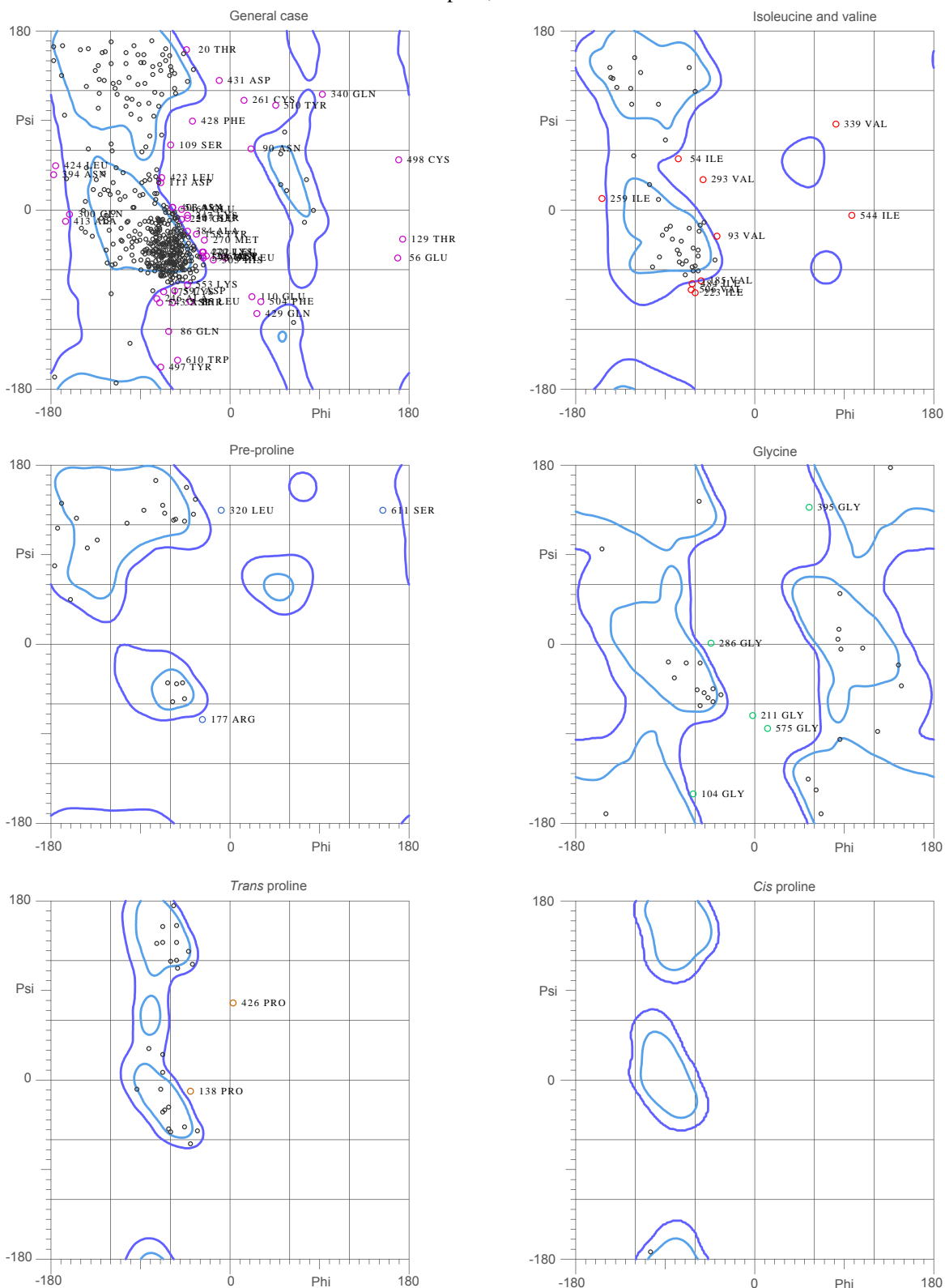


MolProbity Ramachandran analysis

1r4l.H.pdb, model 1



47.0% (100/210) of all residues were in favored (90%) regions.
50.0% (105/210) of all residues were in allowed (10%) regions.
There were 0 outliers (0% out).

Residue	Phi (deg)	Psi (deg)	Category
20 THR	10.0	10.0	Favored
431 ASP	10.0	10.0	Favored
261 CYS	10.0	10.0	Favored
510 TYR	10.0	10.0	Favored
340 GLN	10.0	10.0	Favored
428 PHE	10.0	10.0	Favored
109 SER	10.0	10.0	Favored
90 ASN	10.0	10.0	Favored
498 CYS	10.0	10.0	Favored
424 LEU	10.0	10.0	Favored
394 ASP	10.0	10.0	Favored
413 ASN	10.0	10.0	Favored
423 LEU	10.0	10.0	Favored
411 ASP	10.0	10.0	Favored
410 THR	10.0	10.0	Favored
384 ALA	10.0	10.0	Favored
270 MET	10.0	10.0	Favored
130 LEU	10.0	10.0	Favored
129 THR	10.0	10.0	Favored
56 GLU	10.0	10.0	Favored
86 GLN	10.0	10.0	Favored
610 TRP	10.0	10.0	Favored
497 TYR	10.0	10.0	Favored
320 LEU	10.0	10.0	Favored
611 SER	10.0	10.0	Favored
177 ARG	10.0	10.0	Favored
426 PRO	10.0	10.0	Favored
138 PRO	10.0	10.0	Favored
395 GLY	10.0	10.0	Favored
286 GLY	10.0	10.0	Favored
211 GLY	10.0	10.0	Favored
575 GLY	10.0	10.0	Favored
104 GLY	10.0	10.0	Favored