

# Package ‘annaffy’

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**Title** Annotation tools for Affymetrix biological metadata

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**Depends** R (>= 2.5.0), methods, Biobase, BiocManager, GO.db

**Imports** AnnotationDbi (>= 0.1.15), DBI

**Suggests** hgu95av2.db, multtest, tcltk

**Description** Functions for handling data from Bioconductor Affymetrix annotation data packages. Produces compact HTML and text reports including experimental data and URL links to many online databases. Allows searching biological metadata using various criteria.

**License** LGPL

**LazyLoad** yes

**biocViews** OneChannel, Microarray, Annotation, GO, Pathways, ReportWriting

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## Contents

.aaf.character . . . . .	2
.aaf.goterm . . . . .	3
.aaf.integer . . . . .	4
.aaf.raw . . . . .	4
aaf.handler . . . . .	5
aafChromLoc . . . . .	6
aafChromLoc-class . . . . .	7
aafChromosome . . . . .	7

aafChromosome-class . . . . .	8
aafCytoband . . . . .	9
aafCytoband-class . . . . .	9
aafDescription . . . . .	10
aafDescription-class . . . . .	11
aafExpr . . . . .	12
aafGenBank . . . . .	12
aafGenBank-class . . . . .	13
aafGO . . . . .	13
aafGO-class . . . . .	14
aafGOItem-class . . . . .	15
aafIntensity-class . . . . .	16
aafList-class . . . . .	16
aafLocusLink . . . . .	17
aafLocusLink-class . . . . .	18
aafPathway . . . . .	19
aafPathway-class . . . . .	19
aafPathwayItem-class . . . . .	20
aafProbe . . . . .	21
aafProbe-class . . . . .	22
aafPubMed . . . . .	22
aafPubMed-class . . . . .	23
aafSearchGO . . . . .	24
aafSearchText . . . . .	24
aafSigned-class . . . . .	25
aafSymbol . . . . .	26
aafSymbol-class . . . . .	27
aafTable . . . . .	27
aafTable-class . . . . .	28
aafTableAnn . . . . .	29
aafTableFrame . . . . .	30
aafTableInt . . . . .	31
chkPkgs . . . . .	31
getCSS-methods . . . . .	32
getHTML-methods . . . . .	32
getTD-methods . . . . .	33
getText-methods . . . . .	33
getURL-methods . . . . .	34
is.annpkg . . . . .	34
selectorWidget . . . . .	35

**Index** **36**

---

.aaf.character	<i>Generic constructor for classes extending character</i>
----------------	--

---

**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](mailto:annaffy@colinsmith.org)>

---

.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:XXXXXX
-----	--

### 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.integer                      *Generic constructor for classes extending integer*

---

**Description**

Retrieve annotation from an integer data source.

**Usage**

```
.aaf.integer(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>

---

.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>

---

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>

---

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**

probeids	character vector containing probe ids
chip	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>

**See Also**

[aafChromLoc-class](#)

**Examples**

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

---

aafChromLoc-class	<i>Class aafChromLoc, a class for gene chromosome locations</i>
-------------------	---

---

**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](#)

---

aafChromosome	<i>Constructor for aafChromosome objects</i>
---------------	--

---

**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])
}
```

---

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>

**See Also**

[aafChromosome](#)



---

aafCytoband	<i>Constructor for aafCytoband objects</i>
-------------	--

---

**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>

**See Also**

[aafCytoband-class](#)

**Examples**

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

---

aafCytoband-class	<i>Class aafCytoband, a class for cytoband data</i>
-------------------	---

---

**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 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>

**See Also**

[aafCytoband](#)

---

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])  
}
```

---

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>

**See Also**

[aafDescription](#)

---

aafExpr	<i>Sample ExpressionSet used for demonstration purposes</i>
---------	---

---

**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	<i>Constructor for aafGenBank objects</i>
------------	---

---

**Description**

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

**Usage**

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

**Arguments**

probeids	character vector containing probe ids
chip	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>

**See Also**

[aafGenBank-class](#)

**Examples**

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

---

aafGenBank-class	<i>Class aafGenBank, a class for GenBank accession numbers</i>
------------------	--

---

**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>

**See Also**

[aafGenBank](#)

---

aafGO	<i>Constructor for aafGO objects</i>
-------	--------------------------------------

---

**Description**

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

**Usage**

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

**Arguments**

probeids	character vector containing probe ids
chip	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>

**See Also**

[aafGO-class](#)

**Examples**

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

---

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](mailto: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

*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**

probeids            character vector containing probe ids

chip                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>

**See Also**

[aafLocusLink-class](#)

**Examples**

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

---

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@colinasmith.org](mailto:annaffy@colinasmith.org)>

**See Also**

[aafLocusLink](#)

---

aafPathway	<i>Constructor for aafPathway objects</i>
------------	---

---

**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])  
}
```

---

aafPathway-class	<i>Class aafPathway, a class for KEGG pathway ids</i>
------------------	---

