

## Tetrameric structure of the flagellar cap protein FliD from *Serratia marcescens*

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The bacterial flagellum is a complex nanomachine that is used for motility. The flagellar capping protein FliD plays an essential role in flagellar growth by repetitively inserting a nascent flagellin protein at the distal end of the flagellum. FliD functions as an oligomer. Previous structural studies of FliD proteins revealed that FliD adopts a pentameric or a hexameric structure depending on the bacterial species. Here, we report the tetrameric structures of the D2 and D3 domains of *Serratia marcescens* FliD (smFliD) in two crystal forms. smFliD represents the lowest oligomeric state among structurally characterized FliD caps. Our structure-based comparative analysis of FliD structures highlights several common features of FliD oligomers, such as a head-to-tail organization, a star plate shape, and the primary binding interface, despite their different oligomeric states. However, the smFliD tetramer is characterized with a unique secondary binding interface that reinforces oligomerization. Thus, we conclude that bacteria assemble FliD monomers into diverse oligomers that range from tetramers to hexamers for flagellar growth through common but specific structural mechanisms.

Key words: FliD, *Serratia marcescens*, Crystal structure, Tetramer.