

**W0358**

**Crystal Structure of a Putative pduO-type ATP:cobalamin Adenosyltransferase from *Mycobacterium tuberculosis*.** Jin Ho Moon<sup>1</sup>, Anthony Kaviratne<sup>1</sup>, Minmin Yu<sup>2</sup>, Evan H. Bursey<sup>2</sup>, Li-Wei Hung<sup>3</sup>, Timothy P. Lakin<sup>4</sup>, Brent W. Segelke<sup>4</sup>, Thomas C. Terwilliger<sup>1</sup>, Chang-Yub Kim<sup>1</sup>, <sup>1</sup>Bioscience Div., Los Alamos National Laboratory, Los Alamos, NM 87545 <sup>2</sup> Physical Biosciences Div., Lawrence Berkeley National Berkeley, Berkeley, CA 94720 <sup>3</sup> Biological and Quantum Physics Group, Physics Div., Los Alamos National Laboratory, Los Alamos, NM 87545 <sup>4</sup> Biosciences Div., Lawrence Livermore National Laboratory, Livermore CA 94551.

ATP:cobalamin adenosyltransferase catalyze the final step in the conversion of Vitamin B<sub>12</sub> into coenzyme B<sub>12</sub> (adenosylcobalamin). Three classes of this enzyme have been identified cobA, pduO and eufT based on primary sequences. The gene coding Rv1314c from *Mycobacterium tuberculosis* classified to pduO type. The pduO members are associated with genes encoding adenosylcobalamin-dependent diol or glycerol dehydratase or methylmalony-CoA mutase. We have determined the crystal structure of a putative pduO-type ATP:cobalamin adenosyltransferase from *Mycobacterium tuberculosis* at 2.0 Å resolution by multiple wavelength anomalous dispersion experiments using bromide ion as anomalous scatterers. The monomer consists of a five-helix bundle and two short beta strands. And the oligomeric structure has shown to be trimer which is formed by the interactions between the helix.