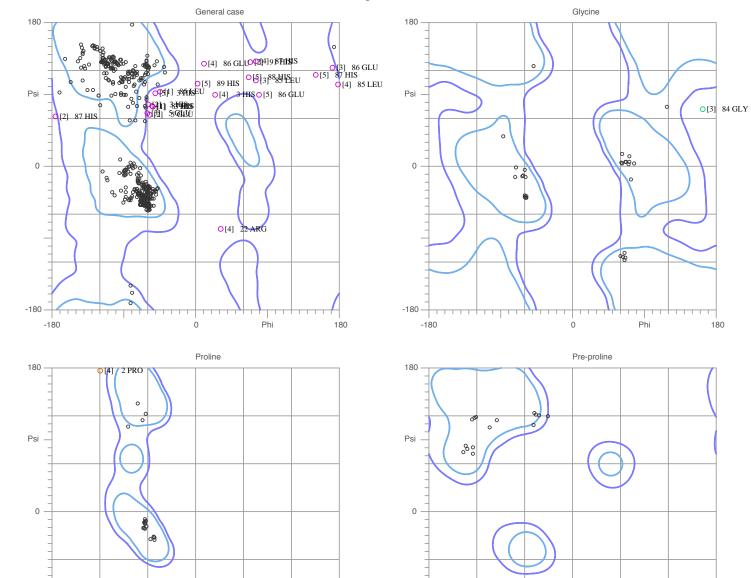
2KZV_AF.pdb, all models



90.4% (407/450) of all residues were in favored (98%) regions. 95.1% (428/450) of all residues were in allowed (>99.8%) regions.

There were 22 outliers (phi, psi):

[1] 3 HIS (-54.8, 75.1)

-180

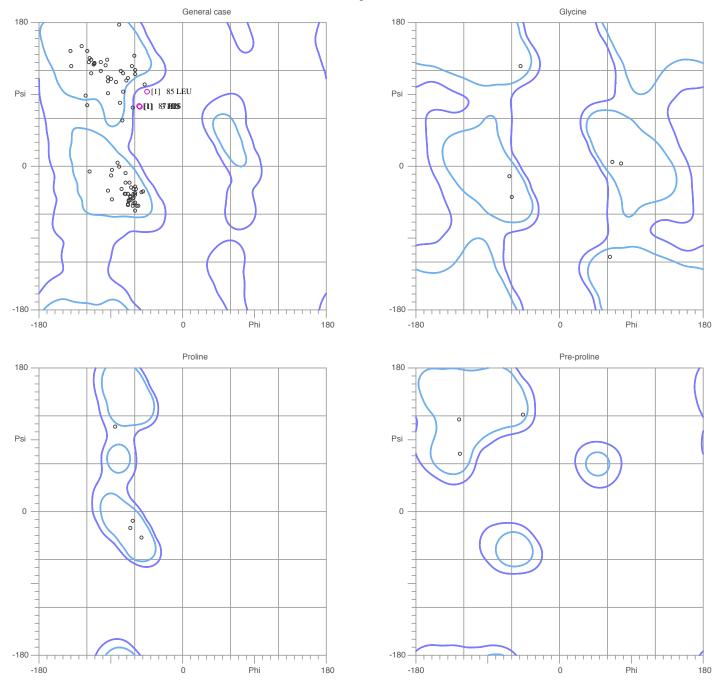
- [1] 85 LEU (-45.3, 94.3)
- [1] 87 HIS (-55.7, 76.2)
- [2] 3 HIS (-60.5, 78.9)
- [2] 5 GLU (-58.0, 65.3) [2] 87 HIS (-176.9, 63.4)
- [2] 91 HIS (68.4, 131.8)
- [3] 5 GLU (-61.1, 67.8)
- [3] 84 GLY (163.0, 72.0)

[3] 85 LEU (75.4, 108.3)

-180

- [3] 86 GLU (171.8, 124.6)
- [4] 2 PRO (-120.7, 177.8)
- [4] 3 HIS (24.9, 90.0)
- [4] 22 ARG (32.0, -78.8)
- [4] 85 LEU (178.0, 103.5)
- [4] 86 GLU (10.2, 130.0)
- [4] 87 HIS (75.5, 132.8)
- 3 HIS (-51.9, 92.2)
- [5] 86 GLU (79.4, 90.9)
- [5] 87 HIS (150.6, 115.5)
- [5] 88 HIS (67.0, 112.2)
- [5] 89 HIS (2.1, 104.2)

