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Introduction of aromatic residue in alpha-helices of *Bacillus Lip B* to improve its thermo stability: A110Y and N195Y mutants by site directed mutagenesis

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Bacillus lipase is an industrial important bacterial lipase because these are easily produced and display high tolerance for alkaline conditions and organic solvents. Bacillus lipase had been successfully evolved for thermo adaptation both by directed evolution and random mutagenesis. Introduction of aromatic interaction had been a rational basis for structure-function analysis of protein for thermal adaptation. Tyrosine is observed to have high residency within alpha helix of thermo-stable protein. Hence A110 and N195 residues within alpha helix of bacillus lipase were targeted for substitution with tyrosine. Variant A110Y was similar in behavior to WT with only mild enhancement in its thermo stability. N195Y showed significant deviation in features as temp. Stability, pH optima, substrate specificity and specific activity with respect to WT. Modeled structure represented the formation of additional interhelical aromatic and polar interaction by Y195 as molecular basis of structural and functional deviation of variant N195Y.

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