

Submitting Specimen and Imaging Data (H&E, IF, ISH, etc)

This page provides instructions for adding specimen and imaging data (such as histology, immunohistochemical, in situ hybridization images, etc) 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.

Related materials

- [Tutorial slides from 5/30/2019 - Model V2](#)
- [Webinar from 5/30/2019](#)

Overview of specimen data submission process

The following are the basic steps you'll take to add specimen and imaging data. Note that you will see many other possible fields/tables you can add and the more information you provide, the more discoverable is your data.

The following are the minimum requirements:

1. [Join \(if you haven't already\) the kidney-writers access group.](#)
2. [Create a Specimen record](#) for each unit of tissue used in an experiment - this is the base metadata record that all related data and tables will link to.
3. Add an [Anatomical Source](#) - this is a metadata field that indicates the anatomical region appearing on the slide as a whole.
4. [Add at least one Image record](#). You can also [batch add images](#) in the browser or use our client tools to do a bulk upload (TBD).
5. [Add an Specimen Antibody record](#) if an antibody was used to stain the slide.
6. [Add a Specimen Probe Association record](#) if a probe was used to probe for a gene.
7. [Add Specimen Expression records](#) if gene expression was scored (for ISH).
8. [Stages and timing for human organoid specimens](#)
9. [Review internally and then submit to the Hub](#) when you're finished via the *Curation Status* field.

Here are the details for each step.

1. Join the kidney-writers group.

- Join the [kidney-writer group](#) by [clicking on this link](#).
- When you click the [kidney-writer group](#) link, if you have never used Globus before, you will be given various choices for logging in: via existing credentials (your institution, Google, or ORCID ID) or by creating a new Globus ID. We recommend using an existing credential if that is available.
- For detailed instruction on how to join different GUDMAP/RBK group, visit [Accessing GUDMAP and RBK Resources](#). If you have any problems, please email help@gudmap.org or help@rebuildingakidney.org.

2. Create a Specimen record

The first thing you'll do is create the base metadata record which describes the Specimen (slide). A specimen is a unit of tissue from a single organism (person/mouse/zebrafish).

Once you create this, then you'll add the Specimen data (ie, upload image files) and link it to this record.

1. Go to a *Specimen* data page and log in: *Search > Gene Expression > Specimens* or use this link: [For GUDMAP](#).
2. Log in and then click + Create in the header.

Actions	RID ↑	Images ↑	Genes ↑	Species ↑	Stage ↑	Anatomical
	Q-29HW	Image 1 of 1		Homo sapiens	CS13	gudmap-legacy:kidr
	Q-2964	Image 1 of 1		Homo	CS15	gudmap-

3. Fill out the form fields.

There are a few fields that are required or you may not save the form (these are indicated with the red asterisk *).

However, we recommend filling in as many fields as possible. The more fields you fill out the more ways users can find your data. For example, if you include the species and age stage, then this data will show up for Specimen searches for that specific species and age stage.

Required fields - click the dropdown field and choose the appropriate value:

- Species: *Homo sapiens, Mus musculus*
- Assay type: The imaging related types are *IHC, ISH, and Histology*.
- Stage: The Theiler or Carnegie stage (preferred). If you cannot provide the stage, there is also the Chronological Age field where you can type in the age.
- Sex: Choose a value from the dropdown menu.
- How the sample was prepared:
 - Preparation
 - Fixation
 - Embedding
- Curation Status: Your relevant choices are *In Preparation* (ie, draft mode), *PI Review* (whatever your internal final

level of review is), and *Submitted* (when you are finished and ready to send to the Hub for further curation before we release it). For more information, see

- Principal Investigator: Choose the appropriate Principal Investigator. If your PI is not on the list, click the plus sign just to the top right of the list to create a new record for them.
- Consortium: GUDMAP, RBK, KPMP or External

These fields may not be required but are useful:

- Internal ID: A useful field for your own lab's tracking purposes.
- Information about the organism:
 - Strain
 - Wild Type
 - Phenotype
 - Cell Line
- Descriptive fields:
 - Upload Notes
 - Probe Usage Notes
- Parent Specimen: If you've subdivided a biological sample, you can create a Specimen record for the original sample and designate it as the "parent" of the Specimen records for all the subdivided samples.
- Representative Image: This is an optional thumbnail of the image. If you do not add one, the system will automatically select the thumbnail from the first image record.

