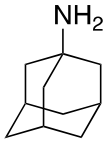
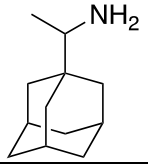
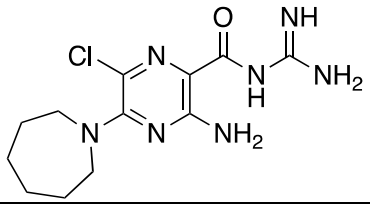
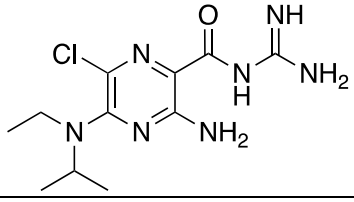
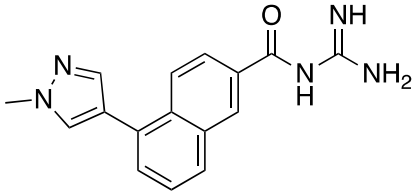
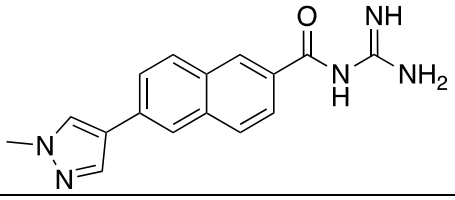
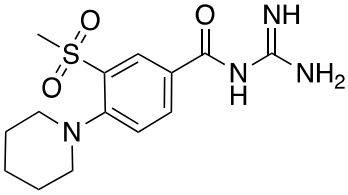
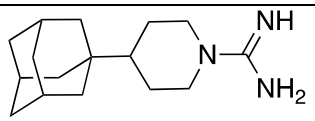
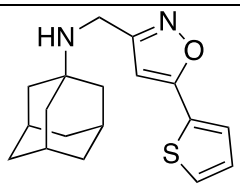
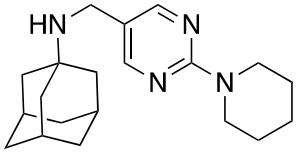
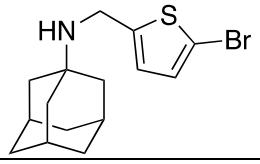
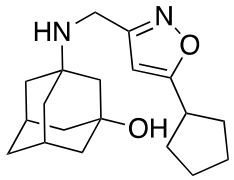
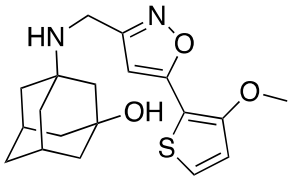
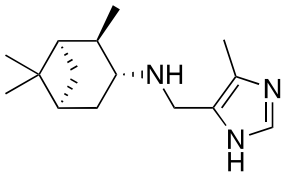
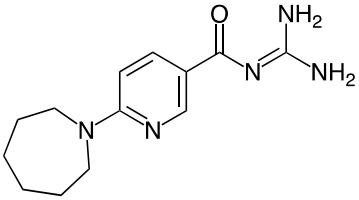
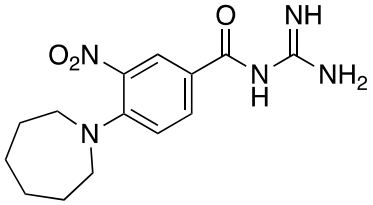
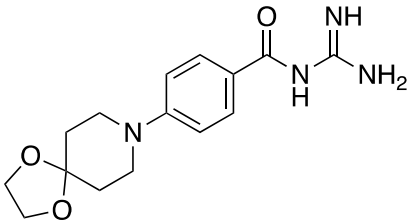
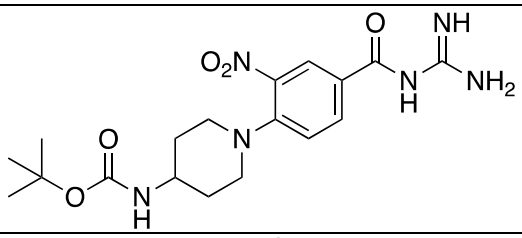
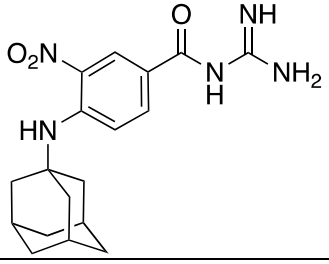
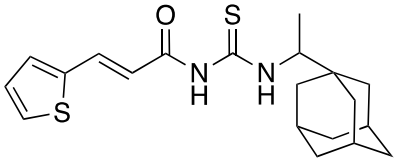
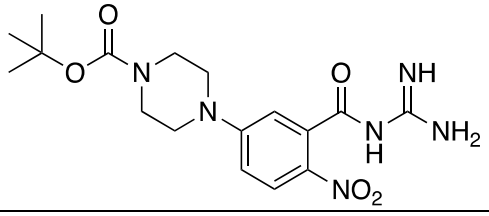
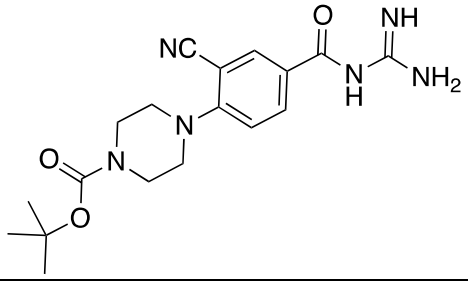
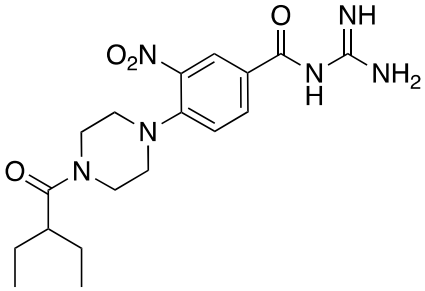
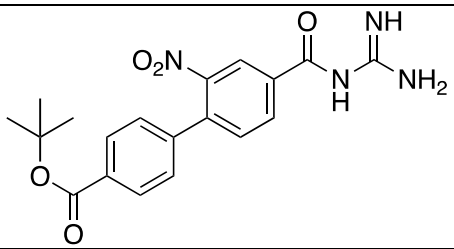
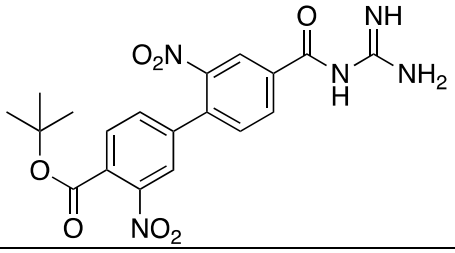
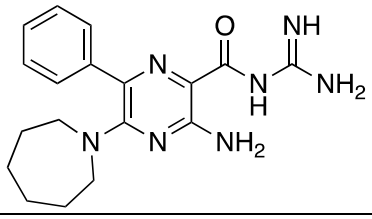
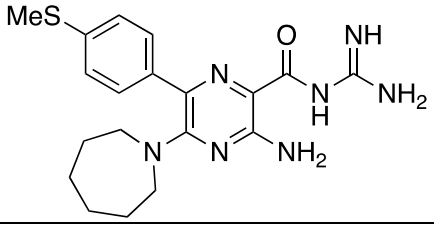
Supplementary Data

