

FULL-LENGTH 16S rRNA Sequencing SERVICE



SOIL SAMPLE



FOOD SAMPLE



WATER SAMPLE

What is Full Length 16S rRNA Sequencing?

16S rRNA is an important gene found in bacteria that codes one of the ribosomal RNAs, a fundamental component of the bacterial ribosome. Due to its importance, this gene is passed down to the next generation and so can be found in all bacteria. This property is what makes this gene suitable as a marker gene since the species of bacteria can be identified using the gene. Full length 16S rRNA sequencing is expanding on that fact by employing Next Generation Sequencing (NGS) for identifying not only one species but the whole population of bacteria found in an ecological system at once. Since its inception, this method has been used to identify the species of all bacteria found in soil (agricultural soil, contaminated soil, and so on), in water (fresh water, marine water, wastewater, etc), in food (fermented food, spoiled food, etc), and in veterinary and human medicine (bodily fluids, intestinal scrape, stool, etc).

WHY CHOOSE

Full Length 16S rRNA Over Partial Length 16S rRNA for Amplicon Sequencing?

The complete length of 16S rRNA gene is around **1500-1600 bp** allowing for more information to be utilized for species identification. Meanwhile, **partial length uses a short fragment of the gene, usually around 300-500 bp**, meaning not all information can be obtained. Limited by the information availability, partial-length method can only be used to identify the genus name of bacteria. In contrast, **the full-length method can be used to identify the species name.** Genetika Science Indonesia is offering full length amplicon sequencing for metagenomics using GridION from Oxford Nanopore Technologies (ONT).

Sample Requirement & Deliverables Key

SAMPLE REQUIREMENT:

Platform : ONT GridION system
Sample Type : Raw sample or Genomic DNA

For genomic DNA samples:

- Amount: 100 ng (Nanodrop)
- Volume : 30 µL
- Purity : A260/A280 = 1.8-2.0 & A260/A230 = 2.0-2.2

For better result, here are some of our sampling technique recommendations:

• Use aseptic technique when taking any samples to prevent any unwanted cross-contamination.

• If the microbial composition data is time-sensitive (e.g samples involving fermentation), extract the genomic DNA immediately after sampling or keep the sample in -20 °C or below.

• When applicable, consider concentrating any liquid sample with low or sparse abundance using either filtration or centrifugation to improve species detection.

SOME OF THE KEY DELIVERABLES FOR AMPLICON SEQUENCING:

- Raw sequencing data in fastq format.
- Sequencing data QC.
- Bioinformatic analysis, includes:
 - Taxonomy annotation and abundance.
 - Sankey diagram.
 - Alpha diversity indices.
 - Beta diversity statistical analysis (Ordination plot such as NMDS and PCoA).
 - Various diagrams and charts (Bar chart, Krona, Venn diagram, Heatmap).
 - Statistical tests (t-test, ANOSIM, MRPP, LefSe).

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