Submitting Histology Data

This page provides instructions for adding histological (H&E) images to the GUDMAP/RBK Data Explorer.

If you have any questions or feedback, please send them to your consortium's help email: help@gudmap.org or help@rebuildingakidney.org

We also have the following training materials available:

- Webinar Slides
- Webinar Replay (18:40)
- Tutorial Videos (Coming Soon)

Overview

Adding histological slides involve the following steps:

- Make sure you are in the correct Globus authentication group, kidney-writers, and that you are logged in.
- Create a new Histological Slide record.
- Fill out the form and upload your CZI file.
- Once the slide is submitted to the Hub (via the *Curation Status* field), the system will process the image.
- The image is then displayed in the browser via a special viewer that displays channels, a scale bar, and allows you to zoom in and out and create annotations.

Schema
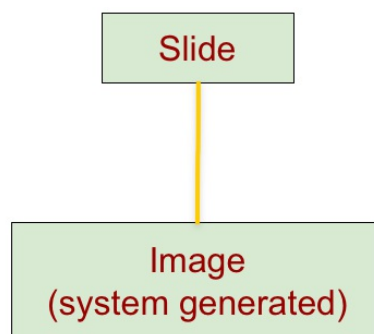
The schema for histological slides is very simple - the record for the slide and then the system-generated image.

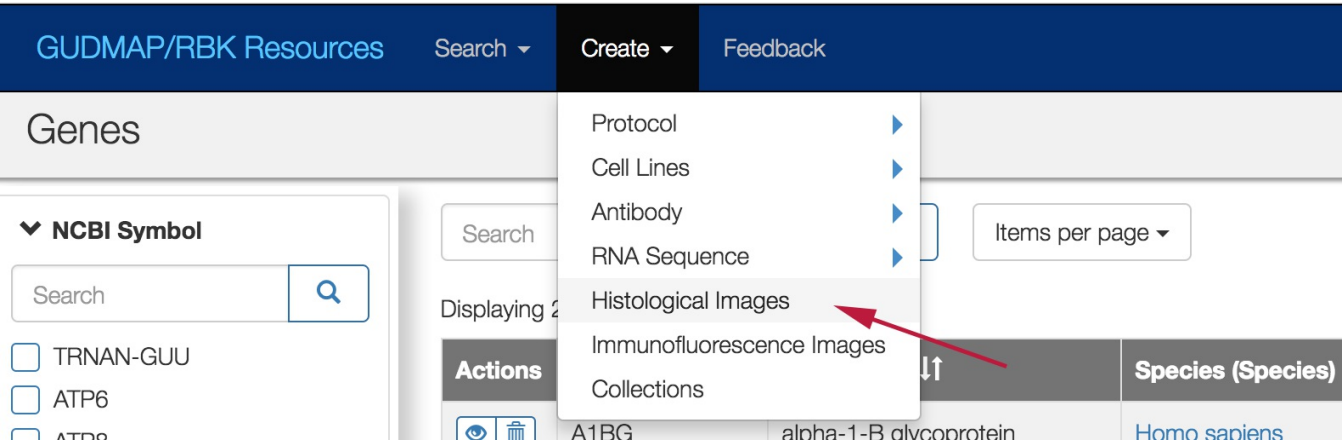# Are you in the `kidney-writers` group?

If you haven't already done so, go to this link to join the group: https://www.globus.org/app/groups/af0b4010-5b75-11e6-9575-22000aef184d/about

You can find more details about this process at Accessing GUDMAP and RBK Resources.

1. Create Histological Slide record

- In the top navigation bar, click *Create > Histological Images*.

