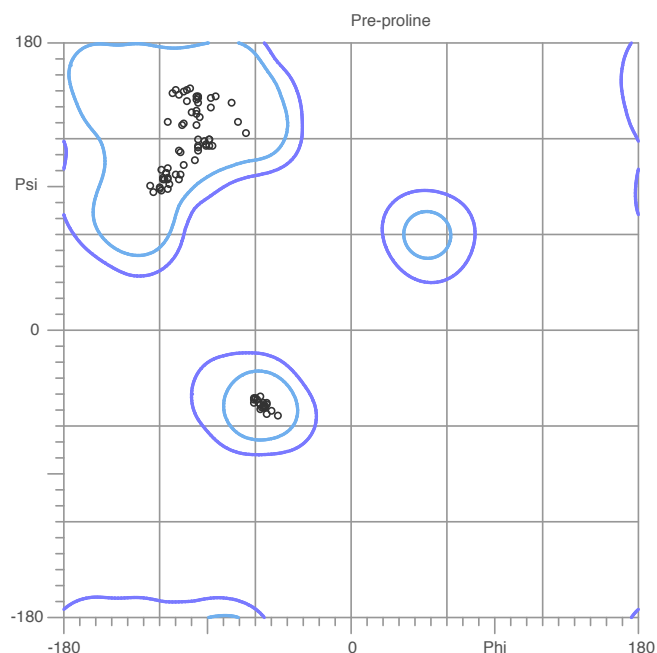
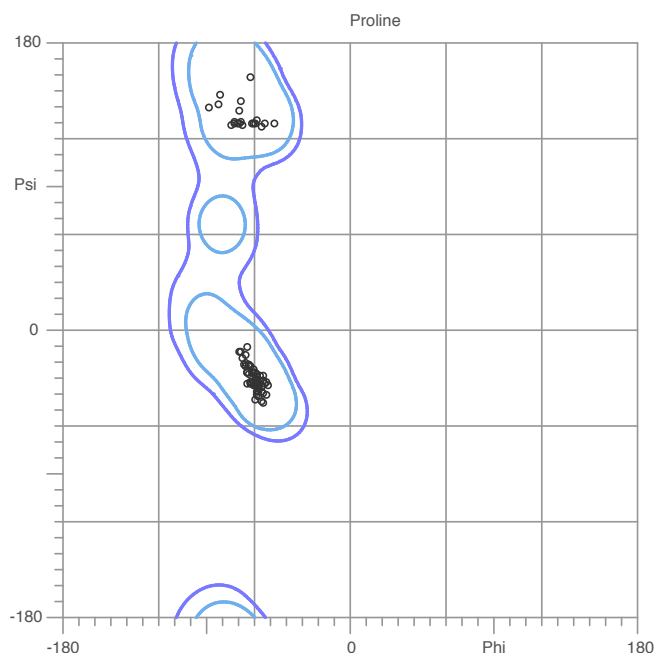
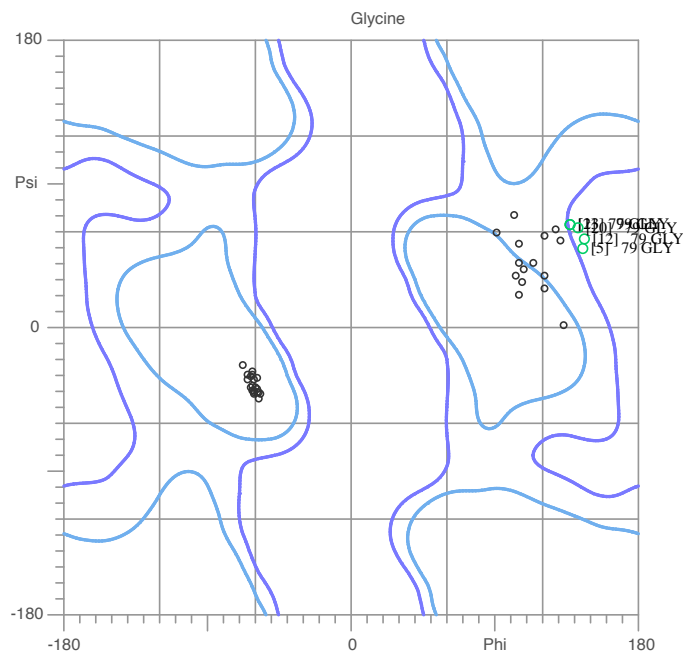
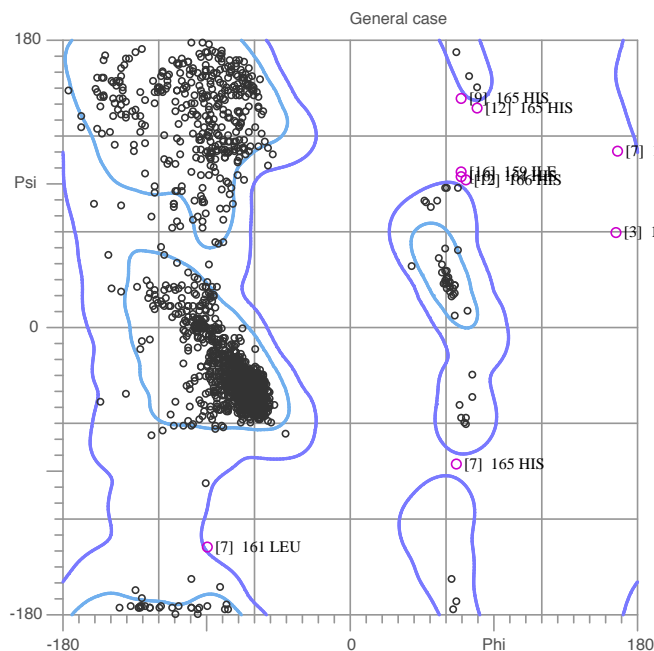


