



CANADA'S MICHAEL SMITH  
GENOME SCIENCES CENTRE

*From Nobel roots.*

## INTRODUCTION TO OUR COLLABORATIVE SERVICES



### A GUIDE TO WORKING WITH US

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## ABOUT US

Our **CAP, DAP, ISO 15189**, and **ISO 27001** certified technology platform is a high-throughput, large-scale DNA and RNA sequencing and analysis facility that has been designed to maximize analytical capacity, diversity, efficiency, scalability and flexibility.

Our state-of-the-art clinical, sequencing, bioinformatics, and proteomics platforms are ready to be put to use for your research or clinic.

We partner with researchers, guide experimental design, execute high quality processing of complex and valuable biological samples and provide extensive bioinformatics analyses with the aim of making genomics research accessible to our partners and collaborators within the scientific community.

Please feel free to contact us at [SOW@bcgsc.ca](mailto:SOW@bcgsc.ca) if you have any questions about the services we provide.

## ABOUT THIS GUIDE

This user guide is an introduction to the process of submitting samples and working with us.

When you're ready to submit a sample, please refer to the corresponding user guide on [bcgsc.ca/services](http://bcgsc.ca/services) for details about sample requirements, online sample submission, and sample shipping.

## CONTACTS

Submissions

[GSC\\_submissions@bcgsc.ca](mailto:GSC_submissions@bcgsc.ca)

Statements of Work

[SOW@bcgsc.ca](mailto:SOW@bcgsc.ca)

Data Support and Access

[data\\_support@bcgsc.ca](mailto:data_support@bcgsc.ca)

Shipping

[GSC\\_submissions@bcgsc.ca](mailto:GSC_submissions@bcgsc.ca)

General

[info@bcgsc.ca](mailto:info@bcgsc.ca)



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## 1. WELCOME TO THE GSC

This guide will provide helpful information that will assist you in navigating our sample submission system.

If you have any questions, please contact us at [GSC\\_Submissions@bcgsc.ca](mailto:GSC_Submissions@bcgsc.ca).



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## 2. FROM SERVICE REQUEST TO DATA DISSEMINATION

1. [Fill out a service request form](#)  
One of our team members will contact you shortly.
2. [Statement of Work \(SOW\)](#)  
Our team will work with you to create a SOW for your project.
3. [Create a LIMS account](#)  
A LIMS account is needed for online sample submission and tracking.
4. [Sample submission](#)  
Follow the appropriate GSC User Guide.
5. [Sample tracking](#)  
Track the status of your samples in LIMS.
6. [Get your data](#)  
Download your data directly.



### 3. SERVICE REQUEST FORM

Let us know how we can help you by filling out our online service request form at [bcgsc.ca/form/service-request](https://bcgsc.ca/form/service-request).

When filling out the form, tell us about your project and which services you are interested in. One of our team members will get back to you within two business days.

#### Collaborative Services Inquiries

Indicates required field

*Thank you for your interest in our Collaborative Services. For us to provide you with information most suitable for your work, please fill out the form below with your contact details, a brief description of your project and which of the services you are interested in.*

##### Submitter Name

Submitter first name

Submitter last name

Submitter position

Email

Confirm email

Phone number

Institution

Province/State

Country

##### Principal Investigator Name (If different from Submitter)

Principal investigator first name

Principal investigator last name

##### Which products are you interested in:

###### Sequencing

- ☐ Clinical
- ☐ Genome
- ☐ Exome
- ☐ Transcriptome
- ☐ Epigenome
- ☐ miRNA
- ☐ Other...

###### Bioinformatics

- ☐ Genome assembly
- ☐ Alignment to reference genome
- ☐ Expression analysis
- ☐ Somatic analysis
- ☐ Structural variant analysis
- ☐ Epigenetic analysis
- ☐ Cancer immune-genetics analysis
- ☐ Submission to a public repository
- ☐ Other...

###### Proteomics

- ☐ Quantitative global proteomics
- ☐ Targeted proteomics
- ☐ Small molecule quantification
- ☐ Protein biochemistry



## 4. STATEMENT OF WORK (SOW)

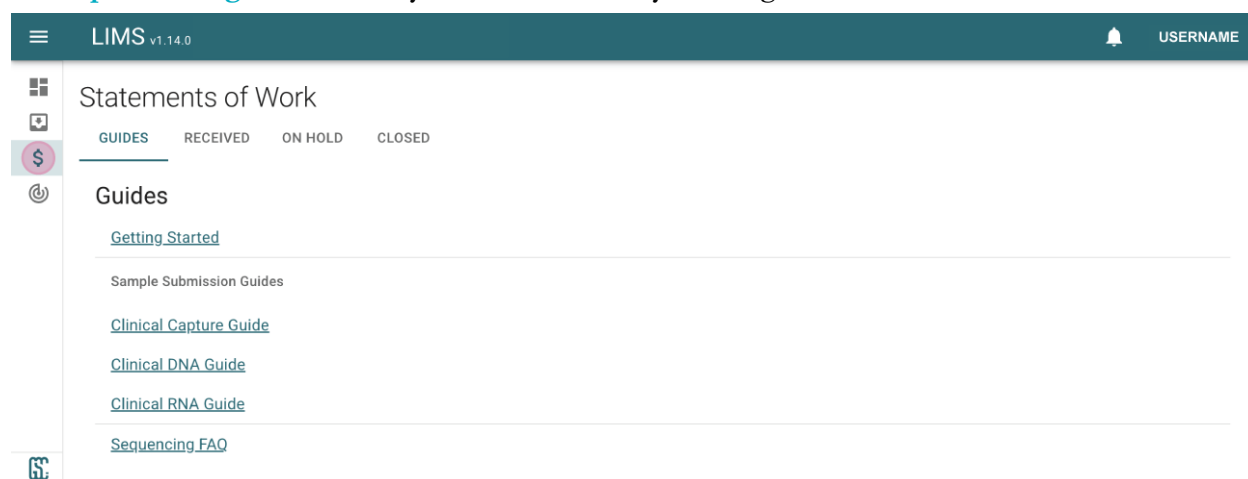
### 4.1. WHAT IS A SOW?

