Poster Presentation

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Macromolecule solution studies with high brilliance, low background SAXS camera

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Small angle x-ray scattering technique is a powerful method to study the 3D envelope of proteins or the arrangement of individual domains in protein complexes through minimized sample preparation. SAXS is thus becoming a mainstream technique to study macromolecules in solutions in an interdisciplinary approach combined with NMR and Electron Microscopy. This is symbolized by a fast growing number of structures published, and initiatives on SAS structures publication guidelines[1]. Progress in instrumentation also led to emergence of high quality laboratory bio SAXS equipments. We will present the impact of relevant equipment features on structure characterization through data measurements examples on various protein samples. Using a high flux with controlled beam properties (size and divergence) at detector plane is important to achieve sufficient signal to noise at larger wave vectors (Q) range together with the capability to measure large protein complexes (related to minimum wave vector detectable, Qmin). We will be discussing figure of merits for evaluating data quality at high Q range and presenting the impact of incident flux and various detection schemes on such criteria. Data measurements on large protein complexes will be shown highligthing the impact of instrument Qmin. Low backgroung scattering generation inside SAXS camera and low noise detection are other critical requirements for faithful and accurate sample to buffer data subtraction. A new generation of scatterless collimation with variable resolution, and improved sample environments open the door to unprecedented ratios of primary beam intensity to background and to measurements on weakly scattering samples. Impact on data quality will be emphasized. Data processing and struture modeling of various proteins of different sizes acquired with laboratory SAXS camera using low maintenance high brighness source will be presented and compared to synchrotron data.

[1] *Jacques et al. (2012) Acta Cryst. D64, 620*

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