

16S and ITS Microbiome Analysis at IGA Tech

High-Throughput Amplicon Generation, Sequencing and Analysis

Amplicon Sequencing

Choose your option of amplicon sequencing:

Bacterial microbiome analysis:

16S V3+V4 region, Primer combination: 341F – 805R1

Fungal microbiome analysis:

ITS ITS 1 region, Primer combination: ITS1–ITS4

18S 18S region, Primer combination: 18S_566F-18S_1200R



Complete Service

Send us your gDNA samples and make use of our Complete Service:

As an additional service we can offer also the **purification of gDNA** from various starting material. Please **check availability** for your specific material.

16S metagenomics: increasing efficiency when investigating microbial communities associated with a eukaryotic host by blocking amplification of contaminating sequences from plastid and mitochondria.

Price MiSeq 2x300bp, min 100.000 fragments (200.000 reads):

12-23 samples = 87 €/sample

24-47 samples = 66 €/sample

+ 48 samples = 56 €/sample

Price MiSeq 2x300bp, min 50.000 fragments (100.000 reads):

12-23 samples = 70 €/sample

24-47 samples = 50 €/sample

+ 48 samples = 38 €/sample

Price HiSeq2500 2x250bp, 250.000 fragments (500.000 reads):

Minimum of 288 samples = 44 €/sample

Details:

- Quality control and fluorescent quantification
- Normalization
- Blocking amplification of contaminating 16S originating from the eukaryotic host's genome, plastid and mitochondria
- Amplicon generation
- Double indexing, quality check, quantification, normalization and pooling of amplicons
- Illumina MiSeq sequencing
- MiSeq Output 30-35 Mreads
- Illumina HiSeq2500 sequencing
- HiSeq2500 Output 180-200Mreads
- De-multiplexing of reads based on Illumina indexing system
- Free Illumina App analysis for Mi-Seq samples
- Data delivery via server

Ready to load libraries

Sequence your ready to load libraries:

Price MiSeq run
2.700 €

Price HiSeq2500 run
5.000 €

Details:

- Illumina MiSeq sequencing
- MiSeq Output 30-35 M reads
- Illumina HiSeq2500 sequencing
- HiSeq2500 Output 180-200Mreads
- De-multiplexing of reads
- Free Illumina App analysis for Mi-Seq samples
- Data delivery via server

Bioinformatics pipeline

From taxonomic abundance to integrated diversity analyses:

Price:

12-23 samples = 25 €/sample

24-47 samples = 20 €/sample

+ 48 samples = 15 €/sample

+ 288 samples = 8 €/sample

Details:

- OTU clustering, taxonomy, assignment, alpha/beta diversity, PCoA and taxonomic enrichment testing (on request). Sample stratification on metadata factors.
- Reference databases:
 - 16S: modified GreenGene database
 - 18S: internal database
 - ITS: UNITE database

Application

Please contact us if you are interested in further service options or other gene regions and we will find your optimal solution

- **Environmental** Metagenomics
- **Human** or **Animal** Microbiome
- **Sterility** Monitoring
- Detection of **Contamination**
- **Biosafety** Monitoring
- **Food Quality**
- **Clinical** Samples