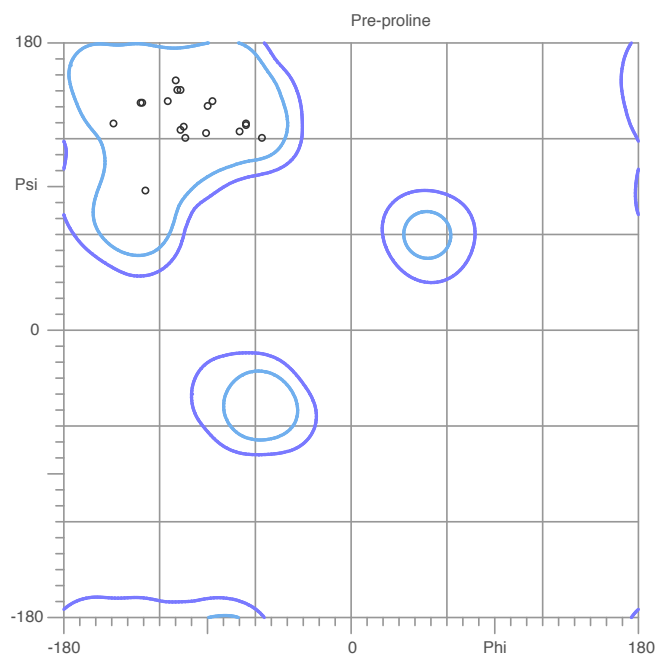
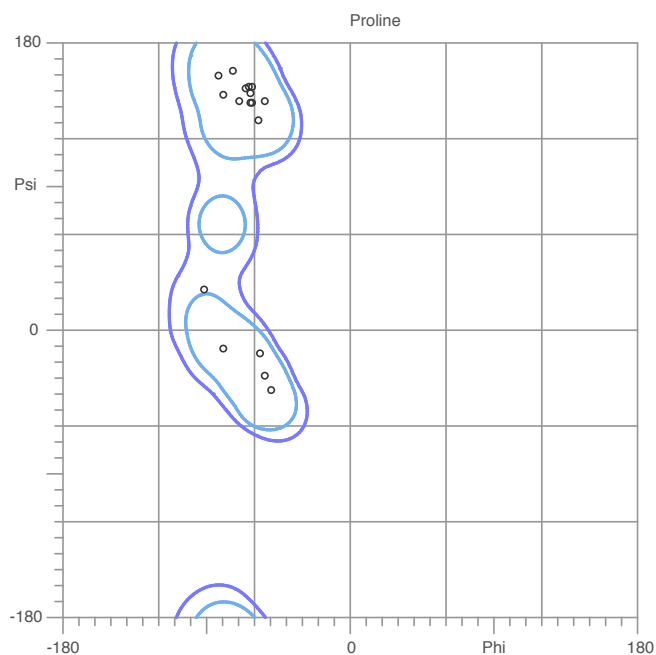
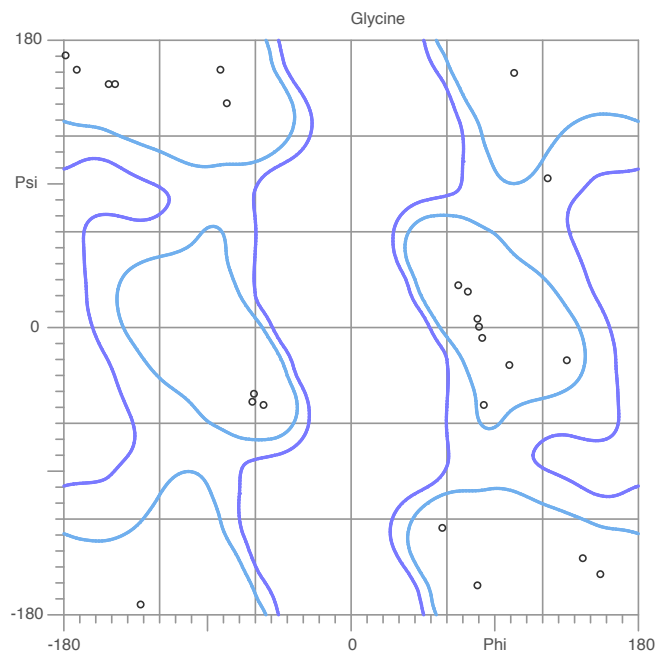
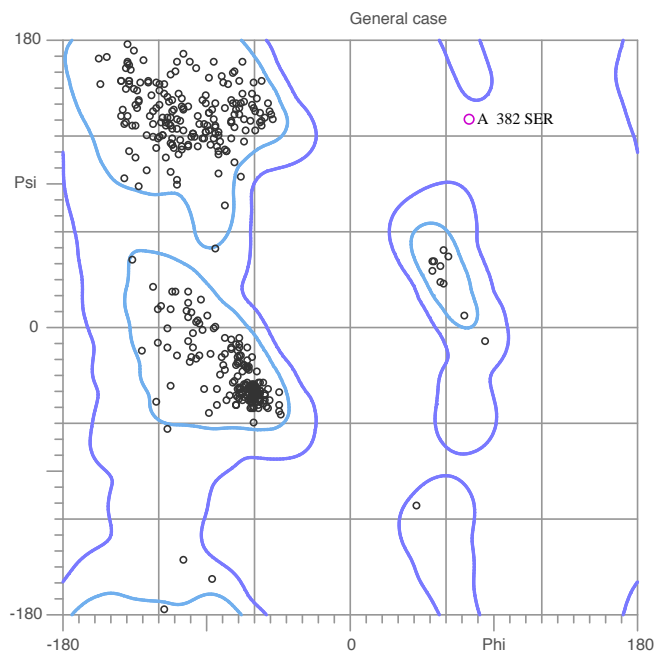


# MolProbity Ramachandran analysis

3NHE.pdb, model 1



97,7% (425/435) of all residues were in favored (98%) regions.  
99,8% (434/435) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

A 382 SER (74,6, 131,8)

<http://kinemage.biochem.duke.edu>

Lovell, Davis, et al. Proteins 50:437 (2003)