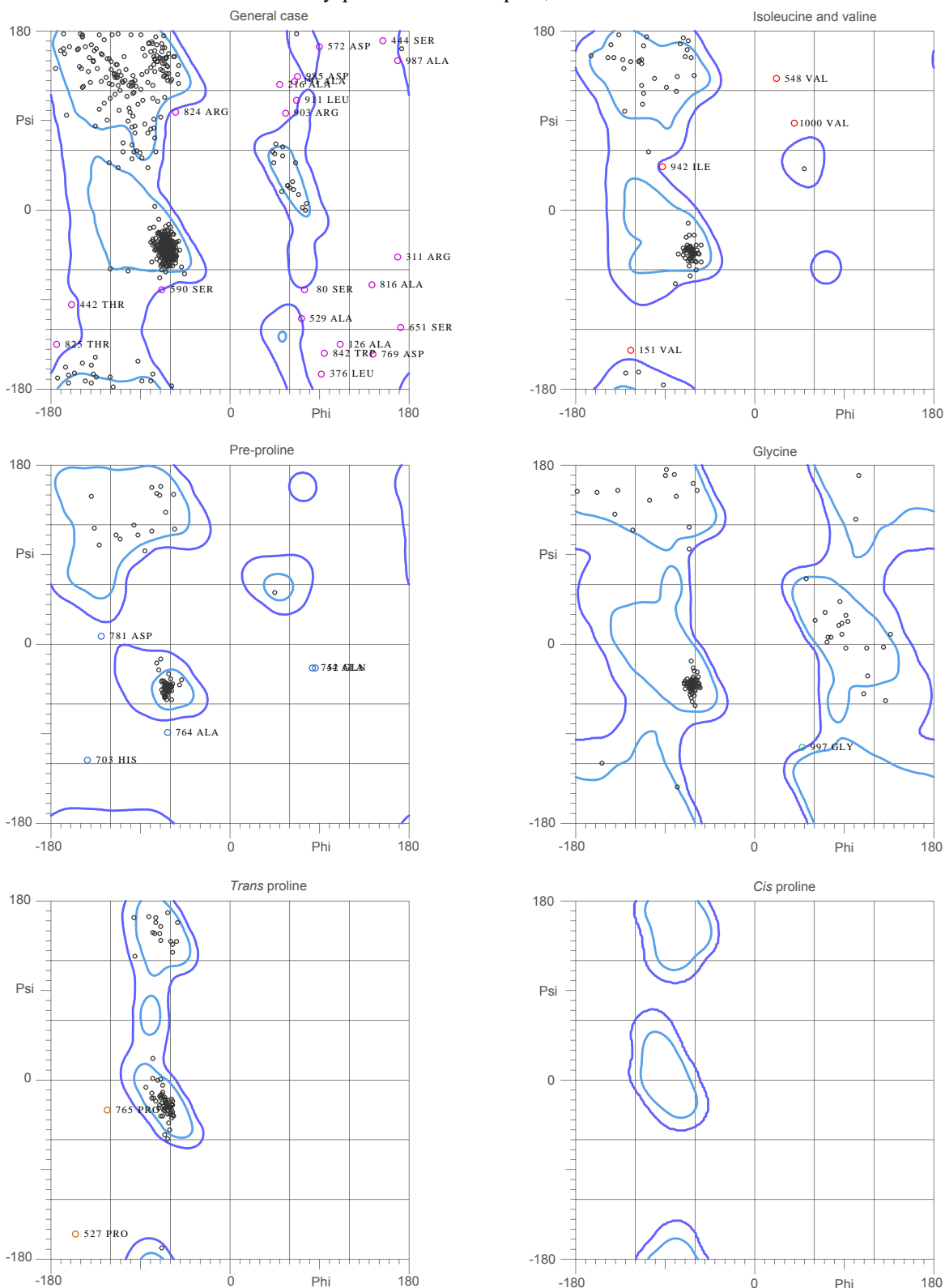


MolProbity Ramachandran analysis

1yq2.B99990009.pdb, model 1



96% of residues in all categories were in favored (blue) regions.
No outliers (red) were observed in disallowed (red) regions.

Residue (chain ID, residue number)

60 ALA (A, 265)
61 SER (A, 461)
62 ASP (A, 572)
63 VAL (A, 580)
64 THR (A, 590)
65 LEU (A, 651)
66 ARG (A, 703)
67 ALA (A, 742)
68 ASP (A, 781)
69 THR (A, 825)
70 THR (A, 842)
71 TRP (A, 842)
72 ALA (A, 816)
73 SER (A, 651)
74 ALA (A, 529)
75 ARG (A, 311)
76 LEU (A, 376)
77 ASP (A, 769)
78 ASP (A, 985)
79 ALA (A, 987)
80 SER (A, 80)
81 ARG (A, 903)
82 LEU (A, 911)
83 ALA (A, 216)
84 THR (A, 442)
85 SER (A, 444)
86 VAL (A, 548)
87 VAL (A, 1000)
88 GLY (A, 997)
89 PRO (A, 527)
90 PRO (A, 765)