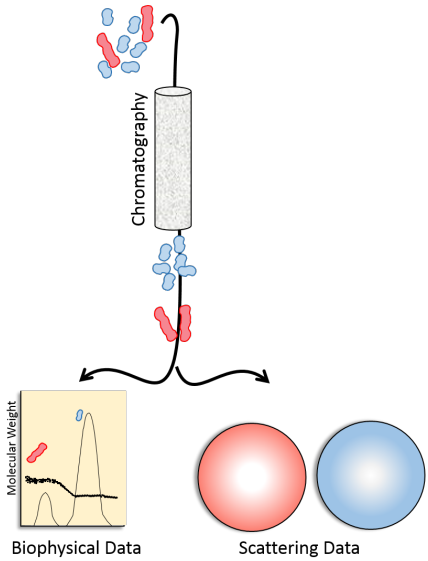

Figure 1.

Keywords: in-line purification, alternative methods, biophysical characterization

MS1-P3 Small-Angle-X ray-Scattering (SAXS) studies of the low-resolution structure of the ribosomal GTPase EFL1, the SBDS protein and their complex

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Ribosome biogenesis is closely linked to the cell growth and proliferation. Dysregulation of this process causes several diseases collectively known as ribosomopathies. One of them is the Shwachman-Diamond Syndrome, and the SBDS protein mutated in this disease participates with EFL1 in the cytoplasmic maturation of the 60S subunit. Recently, we have shown that the interaction of EFL1 with SBDS resulted in a decrease of the Michaelis-Menten constant (K_M) for GTP and thus SBDS acts as a GEF for EFL1 (1). Subsequent studies demonstrated that SBDS debilitates the interaction of EFL1 with GDP without altering that for GTP (2). The interaction of EFL1 alone or in complex with SBDS to guanine nucleotides is followed by a conformational rearrangement. Understanding the molecular strategy used by SBDS to disrupt the binding of EFL1 for GDP and the associated conformational changes will be key to understand their mode of action and alterations occurring in the disease. In this study, we aim to show the conformational changes resulting from the interactions between EFL1 and its binding partners, the SBDS protein and the guanine nucleotides using SAXS technique (3). SAXS provided structural information of the proteins (Fig.1) and their conformational changes (4,5).

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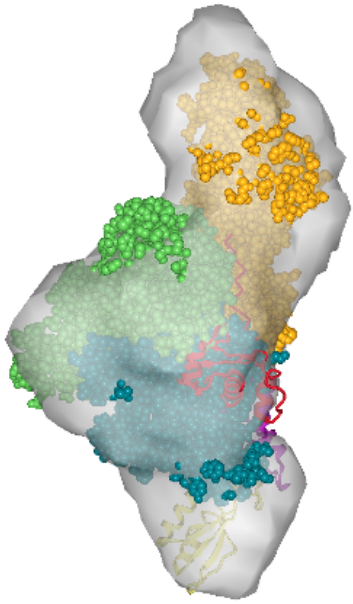

Figure 1. Efl1-Sdo1 complex model fitted into SAXS map. SAXS map obtained from ab-initio model [DAMMIF: Franke, D. and Svergun, D.I. (2009) *J. Appl. Cryst.*, 42, 342-346]. Complex model obtained by a simutaneous docking into SAXS map [Sculptor: Birmans *et al* (2011). *J. Struct Biol*. 173 428-435]

Keywords: Shwachman-Diamond Syndrome, Elongation factor-like 1, ribosomopathy, biosaxs

MS2 Development of new types of sample preparation (both XFEL & synchrotrons)

Chairs: Jörg Standfuss, Gwyndaf Evans

MS2-P1 Structure Determination of Membrane (and Soluble) Proteins Using In Meso In Situ Serial X-ray Crystallography at Room and Cryogenic Temperatures

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The lipid cubic phase continues to grow in popularity as a medium in which to generate crystals of membrane and soluble proteins for high-resolution X-ray structure determination (**1, 2**). To date, the PDB includes 313 records with 105 unique structures attributed to the *in meso* method (**2**). The most successful *in meso* protocol uses glass sandwich crystallization plates, but they are challenging to harvest crystals from. Here, we present a novel *in meso in situ* serial crystallography (IMISX) method which employs a thin cyclic olefin copolymer (COC) windowed plate for *in situ* data collection (**3**). The bolus of mesophase in which crystals grow on the plate contains tens to hundreds of crystals that are clearly visible with an in-line microscope at macromolecular crystallography synchrotron beamlines at both room and cryogenic temperatures. The data acquisition software DA+ GUI at the PX I (X10SA) and PXII (X06SA) beamlines at the Swiss Light Source (SLS) provides a semi-automated 'select and collect' protocol for serial crystallographic data collection with IMISX samples. The method has been demonstrated with β_2AR, AlgE, $PepT_{St}$ and DgkA as model membrane proteins and with lysozyme and insulin as test soluble proteins at room and/or at cryogenic temperatures (**3, 4**). Structures were solved by molecular replacement or by experimental phasing using bromine and native sulfur SAD methods to