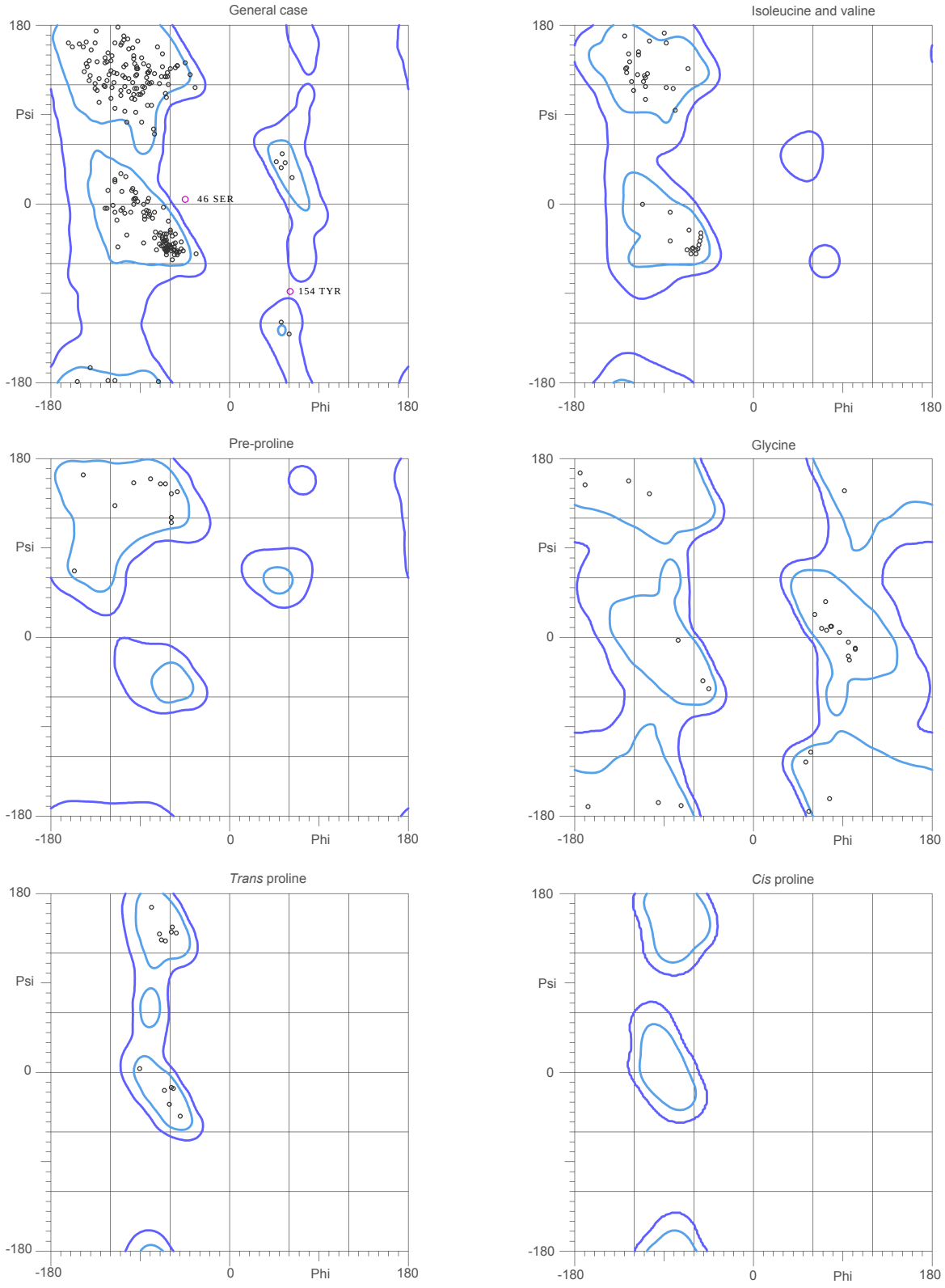
MolProbity Ramachandran analysis

5reh.H.pdb, model 1



96.8% (301/311) of all residues were in favored (98%) regions.
99.4% (309/311) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
46 SER (-45.9, 5.4)
154 TYR (61.9, -88.4)

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