Crystal structure of the *Bc*ZBP, a zinc-binding protein from *Bacillus cereus*

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Bacillus cereus is an opportunistic pathogenic bacterium closely related to *Bacillus anthracis*, the causative agent of anthrax in mammals. A significant portion of the *B. cereus* chromosomal genes are common to *B. anthracis*. The homologues include almost all the putative chromosomal virulence and surface proteins of *B. anthracis*, although *B. cereus* is not associated with anthrax. *B. cereus* provides thus a convenient model organism for studying the corresponding proteins of the highly infectious *B. anthracis*. The *Bc*ZBP protein of *B. cereus*, is encoded from the *bc1534* gene which has three homologues to *B. anthracis*. The protein exhibits deacetylase activity with the N-acetyl moiety of the N-acetylglucosamine and the di- and tri-acetylchitobiose. However, neither the specific substrate of the *Bc*ZBP nor the biochemical pathway have been conclusively identified. We have determined the crystal structure of *Bc*ZBP at 1.8 Å resolution. The N-terminal part of the 234 amino acid protein adopts a Rossmann fold while the C-terminal part constists of two β-strands and two α-helices. In the crystal the protein forms a compact hexamer, in agreement with solution data. A zinc binding site and a potential active site have been identified in each monomer. These sites have extensive similarities to those found in two known zinc-dependent hydrolases with deacetylase activity, MshB and LpxC, despite a low degree of amino acid sequence identity. Functional implications and a possible catalytic mechanism can be deduced from the crystal structure.

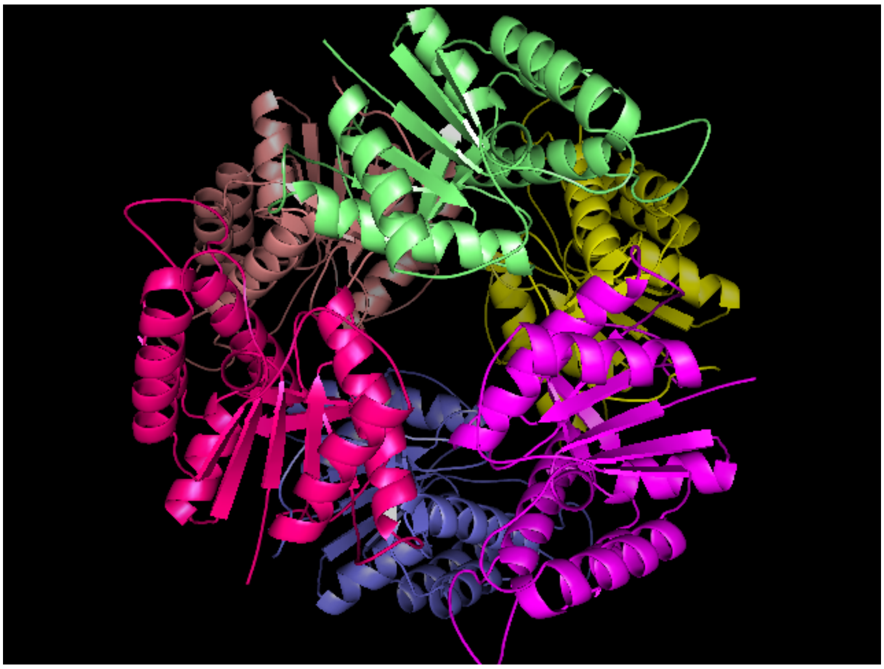

Figure 1: Structure of the *Bc*ZBP hexamer

References

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