

Crystallization and Preliminary X-ray Crystallography of the Outer Membrane Cytochrome OmcA from *Shewanella oneidensis* MR-1

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DOE/Office of Science/Biological & Environmental Research

Objective

- Determine the molecular structure of the outer membrane cytochrome OmcA to elucidate molecular mechanisms of dissimilatory metal-reducing bacteria.

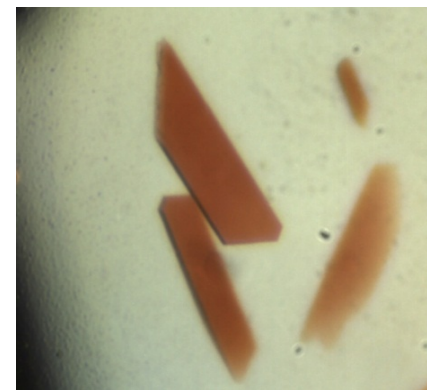
New Science

- Optimization of OmcA crystallization conditions to improve crystal quality for X-ray crystallographic studies.
- Collection of single-crystal X-ray diffraction data on an OmcA crystal to a resolution of 3.25 Å.

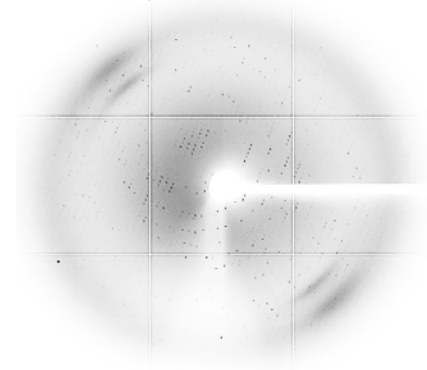
Significance

- Our X-ray crystallographic data is currently being used to determine the three-dimensional molecular structure of OmcA. The structure of OmcA will reveal important molecular details of how extracellular electron transfer might occur in biological dissimilatory reduction pathways.

OmcA Crystal



X-ray Diffraction



Tomanicek, S.J., A. Johs, M.S. Sawhney, L. Shi and L. Liang. 2012. Crystallization and preliminary X-ray crystallographic studies of the outer membrane cytochrome OmcA from *Shewanella oneidensis* MR-1. Acta Crystallogr. Sect. F 68:53-55 (doi:10.1107/S1744309111046082).

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The outer membrane cytochrome OmcA functions as a terminal metal reductase in the dissimilatory metal-reducing bacterium *Shewanella oneidensis* MR-1. The ten-heme centers shuttle electrons from the transmembrane donor complex to extracellular electron acceptors. Here, the crystallization and preliminary crystallographic analysis of OmcA are reported. Crystals of OmcA were grown by the sitting-drop vapor-diffusion method using PEG 20,000 as a precipitant. The OmcA crystals belonged to space group $P2_1$, with unit-cell parameters $a = 93.0$, $b = 246.0$, $c = 136.6$ Å, $\alpha = 90$, $\beta = 97.8$, $\gamma = 90$. X-ray diffraction data were collected to a maximum resolution of 3.25 Å.

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