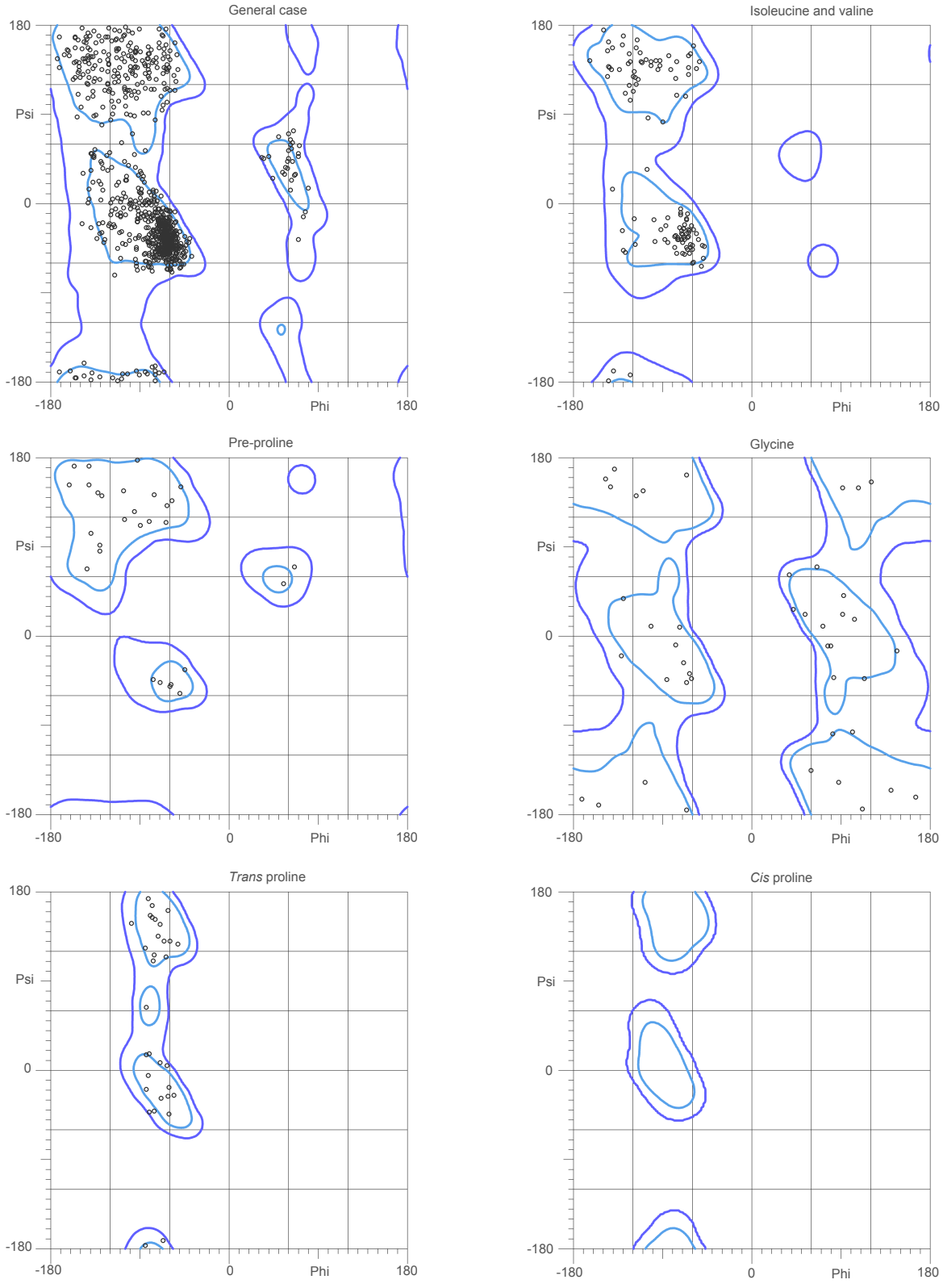
MolProbity Ramachandran analysis

6x2g.H.pdb, model 1



88.0% (899/1022) of all residues were in favored (98%) regions.
100.0% (1022/1022) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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