

Functional characterization and structural modeling of synthetic polyester-degrading hydrolases from *Thermomonospora curvata*

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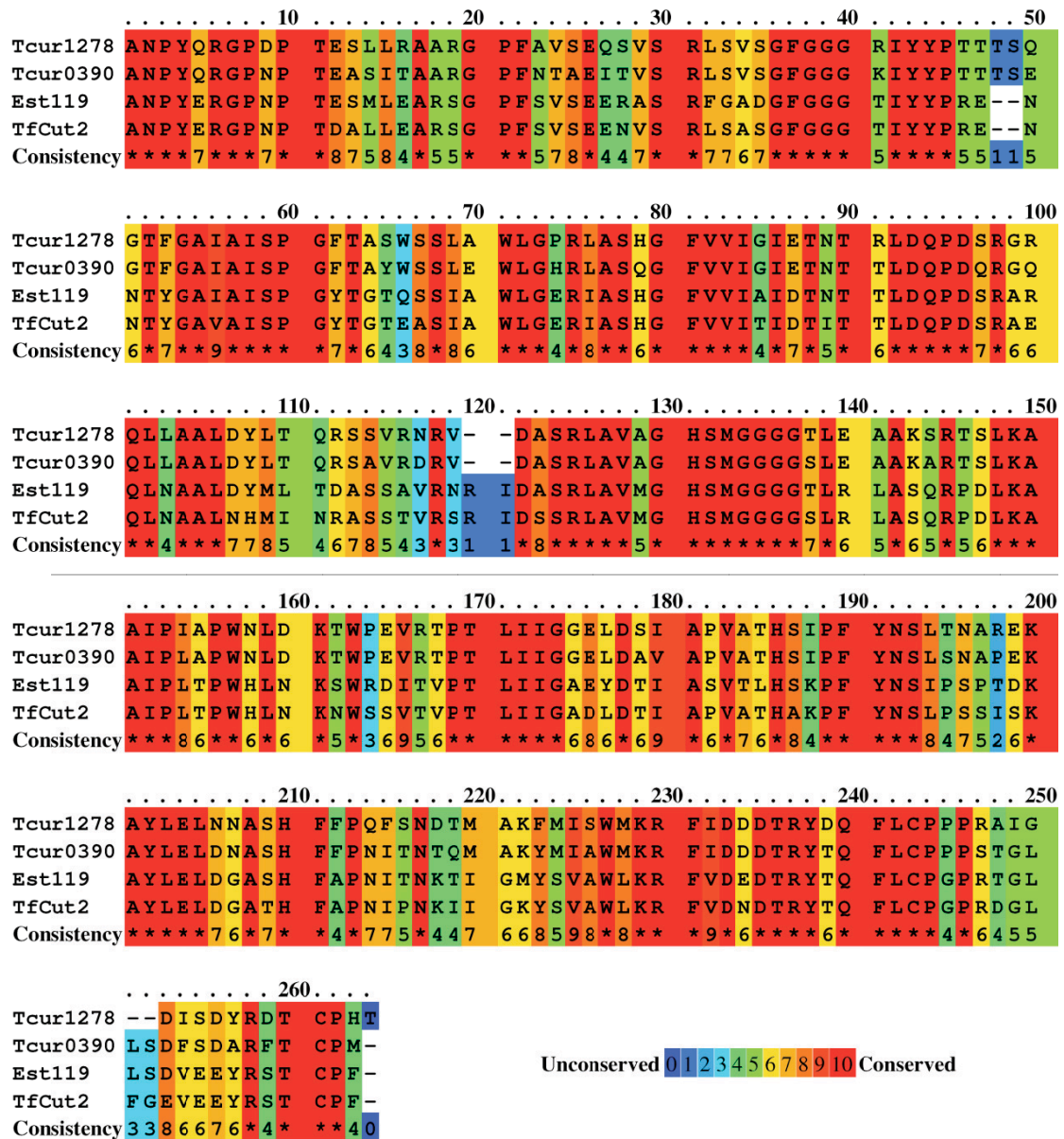


Fig. S1. Alignment of the mature protein sequences of Tcur1278, Tcur0390, TfCut2 and Est119 polyester hydrolases. The regions of similarity of individual amino acid residues are indicated with colors from blue, unconserved to red, conserved. The multiple sequence alignment was performed with the PRALINE web server (Simossis and Heringa 2005).

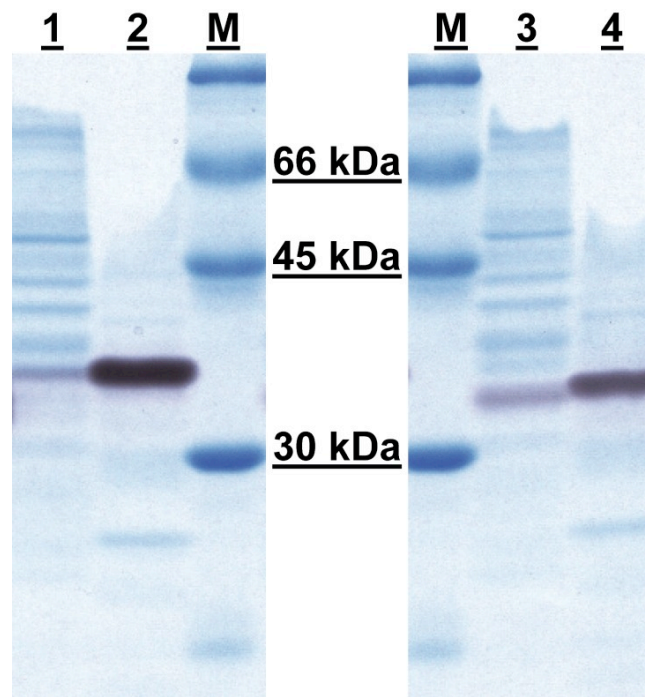


Fig. S2. SDS PAGE analysis of Tcur0390 (lanes 1-2) and Tcur1278 (lanes 3-4). 10 μ g of crude cell lysate (1, 3) and eluate obtained after IMAC purification (2, 4) were loaded in each lane; protein size markers (M). The gel was first stained with Fast Red dye for esterase activity against 1-naphthyl acetate (purple bands) followed by staining with Coomassie Brilliant Blue (blue bands).