

# Three-dimensional structure of a new member of the $\alpha$ -amylase family

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We describe the 3-D structure of a new  $\alpha$ -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 ( $\beta/\alpha$ )<sub>8</sub>-barrel fold (MOTIF & DOMAIN, 1995), described originally in the structure of an interesting enzyme (FIRST et al., 1985). etc., etc.

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## References

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