STRUCTURAL BIOLOGY COMMUNICATIONS

Volume 73 (2017)

Supporting information for article:

Crystal structure of enolase from *Drosophila melanogaster*

Congcong Sun, Baokui Xu, Xuyan Liu, Zhen Zhang and Zhongliang Su

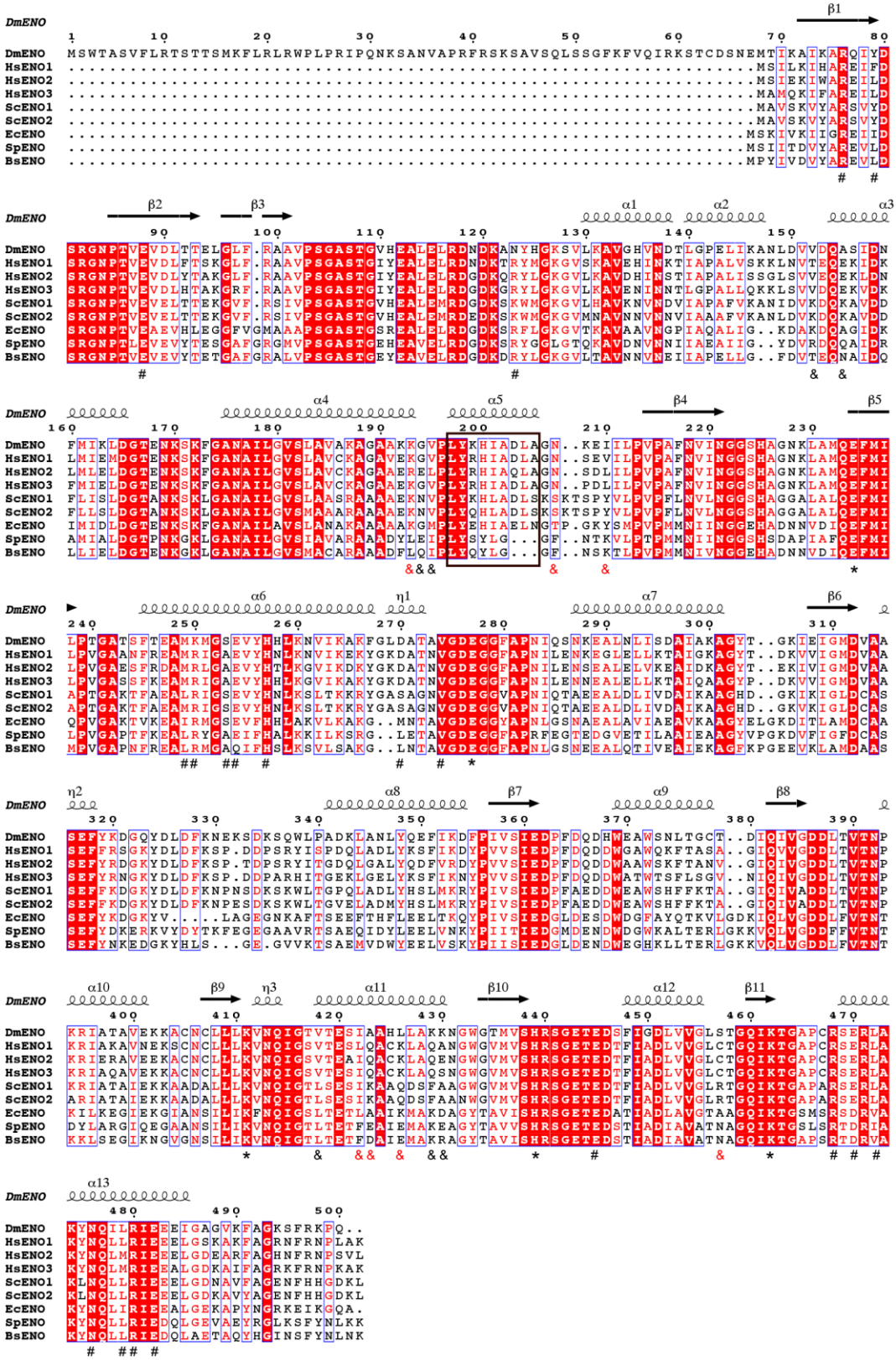

Figure S1 Sequence alignment of enolase proteins from different species including

Drosophila melanogaster, *Homo sapiens*, *Saccharomyces cerevisiae*, *Escherichia coli*,

Streptococcus pneumonia and *Bacillus subtilis* was performed with Clustal Omega and ESPript (Gouet *et al.*, 1999, Sievers *et al.*, 2011). The secondary structure is shown according to the structure of DmENO (69-500, isoform 2). Residues in DmENO dimeric interface are highlighted by number sign (#). Residues responsible for substrate binding and catalysis are highlighted by asterisk (*). Residues in SpENO octameric interface are highlighted by ampersand sign (&). Residues that conserved in SpENO and BsENO, but not in DmENO, are highlighted by red ampersand sign (&). Residues corresponding to the α5 helix of DmENO were indicated by a black box.

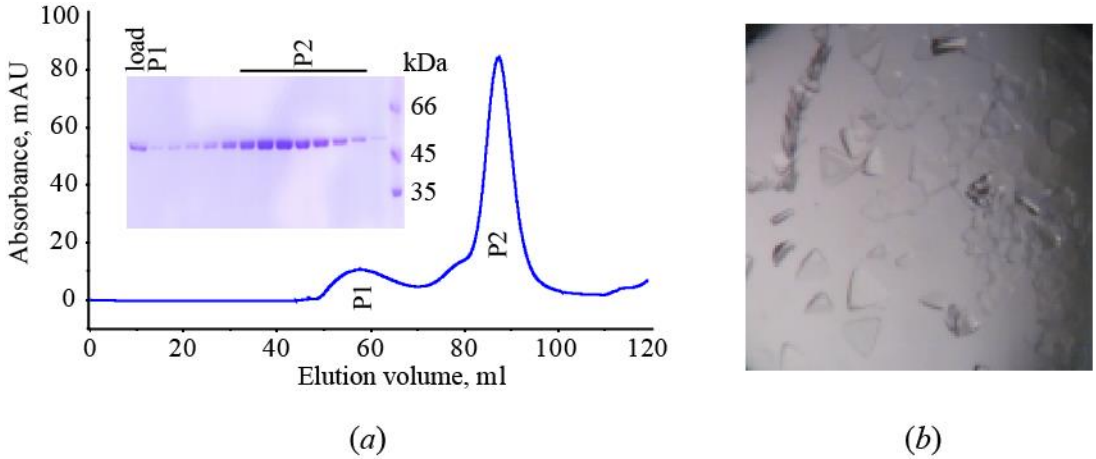

Figure S2 (*a*) Elution profile of DmENO from a HiLoad 16/60 Superdex 200 pg column. Inset, reducing SDS-PAGE for elution samples. (*b*) Crystals for X-ray diffraction experiment.

References

Gouet, P., Courcelle, E., Stuart, D. I. & Metoz, F. (1999). *Bioinformatics* **15**, 305-308.

Sievers, F., Wilm, A., Dineen, D., Gibson, T. J., Karplus, K., Li, W., Lopez, R., McWilliam, H., Remmert, M., Soding, J., Thompson, J. D. & Higgins, D. G. (2011). *Mol. Syst. Biol.* **7**, 539.