A **Statement of Work (SOW)** is a formal document that outlines the scope of work and cost estimates for GSC services based on a project's request.

*A signed SOW is required for submission of samples for sequencing or other activities.*

If you do not have a SOW and would like to submit samples for sequencing, please contact us ([SOW@bcgsc.ca](mailto:SOW@bcgsc.ca)).

If you already have a signed SOW in place, or you have been provided access to one by the **Principal Investigator (PI)**, they can be accessed by clicking on the **SOWs icon \$**.



### 4.2. ACCOUNT CREATION

Adding new users to a SOW will automatically create new accounts in the system.

Account username and temporary password will be sent in an e-mail from [LIMS@bcgsc.ca](mailto:LIMS@bcgsc.ca).

You may need to add [LIMS@bcgsc.ca](mailto:LIMS@bcgsc.ca) to your safe sender list. Upon first login, you will be prompted to set a new password to successfully activate your account.

### 4.3. SOW PERMISSIONS

The **Principal Investigator (PI)** named on each SOW will have all permissions as described below. PIs are able to add additional users to every SOW, and assign permissions as appropriate. If you require additional permissions for any SOW, please contact your PI.



## 4.4. SOW PERMISSION LEVELS

### 4.4.1. BASIC ACCESS

Ability to view the SOW details on the homepage. All users associated with a SOW have this level of access.

### 4.4.2. DISSEMINATION EDITOR

Ability to add/remove users from the dissemination list and the [secure FTP \(SFTP\)](#) access list.

### 4.4.3. DELEGATE

Ability to add/remove users from the SOW, the dissemination list, the SFTP access list, and the submitter access list.

### 4.4.4. SUBMITTER

Ability to initiate, edit, and submit sample submission forms.

### 4.4.5. DISSEMINATION LIST MEMBER

Will receive an email from the GSC when data generated under the SOW is available. This list is maintained by the PI or those they designate as a [Dissemination Editor](#).

### 4.4.6. SFTP ACCESS LIST MEMBER

If your [Statement of Work](#) is scheduled to receive data via our SFTP site, the PI named on the SOW and SFTP access list members will be able to access the SFTP site for data download.

This option will not be available if your data is accessed directly through GSC file systems.



## 5. SUBMITTING SAMPLES

If you have the [Submitter](#) permission, you have the ability to submit samples under the respective SOW. The submission form can be accessed by clicking on the [Submissions](#) button in the left panel.

*The online submission form must be completed and approved prior to submitting your samples to the GSC.*

### 5.1. USER GUIDES

Please refer to the following [User Guides](#) on [bcgsc.ca/services](http://bcgsc.ca/services) before preparing and submitting your samples. These guides also provide sample shipping requirements and drop-off instructions.

| DNA SAMPLES   | RNA SAMPLES       | CONSTRUCTED LIBRARIES |
|---------------|-------------------|-----------------------|
| BODILY FLUIDS | CELLS             | METAGENOMES           |
| TISSUE        | FFPE TISSUE       | FFPE TISSUE BLOCK     |
| CGL CLINICAL  | ADAPTIVE SAMPLING |                       |

### 5.2. ACCREDITATION

All clinical testing must be performed in [CAP](#) or [DAP-accredited](#) laboratories or laboratories accredited by an established international standard from a recognized organization. This includes all components of testing that may impact the quality of the test result, including isolation or extraction of nucleic acids.

The GSC will ask to provide a certificate of accreditation or may choose to have our clients formally attest that extracted nucleic acid submitted for testing has been isolated or extracted in an appropriately accredited laboratory.

