

# CHAPTER 4

## CREATING AND MANAGING EXPERIMENTS

The following topics are part of this chapter:

*Submitting an Experiment Proposal* on page 44

*Updating an Experiment proposal* on page 60

*Managing Experiment Visibility* on page 57

### Overview of an Experiment

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In a caArray Experiment, you can capture all relevant information as you create the project. This includes general information about the experiment, such as the experimental design and experimental factors, associated publications, biological samples, quality control and data processing steps, and so forth. You then upload all of the research data files related to the hybridizations performed in the Experiment, and link the sample information you submitted 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 [the following table Table 4.1](#):

Term	Definition	Example
<b>Experiment</b>	A complete set of annotated hybridizations performed on arrays for a common purpose.	An experiment to identify lung adenocarcinoma subtypes based on gene expression patterns (signatures).
<b>Hybridization</b>	The process of incubating one or more labeled extracts with an array.	A fluorescent-labeled cDNA extract from prostate tumor is hybridized on a custom-made 10K cDNA array.
<b>Experiment Record--not in 2.0??</b>	The (database) record which describes and identifies a microarray experiment.	Dr. James submitted a description of her experiment to caArray, and that information is now an Experiment record in the caArray database.

Table 4.1 *Elements of a caArray Experiment*

See also [Submitting an Experiment Proposal](#)

## Submitting an Experiment Proposal

**Note:** 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.

[Search experiments first?](#)

[Can only a PI create Experiment in 2.0?](#)

Adding an Experiment in caArray involves two main segments:]

1. Creating an Experiment with appropriate characteristics and annotations
2. Uploading the experimental research data files into caArray and associating them with the appropriate Experiment

With the appropriate permissions, you can create, edit and submit an Experiment with its corresponding annotations. A minimum set of information must be entered for an Experiment prior you can submit it, but almost as soon as a project is begun, you can save it as a draft to be retrieved and completed at a later time. Alternatively, you can have another designee with appropriate permissions complete the submission.

[Move these somewhere else:.](#)

<b>Organisms</b>	<a href="#">Definition needed</a>
<b>Assay Providers</b>	<a href="#">Definition needed</a> In the caArray context, a person or an organization associated with an entry in the program
<b>Unique Array Designs</b>	Descriptions of microarrays that include such information as array layout and design and the technology used to create a microarray.

<b>Hybridizations</b>	The process of incubating one or more labeled extracts with an array. Hybridization methods form the basis for microarray techniques.
<b>Registered Institution</b>	<u>Cancer center, academic institution, laboratory or commercial vendor with an established caArray account??</u>
<b>Registered Users</b>	<u>Person with a validated caArray User Account. May or may not be associated with a Registered Institution.</u>

## Creating an Experiment

To create an Experiment in caArray, follow these steps:

I'm a little confused by the use of the term "Proposed" and "proposal" in the UC docs. Please clarify.

1. Go to the NCICB caArray login page <http://array.nci.nih.gov> and log in.

Once you are on the caArray Portal Welcome login page, the browser displays the Experiment workspace.

2. On the left sidebar, click **Create/Propose Experiment**. This opens a tab for entering overall characteristics for the Experiment.

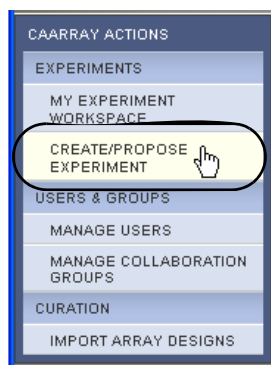


Figure 4.1 Create/Propose Experiment on left sidebar

## Overview Tab

When you create a new experiment in caArray, the Overview tab initially displays alone in the user interface. Once you enter the appropriate information on this tab and save it, other tabs, also necessary for adding Experiment information display as well.

To complete the Overview tab, follow these steps:

1. On the Overview tab, enter the appropriate information for Overall Experiment Characteristics<sup>1</sup> as described in the following [table](#).

Experiment: New Experiment

Overview

Overall Experiment Characteristics

The Overall Experiment Characteristics represent the minimum set of attributes required to submit an experiment for review. Required fields are marked with 'asterisks'.

