

# CAARRAY 1.3.1

*User's Guide*



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# CHAPTER 1

## USING THE CAARRAY GUIDE

This chapter introduces you to the *caArray 1.3.1 User's Guide* and suggests ways you can maximize its use.

Topics in this chapter include:

- *Introduction to the caArray User's Guide* on this page
- *Organization of this Guide* on this page
- *Document Text Conventions* on page 2

### Introduction to the caArray User's Guide

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The *caArray 1.3.1 User's Guide* is the companion documentation to the caArray software application. The *caArray User's Guide* includes information and instructions for the end user about using caArray.

### Organization of this Guide

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The *caArray 1.3.1 User's Guide* contains the following chapters:

**Chapter 1 Using the caArray User's Guide**—This chapter provides information about using the caArray User's Guide.

**Chapter 2 About caArray**—This chapter provides an overview of the caArray infrastructure including a discussion on Model Driven Architecture, *n*-tier architecture with open APIs, use of controlled vocabularies, and registered metadata. It also includes a description about the workflow in caArray and the rationale for creating caArray objects, the Experiments comprised of those objects as well as data files uploaded to those Experiments.

**Chapter 3 Navigating the caArray Application**—This chapter provides details about launching caArray, navigating the interface, accessing online help and performing basic

functions in caArray such as searching caArray, submitting and modifying caArray objects.

**Chapter 4 Creating and Managing User Accounts**—This chapter describes how to create and manage user accounts in caArray.

**Chapter 5 Contacts**—This chapter describes the process for creating and working with Contacts, namely individual and group contacts in caArray.

**Chapter 6 Protocols**—This chapter details instructions for creating and working with Protocols in caArray.

**Chapter 7 Arrays and Array Designs**—This chapter provides information about creating and working with Array Design models as well as Array objects in caArray.

**Chapter 8 Ontologies**—This chapter describes the MGED ontology-based structure and the database resources used for organizing and using controlled vocabulary terms in caArray.

**Chapter 9 Biomaterials**—This chapter provides the details for creating and annotating biomaterials in caArray.

**Chapter 10 Experiments**—This chapter describes the processes for using components created in caArray and data files uploaded into caArray to create a caArray object called an Experiment.

**Appendix A**—This appendix provides a glossary of words relative to microarray techniques in general and caArray in particular.

**Index**—This section of the guide provides a complete index.

## Document Text Conventions

Table 1.1 illustrates how text conventions are represented in this guide. The various typefaces differentiate between regular text and menu commands, keyboard keys, toolbar buttons, dialog box options and text that you type.

<i>Convention</i>	<i>Description</i>	<i>Example</i>
<b>Bold &amp; Capitalized Command</b> <b>Capitalized command &gt; Capitalized command</b>	Indicates a Menu command Indicates Sequential Menu commands	<b>Admin &gt; Refresh</b>
TEXT IN SMALL CAPS	Keyboard key that you press	Press ENTER
TEXT IN SMALL CAPS + TEXT IN SMALL CAPS	Keyboard keys that you press simultaneously	Press SHIFT + CTRL and then release both.
Monospace type	Used for filenames, directory names, commands, file listings, and anything that would appear in a Java program, such as methods, variables, and classes.	URL_definition ::= url_string
<b>Boldface type</b>	Options that you select in dialog boxes or drop-down menus. Buttons or icons that you click.	In the Open dialog box, select the file and click the <b>Open</b> button.

Table 1.1 caArray Guide Text Conventions

<b>Convention</b>	<b>Description</b>	<b>Example</b>
<i>Italics</i>	Used to reference other documents, sections, figures, and tables.	<i>caCORE Software Development Kit 1.0 Programmer's Guide</i>
<i>Italic boldface monospace type</i>	Text that you type	In the New Subset text box, enter <i>Proprietary Proteins</i> .
<b>Note:</b>	Highlights a concept of particular interest	<b>Note:</b> This concept is used throughout the installation manual.
<b>Warning!</b>	Highlights information of which you should be particularly aware.	<b>Warning!</b> Deleting an object will permanently delete it from the database.
{ }	Curly brackets are used for replaceable items.	Replace {root directory} with its proper value, such as c:\cabio

Table 1.1 caArray Guide Text Conventions (Continued)





# CHAPTER 2

## ABOUT CAARRAY

This chapter describes briefly the microarray process as well as the caArray software.

Topics in this chapter include:

- [caArray Overview](#) on this page
- [Objectives of caArray](#) on page 5

### caArray Overview

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caArray is designed by the National Cancer Institutes Center for Bioinformatics (NCICB) to manage and promote the sharing of microarray data among the investigators and organizations committed to conquering cancer.

Gene expression profiling using microarray technologies can be used to discover molecular signatures associated with different types of cancer. Gene expression profiling produces very large quantities of data that represents an unprecedented research and therapeutic resource.

The NCICB cancer array informatics project, caArray, is designed to make it easier to store, annotate, search and share microarray data related to cancer research. caArray currently supports submission of Affymetrix, GenePix and ImaGene file formats, as well as the import of microarray data in the standard XML based format, MAGE-ML.

### Objectives of caArray

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caArray was developed with the following primary objectives:

1. To make well-annotated microarray data publicly available. caArray provides web-based data submission forms to capture MIAME 1.1 compliant annotations. caArray uses terms from controlled vocabularies organized in an MGED ontology structure to annotate biomaterials used in microarray experiments.

2. To record and store information and laboratory data generated from microarray experiments as caArray objects compiled into caArray Experiments.
3. To provide caBIG-compliant architecture and application programming interfaces (APIs), thus promoting data sharing and programmatic data access in the caGrid.
4. To make the caArray programming code freely available with minimal restrictions in an open source environment. This allows caArray to be utilized, modified and extended by the science and cancer research community as a whole. (Additional information on open source software can be found at: <http://www.opensource.org/docs/definition.php>)

**NOTE:** To utilize the open source tools available with caArray, you can access the source code and application programming interfaces (APIs) on the NCICB download site at <http://ncicb.nci.nih.gov/download/>.

## caArray Standards

As research and technology expand, it is of critical importance that established standards be used to ensure better and more accurate data collection and experiment results. Removing ambiguity by using standardized terminologies is one of the cornerstones of caArray. caArray is designed to support the international standard for microarray data, MAGE, and caBIG compatibility guidelines.

**MAGE-ML** — **M**icroarray **G**ene **E**xpression **M**arkup **L**anguage is a standard data exchange format for microarray data. MAGE-ML uses e**X**tensible **M**arkup **L**anguage (XML), which provides a consistent way to label data. MAGE-ML can be automatically derived from Microarray Gene Expression Object Model (MAGE-OM), which is developed and described in Unified Modeling Language (UML). A broad range of computer programs can process XML-labeled data, making it a valuable tool for both analysis and input. For more information about MAGE-ML, refer to the website: <http://www.mged.org/Workgroups/MAGE/introduction.html>.

**MIAME 1.1** — **M**inimum **I**nformation **A**bout a **M**icroarray **E**xperiment describes the minimum information necessary to enable unambiguous interpretation of microarray experiments. Although details for particular experiments may differ, the MIAME objective is to define common elements among most experiments such as information on experiment and Array Design, samples, protocols and measurements. MIAME is not a formal specification, but a set of guidelines. For more information about MIAME 1.1, refer to the website: <http://www.mged.org/miame>.

**caBIG Silver-Level Compatibility** — This term refers to the National Cancer Institute Bioinformatics (NCICB) Cancer Biomedical Informatics Grid (caBIG) Compatibility Guidelines. caBIG is a common, extensible informatics platform that integrates diverse data types and supports interoperable analytic tools. This platform allows research groups access to the extensible collection of emerging cancer research data, while supporting their individual research. For more information about caBIG, refer to the website: <http://cabig.nci.nih.gov>. caBIG-Silver is a compatibility reference indicating that the software being used to submit and share cancer-related data meets or exceeds the Silver level of compliance. A description of the various caBIG guidelines and compliance levels such as bronze, silver and gold can be found at this website: [http://cabig.nci.nih.gov/caBIG/cabigifs/caBIG\\_Compatibility.pdf](http://cabig.nci.nih.gov/caBIG/cabigifs/caBIG_Compatibility.pdf).

## Security Structure

caArray is designed to provide maximum flexibility in the collaborative sharing of microarray data, while allowing users and data managers to make choices regarding who can access the data submitted. Three levels of security and visibility are available in caArray:

- **Public** permissions or visibility gives anyone the ability to view the data, but with Read-Only access. The only person who can modify Public data is the owner of the data. Once your microarray experiment has been published, you may choose to make your experimental data public; anyone can view the data, but after publishing, ownership of the data is moved to the NCICB. Only the NCICB data curator can modify the data at that point.
- **Private** access or visibility restricts access to the data, allowing only the owner the ability to view the data.

*Example:* if you are in the initial information-gathering stage of a microarray experiment, you may choose to make the information available to only yourself.

**Note:** In caArray, if no visibility is selected when you are submitting or modifying an object, the default visibility is “Private”.

- **Group-level/Consortium** access or visibility allows only specified individuals or groups, as specified by the owner to view the microarray data. Groups have “read-only” privileges with exceptions granted to persons assigned “curation” status; they are allowed “modify” privileges. Curation status must be requested through NCICB Application Support.

*Example:* If you are working on a collaborative effort with colleagues in your lab as well as with investigators at a different research facility, you may choose to make your specified data available to a group/consortium; the consortium has read-only access to the referenced objects. Only you and others in the group specified as Curators can modify the data.

Visibility can be designated with multiple choices. For example, if you assign Public visibility as well as a specific group for an object, the object is available for viewing to everyone, but only the members of the group assigned curation privileges can modify the object. The advantage to this arrangement is that a user with appropriate permissions can search for and display all objects assigned specified curation privileges.

## caArray Workflow

To best understand the caArray workflow and its relationships to the functions and roles of caArray, one must understand the definition of a caArray Experiment. An Experiment is comprised of many models of information recorded in caArray that contribute to an caArray Experiment object. These are not only described as follows, but chapters in this caArray User’s Guide correspond to each of these components:

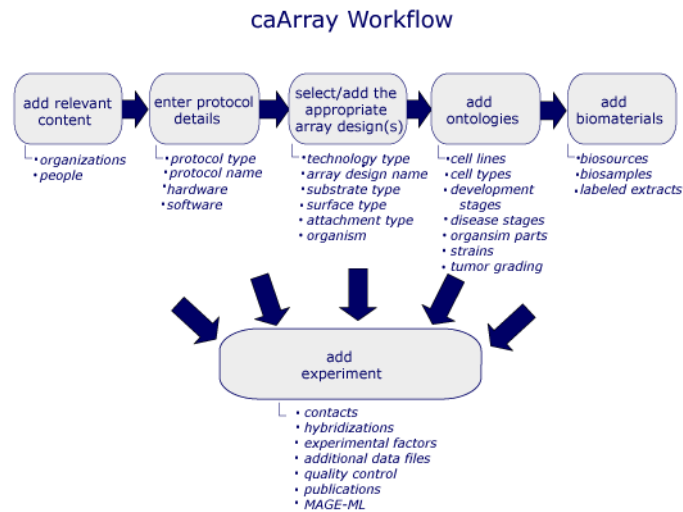
- **Contacts** — Author/creator/organization or other individuals or groups associated with an experiment such as a Principal Investigator (PI), manufacturer of equipment, etc.
- **Protocols** — Includes the details of all protocols, equipment, associated hardware and/or software, descriptions of standard operating procedures (SOPs)

and/or steps involved in extracting or labeling biomaterials, hybridizations, and so forth.

- **Array Designs and Arrays** — Details outlining the microarray chip design and utilization
- **Ontologies** — Controlled vocabulary terms used in caArray to annotate biomaterials
- **Biomaterials** — Materials of biological origin including biosources, biosamples and labeled extracts used in microarray experiments

Because there are dependencies between objects in caArray, it is important that you follow the logical flow of tasks suggested in the workflow shown in [Figure 2.1](#) as you create these objects. Below each step in the workflow figure, objects that can be created in caArray and that are related to that step are listed. For more information about each, see the related chapters in this guide.

As you define the details of all of these components of a microarray experiment, associations between objects are identified and relationships are established. Then an Experiment object is created, incorporating the associated objects that comprise the experiment. These components of an Experiment are then used to annotate microarray hybridization data and raw data files that are uploaded and parsed into the caArray database.



*Figure 2.1 caArray Workflow. Each step in the workflow is described in its text and also serves as a hypertext link to a corresponding caArray viewer. Some steps in the workflow have dependencies on previous tasks. They are described, where appropriate, in this user's guide.*

# CHAPTER 3

## NAVIGATING THE SYSTEM

This chapter introduces you to the caArray interface and its navigation as well as to global operations used in all of the caArray viewing windows.

Topics in this chapter include:

- *Launching caArray* on this page
- *Creating a User Account* on page 11
- *Getting Help* on page 11
- *Navigating through the caArray Workflow* on page 15
- *The caArray Interface* on page 16
- *Access to Public Data in caArray Before Login* on page 16
- *Elements of the caArray Viewer* on page 16

### Launching caArray

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The caArray application can be accessed in three ways:

1. Use this URL to go directly to the caArray login page at NCICB: <http://caarraydb.nci.nih.gov>. Continue to the *caArray New User Account and Login* section on page 10 and *Figure 3.2*.
2. From the caArray Data Portal on the NCICB website, <http://caarraydb.nci.nih.gov/caarray/index.jsp>
3. A version downloaded at your site. On the first download, you must install the software. For instructions about doing so, see your local administrator and/or refer to the *caArray Local Installation Guide* that can be downloaded from the caArray download page: [http://ncicb.nci.nih.gov/download\\_files/caArray/caarray\\_portal/caArray-1\\_2-Local\\_Install.pdf](http://ncicb.nci.nih.gov/download_files/caArray/caarray_portal/caArray-1_2-Local_Install.pdf)

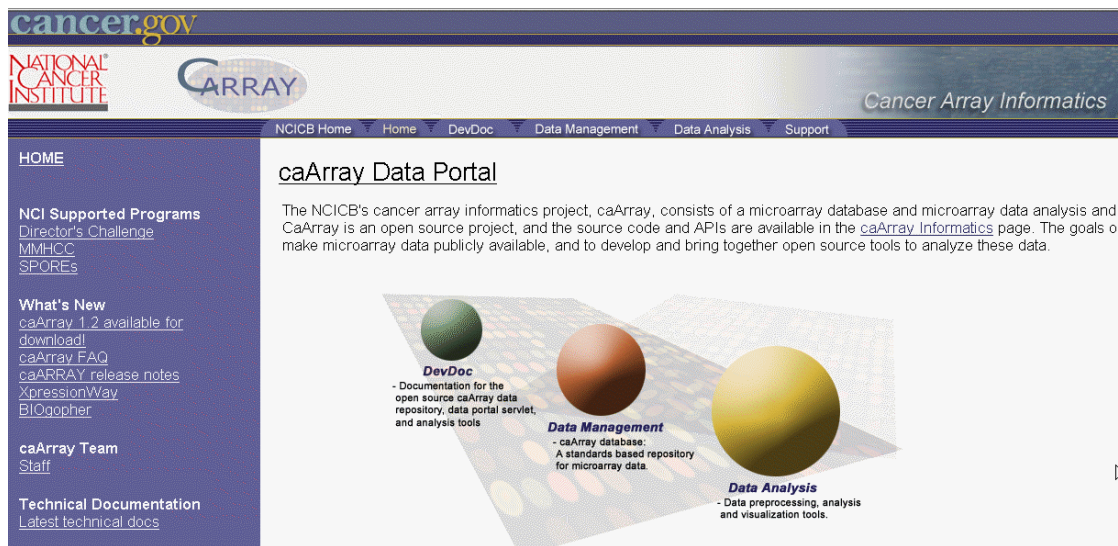
**Note:** If you are using a local installation of caArray, contact your Principal Investigator/Laboratory Manager/System Administrator for the correct URL for your use.

In the instance of #2 or #3, from the Data Portal page, you proceed in caArray in the very same way:

- Click **Data Management** under the center sphere on the page to open the caArray application (*Figure 3.1*).

The DevDoc and Data Analysis options on the Data Portal page are peripheral features of the caArray project.

- **DevDoc** opens documentation about the caArray data repository, the data portal servlet, and available microarray analysis tools (*Figure 3.1*).
- **Data Analysis** provides access to data pre-processing, data analysis and visualization tools themselves (*Figure 3.1*).



*Figure 3.1 caArray data portal page. Click the Data Management hyperlink to go to the caArray login page.*

## caArray New User Account and Login

Once you are on the login page, you can register as a new user or log in if you already have a user account (*Figure 3.2*):





Figure 3.2 caArray login page

- If you already have a caArray user account, enter the login information and click **Login**.
- To register for a new user account, see the following section for more information.

## Creating a User Account

Each user of caArray is given a unique userID and password. The UserID and password you are assigned determines your access rights for the software.

To set-up a user account, you must complete one of these steps:

- Go to the NCICB caArray login page <http://caarraydb.nci.nih.gov/caarray/> and click on the **Register** button. Follow the screen prompts to complete the registration.
- As an alternative, to set up a user account, contact NCICB Application Support:
  - Email at [NCICB@pop.nci.nih.gov](mailto:NCICB@pop.nci.nih.gov)
  - Phone at 888-478-4423 (toll-free) or 301-451-4384 (local)

## Getting Help

If you need help, caArray's online help guide and context-sensitive help topics are available. To access help in using caArray, use any of the following methods:

- Click the **Help** button that displays in many viewers and/or dialog boxes. This generally opens context-sensitive topics.

- In any caArray viewer, click the **Help** button on the lower-left vertical navigation menu (*Figure 3.3*).



Figure 3.3 Help option on Quick Links menu

**Note:** If the Help window does not appear, request that your Systems Administrator turn off any pop-up blockers installed on your computer's browser. Pop-up blockers can interfere with displaying the second help window.

- During the display of any help topic, you can select from the **Help** topic index that displays at the left side of the screen (*Figure 3.4*). For more information, see the section that follows.

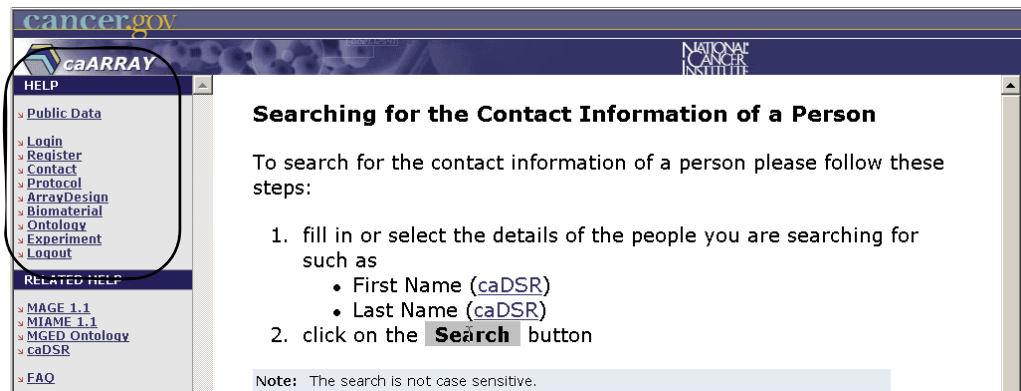


Figure 3.4 Online Help menu items are marked on the left. A typical topic displays in the right-hand panel.

- In any caArray viewer, click the **Help** button on the left vertical navigation menu.

**Note:** If the Help window does not appear, request that your Systems Administrator turn off any pop-up blockers installed on your computer's browser. Pop-up blockers can interfere with displaying the second help window.

## Help Topics Index

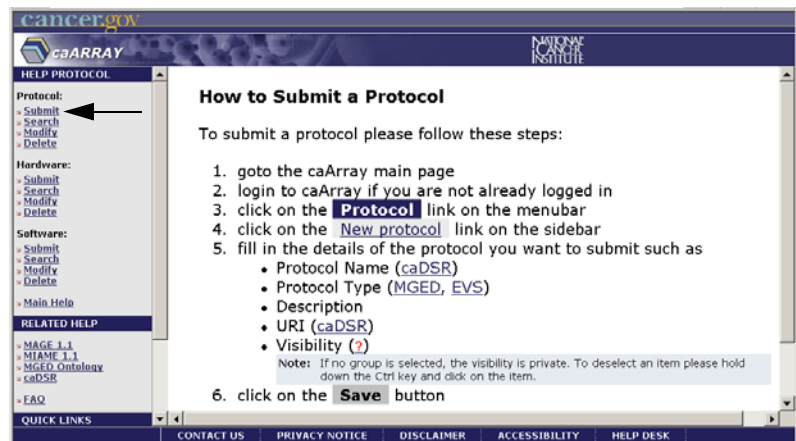
The index of Help topics displayed at the top vertical navigation menu at left of the viewer window shows online help topics related to caArray. When you click on any pertinent option, the viewer displays a related topic (if there are no associated subtopics) or a list of related subtopics. Click any listed option to open a related topic that guides you through the steps necessary to complete a task. In the case of the example shown



in [Figure 3.5](#) and [Figure 3.6](#), clicking the **Protocol** option opens a list of subtopics related to **Protocols**. Clicking on the **Submit** sub-topic opens the topic that describes **How to Submit a Protocol**.



*Figure 3.5 caArray Help menu*



*Figure 3.6 The Protocol sub-menu opens when you click on the Protocol option. Click on a sub-menu option to open the related topic.*

Use the back or forward arrows located on the standard toolbar of the browser displaying online help to move back and forth between various menus and help pages.

**Note:** Using the back or forward arrows in the browser does not work in the caArray program itself.

## Related Help

The **Related Help** menu located at the left of the browser window (lower left in [Figure 3.5](#)) provides links to topics or web pages that provide detailed information about MAGE 1.1, MIAME 1.1 and MGED Ontology standards.

- MAGE 1.1 describes data standards developed for gene expression data, annotations, and data exchange format.
- MIAME1.1. is a standard or guideline for the minimum amount of information required to make a microarray record useful to others.
- MGED Ontology is a controlled vocabulary that concisely defines terms as they relate to Microarrays and caArray as a whole.
- caDSR links to the caArray common data elements (CDEs) stored in the NCICB's metadata repository, caDSR.
- The Frequently Asked Questions (FAQ) menu provides user-friendly answers to common questions in caArray.

## Quick Links

The **Quick Links** on the left-hand navigation menu in most caArray viewers provide sources for caArray-related bioinformatics information on the Internet (*Figure 3.7*).

QUICK LINKS
NCI HOME
NCICB HOME
CANCER.GOV
caARRAY WEBSITE
NCICB Support

Figure 3.7 Quick Links menu options

These include:

- **NCI Home** (<http://www.nci.nih.gov/>) is a link to the home page of the National Cancer Institute.
- **NCICB Home** (<http://ncicb.nci.nih.gov/>) is a link to the NCI Center for Bioinformatics home page.
- **caArray website** (<http://caarray.nci.nih.gov/>) link has several internal and external links of interest
- **NCICB support** <http://ncicbsupport.nci.nih.gov/sw/> opens to a caArray project page; NCICB Application Support subjects (with active hypertext links) display in the left-hand panel of the browser window *Figure 3.8*.

The screenshot shows the NCICB Support Home page. On the left is a navigation menu titled "NCICB Support Home:" with a sub-section "Application Support for:" listing various tools and databases. On the right is the main content area titled "caArray" with sections for "Project Site", "caArray Applications", "caArray Data Portal", "caWorkbench", "WebCGH", and "caArray FAQs".

