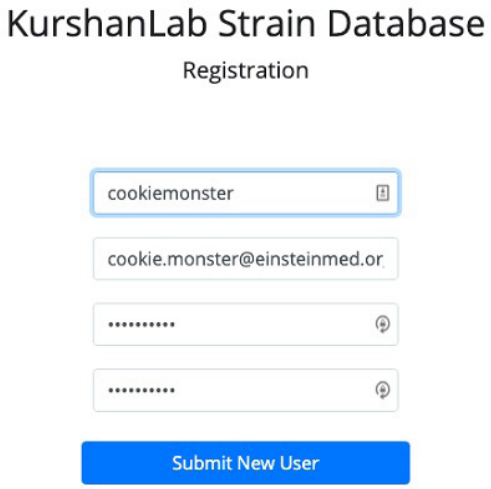
Instructions for the KurshanLab Strain Database

This guide explains how to use the KurshanLab Strain Database. If you are a first-time user, please proceed to the Registering section.

Registering

Follow the instructions below to register for the first time. *You must do this step from an on-campus connected computer.*

1 Go to `https://kurshanlabdatabase.org/start/registration_landing.php`.



2 Pick a username.

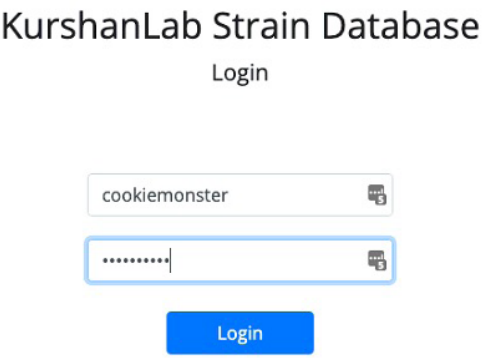
3 Enter your email address.

4 Make up a password. Ideally, *I recommend using a password manager like LastPass that will automatically pick a non-guessable password, remember it for you, and ensure the site you're on is the real site*, but if not the best passwords take elements, like the first character, from a memorable sentence and convert it to a password. For example, *tqbfj0t1d* was taken from *The quick, brown fox jumped over the lazy dog.* Note that some letters were changed to numbers.

5 Click **Submit New User**.

Logging in

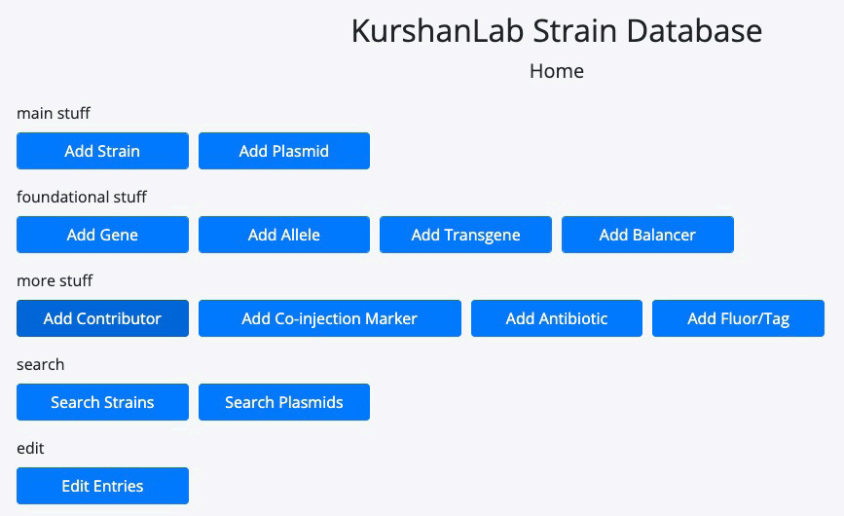
Once you're registered, the screen shifts to the login landing page.



The main URL for the database is `https://kurshanlabdatabase.org`. *Bookmark this URL, so you're always sure you're going to the real site, and not to a fake, phished site.*

1 Enter your credentials and click **Login**.

You are directed to the home page of the online database.

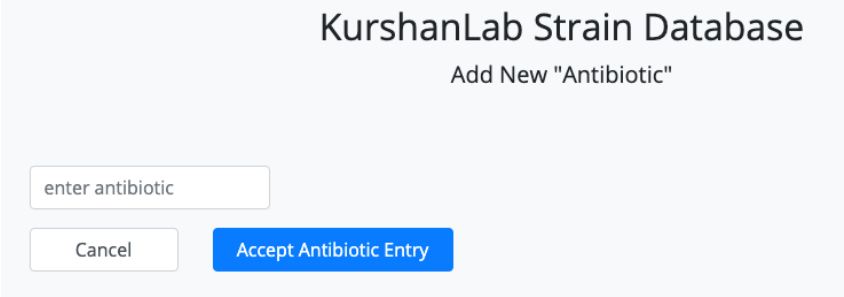


This screen is organized into a number of sections. First, you'll be doing three major operations with the database: entering new data, editing existing data and searching for data. Since you'll be spending a lot of time entering data, it takes up the first three sections. Editing, which will be less frequent, is relegated to a single button at the bottom.

