

# Package ‘AffyCompatible’

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**Type** Package

**Title** Affymetrix GeneChip software compatibility

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**Depends** R (>= 2.7.0), XML (>= 2.8-1), RCurl (>= 0.8-1), methods

**Imports** Biostrings

**Description** This package provides an interface to Affymetrix chip annotation and sample attribute files. The package allows an easy way for users to download and manage local data bases of Affymetrix NetAffx annotation files. The package also provides access to GeneChip Operating System (GCOS) and GeneChip Command Console (AGCC)-compatible sample annotation files.

**License** Artistic-2.0

**biocViews** Infrastructure, Microarray, OneChannel

**NeedsCompilation** no

## R topics documented:

AffyCompatible-package	2
accessors	2
AffyCompatible-class	3
Internal-class	4
NetAffxResource	4
NetAffxResource-class	5
readArr	8
readMage	8
readNetAffx	9
readXml	10
xclass	11
xmlValue.XMLAttributeValue	12
zzz-ARRCompatibility-class	12
zzz-DTTCCompatibility-class	13
zzz-NetAffxCompatibility-class	14
<b>Index</b>	<b>16</b>

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AffyCompatible-package

*Affymetrix chip annotation and sample attribute management*

---

## Description

This package manages Affymetrix NetAffx annotation files, and parses MAGE and ARR sample attribute files into R data structures.

NetAffx provides a way to manage the diverse annotation files provided by Affymetrix for their arrays.

ARR files provide attribute information about samples used in an experiment. These files are created, for instance, by the GeneChip Command Console or compliant applications, or

MAGE files also provide information about samples. Support in this package is for MAGE produced by Affymetrix GCOS compliant applications, and emphasizes sample description and processing.

## Details

Package details are available in the DESCRIPTION file of the package, or with the R command `packageDescription("AffyCompatible")`

Overviews of how to use the functionality of this package are available in the package vignettes. See `vignette(package="AffyCompatible")`.

## Author(s)

Written by Martin Morgan.

Maintainer: Martin Morgan <martin.t.morgan@gmail.com>

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accessors

*Access NetAffxResource-class content*

---

## Description

These functions exist to access the information represented in objects of `linkS4class{NetAffxResource}` and related classes.

## Usage

```
annotationsFile(x)
directory(x)
password(x)
user(x)
```

## Arguments

x                    An object for which the accessor is defined.

**Value**

See, e.g., `help('directory,NetAffxResource-method')` for values returned by specific methods.

**Author(s)**

Martin Morgan

**See Also**

[NetAffxResource](#)

---

AffyCompatible-class    *Virtual classes defining the "AffyCompatibility" hierarchy*

---

**Description**

The classes `AffyCompatible`, `DTTCompatibility`, `ARRCompatibility`, and `NetAffxCompatibility` define the overall class hierarchy in this package. Information about these classes is not usually relevant to the user.

**Objects from the Class**

These are virtual classes: no objects may be created from them.

**Methods**

`show` signature(object = "AffyCompatible"): for each slot, provide the slot name, and then invoke `show` for the slot content.

**Author(s)**

Martin Morgan

**Examples**

```
showClass(getClass("NetAffxCompatibility",
  where=getNamespace("AffyCompatible")))
```

---

Internal-class                      *(Internal) Represent 'typed associations' from XML documents*

---

### Description

This internal class represents 'typed associates' (vectors of identically-typed objects) that appear as vectors to the R user.

### Objects from the Class

Objects are created internally, during XML document parsing.

### Slots

`.Data`: Object of class "list" containing the association objects  
`.extends`: Object of class "character" and length 1 describing the class each element in `.Data` must extend

### Extends

Class "[list](#)", from data part. Class "[vector](#)", by class "list", distance 2.

### Methods

[ signature(x = ".TypedAssociation", i = "numeric", j = "missing"): Subset the typed association, returning a typed association with elements i.  
 [ signature(x = ".TypedAssociation", i = "ANY", j = "ANY"): This method is present to stop access to subsetting methods for class list; it has no user-visible functionality.  
**show** signature(object = ".TypedAssociation"): Compactly display the typed associate, e.g., for `.extends=Foo` and length 5, display `Foo(5)`.

### Author(s)

Martin Morgan

---

NetAffxResource                      *Create and access a NetAffxResource database*

---

### Description

Use this function to create and access a NetAffxResource database.

### Usage

```
NetAffxResource(user = character(0),
  password = character(0),
  affxLicence = "FHCR0607",
  directory = tempdir(), ...)
```

## Arguments

user	Length 1 character vector containing the Affymetrix user name authorized to access the NetAffx resource.
password	Length 1 character vector containing the Affymetrix password of the user.
affxLicence	Length 1 character vector containing the Affymetrix licence (typically application specific, i.e., the specified licence covers AffyCompatible).
directory	(Optional) length 1 character vector providing the full path to the local directory where the NetAffx database and files will be managed. Defaults to a session-specific temporary directory.
...	Additional arguments, not currently used.

## Details

NetAffxResource creates a [NetAffxResource](#) object that manages a data base of NetAffx resources. The data base is located on the user file system as indicated by the directory argument. It is populated when the user requests specific files.

Users should provide a directory argument, so that the data base can be reused across sessions. This means that large files are only downloaded once.

Additional details are provided in the vignette accompanying this package.

## Value

[NetAffxResource](#).

## Author(s)

Martin Morgan

## See Also

[NetAffxResource](#). The vignette ‘Annotations with NetAffx’.

---

NetAffxResource-class *Manage NetAffx annotations*

---

## Description

This class is for accessing and retrieving NetAffx annotation files for Affymetrix chips. It requires that the user has established an account with Affymetrix. Detailed usage is described in the ‘Annotations with NetAffx’ vignette.

## Objects from the Class

Objects are created by calls of the form `NetAffxResource(user="user@research.org", password="terces")`, as illustrated below and in the ‘Annotations with NetAffx’ vignette.

**Slots**

**user:** Object of class "character" containing the full user name (typically an email address) obtained when the user registers with Affymetrix.

**password:** Object of class "character" containing the password associated with the Affymetrix user name. The password is entered and stored in plain text, and should not be considered secure within Bioconductor.

**affxLicence:** Object of class "character" containing the licence, obtained from Affymetrix, for retrieving NetAffx annotations. The licence is usually software specific (e.g., for the Affy-Compatible package of Bioconductor). Users will not usually change the default value.

**directory:** Object of class "character", containing the local directory path where the NetAffx data base and annotation files will reside.

**annotationsFile:** Object of class "character" containing the file name of the NetAffx data base. Users will not usually change the default value.

**affxUrl:** Object of class "character" containing the URL used to download the NetAffx annotations file. Users will not usually change the default value.

**Extends**

Class "[NetAffxCompatibility](#)", directly. Class "[AffyCompatible](#)", by class "NetAffxCompatibility", distance 2.

**Methods**

[[ signature(x = "NetAffxResource", i = "numeric", j = "missing")

[[ signature(x = "NetAffxResource", i = "character", j = "missing"): Retrieve an object representing all NetAffx annotations available for an array. The argument i may be a numeric index or character string corresponding to an array name returned by names(x).

[[ signature(x = "NetAffxResource", i = "numeric", j = "numeric")

[[ signature(x = "NetAffxResource", i = "character", j = "numeric")

[[ signature(x = "NetAffxResource", i = "numeric", j = "character")

[[ signature(x = "NetAffxResource", i = "character", j = "character"): Retrieve an object representing a specific annotation for an array. The argument i may be a numeric index or character string corresponding to an array name returned by names(x). The argument j may be a numeric index or character string corresponding to an annotation returned by description(x[[i]]).

**affxLicence** signature(x = "NetAffxResource"): the character string representation of the licence used to access the NetAffx site.

**affxUrl** signature(x = "NetAffxResource"): the url used to access the NetAffx site.

**annotationsFile** signature(x = "NetAffxResource"): the file name of NetAffx data base, as stored on the local disk of the user.

**directory** signature(x = "NetAffxResource"): the directory in which the NetAffx data base and annotation files are stored on the local disk of the user.

**names** signature(x = "NetAffxResource"): the names of the arrays for which annotations are available.

**password** signature(x = "NetAffxResource"): The password associated with the user name obtained when the user registered with Affymetrix. The password is entered and stored as plain text, and is not secure.

**readAnnotation** signature(netAffxResource = "NetAffxResource", array = "numeric", annotation = "num

**readAnnotation** signature(netAffxResource = "NetAffxResource", array = "numeric", annotation = "cha

**readAnnotation** signature(netAffxResource = "NetAffxResource", array = "character", annotation = "n

**readAnnotation** signature(netAffxResource = "NetAffxResource", array = "character", annotation = "c

**readAnnotation** signature(netAffxResource = "NetAffxResource", array = "missing", annotation = "Aff

Read a specific annotation file as an R object. For the first four methods, array, if present, indexes or names the array while annotation indexes or names the annotation. All methods also accept content = "logical" to indicate whether the content of the file should be returned if possible (content=TRUE, default) or only the path to the local file (content=FALSE) and update = "logical" indicating whether the file should be read from disk if available (update=FALSE, default) or retrieved from the NetAffx web site (update=TRUE). readAnnotation parses CSV, Tabular, and PSI files to data frames, and reads FASTA files to a list of description / sequence pairs (see Biostrings::readFASTA).

The ... argument is passed to corresponding read functions. CSV files are parsed using read.csv(conn, ...), Tabular files with read.delim(conn, ...), PSI files with read.delim(conn, header=FALSE, skip=1, sep="\t", ...), and FASTA with readFASTA(conn, ...).

**show** signature(object = "NetAffxResource"): compactly show the NetAffxResource object.

**user** signature(x = "NetAffxResource"): The user name (typically email address) obtained when the user registers with the Affymetrix web site.

## Author(s)

Martin Morgan <mtmorgan@fhcrc.org>

## See Also

Vignette 'Annotations with NetAffx'. Affymetrix user login site <https://www.affymetrix.com/site/login/login.affx>.

[.Rprofile](#) for ways to automatically set variables (such as password, and directory) for each session.

## Examples

```
## password must be obtained by the user
rsrc <- NetAffxResource(user="mtmorgan@fhcrc.org", password=password)
head(names(rsrc))
affxDescription(rsrc[["Bovine"]])
## paradigm to display all elements of 'annotation'
sapply(affxAnnotation(rsrc[["Bovine"]]), force)
## obtain and read a single annotation
anno <- rsrc[["Porcine"], "Annotations, CSV format"]
df <- readAnnotation(rsrc, annotation=anno)
```

readArr

*Read ARR sample attribute files*

---

**Description**

This functions reads the content of Affymetrix ARR sample attribute files created by GeneChip(R) Command Console. Objects are represented as R classes. Navigation and extraction of data are described in the vignette ‘Retrieving MAGE and ARR sample attributes’.

**Usage**

```
readArr(fls, ...)
```

**Arguments**

<code>fls</code>	A character vector containing the paths to files to be read.
<code>...</code>	Additional arguments, currently unused.

**Value**

An object or list of objects of class `ArrayFileSet`, depending on whether one or several file paths are provided.

**Author(s)**

Martin Morgan

**See Also**

The vignette ‘Retrieving MAGE and ARR sample attributes’ for detailed illustration of use. [xclass](#) and [readXml](#) for advanced access methods.

**Examples**

```
dir <- system.file("extdata", "ARR", package="AffyCompatible")
fls <- list.files(dir, full=TRUE)
readArr(fls[[1]])
readArr(fls)
```

---

readMage*Read DTT (MAGE) sample attribute files*

---

**Description**

This functions reads the content of Affymetrix DTT (MAGE) sample attribute files created by GCOS. Objects are represented as R classes. Navigation and extraction of data are described in the vignette ‘Retrieving MAGE and ARR sample attributes’.



**Usage**

```
readMage(fls, ...)
```

**Arguments**

`fls` A character vector containing the paths to files to be read.  
`...` Additional arguments, currently unused.

**Value**

An object or list of objects of class `ArrayFileSet`, depending on whether one or several file paths are provided.

**Author(s)**

Martin Morgan

**See Also**

The vignette ‘Retrieving MAGE and ARR sample attributes’ for detailed illustration of use. [xclass](#) and [readXml](#) for advanced access methods.

**Examples**

```
dir <- system.file("extdata", "DTT", package="AffyCompatible")
fls <- list.files(dir, full=TRUE)
basename(fls)
readArr(fls[[1]])
```

---

readNetAffx

*Update or read a NetAffx data base*

---

**Description**

This function provides a way to read or update a NetAffx data base. The usual use for this is to force the data base description to be updated (by accessing the Affymetrix web site) or to retrieve the entire list of NetAffx resource data base. A more normal use case is to

**Usage**

```
readNetAffx(netAffxResource, update = FALSE, ...)
```

**Arguments**

`netAffxResource` An object of class [NetAffxResource](#) containing the path to the local data base, and permissions for access the Affymetrix NetAffx resource.  
`update` An object of logical(1) indicating whether the data base is to be updated (TRUE) or not.  
`...` Additional arguments, not currently used.

**Value**

An object representing the annotations found; see [NetAffxResource](#) for additional details.

**Author(s)**

Martin Morgan

**Examples**

```
## retrieve all annotations
## Not run:
example("NetAffxResource-class")
readNetAffx(rsrc)

## End(Not run)
```

---

readXml	<i>(Advanced) Read XML files of Affymetrix sample attributes or annotation</i>
---------	--

---

**Description**

This functions reads the content of Affymetrix DTT (MAGE) or ARR sample files, or AffxNetAffx-AnnotFile array annotation files, return an internal representation of the underlying XML. The return value can be used with [xclass](#) to rapidly create R objects representing deeply nested nodes of the document. The return value can also be used with `xpathApply` in the XML package for access to character-based representation of the data.

**Usage**

```
readXml(f1, ...)
```

**Arguments**

f1	A length-1 character vector giving the full path to the file to be parsed.
...	Additional arguments, passed to <code>xmlTreeParse</code> .

**Value**

An object of class `XMLInternalDocument`.

**Author(s)**

Martin Morgan

**See Also**

The vignettes ‘Retrieving MAGE and ARR sample attributes’ and ‘Annotation retrieval with `NetAffxResource`’ for detailed illustration of use.

[xclass](#) for instantiating objects from `xpath` queries.

**Examples**

```
mageDir <- system.file("extdata", "DTT", package="AffyCompatible")
mageFiles <- list.files(mageDir, full=TRUE)
xml <- readXml(mageFiles[[1]])
xclass(xml, "//MeasuredBioAssay")[[1]]
```

---

xclass

*(Advanced) Construct R objects from XML document queries*


---

**Description**

This function takes an xml object, created from [readXml](#), and an xpath query referencing an element of the document, and returns an R object representing the element.

The xpath query must retrieve an element, not an attribute.

**Usage**

```
xclass(doc, xpathq, prefix = character(0))
```

**Arguments**

doc	An XMLInternalDocument retrieved using <a href="#">readXml</a> .
xpathq	A length-1 character string representing an xpath query into the document.
prefix	A prefix used to map, when necessary, between the XML class name and the corresponding R class. For NetAffx-based classes, the prefix is 'Affx'; no prefix is required for DTT or ARR documents.

**Value**

An R object corresponding to the class(es) referenced by the xpath query.

**Author(s)**

Martin Morgan

**References**

<http://www.w3.org/TR/xpath> provides a very useful description of xpath. Additional references are in the vignette 'Retrieving MAGE and ARR sample attributes'.

**See Also**

The vignettes 'Retrieving MAGE and ARR sample attributes' and 'Annotation retrieval with NetAffxResource' for detailed illustration of use.

[readXml](#) for appropriately reading XML documents.

**Examples**

```
example(readXml)
```

---

```
xmlValue.XMLAttributeValue
```

*Additional functions defined in AffyCompatible*

---

### Description

This page documents additional, miscellaneous, functions defined by AffyCompatible

### Usage

```
## S3 method for class 'XMLAttributeValue'
xmlValue(x, ignoreComments = FALSE, recursive = TRUE,
         encoding=XML:::CE_NATIVE, trim=FALSE)
```

### Arguments

x	An object of class XMLAttributeValue.
ignoreComments	Logical; ignored by the xmlValue.XMLAttributeValue method
recursive	ignored
encoding	File encoding
trim	Remove trailing whitespace? Ignored by this method

### Value

A character vector (usually length 1) containing the character representation of the XML attribute.

---

```
zzz-ARRCompatibility-class
```

*(Auto-generated) classes and methods for navigating ARR sample attributes.*

---

### Description

These classes and methods facilitate navigation of the Affymetrix ARR sample attribute files. ARR files are generated by the Affymetrix AGCC (GeneChip(R) Command Console) application. Specifically, the classes are R representations of the Affymetrix classes defined in ArraySetAndTemplate-File.dtd. The 'show' methods for these classes indicate how objects are to be accessed; details are in the 'Retrieving MAGE and ARR sample attributes' vignette.

### Objects from the Class

Objects are created internally, by parsing XML retrieved from ARR, and are not created directly by the user.

### Slots

Objects have a variety of slots. To discover slot names and content type, see the slotNames portion of the example, below.

**Extends**

Class "ARRCompatibility", directly. Class "AffyCompatible", by class "ARRCompatibility", distance 2.

**Methods**

'Accessor' methods are defined on auto-generated classes to access slot content.

Accessors are apparent from displaying the object; each line of the display is of the form accessor: content. To retrieve the content of an instance object, invoke accessor(object).

Some objects contains several instances of another object. These 'typed associations' are represented by the `.TypedAssociation` class, and are navigated or subset as one would a standard R vector, e.g., using `[, [[`. A useful paradigm for displaying all instances is illustrated in the vignette.

**Author(s)**

Martin Morgan <mtmorgan@fhcrc.org>

**See Also**

Vignette 'Retrieving MAGE and ARR sample attributes'.

**Examples**

```
## defined and auto-generated classes
names(slot(getClass("ARRCompatibility",
                  where=getNamespace("AffyCompatible")),
       "subclasses"))
```

---

zzz-DTTCompatibility-class

*(Auto-generated) classes and methods for navigating DTT sample attributes.*

---

**Description**

These classes and methods facilitate navigation of the Affymetrix DTT sample attribute files. DTT files are generated by the Affymetrix GCOS application. Specifically, the classes are R representations of the Affymetrix classes defined in MAGE-ML.dtd. The 'show' methods for these classes indicate how objects are to be accessed; details are in the 'Retrieving MAGE and ARR sample attributes' vignette.

**Objects from the Class**

Objects are created internally, by parsing XML retrieved from ARR, and are not created directly by the user.

**Slots**

Objects have a variety of slots. To discover slot names and content type, see the slotNames portion of the example, below.

**Extends**

Class "DTTCompatibility", directly. Class "AffyCompatible", by class "DTTCompatibility", distance 2.

**Methods**

'Accessor' methods are defined on auto-generated classes to access slot content.

Accessors are apparent from displaying the object; each line of the display is of the form accessor: content. To retrieve the content of an instance object, invoke accessor(object).

Some objects contains several instances of another object. These 'typed associations' are represented by the `.TypedAssociation` class, and are navigated or subset as one would a standard R vector, e.g., using `[, [[`. A useful paradigm for displaying all instances is illustrated in the vignette.

**Author(s)**

Martin Morgan <mtmorgan@fhcrc.org>

**See Also**

Vignette 'Retrieving MAGE and ARR sample attributes'.

**Examples**

```
## defined and auto-generated classes
names(slot(getClass("DTTCompatibility",
                    where=getNamespace("AffyCompatible")),
        "subclasses"))
```

---

zzz-NetAffxCompatibility-class

*(Auto-generated) classes and methods for navigating NetAffx resources*

---

**Description**

These classes and methods facilitate navigation of the NetAffx resource data base. They are R representations of the Affymetrix classes defined in NetAffxAnnotFileList.dtd. The 'show' methods for these class indicate how objects are to be accessed; details are in the 'Annotations with NetAffx' vignette.

The auto-generated classes are discoverable as indicated in the example below.

**Objects from the Class**

Objects are created internally, by parsing XML retrieved from the local NetAffx data base or from the Affymetrix web site.

**Slots**

Objects have a variety of slots. To discover slot names and content type, see the slotNames portion of the example, below.

**Extends**

Class "[NetAffxCompatibility](#)", directly. Class "[AffyCompatible](#)", by class "NetAffxCompatibility", distance 2.

**Methods**

'Read' methods are defined on auto-generated classes to access slot content.

Accessors are apparent from displaying the object; each line of the display is of the form accessor: content. To retrieve the content of an instance object, invoke `accessor(object)`.

