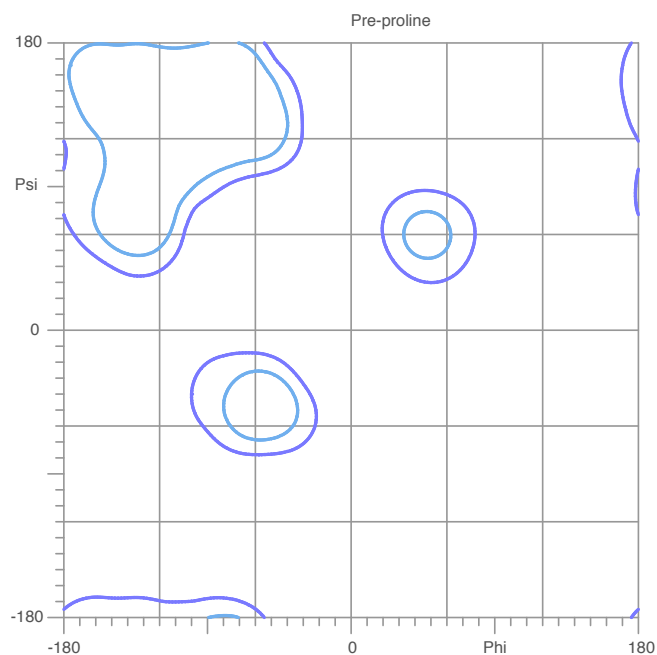
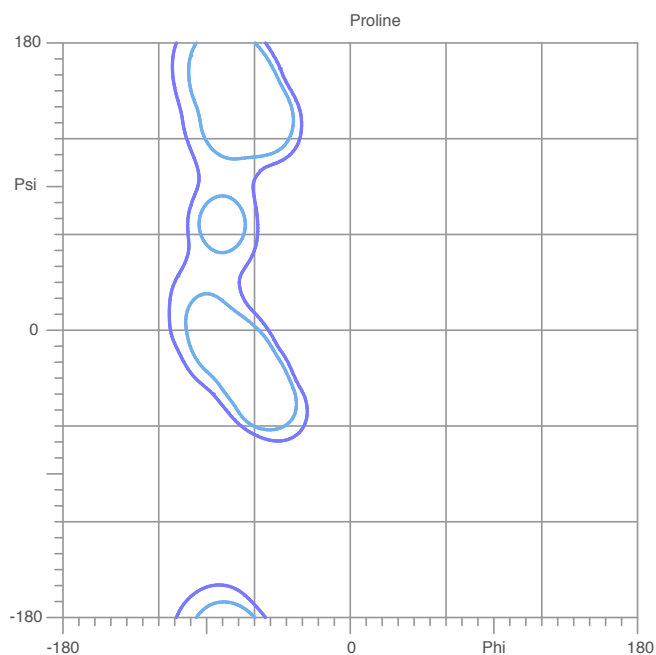
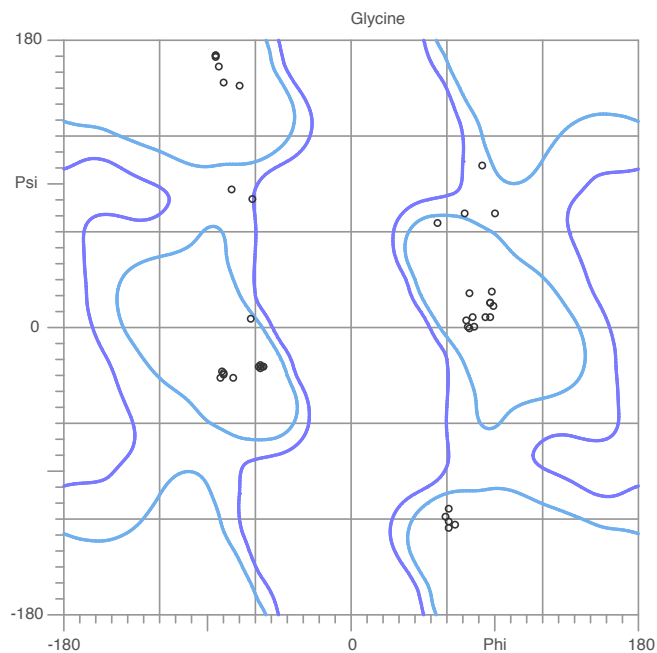
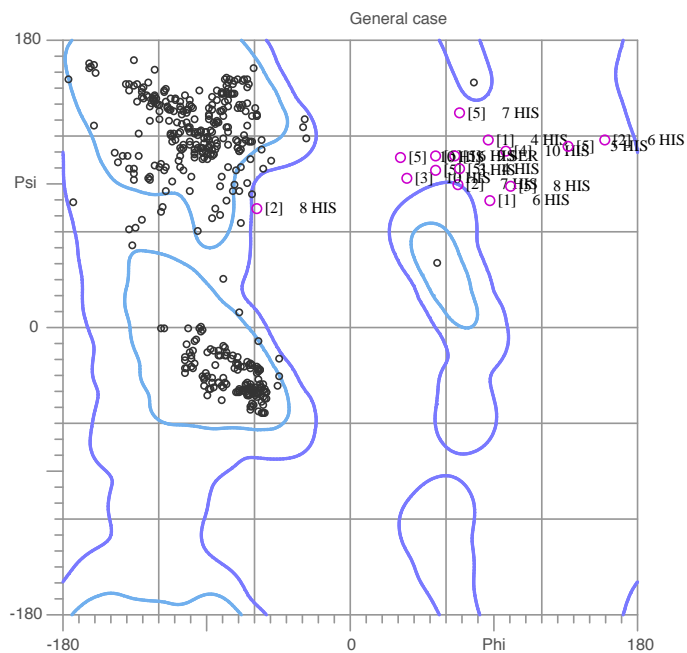