Once you have filled out the fields, click the Submit button at the top of the form.

Tips for navigating the base Specimen record

- The Contents sidebar (on the right) is a table of contents of all associated records for the Specimen.
- The default is to show all possible records that you could link to the Specimen. To hide the empty ones, click "Hide Empty Records" in the header.

3. Add the Anatomical Source

On the new base Specimen record, you can now indicate the Anatomical Source. Among the top rows of the record, look for "Anatomical Source". To the right of this field, click the **Add** button. Start typing a term and choose your term from the list, then click Submit.

RID	N-GHT2
Gene	Pcnt
Species	Mus musculus
Stage	TS17
Assay Type	ISH
Preparation	wholemount
Anatomical Source	genitourinary system (TS13-TS28)
Fixation	4% paraformaldehyde
Strain	CD1
Wild Type	Wild Type
Experiment Note	Embryo dissected below the forelimb and sagittally bisected down the midline to reveal the urogenital system. The caudal end is on the right. 2 No. Embryos.WMISH030106 Sample6.

Contents

- Main
- Images (2)
- Specimen Expression (1)
- Specimen Probe Association (1)
- Probes (1)

3.1. To add the same anatomical source to several Specimen records

This is a great shortcut if you have many Specimen records that you want to add the same Anatomical Source. You can do an anatomy search for the term and then link multiple Specimen records to it:

- Go to *Search > Anatomy Terms > Faceted Search* in the menu.
- Search or filter to find the anatomical term you need and click its eye icon.
- Click **Specimens** in the right Content sidebar or scroll down to that section, then click **Add** to the right of the table.
- In this window, you can filter or search for your Specimens, select the ones you want to associate with this anatomical term, and click **Submit**.

Add related records

To finish, you'll need to add some related records:

- For all imaging data types, you'll need to add at least one Image record.
- If an antibody was used to stain the slide, you'll need to add an Antibody record.
- If a probe was used to probe for a gene, you'll need to add a Probe record.
- If you examined the slide and scored expression values (*present, not present, etc.*) for a gene, you'll need to add

Specimen Expression records.

4. Add Image Records (all imaging data)

For each image, you will need to add an Image record.

From your base Specimen record, scroll down and find the Images table and click the [Add](#) link to the right.

The screenshot shows a GUDMAP/RBK interface for a specimen record titled "GUDMAP:16-CT5G". The "Images" table is displayed, showing no results found. The "Add" button is highlighted with a red box. To the right, a sidebar lists various related records: Images (0), Derived Specimens (0), Specimen Expression (0), Specimen Allele (0), Specimen Probe Association (0), Probes (0), Specimen Antibody (0), and Anchor Gene Specimen (0).

This will open the Create Record form.

The screenshot shows a "Create Record" form for an IMAGE entry. The "Original File URL" field includes a "Select file" button. Other fields include Record Number, RID, Specimen, Notes, Curation Status, Principal Investigator, Consortium, Media Type, Thumbnail URL, and Release Date.

Fill out the fields on this form. Use the Original File URL field to upload your image file and click [Submit](#) to save the record.

4.1. Processing CZI files

Where applicable, we encourage submitting CZI files. The system will convert CZI files for in-browser viewing. This may take a few hours but it will automatically appear once it has been converted.

The browser will allow the user to manipulate channels and zoom in to see details in high resolution.

4.1.2. Note about Viewing 3D Images

In the future, we plan to support 3D viewing. Until then, users will need to download the file and use your own local tools for viewing 3D images.

