

## MS07-P01 | CRYSTAL STRUCTURE OF THE CELL WALL BINDING DOMAIN OF A NOVEL BACTERIOPHAGE PBC5 ENDOLYSIN AND ITS PEPTIDOGLYCAN INTERACTION

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Phage endolysins are hydrolytic enzymes that cleave the bacterial cell wall during the lytic cycle. In this study, we isolated the bacteriophage PBC5 against *Bacillus cereus*, a major foodborne pathogen, and describe the molecular interaction between its endolysin LysPBC5 and the host peptidoglycan structure. LysPBC5 has an N-terminal glycoside hydrolase 25 domain, and a C-terminal cell-wall binding domain (CBD) that is crucial for specific cell-wall recognition and lysis. The crystal and solution structure of CBD reveals tandem SH3b domains that are tightly engaged with each other. CBD binds to peptidoglycan in a bidentate manner via distal beta-sheet motifs with pseudo two-fold symmetry, which can explain its high affinity and host specificity. CBD primarily interacts with the glycan strand of the peptidoglycan layer instead of the peptide crosslink, implicating the tertiary structure of peptidoglycan as the recognition motif of endolysins