Structure of bundled tail fibers

Following our recent report on the capsid structure of A-1 (L), here we present the high-resolution cryo-EM structure of its intact tail machine including the neck, tail and attached...

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; ...

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 ...

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.

The Fraction 252 module first applies the sDp approach to find possible domains in the structure (ii) and the 253 sequence of these domains are arranged in consecutive pairs to create fractions (iii).

As the host receptors continuously evolve, the genes present in the tail fibers, tailspikes or tail appendages are selectively pressured to adapt to the ever-changing target, which can range from ...

Bacteriophage lambda has a double-stranded DNA genome and a long, flexible, non-contractile tail encoded by a contiguous block of 11 genes downstream of the head genes. The tail ...

In this study, we identified a new structure of the podophage with three types of tail fibers, and such phages with different types of fibers may have a broad host range and/or infect host cells ...

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 ...

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