**NCICB Support Home:**

**Application Support for:**

- Cancer Centralized Clinical Database (C3D)
  - Oracle Clinical RDC
  - Oracle Discover
  - Integrated Review
- caArray
  - caArray Data Portal
  - caWorkbench
  - WebCGH
- caDSR Applications
  - caDSR Administration Tool
  - CDE Browser
  - CDE Curation Tool
  - caDSR Sentinel Tool
- Cancer Images Database (caIMAGE)
- Cancer Laboratory Information Management System (caLIMS)
- Cancer Model Organisms Database (caMOD)
- Cancer Molecular Analysis Project (CMAP)
- Centra
- Clinical Research Information Exchange (CRIX)
  - Firebird
- DCP Enterprise System Knowledgebase (DESK)
- Enterprise Vocabulary Services (EVS)
  - NCI Metathesaurus
  - NCI Thesaurus

**Programming & API Support**

**caArray**

**Project Site**

Click **HERE** for project details and background information.

**caArray Applications**

**caArray Data Portal**

URL: <http://caarraydb.nci.nih.gov/>  
Download: <http://ncicb.nci.nih.gov/download/index.jsp>

**caWorkbench**

Download: <http://ncicb.nci.nih.gov/download/index.jsp>

**WebCGH**

URL: <http://webcgh.nci.nih.gov>  
Instructions: [http://caarray.nci.nih.gov/data\\_analysis/webcgh](http://caarray.nci.nih.gov/data_analysis/webcgh)

**caArray FAQs**

Click **HERE** to search our dynamic caArray FAQ knowledgebase.

Figure 3.8 An example of the NCICB quick Link help topic

## Navigating through the caArray Workflow

Once you have logged in, caArray opens to the workflow page (*Figure 3.9*):

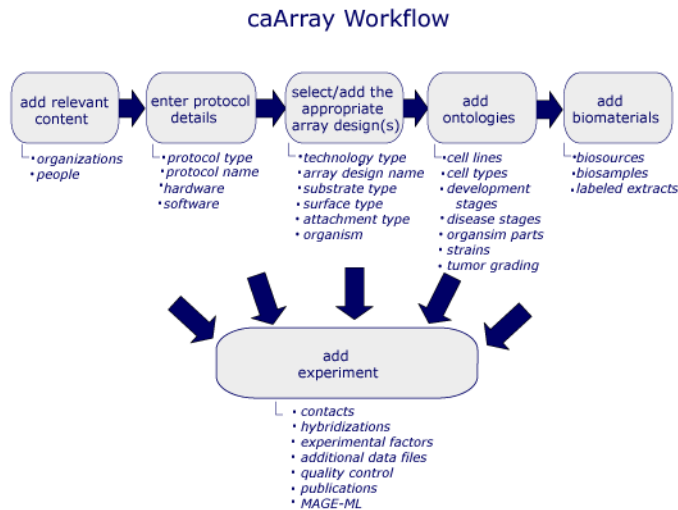


Figure 3.9 caArray Workflow

The workflow is designed to follow a logical flow of tasks as they should be completed in caArray. For more information about the workflow logic, see *caArray Workflow* on page 7. Each step in the workflow is described in its text; accompanying sub-topics represent objects that you can create in the corresponding section of caArray.

Each segment of the workflow figure (*Figure 3.9*) serves as a hypertext link to a corresponding caArray viewer. Click on your selection in the workflow to take you to the appropriate viewer(s) for completing your designated task(s).

**Note:** An alternative way to navigate to different caArray viewers is to mouse over and click the task tabs along the top of the page above the workflow (*Figure 3.10*). The tasks are organized from left to right in the logical order of workflow tasks, .

caArray Workflow

```

graph TD
    A[add relevant content] --> B[enter protocol details]
    B --> C[select/add the appropriate array design(s)]
    C --> D[add ontologies]
    D --> E[add biomaterials]
  
```

**add relevant content**

- organizations
- people

**enter protocol details**

- protocol type
- protocol name
- hardware
- software

**select/add the appropriate array design(s)**

- technology type
- array design name
- substrate type
- surface type

**add ontologies**

- cell lines
- cell types
- development stages

**add biomaterials**

- biosources
- biosamples
- labeled extracts

Figure 3.10 caArray task tabs

## The caArray Interface

The caArray provides a user-friendly interface to display options relating to the context in which you are working. For example, if you are adding contacts to caArray, you will not see protocol data.

The three most common uses of caArray are the following:

- Search public or private data already in the caArray system
- Submit new data, or modify existing data ( with appropriate permissions)
- User and group management and data curation (with appropriate permissions)

### Access to Public Data in caArray Before Login

caArray allows any user, without logging in, the ability to search any publicly-available caArray data. The Search Experiments, Search Array Designs and Search Protocols and other similar options are visible on the caArray homepage, the same page used to log in to caArray. Click on any of these hypertext links to begin the search process (Figure 3.11).

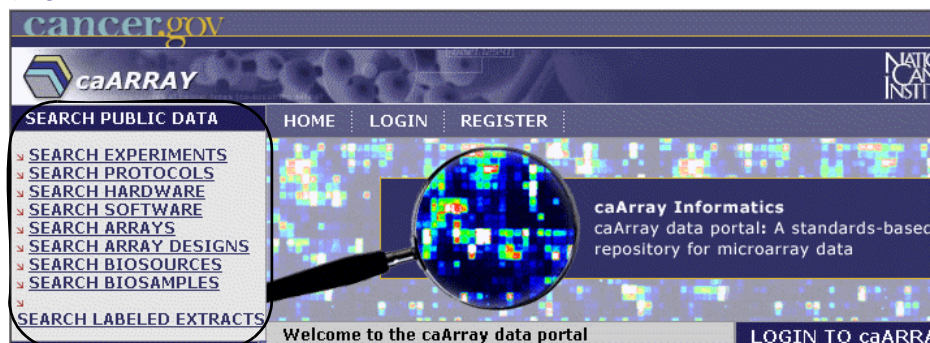


Figure 3.11 Search Public Data options in caArray before login

Menu options for launching searches are more extensive if you log in, because then you will have access to all objects to which you have been granted visibility. Options allowing you to submit, view, modify, and add microarray experiment data to caArray are dependent on your user privileges, once you are logged in. See Table 4.1 for more information.

**Note:** You must obtain a user account from the help desk in order to log in. For more information, see *Creating a User Account* on page 11.

### Elements of the caArray Viewer

Upon login, an array of task tabs displays across the top of the caArray viewing window. The task tabs represent the categories in which you must complete tasks to be submitted to a caArray Experiment; the tabs are placed in the logical order of a caArray workflow.

The task tabs are:

- **Contacts**
- **Protocols**

- **Arrays**
- **Ontologies**
- **Biomaterials**
- **Experiments**

When you select a task tab, the viewer opens to the corresponding section of caArray, and the menu choices on the left navigation menu correspond to the task tab you have selected. At the minimum, each task tab allows you to search and submit those items related to the task (when you are logged in).

Each of the tasks is described in separate chapters in this user's guide.

**Note:** The available options depend on your user privileges. See Table 4.1 for more information.

Additionally, online help and additional resource links remain fixed through all the viewing windows.

### Descriptions of Elements in the caArray Viewer

The terms in Table 3.1 identify and describe elements of a caArray browser window.

<b>Term</b>	<b>Definition</b>
Left Vertical Navigation Menu	Hypertext links associated with the selected task tab; Online Help options; NCICB Quick Links.
Online help	caArray documentation accessed from your computer screen providing help and answers for questions about using the software
Related help	These topics display in every caArray Help browser window.
Standard toolbar	Displays at the top of every browser window
MAGE 1.1	Related Help hypertext link. MAGE 1.1 is a widely-used microarray data standard.
MIAME 1.1	Related Help hypertext link. MIAME1.1. is a standard or guideline for the minimum amount of information required to make a microarray record useful to others.
MGED Ontology	Related Help hypertext link. MGED Ontology is a controlled vocabulary that concisely defines terms as they relate to Microarrays and caArray as a whole
Quick Links	The NCICB Quick Links on the left-hand menu provide sources for caArray-related bioinformatics information on the Internet.
Search {caArray database objects}	Link in upper left-hand corner of caArray browser window. Clicking this button opens the query window associated with the open task tab where you can craft your queries.
Interface	The caArray interface is a browser window, customized to correspond to task tabs or hypertext links you have selected.

Table 3.1 Elements of the caArray browser window

<b>Term</b>	<b>Definition</b>
Task tabs	Located across the top of the caArray browser window in the order of a logical caArray workflow. Task tabs represent the tasks you need to complete to create as components of an experiment
Contacts	One of the caArray task tabs. In the caArray context, a <b>person</b> or an <b>organization</b> associated with an entry in the program
Protocols	One of the caArray task tabs. In the caArray context, a microarray procedure or any other protocols that contribute to a microarray procedure, such as hybridization or image acquisition protocol, hardware and software used in an experiment.
Array Designs	One of the caArray task tabs. Descriptions of microarrays that include such information as array layout and design and the technology used to create a microarray.
Ontologies	One of the caArray task tabs. Based on an MGED structure and controlled vocabulary terms from various standardized database resources. These terms are used to annotate biomaterials in caArray.
Biomaterials	One of the caArray task tabs. The materials of biological origin used in microarray experiments, such as hybridizations.
Experiments	One of the caArray task tabs. Comprised of a complete set of contacts, protocols and hybridizations, arrays, Array Designs, ontologies, and biomaterials performed on or associated with microarrays.

*Table 3.1 Elements of the caArray browser window*

# CHAPTER 4

## CREATING AND MANAGING USER ACCOUNTS

This chapter describes the process for creating and managing accounts for users of caArray.

Topics in this chapter include:

- *Creating caArray Accounts* on this page
- *Managing Access to caArray Data* on page 20

### Creating caArray Accounts

---

#### Creating a User Account

Because microarray experiment data can be highly confidential and proprietary, it is critical that caArray includes security measures to ensure the highest level of confidentiality. One of the ways in which caArray implements security measures is by creating user accounts. User accounts are created from specific information gathered from the user.

To access non-public data in caArray, you must have a caArray account. To create a caArray user account,

- Contact NCICB Application Support:
  - Email at [NCICB@pop.nci.nih.gov](mailto:NCICB@pop.nci.nih.gov)
  - Phone at 888-478-4423 (toll-free) or 301-451-4384 (local)

OR

- Go to the NCICB caArray login page <http://caarraydb.nci.nih.gov/caarray/> and click the **Register** button. Enter the requested information, as displayed in Figure



Figure 4.1 and itemized below the figure. Follow the screen prompts to complete the registration.

\* indicates a required field

REGISTER FOR AN ACCOUNT					
* AFFILIATION	Grand Fork Laboratory			* LAST NAME	James
* FIRST NAME	Jane	MIDDLE INITIAL	B.		
* ADDRESS 1	12345 Isaac Newton Ln	ADDRESS 2			
* CITY	Chicago	* STATE	IL	* ZIP	64598
* COUNTRY		* PHONE		* EMAIL	

Figure 4.1 User account registry form

You must provide the following information in order to obtain a caArray account<sup>1</sup>:

- \*Affiliation
- \*First and Last Names
- \*Complete Address, including country
- \*Telephone number
- \*Email address

## Creating a Group

Periodically, when documenting experiments, more than one person or group is involved in the input and analysis of data. Creating a group is important to allow designated users or groups to access, input and analyze data. To create a group, you must provide NCICB Application Support ([ncicb@pop.nci.nih.gov](mailto:ncicb@pop.nci.nih.gov)) the following information:

- Your name
- Your email address
- Your telephone number
- The name of the group you want to create
- The names of the persons to be included in the group

## Managing Access to caArray Data

---

### Requesting Access to caArray Records

Much of the information provided by others is proprietary, and not yet public. The owner of private data determines who has access to proprietary data.

To request access to caArray records submitted or “owned” by existing caArray Contacts, whether persons or organizations, you must contact NCICB Application Support, [ncicb@pop.nci.nih.gov](mailto:ncicb@pop.nci.nih.gov). In your contact email, you must include the following information:

- Your name

---

1. Items with an asterisk are required fields.



- Your email address
- Name of the owner of the information you wish to access (person or organization)
- The specific information you wish to access, indicated by accession numbers or other unique identifying information available in the caArray records.
- A concise but complete statement of the reason you wish to be granted access to this information.

## Granting Others Access to Your Work

You can choose to grant others access to your work so that they can review your experiments, compare experimental design, compare results, etc. To assign access to others, you must contact NCICB Application Support, [ncicb@pop.nci.nih.gov](mailto:ncicb@pop.nci.nih.gov). In your contact email, you need to include all of the following information:

- Your name
- Your email address
- Your telephone number
- The name(s) of the person or persons, and/or the organization or organizations, to which you wish to grant access and the name of the group with which the new users should be associated
- The contact telephone numbers and email addresses for all persons and organizations to be granted access
- The level of access that you wish to grant to each person/group (**Read only**, **Read and Modify**).

**Note:** If only certain records are to be accessed, this must be explicitly indicated by accession numbers or other unique information that is part of the caArray records or class of records in question.

## Visibility

In caArray, the term “visibility” is used to describe the access to objects granted to logged in users. Table 4.1 describes visibility options and their interpretation.

**Note:** To deselect a Visibility option, press CTRL + click on the item.

<i>Term</i>	<i>Definition</i>
<b>Public</b>	Anyone can view all records, with <b>Read-Only</b> access.
<b>Private</b>	Can be viewed only by submitter (“owner”) of object. <b>Private</b> is assigned by default if no other <b>Visibility</b> option(s) are selected when an object is created.

Table 4.1 caArray visibility and permission settings

<b>Term</b>	<b>Definition</b>
<b>Public + Group</b>	Anyone can view all records, with <b>Read-Only</b> access. Modify privileges are assigned to members of the specified group(s) who are assigned "Curation" privileges. <b>Note:</b> The advantage to assigning a group access to data that is already Public, is in being able to isolate objects with that group's visibility. For example, the user (with appropriate visibility) could locate from the Public objects, all Experiments tagged with the group's visibility.
<b>Read-Only</b>	Permission only to view records created by other persons or organizations
<b>Delete</b>	Permission to delete records created by other persons or organizations
<b>Read/Modify</b>	Permission to view and/or modify records created by other persons or organizations

Table 4.1 caArray visibility and permission settings

# CHAPTER 5 CONTACTS

This chapter describes the process for managing Contact information in caArray.

Topics in this chapter include:

- [Contacts Overview](#) on this page
- [Contacts Workflow](#) on page 24

## Contacts Overview

---

A caArray Contact is described as a **Person** or an **Organization** associated with an entry in the program. For example, the principal investigator of a caArray Experiment is a Contact, as is the Organization with which he or she is affiliated. caArray provides the means to search and/or add new persons or organizations and relevant identifying information. This can assist anyone in the microarray community who needs to locate or contact specific individuals or organizations who might be part of the caArray database. Supplying Contact information is another way to interact with colleagues and institutions.

To successfully build and submit an Experiment in caArray, Contacts are required. Any individual or organization with responsibility for the Experiment such as a principal investigator, research scientist, technical contact, sales representative should be “created” as a Contact. For more information, see [Contacts Workflow](#) on page 24.

**Note:** A Contact person must be associated with an Contact organization. If you plan to add a new Contact, be sure to create the appropriate Contact organization first. For more information, see [Submitting a New Organization Contact](#) on page 25.

Contacts require information such as name, mailing address, phone numbers and email addresses. Table 5.1 defines terms associated with caArray Contacts.

<b>Term</b>	<b>Definition</b>
<b>Contact</b>	A caArray record containing contact information such as addresses and telephone numbers for a person or organization
<b>Person</b>	An individual associated with a caArray contact record
<b>Organization</b>	An organization associated with a caArray contact record
<b>Experiment</b>	The complete set of bioassays (including hybridizations) and their descriptions performed as an experiment for a common purpose.
<b>Search Organization</b>	Search feature which verifies the existence of a Contact Organization in caArray.
<b>Search People</b>	Search feature which verifies the existence of a Contact Person in caArray.
<b>New Organization</b>	caArray feature that allows you to add a new Contact Organization.
<b>New Person</b>	caArray feature that allows you to add a new Contact Person.

Table 5.1 Terms and features in caArray relating to Contacts

## Contacts Workflow

When creating and managing contacts in caArray, complete the following steps in their suggested order.

1. If you are adding a New Person Contact, verify that the Contact Organization in which the person is affiliated exists. Use the Search options, searching for an organization.
 

**Note:** If the Organization does not exist, add the New Organization first before adding the New Person, as a person **MUST** be affiliated with an organization.
2. Before adding a New Person Contact, launch a search to determine if the contact already exists in the system. Use the Search options, searching **People**.
3. If the Contact does not exist, add a **New Organization**, a **New Person**, or both.

## Working with a Contact Organization

### Searching for an Organization

To search for an Organization, follow these steps:

1. Log in on the caArray main page.
2. Select the **Contacts** task tab.
3. Click the **Search Organization** option on the upper left navigation menu.
4. Provide searchable information. You can search by:
  - **Organization** (an organization associated with a Contact) (*Figure 5.1*).

**Note:** The search is case insensitive and wild cards are always implied, for example: "Affy", "affy", "metri" will all return Affymetrix as organization or any others containing these strings.

5. Click the **Search** button to execute the search.

**Note:** By clicking the **Search** button without setting parameters, the search is unrestricted; all Organizations then display in the **Search Results** section.

If the Organization exists, its name displays in the Search Result section (*Figure 5.1*).

The screenshot shows two parts of a web interface. The top part is titled "SEARCH ORGANIZATIONS" and contains a text input field with "Affymetrix" entered, and three buttons: "Search", "Reset", and "Help". The bottom part is titled "SEARCH RESULTS" and shows "One item found." Below this is a table with two columns: "Name" and "Address". The "Name" column contains a link to "Affymetrix".

Figure 5.1 Search Organization query and results

6. To see the details of the Organization, click the **Organization Name**.
7. To reset the form to try another search, select the **Reset** button.

## Submitting a New Organization Contact

To submit contact information for a New Organization contact, follow these steps:

1. Log in on the caArray main page.
2. Select the **Contacts** task tab.
3. Select the **New Organization** link on the left navigation menu.
4. Complete the Contact information, as demonstrated in *Figure 5.2*:

The screenshot shows the "ORGANIZATION DETAILS" form on the National Cancer Institute website. The form has a navigation bar at the top with links: HOME, CONTACTS, PROTOCOLS, ARRAYS, ONTOLOGIES, BIOMATERIALS, EXPERIMENTS. Below the navigation bar is a note: "\* indicates a required field". The form fields are:
 

- \* Name: University of Maryland Baltimore
- \* Address: 701 East Pratt Street
- \* City: Baltimore
- \* State: Maryland
- \* Zip: 12130
- \* Country: U.S.A.
- Phone Number: (empty)
- Fax Number: (empty)
- Email Address: (empty)
- Url: (empty)

 At the bottom right of the form are three buttons: "Submit", "Cancel", and "Help".

Figure 5.2 Entering a new organization

2. Items with an asterisk are required fields.

5. Click the **Submit** button.
6. Review the details and click the **Done** button.

## Modifying Contact Information for an Organization

To modify contact information for an Organization, follow these steps:

1. Search for the **Organization** whose information you want to modify. (See *Working with a Contact Organization* on page 24.)
2. Select the name of the **Organization** in the **Search Results** section to access the organization contact information.
3. Click the **Modify** button.
4. Make any necessary changes.
5. Click the **Save** button to save the modifications, or click the **Cancel** button to disregard the changes.

**Note:** You can do this if you have the Visibility settings allowing you to modify the contact information. If you do not, a notice displays informing you you cannot modify the contact (*Figure 6.3*).

## Deleting a Contact Organization

To delete the contact information of an Organization follow these steps:

1. Search for the **Organization** you want to delete. (See *Working with a Contact Organization* on page 24.)
2. Select the name of the **Organization** you want to delete in the **Search Results** section.
3. Click the **Delete** button.
4. Confirm the deletion by clicking the **OK** button.

- Notes:**
- You can delete a contact organization only if you have permissions and if the organization is not currently referenced in caArray.
  - Deleting an organization cannot be undone.

## Working with a Contact Person

---

### Searching for a Person

To search for a Contact Person, follow these steps:

1. Log in on the caArray main page.
2. Select the **Contacts** task tab.
3. Select the **Search People** option on the left navigation menu.

**Note:** By clicking the **Search** button without setting parameters, the search is unrestricted; all People then display in the **Search Results** section.

4. Provide searchable information. You can search by:
  - **First Name**

◦ **Last Name**

**Note:** The search is case insensitive and wild cards are always implied on both sides of the query string.

5. Click the **Search** button to execute the search.

If the person exists, the name displays in the **Search Result** section (*Figure 5.3*).

The screenshot shows the caArray website interface. At the top, there are logos for cancer.gov, caARRAY, and the NATIONAL CANCER INSTITUTE. A navigation bar includes links for HOME, CONTACTS, PROTOCOLS, ARRAYS, ONTOLOGIES, BIOMATERIALS, EXPERIMENTS, and LOGOUT. On the left, a sidebar menu lists options like SEARCH PEOPLE, NEW PERSON, SEARCH ORGANIZATIONS, and NEW ORGANIZATION, along with QUICK LINKS such as NCI HOME, NCICB HOME, caARRAY WEBSITE, NCICB SUPPORT, and HELP. The main content area is titled 'SEARCH PEOPLE' and contains two input fields: 'First Name' with the value 'Bill' and 'Last Name' with the value 'Hadfield'. Below these fields are 'Search', 'Reset', and 'Help' buttons. Underneath, a 'SEARCH RESULTS' section indicates 'One item found.' and displays a table with columns for First Name, Last Name, and Email. The table contains one row with the values 'Bill', 'Hadfield', and 'hadfielj@mail.nih.gov'.

First Name	Last Name	Email
Bill	Hadfield	hadfielj@mail.nih.gov

*Figure 5.3 caArray Search People query and results*

6. To see the details about a person, select the person's name.
7. To reset the form to try another search, select the **Reset** button.

## Submitting a New Person Contact

To submit contact information for a new Person Contact, follow these steps:

1. Log in on the caArray main page.
2. Select the **Contacts** task tab.
3. Select the **New Person** link on the left navigation menu.

- Complete the contact information, as demonstrated in *Figure 5.4*<sup>3</sup>:

PERSON DETAILS	
* First Name	Jane
Middle Initials	M.
* Last Name	Brown
* Address	1234 Personality Lane
Phone Number	
Fax Number	
Email Address	
Url	
* Affiliation	<div style="border: 1px solid black; padding: 2px;">           Clontech            Columbia University            Cooperative Human Tissue Network            Cornell University Hospital            Dana Farber Cancer Institute            Department of Biostatistics, Harvard School of Public Health            Genome Institute of Singapore            Georgetown University  <b>Hewlett Packard</b>            Insightful Corp         </div> <p>If the Organization you would like to select is not listed, you can add this Organization to the caArray database (<a href="#">How?</a>).</p>

Figure 5.4 The form for submitting information for a new Person Contact

- Click the **Submit** button.
- Review the details and click the **Done** button.

## Modifying Contact Information for a Person

To modify contact information for a Person, follow these steps:

- Search for the person whose information you want to modify (see *Working with a Contact Person* on page 26).
- In the **Search Results** section, select the name of the person to access the individual's contact information.
- Click the **Modify** button.
- Make any necessary changes.
- Click the **Save** button to save the modifications, or click the **Cancel** button to disregard the changes.

- Note:**
- You can do this only if you have the Visibility settings allowing you to modify the contact information. If you do not, a notice displays informing you you cannot modify the contact (*Figure 6.3*).

## Deleting a Contact Person

To delete the contact information of a Person, follow these steps:

- 
- Items with an asterisk are required fields.



1. Search for the person you want to delete (see *Working with a Contact Person* on page 26).
2. Select the name of the person you want to delete in the **Search Results** section.
3. Select the **Delete** button.
4. Confirm the deletion by clicking **OK**.

- Note:**
- You can delete a contact person only if you have permissions and if the organization is not currently referenced in caArray.
  - Deleting a person cannot be undone.



