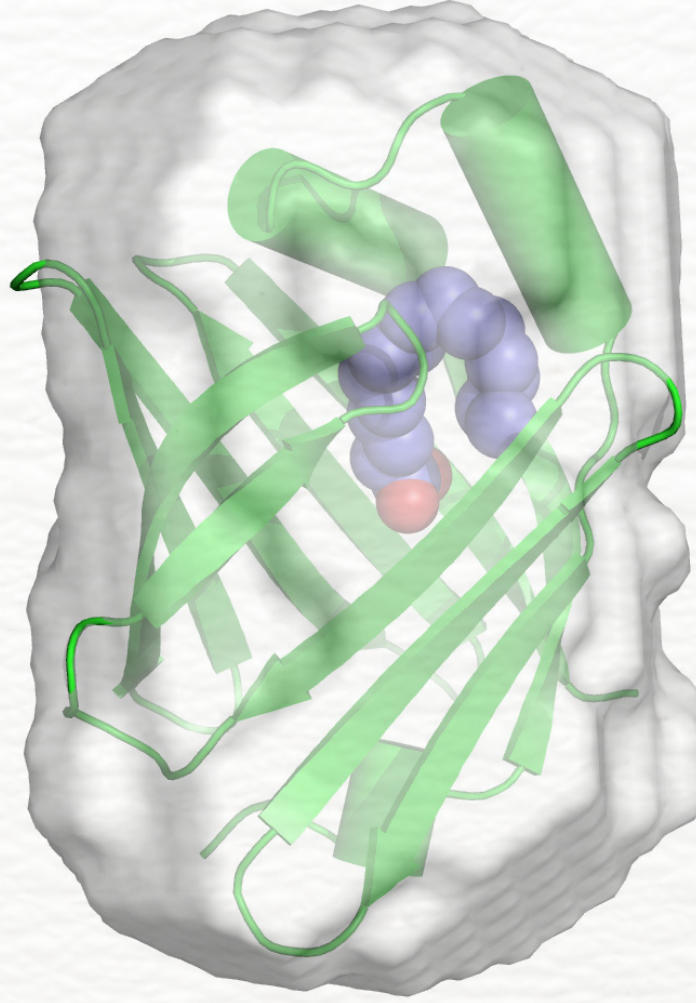


MINISYMPOSIUM

HYBRID STRUCTURAL APPROACHES FOR CLUES TO PROTEIN FUNCTION

27 MAY 2011
14:00 HALL B



Greasy encounters: Structural biology of myelin, a multilayered membrane in the vertebrate nervous system

Petri Kursula

Centre for Structural Systems Biology (CSSB-HZI), DESY, Hamburg, Germany and Department of Biochemistry, University of Oulu, Oulu, Finland

The rapid transduction of nerve impulses is mandatory for vertebrates. This is made possible by the presence of the myelin sheath, a tightly packed multilayered membrane structure wrapped around selected axons in the nervous system. Biochemically, myelin is a unique biological membrane, carrying a specific set of proteins. Many of the myelin proteins are involved also in neurological disease, such as multiple sclerosis. Our project focuses on obtaining detailed structure-function information on the myelin-associated proteins, most of which are either integral of peripheral membrane proteins. Selected examples from our research projects, utilizing synchrotron-based and complementary biophysical and biochemical methods will be discussed.



AGENDA

the event starts at 14:00
and takes place in lecture hall B Kemencentrum

14⁰⁰ Greasy encounters: Structural biology of myelin, a multilayered membrane in the vertebrate nervous system

Petri Kursula

*Centre for Structural Systems Biology, DESY, Hamburg, Germany
& Department of Biochemistry, University of Oulu, Finland*

Coffee break

15¹⁵ Unexpected features of yeast LTA4 Hydrolase

Marjolein Thunnissen

CMPS, Lund University

16⁰⁰ Using complementary structural biology methods to study allosteric regulation in ribonucleotide reductase

Derek T. Logan

CMPS, Lund University

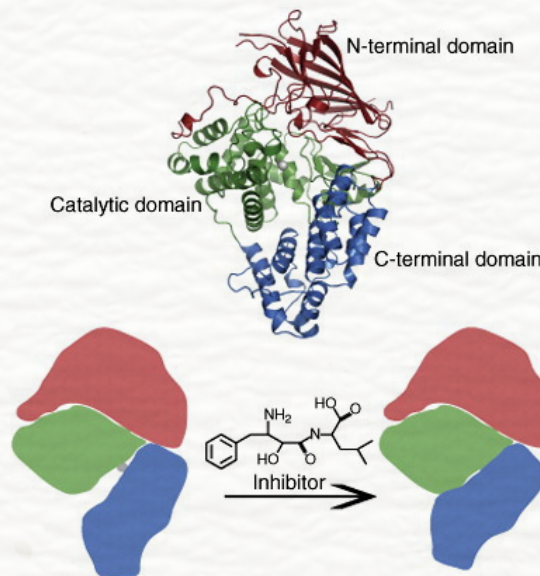
after the talks
pub in CMPS coffee room

Unexpected features of yeast LTA4 Hydrolase

Marjolein Thunnissen

CMPS, Lund University, Sweden

Vertebrate leukotriene A(4) hydrolases are bifunctional zinc metalloenzymes with an epoxide hydrolase and an aminopeptidase activity. In contrast, highly homologous enzymes from lower organisms only have the aminopeptidase activity. From sequence comparisons, it is not clear why this difference occurs. In order to obtain more information on the evolutionary relationship between these enzymes and their activities, the structure of a closely related leucine aminopeptidase from *Saccharomyces cerevisiae* that shows only a very low epoxide hydrolase activity was determined. An unexpected opening of the active site was observed and both this and the evolutionary relationships between the enzymes will be discussed.



Using complementary structural biology methods to study allosteric regulation in ribonucleotide reductase

Derek T. Logan

CMPS, Lund University, Sweden

Ribonucleotide reductases (RNRs) are one of the most essential enzymes for all cellular life, being solely responsible for the last dedicated step of synthesis of the building blocks of DNA, the deoxyribonucleoside triphosphates, or dNTPs. Since the discovery of RNRs by Peter Reichard in Sweden in the late 1950s they have been the subject of intensive research due to their complex radical chemistry and equally complex allosteric regulation. The latter occurs on two levels: overall activity and substrate specificity. The activity must be regulated in order to ensure the correct overall levels of dNTPs as a function of cellular life cycle. ATP activates the enzyme while dATP turns it off. The substrate specificity must be regulated to ensure balanced dNTP pools, disturbance of which can lead to serious disorders. Our studies and those of others have led to an increasingly detailed picture of the structural basis for allosteric regulation of substrate specificity, but activity regulation has remained more obscure. In recent years the role of large oligomeric protein complexes in this regulation has been re-emphasized. Their stoichiometry differs between prokaryotes and eukaryotes. We are studying these using a combination of X-ray crystallography, cryo-electron microscopy and small angle X-ray scattering, in order to unravel the secrets of differential regulation by ATP and dATP as well as understand how this regulation has developed during evolution.

