

Supporting Information

Rapid Prediction of Possible Inhibitors for SARS-
CoV-2 Main Protease using Docking and FPL
Simulations

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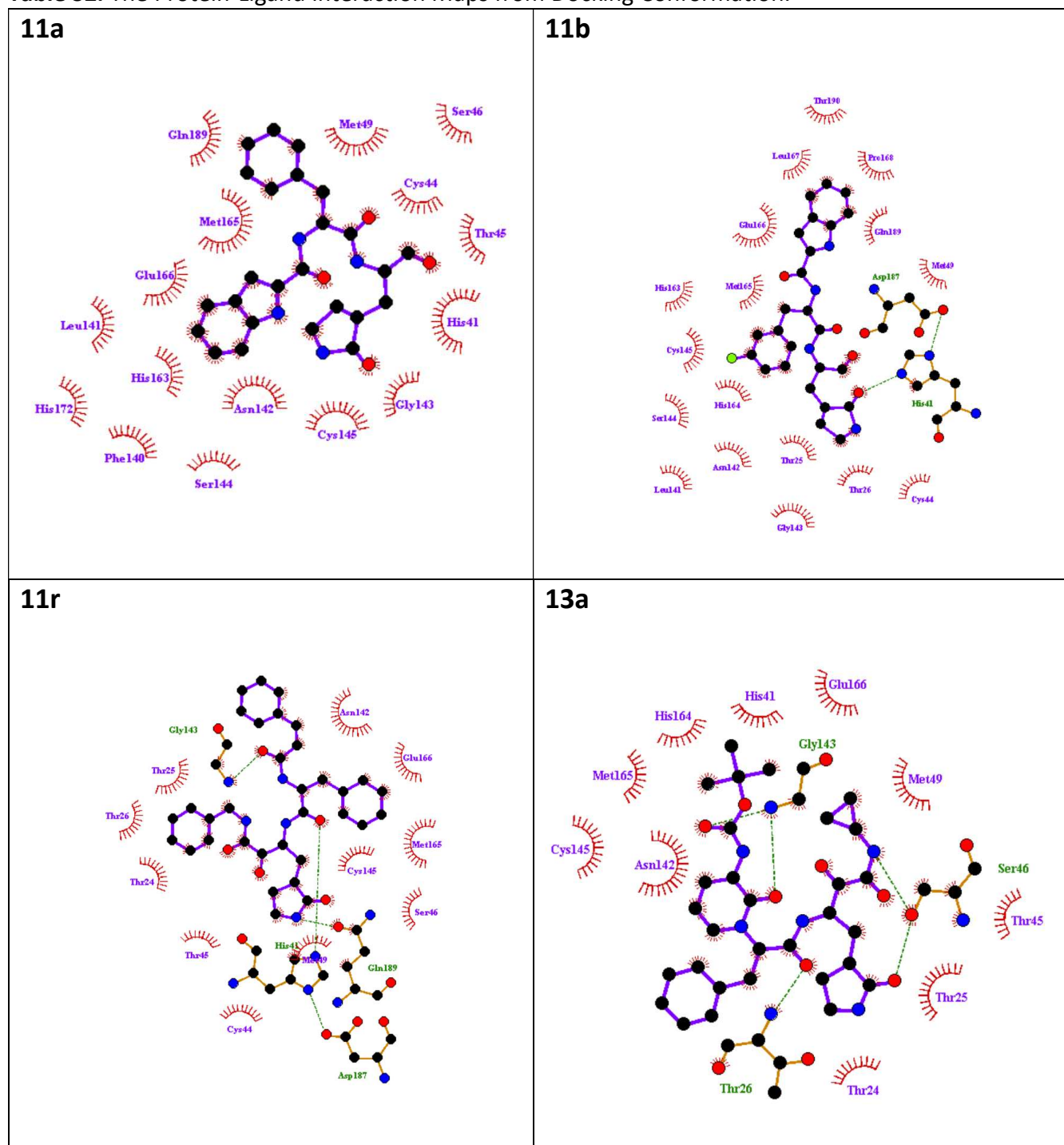
*Email: ngosontung@tdtu.edu.vn

Table 1. Comparison of the docking results of available inhibitors on the SARS-CoV-2 monomer and dimer.

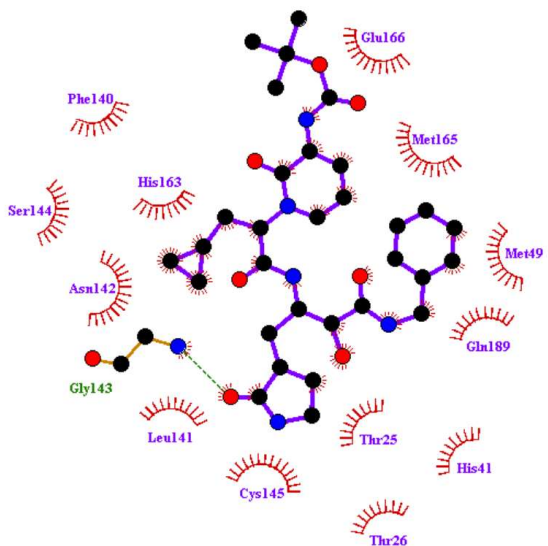
N ^o	Name	$\Delta G_{\text{Dock}}^{\text{Monomer}}$	$\Delta G_{\text{Dock}}^{\text{Dimer}}$
1	11r	-6.5	-7.0
2	13a	-6.5	-6.3
3	13b	-6.3	-7.3
4	11a	-6.8	-7.3
5	11b	-7.0	-7.7
6	<i>Carmofur</i>	-5.7	-5.9
7	<i>Disulfiram</i>	-3.8	-4.2
8	<i>Ebselen</i>	-5.6	-6.2
9	<i>PX-12</i>	-3.8	-4.1
10	<i>Shikonin</i>	-6.1	-6.9
11	<i>Tideglusib</i>	-6.6	-6.6

The unit is in kcal mol⁻¹.

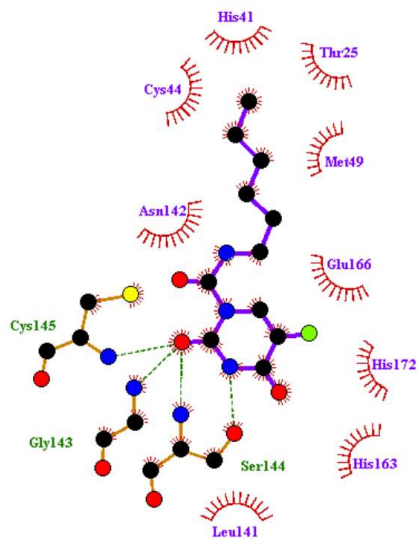
Table S2. The Protein-Ligand Interaction Maps from Docking Conformation.



