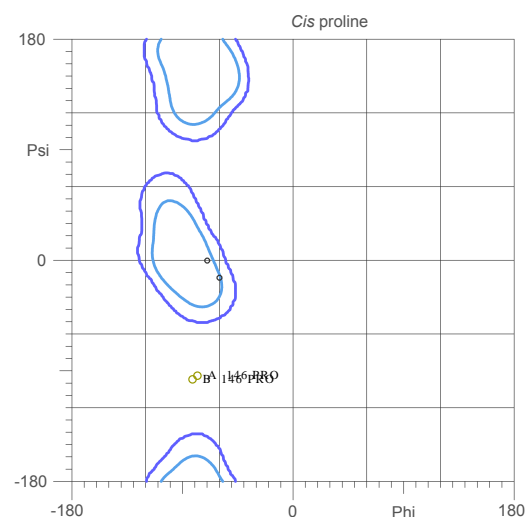
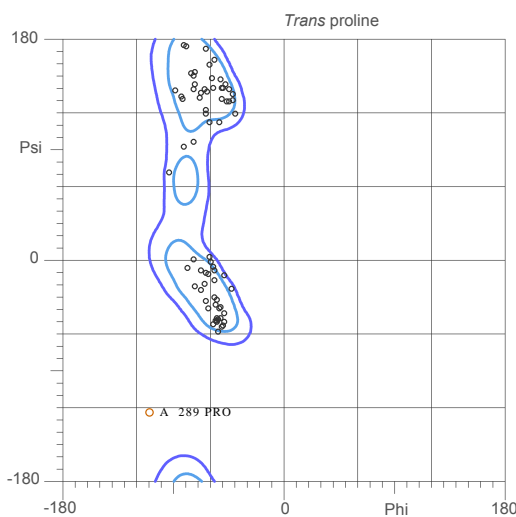
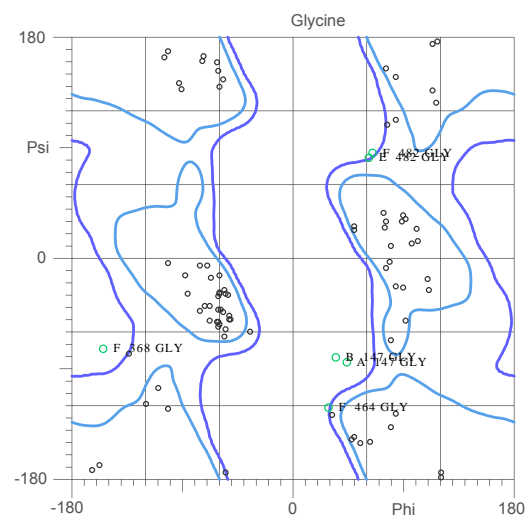
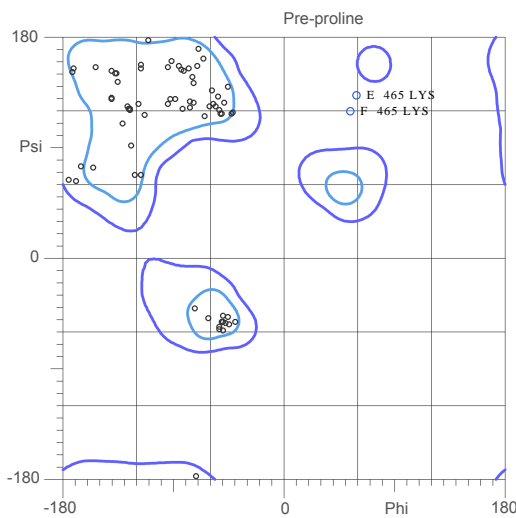
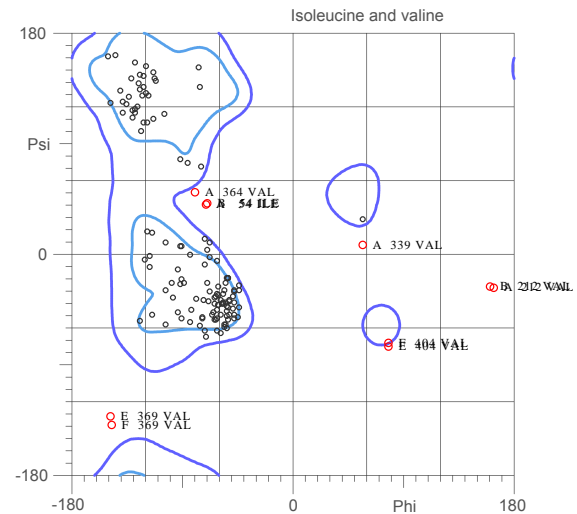
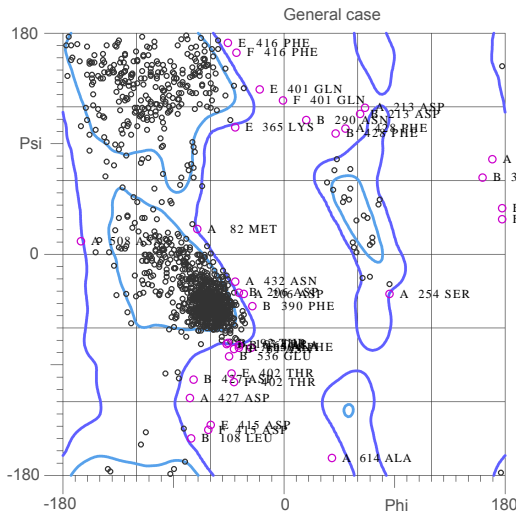