---

**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 (no longer supported)

**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](#)

---

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])  
}
```

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](#)

---

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**

probeids            character vector containing probe ids

chip                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>

**See Also**

[aafPubMed-class](#)

**Examples**

```
if (require(hgu95av2.db)) {  
  data(aafExpr)  
  probes <- featureNames(aafExpr)  
  pmids <- aafPubMed(probes, "hgu95av2.db")  
  show(pmids[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>

**See Also**[aafPubMed](#)

---

`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**

<code>chip</code>	name of the chip data package
<code>ids</code>	numeric or character vector of GO ids
<code>descendants</code>	logical, include GO descendants?
<code>logic</code>	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	<i>Class aafSigned, a class for signed numerical data</i>
-----------------	---

---

**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>

**See Also**

[aafTable](#)

---

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**

probeids	character vector containing probe ids
chip	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>

**See Also**

[aafSymbol-class](#)

**Examples**

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

---

aafSymbol-class	<i>Class aafSymbol, a class for gene symbols</i>
-----------------	--

---

**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>

**See Also**

[aafSymbol](#)

---

aafTable	<i>Constructor for aafTable objects</i>
----------	---

---

**Description**

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

**Usage**

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

**Arguments**

...	named arguments, one for each column
items	alternatively a named list of the items to be put in the table
colnames	character vector of column names
probeids	character vector of probe ids associated with each row
signed	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](#)

---

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](#)

---

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](#)

---

aafTableFrame	<i>Constructor for aafTable objects from data frames</i>
---------------	--

---

**Description**

Constructs an aafTable object given a data frame.

**Usage**

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

**Arguments**

frame	data frame to be converted to the table
colnames	character vector of column names
probeids	character vector of probe ids associated with each row
signed	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	<i>Constructor for aafTable objects from ExpressionSets</i>
-------------	---

---

**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](#)

---

chkPkgs	<i>A Function to Check for and Install Missing Annotation Packages</i>
---------	--

---

**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>

**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**

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

# Index

## \* classes

- aafChromLoc-class, 7
- aafChromosome-class, 8
- aafCytoband-class, 9
- aafDescription-class, 11
- aafGenBank-class, 13
- aafGO-class, 14
- aafGOItem-class, 15
- aafIntensity-class, 16
- aafList-class, 16
- aafLocusLink-class, 18
- aafPathway-class, 19
- aafPathwayItem-class, 20
- aafProbe-class, 22
- aafPubMed-class, 23
- aafSigned-class, 25
- aafSymbol-class, 27
- aafTable-class, 28

## \* datasets

- aafExpr, 12

## \* file

- .aaf.character, 2
- .aaf.goterm, 3
- .aaf.integer, 4
- .aaf.raw, 4
- aaf.handler, 5
- aafChromLoc, 6
- aafChromosome, 7
- aafCytoband, 9
- aafDescription, 10
- aafGenBank, 12
- aafGO, 13
- aafLocusLink, 17
- aafPathway, 19
- aafProbe, 21
- aafPubMed, 22
- aafSearchGO, 24
- aafSearchText, 24
- aafSymbol, 26
- aafTable, 27
- aafTableAnn, 29
- aafTableFrame, 30
- aafTableInt, 31

- is.annpkg, 34
- selectorWidget, 35

## \* internal

- .aaf.character, 2
- .aaf.goterm, 3
- .aaf.integer, 4
- .aaf.raw, 4
- chkPkgs, 31

## \* methods

- getCSS-methods, 32
- getHTML-methods, 32
- getTD-methods, 33
- getText-methods, 33
- getURL-methods, 34

- .aaf.character, 2
- .aaf.goterm, 3
- .aaf.integer, 4
- .aaf.raw, 4
- [, aafList-method (aafList-class), 16
- [, aafTable-method (aafTable-class), 28
- [[, aafTable-method (aafTable-class), 28
- \$.aafTable (aafTable-class), 28

- aaf.handler, 5
- aafChromLoc, 6, 7
- aafChromLoc-class, 6, 7
- aafChromosome, 7, 8
- aafChromosome-class, 8, 8
- aafCytoband, 9, 9, 10
- aafCytoband-class, 9, 9, 33, 34
- aafDescription, 10, 11
- aafDescription-class, 10, 11
- aafExpr, 12
- aafGenBank, 12, 13
- aafGenBank-class, 12, 13, 34
- aafGO, 13, 14, 15
- aafGO-class, 14, 14, 15, 32–34
- aafGOItem, 15
- aafGOItem (aafGOItem-class), 15
- aafGOItem-class, 15, 33, 34
- aafIntensity, 31
- aafIntensity (aafIntensity-class), 16
- aafIntensity-class, 16, 33
- aafList, 15, 20

