Supplementary Data

The Integration of Pharmacophore-Based 3D QSAR Modeling and Virtual Screening in Identification of Natural Product Inhibitors against SARS-CoV-2

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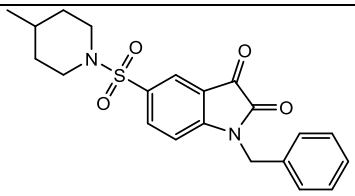
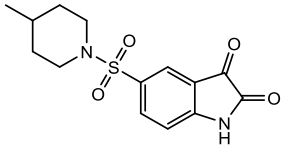
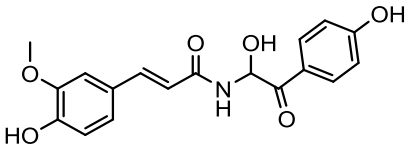
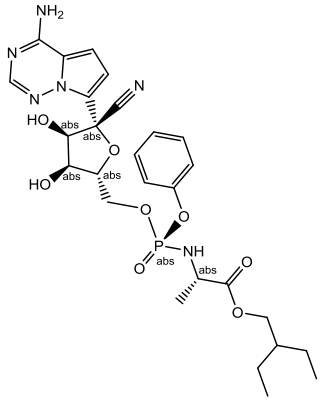
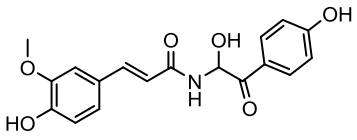
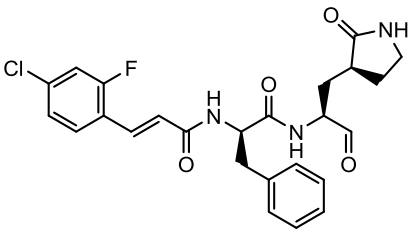
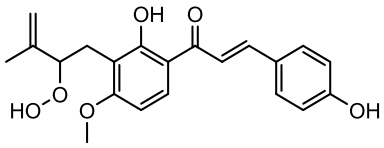
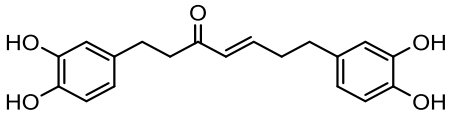
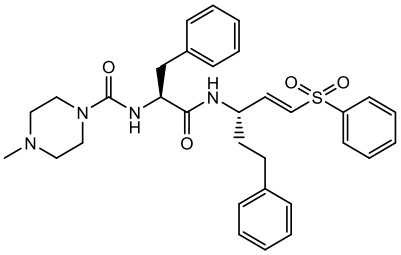
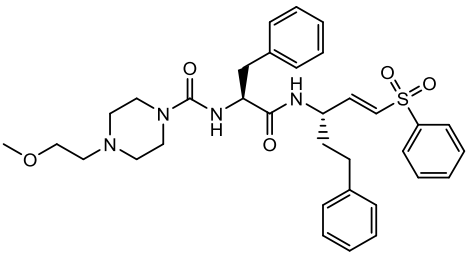
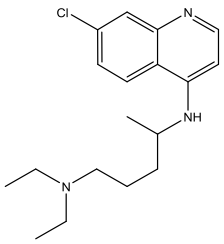
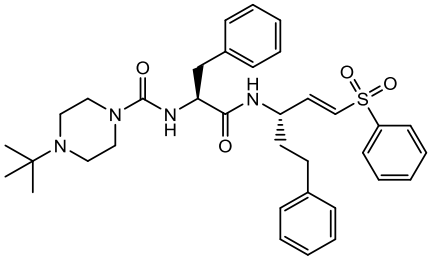
