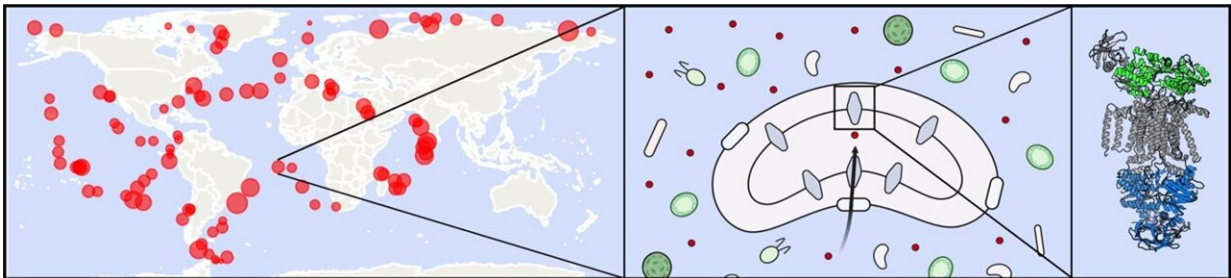


# How the oceans' most abundant bacteria impact global nutrient flows

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An example of a transport protein in a SAR11 bacterium and its distribution in samples of ocean from across the world. Because of their abundance, these transport proteins are widely distributed throughout the ocean and have a global impact on uptake of organic matter in the ocean. Created with Biorender.com. Credit: Clifton et al.

If you were to collect all the organisms from the ocean surface down to 200 meters, you'd find that SAR11 bacteria, though invisible to the naked eye, would make up a fifth of the total biomass. These bacteria, also known as Pelagibacterales, have evolved to thrive in nutrient-poor marine environments and play a significant role in global nutrient cycles. Despite their importance, the mechanisms behind their impact on the planetary ecosystem have remained unclear.

But now, a *Nature* paper by researchers from the Okinawa Institute of Science and Technology (OIST) [sheds light on a crucial aspect](#) of these

bacteria.

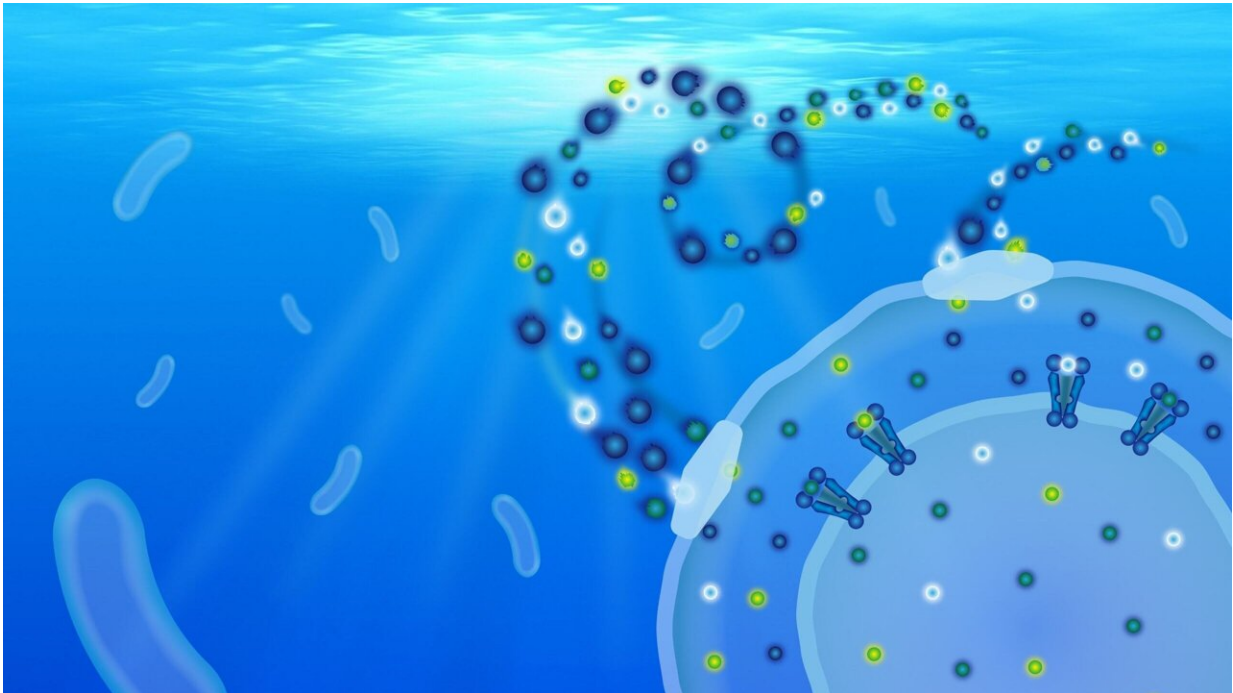
"We knew that SAR11 is a key player in important nutrient cycles, such as carbon and sulfur exchanges, but we didn't know the full extent," explains Dr. Ben Clifton, first author of the paper, adding that "now, by comprehensively mapping out the [transport proteins](#) of the bacteria, we have a much better picture of how SAR11 slots into these cycles."

Professor Paola Laurino, the senior author, credits global seawater sampling projects like the Tara Oceans project for providing the metagenomic data that made this breakthrough possible: "these datasets have allowed us to link genomic data to protein function."

## **Piecing together the protein puzzle**

Transport proteins are vital for moving nutrients in and out of [bacterial cells](#), shaping how bacteria interact with their environment. This is especially significant for SAR11 bacteria, whose [nutrient uptake](#) has a broad impact on global nutrient cycles. But despite their abundance in the oceans, these bacteria are difficult to study due to their specific growth requirements.

To overcome this, the researchers genetically modified E. coli bacteria to express SAR11 transport proteins, allowing them to study the proteins in the lab.



Artist impression of the transport proteins of SAR11 bacteria. Credit: Kaori Serakaki, OIST

Analyzing these genes across the SAR11 metagenome—the [genetic material](#) common to all SAR11 species—required global data, which was made possible by extensive genomic databases. The team identified genes linked to crucial marine processes, such as a protein that interacts with DMSP, a compound vital to the sulfur cycle and climate regulation.

In total, they discovered 13 transport proteins, including those for DMSP, [amino acids](#), glucose, and taurine, all of which have significant environmental roles.

## The logistics of global nutrient cycles

"Through these experiments, we discovered specific properties of

transport proteins that enable SAR11 bacteria to thrive in nutrient-poor environments. This could not have been discovered from just looking at the genomic makeup alone," summarizes Dr. Clifton.

However, the team's research on SAR11 is far from over. Having identified the proteins responsible for nutrient transport, they are now delving into the [metabolic pathways](#) to understand how these nutrients are utilized and converted within the bacteria. Additionally, in collaboration with the Weizmann Institute of Science, they are exploring how SAR11 interacts with its environment before absorbing nutrients.

This study is part of a growing trend that links environmental DNA to [protein function](#), paving the way for new discoveries about how microscopic life forms influence global processes.

As Prof. Laurino puts it, "By bridging the macro perspective of marine diversity and the micro perspective of protein biochemistry, we're setting the stage for further questions about how bacterial proteins fit into global nutrient cycles, and how these bacteria contribute to, and are affected by, climate change and shifts in ocean biodiversity."

**More information:** Paola Laurino, The ultra-high affinity transport proteins of ubiquitous marine bacteria, *Nature* (2024). [DOI: 10.1038/s41586-024-07924-w](#).  
[www.nature.com/articles/s41586-024-07924-w](http://www.nature.com/articles/s41586-024-07924-w)

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