

Supplementary: Development of a Fingerprint-Based Scoring Function for the Prediction of the Binding Mode of Carbonic Anhydrase II Inhibitors

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W005	0	0	0	0	0	0	0
Y007	0	0	0	0	0	0	0
F020	0	0	0	0	0	0	0
R 058	0	0	0	0	0	0	0
L060	0	0	0	0	0	0	0
N062	0	0	0	0	0	0	0
H064	0	0	0	0	0	0	0
A065	0	0	0	0	0	0	0
F066	0	0	0	0	0	0	0
Q067	0	0	0	0	0	0	0
E069	0	0	0	0	0	0	0
D072	0	0	0	0	0	0	0
I091	0	0	0	0	0	0	0
Q092	0	1	0	0	0	0	0
F093	0	0	0	0	0	0	0
H094	0	0	0	0	1	1	0
F095	0	0	0	0	0	0	0
H096	0	0	0	0	0	0	0
H119	0	0	0	0	0	0	0
V121	0	0	0	0	0	0	0
H122	0	0	0	0	0	0	0
W123	0	0	0	0	0	0	0
D129	0	0	0	0	0	0	0
F130	0	0	1	0	1	0	0
G131	0	0	0	0	0	0	0
K132	0	0	0	0	0	0	0
A133	0	0	0	0	0	0	0
V134	0	0	0	0	0	0	0
Q135	0	0	0	0	0	0	0
L140	0	0	0	0	0	0	0
V143	0	0	0	0	0	0	0
S196	0	0	0	0	0	0	0
L197	0	0	1	0	0	0	0
T198	0	1	0	0	0	0	0
T199	0	1	0	0	0	0	0
P200	0	0	0	0	0	0	0
P201	0	0	0	0	0	0	0
L202	0	0	0	0	0	0	0
L203	0	0	0	0	0	0	0
C205	0	0	0	0	0	0	0
V206	0	0	0	0	0	0	0
W208	0	0	0	0	0	0	0
N243	0	0	0	0	0	0	0

Figure S1. Fingerprint analysis of the interaction between 5-[(phenylsulfonyl)amino]-1,3,4-thiadiazole-2-sulfonamide and CAII (PDB code 3DBU).

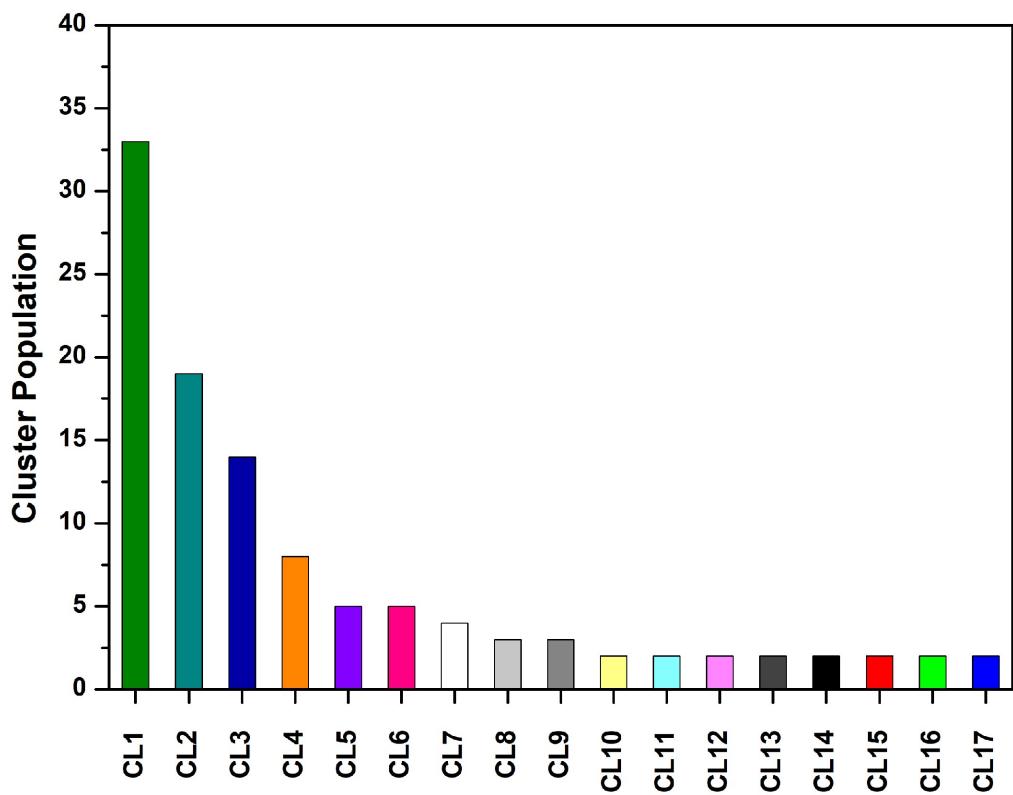


Figure S2. Similarity analysis of the deposited ligand-CAII X-ray complexes on the basis of the Tc-IFP score.

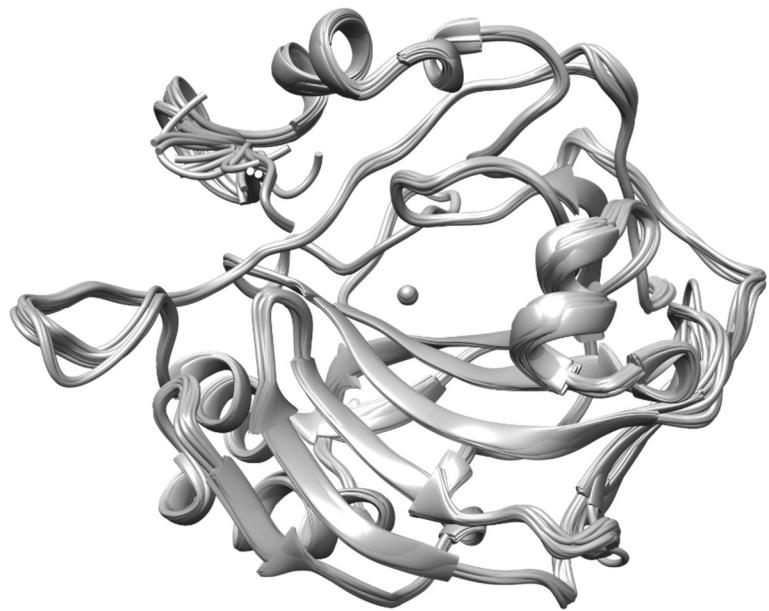


Figure S3. Superimposition of the 127 CAII X-ray structures.

