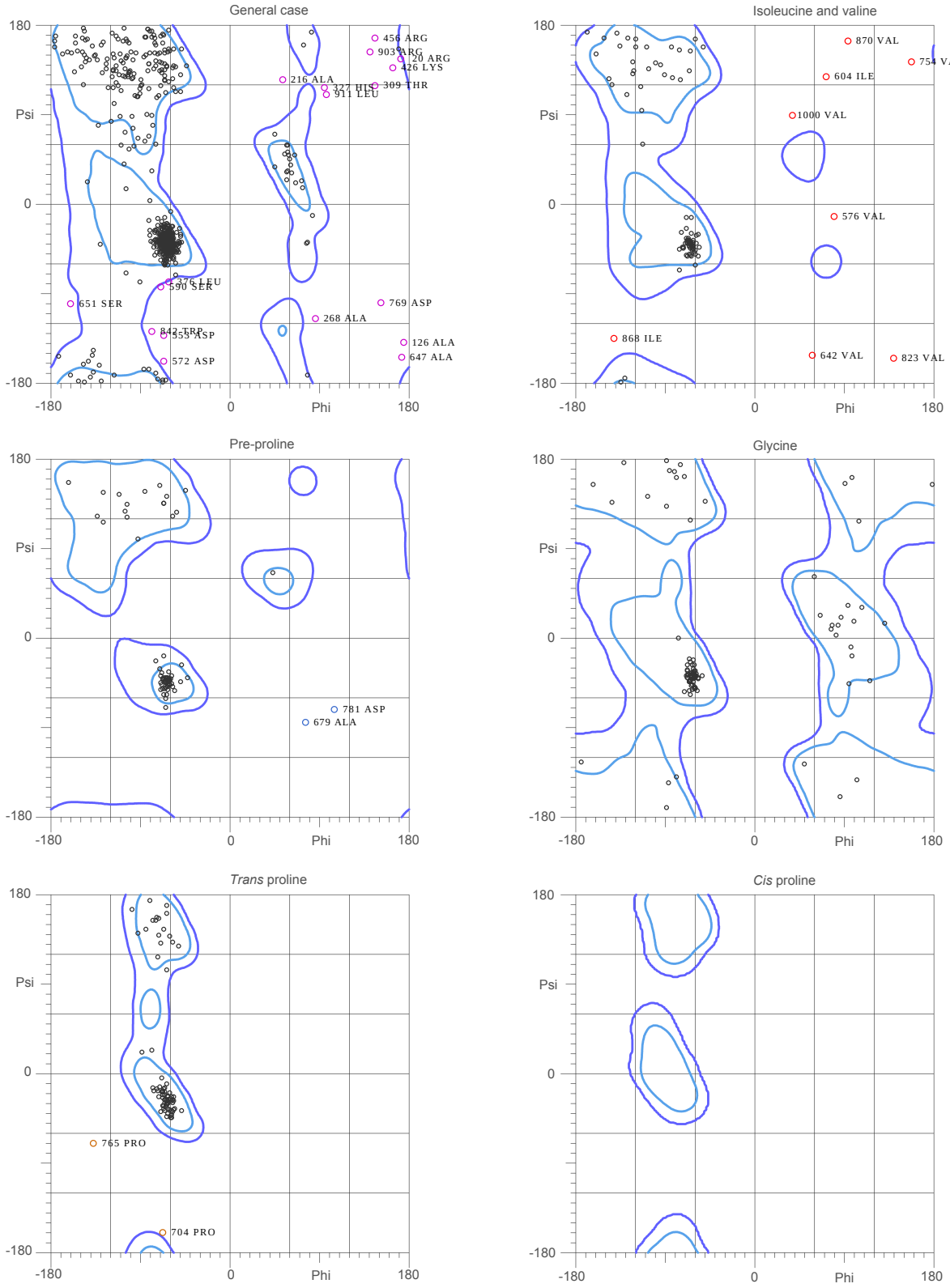
MolProbity Ramachandran analysis

1yq2.B99990018.pdb, model 1



91.8% (926/1008) of all residues were in favored (98%) regions.
97.1% (980/1010) of all residues were in allowed (>99.8%) regions.

There were 10 outliers (pks, pcs):
20 ARG (172.7, 147.5)
120 ARG (-154.1, 150.9)
216 ALA (52.6, -130.8)
268 ALA (86.9, -115.9)
309 THR (140.6, 128.9)
327 HIS (95.1, 118.7)
376 LEU (-62.0, -78.2)
426 LYS (164.5, 158.4)
456 ARG (148.7, 168.7)
553 ASP (-67.3, -132.4)
572 ASP (-87.2, -139.0)
576 VAL (95.6, -12.9)
590 SER (-61.1, 151.1)
666 GLN (72.3, 129.7)
642 VAL (58.7, -153.5)
647 ALA (177.6, -154.7)
651 SER (-161.5, -180.9)
679 ALA (76.2, -81.6)
704 PRO (-68.2, -168.8)
754 VAL (158.7, 144.9)
765 PRO (-156.8, -78.8)
769 ASP (-64.4, 151.1)
781 ASP (145.4, -75.8)
823 VAL (140.2, -156.0)
842 TRP (-79.1, -138.0)
868 ILE (-142.3, -135.0)
870 VAL (93.0, 165.3)
903 ARG (141.9, 154.2)
911 LEU (97.9, 111.8)
1000 VAL (58.8, 90.0)

http://kinemage.biochem.duke.edu

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