Electronic Supplementary Material (ESI) for RSC Advances.

Exploring the Binding Mode and Thermodynamics of Inverse Agonists against Estrogen-related Receptor alpha

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Table S1. Molecular docking results for the ERRα and inverse agonist ligands.

Compound	Autodock Binding Energy (kcal/mol)	Hydrophobic Contacts	Hydrogen Bonds
comp 1	-	V321, L324, F328, E331, V366, F382, L386, A396, G397, L398, F495, L500	-
comp 2a (SO2 IN)	-7.7	V321, L324, F328, E331, M362, L365, V366, V369, F382, L386, A396, L398, V491, F495, V498, L500	-
comp 2b	-6.2	V321, L324, S325, F382, L386, G397, L398, F495, V498, L500	A396
comp 3a (SO2 IN)	-7.6	L318, P319, V321, F328, E331, M362, L365, V366, V369, F382, L386, L388, A395, A396, G397, L398, L400, L405, V491, F495, V498, L500	-
comp 3b	-6.9	V321, L324, L327, F328, E331, L365, V366, V369, F382, A395, A396, L398, L405, F495, V498	G397
XCT790	-10.0	V321, L324, F328, E331, F382, A396, G397,	-

		L398, V491, H494, F495, V498, L500	

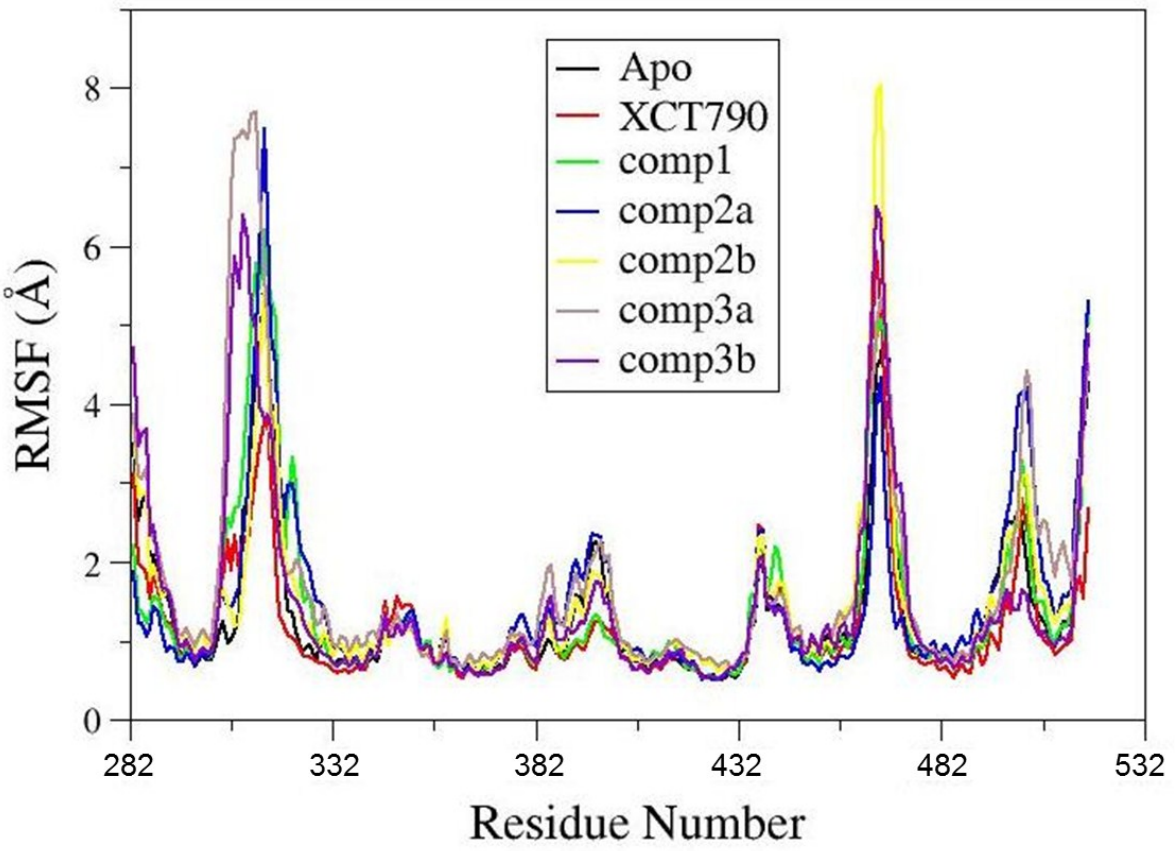

Figure S1. Root-mean-square fluctuation (RMSF) *vs* residue index for the ERRα apo structure and inhibitor bound complexes.

