The Role of Nonconserved Residues of Archaeoglobus fulgidus Ferritin on Its Unique Structure and Biophysical Properties*

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Background: Archaeoglobus fulgidus ferritin (Afftn) assembles with unique tetrahedral symmetry and four large pores.

Results: The Afftn K150A/R151A double mutant forms a closed octahedral assembly with reduced iron release rates relative to the tetrahedral assembly.

Conclusion: The K150A/R151A substitution alters the symmetry type of the ferritin cage.

Significance: The Afftn can be modulated for tuning molecular release from the cavity.

Archaeoglobus fulgidus ferritin (Afftn) is the only tetracossameric ferritin known to form a tetrahedral cage, a structure that remains unique in structural biology. As a result of the tetrahedral (2-3) symmetry, four openings (~45 Å in diameter) are formed in the cage. This open tetrahedral assembly contradicts the paradigm of a typical ferritin cage: a closed assembly having octahedral (4-3-2) symmetry. To investigate the molecular mechanism affecting this atypical assembly, amino acid residues Lys-150 and Arg-151 were replaced by alanine. The data presented here shed light on the role that these residues play in shaping the unique structural features and biophysical properties of the Afftn. The x-ray crystal structure of the K150A/R151A mutant, solved at 2.1 Å resolution, indicates that replacement of these key residues flips a “symmetry switch.” The engineered molecule no longer assembles with tetrahedral symmetry but forms a typical closed octahedral ferritin cage. Small angle x-ray scattering reveals that the overall shape and size of Afftn and Afftn-AA in solution are consistent with those observed in their respective crystal structures. Iron binding and release kinetics of the Afftn and Afftn-AA were investigated to assess the contribution of cage openings to the kinetics of iron oxidation, mineralization, or reductive iron release. Identical iron binding kinetics for Afftn and Afftn-AA suggest that Fe(II) ions do not utilize the triangular pores for access to the catalytic site. In contrast, relatively slow reductive iron release was observed for the closed Afftn-AA, demonstrating involvement of the large pores in the pathway for iron release.

Ferritin is a virtually ubiquitous intracellular iron storage protein. The ferritin archetype consists of a multisubunit protein complex composed of 24 polypeptides, which self-assemble into a hollow cage structure having octahedral (4-3-2) symmetry, with external and internal diameters of ~12 and 8 nm, respectively (1, 2). Excess iron in the blood is stored in ferritin as an insoluble ferric compound that is released in soluble ferrous form during iron starvation to maintain iron homeostasis. Conversion of Fe(II) to Fe(III) in the ferritin protein complex is catalyzed by a ferroxidase center located within the hydrophilic interior of individual subunits. A mineral ferrihydrite, [FeO(OH)]n[FeO(H2PO4)] core is subsequently formed by accumulation of insoluble ferric iron at a nucleation site located within the ferritin cage (3–5). The ferrihydrite core may be reduced by ascorbic acid or other reducing agents to produce soluble Fe(II) in vitro (6, 7).

In general, channels of 3–5 Å diameter that are located at 3- and 4-fold molecular symmetry axes, connect the inner cavity to the ferritin surface, and are proposed as routes for inward and outward movement of ions, protons, and small molecules (3–9). The 3-fold symmetric channels are established as the main pathway for entry of Fe(II) ions into the cavity, whereas the function of 4-fold symmetric channels remains controversial (7, 8). Some studies have proposed the 4-fold symmetric channels as the exit route for protons and Fe(III) (3, 6).

