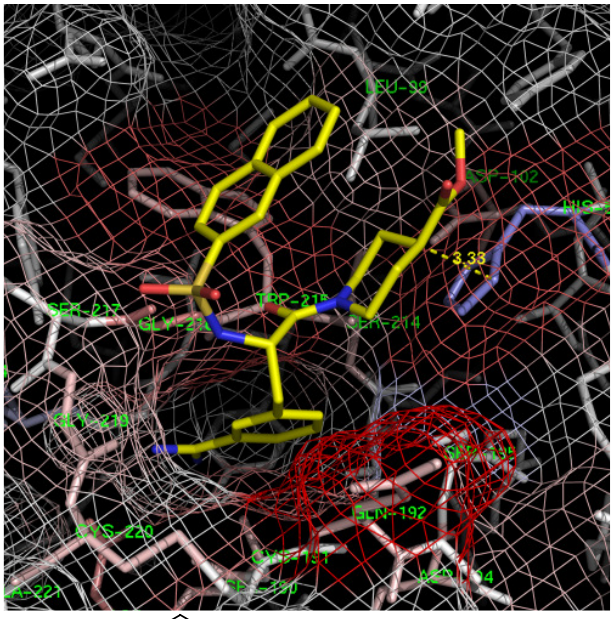
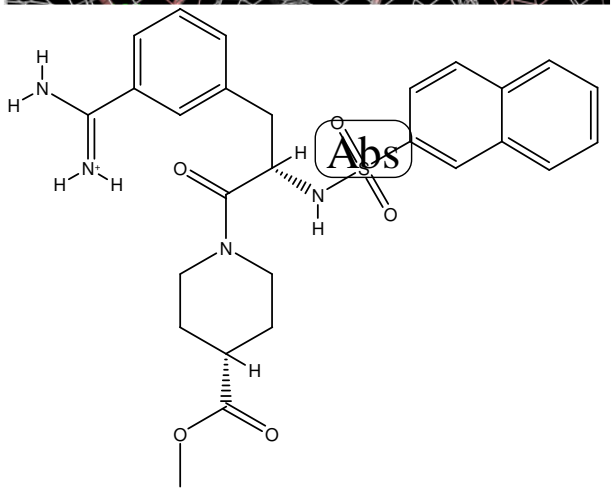
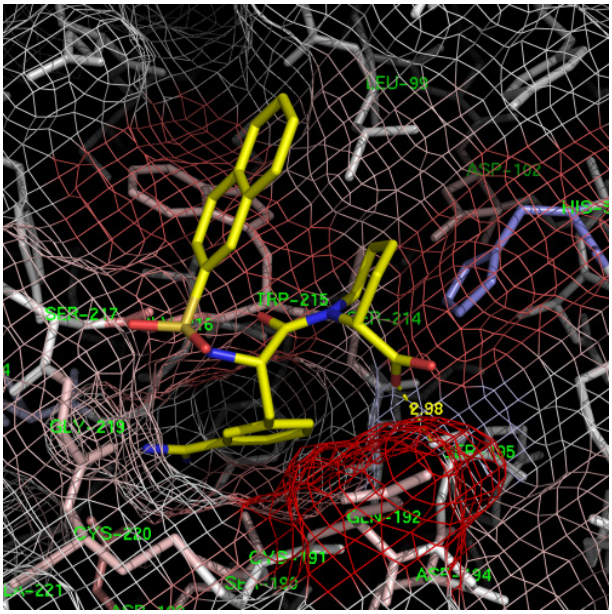
trypsin inhibitors

