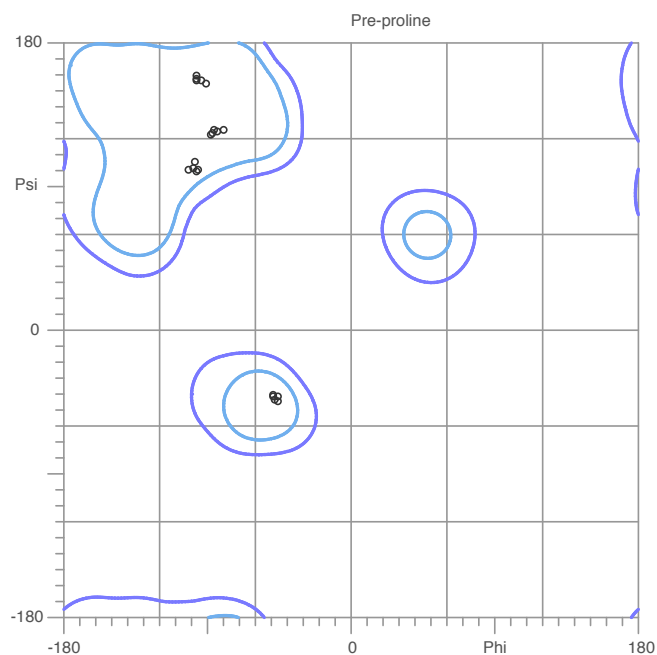
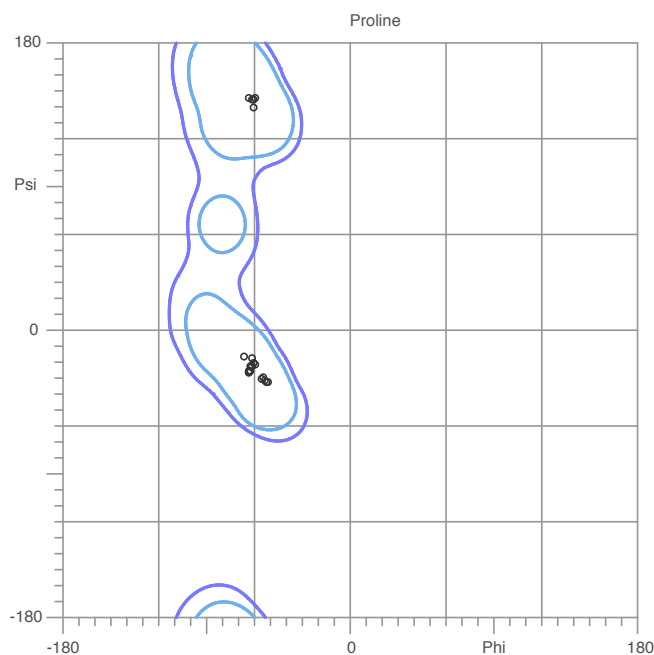
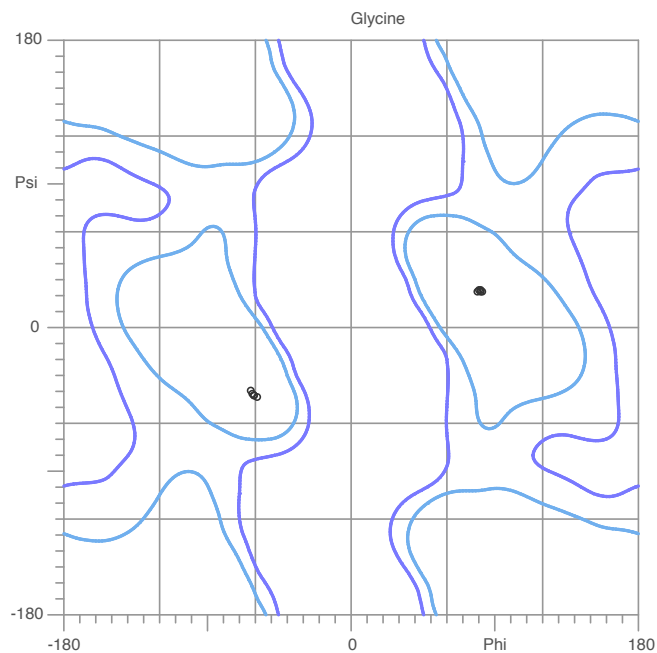
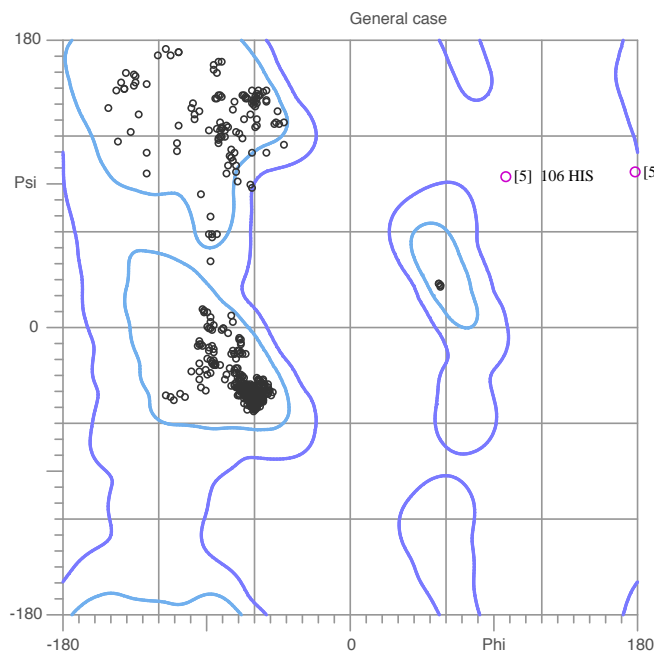