When entering new data, strains and plasmids are the major focus. However, the database is setup such that all the material required for these entities idividually such alleles and fluoro/tags need to be entered first. That is, if you need a specific allele for a given strain, you must first click the Add Allele button and enter that info there first. Once all the information associated with the new strain has been entered separately, only then should you enter the strain info via the Add Strain button.

Adding More Stuff

The steps for entering an item in the **more stuff** category is pretty straightforward.



You can always get back to the Home screen without any changes by clicking the **Cancel** button.

Here's an example showing how to add the antibiotic *erythromycin*.

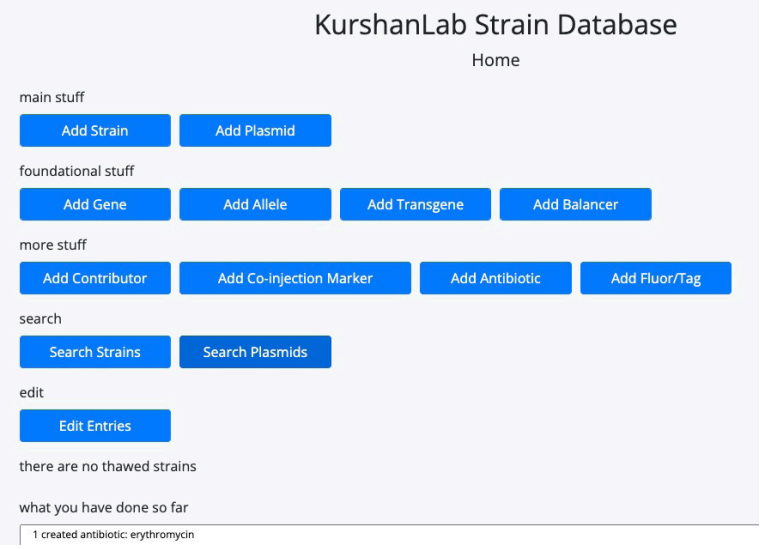
1 Click **Add Antibiotic** in the Home screen. This presents the Add Antibiotic screen shown above.

2 In the **enter antibiotic** field, type `erythromycin`.

3 Click **Accept Antibiotic Entry**.

You will be returned to the Home screen, but something here has changed. See

Add Balancer is a new addition. The name allows freeform editing. It requires at least one chromosome designation, which defaults to I. If a second chromosome is specified, it must be different from the first one.



Similarly, if you ever run into text that clearly indicates something is amiss, take a screenshot and let me know ASAP.

the picture above. Under where it says **what you have done so far,** it indicates that you added the antibiotic erythromycin. This area of the home screen is a running log of everything you add or edit during a single session of using the database. After every addition or edit, please pay close to attention to the log to ensure the database has recorded everything you're doing. If at any time, something you added or edited wasn't recorded in the log, or the log contains an error, ***please stop working on the database and contact me ASAP***. It's likely you've run into a bug.

If you inadvertently attempt to add a duplicate item of any entitiy, the log will let you know, and the item will not actually be added twice.

To add an allele, if you know the gene it's associated with it, you should first enter it using the **Add Gene** action. However, you will be able to edit the allele at any time later, so it's not absolutely mandatory to have the gene name on hand.

The add allele screen is one of the more complex screens because how an allele gets named depends upon its source, whether it was produced in house, *lab-produced*, or obtained from an outside source, *externally-sourced*. You must choose one or the other. If you choose lab-produced, the database gives you the next name to be assigned, a tentative designation.

However, whether the allele gets this designation depends on whether someone else in the lab is also entering alleles at the same time. They, too, will see the same designation, and the person who clicks the **Accept** button first gets that designation and the other user gets next successive designation.

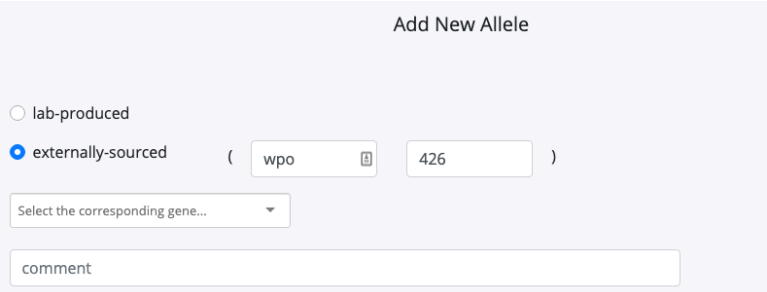
Adding an Allele

1 If you know the gene this allele is associated with, add it first to the database by using the **Add Gene** action in the Home screen.

2 Determine whether the allele is **lab-produced** or **externally-sourced** and choose the corresponding radio button. The screenshot on the next page shows how externally-sourced looks with a name already entered.

3 If the allelle is externally-sourced, enter its designation, letters and numbers into the indicated fields. Leave out the parentheses.

