



Fig. S5. Comparison of potential oxyanion hole residues in OafA and OafB. A. Homology model of OafA_{STM}^{C-long} (yellow) modelled on the structure of OafB (grey, extension in orange and additional helix in teal). Catalytic triad and potential oxyanion hole residues shown as sticks. Residues indicated with OafA first. Both Ser 437 side chain and Leu 438 backbone amide are in close proximity to catalytic triad and active site sulfate. B. Sequence alignment of OafA from *Salmonella* ser. Typhimurium and OafB from Typhimurium and Paratyphi A serovars of *Salmonella* from OafA residues 410-450. Alignments were carried out using Tcoffee with default settings. Red Box highlights predicted replacements for catalytic block II glycine.