

Details

CAU - Microbiome Laboratory (CAU-Microbiome)

The focus of our microbiome laboratory is the identification of genetic and non-genetic factors that shape the microbiome. Multi-OMICS studies integrating microbial profiles, metabolic, genetic, phenotypic and nutritional data are performed under standardized high-throughput methods to identify relevant factors and mechanisms. The Microbiome laboratory at the Institute of Clinical Molecular Biology of the Christian-Albrechts-University of Kiel and the University Medical Center Schleswig-Holstein has established methods to determine bacterial richness and ASVs in a given sample (Who's there? 16S rDNA high-throughput sequencing). In addition, we offer metagenome (Who is there and what are they doing?) and metatranscriptome sequencing (Who is there and what cellular processes are they performing?) on Illumina MiSeq and NovaSeq instruments. In addition, a pipeline has been established for genome sequencing of individual bacteria and detection of their genetic variation, e.g. for identification of resistance genes. We also offer a broad portfolio of extraction methods for different sample types (stool, swabs, soil) derived from different hosts and environments, and the analytical tools are scalable, partially automated, and applicable in experiments ranging from a few observation points to larger cohorts with thousands of patients.

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[To website](#)

Host Institution

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<http://www.uni-kiel.de>
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Scientific Domain

Primary Subjects:

- Biology
- Medicine

Secondary Subjects:

- Agriculture, Forestry, Horticulture and Veterinary Medicine

Category

Genomic, Transcriptomic, Proteomics and Metabolomics Facilities

Scientific Services

The Microbiome Laboratory offers services within the framework of scientific cooperation in the field of consulting, implementation and evaluation of questions related to the determination of microbial diversity using high-throughput sequencing. The services of the microbiome laboratory include project planning (strategic planning, initialization of sample collection), subsequent coordination of the technical implementation of the project (sample logistics, evaluation of quality controls, troubleshooting, etc.) as well as the selection and implementation of appropriate

methodology (extraction of nucleic acids and subsequent investigation of microbial diversity via amplicon and metagenome sequencing in high throughput). Furthermore, support is offered for the bioinformatic evaluation of generated sequencing data, also with regard to the publication of the results in suitable journals.

Scientific Equipment

- QIAcube Connect
- QIAcube classic
- QIAcube classic
- QIAxcel
- Tecan Freedom Evo 150
- LightCycler® 480 Instrument II
- SpeedMill PLUS
- SpeedMill PLUS
- PCR Clean Bench

Keywords

- Microbiom
- Microbiota
- Amplicon-Sequencing
- Metagenomik
- Next-Generation-Sequencing
- Stool samples
- Swab samples

Networks

DFG NGS competence network (NGS-CN)

<https://www.ngscn-ccu.uni-bonn.de/en>

NFDI4Microbiota

<https://nfdi4microbiota.de/>

Users per annum

Internal Users: 30

External Users in total: 30

External Users: 20

External Users in the EU: 7

External Users outside of EU: 3