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1 Fusion of amyloid beta with ferritin yields an isolated  
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17 **Keywords:** Ferritin cage; Amyloid beta;  $\beta$ -sheet-rich oligomer; High-speed AFM.

1 **Abstract**

2 Alzheimer's disease is a severe brain condition caused by the formation of amyloid plaques  
3 composed of amyloid beta (A $\beta$ ) peptide. These peptides form oligomer, protofibril, and fibril  
4 before deposition into amyloid plaques. Among these intermediates, A $\beta$  oligomers (A $\beta$ O) were  
5 found to be the most toxic and therefore an appealing target for drug development and  
6 understanding their role in the disease. However, precise isolation and characterization of A $\beta$ O  
7 have proven challenging because A $\beta$ O tend to aggregate and form heterogeneous mixtures in  
8 solution. As a solution, we genetically fused the A $\beta$  peptide with a ferritin monomer. Such fusion  
9 allowed to encapsulate precisely 24 A $\beta$  peptides inside the 24-mer ferritin cage. Using high-speed  
10 atomic force microscopy (HS-AFM), we disassembled the ferritin and directly visualized the A $\beta$   
11 core enclosed within the cage. The thioflavin-T assay (ThT) and attenuated total reflection infrared  
12 spectroscopy (ATR-IR) reveal the presence of  $\beta$ -sheet structure in the encapsulated oligomeric  
13 aggregate. Gallic acid, an amyloid inhibitor can inhibit the fluorescence of ThT bounded A $\beta$ O. Our  
14 approach represents a significant advance in the isolation and characterization of a  $\beta$ -sheet rich  
15 A $\beta$ O and is expected to be useful for future studies of other disordered peptides such as  $\alpha$ -synuclein  
16 and tau.

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## 1 **Introduction**

2 Protein cages have gained significant attention in biomaterials science due to their well-defined  
3 capsule-like structures with monodisperse sizes.<sup>1, 2</sup> These cages are formed by self-assembly of  
4 protein monomers. Virus-like particles, ferritin, heat-shock proteins and chaperonins are typical  
5 examples of protein cages.<sup>3</sup> Such particles serve various purposes, such as templates for  
6 synthesizing nanomaterials, drug delivery vehicles, and catalytic reaction chambers.<sup>4</sup> Recently, it  
7 was found that larger biomolecules such as proteins and enzymes can be encapsulated within these  
8 cages without compromising their original functions.<sup>5-8</sup> Those reports suggests that the confined  
9 environment in protein cages can maintain the native folded state of the encapsulated biomolecules.  
10 Based on this understanding, we aimed to utilize protein cages to isolate and investigate the  
11 properties of disordered proteins, which are challenging to study in solution due to their tendency  
12 to form aggregates and deposits. In this work, we focused on isolating A $\beta$  peptides into a typical  
13 host protein cage, ferritin and allow the encapsulated A $\beta$  peptides to form oligomer inside the cage  
14 (Figure 1).

15 Amyloid  $\beta$  (A $\beta$ ) peptide is known to be involve in Alzheimer's disease (AD) which is a  
16 neurodegenerative disorder in mammals (Figure 1c).<sup>9</sup> These peptides readily oligomerize and form  
17 protofibril and fibril, which finally accumulate in pathogenic plaques.<sup>10</sup> Most of the current  
18 research on A $\beta$  peptide primarily focuses on efforts to understand the molecular mechanisms  
19 behind A $\beta$  oligomerization and fibril formation.<sup>11</sup> Studies have indicated that A $\beta$  oligomers (A $\beta$ Os)  
20 are the most toxic and pathogenic form of A $\beta$ .<sup>12-15</sup> This makes A $\beta$ Os an appealing target for  
21 developing oligomer-specific drugs, exploring their properties and roles in the disease, and  
22 understanding the mechanism of fibril formation.<sup>15, 16</sup>

23 However, analyzing A $\beta$ Os in detail, including their dynamic features in solution, is challenging  
24 due to their transient nature, aggregation tendency, heterogeneity, and difficulties in isolating well-

1 defined oligomers.<sup>17-20</sup> Several strategies have been used to address these issues, such as  
2 encapsulating A $\beta$  monomers into reverse micelles and promoting the formation of extended  $\beta$ -  
3 strands, which are believed to be the nuclei of fibril formation.<sup>21, 22</sup> Similarly, neurotoxic A $\beta$ Os  
4 were prepared through disulfide bond formation.<sup>23</sup> High-speed atomic force microscopy (HS-  
5 AFM) has also been utilized to study A $\beta$  peptide aggregation and fibril formation.<sup>24</sup> Another  
6 approach involves preparing A $\beta$ Os through photo-crosslinking treatment to investigate their  
7 nanoscale dynamics.<sup>25, 26</sup> Computational studies have proposed that a crowded molecular  
8 environment can stabilize A $\beta$  aggregation.<sup>27</sup> Therefore, if the A $\beta$ Os are not protected, they become  
9 prone to aggregation over time and are more likely to enhance the aggregation at high concentration.

10 In this study, we aimed to isolate a defined number of A $\beta$  monomers within a confined protein  
11 environment that allows them to interact freely and form oligomers. The use of a protein cage offers  
12 several advantages, including genetic fusion for precise encapsulation of A $\beta$  monomers, prevention  
13 of aggregation of A $\beta$ Os, and provision of pores on the cage surface which permit entry of small  
14 molecules to influence the oligomer properties. Considering these factors, we selected the ferritin  
15 protein cage as a suitable template for isolating a defined number of A $\beta$  peptides.

16 Ferritin stands out among other protein cages due to its unique structural features and exceptional  
17 characteristics. It exhibits remarkable thermal stability at temperatures as high as 100°C and  
18 maintains its integrity over a broad pH range of 2 to 11.<sup>28</sup> The spherical ferritin cage is formed by  
19 self-assembly of 24 subunits, which creates an internal space with a diameter of 8 nm (Figure 1b).  
20 Since the C-terminal ends of the subunits are located inside the cage, a genetic fusion of A $\beta$  at each  
21 of the C-terminal ends was expected to result in encapsulation of 24 peptides into the cage (Figure  
22 1b and 1d).

