METADATA COMMONS USER GUIDE

Last revised December 18, 2024

This user guide provides a step-by-step manual about how to navigate and use the features on [metadatacommons.com.](metadatacommons.com)

Table of Contents

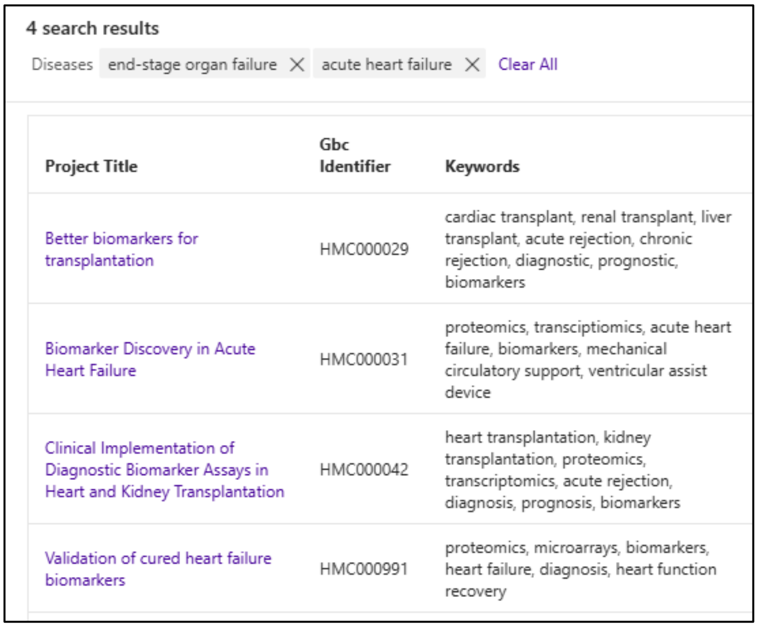
Navigating Metadata Submissions

To browse and search for project metadata, navigate to the **Search Metadata Commons** tab.

Filtering

Filter for desired sorting categories by using the left panel.

Selecting multiple options within a category increases the scope of your search (results matching any of your selected options within a category will be displayed). For example, filtering for both end-stage organ failure and acute heart failure within **Diseases** returns all four projects that contain end-stage organ failure OR acute heart failure.

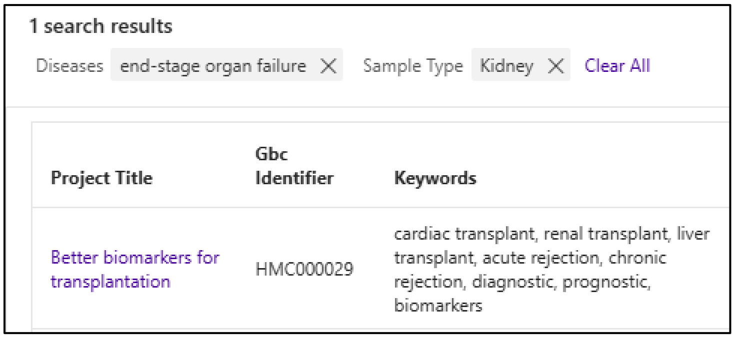


4 search results

Diseases end-stage organ failure acute heart failure

Project Title	Gbc Identifier	Keywords
Better biomarkers for transplantation	HMC000029	cardiac transplant, renal transplant, liver transplant, acute rejection, chronic rejection, diagnostic, prognostic, biomarkers
Biomarker Discovery in Acute Heart Failure	HMC000031	proteomics, transciptiomics, acute heart failure, biomarkers, mechanical circulatory support, ventricular assist device
Clinical Implementation of Diagnostic Biomarker Assays in Heart and Kidney Transplantation	HMC000042	heart transplantation, kidney transplantation, proteomics, transcriptomics, acute rejection, diagnosis, prognosis, biomarkers
Validation of cured heart failure biomarkers	HMC000991	proteomics, microarrays, biomarkers, heart failure, diagnosis, heart function recovery

Selecting multiple options across categories decreases the scope of your search (results matching all your selected options across categories will be displayed). For example, filtering for end-stage organ failure within **Diseases** and kidney samples within **Samples** returns one project containing both that disease AND that sample type.