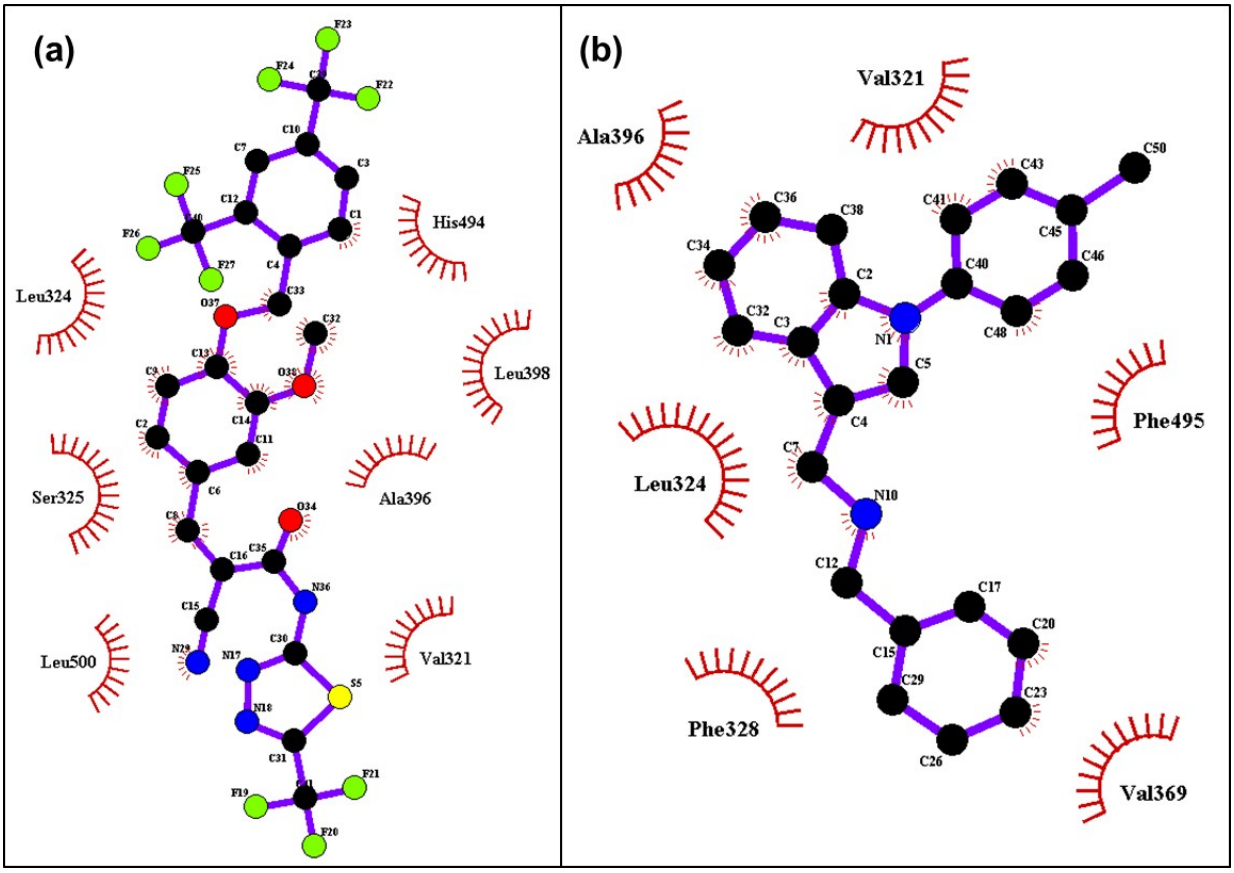

Figure S2. The interaction of XCT790 (a) and compound 1 (b) in the ligand binding domain of ERRα from the top cluster extracted from the MD trajectory.

