htatranscriptcluster.db
March 27, 2024

htatranscriptclusterACCNUM
Map Manufacturer identifiers to Accession Numbers

Description
htatranscriptclusterACCNUM 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 <- hta20transcriptclusterACCNUM
# 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
hta20transcriptclusterALIAS2PROBE

Map between Common Gene Symbol Identifiers and Manufacturer Identifiers

Description

hta20transcriptclusterALIAS 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

```r
## 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(hta20transcriptclusterALIAS2PROBE)
if(length(xx) > 0){
  # Get the probe identifiers for the first two aliases
  xx[1:2]
  # Get the first one
  xx[[1]]
}
```
Welcome to the hta20transcriptcluster.db annotation Package. The purpose of this package is to provide detailed information about the hta20transcriptcluster 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

```r
## select() interface:
## Objects in this package can be accessed using the select() interface
## from the AnnotationDbi package. See ?select for details.
columns(hta20transcriptcluster.db)

## Bimap interface:
## The 'old style' of interacting with these objects is manipulation as
## bimaps. While this approach is still available we strongly encourage the
## use of select().
ls("package:hta20transcriptcluster.db")
```

Map Manufacturer IDs to Chromosomes

**Description**

hta20transcriptclusterCHR 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
hta20transcriptclusterCHRLENGTHS

See Also

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

Examples

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

## Bimap interface:
x <- hta20transcriptclusterCHR
# 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]]
}
```

hta20transcriptclusterCHRLENGTHS

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

Description

hta20transcriptclusterCHRLENGTHS 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

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

tt <- hta20transcriptclusterCHRLENGTHS
# Length of chromosome 1
tt["1"]

**Description**

hta20transcriptclusterCHRLOC 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 (Homo sapiens)

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

**See Also**

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

**Examples**

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

## Bimap interface:
x <- hta20transcriptclusterCHRLOC
# 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
```
Map Ensembl gene accession numbers with Entrez Gene identifiers

**Description**

*hta20transcriptclusterENSEMBL* is an R object that contains mappings between manufacturer identifiers and Ensembl gene accession numbers.

**Details**


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**

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

# Bimap interface:
x <- hta20transcriptclusterENSEMBL
# 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
```
hta20transcriptclusterENTREZID

Map between Manufacturer Identifiers and Entrez Gene

Description

hta20transcriptclusterENTREZID 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 consensus 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


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 <- hta20transcriptclusterENTREZID
# 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]]
}

hta20transcriptclusterENZYME

Maps between Manufacturer IDs and Enzyme Commission (EC) Numbers

Description

hta20transcriptclusterENZYME is an R object that provides mappings between manufacturer identifiers and EC numbers. hta20transcriptclusterENZYME2PROBE is an R object that maps Enzyme Commission (EC) numbers to manufacturer identifiers.

Details

When the hta20transcriptclusterENZYME 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 hta20transcriptclusterENZYME2PROBE, 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 hta20transcriptclusterENZYME2PROBE, 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](http://www.chem.qmul.ac.uk/iupac/jcbn/index.html#6)


References


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 <- hta20transcriptclusterENZYME
# 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 hta20transcriptclusterENZYME2PROBE to a list to see inside
x <- hta20transcriptclusterENZYME2PROBE
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]]
}
```
hta20transcriptclusterGENENAME

*Map between Manufacturer IDs and Genes*

**Description**

hta20transcriptclusterGENENAME 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**

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

## Bimap interface:
x <- hta20transcriptclusterGENENAME
# 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]]
}
```
**hta20transcriptclusterGO**

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

---

**Description**

hta20transcriptclusterGO 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 (hta20transcriptclusterGO2PROBE) do NOT associate the child terms from the GO ontology with the gene. Only the directly evidenced terms are represented here.

hta20transcriptclusterGO2ALLPROBES 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 hta20transcriptclusterGO2PROBE.

**Details**

If hta20transcriptclusterGO 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

If hta20transcriptclusterGO2ALLPROBES or hta20transcriptclusterGO2PROBE 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 an 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/go-basic.obo With a date stamp from the source of: 2021-02-01

References

See Also
• hta20transcriptclusterGO2ALLPROBES
• AnnotationDb-class for use of the select() interface.

Examples

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

## Bimap interface:
x <- hta20transcriptclusterGO
# 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 <- hta20transcriptclusterGO2PROBE
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]
```
hta20transcriptclusterMAP

Map between Manufacturer Identifiers and cytogenetic maps/bands

Description

hta20transcriptclusterMAP is an R object that provides mappings between manufacturer identifiers and cytoband locations.

Details

Each manufacturer identifier is mapped to a vector of cytoband locations. The vector length may be one or longer, if there are multiple reported chromosomal locations for a given gene. An NA is reported for any manufacturer identifiers that cannot be mapped to a cytoband at this time.