- The "Create Histological Slide Record" form appears:

- Select the values for each relevant field. The **required** fields are listed, but the more fields you fill out the easier the data is to find:

  - *Name*: Please use a short descriptive name to help users understand what the image represents.
  - *Download Link*: Upload the raw CZI file.
  - *Tissue*
  - *Age Stage*
  - *Specimen Fixation*
  - *Embedding Medium*
  - *Staining Protocol*
  - *Curation Status*: Choose either:
    - *In Preparation*: Use this status while still drafting the data.
    - *PI Review*: Use this status when your data is ready for internal review.
    - *Submitted*: Use this status when your data is ready for Hub review.
    - **Note:** Your data will **not** be viewable publicly until approved for *Release* by the Hub. For a complete description of the Curation Process, click here.

  - *Principal Investigator*
  - *Data Provider*
  - *Consortium*

- Scroll back up to the top of the page and click the *Submit* button to save the record.

2. Reviewing and Submitting Histological slides

Note: By the hard launch of the new GUDMAP site in April, there will be dashboards and email notifications to make this process more straightforward. In the meantime, here is how a project's PI or designated reviewer can find their project's data with a Curation Status of "PI Review"

- Make sure you are logged in.

- From the navigation bar, click *Search > Gene Expression Data > Histological Images*.

- In the faceting sidebar on the left, scroll to **Curation Status** and choose *PI Review*. Note: Keep in mind that the data submitter may have forgotten to set the Curation Status field, in which case the status would still be *In Preparation*.

- In the faceting sidebar, scroll to **Principal Investigator** and choose your project's PI. Now you should see the data you need to review.

- When your record is approved internally, change *Curation Status* to *Submitted* to send it to the Hub (click here for the full Curation Workflow).

3. Processing the CZI file

Once you have finished any internal review designated by your lab and you set the *Curation Status* to *Submitted*, the CZI file will be added to the system queue for processing.

The system runs a script every hour that looks in the queue and processes the CZI files there, which will take an additional 30 minutes per file. So it may take up to 1-2 hours for your CZI file to be processed and available in the viewer. The raw file is then immediately available.
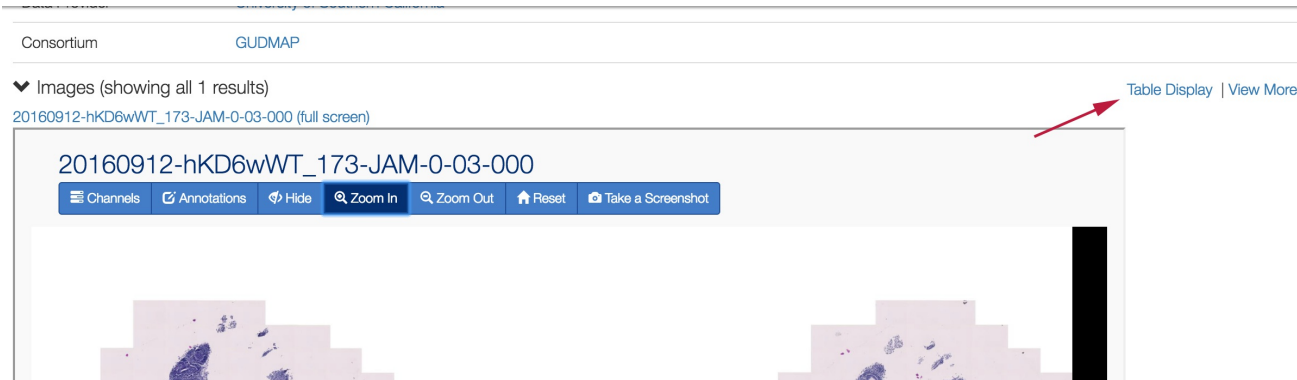
Here is an example of a processed CZI file within the viewer:

4. Deleting Histological Slides

To delete the Histological slide record, you must first delete the system-generated image.

- Go to the record you want to delete (see previous section).

- Scroll down to the "Images" section and click "Table Display" (a link to the right side of the section).

- For each image, click the trashcan (Delete) icon in the "Actions" column. A confirmation window will open - click "Confirm".

- Once all the images in this table are deleted, scroll back up to the top of the record and click "Delete" in the record header.