Batch Add Image Records

If uploading more than one image record, you can click the plus sign (+) to open multiple records.

The screenshot shows a user interface for adding image records. At the top, there's a header bar with 'Feedback' and an email address 'cristina@globusid.org'. Below the header, there's a large input field for file uploads. In the top right corner of this field, there's a red-bordered button containing a blue '+' sign and a downward arrow. To the right of this button is a 'Submit' button. The main area below the input field contains several empty, light-grey rectangular boxes, likely for individual image records. At the bottom right of the main area, there are some small, faint icons.

The screenshot shows a 'Create Records' page for 'IMAGE' type. The top navigation bar includes 'GUDMAP/RBK Resources', 'Search', 'Create', 'Dashboards (requires login)', 'Help', and 'Feedback', along with the email 'cristina@globusid.org'. The main area is titled 'Create Records' and contains a grid of 12 fields for entering data. Each field has a red-bordered '+' button in its top right corner. The fields include: Record Number (1), RID (Automatically generated), Specimen (GUDMAP:16-CT5Q), Original File URL (No file Selected, Select file), Notes (empty), Curation Status (In Preparation, X, Select), Principal Investigator (Select a value, Select), Consortium (Select a value, Select), Media Type (Select a value, Select), Thumbnail URL (No file Selected, Select file), and Release Date (Automatically generated). The entire grid is enclosed in a red border.

Tip: If you are using similar field values - fill in the values of the field before you click the plus sign and those values will propagate to the duplicate record forms.

If you decide you do not want that one of the records, just click the x icon to delete. A popup window will ask you to confirm you want to delete the record.

The screenshot shows a table-based form for a specimen record. The first row contains a header with a blue 'X' icon, the number '2', and a 'Submit' button. Below this are several rows of data:

- Row 1:** A blue 'X' icon, a grey box, and the text "Automatically generated".
- Row 2:** A grey box and the text "GUDMAP:16-CT5G".
- Row 3:** A 'Select file' button and the text "No file Selected".
- Row 4:** An empty grey box.
- Row 5:** A 'Select file' button and the text "In Preparation".

In the top right corner of the form area, there is a red-bordered box containing a blue 'X' icon.

When you are finished, click Submit to save the record.

5. Add an Antibody record if an antibody was used to stain the slide

Go to the *Specimen Antibody* table and click **Add** to add an antibody.

The screenshot shows the "Specimen Antibody" table for the specimen "GUDMAP:16-CT5G". The table has three main sections:

- Specimen Antibody:** This section is currently empty, indicated by "NO Results Found". It includes a red-bordered "Add" button and a "View More" link.
- Anchor Gene Specimen:** This section is also empty, indicated by "NO Results Found". It includes an "Add" and "View More" link.
- Marker Gene Specimen:** This section is also empty, indicated by "NO Results Found". It includes an "Add" and "View More" link.

On the right side of the table, there is a sidebar titled "Images (1)" which lists various related records and associations, such as "Derived Specimens (0)", "Specimen Expression (0)", etc.

The *Create Record* form for the Specimen Antibody appears.

GUDMAP/RBK Resources Search ▾ Create ▾ Dashboards (requires login) ▾ Help ▾ Feedback cristina@globusid.org ▾

Create Record

SPECIMEN ANTIBODY

* indicates required field

Record Number	1
* Specimen RID	GUDMAP:16-CT5G
* Antibody RID	Select a value
Dilution	
Detection Method	
Lab ID	
Detection Notes	
Secondary Antibody	
RID	Automatically generated

[Submit](#) [+](#) [▼](#)

Many of the fields on this page are automatically generated. The important thing to fill out here is the *Antibody RID* to indicate the antibody company. Click the field to see a list of companies.