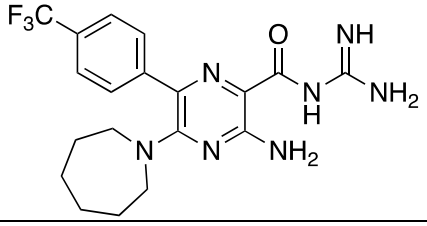
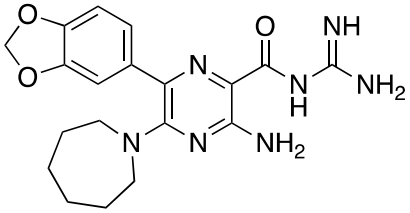
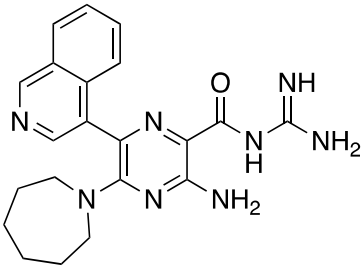
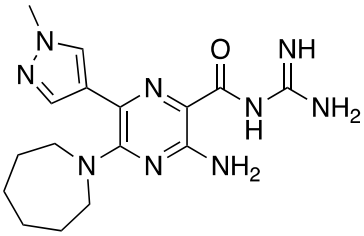
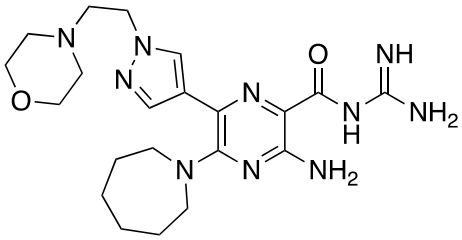
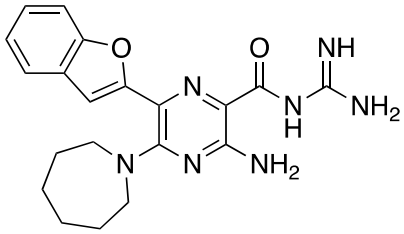
Table S1. The panel of small molecules screened against SARS-CoV-2 E protein.