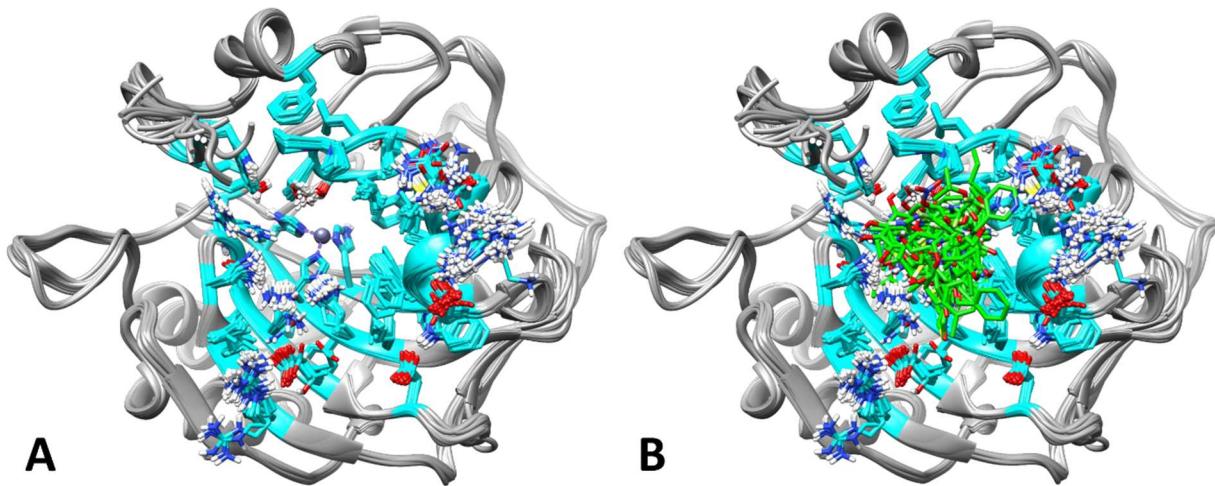
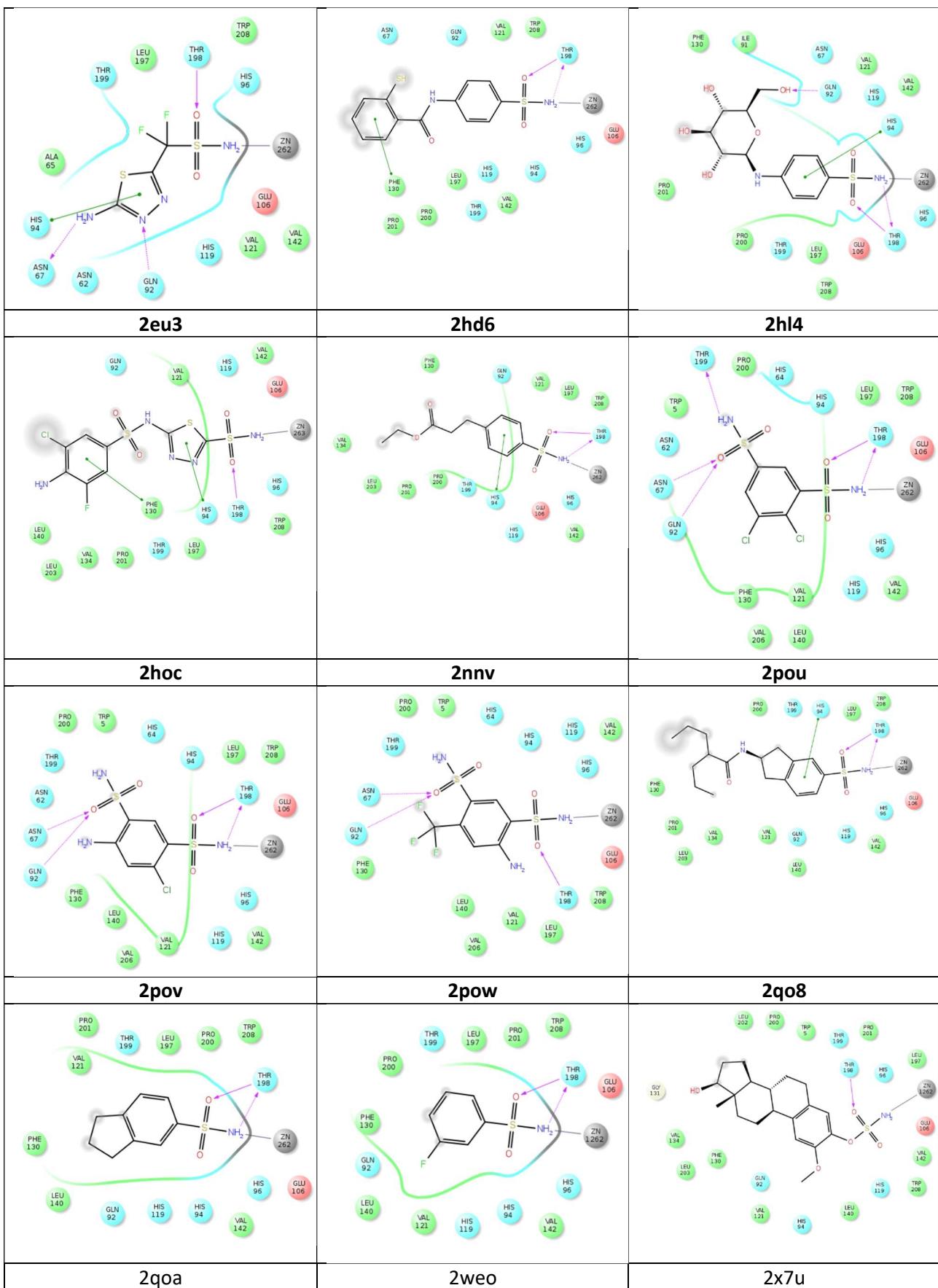
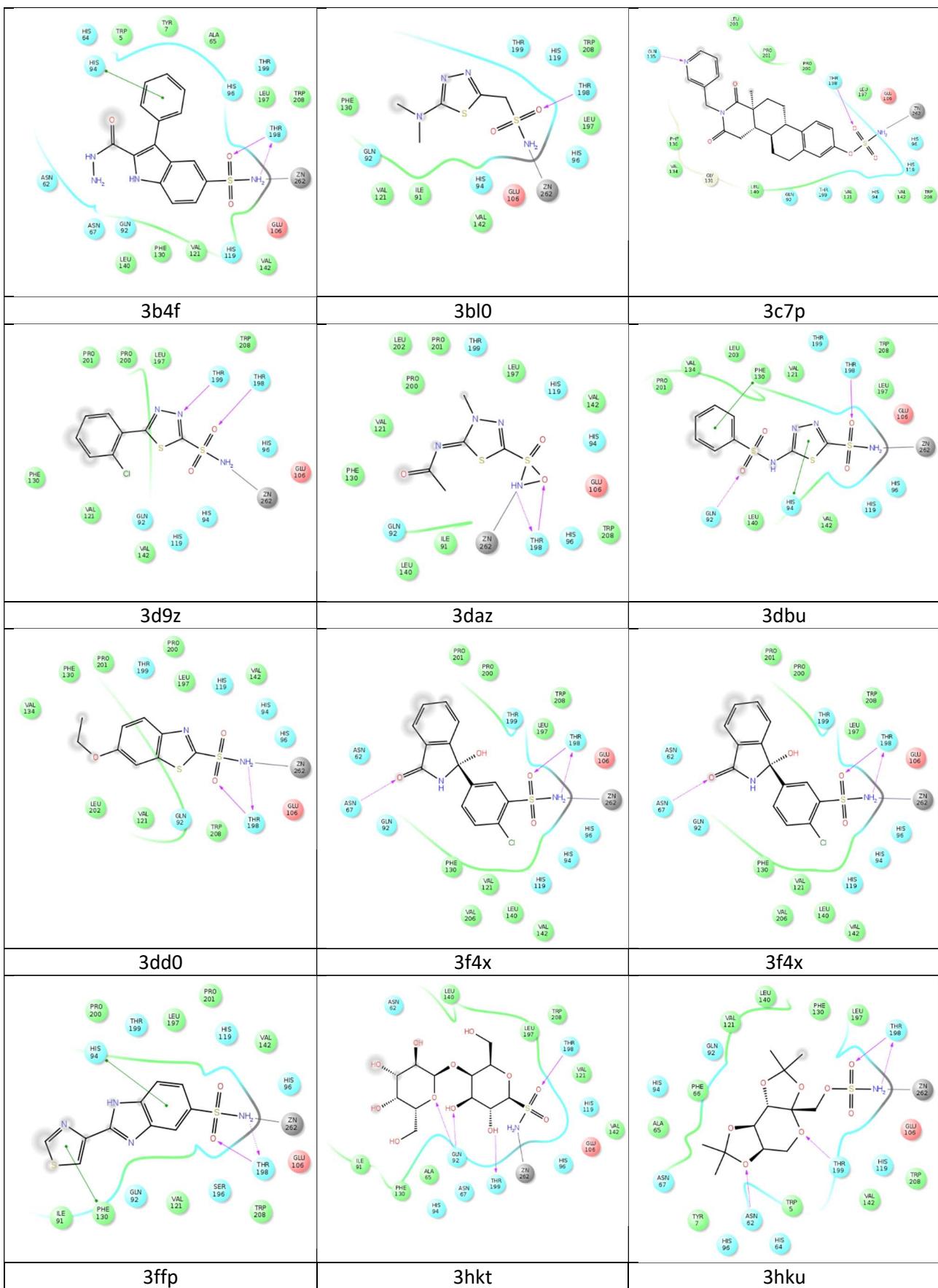
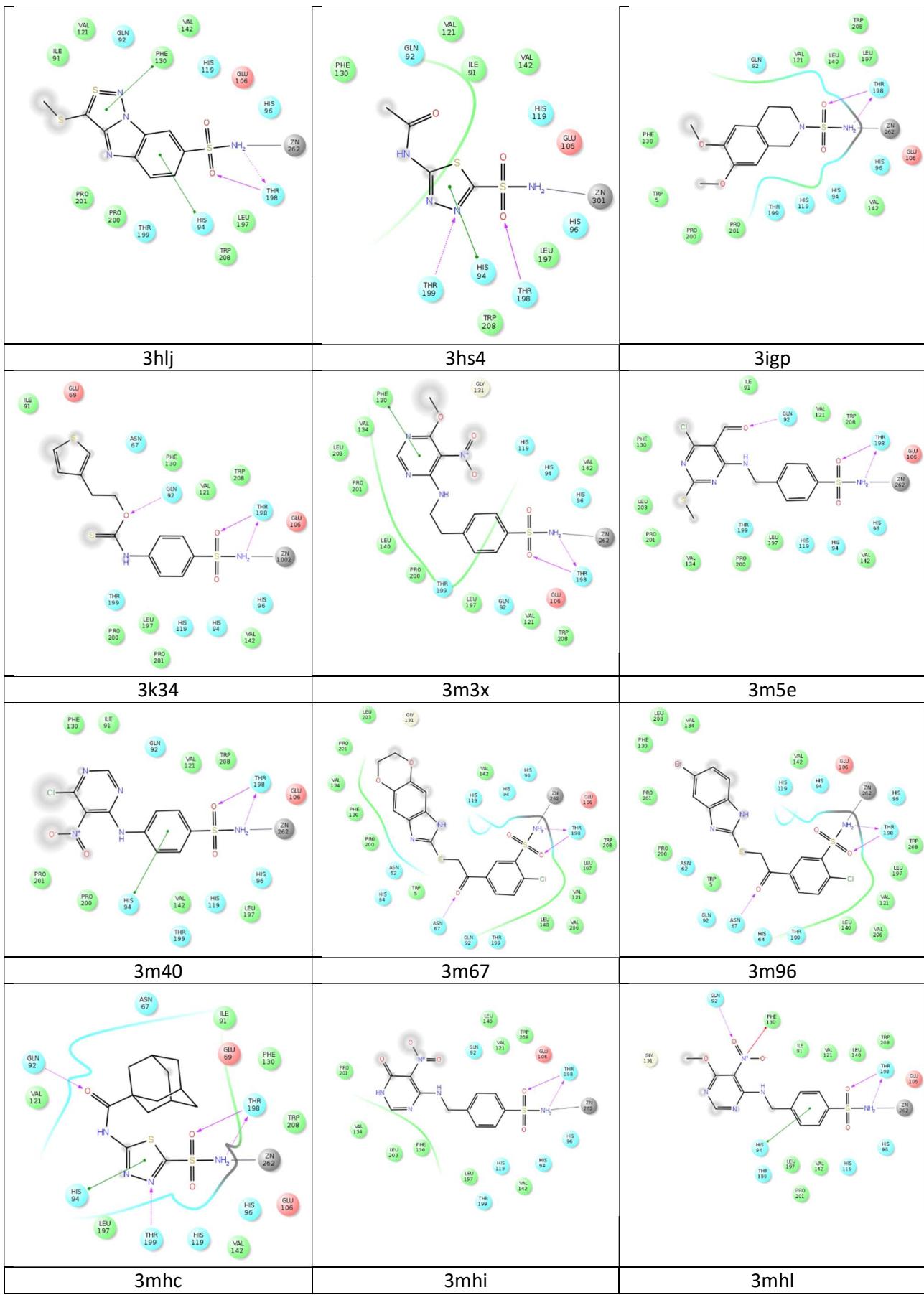


