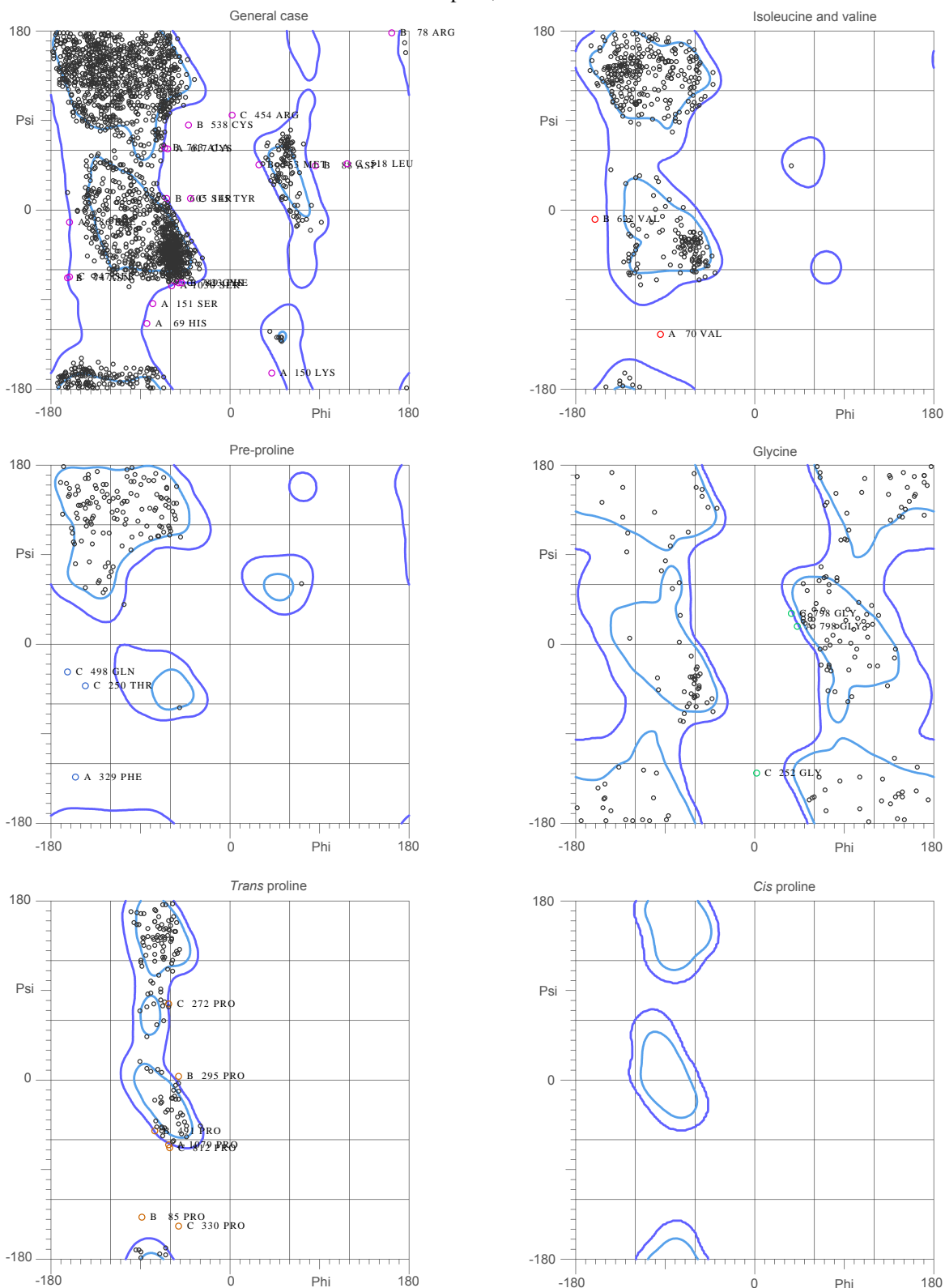


MolProbity Ramachandran analysis

7cn9.H.pdb, model 1



75 (18) (2000) of all residues were in favored (blue) regions.
 96 (19) (2000) of all residues were in allowed (cyan) regions.
 None were in disallowed (red) regions.

Residue Name (Chain ID, Residue Number, Conformation):

- A: 69 (MET) (1A)
- A: 70 (VAL) (1A)
- A: 76 (SER) (1A)
- A: 77 (MET) (1A)
- A: 78 (ARG) (1A)
- A: 85 (PRO) (1A)
- A: 94 (ASN) (1A)
- A: 98 (GLY) (1A)
- A: 103 (SER) (1A)
- A: 106 (TYR) (1A)
- A: 150 (LYS) (1A)
- A: 151 (SER) (1A)
- B: 518 (LEU) (1B)
- B: 538 (CYS) (1B)
- B: 563 (MET) (1B)
- B: 605 (SER) (1B)
- B: 606 (TYR) (1B)
- B: 622 (VAL) (1B)
- B: 767 (ALA) (1B)
- B: 78 (ARG) (1B)
- C: 230 (THR) (1C)
- C: 251 (GLY) (1C)
- C: 272 (PRO) (1C)
- C: 295 (PRO) (1C)
- C: 330 (PRO) (1C)
- C: 398 (GLY) (1C)
- C: 454 (ARG) (1C)
- C: 498 (GLN) (1C)