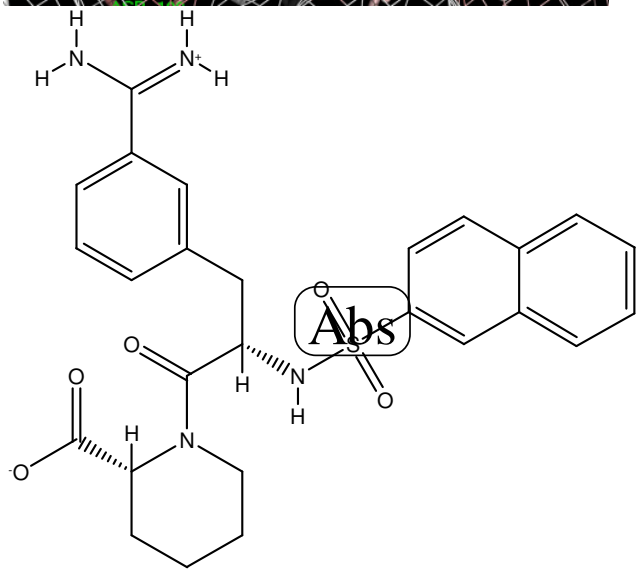
Analyzing the inhibitors described in (Renatus, et al., 1998).
The docking solutions have very high RMSD (> 5 Å).



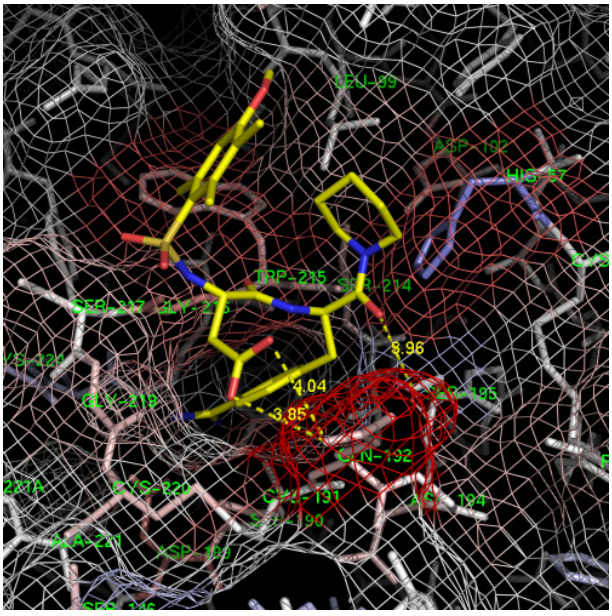


B11/1k1j 0.021 µM -10.5 kcal/mol
docked ΔG predicted: -10.4, ΔG 5th ranked: -8.4
Positive vdw interaction to His57 without poloar interactions.

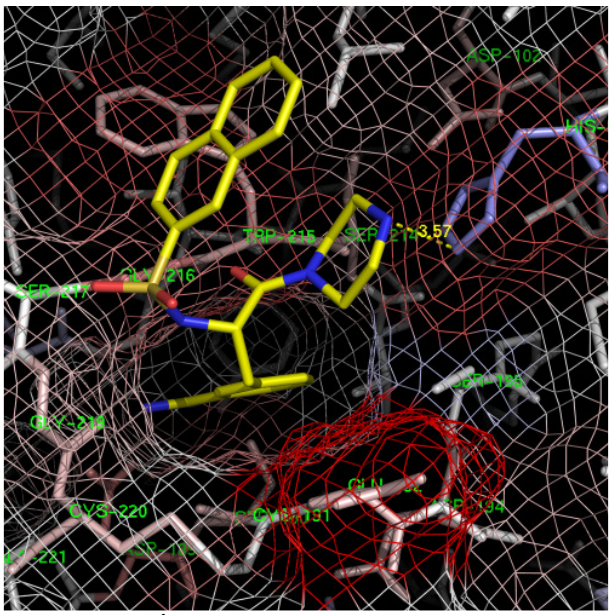


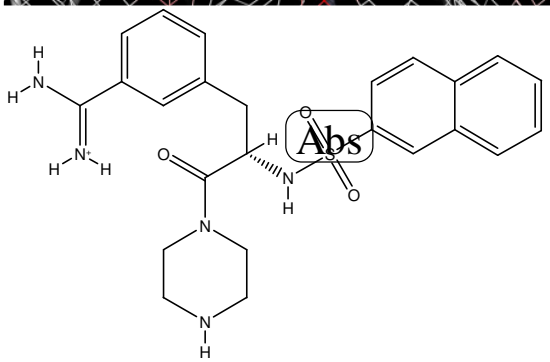


B12/1k1i 0.66 μM -8.4 kcal/mol
docked ΔG predicted: -9.4, ΔG 5th ranked: -8.9
Negative vdw interaction to Ser195.

