Electronic Supplementary Information (ESI)

Insight into the structural stability of Coumestrol with Human Estrogen Receptor α and β subtypes: A combined approach involving docking and molecular dynamics simulation studies

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Table S1 AutoDock analysis of docked coumestrol with ERβ protein without removing active site water molecule

AutoDock Parameter	Coumestrol-ERβ
Binding energy (kcal/mol)	-9.0
Inhibition constant (nM)	253.57
Intermolecular energy	-9.57
Van der Waals H-bond desolvation energy	-8.97
AutoDock refRMS	35.21
No. of Hydrogen bonds	5
Residues involved in hydrogen bonding	Glu305, Leu339, Arg346, Gly472, His475

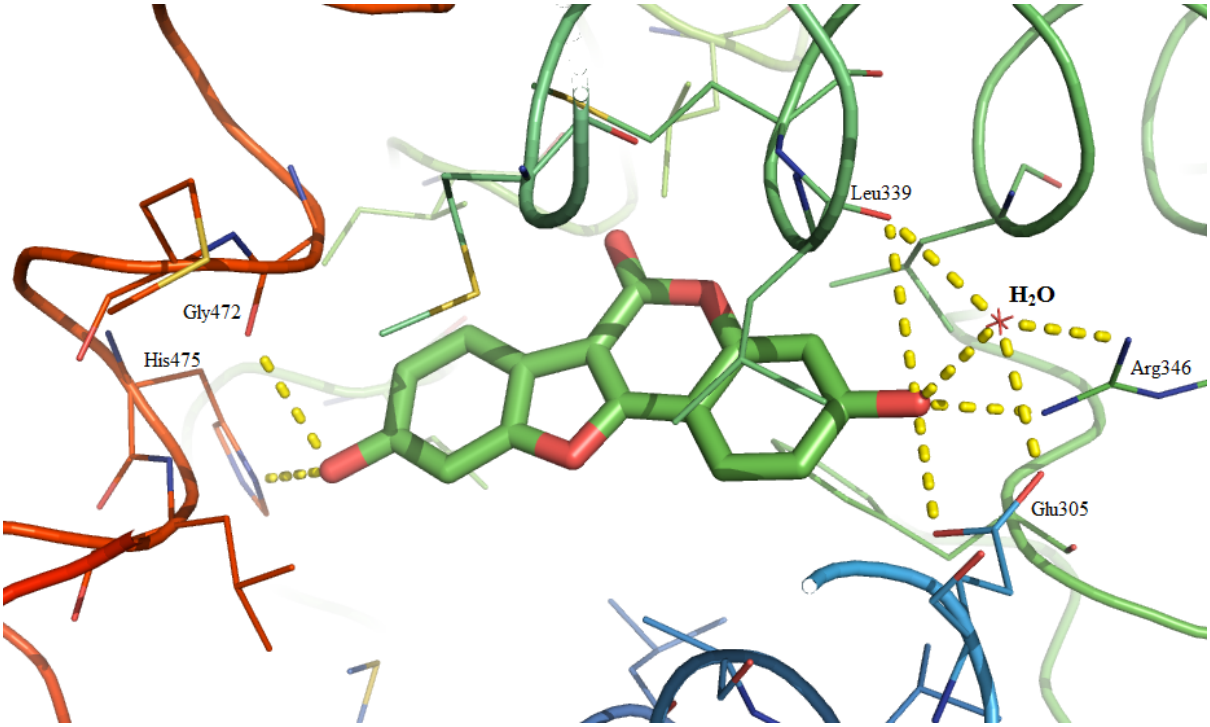

Fig. S1 Binding modes of coumestrol docked into human ERβ binding site without removing active site water molecule. Coumestrol forms 5 hydrogen bonds with ERβ residues. Water molecule in ERβ system is represented by red '*'.