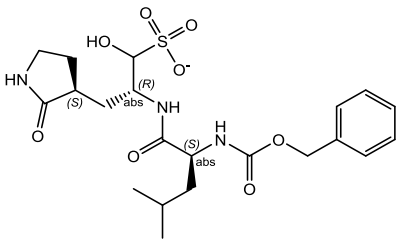
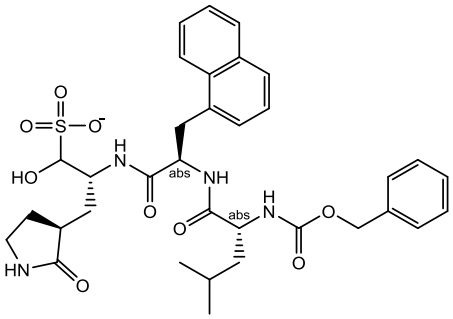
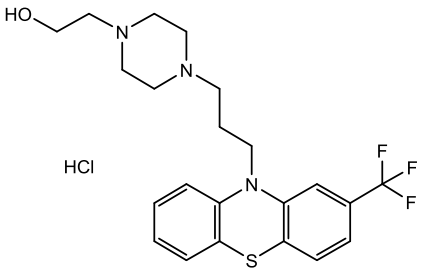
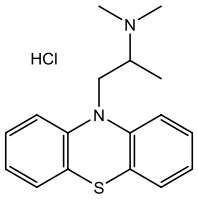
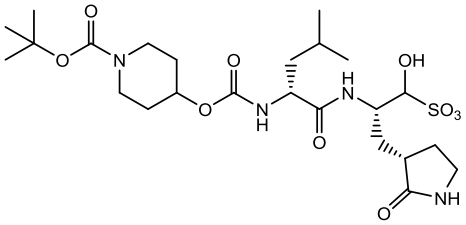
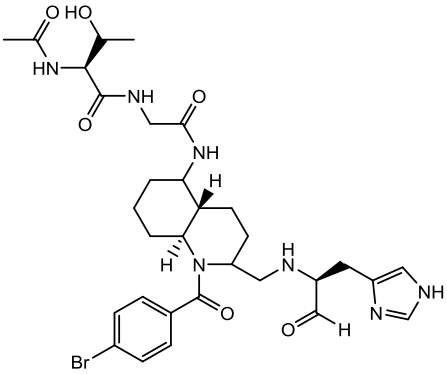
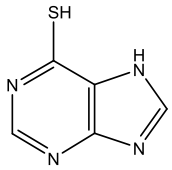
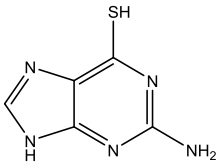
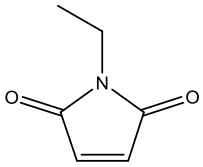
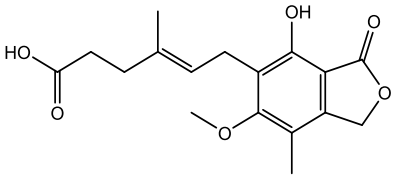
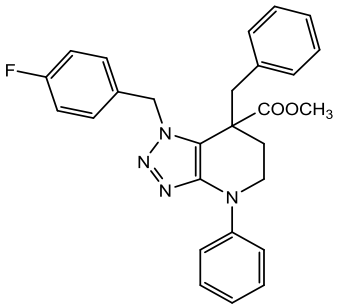
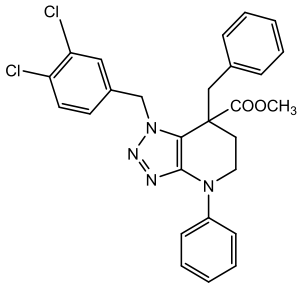
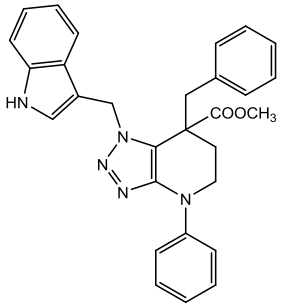
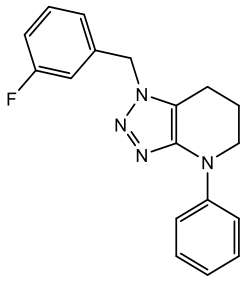
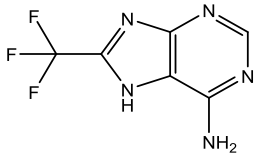
Table S1- 2D structures of 31 SARS coronavirus inhibitors with their Experimental and Predicted pIC50 Values