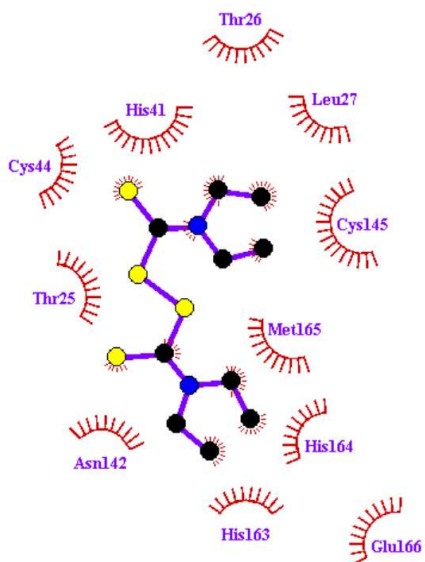
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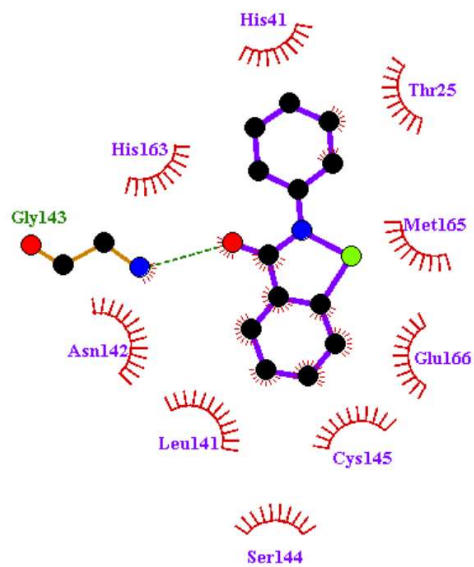
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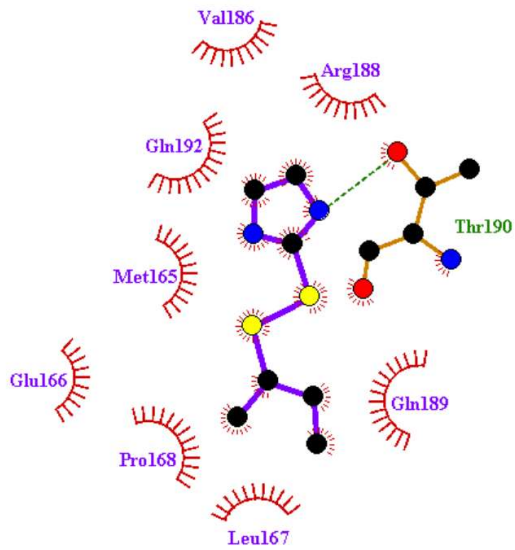
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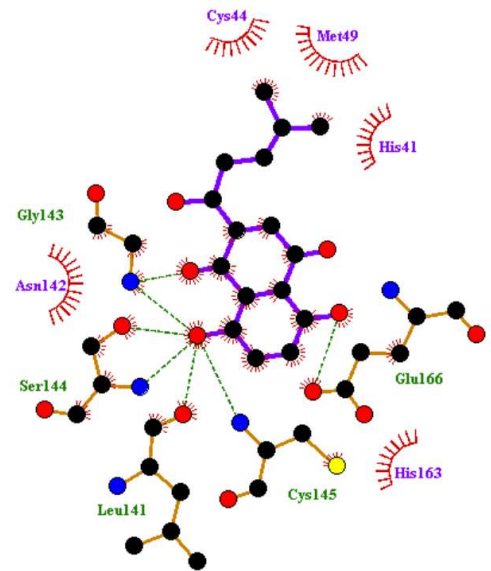
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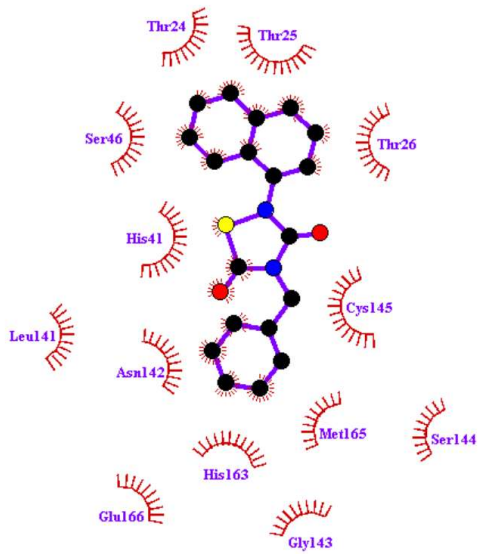
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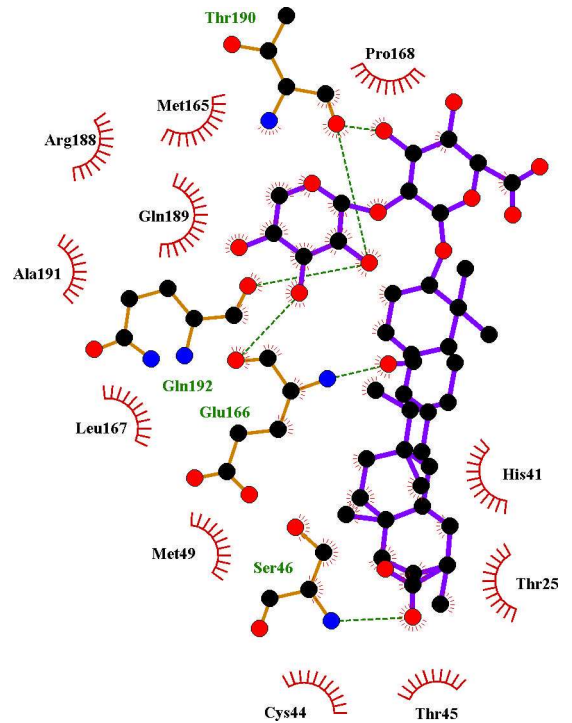
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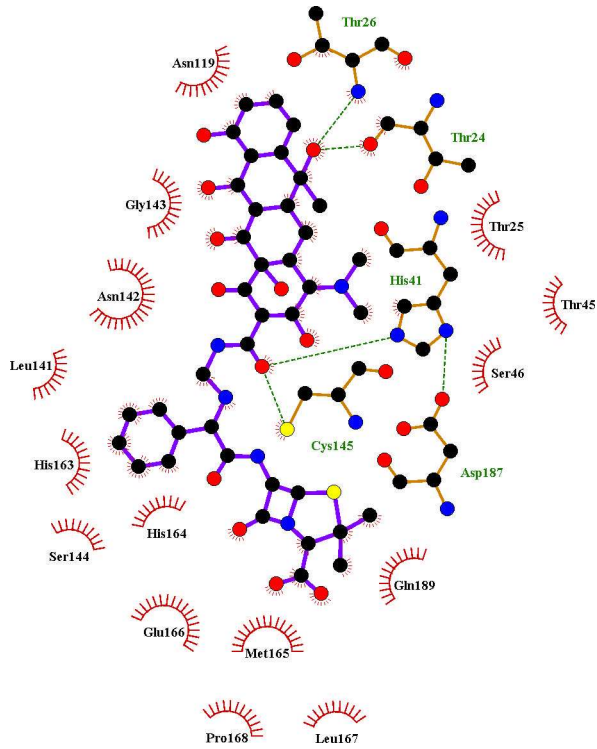
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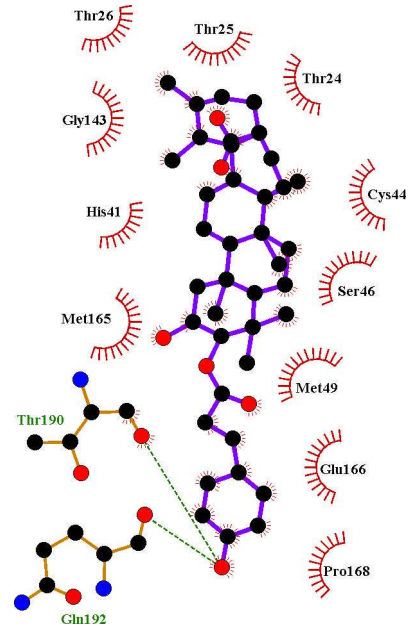
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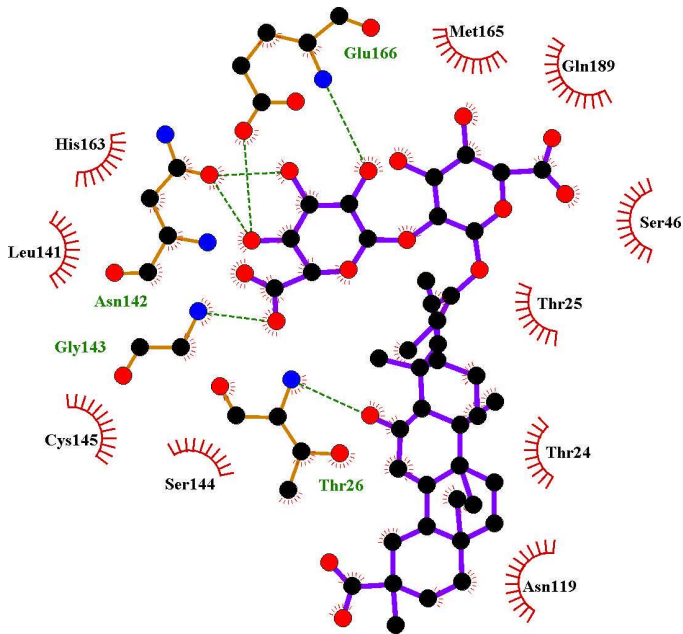
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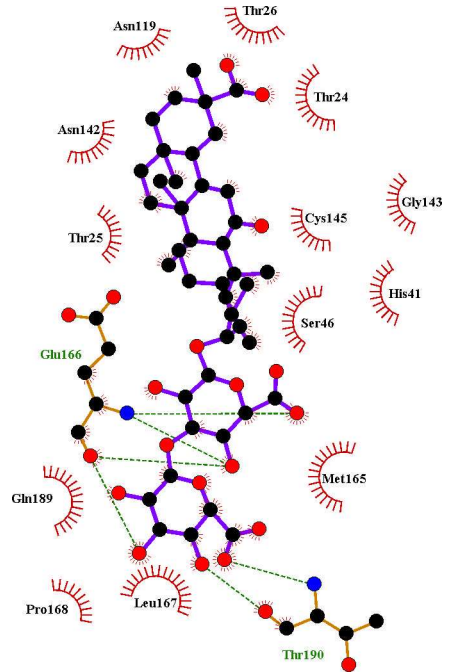
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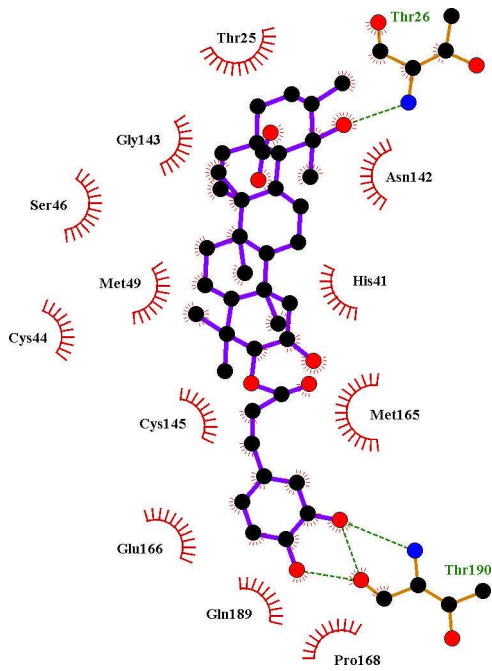
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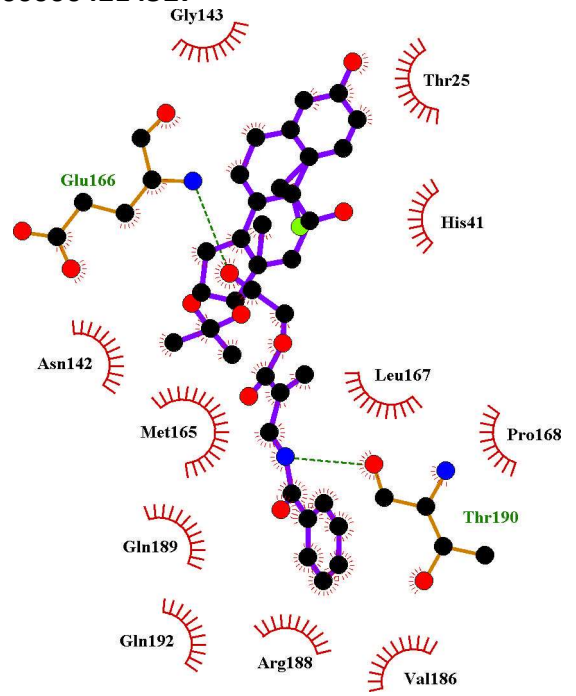
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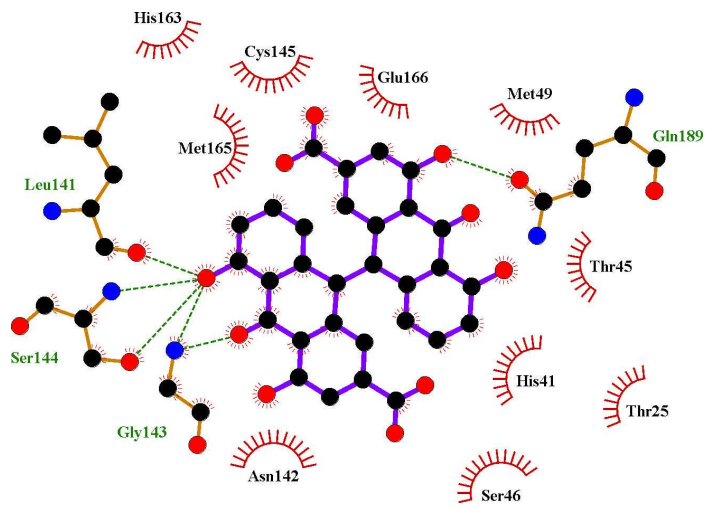
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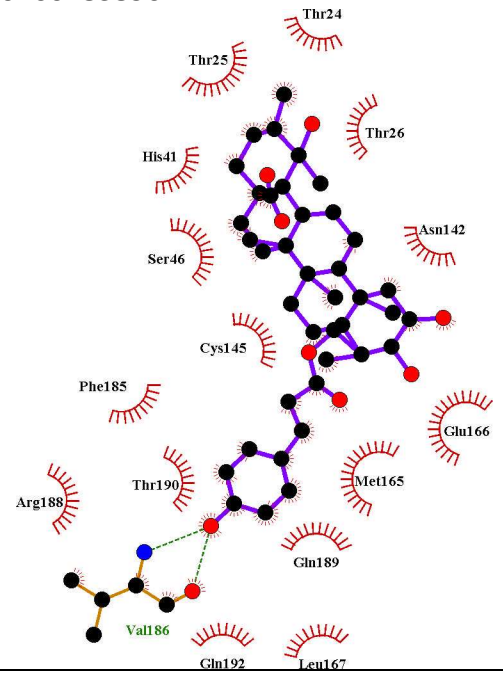
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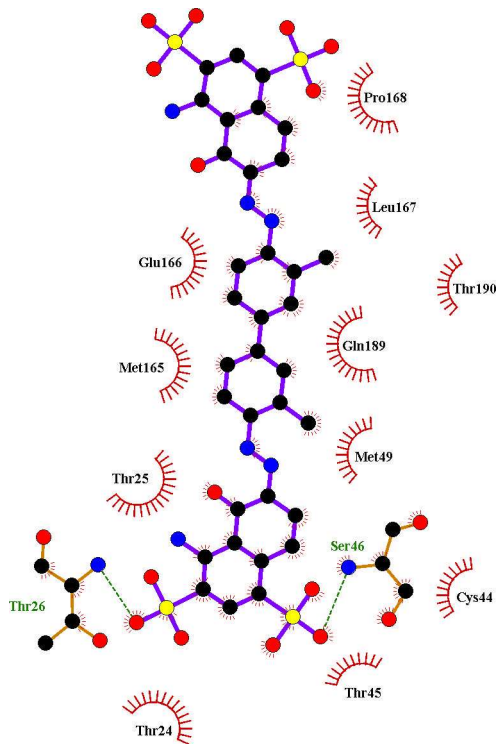
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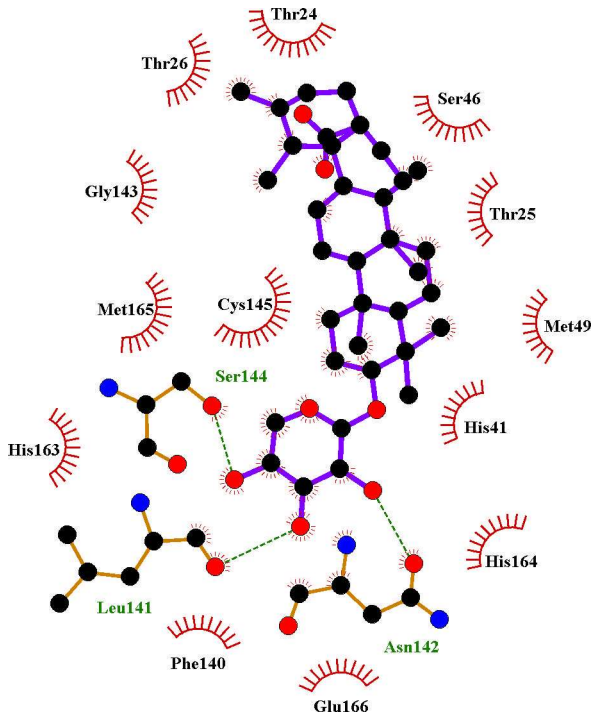
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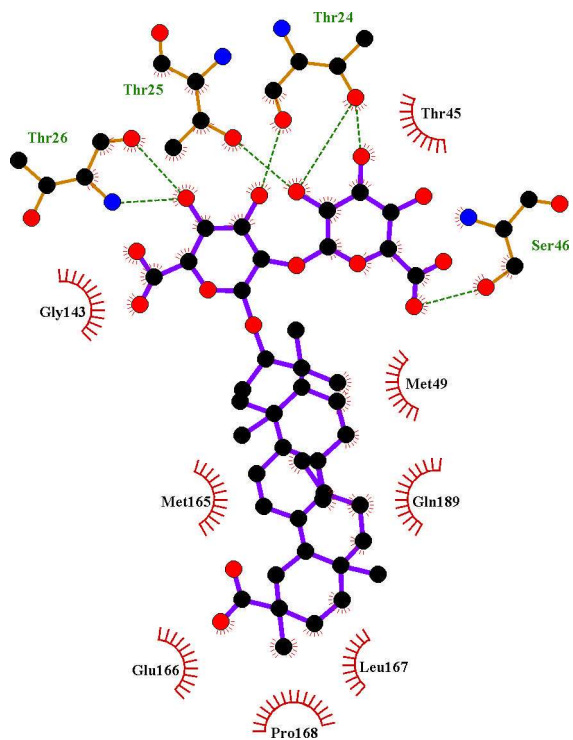
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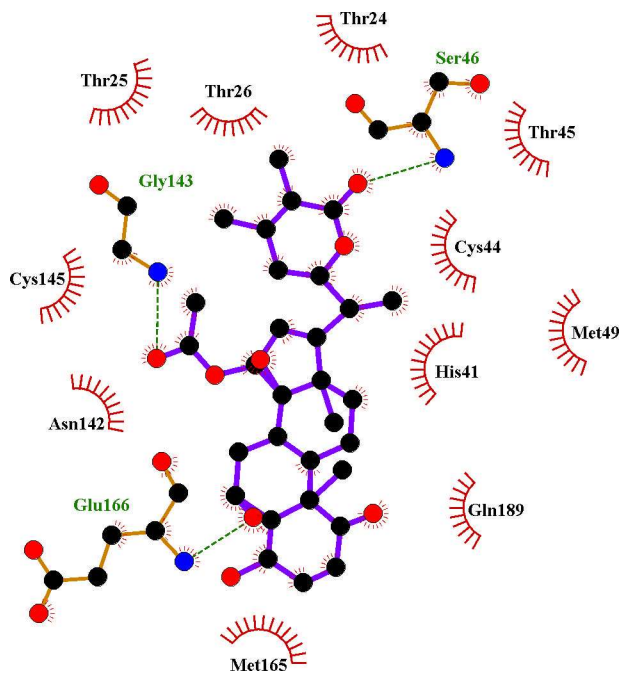
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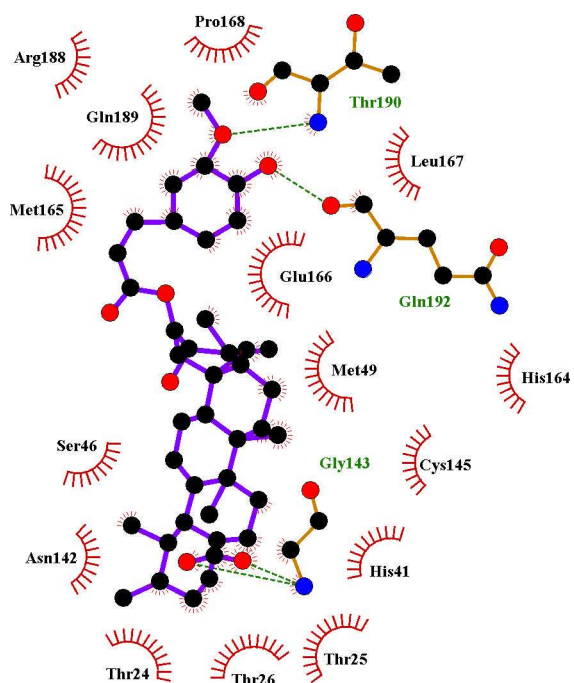
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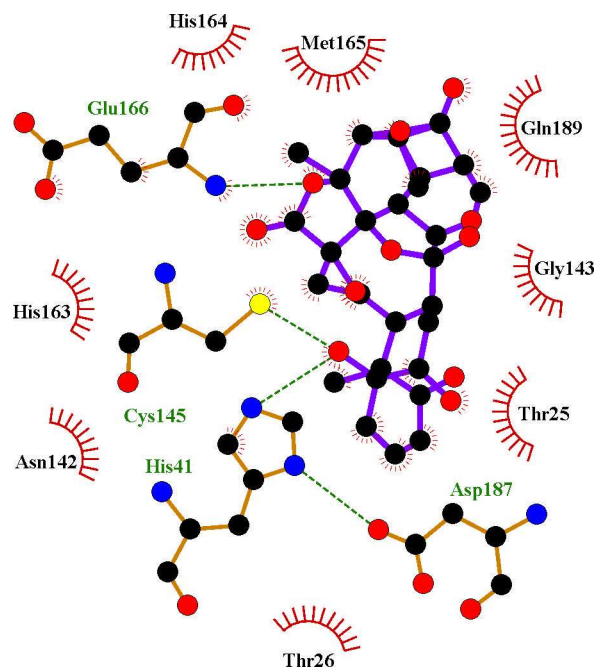
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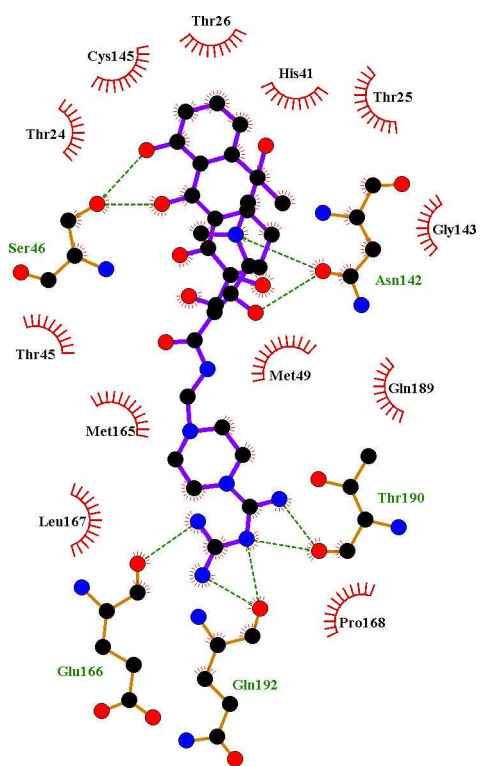
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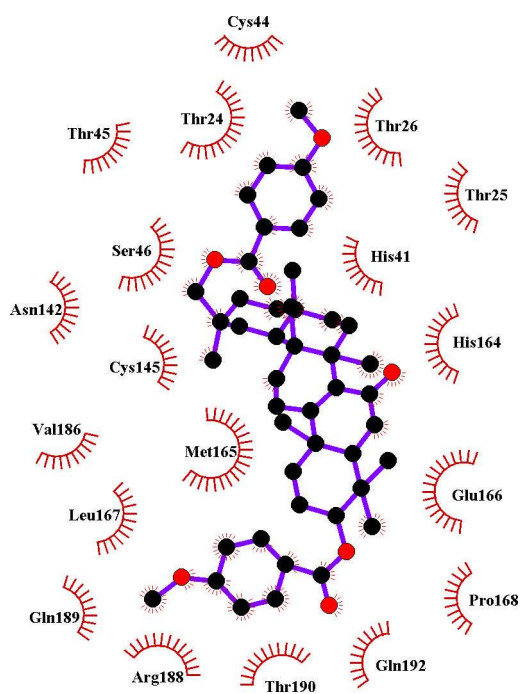
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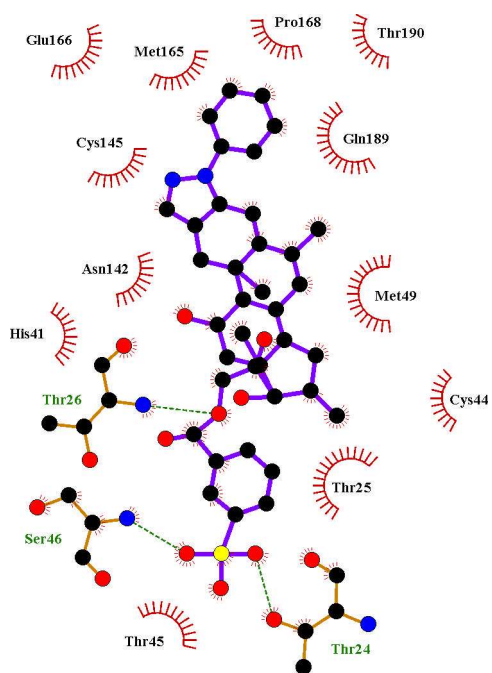
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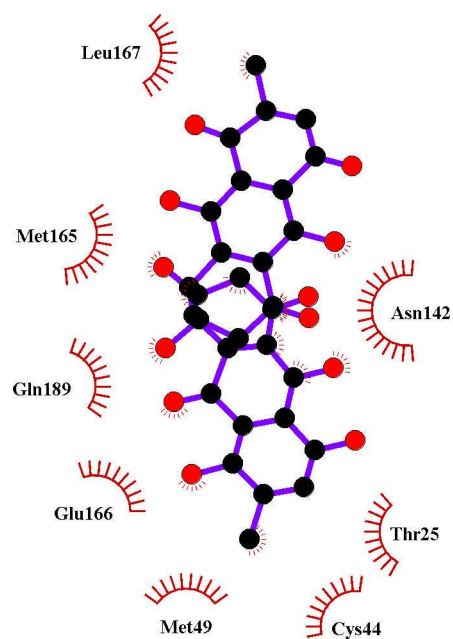
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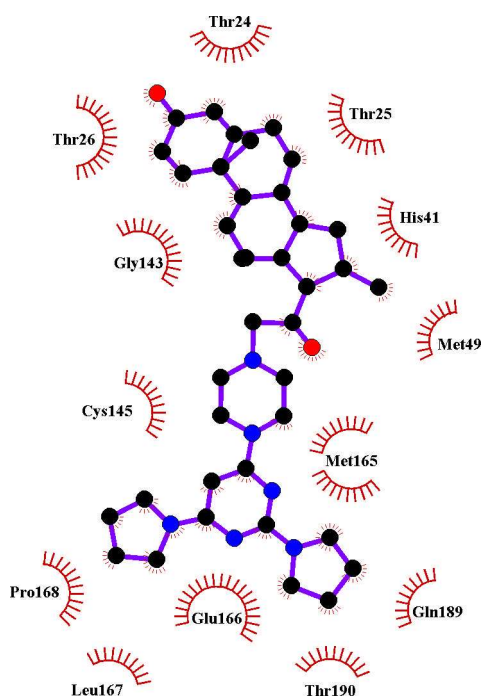
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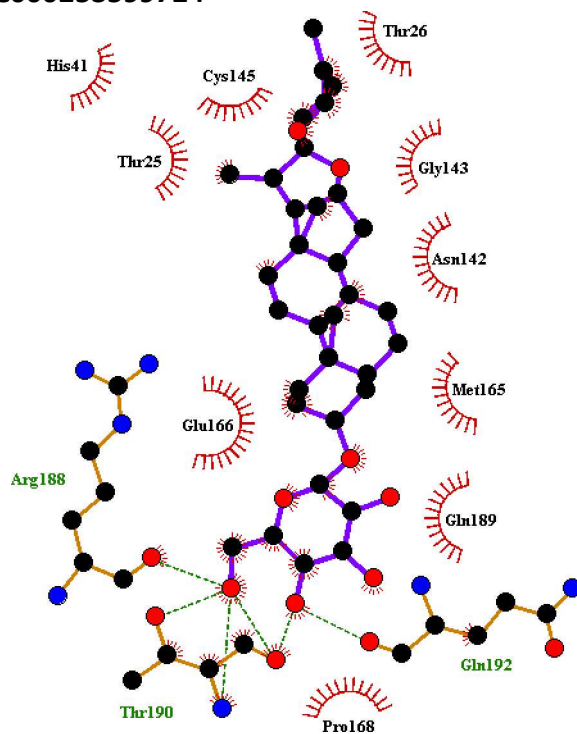
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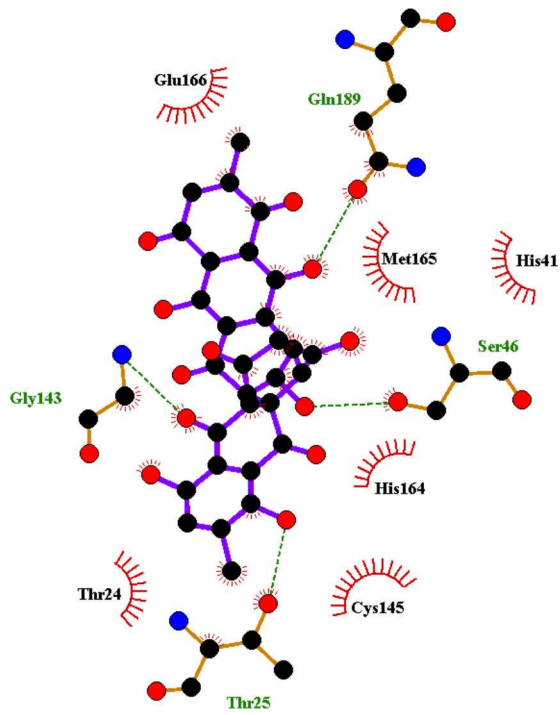
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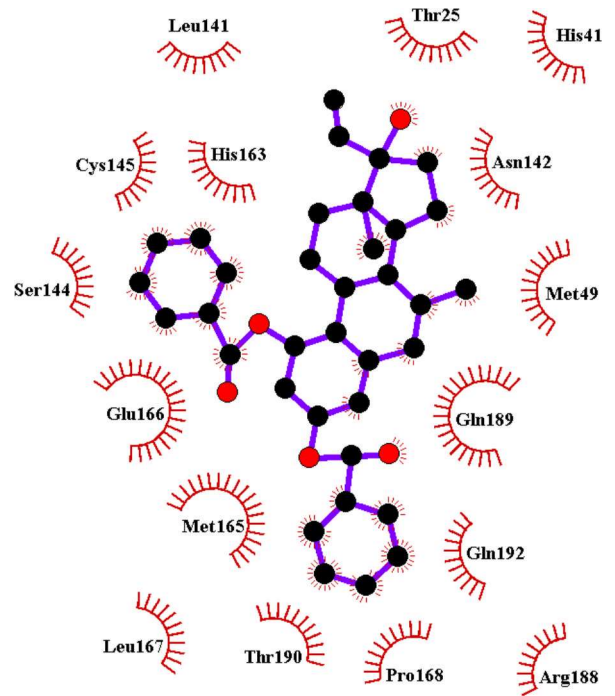
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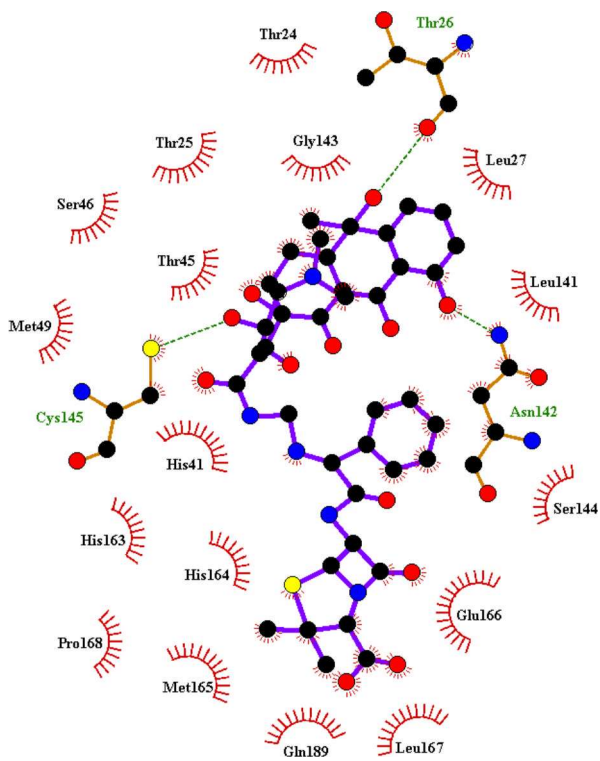