MolProbity Ramachandran analysis

2KOB.pdb, all models



96.1% (2037/2120) of all residues were in favored (98%) regions.
99.3% (2106/2120) of all residues were in allowed (>99.8%) regions.

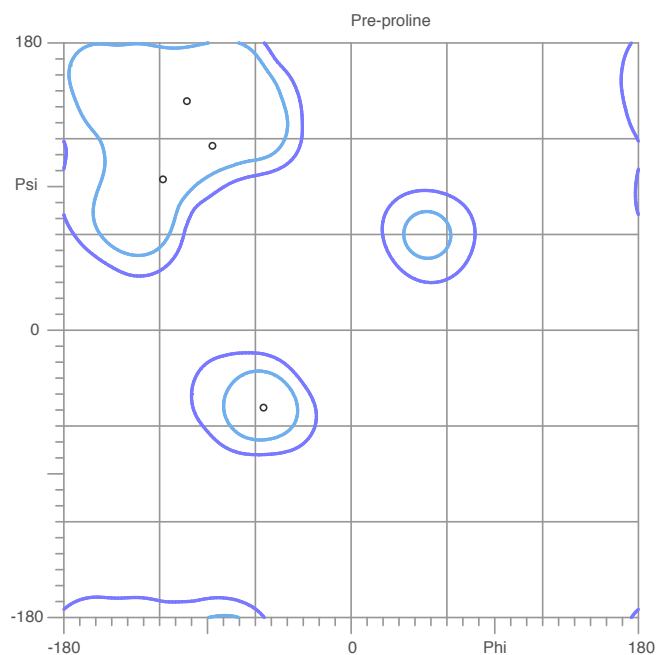
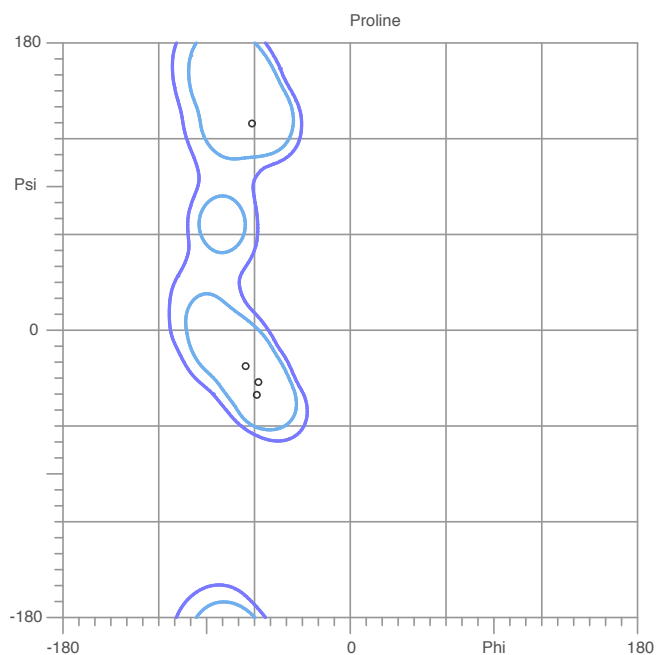
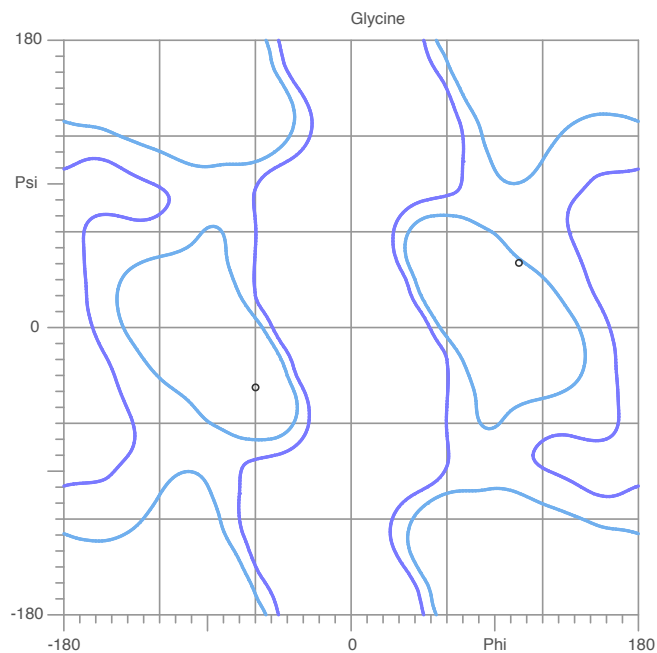
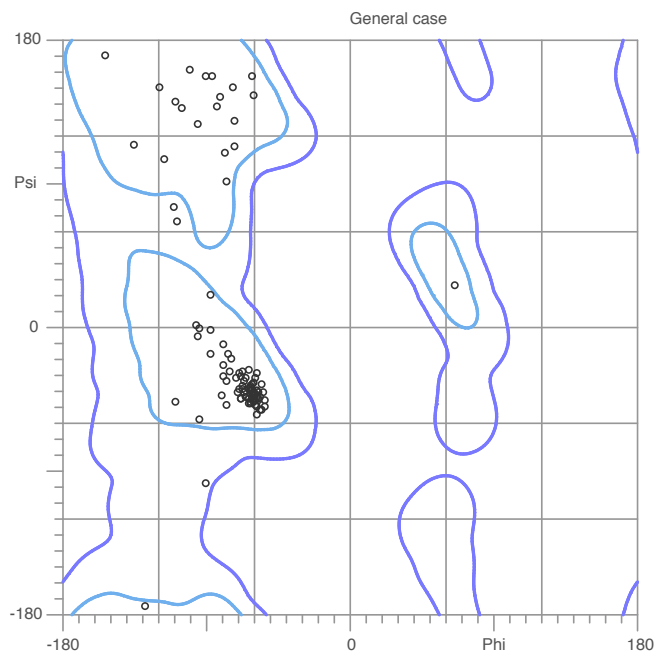
There were 14 outliers (phi, psi):

- [2] 79 GLY (137.6, 65.2)
- [3] 164 HIS (166.4, 60.8)
- [5] 79 GLY (145.9, 50.4)
- [7] 161 LEU (-90.8, -137.3)
- [7] 165 HIS (66.7, -85.2)

- [7] 166 HIS (167.1, 111.1)
- [9] 165 HIS (69.3, 144.7)
- [12] 79 GLY (146.5, 56.4)
- [12] 165 HIS (79.6, 138.7)
- [12] 166 HIS (72.2, 93.0)
- [13] 79 GLY (137.5, 65.8)
- [16] 159 ILE (69.0, 98.7)
- [16] 164 HIS (69.1, 95.1)
- [20] 79 GLY (142.3, 64.0)