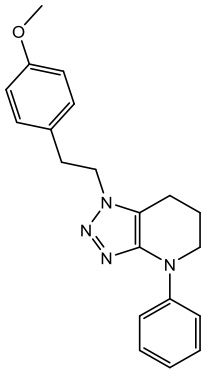
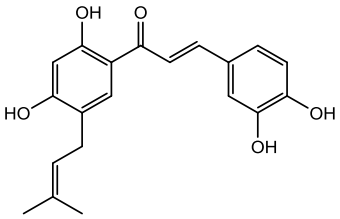
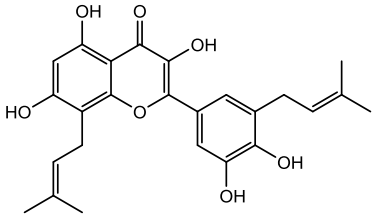
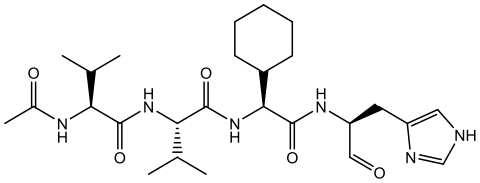
No.	name	structure	IC_{50} (μM)	pIC_{50}	Predicted pIC_{50}	Compound set
1	SARS-CoV-3CLpro		1.04	5.98	5.38	test
2	SARS-CoV-3CLpro		1.18	5.92	4.98	test
3	-		15.8	4.80	4.86	training
4	Remdesivir (GS-5734)		0.074	7.13	5.27	test
5	-		15.8	4.80	5.3	test

6	-		1.17	5.93	5.88	training
7	-		7.1	5.14	5.16	training
8	Dehydrohirsutanonol)		4.1	5.38	6.05	test
9	k11777		0.00032	9.49	9.49	training
10	SMDC-256159		0.00007	10.15	10.11	training
11	chloroquine		8.8	5.05	5.01	training

12	SMDC-256160		0.00008	10.09	9.11	test
13	GC376		0.04	7.39	7.43	training
14	NPL64		0.84	6.07	6.06	training
15	Fluphenazine hydrochloride		20	4.69	5.96	test
16	Promethazine hydrochloride		29	4.53	5.44	test
17	-		5.1	5.29	5.31	training

18	-		26	4.58	4.52	training
19	6-Mercaptopurine		26.9	4.57	4.56	training
20	6-Thioguanine		24.4	4.61	4.49	training
21	N-Ethylmaleimide		45	4.34	4.53	training
22	Mycophenolic acid (Myfortic)		247.6	3.60	5.73	test

23	-		8.95	5.04	5.54	test
24	-		9.45	5.02	5.04	training
25	-		9.45	5.02	4.98	training
26	-		11.95	4.92	4.86	training
27	(f2124-0890)		11	4.95	4.85	test

28	-		8.9	5.05	5.04	training
29	Broussochalcone A		9.2	5.03	5.01	test
30	Broussonol D		3.7	5.43	5.42	training
31	-		0.098	7.00	7.05	training

