



**KSCSTE - CENTRE FOR WATER RESOURCES  
DEVELOPMENT AND MANAGEMENT**  
**ജലവിഭവ വികസന വിനിയോഗ കേന്ദ്രം**

An Institution of Kerala State Council for Science, Technology & Environment, Govt. of Kerala  
കേരള ശാസ്ത്ര സാങ്കേതിക പരിസ്ഥിതി കൗൺസിൽ സ്ഥാപനം, കേരള സർക്കാർ



No:CWRDM/18/2026-A2

27-01-2026

**QUOTATION NOTICE**

Competitive Quotations in sealed covers are invited from the reputed firms for Metagenomic sequencing of water samples based on the details furnished below:-

Sl.NO	Item	Quantity	Amount(GST Incl)
1	Metagenomic sequencing of water samples (As per Technical Specification and Analytical requirements)	Per sample	

**Technical Specifications and Analytical requirements for shotgun metagenomic sequencing of water samples**

**1. Scope of Project:** Shotgun Metagenomic Sequencing and Microbial Community Analysis of Water Samples to characterize microbial diversity, functional potential, antibiotic resistance determinants, and virulence-associated genes.

**Sample type:** Canal and/or River water

**2. Sample Processing and DNA Extraction**

The service provider shall:

- Perform DNA extraction using a validated environmental DNA extraction protocol.
- Conduct DNA quality assessment, including Quantification using Qubit or equivalent fluorometric method, Purity assessment using A260/280 and A260/230 ratios, Integrity evaluation using agarose gel electrophoresis or Tape Station/Bioanalyzer
- DNA quality metrics and extraction reports shall be provided prior to library preparation.

**3. Library Preparation and Sequencing**

- The service provider shall perform library preparation for Shotgun metagenomic sequencing and Library QC (Library concentration measurement, Fragment size distribution profiling, Screening for adapter contamination)
- Sequencing Platform: Illumina Paired-End 150 bp (PE150)
- Minimum Data Output: 8-10 GB data per sample

**Sequencing must be conducted ensuring high-quality paired-end reads suitable for downstream metagenomic analysis.**

#### **4. Bioinformatics Analysis Requirements**

The provider shall perform Raw Data Processing and Quality Control. Remove adapters and low-quality bases, Filter short and low-complexity reads, Remove host DNA contamination, where applicable, Provide QC reports (e.g., FastQC/MultiQC)

##### **a. De Novo Assembly and Taxonomic Profiling**

The provider shall perform De novo assembly of sequencing reads, Taxonomic classification and profiling covering Bacteria, Fungi, Protozoa, and DNA viruses. Taxonomic profiling tools such as Kraken2/Bracken/MetaPhlAn (or equivalent) may be used. Assembly statistics shall be reported.

##### **b. Microbial Diversity Analysis**

Alpha Diversity Indices (Observed, Chao1, ACE, Shannon, Simpson, Inverse Simpson, Fisher)

Beta Diversity Metrics (Bray–Curtis, Jaccard)

The provider shall supply both numerical data tables and graphical visualizations including Rarefaction Curves.

##### **c. Functional Annotation and Resistome Analysis**

Analysis shall include Antibiotic Resistance Gene (ARG) detection using recognized AMR databases (CARD, ResFinder, and MEGARes), Virulence factor detection using VFDB or equivalent and Functional annotation using KEGG, GO, COG databases

**d) Summarized pathway, resistome, and virulome reports shall be included.**

#### **5. Reporting and Data Deliverables**

The following outputs shall be provided for each sample

- a. Raw sequencing reads in FASTQ format (R1 and R2)
- b. Assembled contigs in FASTA format
- c. Taxonomy tables and abundance matrices (Excel format) from Kingdom to Genus
- d. Taxonomic classification output files (including Kraken2 results)
- e. Visualization outputs including Taxonomy abundance bar plots, Krona charts,
- f. Sankey plots Alpha diversity plots and tables
- g. Beta diversity plots and tables
- h. Rarefaction curves
- i. Antibiotic resistance gene detection reports
- j. Virulence gene detection summary
- k. KEGG/GO/COG functional annotation reports

#### **Terms and Conditions:-**

1. Quotation shall be submitted with all required details in sealed envelopes superscribed as 'Quotation for Metagenomic sequencing of water samples' **on or before 03-02-2026, 5 PM.**
2. Quotation which does not conform to the terms and conditions (clauses) of this Notification will be rejected.
3. " In case of any matter which is not covered by this Quotation Notice, or the general terms and conditions of the contract or the specifications etc. as given herewith, the decision of the Executive Director, CWRDM shall be binding on the bidder.
4. The acceptance of this Quotation rests with the competent authorities as per the rules of the CWRDM.
5. Any further information regarding this quotation which the CWRDM do not consider to be kept confidential, can be obtained from Office of the CWRDM during working hours on any day prior to the last date fixed for the receipt of Quotation (**Contact Number 0495- 2351888**).
6. Quotation will be opened on the next working day after the due date at 3 PM.
7. The rate quoted in the Quotation should be valid for **1 year** inclusive of all cost, including, taxes, transportation and handling charges, etc if any and the material should be delivered at CWRDM , Kunnamangalam, Kozhikode-673571, Kerala.
8. The maximum period required for delivery should be mentioned in the quotation.
9. No representation for enhancement of price once accepted will be considered during the currency of the contract.
10. All graphical results shall be supplied in PDF and JPG format.
11. **The service provider shall supply a brief methods document describing Software tools used, Database versions, Default or custom parameters applied. This is required to ensure reproducibility and transparency.**
12. **The provider shall ensure secure handling and storage of all samples and data, confidentiality of project results**
13. **The expected turnaround time from sample submission to final report delivery shall be indicated in the quotation.**

**Registrar**

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