



Creating an order in B-Fabric for Illumina / Short Read Sequencing: RNA and DNA Samples

Important: Please precisely follow the instructions below when submitting **RNA or DNA samples for library preparation**.
If you are submitting **ready-made libraries**, please select the Service Type “**Ready-made Libraries Sequencing**” instead.

If you are submitting **Single-Cell Suspensions for library preparation**, please select the Service Type “**Single Cell Sequencing**” instead.

RNA samples

1. We need 300ng-2ug for standard library prep. Please check our application page for the requirements of the specific protocols <https://fgcz-intranet.uzh.ch/FullServiceSequencing>
Dilute the samples to the same concentration. We prefer 100ng/ul, the lowest possible concentration is 2ng/ul for standard library prep. If this is not possible, please dilute to the highest concentration possible compared to your other samples.
For low input RNA samples, please check with your coach as this will depend on the library prep kit.
2. Please dilute your samples in water or EB buffer.
3. Please use 1.5 ml Eppendorf tubes. **For large orders (>32 samples) we encourage you to submit your samples in plates. The following plates (or similar) should be used:**
 - Eppendorf twin.tec®-PCR-Platte 96 LoBind semi-skirted or skirted
 - BioRad Hard-Shell® 96-Well PCR Plates

DNA samples

1. We need 100ng-500ng for standard library prep. Please check our application page for the requirements of the specific protocols <https://fgcz-intranet.uzh.ch/FullServiceSequencing>
Dilute the samples to the same concentration. We prefer 100ng/ul, the lowest possible concentration is 2ng/ul for standard library prep. If this is not possible, please dilute to the highest concentration possible compared to your other samples.
For low input DNA samples, please check with your coach as this will depend on the library prep kit.
2. Please dilute your samples in water or EB buffer.
3. Please use 1.5 ml Eppendorf tubes. **For large orders (>32 samples) we encourage you to submit your samples in plates. The following plates (or similar) should be used:**
 - Eppendorf twin.tec®-PCR-Platte 96 LoBind semi-skirted or skirted
 - BioRad Hard-Shell® 96-Well PCR Plates
4. Please run your samples in a gel and attach the picture in the comments section of the order.



1.1) Order submission: step-by-step guide: **samples delivered in TUBES**

For large orders (>32 samples) we encourage you to submit your samples in plates. You need the explicit approval of your coach in case you want to deliver more than 32 samples in tubes.

When delivering **samples in plates** please follow the instructions found [here](#).

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



3. Click on the “Create Order” button.
4. Under “**Service Area**”, click on “**High Throughput Sequencing**” and fill up the form (select application, instrument, library protocol etc.) as best you can. If you indicate “*I don’t know*”, your coach will get in touch with you to clarify your order.

Select the option “**Tube**” for the Sample Submission and indicate the number of physical tubes you want to deliver.

Create Order

Service Type *

Service Area	Service Type
No Filter	
<input type="radio"/> Proteomics / Protein analysis	Amino Acid Analysis
<input type="radio"/> Metabolomics (REFINE 2020)	Biophysics Lab Services
<input type="radio"/> Metabolomics (REFINE 2020)	Biophysics User Lab
<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"/> Proteomics / Protein analysis	Glycan/Glycoprotein
<input checked="" type="radio"/> Genomics	High Throughput Sequencing (NGS)
<input type="radio"/> Proteomics / Protein analysis	Intact Mass Determination
<input type="radio"/> Genomics	Long Read Sequencing

Total: 18 / 18 Rows

required

Selected Service Type High Throughput Sequencing (NGS)

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

Sequencing Application * Whole Genome Sequencing

Library Protocol * NEB Ultra II

Number of Samples * 2 Please provide sample details later in the edit order items form!

Insert Size (nt)

Instrument * Illumina Novaseq 6000

Data Package/Run Unit * Data Package (~200M Reads)

Total Number of Units * 1

Read Configuration * Paired End 150 bp

Data Storage Model * Data Delivery Only (without bioinformatics analysis and support)

Bioinformatics Analysis and Support (including data delivery)

Remarks



Note: Please indicate any special instruction in the “Remarks” field.