MolProbity Ramachandran analysis

2KOB_AF.pdb, all models



98.5% (522/530) of all residues were in favored (98%) regions.
99.6% (528/530) of all residues were in allowed (>99.8%) regions.

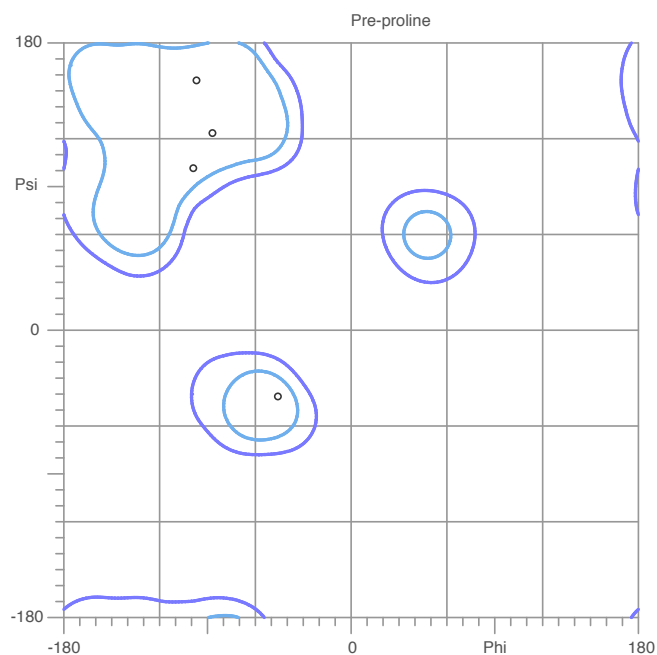
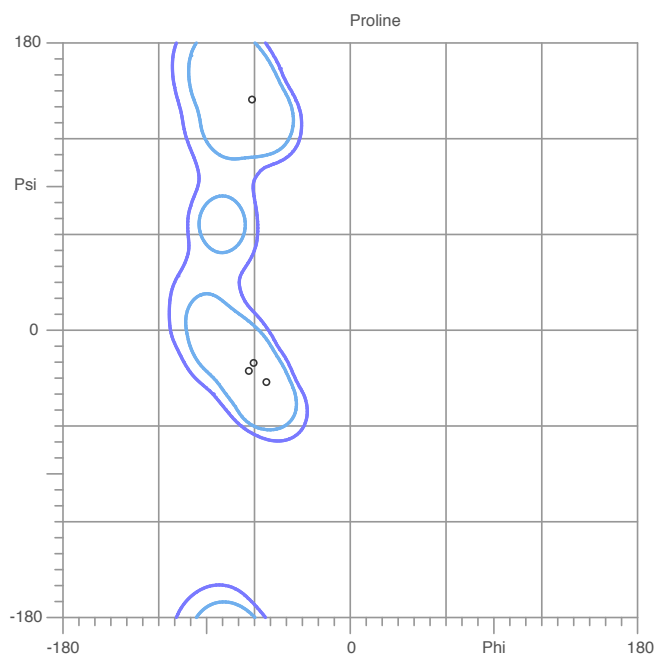
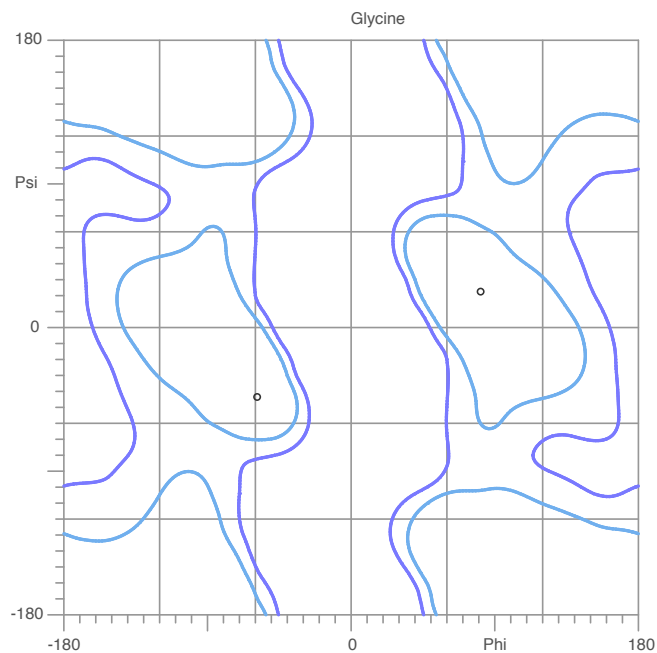
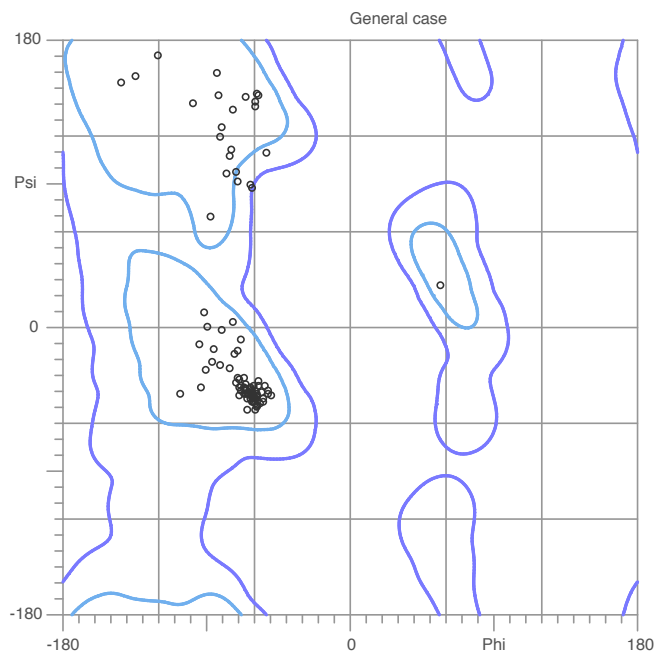
There were 2 outliers (phi, psi):