23 Herein, we demonstrated the genetic fusion of A $\beta$ 42 at the C-terminal end of the ferritin cage to  
24 induce the formation of A $\beta$ O within the restricted protein environment (Figure 1d). We have

1 chosen *E. coli* as the host for expressing Fr-A $\beta$ 42 monomers due to its widespread use in efficient  
2 recombinant protein expression and its ability to provide the necessary cellular environment for  
3 forming 24-mer ferritin cage assembly.<sup>29</sup> Transmission electron microscopy (TEM) analysis  
4 revealed that the ferritin cage containing A $\beta$ 42 forms a well-defined spherical cage structure rather  
5 than aggregating randomly. Using high-speed AFM (HS-AFM), we directly visualized the  
6 encapsulated A $\beta$  core by disassembling the cage in solution. The Thioflavin-T (ThT) assay  
7 indicated the formation of A $\beta$ O. The ThT-A $\beta$ O complex can be inhibited by gallic acid, a typical  
8 amyloid inhibitor. Attenuated total reflectance-infrared spectroscopy (ATR-IR) measurements  
9 confirmed the  $\beta$ -sheet structures within the A $\beta$  core. Previous efforts to study A $\beta$ O in solution were  
10 challenged due to a lack of suitable methods to stop aggregation. Our methodology allows precise  
11 isolation of a defined  $\beta$ -sheet-rich oligomer fused with the protein cage, which can be used to  
12 conduct in-depth studies on the properties and behavior of A $\beta$ O.

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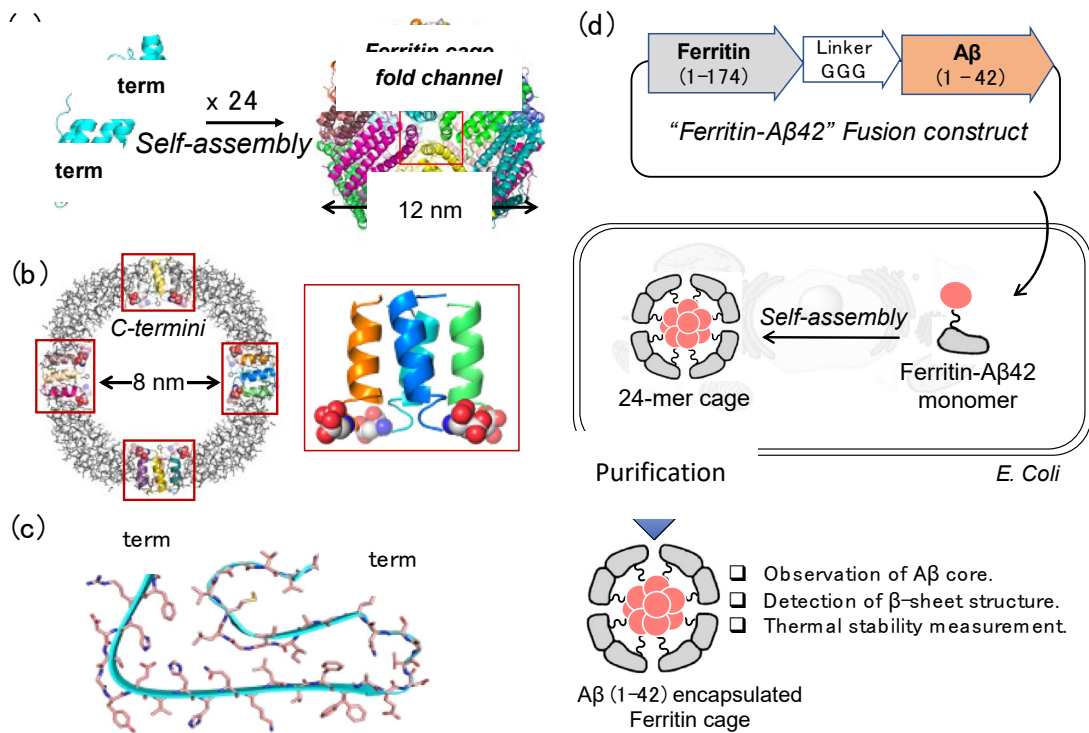
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2 **Figure 1: In-cell packaging of a defined number of Aβ peptides fused with the ferritin cage**  
 3 **monomer.** (a) Self-assembly of the 24 ferritin monomers to form a spherical cage structure  
 4 showing the 4-fold symmetry facing forward (pdb: 1DAT). (b) Interior structure of the ferritin cage  
 5 showing the position of E-helices (cartoon) and C-termini along with an expanded view of four E-  
 6 helices. The C-terminal residue, Asp174 is shown with a sphere model. **The selected square areas**  
 7 **represent the positions of 4 E-helices at the 4-fold symmetric channels, with one of them shown in**  
 8 **an enlarged view.** (c) Monomeric structure of a typical Aβ peptide from a fibrillar structure (pdb:  
 9 6SZF). (d) Schematic illustration showing the genetic fusion of the Aβ peptide at the C-terminal  
 10 end of the ferritin monomer through a flexible GGG linker and encapsulation of the fused peptides  
 11 into the 24-mer cage during the assembly of the Fr-Aβ monomer inside the *E. Coli* cell.

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## 1 **Results**

### 2 **Design and in-cell packaging of A $\beta$ peptides into the ferritin cage**

#### 3 **Design and preparation**

4 Recombinant horse spleen apo-ferritin (apo-rHLFr) was employed as a suitable template for  
5 encapsulating A $\beta$  peptides because this ferritin can be expressed in high yield, easily crystallized  
6 and is very stable. The C-terminal end of apo-rHLFr (FrWT) is located inside the cage (Figure 1b).  
7 To enable free interaction among A $\beta$  peptides and oligomer formation, we fused a full-length of  
8 A $\beta$  peptide with 42 residues to FrWT with a GGG linker (Figure 1d and Table S1-3). During the  
9 expression of **Fr-A $\beta$ 42** monomer in *E. coli* cells and subsequent assembly formation, the 24 A $\beta$   
10 peptides can be encapsulated within the ferritin cage (**Fr-A $\beta$ 42** for 42 A $\beta$  residues) (Figure 1d).  
11 The inherent tendency of A $\beta$  peptides to interact with each other is likely involved during the  
12 encapsulation process. The resulting 24-mer ferritin cage was purified by cell disruption and heat  
13 treatment at 70°C for 15 minutes, followed by anion exchange and size exclusion chromatography  
14 (see supporting information). Although the protein expression level of **Fr-A $\beta$ 42** was found less  
15 compared to FrWT, we successfully isolated and purified the **Fr-A $\beta$ 42** containing A $\beta$  in a sufficient  
16 yield for comprehensive characterization including protein crystallization (Figure S1a,b and Figure  
17 1). The isolated yield of **Fr-A $\beta$ 42** per 1 g of cells was 0.1 mg, which is less than that of FrWT (9.5  
18 mg). Other than low expression, the intrinsic aggregation nature of the A $\beta$ , a section of **Fr-A $\beta$ 42**  
19 might not form the 24-mer cage which could attribute to the low recovery yield.