Some objects contains several instances of another object. These 'typed associations' are represented by the [.TypedAssociation](#) class, and are navigated or subset as one would a standard R vector, e.g., using `[, [[]`. A useful paradigm for displaying all instances is illustrated on the [NetAffxResource](#) page.

**Author(s)**

Martin Morgan <[mtmorgan@fhcrc.org](mailto:mtmorgan@fhcrc.org)>

**See Also**

Vignette 'Annotations with NetAffx'. Affymetrix user login site <https://www.affymetrix.com/site/login/login.affx>.

[NetAffxResource](#) for creating and managing the NetAffx data base.

[NetAffxResource](#) for navigating the data base.

**Examples**

```
## defined and auto-generated classes
getClass("NetAffxCompatibility", where=getNamespace("AffyCompatible"))

## slots of an auto-generated class
getSlots(getClass("AffxNetAffxAnnotFileList",
  where=getNamespace("AffyCompatible")))

## Not run:
example("NetAffxrResource-class")

## End(Not run)
```

# Index

- \*Topic **classes**
  - AffyCompatible-class, 3
  - Internal-class, 4
  - NetAffxResource-class, 5
  - readArr, 8
  - readMage, 8
  - zzz-ARRCompatibility-class, 12
  - zzz-DTTCompatibility-class, 13
  - zzz-NetAffxCompatibility-class, 14
- \*Topic **database**
  - NetAffxResource, 4
  - readNetAffx, 9
- \*Topic **manip**
  - readXml, 10
  - xclass, 11
  - xmlValue.XMLAttributeValue, 12
- \*Topic **methods**
  - accessors, 2
- \*Topic **package**
  - AffyCompatible-package, 2
- .Rprofile, 7
- .TypedAssociation, 13–15
- .TypedAssociation-class
  - (Internal-class), 4
- [, .TypedAssociation, ANY, ANY-method
  - (Internal-class), 4
- [, .TypedAssociation, numeric, missing, ANY-method
  - (Internal-class), 4
- [, .TypedAssociation, numeric, missing-method
  - (Internal-class), 4
- [[, NetAffxResource, character, character-method
  - (NetAffxResource-class), 5
- [[, NetAffxResource, character, missing-method
  - (NetAffxResource-class), 5
- [[, NetAffxResource, character, numeric-method
  - (NetAffxResource-class), 5
- [[, NetAffxResource, numeric, character-method
  - (NetAffxResource-class), 5
- [[, NetAffxResource, numeric, missing-method
  - (NetAffxResource-class), 5
- [[, NetAffxResource, numeric, numeric-method
  - (NetAffxResource-class), 5
- accession (zzz-DTTCompatibility-class), 13
- accession, DatabaseEntry-method
  - (zzz-DTTCompatibility-class), 13
- accessions\_assnlist
  - (zzz-DTTCompatibility-class), 13
- accessions\_assnlist, BibliographicReference-method
  - (zzz-DTTCompatibility-class), 13
- Accessions\_assnlist-class
  - (zzz-DTTCompatibility-class), 13
- accessionVersion
  - (zzz-DTTCompatibility-class), 13
- accessionVersion, DatabaseEntry-method
  - (zzz-DTTCompatibility-class), 13
- accessors, 2
- acpassword (NetAffxResource), 4
- action (zzz-DTTCompatibility-class), 13
- action, Audit-method
  - (zzz-DTTCompatibility-class), 13
- action\_assn
  - (zzz-DTTCompatibility-class), 13
- action\_assn, Treatment-method
  - (zzz-DTTCompatibility-class), 13
- Action\_assn-class
  - (zzz-DTTCompatibility-class), 13
- actionMeasurement\_assn
  - (zzz-DTTCompatibility-class), 13
- actionMeasurement\_assn, Treatment-method
  - (zzz-DTTCompatibility-class), 13
- ActionMeasurement\_assn-class
  - (zzz-DTTCompatibility-class), 13



- activityDate
  - (zzz-DTTCompatibility-class),  
13
- activityDate,ProtocolApplication-method
  - (zzz-DTTCompatibility-class),  
13
- address(zzz-DTTCompatibility-class), 13
- address,Organization-method
  - (zzz-DTTCompatibility-class),  
13
- address,Person-method
  - (zzz-DTTCompatibility-class),  
13
- adjustments\_assnlist
  - (zzz-DTTCompatibility-class),  
13
- adjustments\_assnlist,ArrayManufactureDeviation-method(zzz-DTTCompatibility-class),  
13
- Adjustments\_assnlist-class
  - (zzz-DTTCompatibility-class),  
13
- affiliation\_assnref
  - (zzz-DTTCompatibility-class),  
13
- affiliation\_assnref,Person-method
  - (zzz-DTTCompatibility-class),  
13
- Affiliation\_assnref-class
  - (zzz-DTTCompatibility-class),  
13
- affxAnnotation
  - (zzz-NetAffxCompatibility-class),  
14
- affxAnnotation,AffxArray-method
  - (zzz-NetAffxCompatibility-class),  
14
- AffxAnnotation-class
  - (zzz-NetAffxCompatibility-class),  
14
- affxArray
  - (zzz-NetAffxCompatibility-class),  
14
- affxArray,AffxNetAffxAnnotFileList-method
  - (zzz-NetAffxCompatibility-class),  
14
- affxArray,Array\_assnlist-method
  - (zzz-DTTCompatibility-class),  
13
- AffxArray-class
  - (zzz-NetAffxCompatibility-class),  
14
- affxCategory
  - (zzz-DTTCompatibility-class),  
13
- affxCategory,OntologyEntry-method
  - (zzz-DTTCompatibility-class),  
13
- affxComment
  - (zzz-NetAffxCompatibility-class),  
14
- affxComment,AffxAnnotation-method
  - (zzz-NetAffxCompatibility-class),  
14
- affxComment,PhysicalArray-method
  - (zzz-ARRCompatibility-class),  
12
- AffxComment-class
  - (zzz-NetAffxCompatibility-class),  
14
- affxCompression
  - (zzz-NetAffxCompatibility-class),  
14
- affxCompression,AffxUrl-method
  - (zzz-NetAffxCompatibility-class),  
14
- affxCrc32
  - (zzz-NetAffxCompatibility-class),  
14
- affxCrc32,AffxFile-method
  - (zzz-NetAffxCompatibility-class),  
14
- affxCrc32,AffxUrl-method
  - (zzz-NetAffxCompatibility-class),  
14
- affxDate
  - (zzz-NetAffxCompatibility-class),  
14
- affxDate,AffxFile-method
  - (zzz-NetAffxCompatibility-class),  
14
- affxDate,Audit-method
  - (zzz-DTTCompatibility-class),  
13
- affxDescription
  - (zzz-NetAffxCompatibility-class),  
14
- affxDescription,AffxAnnotation-method
  - (zzz-NetAffxCompatibility-class),  
14
- affxDescription,AffxArray-method
  - (zzz-NetAffxCompatibility-class),  
14
- affxEnd(zzz-DTTCompatibility-class), 13

- affxEnd, CompositePosition-method  
(zzz-DTTCompatibility-class),  
13
- affxEnd, ReporterPosition-method  
(zzz-DTTCompatibility-class),  
13
- affxEnd, SequencePosition-method  
(zzz-DTTCompatibility-class),  
13
- affxFile  
(zzz-NetAffxCompatibility-class),  
14
- affxFile, AffxAnnotation-method  
(zzz-NetAffxCompatibility-class),  
14
- AffxFile-class  
(zzz-NetAffxCompatibility-class),  
14
- affxImage (zzz-DTTCompatibility-class),  
13
- affxImage, PhysicalBioAssayData\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- affxLicence  
(zzz-NetAffxCompatibility-class),  
14
- affxLicence, NetAffxResource-method  
(NetAffxResource-class), 5
- affxName  
(zzz-NetAffxCompatibility-class),  
14
- affxName, AffxArray-method  
(zzz-NetAffxCompatibility-class),  
14
- affxName, AffxFile-method  
(zzz-NetAffxCompatibility-class),  
14
- AffxNetAffxAnnotFileList-class  
(zzz-NetAffxCompatibility-class),  
14
- affxOrder (zzz-DTTCompatibility-class),  
13
- affxOrder, BioDataCube-method  
(zzz-DTTCompatibility-class),  
13
- affxOrder, Treatment-method  
(zzz-DTTCompatibility-class),  
13
- affxPerson  
(zzz-DTTCompatibility-class),  
13
- affxPerson, Contact\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- affxPerson, Person\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- affxRow (zzz-DTTCompatibility-class), 13
- affxRow, FeatureLocation-method  
(zzz-DTTCompatibility-class),  
13
- affxRow, Zone-method  
(zzz-DTTCompatibility-class),  
13
- affxSequence  
(zzz-DTTCompatibility-class),  
13
- affxSequence, BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- affxSize  
(zzz-NetAffxCompatibility-class),  
14
- affxSize, AffxFile-method  
(zzz-NetAffxCompatibility-class),  
14
- affxSize, AffxUrl-method  
(zzz-NetAffxCompatibility-class),  
14
- affxStart (zzz-DTTCompatibility-class),  
13
- affxStart, CompositePosition-method  
(zzz-DTTCompatibility-class),  
13
- affxStart, ReporterPosition-method  
(zzz-DTTCompatibility-class),  
13
- affxStart, SequencePosition-method  
(zzz-DTTCompatibility-class),  
13
- affxStatus  
(zzz-NetAffxCompatibility-class),  
14
- affxStatus, AffxNetAffxAnnotFileList-method  
(zzz-NetAffxCompatibility-class),  
14
- AffxStatus-class  
(zzz-NetAffxCompatibility-class),  
14
- affxText (zzz-DTTCompatibility-class),  
13
- affxText, Description-method  
(zzz-DTTCompatibility-class),  
13

- affxText,Protocol-method  
(zzz-DTTCompatibility-class),  
13
- affxTitle (zzz-DTTCompatibility-class),  
13
- affxTitle,BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- affxTitle,Protocol-method  
(zzz-DTTCompatibility-class),  
13
- affxType  
(zzz-NetAffxCompatibility-class),  
14
- affxType,AffxAnnotation-method  
(zzz-NetAffxCompatibility-class),  
14
- affxType,AffxFile-method  
(zzz-NetAffxCompatibility-class),  
14
- affxUrl  
(zzz-NetAffxCompatibility-class),  
14
- affxUrl,AffxFile-method  
(zzz-NetAffxCompatibility-class),  
14
- affxUrl,NetAffxResource-method  
(NetAffxResource-class), 5
- AffxUrl-class  
(zzz-NetAffxCompatibility-class),  
14
- affyBarcode  
(zzz-ARRCompatibility-class),  
12
- affyBarcode,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- AffyCompatible, 6, 13–15
- AffyCompatible  
(AffyCompatible-package), 2
- AffyCompatible-class, 3
- AffyCompatible-package, 2
- analysisResults\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- analysisResults\_assnreflist,Experiment-method  
(zzz-DTTCompatibility-class),  
13
- AnalysisResults\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- annotations\_assnlist  
(zzz-DTTCompatibility-class),  
13
- annotations\_assnlist,Description-method  
(zzz-DTTCompatibility-class),  
13
- annotations\_assnlist,ExperimentalFactor-method  
(zzz-DTTCompatibility-class),  
13
- Annotations\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- annotationsFile (accessors), 2
- annotationsFile,NetAffxResource-method  
(NetAffxResource-class), 5
- Array-class  
(zzz-DTTCompatibility-class),  
13
- array\_assnlist  
(zzz-DTTCompatibility-class),  
13
- array\_assnlist,Array\_package-method  
(zzz-DTTCompatibility-class),  
13
- Array\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- array\_assnref  
(zzz-DTTCompatibility-class),  
13
- array\_assnref,BioAssayCreation-method  
(zzz-DTTCompatibility-class),  
13
- array\_assnref,Hybridization-method  
(zzz-DTTCompatibility-class),  
13
- Array\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- array\_package  
(zzz-DTTCompatibility-class),  
13
- array\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- Array\_package-class  
(zzz-DTTCompatibility-class),  
13
- array\_ref (zzz-DTTCompatibility-class),  
13
- array\_ref,Array\_assnref-method  
(zzz-DTTCompatibility-class),  
13

- array\_ref,Arrays\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- Array\_ref-class  
(zzz-DTTCompatibility-class),  
13
- arrayAttribute  
(zzz-ARRCompatibility-class),  
12
- arrayAttribute,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- ArrayAttribute-class  
(zzz-ARRCompatibility-class),  
12
- arrayDesign  
(zzz-DTTCompatibility-class),  
13
- arrayDesign,ArrayDesign\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- ArrayDesign-class  
(zzz-DTTCompatibility-class),  
13
- arrayDesign\_assnlist  
(zzz-DTTCompatibility-class),  
13
- arrayDesign\_assnlist,ArrayDesign\_package-method  
(zzz-DTTCompatibility-class),  
13
- ArrayDesign\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- arrayDesign\_assnref  
(zzz-DTTCompatibility-class),  
13
- arrayDesign\_assnref,Array-method  
(zzz-DTTCompatibility-class),  
13
- ArrayDesign\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- arrayDesign\_package  
(zzz-DTTCompatibility-class),  
13
- arrayDesign\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- ArrayDesign\_package-class  
(zzz-DTTCompatibility-class),  
13
- arrayDesign\_ref  
(zzz-DTTCompatibility-class),  
13
- arrayDesign\_ref,ArrayDesign\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- ArrayDesign\_ref-class  
(zzz-DTTCompatibility-class),  
13
- arrayGroup  
(zzz-DTTCompatibility-class),  
13
- arrayGroup,ArrayGroup\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- ArrayGroup-class  
(zzz-DTTCompatibility-class),  
13
- arrayGroup\_assnlist  
(zzz-DTTCompatibility-class),  
13
- arrayGroup\_assnlist,Array\_package-method  
(zzz-DTTCompatibility-class),  
13
- ArrayGroup\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- arrayGroup\_assnref  
(zzz-DTTCompatibility-class),  
13
- arrayGroup\_assnref,Array-method  
(zzz-DTTCompatibility-class),  
13
- ArrayGroup\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- arrayGroup\_ref  
(zzz-DTTCompatibility-class),  
13
- arrayGroup\_ref,ArrayGroup\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- ArrayGroup\_ref-class  
(zzz-DTTCompatibility-class),  
13
- arrayIdentifier  
(zzz-DTTCompatibility-class),  
13
- arrayIdentifier,Array-method  
(zzz-DTTCompatibility-class),  
13
- arrayManufacture  
(zzz-DTTCompatibility-class),

- 13
- arrayManufacture, ArrayManufacture\_assnlist-method 12
- (zzz-DTTCompatibility-class),
- 13
- ArrayManufacture-class
- (zzz-DTTCompatibility-class),
- 13
- arrayManufacture\_assnlist
- (zzz-DTTCompatibility-class),
- 13
- arrayManufacture\_assnlist, Array\_package-method
- (zzz-DTTCompatibility-class),
- 13
- ArrayManufacture\_assnlist-class
- (zzz-DTTCompatibility-class),
- 13
- arrayManufacture\_ref
- (zzz-DTTCompatibility-class),
- 13
- arrayManufacture\_ref, Information\_assnref-method
- (zzz-DTTCompatibility-class),
- 13
- ArrayManufacture\_ref-class
- (zzz-DTTCompatibility-class),
- 13
- arrayManufactureDeviation
- (zzz-DTTCompatibility-class),
- 13
- arrayManufactureDeviation, ArrayManufactureDeviations\_assnlist-method
- (zzz-DTTCompatibility-class),
- 13
- ArrayManufactureDeviation-class
- (zzz-DTTCompatibility-class),
- 13
- arrayManufactureDeviations\_assnlist
- (zzz-DTTCompatibility-class),
- 13
- arrayManufactureDeviations\_assnlist, Array-method
- (zzz-DTTCompatibility-class),
- 13
- ArrayManufactureDeviations\_assnlist-class
- (zzz-DTTCompatibility-class),
- 13
- arrayManufacturers\_assnreflist
- (zzz-DTTCompatibility-class),
- 13
- arrayManufacturers\_assnreflist, ArrayManufacture-method
- (zzz-DTTCompatibility-class),
- 13
- ArrayManufacturers\_assnreflist-class
- (zzz-DTTCompatibility-class),
- 13
- arrayName (zzz-ARRCompatibility-class),
- 12
- arrayName, PhysicalArray-method
- (zzz-ARRCompatibility-class),
- 12
- arrays\_assnreflist
- (zzz-DTTCompatibility-class),
- 13
- arrays\_assnreflist, ArrayGroup-method
- (zzz-DTTCompatibility-class),
- 13
- arrays\_assnreflist, ArrayManufacture-method
- (zzz-DTTCompatibility-class),
- 13
- Arrays\_assnreflist-class
- (zzz-DTTCompatibility-class),
- 13
- ArraySetFile-class
- (zzz-ARRCompatibility-class),
- 12
- arraySpacingX
- (zzz-DTTCompatibility-class),
- 13
- arraySpacingX, ArrayGroup-method
- (zzz-DTTCompatibility-class),
- 13
- arraySpacingY
- (zzz-DTTCompatibility-class),
- 13
- arraySpacingY, ArrayGroup-method
- (zzz-DTTCompatibility-class),
- 13
- arrayXOrigin
- (zzz-DTTCompatibility-class),
- 13
- arrayXOrigin, Array-method
- (zzz-DTTCompatibility-class),
- 13
- arrayYOrigin
- (zzz-DTTCompatibility-class),
- 13
- arrayYOrigin, Array-method
- (zzz-DTTCompatibility-class),
- 13
- ARRCompatibility, 13
- ARRCompatibility-class
- (AffyCompatible-class), 3
- associations\_assnlist
- (zzz-DTTCompatibility-class),
- 13
- associations\_assnlist, OntologyEntry-method
- (zzz-DTTCompatibility-class),

- 13
- Associations\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- audit (zzz-DTTCompatibility-class), 13
- audit, AuditTrail\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Audit-class  
(zzz-DTTCompatibility-class),  
13
- auditAndSecurity\_package  
(zzz-DTTCompatibility-class),  
13
- auditAndSecurity\_package, MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- AuditAndSecurity\_package-class  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, Array-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, ArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, ArrayManufacture-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, Audit-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, BioAssayCreation-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, BioAssayDataCluster-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, BioAssayDimension-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, BioAssayMap-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, BioAssayTreatment-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, BioSample-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, BioSource-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, Channel-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, CompositeCompositeMap-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, CompositeGroup-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, CompositeSequence-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, CompositeSequenceDimension-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, Compound-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, Database-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, DerivedBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, DerivedBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, DerivedSignal-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, Description-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, Error-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist, ExpectedValue-method  
(zzz-DTTCompatibility-class),  
13

- auditTrail\_assnlist,Experiment-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,ExperimentalFactor-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,ExperimentDesign-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,FactorValue-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Failed-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Feature-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,FeatureDimension-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,FeatureExtraction-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,FeatureGroup-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,FeatureReporterMap-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Fiducial-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Hardware-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,HardwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Hybridization-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Image-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,ImageAcquisition-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,LabeledExtract-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,ManufactureLIMS-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,ManufactureLIMSBiomaterial-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,MeasuredBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,MeasuredBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,MeasuredSignal-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Node-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,NodeContents-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Organization-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Parameter-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Person-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,PhysicalArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,PhysicalBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,PresentAbsent-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Protocol-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,ProtocolApplication-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,PValue-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,QuantitationTypeDimension-method  
(zzz-DTTCompatibility-class),

- 13
- auditTrail\_assnlist,QuantitationTypeMap-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Ratio-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Reporter-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,ReporterCompositeMap-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,ReporterDimension-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,ReporterGroup-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Security-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,SecurityGroup-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,SeqFeature-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Software-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,SoftwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,SpecializedQuantitationType-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Transformation-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Treatment-method  
(zzz-DTTCompatibility-class),  
13
- auditTrail\_assnlist,Zone-method  
(zzz-DTTCompatibility-class),  
13
- AuditTrail\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- authors (zzz-DTTCompatibility-class), 13
- authors,BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- 13
- barcode (zzz-DTTCompatibility-class), 13
- barcode,ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- basis (zzz-DTTCompatibility-class), 13
- basis,SeqFeature-method  
(zzz-DTTCompatibility-class),  
13
- bibliographicReference  
(zzz-DTTCompatibility-class),  
13
- bibliographicReference,BibliographicReferences\_assnlist  
(zzz-DTTCompatibility-class),  
13
- BibliographicReference-class  
(zzz-DTTCompatibility-class),  
13
- bibliographicReferences\_assnlist  
(zzz-DTTCompatibility-class),  
13
- bibliographicReferences\_assnlist,Description-method  
(zzz-DTTCompatibility-class),  
13
- BibliographicReferences\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- bioAssay\_assnlist  
(zzz-DTTCompatibility-class),  
13
- bioAssay\_assnlist,BioAssay\_package-method  
(zzz-DTTCompatibility-class),  
13
- BioAssay\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- bioAssay\_assnref  
(zzz-DTTCompatibility-class),  
13
- bioAssay\_assnref,BioAssayTuple-method  
(zzz-DTTCompatibility-class),  
13
- BioAssay\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- bioAssay\_package  
(zzz-DTTCompatibility-class),  
13
- bioAssay\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- BioAssay\_package-class



