



Application for beam time at ESRF – Report_MX1179

Achievements

We have determined the first X-ray structure of a large heterooligomeric eukaryotic Pfk from yeast *Pichia pastoris* at 3.05 Å in the T state, also including data collected at the ESRF [1]. The enzyme of $(\alpha\beta\gamma)_4$ composition contains a unique γ -subunit. A surprising result was also the structure of the N-terminal domains, which are not present in the bacterial enzymes. These domains are related to glyoxalase I, but the active sites are no longer functional. The aim of further experiments is to determine structures of the R-state and to characterize the allosteric switch and the effector binding sites.

References

[1] Sträter N., Marek S., Kuettner E.B., Kloos M., Keim A., Brüser A., Kirchberger J., Schöneberg T. (2011) Molecular architecture and structural basis of allosteric regulation of eukaryotic phosphofructokinases. *FASEB J.* 2011, 25, 89-98.