MolProbity Ramachandran analysis

2KJR_AF.pdb, all models



90.8% (422/465) of all residues were in favored (98%) regions.
96.8% (450/465) of all residues were in allowed (>99.8%) regions.

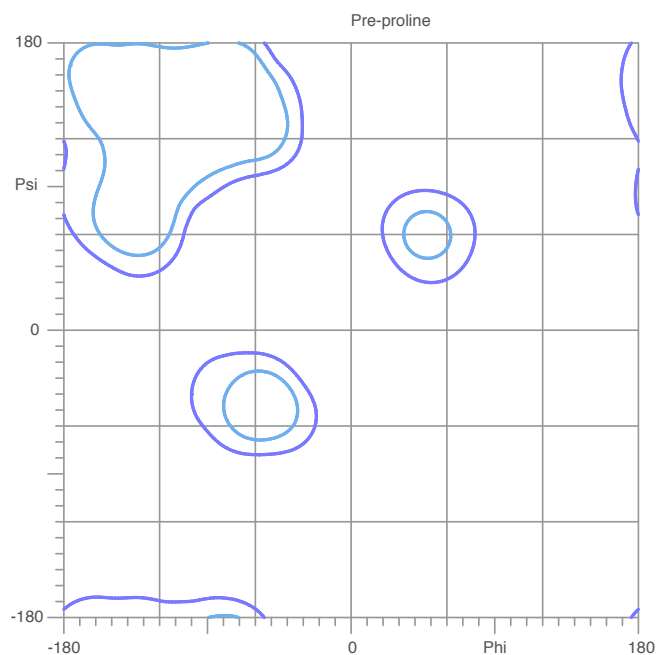
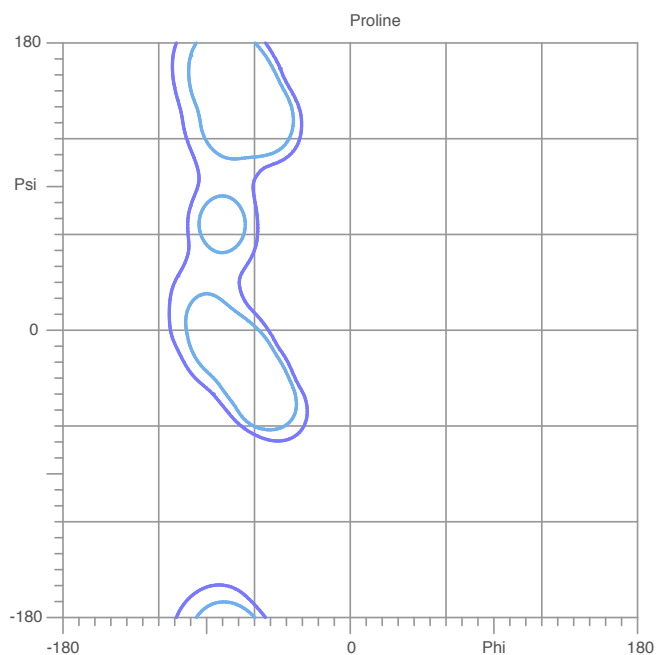
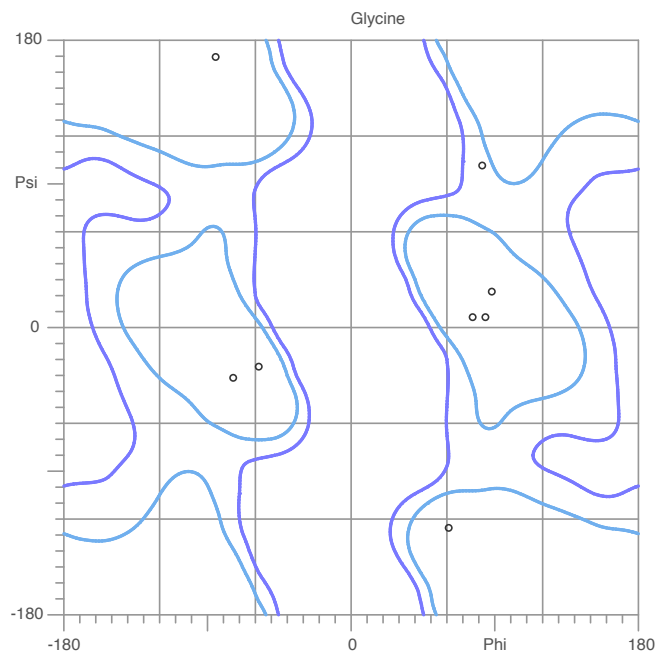
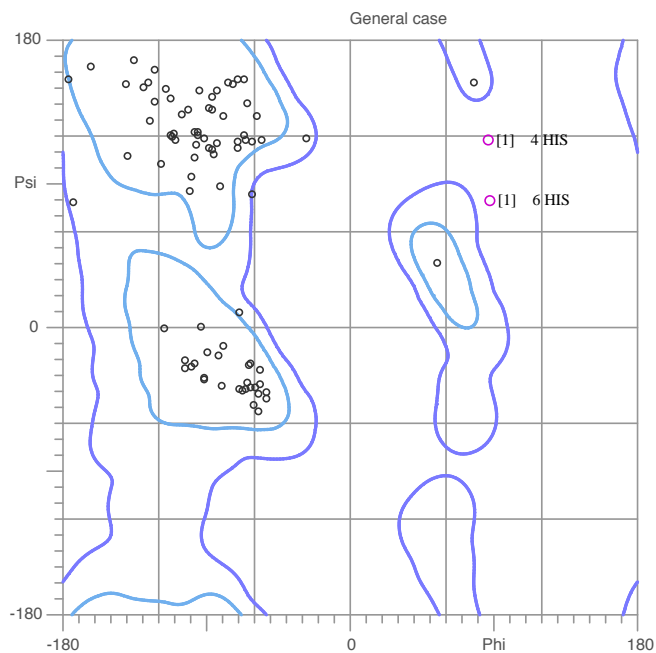
There were 15 outliers (phi, psi):