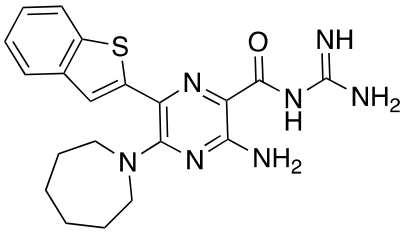
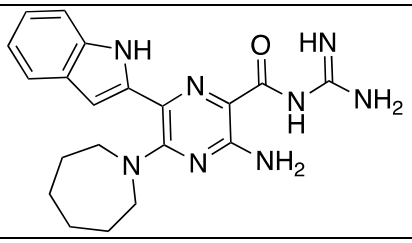
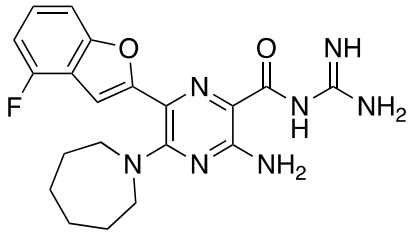
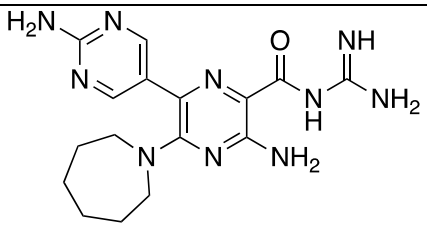
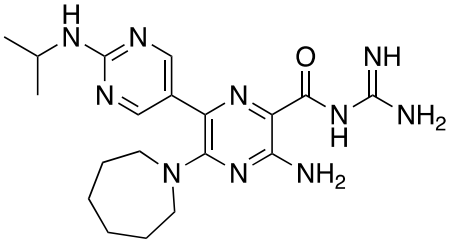
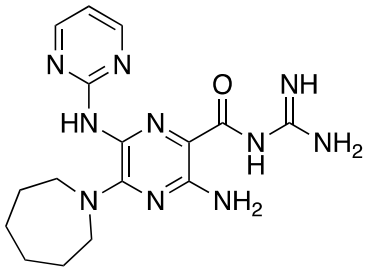
Compound Name/Number	Structure	XP Docking Score	Glide Induced Fit Docking
amantadine		-2.257	-3.995
rimantadine		-3.885	-5.046
HMA		-6.246	-5.326
EIPA		-7.878	-4.905
BIT225 [55]		-4.560	-7.515
BIT314 [55]		-5.445	-7.796
63		-5.664	-5.989

