

Potential role of the host-derived cell-wall binding domain of endolysin CD16/50L as a molecular anchor in preservation of uninfected *Clostridioides difficile* for new rounds of phage infection

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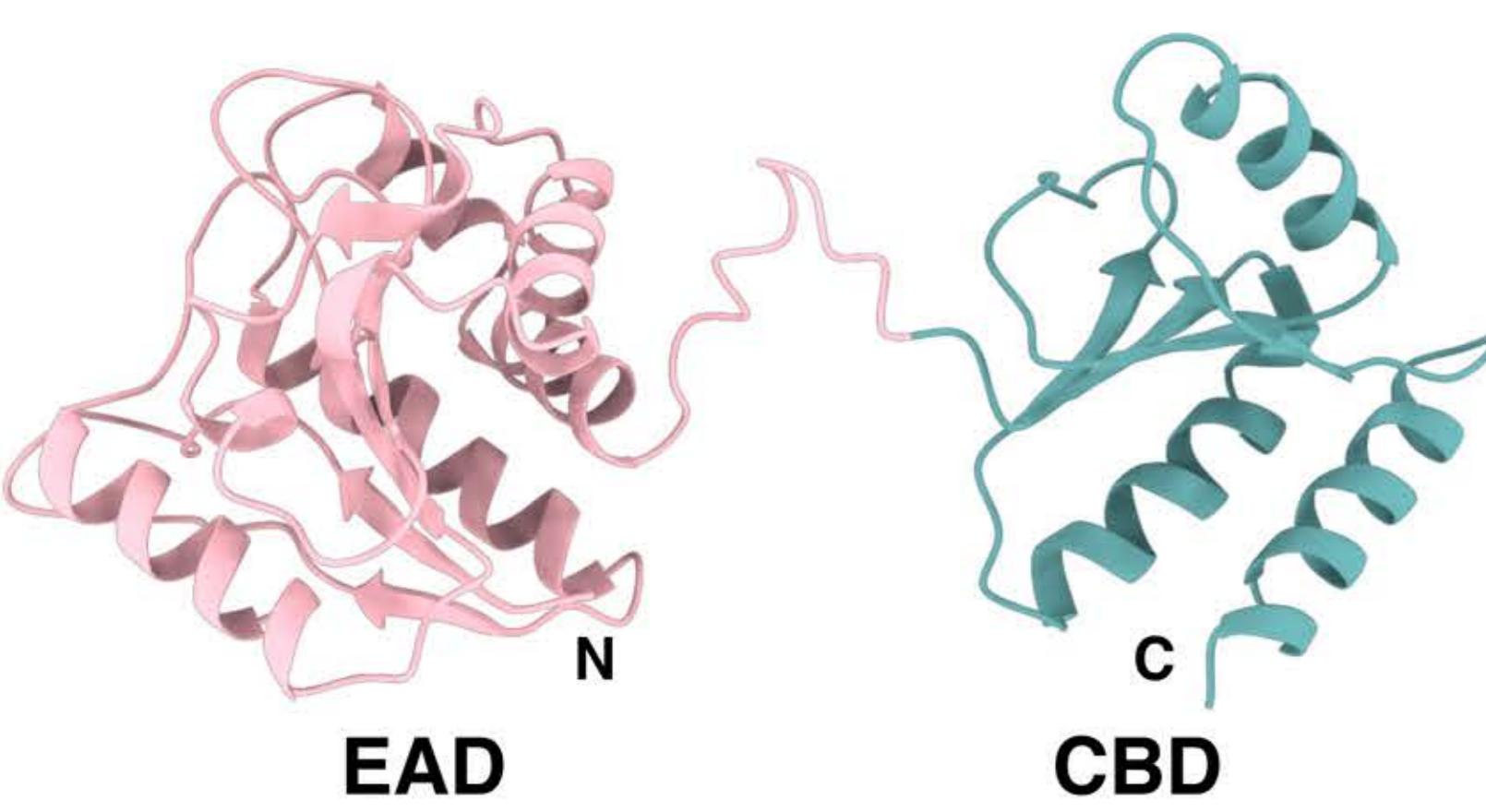
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Abstract

