## **KNI** Regulation of ArfGTPases in Cellular Traffic Jacqueline Cherfils, *Laboratoire d'Enzymologie et Biochimie Structurales, CNRS, Gif-sur-Yvette, France.* E-mail: cherfils@lebs.cnrs-gif.fr

Small GTPasesactuate a variety of functional switches that are pivotal for cell dynamics. The GTPases witch is turned on by guanine nucleotide exchange factors (GEFs), which stimulate the dissociation of the tightly bound GDP nucleotide and its replacement by GTP, and turned off by GAPs, which accelerate the intrinsically slow hydrolysis of GTP. In this talk, I will focus on ArfGTPases, which are central regulators of almostevery aspect of cellular traffic, and are involved in human diseases including infections and cancer. ArfGTPases are activatedon cellular membranes by different Arf GEFs families, which carry a common GEF domain (Sec7 domain), associated with various non-catalytic domains. Recent studies combining crystallography, SAXS and NMR with biochemical reconstitutions of the GDP/GTP exchange reaction on artificial membranes have uncovered sophisticated regulatory mechanisms, which pave the way for inhibitorystrategies.

## Keywords : Small GTPases ;Traffic ; Inhibition

**KN2** Structure solution from powder diffraction; new developments, applications and avenues. <u>Maryjane</u> <u>Tremayne</u>, School of Chemistry, University of Birmingham, Edgbaston, Birmingham, B15 2TT, UK. E-mail: m.tremayne@bham.ac.uk

Over the last two decades, the development of crystal structure solution techniques from powder diffraction data has revolutionised our expectations of what can be achieved within this field. Advances in instrumentation, the development of new algorithms and a change in ethos and approach to structure solution has taken us from the determination and refinement of small molecules to the structural investigation of proteins from powder diffraction data. In this lecture, key advances in the field will be discussed, with a focus on those developments that have led directly to significant breakthrough both in the complexity and the number of organic crystalline structures determined by powder diffraction data [1-3]. The impact of structure solution approaches such as direct space algorithms, charge flipping and complementary techniques will be discussed, although the main emphasis of the presentation will be on the application of these techniques across fields in which knowledge of the crystal structure of molecular solids is crucial. Examples will be presented to demonstrate the current state-of-the-art in application, including forms from across the pharmaceutical and biochemical sciences, and the structure elucidation of molecular materials designed with particular structure-property relationships in mind. Possible new developments will then be discussed in the context of data limitation, accuracy and precision of structures and potential new avenues of application and development.

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Keywords: powder diffraction; organic crystalline structures; structure determination methods