

Supplementary material

Development of novel HER2 inhibitors against gastric cancer derived from flavonoid source of *Syzygium alternifolium* through molecular dynamics and pharmacophore based screening

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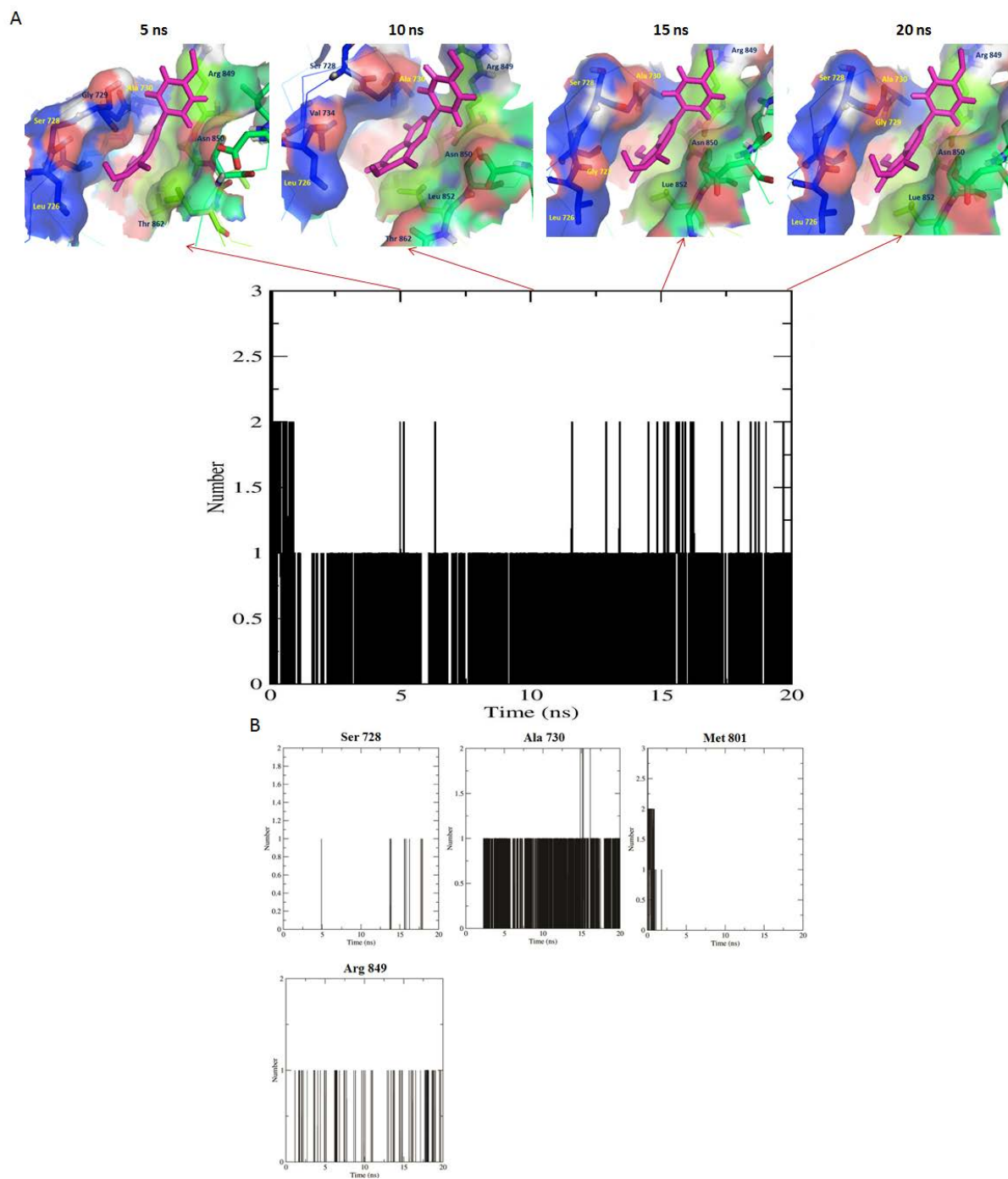


Figure S1A. The snapshots of docking pose of compound **1** and total H-bond intensity at various time scale intervals in 20 ns complex MD simulations with HER2, **B.**Hydrogen bonds diagram between compound **1** and active site residues viz., Ser728, Ala730, Met801 and Arg849 of HER2, Black squares indicate the presence of H-bond and white ones correspond to the absence of H-bond throughout the time scale of 20 ns MD simulations.