Experiment Title\*:

Status: Draft

Experiment Identifier:

Service Type\*:

Assay Type\*:

Provider\*:

Array Designs:

Organism\*:

Tissue Sites\*:

Selected Tissue Sites

Tissue Types\*:

Selected Tissue Types

Cell Types\*:

Selected Cell Types

Conditions\*:

Selected Conditions

Overview Tab Field	Description
Experiment Title	Title designate by the PI or other user creating the Experiment
Status	Draft or Completed?
Experiment Identifier	<p>This project Identifier is autogenerated by caArray upon the initial save of the Experiment. The Experiment Identifier is not editable. The ID is generated using the following convention:</p> <p>The PI last name-5 char autonumber truncated to first 5 characters <a href="#">each particular attribute</a>. Example: klemm-90765. <a href="#">Significance of "90765"? ID produced is directly accessible via a URL. <u>How? Where would one see the URL?</u></a></p>

1. Fields with a red asterisk \* are required.

Overview Tab Field	Description
<b>Service Type</b>	<p>Service Type is <u>describe..</u>. Select from the drop-down menu the appropriate service type. <u>What happens when these options are selected? I see in UC with Publish, caArray messages PI that "submission to a lab is removed. I'd like to talk with you about this.</u></p> <p>Options are: <u>descriptions of each</u></p> <ul style="list-style-type: none"> <li>• <b>Full</b></li> <li>• <b>Partial</b></li> <li>• <b>Analysis</b></li> <li>• <b>Publish</b> <u>for "bulk upload of data". "Intended to provide means to annotate this data, but higher priority is to make data available to caA community." Does selecting <b>Publish</b> service type automatically set the bulk upload in motion? I don't think so, but had to ask.</u></li> </ul>
<b>Assay Type</b>	<p>Select from the drop-down menu the appropriate assay type.</p> <p>Options are: <u>descriptions?</u></p> <ul style="list-style-type: none"> <li>• Gene Expression</li> <li>• DNA</li> <li>• SNP</li> <li>• aCGH</li> </ul>
<b>Provider</b>	<p>Select from the drop-down menu the provider of the array. Note: Only Affymetrix or Illumina are supported in caArra 2.0.</p> <p>Once selected, caArray automatically loads a corresponding list of Array Designs (next field)</p>
<b>Array Design</b>	Select an array design from the automatically-generated list of array designs corresponding to the Provider you selected.
<b>Organism</b>	<u>Organism that is the source of the sample biomaterial?</u> Select from the drop-down menu the appropriate organism
<b>Tissue Sites</b>	<p>Click the source of the tissue used in the array. If the appropriate site is not listed, enter the tissue site in the filter text box and click <b>Add</b>.</p> <p><u>Source of the tissue used in the array? The probe, in other words? . How do the filters in these next several fields work? What do I choose here if E. coli is my organism? E.coli obviously does not have a "Leg" but I can't see an appropriate choice. I guess that's when a user would add a new definition.</u></p> <p><u>Jill, add Manage Vocabularies section for adding terms to these 4 fields.</u></p>
<b>Tissue Types</b>	<p>Click the tissue type used in the array. If the appropriate type is not listed, enter the tissue type in the filter text box and click <b>Add</b>.</p> <p><u>Select the type of tissue (that comes from the tissue site?) used in the array</u></p>
<b>Cell Types</b>	<p>Click the type of cells used in the array. If the appropriate site is not listed, enter the cell type in the filter text box and click <b>Add</b>.</p> <p><u>Select the type of cells used in the array. Cell preps like cell lysate?</u></p>

Overview Tab Field	Description
Conditions	<u>Do you mean type of cancer? That's what it looks like from some samples in the app.</u>

Table 4.2 Field for Overall Experiment Characteristics

- After entering the information, click the **Save** button at the bottom of the page. Upon saving, caArray validates required fields and saves the Experiment as a draft. A confirmation messages displays, verifying that the proposal is saved.

When you save the draft, other tabs used for adding additional information for the Experiment display. Proceed to the **Contacts** tab.

