

Supplementary Materials

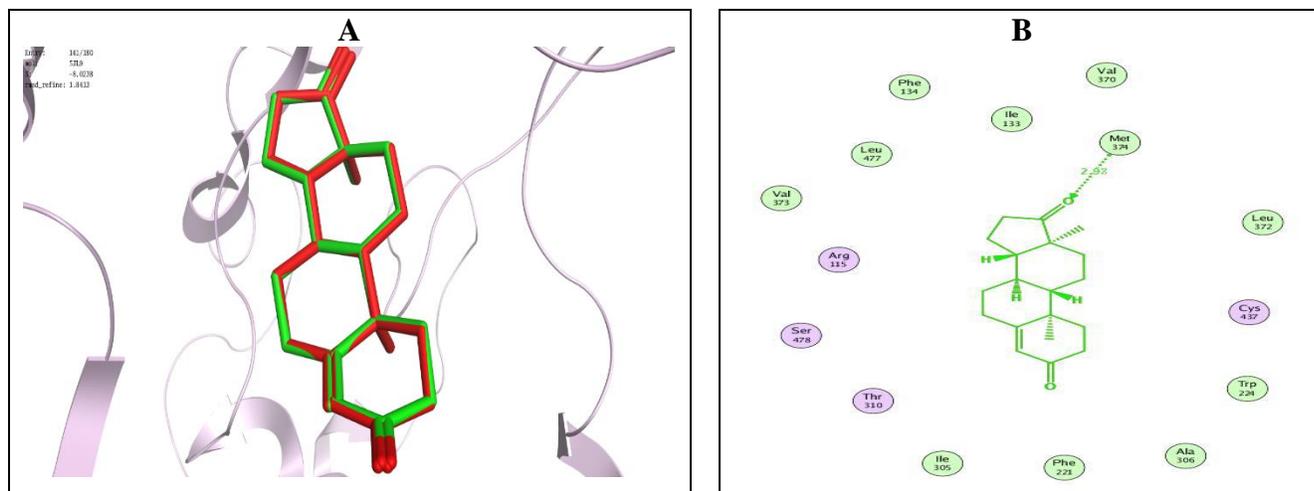


Figure S1: (A) 3D diagram and (B) 2D overlay disclosing the superimposition of the native co-crystallized ligand (green), and the redocked co-crystallized ligand (Red) at aromatase enzyme with RMSD value of 1.84 Å for docking program validation.

