Welcome to eagle-i

Open network. Open access. Open source.

eagle-i is a free, web-based application that collects information about biomedical research resources available at participating universities, and describes them so that researchers can easily search for and discover the tools they need, accelerate their research, and do more with less.

The eagle-i platform consists of two primary components:

- The eagle-i **search engine** is semantic and ontology-driven. When a search string of one or more characters is typed into the search bar, auto-suggest displays a list of possible options. You can select one of the suggestions by clicking on it, or continue to complete the search string to get more precise suggestions. By default, the search application searches all institutions and all resources within the eagle-i network, but you can filter by a single institution, core laboratory, or type of resource.
- The **SWEET** (Semantic Web Entry and Editing Tool) is a data collection tool that allows anyone with appropriate credentials to capture and manage information about research resources, people, and organizations within their institution and then share this information with the eagle-i Network. Depending on the workflow chosen by each member institution, different users may be responsible for adding resources and annotations, and for checking the information for accuracy and consistency before it is made available in the search application.

In continuous development since early 2010, eagle-i is now a mature platform in use at 25 institutions across the United States. The free software is an open source project, and we welcome institutions adopting it and participating in this growing network. The data in the system is also open access; anyone — regardless of affiliation — is welcome to search for resources or download the Linked Open Data directly.

eagle-i Resources

eagle-i collects information about the following types of biomedical research resources:

- Biological Specimens
- Databases
- Antibodies
- Cell Lines

- Human Studies
- Instruments
- Organisms and Viruses
- Cores Labs and other Organizations
- People
- Protocols and Documents
- Reagents
- Research Opportunities
- Services
- Software
- Chemical Reagents
- Constructs
- Gene Knockdown Reagents
- Microarrays
- Nucleic Acid Reagents
- Protein Reagents
- Chemical Libraries
- Nucleic Acid Libraries
- Peptide Libraries
- Organism Libraries

Note: Sharing information with eagle-i **does not necessitate** sharing the resource with anyone who asks; resource providers retain control over when, how, and under what conditions their resources may be used.

About These Training Materials

These training materials correspond to Application Version: 3.0.2 / Ontology Version: 1.9.3 in the SWEET, and are intended as a reference guide for users entering and maintaining information about resources at their institution. Additional documents and videos can be found at: http://open.med.harvard.edu/display/eaglei/Training.

The development of training materials was supported by NIH contract "open-i" (101180SB23), which aims to make Linked Open Data available from four Clinical and Translational Science institutions: Harvard University, Vanderbilt University, Oregon Health and Sciences University and Vanderbilt University. These materials will support the ongoing use and operational support of the servers, databases, and tools necessary for the LOD survivability at the open-i sites.

These documents may also be adapted/repurposed for any institution that has adopted the eagle-i software.

Using the SWEET Training Server

A training server where users can practice adding and editing records using the SWEET is available at: https://training.eagle-i.net:8443/datatools/. Records entered on the training SWEET will never be available in the search application, although other training users will be able to see and possibly modify them if they are left unlocked. The dataset is periodically refreshed by Central eagle-i staff.

To access the SWEET Training Server, log in with the username and password: **demo**. This will provide a demonstration of what the most comprehensive SWEET access (level 4) looks like. Alternatively, you may login using a different level of access with one of the following usernames/passwords: L3/Level3; L2/Level2; L1/Level1.

For more details on which actions are permitted using the different permission levels, see the section on Access Level Details.

Glossary of Common Terms

ACCESS PERMISSION LEVEL – determines which actions you can take to modify records in different states. Determined by your role and assigned by your institutional administrator.

ANNOTATION – refers to both the activity of describing the properties of a resource, and to the descriptions themselves. (e.g. You annotate a record by filling out its fields, thus creating annotations.)

CURATION – describes a range of activities and processes related to the creation, management, maintenance, and validation of information in eagle-i. All records must conform to certain standards before being published in the repository. Data curators provide data quality assurance by ensuring that resources in the eagle-i repository are accurate, up-to-date, and described in a manner that is both consistent with other, similar resources and useful to search users.

FIELD – each record contains multiple fields which each describe one facet of the resource. Fields are determined by properties in the ontology.

LIFECYCLE – refers to the different stages in the typical lifespan of record as it passes through the eagle-i workflow, from creation through removal/preservation. Each stage of the lifecycle corresponds to a different record status.

ONTOLOGY – a formal structural framework used to represent concepts and relationships in a certain domain. The eagle ontology describes groups (classes) of terms relating to biomedical research.

RECORD – a digital form used to describe each instance of a resource, person, or organization in the eagle-i repository.

REPOSITORY – the back-end database that stores eagle-i resource information entered using the SWEET.

ROLE – the tasks an eagle-i user is responsible for completing at his or her institution. Data collection, data entry, and data management/curation (or some combination thereof) are all examples of different roles a user may have.

SEARCH APPLICATION – the search engine allowing users to browse or search for published eagle-i resources from all member institutions.

STATUS/STATE – refers to the stage of a record in the workflow. The four eagle-i states are: Draft (in progress), In Curation (in review), Published (publicly visible), and Withdrawn (retired).

STUB – an unfinished record created from within another record, containing only a name and type. Stub records almost always require further annotation in order to be considered valid for publication.

SYNONYM – an alternate name for a term. Synonyms have an equivalent meaning to the preferred term and will often be an abbreviation or less formal terminology. They are captured in the ontology to aid in resource annotation and retrieval, and can be used interchangeably in the autosuggest.

SWEET – Semantic Web Entry and Editing Tool. The tool used to enter, modify and maintain information about eagle-i resources. Sometimes referred to as simply the data tool.

TERM – controlled vocabulary terms must be selected in fields that are populated from the ontology. If the most accurate term to describe a resource is not currently in the ontology, users can request that it be added. Most terms have definitions and synonyms.

TYPE – refers to the hierarchical categories of concepts (e.g. resources, organizations, people) in the eagle-i ontology. Every record in the SWEET has a Type field which must be filled with term corresponding to either a type (parent) or sub-type (child). Also known as "Classes."

Accessing the SWEET

SWEET *Semantic Web Entry & Editing Tool*

The eagle-i SWEET (**S**emantic **W**eb **E**ntry and **E**diting **T**ool) is eagle-i's web-based data entry tool. Anyone with appropriate credentials can use this tool to enter and manage data in the eagle-i repository. Resources published in the SWEET are visible to the public in the eagle-i search application.

Each institution that uses eagle-i software has a separate installation of the SWEET. To manage resources related to a particular institution, you must have login access to that specific SWEET.

Requesting a new user account

Login credentials for the SWEET are assigned by each institution. If you need access to multiple institutions, you must request access separately for each one.

To request login credentials:

1. Find the URL of your institutional SWEET: https://www.eagle-i.net/help/data-entry-tool-links/. Clink the link to open the SWEET.
2. On the login screen, click **Request your username and password**.
3. The Feedback dialog opens. Provide the required information and select **Entering resources into the eagle-i web application**.
4. Click on **Submit** when done.

Changing or resetting your password

You can change or reset your password at any time. To change your SWEET password:

1. Log into your institutional SWEET using your current password.
2. Click the **Change Password** link at the top of the page.
3. A repository login dialog appears. Log in to the repository with your current credentials.
4. The Change Password dialog appears. Type your current password. Type a new password (twice). Click **Submit** to save the new password or **Reset Form** to clear the fields.

If the **Request your username and password** and **Change Password** links do not appear, your institution may be using a separate login system. Contact your local eagle-i representative to gain access.

Navigating the SWEET Menu

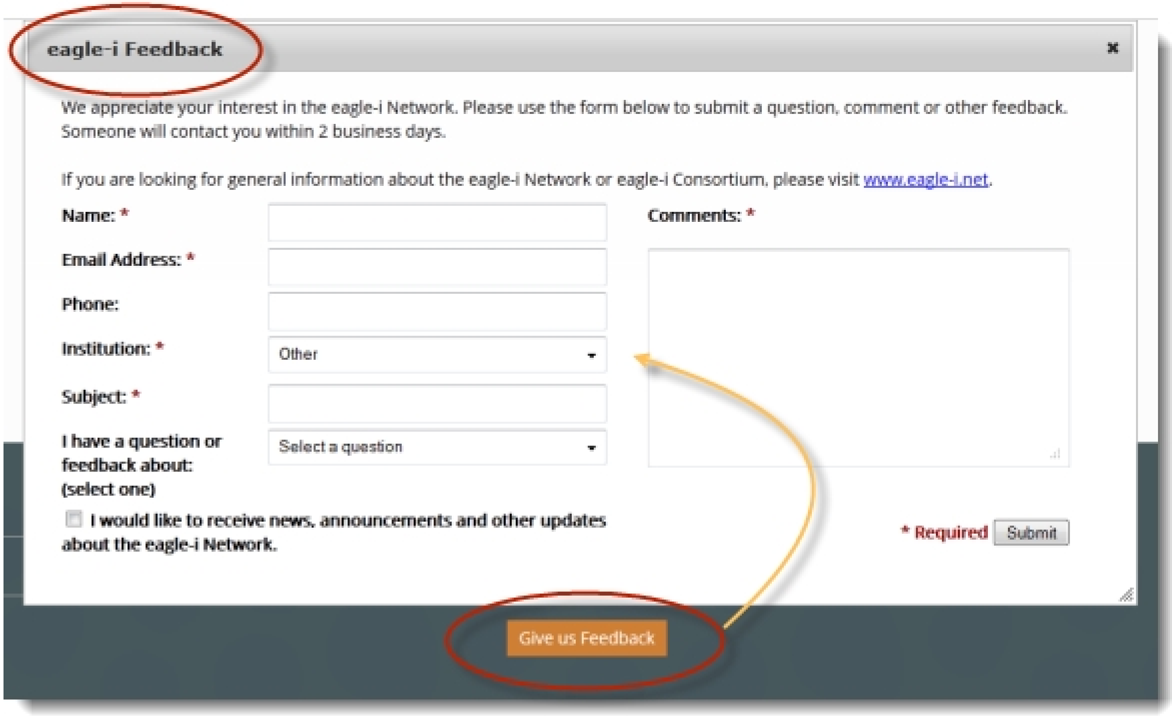
The following menu tabs provide navigation from anywhere in SWEET:

- **eagle-i Home**—Opens the eagle-i home page, including the eagle-i Search engine.
- **Institution Home—**Opens your institution specific home page where you can find summary lists of participating resource providers at your institution as well as other useful links.
- **Help**—Opens the online SWEET Help.
- **Ontology Browser**—Allows you to explore the eagle-i ontology. See the Ontology Browser section for more information.
- **Change Password**—Opens the change password dialog.

If the **Change Password** link does not appear, your institution may be using a separate login system. Contact your local eagle-i representative for more information.

Sending Feedback

The Feedback button located at the bottom of all eagle-i pages opens a feedback form where you can submit questions or comments.



eagle-i Feedback

We appreciate your interest in the eagle-i Network. Please use the form below to submit a question, comment or other feedback. Someone will contact you within 2 business days.

If you are looking for general information about the eagle-i Network or eagle-i Consortium, please visit www.eagle-i.net.

Name: *

Email Address: *

Phone:

Institution: * Other

Subject: *

I have a question or feedback about: (select one) Select a question

Comments: *

☐ I would like to receive news, announcements and other updates about the eagle-i Network.

To leave feedback:

1. Click Feedback on the right side of the page.
2. Complete all required fields. Click Submit.

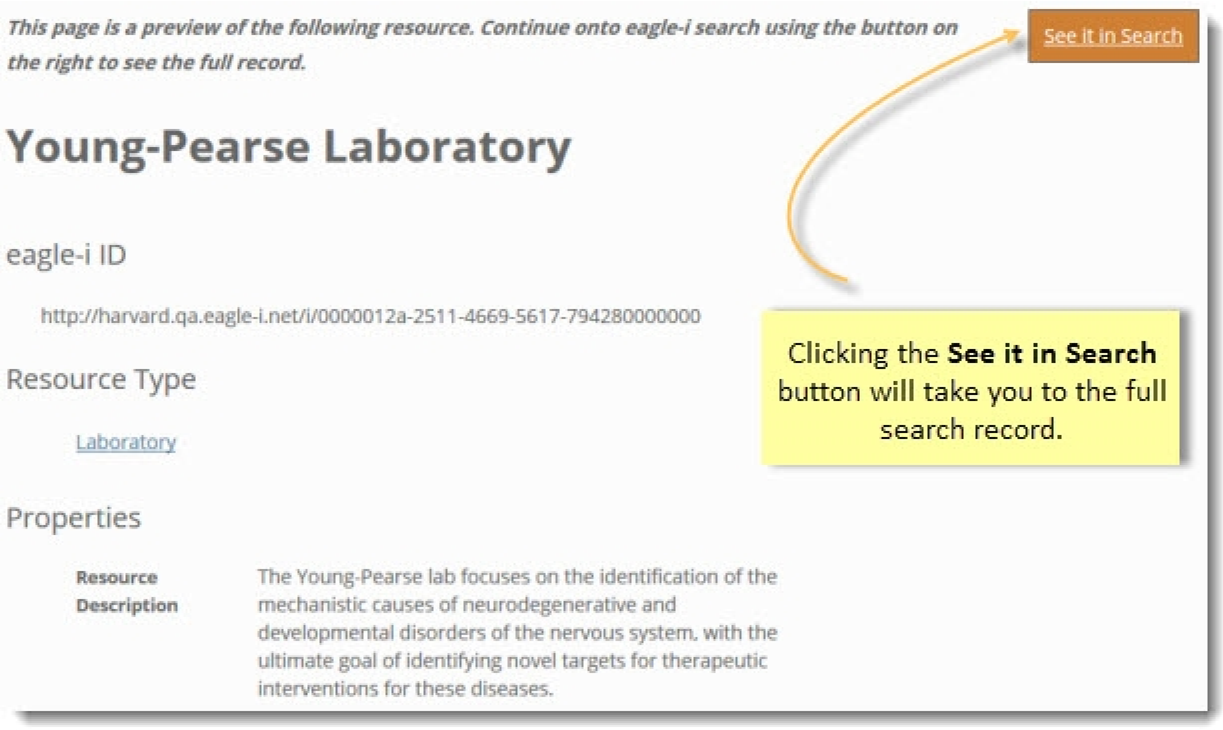
Citing eagle-i Resources

Each eagle-i resource has a unique identifier (URI, or Uniform Resource Identifier) that can be used in a citation for that resource. To find the identifier in a published record,click the **Cite this resource** button:

APP cKO x Cre ER

Mus musculus

Each eagle-i URI is a resolvable link that leads to a dissemination page containing information about the record and a link to it in the search application.



This page is a preview of the following resource. Continue onto eagle-i search using the button on the right to see the full record.

Young-Pearse Laboratory

eagle-i ID

http://harvard.qa.eagle-i.net/i/0000012a-2511-4669-5617-794280000000

Resource Type

Laboratory

Properties

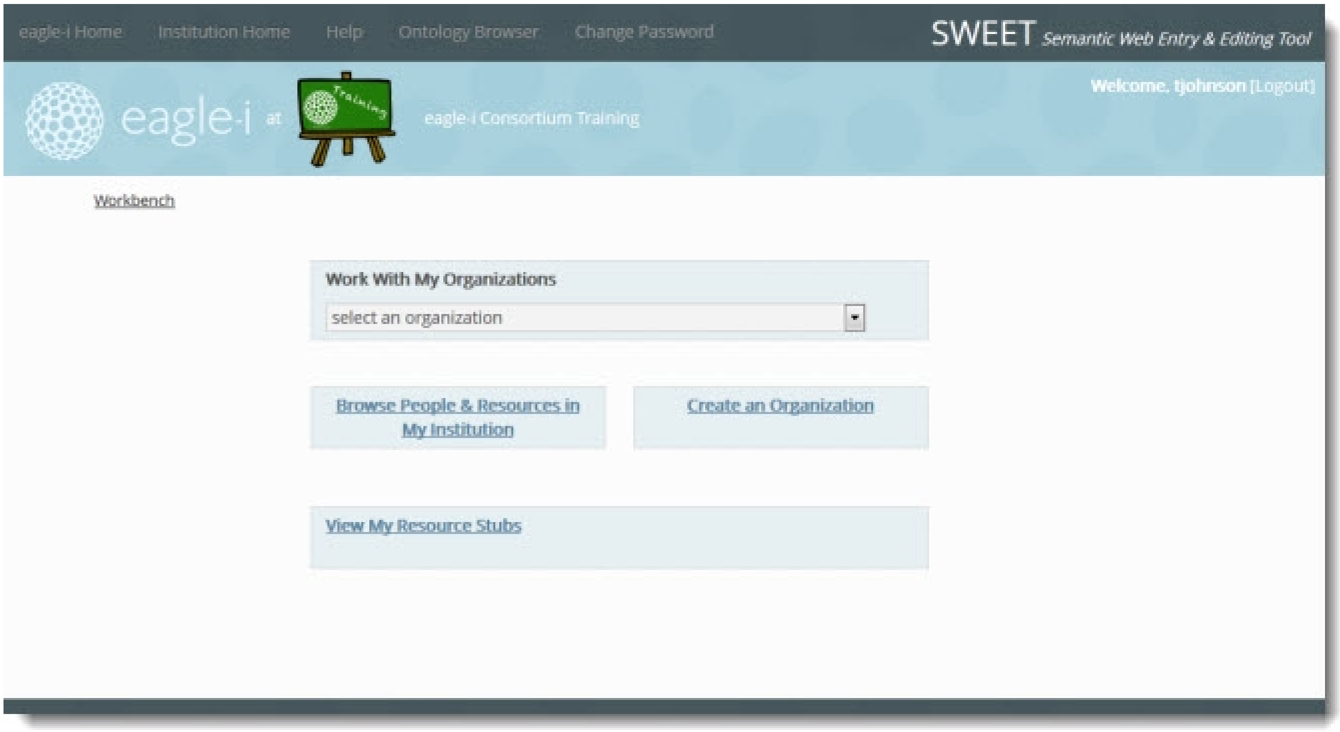
Resource Description	The Young-Pearse lab focuses on the identification of the mechanistic causes of neurodegenerative and developmental disorders of the nervous system, with the ultimate goal of identifying novel targets for therapeutic interventions for these diseases.

Clicking the **See it in Search** button will take you to the full search record.

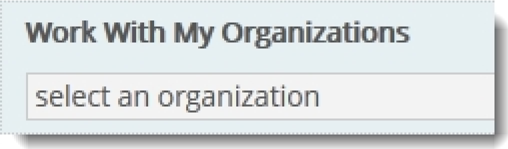
For citation guidelines and examples for different resource types, see: http://www.eagle-i.net/participate/citing-an-eagle-i-resource/.

Navigating the Workbench

After logging into the SWEET, the first page you see is the Workbench.



From the Workbench you have access to the following:



Work With My Organizations — This menu allows quick access to organizations within your institution (with the exception of private companies). Note that this includes all organizations at your institution, not just ones created or owned by you.

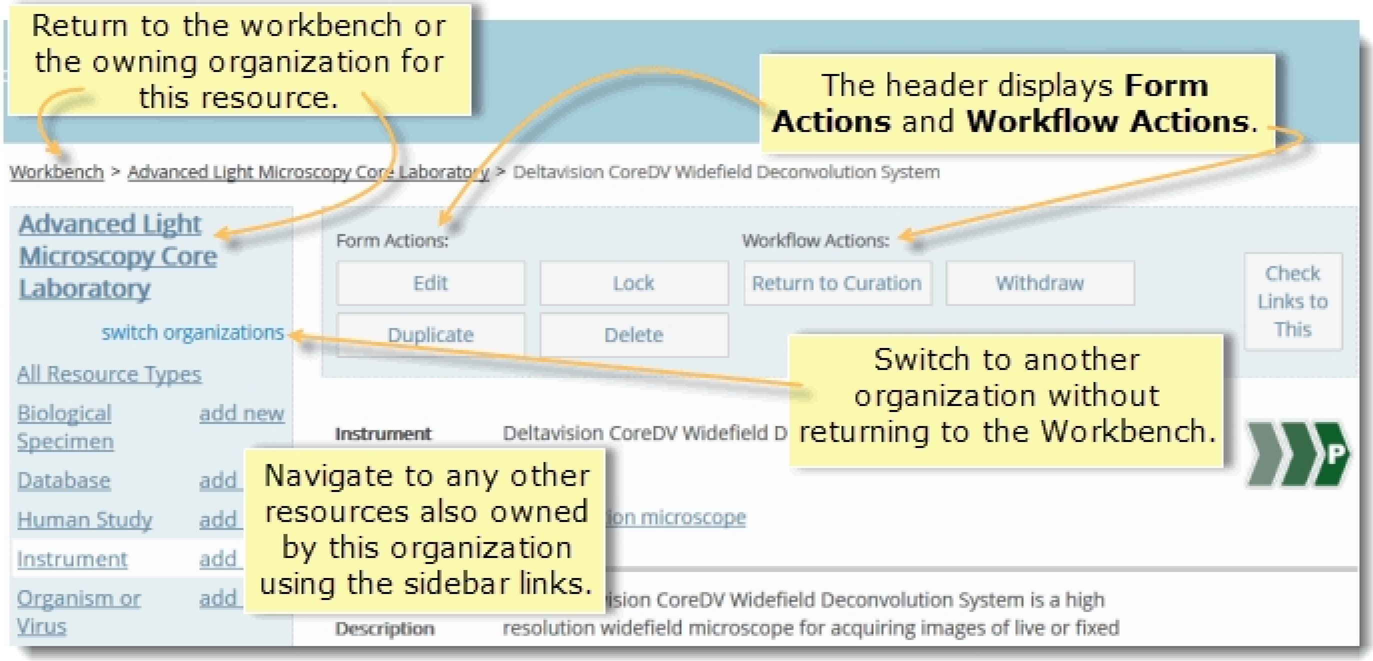
Browse People & Resources in My Institution — Allows you to browse lists of people, organization (including private companies), and resource records within your institution. See Navigating Lists for more information.

Create an Organization — Creates a new organization record, such as a research or core laboratory, to which you can subsequently add descriptive information and resources.

View My Resource Stubs — Stub records are incomplete records that were created as links from within another record, and contain only a name and type. Until these records have been edited and saved, your stubs are listed in the **View My Resource Stubs** section, so it is easy to find and annotate them more completely. See the Resource Stubs section for more information.

About Records

Records are web forms are used to add or modify information in eagle-i. A single record describes a single resource, person, or organization.



Return to the workbench or the owning organization for this resource.

The header displays **Form Actions** and **Workflow Actions**.

Switch to another organization without returning to the Workbench.

Navigate to any other resources also owned by this organization using the sidebar links.

Note: Fields available within forms change based on the specific sub-type of the record; for example, choosing Antibody as a sub-type of reagent will bring up different fields than choosing Cell line. In general, it is best to select the most appropriate top-level fields before continuing editing a form.

Navigating Records

Every record form is composed of the following sections:

Left Sidebar

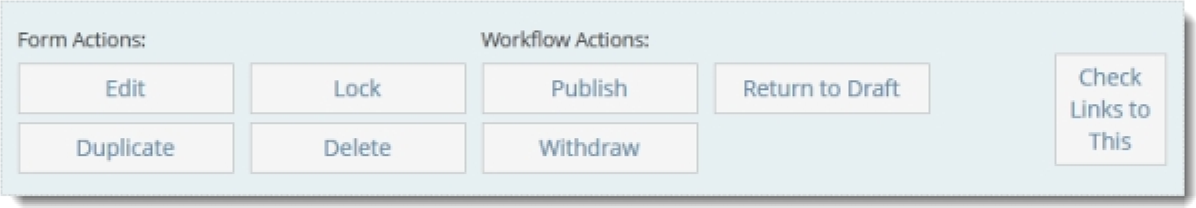
The sidebar to the left of each record provides the ability to navigate through the resources associated with that organization. From the sidebar, you can select the following:

- **Name of the selected organization** — the name in bold type at the top is the organization associated with the selected resource. Selecting the name link opens the overview record for that organization.
- **Switch Organizations** — click to open a drop-down list of all other resource providing organizations within your institution. Click to select a different organization.

- **View All Resource Types** — click any of the resource type names to see any resources of that type belonging to this organization, or click **All Resource Types** at the top to see all resources associated with this organization.
- **Add New** — click to add a new resource of that type to this organization.

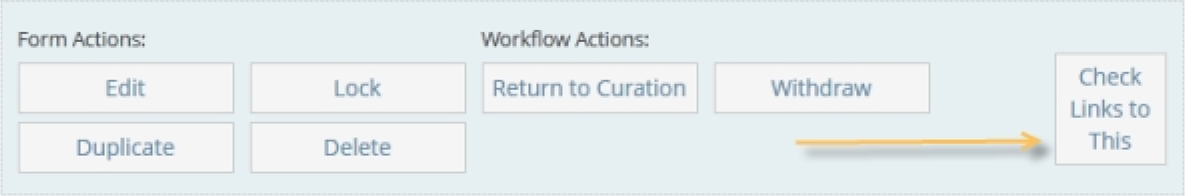
Form Actions and Workflow Actions panel

Located at the top of page. Use **Form Actions** to: edit, duplicate, delete, and lock and unlock records. Use **Workflow Actions** to change the status of any record.

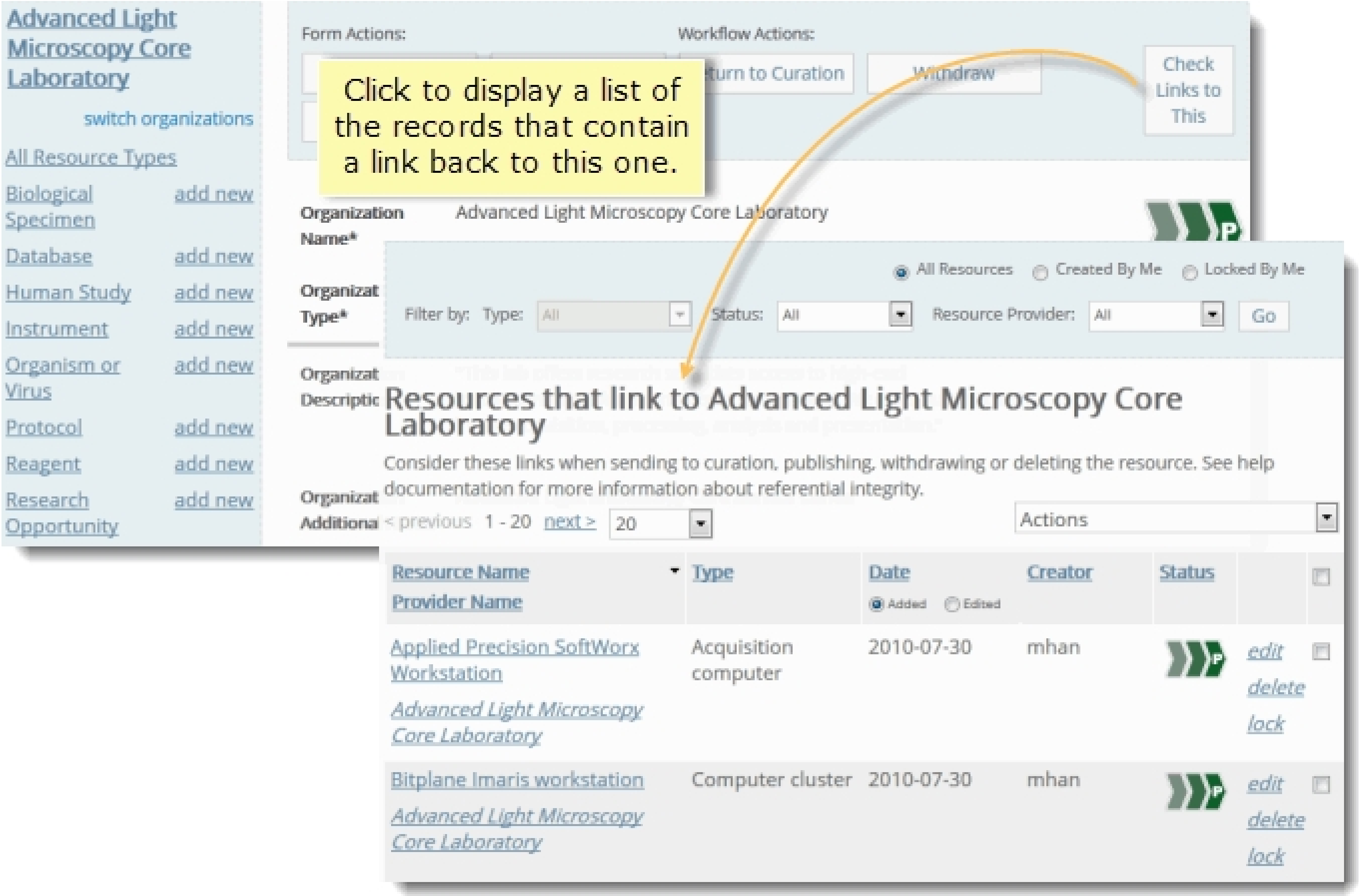


Note: The specific actions that display on each record depend on its workflow status and whether or not it is currently being edited. Actions may display but not currently be available; these appear grayed out.

Check Links to This



After a form has been saved for the first time, this button appears in the workflow actions section at the top of the record. Clicking this button displays a list of other resources that reference this one.



Click to display a list of the records that contain a link back to this one.

Organization Name*: Advanced Light Microscopy Core Laboratory

Filter by: Type: All Status: All Resource Provider: All

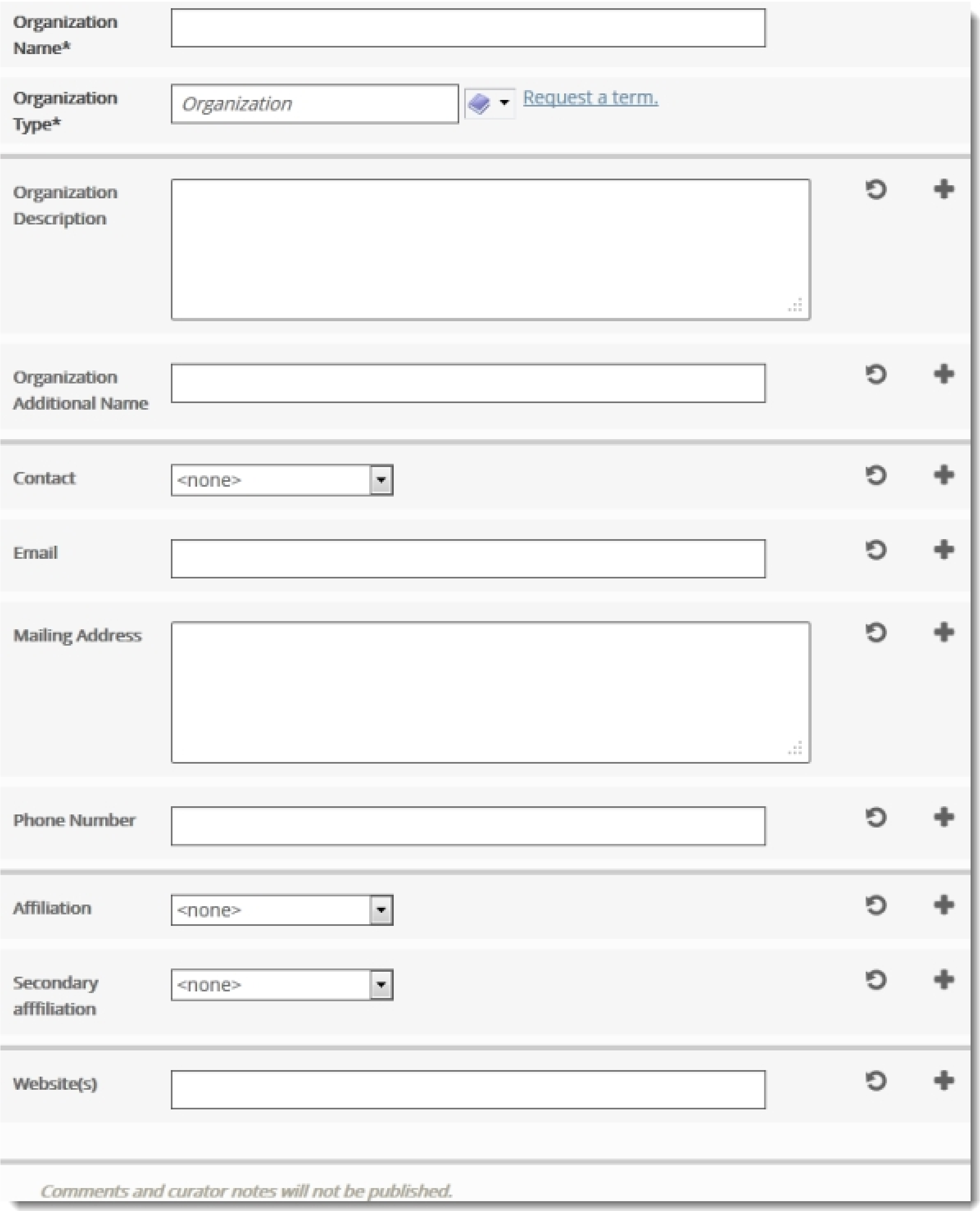
Resources that link to Advanced Light Microscopy Core Laboratory

Consider these links when sending to curation, publishing, withdrawing or deleting the resource. See help documentation for more information about referential integrity.

Resource Name Provider Name	Type	Date ● Added ○ Edited	Creator	Status		☐
Applied Precision SoftWorx Workstation *Advanced Light Microscopy Core Laboratory*	Acquisition computer	2010-07-30	mhan	P	*edit* *delete* *lock*	☐
Bitplane Imaris workstation *Advanced Light Microscopy Core Laboratory*	Computer cluster	2010-07-30	mhan	P	*edit* *delete* *lock*	☐

Main Body

This area is located in the center of the page and contains all the fields used to describe the resource, beginning with the Name field and ending with the Comments and Curator Notes fields.



Any information entered into the form fields in the main body of the record will be visible in the search application after the record is published, except for address, contact information (hidden for privacy reasons) and the Comments and Curator Notes fields.

Metadata

This section is located at the bottom of the page. Click ▶ to expand or collapse this area. Information entered in this section is NOT visible using eagle-i search.

The Metadata section includes:

- The **unique identifier** for the record (URI).
- **Provenance data** about the record (when and by whom it was created and last modified).
- **Hidden fields** that have been removed from the main body of the record due to ontology changes. In most cases, these are because we no longer collect that information, or collect it in another field instead.
- **Saved term requests.**
- Saved information from the **Comments and Curator Notes** fields.

Eagle-i unique ID	http://harvard.qa.eagle-i.net/i/0000012c-64ed-0030-c437-ff0b80000000

Metadata properties:

Last Modification Date	2013-02-25T12:13:10.714-06:00
Creation Date	2010-11-19T10:20:06.264-06:00
Creator	rgarces (Robert Garces)
Workflow State	Published
Contributor	tjohnson (Tenille Johnson)

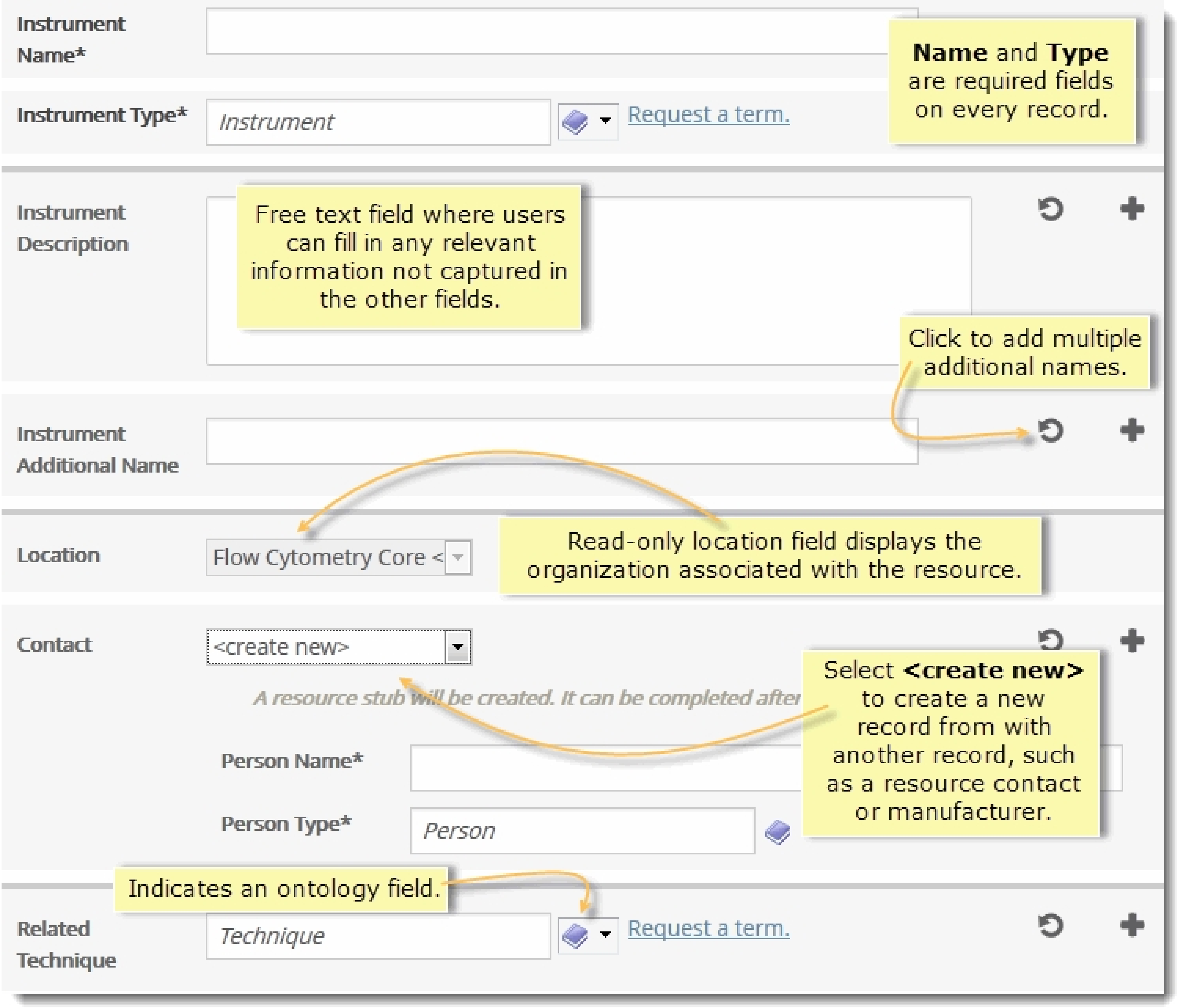
Other properties:

Comments	TJ: Website URL updated on 2/25/13. Director to contact with updates services in March.

Before publishing, you should check this section for any data that should be migrated to another more appropriate field in the main body of the page, or for any notes from other users that could be important.

Types of Fields

Most record forms contain a combination of free text fields, fields populated with controlled vocabulary from the eagle-i ontology, and fields populated with links to other eagle-i records. This screen capture is an example of the types of fields used to describe a new instrument:



Instrument Name*

Instrument Type* Instrument Request a term.

Name and **Type** are required fields on every record.

Instrument Description

Free text field where users can fill in any relevant information not captured in the other fields.

Click to add multiple additional names.

Instrument Additional Name

Location Flow Cytometry Core <

Read-only location field displays the organization associated with the resource.

Contact <create new>

A resource stub will be created. It can be completed after

Person Name*

Person Type* Person

Select **<create new>** to create a new record from with another record, such as a resource contact or manufacturer.

Indicates an ontology field.

Related Technique Technique Request a term.

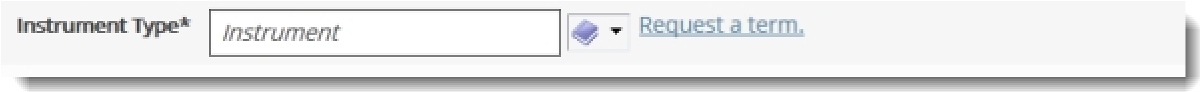
Free Text Fields

These fields can accept any standard text:

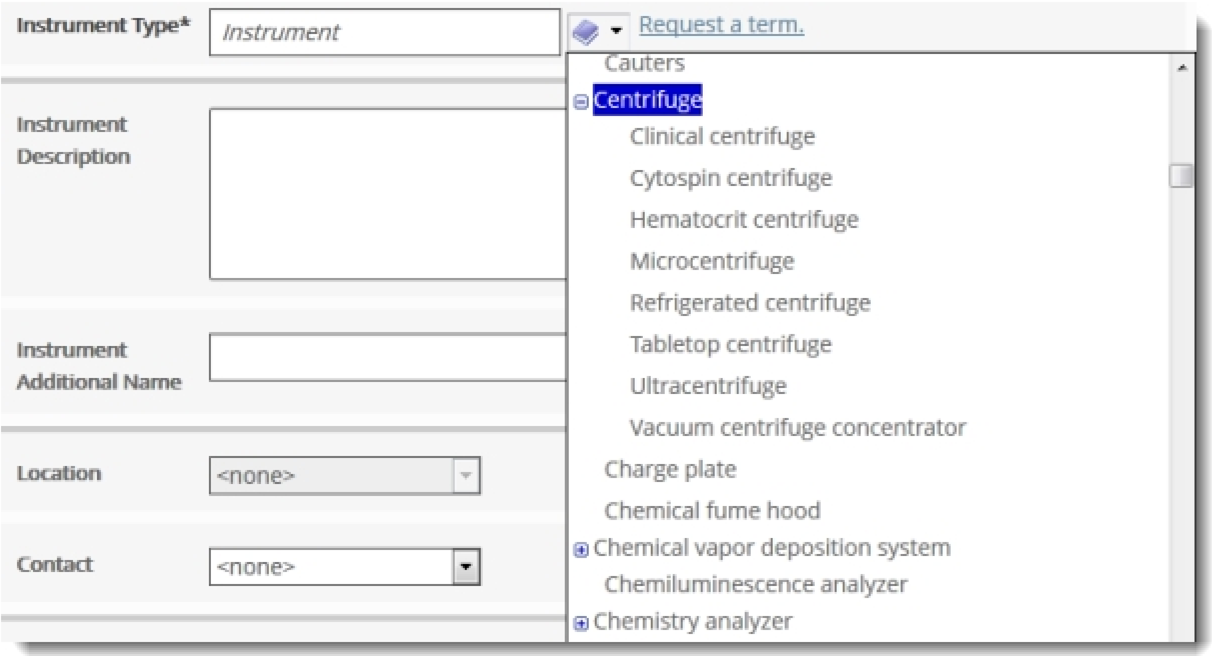
For specific guidelines on the format and content of what should be annotated in each free text field, see the appropriate topic in the SWEET General Annotation Guide.

Ontology / Controlled Vocabulary Fields

An icon depicting a blue book denotes a field that must be annotated using a controlled vocabulary term from the ontology.



Choose a term either by typing in the field and selecting one of the auto-suggestions, or by clicking the icon to browse a list of possible terms, arranged in a hierarchy. Clicking the + or - next to a term in the list will close or open that branch of the hierarchy. Clicking on a term will select it for the field.

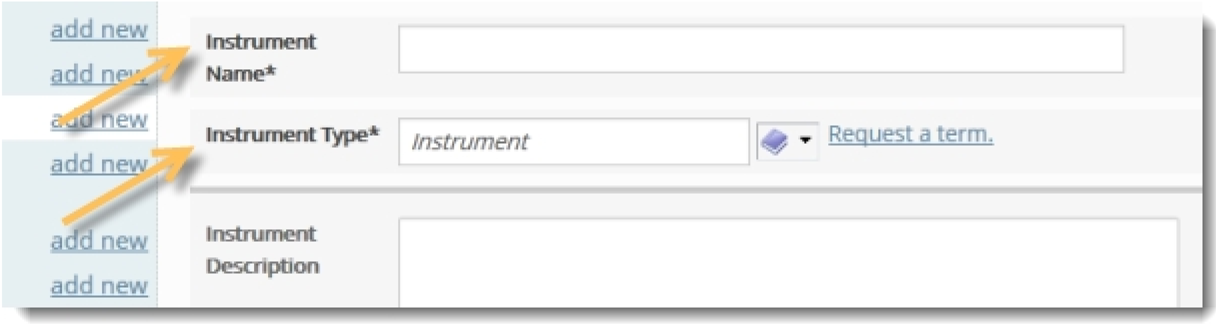


If the exact term needed is not available in the ontology, select the next most accurate term, and submit a term request for the more specific one you would like to use. See Submitting a Term Request for more detail.

Synonyms for the preferred ontology term will show up in autosuggest. If you select a synonym, the preferred term will automatically display in the field.

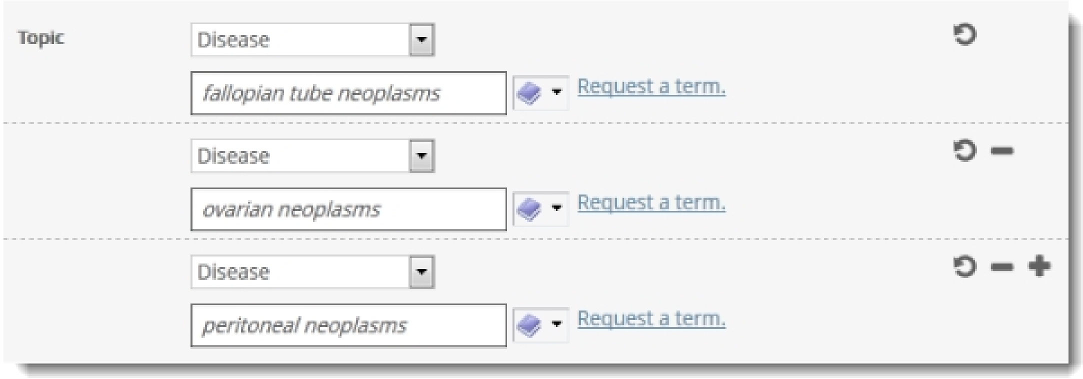
Required Fields

For each resource type, there are a number of fields that are required in order for the record to be valid. Required field titles are marked with **bold text** and an asterisk (*****).



Repeatable Fields

Most form fields allow multiple entries for the same field, for example, multiple contacts for a resource or organization, or multiple topics for a Human Study. If more than one value applies to a particular field, each separate value should be entered in a separate line.



The plus, minus and refresh icons to the right of each repeatable field allow you to add, remove and clear additional lines:

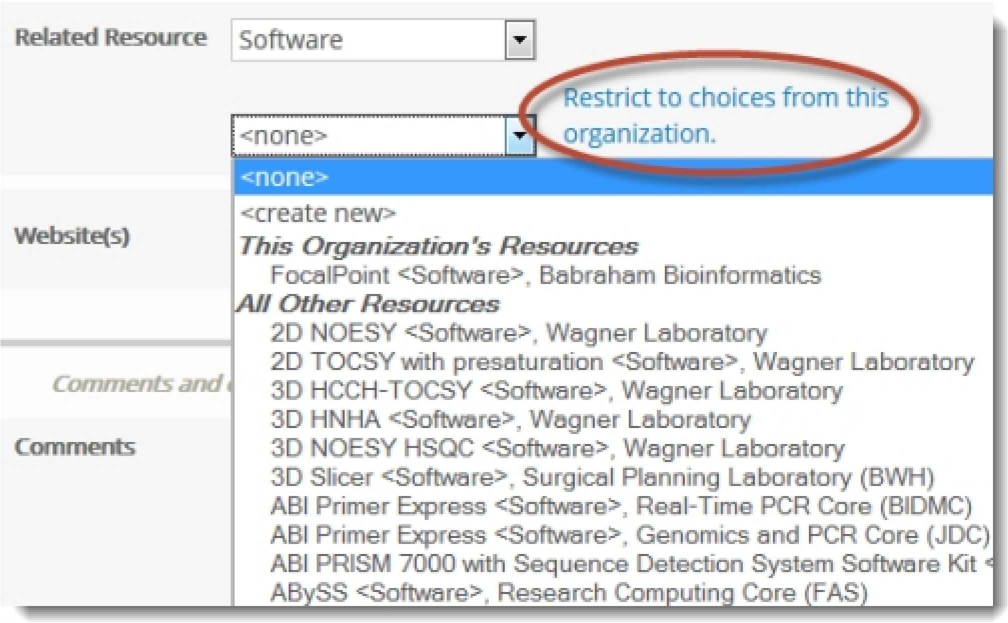
- ⟲ — clears the information without removing the line.
- ▬ — removes the line entirely from the form.
- ✚ — adds additional lines to the field. New lines can only be added from the last line in every repeatable field.

Most fields When you see **NR** on the field annotation tables, it indicates a non-repeatable field.

Fields Linking to Other Records

In a field that links to other eagle-i records, you can either link to an existing record or create a new record from within that field. To see if the resource you want to link to already has an existing eagle-i record, browse the drop-down list for that field. By default, most display a list of only the records associated with that particular organization.

To see all possible records from the entire institution, toggle the **See choices from all organizations** link to the right side of the drop-down list. Records within that organization will still be listed at the top, under the header: **This Organization's Resources**. The rest will be listed in alphabetical order, underneath the header: **All Other Resources**. Toggle the **Restrict to choices from this organization** link to return to only a view of the resources associated with that organization.

