

## W0130

**Crystallization of a Large Single Crystal of  $\beta$ -lactoglobulin for Neutron Protein Crystallography.** D. Yagi<sup>1</sup>, Y. Ohnishi<sup>2</sup>, I. Tanaka<sup>1</sup>, N. Niimura<sup>1</sup>, <sup>1</sup>Ibaraki Univ., <sup>2</sup>Kaken, Hitachi City 316 8511, Japan.

$\beta$ -lactoglobulin is a typical model globular protein for studies of protein folding. The  $\beta$  sheets structure is formed through  $\alpha$ -helix structure in folding process. ( $\alpha$ - $\beta$  transition) The  $\alpha$ - $\beta$  transition includes the rearrangement of H-bonds from intra- $\alpha$ -helix to inter-  $\beta$  strands. In order to elucidate the  $\alpha$ - $\beta$  transition from the atomic view point of H-bonds, the neutron diffraction experiment of  $\beta$ -lactoglobulin has been scheduled.

Neutron diffraction needs a large single crystal of protein. The large single crystal of  $\beta$ -lactoglobulin (1mm $\times$ 0.4mm $\times$ 0.5mm in size) has been grown in the meta-stable zone on the basis of the crystallization phase diagram, which has been determined by a dialysis method. The quality of the crystal was assessed by the developed Wilson plot method. The preliminary neutron diffraction from the crystal has been carried out.