Adam Tas Corridor Energy

Sequence of bundled tail fibers

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Cauda Equina: Understanding the Horse's Tail Bundle of

The cauda equina is a group of nerve fibers that begin at the lower end of the spinal cord, below the level of the first lumbar vertebrae. The term "cauda equina" means "horse's tail" in Latin, and this

Phage tail fibre assembly proteins employ a modular structure to drive

The crystal structure of a complex between the tail fibre and tail fibre assembly (Tfa) protein of Escherichia coli phage Mu reveals the mechanisms by which Tfa regulates fibre assembly

Structural Insights into the Chaperone-Assisted

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

Determination of the three-dimensional structure of bacteriophage Mu

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

Towards a complete phage tail fiber structure atlas.

Additionally, we conducted a structural classification of 67 fibers and their domains, which identified 16 well-defined tail fiber classes and 89 domains. Our findings suggest the existence of

fiber bundle in nLab

1. Idea A fibre bundle or fiber bundle is a bundle in which every fibre is isomorphic, in some coherent way, to a standard fibre or typical fiber. Usually one also requires that it be locally

Eliminates cable excess length and pigtail splice storage.
Designed for high-efficiency onsite installation.

RBPseg: Toward a complete phage tail fiber structure atlas

Here, we propose a pipeline, RBPseg, that defines major domains and segmentation hotspots based on tail fiber primary structure using ESMFold and a

Topology of Fiber Bundles: General Theory of Bundles

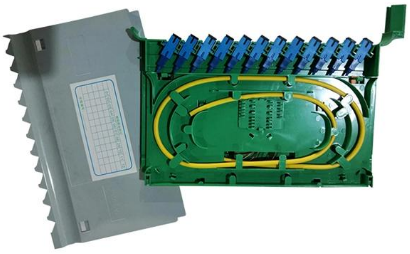
Since a bundle in topology is a union of fibers parametrized by its base space and glued together by the topology of its total space, it provides a basic underlying structure for both the fiber

(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

Nearly complete structure of bacteriophage DT57C reveals

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.

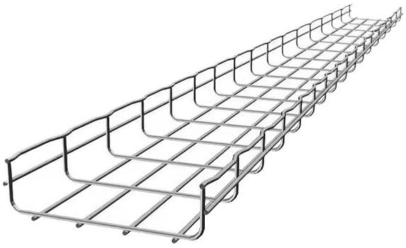


Assembly of bacteriophage T4 tail fibers: Identification and

Formation of both the tail fiber and the baseplate of bacteriophage T4 depends on the product of T4 gene 57. A single amber mutation in that gene causes loss of two T4-specific proteins. Their

Fiber tail fiber characteristics

The ST-type pigtail is usually used for wiring equipment, such as fiber distribution frames, fiber modules, etc. The bundled pigtail has only one end with

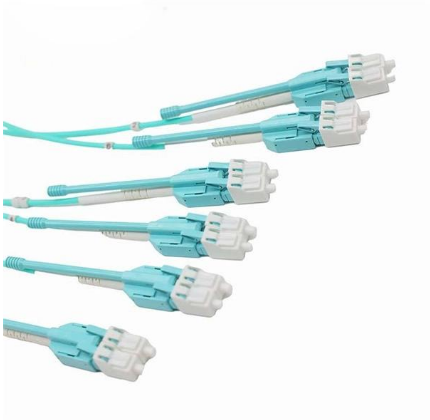


RCSB PDB

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

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.



The structure of Shigella virus Sf14 reveals the presence

The tail structure is overall similar to many Mu-like viruses 15, with its use of two tail fibers having implications for host range and recognition 16.

FIG. 4. Tail fiber sequence and binding analysis. (A)

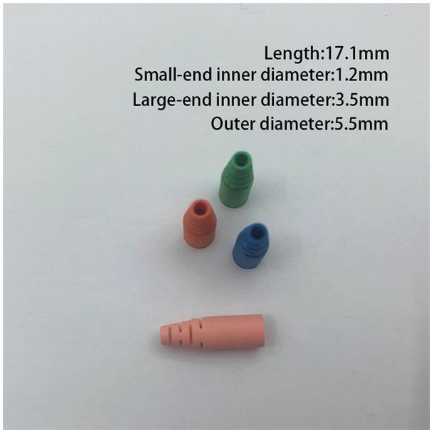
We show that after capsids complete DNA packaging at the surface of the phage nucleus, tails assemble and attach to capsids, and these particles accumulate

Architecture of the bacteriophage lambda tail

Here, we present a high-resolution structure of the tail complex of bacteriophage lambda determined by cryoelectron microscopy. Most component proteins of the lambda tail were

Structure, function and assembly of the long, flexible tail of

The assembly pathway of the capsid and of the long tail are independent: DNA-full capsids and assembled tails connect to form the complete virion, which is liberated with cell lysis.

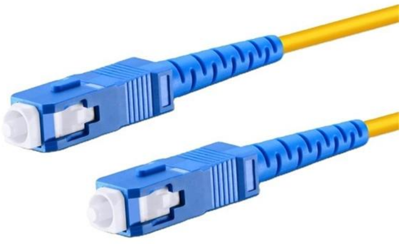


Dissecting neurofilament tail sequence-phosphorylation

We address this challenge by investigating how the tails' stoichiometry and unique sequence features govern brush structure. We find that sequence charge

Explore the world of phage tail fibres in our latest preprint

Additionally, we conducted a structural classification of 67 fibers and their domains, which identified 16 well-defined tail fiber classes and 89 domains.



Dissecting neurofilament tail sequence-phosphorylation-structure

However, the field still lacks a sequence-to-structure paradigm linking NF tail amino acid sequence features to the structure and organization of the NF tail layer. Efforts to define sequence

Tail Fiber: Types, Functions, and Common Interfaces

Similar to fiber optic jumpers, tail fibers are classified into single-mode and multimode types, differing in color, wavelength, and transmission distances. Generally, multimode tail fibers are

Chapter 20965

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

RBPseg: Toward a complete phage tail fiber structure atlas

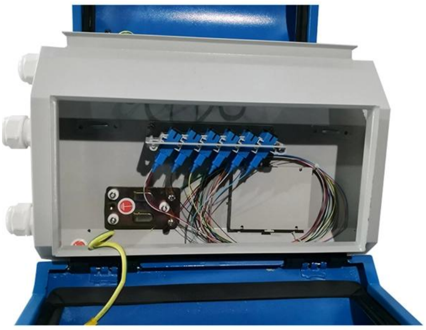
RBPseg enables accurate modeling of tail fiber structure, providing the first comprehensive tail fiber structure atlas.

Structure of the receptor-binding carboxy-terminal domain of

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.

Assembly of bacteriophage T4 tail fibers: The sequence of gene

Intermediates in bacteriophage T4 tail fiber assembly, which accumulate in cells infected with mutants blocked at various stages of tail fiber formation, have been fractionated by velocity sedimentation and



Architecture of the bacteriophage lambda tail: Structure

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

(PDF) Towards a complete phage tail fiber structure atlas

This method segments the tail fiber sequences into smaller fractions, preserving domain boundaries. These segments are then predicted in parallel

Fiber Bundles

Fiber Bundles 'short exact sequence of spaces' A X X/A gives rise to a long exact se-quence of homology groups, but not to a long exact sequence of homotopy groups due to the failure of

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