

AffyCompatible

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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")))
```

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>

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 "NetAffx-Compatibility", 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 = "numeric", ...)

readAnnotation signature(netAffxResource = "NetAffxResource", array = "numeric", annotation = "character", ...)

readAnnotation signature(netAffxResource = "NetAffxResource", array = "character", annotation = "numeric", ...)

readAnnotation signature(netAffxResource = "NetAffxResource", array = "character", annotation = "character", ...)

readAnnotation signature(netAffxResource = "NetAffxResource", array = "missing", annotation = "AffxAnnotation", ...): 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 `Biostings::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", "BLASTP annotations, CSV Format"]]
df <- readAnnotation(rsrc, annotation=anno)
```

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

<code>user</code>	Length 1 character vector containing the Affymetrix user name authorized to access the NetAffx resource.
<code>password</code>	Length 1 character vector containing the Affymetrix password of the user.
<code>affxLicence</code>	Length 1 character vector containing the Affymetrix licence (typically application specific, i.e., the specified licence covers AffyCompatible).
<code>directory</code>	(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.
<code>...</code>	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`’.

`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	<i>Update or read a NetAffx data base</i>
-------------	---

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 <code>NetAffxResource</code> 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(fl, ...)
```

Arguments

`fl` A length-1 character vector giving the full path to the file to be parsed.
`...` Additional arguments, passed to `xmlTreeParse`.

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 [readXml](#).
`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)
```

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 class 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>

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)
```

```
xmlValue.XMLAttributeValue
```

Additional functions defined in AffyCompatible

Description

This page documents additional, miscellaneous, functions defined by AffyCompatible

Usage

```
xmlValue.XMLAttributeValue(x, ignoreComments = FALSE, recursive = TRUE)
```

Arguments

<code>x</code>	An object of class <code>XMLAttributeValue</code> .
<code>ignoreComments</code>	Logical; ignored by the <code>xmlValue.XMLAttributeValue</code> method
<code>recursive</code>	ignored

Value

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

```
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 `.extneds=Foo` and length 5, display `Foo(5)`.

Author(s)

Martin Morgan

Index

*Topic classes

AffyCompatible-class, 2
 Internal-class, 14
 NetAffxResource-class, 3
 readArr, 6
 readMage, 7
 zzz-ARRCompatibility-class, 10
 zzz-DTTCompatibility-class, 11
 zzz-NetAffxCompatibility-class, 12

*Topic database

NetAffxResource, 5
 readNetAffx, 8

*Topic manip

readXml, 8
 xclass, 9
 xmlValue.XMLAttributeValue, 14

*Topic methods

accessors, 1

*Topic package

AffyCompatible-package, 2
 .Rprofile, 5
 .TypedAssociation, 11-13
 .TypedAssociation-class
 (*Internal-class*), 14
 [, .TypedAssociation, ANY, ANY-method
 (*Internal-class*), 14
 [, .TypedAssociation, numeric, missing, ANY-method
 (*Internal-class*), 14
 [, .TypedAssociation, numeric, missing-method
 (*Internal-class*), 14
 [[, NetAffxResource, character, character-method
 (*NetAffxResource-class*), 3
 [[, NetAffxResource, character, missing-method
 (*NetAffxResource-class*), 3
 [[, NetAffxResource, character, numeric-method
 (*NetAffxResource-class*), 3
 [[, NetAffxResource, numeric, character-method
 (*NetAffxResource-class*), 3
 [[, NetAffxResource, numeric, missing-method

 (*NetAffxResource-class*), 3
 [[, NetAffxResource, numeric, numeric-method
 (*NetAffxResource-class*), 3

accession
 (*zzz-DTTCompatibility-class*), 11
 accession, DatabaseEntry-method
 (*zzz-DTTCompatibility-class*), 11
 accessions_assnlist
 (*zzz-DTTCompatibility-class*), 11
 accessions_assnlist, BibliographicReference-method
 (*zzz-DTTCompatibility-class*), 11
 accessionVersion
 (*zzz-DTTCompatibility-class*), 11
 accessionVersion, DatabaseEntry-method
 (*zzz-DTTCompatibility-class*), 11
 accessors, 1
 action
 (*zzz-DTTCompatibility-class*), 11
 action, Audit-method
 (*zzz-DTTCompatibility-class*), 11
 action_assn
 (*zzz-DTTCompatibility-class*), 11
 action_assn, Treatment-method
 (*zzz-DTTCompatibility-class*), 11
 actionMeasurement_assn
 (*zzz-DTTCompatibility-class*), 11
 actionMeasurement_assn, Treatment-method
 (*zzz-DTTCompatibility-class*), 11
 actionDate
 (*zzz-DTTCompatibility-class*), 11

- activityDate, ProtocolApplication-method (zzz-ARRCompatibility-class),
 (zzz-DTTCompatibility-class), 10
 11
- address (zzz-DTTCompatibility-class), 11
- address, Organization-method (zzz-DTTCompatibility-class), 11
- address, Person-method (zzz-DTTCompatibility-class), 11
- adjustments_assnlist (zzz-DTTCompatibility-class), 11
- adjustments_assnlist, ArrayManufactureDeviation-method (zzz-DTTCompatibility-class), 11
- affiliation_assnref (zzz-DTTCompatibility-class), 11
- affiliation_assnref, Person-method (zzz-DTTCompatibility-class), 11
- affxAnnotation (zzz-NetAffxCompatibility-class), 12
- affxAnnotation, AffxArray-method (zzz-NetAffxCompatibility-class), 12
- affxArray (zzz-NetAffxCompatibility-class), 12
- affxArray, AffxNetAffxAnnotFileList-method (zzz-NetAffxCompatibility-class), 12
- affxArray, Array_assnlist-method (zzz-DTTCompatibility-class), 11
- affxCategory (zzz-DTTCompatibility-class), 11
- affxCategory, OntologyEntry-method (zzz-DTTCompatibility-class), 11
- affxComment (zzz-NetAffxCompatibility-class), 12
- affxComment, AffxAnnotation-method (zzz-NetAffxCompatibility-class), 12
- affxComment, PhysicalArray-method (zzz-NetAffxCompatibility-class),
- affxCompression (zzz-NetAffxCompatibility-class), 12
- affxCompression, AffxUrl-method (zzz-NetAffxCompatibility-class), 12
- affxCrc32 (zzz-NetAffxCompatibility-class), 12
- affxCrc32, AffxFile-method (zzz-NetAffxCompatibility-class), 12
- affxCrc32, AffxUrl-method (zzz-NetAffxCompatibility-class), 12
- affxDate (zzz-NetAffxCompatibility-class), 12
- affxDate, AffxFile-method (zzz-NetAffxCompatibility-class), 12
- affxDate, Audit-method (zzz-DTTCompatibility-class), 11
- affxDescription (zzz-NetAffxCompatibility-class), 12
- affxDescription, AffxAnnotation-method (zzz-NetAffxCompatibility-class), 12
- affxDescription, AffxArray-method (zzz-NetAffxCompatibility-class), 12
- affxEnd (zzz-DTTCompatibility-class), 11
- affxEnd, CompositePosition-method (zzz-DTTCompatibility-class), 11
- affxEnd, ReporterPosition-method (zzz-DTTCompatibility-class), 11
- affxEnd, SequencePosition-method (zzz-DTTCompatibility-class), 11
- affxFile (zzz-NetAffxCompatibility-class), 12
- affxFile, AffxAnnotation-method (zzz-NetAffxCompatibility-class),

- 12
 affxImage
 (*zzz-DTTCompatibility-class*), 11
- affxImage, *PhysicalBioAssayData_assnlist*-method
 (*zzz-DTTCompatibility-class*), 11
- affxLicence
 (*zzz-NetAffxCompatibility-class*), 12
- affxLicence, *NetAffxResource*-method
 (*NetAffxResource-class*), 3
- affxName
 (*zzz-NetAffxCompatibility-class*), 12
- affxName, *AffxArray*-method
 (*zzz-NetAffxCompatibility-class*), 12
- affxName, *AffxFile*-method
 (*zzz-NetAffxCompatibility-class*), 12
- affxOrder
 (*zzz-DTTCompatibility-class*), 11
- affxOrder, *BioDataCube*-method
 (*zzz-DTTCompatibility-class*), 11
- affxOrder, *Treatment*-method
 (*zzz-DTTCompatibility-class*), 11
- affxPerson
 (*zzz-DTTCompatibility-class*), 11
- affxPerson, *Contact_assnlist*-method
 (*zzz-DTTCompatibility-class*), 11
- affxPerson, *Person_assnlist*-method
 (*zzz-DTTCompatibility-class*), 11
- affxRow
 (*zzz-DTTCompatibility-class*), 11
- affxRow, *FeatureLocation*-method
 (*zzz-DTTCompatibility-class*), 11
- affxRow, *Zone*-method
 (*zzz-DTTCompatibility-class*), 11
- affxSequence
 (*zzz-DTTCompatibility-class*), 11
- affxSequence, *BioSequence*-method
 (*zzz-DTTCompatibility-class*), 11
- affxSize
 (*zzz-NetAffxCompatibility-class*), 12
- affxSize, *AffxFile*-method
 (*zzz-NetAffxCompatibility-class*), 12
- affxSize, *AffxUrl*-method
 (*zzz-NetAffxCompatibility-class*), 12
- affxStart
 (*zzz-DTTCompatibility-class*), 11
- affxStart, *CompositePosition*-method
 (*zzz-DTTCompatibility-class*), 11
- affxStart, *ReporterPosition*-method
 (*zzz-DTTCompatibility-class*), 11
- affxStart, *SequencePosition*-method
 (*zzz-DTTCompatibility-class*), 11
- affxStatus
 (*zzz-NetAffxCompatibility-class*), 12
- affxStatus, *AffxNetAffxAnnotFileList*-method
 (*zzz-NetAffxCompatibility-class*), 12
- affxText
 (*zzz-DTTCompatibility-class*), 11
- affxText, *Description*-method
 (*zzz-DTTCompatibility-class*), 11
- affxText, *Protocol*-method
 (*zzz-DTTCompatibility-class*), 11
- affxTitle
 (*zzz-DTTCompatibility-class*), 11
- affxTitle, *BibliographicReference*-method
 (*zzz-DTTCompatibility-class*), 11
- affxTitle, *Protocol*-method
 (*zzz-DTTCompatibility-class*), 11
- affxType
 (*zzz-NetAffxCompatibility-class*), 12
- affxType, *AffxAnnotation*-method
 (*zzz-NetAffxCompatibility-class*), 12

- 12
 affxType, AffxFile-method
 (zzz-NetAffxCompatibility-class),
 12
- affxUrl
 (zzz-NetAffxCompatibility-class),
 12
- affxUrl, AffxFile-method
 (zzz-NetAffxCompatibility-class),
 12
- affxUrl, NetAffxResource-method
 (NetAffxResource-class), 3
- affyBarcode
 (zzz-ARRCompatibility-class),
 10
- affyBarcode, PhysicalArray-method
 (zzz-ARRCompatibility-class),
 10
- AffyCompatible, 3, 10, 12, 13
- AffyCompatible
 (AffyCompatible-package), 2
- AffyCompatible-class, 2
- AffyCompatible-package, 2
- analysisResults_assnreflist
 (zzz-DTTCompatibility-class),
 11
- analysisResults_assnreflist, Experiment-method
 (zzz-DTTCompatibility-class),
 11
- annotations_assnlist
 (zzz-DTTCompatibility-class),
 11
- annotations_assnlist, Description-method
 (zzz-DTTCompatibility-class),
 11
- annotations_assnlist, ExperimentalFactor-method
 (zzz-DTTCompatibility-class),
 11
- annotationsFile (accessors), 1
- annotationsFile, NetAffxResource-method
 (NetAffxResource-class), 3
- array_assnlist
 (zzz-DTTCompatibility-class),
 11
- array_assnlist, Array_package-method
 (zzz-DTTCompatibility-class),
 11
- array_assnref
 (zzz-DTTCompatibility-class),
 11
- array_assnref, BioAssayCreation-method
 (zzz-DTTCompatibility-class),
 11
- array_assnref, Hybridization-method
 (zzz-DTTCompatibility-class),
 11
- array_package
 (zzz-DTTCompatibility-class),
 11
- array_package, MAGE-ML-method
 (zzz-DTTCompatibility-class),
 11
- array_ref
 (zzz-DTTCompatibility-class),
 11
- array_ref, Array_assnref-method
 (zzz-DTTCompatibility-class),
 11
- array_ref, Arrays_assnreflist-method
 (zzz-DTTCompatibility-class),
 11
- arrayAttribute
 (zzz-ARRCompatibility-class),
 10
- arrayAttribute, PhysicalArray-method
 (zzz-ARRCompatibility-class),
 10
- arrayDesign
 (zzz-DTTCompatibility-class),
 11
- arrayDesign, ArrayDesign_assnlist-method
 (zzz-DTTCompatibility-class),
 11
- arrayDesign_assnlist
 (zzz-DTTCompatibility-class),
 11
- arrayDesign_assnlist, ArrayDesign_package-method
 (zzz-DTTCompatibility-class),
 11
- arrayDesign_assnref
 (zzz-DTTCompatibility-class),
 11
- arrayDesign_assnref, Array-method
 (zzz-DTTCompatibility-class),
 11
- arrayDesign_package
 (zzz-DTTCompatibility-class),
 11
- arrayDesign_package, MAGE-ML-method
 (zzz-DTTCompatibility-class),
 11
- arrayDesign_ref
 (zzz-DTTCompatibility-class),
 11

arrayDesign_ref, ArrayDesign_assnref-method	(zzz-DTTCompatibility-class),	11	arrayManufactureDeviation, ArrayManufactureDeviation	(zzz-DTTCompatibility-class),	11
arrayGroup	(zzz-DTTCompatibility-class),	11	arrayManufactureDeviations_assnlist	(zzz-DTTCompatibility-class),	11
arrayGroup, ArrayGroup_assnlist-method	(zzz-DTTCompatibility-class),	11	arrayManufactureDeviations_assnlist, Array-method	(zzz-DTTCompatibility-class),	11
arrayGroup_assnlist	(zzz-DTTCompatibility-class),	11	arrayManufacturers_assnreflist	(zzz-DTTCompatibility-class),	11
arrayGroup_assnlist, Array_package-method	(zzz-DTTCompatibility-class),	11	arrayManufacturers_assnreflist, ArrayManufacturers	(zzz-DTTCompatibility-class),	11
arrayGroup_assnref	(zzz-DTTCompatibility-class),	11	arrayName	(zzz-ARRCompatibility-class),	10
arrayGroup_assnref, Array-method	(zzz-DTTCompatibility-class),	11	arrayName, PhysicalArray-method	(zzz-ARRCompatibility-class),	10
arrayGroup_ref	(zzz-DTTCompatibility-class),	11	arrays_assnreflist	(zzz-DTTCompatibility-class),	11
arrayGroup_ref, ArrayGroup_assnref-method	(zzz-DTTCompatibility-class),	11	arrays_assnreflist, ArrayGroup-method	(zzz-DTTCompatibility-class),	11
arrayIdentifier	(zzz-DTTCompatibility-class),	11	arrays_assnreflist, ArrayManufacture-method	(zzz-DTTCompatibility-class),	11
arrayIdentifier, Array-method	(zzz-DTTCompatibility-class),	11	arraySpacingX	(zzz-DTTCompatibility-class),	11
arrayManufacture	(zzz-DTTCompatibility-class),	11	arraySpacingX, ArrayGroup-method	(zzz-DTTCompatibility-class),	11
arrayManufacture, ArrayManufacture_assnlist-method	(zzz-DTTCompatibility-class),	11	arraySpacingY	(zzz-DTTCompatibility-class),	11
arrayManufacture_assnlist	(zzz-DTTCompatibility-class),	11	arraySpacingY, ArrayGroup-method	(zzz-DTTCompatibility-class),	11
arrayManufacture_assnlist, Array_package-method	(zzz-DTTCompatibility-class),	11	arrayXOrigin	(zzz-DTTCompatibility-class),	11
arrayManufacture_ref	(zzz-DTTCompatibility-class),	11	arrayXOrigin, Array-method	(zzz-DTTCompatibility-class),	11
arrayManufacture_ref, Information_assnref-method	(zzz-DTTCompatibility-class),	11	arrayYOrigin	(zzz-DTTCompatibility-class),	11
arrayManufactureDeviation	(zzz-DTTCompatibility-class),	11			

