



Figure S3. Superimposition of Tle1 and Tle4 with the structural model for the Tle^{ECL} lipase domain. The AlphaFold2 model of the Tle^{ECL} lipase domain was superimposed onto the structures of Tle1 (PDB: 4O5P) and Tle4 (PDB: 4R1D) from *Pseudomonas aeruginosa* PAO1. The predicted active-site residues Ser341 and His448 are indicated in the Tle^{ECL} model, and corresponding Tle1 and Tle4 catalytic residues are rendered as spheres in the structure overlays.