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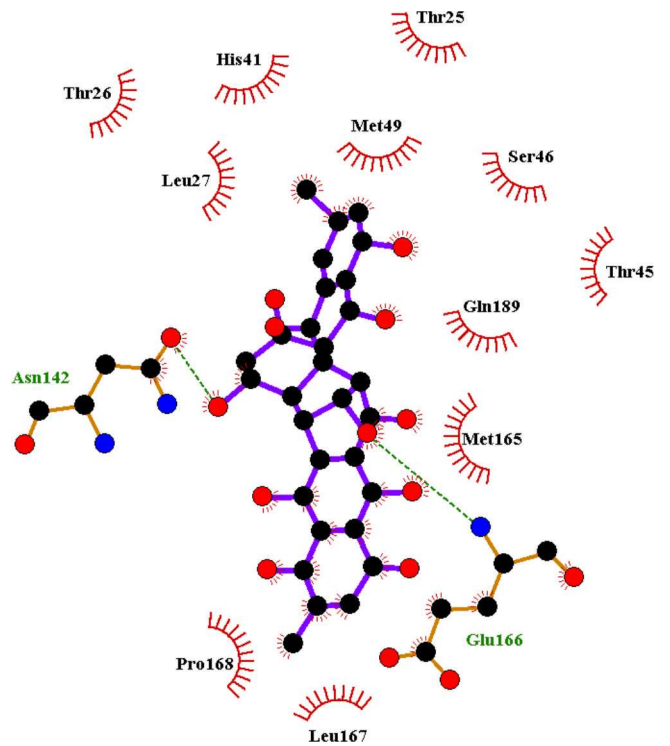
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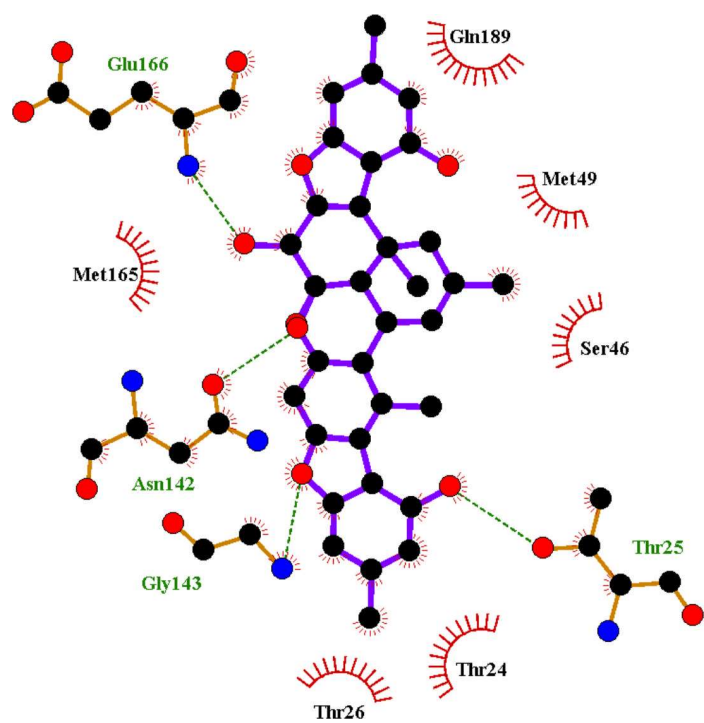
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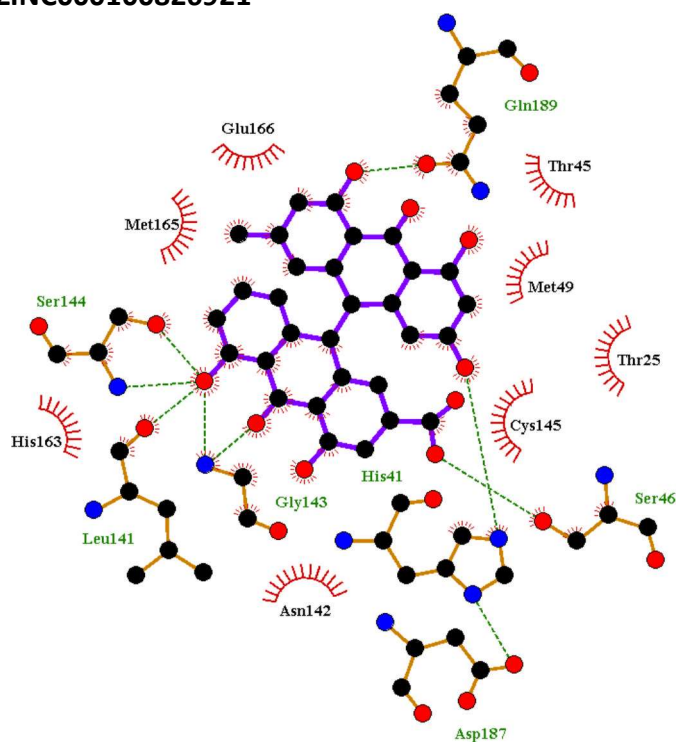
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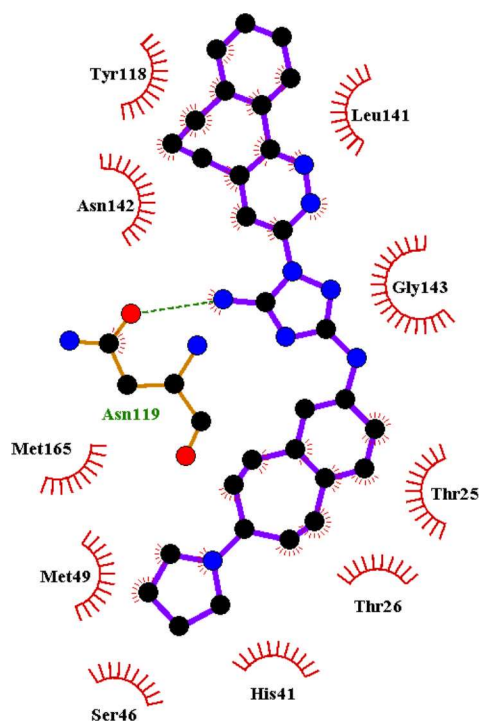
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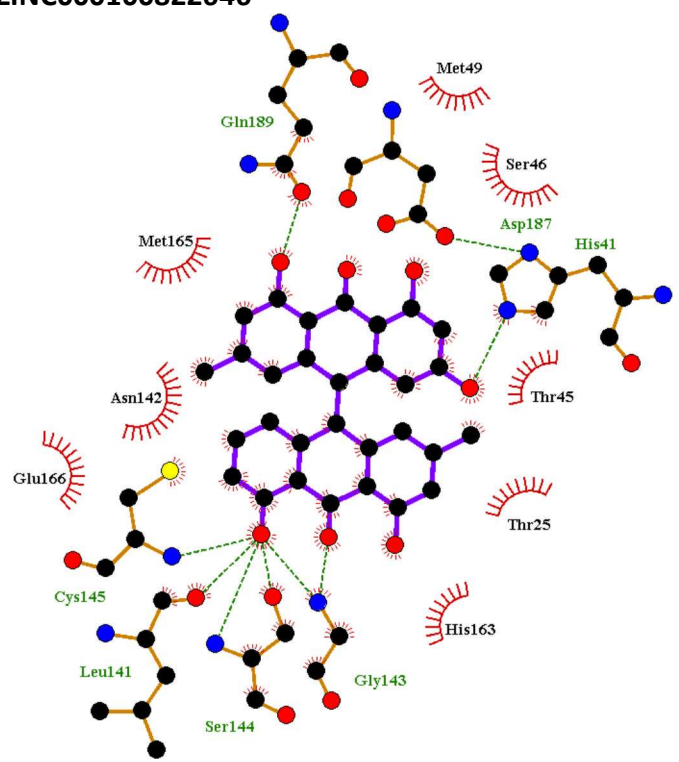
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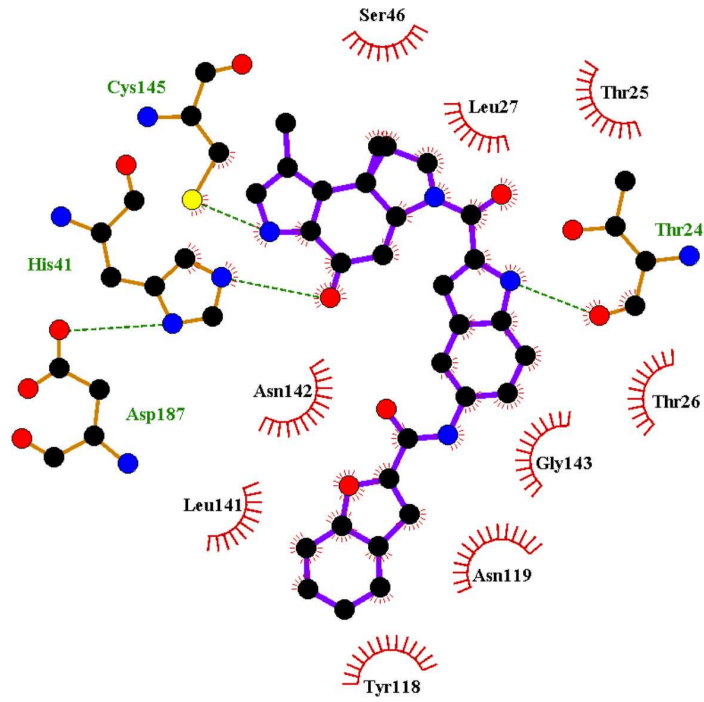
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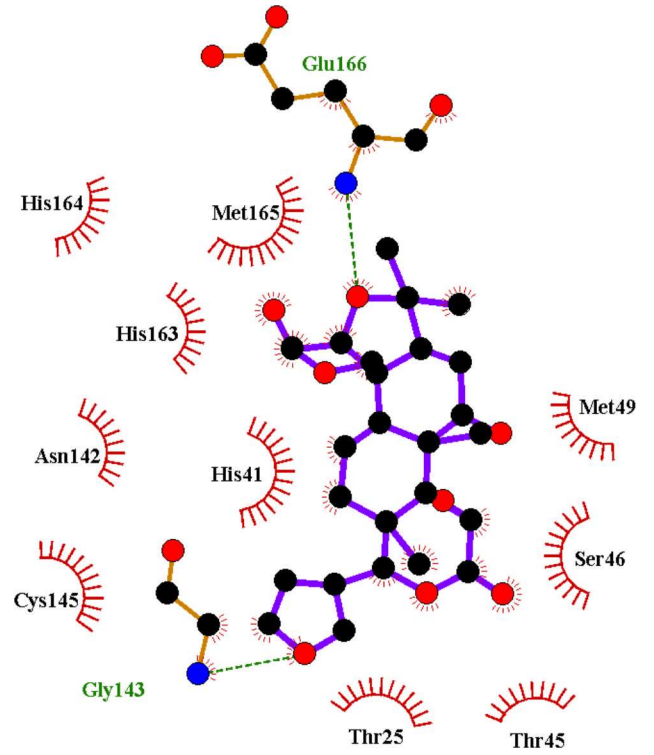
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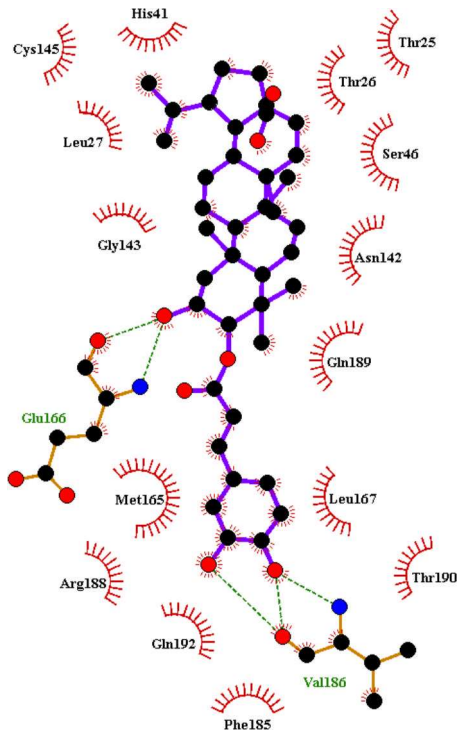
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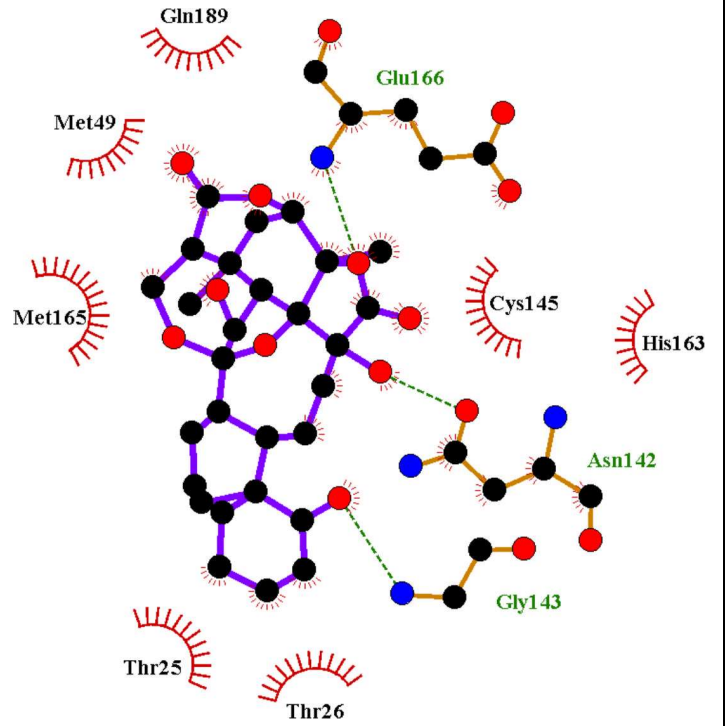
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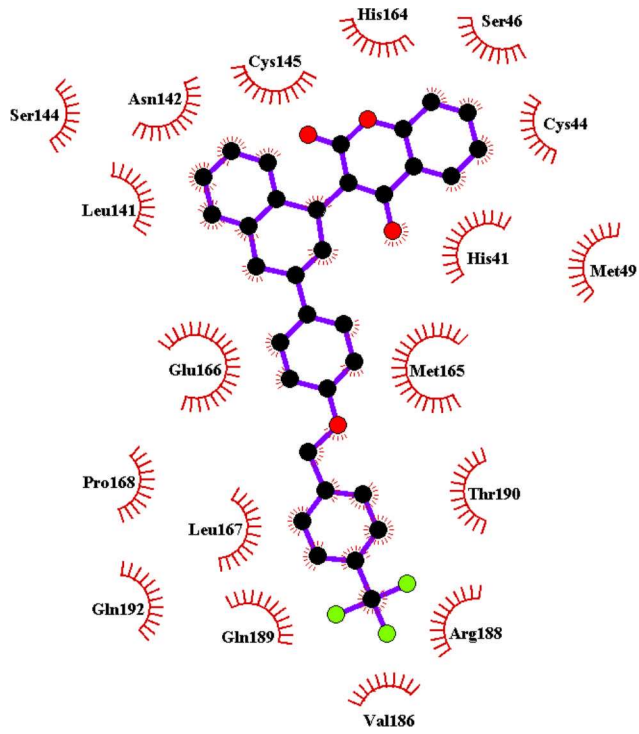
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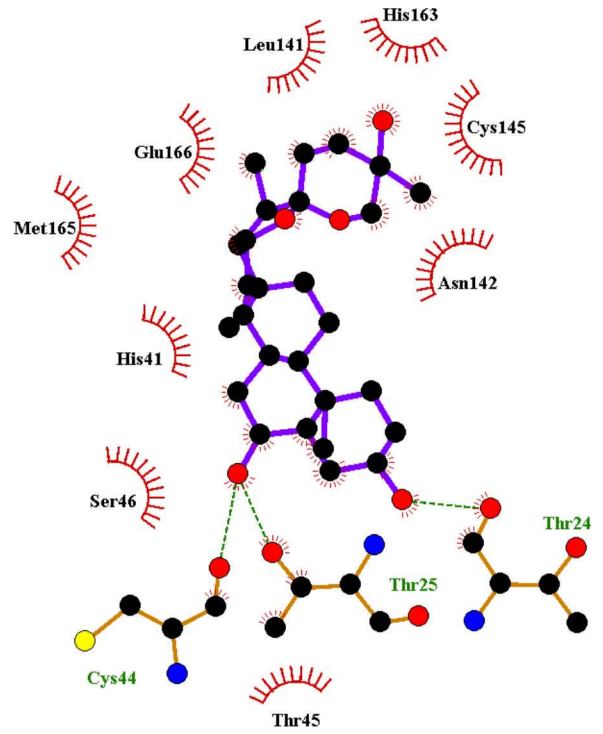
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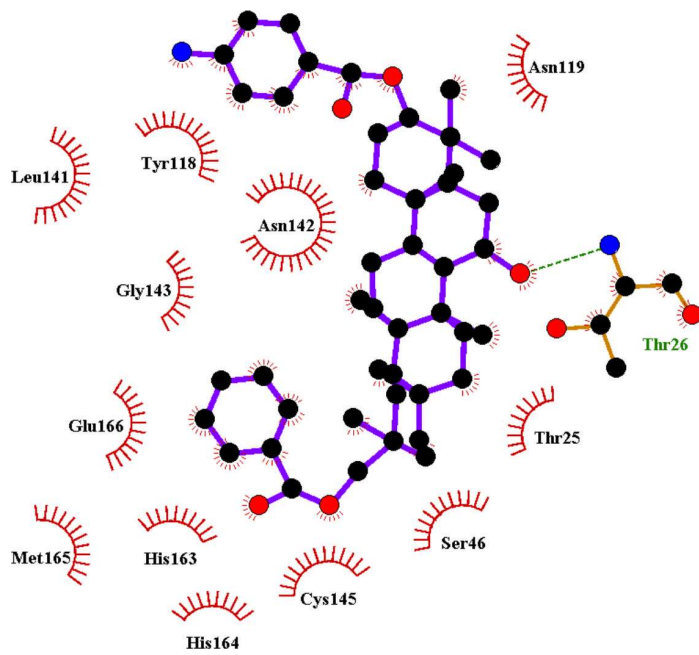
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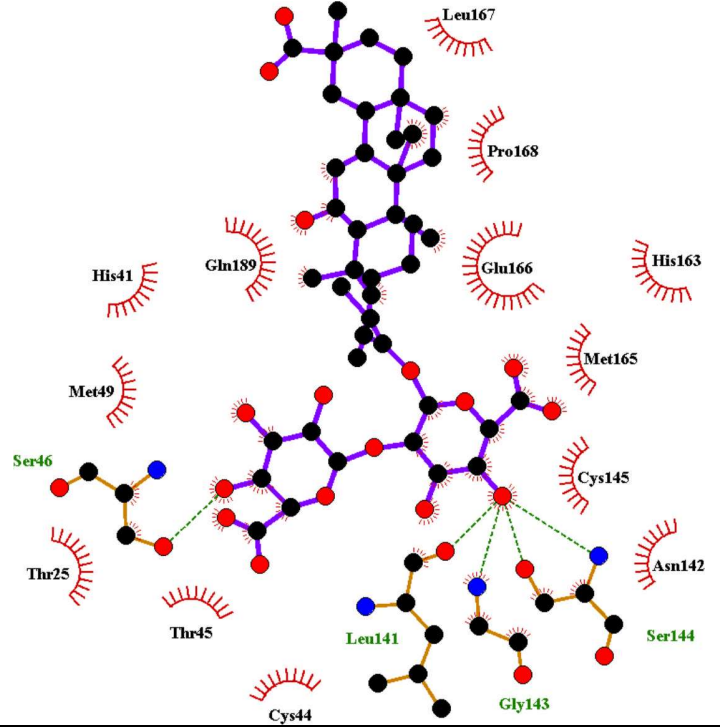
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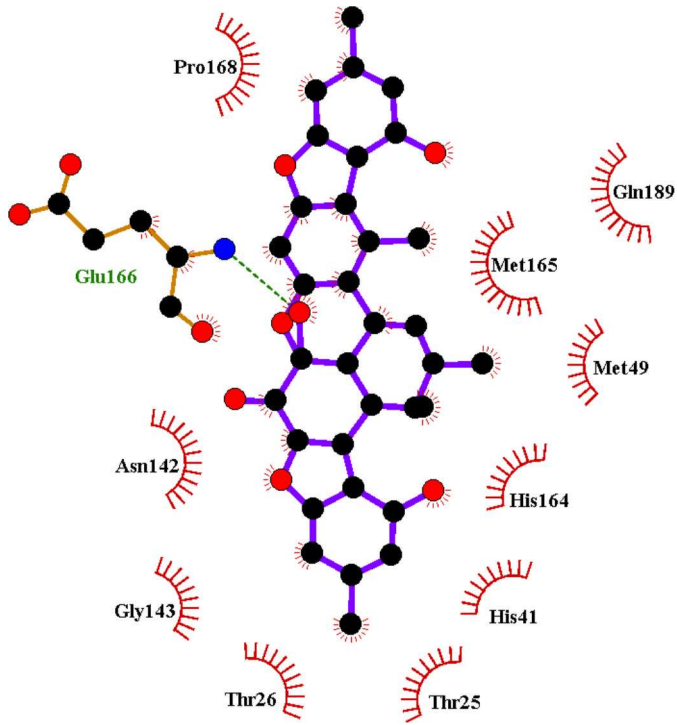
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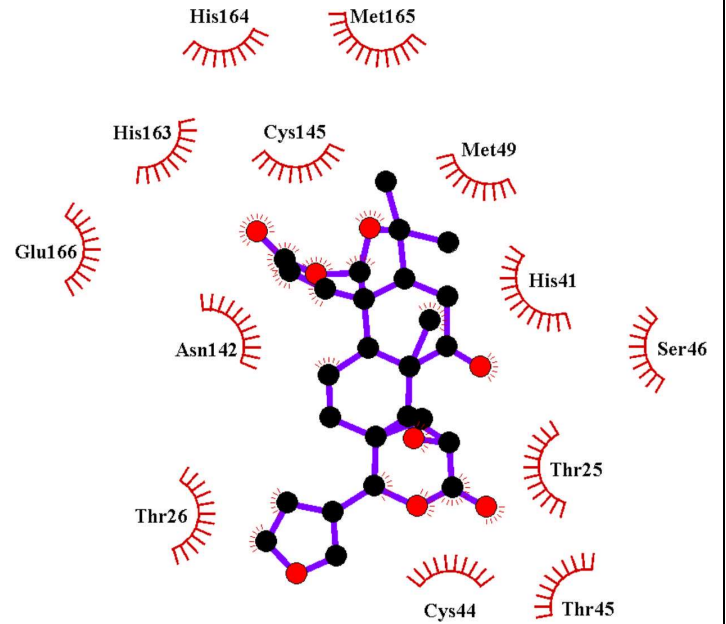
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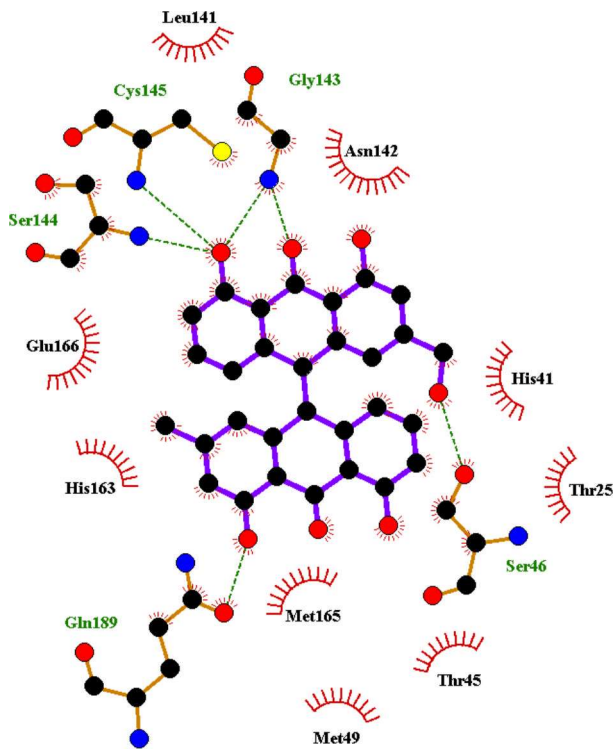
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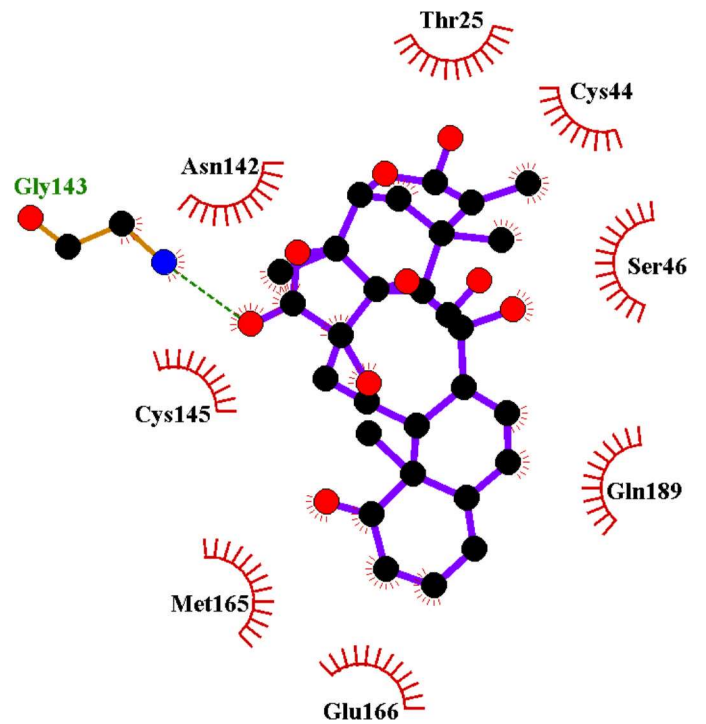
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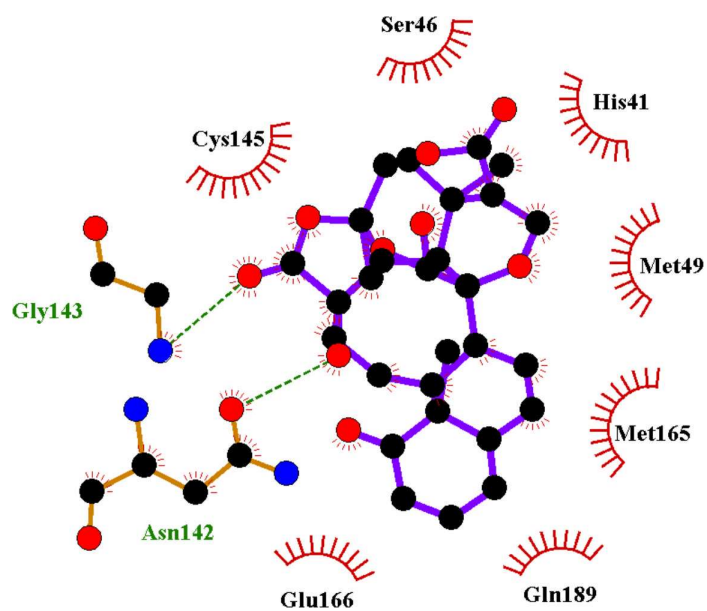
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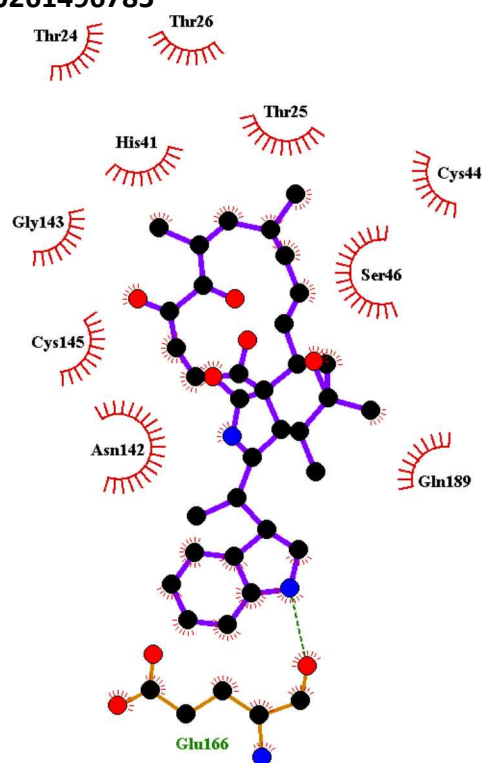
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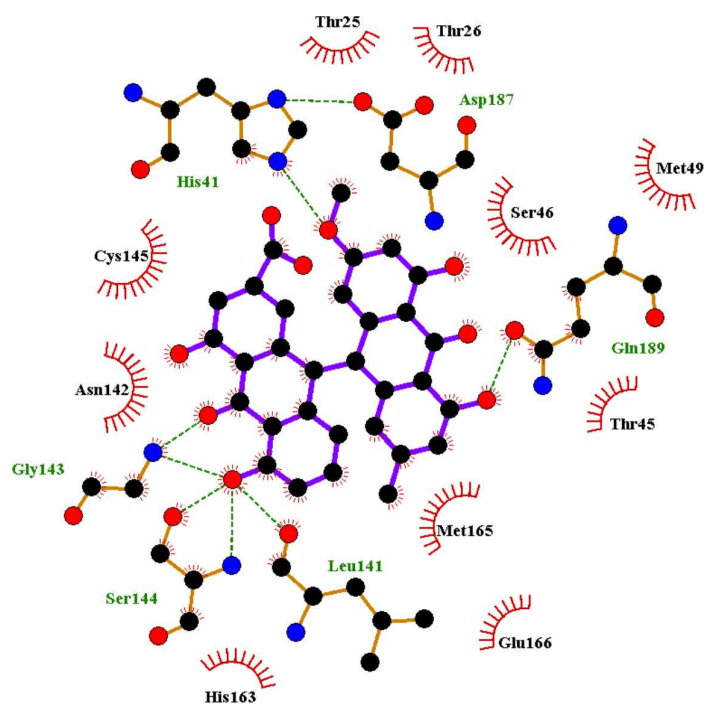
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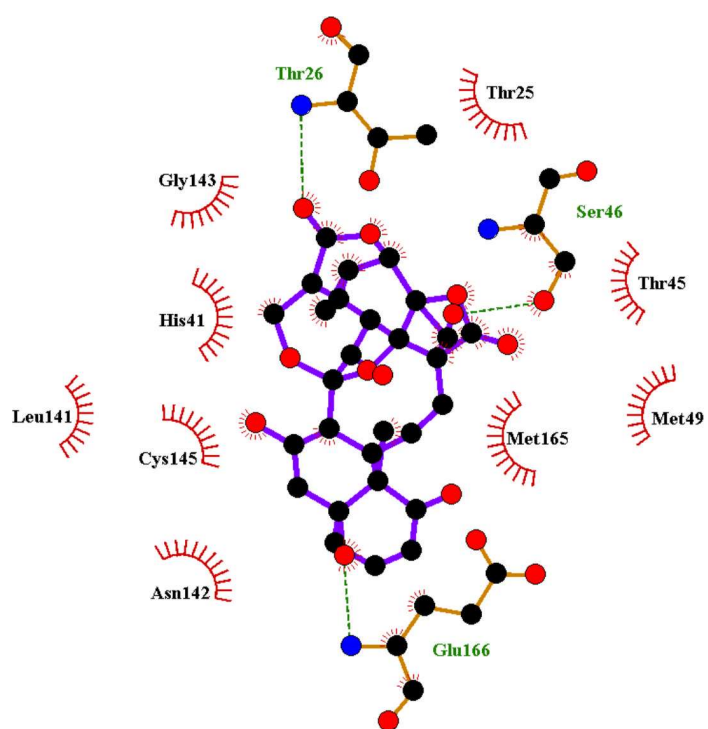
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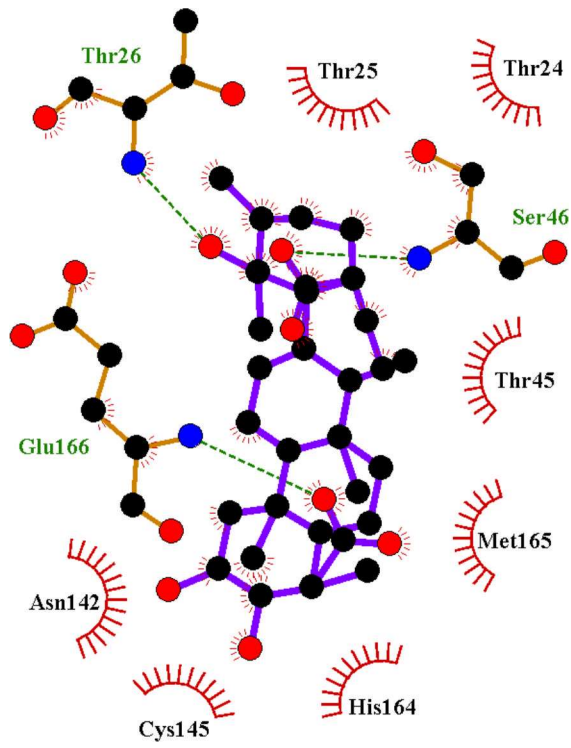
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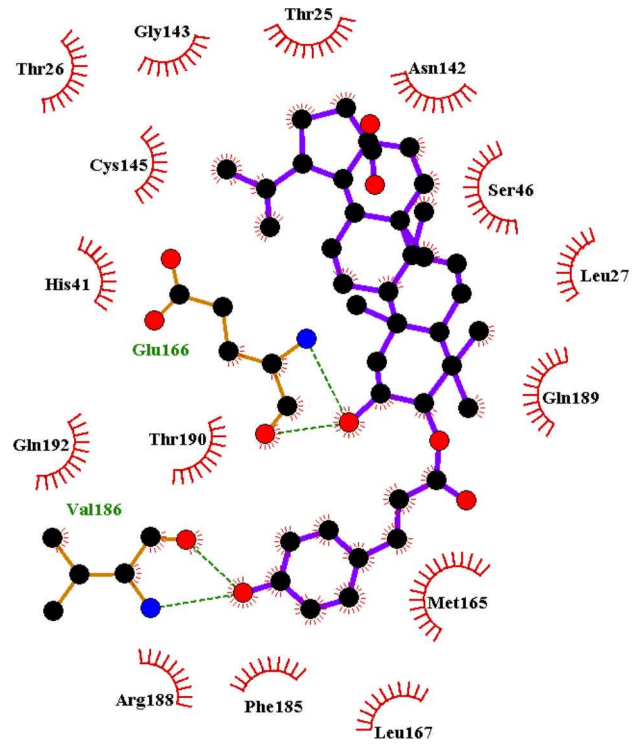
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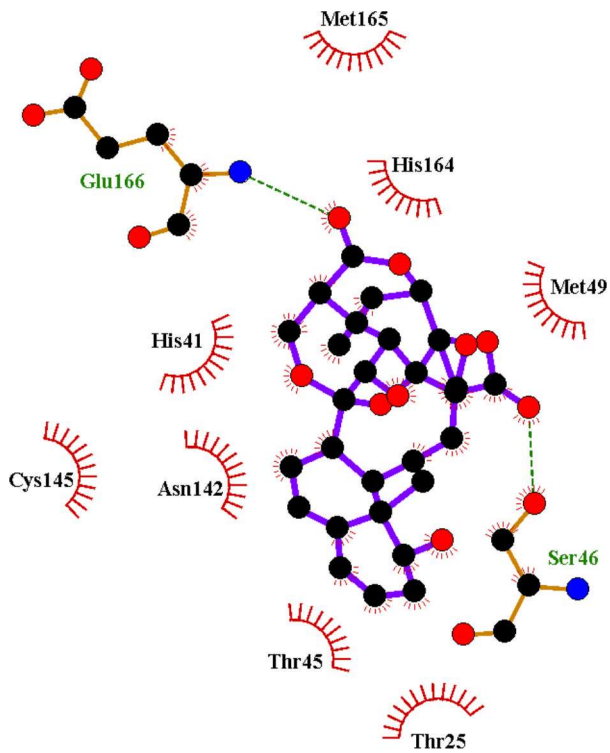
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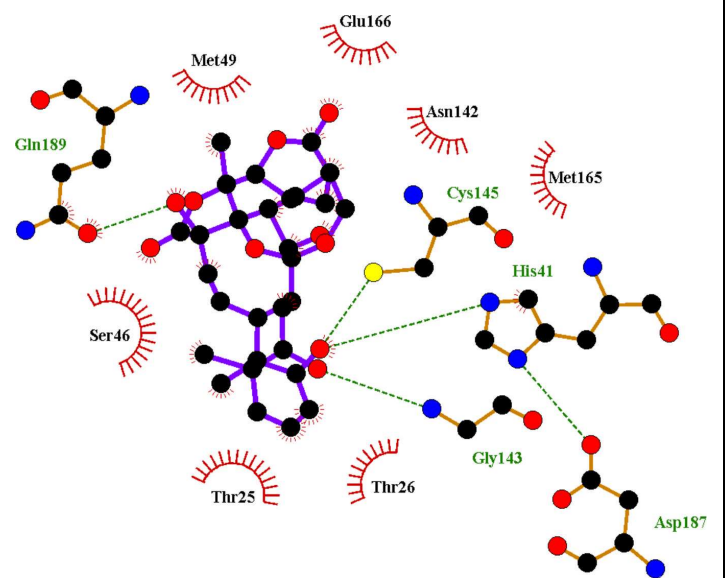
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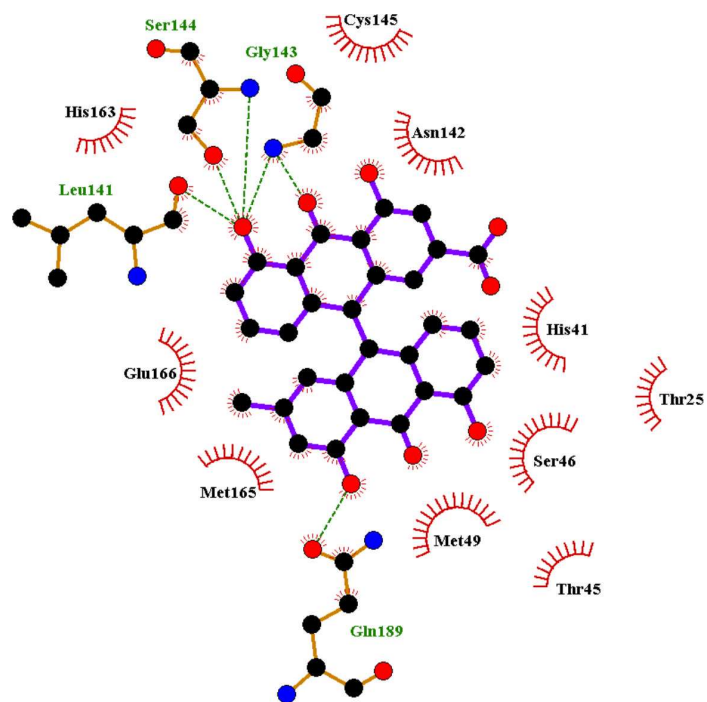
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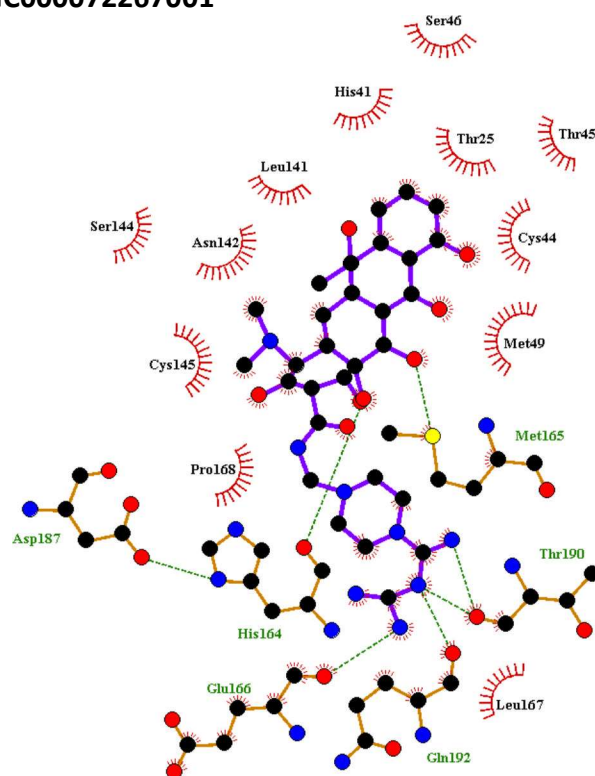
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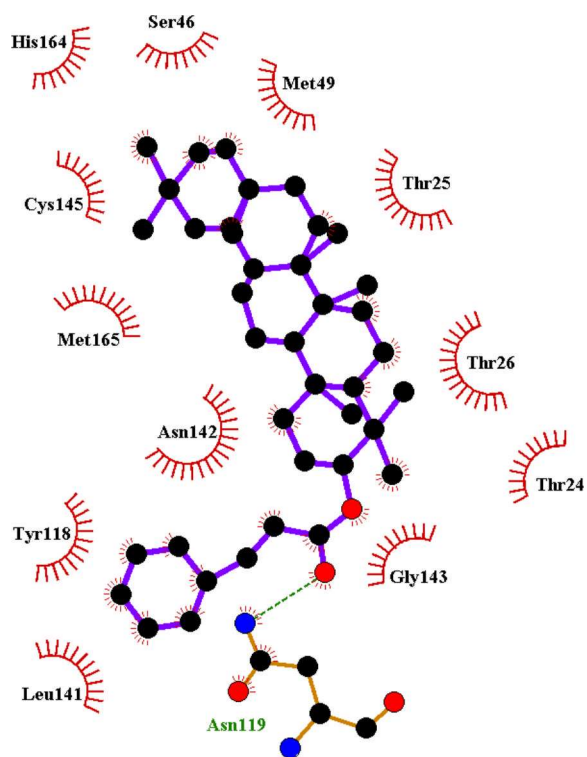
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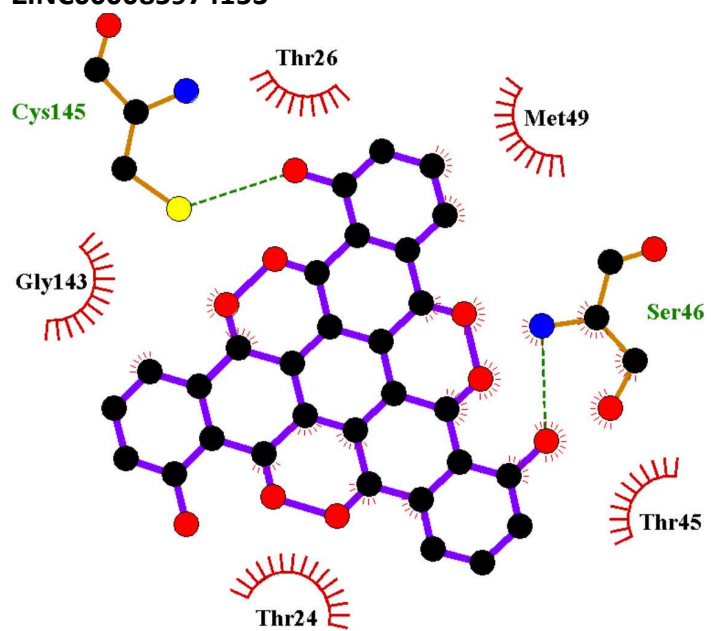


