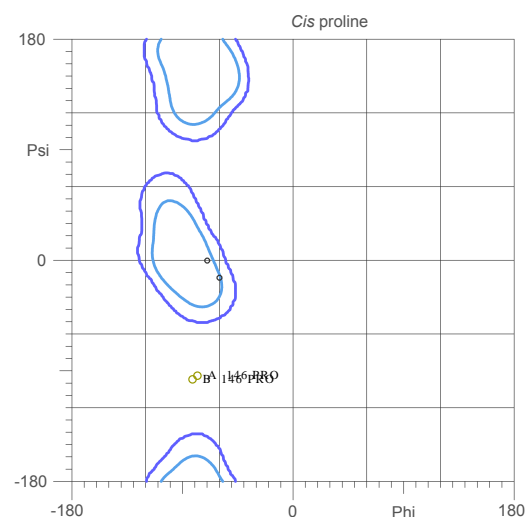
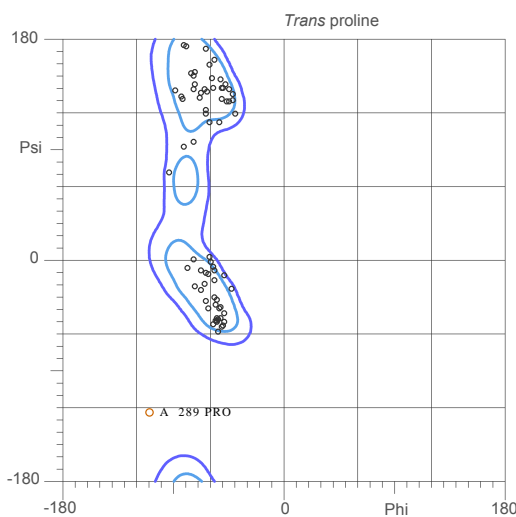
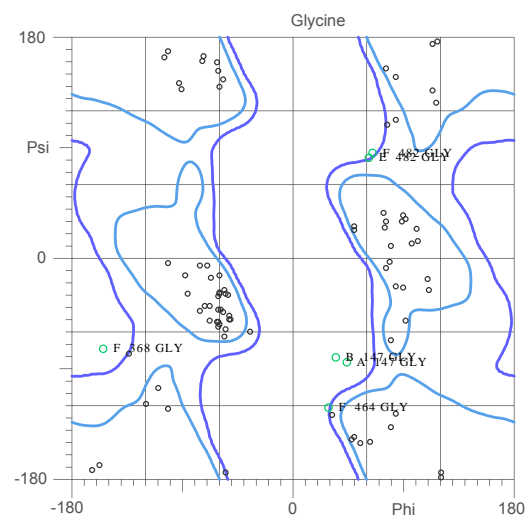
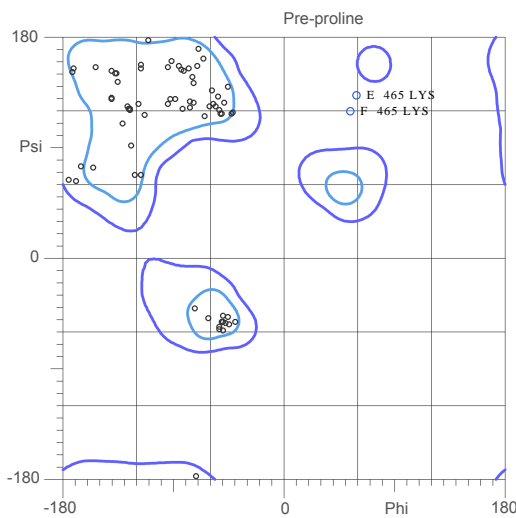
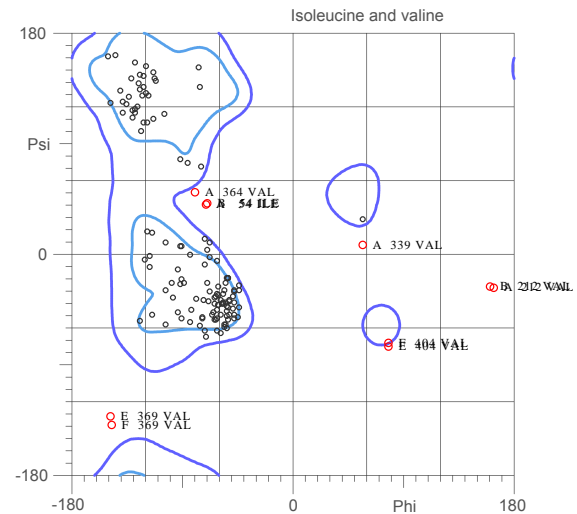
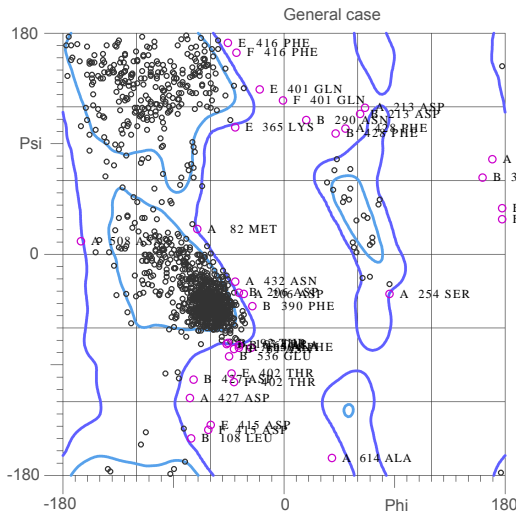


