

CAARRAY 1.6

User's Guide



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USING THE CAARRAY USER'S GUIDE

This chapter introduces you to the *caArray 1.6 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
- [User's Manual Text Conventions](#) on page 2

Introduction to the caArray User's Guide

The *caArray 1.6 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

The *caArray 1.6 User's Guide* contains the following chapters:

Chapter 1 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 2 Getting Started in caArray—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 3 User Account Management—This chapter describes how to create and manage user accounts in caArray.

Chapter 4 Contacts—This chapter describes the process for creating and working with Contacts, namely individual and group contacts in caArray.

Chapter 5 Protocols—This chapter details instructions for creating and working with Protocols in caArray.

Chapter 6 Arrays and Array Designs—This chapter provides information about creating and working with Array Design models as well as Array objects in caArray.

Chapter 7 Controlled Vocabulary Terms—This chapter describes the means for accessing, using and adding standardized terms from Internet sources in the Controlled Vocabulary Terms section in caArray

Chapter 8 Biological Source Materials—This chapter describes the creation, annotation, and management of biological source materials in caArray.

Chapter 9 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.

User's Manual Text Conventions

Table 2.1 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.

Convention	Description	Example
Bold & Capitalized Command Capitalized command > Capitalized command	Indicates a Menu command Indicates Sequential Menu commands	Admin > Refresh
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
Boldface type	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 Open button.
<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>

Table 2.1 caArray Guide Text Conventions

Convention	Description	Example
Note:	Highlights a concept of particular interest	Note: This concept is used throughout the installation manual.
Warning!	Highlights information of which you should be particularly aware.	Warning! 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 2.1 caArray Guide Text Conventions (Continued)

CHAPTER 1

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 this page
- [caArray Workflow](#) on page 7

caArray Overview

caArray is a data portal 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. caArray consists of a database and database repository and web-based data annotation forms.

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

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: <https://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: https://cabig.nci.nih.gov/workspaces/VCDE/Documents/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

Important! Because there are dependencies between models of information in caArray that comprise an Experiment, it is important that you create objects in caArray in the order discussed and displayed in this section shown in *Figure 1.1* If you do not do so, as you create an Experiment, you may find yourself thwarted by lack of a previously defined data element, and required to abandon partially filled out screens to work backwards.

Follow the numbered steps to create the listed objects. Chapters in this caArray User’s Guideonline help correspond to each of these headings:

Contacts

1. Create Organization--manufacturer of equipment, etc.
2. Create People associated with an experiment such as a Principal Investigator (PI), manufacturer of equipment, etc.

Protocols

3. Create Protocol Hardware associated with experiment.
4. Create Protocol Software associated with experiment.
5. Create Protocol including standard operating procedures (SOPs) and/or steps involved in extracting or labeling biomaterials, hybridizations, and so forth.

Array Designs and Arrays

6. Create Array Designs, details outlining the microarray chip design and utilization.

Controlled Vocabulary Terms

7. Identify controlled vocabulary terms used in caArray to annotate biomaterials.

Biological Source Materials

8. Create Source Materials, Sample Extracts, and Labeled Extracts--materials of biological origin used in microarray experiments

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.

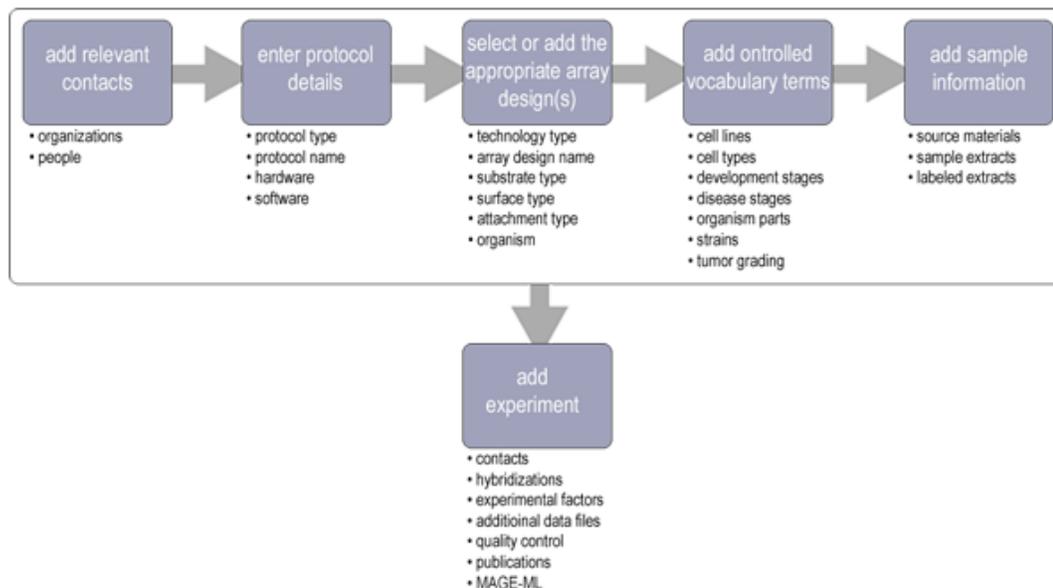


Figure 1.1 caArray Workflow. Each step in the workflow is described in its text and also serves as a hypertext link to a corresponding caArray viewer. Some steps in the workflow have dependencies on previous tasks. They are described, where appropriate, in this user's guide.

CHAPTER 2

GETTING STARTED IN CAARRAY

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
- *Requesting a User Account* on page 13
- *Using caArray Online Help* on page 14
- *Navigating through the caArray Workflow* on page 17
- *The caArray Interface* on page 17
- *Access to Public Data in caArray Before Login* on page 18
- *Elements of the caArray Viewer* on page 18

Launching caArray

Note: Internet Explorer 6.0 is the supported platform for caArray 1.6. If you have questions about this, contact NCICB Application Support, <http://ncicbsupport.nci.nih.gov/sw/>.

The caArray application can be accessed in two ways:

1. Use this URL to go directly to the caArray login page at NCICB: <https://caarraydb.nci.nih.gov/caarray/>. Continue to the *caArray New User Account and Login* section on page 12 and *Figure 2.2*.
2. If a version has been 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/downloadcaarray.jsp>.

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.

If by chance, you navigate to the caArray website instead of the data portal page (#1), you can proceed to caArray from there. On the website, follow this step to go to the caArray data portal:

- Click **Data Management** under the center sphere to open the caArray application (*Figure 2.1*).

The DevDoc and Data Analysis options on the caArray website 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 2.1*).
- **Data Analysis** provides access to data pre-processing, data analysis and visualization tools themselves.

The Cancer Biomedical Informatics Grid™, caBIG™ program is developing tools for microarray data analysis and annotation. Several of these tools, for example, geWorkbench and GenePattern can be used to access and analyze data stored in caArray. A complete inventory of caBIG tools and resources is available at https://cabig.nci.nih.gov/inventory/inventory_a-z/document_view.

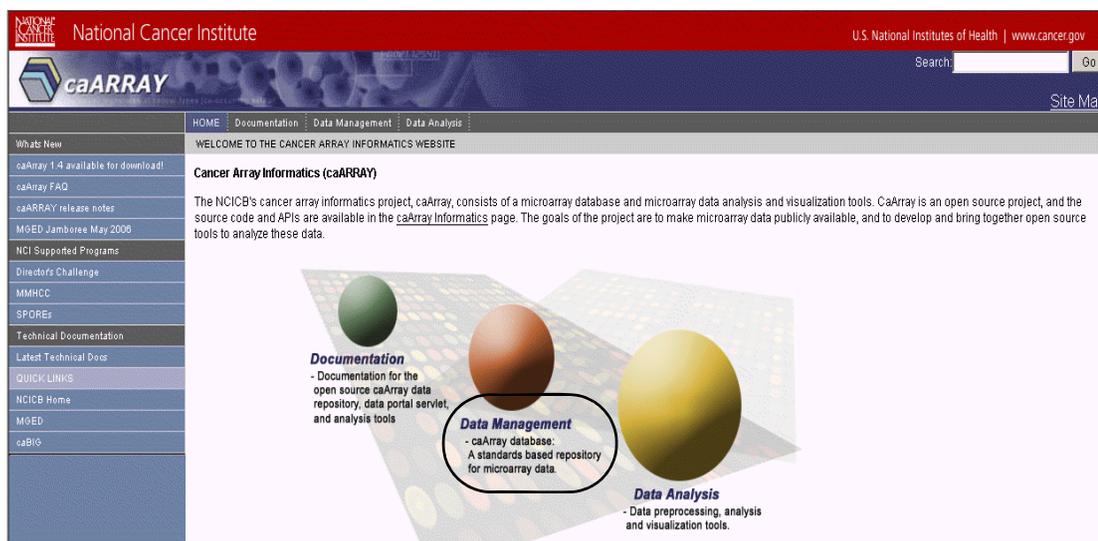


Figure 2.1 caArray data portal page. Click the Data Management hyperlink to go to the caArray login page.

caArray New User Account and Login

Once you are on the login page, you can perform a search of caArray objects without being logged in. On the left sidebar, click any of the **Search [object]** buttons to launch a search. For more information about executing a search, open the online help context sensitive topic from the Search form that opens after you click the appropriate button.

You can do that by clicking the (?) button on the screen.

From this login screen, you can also initiate an initiation of a MAGE-ML file. To do so, click the **Validate MAGE-ML** hypertext link on the left sidebar. That launches caAMEL, a companion tool to caArray that validates and imports MAGE-ML files into caArray. Refer to the *caAMEL 1.0 User's Guide* (<https://caarraydb.nci.nih.gov/caamel/>) for more information.

From the login screen, to register as a new user or log in if you already have a user account (*Figure 2.2*):



Figure 2.2 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.

Requesting a User Account

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

- Go to the NCICB caArray login page <https://caarraydb.nci.nih.gov/caarray/> and click on the **Register** button. Enter the appropriate information in the Register for an Account form. Click **Submit** to request the new account; click **Reset** to clear the form.
- As an alternative, contact NCICB Application Support:
 - NCICB@pop.nci.nih.gov
 - Phone 888-478-4423 (toll-free) or 301-451-4384 (local)

Once the request for a new account is sent to NCICB, it takes 24-48 hours to process. You will receive an email response when the account has been activated.

The UserID and password you are assigned determines your access rights for the software.

Using caArray Online Help

The online help explains how to use all of the features of the caArray portal.

To access online help in caArray, use any of the following methods:

- Click the **Help** menu option on the top menu bar to open the complete online help project.
Note: You can access online help without being logged into caArray.
- Click the **Help** icon or button at the top of each page to open a context-sensitive topic. Context-sensitive help displays information that corresponds to the page from which help was opened.

Once you are in online help, several options help you locate topics of interest.

- Click the **Show in Contents** button () at the top left of the help page to open the complete online help table of contents and locate your current topic in the table.
- The breadcrumb trail at the top of the page shows the relative location of the current help topic relative to neighboring topics. Click a breadcrumb link to display that help topic.
- Click the **Back** or **Forward** links at the top of the page to display help topics you have previously viewed.
- Follow hypertext links or the **Related Topics** buttons in the help topics to open other closely related topics. If the current help page has related topics associated with it, you can also view them by clicking the **Related Topics** button () at the top right of the help page.
- Locate topics using the table of contents that displays in the left pane of the online help project or the **Index** tab that displays at the top of the Table of Contents pane.
- Perform word searches of Help by entering query text in the search text box.
- Print the current topic by clicking the **Print** button () at the top right of the help page.

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 2.3*).



Figure 2.3 Quick Links menu options

These include:

- **NCI Home** (<http://www.cancer.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** (<https://caarraydb.nci.nih.gov/caarray/>) 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 2.4).

National Cancer Institute

Center for Bioinformatics

HOME ABOUT NCICB INFRASTRUCTURE TOOLS PROJECTS DOWNLOADS TRAINING SUPPORT

Support

Welcome to the NCICB Application Support Site

The NCICB Application Support Group is dedicated to helping you use NCICB tools and resources to maximum benefit. We're here to help you find what you need, use and re-use our software, integrate data and applications, and facilitate the sharing of information and resources.

Telephone: 301-451-4384 or toll free: 888-478-4423
Email: ncicb@pop.nci.nih.gov

Telephone support is available Monday to Friday, 8 am – 8 pm Eastern Time, excluding government holidays. You may leave a message, send an email or submit a support request via the Web at any time.

When submitting support requests via email, please include:

- your contact information
- the name of the application/tool you are using
- the URL if it is a Web-based application
- a description of the problem and steps to recreate it
- the text of any error messages you have received

For more information on a specific application, follow the links below, or go to the **Supported Applications List** for a detailed breakout of all supported applications.

CONTENTS

Cancer Centralized Clinical Database (C3D)	Centra
caArray	Clinical Research Information Exchange (CRIX)
caDSR Applications	DCP Enterprise System Knowledgebase (DESK)
Cancer Images Database (caIMAGE)	Enterprise Vocabulary Services (EVS)
Cancer Laboratory Information Management System (caLIMS)	Programming & API Support
Cancer Model Organisms Database (caMOD)	

NCICB User Applications Manual

The NCICB User Applications Manual provides a thorough introduction to NCICB applications.

Web Self-Service

[Search FAQs](#)

Search our dynamic knowledgebase of Frequently Asked Questions (FAQs).

Figure 2.4 An example of the NCICB Quick Link help topic, in this case NCICB Application Support page.

Navigating through the caArray Workflow

Once you have logged in, caArray opens to the workflow page (*Figure 2.5*):

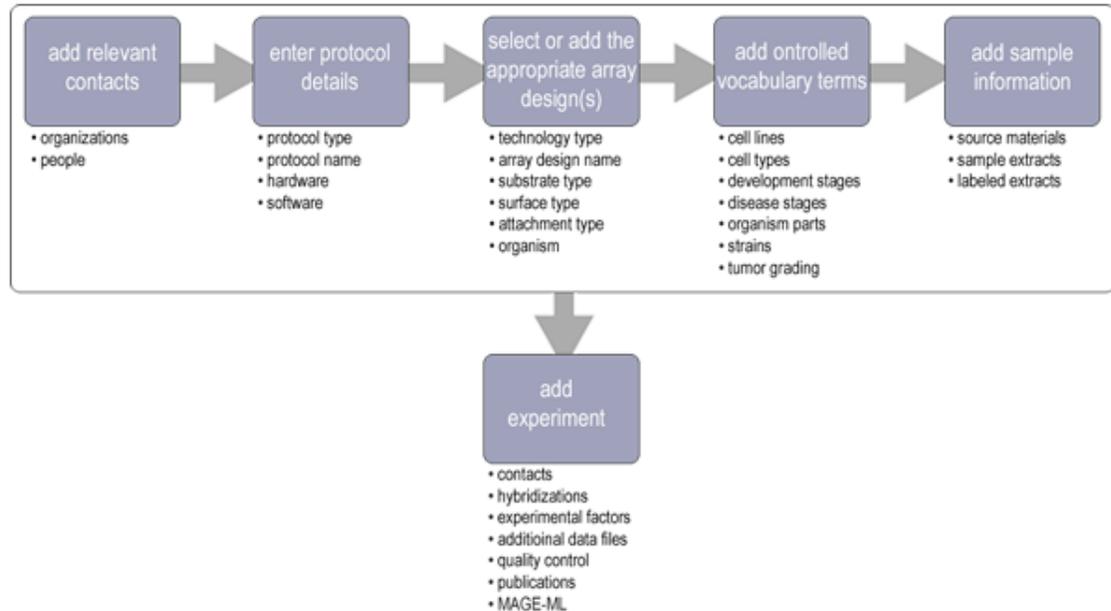


Figure 2.5 caArray Workflow

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 2.5*) 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 2.6*). The tasks are organized from left to right in the logical order of workflow tasks, .

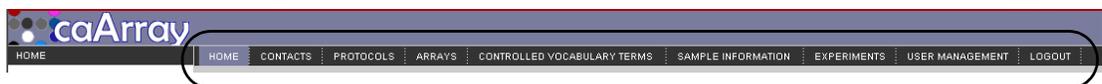


Figure 2.6 caArray task tabs

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. See *caArray New User Account and Login* on page 12. Click on any of these hypertext links to begin the search process (*Figure 2.7*).

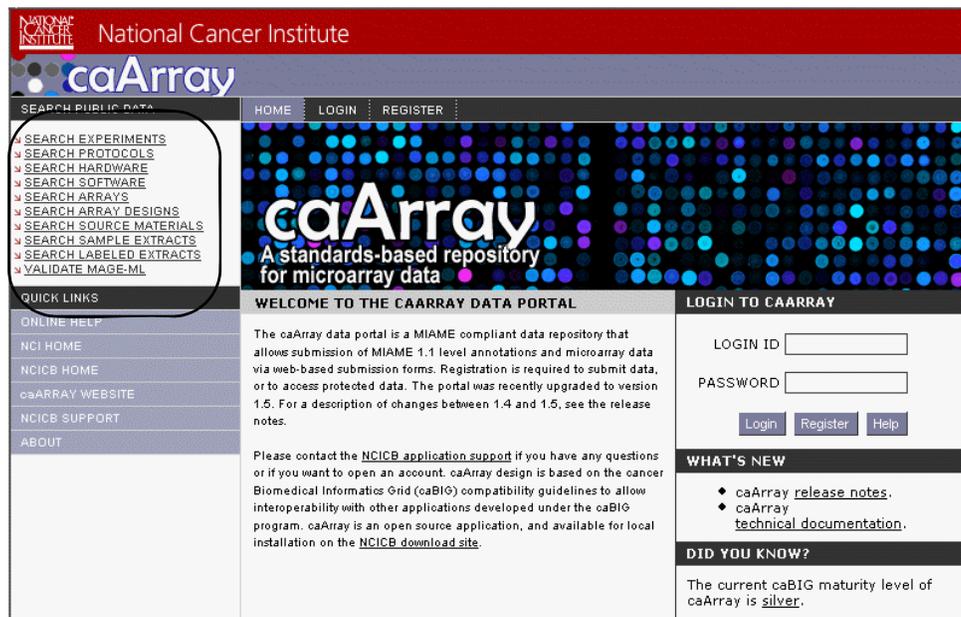


Figure 2.7 Search Public Data options in caArray before login

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 2.1 for more information.