Table S3. The obtained values of the molecular docking and FPL simulations.

N ^o	ZINC ID	Name	ΔG_{Dock}^a	F_{Max}^b	W^c	$\Delta G_{\text{FPL}}^{\text{Pre d}}$
1	ZINC000253599724	Asparagoside A	-8.9	534.1 ± 41.0	61.9 ± 3.8	-8.96
2	ZINC000100774275	Rubroskyrin	-9.0	579.1 ± 30.2	60.9 ± 3.5	-8.91
3	ZINC000004215844	Etamestrol	-9.0	560.6 ± 39.0	59.5 ± 4.3	-8.83
4	ZINC000085537129	Penimocycline	-8.9	569.8 ± 25.6	58.0 ± 3.1	-8.75
5	ZINC000100774279	Deoxyrubroskyrin	-9.2	582.1 ± 32.9	57.7 ± 5.6	-8.73
6	ZINC000100777465	Physalin G	-9.2	637.5 ± 43.4	57.6 ± 4.2	-8.72
7	ZINC000113198271	Altiratinib	-8.9	533.4 ± 25.1	57.2 ± 3.3	-8.70
8	ZINC000085488845	Bisodiospyrin	-9.6	559.1 ± 38.9	56.9 ± 4.2	-8.69
9	ZINC000095564635	Afoxolaner	-8.9	485.8 ± 29.1	56.8 ± 4.0	-8.68
10	ZINC000100772783	Asticolorin A	-9.3	596.3 ± 33.8	56.7 ± 2.5	-8.68
11	ZINC000100826921	Rheidin A	-9.8	608.3 ± 24.5	55.1 ± 1.9	-8.59
12	ZINC000051951668	R428	-9.0	550.1 ± 28.3	54.9 ± 2.4	-8.57
13	ZINC000100822646	Palmidin C	-9.9	604.0 ± 24.7	54.0 ± 2.5	-8.53
14	ZINC000004214742	Undefined	-9.1	512.6 ± 23.5	53.9 ± 3.2	-8.52
15	ZINC000239329011	Limonin	-9.1	610.3 ± 41.0	53.3 ± 2.5	-8.49
16	ZINC000118937393	2alpha-Hydroxypyraacrenic acid	-9.0	446.6 ± 31.0	53.3 ± 5.3	-8.48
17	ZINC000103941727	Physalin B	-9.0	578.8 ± 19.5	53.1 ± 1.8	-8.47
18	ZINC000043061730	Flocoumafen	-9.0	550.8 ± 14.7	53.0 ± 2.4	-8.47
19	ZINC000256421903	Asperagenin	-9.0	589.6 ± 43.0	52.2 ± 3.0	-8.42
20	ZINC000150353464	7-Epizucchini Factor A	-9.1	561.3 ± 43.5	52 ± 4.2	-8.41
21	ZINC000253527861	Glycyrrhizin	-8.9	513.4 ± 47.2	52 ± 6.2	-8.41
22	ZINC000100772795	Asticolorin B	-8.9	570.4 ± 37.7	51.6 ± 3.3	-8.39
23	ZINC000095619883	Jangomolide	-9.2	590.7 ± 30.5	51.2 ± 2.7	-8.37
24	ZINC000100822774	Palmidin B	-9.2	567.3 ± 30.7	50.9 ± 2.5	-8.35
25	ZINC000100783375	25,27-Dihydro-4,7-didehydro-7-deoxyphysalin A	-9.1	571.5 ± 18.1	50.5 ± 1.7	-8.33
26	ZINC000100783373	4,7-Didehydroneophysalin B	-9.7	591.2 ± 54.3	50.4 ± 6.8	-8.32

