

Exploiting contrast variation in Small-Angle Neutron Scattering to resolve the individual subunit structures of a membrane protein complex

Christopher L. Johnson¹, Luke A. Clifton², Alexandra Solovyova¹, Phil Callow³, Kevin L. Weiss⁴, Helen Ridley¹, Anton P. le Brun⁴, Stephen A. Holt⁴, Jeremy H. Lakey¹.

¹Institute for Cell and Molecular Biosciences, The Medical School, Newcastle University, Newcastle, United Kingdom, ²ISIS Spallation Neutron Source, Rutherford Appleton Laboratory, Harwell Science and Innovation Campus, Didcot, United Kingdom, ³Institut Laue Langevin, Grenoble, France, ⁴Bragg Institute, Australian Nuclear Science and Technology Organisation, Kirrawee DC, NSW, Australia.

We wish to understand the mechanism by which colicins translocate across the outer-membrane of competing bacteria to mediate cell death. Pore-forming colicin N hijacks *E. coli* outer-membrane protein OmpF and exploits it as both a receptor and translocator to cross the outer-membrane [1]. It is currently a matter of debate if the translocation route taken by colicin N is through the OmpF internal pore or via the external protein-lipid interface. Recent electron microscopy data from our laboratory suggests the latter route for translocation [2]. In order to re-address this question we undertook Small-Angle Neutron Scattering (SANS) experiments. By using a combination of deuterated OmpF and hydrogenated colicin N we were able to define the three dimensional structure of the colicin N-OmpF complex. This revealed that colicin N inserts into clefts on the outside of the OmpF trimer, supporting the case for translocation via the protein-lipid interface. To our knowledge, this is the first example of exploiting contrast variation in SANS to resolve the individual subunit structures of a membrane protein complex.

1. El Kouhen, R., et al., Eur J Biochem, 1993. **214**(3)
2. Baboolal, T.G., et al., Structure, 2008. **16**(3)