## Microsymposium

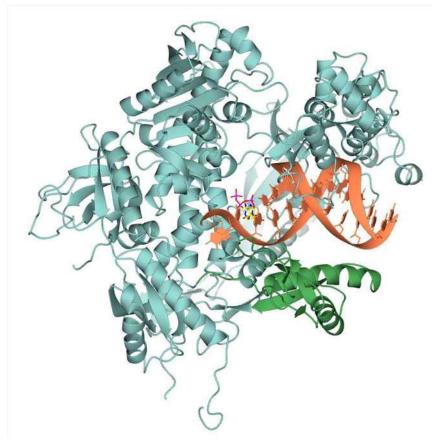
## MS13.003

## Structural basis for processive DNA synthesis by yeast DNA polymerase $\varepsilon$

M. Hogg<sup>1</sup>, P. Osterman<sup>1</sup>, G. Bylund<sup>1</sup>, R. Ganai<sup>1</sup>, E. Lundström<sup>1</sup>, <u>E. Sauer-Eriksson<sup>2</sup></u>, E. Johansson<sup>1</sup> <sup>1</sup>Umea University, Department of Medical Biochemistry and Biophysics, Umea, Sweden, <sup>2</sup>Umea University, Department of Chemistry, Umea, Sweden

DNA polymerase  $\varepsilon$  (Pol  $\varepsilon$ ) is a high-fidelity polymerase that participates in leading-strand synthesis during eukaryotic DNA replication in eukaryotic cells. The 2.2 Å ternary structure of the 142 kDa catalytic core of Pol  $\varepsilon$  from Saccharomyces cerevisiae in complex with DNA and an incoming nucleotide has recently been determined [1]. The structure provides information about the selection of the correct nucleotide and the positions of amino acids that might be critical for proofreading activity. Pol  $\varepsilon$  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 (i.e. the P-domain) that allows Pol  $\varepsilon$  to encircle the nascent doublestranded DNA and enhance processifivity of the polymerase. The structure provides valuable insights into the similarities and differences between Pol  $\varepsilon$  and other B-family polymerases, and suggests possible mechanisms responsible for the high processivity and fidelity of Pol  $\varepsilon$ .

[1] Hogg et al., 2014, NSMB, 21, 49-55



Keywords: DNA polymerase, Protein-nucleic acid interaction, replication