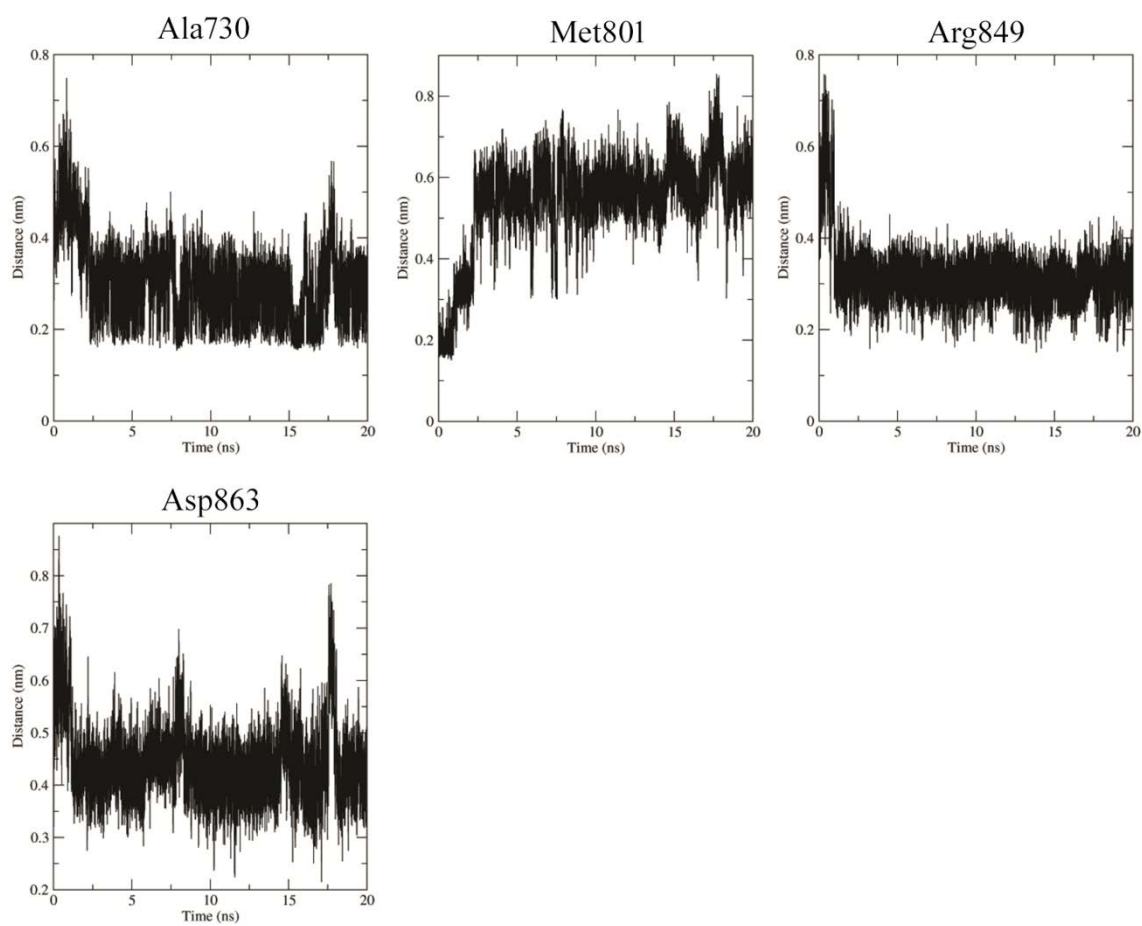


Figure S2 Distance between hydrogen bonding residues viz., Ala 730, Met 801, Arg 849, and Asp 863 with compound **1** in a complex protein of HER2b, comparatively depicted throughout 20 ns simulation period.

