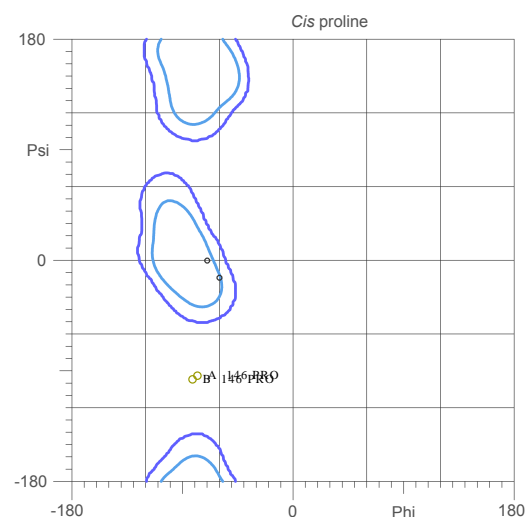
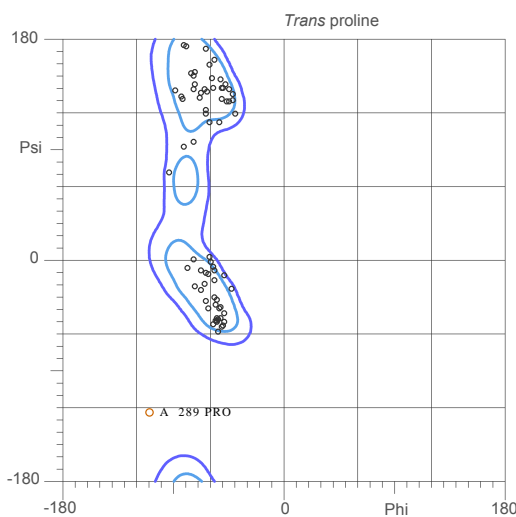
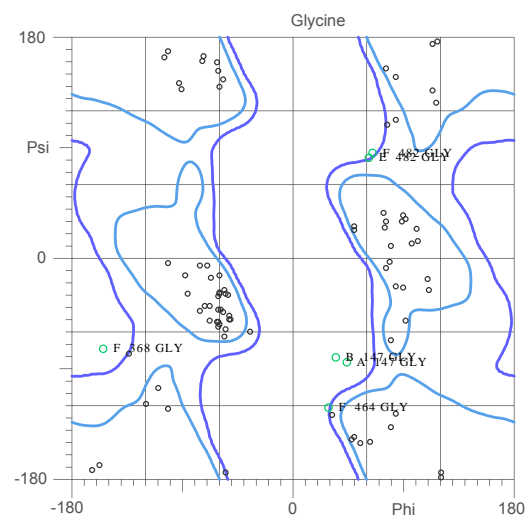
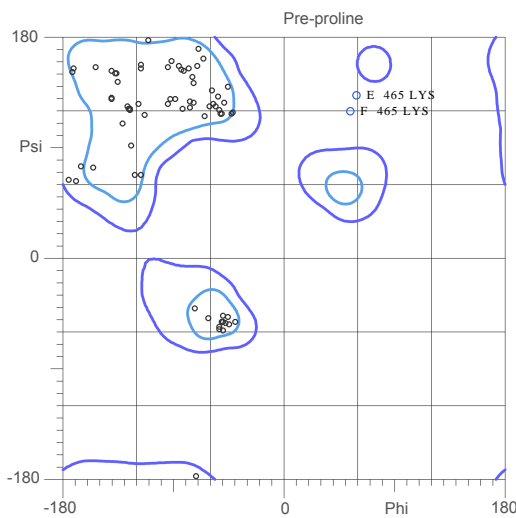
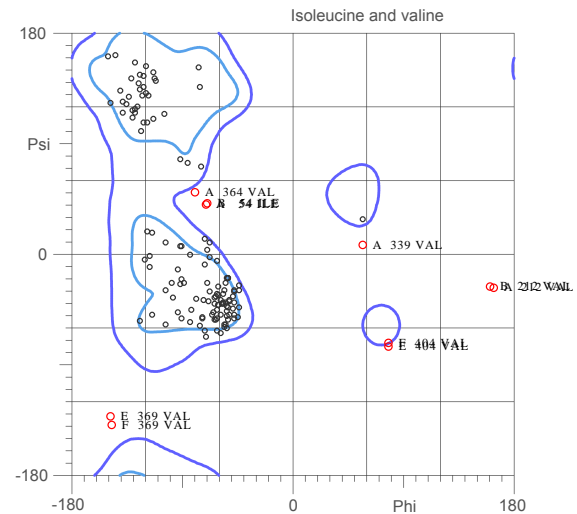
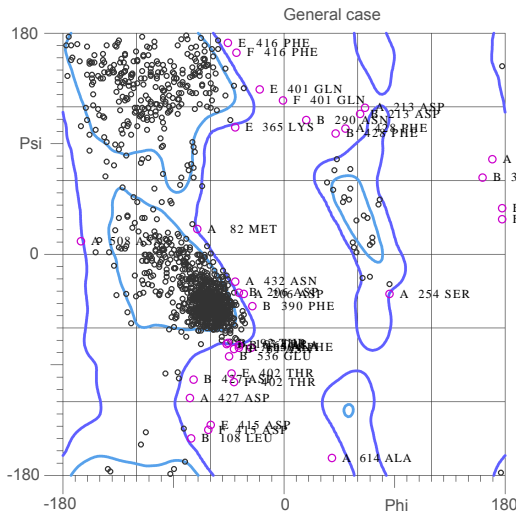


