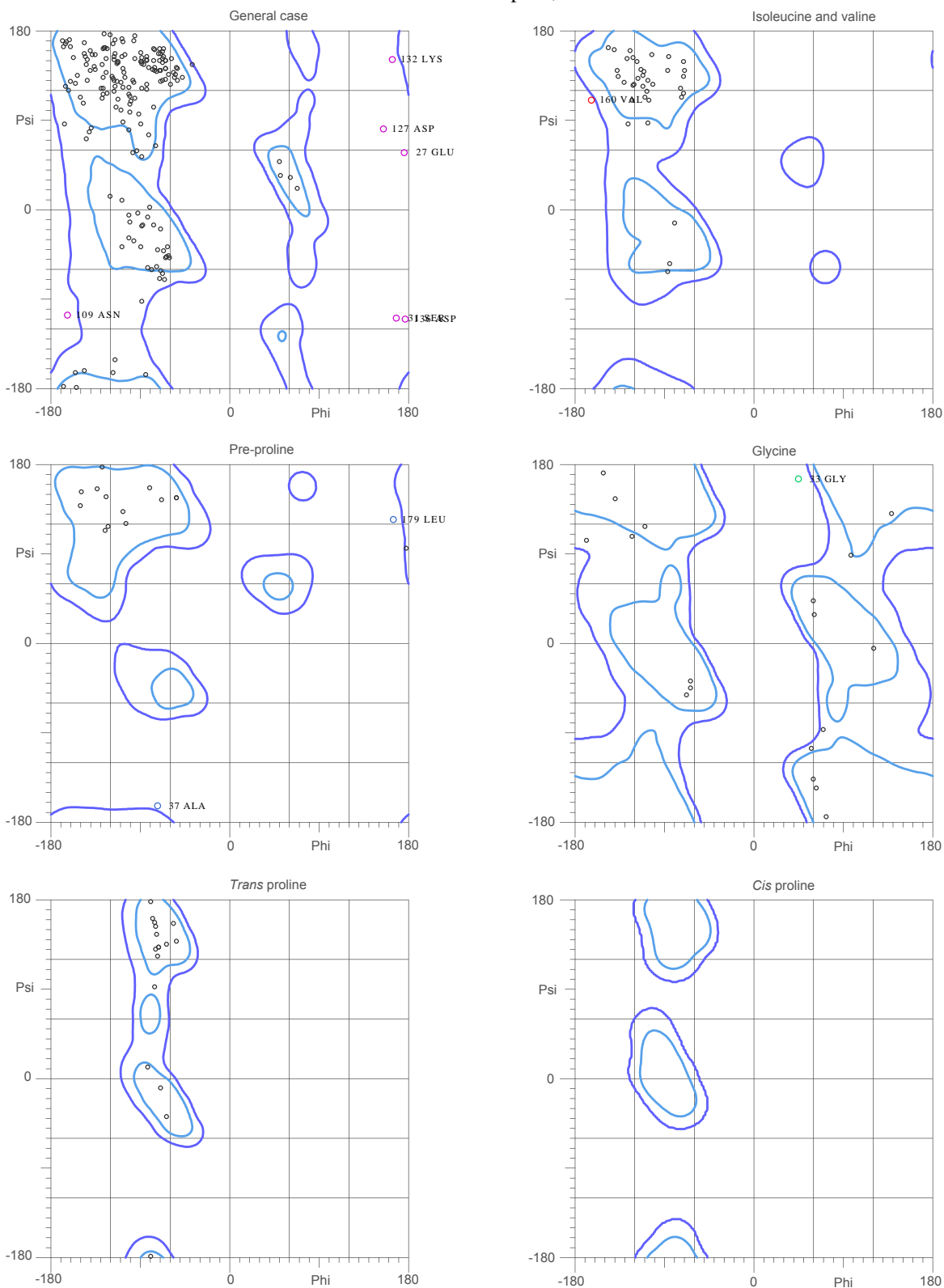# MolProbity Ramachandran analysis

1a02N.B99990038.pdb, model 1

85,6% (238/278) of all residues were in favored (98%) regions.
96,4% (268/278) of all residues were in allowed (>99.8%) regions.

There were 10 outliers (phi, psi):
  27 GLU (176,7, 58,0)
  31 SER (168,5, -109,2)
  33 GLY (45,4, 166,3)
  37 ALA (-73,9, -164,8)
  109 ASN (-164,2, -106,9)
  127 ASP (155,1, 82,3)
  132 LYS (164,9, 152,8)
  136 ASP (177,3, -110,0)
  160 VAL (-164,5, 111,6)
  179 LEU (165,8, 125,6)

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