Crystallizing protein assemblies via free and grafted linkers

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In this study we introduce a coarse-grained molecular dynamics simulation approach for studying the effects of linker length, geometry, and concentration on the stability of metal anchored ferritin protein crystallizing assembly. This model assumes that the anchored metal ions are sufficiently stable on the protein surface for holding proteins in the crystalline structures via linkers. By simulating a system of proteins (eight metal ion anchored sites per protein) and linkers (two free ends per linker), we find that there is a range of optimal linker lengths for crystalline order. The optimal linker length is found to depend on the linker to protein concentration ratio and binding energy. We also examine the case of grafted flexible linkers on the protein surface as an alternative route for constructing highly porous crystalline structures. Our study demonstrates that the length of grafted linkers is a better tunable parameter than the length of free linkers to achieve high porosity protein superlattices.

Significance and Impact

The computationally inexpensive method that we introduce in this study is potentially useful to design open crystalline structures of proteins and serves as a guide for constructing higher order assemblies of complex molecules.

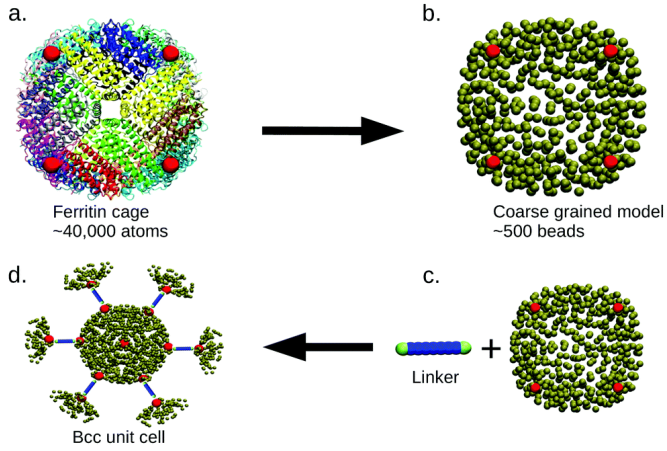

Figure: Detailed structure of a ferritin protein, coarse-grained models of a protein and a linker, and an assembly of proteins in a bcc unit cell. (a) Front view of a ferritin cage (PDB code: 5CMQ) with anchored metal ions. There are 8 metal ion anchored sites per protein which are represented by small red spheres separated by 72 Å. In experiments,2,4 metal ions are anchored on protein surfaces after replacing threonine amino acid at position 122 with histidine. (b) A coarse grained model of a ferritin cage which is composed of 500 beads. (c) A system of coarse-grained linker and protein. The linker has identical beads at two ends (colored in green). The linear density of beads is approximated by $\frac{L}{5}$.Å^{-1}. (d) Proteins in a bcc unit cell held by linkers through the metallic ion installed sites.

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