## Contacts Tab

A caArray Contact is a person (or organization??) associated with an Experiment, either as a Principal Investigator (PI) or the Point of Contact (POC). The Contact does not have to be a registered user of caArray.

To enter contact information for the Experiment, follow these steps:

- On the Contacts tab, enter information for the fields described in Table xx. How is this information "made available automatically." (from UC doc)? There are no drop down menus for selecting pre-entered information.

Contact Fields	Description
P.I First Name	First and last names of the Principle Investigator
P.I Last Name	
Email Address	Email address of the P.I.
Phone	Phone number of the P.I.
Is the P.I. the P.O.C. (point of contact for the Experiment)?	Select <b>Yes</b> or <b>No</b> . If answer is <b>No</b> , caArray opens additional text boxes where you can add contact information for the project Point of Contact (POC). <u>Does POC have to be registered user of caArray.</u>

Table 4.3

- Click **Save**.
- Proceed to the Annotations tab.

## Annotations Tab

The Annotations tab opens with seven subtabs for entering annotation data for the Experiment you are creating. Enter the appropriate information as described below for each of the seven subtabs.

**Note:** You must enter at least one Experimental Factor used in the design. Why is it so important to mention this specifically. There are many other required fields when creating an Experiment.

## Experimental Design

1. Enter on the Experimental Design subtab (under the Annotations Tab) the appropriate information as described in Table sss<sup>1</sup>.

<b>Experimental Design Fields</b>	<b>Description</b>
Experimental Design Type*	Select the Experimental Design type among the options in the drop-down menu.
Experimental Design	<u>Is this field for a description? Then say so (like the next field).</u>
Experimental Design Quality Control Description	Enter a description for the Quality Control used for the Experiment.
Quality Control Types	Select the QC type in the scroll down list.
Replicate Description	<u>Define in context of caArray?</u> Enter a description of the Replicate.
Replicate Types	Select the Replicate Types from the scroll down list. <u>Since Types is plural, select more than one?</u>

Table 4.4

2. Click **Save**.
3. Proceed to the Experimental Factors subtab.

## Experimental Factors

Experimental Factor are the define... The Experimental Factors subtab (under the Annotations Tab) displays any previous Experimental Factors that may have been added previously to the Experiment you are creating.

1. Click the **Add a New Experimental Factor** button to add a new Experimental Factor.
2. In the form that opens, enter a name for the new factor. This is a required field, as indicated by the red asterisk\*<sup>2</sup>.
3. Click **Save**. The name of the factor now displays on the Experimental Factors subtab.
4. Repeat steps 1 & 2 as often as needed to enter all the Experimental Factors for this Experiment.
5. Click **Save**.

How is the category (field for a saved Exp. Factor) determined or specified?

6. Proceed to the Sources subtab.

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1. Fields with a red asterisk \* are required.  
2. Fields with a red asterisk \* are required.

## Sources

In the context of 2.0, the Sources, Samples, Extracts and Labeled Extracts seem to correlate with the biological materials described in caArray 1.6. Please read material I've pasted from previous user's guide and correct it appropriately for 2.0. Perhaps rather than entering comments, it would be better for us to talk about it, then I can modify the content appropriately.

Material from 1.x user's guides starts here:

## 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 [the figure below Figure 4.2](#) 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.

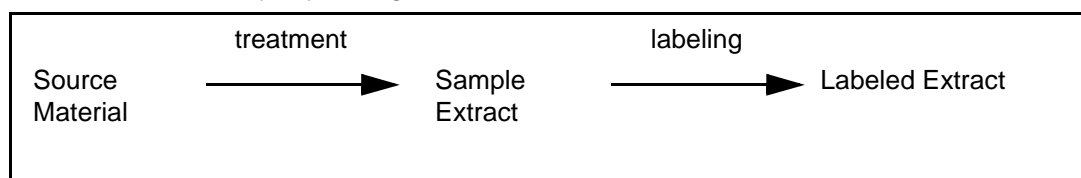


Figure 4.2 Biomaterials components and their relationship in caArray

The nature of each type of biomaterial is defined in varying dialog boxes in caArray. The relevant fields for each is described in [the associated topics Table 4.5, Table 4.6, and Table 4.7](#).