Choose Antibodies

Search 50 Items per page ▾

Displaying 50 of 223 Records

Select	RID ↑	Catalog Number ↑	Company Name ↑	Host Species ↑	Host_Monoclonal ↑	Protein Target ↑	Product Name ↑	Validation Thumbnail ↑	Curation Status ↑
<input checked="" type="checkbox"/>	14-45F6	ab10805	Abcam	Mus musculus	yes	5-methylcytosine (5-mC)	Anti-5-methylcytosine (5-mC)		Release
<input checked="" type="checkbox"/>	W-R9BM	ab109004	Abcam	rabbit	yes	ACPP	Anti-prostatic acid phosphatase antibody		Release
<input checked="" type="checkbox"/>	S-2A2T	MA1-37021	Thermo Scientific		yes	ACTA1	Skeletal Muscle Actin Antibody		Release
<input checked="" type="checkbox"/>	Q-BH9R	ab124964	Abcam	rabbit	yes	ACTA2	Anti-alpha smooth muscle Actin antibody [EPR5368]		Release
<input checked="" type="checkbox"/>	Q-BH9Y	ab32575	Abcam	rabbit		ACTA2	Anti-alpha smooth muscle Actin antibody		Release

If you do not see the antibody company listed, click the plus (+) sign to add it.

Choose Antibodies

Search 50 Items per page ▾

Displaying 50 of 223 Records

Select	RID ↑	Catalog Number ↑	Company Name ↑	Host Species ↑	Host_Monoclonal ↑	Protein Target ↑	Product Name ↑	Validation Thumbnail ↑	Curation Status ↑
<input checked="" type="checkbox"/>	14-45F6	ab10805	Abcam	Mus musculus	yes	5-methylcytosine (5-mC)	Anti-5-methylcytosine (5-mC)		Release
<input checked="" type="checkbox"/>	W-R9BM	ab109004	Abcam	rabbit	yes	ACPP	Anti-prostatic acid phosphatase antibody		Release
<input checked="" type="checkbox"/>	S-2A2T	MA1-37021	Thermo Scientific		yes	ACTA1	Skeletal Muscle Actin Antibody		Release
<input checked="" type="checkbox"/>	Q-BH9R	ab124964	Abcam	rabbit	yes	ACTA2	Anti-alpha smooth muscle Actin antibody [EPR5368]		Release
<input checked="" type="checkbox"/>	Q-BH9Y	ab32575	Abcam	rabbit		ACTA2	Anti-alpha smooth muscle Actin antibody		Release

6. Add Specimen Probe Association if a probe was used to probe for a gene

If you want to associate one or more genes with this specimen, you'll need to populate the *Specimen Probe Association* table. In the following screenshot, two tables are highlighted. Specimen Probe Association is where you will associate the probe(s) with the data. The *Probe* table will display details of the probe(s) you chose - you do not manually add anything to this table.

Of course, to add a record to the Specimen Probe Association table, you'll click the [Add](#) link.

The screenshot shows the GUDMAP/RBK interface with the following details:

- Header:** GUDMAP/RBK Resources, Search, Create, Dashboards (requires login), Help, Feedback, cristina@globusid.org.
- Main Content:**
 - Specimen:** GUDMAP:16-CT5G
 - Specimen Probe Association:** No results found. A red box highlights the "Add" button and the "View More" link.
 - Probes:** No results found. A red box highlights the "View More" link.
- Sidebar:** Contains links to other sections like Main, Images, Derived Specimens, etc.

Here is how it looks after adding a probe to the Specimen Association Table:

The screenshot shows the GUDMAP/RBK interface with the following details:

- Specimen Probe Association:** Showing all 1 results. A red box highlights the "View More" link.
- Probes:** Showing all 1 results. A red box highlights the "View More" link.
- Probe Details:** Shows a single entry for GenBank:AF323497.1 - probe for SIX1.
- Sidebar:** Contains links to other sections like Specimen Expression, Specimen Allele, etc.

7. Add Specimen Expression record (if gene expression was scored)

For In Situ Hybridization data, you'll also add scored expression regions. Scroll down to the *Specimen Expression* table and click [Add](#).