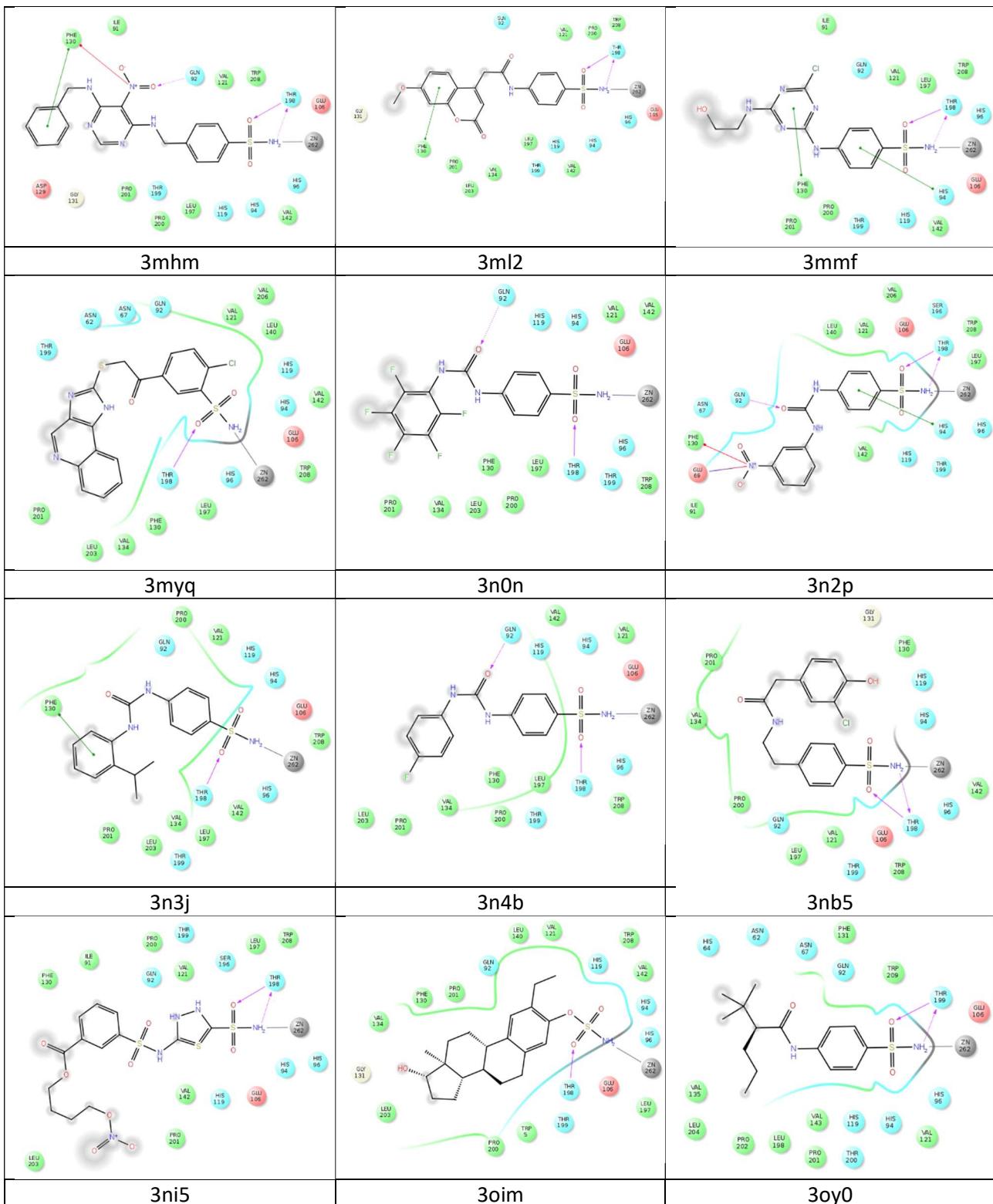
Figure S4. Protein binding site mapped by the CAII-rIFP. (A) The 44 residues of the 127 CAII X-ray structures whose interactions are mapped by the CAII-rIFP are showed in cyan sticks, while the co-crystallized ligands are hidden. (B) The 127 co-crystallized ligands are also shown in green sticks.