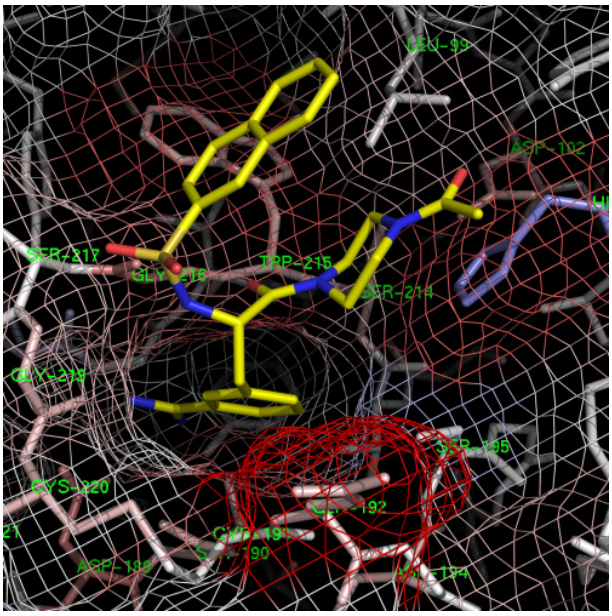


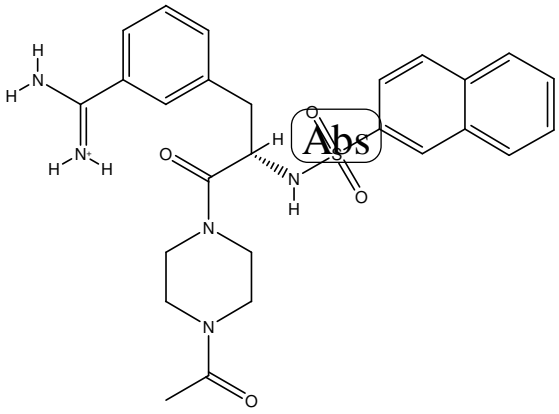
B08/1k1n 0.42 µM -8.7 kcal/mol
docked ΔG bind elec predicted: -7.2, ΔG 5th ranked: -11.2
Negative vdw interaction to Ser195 like in B12, but the carboxy group has a positive vdw/elec influence to Gln192.