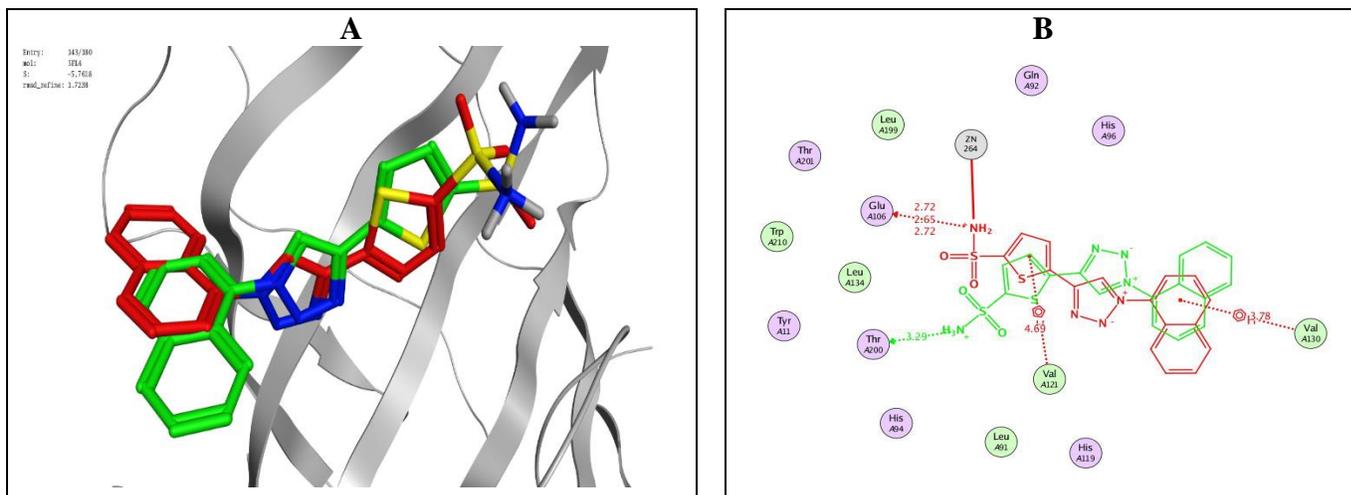


Figure S2: (A) 3D diagram and (B) 2D overlay disclosing the superimposition of the native co-crystallized ligand (green), and the redocked co-crystallized ligand (Red) at CA IV with RMSD value of 1.72 Å for docking program validation.

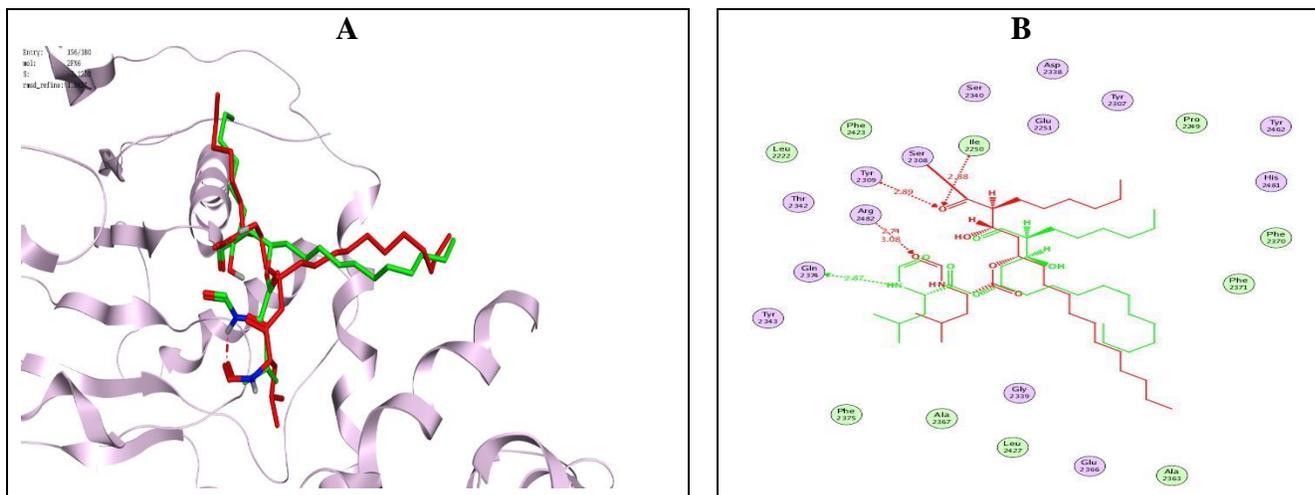


Figure S3: (A) 3D diagram and (B) 2D overlay disclosing the superimposition of the native co-crystallized ligand (green), and the redocked co-crystallized ligand (Red) at **FAS** with RMSD value of 1.88 Å for docking program validation.