Note: You must obtain a user account from the help desk in order to log in. For more information, see *Requesting a User Account* on page 13.

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**

- **Controlled Vocabulary Terms**
- **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 [Security Structure](#)). For descriptions of all interface features, see Table 2.1.

Online help and additional resource links remain fixed through all the viewing windows.

Descriptions of Elements in the caArray Viewer

The terms in Table 2.1 identify and describe elements of a caArray browser window.

Term	Definition
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
Standard toolbar	Displays at the top of every browser window
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.
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 person or an organization 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.

Table 2.1 Elements of the caArray browser window

Term	Definition
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.
Controlled Vocabulary Terms	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, Controlled Vocabulary Terms, and biomaterials performed on or associated with microarrays.

Table 2.1 Elements of the caArray browser window (Continued)

CHAPTER 3

USER ACCOUNT MANAGEMENT

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

Note: The options for performing user management tasks are visible in caArray on the User Management tab that displays upon login, only if you have these Admin privileges.

Topics in this chapter include:

- *User Management* on this page
- *Searching for a User* on page 22
- *Creating a New User Account* on page 25
- *Searching for a Group* on page 27
- *Creating a Group* on page 28
- *Granting Others Access to Your Work* on page 30
- *Visibility* on page 31

User Management

Within caArray, two types of user roles can be assigned:

1. **User**--A regular user of caArray.
2. **Admin User** --This user has access to the User Management features of the caArray application. An Admin User can create/view/update users and groups within the system.

Group roles in which groups are created and users assigned to groups can also be executed in caArray by an Admin User.

Note: The options for performing user management tasks are visible in caArray on the User Management tab that displays upon login, only if you have these Admin privileges.

In caArray, you will not see buttons for actions to which you do not have permissions. For example, the only user who can modify or delete some objects in the caArray database is the “owner” of the original object, i.e. the user who created the object. In other instances, any user can edit or modify some objects. In the case of Controlled Vocabulary Terms (CVT), noone can delete a term, even if you created it.

A good rule of thumb to follow is if you can see a **Modify** button or **Delete** option, then you can modify or delete an object. If you cannot see those options, then you cannot edit or delete the object.

Searching for a User

It is advisable, before creating a new user account in caArray, to perform a search to ascertain whether the user already has an account. By default, when you click the User Management tab, this search page displays.

- Notes**
- This search feature is a part of User Management, accessible only to Admin Users. If you do not have these privileges, you cannot see the options and features described in this section. For more information, see *User Management* on page 21.
 - This user search is to locate a person with an existing user account in caArray. This search is completely different than a Person search, described in *Contacts* on page 33, which searches for persons identified with key roles in Protocols, Arrays, Experiments, and so forth.

To search for a user in caArray, follow these steps:

1. Click the **User Management** task tab or click the **Search for User** link on the left sidebar in the caArray portal.

SEARCH USERS	
Login Name	<input type="text" value="jgreen"/>
First Name	<input type="text" value="John"/>
Last Name	<input type="text" value="Green"/>
Institution	<input type="text" value="imagine"/>
E-Mail Address	<input type="text" value="jgreen@imagine.com"/>
User Role	<input type="text" value="Both"/>
User Status	<input type="text" value="Active"/>

Figure 3.1 Search Users form

2. On the Search for User form that opens (*Figure 3.1*), complete the following fields that identify the user for whom you are searching:
 - **Login Name**
 - **First Name**
 - **Last Name**
 - **Institution**
 - **Email address**

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

3. Click the **Search** button.

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

Search results display on the same page, below the Search Users form. If you do not locate the User you want, you can click the New User hyperlink on the left navigation sidebar to create a new user.

User Search Results

Search results display a list of users meeting the search criteria. If no criteria were entered, a list of all the users in the system is returned. The initial list is sorted in ascending order of users' last names. All columns in the search results are sortable.

To view details for a search hit, click the hypertext link in the **User Name** or **Login Name** columns corresponding to the result.

If the appropriate user is not found in the search, you as an Admin User can create a new user by clicking the New User link on the left navigation sidebar. For more information, see *Creating a New User Account* on page 25.

Viewing User Details

From a list of user search hits, a logged in Admin User can view the user details. To do so, click the hypertext link corresponding to the user in the **User Name** or **Login Name** columns.

The User Details page displays user information in read-only format (*Figure 3.2*).

USER DETAILS	
Login Name	jgreen
User Role In System	Admin User
First Name	John
Last Name	Green
E-Mail Address	jgreen@imagine.com
Title	
Institution	Imagine
Department	Array research
Location	Staten Island, N.Y.
Status	Active
Start Date	12/05/2006
End Date	

Figure 3.2 User Details page

Click **Done** to close the page.

Modifying User Details

To modify the details for a registered caArray user, in the User Details dialog box, click the **Modify** button. This opens the Modify User dialog box (*Figure 3.3*).

* indicates a required field

MODIFY USER	
* Login Name	<input type="text" value="jgreen"/>
* Password	<input type="password" value="*****"/>
* Confirm Password	<input type="password" value="*****"/>
Is Admin User?	<input checked="" type="checkbox"/>
* First Name	<input type="text" value="John"/>
* Last Name	<input type="text" value="Green"/>
Email Address	<input type="text" value="jgreen@imagine.com"/>
Title	<input type="text"/>
* Institution	<input type="text" value="imagine"/>
Department	<input type="text" value="Array research"/>
Location	<input type="text" value="Staten Island, N.Y."/>
Status	Active <input type="button" value="Disable User"/>
* Start Date	<input type="text" value="12/05/2006"/> mm/dd/yyyy
End Date	<input type="text"/> mm/dd/yyyy

Figure 3.3 Modify User page

On the Modify User page, as an Admin User, you can perform the following edits:

- Update a User Role.
- Activate a User by clicking the corresponding button. This clears the End date field, indicating an Active user.
- Update an email address.
- Update the institution, its department and location, with which the user is associated.
- Inactivate a User by clicking the corresponding button. When you click this button, the End date sets to the previous calendar date. This indicates an Inactive user.
- Indicate a Start Date for activating the user.
- Enter an End Date.
- Click a **Manage Groups** button to open a page where you can add a User to an existing group or remove a user from a group. See *Managing a Group* on page 29.

Once you have reviewed and/or edited the user information, click **Save** for saving it, or **Cancel** to indicate no modifications.

Creating a New User Account

A person who wants to be caArray user can apply for a user account through NCICB Application Support (see *Requesting an Account Through NCICB Application Support* on page 25) or can be added as a new user by a User with Admin privileges.

If you are an Admin User, before creating a new user account in caArray, you should perform a search to ascertain whether the user already has an account. For more information, see *Searching for a User* on page 22.

To create a new user account, as an Admin User, follow these steps:

1. Click the **User Management** task tab on the caArray menu bar.
2. On the left sidebar, click the **New User** link.
3. Complete the following information for the new user¹:
 - **Login Name***
 - **Password*²**
 - **Confirm Password***
 - **Is Admin User**--Check to indicate that the user will be an Admin User
 - **First Name***
 - **Last Name***
 - **E-mail Address**
 - **Title**
 - **Institution***
 - **Department**
 - **Location**
 - **Start Date***--format dd/mm/yyyy
 - **End Date**--format dd/mm/yyyy
4. Click **Submit** to save the user information. When successfully saved, the Users Details screen displays. Click **Cancel** to display the User Search page without creating the new user account.

Requesting an Account Through NCICB Application Support

To request a caArray user account from NCICB Application Support, complete one of the following steps:

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

-
1. Items with an asterisk are required fields
 2. Password and Confirm Password fields display only with a local installation of caArray (using database for authentication). For installations that authenticate via LDAP, these fields never display and hence are not required.

OR

- Go to the NCICB caArray login page <https://caarraydb.nci.nih.gov/caarray/> and click the **Register** button. Enter the requested information, as displayed in *Figure 3.4* and itemized below the figure. Follow the screen prompts to complete the registration.

* indicates a required field

REGISTER FOR AN ACCOUNT					
* AFFILIATION	<input type="text"/>				
* FIRST NAME	<input type="text"/>	MIDDLE INITIAL	<input type="text"/>	* LAST NAME	<input type="text"/>
* ADDRESS 1	<input type="text"/>	ADDRESS 2	<input type="text"/>		
* CITY	<input type="text"/>	* STATE	<input type="text"/>	* ZIP	<input type="text"/>
* COUNTRY	<input type="text"/>	* PHONE	<input type="text"/>	* EMAIL	<input type="text"/>

Figure 3.4 User account registry form

You must provide the following information in order to obtain a caArray account³:

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

Disabling a User

An Admin User can disable a caArray user account. This does not remove the underlying record, but after performing this task, the user account status will display on the Modify User Details page as disabled.

To disable a user, follow these steps:

- Perform a search to locate the user. For more information, see *Searching for a User* on page 22.
- Click the user name link in the search results to open the User Details page.
- Click the **Modify** button in the lower right-hand corner to open the Modify User Details page.
- Click the **Disable User** button next to the **User Status**. This action sets the end date set as the previous calendar day.

Note: The status of the user is reflected by the End Date. Clicking the **Disable User** button populates the end date field with the previous day's date. You can also disable the user by entering a previous end date in the field manually, thus inactivating the user.

- Click **Save**. Upon a successful save, the user account is deemed to be inactive.

- Items with an asterisk are required fields.

Activating a User

An Admin User can activate a caArray user account. The user account is noted on the Modify User Details page as **Active**.

To activate a user, follow these steps:

1. Perform a search to locate the user. For more information, see *Searching for a User* on page 22.
2. Click the user name link in the search results to open the User Details page.
3. Click the **Modify** button to open the Modify User Details page.
4. Click the **Activate User** button next to the User Status.

Note: The status of the user is determined by the End Date. Clicking the **Activate User** button clears the end date field, if it was populated. You can also activate the user by clearing the end date field manually. You, as an Admin User, can type in a future end date, if you wish.

5. Click **Save**. Upon a successful save, the user account is immediately activated, indicated on the User Details page by the lack of an end date set.

Searching for a Group

This search feature is a part of User Management, accessible only to Admin Users.

To ascertain whether a particular user's group already exists in caArray, follow these steps:

1. Click the **User Management** task tab on the caArray menu bar.
2. On the left sidebar in the caArray portal, click the **Search for Group** link.
3. On the Search for Groups form (*Figure 3.5*), complete the following field that identifies the group for which you are searching:

◦ **Group Name**

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

4. Click the **Search** button.

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

SEARCH GROUPS	
Group Name	<input type="text"/>

SEARCH RESULTS	
3 items found, displaying all items.	
Group Name	
SAM	
caArray Developers	
Public	

Figure 3.5 Search Results display on the same page as the Search Groups form

Search results display on the same page, below the Search Group form. If you do not locate the group you want, you can click the New Group hyperlink on the left navigation sidebar to create a new group.

Group Search Results

Group search results display below the Search Groups form, displaying a list of groups meeting the search criteria (*Figure 3.5*). If no criteria were entered, a list of all the groups in the system is returned. The initial list is sorted in ascending order of group names. Columns are sortable.

To view details for a search hit, click the hypertext link in the **User Name** or **Login Name** columns corresponding to the result.

If the appropriate group is not found in the search, you as an Admin User can create a new group by clicking the **New Group** link on the left navigation sidebar. For more information, see *Creating a Group* on page 28.

Viewing Group Details

From a list of group search hits, as a logged in Admin User, you can view the group details. To do so, click the hypertext link corresponding to the group. The group details lists all users in the group, along with their role.

The Group Details page display group information in read-only format.

Click **Done** to close the page. Click **Modify** to open the Modify Groups page.

Modifying Group Details

To modify the group details, follow these steps:

1. Click **Modify** to display the Modify Groups screen where you can perform the following edits to modify the group.
2. On this page, as an Admin User, you can perform the following edits:
 - Edit the Group Name. (A Group Name should be unique within the system.)
 - Edit the Group Description.
 - View users within the group.
 - Update Group information.
 - View user details using the hypertext link corresponding to a user in the group.
 - Add a User to an existing group.

Creating a Group

A group can be created as a response to a request submitted to the NCICB Application Support (ncicb@pop.nci.nih.gov) or by an Admin User.

If you are an Admin User, before creating a new group in caArray, you should perform a search to ascertain whether the group already exists. For more information, see *Searching for a Group* on page 27.

To create a group as an **Admin User**, follow these steps:

1. Click the **User Management** task tab on the caArray menu bar.
2. On the left sidebar, click the **New Group** hypertext option.
3. On the New Group form, enter the following information⁴:
 - **Group name***
 - **Group description**
4. Click **Submit** to save the group information. Upon a successful save, a Group Details page displays. Click **Cancel** to abort group creation; this opens the Group Search screen by default.

Managing a Group

Once a group is created, If you have Admin privileges, you can assign a user to a specific group, or you can remove a user from a group.

To assign a user to a group, follow these steps:

1. Perform a search for the user to be added to one or more groups. For more information, see *Searching for a User* on page 22.
2. Click the hypertext link in the **User Name** or **Login Name** columns corresponding to the user.
3. On the User Details page, click the **Manage Groups** button.

The Manage Groups for User page displays the user information, as well as User Groups information.

The User Groups page displays a list of all groups existing in the caArray system.

- a. Each Group Name is hyperlinked to the Group Details page.
- b. Each Group Name has a corresponding drop-down menu that lists three options:

--**Not Assigned**--If selected, this group is not currently assigned to the user

--**Group Member**--If selected, this user is a member of this group

--**Group Curator**--if selected, this member has a curator role for the group. A Curator role is assigned to a user for a specific group. This role allows the Curator to modify an experiment that they are not the owner of, if the experiment is visible to the group.”

Note: A Curator cannot upload or create attachments for the experiment.

4. As an Admin User, you can perform the following tasks:
 - a. Remove an assigned group from the user by clicking **Not Assigned**.
 - a. Assign regular membership in a group to a user by clicking **Group Member**.
 - a. Assign “curator” membership in a group to a user by clicking **Group Curator**.

4. Items with an asterisk are required fields.

5. Click **Save** to save the group assignments/modifications; they will display on the User Details page. Click Cancel to abort group assignment for this user. This returns you to the User Details page.

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. In your contact email, you must include the following information:

- Your name
- 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*. 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 3.1 describes visibility options and their interpretation.

Note: When specifying visibility, to make multiple selections, press the CTRL key and click on all items you want to select. To deselect a visibility option, press CTRL + click on the item.

Term	Definition
Public	Anyone can view all records, with Read-Only access.
Private	Can be viewed only by submitter (“owner”) of object. Private is assigned by default if no other Visibility option(s) are selected when an object is created.
Public + Group	Anyone can view all records, with Read-Only access. Modify privileges are assigned to members of the specified group(s) who are assigned “Curation” privileges. Note: 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.
Read-Only	Permission only to view records created by other persons or organizations
Delete	Permission to delete records created by other persons or organizations
Read/Modify	Permission to view and/or modify records created by other persons or organizations

Table 3.1 caArray visibility and permission settings

The visibility of items is relevant when a user performs a search. In the list of search results only items are displayed which are “visible” for the user who performed the search.

CHAPTER 4 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 34
- [Working with a Contact Organization](#) on page 34
- [Working with a Contact Person](#) on page 37

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 34.

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 35.

Contacts require information such as name, mailing address, phone numbers and email addresses. Table 4.1 defines terms associated with caArray Contacts.

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

Table 4.1 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 4.1).

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 Results section (Figure 4.1).

Name	Address
Advantage Technology Center (ATC)	8717 Grovemont Circle, Gaithersburg, MD, 20877, USA
Affymetrix	
Albert Einstein Cancer Center	111 East 210th Street, Bronx, NY, 10467, United States
Arcturus Bioscience, Inc	400 Logue Avenue, Mountain View, CA, 94043, USA
Ardais Corporation	xxx,xxx,xx,xxxxx, USA
Axon Instruments	3280 Whipple Road, Union City, CA, 94587, USA

Figure 4.1 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 following contact information⁵ (Figure 4.2:

HOME CONTACTS PROTOCOLS ARRAYS CONTROLLED VOCABULARY TERMS SAMPLE INFORMATION EXPERIMENTS

Contacts: Add New Organization

A contact person must be associated with an organization. If you plan to add a new contact, be sure to create the appropriate organization first.