4 Choose the appropriate gene from the dropdown **Select the corresponding gene….**



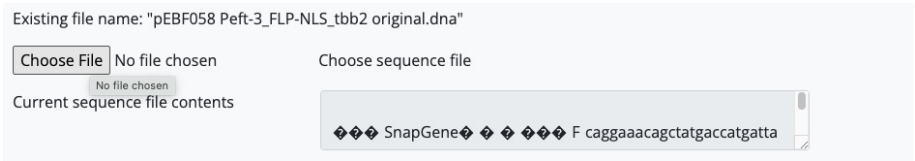
A word on how these dropdowns work. You don't necessarily have to scroll to select from the dropdown. You can filter the results by typing out your entry. So to select a gene named **pwf-303**, simply start by typing, `pwf`. But be sure to actually select the item from the list, that actually adds it. Note that for some dropdowns, such as adding fluoro/tags to plasmids, multiple entries are allowed.

Everywhere in the database, comments can be up to 768 characters.

5 You may enter a comment if one is appropriate.

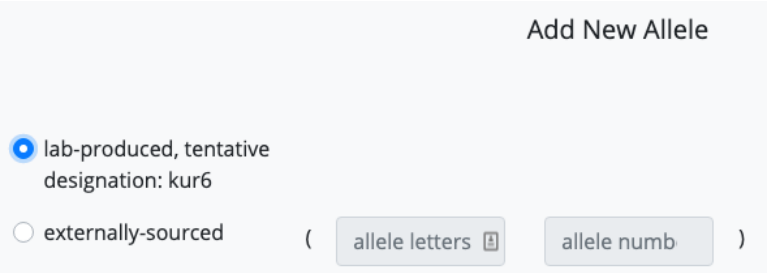
6 If you have the ape sequence file, enter its contents by clicking the **Browse** button and selecting the file. The contents of the file is displayed in the field alongside the label **Current sequence file contents**.

You can't copy the contents of a sequence file from this page and manually move it to a file. Use the download button in the **Search Results** page instead.



7 Click the **Accept Gene Entry** button.

The screen below shows an example of what a tentative designation looks like when adding a lab-produced allele.



Adding a Transgene

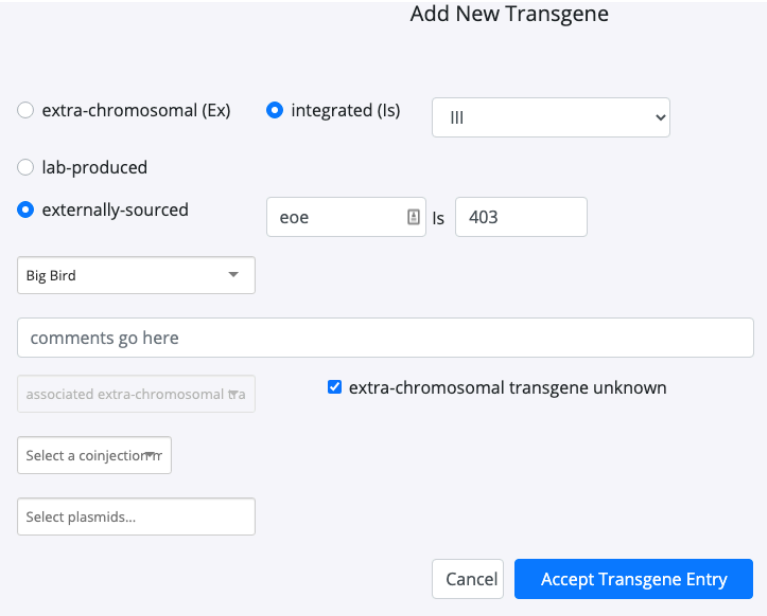
1 Before entering the Add Transgene screen, be sure you've added the relevant contributors, coinjection markers, extra-chromosomal parent transgene, and plasmids (adding plasmids are discussed later).

2 In addition to their lab-produced/externally-sourced state, transgenes can be **integrated** or **extra-chromosomal**. Select the appropriate choice.

Remember that the lab-produced name is tentative. If someone is editing the same screen the same way and accepts before you do, their transgene will get the indicated designation, and yours will get the next one.

3 Choose the corresponding button for whether the transgene is **lab-produced** or **externally-sourced**.

When you make these two sets of choices, the designation will adjust accordingly. For example, for externally-sourced, as you can see in the screenshot on the next page, there is an **Is** between the fields **eoe** and **403**. The **Ex** or **Is** display at that location only for externally-sourced transgenes. For lab-produced ones, it displays the full tentative designation alongside the phrase **lab-produced**.



4 Choose the appropriate choice for **externally-sourced** and **lab-produced**. For externally-sourced, you need to fill out the letter and number designation in the appropriate fields.

The contributor is the person or entity that produced the transgene. It's not necessarily who is entering the information. The database records that separately automatically.

5 Select the **contributor**.

6 If there is a comment, enter it in the **comments** field.

7 If the transgene is integrated, there may be an extra-chromosomal parent associated with it. If so, choose it from the corresponding dropdown. Otherwise, if the parent is unknown, you can check the **extra-chromosomal transgene unkown** button and then follow the remaining instructions.

8 For extra-chromosomal transgenes, select its coinjection marker from the **Select a coinjection marker…** dropdown.

9 Also for extra-chromosomal transgenes, select the appropriate plasmids from the **Select Plasmids…** dropdown. You may select multiple plasmids with this particular dropdown.

10 Click **Accept Transgene Entry**.

Adding a Strain

1 Before you begin, ensure that all dependent elements such genes, alleles and transgenes, have already been entered into the database. You can open the Strain screen and do a quick search to see if everything you need is actually there.

