



Figure S1: Multiple sequence alignment of LysB-D29 with relative members of the α/β hydrolase family including *Penicillium purpureogenum* Acetylxylin esterase (**PPA**), *Fusarium solani* cutinase (**FSC**), *Humicola insolens* cutinase (**HIC**) and *Trichoderma reesei* cutinase (**TRC**). Identical residues are labeled by *asterisk*, conserved residues labeled by *colon* and *full stop* indicating semi-conserved residues. Residues forming the active site are shaded in red color. Region-1 (lid domain) in **TRC** is highlighted in yellow, Region-2 is highlighted in gray, Region-3 (linker domain in LysB-D29) and acyl binding site in **PPA** esterase and all cutinases are highlighted in green. Oxyanion hole and GXP residues are highlighted in pink.