GETTING STARTED

Your starter guide to working with
Canada's Michael Smith Genome Sciences Centre

BC CANCER RESEARCH
Provincial Health Services Authority

CANADA'S MICHAEL SMITH GENOME SCIENCES CENTRE

Bringing Genomics to Life.

ABOUT US

The GSC's CAP, DAP 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** if you have any questions about the services we provide.

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www.bcgsc.ca | info@bcgsc.ca | @BCCancer_GSC

CONTENT

WELCOME

TO THE GSC

Our Getting Started Guide will provide helpful information that will assist you in navigating our online submission website. Please contact us at **GSC_Submissions@bcgsc.ca** at any time if you have any questions.

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 User Guide.

5 SAMPLE TRACKING

Track of the status of your samples in LIMS.

6 GET YOUR DATA

Download your data directly.

① SERVICE REQUEST FORM

Let us know how we can help you by filling out our online service request form available **here**. Tell us about your project and which services you are interested in.

One of our team members will get back to you within 24 hours on Mondays to Fridays, 9 am to 5 pm.

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.

| First name | | Last name | |

| Email | | Confirm email | |

| Phone number |

| Job title |

| Institution |

| Province/State ⌄ | Country ⌄ |

2 STATEMENT OF WORK

A Statement of Work (SOW) is a formal document required for submission of samples for sequencing or other services. If you do not have a SOW and would like to submit samples for sequencing, please contact us at SOW@bcgsc.ca. If you already have a signed SOW in place, or you have been provided access to one by your principal investigator (PI), they can be accessed by clicking on the "SOWs" button in the navigation panel in our laboratory information management system (LIMS).

(3) LIMS ACCOUNT

Adding new users to a SOW will automatically create new accounts to the GSC Sample Submission Interface. Account username and temporary password will be sent in an e-mail from LIMS@bcgsc.ca. You may need to add LIMS@bcgsc.ca in a Safe Sender list. Upon first log-in, you will be prompted to set a new password to successfully activate your account.

SOW Permissions

The PI named on each SOW will have all permissions as described below. PIs are able to add additional contacts to an SOW, and assign permissions as appropriate. If you require additional permissions for any SOW, please contact your PI.

Permission levels

- **Basic Access User**: view the SOW details on the homepage; all users associated with a SOW have this level of access.

- **Dissemination Editor**: add/remove users from the dissemination list.

- **Permissions Editor**: add/remove users from the SOW, the sFTP access list and the submitter access list.

- **Submitter**: initiate, edit and submit sample submission forms.

Additional Permissions

- **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.

- **sFTP Access Member**: For those SOWs that receive their data via our secure sFTP site, the PI named on the SOW or those they delegate 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. Delegates can only be added to sFTP Access list when they are assigned as a user on the SOW with a minimum permission access level of Basic Access User.

4 SAMPLE SUBMISSION

If you have '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.

Please refer to the following guides prior to preparing and submitting your samples:

[User guide: DNA sequencing](#)

[User guide: RNA sequencing](#)

[User guide: constructed libraries](#)

5 SAMPLE TRACKING

The sample tracker can be accessed by clicking on the "Sample Status" button in the left pane. This tab allows you to track any sample you have submitted. You can search for samples using the submission name assigned to each unique submission.

6 GET YOUR DATA

All collaborators 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 in addition to the previously uploaded data sets from the same project. This allows the collaborator to track sequence data as it is generated. **Data will be automatically deleted from the download site after two weeks**. If you are unable to download your data within two weeks, please contact us to reupload your data. If at that time your data are still available for upload, there may be an additional cost for the re-posting. By default the notification email will be sent to the PI listed on the sample submission and submitter of the samples. Additional email recipients can be specified during submission.

Once the notification email has been sent, a separate email with login and password details for the sFTP site will be sent to the PI. To protect the privacy of your data, subsequent amendments to the recipient list and creation of additional sFTP accounts will require approval from the PI. If you do not have a sFTP client on your computer, you will need to download and install one before you are able to access your data. Please visit **our webpage** for a list of some recommended clients that can be downloaded for free, along with links to installation instructions.

ALIGNMENTS

The costs for Illumina sequencing include provision of bam and/or fastq for all sequenced libraries.

Default alignment by STAR to the full read length using GRCh38 and Ensembl99 for all externally and internally constructed RNA libraries with BAM/fastq only deliverable, unless otherwise requested by the Project and confirmed with the GSC.

Default alignment by STAR to the full read length using GRCh37 and Ensembl75 for hg19 requests, unless otherwise requested by the Project and confirmed with the GSC.

Default alignment by Minimap2 to GRCh38 for all genome libraries, unless otherwise requested by the Project and confirmed with the GSC. Alignment to GRCh37 is available on request.

TERMS OF SERVICE

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

Where warranted due to a collaborator's requirements, 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 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 or to enable enhanced/faster service with surcharges or premiums. However, the automation and scalability of our pipelines do result in a reduced cost per sample for larger batches.

ACKNOWLEDGEMENT POLICY

In order to gauge our scientific impact we attempt to track all of our contribution to the scientific community. 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 in any or all of the following ways:

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

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.

We kindly ask that acknowledgement of the work of the GSC be included in peer-reviewed publications. 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 on the **About Us** page.

In addition, 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*".

We would be very pleased to receive notification when collaborators publish papers acknowledging the GSC.

Technology platform

Echelon Innovation Centre
570 West 7th Avenue
Vancouver, B.C. V5Z 4S6
Phone: 604-707-5900

Ash St.

Cambie St.

W. 7th Ave.

W. 8th Ave.

W. Broadway

W. 10th Ave.

Heather St.

Research department

BC Cancer Research Centre
675 West 10th Avenue
Vancouver, B.C. V5Z 1L3
Phone: 604-675-8000

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