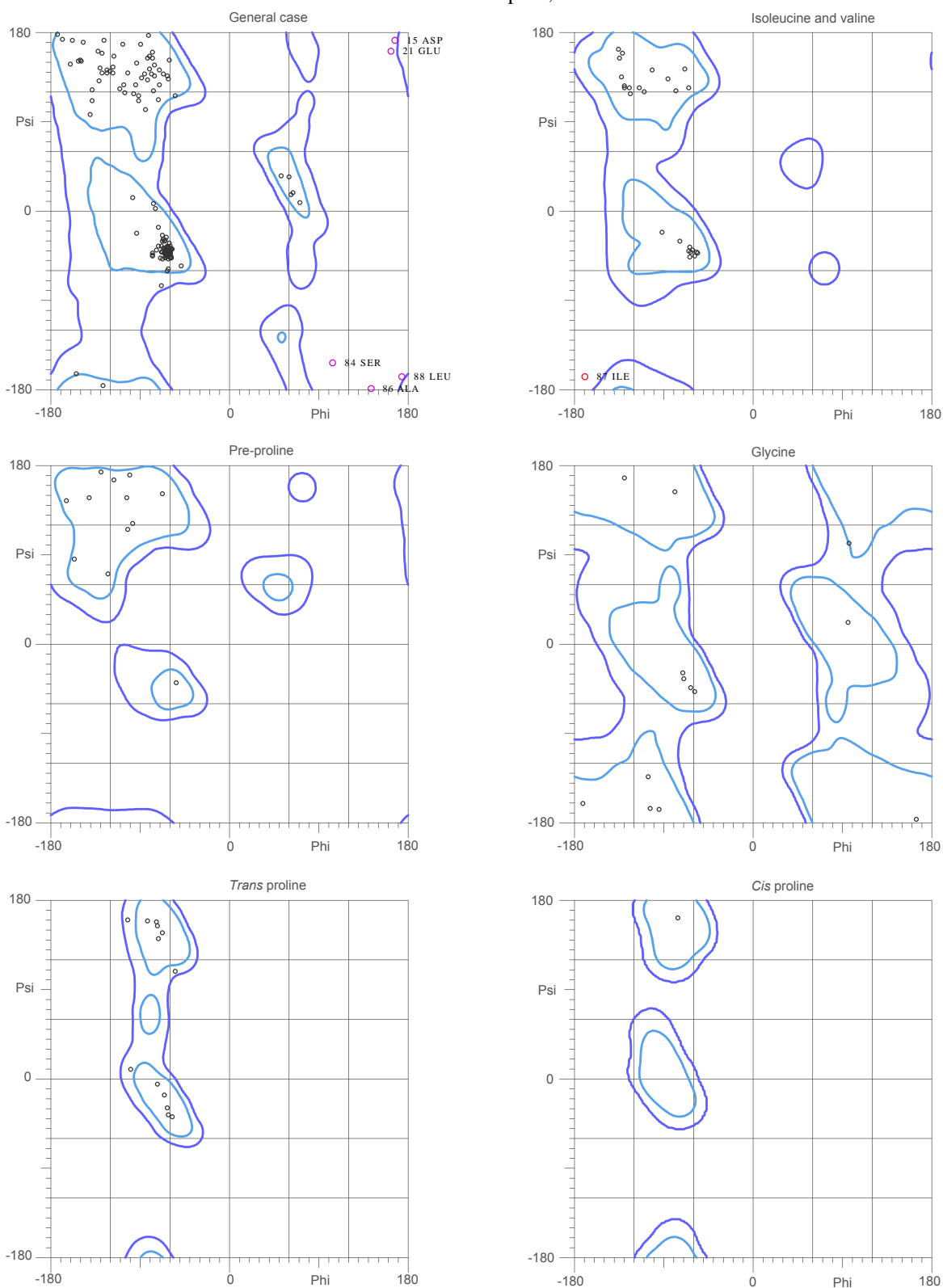# MolProbity Ramachandran analysis

1at3A.B99990042.pdb, model 1

94,4% (203/215) of all residues were in favored (98%) regions.
97,2% (209/215) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
    15 ASP (167,7, 174,0)
    21 GLU (163,7, 162,5)
    84 SER (104,4, -153,6)
    86 ALA (143,1, -179,7)
    87 ILE (-170,5, -167,4)
    88 LEU (174,4, -167,8)

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