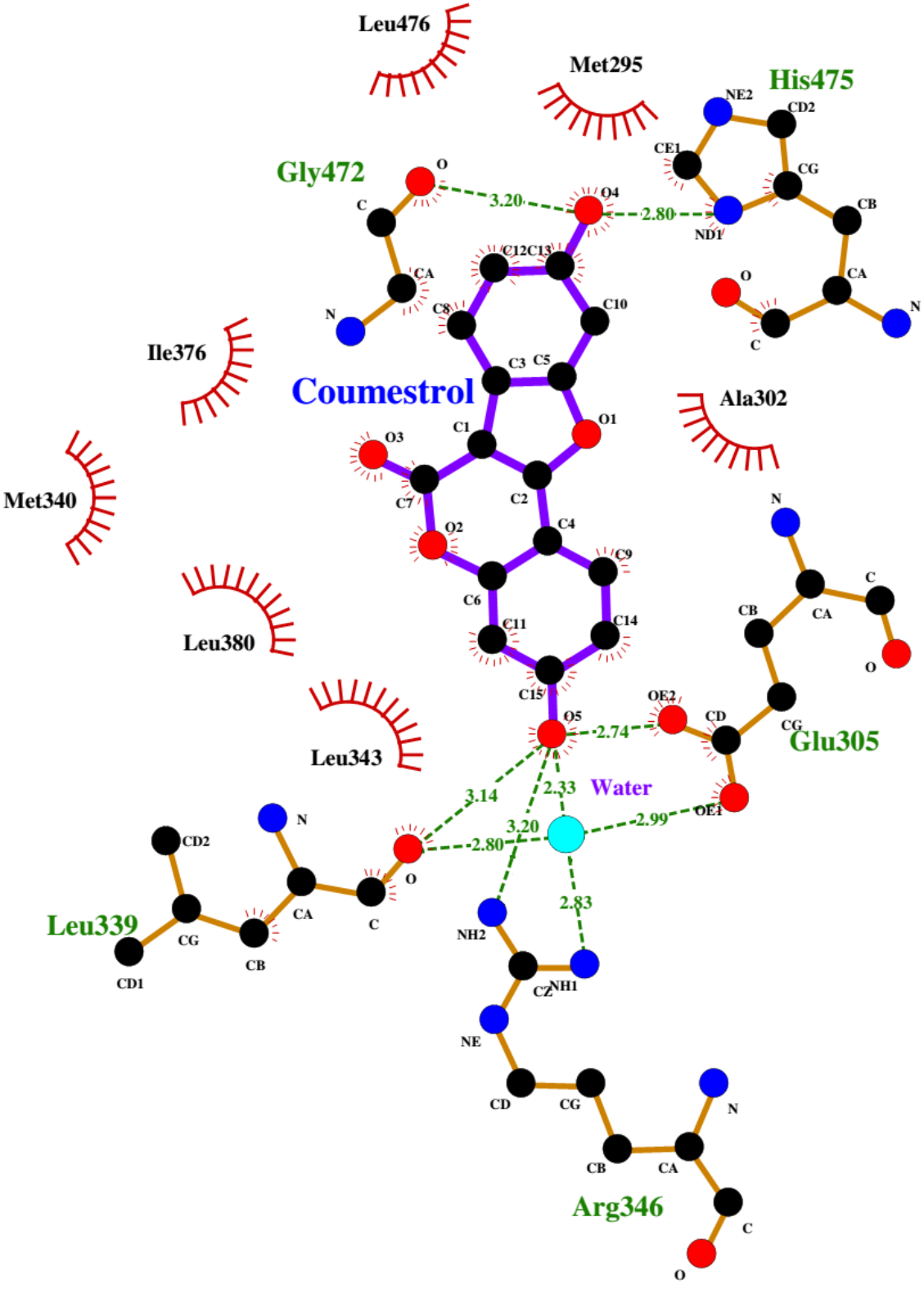

Fig. S2 Detailed interaction view of coumestrol with human ERβ (with active site water molecule) by Ligplot.