- [1] 4 HIS (86.3, 118.8)
 [1] 6 HIS (87.8, 80.5)
 [2] 6 HIS (159.1, 118.5)
 [2] 7 HIS (67.7, 90.2)
 [2] 8 HIS (-59.2, 75.0)

- [3] 10 HIS (35.9, 94.1)
 [4] 10 HIS (97.2, 111.1)
 [5] 3 HIS (53.9, 99.7)
 [5] 4 HIS (68.8, 101.0)
 [5] 5 HIS (136.1, 114.8)
 [5] 6 HIS (53.5, 108.3)
 [5] 7 HIS (68.6, 135.8)
 [5] 8 HIS (100.1, 90.0)
 [5] 9 SER (65.3, 108.7)
 [5] 10 HIS (31.7, 107.9)

MolProbity Ramachandran analysis

2KJR_AF.pdb, model 1



90.3% (84/93) of all residues were in favored (98%) regions.
97.8% (91/93) of all residues were in allowed (>99.8%) regions.

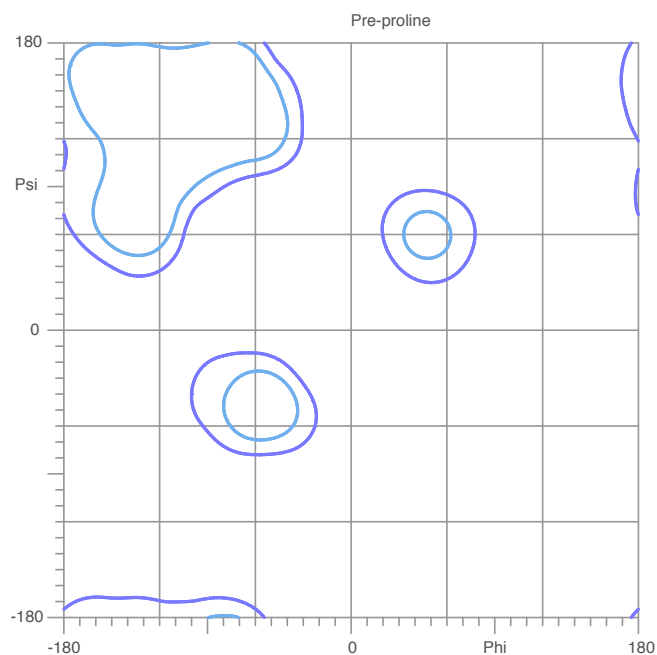
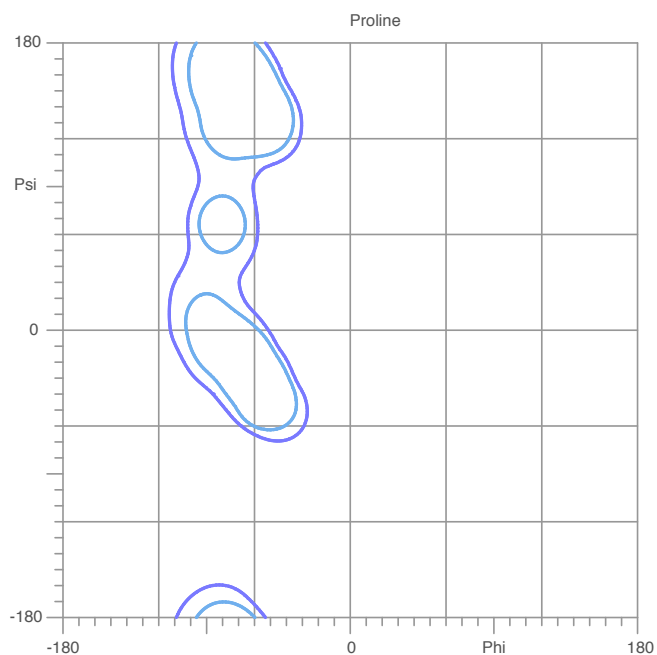
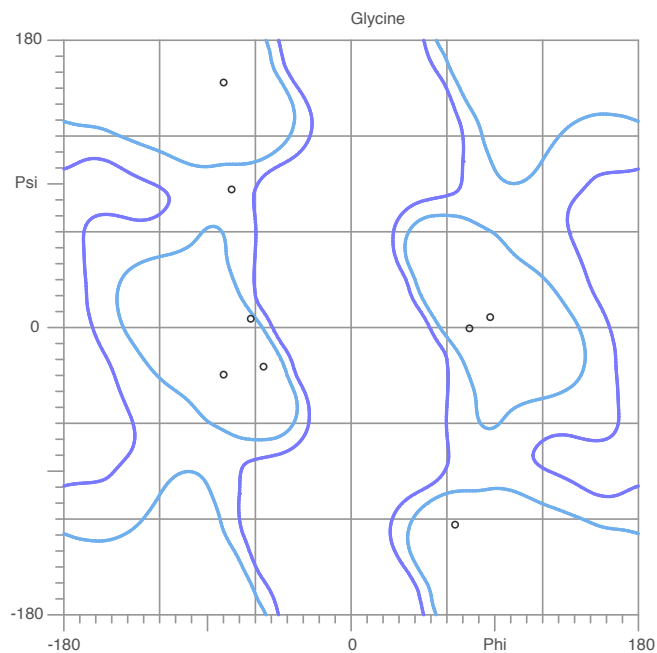
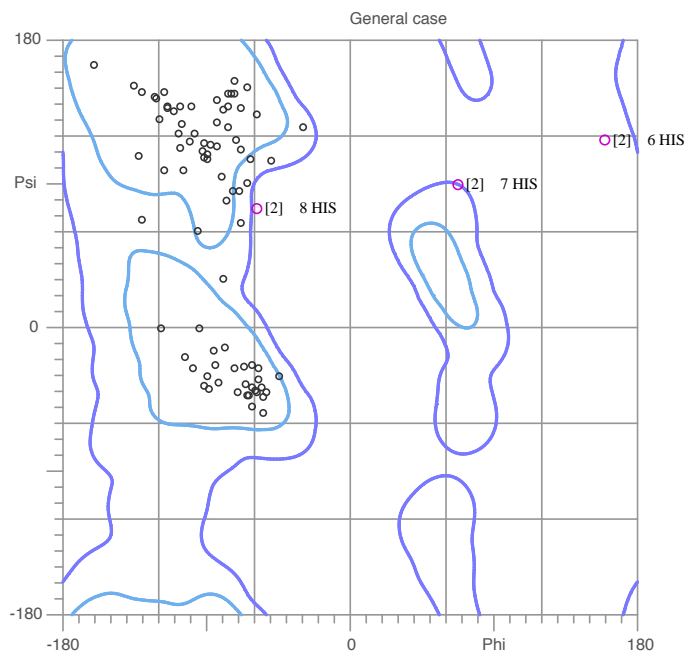
There were 2 outliers (phi, psi):

[1] 4 HIS (86.3, 118.8)

[1] 6 HIS (87.8, 80.5)