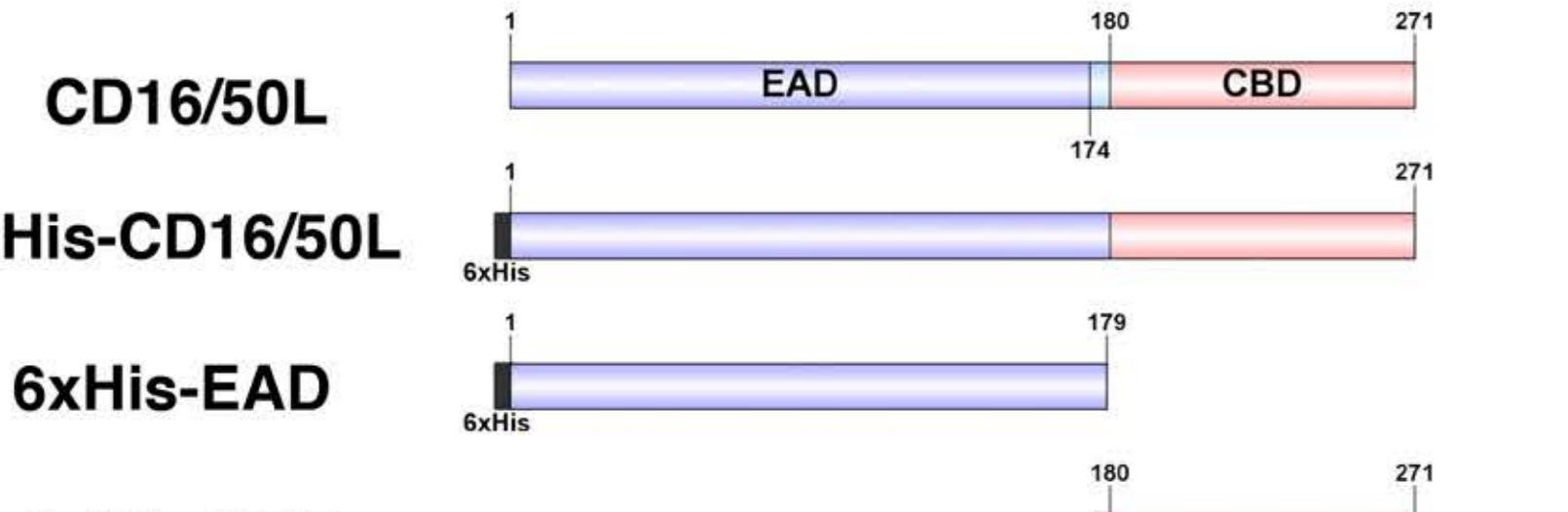
Endolysin is a phage-encoded cell-wall hydrolase which degrades the peptidoglycan layer of the bacterial cell wall. The enzyme is often expressed at the late stage of the phage lytic cycle and is required for progeny escape. Endolysins of bacteriophage that infect Gram-positive bacteria often comprises two domains: a peptidoglycan hydrolase and a cell-wall binding domain (CBD). Although the catalytic domain of endolysin is relatively well-studied, the precise role of CBD is ambiguous and remains controversial. Here, we focus on the function of endolysin CBD from a recently isolated *Clostridioides difficile* phage. We found that the CBD is not required for lytic activity, which is strongly prevented by the surface layer of *C. difficile*. Intriguingly, hidden Markov model analysis suggested that the endolysin CBD is likely derived from the CWB2 motif of *C. difficile* cell-wall proteins but possesses a higher binding affinity to bacterial cell-wall polysaccharides. Moreover, the CBD forms a homodimer, formation of which is necessary for interaction with the surface saccharides. Importantly, endolysin diffusion and sequential cytolytic assays showed that CBD of endolysin is required for the enzyme to be anchored to post-lytic cell-wall remnants, suggesting its physiological roles in limiting diffusion of the enzyme, preserving neighboring host cells, and thereby enabling the phage progeny to initiate new rounds of infection. Taken together, this study provides an insight into regulation of endolysin through CBD and can potentially be applied for endolysin treatment against *C. difficile* infection.

