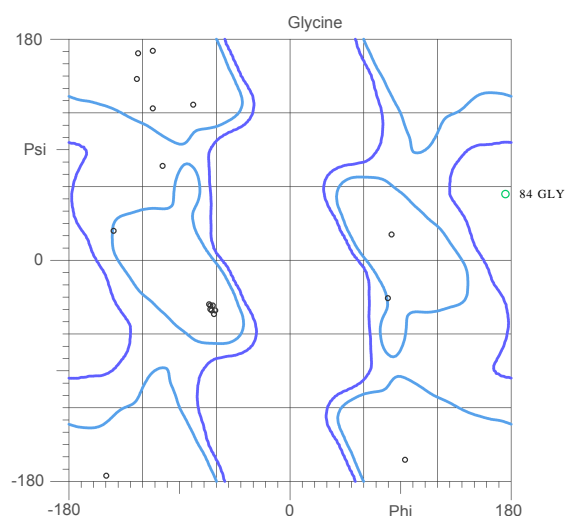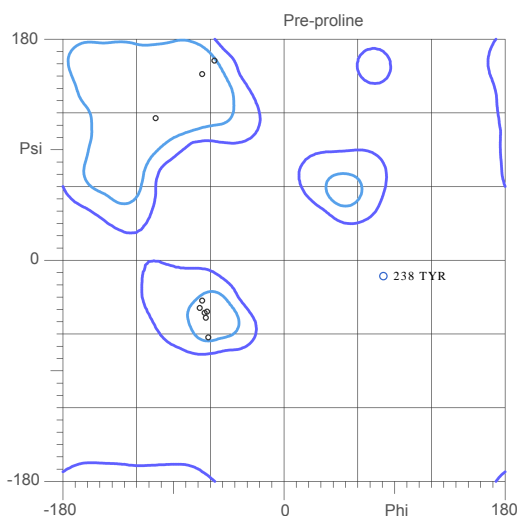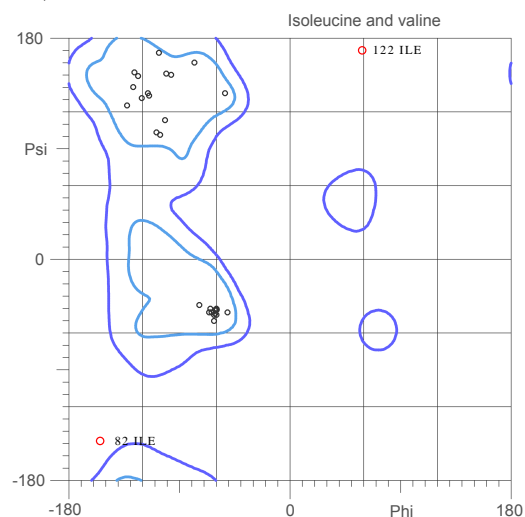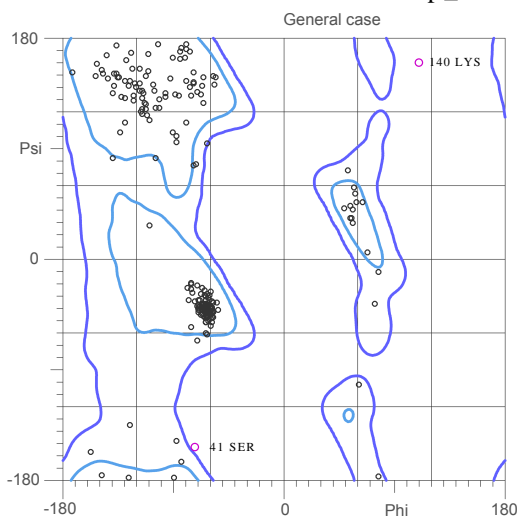# MolProbity Ramachandran analysis

1amp_.B99990019.pdb, model 1
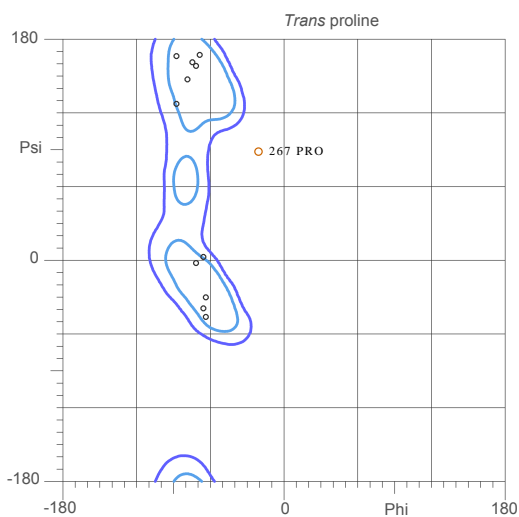
92,0% (266/289) of all residues were in favored (98%) regions.
97,6% (282/289) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
    41 SER (-73,9, -153,4)
    82 ILE (-155,7, -149,0)
    84 GLY (176,9, 54,6)
    122 ILE (59,9, 171,7)
    140 LYS (110,7, 161,7)
    238 TYR (81,4, -14,0)
    267 PRO (-21,0, 89,6)

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