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Crystalline Cyclophane–Protein Cage Frameworks

Ngong Kodiah Beyeh,†,‡,§ Nonaapp,† Ville Liljestrom,† Joona Mikkila,‖ Antti Korpi,‖ Davide Bochicchio,† Giovanni M. Pavan,‖ Olli Ikkala,‖ Robin H. A. Ras,‖∥ and Mauri A. Kostiainen∗,†,‖∥

†HYBER Centre of Excellence, Department of Applied Physics, Aalto University, FI-00076 Aalto, Finland
‡Department of Chemistry and Biochemistry, University of Windsor, N9B 3P4 Windsor, Canada
§Department of Chemistry, Oakland University, 146 Library Drive, Rochester, Michigan 48309-4479, United States
‖Department of Bioproducts and Biosystems, Aalto University, FI-00076 Aalto, Finland
∥Department of Innovative Technologies, University of Applied Sciences and Arts of Southern Switzerland, CH-6928 Manno, Switzerland

Supporting Information

ABSTRACT: Cyclophanes are macrocyclic supramolecular hosts famous for their ability to bind atomic or molecular guests via noncovalent interactions within their well-defined cavities. In a similar way, porous crystalline networks, such as metal–organic frameworks, can create microenvironments that enable controlled guest binding in the solid state. Both types of materials often consist of synthetic components, and they have been developed within separate research fields. Moreover, the use of biomolecules as their structural units has remained elusive. Here, we have synthesized a library of organic cyclophanes and studied their electrostatic self-assembly with biological metal-binding protein cages (ferritins) into ordered structures. We show that cationic pillar[5]arenes and ferritin cages form biohybrid cocrystals with an open protein network structure. Our cyclophane–protein cage frameworks bridge the gap between molecular frameworks and colloidal nanoparticle crystals and combine the versatility of synthetic supramolecular hosts with the highly selective recognition properties of biomolecules. Such host–guest materials are interesting for porous material applications, including water remediation and heterogeneous catalysis.

KEYWORDS: protein cage, cyclophane, pillararene, crystal, self-assembly, electrostatic binding

Supramolecular materials rely often on macrocycles, such as cyclophanes consisting of aromatic rings and aliphatic carbons, to achieve host–guest chemistry. 1 Calixarenes 2 and pillararenes 3 are well-known cyclophanes, capable of forming cup- and barrel-shaped cavities, respectively. Their ability to bind various small molecular guests is well-established and can be tuned through synthetic modifications. In particular, the guest binding of pillararene hosts changes dramatically when the number or OH group substitution of the hydroquinone units is modified. 4 This variability has made pillararenes relevant to applications, for example, in rapid removal of organic micropollutants from water, 5 host–guest complexation of drug molecules, 6 all-solid-state lithium batteries, 7 and artificial membrane channels. 8

The cavity type of the materials can be further modified by arranging the building blocks into crystalline networks. 9

Metal–organic frameworks (MOFs) are a classic example that can achieve very high surface area and uptake of various gases, 10 (chiral) catalysts, 11 or even a large biomolecular guest such as proteins and DNA. 12–15 Furthermore, pillararenes have been crystallized into porous structures alone 16 or together with MOFs 17 to form highly porous structures that can be used, for example, to molecularly sort alkanes. 18 Beyond the small molecular host, colloidal nanoparticle supraspheres can be organized into higher-order structures. Their interparticle voids can be several nanometers in diameter and have recently been demonstrated to efficiently take up hydrophobic guest molecules 19 or to reversibly trap molecules for enhanced remediation.
reactivity and stereoselectivity.\textsuperscript{20} Incorporating MOFs into a mesoporous structure can further improve mass diffusion properties of the material, which highlights the importance of hierarchical frameworks in single-crystalline form.\textsuperscript{21}