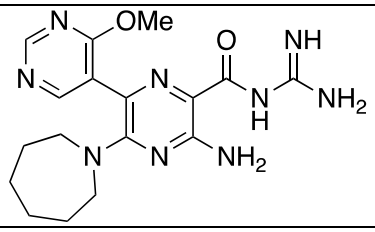
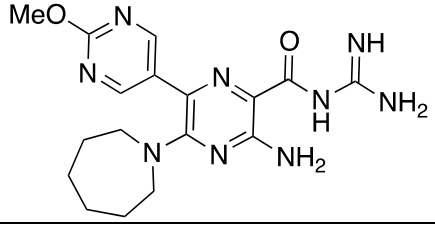
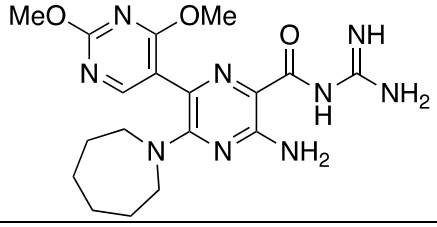
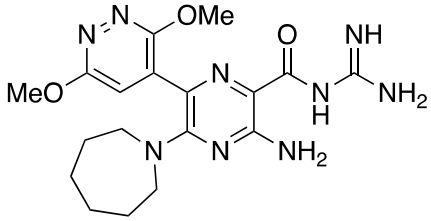
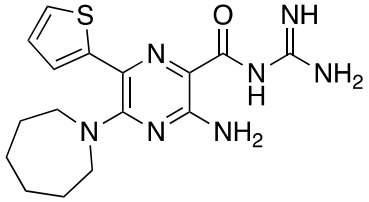
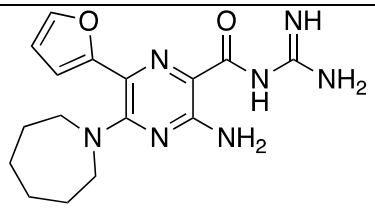
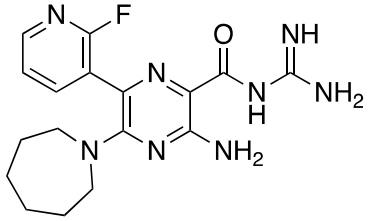
Compound Name/Number	Structure	XP Docking Score	Glide Induced Fit Docking
64 [56]		-7.720	-7.399
M2WJ332 [56]		-5.841	-7.100
69 [56]		-4.543	-6.742
65 [60]		-4.734	-5.842
66 [59]		-5.713	-8.355
67 [57,58]		-5.709	-7.264
68		-4.251	-5.025
9		-5.541	-6.420

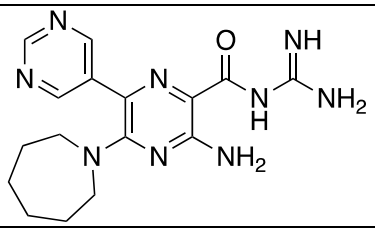
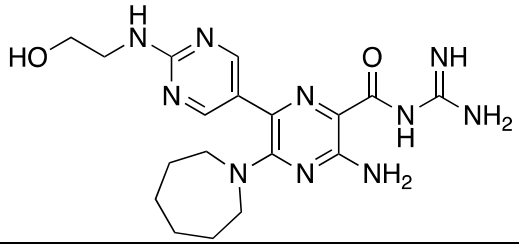
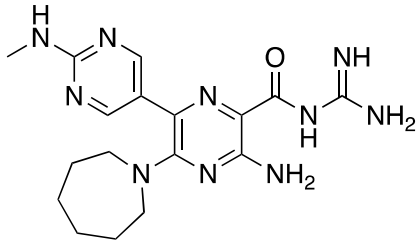
Compound Name/Number	Structure	XP Docking Score	Glide Induced Fit Docking
11		-5.588	N/A
34		-3.711	-6.311
35		-4.201	-6.592
36		-4.894	-5.322
37		-4.769	-8.507
33		-8.201	-5.576

Compound Name/Number	Structure	XP Docking Score	Glide Induced Fit Docking
22		-5.449	-6.643
38		-3.288	-6.280
26		-5.285	-7.397
27		-4.533	-6.353
39		-4.556	-6.591
40		-4.271	-6.871

Compound Name/Number	Structure	XP Docking Score	Glide Induced Fit Docking
41		-2.736	-5.638
42		-4.288	-6.307
43		-4.808	-6.624
44		-3.844	-4.271
45		-3.005	-4.810
46		-2.578	-5.480

Compound Name/Number	Structure	XP Docking Score	Glide Induced Fit Docking
47		-2.936	-5.290
48		-4.403	-5.305
49		-5.020	-6.367
50		-4.105	-7.8
51		-3.214	-3.886
52		-4.531	-6.591