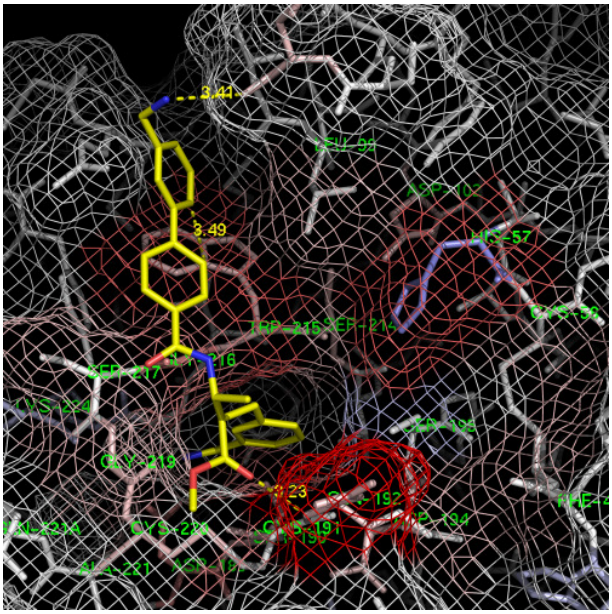


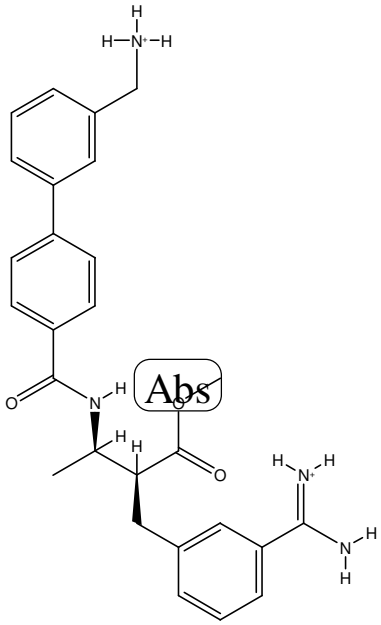
B10/1k1l 0.12 µM -9.4 kcal/mol
docked ΔG bind elec predicted: -8.9, ΔG 5th ranked: -9.1
Negative elec interaction of N of piperazine to His57.



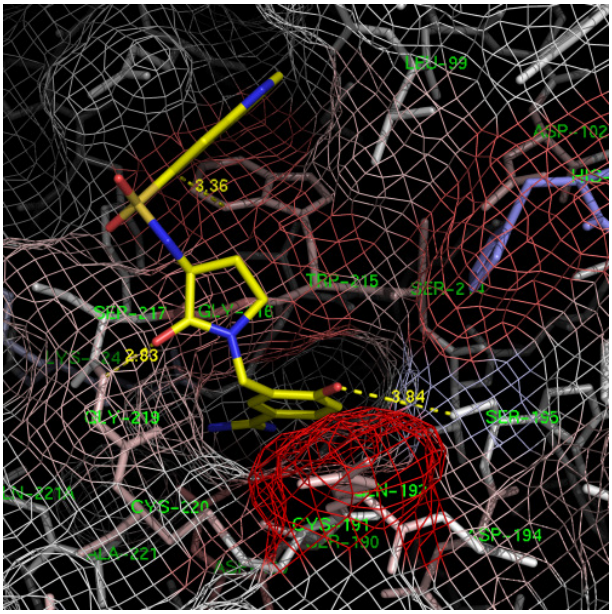


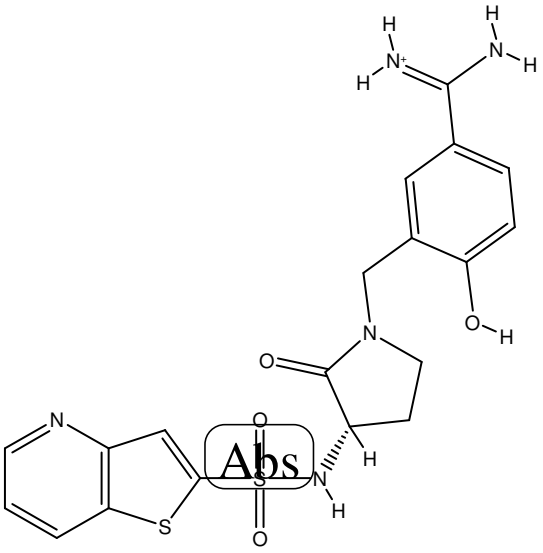
B09/1k1m 0.045 μM -10.0 kcal/mol
docked/predicted: ΔG bind elec: -8.4, ΔG 5th ranked: -9.4
The negative elec interaction of unsubstituted N of piperazine (B10) is avoided by conjugated C=O.



