Sequence of bundled tail fibers

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 ...

In this paper, we introduce RBPseg, a method that combines monomeric ESMfold predictions with a novel sigmoid distance pair (sDp) protein ...

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 ...

Sequence conservation was calculated using the 730 multiple sequence alignment (MSA) of each TC class, highlighting regions of high (1) and low 732 731 (-3) conservation across the members.

Here, we will discuss the function and dynamics of the tail of the Caudovirales. We will examine the similarities and differences of all three families belonging to this order and point out specific ...

In this paper, we introduce RBPseg, a method that combines monomeric ESMfold predictions with a novel sigmoid distance pair (sDp) protein segmentation technique. This method ...

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.

At the first step of phage infection, the receptor-binding proteins (RBPs) such as tail fibers are responsible for recognizing specific host surface receptors. The proper folding and assembly of ...

This study shows that the tail tips, the most diversified region across bacteriophage lambda and other long-tailed phages (or tail-like machines), contain conserved domains, which ...

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- ...

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