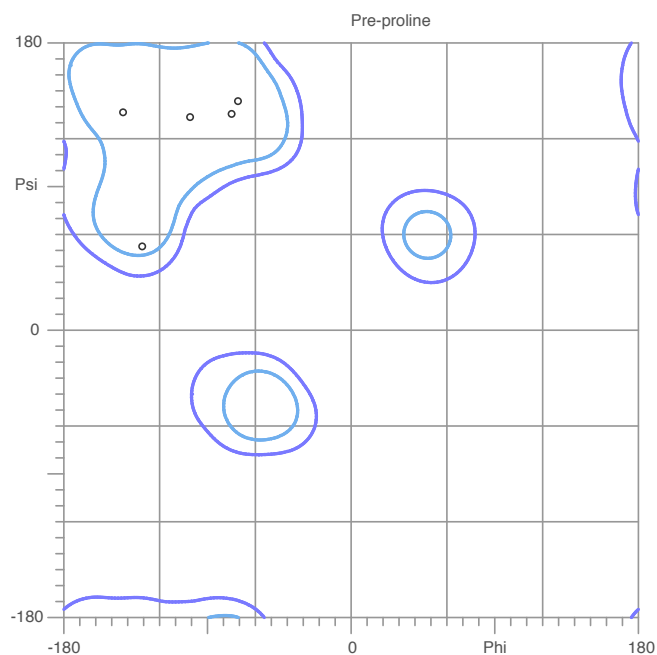
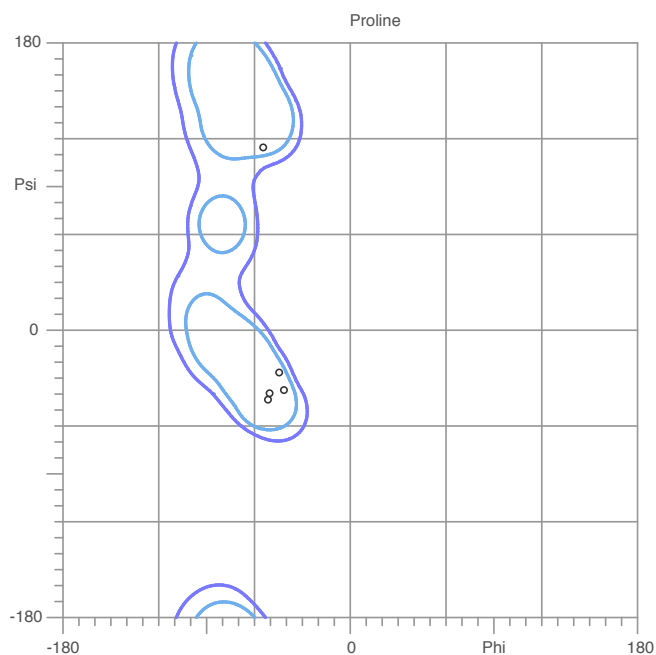
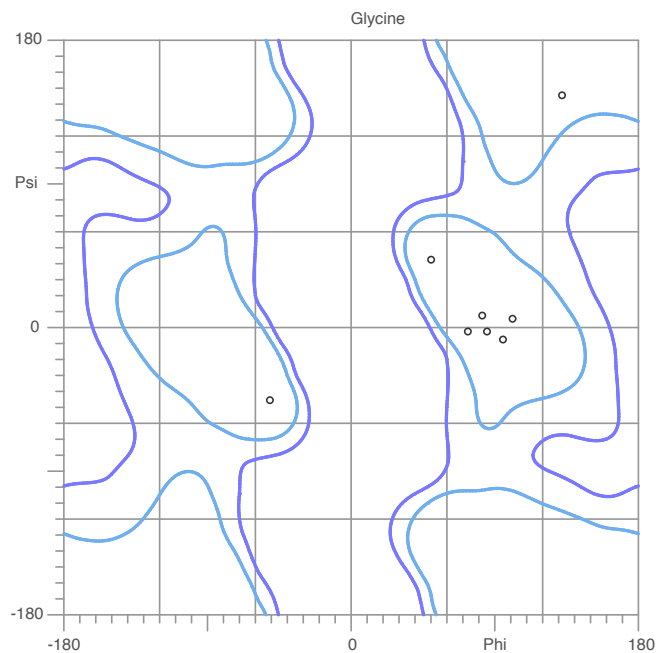
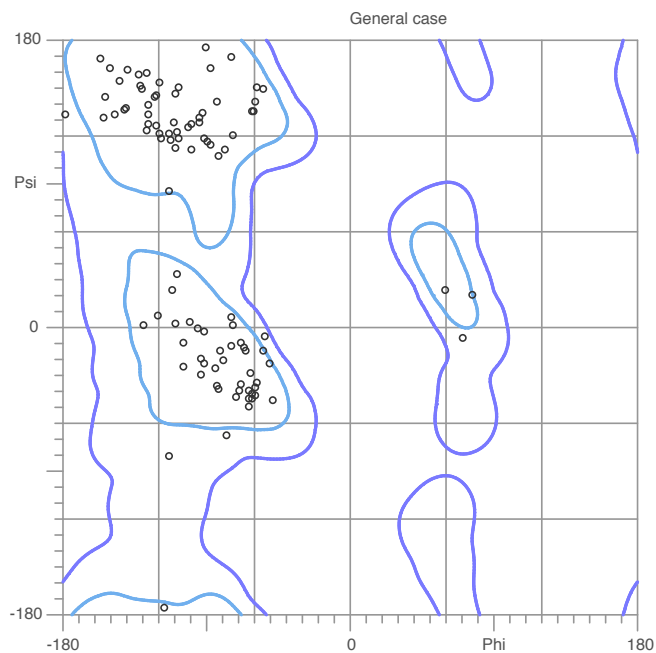


# MolProbity Ramachandran analysis

UUR17A\_XRay\_em\_bcr3.pdb, model 1



94.9% (112/118) of all residues were in favored (98%) regions.

100.0% (118/118) 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)