The diversity of synthetic host molecules is rich and expanding; however, they are still much less sophisticated than those observed in nature.\textsuperscript{22} Naturally occurring protein-based hosts have evolved to carry out highly specific functions.\textsuperscript{23} Among these, ferritins are a key class of protein cages that are responsible for the nucleation and storage of elementary iron in living organisms.\textsuperscript{24} They have also been shown to function as versatile supramolecular templates for the synthesis of different inorganic materials\textsuperscript{25} and encapsulation of active biomolecules.\textsuperscript{26} The exactly defined structure of ferritin can also be utilized to prepare large 3D crystal structures using a protein–metal–organic approach\textsuperscript{27} or electrostatic interactions.\textsuperscript{28,29} An intriguing feature of such structures is that they can be used to direct the formation of nanoparticle superlattices, as placing an inorganic particle inside the cage does not affect its capability to form ordered structures.\textsuperscript{30,31} Furthermore, apoferritin single crystals have been utilized for structural characterization of the formation of sub-nanoclusters within the ferritin cage.\textsuperscript{32} In general, protein crystals with large voids can function in ways similar to those of other porous structures and host various guests \textit{via} supramolecular interactions.\textsuperscript{33–36}

In this article, we present a framework material that combines synthetic cyclophane hosts and native metal-binding protein cages. The advantage is that such an approach offers means to combine different hosts with specific recognition properties. Such materials have been shown to exhibit improved mass diffusion properties, and they enable binding of organic molecules close to catalytically active inorganic centers, which can be used to develop efficient and recyclable catalysts.\textsuperscript{21} We describe the synthesis of several cationic cyclophane hosts, consisting of resorcinarenes and pillararenes and show that hosts with more than five protonatable amines can efficiently bind negatively charged apoferritin protein cage particles and form large complexes. When the number and orientation of electrostatic interactions between the host and apoferritin are optimized, the system self-assembles into a porous cyclophane–protein cage framework (CPF). In the case of symmetrically cationic pillar[5]arene with 10 cationic charges, the CPF adopts a crystal structure where the apoferritin forms a face-centered cubic (fcc) lattice, and the pillar[5]arene hosts are electrostatically bridging the protein lattice and occupying the void spaces between the particles.

RESULTS AND DISCUSSION

Apoferritin (aFT) from \textit{Pyrococcus furiosus} was chosen as the protein part due to its well-defined size (diameter \textsimeq{} 12 nm), spherical shape, and hollow cavity of \textsimeq{} 8 nm. The cage consists of 24 protein subunits with 432 point group symmetry (Figure 1a) and has a total molecular weight of approximately 0.5 MDa.\textsuperscript{37} There are eight three-fold and six four-fold channels that span the cage and allow diffusion into the cavity. The cationic resorcin[4]arene hosts were synthesized by reacting the upper rim 2-position of the phenyl group with benzyloxycarbonyl (Boc)-protected amine in the presence of excess formaldehyde in a Mannich condensation reaction.\textsuperscript{38,39} Finally, the Boc protection was removed using acid hydrolysis to achieve resorcin[4]arene hosts with 4, 8, and 16 amines (hosts R(4+), R(8+), and R(16+), respectively). Additionally, a negatively charged control resorcinarene R(4–) was prepared. The synthesis of pillar[5]arenes with 5 (P(5+)) or 10 (P(10+)) quaternized amines was carried out by first preparing the macrocycle with either ethyl bromide or with ethylenediamine methyl acetate functionalization and finally

Figure 1. Apoferritin and supramolecular hosts used for the crystal preparation. (a) Recombinant apoferritin from \textit{Pyrococcus furiosus} (PDB id: 2JD6) with a diameter of \textsimeq{} 12 nm. (b) Synthesis of the charged resorcin[4]arene (R) hosts. (c) Synthesis of the cationic pillar[5]arene (P) hosts. (d) Schematic presentation of all the hosts used in this study. Diameters (d\textsubscript{host}) of the cationic hosts are approximately 1.5–2 nm.
converted to quaternary ammonium groups by either trimethylamine (P(10+)) or methyl iodide (P(5+)) treatment. The key synthesis steps and a schematic presentation of all the prepared cationic hosts are presented in Figure 1 b−d, respectively. Full experimental details together with characterization data are given in the Supporting Information section 1 (Schemes S1−S4 and Figures S1−S6).

