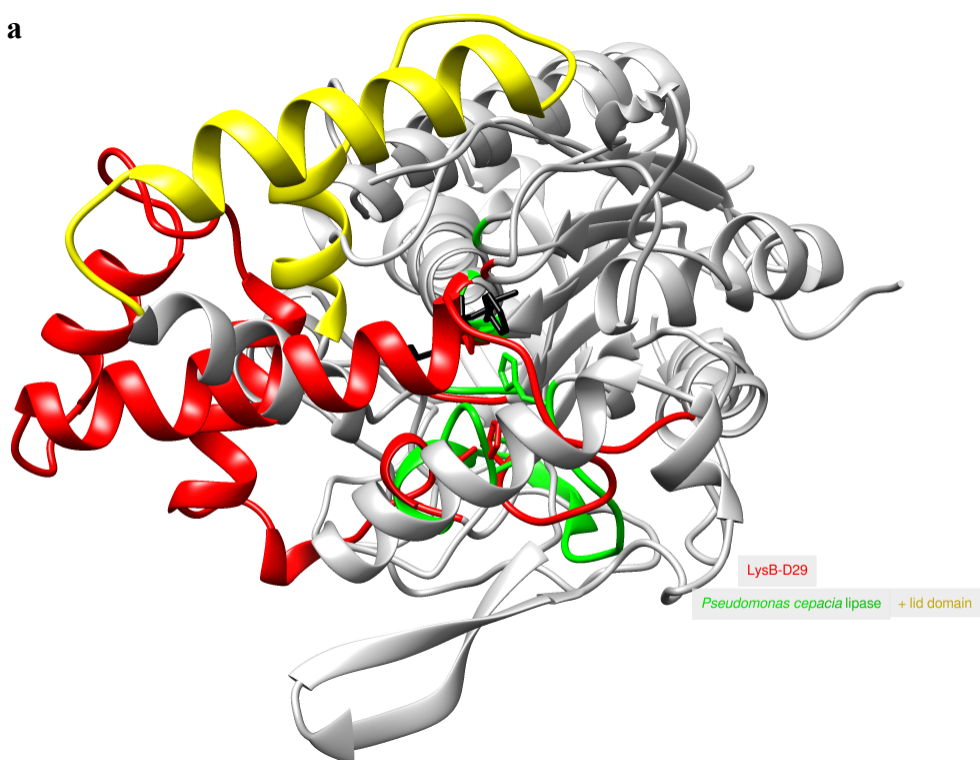
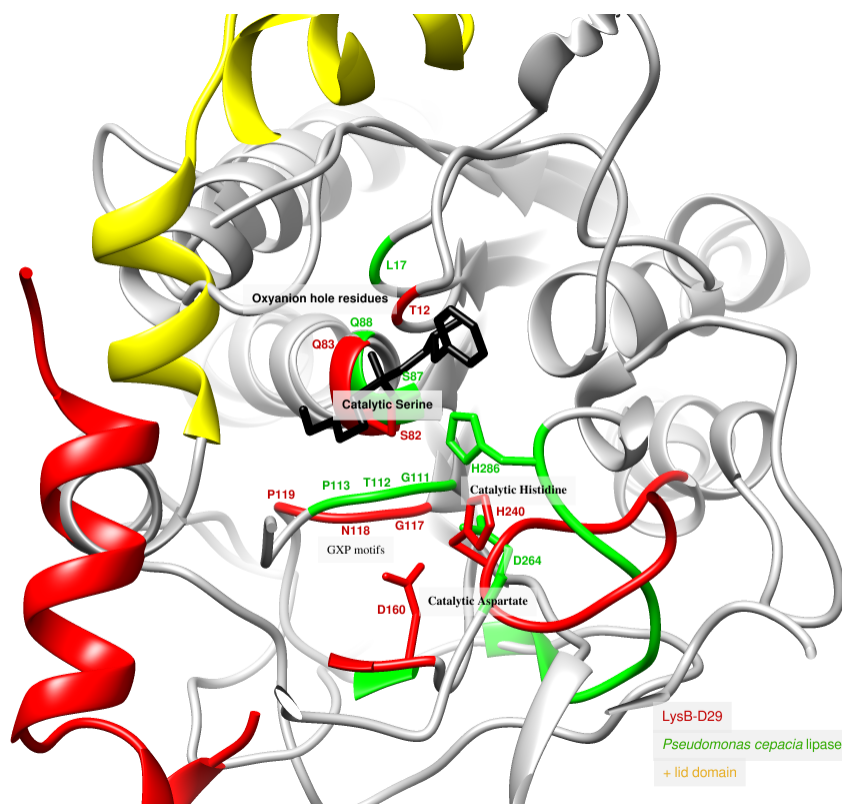