Cytogenetic bands for most higher organisms are labeled p1, p2, p3, q1, q2, q3 (p and q are the p and q arms), etc., counting from the centromere out toward the telomeres. At higher resolutions, sub-bands can be seen within the bands. The sub-bands are also numbered from the centromere out toward the telomere. Thus, a label of 7q31.2 indicates that the band is on chromosome 7, q arm, band 3, sub-band 1, and sub-sub-band 2.

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


See Also

- AnnotationDb-class for use of the select() interface.
Examples

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

## Bimap interface:
x <- hta20transcriptclusterMAP
# Get the probe identifiers that are mapped to any cytoband
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0) {
  # Get the MAP for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

### hta20transcriptclusterMAPCOUNTS

*Number of mapped keys for the maps in package hta20transcriptcluster.db*

#### Description

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

hta20transcriptclusterMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package hta20transcriptcluster.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.

### hta20transcriptclusterOMIM

*Map between Manufacturer Identifiers and Mendelian Inheritance in Man (MIM) identifiers*

#### Description

hta20transcriptclusterOMIM is an R object that provides mappings between manufacturer identifiers and OMIM identifiers.
Details

Each manufacturer identifier is mapped to a vector of OMIM identifiers. The vector length may be
one or longer, depending on how many OMIM identifiers the manufacturer identifier maps to. An
NA is reported for any manufacturer identifier that cannot be mapped to an OMIM identifier at this
time.

OMIM is based upon the book Mendelian Inheritance in Man (V. A. McKusick) and focuses primarily
on inherited or heritable genetic diseases. It contains textual information, pictures, and reference
information that can be searched using various terms, among which the MIM number is one.

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


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 <- hta20transcriptclusterOMIM
# Get the probe identifiers that are mapped to a OMIM ID
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes][1:300])
if(length(xx) > 0) {
  # Get the OMIM for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}

hta20transcriptclusterORGANISM

The Organism information for hta20transcriptcluster

Description

hta20transcriptclusterORGANISM is an R object that contains a single item: a character string that
names the organism for which hta20transcriptcluster was built. hta20transcriptclusterORGPKG 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, hta20transcriptclusterORGANISM provides a simple way to programmatically extract the organism name. hta20transcriptclusterORGPKG 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 centric information is ultimately extracted from. The full package name will always be this string plus the extension ".db". But most programatic acces will not require this extension, so its more convenient to leave it out.

See Also

• AnnotationDb-class for use of the select() interface.

Examples

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

## Bimap interface:
hta20transcriptclusterORGANISM
hta20transcriptclusterORGPKG
```

Description

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

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

htapathsclPATH2PROBE 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.ad.jp/pub/kegg/genes

With a date stamp from the source of: 2011-Mar15
hta20transcriptclusterPFAM

Maps between Manufacturer Identifiers and PFAM Identifiers

Description

hta20transcriptclusterPFAM 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.
Description

hta20transcriptclusterPMID is an R object that provides mappings between manufacturer identifiers and PubMed identifiers. hta20transcriptclusterPMID2PROBE is an R object that provides mappings between PubMed identifiers and manufacturer identifiers.

Details

When hta20transcriptclusterPMID 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 hta20transcriptclusterPMID2PROBE 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


See Also

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

Examples

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

## Bimap interface:
x <- hta20transcriptclusterPMID
# 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 <- hta20transcriptclusterPMID2PROBE
mapped_probes <- mappedkeys(x)
# Now convert the reverse map object hta20transcriptclusterPMID2PROBE 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")
    }
}

hta20transcriptclusterPROSITE

Maps between Manufacturer Identifiers and PROSITE Identifiers

Description

hta20transcriptclusterPROSITE 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.
Map between Manufacturer Identifiers and RefSeq Identifiers

**Description**

hta20transcriptclusterREFSEQ 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\_XXXXX**: RefSeq accessions for genomic region (nucleotide) records
- **NM\_XXXXX**: RefSeq accessions for mRNA records
- **NC\_XXXXX**: RefSeq accessions for chromosome records
- **NP\_XXXXX**: RefSeq accessions for protein records
- **XR\_XXXXX**: RefSeq accessions for model RNAs that are not associated with protein products
- **XM\_XXXXX**: RefSeq accessions for model mRNA records
- **XP\_XXXXX**: RefSeq accessions for model protein records

Where XXXXX is a sequence of integers.


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**


**See Also**

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

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

## Bimap interface:
x <- hta20transcriptclusterREFSEQ
# 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]]
}
```

hta20transcriptclusterSYMBOL

Map between Manufacturer Identifiers and Gene Symbols

Description

hta20transcriptclusterSYMBOL 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


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 <- hta20transcriptclusterSYMBOL
# 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]]
}

Description

hta20transcriptclusterUNIPROT 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 <- hta20transcriptclusterUNIPROT
# 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]])
hta20transcriptcluster_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

hta20transcriptcluster_dbconn()
hta20transcriptcluster_dbfile()
hta20transcriptcluster_dbschema(file="", show.indices=FALSE)
hta20transcriptcluster_dbInfo()

Arguments

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

Details

hta20transcriptcluster_dbconn returns a connection object to the package annotation DB. IMPORTANT: Don’t call dbDisconnect on the connection object returned by hta20transcriptcluster_dbconn or you will break all the AnnObj objects defined in this package!
hta20transcriptcluster_dbfile returns the path (character string) to the package annotation DB (this is an SQLite file).
hta20transcriptcluster_dbschema prints the schema definition of the package annotation DB.
hta20transcriptcluster_dbInfo prints other information about the package annotation DB.

