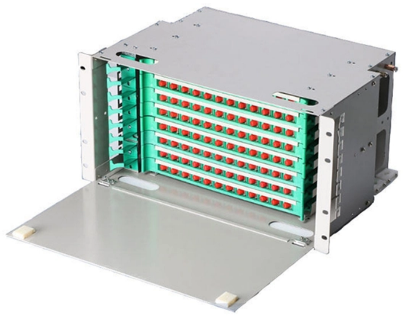
Optics & Photonics

Budowa Silesia Photonics

Tail Fiber Disc Chromatography



Overview

Here, by developing direct receptor binding assays, extensive mutational and biochemical analyses, and structural modeling, we discovered that the ball-shaped tip of the LTF, a trimer of gene product 37, consists of three sets of symmetrically alternating binding sites for LPS and/or OmpC. Long tail fibers consist of a phage-proximal and a phage-distal rod, each around 80 nm long and attached to each other at a slight angle. The phage-distal rod. Cronobacter sakazakii is a Gram-negative pathogen that causes severe infections such as neonatal meningitis and sepsis. These segments are then predicted in parallel using AF2M and assembled into a 26 full fiber model., Ronda de Poniente, 12 – 2 C, 28760 Tres Cantos, Madrid, Spain 2Departamento de Física de la Materia Condensada, Universidad Autónoma de Madrid. Viral fibers play a central role in many virus infection mechanisms since they recognize the corresponding. The tailed phage T4 encodes a specialized device for this purpose, the long tail fiber (LTF), which allows the virus to move on the bacterial surface and find a suitable site for infection.

Article Content

Ares_viral_fibers_AAM

We report herein on the mechanical properties of gp37 fibers such as the Young''s modulus, the breaking force and stiffness, which we have obtained by Atomic Force Microscopy and Finite Element ...

Molecular anatomy of the receptor binding module of a ...

Here, we provide the first molecular description of a tail fiber tip. Extensive mutational, structural, and biochemical analyses show that the ball-shaped tip contains patches of binding sites ...

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.

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). Each section was analyzed separately to ...

Modified Bacteriophage Tail Fiber Proteins for Labeling, ...

In this chapter, we describe the development of the Salmonella phage S16 LTF (S16 LTF) into an affinity molecule as part of a novel assay to detect Salmonella cells.

Amino acid residues in the tail fiber differentiate the host ...

Accurate recognition and attachment to the bacterial host, mediated by tail fibers, are crucial for successful phage infection. Understanding the mechanisms underlying host specificity of ...

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.

Functional domains of Acinetobacter bacteriophage tail fibers

To further explore the functional domains associated with depolymerase activity, tail-associated proteins of 71 sequenced and fully characterized phages were identified from published ...

Bacteriophage T4 long tail fiber domains

In this review, we discuss what is known about the detailed structure and function of the different long tail fiber domains. Partial crystal structures of gp34 and gp37 have revealed the presence of new ...

Determination of the three-dimensional structure of bacteriophage Mu ...

In this study, we determined the X-ray structure of the C -terminal LPS-binding domain of the Mu (−) tail fiber, the alternative tail fiber gp52, to understand the mechanism by which the two tail ...

Contact Us

For more information, pricing, or custom solutions, please contact us:

Website: https://www.budowasilesia.pl
Email: contact@budowasilesia.pl
Phone: +48 537 192 846
Address: ul. Chorzowska 45, 40-001 Katowice, Silesian Voivodeship, Poland