- [Source Material](#)
- [Sample Extracts](#)
- [Labeled Extracts](#)

## Source Material

The term Source Material refers specifically to original source material before it is treated. The nature of Source Materials in caArray is described in [the following table Table 4.5<sup>1</sup>](#):

Source Material Fields		
Field	Description	Example
<b>Source Material Name</b>	Name given to Source Material sample <b>Note:</b> It is a good idea to clearly name Source Materials	
<b>Description</b>	Description of the Source Material.	
<b>*Material Type</b>	Controlled terms for the state of the Source Material	Organism part; cell line
<b>*Organism</b>	Documents the species from which the Source Material is obtained.	<i>Homo sapiens</i>
<b>*Provider</b>	The name of the organization or individual who provided the Source Material	NIH Clinical Center
<b>*Source Material Type</b>	Controlled terms for the type of the Source Material	Lung Biopsy Sample--PatientX
<b>Visibility</b>	Defines permissions for those who can use your Source Material for documentation. Options include Private, Public and designated groups. <b>Note:</b> If no option is selected for visibility, by default, <b>Private</b> is selected, meaning only the owner can view and modify the object. See <a href="#">Visibility</a> on page 31.	Private

Table 4.5 [Fields for documenting Source Materials](#)

[Sample Extracts](#)

[Labeled Extracts](#)

[Overview of Biological Source Materials](#)

1. Items with an asterisk are required fields when adding a new Source Material. See [Adding a Source Material](#) on page 87.

## Sample Extracts

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 [the following table Table 4.6](#):

Sample Extract Fields		
Field	Description	Example
<b>Material Type</b>	Controlled terms for the type of the Sample Extract.	cDNA, total RNA
<b>Source Material</b>	The source from which the Sample Extract was derived <b>Note:</b> 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	Lung cancer biopsy_1
<b>Organism</b>	Documents the species from which the Sample Extract was derived	<i>Homo sapiens</i>
<b>Visibility</b>	Defines permissions for those who can use your Sample Extract for documentation. <b>Note:</b> 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. See <a href="#">Visibility</a> on page 31.	

Table 4.6 *Fields for documenting Sample Extracts*

### Source Material

### Labeled Extracts

### Overview of Biological Source Materials

## Labeled 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 [the following table Table 4.7](#):

Labeled Extract Fields		
Field	Description	Example
<b>Material Type</b>	Controlled terms for the state of the Labeled Extract.	cDNA, total RNA

Table 4.7 *Fields for documenting Labeled Extracts*

Labeled Extract Fields		
Field	Description	Example
<b>Organism</b>	Documents the species from which the Labeled Extract was derived	<i>Homo sapiens</i>
<b>Visibility</b>	Defines permissions for those who can use your Labeled Extract for documentation. <b>Note:</b> 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
<b>Sample Extract</b>	The Sample Extract source from which the Labeled Extract was derived <b>Note:</b> 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
<b>Labeled Extract Name</b>	Name given to the Labeled Extract	Cy5-labeled lung tumor RNA

Table 4.7 *Fields for documenting Labeled Extracts*

Material from 1.x ends here.

New for 2.0:

A source is any biological site from which the tissue for the array is derived. Add to Glossary.

The Sources subtab (under the Annotations Tab) displays any Sources that may have been added previously to the Experiment you are creating.

To add a Source, follow these steps:

1. click the **Add a New Source** button to add a new Source.
2. In the Sources form that opens, enter the information as described in table sss.

Source Fields	Description
Source Name	Name assigned to the source
Description	Description of the source
Tissue Site	Site where the source tissue was derived. Select or enter a new value in the Filter text box and click <b>Add</b> .

Table 4.8

3. Click **Save** to save the Source to the Experiment.

When is other data about sample entered (the fields that display on the Sources tab--Organism, Related Samples)?

- Repeat steps 1-3 as often as necessary to add all appropriate Sources to the Experiment.

