[MS5-P43] Crystal structure of the bacterial type II secretion system secretin/pilotin complex Shuang Gu, Saima Rehman, Richard W. Pickersgill.

Chemistry and Biochemistry Division, SBCS, Queen Mary University of London, London E1 4NS
E-mail: s.gu@qmul.ac.uk

We are investigating the architecture of the type II secretion system from the inner membrane platform to the outer membrane secretin/ pilotin complex. Here we present our work on the secretin/pilotin complex. The secretins are a family of large multimeric channels in the outer membrane of Gram- negative bacteria that are involved in protein export [1-4]. In *Dickeya dadantii* and many other pathogenic bacteria a lipoprotein pilotin targets the secretin subunits to the outer membrane allowing a functional type II secretion system to be assembled [5,6]. Electron microscopy reveals the pilotin as radial spokes protruding from the secretin dodecamer [7,8]. We established that the extreme C-terminal region of the secretin becomes ordered on binding to the pilotin; that the pilotin is an unusual 4 α-helical bundle and we elucidated the crystal structure of the C-terminal peptide of the secretin subunit bound to its cognate pilotin [9,10]. In this complex the secretin peptide forms just under four turns of α-helix the third turn of which binds tight up against the first helix of the pilotin so that the hydrophobic residues of the secretin helix can bind to the hydrophobic surface of the pilotin. The secretin helix binds parallel to the first part of the forth helix of the pilotin and an N-capping aspartate encourages helix formation and binding by interacting favourably with the helix dipole of the helical secretin peptide. The structure of the phytopathogenic *Dickeya dadantii* secretin/ pilotin complex described here is a paradigm for this interaction in the OutS-PulS family of pilotins which is essential for the correct assembly of the type II secretin system of several potent human adversaries including enterohemorrhagic *E. coli* and *Klebsiella oxytoca*.

Keywords: type II secretion system; secretin/pilotin complex

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