The crystal structure of the Archaeoglobus fulgidus ferritin (Afftn)5 (Protein Data Bank code 1SQ3; Fig. 1) represents the first report of an archaeal ferritin structure. The report describes a tetracossameric ferritin shell with unprecedented tetrahedral (2-3) symmetry, which remains unique in structural biology (10). As a consequence of the tetrahedral assembly of the molecule, four large triangular pores (~45 Å diameter) are

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5 The abbreviations used are: Afftn, A. fulgidus ferritin; PfFtn, P. furiosus ferritin; SAXS, small angle x-ray scattering; RMSD, root mean square deviation.
Roles of Nonconserved Residues on Unique AfFtn Features

**EXPERIMENTAL PROCEDURES**

**Gene Expression and Protein Purification**—The AfFtn gene (AF0834) was cloned into NdeI and BamHI sites of a pET-11a expression vector (Novagen). K150A/R151A mutation was constructed by PCR-based site-directed mutagenesis using duplex primers and the AF0834 gene as the template. The mutations were inserted within primer sequences. The PfFtn gene was cloned into NdeI and Sall restriction sites of the vector pET24a(+) (11). Recombinant plasmids were stored in Escherichia coli DH5α.

For overexpression, *E. coli* expression strain (BL21(DE3) CodonPlus-RIL) was transformed with the constructs, and protein production was done in LB medium inoculated with an overnight culture. The genes were induced for 4 h by the addition of 1 mM isopropyl β-D-thiogalactopyranoside when $A_{600}$ was between 0.6 and 0.8. AfFtn and AfFtn-AA were purified by hydrophobic interaction chromatography after thermal purification of the cell lysate at 85 °C for 10 min following previously described method (10). Chromatography was performed on an ÄKTA-Explorer FPLC system (GE Healthcare) using HiPrep 16/10 Phenyl FF (high sub) column equilibrated with 25 mM HEPES buffer containing 50 mM NaCl and 500 mM (NH₄)₂SO₄, pH 7.5. The eluted fractions containing the purified protein without (NH₄)₂SO₄ were pooled. PfFtn was produced and purified following previously published method (9). All proteins were stored at 4 °C until use.

**Protein and Iron Assay**—Protein concentration was measured by bicinchoninic acid method following the manufacturer’s protocol using bovine serum albumin as the standard (RCA protein assay kit; Thermo Scientific). Iron was determined spectrophotometrically by adding 20 mM dithionite to convert total iron into the ferrous form in the presence of bathophenanthroline sulfonic acid to form an iron complex following a method described by Bonomi and Pagani (12) with slight modification. Briefly, the ferritin samples were denatured by treating with 50 mM HNO₃ and mixed with 20 mM bathophenanthroline sulfonic acid, 20 mM dithionite, and 250 mM Tris buffer, pH 8.0. The mixture was incubated overnight, and iron concentration was measured from the absorbance of the complex at 538 nm ($\varepsilon_{538} = 22.1\text{ M}^{-1}\text{ cm}^{-1}$).

**Self-assembly Study**—Salt-mediated self-assembly was studied with apoferritin aliquots incubated overnight with different NaCl concentrations (in 25 mM HEPES buffer, pH 7.5). Molecular sizes of different AfFtn oligomers were determined by size exclusion chromatography using Superdex 200 10/300 GL column (GE Healthcare). The column was equilibrated with 25 mM HEPES, pH 7.5, containing NaCl at the same concentration in which the protein was preincubated, and the same buffer was used as mobile phase. Molecular masses of each oligomeric species were determined by comparing their elution volumes with the elution volumes of standard proteins in the same salt concentration.

The self-assembly was confirmed from the change of hydrodynamic diameter at different salt concentrations as detected by dynamic light scattering (Zetasizer Nano ZS; Malvern Instruments) technique. For salt-mediated self-assembly, the AfFtn and AfFtn-AA preparations were preincubated...
calculation was performed on the protein interfaces, surfaces, and assemblies online portal (PDBePISA).

