

An early diverging SQR enzyme in Antarctic *Gloeobacteriales* indicates sulfide tolerance in thylakoid-lacking cyanobacteria



Louise Hambücken¹, Edi Sudianto¹, Elie Verleyen², Jimmy H. Saw³, Denis Baurain¹ and Luc Cornet¹
Published in *Spectrum* (2026)

¹ University of Liège, Department of Life Sciences, Bât. B22, Quartier Vallée 1, chemin de la Vallée 4, Liège, 4000, Belgium

² Ghent University, Department of Biology / Protistology and Aquatic Ecology, Krijgslaan 297 (S8), Gent, 9000, Belgium

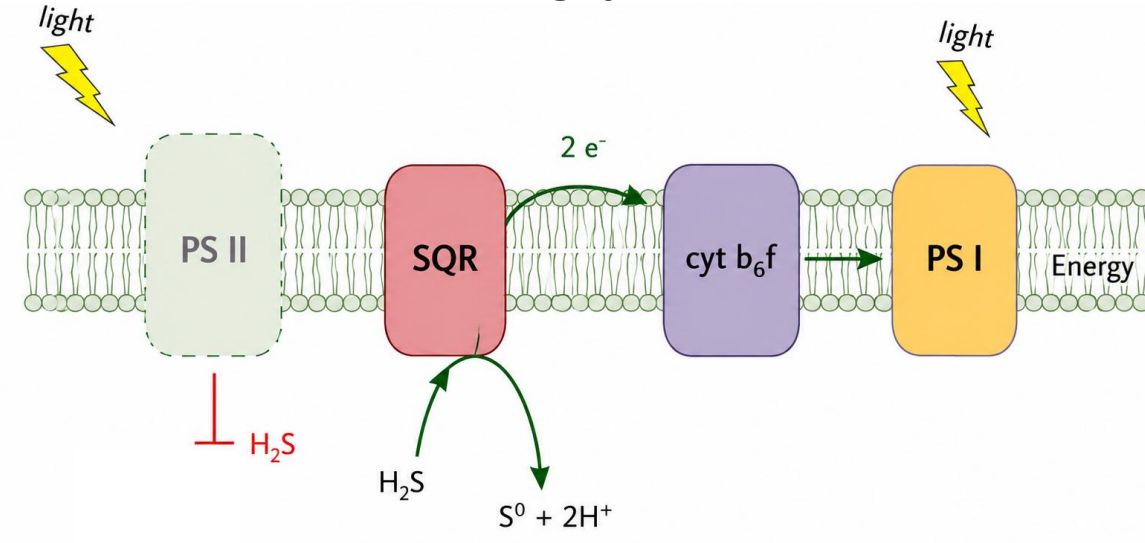
³ The George Washington University, Department of Biological Sciences, Science and Engineering Hall, 800 22nd St. NW, Suite 6000, Washington DC, 20052, USA



Research Background

SQR-mediated sulfide tolerance

Sulfide oxidoreductases (SQRs) oxidize sulfide and transfer electrons to the quinone pool. They may support sulfide-driven **anoxygenic photosynthesis** when oxygenic photosynthesis is impaired, notably because sulfide strongly **inhibits Photosystem II**.



