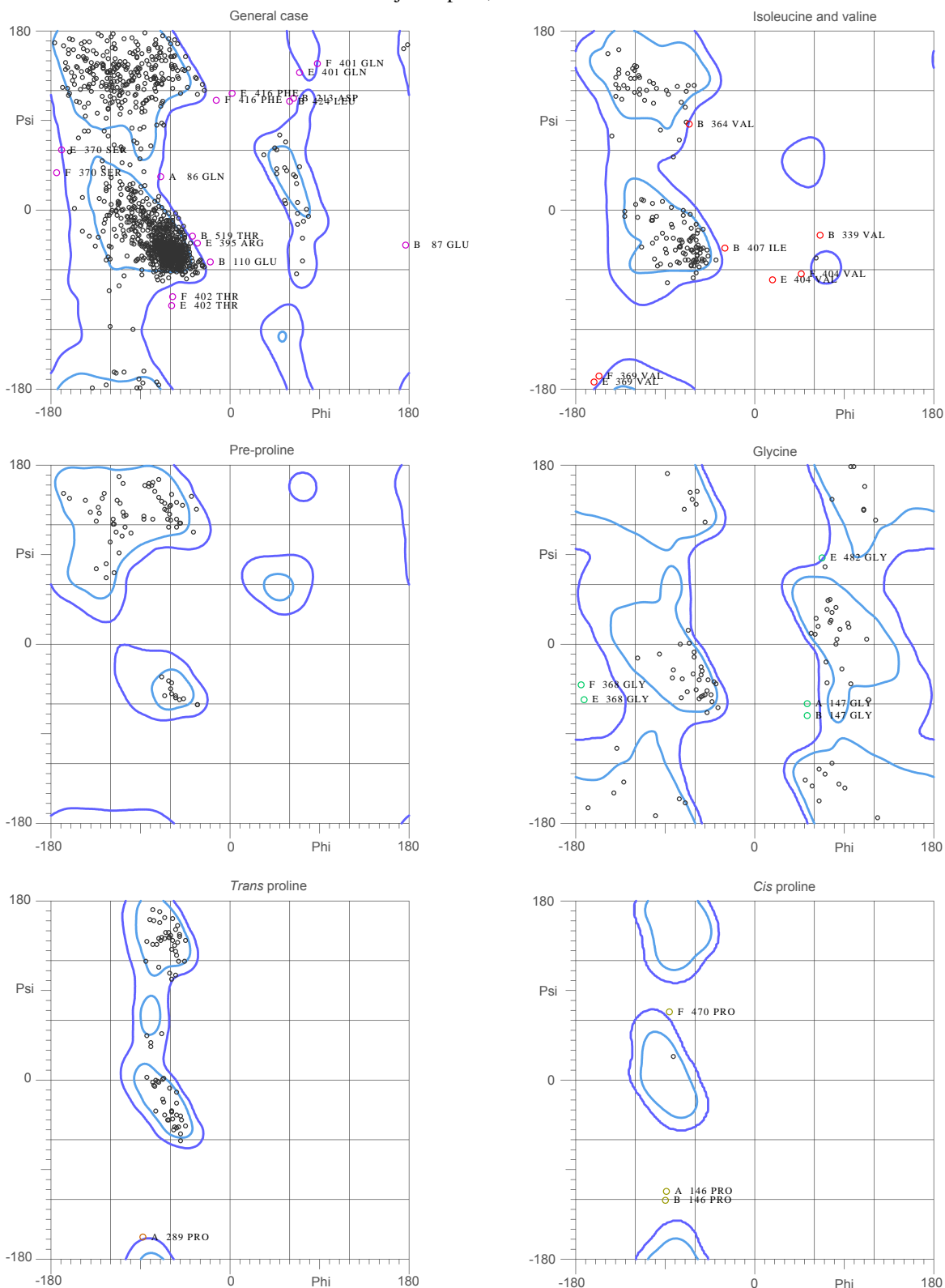


MolProbity Ramachandran analysis

2ajf.H.pdb, model 1



87.0% (1249/1436) of all residues were in favored (98%) regions.
10.0% (143/1436) of all residues were in allowed (1.0%) regions.

There were 53 outliers (3.6%):

A 86 GLN (Phi, Psi)
A 124 ASP (Phi, Psi)
A 146 PRO (Phi, Psi)
A 147 GLY (Phi, Psi)
A 289 PRO (Phi, Psi)
A 370 SER (Phi, Psi)
A 401 GLN (Phi, Psi)
A 402 THR (Phi, Psi)
B 110 GLU (Phi, Psi)
B 124 ASP (Phi, Psi)
B 146 PRO (Phi, Psi)
B 147 GLY (Phi, Psi)
B 339 VAL (Phi, Psi)
B 364 VAL (Phi, Psi)
B 407 ILE (Phi, Psi)
E 368 GLY (Phi, Psi)
E 369 VAL (Phi, Psi)
E 395 ARG (Phi, Psi)
E 401 GLN (Phi, Psi)
E 402 THR (Phi, Psi)
E 404 VAL (Phi, Psi)
E 482 GLY (Phi, Psi)
F 368 GLY (Phi, Psi)
F 369 VAL (Phi, Psi)
F 401 GLN (Phi, Psi)
F 402 THR (Phi, Psi)
F 416 PHE (Phi, Psi)
F 470 PRO (Phi, Psi)