

**Friday, March 14, Session II****L9****MACROMOLECULAR CRYSTALLOGRAPHY WITH THE PHOTON 100 DETECTOR****Vernon Smith***Bruker AXS, Germany*

In recent years, a number of significant developments have taken place in the technology of home-lab single crystal diffraction instruments. These developments are driven by the need to meet the requirements of laboratories addressing increasingly challenging projects.

This presentation will provide an introduction to modern home-lab X-ray instrumentation and discuss how the characteristics of the PHOTON 100 detector - contribute to the collection of high quality:

Several challenging cases will be discussed to illustrate how the experimental set-up influences data quality:

Collecting data for atomic resolution structure determination

*De novo* structure determination of native proteins using single wavelength anomalous dispersion (SAD)  
Structure determination of large macromolecular complexes crystallising with very large unit cell dimensions.

**L10****LATEST DEVELOPMENTS FOR LIFE SCIENCE FROM RIGAKU****Jiří Maršík***Rigaku Innovative, Prague***L11****X-RAY STRUCTURAL ANALYSIS OF CARBONIC ANHYDRASE AND CARBORANE-BASED INHIBITORS COMPLEXES****Jiří Brynda<sup>1,2</sup>, Pavel Mader<sup>1,2</sup>, Václav Šícha<sup>3</sup>, Milan Fábry<sup>1</sup>, Bohumír Grüner<sup>3</sup>, Petr Cígler<sup>2</sup>,  
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Human carbonic anhydrases (CA) are zinc metallo-enzymes that play an important role in many physiological processes. To date, 15 human CA isozymes have been identified. Many experimental evidence also suggests involvement of CAs in various pathological processes, e.g. tumorigenicity, thus, many CA isozymes are recognized as diagnostic and therapeutic targets. About 30 CA inhibitors are used clinically as drugs. The traditional CA inhibitors contain a sulfonamide or sulfamide moiety that coordinates the zinc cation located in the CA catalytic site. Although

the conical active site clefts of different human CA isoenzymes are conserved, variations in aminoacid residues exist at the entrance to the active site. These surface pockets with different shape and hydrophobicity can be exploited to design specific inhibitors. With the help of manual molecular docking into the active site of CAII, we designed new molecule, which contains a sulfamide group connected to a carborane cluster intended to optimally fill the enzyme active site entry.