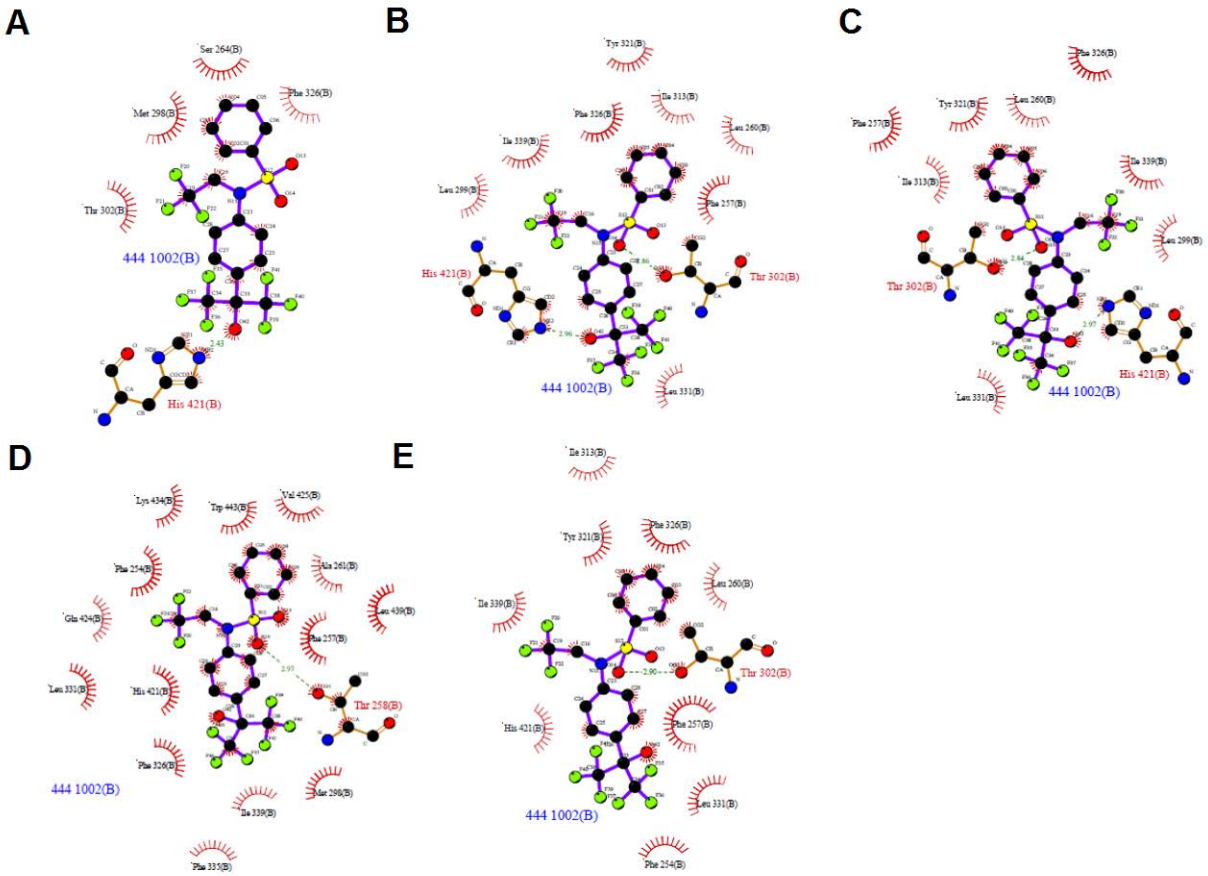

Fig. S2: Schematic representations of molecular interactions between the key amino acid residues, H421 and W444, lining the LXRα ligand binding pocket and T-0901317 have been generated using LIGPLOT. Hydrogen bonds and hydrophobic interactions of LXRα (A) wild-type, (B) H383E, (C) E387Q, (D) L414R, and (E) R415A with T-0901317 have been depicted. Dashed lines represent hydrogen bonds and spiked residues form hydrophobic contacts with the ligand.