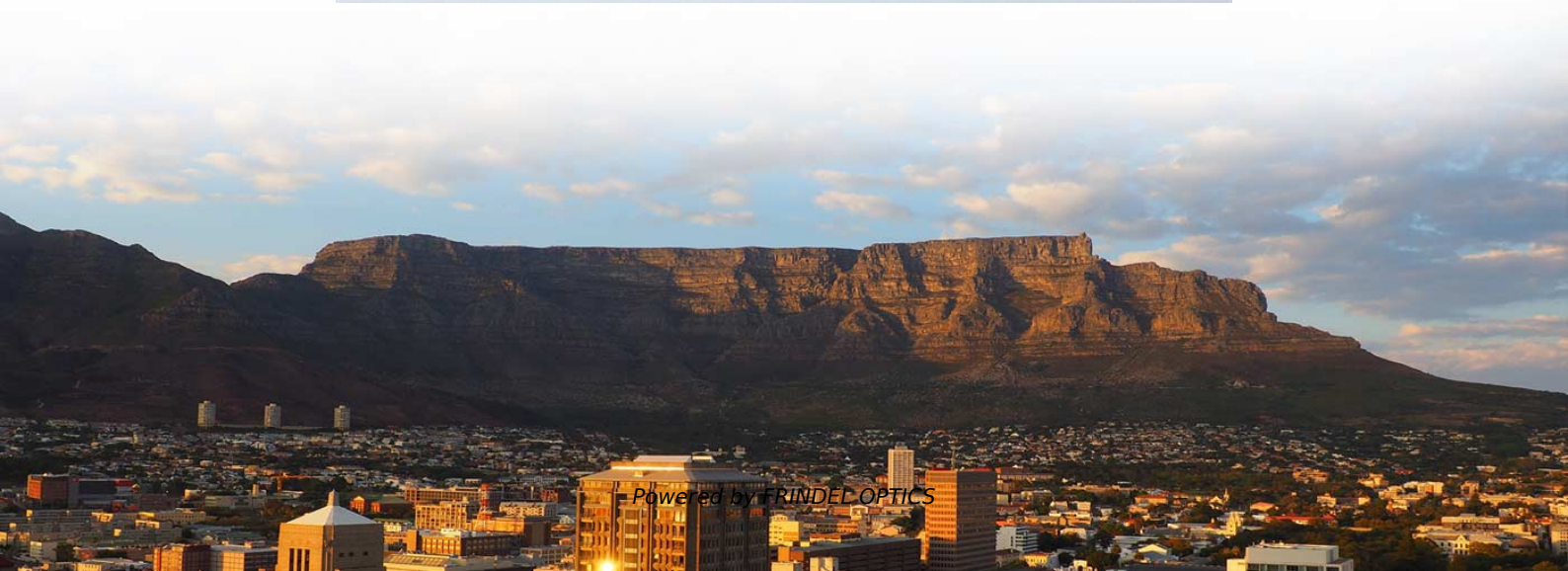


Standardized Binding of Tail Fibers





Standardized Binding of Tail Fibers



Tail fiber function and structure , Bacteriophage T4 Tail

Bacteriophage T4 has two sets of tail fibers, long tail fibers that are the initial receptor binding proteins and short tail fibers that bind subsequently and trigger the

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Chapter 20965

This regulation might prevent the inadvertent binding of the tail fibers to the host in conditions that are unfavorable. In vitro, retraction and extension can be controlled by pH, ionic strength, temperature

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Structures of the tailed bacteriophages that infect Gram-positive

Assembly of tail fibers from some bacteriophage requires the aid of an 'autochaperone' as shown for the phi29 tail appendage . The precursor protein of the phi29 tail fiber contains an ATP

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Phage tail fibre assembly proteins employ a modular structure to drive

Despite the wide occurrence of Tfa proteins, their functional mechanism has not been elucidated. Here, we investigate the tail fibre and Tfa of Escherichia coli phage Mu.



Towards a complete phage tail fiber structure atlas.

Bacteriophages use receptor-binding proteins (RBPs) to adhere to bacterial hosts. Understanding the structure of these RBPs can provide insights into their target interactions. Tail

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Targeting mechanisms of tailed bacteriophages

The short tail fibre is hinged with the receptor-binding region hidden in the baseplate and enables binding, and it rotates and extends in a process

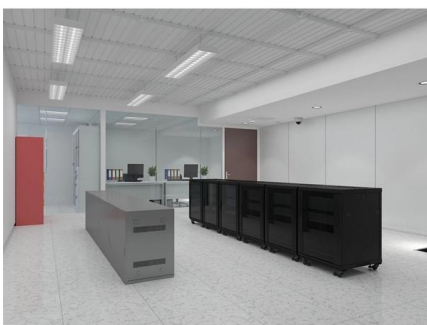
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What are tail fibers and their role in phage infection?

Tail fibers are specialized protein appendages on bacteriophages that recognize and attach to specific bacterial host cell receptors, initiating viral infection.

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RBPseg: Toward a complete phage tail fiber structure atlas

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

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(PDF) Mapping the Tail Fiber as the Receptor Binding

The tail fiber of phages contains receptor-binding proteins that bind with cell surface receptors . No presumed antibiotic resistance genes or virulence

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Evaluating Phage Tail Fiber Receptor-Binding Proteins Using a

In this manuscript, we used a fusion protein comprised of an N-terminal bioluminescent tag translationally fused to T4's long tail fiber binding tip (gp37) to evaluate and quantify gp37's

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(PDF) Molecular Anatomy of the Receptor Binding

Organization of the bacteriophage T4 long tail fiber. (A) A structural model of bacteriophage T4 virion showing the head, the tail, and the long tail fibers.

