Our technical equipment

- Sequencers
  - NovaSeq 6000 (Illumina): 0.65 - 10 billion reads per run, 35 - 500 cycles
  - NextSeq 500 (Illumina): 130 - 400 million reads per run, 75 - 300 cycles
  - Access to MiSeq (Illumina): 1 - 25 million reads per run, 50 - 600 cycles

- Quality Control
  - Tape Station 4200 (Agilent)
  - Bioanalyzer (Agilent)

- Quantification
  - Quantus (Promega)
  - Nanodrop ND-1000 (Thermo Scientific)
  - Access to qPCR CFX Opus 96 (BioRad)

- Nucleic Acid Isolation
  - Maxwell RSC: DNA blood, tissue and cells
  - Maxwell RSC: miRNA tissue, serum and plasma

- Fragmentation
  - Covaris M220 ultrasonicator
  - Volumes of 55 µl or 130 µl

- Automation/Single Cell dispensation
  - CellenOne F1.4 (Cellenion)
  - Mosquito platform (SPT Labtech)

Who can you contact at the Genomics Facility?

Prof. Dr. Ingo Kurth
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Dr. Julia Franzen
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Tel.: +49 241 80 36537

Would you like to discuss your NGS project with us?
Please feel free to contact any member of our team!
Lab technicians: Jasmin Hübner, Tel.: +49 241 80 88614
Anna Rudzinski, Tel.: +49 241 80 89936
Bioinformaticians: Chao-Chung Kuo, Tel.: +49 241 80 35296
Lin Gan, Tel.: +49 241 80 89684

Core Facilities – Technologies, equipment and expertise for ambitious research goals

The Interdisciplinary Center for Clinical Research (IZKF) provides valuable resources for a cost-effective, high-quality research environment.

A wide range of technologies and state-of-the-art equipment are available for all RWTH Aachen University researchers. Experienced technology experts provide services at every stage of the research process, including experimental design, method development, sample work-up, and data interpretation, on a partial cost recovery basis.

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How can we support your research?

Next generation sequencing (NGS) has become the state of the art technology for high-throughput DNA and RNA sequence analysis. The method offers several advantages in comparison to other technologies:

- A priori knowledge of the sequences is not required
- It provides single nucleotide resolution
- NGS only requires small amounts of DNA or RNA input
- It can cover whole genomes/transcriptomes
- Prices for the technology are constantly decreasing

Preparation of samples for high-quality sequencing is very complex and requires intensive training. The Genomics Facility provides the necessary expertise and sequencing equipment for several standardised NGS protocols. Furthermore, we support researchers every step of the way from the initial experimental design to the final data analysis and visualization of the results.

Which NGS methods do we offer?

Genomics:
- Whole genome sequencing
- De novo sequencing
- Amplicon sequencing
- Whole exome sequencing

Transcriptomics:
- 3’mRNA sequencing
- Total RNA sequencing
- mRNA sequencing
- microRNA sequencing

Epigenetics:
- ATAC sequencing
- ChiP sequencing

Single Cell:
- Single cell RNA sequencing
- Single cell ATAC sequencing
- Single cell VDJ sequencing

What do we process your project?

1. Do you want to use next-generation sequencing for your project but do not know where to start? Contact us, and we will advise you on the best approach for your experimental goals.

2. If you decide to use our service, simply submit an online request form. The form will provide us with all the necessary information for your project.

3. Bring your samples to the facility and we will perform initial quality controls and start to process them for sequencing.

4. Only high-quality sequencing libraries will be used for the actual sequencing.

5. You can choose whether you would like us to provide data analysis or if you would rather perform the analysis yourself.

6. If your results are published in a scientific journal, please remember to acknowledge the work of the Genomics Facility.

What else do we offer to support you?

Quality control and quantification of DNA/RNA
Quality control (QC) of library preparations is essential for all next generation sequencing (NGS) experiments. As a standard, our library preparation service for NGS includes sample quantification by fluorometric measurements with the Promega Quantus and subsequent QC with the Agilent TapeStation or Bioanalyzer. In addition, we offer these QC services independently from our NGS services.

Automated isolation of nucleic acids.
The Genomics Facility utilizes the automated Maxwell RSC instrument from Promega to provide high quality DNA/RNA extraction. We commonly offer DNA/RNA extractions from blood, tissues or cells. We are happy to discuss if we can implement a Maxwell RSC solution for your specific research question.

Fragmentation
While preparing intact high molecular weight DNA and preventing shearing throughout most workflow steps is important, DNA fragmentation is a necessary step in sample preparation for most short-read sequencing platforms. In the Genomics Facility, we offer DNA fragmentation with the Covaris ultrasonicator.

What can you expect from our Bioinformatics Service?

For the bioinformatics analysis of your data, you can choose whether you would only like to receive the raw bcl files from the sequencer or if you would rather book one of our analysis packages:

- **FASTQ files and QCs**
  In our simplest package, we perform the demultiplexing for you and provide quality reports for the FASTQ files.

- **Basic analysis**
  The basic analysis contains standardized analysis pipelines for our commonly offered NGS protocols without too much customization.

- **Advanced analysis**
  The advanced analysis is customized for the specific needs of your project.

For all packages, you will receive a report with a detailed description of the analyses performed, and you can further discuss the results with our bioinformaticians.

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