regulatory proteins essential for this process. SM proteins are thought to regulate fusion by interaction with the SNARE protein Syntaxin (Sx). Different binding modes for the SM-Sx interaction have been observed: binding to the closed conformation (neuronal system [1]) binding to the N-terminus of the Sx protein (yeast Golgi-ER system [2] and GLUT4 system [3,4]) and to the SNARE ternary complex (yeast exocytotic system [5]). The role of SM proteins in vesicle fusion has been disputed partly due to the different binding modes. Binding to the closed mode inhibits the formation of the ternary complex, negatively regulating vesicle fusion. Whereas binding via the N-terminus of Sx facilitates binding to the ternary complex and positively regulates fusion [3]. Our research focus is on Munc18c and Sx4, the SM and Sx protein respectively, involved in GLUT4 vesicle transport to the plasma membrane in response to insulin signalling. We have used biophysical techniques such as ITC and small angle scattering (SAS) to further characterize the molecular details of the Munc18c-Sx4 interaction. The findings using these techniques, specifically the possible conformational changes of Sx4 on binding to Munc18c will be discussed.

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Keywords: protein-protein interactions, biophysical methods, SAS

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Atomic-level models of the bacterial carboxysome shell
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The carboxysome is a bacterial microcompartment, roughly 1000Å in diameter, that sequesters enzymes involved in carbon fixation. The shell is built from several thousand protein subunits and resembles a viral capsid. We have previously solved the crystal structures of hexameric carboxysome shell subunits, which suggest their roles in forming flat facets of the polyhedral shell (Kerfeld, et al., Science 2005). There are three structures of homologous hexameric shell proteins solved from one class of carboxysome (beta-type) and one structure solved from another class of carboxysome (alpha-type) (Tsai, et al, PloS Biol 2007). The comparison of these hexameric proteins shows interesting characteristics in sheet packing and residue interactions between adjacent hexamers. Furthermore, the recently determined structures of CcmL and CsoS4A subunits from the two classes of carboxysomes possess predominantly β-sheet structures and assemble as pentamers whose size and shape are compatible in forming icosahedral vertices of the protein shell. Combining these pentamers with the hexamers gives two plausible, preliminary atomic models for the carboxysome shell (Tanaka, et al., Science 2008).

Keywords: photosynthesis, membrane proteins, anomalous diffraction

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Crystallization and structure determination of the phycobilisome complex
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