

Prediction the structure of the psbU protein using the method homology modeling

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Abstract: PsbU is a luminal peripheral protein in the photosystem II (PS II) complex of cyanobacteria and red algae. PsbU provides a stable architecture for the oxygen-evolving system in cyanobacterial photosystem II [1-3]. From the psbU protein, no structural files were reported to create a three-dimensional (3D) structure either experimentally or through modeling in databases. So we use the Homology Modeling method, which is the best way to determine and predict the structure of proteins, and we model the protein.

After performing the Alignment, three proteins 2AXT_U, 4IL6_U and 3A0B_U were used as templates for modeling. These three proteins are part of PS II. These three proteins have 65% Identity of the amino acid sequences with the psbU protein, which indicates the homology of the psbU protein with the three proteins mentioned evolutionarily. Therefore, it is expected that these three proteins will have the same structure and function with the psbU protein. After modeling using these three proteins, and preparing the Ramachandran map, which is used as a Validation Test for measuring and evaluating the protein, finally, the 4IL6_U protein was selected as the best template for modeling.

Keywords: psbU protein; homology modeling; photosystem II

References

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