The screenshot shows the GUDMAP/RBK interface with the following navigation bar:

- GUDMAP/RBK Resources
- Search ▾
- Create ▾
- Dashboards (requires login) ▾
- Help ▾
- Feedback
- cristina@globusid.org ▾

The main content area displays the following sections:

- GUDMAP:16-CT5G SPECIMEN**
- Actions RID ↑ Images ↑**
- Genes ↑ Species ↑ Stage ↑ Anatomical Sources Assay Type ↑**
- No Results Found
- Specimen Expression (no results found)**
- Add View More**
- Actions Expression Scored ↑ Strength ↑ Pattern ↑ Density ↑ Density Change ↑ Density Note ↑ Notes ↑**
- No Results Found
- Specimen Allele (no results found)**
- Add View More**
- Actions Allele RID ↑ Reporter ↑ Visualization Method ↑ First Chromosome ↑ Second Chromosome ↑ Order ↑ Notes ↑ Consortium ↑**

A sidebar on the right lists various links under the heading "Contents":

- Main
- Images (1)**
- Derived Specimens (0)
- Specimen Expression (0)
- Specimen Allele (0)
- Specimen Probe Association (0)
- Probes (0)

The Create Record: Specimen Expression form appears. There are various descriptive fields you can fill out, but at the very least, you'll need to indicate the anatomical region and its expression score (the strength of expression in that region).

The screenshot shows the "Create Record" form for "SPECIMEN EXPRESSION". The top navigation bar is identical to the previous screenshot.

The form fields include:

- Record Number: 1
- * Specimen: GUDMAP:16-CT5G
- * Expression Scored: Select a value (highlighted with a red box)
- Strength: Select a value
- Strength Modifier: Select a value
- Pattern: Select a value
- Pattern Location: Select a value
- Density: Select a value
- Density Change: Select a value
- Density Magnitude: Select a value
- Density Relative To: Select a value
- Density Note: Select a value

Buttons at the top right include "Submit" and "+ / -" for expanding/collapsing sections.

Click the *Expression Scored* field to choose the anatomical region.

Click the *Strength* field to choose from *uncertain*, *present*, and *not detected*.

The click Submit to save the Specimen Expression record.

8. Stages/Timing for Human Organoid Specimens

Kidney organoids are derived from pluripotent stem cells (ESC or iPSC) using a variety of possible protocols. To help standardize assignment of stages of organoid development, we will adopt the convention found in the published literature. This defines the onset of induction as Day 0.

- Day 0 = Induction of iPSCs or ESCs to begin differentiation (i.e. CHIR99021 added)

Each protocol may vary in the rate of formation subsequent to induction, thus the protocol used for a given experiment must be clearly documented with an entered specimen. This can be a reference to a protocol in the GUDMAP

database, or the published paper that details the approach (include PMCID/PMID number).

REFERENCES:

Takasato M, Er PX, Chiu HS, Maier B, Baillie GJ, Ferguson C, Parton RG, Wolvetang EJ, Roost MS, Chuva de Sousa Lopes SM, Little MH, 2015. Kidney organoids from human iPS cells contain multiple lineages and model human nephrogenesis. *Nature* 526, 564–568. PMID: 26444236

Morizane R, Lam AQ, Freedman BS, Kishi S, Valerius MT, Bonventre JV, 2015. Nephron organoids derived from human pluripotent stem cells model kidney development and injury. *Nat Biotechnol* 33, 1193–1200. PMCID: PMC4747858

9. Submit and Releasing your Data

Once you have completed the record and any internal review and are ready to submit to the Hub, edit the Specimen base record.

RID	16-CT5G
Gene	None
Protein	None
Species	<i>Mus musculus</i>

Scroll down to the *Curation Status* field and change the status to Submitted. Then click the Submit button to save the record.

This record will then go to Biocuration Review and the biocurator may contact you to clarify something or to correct an aspect of the data before they update the status to Released. Only when at this point can the public view the data.