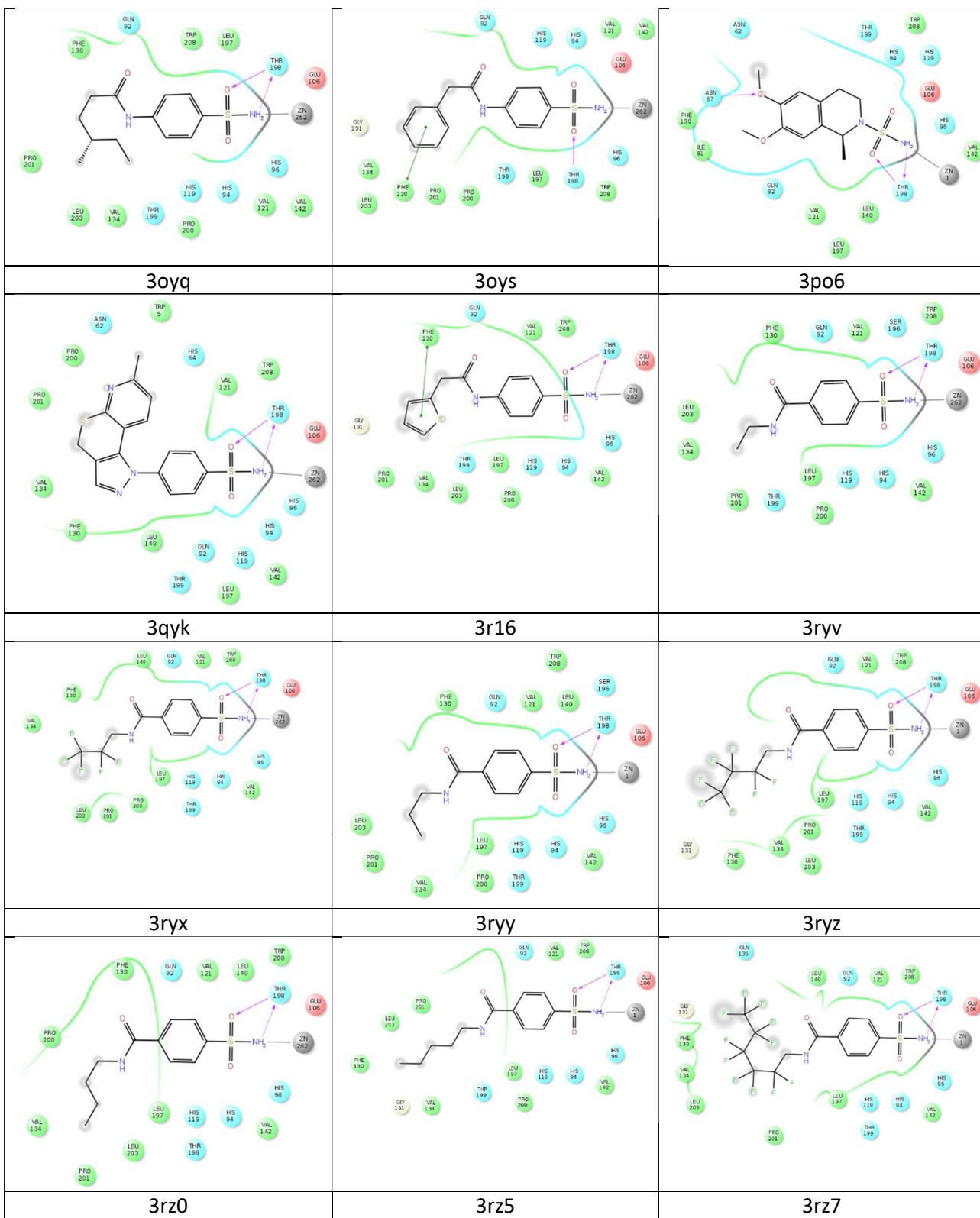
Table S1. Structure and interactions of the 127 ligands co-crystallized with CAII.

