

# gahgu133b.db

February 28, 2017

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gahgu133bALIAS

*Map between Manufacturer IDs and Genes Alias*

---

## Description

gahgu133bALIAS is an R object that maps manufacturer identifiers to the corresponding gene alias.

## Details

Each manufacturer identifier maps to a vector containing the gene alias. If the gene alias is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

## Examples

```
x <- gahgu133bALIAS
# Get the probe identifiers that are mapped to gene alias
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the gene ALIAS for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

gahgu133bALIAS2PROBE

*Map between Common Gene Symbol Identifiers and probeset Identifiers*

---

## Description

gahgu133bALIAS is an R object that provides mappings between common gene symbol identifiers and probeset identifiers.

**Details**

Each gene symbol is mapped to a vector of probeset identifiers. The vector contains all probeset identifiers that are found for that symbol. An NA is reported for any gene symbol that cannot be mapped to any probeset 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: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
# Convert the object to a list
xx <- as.list(gahgu133bALIAS2PROBE)
if(length(xx) > 0){
  # Get the probe identifiers for the first two aliases
  xx[1:2]
  # Get the first one
  xx[[1]]
}
```

---

gahgu133b.db

*Bioconductor annotation data package*


---

**Description**

Welcome to the gahgu133b.db annotation Package. The purpose of this package is to provide detailed information about the gahgu133b platform.

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

```
ls("package:gahgu133b.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:gahgu133b.db")
```

---

gahgu133bCHR

*Map probeset IDs to Chromosomes*


---

**Description**

gahgu133bCHR is an R object that provides mappings between a probeset identifier and the chromosome that contains the gene of interest.

**Details**

Each probeset identifier maps to a vector of chromosomes. If the chromosomal location is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bCHR
# 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]]
}
```

---

gahgu133bCHRLOC

*Map probeset IDs to Chromosomal Location*


---

**Description**

gahgu133bCHRLOC is an R object that maps probeset 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 probeset identifier maps to a named vector of chromosomal locations, where the name indicates the chromosome. 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.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bCHRLOC
# 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]]
}
```

---

gahgu133bDESCRIPTIONS *Map between probeset IDs and gene descriptions*

---

### Description

gahgu133bDESCRIPTIONS is an R object that maps probeset identifiers to the corresponding gene name.

### Details

Each probeset identifier maps to a named vector containing the gene descriptions. The vector name corresponds to the source of each description. If the gene name is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

### Examples

```
x <- gahgu133bDESCRIPTIONS
# Get the probe identifiers that are mapped to a gene description
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the DESCRIPTIONS for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

gahgu133bENTREZID *Map between probeset Identifiers and Entrez Gene*

---

### Description

gahgu133bENTREZID is an R object that provides mappings between probeset identifiers and Entrez Gene identifiers. gahgu133bENTREZID2PROBE provides the reverse mapping.

### Details

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

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bENTREZID
# 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]]
}
```

---

gahgu133bGENECARDSID *Map between probeset IDs and Genes*

---

**Description**

gahgu133bGENECARDSID is an R object that maps probeset identifiers to the corresponding Genecards id.

**Details**

Each probeset identifier maps to a vector containing the Genecards id.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bGENECARDSID
# Get the probe identifiers that are mapped to a Genecards id.
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the GENECARDSID for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

gahgu133bGENEEND *Map between probeset IDs and Genes end*

---

**Description**

gahgu133bGENEEND is an R object that maps probeset identifiers to the corresponding gene end.

**Details**

Each probeset identifier maps to a vector containing the gene end. If the gene end is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bGENEEND
# Get the probe identifiers that are mapped to a gene end
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the GENEEND for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

gahgu133bGENENAME      *Map between probeset IDs and Genes*

---

**Description**

gahgu133bGENENAME is an R object that maps probeset identifiers to the corresponding gene name.