**SAXS Studies**—SAXS data were collected on a Rigaku BioSAXS-1000 system configured with a Rigaku FR-E+ Super-bright rotating anode generator operating at 2.475 kW. The BioSAXS-1000 system is a two-dimensional Kratky SAXS camera that utilizes a point focus source, a Kratky block for beam collimation, and a Dectris Pilatus 100K detector. The Pilatus 100K is a hybrid pixel array detector that provides high sensitivity and low readout noise, both of which are ideal for measuring the very low SAXS signal provided by most macromolecules in solution. The sample to camera distance is ~500 mm, and the q range is 0.008–0.65 Å⁻¹. The BioSAXS-1000 beam path was evacuated to reduce absorption of the scattered x-rays by air. The data collection and scattering-derived parameters are shown on Table 2.

To test for concentrations effects, the sample was serially diluted 50 and 25% with buffer (25 mM HEPES, pH 7.5, containing 500 mM NaCl and 4% glycerol). Prior to SAXS measurements, each sample was centrifuged for 10 min at 4 °C at 10,000 rpm. Then ~20 µl of sample was pipetted into 1.0-mm quartz capillary cells that were sealed at each end with screw caps and O-rings for measurement under vacuum. Both buffer and sample solutions were measured in the same capillary cell for proper buffer subtraction. For each sample and buffer measurement, two scans of 30 min were collected. All data were collected at 4 °C.

Following direct beam and sample to detector distance calibration with a silver behenate standard, the SAXS images from the x-ray detector were azimuthally averaged to obtain onedimensional scattering profiles using SAXS Lab. Duplicate scattering profiles were averaged together, and the averaged buffer profiles were subtracted from the average sample profiles using PRIMUS (23). The resulting scattering data are shown as a function of increasing q. Following buffer subtraction, Guinier plots were prepared using PRIMUS (23) for each sample dilution to assess sample quality, determine the forward scattering intensity, I(0), and determine the radius of gyration, \( R_g \). Low resolution data to q < 1.3 \( R_g \) were used to define the Guinier region and determine \( R_g \). GNOM was used to calculate the indirect Fourier transformation of the scattering data from reciprocal space to real space as expressed in the pair distance.
Roles of Nonconserved Residues on Unique AfFtn Features

FIGURE 2. A, size exclusion chromatogram showing elution volumes of different oligomeric species of AfFtn (black) and AfFtn-AA (red) in the presence of 600 mM NaCl (solid lines) and 20 mM NaCl (dashed lines). A systematic shift toward higher elution volume was observed for both experimental samples (solid lines) and molecular mass standards (not shown) at 600 mM NaCl relative to that in 20 mM NaCl. B, distribution of 24-mer in AfFtn (black) and AfFtn-AA (red) solutions in the presence of different NaCl concentrations as determined by size exclusion chromatography.

distribution function, \( P(r) \). The \( R_g \) and \( I(0) \) from the \( P(r) \) are also reported. The molecular masses were estimated using the experimentally determined forward scattering value, \( I(0) \), using a glucose isomerase standard and from the calculated Porod volume,

\[
V = 2\pi^2 \cdot (I(0)/Q)
\]

by using the program \( \text{datPOROD} \) (24) and the web service \( \text{SAXSMoW} \) (25). Ten low resolution \( \text{ab initio} \) shape models were calculated using the program \( \text{DAMMIF} \) (24).

These models were subsequently aligned and averaged with the programs \( \text{SUPCOMB} \) (26) and \( \text{DAMAVER} \) (27). The filtered SANS model and the sample crystal structures were superimposed with \( \text{SUPCOMB} \) (26). The dry volume and partial specific volume were calculated from the sequence of the monomeric species using the web service (28).

Iron Binding—Iron loading (mineralization) of ferritin was performed following a previously described method (4). Briefly, freshly prepared ferrous sulfate solution in 0.1% HCl was added to apoferritin solution followed by incubation for 1 h at room temperature and overnight at 4 °C.

