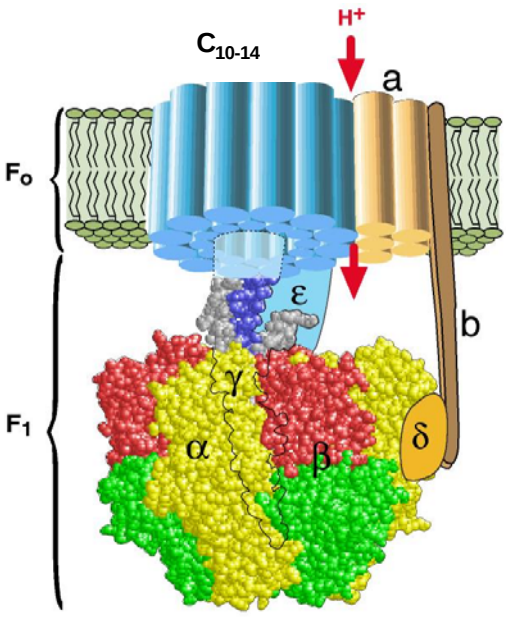
Structural investigations of the ATP-Synthase
(Ben Varco-Merth)

One of the most important proteins in energy transduction is ATP-Synthase (F_0F_1). This membrane-bound enzyme complex is present in all living organisms. It catalyzes the synthesis of ATP from ADP and P_i , driven by a transmembrane electrochemical potential of protons or sodium ions. The enzyme complex consists of two distinct structural and functional domains: A membrane intrinsic proton translocation system (the F_0 part), which is structurally connected by at least two "stalks" to the membrane extrinsic domain (the F_1 part), which in turn harbors the nucleotide binding sites. The structure of the F_1 domain was solved by X-ray structure analysis in 1994 by Abrahams and coworkers [1]. In 1999, a three-dimensional structural model at 3.9 Å was published on yeast-ATP-Synthase, including a ring of 10 subunits c, being part of the proton translocating channel [2]. The molecular elucidation of the coupling mechanism still suffers from the lack of information on the complete structure of the membrane-intrinsic proton translocation machinery and the energy transducing stalk region of the protein complex.



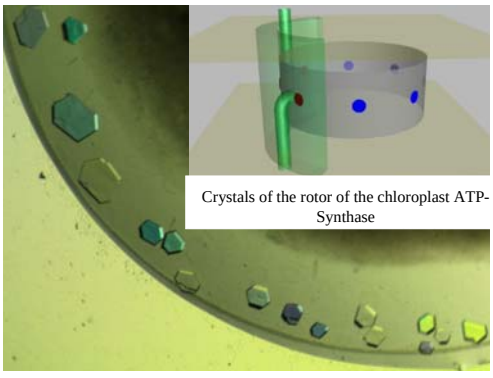
H. Wang and G. Oster (1998). Nature 396:279-282.

Structural model of the ATP-Synthase

The major aim of the project on the ATP-Synthase is to get detailed structural information on the proton conducting part (F0) of the enzyme as well as the coupling between the F0 and F1 part.

We follow a dual strategy for the structure determination:

- ♦ Crystallization of the intact ATP-Synthase
- ♦ Crystallization of subcomplexes of the F0 part



Crystals of the rotor of the chloroplast ATP-Synthase

Crystals of the rotor of the ATP-Synthase.

[1] Abrahams, J.P. , Leslie, A.G.W. , Lutter, R. and Walker, J.E. (1994) Nature 370, 621-628
[2] Stock, D., Leslie, A.G. and Walker, J.E. (1999) Science 286, 1700-1705