Compound Name/Number	Structure	XP Docking Score	Glide Induced Fit Docking
53		-4.112	-5.539
54		-4.112	-7.129
55		-3.866	-3.198
56		-2.696	-5.785
57		-3.689	-6.810
58		-4.144	-6.359
59		-4.106	-4.791

Compound Name/Number	Structure	XP Docking Score	Glide Induced Fit Docking
60		-4.556	-9.159
61		-5.375	-7.621
62		-4.548	-7.280

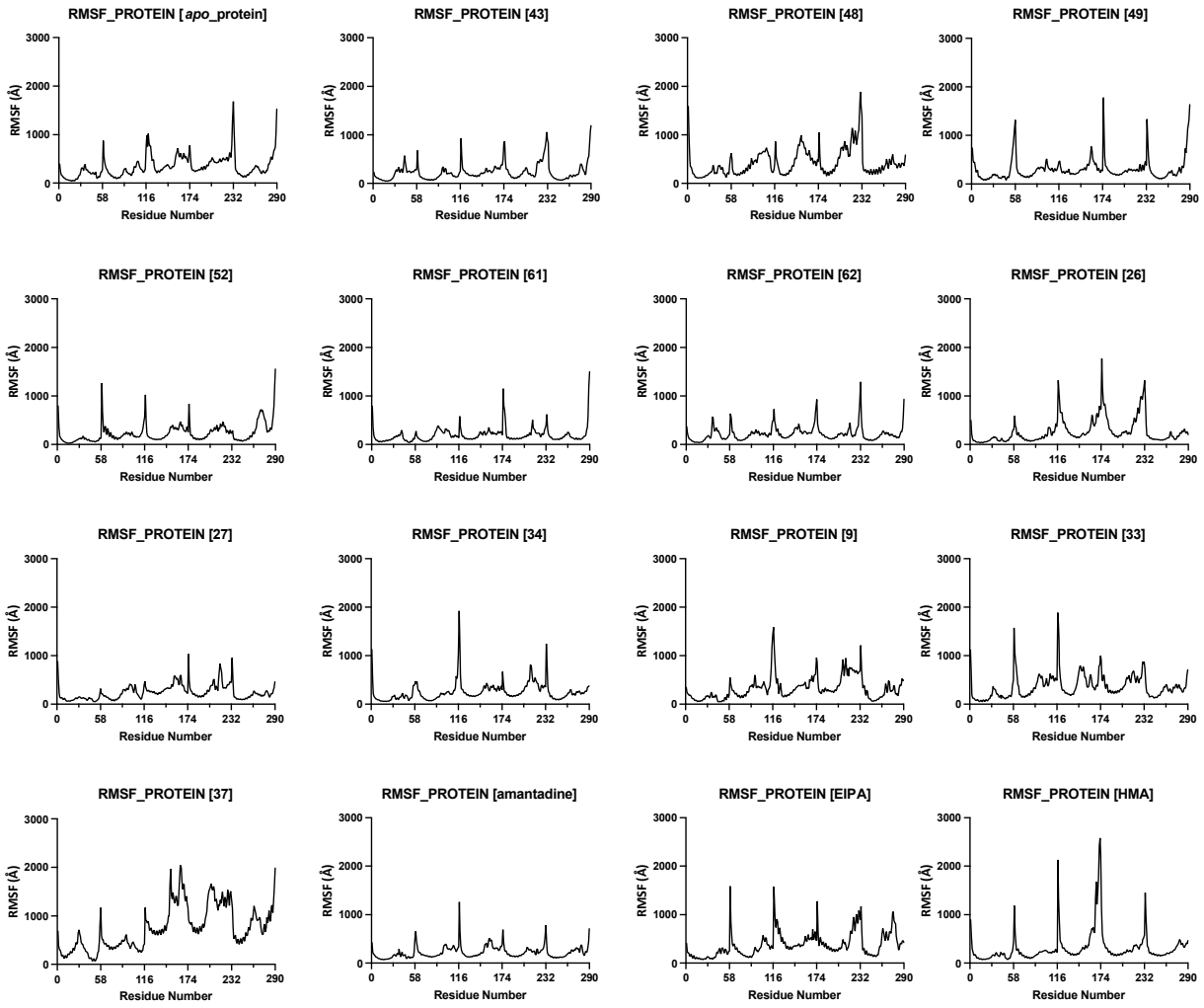


Figure S1. RMSF graphs of the five chains of the protein systems.