- 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**.
- 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. Would you like to add already existing samples from previous orders within the same project, please click on “Add Item(s) Using Samples”.

Edit Order Items

Delete	Tube Id	Sample Name *	Species *	Concentration (ng/µl) *	Extraction Protocol *	Source Type *	Barcode/Index	Total Amount (µg)	Volume (µl)	Description
Delete	p2220_6155/1	abc	Mus musculus (house m	100	custom	Genomic DNA		10000	100	
Delete	p2220_6155/2	gzt	Mus musculus (house m	100	custom	Genomic DNA		10000	100	
Total: 2 / 2 Rows										

1 Add Item(s) | Add Item(s) Using Samples | Create Annotation

Save Cancel

- Enter the information about your samples like **Sample Name, Species, Concentration, Extraction Protocol etc.**

Assign sample attributes by copy and paste from a local spreadsheet

If you would like to assign sample attributes in bulk, you may copy/paste values from a local spreadsheet (see below):

Add/Edit Items, i.e., the sample and service details of this order Please click on the "Add Item(s)" button to add new items.

Delete	Clone	Tube Id	Sample Name *	Species *	Concentration (ng/µl) *	Extraction Protocol *	Source Type *
Delete		p2220_26384/1		Select Item			
Delete		p2220_26384/2		Select Item			
Delete		p2220_26384/3		Select Item			
Delete		p2220_26384/4		Select Item			
Delete		p2220_26384/5		Select Item			
Delete		p2220_26384/6		Select Item			
Delete		p2220_26384/7		Select Item			
Delete		p2220_26384/8		Select Item			
Delete		p2220_26384/9		Select Item			
Delete		p2220_26384/10		Select Item			
		p2220_26384/11		Select Item			
		p2220_26384/12		Select Item			
		p2220_26384/13		Select Item			
		p2220_26384/14		Select Item			
		p2220_26384/15		Select Item			
		p2220_26384/16		Select Item			

1 Add Item(s) | Add Item(s) Using Samples | **Excel Edit**

Save Cancel

Edit Sample Details

	Tube Id	Name	Species	Concentration (ng/µl)	Extraction Protocol	Source Type
1	p2220_26384/1					
2	p2220_26384/2					
3	p2220_26384/3					
4	p2220_26384/4					
5	p2220_26384/5					
6	p2220_26384/6					
7	p2220_26384/7					
8	p2220_26384/8					
9	p2220_26384/9					
10	p2220_26384/10					
11	p2220_26384/11					
12	p2220_26384/12					
13	p2220_26384/13					
14	p2220_26384/14					
15	p2220_26384/15					
16	p2220_26384/16					

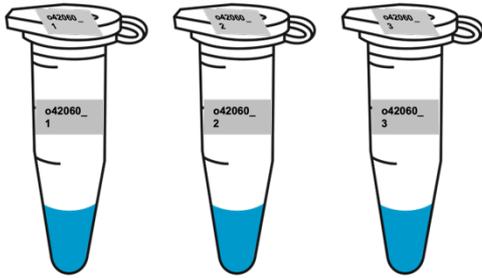
Apply Cancel

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After clicking on “**Excel Edit**”, a pop-up window will open. You must then copy the attributes from your local spreadsheet, navigate to the pop-up window, and press Ctrl + V to assign your values directly to the samples.

The pop-up table works very similar to Excel and can be auto-filled the same way.

- Please leave the **Tube Id** unchanged and use these numbers (Order ID, e.g. o26381/1) when labeling your tubes. Please label your tubes on **top and on the side** with the Tube ID.



9. Click on “Save”
10. Click on “Submit Order” button on the bottom of the page.
11. Your project coach will check the order, accept the order and will add an offer based on your order. Please check the offer and if everything is in order, please bring the samples together with the signed offer and confirmation form.

