F_oF_1-ATP synthase subunit α – A tale of two fragments

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The F_oF_1-ATP synthase is a reversible nanomotor synthesizing ATP in bacteria and eukaryotic mitochondria. The core catalytic F_1 moiety of this multisubunit complex is formed by a globular hexamer of alternating subunits α and β sitting on a central stalk consisting of subunit γ and small subunits δ and ε [1]. The composition and structure of the core F_1-ATPase is believed to be strictly conserved throughout evolution [1], however this notion is based on the established structures of F_oF_1-ATP synthase complexes of bacteria and model eukaryotes and may not reflect full eukaryotic diversity. Several reports have indicated that the Euglenozoa F_1-ATPase subunit α is split into two fragments, presumably by proteolytic cleavage [2–5]. Both fragments stay associated with the complex. This feature appears to have no parallel in any other group of organisms. In this project, we are investigating whether α cleavage results in novel features of this key enzyme, that are important for the structure/function of F_oF_1-ATP synthase in trypanosomes. We also aim to identify the protease responsible.

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