- 11
- arrayYOrigin, Array-method
 - (zzz-DTTCompatibility-class),
 - 11
- ARRCompatibility, 10
- ARRCompatibility-class
 - (AffyCompatible-class), 2
- associations_assnlist
 - (zzz-DTTCompatibility-class),
 - 11
- associations_assnlist, OntologyEntry-method
 - (zzz-DTTCompatibility-class),
 - 11
- audit
 - (zzz-DTTCompatibility-class),
 - 11
- audit, AuditTrail_assnlist-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditAndSecurity_package
 - (zzz-DTTCompatibility-class),
 - 11
- auditAndSecurity_package, MAGE-ML-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, Array-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, ArrayDesign-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, ArrayGroup-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, ArrayManufacture-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, Audit-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, BibliographicReference-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, BioAssayCreation-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, BioAssayDataCluster-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, BioAssayDimension-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, BioAssayMap-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, BioAssayTreatment-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, BioSample-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, BioSequence-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, BioSource-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, Channel-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, CompositeCompositeMap-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, CompositeGroup-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, CompositeSequence-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, CompositeSequenceDimension-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, Compound-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, Database-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, DerivedBioAssay-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, DerivedBioAssayData-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, DerivedSignal-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, Description-method
 - (zzz-DTTCompatibility-class),
 - 11
- auditTrail_assnlist, Error-method

(*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, ExpectedValue-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Experiment-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, ExperimentalFactor-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, ExperimentalDesign-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, FactorValue-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Failed-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Feature-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, FeatureDimension-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, FeatureExtraction-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, FeatureGroup-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, FeatureReporterMap-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Fiducial-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Hardware-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, HardwareApplication-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Hybridization-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Image-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, ImageAcquisition-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, LabeledExtract-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, MAGE-ML-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, ManufactureLIMS-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, ManufactureLIMSBiomaterial-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, MeasuredBioAssay-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, MeasuredBioAssayData-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, MeasuredSignal-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Node-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, NodeContents-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Organization-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Parameter-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Person-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, PhysicalArrayDesign-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, PhysicalBioAssay-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, PresentAbsent-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, Protocol-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11
 auditTrail_assnlist, ProtocolApplication-method (*zzz-DTTCompatibility-class*), 11
 (*zzz-DTTCompatibility-class*), 11
 11

auditTrail_assnlist, PValue-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, QuantitationTypeDimension-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, QuantitationTypeMap-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, Ratio-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, Reporter-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, ReporterCompositeMap-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, ReporterDimension-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, ReporterGroup-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, Security-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, SecurityGroup-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, SeqFeature-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, Software-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, SoftwareApplication-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, SpecializedQuantitationType-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, Transformation-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, Treatment-method (zzz-DTTCompatibility-class), 11
 auditTrail_assnlist, Zone-method (zzz-DTTCompatibility-class), 11
 authors, BibliographicReference-method (zzz-DTTCompatibility-class), 11
 authors, barcode (zzz-DTTCompatibility-class), 11
 authors, barcode, ArrayGroup-method (zzz-DTTCompatibility-class), 11
 authors, basis (zzz-DTTCompatibility-class), 11
 authors, basis, SeqFeature-method (zzz-DTTCompatibility-class), 11
 authors, bibliographicReference (zzz-DTTCompatibility-class), 11
 authors, bibliographicReference, BibliographicReferences (zzz-DTTCompatibility-class), 11
 authors, bibliographicReferences_assnlist (zzz-DTTCompatibility-class), 11
 authors, bibliographicReferences_assnlist, Description-r (zzz-DTTCompatibility-class), 11
 authors, bioAssay_assnlist (zzz-DTTCompatibility-class), 11
 authors, bioAssay_assnlist, BioAssay_package-method (zzz-DTTCompatibility-class), 11
 authors, bioAssay_assnref (zzz-DTTCompatibility-class), 11
 authors, bioAssay_assnref, BioAssayTuple-method (zzz-DTTCompatibility-class), 11
 authors, bioAssay_package (zzz-DTTCompatibility-class), 11
 authors, bioAssay_package, MAGE-ML-method (zzz-DTTCompatibility-class), 11
 authors, bioAssayCreation (zzz-DTTCompatibility-class), 11
 authors, bioAssayCreation, BioAssayCreation_assn-method (zzz-DTTCompatibility-class), 11

11	bioAssayDimension, BioAssayDimension_assnlist-method (zzz-DTTCompatibility-class),	11
bioAssayCreation_assn (zzz-DTTCompatibility-class),	11	bioAssayDimension_assnlist (zzz-DTTCompatibility-class),
11	bioAssayCreation_assn, PhysicalBioAssay-method (zzz-DTTCompatibility-class),	11
bioAssayCreation_assn, PhysicalBioAssay-method (zzz-DTTCompatibility-class),	11	bioAssayDimension_assnlist, BioAssayData_package-method (zzz-DTTCompatibility-class),
11	bioAssayData_assnlist (zzz-DTTCompatibility-class),	11
bioAssayData_assnlist (zzz-DTTCompatibility-class),	11	bioAssayDimension_assnref (zzz-DTTCompatibility-class),
11	bioAssayData_assnlist, BioAssayData_package-method (zzz-DTTCompatibility-class),	11
bioAssayData_assnlist, BioAssayData_package-method (zzz-DTTCompatibility-class),	11	bioAssayDimension_assnref, DerivedBioAssayData-method (zzz-DTTCompatibility-class),
11	bioAssayData_assnreflist (zzz-DTTCompatibility-class),	11
bioAssayData_assnreflist (zzz-DTTCompatibility-class),	11	bioAssayDimension_assnref, MeasuredBioAssayData-method (zzz-DTTCompatibility-class),
11	bioAssayData_assnreflist, Experiment-method (zzz-DTTCompatibility-class),	11
bioAssayData_assnreflist, Experiment-method (zzz-DTTCompatibility-class),	11	bioAssayDimension_assnref, NodeContents-method (zzz-DTTCompatibility-class),
11	bioAssayData_package (zzz-DTTCompatibility-class),	11
bioAssayData_package (zzz-DTTCompatibility-class),	11	bioAssayDimension_ref (zzz-DTTCompatibility-class),
11	bioAssayData_package, MAGE-ML-method (zzz-DTTCompatibility-class),	11
bioAssayData_package, MAGE-ML-method (zzz-DTTCompatibility-class),	11	bioAssayDimension_ref, BioAssayDimension_assnref (zzz-DTTCompatibility-class),
11	bioAssayDataCluster (zzz-DTTCompatibility-class),	11
bioAssayDataCluster (zzz-DTTCompatibility-class),	11	bioAssayFactorValues_assnreflist (zzz-DTTCompatibility-class),
11	bioAssayDataCluster, BioAssayDataCluster_assnlist-method (zzz-DTTCompatibility-class),	11
bioAssayDataCluster, BioAssayDataCluster_assnlist-method (zzz-DTTCompatibility-class),	11	bioAssayFactorValues_assnreflist, DerivedBioAssayData-method (zzz-DTTCompatibility-class),
11	bioAssayDataCluster_assnlist (zzz-DTTCompatibility-class),	11
bioAssayDataCluster_assnlist (zzz-DTTCompatibility-class),	11	bioAssayFactorValues_assnreflist, MeasuredBioAssayData-method (zzz-DTTCompatibility-class),
11	bioAssayDataCluster_assnlist, HigherLevelAnalysis_package-method (zzz-DTTCompatibility-class),	11
bioAssayDataCluster_assnlist, HigherLevelAnalysis_package-method (zzz-DTTCompatibility-class),	11	bioAssayFactorValues_assnreflist, PhysicalBioAssayData-method (zzz-DTTCompatibility-class),
11	bioAssayDataCluster_ref (zzz-DTTCompatibility-class),	11
bioAssayDataCluster_ref (zzz-DTTCompatibility-class),	11	bioAssayMap (zzz-DTTCompatibility-class),
11	bioAssayDataCluster_ref, AnalysisResults_assnreflist-method (zzz-DTTCompatibility-class),	11
bioAssayDataCluster_ref, AnalysisResults_assnreflist-method (zzz-DTTCompatibility-class),	11	bioAssayMap, BioAssayMap_assnlist-method (zzz-DTTCompatibility-class),
11	bioAssayDataSources_assnreflist (zzz-DTTCompatibility-class),	11
bioAssayDataSources_assnreflist (zzz-DTTCompatibility-class),	11	bioAssayMap_assnlist (zzz-DTTCompatibility-class),
11	bioAssayDataSources_assnreflist, Transformation_package-method (zzz-DTTCompatibility-class),	11
bioAssayDataSources_assnreflist, Transformation_package-method (zzz-DTTCompatibility-class),	11	bioAssayMap_assnlist, BioAssayData_package-method (zzz-DTTCompatibility-class),
11	bioAssayDimension (zzz-DTTCompatibility-class),	11
bioAssayDimension (zzz-DTTCompatibility-class),	11	bioAssayMap_ref (zzz-DTTCompatibility-class),
11		

(zzz-*DTTCompatibility-class*), 11
 11 bioAssayTuple
 bioAssayMap_ref, BioAssayMaps_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioAssayTuple, BioAssayTuples_assnlist-method
 bioAssayMap_ref, DerivedBioAssayMap_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioAssayTuples_assnlist
 bioAssayMapping (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioAssayTuples_assnlist, BioDataTuples-method
 bioAssayMapping, BioAssayMapping_assn-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioDataCube
 bioAssayMapping_assn (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioDataCube, BioDataValues_assn-method
 bioAssayMapping_assn, Transformation-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioDataTuples
 bioAssayMaps_assnreflist (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioDataTuples, BioDataValues_assn-method
 bioAssayMaps_assnreflist, BioAssayMapping-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioDataValues_assn
 bioAssayMapTarget_assnref (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioDataValues_assn, DerivedBioAssayData-method
 bioAssayMapTarget_assnref, BioAssayMap-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioDataValues_assn, MeasuredBioAssayData-method
 bioAssays_assnreflist (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioEvent_package
 bioAssays_assnreflist, BioAssayDimension-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioEvent_package, MAGE-ML-method
 bioAssays_assnreflist, Experiment-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 biologicalCharacteristics_assnreflist
 bioAssayTreatment (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 biologicalCharacteristics_assnreflist, Composit
 bioAssayTreatment, BioAssayTreatments_assnlist (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioMaterial_assnlist
 bioAssayTreatments_assnlist (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11 bioMaterial_assnlist, BioMaterial_package-method
 bioAssayTreatments_assnlist, PhysicalBioAssay-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11

bioMaterial_assnref (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterial_assnref, BioMaterialMeasurement-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterial_assnref, ManufactureLIMS-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterial_assnref, ManufactureLIMSBiomaterial-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterial_package (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterial_package, MAGE-ML-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterialMeasurement (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterialMeasurement, SourceBioMaterialMeasurements_assnlist-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterialPlateCol (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterialPlateCol, ManufactureLIMSBiomaterial-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterialPlateIdentifier (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterialPlateIdentifier, ManufactureLIMSBiomaterial-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterialPlateRow (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioMaterialPlateRow, ManufactureLIMSBiomaterial-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioSample (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioSample, BioMaterial_assnlist-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioSample_ref (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioSample_ref, BioMaterial_assnref-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 bioSequence (zzz-DTTCompatibility-class), 11
 bioSequence, BioSequence_assnlist-method (zzz-DTTCompatibility-class), 11
 bioSequence_assnlist (zzz-DTTCompatibility-class), 11
 bioSequence_package (zzz-DTTCompatibility-class), 11
 bioSequence_package, MAGE-ML-method (zzz-DTTCompatibility-class), 11
 bioSequence_ref (zzz-DTTCompatibility-class), 11
 bioSequence_ref, BiologicalCharacteristics_assnlist-method (zzz-DTTCompatibility-class), 11
 bioSequence_ref, ImmobilizedCharacteristics_assnlist-method (zzz-DTTCompatibility-class), 11
 bioSource (zzz-DTTCompatibility-class), 11
 bioSource, BioMaterial_assnlist-method (zzz-DTTCompatibility-class), 11
 bioSource_ref (zzz-DTTCompatibility-class), 11
 bioSource_ref, BioMaterial_assnref-method (zzz-DTTCompatibility-class), 11
 bqs_package (zzz-DTTCompatibility-class), 11
 bqs_package, MAGE-ML-method (zzz-DTTCompatibility-class), 11
 category_assn (zzz-DTTCompatibility-class), 11
 category_assn, ExperimentalFactor-method (zzz-DTTCompatibility-class), 11

- 11
- channel
 - (zzz-*DTTCompatibility-class*), 11
- channel, Channel_assnlist-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnlist
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnlist, BioAssay_package-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref, DerivedSignal-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref, Error-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref, ExpectedValue-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref, Failed-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref, MeasuredSignal-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref, PresentAbsent-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref, PValue-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref, Ratio-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_assnref, SpecializedQuantitationType-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_ref
 - (zzz-*DTTCompatibility-class*), 11
- channel_ref, Channel_assnref-method
 - (zzz-*DTTCompatibility-class*), 11
- channel_ref, Channels_assnreflist-method
 - (zzz-*DTTCompatibility-class*), 11
- channels_assnreflist
 - (zzz-*DTTCompatibility-class*), 11
- channels_assnreflist, DerivedBioAssay-method
 - (zzz-*DTTCompatibility-class*), 11
- channels_assnreflist, Image-method
 - (zzz-*DTTCompatibility-class*), 11
- channels_assnreflist, MeasuredBioAssay-method
 - (zzz-*DTTCompatibility-class*), 11
- channels_assnreflist, PhysicalBioAssay-method
 - (zzz-*DTTCompatibility-class*), 11
- characteristics_assnlist
 - (zzz-*DTTCompatibility-class*), 11
- characteristics_assnlist, BioSample-method
 - (zzz-*DTTCompatibility-class*), 11
- characteristics_assnlist, BioSource-method
 - (zzz-*DTTCompatibility-class*), 11
- characteristics_assnlist, LabeledExtract-method
 - (zzz-*DTTCompatibility-class*), 11
- clusterBioAssayData_assnref
 - (zzz-*DTTCompatibility-class*), 11
- clusterBioAssayData_assnref, BioAssayDataCluster-method
 - (zzz-*DTTCompatibility-class*), 11
- column
 - (zzz-*DTTCompatibility-class*), 11
- column, FeatureLocation-method
 - (zzz-*DTTCompatibility-class*), 11
- column, Zone-method
 - (zzz-*DTTCompatibility-class*), 11
- componentCompounds_assnlist
 - (zzz-*DTTCompatibility-class*), 11
- componentCompounds_assnlist, Compound-method
 - (zzz-*DTTCompatibility-class*), 11
- composite_assnref
 - (zzz-*DTTCompatibility-class*), 11
- composite_assnref, CompositePosition-method

	(<i>zzz-DTTCompatibility-class</i>),	11	
compositeCompositeMap	(<i>zzz-DTTCompatibility-class</i>),	11	compositeGroups_assnreflist, ArrayDesign-method
compositeCompositeMap, CompositeCompositeMap	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeCompositeMap, CompositeCompositeMap	(<i>zzz-DTTCompatibility-class</i>),	11	compositeGroups_assnreflist, PhysicalArrayDesign-method
compositeCompositeMap, DesignElementMap	(<i>zzz-DTTCompatibility-class</i>),	11	compositePosition
compositeCompositeMap_assnlist	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeCompositeMap_assnlist, DesignElement	(<i>zzz-DTTCompatibility-class</i>),	11	compositePosition, CompositePositionSources_assnlist
compositeCompositeMap_ref	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeCompositeMap_ref, CompositeCompositeMap	(<i>zzz-DTTCompatibility-class</i>),	11	compositePosition, Coordinate_assn-method
compositeCompositeMap_ref, CompositeCompositeMap	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeCompositeMap_ref, DesignElementMaps	(<i>zzz-DTTCompatibility-class</i>),	11	compositePositionSources_assnlist
compositeCompositeMaps_assnreflist	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeCompositeMaps_assnreflist, CompositeCompositeMaps	(<i>zzz-DTTCompatibility-class</i>),	11	compositePositionSources_assnlist, CompositeCoordinate
compositeCompositeMaps_assnreflist, CompositeCompositeMaps	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeCompositeMaps_assnreflist, DesignElementMaps	(<i>zzz-DTTCompatibility-class</i>),	11	compositeSequence
compositeCompositeMaps_assnreflist	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeCompositeMaps_assnreflist, CompositeCompositeMaps	(<i>zzz-DTTCompatibility-class</i>),	11	compositeSequence, CompositeSequence_assnlist-method
compositeGroup	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeGroup, CompositeGroup_assnlist-method	(<i>zzz-DTTCompatibility-class</i>),	11	compositeSequence, DesignElement_assnlist-method
compositeGroup_assnlist	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeGroup_assnlist, ArrayDesign_package-method	(<i>zzz-DTTCompatibility-class</i>),	11	compositeSequence_assnlist
compositeGroup_ref	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
compositeGroup_ref, CompositeGroups_assnreflist-method	(<i>zzz-DTTCompatibility-class</i>),	11	compositeSequence_assnlist, DesignElement_package
compositeGroups_assnreflist	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
	(<i>zzz-DTTCompatibility-class</i>),	11	compositeSequence_assnref
	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
	(<i>zzz-DTTCompatibility-class</i>),	11	compositeSequence_assnref, CompositeCompositeMap
	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
	(<i>zzz-DTTCompatibility-class</i>),	11	compositeSequence_ref
	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),
	(<i>zzz-DTTCompatibility-class</i>),	11	compositeSequence_ref, Composite_assnref-method
	(<i>zzz-DTTCompatibility-class</i>),	11	(<i>zzz-DTTCompatibility-class</i>),

