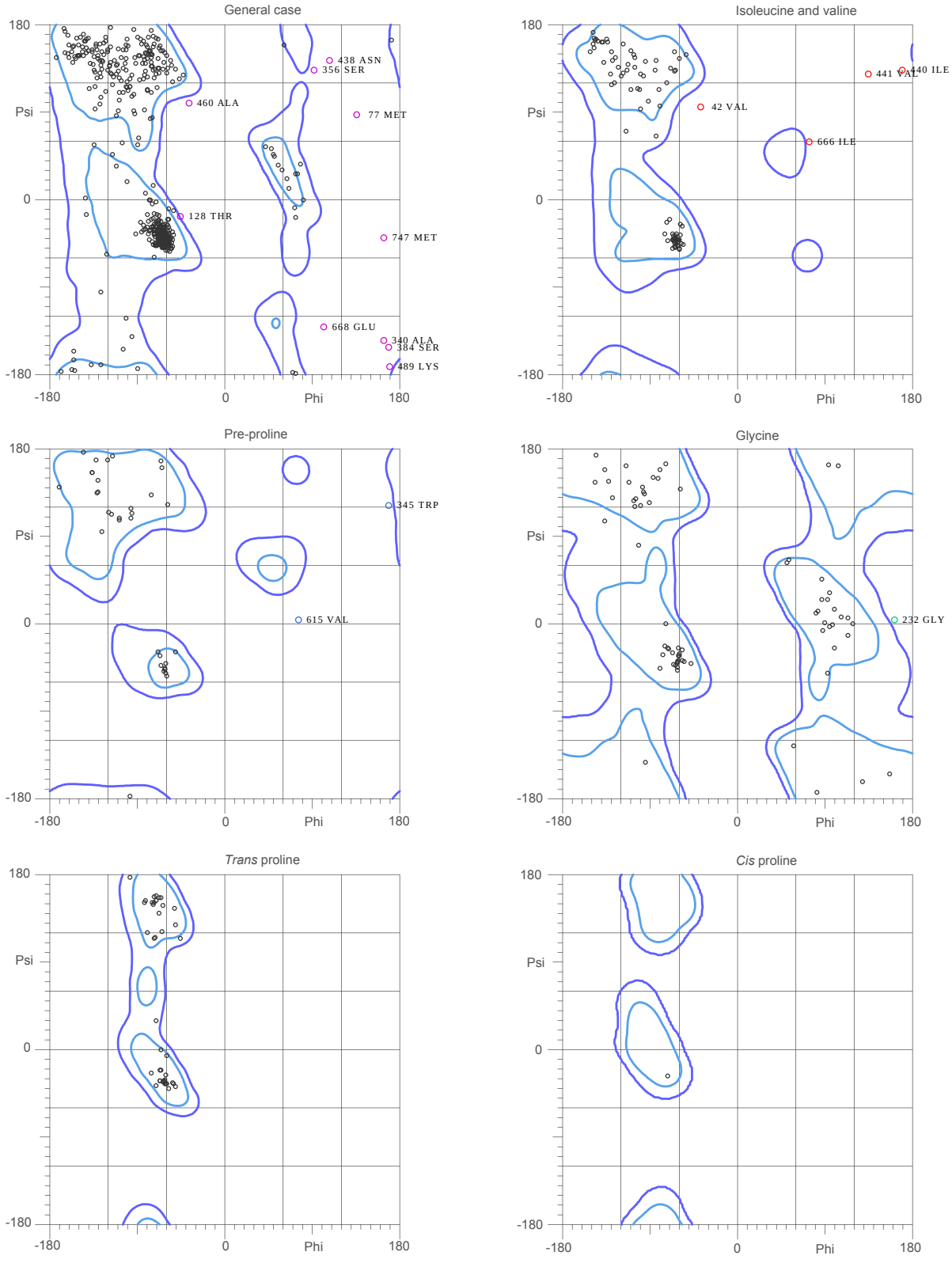
MolProbity Ramachandran analysis

1aco_.B99990037.pdb, model 1



92,5% (695/751) of all residues were in favored (98%) regions.
97,7% (734/751) of all residues were in allowed (>99.8%) regions.

There were 17 outliers (phi, psi):
42 VAL (-38,7, 96,5)
77 MET (136,8, 88,5)
128 THR (-46,5, -17,7)
232 GLY (162,1, 4,2)
340 ALA (164,9, -145,6)
345 TRP (169,2, 122,9)
356 SER (92,9, 134,8)
384 SER (169,4, -152,4)
438 ASN (108,8, 144,8)
440 ILE (170,3, 134,0)
441 VAL (135,4, 130,8)
460 ALA (-37,2, 100,1)
489 LYS (170,0, -172,9)
615 VAL (76,0, 4,1)
666 ILE (74,2, 60,9)
668 GLU (102,2, -131,6)
747 MET (164,7, -39,5)

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