* indicates a required field

ORGANIZATION DETAILS	
* Name	Albion Therapeutics
* Address	123 Array Avenue
* City	Porterville
* State	Wisconsin
* Zip	54321
* Country	USA
Phone Number	
Fax Number	
Email Address	
Url	

Submit Cancel

Figure 4.2 Entering a new organization

- o **Name***
 - o **Address***
 - o **City***
 - o **State***
 - o **Zip***
 - o **Country***
 - o **Phone Number**
 - o **Fax Number**
 - o **Email Address**
 - o **URL**
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 34.)
2. Select the name of the **Organization** in the **Search Results** section to access the organization contact information.
3. Click the **Modify** button.

5. Items with an asterisk are required fields.

Note: You can do this if you have the Visibility settings allowing you to modify the contact information. If you do not, the **Modify** button does not display on the screen.

4. Make any necessary changes.
5. Click the **Save** button to save the modifications, or click the **Cancel** button to disregard the changes.

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 34.)
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 4.3).

Figure 4.3 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.
4. Complete the following contact information⁶ (Figure 4.4)

Figure 4.4 The form for submitting information for a new Person Contact

6. Items with asterisks are required fields.

- **First Name***
- **Middle Initials**
- **Last Name***
- **Address***
- **Phone Number**
- **Fax Number**
- **Email Address**
- **URL**
- **Affiliation***

Select the institute/center if it is listed.

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

Modifying Contact Information for a Person

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

1. Search for the person whose information you want to modify (see *Working with a Contact Person* on page 37).
2. In the **Search Results** section, select the name of the person to access the individual's 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 only if you have the Visibility settings allowing you to modify the contact information. If you do not, the Modify button does not display on the screen. See *Visibility* on page 31 for more information.
 - Deleting a person cannot be undone.

Deleting a Contact Person

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

1. Search for the person you want to delete (see *Working with a Contact Person* on page 37).
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**.

- Notes:**
- 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 5 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
- [Protocol Workflow](#) on page 42

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.

- Notes:**
- 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 31.

- 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 add 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 adding your experiment, you will be unable to successfully complete the submission of hybridization files. For more information on hybridizations and Experiment submissions, see *Adding a New Experiment* on page 104.

Protocol 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 5.1.

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

Protocol Searchable Fields	Description
Protocol Type	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.
Protocol Name	Enter the name to be searched.
Visibility	Select the option describing the visibility assigned to the query Protocol. Options include Private, Public and groups assigned Read/Modify visibility. Note: If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify it.

Table 5.1 Protocols searchable fields

4. 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 5.1).

[HOME](#) | [CONTACTS](#) | [PROTOCOLS](#) | [ARRAYS](#) | [CONTROLLED VOCABULARY TERMS](#) | [SAMPLE INFORMATION](#) | [EXPERIMENTS](#)

Protocol: Search Protocols

SEARCH PROTOCOLS ?

Protocol Type	All
Protocol Name	<input style="width: 90%;" type="text"/>
Visibility	All

SEARCH RESULTS

114 items found, displaying 1 to 20. [First/Prev] 1, 2, 3, 4, 5, 6 [Next/Last]

Protocol Name	Protocol Type
adstflk	linear amplification
Affy U133B	hybridization
Affymatrix feature extraction u95av2	feature extraction
Affymatrix hybridization u95av2	hybridization
Affymatrix u95av2 image acquisition	image acquisition
Affymatrix GeneChip HG-U133 Feature Extraction	feature extraction
Affymatrix GeneChip HG-U133 Image Acquisition	image acquisition
Affymatrix GeneChip HG-U133 Plus2 Hybridization Protocol	hybridization
Affymatrix GeneChip HG-U133 Plus2 Hybridization Protocol	hybridization

Figure 5.1 Results from an unrestricted Protocol search.

5. To see the details of a protocol, click the Protocol name.
6. 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 5.2 on page 45):
 - **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.

Adding 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 5.2*⁷ and described in *Table 5.2*.

Protocol: Add Hardware

* indicates a required field

ADD NEW HARDWARE ?

* **Name** GeneChip(R) Fluidics

* **Model** 450

* **Type** wash_station Specify New Type:

* **Make** Affymetrix

* **Manufacturer** Affymetrix

URI

Visibility
 Public
 caBIG
 Curation
 Curation Team - delete
 Curation Team - make public
 DC Lung Study
 DC Prostate Study
 GMDI_Group
 JenLab
 MAGE-OM API users

Note: **Private** visibility is always selected by default. If you would like this item to have only private visibility (only be visible to you), you do not need to make any selections. If you want to have this item be visible to others, select the additional group(s). Hold CTRL key and click an item to select or deselect multiple items. Hold CTRL key and click an item to deselect it.

Figure 5.2 Adding new hardware

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

Table 5.2 Hardware submission fields

7. Items with an asterisk are required fields

5. Click the **Submit** button.

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 44.
4. Click the **Hardware Name** to be modified in the **Search Results** to see the detailed information.
5. Click the **Modify** button.

Note: You can do this only if you have the Visibility settings allowing you to modify the hardware. If you do not, you will not see the **Modify** button. For more information, see *Visibility* on page 31.

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.

Deleting Hardware

To delete Hardware, follow these steps:

1. Search for the Hardware you want to delete. (See *Searching for Hardware* on page 44.)
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 31.

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 5.3 on page 47):
 - **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.

- 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.

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

Adding New Software

To add New Software, follow these steps:

- Log in on the caArray main page.
- Select the **Protocols** task tab.
- Select **New Software** from the left navigation menu.
- Complete the details of the software you are submitting, as demonstrated in *Figure 5.3* and described in *Table 5.3*⁸

Protocol: Add Software

* indicates a required field

ADD NEW SOFTWARE ?

* Name	<input type="text" value="GenePix Pro"/>	
* Type	array_manufacture_software	Specify New Type: <input type="text"/>
* Manufacturer	Axon Instruments	
URI	<input type="text"/>	
Visibility	<div style="border: 1px solid gray; padding: 2px;"> <ul style="list-style-type: none"> Public caBIG Curation Curation Team - delete Curation Team - make public DC Lung Study DC Prostate Study GMDL_Group JenLab MAGE-OM API users </div>	

Note: **Private** visibility is always selected by default. If you would like this item to have only private visibility (only be visible to you), you do not need to make any selections. If you want to have this item be visible to others, select the additional group(s). Hold CTRL key and click an item to select or deselect multiple items. Hold CTRL key and click an item to deselect it.

Figure 5.3 Adding new software details

Software Submission Fields	Description	Example
*Name	Full name of the software	GenePix Pro 3.0.1.22
*Type	Descriptor of the type of software	Microarray image analysis software
*Manufacturer	Name of the manufacturer of the software	Axon Instrument

Table 5.3 Adding new software submission fields

- Items with an asterisk are required fields.

Software Submission Fields	Description	Example
URI	Uniform Resource Indicator for the manufacturer	http://www.moleculardevices.com/
Visibility	<p>Visibility assigned to the query Hardware. Options include Private, Public and groups assigned Read/Modify visibility.</p> <p>Note: 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 5.3 Adding new software submission 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 46.
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.

Note: You can do this only if you have the Visibility settings allowing you to modify the software. If you do not, you will not see the **Modify** button. For more information, see *Visibility* on page 31.

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.

Deleting Software

To delete Software, follow these steps:

1. Search for the **Software** you want to delete. (See *Searching for Software* on page 46.)
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.

- 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 31.

Adding a New Protocol

To add a New Protocol, follow these steps:

- Log in on the caArray main page.
- Select the **Protocols** task tab.
- Select **New Protocol** from the left navigation menu.
- Complete the details of the Protocol you are submitting as demonstrated in *Figure 5.4* and described in [Table 5.4](#)⁹.

Protocol: Add Protocol

* indicates a required field

ADD NEW PROTOCOLS

* **Name** Affymetrix U9Sav2Image Acquisition

* **Type** image_acquisition Specify New Type: Array Manufacturing Protocol

Add your own description of your protocol to this text box.

Description

URI

* **Visibility**

Public
caBIG
Curation
Curation Team - delete
Curation Team - make public
DC Lung Study
DC Prostate Study
GMDL_Group
JenLab
IMAGE-OM API users

Note: **Private** visibility is always selected by default. If you would like this item to have only private visibility (only be visible to you), you do not need to make any selections. If you want to have this item be visible to others, select the additional group(s). Hold CTRL key and click an item to select or deselect multiple items. Hold CTRL key and click an item to deselect it.

Submit Cancel

Figure 5.4 Adding a new Protocol

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

Table 5.4 Protocol submission fields

- Items with an asterisk are required fields.

Protocol Submission Fields	Description	Example
Description	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
URI	Uniform Resource Identifiers of the protocol, if available and appropriate	URI used in MAGE
Visibility	Visibility assigned to the query Hardware. Options include Private, Public and groups assigned Read/Modify visibility. Note: If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify the object. For more information, see <i>Visibility</i> on page 31.	Public

Table 5.4 Protocol submission fields

- Click **Submit**. This opens the Protocol Details page (Figure 5.5).

Protocol: Protocol Details

PROTOCOL DETAILS	
Name	Affymetrix U9Sav2Image Acquisition
Type	image_acquisition
Description	Add your own description of your protocol to this text box.
URI	
Visibility	Public

Done Modify Delete

PARAMETERS

Add Parameter

HARDWARE ASSOCIATIONS

Add Hardware Association

SOFTWARE ASSOCIATIONS

Add Software Association

Figure 5.5 Protocol Details page

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

Protocol Parameter

A parameter is a protocol detail. It can be associated with a protocol, a hardware protocol, or a software protocol. An example of a parameter would be numerical parameters such as incubation temperatures, or quantities of reagents added.

When associating a parameter with a protocol, note that 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.

* indicates a required field

ADD PARAMETER	
* Name	<input type="text"/>
Default Value	<input type="text"/>
* Unit Type	<input type="text"/> *
* Unit	select Unit Type first <input type="text"/>
* Type	<input type="text"/>

Figure 5.6 Add [Protocol] Parameters dialog box

In the Add Parameter dialog box (Figure 5.6), you can define Protocol details¹⁰. An example of parameters would be numerical parameters such as incubation temperatures, or quantities of reagents added.

- o ***Name**
- o **Default Value**
- o ***Unit type**
- o ***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.

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

Note: This list contains only submitted hardware; if you do not see your hardware on the list, you must first submit New Hardware. See *Adding New Hardware* on page 44 for more information.
- Associate software with the Protocol you are adding by selecting the **Software Association** button (if applicable).

Note: This list contains only submitted software; if you do not see your software protocol on the list, you must first submit New Software. See *Adding New Software* on page 47 for more information.)
- When you have finished specifying these parameters, click **Done**.

Modifying a Protocol

To modify an existng Protocol, follow these steps:

- Log in on the caArray main page.
 - Select the **Protocols** task tab.
-
- Items with an asterisk are required fields.

3. Search for the appropriate protocol using the **Search Protocol** function. (See *Searching for an Existing Protocol* on page 42 for more information.)
4. In the **Search Results**, click the Protocol name to access its detailed information.
5. Click the **Modify** button.
Note: You can do this only if you have the Visibility settings allowing you to modify the protocol. If you do not, the Modify button does not display on the screen. For more information, see *Visibility* on page 31.
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.

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 42.)
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 31.

CHAPTER 6

ARRAYS AND ARRAY DESIGNS

This chapter describes the processes for working with Arrays and Array Designs 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 54
- *Managing Array Designs* on page 54
- *Managing Arrays* on page 61

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 111 in [Adding a New Experiment](#).

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 6.1:

Array Designs Searchable Fields	Description
Technology Type	Select from the drop-down menu the technology type or platform of the reporters on the array. All is the default setting.
Surface Type	Select from the drop-down menu a controlled term for descriptors for coating of the substrate. All is the default setting.
Organism	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. All is the default setting.
Array Design Name	Enter the name for the Array Design
Attachment Type	Select from the drop-down menu the method by which the element (reporter) sequences are physically attached to the array. All is the default setting.
Identifier	caArray identifier
Array Design Provider	Select from the drop-down menu the name of the provider of the Array Design. All is the default setting.
Strand Type	Select from the drop-down menu a descriptor of the strand type to which the sequence feature belongs. All is the default setting.
Visibility	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. All is the default setting.

Table 6.1 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 which you are authorized to view

in caArray will display in the Search Results section of your browser (Figure 6.1).

The screenshot shows the 'Arrays: Search Array Designs' page. At the top is a navigation bar with links: HOME, CONTACTS, PROTOCOLS, ARRAYS, CONTROLLED VOCABULARY TERMS, SAMPLE INFORMATION, EXPERIMENTS, USER MANAGEMENT. Below the navigation bar is a search filter section with the following fields:

- Technology Type: All
- Array Design Name: (text input)
- Array Design Provider: All
- Surface Type: All
- Attachment Type: All
- Strand Type: All
- Organism: All
- Identifier: (text input)
- Visibility: All

Buttons for 'Search' and 'Reset' are located to the right of the filters. Below the filters is the 'SEARCH RESULTS' section, which indicates '42 items found, displaying 1 to 20.' and includes navigation links: [First/Prev] 1, 2, 3 [Next/Last]. The results are displayed in a table:

Design Name	Identifier
Amir's ga	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897535941627:1
Aronow P9	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897591972003:1
HG-U133A	Affymetrix.com:PhysicalArrayDesign:HG-U133A
hg-u133a	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897590577522:1
hg-u133a	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897590577520:1
HG-U133a/b	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897590577538:1
hg-u133a/b	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897590577524:1
Hg-U133a/b	gov.nih.nci.ncicb.caarray:PhysicalArrayDesign:1015897590577535:1

Figure 6.1 Array Design search results (unrestricted)

- To see the details of a particular Array Design, select its name (Figure 6.2).

Array Design: HG-U133A

The screenshot shows the 'GENERAL ARRAY DESIGN INFORMATION' section for 'HG-U133A'. It includes a table of key attributes:

Array Design Name:	HG-U133A
Array Version:	1.0
Technology Type:	in_situ_oligo_features
Surface Type:	glass
Attachment Type:	Unknown
Strand Type:	Unknown
Organism:	Unknown
Array Description:	

Buttons for 'Done', 'Modify', and 'Delete' are located below the table. Below this is the 'VISIBILITIES' section with a 'Visibility' dropdown set to 'Public' and a 'Modify' button. The 'REPORTERS' section shows 'Number of features: 506944' and a 'Download MAGE-ML' link. The 'DESIGN PROVIDERS' section is a table:

Name	Affiliation	URI	Address	Phone	Fax	Action
Affymetrix		http://www.affymetrix.com				Remove

An 'Add Provider' button is located below the table. The 'PROTOCOLS' section at the bottom has an 'Apply Protocol' button.

Figure 6.2 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 59.

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.

The **Design Providers** section is populated with details about the source of an Array Design, if such information has been defined.

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

Adding a New Array Design

Note: The caArray portal currently accepts the submission of the following formats of array design files: .GAL, .CDF (Affymetrix) and .CSV (Illumina). For GenePix, Agilent and Imagene arrays, an array design file may not be available in all cases. When that is true, caArray can use the array design information contained in the hybridization data files to generate these designs. The first time a hybridization data file for a non-uploaded array design is loaded to caArray, caArray populates the array design from the layout information in the hybridization data file. For more information about working with hybridization files, see *Uploading a Hybridization File* on page 108.

If you have other Array Design types you would like to import to caArray, you must contact NCICB Application Support, <mailto:NCICB@pop.nci.nih.gov>.

To add 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 6.3*):

Arrays: New Array Design Information

* indicates a required field

ARRAY REPORTERS INFORMATION	
Check to upload file:	<input checked="" type="checkbox"/>
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.	
Type of Upload:	GAL file

NEW ARRAY DESIGN INFORMATION	
* Array Design Name:	<input type="text"/>
Array Version:	<input type="text"/>
Technology Type:	In_situ_oligo_features
Surface Type:	polylysine
Attachment Type:	covalent
Strand Type:	double_stranded
Organism:	Escherichia coli
* Array Description:	<input type="text"/>

ARRAY DESIGN VISIBILITY INFORMATION	
	Public caBIC Curation

Figure 6.3 caArray page for defining information for a new Array Design

a. **Array Reporters Information** section —

Check to Upload File — Check if you want to upload the array design file; leave it clear to create an array design place holder. You can come back and upload the array design file later.

Type of Upload — From the drop-down menu, select among these four options:

--**Affymetrix CDF** if you are uploading an Affymetris Chip Definition File.

--**GAL File** if you are using a Genepix-generated GAL.

--**GAL converted from UCSF Spot** if you are uploading a UCSF Spot Design converted GAL format.

--**Illumina Content Descriptor CSV** if you are uploading an Illumina CSV-based content descriptor.

Upload — Browse to locate the appropriate array design data file based upon your selection.

Note: The preferred method for loading array design annotations is from an array design data file (for example a GenePix .GAL file). For GenePix, Agilent and Imagene, an array design data file may not be available in all cases. When an array design data file is not available for these types, caArray can use the array design annotations contained in the

hybridization data files generated from these designs. The **first** time hybridization data for an un-uploaded array design is loaded to caArray, caArray will populate the array design from the layout information in the hybridization data file.

- b. **New Array Design Information** section — Enter or select valid values for the Array Design. Table 6.2 describes the fields of the page¹¹.

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

Table 6.2 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 adding. 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 31.

4. Click the **Save** button

Modifying an Array Design

To modify an existing Array Design, 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 6.3 on page 61.