## Samples Tab

Samples are the original source biomaterials before any treatment events. *Example:* Tissue sample or biopsy material. The Samples subtab (under the Annotations Tab) displays any previous Samples that may have been added previously to the Experiment you are creating. A Sample is a ...define for the array.

- Click the **Add a New Sample** button to add a new Sample.
- In the Sample form that opens, enter the information described in Table ss.

<b>Samples Fields</b>	<b>Description</b>
Sample Name	Name assigned to the sample
Description	Description of the sample
Source(s)	Source where the sample tissue was derived. Select or enter a new value in the Filter text box and click <b>Add</b> .

- Click **Save**. When is other data about sample entered (the fields that display on the Samples tab- Organism, Extracts. what is the Download button for?)

The name of the Sample(s) now displays on the Samples subtab.

- Repeat steps 1 - 3 as often as needed to enter all the Samples used in this Experiment.
- Proceed to the Extracts tab.

## Extracts Tab

An Extract is a biological sssss for the array. (Definition from 1.6??)

The Extracts subtab (under the Annotations Tab) displays any Extracts that may have been added previously to the Experiment you are creating.

- Click the **Add a New Extract** button to add a new Extract.
- In the Extract form that opens, enter the information described in Table ss.

<b>Extracts Fields</b>	<b>Description</b>
Extract Name*	Name assigned to the Extract
Description	Description of the extract
Sample*	Sample from which the Extract was derived. Select or enter a new value in the Filter text box and click <b>Add</b> .

- Click **Save**. The name of the Extract now display on the Extracts subtab. When is other data about extract entered (the field that display on the Extracts tab-- Nucleic Acid Type, Labeled Extracts.)?
- Repeat steps 1 - 3 as often as needed to enter all the Extracts used in this Experiment.
- Proceed to the Labeled Extracts subtab.

## Labeled Extracts Tab

A Labeled Extract is a biological sssss for the array. (Definition from 1.6??)

The Labeled Extracts subtab (under the Annotations Tab) displays any Labeled Extracts that may have been added previously to the Experiment you are creating.

1. Click the **Add a New Labeled Extract** button to add a new Labeled Extract.
2. In the Labeled Extract form that opens, enter the information described in Table ss.

<i><b>Labeled Extracts Fields</b></i>	<i><b>Description</b></i>
Labeled Extract Name*	Name assigned to the Extract
Description	Description of the extract
Extracts*	Extract from which the Labeled Extract was derived. Select or enter a new value in the Filter text box and click <b>Add.</b> <u>?? no Add button.</u>

3. Click **Save**. The name of the Extract now display on the Extracts subtab. When is other data about extract entered (the fields that display on the Labeled Extracts tab--Labels Used, Amount, Protocol.)?
4. Repeat steps 1 - 3 as often as needed to enter all the Extracts used in this Experiment.
5. Click **Save**. The name of the Labeled Extract(s) now displays on the Labeled Extracts subtab.
6. Proceed to the Hybridizations subtab.

## Hybridizations Tab

The Hybridizations subtab (under the Annotations Tab) displays any Hybridization information that may have been added previously to the Experiment you are creating.

Where does one enter Protocol information in 2.0? This is obviously crucial information.

1. Click the **Add a New Hyrbridization** button to add a new Hybridization.
2. In the Hybridizations form that opens, enter the information described in Table ss.

<i><b>Hyrbridizations Fields</b></i>	<i><b>Description</b></i>
Hybridization Name*	Name assigned to the Extract
Labeled Extract*	Labeled Extract used in the hybridization protocol. Select or enter a new value in the Filter text box and click <b>Add.</b> <u>?? no Add button.</u>

3. Click **Save**. The name of the Extract now display on the Extracts subtab. When is other data about hybridization entered (the field that display on the LE tab--Uncompressed Size.)?
4. Possible to add more than one hybridization?

- Click **Save**. The name of the Hybridization now displays on the Hybridizations subtab.
- Proceed to the Data tab.

## Data Tab

The Data tab is the vehicle for uploading, validating, importing and downloading data relating to caArray Experiments. When you click on the Data tab, four subtabs where you initiate data-related tasks display. They are described in Table ss.