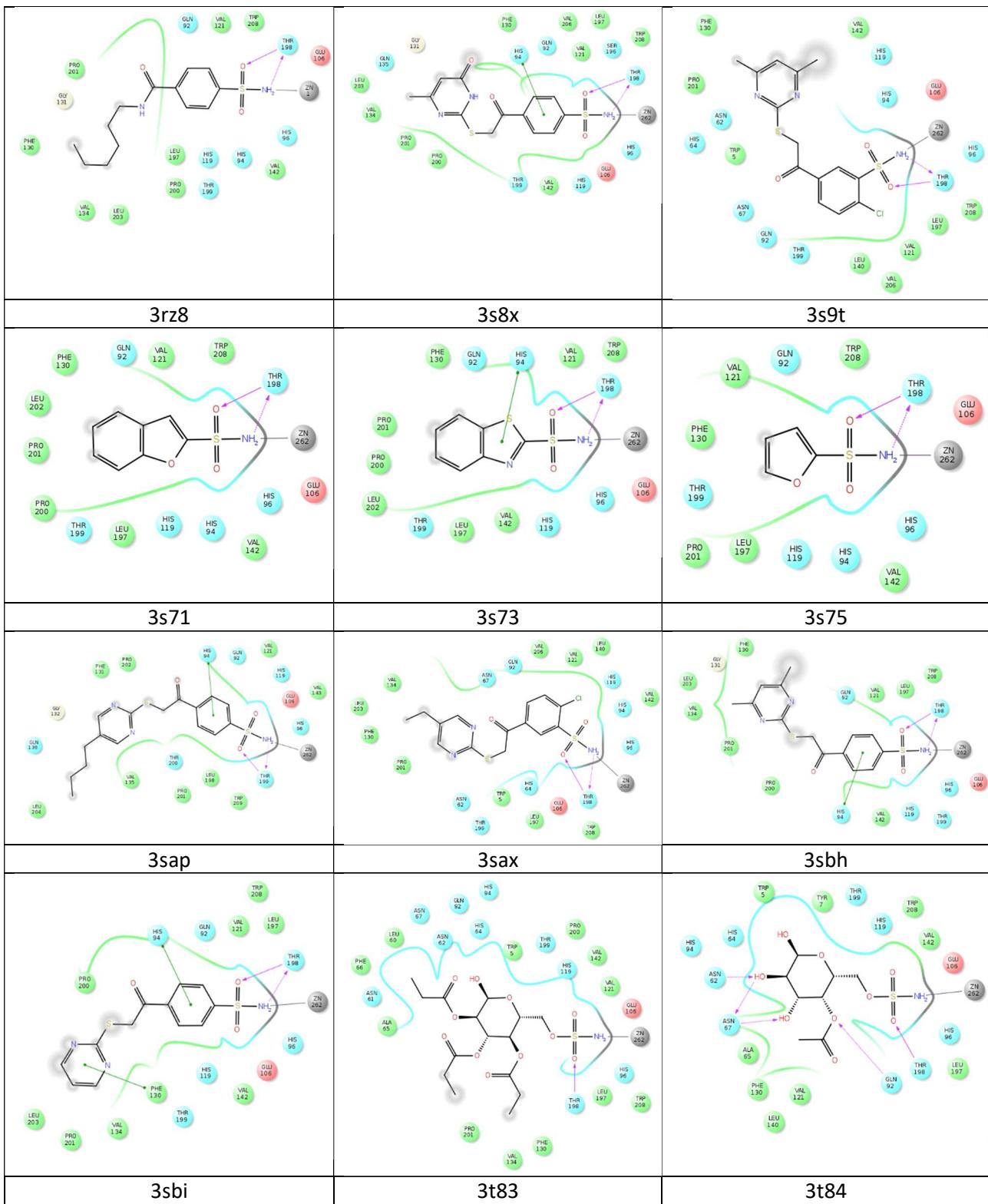


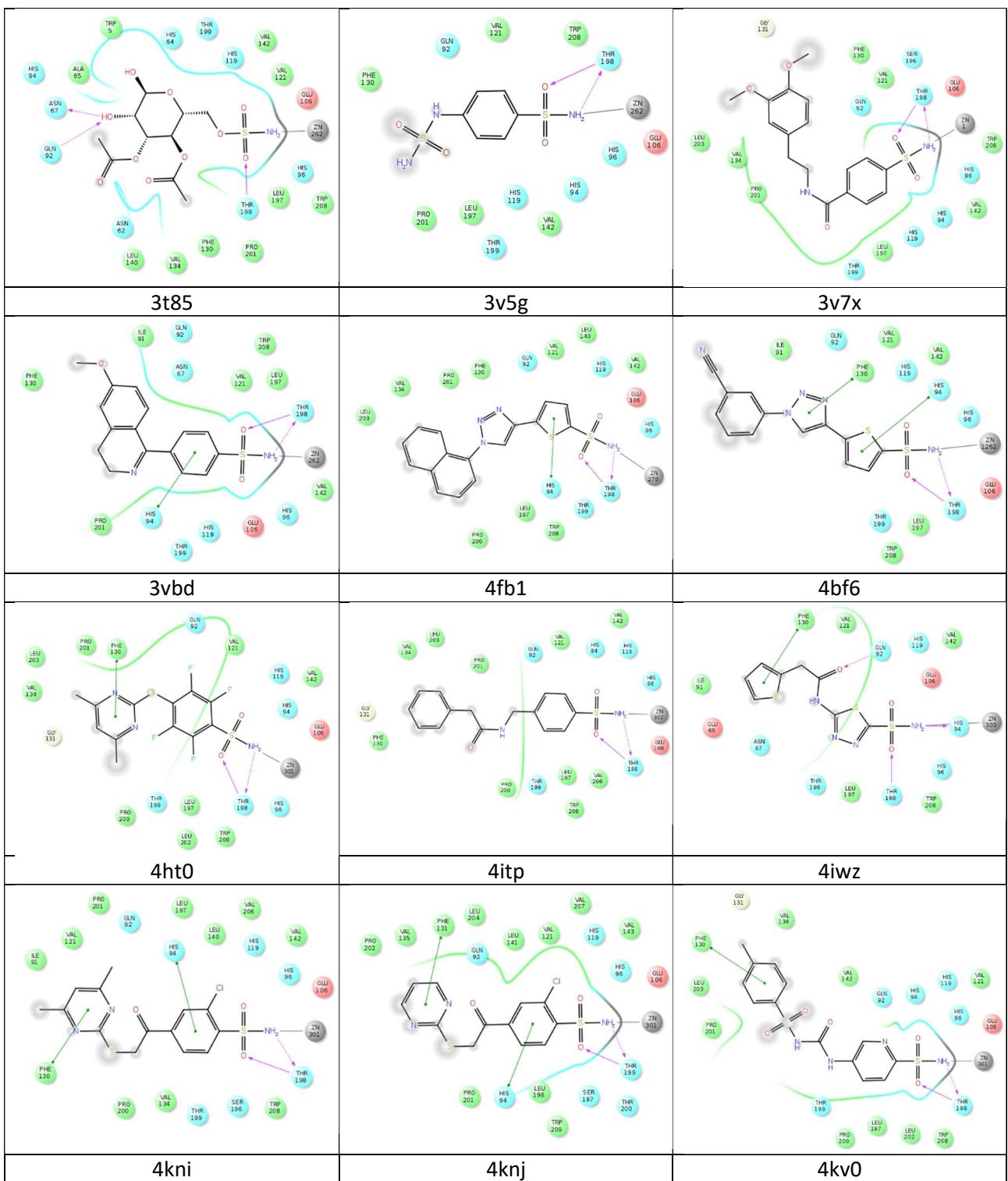


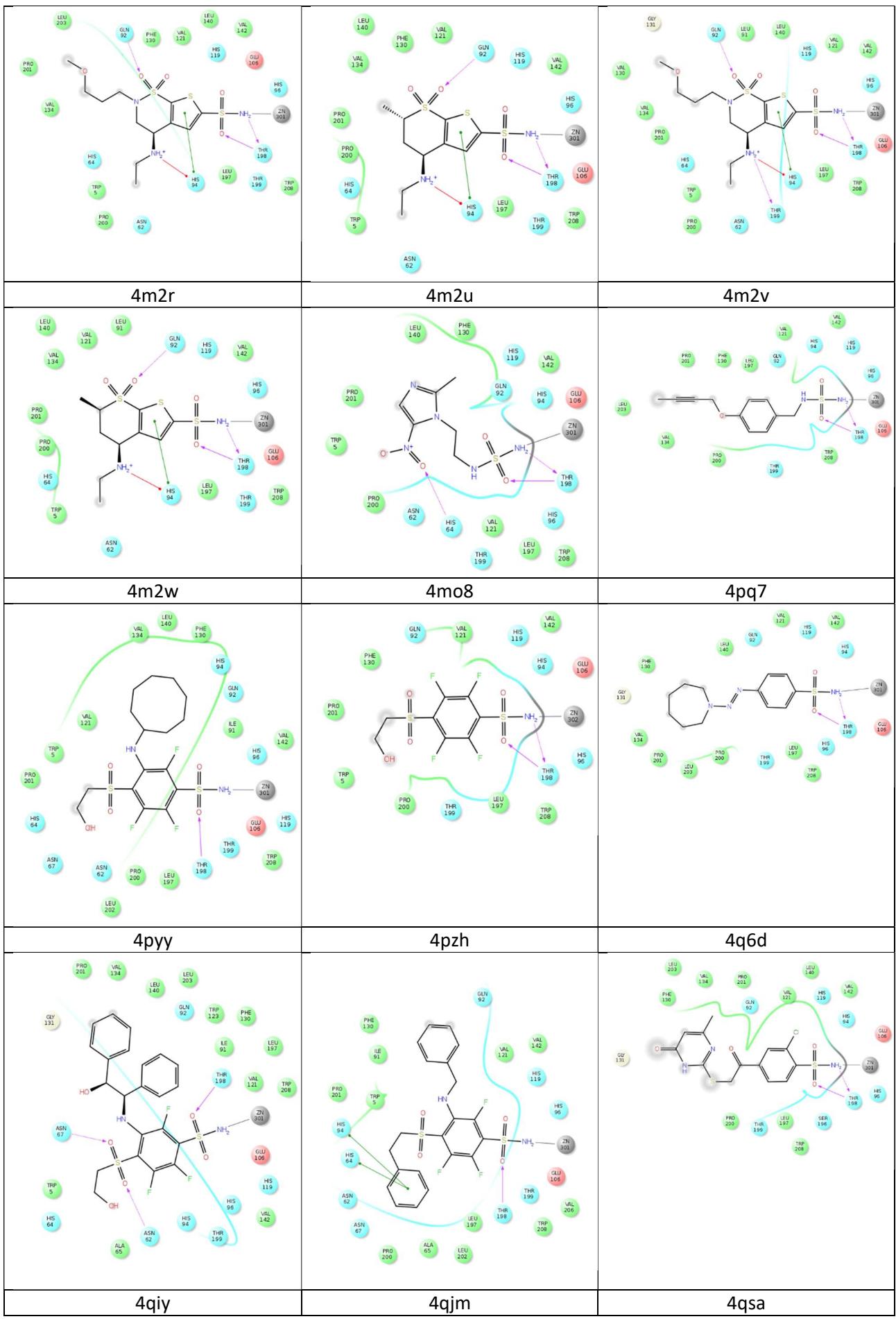


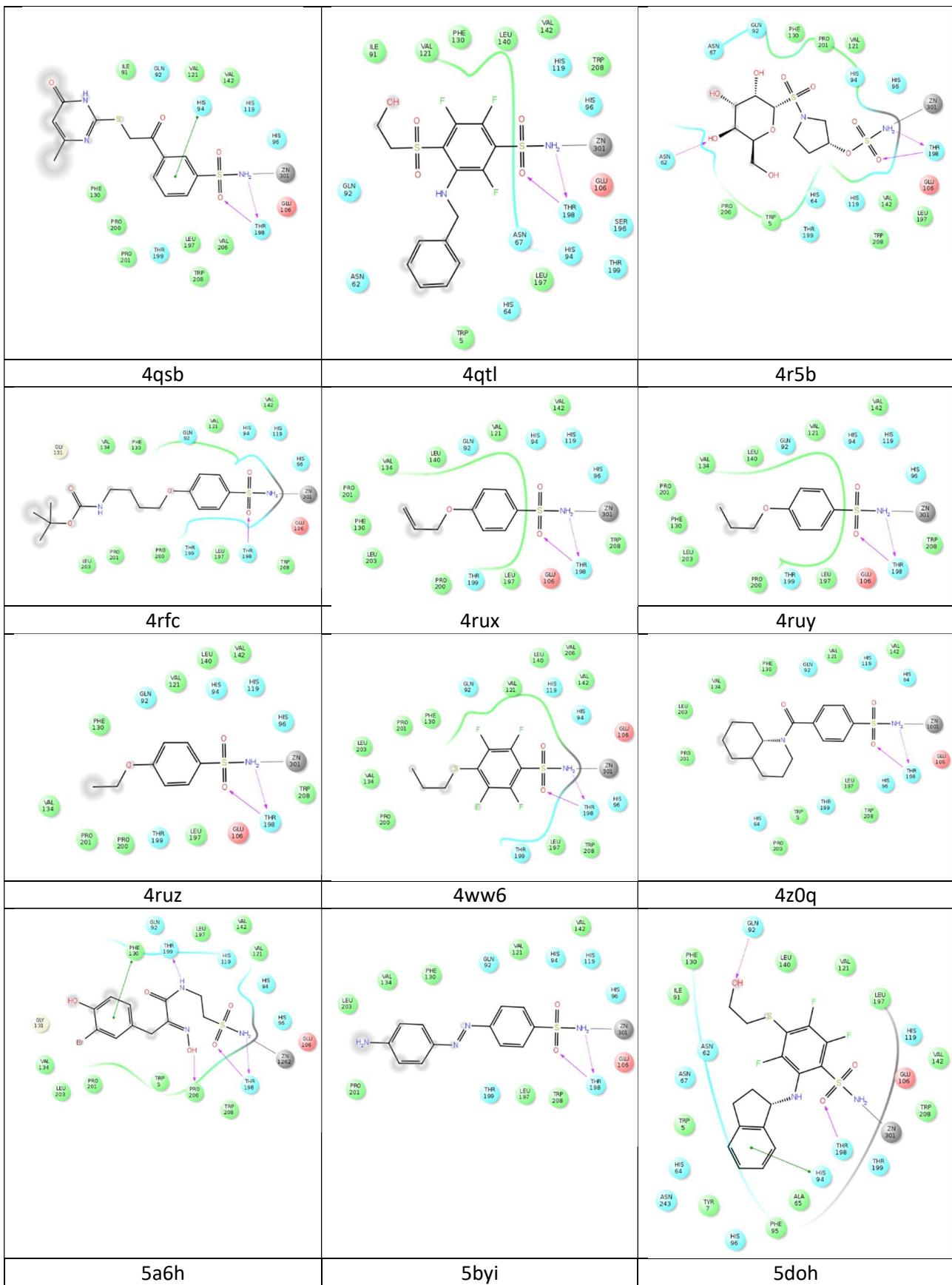


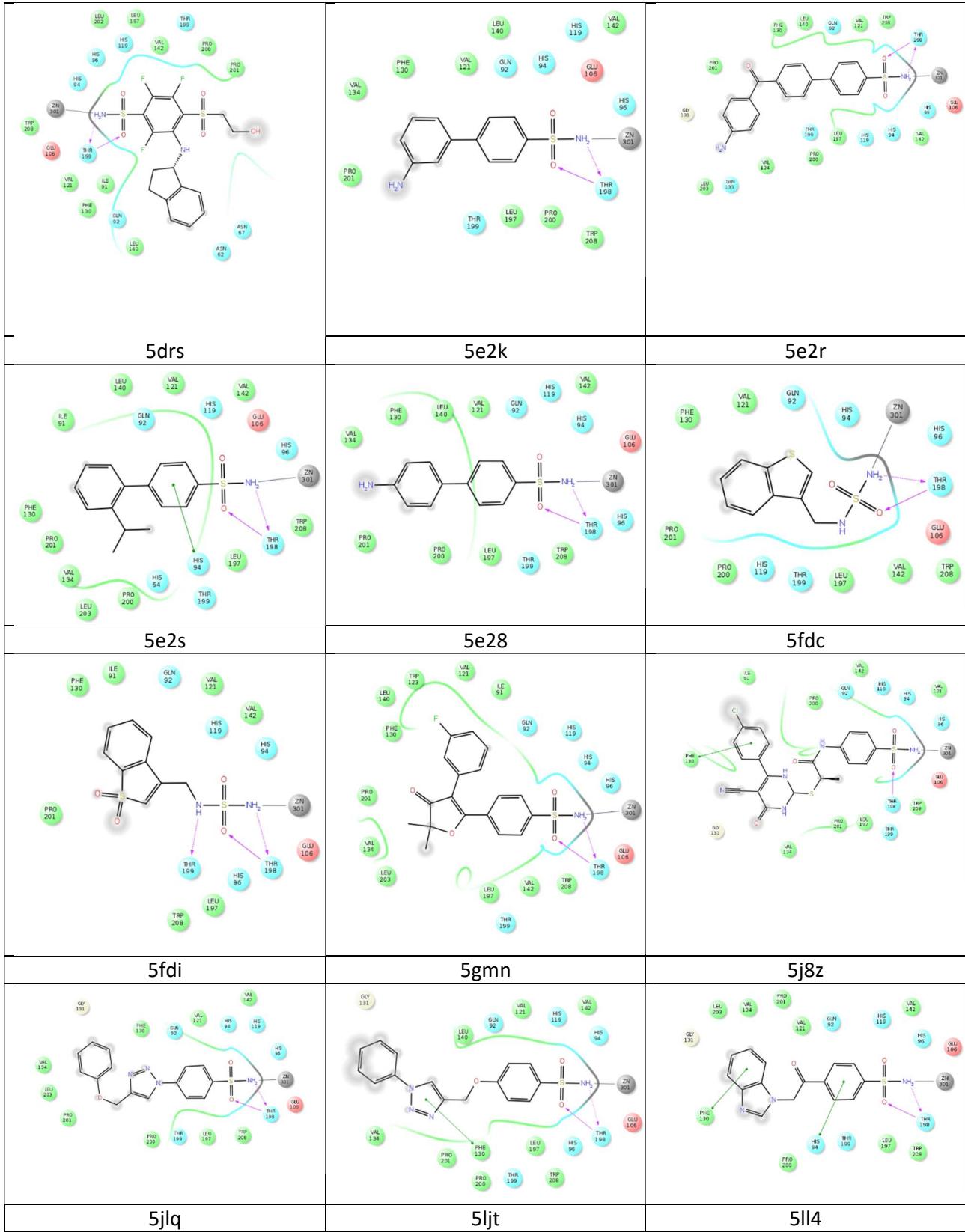












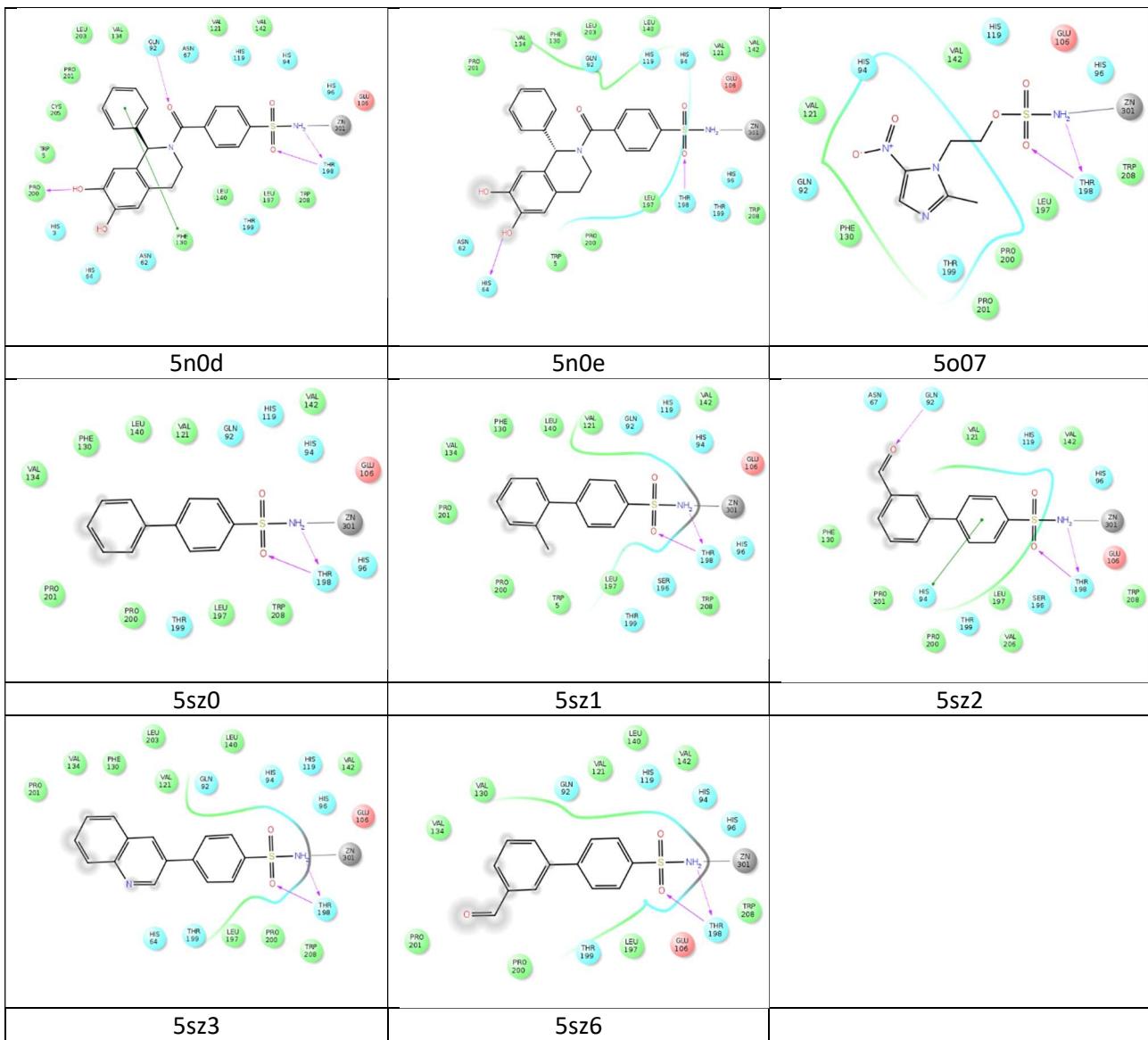
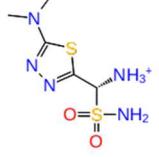
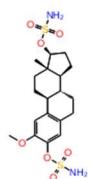
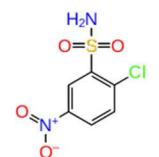
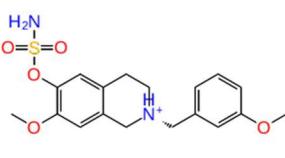
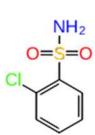
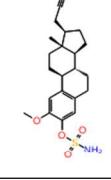