#### 20 **Characterization**

21 Subsequently, the purified **Fr-A $\beta$ 42** was subjected to comprehensive spectral and analytical  
22 characterization. Native polyacrylamide gel electrophoresis (PAGE) analysis of **Fr-A $\beta$ 42** showed  
23 banding patterns similar to those of FrWT. This indicates that the fused A $\beta$  peptides are effectively  
24 packed into the ferritin cage in *E. coli* without altering its original size (Figure 2a). This finding is

1 further supported by size exclusion chromatography (SEC), which revealed identical elution times  
2 for FrWT and **Fr-A $\beta$ 42** (Figure S1). The successful fusion of A $\beta$  peptides within the ferritin cage  
3 was confirmed by the matrix-assisted laser desorption ionization time-of-flight mass spectrometric  
4 analysis (MALDI-TOF). The calculated mass for **Fr-A $\beta$ 42** is 24,513 Da, and the observed mass is  
5 **24,513 Da** (Figure 2b). **We also measured the zeta potential of both FrWT and Fr-A $\beta$ 42 which are**  
6 **-6.8 mV and -6.2 mV, respectively, which suggest that the surface properties of the ferritin cage**  
7 **remained same.**

8 The hydrodynamic diameter based on volume percentages of FrWT and **Fr-A $\beta$ 42** measured  
9 by dynamic light scattering (DLS) were found to be  $13.4 \pm 1.4$  and  $13.4 \pm 0.7$  nm, respectively in  
10 50 mM Tris-HCl (pH 8.0) / 0.15 M NaCl (Figure 2c). The transmission electron microscopic  
11 (TEM) analysis revealed spherical shapes of FrWT and **Fr-A $\beta$ 42** with diameters of  $13.6 \pm 0.9$  and  
12  $13.7 \pm 0.6$  nm, respectively (Figure 2d and 2e). This suggests that the encapsulation of A $\beta$  peptides  
13 does not cause a significant change in the size of the ferritin cage.

#### 14 **X-ray crystal structure analysis**

15 To gain atomic-level insights into the structure, **Fr-A $\beta$ 42** was crystallized, and its structure was  
16 determined by X-ray crystallography at a resolution of 2.0 Å (Table S4). Although we modeled the  
17 overall ferritin cage structure, the A $\beta$  core was left unmodelled due to insufficient electron density  
18 at the center of the cage (Figure S2). **It is to be noted that, A $\beta$ , being an inherently disordered**  
19 **peptide, lacks a fixed structure and that might be the reason for not observing any density of the**  
20 **fused A $\beta$  peptide in the  $2F_o-F_c$  map. A similar phenomena was also previously observed when**  
21 **ferritin was fused with metal binding peptide which was not appeared in the crystal structure.**<sup>30, 31</sup>

22 The **root mean square deviation** (RMSD) of C $\alpha$  atoms of the protein chain from that of FrWT (PDB  
23 ID: 1DAT) is only 0.183. This result provides further support for our interpretation that the fusion  
24 and encapsulation of A $\beta$  peptides does not affect the overall ferritin cage structure. Notably, the

1 four E-helices of the **Fr-A $\beta$ 42** cage were observed in the usual position (Figure S2e). This suggests  
2 that the ferritin cage is folded into its native "flip" conformation in contrast to the "flop"  
3 conformation in which the E-helices are located outside the cage due to the fusion of long peptides  
4 (Table S5). This signifies that the fused A $\beta$  peptide core is located inside the cage.

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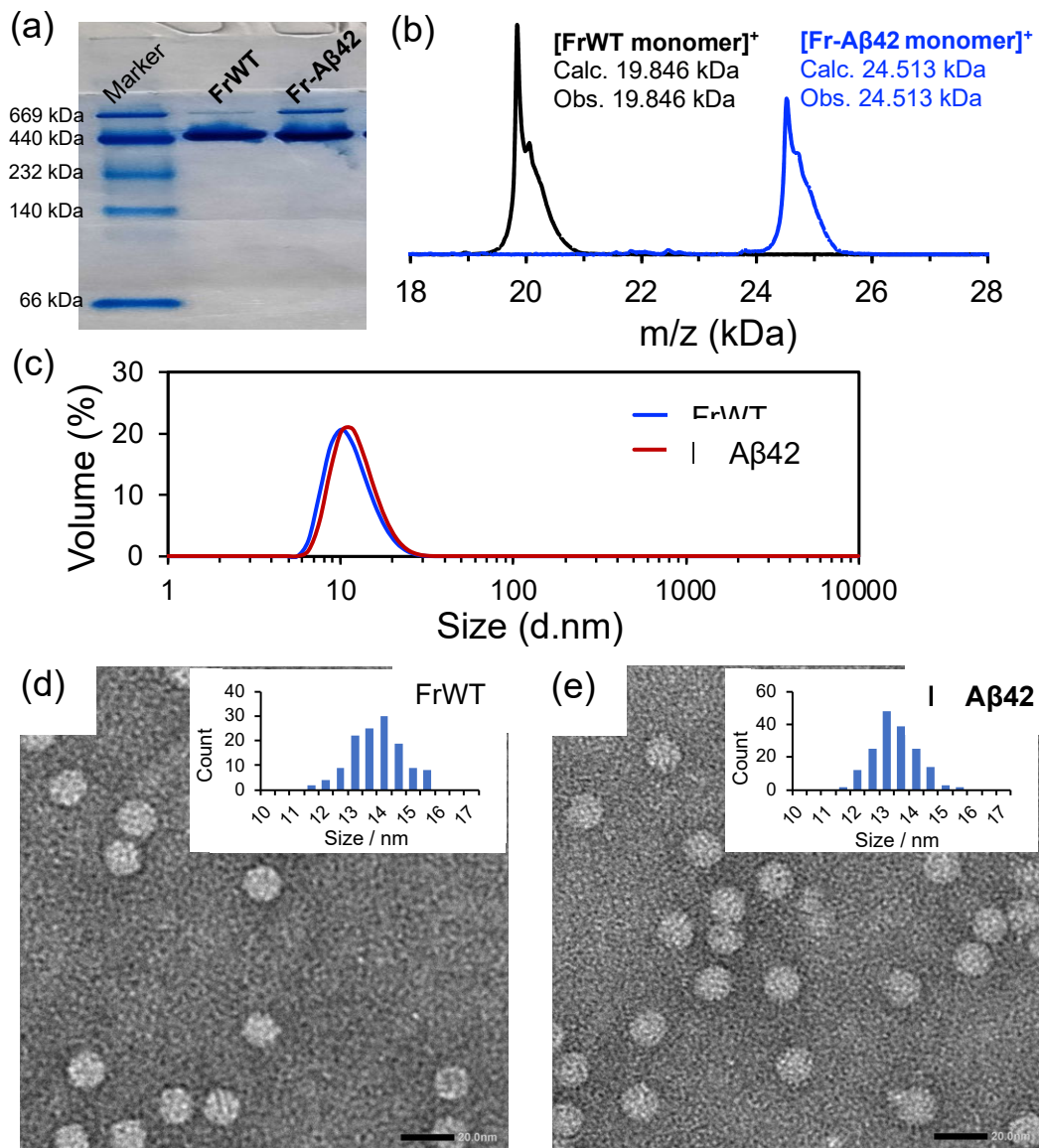
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 2 **Figure 2: Characterization of the A $\beta$  encapsulated ferritin cage, Fr-A $\beta$ 42.** (a) Native  
 3 **polyacrylamide gel electrophoresis** (PAGE) banding pattern of FrWT and Fr-A $\beta$ 42. (b) **Matrix-**  
 4 **assisted laser desorption ionization time-of-flight mass spectrometric analysis (MALDI-TOF)** mass  
 5 of FrWT and Fr-A $\beta$ 42 monomer. (c) Hydrodynamic diameter of FrWT and Fr-A $\beta$ 42 in 50 mM  
 6 Tris-HCl (pH 8) / 0.15 M NaCl. (d-e) **Transmission emission microscopy** (TEM) images showing  
 7 the spherical shape of FrWT and Fr-A $\beta$ 42. Staining: 1 min in 1% Methyl amine tungstate  
 8 (Nanoprobes). Scale bar: 20 nm.