compositeSequence_ref, CompositeSequence_assnref-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compositeSequence_ref, CompositeSequences_assnref-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compositeSequence_ref, DesignElement_assnref-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compositeSequenceDimension (zzz-DTTCompatibility-class), 11
 compositeSequenceDimension, DesignElementDimension-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compositeSequenceDimension_ref (zzz-DTTCompatibility-class), 11
 compositeSequenceDimension_ref, DesignElementDimension_ref-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compositeSequences_assnreflist (zzz-DTTCompatibility-class), 11
 compositeSequences_assnreflist, CompositeGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compositeSequences_assnreflist, CompositeSequence-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compound (zzz-DTTCompatibility-class), 11
 compound, Compound_assnlist-method (zzz-DTTCompatibility-class), 11
 compound_assnlist (zzz-DTTCompatibility-class), 11
 compound_assnlist, BioMaterial_package-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compound_assnref (zzz-DTTCompatibility-class), 11
 compound_assnref, CompoundMeasurement-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compound_ref (zzz-DTTCompatibility-class), 11
 compound_ref, Compound_assnref-method (zzz-DTTCompatibility-class), 11
 compound_ref, Labels_assnreflist-method (zzz-DTTCompatibility-class), 11
 compoundIndices_assnlist (zzz-DTTCompatibility-class), 11
 compoundIndices_assnlist, Compound-method (zzz-DTTCompatibility-class), 11
 compoundMeasurement (zzz-DTTCompatibility-class), 11
 compoundMeasurement, ComponentCompounds_assnlist-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compoundMeasurement, CompoundMeasurements_assnlist-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 compoundMeasurements_assnlist (zzz-DTTCompatibility-class), 11
 compoundMeasurements_assnlist, Treatment-method (zzz-DTTCompatibility-class), 11
 concentrationUnit (zzz-DTTCompatibility-class), 11
 concentrationUnit, Unit_assn-method (zzz-DTTCompatibility-class), 11
 confidenceIndicators_assnreflist (zzz-DTTCompatibility-class), 11
 confidenceIndicators_assnreflist, DerivedSignal-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 confidenceIndicators_assnreflist, Error-method (zzz-DTTCompatibility-class), 11
 confidenceIndicators_assnreflist, ExpectedValue-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 confidenceIndicators_assnreflist, Failed-method (zzz-DTTCompatibility-class), 11
 confidenceIndicators_assnreflist, MeasuredSignal-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 confidenceIndicators_assnreflist, PresentAbsent-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11

11 controlType_assn, Feature-method
 confidenceIndicators_assnreflist, PValue-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 controlType_assn, Reporter-method
 confidenceIndicators_assnreflist, Ratio-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 coordinate_assn
 confidenceIndicators_assnreflist, SpecializedQuantitationType-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 coordinate_assn, SeqFeatureLocation-method
 contact_assnlist (zzz-DTTCompatibility-class), 11
 11 createdBy
 contact_assnlist, AuditAndSecurity_package-method (zzz-ARRCompatibility-class),
 (zzz-DTTCompatibility-class), 10
 11 createdBy, ArraySetFile-method
 contacts_assnreflist (zzz-DTTCompatibility-class), 10
 11 createdBy, PhysicalArray-method
 contacts_assnreflist, Database-method (zzz-ARRCompatibility-class),
 (zzz-DTTCompatibility-class), 10
 11 createdBy, TemplateFile-method
 containedFeatures_assnreflist (zzz-ARRCompatibility-class),
 (zzz-DTTCompatibility-class), 10
 11 createdBy, ArraySetFile-method
 containedFeatures_assnreflist, FeatureDimension-method (zzz-ARRCompatibility-class),
 (zzz-DTTCompatibility-class), 10
 11 createdBy, PhysicalArray-method
 control (zzz-ARRCompatibility-class), 10
 10 createdBy, TemplateFile-method
 control, UserAttribute-method (zzz-ARRCompatibility-class), 10
 10 createdBy, ArraySetFile-method
 controlFeatures_assnreflist (zzz-DTTCompatibility-class), 10
 11 createdBy, PhysicalArray-method
 controlFeatures_assnreflist, Feature-method (zzz-ARRCompatibility-class),
 (zzz-DTTCompatibility-class), 10
 11 createdBy, TemplateFile-method
 controlledFeatures_assnreflist (zzz-ARRCompatibility-class), 10
 10 createdBy, ArraySetFile-method
 controlledFeatures_assnreflist, Feature-method (zzz-ARRCompatibility-class),
 (zzz-DTTCompatibility-class), 10
 11 database
 controlType_assn (zzz-DTTCompatibility-class), 11
 11 database, Database_assnlist-method
 controlType_assn, CompositeSequence-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 database_assnlist

	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
database_assnlist, Description_package-method	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11
database_assnref	dataFormat	
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
database_assnref, DatabaseEntry-method	dataFormat, DataExternal-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
database_ref	dataFormatInfoURI	
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
database_ref, Database_assnref-method	dataFormatInfoURI, DataExternal-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
databaseEntry	dataInternal	
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
databaseEntry, Accessions_assnlist-method	dataInternal, DataInternal_assn-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
databaseEntry, DatabaseReferences_assnlist-method	dataInternal_assn	
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
databaseEntry, ExternalLIMS_assn-method	dataInternal_assn, BioDataCube-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
databaseEntry, IdentifierLIMS_assn-method	dataType_assn	
	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
databaseEntry, OntologyReference_assn-method	dataType_assn, DerivedSignal-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
databaseEntry, SequenceDatabases_assnlist-method	dataType_assn, Error-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
databaseReferences_assnlist	dataType_assn, ExpectedValue-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
databaseReferences_assnlist, Description-method	dataType_assn, Failed-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
dataExternal	dataType_assn, MeasuredSignal-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
dataExternal, DataExternal_assn-method	dataType_assn, NodeValue-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11
	11	
dataExternal_assn	dataType_assn, Parameter-method	
	(<i>zzz-DTTCompatibility-class</i>),	11
	(<i>zzz-DTTCompatibility-class</i>),	11

- dataType_assn, PresentAbsent-method
 (*zzz-DTTCompatibility-class*),
 11
- dataType_assn, PValue-method
 (*zzz-DTTCompatibility-class*),
 11
- dataType_assn, Ratio-method
 (*zzz-DTTCompatibility-class*),
 11
- dataType_assn, SpecializedQuantitationType-method
 (*zzz-DTTCompatibility-class*),
 11
- datum
 (*zzz-DTTCompatibility-class*),
 11
- datum, Datum_assn-method
 (*zzz-DTTCompatibility-class*),
 11
- datum_assn
 (*zzz-DTTCompatibility-class*),
 11
- datum_assn, QuantitationTypeTuple-method
 (*zzz-DTTCompatibility-class*),
 11
- defaultValue
 (*zzz-ARRCompatibility-class*),
 10
- defaultValue, UserAttribute-method
 (*zzz-ARRCompatibility-class*),
 10
- defaultValue_assn
 (*zzz-DTTCompatibility-class*),
 11
- defaultValue_assn, Parameter-method
 (*zzz-DTTCompatibility-class*),
 11
- defectType_assn
 (*zzz-DTTCompatibility-class*),
 11
- defectType_assn, FeatureDefect-method
 (*zzz-DTTCompatibility-class*),
 11
- defectType_assn, ZoneDefect-method
 (*zzz-DTTCompatibility-class*),
 11
- deltaX
 (*zzz-DTTCompatibility-class*),
 11
- deltaX, PositionDelta-method
 (*zzz-DTTCompatibility-class*),
 11
- deltaY
 (*zzz-DTTCompatibility-class*),
 11
- deltaY, PositionDelta-method
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssay
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssay, BioAssay_assnlist-method
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssay, DerivedBioAssay_assnlist-method
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssay_ref
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssay_ref, BioAssay_assnref-method
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssay_ref, BioAssayMapTarget_assnref-
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssay_ref, BioAssays_assnreflist-meth
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssay_ref, SourceBioAssays_assnreflis
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssay_ref, TopLevelBioAssays_assnrefl
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssayData
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssayData, BioAssayData_assnlist-meth
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssayData, DerivedBioAssayData_assnli
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssayData_assnreflist
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssayData_assnreflist, DerivedBioAssa
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssayData_ref
 (*zzz-DTTCompatibility-class*),
 11
- derivedBioAssayData_ref, BioAssayData_assnrefli
 (*zzz-DTTCompatibility-class*),
 11

[11](#) description, QualityControlDescription_assn-method
 derivedBioAssayData_ref, BioAssayDataSources_assnmethod (zzz-DTTCompatibility-class), [11](#)
[11](#) description, ReplicateDescription_assn-method
 derivedBioAssayData_ref, ClusterBioAssayData_assnmethod (zzz-DTTCompatibility-class), [11](#)
[11](#) description_package
 derivedBioAssayData_ref, DerivedBioAssayData_assnmethod (zzz-DTTCompatibility-class), [11](#)
[11](#) description_package, MAGE-ML-method
 derivedBioAssayData_ref, DerivedBioAssayDataTargetAssnmethod (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist
 derivedBioAssayMap_assnreflist (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, Array-method
 derivedBioAssayMap_assnreflist, DerivedBioAssayMap_assnmethod (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, ArrayDesign-method
 derivedSignal (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, ArrayGroup-method
 derivedSignal, QuantitationType_assnlist-method (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, ArrayManufacture-method
 derivedSignal_ref (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, Audit-method
 derivedSignal_ref, QuantitationType_assnref-method (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, BibliographicReference-method
 derivedSignal_ref, QuantitationTypes_assnreflist-method (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, BioAssayCreation-method
 derivedSignal_ref, SourcesQuantitationType_assnmethod (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, BioAssayDataCluster-method
 derivedSignal_ref, TargetQuantitationType_assnmethod (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, BioAssayDimension-method
 description (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, BioAssayMap-method
 description, Descriptions_assnlist-method (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, BioAssayTreatment-method
 description, NormalizationDescription_assnmethod (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, BioSample-method
 description, OntologyEntry-method (zzz-DTTCompatibility-class), [11](#)
[11](#) descriptions_assnlist, BioSequence-method

(zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, FactorValue-method
 descriptions_assnlist, BioSource-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, Failed-method
 descriptions_assnlist, Channel-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, Feature-method
 descriptions_assnlist, CompositeCompositeMap-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, FeatureDimension-method
 descriptions_assnlist, CompositeGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, FeatureExtraction-method
 descriptions_assnlist, CompositeSequence-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, FeatureGroup-method
 descriptions_assnlist, CompositeSequenceDimension-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, FeatureReporterMap-method
 descriptions_assnlist, Compound-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, Fiducial-method
 descriptions_assnlist, Database-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, Hardware-method
 descriptions_assnlist, DerivedBioAssay-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, HardwareApplication-method
 descriptions_assnlist, DerivedBioAssayData-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, Hybridization-method
 descriptions_assnlist, DerivedSignal-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, Image-method
 descriptions_assnlist, Description-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, ImageAcquisition-method
 descriptions_assnlist, Error-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, LabeledExtract-method
 descriptions_assnlist, ExpectedValue-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, MAGE-ML-method
 descriptions_assnlist, Experiment-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, ManufactureLIMS-method
 descriptions_assnlist, ExperimentalFactor-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 descriptions_assnlist, ManufactureLIMSBiomaterial-method
 descriptions_assnlist, ExperimentDesign-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11

descriptions_assnlist, MeasuredBioAssay-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, MeasuredBioAssayData-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, MeasuredSignal-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Node-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, NodeContents-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Organization-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Parameter-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Person-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, PhysicalArrayDesign-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, PhysicalBioAssay-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, PresentAbsent-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Protocol-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, ProtocolApplication-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, PValue-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, QuantitationTypeDimensions-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, QuantitationTypeMap-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Ratio-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Reporter-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, ReporterCompositeMap-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, ReporterDimension-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, ReporterGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Security-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, SecurityGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, SeqFeature-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Software-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, SoftwareApplication-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, SpecializedQuantitationType-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Transformation-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Treatment-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 descriptions_assnlist, Zone-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 designElement_assnref (zzz-DTTCompatibility-class), 11
 designElement_assnref, DesignElementTuple-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 designElement_package (zzz-DTTCompatibility-class), 11
 designElement_package, MAGE-ML-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 designElementDimension_assnlist (zzz-DTTCompatibility-class), 11

- [11](#) designProviders_assnreflist, PhysicalArrayDesign-
 designElementDimension_assnlist, BioAssayDataPackageCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) directory (accessors), [1](#)
 designElementDimension_assnref directory, NetAffxResource-method
 (zzz-DTTCompatibility-class), (NetAffxResource-class), [3](#)
[11](#) distanceUnit
 designElementDimension_assnref, DerivedBioAssayData-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit, DistanceUnit_assn-method
 designElementDimension_assnref, MeasuredBioAssayData-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit, Unit_assn-method
 designElementDimension_assnref, NodeContents-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit_assn
 designElementMapping (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit_assn, ArrayGroup-method
 designElementMapping, DesignElementMapping_assn-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit_assn, FeatureGroup-method
 designElementMapping_assn (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit_assn, Fiducial-method
 designElementMapping_assn, Transformation-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit_assn, Position-method
 designElementMaps_assnreflist (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit_assn, PositionDelta-method
 designElementMaps_assnreflist, DesignElementMapping-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit_assn, Zone-method
 designElementTuple (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit_assn, ZoneGroup-method
 designElementTuple, DesignElementTuples_assnlist-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) distanceUnit_assn, ZoneLayout-method
 designElementTuples_assnlist (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) DTTCompatibility, [12](#)
 DTTCompatibility-class
 designElementTuples_assnlist, BioAssayTuple-method (zzz-DTTCompatibility-class), [2](#)
 (zzz-DTTCompatibility-class),
[11](#) editor
 designProviders_assnreflist (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) editor, BibliographicReference-method
 designProviders_assnreflist, ArrayDesign-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), [11](#)
[11](#) email

- (zzz-DTTCompatibility-class), 11
- email, Organization-method (zzz-DTTCompatibility-class), 11
- email, Person-method (zzz-DTTCompatibility-class), 11
- error (zzz-DTTCompatibility-class), 11
- error, ConfidenceIndicator_assnlist-method (zzz-DTTCompatibility-class), 11
- error, QuantitationType_assnlist-method (zzz-DTTCompatibility-class), 11
- error_ref (zzz-DTTCompatibility-class), 11
- error_ref, ConfidenceIndicators_assnreflist-method (zzz-DTTCompatibility-class), 11
- error_ref, QuantitationType_assnref-method (zzz-DTTCompatibility-class), 11
- error_ref, QuantitationTypes_assnreflist-method (zzz-DTTCompatibility-class), 11
- error_ref, SourcesQuantitationType_assnreflist-method (zzz-DTTCompatibility-class), 11
- error_ref, TargetQuantitationType_assnref-method (zzz-DTTCompatibility-class), 11
- expectedValue (zzz-DTTCompatibility-class), 11
- expectedValue, ConfidenceIndicator_assnlist-method (zzz-DTTCompatibility-class), 11
- expectedValue, QuantitationType_assnlist-method (zzz-DTTCompatibility-class), 11
- expectedValue_ref (zzz-DTTCompatibility-class), 11
- expectedValue_ref, ConfidenceIndicators_assnreflist-method (zzz-DTTCompatibility-class), 11
- expectedValue_ref, QuantitationType_assnref-method (zzz-DTTCompatibility-class), 11
- expectedValue_ref, QuantitationTypes_assnreflist-method (zzz-DTTCompatibility-class), 11
- expectedValue_ref, SourcesQuantitationType_assnreflist-method (zzz-DTTCompatibility-class), 11
- expectedValue_ref, TargetQuantitationType_assnreflist-method (zzz-DTTCompatibility-class), 11
- experiment (zzz-DTTCompatibility-class), 11
- experiment, Experiment_assnlist-method (zzz-DTTCompatibility-class), 11
- experiment_assnlist (zzz-DTTCompatibility-class), 11
- experiment_assnlist, Experiment_package-method (zzz-DTTCompatibility-class), 11
- experiment_package (zzz-DTTCompatibility-class), 11
- experiment_package, MAGE-ML-method (zzz-DTTCompatibility-class), 11
- experimentalFactor (zzz-DTTCompatibility-class), 11
- experimentalFactor, ExperimentalFactors_assnlist-method (zzz-DTTCompatibility-class), 11
- experimentalFactor_ref (zzz-DTTCompatibility-class), 11
- experimentalFactor_ref, ExperimentalFactor_assnlist-method (zzz-DTTCompatibility-class), 11
- experimentalFactors_assnlist (zzz-DTTCompatibility-class), 11
- experimentalFactors_assnlist, ExperimentDesign-assnlist-method (zzz-DTTCompatibility-class), 11
- experimentDesign (zzz-DTTCompatibility-class), 11
- experimentDesign, ExperimentDesigns_assnlist-method (zzz-DTTCompatibility-class), 11