# CHAPTER 6 PROTOCOLS

This chapter describes the elements of and the steps for working with a microarray procedure in caArray.

Topics in this chapter include:

- [Protocol Overview](#) on this page
- [Protocols Workflow](#) on page 32

## Protocol Overview

---

In caArray, Protocols are the foundation of a microarray experiment. A caArray Protocol provides clear and detailed documentation about the precise actions taken in any procedure that might be part of an experiment. For example, a Protocol could describe the steps a laboratory used for designing and creating its own microarray chip. A Protocol could describe the precise actions taken for running a hybridization or in creating an image file of the results. It might describe hardware used in an experiment, such as a chip scanner like the GenePix 4000A. It then would include the software, such as GenePix Pro, used in conjunction with the hardware to extract features of an array.

**Note:** Protocols do not include hardware/software or other procedures relating to the *statistical* analysis of microarray results.

Protocols can be saved for your own reuse or for sharing with colleagues. They can be easily modified, eliminating the need to rewrite an entire procedure. To prevent misinterpretation, Protocols should be clearly and objectively written.

Note that with every Protocol object you create in caArray, you can define its visibility, in other words, its access to other users of caArray. For more information about visibility options, see [Visibility](#) on page 21.

Note that if no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify it.

The Protocols task tab in caArray displays six basic functions that allow you to search or add new protocol-related objects:

- **Search Hardware**
- **New Hardware**
- **Search Software**
- **New Software**
- **Search Protocol**
- **New Protocol**

All of these functions relate to items that must be considered when writing a caArray Protocol. For example, most experiments require at least one **Hardware Protocol** (for example, the scanner to scan the microarray) and one **Software Protocol** (an application used in conjunction with the scanner hardware to identify the characteristics of the microarray).

**Important!** In caArray, you must submit Protocols prior to submitting an Experiment. As part of the Experiment submission process, you must select the Protocols as well as define the hybridizations you used in the experiment. If you have not submitted your Protocols prior to submitting your experiment, you will be unable to successfully complete the submission of hybridization files. For more information on hybridizations and Experiment submissions, see *Submitting a New Experiment* on page 94.

## Protocols Workflow

---

When creating and managing Protocols in caArray, complete the following steps in their suggested order.

1. See if a specific protocol already exists by searching protocols.
2. If a specific protocol does not exist:
  - a. Verify that the appropriate hardware exists in caArray by searching for Hardware.
  - b. If the hardware does not exist, add hardware.
  - c. Verify that the appropriate software exists, by searching Software.
  - d. If software does not exist, add software.
3. Add a New Protocol.
4. Modify a Protocol when the need exists. You can do this only if you have permissions, either as the author of the protocol or as designated by the author of the protocol.

### Searching for an Existing Protocol

To search for an existing protocol, follow these steps:

1. Log in on the caArray main page.
2. Select the **Protocols** task tab.
3. Provide searchable information. You can search by the fields listed in Table 6.1.

**Note:** The search is case insensitive; wild cards are always implied on both sides of the query string.

<b>Searchable Fields</b>	<b>Description</b>
<b>Protocol Type</b>	Select from the drop-down list. This gives you a good idea about the broad range of Protocols that can and should be included as you add components that will comprise your caArray Experiment.
<b>Protocol Name</b>	Enter the name to be searched.
<b>Visibility</b>	Select the option describing the visibility assigned to the query Protocol. Options include Private, Public and groups assigned Read/Modify visibility.  <b>Note:</b> If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify it.

Table 6.1 Protocols searchable fields

- Click the **Search** button. If the protocol exists, it displays in the Search Results section.

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all Protocols will display in the Search Results (Figure 6.1).

SEARCH PROTOCOLS	
Protocol Type	<input type="text" value="All"/>
Protocol Name	<input type="text"/>
Visibility	<input type="text" value="All"/>
<input type="button" value="Search"/> <input type="button" value="Reset"/> <input type="button" value="Help"/>	

SEARCH RESULTS	
80 items found, displaying 1 to 20. [First/Prev] 1, 2, 3, 4 [Next/Last]	
Protocol Name	Protocol Type
<a href="#">Affymatrix hybridization u95av2</a>	hybridization
<a href="#">Affymatrix u95av2 Image acquisition</a>	image acquisition
<a href="#">Affymetrix GeneChip HG-U133 Feature Extraction</a>	feature extraction
<a href="#">Affymetrix GeneChip HG-U133 Image Acquisition</a>	image acquisition
<a href="#">Affymetrix hybridisation EUK-GE 3v2</a>	hybridization
<a href="#">Amir's Array Manufacture</a>	array manufacturing protocol
<a href="#">Amir's feature extraction</a>	feature extraction
<a href="#">Amir's Hybridization</a>	hybridization
<a href="#">Amir's Image Acquisition</a>	image acquisition

Figure 6.1 Results from an unrestricted Protocol search.

- To see the details of a protocol, click the Protocol name.
- To reset the form in order to try another search, select the **Reset** button.

## Searching for Hardware

Any hardware used in a microarray experiment must be entered into caArray as a Hardware object.

To search to see if the **Hardware** already exists in caArray, follow these steps:

1. Log in on the caArray main page.
2. Select the **Protocols** task tab.
3. Select **Search Hardware** from the left navigation menu.
4. Provide searchable information. You can search by any of the following fields, (descriptions for these fields are included in Table 6.2 on page 35):
  - **Hardware Name**
  - **Hardware Model**
  - **Hardware Type**
  - **Hardware Make** (*refers to the same information as Manufacturer*)
  - **Hardware Manufacturer**
  - **Visibility**

**Note:** The search is case insensitive; wild cards are always implied on both sides of the query string.

5. Click the **Search** button. If the hardware exists, it displays in the Search Results section.

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all Hardware will display in the Search Results.

6. To see the details of a particular hardware record, click the hardware name.
7. To reset the form in order to try another search, click the **Reset** button.

## Submitting New Hardware

To submit **New Hardware** follow these steps:

1. Log in on the caArray main page.
2. Select the **Protocols** task tab.
3. Select **New hardware** from the left navigation menu.

4. Select or enter the requested information as demonstrated in [Figure 6.2](#)<sup>4</sup> and described in [Table 6.2](#).

\* indicates a required field

**ADD NEW HARDWARE**

\* Name: GeneChip(R) Fluidics S

\* Model: 450

\* Type: wash\_station Specify New Type:

\* Make: Affymetrix

\* Manufacturer: Affymetrix

URI: http://www.affymetrix.

Visibility: Public  
caArray Developers  
AMDEC Consortium  
ISPY Consortium  
UAT Test

Submit Cancel Help

Figure 6.2 Adding new hardware

<b>Submission Fields</b>	<b>Description</b>	<b>Example</b>
<b>*Name</b>	Full name of the hardware	GeneChip® Fluidics Station 450
<b>*Model</b>	Descriptor of the model	450
<b>*Type</b>	Descriptor for the hardware type	Wash station
<b>*Make</b>	Make of the hardware	Affymetrix
<b>*Manufacturer</b>	Manufacturer of the hardware	Affymetrix
<b>URI</b>	Uniform Resource Identifier for the hardware manufacturer	<a href="http://www.affymetrix.com">http://www.affymetrix.com</a>
<b>Visibility</b>	Visibility assigned to the query Hardware. Options include Private, Public and groups assigned Read/Modify visibility. <b>Note:</b> If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify it.	Private

Table 6.2 Hardware fields

5. Click the **Submit** button.

4. Items with an asterisk are required fields

## Modifying Hardware

To modify Hardware, follow these steps:

1. Log in on the caArray main page.
2. Select the **Protocols** task tab.
3. Search for the appropriate hardware using the **Search Hardware** function. See *Searching for Hardware* on page 33.
4. Click the **Hardware Name** to be modified in the **Search Results** to see the detailed information.
5. Click the **Modify** button.
6. Make any appropriate changes to the hardware details.
7. Select the **Save** button to save the modifications, or select the **Cancel** button to disregard the changes.

**Note:** You can do this only if you have the Visibility settings allowing you to modify the hardware. If you do not, a notice displays informing you that you cannot modify the object (*Figure 6.3*).

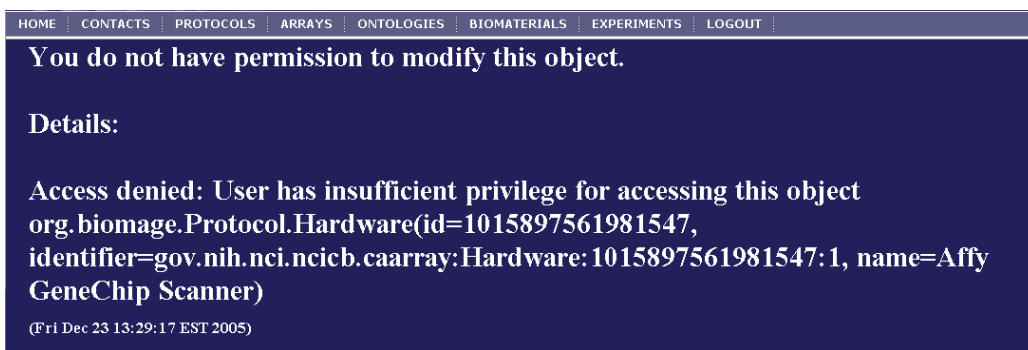


Figure 6.3 Permission to modify an object denied notice

## Deleting Hardware

To delete Hardware, follow these steps:

1. Search for the Hardware you want to delete. (See *Searching for Hardware* on page 33.)
2. Click the name of the **Hardware** you want to delete in the **Search Results** section. This opens the detail page for the selected object.
3. Click the **Delete** button.
4. Confirm the deletion by clicking the **OK** button.

- Notes:**
- Deleting a Hardware object cannot be undone.
  - You can delete an Hardware only if you have the appropriate permissions to do so. For more information, see *Visibility* on page 21.

## Searching for Software

To Search Software follow these steps:



1. Log in on the caArray main page.
2. Select the **Protocols** task tab.
3. Click **Search Software** from the left navigation menu.
4. Provide searchable information. You can search by the following fields, (descriptions are included in Table 6.3 on page 38):
  - **Software type**
  - **Software name**
  - **Software manufacturer**
  - **Visibility**

**Note:** The search is case insensitive; wild cards are always implied on both sides of the query string.
5. Click the **Search** button. Existing software displays in the **Search Results**.
 

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all Software will display in the Search Results.
6. To see the details of the software, select the Software name.
7. To reset the form in order to try another search, click the **Reset** button.

## Submitting New Software

To submit New Software, follow these steps:

1. Log in on the caArray main page.
2. Select the **Protocols** task tab.
3. Select **New Software** from the left navigation menu.
4. Complete the details of the software you are submitting, as demonstrated in [Figure 6.4<sup>5</sup>](#) and described in Table 6.3.

HOME   CONTACTS   PROTOCOLS   ARRAYS   ONTOLOGIES   BIOMATERIALS   EXPERIMENTS   LOGOUT	
* indicates a required field	
<b>ADD NEW SOFTWARE</b>	
* Name	<input type="text" value="GenePix Pro"/>
* Type	<input type="text" value=""/> Specify New Type: <input type="text" value="image analysis software"/>
* Manufacturer	<input type="text" value="Axon Instruments"/>
URI	<input type="text" value="http://www.moleculardevices.com/"/>
Visibility	<input type="text" value="Public"/> <input type="text" value="caArray Developers"/> <input type="text" value="AMDEC Consortium"/> <input type="text" value="ISPY Consortium"/> <input type="text" value="UAT Test"/>
<input type="button" value="Submit"/> <input type="button" value="Cancel"/> <input type="button" value="Help"/>	

---

5. Items with an asterisk are required fields.

Figure 6.4 Adding new software

<b>Submission Fields</b>	<b>Description</b>	<b>Example</b>
<b>*Name</b>	Full name of the software	GenePix Pro 3.0.1.22
<b>*Type</b>	Descriptor of the type of software	Microarray image analysis software
<b>*Manufacturer</b>	Name of the manufacturer of the software	Axon Instrument
<b>URI</b>	Uniform Resource Indicator for the manufacturer	<a href="http://www.moleculardevices.com/">http://www.moleculardevices.com/</a>
<b>Visibility</b>	<p>Visibility assigned to the query Hardware. Options include Private, Public and groups assigned Read/Modify visibility.</p> <p><b>Note:</b> If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify it.</p>	Private

Table 6.3 Software fields

5. Click the **Submit** button.

## Modifying Software

To modify Software, follow these steps:

1. Log in on the caArray main page.
2. Select the **Protocols** task tab.
3. Search for the appropriate software using the **Search Software** function. See **Searching for Software** on page 36.
4. Select the software to modify in the **Search Result** section.
5. Click the Software Name to access the detailed information about the software.
6. Click the **Modify** button.
7. Make appropriate changes to the software details.
8. Click the **Save** button to save the modifications, or select the **Cancel** button to disregard the changes.

**Note:** You can do this only if you have the Visibility settings allowing you to modify the software. If you do not, a notice displays informing you you cannot modify the object (example in [Figure 6.3](#)).

## Deleting Software

To delete Software, follow these steps:

1. Search for the **Software** you want to delete. (See *Searching for Software* on page 36.)
2. Click the name of the **Software** you want to delete in the **Search Results** section. This opens the detail page for the selected object.
3. Click the **Delete** button.
4. Confirm the deletion by clicking the **OK** button.

- Notes:**
- Deleting a software object cannot be undone.
  - You can delete an software only if you have the appropriate permissions to do so. For more information, see *Visibility* on page 21.

## Submitting a New Protocol

To submit a New Protocol, follow these steps:

1. Log in on the caArray main page.
2. Select the **Protocols** task tab.
3. Select **New Protocol** from the left navigation menu.
4. Complete the details of the Protocol you are submitting as demonstrated in *Figure 6.5* and described in Table 6.4)<sup>6</sup>.

\* indicates a required field

ADD NEW PROTOCOL	
* Name	<input type="text" value="Affymetrix u95av2 image acquisition"/>
* Type	<input type="text" value="image_acquisition"/> <input type="button" value="Specify New Type:"/> <input type="text" value="array manufacturing protocol"/>
Description	<input type="text" value="Add your own description of the Protocol to this text box."/>
URI	<input type="text"/>
Visibility	<input type="text" value="Public"/> <input type="text" value="caArray Developers"/> <input type="text" value="AMDEC Consortium"/> <input type="text" value="ISPY Consortium"/> <input type="text" value="UAT Test"/>

Figure 6.5 Adding a new Protocol

<b>Submission Fields</b>	<b>Description</b>	<b>Example</b>
<b>*Name</b>	Name of the protocol	lung tissue RNA extraction
<b>*Type</b>	Descriptor of the type of protocol	array manufacturing protocol; reverse transcription; RNA extraction; labeling protocol

6. Items with an asterisk are required fields.

<b>Submission Fields</b>	<b>Description</b>	<b>Example</b>
<b>Description</b>	Description of the protocol procedure. Include any and all appropriate details such as the detailed steps taken in a laboratory procedure	Description of a procedure for labeling RNA with fluorescent tags to be used in hybridization procedure
<b>URI</b>	Uniform Resource Identifiers of the protocol, if available and appropriate	URI used in MAGE
<b>Visibility</b>	Visibility assigned to the query Hardware. Options include Private, Public and groups assigned Read/Modify visibility. <b>Note:</b> If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify the object.	Public

Table 6.4 Protocol fields

- Click **Submit**. This opens the Protocol Details page (Figure 6.6).

The screenshot shows the 'PROTOCOL DETAILS' page. It contains a table with the following data:

Name	lung tissue RNA extraction
Type	nucleic_acid_extraction
Description	
URI	
Visibility	private

Below the table are three buttons: Done, Modify, and Delete. Underneath are three sections: 'PARAMETERS' with an 'Add Parameter' button; 'HARDWARE ASSOCIATIONS' with a dropdown menu and an 'Add Hardware Association' button; and 'SOFTWARE ASSOCIATIONS' with a dropdown menu and an 'Add Software Association' button.

Figure 6.6 Protocol Details page

- Click the **Add Parameter** button. (This step is optional.)

\* indicates a required field

The screenshot shows the 'ADD PARAMETER' form. It contains the following fields:

- \* Name: Text input field
- Default Value: Text input field
- \* Unit Type: Dropdown menu
- \* Unit: Text input field with a dropdown menu showing 'select Unit Type first'
- \* Type: Dropdown menu

At the bottom right are two buttons: Submit and Cancel.

Figure 6.7 Add [Protocol] Parameters dialog box

In the Add Parameter dialog box ([Figure 6.7](#)), you can define Protocol details<sup>7</sup>. An example of parameters would be numerical parameters such as incubation temperatures, or quantities of reagents added.

- **\*Name**
- **Default Value**
- **\*Unit type**
- **\*Type**

**Note:** These kinds of details do not have to be added here. They could be added as part of step by step instructions added to the Protocol description.

7. Click **Submit** to add the parameters.
8. Back on the Protocol Details page, associate hardware with the new Protocol you are submitting by clicking the **Hardware Association** button (if applicable).

**Note:** This list contains only submitted hardwares; if you do not see your hardware on the list, you must first submit New Hardware. See [Submitting New Hardware](#) on page 34 for more information.

9. Associate software with the Protocol you are submitting by selecting the **Software Association** button (if applicable).

**Note:** This list contains only submitted softwares; if you do not see your software protocol on the list, you must first submit New Software. See [Submitting New Software](#) on page 37 for more information.)

10. When you have finished specifying these parameters, click **Done**.

## Modifying a Protocol

To modify an existing Protocol, follow these steps:

1. Log in on the caArray main page.
2. Select the **Protocols** task tab.
3. Search for the appropriate protocol using the **Search Protocol** function. (See [Searching for an Existing Protocol](#) on page 32 for more information.)
4. In the **Search Results**, click the Protocol name to access its detailed information.
5. Click the **Modify** button.
6. Make appropriate changes to the protocol details.
7. Click the **Save** button to save the modifications, or click the **Cancel** button to disregard the changes.

**Note:** You can do this only if you have the Visibility settings allowing you to modify the protocol. If you do not, a notice displays informing you you cannot modify the object (example in [Figure 6.3](#)).

---

7. Items with an asterisk are required fields.

## Deleting a Protocol

To delete a Protocol object, follow these steps:

1. Search for the Protocol you want to delete. (See *Searching for an Existing Protocol* on page 32.)
2. Click the name of the Protocol you want to delete in the **Search Results** section. This opens the detail page for the selected object.
3. Click the **Delete** button.
4. Confirm the deletion by clicking the **OK** button.

**Notes:**

- Deleting a Protocol object cannot be undone.
- You can delete a Protocol only if you have the appropriate permissions to do so. For more information, see *Visibility* on page 21.

# CHAPTER 7

## ARRAYS AND ARRAY DESIGNS

This chapter describes Arrays and Array Designs in caArray. In caArray, Array Designs are the descriptions of microarrays that include such information as array layout and design, and Arrays are the actual microarrays used in the Experiment.

Topics in this chapter include:

- *Array Designs/Array Overview* on this page
- *Array Designs Workflow* on page 44
- *Managing Array Designs* on page 44
- *Managing Arrays* on page 51

### Array Designs/Array Overview

---

In the context of caArray, it is important to differentiate between Array Designs and Arrays, as both are listed on the **Arrays** tab.

- **Array Design:** A file that explains the design of a microarray. The description includes such information as the array layout and design, its substrate, its surface type, its attachment type and the array strand type.  
An Array Design file defines the coordinates of each gene, its microarray surface, its attachment type, and its substrate. An Array Design is to a microarray as a blueprint is to a house.
- **Array:** The actual microarray slides that are used in an Experiment. In caArray, one and only one Array object corresponds to each hybridization data file. Hence, 100 hybridization files = 100 array objects. Using the blueprint analogy, as 100 houses could be built from one blueprint, 100 Arrays can correspond to one Array Design.)

The ability to define, add and search Array and Array Designs provides the documentation needed to reproduce precise array configurations in protocols and experiments. Well-written and well-documented Array Designs stored in caArray can be reused and modified with minimal effort.

The Arrays task tab features three basic functions: **Add**, **Search** and **Modify** an Array or an Array Design. The **Add** and **Search** are available as links at the upper part of the left side panel, and **Modify** can be performed after a search has located an Array or Array Design.

- **New Array or Array Design** — If an Array or an Array Design does not exist, you can add a new one.
- **Search Array or Array Design** — You can locate an Array Design or an Array existing in caArray to review the object details.
- **Modify Array or Array Design** — With appropriate permissions, either as the author of an Array or Array Design or as designated by the author of the Array or Array Design, you can modify the details of an array.

**Note:** In caArray, after specifying the Array Design that corresponds to a hybridization file to be uploaded, and you create an array for the file, caArray copies the specified Array file for each similar hybridization file you will upload. For more information, see boxed text on page 101.

## Array Designs Workflow

---

A caArray microarray workflow can consist of any or all of the following tasks:

1. Because an Array Design is like a blueprint for an Array, you must create an Array Design in caArray before any corresponding Arrays are added. First, search caArray to see if a specific Array Design exists in caArray.
2. Add a new Array Design, if it does not exist.
3. Add a new Array, based on a specified Array Design.
4. Modify an Array or Array Design.

**Note:** There are many dependencies in this chapter which require naming objects such as Contact person(s) or organizations, Protocols, and so forth when you are creating Array Designs and/or Arrays. If you have not already created these preliminary objects, you must do so before you can complete the directions in this chapter.

## Managing Array Designs

---

### Searching Array Designs

To search **Array Designs**, follow these steps:

1. Log in on the caArray main page.
2. Select the **Arrays** task tab; this opens the Search Array Designs page.



3. Provide searchable information. You can search by using any of the fields in Table 7.1:

<b>Searchable Fields</b>	<b>Description</b>
<b>Technology Type</b>	Select from the drop-down menu the technology type or platform of the reporters on the array. <b>All</b> is the default setting.
<b>Surface Type</b>	Select from the drop-down menu a controlled term for descriptors for coating of the substrate. <b>All</b> is the default setting.
<b>Organism</b>	Select from the drop-down menu the genus and species of the organism from which the cells/nucleic acid used for the microarray experiment was derived. <b>All</b> is the default setting.
<b>Array Design Name</b>	Enter the name for the Array Design
<b>Attachment Type</b>	Select from the drop-down menu the method by which the element (reporter) sequences are physically attached to the array. <b>All</b> is the default setting.
<b>Identifier</b>	caArray identifier
<b>Array Design Provider</b>	Select from the drop-down menu the name of the provider of the Array Design (most likely, a custom Array Design). <b>All</b> is the default setting.
<b>Strand Type</b>	Select from the drop-down menu a descriptor of the strand type to which the sequence feature belongs. <b>All</b> is the default setting.
<b>Visibility</b>	Select from the drop-down menu the Visibility type. Visibility allows you to define permissions for who can use your Array Design or Array for documentation. Options can include groups created in caArray. <b>All</b> is the default setting.

Table 7.1 Array Designs searchable fields

**Note:** The search is case insensitive; wild cards are always implied on both sides of the query string.

4. Click the **Search** button. If the Array Design exists, it will be listed in the Search Results section.

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all Array Designs in caArray will display in the Search Results section of your browser (*Figure 7.1*).

