## Protein cages architectures: biomineralization, nucleic acid encapsidation, and applications in nanoscience

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Protein cage architectures from the iron storage protein ferritin, Cowpea chlorotic mottle virus (CCMV), the small heat shock protein from *Methanococcus jannaschii*, and a Dps protein from *Sulfolobus solfataricus* have been used as models for understanding the basis for molecular host-guest encapsulation. This approach has been inspired by models for biomineralization and viral encapsidation. We have explored modifications to the exterior and interior interfaces while maintaining assembly of stable cage architectures, allowing us to utilize the high symmetry to engineer unique functionality for highly ordered multivalent presentation. These modifications have a profound influence on packaging and interaction of the encapsulated guest with the protein interfaces. Modifications to the interfaces between subunits have been made, which influence structural transitions of the cages as well as metal binding affinity.

Using a solid-state approach we have shown that the symmetry of the CCMV capsid can be broken to allow differentiation of modified sites within the icosahedral capsid. A robust *in vitro* assembly system for CCMV has also allowed us to direct the mixed assembly of differentially modified subunits to generate symmetry broken, multiply labeled capsids. The role of protein interfaces in assembled protein cage architectures has been explored to understand and exploit packaging of materials as diverse as nucleic acid, drugs, and inorganic magnetic and catalytic materials. The library of sizes of these cages has allowed us to explore the size dependent properties of protein-encapsulated materials.