27	ZINC000261496785	Chaetoglobosin N	-9.2	549 ± 29.9	49.6 ± 2.1	-8.28
28	ZINC000100826926	Rheidin C	-9.9	568.6 ± 42.4	48.8 ± 4.1	-8.23
29	ZINC000100777456	Physalin E	-9.2	487.4 ± 42.0	46.4 ± 3.8	-8.1
30	ZINC000100779057	Corosin	-8.9	502.3 ± 32.9	45.5 ± 2.7	-8.05
31	ZINC000118937472	3-O-p-trans-Coumaroylalphitollic acid	-9.0	449.3 ± 22.7	45.5 ± 2.8	-8.05
32	ZINC000100783384	Isophysalin B	-9.0	509.3 ± 24.4	44.5 ± 2.8	-7.99
33	ZINC000100777392	Physalin H	-9.2	467.4 ± 14.5	44.2 ± 1.9	-7.98
34	ZINC000100782938	Physalin N	-9.4	499.6 ± 38.2	43.9 ± 3.9	-7.96
35	ZINC000150353094	Zucchini Factor B	-9.3	411.8 ± 18.2	42.2 ± 1.7	-7.87
36	ZINC000100783281	Physalin P	-9.1	482.8 ± 19.4	38.9 ± 2.5	-7.84
37	ZINC000070450821	Sennidin C	-9.1	406.0 ± 18.0	38.1 ± 3.1	-7.64
38	ZINC000100826931	Rheidin B	-9.7	450.9 ± 37.5	37.2 ± 4.4	-7.58
39	ZINC000072267001	Guamecycline	-9.4	409.8 ± 41.9	36.7 ± 6.1	-7.56
40	ZINC000100777664	Germanicol Cinnamate	-9.6	389.5 ± 20.9	34.5 ± 2.2	-7.44
41	ZINC000085974153	Trisjuglone	-9.3	406.2 ± 16.0	32.9 ± 2.6	-7.35

^aThe docking affinity was calculated using the Autodock Vina package. ^bThe obtained value of the mean rupture force F_{Max} and ^cthe recorded metric of the pulling work W . ^dThe predicted binding free energy $\Delta G_{\text{FPL}}^{\text{Pre}}$ was attained using Eq. (1). The computed error was the standard error of the average. The unit of energy and force are in kcal mol⁻¹ and pN, respectively.