Binding kinetics was studied in dilute protein solutions (0.01 mg/ml) to avoid fast autoxidation at higher \( \text{Fe}^{2+} \) concentrations. The reaction was monitored colorimetrically by measuring the absorbance increase at 315 nm. The reaction was started by addition of 10 \( \mu \)l of freshly prepared 10 mM ferrous sulfate solution in 0.1% HCl to 1 ml of 0.01 mg/ml ferritin solution (in 100 mM HEPES, pH 7.0) preincubated at 20 °C in a temperature-controlled spectrophotometer. The binding kinetics of AfFtn and AfFtn-AA was compared with that of PfFtn.

Iron Release—The iron release profiles of mineralized ferritins were studied at 70 °C in the presence of 10 mM ascorbate (reducing agent) and 1 mM ferrozine. The final protein concentration was maintained at 0.05 mg/ml in 0.1 M HEPES, pH 7.0. Mineralized ferritin solution (loaded with \( \sim 1200 \text{ Fe/24-mer} \) was incubated with 1 mM ferrozine in a temperature-controlled spectrophotometer. The reaction was started by addition of 10 \( \mu \)l of 1 M ascorbate, and iron release was studied by monitoring the formation of \( \text{Fe}^{2+} \)-ferrozine complex at 562 nm. Iron release kinetics of AfFtn and AfFtn-AA was compared with PfFtn.

RESULTS AND DISCUSSION

AfFtn and AfFtn-AA Show Comparable Self-assembly Pattern—AfFtn has been shown to exist primarily as dimer and fully assembled 24-mer at 20 and 600 mM NaCl concentrations, respectively (10, 29). Size exclusion chromatography and dynamic light scattering studies at different salt concentrations suggest that the self-assembly of AfFtn-AA is also dependent on ionic strength. At all ionic strengths tested (ranging from 20 to 600 mM) AfFtn and AfFtn-AA eluted primarily in two peaks corresponding to dimer (\( \approx 45 \text{kDa} \)) and 24-mer (\( \approx 490 \text{kDa} \)) (Fig. 2A). No other oligomeric species corresponding to theoretical intermediates in the self-assembly process were observed. For both AfFtn and AfFtn-AA, the 24-mer to dimer ratio gradually increased with increasing ionic strength, but the AfFtn-AA consistently contained a higher proportion of 24-mer when compared with AfFtn (Fig. 2). At low ionic strength, AfFtn eluted as a single peak corresponding to dimer, whereas \( \sim 15\% \) of the AfFtn-AA was eluted as a 24-mer. In buffer containing 600 mM NaCl, 100% of the AfFtn-AA preparation was converted to 24-mer, whereas \( \sim 4\% \) of AfFtn remained in the dimeric state. Further supporting the observed salt-mediated self-assembly of these proteins, increased hydrodynamic diameters of AfFtn and AfFtn-AA were also observed in dynamic light scattering analysis after addition of 600 mM NaCl (Fig. 3). These observations indicate that the replacement of Lys-150 and Arg-151 amino acid residues has a minimal effect on the solution properties of AfFtn-AA. It is also to be noted that the salt-mediated self-assembly is reversible and operates in a very similar manner for both AfFtn and AfFtn-AA. The small increase in the ratio of 24-mer to dimer in solutions of AfFtn-AA indicates a shift in equilibrium,
away from dimeric species, most likely because of a lower energy 24-mer end product.

Analysis of crystal structures identified several hydrophobic contacts at the subunit interfaces that appear to be important for stabilization of the self-assembled 24-mer structures of AfFtn and AfFtn-AA. Salt-mediated self-assembly is caused by enhanced hydrophobic interactions at high ionic strength, and a clear shift is observed in the oligomeric state with increased NaCl concentrations (Fig. 2B). The reversible salt-mediated process supports hydrophobic interactions as a key force in shifting the dimeric structures to 24-meric cage. In addition, substitution of hydrophilic Lys-150 and Arg-151 residues of AfFtn with hydrophobic alanine in AfFtn-AA fits with the observation of a shift in equilibrium toward 24-mer in AfFtn-AA compared with wild-type AfFtn. The substitution removes destabilizing forces (i.e., steric clashes and repulsive charges) and allows enhanced interactions between subunits in the assembled AfFtn-AA, hence increasing the proportion of 24-mer in AfFtn-AA as compared with the wild-type AfFtn.