Initially, the hosts’ ability to bind and complex aFT into larger assemblies was studied by following the increase in count rate with dynamic light scattering (DLS). An aqueous solution of aFT (100 mg L⁻¹) was slowly titrated with the host (0−80 mg L⁻¹). The assemblies form almost instantaneously after host addition. Figure 2a presents the titration curves for all host compounds. The hosts with a high number of cationic amines (R(16+), R(8+), and P(10+)) were able to fully complex aFT at low concentrations (cₖₕ < 20 mg L⁻¹) as indicated by the rapid increase in the observed count rate and hydrodynamic diameter (to ~2 μm, Figure S7a). In the case of P(10+), maximum intensity is achieved at 12 mg L⁻¹, which corresponds to approximately 25 hosts per aFT. However, the hosts with an intermediate amount of positive charges ((R(4+) and P(5+)) were able to bind the aFT but at much higher concentrations (cₖₕ > 50 mg L⁻¹) and lower final count rate. As expected, the negatively charged resorcinarene R(4−) was not able to interact efficiently with aFT due to the lack of attractive electrostatic interactions, and consequently, no changes in the count rate were observed.

Because the electrostatic interactions are sensitive to the presence of electrolytes and can be screened by increasing the electrolyte concentrations, we studied how the assemblies are affected by the addition of NaCl (0−200 mM). All complexes could be disassembled by NaCl addition (Figure 2b). In the case of P(10+), the disassembly was more complete than with the other hosts and took place at NaCl concentrations above 30 mM. Full disassembly of these complexes could also be induced by lowering the pH close to the isoelectric point of aFT (~4.5) or by temperature increase to 60 °C (Figure S8). The resorcinarene host-based assemblies did not disassemble completely at medium 50 mM NaCl concentration, which can be explained by their partial amphiphilic nature and the presence of attractive hydrophobic interactions between the building blocks. At 200 mM NaCl concentration, the complexes are almost fully disassembled and free aFT particles are mostly observed (Figure S7b). Electrophoretic mobility and ζ-potential (ζp) measurements presented in Figure 2c verify the overall negative charge of the free aFT particles (ζp...
cannot provide su
R(16+)
the
P(10+)
optimized. Only the
ordered frameworks with aFT even when thoroughly
scattering (SAXS) to estimate the degree of crystallinity.
concentrations (0
therefore assembled with aFT in a range of di
entirely, as already shown by the DLS data. All hosts were
attractive interactions and prevents assembly formation almost
concentration that modulates the electrostatic interactions.

Figure 3. Cryo-TEM and optical microscopy imaging of the crystals. (a) Cryo-TEM image of vitri
ed sample from the freshly prepared solution of
aFT particles is clearly visible. Low-magni
definition of the aFT, which explains why it is only weakly
detectable at ∼0.061 Å⁻¹. The lattice constant aSAXS was
estimated from the SAXS data by plotting the quadratic Miller
indices against the measured q values (Figure 2e inset). A linear regression yielded
yielded \( \sqrt{h^2 + k^2 + l^2} \) = 32.67 Å (Å⁻¹), and
for the observed fcc lattice, \( a_{SAXS} = 2\pi \times 32.67 \) Å = 20.5 nm. The
comparison to a simulated scattering curve from a finite
fcc model and the corresponding structure factor (\( S(q) \)) confirms the
\( \text{Fm} \overline{3} \text{m} \) Bravais lattice space group (number 225).
The calculated nearest neighbor aFT center-to-center distance is 14.5 nm, which leaves a ∼2.5 nm space between the adjacent
aFT particles. These dimensions correspond well with the size of
the aFT cage (\( d_{aFT} \sim 12 \) nm) separated by the P(10+) host
(\( d_{host} \sim 1.5 \) nm).