2 Choose the associated gene (allele)('s) from the **Select genes (alleles)** dropdown. The field accepts multiple entries.

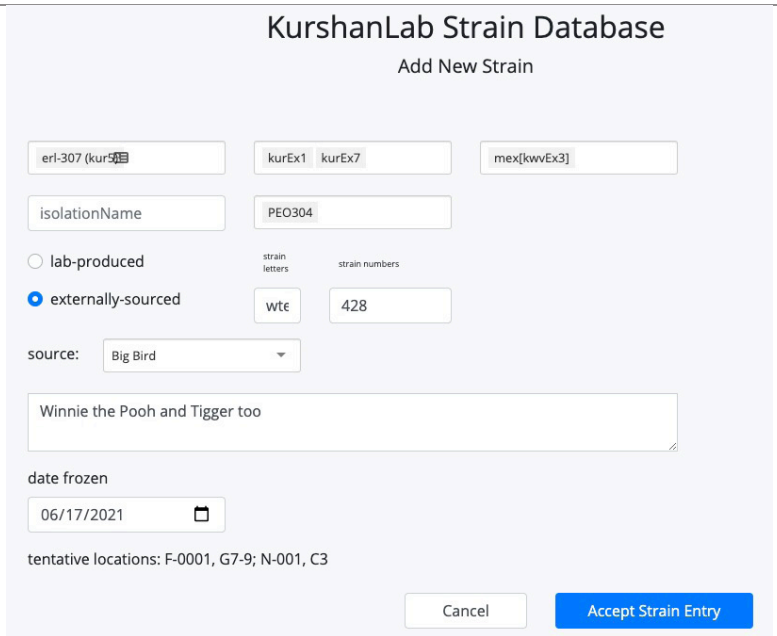
3 Choose the associated transgenes in the **Select transgenes** dropdown. The field accepts multiple entries.

4 Choose any associated balancers in the **Select balancers** dropdown. The field accepts multiple entries.

5 Check the radio button corresponding to whether the strain is lab-produced or externally-sourced. If it's lab-produced, it will receive a tentative designation. If it's externally-sourced, enter the corresponding letters and numbers in the corresponding fields.

6 Enter the contributor in the **contributor** field.

When you edit a strain, there will be other fields including date thawed and whether the strain is the last tube. These will be discussed later in the manual.



7 If any comments are appropriate, enter them in the **comments** field.

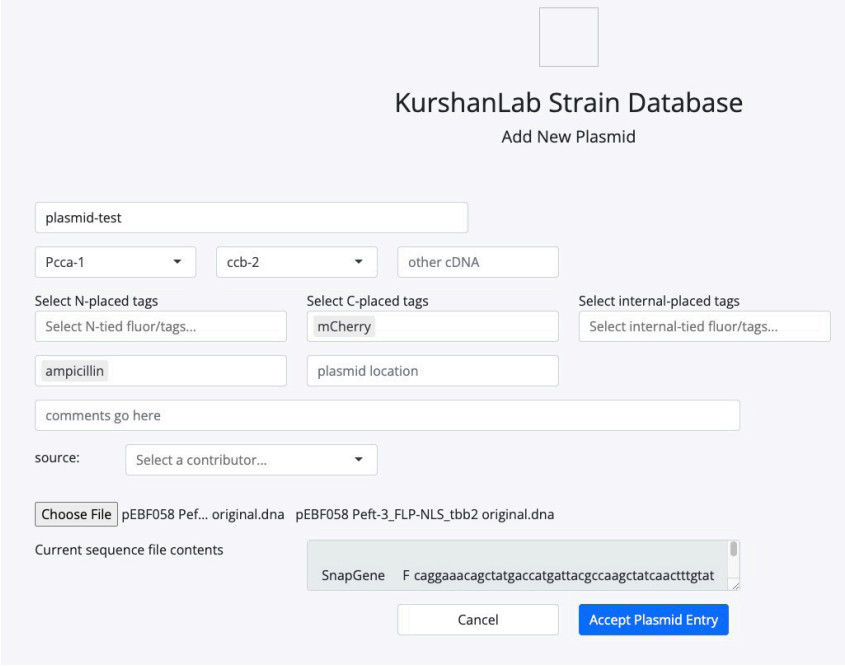
Below the date frozen field is the tentative designation for the freezer and nitrogen locations. Ensure that it matches what you expect, but note that as before with these tentative designations that if another user is entering a strain at the same time and beats you to accepting, their strain will get that designation, and you will get the next one.

8 Enter the date the strain was frozen in the corresponding field. Clicking the calendar icon brings up a date picker window that makes it easy to directly select a date. This field is mandatory, so if you don't have the actual date, enter something that makes sense and you can edit it later.

9 Click **Accept Strain Entry**.

Adding a Plasmid

1 Before you begin, ensure that all dependent elements such genes, collaborators and fluoro/tags, have already been entered into the database.



2 Enter the name for the plasmid in the corresponding field, **enter the plasmid name**.

3 Choose the promoter from the **Select a promoter…** dropbown.

4 Choose the gene from the **Select a gene…** dropdown.

5 Enter any cDNA into the **cDNA** field.

6 Select the corresponding fluoro/tags for each of the three different fields, **Select N-placed tags**, **Select C-placed tags** and **Select internal-placed tags**.