MolProbity Ramachandran analysis

3d0i.H.pdb, model 1



87.1% (131/150) of all residues were in favored (98%) regions.
No. of outliers of all residues were in allowed (100%) regions.

Shown here: 37 outliers (Phi, Psi):

A 342A (71.4, 45.3)	B 290A (107.1, 112.3)
A 342B (71.4, 45.3)	B 290B (107.1, 112.3)
A 342C (71.4, 45.3)	B 290C (107.1, 112.3)
A 342D (71.4, 45.3)	B 290D (107.1, 112.3)
A 342E (71.4, 45.3)	B 290E (107.1, 112.3)
A 342F (71.4, 45.3)	B 290F (107.1, 112.3)
A 342G (71.4, 45.3)	B 290G (107.1, 112.3)
A 342H (71.4, 45.3)	B 290H (107.1, 112.3)
A 342I (71.4, 45.3)	B 290I (107.1, 112.3)
A 342J (71.4, 45.3)	B 290J (107.1, 112.3)
A 342K (71.4, 45.3)	B 290K (107.1, 112.3)
A 342L (71.4, 45.3)	B 290L (107.1, 112.3)
A 342M (71.4, 45.3)	B 290M (107.1, 112.3)
A 342N (71.4, 45.3)	B 290N (107.1, 112.3)
A 342O (71.4, 45.3)	B 290O (107.1, 112.3)
A 342P (71.4, 45.3)	B 290P (107.1, 112.3)
A 342Q (71.4, 45.3)	B 290Q (107.1, 112.3)
A 342R (71.4, 45.3)	B 290R (107.1, 112.3)
A 342S (71.4, 45.3)	B 290S (107.1, 112.3)
A 342T (71.4, 45.3)	B 290T (107.1, 112.3)
A 342U (71.4, 45.3)	B 290U (107.1, 112.3)
A 342V (71.4, 45.3)	B 290V (107.1, 112.3)
A 342W (71.4, 45.3)	B 290W (107.1, 112.3)
A 342X (71.4, 45.3)	B 290X (107.1, 112.3)
A 342Y (71.4, 45.3)	B 290Y (107.1, 112.3)
A 342Z (71.4, 45.3)	B 290Z (107.1, 112.3)