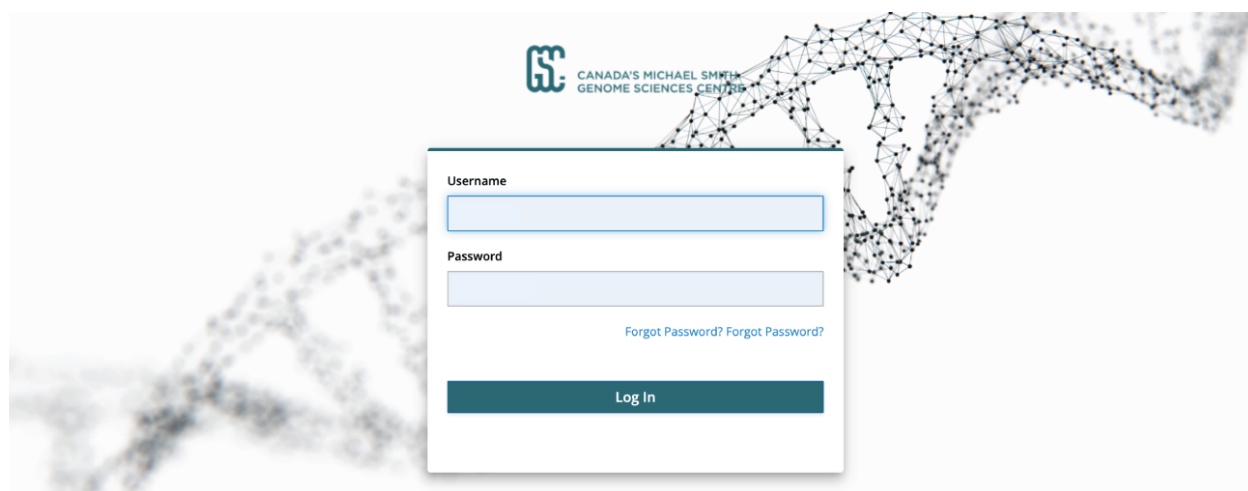


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## 6. ONLINE SAMPLE SUBMISSION AND TRACKING

Our [Online Sample Submission System](#) allows you to submit and track your samples.

If you have any questions, contact us at [GSC Submissions@bcgsc.ca](mailto:GSC_Submissions@bcgsc.ca).



### 6.1. LOGGING IN

1. Go to [bcgsc.ca/samplesubmissions](https://bcgsc.ca/samplesubmissions). Please use Firefox or Google Chrome browsers.
2. Enter your username and password, and then click **Log In**. If you do not yet have an account, contact us [SOW@bcgsc.ca](mailto:SOW@bcgsc.ca).
3. Once you're logged in, you'll be presented with a menu of choices.
4. You can expand and collapse the menu by clicking on the hamburger icon (top left).
5. You can **log out** anytime by clicking on your **user name** (top right).