1 search results

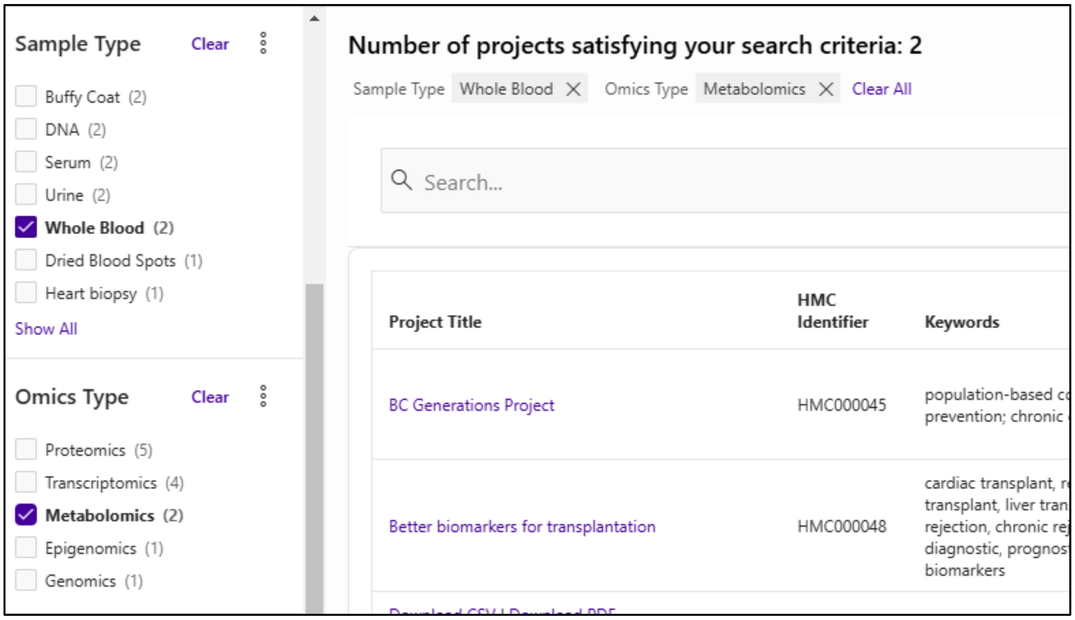
Diseases end-stage organ failure Sample Type Kidney

Project Title	Gbc Identifier	Keywords
Better biomarkers for transplantation	HMC000029	cardiac transplant, renal transplant, liver transplant, acute rejection, chronic rejection, diagnostic, prognostic, biomarkers

For **Cohort Size**, enter your desired cohort size from smallest to largest (inclusive).

For **all other filters**, click Show All to see all filter selections.
Click the three dots symbol ⋮ then click ‘Filter’ to type in and search for a specific filter selection, if one exists.

For **Sample Type** and **Omics Type**, note that the Metadata Commons was designed to support projects utilizing multiple omics types (multiomics), which is why each sample type has an omics type. However, the current filtering capabilities of the platform cannot filter for a sample type that belongs to a specific omics type and vice versa.
For example, if you try to specifically filter projects with whole blood samples focused on metabolomics, the projects that appear will necessarily have whole blood samples and metabolomics-related samples, but not necessarily have them paired.


Sample Type Clear ⋮
☐ Buffy Coat (2)
☐ DNA (2)
☐ Serum (2)
☐ Urine (2)
☑ **Whole Blood (2)**
☐ Dried Blood Spots (1)
☐ Heart biopsy (1)
Show All

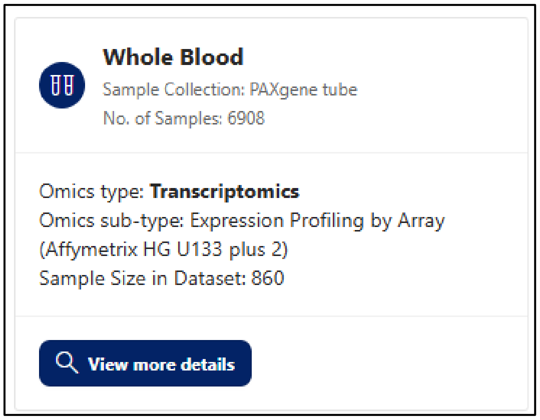
Omics Type Clear ⋮
☐ Proteomics (5)
☐ Transcriptomics (4)
☑ **Metabolomics (2)**
☐ Epigenomics (1)
☐ Genomics (1)

Number of projects satisfying your search criteria: 2
Sample Type: Whole Blood ✕ Omics Type: Metabolomics ✕ Clear All

