IGATech

Microbiome Analysis

SAMPLE SPREADSHEET

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Do you have any questions?
Contact us!

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Targeted and complete analyses

Choose your method:

Metabarcoding:
16S: V1-V3; V5-V6; V4; V3-V4
ITS: ITS1-ITS2; ITS1-ITS4
18S: choice of 563F, 574F, 1132R, 1391F, EuKB_rev

Shotgun metagenomics (WGS)

Metatranscriptomics (RNA-Seq)

Complete Service

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

Purification of gDNA / RNA from various starting material. Please enquire.

Optimized protocols for depletion of unwanted sequences:
rRNA depletion
host mRNA depletion
mitochondrial / plastid 16S rRNA

MiSeq 2x300bp, min 50.000 fragments:
12-23 samples = 48 €/sample
24-47 samples = 41 €/sample
+ 48 samples = 38 €/sample

NovaSeq 2x250bp, 100.000+ fragments:
Minimum of 768 samples = 24 €/sample

WGS 2x150bp, min 5M reads:
12-23 samples = 178 €/sample
24-48 samples = 168 €/sample
48-96 samples = 163 €/sample
+ 96 samples = 99 €/sample

Metatranscriptomics, 30M reads:
With enrichment workflow. Starting from 381€/sample

* For variable depth or different multiplexing please enquire.

Your libraries

Sequence your custom libraries:

MiSeq (2x300bp)
3.390 €

NovaSeq (1 lane - 1300M reads, 150bp paired)
6.490€

NovaSeq (2 lane - 1300M reads, 250bp paired)
10.380€

Includes:

- Free Illumina App analysis for Mi Seq samples (on request)
- Library normalization (up to 192 samples)

Bioinformatics pipeline

From taxonomic abundance to integrated diversity analyses:

Amplicon Analysis
12-36 samples = 600 €
37-96 samples = 900 €
Additional 48 samples = 200 €

* For WGS Analysis please enquire.

OTU clustering, taxonomy, assignment, alpha/beta diversity, PCoA and taxonomic enrichment testing (on request). Sample stratification on metadata factors.

Details:

- Metabarcoding pipeline based on QIIME framework
- Metagenomics / Metatranscriptomics analyses are based on HUMAnN2 framework

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
- Detection of **Contamination**
- **Biosafety Monitoring**
- **Food Quality**
- **Clinical Samples**