The Crystal Structure of AfFtn-AA Indicates Rearrangement of Molecular Quaternary Symmetry—Based on the crystal structure of AfFtn, the amine side chain of the AfFtn Lys-150 residue forms a hydrogen bond with the backbone O at Met-111, an interaction that likely stabilizes the unusual structure with tetrahedral symmetry (Figs. 4A and 5A). The AfFtn Arg-151 side chain is positioned such that it would prohibit assem-

**FIGURE 3.** Hydrodynamic diameters of AfFtn (black) and AfFtn-AA (red) in the presence of 600 mM NaCl (solid lines) and 20 mM NaCl (dashed lines) as determined by dynamic light scattering. The hydrodynamic diameters were measured as follows: AfFtn, 9.4 nm (20 mM) and 14.0 nm (600 mM); and AfFtn-AA, 9.2 nm (20 mM) and 14.0 nm (600 mM).

**FIGURE 4.** A and B, crystal structure of AfFtn (A) and AfFtn-AA (B). C and D, overlay of the filtered (red) and averaged (gray) envelopes (both calculated from SAXS data) of AfFtn (C) and AfFtn-AA (D) with the respective crystal structures (dark maroon). The averaged envelope (or bead model) is produced by DAMAVER and represents the total spread of all the individual superposed models. The filtered envelope is produced by DAMFILT, which removes low occupancy and loosely connected atoms from the averaged envelope to generate a compact, more probable model.
bly of a closed octahedral structure by sterically blocking association of helices at the octahedral 4-fold interface (10). Moreover, these nonconserved amino acid residues contribute to the formation of positively charged clusters located at apices of the triangular open pores. Replacement of these bulky positively charged side chains with the small uncharged side chain of an alanine residue is hypothesized to decrease the positive surface potential at the triangle apices. Therefore, Lys-150 and Arg-151 residues seem critical for the unique open pore structure of AfFtn.

Replacement of the two key amino acids causes a massive rearrangement of the quaternary structure; cage assembly is switched from tetrahedral in AfFtn to octahedral symmetry for the AfFtn-AA. The crystal structure of AfFtn-AA (Protein Data Bank code 3KX9) clearly demonstrates this symmetry switch as a closed protein cage with octahedral symmetry is observed (Fig. 4B).

In AfFtn, pairs of adjacent Arg-151 residues are located ~49 Å apart at each apex of the large triangular pores (Figs. 1 and 5A). In the AfFtn-AA crystal structure, four mutant residues (Ala-151) are rearranged to pack closely (~4 Å apart) at the 4-fold symmetry interfaces (Fig. 5B). This packing appears to stabilize the closed structure through Ala-151–Ala-151 hydrophobic interactions. The closed structure has a slightly smaller diameter than AfFtn based on the crystal structures. The calculated accessible surface area for AfFtn-AA is also smaller (146,140 Å²) compared with AfFtn (156,450 Å²) but has a larger buried surface area (77,800 Å²) compared with AfFtn (64,950 Å²). The decrease in the accessible surface area from AfFtn to AfFtn-AA may serve as an approximate measurement of the free energy difference between the two types of cages (30, 31). Thus, by closing the triangular pore in AfFtn-AA, the buried surface area is increased, and the octahedral cage is thermodynamically more stable than the tetrahedral AfFtn cage. The direct evidence of the increased stability is the observed shift in the solution equilibrium.

SAXS data reveal that the overall shape and size of AfFtn and AfFtn-AA in solution are consistent with their respective crystal structures (Fig. 4, C and D). Specifically, structural parameters (D_max, R_g, and molecular mass) calculated from the SAXS data are consistent with those from the crystal structure (Table 3). The structural parameters are smaller for AfFtn-AA relative to AfFtn by 3–6 and 2–4 Å, respectively, across the concentration range. This would be consistent with a closed conformation for AfFtn-AA versus an open conformation for AfFtn. SAXS profiles and Kratky plots show several peaks, as expected for hollow spheres. Also, the shape of the pair-distance distribution function for both AfFtn and AfFtn-AA is typical of hollow spheres, with a maximum shifted toward a distance larger than D_max/2 (Fig. 6).

