



# **IZKF Genomics Facility**

# **User Regulations as of April 2022**

### Introduction

The IZKF Genomics Facility offers state-of-the-art sequencing and bioinformatics services as well as all basic lab services, required for high quality preparations of sequencing libraries. The goal of the facility is to provide all members of the medical faculty of RWTH Aachen, as well as all RWTH Aachen scientists and external users with highly standardized workflows for reproducible sequencing results. To achieve these high quality results, the staff of the Genomics facility supports the users during every step of the sequencing project including experimental design, sample preparation, data generation and analysis. In order to guarantee a smooth working process, all users of the Genomics facility must adhere to the regulations described in the following paragraphs.

# Offered services and equipment

All offered services will be provided by the IZKF Genomics facility staff. Usage of the sequencers needs a high level of training and expertise and user traffic in the Genomics facility labs should be kept to a minimum to prevent contamination of the labs with nucleic acids. Therefore, handling of the instruments at the IZKF Genomics facility by external users is only permitted in rare exemptions by highly trained personnel and only upon an upfront agreement with the Genomics facility management.

In particular, we can offer the following services and instruments at the Genomics facility:

#### Sequencing:

- Total RNA, mRNA, 3'mRNA
- miRNA
- Amplicons
- single cell RNA, single cell ATAC, single cell VDJ
- Whole genome sequencing
- ATACseq
- ChIPseq

#### **Basic lab:**

- Quantification of RNA/DNA
- Quality control of RNA/DNA
- RNA/DNA isolation from tissue, cells, blood, serum, plasma
- DNA fragmentation
- Single cell suspension

### Illumina Sequencers:

- NovaSeq
- NextSeq
- MiSeq

### **Equipment:**

- Quantus
- TapeStation
- Bioanalyzer
- Maxwell
- Covaris
- CellenOne

#### **Bioinformatics:**

- Raw data
- FASTQ files only
- Basic analysis
- Advanced analysis

#### Servers:

 4 dedicated servers with a total of 296 cores and 2.1 TB RAM and disk space of 118.6 TB

# User's service requests

Service requests of users to the IZKF Genomics Facility can be submitted online at the following address: <a href="https://genomics.rwth-aachen.de/services/">https://genomics.rwth-aachen.de/services/</a>

With the submission of a service request users agree to the user regulations and policies of the IZKF Genomics Facility. The IZKF Genomics facility reserves the right to reject user requests if they are not feasible within the Genomic facility's capacities.

# Sample submission and service hours

Samples can be submitted at any time during the facility's working hours from Monday until Friday between 8:30 h and 16:00 h. A service request and corresponding sample sheet need to be submitted online (<a href="https://genomics.rwth-aachen.de/services/">https://genomics.rwth-aachen.de/services/</a>) before samples can be transferred to the Genomics facility. The labeling of sample tubes is specified in the sample sheet that can be found online. Users should specify the date of sample submission in the online request form. If the sample submission date needs to be rescheduled, users should contact the Genomics facility staff directly (genomicsfacility@ukaachen.de).

Users can submit their samples to the Genomics facility staff at university hospital Aachen, floor 3, corridor 43 (between elevator C3 and C4), room 7.

### Data analysis

The Genomics Facility provides various bioinformatic analyses from FASTQ file generation to basic or advanced analysis. The basic analysis provides the standard analysis procedure for a given NGS methodology without too much customization. Anything beyond the standard pipeline is considered as advanced analysis which requires additional charge and co-authorship. The advanced analysis will be customized to the need of the project and the expertise in the facility. Costs for the advanced analysis will depend on the required time of the analysis. The content of the advanced analysis will be discussed in detail upfront with the users and a quote will be sent to the user, including information on the estimated duration and pricing for the advanced analysis.

