

Cryo-EM structure of a functional monomeric photosystem I from *Thermosynechococcus elongatus* reveals red chlorophyll cluster

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A high-resolution structure of trimeric cyanobacterial Photosystem I (PSI) from *Thermosynechococcus elongatus* was reported as the first atomic model of PSI almost 20 years ago. However, the monomeric PSI structure has not yet been reported despite long-standing interest in its structure and extensive spectroscopic characterization of the loss of red chlorophylls upon monomerization. Here, we describe the structure of monomeric PSI from *Thermosynechococcus elongatus* BP-1 as determined by single particle cryo-EM using the CRYO ARM 200 (JEOL). Comparison with the trimer structure gave detailed insights into monomerization-induced changes in both the central trimerization domain and the peripheral regions of the complex. Monomerization-induced loss of red chlorophylls is assigned to a cluster of chlorophylls adjacent to PsaX. Based on our findings, we propose a role of PsaX in the stabilization of red chlorophylls and that lipids of the surrounding membrane present a major source of thermal energy for uphill excitation energy transfer from red chlorophylls to P700.

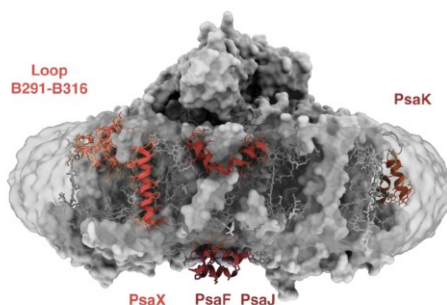


Figure 1. Single particle cryo-EM structure of cyanobacterial monomeric PSI revealing regions of disorder (labeled in red) induced by the monomerization of its trimeric form.

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