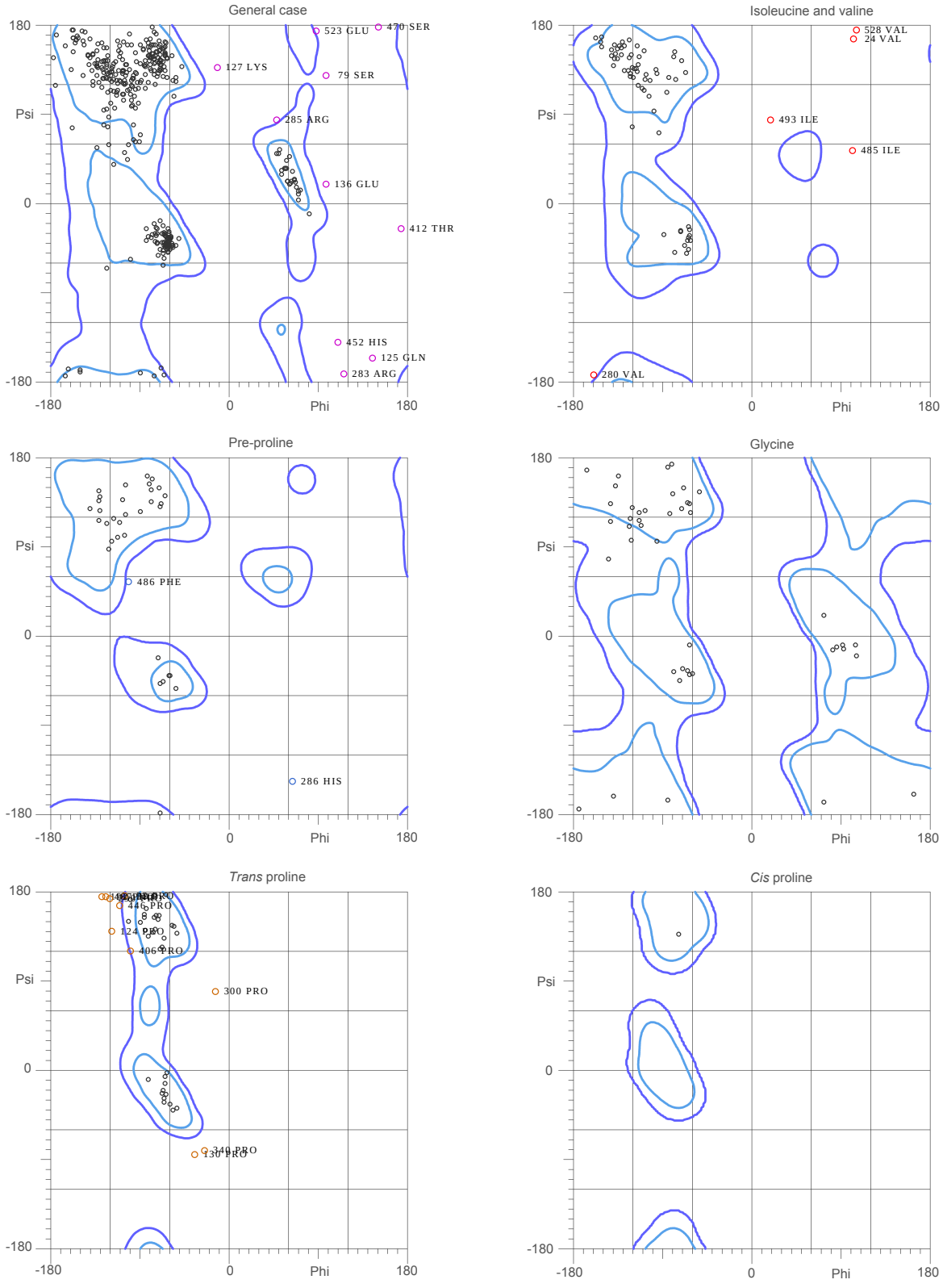
MolProbity Ramachandran analysis

1aozA.B99990041.pdb, model 1



89.1% (490/550) of all residues were in favored (98%) regions.
95.1% (523/550) of all residues were in allowed (>=98.8%) regions.

These were 27 outliers (phi, psi):
24 VAL (103.1, 167.3)
32 PRO (-106.3, 177.4)
79 SER (98.1, 158.6)
124 PRO (-119.6, 141.6)
125 GLN (143.3, -116.0)
127 LYS (-52.4, 138.8)
130 PRO (-51.3, -85.7)
136 GLU (98.0, 49.3)
192 PRO (-129.3, 176.4)
280 VAL (-168.7, -173.9)
283 ARG (136.1, -172.2)
285 ARG (48.7, 85.6)
286 HIS (64.3, -147.8)
298 PRO (-121.9, 174.8)
300 PRO (-54.3, 80.8)
340 PRO (-75.6, -95.4)
406 PRO (-101.0, 121.4)
412 THR (178.4, -35.8)
446 PRO (-111.2, 167.8)
452 HIS (113.0, -148.5)
470 SER (112.8, 175.2)
485 ILE (102.3, 53.8)
486 PHE (-102.3, 55.8)
487 PRO (-125.2, 179.3)
493 ILE (91.2, 81.5)
523 GLU (88.8, 175.4)
528 VAL (106.2, 176.4)

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