

## Construction of a closed regular-triangle trimer of helix-linked cytochrome *c*<sub>555</sub> using sortase A

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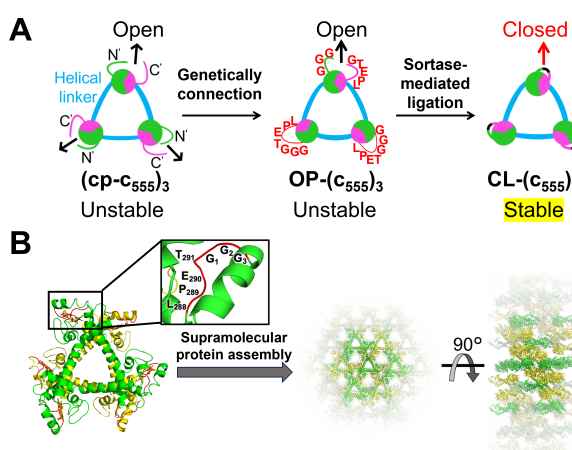
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Protein-based supramolecules require precise arrangement of building blocks for controlling the protein assembly. The building block regular-triangle trimer (cp-*c*<sub>555</sub>)<sub>3</sub> has previously been constructed from cp-*c*<sub>555</sub>, which is an α-helix-linked circular permutant of *Aquifex aeolicus* cyt *c*<sub>555</sub>.<sup>[1]</sup> However, (cp-*c*<sub>555</sub>)<sub>3</sub> may dissociate to monomers. To stabilize the triangle structure, a closed regular-triangle of three cp-*c*<sub>555</sub> molecules is constructed by covalently connecting terminal regions using sortase-mediated ligation (SML). Comparing SML using sortase A for six (cp-*c*<sub>555</sub>)<sub>3</sub> variants, the variant with GGG

at the N-terminus and LPETG at the C-terminus reacted most efficiently. OP-(*c*<sub>555</sub>)<sub>3</sub>, a genetically connected molecule of three cp-*c*<sub>555</sub> molecules containing the optimized sequence for SML, was designed to increase the SML product yield. OP-(*c*<sub>555</sub>)<sub>3</sub> was expressed in *E. coli* cells and the terminal regions were connected by SML, generating a closed regular-triangle CL-(*c*<sub>555</sub>)<sub>3</sub> (Fig. 1A). CL-(*c*<sub>555</sub>)<sub>3</sub> showed higher thermostability than (cp-*c*<sub>555</sub>)<sub>3</sub> and OP-(*c*<sub>555</sub>)<sub>3</sub>. The structural stability of CL-(*c*<sub>555</sub>)<sub>3</sub> was confirmed by high speed-AFM observation. The crystal structure of CL-(*c*<sub>555</sub>)<sub>3</sub> revealed two stacked CL-(*c*<sub>555</sub>)<sub>3</sub> triangle molecules (Fig. 1B) with a covalent linkage across the terminal regions (red loops in Fig. 1B). Additionally, the stacked CL-(*c*<sub>555</sub>)<sub>3</sub> triangles packed into a nanoporous supramolecular structure (Fig. 1B), constructing two pores with diameters of approximately 16 and 30 Å. These results provide a method to stabilize building block proteins, enabling a unique nanoporous assembly with fixed pore sizes. By adjusting helical lengths, assemblies with tunable pore sizes may be constructed for capturing large target molecules.

[1] A. Oda, et al., *Chem. Asian J.* **2018**, 13, 964.



**Fig. 1.** (A) Schematic representation of construction a closed regular-triangle CL-(*c*<sub>555</sub>)<sub>3</sub> by SML. (B) Crystal structures of CL-(*c*<sub>555</sub>)<sub>3</sub> and its nanoporous supramolecular assembly (PDB ID: 9L08).