11. Items with an asterisk are required fields.

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

Array Design: HG-U133A

GENERAL ARRAY DESIGN INFORMATION ?	
Array Design Name:	HG-U133A
Array Version:	1.0
Technology Type:	in_situ_oligo_features
Surface Type:	glass
Attachment Type:	Unknown
Strand Type:	Unknown
Organism:	Unknown
Array Description:	

Done **Modify** Delete

VISIBILITIES	
Visibility:	Public

Modify

REPORTERS	
Number of features:	506944
Array Design File	Download MAGE-ML

DESIGN PROVIDERS						
Name	Affiliation	URI	Address	Phone	Fax	Action
Affymetrix		http://www.affymetrix.com				Remove

Add Provider

PROTOCOLS
Apply Protocol

Figure 6.4 Information displays for an existing Array Design. To modify the object, click the **Modify** button. See accompanying text.

- Click the **Modify** button in either the **General Array Design Information** section or in the **Visibilities** section.

Note: You can do this only if you have the Visibility settings allowing you to modify the array design. If you do not, you will not see the **Modify** button. For more information, see *Visibility* on page 31.
- Make appropriate changes to the Array Design details. (Fields are identical to those described in Table 6.2.)
- 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 or later.
 - The **Number of Features** equals the number of spots on the microarray.
- 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 4 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.

Deleting an Array Design

To delete an Array, follow these steps:

- Search for the **Array Design** you want to delete. (See *Searching Array Designs* on page 54 or *Searching Arrays* on page 61.)
- 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.
- Click the **Delete** button.
- Confirm the deletion by clicking the **OK** button.

- Notes:**
- Deleting an Array Design is a complex and time consuming task. If you encounter any problem, contact NCICB application support.
 - 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 31.

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 54. 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:

- Log in on the caArray main page.
- Select the **Arrays** task tab.
- Click **Search Arrays** from the left navigation menu.
- In the Search dialog box, provide searchable information. You can search by using any of the fields in Table 6.3.

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

Array Searchable Fields	Description	Example
Array Name	Name of the array	ATC_John_BC_BRCA1_01
Array Design	Select from the Array Designs drop-down list.	Hg-u133a

Table 6.3 Searchable fields for Arrays

Array Searchable Fields	Description	Example
Manufacturing Protocol	Select from the Array Manufacturing Protocols drop-down list.	Hg-u133a Protocol
Manufacture Date (range)	Range of dates the array was manufactured	01/01/05 02/01/05
Array Manufacturer	Select from Array manufacturer drop-down list	Affymetrix
Substrate Type	Controlled terms for descriptors of types of array substrates	Glass
Visibility	Allows you to define permissions for who can use your Array for documentation. Options can include groups created in caArray.	Public

Table 6.3 Searchable fields for Arrays (Continued)

5. Click the **Search** button.

Note: If you click **Search** without defining any query parameters, the search is unrestricted and all Arrays you are authorized to see in caArray will display in the Search Results section of your browser (*Figure 6.1*).

If the array you searched for exists, you will see it in the list on the search result page.

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

Adding a New Array

Note: When adding a new Array, you may select a Protocol in caArray of “Array Manufacturing” type that describes the manufacturer 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 *Adding a New Protocol* on page 49.

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 6.5* and described in *Table 6.4*¹²:

Arrays: Submit New Array

* Indicates a required field

SUBMIT NEW ARRAY	
* Array Name:	ATC_John_BC_BRCA1_01
Array Barcode:	
* Array Design:	HG-u133a/b
Array Substrate Type:	glass
Array Manufacturer:	<ul style="list-style-type: none"> Advantage Technology Center (ATC) Affymetrix Albert Einstein Cancer Center Arcturus Bioscience, Inc Ardais Corporation Axon Instruments B. Soares Laboratory Basel Institute for Immunology Baylor College of Medicine BIMAS BioDiscovery, Inc. BioFortis, Inc. Biozentrum, University of Basel Center for Cardiovascular Bioinformatics and Modeling Children's Hospital Los Angeles, Keck School of Medicine, University of Southern California Children's Hospital Los Angeles, Keck School of Medicine, University of Southern California City of Hope National Medical center Clontech Columbia University Cooperative Human Tissue Network
Array Manufacture Date:	
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:	<ul style="list-style-type: none"> Public caBIG Curation Curation Team - delete Curation Team - make public DC Lung Study DC Prostate Study

Figure 6.5 Adding a new Array

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

Table 6.4 Fields for adding a new Array

12. Items with an asterisk are required fields.

Array Submission Fields	Description	Example
Array Manufacture Date	Date of array manufacture	01/01/05
Array Width	Array width in millimeters	
Array Length	Array length in millimeters	
Array Orientation Mark	Mark made on microarray slide which is used as a point of reference for orientation of the slide	#
Array Orientation Mark Position	Position where the mark was made; from drop-down list	Left
Array Description	Description for the Array	
Visibility	Allows you to define permissions for who can use your Array for documentation. Options can include groups created in caArray.	Private

Table 6.4 Fields for adding a new Array (Continued)

Note: In naming an Array, we suggest you follow a convention so that it can be easily identified. In Table 6.4, 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 *Adding a New Protocol* on page 49.

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:	http://arraytracker.nci.nih.gov/index.shtml			
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
			Name Value Type	
Software:	Release Date	<input type="text"/>		
	Version	<input type="text"/>		
	NAME	TYPE	MANUFACTURER	PARAMETERS
	GenePix Pro 3.0.1.22_feature	feature_extraction_software	Axon Instruments	Name Value Type
			st para 4 float	
Save Cancel				

Figure 6.6 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 (Figure 6.6), you must add the **Activity Date** and select the **Performer**.
- Click **Save**. This associates the Protocol you selected with the Array you are adding.

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. See *Searching Arrays* on page 61 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, if it was applied to the Array when it was created (*Figure 6.7*).

ARRAY DETAILS																							
Array Name:	nci432																						
Array Barcode:																							
Array Design:	10k_print2																						
Array Substrate Type:	glass																						
Array Manufacturer:																							
Array Manufacture Date:	5/10/00																						
Array Width:																							
Array Length:																							
Array Orientation Mark:																							
Array Orientation Mark Position:																							
Array Description:																							
Array Visibility:	Public																						
<input type="button" value="Done"/> <input type="button" value="Modify"/> <input type="button" value="Remove"/>																							
PROTOCOL APPLICATION																							
Protocol ID:	URN:LSID:smd.stanford.edu:process:printing/MAGE.Protocol																						
Activity Date:	5/10/00																						
Performer:	Tina Boussard																						
Protocol Name:	printing protocol																						
Protocol Description:	Material is transferred from microtiter plate wells to the slide surface by an automated print head.																						
Hardware:	<table border="1"> <thead> <tr> <th>NAME</th> <th>MODEL</th> <th>TYPE</th> <th>MAKE</th> <th>PARAMETERS</th> </tr> </thead> <tbody> <tr> <td>printer</td> <td></td> <td>arrayer</td> <td></td> <td> <table border="1"> <thead> <tr> <th>Name</th> <th>Value</th> <th>Type</th> </tr> </thead> <tbody> <tr> <td>printer used</td> <td>B001</td> <td></td> </tr> <tr> <td>pin configuration</td> <td>Standard</td> <td></td> </tr> <tr> <td></td> <td>4-tip</td> <td></td> </tr> </tbody> </table> </td> </tr> </tbody> </table>	NAME	MODEL	TYPE	MAKE	PARAMETERS	printer		arrayer		<table border="1"> <thead> <tr> <th>Name</th> <th>Value</th> <th>Type</th> </tr> </thead> <tbody> <tr> <td>printer used</td> <td>B001</td> <td></td> </tr> <tr> <td>pin configuration</td> <td>Standard</td> <td></td> </tr> <tr> <td></td> <td>4-tip</td> <td></td> </tr> </tbody> </table>	Name	Value	Type	printer used	B001		pin configuration	Standard			4-tip	
	NAME	MODEL	TYPE	MAKE	PARAMETERS																		
printer		arrayer		<table border="1"> <thead> <tr> <th>Name</th> <th>Value</th> <th>Type</th> </tr> </thead> <tbody> <tr> <td>printer used</td> <td>B001</td> <td></td> </tr> <tr> <td>pin configuration</td> <td>Standard</td> <td></td> </tr> <tr> <td></td> <td>4-tip</td> <td></td> </tr> </tbody> </table>	Name	Value	Type	printer used	B001		pin configuration	Standard			4-tip								
Name	Value	Type																					
printer used	B001																						
pin configuration	Standard																						
	4-tip																						
Software:	<table border="1"> <thead> <tr> <th>NAME</th> <th>TYPE</th> <th>MANUFACTURER</th> <th>PARAMETERS</th> </tr> </thead> <tbody> <tr> <td></td> <td></td> <td></td> <td></td> </tr> </tbody> </table>	NAME	TYPE	MANUFACTURER	PARAMETERS																		
NAME	TYPE	MANUFACTURER	PARAMETERS																				
Protocol Parameters:	<table border="1"> <thead> <tr> <th>NAME</th> <th>VALUE</th> <th>UNIT</th> <th>TYPE</th> </tr> </thead> <tbody> <tr> <td></td> <td></td> <td></td> <td></td> </tr> </tbody> </table>	NAME	VALUE	UNIT	TYPE																		
NAME	VALUE	UNIT	TYPE																				
<input type="button" value="Remove"/>																							

Figure 6.7 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 51.
- 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 54 or *Searching Arrays* on page 61.)
- 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 31.

Importing MAGE-ML Documents

From the Array Design page, you can launch an import of MAGE-ML documents. For more information, see *Importing MAGE-ML Files* on page 118.

CHAPTER 7

CONTROLLED VOCABULARY TERMS

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

Topics in this chapter include:

- *The Importance of a Controlled Vocabulary* on this page
- *General Overview of the Controlled Vocabulary in caArray* on page 70
- *Workflow for Searching and Adding Terms in caArray* on page 72

The Importance of a Controlled Vocabulary

The use of a controlled vocabulary is fundamental when annotating microarray data in caArray. By using terms from controlled vocabularies, formal classifications of the entries and specified relationships of the terms are established in specified domains of knowledge. 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 microdissection—or whether the tissue represents a mixture of normal and cancerous cells.

Note: While it is recommended that you use terms from a controlled vocabulary, caArray makes it possible to enter terms defined in any specific domain, as long as you can reference a website URI and accession number as the source of that term.

The Controlled Vocabulary Terms feature is used in caArray only to annotate Biomaterials as they are created or modified. For more information, see [Chapter Biological Source Materials](#).

General Overview of the Controlled Vocabulary in caArray

Once you log in to caArray, select the **Controlled Vocabulary Terms** task tab. In a caArray viewer, the Controlled Vocabulary Term entries listed at the upper left of the viewer window are actually Microarray Gene Expression Data (MGED) terms that outline groupings of individual vocabulary terms that reside in caArray (*Figure 7.1*). The MGED ontology provides the structure, the method for organizing these standardized terms in caArray.

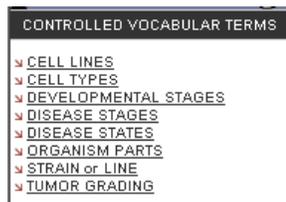


Figure 7.1 Controlled Vocabulary Terms menu options in caArray are based on MGED

The 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://nciterms.nci.nih.gov/NCIBrowser/Dictionary.do>

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

The MGED ontology (MO) provides terms for microarray experiment annotation. However, there are cases when MO points to external controlled vocabularies, and in caArray these cases are annotated using the controlled vocabulary section of the application. That is why this comprehensive section in caArray is called “Controlled Vocabulary Terms”.

List of Common Controlled Vocabulary Terms and Definitions

The options defined in Table 7.9 and *Figure 7.1* represent the Controlled Vocabulary Term categories in caArray which you can search or modify with new terms. This list is accessible in the left sidebar of the the application.

Controlled Vocabulary Term Category	Description
Cell Lines	Identifiers for established cultures of metazoan cells used as biomaterial in caArray protocols or experiments.
Cell Types	Types of unmixed cell used in a caArray experiment.
Developmental Stages	Stages of development in an organism's life cycle from which biomaterial was extracted.

Table 7.1 List of caArray Ontology categories and their MO definitions

Controlled Vocabulary Term Category	Description
Disease Stages	The stage or progression of a disease in an organism, which includes pathological staging of cancers or other measures for other types of diseases.
Disease States	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.
Organism Parts	Parts of an organism's anatomy or substances from an organism which the biomaterial was derived, excluding cells.
Strain or Line	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.
Tumor Grading	A descriptor used in cancer biology that describes abnormalities of tumor cells

Table 7.1 List of caArray Ontology categories and their MO definitions (Continued)

Using the common language elements provided by the Controlled Vocabulary Terms, caArray provides an efficient and effective way to search for terminology stored in caArray. See *Searching for Vocabulary Terms in caArray* on page 73 for explicit instructions for searching for entities in the caArray.

Vocabulary Term Search Overview

Once the **Controlled Vocabulary Terms** tab is open, the Controlled Vocabulary Term 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 7.2*). To illustrate the organization of the vocabulary terms in caArray, click the **Search** button in the Search dialog box 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 7.2)

Controlled Vocabulary: Search Organism Parts

SEARCH ORGANISM PARTS			
Organism Part Name	<input type="text"/>		
Public Database	All	▼	
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			
32 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	http://nciterns.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?bookmarktag=1&conceptname=Brain
Breast	NCI_Thesaurus	C12971	http://nciterns.nci.nih.gov/NCIBrowser/ConceptReport.jsp?dictionary=NCI_Thesaurus&code=C12971
Cerebellum	NCI_Thesaurus		
Colon	NCI_Thesaurus		
Femur	CellML		
Germinal Center	NCI_Thesaurus		
Kidney	CellML		
Kidney	NCI_Thesaurus		
Liver	NCI_Thesaurus	C12392	http://nciterns.nci.nih.gov
Lung	NCI_Thesaurus		
Lymphoid tissue	NCI_Thesaurus	C13049	
Lymph Node	NCI_Thesaurus	C12745	
Mesothelium	NCI_Thesaurus		
murine mammary gland	NCI_Thesaurus	C23302	
Ovary	NCI_Thesaurus	C101764	http://nciterns.nci.nih.gov/NCIBrowser/Connect.do?dictionary=MGED_Ontology&bookmarktag=1
Ovary	NCI_Thesaurus		
Pancreas	NCI_Thesaurus		

Figure 7.2 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 and accession number are referenced.

Search Results Overview

The Vocabulary Term **Search Results** section displays a list of all vocabulary terms in caArray that relate to the selected entry. 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 7.2). Many vocabulary terms include the accession number for the term in the controlled vocabulary that is the source for the term (column 3, Figure 7.2). Some vocabulary terms also include a URI link that takes you directly to the source database (column 4, Figure 7.2). If you want more information about the term, click the link that goes directly to the database. For more information, see *Adding a Vocabulary Term* on page 75.

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.

Workflow for Searching and Adding Terms in caArray

When working with Controlled Vocabulary Terms 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 [Adding a Vocabulary Term](#) on page 75.

2. If the term you are seeking is not located in caArray, follow the directions for adding the term. This procedure includes directions for locating the term in a public database. For more information, see [Adding a Vocabulary Term](#) on page 75.

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 [Adding a Vocabulary Term](#) on page 75.

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

1. Log in on the caArray main page.
2. Select the **Controlled Vocabulary Terms** task tab.
3. Select from among the following Controlled Vocabulary Terms listed on the left navigation menu. (These are defined in Table 7.1 on page 70):
 - **Cell Lines**
 - **Cell Types**
 - **Developmental Stages**
 - **Disease Stages**
 - **Disease States**
 - **Organism Parts**
 - **Strain or Line**
 - **Tumor Grading**

Note: Each of these Controlled Vocabulary Term 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 7.3](#) and described below the figure.

Controlled Vocabulary: Search Organism Parts

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

Figure 7.3 Search Organism Parts dialog box

Note: The form for launching a search for Strain or Line terms requires you to select between **Ecotype** or **Cultivar**. This is the only variation in the search fields among all term categories.

- **{Controlled Vocabulary Term 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.

5. Click the **Search** button. The results display in the Search Results section of your browser (*Figure 7.4*).

Controlled Vocabulary: Search Organism Parts

SEARCH ORGANISM PARTS ?			
Organism Part Name	liver		
Public Database	All		
Accession Number			
<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	C12392	http://nciterns.nci.nih.gov

Figure 7.4 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 7.5*).

Controlled Vocabulary: Search Organism Parts

SEARCH ORGANISM PARTS ?			
Organism Part Name			
Public Database	All		
Accession Number			
<input type="button" value="Search"/> <input type="button" value="Reset"/> <input type="button" value="Submit New Organism Part"/>			
SEARCH RESULTS			
32 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	http://nciterns.nci.nih.gov/NCIBrowser/GetRoleAndProperty.do?bookmarktag=1&con
Breast	NCI_Thesaurus	C12971	http://nciterns.nci.nih.gov/NCIBrowser/ConceptReport.jsp?dictionary=NCI_Thesauru
Cerebellum	NCI_Thesaurus		
Colon	NCI_Thesaurus		
femur	CellML		
Germinal Center	NCI_Thesaurus		
kidney	CellML		
Kidney	NCI_Thesaurus		
Liver	NCI_Thesaurus	C12392	http://nciterns.nci.nih.gov
Lung	NCI_Thesaurus		
Lymphoid tissue	NCI_Thesaurus	C13049	
Lymph Node	NCI_Thesaurus	C12745	

Figure 7.5 Search Results for an unrestricted Organism Parts search

6. To reset the form in order to try another search, click the **Reset** button in the Search {category} dialog box.
7. Interpreting search results:
 - a. 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.
 - b. 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, [Adding a Vocabulary Term](#).
8. To reset the form in order to try another search, click the **Reset** button in the Search {category} dialog box.