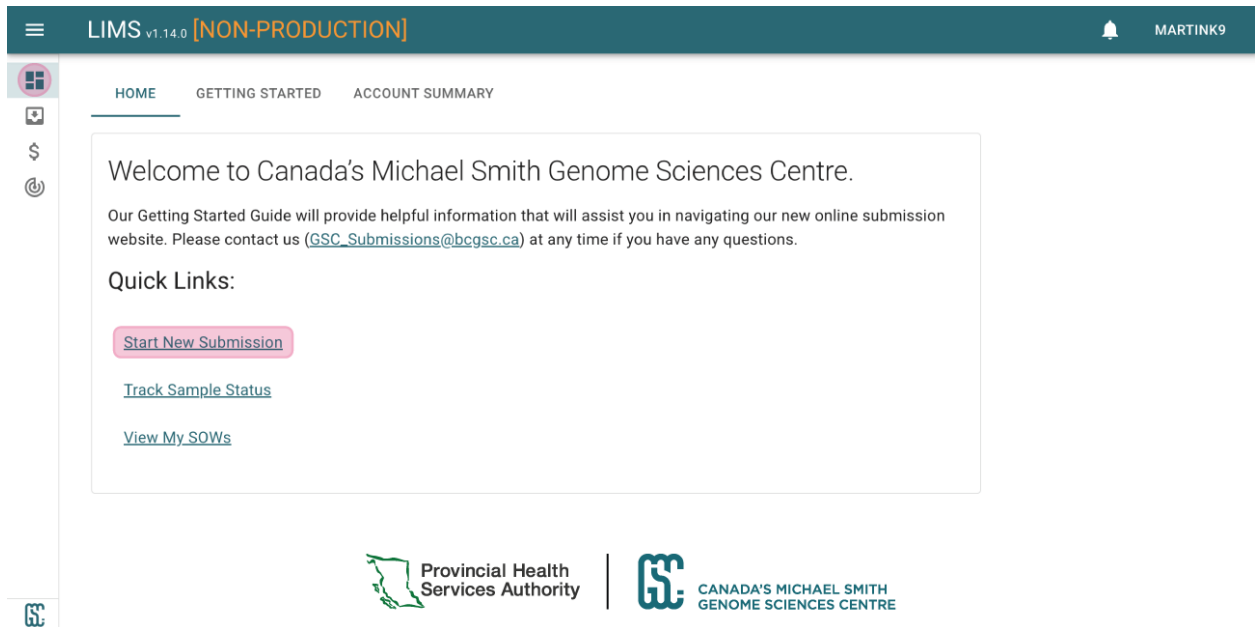


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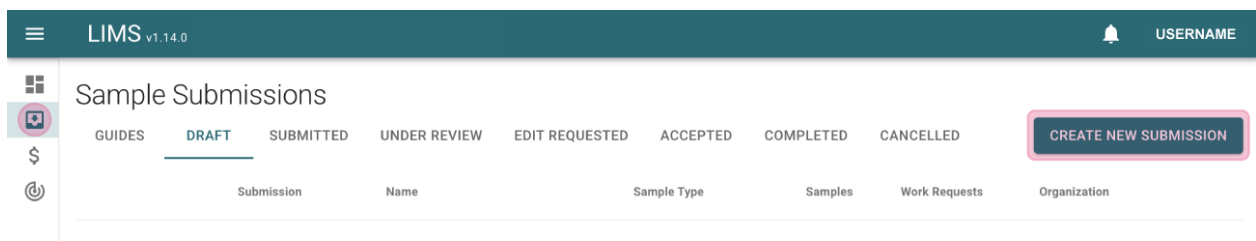
## 6.2. INITIATING A SUBMISSION

You can start a new sample submission in one of two ways.

1. Click the **Dashboard icon**  in the left panel and then click on **Start New Submission** under **Quick Links**.



2. Alternatively, click the **Submission icon**  in the left panel, and then click **Create New Submission**.





## 6.2.1. ENTERING SUBMISSION DETAILS

LIMS v1.14.0 USERNAME

Create a New Submission

Submission Name

Type of Submission \*

Statement of Work \*

How many samples are you submitting? \*

START DRAFT

1. Enter the details of your submission. Mandatory fields are denoted by \*. *Only one sample type is allowed per submission.*
  - 1.1. If you are submitting your sample on an [Axygen plate](#), you will be provided with an option to [request a barcoded plate](#). We will contact you when the plate is ready to be picked up from the GSC or shipped to your lab.
  - 1.2. If you choose to have the plate shipped, we will ask you to provide your shipping address and FedEx account number.
2. *Taxonomy:* You may enter multiple Taxonomy IDs per submission. Search for the taxa of your samples by entering the [NCBI Taxonomy ID](#) (e.g., [9606](#)) or name (e.g., [human](#)). Only selected, [Taxonomy IDs](#) will be available later in the [Sample information](#) section under the [Taxonomy field](#).
  - 2.1. If your sample's taxonomy is [unidentified](#), use code [32644](#).

LIMS v1.14.0 USERNAME

What are the taxa of your samples? (Search by name or NCBI Taxonomy ID) \*

Homo sapiens - human [9606] Populus trichocarpa - black cottonwood [3694]

start typing for options

| Taxonomy | Reference Genome | Dissemination |
|----------|------------------|---------------|
| 9606     |                  | BAM/FASTQ     |
| 3694     |                  | BAM/FASTQ     |

3. *Sample Options:* Select all options that apply to your sample. Depending on your sample options, you will be asked to complete additional fields on the [sample submission form](#),



4. *Prepopulate the form by uploading an Excel file:* Users who submit samples frequently may choose to prepopulate the sample information form by [uploading an Excel file](#).

The screenshot shows the LIMS v1.14.0 interface. On the left is a sidebar with icons for various sample types: Amplicons, Canadian Precision Health Initiative (CPHI), cDNA, Cell Lines, CHIP, Nanopore Adaptive Sampling, and Xenograft. The main area has a header with 'LIMS v1.14.0' and a 'USERNAME' field. Below the sidebar, there is a section titled 'Prepopulate the form by uploading an excel file' which is checked. Below this are two buttons: 'DOWNLOAD TEMPLATE' and 'UPLOAD EXCEL FILE'. Further down, there is a section titled 'Upon completion of project (choose one) \*' with two radio button options: 'Return unused sample.' (with a note 'GSC will return any residual sample at submitter's expense.') and 'Destroy unused sample.' (with a note 'GSC will destroy any remaining sample at completion of project').

- 4.1. Click the [Prepopulate checkbox](#).
- 4.2. Click [Download template](#).
- 4.3. Enter your sample information directly into the Excel file that was generated:
- 4.3.1. You can copy and paste entries from a pre-existing Excel file that contains your sample information.
  - 4.3.2. If a field has a drop-down menu, you must select from the available options.
  - 4.3.3. Some fields may require validation after the sample information form has been populated.
  - 4.3.4. All fields do not need to be completed in order to use this feature to prepopulate the sample information form.
  - 4.3.5. Any missing or invalid fields can be corrected within the actual sample information form.
- 4.4. Once completed, save the Excel file on your computer.
- 4.5. Go back to the [Create a New Submission](#) page and click [Upload Excel file](#).
- 4.6. A dialogue window will open that allows you to navigate to the location on your computer where you saved the Excel file.
- 4.7. The [Sample Information](#) section will be auto-populated based on the entries in the Excel file.



## 6.2.2. ENTERING SAMPLE DETAILS

Once you have started your draft submission, you can always go back to the [Set Up](#) section to edit submission details. The submission type, [SOW](#), [associated project](#), and [number of samples](#) will not be editable.

