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## Model, structure and function of a bacterial virulence factor

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Bacterial virulence factors are essential for pathogens to disrupt host defense mechanisms and survive in the host. Our study focuses on a specific virulence factor, a membrane protein of unknown structure and function, common to several major bacterial pathogens.

First, combining structure prediction using AlphaFold and evolutionary trace using ConSurf has not only revealed an original fold but also a particular multimeric organization. This peculiar multimeric organization was subsequently confirmed by native mass spectrometry. Cryo-electron microscopy has been finally used to solve the first-ever structure of the full-length protein.

These data revealed, for the first time, an original channel organization opening new insight on the real function of this virulence factor. Understanding the structure and molecular details to evaluate the dynamic and the function shall guide the design of novel anti-infectious strategies.

### Session

Structural biology

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