

Start up a HiSeq sequencing project

1. [Buy necessary kits and reagents](#)

Sample prep kits are bought and delivered to your own lab. The sample prep will be performed at your own lab.

In order to avoid transporting the sequencing reagents up and down with risk of thawing, make sure to use our delivery address and contact person for sequencing kits: (UNIV ANTWERPEN-CHARLOTTE CLAES, DEPARTMENT OF MEDICAL GENETICS, PRINS BOUDEWIJNLAAN 43, EDEGEM, 2650, BELGIË).

Please forward the mail with your order and shipping notification to ngs@uantwerpen.be. This way we know what to expect. We'll take care of the package as soon as it arrives and store it in the correct way. For Illumina kit and pricing information, contact customerService@illumina.com.

IMPORTANT REMARK: Our HiSeq device can only run on [high output v3](#), [rapid v1](#) and [rapid v2](#)!

2. [Schedule your experiment](#)

Book a run with the online reservation tool (<http://ngs.uantwerpen.be/booking/>). Contact ngs@uantwerpen.be to create a new account.

- Log in/ create a new account
- my account – profile: contains your personal information
- my account – notification preferences: settings for email notifications
- schedule – resource calendar: overview of all planned runs, can be filtered by equipment
- schedule – my calendar: overview of all your personal runs
- To make a reservation: schedule – bookings:
 - ✓ Select the preferred equipment on an available date, a reservation screen opens.
 - ✓ Choose start and end point (take into account the min/ max reservation time). Please take the following runtimes into account when making equipment reservations

HiSeq run times			
High Output Run Mode		Rapid Run Mode	
TruSeq SBS v3		HISEQ Rapid SBS Kit v2	
1x36	2 days	1x36	7 hr
2x50	5.5 days	2x50	16 hr
2x100	11 days	2x100	27 hr
		2x150	40 hr
		2x250	60 hr

- ✓ Entitle the run with a clear name containing your institute and project.
- ✓ Complete the entire form
- ✓ After saving, your reservation will be send for approval to the administrators.
- ✓ Twice a week, an administrator will approve the reservations.

3. [Perform sample prep](#)

Check you've all the user-supplied materials, instruments and reagents available.

4. [Create sample sheet](#)

Create a sample sheet in [Illumina Experiment Manager \(v1.9-11\)](#) using the correct settings. Create sample sheet -> HiSeq -> HiSeq 1500 -> HiSeq fastq only
Don't use: ', ; - . or spaces in the samplesheet, only _ is allowed.

OPTION 1: For 'Sample Project', fill in the correct data destination folder for each sample For

Data destination	Sample Project	Notification
FTP server	Real_Name@F	Automatic email notification will be send when run or analysis is finished.
Exome pipeline only for registered Galaxy users	Real_Name@E	
CLC Genomics Workbench only for registered CLC users	Real_Name@C	
Galaxy only for registered Galaxy users	Real_Name@G	
Galaxy en CLC only for registered galaxy and CLC users	Real_Name@B	
UZA SeqPilot only for registered UZA users	Real_Name@S	
/home folder only for command line users	Real_Name@H	

For correct "Real_Name", contact NGS team

OPTION 2: For 'Investigator Name', fill in your email address. Data will be send to FTP server.

Deliver the sample sheet to us (ngs@uantwerpen.be or USB key) at least 24h before the run starts. The responsible will copy the sheet to a server. No USB keys are plugged into HiSeq!

5. [Quantification of the library](#)

An accurate quantification of the library is very important. For HiSeq applications we prefer [qPCR measurement](#) (using KAPA Library Quantification Kit, Illumina platforms KK4824).

The delivered library has to be diluted to 2nM.

As NexteraXT protocols include a normalization step, no concentration measurement is needed.

6. [Actual sequencing at CMG](#)

Deliver your library at least 24h before the run starts. Only trained people can start up the HiSeq sequencer.

7. [Data extraction](#)

A notification will be send to you, when your run is finished.

When data is send to the public FTP server; after downloading and storing your data, please delete them on the FTP server.

By default, all data will be deleted from our servers automatically after 3 months.