experimentDesigns_assnlist	(<i>zzz-DTTCompatibility-class</i>),	(<i>zzz-DTTCompatibility-class</i>),
11	11	11
experimentDesigns_assnlist, Experiment-method	(<i>zzz-DTTCompatibility-class</i>),	factorValue_ref
11	11	(<i>zzz-DTTCompatibility-class</i>),
exportedFromDB	(<i>zzz-DTTCompatibility-class</i>),	factorValue_ref, BioAssayFactorValues_assnrefl
11	11	(<i>zzz-DTTCompatibility-class</i>),
exportedFromDB, ExternalReference-method	(<i>zzz-DTTCompatibility-class</i>),	factorValues_assnlist
11	11	(<i>zzz-DTTCompatibility-class</i>),
exportedFromServer	(<i>zzz-DTTCompatibility-class</i>),	factorValues_assnlist, ExperimentalFactor-metho
11	11	(<i>zzz-DTTCompatibility-class</i>),
exportedFromServer, ExternalReference-method	(<i>zzz-DTTCompatibility-class</i>),	failed
11	11	(<i>zzz-DTTCompatibility-class</i>),
exportID	(<i>zzz-DTTCompatibility-class</i>),	failed, QuantitationType_assnlist-method
11	11	(<i>zzz-DTTCompatibility-class</i>),
exportID, ExternalReference-method	(<i>zzz-DTTCompatibility-class</i>),	failed_ref
11	11	(<i>zzz-DTTCompatibility-class</i>),
exportName	(<i>zzz-DTTCompatibility-class</i>),	failed_ref, QuantitationType_assnref-method
11	11	(<i>zzz-DTTCompatibility-class</i>),
exportName, ExternalReference-method	(<i>zzz-DTTCompatibility-class</i>),	failed_ref, QuantitationTypes_assnreflist-metho
11	11	(<i>zzz-DTTCompatibility-class</i>),
externalLIMS_assn	(<i>zzz-DTTCompatibility-class</i>),	failed_ref, SourcesQuantitationType_assnreflist
11	11	(<i>zzz-DTTCompatibility-class</i>),
externalLIMS_assn, Compound-method	(<i>zzz-DTTCompatibility-class</i>),	failed_ref, TargetQuantitationType_assnref-meth
11	11	(<i>zzz-DTTCompatibility-class</i>),
externalReference	(<i>zzz-DTTCompatibility-class</i>),	failTypes_assnlist
11	11	(<i>zzz-DTTCompatibility-class</i>),
externalReference, ExternalReference_assn-method	(<i>zzz-DTTCompatibility-class</i>),	failTypes_assnlist, Reporter-method
11	11	(<i>zzz-DTTCompatibility-class</i>),
externalReference_assn	(<i>zzz-DTTCompatibility-class</i>),	fax(<i>zzz-DTTCompatibility-class</i>),
11	11	11
externalReference_assn, Description-method	(<i>zzz-DTTCompatibility-class</i>),	fax, Organization-method
11	11	(<i>zzz-DTTCompatibility-class</i>),
factorValue	(<i>zzz-DTTCompatibility-class</i>),	fax, Person-method
11	11	(<i>zzz-DTTCompatibility-class</i>),
factorValue, FactorValues_assnlist-method	(<i>zzz-DTTCompatibility-class</i>),	feature
11	11	(<i>zzz-DTTCompatibility-class</i>),

- feature, DesignElement_assnlist-method (zzz-DTTCompatibility-class), 11
- feature, Features_assnlist-method (zzz-DTTCompatibility-class), 11
- feature_assnref (zzz-DTTCompatibility-class), 11
- feature_assnref, FeatureDefect-method (zzz-DTTCompatibility-class), 11
- feature_assnref, FeatureInformation-method (zzz-DTTCompatibility-class), 11
- feature_assnref, ManufactureLIMS-method (zzz-DTTCompatibility-class), 11
- feature_assnref, ManufactureLIMSBiomaterial-method (zzz-DTTCompatibility-class), 11
- feature_ref (zzz-DTTCompatibility-class), 11
- feature_ref, ContainedFeatures_assnreflist-method (zzz-DTTCompatibility-class), 11
- feature_ref, ControlFeatures_assnreflist-method (zzz-DTTCompatibility-class), 11
- feature_ref, ControlledFeatures_assnreflist-method (zzz-DTTCompatibility-class), 11
- feature_ref, DesignElement_assnref-method (zzz-DTTCompatibility-class), 11
- feature_ref, Feature_assnref-method (zzz-DTTCompatibility-class), 11
- featureDefect (zzz-DTTCompatibility-class), 11
- featureDefect, FeatureDefects_assnlist-method (zzz-DTTCompatibility-class), 11
- featureDefects_assnlist (zzz-DTTCompatibility-class), 11
- featureDefects_assnlist, ArrayManufactureDevice_assnlist-method (zzz-DTTCompatibility-class), 11
- featureDimension (zzz-DTTCompatibility-class), 11
- featureDimension, DesignElementDimension_assnlist-method (zzz-DTTCompatibility-class), 11
- featureDimension_ref (zzz-DTTCompatibility-class), 11
- featureDimension_ref, DesignElementDimension_assnlist-method (zzz-DTTCompatibility-class), 11
- featureExtraction (zzz-DTTCompatibility-class), 11
- featureExtraction, FeatureExtraction_assnlist-method (zzz-DTTCompatibility-class), 11
- featureExtraction_assn (zzz-DTTCompatibility-class), 11
- featureExtraction_assn, MeasuredBioAssay-method (zzz-DTTCompatibility-class), 11
- featureGroup (zzz-DTTCompatibility-class), 11
- featureGroup, FeatureGroups_assnlist-method (zzz-DTTCompatibility-class), 11
- featureGroup_ref (zzz-DTTCompatibility-class), 11
- featureGroup_ref, FeatureGroup_assnref-method (zzz-DTTCompatibility-class), 11
- featureGroups_assnlist (zzz-DTTCompatibility-class), 11
- featureGroups_assnlist, ArrayDesign-method (zzz-DTTCompatibility-class), 11
- featureGroups_assnlist, PhysicalArrayDesign-method (zzz-DTTCompatibility-class), 11
- featureHeight (zzz-DTTCompatibility-class), 11
- featureHeight, FeatureGroup-method (zzz-DTTCompatibility-class), 11
- featureInformation (zzz-DTTCompatibility-class), 11

- 11
- featureInformation, FeatureInformationSources(assignment-method) (zzz-DTTCompatibility-class), 11
- featureInformationSources(assignment-method) (zzz-DTTCompatibility-class), 11
- featureInformationSources_assnlist (zzz-DTTCompatibility-class), 11
- featureInformationSources_assnreflist (zzz-DTTCompatibility-class), 11
- featureInformationSources_assnreflist, Reporter-method (zzz-DTTCompatibility-class), 11
- featureLength (zzz-DTTCompatibility-class), 11
- featureLength, FeatureGroup-method (zzz-DTTCompatibility-class), 11
- featureLIMSSs_assnlist (zzz-DTTCompatibility-class), 11
- featureLIMSSs_assnlist, ArrayManufacture-method (zzz-DTTCompatibility-class), 11
- featureLocation (zzz-DTTCompatibility-class), 11
- featureLocation, FeatureLocation_assn-method (zzz-DTTCompatibility-class), 11
- featureLocation_assn (zzz-DTTCompatibility-class), 11
- featureLocation_assn, Feature-method (zzz-DTTCompatibility-class), 11
- featureReporterMap (zzz-DTTCompatibility-class), 11
- featureReporterMap, DesignElementMap_assnlist-method (zzz-DTTCompatibility-class), 11
- featureReporterMap, FeatureReporterMap_assnlist-method (zzz-DTTCompatibility-class), 11
- featureReporterMap_assnlist (zzz-DTTCompatibility-class), 11
- featureReporterMap_assnlist, DesignElement_pac(assignment-method) (zzz-DTTCompatibility-class), 11
- featureReporterMap_ref (zzz-DTTCompatibility-class), 11
- featureReporterMap_ref, DesignElementMaps_assnlist-method (zzz-DTTCompatibility-class), 11
- featureReporterMap_ref, FeatureReporterMaps_assnlist-method (zzz-DTTCompatibility-class), 11
- featureReporterMaps_assnreflist (zzz-DTTCompatibility-class), 11
- featureReporterMaps_assnreflist, Reporter-method (zzz-DTTCompatibility-class), 11
- features_assnlist (zzz-DTTCompatibility-class), 11
- features_assnlist, FeatureGroup-method (zzz-DTTCompatibility-class), 11
- featureShape_assn (zzz-DTTCompatibility-class), 11
- featureShape_assn, FeatureGroup-method (zzz-DTTCompatibility-class), 11
- featureWidth (zzz-DTTCompatibility-class), 11
- featureWidth, FeatureGroup-method (zzz-DTTCompatibility-class), 11
- fiducial (zzz-DTTCompatibility-class), 11
- fiducial, Fiducials_assnlist-method (zzz-DTTCompatibility-class), 11
- fiducials_assnlist (zzz-DTTCompatibility-class), 11
- fiducials_assnlist, ArrayGroup-method (zzz-DTTCompatibility-class), 11
- fiducialType_assn (zzz-DTTCompatibility-class), 11
- fiducialType_assn, Fiducial-method (zzz-DTTCompatibility-class), 11
- filenameURI (zzz-DTTCompatibility-class), 11
- filenameURI, DataExternal-method

- (zzz-DTTCompatibility-class), 11
- firstName
 - (zzz-DTTCompatibility-class), 11
- firstName, Person-method
 - (zzz-DTTCompatibility-class), 11
- format_assn
 - (zzz-DTTCompatibility-class), 11
- format_assn, Image-method
 - (zzz-DTTCompatibility-class), 11
- guid
 - (zzz-ARRCompatibility-class), 10
- guid, ArraySetFile-method
 - (zzz-ARRCompatibility-class), 10
- guid, PhysicalArray-method
 - (zzz-ARRCompatibility-class), 10
- guid, TemplateFile-method
 - (zzz-ARRCompatibility-class), 10
- hardware
 - (zzz-DTTCompatibility-class), 11
- hardware, Hardware_assnlist-method
 - (zzz-DTTCompatibility-class), 11
- hardware_assnlist
 - (zzz-DTTCompatibility-class), 11
- hardware_assnlist, Protocol_package-method
 - (zzz-DTTCompatibility-class), 11
- hardware_assnref
 - (zzz-DTTCompatibility-class), 11
- hardware_assnref, HardwareApplication-method
 - (zzz-DTTCompatibility-class), 11
- hardware_assnref, Software-method
 - (zzz-DTTCompatibility-class), 11
- hardware_ref
 - (zzz-DTTCompatibility-class), 11
- hardware_ref, Hardware_assnref-method
 - (zzz-DTTCompatibility-class), 11
- hardware_ref, Hardware_assnreflist-method
 - (zzz-DTTCompatibility-class), 11
- hardwareApplication
 - (zzz-DTTCompatibility-class), 11
- hardwareApplication, HardwareApplications_assnlist-method
 - (zzz-DTTCompatibility-class), 11
- hardwareApplications_assnlist
 - (zzz-DTTCompatibility-class), 11
- hardwareApplications_assnlist, ProtocolApplications_assnlist-method
 - (zzz-DTTCompatibility-class), 11
- hardwareManufacturers_assnreflist
 - (zzz-DTTCompatibility-class), 11
- hardwareManufacturers_assnreflist, Hardware-manufacturers-assnreflist-method
 - (zzz-DTTCompatibility-class), 11
- hardwares_assnreflist
 - (zzz-DTTCompatibility-class), 11
- hardwares_assnreflist, Protocol-method
 - (zzz-DTTCompatibility-class), 11
- higherLevelAnalysis_package
 - (zzz-DTTCompatibility-class), 11
- higherLevelAnalysis_package, MAGE-ML-method
 - (zzz-DTTCompatibility-class), 11
- hybridization
 - (zzz-DTTCompatibility-class), 11
- hybridization, BioAssayCreation_assn-method
 - (zzz-DTTCompatibility-class), 11
- identifier
 - (zzz-DTTCompatibility-class), 11
- identifier, Array-method
 - (zzz-DTTCompatibility-class), 11
- identifier, Array_ref-method
 - (zzz-DTTCompatibility-class), 11
- identifier, ArrayDesign-method

- (zzz-*DTTCompatibility-class*),
11
- identifier, ArrayDesign_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, ArrayGroup-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, ArrayGroup_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, ArrayManufacture-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, ArrayManufacture_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssay_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssayCreation-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssayData_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssayDataCluster-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssayDataCluster_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssayDimension-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssayDimension_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssayMap-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssayMap_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioAssayTreatment-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioMaterial_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioSample-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioSample_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioSequence-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioSequence_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioSource-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, BioSource_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, Channel-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, Channel_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, CompositeCompositeMap-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, CompositeCompositeMap_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, CompositeGroup-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, CompositeGroup_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, CompositeSequence-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, CompositeSequence_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, CompositeSequenceDimension-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, CompositeSequenceDimension_ref-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, Compound-method
 (zzz-*DTTCompatibility-class*),
11
- identifier, Compound_ref-method
 (zzz-*DTTCompatibility-class*),
11

identifier, ConfidenceIndicator_ref-method	(zzz-DTTCompatibility-class), 11	identifier, ExperimentalFactor-method	(zzz-DTTCompatibility-class), 11
identifier, Contact_ref-method	(zzz-DTTCompatibility-class), 11	identifier, ExperimentalFactor_ref-method	(zzz-DTTCompatibility-class), 11
identifier, Database-method	(zzz-DTTCompatibility-class), 11	identifier, FactorValue-method	(zzz-DTTCompatibility-class), 11
identifier, Database_ref-method	(zzz-DTTCompatibility-class), 11	identifier, FactorValue_ref-method	(zzz-DTTCompatibility-class), 11
identifier, DerivedBioAssay-method	(zzz-DTTCompatibility-class), 11	identifier, Failed-method	(zzz-DTTCompatibility-class), 11
identifier, DerivedBioAssay_ref-method	(zzz-DTTCompatibility-class), 11	identifier, Failed_ref-method	(zzz-DTTCompatibility-class), 11
identifier, DerivedBioAssayData-method	(zzz-DTTCompatibility-class), 11	identifier, Feature-method	(zzz-DTTCompatibility-class), 11
identifier, DerivedBioAssayData_ref-method	(zzz-DTTCompatibility-class), 11	identifier, Feature_ref-method	(zzz-DTTCompatibility-class), 11
identifier, DerivedSignal-method	(zzz-DTTCompatibility-class), 11	identifier, FeatureDimension-method	(zzz-DTTCompatibility-class), 11
identifier, DerivedSignal_ref-method	(zzz-DTTCompatibility-class), 11	identifier, FeatureDimension_ref-method	(zzz-DTTCompatibility-class), 11
identifier, DesignElement_ref-method	(zzz-DTTCompatibility-class), 11	identifier, FeatureExtraction-method	(zzz-DTTCompatibility-class), 11
identifier, DesignElementDimension_ref-method	(zzz-DTTCompatibility-class), 11	identifier, FeatureGroup-method	(zzz-DTTCompatibility-class), 11
identifier, DesignElementMap_ref-method	(zzz-DTTCompatibility-class), 11	identifier, FeatureGroup_ref-method	(zzz-DTTCompatibility-class), 11
identifier, Error-method	(zzz-DTTCompatibility-class), 11	identifier, FeatureReporterMap-method	(zzz-DTTCompatibility-class), 11
identifier, Error_ref-method	(zzz-DTTCompatibility-class), 11	identifier, FeatureReporterMap_ref-method	(zzz-DTTCompatibility-class), 11
identifier, ExpectedValue-method	(zzz-DTTCompatibility-class), 11	identifier, Hardware-method	(zzz-DTTCompatibility-class), 11
identifier, ExpectedValue_ref-method	(zzz-DTTCompatibility-class), 11	identifier, Hardware_ref-method	(zzz-DTTCompatibility-class), 11
identifier, Experiment-method			

