illuminaRatv1.db

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Description

illuminaRatv1ACCNUM 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: 2015-Mar17

Examples

```r
x <- illuminaRatv1ACCNUM
# Get the probe identifiers that are mapped to an ACCNUM
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the ACCNUM for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```
 illuminaRatv1ALIAS2PROBE

Map between Common Gene Symbol Identifiers and Manufacturer Identifiers

Description

illuminaRatv1ALIAS 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: 2015-Mar17

Examples

# Convert the object to a list
xx <- as.list(illuminaRatv1ALIAS2PROBE)
if(length(xx) > 0){
  # Get the probe identifiers for the first two aliases
  xx[1:2]
  # Get the first one
  xx[[1]]
}

 illuminaRatv1.db  Bioconductor annotation data package

Description

Welcome to the illuminaRatv1.db annotation Package. The purpose of this package is to provide detailed information about the illuminaRatv1 platform. This package is updated biannually.

You can learn what objects this package supports with the following command:

ls("package:illuminaRatv1.db")

Each of these objects has their own manual page detailing where relevant data was obtained along with some examples of how to use it.
Examples

ls("package:illuminaRatv1.db")

---

**illuminaRatv1CHR**  
*Map Manufacturer IDs to Chromosomes*

**Description**

**illuminaRatv1CHR** 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: 2015-Mar17

**Examples**

```r
x <- illuminaRatv1CHR
# Get the probe identifiers that are mapped to a chromosome
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the CHR for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

**illuminaRatv1CHRLENGTHS**  
*A named vector for the length of each of the chromosomes*

**Description**

**illuminaRatv1CHRLENGTHS** 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.

Examples

```r
tt <- illuminaRatv1CHRLENGTHS
# Length of chromosome 1
 tt["1"]
```

 illuminaRatv1CHRLOC  
Map Manufacturer IDs to Chromosomal Location

Description

illuminaRatv1CHRLOC 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 (Rattus norvegicus) ftp://hgdownload.cse.ucsc.edu/goldenPath/rn6 With a date stamp from the source of: 2014-Aug1

Examples

```r
x <- illuminaRatv1CHRLOC
# Get the probe identifiers that are mapped to chromosome locations
 mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
    # Get the CHRLOC for the first five probes
    xx[1:5]
    # Get the first one
    xx[[1]]
}
```
illuminArnRatv1ENSEMBL

Description

illuminArnRatv1ENSEMBL 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 is 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.

Examples

x <- illuminArnRatv1ENSEMBL
# 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])
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:
# Convert to a list
xx <- as.list(illuminaRatv1ENSEMBL2PROBE)
if(length(xx) > 0){
  # Gets the entrez gene IDs for the first five Ensembl IDs
  xx[1:5]
  # Get the first one
  xx[[1]]
}
illuminaRatv1ENTREZID  
*Map between Manufacturer Identifiers and Entrez Gene*

**Description**

 illuminaRatv1ENTREZID 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 cannot 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: 2015-Mar17

**References**


**Examples**

```r
x <- illuminaRatv1ENTREZID
# 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])
if(length(xx) > 0) {
    # Get the ENTREZID for the first five probes
    xx[1:5]
    # Get the first one
    xx[[1]]
}
```

illuminaRatv1ENZYME  
*Maps between Manufacturer IDs and Enzyme Commission (EC) Numbers*

**Description**

illuminaRatv1ENZYME is an R object that provides mappings between manufacturer identifiers and EC numbers. illuminaRatv1ENZYME2PROBE is an R object that maps Enzyme Commission (EC) numbers to manufacturer identifiers.
**Details**

When the illuminaRatv1ENZYME maping 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 illuminaRatv1ENZYME2PROBE, 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/](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 illuminaRatv1ENZYME2PROBE, 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)

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

**References**


**Examples**

```r
x <- illuminaRatv1ENZYME
# 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])
if(length(xx) > 0) {
  # Get the ENZYME for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```
 illuminaRatv1GENENAME  

Map between Manufacturer IDs and Genes

Description

illuminaRatv1GENENAME 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: 2015-Mar17

Examples

