Electronic Supplementary Material (ESI) for RSC Advances.

Supplementary materials

β-sitosterol and oleanolic acid as anticancer potential through inhibition of human estrogenic *17beta-hydroxysteroid dehydrogenase type-1* based on *in silico* approach

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Tables:

Table S1 Drug-likeness: Physicochemical properties, Lipinski's rule of five, and Veber's rule.

Parameters	**TES**	**C1**	**C2**
Physicochemical			
Log $P_{o/w}$ (X LogP3)	3.32	9.34	7.49
Log S (ESOL)	-3.72	-7.90	-7.32
Fraction Csp3	0.84	0.93	0.90
Lipinski's rule (RO5)			
M LogP	3.59	6.73	5.82
MW (g/mol)	288.42	414.71	456.70
∑ HBD	1	1	2
∑ HBA	2	1	3
Veber's rule			
Rot. Bonds	0	6	1
TPSA ($Å^2$)	37.30	20.23	57.53
Lipinski and Veber valiations/n	0	1	1

Table S2 ADMET prediction of candidates used pkCSM server.

Parameters	TES	C1	C2
Absorption			
Water solubility (log mol/L)	-4.73	-6.88	-4.07
Caco-2 Permeability (log Papp in 10^{-6} cm/s)	1.54	1.21	1.36
Intestinal Absorption-Human (% Absorbed)	96.53	94.07	98.08
Distribution			
CNS permeability (log PS)	-2.07	-1.33	-1.01
BBB Permeability (log BB)	0.16	0.79	-0.63
Metabolism			
CYP1A2 Inhibitor	No	No	No
CYP2C19 Inhibitor	No	No	No
CYP2C9 Inhibitor	No	No	No
CYP2D6 Inhibitor	No	No	No
CYP3A4 Inhibitor	No	No	No
Excretion			
Total Clearance (log mL/min/Kg)	0.92	0.62	-0.08
Renal OCT2 Substrate	Yes	No	No
Toxicity			
AMES Toxicity	No	No	No
Hepatotoxicity	No	No	Yes
Skin Sensitisation	No	No	No

Table S3 Molecular docking results to identify the ligand- HSD17B1 Interaction.

Complex	Interactions		Distance (Å)	Types
	From	To		
TES- HSD17B1	His221(HE2)	O17	1.76	Conventional hydrogen bond
	H-O17	Glu282:OE2	2.10	Conventional hydrogen bond
	Pro187(Alkyl)	Ring B	4.64	Alkyl
	Val225(Alkyl)	Ring C	4.27	Alkyl
	C15	Leu149(Alkyl)	4.44	Alkyl
	C18	Leu149(Alkyl)	4.33	Alkyl
	Tyr218(Pi-Orbitals)	C18	5.28	Pi-Alkyl
	His221(Pi-Orbitals)	C18	5.27	Pi-Alkyl
	Phe259(Pi-Orbitals)	C15	4.58	Pi-Alkyl
C1-HSD17B1	C18	Leu149(Alkyl)	5.07	Alkyl
	C19	Val188(Alkyl)	4.80	Alkyl
	C1	Cys185(Alkyl)	4.46	Alkyl
	C21	Pro187(Alkyl)	4.35	Alkyl
	$C24^2$	Val143(Alkyl)	4.28	Alkyl
	$C24^2$	Met147(Alkyl)	4.84	Alkyl
	$C24^2$	Leu149(Alkyl)	4.70	Alkyl
	C27	Leu149(Alkyl)	4.57	Alkyl
	C27	Val283(Alkyl)	4.78	Alkyl
	Tyr155(Pi-Orbitals)	C18	4.75	Pi-Alkyl
	Tyr155(Pi-Orbitals)	C5=C6 (Ring B)	5.46	Pi-Alkyl
	Tyr218(Pi-Orbitals)	C27	4.99	Pi-Alkyl
	His221(Pi-Orbitals)	C26	4.36	Pi-Alkyl
	His221(Pi-Orbitals)	C27	4.89	Pi-Alkyl
	Phe259(Pi-Orbitals)	$C24^2$	4.17	Pi-Alkyl
C2-HSD17B1	Ser142(HG)	O28a	1.82	Conventional hydrogen bond
	Tyr155(HH)	O28a	2.00	Conventional hydrogen bond
	H-O28a	Gly186(O)	1.75	Conventional hydrogen bond
	Ser142(HB3)	O28a	2.66	Carbon hydrogen bond
	C30	Leu149(Alkyl)	5.27	Alkyl
	Tyr155(Pi-Orbitals)	C12=C13 (Ring C)	5.48	Pi-Alkyl
	Tyr155(Pi-Orbitals)	C30	4.64	Pi-Alkyl