## 1 Visualization of the encapsulated A $\beta$ peptides by high-speed AFM (HS-AFM)

2 After successfully isolating and characterizing **Fr-A $\beta$ 42**, we aimed to visualize the encapsulated  
3 A $\beta$ O by HS-AFM, which is a powerful tool for investigating the dynamics of protein structures.<sup>24</sup>  
4 Visualizing the A $\beta$ O core directly is challenging because it is located inside the ferritin cage and  
5 covered by the protein shell (Figure 2e). To overcome this issue, we disassembled the ferritin cage  
6 during the HS-AFM measurement to visualize the A $\beta$ O.<sup>32</sup>

7 To facilitate the disassembly process, we conducted HS-AFM measurements at pH 2.3 (50  
8 mM Gly-HCl / 0.1 M KCl), as the ferritin cage is known to start disassembling at lower pH levels.<sup>33</sup>  
9 At first, we focused on a single **Fr-A $\beta$ 42** cage and captured snapshots of it at various intervals until  
10 disassembly occurred. Figure 3a and Figure S3 with selected HS-AFM snapshots (Movie 1 and  
11 Movie 2) present two examples of the dynamic disassembly of a single **Fr-A $\beta$ 42** cage. The HS-  
12 AFM movie 1 revealed that after 6.3 sec (Figure 3a), the spherical structure of the **Fr-A $\beta$ 42** cage  
13 collapses and exposes the A $\beta$  core into the buffer at 6.9 sec. At 12s, the amyloid core, surrounded  
14 by disassembled ferritin subunits, becomes clearly visible, producing a flower-like shape with a  
15 central core (Figure 3a, Movie 1). Such a unique shape was not observed for the FrWT (Figure 3b  
16 and Movie 3).

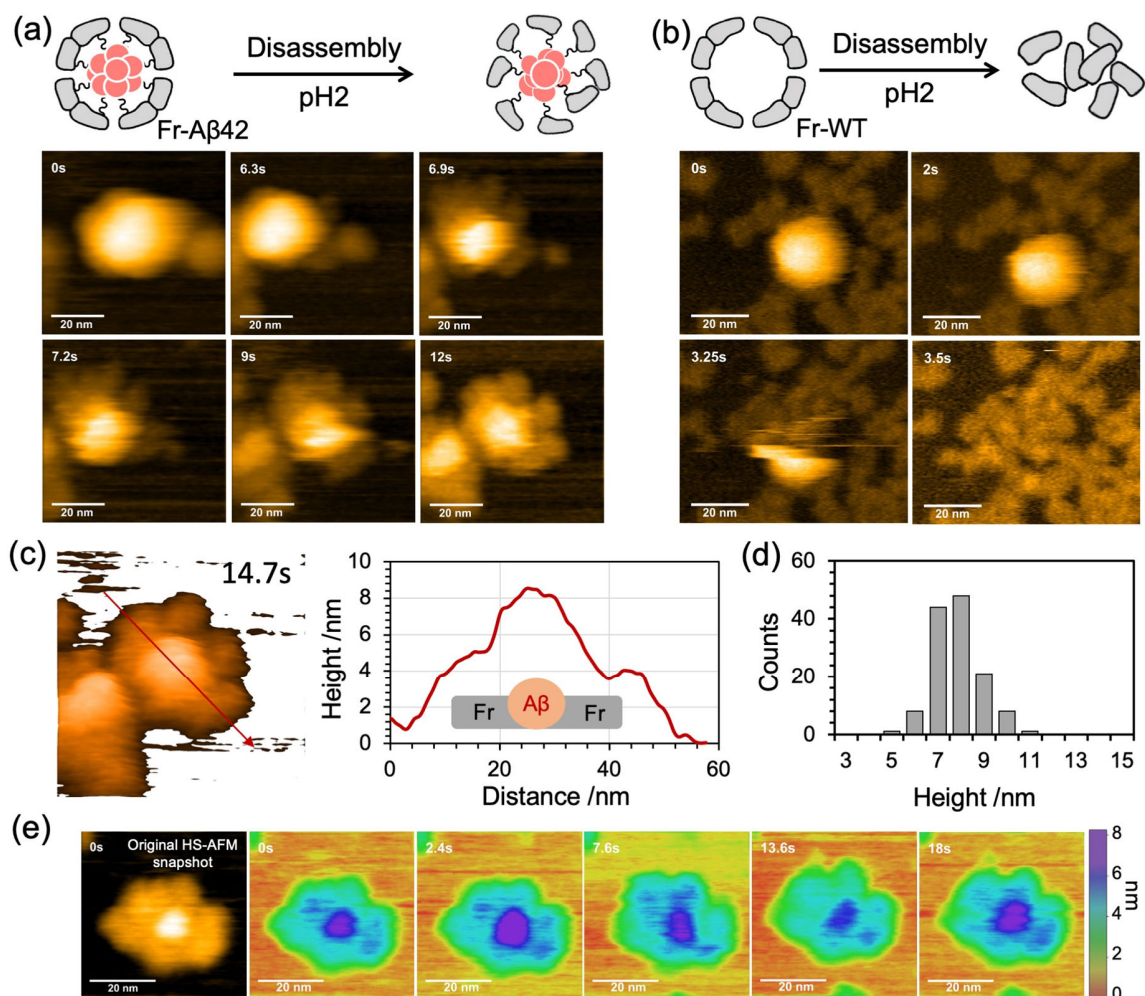
17 The height distribution profile of one of the typical flower-like structures indicates that the  
18 height of the amyloid core is higher than that of the surrounding ferritin subunits (Figure 3c). The  
19 average size of the disassembled **Fr-A $\beta$ 42** cage, including the amyloid core surrounded by the  
20 ferritin subunit, is 28 nm, which is nearly double that of an intact ferritin cage (Figure 3c). At this  
21 pH, various types of A $\beta$  core were observed in the solution. The average height of the amyloid core  
22 is 7.7 nm (Figure 3c and 3d) in comparison to height of ferritin subunits which is approximately 4  
23 nm (Figure 3c). The ferritin cage is usually 12 nm in size, but when it disassembles at a low pH,  
24 the subunits drift apart and lose their globular shape.<sup>33</sup> The disassembled ferritin subunits in **Fr-**