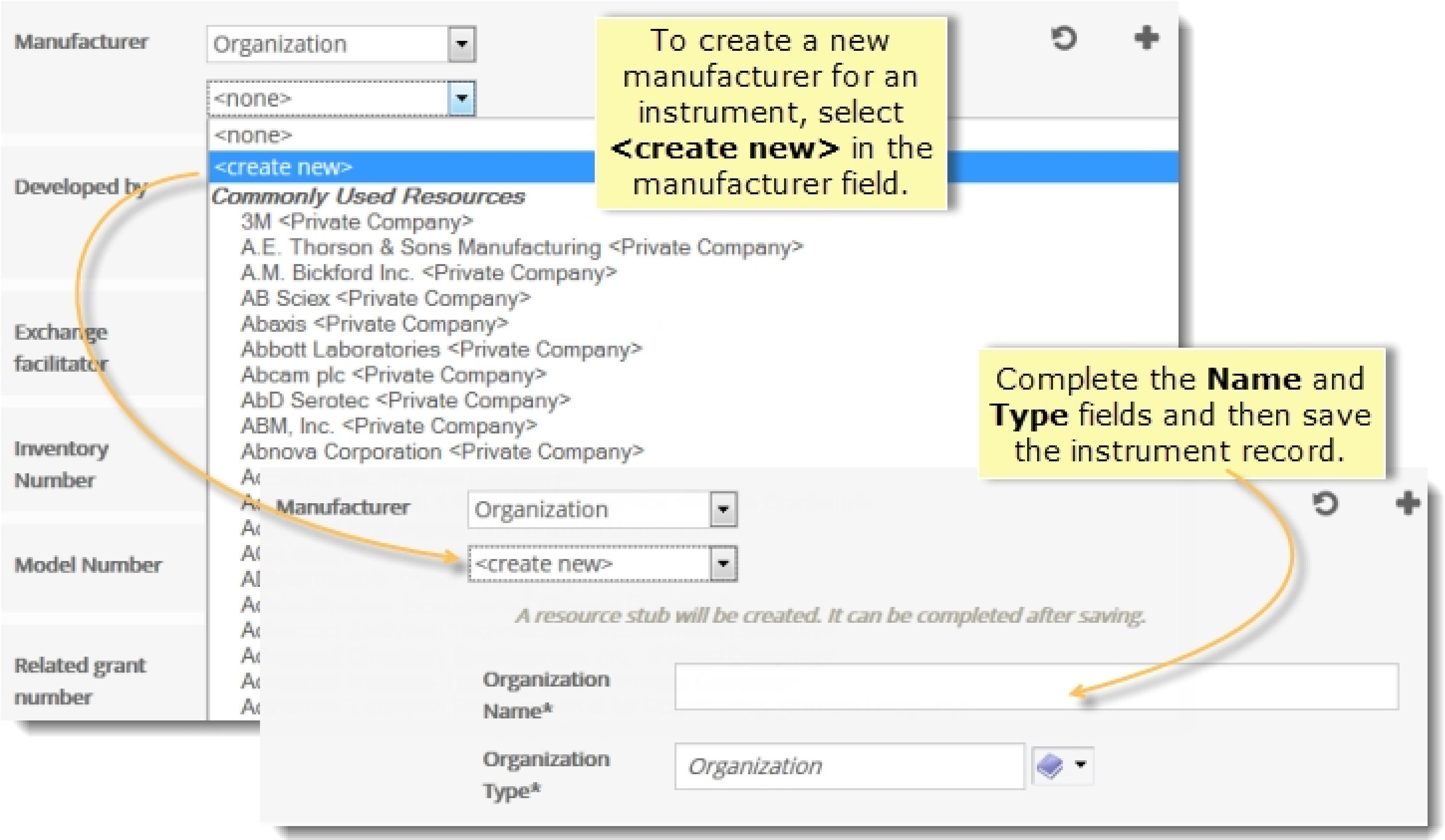


Restrict to choices from this organization.

In certain fields, a third list of existing records may display at the top, under the heading: **Commonly Used Resources**. See Centrally Curated Resources for more details.

Type a letter to jump to the beginning of that section of the list. If the record you want to link to does not exist, select <create new> in the drop-down list.

Example: Suppose you are creating a new instrument record for a microscope, but there is no existing record for the manufacturer. Using this option, you can create a new organization stub record for the manufacturer while still editing instrument record.



To create a new manufacturer for an instrument, select **<create new>** in the manufacturer field.

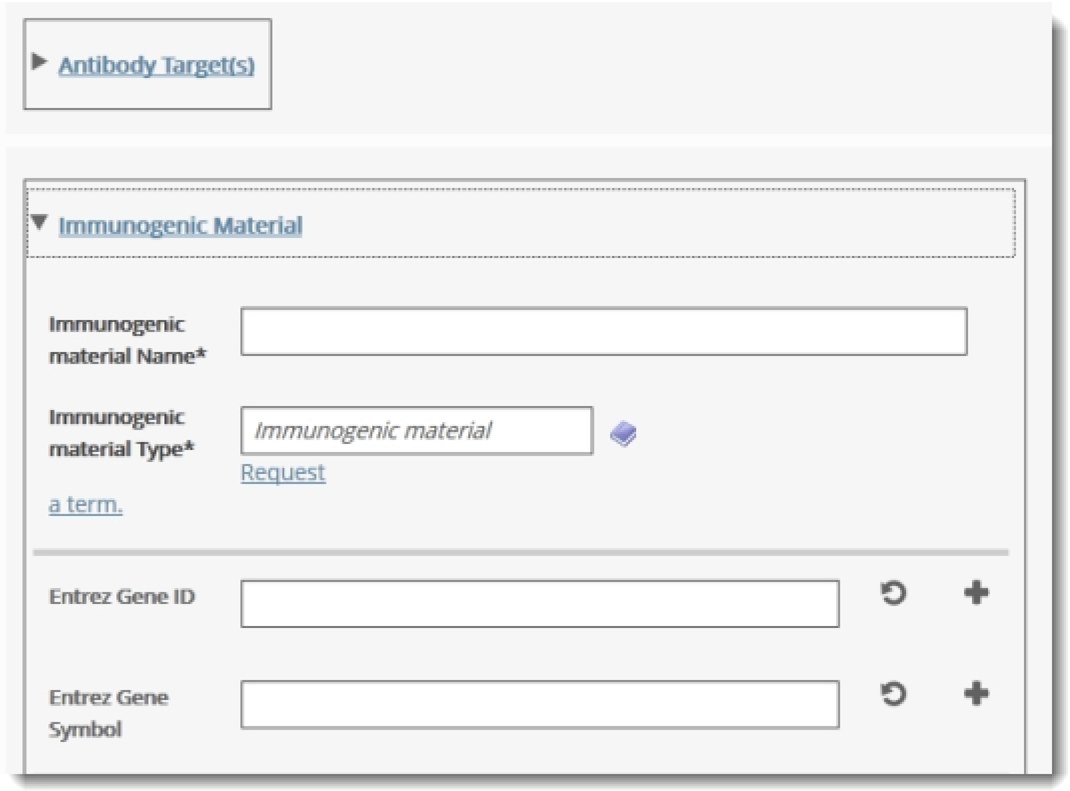
Complete the **Name** and **Type** fields and then save the instrument record.

A resource stub will be created. It can be completed after saving.

See the section on Linking Records for more information about working with linked data.

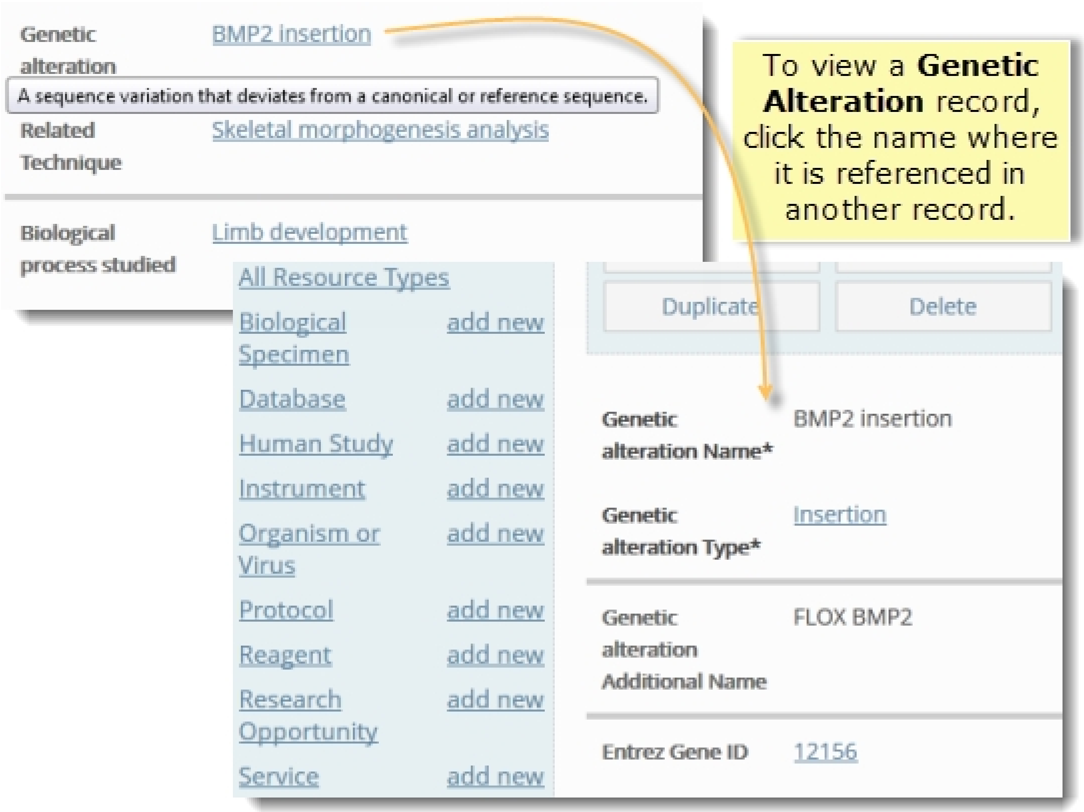
Embedded Fields

Embedded fields can be expanded to display two or more fields pertaining to a separate but related resource. For example, information about Antibody Targets and Immunogenic Material are captured in embedded fields in Antibody records.



Clicking on the field title will expand or collapse the rest of the embedded record.

Like fields that link to Genetic Alterations records, embedded fields are used by eagle-i search to return their referencing types.


Genetic alteration: BMP2 insertion

A sequence variation that deviates from a canonical or reference sequence.

Related Technique: Skeletal morphogenesis analysis

Biological process studied: Limb development

Genetic alteration Name*: BMP2 insertion

Genetic alteration Type*: Insertion

Genetic alteration Additional Name: FLOX BMP2

Entrez Gene ID: 12156

To view a **Genetic Alteration** record, click the name where it is referenced in another record.

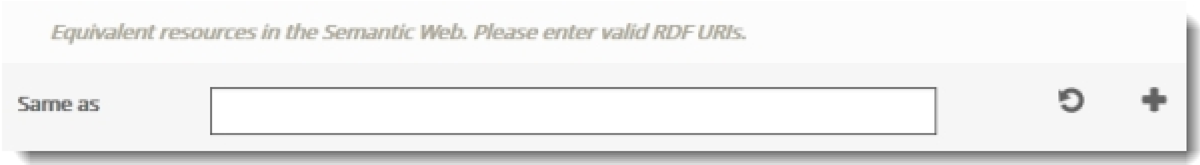
Example: If a match is made on a gene in a Construct Insert, search returns the construct that references it.

However, whereas Genetic Alterations are reusable (e.g. the same allele can be referenced by two different mouse lines), embedded fields are not (e.g. each construct insert can be embedded in only one construct reagent record).

Institution Specific Annotations

This section will only display above the **Comments** if your institution has chosen to add any local fields. Fields in this sections will not be included in the Annotation Guidelines or visible in the Ontology Browser, as they are not part of the central eagle-i Ontology. Questions about annotations in this section should be directed to the local contact at that institution.

The 'Same As' Field


Equivalent resources in the Semantic Web. Please enter valid RDF URIs.

Same as

The **Same As** field displays on every form underneath **Comments** and **Curator Notes** fields. This field should ONLY be used to capture valid RDF URIs of equivalent resources in the Semantic Web. If you have any questions about what constitutes a valid RDF URI, please leave this field blank and consult with an eagle-i curator.

Creating New Resource Records

Resources can be added by anyone with SWEET access and follow the same workflow as organizations: after a resource record is created, it is sent to curation to be reviewed and then published. See the annotation guidelines for each individual resource type for more information.

To add new resources:

1. Resource types are listed in the sidebar of every organization record. Click **add new** to open a new record form for that type. Forms are ontology driven, meaning each form will be slightly different.
2. Alternatively, you may wish to duplicate an existing record.
3. Complete all the required fields in red. Hover over the field names in the SWEET to see a brief explanation ("tool tip") of every field.
4. Complete any additional fields. See the SWEET General Annotation Guide for each individual resource type for more information about each field.
5. Click **Save**. This saves the resource as a record in the repository. The record is automatically assigned **Draft** status. If the resource links to unfinished resources, you'll need to complete these resource **Stubs** prior to sending the resource to curation.

After you save the resource you can **Unlock** the record if you want other users at your institution to edit this resource.

Next Step: Send the record to curation for review and to be published.

Editing Records

Records can be edited from any state. See the Access Level Details section for more information about which levels grant access to edit records in different states.

Note: You may only edit records that are not currently locked or being edited by another user.

Typical modifications include updating incorrect or outdated information, or adding new information. Edits made to published records are immediately visible in the search application. Published records should only be sent back to curation or draft status if the requested changes need to be made by someone with a lower access permission level, or if the current information is incorrect and should not be publicly displayed, but updated information is not yet available.

To edit a record:

1. Locate the resource.
2. Click **Edit**.
3. When you have finished modifying the record, click **Save** to save the changes and leave the record locked so only you can access it. Or if you want to allow someone else to edit the record, click **Save and unlock**.

If a record is closed without saving, any changes that were made will be lost. Therefore, if making numerous or complicated modifications, it may be a good idea to preemptively **Save** and **Edit** certain individual changes as they are made.

Locking and Unlocking Records

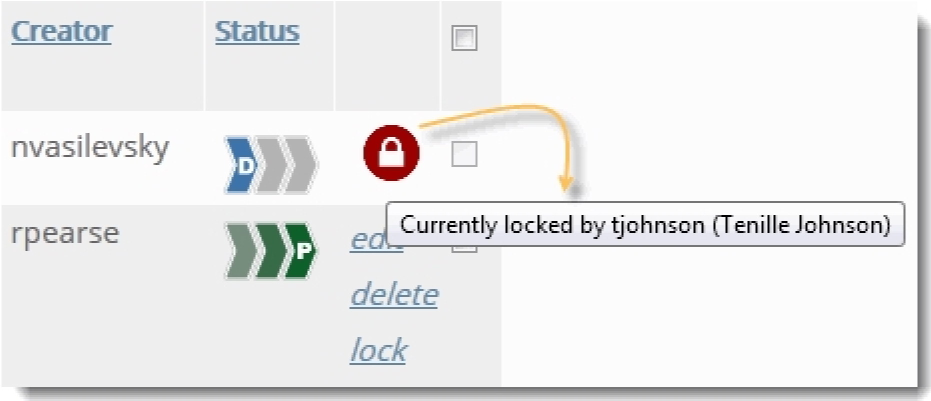
Locking places a hold on the record so that only the person who has locked it can edit it. Unlocking a record means it may be locked and edited by any user with the appropriate permissions. You can change the ownership status of a single record by clicking the **Lock** or **Unlock** buttons from within that record or from within a list.

Note: ownership of a record via locking should not be confused with ownership of the actual resource.

The SWEET automatically locks records while they are being edited. This prevents two people from making changes to the same record at the same time. When you are finished editing, you can choose to either **Save** or **Save and unlock** the record:

- **Save** will preserve the current edits but leave the record locked so that no other user can edit it. A green icon of a lock and key displays in the upper right corner of the main body of any record you have locked, regardless of whether or not you are currently editing it.
- **Save and unlock** will save the current edits and also automatically release the lock.

In the list view, records locked by other users are represented with an orange icon of a lock in the far right column. Hovering over the icon will display the name of the user who has locked the record. Unlocked records or records locked by you display the following options instead of the lock icon: **Edit**, **Delete**, and **Lock**.



Currently locked by tjohnson (Tenille Johnson)

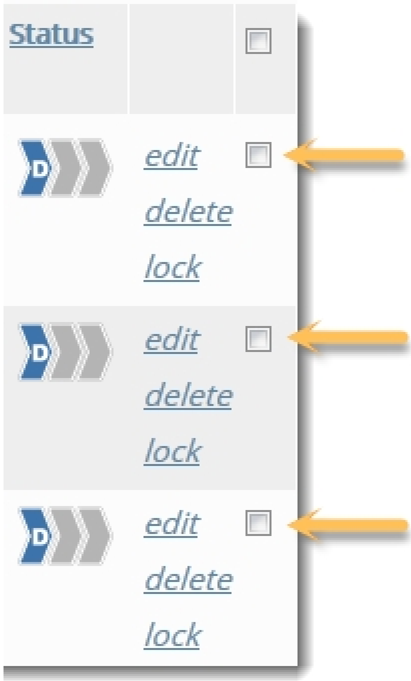
Users can also choose to manually lock records they are not currently working on, either to prevent other users from editing them, or to make it easy to filter a subset of records from a larger list. For example, suppose you are about to edit several related records, a process that may take you most of the day. By locking all of the records you ensure that each record will be available and unchanged when you are ready to make your changes. From any list, you can select **Locked by me** to display only the records you have currently locked.

In most circumstances, however, it is best practice to leave any published, in curation, or withdrawn records you are not currently working on unlocked so that other users can edit them as needed.

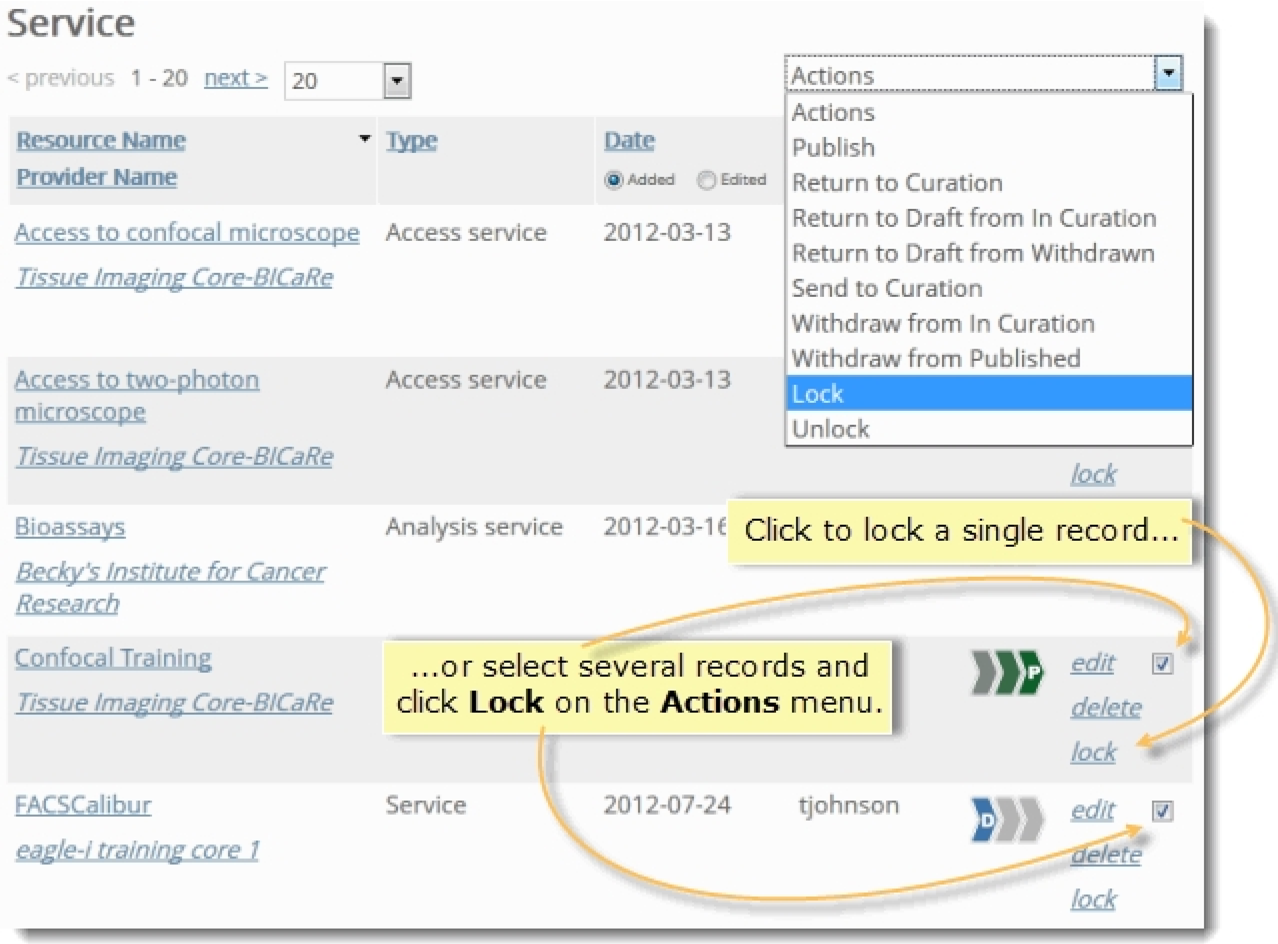
Note: when the status of a record changes, it is automatically returned to an unlocked state and must be manually locked again in order to keep other users from making changes to it.

To Lock or Unlock multiple records:

1. From any list, click the check box next to one or more records.



2. From the Actions drop-down menu, select **Lock** or **Unlock**.



Resource Name Provider Name	Type	Date				
Access to confocal microscope *Tissue Imaging Core-BICaRe*	Access service	2012-03-13				
Access to two-photon microscope *Tissue Imaging Core-BICaRe*	Access service	2012-03-13			*lock*	
Bioassays *Becky's Institute for Cancer Research*	Analysis service	2012-03-1				
Confocal Training *Tissue Imaging Core-BICaRe*				P	*edit* *delete* *lock*	☑
FACSCalibur *eagle-i training core 1*	Service	2012-07-24	tjohnson	D	*edit* *delete* *lock*	☑

Click to lock a single record...

...or select several records and click **Lock** on the **Actions** menu.

3. A list of selected resources appears. Click **Confirm**.

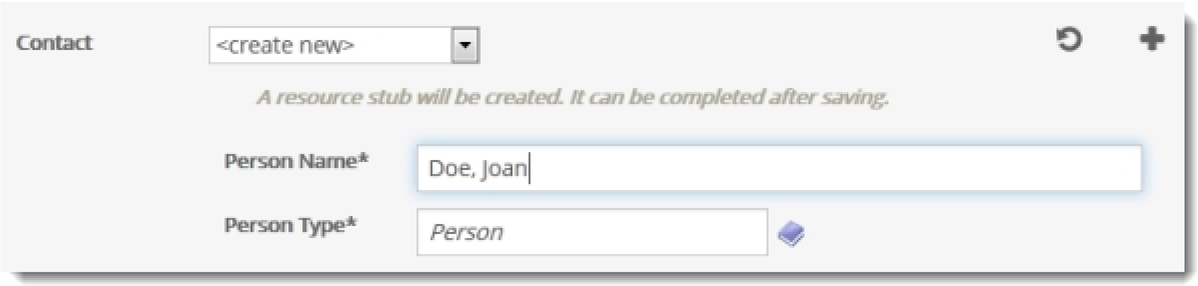
Note: You can only lock a record that has not already been locked by someone else.

About Resource Stubs

Stub records are incomplete records that were created as links from within another record and contain two fields: name and type. Stub records you create are listed in the **View My Resource Stubs** section from the **Workbench** so they are easy to find and further annotate. Once they have been edited and saved, they will no longer appear in this section.

To create, view, and complete a single resource stub:

1. From a field that links to another record, select <create new>.



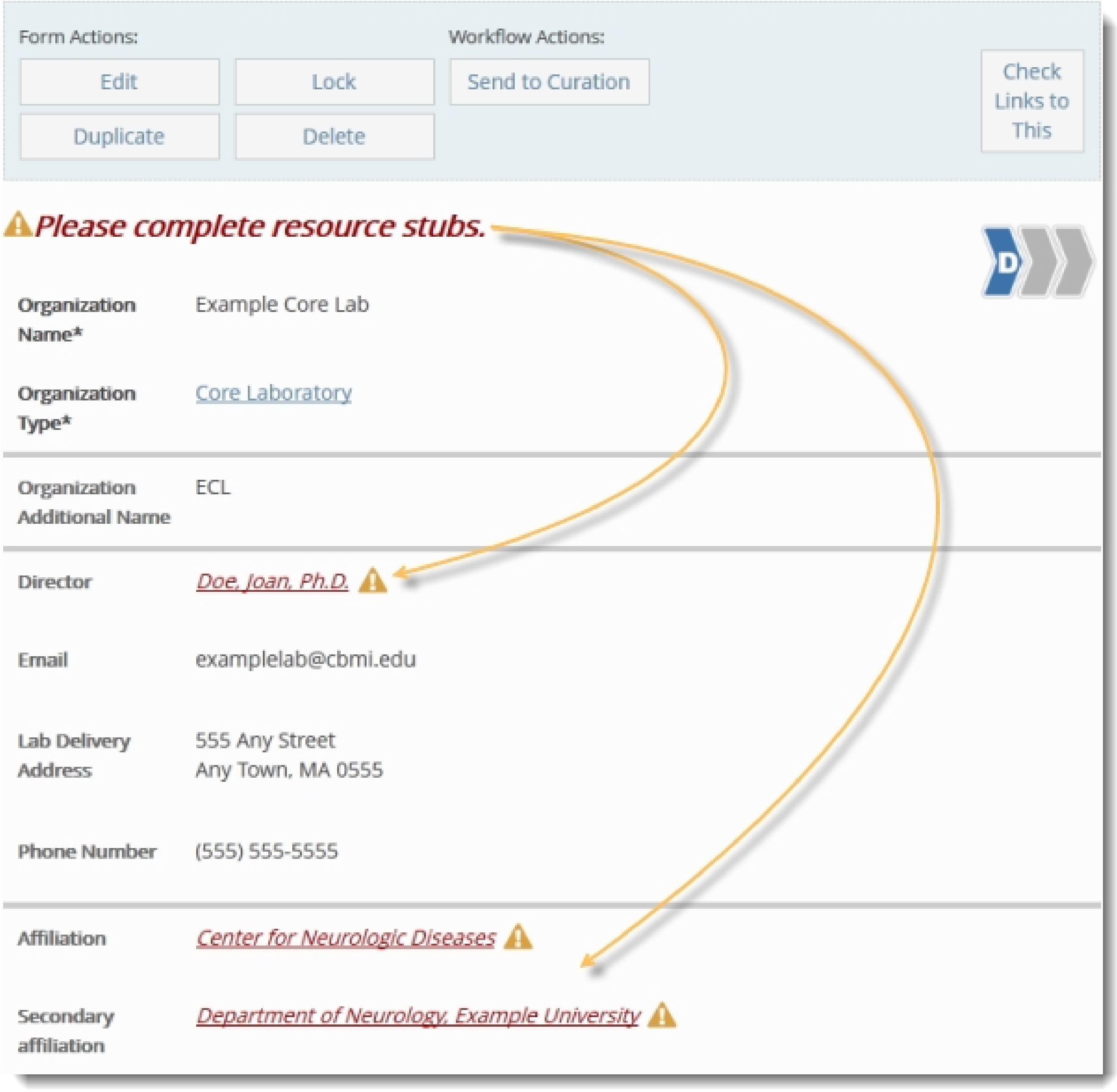
Contact <create new>

A resource stub will be created. It can be completed after saving.

Person Name* Doe, Joan

Person Type* Person

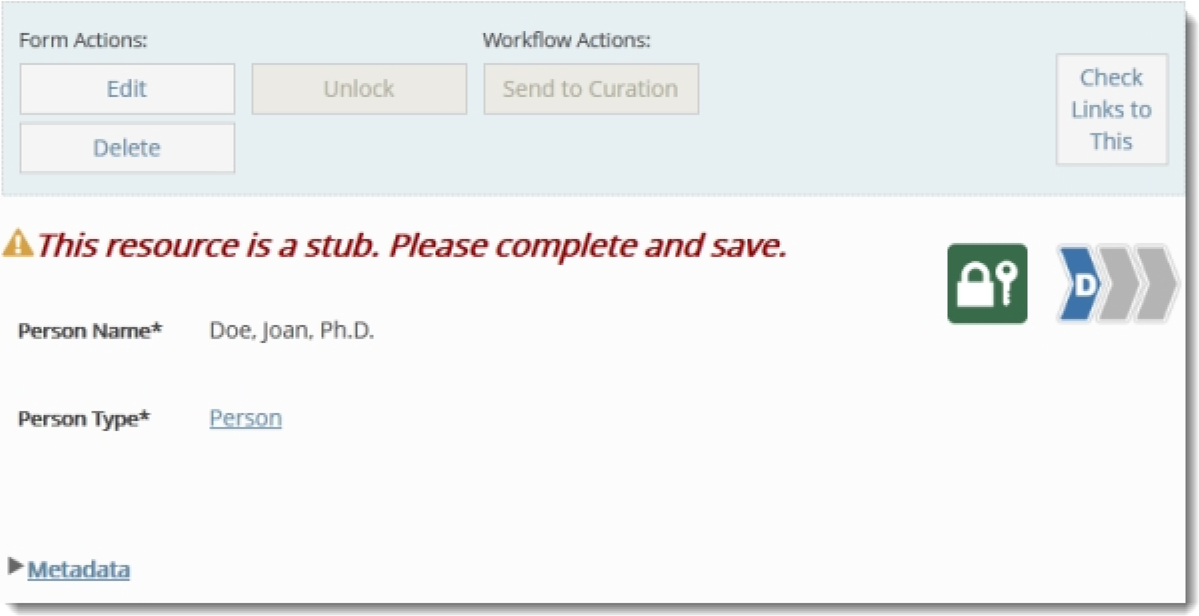
2. Fill in the name and type fields.
3. Click **save**. A message at the top of the record instructs you to complete your resource stubs , which are now highlighted in red with a yellow icon next to them.



⚠ *Please complete resource stubs.*

Organization Name*	Example Core Lab
Organization Type*	Core Laboratory
Organization Additional Name	ECL
Director	*Doe, Joan, Ph.D.* ⚠
Email	examplelab@cbmi.edu
Lab Delivery Address	555 Any Street Any Town, MA 0555
Phone Number	(555) 555-5555
Affiliation	*Center for Neurologic Diseases* ⚠
Secondary affiliation	*Department of Neurology, Example University* ⚠

4. Click on the name of any resource stub to open the associated draft record. A message at the top of the record informs you that you are viewing a stub record and instructs you to complete and save the record.



This resource is a stub. Please complete and save.

Person Name* Doe, Joan, Ph.D.

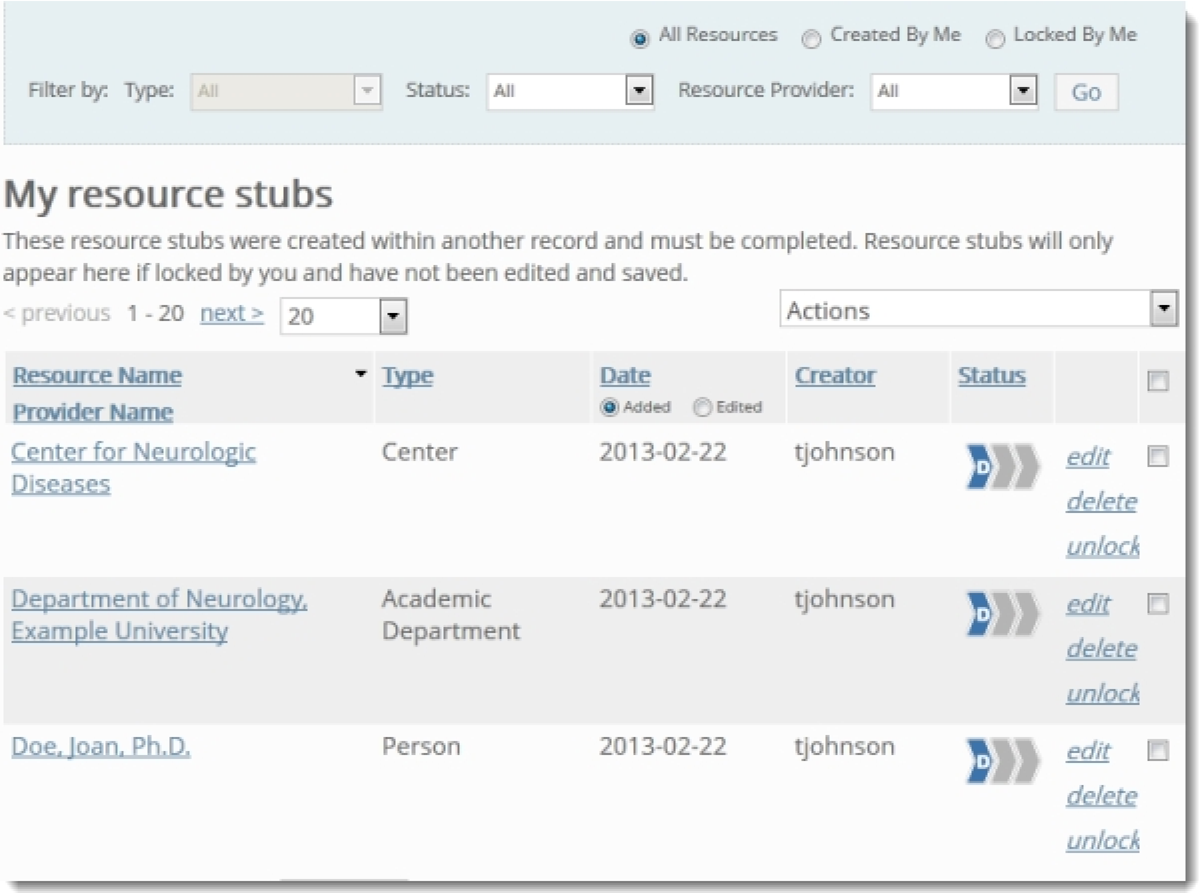
Person Type* Person

5. Click the **edit** button and add any additional information needed to complete the record, then save. The record is no longer considered a stub.

If you do not wish to complete a stub record immediately after completing it, the **Resource Stubs** section in the **Workbench** allows you easily find it again at a later date.

To view all of your Resource Stubs:

1. Open the Workbench.
2. Click **Resource Stubs** to open the list of resources requiring your review and or completion.



● All Resources ○ Created By Me ○ Locked By Me

Filter by: Type: All Status: All Resource Provider: All Go

My resource stubs

These resource stubs were created within another record and must be completed. Resource stubs will only appear here if locked by you and have not been edited and saved.

< previous 1 - 20 next > 20 Actions

Resource Name Provider Name	Type	Date ● Added ○ Edited	Creator	Status		☐
Center for Neurologic Diseases	Center	2013-02-22	tjohnson	D	*edit* *delete* *unlock*	☐
Department of Neurology, Example University	Academic Department	2013-02-22	tjohnson	D	*edit* *delete* *unlock*	☐
Doe, Joan, Ph.D.	Person	2013-02-22	tjohnson	D	*edit* *delete* *unlock*	☐

Note: Only unedited stub records that have been locked by you will appear in this list. Once you edit or unlock any of the records in the Resource Stubs section, they disappear from the list.

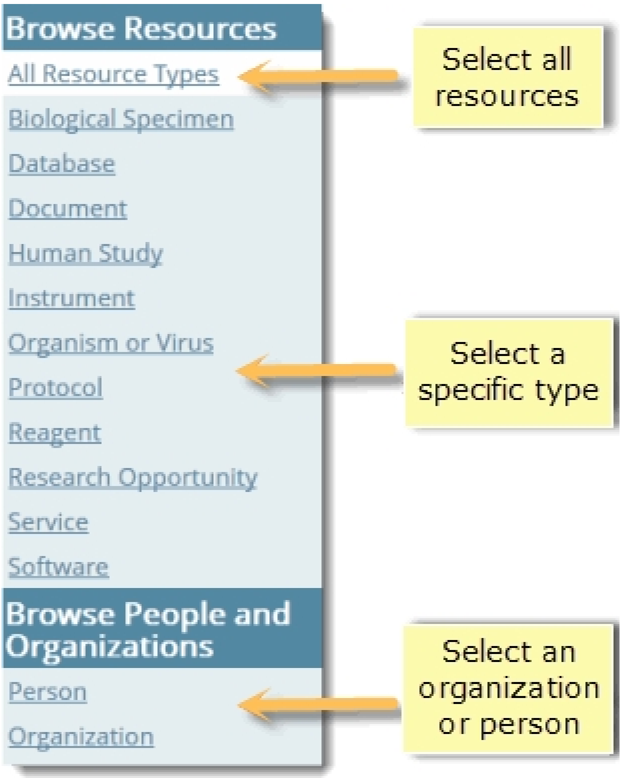
Navigating Lists

Records are organized and displayed in variety of lists in the SWEET. You can view lists of records only associated with a particular organization at your institution, or lists of records associated with *all* organizations at your institutions.

To display all people, organizations and resources for your institution:

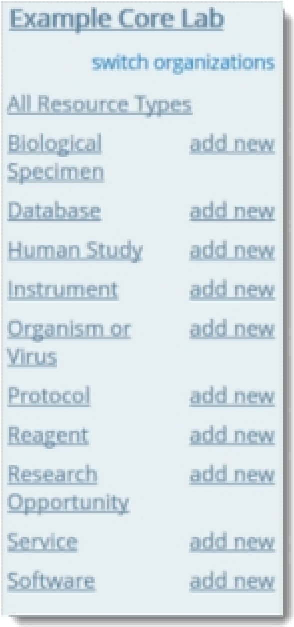
1. From the Workbench, click **Browse People & Resources in My Institution**.
2. To view a lists of resource records, select a specific resource type from the left navigation menu or click **All Resource Types** to display all resources owned by your institution.
3. To view a list of people are your institution, click **Person**.
4. To view a list of organizations affiliated with your institution, click **Organization**.

Note: Due to the large number of resources at some institutions, clicking **All Resource Types** may take slightly longer to display.



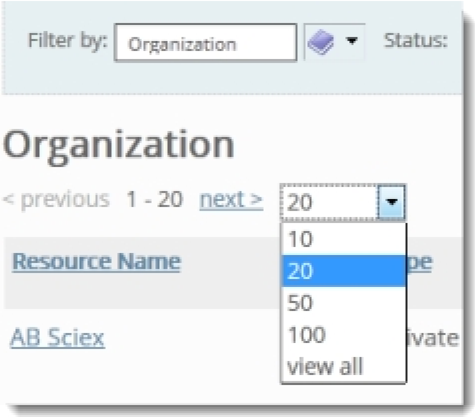
To display resources associated with a single organization:

1. Open an organization record.
2. Use the links in the left sidebar to open lists of different resources associated with that organization:



Changing the number of records displayed

The SWEET displays only the first 20 records of any list by default. You can choose to display 10, 50, 100, or all records in the list instead by selecting one of these options at the top left of every list.

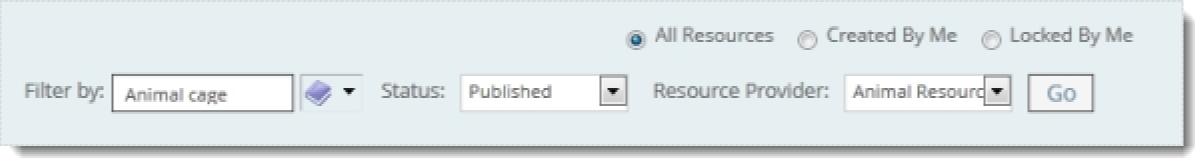


Note: selecting **view all** may result in longer load times for larger lists.

Use the **next** or **previous** links to navigate to the next or previous page of records in the list when not viewing all.

Filtering lists

All lists in the SWEET allow filtering based on one of more of the following categories:



● All Resources ○ Created By Me ○ Locked By Me

Filter by: Animal cage

Status: Published

Resource Provider: Animal Resourc

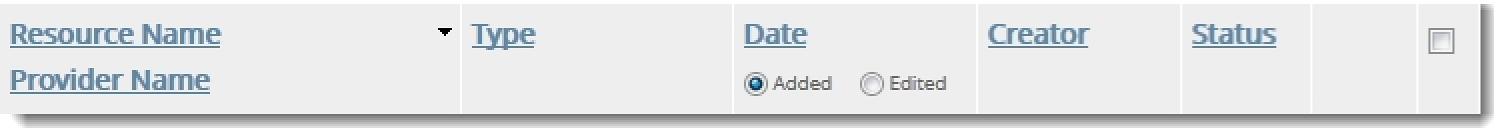
- **Type** — Filters by the selected resource type. To further narrow your search, use the taxonomy browser. For each resource, browse through the taxonomy hierarchy then click to drill down to lower hierarchical levels.
- **Status** — Filters by draft, in curation, published, and withdrawn records.
- **Organization** — Filters by resources or people owned by the organization selected.
- **Creator/Lock Owner** — Filters by records created or locked by the current user.

To apply a combination of filters for Type, Status, or Organization, select one or more and then click **Go.** Filters that are not available for the records listed are grayed out.

To view only resources in a particular list that you have locked, select **Locked By Me**. To view only resources in a list that you created, select **Created By Me**. In most lists of records, all resources are displayed by default. Select **All Resources** to return to the default view.

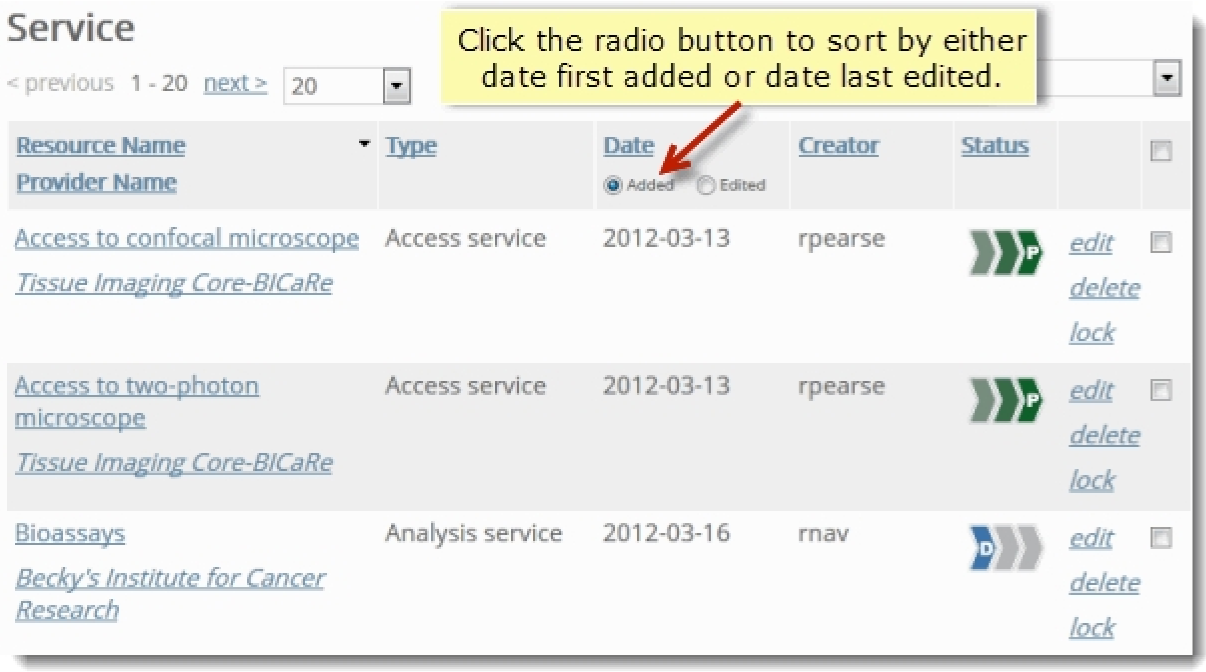
Sorting lists

All lists of records can be sorted by the following categories:



Resource Name Provider Name	Type	Date ● Added ○ Edited	Creator	Status		☐

- **Resource Name** — The contents of the resource name field. Displayed in the same column as the provider name.
- **Provider Name** — The name of the owning organization for the resource. Displays in all lists of resources and people, in the same column as the resource name.
- **Type** — The contents of the resource type field, which is drawn from the ontology.
- **Date Added** — The date the record was created. Displayed in the same column as the date edited. To sort by this, select the radio button next to **Added** and click the **Date** link at the top of the column.
- **Date Edited** — The date the record was last saved. Displayed in the same column as the date added. To sort by this, select the radio button next to **Edited** and click the **Date** link at the top of the column.



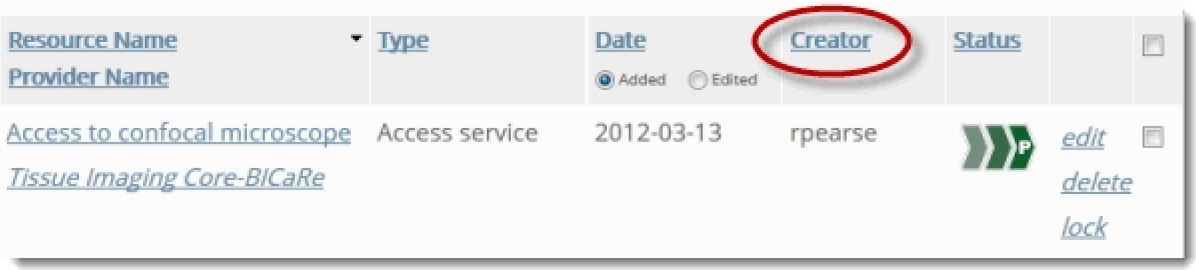
Service

< previous 1 - 20 next > 20

Click the radio button to sort by either date first added or date last edited.

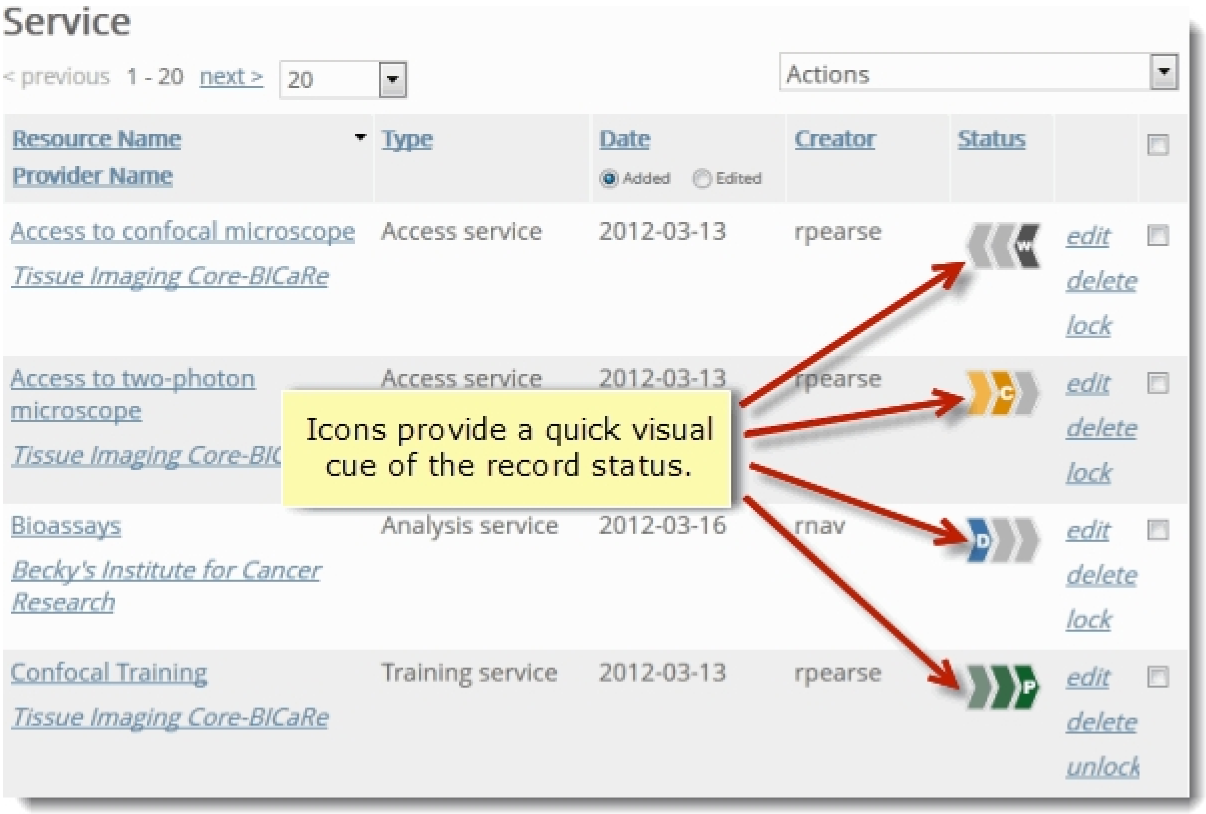
Resource Name Provider Name	Type	Date ● Added ○ Edited	Creator	Status		☐
Access to confocal microscope *Tissue Imaging Core-BICaRe*	Access service	2012-03-13	rpearse	P	*edit* *delete* *lock*	☐
Access to two-photon microscope *Tissue Imaging Core-BICaRe*	Access service	2012-03-13	rpearse	P	*edit* *delete* *lock*	☐
Bioassays *Becky's Institute for Cancer Research*	Analysis service	2012-03-16	rnav	D	*edit* *delete* *lock*	☐

- **Creator** — The name of the user who created the record.



