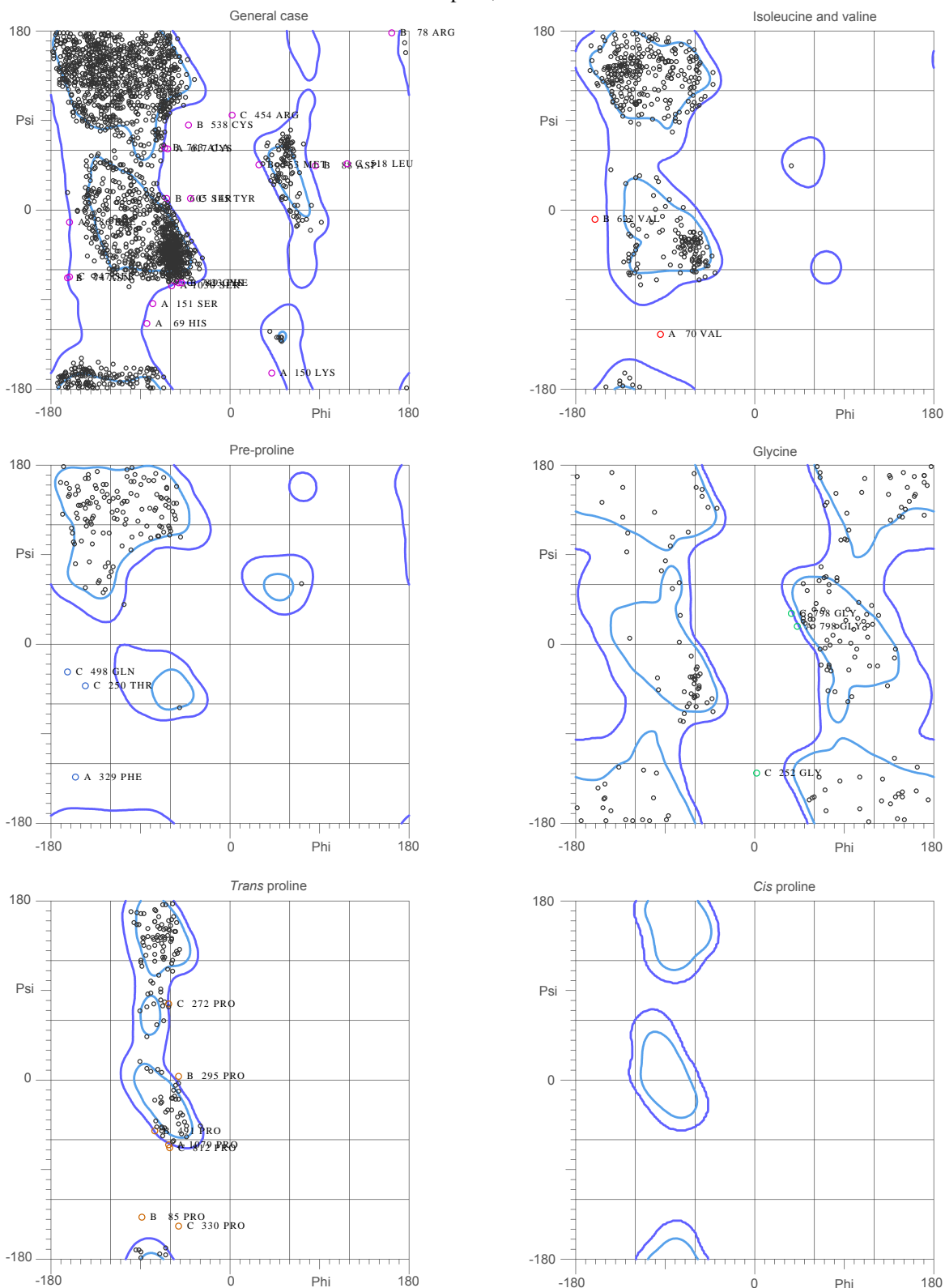


MolProbity Ramachandran analysis

7cn9.H.pdb, model 1



7cn9 (200808) of all residues were in favored (98%) regions.
No (0%) outliers or all residues were in allowed (100%) regions.

Residues (chain, residue, type):

- A: 69 (MET), 150 (LYS)
- B: 78 (ARG), 518 (LEU), 538 (CYS), 605 (SER), 605 (TYR), 653 (MET), 767 (ALA), 947 (ASN)
- C: 454 (ARG), 98 (GLY), 230 (THR), 251 (GLY), 272 (PRO), 295 (PRO), 330 (PRO), 498 (GLN)
- K: 1033 (SER)