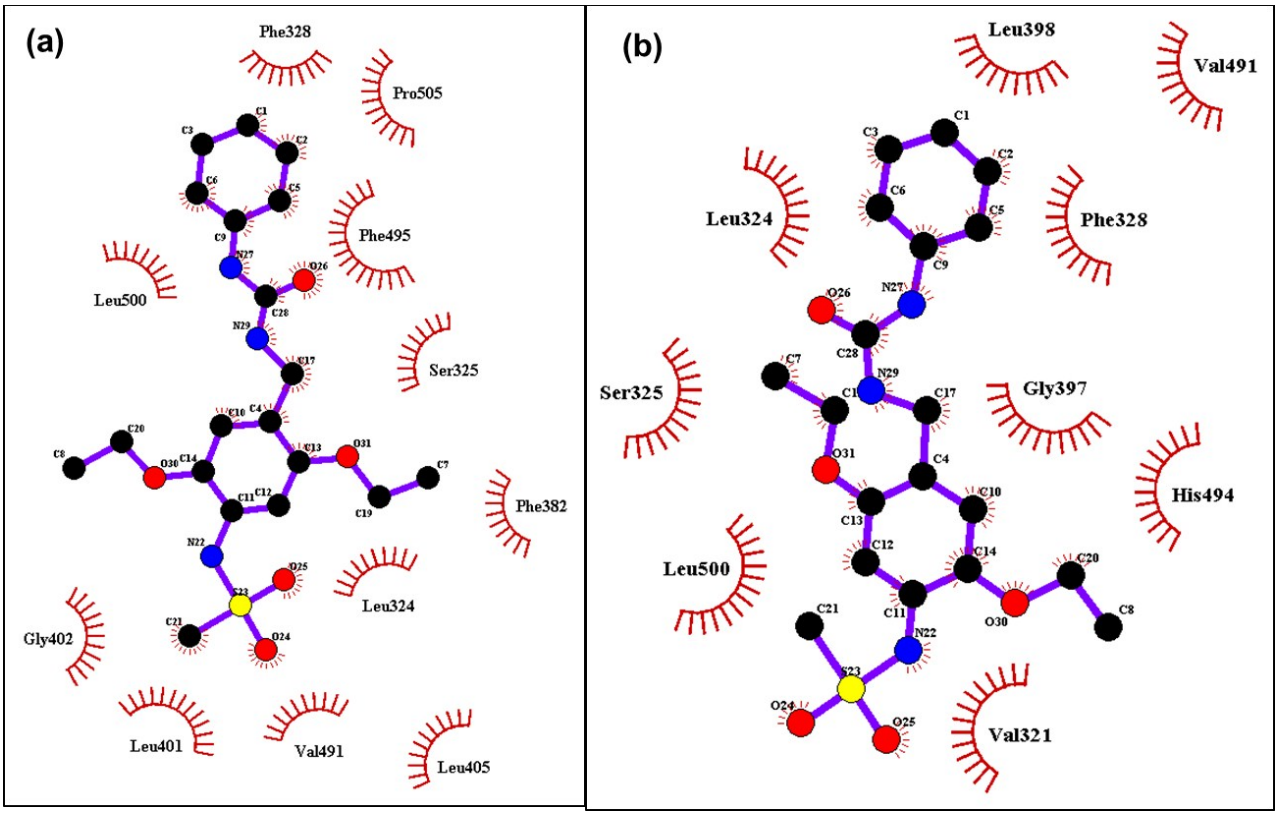

Figure S3. The interaction of compound 2a (a) and compound 2b (b) in the ligand binding domain of ERRα from the top cluster extracted from the MD trajectory.

