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Exploring bacteria through X-rays

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Summary

Studying the 3D structure of a bacterial protein leads to the understanding of its function. This can lead to greater insight in its involvement in pathogenesis with a view to developing new drugs and therapies against a range of diseases caused by microorganisms.

Epsilon toxin is one of the most potent toxins of the Clostrial family and can cause severe diseases mainly to animals and potentially result in huge economical loses to the farming industry. Crystallisation experiments have been performed to investigate the structure of a less toxic mutant. The result was the 3D crystal structure of this mutant solved at 2.4A without significant differences from the wild type protein as reflected by the RMSD of 0.54A. In addition to this, thermofluor stability assay was carried out for the identification of a putative receptor working as a potential inhibitor of ε-toxin.

On the other hand, pathogenic YopM from Yersinia species form complexes with functional interaction partners like kinases and helicases. These suppress and reorient the host immune system to promote infection of lympathic tissues, inner organs and vasculature. In order to understand the YopM function, it is very important to investigate the amino acids of the interactive surface and this can be achieved by characterising the structure in its complexes. The characterisation methods will be used in this study are the X-ray Crystallography, the Small angle Scattering and the Serial Femtosecond Crystallography using X-ray lasers.

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