

Three-dimensional structure of a new member of the α -amylase family

Eve N. PRETTY¹, John S. DILIGENT², Ann D. TALENTED^{2,3} & Gregory F. CLEVER^{1,4}

¹ Department of ..., ... Faculty ..., ... School ..., Street No., Postal zip, City, State

² Brewery..., ... Corporation ..., Street No., Postal zip, City, State

³ Institute of ..., ...Academy ..., Street No., Postal zip, City, State; e-mail: talented@academy.xy

⁴ Department of..., ... Faculty ..., ... University ..., Street No., Postal zip, City, State

We describe the 3-D structure of a new α -amylase family member. According to its amino acid sequence (HOLMES, 1990), The structure was solved using the method by ALIBABA et al. (2000), The enzyme adopts the structure of a classical (β/α)₈-barrel fold (MOTIF & DOMAIN, 1995), described originally in the structure of an interesting enzyme (FIRST et al., 1985). etc., etc.

Acknowledgement(s)

References

- ALIBABA, A.B., ALIDEDO, C.D. & ALIDETI, E.F. 2000. *J. Unbeliev. Methods* **12**, 345-355.
FIRST, G.H., SECOND, I.J. & THIRD, K.L. 1985. *J. Struct. Compet.* **67**, 890-899.
HOLMES, S. 1990. *Fancy Res.* **987**, 654-663.
MOTIF, M.N. & DOMAIN, O.P. 1995. *Mol. Pattern Evol.* **3**, 21-33.