[5] 105 HIS (178.6, 98.9)

[5] 106 HIS (97.5, 95.1)

MolProbity Ramachandran analysis

2KOB_AF.pdb, model 1



96.2% (102/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

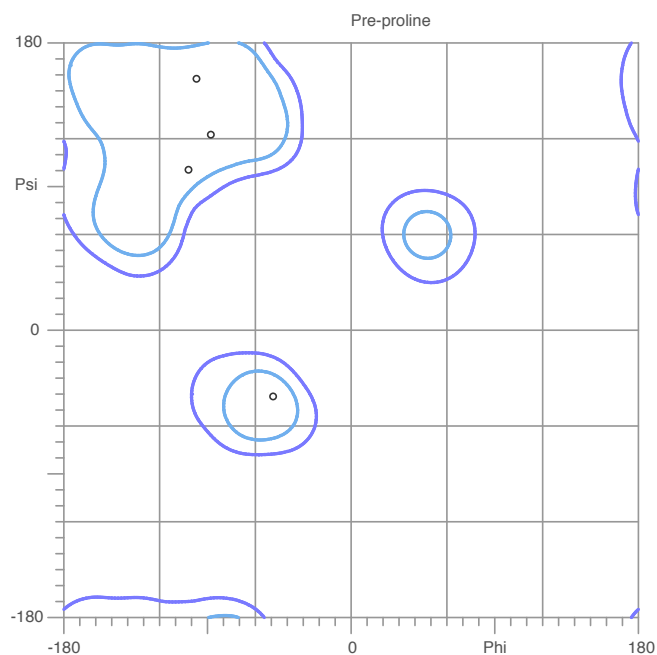
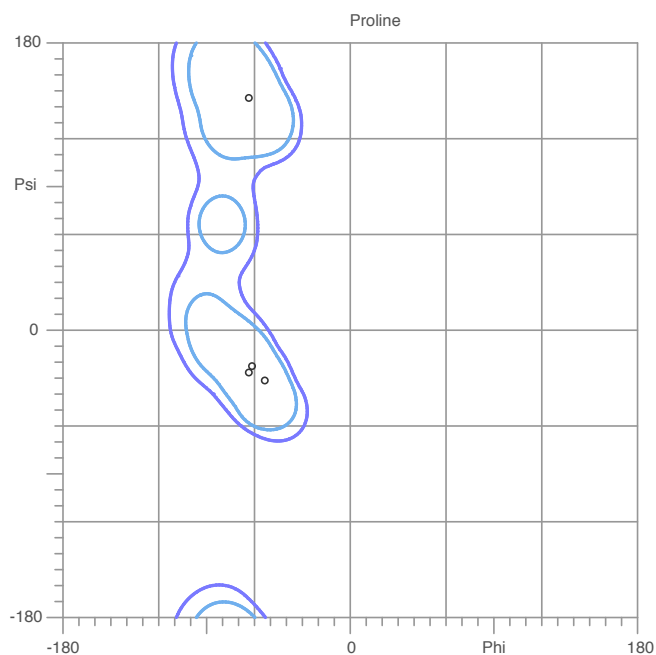
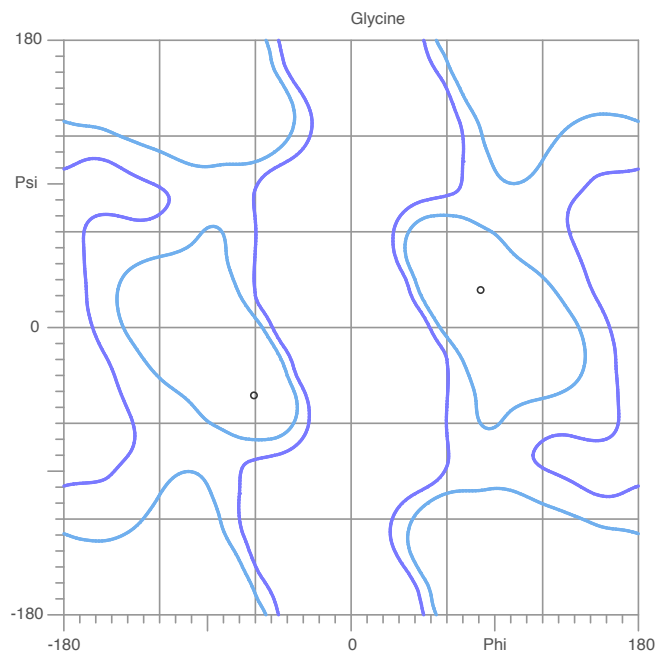
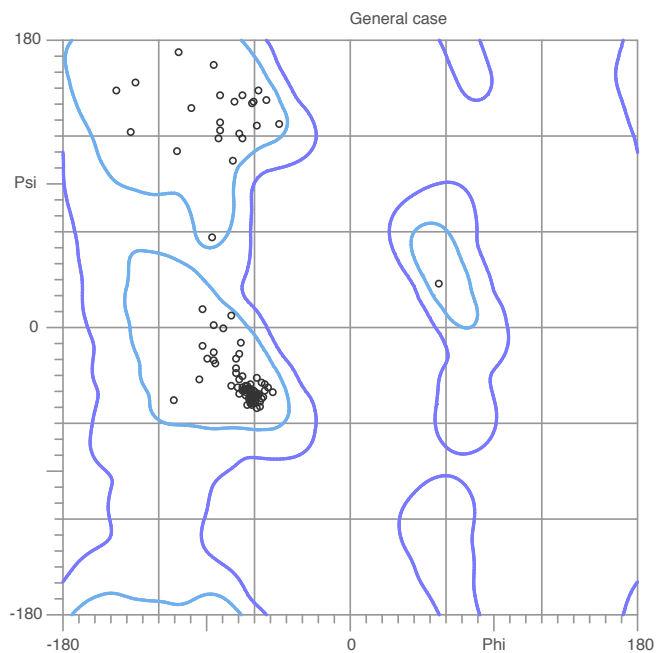
There were no outliers.

