**Poster Presentation**

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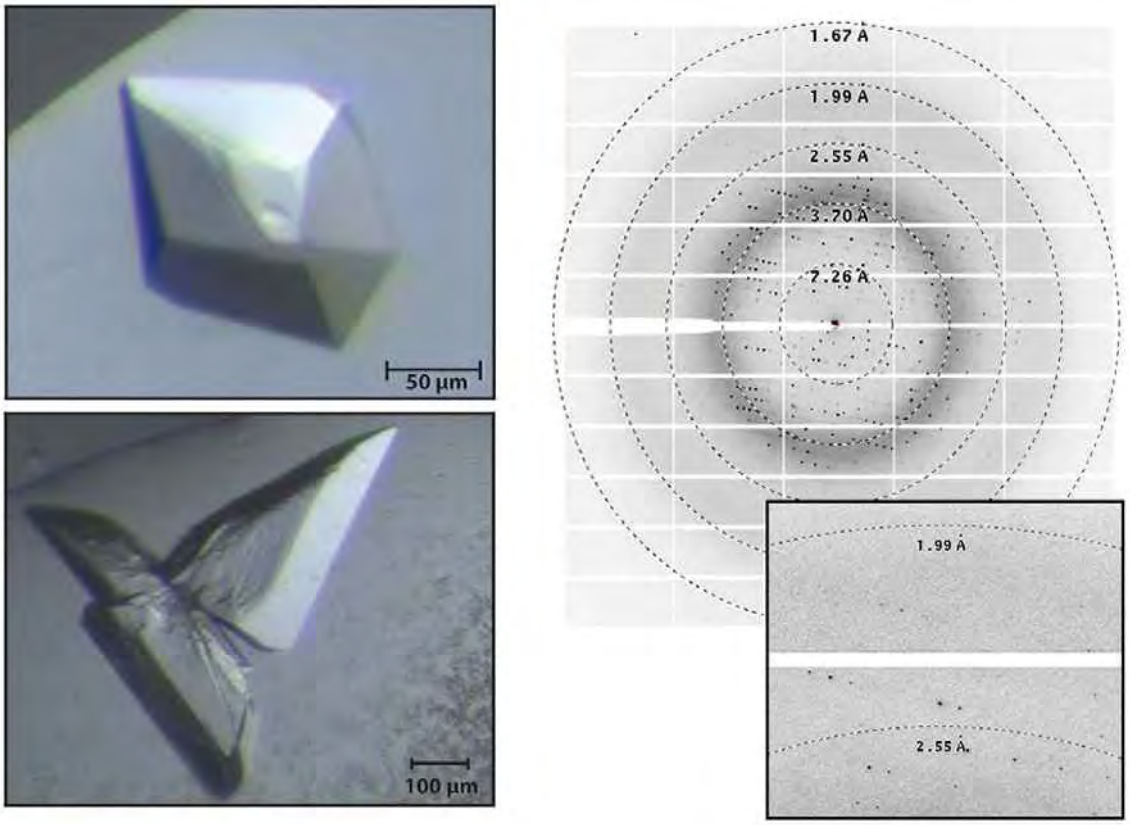
## *Structural characterisation of a Fic protein from Clostridium difficile*

D. Welner[1], E. Dedic[1], H. van Leeuwen[2], E. Kuijper[2], R. Jorgensen[1] Jorgensen[1], R. Jorgensen[1]

*[1]Statens Serum Institut, Microbiology and Infection Control, Copenhagen, Denmark, [2]Leiden University Medical Center, Department of Medical Microbiology, Center of Infectious Diseases, Leiden, The Netherlands*

Fic domains in proteins are found in abundance in nature from the simplest prokaryotes to animals. Interestingly, Fic domains found in two virulence factors of gram-negative bacteria have recently been demonstrated to catalyse the transfer of an AMP moiety from ATP to small host GTPases (1,2). This post-translational modification has received considerable interest and a role for adenylylation in pathology and physiology is emerging. We have structurally characterised a newly identified Fic protein of the pathogenic gram-positive bacterium Clostridium difficile. A constitutively active inhibitory helix mutant of C. difficile Fic was purified, crystallised and data collected to 1.7 Å resolution. The structure confirms C. difficult Fic protein as an ATP binding protein and reveal a binding site similar to other confirmed virulent Fic proteins. Surprisingly, this gram-positive Fic protein does not seem to target GTPases in humans and currently target identification is being chased. The current status of the project will be presented.

***[1]*** *Yarbrough, M. L., Li, Y., Kinch, L. N., Grishin, N. V., Ball, H. L. & Orth, K. (2009). Science 323, 269-272.,* ***[2]*** *Worby, C. A., Mattoo, S., Kruger, R. P., Corbeil, L. B., Koller, A., Mendez, J. C., Zekarias, B., Lazar, C. & Dixon, J. E. (2009). Mol Cell 34, 93-103.*

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