Cyanobacteria in Proterozoic euxinic oceans

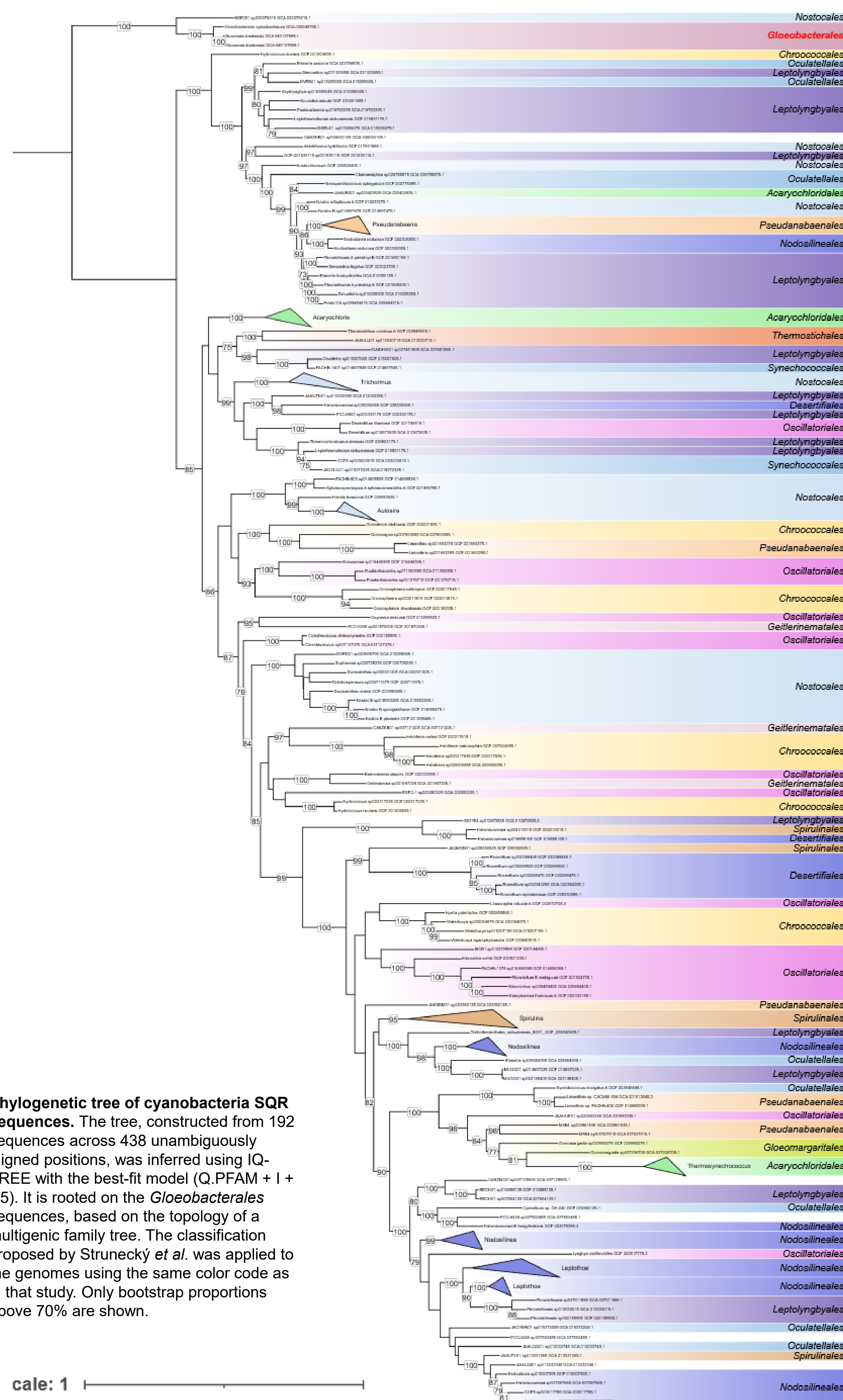
The capacity of switching from oxygenic to **anoxygenic photosynthesis** may have been particularly important during the **early diversification of cyanobacteria** in Proterozoic oceans, where locally anoxic and sulfidic, or **euxinic**, waters occurred within the photic zone. Cyanobacteria may therefore have experienced **fluctuating oxygenated and sulfide-rich conditions**, favouring the coexistence of oxygenic and anoxygenic photosynthesis.

Antarctic *Gloeobacteriales* as a model system

Gloeobacteriales are the **earliest-diverging** cyanobacterial order and **lack thylakoids**, with their photosynthetic electron transport chain located in the cytoplasmic membrane. **Antarctic lakes can develop localized anoxic and sulfidic zones**, making these environments valuable natural systems for investigating **ancient cyanobacterial adaptations** to euxinic conditions.

