


Mechanistic origins of dynamic instability in filaments from the phage tubulin, PhuZ

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Authors	Zehr, EA, Rohou A, Liu Y, Verba KA, Pogliano J, Grigorieff N, Agard DA
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Abstract A bacteriophage-encoded tubulin homologue, PhuZ, harnesses dynamic instability to position genomes of λ KZ-like bacteriophage at the midline of their *Pseudomonas* hosts, facilitating phage infectivity. While much has been learned about molecular origins of microtubule dynamics, how GTP binding and hydrolysis control dynamics in the divergent 3-stranded PhuZ filaments is not understood. Here we present cryo-EM reconstructions of the PhuZ filament in a pre-hydrolysis (3.5 Å) and three post-hydrolysis states (4.2 Å, 7.3 Å and 8.1 Å resolutions), likely representing distinct depolymerization stages. Core polymerization-induced structural changes reveal similarities to $\alpha\beta$ -tubulin, suggesting broad conservation within the tubulin family. By contrast, GTP hydrolysis is sensed quite differently and is communicated by the divergent PhuZ C-terminus to the lateral interface, leading to PhuZ polymer destabilization. This provides a contrasting molecular description of how nucleotide state can be harnessed by the tubulin fold to regulate filament assembly, metastability and disassembly.

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