

**NON-NATURAL AMINO ACIDS: 462 (METHODS IN  
ENZYMولوجY)**

**Therease Madson**

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Table 1 Parameters derived from computational and crystal structure analysis. Manipulation of enzyme properties by noncanonical amino acid incorporation.

This analysis used a fixed-backbone technique [ ]. De novo design of the hydrophobic surface. Protein stabilization by hydrophobic interactions at the surface. In general, one of the big challenges in enzyme engineering is to accurately predict how mutations will affect enzyme function.

The size difference between valine and the adjacent residue allowed a comparison of the structural and energetic consequences of mutations in a solvated hydrophobic cavity. Effect of cavity-creating mutations in the hydrophobic core of chymotrypsin inhibitor