

**Friday 23 May 2014, at 10:30
Seminar Room**

SINGLE CRYSTAL ABSORPTION MICROSPECTROPHOTOMETRY AND X-RAY CRYSTALLOGRAPHY: THE PERFECT MARRIAGE.

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More than 90,000 structures are deposited in the PDB. For the majority of these structures functional properties in the crystalline state has not been tested. Lattice forces, crystal packing and conformation selection by crystallization might cause protein structures determined in the crystal to be different from the predominant and functionally-relevant conformation(s) present in solution. Single crystal polarized absorption microspectrophotometry is an approach perfectly suited to answer to the following questions: i) is the structure in the crystal the same as in solution?, ii) is a protein active in the crystal?, iii) can meta-stable intermediates be accumulated in the crystal, thus allowing cryo-crystallography-based structural determinations and structure-based functional mechanisms to be proposed on the basis of more than just the native protein structure? iv) Can meaningful structure-function correlations be obtained from thermodynamic and kinetic measurements carried out in the crystal?

Selected cases will be discussed during the seminar to answer these questions.

Overall, both “couple” fights and “couple” synergies contribute to a better understanding on how proteins work.

Not registered users are advised to arrive early, to allow time for issuing a visitor's pass at the entrance

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