a gene name
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0) {
  # Get the GENENAME for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

`mta10transcriptclusterGO`*Maps between manufacturer IDs and Gene Ontology (GO) IDs*

---

**Description**

`mta10transcriptclusterGO` is an R object that provides mappings between manufacturer identifiers and the GO identifiers that they are directly associated with. This mapping and its reverse mapping (`mta10transcriptclusterGO2PROBE`) do NOT associate the child terms from the GO ontology with the gene. Only the directly evidenced terms are represented here.

`mta10transcriptclusterGO2ALLPROBES` is an R object that provides mappings between a given GO identifier and all of the manufacturer identifiers annotated at that GO term OR TO ONE OF IT'S CHILD NODES in the GO ontology. Thus, this mapping is much larger and more inclusive than `mta10transcriptclusterGO2PROBE`.

**Details**

If `mta10transcriptclusterGO` is cast as a list, each manufacturer identifier is mapped to a list of lists. The names on the outer list are GO identifiers. Each inner list consists of three named elements: GOID, Ontology, and Evidence.

The GOID element matches the GO identifier named in the outer list and is included for convenience when processing the data using 'lapply'.

The Ontology element indicates which of the three Gene Ontology categories this identifier belongs to. The categories are biological process (BP), cellular component (CC), and molecular function (MF).

The Evidence element contains a code indicating what kind of evidence supports the association of the GO identifier to the manufacturer id. Some of the evidence codes in use include:

IMP: inferred from mutant phenotype

IGI: inferred from genetic interaction

IPI: inferred from physical interaction

ISS: inferred from sequence similarity

IDA: inferred from direct assay

IEP: inferred from expression pattern

IEA: inferred from electronic annotation

TAS: traceable author statement

NAS: non-traceable author statement

ND: no biological data available

IC: inferred by curator

A more complete listing of evidence codes can be found at:

<http://www.geneontology.org/GO.evidence.shtml>

If `mta10transcriptclusterGO2ALLPROBES` or `mta10transcriptclusterGO2PROBE` is cast as a list, each GO term maps to a named vector of manufacturer identifiers and evidence codes. A GO identifier may be mapped to the same manufacturer identifier more than once but the evidence code can be different. Mappings between Gene Ontology identifiers and Gene Ontology terms and other information are available in a separate data package named GO.

Whenever any of these mappings are cast as a `data.frame`, all the results will be output in an appropriate tabular form.

Mappings between manufacturer identifiers and GO information were obtained through their mappings to manufacturer identifiers. NAs are assigned to manufacturer identifiers that can not be mapped to any Gene Ontology information. Mappings between Gene Ontology identifiers and Gene Ontology terms and other information are available in a separate data package named GO.

All mappings were based on data provided by: Gene Ontology <http://current.geneontology.org/ontology/gobasic.obo> With a date stamp from the source of: 2021-02-01

## References

<ftp://ftp.ncbi.nlm.nih.gov/gene/DATA/>

## See Also

- [mta10transcriptclusterGO2ALLPROBES](#)
- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterGO
# Get the manufacturer identifiers that are mapped to a GO ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes][1:300])
if(length(xx) > 0) {
  # Try the first one
  got <- xx[[1]]
  got[[1]][["GOID"]]
  got[[1]][["Ontology"]]
  got[[1]][["Evidence"]]
}
# For the reverse map:
x <- mta10transcriptclusterGO2PROBE
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes][1:300])
if(length(xx) > 0){
  # Gets the manufacturer ids for the top 2nd and 3rd GO identifiers
  goids <- xx[2:3]
```

```

    # Gets the manufacturer ids for the first element of goids
    goids[[1]]
    # Evidence code for the mappings
    names(goids[[1]])
  }