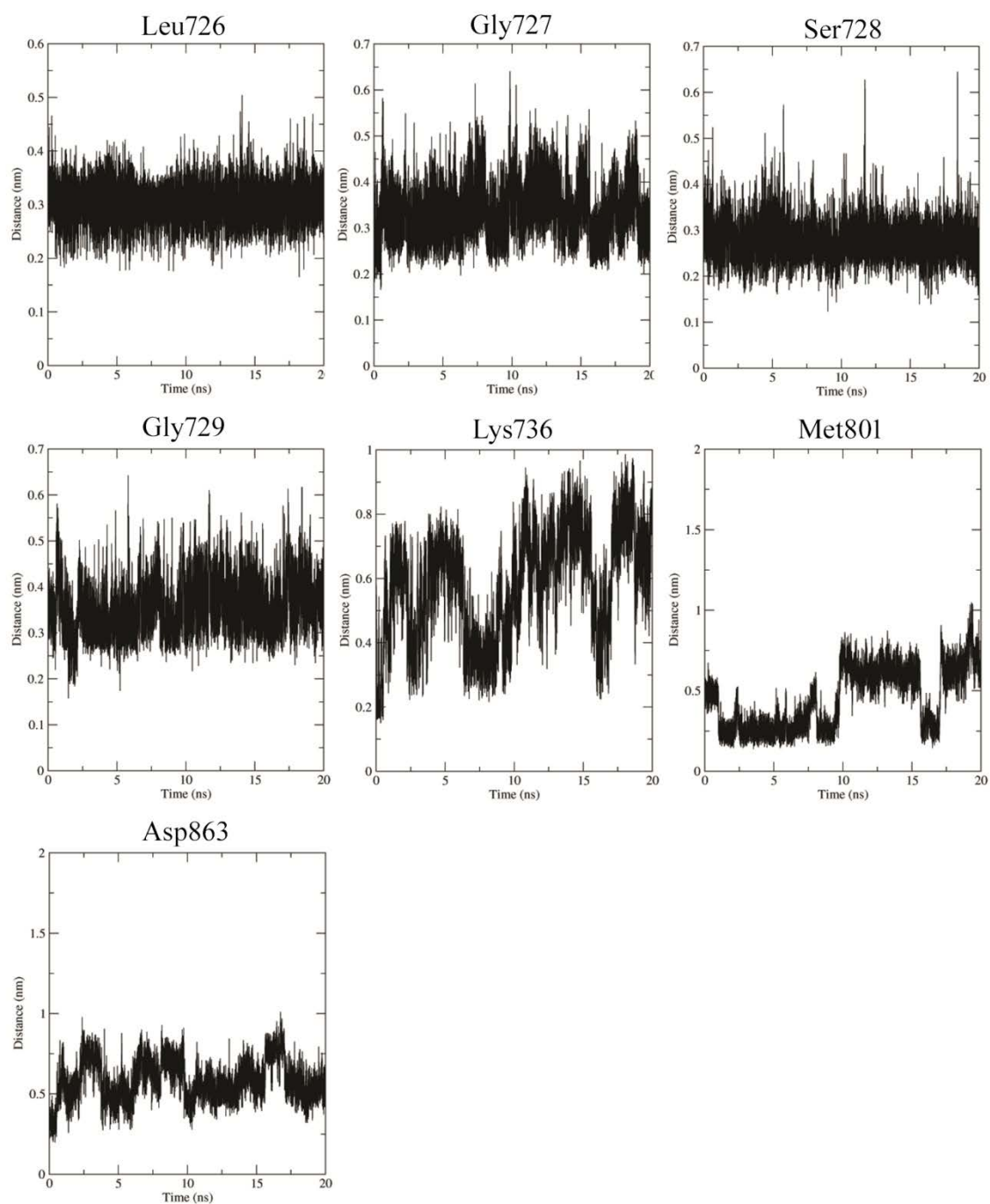


Figure. S3Distance between hydrogen bonding residues viz. Leu 726,Gly 727, Ser 728, Gly 729,Lys 736, Met 801, and Asp 863 with compound **2** in a complex protein of HER2c, comparatively depicted throughout 20 ns simulation period.