MolProbity Ramachandran analysis

3d0i.H.pdb, model 1



87.1% (131/150) of all residues were in favored (98%) regions.

96.7% (145/150) of all residues were in allowed (99.8%) regions.

There were 37 outliers (Phi, Psi):

A 340 GLN (Phi, Psi)
B 340 GLN (Phi, Psi)
E 370 SER (Phi, Psi)
F 370 SER (Phi, Psi)
A 254 SER (Phi, Psi)
E 416 PHE (Phi, Psi)
F 416 PHE (Phi, Psi)
E 401 GLN (Phi, Psi)
F 401 GLN (Phi, Psi)
B 290 ASP (Phi, Psi)
E 365 LYS (Phi, Psi)
A 82 MET (Phi, Psi)
A 432 ASN (Phi, Psi)
B 296 ASP (Phi, Psi)
B 390 PHE (Phi, Psi)
A 536 GLU (Phi, Psi)
E 402 THR (Phi, Psi)
F 402 THR (Phi, Psi)
A 427 ASP (Phi, Psi)
E 415 ASP (Phi, Psi)
B 108 LEU (Phi, Psi)
A 614 ALA (Phi, Psi)
E 465 LYS (Phi, Psi)
F 465 LYS (Phi, Psi)
F 482 GLY (Phi, Psi)
F 368 GLY (Phi, Psi)
A 149 GLY (Phi, Psi)
F 464 GLY (Phi, Psi)
A 289 PRO (Phi, Psi)
A 149 PRO (Phi, Psi)

A 340 GLN (Phi, Psi)
B 340 GLN (Phi, Psi)
E 370 SER (Phi, Psi)
F 370 SER (Phi, Psi)
A 254 SER (Phi, Psi)
E 416 PHE (Phi, Psi)
F 416 PHE (Phi, Psi)
E 401 GLN (Phi, Psi)
F 401 GLN (Phi, Psi)
B 290 ASP (Phi, Psi)
E 365 LYS (Phi, Psi)
A 82 MET (Phi, Psi)
A 432 ASN (Phi, Psi)
B 296 ASP (Phi, Psi)
B 390 PHE (Phi, Psi)
A 536 GLU (Phi, Psi)
E 402 THR (Phi, Psi)
F 402 THR (Phi, Psi)
A 427 ASP (Phi, Psi)
E 415 ASP (Phi, Psi)
B 108 LEU (Phi, Psi)
A 614 ALA (Phi, Psi)
E 465 LYS (Phi, Psi)
F 465 LYS (Phi, Psi)
F 482 GLY (Phi, Psi)
F 368 GLY (Phi, Psi)
A 149 GLY (Phi, Psi)
F 464 GLY (Phi, Psi)
A 289 PRO (Phi, Psi)
A 149 PRO (Phi, Psi)