

Requesting a LabLink user ID

Before submitting samples for processing and analysis, you must request access to the system. LIMS administrators will then review your request, and once approved, send you a confirmation e-mail.

Because account contact information is tied to a specific e-mail address, this account should be for a **single user**, not a shared, lab account.

To request a LabLink user ID:

- Go to the RTSF Genomics Core LabLink home page: <http://clarity.bch.msu.edu/lablink>
- In the LabLink sidebar at the top-left click Request a User ID. The LabLink Sign Up page opens.
- On the LabLink Sign Up page, complete the form. Mandatory fields are outlined in red:
 - **First name:** Type your first name.
 - **Last name:** Type your last name.
 - **Title:** Optional.
 - **Phone:** Type your phone number.
 - **Fax:** Optional.
 - **Email address:** Type your e-mail address. This e-mail address will be used for all future e-mail correspondence, such as when you forget your password or request a change to your password.
 - **Facility:** Leave this as MSU-GLIMS.
 - **Account name:** Use the arrow at the right to view existing Lab names. If your lab name does not appear on the list type the new lab name in the box.
 - **Supervisor/PI:** If you are not the PI for this lab please enter the PI First name and Last name.
 - **User name:** Type the name you would like to use to create your user ID. You must use a minimum of 1 character and a maximum of 15 characters.
 - **New password:** Type the password you would like to assign to your user ID.
 - **Verify new password:** Re-type the password you would like to assign to your user ID.
- Click Submit.
- A page opens where you can view the information you are about to submit to the system. If everything looks correct, click Agree. If you would like to make changes to your information, click the Back button at the bottom of the page. Do not use your Web Browser's Back button.

After you receive confirmation that your account has been approved you may log in to your account to submit samples.

Submitting samples through LabLink

Creating the submission sheet

Sample information is submitted using a sample submission form, a specially preconfigured Excel worksheet. There are different versions of the sample submission form template available for download depending on the type of project you will be submitting. The different submission sheet templates available and their corresponding project types are:

Bioanalyzer / TapeStation submission in tubes

Used when submitting genomic DNA, total RNA, mRNA, dsDNA PCR products or completed Illumina sequencing libraries for analysis on the Bioanalyzer or TapeStation only. Samples are submitted in individual Eppendorf tubes. A maximum of 15 samples may be submitted in individual tubes, larger submissions must use 96 well plates.

Bioanalyzer / TapeStation submission in 96 well plate(s)

Used when submitting genomic DNA, total RNA, mRNA, dsDNA PCR products or completed Illumina sequencing libraries for analysis on the Bioanalyzer or Fragment Analyzer only. Samples are submitted in 96 well, PCR type plates. Submissions of 16 or more samples must be in plates.

Illumina Amplicon metagenomics samples in 96 well plate(s)

Used when submitting either metagenomic DNA for 16S-V4 library preparation, 16S-V3V4 library preparation or primary PCR products of your amplicon of interest.

Illumina DNA/RNA samples in tubes

Used when submitting DNA or RNA samples for standard Illumina shotgun DNA-Seq, mRNA-Seq, small RNA-Seq or other types of library preparation. Samples are submitted in individual Eppendorf tubes.

Illumina DNA/RNA samples in 96 well plate(s)

Used when submitting DNA or RNA samples for standard Illumina shotgun DNA-Seq, mRNA-Seq, small RNA-Seq or other types of library preparation. Samples are submitted in 96 well, PCR type plates.

Illumina User prepared libraries in tubes

Used when submitting already prepared, Illumina compatible libraries. Libraries are submitted in individual Eppendorf tubes. (See below regarding Index IDs.)

Illumina User prepared libraries in 96 well plate(s)

Used when submitting already prepared, Illumina compatible libraries. Libraries are submitted in 96 well, PCR type plates. (See below regarding Index IDs.)

Illumina User prepared library pool(s)

Used when submitting already prepared AND pooled, Illumina compatible libraries. Library pools are submitted in individual Eppendorf tubes. (See below regarding Index IDs.)