SEARCH RESULTS	
25 items found, displaying 1 to 20. [First/Prev] 1, 2 [Next/Last]	
Design Name	Identifier
<a href="#">Amir's qal</a>	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897535941627:1
<a href="#">DrosGenome1</a>	Affymetrix:DrosGenome1
<a href="#">Extracted SAGE</a>	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897536498758:1
<a href="#">hg-u133a</a>	Affymetrix.com:PhysicalArrayDesign:hg-u133a
<a href="#">hg-u133b</a>	Affymetrix.com:PhysicalArrayDesign:hg-u133b
<a href="#">hg-u133_plus_2</a>	Affymetrix.com:PhysicalArrayDesign:hg-u133_plus_2
<a href="#">hg_u95av2</a>	Affymetrix.com:PhysicalArrayDesign:hg_u95av2
<a href="#">hg_u95b</a>	Affymetrix.com:PhysicalArrayDesign:hg_u95b
<a href="#">hg_u95c</a>	Affymetrix.com:PhysicalArrayDesign:hg_u95c
<a href="#">hg_u95d</a>	Affymetrix.com:PhysicalArrayDesign:hg_u95d
<a href="#">hg_u95e</a>	Affymetrix.com:PhysicalArrayDesign:hg_u95e
<a href="#">hu6800</a>	Affymetrix.com:PhysicalArrayDesign:hu6800
<a href="#">LongSAGE</a>	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897536498743:1
<a href="#">mg_u74av2</a>	Affymetrix.com:PhysicalArrayDesign:mg_u74av2
<a href="#">mg_u74bv2</a>	Affymetrix.com:PhysicalArrayDesign:mg_u74bv2
<a href="#">mg_u74cv2</a>	Affymetrix.com:PhysicalArrayDesign:mg_u74cv2
<a href="#">Mm-Incyte-v1px_16Bx24Cx23R</a>	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897539786308:1
<a href="#">Mm-Incyte-v1px_16Bx24Cx23R</a>	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897540401660:1
<a href="#">moe430a</a>	Affymetrix.com:PhysicalArrayDesign:moe430a
<a href="#">MouseArray</a>	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897536304027:1

Figure 7.1 Array Design search results (unrestricted)

- To see the details of a particular Array Design, select its name (Figure 7.2).

Array Design:

GENERAL ARRAY DESIGN INFORMATION						
Array Design Name:	hg_u95b					
Array Version:	1.0					
Technology Type:	in_situ_oligo_features					
Surface Type:	glass					
Attachment Type:	Unknown					
Strand Type:	Unknown					
Organism:	Unknown					
Array Description:						
<input type="button" value="Done"/> <input type="button" value="Modify"/> <input type="button" value="Remove"/>						
VISIBILITIES						
Visibility:	Public					
<input type="button" value="Modify"/>						
REPORTERS						
Number of features:	409600					
Download Array Design	<a href="#">Download MAGE-ML</a>					
<input type="button" value="Generate MAGE-ML"/> <input type="button" value="Help"/>						
DESIGN PROVIDERS						
Name	Affiliation	URI	Address	Phone	Fax	Action
<input type="button" value="Add Provider"/>						
<input type="button" value="Apply Protocol"/>						

Figure 7.2 Details of an Array Design display when you click on its name

**Note:** If you have appropriate permissions, you can modify Array Design information. For more information, see *Modifying an Array Design* on page 49.

Besides displaying details about the Array Design that were user-defined when the object was created in caArray, the **Reporters** section of the details page also reveals information from the Array Design file that was uploaded into caArray when the object was created.

- The **Number of Features** equals the number of spots of the microarray.
- A **Download MAGE-ML** button is available in the **Reporters** section to allow you to download a file in MAGE-ML format that provides the information needed about the Array Design. For more information, see *caArray Standards* on page 6.
- **Generate MAGE-ML** button is available in the Reporters section; click that button to convert the Array Design file to MAGE-ML format. For more information, see *caArray Standards* on page 6.

The **Design Providers** section is populated if information has been defined for a custom Array Design.

6. To reset the form to try another search, click the **Reset** button.

## Submitting a New Array Design

**Note:** caArray currently only accepts user-submitted *gal-file-format* Array Designs. Because of the computational demand, Affymetrix Array Designs are handled by the caArray team. If you have other Array Design types you would like to import to caArray, you must contact NCICB Application Support, [NCICB@pop.nci.nih.gov](mailto:NCICB@pop.nci.nih.gov).

To submit an **Array Design**, follow these steps:

1. Log in on the caArray main page.
2. Select the **Arrays** task tab.
3. Click **Add Array Design** from the left navigation menu.

The browser opens to a page with three sections (*Figure 7.3*)<sup>8</sup>:

The screenshot displays three sections of the caArray viewer interface:

- ARRAY REPORTERS INFORMATION:**
  - \* **Type of Upload:** GAL file (selected). Note: If MAGE-ML is selected, it is not necessary to fill out the section "NEW ARRAY DESIGN INFORMATION".
  - Important: For uploading MAGE-ML, the selected file must have the .xml extension or be a zip file that contains one or more files with the .xml extension. For uploading GAL, the selected file must have the .gal extension or be a zip file that contains a single file with the .gal extension.
  - \* **Upload:**
    - GAL file: [text box] Browse...
    - MAGE-ML file: [text box] Browse...
    - Optional: File with Annotations (Format): [text box] Browse...
  - Help
- NEW ARRAY DESIGN INFORMATION:**
  - \* **Array Design Name:** Array Design Name: [text box]
  - Array Version:** [text box]
  - Technology Type:** in\_situ\_oligo\_features
  - Surface Type:** polylysine
  - Attachment Type:** covalent
  - Strand Type:** double\_stranded
  - Organism:** Escherichia coli
  - \* **Array Description:** Array Description: [text area]
- ARRAY DESIGN VISIBILITY INFORMATION:**
  - Visibility:**
    - Public
    - caBIG
    - Curation Team - delete
    - Curation Team - make public
    - DC Lung Study
    - DC Prostate Study
    - GMDI\_Group

Figure 7.3 caArray viewer for defining information for a new Array Design

a. **Array Reporters Information** section —

**Type of Upload** — From the drop-down menu, select **MAGE-ML** if you are using a MAGE-ML file as the source for your Array Design. Select **gal** if you are using a gal file as the source for your Array Design.

**Upload** — Browse to locate your MAGE-ML or gal file, or other files that have the appropriate annotations. *Note that if you have other file types, you must first check with NCICB Application Support before uploading these files.*

**Note:** If you select MAGE-ML, skip to the **Visibility** section described below in section c.

8. Items with an asterisk are required fields.

- b. **New Array Design Information** section — Enter or select valid values for the Array Design if you are using a **gal** file instead of a MAGE-ML file. Table 7.2 describes the fields of the page<sup>9</sup>.

<b>Term</b>	<b>Definition</b>	<b>Example</b>
<b>*Array Design Name</b>	Name assigned to the Array Design	Hs-OperonV3.0-v1px
<b>Array Version</b>	Version number of the Array Design	Operon Version 3.0 OLI-GOs
<b>Technology Type</b>	The technology type or platform of the reporters on the array.	Spotted_ds_DNA
<b>Surface Type</b>	Descriptors of array surfaces	Polylysine, aminosi-lane, unknown_surface_type
<b>Attachment Type</b>	Descriptors of array attachments	Covalent, ionic, other
<b>Strand Type</b>	Descriptor of the strand type to which the the sequence feature belongs	Forward strand, reverse strand
<b>Organism</b>	The genus and species of the organism from which the cells/nucleic acid used for the microarray experiment was derived	<i>Mus musculus</i>
<b>*Array Description</b>	Description of the microarray	

Table 7.2 Fields for describing new Array Design

- c. **Visibility** section — Select the group or type of permission you are granting for the Array Design you are submitting. If you do not choose a Visibility, the Array Design visibility defaults to **Private**, giving only you access to the Array Design. For more information about Visibility options, see *Visibility* on page 21.
- d. Click the **Save** button

## Modifying an Array Design

To modify an existing Array, follow these steps:

1. Log in on the caArray main page.
2. Select the **Arrays** task tab; the Search Array Designs page displays.
3. Provide searchable information. You can search by using any of the fields defined in Table 7.1 on page 45.

9. Items with an asterisk are required.

- In the **Search Result** section, click the Array Design name to access its detailed information.

Array Design:

GENERAL ARRAY DESIGN INFORMATION	
Array Design Name:	hg_u95b
Array Version:	1.0
Technology Type:	in_situ_oligo_features
Surface Type:	glass
Attachment Type:	Unknown
Strand Type:	Unknown
Organism:	Unknown
Array Description:	

VISIBILITIES	
Visibility:	Public

REPORTERS	
Number of features:	409600
Download Array Design	Download MAGE-ML

DESIGN PROVIDERS						
Name	Affiliation	URI	Address	Phone	Fax	Action
<input type="button" value="Add Provider"/>						

Figure 7.4 Information displays for an existing Array Design. To modify the object, see the accompanying text.

- Click the **Modify** button in either the **General Array Design Information** section or in the **Visibilities** section.
- Make appropriate changes to the Array Design details. (Fields are identical to those described in Table 7.2.)
- For information about using the MAGE-ML-related links in the **Reporter** section, see page 46.
- In the **Design Providers** section, click **Add Provider** to add details about the source of a custom Array Design. This is an instance of object dependencies in caArray, because in the dialog box that opens, you must select an Individual or organization that has already been entered into caArray. If you have not done so, refer to [Chapter 5 Contacts](#) for more information.  
Once you have selected the contact person or organization, the information from the caArray contact object file displays in this section of the Array Design data form.
- Click the **Save** button to save modifications, or click the **Cancel** button to disregard the changes.

**Note:** You can do this if you have the Visibility settings allowing you to modify the Array Design. If you do not, a notice displays informing you you cannot modify the object.

## Deleting an Array Design

To delete an Array, follow these steps:

1. Search for the **Array Design** you want to delete. (See *Searching Array Designs* on page 44 or *Searching Arrays* on page 51.)
2. Select the name of the **Array Design** you want to delete in the **Search Results** section. This opens the detail page for the selected object.
3. Click the **Delete** button.
4. Confirm the deletion by clicking the **OK** button.

- Notes:**
- Deleting an Array Design or an Array cannot be undone.
  - You can delete an Array Design only if you have the appropriate permissions to do so. For more information, see *Visibility* on page 21.

## Managing Arrays

### Searching Arrays

Every hybridization data file uploaded to caArray must have an associated Array which is built on an Array Design already entered in caArray. Before creating such an Array, search caArray to see if the Array Design already exists. For more information, see *Searching Array Designs* on page 44. You should also search caArray to see if the Array you plan to submit already exists.

To search for an existing Array in caArray, follow these steps:

1. Log in on the caArray main page.
2. Select the **Arrays** task tab.
3. Click **Search Arrays** from the left navigation menu.
4. In the Search dialog box, provide searchable information. You can search by using any of the fields in Table 7.3.

**Note:** The search is case insensitive; wild cards are always implied on both sides of the query string.

<b>Searchable Fields</b>	<b>Description</b>	<b>Example</b>
<b>Array Name</b>	Name of the array	ATC_John_BC_BRCA1_01
<b>Array Design</b>	Select from the <b>Array Designs</b> drop-down list.	Hg-u133a
<b>Manufacturing Protocol</b>	Select from the Array Manufacturing Protocols drop-down list.	Hg-u133a Protocol
<b>Manufacture Date (range)</b>	Range of dates the array was manufactured	01/01/05 02/01/05
<b>Array Manufacturer</b>	Select from Array manufacturer drop-down list	Affymetrix

<b>Searchable Fields</b>	<b>Description</b>	<b>Example</b>
<b>Substrate Type</b>	Controlled terms for descriptors of types of array substrates	Glass
<b>Visibility</b>	Allows you to define permissions for who can use your Array for documentation. Options can include groups created in caArray.	Public

Table 7.3 Searchable fields for Arrays

5. Click the **Search** button.

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all Arrays in caArray will display in the Search Results section of your browser (*Figure 7.1*).

6. If the array you searched for exists, you will see it in the list on the search result page.
7. To see the details of a particular array, click the array name.
8. To reset the form to try another search, click the **Reset** button.

## Submitting a New Array

**Note:** When submitting a new Array, you must select a Protocol in caArray of “Array Manufacturing” type that describes the manufacture of the Array. If you have not already entered such a protocol, you must do so before you can finish adding an Array. For more information, see *Submitting a New Protocol* on page 39.

To add a new Array, follow these steps:

1. Log in on the caArray main page.
2. Select the **Array Design** task tab.
3. Click **Add Array** from the left navigation menu.



4. On the Submit New Array page, enter or select the text fields as demonstrated in *Figure 7.5* and described in Table 7.4<sup>10</sup>:

SUBMIT NEW ARRAY	
* Array Name:	ATC_John_BC_BRCA1_01
Array Barcode:	
* Array Design:	hg-u133b
Array Substrate Type:	glass
Array Manufacturer:	Affymetrix Axon Instruments NCICB TIGR
Array Manufacture Date:	01/01/05
Array Width:	mm
Array Length:	mm
Array Orientation Mark:	#
Array Orientation Mark Position:	left
Array Description:	Add your description of the array in this text box.
Visibility:	Public caArray Developers AMDEC Consortium ISPY Consortium UAT Test

Figure 7.5 Adding a new Array

Submission Fields	Description	Example
*Array Name	Name of the Array	ATC_John_BC_BRCA1_01
Array Barcode	Barcode on the Array	
*Array Design	Select from the drop-down menu the Array Designs that is the basis for this Array.	hg-u133a
Array Substrate type	Controlled terms for descriptors of types of array substrates.	Glass
Array Manufacturer	Method by which the element (reporter) sequences are physically attached to the array	Affymetrix
Array Manufacture Date	Date of array manufacture	01/01/05

10. Items with an asterisk are required fields.

<b>Submission Fields</b>	<b>Description</b>	<b>Example</b>
<b>Array Width</b>	Array width in millimeters	
<b>Array Length</b>	Array length in millimeters	
<b>Array Orientation Mark</b>	Mark made on microarray slide which is used as a point of reference for orientation of the slide	#
<b>Array Orientation Mark Position</b>	Position where the mark was made; from drop-down list	Left
<b>Array Description</b>	Description for the Array	
<b>Visibility</b>	Allows you to define permissions for who can use your Array for documentation. Options can include groups created in caArray.	Private

Table 7.4 Fields for submitting a new Array

**Note:** In naming an Array, we suggest you follow a convention so that it can be easily identified. In Table 7.4, the **Array Name**, *ATC\_John\_BC\_BRCA1\_01*, stands for: Advanced Technology Center, John, Breast Cancer Study, BRCA1, array number 01.

5. Click the **Save** button.
6. You must now select a protocol already in caArray that describes the manufacture of the Array. Click the **Apply Protocol** button.
7. Select the **Array Manufacturing Protocol** from the drop down list.

**Note:** This Protocol must have been submitted as an **Array Manufacturing** type in the Protocols section before it can be displayed in the drop down list. See *Submitting a New Protocol* on page 39.

APPLY A PROTOCOL				
Select Protocol:	Amir's Array Manufacture			
* indicates a required field				
PROTOCOL				
Protocol ID:	gov.nih.nci.ncicb.caarray:Protocol:1015897535941613:1			
* Activity Date:	<input type="text"/>			
* Performer:	Select			
Protocol Name:	Amir's Array Manufacture			
Protocol Description:	The cDNA microarray chips contained 7651 total features and were manufactured at the National Cancer Institute microarray facility.			
URI:	<a href="http://arraytracker.nci.nih.gov/index.shtml">http://arraytracker.nci.nih.gov/index.shtml</a>			
Protocol Parameters:	NAME	VALUE	TYPE	
	test Para	3	float	
Hardware:	Serial Number	<input type="text"/>		
	NAME	MODEL	TYPE	MAKE
	GenePix 4000A	4000A [46480]	array_scanner	Axon Instruments
				<input type="text"/> <input type="text"/> <input type="text"/>
Software:	Release Date	<input type="text"/>		
	Version	<input type="text"/>		
	NAME	TYPE	MANUFACTURER	PARAMETERS

Figure 7.6 Applying an Array Manufacturing Protocol to an Array before its submission

- In the page that opens displaying current array manufacture information for the Protocol you selected, you must add the **Activity Date** and select the **Performer**.
- Click **Save**. This associates the Protocol you selected with the Array are submitting.

## Modifying an Array

To modify an existing Array, follow these steps:

- Log in on the caArray main page.
- Select the **Arrays** task tab.
- Click the **Search Arrays** link.

**Note:** See *Searching Arrays* on page 51 for more information.

- In the **Search Result** section, click the Array name to access its detailed information. Note that the Array Details page that opens displays the Protocol information that was applied to the Array when it was created.

ARRAY DETAILS					
Array Name:	BRCA1 36				
Array Barcode:					
Array Design:	Amir's gal				
Array Substrate Type:	glass				
Array Manufacturer:	Advantage Technology Center (ATC)				
Array Manufacture Date:	1/22/01				
Array Width:					
Array Length:					
Array Orientation Mark:					
Array Orientation Mark Position:					
Array Description:	Array printed for Amir's experiment				
Array Visibility:	Public				

PROTOCOL APPLICATION					
Protocol ID:	gov.nih.nci.ncicb.caarray:Protocol:1015897535941613:1				
Activity Date:	4/22/01				
Performer:	Amir Jazaeri				
Protocol Name:	Amir's Array Manufacture				
Protocol Description:	The cDNA microarray chips contained 7651 total features and were manufactured at the National Cancer Institute microarray facility.				
Hardware:	NAME	MODEL	TYPE	MAKE	PARAMETERS
	GenePix 4000A	4000A [46480]	array_scanner	Axon Instruments	<input type="button" value="Name"/> <input type="button" value="Value"/> <input type="button" value="Type"/>
Software:	NAME	TYPE	MANUFACTURER	PARAMETERS	
	GenePix Pro 3.0.1.22_feature	feature_extraction_software	Axon Instruments	<input type="button" value="Name"/> <input type="button" value="Value"/> <input type="button" value="Type"/>	st para float
Protocol Parameters:	NAME	VALUE	UNIT	TYPE	

Figure 7.7 Array details page that opens for an existing Array

- Click the **Modify** button under the Array Details section.
 

**Note:** You cannot modify the Protocol information from this location. To do so, you can modify it, with proper permissions, only in the Protocol section of caArray. For more information, see *Modifying a Protocol* on page 41.
- Make appropriate changes to the array details.
- Click the **Save** button to save the modifications, or click the **Cancel** button to disregard the changes.
 

**Note:** You can do this if you have the Visibility settings allowing you to modify the Array. If you do not, a notice displays informing you you cannot modify the object.

## Deleting an Array

To delete an Array, follow these steps:

- Search for the **Array Design** or **Array** you want to delete. (See *Searching Array Designs* on page 44 or *Searching Arrays* on page 51.)

2. Select the name of the **Array Design** or **Array** you want to delete in the **Search Results** section. This opens the detail page for the selected object.
3. Click the **Delete** button.
4. Confirm the deletion by clicking the **OK** button.

**Notes:**

- Deleting an Array Design or an Array cannot be undone.
- You can delete an Array only if you have the appropriate permissions to do so. For more information, see *Visibility* on page 21.



# CHAPTER 8 ONTOLOGIES

This chapter describes the process for accessing, using and adding standardized terms from Internet sources in the Ontologies section in caArray. These terms are used in caArray specifically for annotating Biomaterials, essential components of a caArray Experiment.

Topics in this chapter include:

- *The Importance of a Common Language* on this page
- *General Overview of the MGED Ontology* on page 60
- *Workflow for Searching and Submitting Terms in caArray* on page 62

## The Importance of a Common Language

---

The use of common language is fundamental when annotating microarray data in caArray. Precise and standard terminology is important to prevent confusion or personal interpretation when sharing data. For example, when referring to a tumor tissue sample, a standard terminology allows you to easily clarify whether all of the cells in the sample are from the tumor itself—which could be obtained by micro-dissection—or whether the tissue represents a mixture of normal and cancerous cells.

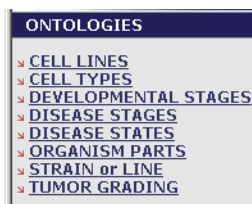
The best way to ensure that investigators utilize a common language is by using terms from controlled vocabularies where formal classifications of the entries and specified relationships of the terms are established in specified domains of knowledge.

**Note:** While it is recommended that you use terms from a controlled vocabulary, caArray makes it possible to enter any term, as long as you can reference a website as the source of that term.

The Ontologies section is used in caArray only to annotate Biomaterials as they are created or modified. For more information, see *Chapter 9 Biomaterials*.

## General Overview of the MGED Ontology

Once you log in to caArray, select the **Ontologies** task tab. In a caArray viewer, the Ontology entries listed at the upper left of the viewer window are MGED terms that outline groupings of individual vocabulary terms that reside in caArray (*Figure 8.1*). The MGED ontology provides the structure, the method for organizing these standardized terms in caArray.



*Figure 8.1 Ontologies menu options in caArray are based on MGED*

The Microarray Gene Expression Data (MGED) Society Ontology Working Group develops terminology and a semantic-based description of microarray experiments called MGED Ontology (MO). For more information on MO, refer to the MO web site, <http://mged.sourceforge.net/ontologies/index.php>. MO can be viewed using the NCI Terminology browser, <http://nciterns.nci.nih.gov/NCIBrowser/Dictionary.do>

In caArray, individual vocabulary listings that are sub-entries to each of these MGED categories are not MGED, but they are all terms, preferably from controlled vocabularies, found in public database resources.

When the MGED ontology points to external vocabularies, or when you locate terms in other controlled vocabulary databases, you can add the appropriate terminology from source vocabularies to caArray.

### List of Common MGED Ontology and Definitions

The options defined in Table 8.9 and *Figure 8.1* represent the MGED entries in caArray which you can search or modify with new terms.

<b>MO Category</b>	<b>Description</b>
<b>Cell Lines</b>	Identifiers for established cultures of metazoan cells used as biomaterial in caArray protocols or experiments.
<b>Cell Types</b>	Types of unmixed cell used in a caArray experiment.
<b>Developmental Stages</b>	Stages of development in an organism's life cycle from which biomaterial was extracted.
<b>Disease Stages</b>	The stage or progression of a disease in an organism, which includes pathological staging of cancers or other measures for other types of diseases.
<b>Disease States</b>	The name of the pathology diagnosed in the organism from which the biomaterial was derived. The disease state is normal if no disease has been diagnosed.

*Table 8.1 List of caArray Ontology categories and their MO definitions*



<b>MO Category</b>	<b>Description</b>
<b>Organism Parts</b>	Parts of an organism's anatomy or substances from an organism which the biomaterial was derived, excluding cells.
<b>Strain or Line</b>	Offspring from animals or plants that have a single ancestral breeding pair or parentage; for microbes, these are isolates derived from nature or in the laboratory.
<b>Tumor Grading</b>	A descriptor used in cancer biology that describes abnormalities of tumor cells

Table 8.1 List of caArray Ontology categories and their MO definitions

Using the common language elements provided by the MGED ontology, caArray provides an efficient and effective way to search for terminology stored in caArray. The next several sections provide explicit instructions for searching for entities in the ontology.

