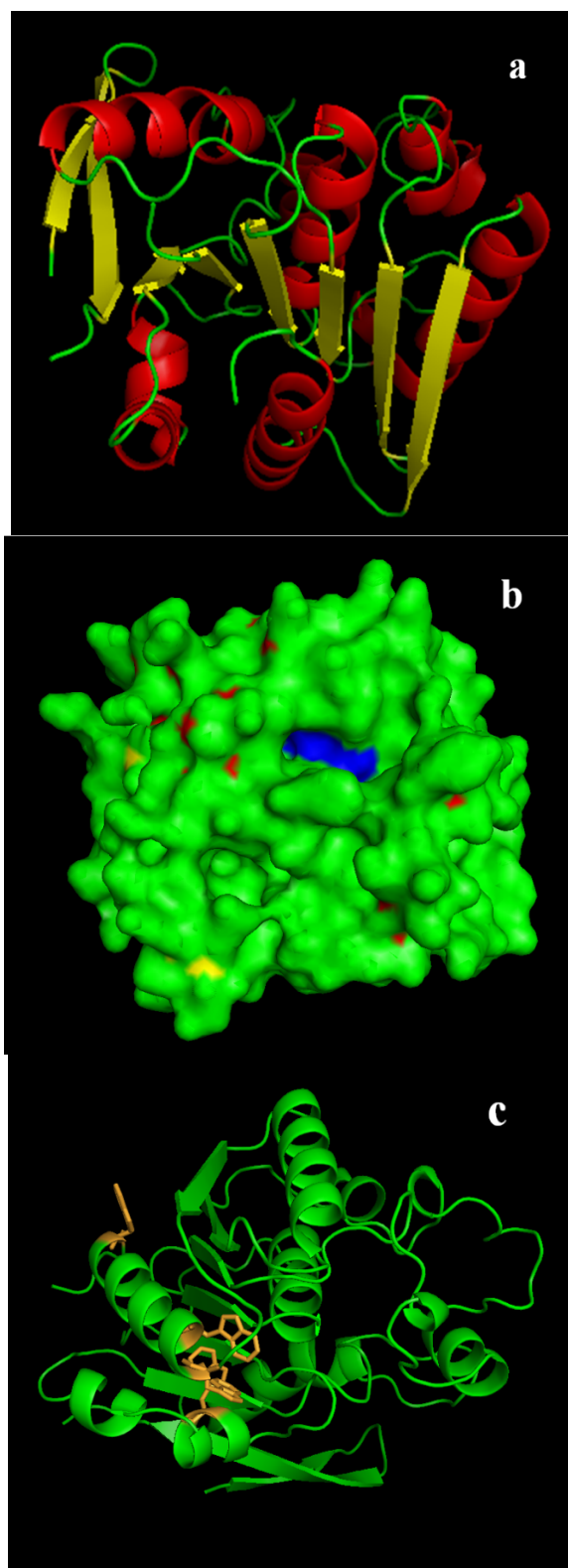


S1 Fig. 3-D structural model of PmEst.



a) Model based on the homology modeling with the crystalline structure of tributyrin esterase (PDB ID: 2UZ0) in cartoon drawing; b) Residues of the esterase domain in PmEst are labeled in blue (on surface view); c) Position of the Trp residues in the 3-D structure of PmEst in cartoon drawing.