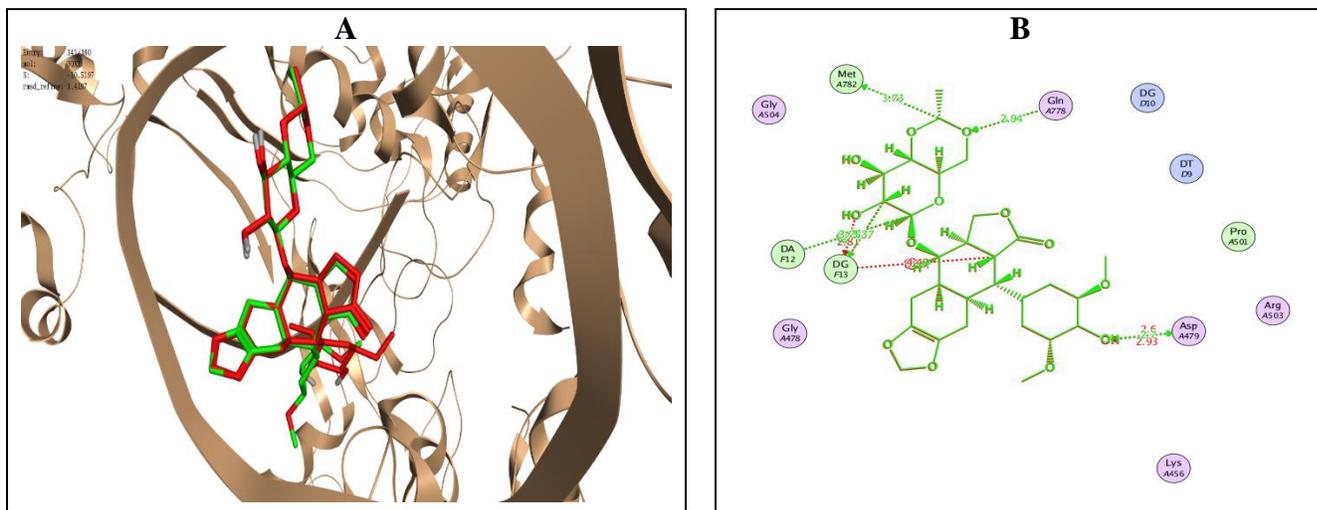


Figure S4: (A) 3D diagram and (B) 2D overlay disclosing the superimposition of the native co-crystallized ligand (green), and the redocked co-crystallized ligand (Red) at **TOP II** with RMSD value of 1.42 Å for docking program validation.

Aromatase			
Comp no.	2D	3D	3D protein
1			
2			
3			
4			

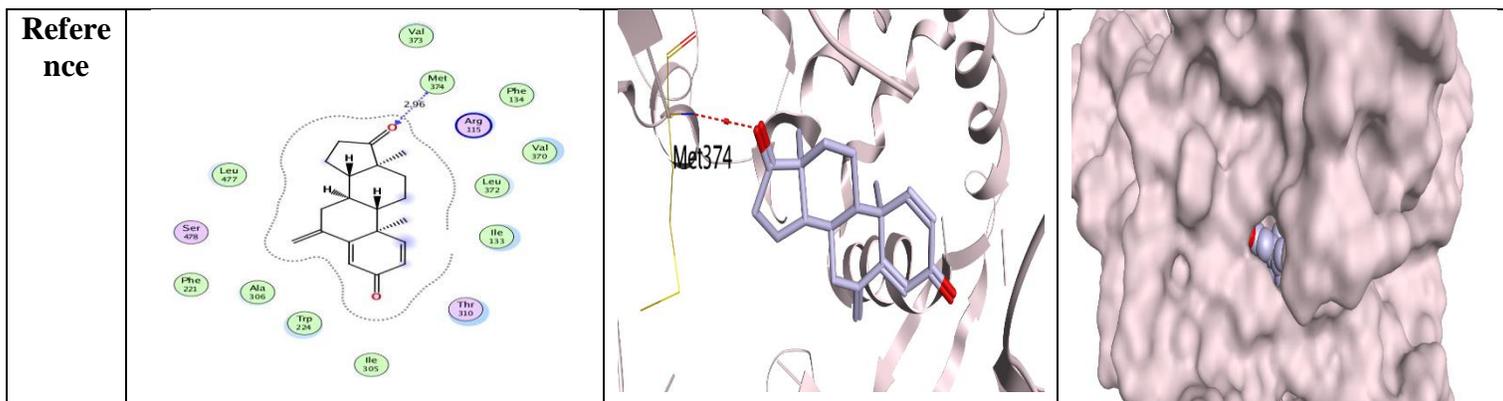


Figure S5: the 2D, 3D, and 3D protein positioning of all investigated compound at the biological target, aromatase.

