OXFORD NANOPORE SEQUENCING

Utilize protein nanopores embedded in a membrane to analyze DNA, RNA and proteins.

Generate long-read lengths, from thousand of bases to entire genomic regions

It is particularly advantageous for de novo sequencing and genome assembly projects

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WHOLE PLASMID

Analyze the entire plasmid sequence, including any complex region, repeats, genes, regulatory elements and more

MOLECULAR BIOLOGY

Crucial for identifying plasmid structure and gene modifications, aiding molecular biologists and genetic engineers in optimizing gene expression and vector design.

MICROBIOLOGY

It helps researchers understand plasmid-borne virulence, resistance genes, and genetic variability in pathogens, aiding in developing targeted therapies, diagnostics, and surveillance.

AGRICULTURAL

It is used in agricultural biotechnology to characterize transgenic constructs, identify unintended genetic modifications, and ensure the safety and stability of GMOs.

ENVIRONMENTAL MICROBIOLOGY

It reveals the genetic potential of environmental microorganisms, aiding in bioremediation, nutrient cycling, and pollutant degradation for sustainable waste management and ecosystem preservation.

ZOOM

LIBRARY KIT

Input	(HMW)	Multiplexing	Platform	Library kit
50ng	Average 10Kbp	Yes (96plex)	GridION	*Rapid Barcoding Kit 96 (Kit 14 chemistry)*

Macrogen Europe recommend to send 10 µl for optimal results

BIOINFORMATICS

DELIVERY	Consensus	Read length vs Read number
	Annotated plasmid	Per position base counts

16S IDENTIFICATION

The 9 variable regions of the 16s rRNA gene has been a standard for taxonomic classification in genomics

The analysis of this gene accross prokaryotic organisms speed up the identification and making it cost-effective

Sequence all the variable regions at the same time

Except for de novo assembly of the full length, it is not necessary to purify cultures

High sequencing depth

APPLICATIONS

Discovery of new species

Classification of a consortium

Studies on environmental samples

Changes in the composition of microbiomes over time

ZOOM

LIBRARY KIT

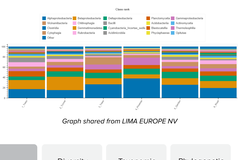
Input	(HMW)	Multiplexing	Platform	Library kit
10ng	Average 1.5Kbp	Yes (24plex)	GridION	*Rapid Barcoding Kit 16 (Kit 14 chemistry)*

Macrogen Europe recommend to send 10 µl for optimal results

BIOINFORMATICS

ABUNDANCE

summarizes microbial presence and abundance across samples, aiding in diversity comparisons and core microbiome identification. It's vital for understanding microbial community dynamics and associations with various conditions.



Graph shared from LIMA EUROPE NV

MORE BI	Diversity indices	Taxonomic lineages	Phylogenetic report

THE HOUSE OF SEQUENCING

Humanizing Genomics macrogen EUROPE

POWERED BY

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