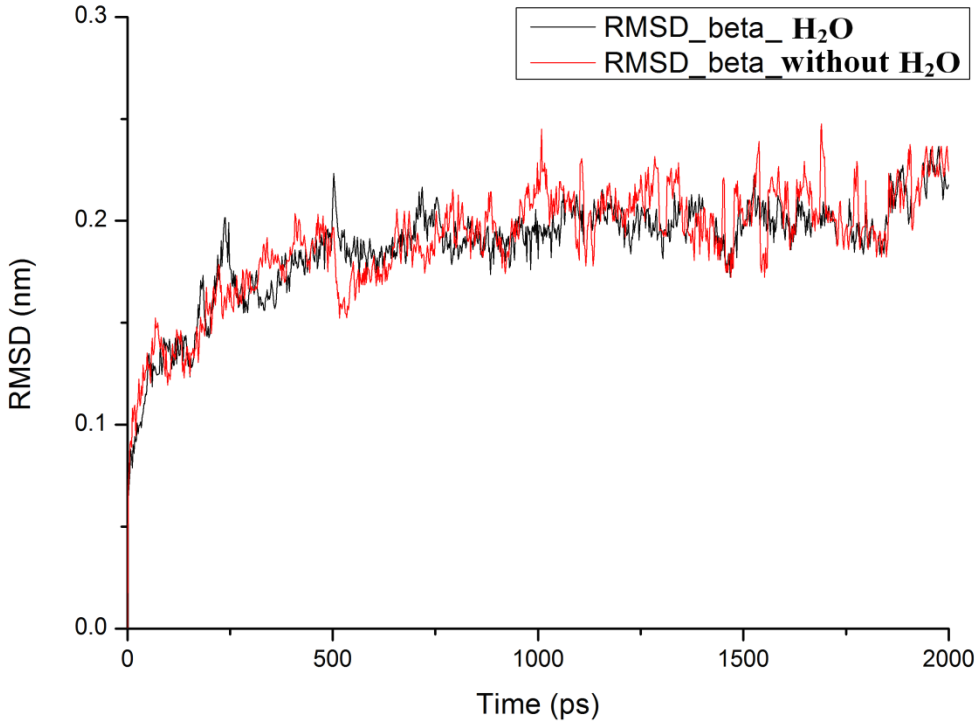

Fig. S3 Backbone RMSD plots of coumestrol-ERβ complex during MD simulation at 300 K. Black colour RMSD plot indicates coumestrol-ERβ complex (with active site water molecule) and red colour RMSD plot indicates coumestrol-ERβ complex (without active site water molecule).

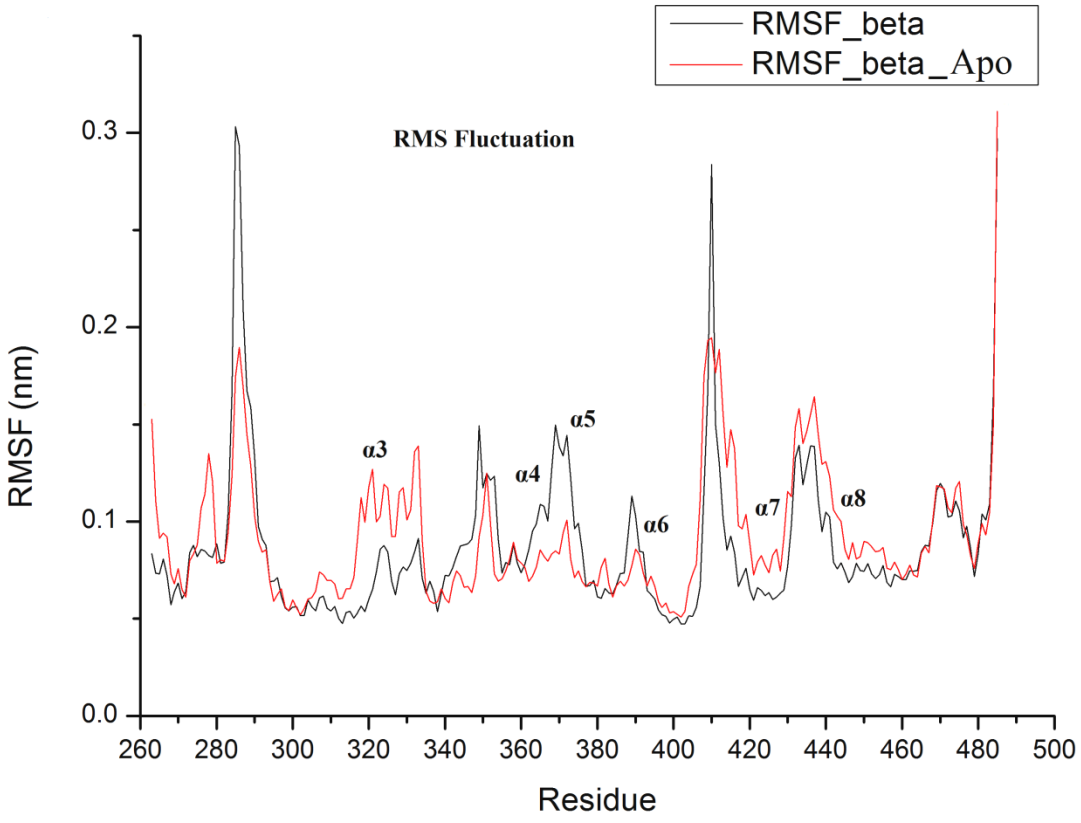

Fig. S4 RMSF of backbone atoms of Apo-ERβ and coumestrol-ERβ complex with active site water molecule at 300 K.