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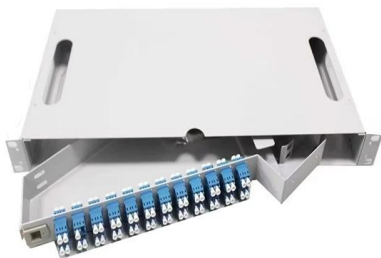




RBPseg: Toward a complete phage tail fiber structure atlas

Here, we introduce RBPseg, a method that combines monomeric ESMFold predictions with a structural-based domain identification approach, to

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Asymmetric Structure of Podophage GP4 Reveals a Novel

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

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Architecture of the bacteriophage lambda tail: Structure

Bacteriophage lambda is an excellent model system to study the tail architecture of bacteriophages. Wang et al. present the cryo-EM structures of the components of the bacteriophage

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Towards a complete phage tail fiber structure atlas

RBPseg workflow in detail, step-by-step demonstrating the 682 architecture of RBPseg using TC14 fiber as example. A FASTA file is input to ESMfold, which 683 generates a monomeric model.

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Structure of the bacteriophage T4 long tail fiber receptor-binding tip

- and irreversibly bind to the outer core region of the lipopolysaccharides (12). This binding is followed by contraction of the outer tail sheath (13, 14), penetration of the bacterial membrane by the hollow

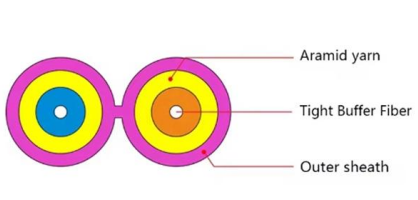
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Amino acid residues in the tail fiber differentiate the host

The predicted structure of the tail fiber revealed that the two amino acid residues are located on the surface of the tail fiber, suggesting that these two

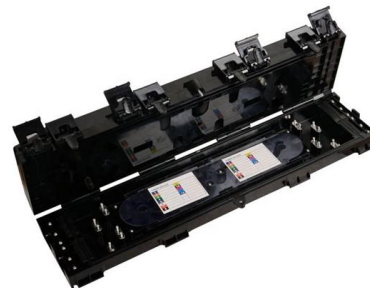
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Ares_viral_fibers_AAM

In the case of phage T4, the initial recognition of the bacterial cell required for the infection, is carried out by the long tail fibers (depicted in Fig. 1a). These fibers reversibly bind to the outer glucose[?]1

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Structural Insights into the Chaperone-Assisted Assembly of a

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

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The C-Terminal Portion of the Tail Fiber Protein of

We fused C-terminal portions of J, the tail fiber protein of ϕ , to maltose-binding protein. Solid-phase binding assays demonstrated that a purified fusion protein

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Phage Proteins Required for Tail Fiber Assembly Also Bind

To initiate their life cycle, phages must specifically bind to the surface of their bacterial hosts. Long-tailed phages often interact with the cell surface using fibers, which are elongated

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RBPseg: Toward a complete phage tail fiber structure atlas

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

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Modified Bacteriophage Tail Fiber Proteins for Labeling,

Phage host range is often determined by their long tail fibers (LTFs) that mediate adsorption of the virus particle to potential bacterial host cells, by binding to specific cell surface

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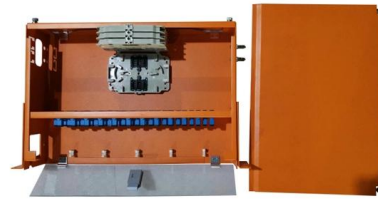
(PDF) Towards a complete phage tail fiber



structure atlas

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

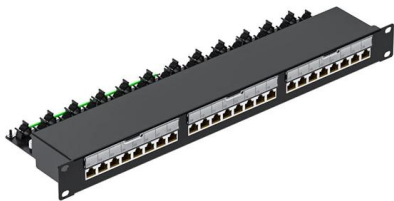
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Phage Proteins Required for Tail Fiber Assembly Also Bind

Tail fibers are long rod-shaped proteins positioned at the tip of the tail and bind specifically to proteins or carbohydrates exposed on the bacterial surface. They are diverse

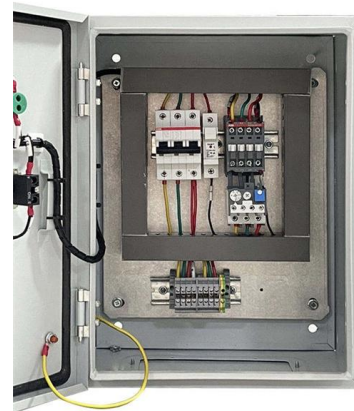
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The Role of Side Tail Fibers during the Infection Cycle of Phage Lambda

Here we utilized fluorescent reporter systems to characterize the effect of the side tail fibers on phage infection. We found that the side tail fibers interfere with phage DNA ejection

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Phage Proteins Required for Tail Fiber Assembly Also Bind Specifically

Phage Proteins Required for Tail Fiber Assembly Also Bind Specifically to the Surface of Host Bacterial Strains.

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Major tail proteins of bacteriophages of the order Caudovirales

The Myoviridae-like tail-morphotype phages do not possess an MTP. Host cell recognition commences by the binding of the distal half-fibers of gp17 to the core heptose region of Escherichia

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Structure of the siphophage neck-Tail complex suggests

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

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<https://frindel.es>