1. There are tools on the top right corner to help you complete each field more conveniently:
  - 1.1. **Paste Range:** Helpful when you have a pre-existing Excel file that you would like to copy and paste line items from. For the fields without a drop-down menu, you can copy and paste directly into the form from your Excel file without using this tool.
  - 1.2. **Fill Down:** Helpful when you have several consecutive rows that will contain the same value.
  - 1.3. **Clear Column:** Helpful when you would like to reset values in the entire column.
2. For additional information on any given field, click the **Information icon** ⓘ next to the column heading:
3. If you enter field values that do not match suggested requirements for a given field (e.g. sample volumes), an **orange warning icon** ⚠ will appear. Please double-check these values. If the information looks correct, you can proceed as is.
4. If field values are missing or do not match strict requirements, a **red warning icon** ❗ will appear. These entries must be corrected before you can submit your sample information form.



## 6.3. WORK REQUESTS

Please refer to your [Statement of Work \(SOW\)](#) to obtain the work request information that will be required in this section.

1. If the samples you are submitting have different library protocols and/or sequencing goals, you will need to click [Add Work Request](#) on the top left corner to be able to enter different work requests for each sample.

LIMS v1.14.0 USERNAME

last saved: 2:29:30 PM

SET UP ✓ SAMPLE INFORMATION \* WORK REQUESTS \* WORK REQUEST ASSIGNMENT \* COMMENTS ✓ PLATE INFORMATION \*

ADD WORK REQUEST REMOVE SELECTED WORK REQUEST

| Library <       | Sequencing <  |                       |                   |                 |           |            |
|-----------------|---------------|-----------------------|-------------------|-----------------|-----------|------------|
| Work Request* ⓘ | Library Type* | Library Protocol*     | Capture Strategy* | Capture Probes* | Platform* | Read Type* |
| 1               | Genome        | Genome (Tagmentation) |                   |                 |           |            |
| 2               | Genome        | PCR-Free Genome       |                   |                 |           |            |

2. Depending on your choices, some work request options may not be available.
3. Once the work request is specified, you will be asked to associate the request with one or more of your samples. See the [Work Request Assignment](#) section below.
4. Enter any additional comments regarding your work request in the [Comments](#) section (e.g. specific pooling strategy).



## 6.4. WORK REQUEST ASSIGNMENT

Once the [Work Requests section](#) has been completed (if applicable), you will need to assign one of the work requests to each sample in the [Work Request Assignment section](#).

Library < Sequencing <

| Work Request* | Library Type* | Library Protocol*     | Capture Strategy* | Capture Probes* | Platform* | Read Type* |
|---------------|---------------|-----------------------|-------------------|-----------------|-----------|------------|
| 1             | Genome        | Genome (Tagmentation) |                   |                 |           |            |
| 2             | Genome        | PCR-Free Genome       |                   |                 |           |            |

PASTE RANGE FILL DOWN CLEAR COLUMN ASSIGN PLATE LOCATION

| Sample Information |            | Analyte Information |                        | Work Requests |                                                                  |
|--------------------|------------|---------------------|------------------------|---------------|------------------------------------------------------------------|
| #                  | Sample ID* | Volume (uL)*        | Concentration (ng/uL)* | Amount (ng)   |                                                                  |
| 1                  | 001-axy    |                     |                        | 0             | <input checked="" type="checkbox"/> 1 <input type="checkbox"/> 2 |
| 2                  | 002-prq    |                     |                        | 0             | <input checked="" type="checkbox"/> 1 <input type="checkbox"/> 2 |
| 3                  | 003-owq    |                     |                        | 0             | <input type="checkbox"/> 1 <input checked="" type="checkbox"/> 2 |
| 4                  | 004-rwx    |                     |                        | 0             | <input type="checkbox"/> 1 <input checked="" type="checkbox"/> 2 |
| 5                  | 005-iqp    |                     |                        | 0             | <input type="checkbox"/> 1 <input checked="" type="checkbox"/> 2 |

1. Assign a work request to each sample by clicking the checkbox under the appropriate [Work Requests](#) column. In the example below, [Work Request 1](#) is assigned to [Samples 1 and 2](#) and [Work Request 2](#) is assigned to [Samples 3, 4, and 5](#).
  - 1.1. You can edit work request details by going back to the [Work Requests section](#).
  - 1.2. If the same work request should be applied to all the samples, simply click the first checkbox, then click [Fill Down](#).



2. The required volume, concentration, and amount are validated based on the library protocol selected. If you are submitting less than the minimum amounts, you will be asked to accept the risks of failure before you can submit your sample information form for review:

Are you sure you want to Submit for Review?

 **Warnings**

**Sample Information**

This does not meet the minimum recommended volume for the selected work requests. We recommend at least 20 uL.

at Volume (uL) in Sample 1234567 [VIEW](#)

**Work Request Assignment**

This does not meet the minimum recommended volume for the selected work requests. We recommend at least 20 uL.

at Volume (uL) in Sample 1234567 [VIEW](#)

The submission amounts which you have indicated may not be sufficient to correctly perform the selected work items, or they may be out of the recommended volume range.

Please consult the [Sequencing FAQ](#) for minimum submission requirements.

☐ I accept the risks

CANCEL

SUBMIT FOR REVIEW



## 6.5. COMMENTS

Use the [Comments Section](#) to provide extra information or details regarding your submission of samples (e.g. specific pooling strategy).