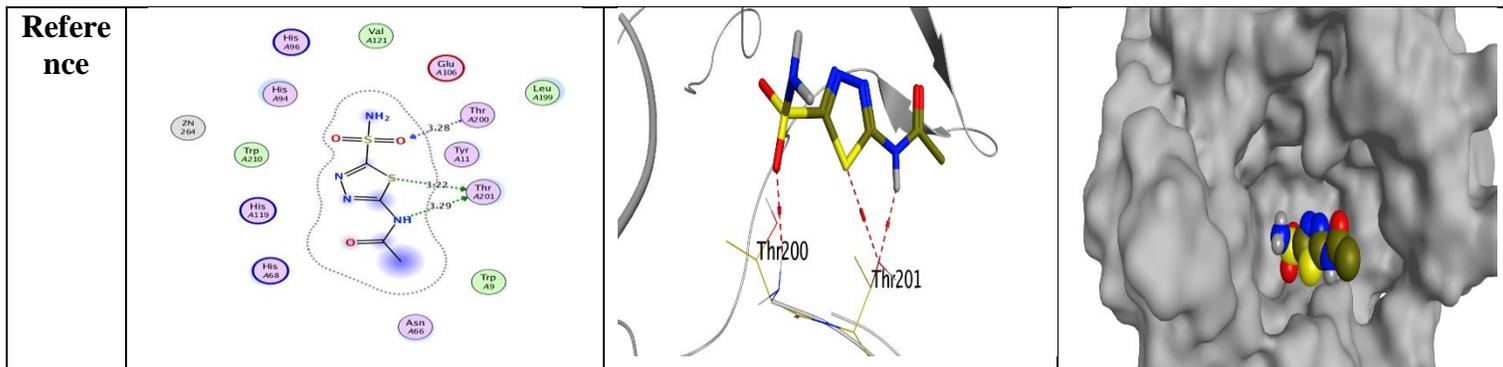
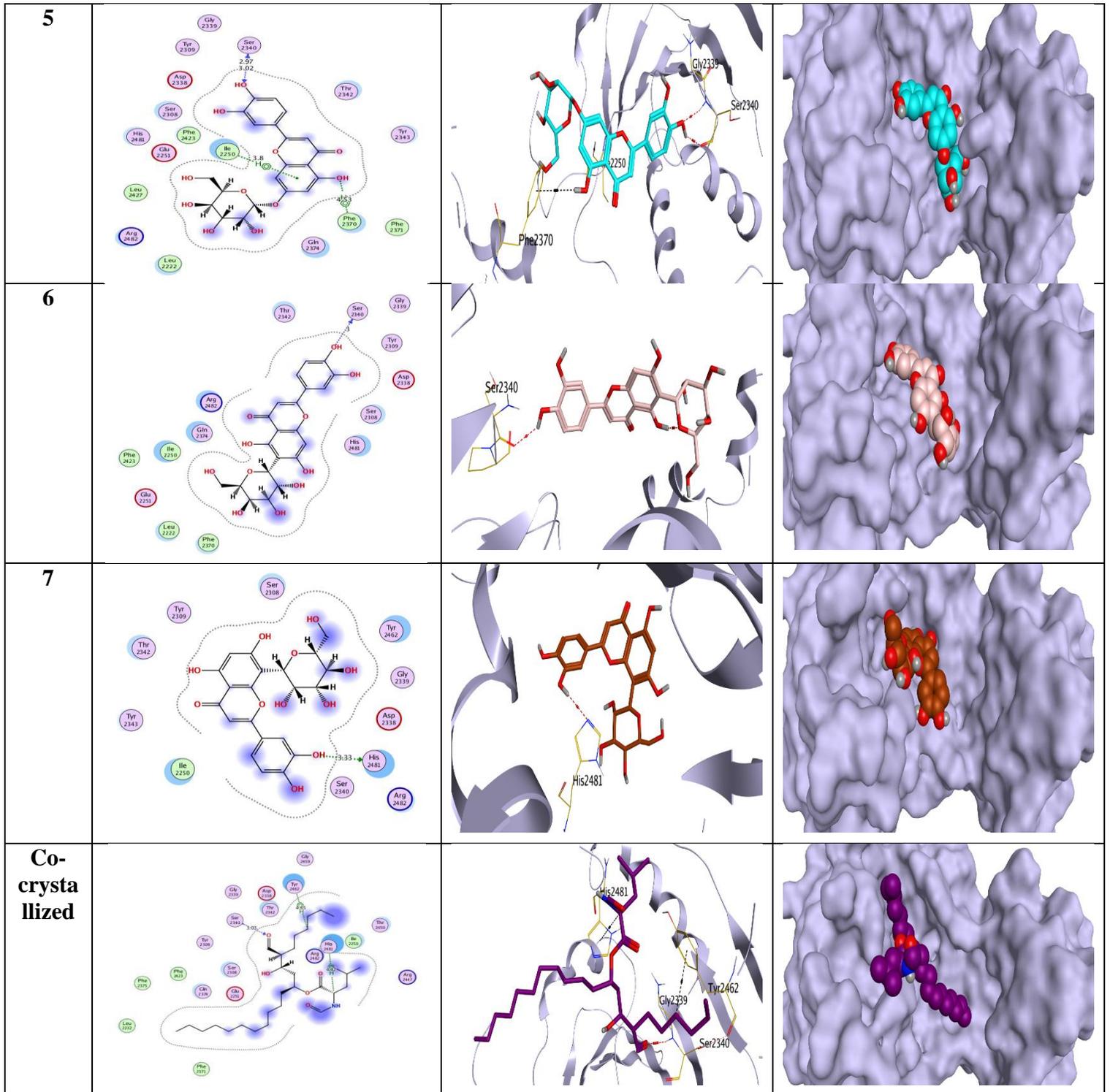