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

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MolProbity Ramachandran analysis

2KOB_AF.pdb, model 2



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

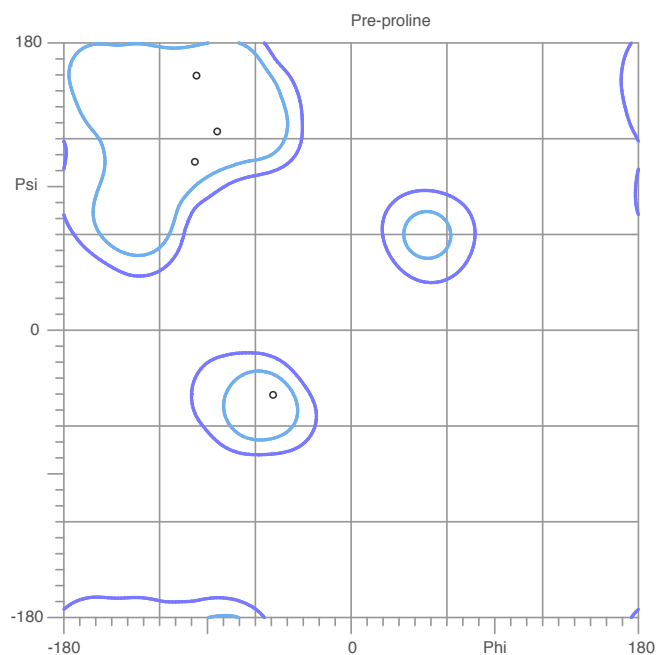
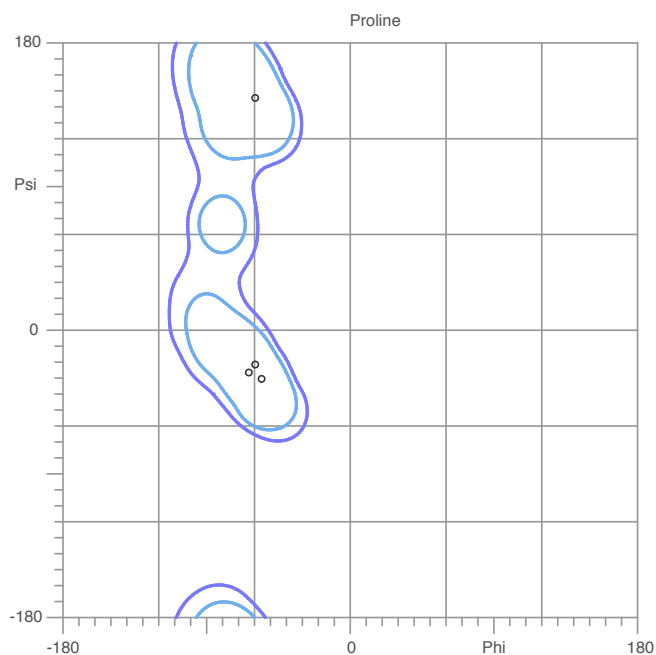
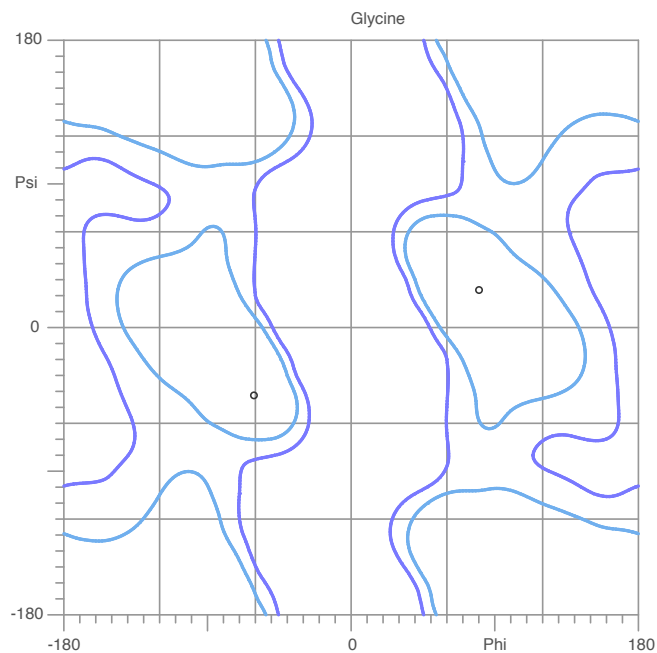
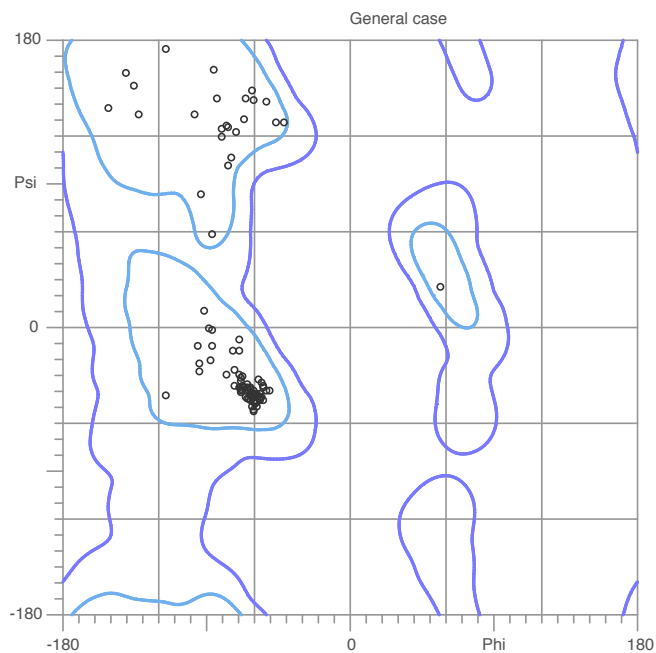
There were no outliers.

