

**P1.1.84. FUNCTIONAL IMPLICATIONS FROM NOVEL
STRUCTURAL FEATURES IN COMPLEX I FROM YARROWIA
LIPOLYTICA**

V. Zickermann¹, M. Radermacher², T. Ruiz², T. Clason², S. Benjamin², B. Wrzesniewska¹, U.
Brandt¹

1 - Zentrum der Biologischen Chemie, Medical School, Universitat Frankfurt, Frankfurt am Main, Germany

2 - Dept. Molecular Physiology and Biophysics, College of Medicine, University of Vermont, Burlington VT, USA

Zickermann@zbc.kgu.de

Complex I is the largest and least understood enzyme of the respiratory chain. An extensive electron microscopic structural analysis of single particles uncovered a number of novel features in a 3 D reconstruction of complex I from *Yarrowia lipolytica*.

Using monoclonal antibodies (Zickermann et al., 2003) and a subcomplex lacking the FP fragment individual subunits can be assigned to distinct subdomains within the peripheral arm.

The membrane arm is curved and viewed from the cytoplasmic side a groove in the direction of the long axis can be seen. On the matrix side the membrane arm shows two major protrusions. From here a highly variable structure originates that forms a second connection between the two arms.

The emerging architecture of complex I has major implications for the understanding of the catalytic mechanism as it seems to rule out a direct coupling between redox chemistry and proton translocation. Instead a growing body of evidence suggests a conformationally driven proton pumping mechanism and it is tempting to speculate that the flexible linker between membrane and peripheral arm is involved in this process.

Zickermann, V., Bostina, M., Hunte, C., Ruiz, T., Radermacher, M. and Brandt, U. (2003) Functional implications from an unexpected position of the 49 kDa subunit of complex I, *J.Biol.Chem.* 278, 29072-29078.