- aafList (aafList-class), 16
- aafList-class, 16, 32–34
- aafLocusLink, 17, 18
- aafLocusLink-class, 17, 18, 34
- aafPathway, 19, 19, 20, 21
- aafPathway-class, 19, 19, 21, 32, 33
- aafPathwayItem, 20
- aafPathwayItem (aafPathwayItem-class), 20
- aafPathwayItem-class, 20, 33, 34
- aafProbe, 21, 22
- aafProbe-class, 21, 22
- aafPubMed, 22, 23, 24
- aafPubMed-class, 23, 23, 32–34
- aafSearchGO, 24, 25
- aafSearchText, 24, 24
- aafSigned (aafSigned-class), 25
- aafSigned-class, 25, 32
- aafSymbol, 26, 27
- aafSymbol-class, 26, 27
- aafTable, 25, 26, 27, 29
- aafTable-class, 28, 28, 30, 31
- aafTableAnn, 29, 29
- aafTableFrame, 29, 30
- aafTableInt, 16, 29, 31
- aafUniGene-class, 34
  
- chkPkgs, 31
- colnames (aafTable-class), 28
- colnames, aafTable-method (aafTable-class), 28
- colnames<- (aafTable-class), 28
- colnames<- , aafTable-method (aafTable-class), 28
  
- dim.aafTable (aafTable-class), 28
  
- Extract, 29
  
- getCSS, 7, 8, 10, 16
- getCSS (getCSS-methods), 32
- getCSS, aafGO-method (aafGO-class), 14
- getCSS, aafList-method (aafList-class), 16
- getCSS, aafPathway-method (aafPathway-class), 19
- getCSS, aafPubMed-method (aafPubMed-class), 23
- getCSS, aafSigned-method (aafSigned-class), 25
- getCSS, ANY-method (getCSS-methods), 32
- getCSS-methods, 32
- getHTML, 7, 8, 10, 11, 13, 16, 18, 22, 25, 27
- getHTML (getHTML-methods), 32
- getHTML, aafGO-method (aafGO-class), 14
- getHTML, aafGOItem-method (aafGOItem-class), 15
- getHTML, aafList-method (aafList-class), 16
- getHTML, aafPathway-method (aafPathway-class), 19
- getHTML, aafPathwayItem-method (aafPathwayItem-class), 20
- getHTML, aafPubMed-method (aafPubMed-class), 23
- getHTML, ANY-method (getHTML-methods), 32
- getHTML-methods, 32
- getTD, 7, 8, 10, 11, 13, 18, 22, 27
- getTD (getTD-methods), 33
- getTD, aafGO-method (aafGO-class), 14
- getTD, aafIntensity-method (aafIntensity-class), 16
- getTD, aafList-method (aafList-class), 16
- getTD, aafPathway-method (aafPathway-class), 19
- getTD, aafPubMed-method (aafPubMed-class), 23
- getTD, aafSigned-method (aafSigned-class), 25
- getTD, ANY-method (getTD-methods), 33
- getTD-methods, 33
- getText, 7, 8, 11, 13, 16, 18, 22, 25, 27
- getText (getText-methods), 33
- getText, aafCytoband-method (aafCytoband-class), 9
- getText, aafGO-method (aafGO-class), 14
- getText, aafGOItem-method (aafGOItem-class), 15
- getText, aafList-method (aafList-class), 16
- getText, aafPathway-method (aafPathway-class), 19
- getText, aafPathwayItem-method (aafPathwayItem-class), 20
- getText, ANY-method (getText-methods), 33
- getText-methods, 33
- getURL, 7, 8, 11, 16, 25, 27
- getURL (getURL-methods), 34
- getURL, aafCytoband-method (aafCytoband-class), 9
- getURL, aafGenBank-method (aafGenBank-class), 13
- getURL, aafGO-method (aafGO-class), 14
- getURL, aafGOItem-method (aafGOItem-class), 15

getUrl, aafList-method (aafList-class),  
16

getUrl, aafLocusLink-method  
(aafLocusLink-class), 18

getUrl, aafPathway-method  
(aafPathway-class), 19

getUrl, aafPathwayItem-method  
(aafPathwayItem-class), 20

getUrl, aafProbe-method  
(aafProbe-class), 22

getUrl, aafPubMed-method  
(aafPubMed-class), 23

getUrl, ANY-method (getUrl-methods), 34

getUrl-methods, 34

is.annpkg, 34

merge.aafTable (aafTable-class), 28

probeids (aafTable-class), 28

probeids, aafTable-method  
(aafTable-class), 28

probeids<- (aafTable-class), 28

probeids<-, aafTable-method  
(aafTable-class), 28

rbind.aafTable (aafTable-class), 28

saveHTML (aafTable-class), 28

saveHTML, aafTable-method  
(aafTable-class), 28

saveText (aafTable-class), 28

saveText, aafTable-method  
(aafTable-class), 28

selectorWidget, 35

show, aafCytoband-method  
(aafCytoband-class), 9

show, aafGOItem-method  
(aafGOItem-class), 15

show, aafList-method (aafList-class), 16

show, aafPathwayItem-method  
(aafPathwayItem-class), 20