Table S4 Post-MD of each system: The average value of trajectories analysis using 100 ns simulation time.

Parameters	**TES-HSD17B1**	**C1-HSD17B1**	**C2-HSD17B1**
Total energy (kcal mol^{-1})	-112530 ± 894.54	-112389 ± 900.94	-112358 ± 900.91
Potential energy (kcal mol^{-1})	-142297 ± 771.59	-142174 ± 777.02	-142134 ± 778.60
Kinetic energy (kcal mol^{-1})	29766 ± 195.71	29784 ± 198.71	29776 ± 196.95
RMSD of complex (nm)	0.26 ± 0.03	0.26 ± 0.03	0.27 ± 0.04
RoG (nm)	19.73 ± 0.14	19.79 ± 0.09	19.89 ± 0.11
RMSF (nm)	1.29 ± 0.41	0.93 ± 0.32	1.24 ± 0.45
SASA (nm)	10.05 ± 1.17	9.46 ± 1.00	12.89 ± 1.02

Figures:

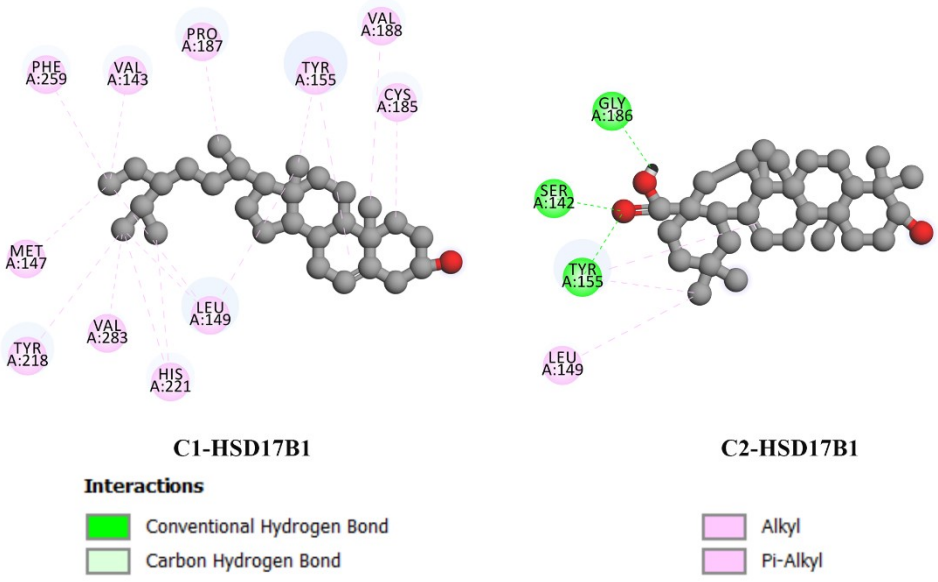

Fig. S1 Molecular docking analysis: The candidate-HSD17B1 Interaction

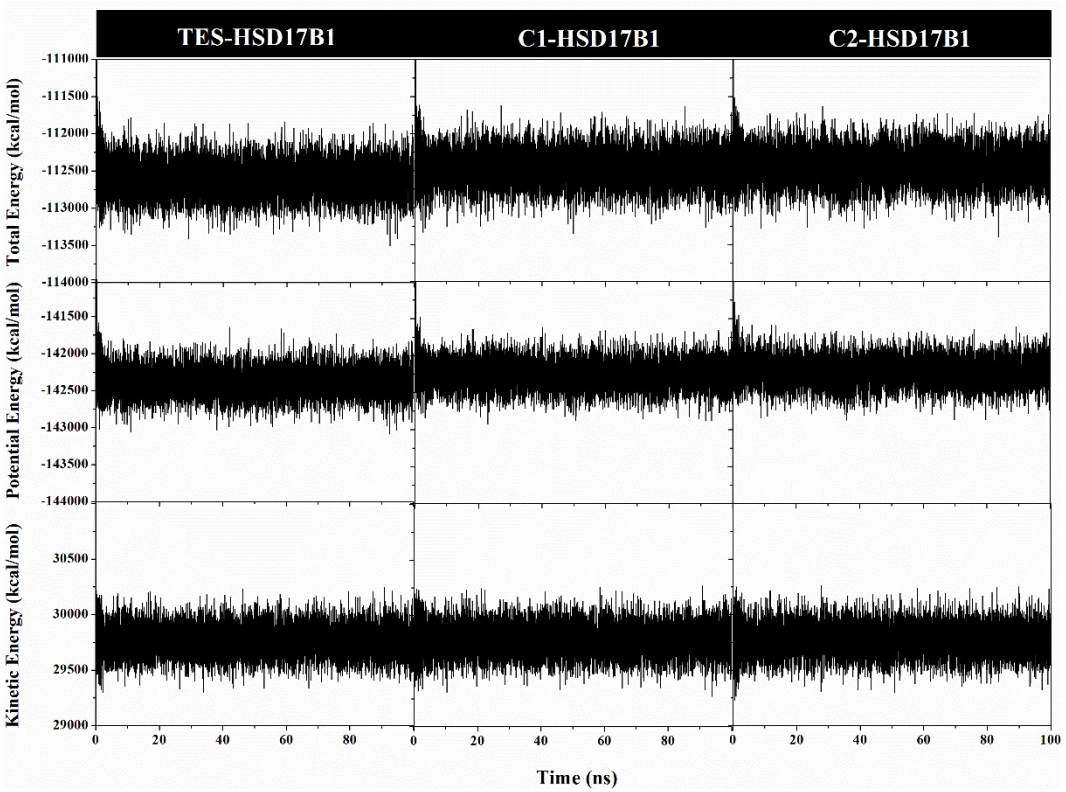

Fig. S2 The *mdout* analysis plotted along 100 ns of MD simulation of each system.