7 Select the associated antibiotics from the **Select antibiotics…** dropdown. This field accepts multiple entries.

8 Enter any comment if appopriate in the **comments go here** field.

9 Choose the contributor in the **Select a contributor…** field.

You will be able to download the contents of the sequence files from the **Search Plasmids** results page.

10 If you have the ape sequence file, enter its contents by clicking the **Browse** button and selecting the file. The contents of the file is displayed in the field alongside the label **Current sequence file contents**.

11 Click the **Accept Plasmid Entry** button.

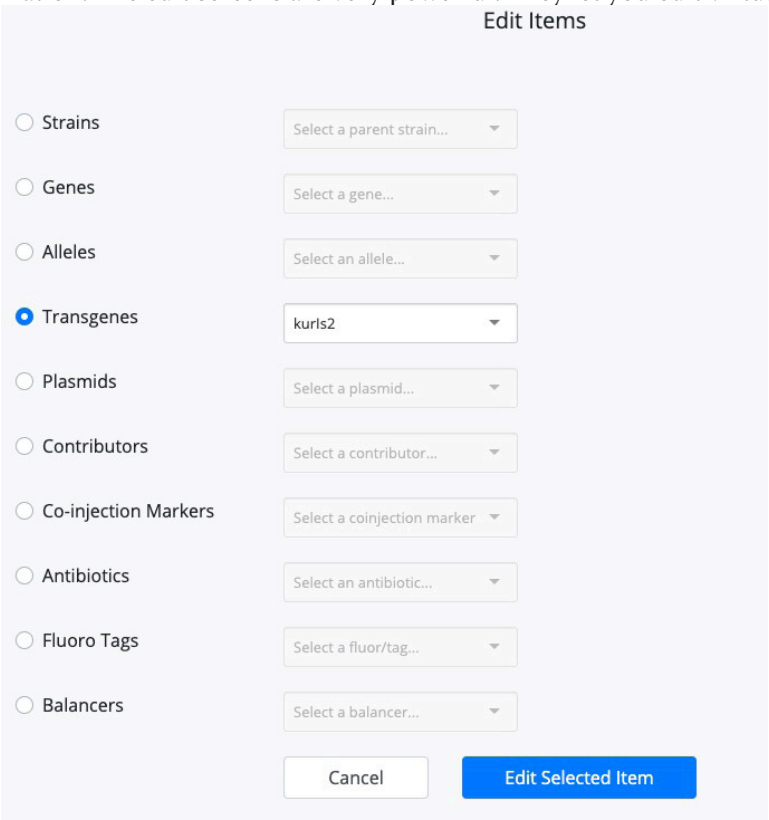
Editing Elements

1 In the Home screen, click the **Edit Entries**… button.

2 In the screen that appears, you are presented with a series of radio buttons, each one corresponding to a different strain element. Choose the one you want to edit, and then choose the specific element you want to edit from the corresponding dropdown. The example screenshot above shows **kuIs2** selected.

3 Click the **Edit Selected Item** to enter the edit screen for this item.

The edit screens are identical to the add screens except they contain all the existing information. The edit screens are very powerful. They let you edit virtually



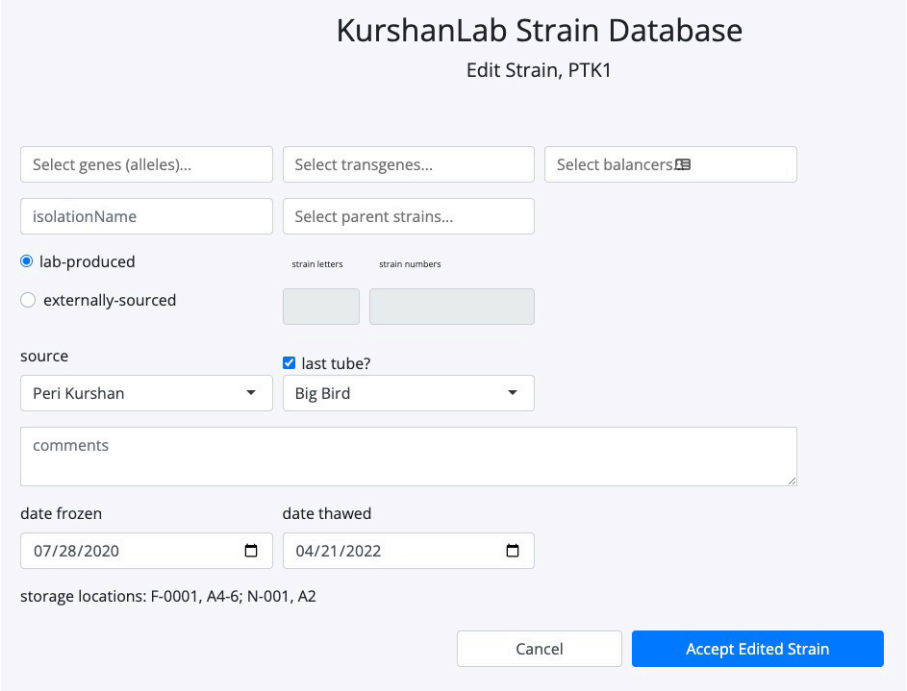
Don't forget you can filter the results by starting to type out the name of the element.

