

## Structural analysis of bacterial transporter protein

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### Introduction

The MexAB-OprM efflux pump of *Pseudomonas aeruginosa* exports xenobiotics including antibiotics out of cells contributing to multiantibiotic of 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.

### Experiments and Results

We collected the data of native crystals using an ADSC detector and synchrotron radiation with 1 Å wavelength and 350mm distance at 95 Kelvin.

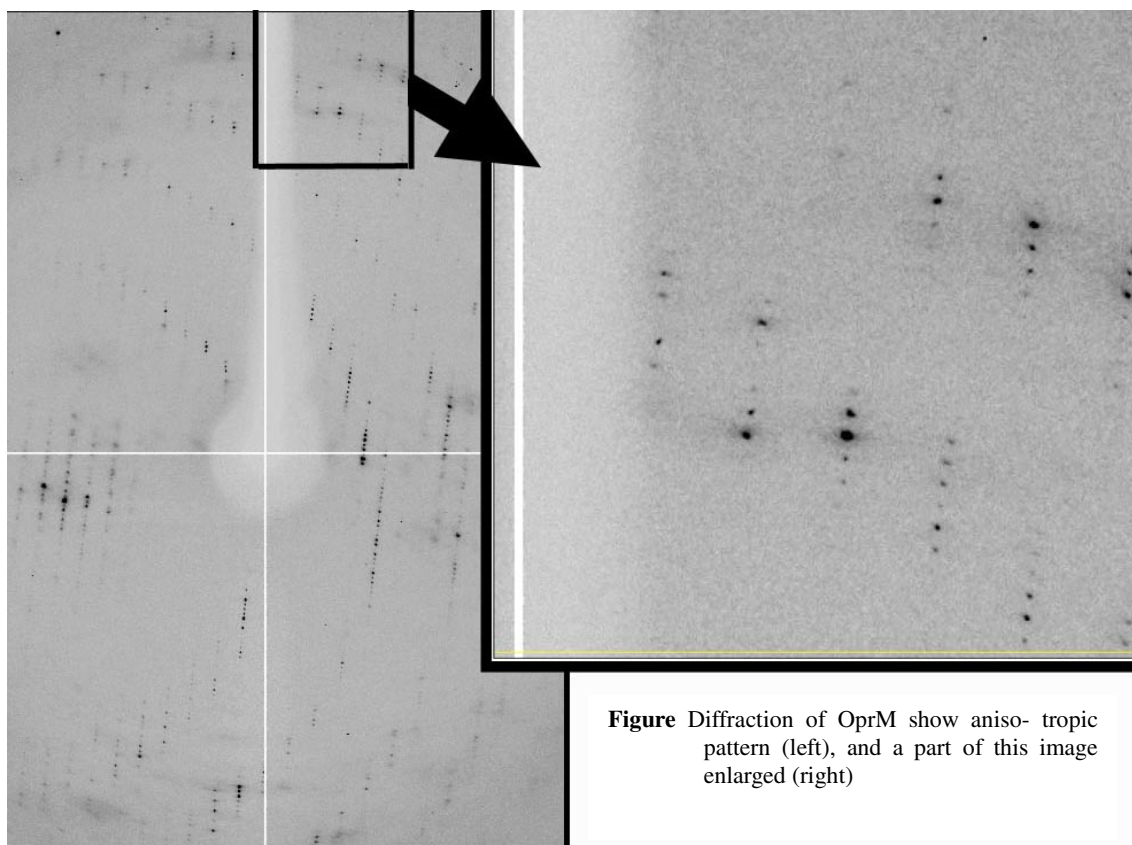
The data were processed using MOSFLM program package. OprM was belonging to rhombohedral space group R32 with unit cell parameters of  $a = b = 85.23 \text{ \AA}$ ,  $c = 1042.66 \text{ \AA}$ . The crystals diffracted beyond 3.4 Å (Figure right), but we have been perplexed with anisotropic diffractive pattern. (Figure left)

Data collections and analysis of derivative crystals are now in 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** Diffraction of OprM show anisotropic pattern (left), and a part of this image enlarged (right)