

W0402

Crystal Structure of a Putative Small Chain Acyl-CoA Transferase (YdiF) and its Complex with Acetyl-CoA. Erumbi S. Rangarajan^{1,2}, Yunge Li², Eunice Ajamian^{1,2}, Pietro Iannuzzi², Stephanie Kernaghan³, Marie Fraser³, Allan Matte², Mirosław Cygler^{1,2}, ¹Dept. of Biochemistry, McGill Univ. Montreal, Canada. ²Biotechnology Research Inst., NRC, 6100 Royalmount, Montreal QC H4P 2R2. ³Dept. of Biological Sciences, Univ. of Calgary, Calgary AB T2N 1N4.

CoA transferases are enzymes of varied substrate specificity and subunit composition. The *Escherichia coli ydiF* gene product is an acyl-CoA transferase that may catalyze the first reaction in short chain fatty acid degradation for the production of energy. The crystal structure of YdiF from *E. coli* O157:H7 has been determined by the multiple anomalous dispersion method and refined at 1.9 Å resolution with a final R-factor of 0.184 and R_{free} of 0.224. The structure belongs to the open α/β-protein class with a fold similar to that of SCOT from pig heart and GCT from *Acidaminococcus fermentans*.

Functional characterization of the YdiF tetramer shows that it acts with various CoA derivatives as donors and the corresponding carboxylic acids as acceptors. The activity profile suggests it to be an acetoacetyl-CoA:acetate CoA transferase. We present here the first co-crystal structure of this family of transferases, bound to acetyl-CoA, and provide mechanistic insight in to the action of this enzyme. Supported by the CIHR to M.C.

