

# annaffy

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.aaf.character      *Generic constructor for classes extending character*

---

### Description

Retrieve annotation from a character data source.

### Usage

```
.aaf.character(probeids, chip, type, class)
```

### Arguments

probeids	character vector containing probe ids
chip	name of chip
type	type of annotation
class	class of object to be created

### Value

A list of objects of class `class` containing the annotation data of from the `type` dataset for the given `probeids`. NA values are returned as empty objects.

### Note

Written at the NASA Center for Computational Astrobiology  
<http://cca.arc.nasa.gov/>

### Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

---

aafChromLoc-class    *Class aafChromLoc, a class for gene chromosome locations*

---

### Description

An abstraction for gene chromosome locations from Bioconductor data packages.

### Objects from the Class

Objects are generally created by the [aafChromLoc](#) constructor. Objects can also be created manually by calls of the form `new("aafChromLoc", description)`.

### Slots

**.Data:** Object of class `integer`

### Extends

Class `integer`, from data part.

### Methods

No methods defined with class "aafChromLoc" in the signature. See generic implementations of [getText](#), [getURL](#), [getHTML](#), [getTD](#), and [getCSS](#).

### Author(s)

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

### See Also

[aafChromLoc](#)

---

aafChromLoc    *Constructor for aafChromLoc objects*

---

### Description

For the given `probeids`, constructs an `aafList` of `aafChromLoc` objects containing annotation data from the `chip` data package.

### Usage

```
aafChromLoc(probeids, chip)
```

### Arguments

<code>probeids</code>	character vector containing probe ids
<code>chip</code>	name of the chip data package

**Value**

An `aafList` of `aafChromLoc` objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafChromLoc-class](#)

**Examples**

```
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  locations <- aafChromLoc(probes, "hgu95av2.db")
  show(locations[6:10])
}
```

---

aafChromosome-class

*Class aafChromosome, a class for gene chromosome assignments*

---

**Description**

An abstraction for gene gene chromosome assignments from Bioconductor data packages.

**Objects from the Class**

Objects are generally created by the `aafChromosome` constructor. Objects can also be created manually by calls of the form `new("aafChromosome", description)`.

**Slots**

**.Data:** Object of class `character`

**Extends**

Class `character`, from data part.

**Methods**

No methods defined with class "aafChromosome" in the signature. See generic implementations of `getText`, `getURL`, `getHTML`, `getTD`, and `getCSS`.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafChromosome](#)

---

aafChromosome      *Constructor for aafChromosome objects*

---

### Description

For the given `probeids`, constructs an `aafList` of `aafChromosome` objects containing annotation data from the `chip` data package.

### Usage

```
aafChromosome(probeids, chip)
```

### Arguments

`probeids`      character vector containing probe ids  
`chip`            name of the chip data package

### Value

An `aafList` of `aafChromosome` objects. NA values are returned as empty objects.

### Author(s)

Colin A. Smith, (annaffy@colinsmith.org)

### See Also

[aafChromosome-class](#)

### Examples

```
if (require(hgu95av2.db)) {  
  data(aafExpr)  
  probes <- featureNames(aafExpr)  
  chromosomes <- aafChromosome(probes, "hgu95av2.db")  
  show(chromosomes[6:10])  
}
```

---

aafCytoband-class      *Class aafCytoband, a class for cytoband data*

---

### Description

An abstraction for cytoband data from Bioconductor data packages.

### Objects from the Class

Objects are generally created by the `aafCytoband` constructor. Objects can also be created manually by calls of the form `new("aafCytoband", band, genbank)`.

**Slots**

**band:** Object of class `character` containing genomic cytoband

**gene:** Object of class `character` containing Gene ID

**Methods**

**getText** (aafCytoband): Returns text of band.

**getURL** (aafCytoband): Returns a URL corresponding entry in NCBI's cytoband map viewer.

See generic implementations of [getHTML](#), [getTD](#), and [getCSS](#).

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafCytoband](#)

---

aafCytoband

*Constructor for aafCytoband objects*

---

**Description**

For the given `probeids`, constructs an `aafList` of `aafCytoband` objects containing annotation data from the `chip` data package.