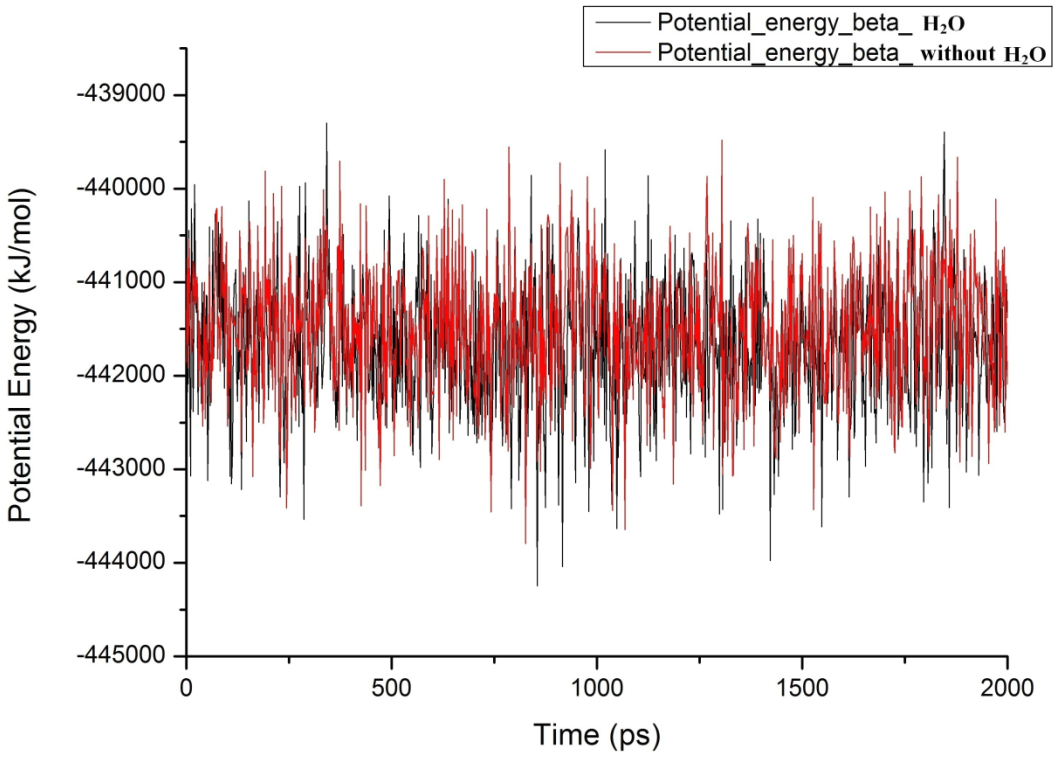

Fig. S5 Potential energy plots of coumestrol-ERβ complex with (shown in black) and without (shown in red) the active site water molecule during MD simulations.