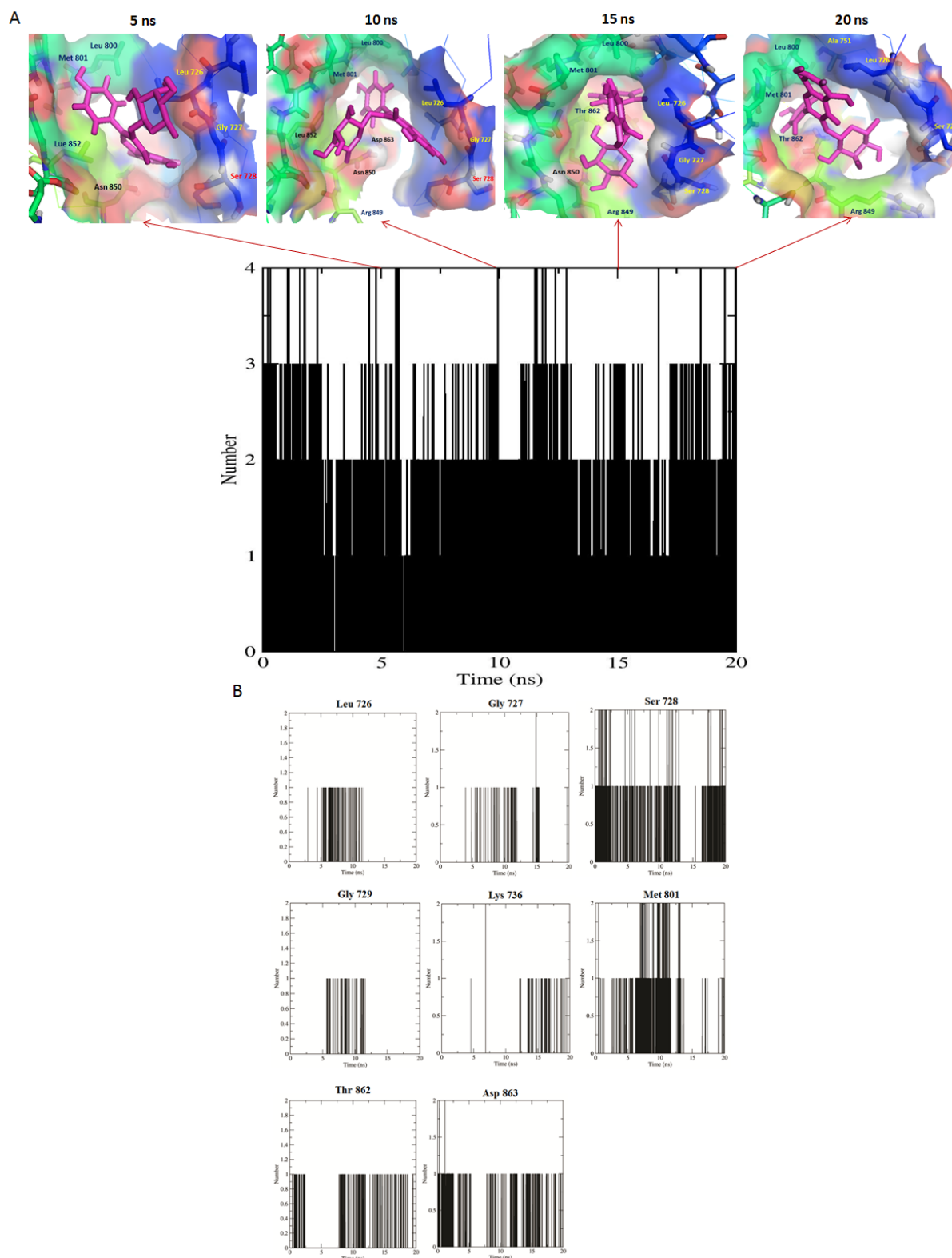


Figure S4 A The snapshots of docking pose of compound **3** and total H-bond intensity at various time scale intervals in 20 ns complex MD simulations with HER2, **B**. Hydrogen bonds diagram between compound **3** and active site residues viz., Leu726, Gly726, Ser728, Gly729, Lys736, Met801, Thr862 and Asp863 of HER2, Black squares indicate the presence of H-bond and white ones correspond to the absence of H-bond throughout the time scale of 20 ns MD simulations.