If you did switch a lab-produced element to an externally-sourced one, its original designation gets retired and does not get reused.

The freezer/nitrogen locations of strains are not editable.

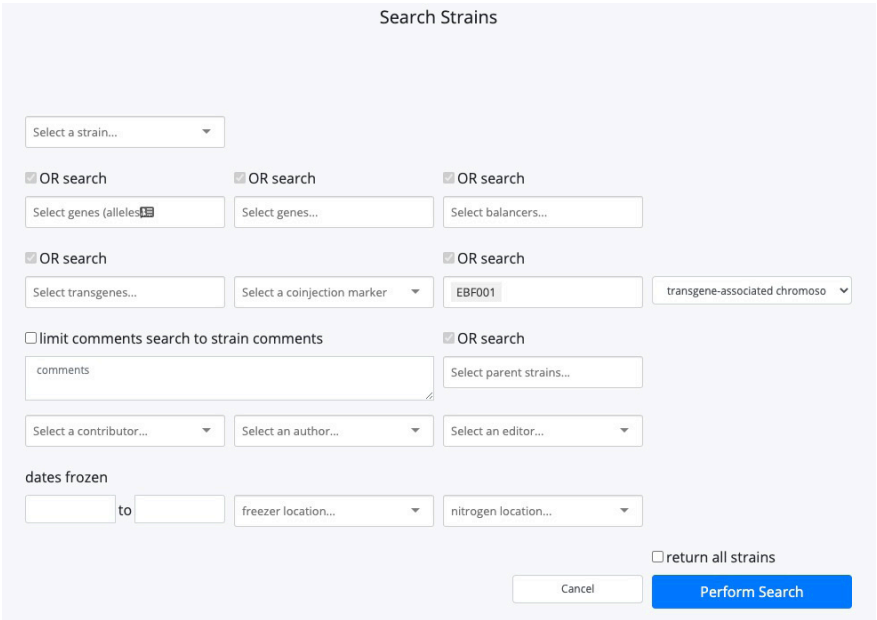
every aspect of every element. For example, you can change a lab-produced transgene to externally-sourced and vice versa. Generally, if you make no changes to an item in an edit screen, the database will log no changes. If you do make a change, the log will reflect that by indicating **updated element x**.

Further, the Edit strain page differs from the Add Strain page. Consider the following screenshot. Here there are a few additional options. Check **last tube?** if this is the last tube being thawed. Indicate who thawed it in the **Select who last vialed…,** and the date it was thawed in **date thawed**.



Searching Strains

The database lets you search for strains and plasmids and presents results includ-



This search is configured to search for strains containing a transgene that itself contains a plasmid named *EBF001*.

ing all the information related to them. For example, if a strain contains an allele associated with a particular gene and that gene has a comment not only will that information display in the results, but you can even search for it, too.

Consider the search screen on the preceding page. Each element is a separate field, but that may fool you into how the search looks for them if you are searching for more than one element at once. There are two ways to construct a search. A search be ANDed or ORed. In an AND search, all the elements must be present in a given strain to be part of the result. In an OR search, the results will contain every strain that contained even just one of the elements being searched for. It is also possible to have a combination where some elements are ANDed and some are ORed.

The search function here uses this combination approach. Comments are always ORed with the other elements, meaning that if you specify a search for a particular comment and, say, a particular allele, you will get results for *both*. However, if you search for strains with, say, a specific allele and a specific transgene, then that search is ANDed and any result has to contain both the allele and the transgene.

But there's more. Within elements where multiple items can be given, such as with alleles or transgenes, the search among *them* is ORed by default. So if you searched for strains with one allele and two transgenes, every result will contain that allele, but it may contain one or the other transgene.

However, above each of these elements is a button where you can uncheck the OR search option. In that case, only strains that contain *all* the elements for that type of element will appear in the results.

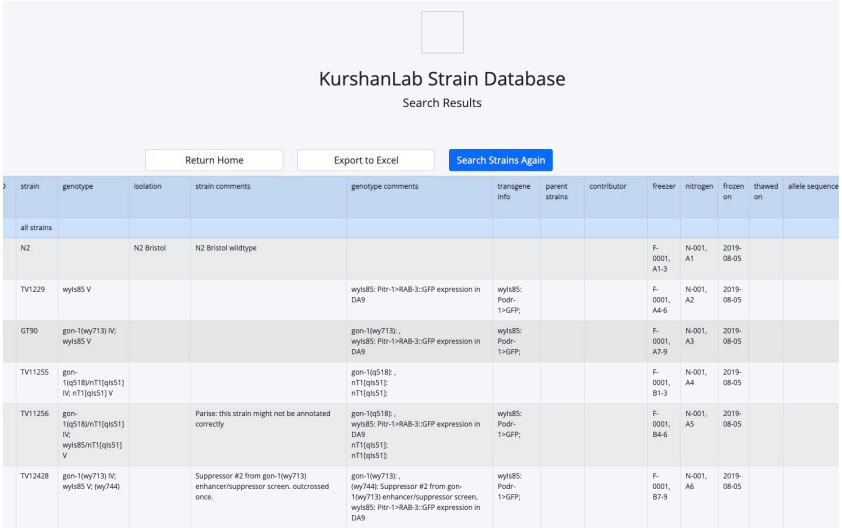
The comments search by default searches for comments not only in the strain itself but in the comments field of any associated element. So if a gene were associated to a given strain by way of an allele, then the search will search that gene's comment field, too. By checking the **limit comments search to strain comments** button, you can restrict the comment search to just the comments of the strains themselves.

