

Tail Fiber Binding Spacing





Tail Fiber Binding Spacing

Major tail proteins of bacteriophages of the order Caudovirales

The tail formation is completed by the binding of six gp17 fiber protein trimers, which are responsible for host cell recognition, onto the gp11-gp12 interface (12).

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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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Organization of the bacteriophage T4 long tail fiber. (A)

The ferrous ions are shown as yellow spheres. from publication: Molecular Anatomy of the Receptor Binding Module of a Bacteriophage Long Tail Fiber , Tailed

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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

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Understanding Bacteriophage Tail Fiber Interaction with

In this review, we comprehensively summarize how the tail fibers of the T4 phage recognize host surface receptors at single-molecule and atomic levels.

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The Structure of the Receptor-binding Domain of the

However, we do not know of a homologous protein where the receptor-binding domain is a monomer, or of a homologous bacteriophage short tail fibre where the receptor-binding domain is

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Bacteriophage T4 long tail fiber domains

Bacteriophage T4 initially recognizes its host cells using its long tail fibers. Long tail fibers consist of a phage-proximal and a phage-distal rod, each around 80 nm long and attached to each

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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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RBPseg: Toward a complete phage tail fiber structure atlas

Bacteriophages use receptor-binding proteins (RBPs) to adhere to bacterial hosts, yet their sequence and structural diversity remain poorly understood. Tail fibers, a major class of RBPs,

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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.

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Determination of the three-dimensional structure of bacteriophage Mu

The phage possesses two types of tail fibers important for host recognition, which enable it to expand its range of hosts. The alternate tail fibers are formed through the action of genes 49-50

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Understanding Bacteriophage Tail Fiber Interaction with Host Surface

Here, we discuss the molecular mechanisms and models of the tail fibers of the well-characterized T4 phage's interaction with host surface receptors. Structure-function knowledge of tail fibers will pave

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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

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The long tail fibers (which have a stoichiometry $(gp34)_3(gp35)_1(gp36)_3(gp37)_3$) bind to the gp9 trimer. These viral adhesins have a tremendous length (1600 Å) and recognize both LPS as well as the

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Chromatin Fiber Folding Directed by Cooperative Histone Tail

In eukaryotic chromatin, islands of histone tail acetylation are found near transcription start sites and enhancers, whereas linker histones (LHs) are localized in intergenic regions with wild

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Structure of the putative long tail fiber receptor-binding tip of a

The structure resembles the receptor-binding tip from the bacteriophage T4 long tail fiber yet showing marked differences in its domain organization, size, sequence identity and metal binding

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Understanding Bacteriophage Tail Fiber Interaction with

Here, we discuss the molecular mechanisms and models of the tail fibers of the well-characterized T4 phage's interaction with host surface receptors.

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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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RCSB PDB

The structure reveals a previously unknown beta-structured fibrous fold, provides insights into the remarkable stability of the fiber, and suggests a framework for

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Structural mechanism of bacteriophage lambda tail's

The C-terminal portion of the tail fiber protein of bacteriophage lambda is responsible for binding to LamB, its receptor at the surface of Escherichia coli K-12.

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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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Structure of the receptor-binding carboxy-terminal

The tail-spike of the podovirus P22 has been studied extensively in terms of carbohydrate binding, hydrolysis, folding, and assembly (17, 18). Much is also

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Architecture of the bacteriophage lambda tail: Structure

To acquire atomic-level structural details, the tail particles were divided into three distinct reconstructions: tail cap, tail tip, and tail fiber (Figure 1 B).



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R pyocin tail fiber structure reveals a receptor-binding domain with a

Although the minimal tail fiber fragment required for specific binding has not been identified, target strain sensitivity switching has been demonstrated by substitution of the region

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