An early diverging SQR enzyme in Antarctic *Gloeobacteriales*

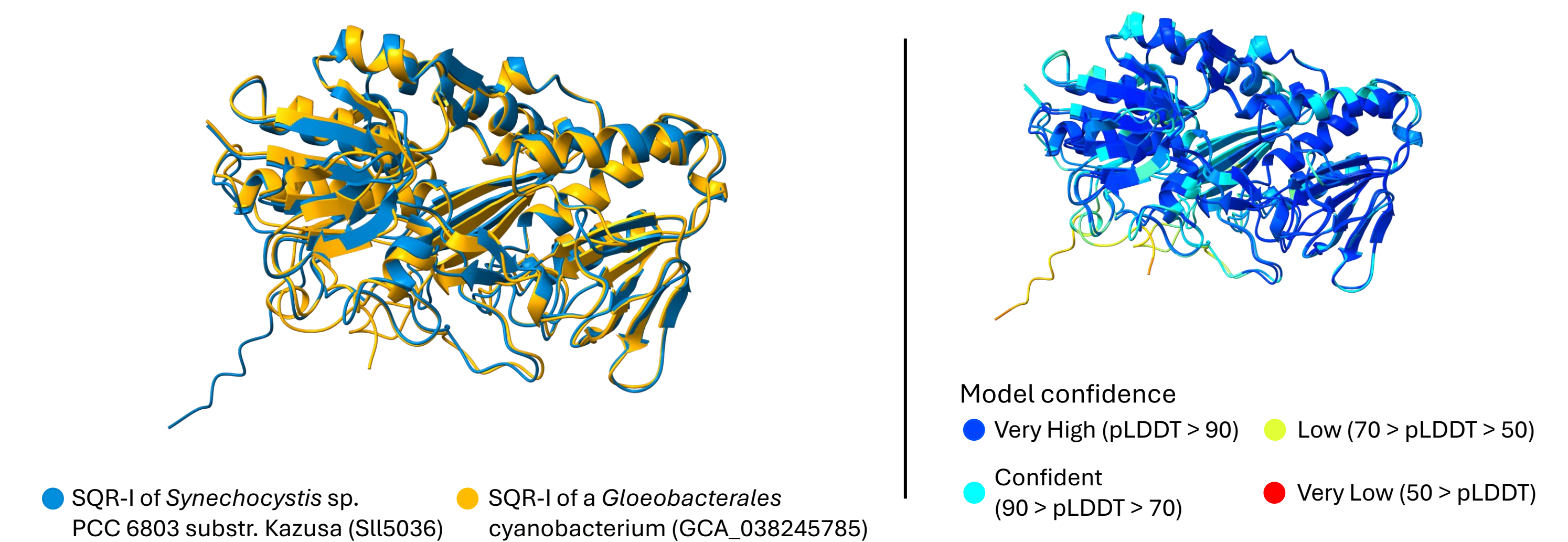
Basal position of three Antarctic *Gloeobacteriales* MAGs in cyanobacterial SQR phylogeny. Searches for orthologous SQR protein sequences against 107,237 representative bacterial genomes (GTDB) revealed that sequences from three Antarctic *Gloeobacteriales* MAGs occupy a strictly basal position within the monophyletic cyanobacterial group. These three sequences were used to root a reduced phylogeny comprising 192 cyanobacterial SQR sequences shown below. Their position is highly consistent with the early divergence of the *Gloeobacteriales* order, strongly suggesting they represent the earliest-diverging cyanobacterial SQR sequences identified to date. The broader phylogeny also indicates recurrent lateral gene transfer later in SQR evolution, evidenced by the intermingling of several other cyanobacterial orders, including *Oscillatoriales* and *Nostocales*, with strong bootstrap support.