MolProbity Ramachandran analysis

2KJR_AF.pdb, model 2



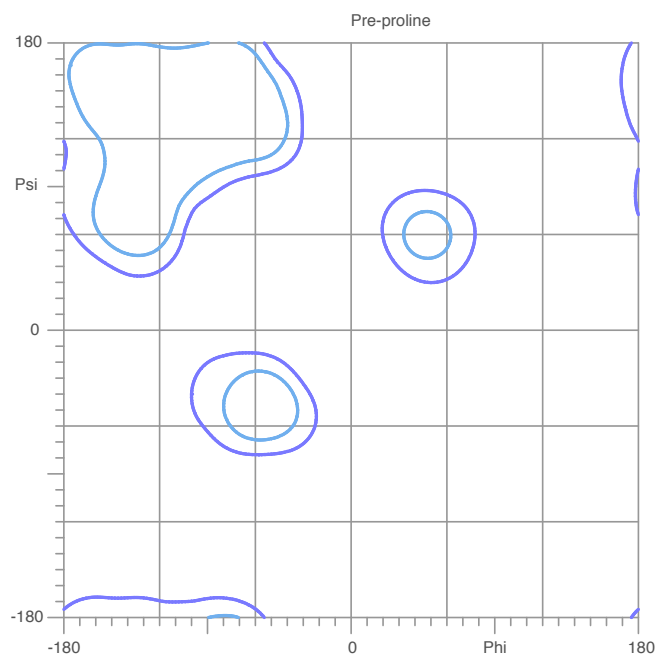
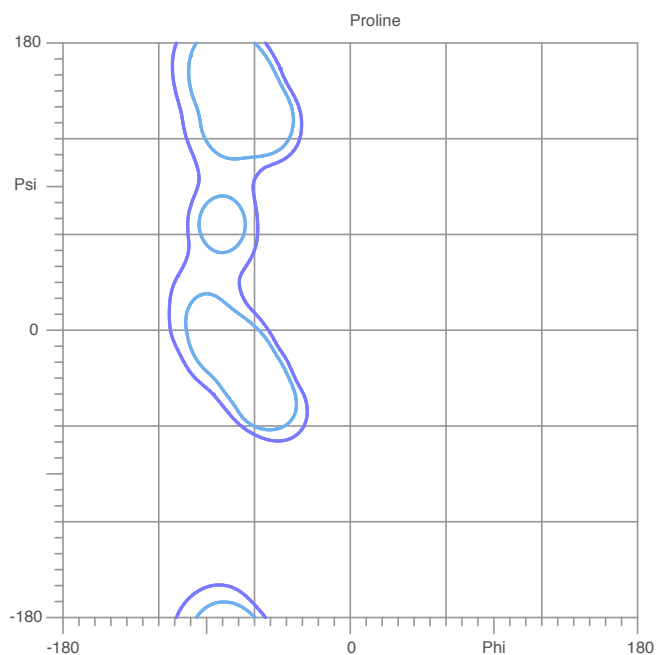
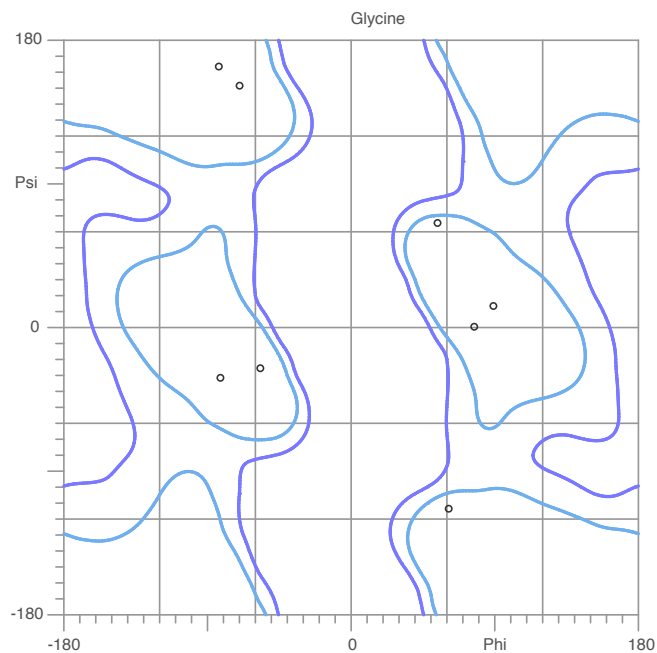
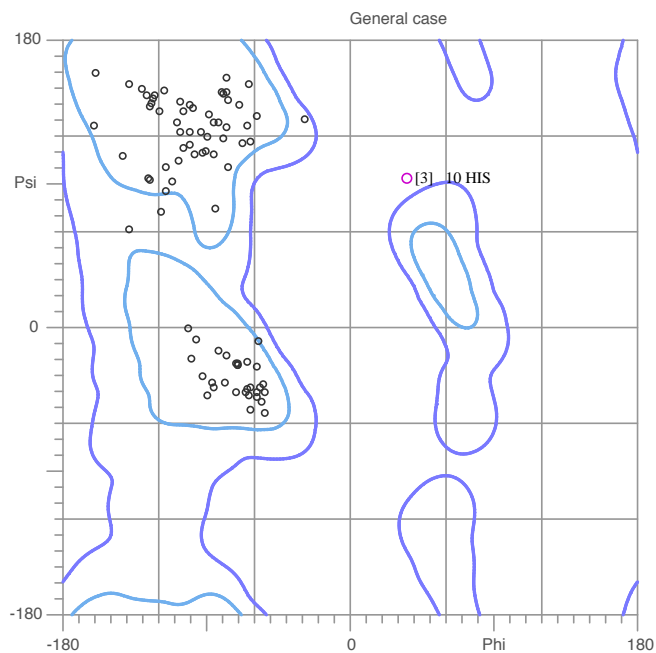
87.1% (81/93) of all residues were in favored (98%) regions.
96.8% (90/93) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 6 HIS (159.1, 118.5)
- [2] 7 HIS (67.7, 90.2)
- [2] 8 HIS (-59.2, 75.0)