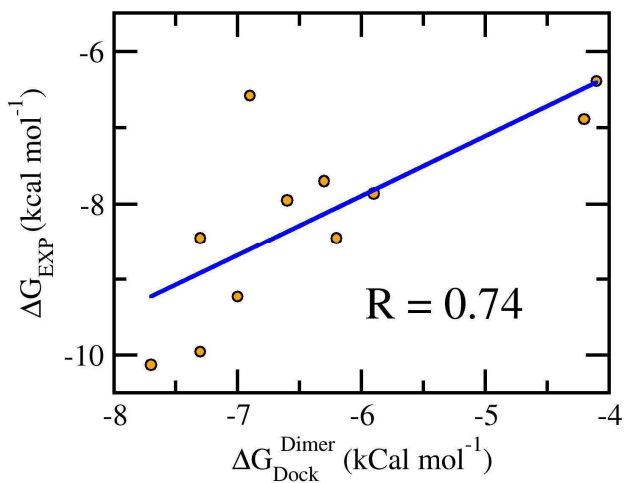
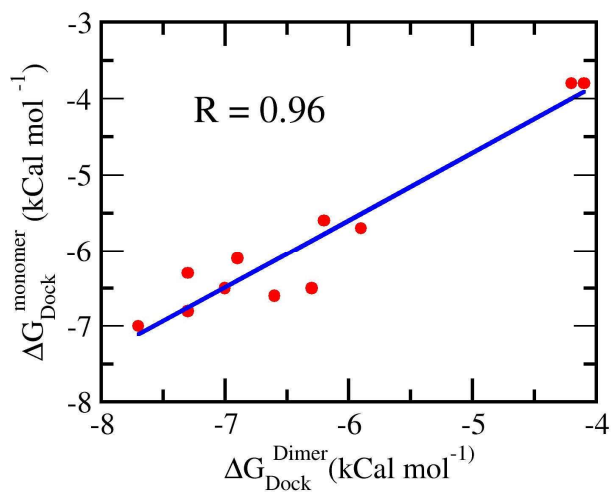
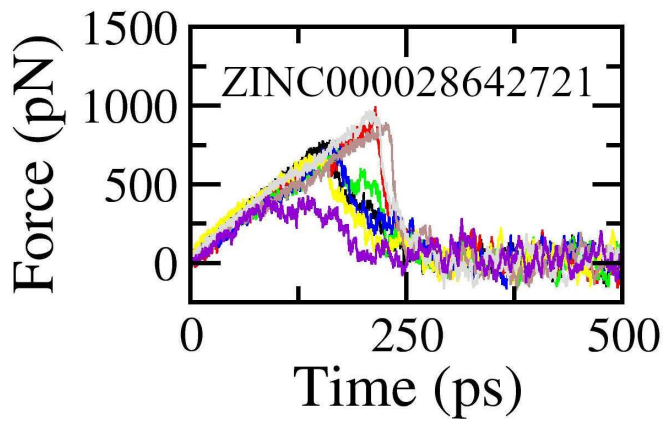
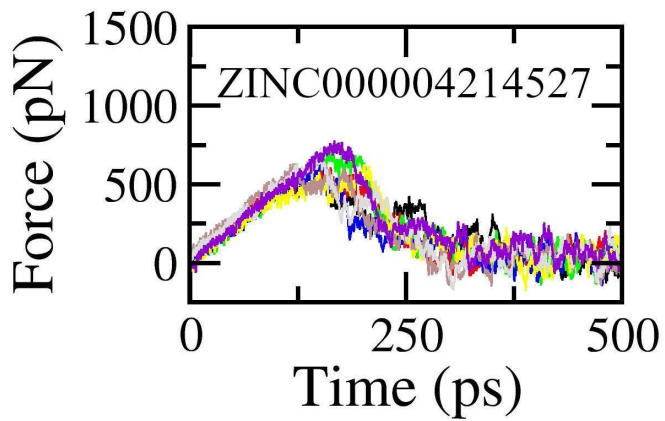
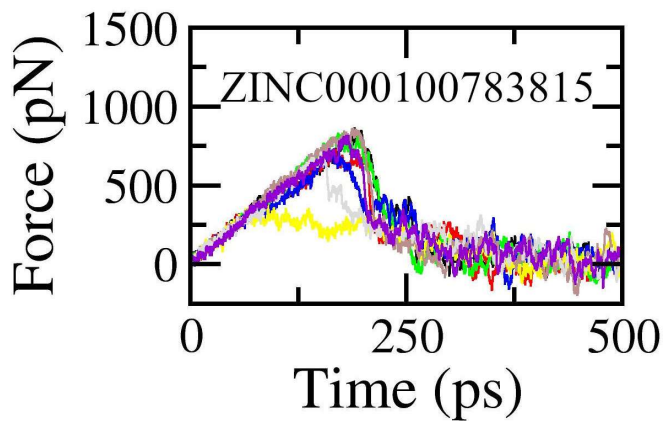
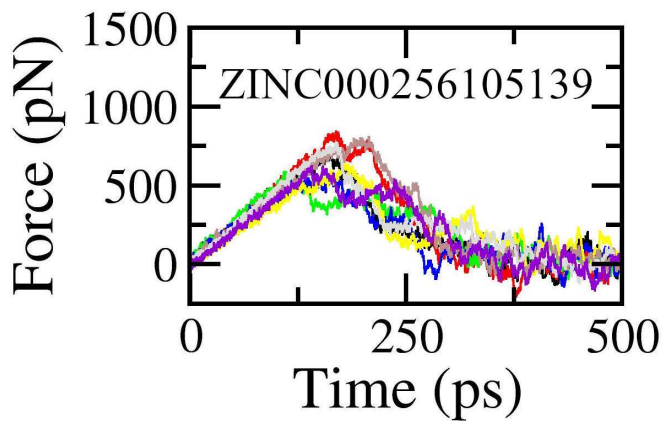
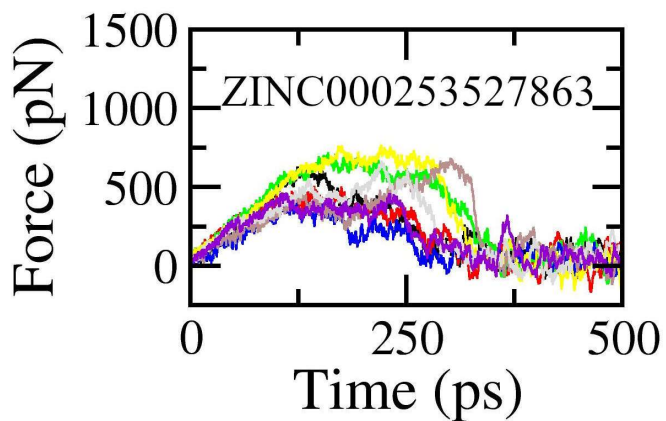
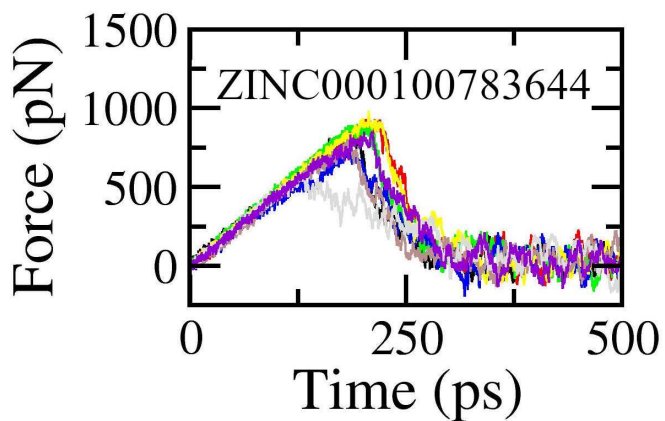
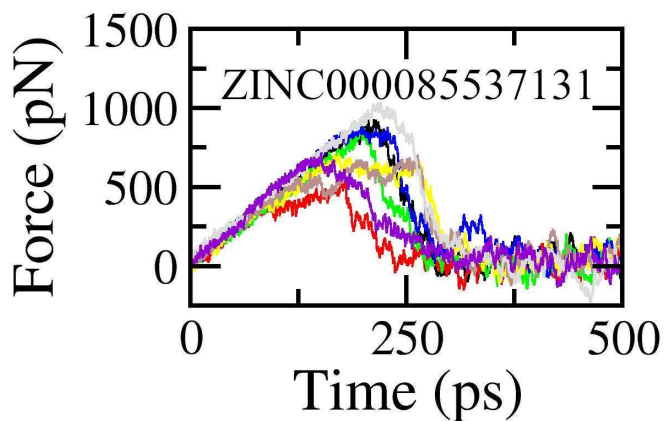
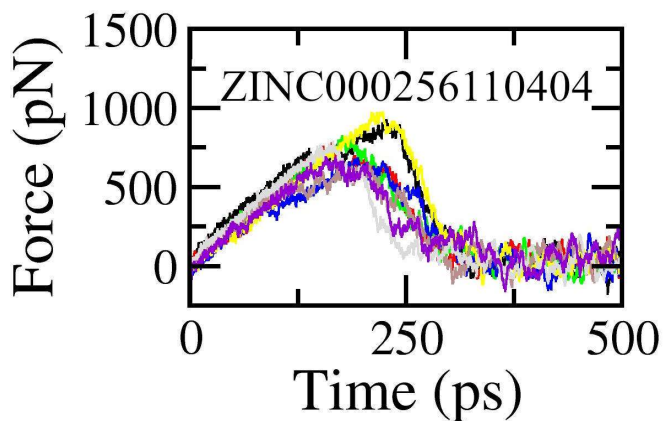
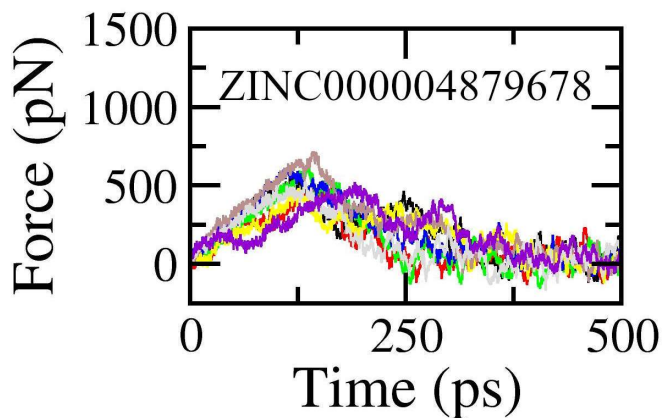
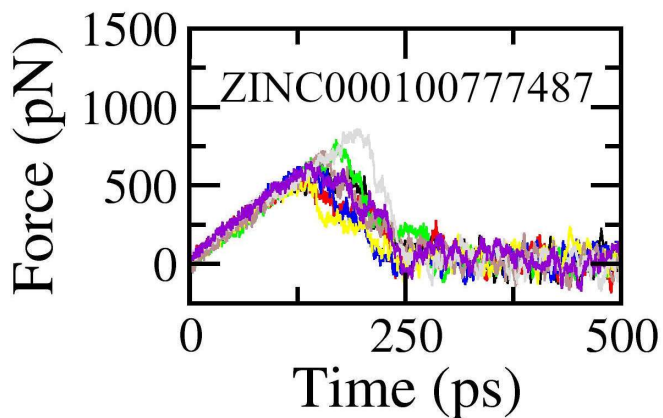
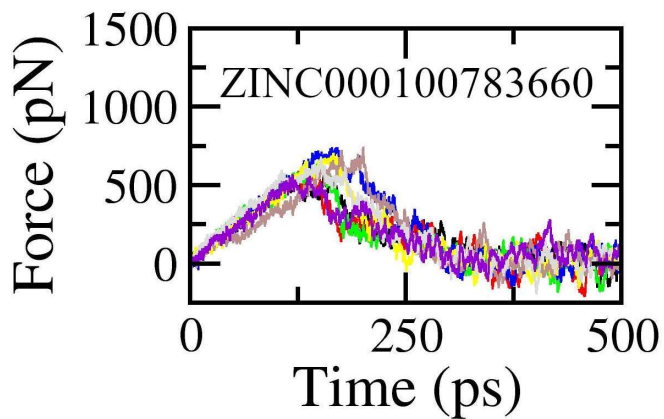
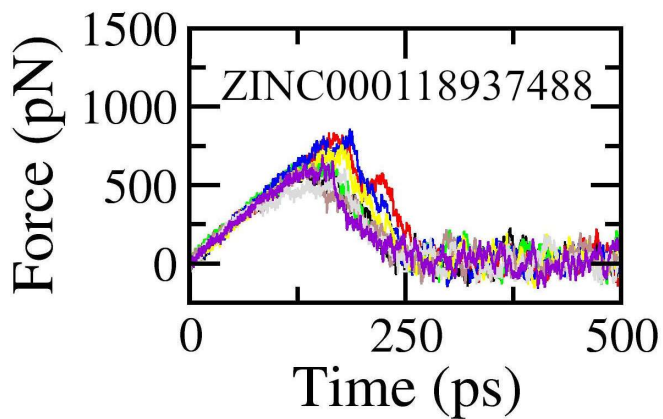
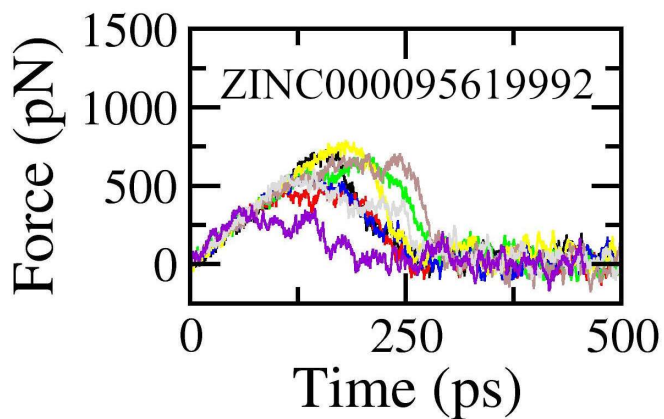
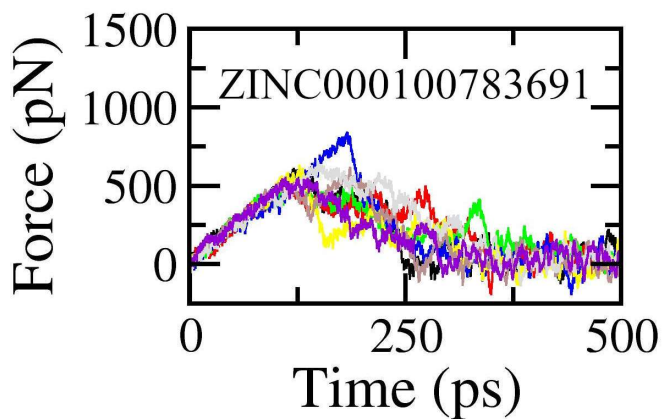
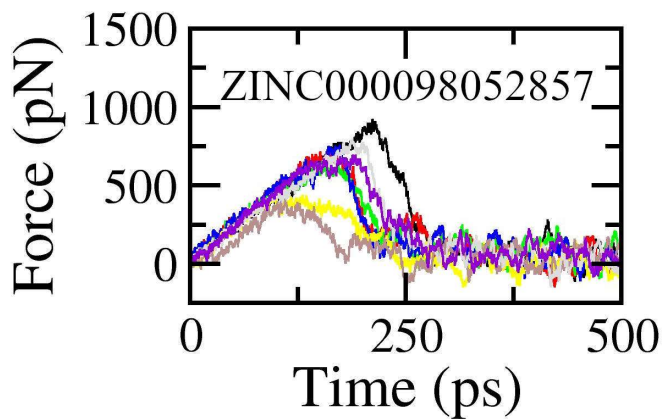
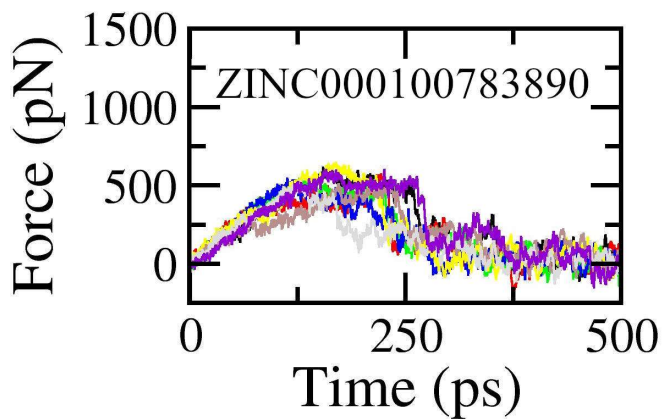
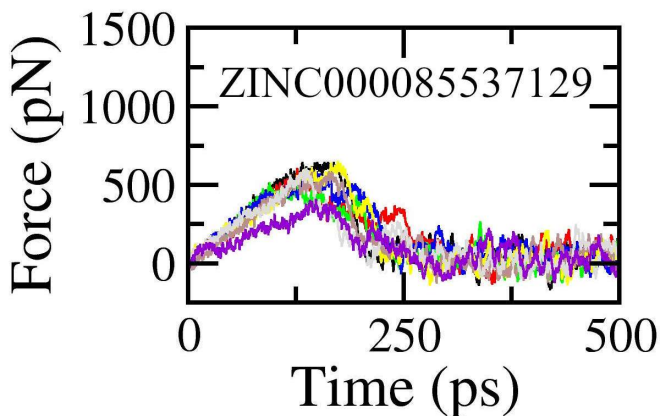
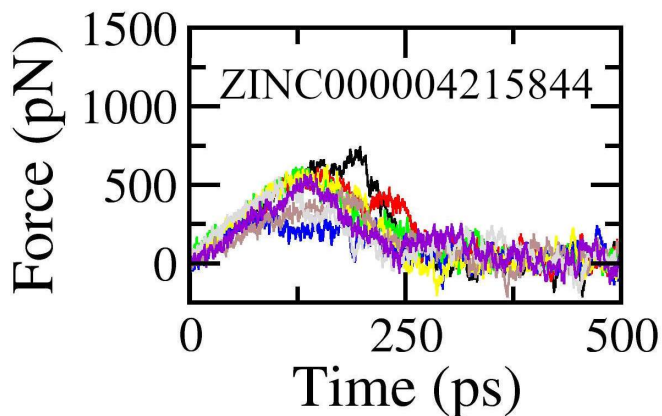
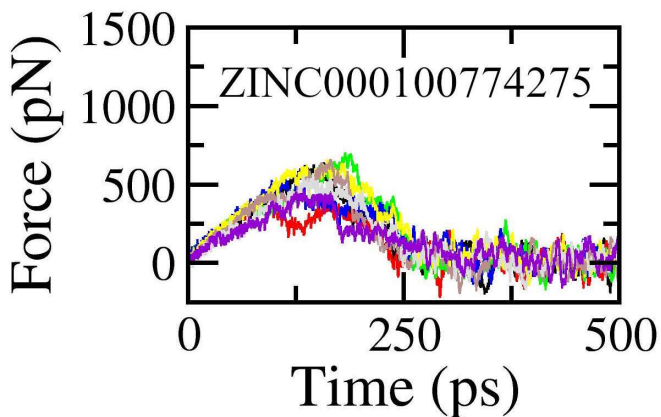
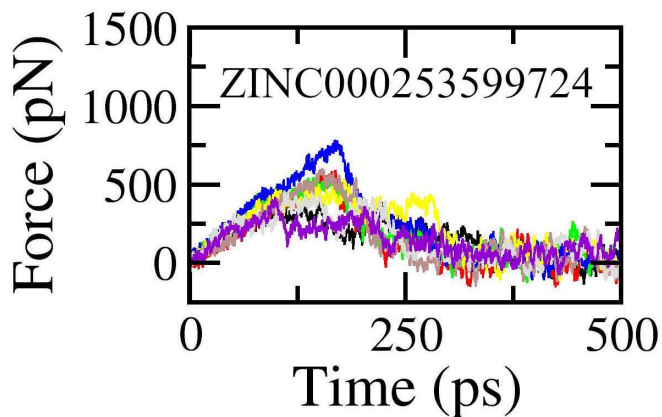
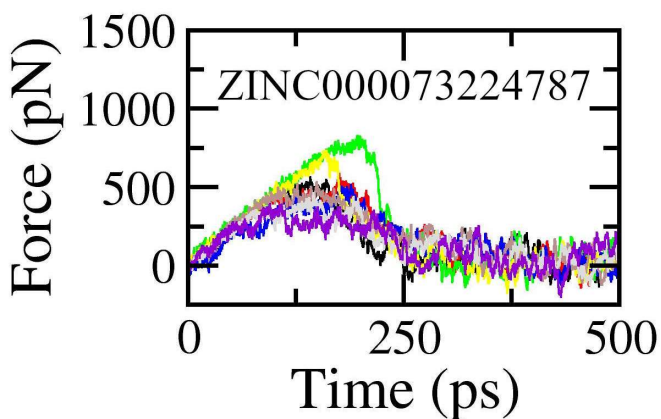
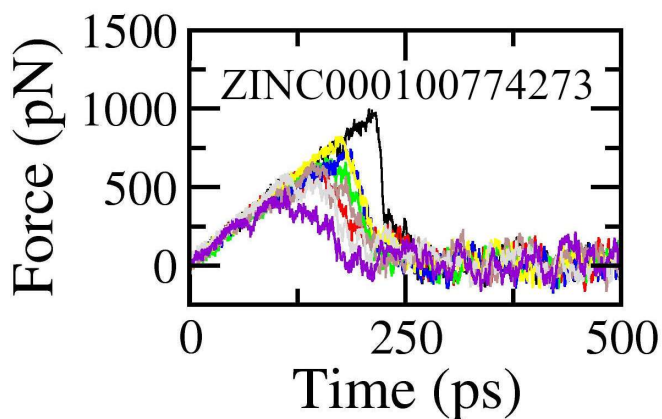
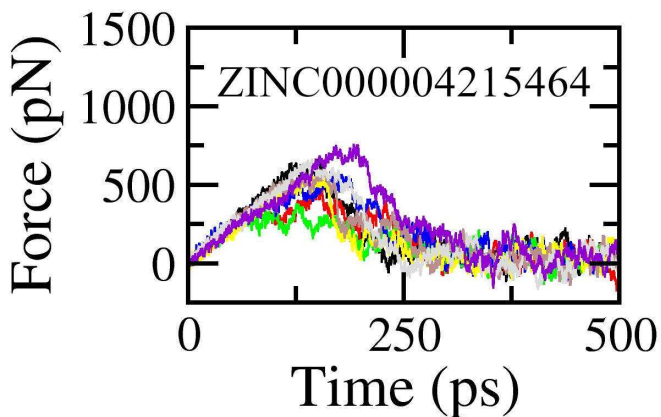
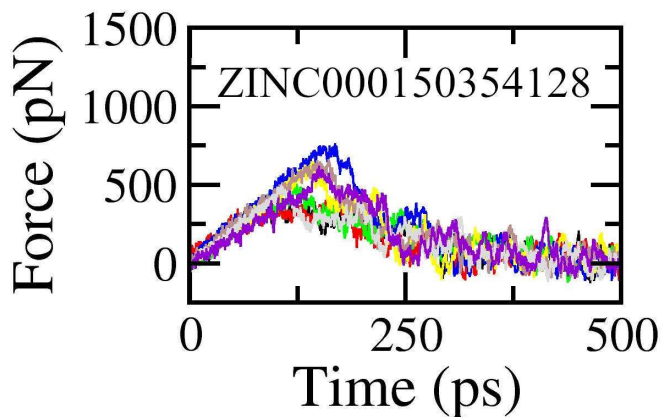
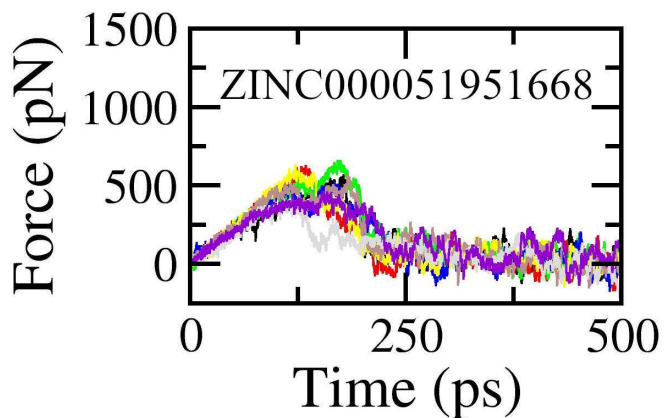
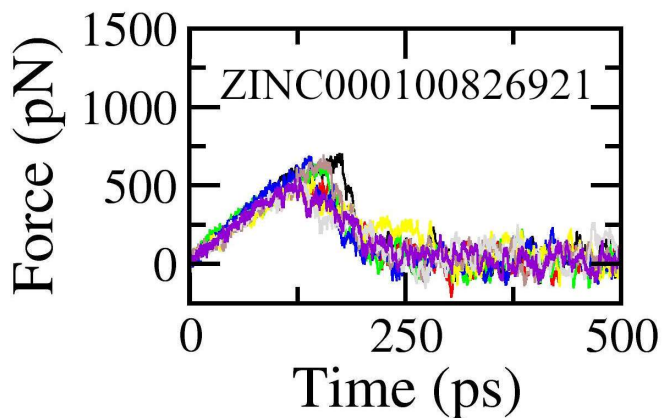
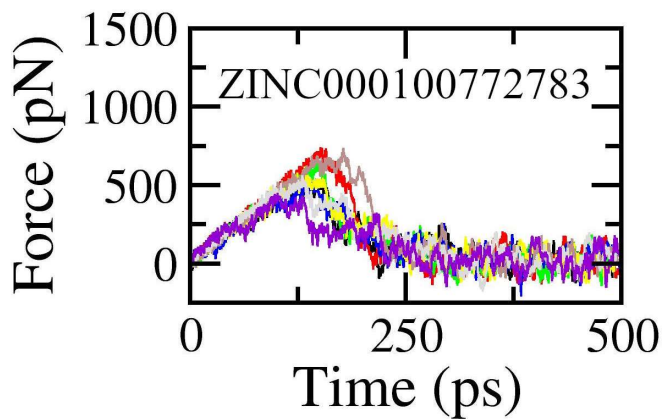
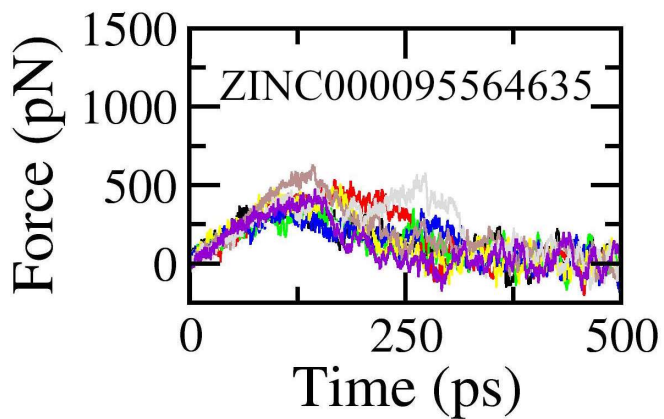
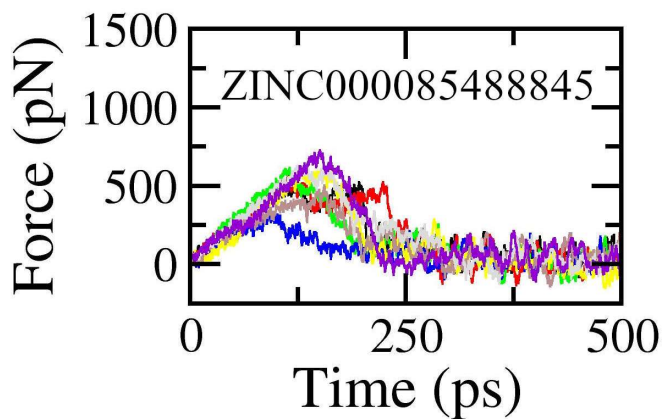
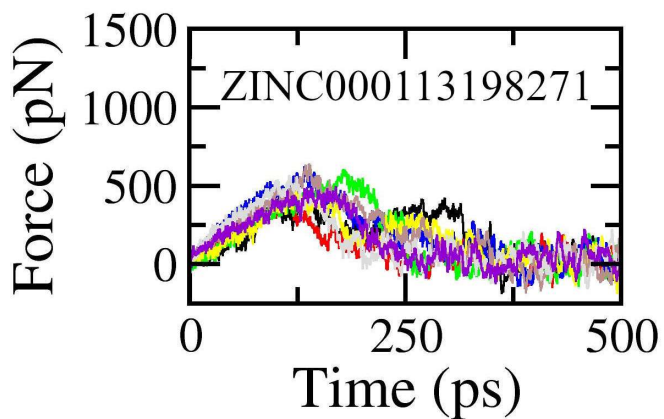
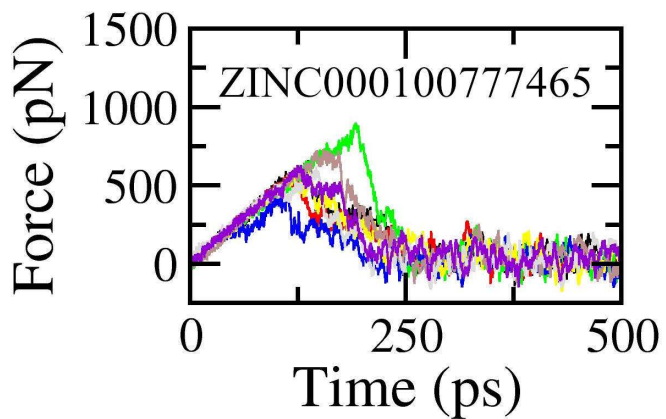
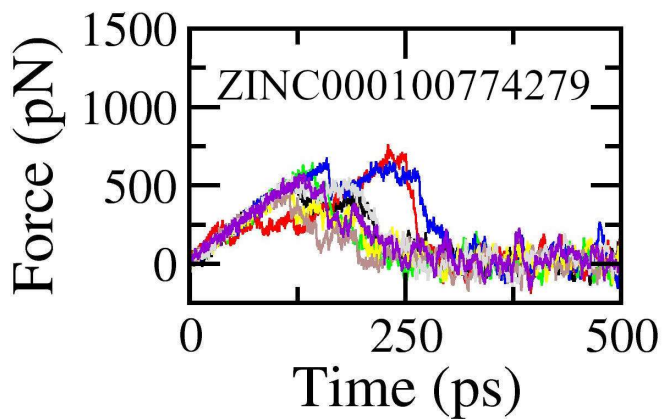