x <- mta10transcriptclusterGO2ALLPROBES
mapped_genes <- mappedkeys(x)
# Convert mta10transcriptclusterGO2ALLPROBES to a list
xx <- as.list(x[mapped_genes][1:300])
if(length(xx) > 0){
  # Gets the manufacturer identifiers for the top 2nd and 3rd GO identifiers
  goids <- xx[2:3]
  # Gets all the manufacturer identifiers for the first element of goids
  goids[[1]]
  # Evidence code for the mappings
  names(goids[[1]])
}

```

---

mta10transcriptclusterMAPCOUNTS

*Number of mapped keys for the maps in package  
mta10transcriptcluster.db*

---

### Description

DEPRECATED. Counts in the MAPCOUNT table are out of sync and should not be used.

mta10transcriptclusterMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package mta10transcriptcluster.db.

### Details

DEPRECATED. Counts in the MAPCOUNT table are out of sync and should not be used.

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.

---

mta10transcriptclusterMGI

*Map MGI gene accession numbers with manufacturer identifiers*

---

### Description

mta10transcriptclusterMGI is an R object that contains mappings between manufacturer identifiers and Jackson Laboratory MGI gene accession numbers.

**Details**

This object is a simple mapping of manufacturer identifiers to MGI gene Accession Numbers.

Mappings were based on data provided by: Entrez Gene ftp://ftp.ncbi.nlm.nih.gov/gene/DATA With a date stamp from the source of: 2021-Apr14

**See Also**

- [AnnotationDb-class](#) for use of the `select()` interface.

**Examples**

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterMGI
# Get the manufacturer IDs that are mapped to an MGI ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes][1:300])
if(length(xx) > 0) {
  # Get the MGI IDs for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
#For the reverse map MGI2EG:
x <- mta10transcriptclusterMGI2PROBE
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes][1:300])
if(length(xx) > 0){
  # Gets the manufacturer IDs for the first five MGI IDs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

mta10transcriptclusterORGANISM

*The Organism information for mta10transcriptcluster*

---

**Description**

mta10transcriptclusterORGANISM is an R object that contains a single item: a character string that names the organism for which mta10transcriptcluster was built. mta10transcriptclusterORGPKG is an R object that contains a character vector with the name of the organism package that a chip package depends on for its gene-centric annotation.

**Details**

Although the package name is suggestive of the organism for which it was built, `mta10transcriptclusterORGANISM` provides a simple way to programmatically extract the organism name. `mta10transcriptclusterORGPKG` provides a simple way to programmatically extract the name of the parent organism package. The parent organism package is a strict dependency for chip packages as this is where the gene cetric information is ultimately extracted from. The full package name will always be this string plus the extension ".db". But most programatic access will not require this extension, so its more convenient to leave it out.

**See Also**

- [AnnotationDb-class](#) for use of the `select()` interface.

**Examples**

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
mta10transcriptclusterORGANISM
mta10transcriptclusterORGPKG
```

---

```
mta10transcriptclusterPATH
```

*Mappings between probe identifiers and KEGG pathway identifiers*

---

**Description**

KEGG (Kyoto Encyclopedia of Genes and Genomes) maintains pathway data for various organisms.

`mta10transcriptclusterPATH` maps probe identifiers to the identifiers used by KEGG for pathways in which the genes represented by the probe identifiers are involved

`mta10transcriptclusterPATH2PROBE` is an R object that provides mappings between KEGG identifiers and manufacturer identifiers.

**Details**

Each KEGG pathway has a name and identifier. Pathway name for a given pathway identifier can be obtained using the KEGG data package that can either be built using `AnnBuilder` or downloaded from Bioconductor <http://www.bioconductor.org>.

Graphic presentations of pathways are searchable at url <http://www.genome.ad.jp/kegg/pathway.html> by using pathway identifiers as keys.

Mappings were based on data provided by: KEGG GENOME <ftp://ftp.genome.jp/pub/kegg/genomes>  
With a date stamp from the source of: 2011-Mar15

**References**

<http://www.genome.ad.jp/kegg/>

**See Also**

- [AnnotationDb-class](#) for use of the `select()` interface.