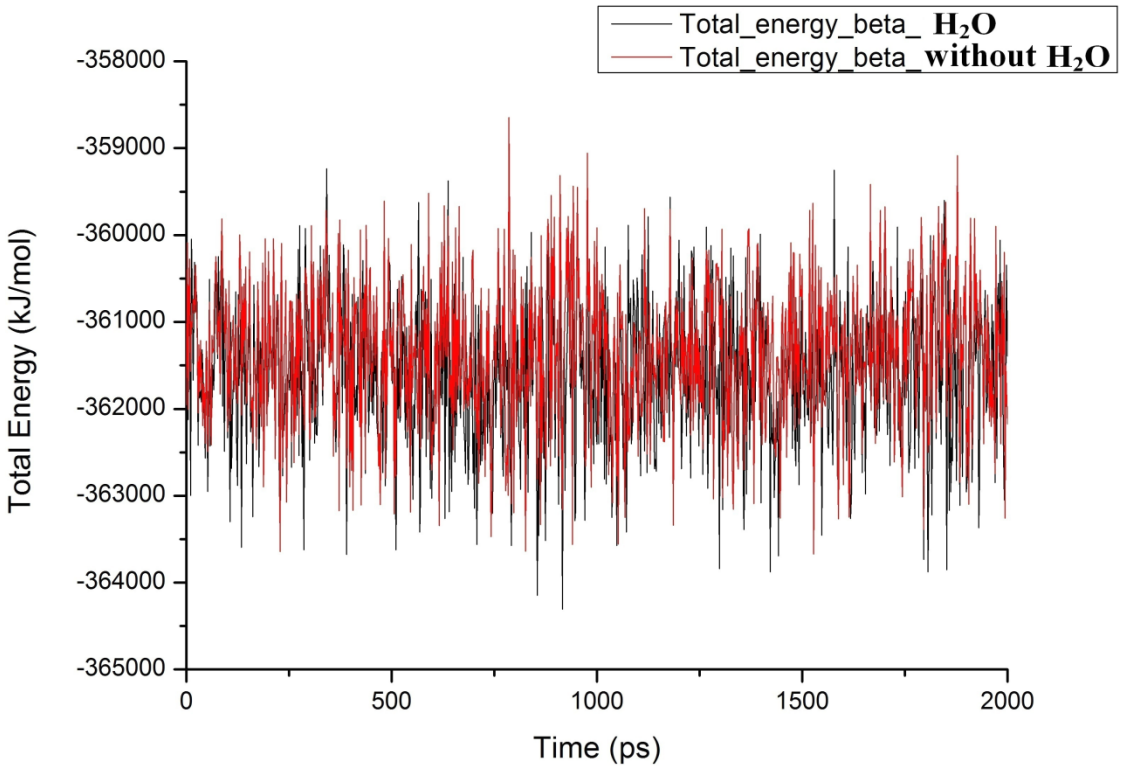

Fig. S6 Total energy plots of coumestrol-ERβ complex with (shown in black) and without (shown in red) the active site water molecule during MD simulations.

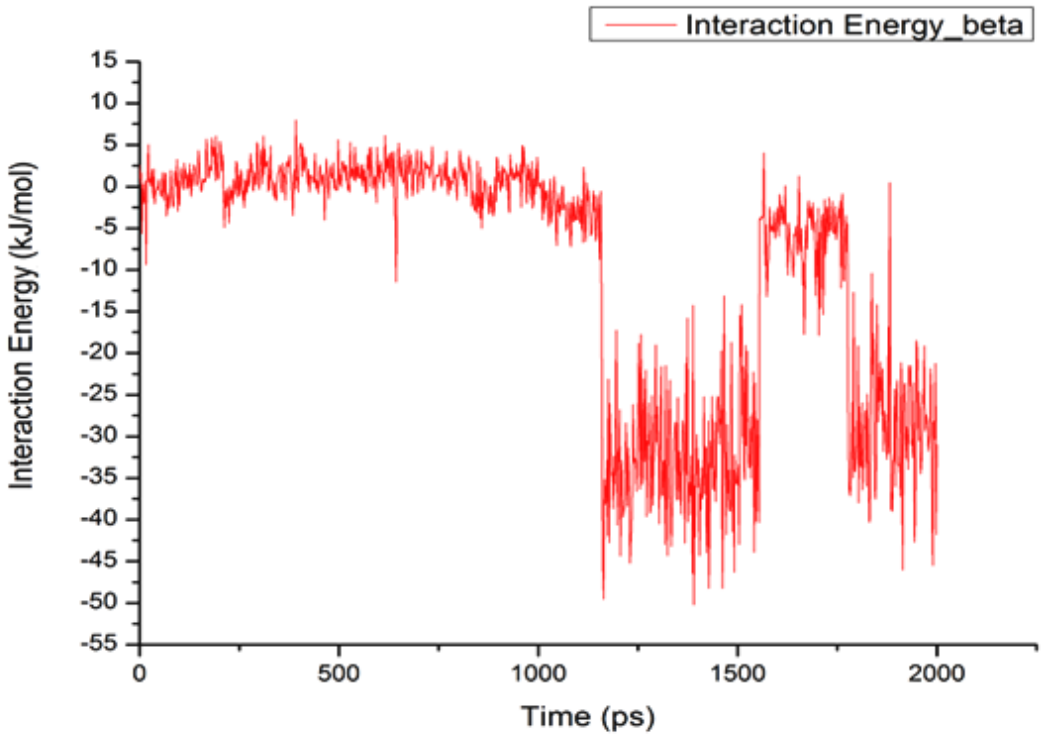

Fig. S7 Interaction energy plot for 2 ns MD simulation of coumestrol-ERβ complex with active site water molecule.

