RECENT APPLICATIONS OF SOLUTION SAXS IN STRUCTURAL BIOLOGY AT THE UNIVERSITY OF AARHUS

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Small-angle x-ray scattering has proven to be an extremely important tool in structural biology, as a low-resolution tool complementary to high resolution protein crystallography. Following the installation of a laboratory-based instrument, at the University of Aarhus in 2001, numerous studies on biomacromolecules in solution have been carried out. The instrument is optimized for solution scattering and provides high quality data. This together with the flexible access to the instrument makes it ideal for studies of delicate biological samples. The talk will review three recent studies in which solution SAXS has provided key information. The first study concerns the yeast elongation factor eEF3[1] which serves an essential function in the translation cycle of fungi. SAXS shows that the solution structure is highly dependent on pH and that at physiological pH, a rotation of one domain in eEF3 of approximately 120^{o} takes place so that a more elongated conformation is formed. In the second study, Exon Junction Core (EJC) complex from higher eukaryotes was investigated[2]. The exon junction complex is organized around a stable core, which serves as a binding platform for numerous factors that influence messenger RNA function. The solution structure of the eukaryotic initiation factor 4AIII (eIF4AIII) which constitutes the central part of the EJC complex, as well as eIF4AIII in complex with a fragment of one of the other four proteins of the EJC complex, MLN51, was investigated. It was shown that the eIF4AIII in both cases adapt an open conformation. For the eIF4AIII+MLN51 it was possible to add the missing flexible parts to the structure. The third example concerns the Mannan-binding lectin[3] (MBL) which is a classic example of a pattern recognition molecule with important roles in innate immunity against microbial infections. The solution scattering SAXS analysis shows that the large MBL complex in solution is folded into a ramified structure with a striking rotational symmetry and a structure permissive of elongation by unbending. Comparison of the structure of the part for which the crystal structure is known suggests a significant conformational change in this part in solution.

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