Results

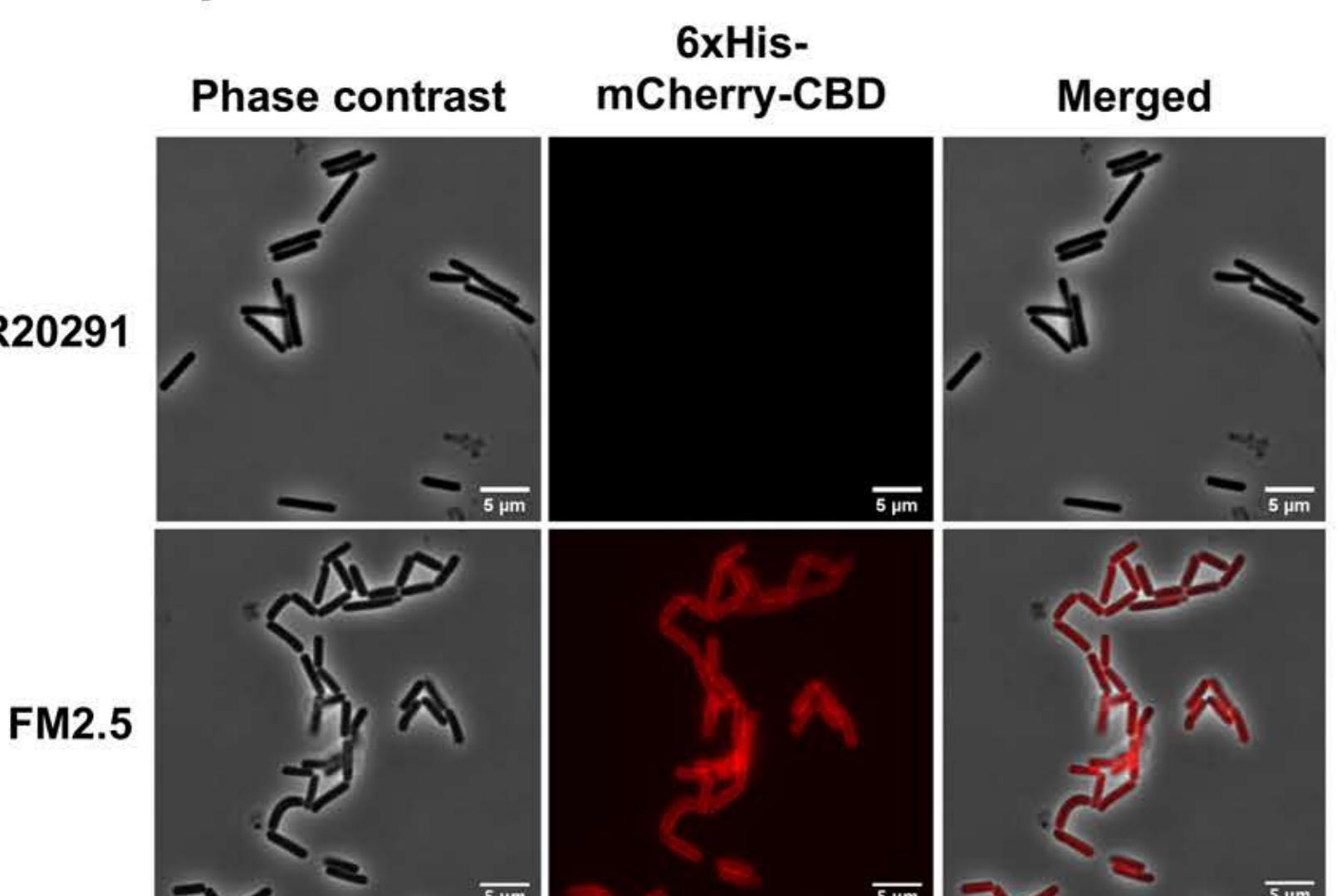
Structure model of CD16/50L by AlphaFold