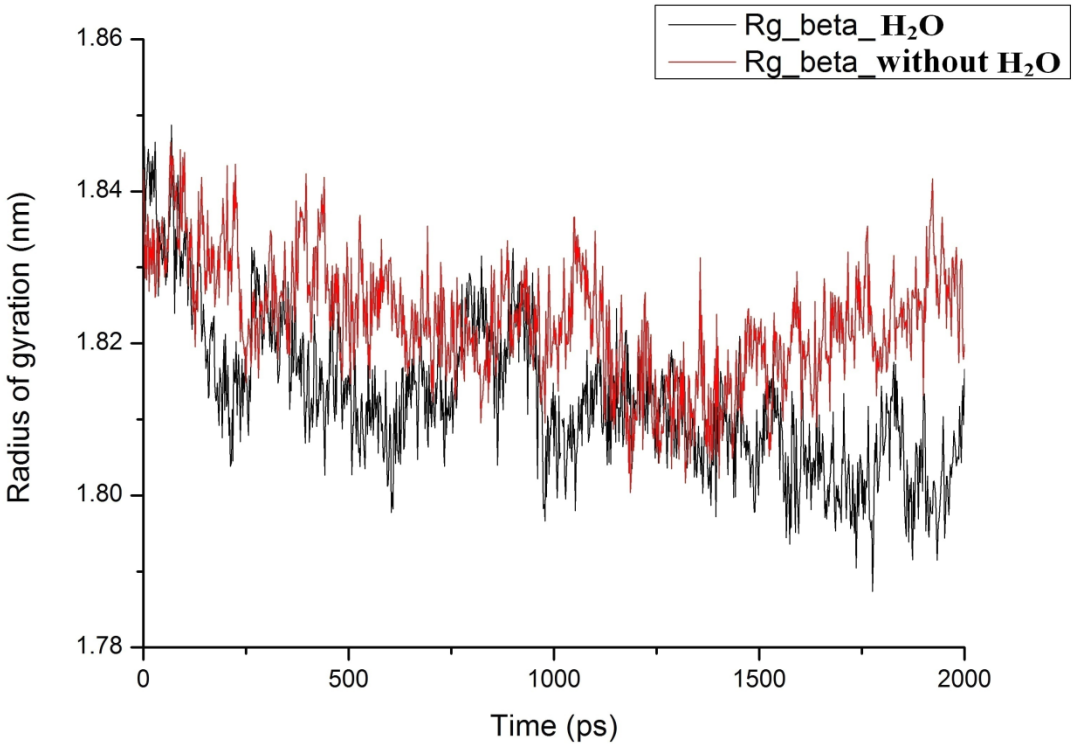

Fig. S8 Variation of gyration radius (R_g) of ERβ backbone atoms calculated as a function of time for coumestrol-ERβ complex with (shown in black) and without (shown in red) the active site water molecule.