## Vocabulary Terms

Once the Ontologies tab is open, the MGED entries in the upper left-hand corner of your browser display as hyperlink menu options. Click on any of these terms to open a related Search dialog box (the top section of [Figure 8.2](#)). To illustrate the organization of the vocabulary terms in caArray, click the **Search** button which launches an unrestricted search for terms related to the top-level entry you selected. The **Search Results** section displays a list of all vocabulary terms in caArray that relate to the selected entry. ([Figure 8.2](#))

SEARCH ORGANISM PARTS			
Organism Part Name	<input type="text"/>		
Public Database	All <input type="button" value="v"/>		
Accession Number	<input type="text"/>		
<input type="button" value="Search"/> <input type="button" value="Reset"/> <input type="button" value="Submit New Organism Part"/>			

SEARCH RESULTS			
27 items found, displaying 1 to 20. [First/Prev] 1, 2 [Next/Last]			
Organism Part Name	Database	Accession Number	Link
<a href="#">Adrenal Gland</a>	NCI_Thesaurus		
<a href="#">Bladder</a>	NCI_Thesaurus		
<a href="#">bone marrow</a>	NCI_Thesaurus		
<a href="#">Brain</a>	NCI_Thesaurus	C12439	<a href="http://ncitterms.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?bookm">http://ncitterms.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?bookm</a>
<a href="#">Breast</a>	NCI_Thesaurus		
<a href="#">colon</a>	NCI_Thesaurus		
<a href="#">femur</a>	CellML		
<a href="#">Kidney</a>	NCI_Thesaurus		
<a href="#">kidney</a>	CellML		
<a href="#">Liver</a>	NCI_Thesaurus		
<a href="#">Lung</a>	NCI_Thesaurus		
<a href="#">Lymphoid tissue</a>	NCI_Thesaurus		
<a href="#">Mesothelium</a>	NCI_Thesaurus		
<a href="#">murine mammary gland</a>	NCI_Thesaurus	C23302	
<a href="#">Ovary</a>	NCI_Thesaurus	C101764	<a href="http://ncitterms.nci.nih.gov/NCIBrowser/Connect.do?dictionary=MGED">http://ncitterms.nci.nih.gov/NCIBrowser/Connect.do?dictionary=MGED</a>
<a href="#">Ovary</a>	NCI_Thesaurus		
<a href="#">Pancreas</a>	NCI_Thesaurus		
<a href="#">Peripheral blood mononuclear cell</a>	NCI_Thesaurus	C12954	<a href="http://ncitterms.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?bookm">http://ncitterms.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?bookm</a>
<a href="#">peripheral blood mononuclear cell</a>	NCI_Thesaurus	C12954	
<a href="#">Peripheral Blood/Bone Marrow</a>	NCICB Seed entries		

<a href="#">CONTACT US</a>	<a href="#">PRIVACY NOTICE</a>	<a href="#">DISCLAIMER</a>	<a href="#">ACCESSIBILITY</a>	<a href="#">APPLICATION SUPPORT</a>
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Figure 8.2 Vocabulary terms in caArray corresponding to the Organism Parts category

**Note:** Although it is recommended that terminology entries in caArray come from public controlled vocabulary databases, any term can be entered into caArray, as long as the source database website is referenced.

The name indicated for each vocabulary term appears exactly as it does in the source database, which is listed in the search results (column 2, [Figure 8.2](#)). Many vocabulary terms include the accession number for the term in the controlled vocabulary that is the source for the term (column 3, [Figure 8.2](#)). Some vocabulary terms also include a URI link that takes you directly to the source database (column 4, [Figure 8.2](#)). If you want more information about the term, click the link that goes directly to the database. For more information, see [Submitting a Vocabulary Term](#) on page 65.

**Note:** In some cases, the URI may not link directly to the source. If the URI is absent or it does not work, you may want to do a web search for the database.

## Getting MGED Ontology Help

On the **Ontologies** task tab, click the **Help** link, the last of the **Quick Links** menu options. On the left navigation Help menu, click the **Ontology** option. Under the **Related Help** option, click the **MGED Ontology** link which opens the MGED Ontology search page where you can find terms and definitions relevant to your query term.

Using the common language elements provided in the MGED ontology categories, caArray provides an efficient and effective way to search for caArray records. The next several sections provide explicit instructions for searching for vocabulary terms in caArray and adding terms when specified terms are not found.

## Workflow for Searching and Submitting Terms in caArray

---

When working with ontologies in caArray, complete the following steps in their suggested order.

1. Search for a term you want to use or are planning to submit to avoid entering duplicate terms into caArray. For more information, see the following section, [Searching for Vocabulary Terms in caArray](#).

**Note:** A search launched as described in this chapter only searches for terms in caArray. To search for terms in public databases, follow the directions in [Submitting a Vocabulary Term](#) on page 65.

2. If the term you are seeking is not located in caArray, follow the directions for submitting the term. This procedure includes directions for locating the term in a public database. For more information, see [Submitting a Vocabulary Term](#) on page 65.

## Searching for Vocabulary Terms in caArray

**Note:** When you launch a search for a vocabulary term in caArray, the search only covers terms existing in caArray. To launch a search in a public database of vocabulary terms, follow the instructions in [Submitting a Vocabulary Term](#) on page 65.

To search for a vocabulary term in caArray, follow these steps:

1. Log in on the caArray main page.

2. Select the **Ontologies** task tab.
3. Select from among the following MGED ontology listed on the left navigation menu. (These are defined in Table 8.1 on page 60):
  - **Cell Lines**
  - **Cell Types**
  - **Developmental Stages**
  - **Disease Stages**
  - **Disease States**
  - **Organism Parts**
  - **Strain or Line**
  - **Tumor Grading**

**Note:** Each of these MGED entries contains related sub-entries that are vocabulary terms from various public databases (preferably from controlled vocabulary databases). It is those vocabulary terms that are used to annotate Biomaterials in caArray.

4. In the Search dialog box that opens, provide searchable information. The searchable fields are demonstrated in [Figure 8.3](#) and described below the figure.

SEARCH ORGANISM PARTS	
Organism Part Name	<input type="text" value="liver"/>
Public Database	<input type="text" value="NCI Thesaurus"/>
Accession Number	<input type="text"/>
<input type="button" value="Search"/> <input type="button" value="Reset"/> <input type="button" value="Submit New Organism Part"/>	

*Figure 8.3 Search Organism Parts dialog box*

- **{Ontology entry} Name**
- **Public Database**—This field refers to the controlled vocabulary that is the source of the term. The drop-down menu gives you a good idea of the variety of source controlled vocabulary databases you can use to find your term.
- **Accession Number**—Identifier in the source database

**Note:** The search is case insensitive; wild cards are always implied on both sides of the query string.

- Click the **Search** button. The results display in the Search Results section of your browser (*Figure 8.4*).

SEARCH ORGANISM PARTS	
Organism Part Name	<input type="text" value="liver"/>
Public Database	All <input type="button" value="v"/>
Accession Number	<input type="text"/>
<input type="button" value="Search"/> <input type="button" value="Reset"/> <input type="button" value="Submit New Organism Part"/>	

SEARCH RESULTS			
One item found.			
Organism Part Name	Database	Accession Number	Link
Liver	NCI_Thesaurus		

Figure 8.4 Term search for query "liver"

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all related terms in caArray display in the Search Results section (*Figure 8.5*).

SEARCH RESULTS			
27 items found, displaying 1 to 20. [First/Prev] 1, 2 [Next/Last]			
Organism Part Name	Database	Accession Number	Link
Adrenal Gland	NCI_Thesaurus		
Bladder	NCI_Thesaurus		
bone marrow	NCI_Thesaurus		
Brain	NCI_Thesaurus	C12439	<a href="http://nciterns.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?">http://nciterns.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?</a>
Breast	NCI_Thesaurus		
colon	NCI_Thesaurus		
femur	CellML		
Kidney	NCI_Thesaurus		
kidney	CellML		
Liver	NCI_Thesaurus		
Lung	NCI_Thesaurus		
Lymphoid tissue	NCI_Thesaurus		
Mesothelium	NCI_Thesaurus		
murine mammary gland	NCI_Thesaurus	C23302	
Ovary	NCI_Thesaurus	C101764	<a href="http://nciterns.nci.nih.gov/NCIBrowser/Connect.do?dictionary=M">http://nciterns.nci.nih.gov/NCIBrowser/Connect.do?dictionary=M</a>
Ovary	NCI_Thesaurus		
Pancreas	NCI_Thesaurus		
Peripheral blood mononuclear cell	NCI_Thesaurus	C12954	<a href="http://nciterns.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?">http://nciterns.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?</a>
peripheral blood mononuclear cell	NCI_Thesaurus	C12954	
Peripheral Blood/Bone Marrow	NCICB Seed entries		

<a href="#">CONTACT US</a>	<a href="#">PRIVACY NOTICE</a>	<a href="#">DISCLAIMER</a>	<a href="#">ACCESSIBILITY</a>	<a href="#">APPLICATION SUPPORT</a>
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Figure 8.5 Search Results for an unrestricted Organism Parts search

- Interpreting search results:
  - If the term exists in caArray, the details recorded in caArray for a particular term display in the **Search Results** columns: the category name, the source database, the accession number in that database, and the URI for that database.
  - If the term is not found in caArray, click the **Submit New {ontology entry name}** button (at the lower right of the Search {ontology entry} dialog box). To continue with the submission process for a new term, see the following section, *Submitting a Vocabulary Term*.
- To reset the form in order to try another search, click the **Reset** button in the Search {category} dialog box.

## Submitting a Vocabulary Term

**Note:** Each vocabulary term in caArray should come from a public database of such terms. Identifying features of the terms in caArray must be identical to these features in the source databases. The procedure in this section includes directions for locating in a public database a term you want to submit.

To submit a vocabulary term to caArray, follow these steps:

1. Log in on the caArray main page.
2. Select the **Ontologies** task tab.
3. Click the Ontologies entry of your choice from the left navigation menu. You should select the MGED entry into which your term would logically fit. These are defined in Table 8.1 on page 60.
4. At the bottom of the search section, select the **Submit New {ontology entry name}** button.

All of the fields in the Add ... dialog box that opens require a text entry except the **Public Database** field. Provide the requested information which varies according to your category selection.

**Note:** Do not add the {category} name to the submission form yet. All fields must be populated with text exactly as it appears in the source database.

5. Open the drop-down menu for **Public Database**. The variety of options in this list demonstrates the wide variety of places where you can search for your vocabulary term.

**Note:** If you plan to add a term related to Cell Lines, in the Add Cell Lines dialog box, click the **Help** button. The context sensitive help topic that opens points the way and includes links to two public databases, ATCC and CAPRI, for finding controlled terms for cell lines. For a case study submitting a specific cell line term to caArray, see *Case Study: Submitting a Cell Line Term into caArray* on page 67.

*This is the only MGED category that has such a help section.*

6. Go to the database where you want to locate a term. The example used is the NCI Thesaurus.
7. Enter the term in the Quick Search text box, for instance, in the NCI Thesaurus. Click the **Go** icon. The viewer displays all related terms (*Figure 8.6*):.

The screenshot shows the National Cancer Institute (NCI) Thesaurus search interface. At the top, there is a navigation bar with the NCI logo and the text 'National Cancer Institute' and 'U.S. National Institutes of Health'. Below this, there are two search boxes: 'Quick Search' and 'Advanced Search'. The 'Quick Search' box contains the text 'prostate gland' and a 'Max Results' dropdown set to '10'. The 'Advanced Search' box has dropdown menus for 'Information about this concept' and 'Accepted\_Therapeutic\_Use\_For'. To the right of the search boxes, it says 'Vocabulary: NCI\_Thes' and 'Concepts visited (during this s' with a list containing 'Prostate Adenoma'. Below the search boxes is a navigation menu with links: 'QUICK LINKS', 'HELP', 'RESULTS', 'CUSTOMIZE', 'ABOUT', 'BROWSE HIERARCHY', and 'LOGOUT'. On the left side, there are links for 'NCI HOME', 'NCICB HOME', 'EVS HOME', 'SITE HOME', and 'KNOWN ISSUES'. The main content area is titled 'Quick Search Results' and displays 'There are 3 concepts matching "prostate gland\*"'. Below this, there are three search results, each with a red icon and a plus sign: 'Murine Prostate', 'Prostate Gland (MMHCC)', and 'Prostate Gland'.

Figure 8.6 NCI Thesaurus search results for "prostate gland"

8. To learn more about the term, follow links within the source database. For example, in the NCI Thesaurus, click on the text icon. By following the links, you can find the accession number for the term in the source database (*Figure 8.7*). You need this reference information to adequately identify a term that you are submitting in caArray; you are also facilitating other users' ability to learn more about the selected term..

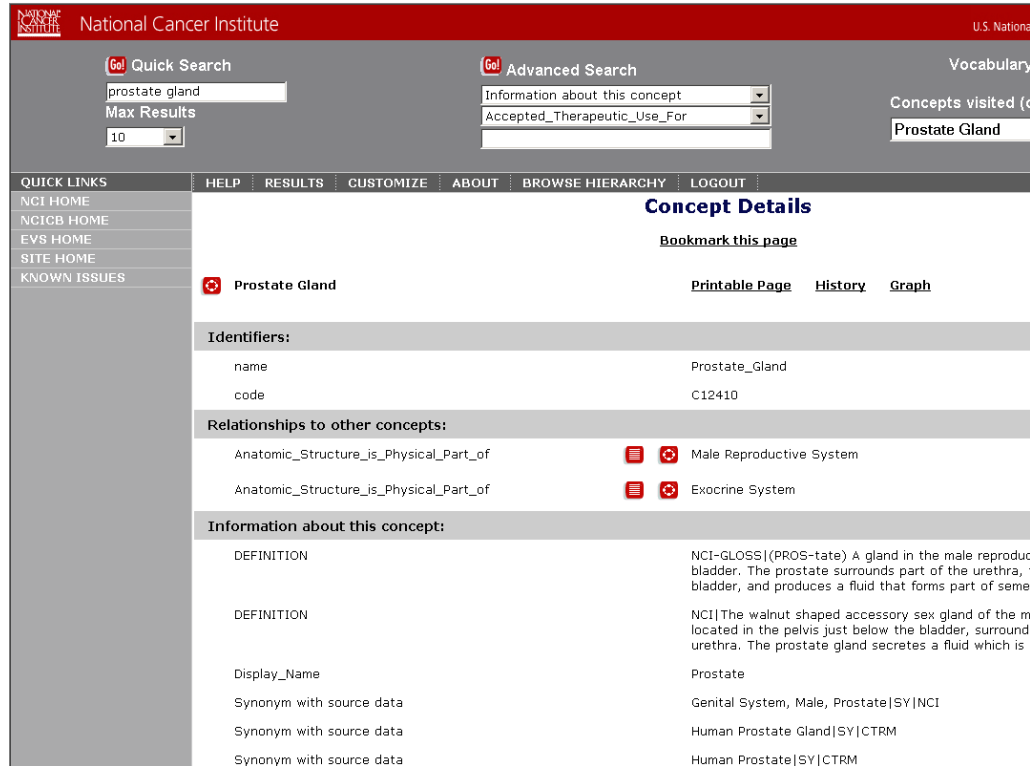


Figure 8.7

9. In the Add {term} dialog box in caArray:
  - a. Enter the term exactly as it appears in your source database: e.g. Prostate\_Gland (*Figure 8.8*).
  - b. Copy and paste the accession number from your source database.
  - c. Enter the URI for the database.

ADD CELL TYPE	
* Cell Type	<input type="text" value="Prostate_Gland"/>
* Public Database	<input type="text" value="NCI_Thesaurus"/>
Accession Number	<input type="text" value="C12410"/>
URI	<input type="text" value="http://nciterms.nci.nih.gov/"/>

\* indicates a required field

Figure 8.8 Adding a Cell Type term

10. Click the **Add** button. This adds the term to caArray.

## Case Study: Submitting a Cell Line Term into caArray

This case study searches for the Colo 320 cell line term in caArray. When it is not found, the appropriate source for the cell line is located. The Colo 320 term is then entered into caArray.

1. Click the **Ontologies** tab at the top of the caArray viewer.
2. Search for all the cell lines in caArray (the default selection when you clicked on Ontologies). Without entering anything in the search text fields, click the **Search** button (the upper section of *Figure 8.9*). This launches an unrestricted search for all Cell Lines terms.

SEARCH CELL LINES			
Cell Line Name	<input type="text"/>		
Public Database	All <input type="button" value="v"/>		
Accession Number	<input type="text"/>		
<input type="button" value="Search"/> <input type="button" value="Reset"/> <input type="button" value="Submit New Cell Line"/>			
SEARCH RESULTS			
18 items found, displaying all items.			
Cell Line Name	Database	Accession Number	Link
<a href="#">H1437</a>	NCI_Thesaurus		
<a href="#">H2009</a>	NCI_Thesaurus		
<a href="#">H2087</a>	NCI_Thesaurus		
<a href="#">H2347</a>	NCI_Thesaurus		
<a href="#">HCC78</a>	NCI_Thesaurus		
<a href="#">JLCELLLINE001sdfsd</a>	MGED Ontology	ACC1234	
<a href="#">JLCELLLINE001sdfsd</a>	MGED Ontology	ACC1234	
<a href="#">MCF-12A</a>	ATCC_Cultures	CRL-10782™	<a href="http://www.atcc.org">http://www.atcc.org</a>
<a href="#">MG 63</a>	CellML		
<a href="#">ovarian surface epithelial cell line</a>	ATCC_Cultures		
<a href="#">Pr111</a>	NCI_Thesaurus		
<a href="#">Pr117</a>	NCI_Thesaurus		
<a href="#">Pr14</a>	NCI_Thesaurus		
<a href="#">Pr14C1</a>	NCI_Thesaurus		
<a href="#">Pr14C2</a>	NCI_Thesaurus		
<a href="#">SAGE cartilage</a>	NCICB Seed entries		
<a href="#">Test cell line</a>	ATCC_Cultures		
<a href="#">TestCellLine2</a>	MGED Ontology		

Figure 8.9 The Search Results in the Cell Lines viewer display cell lines in the caArray database.

3. The **Search Results** section of the viewer (*Figure 8.9*) displays all Cell Lines currently listed in the caArray database. Because the **Colo 320** cell line is not in the list, you must submit the information.
4. Click the **Submit New Cell Line** button. The Add Cell Line dialog box displays (*Figure 8.10*).

ADD CELL LINE	
* Cell Line Name	<input type="text"/>
* Public Database	<input type="button" value="v"/>
Accession Number	<input type="text"/>
URI	<input type="text"/>
* indicates a required field	
<input type="button" value="Add"/> <input type="button" value="Reset"/> <input type="button" value="Cancel"/> <input type="button" value="Help"/>	

Figure 8.10 Add Cell Line dialog box

- Click the **Help** button. The Help topic that opens points to two databases for finding controlled terms for cell lines, ATCC and CAPRI (*Figure 8.11*).

**Submitting Information about a Cell Line**

To submit information about a cell line please follow these steps:

- fill in or select the details of the cell line you want to submit such as
  - Name
  - Database
    - [ATCC Cultures \(MGED, EVS\)](#)
    - [CABRI Human and Animal Cell lines \(MGED, EVS\)](#)
  - Accession Number
  - URI
- click on the **Add** button to save the entered information.

For further information (MAGE specification, MIAME specification and the MGED Ontology) please see the section [Related Help](#).

Figure 8.11 The Help topic for adding a cell line

- Click the link to the ATCC web site; follow the cell line links at the website for locating colo 320. You will discover that **colo 320** is included in the ATCC catalog (*Figure 8.12*).

**ATCC**  
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**Product Description**  
Before submitting an order you will be asked to read and accept the terms and conditions of ATCC's [Material Transfer Agreement](#) or, in certain cases, a depositing institution.

Customers in Europe, Australia, Hong Kong, India, Japan, Korea, New Zealand, Singapore and Taiwan, R.O.C. must contact a [local distributor](#) for an order for ATCC cultures and products.

**Cell Lines**

ATCC® Number: CCL-220.1™  Price: \$315.00

**Designations:** COLO 320HSR [COLO 320 HSR] **Depositors:** GE Moore

**Biosafety Level:** 1 **Shipped:** frozen

**Medium & Serum:** [See Propagation](#) **Growth Properties:** loosely adherent, multicell aggregates

**Organism:** *Homo sapiens* (human) **Morphology:** cells are rounded and refractile

**Source:** Organ: colon  
Disease: colorectal adenocarcinoma  
Tumor stage: Dukes' type C

**Cellular Products:** serotonin; norepinephrine; epinephrine; adrenocorticotrophic hormone (ACTH); parathyroid hormone

Figure 8.12 ATCC website

- Returning to caArray, enter the information from the ATCC web site in the form as shown in *Figure 8.13*.

ADD CELL LINE	
* Cell Line Name	<input type="text" value="COLO 320 HSR"/>
* Public Database	<input type="text" value="ATCC_Cultures"/>
Accession Number	<input type="text" value="CCL-220"/>
URI	<input type="text" value="http://www.atcc.org/"/>

\* indicates a required field

Figure 8.13 Entry form for submitting a new cell line



- Click **Add** to submit the information. caArray displays the information for the newly submitted Cell Line (*Figure 8.14*).

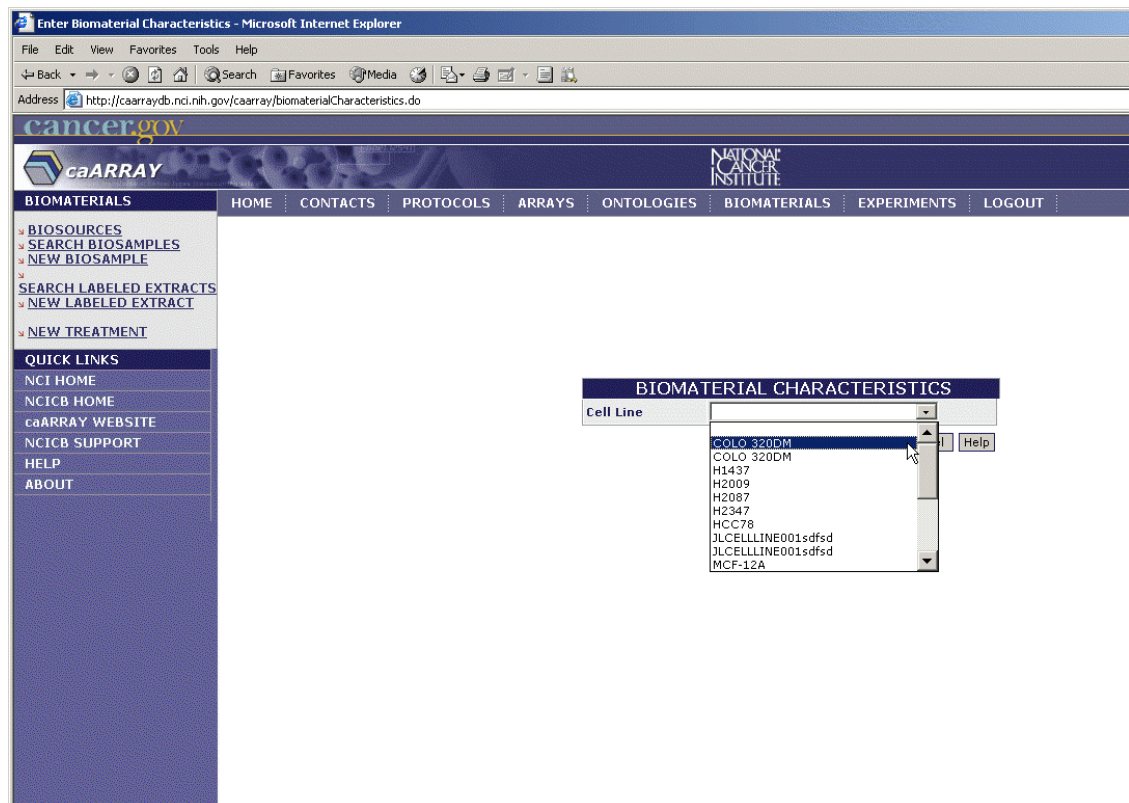
The following record was submitted:

CELL LINE DETAILS	
Cell Line Name	colo 320 HSR
Public Database	ATCC_Cultures
Database Version	
Accession Number	CCL-220
URI	<a href="http://www.atcc.org/">http://www.atcc.org/</a>

*Figure 8.14 A confirmation displays information for a newly submitted cell line*

- Click **Done**, or **Add Another** if you want to submit additional cell line terms.

In the caArray Biomaterials section, when you submit information about Biomaterial Cell Line characteristics, you will be able to see and select the **colo 320** cell line name in the drop down list, as shown in *Figure 8.15*.



*Figure 8.15 The new cell line you submitted displays among the Biomaterial Cell Line characteristics in caArray.*



# 9

## BIOMATERIALS

This chapter describes the creation, annotation, and management in caArray of biomaterial objects, the materials of biological origin used in microarray experiments.