The screenshot displays the LIMS v1.14.0 web interface. At the top, a dark teal header bar contains a menu icon, the text 'LIMS v1.14.0', a notification bell icon, and the placeholder 'USERNAME'. Below the header, a sidebar on the left shows a grid icon, a plus icon, a dollar sign, and a circular icon. The main content area features a horizontal navigation bar with tabs: 'SET UP' (with a green checkmark), 'SAMPLE INFORMATION' (with a red asterisk), 'WORK REQUESTS' (with a red asterisk), 'WORK REQUEST ASSIGNMENT' (with a red asterisk), 'COMMENTS' (with a green checkmark and highlighted in pink), and 'PLATE INFORMATION' (with a red asterisk). Above the 'COMMENTS' tab, there are icons for undo, redo, edit, and view, followed by a 'SAVE' button, a 'SUBMIT FOR REVIEW' button with a dropdown arrow, and a 'STOP EDITING' button. A status message 'last saved: 2:32:26 PM' is positioned above the 'COMMENTS' tab. The 'COMMENTS' section itself is a large, empty text area labeled 'Submission Comments'.



## 6.6. PLATE INFORMATION

If you are submitting **24–92 samples**, you will also need to provide **Plate ID** and **Rac ID** (if applicable) in the **Plate Information section**.

1. **Plate ID** is the name your lab assigns to the plate. You may even handwrite your **SOW number**, **project name**, etc. on the plate and use that as **Plate ID**. If your samples are being submitted on a pre-barcoded plate provided by the GSC, **Plate ID cannot be the same** as **Rac ID**, as **Rac ID** is the internal name used by the GSC.
2. If you have received a pre-barcoded plate from the GSC, please enter the **Rac ID** affixed to the plate. If you have not received the plate yet, you may complete the submission.



## 6.7. FINALIZING YOUR SUBMISSION

Once you have reviewed all the fields and are satisfied with the sample information form, click [Submit for Review](#) on the top right corner.

The screenshot shows the LIMS v1.14.0 interface. At the top, there is a header bar with a menu icon, 'LIMS v1.14.0', a notification bell, and 'USERNAME'. Below the header, there is a toolbar with icons for home, search, edit, and view, along with buttons for 'SAVE', 'SUBMIT FOR REVIEW' (highlighted with a red box), and 'STOP EDITING'. The main content area has a tabbed interface with tabs for 'SET UP', 'SAMPLE INFORMATION', 'WORK REQUESTS', 'WORK REQUEST ASSIGNMENT', 'COMMENTS', and 'PLATE INFORMATION'. The 'SAMPLE INFORMATION' tab is active. Below the tabs, there is a 'jump to section' dropdown menu set to 'Sample Information', and buttons for 'ADD SAMPLE', 'REMOVE SELECTED SAMPLES', 'PASTE RANGE', 'FILL DOWN', 'CLEAR COLUMN', and 'ASSIGN PLATE LOCATION'. A table is displayed with columns for '#', 'Sample ID', 'Plate Location', 'Taxonomy', 'Alternate Sample ID', 'Patient ID', and 'Participant Study ID'. The table has a header row with expandable sections for 'Sample Information' and 'Sample Information'.

1. If any of the samples do not meet the minimum recommended amount, click on the [I accept the risks](#) checkbox in order to proceed.

Are you sure you want to Submit for Review?

The warning dialog box has a title 'Warnings' with a warning icon. It contains two sections: 'Sample Information' and 'Work Request Assignment'. Both sections state: 'This does not meet the minimum recommended volume for the selected work requests. We recommend at least 20 uL. at Volume (uL) in Sample 1234567 VIEW'. Below these sections, there is a paragraph: 'The submission amounts which you have indicated may not be sufficient to correctly perform the selected work items, or they may be out of the recommended volume range. Please consult the [Sequencing FAQ](#) for minimum submission requirements.' At the bottom of the dialog, there is a checkbox labeled 'I accept the risks'.

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SUBMIT FOR REVIEW



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2. If there are any errors that need to be addressed, you will see an [Unable to Submit for Review](#) message. For each error, click [View](#) to go to the cell that must be fixed before submitting.

Unable to Submit for Review

All errors must be resolved before submitting.

 Errors

Sample Information

Field is required.  
at Concentration (nM) in Sample [VIEW](#)

Field is required.  
at Volume (uL) in Sample [VIEW](#)

3. Once your sample information form has been successfully submitted, you will receive [Sample Information Form Received for Review](#) email notification.



