



# Metagenomics

resequencing  
storage genetics  
assembly ncRNA  
custom genotyping  
RNA-seq de novo trio private  
mendelian exome ChIP-seq  
genomics  
bioinformatics  
indel NGS prediction  
target  
metagenomics variation  
SNP diagnostics amplicon  
high-throughput DNA gene expression  
structural variation  
epigenetics GBS personalized  
comparative genomics  
tumor-normal



# NGS Next Generation Services



IGATech is the leading Italian provider of genomic research services using Illumina Next Generation Sequencing (NGS) technology. We are the largest lab in Italy offering these services on a wide range of organisms: we have experience with humans, other animals, plants and microorganisms.

The company has direct access to the scientific and technological resources of its founder, the Institute of Applied Genomics (IGA), which has gained an outstanding reputation in genomic research through participation in genome sequencing projects both at a national and international level.

Among the genomic research services provided, the company also offers a wide variety of bioinformatic services such as conventional and custom analyses and customer-oriented software development.

# Metagenomics

## Qualitative and quantitative analysis of microbial communities

Microbial communities affect human and animal health, support the growth of plants, are critical components of all terrestrial and aquatic ecosystems and can be exploited to produce food, fuels or chemicals. Today, Next-Generation Sequencing technology, with its ability to sequence thousands of organisms in parallel, has revolutionized microbiology by allowing concurrent analysis of whole microbial communities.

IGATech provides Metagenomics NGS testing that can profile entire microbial communities from complex samples, discover new organisms and explore the dynamic nature of microbial populations. We adopt a Next-Generation Sequencing approach, a culture-free method, which enables analysis of the entire microbial community, bacterial and yeast, within a sample. With the ability to combine many samples in a single test, our approach offers a cost-effective method for qualitative and quantitative analysis of heterogeneous communities and identification of strains that may not be found using other methods.

### **16S rRNA SEQUENCING FOR BACTERIAL IDENTIFICATION**

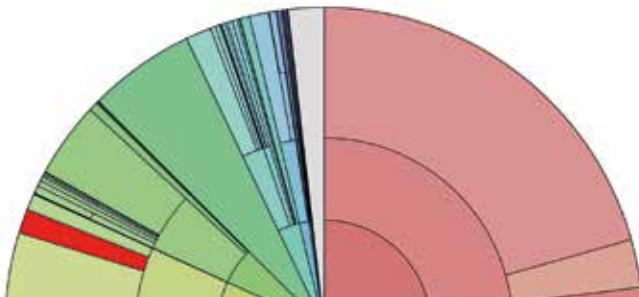
16S rRNA gene is used as a phylogenetic marker of microbial taxa. The 16S rRNA gene occurs in all living organisms, with the notable exception of viruses, and represents more than 80% of total bacterial RNA. The 16S rRNA gene includes interspersed conserved and variable regions, which makes it well suited for PCR amplification and sequencing as well as for the subsequent identification of bacteria present within a given sample.

### **ITS SEQUENCING FOR FUNGAL IDENTIFICATION**

The most widely used genomic region for identifying yeast and other fungal species is the ribosomal Internal Transcribed Spacer (ITS), a short DNA segment that contains enough intra-specific variation to distinguish different species.

### **METAGENOME SEQUENCING**

Metagenome sequencing captures the complete genomes of all the organisms in the microbial population. The comprehensive information obtained by this approach enables accurate phylogenetic inferences of close and distant relatives.



# Services list

## ADVANTAGES

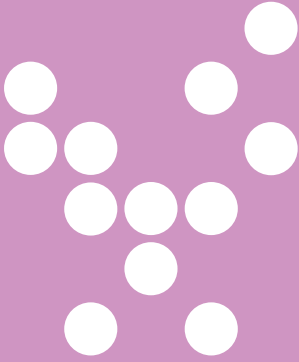
- Qualitative and quantitative analysis
- Ultra-sensitive - identification of strains that may not be found using other methods
- Suitable for any sample type
- Culture-free molecular test
- Cost effective - single test
- Fast turn-around time

## SERVICE DESCRIPTION

- Extraction of the genomic DNA
- Library preparation and sequencing
- Identification based on the best information available on public databases
- Analysis report delivery

Additional custom sequence targets can be analyzed if required or requested.





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