Searching for Strains

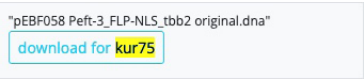
1 Prepare your search. If you want to search for a specific strain, select it from the **Select a Strain…** dropdown. Then proceed to the last step. If you want to search for multiple different elements, all of those elements must be present in a given strain for it to show up in the search results. If you want to search for different instances of the same element, every strain that contains one or more those elements will show up in the results unless you uncheck the **OR search** checkbox in which case, only the results that contain *all* these elements will show. To search for dates frozen, you must enter a range of dates. The dates are inclusive. If you want to search for a freezer or nitrogen location, choose it respectively from the appropriate dropdown. Only populated ones are shown. If you want to display all strains, check the **return all strains** button.

2 Click the **Perform Search** button.

Consider the results screen on the next page. The top row displays the name of each item in the search results. The second row displays what was searched for. The subsequent rows are the results ordered by the internal strain ID. The strain comments gives the comments for the strain, but to view the comments for genes, alleles or transgenes, look in their respective columns. **Click Search Strains Again** to perform another search (note that your original selections will be lost) or **Re-**



If the strain or plasmid has associated sequence files, you can download them by clicking the corresponding download button.



turn Home to go back to the Home screen.

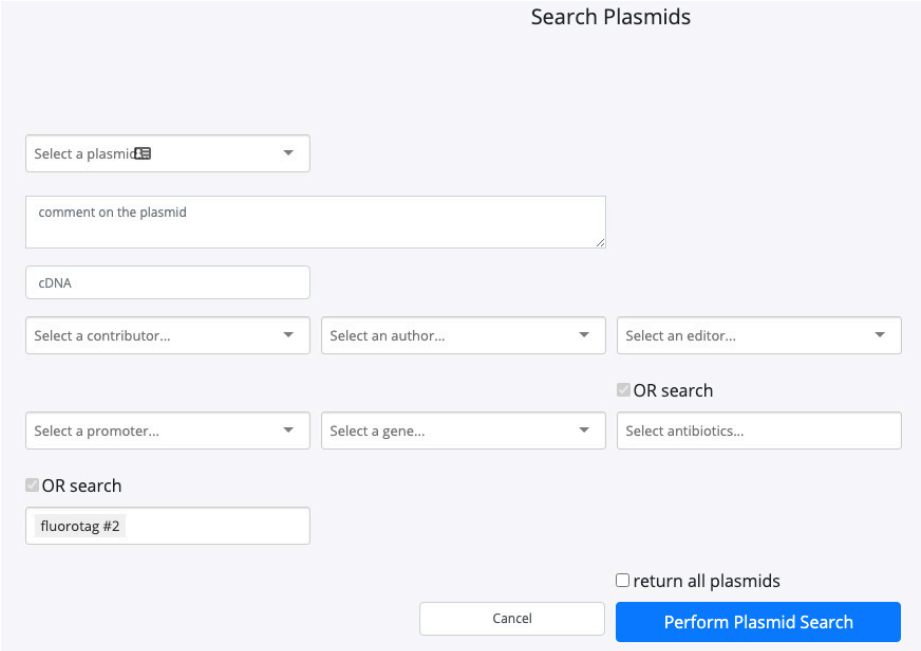
Finally, there is an Export to Excel button. This button is discussed after the section on *Searching for Plasmids*.

Searching for Plasmids

1 Prepare your search. If you want to search for a specific plasmid, select it from the **Select a Plasmid…** dropdown. Then proceed to the last step. If you want to search for multiple different elements, all of those elements must be present in a given plasmid for it to show up in the search results. In searching for antibiotics, you can search for multiple ones, either individually (OR search) or all together. If you want to display all plasmids, check the **return all plasmids** button.

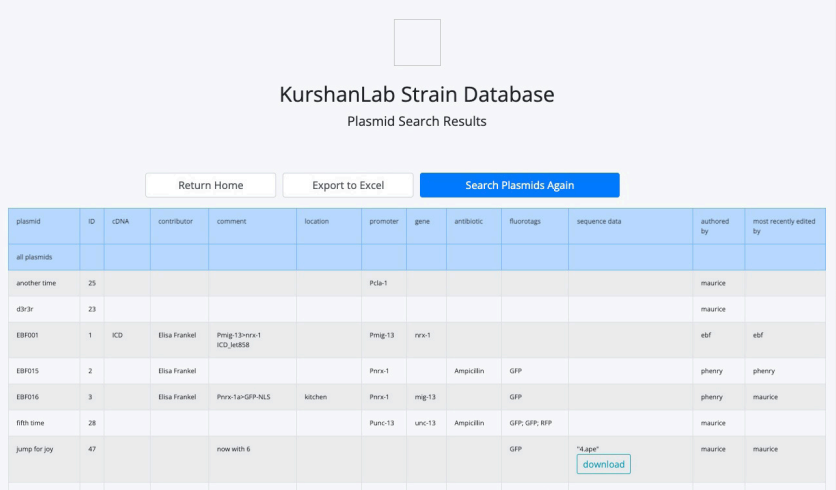
2 Click the **Perform Search** button.

