

Structural analysis of bacterial transporter protein

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Introduction

The MexAB-OprM pump of *Pseudomonas aeruginosa* extrudes antibiotics and confers multi-antibiotic resistance to this hospital pathogen. The pump assembly consists of the proton conducting transporter MexB [3], the membrane fusion protein MexA [1], and the outer membrane protein OprM [2].

An aim of this study is to obtain atomic level three-dimensional structure of these medically important and scientifically interesting transporter proteins and contribute for better understanding of multi-drug resistance systems.

Experiments and Results

We collected the data of OprM and MexA crystals using an ADSC detector exposing 30-40 sec and synchrotron radiation with 0.978 Å wavelength at 300-350mm distance at 95 Kelvin.

The data were processed using HKL2000 program package. OprM belonged to rhombohedral space group R32 with unit cell parameters of $a = b = 85.12\text{Å}$, $c = 1042.90\text{Å}$. MexA belonged to monoclinic space group P21 with unit cell parameters of $a = 129.78$, $b = 179.65\text{Å}$, $c = 213.74\text{Å}$, $\beta = 107.0$ degree. The metal derivative crystals diffracted beyond 3.5 Å. We have been perplexed with anisotropic diffractive pattern for OprM, but not for MexA (figure)

Further data analyses of derivative crystals are on progress.

References

- [1] H. Yoneyama et al., J. Biol. Chem. Vol.275, No.7, pp. 4624-4638 (2000).
- [2] A. Nakajima et al., J. Biol. Chem. Vol.275, No.39, pp. 30064-30068 (2000).
- [3] L. Guan et al., J. Biol. Chem. Vol.274, No.15, pp. 10517-10522 (1999).

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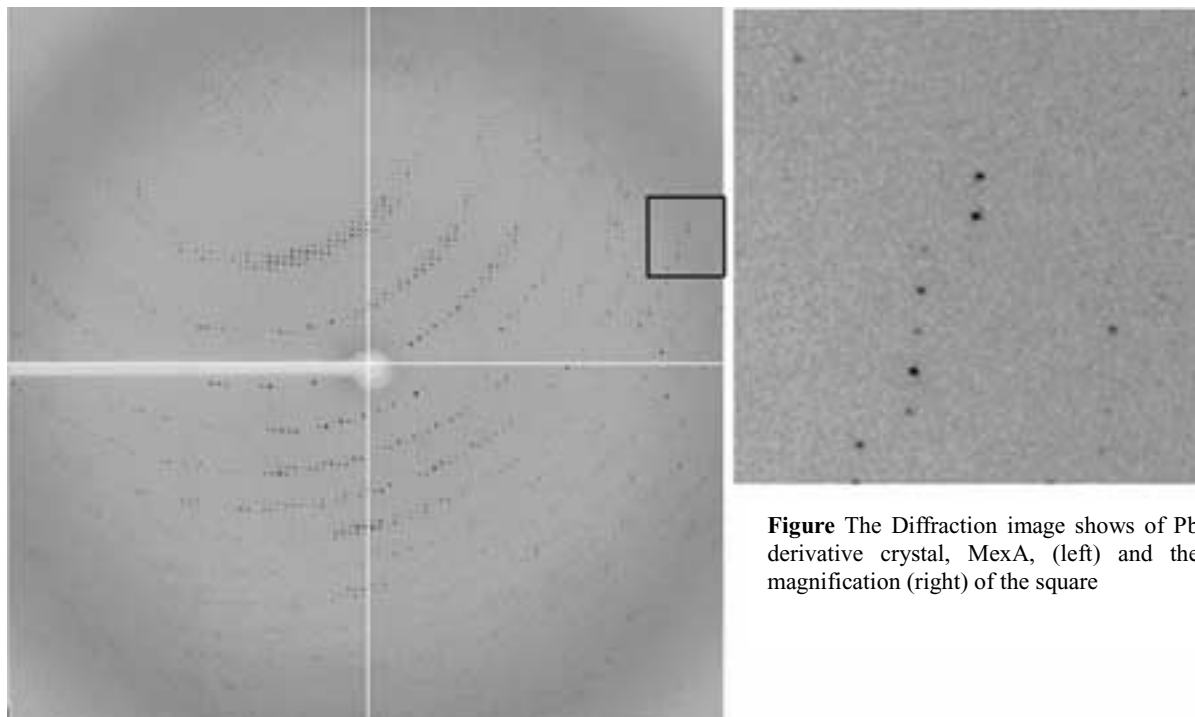


Figure The Diffraction image shows of Pb derivative crystal, MexA, (left) and the magnification (right) of the square