MolProbity Ramachandran analysis

3d0i.H.pdb, model 1



87.1% (131/150) of all residues were in favored (98%) regions.
96.7% (143/148) of all residues were in allowed (100%) regions.

Shown here: 37 outliers (Phi, Psi):

A 340 GLN (17.4, 45.3)	B 340 GLN (17.4, 45.3)
A 82 MET (17.4, 45.3)	B 82 MET (17.4, 45.3)
A 401 GLN (17.4, 45.3)	B 401 GLN (17.4, 45.3)
A 416 PHE (17.4, 45.3)	B 416 PHE (17.4, 45.3)
A 427 ASP (17.4, 45.3)	B 427 ASP (17.4, 45.3)
A 432 ASN (17.4, 45.3)	B 432 ASN (17.4, 45.3)
A 465 LYS (17.4, 45.3)	B 465 LYS (17.4, 45.3)
A 536 GLU (17.4, 45.3)	B 536 GLU (17.4, 45.3)
A 614 ALA (17.4, 45.3)	B 614 ALA (17.4, 45.3)
A 129 PHE (17.4, 45.3)	B 129 PHE (17.4, 45.3)
A 206 ASP (17.4, 45.3)	B 206 ASP (17.4, 45.3)
A 254 SER (17.4, 45.3)	B 254 SER (17.4, 45.3)
A 289 PRO (17.4, 45.3)	B 289 PRO (17.4, 45.3)
A 365 LYS (17.4, 45.3)	B 365 LYS (17.4, 45.3)
A 370 SER (17.4, 45.3)	B 370 SER (17.4, 45.3)
A 402 THR (17.4, 45.3)	B 402 THR (17.4, 45.3)
A 415 ASP (17.4, 45.3)	B 415 ASP (17.4, 45.3)
A 482 THR (17.4, 45.3)	B 482 THR (17.4, 45.3)
A 149 GLY (17.4, 45.3)	B 149 GLY (17.4, 45.3)
A 368 GLY (17.4, 45.3)	B 368 GLY (17.4, 45.3)
A 464 GLY (17.4, 45.3)	B 464 GLY (17.4, 45.3)
A 482 GLY (17.4, 45.3)	B 482 GLY (17.4, 45.3)