Phylogenetic tree of cyanobacteria SQR sequences. The tree, constructed from 192 sequences across 438 unambiguously aligned positions, was inferred using IQ-TREE with the best-fit model (Q.PFAM + I + R5). It is rooted on the *Gloeobacteriales* sequences, based on the topology of a multigenic family tree. The classification proposed by Strunecký *et al.* was applied to the genomes using the same color code as in that study. Only bootstrap proportions above 70% are shown.

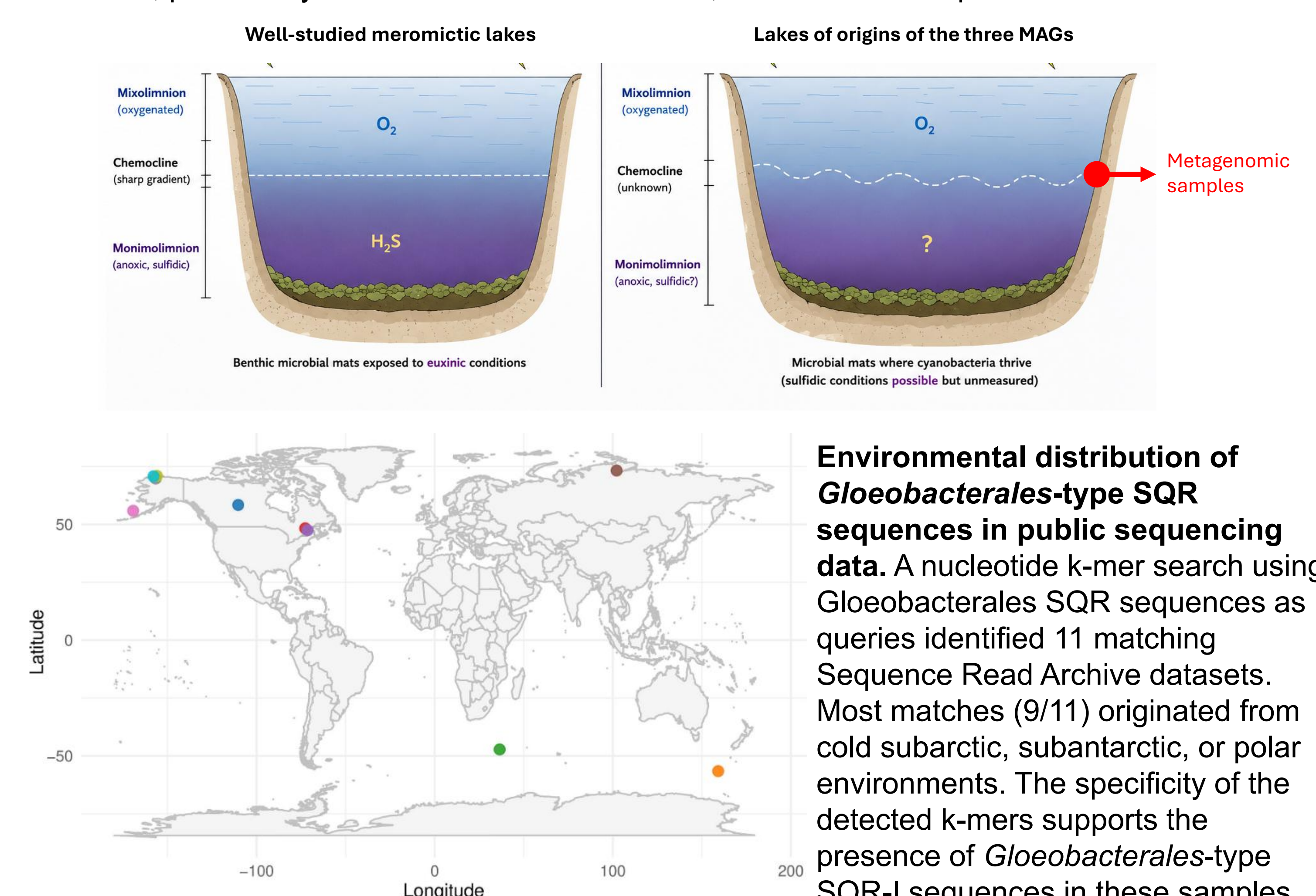
Structural conservation of the active site in Antarctic *Gloeobacteriales* SQR proteins.

