MolProbity Ramachandran analysis

16pk_.B99990038.pdb, model 1
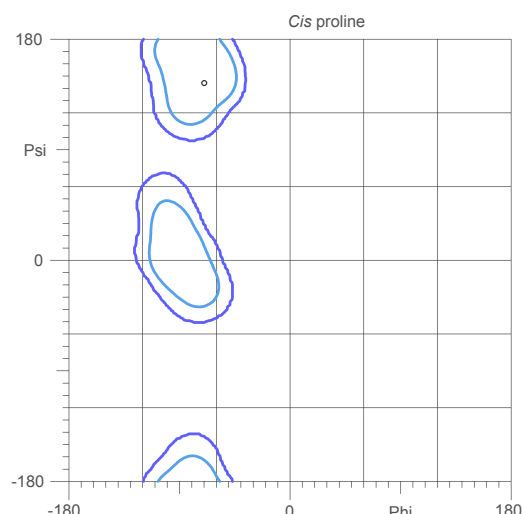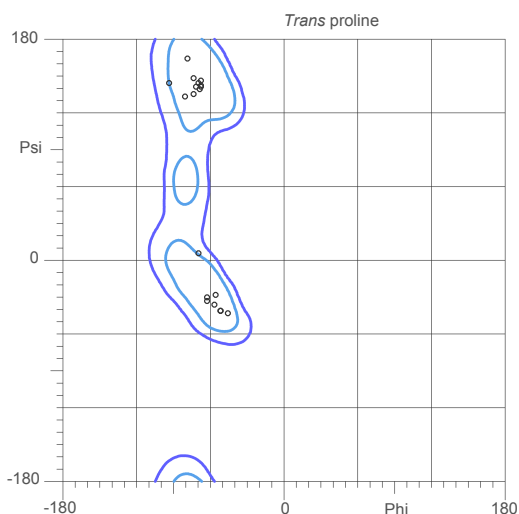
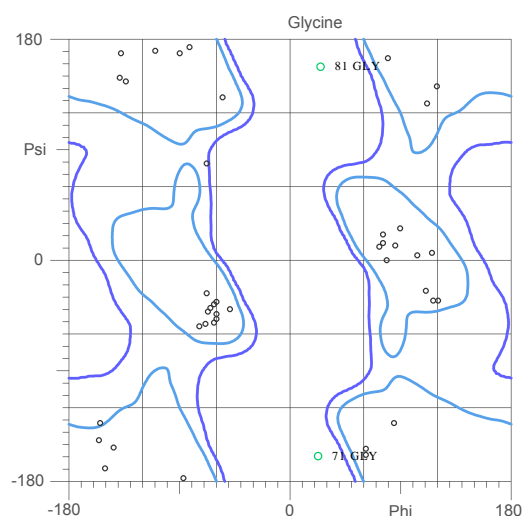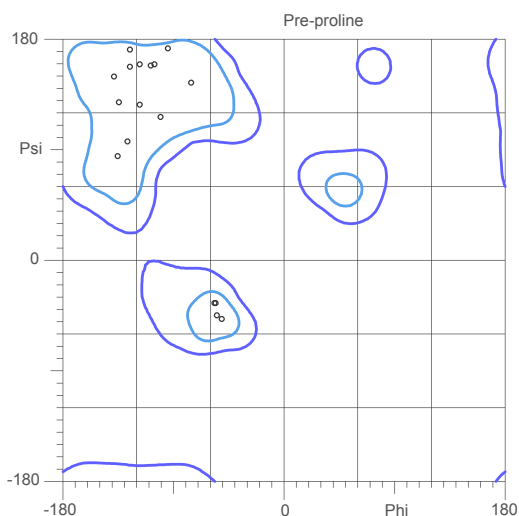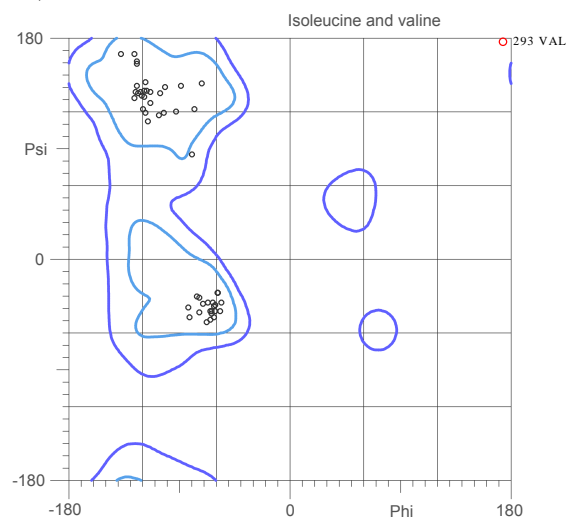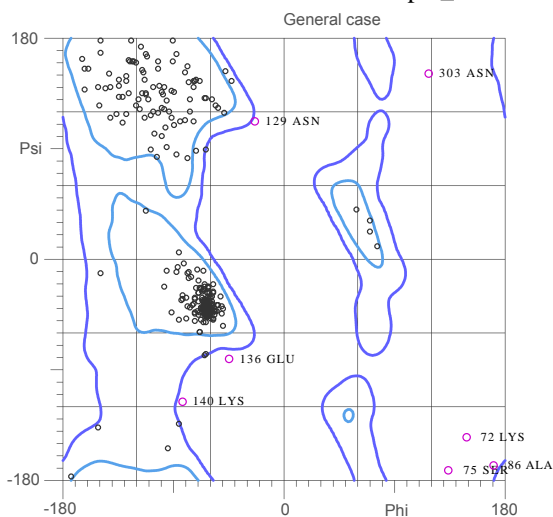
93.7% (387/413) of all residues were in favored (98%) regions.
97.6% (403/413) of all residues were in allowed (>99.8%) regions.

There were 10 outliers (phi, psi):
    71 GLY (23.1, -160.8)
    72 LYS (149.5, -145.8)
    75 SER (134.4, -172.5)
    81 GLY (25.9, 158.5)
    86 ALA (172.0, -168.6)
    129 ASN (-24.7, 113.0)
    136 GLU (-45.3, -81.9)
    140 LYS (-83.9, -116.5)
    293 VAL (174.6, 178.2)
    303 ASN (118.3, 152.4)

http://kinemage.biochem.duke.edu

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