- (zzz-DTTCompatibility-class),  
13
- BioAssay\_ref-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayCreation  
(zzz-DTTCompatibility-class),  
13
- bioAssayCreation,BioAssayCreation\_assn-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayCreation-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayCreation\_assn  
(zzz-DTTCompatibility-class),  
13
- bioAssayCreation\_assn,PhysicalBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayCreation\_assn-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayData\_assnlist  
(zzz-DTTCompatibility-class),  
13
- bioAssayData\_assnlist,BioAssayData\_package-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayData\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayData\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- bioAssayData\_assnreflist,Experiment-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayData\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayData\_package  
(zzz-DTTCompatibility-class),  
13
- bioAssayData\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayData\_package-class  
(zzz-DTTCompatibility-class),  
13
- BioAssayData\_ref-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayDataCluster  
(zzz-DTTCompatibility-class),  
13
- bioAssayDataCluster,BioAssayDataCluster\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayDataCluster-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayDataCluster\_assnlist  
(zzz-DTTCompatibility-class),  
13
- bioAssayDataCluster\_assnlist,HigherLevelAnalysis\_package  
(zzz-DTTCompatibility-class),  
13
- BioAssayDataCluster\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayDataCluster\_ref  
(zzz-DTTCompatibility-class),  
13
- bioAssayDataCluster\_ref,AnalysisResults\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayDataCluster\_ref-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayDataSources\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- bioAssayDataSources\_assnreflist,Transformation-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayDataSources\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayDimension  
(zzz-DTTCompatibility-class),  
13
- bioAssayDimension,BioAssayDimension\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayDimension-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayDimension\_assnlist  
(zzz-DTTCompatibility-class),  
13
- bioAssayDimension\_assnlist,BioAssayData\_package-method  
(zzz-DTTCompatibility-class),  
13

BioAssayDimension\_assnlist-class  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayDimension\_assnref  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayDimension\_assnref,DerivedBioAssayData-method  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayDimension\_assnref,MeasuredBioAssayData-method  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayDimension\_assnref,NodeContents-method  
     (zzz-DTTCompatibility-class),  
     13  
 BioAssayDimension\_assnref-class  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayDimension\_ref  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayDimension\_ref,BioAssayDimension\_assnref-method  
     (zzz-DTTCompatibility-class),  
     13  
 BioAssayDimension\_ref-class  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayFactorValues\_assnreflist  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayFactorValues\_assnreflist,DerivedBioAssay-method  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayFactorValues\_assnreflist,MeasuredBioAssay-method  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayFactorValues\_assnreflist,PhysicalBioAssay-method  
     (zzz-DTTCompatibility-class),  
     13  
 BioAssayFactorValues\_assnreflist-class  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayMap  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayMap,BioAssayMap\_assnlist-method  
     (zzz-DTTCompatibility-class),  
     13  
 BioAssayMap-class  
     (zzz-DTTCompatibility-class),  
     13  
 bioAssayMap\_assnlist  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMap\_assnlist,BioAssayData-package-method  
     (zzz-DTTCompatibility-class),  
     13  
     BioAssayMap\_assnlist-class  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMap\_ref  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMap\_ref,BioAssayMaps\_assnreflist-method  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMap\_ref,DerivedBioAssayMap\_assnreflist-method  
     (zzz-DTTCompatibility-class),  
     13  
     BioAssayMap\_ref-class  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMapping  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMapping,BioAssayMapping\_assn-method  
     (zzz-DTTCompatibility-class),  
     13  
     BioAssayMapping-class  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMapping\_assn  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMapping\_assn,Transformation-method  
     (zzz-DTTCompatibility-class),  
     13  
     BioAssayMapping\_assn-class  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMaps\_assnreflist  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMaps\_assnreflist,BioAssayMapping-method  
     (zzz-DTTCompatibility-class),  
     13  
     BioAssayMaps\_assnreflist-class  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMapTarget\_assnref  
     (zzz-DTTCompatibility-class),  
     13  
     bioAssayMapTarget\_assnref,BioAssayMap-method  
     (zzz-DTTCompatibility-class),  
     13

- 13
- BioAssayMapTarget\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- bioAssays\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- bioAssays\_assnreflist,BioAssayDimension-method  
(zzz-DTTCompatibility-class),  
13
- bioAssays\_assnreflist,Experiment-method  
(zzz-DTTCompatibility-class),  
13
- BioAssays\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayTreatment  
(zzz-DTTCompatibility-class),  
13
- bioAssayTreatment,BioAssayTreatments\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayTreatment-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayTreatments\_assnlist  
(zzz-DTTCompatibility-class),  
13
- bioAssayTreatments\_assnlist,PhysicalBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayTreatments\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayTuple  
(zzz-DTTCompatibility-class),  
13
- bioAssayTuple,BioAssayTuples\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayTuple-class  
(zzz-DTTCompatibility-class),  
13
- bioAssayTuples\_assnlist  
(zzz-DTTCompatibility-class),  
13
- bioAssayTuples\_assnlist,BioDataTuples-method  
(zzz-DTTCompatibility-class),  
13
- BioAssayTuples\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- bioDataCube  
(zzz-DTTCompatibility-class),  
13
- bioDataCube,BioDataValues\_assn-method  
(zzz-DTTCompatibility-class),  
13
- BioDataCube-class  
(zzz-DTTCompatibility-class),  
13
- bioDataTuples  
(zzz-DTTCompatibility-class),  
13
- bioDataTuples,BioDataValues\_assn-method  
(zzz-DTTCompatibility-class),  
13
- BioDataTuples-class  
(zzz-DTTCompatibility-class),  
13
- bioDataValues\_assn  
(zzz-DTTCompatibility-class),  
13
- bioDataValues\_assn,DerivedBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- bioDataValues\_assn,MeasuredBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- BioDataValues\_assn-class  
(zzz-DTTCompatibility-class),  
13
- bioEvent\_package  
(zzz-DTTCompatibility-class),  
13
- bioEvent\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- BioEvent\_package-class  
(zzz-DTTCompatibility-class),  
13
- biologicalCharacteristics\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- biologicalCharacteristics\_assnreflist,CompositeSequence  
(zzz-DTTCompatibility-class),  
13
- BiologicalCharacteristics\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- bioMaterial\_assnlist  
(zzz-DTTCompatibility-class),  
13
- bioMaterial\_assnlist,BioMaterial\_package-method

- (zzz-DTTCompatibility-class),  
13
- BioMaterial\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- bioMaterial\_assnref  
(zzz-DTTCompatibility-class),  
13
- bioMaterial\_assnref,BioMaterialMeasurement-method  
(zzz-DTTCompatibility-class),  
13
- bioMaterial\_assnref,ManufactureLIMS-method  
(zzz-DTTCompatibility-class),  
13
- bioMaterial\_assnref,ManufactureLIMSBiomaterial-method  
(zzz-DTTCompatibility-class),  
13
- BioMaterial\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- bioMaterial\_package  
(zzz-DTTCompatibility-class),  
13
- bioMaterial\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- BioMaterial\_package-class  
(zzz-DTTCompatibility-class),  
13
- BioMaterial\_ref-class  
(zzz-DTTCompatibility-class),  
13
- bioMaterialMeasurement  
(zzz-DTTCompatibility-class),  
13
- bioMaterialMeasurement,SourceBioMaterialMeasurements\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- BioMaterialMeasurement-class  
(zzz-DTTCompatibility-class),  
13
- bioMaterialPlateCol  
(zzz-DTTCompatibility-class),  
13
- bioMaterialPlateCol,ManufactureLIMSBiomaterial-method  
(zzz-DTTCompatibility-class),  
13
- bioMaterialPlateIdentifier  
(zzz-DTTCompatibility-class),  
13
- bioMaterialPlateIdentifier,ManufactureLIMSBiomaterial-method  
(zzz-DTTCompatibility-class),  
13
- 13
- bioMaterialPlateRow  
(zzz-DTTCompatibility-class),  
13
- bioMaterialPlateRow,ManufactureLIMSBiomaterial-method  
(zzz-DTTCompatibility-class),  
13
- bioSample (zzz-DTTCompatibility-class),  
13
- bioSample,BioMaterial\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- BioSample-class  
(zzz-DTTCompatibility-class),  
13
- bioSample\_ref  
(zzz-DTTCompatibility-class),  
13
- bioSample\_ref,BioMaterial\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- BioSample\_ref-class  
(zzz-DTTCompatibility-class),  
13
- bioSequence  
(zzz-DTTCompatibility-class),  
13
- bioSequence,BioSequence\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- BioSequence-class  
(zzz-DTTCompatibility-class),  
13
- bioSequence\_assnlist  
(zzz-DTTCompatibility-class),  
13
- bioSequence\_assnlist,BioSequence\_package-method  
(zzz-DTTCompatibility-class),  
13
- BioSequence\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- bioSequence\_package  
(zzz-DTTCompatibility-class),  
13
- bioSequence\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- BioSequence\_package-class  
(zzz-DTTCompatibility-class),  
13
- bioSequence\_ref

- (zzz-DTTCompatibility-class),  
13
- bioSequence\_ref,BiologicalCharacteristics\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- bioSequence\_ref,ImmobilizedCharacteristics\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- BioSequence\_ref-class  
(zzz-DTTCompatibility-class),  
13
- bioSource (zzz-DTTCompatibility-class),  
13
- bioSource,BioMaterial\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- BioSource-class  
(zzz-DTTCompatibility-class),  
13
- bioSource\_ref  
(zzz-DTTCompatibility-class),  
13
- bioSource\_ref,BioMaterial\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- BioSource\_ref-class  
(zzz-DTTCompatibility-class),  
13
- bqs\_package  
(zzz-DTTCompatibility-class),  
13
- bqs\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- BQS\_package-class  
(zzz-DTTCompatibility-class),  
13
- category\_assn  
(zzz-DTTCompatibility-class),  
13
- category\_assn,ExperimentalFactor-method  
(zzz-DTTCompatibility-class),  
13
- Category\_assn-class  
(zzz-DTTCompatibility-class),  
13
- channel (zzz-DTTCompatibility-class), 13
- channel,Channel\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Channel-class  
(zzz-DTTCompatibility-class),  
13
- channel\_assnlist  
(zzz-DTTCompatibility-class),  
13
- channel\_assnlist,BioAssay\_package-method  
(zzz-DTTCompatibility-class),  
13
- Channel\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref,DerivedSignal-method  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref,Error-method  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref,ExpectedValue-method  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref,Failed-method  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref,MeasuredSignal-method  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref,PresentAbsent-method  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref,PValue-method  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref,Ratio-method  
(zzz-DTTCompatibility-class),  
13
- channel\_assnref,SpecializedQuantitationType-method  
(zzz-DTTCompatibility-class),  
13
- Channel\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- channel\_ref  
(zzz-DTTCompatibility-class),  
13
- channel\_ref,Channel\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- channel\_ref,Channels\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13

- Channel\_ref-class  
(zzz-DTTCompatibility-class),  
13
- channels\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- channels\_assnreflist,DerivedBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- channels\_assnreflist,Image-method  
(zzz-DTTCompatibility-class),  
13
- channels\_assnreflist,MeasuredBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- channels\_assnreflist,PhysicalBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- Channels\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- characteristics\_assnlist  
(zzz-DTTCompatibility-class),  
13
- characteristics\_assnlist,BioSample-method  
(zzz-DTTCompatibility-class),  
13
- characteristics\_assnlist,BioSource-method  
(zzz-DTTCompatibility-class),  
13
- characteristics\_assnlist,LabeledExtract-method  
(zzz-DTTCompatibility-class),  
13
- Characteristics\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- clusterBioAssayData\_assnref  
(zzz-DTTCompatibility-class),  
13
- clusterBioAssayData\_assnref,BioAssayDataCluster-method  
(zzz-DTTCompatibility-class),  
13
- ClusterBioAssayData\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- column (zzz-DTTCompatibility-class), 13
- column,FeatureLocation-method  
(zzz-DTTCompatibility-class),  
13
- column,Zone-method  
(zzz-DTTCompatibility-class),  
13
- componentCompounds\_assnlist  
(zzz-DTTCompatibility-class),  
13
- componentCompounds\_assnlist,Compound-method  
(zzz-DTTCompatibility-class),  
13
- ComponentCompounds\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- composite\_assnref  
(zzz-DTTCompatibility-class),  
13
- composite\_assnref,CompositePosition-method  
(zzz-DTTCompatibility-class),  
13
- Composite\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- compositeCompositeMap  
(zzz-DTTCompatibility-class),  
13
- compositeCompositeMap,CompositeCompositeMap\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- compositeCompositeMap,DesignElementMap\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- CompositeCompositeMap-class  
(zzz-DTTCompatibility-class),  
13
- compositeCompositeMap\_assnlist  
(zzz-DTTCompatibility-class),  
13
- compositeCompositeMap\_assnlist,DesignElement\_package-method  
(zzz-DTTCompatibility-class),  
13
- CompositeCompositeMap\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- compositeCompositeMap\_ref  
(zzz-DTTCompatibility-class),  
13
- compositeCompositeMap\_ref,CompositeCompositeMaps\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- compositeCompositeMap\_ref,DesignElementMaps\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- CompositeCompositeMap\_ref-class  
(zzz-DTTCompatibility-class),  
13
- compositeCompositeMaps\_assnreflist

- (zzz-DTTCompatibility-class), 13
- compositeCompositeMaps\_assnreflist, CompositeSequence-assnreflist-method (zzz-DTTCompatibility-class), 13
- CompositeCompositeMaps\_assnreflist-class (zzz-DTTCompatibility-class), 13
- compositeGroup (zzz-DTTCompatibility-class), 13
- compositeGroup, CompositeGroup\_assnlist-method (zzz-DTTCompatibility-class), 13
- CompositeGroup-class (zzz-DTTCompatibility-class), 13
- compositeGroup\_assnlist (zzz-DTTCompatibility-class), 13
- compositeGroup\_assnlist, ArrayDesign\_package-method (zzz-DTTCompatibility-class), 13
- CompositeGroup\_assnlist-class (zzz-DTTCompatibility-class), 13
- compositeGroup\_ref (zzz-DTTCompatibility-class), 13
- compositeGroup\_ref, CompositeGroups\_assnreflist-method (zzz-DTTCompatibility-class), 13
- CompositeGroup\_ref-class (zzz-DTTCompatibility-class), 13
- compositeGroups\_assnreflist (zzz-DTTCompatibility-class), 13
- compositeGroups\_assnreflist, ArrayDesign-method (zzz-DTTCompatibility-class), 13
- compositeGroups\_assnreflist, PhysicalArrayDesign-method (zzz-DTTCompatibility-class), 13
- CompositeGroups\_assnreflist-class (zzz-DTTCompatibility-class), 13
- compositePosition (zzz-DTTCompatibility-class), 13
- compositePosition, CompositePositionSources\_assnlist-method (zzz-DTTCompatibility-class), 13
- compositePosition, Coordinate\_assn-method (zzz-DTTCompatibility-class), 13
- CompositePosition-class (zzz-DTTCompatibility-class), 13
- compositePositionSources\_assnlist (zzz-DTTCompatibility-class), 13
- compositePositionSources\_assnlist, CompositeCompositeMap-assnreflist-method (zzz-DTTCompatibility-class), 13
- CompositePositionSources\_assnlist-class (zzz-DTTCompatibility-class), 13
- compositeSequence (zzz-DTTCompatibility-class), 13
- compositeSequence, CompositeSequence\_assnlist-method (zzz-DTTCompatibility-class), 13
- compositeSequence, DesignElement\_assnlist-method (zzz-DTTCompatibility-class), 13
- CompositeSequence-class (zzz-DTTCompatibility-class), 13
- compositeSequence\_assnlist (zzz-DTTCompatibility-class), 13
- compositeSequence\_assnlist, DesignElement\_package-method (zzz-DTTCompatibility-class), 13
- CompositeSequence\_assnlist-class (zzz-DTTCompatibility-class), 13
- compositeSequence\_assnref (zzz-DTTCompatibility-class), 13
- compositeSequence\_assnref, CompositeCompositeMap-method (zzz-DTTCompatibility-class), 13
- CompositeSequence\_assnref-class (zzz-DTTCompatibility-class), 13
- compositeSequence\_ref (zzz-DTTCompatibility-class), 13

compositeSequence\_ref, Composite\_assnref-method 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequence\_ref, CompositeSequence\_assnref-method 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequence\_ref, CompositeSequences\_assnreflist-method 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequence\_ref, DesignElement\_assnref-method 13  
     (zzz-DTTCompatibility-class), 13  
 CompositeSequence\_ref-class 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequenceDimension 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequenceDimension, DesignElementDimension\_assnlist-method 13  
     (zzz-DTTCompatibility-class), 13  
 CompositeSequenceDimension-class 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequenceDimension\_ref 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequenceDimension\_ref, DesignElementDimension\_assnref-method 13  
     (zzz-DTTCompatibility-class), 13  
 CompositeSequenceDimension\_ref-class 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequences\_assnreflist 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequences\_assnreflist, CompositeGroup-method 13  
     (zzz-DTTCompatibility-class), 13  
 compositeSequences\_assnreflist, CompositeSequenceDimension-method 13  
     (zzz-DTTCompatibility-class), 13  
 CompositeSequences\_assnreflist-class 13  
     (zzz-DTTCompatibility-class), 13  
 compound (zzz-DTTCompatibility-class), 13  
 compound, Compound\_assnlist-method 13  
     (zzz-DTTCompatibility-class), 13  
 Compound-class 13  
     (zzz-DTTCompatibility-class), 13  
     compound\_assnlist (zzz-DTTCompatibility-class), 13  
     compound\_assnlist, BioMaterial\_package-method (zzz-DTTCompatibility-class), 13  
     Compound\_assnlist-class (zzz-DTTCompatibility-class), 13  
     compound\_assnref (zzz-DTTCompatibility-class), 13  
     compound\_assnref, CompoundMeasurement-method (zzz-DTTCompatibility-class), 13  
     Compound\_assnref-class (zzz-DTTCompatibility-class), 13  
     compound\_ref (zzz-DTTCompatibility-class), 13  
     compound\_ref, Compound\_assnref-method (zzz-DTTCompatibility-class), 13  
     compound\_ref, Labels\_assnreflist-method (zzz-DTTCompatibility-class), 13  
     Compound\_ref-class (zzz-DTTCompatibility-class), 13  
     compoundIndices\_assnlist (zzz-DTTCompatibility-class), 13  
     compoundIndices\_assnlist, Compound-method (zzz-DTTCompatibility-class), 13  
     CompoundIndices\_assnlist-class (zzz-DTTCompatibility-class), 13  
     compoundMeasurement (zzz-DTTCompatibility-class), 13  
     compoundMeasurement, ComponentCompounds\_assnlist-method (zzz-DTTCompatibility-class), 13  
     compoundMeasurement, CompoundMeasurements\_assnlist-method (zzz-DTTCompatibility-class), 13  
     CompoundMeasurement-class (zzz-DTTCompatibility-class), 13