Value

hta20transcriptcluster_dbconn: a DBIConnection object representing an open connection to the package annotation DB.
hta20transcriptcluster_dbfile: a character string with the path to the package annotation DB.
hta20transcriptcluster_dbschema: none (invisible NULL).
hta20transcriptcluster_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(hta20transcriptcluster_dbconn(), "SELECT COUNT(*) FROM probes")

hta20transcriptcluster_dbschema()

hta20transcriptcluster_dbInfo()
Index

* datasets
  hta20transcriptcluster.db, 3
  hta20transcriptcluster_dbconn, 23
  hta20transcriptclusterACCNUM, 1
  hta20transcriptclusterALIAS2PROBE, 2
  hta20transcriptclusterCHR, 3
  hta20transcriptclusterCHRLENGTHS, 4
  hta20transcriptclusterCHRLOC, 5
  hta20transcriptclusterENSEMBL, 6
  hta20transcriptclusterENTREZID, 7
  hta20transcriptclusterENZYME, 8
  hta20transcriptclusterGENENAME, 10
  hta20transcriptclusterGO, 11
  hta20transcriptclusterMAP, 13
  hta20transcriptclusterMAPCOUNTS, 14
  hta20transcriptclusterOMIM, 14
  hta20transcriptclusterORGANISM, 15
  hta20transcriptclusterPATH, 16
  hta20transcriptclusterPFAM, 17
  hta20transcriptclusterPMID, 18
  hta20transcriptclusterPROSITE, 19
  hta20transcriptclusterREFSEQ, 20
  hta20transcriptclusterSYMBOL, 21
  hta20transcriptclusterUNIPROT, 22

* utilities
  hta20transcriptcluster_dbconn, 23

AnnDbObj, 23

cat, 23
checkMAPCOUNTS, 14

dbconn, 24
dbConnect, 24
dbDisconnect, 23
dbfile, 24
dbGetQuery, 24
dbInfo, 24
dbschema, 24

hta20transcriptcluster
  (hta20transcriptcluster.db), 3
hta20transcriptcluster.db, 3
hta20transcriptcluster_dbconn, 23
hta20transcriptcluster_dbfile
  (hta20transcriptcluster_dbconn), 23
hta20transcriptcluster_dbInfo
  (hta20transcriptcluster_dbconn), 23
hta20transcriptcluster_dbschema
  (hta20transcriptcluster_dbconn), 23
hta20transcriptclusterACCNUM, 1
hta20transcriptclusterALIAS2PROBE, 2
hta20transcriptclusterCHR, 3
hta20transcriptclusterCHRLengths, 4
hta20transcriptclusterCHRLOC, 5
hta20transcriptclusterCHRLOCEND
  (hta20transcriptclusterCHRLOC), 5
hta20transcriptclusterENSEMBL, 6
hta20transcriptclusterENSEMBL2PROBE
  (hta20transcriptclusterENSEMBL), 6
hta20transcriptclusterENTREZID, 7
hta20transcriptclusterENZYME, 8
hta20transcriptclusterENZYME2PROBE
  (hta20transcriptclusterENZYME), 8
hta20transcriptclusterGENENAME, 10
hta20transcriptclusterGO, 11
hta20transcriptclusterG02ALLPROBES, 12
hta20transcriptclusterG02ALLPROBES
  (hta20transcriptclusterGO), 11
hta20transcriptclusterG02PROBE
  (hta20transcriptclusterGO), 11
hta20transcriptclusterLOCUSID
  (hta20transcriptclusterENTREZID), 7
hta20transcriptclusterMAP, 13
hta20transcriptclusterMAPCOUNTS, 14
hta20transcriptclusterOMIM, 14
hta20transcriptclusterORGANISM, 15
hta20transcriptclusterORGPKG
  (hta20transcriptclusterORGANISM), 15
hta20transcriptclusterPATH, 16
hta20transcriptclusterPATH2PROBE
  (hta20transcriptclusterPATH), 16
hta20transcriptclusterPFAM, 17
hta20transcriptclusterPMID, 18
hta20transcriptclusterPMID2PROBE
  (hta20transcriptclusterPMID), 18
hta20transcriptclusterPROSITE, 19
hta20transcriptclusterREFSEQ, 20
hta20transcriptclusterSYMBOL, 21
hta20transcriptclusterUNIPROT, 22
hta20transcriptclusterUNIPROT2PROBE
  (hta20transcriptclusterUNIPROT), 22