1 **Aβ42** generate the distinctive flower-like structure, allowing the amyloid core to remain in its  
2 oligomeric configuration through Aβ-Aβ interactions.

3 Monitoring an amyloid core in the flower-like structure over time, we observed dynamic  
4 changes in its shape, which indicate a transition from globular to linear/deformed and then to  
5 globular again (Figure 3e, Figure S5, Movie 4 and Movie 5). This feature is consistent with the  
6 typical behavior of AβO, which was previously shown to be dynamic in nature and undergo shape  
7 alterations from globular to linear.<sup>25</sup>

8 Due to the restricted cage size, the encapsulated AβO might not exhibit dynamic behavior  
9 and maintain a globular shape. However, after disassembling the ferritin cage, the amyloid core  
10 became exposed to the solution and became dynamic. Notably, the disassembled ferritin subunits  
11 prevent the amyloid core from aggregating, which allowed us to characterize its dynamic nature in  
12 solution.

13 We need to mention that, although we visualized the encapsulated AβO by HS-AFM, the biological  
14 and atomic level properties of the AβO might differ from those found in Alzheimer's disease  
15 patient as the measurement was done under acidic conditions (pH 2.3). Nevertheless, HS-AFM is  
16 the only method that enables direct visualization of the globular shape and the dynamic nature of  
17 AβO exposed from the ferritin cage. This approach overcame the challenge of directly visualizing  
18 the core and provided important insights into the dynamic nature of AβO. In the flower-like  
19 structure, the amyloid core is wrapped by the fused ferritin subunits. This demonstrates that due to  
20 Aβ-Aβ interaction, the oligomeric state remained intact, otherwise it would have been drift apart  
21 as shown in Figure 3b.



1  
2 **Figure 3: Visualization of Aβ core by high-speed AFM (HS-AFM).** (a) HS-AFM snapshots of  
3 the dynamic observation of a single molecule **Fr-Aβ42** in pH 2.3 (50 mM Gly-HCl-100 mM KCl).  
4 (b) HS-AFM snapshots of the disassembly of FrWT under similar condition as for **Fr-Aβ42**. (c)  
5 Three-dimensional image of a HS-AFM snapshot (14.7s) of the disassembly of **Fr-Aβ42** and the  
6 corresponding height profile analysis. **The height profile was measured along the red arrow.** (d)  
7 The height distribution profile of the Aβ cores obtained after the disassembly of **Fr-Aβ42** at pH2.3.  
8 (e) Heat-plot showing the time-dependent dynamic structural changes of a flower-like structure  
9 overtime. The purple color indicates highest height corresponding to the Aβ core which changed  
10 with time.

11

## 1 Evidence of $\beta$ -sheet-rich amyloid core in Fr-A $\beta$ 42.

### 2 **Thioflavin T (ThT) assay**

3 We conducted a ThT assay to explore the secondary structure of **Fr-A $\beta$ 42**.<sup>34, 35</sup> ThT is a  
4 nonfluorescent dye that exhibits blue fluorescence upon specific binding to  $\beta$ -sheet structures.  
5 **Ferritin cage consists of 8 symmetric three-fold channels (Figure S2b) through which large**  
6 **molecules like Zn-phthalocyanine (Approx. size: 15.7 Å x 15.7 Å; CCDC No. 1013162) can enter**  
7 **into the cage simply by incubating at room temperature.<sup>36</sup> Therefore, being smaller in size in**  
8 **comparison to Zn-phthalocyanine, ThT dye (14.1 Å x 4.6 Å ; CCDC No. 1816441) is expected to**  
9 **enter into the cage and binds to  $\beta$ -sheet structure if present.** The **Fr-A $\beta$ 42** solution, when incubated  
10 with ThT, shows a strong fluorescence band at 480 nm, while no fluorescence is observed for FrWT  
11 under similar experimental conditions (Figure 4a). This finding suggests the presence of  $\beta$ -sheet  
12 structures in **Fr-A $\beta$ 42** and the formation of an oligomer inside the ferritin cage.

13 To confirm that the observed ThT fluorescence in our assay was not due to ThT self-  
14 aggregation or other phenomena in solution, size exclusion chromatography was performed using  
15 an incubated mixture of ThT and **Fr-A $\beta$ 42** (Figure 4b). Protein absorbance at 280 nm and ThT  
16 fluorescence (FL) at 480 nm were monitored simultaneously. No fluorescence peak was observed  
17 in the elution profile of FrWT (Figure 4b(i)). In contrast, **Fr-A $\beta$ 42** showed coexistence of UV and  
18 FL peaks in the elution profile at 10 min. This indicates that the ThT fluorescence originates from  
19 the ferritin cage containing A $\beta$  core.

