



	<b>Experiment title:</b> Crystal structure of eukaryotic DNA polymerase epsilon	<b>Experiment number:</b> MX 1449
<b>Beamline:</b> ID23-2	<b>Date of experiment:</b> from: Oct 3rd, 2012 to: Oct 4th, 2012	<b>Date of report:</b>
<b>Shifts:</b> 2	<b>Local contact(s):</b> Matthew Bowler	<i>Received at ESRF:</i>
<b>Names and affiliations of applicants (* indicates experimentalists):</b> <b>Matthew Hogg</b> <b>Elisabeth Sauer-Eriksson</b> <b>Erik Johansson</b>		

## Report:

**We were assigned 2 shifts at beamline ID23-1, but due to technical problems (alignment) with that beamline we were unable to collect usable datasets. Fortunately, the microfocus beamline ID23-2 was not used by others and we were able to collect datasets that allowed us to solve the structure of the catalytic core (142 kDa) of DNA polymerase epsilon at 2.2 Å resolution.**

DNA polymerase  $\epsilon$  (Pol  $\epsilon$ ) is a high-fidelity polymerase that has been shown to participate in leading-strand synthesis during DNA replication in eukaryotic cells. We present here a ternary structure of the catalytic core of Pol  $\epsilon$  (142 kDa) from *Saccharomyces cerevisiae* in complex with DNA and an incoming nucleotide. This structure provides information about the selection of the correct nucleotide and the positions of amino acids that might be critical for proofreading activity. Pol  $\epsilon$  has the highest fidelity among B-family polymerases despite the absence of an extended  $\beta$ -hairpin loop that is required for high-fidelity replication by other B-family polymerases. Moreover, the catalytic core has a new domain that allows Pol  $\epsilon$  to encircle the nascent double-stranded DNA. Altogether, the structure provides an explanation for the high processivity and high fidelity of leading-strand DNA synthesis in eukaryotes.

Hogg, M., Osterman, P., Bylund, G.O., Ganai, R.A., Lundström, E.-B., Sauer- Eriksson, A.E. and Johansson, E. (2014) Structural basis for processive DNA synthesis by yeast DNA polymerase  $\epsilon$ . *Nature Structural & Molecular Biology* 21:49-55