Nanopore DNA/RNA samples in tubes

Used when submitting DNA, cDNA or RNA samples for Oxford Nanopore library preparation and sequencing. Samples are submitted in individual Eppendorf tubes.

NanoString expression analysis

Used when submitting RNA or lysed cells for NanoString nCounter expression analysis projects. In addition to Sample information you must also provide information about the NanoString expression Panel (CodeSet) which is to be used for your experiment.

There are specific instructions provided for each submission type in the corresponding Excel template file. Carefully read and follow these instructions as you fill out your sample sheet.

When submitting prepared libraries for sequencing, either as individual libraries or pool(s) each library must have an Index ID associated with it. Only Index IDs already preconfigured in the ClarityLIMS system may be used and they must be entered on your sample sheet in a very specific format. There are two additional Excel files available for download which include all the acceptable index IDs currently available; one file includes Single Index IDs and the other Dual Index IDs. Download the appropriate file, and follow the instructions in that file to copy and paste exactly the correct Index IDs for each library.

NOTE: If you are unable to find an appropriate Index ID for your libraries then please contact the MSU Genomics Core at gtsf@msu.edu for help. DO NOT proceed with your submission until you have consulted with the genomics core.

Double check the information for errors and save the Excel file in a convenient location on your computer.

Create your project and upload sample information

When submitting samples, you are first asked to create a Project. This is because the LIMS uses Projects as the foundation for all work performed in the system. A Project stores the information about the user who creates it, significant dates, the status of the Project, permissions, and any user-defined information that a lab would like to collect. After creating a Project, you can add samples to the Project and the lab will then run Processes on those samples to perform the desired analysis.

To specify the Project that will contain your samples:

- In the LabLink sidebar to the left, click Submit Samples. The Sample Submission - Create a New Project page opens.
- On the Sample Submission - Create a New Project page, fill in the fields. Mandatory fields are outlined in red:
- **Project name:** Type a name for the Project. This Project name should be relatively short but meaningful. The name may only contain letters, digits, dashes (-) and underscores (_). NO SPACES, PERIODS OR OTHER PUNCTUATION MARKS ARE PERMITTED IN THE PROJECT NAME.
- **Project Type:** Select the appropriate project type from the drop down menu
- **Long Project Name:** (Optional) This field allows you to provide a more descriptive project name if you wish; it is solely for your information.
- **Payment Method:** Select one of the payment methods from the pop-up list (use arrow at right).
- **Account number:**
 - If you selected MSU Account above please enter the MSU Account number here. Include the subaccount information if you are using one.
 - If you selected PO please enter your institutions Purchase Order number here and submit a copy of your PO along with your sample submission form.
 - If Credit Card or Other please contact the RTSF Genomics Core to discuss payment. DO NOT ENTER YOUR CREDIT CARD NUMBER ON THIS FORM!
 - Payment information must be entered or otherwise provided to the RTSF Genomics Core before any work will be performed on your samples.
- **Note:** (Optional) Enter any additional information you feel is necessary such as special handling instructions, additional sample information, etc.
- Click Next.

The Enter Sample Information for Project page opens where you can add samples to the Project.

- Click the "Choose File" button. From the File Open dialog that appears locate and select the Excel file you created above.
- Click "Next". The submission system will read the Excel file. If an error is encountered it will be reported at the top of the screen. Correct the information in the Excel file, save it and repeat the step above.

The Review Your Samples page will appear.

- Review the information for your samples. If you see an error, click the "Back" button at the bottom of the page. This will return you to the previous page. Make changes to your Excel file, save the new version and repeat the upload process above.
- If all information in the table is correct click "Agree".

The Summary of Submitted Samples page will appear.

- Click Print.
- Sign the form (only one signature is required).
- Submit the signed copy of your form along with your samples to the RTSF Genomics Core submission -20°C freezer outside of Room S-18 Plant Biology Laboratories Building.