Quaternary Structures of the AfFtn-AA Resemble PfFtn More Closely than AfFtn—Hexamer is a widely proposed intermediate in self-assembly of ferritin cages despite the absence of any experimental observations (9, 10, 32). The structural conformation of hexameric intermediate may reflect the symmetry of 24-meric ferritin cage. Structural superimposition of AfFtn, AfFtn-AA, and PfFtn monomers, dimers, and hexamers shows that the primary, secondary, and tertiary structures of AfFtn-AA are closely related to AfFtn and PfFtn (Fig. 7). As expected for the monomer, AfFtn-AA is more structurally related to AfFtn.
Roles of Nonconserved Residues on Unique AfFtn Features

| TABLE 3 | Comparison of $D_{\text{max}}$, $R_g$ values, and molecular mass calculated from the SAXS data and the crystal structure of apo AfFtn and AfFtn-AA |
|---------|------------------------------------------------------------------------------------|
|          | **SAXS**                                                                 |
|          | 8 mg/ml  | 4 mg/ml  | 2 mg/ml  | Average  | Structure  |
| $D_{\text{max}}$ (Å) | AfFtn   | 131      | 133      | 133      | 133        | AfFtn-AA  | 129      | 128      | 130      | 129        | 136        |
| $R_g$ (Å) from $P(r)$ | AfFtn   | 55.46    | 55.63    | 55.55    | 55.55     | 57.25      | AfFtn-AA  | 53.18    | 53.26    | 53.42    | 53.29     | 53.61      |
| Molecular mass (kDa) from Porod volume//(0)//SAXSMoW | AfFtn   | 425.1/435.0/459.5 | 440.5/436.8/471.2 | 441.2/435.2/471.1 | 487.6/484.2 |
|          | AfFtn-AA  | 442.2/436.3/463.8 | 446.9/433.9/482.7 | 455.2/443.9/477.4 | 484.2 |

* Calculated from the crystal structure using both CRYSTOL and Moleman2.
* Calculated from the sequence using ProtParam tool.

![Normalized pair-distance distribution function plots for three concentrations of AfFtn (A) and AfFtn-AA (B) obtained from 30-min exposures.](image)

Fig. 6. Normalized pair-distance distribution function plots for three concentrations of AfFtn (A) and AfFtn-AA (B) obtained from 30-min exposures. Blue, 8 mg/ml; red, 4 mg/ml; green, 2 mg/ml protein concentration. The shape of the pair-distance distribution function for both AfFtn and AfFtn-AA is typical of hollow spheres. Average $D_{\text{max}}$ values of AfFtn and AfFtn-AA are calculated as 133 and 129 Å, respectively.

(RMSD = 0.393 Å) than PfFtn (RMSD = 0.648 Å). However, at the level of quaternary subassembly components (dimers and hexamers), AfFtn-AA is actually more closely related to PfFtn (dimer and hexamer RMSDs = 0.775 and 0.881 Å, respectively) than AfFtn (dimer and hexamer RMSDs = 0.820 and 1.066 Å, respectively). Despite relatively low similarity in primary, secondary, and tertiary structure, the quaternary structure of the octahedral AfFtn-AA and PfFtn resemble each other most closely, both in the symmetry class of the 24-mer and in the structural relatedness of their quaternary dimeric and hexameric building blocks. In contrast, although AfFtn-AA and AfFtn have 99% sequence identity and virtually identical subunit structure, the quaternary building blocks are less structurally related, relative to PfFtn, and the cages assemble with divergent symmetry (octahedral versus tetrahedral).