Adding 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 **Controlled Vocabulary Terms** task tab.
3. Click the Controlled Vocabulary Terms 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 7.1 on page 70.
4. At the bottom of the search section, select the **Submit New {Controlled Vocabulary Term entry name}** button.

All of the fields in the Add {Controlled Vocabulary Term category} 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.

- 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 adding a specific cell line term to caArray, see *Case Study: Adding a Cell Line Term to caArray* on page 77.

This is the only Controlled Vocabulary Terms category in caArray that has such a help section.

- Go to the database where you want to locate a term. The example used is the NCI Thesaurus.
- 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 7.6*).



Figure 7.6 NCI Thesaurus search results for “prostate gland”

- 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 7.7*). You need this reference information to adequately identify a term that you are

adding in caArray; you are also facilitating other users' ability to learn more about the selected term.

The screenshot shows the NCI website interface. At the top, there is a search bar with 'prostate gland' entered and 'Max Results' set to 10. The 'Advanced Search' section is also visible. The main content area is titled 'Concept Details' for 'Prostate Gland'. It includes a 'Bookmark this page' link and a 'Printable Page' link. The 'Identifiers' section shows the name 'Prostate_Gland' and the code 'C12410'. The 'Relationships to other concepts' section lists 'Anatomic_Structure_is_Physical_Part_of' relationships with 'Male Reproductive System' and 'Exocrine System'. The 'Information about this concept' section provides a definition: 'NCI-GLOSS|(PROS-tate) A gland in the male reproductive bladder. The prostate surrounds part of the urethra, bladder, and produces a fluid that forms part of semen.' Other information includes the display name 'Prostate', and synonyms with source data: 'Genital System, Male, Prostate|SY|NCI', 'Human Prostate Gland|SY|CTRM', and 'Human Prostate|SY|CTRM'.

Figure 7.7 Concept details for query subject

9. In the Add {term} dialog box in caArray:
 - a. Enter the term exactly as it appears in your source database: for example, Prostate_Gland (Figure 7.8).
 - b. Copy and paste the accession number (required field) from your source database.
 - c. Enter the URI for the database.

Controlled Vocabulary: Add Cell Type

The screenshot shows the 'ADD CELL TYPE' dialog box. It has four input fields: 'Cell Type' with the value 'prostate gland', 'Public Database' with a dropdown menu showing 'NCI_Thesaurus', 'Accession Number' with the value 'C12410', and 'URI' with the value 'http://nciterns.nci.nih.gov/'. There are 'Add', 'Reset', and 'Cancel' buttons at the bottom right. A note at the bottom left states '* indicates a required field'.

Figure 7.8 Adding a Cell Type term

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

Case Study: Adding a Cell Line Term to 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 **Controlled Vocabulary Terms** tab at the top of the caArray viewer.
2. Search for all the cell lines in caArray (the default selection when you clicked on Controlled Vocabulary Terms). Without entering anything in the search text fields, click the **Search** button (the upper section of *Figure 7.9*). This launches an unrestricted search for all Cell Lines terms.

Controlled Vocabulary: Search Cell Lines

SEARCH CELL LINES ?

Cell Line Name	<input type="text"/>	
Public Database	All	▼
Accession Number	<input type="text"/>	

SEARCH RESULTS

29 items found, displaying 1 to 20. [\[First/Prev\]](#) **1, 2** [\[Next/Last\]](#)

Cell Line Name	Database	Accession Number	Link
BT-474	ATCC_Cultures	HTB-20	
colo_320_HSR	ATCC_Cultures	CCL-220	http://www.atcc.org/
COLO_320DM	ATCC_Cultures	CCL-220	http://www.atcc.org
COLO_320DM	ATCC_Cultures	CCL-320	http://www.atcc.org/
HCC78	NCI_Thesaurus		
JLCELLINE001sdfsd	MGED Ontology	ACC1234	
JLCELLINE001sdfsd	MGED Ontology	ACC1234	
MCF-12A	ATCC_Cultures	CRL-10782	http://www.atcc.org
MCF-7	ATCC_Cultures	HTB-22	http://www.atcc.org
MDA-MB-231	ATCC_Cultures	HTB-26	http://www.atcc.org
MDA-MB-453	ATCC_Cultures	HTB-131	http://www.atcc.org
MDA-MB-453	ATCC_Cultures	HTB-131	http://www.atcc.org
MG-63	ATCC_Cultures	CRL-1427	http://www.atcc.org
NCL-H1437	ATCC_Cultures	CRL-5872	http://www.atcc.org
NCL-H2009	ATCC_Cultures	CRL-5911	http://www.atcc.org
NCL-H2087	ATCC_Cultures	CRL-5922	http://www.atcc.org
NCL-H2347	ATCC_Cultures	CRL-5942	http://www.atcc.org
ovarian surface epithelial cell line	ATCC_Cultures		
Pr111	Adult_Mouse_Anatomy	NCI-CCR	http://www.cancer.gov/

Figure 7.9 The Search Results in the Cell Lines viewer display cell lines in the caArray database.

3. The **Search Results** section of the viewer (*Figure 7.9*) 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 7.10*).

Controlled Vocabulary: Add Cell Line

* indicates a required field

ADD CELL LINE ?

* Cell Line Name	<input type="text"/>	
* Public Database		▼
Accession Number	<input type="text"/>	
URI	<input type="text"/>	

Figure 7.10 Add Cell Line dialog box

5. Click the **Help** button. The Help topic that opens points to two databases for finding controlled terms for cell lines, ATCC and CAPRI (*Figure 7.11*).

Experiments > Importing MAGE-ML Files > Adding Information About a Cell Line

Adding Information About a Cell Line

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

1. From the caArray main page, click **Controlled Vocabulary Terms** on the menu bar.
2. Click the **Cell Lines** link on the left side bar.
3. In the lower right hand corner of the Search Cell Lines form, click the **Submit New Cell Line** button.
4. Enter or select the details of the cell line you want to submit such as

a. **Name**

b. **Database**

-- ATCC Cultures, (MGED, EVS)

-- CABRI Human and Animal Cell lines, (MGED, EVS)

3. **Accession Number**

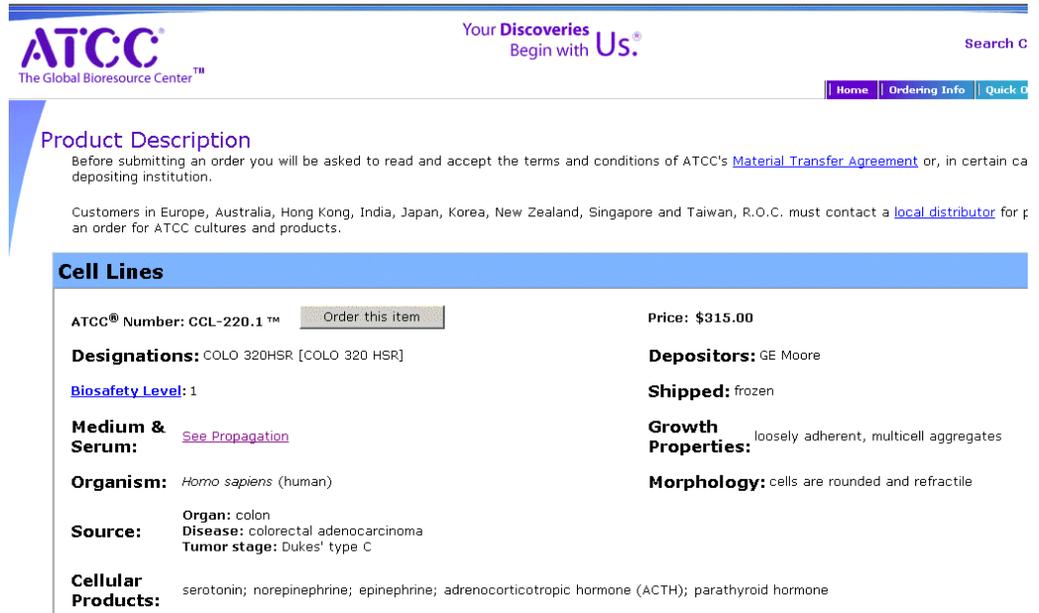
4. **URI**

6. Click **Add** to save the entered information.

Related Topics 

Figure 7.11 The Help topic for adding a cell line

6. 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 7.12).



The screenshot shows the ATCC website interface. At the top, the ATCC logo is on the left, and the slogan "Your Discoveries Begin with Us." is on the right. A search bar is located in the top right corner. Below the header, there are navigation links for Home, Ordering Info, and Quick Order. The main content area is titled "Product Description" and includes a disclaimer about terms and conditions. Below this, there is a section for "Cell Lines" with a blue header. The product details for "ATCC® Number: CCL-220.1™" are displayed in a table-like format. The price is listed as \$315.00. Designations include COLO 320HSR [COLO 320 HSR]. Biosafety Level is 1. Medium & Serum information points to a propagation page. The organism is Homo sapiens (human). Source information includes organ (colon), disease (colorectal adenocarcinoma), and tumor stage (Dukes' type C). Cellular Products listed include serotonin, norepinephrine, epinephrine, adrenocorticotropic hormone (ACTH), and parathyroid hormone. Depositors are GE Moore, and the product is shipped frozen. Growth Properties are loosely adherent, multicell aggregates, and Morphology consists of rounded and refractile cells.

ATCC® Number: CCL-220.1™	Order this item	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: <i>Homo sapiens</i> (human)		Morphology: cells are rounded and refractile
Source: Organ: colon Disease: colorectal adenocarcinoma Tumor stage: Dukes' type C		
Cellular Products: serotonin; norepinephrine; epinephrine; adrenocorticotropic hormone (ACTH); parathyroid hormone		

Figure 7.12 ATCC website

- Returning to caArray, enter the information from the ATCC web site in the form as shown in *Figure 7.13*.

Controlled Vocabulary: Add Cell Line

ADD CELL LINE	
* Cell Line Name	COLO 320 HSR
* Public Database	ATCC_Cultures
Accession Number	CCL-220
URI	http://www.atcc.org/

* indicates a required field Add Reset Cancel

Figure 7.13 Entry form for adding a new cell line

- Click **Add** to submit the information. caArray displays the information for the newly submitted Cell Line (*Figure 7.14*).

Controlled Vocabulary: Cell Line Details

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	http://www.atcc.org/

Done Add Another

Figure 7.14 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 Sample Information section, when you submit information about Source Material 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 7.15*.

The screenshot shows the National Cancer Institute caArray interface. The main navigation bar includes 'SAMPLE INFORMATION', 'HOME', 'CONTACTS', 'PROTOCOLS', 'ARRAYS', and 'CONTROLLED VOCABULARY'. On the left, there are links for 'SEARCH SOURCE MATERIALS', 'NEW SOURCE MATERIAL', 'SEARCH SAMPLE EXTRACTS', 'NEW SAMPLE EXTRACT', 'SEARCH LABELED EXTRACTS', and 'NEW LABELED EXTRACT'. Below these are 'QUICK LINKS' such as 'ONLINE HELP', 'NCI HOME', 'NCICB HOME', 'caARRAY WEBSITE', 'NCICB SUPPORT', and 'ABOUT'. The main content area displays the 'SAMPLE INFORMATION CHARACTERISTICS' form. The 'Cell Line' dropdown menu is open, showing a list of cell lines: 'BT-474', 'colo 320 HSR', 'COLO 320 HSR' (highlighted), 'COLO 320DM', 'HCC78', 'JLCELLLINE001 sdfs', 'JLCELLLINE001 sdfs', 'MCF-12A', and 'MCF-7'. The 'Disease State' dropdown is also visible, showing 'BT-474'. There are 'Save' and 'Cancel' buttons at the bottom right of the form.

Figure 7.15 The new cell line you submitted displays among the Source Material (Sample Information) Cell Line characteristics in caArray.

CHAPTER 8

BIOLOGICAL SOURCE MATERIALS

This chapter describes the creation, annotation, and management of biological source materials in caArray.

Topics in this chapter include:

- [Overview of Biological Source Materials](#) on this page
- [Biomaterials Workflow](#) on page 84

Overview of Biological Source Materials

Materials of biological origin are used in microarray experiments, and the state and characteristics of those biomaterials can be objectively documented and described. Biological materials (biomaterials) can be treated, labeled and hybridized on microarrays to study relative expression levels of the genes represented on the microarrays. All categories of biological materials are created in caArray to later be included as essential components in a caArray Experiment.

Many biological materials' characteristics are defined in caArray by terms found in the caArray Controlled Vocabulary Terms. For more information, see [Chapter 9 Controlled Vocabulary Terms](#).

Biological materials in caArray consist of **Source Materials**, **Sample Extracts**, and **Labeled Extracts**, defined below and illustrated in *Figure 8.1* in their hierarchical relationship.

- **Biological material** 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. In caArray, biological materials are divided into three different categories, named below, based on the treatment status of the biomaterial. *Example:* a cDNA preparation from human tumor tissue that has been treated with an anti-cancer drug.

- **Source Materials** are the original source biomaterials before any treatment events. *Example:* Tissue sample or biopsy material.
- **Sample Extracts** are Source Materials after any treatment event. *Example:* A Source Material tissue treated with RNA extraction method yields the Sample Extract, RNA.
- **Labeled Extracts** are Sample Extracts that have been labeled for detection of the nucleic acids. *Example:* The Sample Extract RNA is labeled with a fluorescent dye, yielding the labeled extract RNA.

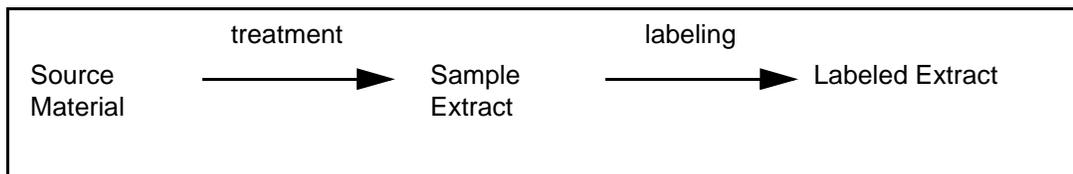


Figure 8.1 Biomaterials components and their relationship in caArray

The nature of each type of biomaterial is defined in varying dialog boxes in caArray. The relevant fields for each is described in Table 8.1, Table 8.2, and Table 8.3.

The term Source Material refers specifically to original source material before it is treated. The nature of Source Materials in caArray is described in Table 8.1¹³:

Source Material Fields		
Field	Description	Example
Source Material Name	Name given to Source Material sample Note: It is a good idea to clearly name Source Materials	
Description	Description of the Source Material.	
*Material Type	Controlled terms for the state of the Source Material	Organism part; cell line
*Organism	Documents the species from which the Source Material is obtained.	<i>Homo sapiens</i>
*Provider	The name of the organization or individual who provided the Source Material	NIH Clinical Center
*Source Material Type	Controlled terms for the type of the Source Material	Lung Biopsy Sample--PatientX

Table 8.1 Fields for documenting Source Materials

13. Items with an asterisk are required fields when adding a new Source Material. See *Adding a Source Material* on page 87.

Source Material Fields		
Field	Description	Example
Visibility	<p>Defines permissions for those who can use your Source Material for documentation. Options include Private, Public and designated groups.</p> <p>Note: If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and modify the object.</p> <p>See <i>Visibility</i> on page 31.</p>	Private

Table 8.1 Fields for documenting Source Materials (Continued)

A Sample Extract represents the sample obtained from the Source Material after it has been processed for use in microarray experiments. The nature of Sample Extracts In caArray is described in Table 8.2:

Sample Extract Fields		
Field	Description	Example
Material Type	Controlled terms for the type of the Sample Extract.	cDNA, total RNA
Source Material	<p>The source from which the Sample Extract was derived</p> <p>Note: If the Source Material does not exist on the Source Material drop-down list, you must first submit the Source Material before you can submit the Sample Extract</p>	Lung cancer biopsy_1
Organism	Documents the species from which the Sample Extract was derived	<i>Homo sapiens</i>
Visibility	<p>Defines permissions for those who can use your Sample Extract for documentation.</p> <p>Note: Visibility of the Sample Extract inherits the visibility of the Source Material from which Sample Extract is derived. If the visibility of the Source Material is private, then the visibility of the Sample Extract is private as well.</p> <p>See <i>Visibility</i> on page 31.</p>	

Table 8.2 Fields for documenting Sample Extracts

A Labeled Extract is a Sample Extract 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 8.3:

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

Table 8.3 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 caArray to determine if the following biomaterials already exist in caArray:
 - Source Material
 - Sample Extract related to Source Material
 - Labeled extracts related to the Source Materials' Sample Extracts
2. If the specified biomaterial is not already in caArray, submit or add a new:
 - Source Material
 - Sample Extract related to a newly submitted Source Material
 - Labeled Extracts related to a newly submitted Sample Extract

3. Modify or delete an existing biomaterial.

Working with Source Materials

Searching for a Source Material

To search **Source Materials**, follow these steps:

1. Log in on the caArray main page.
2. On the menu bar, select the **Sample Information** task tab.

OR

3. Click **Source Materials** from the left sidebar menu, under **Sample Information**. The Search Source Materials dialog displays in the browser (*Figure 8.2*).
4. Provide searchable information. You can search by using any of the following fields (defined in Table 8.1 on page 82):
 - **Material Type**
 - **Organism**
 - **Source Material Name**
 - **Source Material Type**
 - **Provider**
 - **Visibility**

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

5. To clear the form in order to try another search, click the **Reset** button.
6. Click the **Search** button. If the Source Material exists in caArray, it will display in the **Search Results** section (*Figure 8.2*).