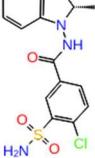
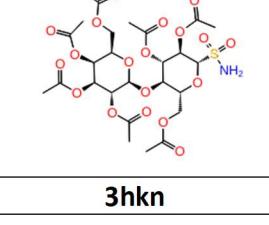
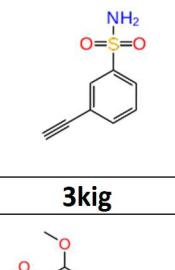
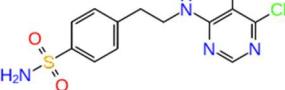
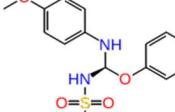
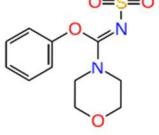
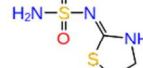
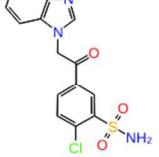
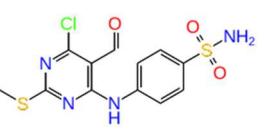
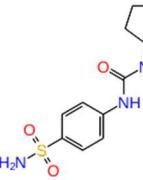
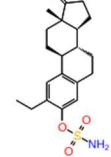
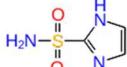
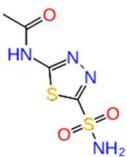