- (zzz-DTTCompatibility-class),  
13
- controlledFeatures\_assnreflist,Feature-method  
(zzz-DTTCompatibility-class),  
13
- ControlledFeatures\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- controlType\_assn  
(zzz-DTTCompatibility-class),  
13
- controlType\_assn,CompositeSequence-method  
(zzz-DTTCompatibility-class),  
13
- controlType\_assn,Feature-method  
(zzz-DTTCompatibility-class),  
13
- controlType\_assn,Reporter-method  
(zzz-DTTCompatibility-class),  
13
- ControlType\_assn-class  
(zzz-DTTCompatibility-class),  
13
- coordinate\_assn  
(zzz-DTTCompatibility-class),  
13
- coordinate\_assn,SeqFeatureLocation-method  
(zzz-DTTCompatibility-class),  
13
- Coordinate\_assn-class  
(zzz-DTTCompatibility-class),  
13
- createdBy (zzz-ARRCompatibility-class),  
12
- createdBy,ArraySetFile-method  
(zzz-ARRCompatibility-class),  
12
- createdBy,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- createdBy,TemplateFile-method  
(zzz-ARRCompatibility-class),  
12
- createdDateTime  
(zzz-ARRCompatibility-class),  
12
- createdDateTime,ArraySetFile-method  
(zzz-ARRCompatibility-class),  
12
- createdDateTime,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- createdDateTime,TemplateFile-method  
(zzz-ARRCompatibility-class),  
12
- createdStep  
(zzz-ARRCompatibility-class),  
12
- createdStep,ArraySetFile-method  
(zzz-ARRCompatibility-class),  
12
- createdStep,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- database (zzz-DTTCompatibility-class),  
13
- database,Database\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Database-class  
(zzz-DTTCompatibility-class),  
13
- database\_assnlist  
(zzz-DTTCompatibility-class),  
13
- database\_assnlist,Description\_package-method  
(zzz-DTTCompatibility-class),  
13
- Database\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- database\_assnref  
(zzz-DTTCompatibility-class),  
13
- database\_assnref,DatabaseEntry-method  
(zzz-DTTCompatibility-class),  
13
- Database\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- database\_ref  
(zzz-DTTCompatibility-class),  
13
- database\_ref,Database\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- Database\_ref-class  
(zzz-DTTCompatibility-class),  
13
- databaseEntry  
(zzz-DTTCompatibility-class),  
13
- databaseEntry,Accessions\_assnlist-method  
(zzz-DTTCompatibility-class),

- 13
- databaseEntry, DatabaseReferences\_assnlist-method (zzz-DTTCompatibility-class), 13
- databaseEntry, ExternalLIMS\_assn-method (zzz-DTTCompatibility-class), 13
- databaseEntry, IdentifierLIMS\_assn-method (zzz-DTTCompatibility-class), 13
- databaseEntry, OntologyReference\_assn-method (zzz-DTTCompatibility-class), 13
- databaseEntry, SequenceDatabases\_assnlist-method (zzz-DTTCompatibility-class), 13
- DatabaseEntry-class (zzz-DTTCompatibility-class), 13
- databaseReferences\_assnlist (zzz-DTTCompatibility-class), 13
- databaseReferences\_assnlist, Description-method (zzz-DTTCompatibility-class), 13
- DatabaseReferences\_assnlist-class (zzz-DTTCompatibility-class), 13
- dataExternal (zzz-DTTCompatibility-class), 13
- dataExternal, DataExternal\_assn-method (zzz-DTTCompatibility-class), 13
- DataExternal-class (zzz-DTTCompatibility-class), 13
- dataExternal\_assn (zzz-DTTCompatibility-class), 13
- dataExternal\_assn, BioDataCube-method (zzz-DTTCompatibility-class), 13
- DataExternal\_assn-class (zzz-DTTCompatibility-class), 13
- dataFormat (zzz-DTTCompatibility-class), 13
- dataFormat, DataExternal-method (zzz-DTTCompatibility-class), 13
- dataFormatInfoURI (zzz-DTTCompatibility-class), 13
- dataFormatInfoURI, DataExternal-method (zzz-DTTCompatibility-class), 13
- dataInternal (zzz-DTTCompatibility-class), 13
- dataInternal, DataInternal\_assn-method (zzz-DTTCompatibility-class), 13
- DataInternal-class (zzz-DTTCompatibility-class), 13
- dataInternal\_assn (zzz-DTTCompatibility-class), 13
- dataInternal\_assn, BioDataCube-method (zzz-DTTCompatibility-class), 13
- DataInternal\_assn-class (zzz-DTTCompatibility-class), 13
- dataType\_assn (zzz-DTTCompatibility-class), 13
- dataType\_assn, DerivedSignal-method (zzz-DTTCompatibility-class), 13
- dataType\_assn, Error-method (zzz-DTTCompatibility-class), 13
- dataType\_assn, ExpectedValue-method (zzz-DTTCompatibility-class), 13
- dataType\_assn, Failed-method (zzz-DTTCompatibility-class), 13
- dataType\_assn, MeasuredSignal-method (zzz-DTTCompatibility-class), 13
- dataType\_assn, NodeValue-method (zzz-DTTCompatibility-class), 13
- dataType\_assn, Parameter-method (zzz-DTTCompatibility-class), 13
- dataType\_assn, PresentAbsent-method (zzz-DTTCompatibility-class), 13
- dataType\_assn, PValue-method

- (zzz-DTTCompatibility-class),  
13
- dataType\_assn,Ratio-method  
(zzz-DTTCompatibility-class),  
13
- dataType\_assn,SpecializedQuantitationType-method  
(zzz-DTTCompatibility-class),  
13
- DataType\_assn-class  
(zzz-DTTCompatibility-class),  
13
- datum (zzz-DTTCompatibility-class), 13
- datum,Datum\_assn-method  
(zzz-DTTCompatibility-class),  
13
- Datum-class  
(zzz-DTTCompatibility-class),  
13
- datum\_assn  
(zzz-DTTCompatibility-class),  
13
- datum\_assn,QuantitationTypeTuple-method  
(zzz-DTTCompatibility-class),  
13
- Datum\_assn-class  
(zzz-DTTCompatibility-class),  
13
- defaultValue  
(zzz-ARRCompatibility-class),  
12
- defaultValue,UserAttribute-method  
(zzz-ARRCompatibility-class),  
12
- defaultValue\_assn  
(zzz-DTTCompatibility-class),  
13
- defaultValue\_assn,Parameter-method  
(zzz-DTTCompatibility-class),  
13
- DefaultValue\_assn-class  
(zzz-DTTCompatibility-class),  
13
- defectType\_assn  
(zzz-DTTCompatibility-class),  
13
- defectType\_assn,FeatureDefect-method  
(zzz-DTTCompatibility-class),  
13
- defectType\_assn,ZoneDefect-method  
(zzz-DTTCompatibility-class),  
13
- DefectType\_assn-class  
(zzz-DTTCompatibility-class),  
13
- deltaX (zzz-DTTCompatibility-class), 13
- deltaX,PositionDelta-method  
(zzz-DTTCompatibility-class),  
13
- deltaY (zzz-DTTCompatibility-class), 13
- deltaY,PositionDelta-method  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssay  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssay,BioAssay\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssay,DerivedBioAssay\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- DerivedBioAssay-class  
(zzz-DTTCompatibility-class),  
13
- DerivedBioAssay\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssay\_ref  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssay\_ref,BioAssay\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssay\_ref,BioAssayMapTarget\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssay\_ref,BioAssays\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssay\_ref,SourceBioAssays\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssay\_ref,TopLevelBioAssays\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- DerivedBioAssay\_ref-class  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssayData  
(zzz-DTTCompatibility-class),  
13
- derivedBioAssayData,BioAssayData\_assnlist-method  
(zzz-DTTCompatibility-class),  
13

derivedBioAssayData, DerivedBioAssayData\_assnlist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 DerivedBioAssayData-class (zzz-DTTCompatibility-class), 13  
 DerivedBioAssayData\_assnlist-class (zzz-DTTCompatibility-class), 13  
 derivedBioAssayData\_assnreflist (zzz-DTTCompatibility-class), 13  
 derivedBioAssayData\_assnreflist, DerivedBioAssay-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 DerivedBioAssayData\_assnreflist-class (zzz-DTTCompatibility-class), 13  
 derivedBioAssayData\_ref (zzz-DTTCompatibility-class), 13  
 derivedBioAssayData\_ref, BioAssayData\_assnreflist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 derivedBioAssayData\_ref, BioAssayDataSources\_assnreflist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 derivedBioAssayData\_ref, ClusterBioAssayData\_assnref-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 derivedBioAssayData\_ref, DerivedBioAssayData\_assnreflist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 derivedBioAssayData\_ref, DerivedBioAssayDataTarget\_assnref-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 DerivedBioAssayData\_ref-class (zzz-DTTCompatibility-class), 13  
 13  
 DerivedBioAssayDataTarget\_assnref-class (zzz-DTTCompatibility-class), 13  
 13  
 derivedBioAssayMap\_assnreflist (zzz-DTTCompatibility-class), 13  
 13  
 derivedBioAssayMap\_assnreflist, DerivedBioAssay-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 DerivedBioAssayMap\_assnreflist-class (zzz-DTTCompatibility-class), 13  
 (zzz-DTTCompatibility-class), 13  
 13  
 derivedSignal (zzz-DTTCompatibility-class), 13  
 derivedSignal, QuantitationType\_assnlist-method (zzz-DTTCompatibility-class), 13  
 13  
 DerivedSignal-class (zzz-DTTCompatibility-class), 13  
 derivedSignal\_ref (zzz-DTTCompatibility-class), 13  
 derivedSignal\_ref, QuantitationType\_assnref-method (zzz-DTTCompatibility-class), 13  
 13  
 derivedSignal\_ref, QuantitationTypes\_assnreflist-method (zzz-DTTCompatibility-class), 13  
 13  
 derivedSignal\_ref, SourcesQuantitationType\_assnreflist-method (zzz-DTTCompatibility-class), 13  
 13  
 derivedSignal\_ref, TargetQuantitationType\_assnref-method (zzz-DTTCompatibility-class), 13  
 13  
 DerivedSignal\_ref-class (zzz-DTTCompatibility-class), 13  
 description (zzz-DTTCompatibility-class), 13  
 description, Descriptions\_assnlist-method (zzz-DTTCompatibility-class), 13  
 description, NormalizationDescription\_assn-method (zzz-DTTCompatibility-class), 13  
 description, OntologyEntry-method (zzz-DTTCompatibility-class), 13  
 description, QualityControlDescription\_assn-method (zzz-DTTCompatibility-class), 13  
 description, ReplicateDescription\_assn-method (zzz-DTTCompatibility-class), 13  
 Description-class (zzz-DTTCompatibility-class), 13  
 description\_package (zzz-DTTCompatibility-class), 13  
 description\_package, MAGE-ML-method (zzz-DTTCompatibility-class), 13

- 13
- Description\_package-class  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Array-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,ArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,ArrayManufacture-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Audit-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,BioAssayCreation-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,BioAssayDataCluster-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,BioAssayDimension-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,BioAssayMap-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,BioAssayTreatment-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,BioSample-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,BioSource-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Channel-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,CompositeCompositeMap-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,CompositeGroup-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,CompositeSequence-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,CompositeSequenceDimension-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Compound-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Database-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,DerivedBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,DerivedBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,DerivedSignal-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Description-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Error-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,ExpectedValue-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Experiment-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,ExperimentalFactor-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,ExperimentDesign-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,FactorValue-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Failed-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Feature-method

- (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, FeatureDimension-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, FeatureExtraction-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, FeatureGroup-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, FeatureReporterMap-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Fiducial-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Hardware-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, HardwareApplication-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Hybridization-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Image-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, ImageAcquisition-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, LabeledExtract-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, MAGE-ML-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, ManufactureLIMS-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, ManufactureLIMSBiomaterial-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, MeasuredBioAssay-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, MeasuredBioAssayData-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, MeasuredSignal-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Node-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, NodeContents-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Organization-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Parameter-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Person-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, PhysicalArrayDesign-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, PhysicalBioAssay-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, PresentAbsent-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Protocol-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, ProtocolApplication-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, PValue-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, QuantitationTypeDimension-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, QuantitationTypeMap-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Ratio-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, Reporter-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, ReporterCompositeMap-method (zzz-DTTCompatibility-class), 13
- descriptions\_assnlist, ReporterDimension-method (zzz-DTTCompatibility-class), 13

- descriptions\_assnlist,ReporterGroup-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Security-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,SecurityGroup-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,SeqFeature-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Software-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,SoftwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,SpecializedQuantitationType-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Transformation-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Treatment-method  
(zzz-DTTCompatibility-class),  
13
- descriptions\_assnlist,Zone-method  
(zzz-DTTCompatibility-class),  
13
- Descriptions\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- DesignElement\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- designElement\_assnref  
(zzz-DTTCompatibility-class),  
13
- designElement\_assnref,DesignElementTuple-method  
(zzz-DTTCompatibility-class),  
13
- DesignElement\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- designElement\_package  
(zzz-DTTCompatibility-class),  
13
- designElement\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- DesignElement\_package-class  
(zzz-DTTCompatibility-class),  
13
- (zzz-DTTCompatibility-class),  
13
- DesignElement\_ref-class  
(zzz-DTTCompatibility-class),  
13
- designElementDimension\_assnlist  
(zzz-DTTCompatibility-class),  
13
- designElementDimension\_assnlist,BioAssayData\_package-me  
(zzz-DTTCompatibility-class),  
13
- DesignElementDimension\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- designElementDimension\_assnref  
(zzz-DTTCompatibility-class),  
13
- designElementDimension\_assnref,DerivedBioAssayData-meth  
(zzz-DTTCompatibility-class),  
13
- designElementDimension\_assnref,MeasuredBioAssayData-meth  
(zzz-DTTCompatibility-class),  
13
- designElementDimension\_assnref,NodeContents-method  
(zzz-DTTCompatibility-class),  
13
- DesignElementDimension\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- DesignElementDimension\_ref-class  
(zzz-DTTCompatibility-class),  
13
- DesignElementMap\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- DesignElementMap\_ref-class  
(zzz-DTTCompatibility-class),  
13
- designElementMapping  
(zzz-DTTCompatibility-class),  
13
- designElementMapping,DesignElementMapping\_assn-method  
(zzz-DTTCompatibility-class),  
13
- DesignElementMapping-class  
(zzz-DTTCompatibility-class),  
13
- designElementMapping\_assn  
(zzz-DTTCompatibility-class),  
13
- designElementMapping\_assn,Transformation-method  
(zzz-DTTCompatibility-class),  
13



- 13
- DesignElementMapping\_assn-class  
(zzz-DTTCompatibility-class),  
13
- designElementMaps\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- designElementMaps\_assnreflist, DesignElementMapping-method  
(zzz-DTTCompatibility-class),  
13
- DesignElementMaps\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- designElementTuple  
(zzz-DTTCompatibility-class),  
13
- designElementTuple, DesignElementTuples\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- DesignElementTuple-class  
(zzz-DTTCompatibility-class),  
13
- designElementTuples\_assnlist  
(zzz-DTTCompatibility-class),  
13
- designElementTuples\_assnlist, BioAssayTuple-method  
(zzz-DTTCompatibility-class),  
13
- DesignElementTuples\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- designProviders\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- designProviders\_assnreflist, ArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- designProviders\_assnreflist, PhysicalArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- DesignProviders\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- directory (accessors), 2
- directory, NetAffxResource-method  
(NetAffxResource-class), 5
- distanceUnit  
(zzz-DTTCompatibility-class),  
13
- distanceUnit, DistanceUnit\_assn-method  
(zzz-DTTCompatibility-class),  
13
- distanceUnit, Unit\_assn-method  
(zzz-DTTCompatibility-class),  
13
- DistanceUnit-class  
(zzz-DTTCompatibility-class),  
13
- distanceUnit\_assn  
(zzz-DTTCompatibility-class),  
13
- distanceUnit\_assn, ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- distanceUnit\_assn, FeatureGroup-method  
(zzz-DTTCompatibility-class),  
13
- distanceUnit\_assn, Fiducial-method  
(zzz-DTTCompatibility-class),  
13
- distanceUnit\_assn, Position-method  
(zzz-DTTCompatibility-class),  
13
- distanceUnit\_assn, PositionDelta-method  
(zzz-DTTCompatibility-class),  
13
- distanceUnit\_assn, Zone-method  
(zzz-DTTCompatibility-class),  
13
- distanceUnit\_assn, ZoneGroup-method  
(zzz-DTTCompatibility-class),  
13
- distanceUnit\_assn, ZoneLayout-method  
(zzz-DTTCompatibility-class),  
13
- DistanceUnit\_assn-class  
(zzz-DTTCompatibility-class),  
13
- DTTCompatibility, 14
- DTTCompatibility-class  
(AffyCompatible-class), 3
- editor (zzz-DTTCompatibility-class), 13
- editor, BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- email (zzz-DTTCompatibility-class), 13
- email, Organization-method  
(zzz-DTTCompatibility-class),  
13
- email, Person-method  
(zzz-DTTCompatibility-class),  
13
- error (zzz-DTTCompatibility-class), 13

- error,ConfidenceIndicator\_assnlist-method (zzz-DTTCompatibility-class), 13  
 error,QuantitationType\_assnlist-method (zzz-DTTCompatibility-class), 13  
 Error-class (zzz-DTTCompatibility-class), 13  
 error\_ref (zzz-DTTCompatibility-class), 13  
 error\_ref,ConfidenceIndicators\_assnreflist-method (zzz-DTTCompatibility-class), 13  
 error\_ref,QuantitationType\_assnref-method (zzz-DTTCompatibility-class), 13  
 error\_ref,QuantitationTypes\_assnreflist-method (zzz-DTTCompatibility-class), 13  
 error\_ref,SourcesQuantitationType\_assnreflist-method (zzz-DTTCompatibility-class), 13  
 error\_ref,TargetQuantitationType\_assnref-method (zzz-DTTCompatibility-class), 13  
 Error\_ref-class (zzz-DTTCompatibility-class), 13  
 expectedValue (zzz-DTTCompatibility-class), 13  
 expectedValue,ConfidenceIndicator\_assnlist-method (zzz-DTTCompatibility-class), 13  
 expectedValue,QuantitationType\_assnlist-method (zzz-DTTCompatibility-class), 13  
 ExpectedValue-class (zzz-DTTCompatibility-class), 13  
 expectedValue\_ref (zzz-DTTCompatibility-class), 13  
 expectedValue\_ref,ConfidenceIndicators\_assnreflist-method (zzz-DTTCompatibility-class), 13  
 expectedValue\_ref,QuantitationType\_assnref-method (zzz-DTTCompatibility-class), 13  
 expectedValue\_ref,QuantitationTypes\_assnreflist-method (zzz-DTTCompatibility-class), 13  
 expectedValue\_ref,SourcesQuantitationType\_assnreflist-method (zzz-DTTCompatibility-class), 13  
 expectedValue\_ref,TargetQuantitationType\_assnref-method (zzz-DTTCompatibility-class), 13  
 ExpectedValue\_ref-class (zzz-DTTCompatibility-class), 13  
 experiment (zzz-DTTCompatibility-class), 13  
 experiment,Experiment\_assnlist-method (zzz-DTTCompatibility-class), 13  
 Experiment-class (zzz-DTTCompatibility-class), 13  
 experiment\_assnlist (zzz-DTTCompatibility-class), 13  
 experiment\_assnlist,Experiment\_package-method (zzz-DTTCompatibility-class), 13  
 Experiment\_assnlist-class (zzz-DTTCompatibility-class), 13  
 experiment\_package (zzz-DTTCompatibility-class), 13  
 experiment\_package,MAGE-ML-method (zzz-DTTCompatibility-class), 13  
 Experiment\_package-class (zzz-DTTCompatibility-class), 13  
 experimentalFactor (zzz-DTTCompatibility-class), 13  
 experimentalFactor,ExperimentalFactors\_assnlist-method (zzz-DTTCompatibility-class), 13  
 ExperimentalFactor-class (zzz-DTTCompatibility-class), 13  
 ExperimentalFactor\_assnref-class (zzz-DTTCompatibility-class), 13  
 experimentalFactor\_ref (zzz-DTTCompatibility-class), 13