The Large Triangular Pores Are Involved in the Ascorbate Transport to the Core and Affect the Release Rate but Not the Nucleation Rate—Ferritin is the iron storage protein with oxidoreductase activity. It buffers intracellular and extracellular iron levels by highly coordinated activity of specific ion channels and catalytic centers. Fe$^{2+}$ ions pass through openings on the protein surface to the catalytic centers and are oxidized to Fe$^{3+}$ ions that move to the nucleation site for subsequent bulk mineralization (7). Comparative studies of iron binding/release kinetics of AfFtn and AfFtn-AA were performed to elucidate the role of the distinct triangular pores of AfFtn in the iron transport pathway. The iron binding and release kinetics of AfFtn and AfFtn-AA were also compared with another archaeal ferritin, PfFtn. Fig. 8A shows that iron binding kinetics in all three ferritins have more than one phase. The initial fast reaction is due to immediate oxidation of irons at the ferroxidase center that is followed by a subsequent slower oxidation phase at the nucleation site within the ferritin cavity. The latter phase requires transport of Fe$^{2+}$ ion into the cavity from the external environment. Experiments show virtually identical iron binding kinetics for both AfFtn and AfFtn-AA and suggest that the triangular pores do not play a significant role in the mechanism of Fe$^{2+}$ oxidation. Ion transport through protein is governed by charge distribution of specific ion channels. Fe$^{2+}$ ion intake in ferritin takes place through a very specific pathway, i.e., the hydrophilic 3-fold symmetric channels, which are lined by negatively charged amino acids. From the crystal structure data of frog ferritin, Tosha et al. (7) reported that metal ions need to follow specific ion channels from the 3-fold openings with highly conserved residues to access the catalytic site at the ferritin interior. They showed that the movement of Fe$^{2+}$ ion from the pore opening is guided by the charge distribution of the channel. Mutation of several amino acids on the 3-fold symmetric channel of frog M-ferritin showed that specific residues are essential in each step of Fe$^{2+}$ ion mobility from the channel opening to the nucleation site (8, 33). AfFtn has a second potential route for Fe$^{2+}$ ion entry, i.e., the negatively charged channels previously described as “A” channels (10). These channels are located between the noncrystallographic symmetry axis and...
the large triangular pore. They extend to the ferritin interior and are large enough for transport of Fe$^{2+}$ ions. Although negatively charged 3-fold symmetric channels and A channels of AfFtn appear suitable for inward movement of Fe$^{2+}$ ion, the charge distribution of the large triangular pores may not be favorable for this purpose. Positive electrostatic potential of the triangle apices is extended from the exterior surface of AfFtn, through the pore opening, and onto the interior surface of the AfFtn shell (10). Reasonably, this positive surface potential is unlikely to favor passage of any positively charged moiety through these pores. However, slower Fe$^{2+}$ oxidation in PfFtn may be due to the difference in electrostatic charge in the 3-fold channels of the ferritins isolated from two different species. The 3-fold channels of PfFtn are reported to be less hydrophilic in comparison with that of AfFtn, and this may cause lower affinity of Fe$^{2+}$ ion to the 3-fold symmetric channels of PfFtn than 3-fold symmetric channels of AfFtn or AfFtn-AA (9).

Fig. 8B shows the iron release kinetics by ascorbate-mediated Fe$^{3+}$ reduction. The initial iron release rates of AfFtn, AfFtn-AA, and PfFtn were calculated to be 90, 70, and 57 $\mu$M min$^{-1}$, respectively. The iron release rate of AfFtn-AA is slower than that of AfFtn, which suggests involvement of the triangular pores in reductive iron release from the AfFtn core. However, the contribution of these pores in the iron transport process is yet to be rigorously established. These pores could be used for transport of negatively charged ascorbate to the nucleation site. The relatively small decrease in the iron release rate of the closed AfFtn-AA indicates a minor contribution of the large pores under these conditions. A much larger change would be expected if the triangular pores provide a substantial pathway for ascorbate transport or if transport is not rate-limiting. Similar results were obtained using another reducing agent, i.e., NADH (data not shown). Ascorbate-mediated reduction of ferric core is a common observation in many archetypal ferritins, which further supports the role of the large triangular pores of AfFtn as a route that is additional to the narrow channels generally used for ascorbate transport in ferritins. Like any typical octahedral ferritin, AfFtn-AA may utilize 3- or 4-fold channels for ascorbate transport.

