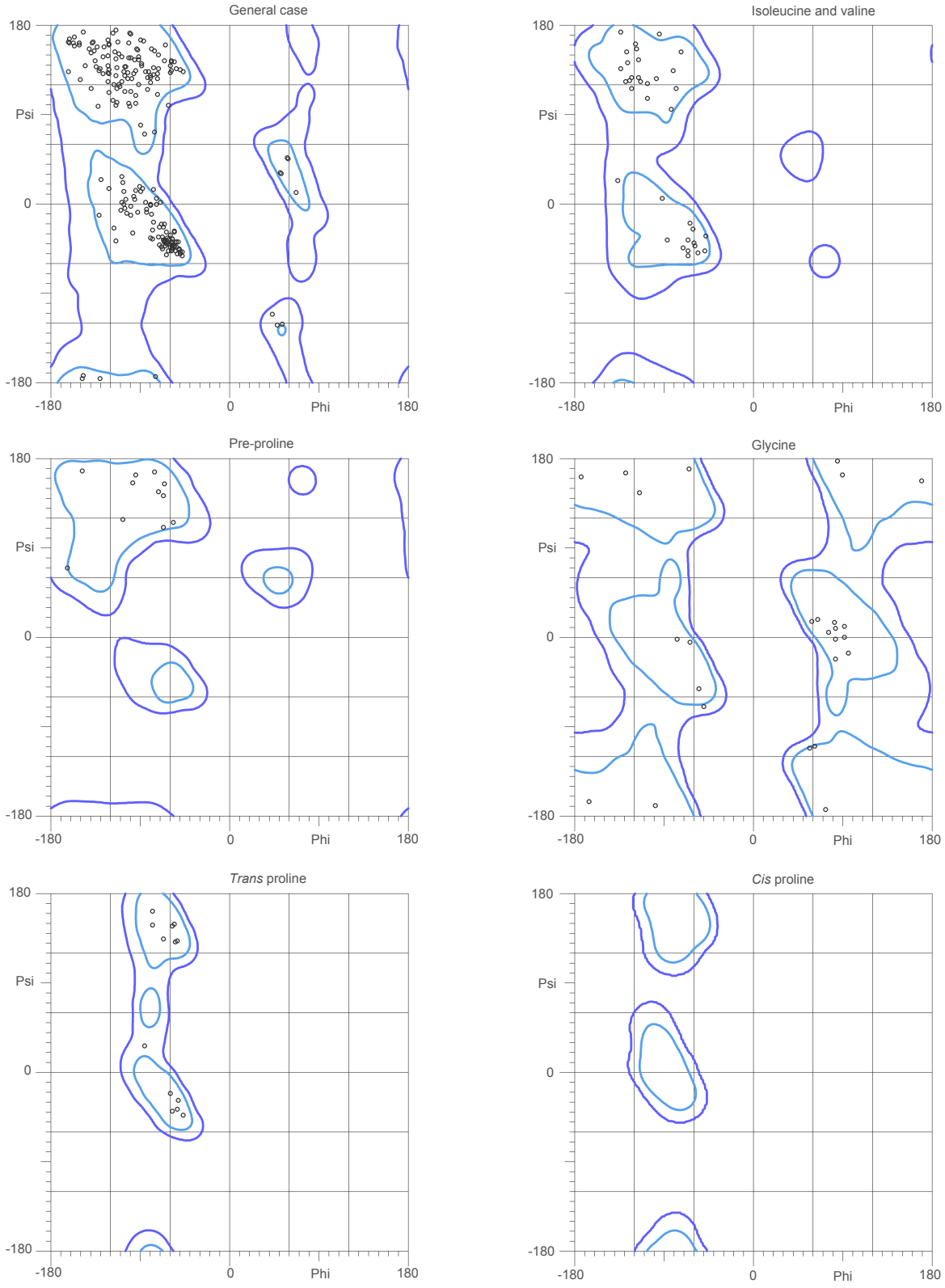
MolProbity Ramachandran analysis

3ea8.H.pdb, model 1



96.7% (294/304) of all residues were in favored (98%) regions.
100.0% (304/304) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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