

CHAPTER 4

CREATING AND MANAGING EXPERIMENTS

The following topics are part of this chapter:

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Submitting an Experiment Proposal

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, as needed. Alternatively, you can have another designee with appropriate privileges complete the submission.

Move these somewhere else:.

Organisms	<u>Definition needed</u>
Assay Providers	<u>Definition needed</u> In the caArray context, a person or an organization associated with an entry in the program

Unique Array Designs	Descriptions of microarrays that include such information as array layout and design and the technology used to create a microarray.
Hybridizations	The process of incubating one or more labeled extracts with an array. Hybridization methods form the basis for microarray techniques.
Registered Institution	<u>Cancer center, academic institution, laboratory or commercial vendor with an established caArray account??</u>
Registered Users	<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**.



Figure 4.1 Create/Propose Experiment on left sidebar

caArray displays a New Experiment page consisting of five tabs, described as follows:

Tab Name	Description
Overview	Overall experiment characteristics
Contacts	Principal Investigator and Contact Data
Annotations	Annotation (containing Experimental Design, Sources, Samples, Extracts**, Labeled Extracts**, Hybridization** subsections)
Data	containing Manage Data and Download Data subsections
Supplemental	Reference documents
Publications	Publications associated with the Experiment

Table 4.1

Sections [do you mean tabs?](#) which must be completed are indicated [how?](#) as well as the required fields within each section before you can save the Experiment.

*The Principal Investigator contact data is made available automatically. [What does this mean?](#)

**These sections are filled out by Lab Member users during the course of executing a full service experiment; they generally are not shown prior to submission).

[Can only PIs enter an Experiment? Does that now \(11/21/07\) mean that any logged in user can do this?](#)

Overview Tab

When creating an Experiment, on the Overview tab, enter the appropriate information for Overall Experiment Characteristics¹. Fields are described in the following [table](#).

Experiment: New Experiment

The screenshot shows the 'Overview' tab for a 'New Experiment'. The main section is 'Overall Experiment Characteristics'. A note states: 'The Overall Experiment Characteristics represent the minimum set of attributes required to submit an experiment for review. Required fields are marked with *asterisks*.' The form contains the following fields and sections:

- Experiment Title:** A text input field.
- Status:** Displayed as 'Draft'.
- Experiment Identifier:** A dropdown menu.
- Service Type:** A dropdown menu with '--Select a Service Type--'.
- Assay Type:** A dropdown menu with '--Select an Assay Type--'.
- Provider:** A dropdown menu with '--Select a Provider--'.
- Array Designs:** A text input field.
- Organism:** A dropdown menu with '--Select an Organism--'.
- Tissue Sites:** A section with a 'Filter:' box, an 'Add' button, and a list of items: Leg, Brain, Cell Line, Feed. To the right is a 'Selected Tissue Sites' box.
- Tissue Types:** A section with a 'Filter:' box, an 'Add' button, and a list of items: whole_organism, cell lysate, organism_part, DNA, total_RNA. To the right is a 'Selected Tissue Types' box.
- Cell Types:** A section with a 'Filter:' box, an 'Add' button, and a list of items: Chromaphine Cells, Brain Tissue. To the right is a 'Selected Cell Types' box.
- Conditions:** A section with a 'Filter:' box, an 'Add' button, and a list of items: Adrenocortical Carcinoma. To the right is a 'Selected Conditions' box.

A 'Save' button is located at the bottom right of the form.

:

Overview Tab Field	Description
Experiment Title	Title designate by the PI or other user creating the Experiment
Status	Draft or Completed?

1. Fields with a red asterisk * are required.

Overview Tab Field	Description
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 <u>each particular attribute</u>. Example: klemm-90765. <u>Significance of "90765"? ID produced is directly accessible via a URL. <u>How? Where would one see the URL?</u></u></p>
Service Type	<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"> • Full • Partial • Analysis • Publish for "bulk upload of data". <u>"Intended to provide means to annotate this data, but higher priority is to make data available to caA community." Does selecting Publish service type automatically set the bulk upload in motion? I don't think so, but <u>had to ask.</u></u>
Assay Type	<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"> • Gene Expression • DNA • SNP • aCGH
Provider	<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>
Array Design	Select an array design from the automatically-generated list of array designs corresponding to the Provider you selected.
Organism	<u>Organism that is the source of the sample biomaterial?</u> Select from the drop-down menu the appropriate organism
Tissue Sites	<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>
Tissue Types	Select the type of tissue (that comes from the tissue site?) used in the array
Cell Types	Select the type of cells used in the array. Cell preps like cell lysate?

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. Would you suggest doing this for each page (tab) before moving onto the next?
- Proceed to the **Contacts** tab.

Contacts Tab

The Contacts tab is one of the six tabs displayed for an Experiment.

