

Request for Proposal “Metagenome Sequencing” 2026

The Chair of Aquaculture and Sea-Ranching at the Faculty of Agriculture, Civil Engineering, and Environmental Sciences at the University of Rostock intends to award a contract for the metagenome sequencing of 70 samples. The contract is expected to be awarded in the 2nd or 3rd quarter of 2026.

Tender period: 10 business days

Description of the scope and content of the bid:

Metagenome sequencing of 70 samples: 2x150bp Illumina paired-end reads with an approximate output of 30 million reads per sample and data transfer of FASTQ files.

Test material:

The microbiome (gut and whole larvae) of juvenile zander, as well as the skin microbiome (swabs) of rainbow trout, are to be examined. Additional samples to be analyzed include the metagenome of water samples, pellet feed, Artemia, green water/microalgae, and swabs of biofilms from rearing tanks.

The extracted gDNA, quantified by fluorometry (Qubit™), will be provided by the client.

Analysis method to be used:

70 x QC and Library Prep Illumina DNA Prep, (M) Tagmentation

1x sequencing on NovaSeq 6000 S1 Rgt Kit v1.5 (300 cycles)

1x sequencing QC and demultiplexing per flow cell

Deliverables:

- FASTQ files
- Report (PDF)
- Kraken 2 report (xslm) (exclusively for prokaryotes (Bacteria and Archaea) for each sample

Optional: Metagenome Analysis Service

- Alpha diversity indices (Gini-Simpson, Chao1, ACE, Shannon, observed species); for each sample at the family, genus (top 10 by OTUs), and species levels (top 20 OTUs) (xslm) (tsv) (png)
- Total number of sequences (total number of OTUs) at the family, genus (Top 10 by OTUs), and species levels (Top 20 OTUs) (xslm) (tsv) (png)
- Relative abundance at the family, genus (Top 10 by OTUs), and species levels (Top 20 OTUs) Bracken/KrakenTools (pdf) (xslm) (tsv) (png)
- Beta diversity indices (Bray-Curtis, PCOA) between selected samples (triplicates) (xslm) (tsv) (png)

(Alpha diversity indices for each sample at the family, genus (both Top 10), and species levels (Top 20) as tables (tsv), graphs (png), and raw data (xslm). Total number of sequences (OTUs) at the family, genus (both Top 10), and species (Top 20) levels as tables (tsv), graphs (png), and raw data (xslm). Beta diversity indices between selected samples (triplicates) as tables (tsv), graphs (png), and raw data (xslm)

Evaluation Criteria and Award

In addition to the “633 Bid Letter” form, please also submit a bid prepared by you with a corresponding description of the services (see Service Evaluation). The price must be stated as a total price including labor hours, additional costs, and VAT.

Price evaluation:

The bid price is weighted at 40%. Price evaluation is based on the total bid price. A maximum of 40 points will be awarded for the total bid price, and the evaluation will be based on a point distribution using linear interpolation:

$$Punkte_i = \frac{P_{max} - P_i}{P_{max} - P_{min}} * L_{max}$$

Pmax = Highest price / hypothetical price twice as high as the lowest offer (Pmin * 2)

Pmin = Lowest price

Pi = Price of the currently considered offer

Lmax = Maximum achievable number of price points = 40 points

Punkte i = Points determined for the respective offer price under consideration

Offers that are higher than the fictitious offer that is twice as expensive automatically receive 0 points.

Performance evaluation:

A maximum of 60 performance points can be earned, corresponding to a weighting of 60%.

The evaluation of bids and allocation of points is based on the following criteria (general evaluation procedure and scope of results): Service included in the bid: yes; if no, then 0 points	Points
Standard library preparation	10
Sequencing (e.g., NovaSeq S1) 2x150bp paired-end reads, at least 20 million reads	15
Sequence quality control	10
Results as FASTQ files, Kraken 2 report	10
Metagenome analysis in the form of tables, diagrams, and graphs	15
Total maximum achievable performance points	60

Award

The bid with the highest total score is the most economically advantageous bid. If multiple bids receive the same score, the bid with the highest total performance score will be awarded the contract.