s1.m6.05 **"The Temptation of Inactivity"**. <u>Richard</u> <u>Pauptit</u>, AstraZeneca, R&D, Global Sciences & Information, Macclesfield, UK. E-mail: richard.pauptit@astrazeneca.com

Keywords: Structure-Based Drug Design; Engineered Protein Constructs; Kinases

When using crystallography to support drug design in a pharmaceutical company environment, there is typically much time pressure and a large number of projects to balance. Whereas there is undeniable value in working on the exact version of the protein one would expect to encounter in vivo, the practicalities of delivering structural information on a relevant time scale have in most cases precluded fastidious working with the full unadulterated enzyme. Fragments of proteins may be more amenable to structural studies even if the activity is compromised. There are many occasions when an enzyme is deliberately inactivated to facilitate study: proteases may be mutated to avoid autodegradation, as kinases may be mutated to avoid autophosphorylation. Surrogate proteins may be used to study drug interactions when the protein of interest is recalcitrant to crystallisation. Of course there are limitations in interpretation of structural results when surrogate or modified protein is used, but in general the systems provide useful information which otherwise is not obtained. The talk will attempt to illustrate this.

s1.m7.o1 Crystal Structure of Cyanobacterial Photosystem II. Tina M. Iverson, Kristina N. Ferreira, Karim Maghlaoui, Jim Barber and <u>So Iwata</u>, *Imperial College London*, *Biological Sciences*, UK. E-mail: s.iwata@ic.ac.uk

Keywords: Membrane Protein; Photosynthesis; MAD

Photosystem II (PSII) is an integral-membrane multi subunit enzyme that uses light energy to initiate the electron transport chain in plants and cyanobacteria. This enzyme complex uses H_2O as the initial electron donor with molecular O_2 as the side product. The crystal structure of cyanobacterial PSII has been determined at 3.5 A resolution. From this data, side chains could be assigned to the model and 19 subunits were assigned. In addition, anomalous scattering techniques have been used to identify the positions of the metals in the Mn_4CaO_4 cofactor that catalyzes the water oxidation chemistry. Modification of the protein preparation and crystallization procedure were critical for obtaining crystals and may prove to be useful as general techniques for the crystallization of membrane proteins.