MolProbity Ramachandran analysis

2KJR_AF.pdb, model 3



95.7% (89/93) of all residues were in favored (98%) regions.
98.9% (92/93) of all residues were in allowed (>99.8%) regions.

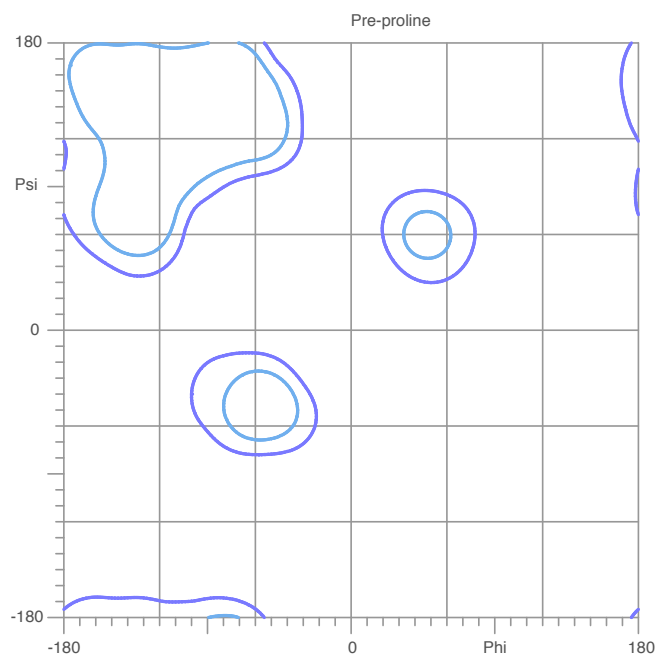
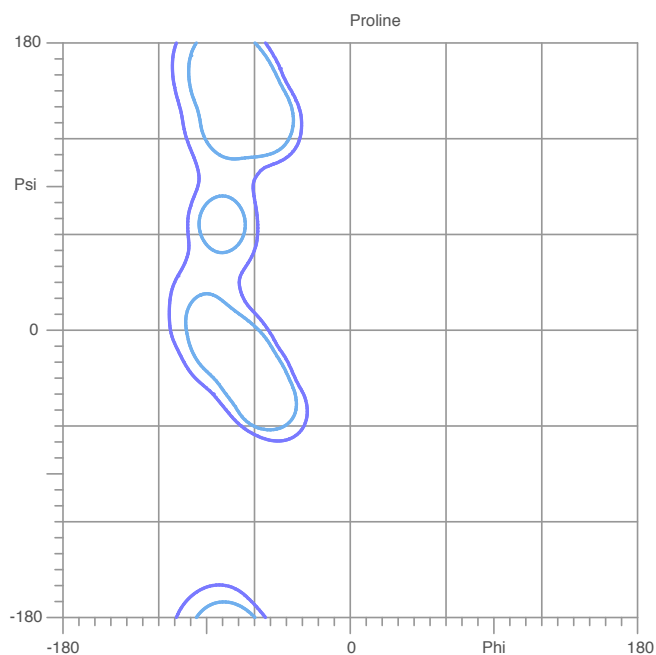
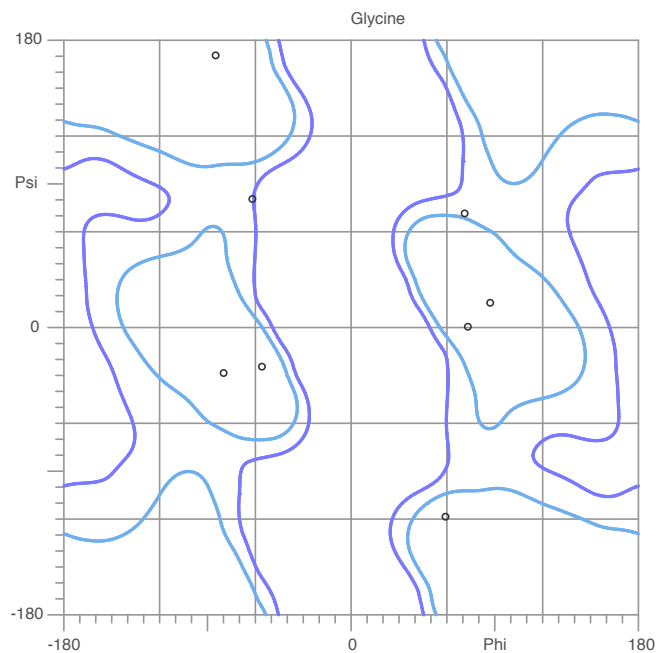
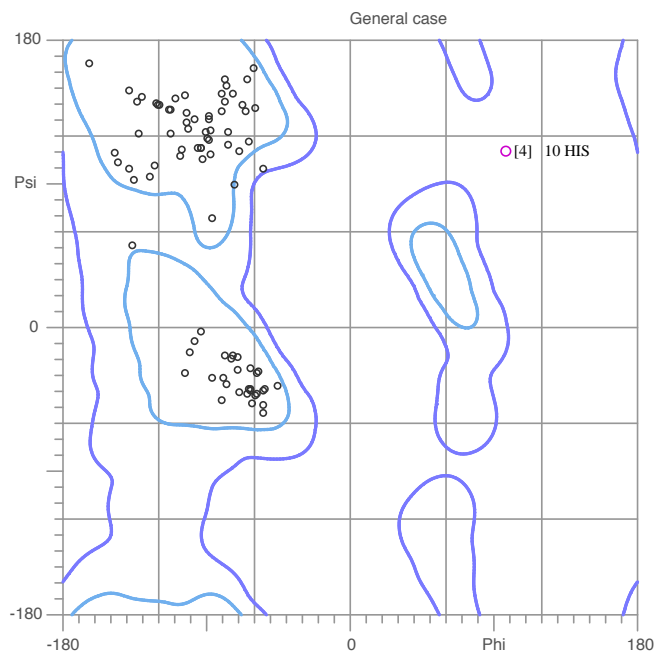
There were 1 outliers (phi, psi):
[3] 10 HIS (35.9, 94.1)