```
x <- illuminaRatv1GENENAME
# 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])
if(length(xx) > 0) {
    # Get the GENENAME for the first five probes
    xx[1:5]
    # Get the first one
    xx[[1]]
}
```
illuminaRatv1GO

Maps between manufacturer IDs and Gene Ontology (GO) IDs

Description

illuminaRatv1GO 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 (illuminaRatv1GO2PROBE) do NOT associate the child terms from the GO ontology with the gene. Only the directly evidenced terms are represented here.

illuminaRatv1GO2ALLPROBES 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 illuminaRatv1GO2PROBE.

Details

If illuminaRatv1GO 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:

If illuminaRatv1GO2ALLPROBES or illuminaRatv1GO2PROBE 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 ftp://ftp.geneontology.org/pub/go/godatabase/archive/latest-lite/ With a date stamp from the source of: 20150314

References


See Also

illuminaRatv1GO2ALLPROBES.

Examples

```r
x <- illuminaRatv1GO
# 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])
if(length(xx) > 0) {
    # Try the first one
got <- xx[[1]]
got[[1]]["GOID"]
got[[1]]["Ontology"]
got[[1]]["Evidence"]
}
# For the reverse map:
# Convert to a list
xx <- as.list(illuminaRatv1GO2PROBE)
if(length(xx) > 0){
    # Gets the manufacturer ids for the top 2nd and 3nd 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]])
}
# Convert illuminaRatv1GO2ALLPROBES to a list
xx <- as.list(illuminaRatv1GO2ALLPROBES)
if(length(xx) > 0){
    # Gets the manufacturer identifiers for the top 2nd and 3nd GO identifiers
    goids <- xx[2:3]
    # Gets all the manufacturer identifiers for the first element of goids
```
illuminaRatv1MAPCOUNTS

Number of mapped keys for the maps in package illuminaRatv1.db

Description

illuminaRatv1MAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package illuminaRatv1.db.

Details

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

See Also

mappedkeys, count.mappedkeys, checkMAPCOUNTS

Examples

illuminaRatv1MAPCOUNTS
mapnames <- names(illuminaRatv1MAPCOUNTS)
illuminaRatv1MAPCOUNTS[mapnames[1]]
scratch <- get(mapnames[1])
sum(!is.na(as.list(scratch)))
count.mappedkeys(scratch)  # much faster!

## Check the "map count" of all the maps in package illuminaRatv1.db
checkMAPCOUNTS("illuminaRatv1.db")

 illuminaRatv1listNewMappings

Custom mappings added to the package

Description

We have used an extensive re-annotation of the illuminaRatv1 probe sequences to provide additional information that is not captured in the standard Bioconductor packages. Whereas Bioconductor annotations are based on the RefSeq ID that each probe maps to, our additional mappings provide data specific to each probe on the platform. See below for details. We recommend using the probe quality as a form of filtering, and retaining only perfect or good probes for an analysis.
Details of custom mappings

**illuminaRatl1listNewMappings** List all the custom re-annotation mappings provided by the package

**illuminaRatl1fullReannotation** Return all the re-annotation information as a matrix

**illuminaRatl1ARRAYADDRESS** Array Address code used to identify the probe at the bead-level

**illuminaRatl1NUID** Lumi’s nuid (universal naming scheme for oligonucleotides) Reference: Du et al. (2007), Biol Direct 2:16

**illuminaRatl1PROBESEQUENCE** The 50 base sequence for the probe

**illuminaRatl1PROBEQUALITY** Quality grade assigned to the probe: “Perfect” if it perfectly and uniquely matches the target transcript; “Good” if the probe, although imperfectly matching the target transcript, is still likely to provide considerably sensitive signal (up to two mismatches are allowed, based on empirical evidence that the signal intensity for 50-mer probes with less than 95% identity to the respective targets is less than 50% of the signal associated with perfect matches *); “Bad” if the probe matches repeat sequences, intergenic or intronic regions, or is unlikely to provide specific signal for any transcript; “No match” if it does not match any genomic region or transcript.

**illuminaRatl1CODOINGZONE** Coding status of target sequence: intergenic / intronic / Transcriptomic (“Transcriptomic” when the target transcript is non-coding or there is no information on the coding sequence)

**illuminaRatl1GENOMICLOCATION** Probe’s genomic coordinates (hg19 for human, mm9 for mouse or rn4 for rat)

**illuminaRatl1GENOMICMATCHSIMILARITY** Percentage of similarity between the probe and its best genomic match in the alignable region, taking the probe as reference

**illuminaRatl1SECONDMATCHES** Genomic coordinates of second best matches between the probe and the genome

**illuminaRatl1SECONDMATCHSIMILARITY** Percentage of similarity between the probe and its second best genomic match in the alignable region, taking the probe as reference

**illuminaRatl1TRANSCRIPTOMICMATCHSIMILARITY** Percentage of similarity between the probe and its target transcript in the alignable region, taking the probe as reference

**illuminaRatl1OTHERGENOMICMATCHES** Genomic coordinates of sequences as alignable with the probe (in terms of number of matching nucleotides) as its main target

**illuminaRatl1REPEATMASK** Overlapping RepeatMasked sequences, with number of bases overlapped by the repeat

**illuminaRatl1OVERLAPINGSNP** Overlapping annotated SNPs

**illuminaRatl1ENTREZREANNOTATED** Entrez IDs

**illuminaRatl1ENSEMBLREANNOTATED** Ensembl IDs

**illuminaRatl1SYMBOLREANNOTATED** Gene symbol derived by re-annotation

**illuminaRatl1REPORTERGROUPID** For probes marked as controls in Illumina’s annotation file, these gives the type of control

**illuminaRatl1REPORTERGROUPNAME** Usually a more informative name for the control type
References

http://remoat.sysbiol.cam.ac.uk

Examples

##See what new mappings are available