- 11
- identifier, Hybridization-method
(zzz-DTTCompatibility-class),
11
- identifier, Image-method
(zzz-DTTCompatibility-class),
11
- identifier, Image_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, ImageAcquisition-method
(zzz-DTTCompatibility-class),
11
- identifier, LabeledExtract-method
(zzz-DTTCompatibility-class),
11
- identifier, LabeledExtract_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, MAGE-ML-method
(zzz-DTTCompatibility-class),
11
- identifier, MeasuredBioAssay-method
(zzz-DTTCompatibility-class),
11
- identifier, MeasuredBioAssay_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, MeasuredBioAssayData-method
(zzz-DTTCompatibility-class),
11
- identifier, MeasuredBioAssayData_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, MeasuredSignal-method
(zzz-DTTCompatibility-class),
11
- identifier, MeasuredSignal_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, Organization-method
(zzz-DTTCompatibility-class),
11
- identifier, Organization_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, Parameter-method
(zzz-DTTCompatibility-class),
11
- identifier, Parameter_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, Person-method
(zzz-DTTCompatibility-class),
11
- identifier, Person_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, PhysicalArrayDesign-method
(zzz-DTTCompatibility-class),
11
- identifier, PhysicalArrayDesign_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, PhysicalBioAssay-method
(zzz-DTTCompatibility-class),
11
- identifier, PhysicalBioAssay_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, PresentAbsent-method
(zzz-DTTCompatibility-class),
11
- identifier, PresentAbsent_ref-method
(zzz-DTTCompatibility-class),
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(zzz-DTTCompatibility-class),
11
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(zzz-DTTCompatibility-class),
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- identifier, PValue-method
(zzz-DTTCompatibility-class),
11
- identifier, PValue_ref-method
(zzz-DTTCompatibility-class),
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(zzz-DTTCompatibility-class),
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- identifier, QuantitationTypeDimension-method
(zzz-DTTCompatibility-class),
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(zzz-DTTCompatibility-class),
11
- identifier, QuantitationTypeMap-method
(zzz-DTTCompatibility-class),
11
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(zzz-DTTCompatibility-class),
11
- identifier, Ratio-method

- (zzz-DTTCompatibility-class),
11
- identifier, Ratio_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, Reporter-method
(zzz-DTTCompatibility-class),
11
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(zzz-DTTCompatibility-class),
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- identifier, ReporterCompositeMap-method
(zzz-DTTCompatibility-class),
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(zzz-DTTCompatibility-class),
11
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(zzz-DTTCompatibility-class),
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(zzz-DTTCompatibility-class),
11
- identifier, ReporterGroup-method
(zzz-DTTCompatibility-class),
11
- identifier, ReporterGroup_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, Security-method
(zzz-DTTCompatibility-class),
11
- identifier, Security_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, SecurityGroup-method
(zzz-DTTCompatibility-class),
11
- identifier, SecurityGroup_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, Software-method
(zzz-DTTCompatibility-class),
11
- identifier, Software_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, SpecializedQuantitationType-method
(zzz-DTTCompatibility-class),
11
- identifier, SpecializedQuantitationType_ref-method
(zzz-DTTCompatibility-class),
11
- (zzz-DTTCompatibility-class),
11
- identifier, StandardQuantitationType_ref-method
(zzz-DTTCompatibility-class),
11
- identifier, Transformation-method
(zzz-DTTCompatibility-class),
11
- identifier, Treatment-method
(zzz-DTTCompatibility-class),
11
- identifier, Zone-method
(zzz-DTTCompatibility-class),
11
- identifier, Zone_ref-method
(zzz-DTTCompatibility-class),
11
- identifierLIMS_assn
(zzz-DTTCompatibility-class),
11
- identifierLIMS_assn, ManufactureLIMS-method
(zzz-DTTCompatibility-class),
11
- identifierLIMS_assn, ManufactureLIMSBIOMATERIAL-method
(zzz-DTTCompatibility-class),
11
- image_ref
(zzz-DTTCompatibility-class),
11
- image_ref, Images_assnreflist-method
(zzz-DTTCompatibility-class),
11
- imageAcquisition
(zzz-DTTCompatibility-class),
11
- imageAcquisition, BioAssayTreatments_assnreflist-method
(zzz-DTTCompatibility-class),
11
- images_assnreflist
(zzz-DTTCompatibility-class),
11
- images_assnreflist, ImageAcquisition-method
(zzz-DTTCompatibility-class),
11
- immobilizedCharacteristics_assnreflist
(zzz-DTTCompatibility-class),
11
- immobilizedCharacteristics_assnreflist, Reporter-method
(zzz-DTTCompatibility-class),
11
- information_assnref
(zzz-DTTCompatibility-class),
11

- information_assnref, Array-method
 (*zzz-DTTCompatibility-class*),
 11
- Internal-class, 14
- isApproximateLength
 (*zzz-DTTCompatibility-class*),
 11
- isApproximateLength, BioSequence-method
 (*zzz-DTTCompatibility-class*),
 11
- isBackground
 (*zzz-DTTCompatibility-class*),
 11
- isBackground, DerivedSignal-method
 (*zzz-DTTCompatibility-class*),
 11
- isBackground, Error-method
 (*zzz-DTTCompatibility-class*),
 11
- isBackground, ExpectedValue-method
 (*zzz-DTTCompatibility-class*),
 11
- isBackground, Failed-method
 (*zzz-DTTCompatibility-class*),
 11
- isBackground, MeasuredSignal-method
 (*zzz-DTTCompatibility-class*),
 11
- isBackground, PresentAbsent-method
 (*zzz-DTTCompatibility-class*),
 11
- isBackground, PValue-method
 (*zzz-DTTCompatibility-class*),
 11
- isBackground, Ratio-method
 (*zzz-DTTCompatibility-class*),
 11
- isBackground, SpecializedQuantitationType-method
 (*zzz-DTTCompatibility-class*),
 11
- isCircular
 (*zzz-DTTCompatibility-class*),
 11
- isCircular, BioSequence-method
 (*zzz-DTTCompatibility-class*),
 11
- isSolvent
 (*zzz-DTTCompatibility-class*),
 11
- isSolvent, Compound-method
 (*zzz-DTTCompatibility-class*),
 11
- issue
 (*zzz-DTTCompatibility-class*),
 11
- issue, BibliographicReference-method
 (*zzz-DTTCompatibility-class*),
 11
- kindCV
 (*zzz-DTTCompatibility-class*),
 11
- kindCV, Measurement-method
 (*zzz-DTTCompatibility-class*),
 11
- labeledExtract
 (*zzz-DTTCompatibility-class*),
 11
- labeledExtract, BioMaterial_assnlist-method
 (*zzz-DTTCompatibility-class*),
 11
- labeledExtract_ref
 (*zzz-DTTCompatibility-class*),
 11
- labeledExtract_ref, BioMaterial_assnref-method
 (*zzz-DTTCompatibility-class*),
 11
- labels_assnreflist
 (*zzz-DTTCompatibility-class*),
 11
- labels_assnreflist, Channel-method
 (*zzz-DTTCompatibility-class*),
 11
- labels_assnreflist, LabeledExtract-method
 (*zzz-DTTCompatibility-class*),
 11
- lastName
 (*zzz-DTTCompatibility-class*),
 11
- lastName, Person-method
 (*zzz-DTTCompatibility-class*),
 11
- length, ArrayGroup-method
 (*zzz-DTTCompatibility-class*),
 11
- length, BioSequence-method
 (*zzz-DTTCompatibility-class*),
 11
- libraryPackageName
 (*zzz-ARRCompatibility-class*),
 10
- libraryPackageName, PhysicalArray-method
 (*zzz-ARRCompatibility-class*),
 10

- list, 14
- lowerRightX
 - (zzz-DTTCompatibility-class), 11
- lowerRightX, Zone-method
 - (zzz-DTTCompatibility-class), 11
- lowerRightY
 - (zzz-DTTCompatibility-class), 11
- lowerRightY, Zone-method
 - (zzz-DTTCompatibility-class), 11
- make
 - (zzz-DTTCompatibility-class), 11
- make, Hardware-method
 - (zzz-DTTCompatibility-class), 11
- manufactureLIMS
 - (zzz-DTTCompatibility-class), 11
- manufactureLIMS, FeatureLIMSs_assnlist-method
 - (zzz-DTTCompatibility-class), 11
- manufactureLIMSBiomaterial
 - (zzz-DTTCompatibility-class), 11
- manufactureLIMSBiomaterial, FeatureLIMSs_assnlist-method
 - (zzz-DTTCompatibility-class), 11
- manufacturingDate
 - (zzz-DTTCompatibility-class), 11
- manufacturingDate, ArrayManufacture-method
 - (zzz-DTTCompatibility-class), 11
- massUnit
 - (zzz-DTTCompatibility-class), 11
- massUnit, Unit_assn-method
 - (zzz-DTTCompatibility-class), 11
- masterFileGUID
 - (zzz-ARRCompatibility-class), 10
- masterFileGUID, PhysicalArray-method
 - (zzz-ARRCompatibility-class), 10
- masterFileName
 - (zzz-ARRCompatibility-class), 10
- masterFileName, PhysicalArray-method
 - (zzz-ARRCompatibility-class), 10
- materialType_assn
 - (zzz-DTTCompatibility-class), 11
- materialType_assn, BioSample-method
 - (zzz-DTTCompatibility-class), 11
- materialType_assn, BioSource-method
 - (zzz-DTTCompatibility-class), 11
- materialType_assn, LabeledExtract-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssay
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssay, BioAssay_assnlist-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssay, MeasuredBioAssay_assnlist-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssay_ref
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssay_ref, BioAssay_assnref-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssay_ref, BioAssays_assnreflist-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssay_ref, MeasuredBioAssayTarget_assnreflist-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssay_ref, SourceBioAssays_assnreflist-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssay_ref, TopLevelBioAssays_assnreflist-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssayData
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssayData, BioAssayData_assnlist-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssayData, MeasuredBioAssayData_assnreflist-method
 - (zzz-DTTCompatibility-class), 11
- measuredBioAssayData_assnreflist

	(zzz-DTTCompatibility-class),	11	
	11		measurement_assn
measuredBioAssayData_assnreflist, MeasuredBioAssayData_ref	(zzz-DTTCompatibility-class),	11	(zzz-DTTCompatibility-class),
	11		measurement_assn, BioMaterialMeasurement-method
measuredBioAssayData_ref	(zzz-DTTCompatibility-class),	11	(zzz-DTTCompatibility-class),
	11		measurement_assn, CompoundMeasurement-method
measuredBioAssayData_ref, BioAssayData_assnreflist	(zzz-DTTCompatibility-class),	11	(zzz-DTTCompatibility-class),
	11		measurement_assn, FactorValue-method
measuredBioAssayData_ref, BioAssayDataSources	(zzz-DTTCompatibility-class),	11	(zzz-DTTCompatibility-class),
	11		measurement_package
measuredBioAssayData_ref, ClusterBioAssayData	(zzz-DTTCompatibility-class),	11	(zzz-DTTCompatibility-class),
	11		measurement_package, MAGE-ML-method
measuredBioAssayData_ref, MeasuredBioAssayData	(zzz-DTTCompatibility-class),	11	(zzz-DTTCompatibility-class),
	11		mediaCol
measuredSignal	(zzz-ARRCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		mediaCol, PhysicalArray-method
measuredSignal, QuantitationType_assnreflist-method	(zzz-ARRCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		mediaFileGUID
measuredSignal_ref	(zzz-ARRCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		mediaFileGUID, PhysicalArray-method
measuredSignal_ref, QuantitationType_assnref-method	(zzz-ARRCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		mediaFileName
measuredSignal_ref, QuantitationTypes_assnreflist	(zzz-ARRCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		mediaFileName, PhysicalArray-method
measuredSignal_ref, SourcesQuantitationType_assnref	(zzz-ARRCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		mediaRow
measuredSignal_ref, TargetQuantitationType_assnref	(zzz-ARRCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		mediaRow, PhysicalArray-method
measurement	(zzz-DTTCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		mediaType
measurement, ActionMeasurement_assn-method	(zzz-DTTCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		mediaType, PhysicalArray-method
measurement, DefaultValue_assn-method	(zzz-DTTCompatibility-class),	10	(zzz-ARRCompatibility-class),
	11		members_assnreflist
measurement, Measurement_assn-method	(zzz-DTTCompatibility-class),	11	(zzz-DTTCompatibility-class),
	11		11

members_assnreflist, SecurityGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 midInitials name, ArrayGroup_ref-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 midInitials, Person-method name, ArrayManufacture-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 mismatchInformation name, ArrayManufacture_ref-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 mismatchInformation, MismatchInformation_assnlist-method name, BioAssay_ref-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 mismatchInformation_assnlist name, BioAssayCreation-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 mismatchInformation_assnlist, CompositePosition-method name, BioAssayData_ref-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 mismatchInformation_assnlist, FeatureInformation-method name, BioAssayDataCluster-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 mismatchInformation_assnlist, ReporterPosition-method name, BioAssayDataCluster_ref-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 model name, BioAssayDimension-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 model, Hardware-method name, BioAssayDimension_ref-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 name name, BioAssayMap-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 name, Array-method name, BioAssayMap_ref-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 name, Array_ref-method name, BioAssayTreatment-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 name, ArrayAttribute-method name, BioMaterial_ref-method
 (zzz-ARRCompatibility-class), (zzz-DTTCompatibility-class), 10
 name, ArrayDesign-method name, BioSample-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 name, ArrayDesign_ref-method name, BioSample_ref-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11
 name, ArrayGroup-method name, BioSequence-method
 (zzz-DTTCompatibility-class), (zzz-DTTCompatibility-class), 11

- 11
- name, BioSequence_ref-method
(zzz-DTTCompatibility-class),
11
- name, BioSource-method
(zzz-DTTCompatibility-class),
11
- name, BioSource_ref-method
(zzz-DTTCompatibility-class),
11
- name, Channel-method
(zzz-DTTCompatibility-class),
11
- name, Channel_ref-method
(zzz-DTTCompatibility-class),
11
- name, CompositeCompositeMap-method
(zzz-DTTCompatibility-class),
11
- name, CompositeCompositeMap_ref-method
(zzz-DTTCompatibility-class),
11
- name, CompositeGroup-method
(zzz-DTTCompatibility-class),
11
- name, CompositeGroup_ref-method
(zzz-DTTCompatibility-class),
11
- name, CompositeSequence-method
(zzz-DTTCompatibility-class),
11
- name, CompositeSequence_ref-method
(zzz-DTTCompatibility-class),
11
- name, CompositeSequenceDimension-method
(zzz-DTTCompatibility-class),
11
- name, CompositeSequenceDimension_ref-method
(zzz-DTTCompatibility-class),
11
- name, Compound-method
(zzz-DTTCompatibility-class),
11
- name, Compound_ref-method
(zzz-DTTCompatibility-class),
11
- name, ConfidenceIndicator_ref-method
(zzz-DTTCompatibility-class),
11
- name, Contact_ref-method
(zzz-DTTCompatibility-class),
11
- name, Database-method
(zzz-DTTCompatibility-class),
11
- name, Database_ref-method
(zzz-DTTCompatibility-class),
11
- name, DerivedBioAssay-method
(zzz-DTTCompatibility-class),
11
- name, DerivedBioAssay_ref-method
(zzz-DTTCompatibility-class),
11
- name, DerivedBioAssayData-method
(zzz-DTTCompatibility-class),
11
- name, DerivedBioAssayData_ref-method
(zzz-DTTCompatibility-class),
11
- name, DerivedSignal-method
(zzz-DTTCompatibility-class),
11
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(zzz-DTTCompatibility-class),
11
- name, DesignElement_ref-method
(zzz-DTTCompatibility-class),
11
- name, DesignElementDimension_ref-method
(zzz-DTTCompatibility-class),
11
- name, DesignElementMap_ref-method
(zzz-DTTCompatibility-class),
11
- name, Error-method
(zzz-DTTCompatibility-class),
11
- name, Error_ref-method
(zzz-DTTCompatibility-class),
11
- name, ExpectedValue-method
(zzz-DTTCompatibility-class),
11
- name, ExpectedValue_ref-method
(zzz-DTTCompatibility-class),
11
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(zzz-DTTCompatibility-class),
11
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(zzz-DTTCompatibility-class),
11
- name, ExperimentalFactor_ref-method

