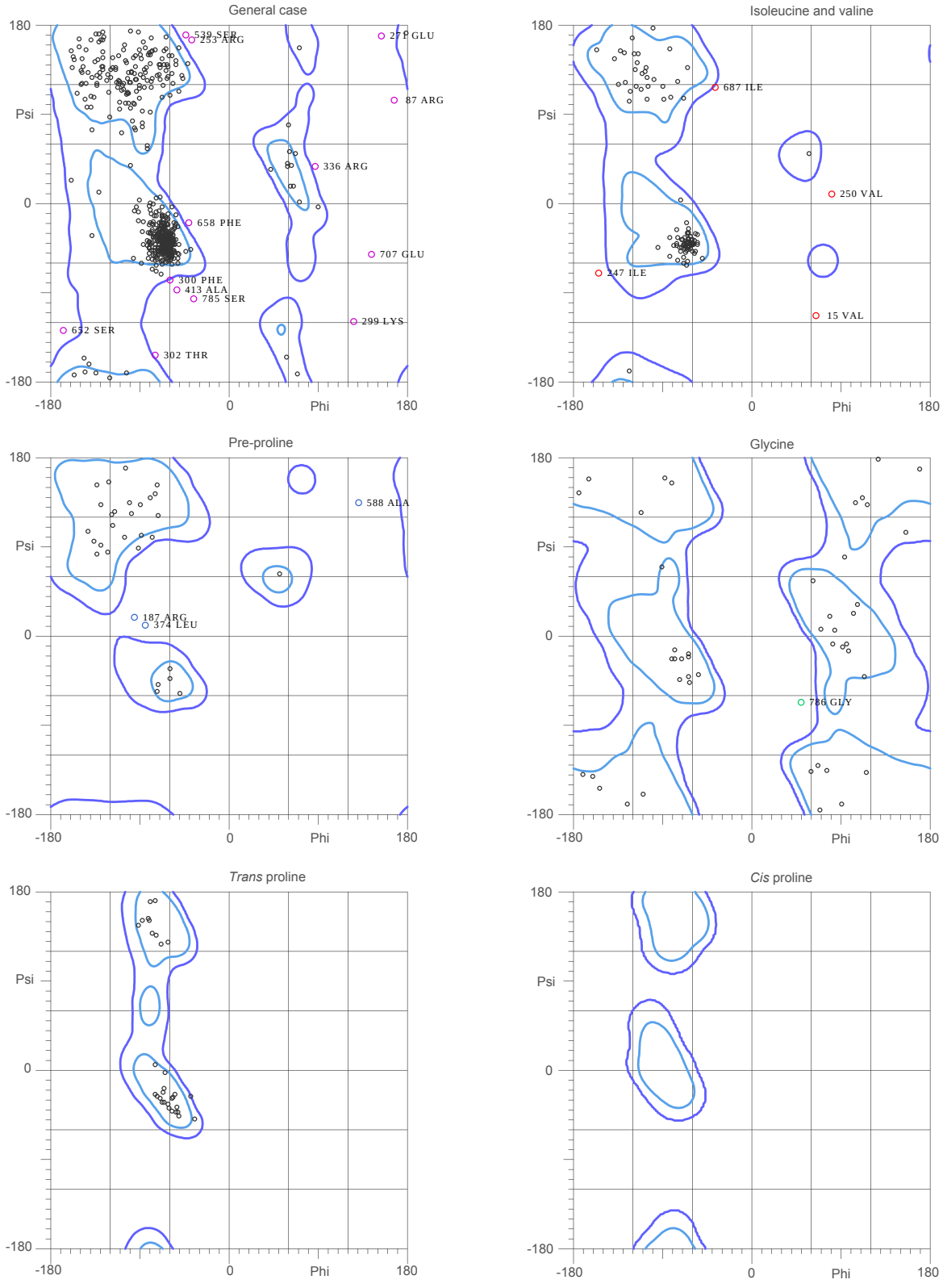
MolProbity Ramachandran analysis

1a8i_.B99990021.pdb, model 1



92,1% (746/810) of all residues were in favored (98%) regions.
97,4% (789/810) of all residues were in allowed (>=98.8%) regions.

There were 21 outliers (phi, psi):
15 VAL (65,8, -113,7)
87 ARG (167,8, 105,1)
187 ARG (-96,5, 19,6)
247 ILE (-155,1, -70,8)
250 VAL (81,0, 10,3)
253 ARG (-38,8, 166,3)
271 GLU (154,4, 170,2)
299 LYS (126,0, -119,1)
300 PHE (-60,7, -77,5)
302 THR (-75,7, -153,5)
336 ARG (87,2, 38,8)
374 LEU (-85,7, 11,5)
413 ALA (-54,0, -87,4)
539 SER (-44,7, 171,4)
588 ALA (131,6, 135,4)
652 SER (-168,3, -128,6)
658 PHE (-61,6, -19,4)
687 ILE (-37,3, 118,8)
707 GLU (144,8, -51,9)
785 SER (-36,7, -96,1)
786 GLY (50,6, -47,9)

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