```r
illuminaRatv1listNewMappings()
```

```r
x <- illuminaRatv1PROBEQUALITY
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
    # Get the PROBEQUALITY for the first five probes
    xx[1:5]
    # Get the first one
    xx[[1]]
}
```

##Overall table of qualities

```r
table(unlist(xx))
```

```r
x <- illuminaRatv1ARRAYADDRESS
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
    # Get the ARRAYADDRESS for the first five probes
    xx[1:5]
    # Get the first one
    xx[[1]]
}
```

##Can do the mapping from array address to illumina ID using a revmap

```r
y<- revmap(illuminaRatv1ARRAYADDRESS)
```

```r
mapped_probes <- mappedkeys(y)
# Convert to a list
yy <- as.list(y[mapped_probes])
if(length(yy) > 0) {
    # Get the ARRAYADDRESS for the first five probes
    yy[1:5]
}
# The Organism information for illuminaRatv1

### Description

`illuminaRatv1ORGANISM` is an R object that contains a single item: a character string that names the organism for which `illuminaRatv1` was built. `illuminaRatv1ORGPKG` 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, `illuminaRatv1ORGANISM` provides a simple way to programmatically extract the organism name. `illuminaRatv1ORGPKG` 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 accesses will not require this extension, so it's more convenient to leave it out.
**Description**

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

 illuminaRatv1PATH maps probe identifiers to the identifiers used by KEGG for pathways in which the genes represented by the probe identifiers are involved

 illuminaRatv1PATH2PROBE 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](http://www.bioconductor.org).


