



# RESEARCH ASSOCIATE FOR THE PROJECT “LARGE SCALE SEQUENCING TO UNRAVEL CARBON CYCLING IN THE ELBE ESTUARY (MICRO)BIOTA” § 28 SUBSECTION 3 HMBHG

**Institution:** Faculty of Mathematics, Informatics and Natural Sciences, Department of Biology, Institute of Cell and Systems Biology of Animals

**Salary level:** EGR. 13 TV-L

**Start date:** as soon as possible, fixed for a period of two years

**Application deadline:** 2022-10-18

**Scope of work:** full-time position suitable for part-time

## Responsibilities

In the period 01.10.2022-31.03.2023 duties primarily include teaching and research. In the period 01.04.2023-30.09.2024 duties include academic services in the project named above.

Research associates may also pursue independent research and further academic qualifications.

## Specific Duties

The research associate will be a member of the DFG funded Research Training Group 2530 (Biota-mediated effects on Carbon cycling in Estuaries) and the adjoining DFG funded Sequencing Project. We will unravel the main microbiome pathways in the sediment's samples along the salinity gradient, the plant rhizospheres and the free water samples. The postdoc researcher will coordinate the main sequencing data analysis of the involved five PhD students and will combine the generated sequencing data (microbiome composition, microbial RNA-Seq, whole genome sequencing), support the PhD students in the annotation and identification of prevailing biota and pathways and support the statistical analysis and data integration. Additionally, the objectives of the postdoc researcher will be to combine the above data of the estuary microbiome composition, the meta-transcriptomes and genomes of each project into major overlapping pathways that are affected by the salinity gradient, seasons and tides, using existing bioinformatics tools. We expect the research associate to add his expertise in statistical analysis and modelling of the generated data and the effects on the Carbon cycling in the Elbe estuary.

Teaching duty of 4 teaching hours in the period from 01.10.2022-31.03.2023.

## Requirements

A university degree in a relevant field plus doctorate.

University degree (PhD, Dr rer nat) in bioinformatics, informatics, biology or a relevant field. The applicant should have sound knowledge and experience in the methods of next generation sequencing techniques and their statistical analysis and annotation. Experience in microbiome amplicon analysis, de novo assembly and analysis of microbial RNA-Seq data and complex shotgun sequencing analysis is desirable. Team spirit, the ability of scientific writing and good communication skills are required. Good oral and written English skills are necessary.

## We offer



Reliable remuneration based on wage agreements



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As a University of Excellence, Universität Hamburg is one of the strongest research universities in Germany. As a flagship university in the greater Hamburg region, it nurtures innovative, cooperative contacts to partners within and outside academia. It also provides and promotes sustainable education, knowledge, and knowledge exchange locally, nationally, and internationally.

Severely disabled and disabled applicants with the same status will receive preference over equally qualified non-disabled applicants.

## Instructions for applying

### Contact

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### Location

Martin-Luther-King-Platz 3  
20146 Hamburg  
[Zu Google Maps](#)

### Reference number

381

### Application deadline

2022-10-18

Send us your complete application documents (cover letter, curriculum vitae, copies of degree certificate[s] and if necessary ID attesting to your disability or proof of equivalent status) via the online application form only.

If you experience technical problems, send an email to [bewerbungen@uni-hamburg.de](mailto:bewerbungen@uni-hamburg.de).  
More information on [data protection](#) in selection procedures.



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