- (zzz-*DTTCompatibility-class*),
11
- name, FactorValue-method
(zzz-*DTTCompatibility-class*),
11
- name, FactorValue_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, Failed-method
(zzz-*DTTCompatibility-class*),
11
- name, Failed_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, Feature-method
(zzz-*DTTCompatibility-class*),
11
- name, Feature_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, FeatureDimension-method
(zzz-*DTTCompatibility-class*),
11
- name, FeatureDimension_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, FeatureExtraction-method
(zzz-*DTTCompatibility-class*),
11
- name, FeatureGroup-method
(zzz-*DTTCompatibility-class*),
11
- name, FeatureGroup_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, FeatureReporterMap-method
(zzz-*DTTCompatibility-class*),
11
- name, FeatureReporterMap_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, Hardware-method
(zzz-*DTTCompatibility-class*),
11
- name, Hardware_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, Hybridization-method
(zzz-*DTTCompatibility-class*),
11
- name, Image-method
(zzz-*DTTCompatibility-class*),
11
- name, Image_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, ImageAcquisition-method
(zzz-*DTTCompatibility-class*),
11
- name, LabeledExtract-method
(zzz-*DTTCompatibility-class*),
11
- name, LabeledExtract_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, MAGE-ML-method
(zzz-*DTTCompatibility-class*),
11
- name, MeasuredBioAssay-method
(zzz-*DTTCompatibility-class*),
11
- name, MeasuredBioAssay_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, MeasuredBioAssayData-method
(zzz-*DTTCompatibility-class*),
11
- name, MeasuredBioAssayData_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, MeasuredSignal-method
(zzz-*DTTCompatibility-class*),
11
- name, MeasuredSignal_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, NameValueType-method
(zzz-*DTTCompatibility-class*),
11
- name, NodeValue-method
(zzz-*DTTCompatibility-class*),
11
- name, Organization-method
(zzz-*DTTCompatibility-class*),
11
- name, Organization_ref-method
(zzz-*DTTCompatibility-class*),
11
- name, Parameter-method
(zzz-*DTTCompatibility-class*),
11
- name, Parameter_ref-method
(zzz-*DTTCompatibility-class*),
11

name, Person-method (zzz-DTTCompatibility-class), 11
 name, Person_ref-method (zzz-DTTCompatibility-class), 11
 name, PhysicalArrayDesign-method (zzz-DTTCompatibility-class), 11
 name, PhysicalArrayDesign_ref-method (zzz-DTTCompatibility-class), 11
 name, PhysicalBioAssay-method (zzz-DTTCompatibility-class), 11
 name, PhysicalBioAssay_ref-method (zzz-DTTCompatibility-class), 11
 name, PresentAbsent-method (zzz-DTTCompatibility-class), 11
 name, PresentAbsent_ref-method (zzz-DTTCompatibility-class), 11
 name, Protocol-method (zzz-DTTCompatibility-class), 11
 name, Protocol_ref-method (zzz-DTTCompatibility-class), 11
 name, PValue-method (zzz-DTTCompatibility-class), 11
 name, PValue_ref-method (zzz-DTTCompatibility-class), 11
 name, QuantitationType_ref-method (zzz-DTTCompatibility-class), 11
 name, QuantitationTypeDimension-method (zzz-DTTCompatibility-class), 11
 name, QuantitationTypeDimension_ref-method (zzz-DTTCompatibility-class), 11
 name, QuantitationTypeMap-method (zzz-DTTCompatibility-class), 11
 name, QuantitationTypeMap_ref-method (zzz-DTTCompatibility-class), 11
 name, Ratio-method (zzz-DTTCompatibility-class), 11
 name, Ratio_ref-method (zzz-DTTCompatibility-class), 11
 name, Reporter-method (zzz-DTTCompatibility-class), 11
 name, Reporter_ref-method (zzz-DTTCompatibility-class), 11
 name, ReporterCompositeMap-method (zzz-DTTCompatibility-class), 11
 name, ReporterCompositeMap_ref-method (zzz-DTTCompatibility-class), 11
 name, ReporterDimension-method (zzz-DTTCompatibility-class), 11
 name, ReporterDimension_ref-method (zzz-DTTCompatibility-class), 11
 name, ReporterGroup-method (zzz-DTTCompatibility-class), 11
 name, ReporterGroup_ref-method (zzz-DTTCompatibility-class), 11
 name, Security-method (zzz-DTTCompatibility-class), 11
 name, Security_ref-method (zzz-DTTCompatibility-class), 11
 name, SecurityGroup-method (zzz-DTTCompatibility-class), 11
 name, SecurityGroup_ref-method (zzz-DTTCompatibility-class), 11
 name, Software-method (zzz-DTTCompatibility-class), 11
 name, Software_ref-method (zzz-DTTCompatibility-class), 11
 name, SpecializedQuantitationType-method (zzz-DTTCompatibility-class), 11
 name, SpecializedQuantitationType_ref-method (zzz-DTTCompatibility-class), 11

- 11
- name, StandardQuantitationType_ref-method
(*zzz-DTTCompatibility-class*),
11
- name, Transformation-method
(*zzz-DTTCompatibility-class*),
11
- name, Treatment-method
(*zzz-DTTCompatibility-class*),
11
- name, UserAttribute-method
(*zzz-ARRCompatibility-class*),
10
- name, Zone-method
(*zzz-DTTCompatibility-class*),
11
- name, Zone_ref-method
(*zzz-DTTCompatibility-class*),
11
- names, AffxArray-method
(*zzz-NetAffxCompatibility-class*),
12
- names, NetAffxResource-method
(*NetAffxResource-class*), 3
- namespace
(*zzz-ARRCompatibility-class*),
10
- namespace, UserAttribute-method
(*zzz-ARRCompatibility-class*),
10
- nameValueType
(*zzz-DTTCompatibility-class*),
11
- nameValueType, PropertySets_assnlist-method
(*zzz-DTTCompatibility-class*),
11
- nameValueType, QualityControlStatistics_assnlist-method
(*zzz-DTTCompatibility-class*),
11
- nameValueType, SummaryStatistics_assnlist-method
(*zzz-DTTCompatibility-class*),
11
- NetAffxCompatibility, 3, 13
- NetAffxCompatibility-class
(*AffyCompatible-class*), 2
- NetAffxResource, 1, 5, 6, 8, 13
- NetAffxResource-accessors
(*accessors*), 1
- NetAffxResource-class, 3
- newSequence
(*zzz-DTTCompatibility-class*),
11
- newSequence, MismatchInformation-method
(*zzz-DTTCompatibility-class*),
11
- node
(*zzz-DTTCompatibility-class*),
11
- node, Nodes_assnlist-method
(*zzz-DTTCompatibility-class*),
11
- nodeContents
(*zzz-DTTCompatibility-class*),
11
- nodeContents, NodeContents_assnlist-method
(*zzz-DTTCompatibility-class*),
11
- nodeContents_assnlist
(*zzz-DTTCompatibility-class*),
11
- nodeContents_assnlist, Node-method
(*zzz-DTTCompatibility-class*),
11
- nodes_assnlist
(*zzz-DTTCompatibility-class*),
11
- nodes_assnlist, BioAssayDataCluster-method
(*zzz-DTTCompatibility-class*),
11
- nodes_assnlist, Node-method
(*zzz-DTTCompatibility-class*),
11
- nodeValue
(*zzz-DTTCompatibility-class*),
11
- nodeValue, NodeValue_assnlist-method
(*zzz-DTTCompatibility-class*),
11
- nodes_value_assnlist
(*zzz-DTTCompatibility-class*),
11
- nodeValue_assnlist, Node-method
(*zzz-DTTCompatibility-class*),
11
- normalizationDescription_assn
(*zzz-DTTCompatibility-class*),
11
- normalizationDescription_assn, ExperimentDesign
(*zzz-DTTCompatibility-class*),
11
- numArrays
(*zzz-DTTCompatibility-class*),
11
- numArrays, ArrayGroup-method

- (*zzz-DTTCompatibility-class*), 11
- numberOfFeatures (*zzz-DTTCompatibility-class*), 11
- numberOfFeatures, ArrayDesign-method (*zzz-DTTCompatibility-class*), 11
- numberOfFeatures, PhysicalArrayDesign-method (*zzz-DTTCompatibility-class*), 11
- numFeaturesPerCol (*zzz-DTTCompatibility-class*), 11
- numFeaturesPerCol, ZoneLayout-method (*zzz-DTTCompatibility-class*), 11
- numFeaturesPerRow (*zzz-DTTCompatibility-class*), 11
- numFeaturesPerRow, ZoneLayout-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntries_assnlist (*zzz-DTTCompatibility-class*), 11
- ontologyEntries_assnlist, BioSequence-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Action_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Annotations_assnlist-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Associations_assnlist-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Category_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Characteristics_assnlist-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, CompoundIndices_assnlist-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, ControlType_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, DataType_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, DefectType_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, FailTypes_assnlist-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, FeatureShape_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, FiducialType_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Format_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, MaterialType_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, OntologyEntries_assnlist-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Parameters_assnlist-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, PolymerType_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Roles_assnlist-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Scale_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Species_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, SubstrateType_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, SurfaceType_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, TechnologyType_assn-method (*zzz-DTTCompatibility-class*), 11
- ontologyEntry, Type_assn-method (*zzz-DTTCompatibility-class*), 11

- ontologyEntry,Types_assnlist-method (zzz-DTTCompatibility-class), 11
- ontologyEntry,Value_assn-method (zzz-DTTCompatibility-class), 11
- ontologyEntry,WarningType_assn-method (zzz-DTTCompatibility-class), 11
- ontologyReference_assn (zzz-DTTCompatibility-class), 11
- ontologyReference_assn,OntologyEntry-method (zzz-DTTCompatibility-class), 11
- organization (zzz-DTTCompatibility-class), 11
- organization,Contact_assnlist-method (zzz-DTTCompatibility-class), 11
- organization,Organization_assnlist-method (zzz-DTTCompatibility-class), 11
- organization_ref (zzz-DTTCompatibility-class), 11
- organization_ref,Affiliation_assnref-method (zzz-DTTCompatibility-class), 11
- organization_ref,ArrayManufacturers_assnreflist-method (zzz-DTTCompatibility-class), 11
- organization_ref,Contacts_assnreflist-method (zzz-DTTCompatibility-class), 11
- organization_ref,DesignProviders_assnreflist-method (zzz-DTTCompatibility-class), 11
- organization_ref,HardwareManufacturers_assnreflist-method (zzz-DTTCompatibility-class), 11
- organization_ref,Members_assnreflist-method (zzz-DTTCompatibility-class), 11
- organization_ref,Owner_assnreflist-method (zzz-DTTCompatibility-class), 11
- organization_ref,Parent_assnref-method (zzz-DTTCompatibility-class), 11
- organization_ref,Performer_assnref-method (zzz-DTTCompatibility-class), 11
- organization_ref,Providers_assnreflist-method (zzz-DTTCompatibility-class), 11
- organization_ref,SoftwareManufacturers_assnreflist-method (zzz-DTTCompatibility-class), 11
- organization_ref,SourceContact_assnreflist-method (zzz-DTTCompatibility-class), 11
- orientationMark (zzz-DTTCompatibility-class), 11
- orientationMark,ArrayGroup-method (zzz-DTTCompatibility-class), 11
- orientationMarkPosition (zzz-DTTCompatibility-class), 11
- orientationMarkPosition,ArrayGroup-method (zzz-DTTCompatibility-class), 11
- originalProjectName (zzz-ARRCompatibility-class), 10
- originalProjectName,ArraySetFile-method (zzz-ARRCompatibility-class), 10
- originRelativeTo (zzz-DTTCompatibility-class), 11
- originRelativeTo,Array-method (zzz-DTTCompatibility-class), 11
- otherKind (zzz-DTTCompatibility-class), 11
- otherKind,Measurement-method (zzz-DTTCompatibility-class), 11
- owner_assnreflist (zzz-DTTCompatibility-class), 11
- owner_assnreflist,Security-method (zzz-DTTCompatibility-class), 11
- pages (zzz-DTTCompatibility-class), 11
- pages,BibliographicReference-method (zzz-DTTCompatibility-class), 11

- parameter
 - parameterValues_assnlist, SoftwareApplication-method (zzz-DTTCompatibility-class), 11
 - parameterTypes_assnlist-method (zzz-DTTCompatibility-class), 11
 - parameter_ref (zzz-DTTCompatibility-class), 11
 - parameter_ref, ParameterType_assnref-method (zzz-DTTCompatibility-class), 11
 - parameters_assnlist (zzz-DTTCompatibility-class), 11
 - parameters_assnlist, BibliographicReference-method (zzz-DTTCompatibility-class), 11
 - parameterType_assnref (zzz-DTTCompatibility-class), 11
 - parameterType_assnref, ParameterValue-method (zzz-DTTCompatibility-class), 11
 - parameterTypes_assnlist (zzz-DTTCompatibility-class), 11
 - parameterTypes_assnlist, Hardware-method (zzz-DTTCompatibility-class), 11
 - parameterTypes_assnlist, Protocol-method (zzz-DTTCompatibility-class), 11
 - parameterTypes_assnlist, Software-method (zzz-DTTCompatibility-class), 11
 - parameterValue (zzz-DTTCompatibility-class), 11
 - parameterValue, ParameterValues_assnlist-method (zzz-DTTCompatibility-class), 11
 - parameterValues_assnlist (zzz-DTTCompatibility-class), 11
 - parameterValues_assnlist, HardwareApplication-method (zzz-DTTCompatibility-class), 11
 - parameterValues_assnlist, ProtocolApplication-method (zzz-DTTCompatibility-class), 11
- parameterValues_assnlist, SoftwareApplication-method (zzz-DTTCompatibility-class), 11
- parent_assnref (zzz-DTTCompatibility-class), 11
- parent_assnref, Organization-method (zzz-DTTCompatibility-class), 11
- password(accessors), 1
- password, NetAffxResource-method (NetAffxResource-class), 3
- patassignmentMethod (zzz-ARRCompatibility-class), 10
- patassignmentMethod, PhysicalArray-method (zzz-ARRCompatibility-class), 10
- performer_assnref (zzz-DTTCompatibility-class), 11
- performer_assnref, Audit-method (zzz-DTTCompatibility-class), 11
- performers_assnreflist (zzz-DTTCompatibility-class), 11
- performers_assnreflist, ProtocolApplication-method (zzz-DTTCompatibility-class), 11
- person_ref (zzz-DTTCompatibility-class), 11
- person_ref, ArrayManufacturers_assnreflist-method (zzz-DTTCompatibility-class), 11
- person_ref, Contacts_assnreflist-method (zzz-DTTCompatibility-class), 11
- person_ref, DesignProviders_assnreflist-method (zzz-DTTCompatibility-class), 11
- person_ref, HardwareManufacturers_assnreflist-method (zzz-DTTCompatibility-class), 11
- person_ref, Members_assnreflist-method (zzz-DTTCompatibility-class), 11
- person_ref, Owner_assnreflist-method (zzz-DTTCompatibility-class), 11
- person_ref, Performer_assnref-method (zzz-DTTCompatibility-class), 11

(zzz-*DTTCompatibility-class*), 11
 11
 person_ref, Performers_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 person_ref, Providers_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 person_ref, SoftwareManufacturers_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 person_ref, SourceContact_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 phone (zzz-*DTTCompatibility-class*),
 11
 phone, Organization-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 phone, Person-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalArray (zzz-*ARRCompatibility-class*),
 10
 physicalArray, PhysicalArrays-method (zzz-*ARRCompatibility-class*),
 (zzz-*ARRCompatibility-class*), 10
 10
 physicalArrayDesign (zzz-*DTTCompatibility-class*),
 11
 11
 physicalArrayDesign, ArrayDesign_assnlist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalArrayDesign_ref (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalArrayDesign_ref, ArrayDesign_assnref-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalArrays (zzz-*ARRCompatibility-class*),
 10
 10
 physicalArrays, ArraySetFile-method (zzz-*ARRCompatibility-class*),
 (zzz-*ARRCompatibility-class*), 10
 10
 physicalBioAssay (zzz-*DTTCompatibility-class*),
 11
 11
 physicalBioAssay, BioAssay_assnlist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay, PhysicalBioAssay_assnlist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay_ref (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay_ref, BioAssay_assnref-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay_ref, BioAssays_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay_ref, PhysicalBioAssay_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay_ref, PhysicalBioAssaySource_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay_ref, PhysicalBioAssayTarget_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay_ref, SourceBioAssays_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay_ref, Target_assnref-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssay_ref, TopLevelBioAssays_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssayData_assnlist (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssayData_assnlist, PhysicalBioAssay_assnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssaySource_assnref (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 physicalBioAssaySource_assnref, FeatureExtractAssayAssayAssnreflist-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 polymerType_assn (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 polymerType_assn, BioSequence-method (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11
 position (zzz-*DTTCompatibility-class*),
 (zzz-*DTTCompatibility-class*), 11
 11

- position, Position_assn-method
 (*zzz-DTTCompatibility-class*),
 11
- position_assn
 (*zzz-DTTCompatibility-class*),
 11
- position_assn, Feature-method
 (*zzz-DTTCompatibility-class*),
 11
- position_assn, Fiducial-method
 (*zzz-DTTCompatibility-class*),
 11
- positionDelta
 (*zzz-DTTCompatibility-class*),
 11
- positionDelta, PositionDelta_assn-method
 (*zzz-DTTCompatibility-class*),
 11
- positionDelta_assn
 (*zzz-DTTCompatibility-class*),
 11
- positionDelta_assn, FeatureDefect-method
 (*zzz-DTTCompatibility-class*),
 11
- positionDelta_assn, ZoneDefect-method
 (*zzz-DTTCompatibility-class*),
 11
- presentAbsent
 (*zzz-DTTCompatibility-class*),
 11
- presentAbsent, QuantitationType_assnlist-method
 (*zzz-DTTCompatibility-class*),
 11
- presentAbsent_ref
 (*zzz-DTTCompatibility-class*),
 11
- presentAbsent_ref, QuantitationType_assnref-method
 (*zzz-DTTCompatibility-class*),
 11
- presentAbsent_ref, QuantitationTypes_assnrefl-method
 (*zzz-DTTCompatibility-class*),
 11
- presentAbsent_ref, SourcesQuantitationType_assnrefl-method
 (*zzz-DTTCompatibility-class*),
 11
- presentAbsent_ref, TargetQuantitationType_assnrefl-method
 (*zzz-DTTCompatibility-class*),
 11
- producerTransformation_assn
 (*zzz-DTTCompatibility-class*),
 11
- producerTransformation_assn, DerivedBioAssayData-method
 (*zzz-DTTCompatibility-class*),
 11
- (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, Array-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, ArrayDesign-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, ArrayGroup-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, ArrayManufacture-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, ArrayManufactureDeviation-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, Audit-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BibliographicReference-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BioAssayCreation-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BioAssayDataCluster-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BioAssayDimension-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BioAssayMap-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BioAssayMapping-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BioAssayTreatment-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BioDataCube-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BioDataTuples-method
 (*zzz-DTTCompatibility-class*),
 11
- propertySets_assnlist, BioMaterialMeasurement-method
 (*zzz-DTTCompatibility-class*),
 11