- experimentalFactor\_ref, ExperimentalFactor\_assnref-method  
(zzz-DTTCompatibility-class), 13
- ExperimentalFactor\_ref-class  
(zzz-DTTCompatibility-class), 13
- experimentalFactors\_assnlist  
(zzz-DTTCompatibility-class), 13
- experimentalFactors\_assnlist, ExperimentDesign-method  
(zzz-DTTCompatibility-class), 13
- ExperimentalFactors\_assnlist-class  
(zzz-DTTCompatibility-class), 13
- experimentDesign  
(zzz-DTTCompatibility-class), 13
- experimentDesign, ExperimentDesigns\_assnlist-method  
(zzz-DTTCompatibility-class), 13
- ExperimentDesign-class  
(zzz-DTTCompatibility-class), 13
- experimentDesigns\_assnlist  
(zzz-DTTCompatibility-class), 13
- experimentDesigns\_assnlist, Experiment-method  
(zzz-DTTCompatibility-class), 13
- ExperimentDesigns\_assnlist-class  
(zzz-DTTCompatibility-class), 13
- exportedFromDB  
(zzz-DTTCompatibility-class), 13
- exportedFromDB, ExternalReference-method  
(zzz-DTTCompatibility-class), 13
- exportedFromServer  
(zzz-DTTCompatibility-class), 13
- exportedFromServer, ExternalReference-method  
(zzz-DTTCompatibility-class), 13
- exportID (zzz-DTTCompatibility-class), 13
- exportID, ExternalReference-method  
(zzz-DTTCompatibility-class), 13
- exportName  
(zzz-DTTCompatibility-class), 13
- exportName, ExternalReference-method  
(zzz-DTTCompatibility-class), 13
- externalLIMS\_assn  
(zzz-DTTCompatibility-class), 13
- externalLIMS\_assn, Compound-method  
(zzz-DTTCompatibility-class), 13
- ExternalLIMS\_assn-class  
(zzz-DTTCompatibility-class), 13
- externalReference  
(zzz-DTTCompatibility-class), 13
- externalReference, ExternalReference\_assn-method  
(zzz-DTTCompatibility-class), 13
- externalReference\_assn  
(zzz-DTTCompatibility-class), 13
- externalReference\_assn, Description-method  
(zzz-DTTCompatibility-class), 13
- ExternalReference\_assn-class  
(zzz-DTTCompatibility-class), 13
- factorValue  
(zzz-DTTCompatibility-class), 13
- factorValue, FactorValues\_assnlist-method  
(zzz-DTTCompatibility-class), 13
- FactorValue-class  
(zzz-DTTCompatibility-class), 13
- factorValue\_ref  
(zzz-DTTCompatibility-class), 13
- factorValue\_ref, BioAssayFactorValues\_assnreflist-method  
(zzz-DTTCompatibility-class), 13
- FactorValue\_ref-class  
(zzz-DTTCompatibility-class), 13
- factorValues\_assnlist  
(zzz-DTTCompatibility-class), 13
- factorValues\_assnlist, ExperimentalFactor-method  
(zzz-DTTCompatibility-class), 13

- FactorValues\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- failed (zzz-DTTCompatibility-class), 13
- failed, QuantitationType\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Failed-class  
(zzz-DTTCompatibility-class),  
13
- failed\_ref  
(zzz-DTTCompatibility-class),  
13
- failed\_ref, QuantitationType\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- failed\_ref, QuantitationTypes\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- failed\_ref, SourcesQuantitationType\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- failed\_ref, TargetQuantitationType\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- Failed\_ref-class  
(zzz-DTTCompatibility-class),  
13
- failTypes\_assnlist  
(zzz-DTTCompatibility-class),  
13
- failTypes\_assnlist, Reporter-method  
(zzz-DTTCompatibility-class),  
13
- FailTypes\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- fax (zzz-DTTCompatibility-class), 13
- fax, Organization-method  
(zzz-DTTCompatibility-class),  
13
- fax, Person-method  
(zzz-DTTCompatibility-class),  
13
- feature (zzz-DTTCompatibility-class), 13
- feature, DesignElement\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- feature, Features\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Feature-class  
(zzz-DTTCompatibility-class),  
13
- feature\_assnref  
(zzz-DTTCompatibility-class),  
13
- feature\_assnref, FeatureDefect-method  
(zzz-DTTCompatibility-class),  
13
- feature\_assnref, FeatureInformation-method  
(zzz-DTTCompatibility-class),  
13
- feature\_assnref, ManufactureLIMS-method  
(zzz-DTTCompatibility-class),  
13
- feature\_assnref, ManufactureLIMSBiomaterial-method  
(zzz-DTTCompatibility-class),  
13
- Feature\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- feature\_ref  
(zzz-DTTCompatibility-class),  
13
- feature\_ref, ContainedFeatures\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- feature\_ref, ControlFeatures\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- feature\_ref, ControlledFeatures\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- feature\_ref, DesignElement\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- feature\_ref, Feature\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- Feature\_ref-class  
(zzz-DTTCompatibility-class),  
13
- featureDefect  
(zzz-DTTCompatibility-class),  
13
- featureDefect, FeatureDefects\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- FeatureDefect-class  
(zzz-DTTCompatibility-class),  
13
- featureDefects\_assnlist  
(zzz-DTTCompatibility-class),  
13

- 13  
 featureDefects\_assnlist,ArrayManufactureDeviation-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureDefects\_assnlist-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureDimension  
 (zzz-DTTCompatibility-class),  
 13  
 featureDimension,DesignElementDimension\_assnlist-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureDimension-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureDimension\_ref  
 (zzz-DTTCompatibility-class),  
 13  
 featureDimension\_ref,DesignElementDimension\_assnref-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureDimension\_ref-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureExtraction  
 (zzz-DTTCompatibility-class),  
 13  
 featureExtraction,FeatureExtraction\_assn-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureExtraction-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureExtraction\_assn  
 (zzz-DTTCompatibility-class),  
 13  
 featureExtraction\_assn,MeasuredBioAssay-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureExtraction\_assn-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureGroup  
 (zzz-DTTCompatibility-class),  
 13  
 featureGroup,FeatureGroups\_assnlist-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureGroup-class  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureGroup\_assnref-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureGroup\_ref  
 (zzz-DTTCompatibility-class),  
 13  
 featureGroup\_ref,FeatureGroup\_assnref-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureGroup\_ref-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureGroups\_assnlist  
 (zzz-DTTCompatibility-class),  
 13  
 featureGroups\_assnlist,ArrayDesign-method  
 (zzz-DTTCompatibility-class),  
 13  
 featureGroups\_assnlist,PhysicalArrayDesign-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureGroups\_assnlist-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureHeight  
 (zzz-DTTCompatibility-class),  
 13  
 featureHeight,FeatureGroup-method  
 (zzz-DTTCompatibility-class),  
 13  
 featureInformation  
 (zzz-DTTCompatibility-class),  
 13  
 featureInformation,FeatureInformationSources\_assnlist-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureInformation-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureInformationSources\_assnlist  
 (zzz-DTTCompatibility-class),  
 13  
 featureInformationSources\_assnlist,FeatureReporterMap-method  
 (zzz-DTTCompatibility-class),  
 13  
 FeatureInformationSources\_assnlist-class  
 (zzz-DTTCompatibility-class),  
 13  
 featureLength  
 (zzz-DTTCompatibility-class),  
 13  
 featureLength,FeatureGroup-method

- (zzz-DTTCompatibility-class),  
13
- featureIMSSs\_assnlist  
(zzz-DTTCompatibility-class),  
13
- featureIMSSs\_assnlist,ArrayManufacture-method  
(zzz-DTTCompatibility-class),  
13
- FeatureIMSSs\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- featureLocation  
(zzz-DTTCompatibility-class),  
13
- featureLocation,FeatureLocation\_assn-method  
(zzz-DTTCompatibility-class),  
13
- FeatureLocation-class  
(zzz-DTTCompatibility-class),  
13
- featureLocation\_assn  
(zzz-DTTCompatibility-class),  
13
- featureLocation\_assn,Feature-method  
(zzz-DTTCompatibility-class),  
13
- FeatureLocation\_assn-class  
(zzz-DTTCompatibility-class),  
13
- featureReporterMap  
(zzz-DTTCompatibility-class),  
13
- featureReporterMap,DesignElementMap\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- featureReporterMap,FeatureReporterMap\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- FeatureReporterMap-class  
(zzz-DTTCompatibility-class),  
13
- featureReporterMap\_assnlist  
(zzz-DTTCompatibility-class),  
13
- featureReporterMap\_assnlist,DesignElement\_package-method  
(zzz-DTTCompatibility-class),  
13
- FeatureReporterMap\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- featureReporterMap\_ref  
(zzz-DTTCompatibility-class),  
13
- featureReporterMap\_ref,DesignElementMaps\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- featureReporterMap\_ref,FeatureReporterMaps\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- FeatureReporterMap\_ref-class  
(zzz-DTTCompatibility-class),  
13
- featureReporterMaps\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- featureReporterMaps\_assnreflist,Reporter-method  
(zzz-DTTCompatibility-class),  
13
- FeatureReporterMaps\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- features\_assnlist  
(zzz-DTTCompatibility-class),  
13
- features\_assnlist,FeatureGroup-method  
(zzz-DTTCompatibility-class),  
13
- Features\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- featureShape\_assn  
(zzz-DTTCompatibility-class),  
13
- featureShape\_assn,FeatureGroup-method  
(zzz-DTTCompatibility-class),  
13
- FeatureShape\_assn-class  
(zzz-DTTCompatibility-class),  
13
- featureWidth  
(zzz-DTTCompatibility-class),  
13
- featureWidth,FeatureGroup-method  
(zzz-DTTCompatibility-class),  
13
- fiducial (zzz-DTTCompatibility-class),  
13
- fiducial,Fiducials\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Fiducial-class  
(zzz-DTTCompatibility-class),  
13
- fiducials\_assnlist

(zzz-DTTCompatibility-class),  
13

fiducials\_assnlist,ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13

Fiducials\_assnlist-class  
(zzz-DTTCompatibility-class),  
13

fiducialType\_assn  
(zzz-DTTCompatibility-class),  
13

fiducialType\_assn,Fiducial-method  
(zzz-DTTCompatibility-class),  
13

FiducialType\_assn-class  
(zzz-DTTCompatibility-class),  
13

filenameURI  
(zzz-DTTCompatibility-class),  
13

filenameURI,DataExternal-method  
(zzz-DTTCompatibility-class),  
13

firstName (zzz-DTTCompatibility-class),  
13

firstName,Person-method  
(zzz-DTTCompatibility-class),  
13

format\_assn  
(zzz-DTTCompatibility-class),  
13

format\_assn,Image-method  
(zzz-DTTCompatibility-class),  
13

Format\_assn-class  
(zzz-DTTCompatibility-class),  
13

guid (zzz-ARRCompatibility-class), 12

guid,ArraySetFile-method  
(zzz-ARRCompatibility-class),  
12

guid,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12

guid,TemplateFile-method  
(zzz-ARRCompatibility-class),  
12

hardware (zzz-DTTCompatibility-class),  
13

hardware,Hardware\_assnlist-method  
(zzz-DTTCompatibility-class),

13

Hardware-class  
(zzz-DTTCompatibility-class),  
13

hardware\_assnlist  
(zzz-DTTCompatibility-class),  
13

hardware\_assnlist,Protocol\_package-method  
(zzz-DTTCompatibility-class),  
13

Hardware\_assnlist-class  
(zzz-DTTCompatibility-class),  
13

hardware\_assnref  
(zzz-DTTCompatibility-class),  
13

hardware\_assnref,HardwareApplication-method  
(zzz-DTTCompatibility-class),  
13

hardware\_assnref,Software-method  
(zzz-DTTCompatibility-class),  
13

Hardware\_assnref-class  
(zzz-DTTCompatibility-class),  
13

hardware\_ref  
(zzz-DTTCompatibility-class),  
13

hardware\_ref,Hardware\_assnref-method  
(zzz-DTTCompatibility-class),  
13

hardware\_ref,Hardwares\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13

Hardware\_ref-class  
(zzz-DTTCompatibility-class),  
13

hardwareApplication  
(zzz-DTTCompatibility-class),  
13

hardwareApplication,HardwareApplications\_assnlist-method  
(zzz-DTTCompatibility-class),  
13

HardwareApplication-class  
(zzz-DTTCompatibility-class),  
13

hardwareApplications\_assnlist  
(zzz-DTTCompatibility-class),  
13

hardwareApplications\_assnlist,ProtocolApplication-method  
(zzz-DTTCompatibility-class),  
13

- HardwareApplications\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- hardwareManufacturers\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- hardwareManufacturers\_assnreflist,Hardware-method  
(zzz-DTTCompatibility-class),  
13
- HardwareManufacturers\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- hardwares\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- hardwares\_assnreflist,Protocol-method  
(zzz-DTTCompatibility-class),  
13
- Hardwares\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- higherLevelAnalysis\_package  
(zzz-DTTCompatibility-class),  
13
- higherLevelAnalysis\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- HigherLevelAnalysis\_package-class  
(zzz-DTTCompatibility-class),  
13
- hybridization  
(zzz-DTTCompatibility-class),  
13
- hybridization,BioAssayCreation\_assn-method  
(zzz-DTTCompatibility-class),  
13
- Hybridization-class  
(zzz-DTTCompatibility-class),  
13
- identifier  
(zzz-DTTCompatibility-class),  
13
- identifier,Array-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Array\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ArrayDesign\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ArrayGroup\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ArrayManufacture-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ArrayManufacture\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssay\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssayCreation-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssayData\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssayDataCluster-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssayDataCluster\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssayDimension-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssayDimension\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssayMap-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssayMap\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioAssayTreatment-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioMaterial\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioSample-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioSample\_ref-method  
(zzz-DTTCompatibility-class),  
13



- 13
- identifier,BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioSequence\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioSource-method  
(zzz-DTTCompatibility-class),  
13
- identifier,BioSource\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Channel-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Channel\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,CompositeCompositeMap-method  
(zzz-DTTCompatibility-class),  
13
- identifier,CompositeCompositeMap\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,CompositeGroup-method  
(zzz-DTTCompatibility-class),  
13
- identifier,CompositeGroup\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,CompositeSequence-method  
(zzz-DTTCompatibility-class),  
13
- identifier,CompositeSequence\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,CompositeSequenceDimension-method  
(zzz-DTTCompatibility-class),  
13
- identifier,CompositeSequenceDimension\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Compound-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Compound\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ConfidenceIndicator\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier>Contact\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Database-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Database\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,DerivedBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- identifier,DerivedBioAssay\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,DerivedBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- identifier,DerivedBioAssayData\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,DerivedSignal-method  
(zzz-DTTCompatibility-class),  
13
- identifier,DerivedSignal\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,DesignElement\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,DesignElementDimension\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,DesignElementMap\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Error-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Error\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ExpectedValue-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ExpectedValue\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier,Experiment-method  
(zzz-DTTCompatibility-class),  
13
- identifier,ExperimentalFactor-method

- (zzz-DTTCompatibility-class),  
13
- identifier, ExperimentalFactor\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier, FactorValue-method  
(zzz-DTTCompatibility-class),  
13
- identifier, FactorValue\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier, Failed-method  
(zzz-DTTCompatibility-class),  
13
- identifier, Failed\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier, Feature-method  
(zzz-DTTCompatibility-class),  
13
- identifier, Feature\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier, FeatureDimension-method  
(zzz-DTTCompatibility-class),  
13
- identifier, FeatureDimension\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier, FeatureExtraction-method  
(zzz-DTTCompatibility-class),  
13
- identifier, FeatureGroup-method  
(zzz-DTTCompatibility-class),  
13
- identifier, FeatureGroup\_ref-method  
(zzz-DTTCompatibility-class),  
13
- identifier, FeatureReporterMap-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- identifier, Hardware-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- 13
- identifier, Image-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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13
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13
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13
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13
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13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13

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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
13
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13
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13
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13
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13
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13
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- 13
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13
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13
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(zzz-DTTCompatibility-class),  
13
- IdentifierLIMS\_assn-class  
(zzz-DTTCompatibility-class),  
13
- Image-class  
(zzz-DTTCompatibility-class),  
13
- image\_ref (zzz-DTTCompatibility-class),  
13
- image\_ref,Images\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- Image\_ref-class  
(zzz-DTTCompatibility-class),  
13
- imageAcquisition  
(zzz-DTTCompatibility-class),  
13
- imageAcquisition,BioAssayTreatments\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- ImageAcquisition-class  
(zzz-DTTCompatibility-class),  
13
- images\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- images\_assnreflist,ImageAcquisition-method  
(zzz-DTTCompatibility-class),  
13
- Images\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- immobilizedCharacteristics\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- immobilizedCharacteristics\_assnreflist,Reporter-method  
(zzz-DTTCompatibility-class),  
13
- ImmobilizedCharacteristics\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- information\_assnref  
(zzz-DTTCompatibility-class),  
13
- information\_assnref,Array-method  
(zzz-DTTCompatibility-class),  
13
- Information\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- Internal-class, 4
- isApproximateLength  
(zzz-DTTCompatibility-class),  
13
- isApproximateLength,BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- isBackground  
(zzz-DTTCompatibility-class),  
13
- isBackground,DerivedSignal-method  
(zzz-DTTCompatibility-class),  
13
- isBackground,Error-method  
(zzz-DTTCompatibility-class),  
13
- isBackground,ExpectedValue-method  
(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
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13
- isBackground,PValue-method  
(zzz-DTTCompatibility-class),  
13
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- (zzz-DTTCompatibility-class),  
13
- isBackground, SpecializedQuantitationType-method  
(zzz-DTTCompatibility-class),  
13
- isCircular  
(zzz-DTTCompatibility-class),  
13
- isCircular, BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- isSolvent (zzz-DTTCompatibility-class),  
13
- isSolvent, Compound-method  
(zzz-DTTCompatibility-class),  
13
- issue (zzz-DTTCompatibility-class), 13
- issue, BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- kindCV (zzz-DTTCompatibility-class), 13
- kindCV, Measurement-method  
(zzz-DTTCompatibility-class),  
13
- labeledExtract  
(zzz-DTTCompatibility-class),  
13
- labeledExtract, BioMaterial\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- LabeledExtract-class  
(zzz-DTTCompatibility-class),  
13
- labeledExtract\_ref  
(zzz-DTTCompatibility-class),  
13
- labeledExtract\_ref, BioMaterial\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- LabeledExtract\_ref-class  
(zzz-DTTCompatibility-class),  
13
- labels\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- labels\_assnreflist, Channel-method  
(zzz-DTTCompatibility-class),  
13
- labels\_assnreflist, LabeledExtract-method  
(zzz-DTTCompatibility-class),  
13
- Labels\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- lastName (zzz-DTTCompatibility-class),  
13
- lastName, Person-method  
(zzz-DTTCompatibility-class),  
13
- length, ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- length, BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- libraryPackageName  
(zzz-ARRCompatibility-class),  
12
- libraryPackageName, PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- list, 4
- lowerRightX  
(zzz-DTTCompatibility-class),  
13
- lowerRightX, Zone-method  
(zzz-DTTCompatibility-class),  
13
- lowerRightY  
(zzz-DTTCompatibility-class),  
13
- lowerRightY, Zone-method  
(zzz-DTTCompatibility-class),  
13
- MAGE-ML-class  
(zzz-DTTCompatibility-class),  
13
- make (zzz-DTTCompatibility-class), 13
- make, Hardware-method  
(zzz-DTTCompatibility-class),  
13
- manufactureLIMS  
(zzz-DTTCompatibility-class),  
13
- manufactureLIMS, FeatureLIMSS\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- ManufactureLIMS-class  
(zzz-DTTCompatibility-class),  
13
- manufactureLIMSBiomaterial  
(zzz-DTTCompatibility-class),  
13

- manufactureLIMSBiomaterial, FeatureLIMSS\_assnlist-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- ManufactureLIMSBiomaterial-class  
 (zzz-DTTCompatibility-class),  
[13](#)
- manufacturingDate  
 (zzz-DTTCompatibility-class),  
[13](#)
- manufacturingDate, ArrayManufacture-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- massUnit (zzz-DTTCompatibility-class),  
[13](#)
- massUnit, Unit\_assn-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- MassUnit-class  
 (zzz-DTTCompatibility-class),  
[13](#)
- masterFileGUID  
 (zzz-ARRCompatibility-class),  
[12](#)
- masterFileGUID, PhysicalArray-method  
 (zzz-ARRCompatibility-class),  
[12](#)
- masterFileName  
 (zzz-ARRCompatibility-class),  
[12](#)
- masterFileName, PhysicalArray-method  
 (zzz-ARRCompatibility-class),  
[12](#)
- materialType\_assn  
 (zzz-DTTCompatibility-class),  
[13](#)
- materialType\_assn, BioSample-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- materialType\_assn, BioSource-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- materialType\_assn, LabeledExtract-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- MaterialType\_assn-class  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssay  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssay, BioAssay\_assnlist-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssay, MeasuredBioAssay\_assnlist-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- MeasuredBioAssay-class  
 (zzz-DTTCompatibility-class),  
[13](#)
- MeasuredBioAssay\_assnlist-class  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssay\_ref  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssay\_ref, BioAssay\_assnref-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssay\_ref, BioAssays\_assnreflist-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssay\_ref, MeasuredBioAssayTarget\_assnref-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssay\_ref, SourceBioAssays\_assnreflist-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssay\_ref, TopLevelBioAssays\_assnreflist-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- MeasuredBioAssay\_ref-class  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssayData  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssayData, BioAssayData\_assnlist-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssayData, MeasuredBioAssayData\_assnlist-method  
 (zzz-DTTCompatibility-class),  
[13](#)
- MeasuredBioAssayData-class  
 (zzz-DTTCompatibility-class),  
[13](#)
- MeasuredBioAssayData\_assnlist-class  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssayData\_assnreflist  
 (zzz-DTTCompatibility-class),  
[13](#)
- measuredBioAssayData\_assnreflist, MeasuredBioAssay-method  
 (zzz-DTTCompatibility-class),  
[13](#)

