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A multi-purpose neutron diffractometer at the ILL: the state-of-the-art of D19

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D19 is a four-circle monochromatic diffractometer installed on the thermal guide H11 at the Institute Laue-Langevin. It is a unique instrument that combines an intense thermal beam, a flexible monochromator/optical arrangement and a 120° horizontal by 30° vertical position sensitive He detector, to produce a diffractometer that is easily optimised for neutron diffraction studies of large chemical systems, fiber diffraction studies of natural and synthetic polymers, and crystallographic studies of small molecular systems. The total refurbishment of the instrument, funded by EPSRC, was completed in 2007. Since then, D19 has been producing valuable data in both fundamental research and industrial applications. The new challenges that face D19 include: faster data acquisition (e.g. optimisation of the strategy for sampling reciprocal space), measurement of smaller and smaller samples and new sample environments (for example a N2-cryostream for moderately low temperature measurements).

In order to illustrate the spread of science that can be studied on D19 few examples will be presented: i) the role of metal ions and hydrogen atoms in the reaction of D-xylose isomerase with sugar; ii) hydrogen bonds dynamics of ammonia on cellulose; iii) binding coordination and dynamics of dihydrogen ligands in transition metal catalytic systems; iv) the study of texture in submarine rocks.

Keywords: instrumentation, neutron, diffraction


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The recognition of endocytic signal sequences by the AP2 complex

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Membrane proteins are packaged for transport between the different membrane compartments of eukaryotic cells into small vesicles formed by an elaborate system of cytoplasmic proteins. Selection of cargo for vesicle formation at the plasma membrane (endocytosis) is generally mediated directly or indirectly by the heterotetrameric clathrin adaptor complex AP2, which binds short sequence recognition motifs of two types, YxxΦ (tyrosine-based motif, where Φ is a hydrophobic residue) and [DE]xxxLL (acidic dileucine motif). The structure of the 200KDa AP2 “core” crystallised in the absence of peptides showed a closed conformation, with binding sites for both types of motifs blocked, and indeed AP2 in solution does not bind motif peptides. AP2 is activated by binding to negatively charged membranes containing phosphatidylinositol-(4,5)-bisphosphate. We were able to trap the activated “open” conformation in crystals grown with a YxxΦ peptide, and this structure shows a large conformational change compared to the closed “locked” conformation, with the YxxΦ-binding domain moving out of the “bowl” formed by the other subunits. This places both peptide sites on the positively-charged face of the complex, allowing simultaneous interaction with cargo motifs and the membrane. Thus AP2 functions as a plasma membrane-activated switch for endocytic cargo recognition.

Keywords: membrane associated proteins, protein-peptide interactions, conformational change


Keywords: x-ray, synchrotron, coherence.