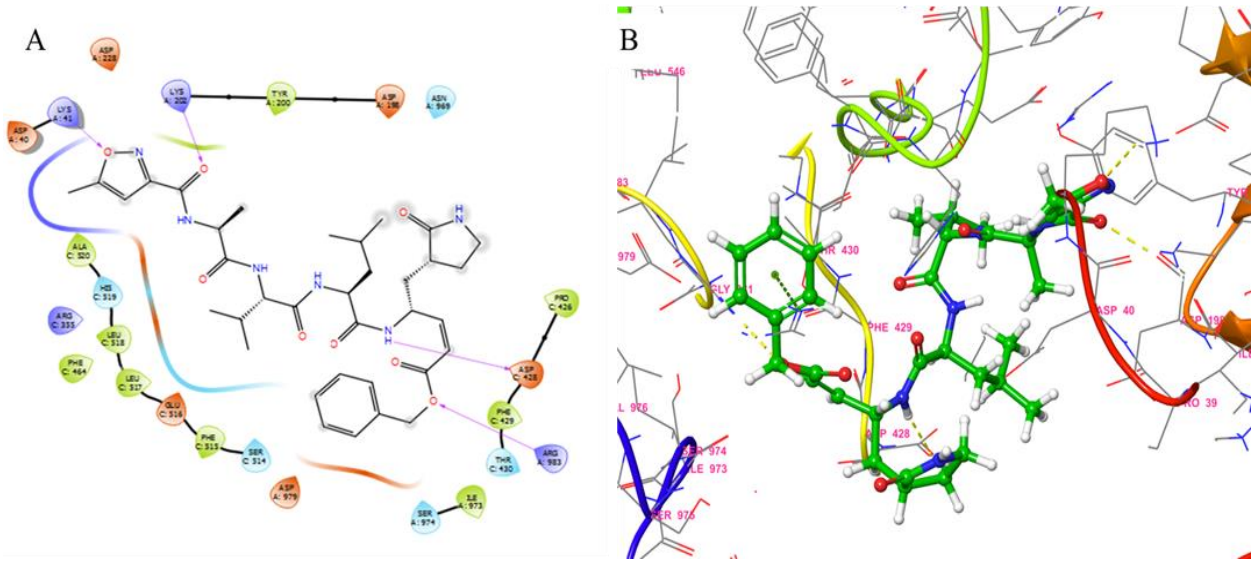


Figure S1- The binding pose of the Spike ectodomain - N3 complex. A: 3D interaction, B: 2D interaction