**Details**

Each probeset identifier maps to a vector containing the gene name. If the gene name is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bGENENAME
# 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]]
}
```

---

gahgu133bGENESTART      *Map between probeset IDs and Genes start*

---

**Description**

gahgu133bGENESTART is an R object that maps probeset identifiers to the corresponding gene start.

## Details

Each probeset identifier maps to a vector containing the gene start. If the gene start is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

## Examples

```
x <- gahgu133bGENESTART
# Get the probe identifiers that are mapped to a gene start
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the GENESTART for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

gahgu133bGENESTRAND    *Map between probeset IDs and Genes strand*

---

## Description

gahgu133bGENESTRAND is an R object that maps probeset identifiers to the corresponding gene strand.

## Details

Each probeset identifier maps to a vector containing the gene strand. If the gene strand is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

## Examples

```
x <- gahgu133bGENESTRAND
# Get the probe identifiers that are mapped to a gene strand
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the GENESTRAND for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

gahgu133bGO

*Map between probset IDs and Gene Ontology (GO)***Description**

gahgu133bGO is an R object that provides mappings between probesets and the GO identifiers that they are directly associated with.

**Details**

Each probeset 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 Entrez Gene id. 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

NAs are assigned to probe 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.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bGO
# Get the probe identifiers that are mapped to a GO ID
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Try the first one
  got <- xx[[1]]
  got[[1]][["GOID"]]
  got[[1]][["Ontology"]]
}
```



```

      got[[1]][["Evidence"]]
    }

```

---

gahgu133bGO2PROBE      *Map between Gene Ontology (GO) and probesets*

---

## Description

gahgu133bGO2PROBE is an R object that provides mappings between GO identifiers and probesets.

## Details

Each GO term maps to a named vector of probesets. The name associated with each probeset corresponds to the evidence code for that GO identifier. The evidence code indicates what kind of evidence supports the association between the GO and Entrez Gene identifiers. Evidence codes currently 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 GO identifier may be mapped to the same probe 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.

Mappings were based on data provided by:

Genecards ( <http://www.genecards.org> ) on 2010-Nov22

## Examples

```

# Convert to a list
xx <- as.list(gahgu133bGO2PROBE)
if(length(xx) > 0){
  # Get the probe identifiers for the top 2nd and 3rd GO identifiers
  goids <- xx[2:3]
  # Get the probe identifiers for the first element of goids
  goids[[1]]
  # Evidence code for the mappings
  names(goids[[1]])
}

```

gahgu133bINTERPRODOMAIN

*Map between Manufacturer IDs and Genes*

---

**Description**

gahgu133bINTERPRODOMAIN is an R object that maps probeset identifiers to the corresponding Interpro domain.

**Details**

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

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bINTERPRODOMAIN
# Get the probe identifiers that are mapped to an Interpro domain
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the INTERPRODOMAIN for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

gahgu133bINTERPROID*Map between probesets and Interpro ID*

---

**Description**

gahgu133bINTERPROID is an R object that maps manufacturer identifiers to the corresponding Interpro ID.

**Details**

Each probeset maps to a named vector containing the Interpro IDs. If the Interpro ID is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bINTERPROID
# Get the probe identifiers that are mapped to an Interpro ID
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the INTERPROID for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

gahgu133bKEGGID

*Map between probesets and KEGG pathway ID***Description**

gahgu133bKEGGID is an R object that maps probe identifiers to the corresponding KEGG pathway ID.

**Details**

Each probeset maps to a vector containing the KEGG pathway ID. If the KEGG pathway ID is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bKEGGID
# 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 KEGGID for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

gahgu133bKEGGNAME

*Map between probesets and KEGG pathway name***Description**

gahgu133bKEGGNAME is an R object that maps probe identifiers to the corresponding KEGG pathway name.

