MolProbity Ramachandran analysis

1air_.B99990030.pdb, model 1
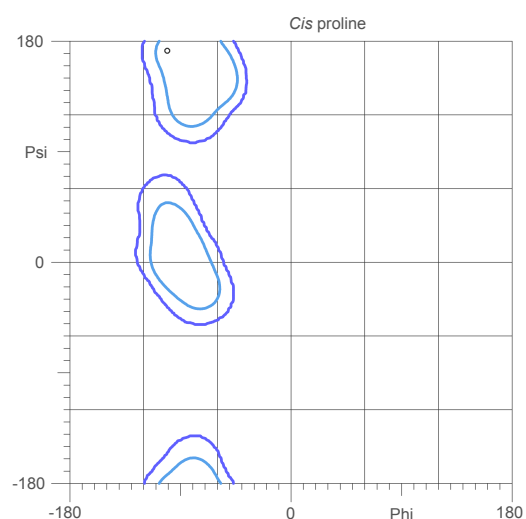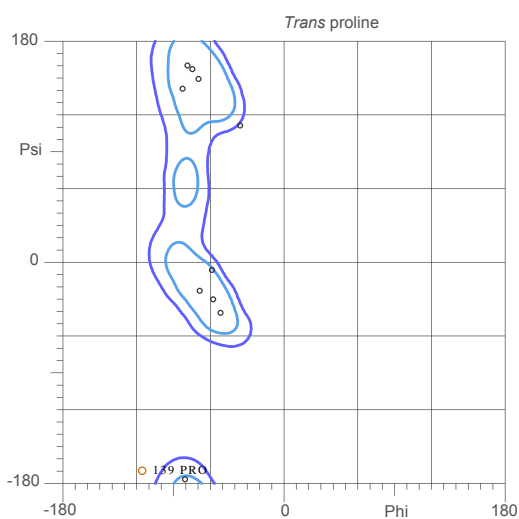
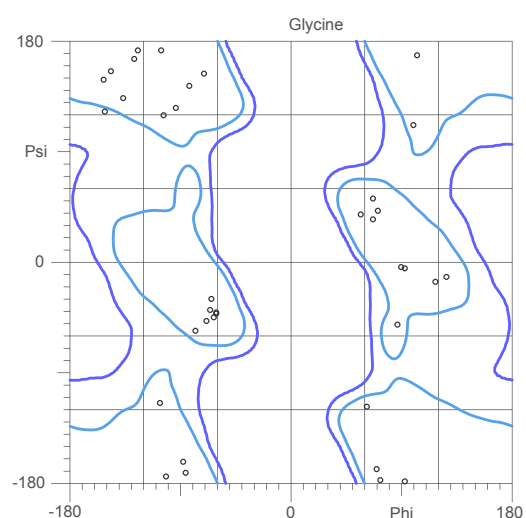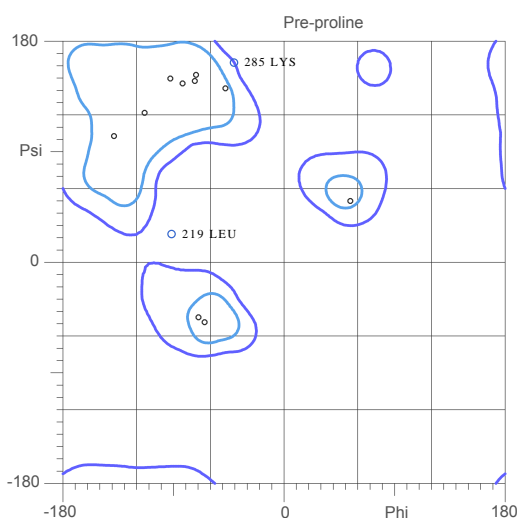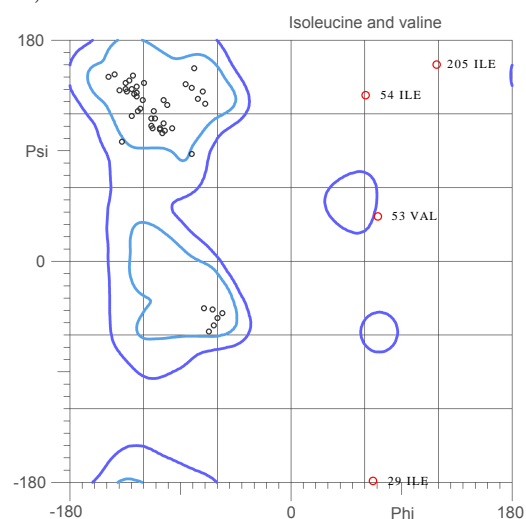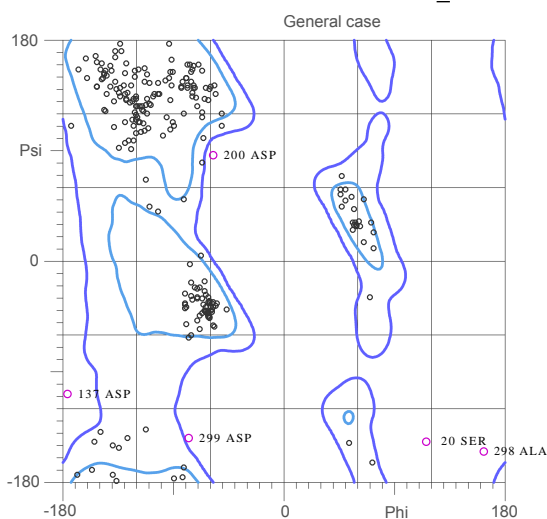

88.9% (311/350) of all residues were in favored (98%) regions.
96.6% (338/350) of all residues were in allowed (>99.8%) regions.

There were 12 outliers (phi, psi):
    20 SER (116.1, -147.9)
    29 ILE (67.4, -179.6)
    53 VAL (71.5, 37.9)
    54 ILE (61.9, 136.5)
    137 ASP (-177.3, -108.8)
    139 PRO (-116.8, -170.1)
    200 ASP (-58.5, 87.3)
    205 ILE (119.1, 161.1)
    219 LEU (-92.4, 23.4)
    285 LYS (-41.1, 163.4)
    298 ALA (163.7, -155.0)
    299 ASP (-78.6, -144.2)

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