CRYSTAL STRUCTURE OF A NOVEL *(R)*-SELECTIVE AMINE TRANSAMINASE AND APPROACHES TO BROADEN ITS SUBSTRATE SCOPE BY RATIONAL ENGINEERING

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We recently identified a novel *(R)*-selective amine transaminase (ATA); now we want to broaden its substrate scope since ATAs are promising biocatalysts for the production of chiral amines [1]. In general, aminotransferases are pyridoxal-5′-phosphate (PLP)-dependent enzymes, which reversibly catalyze the transfer of an amino group from an amino donor to a ketone or aldehyde, resulting in the formation of chiral amines. The conversion of bulky ketones to amines is especially interesting because they serve as drug-precursors. In most cases, bulky ketones are not naturally converted. For this reason, protein engineering methods are applied. There are two approaches: random and rational. While we also use the random approach, rational engineering seems to be more effective for our purpose. We use the protein crystal structure to predict impactful amino acid exchanges to improve transamination activity. In this work, we present the characteristics of our novel *(R)*-selective ATA and show its crystal structure with the PLP bound to the active site lysine. Furthermore, we compare our ATA to existing *(R)*-selective ATA structures [2] and explain our approach to broaden the substrate scope by rational engineering.

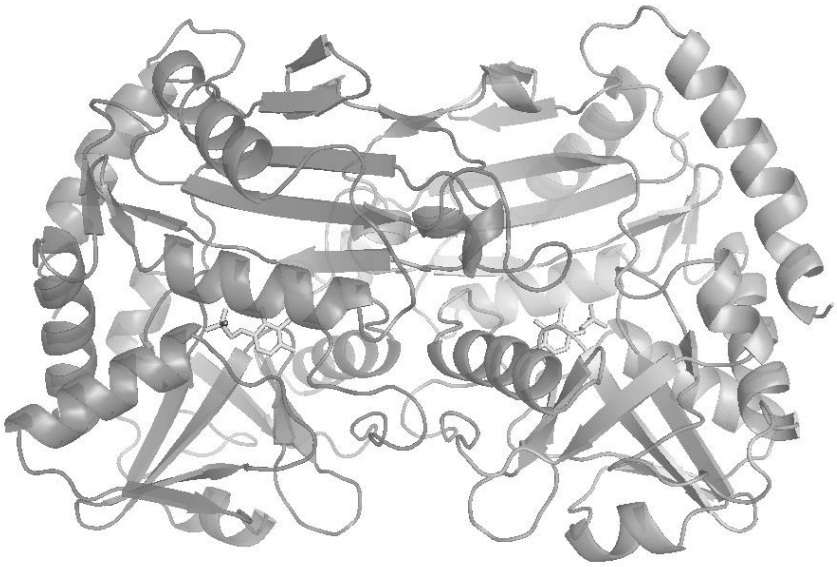

Figure 1 – Crystal structure of the new (R)-selective amine transaminase

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