

Creating an order in B-Fabric for Long Read Sequencing

- 1) Please login to your project main page B-Fabric. If you have more than one project @FGCZ, please make sure you are in the correct project page.
- 2) Click on the “Orders” listed on the left part of the screen:

Details	
Members	3
Comments	0
Samples	0
Extracts	0
Workunits	0
Resources	0
Experiment Definitions	0
Orders	0
Charges	0
Bookings	0
Instrument Reservations	0
Reviews	0
Mails	
Tree	

- 3) Under “Service Area”, select “Genomics” from the drop down menu.

Create Order

Internal * No Yes

Service Type *

	Service Type
<input type="radio"/>	No Filter
<input checked="" type="radio"/>	Genomics
<input type="radio"/>	Metabolomics (REFINE 2020)
<input type="radio"/>	Proteomics / Protein analysis
<input type="radio"/>	Genomics
<input type="radio"/>	Genomics
<input type="radio"/>	Genomics
<input checked="" type="radio"/>	Genomics
<input type="radio"/>	Genomics
<input type="radio"/>	Genomics

Total: 7 / 18 Rows 1 10 CSV

Selected Service Type Long Read Sequencing

- 4) Under “Service Area”, click on “Long Read Sequencing” and fill up the form (select application, instrument, library protocol...). See Example below.

Create Order

Internal No Yes

Service Type *

Service Area	Service Type
No Filter	
<input type="radio"/> Genomics	Genome Informatics
<input type="radio"/> Genomics	Genomics User Lab - Bench Access (QC, Library Prep, Sonication)
<input type="radio"/> Genomics	Genomics User Lab - Walk-in Sequencing Access
<input type="radio"/> Genomics	High Throughput Sequencing (NGS)
<input checked="" type="radio"/> Genomics	Long Read Sequencing
<input type="radio"/> Genomics	Optical Mapping User Lab
<input type="radio"/> Genomics	Single Cell Sequencing
<input type="radio"/> Metabolomics (REFINE 2020)	Biophysics Lab Services
<input type="radio"/> Metabolomics (REFINE 2020)	Biophysics User Lab
<input type="radio"/> Metabolomics (REFINE 2020)	Metabolomics Bioinformatics Services

Total: 16 / 16 Rows 1 2 10 CSV

Selected Service Type Long Read Sequencing

Technologies General Genomics/Transcriptomics Metabolomics/Biophysics Proteomics

Instruction Link [Please click here for order form instructions!](#)

Sequencing Application * Genome de novo Sequencing

Instrument * PacBio Sequel II

Library Protocol * HiFi Standard protocol, 17-22kb library

Number of Physical Tubes * 1 Please provide sample details later in the edit order items form!

Insert Size (nt) 20000

Data Package/Run Unit * SMRT Cell 8M, 30h movie (HiFi, IsoSeq, very large amplicons)

Total Number of Units *

Demultiplexing * No

Data Storage Model Data Delivery Only (without bioinformatics analysis and support)
 Bioinformatics Analysis and Support (including data delivery)

Remarks

- 5) Check if the billing address is correct. Please note that ETH/UZH users will be required to enter their fund number for invoicing. If not sure about the fund number please ask your group leader. Click on agree and Save.

* I agree to the Terms and Conditions and confirm that the billing address above is correct

Custom Attribute Name	Value
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Save Cancel

- 6) Please enter the number of samples you would like to submit. Would you like to add new samples please click on “Add Item(s)” Would you like to add already existing samples from previous orders with in the same project, please click on “Add Item(s) Using Samples.

Add/Edit items, i.e., the sample and service details of this order

1 Add Item(s) Add Item(s) Using Samples

Save Cancel

- 7) A table will open with fields for the number of samples you have chosen. If you have more samples, add any number of the fields by using the “Add Item(s)” option.

Add/Edit items, i.e., the sample and service details of this order

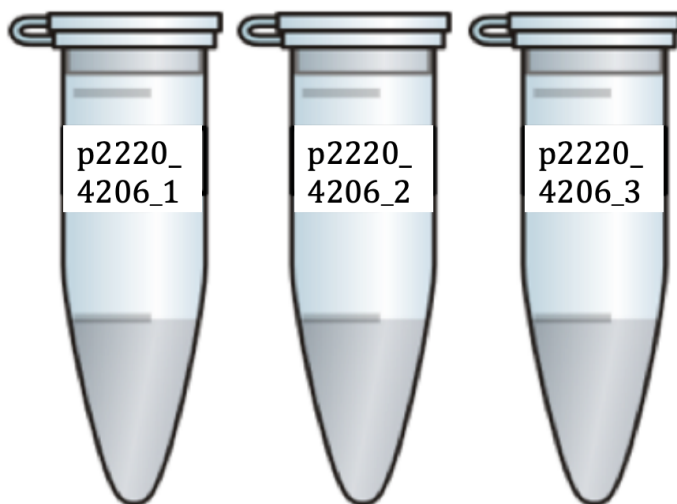
Delete	Clone	Tube Id	Sample Name *	Species *	Concentration (ng/µl) *	Extraction Protocol *	Source Type *	Total Amount (µg)	Barcode1	Volume (µl)
Delete		p2678_22639/1	Novo_1	Sus Linnaeus (Pig)	150	Custom	Genomic DNA	15000		100

Total: 1 / 1 Rows

1 Add Item(s) Add Item(s) Using Samples

Save Cancel

- 8) Enter the information about your samples like Sample Name, Species, Concentration, Extraction Protocol....
- 9) Please leave the Tube Id unchanged and use these numbers (project ID + Order ID) when labeling your tubes.



- 10) Save
- 11) Click on “**Submit Order**” button at the bottom of the page

After order submission, your order will be reviewed by the FGCZ. You will be notified by email when the order is accepted. Upon order acceptance, you can then deliver your samples to the FGCZ. You will be able to monitor the status of your order under the status section on the same page.