<b>Data Tabs</b>	<b>Description</b>
Manage Data	
Imported Data	Define
Supplemental Files	Define
Download Data	

[Flesh out this section.](#)

[For more information about submitting data to an Experiment, see Chapter 5 Submitting Data to an Experiment.](#)

## Publications

This tab allows you to create, edit or delete associations of publications with the Experiment you are creating or editing. You can add manuscripts, abstracts and posters as well as any journal publications or books [\(true?\)](#).

To add publication associations, follow these steps:

- Locate the Experiment for which you want to associate publications.
- Click the **Publications** tab.
- Click the **Add a New Publication** button.
- On the form that opens, enter the appropriate information in the fields provided (and described in [table ss](#)).<sup>1</sup>.

<b>Publications Fields</b>	<b>Description</b>
Title*	
Authors	
URL	
<u><a href="#">DOI</a></u>	
Editor	
Pages	Where appropriate, enter the page number(s) of the article your are referencing
Publisher	

1. Fields with a red asterisk \* are required.

<b>Publications Fields</b>	<b>Description</b>
PubMedID	
Volume	
Year	
Publication	
Type	Select in the drop-down menu the publication type.
Status	Select in the drop-down menu the publish status: <b>Published, In Preparation, Submitted</b>

5. After entering the appropriate information, click **Save**. A message displays verifying that the publication was successfully saved with the Experiment.

The System saves the Experiment, informs the Principal Investigator and the Lab Administrator via email of the submission (including the experiment url) and returns the Principal Investigator to their workspace updated with the state of the project.

## Managing Experiment Visibility

Once you create and Experiment draft, it is listed on the My Experiment Workspace. At that point, you can review and or modify the access of other users to the project.

To assign or modify Experiment visibility, follow these steps:

1. Click on the icon in the Permissions column that corresponds to the Experiment.
2. The Experiment Permissions page that opens displays two visibility categories:
  - a. Browsability--The default setting is "Not Browsable. To change the setting to Browsable, click the Toggle button.
  - b. Policies--The only option here is to click the **Use TCGA Policy** check box. The Cancer Genome Atlas (TCGA) has established a policy in which only 4 fields of annotation can be provided to the open public:
    - Clinical Diagnosis
    - Histologic Diagnosis
    - Tissue Anatomic Site
    - Pathologic Status

If you check the box, the same access standard will apply to your Experiment.Visibility.

**Note:** At this point, visibility cannot be assigned to Collaboration Groups.

### Online Help

Revise: Easily accessible and prominent informational text indicating the distinction between public, institutional and collaboration group access as well as the type of access control available (Read and Read Selective; Edit and Edit Selective; and None) is vital to understanding the nuances of this use case.

## Managing Access to caArray Data

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This is from previous manual. When I get time to work through it, it will probably be removed.

### Requesting Access to caArray Records

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

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

- Your name
- 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*

*Visibility*

*Security Structure Reword to reflect 2.0*

### 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.

*Work on redundancy. Don't know if this still applies or not. Put in creating and managing experiments??*

*Visibility*

*Security Structure Reword to reflect 2.0*

## Visibility

In caArray, the term “visibility” is used to describe the access to objects granted to logged in users. The following table [Table 4.9](#) 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.

<b>Term</b>	<b>Definition</b>
<b>Public</b>	Anyone can view all records, with <b>Read-Only</b> access.
<b>Private</b>	Can be viewed only by submitter (“owner”) of object. <b>Private</b> is assigned by default if no other <b>Visibility</b> option(s) are selected when an object is created.
<b>Public + Group</b>	Anyone can view all records, with <b>Read-Only</b> access. Modify privileges are assigned to members of the specified group(s) who are assigned “Curation” privileges.  <b>Note:</b> The advantage to assigning a group access to data that is already Public, is in being able to isolate objects with that group’s visibility. For example, the user (with appropriate visibility) could locate from the Public objects, all Experiments tagged with the group’s visibility.
<b>Read-Only</b>	Permission only to view records created by other persons or organizations
<b>Delete</b>	Permission to delete records created by other persons or organizations
<b>Read/Modify</b>	Permission to view and/or modify records created by other persons or organizations

Table 4.9 *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.