**Usage**

```
aafCytoband(probeids, chip)
```

**Arguments**

`probeids`      character vector containing probe ids

`chip`            name of the chip data package

**Value**

An `aafList` of `aafCytoband` objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafCytoband-class](#)

## Examples

```
if (require(hgu95av2.db)) {  
  data(aafExpr)  
  probes <- featureNames(aafExpr)  
  bands <- aafCytoband(probes, "hgu95av2.db")  
  show(bands[6:10])  
}
```

---

aafDescription-class

*Class aafDescription, a class for gene descriptions*

---

## Description

An abstraction for gene description from Bioconductor data packages.

## Objects from the Class

Objects are generally created by the [aafDescription](#) constructor. Objects can also be created manually by calls of the form `new("aafDescription", description)`.

## Slots

**.Data:** Object of class character

## Extends

Class character, from data part.

## Methods

No methods defined with class "aafDescription" in the signature. See generic implementations of [getText](#), [getURL](#), [getHTML](#), and [getTD](#).

## Author(s)

Colin A. Smith, <[annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)>

## See Also

[aafDescription](#)

---

aafDescription      *Constructor for aafDescription objects*

---

### Description

For the given probeids, constructs an aafList of aafDescription objects containing annotation data from the chip data package.

### Usage

```
aafDescription(probeids, chip)
```

### Arguments

probeids	character vector containing probe ids
chip	name of the chip data package

### Value

An aafList of aafDescription objects. NA values are returned as empty objects.

### Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

### See Also

[aafDescription-class](#)

### Examples

```
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  descriptions <- aafDescription(probes, "hgu95av2.db")
  show(descriptions[6:10])
}
```

---

aafExpr      *Sample ExpressionSet used for demonstration purposes*

---

### Description

Contains expression values for 250 probe ids with 8 samples. Two covariates are provided. Expression comes from the hgu95av2 chip.

### Details

The data is real but anonymized. 250 genes expression values were chosen at random from an existing ExpressionSet. Another 250 probe ids were selected at random and were assigned to the expression values. That way, expression values do not correspond to the true probe ids.

Post-processing was done with `rma()` in `affy` 1.2.23.



---

aafGenBank-class     *Class aafGenBank, a class for GenBank accession numbers*

---

### Description

An abstraction for GenBank accession numbers from Bioconductor data packages.

### Objects from the Class

Objects are generally created by the [aafGenBank](#) constructor. Objects can also be created manually by calls of the form `new("aafGenBank", accnum)`.

### Slots

**.Data:** Object of class `character`

### Extends

Class `character`, from data part.

### Methods

**getURL** (aafGenBank): Returns a URL to the corresponding entry in NCBI's GenBank database. See generic implementations of [getText](#), [getHTML](#), and [getTD](#).

### Author(s)

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

### See Also

[aafGenBank](#)

---

aafGenBank     *Constructor for aafGenBank objects*

---

### Description

For the given `probeids`, constructs an `aafList` of `aafGenBank` objects containing annotation data from the `chip` data package.

### Usage

```
aafGenBank(probeids, chip)
```

### Arguments

<code>probeids</code>	character vector containing probe ids
<code>chip</code>	name of the chip data package

**Value**

An `aafList` of `aafGenBank` objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafGenBank-class](#)

**Examples**

```
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  gbs <- aafGenBank(probes, "hgu95av2.db")
  show(gbs[6:10])
}
```

---

aafGO-class

*Class aafGO, a class for gene ontology ids*

---

**Description**

An abstraction for gene ontology ids from Bioconductor data packages. This class is actually extends `aafList` and holds `aafGOItem` objects which have the actual annotation data.

**Objects from the Class**

Objects are generally created by the `aafGO` constructor. Objects can also be created manually by calls of the form `new("aafGO", list(goitems))`.

**Slots**

**.Data:** Object of class `list`

**Extends**

Class `aafList`, from data part.

**Methods**

**getText** (aafGO): Returns a comma delimited list of the individual `aafGOItem` objects.

**getURL** (aafGO): Returns a single URL to an AmiGO page which displays all the gene ontology identifiers in an hierarchical listing.

**getHTML** (aafGO): Returns an HTML representation of each of the individual `aafGOItem` objects, concatenated together.

**getTD** (aafGO): Returns an HTML table cell representation with the class set to "aafGO".

**getCSS** (aafGOItem): Returns a line of CSS that indents GOItem paragraphs.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafGO](#), [aafGOItem](#), [aafList](#)

---

aafGOItem-class      *Class aafGOItem, a class for gene ontology id elements*

---

**Description**

An abstraction for gene ontology id elements from Bioconductor data packages. Multiple instances of this class are held by the wrapper class `aafGO`.

