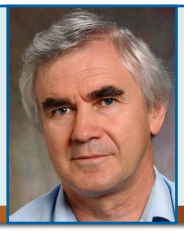

Protein Crystallography and Engineering Professor David Ollis

The group works at the interface between chemistry and biology. Our major interest is in working out how proteins function and how they might be modified for new and useful purposes. The laboratory routinely uses X-ray crystallography to obtain structures that can be used to better understand protein function. Directed evolution is used to produce mutant proteins that frequently have interesting properties that can be utilised in industrial and environmental applications. These mutants can also be analysed using a variety of techniques, including X-ray crystallography, to further understand the detailed mechanics of protein function.

In the past year, we have published a paper that describes the importance of enzyme inhibitors in the evolution of new enzymes. We have also developed methods to allow *Escherichia coli* to grow by using common pesticides, like Paraoxon, as the sole source of phosphorous. This latter discovery greatly facilitates the directed evolution of pesticide degrading enzymes. We have also solved the structure of the *N*-terminal domain of *E. coli* glutamine synthetase adenylyl transferase.

Structure of a Regulatory Protein Involved in Nitrogen Uptake by Bacteria

Over the last year the structure of the *N*-terminal domain of *E. coli* glutamine synthetase adenyl transferase (AT-N) was determined. This was a collaborative effort with a group in the James Cook University, Townsville. *(With P D Carr, Y Xu, and S Vasudevan [James Cook U])*

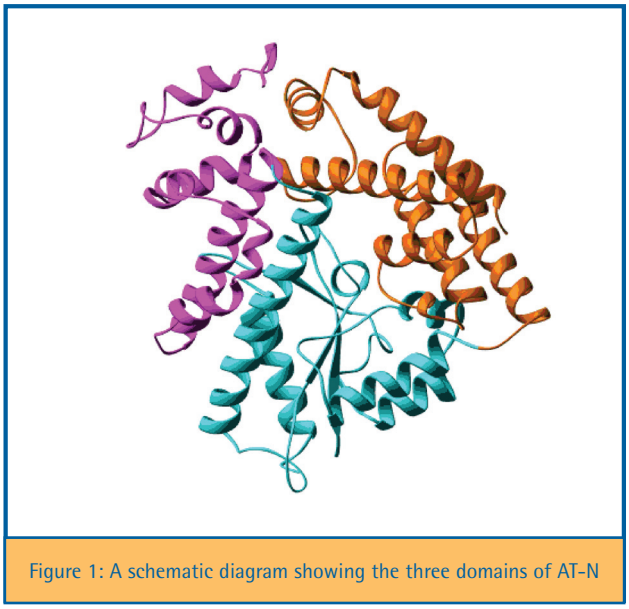

Figure 1: A schematic diagram showing the three domains of AT-N

Enzyme Engineering with an Organophosphate Degrading Enzyme

We have cloned and expressed an enzyme from *Enterobacter aerogenes* (GpdQ) that is capable of rapidly degrading phosphate diesters such as dimethyl phosphate. When this enzyme is co-expressed in *E. coli* with the organophosphate degrading enzyme from *Agrobacterium radiobacter* (OPDA), *E. coli* can use organophosphate pesticides as the sole form of phosphate for its growth. This has facilitated the directed evolution of OPDA and enabled us to improve the catalytic activity of OPDA towards a number of substrates. *(With P D Carr, J-W Liu, S Yu-McLoughlin)*

The β-subunit of the IL-5 Receptor – Identifying the Interaction Site

IL-5 is a regulator of growth, differentiation and activation of the white blood cell eosinophils. These cells are of major importance in the body's response to invasion by parasites and asthma inducing aeroallergens. Structure based site-directed mutagenesis of the β-common receptor successfully identified amino acid residues that are crucial for binding the cytokines IL-3, IL-5 and GM-CSF. *(With P D Carr, J Murphy, and I G Young [JCSMR, ANU])*

The Structure of an Intein

We have obtained the structure of the protein splicing intein from the DnaB gene of *Synechocystis sp.* PCC6803. *(With P D Carr, N E Dixon, and K Alexandrov, A Rak [Max-Planck Institute for Molecular Physiology, Dortmund, Germany])*

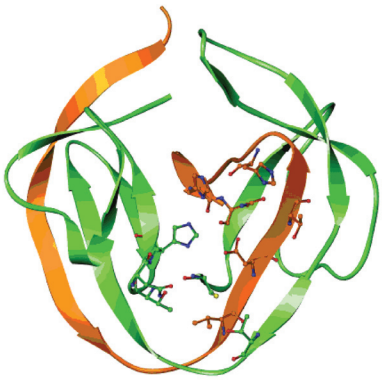

Figure 2: Schematic diagram of the DnaB intein.

http://rsc.anu.edu.au/research/ollis.php