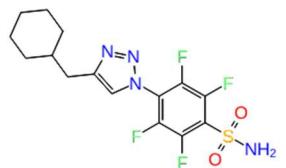
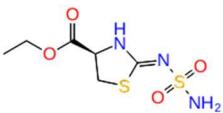
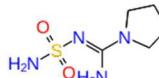
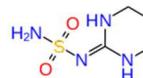
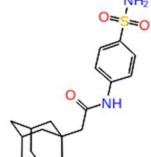
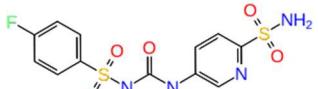
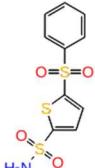
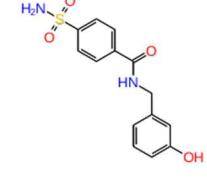
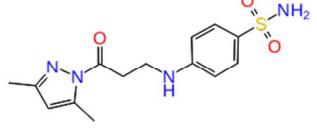
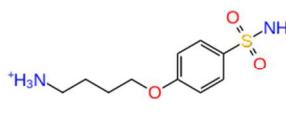
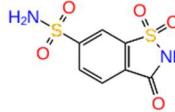
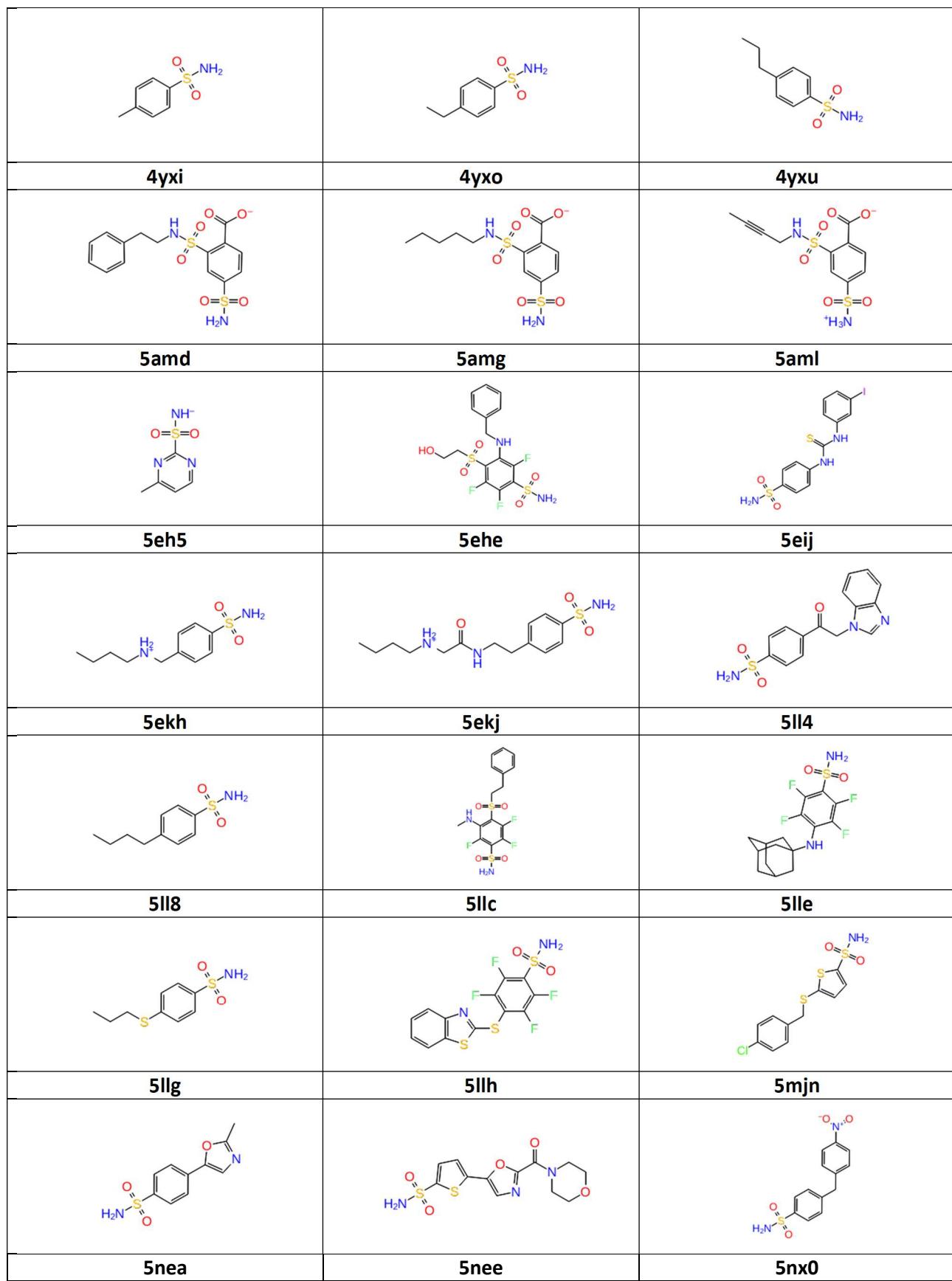