**Objects from the Class**

Objects are generally created by the `aafGO` constructor. Objects can also be created manually by calls of the form `new("aafGOItem", id, name, type)`.

**Slots**

**id:** Object of class `character` containing GO id  
**name:** Object of class `character` containing textual name  
**type:** Object of class `character` containing GO subtype  
**evid:** Object of class `character` containing GO evidence code

**Methods**

**getText** (aafGOItem): Returns textual representation formatted "id: name".  
**getURL** (aafGOItem): Returns a URL to the corresponding gene ontology entry on AmiGO.  
**getHTML** (aafGOItem): Returns an HTML representation including the URL link, gene ontology name, and rollover subtype.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafGO-class](#), [aafGO](#)

---

`aafGO`*Constructor for aafGO objects*

---

**Description**

For the given `probeids`, constructs an `aafList` of `aafGO` objects containing annotation data from the chip data package.

**Usage**

```
aafGO(probeids, chip)
```

**Arguments**

<code>probeids</code>	character vector containing probe ids
<code>chip</code>	name of the chip data package

**Value**

An `aafList` of `aafGO` objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafGO-class](#)

**Examples**

```
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  gos <- aafGO(probes, "hgu95av2.db")
  show(gos[6:10])
}
```

---

`.aaf.goterm`*Fetch Gene Ontology term information*

---

**Description**

Given a Gene Ontology number, return its type and name.

**Usage**

```
.aaf.goterm(num)
```

**Arguments**

num                    Gene Ontology number - should be formatted GO:XXXXXXX

**Value**

A list with components

type                    Type of GO record, either Biological Process, Cellular Component, or Molecular Function.

name                    A character vector containing the GO name.

**Note**

Written at the NASA Center for Computational Astrobiology  
<http://cca.arc.nasa.gov/>

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

---

aaf.handler                    *Handle fetching annotation data columns*

---

**Description**

Dispatches requests for annotation data to the correct function. Alternatively returns a list of all the columns it supports.

**Usage**

```
aaf.handler(probeids, chip, name)
```

**Arguments**

probeids                character vector containing probe ids

chip                    name of chip

name                    name of the column of data to return

**Value**

An `aafList` containing objects of the proper class.

If no arguments are passed, it will return a character vector of the columns currently supported.

**Note**

Written at the NASA Center for Computational Astrobiology  
<http://cca.arc.nasa.gov/>

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

---

`.aaf.integer`      *Generic constructor for classes extending integer*

---

### Description

Retrieve annotation from an integer data source.

### Usage

```
.aaf.integer(probeids, chip, type, class)
```

### Arguments

<code>probeids</code>	character vector containing probe ids
<code>chip</code>	name of chip
<code>type</code>	type of annotation
<code>class</code>	class of object to be created

### Value

A list of objects of class `class` containing the annotation data of from the `type` dataset for the given `probeids`. NA values are returned as empty objects.

### Note

Written at the NASA Center for Computational Astrobiology  
<http://cca.arc.nasa.gov/>

### Author(s)

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

---

`aafIntensity-class`      *Class aafIntensity, a class for gene expression values*

---

### Description

A class for displaying gene expression values with a green background of differing intensities.

### Objects from the Class

Objects are generally created by the `aafTableInt` constructor. Objects can also be created manually by calls of the form `new("aafIntensity", intensity)`.

### Slots

**.Data:** Object of class `numeric`

**Extends**

Class `numeric`, from data part.

**Methods**

**getTD** (aafIntensity): Returns an HTML table cell with background varying from white to green depending on intensity. Scaling is controlled by two options, `minIntensity` (fully white) and `maxIntensity` (fully green), usually set by `writeHTML`.

See generic implementations of `getText`, `getURL`, `getHTML`, and `getCSS`.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafTableInt](#)

---

aafList-class

*Class aafList, a specialized subclass of list*

---

**Description**

A class for lists of annotation data objects.

**Objects from the Class**

Objects are generally created by any of the annotation data constructors that are also part of this package. Objects can also be created manually by calls of the form `new("aafList", list)`.

**Slots**

**.Data:** Object of class `list`

**Extends**

Class `list`, from data part.

**Methods**

**getText** (aafList): Returns a character vector containing textual representations of every item.

**getURL** (aafList): Returns a character vector containing single URLs (if possible) of every item.

**getHTML** (aafList): Returns a character vector containing HTML representations of every item.

**getTD** (aafList): Returns a character vector containing HTML table cell representations of every item.

**getCSS** (aafList): Returns `getCSS()` of the first item in the list.

**[** (aafList): Returns a subset of `aafList` as another `aafList` object.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

---

aafLocusLink-class *Class aafLocusLink, a class for LocusLink ids*

---

### Description

An abstraction for LocusLink ids from Bioconductor data packages.

