



10 SECONDS OVERVIEW

- » Next generation sequencing of complex metagenomes
- » Characterisation of microorganisms without the restriction of taxonomic gene markers
- » Proprietary DNA extraction protocols
- » ISO 17025 accredited sequencing

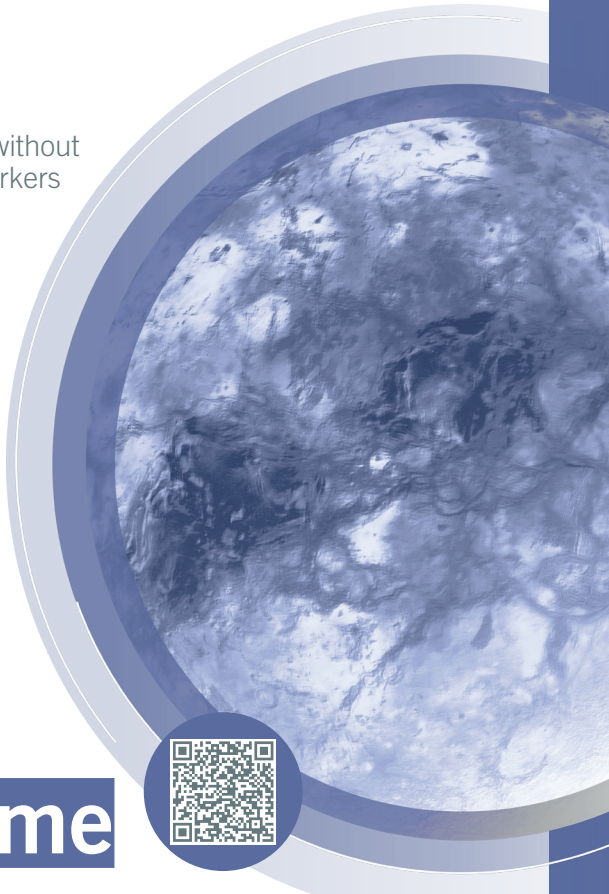
APPLICATIONS

- » Identify novel pathogens
- » Obtain a broad overview of genera in complex communities
- » Detect antibiotic resistance markers and virulence markers
- » Functional profiling & KEGG pathway analysis



INVIEW

Metagenome



SPECIFICATIONS

Library type	Whole genome library	
Starting material	All types of feces, food, environmental and other sample types	
Sequencing technology	Illumina	
Sequencing mode	150 bp paired-end reads	
Number of guaranteed reads	Multiples of 10M paired-end reads	
Delivery time	12 days	
Bioinformatic analysis	EXPLORE	ADVANCE
Deliverables	• FastQ Files (sequences and quality scores) • Phylum, genus and species level OTU abundance tables and graphs • Species diversity indices and plots • Rarefaction curves • Comprehensive Data Analysis Report	• FastQ Files (sequences and quality scores) • Phylum, genus and species level OTU abundance tables and graphs • Species diversity indices and plots • Rarefaction curves • KEGG annotation tables and graphs • Antibiotic resistance and virulence tables and graphs • Correlation plots • Comprehensive Data Analysis Report

BEST SUITED FOR

Taxonomic profiling	✓	✓
Characterisation of bacteria, archaea, viruses, protozoa, fungi	✓	✓
Identification of virulence factors		✓
Detection of antibiotic resistance genes		✓
Functional profiling		✓