Experimental Report

Proposal:	8-02-707	Council:	10/2014		
Title:	SANS Study of the Structure of Photosynthetic Membrane Proteins in Solution				
This proposal is a new proposal					
Researh Area:	Soft condensed matter				
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Local Contact:	MARTEL Anne				
Samples:	Photosynthetic Membrane Proteins				
Instrument	Req. Days	s All. Days	From	То	
D33	0	2	18/04/2015	20/04/2015	
Abstract:					

SANS study of the structure of photosynthetic membrane proteins in solution Introduction

Oxygenic photosynthesis, which performs a transformation of the light energy into a storable form of the chemical energy, is the principal energy converter on earth, that has been developed in green plants and cyanbacteria over millions years by nature. Conversion of light to chemical energy at Photosystem II is associated with charge separation across the thylakoid membrane. The structure of PS II complexes has been already studied by a number of different techniques, e.g., its structure is well established by X-ray crystallography to a resolution of 1.9 Å at ultra low temperatures [1]. It is known that PS II is composed of at least 17 subunits [2] of which 14 are located within the photosynthetic membrane. In the crystal structure, PS II occurs as a homodimer with the longest dimensions of the membrane integral part 190 Å x 100 Å, which is 40 Å thick and extends from the stromal side of the membrane by no more than 10 Å. At the same time the luminal side of each monomer has prominent protrusions up to 55 Å above the membrane [3]. Nevertheless, the direct structural information about the properties of isolated PS II core complex stabilized with detergents at native environmental conditions has been missed so far. It has been shown for a number of proteins that the protein-detergent interactions have an influence on the membrane proteins structure that in some cases deviates from those determined by crystallographic techniques [4-7].

The structure of the core complex of Photosystem II (PS II), which was isolated and stored in a solution of the dodecyl- β -D-maltoside (β DM) detergent and of the octaethylene glycol monodecyl (C₁₂E₈) detergent, has been investigated by small-angle neutron scattering (SANS). In order to investigate independently the protein and the detergent structure, two different D₂O/H₂O contrast match points was used. The topological shape of PS II has been determined by applying ab initio shape restoration methods from the SANS data at the contrast match point of the detergents. The interaction of the protein and detergents was studied from the SAXS curves and also from the SANS curves, measured at the contrast match point for the protein and in 75% D₂O contrast. Our data analysis shows that there is a monolayer of the detergent surrounding the protein as a kind of protection belt. The SANS data also proves that the β DM detergent prevents an aggregation of PS II protein.

As a short conclusion, this work proves that natively structure PS II can be produced for functional characterization at physiological conditions.

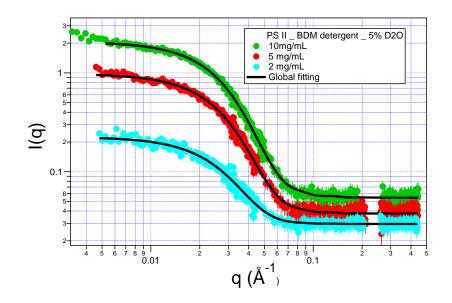


Figure 1. SANS curves from PS II isolated protein in β DM detergent measured in 5% D₂O contrast (green dots correspond to the protein concentration of 10 mg/mL, red dots – 5mg/mL and light blue dots – 2 mg/mL) by the elliptical cylinder model (black lines).

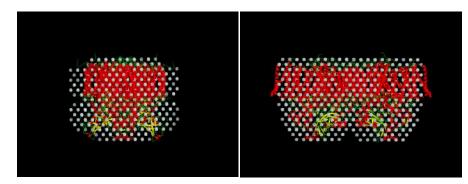


Figure 2. Comparison of restored low-resolution structural model (grey balls) and high-resolution PS II crystal structure (red ribbons).

References:

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