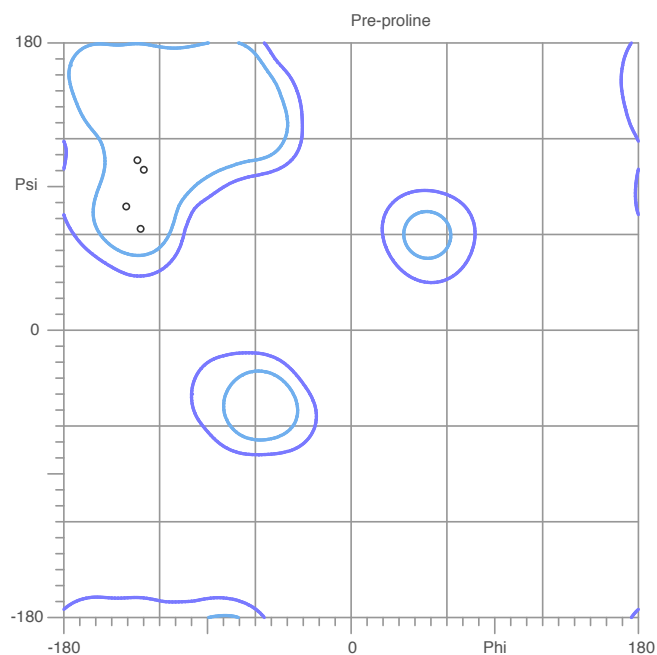
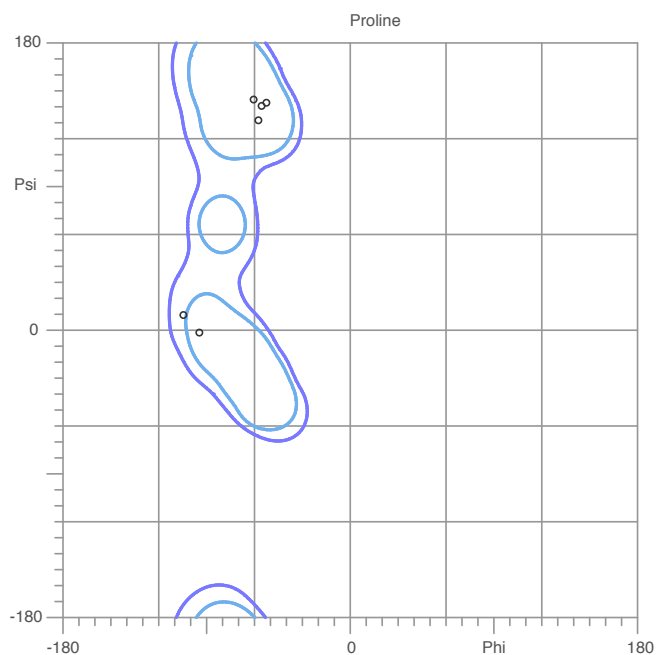
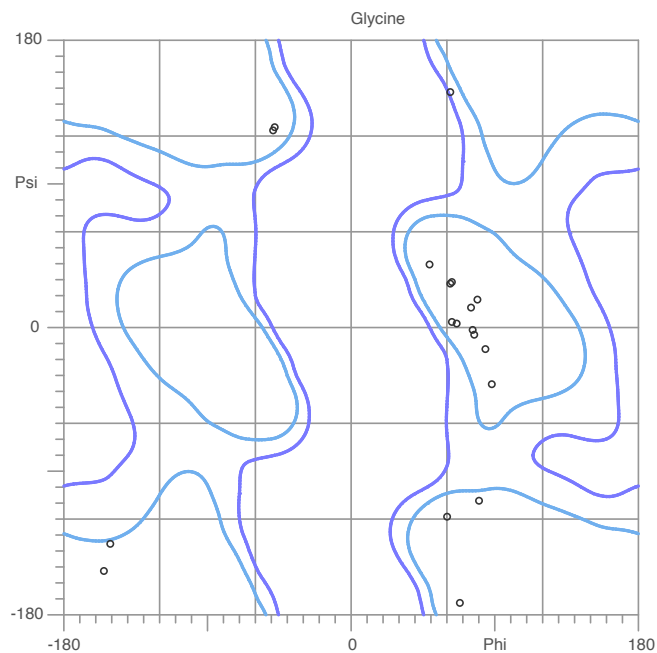
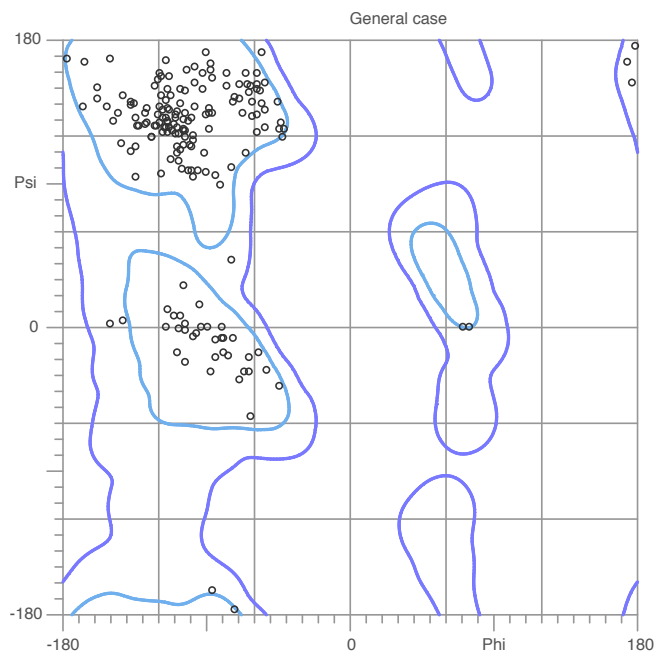


MolProbity Ramachandran analysis

HR5546A_XRay_em_bcr3.pdb, model 1



94.7% (198/209) of all residues were in favored (98%) regions.

100.0% (209/209) 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)