

Crystal Structure of Psb27 from *T. elongatus* and its Association with Dimeric Photosystem II

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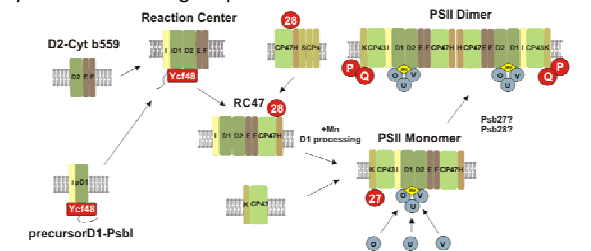
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Repair and assembly of Photosystem II

Several proteins have recently been identified as playing accessory roles in Photosystem II, either regulating activity or involved in the assembly and repair of the complex. This study focuses on Psb27, which is found in oxygenic phototrophs from cyanobacteria to higher plants.



Accessory proteins (in red) involved in the repair, assembly and activity of cyanobacterial PSII

3D structures of PSII assembly factors

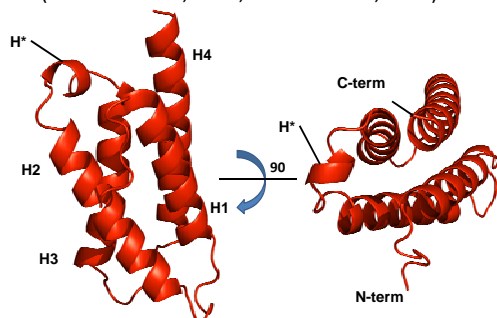
PSII accessory proteins include Psb27, Psb28, Psb29, CyanoP and CyanoQ. Psb27 is a lipoprotein (of approximately 11 kDa) which is thought to bind to the luminal side of monomeric PSII core complexes, preventing binding of the PsbO, PsbU and PsbV extrinsic proteins (Nowaczyk *et al.*, 2006). Psb27 has been assigned a role in regulating the assembly of the Mn₄Ca cluster involved in water oxidation (Roose and Pakrasi, 2008). Recently, the crystal or NMR structures of several assembly factors have been reported. This study focuses on the crystal structure of Psb27 from *Thermosynechococcus elongatus*.



3D crystal structures of Ycf48 (Blue, pdb 2XB6), CyanoP (Orange, pdb 2XB3, Michoux *et al.*, 2010) from *T. elongatus* and NMR structure of Psb27 from *Synechocystis* 6803 (Purple, pdb 2KVO).

Psb27 crystal structure

T. elongatus Psb27, lacking the signal peptide and the lipid-binding Cys₂₂ residue, was expressed in *E. coli* with an N-terminal His-tag, which was removed following purification. The crystal structure was solved at 1.7Å through molecular replacement using previously published NMR structure (pdb 2KMF). The structure is a four-helix bundle (H1-H4), similar to the recently published structures of Psb27 from *Synechocystis* 6803 obtained by NMR (Cormann *et al.*, 2009; Mabbitt *et al.*, 2009).

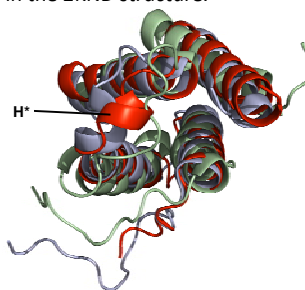


Cartoon representation of Psb27 from *T. elongatus*.

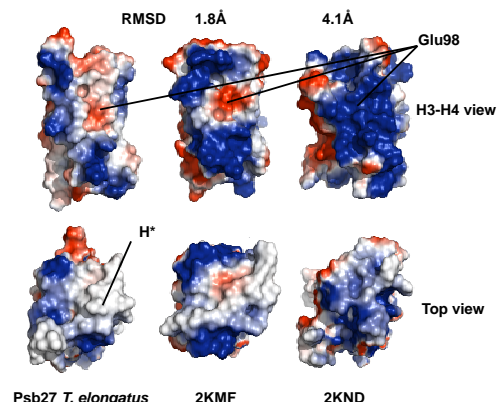
Comparison with known Psb27 structures

The determination of the crystal structure of Psb27 from *T. elongatus* allowed a direct comparison with previously reported NMR structures of Psb27 from *Synechocystis* 6803 which shares 50% sequence identity. Psb27 from *T. elongatus* has an extra short helix (H*) located between helices 2 and 3. The surface charge is similar to that calculated for 2KMF, but different to 2KND.

This difference is primarily due to the Glu₉₈ residue, which is buried in the 2KND structure.



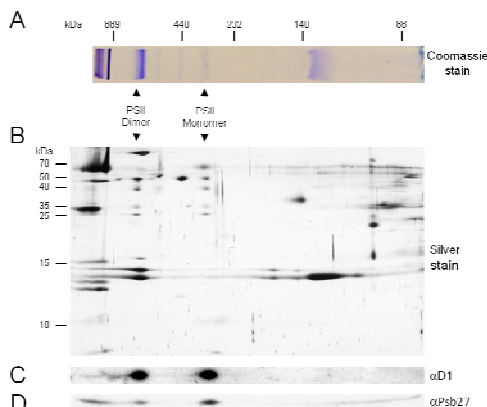
Alignment of 3D structures from *T. elongatus* (in red) and from *Synechocystis* (light blue, pdb 2KMF; light green, pdb 2KND).



Comparison of surface charges between Psb27 from *T. elongatus* and *Synechocystis* (pdb 2KMF and 2KND).

Identification of Psb27 in monomeric and dimeric PSII complexes

The presence of Psb27 within thylakoid membranes isolated from *T. elongatus* was assessed by immunoblotting 2D Blue Native (BN)/SDS PAGE gels (A, B) with specific antibodies raised against Psb27 and D1 (C, D). The results indicate that Psb27 is part of both monomeric and dimeric PSII, as well as larger complexes, in contrast to previous findings.



Dodecylmaltoside solubilised thylakoid proteins from *T. elongatus* were separated by BN-PAGE (A). The lanes were then cut, solubilised and run on a 18% (w/v) 2nd dimension SDS PAGE gel (B). Gels were stained using Coomassie (A), silver (B) or immunoblotted with specific antibodies raised against D1 (C) and Psb27 (D).

Conclusions

- 1- The 3D crystal structure of Psb27 from *T. elongatus* is more similar to the 2KMF NMR model from *Synechocystis* and contains a new helical region (H*) not present in previous models.
- 2- The surface charge model of Psb27 from *T. elongatus* indicates that interaction between Psb27 and PSII may be localised to the H4 helix only instead of both H3 and H4 (Cormann *et al.*, 2009).
- 3- Psb27 is found in both monomeric and dimeric PSII

References

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