

**CRYSTAL STRUCTURE OF AN ENZYME INVOLVED IN THE BIOSYNTHESIS
OF ISOPRENOIDS:
4-diphosphocytidyl-2C-methyl-D-erythritol kinase from *E. coli*,
a potential drug target.**

L. Miallau^{1,2}, M. S. Alphey¹, L. E. Kemp¹, G. A. Leonard², S. M. McSweeney², S. Hecht³, A. Bacher³, W. Eisenreich³, F. Rohdich³ and W. N. Hunter¹

1 University of Dundee, Dundee, Scotland; 2 ESRF, Grenoble, France; 3 Technische Universität München, Garching, Germany.

Isoprenoids are a diverse family of compounds consisting of isoprene units (five-carbons units) and are involved in many biological functions such as electron transport, hormone based signaling, apoptosis, also they provide structural components of cell membranes. In contrast to mammals, some pathogenic agents such as those responsible for serious human disease including leprosy, malaria, bacterial meningitis, tuberculosis and certain types of pneumonia use the non-mevalonate pathway to synthesis those compounds. If we could disrupt this pathway, it might provide the first step in the development of a broad-spectrum antimicrobial agent. With this in mind, we solved the structure of the 4-diphosphocytidyl-2C-methyl-D-erythritol kinase (CDP-ME kinase). The resulting model reveals information as to the specificity and the catalytic mechanism of the enzyme.

References

Rohdich, F., Hecht, S., Bacher, A. & Eisenreich, W. Deoxyxylulose phosphate pathway of isoprenoid biosynthesis. Discovery and function of *ispDEFGH* genes and their cognate enzymes. *Pure Appl. Chem.* **75**, 393-405 (2003).