A030 · Collective Dynamics of Confined Water in Amyloid Fibrils

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Collective Dynamics of Confined Water in Amyloid Fibrils

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Abstract

Amyloid fibrils are stable protein assemblies whose structures depend on sequence, packing, and growth conditions. We show by all-atom molecular-dynamics simulations that water inside SAA fibrils does not behave as bulk water or ordinary surface hydration water. Instead, the fibril architecture organizes internal water into distinct dynamical states, from slip-like diffusive channels to rattle-like structured water wires. This raises fundamental questions about how confined water contributes to amyloid stability, polymorphism, and biological nanoconfinement. The structural analysis of serum amyloid A fibrils reveals internal channels filled with water, ranging from large hydrated cavities to narrow water wires. Because these waters are buried within the amyloid core, they are often treated as trapped solvent occupying preformed pores. SAA fibrils host internal water channels spanning distinct pore environments–from wider, Rahman "slip-like" diffusive channels to narrow, Rahman "rattle-like" and strongly structured water wires–yet it remains unclear how the local channel microenvironment controls water's dynamical state and thermodynamic signatures. Borrowing concepts from statistical mechanics, we decompose the VACF into "slipping" (diffusive, zero-frequency contributions) versus "rattling" (caged, finite-frequency contributions) dynamics. Further, we explore diffusivity, fluidity, and entropy without invoking harmonic approximation among these channels using FRESEAN analysis along with the 2PT model.