



Professional activity

Chris Rinke completed his PhD at the Department of Marine Biology at the University of Vienna, Austria, followed by a two-and-a-half-year postdoc at Washington State University (WSU) in the USA. At WSU, he worked on deep-sea projects that enabled him to dive with the research submarine Alvin to deep-sea hot springs at a depth of over 2000 m. He used a second postdoctoral stay at the Joint Genome Institute (JGI) of the Lawrence Berkeley National Laboratory in California to work on a single-cell genomics methods to recover genomes of uncultured bacteria and archaea. He then moved to the Australian Centre for Ecogenomics (ACE) at the University of Queensland in Brisbane, Australia, where he secured the prestigious Future Fellowship

and started his own research group in Microbial Genomics. Following a move to Europe, he is now Professor of Environmental Microbiology at the University of Innsbruck, Austria and Honorary Professor at the University of Queensland, Australia. Since November 2021 Chris's publication record has been recognised by the Clarivate "Highly Cited Researchers" list, which highlights the world's top one percent of researchers.

The Rinke Lab uses various 'omics' methods to analyze genomes, transcripts, proteins and metabolites of environmental samples - hence the name of the group "Environmental Omics", also known by the abbreviation "E-Omics". Current research areas include: 1) microbial biodegradation of synthetic polymers, e.g. multi-omics analyses of gut microbiomes from superworms on a plastic diet, 2) ecosystem functions of uncharacterised and rare microbes in anthropogenically impacted environments, such as rivers and coastal waterways, 3) novel microbial taxa from extreme environments ranging from deep-sea sediments to terrestrial hot springs, 4) curation and extension of the Genome Taxonomy Database (GTDB; gtdb.ecogenomic.org) to establish a standardised microbial taxonomy based on genome phylogeny.

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Abstract:

Over the past few years, our understanding of the tree of life has undergone a profound transformation. Culture-independent techniques, such as metagenomics and single-cell genomics have generated an unprecedented wealth of sequencing data. These approaches have enabled the recovery of vast numbers of microbial genomes, including those from previously uncultured microorganisms. This genomic data has revolutionized microbial taxonomy by facilitating the development of systematic classifications based on evolutionary relationships. Furthermore, it has opened new avenues for exploring ecosystems at both genomic and viromic levels, characterizing novel taxa, and advancing applied research.