Resource Name Provider Name	Type	Date ● Added ○ Edited	Creator	Status		☐
Access to confocal microscope *Tissue Imaging Core-BICaRe*	Access service	2012-03-13	rpearse	P	*edit* *delete* *lock*	☐

- **Status** — Displays an icon corresponding to each record’s state: Draft, In Curation, Published or Withdrawn.



Resource Name Provider Name	Type	Date ● Added ○ Edited	Creator	Status		☐
Access to confocal microscope *Tissue Imaging Core-BICaRe*	Access service	2012-03-13	rpearse	W	*edit* *delete* *lock*	☐
Access to two-photon microscope *Tissue Imaging Core-BIC*	Access service	2012-03-13	rpearse	C	*edit* *delete* *lock*	☐
Bioassays *Becky's Institute for Cancer Research*	Analysis service	2012-03-16	rnav	D	*edit* *delete* *lock*	☐
Confocal Training *Tissue Imaging Core-BICaRe*	Training service	2012-03-13	rpearse	P	*edit* *delete* *unlock*	☐

Icons provide a quick visual cue of the record status.

Columns are sorted in ascending order by default. Click the column name again to sort in descending order instead.

Working With Linked Data

In eagle-i, it is possible to connect resources by creating links between records. This leverages the semantic power of linked data to help make search results more useful and guide users to resources they not otherwise have found. However, linking records also means that any changes made to one record may affect many other records in ways that may not always obvious in the SWEET.

Example: Just as labs and resources may be published or sent to curation separately, changing the status of a lab record will not automatically affect the status of any of its associated resources. Therefore, before taking any of those actions, you should take care to make sure any records that are linked will not be negatively impacted. To help with this, when changing the state of a record, the system will prompt you to also perform the same action on any linked records that are currently in the same state.

Common issues that may occur with linked records include links to deleted or unpublished records, and the inadvertent creation of orphaned records.

- Links to deleted records
- Links to orphaned records

- Links to unpublished records

Performing actions on linked records

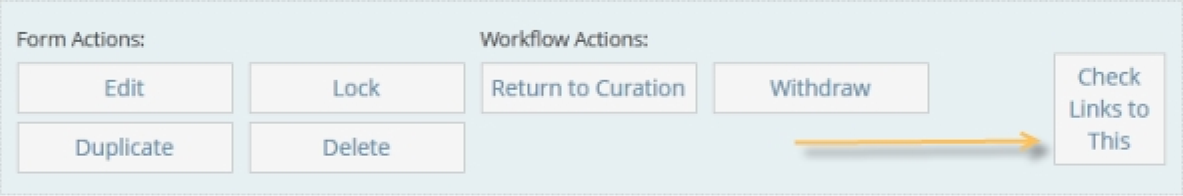
To avoid these types of linked data errors:

- Use the **Check Links to This** button located at the top of each record before deleting any record, regardless of publication status, or before removing any published record from visibility in the search application.
- Never publish a record without examining any linked records to make sure they are also complete and published. Commonly referenced types of resources to look out for are:
  - Owning organizations such as labs, centers, institutes, etc.
  - Contact people
  - Manufacturers and affiliates
  - Instruments, software, organisms and reagents that are related to services

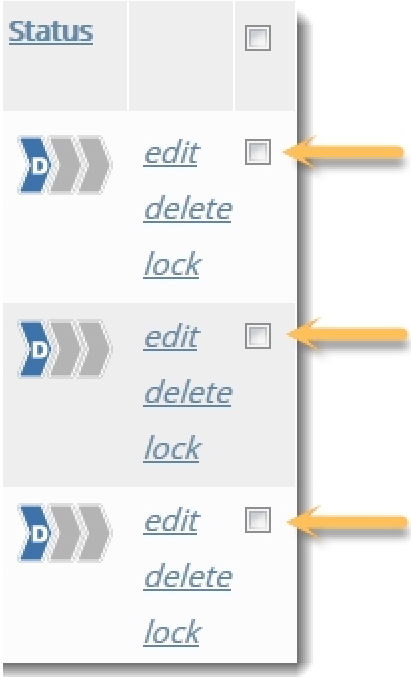
If a previously published laboratory record needs to be removed from visibility in search for any reason, all associated resources should be manually redirected or removed at the same time.

To perform an operation on all resources associated to an organization:

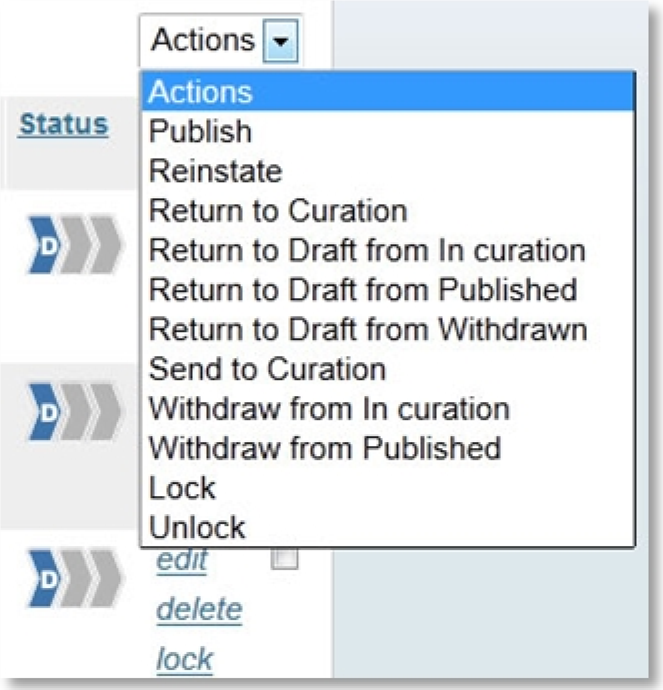
1. Select the **Check links to this** button from the laboratory record.



2. Use the check boxes on the right to select one or more resources.



3. Select an Action to apply to all. (There is no bulk delete. You must delete resources individually.)



Note: You will only see actions that you have permission to take. (e.g. Users with level 1 access will only see Send to Curation, Lock, and Unlock, while users with level 4 access will see many more options.)

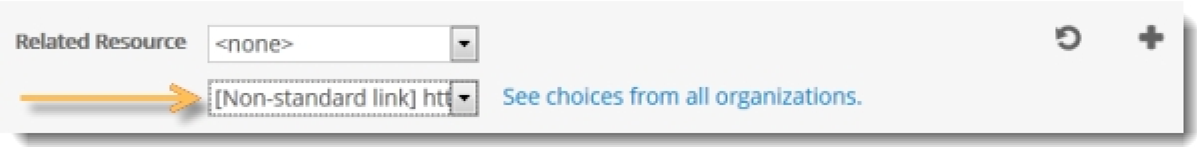
Links to Deleted Records

Fields populated by links to other eagle-i records that no longer exist in the repository will simply not display in the search application. In the SWEET, however, they will appear as the deleted record's URI. These are problematic because there is no way to identify the content of a deleted record from its URI alone, much less the context for how, why, when, or by whom it was deleted.

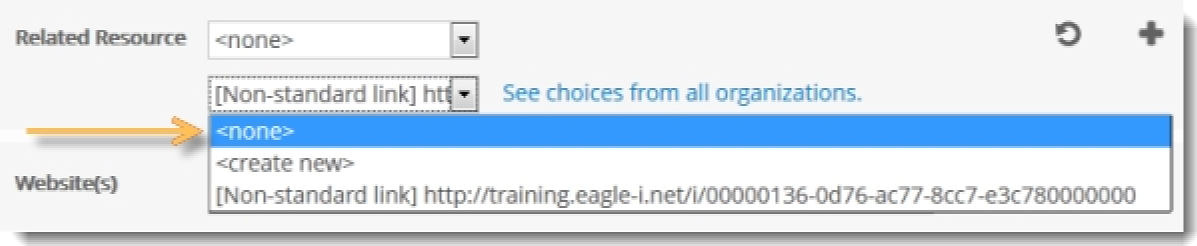
In addition, records are often removed because they duplicate other records; but once they have been deleted, there is no easy way to track the deleted links their removal might have created, meaning those connections may be unnecessarily lost. Therefore, best practice is to replace or remove all links before deleting a record, using the Check Links to This button at the top of every record.

To remove a deleted link:

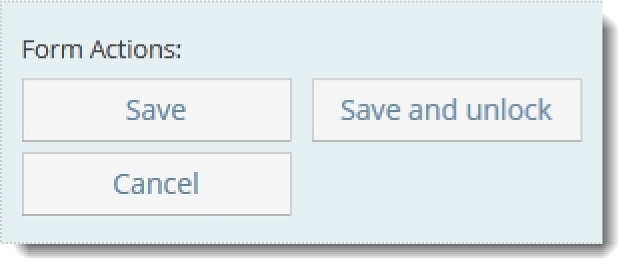
1. In edit mode, the field containing the broken link will display as **[Non-standard link]**.



2. Select any other record from the drop-down list or select **<none>** if this link simply needs to be removed.



3. **Save** or **Save and unlock** the record. The link to the deleted record should no longer display.



Note: If it is necessary to leave a link to a deleted record, you should leave a brief comment or explanation in the **Comments** field to avoid confusion in the future.

Links to Unpublished Records

Published records linking to unpublished records differ from links to deleted records in that they refer to records that still exist in the repository. But they behave like links to deleted records in the search application, meaning that those connections will not be visible to search users.

Links to unpublished records are hard to spot in the SWEET, as there is no way to tell simply from looking at a record what the status of all the records it links to is. However, when you change the status of a record, the system will ask if you also want to change the status of any linked records which are currently in the same state. For example, if you publish a record from curation and there is linked contact person for the lab also in curation, a pop up message will ask if you also want to publish the contact. Select Yes to change the state of the linked record(s). Select No to leave the linked record(s) in their existing state; the original record’s state will still be changed even if you select No.

Note: This applies only to records directly referenced with a link on the record whose state is being changed. In other words, the pop up will not include all resources associated with an organization if they are not directly linked from a field in the organization record

Orphaned Records

In some cases, it may be necessary to publish a record without publishing all of the records associated with it. But you should **never** publish a resource without publishing its owning organization and contact person. This creates an orphaned record in the search application, as location and contact information will be invisible to search user.

If an owning organization record needs to be removed from search either by being deleted, withdrawn, returned to curation, or locally published, all attached resources should be dealt with similarly—unless they are shared by another organization. For instance, if a person is the director of multiple labs, their person record should remain published even if one of the labs is withdrawn. If the person is attached only to the lab being removed, their person record should be removed as well. **No resource record should ever be published unless it is attached to a published organization.**

Note: If a non-owning organization record that is not ready to be published is linked from another record, then you should use your best judgment on whether or not to publish any linking records. It may be preferable to publish a record that is incomplete because of an unpublished link than to leave it unpublished.

Merging Records

Merging records is currently a manual process. You may find it necessary to merge records for a variety of reasons (e.g. in the course of cleaning up duplicate records, or if a data collector has created individual records for multiple copies of the same instrument model within the same lab).

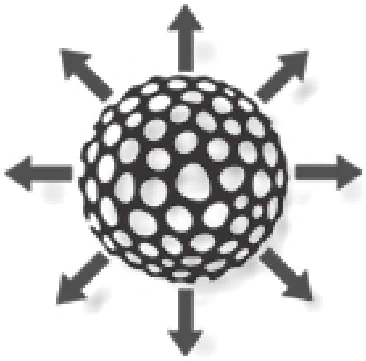
To determine which records should be kept and which should be deleted:

1. In general, already published records should be kept over unpublished records.
2. If none of the records have been published (or if all have been published), use the **Check links to this** button to determine which record has the least amount of links to be replaced. The one linked the most should be kept.
3. All other factors being equal, keep the record that contains the most information.

Note: These types of erroneous duplicates should not be confused with records created using the Duplicate button. This button is intended to aid in the creation of multiple records for resources which are separate but have similar properties.

If the records being deleted contain any information that is missing from the record being kept, that data must be manually migrated (i.e. copied and pasted into the appropriate field in the record being kept) before continuing.

Any links to the records being deleted must also be replaced prior to deletion. Use **Check Links to This** to determine if and where the record is linked on other records so that those links can be removed or replaced, as applicable. See the Working With Linked Data section for more detail.

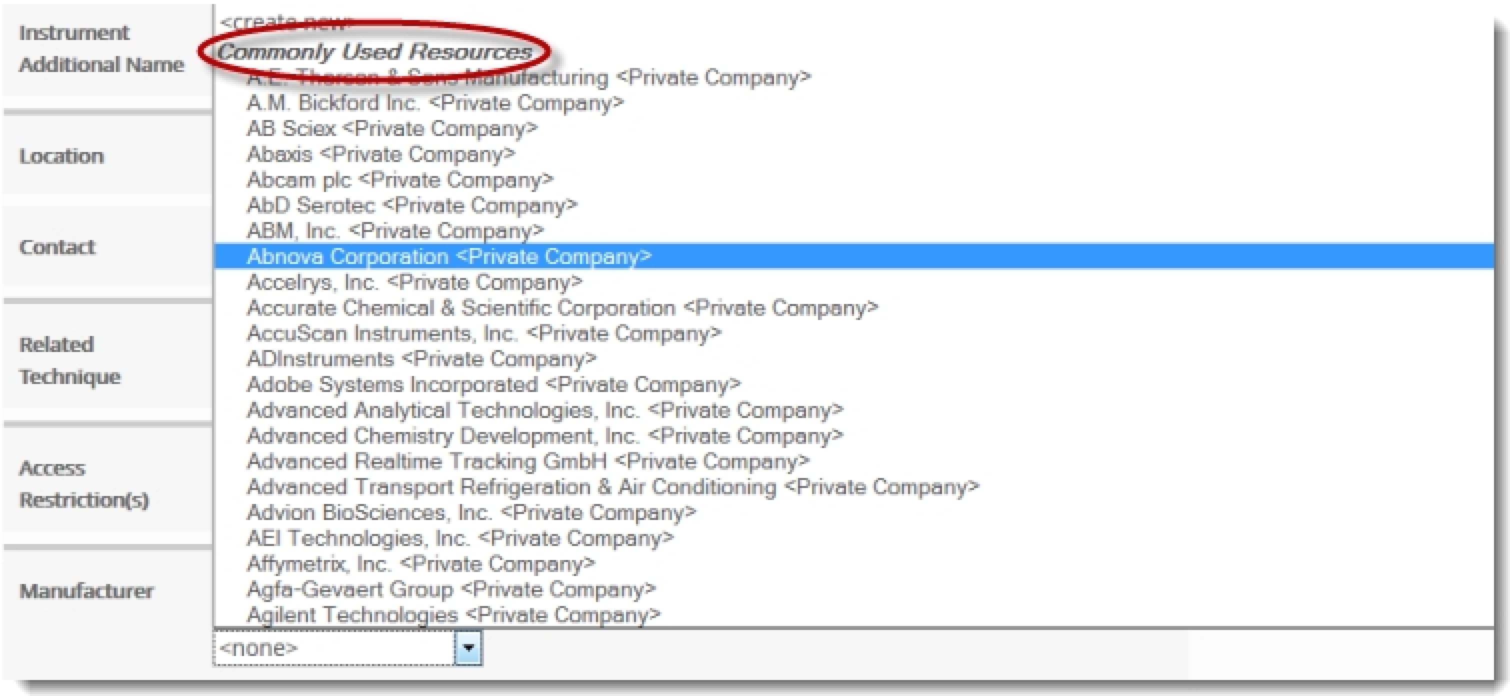


Centrally Curated Resources

Centrally Curated Resources, sometimes also known as **Commonly Used Resources** or **Globals**, represent resources that can be linked to from multiple institutions. Centrally curated records exist for source organisms, as well as for private companies and government agencies, which can be referenced as manufacturers or funding agencies for many resources across all institutions in the eagle-i Network. These records are added and maintained by the central eagle-i team, and then shared among all institutions in the Network.

Linking to Centrally Curated Resources

If any shared records are available in a drop-down list, they will be listed at the top of the list under the header: **Commonly Used Resources**.



To link a local resource, such as an instrument or piece of software, to a centrally curated resource, such as a manufacturer, select the company name from the list of commonly used resources, and save the instrument or software record linking to it.

Adding and Editing Centrally Curated Records

New centrally curated records are added by the central eagle-i curation team. If the organism, private company, or government agency needed does not currently exist on the commonly used resource list, simply add a local record using **<create new>** as you normally would. Locally created records representing commonly used resources may be periodically migrated to centrally curated records by the central team.

This process should be invisible to local users, though you will not be able to edit or make changes to the status of any centrally curated records. To suggest an update to a centrally curated record, please contact the central curation team using the Feedback form.

Extract, Transform and Load (ETL)

ETL (Extract, Transform and Load) is a process that can be used to bulk upload data into the SWEET. Experienced users can use the eagle-i SWIFT (Semantic Web Ingest from Tables) toolkit to ETL data into any eagle-i repository. Currently the toolkit supports only spreadsheets as input files, and due to the time needed to format files for ETL, it should typically be reserved for large or complicated data sets that would be too time-consuming to enter manually.

For more information about how to use SWIFT, please refer to the technical documentation.

Data Entry and Annotation Workflow

This sections contains the entire eagle-i workflow from start to finish. You may not be responsible for some of these steps, but understanding the workflow as a whole may help you better understand your role in eagle-i at your institution. Watch this video tutorial for a demonstration of SWEET workflow.

Records in the SWEET progress through a life cycle where each stage is defined by a status, or state. There are four states in a typical record lifecycle:

Draft — New resources are created as drafts, and remain in a Draft state until they are complete. Draft records are not publicly visible to anyone without a SWEET login.

In Curation — Records In Curation are ready for review to make sure they meet eagle-i guidelines. Records in curation are not publicly visible to anyone without a SWEET login.

Published — Published records have been curated and are visible in eagle-i search. At some institutions, an additional publish locally option may be available.

Withdrawn — Retired records that are not visible in eagle-i search, but are still kept in the repository for archival purposes. Anyone with a direct link to a withdrawn resource will still be able to view a dissemination page containing information about that resource, but they will not appear as search results.

Records may also be deleted entirely from the eagle-i repository. However, as this is a permanent action, it should be used only with caution.

An icon indicating its status displays in the upper right corner of every record. A legend for the icons is available under the left sidebar. Not all users have the ability to modify records in all states. Your access permission level is set by a system administrator, and will allow you to pass records through all or part of the typical record life cycle as needed for your role at your institution.

Access Level Details

All users with access to the SWEET are able to create, edit, share or delete records while they are in draft form. However, higher permission levels will have access to records in curation or records that have been published or withdrawn. The different levels of access are summarized below, and are granted by a system administrator to suit your role at your institution:

	Level 1	**Level 2**	**Level 3**	**Level 4**
View records in any state	Yes	Yes	Yes	Yes
Create Draft records	Yes	Yes	Yes	Yes

Edit and delete Draft records	Yes	Yes	Yes	Yes
Send records to In Curation	Yes	Yes	Yes	Yes
Edit and Delete records In Curation	No	Yes	Yes	Yes
Return records from Curation to Draft	No	Yes	Yes	Yes
Publish records	No	No	Yes	Yes
Edit Published records	No	No	Yes	Yes
Delete Published records	No	No	No	Yes
Return Published record to Curation	No	No	Yes	Yes
Withdraw from In Curation	No	No	No	Yes
Withdraw from Published	No	No	Yes	Yes
Delete Withdrawn records	No	No	No	Yes
Reinstate from Withdrawn to Draft	No	No	Yes	Yes

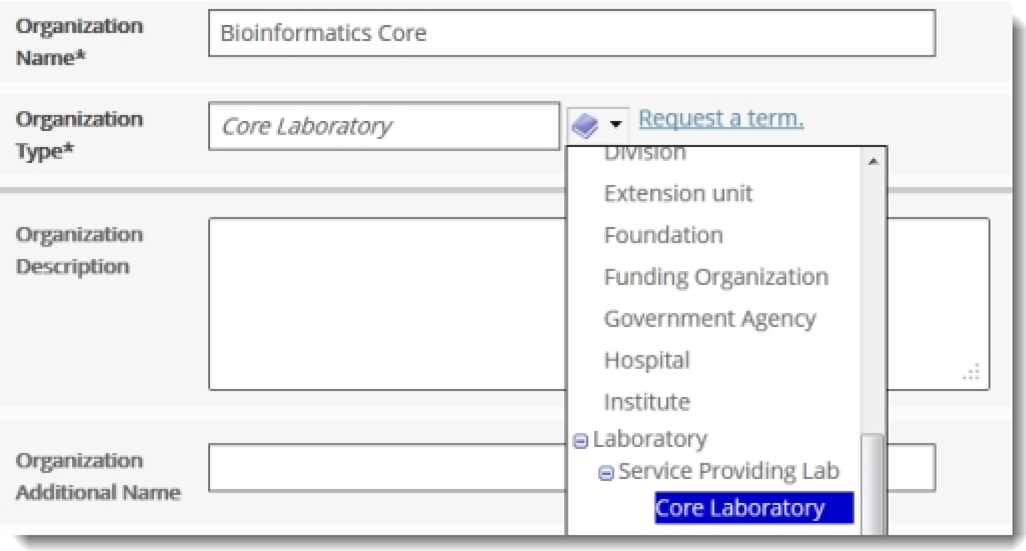
Step 1: Creating Records in Draft

Every resource and most people in eagle-i must be associated with a providing organization. This means that before you can add resources, you must first add an organization record for the resource provider.

To add an organization:

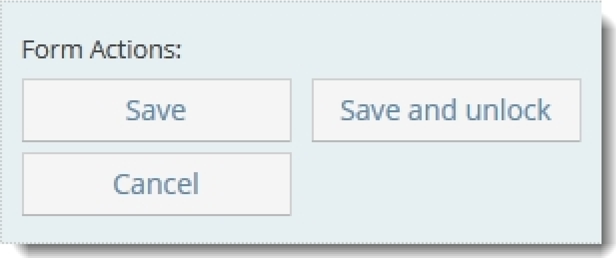
1. Open the SWEET, and click **Create an Organization** to open a blank record form.

2. Annotate the **Organization Name** and **Organization Type** required fields. The other fields displayed vary depending on the type of organization chosen. Add as much additional information as possible in the remaining fields. For detailed descriptions of every field, see the SWEET General Annotation Guide.


Organization Name*: Bioinformatics Core

Organization Type*: *Core Laboratory*

3. **Save** or **Save and Unlock** the record when finished. After saving the record, if the organization has a sub-type that allows you to add resources, the left sidebar will populate with links allowing you to add additional resources to the organization.



Note: you **must** choose an appropriate organization sub-type (i.e. *Core Laboratory*, *Center*, *Institution*, etc.) in the type field in order to add resources; organizations left with the root *Organization* type or the *Private Company* sub-type will not have this functionality.

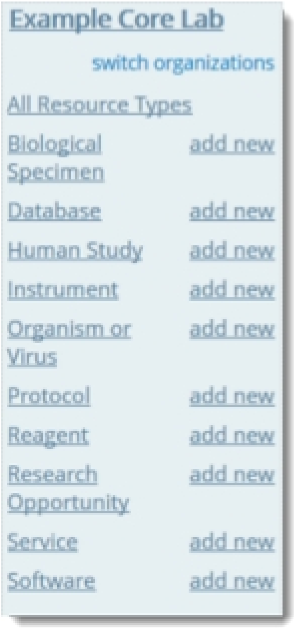
If you created any stub records for people or affiliated organizations, you should open them and add as much information as possible for each. Stub records cannot be sent to curation until they have been edited and saved at least once. After the stub records have been annotated, save the changes and return to the original organization record you just created.

Tip: To open stub records without leaving the record you are currently viewing, right-click on the name of the stub and open it in a new tab or window.

Next: Add resources

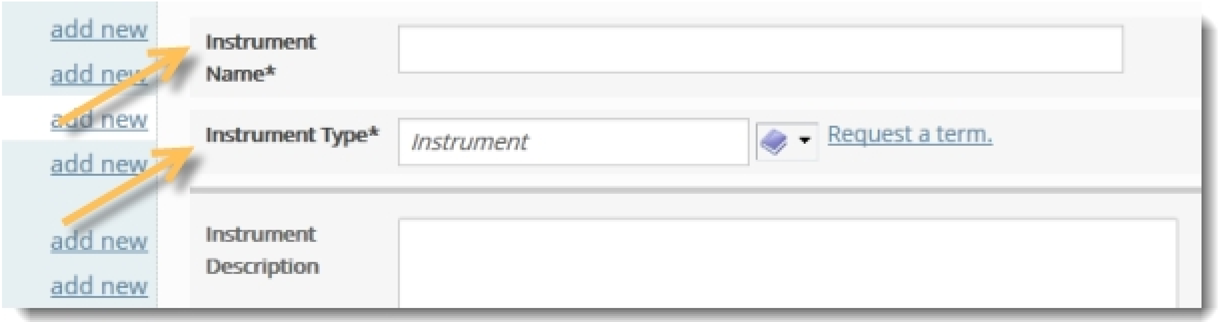
To add new resources:

1. Resource types are listed in the sidebar of every organization record. Click **add new** to open a new record form for that type. Forms are ontology driven, meaning each form will be slightly different.

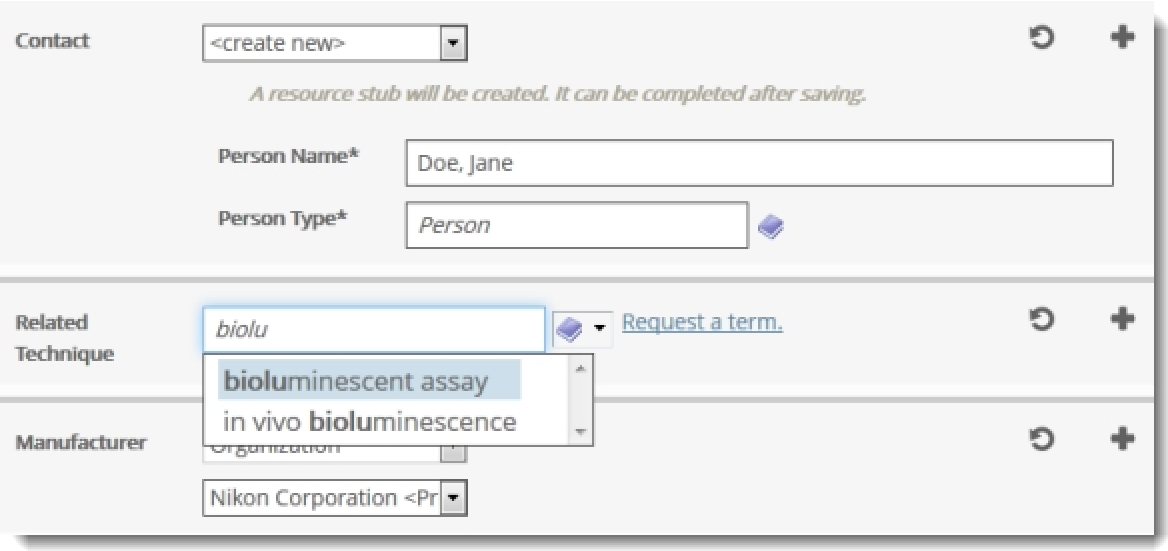


2. Alternatively, you may wish to duplicate an existing record.

3. Complete all the required fields in red. Hover over the field names in the SWEET to see a brief explanation ("tool tip") of every field.



4. Complete any additional fields. See the SWEET General Annotation Guide for each individual resource type for more information about each field.



Contact <create new>

A resource stub will be created. It can be completed after saving.

Person Name* Doe, Jane

Person Type* Person

Related Technique biolu

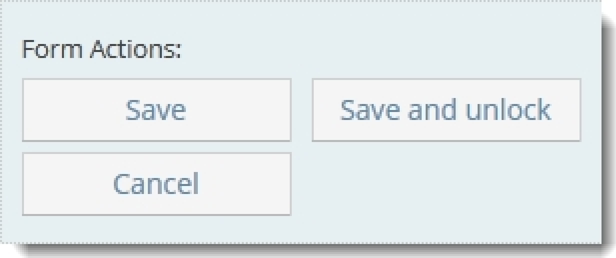
- bioluminescent assay
- in vivo bioluminescence

Request a term.

Manufacturer Organization

Nikon Corporation <Pr

5. Click **Save**. This saves the resource as a record in the repository. The record is automatically assigned **Draft** status. If the resource links to unfinished resources, you'll need to complete these resource **Stubs** prior to sending the resource to curation.



After you save the resource you can **Unlock** the record if you want other users at your institution to edit this resource.

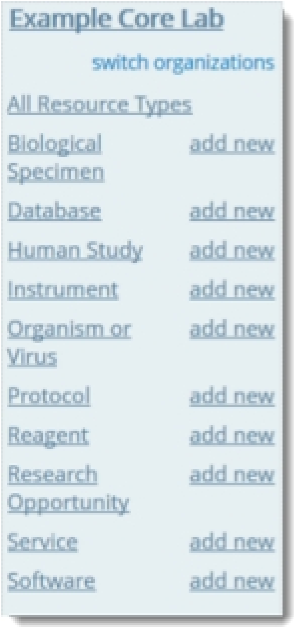
Optional Step: Duplicating Records

If you are entering multiple resources with similar properties, it may save time to use the duplicate button to create multiple copies of a single record. When you duplicate a record, this copies all editable fields in the original resource except for the name field. You can then modify or add information to make it specific to the new resource.

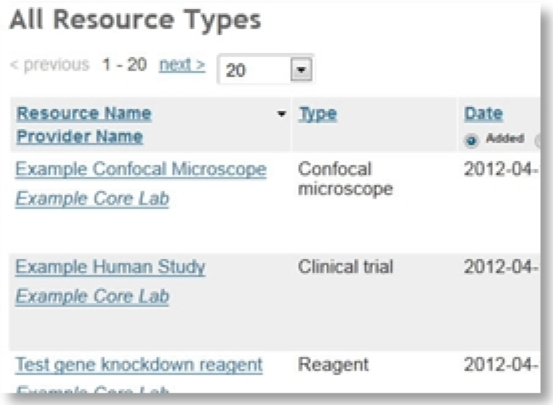
Note: You do not need to be the owner of a resource to duplicate it.

To duplicate a resource record:

1. Open a list of records for an organization by selecting either **All Resource Types** or a specific Resource Type link on the left sidebar.



2. Locate the record you wish to duplicate from the list. You can duplicate only one record at a time. Click the resource's name to open the record.

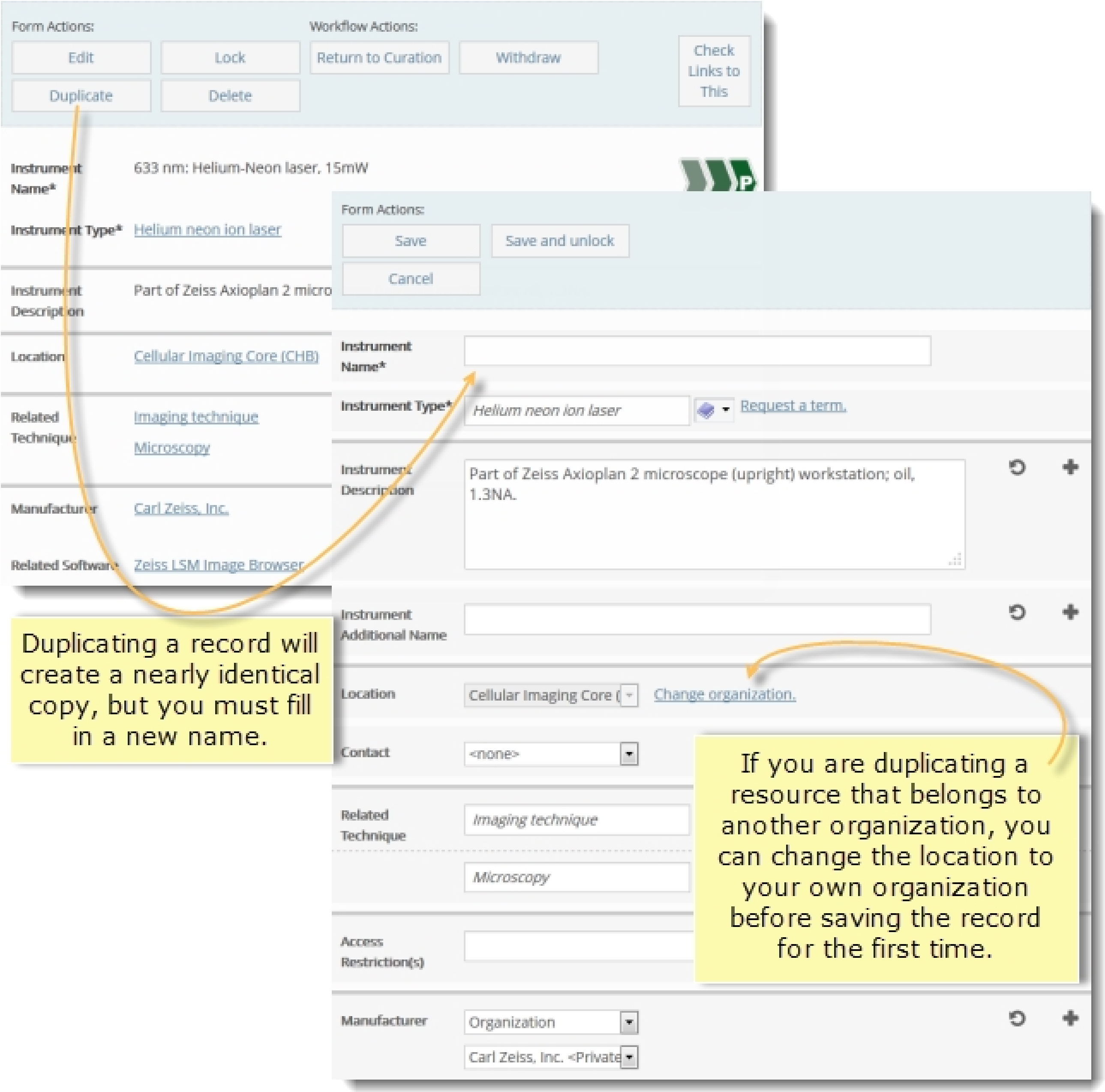


All Resource Types

< previous 1 - 20 next > 20

Resource Name Provider Name	Type	Date Added
Example Confocal Microscope *Example Core Lab*	Confocal microscope	2012-04-
Example Human Study *Example Core Lab*	Clinical trial	2012-04-
Test gene knockdown reagent	Reagent	2012-04-

3. From the **Form Actions** menu, click **Duplicate**. A copy of the resource appears.



Instrument Name*: 633 nm: Helium-Neon laser, 15mW

Instrument Type*: Helium neon ion laser

Instrument Description: Part of Zeiss Axioplan 2 micro

Location: Cellular Imaging Core (CHB)

Related Technique: Imaging technique
Microscopy

Manufacturer: Carl Zeiss, Inc.

Related Software: Zeiss LSM Image Browser

Duplicating a record will create a nearly identical copy, but you must fill in a new name.

Instrument Name*:

Instrument Type*: Helium neon ion laser

Instrument Description: Part of Zeiss Axioplan 2 microscope (upright) workstation; oil, 1.3NA.

Instrument Additional Name:

Location: Cellular Imaging Core (

Contact: <none>

Related Technique: Imaging technique
Microscopy

Access Restriction(s):

Manufacturer: Organization
Carl Zeiss, Inc. <Private

If you are duplicating a resource that belongs to another organization, you can change the location to your own organization before saving the record for the first time.

4. If the resource being duplicated belongs to a different organization from you're own, click **Change organization** next to the **Location** field and change the location to your own organization.
5. You must enter a new Name for the duplicate resource. Make necessary edits and then **Save** or **Save and unlock** the record.

You can duplicate resources owned by other organizations as well as resources owned by your own. Once you have duplicated the record, Click Change Organization to change the organization associated with the duplicated resource. Select the new organization. Then, click **Save**.

Step 2: Sending Records to Curation

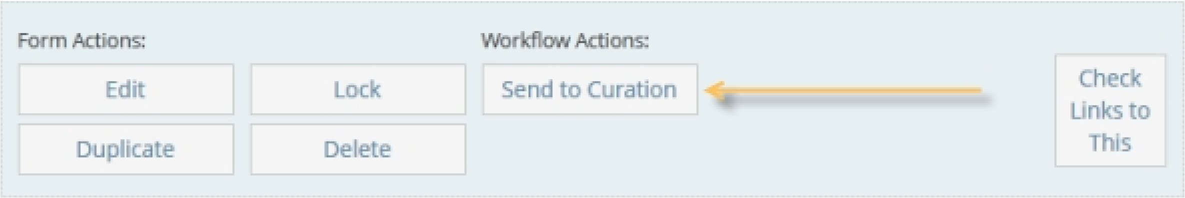
After a record has been created and annotated as completely as possible, the next step in the workflow is to send it to curation. All users have the ability to send records from draft to curation. If your role does not grant you access to edit and publish records in curation, then another user will review the records you send to curation. During the curation process, curators review the data and make any necessary annotations prior to publishing.

Note: When you send an organization to curation, you are only sending the organization record, not all of the resources associated with it. While it is possible to send records to curation piecemeal, it is recommended that you send as many connected records to curation together as possible in order to facilitate timely curation. Resources sent to curation without an owning organization or associated contact email will not be published.

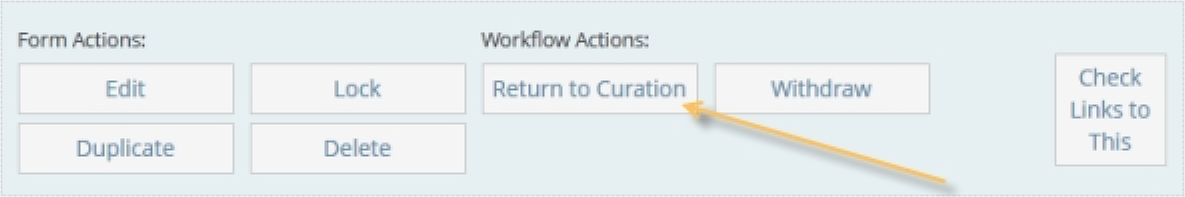
To send a single record to Curation:

Open a single record.

1. If the record is a draft, click Send to Curation.

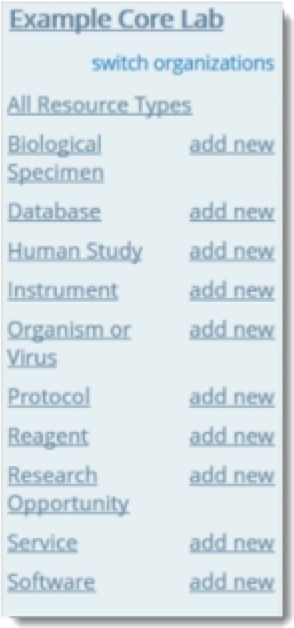


2. If the record is currently published, click Return to Curation.



To send multiple records to Curation:

1. Open a list of records belonging to an organization by selecting either All Resource Types or a specific Resource Type link on the left sidebar.



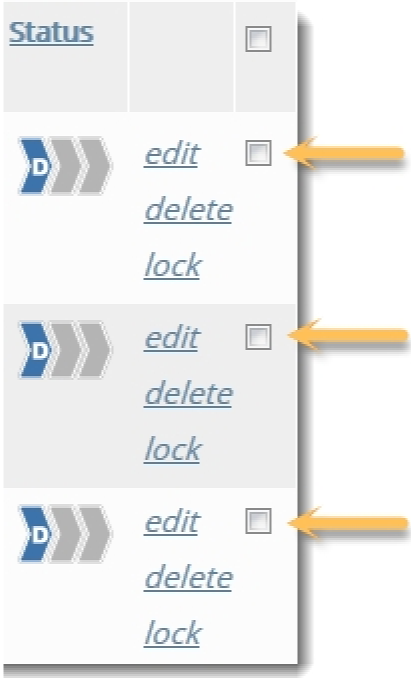
Example Core Lab

switch organizations

All Resource Types

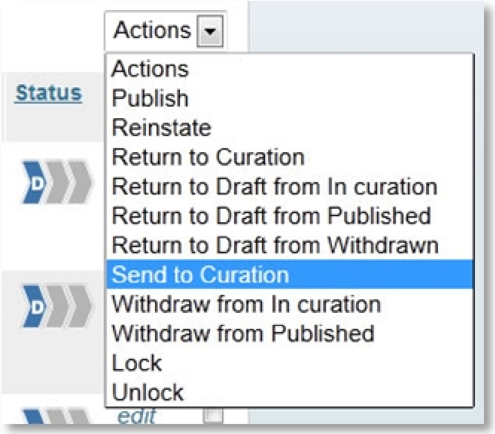
Biological Specimen	add new
Database	add new
Human Study	add new
Instrument	add new
Organism or Virus	add new
Protocol	add new
Reagent	add new
Research Opportunity	add new
Service	add new
Software	add new

2. In the resource list, select the checkbox beside all the records that should be sent to curation.



Status		☐
D	edit delete lock	☐
D	edit delete lock	☐
D	edit delete lock	☐

3. From the Actions drop-down menu, select **Send To Curation** or **Return to Curation**, depending on record status.



Send to Curation will only send records in Draft state to curation, even if Published records are also selected. Similarly, **Return to Curation** will only send Published records to curation, even if Draft records are also selected. If a stub record is among the resources selected sending multiple records to curation, you see the error: *Please finish reviewing <resource name> before trying to Send to Curation.*

Step 3: Reviewing and Publishing Records

All eagle-i records must be checked for consistency and accuracy before being published in the repository. Data curators provide this data quality assurance by reviewing resources sent to curation and ensuring they conform to the annotation guidelines. If more information is required, they may return the records to draft so the record creator can edit it; if the records are complete, they are published and made visible in the eagle-i search application. Data curators also provide data management support by keeping resource information current.

Note: there is no automated process for notifying curators when new records have been submitted for curation. You will need to set up your own systems of communication with resource collectors, monitor the SWEET, and/or run regular data queries to see records in Curation at your institution.

Reviewing by Organization

Because eagle-i resources are organized and displayed by their providing organization, it is generally helpful to review them within that context. Reviewing all of the resources from one organization before moving on to another organization's resources allows you to check for internal consistency, weed out accidental duplicates that might have been entered, and consolidate records where necessary.

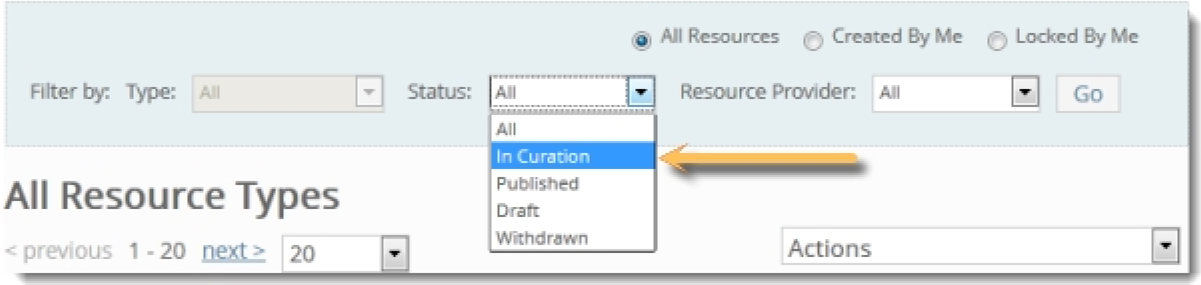
Typically, records that should be combined are:

- Sparsely annotated service records that describe variations on the same service. For search usability, it is better to combine these under a single service record with a broad title and list the individual service variations in the resource description.
- Multiple copies of the same instrument owned by the same lab. These should be described in one record. Note how many of that instrument is available in the resource description.

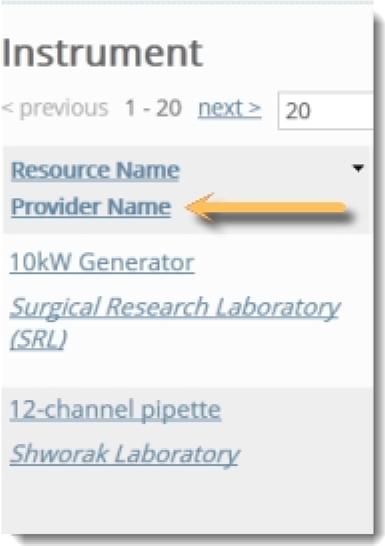
To review records by organization:

1. From the Workbench click Browse People & Resources in My Institution.

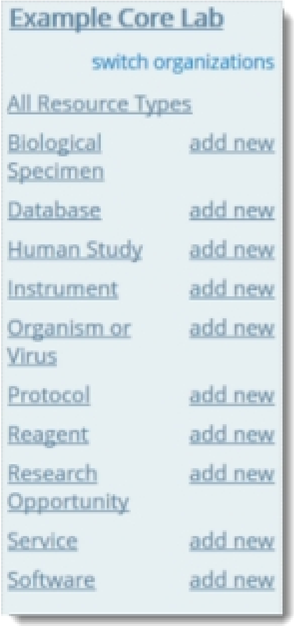
2. Filter the list by status. Select In Curation from the Status drop-down filter list.



3. The name of the owning organization is displayed in italics underneath each resource name in the list. All resources at your institution are displayed in alphabetical order by default. You can sort by Provider Name to see resources belonging to the same organization grouped together.



4. Or simply click on a resource to open the record, then use the left sidebar—now populated with information specific to the provider for that resource—to navigate through other resources within that organization.



5. Because required fields are different depending on the resource type, you should start by reviewing the resource **Name** and **Type** fields.

For more information, see the Data validation and consistency and How to publish records sections.

Data Validation and Annotation Consistency

Curation is more than just proofreading.

You should ensure that the data is as robust and complete as possible before publishing it. When curating a laboratory or another type of resource owning organization, it is best practice to compare the information in the SWEET with information available on the organization's website. If there is information on the site that is missing from the records, it should be updated in eagle-i, unless there is reason to believe the website is out of date. Manufacturers' sites can also be a good source of information for instruments, software, reagents, and protocols. Any questions should be brought to the attention of the record creator.

See the SWEET General Annotation Guide for specific guidelines pertaining to each resource type.

Data Validation

When reviewing records, check to ensure:

- All required fields are complete. Note that required fields vary depending on type.
- Additional fields are complete whenever information is available.

- Data is recorded in the correct field: for example, the study's CT.gov URL is in the ClinicalTrials.gov URL field, not the website (s) field.
- Data is contextually accurate: For example, would a user be surprised if they searched for the contents of any of the record's properties and got the record as a result?
- Was there a term request associated with this record? If so, does the request represent a truly unique concept, or should the record have been annotated with another existing term?
- Data is contextually consistent. In other words, the metadata from the ontology is applied consistently with that of similar records.
- Links between the record and other resource records are correct, and the records to which your resource links are all also published.

Annotation Consistency

The wide range of annotation and domain expertise among the individual data collectors means that incoming data may be wildly inconsistent. You are responsible for maintaining not only a certain standard of quality in the data, but also for ensuring that the data is described in a similar manner within each institutional repository as well as across the entire network.

There are several general methods for maintaining annotation consistency. In addition to referencing the topics in these guidelines, it is best practice to:

- Use the eagle-i search application to review how other similar records have been annotated.
- Perform periodic automated (SPARQL queries) and manual data quality spot checks to ensure uniformity and correct human error in the data.
- Reach out to other curators. Curation is collaborative by nature. Curators are strongly encouraged to communicate with one another and with other domain experts over any questions relating to consistency and overall data quality.

Publishing Records

Once you have completed your review, publish the record along with any associated records that have also passed through curation.

Things to look out for:

- All published eagle-i resources must be linked to a published organization. Although the system allows records for organizations to be submitted for curation independently from other resources associated with them, they should not be published unless they are referenced by another published record as a resource provider, affiliate, or manufacturer.
- Core laboratories should not be published unless they are associated with at least one published service record.
- Every published resource-owning organization needs at least one associated email address in order for the **Send Message to Resource Contact** button to function correctly in search. An email address can be associated with an organization by

entering the an email address in the Email field on either the organization record itself, or in a published contact, PI, or Director person record related to that organization.