Once you are at the door of the FGCZ you can call the **Genomics Sample Delivery number (reachable from 09:00-17:00)**.

Do not bring the samples if your order has not been accepted by your coach!

IMPORTANT: Once you bring or sent the samples, we will process the samples according to the order details accepted by your coach in Bfabric. We will only refer to the order form on the offer and NOT look at any off-Bfabric communication you had with any staff member.

12. The signed confirmation form means that you agree to our terms and conditions.
13. You will receive status updates every time a milestone is reached in the processing of your order. The current state can always be checked on the order page.

Sequencing Output [Disclaimer]: Please note that we cannot guarantee the exact read numbers per sample but do our best to provide the requested amount of data.



1.2) Order submission: step-by-step guide: **samples delivered in PLATES**

When delivering **samples in tubes** please follow the instructions found [here](#).

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



3. Click on the “Create Order” button.
4. Under “**Service Area**”, click on “**High Throughput Sequencing**” and fill up the form (select application, instrument, library protocol etc.) as best you can. If you indicate “*I don’t know*”, your coach will get in touch with you to clarify your order.

Select the option “**Plate**” for the Sample Submission (see below) and indicate the number of physical plates you want to deliver.

Selected Service Type High Throughput Sequencing (NGS)

Technologies General Genomics/Transcriptomics Metabolomics/Biophysics Proteomics

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

Sample Submission * Plate Tube

Sequencing Application * Whole Genome Sequencing

Library Protocol * Illumina Truseq Nano

Number of Plates * 2 Please provide plate details later in the edit order items form!

Insert Size (nt)

Instrument Illumina Novaseq 6000 #1

Data Package/Run Unit * Data Package (200M reads) (~200M Reads)

Total Number of Units * 1.00

Read Configuration * Paired End 150 bp

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

Note: Please indicate any special instruction in the “Remarks” field.

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



	Position	Name
1	A1	a
2	B1	b
3	C1	c
4	D1	
5	E1	
6	F1	
7	G1	

Define the **Plate Name**, **Plate Layout** (Standard: *96-well*) and **Sample Assignment Order** (Standard: *Column-wise*).

Click on “**Assign Samples**” and copy and paste your sample names from an excel spreadsheet. **Please make sure that the plate positions and sample names match!**

Important: When submitting samples in plates please note that **row-wise sample assignment is not allowed without explicit approval by your coach**. Whenever possible please assign the samples column-wise without any blank wells.

7. Click on “Save”.
8. You will be forwarded to the screen seen below. Click on “**Edit Samples**” for each plate and fill out the mandatory additional fields for the samples on that plate. Please note that you can also use mock values for fields like “*Concentration*” in case this is not relevant for you.

Order Items (2)

This order is NOT submitted yet: DO NOT send or bring any samples!

Samples on Plate	Order Item Id	Plate Name	Plate Layout	Sample Assignment Order	Charges	Created By	Created	Modified By	Modified
Edit Samples (96)	161362	PlateTest1	96-well	Column	0	simongruter	2021-11-01 14:36:39	simongruter	2021-11-01 14:36:39
Edit Samples (96)	161363	PlateTest2	96-well	Column	0	simongruter	2021-11-01 14:36:40	simongruter	2021-11-01 14:36:40

Total: 2 / 2 Rows

Edit Order Items Show Samples on Plate

9. Please use the **Plate Name** and the **Tube Id** (Order ID, e.g. o26381/1) when labeling your plates. Please label your plates on **top and on the side**.
10. Click on “Submit Order” button on the bottom of the page.
11. Your project coach will check the order, accept the order and will add an offer based on your order. Please check the offer and if everything is in order, please bring the samples together with the signed offer and confirmation form.

Once you are at the door of the FGCZ you can call the **Genomics Sample Delivery number (reachable from 09:00-17:00)**.

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Sequencing Output [Disclaimer]: Please note that we cannot guarantee the exact read numbers per sample but do our best to provide the requested amount of data.