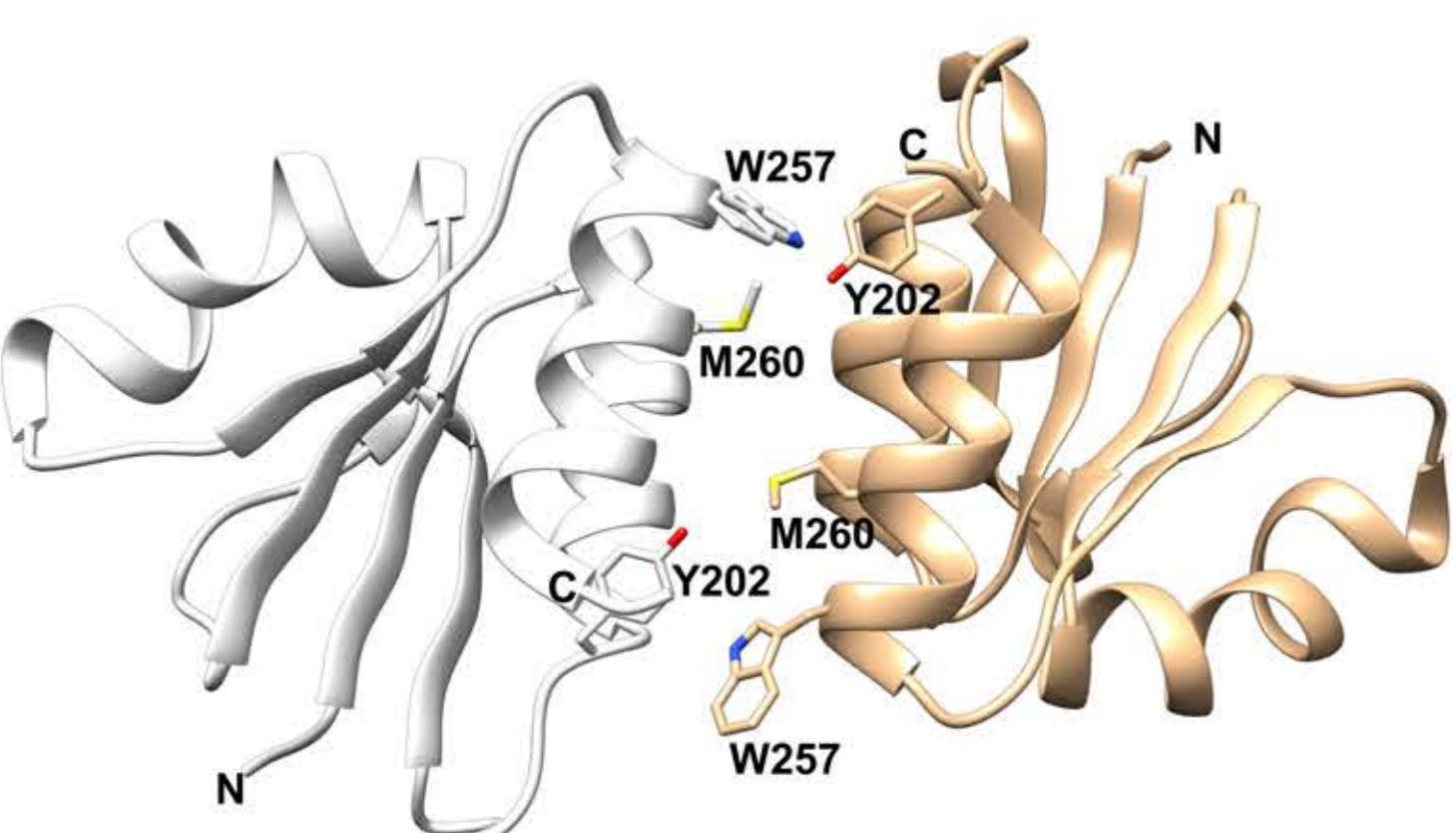
Schematic of CD16/50L variants



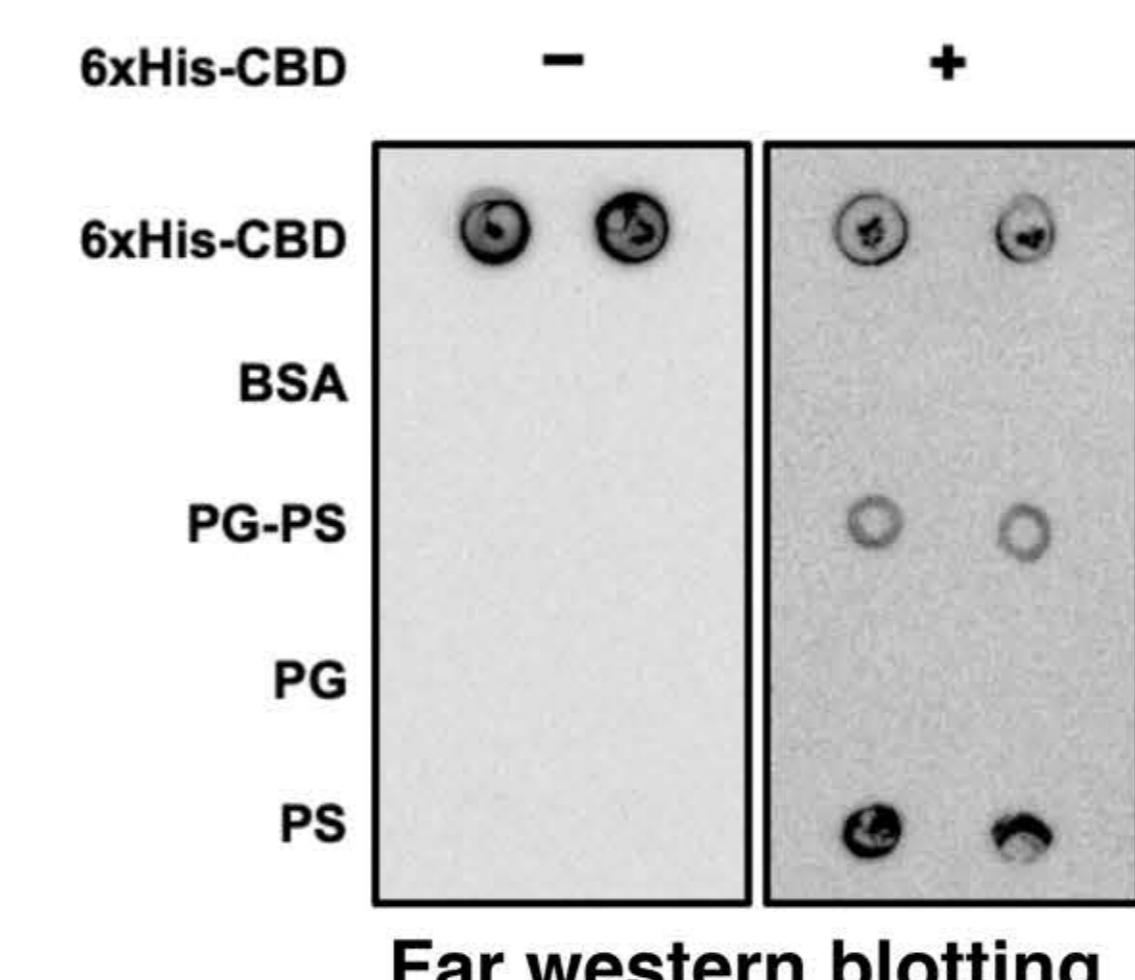