Topics in this chapter include:

- [Overview of Biomaterials](#) on this page
- [Biomaterials Workflow](#) on page 74

### Overview of Biomaterials

---

Materials of biological origin are used in microarray experiments, and the state and characteristics of those biomaterials can be objectively documented and described. Biomaterials can be treated, labeled and used in hybridization procedures. They provide signals that indicate the presence, absence or relative expression level of specific gene products or other materials. Biomaterials are created in caArray to later be included as essential components in a caArray Experiment.

Many biomaterials' characteristics are defined in caArray by terms found in the caArray Ontologies. For more information, see [Chapter 8 Ontologies](#).

Biomaterials in caArray consist of **Biosources**, **Biosamples**, and **Labeled Extracts**, defined below and illustrated in [Figure 9.1](#) in their hierarchical relationship.

- **Biomaterial** is a comprehensive term meaning any substance of biological origin used in microarray experiments. Biomaterials can be untreated, treated and/or labeled for use in microarray experiments. *Example:* a cDNA preparation from human tumor tissue that has been treated with an anti-cancer drug.
- **Biosources** are the original source biomaterials before any treatment events. *Example:* Tissue sample or biopsy material.
- **Biosamples** are Biosources after any treatment event. *Example:* A biosource tissue treated with RNA extraction method yields the biosample, RNA.

- **Labeled Extracts** are biosamples that have been labeled for detection of the nucleic acids. *Example:* The biosample RNA is labeled with a fluorescent dye, yielding the labeled extract RNA.



Figure 9.1 Biomaterials components and their relationship in caArray

The nature of each type of biomaterial is defined in varying dialog boxes in caArray. The relevant fields for each is described in Table 9.1, Table 9.2, and Table 9.3.

The term Biosource refers specifically to original source material before it is treated. The nature of Biosources in caArray is described in Table 9.1<sup>11</sup>:

Biosource Fields		
Field	Description	Example
* <b>Biosource Name</b>	Name given to biosource sample <b>Note:</b> It is a good idea to clearly name biosources	LungSamplePatientX
<b>Description</b>	A brief description about the biosource; limited to 4000 characters	Lung sample obtained from a female patient age 65 with carcinoma using...
* <b>Material Type</b>	Controlled terms for the state of the Biosource	Nuclear RNA
* <b>Organism</b>	Documents the species from which the biosource is obtained.	<i>Homo sapiens</i>
<b>Specify New Organism</b>	Document a species <i>only if</i> the species is not in <b>Organism</b> field drop down list <b>Note:</b> Rarely needs to be user defined, as the majority of commonly used organisms are already available in the <b>Organism</b> field drop-down list.	<i>Saccharomyces cerevisiae</i>
* <b>Provider</b>	The name of the organization or individual who provided the sample	NIH Clinical Center
* <b>Biosource Type</b>	The state of the biosource when received	Fresh_sample; Blood; Paraffin_sample

Table 9.1 Fields for documenting Biosources

11. Items with an asterisk are required fields when submitting a new Biosource. See on page 76.

Biosource Fields		
Field	Description	Example
<b>Specify New Biosource Type</b>	Document a biosource type <i>only if</i> the biosource is not in the biosource type drop down list. <b>Note:</b> Rarely needs to be user defined, as a majority of the common used biosource types are already available in the <b>Biosource Type</b> field drop down list.	
<b>Visibility</b>	Defines permissions for those who can use your biosource for documentation. Options include Private, Public and designated groups. <b>Note:</b> If no option is selected for visibility, by default, <b>Private</b> is selected, meaning only the owner can view and modify the object.	Private

Table 9.1 Fields for documenting Biosources

A Biosample represents the sample obtained from the biosource after it has been processed for use in microarray experiments. The nature of Biosamples In caArray is described in Table 9.2:

Biosample Fields		
Field	Description	Example
<b>Sample Name</b>	Name given to the biosample	Lung Tumor RNA
<b>Biosource</b>	The source from which the sample was derived <b>Note:</b> If the biosource does not exist on the Biosource drop-down list, you must first submit the Biosource before you can submit the Biosample	Lung cancer biopsy_1
<b>Organism</b>	Documents the species from which the Biosample was derived	<i>Homo sapiens</i>
<b>Material Type</b>	Controlled terms for the state of the Bio-Sample.	cDNA, total RNA
<b>Visibility</b>	Defines permissions for those who can use your biosource for documentation. <b>Note:</b> Visibility of the biosample inherits the visibility of the biosource from which biosample is derived. If the visibility of the biosource is private, then the visibility of the biosample is private as well.	

Table 9.2 Fields for documenting Biosamples

A Labeled Extract is a Biosample that has been labeled with signal emitters such as fluorescent materials for nucleic acid detection. Labeled Extracts are detected by automated equipment. The nature of Labeled Extracts in caArray is described in the fields in Table 9.3:

Labeled Extract Fields		
Field	Description	Example
<b>Labeled Extract Name</b>	Name given to the Labeled Extract	Cy5-labeled lung tumor RNA
<b>Biosample</b>	The Biosample source from which the Labeled Extract was derived <b>Note:</b> If the Biosample does not exist on the Biosample drop-down list, you must first submit the Biosample before you can add the Labeled Extract	Lung_Cancer_1_RNA
<b>Organism</b>	Documents the species from which the Labeled Extract was derived	<i>Homo sapiens</i>
<b>Material Type</b>	Controlled terms for the state of the Labeled Extract.	cDNA, total RNA
<b>Visibility</b>	Defines permissions for those who can use your biosource for documentation. <b>Note:</b> Visibility of the Labeled Extract inherits the visibility of the Biosample from which Labeled Extract is derived.	Lung Cancer Consortium of the Pacific Northwest

Table 9.3 Fields for documenting Labeled Extracts

## Biomaterials Workflow

Biomaterials, which are used in microarray experiments, primarily in hybridization techniques, are created in caArray to later be included as components when caArray Experiments are created.

When working with biomaterials in caArray, it is important to complete the steps in the workflow in their suggested order, because of the dependencies between objects.

1. Search Biomaterials to determine if the following biomaterials already exist in caArray:
  - Biosource
  - Biosample related to Biosource
  - Labeled extracts related to the Biosources' Biosamples
2. If the specified biomaterial is not already in caArray, submit or add a new:
  - Biosource
  - Biosample related to a newly submitted Biosource
  - Labeled Extracts related to a newly submitted Biosample
3. Modify or delete an existing biomaterial.

## Working with Biosources

### Searching for a Biosource

To search **Biosources**, follow these steps:

1. Log in on the caArray main page.
2. At the upper left of your browser, select the **Biomaterials** task tab.
3. Click **Biosources** from the left navigation menu. The Search Biosources dialog displays in the browser (top segment of [Figure 9.2](#)).
4. Provide searchable information. You can search by using any of the following fields (defined in Table 9.1 on page 72):
  - **Material Type**
  - **Organism**
  - **Biosource Name**
  - **Biosource Type**
  - **Visibility**

**Note:** The search is case insensitive; wild cards are always implied on both side of the query string.

5. Click the **Search** button. If the biosource exists in caArray, it will display in the **Search Results** section ([Figure 9.2](#)).

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all Biosources in caArray display in the Search Results section.

SEARCH BIOSOURCES			
Material Type	<input type="text" value="All"/>	Biosource Type	<input type="text" value="All"/>
Organism	<input type="text" value="All"/>	Provider	<input type="text" value="All"/>
Biosource Name	<input type="text"/>	Visibility	<input type="text" value="All"/>
<input type="button" value="Search"/> <input type="button" value="Reset"/> <input type="button" value="Help"/> <input type="button" value="Submit New Biosource"/>			

SEARCH RESULTS				
539 items found, displaying 1 to 20. <a href="#">[First/Prev]</a> <a href="#">1</a> , <a href="#">2</a> , <a href="#">3</a> , <a href="#">4</a> , <a href="#">5</a> , <a href="#">6</a> , <a href="#">7</a> , <a href="#">8</a> <a href="#">[Next/Last]</a>				
Biosource Name	Material Type	Organism	Description	
<a href="#">100c Lung cell line_HCC78</a>	cell	Homo sapiens		
<a href="#">101 tissue Non Neoplastic Liver</a>	organism_part	Homo sapiens		
<a href="#">101c Lung cell line_H2009</a>	cell	Homo sapiens		
<a href="#">102 tissue Leiomyoma</a>	organism_part	Homo sapiens		
<a href="#">103 tissue Malignant G1 Stromal Tumor</a>	organism_part	Homo sapiens		
<a href="#">112c Lung cell line_H2347</a>	cell	Homo sapiens		
<a href="#">117 tissue Leiomyoma</a>	organism_part	Homo sapiens		
<a href="#">118 tissue Large Cell Lymphoma</a>	organism_part	Homo sapiens		
<a href="#">119 tissue Malignant G1 Stromal Tumor</a>	organism_part	Homo sapiens		
<a href="#">120 tissue Adrenal Cortical Adenoma</a>	organism_part	Homo sapiens		
<a href="#">121 tissue Stomach Adenocarcinoma</a>	organism_part	Homo sapiens		

*Figure 9.2 Biosource unrestricted search results*

- To see the details corresponding to a particular biosource, click the **Biosource** name. This opens the Biosource Details page (*Figure 9.3*).

BIOSOURCE DETAILS	
Biosource Name	76c_Lung cell line_H2347
Description	
Material Type	cell
Organism	Homo sapiens
Provider	NCI
Biosource Type	frozen_sample
Visibility	Public

BIOMATERIAL CHARACTERISTICS	
Cell Type	Epithelial

*Figure 9.3 The Biosource Details page displays information about the Biosource*

The Biosource Details page displays characteristics defined when the Biosource object was submitted to caArray. The Biomaterials characteristics display vocabulary term(s) assigned to this Biosource from the caArray Ontologies.

- To reset the form in order to try another search, click the **Reset** button.

### Submitting a Biosource

To submit/add a Biosource, follow these steps:

- Log in on the caArray main page.
- Select the **Biomaterials** task tab.
- At the upper left of your browser, select **Biosources**.
- At the bottom right of the Search Biosources form, click the **Submit New Biosource** button



5. Complete the Biosource fields, as demonstrated in [Figure 9.4](#)<sup>12</sup>. (Biosource terms are defined in Table 9.1 on page 72).

Figure 9.4 Adding a new Biosource

6. Click the **Save** button to submit the Biosource to caArray.
7. In the Biosource Details page that opens, specify the biosource characteristics by clicking the **Modify Characteristics** button.
- This opens a **Biosource Characteristics** list box where you can select one or multiple characteristics that you want associated with the Biosource you are submitting. (Many of the terms are found in the controlled vocabulary section of caArray Ontologies, while others represent static information such as age.)
8. Select one or multiple fields which are applicable: hold the CTRL key and click to select non-contiguous fields.

Figure 9.5 Biosource Characteristics dialog box

12. Items with an asterisk are required fields.

- Click **Next** to continue.

Whatever characteristics you selected in the previous dialog box become fields in the dialog that now opens (*Figure 9.6*). Some fields are drop-down lists for you to make selections from pre-defined vocabulary terms and some are text fields where you enter your own text preference(s). An example is the Temperature field. You would not do a search for temperature "37 fahrenheit", but you could enter that in a text box.

BIOMATERIAL CHARACTERISTICS	
Age	Single Age Entry <input type="text" value="32"/> years <input type="text" value=""/>
	Initial Time Point: <input type="text" value="beginning_of_stage"/>
Cell Type	<input type="text" value="Epithelial"/>
Disease State	<input type="text" value="Normal"/>
Organism Part	<input type="text" value="Prostate"/>
Sex	<input type="text" value="male"/>
Temperature	<input type="text" value="37"/>
<input type="button" value="Save"/> <input type="button" value="Cancel"/> <input type="button" value="Help"/>	

Figure 9.6 Dialog box for specifying Biosource characteristics

- Select or enter the Biomaterial Characteristics in the fields provided. Click **Save** to save your changes or click the **Cancel** button to disregard the changes.
- Back in the Biosources Details page, click **Done** to complete the submission. For further information, see *Related Help* on page 13.

## Modifying a Biosource

To modify a Biosource, follow these steps:

- Log in on the caArray main page.
- Select the **Biomaterials** task tab.
- At the upper left of your browser, click **Biosources**.
- Launch a search for the biosource you want to modify. For more information, see *Searching for a Biosource* on page 75.
- Click the **Biosource Name** in the Biosource **Search Results** section. This opens the Biosource Details page.

BIOSOURCE DETAILS	
Biosource Name	76c_Lung cell line_H2347
Description	
Material Type	cell
Organism	Homo sapiens
Provider	NCI
Biosource Type	frozen_sample
Visibility	Public
<input type="button" value="Done"/> <input type="button" value="Modify"/> <input type="button" value="Delete"/>	
BIOMATERIAL CHARACTERISTICS	
Cell Type	Epithelial
<input type="button" value="Modify Characteristics"/>	

Figure 9.7 Biosource details page

6. To modify the Biosource details, click the **Modify** button.

\* indicates a required field

UPDATE BIOSOURCE			
* Biosource Name	<input type="text" value="lung_sample_patient 47"/>		
Description	<input type="text"/>		
* Material Type	<input type="text" value="cell"/>	Specify New Type:	<input type="text"/>
* Organism	<input type="text" value="Homo sapiens"/>	Specify New Type:	<input type="text"/>
* Provider	<input type="text" value="BioDiscovery, Inc."/>		
* Biosource Type	<input type="text" value="biopsy"/>	Specify New Type:	<input type="text"/>
* Visibility	<input type="text" value="Public"/> <input type="text" value="caBIG"/> <input type="text" value="Curation Team - delete"/> <input type="text" value="Curation Team - make public"/> <input type="text" value="DC Lung Study"/> <input type="text" value="DC Prostate Study"/> <input type="text" value="GMDI_Group"/> <input type="text" value="JenLab"/> <input type="text" value="MAGE-OM API users"/> <input type="text" value="NCICB"/>		

Figure 9.8 Dialog box for modifying a Biosource object

7. The Update Biosource dialog box displays current information for the open Biosource (Figure 9.8). Modify the information according to your preference. (Each field is described in Table 9.1 on page 72.)
8. Click **Save**. This returns you to the Biosource Details page.
9. Click the **Modify Characteristics** button.
- This opens a biomaterial characteristics drop-down list where you can select one or multiple characteristics that you want associated with the Biosource you are modifying. (Many of the terms are found in the controlled vocabulary section of caArray Ontologies, while others represent static information such as age.)
10. Use CTRL + click to select multiple non-contiguous fields. Click **Next** to continue.

BIOMATERIAL CHARACTERISTICS	
Cell Line	<input type="text" value="ovarian surface epithelial cell line"/>
Generation	<input type="text"/>
Genotype	<input type="text"/>

Figure 9.9 Dialog box for specifying Biomaterial characteristics

Whatever characteristics you selected in the previous dialog box become fields in the dialog that now opens (Figure 9.9). Some fields are drop-down lists for you to make selections from pre-defined controlled vocabulary terms and some are text fields where you enter your own text preference(s).

11. Select or enter the Biomaterial Characteristics in the fields provided.
12. Click **Save** to save your changes or click the **Cancel** button to disregard the changes.

13. Back in the Biosource Details page, click **Done** when you are finished modifying the object.

**Note:** You can do this if you have the Visibility settings allowing you to modify the Biosource. If you do not, a notice displays informing you that you cannot modify the object.

## Deleting a Biosource

To delete a Biosource, follow these steps:

1. Log in on the caArray main page.
2. Select the **Biomaterials** task tab.
3. At the upper left of your browser, click the **Biosources** option.
4. Launch a search for the biomaterial you want to delete. See [Searching for a Biosource](#) on page 75 for more information.
5. In the **Search Results** section of the page, select the name of the biomaterial to be deleted.
6. On the Biosource Details page, click the **Delete** button
7. Confirm the deletion by selecting the **OK** button

- Notes:**
- You can delete a Biosource only if you have the appropriate permissions to do so. For more information, see *Visibility* on page 21. Additionally, if an experiment that uses the biosource has been submitted or published, the biosource *cannot* be deleted.
  - You must also delete all associated Biosamples and Labeled Extracts to delete a Biosource.
  - Deleting a biomaterial cannot be undone.

## Working with Biosamples

### Searching for a Biosample

To search **Biosamples**, follow these steps:

1. Log in on the caArray main page.
2. Select the **Biomaterials** task tab
3. At the upper left of your browser, select **Search Biosamples**.
4. Provide searchable information. You can search by using any of the following fields (defined in Table 9.2 on page 73):
  - **Sample Name**
  - **Biosource** (from which the Biosample is derived)
  - **Organism**
  - **Material Type**
  - **Visibility**

**Note:** The search is case insensitive; wild cards are always implied on both side of the query string.

5. Click the **Search** button

If the Biosample exists, it will display in the **Search Results** section

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all Biosamples in caArray display in the Search Results section.

6. To see the details corresponding to a particular biosample, click the **Biosample** name.
7. To reset the form in order to try another search, click the **Reset** button.

## Submitting a Biosample

There are three steps in submitting a biosample: 1) identifying the Biosource from which the Biosample is derived; 2) identifying a treatment to the Biosample; and 3) identifying a protocol describing the treatment of the Biosample.

- Notes:**
- If you have not submitted the protocol for the type of treatment you selected in the previous step, you must first submit the protocol before you can submit your Biosample (see *Submitting a New Protocol* on page 39 for more information).
  - You must also create a Biosource before you can create a Biosample.

To submit a Biosample, follow these steps:

### Step 1 – Identifying a Biosource

1. Log in on the caArray main page.
2. Select the **Biomaterials** task tab.
3. Select **New Biosample** from the left navigation menu.
4. In the **Biomaterial Treatment** dialog box that opens, enter or select the requested information as demonstrated in *Figure 9.10*. Parameters are described in Table 9.4<sup>13</sup>.

Figure 9.10 Biomaterials Treatment dialog box

<b>Submission Terms</b>	<b>Definition</b>
<b>*Select Source Biomaterial</b>	The organ or tissue source of the material

13. Items with an asterisk are required fields.

<b>Submission Terms</b>	<b>Definition</b>
<b>*Name of Resulting Biomaterial</b>	Name of the biomaterial after it has been processed.
<b>*Type of Resulting Biomaterial</b>	Type of the biomaterial after it has been processed.
<b>Description of Resulting Biomaterial</b>	Description of the biomaterial after it has been processed.

Table 9.4 Fields describing Biomaterials Treatment

- Click **Next** to continue. A new viewer opens that displays the information you have just entered (top segment of [Figure 9.11](#)).

**CREATE NEW TREATMENT**

BIOMATERIAL INFORMATION	
Source Biomaterial	118 tissue Large Cell Lymphoma
Name Of Resulting Biomaterial	lymphoma
Material Type Of Resulting Biomaterial	cell_lystate
Description Of Resulting Biomaterial	

ADD NEW TREATMENT EVENT			
* Treatment Type	<input type="text"/>		
Measurement	Value: <input type="text"/>	Unit Type:	<input type="text"/>
Compound Measurement			
Compound	<input type="text"/>	Value: <input type="text"/>	Unit Type: <input type="text"/>
			<input type="button" value="Add Compound Measurement"/>
* indicates a required field			
		<input type="button" value="Apply Protocol"/>	<input type="button" value="Add Treatment"/>
		<input type="button" value="Done"/>	

Figure 9.11 Dialog box for describing treatment of a biosample

### Step 2 – Identifying a Treatment

- In the **Add New Treatment Event** section ([Figure 9.11](#)), enter the requested information, described in Table 9.5<sup>14</sup>:

<b>Submission Terms</b>	<b>Definition</b>	<b>Example</b>
<b>*Treatment Type</b>	The type of protocol by which an input biomaterial is treated.	Incubate
<b>Measurement</b> <ul style="list-style-type: none"> <li>• Value</li> <li>• Unit type</li> </ul>	The measurement of the treatment	15 minutes
<b>Compound measurement</b> <ul style="list-style-type: none"> <li>• Compound</li> <li>• Value</li> <li>• Unit type</li> </ul>	The compound and measurement applied to the treatment	1 mmol

<sup>14</sup>Items with an asterisk are required fields.

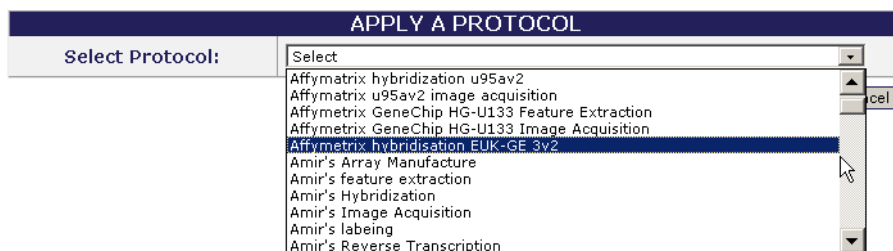
Table 9.5 Fields describing a new biomaterials treatment

**Note:** The Compound Measurement is optional. If there's no compound applied, skip to step 3. If a compound is applied, fill in the fields and click the **Add Compound Measurement** button.

### Step 3 – Identifying a Protocol

**Note:** If you have not submitted the protocol for the type of treatment you selected in the previous step, you must first do so before you can finish submitting your Biosample (see *Submitting a New Protocol* on page 39 for more information).

1. Click the **Apply Protocol** button.
2. Select the protocol for the treatment from the drop down list.



3. Click **Continue**.
4. Complete the following information
  - **Activity Date**
  - **Performer**

**Note:** Performer is a contact added in the Contact task tab. If the appropriate name is missing, you must add it in the Contacts task tab prior to completing this section. For more information, see *Submitting a New Person Contact* on page 27.

5. Click the **Add Treatment** button.
6. If there are more treatments, repeat steps 1-5. If there are no more treatments, click **Done** to submit the Biosample.

### Modifying a Biosample

To modify a Biosample, follow these steps:

1. Log in on the caArray main page.
2. Select the **Biomaterials** task tab.
3. Select **Search Biosample**, and launch the search for the Biosample you want to modify. For more information, see *Searching for a Biosample* on page 80.

- Click the **Biosample Name** in the biosample **Search Results** section. This opens the Biosample Details page (*Figure 9.12*).

BIOSAMPLE: cell line cDNA

BIOSAMPLE DETAILS	
Source Biomaterials	Ovarian surface epithelial cell line
Sample Type	complementary DNA
Description	cell line cDNA for microarray experiment
<input type="button" value="Done"/> <input type="button" value="Modify"/> <input type="button" value="Delete"/>	

BIOMATERIAL CHARACTERISTICS	
Cell Line	ovarian surface epithelial cell line
Disease State	Normal

TREATMENT 1	
Treatment Type	nucleic_acid_extraction
Measurement	

PROTOCOL APPLICATION SUMMARY	
Protocol Name	Amir's RNA Extract
Protocol Type	nucleic_acid_extraction
Activity Date	1/5/01
Performer	Amir A. Jazaeri
Measurement	
Parameters	

|

TREATMENT 2	
Treatment Type	reverse_transcription
Measurement	

PROTOCOL APPLICATION SUMMARY	
Protocol Name	Amir's Reverse Transcription
Protocol Type	reverse_transcription
Activity Date	1/5/01
Performer	Amir A. Jazaeri
Measurement	
Parameters	

|

Figure 9.12 Biosample Details page where you can modify the object

- To modify the Biosample details, click the **Modify** button below the top section of the page.
- Modify the Biosample details (defined in Table 9.2 on page 73) and click **Submit Changes** to save the changes or **Cancel** to abort the changes.
- To modify any of the treatment sections, click the corresponding **Modify Treatment** button and make the preferred changes.

**Note:** You cannot make changes in a Protocol in this section. You must open the Protocols section of caArray to modify a Protocol. For more information, see *Modifying a Protocol* on page 41.

- In each of the appropriate viewers, click the **Save** button to save the modifications, or select the **Cancel** button to disregard the changes.

