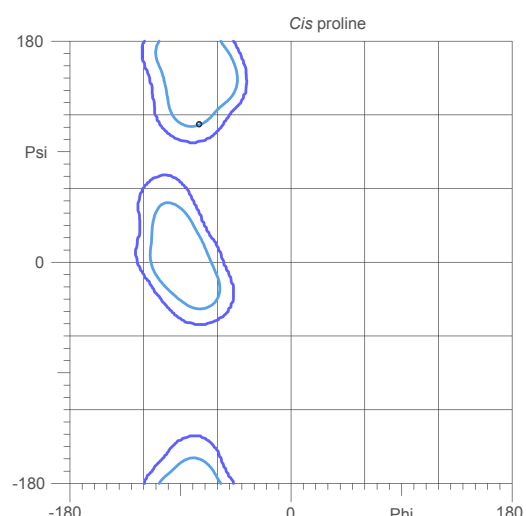
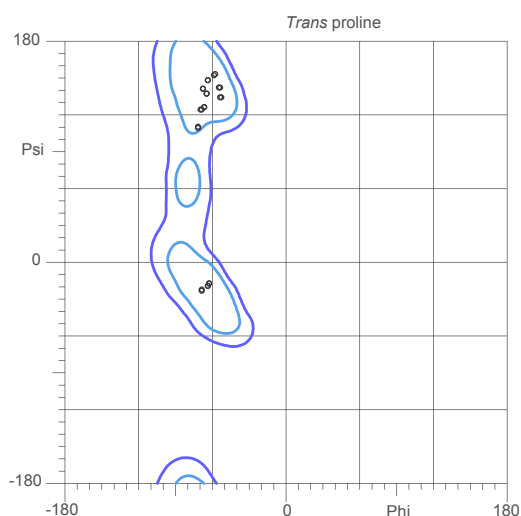
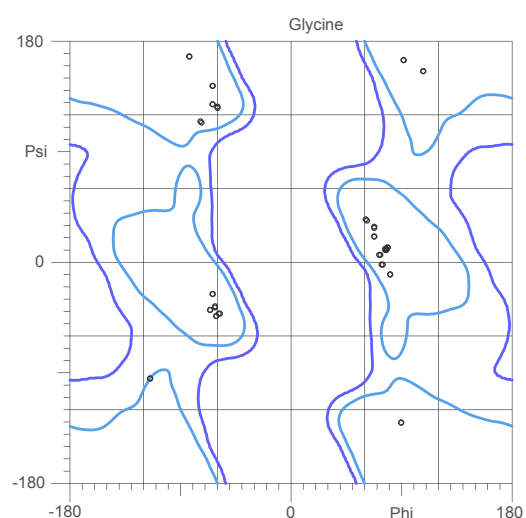
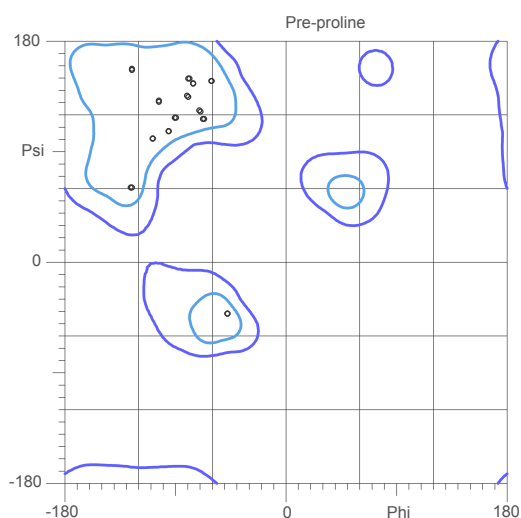
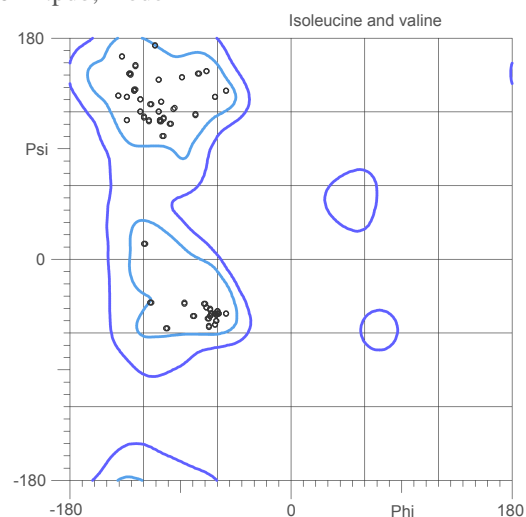
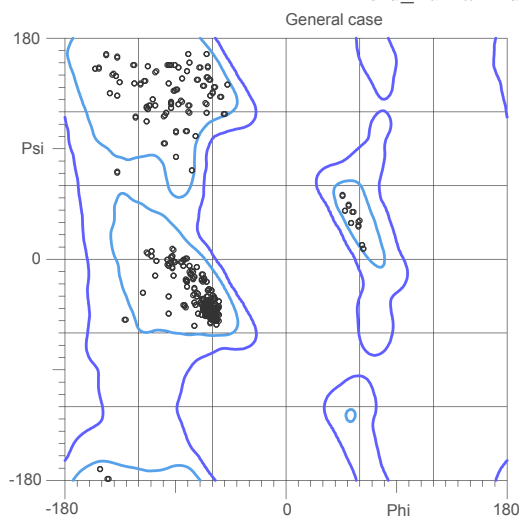


# MolProbity Ramachandran analysis

fold\_humanmdh1\_model\_0FH.pdb, model 1



98.9% (655/662) of all residues were in favored (98%) regions.  
100.0% (662/662) of all residues were in allowed (>99.8%) regions.

There were no outliers.