MeasuredBioAssayData\_assnreflist-class (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 measurement, ActionMeasurement\_assn-method  
 measuredBioAssayData\_ref (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 measurement, DefaultValue\_assn-method  
 measuredBioAssayData\_ref, BioAssayData\_assnreflist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 measurement, Measurement\_assn-method  
 measuredBioAssayData\_ref, BioAssayDataSources\_assnreflist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 Measurement-class  
 measuredBioAssayData\_ref, ClusterBioAssayData\_assnreflist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 measurement\_assn  
 measuredBioAssayData\_ref, MeasuredBioAssayData\_assnreflist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 measurement\_assn, BioMaterialMeasurement-method  
 MeasuredBioAssayData\_ref-class (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 measurement\_assn, CompoundMeasurement-method  
 MeasuredBioAssayTarget\_assnref-class (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 measurement\_assn, FactorValue-method  
 measuredSignal (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 Measurement\_assn-class  
 measuredSignal, QuantitationType\_assnlist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 measurement\_package  
 MeasuredSignal-class (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 measurement\_package, MAGE-ML-method  
 measuredSignal\_ref (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 Measurement\_package-class  
 measuredSignal\_ref, QuantitationType\_assnref-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 mediaCol (zzz-ARRCompatibility-class),  
 mediaCol, PhysicalArray-method  
 measuredSignal\_ref, QuantitationTypes\_assnreflist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 12  
 (zzz-ARRCompatibility-class),  
 measuredSignal\_ref, SourcesQuantitationType\_assnreflist-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 12  
 mediaFileGUID  
 (zzz-ARRCompatibility-class),  
 measuredSignal\_ref, TargetQuantitationType\_assnref-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 12  
 mediaFileGUID, PhysicalArray-method  
 (zzz-ARRCompatibility-class),  
 MeasuredSignal\_ref-class (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 12  
 mediaFileName  
 (zzz-ARRCompatibility-class),  
 measurement 12

- mediaFileName,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- mediaRow (zzz-ARRCompatibility-class),  
12
- mediaRow,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- mediaType (zzz-ARRCompatibility-class),  
12
- mediaType,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- members\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- members\_assnreflist,SecurityGroup-method  
(zzz-DTTCompatibility-class),  
13
- Members\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- midInitials  
(zzz-DTTCompatibility-class),  
13
- midInitials,Person-method  
(zzz-DTTCompatibility-class),  
13
- mismatchInformation  
(zzz-DTTCompatibility-class),  
13
- mismatchInformation,MismatchInformation\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- MismatchInformation-class  
(zzz-DTTCompatibility-class),  
13
- mismatchInformation\_assnlist  
(zzz-DTTCompatibility-class),  
13
- mismatchInformation\_assnlist,CompositePosition-method  
(zzz-DTTCompatibility-class),  
13
- mismatchInformation\_assnlist,FeatureInformation-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- MismatchInformation\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- model (zzz-DTTCompatibility-class), 13
- model,Hardware-method  
(zzz-DTTCompatibility-class),  
13
- name (zzz-DTTCompatibility-class), 13
- name,Array-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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12
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13
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13
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13
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13
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13
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13
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13
- name,BioAssayDimension\_ref-method  
(zzz-DTTCompatibility-class),  
13



- [13](#)
- name, BioAssayMap-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, BioAssayMap\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
- name, BioSequence-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, BioSequence\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
- name, Channel-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
- name, CompositeCompositeMap\_ref-method  
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[13](#)
- name, CompositeGroup-method  
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[13](#)
- name, CompositeGroup\_ref-method  
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[13](#)
- name, CompositeSequence-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, CompositeSequence\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, CompositeSequenceDimension-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, CompositeSequenceDimension\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, Compound-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, Compound\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, ConfidenceIndicator\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, Contact\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, Database-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, Database\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, DerivedBioAssay-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, DerivedBioAssay\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, DerivedBioAssayData-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, DerivedBioAssayData\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, DerivedSignal-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, DerivedSignal\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, DesignElement\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, DesignElementDimension\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, DesignElementMap\_ref-method

- (zzz-DTTCompatibility-class),  
13
- name,Error-method  
(zzz-DTTCompatibility-class),  
13
- name,Error\_ref-method  
(zzz-DTTCompatibility-class),  
13
- name,ExpectedValue-method  
(zzz-DTTCompatibility-class),  
13
- name,ExpectedValue\_ref-method  
(zzz-DTTCompatibility-class),  
13
- name,Experiment-method  
(zzz-DTTCompatibility-class),  
13
- name,ExperimentalFactor-method  
(zzz-DTTCompatibility-class),  
13
- name,ExperimentalFactor\_ref-method  
(zzz-DTTCompatibility-class),  
13
- name,FactorValue-method  
(zzz-DTTCompatibility-class),  
13
- name,FactorValue\_ref-method  
(zzz-DTTCompatibility-class),  
13
- name,Failed-method  
(zzz-DTTCompatibility-class),  
13
- name,Failed\_ref-method  
(zzz-DTTCompatibility-class),  
13
- name,Feature-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- name,FeatureDimension-method  
(zzz-DTTCompatibility-class),  
13
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13
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13
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13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- name,Image-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- name,MeasuredSignal-method  
(zzz-DTTCompatibility-class),  
13

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(zzz-DTTCompatibility-class),  
[13](#)
- name, NameValueType-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, NodeValue-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, Organization-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
- name, Person-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
- name, PhysicalArrayDesign\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, PhysicalBioAssay-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
- name, PresentAbsent-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
- name, Protocol-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, Protocol\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, PValue-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, PValue\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, QuantitationType\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, QuantitationTypeDimension-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
[13](#)
- name, Ratio-method  
(zzz-DTTCompatibility-class),  
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- name, Ratio\_ref-method  
(zzz-DTTCompatibility-class),  
[13](#)
- name, Reporter-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
- name, ReporterCompositeMap-method  
(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
[13](#)
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
[13](#)
- name, Security-method  
(zzz-DTTCompatibility-class),

- 13
- name, Security\_ref-method  
(zzz-DTTCompatibility-class),  
13
- name, SecurityGroup-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- name, SpecializedQuantitationType-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- name, Transformation-method  
(zzz-DTTCompatibility-class),  
13
- name, Treatment-method  
(zzz-DTTCompatibility-class),  
13
- name, UserAttribute-method  
(zzz-ARRCompatibility-class),  
12
- name, Zone-method  
(zzz-DTTCompatibility-class),  
13
- name, Zone\_ref-method  
(zzz-DTTCompatibility-class),  
13
- names, AffxArray-method  
(zzz-NetAffxCompatibility-class),  
14
- names, NetAffxResource-method  
(NetAffxResource-class), 5
- namespace (zzz-ARRCompatibility-class),  
12
- namespace, UserAttribute-method  
(zzz-ARRCompatibility-class),  
12
- nameValueType  
(zzz-DTTCompatibility-class),  
13
- nameValueType, PropertySets\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- nameValueType, QualityControlStatistics\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- nameValueType, SummaryStatistics\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- NameValueType-class  
(zzz-DTTCompatibility-class),  
13
- NetAffxCompatibility, 6, 15
- NetAffxCompatibility-class  
(AffyCompatible-class), 3
- NetAffxResource, 3, 4, 5, 9, 10, 15
- NetAffxResource-accessors (accessors), 2
- NetAffxResource-class, 5
- newSequence  
(zzz-DTTCompatibility-class),  
13
- newSequence, MismatchInformation-method  
(zzz-DTTCompatibility-class),  
13
- node (zzz-DTTCompatibility-class), 13
- node, Nodes\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Node-class  
(zzz-DTTCompatibility-class),  
13
- nodeContents  
(zzz-DTTCompatibility-class),  
13
- nodeContents, NodeContents\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- NodeContents-class  
(zzz-DTTCompatibility-class),  
13
- nodeContents\_assnlist  
(zzz-DTTCompatibility-class),  
13
- nodeContents\_assnlist, Node-method  
(zzz-DTTCompatibility-class),  
13
- NodeContents\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- nodes\_assnlist  
(zzz-DTTCompatibility-class),

- 13
- nodes\_assnlist, BioAssayDataCluster-method  
(zzz-DTTCompatibility-class),  
13
- nodes\_assnlist, Node-method  
(zzz-DTTCompatibility-class),  
13
- Nodes\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- nodeValue (zzz-DTTCompatibility-class),  
13
- nodeValue, NodeValue\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- NodeValue-class  
(zzz-DTTCompatibility-class),  
13
- nodeValue\_assnlist  
(zzz-DTTCompatibility-class),  
13
- nodeValue\_assnlist, Node-method  
(zzz-DTTCompatibility-class),  
13
- NodeValue\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- normalizationDescription\_assn  
(zzz-DTTCompatibility-class),  
13
- normalizationDescription\_assn, ExperimentDesign-method  
(zzz-DTTCompatibility-class),  
13
- NormalizationDescription\_assn-class  
(zzz-DTTCompatibility-class),  
13
- numArrays (zzz-DTTCompatibility-class),  
13
- numArrays, ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- numberOfFeatures  
(zzz-DTTCompatibility-class),  
13
- numberOfFeatures, ArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- numberOfFeatures, PhysicalArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- numFeaturesPerCol  
(zzz-DTTCompatibility-class),  
13
- numFeaturesPerCol, ZoneLayout-method  
(zzz-DTTCompatibility-class),  
13
- numFeaturesPerRow  
(zzz-DTTCompatibility-class),  
13
- numFeaturesPerRow, ZoneLayout-method  
(zzz-DTTCompatibility-class),  
13
- ontologyEntries\_assnlist  
(zzz-DTTCompatibility-class),  
13
- ontologyEntries\_assnlist, BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- OntologyEntries\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- ontologyEntry  
(zzz-DTTCompatibility-class),  
13
- ontologyEntry, Action\_assn-method  
(zzz-DTTCompatibility-class),  
13
- ontologyEntry, Annotations\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
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- ontologyEntry, CompoundIndices\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
13

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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
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13
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13
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(zzz-DTTCompatibility-class),  
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(zzz-DTTCompatibility-class),  
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- ontologyEntry, WarningType\_assn-method  
(zzz-DTTCompatibility-class),  
13
- OntologyEntry-class  
(zzz-DTTCompatibility-class),  
13
- ontologyReference\_assn  
(zzz-DTTCompatibility-class),  
13
- ontologyReference\_assn, OntologyEntry-method  
(zzz-DTTCompatibility-class),  
13
- OntologyReference\_assn-class  
(zzz-DTTCompatibility-class),  
13
- organization  
(zzz-DTTCompatibility-class),  
13
- organization, Contact\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- organization, Organization\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Organization-class  
(zzz-DTTCompatibility-class),  
13
- Organization\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- organization\_ref  
(zzz-DTTCompatibility-class),  
13
- organization\_ref, Affiliation\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- organization\_ref, ArrayManufacturers\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- organization\_ref, Contacts\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- organization\_ref, DesignProviders\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- organization\_ref, HardwareManufacturers\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- organization\_ref, Members\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- organization\_ref, Parent\_assnref-method  
(zzz-DTTCompatibility-class),

- 13
- organization\_ref, Performer\_assnref-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- organization\_ref, SoftwareManufacturers\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- organization\_ref, SourceContact\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- Organization\_ref-class  
(zzz-DTTCompatibility-class),  
13
- orientationMark  
(zzz-DTTCompatibility-class),  
13
- orientationMark, ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- orientationMarkPosition  
(zzz-DTTCompatibility-class),  
13
- orientationMarkPosition, ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- originalProjectName  
(zzz-ARRCompatibility-class),  
12
- originalProjectName, ArraySetFile-method  
(zzz-ARRCompatibility-class),  
12
- originRelativeTo  
(zzz-DTTCompatibility-class),  
13
- originRelativeTo, Array-method  
(zzz-DTTCompatibility-class),  
13
- otherKind (zzz-DTTCompatibility-class),  
13
- otherKind, Measurement-method  
(zzz-DTTCompatibility-class),  
13
- owner\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- owner\_assnreflist, Security-method  
(zzz-DTTCompatibility-class),  
13
- Owner\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- pages (zzz-DTTCompatibility-class), 13
- pages, BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- parameter (zzz-DTTCompatibility-class),  
13
- parameter, ParameterTypes\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Parameter-class  
(zzz-DTTCompatibility-class),  
13
- parameter\_ref  
(zzz-DTTCompatibility-class),  
13
- parameter\_ref, ParameterType\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- Parameter\_ref-class  
(zzz-DTTCompatibility-class),  
13
- parameters\_assnlist  
(zzz-DTTCompatibility-class),  
13
- parameters\_assnlist, BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- Parameters\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- parameterType\_assnref  
(zzz-DTTCompatibility-class),  
13
- parameterType\_assnref, ParameterValue-method  
(zzz-DTTCompatibility-class),  
13
- ParameterType\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- parameterTypes\_assnlist  
(zzz-DTTCompatibility-class),  
13
- parameterTypes\_assnlist, Hardware-method  
(zzz-DTTCompatibility-class),  
13
- parameterTypes\_assnlist, Protocol-method  
(zzz-DTTCompatibility-class),  
13
- parameterTypes\_assnlist, Software-method  
(zzz-DTTCompatibility-class),

- 13
- ParameterTypes\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- parameterValue  
(zzz-DTTCompatibility-class),  
13
- parameterValue,ParameterValues\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- ParameterValue-class  
(zzz-DTTCompatibility-class),  
13
- parameterValues\_assnlist  
(zzz-DTTCompatibility-class),  
13
- parameterValues\_assnlist,HardwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- parameterValues\_assnlist,ProtocolApplication-method  
(zzz-DTTCompatibility-class),  
13
- parameterValues\_assnlist,SoftwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- ParameterValues\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- parent\_assnref  
(zzz-DTTCompatibility-class),  
13
- parent\_assnref,Organization-method  
(zzz-DTTCompatibility-class),  
13
- Parent\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- password (accessors), 2
- password,NetAffxResource-method  
(NetAffxResource-class), 5
- patassignmentMethod  
(zzz-ARRCompatibility-class),  
12
- patassignmentMethod,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- performer\_assnref  
(zzz-DTTCompatibility-class),  
13
- performer\_assnref,Audit-method  
(zzz-DTTCompatibility-class),  
13
- Performer\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- performers\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- performers\_assnreflist,ProtocolApplication-method  
(zzz-DTTCompatibility-class),  
13
- Performers\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- Person-class  
(zzz-DTTCompatibility-class),  
13
- Person\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- person\_ref  
(zzz-DTTCompatibility-class),  
13
- person\_ref,ArrayManufacturers\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,Contacts\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,DesignProviders\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,HardwareManufacturers\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,Members\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,Owner\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,Performer\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,Performers\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,Providers\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,SoftwareManufacturers\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- person\_ref,SourceContact\_assnreflist-method



- (zzz-DTTCompatibility-class),  
13
- Person\_ref-class  
(zzz-DTTCompatibility-class),  
13
- phone (zzz-DTTCompatibility-class), 13
- phone, Organization-method  
(zzz-DTTCompatibility-class),  
13
- phone, Person-method  
(zzz-DTTCompatibility-class),  
13
- physicalArray  
(zzz-ARRCompatibility-class),  
12
- physicalArray, PhysicalArrays-method  
(zzz-ARRCompatibility-class),  
12
- PhysicalArray-class  
(zzz-ARRCompatibility-class),  
12
- physicalArrayDesign  
(zzz-DTTCompatibility-class),  
13
- physicalArrayDesign, ArrayDesign\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- PhysicalArrayDesign-class  
(zzz-DTTCompatibility-class),  
13
- physicalArrayDesign\_ref  
(zzz-DTTCompatibility-class),  
13
- physicalArrayDesign\_ref, ArrayDesign\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- PhysicalArrayDesign\_ref-class  
(zzz-DTTCompatibility-class),  
13
- physicalArrays  
(zzz-ARRCompatibility-class),  
12
- physicalArrays, ArraySetFile-method  
(zzz-ARRCompatibility-class),  
12
- PhysicalArrays-class  
(zzz-ARRCompatibility-class),  
12
- physicalBioAssay  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay, BioAssay\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay, PhysicalBioAssay\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- PhysicalBioAssay-class  
(zzz-DTTCompatibility-class),  
13
- PhysicalBioAssay\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- PhysicalBioAssay\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay\_ref  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay\_ref, BioAssay\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay\_ref, BioAssays\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay\_ref, PhysicalBioAssay\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay\_ref, PhysicalBioAssaySource\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay\_ref, PhysicalBioAssayTarget\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay\_ref, SourceBioAssays\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay\_ref, Target\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssay\_ref, TopLevelBioAssays\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- PhysicalBioAssay\_ref-class  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssayData\_assnlist  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssayData\_assnlist, PhysicalBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- PhysicalBioAssayData\_assnlist-class  
(zzz-DTTCompatibility-class),

- 13
- physicalBioAssaySource\_assnref  
(zzz-DTTCompatibility-class),  
13
- physicalBioAssaySource\_assnref,FeatureExtraction-method  
(zzz-DTTCompatibility-class),  
13
- PhysicalBioAssaySource\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- PhysicalBioAssayTarget\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- polymerType\_assn  
(zzz-DTTCompatibility-class),  
13
- polymerType\_assn,BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- PolymerType\_assn-class  
(zzz-DTTCompatibility-class),  
13
- position (zzz-DTTCompatibility-class),  
13
- position,Position\_assn-method  
(zzz-DTTCompatibility-class),  
13
- Position-class  
(zzz-DTTCompatibility-class),  
13
- position\_assn  
(zzz-DTTCompatibility-class),  
13
- position\_assn,Feature-method  
(zzz-DTTCompatibility-class),  
13
- position\_assn,Fiducial-method  
(zzz-DTTCompatibility-class),  
13
- Position\_assn-class  
(zzz-DTTCompatibility-class),  
13
- positionDelta  
(zzz-DTTCompatibility-class),  
13
- positionDelta,PositionDelta\_assn-method  
(zzz-DTTCompatibility-class),  
13
- PositionDelta-class  
(zzz-DTTCompatibility-class),  
13
- positionDelta\_assn  
(zzz-DTTCompatibility-class),  
13
- positionDelta\_assn,FeatureDefect-method  
(zzz-DTTCompatibility-class),  
13
- positionDelta\_assn,ZoneDefect-method  
(zzz-DTTCompatibility-class),  
13
- PositionDelta\_assn-class  
(zzz-DTTCompatibility-class),  
13
- presentAbsent  
(zzz-DTTCompatibility-class),  
13
- presentAbsent,QuantitationType\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- PresentAbsent-class  
(zzz-DTTCompatibility-class),  
13
- presentAbsent\_ref  
(zzz-DTTCompatibility-class),  
13
- presentAbsent\_ref,QuantitationType\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- presentAbsent\_ref,QuantitationTypes\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- presentAbsent\_ref,SourcesQuantitationType\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- presentAbsent\_ref,TargetQuantitationType\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- PresentAbsent\_ref-class  
(zzz-DTTCompatibility-class),  
13
- producerTransformation\_assn  
(zzz-DTTCompatibility-class),  
13
- producerTransformation\_assn,DerivedBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- ProducerTransformation\_assn-class  
(zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist  
(zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist,Array-method  
(zzz-DTTCompatibility-class),

- 13  
propertySets\_assnlist,ArrayDesign-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,ArrayManufacture-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,ArrayManufactureDeviation-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,Audit-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioAssayCreation-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioAssayDataCluster-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioAssayDimension-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioAssayMap-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioAssayMapping-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioAssayTreatment-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioDataCube-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioDataTuples-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioMaterialMeasurement-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioSample-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioSequence-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,BioSource-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,Channel-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,CompositeCompositeMap-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,CompositeGroup-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,CompositePosition-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,CompositeSequence-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,CompositeSequenceDimension-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,Compound-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,CompoundMeasurement-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,ConcentrationUnit-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,Database-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,DatabaseEntry-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,DerivedBioAssay-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,DerivedBioAssayData-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,DerivedSignal-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,Description-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,DesignElementMapping-method  
(zzz-DTTCompatibility-class),  
13  
propertySets\_assnlist,DistanceUnit-method

