**Crystal Structures of Cyanobacterial Heme Oxygenases**

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Heme oxygenase (HO) catalyzes heme degradation utilizing $O_2$ and reducing equivalents. In mammals, HO is involved in iron homeostasis, whereas in plants, algae, and cyanobacteria, it is utilized for producing photoreceptor and light-harvesting pigments.

We determined structures of heme bound HOs from cyanobacterium, *Synechocystis* sp. PCC 6803 (Syn HO-1 and Syn HO-2) by molecular replacement using mammalian HO structure. Syn HO-2 crystals were non-merohedral twin and diffraction data were detwinned for refinement. Overall folding and heme environment of each Syn HO-1 and Syn HO-2 is similar to that of mammalian HO, however, two characteristic features are seen in Syn HO-1 and Syn HO-2. One is charge distribution; basic patch of Syn HO-1, where Syn HO-1 interacts with redox partner, is narrower than that of mammalian HO. Different charge distribution between Syn HO-1 and mammalian HO would reflect the different molecular size between their redox partners. The other is oligomeric state; Syn HO-2 forms dimer although other HOs including Syn HO-1 are monomer. Different oligomerization between Syn HO-1 and Syn HO-2 would contribute to the selection of their redox partners four ferredoxin paralogs in this bacterium.

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