- When reviewing an Experiment, you can select the Contacts tab to review xxxxx.
- When you are creating an Experiment, select this tab to identify players in the Experiment.
- 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.
- To enter Contact information for the Experiment, follow these steps:
 - On the Contact tab, enter information for the fields described in Table xx. How is this information "made available automatically."? 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)?	<p>Select Yes or No. If answer is No, caArray opens new text boxes where you can add contact information for the POC. Does POC have to be registered user of caArray.</p> <p><u>Will a list display of caArray users from which you can select another POC? This is described in UC, I believe. Is this correct?</u></p>

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 sss¹.

Experimental Design Fields	Description
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	Select the Quality Control type from the scroll down list.
Quality Control Types	
Replicate Description	
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. Proceed to the Experimental Factors subtab.

Experimental Factors

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*.
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. Proceed to the Sources subtab.

1. Fields with a red asterisk * are required.

Sources

The Sources subtab (under the Annotations Tab) displays any previous Sources that may have been added previously to the Experiment you are creating. A source is any biological site from which the tissue for the array is derived. [Add to Glossary.](#)

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

3. The Principal Investigator comes to the Sources portion of the project proposal and the System offers three options for the entering of Source data. [I don't see these three options on the Sources tab.](#)
 - a. [Manual Entry](#)
 - b. [Import data](#)
 - c. [Pull from caTissue](#)
4. The Principal Investigator chooses to enter the elements manually. [As I see it, that is the only option.](#)
5. Click **Save**. The name of the source now displays on the Source subtab.

[Can user add more than one Source for an Experiment? I think not.](#)

6. Proceed to the Samples subtab.
7. 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.
8. The Principal Investigator chooses to Copy the Existing Source.
9. 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.

Samples Tab

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 biologicalsssss for the array.

1. Click the **Add a New Sample** button to add a new Sample.
2. In the Sample form that opens, enter the name and description of the Sample. When is other data about sample entered (the fields that display on the Samples tab.)?
3. Repeat steps 1 & 2 as often as needed to enter all the Samples used in this Experiment.
4. Click **Save**. The name of the Sample(s) now displays on the Samples subtab.
5. Proceed to the Extracts tab.
6. 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
7. The Principal Investigator chooses to enter the elements manually.
8. The System displays the elements for describing a sample entering each required field for each sample used in the experiment.
9. The Principal Investigator saves the entry.
10. 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.
11. The Principal Investigator chooses to Copy the Existing Sample.
12. 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.

Extracts Tab

The Extracts subtab (under the Annotations Tab) displays any previous Extracts that may have been added previously to the Experiment you are creating. An Extract is a biological sssss for the array.

1. Click the **Add a New Extract** button to add a new Extract.
2. In the Extract form that opens, enter the name and description of the Extract. When is other data about extract entered (the fields that display on the Samples tab.)?
3. Repeat steps 1 & 2 as often as needed to enter all the Extracts used in this Experiment.
4. Click **Save**. The name of the Extracts now display on the Extracts subtab.
5. Proceed to the Labeled Extracts subtab.

Labeled Extracts Tab

The Labeled Extracts subtab (under the Annotations Tab) displays any previous Labeled Extracts that may have been added previously to the Experiment you are creating. An Labeled Extract is a biological sssss for the array.

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 name and description of the Extract. When is other data about extract entered (the fields that display on the Samples tab.)?
3. Repeat steps 1 & 2 as often as needed to enter all the Labeled Extracts used in this Experiment.
4. Click **Save**. The name of the Labeled Extract(s) now displays on the Labeled Extracts subtab.
5. Proceed to the Hybridizations subtab.

Hybridizations Tab

The Hybridizations subtab (under the Annotations Tab) displays any previous Hybridization information that may have been added previously to the Experiment you are creating. An Hybridization is a biological sssss for the array.

1. Click the **Add a New Hyrbridization** button to add a new Hybridization.
2. In the Hybridizations form that opens, enter the name and description of the Hybridization. When is other data about extract entered (the fields that display on the Samples tab.)?
3. Repeat steps 1 & 2 as often as needed to enter all the Hybridizations used in this Experiment. Can enter more than one?
4. Click **Save**. The name of the Hybridization now displays on the Hybridization subtab.
5. Proceed to the Data tab.

Data Tab

The Data tab is the vehicle for uploading, validating, importing and downloading data relating to caArray Experiments. For more information about submitting data to an Experiment, see Chapter 5 Submitting Data to an Experiment.

Supplemental Tab

Publications

This tab allows you to create, edit or delete publications associated 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:

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

<i>Publications Fields</i>	<i>Description</i>
Title*	
Authors	
URL	
DOI	
Editor	
Pages	Where appropriate, enter the page number(s) of the article you are referencing
Publisher	
PubMedID	
Volume	
Year	
Publication	
Type	Select in the drop-down menu the publication type.
Status	Select in the drop-down menu the publish status: Published, In Preparation, Submitted

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.

Save a Draft

1. At Step 4 of Basic flow, but subsequently available between steps 5-20, the PI selects to save a draft of the experiment.

1. Fields with a red asterisk * are required.

2. System validates required fields, saves the E as a draft, and displays confirmation that proposal was saved. Return to Step 4 of basic flow.
3. How do you go from the Save draft to a final submission and approval of the Experiment?