Figure S6: the 2D, 3D, and 3D protein positioning of all investigated compound at the biological target, CA IX.

Comp no.	FAS		
	2D	3D	3D protein
1			
2			
3			
4			



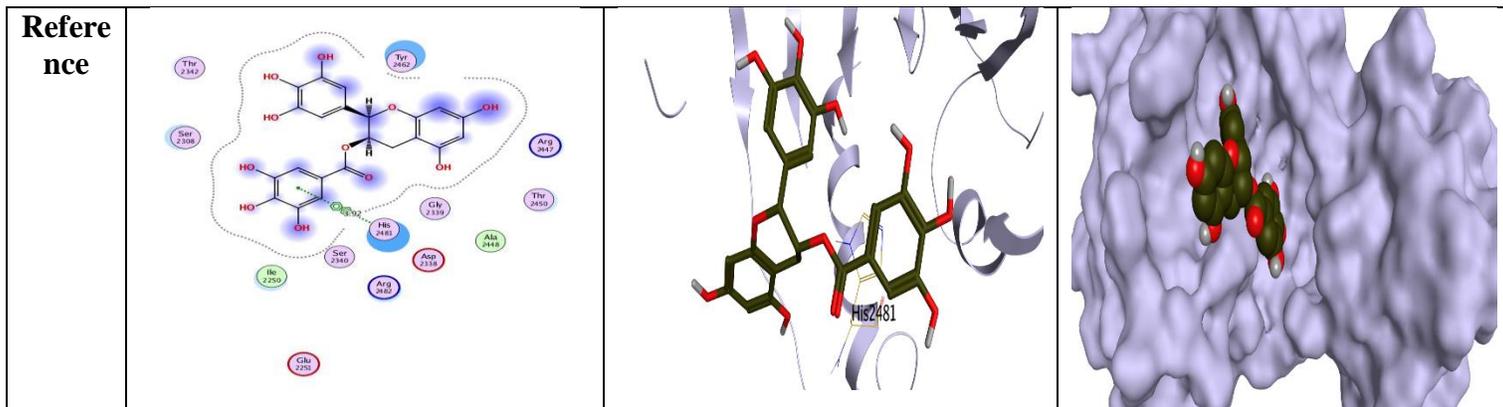


Figure S7: the 2D, 3D, and 3D protein positioning of all investigated compound at the biological target, FAS.

