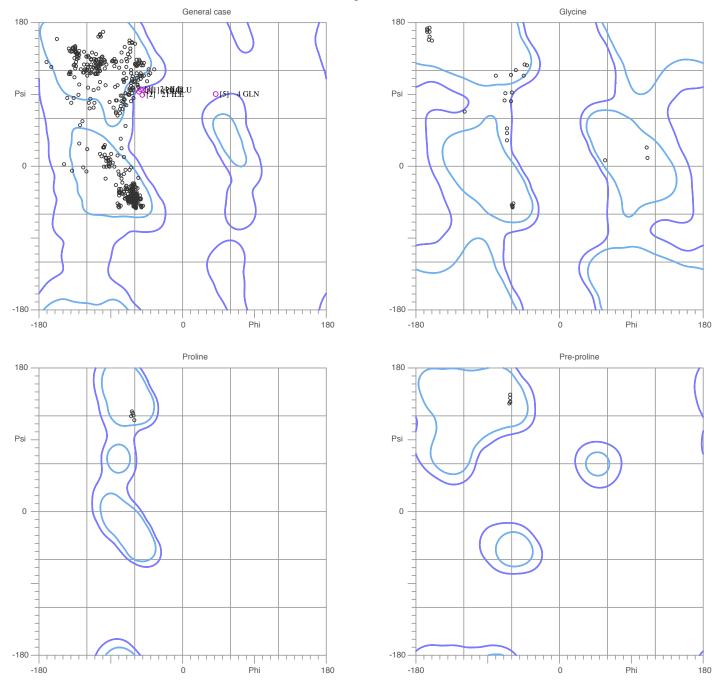
2KHD\_AF.pdb, all models

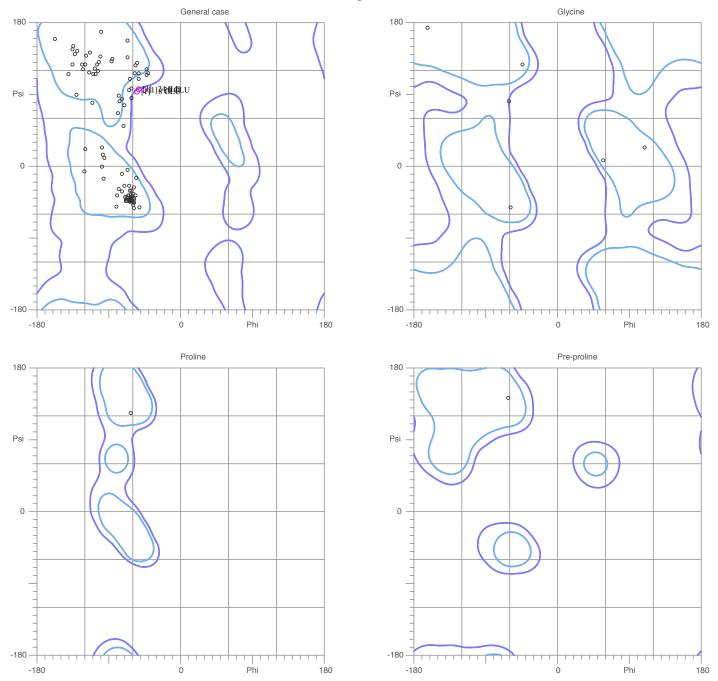


89.1% (472/530) of all residues were in favored (98%) regions. 99.1% (525/530) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [1] 8 GLU (-55.2, 94.6)
- [1] 20 GLU (-46.5, 96.7)
- [1] 24 ILE (-53.8, 97.1)
- [2] 21 ILE (-51.9, 90.1)
- [5] 4 GLN (41.9, 91.1)

2KHD\_AF.pdb, model 1

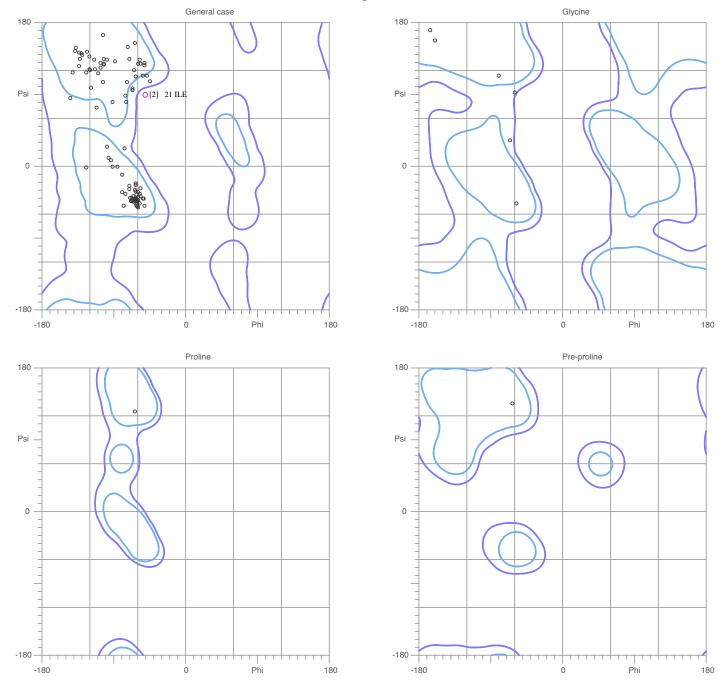


87.7% (93/106) of all residues were in favored (98%) regions. 97.2% (103/106) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 8 GLU (-55.2, 94.6)
- [1] 20 GLU (-46.5, 96.7)
- [1] 24 ILE (-53.8, 97.1)

