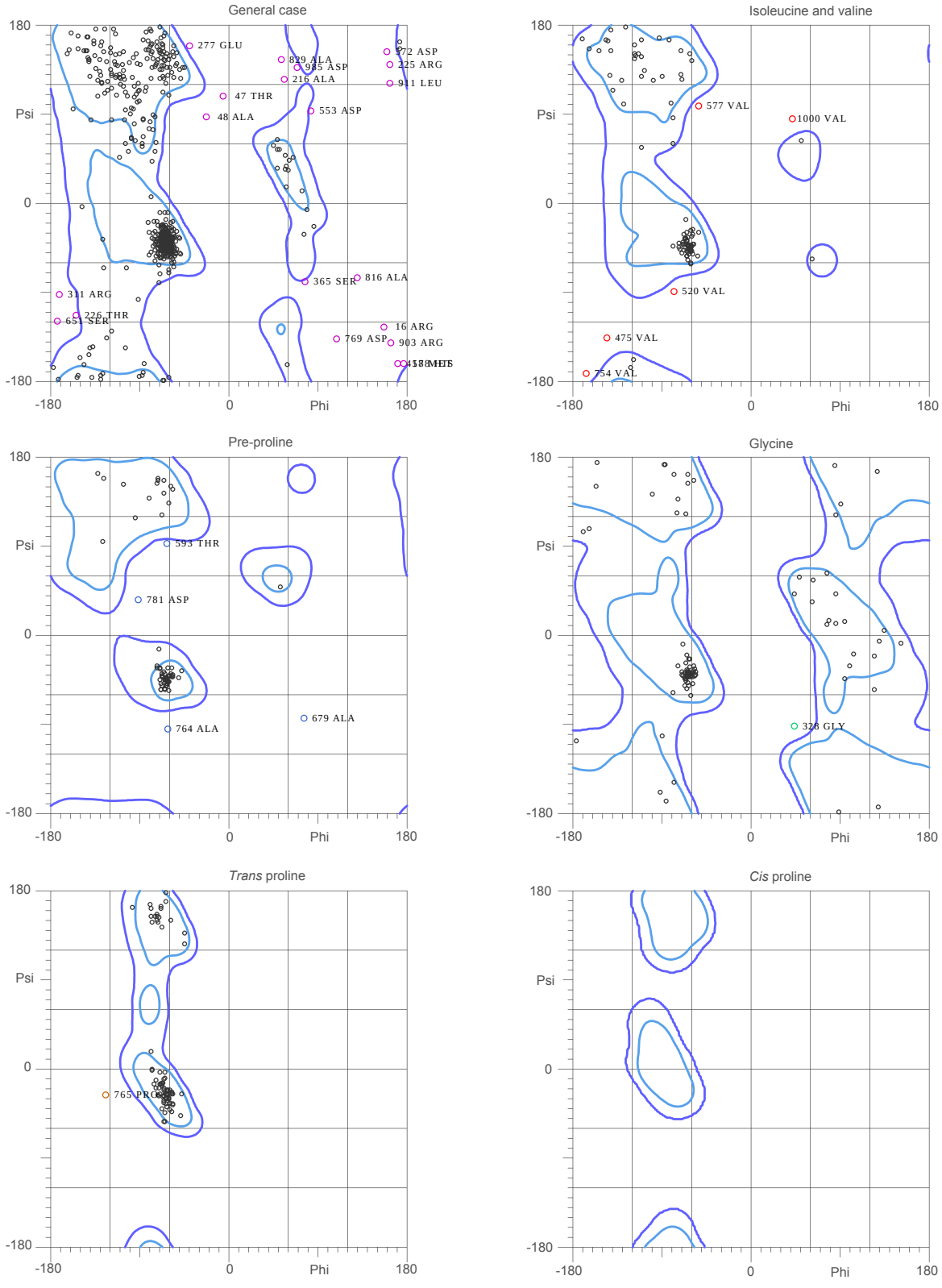
MolProbity Ramachandran analysis

1yq2.B99990013.pdb, model 1



98.3% (9/10/1010) of all residues were in favored (98%) regions.
97.0% (987/1010) of all residues were in allowed (>99.8%) regions.

There were 31 outliers (pb, psi):

16 ARG (117.5, -120.5)
47 THR (-6.4, 118.0)
48 ALA (-23.9, 88.0)
216 ALA (56.5, 127.0)
225 ARG (104.0, 141.5)
226 THR (-115.9, -115.4)
277 GLU (-40.5, 160.0)
311 ARG (-172.6, -92.4)
328 GLY (-42.5, -52.9)
365 SER (77.5, -86.0)
418 MET (171.6, -163.1)
475 VAL (-146.1, -156.3)
520 VAL (-76.5, -89.3)
553 ASP (85.4, 94.9)
572 ASP (100.4, 104.4)
577 VAL (-53.5, 98.4)
578 HIS (177.5, -162.5)
593 THR (-63.4, 94.0)
651 SER (-174.7, -119.6)
679 ALA (76.2, -84.6)
754 VAL (-100.0, -172.9)
764 ALA (-62.8, -95.4)
765 PRO (-125.4, -36.9)
769 ASP (100.7, -157.2)
781 ASP (-63.2, 36.9)
816 ALA (158.7, -75.6)
829 ALA (55.5, 146.4)
903 ARG (104.7, -161.4)
911 LEU (143.4, 122.3)
985 ASP (65.6, 110.8)
1000 VAL (42.9, 86.8)

http://kinemage.biochem.duke.edu

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