**Details**

Each probeset maps to a named vector containing the KEGG pathway name. The vector name corresponds to the KEGG pathway ID. If the KEGG pathway name is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bKEGGNAME
# Get the probe identifiers that are mapped to a KEGG pathway name
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the KEGGNAME for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

gahgu133bMAPCOUNTS      *Number of mapped keys for the maps in package gahgu133b.db*

---

**Description**

gahgu133bMAPCOUNTS provides the "map count" (i.e. the count of mapped keys) for each map in package gahgu133b.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**

```
gahgu133bMAPCOUNTS
mapnames <- names(gahgu133bMAPCOUNTS)
gahgu133bMAPCOUNTS[mapnames[1]]
x <- get(mapnames[1])
sum(!is.na(as.list(x)))
count.mappedkeys(x)    # much faster!

## Check the "map count" of all the maps in package gahgu133b.db
checkMAPCOUNTS("gahgu133b.db")
```

---

gahgu133bORGANISM      *The Organism for gahgu133b*

---

### Description

gahgu133bORGANISM is an R object that contains a single item: a character string that names the organism for which gahgu133b was built.

### Details

Although the package name is suggestive of the organism for which it was built, gahgu133bORGANISM provides a simple way to programmatically extract the organism name.

### Examples

```
gahgu133bORGANISM
```

---

gahgu133bSWISSPROTID      *Map between probesets and Genes*

---

### Description

gahgu133bSWISSPROTID is an R object that maps probe identifiers to the corresponding swissprot id.

### Details

Each probeset maps to a vector containing the swissprot id. If the swissprot id is unknown, the vector will contain an NA.

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

### Examples

```
x <- gahgu133bSWISSPROTID
# Get the probe identifiers that are mapped to a swissprot id
mapped_probes <- mappedkeys(x)
# Convert to a list
xx <- as.list(x[mapped_probes])
if(length(xx) > 0) {
  # Get the SWISSPROTID for the first five probes
  xx[1:5]
  # Get the first one
  xx[[1]]
}
```

---

gahgu133bSYMBOL      *Map between probeset and Gene Symbols*

---

### Description

gahgu133bSYMBOL is an R object that provides mappings between probeset and gene abbreviations. gahgu133bSYMBOL2PROBE provides the reverse mapping.

### Details

Each probeset 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: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

### References

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

### Examples

```
x <- gahgu133bSYMBOL
# 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]]
}
```

---

gahgu133bUNIPROT      *Map Uniprot accession numbers with probeset identifiers*

---

### Description

gahgu133bUNIPROT is an R object that contains mappings between probeset identifiers and Uniprot accession numbers.

### Details

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

Mappings were based on data provided by: Genecards ( <http://www.genecards.org> ) on 2010-Nov22

**Examples**

```
x <- gahgu133bUNIPROT
# Get the probeset 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]]
}
```

gahgu133b\_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**

```
gahgu133b_dbconn()
gahgu133b_dbfile()
gahgu133b_dbschema(file="", show.indices=FALSE)
gahgu133b_dbInfo()
```

**Arguments**

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

**Details**

`gahgu133b_dbconn` returns a connection object to the package annotation DB. **IMPORTANT:** Don't call `dbDisconnect` on the connection object returned by `gahgu133b_dbconn` or you will break all the `AnnDbObj` objects defined in this package!

`gahgu133b_dbfile` returns the path (character string) to the package annotation DB (this is an SQLite file).

`gahgu133b_dbschema` prints the schema definition of the package annotation DB.

`gahgu133b_dbInfo` prints other information about the package annotation DB.

**Value**

`gahgu133b_dbconn`: a `DBConnection` object representing an open connection to the package annotation DB.

`gahgu133b_dbfile`: a character string with the path to the package annotation DB.

`gahgu133b_dbschema`: none (invisible NULL).

`gahgu133b_dbInfo`: none (invisible NULL).

**See Also**

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

**Examples**

```
## Count the number of rows in the "probes" table:  
dbGetQuery(gahgu133b_dbconn(), "SELECT COUNT(*) FROM probes")  
  
## The connection object returned by gahgu133b_dbconn() was created with:  
dbConnect(SQLite(), dbname=gahgu133b_dbfile(), cache_size=64000, synchronous=0)  
  
gahgu133b_dbschema()  
  
gahgu133b_dbInfo()
```



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