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

Sample Information: Search Source Materials

SEARCH SOURCE MATERIALS ?			
Material Type	All	Source Material Type	All
Organism	All	Provider	All
Source Material Name		Visibility	All

SEARCH RESULTS			
2,259 items found, displaying 1 to 20. [First/Prev] 1 , 2 , 3 , 4 , 5 , 6 , 7 , 8 [Next/Last]			
Source Material Name	Material Type	Organism	Description
cDNA from diffuse large B-cell lymphoma 11	organism_part		
MET6_U95Av2 prostate tumor	organism_part		
100c_Lung cell line_HCC78	cell		
100c_Lung cell line_HCC78_09/23/03_L_20060912_12-12-37-780_CL2003092302AA	cell		
101 tissue Non Neoplastic Liver	organism_part		
101c_Lung cell line_H2009	cell		
101c_Lung cell line_H2009_09/23/03_L_20060912_12-12-37-780_CL2003092303AA	cell		
101 tissue Non Neoplastic Liver_09/23/03_L_20060912_12-12-37-780_CL2003092308AA	organism_part		
102 tissue Leiomyoma	organism_part		
10219-10218_1656_GBM_133A_8-13-02	organism_part		
102 tissue Leiomyoma_09/23/03_L_20060912_12-12-37-780_CL2003092311AA	organism_part		
103 tissue Malignant G1 Stromal Tumor	organism_part		
103 tissue Malignant G1 Stromal Tumor_09/23/03_L_20060912_12-12-37-780_CL2003092310AA	organism_part		

Figure 8.2 Search Source Materials/Source Material unrestricted search results

- To see the details corresponding to a particular Source Material, click the **Source Material** name. This opens the Source Material Details page (Figure 8.3).

SOURCE MATERIAL DETAILS ?	
MAGE Identifier	gov.nih.nci.ncicb.caarray:BioSource:1015897589991538:1
Source Material Name	cDNA from diffuse large B-cell lymphoma 11
Description	
Material Type	organism_part
Organism	Homo sapiens
Provider	Dana Farber Cancer Institute
Source Material Type	frozen_sample
Visibility	Public

SAMPLE INFORMATION CHARACTERISTICS	
Cell Type	B-Lymphocyte
Disease Stage	IPI low
Disease State	Diffuse large B-cell Lymphoma
Individual	DLBC11
Organism Part	Lymphoid tissue

Figure 8.3 The Source Material Details page displays information about the Source Material

The Source Material Details page displays characteristics defined when the Source Material object was submitted to caArray. The Biomaterials

characteristics display vocabulary term(s) assigned to this Source Material from the caArray Controlled Vocabulary Terms.

Adding a Source Material

To submit/add a Source Material, follow these steps:

1. Log in on the caArray main page.
2. Select the **Sample Information** task tab.
3. At the upper left of your browser, select **Source Materials**.
4. At the bottom right of the Search Source Materials form, click the **Submit New Source Material** button
5. Complete the Source Material fields, as demonstrated in *Figure 8.4*. (Source Material terms are defined in Table 8.1 on page 82).

Sample Information: Add Source Materials

* indicates a required field

NEW SOURCE MATERIAL ?

* **Source Material Name**

Description
 Example: Lung sample obtained using... from a female patient age 65 with carcinoma...

* **Material Type** Specify New Type:

* **Organism** Specify New Type:

* **Provider**

* **Source Material Type** Specify New Type:

Visibility
 caBIG
 Curation
 Curation Team - delete
 Curation Team - make public
 DC Lung Study
 DC Prostate Study
 GMDL_Group
 JenLab
 MAGE-OM API users

Figure 8.4 Adding a new Source Material

6. Click the **Save** button to submit the Source Material to caArray.
7. In the Source Material Details page that opens, specify the Source Material characteristics by clicking the **Modify Characteristics** button.

This opens a **Source Material Characteristics** list box where you can select one or multiple characteristics that you want associated with the Source Material you are adding. (Many of the terms are found in the controlled vocabulary section of caArray Controlled Vocabulary Terms, while others represent static information such as age.)

- Select one or multiple fields which are applicable: hold the CTRL key and click to select non-contiguous fields (*Figure 8.6*).

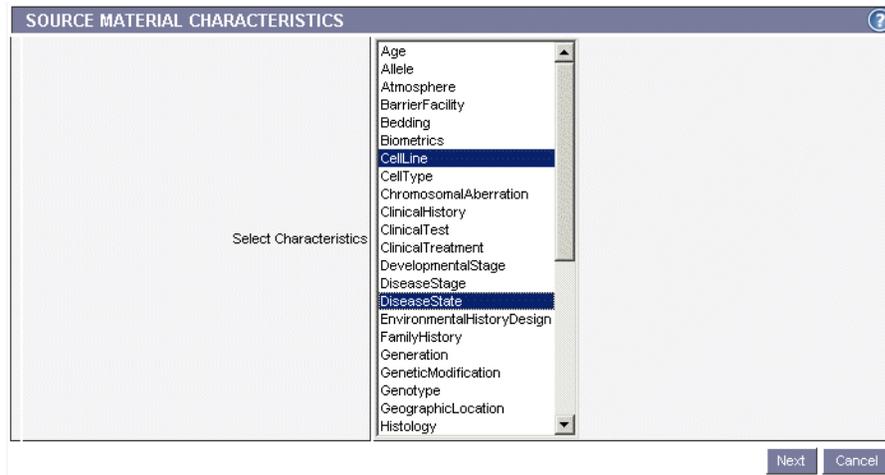


Figure 8.5 Source Material Characteristics dialog box

- Click **Next** to continue.

Whatever characteristics you selected in the previous dialog box become fields in the dialog that now opens (*Figure 8.6*). 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). For example, the Temperature field does not offer a drop-down list showing “37 Fahrenheit”, but you could enter that in the text box.

Figure 8.6 Dialog box for specifying Source Material “Sample Information” 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 Source Materials Details page, click **Done** to complete the submission.

Modifying a Source Material

To modify a Source Material, follow these steps:

- Log in on the caArray main page.
- Select the **Biomaterials** task tab.

- At the upper left of your browser, click **Source Materials**.
- Launch a search for the Source Material you want to modify. For more information, see *Searching for a Source Material* on page 85.
- Click the **Source Material Name** in the Source Material **Search Results** section. This opens the Source Material Details page (*Figure 8.7*).

SOURCE MATERIAL DETAILS ?	
MAGE Identifier	gov.nih.nci.ncicb.caarray:BioSource:1015897589991538:1
Source Material Name	cDNA from diffuse large B-cell lymphoma 11
Description	
Material Type	organism_part
Organism	Homo sapiens
Provider	Dana Farber Cancer Institute
Source Material Type	frozen_sample
Visibility	Public
<input type="button" value="Done"/>	

SAMPLE INFORMATION CHARACTERISTICS	
Cell Type	B-Lymphocyte
Disease Stage	PI low
Disease State	Diffuse large B-cell Lymphoma
Individual	DLBC11
Organism Part	Lymphoid tissue

Figure 8.7 Source Material details page

- To modify the Source Material details, click the **Modify** button.

* indicates a required field

UPDATE SOURCE MATERIAL	
* Source Material Name	<input type="text" value="Lung from patient #1"/>
Description	<input type="text"/>
* Material Type	<input type="text" value="organism_part"/> <input type="button" value="Specify New Type:"/>
* Organism	<input type="text" value="Homo sapiens"/> <input type="button" value="Specify New Type:"/>
* Provider	<input type="text" value="NCICB"/>
* Source Material Type	<input type="text" value="frozen_sample"/> <input type="button" value="Specify New Type:"/>
* Visibility	<input type="text" value="Public"/> <input type="text" value="SAM"/> <input type="text" value="caArray Developers"/>

Figure 8.8 Dialog box for updating a Source Material object

- The Update Source Material dialog box displays current information for the open Source Material (*Figure 8.8*). Modify the information according to your preference. (Each field is described in Table 8.1 on page 82.)
- Click **Save**. This returns you to the Source Material Details page.
- Click the **Modify Characteristics** button.

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

This opens a **Source Material Characteristics** panel/list where you can select one or multiple characteristics that you want associated with the Source Material you are modifying (*Figure 8.9*). (Many of the terms are found in the controlled vocabulary section of caArray Controlled Vocabulary Terms, while others represent static information such as age.)

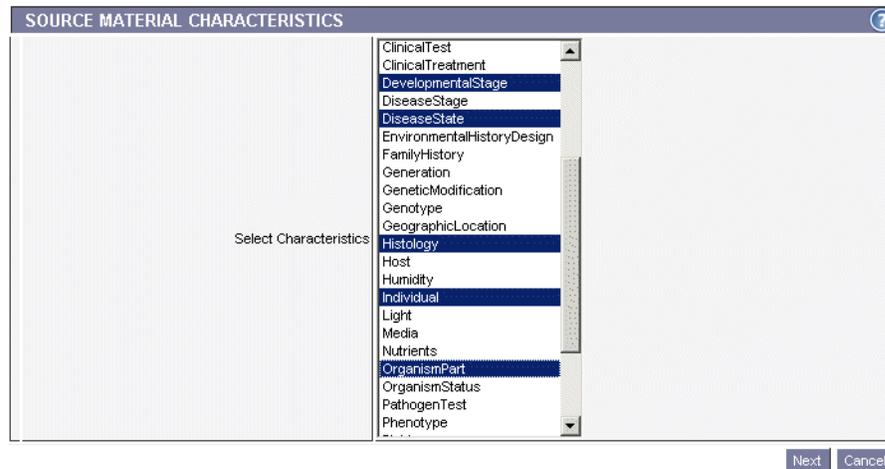


Figure 8.9 Dialog box for specifying Biomaterial characteristics

- Use CTRL + click to select multiple non-contiguous fields. Click **Next** to continue.

Whatever characteristics you selected in the previous dialog box become fields in the Sample Information Characteristics dialog box that now opens (*Figure 8.10*). 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).

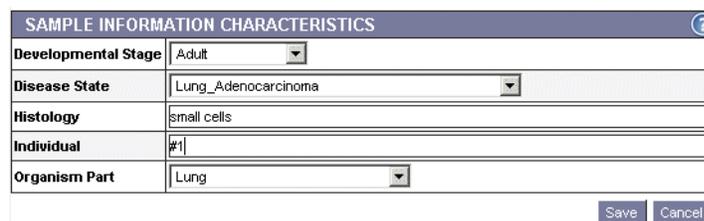


Figure 8.10 Dialog box for specifying Biomaterial characteristics

- Select or enter the Sample Information Characteristics in the fields provided.
- Click **Save** to save your changes or click the **Cancel** button to disregard the changes.
- Back in the Source Material Details page, click **Done** when you are finished modifying the object.

Deleting a Source Material

To delete a Source Material, follow these steps:

1. Log in on the caArray main page.
2. Select the **Sample Information** task tab.
3. At the upper left of your browser, click the **Source Materials** option.
4. Launch a search for the biomaterial you want to delete. See *Searching for a Source Material* on page 85 for more information.
5. In the **Search Results** section of the page, note the name of the Source Material to be deleted.
6. In the last column, on the row corresponding to the Source Material name, click the **Delete** hypertext link.
7. Confirm the deletion by selecting the **OK** button

Notes:

- The **Delete** option displays only if you have the appropriate permissions to perform the delete task. For more information, see *Visibility* on page 31. Additionally, if an experiment that uses the Source Material has been submitted or published, the Source Material *cannot* be deleted.
- You must also delete all associated Sample Extracts and Labeled Extracts before you can delete a Source Material.
- Deleting a biomaterial cannot be undone.

Working with Sample Extracts

Searching for a Sample Extract

To search **Sample Extracts**, follow these steps:

1. Log in on the caArray main page.
2. Select the **Sample Information** task tab
3. At the upper left of your browser, select **Search Sample Extracts**.
4. Provide searchable information. You can search by using any of the following fields (defined in Table 8.2 on page 83):
 - **Sample Name**
 - **Material Type**
 - **Source Material** (from which the Sample Extract is derived)
 - **Organism**
 - **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 Sample 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 Sample Extracts in caArray display in the Search Results section.

6. To see the details corresponding to a particular Sample Extract, click the **Sample Extract** name. Details may include Sample Information Characteristics and treatments associated with the extract.
7. To reset the form in order to try another search, click the **Reset** button.

Adding a Sample Extract

There are three steps in adding a Sample Extract: 1) identifying the Source Material from which the Sample Extract is derived; 2) identifying a treatment to the Sample Extract; and 3) identifying a protocol describing the treatment of the Sample Extract.

- 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 Sample Extract (see *Adding a New Protocol* on page 49 for more information).
 - You must also create a Source Material before you can create a Sample Extract.

To submit a Sample Extract, follow these steps:

Step 1 – Identifying a Source Material

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

In the **Sample Extract** dialog box that opens, enter or select the requested information as demonstrated in . Parameters are described in Table 8.4¹⁴.

SAMPLE EXTRACT	
* Select Source Sample	Lung from patient #1
* Name of Resulting Sample	user-defined name for new sample extract
* Type of Resulting Sample	cell_lystate Specify New Type:
Description of Resulting Sample	Enter description of new sample extract here

* indicates a required field

Figure 8.11 Sample Extract dialog box for entering definitions of new Sample Extract

Submission Terms	Definition
* Select Source Sample	The cells, organ or tissue source of the material
* Name of Resulting Sample	Name of the sample after it has been processed.
* Type of Resulting Sample	Type of the sample after it has been processed.

Table 8.4 Fields describing new Sample Extract

14. Items with an asterisk are required fields.

Submission Terms	Definition
Specify New Type	If the type is not on the previous list, enter the new type of the sample.
Description of Resulting Sample	Description of the sample after it has been processed.

Table 8.4 Fields describing new Sample Extract (Continued)

- Click **Next** to continue. A new viewer opens that displays the information you have just entered (top segment of Figure 8.12).

Sample Information: Add Sample Extract

SAMPLE INFORMATION

Source Sample	Lung sample patient
Name Of Resulting Sample	lung tumor extract
Material Type Of Resulting Sample	genomic_DNA
Description Of Resulting Sample	Enter description in this field.

ADD NEW TREATMENT EVENT

* Treatment Type: harvest

Measurement Value: [] Unit Type: []

Compound Measurement

Compound: [] Value: [] Unit Type: []

Add Compound Measurement

* indicates a required field

Apply Protocol Add Treatment Done

Figure 8.12 Dialog box displaying initial definition of Sample Extract source material

Step 2 – Identifying a Treatment for a Sample Extract

- In the **Add New Treatment Event** section (Figure 8.12), enter the requested information, described in Table 8.5¹⁵:

Submission Terms	Definition	Example
*Treatment Type	The type of protocol by which an input biomaterial is treated.	Incubate
Measurement <ul style="list-style-type: none"> Value Unit type 	The measurement of the treatment	15 minutes

Table 8.5 Fields describing the treatment event that resulted in the new Sample Extract

15. Items with an asterisk are required fields.

Submission Terms	Definition	Example
Compound measurement <ul style="list-style-type: none"> • Compound • Value • Unit type 	The compound and measurement applied to the treatment	1 mmol

Table 8.5 Fields describing the treatment event that resulted in the new Sample Extract

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 for a Sample Extract

Note: If you have not identified the protocol for the type of treatment you selected in the previous step, you must first do so before you can finish adding your Sample Extract (see *Adding a New Protocol* on page 49 for more information).

1. Click the **Apply Protocol** button.
2. Select the protocol for the treatment from the drop down list (*Figure 8.13*).

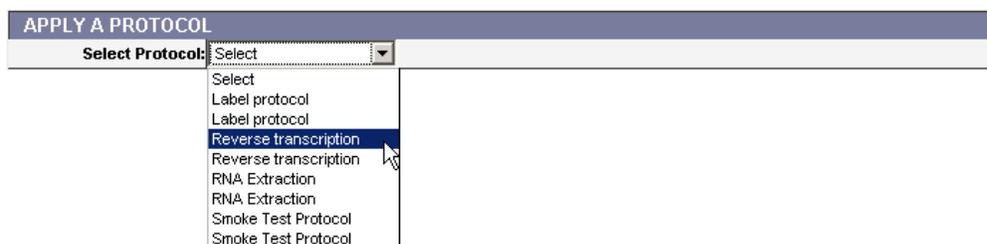


Figure 8.13 Select Protocol drop-down list

3. Once select, the Protocol information displays. Click **Continue**.
4. On the new form that opens, 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 38.

5. Click the **Add Treatment** button.

The treatment information displays after you have selected it.

