

Supplementary figures

Fig. S1. Alignment of sequences of human UNG nuclear isoform (human_UNG2) and *S. purpuratus* putative uracil-DNA glycosylase (XP_791566.1). Residues responsible for interaction with DNA are marked by asterisks based on human UNG X-ray structure.¹ Identical, highly conserved, and moderately conserved residues in the alignment are labeled by black, dark grey, and light grey boxes, respectively. The alignment and conservation values were produced with Clustal Omega.²

Supplementary references

- 1 S. S. Parikh, C. D. Mol, G. Slupphaug, S. Bharati, H. E. Krokan and J. A. Tainer, *EMBO J.*, 1998, **17**, 5214–5226.
- 2 F. Sievers, A. Wilm, D. Dineen, T. J. Gibson, K. Karplus, W. Li, R. Lopez, H. McWilliam, M. Remmert, J. Söding, J. D. Thompson and D. G. Higgins, *Mol. Syst. Biol.*, 2011, **7**, 539.