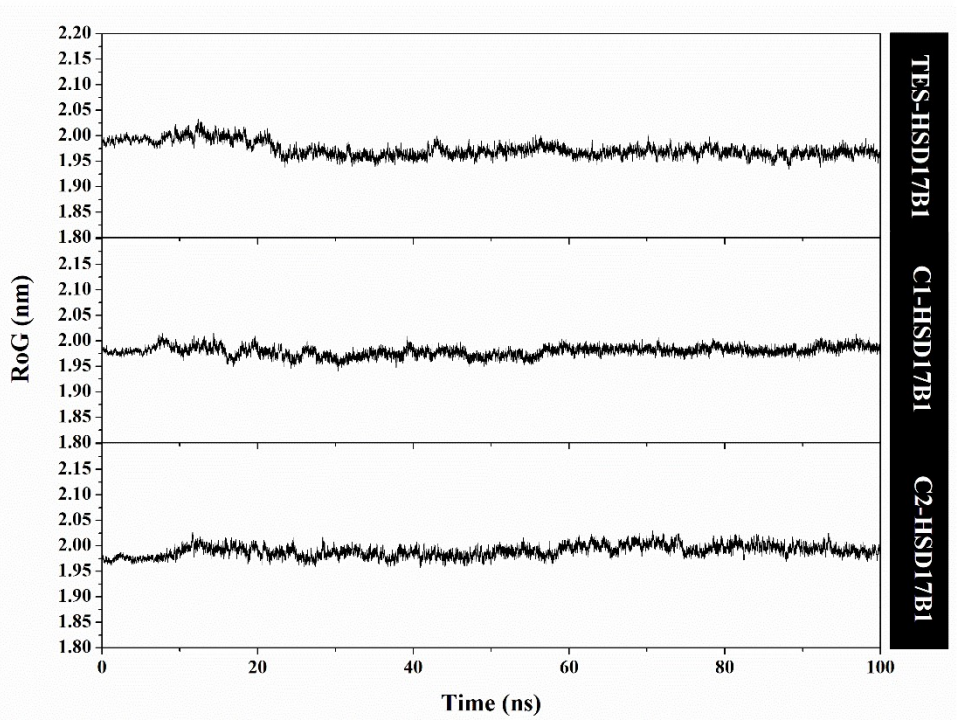

Fig. S3 Trajectories analysis: Radius of gyration of each system plotted along the 100 ns of MD simulation.

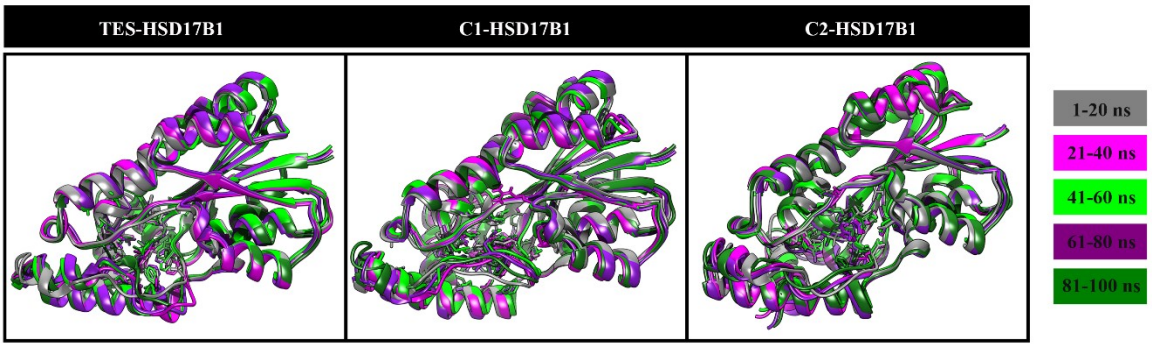

Fig. S4 The average conformational of each complex was plotted along 100 ns for each period.

