



USER MEETING 2016

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National Centre for Synchrotron Science



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Observing proteins at play: structural techniques to probe function

Friday, 25 November 2016 13:30 (30)

We have used protein crystallography and small angle X-ray scattering to understand the way that enzymes respond to remote signals – a process known as allostery (from the Greek *allos* meaning “other” and *stereos* meaning “solid”). Allostery is critical to the control of metabolism, and although allostery has been known for many years, it is only more recently that the molecular networks that govern this communication in proteins have begun to be unravelled in detail.

We have used a combination of structural, computational and biophysical approaches to examine the allosteric function of several enzymes that operate at important control points in key metabolic pathways. We have used crystallography and small angle X-ray scattering to demonstrate significant changes in structure and dynamics are part of the allosteric response. Our studies have revealed the details of the molecular events that are associated with the allosteric response and shed light on the evolution of allosteric properties by enzymes.

Keywords or phrases (comma separated)

SAXS, Allostery, enzyme regulation,

Are you a student?

No

Do you wish to take part in the Student Poster Slam?

No

Are you an ECR? (<5 yrs since PhD/Masters)

No

What is your gender?

Female

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