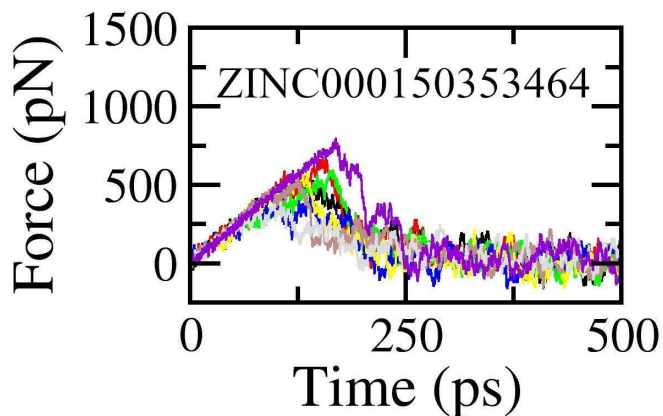
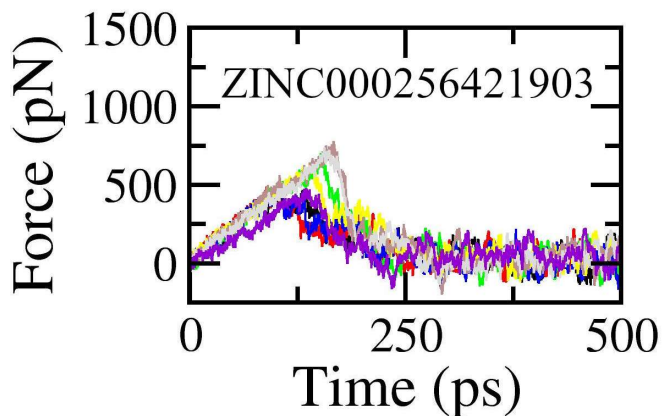
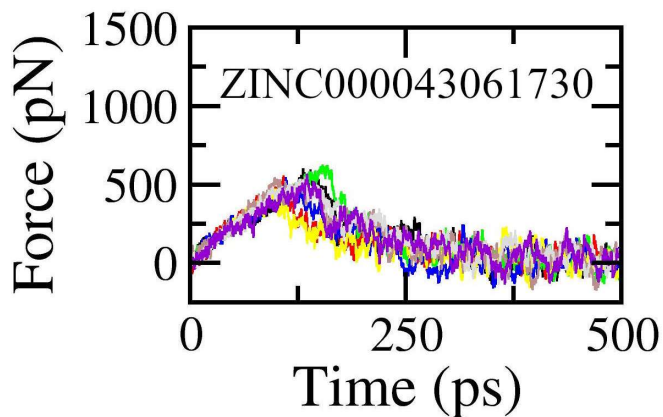
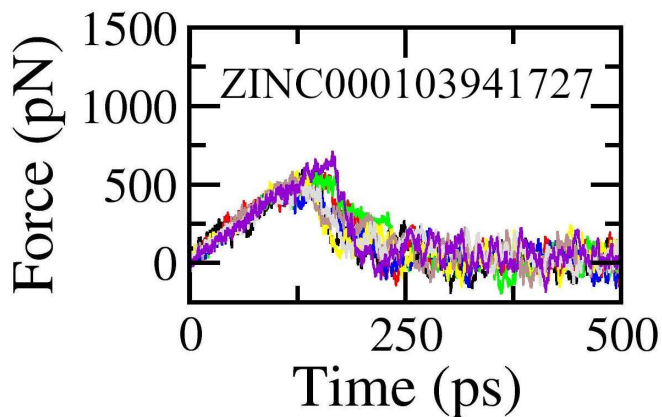
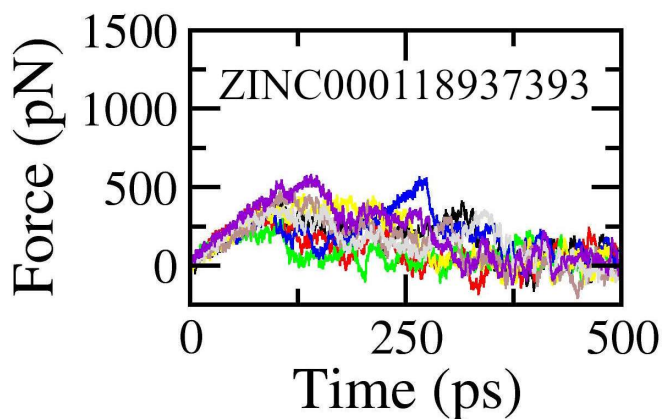
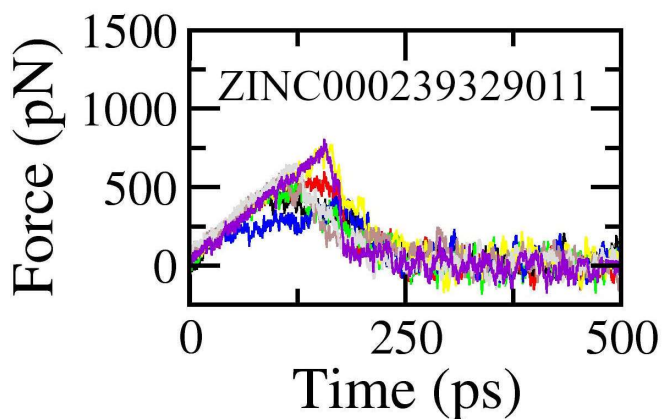
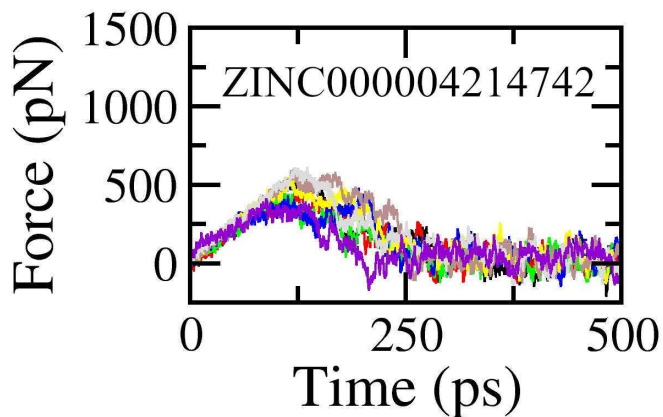
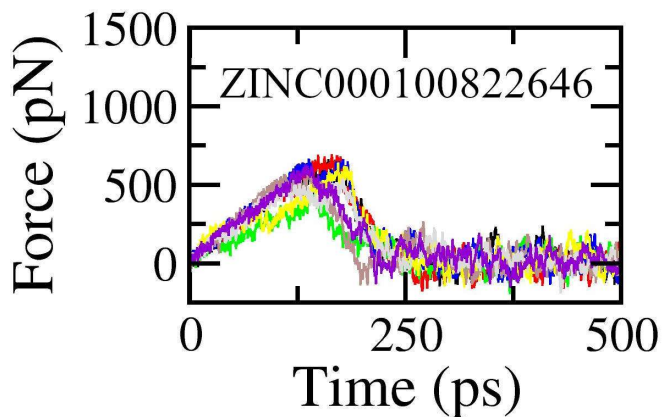
Figure S1. Association between the docking energy $\Delta G_{\text{Dock}}^{\text{monomer}}$ versus $\Delta G_{\text{Dock}}^{\text{Dimer}}$ (left) and $\Delta G_{\text{Dock}}^{\text{Dimer}}$ versus ΔG_{EXP} (right).