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

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MolProbity Ramachandran analysis

2KOB_AF.pdb, model 3



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

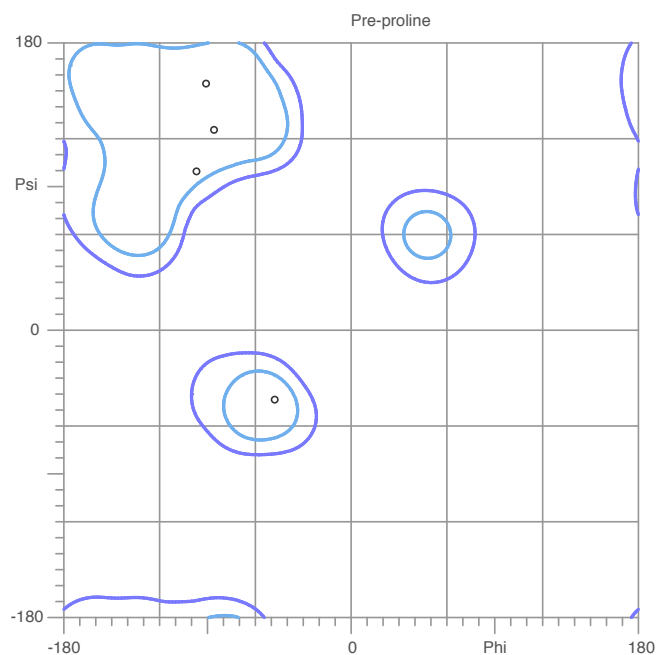
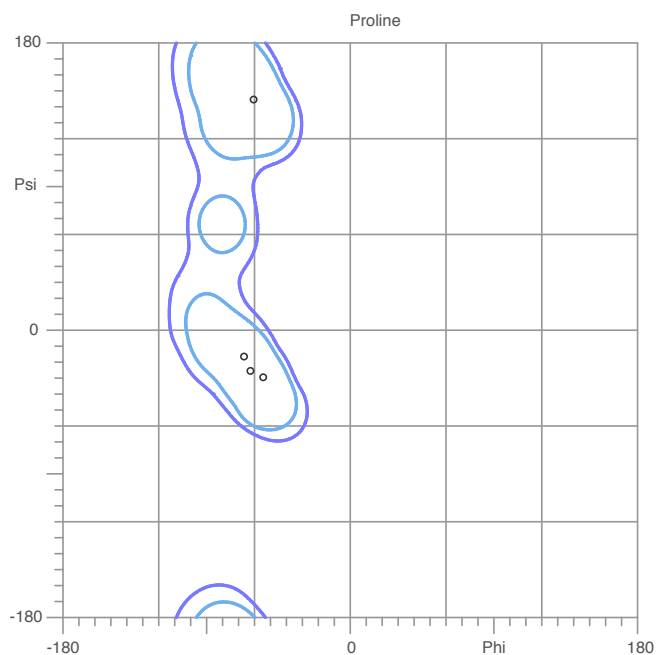
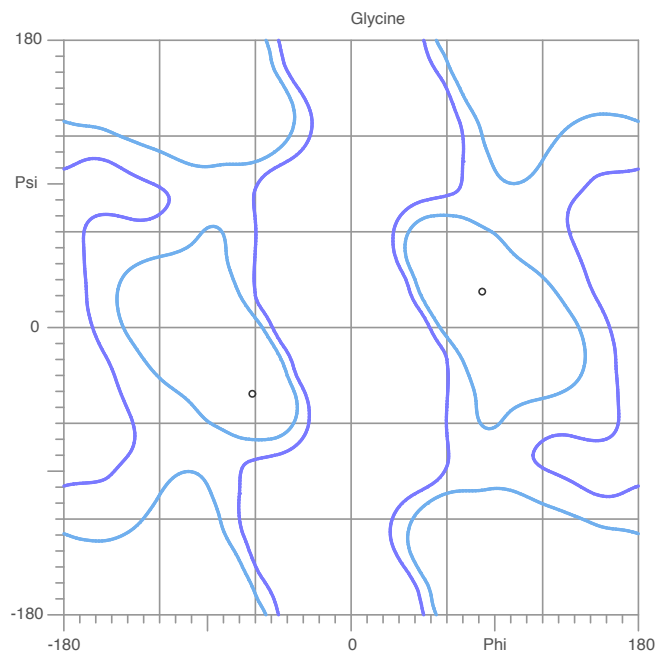
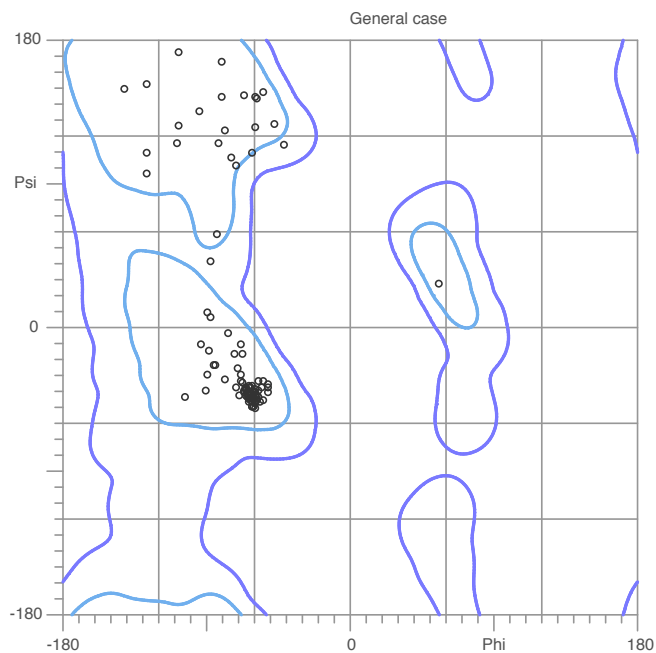
There were no outliers.