- (zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist,Error-method  
(zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist,ExpectedValue-method  
(zzz-DTTCompatibility-class),  
13
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13
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(zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist,ExperimentDesign-method  
(zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist,ExternalReference-method  
(zzz-DTTCompatibility-class),  
13
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13
- propertySets\_assnlist,Failed-method  
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13
- propertySets\_assnlist,Feature-method  
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13
- propertySets\_assnlist,FeatureDefect-method  
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13
- propertySets\_assnlist,FeatureDimension-method  
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13
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13
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13
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13
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13
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13
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13
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13
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13
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13
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13
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13
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13
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13
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13

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13
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13
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(zzz-DTTCompatibility-class),  
13
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13
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13
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13
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13
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13
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13
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13
- propertySets\_assnlist,ReporterGroup-method  
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13
- propertySets\_assnlist,ReporterPosition-method  
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13
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13
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13
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13
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13
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13
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13
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13
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(zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist,TemperatureUnit-method  
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13
- propertySets\_assnlist,TimeUnit-method  
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13

- 13
- propertySets\_assnlist,Transformation-method  
(zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist,Treatment-method  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist,ZoneDefect-method  
(zzz-DTTCompatibility-class),  
13
- propertySets\_assnlist,ZoneGroup-method  
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13
- propertySets\_assnlist,ZoneLayout-method  
(zzz-DTTCompatibility-class),  
13
- PropertySets\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- protocol (zzz-DTTCompatibility-class),  
13
- protocol,Protocol\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Protocol-class  
(zzz-DTTCompatibility-class),  
13
- protocol\_assnlist  
(zzz-DTTCompatibility-class),  
13
- protocol\_assnlist,Protocol\_package-method  
(zzz-DTTCompatibility-class),  
13
- Protocol\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- protocol\_assnref  
(zzz-DTTCompatibility-class),  
13
- protocol\_assnref,ProtocolApplication-method  
(zzz-DTTCompatibility-class),  
13
- Protocol\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- protocol\_package  
(zzz-DTTCompatibility-class),  
13
- protocol\_package,MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- Protocol\_package-class  
(zzz-DTTCompatibility-class),  
13
- protocol\_ref  
(zzz-DTTCompatibility-class),  
13
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(zzz-DTTCompatibility-class),  
13
- Protocol\_ref-class  
(zzz-DTTCompatibility-class),  
13
- protocolApplication  
(zzz-DTTCompatibility-class),  
13
- protocolApplication,ProtocolApplications\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- ProtocolApplication-class  
(zzz-DTTCompatibility-class),  
13
- protocolApplications\_assnlist  
(zzz-DTTCompatibility-class),  
13
- protocolApplications\_assnlist,ArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- protocolApplications\_assnlist,ArrayManufacture-method  
(zzz-DTTCompatibility-class),  
13
- protocolApplications\_assnlist,BioAssayCreation-method  
(zzz-DTTCompatibility-class),  
13
- protocolApplications\_assnlist,BioAssayMap-method  
(zzz-DTTCompatibility-class),  
13
- protocolApplications\_assnlist,BioAssayTreatment-method  
(zzz-DTTCompatibility-class),  
13
- protocolApplications\_assnlist,CompositeCompositeMap-method  
(zzz-DTTCompatibility-class),  
13
- protocolApplications\_assnlist,FeatureExtraction-method  
(zzz-DTTCompatibility-class),  
13
- protocolApplications\_assnlist,FeatureReporterMap-method  
(zzz-DTTCompatibility-class),

- 13  
 PValue-class  
 protocolApplications\_assnlist,Hybridization-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 pvalue\_ref  
 protocolApplications\_assnlist,ImageAcquisition-method(zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 pvalue\_ref,ConfidenceIndicators\_assnreflist-method  
 protocolApplications\_assnlist,PhysicalArrayDesign-method(zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 pvalue\_ref,QuantitationType\_assnref-method  
 protocolApplications\_assnlist,QuantitationTypeMap-method(zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 pvalue\_ref,QuantitationTypes\_assnreflist-method  
 protocolApplications\_assnlist,ReporterCompositeMap-method(zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 pvalue\_ref,SourcesQuantitationType\_assnreflist-method  
 protocolApplications\_assnlist,Transformation-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 pvalue\_ref,TargetQuantitationType\_assnref-method  
 protocolApplications\_assnlist,Treatment-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 PValue\_ref-class  
 ProtocolApplications\_assnlist-class (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13  
 13  
 providers\_assnreflist  
 quality (zzz-DTTCompatibility-class), 13  
 quality,ManufactureLIMS-method  
 (zzz-DTTCompatibility-class),  
 13  
 providers\_assnreflist,Experiment-method  
 quality,ManufactureLIMSBiomaterial-method  
 (zzz-DTTCompatibility-class),  
 13  
 13  
 Providers\_assnreflist-class  
 qualityControlDescription\_assn  
 (zzz-DTTCompatibility-class),  
 13  
 13  
 publication  
 qualityControlDescription\_assn,ExperimentDesign-method  
 (zzz-DTTCompatibility-class),  
 13  
 13  
 publication,BibliographicReference-method  
 QualityControlDescription\_assn-class  
 (zzz-DTTCompatibility-class),  
 13  
 13  
 publisher (zzz-DTTCompatibility-class),  
 qualityControlStatistics\_assnlist  
 (zzz-DTTCompatibility-class),  
 13  
 13  
 publisher,BibliographicReference-method  
 qualityControlStatistics\_assnlist,ArrayManufacture-meth  
 (zzz-DTTCompatibility-class),  
 13  
 13  
 pvalue (zzz-DTTCompatibility-class), 13  
 qualityControlStatistics\_assnlist,BioSample-method  
 (zzz-DTTCompatibility-class),  
 13  
 13  
 pvalue,ConfidenceIndicator\_assnlist-method  
 qualityControlStatistics\_assnlist,BioSource-method  
 (zzz-DTTCompatibility-class),  
 13  
 13  
 pvalue,QuantitationType\_assnlist-method  
 (zzz-DTTCompatibility-class),  
 13  
 13

- qualityControlStatistics\_assnlist, LabeledExtract-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13
- QualityControlStatistics\_assnlist-class  
 (zzz-DTTCompatibility-class), 13
- quantitationDimension\_assnref  
 (zzz-DTTCompatibility-class), 13
- quantitationDimension\_assnref, NodeContents-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13
- QuantitationDimension\_assnref-class  
 (zzz-DTTCompatibility-class), 13
- quantitationType\_assnlist  
 (zzz-DTTCompatibility-class), 13
- quantitationType\_assnlist, QuantitationType\_package-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13
- QuantitationType\_assnlist-class  
 (zzz-DTTCompatibility-class), 13
- quantitationType\_assnref  
 (zzz-DTTCompatibility-class), 13
- quantitationType\_assnref, QuantitationTypeTuple-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13
- QuantitationType\_assnref-class  
 (zzz-DTTCompatibility-class), 13
- quantitationType\_package  
 (zzz-DTTCompatibility-class), 13
- quantitationType\_package, MAGe-ML-method  
 (zzz-DTTCompatibility-class), 13
- QuantitationType\_package-class  
 (zzz-DTTCompatibility-class), 13
- QuantitationType\_ref-class  
 (zzz-DTTCompatibility-class), 13
- quantitationTypeDimension  
 (zzz-DTTCompatibility-class), 13
- quantitationTypeDimension, QuantitationTypeDimension\_assnref-method (zzz-DTTCompatibility-class),  
 (zzz-DTTCompatibility-class), 13
- QuantitationTypeDimension-class  
 (zzz-DTTCompatibility-class), 13
- quantitationTypeDimension\_assnlist  
 (zzz-DTTCompatibility-class), 13
- quantitationTypeDimension\_assnlist, BioAssayData\_package  
 (zzz-DTTCompatibility-class), 13
- QuantitationTypeDimension\_assnlist-class  
 (zzz-DTTCompatibility-class), 13
- quantitationTypeDimension\_assnref  
 (zzz-DTTCompatibility-class), 13
- quantitationTypeDimension\_assnref, DerivedBioAssayData-  
 (zzz-DTTCompatibility-class), 13
- quantitationTypeDimension\_assnref, MeasuredBioAssayData-  
 (zzz-DTTCompatibility-class), 13
- QuantitationTypeDimension\_assnref-class  
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- quantitationTypeDimension\_ref  
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- quantitationTypeDimension\_ref, QuantitationDimension\_assnref  
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- QuantitationTypeDimension\_ref-class  
 (zzz-DTTCompatibility-class), 13
- quantitationTypeMap  
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- quantitationTypeMap, QuantitationTypeMap\_assnlist-method  
 (zzz-DTTCompatibility-class), 13
- QuantitationTypeMap-class  
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- quantitationTypeMap\_assnlist  
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- quantitationTypeMap\_assnlist, BioAssayData\_package-method  
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- QuantitationTypeMap\_assnlist-class  
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- 13
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  - (zzz-DTTCompatibility-class),
  - 13
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- quantitationTypeMaps\_assnreflist, Error-method
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  - (zzz-DTTCompatibility-class),
  - 13
- quantitationTypeTuple, QuantitationTypeTuples\_assnreflist-method
  - (zzz-DTTCompatibility-class),
  - 13
- QuantitationTypeTuple-class
  - (zzz-DTTCompatibility-class),
  - 13
- quantitationTypeTuples\_assnreflist
  - (zzz-DTTCompatibility-class),
  - 13
- quantitationTypeTuples\_assnreflist, DesignElementTuple-method
  - (zzz-DTTCompatibility-class),
  - 13
- QuantitationTypeTuples\_assnreflist-class
  - (zzz-DTTCompatibility-class),
  - 13
- quantityUnit
  - (zzz-DTTCompatibility-class),
  - 13
- quantityUnit, Unit\_assnreflist-method
  - (zzz-DTTCompatibility-class),
  - 13
- QuantityUnit-class
  - (zzz-DTTCompatibility-class),
  - 13
- ratio (zzz-DTTCompatibility-class), 13
- ratio, QuantitationType\_assnreflist-method
  - (zzz-DTTCompatibility-class),
  - 13

- Ratio-class (zzz-DTTCompatibility-class), 13
- ratio\_ref (zzz-DTTCompatibility-class), 13
- ratio\_ref, QuantitationType\_assnref-method (zzz-DTTCompatibility-class), 13
- ratio\_ref, QuantitationTypes\_assnreflist-method (zzz-DTTCompatibility-class), 13
- ratio\_ref, SourcesQuantitationType\_assnreflist-method (zzz-DTTCompatibility-class), 13
- ratio\_ref, TargetQuantitationType\_assnref-method (zzz-DTTCompatibility-class), 13
- Ratio\_ref-class (zzz-DTTCompatibility-class), 13
- readAnnotation (NetAffxResource-class), 5
- readAnnotation, NetAffxResource, character, character-method (NetAffxResource-class), 5
- readAnnotation, NetAffxResource, character, numeric-method (NetAffxResource-class), 5
- readAnnotation, NetAffxResource, missing, AffxAnnotation-method (NetAffxResource-class), 5
- readAnnotation, NetAffxResource, numeric, character-method (NetAffxResource-class), 5
- readAnnotation, NetAffxResource, numeric, numeric-method (NetAffxResource-class), 5
- readArr, 8
- readMage, 8
- readNetAffx, 9
- readXml, 8, 9, 10, 11
- regions\_assnlist (zzz-DTTCompatibility-class), 13
- regions\_assnlist, SeqFeature-method (zzz-DTTCompatibility-class), 13
- Regions\_assnlist-class (zzz-DTTCompatibility-class), 13
- releaseDate (zzz-DTTCompatibility-class), 13
- releaseDate, SoftwareApplication-method (zzz-DTTCompatibility-class), 13
- replacedLength (zzz-DTTCompatibility-class), 13
- replacedLength, MismatchInformation-method (zzz-DTTCompatibility-class), 13
- replicateDescription\_assn (zzz-DTTCompatibility-class), 13
- replicateDescription\_assn, ExperimentDesign-method (zzz-DTTCompatibility-class), 13
- Reporter-class (zzz-DTTCompatibility-class), 13
- Reporter-methods (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist, DesignElement\_assnlist-method (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist, Reporter\_assnlist-method (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist-class (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist, DesignElement\_package-method (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist-method (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist, FeatureReporterMap-method (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist, ReporterPosition-method (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist-class (zzz-DTTCompatibility-class), 13
- Reporter\_assnlist, ReporterPosition-method (zzz-DTTCompatibility-class), 13
- Reporter\_ref (zzz-DTTCompatibility-class), 13
- Reporter\_ref, DesignElement\_assnref-method (zzz-DTTCompatibility-class), 13

- reporter\_ref,Reporter\_assnref-method (zzz-DTTCompatibility-class), 13
- reporter\_ref,Reporters\_assnreflist-method (zzz-DTTCompatibility-class), 13
- Reporter\_ref-class (zzz-DTTCompatibility-class), 13
- reporterCompositeMap (zzz-DTTCompatibility-class), 13
- reporterCompositeMap,DesignElementMap\_assnlist-method(zzz-DTTCompatibility-class), 13
- reporterCompositeMap,ReporterCompositeMap\_assnlist-method(zzz-DTTCompatibility-class), 13
- ReporterCompositeMap-class (zzz-DTTCompatibility-class), 13
- reporterCompositeMap\_assnlist (zzz-DTTCompatibility-class), 13
- reporterCompositeMap\_assnlist,DesignElement\_package-method (zzz-DTTCompatibility-class), 13
- ReporterCompositeMap\_assnlist-class (zzz-DTTCompatibility-class), 13
- reporterCompositeMap\_ref (zzz-DTTCompatibility-class), 13
- reporterCompositeMap\_ref,DesignElementMaps\_assnreflist(zzz-DTTCompatibility-class), 13
- reporterCompositeMap\_ref,ReporterCompositeMaps\_assnreflist(zzz-DTTCompatibility-class), 13
- ReporterCompositeMap\_ref-class (zzz-DTTCompatibility-class), 13
- reporterCompositeMaps\_assnreflist (zzz-DTTCompatibility-class), 13
- reporterCompositeMaps\_assnreflist,CompositeSequence-method (zzz-DTTCompatibility-class), 13
- ReporterCompositeMaps\_assnreflist-class (zzz-DTTCompatibility-class), 13
- reporterDimension (zzz-DTTCompatibility-class), 13
- reporterDimension,DesignElementDimension\_assnlist-method (zzz-DTTCompatibility-class), 13
- ReporterDimension-class (zzz-DTTCompatibility-class), 13
- reporterDimension\_ref (zzz-DTTCompatibility-class), 13
- reporterDimension\_ref,DesignElementDimension\_assnref-method(zzz-DTTCompatibility-class), 13
- ReporterDimension\_ref-class (zzz-DTTCompatibility-class), 13
- reporterGroup (zzz-DTTCompatibility-class), 13
- reporterGroup,ReporterGroup\_assnlist-method (zzz-DTTCompatibility-class), 13
- ReporterGroup-class (zzz-DTTCompatibility-class), 13
- reporterGroup\_assnlist (zzz-DTTCompatibility-class), 13
- reporterGroup\_assnlist,ArrayDesign\_package-method (zzz-DTTCompatibility-class), 13
- ReporterGroup\_assnlist-class (zzz-DTTCompatibility-class), 13
- reporterGroup\_ref (zzz-DTTCompatibility-class), 13
- reporterGroup\_ref,ReporterGroups\_assnreflist-method (zzz-DTTCompatibility-class), 13
- ReporterGroup\_ref-class (zzz-DTTCompatibility-class), 13
- reporterGroups\_assnreflist (zzz-DTTCompatibility-class), 13
- reporterGroups\_assnreflist,ArrayDesign-method (zzz-DTTCompatibility-class), 13
- reporterGroups\_assnreflist,PhysicalArrayDesign-method (zzz-DTTCompatibility-class), 13

- 13
- ReporterGroups\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- reporterPosition  
(zzz-DTTCompatibility-class),  
13
- reporterPosition,Coordinate\_assn-method  
(zzz-DTTCompatibility-class),  
13
- reporterPosition,ReporterPositionSources\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- ReporterPosition-class  
(zzz-DTTCompatibility-class),  
13
- reporterPositionSources\_assnlist  
(zzz-DTTCompatibility-class),  
13
- reporterPositionSources\_assnlist,ReporterCompositeMap-method  
(zzz-DTTCompatibility-class),  
13
- ReporterPositionSources\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- reporters\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- reporters\_assnreflist,ReporterDimension-method  
(zzz-DTTCompatibility-class),  
13
- reporters\_assnreflist,ReporterGroup-method  
(zzz-DTTCompatibility-class),  
13
- Reporters\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- required(zzz-ARRCompatibility-class),  
12
- required,UserAttribute-method  
(zzz-ARRCompatibility-class),  
12
- roles\_assnlist  
(zzz-DTTCompatibility-class),  
13
- roles\_assnlist,Organization-method  
(zzz-DTTCompatibility-class),  
13
- roles\_assnlist,Person-method  
(zzz-DTTCompatibility-class),  
13
- Roles\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- scale\_assn  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,DerivedSignal-method  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,Error-method  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,ExpectedValue-method  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,Failed-method  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,MeasuredSignal-method  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,NodeValue-method  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,PresentAbsent-method  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,PValue-method  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,Ratio-method  
(zzz-DTTCompatibility-class),  
13
- scale\_assn,SpecializedQuantitationType-method  
(zzz-DTTCompatibility-class),  
13
- Scale\_assn-class  
(zzz-DTTCompatibility-class),  
13
- security(zzz-DTTCompatibility-class),  
13
- security,Security\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Security-class  
(zzz-DTTCompatibility-class),  
13
- security\_assnlist  
(zzz-DTTCompatibility-class),  
13
- security\_assnlist,AuditAndSecurity\_package-method  
(zzz-DTTCompatibility-class),  
13

- Security\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- security\_assnref  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Array-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,ArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,ArrayManufacture-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Audit-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,BioAssayCreation-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,BioAssayDataCluster-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,BioAssayDimension-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,BioAssayMap-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,BioAssayTreatment-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,BioSample-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,BioSource-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Channel-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,CompositeCompositeMap-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,CompositeGroup-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,CompositeSequence-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,CompositeSequenceDimension-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Compound-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Database-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,DerivedBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,DerivedBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,DerivedSignal-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Description-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Error-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,ExpectedValue-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Experiment-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,ExperimentalFactor-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,ExperimentDesign-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,FactorValue-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Failed-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref,Feature-method  
(zzz-DTTCompatibility-class),

- 13
- security\_assnref, FeatureDimension-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, FeatureExtraction-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, FeatureGroup-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, FeatureReporterMap-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Fiducial-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Hardware-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, HardwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Hybridization-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Image-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, ImageAcquisition-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, LabeledExtract-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, MAGE-ML-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, ManufactureLIMS-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, ManufactureLIMSBiomaterial-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, MeasuredBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, MeasuredBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, MeasuredSignal-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Node-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, NodeContents-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Organization-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Parameter-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Person-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, PhysicalArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, PhysicalBioAssay-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, PresentAbsent-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Protocol-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, ProtocolApplication-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, PValue-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, QuantitationTypeDimension-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, QuantitationTypeMap-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Ratio-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Reporter-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, ReporterCompositeMap-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, ReporterDimension-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, ReporterGroup-method

- (zzz-DTTCompatibility-class),  
13
- security\_assnref, Security-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, SecurityGroup-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, SeqFeature-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Software-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, SoftwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, SpecializedQuantitationType-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Transformation-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Treatment-method  
(zzz-DTTCompatibility-class),  
13
- security\_assnref, Zone-method  
(zzz-DTTCompatibility-class),  
13
- Security\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- security\_ref  
(zzz-DTTCompatibility-class),  
13
- security\_ref, Security\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- Security\_ref-class  
(zzz-DTTCompatibility-class),  
13
- securityGroup  
(zzz-DTTCompatibility-class),  
13
- securityGroup, SecurityGroup\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- SecurityGroup-class  
(zzz-DTTCompatibility-class),  
13
- securityGroup\_assnlist  
(zzz-DTTCompatibility-class),  
13
- securityGroup\_assnlist, AuditAndSecurity\_package-method  
(zzz-DTTCompatibility-class),  
13
- SecurityGroup\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- securityGroup\_ref  
(zzz-DTTCompatibility-class),  
13
- securityGroup\_ref, SecurityGroups\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- SecurityGroup\_ref-class  
(zzz-DTTCompatibility-class),  
13
- securityGroups\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- securityGroups\_assnreflist, Security-method  
(zzz-DTTCompatibility-class),  
13
- SecurityGroups\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- seqFeature  
(zzz-DTTCompatibility-class),  
13
- seqFeature, SeqFeatures\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- SeqFeature-class  
(zzz-DTTCompatibility-class),  
13
- seqFeatureLocation  
(zzz-DTTCompatibility-class),  
13
- seqFeatureLocation, Regions\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- seqFeatureLocation, Subregions\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- SeqFeatureLocation-class  
(zzz-DTTCompatibility-class),  
13
- seqFeatures\_assnlist  
(zzz-DTTCompatibility-class),  
13
- seqFeatures\_assnlist, BioSequence-method  
(zzz-DTTCompatibility-class),  
13