11
 propertySets_assnlist, BioSample-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, BioSequence-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, BioSource-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, Channel-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, CompositeCompositeMap-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, CompositeGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, CompositePosition-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, CompositeSequence-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, CompositeSequenceDimension-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, Compound-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, CompoundMeasurement-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, ConcentrationUnit-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, Database-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, DatabaseEntry-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, DerivedBioAssay-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, DerivedBioAssayData-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, DerivedSignal-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11
 propertySets_assnlist, Description-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, DesignElementMapping-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, DistanceUnit-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, Error-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, ExpectedValue-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, Experiment-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, ExperimentalFactor-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, ExperimentDesign-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, ExternalReference-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, FactorValue-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, Failed-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, Feature-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, FeatureDefect-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, FeatureDimension-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, FeatureExtraction-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, FeatureGroup-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, FeatureInformation-method
 (zzz-DTTCompatibility-class),
 11
 11
 propertySets_assnlist, FeatureLocation-method

(zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, NameValueType-method
 propertySets_assnlist, FeatureReporterMap-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, Node-method
 propertySets_assnlist, Fiducial-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, NodeContents-method
 propertySets_assnlist, Hardware-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, NodeValue-method
 propertySets_assnlist, HardwareApplication-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, OntologyEntry-method
 propertySets_assnlist, Hybridization-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, Organization-method
 propertySets_assnlist, Image-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, Parameter-method
 propertySets_assnlist, ImageAcquisition-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, ParameterValue-method
 propertySets_assnlist, LabeledExtract-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, Person-method
 propertySets_assnlist, MAGE-ML-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, PhysicalArrayDesign-method
 propertySets_assnlist, ManufactureLIMS-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, PhysicalBioAssay-method
 propertySets_assnlist, ManufactureLIMSBiomaterial-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, Position-method
 propertySets_assnlist, MassUnit-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, PositionDelta-method
 propertySets_assnlist, MeasuredBioAssay-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, PresentAbsent-method
 propertySets_assnlist, MeasuredBioAssayData-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, Protocol-method
 propertySets_assnlist, MeasuredSignal-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, ProtocolApplication-method
 propertySets_assnlist, Measurement-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, PValue-method
 propertySets_assnlist, MismatchInformation-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11

propertySets_assnlist, QuantitationTypeDimensions-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, TemperatureUnit-method
 propertySets_assnlist, QuantitationTypeMap-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, TimeUnit-method
 propertySets_assnlist, QuantitationTypeMapping-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, Transformation-method
 propertySets_assnlist, QuantityUnit-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, Treatment-method
 propertySets_assnlist, Ratio-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, VolumeUnit-method
 propertySets_assnlist, Reporter-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, Zone-method
 propertySets_assnlist, ReporterCompositeMap-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, ZoneDefect-method
 propertySets_assnlist, ReporterDimension-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, ZoneGroup-method
 propertySets_assnlist, ReporterGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 propertySets_assnlist, ZoneLayout-method
 propertySets_assnlist, ReporterPosition-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 protocol
 propertySets_assnlist, Security-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 protocol, Protocol_assnlist-method
 propertySets_assnlist, SecurityGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 protocol_assnlist
 propertySets_assnlist, SeqFeature-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 protocol_assnlist, Protocol_package-method
 propertySets_assnlist, SeqFeatureLocation-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 protocol_assnref
 propertySets_assnlist, SequencePosition-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 protocol_assnref, ProtocolApplication-method
 propertySets_assnlist, Software-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 protocol_package
 propertySets_assnlist, SoftwareApplication-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 11 protocol_package, MAGE-ML-method
 propertySets_assnlist, SpecializedQuantitationType-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11

- 11
 protocol_ref
 (zzz-DTTCompatibility-class),
 11
 protocol_ref, Protocol_assnref-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplication
 (zzz-DTTCompatibility-class),
 11
 protocolApplication, ProtocolApplications_assnref-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, ArrayDesign-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, ArrayManufacture-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, BioAssayCreation-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, BioAssayMap-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, BioAssayTreatment-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, CompositeCompositeMap-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, FeatureExtractor-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, FeatureReporterMap-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, Hybridization-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, ImageAcquisition-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, PhysicalArrayDesign-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, QuantitationTypeMap-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, ReporterComposition-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, Transformation-method
 (zzz-DTTCompatibility-class),
 11
 protocolApplications_assnlist, Treatment-method
 (zzz-DTTCompatibility-class),
 11
 providers_assnreflist
 (zzz-DTTCompatibility-class),
 11
 providers_assnreflist, Experiment-method
 (zzz-DTTCompatibility-class),
 11
 publication
 (zzz-DTTCompatibility-class),
 11
 publication, BibliographicReference-method
 (zzz-DTTCompatibility-class),
 11
 publisher
 (zzz-DTTCompatibility-class),
 11
 publisher, BibliographicReference-method
 (zzz-DTTCompatibility-class),
 11
 pvalue
 (zzz-DTTCompatibility-class),
 11
 pvalue, ConfidenceIndicator_assnlist-method
 (zzz-DTTCompatibility-class),
 11
 pvalue, QuantitationType_assnlist-method
 (zzz-DTTCompatibility-class),
 11
 pvalue_ref
 (zzz-DTTCompatibility-class),
 11
 pvalue_ref, ConfidenceIndicators_assnreflist-method
 (zzz-DTTCompatibility-class),
 11
 pvalue_ref, QuantitationType_assnref-method
 (zzz-DTTCompatibility-class),
 11
 pvalue_ref, QuantitationTypes_assnreflist-method
 (zzz-DTTCompatibility-class),
 11
 pvalue_ref, SourcesQuantitationType_assnreflist-method
 (zzz-DTTCompatibility-class),
 11
 pvalue_ref, TargetQuantitationType_assnref-method

- (zzz-*DTTCompatibility-class*), 11
- quality
 - (zzz-*DTTCompatibility-class*), 11
- quality, ManufactureLIMS-method
 - (zzz-*DTTCompatibility-class*), 11
- quality, ManufactureLIMSBiomaterial-method
 - (zzz-*DTTCompatibility-class*), 11
- qualityControlDescription_assn
 - (zzz-*DTTCompatibility-class*), 11
- qualityControlDescription_assn, ExperimentDesign-method
 - (zzz-*DTTCompatibility-class*), 11
- qualityControlStatistics_assnlist
 - (zzz-*DTTCompatibility-class*), 11
- qualityControlStatistics_assnlist, ArrayManufacture-method
 - (zzz-*DTTCompatibility-class*), 11
- qualityControlStatistics_assnlist, BioSample-method
 - (zzz-*DTTCompatibility-class*), 11
- qualityControlStatistics_assnlist, BioSource-method
 - (zzz-*DTTCompatibility-class*), 11
- qualityControlStatistics_assnlist, LabeledExtract-method
 - (zzz-*DTTCompatibility-class*), 11
- quantitationDimension_assnref
 - (zzz-*DTTCompatibility-class*), 11
- quantitationDimension_assnref, NodeContents-method
 - (zzz-*DTTCompatibility-class*), 11
- quantitationType_assnlist
 - (zzz-*DTTCompatibility-class*), 11
- quantitationType_assnlist, QuantitationType_package-method
 - (zzz-*DTTCompatibility-class*), 11
- quantitationType_assnref
 - (zzz-*DTTCompatibility-class*), 11
- quantitationType_assnref, QuantitationTypeTuple-method
 - (zzz-*DTTCompatibility-class*), 11
- quantitationType_package
 - (zzz-*DTTCompatibility-class*), 11
- quantitationType_package, MAGE-ML-method
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension, QuantitationTypeDimension
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension_assnlist
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension_assnlist, BioAssayData
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension_assnref
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension_assnref, DerivedBioAssayData
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension_assnref, MeasuredBioAssayData
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension_ref
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension_ref, QuantitationDimension
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeDimension_ref, QuantitationTypeDimension
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeMap
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeMap, QuantitationTypeMap_assnlist
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeMap_assnlist
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeMap_assnlist, BioAssayData_package
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeMap_ref
 - (zzz-*DTTCompatibility-class*), 11
- quantitationTypeMap_ref, QuantitationTypeMaps
 - (zzz-*DTTCompatibility-class*), 11

quantitationTypeMapping (zzz-DTTCompatibility-class), 11
 quantitationTypeMapping, QuantitationTypeMapping_assnreflist-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMapping_assn (zzz-DTTCompatibility-class), 11
 quantitationTypeMapping_assn, Transformation-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist, DerivedSignal-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist, Error-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist, ExpectedValue-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist, Failed-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist, MeasuredSignal-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist, PresentAbsent-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist, PValue-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist, QuantitationTypeMapping-method (zzz-DTTCompatibility-class), 11
 quantitationTypeMaps_assnreflist, Ratio-method (NetAffxResource-class), 3
 quantitationTypeMaps_assnreflist, SpecializedQuantitationType-method (NetAffxResource-class), 3
 quantitationTypes_assnreflist (NetAffxResource-class), 3
 quantitationTypes_assnreflist, QuantitationTypeMappings-method (NetAffxResource-class), 3
 quantitationTypeTuple readAnnotation, 6
 readMage, 7

- readNetAffx, 8
 readXml, 6, 7, 8, 9, 10
 regions_assnlist
 (zzz-DTTCompatibility-class),
 11
 regions_assnlist, SeqFeature-method
 (zzz-DTTCompatibility-class),
 11
 releaseDate
 (zzz-DTTCompatibility-class),
 11
 releaseDate, SoftwareApplication-method
 (zzz-DTTCompatibility-class),
 11
 replacedLength
 (zzz-DTTCompatibility-class),
 11
 replacedLength, MismatchInformation-method
 (zzz-DTTCompatibility-class),
 11
 replicateDescription_assn
 (zzz-DTTCompatibility-class),
 11
 replicateDescription_assn, ExperimentDesign-method
 (zzz-DTTCompatibility-class),
 11
 reporter
 (zzz-DTTCompatibility-class),
 11
 reporter, DesignElement_assnlist-method
 (zzz-DTTCompatibility-class),
 11
 reporter, Reporter_assnlist-method
 (zzz-DTTCompatibility-class),
 11
 reporter_assnlist
 (zzz-DTTCompatibility-class),
 11
 reporter_assnlist, DesignElement_package-method
 (zzz-DTTCompatibility-class),
 11
 reporter_assnref
 (zzz-DTTCompatibility-class),
 11
 reporter_assnref, FeatureReporterMap-method
 (zzz-DTTCompatibility-class),
 11
 reporter_assnref, ReporterPosition-method
 (zzz-DTTCompatibility-class),
 11
 reporter_ref
 (zzz-DTTCompatibility-class),
 11
 reporter_ref, DesignElement_assnref-method
 (zzz-DTTCompatibility-class),
 11
 reporter_ref, Reporter_assnref-method
 (zzz-DTTCompatibility-class),
 11
 reporter_ref, Reporters_assnreflist-method
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMap
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMap, DesignElementMap_assnlist
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMap, ReporterCompositeMap_assnlist
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMap_assnlist
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMap_assnlist, DesignElement_package
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMap_ref
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMap_ref, DesignElementMaps_assnlist
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMap_ref, ReporterCompositeMaps_assnlist
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMaps_assnreflist
 (zzz-DTTCompatibility-class),
 11
 reporterCompositeMaps_assnreflist, CompositeSeq
 (zzz-DTTCompatibility-class),
 11
 reporterDimension
 (zzz-DTTCompatibility-class),
 11
 reporterDimension, DesignElementDimension_assnlist
 (zzz-DTTCompatibility-class),
 11
 reporterDimension_ref
 (zzz-DTTCompatibility-class),
 11
 reporterDimension_ref, DesignElementDimension_assnlist
 (zzz-DTTCompatibility-class),
 11

reporterGroup (zzz-ARRCompatibility-class), 10
 (zzz-DTTCompatibility-class), 11
 reporterGroup, ReporterGroup_assnlist-method (zzz-ARRCompatibility-class), 10
 (zzz-DTTCompatibility-class), 11
 reporterGroup_assnlist (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterGroup_assnlist, ArrayDesign_package-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterGroup_ref (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterGroup_ref, ReporterGroups_assnreflist-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterGroups_assnreflist scale_assn, DerivedSignal-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterGroups_assnreflist, ArrayDesign-method scale_assn, Error-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterGroups_assnreflist, PhysicalArrayDesign-method scale_assn, ExpectedValue-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterPosition scale_assn, Failed-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterPosition, Coordinate_assn-method scale_assn, MeasuredSignal-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterPosition, ReporterPositionSources_assnlist-method scale_assn, NodeValue-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterPositionSources_assnlist scale_assn, PresentAbsent-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporterPositionSources_assnlist, ReporterCompositeMap-method scale_assn, PValue-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporters_assnreflist scale_assn, Ratio-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporters_assnreflist, ReporterDimension-method scale_assn, SpecializedQuantitationType-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 reporters_assnreflist, ReporterGroup-method (zzz-DTTCompatibility-class), 11
 (zzz-DTTCompatibility-class), 11
 required security (zzz-DTTCompatibility-class), 11
 security, Security_assnlist-method (zzz-DTTCompatibility-class), 11

- 11
security_assnlist
(zzz-*DTTCompatibility-class*),
11
- security_assnlist, AuditAndSecurity_package-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref
(zzz-*DTTCompatibility-class*),
11
- security_assnref, Array-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, ArrayDesign-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, ArrayGroup-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, ArrayManufacture-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, Audit-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, BibliographicReference-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, BioAssayCreation-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, BioAssayDataCluster-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, BioAssayDimension-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, BioAssayMap-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, BioAssayTreatment-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, BioSample-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, BioSequence-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, BioSource-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, Channel-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, CompositeCompositeMap-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, CompositeGroup-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, CompositeSequence-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, CompositeSequenceDimension-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, Compound-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, Database-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, DerivedBioAssay-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, DerivedBioAssayData-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, DerivedSignal-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, Description-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, Error-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, ExpectedValue-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, Experiment-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, ExperimentalFactor-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, ExperimentDesign-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, FactorValue-method
(zzz-*DTTCompatibility-class*),
11
- security_assnref, Failed-method

- (*zzz-DTTCompatibility-class*), 11
- security_assnref, Feature-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, FeatureDimension-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, FeatureExtraction-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, FeatureGroup-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, FeatureReporterMap-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Fiducial-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Hardware-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, HardwareApplication-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Hybridization-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Image-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, ImageAcquisition-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, LabeledExtract-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, MAGE-ML-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, ManufactureLIMS-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, ManufactureLIMSBiomaterial-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, MeasuredBioAssay-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, MeasuredBioAssayData-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, MeasuredSignal-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Node-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, NodeContents-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Organization-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Parameter-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Person-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, PhysicalArrayDesign-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, PhysicalBioAssay-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, PresentAbsent-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Protocol-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, ProtocolApplication-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, PValue-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, QuantitationTypeDimension-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, QuantitationTypeMap-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Ratio-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, Reporter-method (*zzz-DTTCompatibility-class*), 11
- security_assnref, ReporterCompositeMap-method (*zzz-DTTCompatibility-class*), 11

- security_assnref, ReporterDimension-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, ReporterGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, Security-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, SecurityGroup-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, SeqFeature-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, Software-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, SoftwareApplication-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, SpecializedQuantitationType-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, Transformation-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, Treatment-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_assnref, Zone-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_ref (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 security_ref, Security_assnref-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 securityGroup (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 securityGroup, SecurityGroup_assnlist-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 securityGroup_assnlist (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 securityGroup_assnlist, AuditAndSecurity_package-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 securityGroup_ref securityGroup_ref, SecurityGroups_assnreflist-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 securityGroups_assnreflist (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 securityGroups_assnreflist, Security-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 seqFeature (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 seqFeature, SeqFeatures_assnlist-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 seqFeatureLocation seqFeatureLocation (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 seqFeatureLocation, Regions_assnlist-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 seqFeatureLocation, Subregions_assnlist-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 seqFeatures_assnlist (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 seqFeatures_assnlist, BioSequence-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 sequenceDatabases_assnlist (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 sequenceDatabases_assnlist, BioSequence-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 sequencePosition (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 sequencePosition, Coordinate_assn-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 serialNumber (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 serialNumber, HardwareApplication-method (zzz-DTTCompatibility-class),
 (zzz-DTTCompatibility-class), 11
 show, .TypedAssociation-method (Internal-class), 14