The presentation of residue numbers are sequential and the graphs are labelled by the respective bound-ligands. Highest degree of fluctuation observed at the C-terminal end of the TM helix of each monomer within the protein-ligand complex. The number in the graph title refers to the compound number from Table 1.

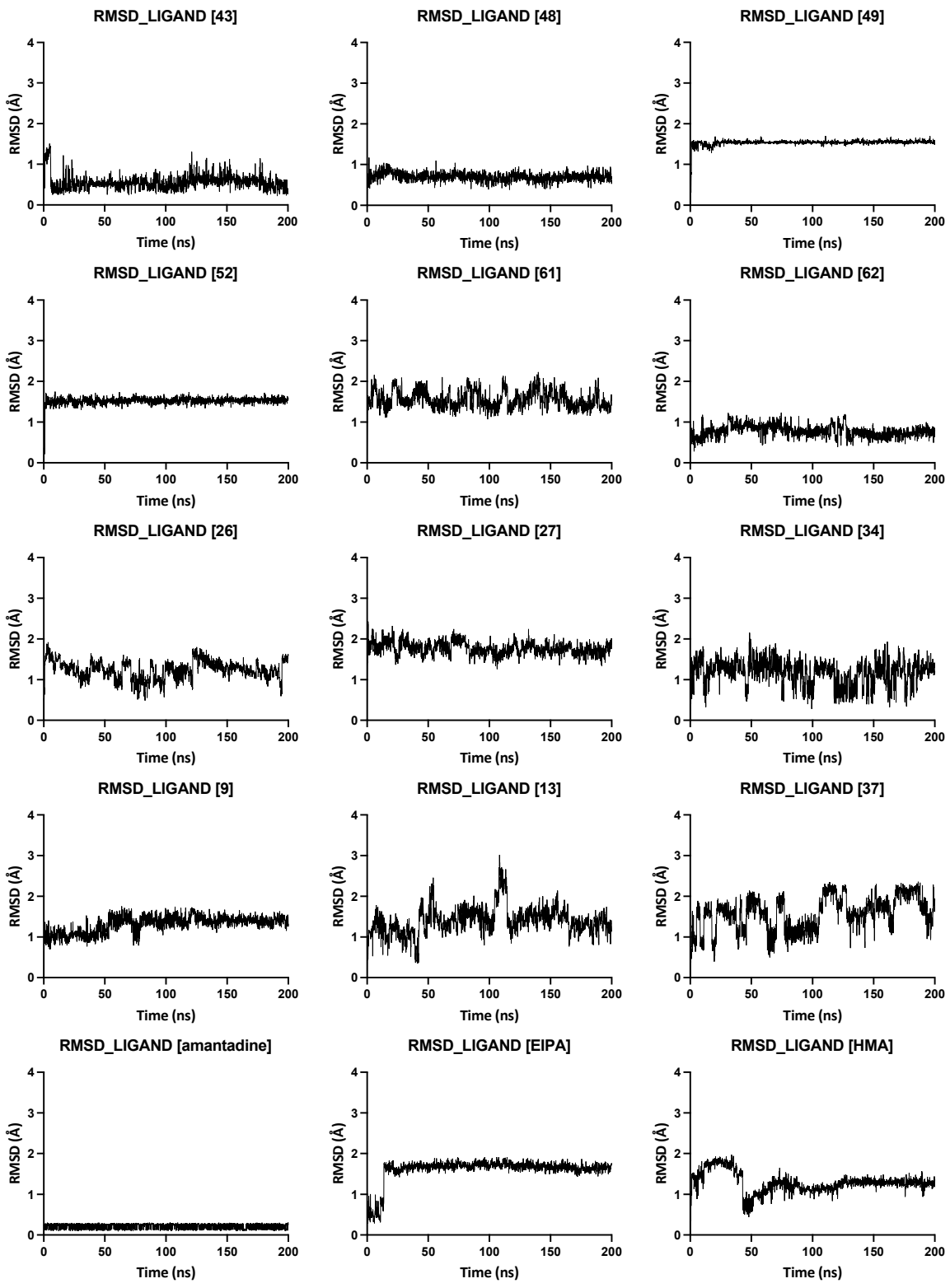


Figure S2. RMSD graphs of the ligands during MD simulations.