Reductive iron release from ferritin core is a complex process that depends on access of the reducing agent to the ferric core and the transport of reduced Fe$^{2+}$ ion from the interior to the channel openings (34, 35). The existing literature evidence suggests that both 3- and 4-fold channels are associated with the reductive iron release mechanism (3, 6, 36, 37). The 4-fold
Roles of Nonconserved Residues on Unique AfFtn Features

channels were predicted as the route for proton and Fe$^{2+}$ ion transport during mineralization and demineralization (3, 6). In two different studies, the 3-fold channels of horse ferritin were locally unfolded by mutation of conserved amino acids in the 3-fold channels. The mutations resulted in increased Fe$^{3+}$ release rates, and the authors proposed involvement of the 3-fold channels in the mechanism of reductive iron release (36, 37). Another study observed iron release as a multistep procedure involving hydrolysis of Fe-O/OH-Fe bridges, chelation of iron inside the ferritin cage, and/or transfer of iron to the chelator outside the ferritin (4). This study further described the ferritin channel as a gated pore. Control of reductive iron release was explained by controlled access of reducing/chelating agents to the ferric core by altering the structure of these gated pores.

Based on the charge distribution of the triangular pores of AfFtn and our experimental observations, we hypothesize that these pores are used for entry of negatively charged ascorbate but have no role in the transport of positively charged Fe$^{2+}$ ion. The large triangular pores allow faster ascorbate transport to the AfFtn core and, hence, an increased rate of Fe$^{3+}$ reduction compared with AfFtn-AA. The closed octahedral cage of AfFtn-AA limits access of ascorbate into the ferritin interior, which leads to relatively slow rates of Fe$^{3+}$ reduction. Considering the major structural differences in tetrahedral and octahedral assemblies, it is possible that features distinct from the pores contribute to the slower iron release rate observed in AfFtn-AA. Further studies will be required to verify the precise molecular components involved in the complex process of iron release from these fascinating iron storage proteins.

**Conclusion**—Using x-ray crystal structures, SAXS, and kinetic data, we demonstrate that the triangular pores of AfFtn are not artifacts of crystallization and that the Lys-150 and Arg-151 residues are critical for stabilization of the open pore tetrahedral structure of AfFtn. The data presented here further indicate that the large pores are involved in reductive iron release from AfFtn. Substitution of the bulky positively charged side chains of Lys-150 and Arg-151 with the small hydrophobic side chain of alanine results in a massive rearrangement in the quaternary structure and a switch from tetrahedral to octahedral symmetry. The mutations remove sterically clashing and provide enhanced hydrophobic interactions at the 4-fold interface, allowing subunits to self-assemble into a closed archetypal ferritin cage with slightly smaller dimensions compared with the wild type. With the caveat of unavoidable differences between conditions in crystallization and solution experiments, the structural parameters obtained from SAXS are consistent with those obtained from the crystal structures.

Analysis of the crystal structures and the observation of self-assembly in conditions of high ionic strength also indicate hydrophobic interactions as key forces that stabilize the cage structures of both AfFtn and AfFtn-AA. Elimination of the large triangular pores results in slower reduction of Fe$^{3+}$ core but does not affect the rate of Fe$^{2+}$ oxidation and suggests that these pores are not involved in Fe$^{2+}$ ion transport. However, understanding the exact function of these pores and their exact role in the reductive release of the Fe$^{3+}$ core will require further research.

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