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Understanding the interaction between the *Proteus mirabilis* Scs proteins using neutron scattering

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Correctly forming disulphide bonds is critical to the folding of a wide variety of proteins. Bacterial virulence factors are one class of proteins containing disulfide bonds, thus, an approach to disarm virulent bacterial might involve shutting down the machinery involved in the formation of disulfide bonds. The suppressor of copper sensitivity (Scs) proteins form part of the disulfide bond forming machinery in bacteria, and it is hoped that determining the structure of molecules such as this may lead to the development of new classes of antibiotics. There are four Scs proteins (ScsA, B, C and D) present in numerous Gram-negative bacteria, and few have been structurally characterised. In this work, we have created cysteine variants of PmScsC and PmScsB to produce a stable complex and using small-angle X-ray and neutron scattering with contrast variation, we have determined the low-resolution structure of the PmScsC–PmScsB complex.

Topic

Biology

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