Sucrose isomerases, which are identified in several microorganisms, catalyze the isomerization of sucrose into variable amounts of isomaltulose (α-D-glucosylpyranosyl-1,6-D-fructofuranose) and trehalulose (α-D-glucosylpyranosyl-1,1-D-fructofuranose) with the formation of glucose and fructose as by-products. The product ratio depends mainly on the bacterial strain but also on the temperature, pH and reaction conditions. Crystal structures of sucrose isomerases with distinct product specificity and physico-chemical parameters were determined: MutB, a trehalulose synthase from Pseudomonas mesoacidophila MX-45, and SmuA, a isomaltulose synthase from Protaminobacter rubrum. These enzymes display a catalytic core and an active site architecture characteristic of glycoside hydrolase family 13 enzymes. Substrate recognition and processing as well as the reaction mechanism and specificity were earlier investigated for MutB pointing out the important role of an aromatic clamp and of the residues interacting with the substrate. This clamp is a key player in the catalytic mechanism controlling/modulating the entrance/exit of the substrate/product. It might determine in direct line with the kinetics parameters of the enzyme, the time that the substrate stays in the pocket and favors or penalizes the tautomerization event required for trehalulose formation. Typical and specific structural features linked to the product specificity and the reaction mechanism in general will be discussed.