

### Crystal Structure of L-phenylalanine Oxidase

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L-phenylalanine oxidase (PAO) from *Pseudomonas* sp. P-501 catalyzes both oxidative deamination ( $\beta$ -phenylpyruvic acid is product) and oxygenative decarboxylation ( $\alpha$ -phenylacetamide is product). The enzyme contains two mol of noncovalent FAD. The enzyme is expressed as a proenzyme that has a noncatalytic polypeptide at the N-terminal end and is activated by proteolysis [1].

The proenzyme of PAO (proPAO) has been crystallized by the hanging-drop vapor-diffusion method using ammonium sulfate as a precipitant. The crystal belongs to space group  $P2_12_12$ , with unit-cell parameters ( $a = 141.8 \text{ \AA}$ ,  $b = 145.4 \text{ \AA}$ ,  $c = 82.2 \text{ \AA}$ ) and contains two molecules in the asymmetric unit. The X-ray diffraction data were collected to a resolution of  $1.9 \text{ \AA}$  at the NW-12 beamline in the Photon Factory.

We determined the crystal structure of proPAO using selenomethionine-derivative crystal and SAD method. The crystal structure was not able to solve by MAD method, because the crystal received big damage by the radiation and did not keep isomorphism between the data sets. Crystal structure of PAO is a dimer form. The active site is like a funnel. The prosequence enters the funnel and bonds to the active site residues. It thus appears that prosequence is a substrate mimic and keeps inactive form.

[1] Haruo S., *et al.*, *J. Biochem.*, 2004, **136**, 617.

**Keywords: flavoprotein, SAD, enzyme activity mechanism**