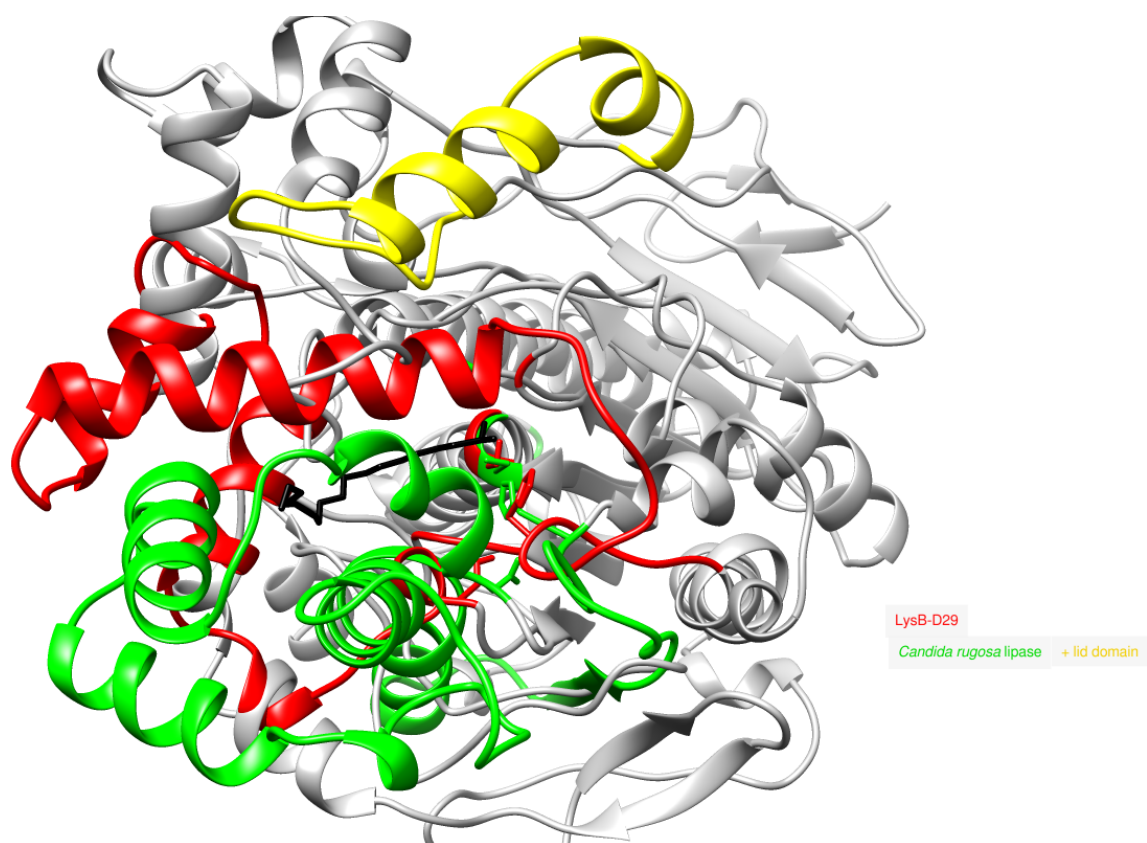
**a**



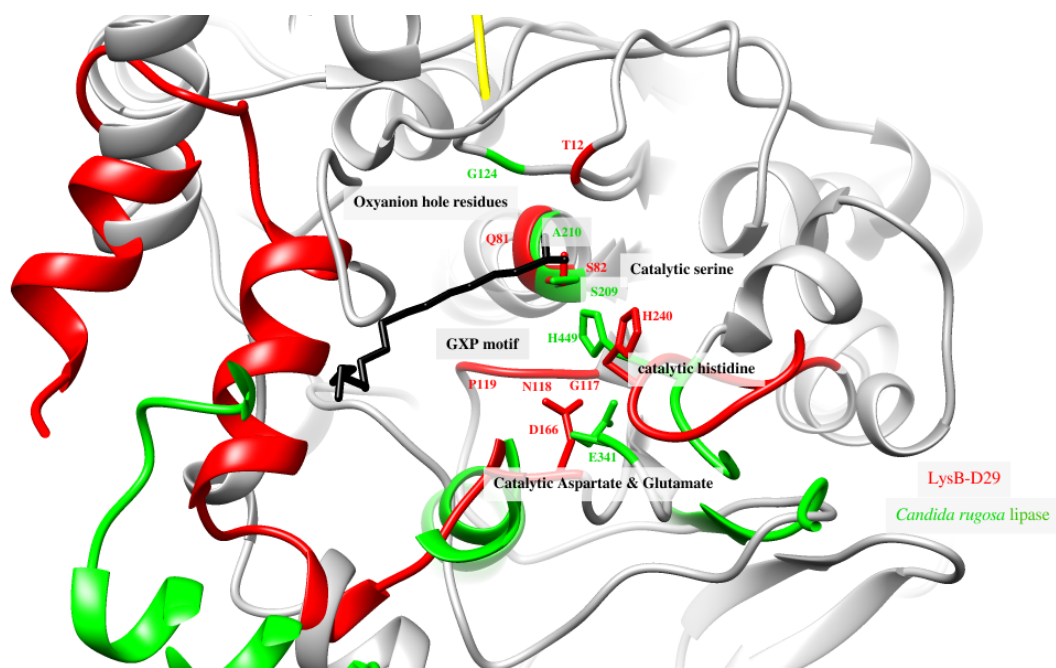
**b**



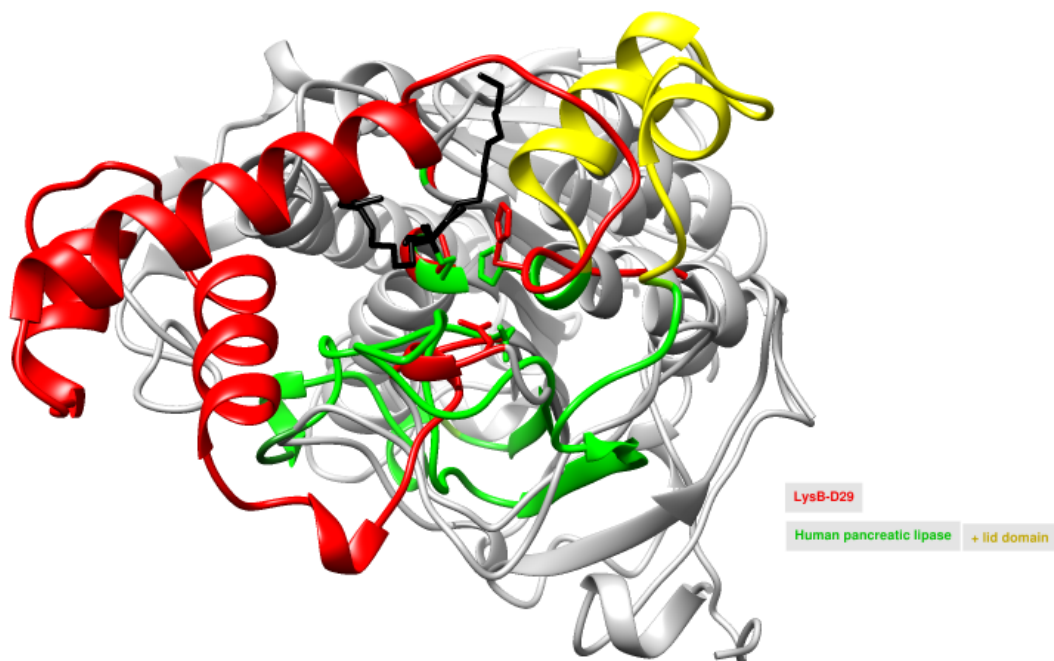
c



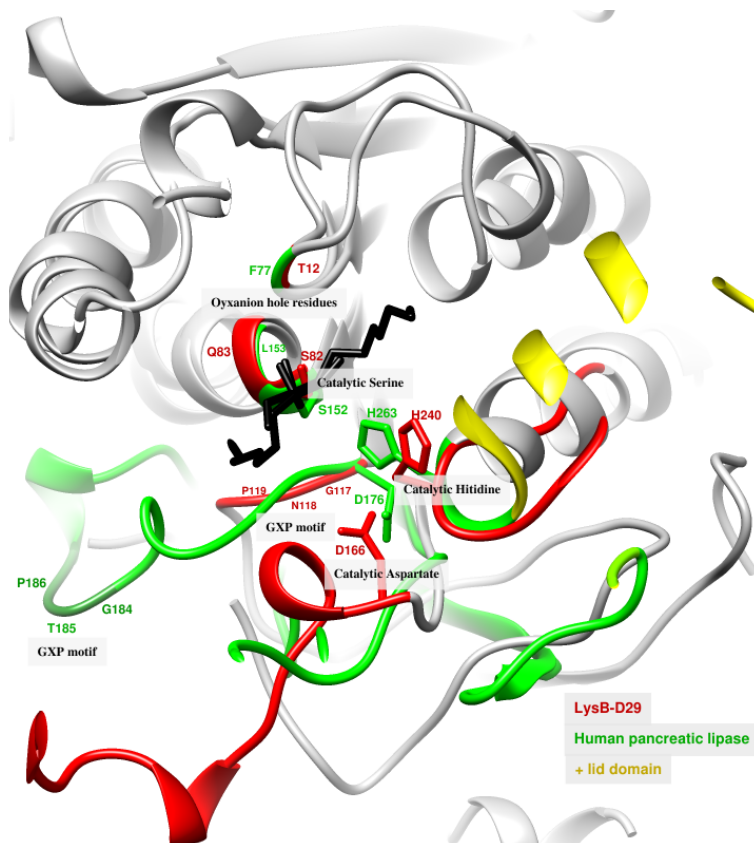
d



e



f



**Figure S4. Total alignment** of three-dimensional structural alignment of 3D structures of LysB-D29 and its relative members of the  $\alpha/\beta$  hydrolase family including: (a) *Pseudomonas cepacia* lipase, (c) *Candida rugosa* lipase and (e) Human pancreatic lipase, showing lid domain (yellow), linker domain of LysB-D29 (red color) and acyl binding site in lipases (green color). **Focus views** of (b) alignment of

LysB-D29 to *P. cepacia*, **(d)** alignment of LysB-D29 to *C. rugosa* and **(f)** alignment of LysB-D29 to Human pancreatic lipase, showing triad residues, oxyanion hole residues, GXP residues in red color (LysB-D29) and green color (aligned lipases) and co-crystalized inhibitor molecule (black color).