Molecular Basis of Encapsulation of Positively Supercharged Species by Ferritin
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Purpose

- Protein-protein host-guest systems have a broad range of applications including chemical sensing, separations, materials science, catalysis, and pharmaceutics. Ferritin with its self-assembling, high-biocompatibility, and negatively charged inner core is an attractive host system for positively charged species. It’s been shown to encapsulate positively charged species such as GFP (green fluorescent protein), carbonic anhydrase II, and gold nanoparticles. We now aim to understand the mechanisms behind encapsulation of positively charged proteins inside the core of ferritin by generating an ensemble of configurations using molecular dynamics.

Background

- Ferritin, a ubiquitous protein across all domains of life, is responsible for maintaining the levels of iron within cells by oxidizing iron into mineralize iron that can be stored within its hollow core for release later.
- Ferritin is composed of 24 subunit of a tetrahedral bundle with a short fifth helix.
- Aftn is the only known ferritin to be able to dissociate into its subunits and reform back to a spherical cage by tuning the salt concentration of the solution. This opens a milder pathway to induce encapsulation of positively charged species such as GFP (green fluorescent protein), carbonic anhydrase II, and gold nanoparticles. We now aim to understand the mechanisms behind encapsulation of positively charged proteins inside the core of ferritin by generating an ensemble of configurations using molecular dynamics.

Experimental Design

Crystal Structures

- Figure on left is a subunit of ferritin, PDB ID: 1SQ3
- Middle Figure is ferritin in its fully assemble state
- Right figure is GFP+36 PDB ID: 2B3P

Simulation Parameters

- NPT Ensemble (constant number of molecules, pressure, and temperature)
- Immers with explicit water molecules in a water box
- Temperature: 300K
- Pressure: 1atm
- Minimized for 1000 steps
- Equilibration time: 40ns

Methodology/ Preliminary Results

1) Find time region where GFP docks onto Ferritin
2) Construct an average contact map between the residues on GFP against residues on ferritin over the trajectory
3) Visually inspect the residue pairs

Table 1. List of residues in contact

<table>
<thead>
<tr>
<th>PDB</th>
<th>residue</th>
<th>contact</th>
</tr>
</thead>
<tbody>
<tr>
<td>1SQ3</td>
<td>1-100</td>
<td>100</td>
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<td>2B3P</td>
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<td>38</td>
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References