### Objects from the Class

Objects are generally created by the `aafLocusLink` constructor. Objects can also be created manually by calls of the form `new("aafLocusLink", id)`.

### Slots

**.Data:** Object of class `integer`

### Extends

Class `integer`, from data part.

### Methods

**getURL** (aafLocusLink): Returns a URL to the corresponding entry in NCBI's LocusLink database. On the rare chance that more than one id is defined, more than one URL will be returned.

See generic implementations of `getText`, `getHTML`, and `getTD`.

### Author(s)

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

### See Also

[aafLocusLink](#)

---

aafLocusLink *Constructor for aafLocusLink objects*

---

### Description

For the given `probeids`, constructs an `aafList` of `aafLocusLink` objects containing annotation data from the `chip` data package.

### Usage

```
aafLocusLink(probeids, chip)
```

### Arguments

<code>probeids</code>	character vector containing probe ids
<code>chip</code>	name of the chip data package



**Value**

An `aafList` of `aafLocusLink` objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafLocusLink-class](#)

**Examples**

```
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  lls <- aafLocusLink(probes, "hgu95av2.db")
  show(lls[6:10])
}
```

---

aafPathway-class    *Class aafPathway, a class for KEGG pathway ids*

---

**Description**

An abstraction for KEGG pathway ids from Bioconductor data packages. This class is actually extends `aafList` and holds `aafPathwayItem` objects which have the actual annotation data.

**Objects from the Class**

Objects are generally created by the `aafPathway` constructor. Objects can also be created manually by calls of the form `new("aafPathway", list(pathwayitems))`.

**Slots**

**.Data:** Object of class `list`

**Extends**

Class `aafList`, from data part.

**Methods**

**getText** (aafGO): Returns a comma delimited list of the individual `aafPathwayItem` objects.

**getURL** (aafGO): Returns zero length character vector because this method is not valid for this class.

**getHTML** (aafGO): Returns an HTML representation of each of the individual `aafPathwayItem` objects, concatenated together.

**getTD** (aafGO): Returns an HTML table cell representation with the class set to "aafPathway".

**getCSS** (aafGO): Returns a line of CSS which intends `PathwayItem` paragraphs.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafPathway](#), [aafPathwayItem](#), [aafList](#)

---

aafPathwayItem-class

*Class aafPathwayItem, a class for KEGG pathway id elements*

---

**Description**

An abstraction for KEGG pathway id elements from Bioconductor data packages. Multiple instances of this class are held by the wrapper class `aafPathway`.

**Objects from the Class**

Objects are generally created by the `aafPathway` constructor. Objects can also be created manually by calls of the form `new("aafPathwayItem", id, name, enzyme)`.

**Slots**

**id:** Object of class `character` containing KEGG pathway id

**name:** Object of class `character` containing textual name

**enzyme:** Object of class `character` containing the Enzyme Commission number if applicable

**Methods**

**getText** (aafPathwayItem): Returns textual representation formatted "id: name".

**getURL** (aafPathwayItem): Returns a URL to the corresponding entry in the Kyoto Encyclopedia of Genes and Genomes database. If there is a corresponding EC number, it will be highlighted in red.

**getHTML** (aafPathwayItem): Returns an HTML representation including the URL link and pathway name.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafPathway-class](#), [aafPathway](#)

---

aafPathway                    *Constructor for aafPathway objects*

---

### Description

For the given `probeids`, constructs an `aafList` of `aafPathway` objects containing annotation data from the `chip` data package.

### Usage

```
aafPathway(probeids, chip)
```

### Arguments

`probeids`            character vector containing probe ids  
`chip`                name of the chip data package

### Value

An `aafList` of `aafPathway` objects. NA values are returned as empty objects.

### Author(s)

Colin A. Smith, (annaffy@colinsmith.org)

### See Also

[aafPathway-class](#)

### Examples

```
if (require(hgu95av2.db)) {  
  data(aafExpr)  
  probes <- featureNames(aafExpr)  
  pathways <- aafPathway(probes, "hgu95av2.db")  
  show(pathways[6:10])  
}
```

---

aafProbe-class            *Class aafProbe, a class for Probe ids*

---

### Description

An abstraction for Affymetrix ProbeSet ids.

