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Here, we introduce RBPseg, a method that combines monomeric ESMFold predictions with a structural- based domain identification approach, to divide tail fiber sequences into ...

In this review, we provide a comprehensive analysis of the various proteins constituting tailed bacteriophages from a structural viewpoint.

Advances in synthetic biology may soon allow a bottom-up approach for engineering custom phages or phage tail fibers, but for this to become reality we must first have a better understanding of phage ...

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Here, we provide the first molecular description of a tail fiber tip. Extensive mutational, structural, and biochemical analyses show that the ball-shaped tip contains patches of binding sites ...

Tail fibres, tail spikes and tail tips function as RBPs, and they specifically recognize host receptors, such as lipopolysaccharide (LPS), teichoic acids and porins. Initial reversible...

To acquire atomic-level structural details, the tail particles were divided into three distinct reconstructions: tail cap, tail tip, and tail fiber (Figure 1 B).

Synonymous with long tail fiber, a long, thin, proteinaceous appendage to phagetails that is found in multiple copies and is involved in the first, typically reversible steps of phage attachment to bacteria.

Tail fiber assembly (Tfa) proteins are a very large family of proteins that serve as chaperones for fiber folding in a wide variety of phages that infect diverse species.

In this study, we have determined the structure of the alternative tail fiber subunit, gp52, and compared it with other tail fibers. The results revealed that Mu phage employs different structural ...

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