2KZV_AF.pdb, model 1

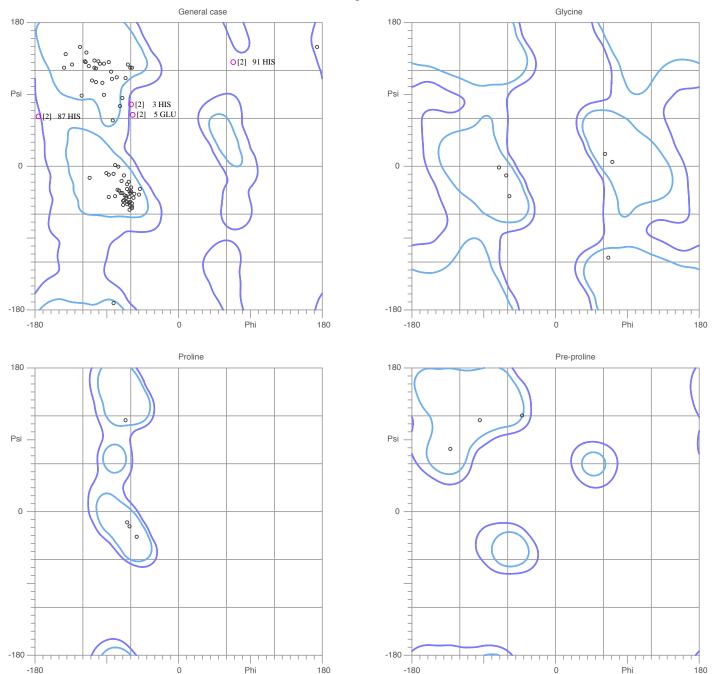


91.1% (82/90) of all residues were in favored (98%) regions. 96.7% (87/90) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 3 HIS (-54.8, 75.1)
- [1] 85 LEU (-45.3, 94.3)
- [1] 87 HIS (-55.7, 76.2)

2KZV_AF.pdb, model 2

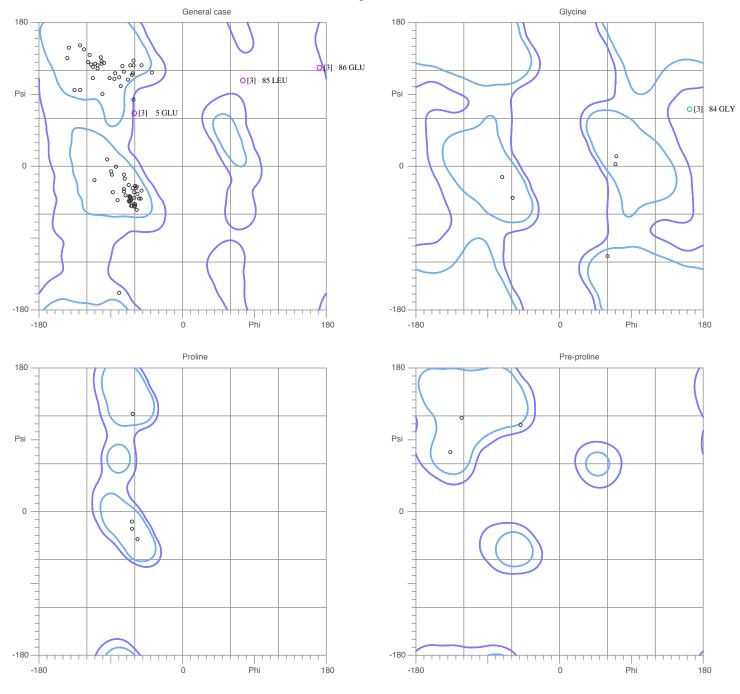


93.3% (84/90) of all residues were in favored (98%) regions. 95.6% (86/90) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [2] 3 HIS (-60.5, 78.9)
- [2] 5 GLU (-58.0, 65.3)
- [2] 87 HIS (-176.9, 63.4)
- [2] 91 HIS (68.4, 131.8)