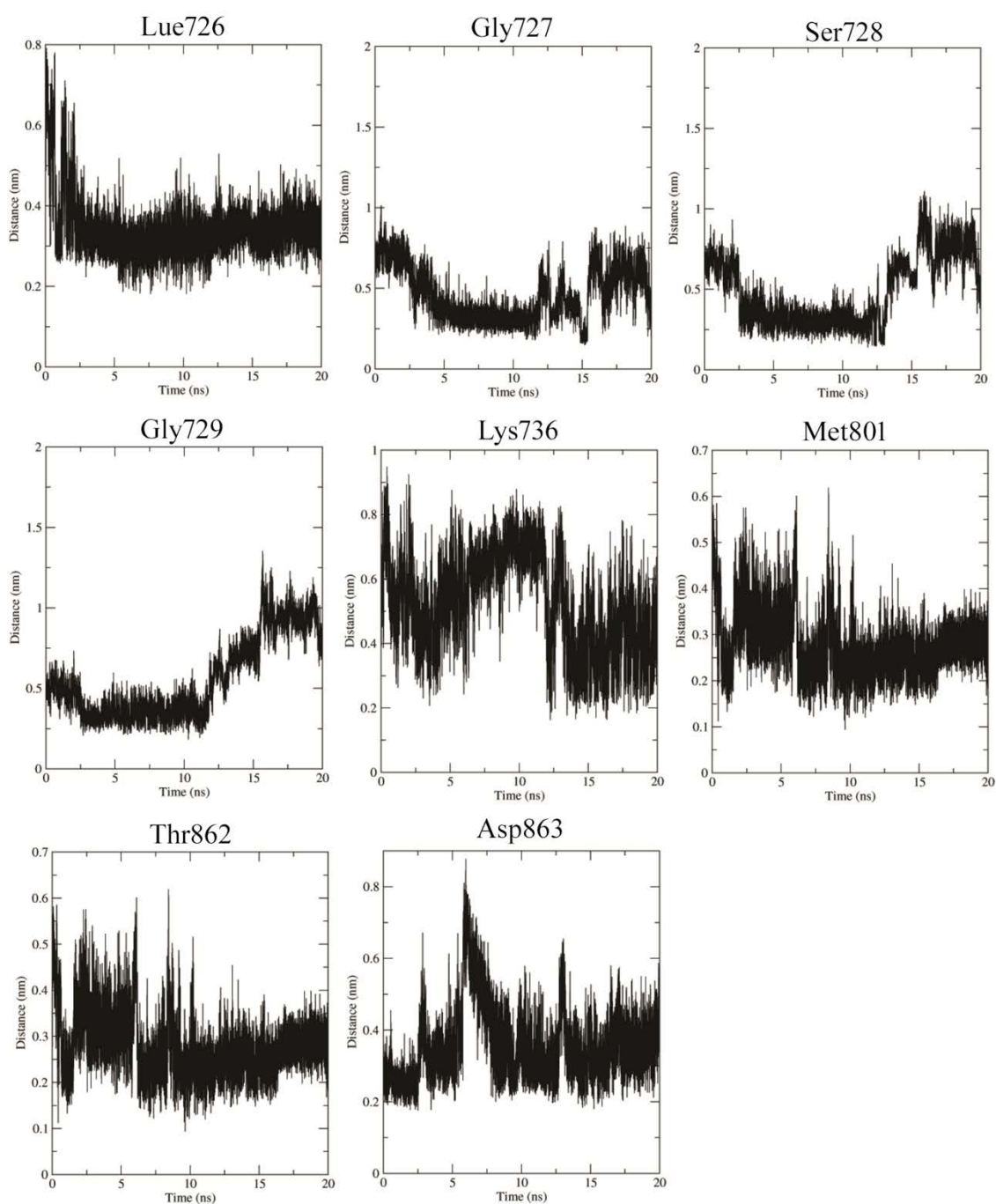


Figure S5 Distance between hydrogen bonding residues viz. Leu 726, Gly 727, Ser 728, Gly 729, Lys 736, Met 801, Thr 862 and Asp 863 with compound **3** in a complex protein of HER2d, comparatively depicted throughout 20 ns simulation period.

