

Preview

Siphophages have a long, flexible, and noncontractile tail that connects to the capsid through a neck. The phage tail is essential for host cell recognition and virus-host cell interactions; moreover, it serves as a channel for genome delivery during infection. Here, using a minimal myocyanophage, termed Pam3, isolated from Lake Chaohu, we demonstrate that the chaperone gp25 forms a stable complex with the tail fiber gp24 at a stoichiometry of 3:3. 1-A cryo-electron microscopy structure of this complex revealed an elongated structure with the gp25. Here, we introduce RBPseg, a method that combines monomeric ESMFold predictions with a structural- based domain identification approach, to divide tail fiber sequences into manageable fractions for high- confidence modeling with AF2M.

Bacteriophage T5, a Siphovirus belonging to the order Caudovirales, has a flexible, three-fold symmetric tail, to which three L-shaped fibres are attached. These

The six bacteriophage T7 tail fibers, homo-trimers of gene product 17, are thought to be responsible for the first specific, albeit reversible, attachment to Escherichia coli lipopolysaccharide.

Hier sollte eine Beschreibung angezeigt werden, diese Seite lässt dies jedoch nicht zu.

Here, we present the structure of DT57C determined by cryo-EM, and an atomic model of the virus, which was further explored using all-atom molecular dynamics simulations.

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The bundled pigtail has only one end with a connector, and the other end is a broken end of an optical fiber, which is connected to other optical fiber

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Phage tail fibres are elongated protein assemblies capable of specific recognition of bacterial surfaces during the first step of viral infection¹⁻⁴.

Commissural fibers act as bridges between the left and right cerebral hemispheres. The most prominent

Large rounded bundle-shaped tail fiber

example is the corpus callosum, a large bundle of fibers that facilitates

In this study, we report the cryo-EM structure of the simplified tail fiber complexed with its chaperone from the myocyanophage Pam3, which provides insights into the assembly mechanism of the tail

The authors present the nearly-complete structure of the DT57C bacteriophage of the Siphovirus family, revealing the molecular architecture of its capsid, neck, tail and tail tip, and

RBPseg enables accurate modeling of tail fiber structure, providing the first comprehensive tail fiber structure atlas.

Cells use the actin cytoskeleton for many of their functions, including their division, adhesion, mechanosensing, endo- and phagocytosis, migration, and invasion.

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