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Penrose-like tilings as geometric constraints on the structures of protein assemblies.

Non-crystallographic symmetry is common in protein assemblies, from icosahedral symmetry in viral capsids to five-fold and seven-fold axial symmetry in C-reactive proteins and chaperonin molecules, respectively. We have shown that the overall organisation of such structures can be predicted using affine extensions of non-crystallographic symmetry. In particular, important insights can be gained not only into the outer surfaces of these clusters, but also in how symmetry is correlated at different radial levels. For example, in applications to viruses, this has led to the discovery of a molecular scaling principle between different viral components. Here I will show that Penrose-like non-crystallographic tilings derived from higher dimensional lattices can be used to provide bounding boxes for proteins in non-crystallographic assemblies.