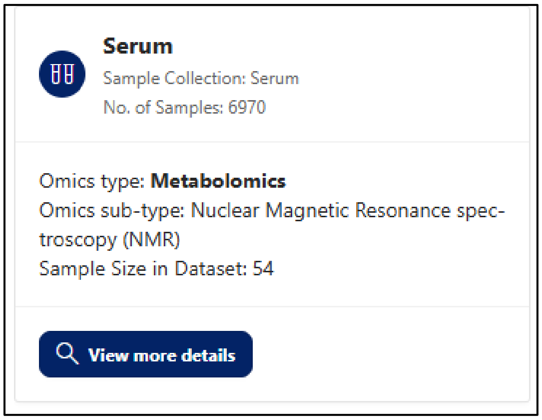
Search...

Project Title	HMC Identifier	Keywords
BC Generations Project	HMC000045	population-based c prevention; chronic
Better biomarkers for transplantation	HMC000048	cardiac transplant, r transplant, liver tran rejection, chronic rej diagnostic, prognos biomarkers

Download CSV | Download PDF


Whole Blood
Sample Collection: PAXgene tube
No. of Samples: 6908

Omics type: **Transcriptomics**
Omics sub-type: Expression Profiling by Array (Affymetrix HG U133 plus 2)
Sample Size in Dataset: 860


Serum
Sample Collection: Serum
No. of Samples: 6970

Omics type: **Metabolomics**
Omics sub-type: Nuclear Magnetic Resonance spectroscopy (NMR)
Sample Size in Dataset: 54

Searching

Search for a specific project or keyword by typing in the search bar, making sure to type in entire words or phrases (typing in parts of words will not yield results).

The total number of projects matching your search is displayed at the top.
Click the ↺ Reset button to remove your search and filter selections.
Scroll down to see the list of projects or to browse.
To download your search results, click the Download CSV | Download PDF buttons at the bottom.

Creating an Account/Logging in

STEP 1

Click the Login button on the top right of the page then click Register .

STEP 2

Enter your details, acknowledge the terms and conditions, and click Create User .

STEP 3

Navigate back to the login page by clicking the Back to Login button. Enter your username and the temporary password sent to your email. Set a personalized password on the screen when prompted.

STEP 4

To log in, click the Login button again. Enter your username and new password, then click the Sign In button.

If you would like to change your account email or delete your account, please contact us.

Customizing Email Notifications

⚠ **Please note that if no selections are made, no email notifications will be sent.**

STEP 1

Log in, go to the top right from the home screen, and click on your username. Select User preferences .

STEP 2

Choose whether you want to be notified if any of your criteria are met by selecting “OR”, or if you want all your criteria to be met by selecting “AND”. An email will be sent to you whenever a new project is submitted that matches this criteria.

STEP 3

To save your preferences, click the Apply Changes button:

You will now receive an email whenever a new submission matching your criteria is published.

Submitting New Metadata

⚠ **Please note that if you are not the principal investigator of the project you want to submit, it is your responsibility to get their approval.**

Step 1. Go to Metadata Submission page.

On the Health Metadata Common's Home page, go to the navigation menu on top of the page and click on the **Metadata Submission** tab. Note that users who are submitting metadata need to create an account and login before being able to access the submission page.

Step 2. Start a New Submission.

On the right of the **Metadata Submission** page, open a new submission form by clicking on the **Start a New Submission** button.

Step 3. Create your draft.

The **project title** is the only information that is required at this step. Once your project title is typed in, click the **Create** button.

Step 4. Fill out the form.

⚠ **We encourage you to provide as much information on the form as possible to facilitate future potential collaborations**.

On the **Metadata Submission** page, find your draft in the summary list.

Click the ✎ icon to edit your draft and continue filling out the submission form at any time.

To delete a draft, click on the **Delete** button at the top. **This action is permanent.**

Click the ❓ icon beside each field to view its help text.

Note that the required fields are indicated on the form with an asterisk (*).

The form consists of 3 main sections:

Project: Information related to the study, investigators, funders.

Cohort: Information related to the enrolled patients, disease/condition studied, types of clinical data collected.

Samples/Omics: Information related to the sample types and if applicable, the omics datasets. This section consists of two linked interactive grids, meaning that every sample type has its own omics datasets. Make sure to select the sample type before filling out the related omics information. To see an example of a filled-out samples/omics section, please go to Section B in the Appendix.