To visualize and further analyze the formed lattices, we
turned to cryogenic transmission electron microscopy (cryo-
TEM). A vitrified sample from the freshly prepared solution of the
crystals was imaged at 300 kV acceleration voltage. Figure
3a shows a typical small crystallite viewed along the [110]
projection axis. The highly ordered arrangement of individual
aFT particles is clearly visible. Low-magnification images
showing multiple highly ordered complexes from random
orientations of the lattices are presented in the Supporting
Information (Figure S9). From these images, it is possible to
find all the expected projections of the fcc lattice. Figure
3b shows the filtered inverse Fourier transform from selected
Fourier components of lattice projections viewed along [100], [110], and [111] projection axes. The observed images match
closely with the expected projections of the model unit cell.

Measuring the dimensions of the lattice along the [110]
projection yields a lattice constant, \( a_{TEM} = 20.5 \) nm, which
matches exactly with the SAXS data.
The relation between the crystal structure and crystal habit can be directly observed when imaging the crystals with optical microscopy. During growth, the crystals develop a clear octahedral habit (Figure 3d), and the dimensions of the crystal can easily be >10 μm (Figure S10a). aFT crystallization has been observed to proceed in the {111} lattice plane by the formation of step edges. Also in the case of aFT−P(10+) crystals, the surface energy is presumably smallest for the close-packed {111} faces, and growth of these eight faces leads to the observed octahedral habit (Figure S10b,c). The structure contains large cavities (Figure 3e), where the largest octahedral and tetrahedral voids are 8.5 and 5.8 nm in diameter, respectively. By assuming a spherical aFT particle with an inner hollow core, the space not occupied by ferritin protein subunits is very large and consists of approximately 66% of the volume of the unit cell (Figure S11). This shows that the structure has a percolated network of large voids between the aFT particles that can be occupied by the P(10+) hosts.

To obtain an insight into the interactions between P(10+) and aFT, we used molecular dynamics simulations. First, an atomistic model for both interacting species (Figure 4a, top) was created. Analysis of the electrostatic potential of the aFT cage surface revealed that it has a net negative charge. There are several negatively charged patches, but most of the negative charge of ferritin is located around the pores present at the three-fold symmetry axes, which constitute potential binding sites for the positively charged P(10+) (Figure 4a, bottom). However, binding to the other negatively charged patches can most likely also take place in this system. The large size of aFT prevents atomistic simulation of the full cage. Thus, as recently done to study the interaction of positively charged binders with viral capsids and microtubules, we first focused on the study of the local binding between one P(10+) and one three-fold binding site on the aFT cage. We cut a portion of the cage constituted by the protein chains surrounding the pore (Figure 4b, black α-helices) and their closest neighbors (gray). One P(10+) molecule was then placed in close vicinity above the pore and was observed to bind and equilibrate onto the cage pore by means of unbiased all-atom molecular dynamics (AA-MD) simulation in explicit water and ions (Figure 4b). Full computational details are provided in the Methods section and in the Supporting Information (Table S1). Metadynamics simulations (Figure 4c) then allowed us to quantify the free energy of binding of P(10+) to the cage pore as ΔG = −13 ± 1.4 kcal mol⁻¹ (average ± standard error). Analysis of the nonbond interactions conducted on the unbiased AA-MD trajectories (Figure 4d) indicated that the P(10+) binding is controlled by favorable interactions with negatively charged...
glutamate (Glu) amino acids (Glu 109/121), particularly dense in the pore region (capturing ~96% of the total nonbond interaction with the surface). Of this interaction with Glu residues, ~70% is controlled by electrostatic interactions (Figure 4d).