2KHD\_AF.pdb, model 2

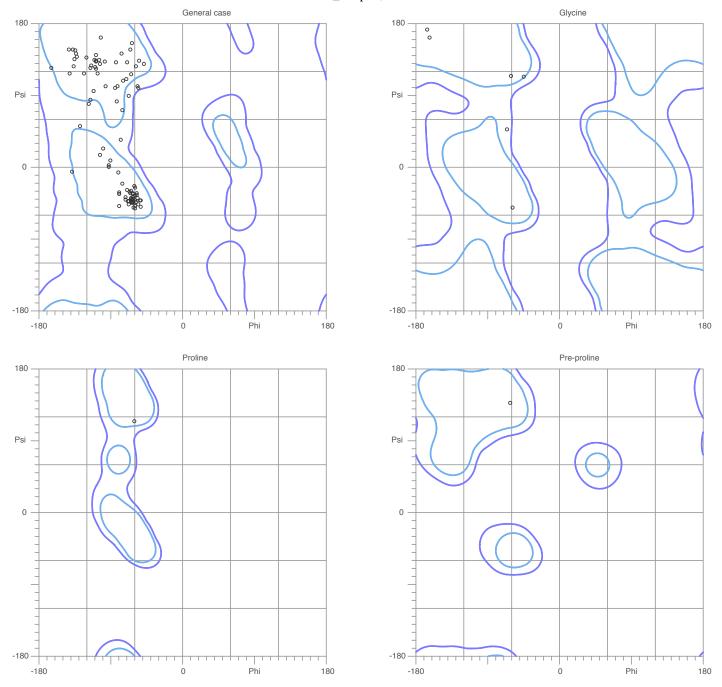


90.6% (96/106) of all residues were in favored (98%) regions. 99.1% (105/106) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[2] 21 ILE (-51.9, 90.1)

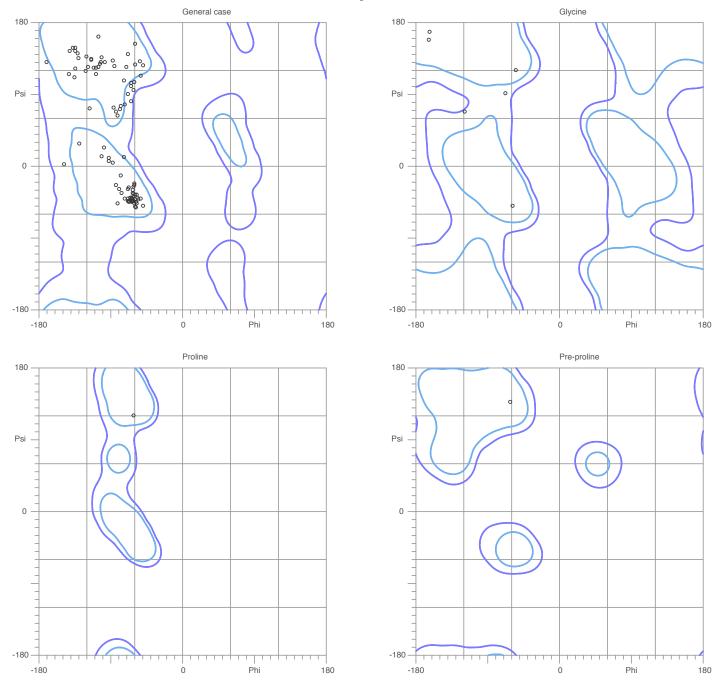
2KHD\_AF.pdb, model 3



91.5% (97/106) of all residues were in favored (98%) regions. 100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

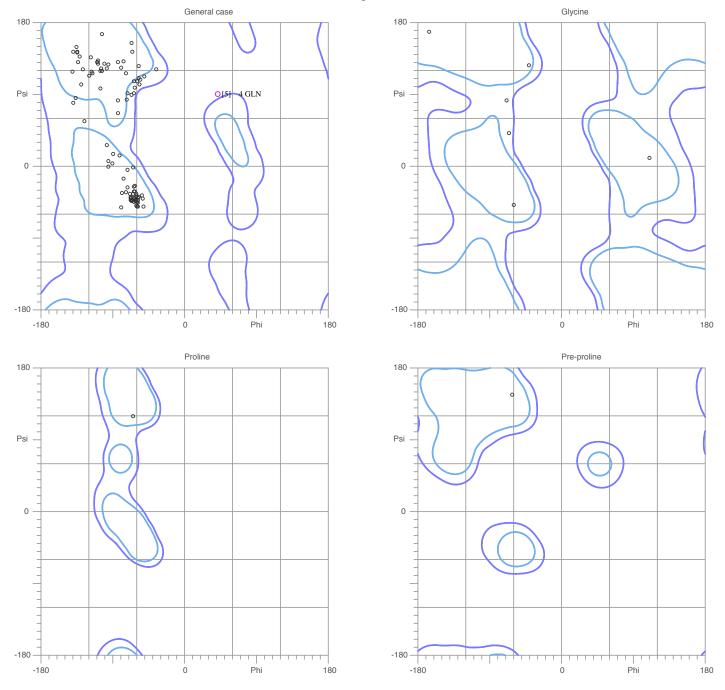
2KHD\_AF.pdb, model 4



89.6% (95/106) of all residues were in favored (98%) regions. 100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

2KHD\_AF.pdb, model 5



85.8% (91/106) of all residues were in favored (98%) regions. 99.1% (105/106) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[5] 4 GLN (41.9, 91.1)