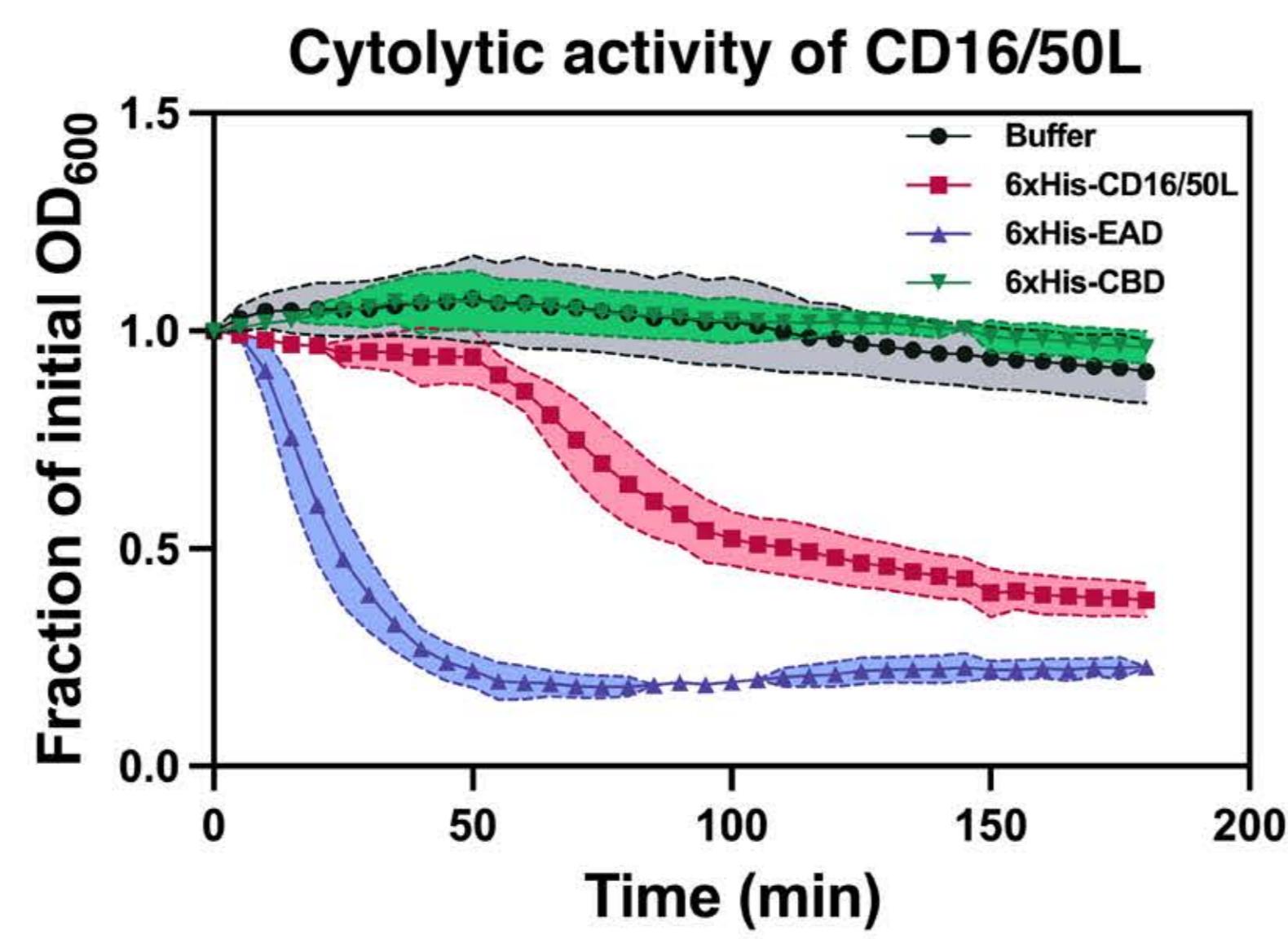
- CD16/50L full-length and EAD able to lyse *C. difficile*.
- CD16/50L is CBD-independent cytolytic activity.