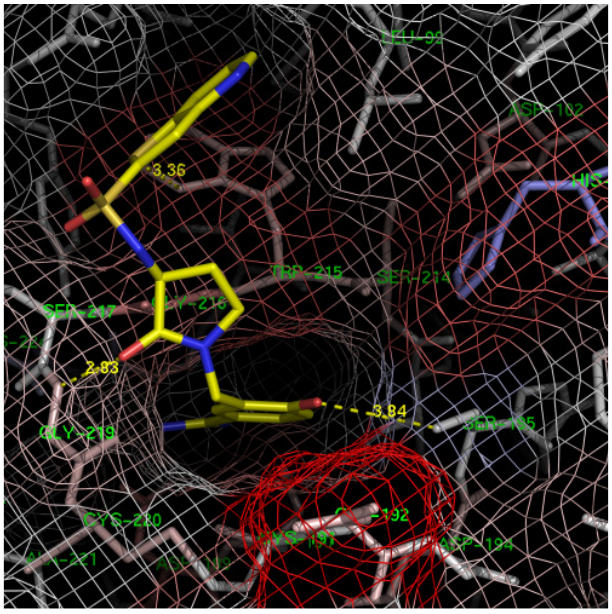


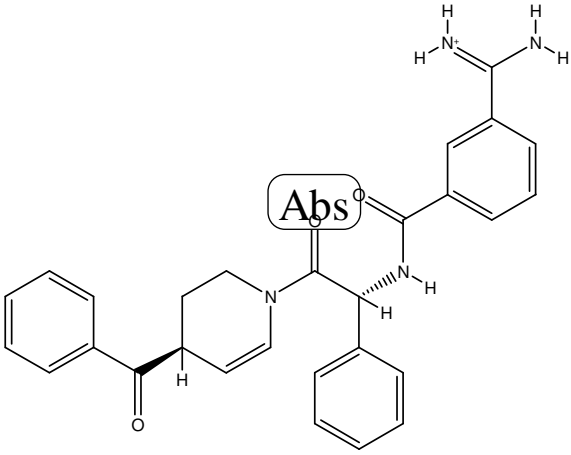
B14/1f0u 0.07 µM -9.8 kcal/mol
docked/predicted: ΔG bind elec: -10.5, ΔG 5th ranked: -10.7
Positive elec interaction to Asn97 and positive vdw/elec interaction to Gln192.



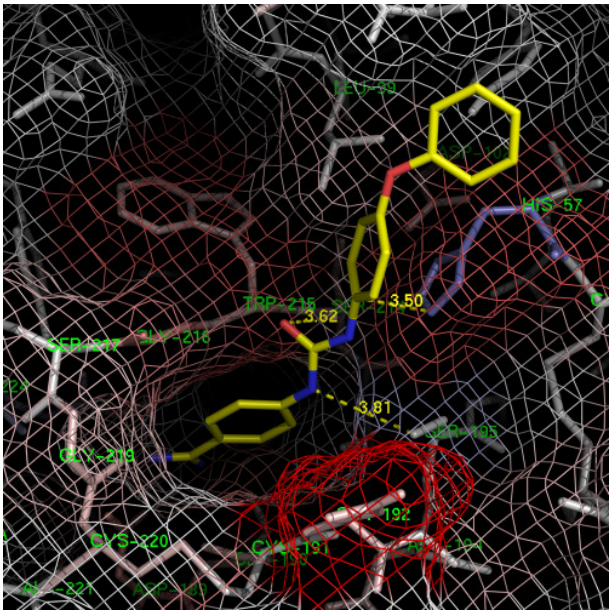


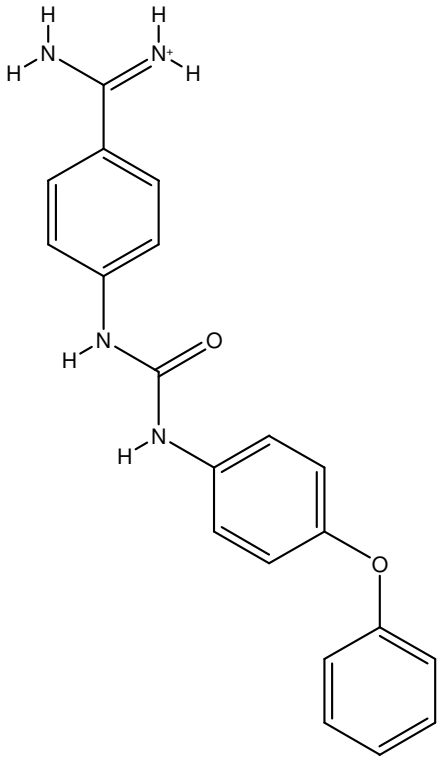
B15/1f0t 1 µM -8.1 kcal/mol
docked/predicted: ΔG bind elec: -9.7, ΔG 5th ranked: -9.8
Positive vdw (and elec) interaction to Trp215 but negative vdw to Ser195. (Similar to B16)



