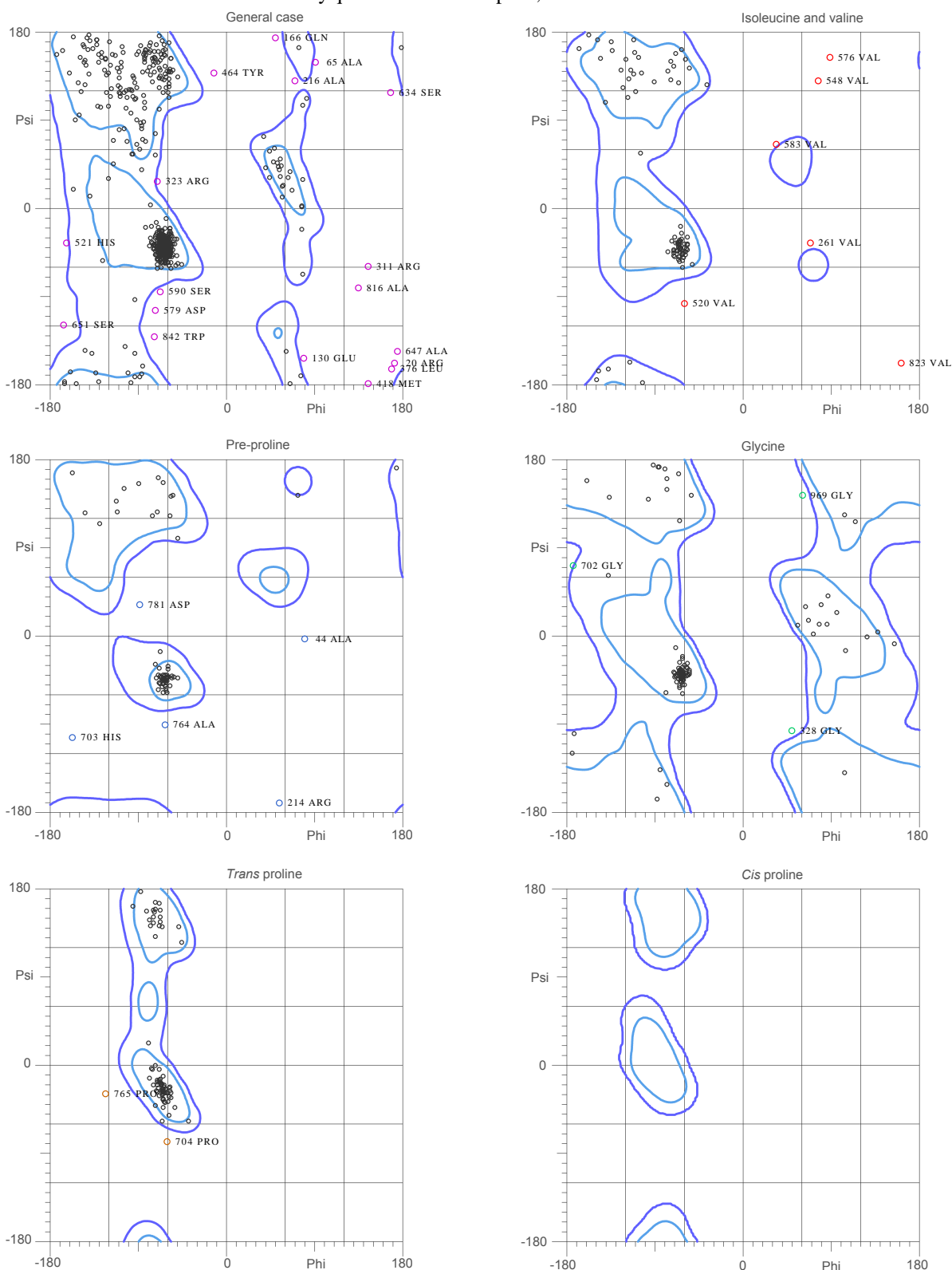


MolProbity Ramachandran analysis

1yq2.B99990010.pdb, model 1



Outliers (residues) of all residues were in favored (blue) regions.
No % in 100 (blue) or 90 (orange) or 50 (red) or 25 (yellow) regions.

Residue name (chain ID, residue number, and B-factor):

- 166 GLN (A, 166, 1.00)
- 65 ALA (A, 65, 1.00)
- 216 ALA (A, 216, 1.00)
- 634 SER (A, 634, 1.00)
- 464 TYR (A, 464, 1.00)
- 323 ARG (A, 323, 1.00)
- 521 HIS (A, 521, 1.00)
- 590 SER (A, 590, 1.00)
- 579 ASP (A, 579, 1.00)
- 842 TRP (A, 842, 1.00)
- 631 SER (A, 631, 1.00)
- 311 ARG (A, 311, 1.00)
- 816 ALA (A, 816, 1.00)
- 130 GLU (A, 130, 1.00)
- 647 ALA (A, 647, 1.00)
- 700 ARG (A, 700, 1.00)
- 418 MET (A, 418, 1.00)