<http://kinemage.biochem.duke.edu>

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

MolProbity Ramachandran analysis

2KJR_AF.pdb, model 4



94.6% (88/93) of all residues were in favored (98%) regions.
98.9% (92/93) of all residues were in allowed (>99.8%) regions.

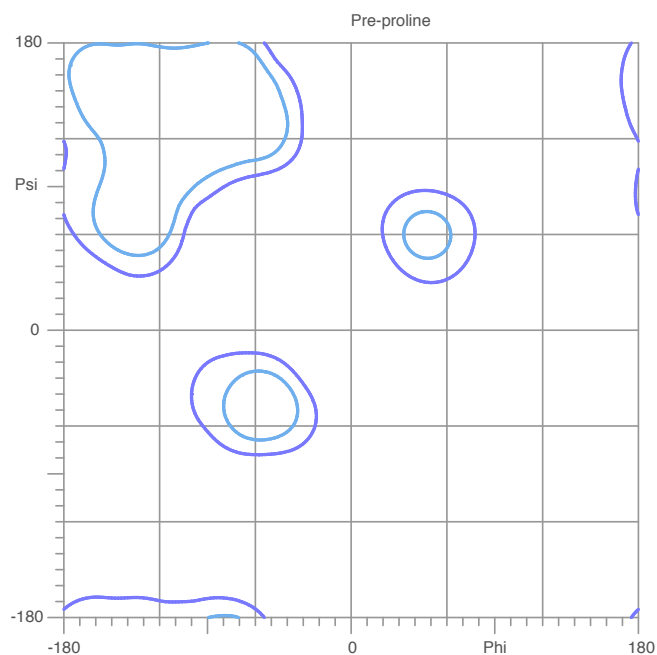
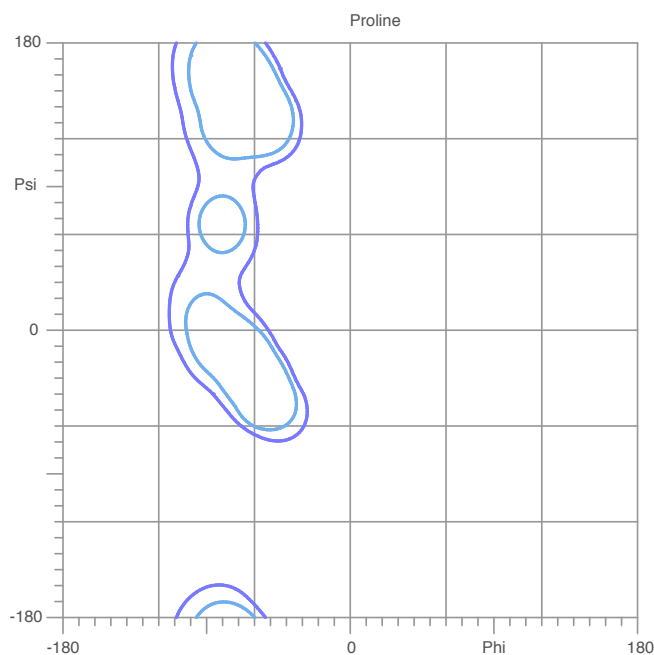
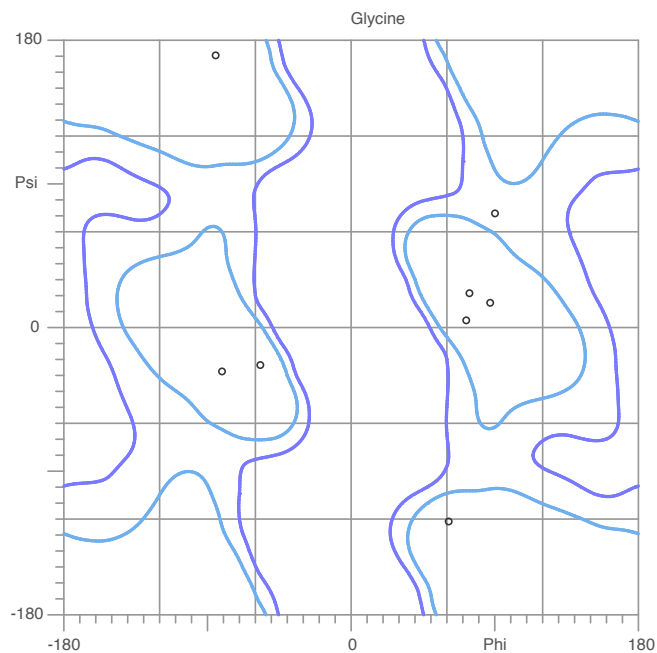
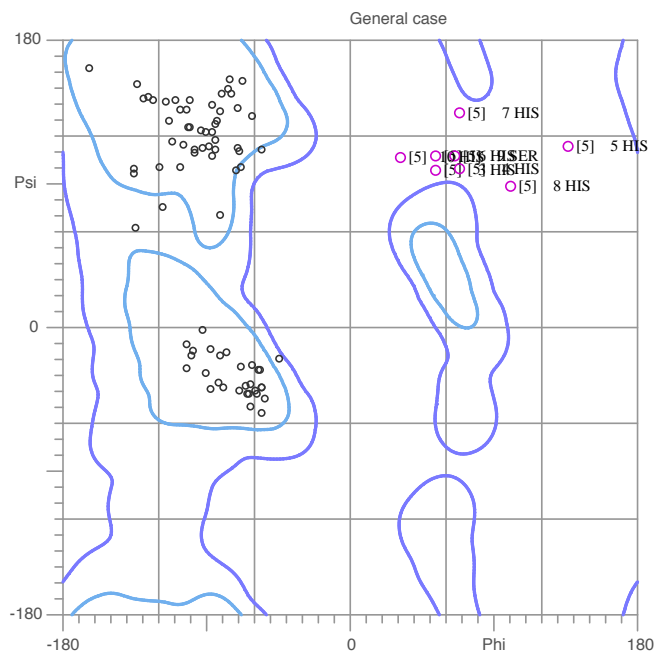
There were 1 outliers (phi, psi):
[4] 10 HIS (97.2, 111.1)

<http://kinemage.biochem.duke.edu>

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

MolProbity Ramachandran analysis

2KJR_AF.pdb, model 5



86.0% (80/93) of all residues were in favored (98%) regions.
91.4% (85/93) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[5] 3 HIS (53.9, 99.7)

[5] 4 HIS (68.8, 101.0)

[5] 5 HIS (136.1, 114.8)

[5] 6 HIS (53.5, 108.3)

[5] 7 HIS (68.6, 135.8)

[5] 8 HIS (100.1, 90.0)

[5] 9 SER (65.3, 108.7)

[5] 10 HIS (31.7, 107.9)