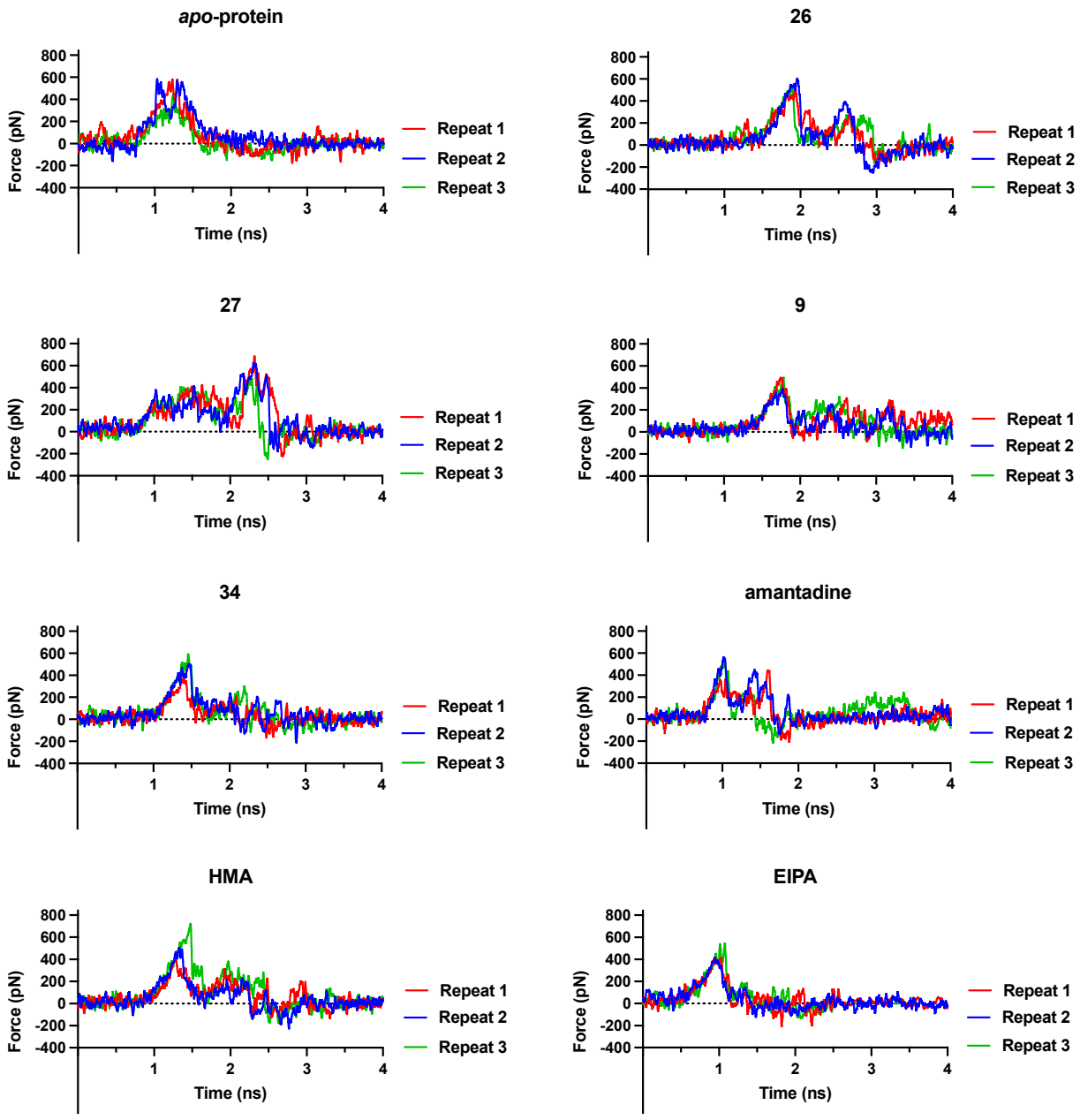


Figure S3. SMD force profile of a sodium ion pulled through the ligand-bound systems.