- show, AffyCompatible-method
(AffyCompatible-class), 2
- show, NetAffxResource-method
(NetAffxResource-class), 3
- software
(zzz-DTTCompatibility-class),
11
- software, Software_assnlist-method
(zzz-DTTCompatibility-class),
11
- software_assnlist
(zzz-DTTCompatibility-class),
11
- software_assnlist, Protocol_package-method
(zzz-DTTCompatibility-class),
11
- software_assnref
(zzz-DTTCompatibility-class),
11
- software_assnref, SoftwareApplication-method
(zzz-DTTCompatibility-class),
11
- software_ref
(zzz-DTTCompatibility-class),
11
- software_ref, Software_assnref-method
(zzz-DTTCompatibility-class),
11
- software_ref, Softwares_assnreflist-method
(zzz-DTTCompatibility-class),
11
- softwareApplication
(zzz-DTTCompatibility-class),
11
- softwareApplication, SoftwareApplications_assnreflist-method
(zzz-DTTCompatibility-class),
11
- softwareApplications_assnlist
(zzz-DTTCompatibility-class),
11
- softwareApplications_assnlist, ProtocolApplication_ref-method
(zzz-DTTCompatibility-class),
11
- softwareManufacturers_assnreflist
(zzz-DTTCompatibility-class),
11
- softwareManufacturers_assnreflist, Software-method
(zzz-DTTCompatibility-class),
11
- softwares_assnreflist
(zzz-DTTCompatibility-class),
11
- softwares_assnreflist, Hardware-method
(zzz-DTTCompatibility-class),
11
- softwares_assnreflist, Protocol-method
(zzz-DTTCompatibility-class),
11
- softwares_assnreflist, Software-method
(zzz-DTTCompatibility-class),
11
- sourceBioAssays_assnreflist
(zzz-DTTCompatibility-class),
11
- sourceBioAssays_assnreflist, BioAssayMap-method
(zzz-DTTCompatibility-class),
11
- sourceBioMaterialMeasurements_assnlist
(zzz-DTTCompatibility-class),
11
- sourceBioMaterialMeasurements_assnlist, BioAssayMap-method
(zzz-DTTCompatibility-class),
11
- sourceBioMaterialMeasurements_assnlist, Hybrid-method
(zzz-DTTCompatibility-class),
11
- sourceBioMaterialMeasurements_assnlist, Treatment-method
(zzz-DTTCompatibility-class),
11
- sourceContact_assnreflist
(zzz-DTTCompatibility-class),
11
- sourceContact_assnreflist, BioSource-method
(zzz-DTTCompatibility-class),
11
- sourcesQuantitationType_assnreflist
(zzz-DTTCompatibility-class),
11
- sourcesQuantitationType_assnreflist, Quantitation-method
(zzz-DTTCompatibility-class),
11
- spacingBetweenCols
(zzz-DTTCompatibility-class),
11
- spacingBetweenCols, ZoneLayout-method
(zzz-DTTCompatibility-class),
11
- spacingBetweenRows
(zzz-DTTCompatibility-class),
11
- spacingBetweenRows, ZoneLayout-method
(zzz-DTTCompatibility-class),
11
- spacingsBetweenZonesX

(zzz-DTTCompatibility-class),	11
11	strandType
spacingsBetweenZonesX, ZoneGroup-method	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	strandType, SeqFeatureLocation-method
spacingsBetweenZonesY	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	subregions_assnlist
spacingsBetweenZonesY, ZoneGroup-method	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	subregions_assnlist, SeqFeatureLocation-method
specializedQuantitationType	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	substrateType_assn
specializedQuantitationType, QuantitationType	(zzz-DTTCompatibility-class),
assnlist-method	11
(zzz-DTTCompatibility-class),	11
11	substrateType_assn, ArrayGroup-method
specializedQuantitationType_ref	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	summaryStatistics_assnlist
specializedQuantitationType_ref, QuantitationType	(zzz-DTTCompatibility-class),
assnref-method	11
(zzz-DTTCompatibility-class),	11
11	summaryStatistics_assnlist, DerivedBioAssayData
specializedQuantitationType_ref, QuantitationTypes	(zzz-DTTCompatibility-class),
assnreflist-method	11
(zzz-DTTCompatibility-class),	11
11	summaryStatistics_assnlist, MeasuredBioAssayData
specializedQuantitationType_ref, SourcesQuantitationType	(zzz-DTTCompatibility-class),
assnreflist-method	11
(zzz-DTTCompatibility-class),	11
11	surfaceType_assn
specializedQuantitationType_ref, TargetQuantitationType	(zzz-DTTCompatibility-class),
assnref-method	11
(zzz-DTTCompatibility-class),	11
11	surfaceType_assn, PhysicalArrayDesign-method
species_assn	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	target_assnref
species_assn, BioSequence-method	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	target_assnref, BioAssayTreatment-method
species_assn, CompositeGroup-method	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	target_assnref, ImageAcquisition-method
species_assn, FeatureGroup-method	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	targetQuantitationType_assnref
species_assn, ReporterGroup-method	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	targetQuantitationType_assnref, Error-method
startCoord	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	targetQuantitationType_assnref, ExpectedValue-r
startCoord, MismatchInformation-method	(zzz-DTTCompatibility-class),
(zzz-DTTCompatibility-class),	11
11	

targetQuantitationType_assnref,PValue-method(*zzz-DTTCompatibility-class*),
 (*zzz-DTTCompatibility-class*), 11
 targetQuantitationType_assnref,QuantitationTypeAssnref-method(*zzz-DTTCompatibility-class*),
 (*zzz-DTTCompatibility-class*), 11
 technologyType_assn
 (*zzz-DTTCompatibility-class*), 11
 technologyType_assn,FeatureGroup-method
 (*zzz-DTTCompatibility-class*), 11
 temperatureUnit
 (*zzz-DTTCompatibility-class*), 11
 temperatureUnit,Unit_assn-method
 (*zzz-DTTCompatibility-class*), 11
 timeUnit
 (*zzz-DTTCompatibility-class*), 11
 timeUnit,Unit_assn-method
 (*zzz-DTTCompatibility-class*), 11
 tolerance
 (*zzz-DTTCompatibility-class*), 11
 tolerance,ArrayManufacture-method
 (*zzz-DTTCompatibility-class*), 11
 tollFreePhone
 (*zzz-DTTCompatibility-class*), 11
 tollFreePhone,Organization-method
 (*zzz-DTTCompatibility-class*), 11
 tollFreePhone,Person-method
 (*zzz-DTTCompatibility-class*), 11
 topLevelBioAssays_assnreflist
 (*zzz-DTTCompatibility-class*), 11
 topLevelBioAssays_assnreflist,ExperimentDesign-method(*zzz-DTTCompatibility-class*),
 (*zzz-DTTCompatibility-class*), 11
 transformation
 (*zzz-DTTCompatibility-class*), 11
 transformation,ProducerTransformation_assn-method(*zzz-DTTCompatibility-class*),
 (*zzz-DTTCompatibility-class*), 11
 treatment
 (*zzz-DTTCompatibility-class*), 11
 treatment,Treatments_assnlist-method
 (*zzz-DTTCompatibility-class*), 11
 treatments_assnlist
 (*zzz-DTTCompatibility-class*), 11
 treatments_assnlist,BioSample-method
 (*zzz-DTTCompatibility-class*), 11
 treatments_assnlist,BioSource-method
 (*zzz-DTTCompatibility-class*), 11
 treatments_assnlist,LabeledExtract-method
 (*zzz-DTTCompatibility-class*), 11
 type
 (*zzz-DTTCompatibility-class*), 11
 type,ArraySetFile-method
 (*zzz-ARRCompatibility-class*), 10
 type,Measurement-method
 (*zzz-DTTCompatibility-class*), 11
 type,NameValueType-method
 (*zzz-DTTCompatibility-class*), 11
 type,PhysicalArray-method
 (*zzz-ARRCompatibility-class*), 10
 type,TemplateFile-method
 (*zzz-ARRCompatibility-class*), 10
 type,UserAttribute-method
 (*zzz-ARRCompatibility-class*), 10
 type_assn
 (*zzz-DTTCompatibility-class*), 11
 type_assn,BioSample-method
 (*zzz-DTTCompatibility-class*), 11
 type_assn,BioSequence-method
 (*zzz-DTTCompatibility-class*), 11
 type_assn,DatabaseEntry-method
 (*zzz-DTTCompatibility-class*), 11
 type_assn,DerivedBioAssay-method
 (*zzz-DTTCompatibility-class*), 11

- 11
- type_assn, Hardware-method
(zzz-DTTCompatibility-class),
11
- type_assn, NodeValue-method
(zzz-DTTCompatibility-class),
11
- type_assn, Protocol-method
(zzz-DTTCompatibility-class),
11
- type_assn, Software-method
(zzz-DTTCompatibility-class),
11
- types_assnlist
(zzz-DTTCompatibility-class),
11
- types_assnlist, CompositeGroup-method
(zzz-DTTCompatibility-class),
11
- types_assnlist, ExperimentDesign-method
(zzz-DTTCompatibility-class),
11
- types_assnlist, FeatureGroup-method
(zzz-DTTCompatibility-class),
11
- types_assnlist, ReporterGroup-method
(zzz-DTTCompatibility-class),
11
- unit_assn
(zzz-DTTCompatibility-class),
11
- unit_assn, Measurement-method
(zzz-DTTCompatibility-class),
11
- unitName
(zzz-DTTCompatibility-class),
11
- unitName, ConcentrationUnit-method
(zzz-DTTCompatibility-class),
11
- unitName, DistanceUnit-method
(zzz-DTTCompatibility-class),
11
- unitName, MassUnit-method
(zzz-DTTCompatibility-class),
11
- unitName, QuantityUnit-method
(zzz-DTTCompatibility-class),
11
- unitName, TemperatureUnit-method
(zzz-DTTCompatibility-class),
11
- unitName, TimeUnit-method
(zzz-DTTCompatibility-class),
11
- unitName, VolumeUnit-method
(zzz-DTTCompatibility-class),
11
- unitNameCV
(zzz-DTTCompatibility-class),
11
- unitNameCV, ConcentrationUnit-method
(zzz-DTTCompatibility-class),
11
- unitNameCV, DistanceUnit-method
(zzz-DTTCompatibility-class),
11
- unitNameCV, MassUnit-method
(zzz-DTTCompatibility-class),
11
- unitNameCV, QuantityUnit-method
(zzz-DTTCompatibility-class),
11
- unitNameCV, TemperatureUnit-method
(zzz-DTTCompatibility-class),
11
- unitNameCV, TimeUnit-method
(zzz-DTTCompatibility-class),
11
- unitNameCV, VolumeUnit-method
(zzz-DTTCompatibility-class),
11
- upperLeftX
(zzz-DTTCompatibility-class),
11
- upperLeftX, Zone-method
(zzz-DTTCompatibility-class),
11
- upperLeftY
(zzz-DTTCompatibility-class),
11
- upperLeftY, Zone-method
(zzz-DTTCompatibility-class),
11
- uri (zzz-DTTCompatibility-class),
11
- uri, BibliographicReference-method
(zzz-DTTCompatibility-class),
11
- uri, Database-method
(zzz-DTTCompatibility-class),
11
- uri, DatabaseEntry-method
(zzz-DTTCompatibility-class),

- 11
- uri, Description-method
(*zzz-DTTCompatibility-class*),
11
- uri, Hardware-method
(*zzz-DTTCompatibility-class*),
11
- uri, Image-method
(*zzz-DTTCompatibility-class*),
11
- uri, Organization-method
(*zzz-DTTCompatibility-class*),
11
- uri, Person-method
(*zzz-DTTCompatibility-class*),
11
- uri, Protocol-method
(*zzz-DTTCompatibility-class*),
11
- uri, Software-method
(*zzz-DTTCompatibility-class*),
11
- user (*accessors*), 1
- user, NetAffxResource-method
(*NetAffxResource-class*), 3
- userAttribute
(*zzz-ARRCompatibility-class*),
10
- userAttribute, UserAttributes-method
(*zzz-ARRCompatibility-class*),
10
- userAttributes
(*zzz-ARRCompatibility-class*),
10
- userAttributes, ArraySetFile-method
(*zzz-ARRCompatibility-class*),
10
- userAttributes, TemplateFile-method
(*zzz-ARRCompatibility-class*),
10
- userAttributeValue
(*zzz-ARRCompatibility-class*),
10
- userAttributeValue, UserAttribute-method
(*zzz-ARRCompatibility-class*),
10
- value
(*zzz-ARRCompatibility-class*),
10
- value, Control-method
(*zzz-ARRCompatibility-class*),
10
- value, Datum-method
(*zzz-DTTCompatibility-class*),
11
- value, Measurement-method
(*zzz-DTTCompatibility-class*),
11
- value, NameValueType-method
(*zzz-DTTCompatibility-class*),
11
- value, NodeValue-method
(*zzz-DTTCompatibility-class*),
11
- value, OntologyEntry-method
(*zzz-DTTCompatibility-class*),
11
- value, ParameterValue-method
(*zzz-DTTCompatibility-class*),
11
- value_assn
(*zzz-DTTCompatibility-class*),
11
- value_assn, FactorValue-method
(*zzz-DTTCompatibility-class*),
11
- vector, 14
- version
(*zzz-ARRCompatibility-class*),
10
- version, ArrayDesign-method
(*zzz-DTTCompatibility-class*),
11
- version, ArraySetFile-method
(*zzz-ARRCompatibility-class*),
10
- version, Database-method
(*zzz-DTTCompatibility-class*),
11
- version, PhysicalArrayDesign-method
(*zzz-DTTCompatibility-class*),
11
- version, SoftwareApplication-method
(*zzz-DTTCompatibility-class*),
11
- version, TemplateFile-method
(*zzz-ARRCompatibility-class*),
10
- volume
(*zzz-DTTCompatibility-class*),
11
- volume, BibliographicReference-method
(*zzz-DTTCompatibility-class*),
11

- volumeUnit
(*zzz-DTTCompatibility-class*),
[11](#)
- volumeUnit, Unit_assn-method
(*zzz-DTTCompatibility-class*),
[11](#)
- warningType_assn
(*zzz-DTTCompatibility-class*),
[11](#)
- warningType_assn, Reporter-method
(*zzz-DTTCompatibility-class*),
[11](#)
- width
(*zzz-DTTCompatibility-class*),
[11](#)
- width, ArrayGroup-method
(*zzz-DTTCompatibility-class*),
[11](#)
- x(*zzz-DTTCompatibility-class*), [11](#)
- x, Position-method
(*zzz-DTTCompatibility-class*),
[11](#)
- xclass, [6-8, 9, 9](#)
- xmlValue.XMLAttributeValue, [14](#)
- y(*zzz-DTTCompatibility-class*), [11](#)
- y, Position-method
(*zzz-DTTCompatibility-class*),
[11](#)
- year
(*zzz-DTTCompatibility-class*),
[11](#)
- year, BibliographicReference-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zone
(*zzz-DTTCompatibility-class*),
[11](#)
- zone, ZoneLocations_assnlist-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zone_assnref
(*zzz-DTTCompatibility-class*),
[11](#)
- zone_assnref, Feature-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zone_assnref, ZoneDefect-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zone_ref
(*zzz-DTTCompatibility-class*),
[11](#)
- zone_ref, Zone_assnref-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneDefect
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneDefect, Adjustments_assnlist-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneGroup
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneGroup, ZoneGroups_assnlist-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneGroups_assnlist
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneGroups_assnlist, PhysicalArrayDesign-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneLayout
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneLayout, ZoneLayout_assn-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneLayout_assn
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneLayout_assn, ZoneGroup-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneLocations_assnlist
(*zzz-DTTCompatibility-class*),
[11](#)
- zoneLocations_assnlist, ZoneGroup-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zonesPerX
(*zzz-DTTCompatibility-class*),
[11](#)
- zonesPerX, ZoneGroup-method
(*zzz-DTTCompatibility-class*),
[11](#)
- zonesPerY
(*zzz-DTTCompatibility-class*),
[11](#)
- zonesPerY, ZoneGroup-method

(*zzz-DTTCompatibility-class*),
11

zzz-.TypedAssociation-class
(*Internal-class*), 14

zzz-AffyCompatible-class
(*AffyCompatible-class*), 2

zzz-ARRCompatibility-class, 10

zzz-DTTCompatibility-class, 11

zzz-NetAffxCompatibility-class,
12