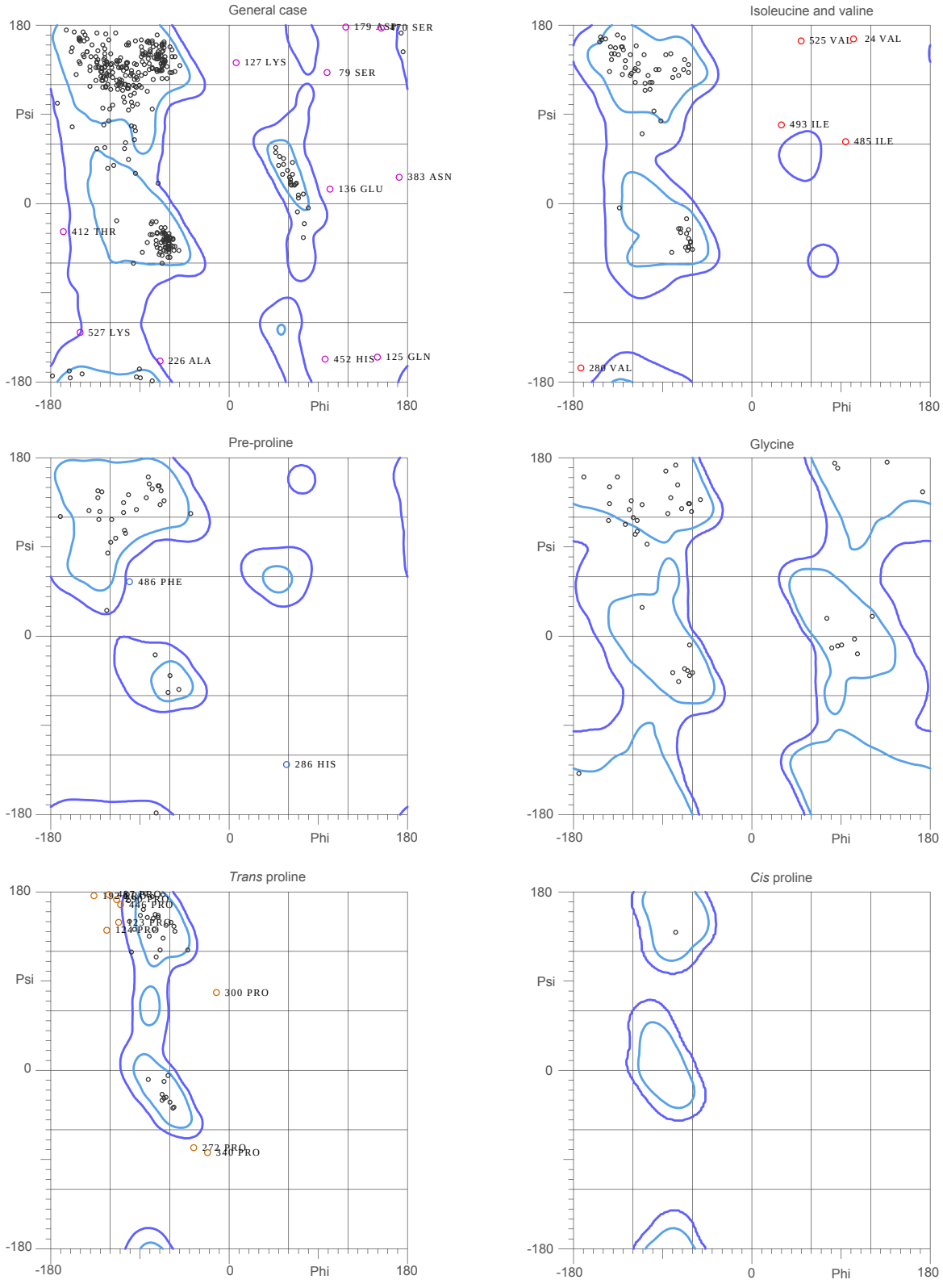
MolProbity Ramachandran analysis

1aozA.B99990001.pdb, model 1



88.0% (484/550) of all residues were in favored (98%) regions.
95.1% (523/550) of all residues were in allowed (>99.8%) regions.

There were 27 outliers (phi, psi):
24 VAL (103.5, 167.7)
79 SER (99.8, 133.9)
123 PRO (-112.1, 158.3)
124 PRO (-124.1, 142.2)
125 GLN (150.6, -155.3)
127 LYS (75.3, 143.9)
136 GLU (102.6, 15.6)
179 ASP (-118.8, 179.4)
192 PRO (-137.2, 177.2)
226 ALA (-76.1, -159.4)
272 PRO (-36.0, -78.1)
280 VAL (-173.8, -166.7)
286 HIS (58.4, -138.4)
298 PRO (-114.4, 173.3)
300 PRO (-64.9, 79.7)
340 PRO (-22.9, -85.5)
383 ASN (172.1, 27.4)
412 THR (-168.4, -28.8)
446 PRO (-110.8, 168.3)
452 HIS (97.4, -157.3)
479 SER (154.5, 178.2)
485 ILE (95.8, 83.1)
486 PHE (-101.9, 56.9)
487 PRO (-122.3, 178.7)
493 ILE (58.3, 88.8)
525 VAL (58.6, 165.6)
527 LYS (-151.2, -130.1)

http://kinemage.biochem.duke.edu

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