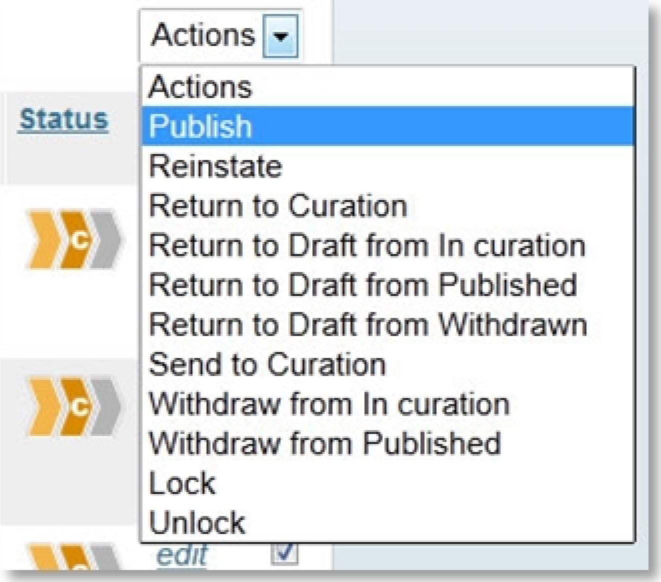
For more information see Working With Linked Data.

To publish multiple resources at the same time:

1. From the Workbench, click Browse People & Resources in My Institution.

2. Filter the list to view the records that are currently in curation. Select one or more resources by clicking the check box.

3. Click Publish in the Actions menu.



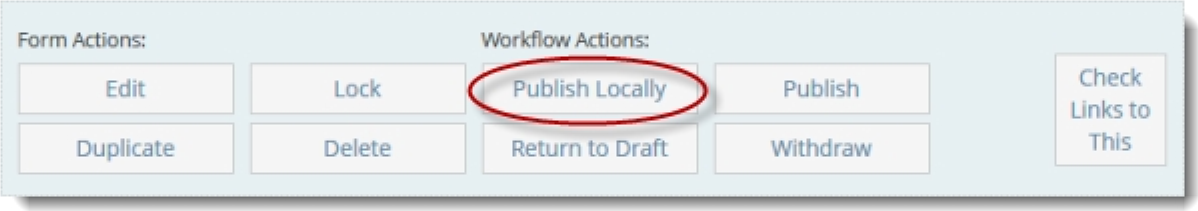
Publishing records with open term requests

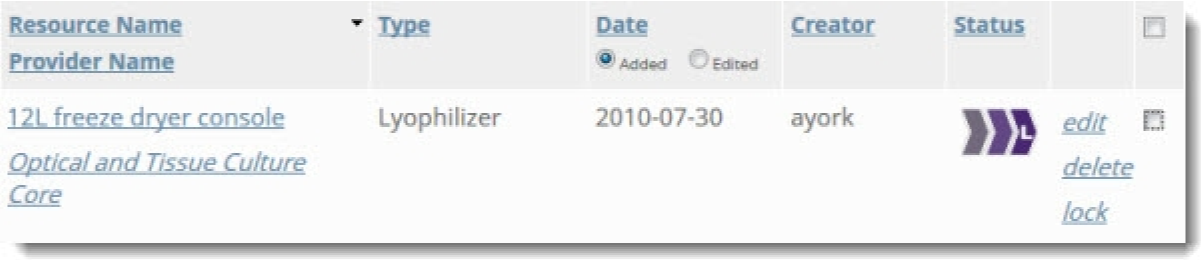
If there is an outstanding term request for a record that is otherwise complete, it should be published. See Publishing Records with Open Term Requests for more details.

Publishing Locally

Some institutions may provide the option to **Publish Locally**. Resources published locally will not be visible in the central eagle-i search, but will be visible in a separate search available only to local users.

If the publish locally option is available, the status legend under the left sidebar will contain a purple icon, and records in curation will contain a **Publish Locally** button to the left of the regular **Publish** button on the **Form Actions** panel:





Resource Name Provider Name	Type	Date ● Added ○ Edited	Creator	Status		☐
12L freeze dryer console *Optical and Tissue Culture Core*	Lyophilizer	2010-07-30	ayork		*edit* *delete* *lock*	☐

Locally published records can either be **Withdrawn** or returned to **Curation**. To move a record from **Published** to **Published Locally**, or vice versa, it must first be sent back to curation and then re-published.

Links between Published and Locally Published records

Links from locally published to regularly published records will be visible in *local* search. However, links from published records to locally published records will **not** be visible in *central* eagle-i search.

Users should take care before locally publishing records to ensure no critical information—such as the contact email—will be removed from records remaining in central eagle-i search. In particular, resource records should **never** be published to central eagle-i search with a locally published owning organization, as this will create the appearance of orphaned records in central search.

Only users with **Level 3** or **Level 4** access permissions will have the ability to publish locally.

Step 4: Withdrawing Records

When a record is withdrawn, the data is retained in the repository but is not visible in search. Withdrawn records can still be viewed, edited, locked/unlocked, or returned to draft in order to start the process through the life cycle again. Some users also have the ability to withdraw records from curation. This access is restricted because typically, only records that have been published should be withdrawn and kept in the system. In certain, rare circumstances, however, it may be necessary to keep a record or collection of records for reference which will never be published for various reasons.

Note: Withdrawn records will not be listed in the drop-down for fields that link to other records *unless* they were already linked in that field prior to being withdrawn.

Who can see withdrawn records?

Anyone with SWEET access can view all the Withdrawn records in that repository. However, withdrawn records are not listed in search auto-suggestions or search results, and links to withdrawn records from published records are not visible in eagle-i search. A public dissemination page will still exist for withdrawn records, but will be visible only to people with a direct link to it.

This record has been removed from eagle-i search; this page is an archival copy only. Use the search bar at the top of the page to look for similar resources in eagle-i.

100x Apo TIRF-85

eagle-i ID

http://harvard.qa.eagle-i.net/i/0000012a-2514-ef2f-5617-794280000067

Resource Type

Objective lens

Properties

Resource Description	Station 4 / Mag:100x DIC N2 Numerical Aperture: 1.49 Immersion Media: Oil
Manufacturer	Nikon Corporation
Model Number	100x Apo TIRF
Location	0000012a-2514-eb96-5617-794280000000

Text indicates this resource is no longer active and/or available for sharing.

What should be withdrawn?

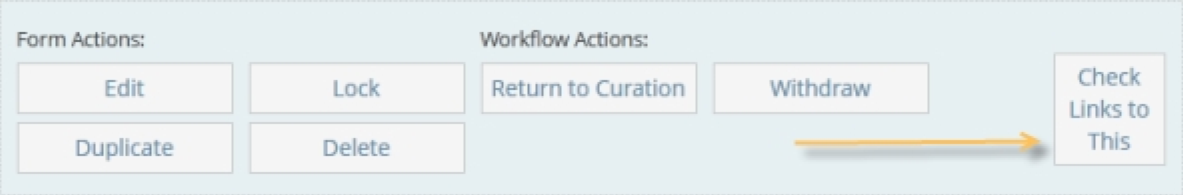
Unlike deleted records, withdrawn records can be both viewed in the SWEET and reinstated in case they become relevant again. In general, previously published records should always be withdrawn rather than deleted, unless they are duplicates of other existing records. This is both for general archival purposes and to ensure that any citations to the resource will still contain a useful link.

You should withdraw any published records of resources that no longer available for sharing, whether temporarily or permanently. For example, an antibody that is no longer in stock, or a service that a lab is currently too busy to offer, but may offer again in the future. The records of organizations and people should also be withdrawn when they are no longer relevant, such as when a lab contact leaves that lab, or a core is closed down.

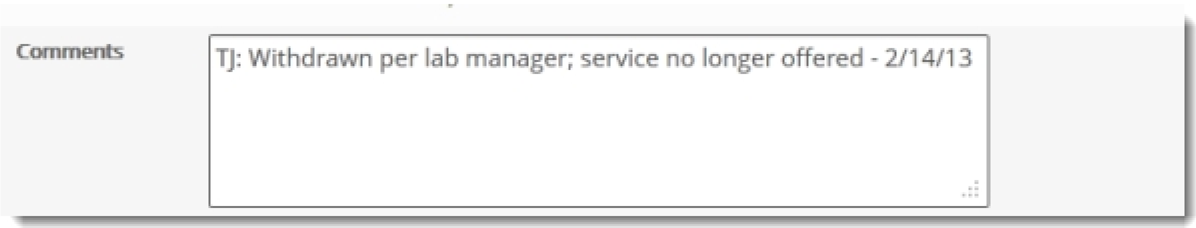
Note: if a record is being removed from public view due to privacy concerns, it should be sent back to Draft rather than withdrawn, as otherwise the information will still remain visible to anyone with the resource ID.

To withdraw a record:

1. Open the record and select the **Check links to this** button. If it is linked to any other resources, determine if those records should be withdrawn as well. If you are withdrawing a laboratory, all of the attached resources and people must also be withdrawn.

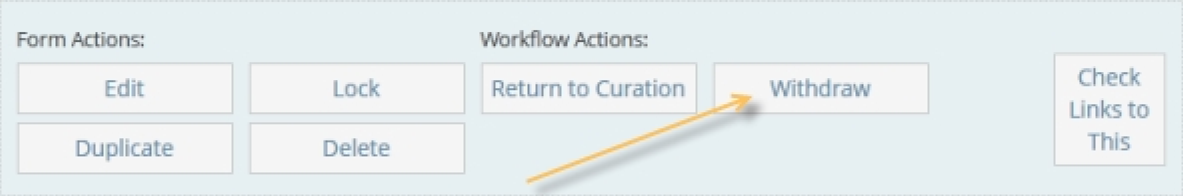


2. Add a note in the Comments field with your initials, explaining why the record was withdrawn.



TJ: Withdrawn per lab manager; service no longer offered - 2/14/13

3. From the **Workflow Actions** menu, click Withdraw.



Next step: Reinstate the record.

Optional Step: Reinstating Records

Records that have been withdrawn can be reinstated back to active status at any time.

To reinstate a withdrawn record:

1. Select Return to Draft from the **Workflow Actions** menu.
2. Update the record as needed.
3. Move the record back up through the workflow until it is published again.

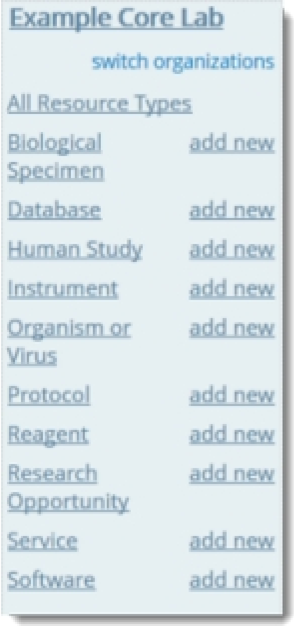
Note: resources associated with withdrawn organizations should only be reinstated along with their owning organization. See Working With Linked Data for more information.

Deleting Records

Records may be deleted from the eagle-i repository entirely, rather than Withdrawn. The distinction between withdrawn records and deleted records is that once deleted, a record cannot be recovered. Therefore, you should use caution before deleting any record. In general, the only records that should be deleted are unpublished, erroneously created, or unnecessary duplicate records. In the case of duplicates, the records should be merged and the duplicate deleted.

To delete a resource record:

1. Open a list of records belonging to an organization by selecting either All Resource Types or a specific Resource Type link on the left sidebar.



Example Core Lab
switch organizations
All Resource Types
Biological Specimen add new
Database add new
Human Study add new
Instrument add new
Organism or Virus add new
Protocol add new
Reagent add new
Research Opportunity add new
Service add new
Software add new

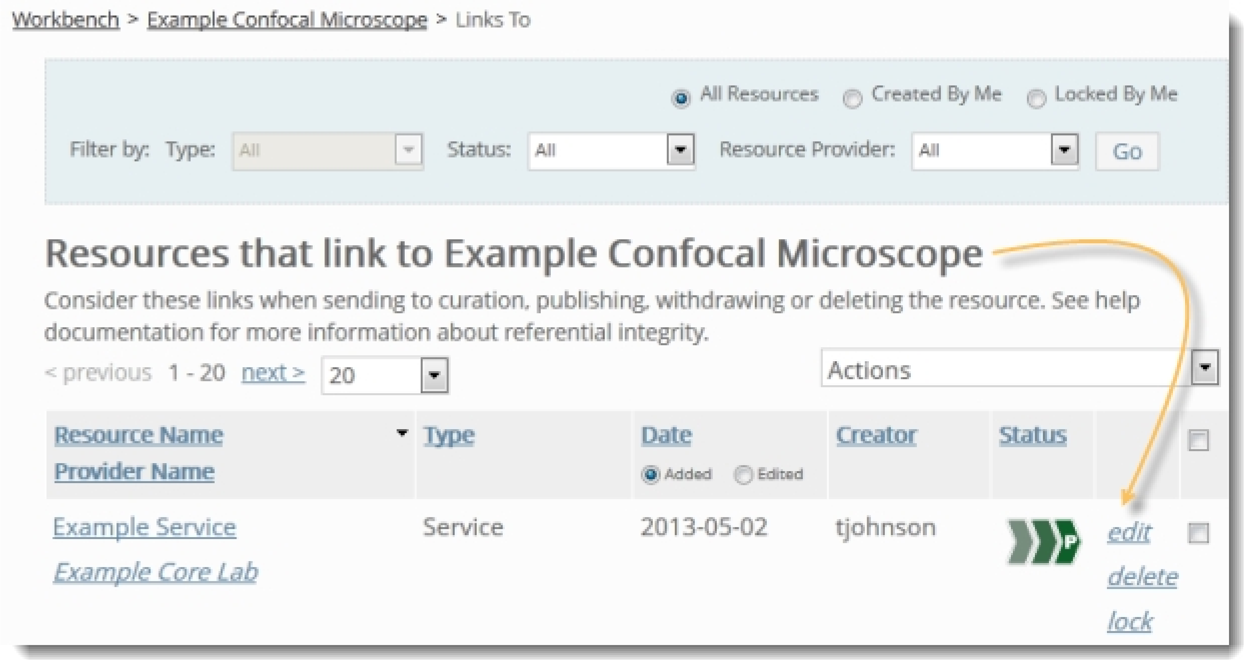
2. Locate the record to delete from the list. You can delete only one record at a time.

All Resource Types

< previous 1 - 20 next > 20

Resource Name Provider Name	Type	Date Added
Example Confocal Microscope *Example Core Lab*	Confocal microscope	2012-04-
Example Human Study *Example Core Lab*	Clinical trial	2012-04-
Test gene knockdown reagent	Reagent	2012-04-

3. Click the resource’s name to open the resource details page and use the Check Links to This button to determine if the resource is linked to any other records.



Workbench > Example Confocal Microscope > Links To

● All Resources ○ Created By Me ○ Locked By Me

Filter by: Type: All Status: All Resource Provider: All

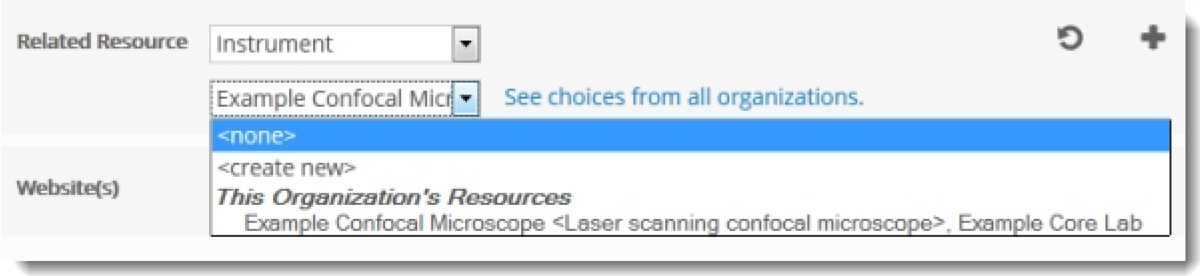
Resources that link to Example Confocal Microscope

Consider these links when sending to curation, publishing, withdrawing or deleting the resource. See help documentation for more information about referential integrity.

< previous 1 - 20 next > 20

Resource Name Provider Name	Type	Date ● Added ○ Edited	Creator	Status		☐
Example Service *Example Core Lab*	Service	2013-05-02	tjohnson	P	*edit* *delete* *lock*	☐

4. Edit those records. Remove or replace those links as necessary.



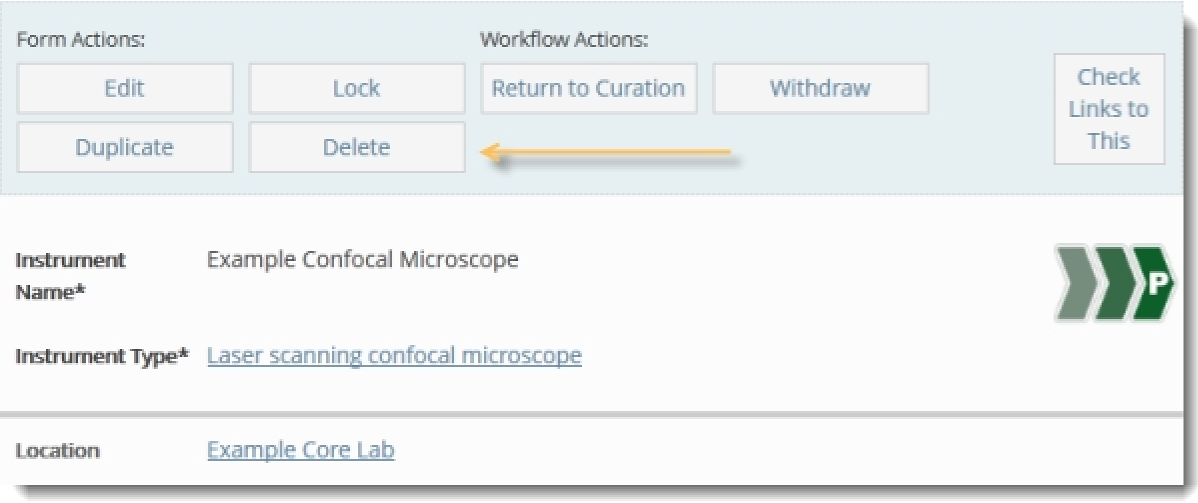
Related Resource Instrument

Example Confocal Micr

See choices from all organizations.

Website(s)

5. Return to the record you wish to delete. Click Delete in the Form Actions panel.



Instrument Name* Example Confocal Microscope

Instrument Type* Laser scanning confocal microscope

Location Example Core Lab

Data Maintenance and Quality Control

Periodic quality control measures need to be taken to ensure the data in the repository stays up to date and accurate, and that connections between records are linked correctly. Data maintenance and quality control activities consist of: refreshing stale information, removing invalid records, updating records to meet any changes to the guidelines or ontology, and ensuring that the necessary connections are visible in the search application. In general, each institution is responsible for maintaining its own data; the central curation and ontology teams may also perform these activities to ensure consistency across all institutions and to update terms or records after an ontology or software release.

There are a number of SPARQL queries that need to be regularly and manually run to perform large-scale quality assurance on the data at all institutions. The table below lists the broad types of queries and the frequency with which they should be run:

DAILY

- Check for records in curation that need to be reviewed

WEEKLY

- Check for Orphaned records:
    - Published resources with an unpublished provider.
    - Published resources that have links to other unpublished records.
- Check that all published resource have published contact information, either in the contact associated with the resource or with the resource's owning organization

MONTHLY

- Check for broken links to external websites.
- Check for records that have same label as type.

POST-RELEASE

- Check for new term requests that have been added to the ontology and now need to be updated in the SWEET.

PERIODICALLY

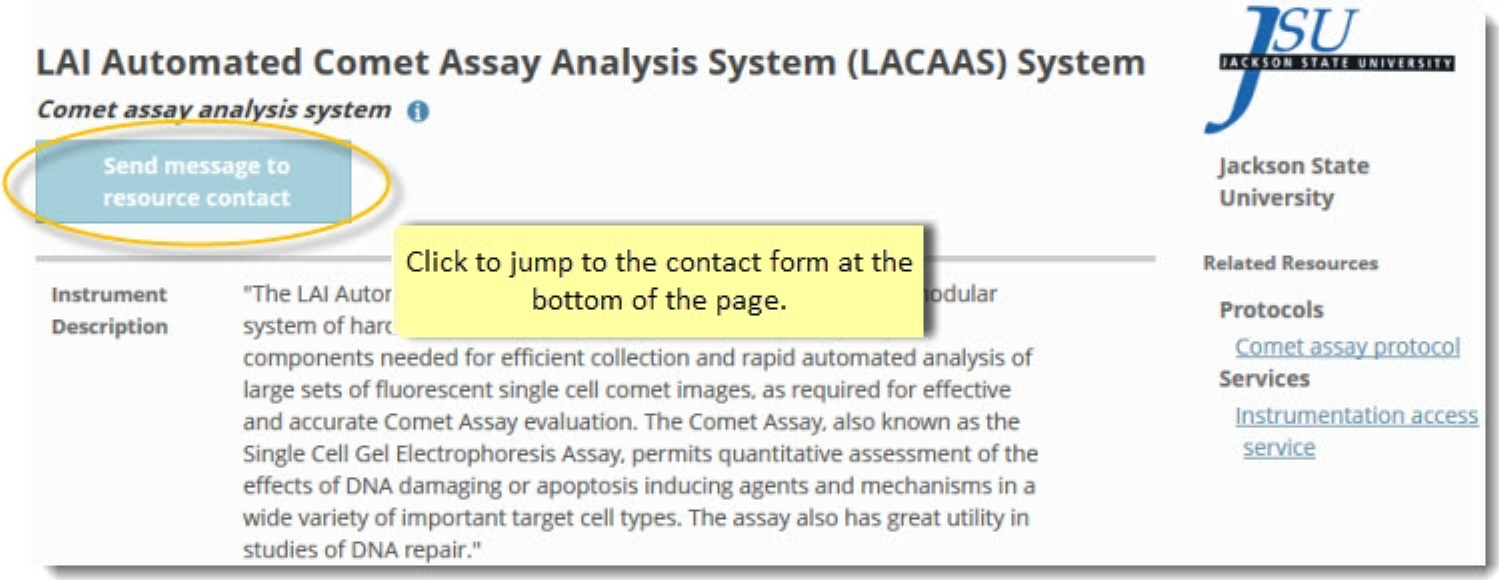
- Check for resource with multiple providers. These may be deliberate but should be verified.
- Check for resources with obsolete types or properties.
- Check for records with no label. These will not be visible in the SWEET and require build team assistance to fix. These are usually the result of an ETL error or data migration error.

Contact Emails and Privacy Concerns

By default, eagle-i hides information related to physical addresses, e-mail addresses, and phone numbers for all organizations and people, in response to the privacy concerns of certain researchers (in particular, research laboratories that work with animals). The affected fields are:

- E-mail
- Lab delivery address
- Mailing address
- Phone number

Although this information can and should be entered in the SWEET, it will not display in the search application. eagle-i search features an anonymous contact button that allows users to email resource owners while protecting their privacy.



LAI Automated Comet Assay Analysis System (LACAAS) System

Comet assay analysis system

Click to jump to the contact form at the bottom of the page.

Instrument Description "The LAI Autor odular system of harc components needed for efficient collection and rapid automated analysis of large sets of fluorescent single cell comet images, as required for effective and accurate Comet Assay evaluation. The Comet Assay, also known as the Single Cell Gel Electrophoresis Assay, permits quantitative assessment of the effects of DNA damaging or apoptosis inducing agents and mechanisms in a wide variety of important target cell types. The assay also has great utility in studies of DNA repair."

Jackson State University

Related Resources

Protocols
Comet assay protocol
Services
Instrumentation access service

When a researcher clicks this button and fills out the provided form, an email is generated and sent to the email address listed as the contact for that resource. In some cases, this may lead to a guided interaction between the person requesting a resource and the resource owner. See Using eagle-i Request for more information.

Designating a resource contact

The contact for a specific resource may be different from the general contact for the owning organization as a whole. If a specific resource contact exists, that name will be listed on the resource details page, and using the contact form will generate a message for that person. If no specific resource contact exists, using the form will generate a message for the next available contact listed on the corresponding organization record for that resource. Contact emails are generated in the following order, depending on which are available:

1. Email of the person listed in the contact field on the resource record.
2. Email entered in the general **Email** field of the resource's owning organization.
3. Email of the **Contact** person for the owning organization.
4. Email of the **PI** for the owning organization.
5. Email of the **PI (co-Investigator)** for the owning organization.
6. Email of the **Director** for the owning organization.
7. Email of any person listed in the **Other members** field for the owning organization.

In order to be used for the anonymous contact form, an email must be entered on a published record. If no valid emails are available for a resource, the eagle-i postmaster will receive any communications generated using the anonymous contact form.

Note: if multiple people are entered in a contact field, the system will randomly choose one as the primary contact. If there's a specific person for different resources, those contacts should be individually added to the appropriate resource records. To designate just one person to receive all contact emails for an organization, either move all but one of the people to the **Other members** field, or add the email of the selected primary contact to the organization's general **Email** field.

De-identifying Lab Names and People

Organizations that wish to anonymously contribute information about their resources to eagle-i can use a less specific name if using their real name would be enough to identify them. For example: a research laboratory working with primates goes by the name "Smith Lab." As the lab wishes to remain anonymous, it could be entered into eagle-i with a more generic name, such as "Primate Research Laboratory."

Instead of creating contact people for these organizations, the email of the designated contact should be entered in the **Email** field on the organization record, along with a note of explanation in the **Comments** field of the lab. If an existing person record needs to be removed from public view due to privacy concerns:

1. Move the record to a Draft or Curation state. It should **not** be Withdrawn, as a public dissemination page will still exist and be visible to anyone who has a direct link to it.
2. If the removed record is the only contact for the organization, migrate the person's email to the **Email** field of the organization record.

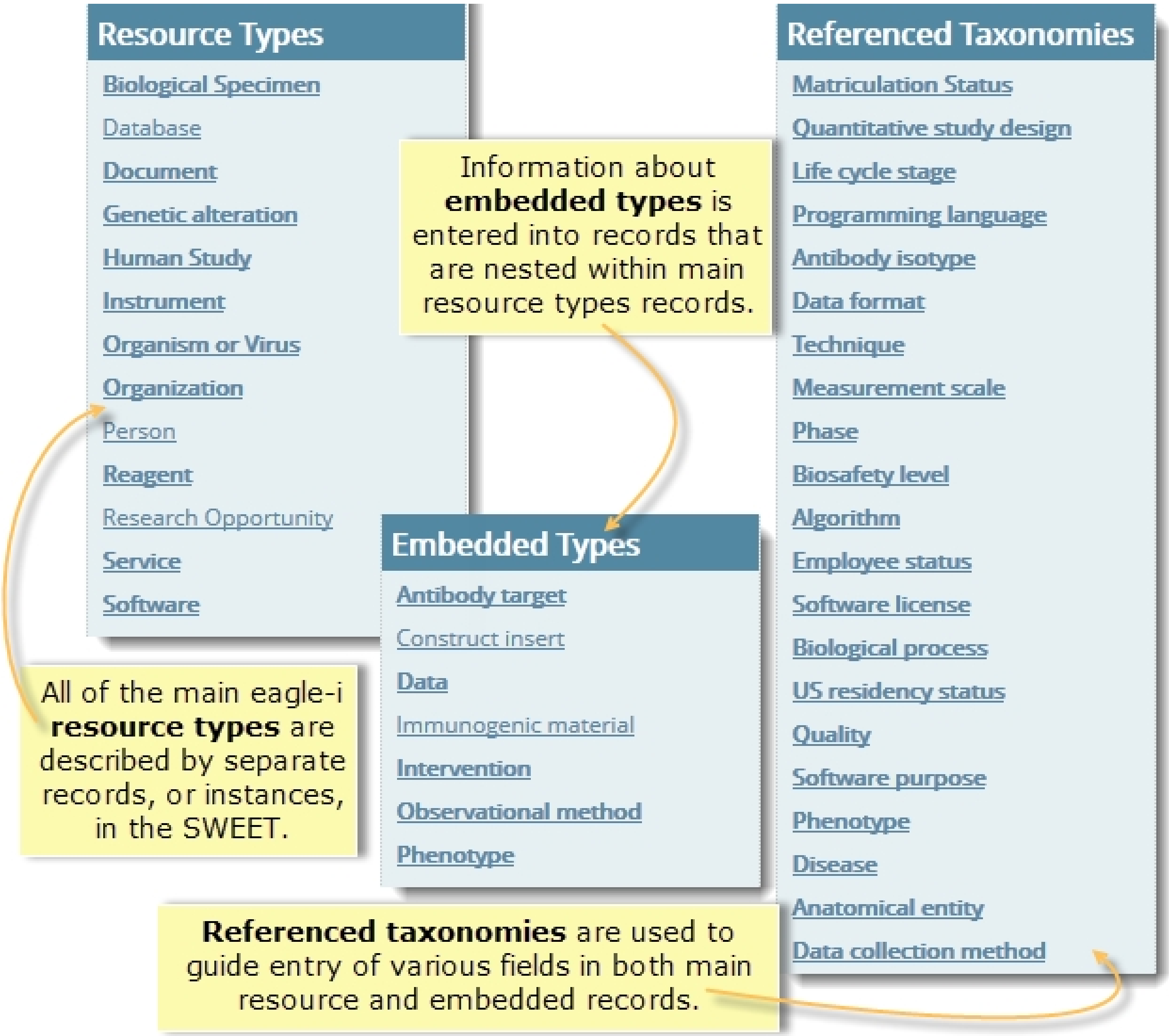
Using the eagle-i Ontology

The eagle-i ontology is maintained by a central team, and drives much of the way information is displayed and annotated in the SWEET. The ontology can aid in both annotation and curation.

- Navigating the eagle-i ontology
- Adding terms to the eagle-i ontology

Using the eagle-i Ontology Browser

The Ontology Browser allows you to look for terms and view definitions, synonyms, related terms, and the properties used to describe them in the SWEET. This information can be used to determine the most appropriate terms to use for annotation.



Information about **embedded types** is entered into records that are nested within main resource types records.

All of the main eagle-i **resource types** are described by separate records, or instances, in the SWEET.

Referenced taxonomies are used to guide entry of various fields in both main resource and embedded records.

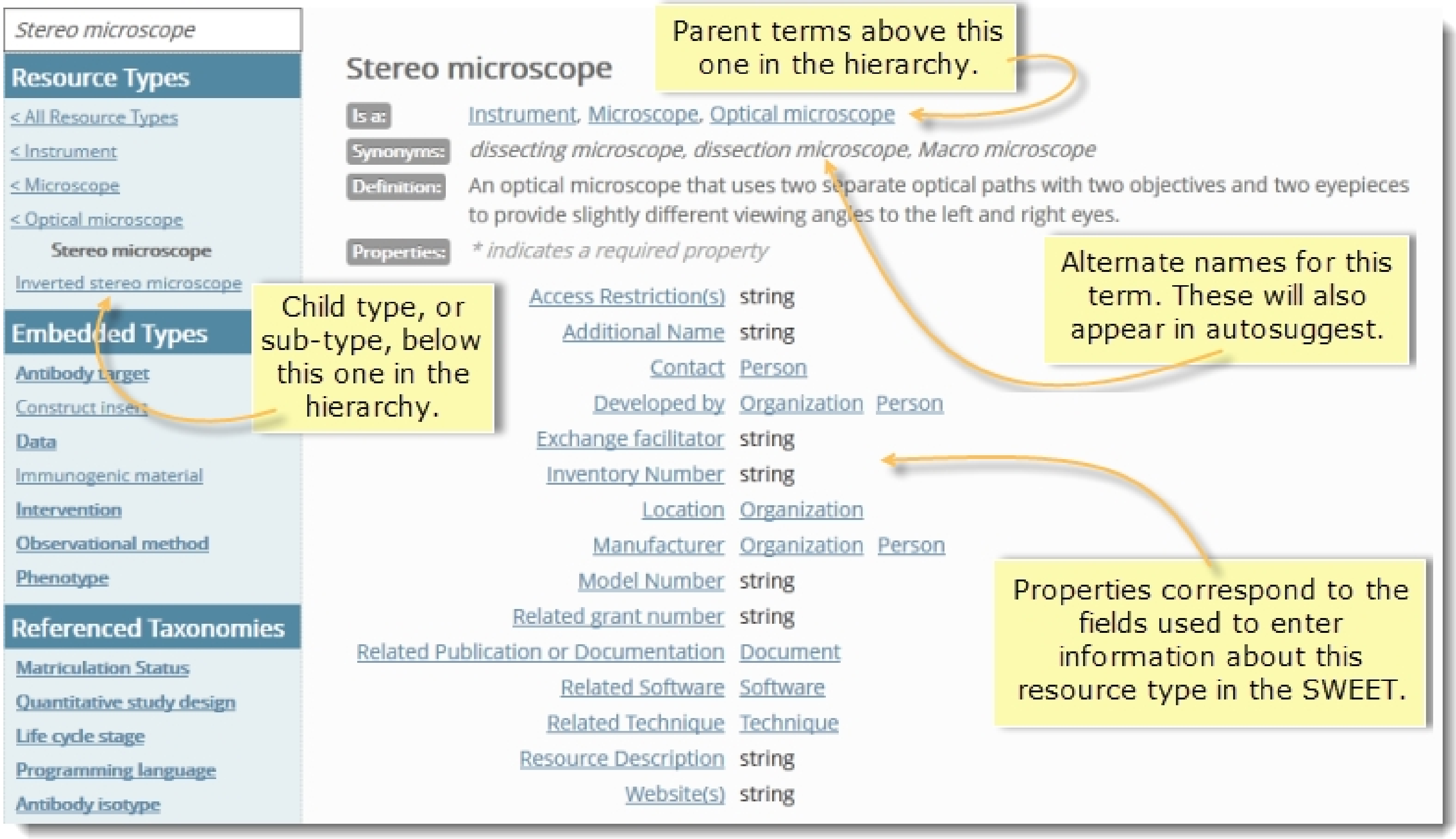
Requests for new terms can be entered by filling out a simple form available in either the SWEET or the ERO Term Tracker. See the Submitting a Term Request section for more detail.

Searching and browsing the ontology

From either the SWEET or the search application, click Help and select the Ontology Browser, or go to https://search.eagle-i.net/-model/.

To find vocabulary terms:

- Browse the term hierarchy in the left sidebar by major resource type. For example: browse instruments, reagents or by the various taxonomies referenced by the eagle-i ontology, such as **Techniques** or **Biological Processes**.
- Click any term to display its information in the main body of the page and its *child terms* (sub-classes) in the sidebar. The selected term appears in the sidebar under a hierarchy of its parent terms (super-classes).



Stereo microscope

Resource Types
< All Resource Types
< Instrument
< Microscope
< Optical microscope
Stereo microscope
Inverted stereo microscope

Embedded Types
Antibody target
Construct insert
Data
Immunogenic material
Intervention
Observational method
Phenotype

Referenced Taxonomies
Matriculation Status
Quantitative study design
Life cycle stage
Programming language
Antibody isotype

Stereo microscope

Is a: Instrument, Microscope, Optical microscope

Synonyms: *dissecting microscope, dissection microscope, Macro microscope*

Definition: An optical microscope that uses two separate optical paths with two objectives and two eyepieces to provide slightly different viewing angles to the left and right eyes.

Properties: ** indicates a required property*

Access Restriction(s)	string
Additional Name	string
Contact	Person
Developed by	Organization Person
Exchange facilitator	string
Inventory Number	string
Location	Organization
Manufacturer	Organization Person
Model Number	string
Related grant number	string
Related Publication or Documentation	Document
Related Software	Software
Related Technique	Technique
Resource Description	string
Website(s)	string

Parent terms above this one in the hierarchy.

Child type, or sub-type, below this one in the hierarchy.

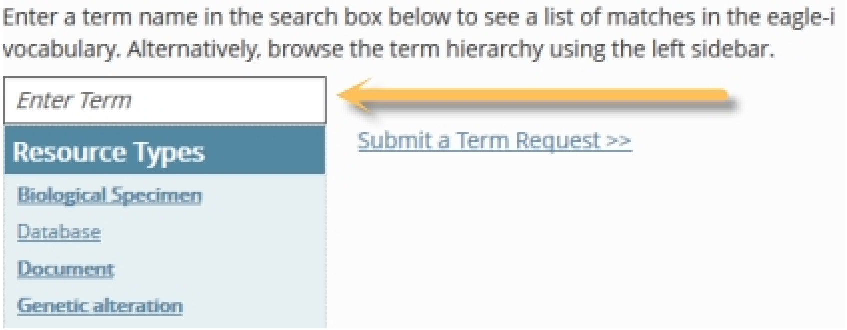
Alternate names for this term. These will also appear in autosuggest.

Properties correspond to the fields used to enter information about this resource type in the SWEET.

- Click any term in any order to view its information. Sidebar items in bold font have child terms; items in plain font do not.

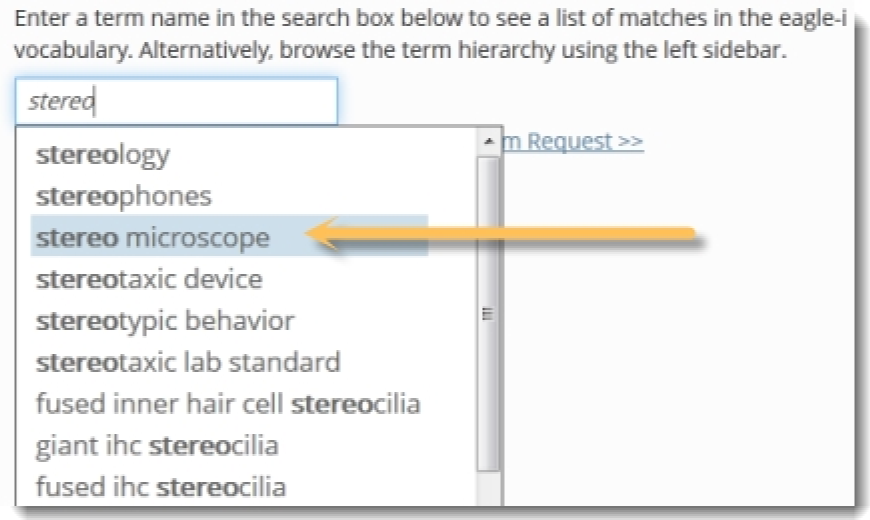
-or-

- Type a term name in the search box above the left sidebar.



Enter a term name in the search box below to see a list of matches in the eagle-i vocabulary. Alternatively, browse the term hierarchy using the left sidebar.

- As you type the query text, you see a list of potential query completions that are generated using auto-suggest technology from the eagle-i ontology.



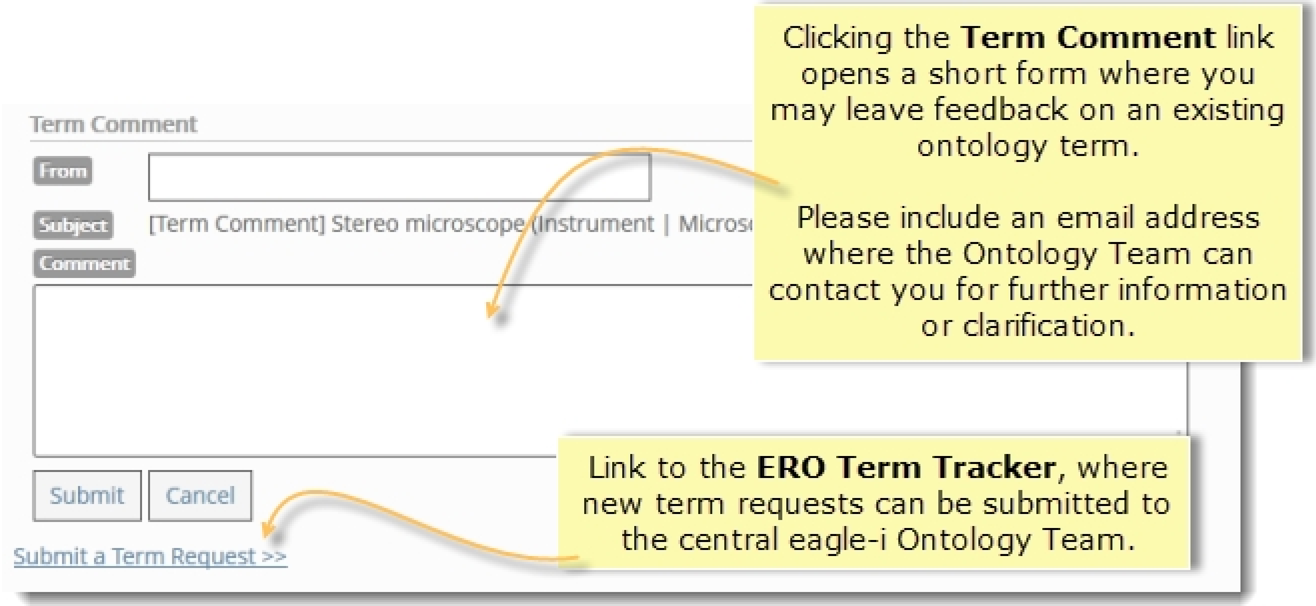
Enter a term name in the search box below to see a list of matches in the eagle-i vocabulary. Alternatively, browse the term hierarchy using the left sidebar.

- To view information about a term, either type in the full, matching term and hit Enter, or click on one of the auto-suggested terms. The selected term is highlighted in the left sidebar with its child terms, if any, displayed below it. The main body of the page contains information that describes a term’s properties and where it fits in the ontology:

- ○ **Is a** - the terms (classes) of which the selected term is a sub-class.
- ○ **Synonyms** – any equivalent terms or alternative names for the selected term.
- ○ **Definition** – describes how the selected term is defined for eagle-i purposes.
- ○ **Properties** – these reflect the data fields that are available for the selected type in the data tool. Click on a property name to toggle its definition into view. Click on a property name to toggle its definition into view.

- Click the **Term Comment** link beneath the properties section for any term to send any feedback about the term to the eagle-i Ontology Team. Feedback could include information such as corrections or suggestions for new synonyms. Click the

Submit a Term Request link to be taken to the ERO Term Tracker. See Submitting Term Requests for more details.



Subject: [Term Comment] Stereo microscope (Instrument | Micros

Clicking the **Term Comment** link opens a short form where you may leave feedback on an existing ontology term.

Please include an email address where the Ontology Team can contact you for further information or clarification.

Link to the **ERO Term Tracker**, where new term requests can be submitted to the central eagle-i Ontology Team.

Limitations

- Because only ten auto-suggestions are displayed at a time, the auto-suggestions for terms that have more than ten matches in the ontology are not a complete representation of every available term.
- To find a term that isn't appearing as an auto-suggestion, users should try different variations of the word. Typing the least common sections of a word or phrase can sometimes bring up more effective results.
- In addition, users should remember that a term that appears in the Ontology Browser may not yet be available for annotation, due to the lag time between ontology updates and new releases of SWEET.

Term Requests

Term requests are one way new terms are added to the eagle-i ontology. If you want to annotate a field with a term that is not currently available, select the next most applicable term, and then submit a term request for the most specific one you would like to use.

Term request topics in this section:

- How to submit a term request
- How to publish records with open term requests
- How to fill term requests

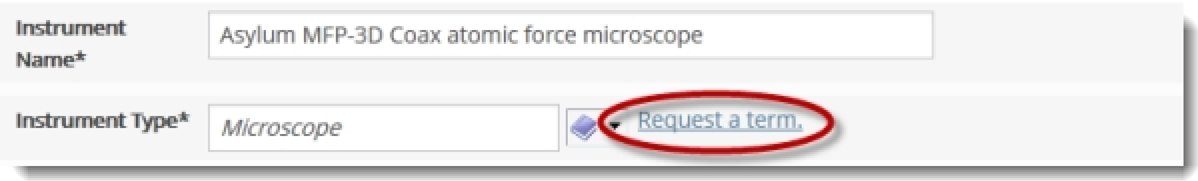
Submitting Term Requests

Any field marked with a blue book icon is an ontology/controlled vocabulary field, meaning that it must be filled with a term from the eagle-i ontology. If the term you want to use is not available, you can request it be added to the ontology by submitting a term request form.

Submitting Term Requests in the SWEET

Procedure for submitting term requests:

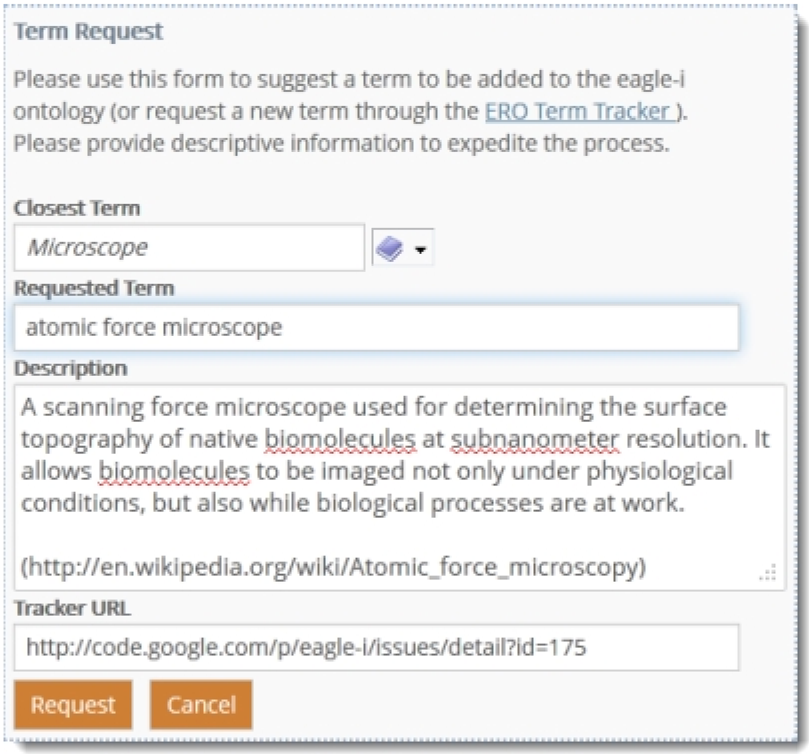
- Use autosuggest or browse the hierarchy of terms under the blue book icon to select the closest existing parent term to the one being requested. If no closer term exists, annotate it with the root type. For example: if the term *atomic force microscope* is being requested, the closest parent term would be *microscope* instead of the root type, "instrument." Only if microscope is not available should this field be left as instrument.



Instrument Name* Asylum MFP-3D Coax atomic force microscope

Instrument Type* Microscope

2. Click the **Request a term** link, found to the right of every ontology/ controlled vocabulary field.
3. A Term Request form appears.
    - If the record has been saved, the **Closest Term** field will be auto-populated with the term selected in step one. If not, you may have to select it again.
    - Either a **Requested Term** name or a **Tracker URL** is required. See below for instructions on the using the ERO Term Tracker.
    - The **Description** field is optional, but providing as much information about the requested term as possible will help the ontology team process your term request more efficiently. The most useful descriptions are definitions of the term being requested along with a corresponding source, i.e. URLs, people, books, etc. Include your name and email if you are willing to be contacted about your request (or would like a notification when it has been filled).



Term Request

Please use this form to suggest a term to be added to the eagle-i ontology (or request a new term through the ERO Term Tracker). Please provide descriptive information to expedite the process.

Closest Term: *Microscope*

Requested Term: atomic force microscope

Description: A scanning force microscope used for determining the surface topography of native biomolecules at subnanometer resolution. It allows biomolecules to be imaged not only under physiological conditions, but also while biological processes are at work.

(http://en.wikipedia.org/wiki/Atomic_force_microscopy)

Tracker URL: http://code.google.com/p/eagle-i/issues/detail?id=175

4. After you have completed the form, click **Request**. Doing so will generate an email notification to the ontology team with your request info.

Note: After the record is saved, anything entered into the Term Request field is displayed in the Metadata section at the bottom of the record. Term requests will not be visible in search.

Using the ERO Term Tracker

The ERO Term Tracker, or Google Code Tracker, is used by the ontology team to log and track term requests. Each term request has a single issue ticket. If a ticket already exists for the term you are requesting, there is no need to create a new one; simply copy the URL of the existing ticket and paste it into the **Tracker URL** field in the term request form in the SWEET.