**Examples**

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterPATH
# Get the probe identifiers that are mapped to a KEGG pathway ID
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0) {
  # Get the PATH for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}

x <- mta10transcriptclusterPATH
mapped_probes <- mappedkeys(x)
# Now convert the mta10transcriptclusterPATH2PROBE object to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0){
  # Get the probe identifiers for the first two pathway identifiers
  xx[1:2]
  # Get the first one
  xx[[1]]
}
```

---

mta10transcriptclusterPFAM

*Maps between Manufacturer Identifiers and PFAM Identifiers*

---

**Description**

mta10transcriptclusterPFAM is an R object that provides mappings between manufacturer identifiers and PFAM identifiers.

**Details**

The bimap interface for PFAM is defunct. Please use `select()` interface to PFAM identifiers. See `?AnnotationDbi::select` for details.



---

`mta10transcriptclusterPMID`*Maps between Manufacturer Identifiers and PubMed Identifiers*

---

## Description

`mta10transcriptclusterPMID` is an R object that provides mappings between manufacturer identifiers and PubMed identifiers. `mta10transcriptclusterPMID2PROBE` is an R object that provides mappings between PubMed identifiers and manufacturer identifiers.

## Details

When `mta10transcriptclusterPMID` is viewed as a list each manufacturer identifier is mapped to a named vector of PubMed identifiers. The name associated with each vector corresponds to the manufacturer identifier. The length of the vector may be one or greater, depending on how many PubMed identifiers a given manufacturer identifier is mapped to. An NA is reported for any manufacturer identifier that cannot be mapped to a PubMed identifier.

When `mta10transcriptclusterPMID2PROBE` is viewed as a list each PubMed identifier is mapped to a named vector of manufacturer identifiers. The name represents the PubMed identifier and the vector contains all manufacturer identifiers that are represented by that PubMed identifier. The length of the vector may be one or longer, depending on how many manufacturer identifiers are mapped to a given PubMed identifier.

Titles, abstracts, and possibly full texts of articles can be obtained from PubMed by providing a valid PubMed identifier. The `pubmed` function of `annotate` can also be used for the same purpose.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2021-Apr14

## References

<https://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=PubMed>

## See Also

- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterPMID
# Get the probe identifiers that are mapped to any PubMed ID
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
```

```

if(length(xx) > 0){
  # Get the PubMed identifiers for the first two probe identifiers
  xx[1:2]
  # Get the first one
  xx[[1]]
  if(interactive() && !is.null(xx[[1]]) && !is.na(xx[[1]]))
    && require(annotate){
      # Get article information as XML files
      xmls <- pubmed(xx[[1]], disp = "data")
      # View article information using a browser
      pubmed(xx[[1]], disp = "browser")
    }
}

x <- mta10transcriptclusterPMID2PROBE
mapped_probes <- mappedkeys(x)
# Now convert the reverse map object mta10transcriptclusterPMID2PROBE to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0){
  # Get the probe identifiers for the first two PubMed identifiers
  xx[1:2]
  # Get the first one
  xx[[1]]
  if(interactive() && require(annotate)){
    # Get article information as XML files for a PubMed id
    xmls <- pubmed(names(xx)[1], disp = "data")
    # View article information using a browser
    pubmed(names(xx)[1], disp = "browser")
  }
}

```

---

mta10transcriptclusterPROSITE

*Maps between Manufacturer Identifiers and PROSITE Identifiers*

---

## Description

mta10transcriptclusterPROSITE is an R object that provides mappings between manufacturer identifiers and PROSITE identifiers.

## Details

The bimap interface for PROSITE is defunct. Please use `select()` interface to PROSITE identifiers. See `?AnnotationDbi::select` for details.

---

`mta10transcriptclusterREFSEQ`*Map between Manufacturer Identifiers and RefSeq Identifiers*

---

## Description

`mta10transcriptclusterREFSEQ` is an R object that provides mappings between manufacturer identifiers and RefSeq identifiers.

## Details

Each manufacturer identifier is mapped to a named vector of RefSeq identifiers. The name represents the manufacturer identifier and the vector contains all RefSeq identifiers that can be mapped to that manufacturer identifier. The length of the vector may be one or greater, depending on how many RefSeq identifiers a given manufacturer identifier can be mapped to. An NA is reported for any manufacturer identifier that cannot be mapped to a RefSeq identifier at this time.

RefSeq identifiers differ in format according to the type of record the identifiers are for as shown below:

NG\XXXXXX: RefSeq accessions for genomic region (nucleotide) records

NM\XXXXXX: RefSeq accessions for mRNA records

NC\XXXXXX: RefSeq accessions for chromosome records

NP\XXXXXX: RefSeq accessions for protein records

XR\XXXXXX: RefSeq accessions for model RNAs that are not associated with protein products

XM\XXXXXX: RefSeq accessions for model mRNA records

XP\XXXXXX: RefSeq accessions for model protein records

Where XXXXXX is a sequence of integers.