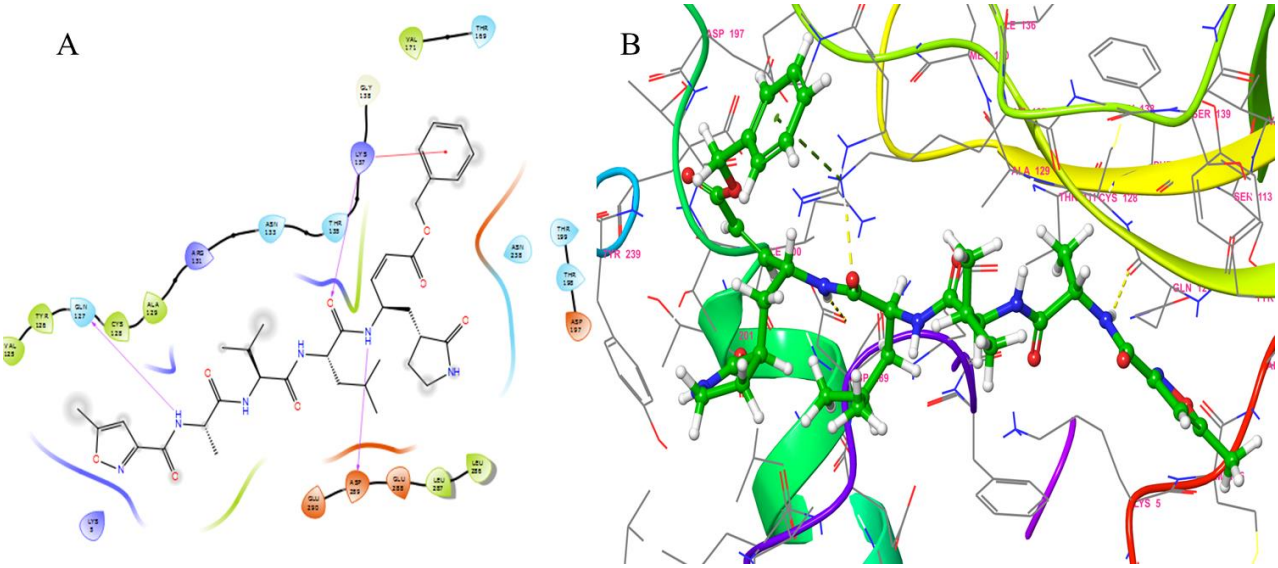


Figure S2- The binding pose of the main protease - N3 complex. A: 3D interaction, B: 2D interaction

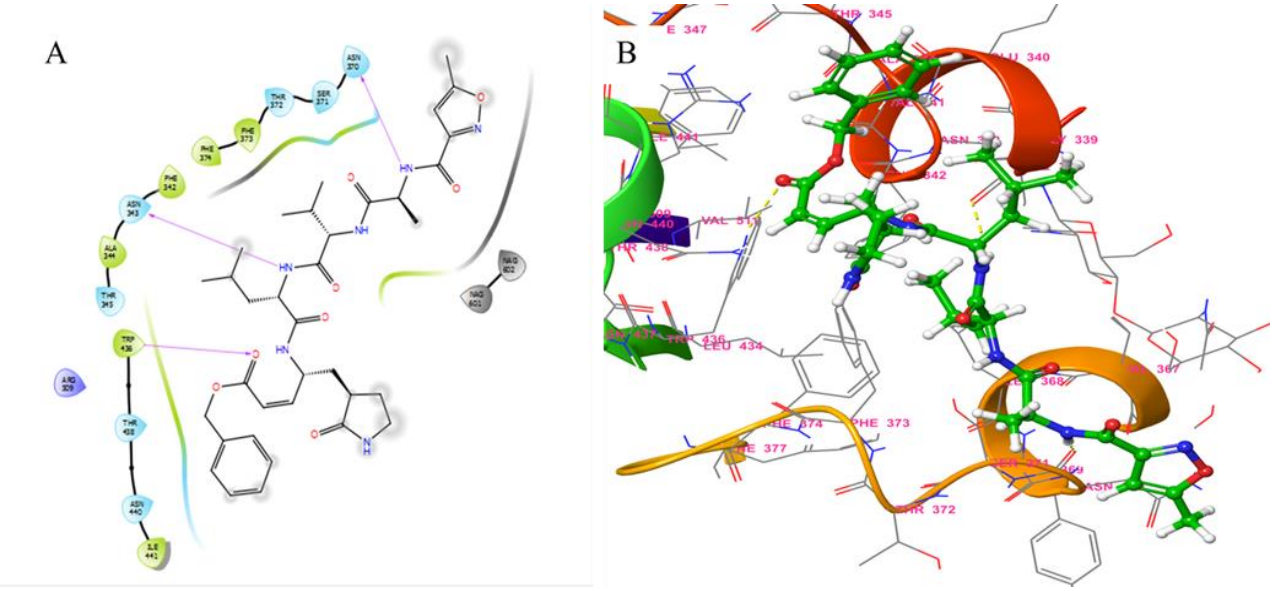


Figure S3- The binding pose of the receptor-binding domain - N3 complex. A: 3D interaction, B: 2D interaction