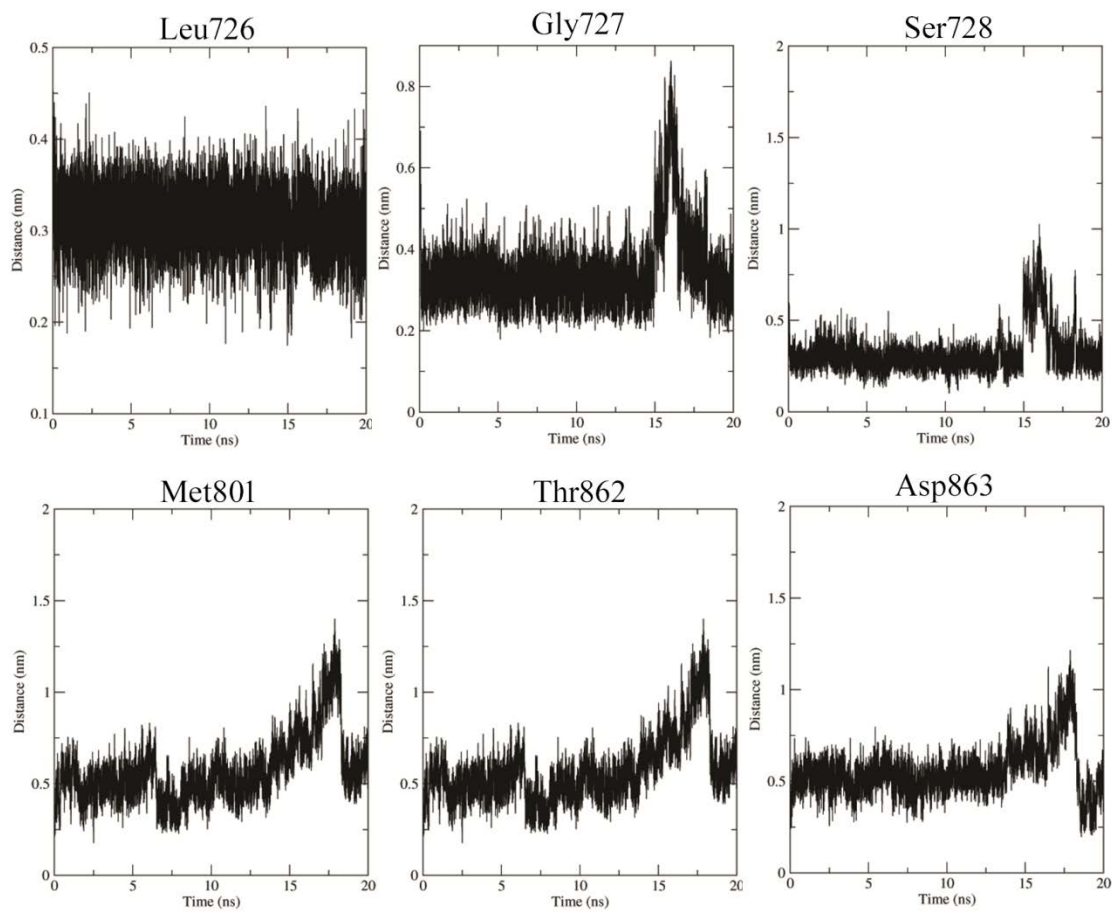


Figure S6 Distance between hydrogen bonding residues viz. Leu 726, Gly 727, Ser 728, Met 801, Thr 862 and Asp 863 with ZINC67903192 in a complex protein of HER2e, comparatively depicted throughout 20 ns simulation period.

Table S1

The list of pharmacophore hits for HER2-Compound **2** complex and its physico-chemical properties.

S.No	mol	rmsd	mseq	b_rotN	Weight	a_acc	a_don	SlogP
1	ZINC67903192	0.536928	1	6	594.522	14	9	-1.5844
2	ZINC67903197	0.582157	2	6	594.522	14	9	-1.5844
3	ZINC59763389	0.796897	3	5	564.496	13	8	-0.9453
4	ZINC59763395	0.783681	4	5	564.496	13	8	-0.9453
5	ZINC85816423	0.601657	5	9	772.662	20	13	-4.0546
6	ZINC85816425	0.601468	6	9	772.662	20	13	-4.0546
7	ZINC85816428	0.736348	7	9	772.662	20	13	-4.0546
8	ZINC85816432	0.736335	8	9	772.662	20	13	-4.0546
9	ZINC85507936	0.629833	9	7	626.52	16	11	-2.9064
10	ZINC85816022	0.582267	10	7	626.52	16	11	-2.9064
11	ZINC85816467	0.791578	11	10	788.661	21	14	-5.0822
12	ZINC85816470	0.650954	12	10	788.661	21	14	-5.0822
13	ZINC85815711	0.651054	13	6	596.494	15	10	-2.2673
14	ZINC85815706	0.582267	14	6	596.494	15	10	-2.2673