*Security Structure Reword to reflect 2.0*

*Work on redundancy. Don't know if this still applies or not. Put in creating and managing experiments??*

*Granting Others Access to Your Work*

From here on, to be reworked:

## Updating an Experiment proposal

Once an Experiment proposal has been created by a Principal Investigator, with the appropriate permissions, you can edit a proposed project to reflect changes as needed or to simply update a proposal in draft status. In fact, to update an Experiment proposal, the Experiment must be in “draft” or “returned for revision” status.

### Only a PI can perform this task?

To update an Experiment proposal, follow these steps:

1. Go to the NCICB caArray login page <http://array.nci.nih.gov> and log in.

Once you are on the caArray Portal Welcome login page, the browser displays the Experiment workspace.

2. Browse or search for the Experiment you want to edit.
3. Select Update Experiment.
4. The System displays all experiments that are in “draft” or “sent for revision” status.
5. The Principal Investigator selects the experiment of interest for updating.
6. The system displays several sections of the experiment proposal – details of which are in Special Requirements – Project Section Attributes and Conditional Logic – presented in the following order –
  - a. Overall Project Characteristics,
  - b. Principal Investigator and Contact Data\*,-- basic contact data displayed with indicator of whether the PI is main point of contact or member of research team is the POC.
  - c. Experimental Design,
  - d. Sources,
  - e. Samples,

Can select to save a draft .

If an entry is not valid, system displays validation message indicating type of info required.

7. The Principal Investigator enters all the required fields for “Overall Project Characteristics” as described in the Special Requirements and moves to the next section.

If an entry incorrectly entered, a “Back function appears. Correct and resubmit proposal.

If PI is not primary point of contact, system present list of associated research scientist from which to pick.

8. Next, the Principal Investigator reviews their abbreviated contact data, displayed in read-only format and validates that they are the primary point of contact for the project.
9. Next, the Principal Investigator enters all required fields in the Experimental Design section, indicating at least one Experimental Factor used in the design.
10. Next, the Principal Investigator comes to the Sources portion of the project proposal and the System offers three options for the entering of Source data
  - a. Manual Entry
  - b. Import data
  - c. Pull from caTissue
11. The Principal Investigator chooses to enter the elements manually.
12. The System displays the elements for describing a source entering each required field for each source used in the experiment.
13. The Principal Investigator saves the entry.
14. The System brings the Principal Investigator to the source just entered and displays the name, description of the initial source entry and the ability to:
  - a. Copy the Existing Source
  - b. Add Another – return to Step 8 of the Basic Flow
  - c. Edit the Existing Source – return to Step 8 of the Basic Flow with the previous entered data available
  - d. Delete the Existing Source – removes the existing source and return to Step 6 of the Basic Flow.
15. The Principal Investigator chooses to Copy the Existing Source.
16. The System copies the source attributes, renames it using the existing source name and adding an incremental number (i.e., Source2, Source3,) and displays the source directly under the existing one, with the ability to edit the name. Steps 8-12 of the Basic Flow can be repeated as often as desired and Step 10 can be repeated against any existing source.
17. The Principal Investigator moves on to the Sample Section and the System provides three options for entry
  - a. Manual Entry
  - b. Import Data
  - c. Pull for caTissue--deferred for 2.0?
18. The Principal Investigator chooses to enter the elements manually.
19. The System displays the elements for describing a sample entering each required field for each sample used in the experiment.
20. The Principal Investigator saves the entry.
21. The System brings the Principal Investigator to the sample just entered and displays the name, description, source, and number of extracts of the that sample entry with the ability to:

- a. Copy the Existing Sample
- b. Add Another – return to Step 15 of the Basic Flow
- c. Edit the Existing Sample – return to Step 15 of the Basic Flow with the previous entered data available
- d. Delete the Existing Sample – removes the existing sample and return to Step 6 of the Basic Flow.