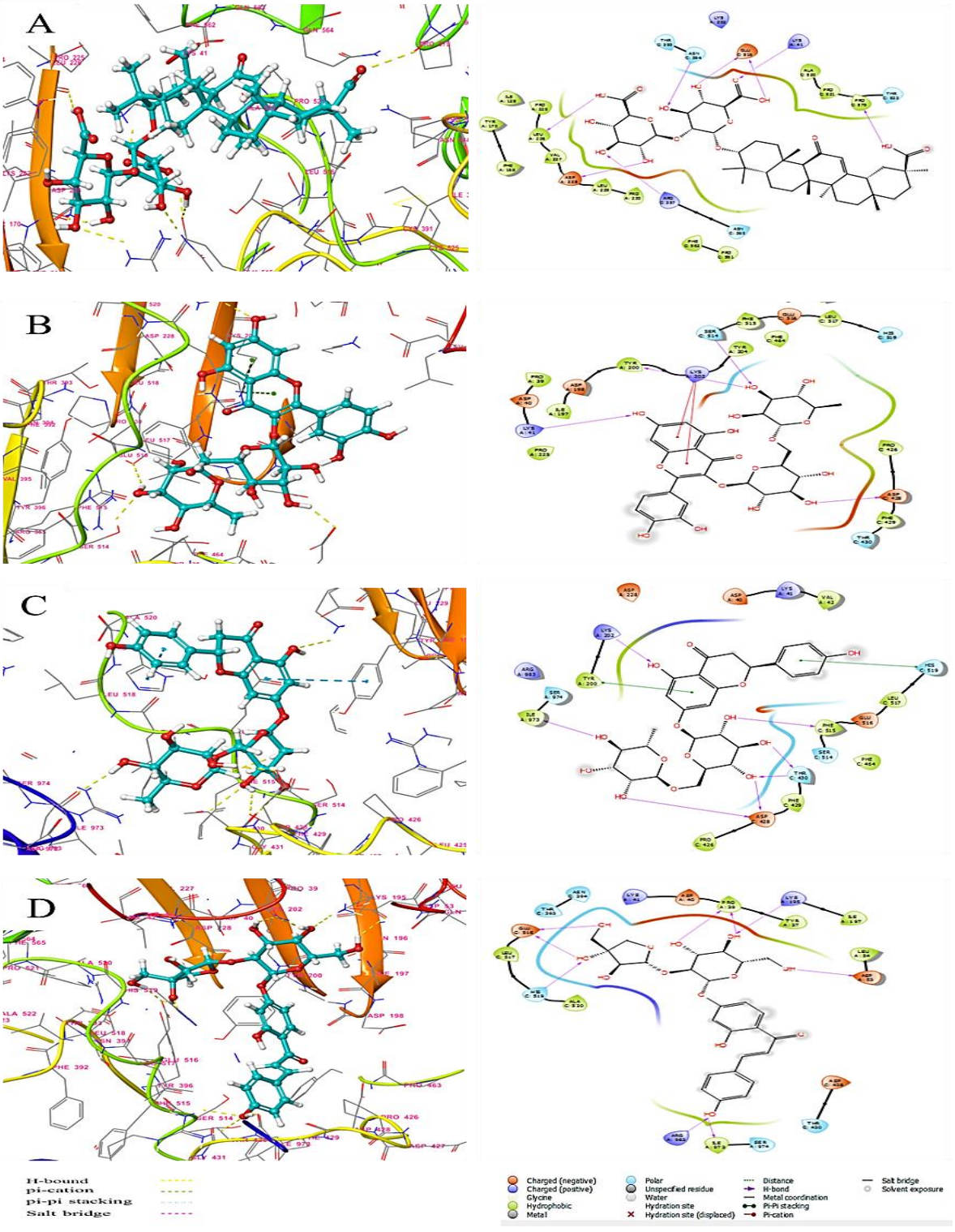


Figure S4- 3D and 2D interaction of Glycyrrhizin (A), Rutin (B), Narirutin (C), and Licuroside (D) with the COVID-19 main protease receptor (PDB ID: 6VYB)

