

Answer key questions on microbial diversity

INVIEW MICROBIOME PROFILING 2.0

In-depth analysis of microbial communities

- Sequencing of multiple hypervariable regions of the 16S rRNA or the ITS regions
- Characterisation of very rare taxa at low densities down to genus level
- Determination of microbial populations of any complexity

INVIEW MICROBIOME HIGH SPECIFICITY

Full-length 16S amplicon sequencing for highest taxonomical resolution

- Ultra-long amplicon sequencing based on PacBio's single molecule, real-time (SMRT®) technology
- Characterisation of microbial communities down to species level
- Perfectly suitable for many research objectives: from clinical to environmental to food microbiology

Deep insights based on sound knowledge

Our goal is to apply cutting-edge technologies and all of our know-how to create flexible and scalable solutions.

GATC Biotech offers a variety of Sequencing Solutions for analysing complex microbial communities.

Fully automated LIMS-controlled workflows allow processing of any type of samples with accurate results in short turnaround times. Furthermore, optimised PCR conditions result in a reduced bias for your microbiome studies. GATC's own bioinformatics pipeline includes a manually curated reference database offering reliable interpretation of your results.

Collaborative interactions ensure the innovative nature of our product portfolio.

Benefit from our experience in the detection of fine differences between microorganisms from various sources, even when they are present at very low densities.



GATC Biotech provides a number of standardised and ISO 17025 accredited next generation sequencing (NGS) solutions.

Visit www.gatc-biotech.com and discover our entire product portfolio, covering Sanger, exome and whole genome sequencing as well as microbiome and epigenetic studies. For maximum flexibility discover **NGSELECT™**, our modular NGS service.



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GATC Sequencing Solutions

Discover the diversity of microbial communities



Why choose INVIEW™ MICROBIOME for your taxonomic studies?

- Highly sensitive, accurate phylogenetic characterisation and quantification down to genus or even species level
- Benefit from full-length 16S amplicon analysis; multiplexing of up to 10 samples
- Characterise hypervariable regions of the 16S rRNA gene and ITS regions with 2 x 300 bp paired-end sequencing; multiplexing of up to 96 samples
- Optimised bioinformatics pipeline for samples of any complexity
- ISO 17025 accredited sequencing available upon request

Service offerings and quality highlights

INVIEW MICROBIOME

Specifications

Product	MICROBIOME PROFILING 2.0	MICROBIOME HIGH SPECIFICITY
Regions for microbial analysis	<ul style="list-style-type: none">• Bacteria: 16S rRNA V1-V3, V3-V5• Fungi: ITS1, ITS2• Archaea: 16S rRNA V4-V6	Full-length 16S amplicon (V1 – V8)
Sequencing technology	MiSeq (Illumina)	PacBio RS II (Pacific Biosciences)
Pre-sequencing	<ul style="list-style-type: none">• PCR amplification of hypervariable regions• Purification of PCR products and attachment of tagged adaptors• Preparative gel purification	<ul style="list-style-type: none">• PCR amplification of whole 16S rRNA gene• Purification of PCR products• Barcoding of PCR products, pooling and standard adapter ligation
Starting material	All kinds of samples can be used from food, clinical, or environmental sources	
Data packages	Multiples of 22,000,000 reads	Multiples of 15,000 reads
Number of samples per data package	Up to 96 samples	Up to 10 samples
Accuracy	> 99 %	> 99,6 %
Detection level	Genus	Species
Deliverables	<ul style="list-style-type: none">• Raw sequencing data (.fasta)• Tables listing all genera present including diversity indices and respective read counts• Results in common file formats (.fastq, .fasta, .tsv, .txt) to be easily handled with standard software for further analysis or visualisation• Visualisation of relative genus or species abundance• Comprehensive GATC Data Analysis Report	

Best suited for

Phylogeny and taxonomy of microorganisms including non-cultivable microorganisms and complex samples, microbiomes of industrial relevance, clinical samples	Any kind of taxonomic studies down to species level
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