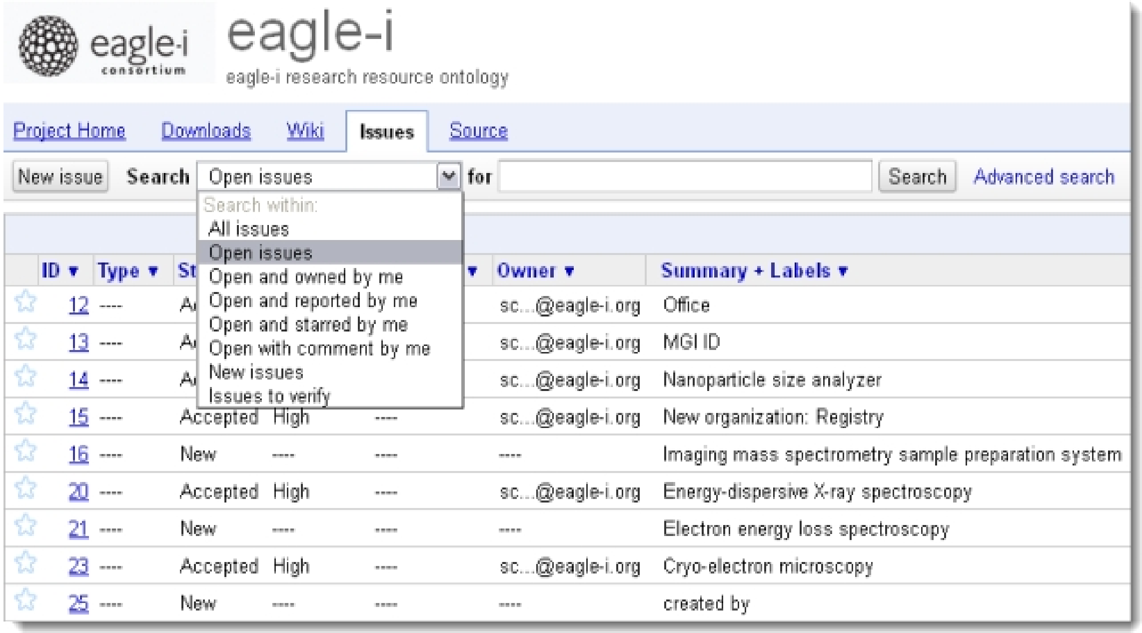
If there is no existing ticket, you can fill the term name in the **Requested Term** field instead. A member of the ontology team will issue a ticket for it in the tracker at a later time. Advanced users may choose to create their own issue tickets in the tracker directly, particularly in cases where the same term request will be applied to multiple records. **If you create your own issue ticket, you must still paste the URL into the Tracker URL field for every record where it should be applied in the SWEET.** This will allow the records to be updated when the term is added.

Note: A valid Google e-mail address is required to use the tracker.

Finding existing issues:

1. Go to the ERO Term Tracker site. Open the **Issues** tab.

2. Search or browse through the **Open issues** for the term you are requesting.



ID	Type	St			Owner	Summary + Labels
12	----	A			sc...@eagle-i.org	Office
13	----	A			sc...@eagle-i.org	MGI ID
14	----	A			sc...@eagle-i.org	Nanoparticle size analyzer
15	----	Accepted	High	----	sc...@eagle-i.org	New organization: Registry
16	----	New	----	----	----	Imaging mass spectrometry sample preparation system
20	----	Accepted	High	----	sc...@eagle-i.org	Energy-dispersive X-ray spectroscopy
21	----	New	----	----	----	Electron energy loss spectroscopy
23	----	Accepted	High	----	sc...@eagle-i.org	Cryo-electron microscopy
25	----	New	----	----	----	created by

3. Click on the **ID** to open any ticket. Copy the full URL into the term request form in the SWEET.

Creating new issues:

1. Create a "New Issue" on the ERO Term Tracker site.

2. Using the text template, provide as much information about the requested term as possible. An example can be found at the bottom of every new ticket.

3. In the **Additional Information** field, include the eagle-i Unique ID (or URI) of the eagle-i records for which the term is needed. The URI can be found in the Metadata section at the bottom of every record. If the term applies to multiple records, please include the URIs for each.

4. Submit the issue ticket.

5. Copy the URL of the issue ticket and paste it into the **Tracker URL** field in any eagle-i records where the term is needed.

Publishing Records with Open Term Requests

Resources with open term requests should be published if they otherwise meet all eagle-i standards.

1. If the requested term has been entered into in the Term Request form without an ERO Term Tracker ID, search the open tracker issues to see if an issue has already been created. If it has not, create the issue, and then copy and paste the ticket

URL into the Tracker URL field.

2. Make sure the closest parent to the term being requested has been selected from the ontology: for example, if the term *confocal microscope* was requested for an instrument type, the closest parent term would be *microscope*, not *instrument*.
3. Publish the record.

Filling Term Requests

New terms that have been added to the ontology are only available in the SWEET after a new release of the software, which occur 2-4 times a year. Typically, members of the central eagle-i curation and ontology teams will update records with outstanding term requests after a new release. To do so:

1. For all term requests with existing issue tickets, run a SPARQL query to find all current records that have open terms requests in the SWEET.
2. Search that list for the term or ticket ID of the term, open those records, and replace the current term in that field with the new term.
3. Use the Comments field to indicate that the term request was filled, along with your initials (for example, 'NV: Filled term request 8/15/2012').

Other users may also fill outstanding term requests if they come across them and notice that the requested term is now available in the ontology.

1. Select the requested term, replacing whatever parent term was originally entered in that field.
2. Delete the Issue ticket information from the Metadata section.
3. Use the Comments field to indicate that the term request was filled, along with your initials (for example, 'NV: Filled term request 8/15/2012').

SWEET General Annotation Guide

This section contains detailed annotation guidelines for entering and reviewing organization, people, and resource records in the eagle-i SWEET.

- Annotation Guidelines for Organizations and People
- Annotation Guidelines for Resources

Standardization and Grammar

The following general standards should be used for all annotations:

- **Capitalization** - Capitalize the first letter of all resource names, unless the official name begins with lowercase, such as "eagle-i" or the software "jMURI". When the resource name contains multiple words, either Sentence Case or Title Case can be used, unless the official name contains specific capitalization, such as company names and publications. The first and last names of all people should be capitalized unless they contain a lowercase prefix.
- **Articles** - Resource names should never begin with “the,” “a” or “an”. The sole exception is publication titles that begin with an article. These should be quoted exactly in the resource name.
- **Quoted material** - Some fields, most often resource descriptions, may contain quoted material from external sources. eagle-i permits publication of quoted material, provided:
  - All quoted text is clearly identified using quotation marks.
  - All quoted material is accompanied by a source URL in the Web site(s) field. If the source is not a web page, then it should be cited using APA Style (http://www.apastyle.org/) underneath the quoted material.
- **Punctuation** - Resource descriptions should always be complete sentences beginning with a capitalized first word and ending with a period. All other fields that contain complete sentences should be properly punctuated. If a field is filled with a sentence fragment, curators should convert this to a full sentence wherever it makes sense to do so, but may leave one or two word fragments as is.
- **Abbreviations** - If there is an abbreviation for a resource name, both the spelled out version and the abbreviation should be included somewhere in the record for search purposes. In general, the abbreviation should be spelled out in the resource name field and the abbreviation itself should go in the Alternate name field, unless the abbreviation is so much more common that seeing the spelled out version in the main name field would cause confusion for users. Any subsequent usage of the name can use the abbreviation for brevity.
- **Numbers** - Per the Microsoft Manual of Style, "Use numerals for 10 and greater. Spell out zero through nine if the number does not precede a unit of measure or is not used as input. For rounds numbers of 1 million or more, use a numeral plus the word, even if the numeral is less than 10."

- **Super/subscripts** - May be represented using either brackets or HTML:
    - Superscripts may be indicated using square brackets around the text. For example, for allele names: $agil^{2J}$ would be entered as agil[2J].
    - Both super- and subscripts can also be represented using the HTML tags <sup> and <sub>. In particular, these tags should be used for resources for which the addition of extra brackets might be misleading. For example: the chemical compound $[^{11}C]CH_3I$ (methyl iodide) would be entered as [¹¹C]CH₃I. In these cases, in order to ensure the resource will still come up in search results, a version of the name without the HTML tags should also be entered in the Additional Name field.
- **Smart quotes** - The system cannot currently support smart quotes. Be sure to replace these when copying and pasting from outside sources.
- **Empty fields** - If a field does not apply, it should be left blank, which means the field will not display. Entering “none” or "n/a" unnecessarily clutters the record.
- **Foreign languages** - If a resource’s proper name is in a language other than English:
    - The Alternate Name field should contain the non-English version of the name.
    - If the resource is a document in another language, or if the record includes a link to a website that is not in English, this should be noted in the resource.
    - The main resource name field should contain the English translation of the name.

External Facilitators

The **External facilitator** field can be used to link to any third-party service that facilitates payment for or access to the lab's services or resources. This link should always be to the corresponding page on the facilitator's website for that lab or resource, and NOT simply to the main page of the facilitator website.

eagle-i currently supports buttons for certain facilitators, using the codes listed below:

External Facilitator	HTML Code
Addgene	<img src=http://eagle-i.net/images/addgene-button-large.png alt='Order from Addgene'>
Coriell Institute	<img src=http://eagle-i.net/images/coriell-button-large.png alt='Order from Coriell'>
Developmental Stud-	<img src=http://eagle-i.net/images/dshb-button-

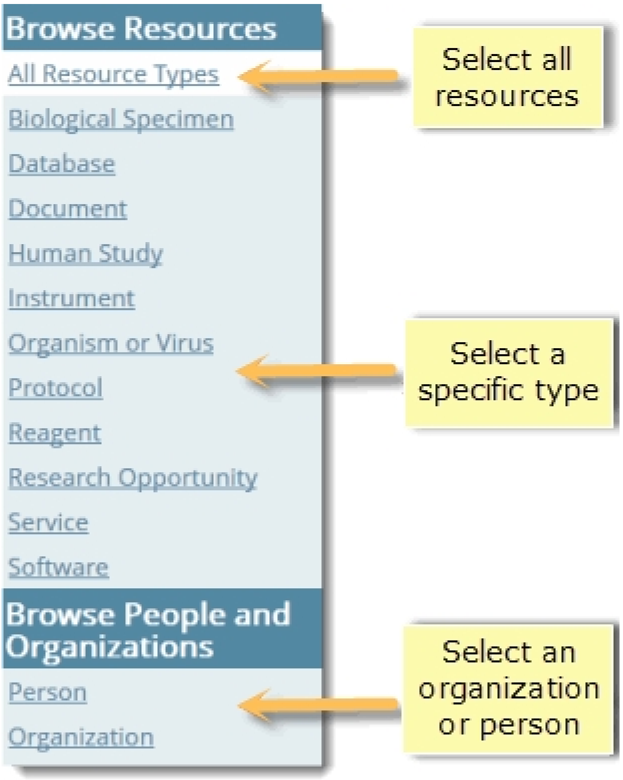
ies Hybridoma Bank	large.png alt='Order from DHSB'>
Jackson Laboratory	<img src=http://eagle-i.net/images/jacksonlabs-button-large.png alt='Order from Jackson Laboratory'>
New York Stem Cell Foundation	<img src=http://eagle-i.net/images/nyscf-button-large.png alt='Order from NYSCF'>
Science Exchange	<img src=http://eagle-i.net/images/se-button-large.png alt='Order from Science Exchange'> Services can be facilitated through Science Exchange
WiCell Research Institute	<img src=http://eagle-i.net/images/wicell-button-large.png alt='Order from WiCell'>

To insert a button into the Exchange facilitator field:

1. Locate the specific URL for the resource to which you wish to link. In most cases, this should contain some sort of ID for the resource. For example: *http://dshb.biology.uiowa.edu/CD31-PECAM-1.*
2. Find the appropriate exchange facilitator in the table above, and copy the text in the **HTML Code** column.
3. Paste the text into the **Exchange facilitator** field in the eagle-i record for that resource.
4. Replace the red **RESOURCE URL** text with the URL from step one.

Annotation Guidelines for Organizations and People

At a high level, *organizations* and *people* are considered resources in the eagle-i system, and as such, they are cataloged with their own individual records that must be sent to curation and published like any other resource. This categorization is confusing and counter-intuitive for many users, so for practical purposes, they are displayed under a separate heading in the Browse People & Resources in My Institution area of the Workbench.



Select all resources

Select a specific type

Select an organization or person

They are also treated separately in terms of usage and content metrics.

E-mail and Privacy

eagle-i currently hides information related to physical addresses, e-mail addresses and phone numbers of all organizations and people, in response to the privacy concerns of certain researchers (in particular, research laboratories that work with animals). Although this information can and should be entered in the SWEET, it will not display in the search application. The affected fields are:

- E-mail
- Lab delivery address

- Mailing address
- Phone number

In some cases, laboratories may also request that existing person records be removed from search to keep even their names from displaying. Those person records should be put into a Draft or Curation state with an explanation added in the **Comments** field. If the removed person’s email was the sole contact email for that organization, either:

1. Add a generic organization email to the organization record.

- or -

2. Migrate the personal email address of the person to the owning organization email field. Because eagle-i uses an anonymous contact form in the search application, the actual email address will remain hidden, but users will still be able to contact the person.

Note: if a record is being removed from public view due to privacy concerns, it should **not** be Withdrawn, as a public dissemination page will still exist, and will be visible to anyone who has a direct link to it. Moving the record to **Draft** or **Curation** will ensure the resource has been completely removed from public view.

Organizations Information and Workflow

Organizations include laboratories and other resource providers, manufacturers, and affiliates. Note that these are not mutually exclusive categories; it is possible for an organization to be listed as an affiliate of or parent organization to other resource-providing organizations while also providing resources itself. Corporate manufacturers should be classified as private companies and are the only type of records that cannot provide resources.

Using the eagle-i Workbench, you can add new organizations or browse existing organization records. From the Workbench, you can select a single organization or you can choose to browse through a list of all of the organizations at your institution.

Browsing / Viewing Organization Records

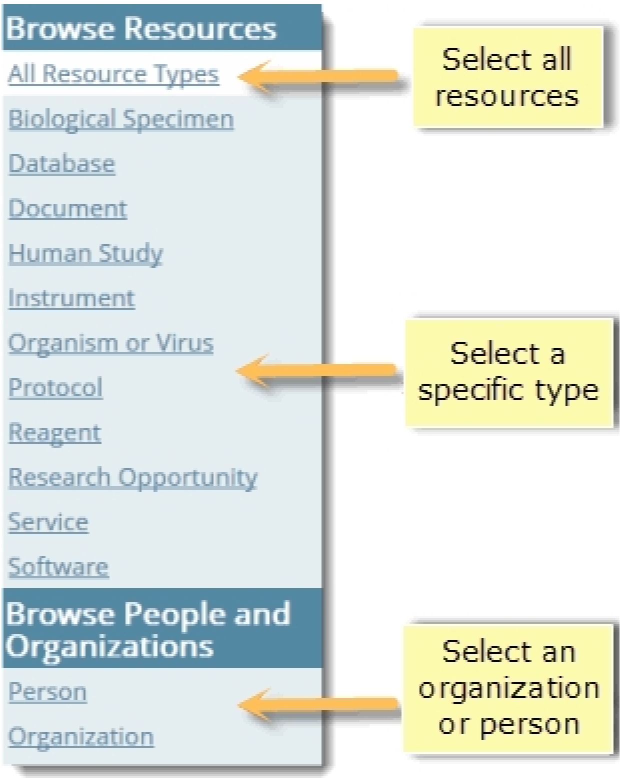
There are several ways to access organization records.

To view organizational records:

- To go directly to a particular resource providing organization, open the **Workbench** and select the organization by name from **Work With My Organizations**. Private Companies are the only type that are excluded. Once you open a record, details about the selected organization are displayed in the center of the page and links to resources associated with that organization are displayed in the Resource Types side bar on the left side of the page.

- or -

- To browse all organizations, including private companies and all potential resource-providing organizations in an institution, click **Browse People and Resources in My Institution**, then *Organization*. Note that inclusion in this list does not guarantee an organization currently contains any resources, merely that it has the ability to do so. From here, you can sort by status to easily find records in curation and/or records that have been locked.



Use the sidebar to the left of each organization record to navigate through the resources associated with that organization.

Creating Organization Records

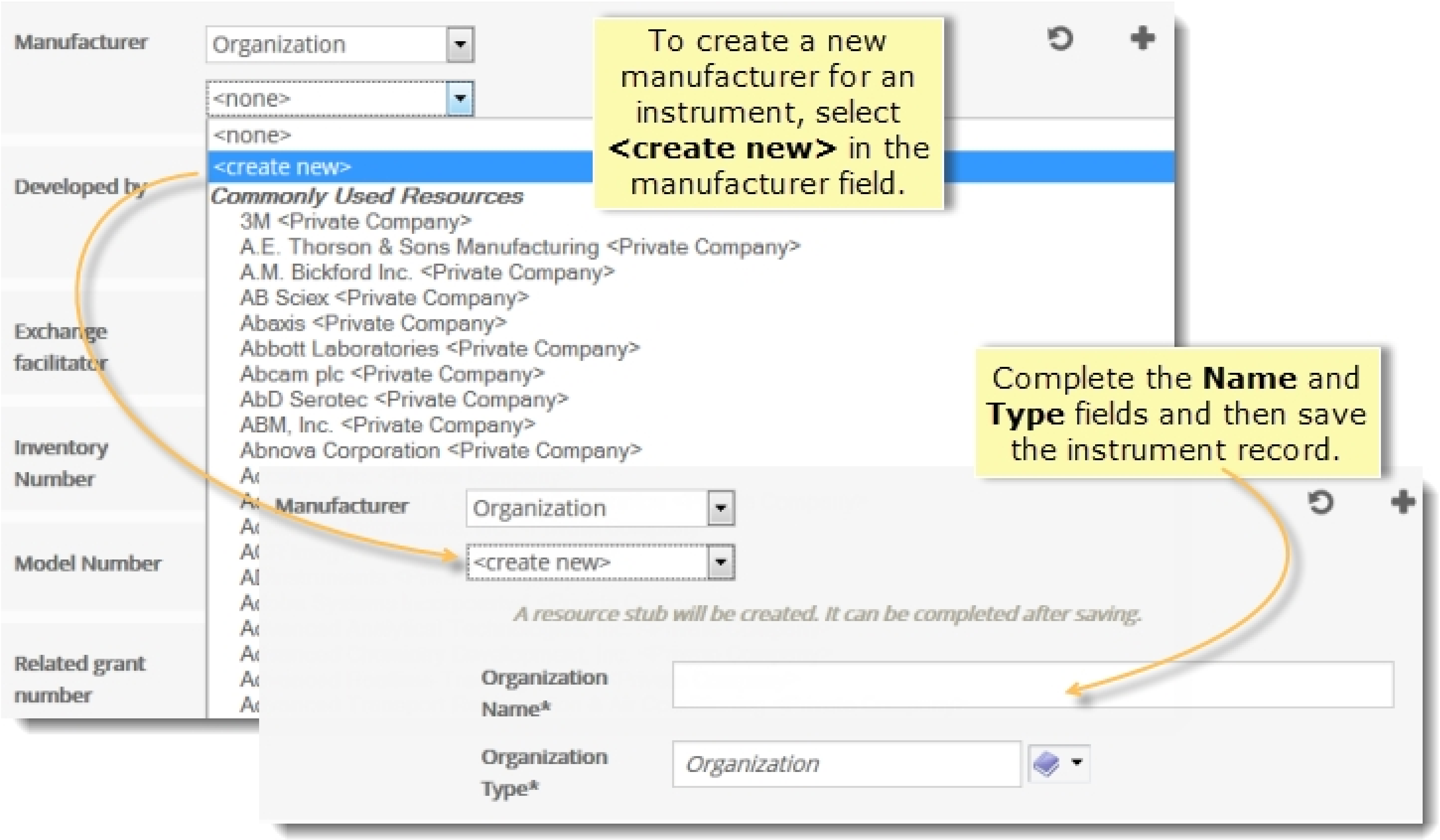
Watch this video tutorial for a demonstration of how to create organization records in the SWEET.

To create an organization record:

- From the Workbench, click **Create an Organization**. Selecting an organization sub-type determines which additional fields will populate the record. Refer to the Organization Field Annotation table for guidelines for entering data.

- or -

- From within another record, use **<create new>** from either the affiliation or manufacturer fields. Organization records that are created from within another record are considered unfinished stub records until they have been edited and saved.



To create a new manufacturer for an instrument, select **<create new>** in the manufacturer field.

Complete the **Name** and **Type** fields and then save the instrument record.

A resource stub will be created. It can be completed after saving.

Next steps: After you save the organization you can:

- Add resources. After the organization record has been added, you can associate resources to this organization. You do not need to wait for the record to be published; as soon as the organization record has been added, resources can be added.

- Send to curation. Use this option when you are ready for the information to be reviewed and published.

- Share the record. Use this option if you want other users at your institution to edit this organization.

Publishing Organization Records

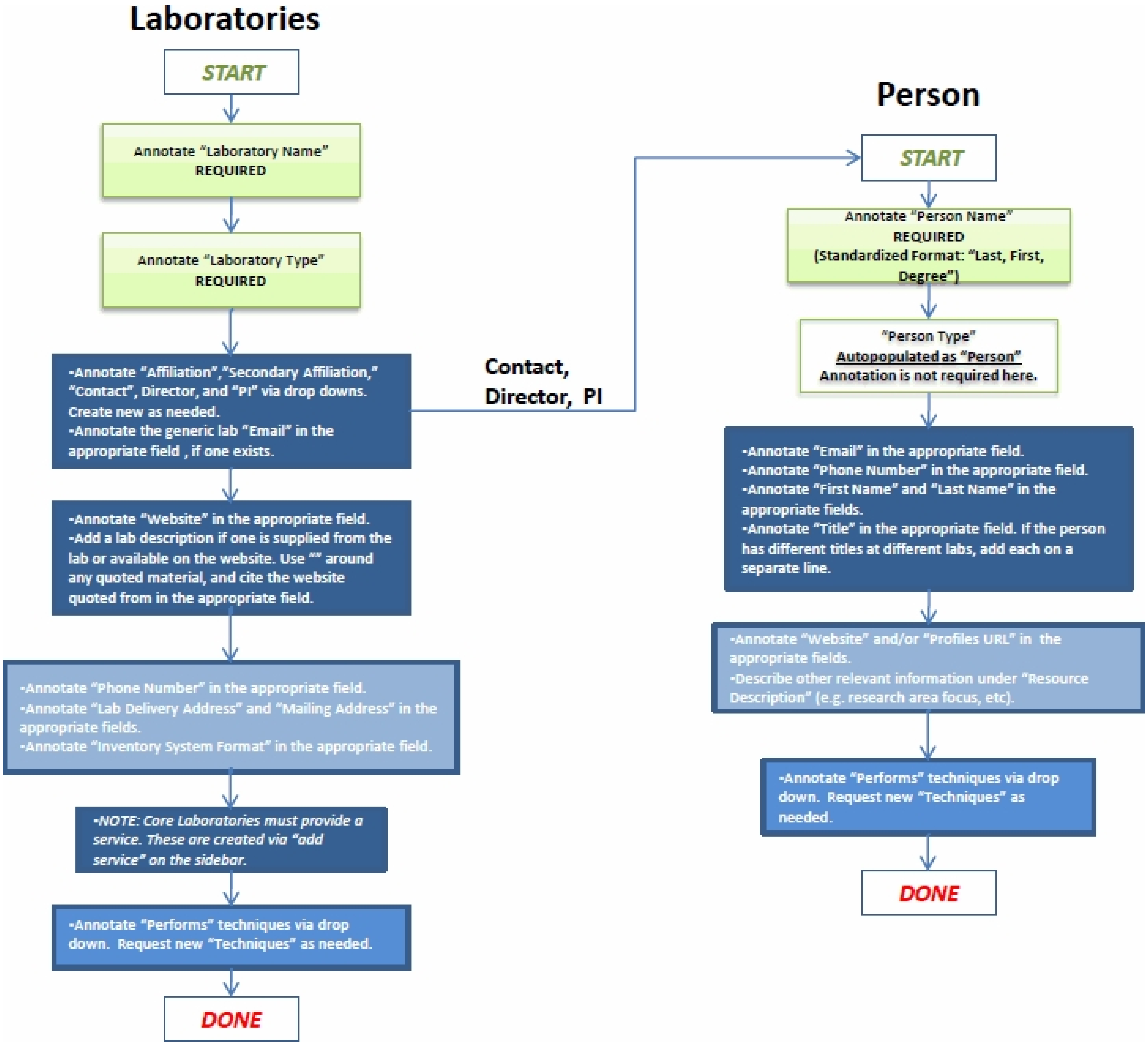
All person records associated with an organization or resource should be published at the same time as the organization record whenever possible. If, for some reason, not all associated person records are ready to be published with the organization record, you should ensure that *there is at least one published contact e-mail address for the organization*. This e-mail address is used when a search user clicks the **Send Message to Resource Contact** button.

See E-mail and Privacy for more information.

About Core Facilities

Core Facilities are a sub-type of organization. The eagle-i ontology defines a Core Facility as a type of laboratory that has the mission of providing services. Although many of the resources offered by Core Facilities are not strictly invisible, they are still extremely valuable, and exposure in eagle-i means that they can be easily discovered by a wider audience—either through directly searching, or through links to other resources they search for (microscopes, for instance).

By definition, every Core Facility must provide at least one service, even if that service is merely access to equipment or facilities. A service is a planned process carried out by an organization with the objective of performing a technique, providing training, providing storage of data or physical resources, or providing access to instruments for another person or organization. See the Service annotation guidelines for more details.



Laboratories

START

Annotate "Laboratory Name" REQUIRED

Annotate "Laboratory Type" REQUIRED

-Annotate "Affiliation","Secondary Affiliation," "Contact", Director, and "PI" via drop downs. Create new as needed.
-Annotate the generic lab "Email" in the appropriate field , if one exists.

-Annotate "Website" in the appropriate field.
-Add a lab description if one is supplied from the lab or available on the website. Use "" around any quoted material, and cite the website quoted from in the appropriate field.

-Annotate "Phone Number" in the appropriate field.
-Annotate "Lab Delivery Address" and "Mailing Address" in the appropriate fields.
-Annotate "Inventory System Format" in the appropriate field.

-NOTE: Core Laboratories must provide a service. These are created via "add service" on the sidebar.

-Annotate "Performs" techniques via drop down. Request new "Techniques" as needed.

DONE

Contact, Director, PI

Person

START

Annotate "Person Name" REQUIRED (Standardized Format: "Last, First, Degree")

"Person Type" Autopopulated as "Person" Annotation is not required here.

-Annotate "Email" in the appropriate field.
-Annotate "Phone Number" in the appropriate field.
-Annotate "First Name" and "Last Name" in the appropriate fields.
-Annotate "Title" in the appropriate field. If the person has different titles at different labs, add each on a separate line.

-Annotate "Website" and/or "Profiles URL" in the appropriate fields.
-Describe other relevant information under "Resource Description" (e.g. research area focus, etc).

-Annotate "Performs" techniques via drop down. Request new "Techniques" as needed.

DONE

Organization Records Field Annotation

Note: NR indicates a non-repeatable field.

Not all types of organization records contain all of the fields listed below, as the fields differ depending on the sub-type chosen. Laboratories are the main type of organization record in the SWEET, and the means by which the majority of eagle-i resources are organized and most easily accessed. They are the only type to contain all of the fields listed. Therefore, it is especially important to make sure the record is typed correctly as a Laboratory or Core Laboratory before annotating or curating it.

Field	Description	Req.	NR
Organization Name	Enter the full organization name. If there are multiple organizations with the same name, disambiguate by adding affiliation information within the title. Example: "Flow Cytometry Core Laboratory (BWH)" vs "Flow Cytometry Core Laboratory (BIDMC)". Note: it is especially critical to ensure that all organizations added using ETL have unique names prior to beginning the process to prevent data merging issues.	Yes	✓
Organization Type	Select the most appropriate type for the organization. For research laboratories, choose the type "Laboratory". Note: Not all labs that provide services are automatically considered core labs. But all published core labs should have at least one published service record.	Yes	✓
Organization Description	Provide a brief overview of the organization. Can include a mission statement, short description of the research focus, services offered, or any other information that describes the organization that is not captured in any of the other fields.		
Organization Additional Name	Any alternate names for the organization. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Contact	Link to the primary contact person for the organization. The same person may also be listed under the **Director** and/or **PI** fields, if appropriate. If multiple contacts are listed, only one will be used for the anonymous contact form in search. To specify a single contact, either move the other contacts to the **Other Members** field or repeat the address of the designated primary contact in the **Email** field. See Contact Emails and Privacy Concerns for more information. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Director	Link to the director of the organization.		
Other members	Link to any additional people associated with this organization. If only one person is listed, or if a person is already listed as the organization **Contact**, **Director** or **PI**, then they should **not** be listed in this field.		
PI	Link to the Principal Investigator (PI) for the organization. This field should be filled separately, even if the **Contact** and the Principal Investigator are the same person. Use the **PI (co-Investigator)** field to note any co- or secondary PIs, if applicable.		
PI (co-Investigator)	Link to any co-Principle Investigators (co- PIs) for the organization. Should be filled separately, even if the **Contact** and co-PI is the same person. This field is meant to distinguish the primary PI from any co- or secondary PIs, and should not be used unless there is also a person listed in the **PI** field.		
Email	Generic contact e-mail address for the organization. This information will not be visible in eagle-i search.		

	Note: It is only necessary to fill this in if there is a generic e-mail for the lab itself, such as: *biomedicallab@harvard.edu*. Personal e-mails belonging to any people associated with the organization should be listed on the records of those individual people, and do not need to be repeated in this field. However, if there are multiple contact people linked to an organization, adding only the email of the primary contact to this field will designate it as the address to be used for the search anonymous contact form.		
Lab Delivery Address	Enter a physical location address for the delivery of packages. This information will not be visible in eagle-i search. Delivery address and mailing address may be identical. Use the following format: Biomedical Lab Harvard University 123 Cambridge Street Cambridge, MA 02138		
Mailing Address	Enter a central mailing address for correspondence. This information will not be visible in eagle-i search. Use same format as **Lab Delivery Address**.		
Phone Number	Enter a contact phone number for the organization. This information will not be visible in eagle-i search. Use the format: (xxx) xxx-xxxx Ext. xxx.		
Affiliation	Link to any the primary institutional and consortial affiliations or certifying organizations. For generic departmental affiliates, format the label as follows: Department of [department name], [institution] (ex. Department of Biology, University of Alaska). Note: the organization that owns the eagle-i repository in which the record is housed (for example: Dartmouth College) does not need to be created as a separate affiliate; the logo for that organization will automatically display to the right of the search record.		
Secondary Affiliation	Link to any secondary institutional and consortial affiliations or certifying organizations.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the lab's services or resources.		
Inventory System Format	Enter the format of the current method used to inventory lab resources, such as LIMS, Excel file, index card file, FileMaker database, 3-ring binder, and so forth. Only for Laboratory and Core Laboratory organization types.		
Performs Technique	Select any techniques used by the organization. Add as many as are applicable. Only for Laboratory and Core Laboratory organization types.		
Website(s)	Enter the URLs of any related external websites, e.g. any separate pages about the organization. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Guidelines for Technology Transfer Offices

Many institutions have an Office of Technology Transfer (TTO) that protects the institution’s intellectual property and helps facilitate potential commercial opportunities developed from research done at that institution.

eagle-i collects information about resources (usually services) provided by these TTOs, also referred to as technology transfer offices. However, these resources tend to be a little different from those typically offered by laboratories. For instance, while tech transfer offices often provide access to physical resources via a license agreement, they do not own the actual resources themselves. Therefore, some additional guidelines apply:

- **Naming conventions** — Like departments, many institutions will have similarly named tech transfer offices. Therefore, each should include the name of the institution to distinguish them in search results, for example, *Technology Transfer Office, Montana State University*
- **General services** — The services offered by tech transfer offices are usually support or access services. Many offices at different institutions will offer the same basic services; the differences will be in the specific research available for commercialization at each institution. To maintain consistency, use the search application to see how similar services have been annotated in the past. Generic services typically offered include:
    - Technology licensing—access service
    - Invention reporting—support service
    - Copyright registration—support service
    - Confidentiality agreements—support service
    - Negotiation of various agreements such as material transfer, facilities/equipment use, non-disclosure, and so on. Generally these are support services, but may be classified as access services depending on the specifics of the type of agreement.
- **Granularity of data collected —** Although more detail is usually preferable, due to the legal sensitivity of many of these resources, different tech transfer offices may wish to limit the exposure on eagle-i to the specific licensing opportunities available at their institutions. Therefore, the annotation guidelines for these types of resources are flexible:
    - A generic "umbrella" licensing service record with a link to the office's website and/or contact information for more detail is sufficient if the office does not wish to share any more granular data.
    - If information about specific licensing opportunities is available, then it should be entered in the resource description along with whatever keywords might be useful for calling up the record in search.
    - If there are too many licensing opportunities to fit in one record, they should be reorganized them into broad categories, if possible. It is not best practice to create individual records for every commercial opportunity at an institution.

People Records Introduction and Workflow

People can be contacts, directors, PIs, manufacturers, developers, and authors in the eagle-i system. Information about each person is captured in a separate record, which can be linked to multiple organizations or resources.

Browsing / Viewing Person Records

Person records can be accessed either by navigating to **Browse People & Resources in My Institution** from the Workbench, or by clicking on the name of the person from within any record from which they are linked. If no specific contact is manually assigned to a resource, the system will infer that the generic contact for the organization is that resource's contact.

Creating Person Records

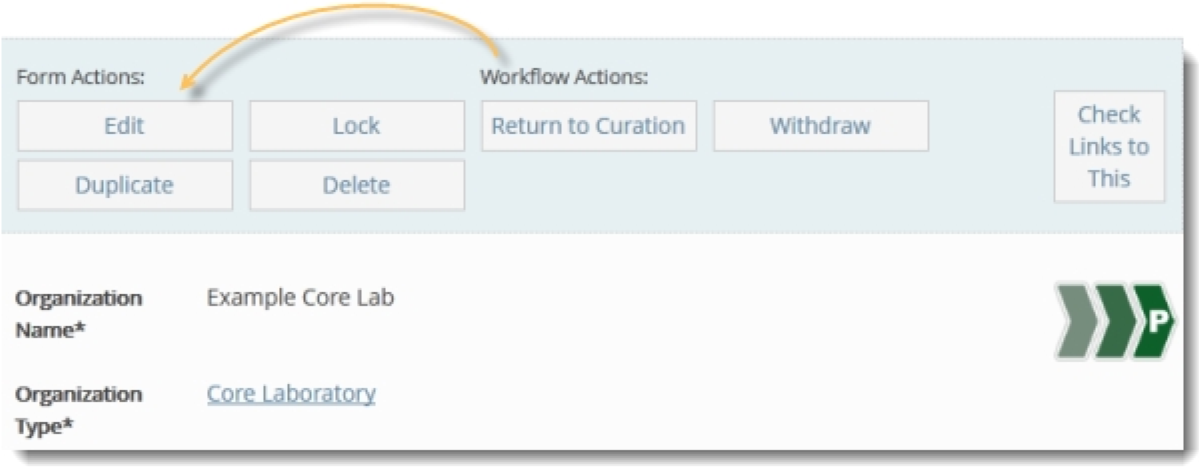
The only way to create new person records is using **<create new>** from within another existing record.

Before adding a person record, you should ensure that a record for that person does not already exist. To check for duplicates, you can either look at the full list of people under **Browse People & Resources in My Institution > Person** or browse through the list of people in the field where you are adding the person.

Remember to check for records beginning with both the first and last names of the person, as sometimes people are entered with both formats in error. If duplicates are found, they will need to be merged. See Merging Records.

To create a person record:

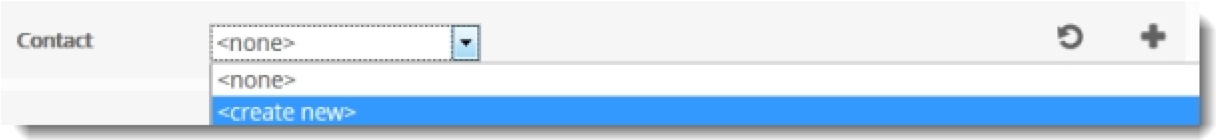
1. Open an existing record and select Edit.



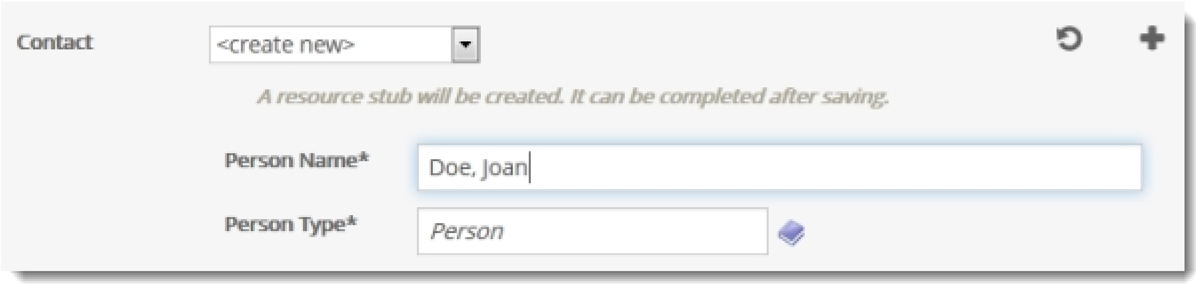
Organization Name* Example Core Lab

Organization Type* Core Laboratory

2. **<create new>** is available from any field that links to a person, including: **Contact**, **Director**, **PI**, **Co-PI**, **Other members**, **Manufacturer**, **Developer**, and **Author**. Before adding a new person, open the drop-down list to show all existing people records at your institution. If you still don't see the person, click **<create new>**.



3. Type the person’s name in the format: last name, first name.



Contact: <create new>

A resource stub will be created. It can be completed after saving.

Person Name*: Doe, Joan

Person Type*: *Person*

4. The new record is added as an unfinished resource stub and will appear in the **View My Resource Stubs** list, found off the main **Workbench**. See the Resource Stubs section for more information.

Publishing Person Records

All person records associated with a resource owning organization should be published at the same time as the organization record whenever possible.

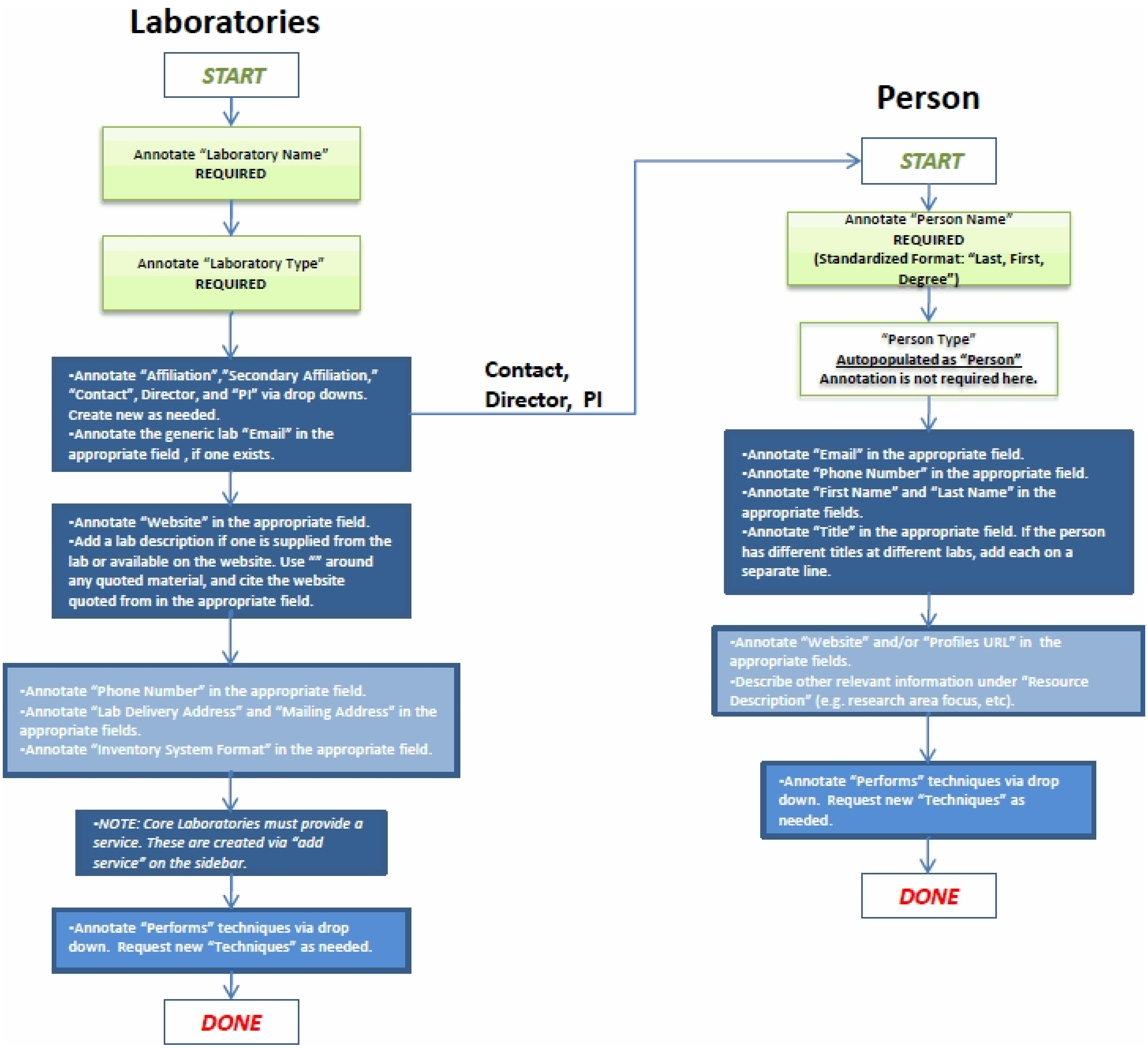
If, for some reason, not all associated person records are ready to be published with the organization or resource record, you should ensure that *there is at least one published contact e-mail address for the resource*. This email address can either be a generic organization email used in the organization record itself, or a personal email for one of the people associated with the organization, and will be used when a search user clicks the **Send Message to Resource Contact** button for any of the organization's resources.

See Email and Privacy for more information.

Withdrawing Person Records

Person records are often withdrawn due to organization staffing changes. Before withdrawing a person record, use the Check Links to This button at the top of the record to make sure the person is not associated with any other published organizations at the institution. If so, then the record should remain published, but any references to the withdrawn organization should be updated.

Note: When withdrawing person records associated with published resource owning organizations, you should ensure that at least one valid email address for the organization is still published, either in the organization record itself or in another published person associated with the organization. If no other valid email remains, contact the lab.



Laboratories

START

Annotate "Laboratory Name"
REQUIRED

Annotate "Laboratory Type"
REQUIRED

-Annotate "Affiliation","Secondary Affiliation," "Contact", Director, and "PI" via drop downs. Create new as needed.
-Annotate the generic lab "Email" in the appropriate field , if one exists.

-Annotate "Website" in the appropriate field.
-Add a lab description if one is supplied from the lab or available on the website. Use "" around any quoted material, and cite the website quoted from in the appropriate field.

-Annotate "Phone Number" in the appropriate field.
-Annotate "Lab Delivery Address" and "Mailing Address" in the appropriate fields.
-Annotate "Inventory System Format" in the appropriate field.

-*NOTE: Core Laboratories must provide a service. These are created via "add service" on the sidebar.*

-Annotate "Performs" techniques via drop down. Request new "Techniques" as needed.

DONE

Contact, Director, PI

Person

START

Annotate "Person Name"
REQUIRED
(Standardized Format: "Last, First, Degree")

"Person Type"
Autopopulated as "Person"
Annotation is not required here.

-Annotate "Email" in the appropriate field.
-Annotate "Phone Number" in the appropriate field.
-Annotate "First Name" and "Last Name" in the appropriate fields.
-Annotate "Title" in the appropriate field. If the person has different titles at different labs, add each on a separate line.

-Annotate "Website" and/or "Profiles URL" in the appropriate fields.
-Describe other relevant information under "Resource Description" (e.g. research area focus, etc).

-Annotate "Performs" techniques via drop down. Request new "Techniques" as needed.

DONE

People Records Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Person Name	Enter in the format: Last name, First name, Degree . (Example: "Smith, John, Ph.D.") List multiple degrees separated by commas, such as: "M.D., Ph.D." Note: if a person is deceased but should still be kept as an active record (for example, in the case of a developer of a particular resource, or author of a paper) this may be indicated by adding "deceased" in parentheses after their name.	**Yes**	✓
Person Type	Pre-filled. No action necessary.	**Yes**	✓
Person Description	Enter any relevant information not captured in any of the other fields. Can include a description of the person's research or professional interests.		
Person Additional Name	Enter any nicknames or additional names for the person here, if requested by the person.		
Email	Enter the preferred contact email for the person. This information will not be visible in eagle-i search. Note: more than one email can be entered, but the system will use only one (selected randomly) for the anonymous contact form in search. Additional email addresses that should not be used as the preferred contact email can be recorded in the **Comments** field instead.		
Mailing address	Mailing address for the person, if applicable. This information will not be visible in eagle-i search. Format as: Biomedical Lab Harvard University PO Box 5678 123 Cambridge Street Cambridge, MA 02138		
Phone Number	Format as (xxx) xxx-xxxx Ext. xxx. This information will not be visible in eagle-i search.		
First Name	Enter the person’s first name. Can include middle names or initials, if applicable.		
Last Name	Enter the person's last name.		
Performs Technique	Select any techniques or expertise for which the person is a contact.		
Profiles URL	Enter the profiles page URL for the person, if one exists. If no profiles page is available, this field should be left blank. This field is specific to institutions that use the open source Profiles Research Networking Software (http://profiles.catalyst.harvard.edu/) developed by Harvard University.		
Title	Enter any professional titles (e.g. Director, Professor, Manager). Each title should be entered in a separate line and should be as specific as possible (e.g. Director, Flow Cytometry Core or Professor of Bioinformatics). If one person is the director of multiple labs, then each should be listed as a distinct title. Note: degree information belongs in the name field rather than the title field.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or university pages for the person, or their personal website or CV. Any pages using the Profiles software should be listed in the **Profiles URL** field. All URLs should include the full address, such as: http://www.eagle-i.net.		

Comments	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Annotation Guidelines for Resource Records

Use the following guidelines when entering or reviewing information about research resources:

- Biological Specimens
- Databases
- Human Studies
- Instruments
- Organisms and Viruses
- Protocols and Documents
- Reagents
- Research Opportunities
- Services
- Software

What is invisible?

eagle-i focuses on resources that are invisible, rare, or unique for their area.

Resource creators and/or providers (typically researchers, such as postdoctoral fellows, graduate students, core facility managers, etc.) may be well aware of what resources they have and regularly use, but fellow colleagues or other researchers often times are not. As a consequence, researchers may waste valuable time and money recreating or purchasing an animal model, DNA construct, or key piece of equipment is already available in a lab nearby. Although some resources (typically unpublished ones) are invisible for a reason, many can and should be shared once the research has been published in a journal. Sharing information about what researchers have opens up the possibility of forming new collaborations to help take their research in new and exciting directions. Of course, it remains up to the resource owner to determine what and how a resource should be shared.

In some cases, resources that might be ubiquitous at one institution will be extremely valuable to a smaller or more rural institution where those resources are scarce. Those resources may be cataloged in eagle-i, but should include a clear resource description that indicates how or why they are important.

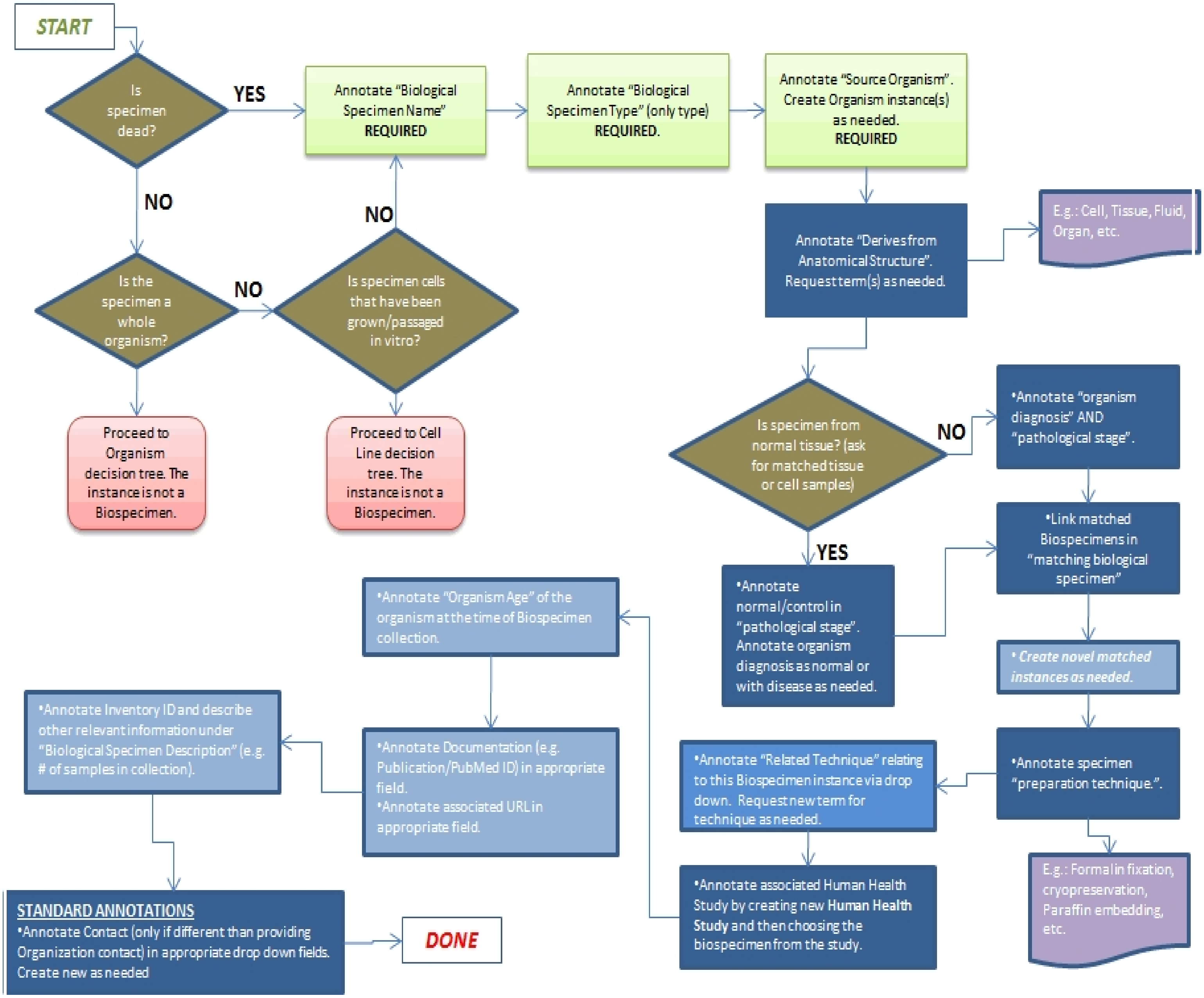
In general, however, eagle-i does not collect information about: refrigerators, Xerox machines, telephone systems, and basic computers and cameras, kit instructions as protocols, and common chemical reagents such as Sodium Chloride (NaCl).