### Objects from the Class

Objects are generally created by the `aafProbe` constructor. Objects can also be created manually by calls of the form `new("aafProbe", id)`.

**Slots**

**.Data:** Object of class character

**Extends**

Class character, from data part.

**Methods**

**getURL** (aafProbe): Returns a URL to the annotation found in the Affymetrix NetAffx Analysis Center.

See generic implementations of [getText](#), [getHTML](#), and [getTD](#).

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafProbe](#)

---

aafProbe

*Constructor for aafProbe objects*

---

**Description**

For the given probeids, constructs an aafList of aafProbe objects.

**Usage**

```
aafProbe (probeids)
```

**Arguments**

probeids      character vector containing probe ids

**Value**

An aafList of aafProbe objects.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafProbe-class](#)

## Examples

```
if (require(hgu95av2.db)) {  
  data(aafExpr)  
  probes <- featureNames(aafExpr)  
  probesets <- aafProbe(probes)  
  getURL(probesets[6:10])  
}
```

---

aafPubMed-class      *Class aafPubMed, a class for PubMed ids*

---

## Description

An abstraction for LocusLink ids from Bioconductor data packages.

## Objects from the Class

Objects are generally created by the [aafPubMed](#) constructor. Objects can also be created manually by calls of the form `new("aafPubMed", id)`.

## Slots

**.Data:** Object of class `integer`

## Extends

Class `integer`, from data part.

## Methods

**getURL** (aafPubMed): Returns a single URL to the corresponding abstracts in NCBI's PubMed database.

**getHTML** (aafPubMed): Returns an HTML link along with the number of abstracts.

**getTD** (aafPubMed): Returns an HTML table cell representation with the class set to "aafPubMed".

**getCSS** (aafPubMed): Returns a line of CSS which centers the PubMed link.

## Author(s)

Colin A. Smith, {[annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)}

## See Also

[aafPubMed](#)

---

`aafPubMed`*Constructor for aafPubMed objects*

---

**Description**

For the given `probeids`, constructs a list of `aafPubMed` objects containing annotation data from the `chip` data package.

**Usage**

```
aafPubMed(probeids, chip)
```

**Arguments**

<code>probeids</code>	character vector containing probe ids
<code>chip</code>	name of the chip data package

**Value**

An `aafList` of `aafPubMed` objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafPubMed-class](#)

**Examples**

```
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  pmids <- aafPubMed(probes, "hgu95av2.db")
  show(pmids[6:10])
}
```

---

`.aaf.raw`*Fetch raw annotation data*

---

**Description**

Retrieve annotation data from a data package, loading the library if necessary.

**Usage**

```
.aaf.raw(probeids, chip, type)
```

**Arguments**

probeids	character vector containing probe ids
chip	name of chip, see details
type	type of annotation, see details

**Details**

The core workings of this function depend on an (informal) protocol used in creating the BioConductor Affymetrix annotation data packages. Based on currently published (and unpublished) data packages, the current protocol includes the following features:

The package is named after the chip, `<chip name>`

The package contains datasets named `<chip name><data type>`

**Value**

A list of annotation data for the given probeids. Each list contains a sub-list containing the actual data.

**Note**

Written at the NASA Center for Computational Astrobiology

<http://cca.arc.nasa.gov/>

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

---

aafSearchGO

*Find probe ids corresponding to GO ids*


---

**Description**

Searches Gene Ontology ids for corresponding probe ids in a given chip, optionally including descendants.

**Usage**

```
aafSearchGO(chip, ids, descendants = TRUE, logic = "OR")
```

**Arguments**

chip	name of the chip data package
ids	numeric or character vector of GO ids
descendants	logical, include GO descendants?
logic	type of logic to use, "AND" or "OR"

**Value**

A character vector of probe ids matching the search criteria.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafSearchText](#)

---

aafSearchText      *Search metadata annotation text*

---

**Description**

Searches Bioconductor metadata annotation package text for specific strings or Perl compatible regular expressions.

**Usage**

```
aafSearchText(chip, colnames, text, logic = "OR")
```

**Arguments**

chip	name of the chip data package
colnames	character vector of metadata column names to search
text	character vector of strings/regular expressions to match
logic	type of logic to use, "AND" or "OR"

**Value**

A character vector of probe ids matching the search criteria.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafSearchGO](#)

**Examples**

```
if (require(hgu95av2.db)) {  
  aafSearchText("hgu95av2.db", "Description", c("kinase", "interferon"))  
  # aafSearchText("hgu95av2.db", c("Gene Ontology", "Pathway"), "ribosome")  
}
```



---

aafSigned-class      *Class aafSigned, a class for signed numerical data*

---

### Description

A class for displaying signed numerical data with different styles depending on the sign.