### 20 **Attenuated total reflectance infrared spectroscopy (ATR-IR) measurement**

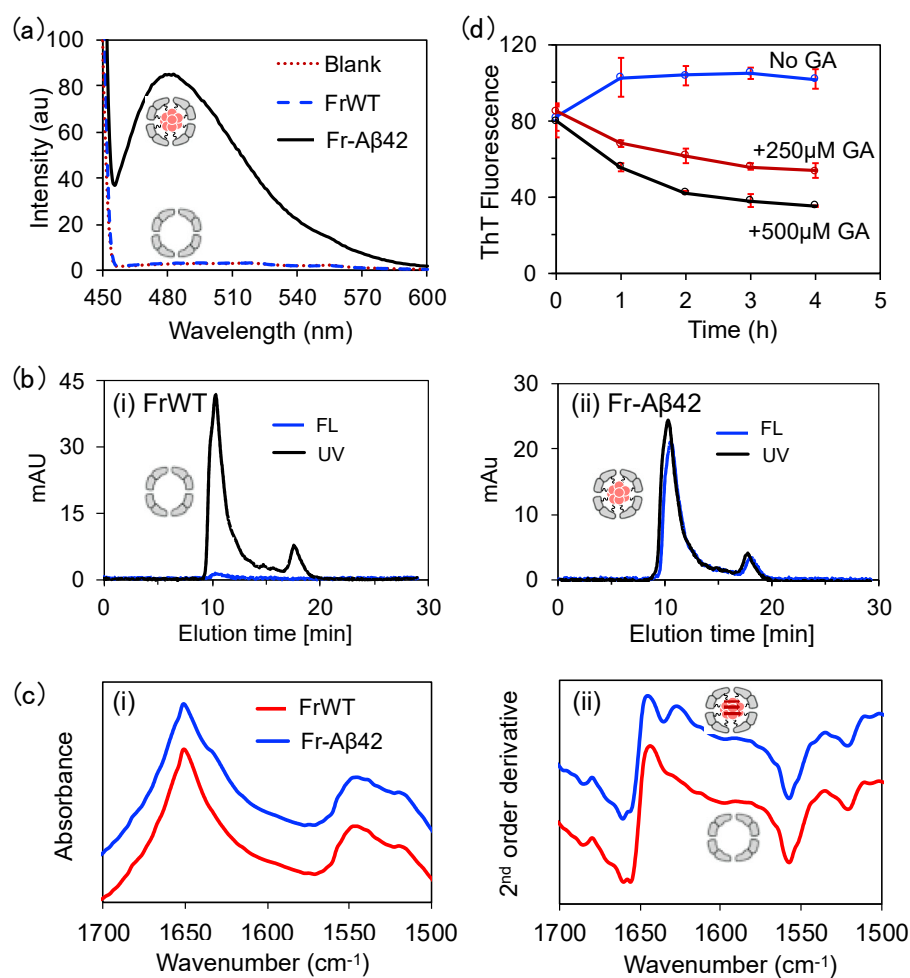
21 For further verification of the presence of a  $\beta$ -sheet in the ferritin cage, we obtained ATR-IR  
22 spectroscopy measurements. The spectrum exhibit the characteristic IR stretching frequency near  
23 1630  $\text{cm}^{-1}$  corresponding to the extended parallel  $\beta$ -stranded structure (Figure 4c).<sup>37, 38</sup> This

1 frequency appears as a shoulder to the amide-I stretching frequency at  $1650\text{ cm}^{-1}$  and is more  
2 prominent in the second derivative plot (Figure 4c(ii)). Importantly, FrWT does not show such a  
3 peak. This supports the presence of a  $\beta$ -sheet rich A $\beta$ O inside **Fr-A $\beta$ 42**. The observed amyloid  $\beta$ -  
4 sheet structure is likely to exist in parallel in nature because the A $\beta$  peptide is fused at the C-  
5 terminal end of each of four parallel E-helices.

6 Overall, the ThT assay and ATR-IR results demonstrate the presence of  $\beta$ -sheet structures  
7 in the encapsulated oligomeric A $\beta$  aggregates inside the ferritin cage.

### 8 **Gallic acid (GA) inhibition assay**

9 Inhibition of fibrilization of A $\beta$  peptides is known to occur in the presence various organic  
10 substances including polyphenolic compounds, such as gallic acid which is known to interact with  
11 the fibrillar A $\beta$  structure.<sup>39-41</sup> In order to test whether the encapsulated oligomeric  $\beta$ -sheet-rich A $\beta$   
12 aggregate inside ferritin cage has any such effect, we chose gallic acid as a starting model inhibitor.  
13 Gallic acid was added during ThT assay and the fluorescence peak at 480 nm was monitored with  
14 time (Figure 4d). It was found that high gallic acid concentration leads to more decrease in the ThT  
15 fluorescence. The ThT fluorescence intensity at 480 nm was found to decrease over time at a  
16 particular inhibitor concentration. Since the rate of gallic acid oxidation is faster in alkaline pH, a  
17 control experiment at pH 6.8 was performed which also showed inhibition of ThT fluorescence at  
18 480 nm but at a slower rate (Figure S6). These results indicate that the gallic acid inhibitor interacts  
19 with the  $\beta$ -sheet rich A $\beta$ O inside the cage and possibly induces structural changes in the ThT-  
20 bounded A $\beta$  core which lead to the release of ThT as well as ThT fluorescence. We observed a  
21 new peak appearing at 510 nm after significance decrease in ThT fluorescence (Figure S6). This  
22 suggests possible formation of a structure with different fluorescence properties involving gallic  
23 acid after the ThT inhibition because ThT fluorescence is specific at 480 nm.<sup>39</sup>