- mCherry-CBD decorated on the S-layer mutant *C. difficile* cells but not wild-type cells



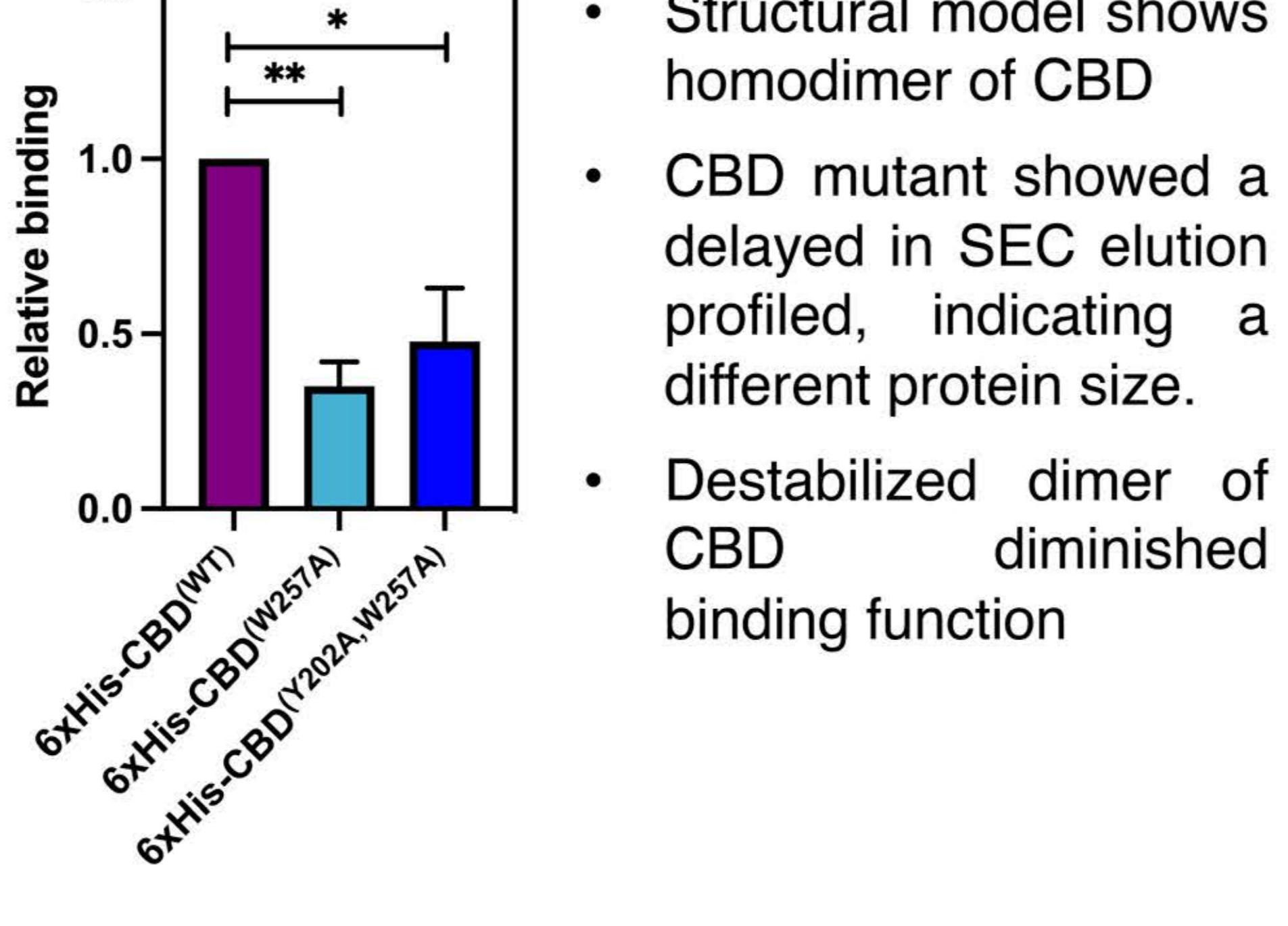
- CD16/50L is modular structure composed of N-terminal enzymatic active domain (EAD) and C-terminal cell-wall binding domain (CBD)
- Sequence-based analysis revealed that EAD contains an amidase function