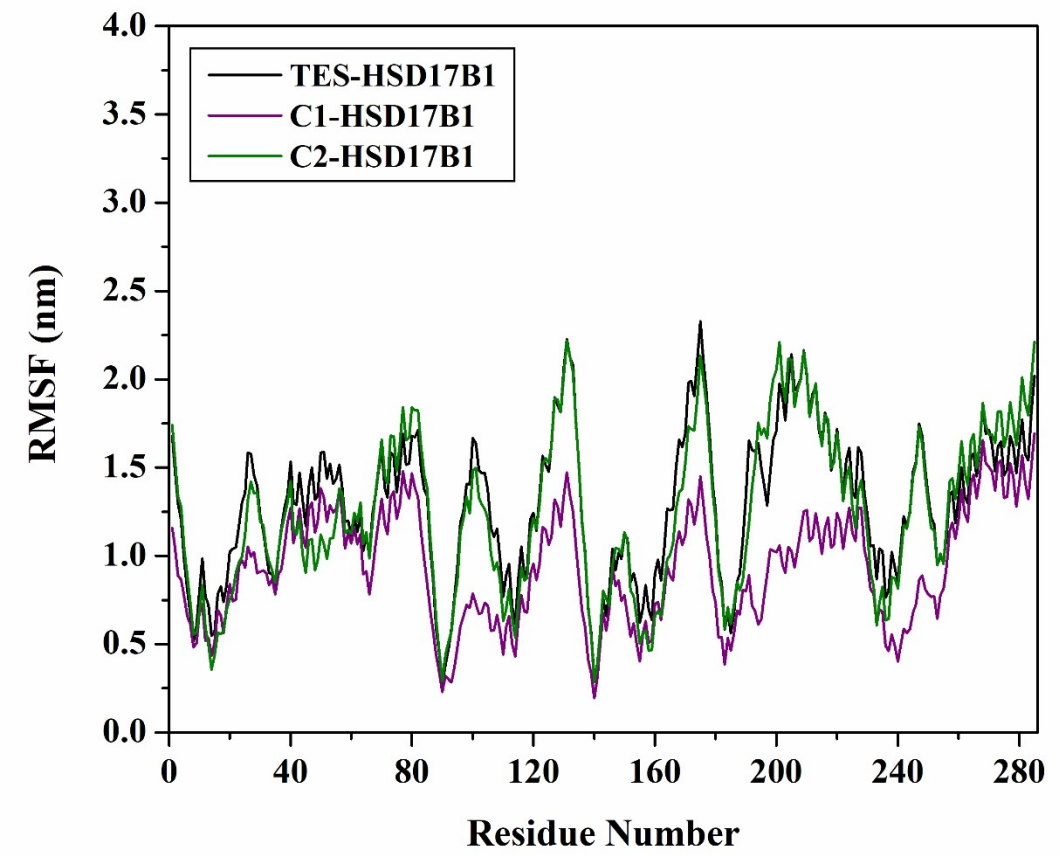

Fig. S5 Trajectories analysis: The root-mean-square fluctuation of each complex was plotted along 100 ns for each period.