Consider the results screen on the next page. The top row displays the name of each item in the search results. The second row displays what was searched for.



This search is configured to search for plasmids containing a fluoro/tag named *fluorotag #2*.

Plasmids that contain sequence data have a **Download** button that you can use to download it to an .ape file.



The subsequent rows are the results ordered by the internal plasmid ID. The plasmid comments gives the comments for the plasmid; it doesn't dig into the comments of the promoter or gene. **Click Search Plasmids Again** to perform another search (note that your original selections will be lost) or **Return Home** to go back to the Home screen. The Export to Excel button is discussed in the next section.

Exporting to Excel

You can export either search results, strain or plasmids, to a tab-separated values file (tsv) that can you can open in Excel. To do so, in the search results page, click the **Export to Excel** button and a tsv file is automatically downloaded to your computer. To open the file in Excel, follow the instructions below depending on your computer platform.

To open tsv files on Windows, follow these instructions

1 In Windows Explorer, right-click on the tsv file and select **Open With** and choose **Choose Another App**.

2 In the dialog that appears, Click **More Apps** and scroll down to where it says **Look for another app on this PC** and click it.

3 Now navigate to Microsoft Excel. The path may vary depending on your version of it. A common path is as follows:

C → **Program Files** → **Microsoft Office** → **root** → **Office 16** → **Excel.exe**

4 Click Open.

To open tsv files on the Mac, follow these instructions

1 In the Finder, right-click on the tsv file and choose **Get Info**.

2 Under the section **Open With**, click the triangle and then choose **Microsoft Excel** from the popup menu.

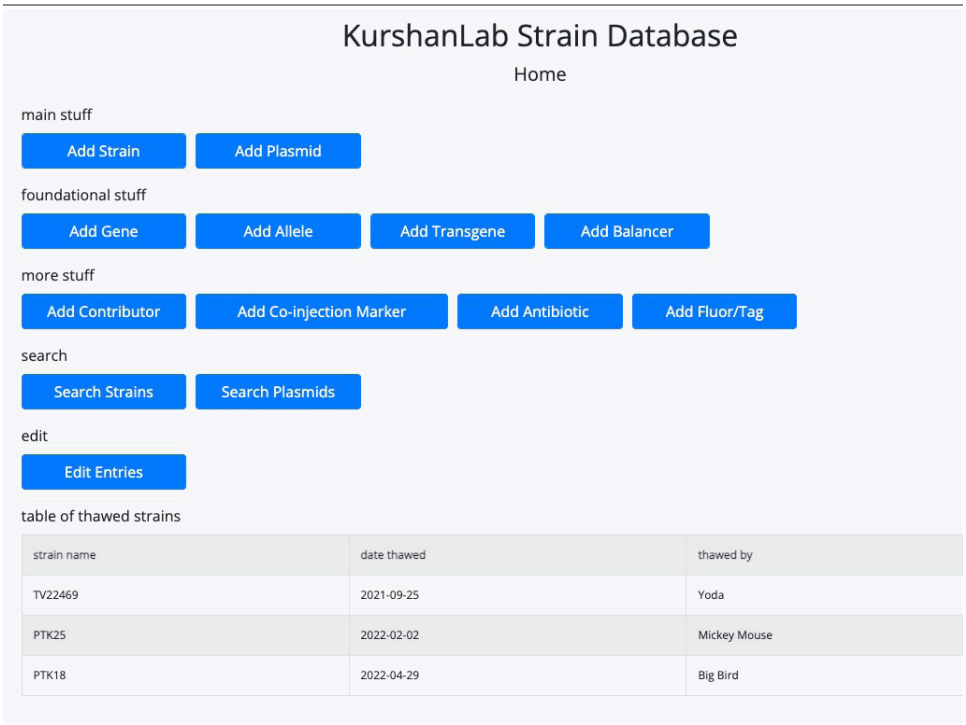
3 Click the **Change All**… button right under this.

4 In the dialog that appears, click **OK**.

Now going forward on your computer, you can open these files directly in Excel.

Reviewing Thawed Strains

Any thawed strains that exist in the database will show up in a table on the home page. Strains appears in reverse chronological order of the thawed date. You can see an example of this on the next page.


KurshanLab Strain Database
Home
main stuff
Add Strain
Add Plasmid
foundational stuff
Add Gene
Add Allele
Add Transgene
Add Balancer
more stuff
Add Contributor
Add Co-injection Marker
Add Antibiotic
Add Fluor/Tag
search
Search Strains
Search Plasmids
edit
Edit Entries
table of thawed strains
strain name
date thawed
thawed by
TV22469
2021-09-25
Yoda
PTK25
2022-02-02
Mickey Mouse
PTK18
2022-04-29
Big Bird