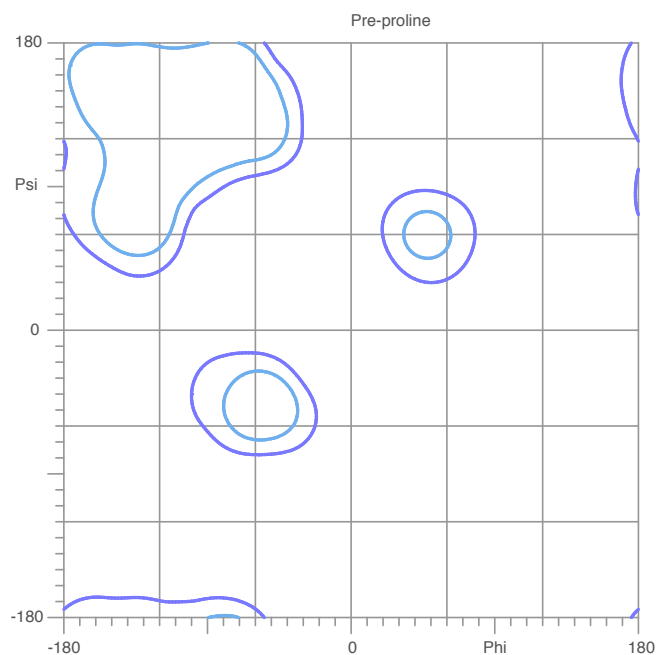
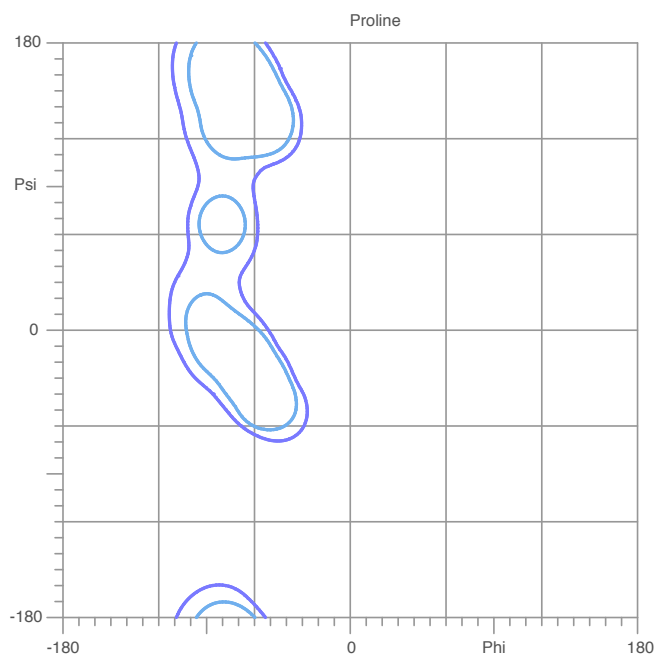
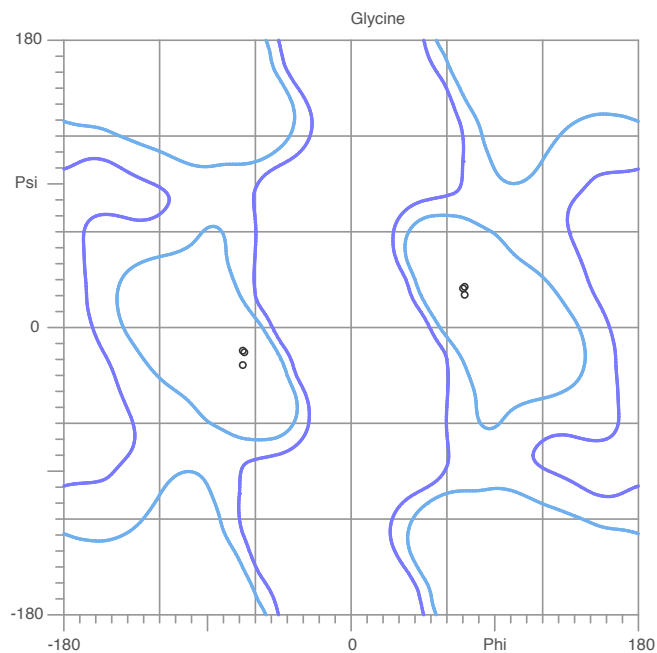
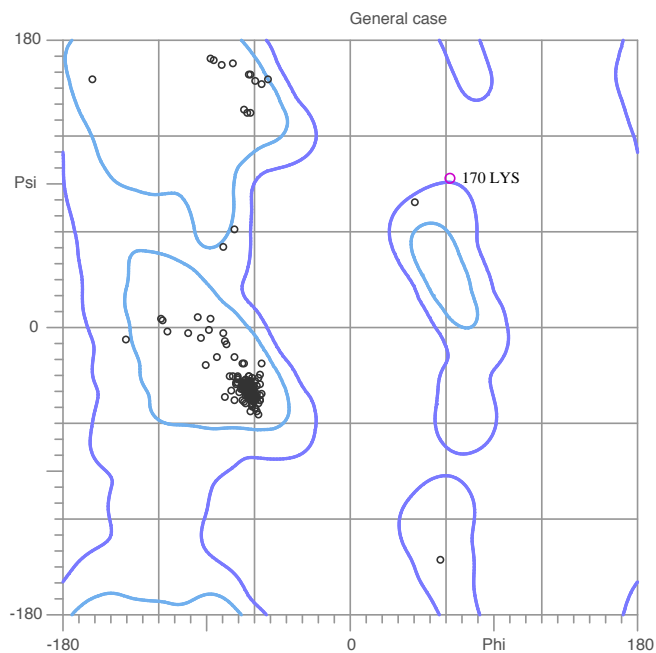


# MolProbity Ramachandran analysis

SR384\_XRay\_em\_bcr3.pdb, model 1



95.9% (142/148) of all residues were in favored (98%) regions.  
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
170 LYS (62.6, 94.7)

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

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