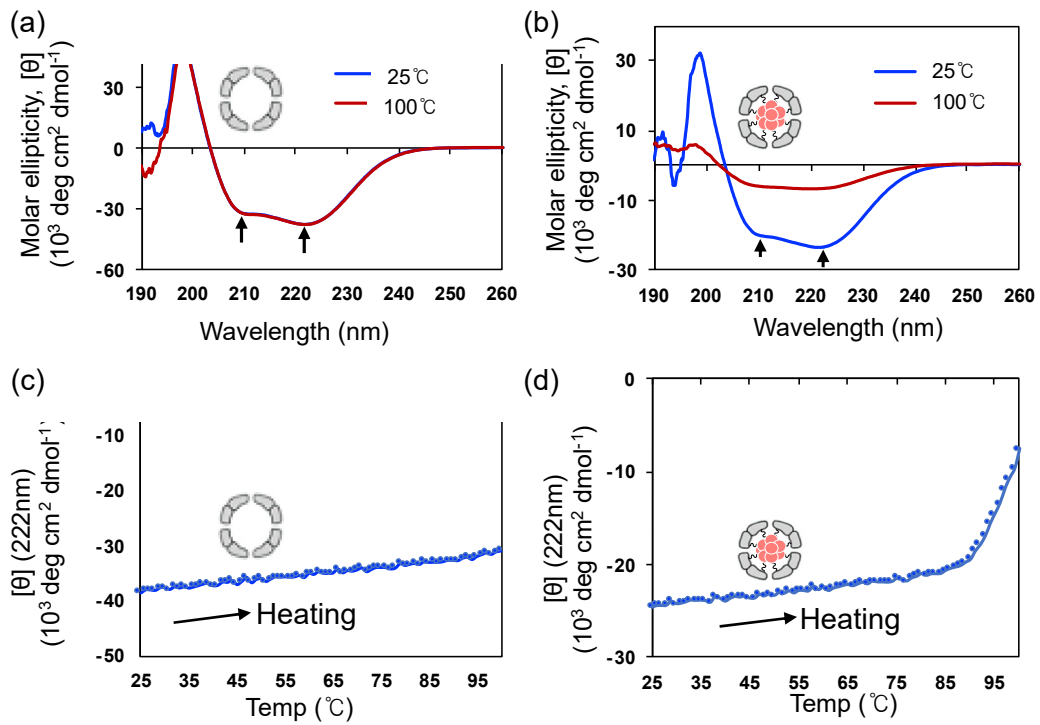
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2 **Figure 4: Evaluation of the  $\beta$ -sheet structure in Fr-A $\beta$ 42.** (a) **Thioflavin-T** (ThT) assay showing  
 3 the appearance of the fluorescence band at 480 nm for **Fr-A $\beta$ 42**. 10  $\mu$ M of ThT and 1  $\mu$ M of protein  
 4 in 50 mM Tris-HCl (pH 8.0) /0.15 M NaCl was used for the study. (b) Size exclusion  
 5 chromatography of the mixtures used for ThT assay showing the coexistence of both UV and ThT  
 6 fluorescence (FL) in the elution profile of FrWT (i) and **Fr-A $\beta$ 42** (ii). Elution buffer: 20 mM Tris-  
 7 HCl. Flow: 0.5 ml/min. (c) **Attenuated Total Reflectance Infrared spectroscopy** (ATR-IR) spectra  
 8 of FrWT and **Fr-A $\beta$ 42** (i) and the corresponding second order derivative plot (ii). The spectra of  
 9 FrWT and **Fr-A $\beta$ 42** are shown as red and blue lines, respectively. (d) Effect on ThT fluorescence  
 10 at 480 nm over time after addition of gallic acid (250  $\mu$ M and 500  $\mu$ M) into **Fr-A $\beta$ 42** solution (10  
 11  $\mu$ M ThT and 1  $\mu$ M protein in 50 mM Tris-HCl (pH 8.0) /0.15 M NaCl. The error bar represents  
 12 standard deviations from three independent experiments.

## 1 Thermal stability measurement of the A $\beta$ encapsulated ferritin cage by circular dichroism 2 (CD) spectroscopy

3 CD measurements were carried out to investigate the changes in secondary structure  
4 observed upon heating (Figure 5). At 25°C, FrWT and Fr-A $\beta$ 42 show the characteristic negative  
5 bands at 208 nm and 222 nm corresponding to the  $\alpha$ -helix structure (Figure 5a and 5b). Although  
6 the presence  $\beta$ -sheet structure was indicated by ThT assay, no distinct absorption band was  
7 observed for the  $\beta$ -sheet structure near 215 nm in the CD spectrum of Fr-A $\beta$ 42 (Figure 5a and 5b).  
8 The secondary structure analysis from the CD spectrum of Fr-A $\beta$ 42 indicates the presence of only  
9 4% of  $\beta$ -sheet structure (Table S6). This suggests that Fr-A $\beta$ 42 has a predominant  $\alpha$ -helix  
10 structure. When the temperature was raised gradually from 25°C to 100°C, the molar ellipticity of  
11 FrWT at 222 nm ( $\theta_{222}$ ) slightly increased, and the CD spectrum after cooling down to RT remained  
12 almost identical to the original CD spectrum (Figure 5a). This suggests that FrWT remains stable  
13 at 100°C. Fr-A $\beta$ 42 showed a different pattern in which the ( $\theta$ )<sub>222</sub> increased slightly up to 85°C in a  
14 manner similar to the pattern of FrWT and then increased sharply up to 100°C (Figure 5c and 5d).  
15 This suggests that Fr-A $\beta$ 42 starts denaturing after 85°C (Figure 5d) by losing its secondary  
16 structures as reflected in the CD spectrum in Figure 5b and Table S6. In HS-AFM measurement,  
17 we found that the A $\beta$ O is dynamic in nature (Figure 3e and Figure S5), higher temperature likely  
18 enhanced their dynamic behavior and impact on the cage stability. As a result, the Fr-A $\beta$ 42  
19 denatured at high temperature which was not observed for FrWT.

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 2 **Figure 5: Measurement of thermal stability of Fr-Aβ42 by Circular dichroism (CD)**  
 3 **spectroscopy.** CD spectra measured at 25°C before heating and after heating at 100°C for (a) FrWT  
 4 and (b) Fr-Aβ42. The arrows indicate the positions of alpha-helix peaks at 208 nm and 222 nm.  
 5 Changes of molar ellipticity at 222 nm,  $(\theta)_{222}$  during heating from 25°C to 100°C with a  
 6 temperature gradient of  $1^\circ\text{C min}^{-1}$  for (c) FrWT and (d) Fr-Aβ42. Measurements were done with  
 7 a protein concentration of 0.1 mg/ml in 50 mM Tris-HCl (pH 8) /0.15 M NaCl.