- SeqFeatures\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- sequenceDatabases\_assnlist  
(zzz-DTTCompatibility-class),  
13
- sequenceDatabases\_assnlist,BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- SequenceDatabases\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- sequencePosition  
(zzz-DTTCompatibility-class),  
13
- sequencePosition,Coordinate\_assn-method  
(zzz-DTTCompatibility-class),  
13
- SequencePosition-class  
(zzz-DTTCompatibility-class),  
13
- serialNumber  
(zzz-DTTCompatibility-class),  
13
- serialNumber,HardwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- show,.TypedAssociation-method  
(Internal-class), 4
- show,AffyCompatible-method  
(AffyCompatible-class), 3
- show,NetAffxResource-method  
(NetAffxResource-class), 5
- software(zzz-DTTCompatibility-class),  
13
- software,Software\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Software-class  
(zzz-DTTCompatibility-class),  
13
- software\_assnlist  
(zzz-DTTCompatibility-class),  
13
- software\_assnlist,Protocol\_package-method  
(zzz-DTTCompatibility-class),  
13
- Software\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- software\_assnref  
(zzz-DTTCompatibility-class),  
13
- software\_assnref,SoftwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- Software\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- software\_ref  
(zzz-DTTCompatibility-class),  
13
- software\_ref,Software\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- software\_ref,Softwares\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- Software\_ref-class  
(zzz-DTTCompatibility-class),  
13
- softwareApplication  
(zzz-DTTCompatibility-class),  
13
- softwareApplication,SoftwareApplications\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- SoftwareApplication-class  
(zzz-DTTCompatibility-class),  
13
- softwareApplications\_assnlist  
(zzz-DTTCompatibility-class),  
13
- softwareApplications\_assnlist,ProtocolApplication-method  
(zzz-DTTCompatibility-class),  
13
- SoftwareApplications\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- softwareManufacturers\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- softwareManufacturers\_assnreflist,Software-method  
(zzz-DTTCompatibility-class),  
13
- SoftwareManufacturers\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- softwares\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- softwares\_assnreflist,Hardware-method  
(zzz-DTTCompatibility-class),  
13



- softwares\_assnreflist,Protocol-method  
(zzz-DTTCompatibility-class),  
13
- softwares\_assnreflist,Software-method  
(zzz-DTTCompatibility-class),  
13
- Softwares\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- sourceBioAssays\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- sourceBioAssays\_assnreflist,BioAssayMap-method  
(zzz-DTTCompatibility-class),  
13
- SourceBioAssays\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- sourceBioMaterialMeasurements\_assnlist  
(zzz-DTTCompatibility-class),  
13
- sourceBioMaterialMeasurements\_assnlist,BioAssayCreation-method  
(zzz-DTTCompatibility-class),  
13
- sourceBioMaterialMeasurements\_assnlist,Hybridization-method  
(zzz-DTTCompatibility-class),  
13
- sourceBioMaterialMeasurements\_assnlist,Treatment-method  
(zzz-DTTCompatibility-class),  
13
- SourceBioMaterialMeasurements\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- sourceContact\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- sourceContact\_assnreflist,BioSource-method  
(zzz-DTTCompatibility-class),  
13
- SourceContact\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- sourcesQuantitationType\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- sourcesQuantitationType\_assnreflist,QuantitationTypeMap-method  
(zzz-DTTCompatibility-class),  
13
- SourcesQuantitationType\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- spacingBetweenCols  
(zzz-DTTCompatibility-class),  
13
- spacingBetweenCols,ZoneLayout-method  
(zzz-DTTCompatibility-class),  
13
- spacingBetweenRows  
(zzz-DTTCompatibility-class),  
13
- spacingBetweenRows,ZoneLayout-method  
(zzz-DTTCompatibility-class),  
13
- spacingsBetweenZonesX  
(zzz-DTTCompatibility-class),  
13
- spacingsBetweenZonesX,ZoneGroup-method  
(zzz-DTTCompatibility-class),  
13
- spacingsBetweenZonesY  
(zzz-DTTCompatibility-class),  
13
- spacingsBetweenZonesY,ZoneGroup-method  
(zzz-DTTCompatibility-class),  
13
- specializedQuantitationType  
(zzz-DTTCompatibility-class),  
13
- specializedQuantitationType,QuantitationType\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- SpecializedQuantitationType-class  
(zzz-DTTCompatibility-class),  
13
- specializedQuantitationType\_ref  
(zzz-DTTCompatibility-class),  
13
- specializedQuantitationType\_ref,QuantitationType\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- specializedQuantitationType\_ref,QuantitationTypes\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- specializedQuantitationType\_ref,SourcesQuantitationType\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- specializedQuantitationType\_ref,TargetQuantitationType\_assnreflist-method  
(zzz-DTTCompatibility-class),  
13
- SpecializedQuantitationType\_ref-class  
(zzz-DTTCompatibility-class),  
13
- species\_assn  
(zzz-DTTCompatibility-class),

- 13
- species\_assn, BioSequence-method  
(zzz-DTTCompatibility-class),  
13
- species\_assn, CompositeGroup-method  
(zzz-DTTCompatibility-class),  
13
- species\_assn, FeatureGroup-method  
(zzz-DTTCompatibility-class),  
13
- species\_assn, ReporterGroup-method  
(zzz-DTTCompatibility-class),  
13
- Species\_assn-class  
(zzz-DTTCompatibility-class),  
13
- StandardQuantitationType\_ref-class  
(zzz-DTTCompatibility-class),  
13
- startCoord  
(zzz-DTTCompatibility-class),  
13
- startCoord, MismatchInformation-method  
(zzz-DTTCompatibility-class),  
13
- strandType  
(zzz-DTTCompatibility-class),  
13
- strandType, SeqFeatureLocation-method  
(zzz-DTTCompatibility-class),  
13
- subregions\_assnlist  
(zzz-DTTCompatibility-class),  
13
- subregions\_assnlist, SeqFeatureLocation-method  
(zzz-DTTCompatibility-class),  
13
- Subregions\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- substrateType\_assn  
(zzz-DTTCompatibility-class),  
13
- substrateType\_assn, ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- SubstrateType\_assn-class  
(zzz-DTTCompatibility-class),  
13
- summaryStatistics\_assnlist  
(zzz-DTTCompatibility-class),  
13
- summaryStatistics\_assnlist, DerivedBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- summaryStatistics\_assnlist, MeasuredBioAssayData-method  
(zzz-DTTCompatibility-class),  
13
- SummaryStatistics\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- surfaceType\_assn  
(zzz-DTTCompatibility-class),  
13
- surfaceType\_assn, PhysicalArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- SurfaceType\_assn-class  
(zzz-DTTCompatibility-class),  
13
- target\_assnref  
(zzz-DTTCompatibility-class),  
13
- target\_assnref, BioAssayTreatment-method  
(zzz-DTTCompatibility-class),  
13
- target\_assnref, ImageAcquisition-method  
(zzz-DTTCompatibility-class),  
13
- Target\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- targetQuantitationType\_assnref  
(zzz-DTTCompatibility-class),  
13
- targetQuantitationType\_assnref, Error-method  
(zzz-DTTCompatibility-class),  
13
- targetQuantitationType\_assnref, ExpectedValue-method  
(zzz-DTTCompatibility-class),  
13
- targetQuantitationType\_assnref, PValue-method  
(zzz-DTTCompatibility-class),  
13
- targetQuantitationType\_assnref, QuantitationTypeMap-method  
(zzz-DTTCompatibility-class),  
13
- TargetQuantitationType\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- technologyType\_assn  
(zzz-DTTCompatibility-class),  
13
- technologyType\_assn, FeatureGroup-method

- (zzz-DTTCompatibility-class),  
13
- TechnologyType\_assn-class  
(zzz-DTTCompatibility-class),  
13
- temperatureUnit  
(zzz-DTTCompatibility-class),  
13
- temperatureUnit,Unit\_assn-method  
(zzz-DTTCompatibility-class),  
13
- TemperatureUnit-class  
(zzz-DTTCompatibility-class),  
13
- TemplateFile-class  
(zzz-ARRCompatibility-class),  
12
- timeUnit (zzz-DTTCompatibility-class),  
13
- timeUnit,Unit\_assn-method  
(zzz-DTTCompatibility-class),  
13
- TimeUnit-class  
(zzz-DTTCompatibility-class),  
13
- tolerance (zzz-DTTCompatibility-class),  
13
- tolerance,ArrayManufacture-method  
(zzz-DTTCompatibility-class),  
13
- tollFreePhone  
(zzz-DTTCompatibility-class),  
13
- tollFreePhone,Organization-method  
(zzz-DTTCompatibility-class),  
13
- tollFreePhone,Person-method  
(zzz-DTTCompatibility-class),  
13
- topLevelBioAssays\_assnreflist  
(zzz-DTTCompatibility-class),  
13
- topLevelBioAssays\_assnreflist,ExperimentDesign-method(zzz-ARRCompatibility-class),  
(zzz-DTTCompatibility-class),  
13
- TopLevelBioAssays\_assnreflist-class  
(zzz-DTTCompatibility-class),  
13
- transformation  
(zzz-DTTCompatibility-class),  
13
- transformation,ProducerTransformation\_assn-method  
(zzz-DTTCompatibility-class),  
13
- Transformation-class  
(zzz-DTTCompatibility-class),  
13
- treatment (zzz-DTTCompatibility-class),  
13
- treatment,Treatments\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Treatment-class  
(zzz-DTTCompatibility-class),  
13
- treatments\_assnlist  
(zzz-DTTCompatibility-class),  
13
- treatments\_assnlist,BioSample-method  
(zzz-DTTCompatibility-class),  
13
- treatments\_assnlist,BioSource-method  
(zzz-DTTCompatibility-class),  
13
- treatments\_assnlist,LabeledExtract-method  
(zzz-DTTCompatibility-class),  
13
- Treatments\_assnlist-class  
(zzz-DTTCompatibility-class),  
13
- type (zzz-DTTCompatibility-class), 13
- type,ArraySetFile-method  
(zzz-ARRCompatibility-class),  
12
- type,Measurement-method  
(zzz-DTTCompatibility-class),  
13
- type,NameValueType-method  
(zzz-DTTCompatibility-class),  
13
- type,PhysicalArray-method  
(zzz-ARRCompatibility-class),  
12
- type,TemplateFile-method  
(zzz-ARRCompatibility-class),  
12
- type,UserAttribute-method  
(zzz-ARRCompatibility-class),  
12
- type\_assn (zzz-DTTCompatibility-class),  
13
- type\_assn,BioSample-method  
(zzz-DTTCompatibility-class),  
13

- type\_assn, BioSequence-method  
(zzz-DTTCompatibility-class),  
[13](#)
- type\_assn, DatabaseEntry-method  
(zzz-DTTCompatibility-class),  
[13](#)
- type\_assn, DerivedBioAssay-method  
(zzz-DTTCompatibility-class),  
[13](#)
- type\_assn, Hardware-method  
(zzz-DTTCompatibility-class),  
[13](#)
- type\_assn, NodeValue-method  
(zzz-DTTCompatibility-class),  
[13](#)
- type\_assn, Protocol-method  
(zzz-DTTCompatibility-class),  
[13](#)
- type\_assn, Software-method  
(zzz-DTTCompatibility-class),  
[13](#)
- Type\_assn-class  
(zzz-DTTCompatibility-class),  
[13](#)
- types\_assnlist  
(zzz-DTTCompatibility-class),  
[13](#)
- types\_assnlist, CompositeGroup-method  
(zzz-DTTCompatibility-class),  
[13](#)
- types\_assnlist, ExperimentDesign-method  
(zzz-DTTCompatibility-class),  
[13](#)
- types\_assnlist, FeatureGroup-method  
(zzz-DTTCompatibility-class),  
[13](#)
- types\_assnlist, ReporterGroup-method  
(zzz-DTTCompatibility-class),  
[13](#)
- Types\_assnlist-class  
(zzz-DTTCompatibility-class),  
[13](#)
- unit\_assn (zzz-DTTCompatibility-class),  
[13](#)
- unit\_assn, Measurement-method  
(zzz-DTTCompatibility-class),  
[13](#)
- Unit\_assn-class  
(zzz-DTTCompatibility-class),  
[13](#)
- unitName (zzz-DTTCompatibility-class),  
[13](#)
- unitName, ConcentrationUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitName, DistanceUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitName, MassUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitName, QuantityUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitName, TemperatureUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitName, TimeUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitName, VolumeUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitNameCV  
(zzz-DTTCompatibility-class),  
[13](#)
- unitNameCV, ConcentrationUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitNameCV, DistanceUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitNameCV, MassUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitNameCV, QuantityUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitNameCV, TemperatureUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitNameCV, TimeUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- unitNameCV, VolumeUnit-method  
(zzz-DTTCompatibility-class),  
[13](#)
- upperLeftX  
(zzz-DTTCompatibility-class),  
[13](#)
- upperLeftX, Zone-method  
(zzz-DTTCompatibility-class),  
[13](#)
- upperLeftY

- (zzz-DTTCompatibility-class),  
13
- upperLeftY, Zone-method  
(zzz-DTTCompatibility-class),  
13
- uri (zzz-DTTCompatibility-class), 13
- uri, BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- uri, Database-method  
(zzz-DTTCompatibility-class),  
13
- uri, DatabaseEntry-method  
(zzz-DTTCompatibility-class),  
13
- uri, Description-method  
(zzz-DTTCompatibility-class),  
13
- uri, Hardware-method  
(zzz-DTTCompatibility-class),  
13
- uri, Image-method  
(zzz-DTTCompatibility-class),  
13
- uri, Organization-method  
(zzz-DTTCompatibility-class),  
13
- uri, Person-method  
(zzz-DTTCompatibility-class),  
13
- uri, Protocol-method  
(zzz-DTTCompatibility-class),  
13
- uri, Software-method  
(zzz-DTTCompatibility-class),  
13
- user (accessors), 2
- user, NetAffxResource-method  
(NetAffxResource-class), 5
- userAttribute  
(zzz-ARRCompatibility-class),  
12
- userAttribute, UserAttributes-method  
(zzz-ARRCompatibility-class),  
12
- UserAttribute-class  
(zzz-ARRCompatibility-class),  
12
- userAttributes  
(zzz-ARRCompatibility-class),  
12
- userAttributes, ArraySetFile-method  
(zzz-ARRCompatibility-class),  
12
- UserAttributes-class  
(zzz-ARRCompatibility-class),  
12
- userAttributeValue  
(zzz-ARRCompatibility-class),  
12
- userAttributeValue, UserAttribute-method  
(zzz-ARRCompatibility-class),  
12
- UserAttributeValue-class  
(zzz-ARRCompatibility-class),  
12
- value (zzz-ARRCompatibility-class), 12
- value, Control-method  
(zzz-ARRCompatibility-class),  
12
- value, Datum-method  
(zzz-DTTCompatibility-class),  
13
- value, Measurement-method  
(zzz-DTTCompatibility-class),  
13
- value, NameValueType-method  
(zzz-DTTCompatibility-class),  
13
- value, NodeValue-method  
(zzz-DTTCompatibility-class),  
13
- value, OntologyEntry-method  
(zzz-DTTCompatibility-class),  
13
- value, ParameterValue-method  
(zzz-DTTCompatibility-class),  
13
- value\_assn  
(zzz-DTTCompatibility-class),  
13
- value\_assn, FactorValue-method  
(zzz-DTTCompatibility-class),  
13
- Value\_assn-class  
(zzz-DTTCompatibility-class),  
13
- vector, 4
- version (zzz-ARRCompatibility-class), 12
- version, ArrayDesign-method  
(zzz-DTTCompatibility-class),

- 13
- version, ArraySetFile-method  
(zzz-ARRCompatibility-class),  
12
- version, Database-method  
(zzz-DTTCompatibility-class),  
13
- version, PhysicalArrayDesign-method  
(zzz-DTTCompatibility-class),  
13
- version, SoftwareApplication-method  
(zzz-DTTCompatibility-class),  
13
- version, TemplateFile-method  
(zzz-ARRCompatibility-class),  
12
- volume (zzz-DTTCompatibility-class), 13
- volume, BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- volumeUnit  
(zzz-DTTCompatibility-class),  
13
- volumeUnit, Unit\_assn-method  
(zzz-DTTCompatibility-class),  
13
- VolumeUnit-class  
(zzz-DTTCompatibility-class),  
13
- warningType\_assn  
(zzz-DTTCompatibility-class),  
13
- warningType\_assn, Reporter-method  
(zzz-DTTCompatibility-class),  
13
- WarningType\_assn-class  
(zzz-DTTCompatibility-class),  
13
- width (zzz-DTTCompatibility-class), 13
- width, ArrayGroup-method  
(zzz-DTTCompatibility-class),  
13
- x (zzz-DTTCompatibility-class), 13
- x, Position-method  
(zzz-DTTCompatibility-class),  
13
- xclass, 8–10, 11
- xmlValue.XMLAttributeValue, 12
- y (zzz-DTTCompatibility-class), 13
- y, Position-method  
(zzz-DTTCompatibility-class),  
13
- year (zzz-DTTCompatibility-class), 13
- year, BibliographicReference-method  
(zzz-DTTCompatibility-class),  
13
- zone (zzz-DTTCompatibility-class), 13
- zone, ZoneLocations\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- Zone-class  
(zzz-DTTCompatibility-class),  
13
- zone\_assnref  
(zzz-DTTCompatibility-class),  
13
- zone\_assnref, Feature-method  
(zzz-DTTCompatibility-class),  
13
- zone\_assnref, ZoneDefect-method  
(zzz-DTTCompatibility-class),  
13
- Zone\_assnref-class  
(zzz-DTTCompatibility-class),  
13
- zone\_ref (zzz-DTTCompatibility-class),  
13
- zone\_ref, Zone\_assnref-method  
(zzz-DTTCompatibility-class),  
13
- Zone\_ref-class  
(zzz-DTTCompatibility-class),  
13
- zoneDefect  
(zzz-DTTCompatibility-class),  
13
- zoneDefect, Adjustments\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- ZoneDefect-class  
(zzz-DTTCompatibility-class),  
13
- zoneGroup (zzz-DTTCompatibility-class),  
13
- zoneGroup, ZoneGroups\_assnlist-method  
(zzz-DTTCompatibility-class),  
13
- ZoneGroup-class  
(zzz-DTTCompatibility-class),  
13
- zoneGroups\_assnlist

(zzz-DTTCompatibility-class),  
13

zoneGroups\_assnlist,PhysicalArrayDesign-method  
(zzz-DTTCompatibility-class),  
13

ZoneGroups\_assnlist-class  
(zzz-DTTCompatibility-class),  
13

zoneLayout  
(zzz-DTTCompatibility-class),  
13

zoneLayout,ZoneLayout\_assn-method  
(zzz-DTTCompatibility-class),  
13

ZoneLayout-class  
(zzz-DTTCompatibility-class),  
13

zoneLayout\_assn  
(zzz-DTTCompatibility-class),  
13

zoneLayout\_assn,ZoneGroup-method  
(zzz-DTTCompatibility-class),  
13

ZoneLayout\_assn-class  
(zzz-DTTCompatibility-class),  
13

zoneLocations\_assnlist  
(zzz-DTTCompatibility-class),  
13

zoneLocations\_assnlist,ZoneGroup-method  
(zzz-DTTCompatibility-class),  
13

ZoneLocations\_assnlist-class  
(zzz-DTTCompatibility-class),  
13

zonesPerX (zzz-DTTCompatibility-class),  
13

zonesPerX,ZoneGroup-method  
(zzz-DTTCompatibility-class),  
13

zonesPerY (zzz-DTTCompatibility-class),  
13

zonesPerY,ZoneGroup-method  
(zzz-DTTCompatibility-class),  
13

zzz-.TypedAssociation-class  
(Internal-class), 4

zzz-AffyCompatible-class  
(AffyCompatible-class), 3

zzz-ARRCompatibility-class, 12

zzz-DTTCompatibility-class, 13

zzz-NetAffxCompatibility-class, 14