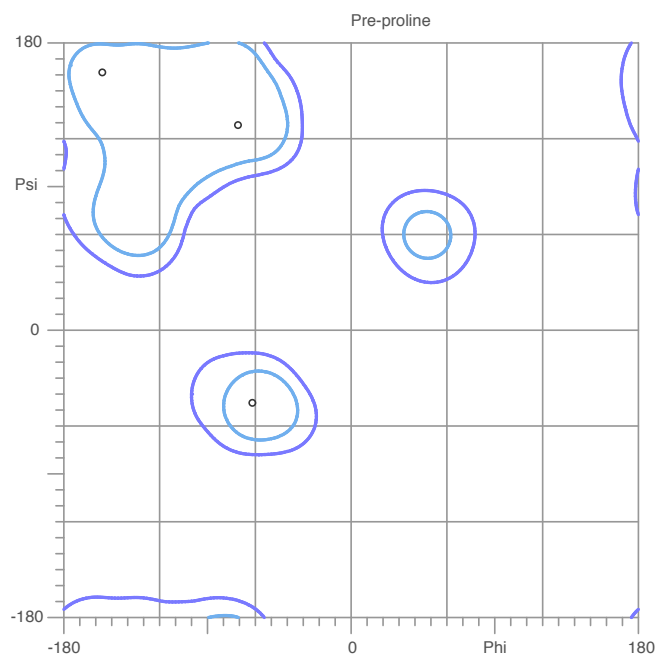
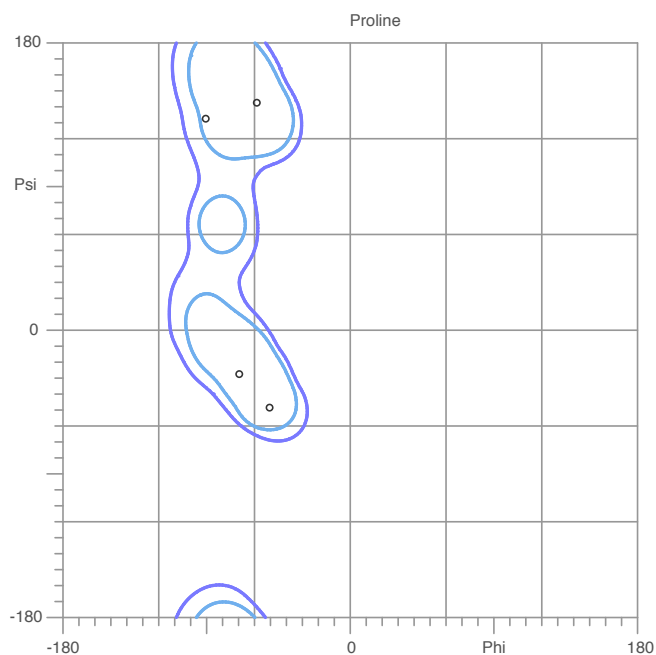
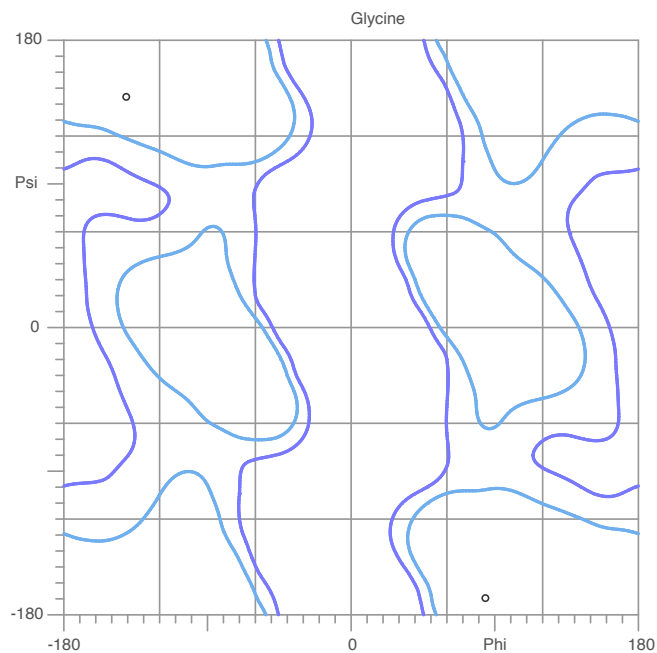
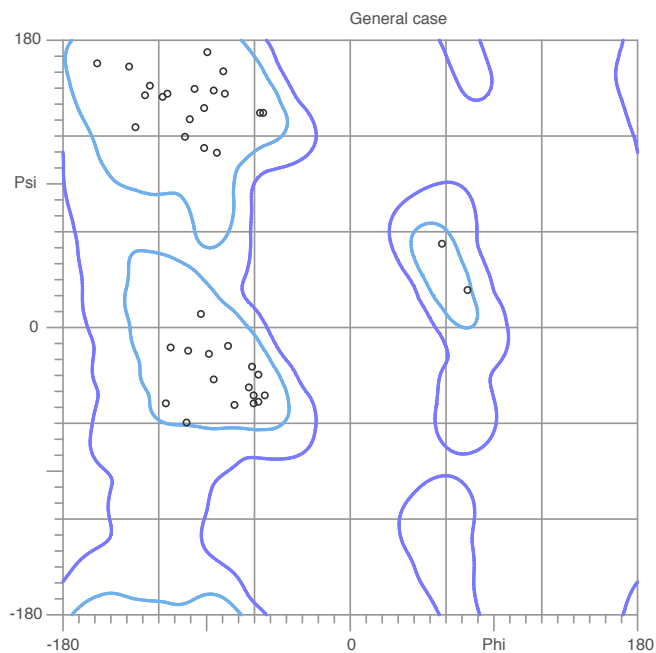


MolProbity Ramachandran analysis

4AAZ_A.pdb, model 1



100,0% (46/46) of all residues were in favored (98%) regions.
100,0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

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