Click Edit or Add Row at the top of the summary table to be able to add your information and edit a row. You can delete a row by clicking on the ☰ icon.

Each section has the following required fields (go to Section A in the Appendix to see all fields):

Section	Field Name	Details
PROJECT	Project Title	Title or name of the project
	Project Description	Describe the study (max 4,000 characters)
	Project Investigators *	First and last names of each investigator
	Contact	Email address of the project leader
	Data Access Request **	URL to data access request webpage
COHORT	Cohort size	Number of patients in the cohort (or estimate)
	Enrollment city/country	Specify where the patients have been enrolled
	Disease/Condition studied *	Disease condition studied
SAMPLES AND OMICS	Sample Type *	List sample types collected
	Omics-type *†	Omics type developed from samples collected
	Omics Sub-type *†	Omics sub-types for each sample type

* Add custom values by typing your own or clicking the ‘+’ button

† If omics type is equal to “Not Analyzed” then the omics sub-type is not required.

** Either an email address or a URL to data access request is required, not both.

Step 5. Submit for Approval

⚠ **Before submitting for approval, make sure you have saved your last changes by clicking the** Apply Changes **button.**

Click the **Submit for Approval** button to submit your metadata.

If any of the required fields are not completed, a window will pop up on the top right corner of the page and specify what information is missing.

Next steps

1. The administrators of the platform will be notified upon your submission and will review it within a week.
2. The result of the review will be sent by email to the user account holder:
   a. **Rejected**: suggestions will be provided, and the submission form can be edited before re-submission.
   b. **Approved**: A data sharing certificate will be attached to the email. If minor changes have been made, they will be specified in the body of the email.
3. Once approved, the project becomes available to the public on the **Home** and **Search** pages.
4. If you would like to edit your submission after it is approved, open your project from the **Metadata Submission** tab and click the **Request Update** button. Your project will be hidden from the public and available as a draft until re-submission.

Resources/Contact

To see our terms and conditions, FAQ, or data literacy webinars, go to the **Resources** tab.

If you have created an account and would like to provide feedback on the Metadata Commons, click on the 💬 icon on the top right of the page to send feedback directly.

To request for help or provide feedback to the Metadata Commons without logging in, please contact us at metadatacommons@genomebc.ca or go to the bottom of the page and click Contact Us to fill out a contact form.

Acknowledgements

We are grateful for the dedicated contributions from Genome BC staff, the valuable feedback from Bill Tam (Thoughtbridge), Raymond Ng (UBC), all beta-testers, and user interview participants, as well as our partners at Oracle Apex and Insum.

We would also like to thank Zsuzsanna Hollander, Annaïck Carles, Mohammed Hasham, and Federica di Palma for their passion and work leading the development of the Metadata Commons.

Thank you to all contributors and users of the Metadata Commons for your continued support!

Appendix

Section A: Metadata Submission Fields

#	Field Name	Details	Section
1	Project Unique Identifier	"HMC" followed by 6 digits	PROJECT
2	**Project Title**	Title or name of the project	
3	**Project Description**	Describe the study (max 4,000 characters)	
4	Project Funder(s)	List of funding sources	
5	**Project Investigators**	First and last name of investigators	
6	Project Institution(s)	Name of every research institution involved in project	
7	Keywords	List keywords related to the project	
8	Publication Link	URL of most relevant publication (e.g., PubMed)	
9*	**Contact Email**	Email address of the project leader	
10*	**Data Access Request URL**	URL to data access request webpage	
11	Study Completed	Has the study been completed	
12	Cohort Name	Name of the patient cohort	COHORT
13	**Cohort Size**	Number of patients in the cohort (or estimate)	
14	Study Design	The type of study (Clinical trial OR Observational OR Prospective, etc.)	
15	**Enrollment Site(s)**	Where patients were enrolled (facility, city, country)	
16	Enrollment Time Window	Time window during which patient enrollment and sample collection took place	
17	**Disease/Condition Studied**	Disease condition studied	
18	Biobanking Consent	Has biobanking consent been obtained from study participants	
19	Medical History	Has medical history been collected	
20	Ethnicity	Has ethnicity been recorded	
21	Time Course	Is time course data available	
22	Patient Phenotypes	List patient phenotypes	
23	Patient Outcomes	List patient outcomes	
24	Clinical Data Types	List the types of clinical data collected for this cohort.	
25	Time Course Data Points	Specify the data points when available	
26	Group Name	Specify patient groups enrolled within the cohort	
27	Inclusion Criteria	List enrollment inclusion criteria for each group	
28	Exclusion Criteria	List enrollment exclusion criteria for each group	
29	**Sample Type**	List sample types collected	SAMPLES AND OMICS
30	Number of Samples	Total number of samples for each sample type collected	
31	Collection Method	Collection method used for each sample type	
32	**Omics-type**	Omics type developed from the samples collected	
33	**Omics Sub-type**	Omics sub-types for each sample type	
34	Sample Size in Dataset	Number of samples for each omics sub-type	
35	Instrument	Instrument used to produce omics data	
36	Experimental Design	Experimental design used to produce omics data	
37	Data Repository Link	Data repository accession number	