### Objects from the Class

Objects are generally created by the [aafTable](#) constructor. Objects can also be created manually by calls of the form `new("aafSigned", signedval)`.

### Slots

**.Data:** Object of class `numeric`

### Extends

Class `numeric`, from data part.

### Methods

**getTD** (aafSigned): Returns an HTML table cell with class differentially set based on sign. `aafSignedPos` is used for positive values. `aafSignedNeg` is used for negative values. `aafSignedZero` is used for zero values.

**getCSS** (aafSigned): Returns two lines of CSS that set the cell background of positive values light blue and negative values light red.

See generic implementations of [getText](#), [getURL](#), and [getHTML](#).

### Author(s)

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

### See Also

[aafTable](#)

---

aafSymbol-class      *Class aafSymbol, a class for gene symbols*

---

### Description

An abstraction for gene symbol from Bioconductor data packages.

### Objects from the Class

Objects are generally created by the [aafSymbol](#) constructor. Objects can also be created manually by calls of the form `new("aafSymbol", description)`.

**Slots**

**.Data:** Object of class `character` with gene symbol

**Extends**

Class `character`, from data part.

**Methods**

No methods defined with class "aafSymbol" in the signature. See generic implementations of [getText](#), [getURL](#), [getHTML](#), and [getTD](#).

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafSymbol](#)

---

aafSymbol

*Constructor for aafSymbol objects*

---

**Description**

For the given `probeids`, constructs a list of `aafSymbol` objects containing annotation data from the `chip` data package.

**Usage**

```
aafSymbol(probeids, chip)
```

**Arguments**

<code>probeids</code>	character vector containing probe ids
<code>chip</code>	name of the chip data package

**Value**

An `aafList` of `aafSymbol` objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafSymbol-class](#)

## Examples

```
if (require(hgu95av2.db)) {  
  data(aafExpr)  
  probes <- featureNames(aafExpr)  
  symbols <- aafSymbol(probes, "hgu95av2.db")  
  show(symbols[6:10])  
}
```

---

aafTableAnn                      *Constructor for aafTable objects from annotation data*

---

## Description

Constructs an aafTable object given a set of probe ids and desired annotation types.

## Usage

```
aafTableAnn(probeids, chip, colnames = aaf.handler(chip = chip), widget = FALSE)
```

## Arguments

probeids	character vector of probe ids
chip	name of the data package in which the annotation data is stored
colnames	character vector of annotation types
widget	boolean, use widget to select columns?

## Value

An aafTable object.

## Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

## See Also

[aafTable-class](#)

---

aafTable-class      *Class aafTable, a tabular microarray data class*

---

## Description

A class for storing and flexible output of microarray data to HTML and text formats.

## Objects from the Class

Objects are generally created by any of the annotation table constructors that are also part of this package. Objects can also be created manually by calls of the form `new("aafList", probeids, table)`.

## Slots

**probeids**: Object of class `character` containing the probe ids for each row of the table.

**table**: Object of class `list` containing `aafList` objects all of the same length, representing the columns of the table. Each item in the list must have a unique name.

## Methods

**probeids** (aafTable): Returns a character vector containing the probe ids for each row of the table.

**probeids<-** (aafTable): Sets the probe ids for the table rows. Can be set to `character(0)` if unknown or not applicable.

**colnames** (aafTable): Returns a character vector containing the names of the columns stored in the table.

**colnames<-** (aafTable): Set the column names for the table. Each must be unique.

**dim** (aafTable): Returns the dimensions of the table.

**merge** (aafTable, aafTable, all = FALSE, all.x = all, all.y = all, suffixes = c(".x", ".y")): Merges two tables together, aligning common probe ids if possible. Duplicate column names are given suffixes to make them unique. Returns the merged table.

**rbind** (aafTable, aafTable, ...): Vertically combines tables by row. Requires that column names be identical and that all tables either have probe ids defined or not.

[ Returns a subset of the table based on [row, column]. Indices may be passed as integers or probe ids/column names.

[[ Returns the given table column. This also supports recursive subsetting to address columns, then cells, then sub-cells (if applicable). See [Extract](#) for more information.

