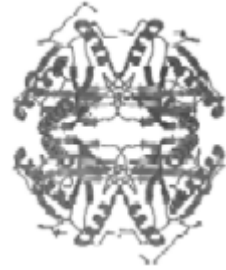


## E0038

**Crystal Structures of Chicken Muscle Lactate Dehydrogenase.** L. Grant, E.R. Greiner, J.M. Warfel, N. Polder, G. Watanabe, C. Smith, B. Rupp, X. Ouyang, S.R. Herron, C.R. Meyer, C. Srinivasan, K.A. Kantardjieff, *et al*, Dept. of Chemistry and Biochemistry and W.M. Keck Foundation Center of Molecular Structure, California State Univ., Fullerton, CA.

Lactate dehydrogenase (LDH) is a tetrameric, 331 residue oxidoreductase essential to ATP synthesis under anaerobic conditions which catalyzes the reversible reduction of pyruvate to lactate. Evolutionary alterations in the flexibility of the molecule and patterns of sequence conservation suggest the active site of LDH-A should be viewed as an extended unit involving most of the enzyme's structure for which substrate binding induces the loop region to fold over the active site. LDH-A was purified from chicken breast muscle and crystals obtained using Hampton screens via vapor diffusion. The native enzyme crystallized in space group  $P2_12_12_1$  with cell dimensions, in Å, of  $a = 84.04$  Å  $b = 126.78$  Å and  $c = 252.74$  Å. A putative pyruvate complex has been crystallized in space group  $C2$  with dimensions of  $a = 75.16$  Å  $b = 152.40$  Å  $c = 142.79$  Å and  $\beta = 93.5^\circ$ .



Crystals were flash cooled and shipped to the Stanford Synchrotron Radiation Laboratory where 1.92 Å native data were collected. The native structure has been solved by molecular replacement using porcine LDH-A as the probe. Data refinement and structure determination of complexed crystals has begun.