# Data management and storage

Data management is the whole process of handling research data, from its entry into the research cycle through to the dissemination, sharing, archiving, and destruction. Due to the limited storage capacity in the Genomics Facility we will store our user's data as indicated below:

TYPE	DEFINITION	STORAGE TIME
		AFTER CLOSING
Raw Data	Raw data means the Binary Base Call (BCL) files generated by the	5 years
	Illumina sequencers.	
Processed	Processed data means the files after bioinformatic analyses such	6 months
Data	as alignment, read counts, peak calling, or differential analysis	
	etc.	

Advanced	Any customized analysis is done for the need of the clients. This	6 months
Analysis	might include figures, tables, or PDF reports.	
Data export	After any analysis is done, the data are exported to the clients via	1 month
	our web server with the given username and password. This access	after submission
	will be terminated within a month.	

Every user should have a plan for his own data. Many grant proposals now require the plan of data management (e.g. DFG Handling of Research Data). Whenever we submit the data to the users, we expect the users to store their data according to their own plans. It is the user's responsibility to keep the data safe and reusable. After we deliver the data to the clients, we will clean the data from our servers according to this policy. Please make sure that you store the data in your lab properly.

If there is no data storage infrastructure available in the lab, we can offer data storage services to keep the data of the users in the Genomics facility for a longer period but this service will be charged.

# **Safety instructions**

The IZKF Genomics facility is located within an S1 safety area. Upon sample submission, users are required to adhere to federal health and safety regulations and obey S1 regulation rules.

Samples which require handling under S2-S4 safety regulations cannot be processed at the IZKF Genomics facility.

# **Costs and payment**

Users are charged for all required reagents and kits, as well as for lab consumables and instrument usage. Furthermore, we charge users for our bioinformatics support depending on the extent to which this support is requested. Prices can vary according to the current list prices of the manufacturers. External users will additionally be charged with a service fee for our support. Users can receive a quote for their specific service demands upon request.

Please be aware that services provided in the second half of the year may not be invoiced until mid-March of the following year. If funds budgeted for services are no longer available at this later billing date (e.g., due to project completion, annuality of appropriated funds), the Facility leadership should be contacted early to arrange a progress payment.

### Order of sample processing

Samples will be processed in the order in which they were scheduled in consultation with the Genomics facility. There are no groups that are given preferential treatment. In very urgent cases (but only if both users agree after prior consultation) the order can be swapped. Unforeseen delays may occur if material is not delivered on time, if manpower is unavailable due to illness, or similar.

## **Failing of experiments**

## Manufacturer-related problems

If problems arise in experiments that are caused by the manufacturer of the materials, the costs incurred at the Genomics Facility for a repeat of the experiment will be charged. The Genomics Facility will be happy to assist in a negotiation with the manufacturer to receive a kit/sequencing cartridge replacement. However, the replacement of a kit/sequencing cartridge cannot be guaranteed by the Genomics Facility.

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**Genomics Facility-related problems** 

If results are not obtained due to handling in the Genomics Facility, the tests will be repeated by the Genomics Facility free of charge for the user. This does not apply to experiments in which the user has

been made aware of potential problems in advance.

**Problems without apparent source** 

We take best care to handle your samples in accordance with current lab standards and perform extensive trouble shooting in case of failure of an experiment. It might still occur that results cannot be obtained without any apparent source of the underlying problem. In such rare cases, the Genomics

facility will charge the users with the incurred costs of the experiment.

**Acknowledgements** 

All users of an IZKF core facility have to acknowledge the support of the respective facility in all relevant publications. Please use the following wording:

"This work was supported by the IZKF Genomics facility, a core facility of the Interdisciplinary Center for Clinical Research (IZKF) Aachen within the Faculty of Medicine at RWTH Aachen University."

OR

"Diese Arbeit wurde unterstützt durch die IZKF Genomics Facility eine Core Facility des Interdisziplinären Zentrums für Klinische Forschung (IZKF) Aachen der Medizinischen Fakultät der

RWTH."

User agreement

All users who make use of any service of the IZKF Genomics Facility declare their agreement with the aforementioned user regulations.

**Contact** 

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