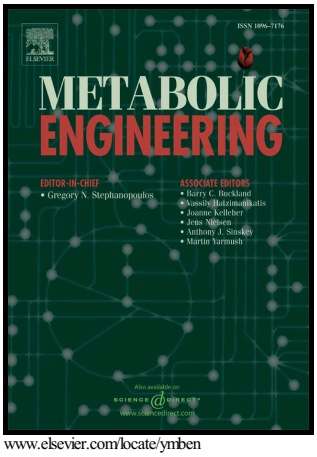

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Uncovering the role of branched-chain amino acid transaminases in *Saccharomyces cerevisiae* isobutanol biosynthesis

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Abstract

Isobutanol and other branched-chain higher alcohols (BCHAs) are promising advanced biofuels derived from the degradation of branched-chain amino acids (BCAAs). The yeast *Saccharomyces cerevisiae* is a particularly attractive host for the production of BCHAs due to its high tolerance to alcohols and prevalent use in the bioethanol industry. Degradation of BCAAs begins with transamination reactions, catalyzed by branched-chain amino acid transaminases (BCATs) located in the mitochondria (Bat1p) and cytosol (Bat2p). However, the roles that these transaminases play in isobutanol production remain poorly understood and obscured by conflicting reports in the literature. In this work, we elucidate the influence of BCATs on isobutanol production in two genetic backgrounds (CEN.PK2-1C and BY4741). In the process,