Structural Studies of the Sucrose Isomerase MutB from *Pseudomonas mesoacidophila*

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The sucrose isomerase, MutB, from *Pseudomonas mesoacidophila* belongs to glycoside hydrolase family 13, and catalyzes the isomerization of sucrose into isomaltulose and trehalulose [1]. The 64 kDa enzyme has been crystallized [2] and the three dimensional structure of MutB has been solved to 1.6 Å resolution by the molecular replacement method using the isomaltulose synthase, PalI, from *Klebsiella* sp. LX3 as a search model [3]. The overall structure of MutB is made up of three domains: an N-terminal and catalytic $(\beta/\alpha)_8$ domain, a subdomain and a C-terminal domain made up of seven β-strands [4].

The structures of various complexes with inhibitors and/or substrate analogues have been obtained and are currently under refinement. Once the detailed analyses of these structures have been completed, a better understanding of the molecular basis of sucrose decomposition, isomerization as well as the selectivity of this enzyme leading to the formation of different products should be gained.

[1] Nagai Y., Sugitani T., Tsuyuki K., *Biosci. Biotechnol. Biochem.,* 1994, **58**, 1789. [2] Ravaud S., Watzlawick H., Haser R., Mattes R., Aghajari N., *Acta Cryst. F.*, 2005, **61**, 100. [3] Zhang D., Li N., Lok S.M., Zhang L.H., Swaminathan K., *J. Biol. Chem.,* 2003, **278**, 35428. [4] Ravaud S., Watzlawick H., Haser R., Mattes R., Aghajari N., *submitted.*

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