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## 1 **Discussions**

2 In this study, we successfully isolated a precisely defined number of A $\beta$  peptides by fusing them  
3 into a self-assembled ferritin cage. Since the self-assembly process occurs inside the cell, one can  
4 expect that the A $\beta$ -A $\beta$  interaction and formation of oligomeric aggregate inside the ferritin cage is  
5 more natural than the same if occur in buffer solution outside the cell. It is important to note that  
6 although the fused A $\beta$  peptides freely interact with each other inside the cage, the characteristic of  
7 the formed oligomeric aggregates might not be the exact same as occurred in Alzheimer's disease  
8 due to fusion. Nevertheless, our method of encapsulation of a fused A $\beta$ O inside the ferritin cage  
9 is valuable for understanding their nature, structure, and properties as they are intrinsically disorder  
10 in nature and difficult to isolate. The restricted environment of the ferritin cage helps A $\beta$ O to avoid  
11 mutual aggregation and preserve the oligomeric nature of the amyloid core encapsulated within the  
12 cage. Previous attempts using reverse micelles to isolate A $\beta$ O<sub>s</sub> showed less stability and onset of  
13 aggregation over time.<sup>22</sup> In our case, the A $\beta$ O inside the ferritin cage remained stable over time  
14 (Figure S1c). As A $\beta$  oligomers are considered the most toxic species in Alzheimer's disease (AD),  
15 our approach is useful for studying the properties, toxicity, and disease-related roles of a precisely  
16 defined isolated A $\beta$ O.

17 It should be noted that retrieving the encapsulated A $\beta$ O out of the cage could be beneficial for  
18 studying oligomer-oligomer interaction that give rise to protofibrils or fibrils, etc. However, it is  
19 challenging to retrieve them because the A $\beta$ O is fused to the ferritin monomer, and the cage can  
20 only disassemble at an extremely acidic pH (<2.0). Our intention was not to conduct those studies  
21 because such investigations can be easily carried out using A $\beta$  peptides in a solution.<sup>18, 24, 42</sup> Rather,  
22 we focused on a method to inhibit the oligomer-oligomer aggregation, which is a common problem  
23 in studying isolated single oligomers.

1 The fusion of foreign proteins and peptides at the C-terminal end of the ferritin cage is not new  
2 (Table S5). Such fusion does not cause any changes in the spherical shape of the ferritin cage.  
3 However, fusion of proteins with over 28 residues causes shifting of the E-helix towards the outside  
4 of the cage (Table S5). Notably, in our case, the strong aggregation propensity of A $\beta$  peptides  
5 which include 42 residues is anticipated to play a crucial role in their encapsulation into the cage  
6 (Figure 1d). Interestingly, the encapsulated 24-mer A $\beta$ O falls in the category of toxic high  
7 molecular weight (HMW) oligomers which could be targets for drug discovery.<sup>43, 44</sup>

8 The A $\beta$  peptide encapsulated ferritin cage was found to be highly stable up to 85 °C, although  
9 not comparable with FrWT which denatured over 100 °C. The inherent disordered nature of the A $\beta$   
10 peptide was considered to be the reason for less stability of Fr-A $\beta$ 42 than FrWT.<sup>45</sup> This is reflected  
11 in the CD spectrum (Figure 5d). Since low temperature (70 °C) was used to denature the impurities  
12 during the Fr-A $\beta$ 42 purification, protein loss due to stability issue might be less. Other than thermal  
13 stability, no noticeable changes in the physicochemical properties was observed. The 24-mer cage  
14 integrity was maintained up to pH2.3 similar to FrWT while the zeta potential and the overall cage  
15 size remained same.

16 Another intriguing aspect of our study is the visualization of A $\beta$  core by HS-AFM and dynamic  
17 changes in shape with time. Such dynamic features indicate that it might be an intermediate of  
18 higher order assembly formation such as fibril. Therefore, targeting this type of A $\beta$ O could stop  
19 formation of fibril.

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## 21 **Conclusions**

22 In conclusion, we have successfully demonstrated a novel method for isolating a single  $\beta$ -  
23 sheet-rich A $\beta$ O within a ferritin cage. This was achieved by fusing the N-terminal of the A $\beta$  peptide

1 to the C-terminal ends of subunits of ferritin. Due to such fusion, when the 24-mer ferritin cage is  
2 formed, 24 A $\beta$  peptides are encapsulated into the cage. The A $\beta$  encapsulated ferritin cage has a  
3 spherical cage structure similar to that of FrWT. The encapsulated A $\beta$  peptide core inside ferritin  
4 was directly visualized by HS-AFM after disassembling the cage. By ThT assay and ATR-IR, we  
5 confirmed the presence of a  $\beta$ -sheet structure in the encapsulated A $\beta$  core. The ThT bounded A $\beta$   
6 core was affected by an amyloid inhibitor, gallic acid. The **Fr-A $\beta$ 42** cage was found to be stable  
7 even at 85°C. The isolation of a single A $\beta$ O through our fusion method holds significant potential  
8 for advancing our understanding of the structure, properties, and dynamics of A $\beta$ O. Since small  
9 molecules such as gallic acid and ThT can enter the cage, our method could be a handy way to  
10 figure out if an oligomer-targeting drug is worth exploring further. The method is useful for other  
11 proteins related to disorders. The exceptional cage stability can be a secure storage space for A $\beta$ O  
12 with an inherent tendency to aggregate. Looking at the big picture, one could use cleavable linkers  
13 to engineer the ferritin cage for therapeutic peptide delivery. Furthermore, our approach may have  
14 broader applications beyond drug discovery, specifically in studying other intrinsically disordered  
15 proteins (IDPs), such as  $\alpha$ -synuclein and tau, which are challenging to analyze because they are  
16 prone to forming aggregates in solution.

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18 **Abbreviations**  
19 A $\beta$ , Amyloid beta ; AD, Alzheimer's Disease; A $\beta$ O, Amyloid beta oligomer; ATR-IR, Attenuated  
20 total reflectance-Fourier transform infrared spectroscopy; CD, Circular Dichroism; FrWT, Ferritin  
21 wildtype; Fr-A $\beta$ 42, Ferritin cage containing 24 A $\beta$  peptides with 42 residues; FL, Fluorescence;  
22 HS-AFM, High-Speed Atomic Force Microscopy; HMW, High molecular weight; IDP,  
23 Intrinsically disordered protein; rHLFr, Recombinant horse spleen L-ferritin; MALDI-TOF,  
24 matrix-assisted laser desorption ionization time-of-flight mass spectrometric mass analysis; PAGE,

1 Polyacrylamide gel electrophoresis; RMSD, Root mean square deviation; SEC, Size exclusion  
2 chromatography; TEM, Transmission Emission Microscopy; ThT, Thioflavin T.

### 3 **Author Contributions**

4 The manuscript was written through contributions of all authors. All authors have given approval  
5 to the final version of the manuscript.

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