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

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

MolProbity Ramachandran analysis

2KOB_AF.pdb, model 4



98.1% (104/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

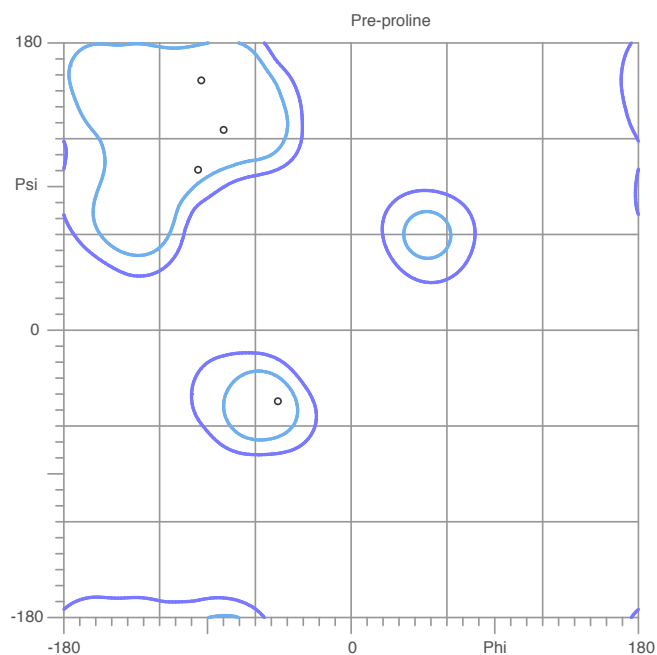
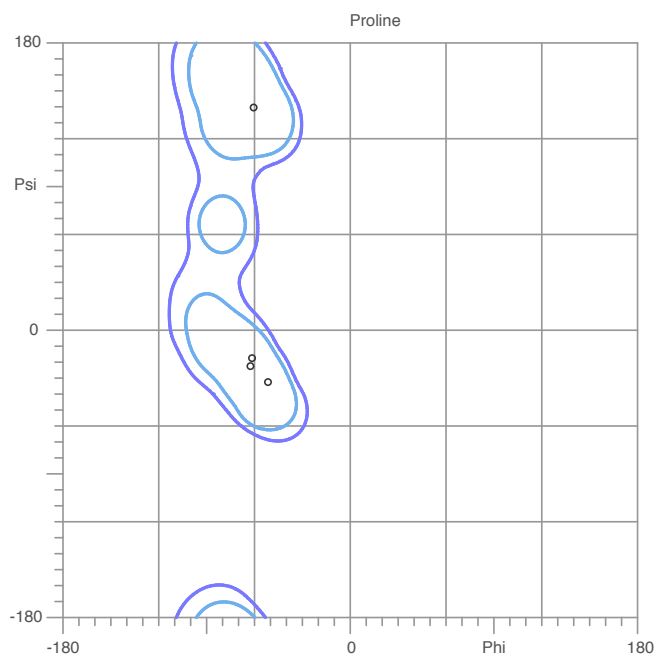
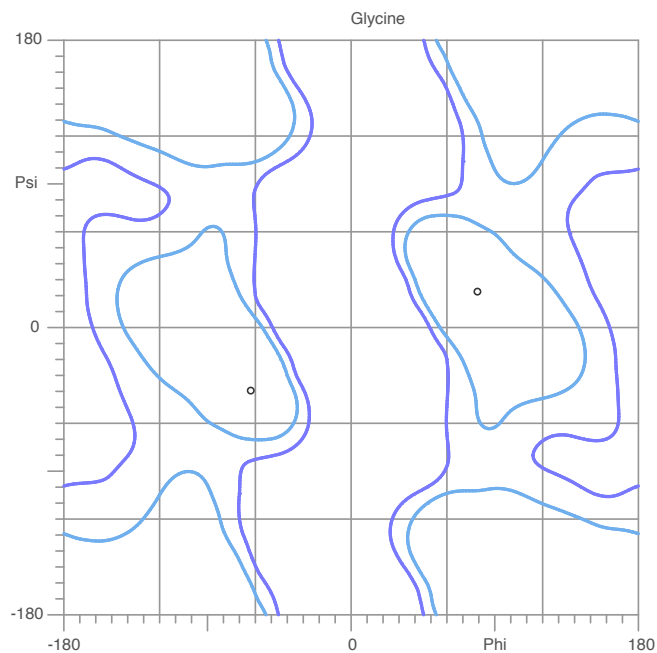
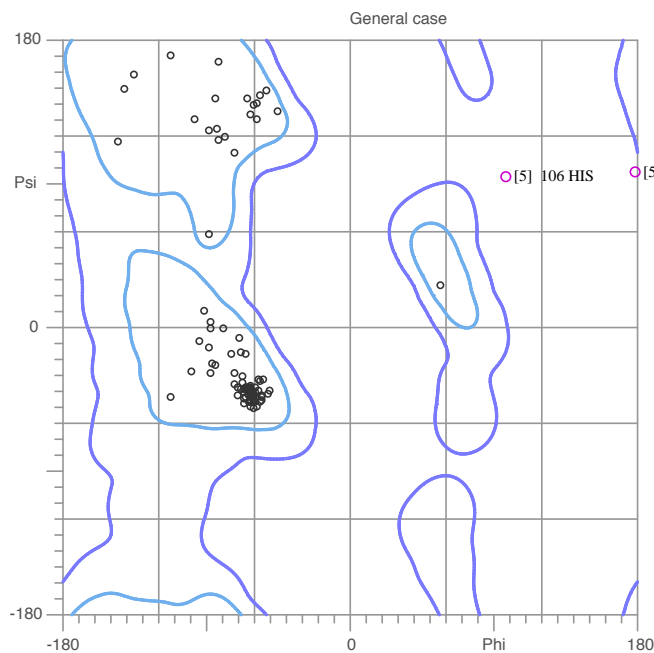
There were no outliers.

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

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

MolProbity Ramachandran analysis

2KOB_AF.pdb, model 5



98.1% (104/106) of all residues were in favored (98%) regions.
98.1% (104/106) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[5] 105 HIS (178.6, 98.9)

[5] 106 HIS (97.5, 95.1)