Biological Specimens Introduction and Workflow

A biospecimen is a portion or quantity of a biological material for use in testing, examination, or study; it can be an individual animal, part of an organism, or something derived from an organism or organisms.

Sometimes people confuse biological specimens with organisms: for example, insect specimens at a museum would be considered biological specimens, not organisms. But trees in an arboretum would be considered organisms. Currently, eagle-i distinguishes these two based first on whether or not the entity is alive. If it is alive, it is not a biological specimen. If it is dead, the most critical information is what species and what anatomical structure the specimen is derived from. If the specimen is live cells that have been passaged in vitro, then it should be annotated as a cell line (or primary culture).

Biological Specimens



Biospecimen Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Biological Specimen Name	Enter a brief by descriptive name for the biological specimen. For example: "Pathological tissue: Breast tissue displaying fibroadenomaor" or "Normal/control pathological tissue: Control breast tissue."	Yes	✓
Biological Specimen Type	Pre-filled. No action necessary.	Yes	✓
Biological Specimen Description	Enter any information that describes the biospecimen but is not captured in any of the other fields. **High value information:** Whether the tissue is normal or diseased; if there is a diseased state and what that is; the nature of any matching specimens. Even though the two specimens can be linked (see below) it may be necessary to further describe the nature of the match: same patient disease vs. normal tissue, siblings, etc. If a description isn't included, then the record creator or a domain expert should be consulted before publishing.		
Biological Specimen Additional Name	Enter any alternate names for the biospecimen. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Diagnosis Description	Enter a description of the clinical diagnosis made on the biological specimen sampled, or the organism from which it was derived at the time of specimen collection.		
Pathological Stage	Enter the stage that has been assigned to the biological specimen, such as: cancer stage, degeneration stage, normal or control.		
Source Organism Type	The species or lab-generated strain of organism from which the specimen was derived. In most cases, this will be a generic organism. See Organisms guidelines for more details. In rare cases, more than one organism can be selected. For example: blood samples or other specimens from two different organisms mixed together. If the same type of specimen is available from multiple organisms, then a separate record should be created for each. Note: this field should only be filled out if the specimen was **not** derived from a human subject. (See the **Source Human Subject** field below.)	Yes	
Organism age at collection	Enter the age of the organism from which the specimen was collected. Can be: days, months, years.		
Source Anatomical Structure	Select the anatomical structure from which the specimen was derived, e.g. Cell, Tissue, Fluid, Organ, etc.		
Source Human Sub-	Link to the individual human subject from which the specimen was derived.		

ject			
Source Specimen	Link to any specimens from which this one was derived.		
Related disease	Select any diseases or conditions indicated by the biological specimen diagnosis or other diagnoses on the organism from which the specimen was derived.		
Related Human Study	Link to any human studies related to the biological specimen. For example: a study in which the specimen was generated or investigated.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the biospecimen.		
Funded by	Link to any organizations that funded the work that produced the specimen.		
Inventory Number	The inventory identifier for the specimen. Can be the internal laboratory ID or a commercial catalog number. External inventory numbers should be formatted with the name of the company followed by a colon and the number, e.g. Cell signaling catalog number: 7634.		
Matching biological specimen	Link to any matched biospecimens, if applicable. A matched pair of biological specimens usually includes a control specimen that is either from a non-affected individual or tissue.		
Related grant number	Grant number for the funding that contributed to the development of the biospecimen. For example: 'U24 RR 029825'.		
Related NCBI Record	A complete URL for any NCBI database record or dataset that was generated about this resource. For example: gene expression analysis data in the Gene Expression Omnibus, genome variation data in dbVar, or sequence read data in the Sequence Read Archive.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the specimen.		
Related Technique	Choose "Biospecimen preparation" from the drop-down to indicate the method of tissue preparation, such as: Formalin fixation, cryopreservation, Paraffin embedding, etc. Choose "Technique" to indicate the method related to or performed using the biospecimen (i.e. techniques for which you can use the specimen or that describe how it was used as a whole). Do not include any techniques used to generate the specimen, such as histological preparation techniques.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Database Introduction and Workflow

A database is an organized collection of data, today typically in digital form. Although databases are described using many of the same fields as pieces of software, they should be categorized separately.

Databases Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Database Name	Enter the most common name for the database.	Yes	✓
Database Type	Pre-filled. No action necessary.	Yes	✓
Database Description	Enter any information that describes the database but is not captured in any of the other fields, such as a brief description of the database’s function.		
Database Additional Name	Enter any alternate names for the database. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Used by	Link to the record of the owning organization that uses the database. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Related Technique	Select any methods related to or performed using the database(in other words, techniques for which you can use the resource or that describe how it was used as a whole). Add as many techniques as are applicable.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Data Input	Describes the type of data contained in the database.		
Topic	Select any organisms, biological processes, or diseases that are the subject matter of the database. If choosing an organism, in most cases, this will be a generic organism. See Organisms guidelines for more details.		
Manufacturer	Link to the organization that created the database, which in many cases may be the owning organization. May also be a person, but only if the person mass produces the database. Use the **Developed by** field for databases not designed for mass distribution.		
Coded in	Select the programming language in which the database is coded.		
Developed by	Any people or organizations who designed or helped develop the database for limited or internal use only. If the database was developed for commercial mass distribution, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the database.		
Operating System	Enter any operating systems with which the database is compatible. Group multiple ver-		

	sions of the same operating system on the same line, for example, "Microsoft Windows XP, Vista, and 7" but use the + function to create a separate line for each operating system if more than one applies to the same piece of software: ▪ Microsoft Windows XP, Vista, and 7 ▪ Mac OS ▪ Linux ▪ Unix The names of common operating systems should be consistently formatted. Use "Microsoft Windows" for all Microsoft operating systems, never just Microsoft or Windows. Use "Mac OS" or "Mac OS X" for Apple operating systems; assume Mac OS as the default if OS X isn't specified.		
Related grant number	Grant number for the funding that contributed to the development of the database. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the database.		
Related Software	Link to any software that is used to operate the database or specifically analyze the data output from the database.		
Version	The version designation associated with the database. This is often a numeral followed by a decimal and another numeral, for example: 2.1.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Genetic Alterations Introduction and Workflow

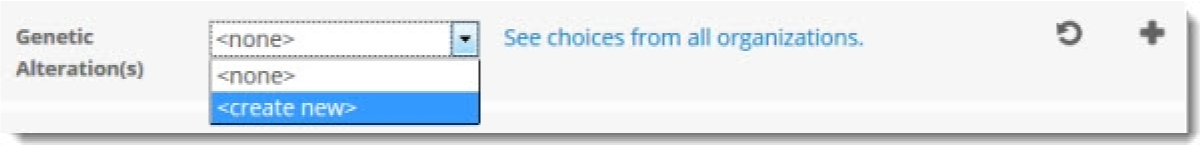
Genetic alteration records describe any variation(s) in sequence carried by a macromolecule or the genome of an organism or cell line that deviates from a canonical or reference sequence. Although genetic alterations are not shareable resources themselves, each genetic alteration in eagle-i is described by a single record, which can be linked to eagle-i resources such as organisms and cell lines.

Creating Genetic Alteration records

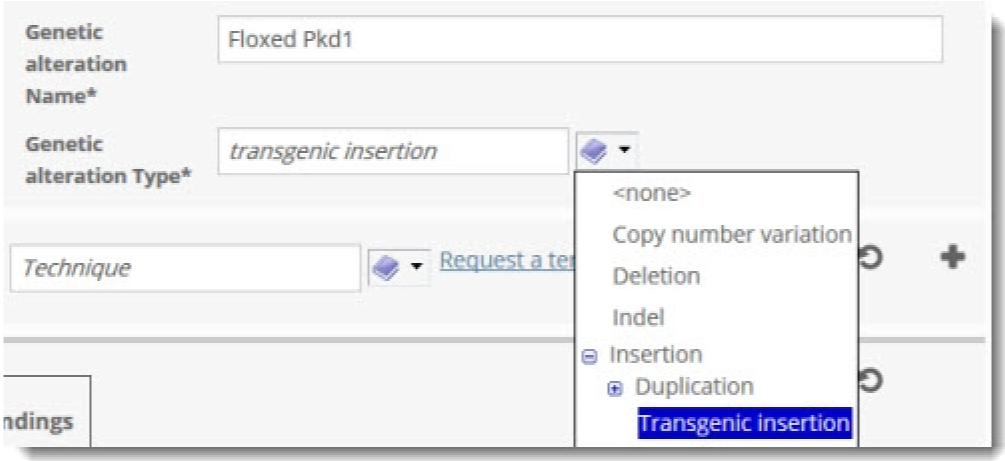
Like person records, genetic alteration records can only be created from within another record. Before creating a new one, click **See choices from all organizations** next to the field to check if a record for the alteration already exists. A single genetic alteration record can be linked to as many other records as are applicable.

To create a genetic alteration record:

1. From any record with the **Genetic Alteration(s)** field, select **<create new>** from the dropdown.



2. Enter a descriptive name and select the appropriate type.


Genetic alteration Name* Floxed Pkd1

Genetic alteration Type* *transgenic insertion*

3. Save the record. The new record is added as an unfinished resource stub and will appear in the **View My Resource Stubs** list, found off the main **Workbench**. Click on the name of the genetic alteration to open the record and enter additional information, such as the Entrez gene ID and symbol.

Note: genetic alteration records must move through the SWEET workflow separately from the records to which they are linked. Always check to make sure any existing genetic alterations you've linked to are published. And if withdrawing a genetic alteration record, use the **Check links to this** button to first see if any other published resources are linking to it.

Available guidelines for Genetic Alteration records

- Annotation guidelines for genetic alteration records

Genetic Alteration Field Annotation

Field	Description	Req.	NR
Genetic Alteration Name	Any alteration in a gene; may be disease causing or a benign, normal variant. Enter the name in the format: "Gene symbol[Allele name]" using either brackets or HTML tags for superscripts. See the guidelines for superscripts for more details. Where possible, use common nomenclature: see the **Gene and protein symbol conventions** table below for examples. If there is no specific nomenclature available, then use the above as default or contact a domain expert.	Yes	✓
Genetic AlterationType	Select the appropriate type. If the genetic alteration type is unknown, annotate up.	Yes	✓
Genetic Alteration Name	Enter any alternate names for the genetic alteration. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		

Entrez Gene ID	If the gene and organism are known, enter the unique identifier assigned to the corresponding record for the affected/mutated gene in the Entrez Gene database (http://www.ncbi.nlm.nih.gov/gene).		
Entrez Gene Symbol	Enter the official symbol for the gene. (e.g. 'SHH' for sonic hedge hog.)		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Human Studies Introduction and Workflow

Human studies (HS) are any research studies where the study population is comprised of humans. You may run across some references to “human health studies” or “HHS” in eagle-i documentation, however this usage presupposes a health-only focus to human research at eagle-i institutions. Because this supposition is limiting and potentially inaccurate, the term “human studies” or “HS” is preferable.

Human studies are unique within eagle-i in that, unlike instruments, software, reagents, biological specimens, or other resources, human studies are research projects themselves rather than the resources used to produce research. An important way these studies are commonly described by scientists is based on aspects of their research design and study population, in other words, “randomized double-blind clinical trial”, “cohort study”, and so on. The understanding and documentation of these design distinctions are a critical part of the meaningful annotation of eagle-i human studies, as evidenced by the role they play in the decision points in the human studies decision tree diagram.

Before you begin annotation, it is helpful to look at a previously curated human study record to get an idea of what a completed and curated record looks like.

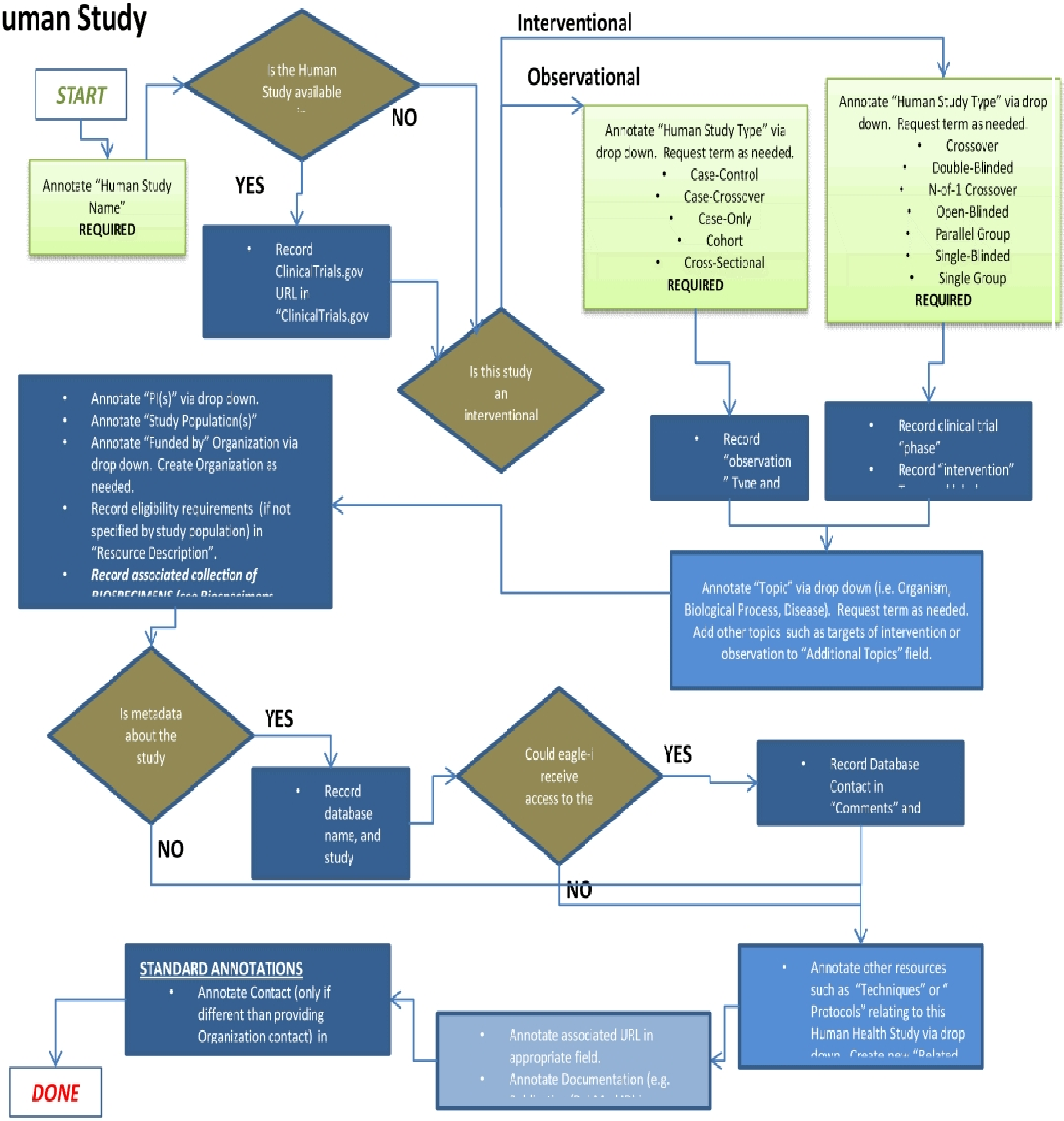
ClinicalTrials.gov Studies

Many human studies have a ClinicalTrials.gov (CT.gov) record. ClinicalTrials.gov is a large federal repository that contains information regarding planned, ongoing, and concluded human studies. Its name is somewhat of a misnomer in that it includes metadata for human studies with any research design, not just clinical trials per se.

If the study you are annotating already has a CT.gov record, it would be helpful know before you start recording information, for two reasons:

1. Some CT.gov records have already been imported into the eagle-i repository. If your study already has a CT.gov record, it may also already have an eagle-i record. Working with that imported record will save you the time of re-recording information, and ensure that there is no duplication of resource records within eagle-i.
2. Even if there is no pre-populated eagle-i record for the study, if it has a CT.gov record, the information it contains may be helpful in filling in the data you need to record. Go to http://clinicaltrials.gov/ and click “Search for clinical trials” to determine if a record exists.

Human Study



Annotate "Human Study Name"
REQUIRED

- Record ClinicalTrials.gov URL in "ClinicalTrials.gov

Annotate "Human Study Type" via drop down. Request term as needed.
- Case-Control
- Case-Crossover
- Case-Only
- Cohort
- Cross-Sectional

REQUIRED

Annotate "Human Study Type" via drop down. Request term as needed.
- Crossover
- Double-Blinded
- N-of-1 Crossover
- Open-Blinded
- Parallel Group
- Single-Blinded
- Single Group

REQUIRED

- Record "observation" Type and
- Record clinical trial "phase"
- Record "intervention"

Annotate "Topic" via drop down (i.e. Organism, Biological Process, Disease). Request term as needed. Add other topics such as targets of intervention or observation to "Additional Topics" field.

- Annotate "PI(s)" via drop down.
- Annotate "Study Population(s)"
- Annotate "Funded by" Organization via drop down. Create Organization as needed.
- Record eligibility requirements (if not specified by study population) in "Resource Description".
- ***Record associated collection of***

- Record database name, and study

- Record Database Contact in "Comments" and

- Annotate other resources such as "Techniques" or " Protocols" relating to this Human Health Study via drop

- Annotate associated URL in appropriate field.
- Annotate Documentation (e.g.

STANDARD ANNOTATIONS
- Annotate Contact (only if different than providing Organization contact) in

Human Study Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Human Study Name	Enter the official name of the study. In the absence of a formal name, it is acceptable to use the title of a journal article or other publication reporting on the study as the study name as long as: 1) the article title does not refer to itself as a publication, which would then not make sense in the human study context; 2) the article title is specific enough to distinguish the specific study being annotated from others that may be related or associated with the same organization or project.	**Yes**	✓
Human Study Type	Select the most specific study type as defined by its research design. Use the eagle-i glossary or consult the Observational Studies chart to see definitions of the study types. If no study type accurately matches the characteristics of the study, submit a term request. **Note on Epidemiological studies:** these are statistical studies on human populations, which attempt to link human health effects to a specified cause. An epidemiological study can only prove that an agent could have caused, but not that it did cause, an effect in any particular case.	**Yes**	✓
Human Study Description	Enter a short, typically one paragraph description of the study to serve as an overview, with particular emphasis on the goals of the research or aspects not recorded in any other field. Some annotators have used the abstract of a journal article describing the study as the description. This is acceptable, and is particularly useful to the reader if it is a structured abstract, as long as the abstract comes from a source that is not copyrighted, such as PubMed. The CT.gov record for the study may also provide information.		
Human Study Additional Name	Enter any alternate names for the study. Should include any abbreviations or alternate spellings. Use separate lines for multiple names. For example: the Third National Health and Nutrition Examination Survey is often called "NHANES 3."		
Performed by	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary contact for information about the study and its associated resources. This may or may not be the same as the Principal Investigator. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
PI (Principal Investigator)	Link to the lead scientist supervising the study and primarily responsibility for its outcome. This field should be filled separately, even if the **Contact** and the Principal Investigator are the same person. Use the **PI (co-Investigator)** field to note any co- or secondary PIs, if applicable.		
PI (co-Investigator)	Link to any co-Principle Investigators (co- PIs) for the study. Should be filled separately, even if the **Contact** and co-PI are the same person. This field is meant to distinguish the primary PI from any co- or secondary PIs, and should not be used unless there is also a person listed in the **PI** field.		
Access Restriction(s)	List any restrictions on the availability of study data. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geo-		

	graphically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Intervention	This box only displays if you have selected an Interventional study type. Click to display two required fields: Name and Type.	**Yes**	
Observational Method	This box only displays if you have selected an Observational study type. Click to display two required fields: Name and Type.	**Yes**	
Topic	Select any organisms, biological processes, or diseases that are the subject matter of the study. If choosing an organism, in most cases, this will be a generic organism. See Organisms guidelines and Using the Topic Field for more details.		
Additional Topic(s)	Record any topics not represented in the **Topic** field. Topics are likely represented conceptually in the study description you have already created. If the study has a ClinicalTrials.gov record, the Medical Subject Headings (MeSH) which appear in the CT.gov record may also provide insight into the topics covered. For more information, see Using the Topic Field.		
Phase	Select the appropriate phase. This field will only appear when “Clinical trial” has been selected as the study type. Clinical trial phases are defined by the U.S. Food and Drug Administration. Studies with formally numbered and reported phases are typically clinical trials. For example, “Phase 2 randomized trial.” The following selections appear in the drop-down list: **Phase 0 trials**—Very limited human exposure, with no therapeutic or diagnostic intent (e.g., screening study, microdose study) **Phase I trials**—Researchers test an experimental drug or treatment in a small group of people (20-80) for the first time to evaluate its safety, determine a safe dosage range, and identify side effects. **Phase II trials**—Experimental study drug or treatment is given to a larger group of people (100-300) to see if it is effective and to further evaluate its safety. **Phase III trials**—Experimental study drug or treatment is given to a larger group of people (100-300) to see if it is effective and to further evaluate its safety **Phase IV trials**—Post marketing studies produce additional information including the documented risks, benefits, and optimal use of an approved therapy. For combined trial phases such as “**Phase I/II trials**” and “**Phase II/III trials**”, use the + to select multiple phases.		
Biological Specimen	Link to any biological specimens used in the study.		
ClinicalTrials.gov url	Enter the full URL for the corresponding study record in the ClinicalTrials.gov repository.		
Funded by	Link to any organizations that funded the study.		
Related Cell Line	Link to any cell lines related to the study.		
Related grant number	Grant number for the funding that contributed to the development of the study. For example: 'U24 RR 029825'.		
Related NCBI Record	Enter the complete URL for any NCBI database records or datasets that generated about this study. For example: gene expression analysis data in the Gene Expression Omnibus, genome variation data in dbVar, or sequence read data in the Sequence Read Archive.		
Related protocol(s)	Link to any protocols used to perform the study.		
Related Publication or Documentation	Link to any journal articles or patents that contain information related to the study.		

Study Population	Briefly summarize the general characteristics of the study population. For example: “3000 lung cancer patients between the ages of 50 and 60 years of age.” Do not copy in the complete text of the ClinicalTrials.gov eligibility criteria or lengthy descriptions from protocols or similar sources.		
Website(s)	Enter the URLs of any external websites related to the study. All URLs should include the full address, such as: http://www.eagle-i.net. Note: ClinicalTrials.gov links should be entered in the corresponding field above. PubMed links should be entered in the record of the corresponding journal article and then linked to the study using the **Related Publication or Documentation** field.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Observational Method

Field	**Description**	**Req.**	**NR**
Observational Method Name	Enter the name of the observational technique which was brought to bear on the topic of the study. For example, the topic of the study may be a biological process, such as speech, and the observational technique a modality such as surveying. When copying from Clinicaltrials.gov, include only the name of the technique.		
Observational Method Type	Select the appropriate observational technique type. Consult the Ontology Browser for definitions of each type.	**Yes**	✓

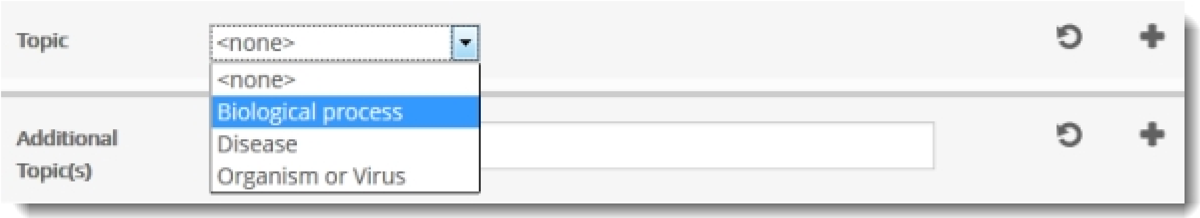
Intervention Table

Field	**Description**	**Req.**	**NR**
Intervention Name	Enter the name of the intervention technique that was brought to bear on the topic of the study. For example, the topic of the study may be a disease and the intervention may be a drug. When copying from Clinicaltrials.gov, include only the name of the technique. For example, enter “Rituximab” and not “Drug: Rituximab.”	**Yes**	✓
Intervention Type	Select the appropriate intervention type. Consult the Ontology Browser for definitions of each type.		

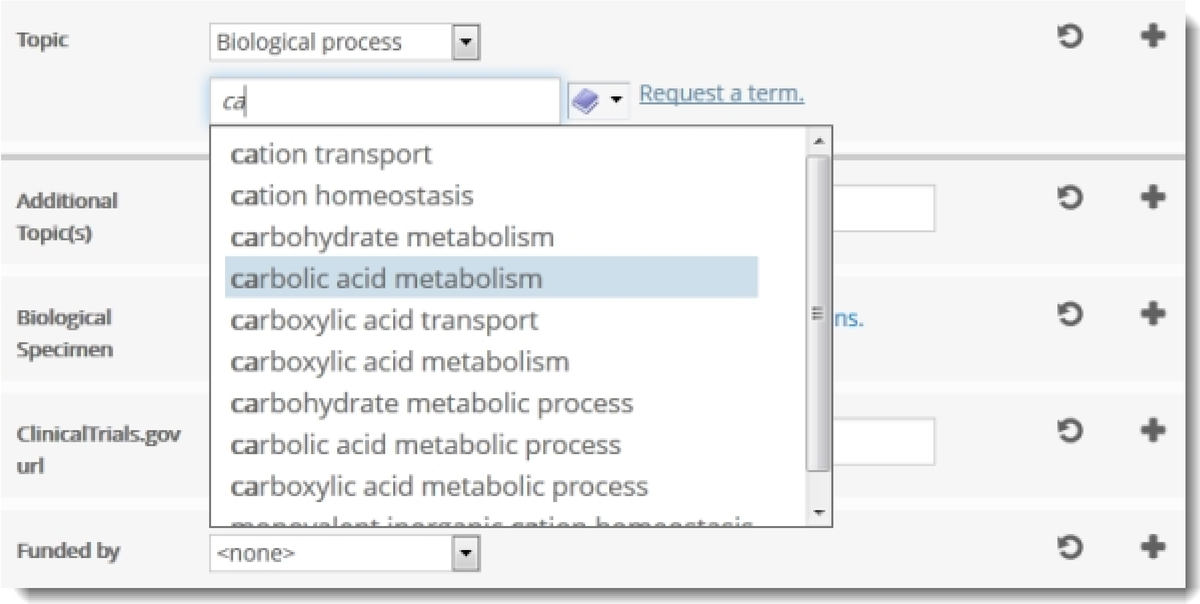
Using the Topic Field

The topic field is tied to the eagle-i ontology, and should only be used to record study topics that are diseases, biological processes, or organisms or viruses. All other topics should be added to the record using the Additional Topic(s) field discussed below. You can search for topics two ways:

1. Select **biological process**, **disease**, or **organism or virus** from the drop-down list.

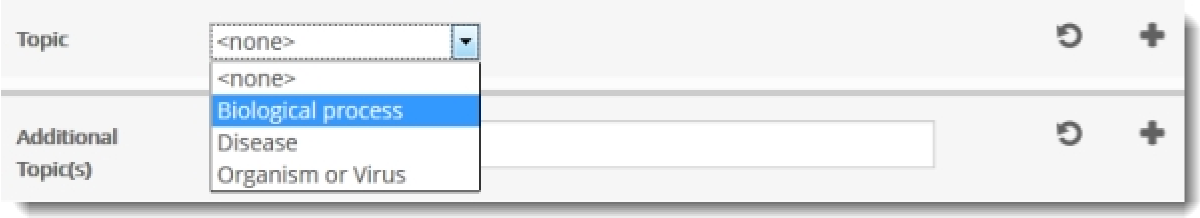


2. Type the topic in the text box. If necessary, use synonyms, word roots, and alternative punctuation forms to find topics. For example, if you cannot find it under "lung", try "pneumo-", "airway", "bronch-", "respiratory", and "breath—" terms; if "Nail-Patella Syndrome" doesn't work, try "Nail Patella Syndrome.

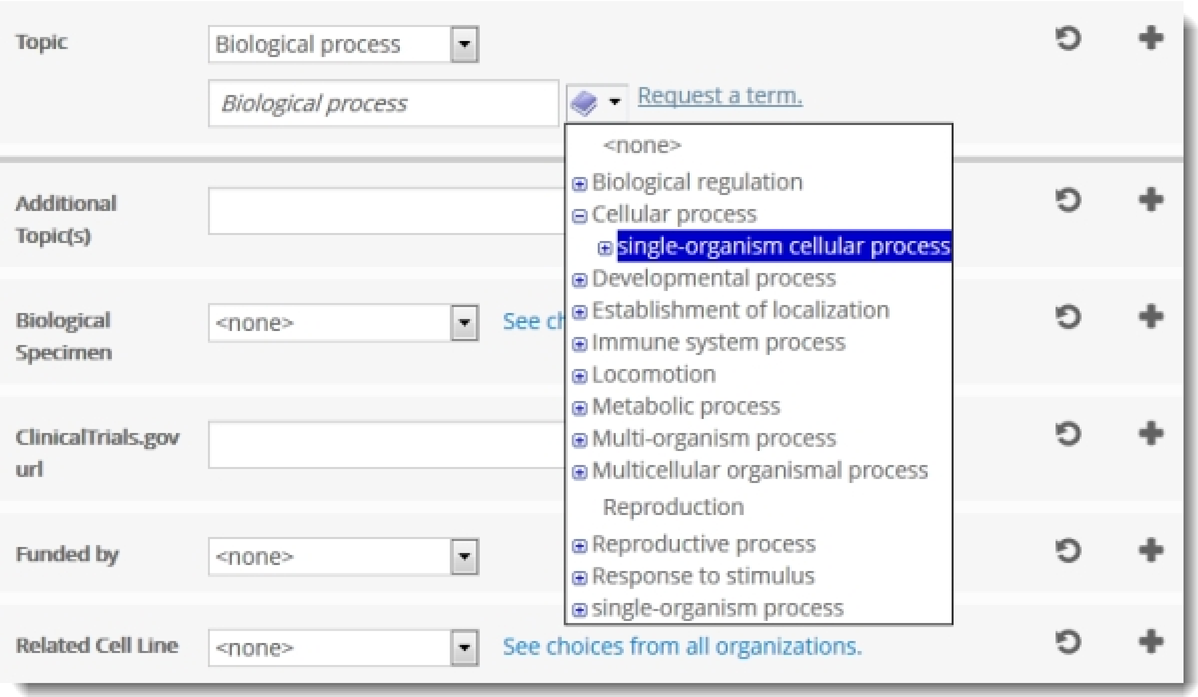


- or -

1. Select one of the three broad topic types from the drop-down list.



2. Click the taxonomy browser and navigate through the related ontology term hierarchies.


Topic Biological process
Biological process
Additional Topic(s)
Biological Specimen <none>
ClinicalTrials.gov url
Funded by <none>
Related Cell Line <none>

If selecting an organism, see the Generic Organisms section.

When the topic is not in the ontology

To build the ontology to meet user needs, it is important for annotators to communicate what ontology concepts are required. If the needed topic term is a disease, biological process, or organism/virus, select the appropriate parent term in the drop-down list and request the new term. See Submitting Term Requests for more information.

Using the additional topic(s) field

This field is used to record any other topics related to the study where the topic is not a disease, biological process, or an organism/virus. This is a free text field. Record only one topic in the box. Click + to add additional boxes and topics.

Table of Study Types

Study Type	Synonyms	ClinicalTrials.gov Definition	Ontology of Clinical Research (OCRe) Definition
Interventional study	Experimental study	Studies in human beings in which individuals are assigned by an investigator based on a protocol to receive specific interventions. Subjects may receive diagnostic, therapeutic or other types of interventions. The assignment of the intervention may or may not be random. The individuals are then followed	An interventional study is a quantitative study that prospectively assigns human participants or groups of humans to one or more health-related interventions to evaluate the effects on health outcomes. Interventions include but are not restricted to drugs, cells and other biological products, sur-

		and biomedical and/or health outcomes are assessed.	gical procedures, radiologic procedures, devices, behavioral treatments, process-of-care changes, preventive care, etc. [adapted from: WHO, available at: http://www.who.int/ictrp/en/]
(Interventional) Single group study		A single arm study.	OCRe: A single group study is an interventional study that has only a single allocation group and no contemporaneous comparison group. A study in which an individual acts has his/her own comparison does not fall into this category, since an individual is not a group.
(Interventional) Parallel study		CTs.gov: participants are assigned to one of two or more groups in parallel for the duration of the study	OCRe: A parallel group study is an interventional study that compares across at least two allocation groups concurrently, each receiving a regimen of interventions (which can be "no intervention").
(Interventional) Cross-over study		CTs.gov: Cross-over: participants receive one of two alternative interventions during the initial phase of the study and receive the other intervention during the second phase of the study.	OCRe: A crossover study is an interventional study where the population is more than a single human subject, in which at least two regimens of interventions are given alternatingly. Upon completion of one regimen, participants are switched to the other. For example, for a comparison of regimens A and B, the participants are randomly allocated to receive them in either the order A, B or the order B, A. Regimens are assigned to and data are analyzed within more than one participant at a time.
(Interventional) Factorial study	Factorial design	CTs.gov: Factorial: two or more interventions, each alone and in combination, are evaluated in parallel against a control group.	OCRe: Factorial design is a trial design used to assess the individual contribution of treatments given in combination, as well as any interactive effect they may have... In a trial using a 2x2 factorial design, participants are allocated to one of four possible combinations... This type of study is usually carried out in circumstances where no interaction is likely.
(Interventional) N-of-1 study	Single patient trial	CTs.gov: no equivalent class.	OCRe: An N-of-1 crossover study is an interventional study where the population is a single human subject and in which at least two regimens of interventions are given alternatingly. Regi-

			mens are assigned to and data are analyzed within one participant at a time.
(Interventional) Quasi-experimental study	quasi-experiment; quasi-random allocation	CTs.gov: no equivalent class.	OCRe: Quasi-random allocation is an allocation scheme that is not random, but is intended to produce similar groups when used to allocate participants. Quasi-random methods include: allocation by the person's date of birth, by the day of the week or month of the year, by a person's medical record number, or just allocating every alternate person. In practice, these methods of allocation are relatively easy to manipulate, introducing selection bias.
Observational study	Non-experimental study	Studies in human beings in which biomedical and/or health outcomes are assessed in pre-defined groups of individuals. Subjects in the study may receive diagnostic, therapeutic, or other interventions, but the investigator does not assign specific interventions to the subjects of the study.	An observational study is a quantitative study in which the investigators do not seek to intervene, and simply observe the course of events. [adapted from: Glossary of Terms in The Cochrane Collaboration]
(Observational) Cohort study	Concurrent study Concurrent cohort study Follow-up study Incidence study Longitudinal study Panel study Prospective study	CTs.gov: Cohort: group of individuals, initially defined and composed, with common characteristics (e.g., condition, birth year), who are examined or traced over a given time period.	OCRe: A cohort study is an observational study in which a defined group of people (the cohort) is followed over time. The outcomes of people in subsets of this cohort are compared, to examine people who were exposed or not exposed (or exposed at different levels) to a particular intervention or other factor of interest. A prospective cohort study assembles participants and follows them into the future. A retrospective (or historical) cohort study identifies subjects from past records and follows them from the time of those records to the present. [Glossary of Terms in The Cochrane Collaboration]
(Observational) Non-concurrent cohort study	Non-concurrent prospective study Retrospective cohort study Historical cohort study Historical prospective study		

(Observational) Case-control study	Case-referent study Retrospective study	CTs.gov: Case-control: group of individuals with specific characteristics (e.g., conditions or exposures) compared to group(s) with different characteristics, but otherwise similar.	OCRe: A case control study is an observational study that compares people with a specific disease or outcome of interest (cases) to people from the same population without that disease or outcome (controls), and which seeks to find associations between the outcome and prior exposure to particular risk factors. [Glossary of Terms in The Cochrane Collaboration]
(Observational) Case-only study		CTs.gov: Case-only: single group of individuals with specific characteristics.	OCRe: no equivalent class.
(Observational) Case-crossover study		CTs.gov: Case-crossover: characteristics of case immediately prior to disease onset (sometimes called the hazard period) compared to characteristics of same case at a prior time (i.e., control period).	OCRe: A case-crossover study is an observational study that aims to answer the question, "Was this event triggered by something unusual that happened just before?" The key feature of the design is each case serves as its own control. The method is analogous to a crossover experiment viewed retrospectively, except the investigator does not control when a patient starts and stops being exposed to the potential trigger. Also, the exposure frequency is typically measured in only a sample of the total time when the patient was at risk of the injury or disease onset. Thus it usually resembles a case-control study more than a retrospective cohort study. The simplest case-crossover design is closely analogous to a traditional matched-pair case-control design. In both, each case has a matched control. In a traditional matched-pair case-control study, the control is a different person at a similar time. In the matched-pair case-crossover design, the control is the same person at a different time [Annu Rev Public Health. 2000;21:193-221.]
(Observational) Cross sectional	Disease-frequency survey Prevalence study Survey	CTs.gov: no equivalent class.	OCRe: A cross-sectional study is an observational study measuring the distribution of some characteristic(s) in a population at a particular point in time. (Also called survey.) [adapted from: Glossary of Terms in The Cochrane Collaboration]

Ecologic or community studies	Ecological study	Geographically defined populations, such as countries or regions within a country, compared on a variety of environmental (e.g., air pollution intensity, hours of sunlight) and/or global measures not reducible to individual level characteristics (e.g., health care system, laws or policies median income, average fat intake, disease rate)	OCRe: An ecologic study is a non individual-human study in which the unit of observation is a population or community.

Human Subjects Introduction and Workflow

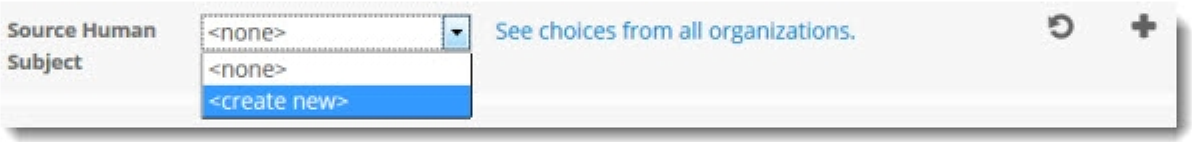
eagle-i collects information about the de-identified individual human subjects of research experiments and the families to which they belong, where useful to help describe the biological materials derived from those subjects. Note that although both describe people, human subject and people records should not be confused.

Creating Human Subject records

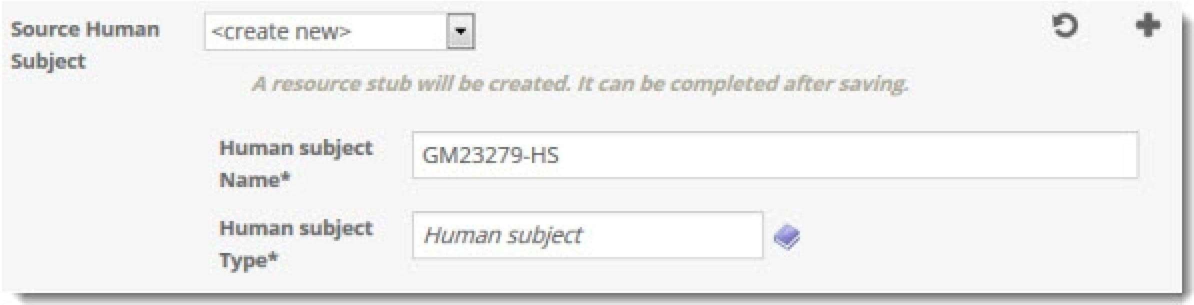
Like other types of records describing people, records for human subjects their families can only be created from within other records. Before creating a new human subject or family record, click **See choices from all organizations** next to the field to check if there's an existing record that can be used instead. A single human subject or family record can be linked to as many other resource records as are applicable.

To create a human subject record:

1. From any record with a **Source Human Subject** or **Family** field, select **<create new>** from the dropdown.



2. Enter a codified or de-identified number to represent the human subject or family. eagle-i does **NOT** collect the names of human subjects or families.


Source Human Subject: <create new>

A resource stub will be created. It can be completed after saving.

Human subject Name*: GM23279-HS

Human subject Type*: *Human subject*

3. Save the record. The new record is added as an unfinished resource stub and will appear in the **View My Resource Stubs** list, found off the main Workbench. Click on the name of the human subject or family to open the record and enter additional information, as applicable.

Note: human subject and family records must move through the SWEET workflow separately from the records to which they are linked. Always check to make sure any existing human subject or family you've linked to are published. And if withdrawing a human subject or family record, use the **Check links to this** button to first see if any other published resources are linking to it.

Available Guidelines for Human Subject records

- Annotation guidelines for human subject records
- Annotation guidelines for family records

Human Subject Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Human Subject Name	Enter a codified or de-identified number to represent the human subject. eagle-i does **NOT** collect the names of Human Subjects.	Yes	✓
Human Subject Type	Pre-filled. No action necessary.	Yes	✓
Human subject Description	Enter any relevant medical information not covered in the other fields.		
Genetic Alteration	**High Value field.** Link to any records describing variations in sequence carried by macromolecules, or organism genomes that deviate from a canonical or reference sequence. Select an existing alteration record or create a new one by entering the name and type. If multiple genes are affected, link to a separate genetic alteration record for each.		
Country of Origin	Enter the country in which the human subject was born.		
Ethnicity	Select the most appropriate ethnic group to which the human subject belongs. For persons with mixed backgrounds, select 'mixed ethnicity' and then use the + button to add a new field for any significant contributing ethnicities.		
Family	Link to the family to which the subject belongs. Check to see if an existing record for the family already exists. If not, create a new one using any existing de-identified name, identifier, or combination thereof from an outside database or registry.		
Relationship to Proband	Where applicable, select the relationship between this human subject and the proband (the primary family member identified as the focus of a biomedical investigation or pedigree).		

Sex	Select the phenotypic sex of the organism.		
Available Medical Records/History	Indicate whether the subject's medical records or history are available. Select <none> if history is unknown.		✓
Clinically Affected	Indicate whether the subject is affected by the disorder or condition under investigation. Select <none> if status is unknown.		✓
Diagnosis	A diagnosis of some disease or disorder made on a human subject, either by a physician or by the subject.		
Phenotype Findings	Captures all observable characteristics or traits of an organism, such as its morphology (e.g. small eye), development, biochemical or physiological properties, behavior, or products of behavior (such as a bird's nest). The phenotype is more atomic than syndrome or disease.		
Related Human Study	Link to any human studies in which the subject participates.		
Infectious History	Infectious history of the human subject, such as previous viral infections that may affect his or her usage of for research.		
Inventory Number	Enter any numerical identifiers for the human subject, if different from the one used in the **Name** field.		
Related grant number	Grant number for the funding that contributed to the research in which the subject is participating. For example: 'U24 RR 029825'.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Family Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Family Name	Enter a codified or de-identified number to represent the family. Can be any existing name, identifier, or combination thereof from another database or registry. eagle-i does **NOT** collect the names of families.	**Yes**	✓
Family Type	Pre-filled. No action necessary.	**Yes**	✓
Family Description	Enter any relevant medical information not covered in the other fields.		
Family Identifier	Where applicable, enter any additional identifiers (OrcID, etc.) for the family found in other databases or registries.		
Website(s)	Enter the URLs of any related external websites pertaining to the family. All URLs should include the full address, such as: http://www.eagle-i.net.		

Diagnosis Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Diagnosis Name	Name of the diagnosis. Can be the same as or a variation on the name of the disease entered in the **Diagnosed Disease** field.	Yes	✓
Diagnosis Type	Pre-filled. No action necessary.	Yes	✓
Diagnosis Description	Free-text description of the diagnosis made on the biological specimen sampled or the organism or human subject from which it derived.		
Diagnosed Disease	A disease assigned by the diagnosis to a patient or subject. Use the '+' button at the right to add additional fields where more than one disease applies.		
Self-Diagnosis?	Indicate 'Yes' if the diagnosis was made by the subject, and 'No' if it was made by a medical professional. Leave as <none> if unknown.		✓
Subject Age at Diagnosis	The age of the subject at the time the initial diagnosis was made.		

Instruments Introduction and Workflow

Instruments are devices that have a mechanical, measurement, or electronic function. Instrument accessories that are part of a particular workstation should only be recorded as separate records if they meet the definition of instrument, in other words, if they perform a specific function, such as mechanical, measurement, or electronic functions; slides, for example, would not be a separate instance, but a photomultiplier would be.

Creating Instrument Records

Watch this video tutorial for a demonstration of how to create instrument records in the SWEET.

Only a single record should be used to represent multiple copies of the same instrument in a single laboratory; indicate the number of instruments available in the Instrument Description field. However, duplicate copies of the same instrument located in *different* laboratories should be represented by separate records.

Note: There is currently no automatic way to record relationships between instruments that are parts of other instruments (in other words, an *objective* is part of a *microscope*).

To manually describe parts of a workstation:

1. Create a stub record for the workstation, typed as whichever type of instrument corresponds to the main component.
2. In the Instrument Description field, include a list of specifically relevant parts or important components that might be queried on.
3. Each of those components should also be recorded in a separate record, with the workstation name included in the **Instrument Description** field.

As instruments are commonly linked to from other types of records, particularly services and software, it is often easiest to create instrument records first.

Instruments Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Instrument Name	Enter any local designation commonly used to refer to the instrument, such as: "96-well plate in storage area." Wherever possible, use manufacturer/model information to distinguish generic instrument labels. **If at all possible, the instrument name should be more specific than the type.**	Yes	✓
Instrument Type	Select the most specific term that accurately represents the instrument. If the most accurate type isn't available, annotate up and submit a term request for the one needed. For example: if "scanning electron microscope" is not available, select "electron microscope" as the next most accurate term in the hierarchy and request "scanning electron microscope" as new term. See Submitting Term Requests for more information.	Yes	✓
Instrument Description	Enter any information that describes the instrument but is not captured in any of the other fields. Can include information about the number of copies of an instrument the lab owns, or any workstation components.		
Instrument Additional Name	Enter any alternate names for the instrument. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field. Note: In some cases, multiple labs may share a single instrument; the instrument should be associated with the organization where it is primary housed or owned. It can be linked to access services associated with other organizations, if needed.		✓
Contact	Link to the primary person responsible for the instrument. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Method related to or performed using the instrument (in other words, techniques for which you can use the resource or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to create the instrument.		
Manufacturer	Name of the organization that created the instrument. May also be a person, but only if the person mass produces the instrument. Use the **Developed by** field for resources designed by a person but not mass produced.		
Developed by	Any people or organizations who designed or helped develop the instrument for limited or internal use only. If the instrument was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the instrument.		
Funded by	Link to any organizations that funded the purchase of the instrument or the work that produced it.		

Inventory Number	Enter the internal laboratory inventory identifier for the instrument. Often used for insurance and control purposes, this may be available via university records or is often recorded on a plate attached to the device itself. Note: if a lab contains multiple copies of the same instrument that differ only by inventory number, create one instrument record and annotate all inventory numbers on separate lines.		
Model Number	Enter the commercial instrument model. Can be a name, number, or combination of both. Fill out even if the information is included in the instrument name field.		
Related grant number	Grant number for the funding that contributed to the development of the instrument. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the instrument.		
Related Software	Link to any software that is used to run the instrument or specifically analyze the data output from the instrument.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Organism and Viruses Introduction and Workflow

Organisms and *viruses* are living systems that are capable of replicating or reproducing in the right environment. Examples: *animal*, *plant*, *bacteria*, *fungus* or *virus*.

Sometimes people confuse biological specimens with organisms: For example, insect specimens at a museum would be considered biological specimens, not organisms. But trees in an arboretum would be considered organisms. Currently, eagle-i distinguishes these two based first on whether or not the entity is alive. If it is alive, it is not a biological specimen. If it is dead, the most critical information is what species and what anatomical structure the specimen is derived from.

Selecting either an organism or a virus in the Organisms and Viruses Type field determines which fields display in the main body of the record. Therefore, it is necessary that this field be annotated correctly before entering or editing new records.