Three replicates are shown labelled by ligand-bound to each protein.

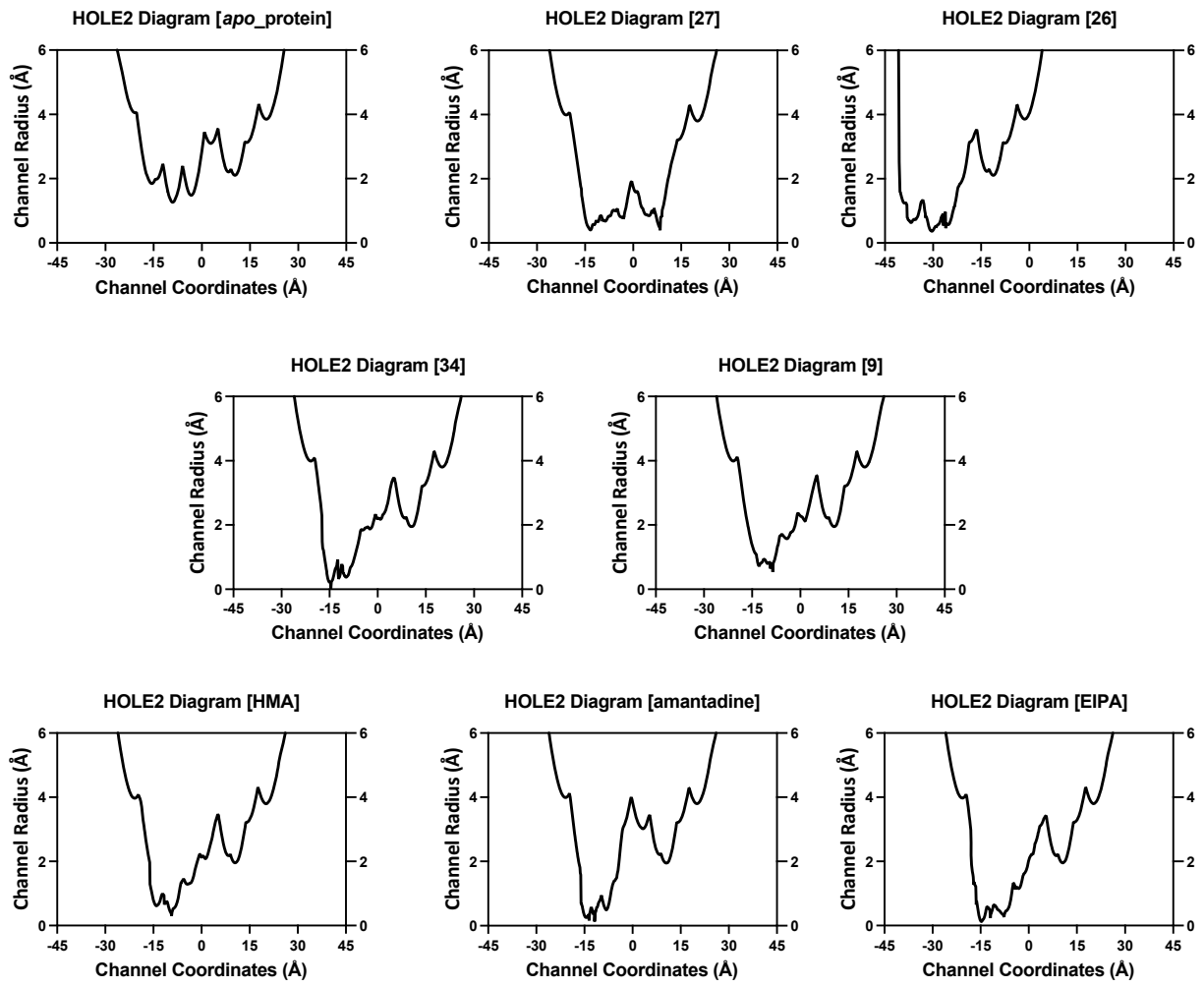


Figure S4. HOLE2 analysis diagram of protein systems bound to ligands.

X-axis represents channel coordinate (Å) and Y-axis shows the channel pore radius (Å) throughout the TMD along Z-axis of the protein. The graphs are titled by the compound number bound to the protein.