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. difficile 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.


**Keywords:** Fic protein, Clostridium difficile, Adenylylating enzyme