**Note:** You can do this only if you have the Visibility settings allowing you to modify the Biosample. If you do not, a notice displays informing you you cannot modify the object.

## Deleting a Biosample

To delete a Biosample, follow these steps:

- Log in on the caArray main page.



2. Select the **Biomaterials** task tab.
3. Select **Search Biosample**, and launch the search for the Biosample you want to modify. For more information, see *Submitting a Biosource* on page 76..
4. Select the **Biosample Name** in the biosample search results section.
5. Click the **Delete** button
6. Confirm the delete by clicking the **OK** button.

- Notes:**
- You can delete a Biosample only if you have the appropriate permissions to do so. For more information, see *Visibility* on page 21. Additionally, if an experiment that uses the Biosample has been submitted or published, the biosource *cannot* be deleted.
  - Deleting a biosample cannot be undone.

## Working with Labeled Extracts

### Searching for a Labeled Extract

To search **Labeled extracts**, follow these steps:

1. Log in on the caArray main page.
2. Select the **Biomaterials** task tab.
3. Select **Search Labeled Extracts** from the left navigation menu
4. Provide searchable information. You can search by using any of the fields described in Table 9.3 on page 74:
  - **Labeled Extract Name**
  - **Biosample** from which it is derived
  - **Organism**
  - **Material Type**
  - **Visibility**

**Note:** The search is case insensitive; wild cards are always implied on both sides of the query string.
5. Click the **Search** button
 

If the Labeled Extract exists, it will display in the Search Results section.

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all Biosources in caArray display in the Search Results section.
6. To see the details corresponding to a particular Labeled Extract, click the **Labeled Extract** name.
7. To reset the form in order to try another search, click the **Reset** button.

### Submitting a Labeled Extract

- Notes:**
- If you have not submitted the protocol describing the procedure in which the Biosample was labeled, forming a Labeled Extract, you must do so before you

can submit a Labeled Extract (see *Submitting a New Protocol* on page 39 for more information).

- You also must have created a Biosource and Biosample before you can create a Labeled Extract.

There are two steps in submitting a Labeled Extract: 1) Identify the label of the Biosample and 2) Identify a Protocol.

To submit a Labeled Extract follow these steps:

### Step 1 – Identifying the Treatment

- Log in on the caArray main page.
- Select the **Biomaterials** task tab.
- Select **New Labeled Extract** from the left navigation menu.
- Complete the **Labeled Extract** fields as demonstrated in *Figure 9.13* and described in Table 9.6<sup>15</sup>.

The screenshot shows a web form titled "BIOMATERIAL LABEL". At the top, there is a navigation bar with tabs: PROTOCOLS, ARRAYS, ONTOLOGIES, BIOMATERIALS, EXPERIMENTS, and LOGOUT. Below the navigation bar, a note states "\* indicates a required field". The form fields are as follows:

- Name of the Resulting Labeled Extract:** Text input field containing "lung tumor RNA".
- Select a BioSample to be Labeled:** Dropdown menu.
- Treatment Type:** Text input field containing "Label".
- Label:** Dropdown menu with "Cy5" selected.
- Amount of Nucleic Acid Labeled:** Text input field containing "10" and a unit dropdown menu with "ug" selected.
- Material Type of the Resulting Labeled Extract:** Dropdown menu with "cell\_lystate" selected.
- Description of the Resulting Labeled Extract:** Text area containing "Cy5-labeled lung tumor RNA".
- Visibility:** A box containing a list of roles: "Public", "caArray Developers", "AMDEC Consortium", "ISPY Consortium", and "UAT Test".

At the bottom right of the form, there are two buttons: "Apply Protocol" and "Cancel".

Figure 9.13 Adding Biomaterial Label information

<b>Submission Terms</b>	<b>Definition</b>
*Name of Resulting Extract	Name of the biomaterial after it has been processed.
*Select a Biosample to be Labeled	Name of the Biosample from which the Labeled Extract will be derived
Treatment Type	The type of protocol by which an input biomaterial is treated.
*Label	The labeling material used for the Labeled Extract
*Amount of Nucleic Acid Labeled	Measurement of the biosample to be labeled
*Material Type of Resulting Labeled Extract	Type of the biomaterial after it has been processed to Labeled Extract

15.Items with an asterisk are required fields.

<b>Submission Terms</b>	<b>Definition</b>
Description of the Resulting Labeled Extract	Description of the Labeled Extract after it has been processed.

Table 9.6 Fields for submitting a new Labeled Extract

5. Click the **Apply Protocol** button.

### Step 2 – Identifying a Protocol

**Note:** If you have not submitted the protocol describing the procedure in which the Biosample was labeled, you must do so before you can finish submitting your Labeled Extract.

6. Select the labeling protocol from the drop down list.
7. Complete the following information:
  - **Activity Date**
  - **Performer**

**Note:** The “Performer” a Contact added in the Contact task tab. If the appropriate name is missing, you must add it in the Contacts task tab prior to completing this section. For more information, see *Submitting a New Person Contact* on page 27.

8. Click the **Save** button

### Modifying a Labeled Extract

To modify a Labeled Extract, follow these steps:

1. Log in on the caArray main page.
2. Select the **Biomaterials** task tab.
3. Select **Search Labeled Extract**.
4. Click the **Labeled Extract Name** in the Labeled Extract search results section. This opens the Labeled Extract Details page (*Figure 9.14*).

The top section of the Labeled Extract Details page includes details that were entered when the Labeled Extract was submitted to caArray. The center section of the page includes Biomaterial Characteristics, also defined when the object was submitted. The bottom section of the page displays features in the Protocol submitted to caArray that described the labeling process for the Biosample from

which the Labeled Extract was derived. This Protocol was identified when the Labeled Extract was submitted to caArray.

LABELED EXTRACT DETAILS	
Biomaterial	Ovarian adenocarcinoma BRCA2 1 cDNA
Name	cy5 labeled tumor BRCA2 1 cDNA
Description	cy5 Labeled tumor cDNA for Amir's microarray experiment.
Label	Cy5
Amount of nucleic acid labeled	4 ug
Material Type	complementary DNA
<input type="button" value="Done"/> <input type="button" value="Modify"/> <input type="button" value="Delete"/>	

BIOMATERIAL CHARACTERISTICS	
Age	71 years Initial Time Point: birth
Developmental Stage	Adult
Disease Stage	Stage IIIC
Disease State	Ovarian Adenocarcinoma
Genotype	BRCA-2
Histology	Clear cell
Individual	BRCA-2 1
Organism Part	Ovary
Organism Status	premortem
Sex	female
Tumor Grading	Grade 3

PROTOCOL			
Protocol ID:	gov.nih.nci.ncicb.caarray:Protocol:1015897536038902:1		
Activity Date:	12/22/05		
Performer:	Amir Jazaeri		
Protocol Name:	Amir's labeling		
Protocol Description:	Four micrograms of amplified RNA was reverse transcribed and directly labeled with cyanine 5-conjugated deoxyuridine 5'-triphosphate (dUTP) (tumor RNA) or cyanine 3-conjugated dUTP (IOSE RNA).		
URI:	<a href="http://www/atc.nci.nih.gov">http://www/atc.nci.nih.gov</a>		
Hardware:	NAME	MODEL	TYPE MAKE
Software:	NAME	TYPE	MANUFACTURER
Protocol Parameters:	NAME	VALUE	DEFAULT VALUE TYPE

Figure 9.14 Labeled Extract details page

5. To modify the Labeled Extract basic details (displayed in the top section), click the **Modify** button just below that section.
6. Modify the **Labeled Extract** details (defined in Table 9.3).
7. Click the **Save** button to save the modifications, or click the **Cancel** button to disregard the changes.
8. The other two sections on this page cannot be modified from this location.
  - To modify the Biomaterial Characteristics, you must return to the originating Biosource to modify its details. For more information, see *Modifying a Biosource* on page 78.
  - To modify the Protocol, you must return to the Protocols section. For more information, see *Modifying a Protocol* on page 41.
9. Click the **Done** button to save the modifications, or click the **Cancel** button to disregard the changes.

**Note:** You can do this only if you have the Visibility settings allowing you to modify the Labeled Extract. If you do not, a notice displays informing you you cannot modify the object.

## Deleting a Labeled Extract

To delete a Labeled Extract, follow these steps:

1. Log in on the caArray main page.
2. Select the **Biomaterials** task tab.
3. Select **Search Labeled Extract**.
4. Click the **Labeled Extract Name** in the **Labeled Extract Search Results** section.
5. Click the **Delete** button.
6. Confirm the deletion by clicking the **OK** button.

- Notes:**
- Only the owner of a Labeled Extract can modify or delete a Labeled Extract. For more information, see *Visibility* on page 21. Furthermore, if an experiment has been submitted or published using the Labeled Extract, the Labeled Extract object cannot be deleted.
  - Deleting a Labeled Extract cannot be undone.



# CHAPTER 10 EXPERIMENTS

This chapter describes the process for creating and working with microarray Experiments in caArray.

Topics in this chapter include:

- [Overview of an Experiment](#) on this page
- [Experiments Workflow](#) on page 92

## Overview of an Experiment

---

In this chapter, all of the objects you have created in previous chapters can now be compiled into a caArray Experiment. Note that all of these objects you now have in your caArray system can be used repeatedly.

In an Experiment, you can capture all relevant information about an Experiment. This includes general information about the experiment, such as the experimental design and experimental factors, associated publications, quality control and data processing steps, and so forth. You should complete the appropriate Contacts, Protocols, Array Designs and Arrays, Ontologies and Biomaterials sections in caArray. These annotations are required as you create a corresponding Experiment. You then upload all of the research data files related to the hybridizations performed in the Experiment, and link the sample information you submitted in the Biomaterials section to the hybridizations.

Besides the option just described to compile components into a caArray Experiment, the Experiments section of caArray also allows you to import microarray data and annotations in MAGE-ML format. In this case, you do not need to add all caArray component objects ahead of time, but you can go directly to Experiment submission of the MAGE-ML file. This, of course, requires that your MAGE-ML document be valid and that it include all the necessary annotations, as defined in MIAME.

The basic elements of a caArray Experiment are described in Table 10.1:

<b>Term</b>	<b>Definition</b>	<b>Example</b>
<b>Experiment</b>	A complete set of annotated hybridizations performed on microarrays for a common purpose.	An experiment to identify lung adenocarcinoma subtypes based on gene expression patterns (signatures).
<b>Hybridization</b>	The process of incubating one or more labeled extracts with an array.	A fluorescent-labeled cDNA extract from prostate tumor is hybridized on a custom-made 10K cDNA array.
<b>Experiment Record</b>	The (database) record which describes and identifies a microarray experiment.	Dr. James submitted a description of her experiment to caArray, and that information is now an Experiment record in the caArray database.

Table 10.1 Elements of a caArray Experiment

## Experiments Workflow

### Notes:

- There are many dependencies in this chapter which require naming objects such as Contact person(s) or organizations, Protocols, Array Designs and/or Arrays and Biomaterials for the Experiments you submit. If you have not already created these preliminary objects, you must do so before you can complete the directions in this chapter.
- In caArray, you can modify any part of your experiment at any time prior to publishing or locking the experiment. Once an experiment has been locked, however, you cannot perform any further modifications on the Experiment. Only NCICB personnel can “unlock” or otherwise modify an Experiment.

Adding an Experiment in caArray involves two main segments:

1. Creating and annotating individual microarray-related objects: people, organizations, equipment used, laboratory procedures and all supplemental data: arrays, array designs, and biomaterials.
2. Uploading the experimental research data files into the system.

When creating and managing Experiments in caArray, complete the following steps in their suggested order.

1. Search caArray to see if the Experiment has already been submitted.
2. If the Experiment does not exist, add a New Experiment.
  - a. Verify that all **Contacts, Protocols, Array Designs, Arrays, Ontologies, and Biomaterials** needed for the experiment have been submitted to caArray. See the appropriate chapters of this guide for more information.
  - b. As requested, create and/or define these elements for the new Experiment.
  - c. Complete the required and/or optimal substeps, adding such information as Experimental Factors, Quality Control steps, additional qualifiers, and so forth.
  - d. Configure the details for the hybridization file upload.



- e. Upload the hybridizations file(s).
  - f. Annotate the hybridization file(s).
3. Submit the **Experiment** into caArray.

## Searching Experiments

To find an existing **Experiment** object in caArray, follow these steps:

1. Log in on the caArray main page.
2. Select the **Experiments** task tab.
3. Select **Search Experiments** from the left navigation menu.
4. Provide searchable information. You can search by the fields listed in Table 10.2<sup>16</sup>:

<i>Submission Fields</i>	<i>Description</i>	<i>Example</i>
<b>*Experiment Name</b>	Name assigned to the Experiment	Lung Adenocarcoma 4912
<b>[Experiment] Identifier</b>	Identification label assigned to the Experiment	gov.nih.nci.ncicb.caarray:Experiment:1015897540503881:1
<b>*Visibility</b>	Visibility assigned to the query Experiment. Options include Private, Public and groups assigned Read/Modify visibility. <b>Note:</b> If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify it.	Public
<b>Principal Investigator</b>	Lead investigator for the project	Dr. Jane James, EcoTest Institute
<b>Experiment Type</b>	Descriptor of the type of the Experiment	Disease_state_design

Table 10.2 Fields for submitting Experiments

**Note:** The search is case insensitive; wild cards are always implied on both sides of the query string.

5. Click the **Search** button. If the experiment exists, it will display in the **Search Results** section.

**Note:** If you click **Search** without defining any query parameters, the search is unrestricted and all Experiments in caArray display in the Search Results section.

---

<sup>16</sup>Items with an asterisk are required fields.

6. To see the details of a particular experiment, click the experiment name. This opens the General Information page of the Experiment. (*Figure 10.1* is an example of a General Information page.)
7. To reset the form to initiate another search, click the **Reset** button.

## Submitting a New Experiment

**Note:** There are many dependencies in this chapter which require naming objects such as Contact person(s) or organizations, Protocols, Array Designs and/or Arrays and Biomaterials for the Experiments you submit. If you have not already created these preliminary objects, you must do so before you can complete the directions in this section.

Submitting an Experiment in caArray involves several sub-steps which require completing information for: **General Experiment Information, Experimental Factors, Publications, Quality Control Steps, Additional Qualifiers, Additional Data Processing, and Additional Upload Files**. One additional and essential sub-step is that for configuring and **uploading a hybridization file**. Each of these is described in this section.

To submit an experiment, follow these steps:

1. Log in on the caArray main page.
2. Select the **Experiments** task tab.
3. Select **New Experiment** from the left navigation menu.

As each of the following forms open, enter or select the appropriate information. Click **Next** as you complete each form.

## General Information

4. In the General Information form, enter or select **General Experiment** information as demonstrated in *Figure 10.1*. Parameters are described in Table 10.3<sup>17</sup>:

\* indicates a required field

NEW EXPERIMENT: GENERAL INFORMATION	
* Title	<input type="text" value="Jill's experiment"/>
* Experiment Completion Date:	<input type="text" value="01/01/05"/>
* Experiment Design Type	<input type="text" value="cellular_modification_design"/> <input type="text" value="cellular_process_design"/> <input type="text" value="cell_cycle_design"/> <input type="text" value="cell_type_comparison_design"/> <input type="text" value="circadian_rhythm_design"/> Other <input type="text"/>
Visibility	<input type="text" value="Public"/> <input type="text" value="caBIG"/> <input type="text" value="Curation Team - delete"/> <input type="text" value="Curation Team - make public"/> <input type="text" value="DC Lung Study"/> <input type="text" value="DC Prostate Study"/> <input type="text" value="GMDI_Group"/> <input type="text" value="JenLab"/> <input type="text" value="MAGE-OM API users"/> <input type="text" value="NCICB"/>
Note: If you do not select any item from the visibility list, it means the visibility of this experiment is private. Hold CTRL key and click the item to deselect it.	
Description/Goal of the experiment	<input type="text" value="Enter a description of the Experiment in this text box."/>
Principal Investigator	<input type="text" value="Jill B. Hadfield"/> If the person you would like to select is not listed, you can add this person to the caArray database ( <a href="#">How?</a> ).
Contact Person	<input type="text" value="please select Contact Person"/> If the person you would like to select is not listed, you can add this person to the caArray database ( <a href="#">How?</a> ).
* Number of Experimental Factors	<input type="text" value="2"/>

Figure 10.1 Adding New Experiment General Information

Submission Fields	Description
*Title	Assign a name to the Experiment.
*Experiment Completion Date	Enter the date the experiment was completed.
*Experiment Design Type	Select the type of the experimental design
*Visibility	Visibility assigned to the query Experiment. Options include <b>Private</b> , <b>Public</b> and groups assigned <b>Read/Modify</b> visibility. <b>Note:</b> If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify it.
Description/Goal of the Experiment	Enter text description of the Experiment.
Principal Investigator	Select the lead investigator for the Experiment
Contact Person	Select the person who can be contacted for information; this can be the same as the PI.

17. Items with an asterisk are required fields.

<b>Submission Fields</b>	<b>Description</b>
<b>*Number of Experimental Factors</b>	Enter the number of experimental factors (the factors in the study that are experimental parameters or regarded as influencing the experimental results.)

Table 10.3 General Experiment fields

5. Click **Next** to continue.

### Experimental Factors

1. Document the Experimental Factors by completing the fields demonstrated in [Figure 10.2](#) and described in [Table 10.4](#)<sup>18</sup>. The number of experimental factors that you enter must equal the number of experimental factors you indicated in the last field in [Figure 10.1](#).

**Note:** You can add only one value for each Experimental Factor. Other values can be added later.

NEW EXPERIMENT: EXPERIMENTAL FACTORS				
#	Factor Name	* Factor Type	Scale	Factor Value
1	<input type="text" value="time interval"/>	<input type="text" value="timepoint (Action)"/>	<input type="text" value="linear_scale"/>	<input type="text" value="1 hour"/>
2	<input type="text" value="tissue type"/>	<input type="text" value="tumor_grading (BioMaterialCharacteristicCategory)"/>	<input type="text" value="unscaled"/>	<input type="text" value="normal"/>

Figure 10.2 Entering Experiment Experimental Factors

<b>Submission Fields</b>	<b>Description</b>
<b>Factor Name</b>	Assign a name to each Experimental Factor.
<b>*Factor Type</b>	Type of experimental factor
<b>Scale</b>	The scale used to represent the value
<b>Factor Value</b>	The value of an experimental factor

Table 10.4 Experimental factors fields

### Other Submission Factors

The General Experiment page displays again, a portion of which is shown in [Figure 10.3](#). Different sections of the page allow you to list and define other submission factors which must be added for the Experiment you plan to submit. Each of these parameters is described in [Table 10.5](#).

<sup>18</sup>Items with an asterisk are required fields.

1. Continue to click **Next** as you finish each window described in the following sections.

ADDITIONAL DATA PROCESSING (DERIVED MEASUREMENTS)				
#	DataTransformation Protocol	Protocol Description	Uploaded files	Action
<a href="#">Add More</a>				

ADDITIONAL UPLOADED FILES			
#	File	Description	Action
<a href="#">Upload More</a>			

MAGE-ML DOWNLOAD
Warning: Generating MAGEML can take from a few minutes up to days depending how much data this experiment has. Usually, uploaded hybridization data accounts for most of an experiment's data.
<a href="#">Generate MAGE-ML</a>

EXPERIMENTAL FACTORS/VARIABLES				
Factor	Factor Type	Scale	Factor Value	Actions
time interval	timepoint	linear_scale	<input type="text"/>	<a href="#">Add</a> <a href="#">Modify</a> <a href="#">Remove</a>
tissue type	Lung	unscaled	<input type="text"/>	<a href="#">Add</a> <a href="#">Modify</a> <a href="#">Remove</a>
<a href="#">Add A New Factor</a>				

PUBLICATIONS				
PubMed ID	Title	Authors	Publication	Actions
<a href="#">Add A New Publication</a>				

QUALITY CONTROL STEPS DESCRIPTION
<a href="#">Add Quality Control</a>

ADDITIONAL QUALIFIERS			
Qualifier name:	Value:	Source	Actions
<a href="#">Add A New Qualifier</a>			

Figure 10.3 Other submission factors must be defined for the Experiment

<b>Submission Factors</b>	<b>Description</b>	<b>Action(s)</b>
<b>Additional Data Processing</b>	Document additional processing of the data such as derived measurements	Click the <b>Add More</b> hyperlink. Fill in the fields and browse for the file to be uploaded. Click <b>Next</b> to continue.
<b>Additional Uploaded Files</b>	Document additional uploaded files.	Click <b>Upload More</b> hyperlink.
<b>MAGE-ML Download</b>	Generates a MAGE-ML Experiment file from the current file	Click <b>Generate MAGE-ML</b> .
<b>Experimental Factors/Variables</b>	Displays factors you just added to the Experiment (see page 96).	Enter additional values for Experimental Factors you defined in the previous step.
<b>Publications</b>	Publication pertinent to the Experiment	Click <b>Add a New Publication</b> .
<b>Quality Control Steps Description</b>	Document quality control steps taken in the Experiment	Click the <b>Add Quality Control</b> hyperlink.
<b>Additional Qualifiers</b>	Document any Additional Qualifiers.	Click the <b>Add New Qualifier</b> Hyperlink.

Table 10.5 Other Factors for an Experiment

- For each section of the page, click **Add {information type}**.
- Enter or select the information, as appropriate. Click the **Save** button between each action, as relevant.

### Uploading a Hybridization File

**Note:** All caArray objects requested in this section must have been created earlier in caArray. If that has not been done, you can go back to the appropriate sections in caArray and create them. During this data upload, you will identify the appropriate objects and associate them with this Experiment. You will add all supplemental information and link everything together in the Experiment you are submitting.

Configuring the hybridization file upload is a fairly involved procedure. During this process, you will be asked to select or define objects or parameters described in Table 10.6.

<b>Hybridization Parameters</b>	<b>Description</b>	<b>Example</b>
<b>Array Design</b>	Information describing the microarray design	hg-u133a
<b>Number of Channels</b>	Number of channels for hybridization	single
<b>Hybridization File Type</b>	Type of software used to generate the hybridization file.	Affymetrix
<b>Array Template</b>	Array created in Arrays chapter from which copies are made for hybridization files	ATC_Jane_BC
<b>Labeled Extract Template</b>	Labeled extract created in Biomaterials chapter, from which copies are made for hybridization files	Cy5_ATC_Jane_BC
<b>Spike Control Template</b>	Labeled extract for detecting spike control (optional object); created in the Biomaterials chapter, from which copies are made for hybridization files	cRNA_BioB
<b>Hybridization Protocol</b>	Protocol describing how the hybridization was carried out; created in Protocol chapter	Hg-u133 Hybridization Protocol
<b>Activity Date</b>	Date on which the protocol was carried out	01/01/05
<b>Performer</b>	Name of person who performed the activity	Dr. Sally Toe

<b>Hybridization Parameters</b>	<b>Description</b>	<b>Example</b>
<b>Image Acquisition Protocol (Not required)</b>	Protocol describing how the image of hybridization was acquired; created in Protocol chapter	Hg-u133 Hybridization Protocol
<b>Feature Extraction Protocol (Not required)</b>	Protocol describing how the intensity of hybridization for each feature was extracted; created in Protocol chapter	Hg-u133 Feature Extraction Protocol

Table 10.6 Hybridization Parameters for Hybridization Upload

1. Click the **Upload Files** link in the **Hybridization File Upload** section (the third section) of the General Information page.

Experiment: Test experiment

GENERAL EXPERIMENT INFORMATION	
Title:	Test experiment
Identifier:	gov.nih.nci.ncicb.caarray:Experiment:1015897589684623:1
Experiment Date:	1/5/05
Experiment Design Type	cell_cycle_design,
Visibility	private
Description/Goal of the experiment:	

Done Lock Modify Delete Help

CONTACTS	
Principal Investigator:	
Contact Person:	

Modify Help

HYBRIDIZATION FILE UPLOAD	
View and Annotate Uploaded Files	<b>Upload Files</b>

Hybridization Files Batch Download

Help

Figure 10.4 Click Upload Files (circled) to begin loading hybridization files

2. In the dialog boxes that open, you must start selecting information. Click **Next** to move between each viewer in the following steps.