Creating Organism Records

Watch this video tutorial for a demonstration of how to create organism records in the SWEET.

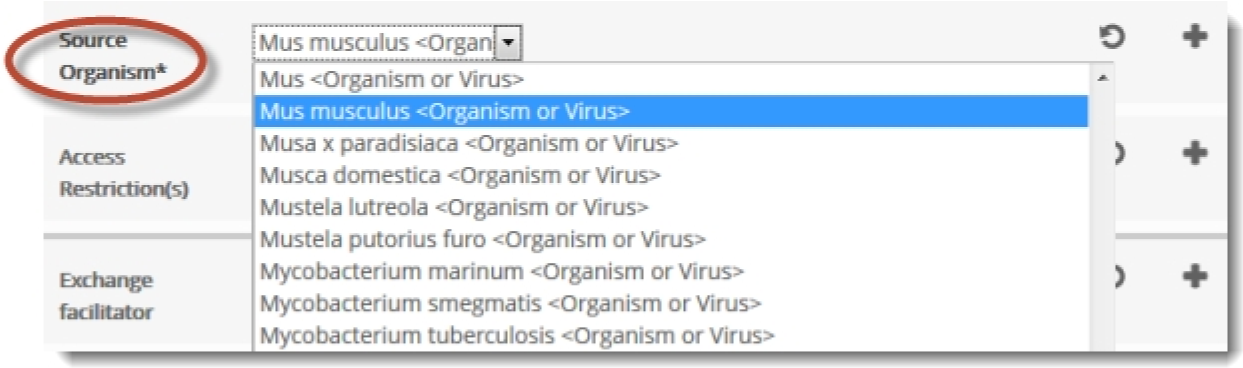
About Model Organisms

eagle-i collects information on organisms that have genetic or epigenetic modifications that allow them to be used as proxies for human diseases. These models are designed to mimic physiological and/or pathological processes that are thought be central to the pathogenesis of human disease. They help translational and pre-clinical investigators perform unlimited genetic, biochemical, physiological and interventional experimentation that would not be possible in humans. When reflective of a human disease process, organisms are critical reagents for the development of new therapeutics. However, model organisms relevant to human disease can be very difficult to find if they are not published and/or are not described in sufficient detail.

About Generic Organisms

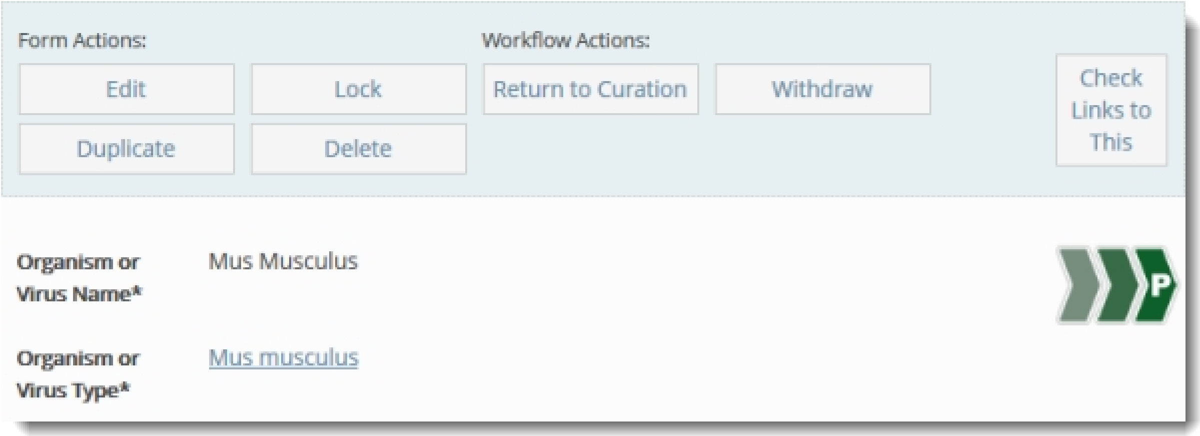
There are two kinds of organism records in eagle-i. The first kind describe a specific organism available for sharing from a laboratory. The majority of the guidelines in this section are applicable only to these kinds of organisms.

The second kind are Generic organism records. These describe a general type of organism, rather than a specific instance of that organism (such as a particular model organism). Generic organisms are not associated with any organization and are not available for sharing; rather, they are used as a way to describe the general source organism type of another resource. For instance, a biospecimen record must include the organism from which that specimen was derived, but in some cases, that organism will not be a part of the laboratory’s resources. In cases like that, the **Source Organism** field should be filled with a link to a generic organism record.



Generic organisms are listed at the top of the **Source Organism** dropdown under the header: **Commonly Used Resources**. Specific, shareable organisms that are available from labs or other organizations in eagle-i are listed underneath the generic organisms under the header: **All Other Resources**.

If you need to link another resource to an organism type that isn't currently available in eagle-i, you can create a new one in the same way as you would create any other new record. However, generic organisms need only have two fields fill in: label and type, with the label exactly the same as the type. For example: label "Mus musculus" of type Mus musculus.



Organism or Virus Name* Mus Musculus

Organism or Virus Type* Mus musculus

Generic organism records are maintained by the central eagle-i team. Any locally created generic organism records will eventually be migrated to a central record that is available to all institutions in the network. See the Centrally Curated Records section for more details.

Super/subscripts

Super- and subscripts may be represented using either brackets or HTML:

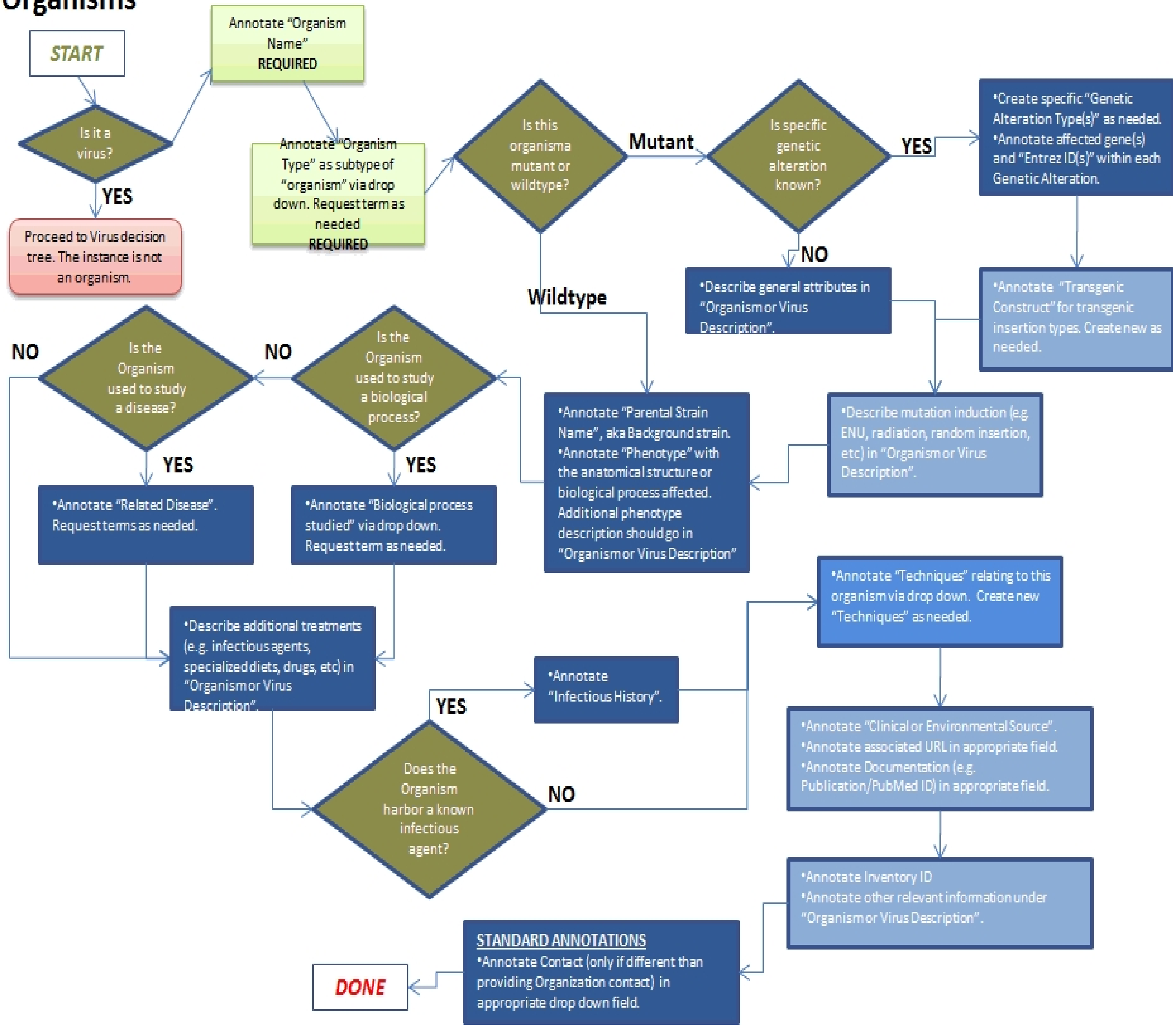
- Superscripts may be indicated using square brackets around the text. For example, for allele names: $agil^{2J}$ would be entered as agil[2J].

- Both super- and subscripts can also be represented using the HTML tags <sup> and <sub>. In particular, these tags should be used for resources for which the addition of extra brackets might be misleading. For example: the chemical compound $[^{11}C]CH_3I$ (methyl iodide) would be entered as [¹¹C]CH₃I. In these cases, in order to ensure the resource will still come up in search results, a version of the name without the HTML tags should also be entered in the Additional Name field.

Available Guidelines for Organism and Virus Records

- Decision Tree for entering Organism records
- Decision Tree for entering Virus records
- Annotation Guidelines for Organism records
- Annotation Guidelines for Virus records

Organisms


START
Is it a virus?
YES
Proceed to Virus decision tree. The instance is not an organism.
Annotate "Organism Name" REQUIRED
Annotate "Organism Type" as subtype of "organism" via drop down. Request term as needed REQUIRED
Is this organisma mutant or wildtype?
Mutant
Is specific genetic alteration known?
YES
•Create specific "Genetic Alteration Type(s)" as needed. •Annotate affected gene(s) and "Entrez ID(s)" within each Genetic Alteration.
NO
•Describe general attributes in "Organism or Virus Description".
•Annotate "Transgenic Construct" for transgenic insertion types. Create new as needed.
Wildtype
•Describe mutation induction (e.g. ENU, radiation, random insertion, etc) in "Organism or Virus Description".
•Annotate "Parental Strain Name", aka Background strain. •Annotate "Phenotype" with the anatomical structure or biological process affected. Additional phenotype description should go in "Organism or Virus Description"
Is the Organism used to study a biological process?
NO
YES
•Annotate "Biological process studied" via drop down. Request term as needed.
Is the Organism used to study a disease?
NO
YES
•Annotate "Related Disease". Request terms as needed.
•Describe additional treatments (e.g. infectious agents, specialized diets, drugs, etc) in "Organism or Virus Description".
Does the Organism harbor a known infectious agent?
YES
•Annotate "Infectious History".
NO
•Annotate "Techniques" relating to this organism via drop down. Create new "Techniques" as needed.
•Annotate "Clinical or Environmental Source". •Annotate associated URL in appropriate field. •Annotate Documentation (e.g. Publication/PubMed ID) in appropriate field.
•Annotate Inventory ID •Annotate other relevant information under "Organism or Virus Description".
STANDARD ANNOTATIONS •Annotate Contact (only if different than providing Organization contact) in appropriate drop down field.
DONE

Organisms Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Organism Name	Enter a label for the organism. If the label contains genotype information and there is no corresponding genetic alteration/mutation type added to the record, then you should create one. If the name does not contain genotype information, the label should be the Latin (binomial) name of the organism. The common (layman's) name can be added in the "Additional name" field.	**Yes**	✓
Organism Type	Select the most specific term that accurately represents the organism type or taxon. If the most accurate type isn't available, annotate up and submit a term request for the one needed. For example: if "Mus musculus" is not a available, select "Mus" as the next most accurate term in the hierarchy and request "Mus musculus" as a new term. If "Mus" is not available, then select "Rodentia," and so forth. See Submitting Term Requests for more information.	**Yes**	✓
Organism or Virus Description	Enter any information that describes the organism but is not captured in any of the other fields, such as how the mutant was generated or any additional treatments. Some helpful definitions: ▪ Wildtype: Refers to the phenotype of the typical form of a species as it occurs in nature. ▪ Mutant: An organism that has characteristics resulting from chromosomal alteration. ▪ Engineered: A mutation that was engineered using recombinant DNA technology. For example: knockout mouse would include inducible knockout or knockin mice. ▪ Induced: A mutation that is induced by administration of a mutagenic reagent. For example: induction of mutations in mice with ENU.		
Organism or Virus Additional Name	Enter any alternate names for the organism. Should include any abbreviations or alternate spellings, such as any genotype names that may be commonly used but do not conform to official nomenclature guidelines. For example: the zebrafish mutant fgf8a[ti282] was originally published as "acerebellar" with the abbreviation "ace"; the former should be used in the Resource Name and the latter listed as an Additional Name. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, uni-		

	versity or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Genetic Alteration(s)	**High Value field.** Link to any records describing variations in sequence carried by macromolecules, or organism genomes that deviate from a canonical or reference sequence. Select an existing alteration record or create a new one by entering the name and type. If multiple genes are affected, link to a separate genetic alteration record for each.		
Related Technique	Method related to or performed using the organism (in other words, techniques for which you can use the organism or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the organism.		
Phenotype findings	Captures all observable characteristics or traits of the organism, such as its morphology (e.g. small eye), development, biochemical or physiological properties, behavior, or products of behavior (such as a bird's nest). The phenotype is more atomic than syndrome or disease.		
Related Disease	**High Value field.** The disease or condition in which the organism manifests or of which the organism is a representation. If at all possible, records for model organisms should include either the related disease, biological process studied, or both. Possible exceptions include: intrinsically rare wildtype organisms, e.g. primates.		
Biological Process Studied	**High value field.** The biological process that is studied in the organism.		
Clinical or Environmental Source	Enter the organism's source environment or clinical setting. For example: clinical isolates or animals captured in the wild vs. lab-reared. Can also include a geographical origin (such as the country name).		
Developed by	Link to any people or organizations who designed or helped develop the resource.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the organism.		
Funded by	Link to any organizations that funded the work that produced the organism.		
Infectious History	**High value field.** The infectious history of the organism, such as previous viral infections that may affect its usage for research. Should not include normal health reporting. Example: "Animal has been exposed to parvo virus."		
Inventory Number	Enter the inventory identifier for the organism. Can be the internal laboratory ID or a commercial catalog number. External inventory numbers should be formatted with the name of the company followed by a colon and the number. For example: "Cell signaling catalog number: 7634".		
Parental Strain Name	**High value field.** Enter the parental strain name of modified organisms. The level of detail given to the background is at the discretion of the researcher. Multiple strains, if important enough to capture, should be entered entered on multiple lines. Use approved nomenclature where applicable. See the **Gene and protein symbol conventions** table below for examples.		
Related grant number	Grant number for the funding that contributed to the development of the organism. For example: 'U24 RR 029825'.		
Related NCBI Record	Enter the complete URLs of any NCBI database records or datasets that were generated about this resource. For example: gene expression analysis data in the Gene Expression Omnibus, genome variation data in dbVar, or sequence read data in the Sequence Read Archive.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the organism.		

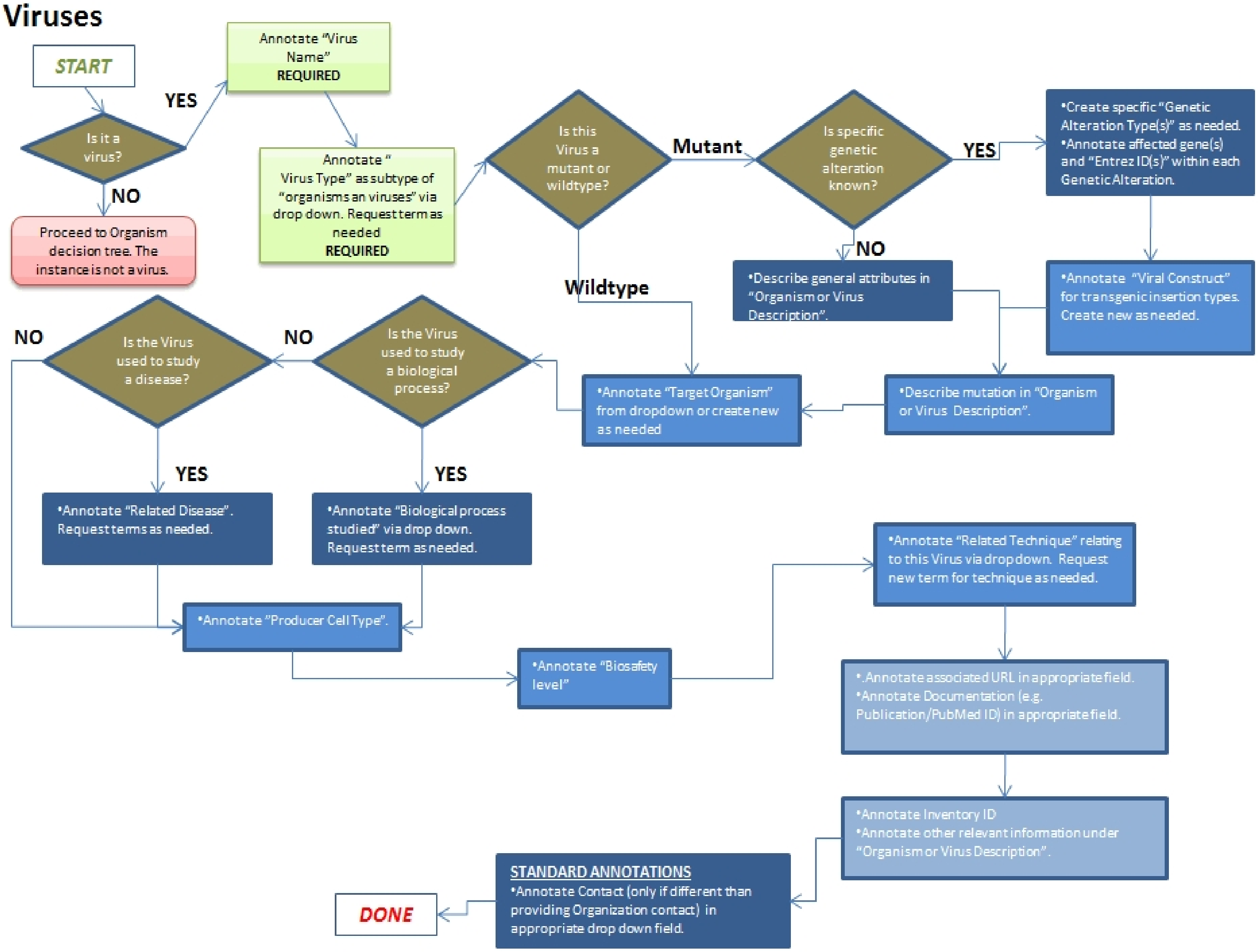
Transgenic Construct	Link to any constructs used to generate a transgenic organism. The relevant insert gene symbol and Entrez gene ID can be captured in the construct record.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net. Note: use the **External facilitator** field for links to commercial vendor order pages, such as JAX.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Gene and protein symbol conventions ("sonic hedgehog" gene)

Examples of common nomenclature: human gene symbols are all capitals (e.g. SHH); mouse gene symbols have the first letter capitalized (Shh). For nomenclature specific to other species, see: http://en.wikipedia.org/wiki/Gene_nomenclature.

Species	**Gene symbol**	**Protein symbol**
Homo sapiens	*SHH*	SHH
Mus musculus, Rattus norvegicus	*Shh*	SHH
Danio rerio	*Shh*	Shh

Viruses


START
Is it a virus?
YES
Annotate "Virus Name" REQUIRED
NO
Proceed to Organism decision tree. The instance is not a virus.
Annotate " Virus Type" as subtype of "organisms an viruses" via drop down. Request term as needed REQUIRED
Is this Virus a mutant or wildtype?
Mutant
Wildtype
Is specific genetic alteration known?
YES
•Create specific "Genetic Alteration Type(s)" as needed.
•Annotate affected gene(s) and "Entrez ID(s)" within each Genetic Alteration.
NO
•Describe general attributes in "Organism or Virus Description".
•Annotate "Viral Construct" for transgenic insertion types. Create new as needed.
•Describe mutation in "Organism or Virus Description".
•Annotate "Target Organism" from dropdown or create new as needed
Is the Virus used to study a biological process?
NO
Is the Virus used to study a disease?
NO
YES
•Annotate "Related Disease". Request terms as needed.
YES
•Annotate "Biological process studied" via drop down. Request term as needed.
•Annotate "Producer Cell Type".
•Annotate "Biosafety level"
•Annotate "Related Technique" relating to this Virus via drop down. Request new term for technique as needed.
•.Annotate associated URL in appropriate field.
•Annotate Documentation (e.g. Publication/PubMed ID) in appropriate field.
•Annotate Inventory ID
•Annotate other relevant information under "Organism or Virus Description".
STANDARD ANNOTATIONS
•Annotate Contact (only if different than providing Organization contact) in appropriate drop down field.
DONE

Viruses Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Virus Name	Enter a label for the virus. If the label contains genotype information and there is no corresponding genetic alteration/mutation type added to the record, then you should create one. If the name does not contain genotype information, the label should be the Latin (binomial) name of the virus. The common (layman's) name can be added in the "Additional name" field.	**Yes**	✓
Virus Type	Select the most specific term that accurately represents the virus type or taxon. If the most accurate type isn't available, annotate up and submit a term request for the one needed. For example: if "Hepatitis B virus" is not a available, select "Hepadnaviridae" as the next most accurate term in the hierarchy and request "Hepatitis B virus" as a new term. See Submitting Term Requests for more information.	**Yes**	✓
Organism or Virus Description	Enter any information that describes the virus but is not captured in any of the other fields, such as how the mutant was generated or any additional treatments.		
Organism or Virus Additional Name	Enter any alternate names for the virus. Should include any abbreviations or alternate spellings, such as any genotype names that may be commonly used but do not conform to official nomenclature guidelines. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Genetic Alteration	**High Value field.** Link to any records describing variations in sequence carried by macromolecules, or organism genomes that deviate from a canonical or reference sequence. Select an existing alteration record or create a new one by entering the name and type. If multiple genes are affected, link to a separate genetic alteration record for each.		
Related Technique	Method related to or performed using the virus (in other words, techniques for which you can use the virus or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the virus.		
Phenotype findings	Captures all observable characteristics or traits of an v, such as its morphology (e.g. small eye), development, biochemical or physiological properties, behavior, or products of behavior (such as a bird's nest). The phenotype is more atomic than syndrome or disease.		
Related disease	The disease of which the virus is a representation.		
Biosafety Level	The level of the biocontainment precaution required to isolate dangerous biological agents in an enclosed facility. The levels of containment range from the lowest biosafety level 1 to the highest at level 4.		

Developed by	Link to any people or organizations who designed or helped develop the virus.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the virus.		
Funded by	Link to any organizations that funded the work that produced the virus.		
Inventory Number	Enter the inventory identifier for the virus. Can be the internal laboratory ID or a commercial catalog number. External inventory numbers should be formatted with the name of the company followed by a colon and the number. For example: "Cell signaling catalog number: 7634".		
Producer Cell Type	Enter the kind of cell in which the virus may be produced. For example: 293T.		
Related grant number	Grant number for the funding that contributed to the development of the virus. For example: U24 RR 029825.		
Related NCBI Record	Enter the complete URLs of any NCBI database records or datasets that were generated about this resource. For example: gene expression analysis data in the Gene Expression Omnibus, genome variation data in dbVar, or sequence read data in the Sequence Read Archive.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the virus.		
Target Organism	Link to the organism that the virus infects.		
Transgenic Construct	Link to any constructs used to generate a transgenic organism. The relevant insert gene symbol and Entrez gene ID can be captured in the construct record.		
Viral Construct	Link to any constructs used to generate active virus.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net. Use the **External facilitator** field for links to commercial vendor order pages.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Phenotype Field Annotations

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Phenotype Name	Name of the phenotype. Should be capitalized.	Yes	✓
Phenotype Type	Select an appropriate sub-type. Subtypes include anatomical phenotypes, phenotypes related to biological processes, and phenotypes specifically designed for mammals. The sub-type selected will determine which additional fields display below.	Yes	✓
Phenotype Description	Enter any information that describes the phenotype but is not captured in any of the other fields.		
Anatomical	Anatomical structure characterized by the phenotype. In the case of a "Gigantic foot" phenotype, 'foot' would be chosen for this field.		

entity			
Biological process	Biological process characterized by the phenotype. In the case of a "Longer hibernation" phenotype, 'hibernation' would be chosen for this field.		
Mammalian phenotype	Mammal-specific phenotype. In the case of an albino rat phenotype, 'absent skin pigmentation' would be chosen for this field.		
Descriptor	Word or phrase used to describe the thing being characterized by the phenotype. In the case of a "Gigantic foot" phenotype, 'gigantic' would be chosen for this field. In the case of a "Longer hibernation" phenotype, 'increased duration' would be chosen for this field.		

Documents and Protocols Introduction and Workflow

eagle-i collects information about physical or electronically formatted documents in the form of protocols, journal articles, and patents.

Note: eagle-i does not store the actual documents themselves; it merely stores metadata about the documents.

Document records may reference and/or be closely related to other resource types, such as techniques, instruments, or human studies, and it is important to keep the differences in mind when annotating documents. There could be a similar name for a technique, an instrument and a document. For example, a protocol for chromatography is a documented plan; it is not the same as chromatography per se, which is a technique. In the same way, a publication reporting on a human study is a document that describes the study. The study will therefore have its own separate record which may have multiple publications associated with it. A document is always a written text that can be referenced either as a physical document or at a URL.

If the actual document is available at an external website, the URL should be included in the record. If the document is not electronically available, but is otherwise valuable, it should still be included in eagle-i. However, it is particularly important to provide a descriptive label, extensive resource description and/or related resources types (techniques, organisms, etc.) for such documents in order to facilitate their identification in the search application.

Protocols

Scientific protocols are detailed plan specifications designed to allow experts to independently reproduce that process. They are often not widely communicated, shared, or available electronically. Therefore, fostering the sharing of protocols is an especially valuable eagle-i service to the scientific community. The exception is commercial protocols, which are not generally considered to be within scope for eagle-i, as they are neither invisible nor rare.

Adding Documents

Protocols are the most common type of document collected in eagle-i, and the only type of document listed on the organizations sidebar in the SWEET. You can add new records for other types of documents from within other resource records. For example, to add a record for a journal article related to an organism:

1. Open the organism record.
2. Select <create new> from the **Related Publication or Documentation** field.
3. Select the "journal article" sub-type and enter the article title.
4. After saving the organism record, open the journal article record and fill in additional information, such as the PubMed ID.

You can also add new document records by clicking the **add new** protocol link on the sidebar of an owning organization. The Document Type field will automatically populate with the type: "protocol". Select another type of document instead. Be sure to do this before filling out any other fields in the record, as the fields will change depending on the type selected. After, complete and save the record as you normally would.

Documents and Protocols Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Document Name	Enter a title for the protocol or document. For example: "DNA extraction from blood protocol." In general, titles should be capitalized. For protocols, add the word "protocol" to the end of the document name where it makes lexical sense. This will help to distinguish them from techniques of the same name in some display contexts.	**Yes**	✓
Document Type	Select the appropriate type. Choosing "Protocol" or "Journal Article" will populate additional fields below.	**Yes**	✓
Document Description	Enter any information not captured in any of the other fields. Can include a brief abstract of the journal article, a description of the protocol or report contents, or a standardized tracking number (such as the SOP number or patent number). Should not contain the actual step-by-step test of the protocol itself.		
Document Additional Name	Enter any alternate names for the document. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Used by	Link to the record of the owning organization. Pre-populated, read-only field. Note: applies to protocols only; journal articles and patents are not directly associated with any single owning organization.		✓
Author	For protocols and patents: select the author from the drop-down list. Add as many authors as needed. For journal articles: at present this field may be left blank for publications that have a PMID ID (see below), as the authors will eventually be pulled from PubMed.		
Contact	Link to the primary person responsible for the document. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Topic	Select any organisms, biological processes, or diseases that are the subject matter of the protocol. If choosing organism, in most cases, this will be a generic organism. See Organisms guidelines for more details.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the document.		
PubMed ID (PMID)	Applies to journal articles only. Annotate the full URL of the PubMed record, which will include the PMID. For example: "http://www.ncbi.nlm.nih.gov/pubmed/3907859."		
Related grant number	Grant number for the funding that contributed to the development of the document. For example: 'U24 RR 029825'.		
Related Publication	Link to any other documents that contain information related to this one.		

or Documentation			
Uses	Link to any instruments, organism or viruses, reagents, software, or techniques that are referenced in the protocol. Add as many as are applicable.		
Website(s)	Enter the URLs of any related external websites, such as a lab page containing or describing the protocol or a full text link to the journal article. PubMed links should be captured in the **PubMed ID** field instead. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Reagents Introduction and Workflow

A reagent is a substance that is used in a chemical reaction or other experimental process to detect, measure, examine or produce other substances. Sometimes people confuse reagents with other biological specimens or organisms. eagle-i collects information about antibodies, cell lines, chemicals, constructs, gene knockdown reagents, micrarrays, nucleic acid reagents, proteins, and reagent libraries.

Creating Reagent Records

When entering resource information in the SWEET, the type of reagent selected in the Reagent Type field determines which fields display in the main body of the record. Therefore, it is necessary that this field be annotated correctly before entering or editing new records.

Special Issues and Workarounds

Greek characters are now fully supported and should be used where applicable. Super/subscripts may be represented using either brackets or HTML:

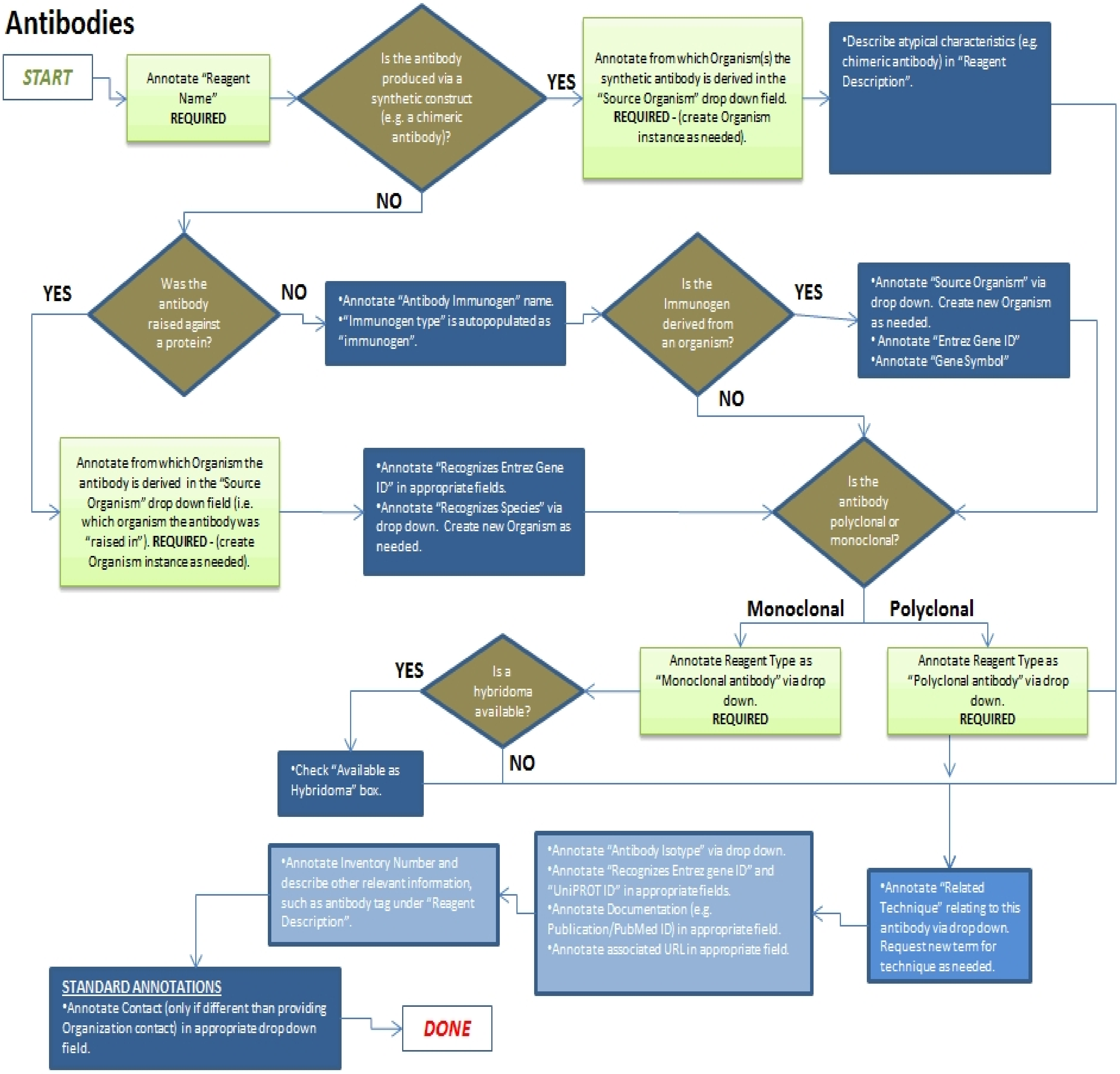
- Superscripts may be indicated using square brackets around the text. For example, for allele names: $agil^{2J}$ would be entered as agil[2J].
- Both super- and subscripts can also be represented using the HTML tags <sup> and <sub>. In particular, these tags should be used for resources for which the addition of extra brackets might be misleading. For example: the chemical compound $[^{11}C]CH_3I$ (methyl iodide) would be entered as [¹¹C]CH₃I. In these cases, in order to ensure the resource will still come up in search results, a version of the name without the HTML tags should also be entered in the Additional Name field.

Available Guidelines for Reagent Records

- Antibodies
- Cell Lines
- Chemical Reagents
- Constructs
- Gene Knockdown Reagents
- Microarrays
- Nucleic Acid Reagents
- Protein Reagents
- Reagent Libraries

Antibodies Introduction and Workflow

Antibodies are reagents comprised of immunoglobulins produced by B cells in response to an antigen. Antibody reagents can be engineered to have specificity for specific antigens.



Antibodies Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter the antibody name. Use the format: “Organism anti-organism Protein.” For example: “Mouse anti-human Tubulin.”	Yes	✓
Reagent Type	Select the appropriate type. If the sub-type isn't specified but the antibody is commercially available, check the manufacturer's online catalog to determine the sub-type.	Yes	✓
Reagent Description	Enter any information that describes the antibody but is not captured in any of the other fields. **High value:** description of atypical characteristics. For example, if the antibody is a synthetic construct.		
Reagent Additional Name	Enter any alternate names for the antibody. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the antibody (in other words, techniques for which you can use the antibody or that describe how it was used as a whole). Choose "Antibody related technique" from the drop-down to see a list common techniques related to antibodies; choose "Technique" to see the full technique hierarchy. Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Source Organism Type	Link to the species or lab-generated strain of organism from which the antibody was derived. In most cases, this will be a generic organism. See Organisms guidelines for more details. Note: In rare cases, more than one organism can be selected. If the same type of antibody is available from multiple organisms, a separate record should be created for each.	Yes	
Antibody Target(s)	A substance that is recognized by the antibody. Most often this is a protein, but it can also include chemicals or biological materials such a cells or organisms.		
Immunogenic Material	A substance used to generate an immune response to produce an antibody. For example: a protein, tissue, or virus.		
Isotype	Select the antibody isotype. This information can often be found on a commercial antibody data sheet from the manufacturer.		
Antibody Registry ID	Enter the unique ID number assigned to the antibody in the Neuroscience Information Framework (NIF) antibody registry (http://www.neuinfo.org/products/antibodyregistry/).		

	Use the format: AB_#######.		
Conjugate	A molecule conjugated to the antibody, which can be used to detect the presence of the antibody.		
Manufacturer	Link to the organization that created the antibody. May also be a person, but only if the person mass produces the antibody. Use the **Developed by** field for antibodies designed by a person but not mass produced.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to any people or organizations who designed or helped develop the antibody for limited or internal use only. If the antibody was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the antibody.		
Funded by	Link to any organizations that funded the purchase of the antibody or the work that produced it.		
Clone ID	Clone identification number assigned to a monoclonal antibody.		
Inventory Number	Enter the laboratory inventory identifier for the antibody. Format should correspond to whatever is used by the lab. For commercial resources, use the **Catalog Number** field instead.		
Lot Number	Enter the antibody lot number assigned by the manufacturer.		
Related grant number	Grant number for the funding that contributed to the development of the antibody. For example: 'U24 RR 029825'.		
Related Hybridoma Cell Line	Link to the hybridoma cell line used to produce the antibody. Applies to Monoclonal antibodies only. Note: A separate record for the hybridoma should only be created/linked to in this field if it is also available for sharing by the lab.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the antibody.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Immunogenic Material Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Immunogen Material Name	Enter the name of the protein or substance that provoked an immune response used to generate the antibody.	Yes	✓
Immunogen Material Type	Select the appropriate type.	Yes	✓

Entrez Gene ID	Enter the unique identifier assigned to the corresponding record in the Entrez Gene database (http://www.ncbi.nlm.nih.gov/gene). Annotate the full URL, which includes the ID.		
Entrez Gene Symbol	Enter the official symbol for the gene. (e.g. 'SHH' for sonic hedge hog.)		

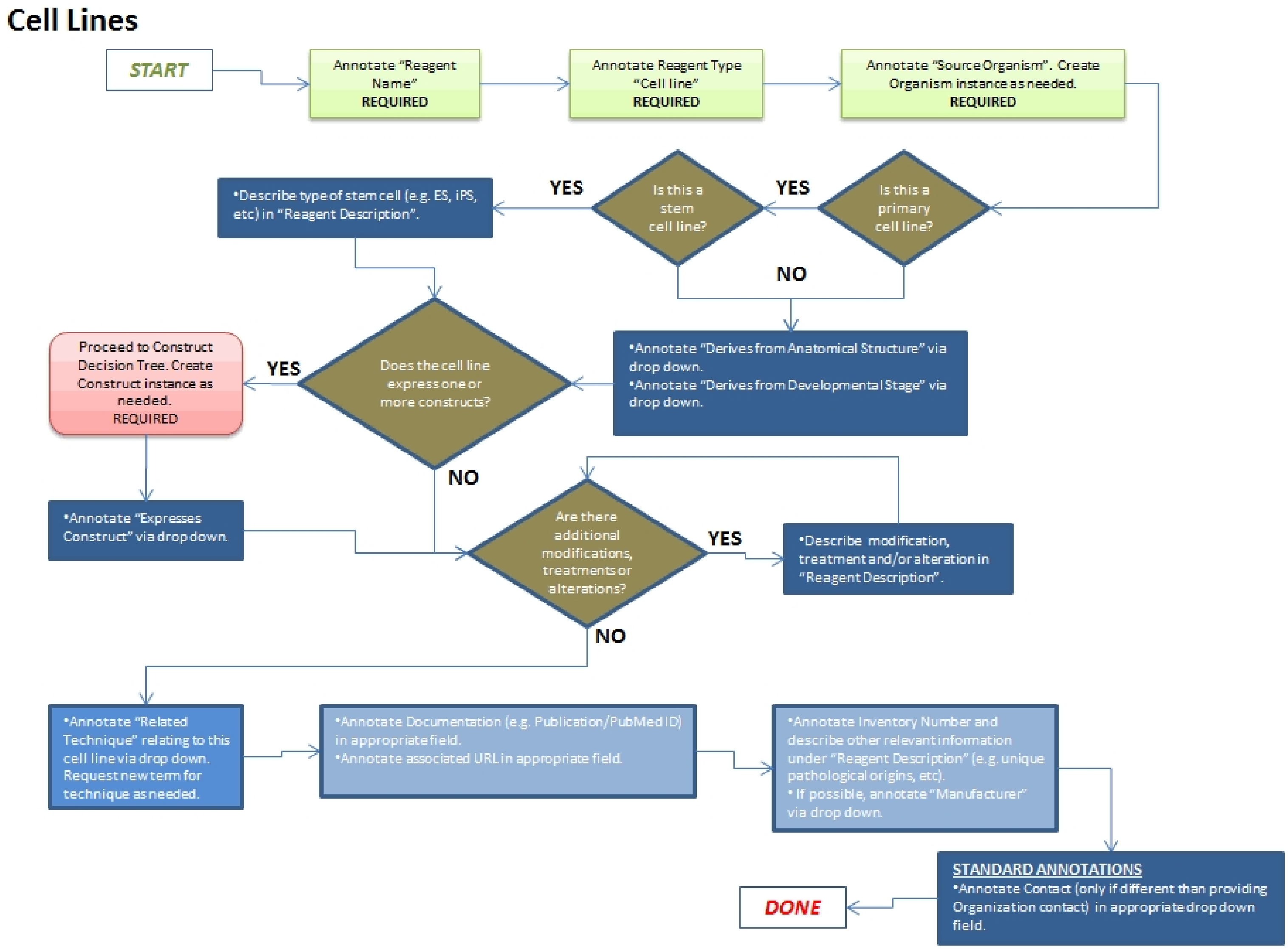
Antibody Target(s)

Note: NR indicates a non-repeatable field.

Field	**Description**	**Req.**	**NR**
Antibody target name	Enter the name of a substance that is recognized by the antibody.	**Yes**	✓
Antibody target type	Select the appropriate type.	**Yes**	✓
Entrez Gene ID	**High value.** Applies to Nucleic acid and Protein targets only. Enter the unique identifier assigned to the corresponding record in the Entrez Gene database (http://www.ncbi.nlm.nih.gov/gene). Annotate the full URL, which includes the ID.		
Entrez Gene Symbol	Applies to Nucleic acid and Protein targets only. Enter the official symbol for the gene. (e.g. 'SHH' for sonic hedge hog.)		
Sequence	Applies to Nucleic acid and Protein targets only. Enter the nucleic acid or protein sequence, such as: ATGCCG or or MATLK.		
Gene Cross Reactivity	Applies to Nucleic acid and Protein targets only. Enter any genes for which the antibody has been shown to cross react.		
Species Reactivity	Link to any organisms in which antibody target is recognized.		
Species Non-Reactivity	Link to any species in which the antibody has been shown not to cross react.		
Target Modification	Applies to Nucleic acid and Protein targets only. Enter the post-transitional modification to the protein, such as: phosphorylation, acetylation, or glycosylation.		
Target Sub Region	Applies to Biomolecular types only. Enter the subregion targeted by the antibody, such as the N- or C-terminus or a specific domain.		
UniPROT ID	Applies to Protein targets only. Enter the unique identifier of the protein from the UniPROT database: http://www.uniprot.org/. Whenever possible, annotate the full URL of the ID, rather than just the ID itself. For example: http://www.uniprot.org/uniprot/A6NMY6.		

Cell Lines Introduction and Workflow

A cell line reagent is a population of cells cultured in vitro that are descended through one or more generations (and possible sub-cultures) from a single primary culture which was originally derived from part of an organism. The cells of such a population share common characteristics.



Cell Lines Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter the cell line name. Should be as specific as possible, with any additional names provided in the appropriate field below. For example: use "HEK 293" instead of just "293." ("Human Embryonic Kidney 293" could be added as an additional name.)	Yes	✓
Reagent Type	Select the appropriate type.	Yes	✓
Reagent Description	Should include any information that describes the cell line but is not captured in any of the other fields. **High value data**: 1) Enter the selectable marker name. Commonly used selectable markers include: Neomycin, Gentamycin, G418, Hygromycin. 2) Describe any modifications, treatments or alterations. Example: information about stable expression of genes, knock-downs, etc.		
Reagent Additional Name	Enter any alternate names for the resource. Should include any abbreviations or alternate spellings. The full name can also be annotated here. For example: an additional name for CHO could be "Chinese hamster ovary cell line." Use separate lines for multiple names. Note: if there is information about the stable expression of a gene, such as "EA.hy926 stably expressing THADA shRNA5," move that to the **Resource Description**.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the cell line. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Genetic Alteration(s)	**High Value field.** Link to any records describing variations in sequence carried by macromolecules, or organism genomes that deviate from a canonical or reference sequence. Select an existing alteration record or create a new one by entering the name and type. If multiple genes are affected, link to a separate genetic alteration record for each.		
Related Technique	Select any methods related to or performed using the cell line (in other words, techniques for which you can use the cell line or that describe how it was used as a whole). For example, transfection or cell proliferation assay. Add as many techniques as are applicable; do not include any techniques used to generate the cell line.		
Source Organism Type	Link to the species or lab-generated strain of organism from which the cell line was derived. In most cases, this will be a generic organism, unless the specific organism is also available for sharing by the lab. See Organisms guidelines for more details. Note: this field should only be filled out if the cell line was **not** derived from a human sub-	Yes	

	ject. (See the **Source Human Subject** field below.)		
Source Anatomical Structure	Select the anatomical structure from which the cell line was derived.		
Source Developmental Stage	Select the developmental stage of the source organism at the time when the biological specimen pertaining to the it was collected.		
Source Human Subject	Link to the individual human subject from which the cell line was derived.		
Subject Age at Sampling	Enter the age of the organism or human subject at the time a biospecimen was collected for use in a technique or investigation (e.g. the collection of cells to generate the iPS cell line).		
Co-Developed Line(s)	Link to any other cell lines co-developed at the same time from the same biological source.		
Differentiated Cell Lines	Link to any available stem cell-derived lines that were generated through differentiation of this stem cell line.		
Differentiated Cell Types	Cell types into which the stem cell line has been shown to be capable of differentiating.		
Expresses Construct(s)	**High value field.** Link to any constructs that have been introduced into the genome of the stable cell line.		
Induction Method	Select the method used to induce pluripotency in the cell line.		
Induction Reagents	Enter a description of the specific reagents/procedures used for inducing pluripotency, including specific genes introduced or modified, vectors used, or facilitating chemicals applied.		
Karyotype Description	Enter any known information about the karyotype of the cells. This can simply indicate whether it's 'normal', 'abnormal', or 'unknown', or provide more precise information, such as an ISCN (International System for Cytogenetic Nomenclature) syntax description of the karyotype.		
Manufacturer	Link to the organization that created the cell line. May also be a person, but only if the person mass produces the cell line. Use the **Developed by** field for resources designed by a person but not mass produced.		
Parental Line	If applicable, link to an existing cell line from which this cell line was derived through an experimental modification or a characterized spontaneous change.		
Potency	Select any types of germ layers into which the cell line is capable of differentiating (e.g. select mesoderm, endoderm, ectoderm, and neural crest if fully pluripotent). If directed differentiation studies have been performed to test capability to form specific cell types, record this information as free text in the general **Reagent Description** field.		
QC Report	A document that describes the results of a study to characterize the molecular and cellular attributes of a cell line, including gene and protein expression patterns, morphological features, genetic variations, and sterility.		
Related Disease	Select any diseases or conditions for which the cell line presents some or all defining characteristics.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to any people or organizations who designed or helped develop the cell line for limited or internal use only. If the cell line was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the cell line.		
Funded by	Link to any organizations that funded the purchase of the cell line or the work that pro-		

	duced it.		
Inventory Number	Enter the laboratory inventory identifier for the cell line. Format should correspond to whatever is used by the lab. For commercial resources, use the **Catalog Number** field instead.		
Related grant number	Grant number for the funding that contributed to the development of the cell line. For example: 'U24 RR 029825'.		
Related NCBI Record	Enter the complete URLs of any NCBI database records or datasets that were generated about this resource. For example: gene expression analysis data in the Gene Expression Omnibus, genome variation data in dbVar, or sequence read data in the Sequence Read Archive.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the cell line.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

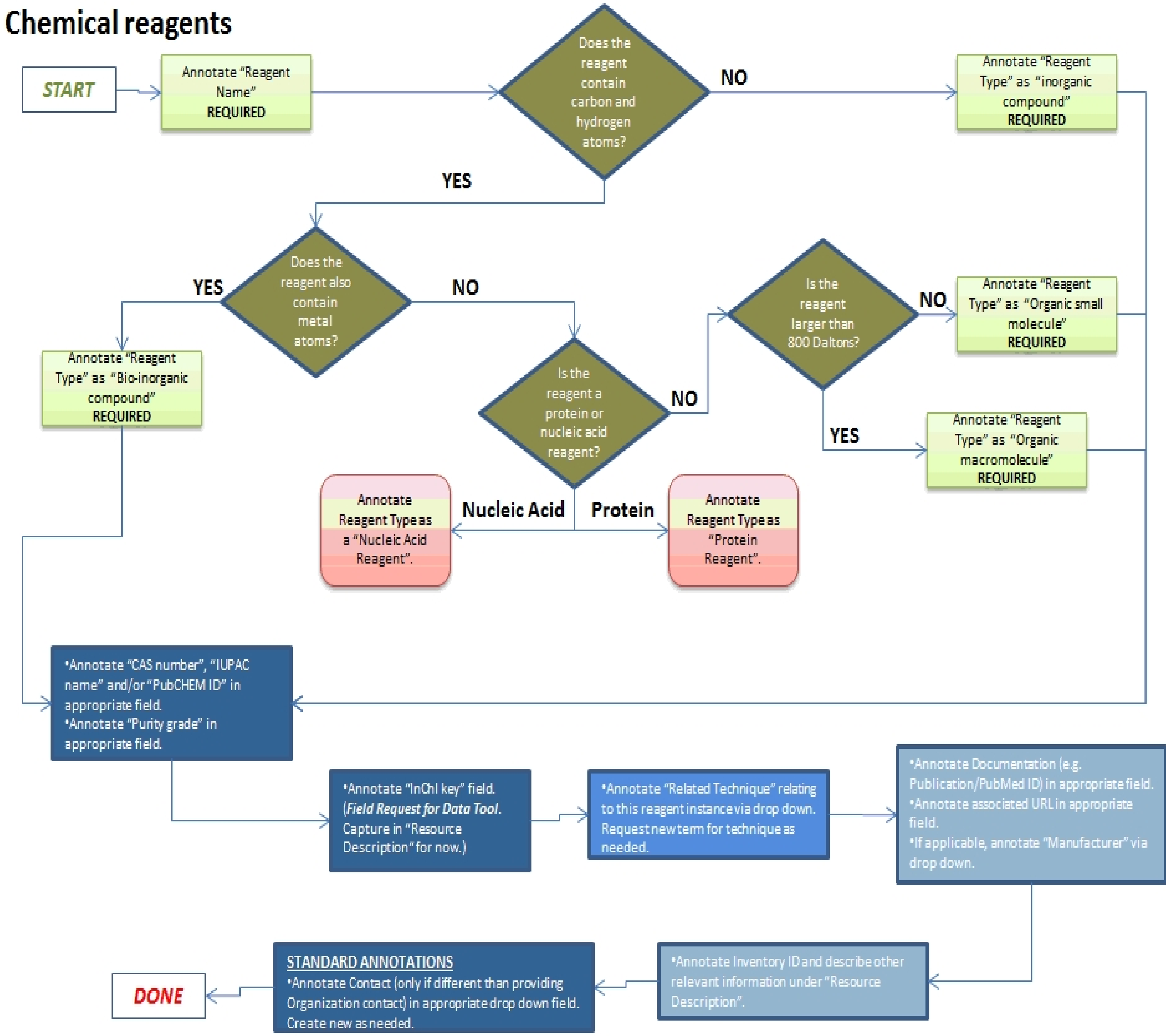
QC Report Field Annotation

Note: NR indicates a non-repeatable field.

