The chloroplast ATP synthase (CF_1F_o) located in the stroma lamellae of the thylakoid membranes shares many structural and functional characteristics with the homologous mitochondrial and bacterial ATPases, but is unique in enzyme activation and in the interaction with specific energy transfer inhibitors. In contrast to ATPases from other species and organelle the activity of the chloroplast enzyme is strongly controlled by the transmembrane proton gradient and the redox state of the γ-subunit in the membrane extrinsic F_1 domain.

We have collected diffraction data on 14 crystals obtained with the purified CF_1F_o-holoenzyme. Data were processed by MOSFLM/SCALA. All crystals showed mosaicities of almost 0.9°, belong to space group *C2* and have unit cell parameter of a = 150.2 Å, b = 99.4 Å, c = 130.7 Å.

In addition several crystals of a F_1-δ subcomplex of the cyanobacterial ATP synthase from *Thermosyechococcus elongatus* BP-1 obtained by a PEG-screen were tested for diffraction on ID-14-1. However, no well-diffracting crystal was found in this initial screen. Optimisation of crystallisation conditions and cryo-conditions are in progress.