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CryoEM of Polymers: From Proteins to Peptides

Cryo-EM has emerged as the main technique for determining the atomic structure of macromolecular assemblies. I will discuss our applications of cryo-EM to a range of polymers, including bacterial and archaeal pili, bacterial and archaeal flagella, extracellular cytochrome filaments that conduct electrons over long distances ("microbial nanowires") and filamentous viruses that infect hosts living in nearly boiling acid. Watson and Crick observed in 1956 that almost all viruses were spherical (icosahedral) or rod-like (helical) and explained this in terms of symmetry: both allowed many copies of a single protein to encapsulate a genome. The basis for spindle-shaped viruses that infect archaea has therefore been a puzzle, as they cannot be explained by either icosahedral or helical symmetry. We show how they actually evolved from helical archaeal viruses, driven by the need to package a larger genome, and that these capsids can be explained by the idea of quasi-equivalence, first postulated by Caspar and Klug in 1962 with regard to icosahedral viruses. The powerful methods that have been developed in cryo-EM of biological complexes can now be readily applied to assemblies of peptides and small molecules. Cryo-EM is thus beginning to make a real impact in areas such as materials science, soft matter and chemistry.