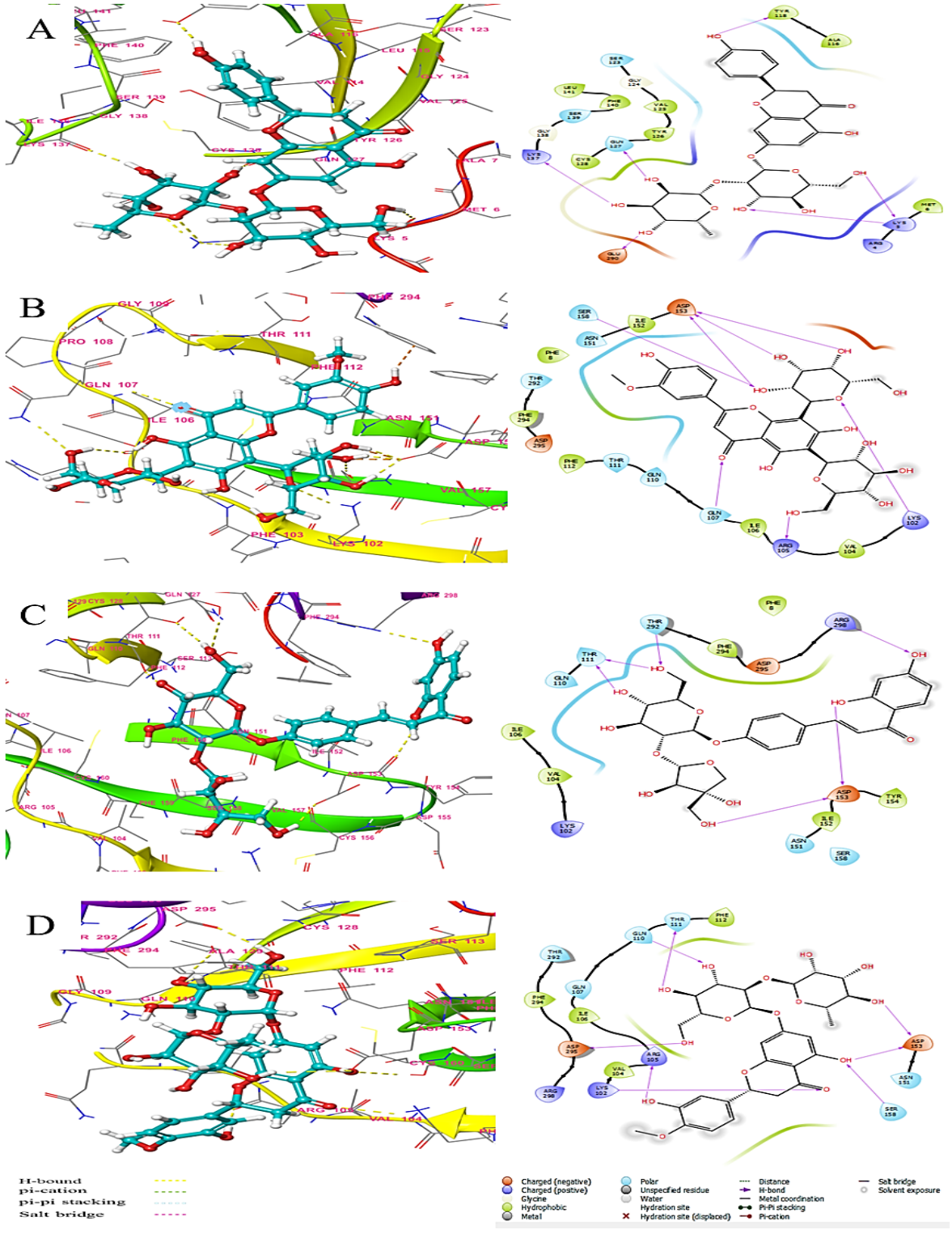


Figure S5- 3D and 2D interaction of Naringin (A), Chrysoeriol 6,8-di-C-gluc (B), Isoliquiritin Apioside (C), and Neohesperidin (D) with the COVID-19 main protease receptor (PDB ID: 6LU7)