15	ZINC85816026	0.650954	15	7	626.52	16	11	-2.9064
16	ZINC85816347	0.751353	16	8	756.663	19	12	-3.027
17	ZINC85816374	0.823635	17	9	772.662	20	13	-4.0546
18	ZINC85816382	0.823287	18	9	772.662	20	13	-4.0546
19	ZINC85816460	0.581897	19	10	788.661	21	14	-5.0822
20	ZINC85816463	0.647945	20	10	788.661	21	14	-5.0822
21	ZINC59764808	0.797006	21	5	580.495	14	9	-1.2397
22	ZINC59764812	0.783414	22	5	580.495	14	9	-1.2397
23	ZINC85531791	0.526649	23	6	610.521	15	10	-1.8788

S.No	mol	rmsd	mseq	b_rotN	Weight	a_acc	a_don	SlogP
24	ZINC59766057	0.745063	24	5	596.494	15	10	-1.5341
25	ZINC59766065	0.742473	25	5	596.494	15	10	-1.5341
26	ZINC85948558	0.774123	26	7	610.521	15	9	-1.9643
27	ZINC85948547	0.774294	27	7	610.521	15	9	-1.9643
28	ZINC86048481	0.644746	28	8	656.546	17	11	-2.8978
29	ZINC86048475	0.644507	29	8	656.546	17	11	-2.8978
30	ZINC85931428	0.773715	30	9	670.573	17	10	-2.5948
31	ZINC85931420	0.77392	31	9	670.573	17	10	-2.5948
32	ZINC59764341	0.62403	32	10	607.497	12	8	-1.8986
33	ZINC59764345	0.62403	33	10	607.497	12	8	-1.8986
34	ZINC59585850	0.712897	34	4	464.379	11	8	-0.7306

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