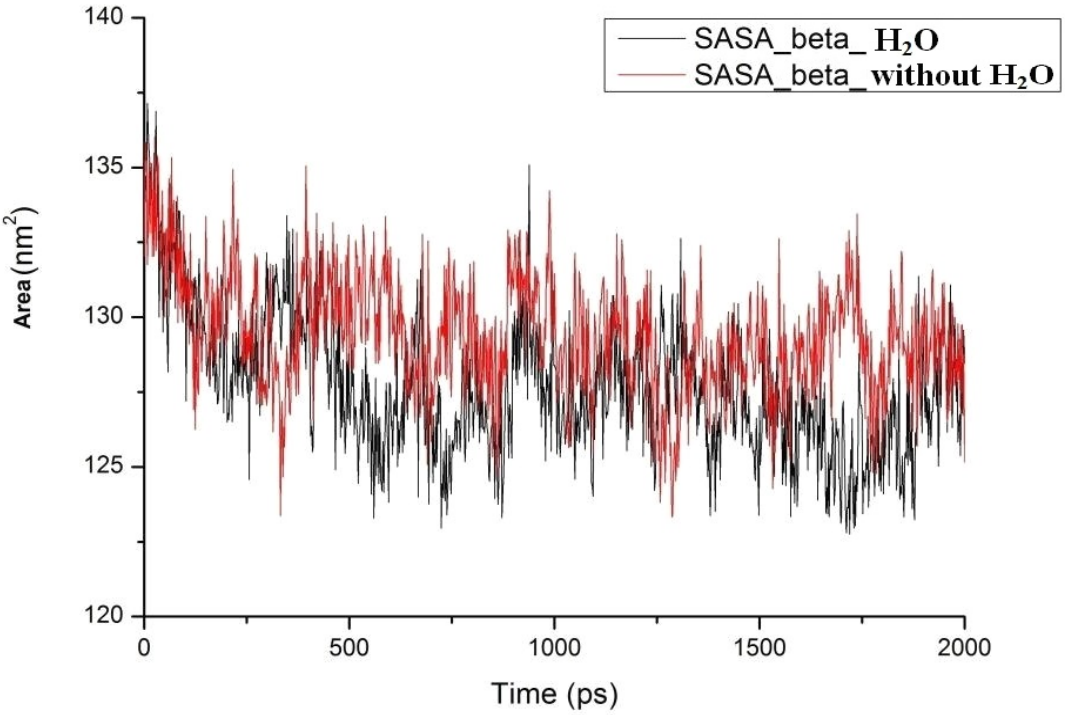

Fig. S9 Solvent accessible surface area (SASA) during 2 ns simulations calculated from trajectory files for coumestrol-ERβ complex with (shown in black) and without (shown in red) the active site water molecule.

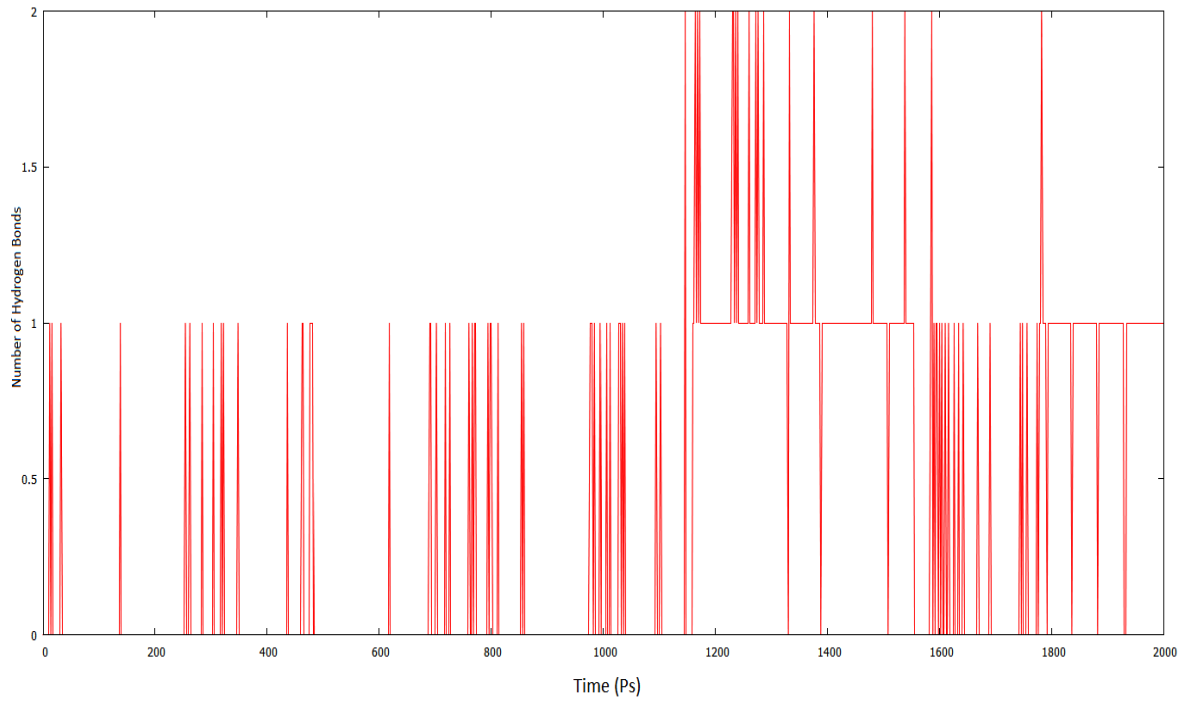

Fig. S10 Stability evaluation of coumestrol-ERβ complex (with active site water molecule) using intermolecular hydrogen bonding pattern as a function of time.