22. The Principal Investigator chooses to Copy the Existing Sample.

23. The System copies the sample attributes, renames it using the existing sample name and adding an incremental number (i.e., Sample2, Sample3,) and displays the sample directly under the existing one, with the ability to edit the name and change the source (if more than one source exists). Steps 15-19 of the Basic Flow can be repeated as often as desired and Step 19 can be repeated against any existing sample.

24. The Principal Investigator is content with the data entered and submits the Project.

The System saves the Project, informs the Principal Investigator and the Lab Administrator via email of the submission (including the project url) and returns the Principal Investigator to their workspace updated with the state of the project.

User can choose one or more array types within given experiment. E.G an SNP genotype project can have both Affy 250 K chips that are .nsp and .sty.

no multiple organisms or platforms.

Can import source and sample annotation or manually enter source and sample annotations. Cannot overwrite or version related to asynchronous importing of annotations.

## Project Characteristics

Represent minimum set of attributes required to submit an Exp for review.

Screen Name	Value	Field Type	Required
Experiment Title	Alpha/Numeric (100 characters)	Text Box	Yes
Experiment Identifier	Auto-generated once saved	Hidden	No
Payment Mechanism	Grant, Purchase Order, Other	List Box	Yes
Payment Number	Alpha/Numeric (100 characters)	Text Box	No
Service Type	Full, Partial, Analysis	List Box	Yes
Platform Type*	Gene Expression, SNP, DNA aCGH	List Box	Yes
Manufacturer	Affymetrix, Agilent, GenePix, Illumina, Imagene, UCSF Spot, Custom*	List Box	No
Array Design	Derived List of Available Designs from Manufacturer	List Box	No
Source	List of available Organisms	Multi-Select	Yes

Tissue Site	List of Available Terms based on Organism	Multi-Select	Yes
Tissue Types	List of Tissue Types (e.g., frozen_tissue_cells)	Multi-Select	Yes
Cell Type	List of Available Terms	Multi-Select	No
Disease/Condition	List of Available Terms	Multi-Select	Yes
Pooled Samples?	Yes/No	Radio	Yes
Sample Types	List of Sample Types based on Platform Type (e.g., DNA for SNP, RNA for Gene Expression)	Multi-Select	Yes

## Experimental Design

Screen Name	Value	Field Type	Required
Experiment Design Type	List of Available Types (e.g., time series, pharmacogenic)	List Box	Yes
Experimental Design	Alpha/Numeric Text (2000 Characters)	Text Area	Yes
Experimental Quality Control Description	Alpha/Numeric Text (2000 Characters)	Text Area	No
Quality Control Types	List of Available Types (biological replicates, peer review)	List Box	No
Replicate Description	Alpha/Numeric Text (2000 Characters)	Text Area	No
Replicate Types	List of Available Types (biological or technical replicates)	List Box	No
Experimental Factors	Name, Description and Category (list)	Mixed with Multiple Factors able to be added	Yes

## Sources

Screen Name	Value	Field Type	Required
Source Name	Alpha/Numeric Text	Text Box	Yes
Source Description	Alpha/Numeric Text (500 characters)	Text Area	No
Organism	Displayed from Project Properties	Read-only	N/A
Organism Part	Displayed from Project Properties – Unless more than one selected, then display the option(s)	Select	Yes
Cell Type			
Strain			
Developmental Stage			
Disease State			

Genetic Variation			
Genotype or Mutation Status			
Age	Numeric value (including 0 and decimal amounts) and a qualifying list (minutes, hours, days, weeks, months, years)		

## Samples

Screen Name	Value	Field Type	Required
Source Name	Alpha/Numeric Text	Text Box	Yes
Source Description	Alpha/Numeric Text (500 characters)	Text Area	No
Organism	Displayed from Project Properties	Read-only	N/A
Organism Part	Displayed from Project Properties – Unless more than one selected, then display the option(s)	Select	Yes
Cell Type			
Strain			
Developmental Stage			
Disease State			
Genetic Variation			
Genotype or Mutation Status			
Age	Numeric value (including 0 and decimal amounts) and a qualifying list (minutes, hours, days, weeks, months, years)		