

Cell Wall Biosynthesis, Folate Retention and Motility: Diverse Roles for a Common Enzyme Scaffold. C.A. Smith,¹ T. Deva², E.N. Baker,² ¹Stanford Synchrotron Radiation Laboratory, Menlo Park, CA 94025 USA, ²School of Biological Sciences, Univ. of Auckland, Auckland, New Zealand.

It is well known in biology that common enzyme architectures are used to catalyze similar reactions from diverse biological systems. The amide-bond ligase family, which includes the bacterial cell wall enzymes MurC, MurD, MurE and MurF, the folate polyglutamylation enzyme FPGS and cyanophycin synthetase, are examples of this. Although the main biological role of these enzymes is to form new amide bonds between diverse molecules, the common underlying reaction is the hydrolysis of ATP. Similarly, in the motor proteins myosin and kinesin, the underlying biochemical reaction is ATP hydrolysis. It is not surprising therefore, that these enzymes, along with many others which catalyze the conversion of ATP to ADP, all have a common scaffold buried within their 3-dimensional structures. We have determined the structure of *E. coli* MurC by Se-Met MAD, thus completing the set of four cell wall ligases from *E. coli*. Structural similarity and conformational diversity between the four ligases will be presented, along with comparisons with FPGS and other members of the ATPase superfamily.