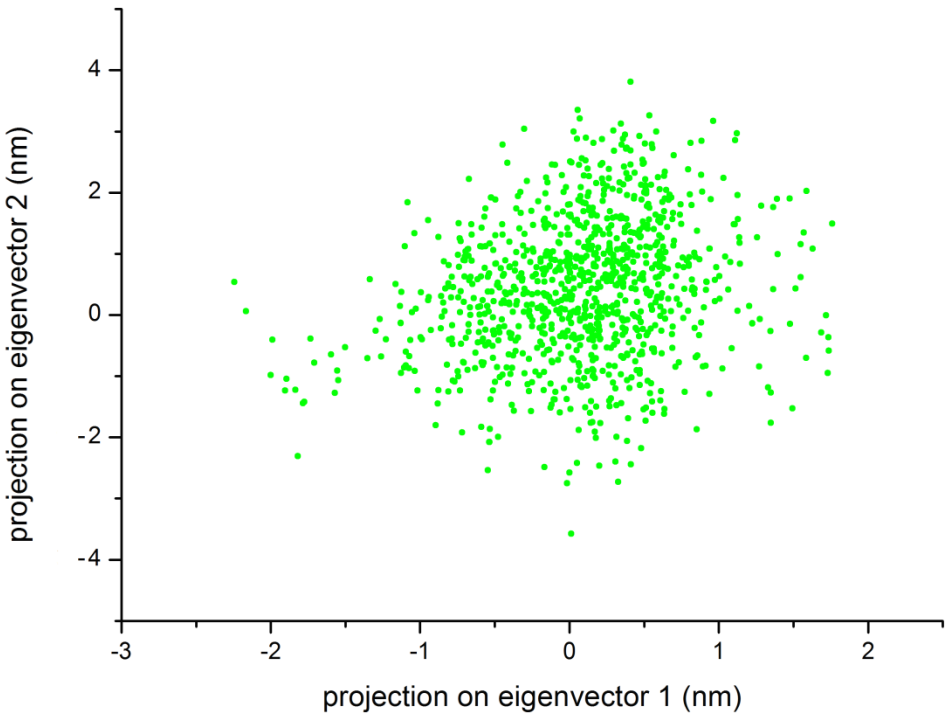

Fig. S11 2D projection of the backbone atoms of coumestrol-ERβ system with active site water molecule over the first two principal components.

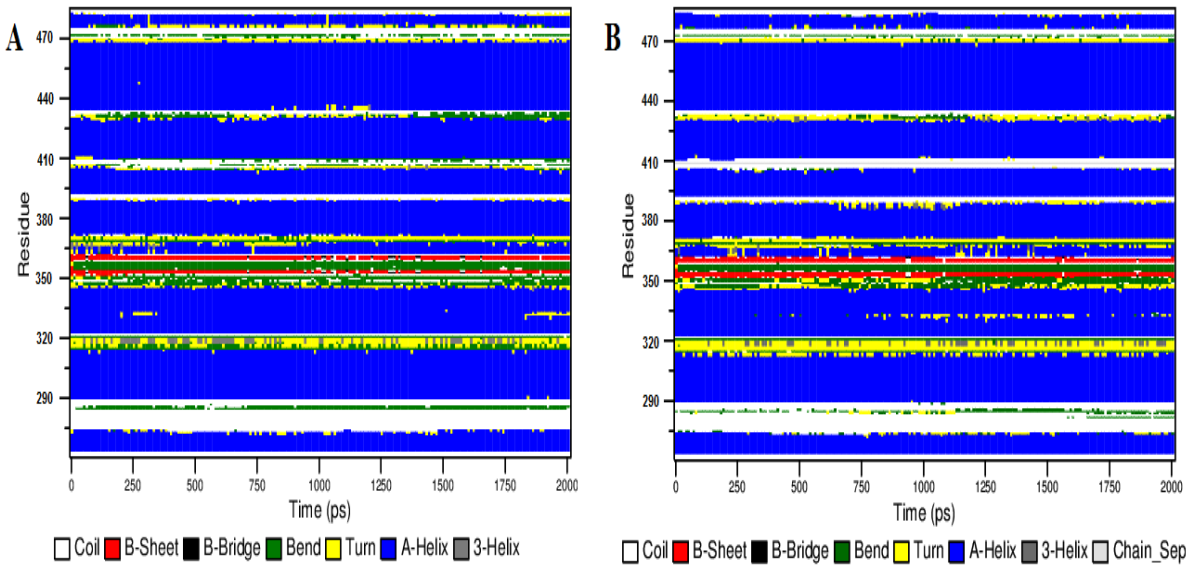

Fig. S12 Secondary structure elements changes during the 2 ns MD simulation at 300 K. (A) Apo-ERβ with active site water molecule and (B) coumestrol-ERβ complex with active site water molecule. The colour scale at the bottom represents the DSSP classification of each secondary structure element.