\$ Returns the given table column.

**saveHTML** (aafTable, filename, title = "Bioconductor Affymetrix Probe Listing", colnames = colnames(aafTable), range = 1:dim(aafTable)[1], open = FALSE, widget = FALSE): Saves the table to HTML with the specified filename and title. Both the columns and the range of table rows can be specified. Range can either be specified as a character vector of probe ids or an integer vector of row positions. One can also specify whether to open the resulting file in the browser and whether to use a widget for column selection.

**saveText** (aafTable, filename, header = TRUE, colnames = colnames(aafTable), range = 1:dim(aafTable)[1], widget = FALSE): Saves the table to tab delimited text with specified filename and optional header. Both the columns and the range of table rows can be specified. Range can either be specified as a character vector of probe ids or an integer vector of row positions. One can also specify whether to use a widget for column selection.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafTable](#), [aafTableFrame](#), [aafTableAnn](#), [aafTableInt](#)

---

aafTableFrame      *Constructor for aafTable objects from data frames*

---

**Description**

Constructs an `aafTable` object given a data frame.

**Usage**

```
aafTableFrame(frame, colnames = names(frame), probeids = row.names(frame),  
              signed = FALSE)
```

**Arguments**

<code>frame</code>	data frame to be converted to the table
<code>colnames</code>	character vector of column names
<code>probeids</code>	character vector of probe ids associated with each row
<code>signed</code>	boolean, should each column be colored based on the sign?

**Value**

An `aafTable` object.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafTable-class](#)

---

aafTableInt                      *Constructor for aafTable objects from ExpressionSets*

---

### Description

Constructs an aafTable object containing expression values given an ExpressionSet.

In the resulting HTML table, the expression values will have backgrounds with varying intensities of green depending on the expression measure.

### Usage

```
aafTableInt(exprSet, colnames = sampleNames(exprSet),
            probeids = featureNames(exprSet))
```

### Arguments

exprSet	object of class ExpressionSet
colnames	character vector of column names
probeids	character vector of probe ids associated with each row

### Value

An aafTable object.

### Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

### See Also

[aafTable-class](#), [aafIntensity](#)

---

aafTable                      *Constructor for aafTable objects*

---

### Description

Constructs an aafTable object given vectors, lists, or aafList objects.

### Usage

```
aafTable(..., items = list(...), colnames = names(items),
         probeids = character(0), signed = FALSE)
```

**Arguments**

<code>...</code>	named arguments, one for each column
<code>items</code>	alternatively a named list of the items to be put in the table
<code>colnames</code>	character vector of column names
<code>probeids</code>	character vector of probe ids associated with each row
<code>signed</code>	boolean, should each column be colored based on the sign?

**Value**

An `aafTable` object.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafTable-class](#)

---

`aafUniGene-class`    *Class aafUniGene, a class for UniGene cluster ids*

---

**Description**

An abstraction for UniGene cluster ids from Bioconductor data packages.

**Objects from the Class**

Objects are generally created by the `aafUniGene` constructor. Objects can also be created manually by calls of the form `new("aafUniGene", id)`.

**Slots**

**.Data:** Object of class `character`

**Extends**

Class `character`, from data part.

**Methods**

**getURL** (`aafUniGene`): Returns a URLs to the corresponding entry in NCBI's UniGene database. On the rare chance that more than one id is defined, more than one URL will be returned.

**getHTML** (`aafUniGene`): Returns an HTML representation with a link to the UniGene database. On the rare chance that more than one id is defined, more than one link will be returned.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

**See Also**

[aafUniGene](#)

---

aafUniGene                      *Constructor for aafUniGene objects*

---

**Description**

For the given probeids, constructs a list of aafUniGene objects containing annotation data from the chip data package.

**Usage**

```
aafUniGene(probeids, chip)
```

**Arguments**

probeids	character vector containing probe ids
chip	name of the chip data package

**Value**

An aafList of aafUniGene objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

[aafUniGene-class](#)

**Examples**

```
if (require(hgu95av2.db)) {  
  data(aafExpr)  
  probes <- featureNames(aafExpr)  
  ugs <- aafUniGene(probes, "hgu95av2.db")  
  show(ugs[6:10])  
}
```

---

chkPkgs                      *A Function to Check for and Install Missing Annotation Packages*

---

**Description**

This is a wrapper function that calls all the necessary functions to detect missing annotation packages, ensure all versions are compatible with the current version of annaffy, and download required packages. This is an internal function and should not be called by the end user.

