

## Electron Crystallography of the *E. coli* Outer Membrane Protein Wza<sub>K30</sub>

C.M. Hill\*, J. Nesper\*\*, C. Whitfield\*\* and G. Harauz\*

\*Department of Molecular Biology and Genetics and \*\*Department of Microbiology,  
University of Guelph, Ontario, Canada, N1G 2W1

The surface-exposed outer membrane lipoprotein Wza<sub>K30</sub> of *E. coli* translocates the K30 capsular polysaccharide to the exterior face of the cell. Transmission electron microscopy of negatively stained Wza<sub>K30</sub> preparations has shown that Wza<sub>K30</sub> peptides assemble into a multimeric ring structure with an apparent central pore large enough to permit the passage of a filamentous polysaccharide [1]. Here we present structural data obtained by using a two-dimensional crystallization approach for integral membrane proteins developed by Lévy et al. [2].

A recombinant form of Wza<sub>K30</sub> incorporating a C-terminal hexahistidine tag was purified from sodium dodecyl sulphate-solubilised outer membranes via Ni<sup>2+</sup> affinity chromatography and solubilised in the detergent SB3-14. Planar crystals of Wza<sub>K30</sub> multimers were then obtained by incubating the preparation under a monolayer incorporating an equal proportion of *E. coli* lipids and a lipid containing a nickel-chelating headgroup. Binding of the hexahistidine tags to the nickel ions presented by these latter lipids permitted concentration of Wza<sub>K30</sub> at the monolayer surface. Detergent was then removed in the presence of free *E. coli* lipid by the incorporation of polystyrene BioBeads<sup>®</sup>. It is proposed that this method results in the replacement of detergent with lipids from the aqueous phase, reconstituting the protein within a bilayer matrix [2].

Upon mounting, dehydration and staining with 2% uranyl acetate, planar arrays of Wza<sub>K30</sub> exhibiting varying degrees of regularity were observed. The individual ring multimers were 7.6 nm in diameter (Figure 1) and were arranged in a square lattice with spacings of 1 nm (Figure 2). These crystals were readily reproducible and work is ongoing to collect a large number of micrographs for averaging and extraction of structural detail by the IMAGIC-5 image processing software package [3].

### References and Acknowledgements

- [1] J. Drummelsmith and C. Whitfield, *EMBO J.* 19 (2000) 57.
- [2] D. Lévy et al., *J. Struct. Biol.* 127 (1999) 44
- [3] M. van Heel et al., *J. Struct. Biol.* 116 (1996) 17.
- [4] This work was supported by the Canadian Institutes of Health Research and the Natural Sciences and Engineering Research Council of Canada.

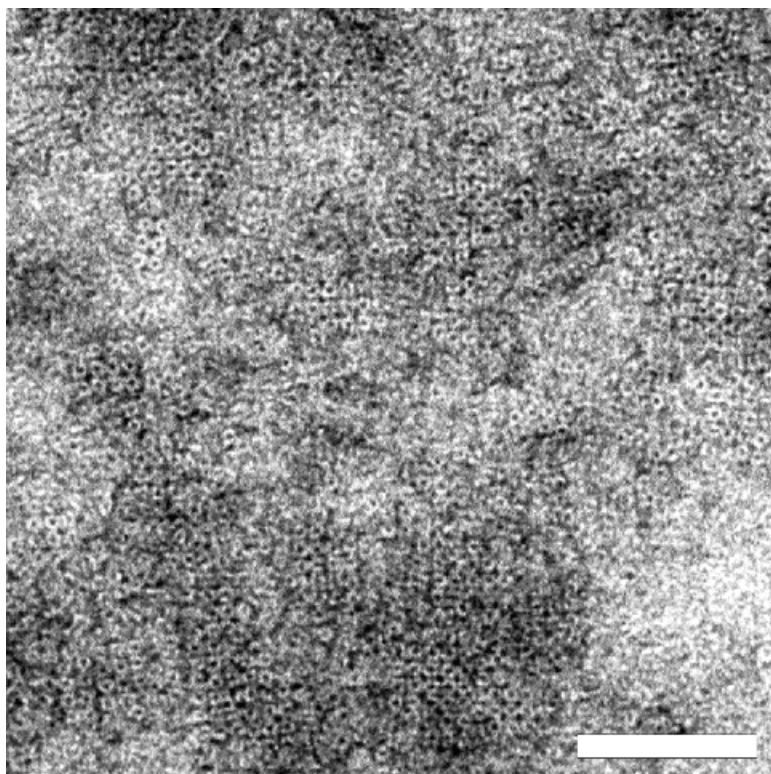


Figure 1  
Planar arrays of anchored  $wza_{K50}$ .  
The protein appears as a ring with a stain filled central core.  
Nominal magnification 20,000x.  
Scale bar represents 100 nm.

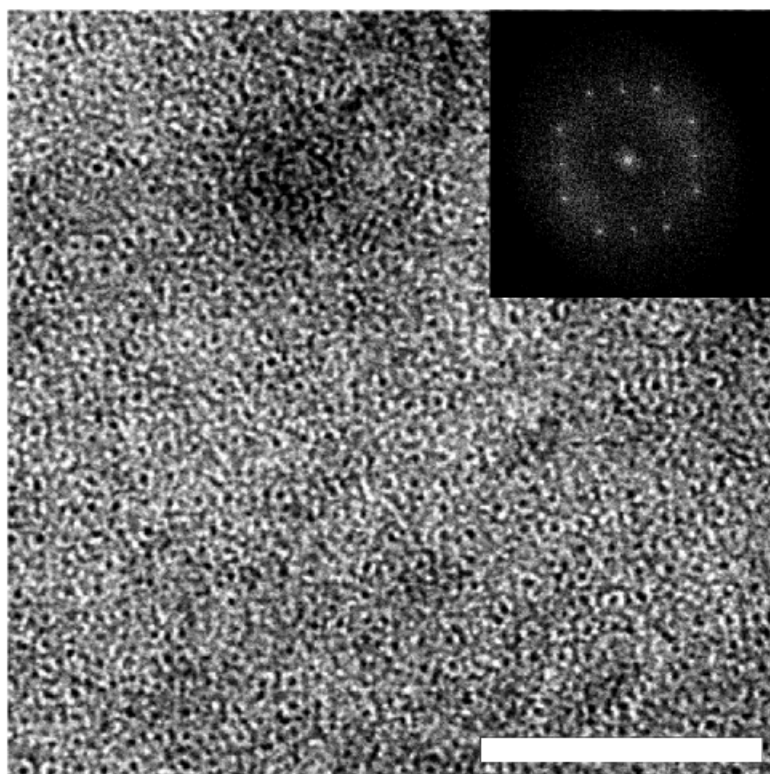


Figure 2  
Ordered planar arrays of anchored  $wza_{K30}$ . *Inset:* Fourier transform analysis reveals two orders of regularity.  
Nominal magnification 31,500x.  
Scale bar represents 100 nm.