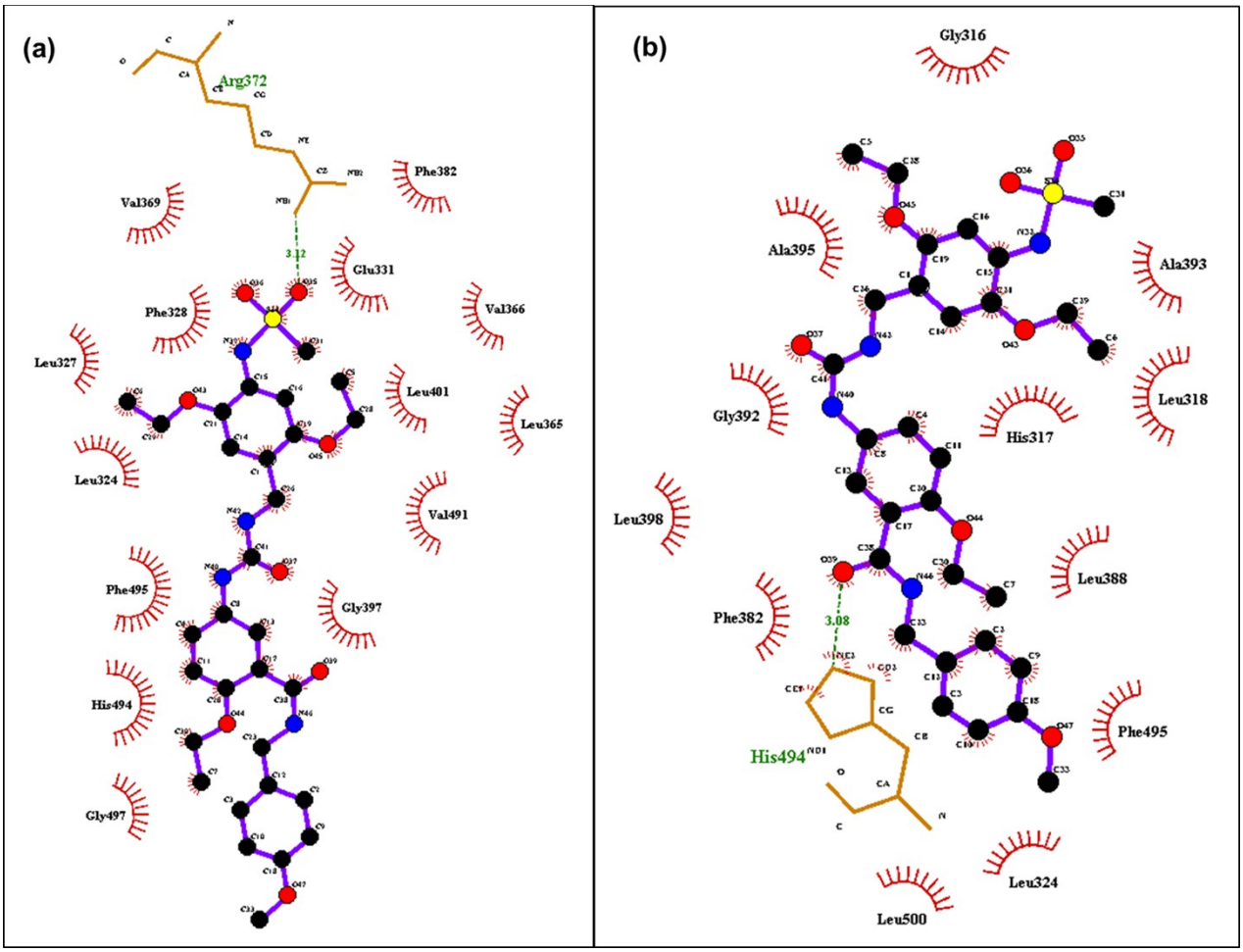

Figure S4. The interaction of compound 3a (a) and compound 3b (b) in the ligand binding domain of ERRα from the top cluster extracted from the MD trajectory.

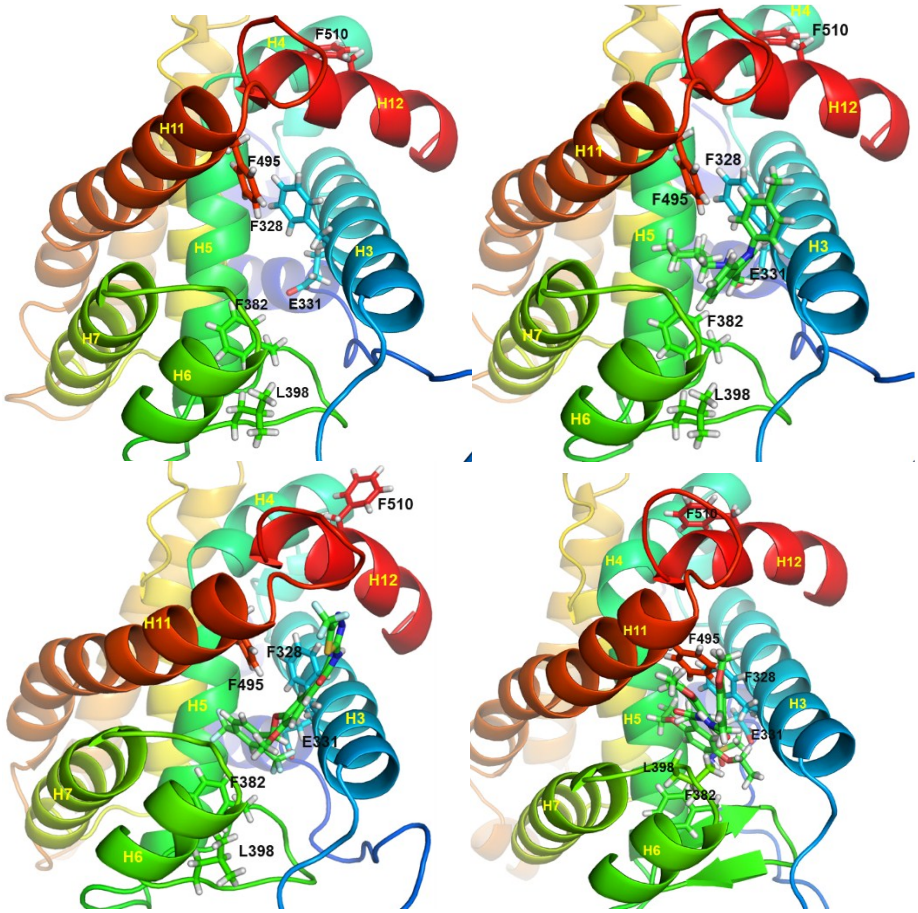

Figure S5. Depiction of aromatic side chains of Phe328(H3), Phe382(H5/H6 loop), Phe495(H11), Phe510(H12) cluster and side chains of Glu331(H3) and Leu398(H6/H7 loop) in the LBP of ERRα. (a)Apo-ERRα; (b) compound 1/ ERRα; (c) XCT790/ ERRα; (d) Compound 3/ERRα