

## Crystallographic Studies of Apo Maize Aldose Reductase

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Maize aldose reductase (AR; EC 1.1.1.21) present in seed endosperm is able to catalyze the reduction of glucose to sorbitol in the polyol pathway. The maize enzyme is a member of the aldo-keto reductase superfamily and, in contrast to human AR, it seems to prefer the conversion of sorbitol into glucose. In humans, the protein is involved in severe diabetic complications. For this reason, the structure of human AR has been extensively studied. However, very few plant ARs have been characterized so far. To better understand maize AR apparent preference for sorbitol over glucose as a substrate, crystallographic studies were initiated and preliminary X-ray diffraction studies were previously reported (Kiyota, E. *et al.*, 2007, *Acta Cryst.* **F63**: 990-992). In this work, the crystal structure of apo maize AR is described. The AR structure with one molecule in the asymmetric unit was solved by an automated molecular replacement procedure implemented in the program *MrBUMP*. Loop regions of the AR structure were built using the Loop module in the ARP/wARP software suite. The final refined structure along with refinement statistics are presented. A comparative analysis is currently in progress and it is expected to shed light into structural features related to the enzymatic mechanism and peculiar activities of maize AR. This work was supported by FAPESP, CNPq and CAPES. We gratefully acknowledge the MX-1/MX-2 beam line staffs and LNLS for beam line time.

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