Validation failure.

1. At step 21 of basic flow, system finds fault with one of the enteries.
2. System displays validation mesage indicating type of ino required.
3. PI corrects entry and resubmits.

Experiment Design attributes in table 2 page 8 of UC.

Sources described p. 8 of UC

Sample described p. 8 & 9 of UC.

4. Project identifier p. 9 of UC

Permissions Tab--column in the Experiment workspace

Managing Experiment Visibility

Initiated by a Data Owner, this use case allows for the promotion of a project's visibility. This action can apply to an entire project or to specific samples within the project. The basic visibility states of the project are: restricted, institution, group, public and collaborator. There is no restriction on changing a project's visibility, though it is not advisable once a publication has been published against the project.

only PIs can make changes

Addition Permissions

Which entities or attributes require permissions not described here? E.g.

- •Certain QuantitationTypes for SNP array data?
- ²Certain characteristics of Sources (e.g. potentially identifying characteristics of human subjects).
- ²Others?

Q. How should non-sample bio-materials be secured? E.g. what if a MAGE-TAB upload only included Extracts and not Samples? A. Through association to the project or a sample (for 2.0)

Q. How should individual data files be secured? A. through association to the project or a sample (for 2.0)

Q. Raw data is associated with a single hybridization, but a DerivedArrayData may be associated with multiple hybridizations. How should sample (or other discrete) permissions be handled for these? A. For 2.0 – within an experiment, the permission as the experiment or sample level will cascade downward to annotation and files

Q. What happens when a SNP human project (with privacy data) becomes public for TCGA? 4 specific fields for human snp projects will be visible to the public:

data owner must be logged in.

Available must exist in a saved state.

Workflow

1. 1.The Data Owner navigates to their workspace and selects one of their experiments they wish to change access permissions from the default “restricted” – which only allows the PI and the Lab to see the experiment.
2. 2.The System displays the experiment description, including the action “Manage Experiment Properties”.
3. 3.The Data Owner chooses the action “Manage Experiment Properties”.
4. 4.The System displays a choice for the type of access desired:
 - a. a.Public Access – whereby anyone with access to the instance’s url would be able to view, download or analyze the data exposed
 - b. b.Group Access – whereby anyone in a recognized group, likely including external institutions – will be able to access the data exposed (deferred from 2.0)
 - c. c.Institutional Access – whereby anyone who is registered with the host institution can gain access
 - d. d.Collaborator Access – whereby user created groups of individuals registered with the installation become available for assigning access to (see Manage Collaborators Use Case)
 - e. e.Explicit Restriction – a special case where the Principle Investigator wants to remove the experiment from view.
 - f. Data Owner can choose to restrict access to only those that received submission of the experiment. System requests confirmation and indicates that the experiment will be removed from all views . Data owner confirms.
5. The Data Owner chooses “Public Access”.
6. The System then requests whether the access is to apply to the entire experiment by supplying the following choices:
 - a. None (meaning the experiment will not be exposed)
 - b. Read (meaning the entire experiment is read only)
 - c. Read Selective (meaning a subset of the experiment will be read only)

Displays a list with all samples identified and their description in a read-only fashion.

 - d. Data owner elects to provide Edit Access at the Experiment level.
 - e. Data owner elects to provide Edit Selective Access at the Experiment level.
 - f. System exposes each sample with ability to select the visibility of the sample as None, Read, Edit (None is default). Data owner chooses access for each sample and saves.
7. The Data Owner chooses Read Selective.

8. The System exposes each sample with the ability to uniquely select the visibility of the sample as either – None or Read – with None as the default displayed for each sample.
9. The Data Owner chooses which samples desired for read access and saves.
10. The System presents a confirmation list (experiment name and affected samples) of the action about to be taken, presenting the ability to
 - a. Confirm Permissions
 - b. [Cancel Permissions](#)

The Data Owner confirms the change in permissions.

Note: At a minimum, The Cancer Genome Atlas, and potentially others, have established a policy where by only 4 fields of annotation can be provided to the open public:

- Clinical Diagnosis
- Histologic Diagnosis
- Tissue Anatomic Site
- Pathologic Status

Other data policies from TCGA can be found in Table 1 of the data policy document:

http://cancergenome.nih.gov/components/TCGA_Human_Subjects_prot_policy.pdf

Note about permissions:

If a sample contains a source that is used in more than 1 experiment, the control of whether or not the group (and the users within it) is constrained by the permissions set on the experiment. The sample in experiment 2 will not be visible or actionable unless the Data Owner (PI, Lab Scientist, Bioinformatician) provides access to the experiment and the group.

In addition, the permission established by the original owner of the data is carried forward as the default permission of the source or sample in question (and the data its associated with). However, the ability for the downstream “owner” to change the visibility of the data within their own experiment is available but that action will not change the visibility of the sample it was taken from – thus breaking the chain of reference in terms of visibility.

Online Help

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

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

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

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 4.5](#) 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 4.5 *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

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)		