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**


**Examples**

```r
x <- illuminaRatv1PATH
# 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])
if(length(xx) > 0){
  # Get the PATH for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}

# Now convert the illuminaRatv1PATH2PROBE object to a list
xx <- as.list(illuminaRatv1PATH2PROBE)
if(length(xx) > 0){
```
# illuminaRatv1PMID

## Maps between Manufacturer Identifiers and PubMed Identifiers

**Description**

`illuminaRatv1PMID` is an R object that provides mappings between manufacturer identifiers and PubMed identifiers. `illuminaRatv1PMID2PROBE` is an R object that provides mappings between PubMed identifiers and manufacturer identifiers.

**Details**

When `illuminaRatv1PMID` 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 `illuminaRatv1PMID2PROBE` 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: 2015-Mar17

**References**


**Examples**

```r
x <- illuminaRatv1PMID
# 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])
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")
  }
}

# Now convert the reverse map object illuminaRatv1PMID2PROBE to a list
xx <- as.list(illuminaRatv1PMID2PROBE)
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")
  }
}

---

**illuminaRatv1REFSEQ**  
*Map between Manufacturer Identifiers and RefSeq Identifiers*

**Description**

*illuminaRatv1REFSEQ* 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: 2015-Mar17

References

Examples

```r
x <- illuminaRatv1REFSEQ
# 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])
if(length(xx) > 0) {
  # Get the REFSEQ for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

 illuminaRatv1SYMBOL  Map between Manufacturer Identifiers and Gene Symbols

Description

illuminaRatv1SYMBOL 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: 2015-Mar17

References

Examples

```r
x <- illuminaRatv1SYMBOL
# 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])
if(length(xx) > 0) {
  # Get the SYMBOL for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

 illuminaRatv1UNIGENE  Map between Manufacturer Identifiers and UniGene cluster identifiers

Description

illuminaRatv1UNIGENE is an R object that provides mappings between manufacturer identifiers and UniGene identifiers.

Details

Each manufacturer identifier is mapped to a UniGene identifier. An NA is reported if the manufacturer identifier cannot be mapped to UniGene at this time.

A UniGene identifier represents a cluster of sequences of a gene. Using UniGene identifiers one can query the UniGene database for information about the sequences or the Entrez Gene database for information about the genes.

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: 2015-Mar17

References


Examples

```r
x <- illuminaRatv1UNIGENE
# Get the probe identifiers that are mapped to a UNIGENE ID
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the UNIGENE for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```
illuminaRatv1UNIPROT  
Map Uniprot accession numbers with Entrez Gene identifiers

Description

illuminaRatv1UNIPROT 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/](http://www.ensembl.org/biomart/martview/)

Examples

```r
x <- illuminaRatv1UNIPROT  
# 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])  
if(length(xx) > 0) {  
  # Get the Uniprot IDs for the first five genes  
  xx[1:5]  
  # Get the first one  
  xx[[1]]  
}
```

illuminaRatv1_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

```r
illuminaRatv1_dbconn()  
illuminaRatv1_dbfile()  
illuminaRatv1_dbschema(file='', show.indices=FALSE)  
illuminaRatv1_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

illuminaRatv1_dbconn returns a connection object to the package annotation DB. IMPORTANT: Don’t call dbDisconnect on the connection object returned by illuminaRatv1_dbconn or you will break all the AnnDbObj objects defined in this package!

illuminaRatv1_dbfile returns the path (character string) to the package annotation DB (this is an SQLite file).

illuminaRatv1_dbschema prints the schema definition of the package annotation DB.

illuminaRatv1_dbInfo prints other information about the package annotation DB.

Value

illuminaRatv1_dbconn: a DBIConnection object representing an open connection to the package annotation DB.

illuminaRatv1_dbfile: a character string with the path to the package annotation DB.

illuminaRatv1_dbschema: none (invisible NULL).

illuminaRatv1_dbInfo: none (invisible NULL).

See Also

dbGetQuery, dbConnect, dbconn, dbfile, dbschema, dbInfo

Examples

## Count the number of rows in the "probes" table:

dbGetQuery(illuminaRatv1_dbconn(), "SELECT COUNT(*) FROM probes")

illuminaRatv1_dbschema()

illuminaRatv1_dbInfo()
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