6. If there are more treatments, repeat steps 1-5. If there are no more treatments, click the **Commit Treatment** button. Then click **Done** to submit the Sample Extract.

Modifying a Sample Extract

To modify a Sample Extract, follow these steps:

1. Log in on the caArray main page.
2. Select the **Sample Information** task tab.
3. Select **Search Sample Extracts** on the left sidebar, and launch the search for the Sample Extract you want to modify. For more information, see *Searching for a Sample Extract* on page 91.
4. Click the **Sample Extract Name** in the [Sample Extract] **Search Results** section. This opens the Sample Extract Details page (*Figure 8.14*).

Sample Extract: prostate carcinoma P1 cDNA

SAMPLE EXTRACT DETAILS	
MAGE Identifier	gov.nih.nci.ncicb.caarray:BioSample:1015897535941596:1
Source Sample	primary prostate carcinoma P1
Sample Type	synthetic_DNA
Description	

Done Modify Delete

SAMPLE INFORMATION CHARACTERISTICS	
Age	66 years
	Initial Time Point: birth
Disease State	Prostate_Adenocarcinoma
Sex	male

TREATMENT 1	
Treatment Type	nucleic_acid_extraction
Measurement	

PROTOCOL APPLICATION SUMMARY	
Protocol Name	MSKCC RNA extraction
Protocol Type	nucleic_acid_extraction
Activity Date	8/1/02
Performer	William Gerald
Measurement	
Parameters	

Modify Treatment

Add New Treatment

Figure 8.14 Sample Extract Details page where you can modify the object

5. To modify the Sample Extract details, click the **Modify** button below the top section of the page.
6. Modify the Sample Extract details (defined in Table 8.2 on page 83) and click **Submit Changes** to save the changes or **Cancel** to abort the changes.
7. 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 51.

8. 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 privileges to modify the Sample Extract. If you do not, a notice displays informing you you cannot modify the object.

Deleting a Sample Extract

To delete a Sample Extract, follow these steps:

1. Log in on the caArray main page.
2. Select the **Sample Information** task tab on the caArray menu bar.
3. Select **Search Sample Extract**, and launch the search for the Sample Extract you want to modify. For more information, see *Adding a Source Material* on page 87.
4. Select the **Sample Extract Name** in the Sample Extract search results section.
5. Click the **Delete** button
6. Confirm the delete by clicking the **OK** button.

- Notes:**
- You can delete a Sample Extract only if you have the appropriate permissions to do so. For more information, see *Visibility* on page 31. Additionally, if an experiment that uses the Sample Extract has been submitted or published, the Source Material *cannot* be deleted.
 - Deleting a Sample Extract 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 **Sample Information** 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 8.3 on page 84:
 - **Material Type**
 - **Sample Extract** from which it is derived
 - **Organism**
 - **Labeled Extract Name**
 - **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 Source Materials in caArray display in the Search Results section.

6. To see the details corresponding to a particular Labeled Extract, click the **Labeled Extract** name.

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

Adding a Labeled Extract

- Notes:
- If you have not submitted the protocol describing the procedure in which the Sample Extract was labeled, forming a Labeled Extract, you must do so before you can submit a Labeled Extract (see *Adding a New Protocol* on page 49 for more information).
 - You also must have created a Source Material and Sample Extract before you can create a Labeled Extract.

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

To submit a Labeled Extract follow these steps:

Step 1 – Identifying the Treatment for a Labeled Extract

- Log in on the caArray main page.
- Select the **Sample Information** task tab.
- Select **New Labeled Extract** from the left navigation menu.
- Complete the **Labeled Extract** fields as demonstrated in *Figure 8.15* and described in Table 8.6¹⁶.

Sample Information: Add Labeled Extract

* indicates a required field

LABELED EXTRACT	
*Select a Sample Extract to be Labeled	cy5 labeled tumor BRCA1 52_2 cDNA_L_20060330_14-12-47-653_JHG-U95Bref-10
*Name of the Resulting Labeled Extract	
Treatment Type	Label
*Label	Cy5
*Amount of Nucleic Acid Labeled	50 ug
*Material Type of the Resulting Labeled Extract	genomic_DNA
Description of the Resulting Labeled Extract	

Apply Protocol Cancel

Figure 8.15 Adding information for a new Labeled Extract

Submission Terms	Definition
*Select a Sample Extract to be Labeled	Name of the Sample Extract from which the Labeled Extract will be derived
*Name of Resulting Extract	Name of the biomaterial after it has been processed.
Treatment Type	The type of protocol by which an input biomaterial is treated.
*Label	The labeling material used for the Labeled Extract

Table 8.6 Fields for adding a new Labeled Extract

16. Items with an asterisk are required fields.

Submission Terms	Definition
*Amount of Nucleic Acid Labeled	Measurement of the Sample Extract to be labeled
*Material Type of Resulting Labeled Extract	Type of the biomaterial after it has been processed to Labeled Extract
Description of the Resulting Labeled Extract	Description of the Labeled Extract after it has been processed.

Table 8.6 Fields for adding a new Labeled Extract (Continued)

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

Step 2 – Identifying a Protocol for a Labeled Extract

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

1. Select the labeling protocol from the drop down list.
2. 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 38.

3. 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 **Sample Information** task tab on the caArray menu bar.
3. On the left sidebar, 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 8.16*).

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 Sample Information, 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 Sample Extract

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

Labeled Extract Details									
MAGE Identifier	gov.nih.nci.ncicb.caarray:LabeledExtract:1015897536220073:1								
Sample Information	Ovarian adenocarcinoma BRCA2 8 cDNA								
Name	Cy5 labeled tumor BRCA2 8 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"/>									
Sample Information Characteristics									
Age	57 years								
Developmental Stage	Initial Time Point: birth Adult								
Disease Stage	Sage IIC								
Disease State	Ovarian Adenocarcinoma								
Genotype	BRCA-2								
Histology	serous								
Individual	BRCA-2 8								
Organism Part	Ovary								
Organism Status	premortem								
Sex	female								
Tumor Grading	Grade 2								
Protocol									
Protocol ID:									
Activity Date:	12/22/05								
Performer:	Amir Jazaeri								
Protocol Name:									
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 (OSE RNA).								
URI:									
Hardware:	<table border="1"> <thead> <tr> <th>NAME</th> <th>MODEL</th> <th>TYPE</th> <th>MAKE</th> </tr> </thead> <tbody> <tr> <td> </td> <td> </td> <td> </td> <td> </td> </tr> </tbody> </table>	NAME	MODEL	TYPE	MAKE				
NAME	MODEL	TYPE	MAKE						
Software:	<table border="1"> <thead> <tr> <th>NAME</th> <th>TYPE</th> <th>MANUFACTURER</th> </tr> </thead> <tbody> <tr> <td> </td> <td> </td> <td> </td> </tr> </tbody> </table>	NAME	TYPE	MANUFACTURER					
NAME	TYPE	MANUFACTURER							
Protocol Parameters:	<table border="1"> <thead> <tr> <th>NAME</th> <th>VALUE</th> <th>DEFAULT VALUE</th> <th>TYPE</th> </tr> </thead> <tbody> <tr> <td> </td> <td> </td> <td> </td> <td> </td> </tr> </tbody> </table>	NAME	VALUE	DEFAULT VALUE	TYPE				
NAME	VALUE	DEFAULT VALUE	TYPE						

Figure 8.16 Labeled Extract details page

- To modify the Labeled Extract basic details (displayed in the top section), click the **Modify** button just below that section.

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 that you cannot modify the object.

- Modify the **Labeled Extract** details (defined in Table 8.3 on page 84).
- Click the **Save** button to save the modifications, or click the **Cancel** button to disregard the changes.
- The other two sections on this page cannot be modified from this location.
 - To modify the Biomaterial Characteristics, you must return to the originating Source Material to modify its details. For more information, see *Modifying a Source Material* on page 88.
 - To modify the Protocol, you must return to the Protocols section. For more information, see *Modifying a Protocol* on page 51.
- Click the **Done** button to save the modifications, or click the **Cancel** button to disregard the changes.

Deleting a Labeled Extract

To delete a Labeled Extract, follow these steps:

- 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 31. 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 9 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 102

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 components 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 describes how to import microarray data and annotations in MAGE-ML format using caAMEL. 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. See [Importing MAGE-ML Files](#) on page 118.

The basic elements of a caArray Experiment are described in Table 9.1:

Term	Definition	Example
Experiment	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).
Hybridization	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.
Experiment Record	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 9.1 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. These tasks have been described in previous chapters of this user's guide
2. Uploading the experimental research data files into the system. This is described in this chapter.

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, Controlled Vocabulary Terms**, and **Biomaterials** needed for the experiment have been submitted to caArray. See the appropriate chapters of this guide for more information.
 - b. As needed, create and/or define these elements for the new Experiment.

- c. On the Experiments page, 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

Before you create an Experiment, you should perform a search to see if the Experiment already exists in the system. 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 9.2¹⁷:

Submission Fields	Description	Example
*Experiment Name	Name assigned to the Experiment	Lung Adenocarcoma 4912
[Experiment] Identifier	Identification label assigned to the Experiment	gov.nih.nci.ncicb.caarray:Experiment:1015897540503881:1
*Visibility	Visibility assigned to the query Experiment. Options include Private, Public and groups assigned Read/Modify visibility. Note: If no option is selected for visibility, by default, Private is selected, meaning only the owner can view and/or modify it. See <i>Visibility</i> on page 31.	Public
Principal Investigator	Lead investigator for the project	Dr. Jane James, EcoTest Institute
Experiment Type	Descriptor of the type of the Experiment	Disease_state_design

Table 9.2 Fields for adding Experiments

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

17. Items with an asterisk are required fields.

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.

6. To see the details of a particular experiment, click the experiment name. This opens the General Information page of the Experiment. (*Figure 9.1* is an example of a General Information page.)
7. To reset the form to initiate another search, click the **Reset** button.

Adding a New Experiment

Adding an Experiment in caArray involves several sub-steps which require completing information described in the following topics, listed in the order in which they should be performed. The forms for entering the appropriate information display on the same Experiment browser window in caArray. By following the links below, you can go directly to the instructions for the specific portion of the form about which you may have questions.

General [Experiment] Information on page 105

Experimental Factors on page 106

Other Submission Factors on page 106

- Contacts
- Additional Data Processing
- Uploading Additional Files
- Publications
- Quality Control Descriptions
- Additional Qualifiers

Uploading a Hybridization File on page 108

Viewing, Adding and Modifying Hybridization Files Annotations on page 115

Note: There are many dependencies in submitting a new Experiment 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 described in the Experiments 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 [Experiment] Information

1. In the General Information form, enter or select **General Experiment** information as demonstrated in *Figure 9.1*. Parameters are described in Table 9.3¹⁸.

Experiment: Add New Experiment

* indicates a required field

NEW EXPERIMENT: GENERAL INFORMATION	
* Title	Jill's Experiment
* Experiment Completion Date:	01/01/05
* Experiment Design Type	<div style="border: 1px solid black; padding: 2px;"> cellular_modification_design cellular_process_design cell_cycle_design cell_type_comparison_design circadian_rhythm_design </div> Other <input type="text"/>
Visibility	<div style="border: 1px solid black; padding: 2px;"> Public caArray Developers caBig </div>
<small>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.</small>	
Description/Goal of the experiment	<input type="text"/>
Principal Investigator	Heiskanen, Mervi A - NCI Center for Bioinfo... <small>If the person you would like to select is not listed, you can add this person to the caArray database (How?).</small>
Contact Person	please select Contact Person <small>If the person you would like to select is not listed, you can add this person to the caArray database (How?).</small>
* Number of Experimental Factors	2

Figure 9.1 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 Private , Public and groups assigned Read/Modify visibility. Note: 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

Table 9.3 General Experiment fields

18. Items with an asterisk are required fields.

Submission Fields	Description
Contact Person	Select the person who can be contacted for information; this can be the same as the PI.
*Number of Experimental Factors	Enter the number of experimental factors (the factors in the study that are experimental parameters or regarded as influencing the experimental results.)

Table 9.3 General Experiment fields (Continued)

2. Click **Next** to continue.

Experimental Factors

1. Document the Experimental Factors by completing the fields as demonstrated in *Figure 9.2* and described in Table 9.5¹⁹. The number of experimental factors that you enter must equal the number of experimental factors you indicated in the last field in *Figure 9.1*.

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

Experiment: Add New Experiment

NEW EXPERIMENT: EXPERIMENTAL FACTORS				
#	Factor Name	* Factor Type	Scale	Factor Value
1	time interval	timepoint (Action)	linear_scale	1 hour
2	issue type	tumor_grading (BioMaterialCharacteristicCategory)	unscaled	normal

Previous Next

Figure 9.2 Entering Experiment Experimental Factors

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

Table 9.4 Experimental factors fields

Other Submission Factors

The General Experiment page displays again after you complete the *Experimental Factors*, a portion of which is shown in *Figure 9.3*. 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 9.5. For more information about each, click its hypertext link.

¹⁹. Items with an asterisk are required fields.

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

CONTACTS ?

Principal Investigator: Mervi A. Heiskanen

Contact Person:

[Modify](#)

HYBRIDIZATION FILE UPLOAD ?

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

HYBRIDIZATION FILES BATCH DOWNLOAD ?

Note: Do not download files immediately after uploading hybridization files. The application needs some time to process files.

ADDITIONAL DATA PROCESSING (DERIVED MEASUREMENTS) ?

#	Data Transformation Protocol	Protocol Description	Uploaded files	Action
				Add More

ADDITIONAL UPLOADED FILES ?

#	File	Description	Action
			Upload More

EXPERIMENTAL FACTORS/VARIABLES ?

Factor	Factor Type	Scale	Factor Value	
time interval	timepoint	linear_scale	1 hour	Remove
			<input type="text"/>	Add
Modify Remove				
tissue type	tumor_grading	unscaled	normal	Remove
			<input type="text"/>	Add
Modify Remove				
Add A New Factor				

Figure 9.3 Other submission factors must be defined for the Experiment

Submission Factors	Description	Action(s)
Contacts	Review and/or modify the contact information you entered in the Contacts section of caArray	Click Modify to open the Experiments:Contacts dialog box where you can modify the information.
Additional Data Processing	Document additional processing of the data such as derived measurements	Click the Add More hyperlink. Fill in the fields and browse for the file to be uploaded. Click Next to continue.
Additional Uploaded Files	Document additional uploaded files.	Click Upload More hyperlink.

Table 9.5 Other Factors for an Experiment

Submission Factors	Description	Action(s)
Experimental Factors/ Variables	Displays factors you just added to the Experiment (see <i>See Experimental Factors</i> on page 106.).	Enter additional values for Experimental Factors you defined in the previous step.
Publications	Publication pertinent to the Experiment	Click Add a New Publication .
Quality Control Steps Description	Document quality control steps taken in the Experiment	Click the Add Quality Control hyperlink.
Additional Qualifiers	Document any Additional Qualifiers.	Click the Add New Qualifier Hyperlink.

Table 9.5 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

See also *Adding a New Experiment* on page 104.

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 adding.

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 9.6.

Hybridization Parameters	Description	Example
Array Design	Information describing the microarray design	hg-u133a
Number of Channels	Number of channels for hybridization	single
Hybridization File Type	Type of software used to generate the hybridization file.	Affymetrix
Array Template	Array created in Arrays chapter from which copies are made for hybridization files	ATC_Jane_BC
Labeled Extract Template	Labeled extract created in the <i>Biological Source Materials</i> chapter, from which copies are made for hybridization files	Cy5_ATC_Jane_BC

Table 9.6 Hybridization Parameters for Hybridization Upload

Hybridization Parameters	Description	Example
Spike Control Template	Labeled extract for detecting spike control (optional object); created in the Biomaterials chapter, from which copies are made for hybridization files	cRNA_BioB
Hybridization Protocol	Protocol describing how the hybridization was carried out; created in Protocol chapter	Hg-u133 Hybridization Protocol
Activity Date	Date on which the protocol was carried out	01/01/05
Performer	Name of person who performed the activity	Dr. Sally Toe
Image Acquisition Protocol (Not required)	Protocol describing how the image of hybridization was acquired; created in Protocol chapter	Hg-u133 Hybridization Protocol
Feature Extraction Protocol (Not required)	Protocol describing how the intensity of hybridization for each feature was extracted; created in Protocol chapter	Hg-u133 Feature Extraction Protocol

Table 9.6 Hybridization Parameters for Hybridization Upload (Continued)

1. Click the **Upload Files** link in the **Hybridization File Upload** section (the third section) of the General Information page (Figure 9.4).

The screenshot shows a web interface with three main sections:

- CONTACTS**: Contains fields for 'Principal Investigator' (Mervi A Heiskanen) and 'Contact Person'. A 'Modify' button is located at the bottom right.
- HYBRIDIZATION FILE UPLOAD**: Contains two buttons: 'View and Annotate Uploaded Files' and 'Upload Files'. The 'Upload Files' button is circled in red.
- HYBRIDIZATION FILES BATCH DOWNLOAD**: Contains a note: 'Note: Do not download files immediately after uploading hybridization files. The application needs some time to process files.'

Figure 9.4 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.

