

## Online Ordering.

## Contact Us.

### Convenient 24/7 ordering

INVIEW products are optimised service packages for common NGS applications that ensure premium data quality combined with attractive prices. They can be ordered online just like all other Eurofins Genomics products.

Microbiome profiling is also available in our online shop.

#### How to order online:

- Open our website: [eurofinsgenomics.eu](https://eurofinsgenomics.eu)
- Click on the "Order Now" button on top of the page and select "INVIEW Microbiome Profiling 3.0"
- Create an account or use the same login credentials as for all other products (e.g. oligos)
- The order page appears (see below)
- Enter all details and place the package in your cart for immediate or later checkout

#### INVIEW Microbiome Profiling 3.0

1 Package Ordering 2 Option Selection 3 Sample Questionnaire

##### Next Generation Sequencing

Name of Project:   
Type of Project:   
Select Package:   
Number of Samples:

##### Package Details:

This INVIEW Microbiome Profiling package offers a highly sensitive identification and classification of the microbial population in any environmental, food or clinical sample. This is accomplished by amplification and Illumina MiSeq sequencing of the hypervariable regions in the 16S rRNA gene or the fungal internal transcribed spacer (ITS) gene.  
With the INVIEW Microbiome Profiling package we amplify and sequence a single target from all DNA samples. Choose this package if your aim is to analyse either the bacterial, the archaeal or the fungal content in your samples.

### Toll free phone numbers

Austria	0800 296 562
Belgium	0800 77862
Denmark	8088 1262
Finland	0800 112 744
France	0800 903 807
Ireland	1800 555 056
Italy	800 785 950
Luxembourg	8002 6418
Netherlands	0800 0226215
Norway	800 138 44
Sweden	020 798 148
Switzerland	0800 562 013
UK	0800 0323 135

**Email:**  
[support-eu@eurofins.com](mailto:support-eu@eurofins.com)

**Phone:**  
**+49 8092 82 89-77**

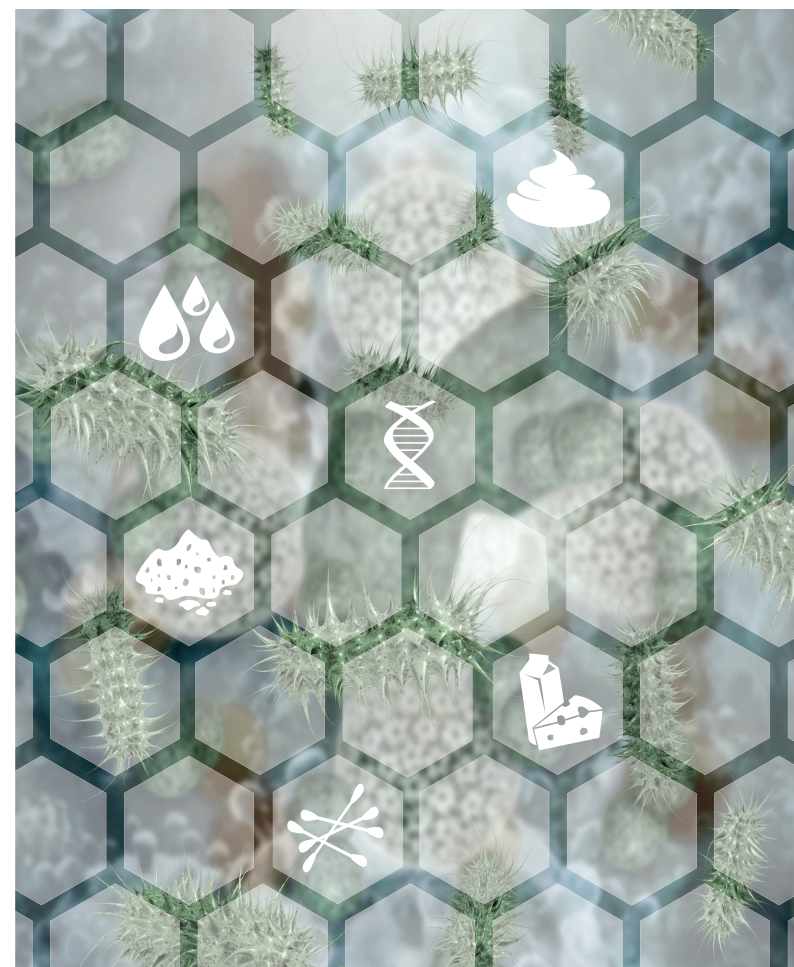
**Official business hours:**  
**8 a.m. – 6 p.m. CET**



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[eurofinsgenomics.com](https://eurofinsgenomics.com)

## INVIEW Microbiome Profiling 3.0

Identify the microbial community  
in your sample.



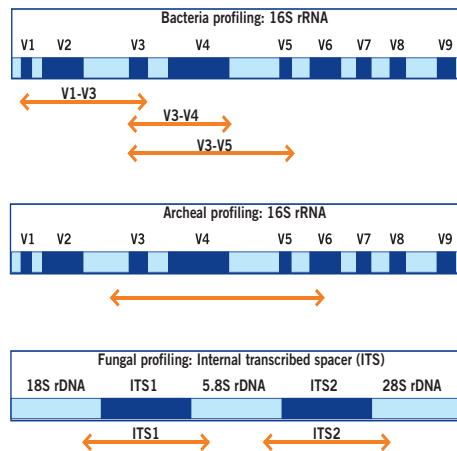
## Microbiome Profiling.

### Flexible layout at premium quality

16S rRNA & ITS sequencing is used for a highly sensitive identification and classification of the microbial population in any environmental, food or clinical sample.

#### Specifications

- Minimum sample number: 6
- Sequencing on MiSeq with 2x 300 bp
- Sorting of reads according to indices & data delivery



#### Possible 16S & ITS regions

- Choose between 6 different regions to be sequenced
- You can order the analysis of 1 - 4 target regions

## Second PCR Option.

### Define your own target regions

Send us your own specific amplicons generated in your lab and we will continue with the purification of the PCR products, the index PCR and sequencing.

With our 2nd PCR Microbiome Profiling Service we offer you full flexibility of the target region combined with cost-effective outsourcing of the remaining processes in an experienced lab.

For this service amplicons need to be generated with NGS primers consisting of the target specific sequences defined by the customer and an Illumina Adaptor sequence (detailed instructions are available in our Sample Submission Guides).

#### Specifications

- Minimum sample number: 6
- Purification of each amplicon you send in
- Generation of the index PCR
- Pooling & normalisation of amplicons
- Sequencing on MiSeq with 2 x 300 bp
- Sorting of reads according to indices & data delivery



The Eurofins Genomics NGS laboratory is GLP and ISO 9001 certified and ISO 17025 accredited.

## Additional Options.

### DNA extraction starting material

- Fermented products (e.g. cheese / yoghurt)
- Enrichment cultures / starter cultures
- Buccal swabs
- Human & animal faeces
- Water & waste water
- Soil & dust samples

### Bioinformatic analysis

- Chimera filtering & read merging
- Picking of OTU representative sequences (Operational Taxonomic Unit)
- Taxonomical assignment and read abundance estimation for all detected OTUs
- Normalised abundance estimation of bacterial and archaeal OTUs considering lineage-specific copy numbers of marker genes