Table S2. Structures of the 70 ligands used as a first external test set.

		
2eu2	2gd8	2h15
		
2qp6	2wd2	2weg
		
2weh	2x7t	3bet
		
3bl1	3hkn	3kig
		
3l14	3m2n	3m2x
		
3m04	3m14	3m98
		
3mho	3mzc	3oku

		
3s76	3v2m	4dz7
		
4dz9	4fpt	4frc
		
4fu5	4fvn	4fvo
		
4ilx	4ito	4kuw
		
4lhi	4mty	4n0x
		
4pyx	4q6e	4rfd
		
4rn4	4xe1	4yx4



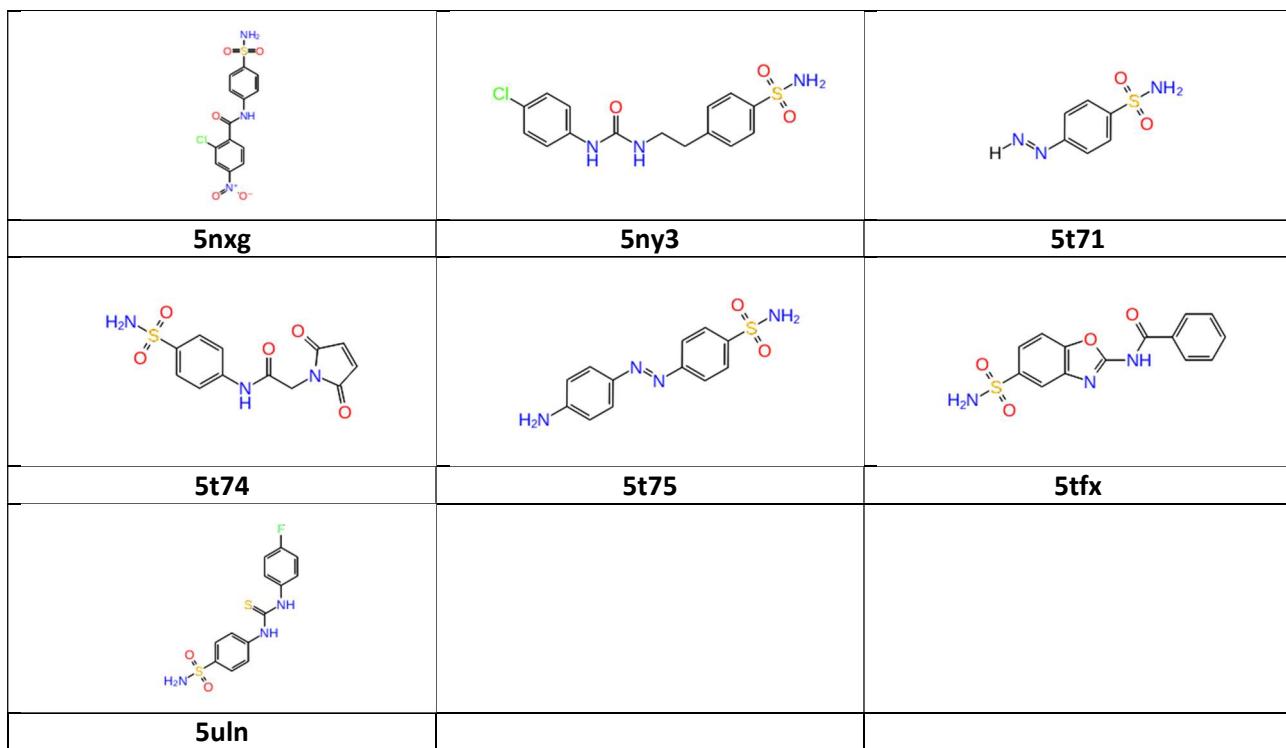


Table S3. Structures of the 15 ligands used as additional external test set.