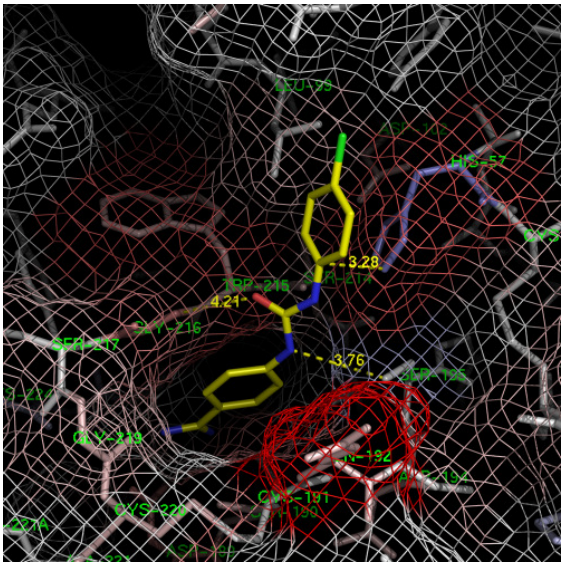


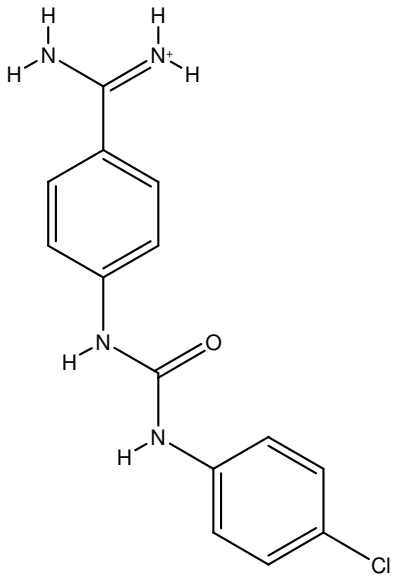
B16/1eb2 1 µM -8.1 kcal/mol
docked/predicted: ΔG bind elec: -7.8, ΔG 5th ranked: -7.2
Positive vdw interaction to Trp215 but negative vdw to Ser195. (similar to B15)



