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Tianyi Chang, Maria G. Pachiadaki, Gregory S. Gavelis, Nicole J. Poulton, Brian Thompson, Corianna Mascena, Keir Macartney, Julia M. Brown, James J. La Clair, Alaina R. Weinheimer, Taichi Yokokawa, Paula Ruiz-Fernández, Julia Anstett, Paul M. Berube, Steven J. Biller, Beth N. Orcutt, Federico Baltar, Michael D. Burkart, Steven J. Hallam, Klaus Jürgens, Osvaldo Ulloa, Takuro Nunoura, **Eva Sintes**, Gerhard J. Herndl, Ramunas Stepanauskas, 2026.

[Single-cell-resolved genome atlas of prokaryoplankton inhabiting the ocean's interior.](#)

Cell. 15 September 2026. <https://doi.org/10.1016/j.cell.2026.08.036>

Abstract: The ocean's aphotic interior harbors three-quarters of planktonic bacteria and archaea (prokaryoplankton), whose composition, ecology, and biotechnological potential remain poorly constrained. To address this knowledge gap, we created Global Oceans Reference Genomes (GORG)-Dark, a dataset of 9,698 genomes from individual prokaryoplankton cells sampled unselectively across a broad range of depths, geographic locations, and environmental conditions below the ocean's photic surface. Biogeographic analyses revealed prokaryoplankton vertical stratification extending to abyssal depths, the presence of particle-attached lineages of Pelagibacterales, and the previously overlooked abundance of Patescibacteria and Nanoarchaeota in the Baltic and Black Seas. We identified coding potential for chemolithoautotrophy, pharmacologically relevant secondary metabolisms, and a distinct type of proteorhodopsins in prokaryoplankton lineages prevalent throughout the aphotic ocean. This study offers a quantitative, global assessment of the composition and coding potential of microorganisms inhabiting the vast ocean's interior and contributes an extensive, single-cell-resolved dataset to microbial oceanography's cyberinfrastructure.

Keywords: single-cell genomics, prokaryoplankton diversity, ocean microbiome, chemolithoautotrophy, proteorhodopsin, bioprospecting, biosynthetic gene cluster, biogeography, biogeochemistry, darobactin.