Field	**Description**	**Req.**	**NR**
Cell line QC report Name	Report name.	**Yes**	✓
Cell line QC report Type	Pre-filled. No action necessary.	**Yes**	✓
Cell line QC report Description	Description of the validation/QC report generated about the cell line.		
Passage Number at Analysis	Passage number of the cell line when the reported analyses were performed.		
Study Type	The type of analysis described by the report. Indicate more than one by using the '+' button to the right, if appropriate.		
Assay(s) Applied	Specific assay(s) used in the generation of data described in the report. Indicate more than one by using the '+' button to the right, if appropriate.		
Website(s)	The URLs of any web addresses pertaining to the QC report.		

Chemical Reagents Introduction and Workflow

Chemical reagents are a material of pure chemical composition, either an element or a compound.



Chemical Reagents Field Annotation

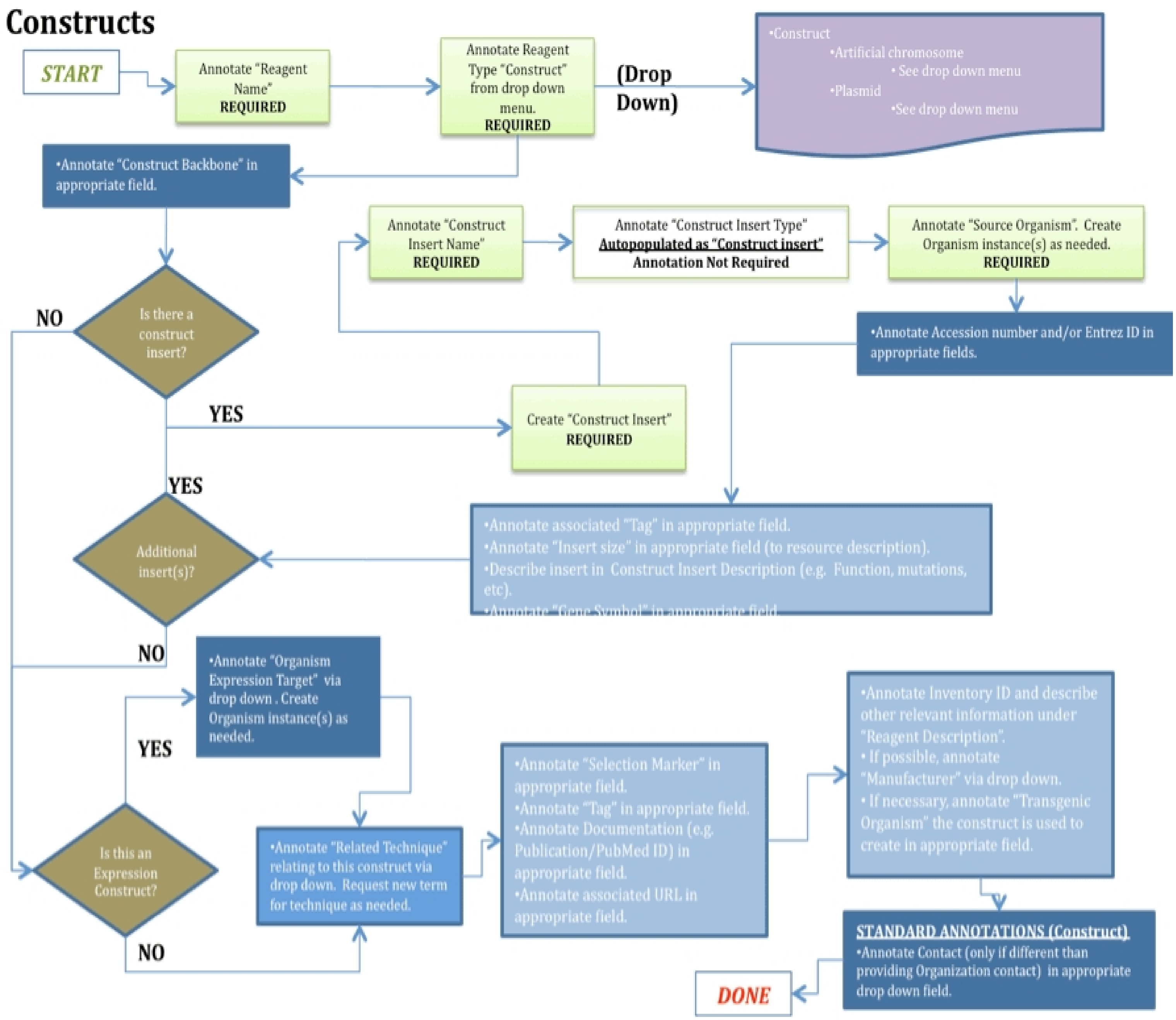
Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter the name of chemical reagent. The full name is preferred ("Sodium hydroxide") but molecular formula may also be used if more common. See the guidelines for superscripts for more details on how to enter molecular formulas.	**Yes**	✓
Reagent Type	Select the appropriate type. If a subtype is not annotated, you may be able to determine its type based on the chemical structure or CAS number, if it is provided.	**Yes**	✓
Reagent Description	Enter any information that describes the chemical but is not captured in any of the other fields.		
Reagent Additional Name	Enter any alternate names for the chemical. Should include any abbreviations or alternate spellings, such as: "NaOH." If the full name was not used in the label, it should be entered here. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the chemical. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the chemical (in other words, techniques for which you can use the resource or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the chemical.		
Manufacturer	Link to the organization that created the chemical. May also be a person, but only if the person mass produces the chemical. Use the **Developed by** field for resources designed by a person but not mass produced.		
CAS Number	**High Value Field.** A unique numeric identifier assigned by the Chemical Abstracts Service. Can contain up to 10 digits, divided by hyphens into three parts, such as this one for Caffeine: 58-08-2. Look up at: http://chem2.sis.nlm.nih.gov/chemidplus/chemidlite.jsp		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to the people or organizations who designed or helped develop the chemical for limited or internal use only. If the chemical was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the chemical.		
Funded by	Link to any organizations that funded the purchase of the cell line or the work that produced it.		

InChi Key	**High Value Field.** Enter the unique identifier assigned to the corresponding record in the InChi Key database: http://cactus.nci.nih.gov/chemical/structure. (InChI keys require special software, but the above link may find them) Example for Ethanol: 1/C2H6O/c1-2-3/h3H,2H2,1H3.		
Inventory Number	The laboratory inventory identifier for the chemical reagent. Format should correspond to whatever is used by the lab. For commercial resources, use the **Catalog Number** field instead.		
IUPAC Name	Enter the name assigned by the International Union of Pure and Applied Chemistry (IUPAC). Caution is necessary when names are long. IUPAC names can be found on MSDS, SciFinder, Merck Index, and the IUPAC database (http://www.chem.qmul.ac.uk/iupac/). For example: 1,3,7-trimethyl- 1H-purine- 2,6(3H,7H)-dione.		
PubChem ID	**High Value Field.** Identifier from the PubChem database of chemical molecules: http://pubchem.ncbi.nlm.nih.gov/. Example for Ethanol: "CID: 702"		
Purity Grade	Enter the purity grade of chemical, often expressed in the product name by means of a quality denomination that follows to the product nomenclature, such as Guaranteed Rights. This website has an example of purity grades: http://www.advtechind.com/grade.htm.		
Related grant number	Grant number for the funding that contributed to the development of the chemical. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the chemical.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Constructs Introduction and Workflow

A construct is a reagent that is a virus or DNA molecule capable of autonomous replication, used as a vehicle to transfer foreign genetic material into a host cell. A construct may contain an insert of DNA from an external source, and may be used for cloning or for expression purposes.



Constructs Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter a brief but descriptive name for the construct. Ideally this should this describe the backbone and insert, or whatever the lab has named it. For example: pBSK-SHH.	**Yes**	✓
Reagent Type	Select the appropriate type. "Expression construct" is an inferred type and should not be selectable. It is inferred when an expression host is chosen.	**Yes**	✓
Reagent Description	Enter any information that describes the construct reagent but is not captured in any of the other fields.		
Reagent Additional Name	Enter any alternate names for the construct. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the construct. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the construct (in other words, techniques for which you can use the resource or that describe how it was used as a whole). Example: transfection or transgenic animal model generation. Add as many techniques as are applicable; do not include any techniques used to generate the construct.		
Sequence	Enter the nucleic acid or protein sequence, such as: ATGCCG or or MATLK.		
Manufacturer	Link to the name of the organization that created the construct. May also be a person, but only if the person mass produces the construct. Use the **Developed by** field for constructs designed by a person but not mass produced.		
Accession Number	The unique identifier of a biological polymer sequence (DNA, RNA, protein) when it is submitted to a sequence database. Example: AC_123456. Note: First two letters can vary; for thorough formatting examples, see: http://www.ncbi.nlm.nih.gov/refseq/ or http://www.ncbi.nlm.nih.gov/nuccore.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Construct Backbone	**High Value Field.** Enter the name of the construct backbone. This label is often the first part of a construct name and refers to the part of the construct that is not the insert. Manufacturer would typically be associated with construct backbone.	**Yes**	
Construct Insert	**High value field**. Identifies the contents of the construct. Not required because there is not always an insert. But the record may be sent to a domain expert for review if the insert is missing. Note: if the construct has more than one gene inserted into it, two construct inserts		

	should be entered, each with their own name, source organism and Entrez Gene IDs. Example: pRS424-ADH/B42-SRB2 should have a separate insert for both the ADH gene and the SRB2 gene. If it is a construct promoter, it should also be included as a separate construct insert.		
Developed by	Link to any people or organizations who designed or helped develop the construct for limited or internal use only. If the resource was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the construct.		
Funded by	Link to any organizations that funded the purchase of the resource or the work that produced it.		
Inventory Number	Enter the laboratory inventory identifier for the construct. Format should correspond to whatever is used by the lab. For commercial resources, use the **Catalog Number** field instead.		
Organism Expression Target	Link to the organism in which the construct is designed to be expressed. For expression constructs only. The generic organism should be annotated. Note: if the organism is a prokaryote, the construct type should be "prokaryotic expression construct" and vice versa. Prokaryote organism types can be verified in the Ontology Browser.		
Related grant number	Grant number for the funding that contributed to the development of the construct. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the construct.		
Selectable Marker	**High Value Field.** Gene that confers antibiotic resistance. Bacterial selection markers and mammalian selection markers should all go in this field; there is no need to indicate which type of marker it is. Enter bacterial selection marker "ampicillin-" as Ampicillin. Enter mammalian selection marker "hygromycin-" as Hygromycin. Enter both "Amp" or "AmpR-" as Ampicillin, and "Kan" or "KanR" as Kanamycin.		
Transgenic Organism	**High Value Field.** Link to any transgenic organism generated using the construct.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Construct Insert Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Construct Insert Name	Enter the name of the insertion. Can be just the gene name, or the gene name with the modification, such as: SHH or SHH[delta]S45A. Annotate Cre as "Cre recombinase." Note: fluorescent markers such as GFP should be annotated in the Tag field.	Yes	✓

Construct Insert Type	Pre-filled. No action necessary.	**Yes**	✓
Construct Insert Description	Enter any information that describes the construct insert but is not captured in any of the other fields, such as the gene name, modification, isoform, etc. Note that reference to a gene name here is informal; please record the specific gene ID in the designated field.		
Entrez Gene ID	**High value field.** Enter the unique identifier assigned to the corresponding record in the Entrez Gene database (http://www.ncbi.nlm.nih.gov/gene). Annotate the full URL, which includes the ID.		
Entrez Gene Symbol	Enter the official symbol for the gene. (e.g. 'SHH' for sonic hedge hog.)		
Sequence	The nucleic acid or protein sequence, such as: ATGCCG or MATLK.		
Accession Number	A the unique identifier of a biological polymer sequence (DNA, RNA, protein) when it is submitted to a sequence database. Example: AC_123456. Note: First two letters can vary; for thorough formatting examples, see: http://www.ncbi.nlm.nih.gov/refseq/ or http://www.ncbi.nlm.nih.gov/nuccore.		
Insert Size	Should be a number labeled with kb or bp. Example: 1.0kb or 1000bp.		
Source Organism	Link to the organism from which the construct insert is derived. In most cases, this will be a generic organism, unless the specific organism is also available for sharing by the lab. See Organisms guidelines for more details. Not required because not all inserts come from an organism; some are synthetic.		
Tag	Expression tag that allows tracking of the RNA or protein. Common examples: GFP, FLAG, HA, HIS, Myc. Should be a tag that is on the insert only. Tags on the plasmid that are not linked to the gene insert should be described in the resource description for the construct.		

Gene Knockdown Reagents Introduction and Workflow

A Gene Knockdown reagent is a reagent that is capable of reducing the expression of a target gene in a biological system.

Gene Knockdown Reagent Field Annotation

Note: NR indicates a non-repeatable field.

Field	**Description**	**Req.**	**NR**
Reagent Name	Enter the name of gene knockdown reagent, such as: SHH siRNA oligo.	**Yes**	✓
Reagent Type	Select the appropriate type.	**Yes**	✓
Reagent Description	Enter any information that describes the gene knockdown reagent but is not captured in any of the other fields.		
Reagent Additional Name	Enter any alternate names for the gene knockdown reagent. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methode related to or performed using the gene knockdown reagent, such as transfection or electroporation. Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Sequence	Enter the nucleic acid or protein sequence. For example: ATGCCG or MATLK.		
Manufacturer	Link to the organization that created the resource. May also be a person, but only if the person mass produces the resource. Use the **Developed by** field for gene knockdown reagents designed by a person but not mass produced.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to any people or organizations who designed or helped develop the resource for limited or internal use only. If the resource was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the gene knockdown reagent.		
Funded by	Link to any organizations that funded the purchase of the resource or the work that produced it.		
Inventory Number	Enter the laboratory inventory identifier for the gene knockdown reagent. Format should correspond to whatever is used by the lab. For commercial resources, use the **Catalog**		

	Number field instead.		
Related grant number	Grant number for the funding that contributed to the development of the gene knock-down reagent. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the resource.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.**Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Microarrays Introduction and Workflow

A microarray reagent is a processed material that is made to be used in an analyte assay. It consists of a physical immobilization matrix in which substances that bind the analyte are placed in regular spatial position.

Microarray Reagent Field Annotation Table

Note: NR indicates a non-repeatable field.

Field	Description	Req	NR
Reagent Name	Enter the name of the microarray reagent, such as: "Affymetrix mouse microarray."	Yes	✓
Reagent Type	Select the appropriate type.	Yes	✓
Reagent Description	Enter any information that describes the microarray reagent but is not captured in any of the other fields.		
Reagent Additional Name	Enter any alternate names for the resource. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the resource (in other words, techniques for which you can use the resource or that describe how it was used as a whole). Example: Affymetrix array. Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Manufacturer	Link to the organization that created the microarray. May also be a person, but only if the person mass produces the microarray. Use the **Developed by** field for microarrays designed by a person but not mass produced.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to any people or organizations who designed or helped develop the resource for limited or internal use only. If the resource was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the microarray.		
Funded by	Link to any organizations that funded the purchase of the resource or the work that produced it.		
Inventory Number	The laboratory inventory identifier for the microarray. Format should correspond to		

	whatever is used by the lab. For commercial resources, use the **Catalog Number** field instead.		
Related grant number	Grant number for the funding that contributed to the development of the microarray. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the resource.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Nucleic Acid Reagents Introduction and Workflow

A Nucleic Acid reagent is a polymer comprised of nucleotides, each of which consists of three components: a nitrogenous heterocyclic base, which is either a purine or a pyrimidine; a pentose sugar; and a phosphate group.

Nucleic Acid Reagents Field Annotation

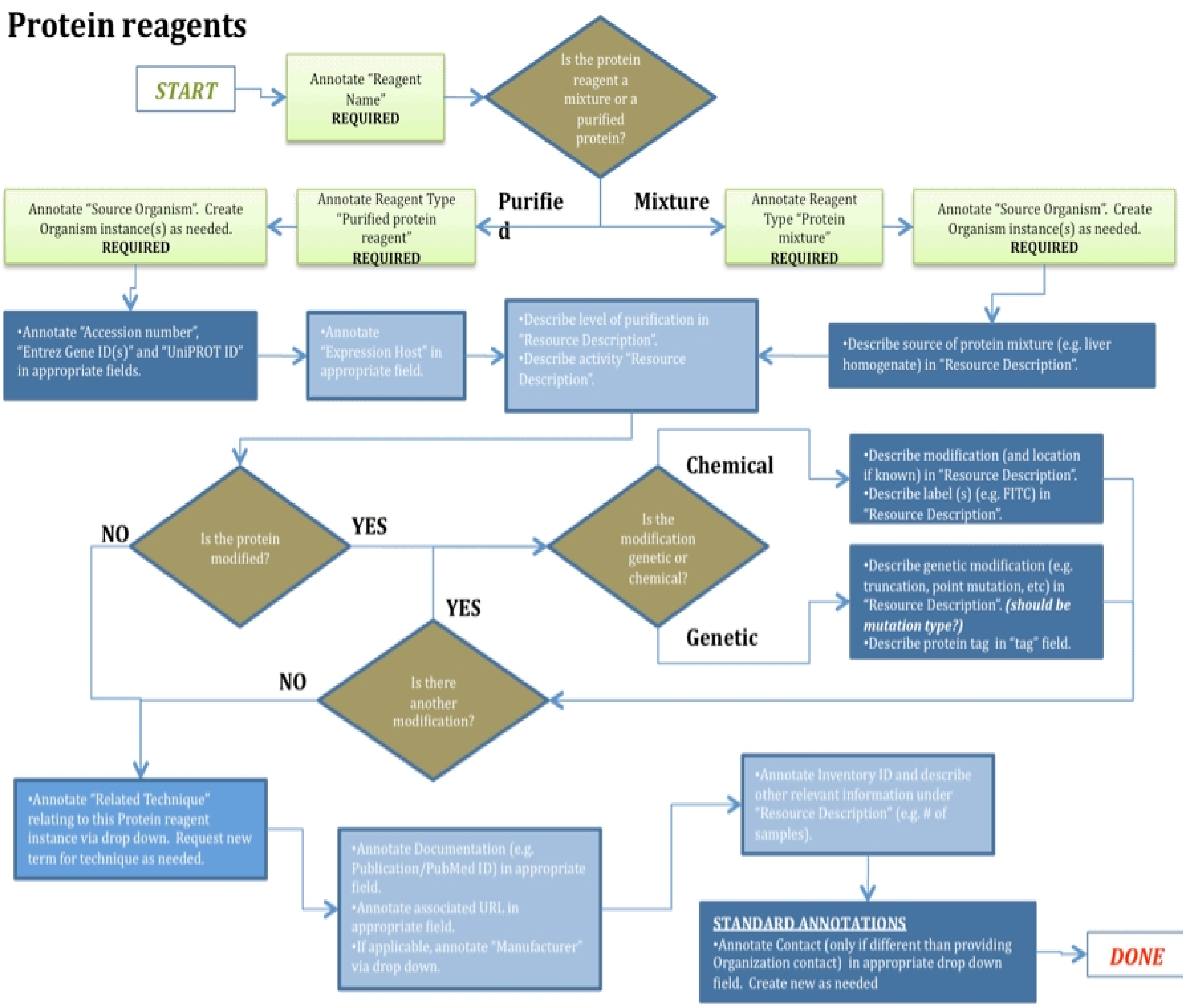
Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter the name of nucleic acid reagent.	**Yes**	✓
Reagent Type	Select the appropriate type.	**Yes**	✓
Reagent Description	Enter any information that describes the nucleic acid reagent but is not captured in any of the other fields. Note: Either the Entrez gene ID OR both the organism and the gene name is required. If the record is missing both, then there should be an explanation in resource description.		
Reagent Additional Name	Enter any alternate names for the resource. Spell out abbreviations such as SHH siRNA-A=Sonic Hedgehog small interfering RNA. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Entrez Gene ID	**High Value Field.** Enter the unique identifier assigned to the corresponding record in the Entrez Gene database (http://www.ncbi.nlm.nih.gov/gene). Annotate the full URL, which includes the ID.		
Entrez Gene Symbol	Enter the official symbol for the gene. (e.g. 'SHH' for sonic hedge hog.)		
Genetic Alteration	**High Value field.** Link to any records describing variations in sequence carried by macromolecules, or organism genomes that deviate from a canonical or reference sequence. Select an existing alteration record or create a new one by entering the name and type. If multiple genes are affected, link to a separate genetic alteration record for each.		
Related Technique	Select any methods related to or performed using the nucleic acid reagent (in other words, techniques for which you can use the resource or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Sequence	The nucleic acid or protein sequence of the nucleic acid reagent, such as: ATGCCG or MATLK.		
Manufacturer	Link to the organization that created the resource. May also be a person, but only if the		

	person mass produces the resource. Use the **Developed by** field for resources designed by a person but not mass produced.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to any people or organizations who designed or helped develop the resource for limited or internal use only. If the resource was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the nucleic acid reagent.		
Funded by	Link to any organizations that funded the purchase of the resource or the work that produced it.		
Inventory Number	Enter the laboratory inventory identifier for nucleic acid reagent. Format should correspond to whatever is used by the lab. For commercial resources, use the **Catalog Number** field instead.		
Related grant number	Grant number for the funding that contributed to the development of the nucleic acid reagent. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the resource.		
Source Organism or Virus	The species or lab-generated strain of organism from which the nucleic acid reagent was derived. In most cases, this will be a generic organism, unless the specific organism is also available for sharing by the lab. See Organisms guidelines for more details.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Protein Reagents Introduction and Workflow

A protein reagent is a sequence of amino acids.



Protein Reagents Field Annotation

For purified proteins: A minimum of either “Accession number”, “Entrez Gene ID(s)” and “UniPROT ID” is required. If all are absent, look up at least one or send back to the record creator. Note: Need to know “Derives from Organism” in order to determine ID#.

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter a brief but descriptive name for the protein. Should describe any modifications, such as tags, etc. For example: SHH-GST.	**Yes**	✓
Reagent Type	Select the appropriate type. If annotated to protein reagent, use the name, Entrez Gene ID, or Accession Number to determine a more specific sub-type. If the resource has a specific protein name, it will be a purified protein reagent in most cases.	**Yes**	✓
Reagent Description	Enter any information that describes the protein but is not captured in any of the other fields. If describing activity, format as “Activity: xxx” Use Gene Ontology for guidance when applicable. **High value data:** 1) Description of source of protein mixture (e.g. liver homogenate) 2) Description of chemical modification (and location, if known) 3) Describe label(s) (e.g. FITC) 4) Description of genetic modification (e.g. truncation, point mutation, etc)		
Reagent Additional Name	Enter any alternate names for the protein. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Entrez Gene ID	**High value field.** Only applies to purified proteins. Enter the unique identifier assigned to the corresponding record in the Entrez Gene database (http://www.ncbi.nlm.nih.gov/gene). Annotate the full URL, which includes the ID.		
Entrez Gene symbol	**High value field.** Enter the official symbol for the gene. (e.g. 'SHH' for sonic hedge hog.) See the **Gene and protein symbol conventions** table below for examples.		
Genetic Alteration	**High Value field.** Link to any records describing variations in sequence carried by macromolecules, or organism genomes that deviate from a canonical or reference sequence. Select an existing alteration record or create a new one by entering the name and type. If multiple genes are affected, link to a separate genetic alteration record for each.		

Related Technique	Select any methods related to or performed using the resource (in other words, techniques for which you can use the resource or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Sequence	Enter the nucleic acid or protein sequence, such as: ATGCCG or MATLK.		
Manufacturer	Link to the organization that created the resource. May also be a person, but only if the person mass produces the resource. Use the **Developed by** field for resources designed by a person but not mass produced.		
Accession Number	**High value field.** Only applies to purified proteins. The unique identifier of a biological polymer sequence (DNA, RNA, protein) when it is submitted to a sequence database. Example: AC_123456. Note: First two letters can vary; for thorough formatting examples, see: http://www.ncbi.nlm.nih.gov/refseq/ and http://www.ncbi.nlm.nih.gov/nuccore.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to any people or organizations who designed or helped develop the protein for limited or internal use only. If the resource was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the protein.		
Expression Host	**High value field.** Host in which the protein was generated. Example: mammalian cells, insect cells, bacterial cells.		
Funded by	Link to any organizations that funded the purchase of the resource or the work that produced it.		
Inventory Number	Enter the laboratory inventory identifier for the resource. Format should correspond to whatever is used by the lab. For commercial resources, use the **Catalog Number** field instead.		
Related grant number	Grant number for the funding that contributed to the development of the protein. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the resource.		
Tag	**High value field.** Enter any expression tags that allow tracking of the RNA or protein. Common examples: GFP, FLAG, HA, HIS, Myc.		
UniPROT ID	**High value field.** Only applies to purified proteins. Enter the unique identifier of the protein from the UniPROT database: http://www.uniprot.org/. Whenever possible, annotate the full URL of the ID, rather than just the ID itself. For example: http://www.uniprot.org/uniprot/A6NMY6.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Gene and protein symbol conventions (“sonic hedgehog” gene)

Examples of common nomenclature: human gene symbols are all capitals (e.g. SHH); mouse gene symbols have the first letter capitalized (Shh). For nomenclature specific to other species, see: http://en.wikipedia.org/wiki/Gene_nomenclature.

Species	**Gene symbol**	**Protein symbol**
Homo sapiens	*SHH*	SHH
Mus musculus, Rattus norvegicus	*Shh*	SHH
Danio rerio	*Shh*	Shh

Reagent Libraries Introduction and Workflow

A Reagent Library consists of a collection of individual reagents of a given type. eagle-i collects information about: Chemical libraries, Nucleic acid libraries, Organism libraries, Peptide libraries.

Available Guidelines for Reagent Library Records

- Annotation Guidelines for Chemical libraries records
- Annotation Guidelines for Nucleic acid libraries records
- Annotation Guidelines for Organism libraries records
- Annotation Guidelines for Peptide libraries records

Chemical Library Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter the name of chemical library.	**Yes**	✓
Reagent Type	Select the appropriate type.	**Yes**	✓
Reagent Description	Enter any information that describes the chemical library but is not captured in any of the other fields.		
Reagent Additional Name	Enter any alternate names for the chemical library. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the chemical library (in other words, techniques for which you can use the resource or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Manufacturer	Link to the organization that created the chemical library. May also be a person, but only if the person mass produces the library. Use the **Developed by** field for resources designed by a person but not mass produced.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to any people or organizations who designed or helped develop the chemical library for limited or internal use only. If the resource was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the chemical library resource.		
Funded by	Link to any organizations that funded the purchase of the resource or the work that produced it.		
Inventory Number	Enter the laboratory inventory identifier for the resource. Format should correspond to whatever is used by the lab. For commercial resources, use the Catalog Number field instead.		
Library Count	Enter the number of elements in the library. Format as number only.		
Library Source	**High value field.** Link to the organization that was the original provider of the library.		

Related grant number	Grant number for the funding that contributed to the development of the chemical library. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the chemical library.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Nucleic Acid Library Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter the name of nucleic acid library.	**Yes**	✓
Reagent Type	Select the appropriate type.	**Yes**	✓
Reagent Description	Enter any information that describes the nucleic acid library but is not captured in any of the other fields.		
Reagent Additional Name	Enter any alternate names for the resource. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the nucleic acid library (in other words, techniques for which you can use the library or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Manufacturer	Link to the organization that created the nucleic acid library. May also be a person, but only if the person mass produces the resource. Use the **Developed by** field for resources designed by a person but not mass produced.		
Bacterial Host Strain	Enter the bacterial strain in which the library is hosted.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to any people or organizations who designed or helped develop the nucleic acid library for limited or internal use only. If the resource was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the nucleic acid library.		
Funded by	Link to any organizations that funded the purchase of the resource or the work that produced it.		
Inventory Number	Enter the laboratory inventory identifier for the resource. Format should correspond to whatever is used by the lab. For commercial resources, use the **Catalog Number** field instead.		

Library Count	Number of elements in the library. Format as number only.		
Library Source	**High value field.** Link to the organization that was the original provider of the library.		
Producer Strain	Enter the bacterial strain used to produce the nucleic acid library.		
Related grant number	Grant number for the funding that contributed to the development of the nucleic acid library. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the nucleic acid library.		
Source Organism or Virus	Link to the species or lab-generated strain of organism from which the resource was derived. In most cases, this will be a generic organism, unless the specific organism is also available for sharing by the lab. See Organisms guidelines for more details.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Peptide Library Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter the name of peptide library.	**Yes**	✓
Reagent Type	Select the appropriate type.	**Yes**	✓
Resource Description	Enter any information that describes the peptide library but is not captured in any of the other fields. Note: All Peptide library records should contain a description (information about what the library contains, applications, etc.).		
Reagent Additional Name	Enter any alternate names for the resource. Should include any abbreviations or alternate spellings for the protein. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the peptide library (in other words, techniques for which you can use the library or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Manufacturer	Link to the organization that created the resource. May also be a person, but only if the person mass produces the resource. Use the **Developed by** field for resources designed by a person but not mass produced.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Derives from Organism	Select the species or lab-generated strain of organism from which the resource was derived. In most cases, this will be a generic organism, unless the specific organism is also available for sharing by the lab. See Organisms guidelines for more details. Note: if this field is missing, there should be an explanation why in resource description (i.e. it is synthetic).		
Developed by	Link to any people or organizations who designed or helped develop the resource for limited or internal use only. If the resource was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the peptide library.		
Funded by	Link to any organizations that funded the purchase of the resource or the work that pro-		

	duced it.		
Inventory Number	Enter the laboratory inventory identifier for the resource. Format should correspond to whatever is used by the lab. For commercial resources, use the Catalog Number field instead.		
Library Count	Enter the number of elements in the library. Format as number only.		
Library Source	**High value field.** Link to the organization that was the original provider of the library.		
Related grant number	Grant number for the funding that contributed to the development of the peptide library. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the peptide library.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Organism Library Field Annotation

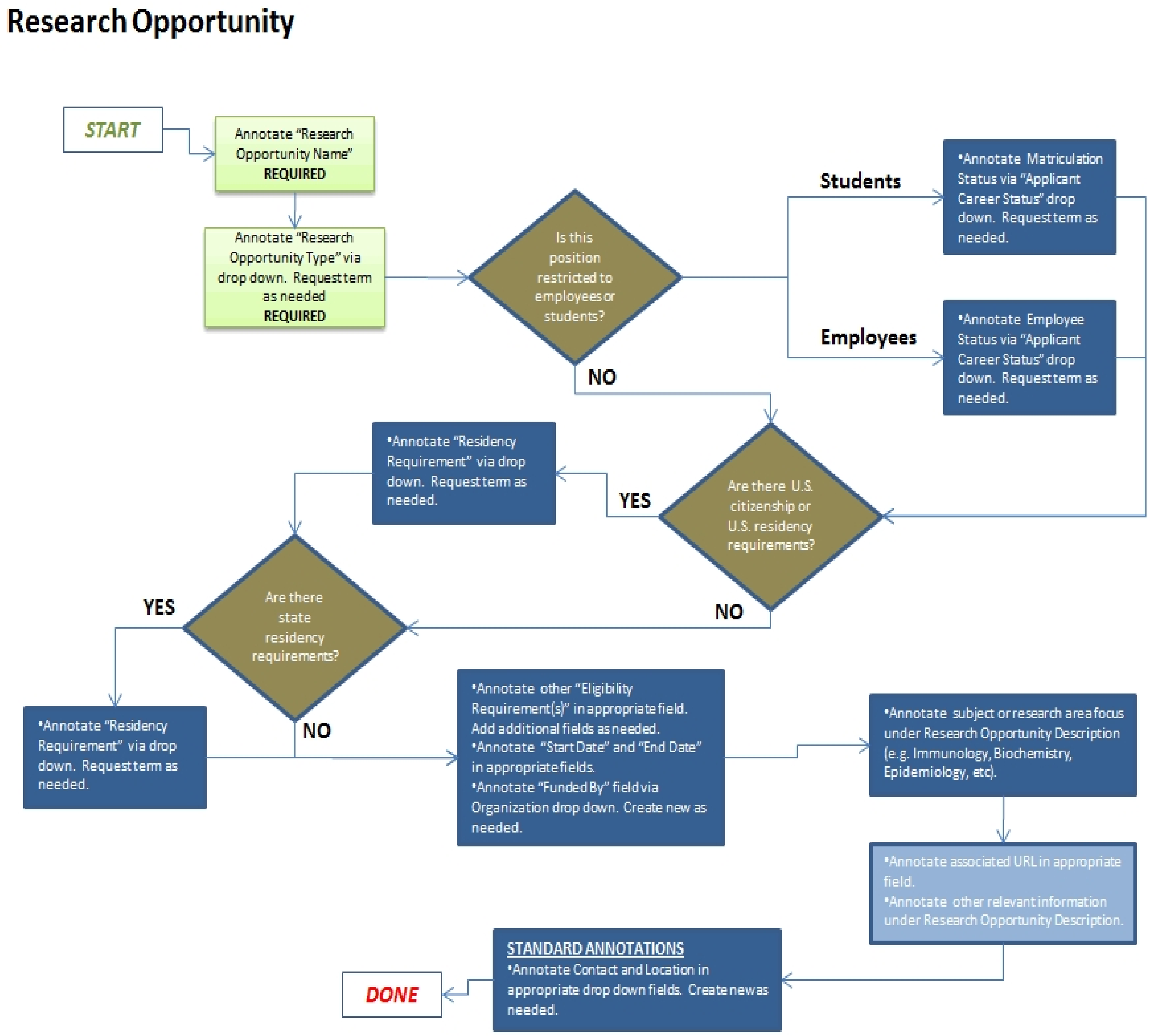
Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Reagent Name	Enter the name of organism library.	Yes	✓
Reagent Type	Select the appropriate type.	Yes	✓
Reagent Description	Enter any information that describes the organism library but is not captured in any of the other fields.		
Reagent Additional Name	Enter any alternate names for the resource. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Location	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the organism library (in other words, techniques for which you can use the library or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Manufacturer	Link to the organization that created the resource. May also be a person, but only if the person mass produces the resource. Use the **Developed by** field for resources designed by a person but not mass produced.		
Catalog Number	Refers to a commercial catalog number. Should be formatted with the name of the company followed by a colon and the number.		
Developed by	Link to any people or organizations who designed or helped develop the resource for limited or internal use only. If the resource was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the organism library.		
Expression vector	Link to the expression vector into which the library is cloned. Lambda phage libraries only.		
Funded by	Link to any organizations that funded the purchase of the resource or the work that produced it.		
Inventory Number	Enter the laboratory inventory identifier for the resource. Format should correspond to whatever is used by the lab. For commercial resources, use the **Catalog Number** field instead.		
Related grant number	Grant number for the funding that contributed to the development of the organism library. For example: 'U24 RR 029825'.		

Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the organism library.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Research Opportunities Introduction and Workflow

Research Opportunities are opportunities to participate in research training. Research opportunities may be available to people at any stage of their career.



Research Opportunity Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Research Opportunity Name	Enter the name of the research opportunity. Example: Postdoctoral Research Fellowships in Biology.	**Yes**	✓
Research Opportunity Type	Pre-filled. No action necessary.	**Yes**	✓
Research Opportunity Description	Enter any information that describes the opportunity but is not captured in any of the other fields.		
Research Opportunity Additional Name	Enter any alternate names for the resource. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Provided By	Link to the record of the owning organization. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Start Date	Earliest date at which the opportunity is available. Format as: MM/DD/YYYY. Example: 07/13/2015.		
End Date	Date at which the opportunity is no longer available. Format as: MM/DD/YYYY. Example: 07/13/2016.		
Access Restriction (s)	List any restrictions on resource availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Additional Topic(s)	Enter any applicable subject areas for the opportunity. For example: Bioinformatics. Level of detail may vary.		
Applicant Career Status	Select the employee and/or matriculation status of applicants that may apply for the research opportunity. Add as many as are applicable.		
Eligibility Requirement	Enter any requirements for research opportunity eligibility, such as: coursework, minimum GPA, state residency, under-represented group status, or field of study. Add as many as are applicable.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the research opportunity.		
Funded By	Link to any organizations providing financial support for the Research Opportunity. In most cases, this will be a government organization, parent organization, or affiliate of the providing organization.		
Related grant number	Grant number for the funding that contributed to the development of the Research Opportunity. For example: 'U24 RR 029825'.		
Residency Requirement	Select the US residency status of applicants who may apply for the research opportunity. Add as many as are applicable.		

Website(s)	Enter the URLs of any related external websites. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Services Introduction and Workflow

A *service* is a planned process carried out by an organization with the objective of performing a technique, providing training, providing storage of data or physical resources, or providing access to instruments for another person or organization.

Service records often reference other types of records, particularly instruments, protocols, software, techniques, and people. Before publishing service record, it is important to open each referenced record to ensure that the correct connections have been made. See Deleting Records for more details on how to deal with incorrect connections.

Core Facilities and Tech Transfer Offices

Although research laboratories, centers and other organizations may sometimes provide services, they are most often associated with core laboratories; by definition, every published core laboratory must have provide at least one published service, even if that service is merely access to equipment or facilities.

If the service is provided by a Technology Transfer Office, see the Technology Transfer Office guidelines for special considerations.

Creating Service Records

Watch this video tutorial for a demonstration of how to create service records in the SWEET.

It is especially important for service records to be well described. Although some service names alone may provide enough of a description, many require more information to make what the service includes clear to users. You should ensure that a concise but complete description is available, either by questioning the record creator or pulling information off of the organization's website.

Consolidating Service Records

In some cases, a record creator may have created multiple individual records that are variations upon a theme and contain very little distinct information other than a service name. You should use your best judgment to determine whether consolidating these records would make more sense from a search user perspective, both aesthetically and content-wise: for example, if a particular core offers a large number of similar tests, but provides no information about each one other than a name, it may be preferable to create one record with a more generic name and include the list of individual tests in the resource description. In this way, the information is still searchable, but avoids having a large number of mostly empty records. If there is detailed information available about each test, however, it may make more sense to leave them as individual records.

To consolidate service records, you must manually copy and paste all relevant information into whatever records are being kept and make sure to re-link any associated records before deleting any of the records not being kept. See guidelines for Merging Records.

Services Field Annotation

Note: NR indicates a non-repeatable field.

Field	Description	Req.	NR
Service Name	Enter a brief but descriptive name for the service. Capitalize the first letter of all services, unless the word is a name that should not be capitalized (e.g. "iPSC line propagation"). Note: Service names should be as clear as possible. For example: "HPV testing" is a sufficiently clear service name; "HPV" alone is ambiguous. If necessary, the word "service" may also be appended to the end of the label to aid in clarity.	Yes	✓
Service Type	Select the most relevant service type. If multiple types are applicable, choose the one that most accurately describes the service, i.e. if both access and training are provided, select the sub-type for whichever aspect should most be emphasized to users. Do not leave as 'Service' if it is at all possible to select a more specific sub-type.	Yes	✓
Service Description	Enter any information that describes the service but is not captured in any of the other fields.		
Service Additional Name	Enter any alternate names for the service. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Service Provided By	Link to the organization that provides the service. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on service availability. This may include both institutional (such as the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the service. Add as many techniques as are applicable.		
Topic	Select any organisms, biological processes, or diseases that are the subject matter of the service. If choosing an organism, in most cases, this will be a generic organism. See Organisms guidelines for more details.		
Fee for Service	Indicate whether there is a fee charged for the service. Select <none> if fee information is unknown.		✓
Service fee URL	Enter the URL of any external websites that contain fee information for the service. Note: in general, specific fee amounts are considered too ephemeral to collect and should not be noted in the record itself unless they will be updated frequently by the resource owner.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the service.		
Related grant number	Grant number for the funding that contributed to the development of the service. For example: 'U24 RR 029825'.		
Related Protocol(s)	Link to any protocols used to perform the service.		

Related Publication or Documentation	Link to any journal articles or patents that contain information related to the service.		
Related Resource	Link to any databases, instruments, organisms, viruses, reagents, or software to which the service provides access or training.		
Website(s)	Enter the URLs of any related external websites. All services should have at least one website, if one is at all available. If no specific page exists for the service, use the main URL for the providing organization website. All URLs should include the full address, such as: http://www.eagle-i.net. Note: if the page deals with fee information, the URL should go in the **Service fee URL** field above; it does not need to be entered in both fields.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Software Introduction and Workflow

Software refers to digitally stored data, such as computer programs and other kinds of information read and written by computers.

Only a single record should be used to represent multiple copies of the same software in a single lab. Type in the number of copies available in the laboratory in the Resource Description, and include any separate version numbers on separate lines in the "Version" field. Multiple copies of the same software located in different laboratories should be represented by separate records.

Collecting Information About Algorithms

The past 10 years have seen an historic pace of technical advancement in DNA sequencing, DNA analysis, and the quantitative chemical analysis of complex mixtures. The resulting precipitous drop in the cost of endeavors like genome sequencing, transcription and protein profiling, and metabolic analyte analysis has produced an explosion of data quantity that has far outpaced the ability to efficiently analyze the results. This, in turn, has resulted in a great demand for better data analysis tools. In response, academic labs have made numerous local breakthroughs in mathematical analysis of complex data sets. These new data analysis methods are routinely incorporated into small, locally developed software programs designed to specifically meet the needs of a specific analytical problem.

Algorithm software produced in labs is generally shared freely with the community but scattered on individual laboratory websites and in open-source repositories. eagle-i collects information about these algorithms and allows organizations to represent software bundles (or tool kits), and to link individual pieces of algorithm software to demonstrate aggregated, multi-algorithm pipelines.

Software Field Annotation

Note: NR indicates a non-repeatable field.

Field	**Description**	**Req.**	**NR**
Software Name	Enter the name of the program. For example: "RNABuilder."	**Yes**	✓
Software Type	Select the type of software. All software that is neither an algorithmic component or suite should be left at just "Software."	**Yes**	✓
Software Description	Enter any information that describes the software but is not captured in any of the other fields. A brief description of the software's function may be useful here.		
Software Additional Name	Enter any alternate names for the resource. Should include any abbreviations or alternate spellings. Use separate lines for multiple names.		
Used by	Link to the record of the owning organization that uses the software. Pre-populated, read-only field.		✓
Contact	Link to the primary person responsible for the resource. Not needed if the same as the contact for the providing organization. Check to make sure a record for the person you want to add does not already exist before creating a new record. If creating a new person record, enter name in the format: Last name, First name, Degree.		
Access Restriction(s)	List any restrictions on resource availability. This may include both institutional (such as		

	the providing laboratory, associated hospital, department, or university) and geographically-defined restrictions (such as metro areas, counties, states, or regions, university or consortium affiliation, professional certification). If more than one restriction applies, enter them on separate lines.		
Related Technique	Select any methods related to or performed using the software (in other words, techniques for which you can use the software or that describe how it was used as a whole). Add as many techniques as are applicable; do not include any techniques used to generate the resource.		
Software purpose	Select the appropriate software objectives. Add as many as are applicable.		
Algorithm used	Select the algorithm that the software uses to complete its objective.		
Data Input	Describes the data put into the software at the start of its process.		
Data Output	Describes the data output after the software process has been run. If the data output is the same as the data input, it is not necessary to fill this field out.		
Manufacturer	Link to the organization that created the software. May also be a person, but only if the person mass produces the software. Use the **Developed by** field for software not designed for mass production.		
Coded in	Select the programming language in which the software is coded.		
Developed by	Link to any people or organizations who designed or helped develop the software for limited or internal use only. If the software was developed for commercial mass production, the **Manufacturer** field should be used instead.		
Exchange facilitator	Enter the URL for any third-party service that facilitates payment for or access to the software.		
Funded by	Link to any organizations that funded the purchase of the software or the work that produced it.		
Operating System	Enter the operating system(s) with which the software is compatible. Group multiple versions of the same operating system on the same line, for example, "Microsoft Windows XP, Vista, and 7" but use the + function to create a separate line for each operating system if multiple ones apply to the same piece of software: ▪ Microsoft Windows XP, Vista, and 7 ▪ Mac OS ▪ Linux ▪ Unix The names of common operating systems should be consistently formatted. Use "Microsoft Windows" for all Microsoft operating systems, never just Microsoft or Windows. Use "Mac OS" or "Mac OS X" for Apple operating systems; assume Mac OS as the default if OS X isn't specified.		
Related data collection method	Select any applicable data collection structures used to generate input data for biostatistical analysis software.		
Related grant number	Grant number for the funding that contributed to the development of the software. For example: 'U24 RR 029825'.		
Related Publication or Documentation	Link to any protocols, journal articles, or patents that contain information related to the software.		
Related study design	Select any applicable study designs used to generate input data for biostatistical analysis software.		

Software license	Select the appropriate type of software license.		
Uses algorithmic software component	Link to any relevant algorithmic component records. Appears only when "Algorithmic software suite" is selected in the type field.		
Version	The version designation associated with the software. This is often a numeral followed by a decimal and another numeral, for example: 2.1.		
Website(s)	Enter the URLs of any related external websites, e.g. any lab or manufacturer pages that provide additional information or where open source software can be downloaded. All URLs should include the full address, such as: http://www.eagle-i.net.		
Comments/Curator Note	**Not visible in search.** Use these fields to capture notes about the record or comments intended for reviewers. Possible uses include explanations for missing information in the record or reasons for withdrawal. Since the system does not track provenance, it is helpful for curators to leave their name and a date when making significant changes.		✓

Data input

Note: NR indicates a non-repeatable field.

Field	**Description**	**Req.**	**NR**
Data Name	Name of the data put into the software or database at the start of its process. May be the same as the **Data Type**, but should be more specific if additional information is available. For example: if the type is "Flow cytometry data," the more specific name might be "Cell quest flow cytometry data."	Yes	✓
Data Type	Select the most accurate data type. If the most accurate type isn't available, annotate up and submit a term request for the one needed.	Yes	✓
Format	Select the appropriate input data format.		
Measurement scale	Select the level of measurement precision used to record the data. Primarily relevant for biostatistical analysis software.		

Data output

Note: NR indicates a non-repeatable field.

Field	**Description**	**Req.**	**NR**
Data Name	Enter the name of the data that results after the software process has been run. May be the same as the **Data Type**, but should be more specific if additional information is available. For example: if the type is "Flow cytometry data," the more specific name might be "Cell quest flow cytometry data."	Yes	✓
Data Type	Select the most accurate data type. If the most accurate type isn't available, annotate up and submit a term request for the one needed.	Yes	✓

Format	Select the appropriate output data format.		
Measurement scale	Select the level of measurement precision used to record the data. Primarily relevant for bio-statistical analysis software.		