**Usage**

```
chkPkgs(pkg)
```



**Arguments**

pkg                    The chip-level annotation package

**Details**

This function checks for the correct chip-level package, and if it is not installed will download and install. In the case that there are two versions of the same package installed, the function will return the library location of the package with the correct version.

**Value**

This function doesn't return anything; it is only called for its side effect of loading or installing a chip-level annotation package.

**Author(s)**

James W. MacDonald <jmacdon@med.umich.edu> and Jeff Gentry <jgentry@jimmy.harvard.edu>

---

getCSS-methods                    *Methods for function getCSS*

---

**Description**

Methods to get relevant stylesheet lines for an object.

**Methods**

**object = ANY** Returns an empty character vector.

**Note**

For information about other implementations of this method, see documentation of the respective class.

**See Also**

[aafList-class](#), [aafPubMed-class](#), [aafGO-class](#), [aafPathway-class](#), [aafSigned-class](#)

---

getHTML-methods      *Methods for function getHTML*

---

### Description

Methods to get an HTML representation of an object.

### Methods

**object = ANY** Returns text of `object` along with URL link if applicable. If `object` is floating point, it displays a fixed number of significant digits as specified by the `sigfigs` option (default 6).

### Note

For information about other implementations of this method, see documentation of the respective class.

### See Also

[aafList-class](#), [aafPubMed-class](#), [aafGO-class](#), [aafGOItem-class](#), [aafPathway-class](#), [aafPathwayItem-class](#)

---

getTD-methods      *Methods for function getTD*

---

### Description

Methods to get an HTML table cell representation of an object.

### Methods

**object = ANY** Returns `<td>` tag containing HTML representation of `object`. Sets class attribute to `class(object)`.

### Note

For information about other implementations of this method, see documentation of the respective class.

### See Also

[aafList-class](#), [aafGO-class](#), [aafPathway-class](#), [aafIntensity-class](#)

---

getText-methods      *Methods for function getText*

---

**Description**

Methods to get a textual representation of an object.

**Methods**

**object = ANY** Returns a comma delimited list of the elements in `list`.

**Note**

For information about other implementations of this method, see documentation of the respective class.

**See Also**

[aafList-class](#), [aafCytoband-class](#), [aafGO-class](#), [aafGOItem-class](#), [aafPathway-class](#), [aafPathwayItem-class](#)

---

getURL-methods      *Methods for function getURL*

---

**Description**

Methods to get a URL link to a web resource for an object.

**Methods**

**object = ANY** Returns an empty character vector.

**Note**

For information about other implementations of this method, see documentation of the respective class.

**See Also**

[aafList-class](#), [aafGenBank-class](#), [aafLocusLink-class](#), [aafCytoband-class](#), [aafUniGene-class](#), [aafPubMed-class](#), [aafGO-class](#), [aafGOItem-class](#), [aafPathwayItem-class](#)

---

`is.annpkg` *Determine if packages contain annotation*

---

### Description

Checks to see that the given packages contain all the necessary annotation environments to be usable by `annaffy`.

### Usage

```
is.annpkg(packages, lib.loc = NULL)
```

### Arguments

`packages` character vector containing package names to check

`lib.loc` a character vector with path names of `R` libraries, or `NULL`. The default value of `NULL` corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.

### Value

A logical vector indicating whether the packages contain annotation data.

### Author(s)

Colin A. Smith, [⟨annaffy@colinsmith.org⟩](mailto:annaffy@colinsmith.org)

### Examples

```
pkgnames <- installed.packages()[,"Package"]
pkgnames <- pkgnames[1:5]
pkgnames[is.annpkg(pkgnames)]
```

---

`selectorWidget` *Dialog to select items from a list*

---

### Description

Presents the user with a dialog box to select items from a list.

### Usage

```
selectorWidget(options, selected = character(0), title = "Selector",
               ordersel = FALSE, ordernsel = FALSE,
               height = max(10, min(20, length(options))))
```

**Arguments**

<code>options</code>	vector, options to be selected from
<code>selected</code>	vector, subset of options selected by default
<code>title</code>	character scalar, window title
<code>ordersel</code>	boolean, keep the selected items in order?
<code>ordernsel</code>	boolean, keep the not selected items in order?
<code>height</code>	scalar, height of the two listboxes

**Value**

A character vector containing the selected items. If a vector of a different class was initially provided, it must be manually coerced back to the correct type.

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)

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