AlphaFold 3 models of *Gloeobacteriales* SQR sequences were structurally aligned with characterized SQR-I proteins. Despite sequence divergence, the predicted overall fold and the spatial arrangement of residues forming the catalytic site are conserved. Mapping of the key active-site residues onto the predicted structures supports the functional assignment of these proteins as SQR and suggests that the Antarctic variants retain the molecular features required for sulfide oxidation.



Potential occurrence of sulfidic conditions in Antarctic lakes harboring the three *Gloeobacteriales* MAGs.

In well-studied meromictic lakes such as Ace Lake and Lake Fryxell, permanent water-column stratification limits mixing and leads to an oxygenated mixolimnion above an anoxic, sulfide-rich monimolimnion, exposing deep benthic microbial mats to euxinic conditions. The lakes from which the three Antarctic *Gloeobacteriales* MAGs were recovered are not formally classified as meromictic, and sulfide concentrations were not measured. Localized sulfidic conditions, particularly within benthic microbial mats, therefore remain possible but unconfirmed.



Environmental distribution of *Gloeobacteriales*-type SQR sequences in public sequencing data. A nucleotide k-mer search using *Gloeobacteriales* SQR sequences as queries identified 11 matching Sequence Read Archive datasets. Most matches (9/11) originated from cold subarctic, subantarctic, or polar environments. The specificity of the detected k-mers supports the presence of *Gloeobacteriales*-type SQR-I sequences in these samples.

Conclusion

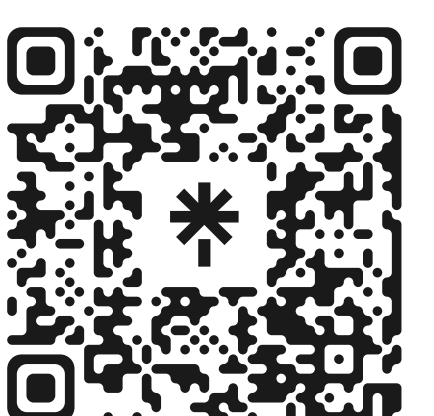
Some Antarctic *Gloeobacteriales* harbor basal SQR-I sequences that retain the **conserved catalytic features** of functional sulfide oxidoreductases. Their presence in early-diverging *Gloeobacteriales* provides **new insights into the early evolution of sulfide tolerance** and potentially sulfide-driven photosynthesis. However, because sulfide was not measured in the lakes or microbial mats from which these genomes originated, the environmental role of **these SQRs remains to be physiologically and ecologically confirmed**.

Related Article

Hambücken, L., Sudianto, E., Verleyen, E., Saw, J. H., Baurain, D., & Cornet, L. (2026). An early diverging SQR enzyme in Antarctic *Gloeobacteriales* indicates sulfide tolerance in thylakoid-lacking cyanobacteria. *Microbiology Spectrum*, 14(6), e00423-26. <https://doi.org/10.1128/spectrum.00423-26>

Acknowledgements

This work was supported by a research grant (PDR T.0018.24 OR-OPHOT-IN-CYN) from the Belgian National Fund for Scientific Research (F.R.S.-FNRS) to DB. LH is a FRIA grantee of the Fonds de la Recherche Scientifique – FNRS. Computational resources were provided by the Consortium des Équipements de Calcul Intensif (CÉCI), funded by the F.R.S.-FNRS under Grant No. 2.5020.11 and by the Walloon Region.



Scan for more information