- Far western blotting revealed the interaction of CBD on peptidoglycan-polysaccharide complex (PG-PS) and PS but not PG alone.

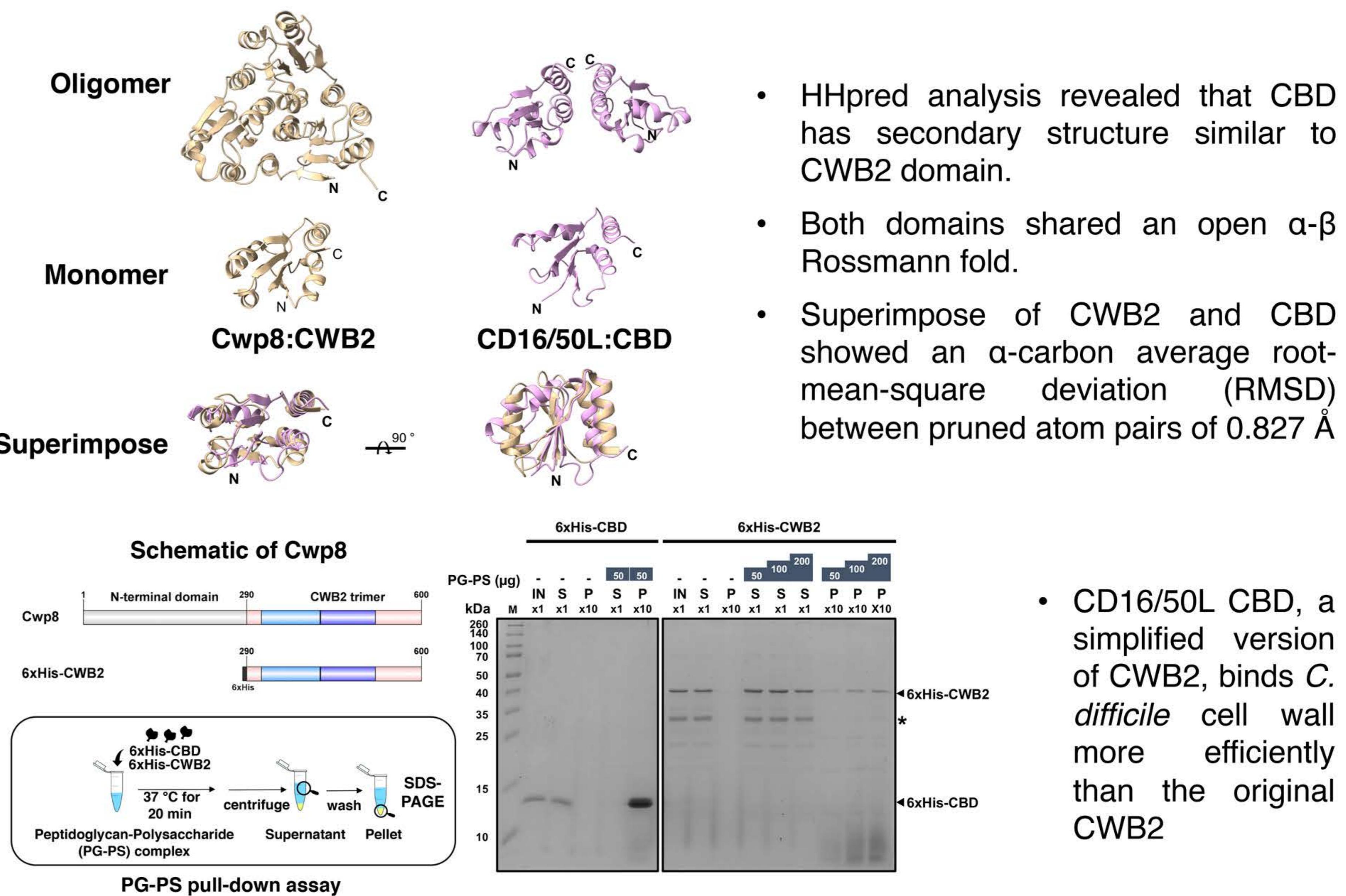
The CBD of CD16/50L forms a homodimer

Binding of CBD WT and mutant

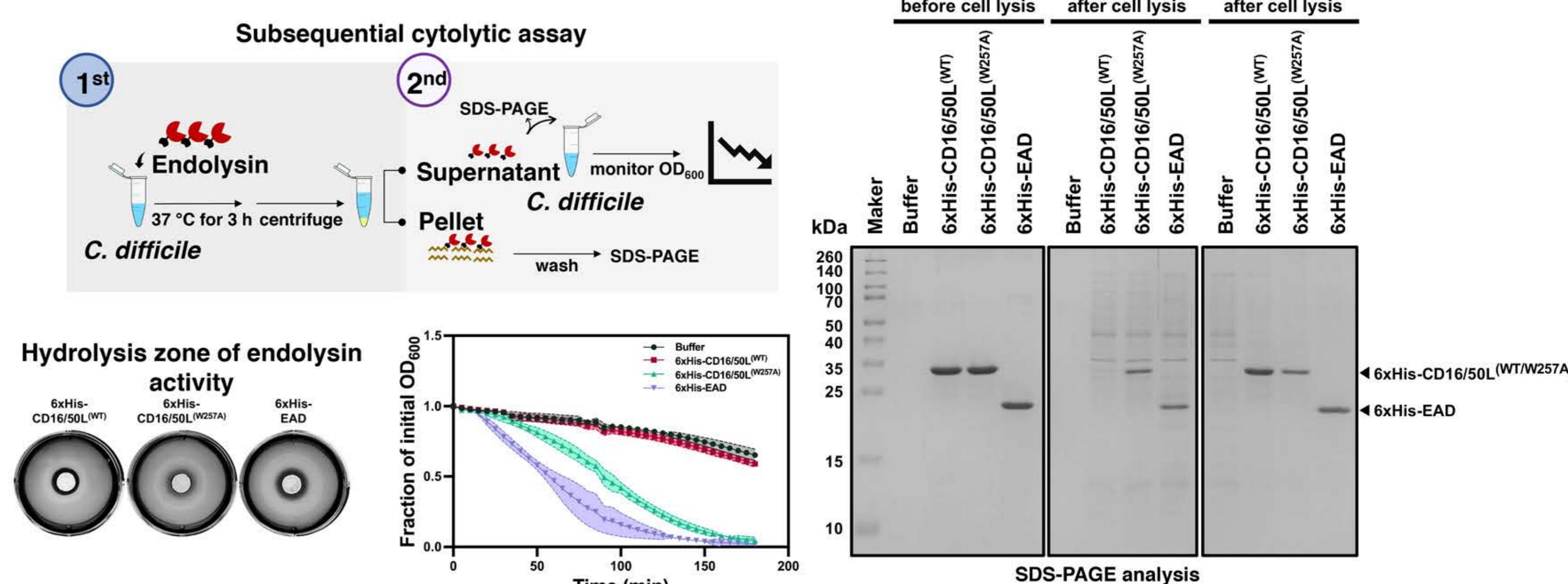


- Structural model shows homodimer of CBD
- CBD mutant showed a delayed in SEC elution profile, indicating a different protein size.
- Destabilized dimer of CBD diminished binding function

The CBD of CD16/50L is evolutionarily homologous to CWB2 domain of *C. difficile* cell wall proteins and binds to PG-PS complex more tightly than the host counterpart



The CBD of CD16/50L anchors the endolysin to bacterial post-lytic remnants and prevents a successive round of cytology



- CBD restricted endolysin diffusion
- CD16/50L WT containing CBD dimer was trapped in bacterial cell wall. While the dimer destabilized of CD16/50L W257A and EAD able to detach from bacterial cell remnants.
- CD16/50L W257A and EAD were able to lyse a fresh batch of *C. difficile* cells
- CBD anchors bacterial cell wall could prevent the neighbor cells from cell lysis which may benefit for progeny phage

Summary

- CD16/50L is modular structure composed of EAD and CBD
- CD16/50L is CBD-independent cytolytic activity.
- CBD binds polysaccharide on bacterial cell wall.
- CBD is homologous to CWB2 domain of *C. difficile* cell-wall proteins.
- CBD forms homodimer which is essential for interaction with bacterial cell
- CBD binds bacterial cell remnant, preventing endolysin diffusion.
- The CBD-cell wall trapping mechanism might be beneficial for bacteriophage

Acknowledgement

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