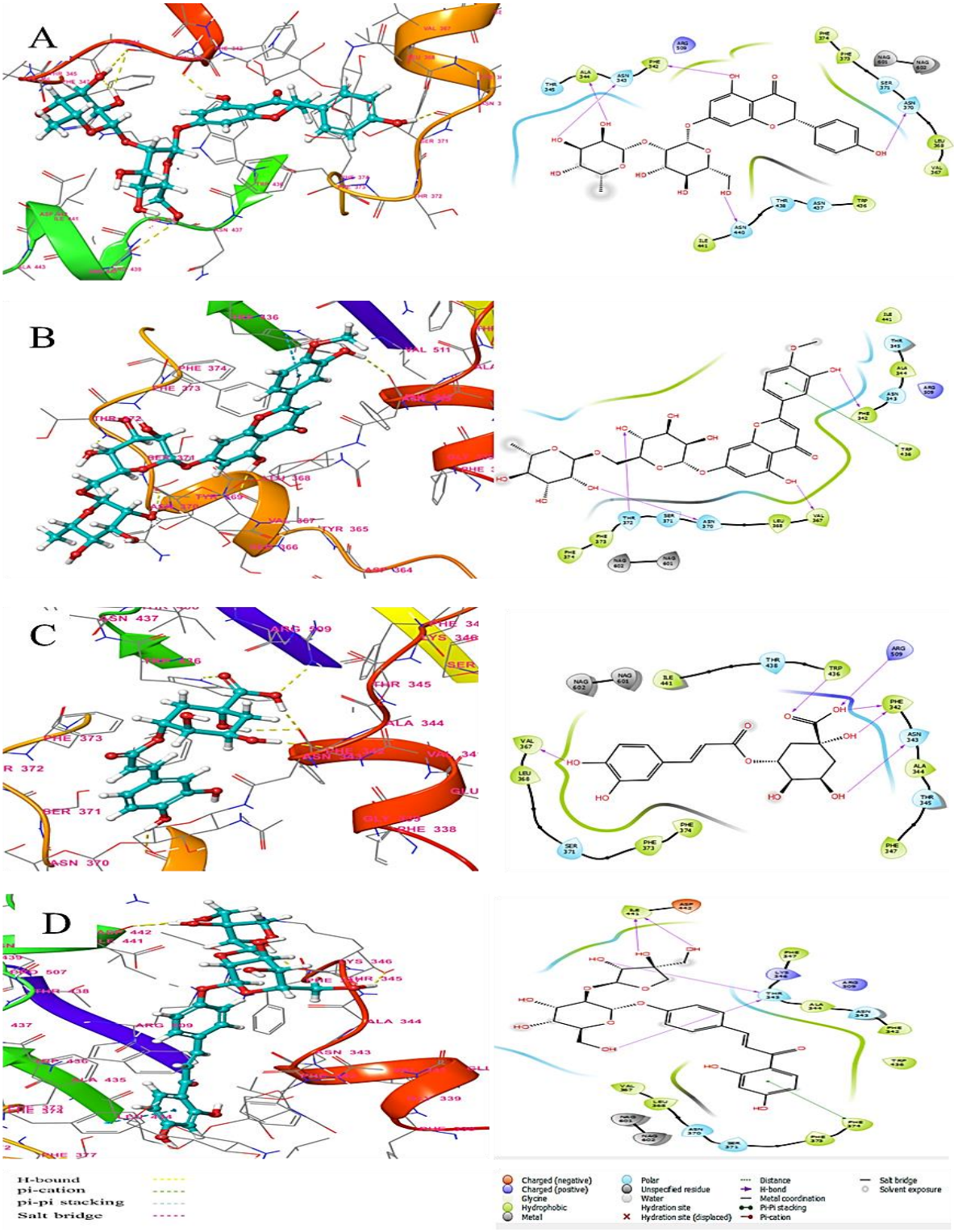


Figure S6- 3D and 2D interaction of Naringin (A), Hesperidin(B), Cholorogenic Acid (C), and Isoliquiritin Apioside (D) with the receptor-binding domain (PDB ID: 6VW1)