Hybridization File Upload

* Indicates a required field

COMMON HYBRIDIZATION INFORMATION (file upload)

* Array Design:	HG-U133_Plus_2
* Number of Channels:	Single
* Hybridization File Type:	Affymetrix

Next Cancel

Figure 9.5 Entering common hybridization information

3. In the Common Hybridization Information dialog box (Figure 9.5), 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 9.5, the Array Design selected is an Affymetrix chip. Affymetrix chips are always single channel.

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 9.6). Options listed here are those that use the Array Design you just selected, in this case, hg u133a.

Hybridization File Upload

COMMON HYBRIDIZATION INFORMATION		
Array Design:	HG-U133_Plus_2	
Number of Channels:	1	
Hybridization File Type:	Affymetrix	
* indicates a required field		
HYBRIDIZATION (FILE UPLOADS)		
Array Identifier Template	Labeled Extract Template	Factor Values
Unknown	* Extract: Cy5 labeled cDNA for ovarian adenocarcinoma 36	time interval 1 hour
	Spiked Control: Select Control	tissue type normal
		Next Cancel

Figure 9.6 Associating the Labeled Extract and Spiked Control with the Array Design

4. Select the following in this dialog box²⁰:
 - **Array Identifier Template**
 - ***[Labeled] Extract Template**
 - **Spiked Control**

20. Items with an asterisk are required fields.

◦ **Factor Values**

Note: The Array Identifier, Labeled Extract and Spiked Control options you select on the form 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 (See Step 10 below in this topic for description), 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 Sample Extract and Source Material)

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

Spiked Control (same with associated Sample Extract and Source Material)

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

5. In the next dialog box that opens (*Figure 9.7*), select the hybridization protocol you created in caArray that corresponds to this Experiment you are submitting.

Hybridization File Upload

COMMON HYBRIDIZATION INFORMATION (file upload) ?	
Array Design:	HG-U133_Plus_2
Number of Channels:	1
Hybridization File Type:	Affymetrix
Array Group Template Name:	
Hybridization Protocol:	Affymetrix Hybridization Protocol ▾

If the protocol you would like to select is not listed, you can add this protocol to the caArray database ([How?](#)).

Figure 9.7 Selecting a Hybridization Protocol

6. In the next dialog box (*Figure 9.8*), enter the **Activity Date** and the **Performer** (the person who performed the hybridization).

Hybridization File Upload

COMMON HYBRIDIZATION INFORMATION (file upload)			
Array Design:	HG-U133_Plus_2		
Number of Channels:	1		
Hybridization File Type:	Affymetrix		
Array Group Template Name:			
Hybridization Protocol:	Affymetrix Hybridization Protocol		
If the protocol you would like to select is not listed, you can add this protocol to the caArray database (How?).			
* indicates a required field			
PROTOCOL			
Protocol ID:	gov.nih.nci.ncicb.caarray.Protocol:1015897524596172-1		
* Activity Date:	01/01/05		
* Performer:	Heiskanen, Mervi A - NCI Center for Bioinfo...		
Protocol Name:	Affymetrix Hybridization Protocol		
Protocol Description:	Fragmented cRNA (15 µg) was used to prepare 300 µL hybridization cocktail (100 mmol/L MES, 1 mol/L NaCl, 20 mmol/L EDTA, 0.01% Tween 20) containing 0.1 mg/mL (3 mL/300 mL) of herring sperm DNA (Promega, Madison, WI, 10 mg/mL) and 500 µg/mL acetylated bovine serum albumin (3 mL/300 mL, Invitrogen, 50 mg/mL). EDTA was obtained from Sigma Chemical, Tween 20 from Pierce Chemical (Rockford, IL), and DEPC-treated water from Ambion. Control cRNA used for comparison of hybridization efficiency between arrays and to standardize the quantitation of measured transcript levels is included as component of Eukaryotic Hybridization Control kit (Affymetrix, 20x) and uses 15 mL/300 mL hybridization cocktail. Before hybridization, the cocktails were heated to 94°C for 5 minutes, equilibrated at 45°C for 5 minutes, and clarified by centrifugation (16,000 × g) at room temperature for 5 minutes. Aliquots of each sample (10 µg fragmented cRNA in 200 µL hybridization cocktail) were prehybridized to U133A arrays at 45°C for 60 minutes and then hybridized for 16 to 18 hours in a rotisserie oven at 60 × g. The arrays were then washed using nonstringent wash buffer (6x saline-sodium phosphate-EDTA) at 25°C followed by stringent wash buffer [100 mmol/L MES (pH 6.7), 0.1 mol/L NaCl, 0.01% Tween 20] at 50°C. After staining with streptavidin-phycoerythrin (Molecular Probes, Eugene, OR), the arrays were washed again with 6x saline-sodium phosphate-EDTA and incubated with biotinylated anti-streptavidin IgG followed by a second staining with streptavidin-phycoerythrin and a third washing with 6x saline-sodium phosphate-EDTA. The arrays were scanned using the GeneArray scanner (Affymetrix). Data analysis was done using Affymetrix GeneChip 5.0 software. Features on the oligonucleotide arrays were carefully reviewed to confirm expression levels and exclude hybridization or washing artifacts.		
URI:			
Protocol Parameters:	NAME	VALUE	TYPE
Next Cancel			

Figure 9.8 Hybridization Protocol Information

7. In the next two dialog boxes (Example in *Figure 9.9*), 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.

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

Hybridization File Upload

COMMON HYBRIDIZATION INFORMATION	
Array Design:	HG-U133_Plus_2
Number of Channels:	1
Hybridization File Type:	Affymetrix
Array Group Template Name:	
Hybridization Protocol Name:	Affymetrix Hybridization Protocol
Image Acquisition Protocol:	select protocol

Protocol: If the protocol you would like to select is not listed, you can add this protocol to the caArray database (How?).

Next Cancel

Figure 9.9 Selecting Image Acquisition Protocol

8. Once you have gone through the IAP and FEP dialog boxes, when you click **Next**, the Java Applet is initiated and the security dialog box opens first (Figure 9.10).

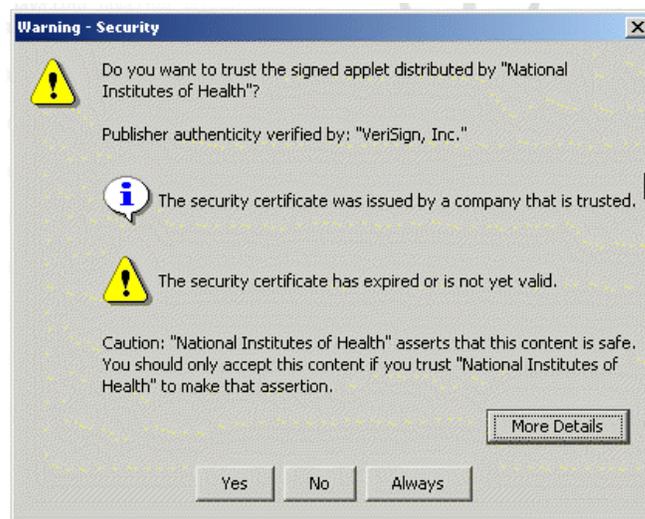


Figure 9.10 Java Applet security dialog box

9. Click **Yes** to verify the running of the applet.

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 9.11). 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.

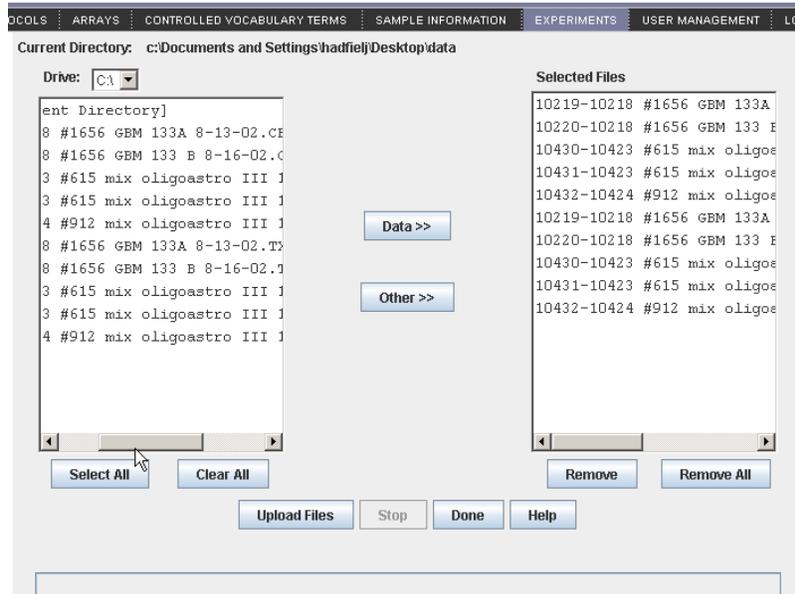


Figure 9.11 File upload applet

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 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 9.12). 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 9.12 File Upload Confirmation dialog

- 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 9.13*). If the file(s) upload fails, that is noted in the **Files Failed** section of the dialog box.

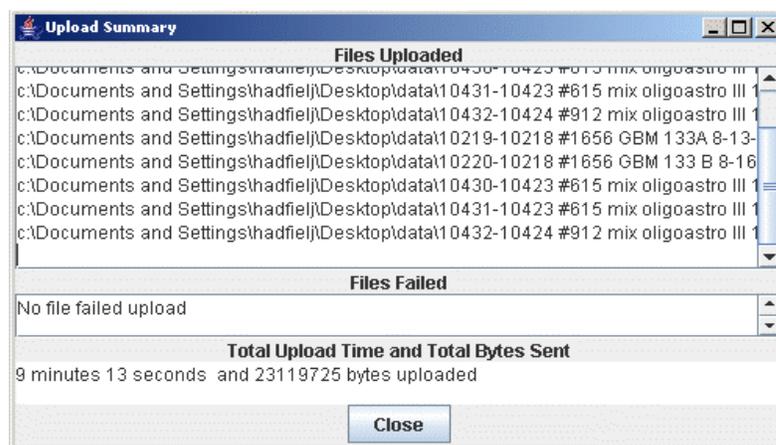


Figure 9.13 Summary dialog box reporting a successful data upload

Additionally, the caArray system sends an email reporting the success or failure of the file upload and subsequent parsing (*Figure 9.14*).



Figure 9.14 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, Adding and Modifying Hybridization Files Annotations

See also *Adding a New Experiment* on page 104

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:

- Search for the experiment you'd like to annotate, as described in *Searching Experiments* on page 103.

- Click on the Experiment to be annotated.
- In the Hybridization File Upload section of the Experiment Details page, click **View and Annotate Uploaded Files** (Figure 9.15).

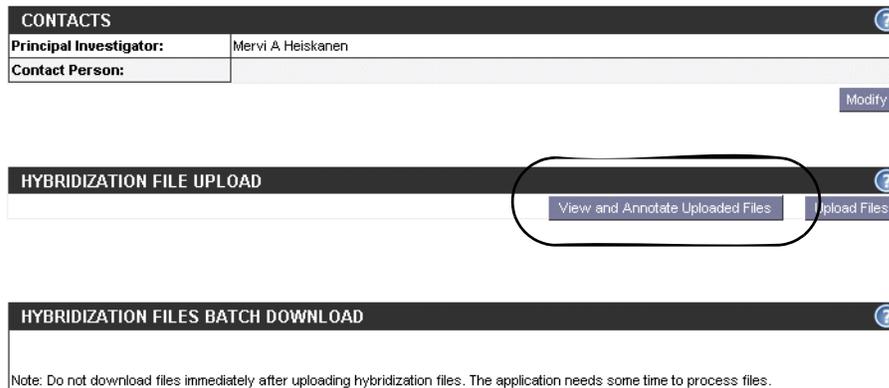


Figure 9.15 Click View and Annotate Uploaded [Hybridization Files] link to annotate files

- Click the **Annotate** link under the **Action** column of the hybridization you would like to update (Figure 9.16).

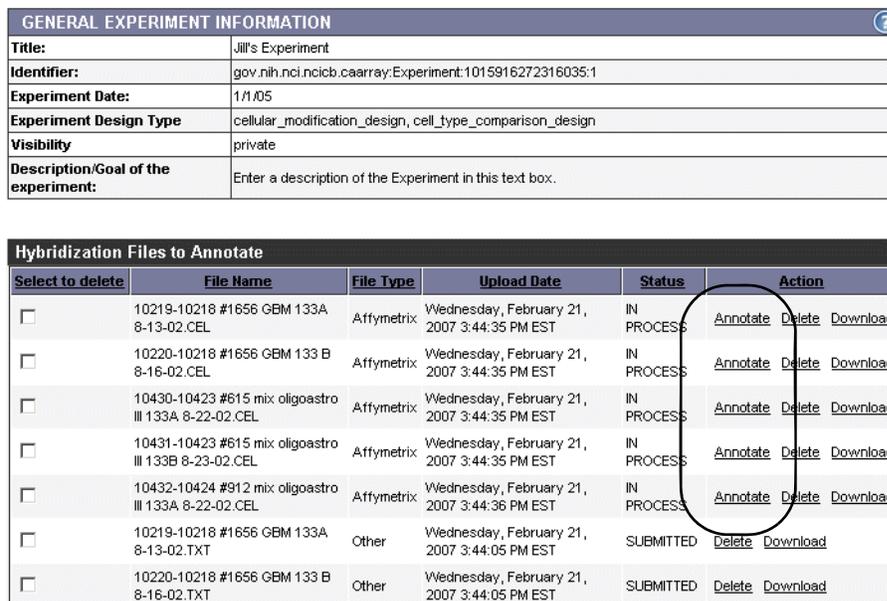


Figure 9.16 Annotate link for updating hybridization file annotations

- To change the Array annotation, click the array name under the **Array Identifier** column (Figure 9.17).



Figure 9.17 Hybridization File Annotation dialogbox for modifying annotations

- Modify the array as described in *Modifying an Array* on page 65.

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 Chapter Biological Source Materials*.
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: 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.

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

Nearly every section of the General Experiment Information page that opens 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 **Modify** button that allows you to modify or add information.

Experiment: General Information

UPDATE GENERAL EXPERIMENT INFORMATION	
*Title:	test 123
*Experiment Date:	1/2/03
*Experiment Design Type	<ul style="list-style-type: none"> all_pairs behavioral_design_type behavior_design binding_site_identification_design cellular_modification_design
Description/Goal of the experiment:	
Visibility:	<ul style="list-style-type: none"> Public caBIG Curation Curation Team - delete Curation Team - make public DC Lung Study DC Prostate Study GMDL_Group JenLab MAGE-OM API users <p><small>Note: Private visibility is always selected by default. If you would like this item to have only private visibility (only be visible to you), you do not need to make any selections. If you want to have this item be visible to others, select the additional group(s). Hold CTRL key and click an item to select or deselect multiple items. Hold CTRL key and click an item to deselect it.</small></p>
<input type="button" value="Save"/> <input type="button" value="Cancel"/>	

Figure 9.18 The Update General Experiment Information page for modifying an Experiment

6. For more information about each section, return to the corresponding directions in the section, *Adding a New Experiment* on page 104.
7. On the Update Experiment page (*Figure 9.18*), modify the experiment details appropriately.
8. 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:

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 you want to modify. For more information, see *Searching Experiments* on page 103.
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.

Importing MAGE-ML Files

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.

You can import valid MAGE ML documents into caArray using caAMEL ("caArray MAGE-ML Loader"). For more information about caAMEL, see <https://caarraydb.nci.nih.gov/caamel/>.

To launch caAMEL, follow these directions:

1. From either the Array Design or Experiment pages, click the **MAGE-ML** hypertext link at the top of the left sidebar (*Figure 9.19*). caAMEL opens in a new browser window.

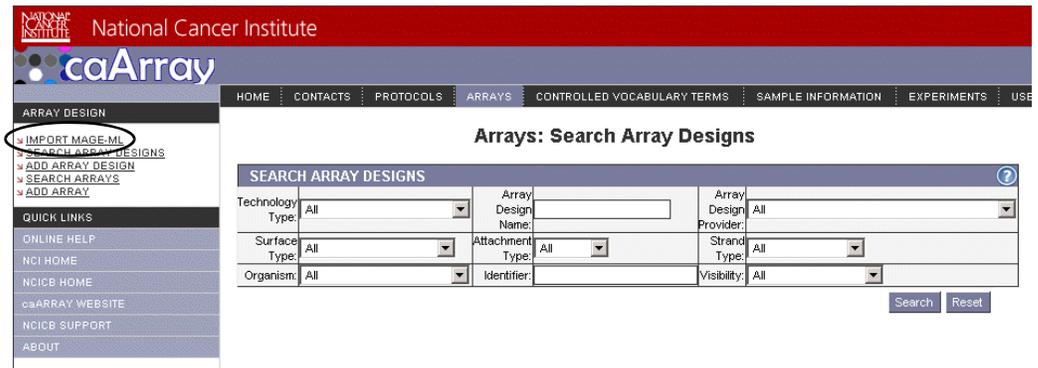


Figure 9.19 MAGE-ML hypertext link from Array Design page

Refer to the *caAMEL 1.6 User's Guide* (<https://caarraydb.nci.nih.gov/caamel/>) for more information about MAGE-ML imports.

APPENDIX

A

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.

Term	Definition
caAMEL	caArray MAGE-ML Loader
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

Term	Definition
URL	Uniform Resource Locators
XML	Extensible Markup Language (http://www.w3.org/TR/REC-xml/) - 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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