Next, starting from the equilibrated 1:1 P(10+)–aFT obtained from AA-MD, we built another molecular model containing a second cage pore region symmetrically bound to the same binder (Figure 4e, 1:2 system). This model was equilibrated in explicit water and counterions by means of AA-MD simulation, providing information on the interactions of P(10+) bridging two cages. The extracted data demonstrated that a single P(10+) can stably interact with two cages. From this AA-MD simulation, we could observe that the interaction is symmetric, indicating that the binding to a second cage does not impair the binding to the first one.

CONCLUSION

We have laid out the rules for preparing framework materials from synthetic cyclophanes and protein cages. A facially symmetric pillar[5]arene with 10 protonatable amines was identified as the optimal host to electrostatically self-assemble with ferritin cages to yield ordered framework structures. The crystals have large interconnected voids between the protein cages that are in the size range of several nanometers. We envision that following the presented design parameters, it is possible to prepare CPFs from a variety of cyclophanes and tune the binding properties of the resulting framework materials. Furthermore, it would be possible to expand the design space of CPFs by using de novo engineered protein cages.44−46 These developments could in the future lead to an efficient heterogeneous catalyst, where the cyclophanes are able to trap guest molecules close to the catalytic sites of the biomolecules,20 multifunctional water remediation materials,47 or preparation of zeolite-type structures with rod-like biomolecules.48

METHODS

Dynamic Light Scattering and ζ-Potential Measurements.

The hydrodynamic diameter (Dh) of the assemblies was measured using a Malvern Instruments DLS device (Zetasizer Nano ZS Series) with a 4 mW He−Ne ion laser at a wavelength of 633 nm and an avalanche photodiode detector at an angle of 173°. Experiments were carried out at 25 °C. Plastibrand semimicro poly(methyl methacrylate) cuvettes and Malvern disposable −cells were used for the measurement. Zeta potentials were measured using Zetasizer Nano ZS Series. Sample-to-detector distance was 1.59 m, and a silver behenate standard sample was used for the calibration of the length of the scattering vector q. One-dimensional SANS data were obtained by azimuthally averaging the 2D scattering data, and the magnitude of the scattering vector q is given by q = 4π sin θ/λ, where 2θ is the scattering angle.

Sample Preparation for SAXS, Cryo-TEM, and Optical Microscopy. Cyclopane−aFT samples were prepared by combining 6 μL of aqueous aFT solution (15 mg mL−1, Pyrococcus furiosus, Molecular Links Rote), 3.5 μL 20 mM Tris pH 8.5 buffer, 1.5 μL of 0−400 mM NaCl solution, and 4 μL of 10 mg mL−1 cyclophane in water, in this order. The samples were gently mixed with a pipet and allowed to set. All-Atom Simulations. All simulations were conducted using the GROMACS 5.1.2 software and the PLUMED 2 plugin.49,50 The atomic model for P(10+) was parametrized with the general Amber force field, and aFT was parametrized using the Amber force field ff12SB. The P(10+) binding energy (ΔG) was calculated from metadynamics simulations. All computational details on the creation of the molecular systems, their equilibration, and the simulation parameters used in AA-MD and metadynamics simulations are provided in the Supporting Information.

ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/acsnano.8b02856.

Details of the synthesis, full experimental methods, additional DLS and TEM analysis (PDF)

AUTHOR INFORMATION

Corresponding Author

E-mail: mauri.kostiainen@aalto.fi.

ORCID

Ngong Kodiah Beyeh: 0000-0003-3935-1812
Nonappa: 0000-0002-6804-4128
Davide Bochicchio: 0000-0002-3682-9086
Giovanni M. Pavan: 0000-0002-3473-8471
Olli Ikkala: 0000-0002-0470-1889
Robin H. A. Ras: 0000-0002-2076-242X
Mauri A. Kostiainen: 0000-0002-8282-2379

Notes

The authors declare no competing financial interest.

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