component of the enzyme proton channel, that was in large part due to a slowering in translation. Interestingly, depletion of subunit *h* resulted in dramatic changes in mitochondrial cristae morphology, which further supports the existence of a link between the ATP synthase and the folding/biogenesis of the inner mitochondrial membrane.

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S1.49 Kinetics of the F-ATPase of *E. coli* before and after blocking the C-terminal end of γ

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The F-ATPase of *E. coli* consists of the F_1 ($\alpha\beta\gamma\delta\varepsilon$) and the F_o (abc) part. The subunits γ, c and ε form the rotor of the protein. Former studies showed that a swivel joint in γ was created after fixing the rotor to the stator. That allows a rotation of γ despite a closed crosslink. In these studies we asked for the location of the swivel joint along the length of γ. For this purpose four new F_1-mutants, that carried a Cysteine at the C-terminal end of γ and a Cysteine at α, were created. Under oxidizing conditions a crosslink between stator- and rotor-subunits could be closed. Using a microvideographic test for single-molecule-rotation the different mutants were tested in respect of their hydrolysing behaviour under reducing and oxidizing conditions. Three mutants showed normal rotational behaviour. The rotational velocity dropped by appr. 25%. One mutant (γG282C) showed rotation despite an intact crosslink (verified by SDS-PAGE with appr. 90% closed crosslink) but the rotational velocity dropped by appr. 56%. The untwisting of the α-helical structure behind γI279 allows rotation around the dihedral angels of the peptide-backbone. This rotation could meet sterical hindrance causing greater activation energy. The untwisting of the α-helical portion of γ is one option for a rotary joint in F_1.

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(S2) Photosystems symposium lecture abstracts

S2/1 Membrane protein structure determination using crystallography and lipidic mesophases
Recent advances and successes

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A primary impasse on the route that leads to membrane protein structure through to activity and function is found at the crystal production stage. Diffraction quality crystals, with which structure is determined, are particularly difficult to prepare currently when a membrane source is used. The reason for this is our limited ability to manipulate proteins with hydrophobic/amphipathic surfaces that are usually enveloped with membrane lipid. More often than not, the protein gets trapped as an intractable aggregate in its watery course from membrane to crystal. As a result, access to the structure and thus function of tens of thousands of membrane proteins is limited. In contrast, a veritable cornucopia of soluble proteins has offered up their structure with insight into function, reflecting the relative ease with which they are crystallized. There exists therefore an enormous need for new ways of producing crystals of membrane proteins. One such promising approach makes use of lipidic liquid crystalline phases (mesophases). In my presentation, I will describe the method, our progress in robotizing and miniaturizing it for high-throughput applications, and our understanding of how it works at a molecular level. Major advances in applying the method for membrane protein structure determination will be presented.

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S2/2 Structure and function of photosynthetic membrane proteins

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Oxygenic photosynthesis is the main biological process on earth that converts the light energy from the sun into chemical energy. The primary step in this energy conversion, the light induced charge separation, is catalyzed by two distinct, membrane intrinsic protein complexes, photosystems I and II. Cyanobacterial Photosystem I consists of 12 protein subunits, to which 127 cofactors are non-covalently bound. It catalyzes the light-driven electron transfer from plastocyanin to ferredoxin. In the talk, the structure of the PSI-Ferredoxin will be presented. The second part of the talk focuses on the chloroplast ATP Synthase. Crystals of an oligomeric form of subunit c were grown from the spinach chloroplast enzyme diffracting as far as 2.5 Å. Though we are currently collecting experimental phases using nobel gases, the high symmetry of the oligomer allows for the determination of valuable structural insights from the native data. The native Patterson reveals the presence of 14-fold symmetry in the oligomer, confirming previous AFM studies. A huge surprise is the finding, that these crystals possess a strong yellow color. The pigment analysis shows that the c-ring chloroplast ATP-synthase contains chlorophylls and carotenoids.

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S2/3 Structural plasticity of the *Rhodobacter* photosystem

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