## 6.8. AFTER SUBMITTING FOR REVIEW

1. Your sample information form will be reviewed for completeness and accuracy. You will then receive **Edits Requested** or **Submission Approved** email notification.
2. For **Edits Requested**:
  - 2.1. In order to resubmit the form, you must confirm or amend all of the fields which have been highlighted yellow or orange by the reviewer. As you address each field in the form, its colour will change to green or blue. When there are no more yellow or orange fields left, you can resubmit.
  - 2.2. Some fields may also contain a comment made by the reviewer, in which case those fields will be marked with a small red triangle. You can hover your mouse over those fields to see the reviewer comments.
  - 2.3. You also have the option of making edits to any field, including those which have not been highlighted by the reviewer. Any such fields will become highlighted purple, and are subject to final review by the GSC Submission team.
  - 2.4. Colors will draw your attention to steps in the process or actions that need to be completed:
    - 2.4.1. **Yellow: Needs Attention** — the reviewer believes an edit may be required.
    - 2.4.2. **Orange: Changed by Reviewer** — the reviewer has already changed the value of this field, and would like you to confirm (or re-edit). Hover over the field with your mouse to see the change that has been made.
    - 2.4.3. **Blue: Amended by Submitter** — to be reviewed by the GSC submission team.
    - 2.4.4. **Green: Confirmed by Submitter** — subject to final review by the GSC submission team.
    - 2.4.5. **Purple: Additional Edit by Submitter** — subject to final review by the GSC submission team.

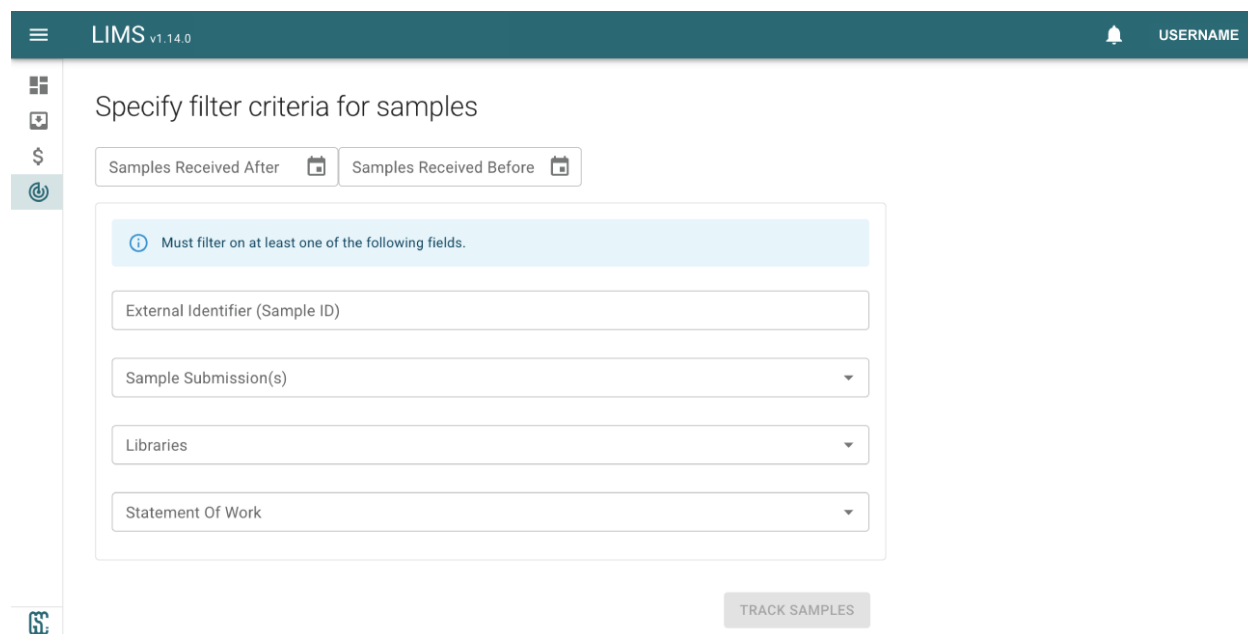


3. You should use the following modes (**Edit**, **Highlight**, and **Read-only**) when addressing reviewer comments and changes:
  - 3.1.  **Edit**: This is the default mode. When in **Edit** mode, you are able to alter any field to change its value. Whenever you have made an edit to a field, it will turn blue or purple.
  - 3.2.  **Highlight**: When you switch to **Highlight** mode, clicking on a field should turn it green. You may highlight a field green to indicate that you agree with an edit made by the reviewer, or that you believe the highlighted field already has the correct value. (Clicking on a field multiple times while in highlight mode will toggle between **unconfirmed** and **confirmed** state.)
  - 3.3.  **Read-only**: All error and warning messages will be hidden.
4. Once your submission has been approved, you will receive a **Submission Approved** email notification with detailed instructions for dropping off or shipping your samples. *An approved submission form is required in order for the GSC to receive samples.*



## 6.9. TRACKING A SAMPLE

The sample tracker can be accessed by clicking on the **Sample Status icon** (  ) in the left pane. Here, you can **search for and track samples** that you have submitted. You can search for samples using the submission name or identifier assigned to each unique submission. You may also track samples by searching the external identifier (**Sample ID**), library name or SOW.



The screenshot shows the LIMS v1.14.0 interface. At the top, there is a header bar with the LIMS logo, version number, and a user profile section with a bell icon and the text 'USERNAME'. On the left, there is a vertical sidebar with icons for home, samples, libraries, and a highlighted 'Sample Status' icon. The main content area is titled 'Specify filter criteria for samples'. It contains two date-based filters: 'Samples Received After' and 'Samples Received Before', each with a calendar icon. Below these is a light blue box with an information icon and the text 'Must filter on at least one of the following fields.' This is followed by four input fields: 'External Identifier (Sample ID)' (text input), 'Sample Submission(s)' (dropdown menu), 'Libraries' (dropdown menu), and 'Statement Of Work' (dropdown menu). At the bottom right of the form area is a grey button labeled 'TRACK SAMPLES'.