\* indicates a required field

COMMON HYBRIDIZATION INFORMATION (file upload)	
* Array Design:	hg-u133a
* Number of Channels:	Single
* Hybridization File Type	Affymetrix

Next Cancel Help

Figure 10.5 Entering common hybridization information

3. In the Common Hybridization Information dialog box (Figure 10.5), select the following information:
  - **Array Design** to be associated with this Experiment. (The drop-down menu lists all Array Designs that have been created in caArray.)

- The **Number of Channels** used for the microarray procedure.
- The **Hybridization File Type**.

Make sure that the information you select matches your other selections. For instance, in [Figure 10.5](#) the Array Design selected is an Affymetrix chip. Affymetrix chips are always single channel.

When you click **Next** in this dialog box, proceeding to the next dialog box is fairly slow.

The next dialog box that opens allows you to define information about the Array object and Labeled Extract to be associated with this Experiment ([Figure 10.6](#)). Options listed here are those that use the Array Design you just selected, in this case, hg u133a.

COMMON HYBRIDIZATION INFORMATION		
Array Design:	hg-u133a	
Number of Channels:	1	
Hybridization File Type:	Affymetrix	

\* indicates a required field

HYBRIDIZATION(FILE UPLOADS)		
Array Identifier Template	Labeled Extract Template	Factor Values
Mof Cells 102_dobbin615	* Extract: cy5 labeled tumor sporadic 100 cDNA	time interval: 1 hour
	Spiked Control: Select Control	tissue type: normal

Next Cancel Help

Figure 10.6 Associating the Labeled Extract and Spiked Control with the Array Design

- Select the following in this dialog box<sup>19</sup>:
  - Array Identifier Template
  - \*[Labeled] Extract Template
  - Spiked Control
  - Factor Values

<sup>19</sup>Items with an asterisk are required fields.



The Array Identifier, Labeled Extract and Spiked Control options you select in [Figure 10.6](#) actually become templates. Because one usually uses the same Array, Labeled Extract and Spiked Control with a selected Array Design, caArray has a copy feature: if you upload 10 hybridization files with the same Array Design (described in [Step 10](#) on page 104), caArray makes 10 copies of the same Array, Labeled Extract and Spiked Control you designated for that Array Design and applies them to each uploaded file. There is, then, no need to identify separately an Array, a Labeled Extract and Spiked Control for each hybridization file to be uploaded.

The Labeling convention for the copies is as follows:

*Array Identifier*

- [Array Identifier Template] + Ascending ID #

*Labeled Extract (same with associated Biosample and Biosource)*

- [Labeled Extract Template Name] + L + Hybridization File Name

*Spiked Control (same with associated Biosample and Biosource)*

- [Spiked Control Template Name] + S + Hybridization File Name

5. In the next dialog box that opens ([Figure 10.7](#)), select the hybridization protocol you created in caArray that corresponds to this Experiment you are submitting.

COMMON HYBRIDIZATION INFORMATION	
Array Design:	hg-u133a
Number of Channels:	1
Hybridization File Type:	Affymetrix
Array Group Template Name:	Mof Cells 102_dobbin615
Hybridization Protocol:	<div style="border: 1px solid black; padding: 2px;"> <span style="border: 1px solid black; display: inline-block; width: 150px; height: 15px; vertical-align: middle;">Affymetrix hybridization u95av2</span> </div> <p>If the protocol you would like to select is not listed, you can add this protocol to the caArray database (<a href="#">How?</a>).</p>
<input type="button" value="Next"/> <input type="button" value="Cancel"/> <input type="button" value="Help"/>	

*Figure 10.7 Selecting a Hybridization Protocol*

6. In the next dialog box (*Figure 10.8*), enter the **Activity Date** and the **Performer** (the person who performed the hybridization).

COMMON HYBRIDIZATION INFORMATION				
Array Design:	hg-u133a			
Number of Channels:	1			
Hybridization File Type:	Affymetrix			
Array Group Template Name:	Mof Cells 102_dobbin615			
Hybridization Protocol:	Jill's If the protocol you would like to select is not listed, you can add this protocol to the caArray database ( <a href="#">How?</a> ).			
* indicates a required field				
PROTOCOL				
Protocol ID:	gov.nih.nci.ncicb.caarray:Protocol:1015897583631207:1			
* Activity Date:	01/01/05			
* Performer:	Jill B. Hadfield			
Protocol Name:	Jill's			
Protocol Description:				
URI:				
Protocol Parameters:	<table border="1"> <thead> <tr> <th>NAME</th> <th>VALUE</th> <th>TYPE</th> </tr> </thead> <tbody> </tbody> </table>	NAME	VALUE	TYPE
NAME	VALUE	TYPE		
<input type="button" value="Next"/> <input type="button" value="Cancel"/> <input type="button" value="Help"/>				

*Figure 10.8 Hybridization Protocol Information*

7. In the next two dialog boxes (Example in *Figure 10.9*), select the Image Acquisition Protocol (IAP) and the Feature Extraction Protocol (FEP). (These have to have been entered in the caArray Protocol section.) Neither of these two protocols are required in your Experiment, so click **Next** to move beyond these pages, if you choose.

**Note:** Remember that hardware and software can be associated when creating a protocol. In both IAPs and FEPs, it is necessary that the software used (the software manufacturer) match the Hybridization File Type selected for the protocol to show up in the dropbox. For example, if a Affymetrix Hybridization File Type is being submitted, it is necessary for the IAP and FEP to have a Software Association with a Software Manufacturer of Affymetrix.

- a. If you select an IAP, you must enter the Activity Date and the Performer.
- b. If you select an FEP, you must enter the Activity Date and the Performer.

\* indicates a required field

PROTOCOL																							
Protocol ID:	gov.nih.nci.ncicb.caarray:Protocol:1015897549070020:1																						
* Activity Date:	<input type="text"/>																						
* Performer:	<input type="text"/>																						
Protocol Name:	Affymatrix u95av2 image acquisition																						
Protocol Description:																							
URI:																							
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Version	<input type="text"/>																						
NAME	TYPE	MANUFACTURER	PARAMETERS																				
Microarray Suite 5.0 image	image_acquisition_software	Affymatrix	<input type="text"/> <input type="text"/> <input type="text"/>																				

Next Cancel Help

Figure 10.9 Defining information for an Image Acquisition Protocol

- Once you have gone through the IAP and FEP dialog boxes, when you click **Next**, the Java Applet is initiated. The security dialog box opens where you verify the running of the applet (Figure 10.10).

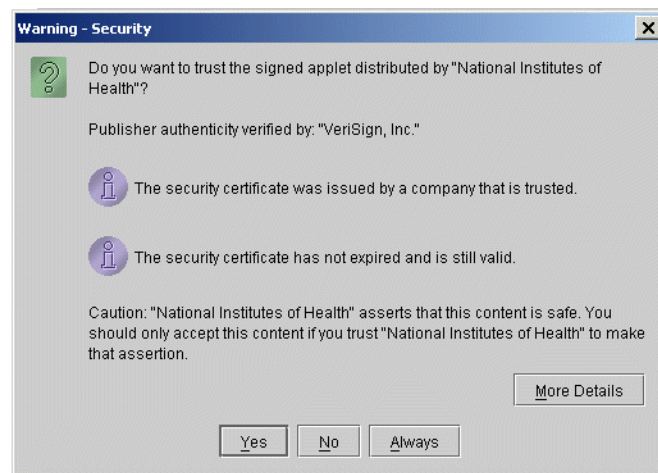


Figure 10.10 Java Applet security dialog box

- Click **Yes**.

**Note:** If you don't have the proper Java Runtime Environment (JRE) installed on your computer, (in caArray, JRE 1.42.06) you will be prompted to install it. After you click **Yes**, follow the installation steps. This takes several minutes.

At this point, a screen opens that looks much like an FTP site dialog box (Figure 10.11). The left side lists the entire directory structure of your local computer, including shared drives that you may have mapped. This is where you will

select the data files to be uploaded into caArray. As you select the files, you will move their identifiers to the right panel, **Selected Files**, in the dialog box.

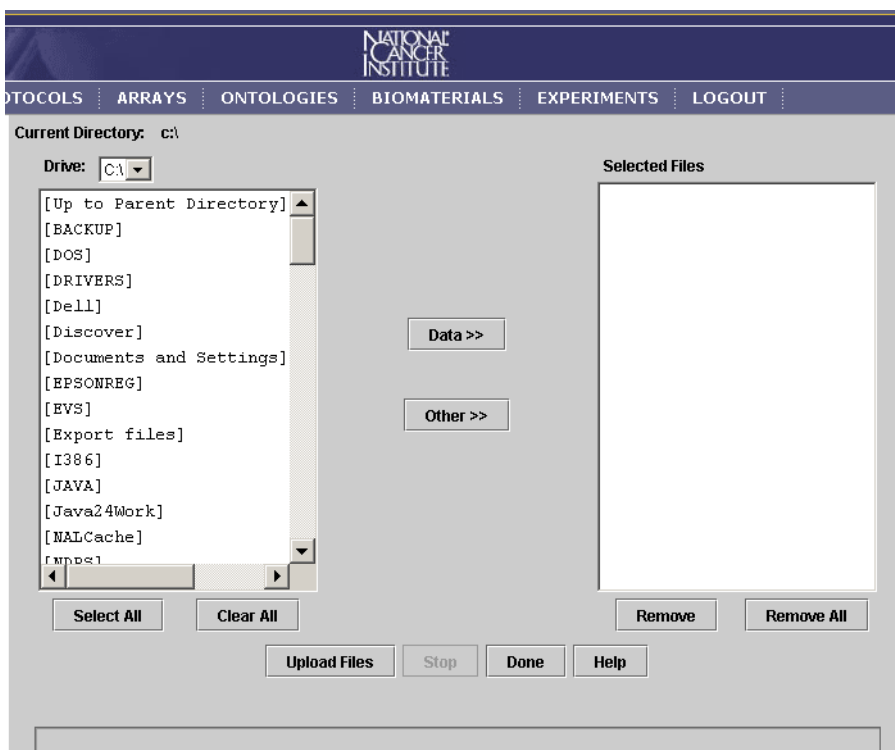


Figure 10.11 File upload applet

10. Click the **Drive:** down arrow to navigate to the drive and directory where your hybridization files are stored. The files you plan to upload can have one of two different tags applied to them:
  - Raw data files should be selected using the **Data>>** button. This will move the files over to the **Selected Files** panel. These files will be parsed into the caArray database where the expression values will be accessible from other data analysis applications.
  - All other supplemental files should be selected using the **Other>>** button. These files will also be moved over to the **Selected Files** panel. These files are just uploaded into the caArray file system and are not parsed into the database.

As you move these files, an intercept opens showing what characters are not acceptable in file titles; it indicates that they will be replaced with an underscore (\_).

11. Click **Upload Files** in the same viewer.

A Confirmation dialog opens to make sure the hybridization data files you selected are correctly associated with the Array Design file you specified in this process (Figure 10.12). If they are not compatible with the Array Design you

specified, the files will not be parsed and you will receive an email saying “File not parsable.”

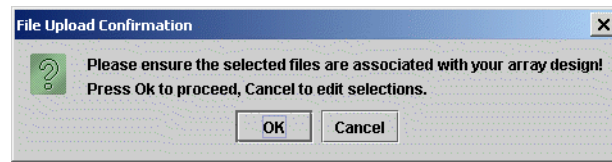


Figure 10.12 File Upload Confirmation dialog

12. Click **OK** to start the uploading. Be patient, as the process may take a while. The files are loaded to the caArray backend.

An Upload Summary dialog box opens, reporting the Upload time and total amount of information sent (Figure 10.13). If the file(s) upload fails, that is noted in the **Files Failed** section of the dialog box.

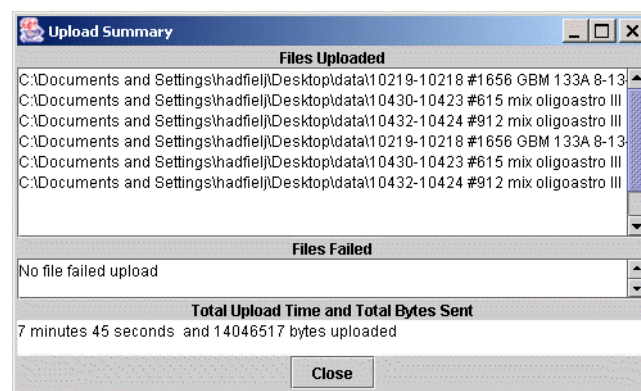


Figure 10.13 Summary dialog box reporting a successful data upload

Additionally, the caArray system sends an email reporting the success or failure of the file upload and subsequent parsing (Figure 10.14).

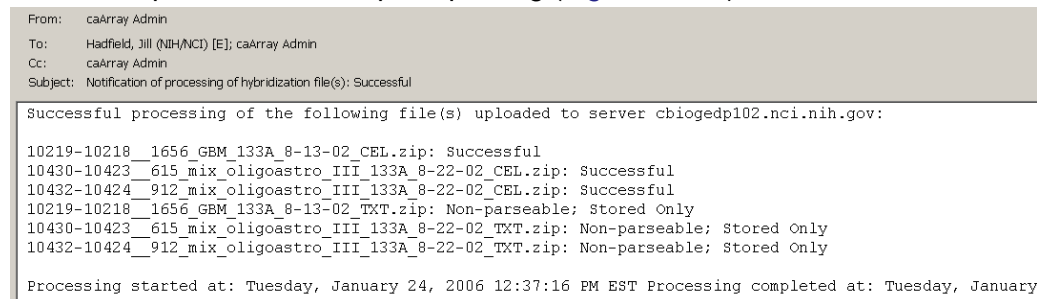


Figure 10.14 Email reporting a successful data upload and parsing of files

**Note:** Wait until you get an e-mail response with the result of the processing of the uploaded files before attempting to access those files.

### Viewing and Modifying Uploaded Hybridization Files Annotations

Because the array and biomaterials associated with each hybridization file are generic templates created prior to uploading, you may need to modify some of them (arrays, biomaterials and/or factor values) if their information varies from the information in the template.

Once you have received an email verifying a successful upload of the files, you can locate and annotate the files.

To annotate each hybridization file, follow these steps:

1. Search for the experiment you'd like to annotate, as described in *Searching Experiments* on page 93.
2. Click on the Experiment to be annotated.
3. In the Hybridization File Upload section of the Experiment Details page, click **View and Annotate Uploaded Files** (*Figure 10.15*).

Title:	Test experiment
Identifier:	gov.nih.nci.ncicb.caarray:Experiment:1015897589684623:1
Experiment Date:	1/5/05
Experiment Design Type	cell_cycle_design,
Visibility	private
Description/Goal of the experiment:	

---

**CONTACTS**

Principal Investigator:	
Contact Person:	

---

**HYBRIDIZATION FILE UPLOAD**

[View and Annotate Uploaded Files](#) | [Upload Files](#)

---

**Hybridization Files Batch Download**

Figure 10.15 Click View and Annotate Uploaded [Hybridization Files] link to annotate files

4. Click the **Annotate** link under the **Action** column of the hybridization you would like to update (*Figure 10.16*).

GENERAL EXPERIMENT INFORMATION	
Title:	Don's Experiment
Identifier:	gov.nih.nci.ncicb.caarray:Experiment:1015897583631001:1
Experiment Date:	1/1/01
Experiment Design Type	clinical_history_design, behavioral_design_type, behavior_design, cellular_modification_design, circadian_rhythm_design, disease_state_design, cell_type_comparison_design, dose_response_design, genetic_modification_design, genotyping_design
Visibility	private
Description/Goal of the experiment:	

Hybridization Files to Annotate					
File Name	File Type	Upload Date	Parsing Status	Action	
10219-10218__1656_GBM_133A_8-13-02_CEL.zip	Affymetrix	12/14/05	Successful	<a href="#">Annotate</a>	<a href="#">Delete</a>
10430-10423__615_mix_oligoastro_III_133A_8-22-02_CEL.zip	Affymetrix	12/14/05	Successful	<a href="#">Annotate</a>	<a href="#">Delete</a>
10432-10424__912_mix_oligoastro_III_133A_8-22-02_CEL.zip	Affymetrix	12/14/05	Successful	<a href="#">Annotate</a>	<a href="#">Delete</a>
10219-10218__1656_GBM_133A_8-13-02_TXT.zip	Other	12/14/05	Successful	<a href="#">Annotate</a>	<a href="#">Delete</a>

Figure 10.16 Annotate link for updating hybridization file annotations

5. To change the Array annotation, click the array name under the **Array Identifier** column (*Figure 10.17*).

HYBRIDIZATION FILE ANNOTATION			
File Names	Array Identifier	Biomaterials	Factor
10219-10218_1656_GBM_133A_8-13-02_CEL.zip	<a href="#">caArray Generated Array/Group</a>	Extract: DSLABELEXTRACT001 L 10219-10218_1656_GBM_133A_8-13-02 Spiked Control: N/A	Tissue Type Time Int

Figure 10.17 Hybridization File Annotation dialog for modifying annotations

6. Modify the array as described in *Modifying an Array* on page 55.
7. To change the Labeled Extract or Spiked Control annotation(s), click the name of the Labeled Extract or Spiked Control under the **Biomaterials** column.
8. Select the **Biomaterials** to modify from the drop-down list.
9. Modify the appropriate Biomaterial as described in [Chapter 9 Biomaterials](#).
10. To change any of the Factor Values, select the **Factor Value** for the hybridization file from the **Factor Names/Values** column.
11. Click **Save** to continue.
12. Click **Done** when you complete the annotation modifications.

**Note:**

## Modifying an Experiment

To modify an Experiment follow these steps:

1. Log in on the caArray main page.
2. Select the **Experiments** task tab.
3. Select **Search/Modify**.
4. Search for the experiment you want to modify.

- Click the **Experiment Name** in the experiment **Search Results** section.

ADDITIONAL DATA PROCESSING (DERIVED MEASUREMENTS)				
#	Data Transformation Protocol	Protocol Description	Uploaded files	Action
<a href="#">Add More</a>				

ADDITIONAL UPLOADED FILES			
#	File	Description	Action
<a href="#">Upload More</a>			

MAGE-ML DOWNLOAD	
Warning: Generating MAGEML can take from a few minutes up to days depending how much data this experiment has. Usually, uploaded hybridization data accounts for most of an experiment's data.	
<a href="#">Generate MAGE-ML</a>	

EXPERIMENTAL FACTORS/VARIABLES				
Factor	Factor Type	Scale	Factor Value	Actions
time interval	timepoint	linear_scale	<input type="text"/>	<a href="#">Add</a> <a href="#">Modify</a> <a href="#">Remove</a>
tissue type	Lung	unscaled	<input type="text"/>	<a href="#">Add</a> <a href="#">Modify</a> <a href="#">Remove</a>
<a href="#">Add A New Factor</a>				

PUBLICATIONS				
PubMed ID	Title	Authors	Publication	Actions
<a href="#">Add A New Publication</a>				

QUALITY CONTROL STEPS DESCRIPTION	
<a href="#">Add Quality Control</a>	

ADDITIONAL QUALIFIERS			
Qualifier name:	Value:	Source	Actions
<a href="#">Add A New Qualifier</a>			

Figure 10.18 Section of General Experiment page for modifying an Experiment

Nearly every section of the General Experiment Information page that opens ([Figure 10.18](#)) allows you to modify or add information: contacts, uploading more files, adding data processing and experimental factors information, new publications, quality control and qualifiers information. Click the appropriate button that allows you to modify or add information.

- For more information about each section, return to the corresponding directions in the previous section, *Submitting a New Experiment* on page 94.
- Modify the experiment details appropriately.
- Select the **Save** button to save the modifications, or select the **Cancel** button to disregard the changes.

**Note:** You can do this if you have the Visibility settings allowing you to modify the Experiment. If you do not, a notice displays informing you you cannot modify the object.

## Deleting an Experiment

To delete an Experiment, follow these steps:

- Log in on the caArray main page.
- Select the **Experiments** task tab.
- Select **Search/Modify** and launch the search for the Experiment you want to modify. For more information, see *Searching Experiments* on page 93.



4. Click the Experiment name in the Experiments **Search Results** section.
5. When the Experiment Details page opens, click **Delete** at the bottom right of the first section of the General Experiment Information section.
6. Confirm the delete by clicking the **OK** button.

- Notes:**
- Only the owner of an Experiment can delete the Experiment.
  - Deleting an Experiment cannot be undone.

## Generating MAGE-ML File from an Experiment

---

Once an Experiment has been submitted, you can create a MAGE-ML-compliant file from the caArray Experiment.

1. Log in on the caArray main page.
2. Select the **Experiments** task tab.
3. Select **Search/Modify** and launch the search for the Experiment for which you want to generate the MAGE-ML file. For more information, see *Searching Experiments* on page 93.
4. Click the Experiment name.
5. Click the **Generate MAGE ML** button to generate a MAGE file.

**Note:** If you modify your experiment after you create this file, the update will not be reflected in the MAGE-ML. To update the MAGE-ML document, you must generate MAGE-ML again to reflect the modifications made.

## Importing MAGE-ML File

---

**Note:** This functionality of ca Array is inactivated in version 1.3.1. It will be reactivated in caArray 1.4.

As an option to creating an Experiment in caArray, you can import a MAGE-ML file into caArray. You needn't associate caArray objects with this file because a MAGE-ML file in XML format represents an entire experiment adequately annotated with all relevant information.

**Note:** caArray supports only MAGE-ML files that are EBI-compliant.

To Import MAGE-ML follow these steps:

1. Log in on the caArray main page.
2. Select the **Experiments** task tab.
3. Select **Import MAGE-ML** from the left navigation menu.
4. Navigate to the MAGE-ML file, using the **Browse** Button.
5. Enter any additional information about the imported MAGE-ML file in the **Message for Curator** section.
6. Click **Upload** to add the MAGE-ML file to your experiment documentation.



## APPENDIX

# 1

## CAARRAY GLOSSARY

Acronyms, objects, tools and other terms referred to in the chapters or appendixes of this caArray User's Guide are described in this glossary.

<i>Term</i>	<i>Definition</i>
caBIG	cancer Biomedical Informatics Grid
caBIO	Cancer Bioinformatics Infrastructure Objects
caCORE	cancer Common Ontologic Representation Environment
caDSR	Cancer Data Standards Repository
caMOD	Cancer Models Database
CGH	Comparative Genomic Hybridization
EBI	European Bioinformatics Institute
EVS	Enterprise Vocabulary Services
MAGE 1.1	MAGE 1.1 is a widely-used microarray data standard or guideline
MAGE-ML software format	XML-based standard for representation of microarray data
MIAME 1.1	MIAME1.1. is a standard or guideline for the minimum amount of information required to make a microarray record useful to others.
MGED Ontology	MGED Ontology is a controlled vocabulary standard that concisely defines terms as they relate to Microarrays and caArray as a whole
MGED	Microarray Gene Expression Data Society
MMHCC	Mouse Models of Human Cancers Consortium
NCI	National Cancer Institute
NCICB	National Cancer Institute Center for Bioinformatics
URI	Uniform Resource Identifier
URL	Uniform Resource Locators

<b>Term</b>	<b>Definition</b>
XML	Extensible Markup Language ( <a href="http://www.w3.org/TR/REC-xml/">http://www.w3.org/TR/REC-xml/</a> ) - XML is a subset of Standard Generalized Markup Language (SGML). Its goal is to enable generic SGML to be served, received, and processed on the Web in the way that is now possible with HTML. XML has been designed for ease of implementation and for interoperability with both SGML and HTML

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