NCBI <https://www.ncbi.nlm.nih.gov/RefSeq/> allows users to query the RefSeq database using RefSeq identifiers.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2021-Apr14

## References

<https://www.ncbi.nlm.nih.gov> <https://www.ncbi.nlm.nih.gov/RefSeq/>

## See Also

- [AnnotationDb-class](#) for use of the `select()` interface.

## Examples

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterREFSEQ
# Get the probe identifiers that are mapped to any RefSeq ID
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0) {
  # Get the REFSEQ for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

mta10transcriptclusterSYMBOL

*Map between Manufacturer Identifiers and Gene Symbols*

---

## Description

mta10transcriptclusterSYMBOL is an R object that provides mappings between manufacturer identifiers and gene abbreviations.

## Details

Each manufacturer identifier is mapped to an abbreviation for the corresponding gene. An NA is reported if there is no known abbreviation for a given gene.

Symbols typically consist of 3 letters that define either a single gene (ABC) or multiple genes (ABC1, ABC2, ABC3). Gene symbols can be used as key words to query public databases such as Entrez Gene.

Mappings were based on data provided by: Entrez Gene <ftp://ftp.ncbi.nlm.nih.gov/gene/DATA> With a date stamp from the source of: 2021-Apr14

## References

<https://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=gene>

## See Also

- [AnnotationDb-class](#) for use of the select() interface.

**Examples**

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterSYMBOL
# Get the probe identifiers that are mapped to a gene symbol
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0) {
  # Get the SYMBOL for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

mta10transcriptclusterUNIPROT

*Map Uniprot accession numbers with Entrez Gene identifiers*

---

**Description**

mta10transcriptclusterUNIPROT is an R object that contains mappings between the manufacturer identifiers and Uniprot accession numbers.

**Details**

This object is a simple mapping of manufacturer identifiers to Uniprot Accessions.

Mappings were based on data provided by NCBI (link above) with an exception for fly, which required retrieving the data from ensembl <http://www.ensembl.org/biomart/martview/>

**See Also**

- [AnnotationDb-class](#) for use of the select() interface.

**Examples**

```
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.

## Bimap interface:
x <- mta10transcriptclusterUNIPROT
# Get the entrez gene IDs that are mapped to an Uniprot ID
mapped_genes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_genes][1:300])
```

```

if(length(xx) > 0) {
  # Get the Uniprot IDs for the first five genes
  xx[1:5]
  # Get the first one
  xx[[1]]
}

```

---

mta10transcriptcluster\_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

```

mta10transcriptcluster_dbconn()
mta10transcriptcluster_dbfile()
mta10transcriptcluster_dbschema(file="", show.indices=FALSE)
mta10transcriptcluster_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

mta10transcriptcluster\_dbconn returns a connection object to the package annotation DB. **IMPORTANT:** Don't call [dbDisconnect](#) on the connection object returned by mta10transcriptcluster\_dbconn or you will break all the [AnnDbObj](#) objects defined in this package!

mta10transcriptcluster\_dbfile returns the path (character string) to the package annotation DB (this is an SQLite file).

mta10transcriptcluster\_dbschema prints the schema definition of the package annotation DB.

mta10transcriptcluster\_dbInfo prints other information about the package annotation DB.

## Value

mta10transcriptcluster\_dbconn: a DBIConnection object representing an open connection to the package annotation DB.

mta10transcriptcluster\_dbfile: a character string with the path to the package annotation DB.

mta10transcriptcluster\_dbschema: none (invisible NULL).

mta10transcriptcluster\_dbInfo: none (invisible NULL).

**See Also**

[dbGetQuery](#), [dbConnect](#), [dbconn](#), [dbfile](#), [dbschema](#), [dbInfo](#)

**Examples**

```
library(DBI)
## Count the number of rows in the "probes" table:
dbGetQuery(mta10transcriptcluster_dbconn(), "SELECT COUNT(*) FROM probes")

mta10transcriptcluster_dbschema()

mta10transcriptcluster_dbInfo()
```

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