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## 7. SAMPLE RETENTION POLICY

Storage of materials for this Project, including the submitted libraries or other materials submitted by the Project ([Original Materials](#)) and any and all subsequent materials produced by the GSC ([Subproducts](#)) will continue for 6 months following data dissemination.

Submitted [Original Materials](#) will be disposed of at the GSC's discretion after [6 months](#) following data dissemination.

If indicated in the approved [Sample Submission Form](#) that the Project would like the Original Materials returned, a written request from the Project for sample return needs to be received within this 6 month period.

The cost of any return shipping (including handling fees, insurance, and courier costs) will be the responsibility of the Project and added to the Project cost.



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## 8. ACCESSING YOUR DATA

Once sequencing has completed and data ready for download, all individuals listed in the [Dissemination List](#) will receive an email informing them that their data is available for download from our SFTP site. The email is a receipt, identifying data that has recently been made available.

Once the notification email has been sent, a separate email with login and password details for the SFTP site will be sent to the individuals listed on the [SFTP Access List](#).

If you do not have an SFTP client on your computer, you will need to download and install one before you are able to access your data. Please refer to this [list of some recommended SFTP clients](#) that can be downloaded for free, along with links to installation instructions.

### 8.1. DATA RETENTION POLICY

Data will be automatically deleted from the download site two weeks after the data dissemination email is sent.

If you are unable to download your data within two weeks, please contact us at [data\\_support@bcgsc.ca](mailto:data_support@bcgsc.ca).

If your data are still available for re-upload, there may be an additional cost.



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## 9. ALIGNMENTS

The costs for sequencing include provision of alignments for all sequenced libraries where applicable. For more information on the GSC's sequence data format, alignment software, and reference(s) used as default or custom-request, visit [bcgsc.ca/services/frequently-asked-questions](https://bcgsc.ca/services/frequently-asked-questions).



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## 10. TERMS OF SERVICE

Platform services at the GSC are collaborative and are available and accessible to any and all researchers. Collaborative services are billed on a cost recovery basis, meaning that we charge only the costs of conducting the service. Pricing is regularly reviewed to accurately reflect costs for the scope and type of work requested.

Where warranted, we can operate on a fee-for-services basis. We encourage the use of the platform for commercial or service-based activity on terms and conditions determined by the [\*Provincial Health Services Authority Technology Development Office\*](#). Regardless of the service type, the order of work and delivery of service follow the principles described below.

For all services, the order of work done is determined on a “first in, first on” principle. We require that all researchers establish a **Statement of Work** with us for their activities prior to the submission of any samples. All work is queued in our systems based on the date of successful sample receipt.

Turnaround times may vary, based not only on the numbers of samples or other work in the queue, but also status of technology development. During times when instrument or systems upgrades are being installed or implemented, turnaround times may be affected while the platform adopts newer, better methods and technology.

Because we operate on a collaborative cost-recovery basis, we are unable to offer volume discounts for large sample sets. However, the automation and scalability of our pipelines do result in a reduced cost per sample for larger batches. Requests for enhanced/faster service are reviewed and considered at a case-by-case basis and may be associated with surcharges or premiums.



## 11. ACKNOWLEDGEMENT POLICY

To gauge our scientific impact and monitor our involvement in the wider scientific community, we make efforts to track our contributions and collaborations. This is done as part of our ongoing support for the activities of our collaborators, as well as to ensure we meet the requirements of both our funding partners and our charter as a non-profit agency.

In order to achieve this, we require our collaborators to acknowledge the work performed by the GSC. We would be very pleased to receive notification when collaborators publish papers acknowledging the GSC.

Acknowledgements can be made in any or all of the following ways:

### 11.1. MINIMUM ACKNOWLEDGEMENT

Peer-reviewed publications should include an acknowledgement of the work conducted by the GSC.

The following sentence can be incorporated into the [Acknowledgements](#) section of the article: *"The authors wish to acknowledge Canada's Michael Smith Genome Sciences Centre, Vancouver, Canada for [activity]."*

A full list of funders of infrastructure and research supporting the services accessed can be found at [bcgsc.ca/about-us](http://bcgsc.ca/about-us).

### 11.2. IN-TEXT ACKNOWLEDGEMENT

Acknowledgements should appear in the text of peer-reviewed publications, for example in the [Materials and Methods](#) section.

A suggested sentence for inclusion is: *"[Activity] was performed by Canada's Michael Smith Genome Sciences Centre, Vancouver, Canada."*

### 11.3. INTELLECTUAL CONTRIBUTIONS

Where intellectual contributions have been made by the GSC, collaborators are required to discuss potential and pending publications based on these contributions with the relevant GSC scientists or staff to identify appropriate co-authorship.

### 11.4. CO-AUTHORSHIP

The GSC does not request or require co-authorship on publications when data has been generated through our cost-recovery collaborative services alone (i.e., when no intellectual contribution has been made).



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*Bringing genomics to life.*