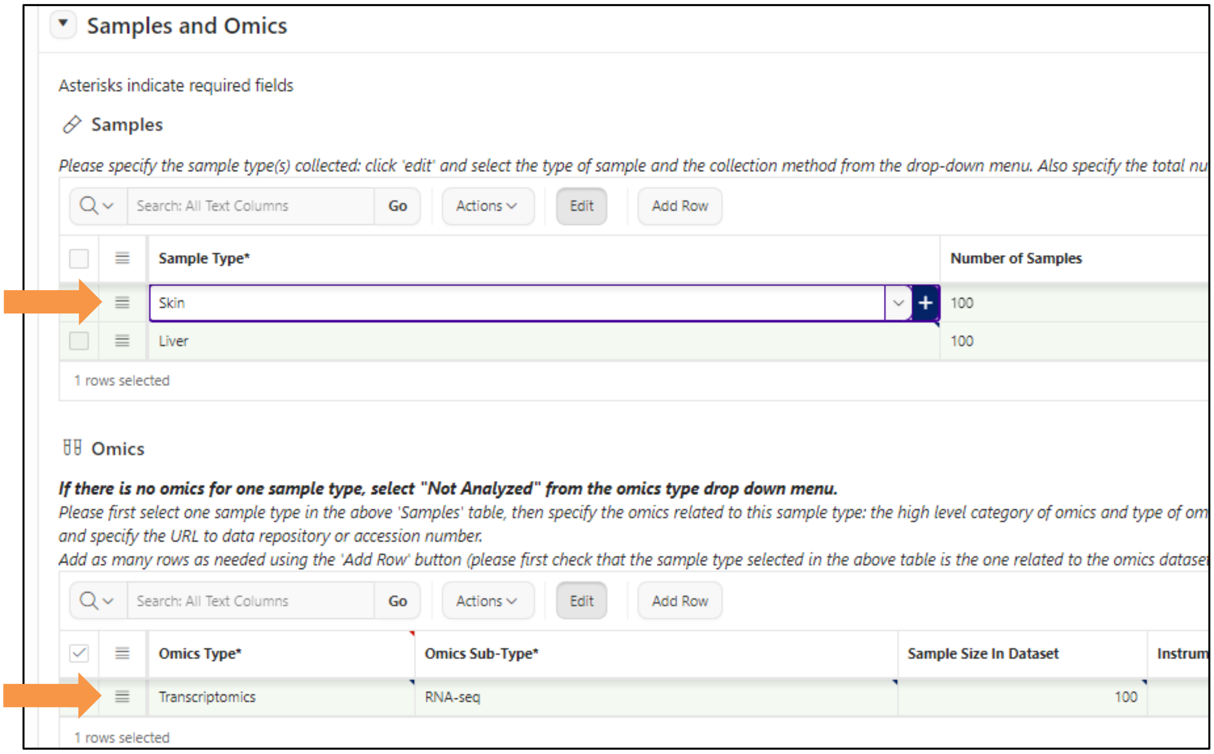
Required fields are **bolded**.

Section B: Sample/Omics Form Section Example

The first sample type `Skin` has `Transcriptomics/RNA-seq` data.