TOP II			
Comp no.	2D	3D	3D protein
1	<p>2D chemical structure of compound 1. Interaction sites are highlighted in blue. Residues shown include DA C12, Gln A479, DT B9, DG C11, Gly A504, Asp A479, Lys A459, Gly A478, Arg A503, Leu A502, and Pro A508. Distances: 3.28, 2.96, 2.86.</p>	<p>3D ribbon diagram of compound 1 (green) in the protein binding pocket. Residues shown include Gly478, Asp479, DT9, and DG10.</p>	<p>3D surface representation of compound 1 (green and red) in the protein binding pocket.</p>
2	<p>2D chemical structure of compound 2. Interaction sites are highlighted in blue. Residues shown include Gln A479, Met A782, DT B9, DA C12, DG C13, Arg A503, and DC C4. Distances: 3.16, 2.99.</p>	<p>3D ribbon diagram of compound 2 (yellow and red) in the protein binding pocket. Residues shown include Arg503 and Met782.</p>	<p>3D surface representation of compound 2 (yellow and red) in the protein binding pocket.</p>
3	<p>2D chemical structure of compound 3. Interaction sites are highlighted in blue. Residues shown include DA C12, DG C13, Gly A504, Arg A503, Leu A502, DT B9, and DA B10. Distances: 3.95, 3.01.</p>	<p>3D ribbon diagram of compound 3 (purple and red) in the protein binding pocket. Residues shown include Arg503, Gly478, Gly478, and Asp.</p>	<p>3D surface representation of compound 3 (purple and red) in the protein binding pocket.</p>
4	<p>2D chemical structure of compound 4. Interaction sites are highlighted in blue. Residues shown include Asp A509, Asp A505, Glu A477, Ser A480, Pro A505, Gly A478, Gly A504, Leu A502, Asp A479, Arg A503, Lys A465, and DT B9. Distances: 3.10, 3.08.</p>	<p>3D ribbon diagram of compound 4 (orange and red) in the protein binding pocket. Residues shown include Asp479 and DT9.</p>	<p>3D surface representation of compound 4 (orange and red) in the protein binding pocket.</p>

5			
6			
7			
Co-crystallized			

Reference

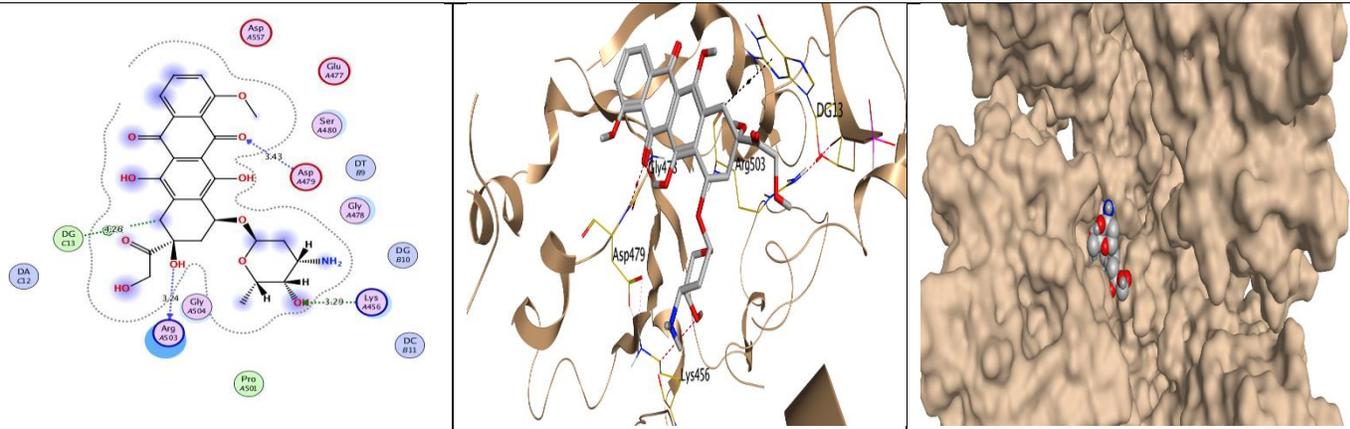


Figure S8: the 2D, 3D, and 3D protein positioning of all investigated compound at the biological target, TOP II.