In Saccharomyces cerevisiae, trehalose is a major reserve carbohydrate involved in reponses to thermal, osmotic, oxidative, and ethanol stresses, as well as the suppression of denatured protein aggregation. Trehalose biosynthesis is a two-step process in which glucose 6-phosphate and UDP-glucose are converted by trehalose-6-phosphate synthase, encoded by TPS1, into alpha,alpha-trehalose 6-phosphate, which is then converted with water into trehalose and phosphate by trehalose-6-phosphate phosphatase, encoded by TPS2. The trehalose biosynthetic pathway can affect glycolysis in that one of its intermediates, trehalose-6-phosphate, inhibits hexokinase activity, which restricts the influx of sugars to glycolysis during the switch to fermentative metabolism. Tps1p and Tps2p are part of the alpha,alpha-trehalose-phosphate synthase complexwith Tps3p and Tsl1p, regulatory proteins with partially overlapping functions, though some Tps1p appears to be present in the cell as a monomer. TPS1, TPS2, TPS3 and TSL1 are coinduced under stress conditions, and corepressed by the Ras-cAMP pathway. Deletion of TPS1 results in loss of both TPS activity and trehalose biosynthesis, whereas deletion of TPS2 results in temperature sensitivity and loss of TPP activity. Deletion of either TPS1 or TPS2 results in a growth defect on fermentable carbon sources. Deletion of either TPS3 or TSL1 has only mild effects, but deletion of both TPS3 and TSL1 results in significant reductions in TPS and TPP activities, as well as reduced trehalose biosynthesis.