



Figure S6. Structure-based sequence alignment of eight class III CoA-transferase superfamily members. This alignment corresponds to the structure superposition in Figure 2B. Secondary structure elements, except 3₁₀ helices, are shown for H6YfdE (PDB entry 4hl6). The active site Asp is indicated by a red triangle. The locations of the ACOCT GNxH loop (PDB entry 4hl6) and FCOCT Gly-rich loop (PDB entries 1p5h, 1pt7, and 3ubm) are underlined in blue. In the YfdE sequence, large domain residues are upper-case and small domain residues are lower-case. The percent identity/similarity for each pair of sequences is given in Table S2.