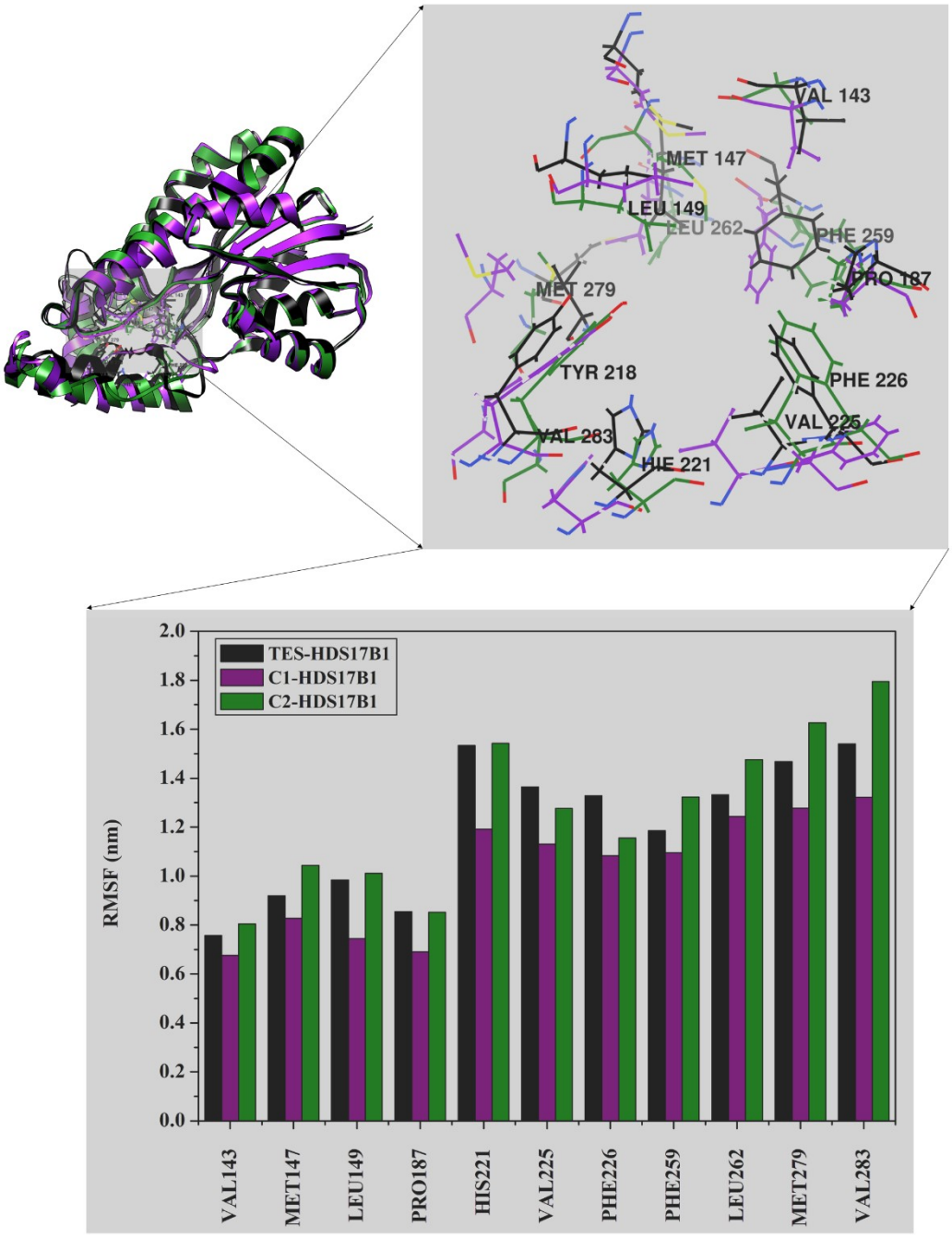

Fig. S6 The key residues conformational on the HSD17B1 active site shows by the RMSF value during the simulation time.

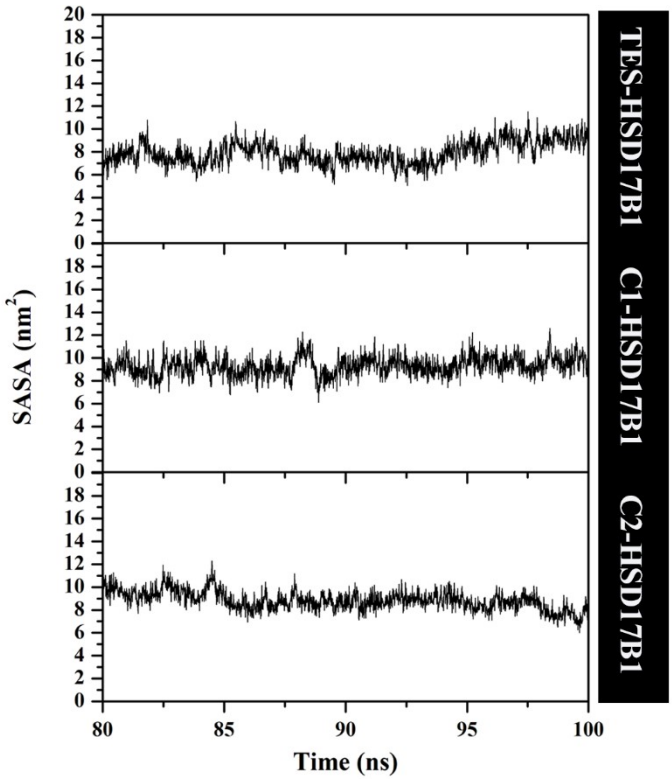

Fig. S7 Trajectories analysis during the simulation over the last 20 ns: The solvent-accessible surface area in the active site (radius 5 Å).