The second sample type `Liver` has `Epigenomics/WGBS-seq` data

Skin samples with Transcriptomics (RNA-seq)



Samples and Omics

Asterisks indicate required fields

Samples

Please specify the sample type(s) collected: click 'edit' and select the type of sample and the collection method from the drop-down menu. Also specify the total nu

☐	Sample Type*	Number of Samples
	Skin	100
☐	Liver	100

Omics

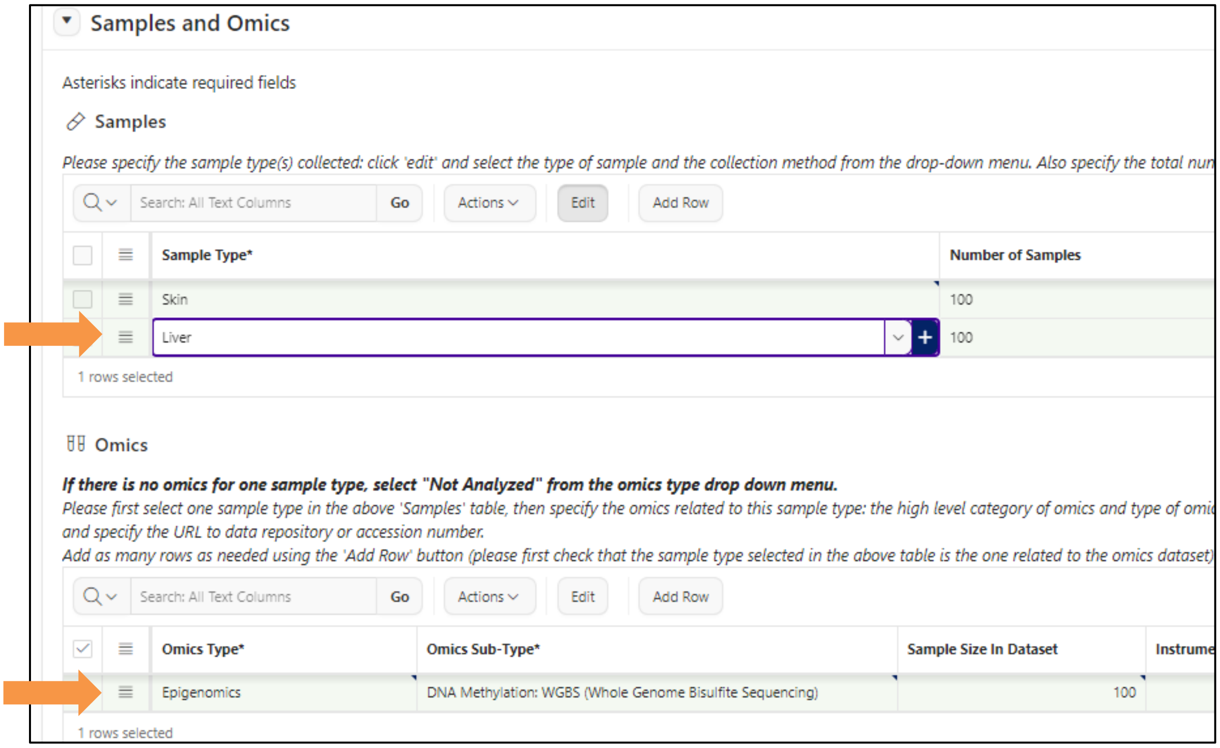
If there is no omics for one sample type, select "Not Analyzed" from the omics type drop down menu.

Please first select one sample type in the above 'Samples' table, then specify the omics related to this sample type: the high level category of omics and type of om and specify the URL to data repository or accession number.

Add as many rows as needed using the 'Add Row' button (please first check that the sample type selected in the above table is the one related to the omics datase

☑	Omics Type*	Omics Sub-Type*	Sample Size In Dataset	Instrum
	Transcriptomics	RNA-seq	100	

Liver samples with Epigenomics (WGBS-seq)



Samples and Omics

Asterisks indicate required fields

Samples

Please specify the sample type(s) collected: click 'edit' and select the type of sample and the collection method from the drop-down menu. Also specify the total nun

☐	Sample Type*	Number of Samples
☐	Skin	100
	Liver	100

Omics

If there is no omics for one sample type, select "Not Analyzed" from the omics type drop down menu.

Please first select one sample type in the above 'Samples' table, then specify the omics related to this sample type: the high level category of omics and type of omi and specify the URL to data repository or accession number.

Add as many rows as needed using the 'Add Row' button (please first check that the sample type selected in the above table is the one related to the omics dataset)

☑	Omics Type*	Omics Sub-Type*	Sample Size In Dataset	Instrume
	Epigenomics	DNA Methylation: WGBS (Whole Genome Bisulfite Sequencing)	100	