

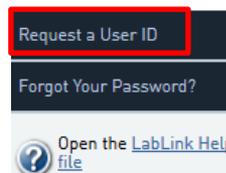
SF LIMS Customer Interface manual

SF LIMS – Create an Account

- Please copy and paste the following url to your web browser. To open this url please make sure that your computer is connected to the nih network.

<http://fr-s-ccrifx-dmo.ncifcrf.gov:8080/lablink/Welcome.do>

- Click on the “Request User ID” tab on the left side bar.



- Fill up all the details and click submit. You will receive an email confirmation, SF will send you confirmation after accepting the request.

Personal Information

First name:

Last name:

Title:

Phone:

Fax:

Email address:

Facility:

Supervisor / PI

First name:

Last name:

Account Information

User name:

New password:

Verify new password:

SF LIMS – Customer Interface

- Url : <http://fr-s-ccrsf-lim-p.ncifcrf.gov:8080/lablink/Welcome.do>
 - Login to interface by using given User Name and Password

Request a User ID

Forgot Your Password?

 Open the [LabLink Help file](#)

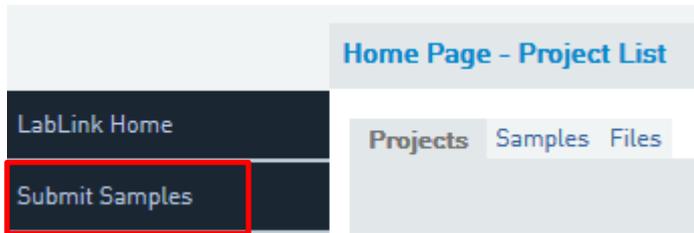
 Are you new to LabLink? To get started, click the 'Request a User ID' link in the LabLink sidebar.

User name:

Password:

SF LIMS – Sample Submission

- Click on Submit Samples which is on the left side bar



- Fill all the details regarding your project

Enter Project Information

Project name:

Principle Investigator Name:

Lab Contact:

Bioinformatics Contact:

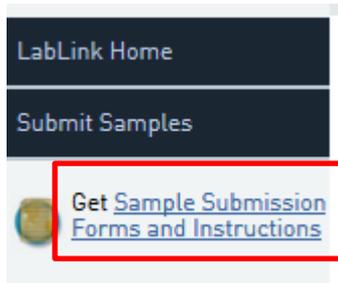
Total Number of Samples:

Project Details:

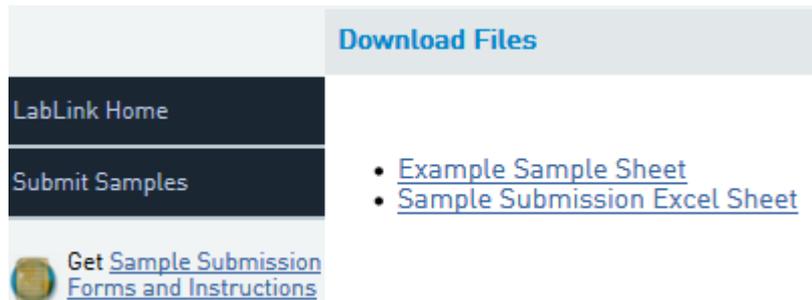
Next Cancel

- After filling the project details, click next

- Now it will ask you to upload the Sample Submission excel file. Which is available by clicking on the “Get Submission Forms and Instructions – Left side bar shown in the image below.



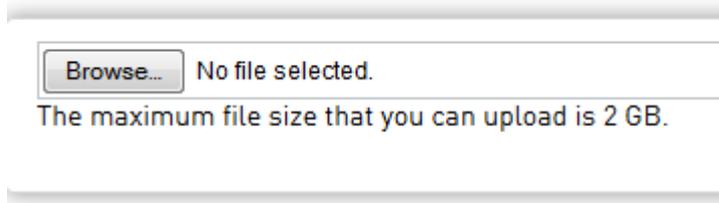
- You can also download the example of submission excel file along with the Sample Submission file.



SF LIMS – Rules of Sample Submission sheet

- If you are sending samples in the “Tube” then leave “Container/Name” and “Sample/Well Location” column blank. These columns are compulsory when you send your samples on plate.
- All the fields are required to be filled before uploading excel file to LIMS.
- UDF/Pooling – how many samples should be pooled along with this sample.
 - i.e. n=3 means pool two other samples submitted in this project along with this sample in to a lane (for Hiseq) or in flowcell (for NextSeq and MiSeq)
 - This step defines how many samples should be run together and SF will strictly follow the information written here so make sure the pooling information is accurate.
- “UDF/Sample Conc.” – Concentration of the sample and “UDF/Volume (uL)” – Volume of the sample must be accurate.
 - For time being you are not allowed to submit data if volume is not between ‘5 to 30’ uL.
 - Exception can be made by requesting to SF lab manager.
- Other Fields
 - UDF/CSAS – CSAS id for this project
 - UDF/Machine Type – which platform your samples should sequence on – i.e. HiSeq, MiSeq or NextSeq
 - UDF/Read Length – desired Read length of your data – option can vary based on sequencer type
 - UDF/Sample Type – type of sample being submitted – i.e. RNA, ChipDNA, gDNA, PCR products
 - UDF/Application – type of application you would like to do – i.e. mRNA Seq, Chip Seq or Exome Seq
 - UDF/Reference Genome – reference you would like to align you data against – i.e. Human hg19, Mouse mm9 etc.

- Upload the excel file back to lims upload interface by clicking “Browse” button and click next.



- It will now prompt you to a screen where you can confirm the submission details. If everything is correct then click next or click back and modify your sample submission excel file and re upload it again.
- It will now ask you “agree” on the sample details. Click “Agree”
- Now print the “Summary of Submitted Sample” . Sign it, scan it and send the printed form to following email : ccrsfhelp@mail.nih.gov

SF LIMS – Track your Samples

- New SF LIMS will allow customer to track their samples
 - It will mention that how many processes have been completed on the sample i.e. “Library preparation and QC validation complete”
- To track the samples
 - Click on the “LabLink Home” which on the left side bar



- Then click on the samples, Here you can track the samples by viewing the “Process Field”.

Projects **Samples** Files Get help for this page

View samples with status: For project:

Name	LIMS ID	Status	Project	Date Received	Last Note	Application	CSAS	Machine Type	Progress	Read Length	Reference Genome	Volume (uL)
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LIMS Support and Contact Information

For questions or ask for LIMS support, please send email to:

keyur.talsania@nih.gov or

SFILLUMINABIOINF@mail.nih.gov