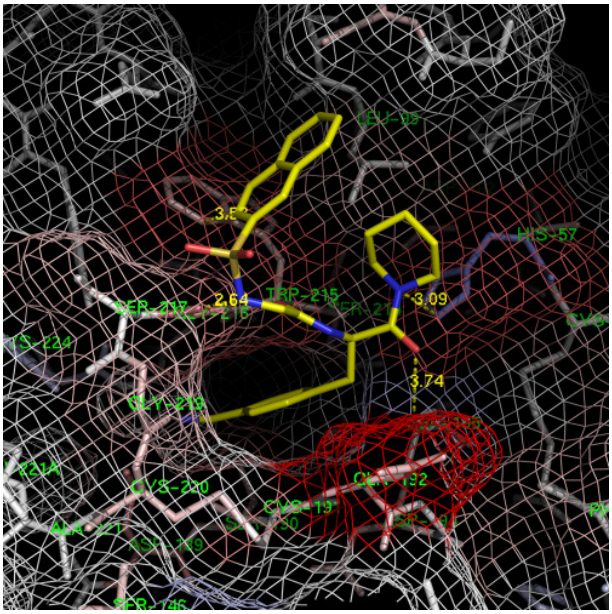


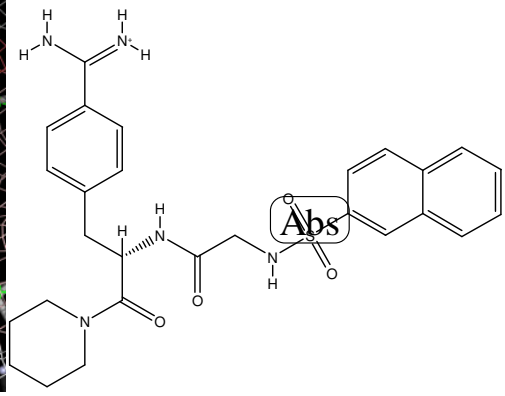
B18/1bjv 3 μM -7.5 kcal/mol
docked/predicted: ΔG bind elec: -9.4, ΔG 5th ranked: -10.7
Positive vdw interaction to His57 but negative vdw to Ser195.



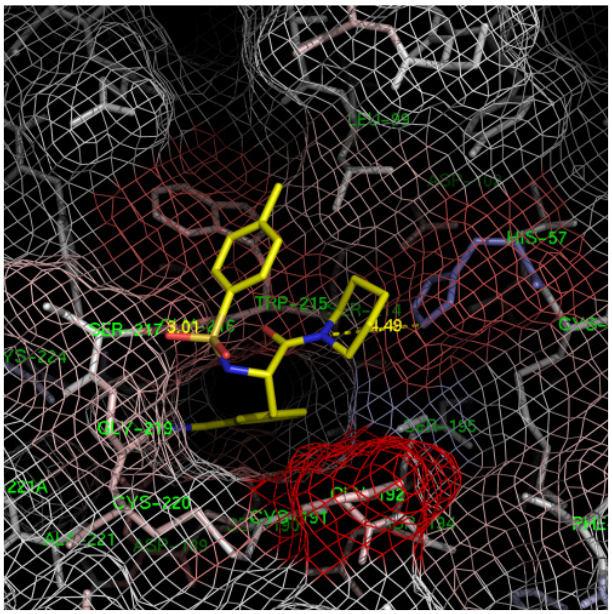


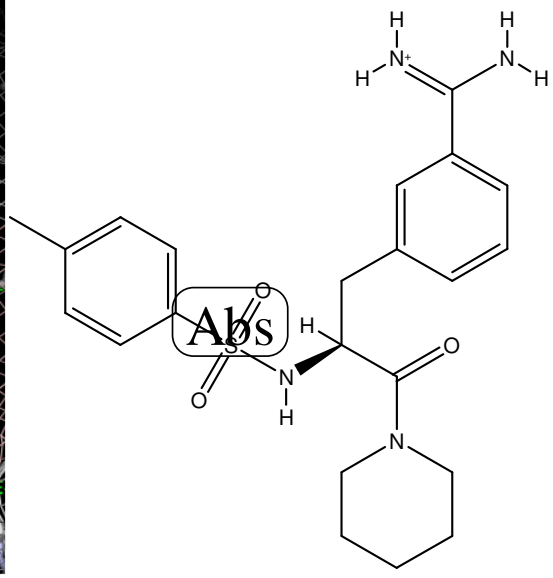
B19/1bju 16 μM -6.5 kcal/mol
docked/predicted: ΔG bind elec: -8.6, ΔG 5th ranked: -8.5, RMSD ~3.5 Å
Positive vdw interaction to His57 but negative vdw to Ser195. (similar to B18)





B06/1ppc 0.7 µM -8.4 kcal/mol
docked/predicted: ΔG bind elec: -10.0, ΔG 5th ranked: -9.9
Positive vdw interaction to His57 and Trp215 but negative vdw to Ser195. Positive elec to Gly216.





B05/1pph 0.7 µM -8.1 kcal/mol
docked/predicted: ΔG bind elec: -8.7, ΔG 5th ranked: -9.0
Positive elec to Gly216.

Renatus, M., Bode, W., Huber, R., Sturzebecher, J. and Stubbs, M.T. (1998) Structural and functional analyses of benzamidine-based inhibitors in complex with trypsin: implications for the inhibition of factor Xa, tPA, and urokinase, *J Med Chem*, **41**, 5445-5456.