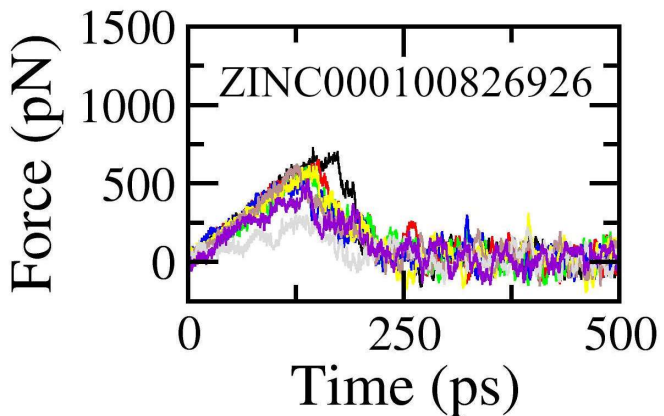
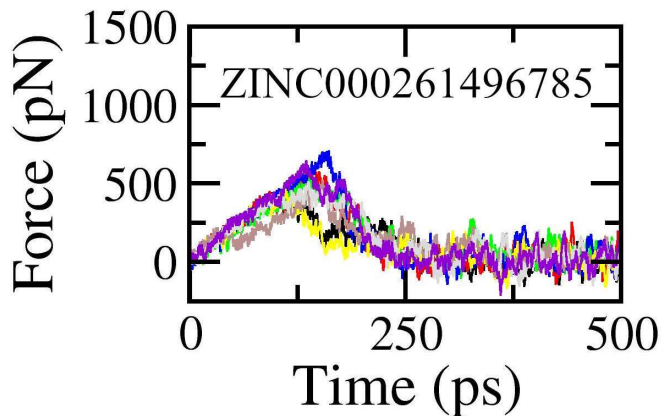
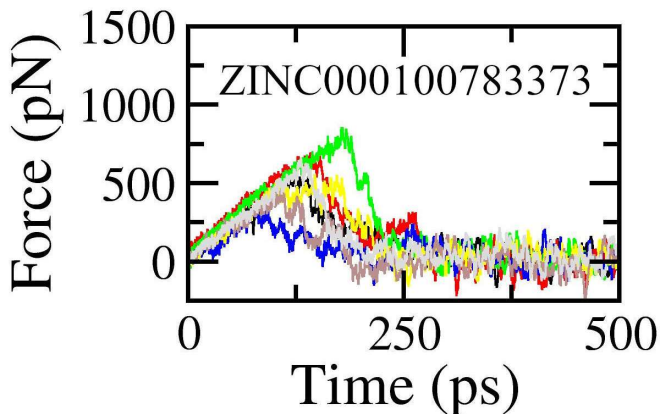
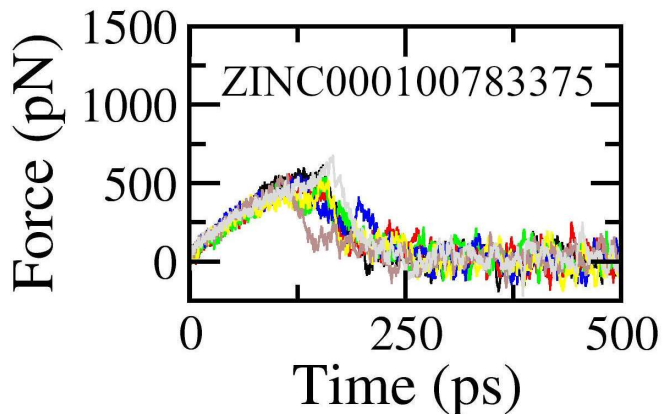
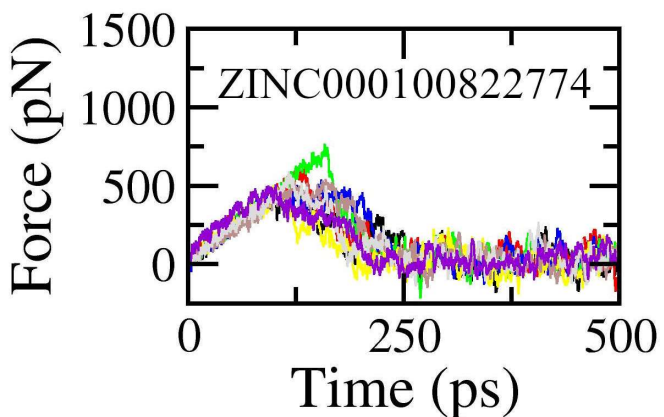
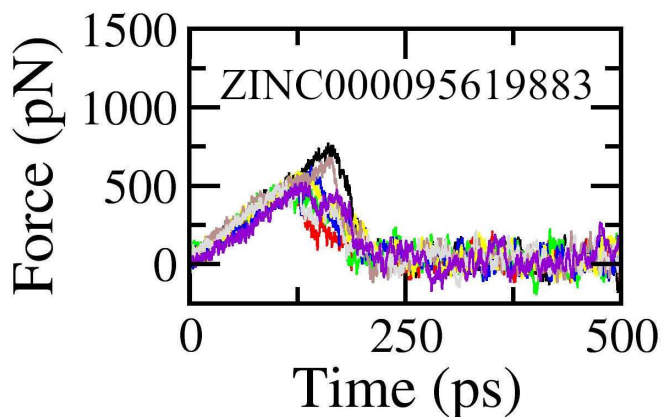
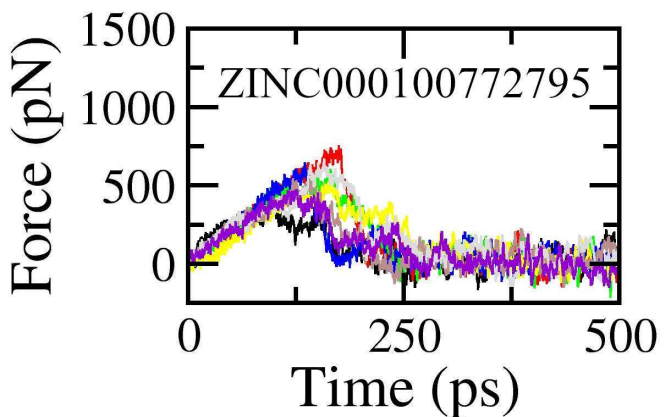
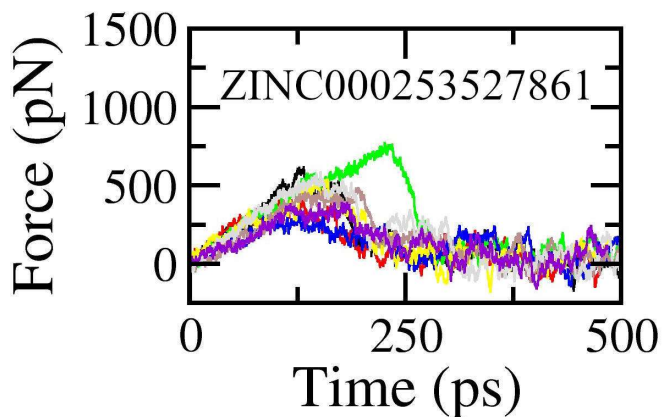


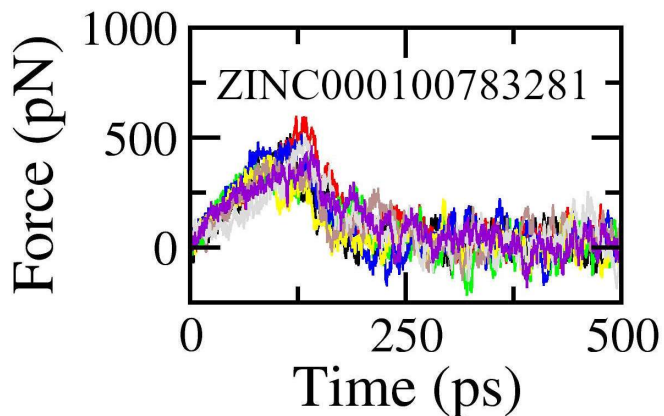
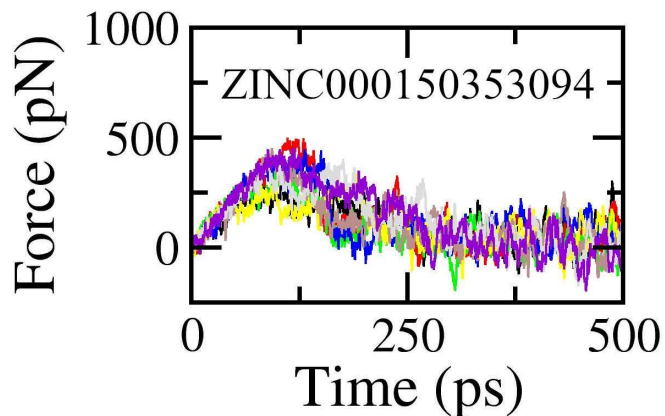
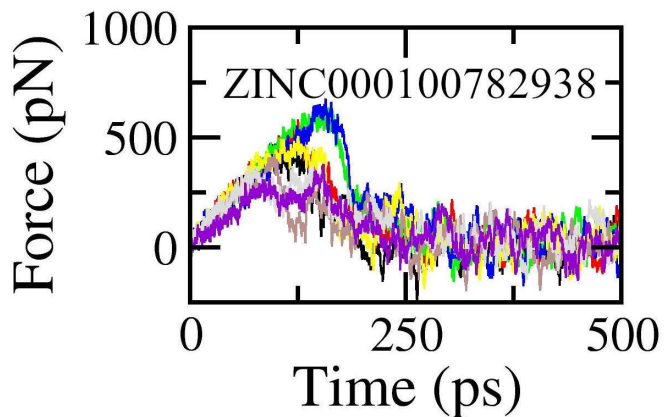
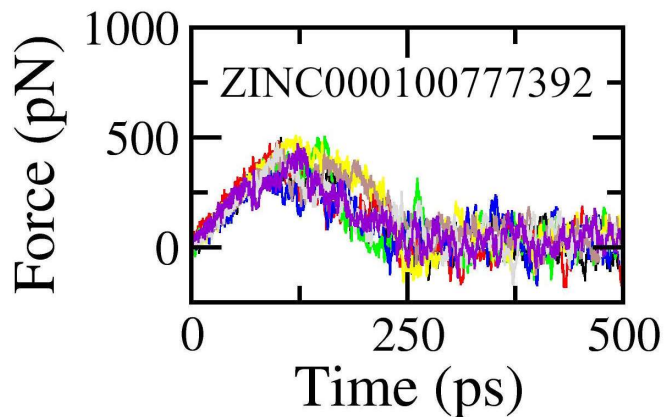
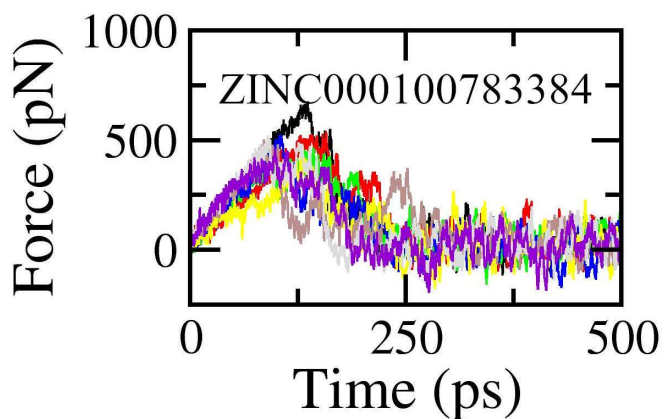
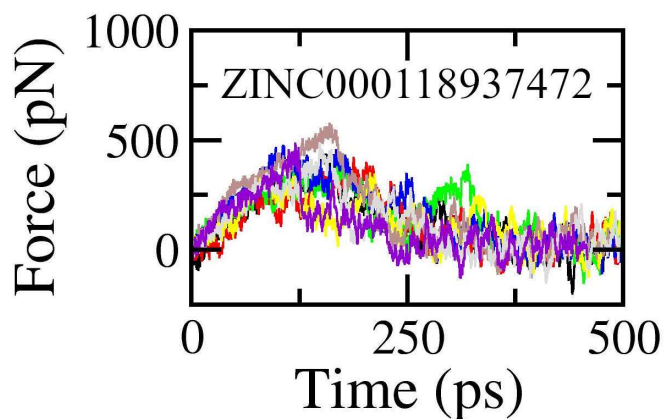
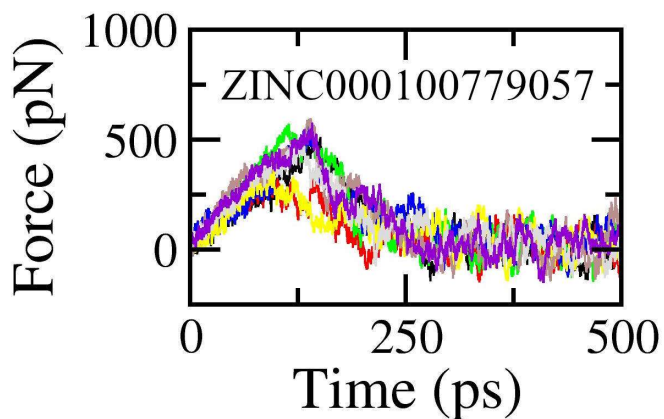
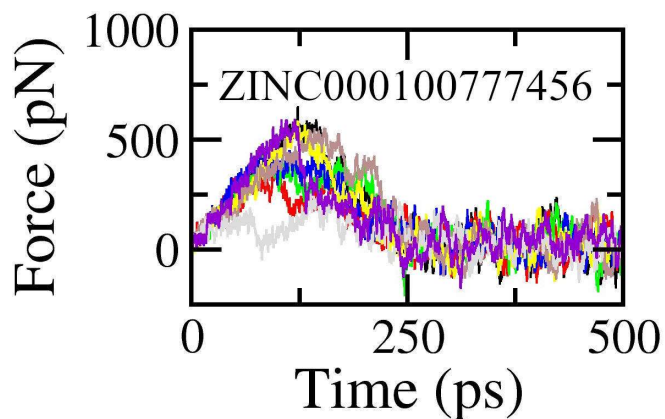












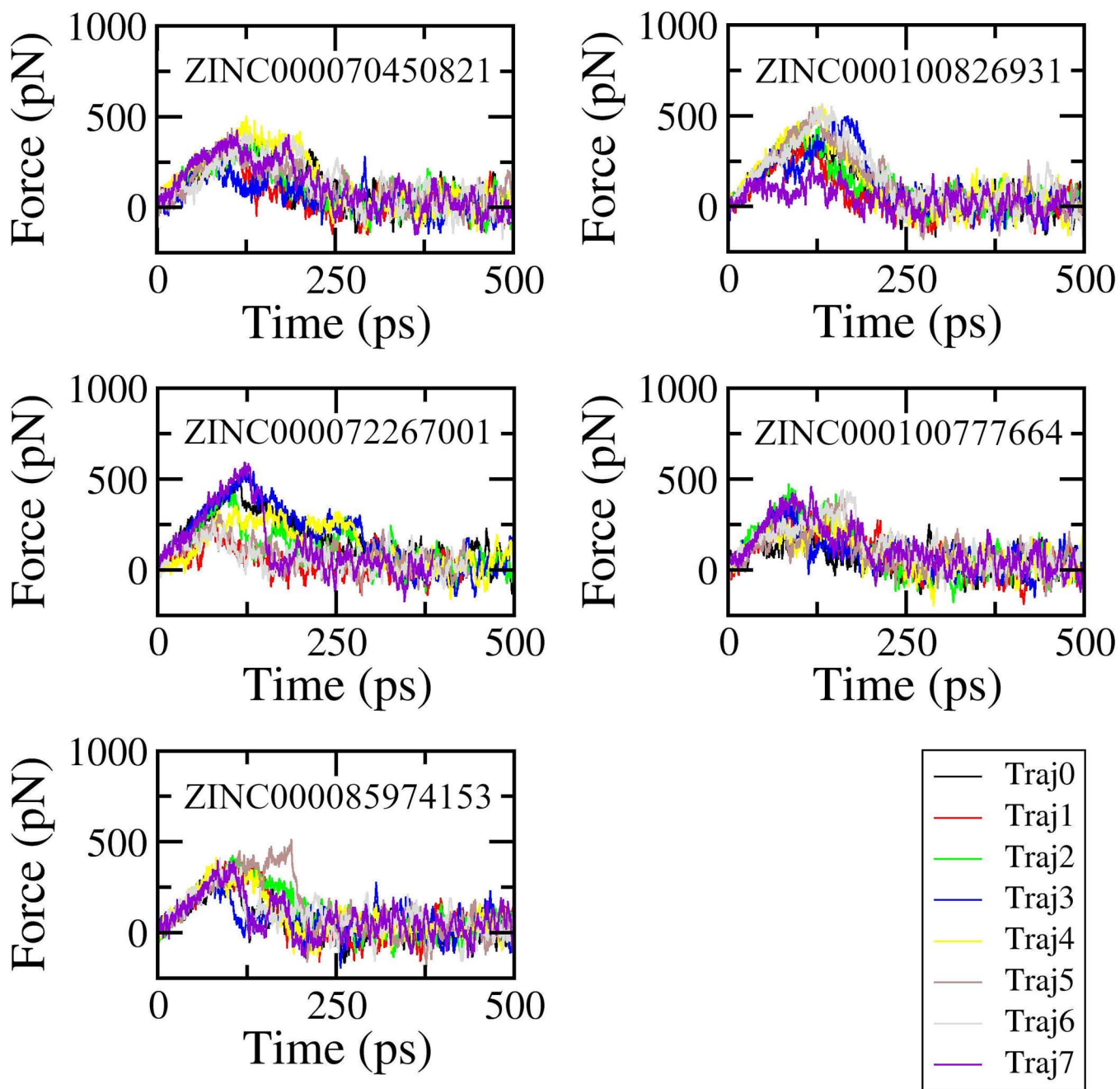


Figure S2. Externally pulling forces in time dependence over 8 independent FPL trajectories.