2KZV_AF.pdb, model 3

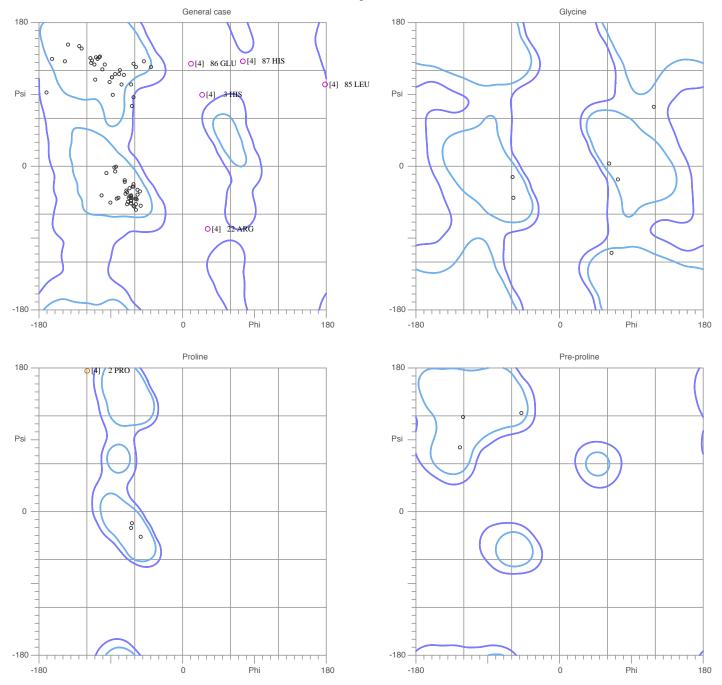


91.1% (82/90) of all residues were in favored (98%) regions. 95.6% (86/90) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [3] 5 GLU (-61.1, 67.8)
- [3] 84 GLY (163.0, 72.0)
- [3] 85 LEU (75.4, 108.3)
- [3] 86 GLU (171.8, 124.6)

2KZV_AF.pdb, model 4



87.8% (79/90) of all residues were in favored (98%) regions. 93.3% (84/90) of all residues were in allowed (>99.8%) regions.

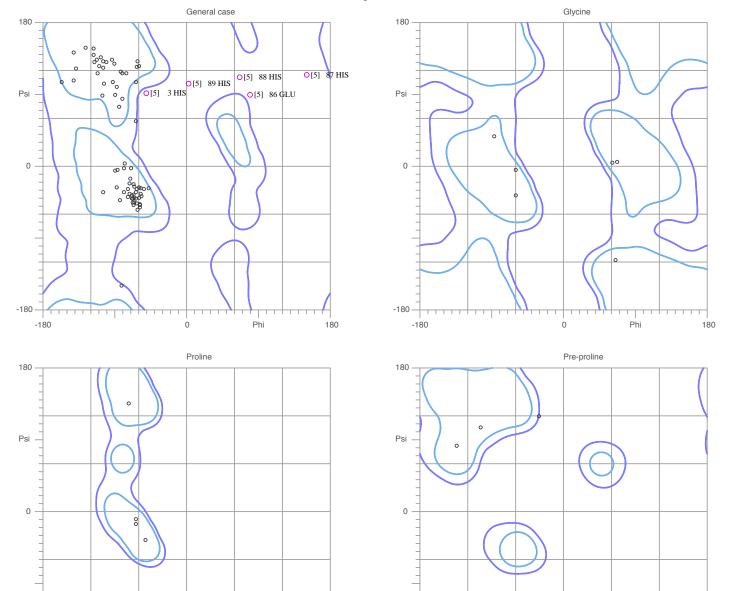
There were 6 outliers (phi, psi):

[4] 2 PRO (-120.7, 177.8)

- [4] 3 HIS (24.9, 90.0)
- [4] 22 ARG (32.0, -78.8)
- [4] 85 LEU (178.0, 103.5)
- [4] 86 GLU (10.2, 130.0)
- [4] 87 HIS (75.5, 132.8)

Lovell, Davis, et al. Proteins 50:437 (2003)

2KZV_AF.pdb, model 5



88.9% (80/90) of all residues were in favored (98%) regions. 94.4% (85/90) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

-180

- [5] 3 HIS (-51.9, 92.2)
- [5] 86 GLU (79.4, 90.9)
- [5] 87 HIS (150.6, 115.5)
- [5] 88 HIS (67.0, 112.2)
- [5] 89 HIS (2.1, 104.2)