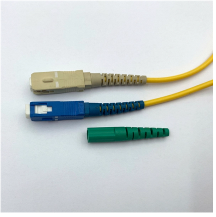
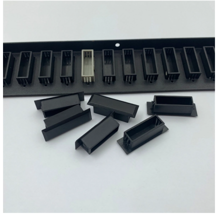
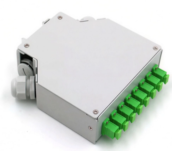
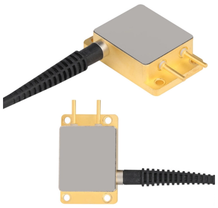
Fiber tail folding range

Overview

The host range of a phage is primarily determined by phage tail fibers (or spikes), which initially mediate reversible and specific recognition and adsorption by susceptible bacteria. Tail fiber assembly (Tfa) proteins are a very large family of proteins that serve as chaperones for fiber folding in a wide variety of phages that infect diverse species. Recent significant advances at single-molecule and atomic levels have begun to unravel the structural organization. In this paper, we introduce RBPseg, a method that combines monomeric 23 ESMfold predictions with a novel sigmoid distance pair (sDp) protein segmentation technique. These segments are then predicted in parallel using AF2M and assembled into a 26 full fiber model.

Fiber tail folding range

	Tail fiber assembly (Tfa) proteins are a very large family of proteins that serve as chaperones for fiber folding in a wide variety of phages that infect diverse species.
	This innovative paper describes how the host range of R-type pyocins can be reprogrammed by replacing parts of the tail fibres between phages with different host ranges.
	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.
	To explore the folding propensity by which these features may govern gene expression, we analyze 20 kb fibers that contain regularly spaced acetylation islands of two sizes (2 or 5 kb) 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.

	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 …
	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 …
	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 tail …
	Through natural evolution and structural modeling, we identified host-range-determining regions (HRDRs) in the T3 phage tail fiber protein and developed a high-throughput strategy to genetically …
	RBPs play a critical role in spatial and temporal positioning of the tail apparatus to the bacterial surface during infection. High-resolution structures of RBPs can be used as "blueprints" to …
	We find that Tfa proteins are comprised of two domains: a non-conserved N-terminal domain that binds to the C-terminal region of the fibre and a conserved C-terminal domain that …

Contact Us

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

Website: https://www.yoahorroenergia.es
Email: hello@yoahorroenergia.es
Phone: +233 54 318 7269
Address: Plot 28, Spintex Road, Accra, Greater Accra, Ghana

This document is for informational purposes only. Specifications subject to change without notice.