MolProbity Ramachandran analysis

2KOB.pdb, model 1



97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

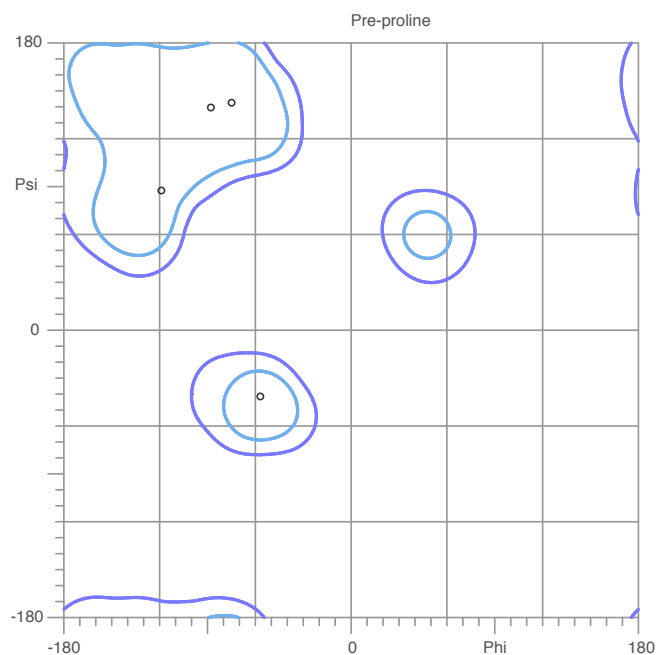
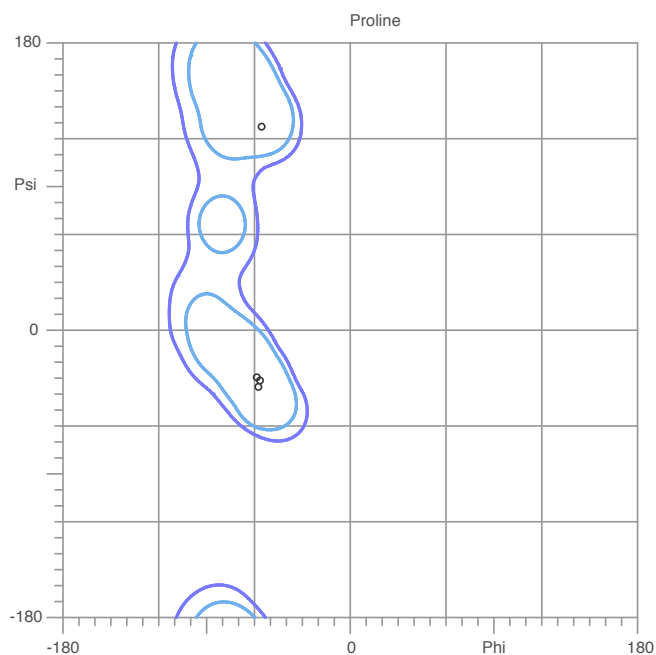
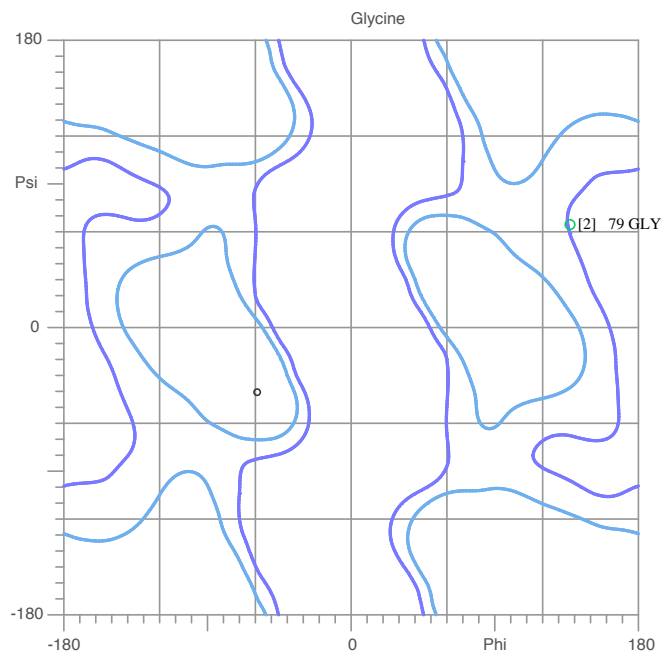
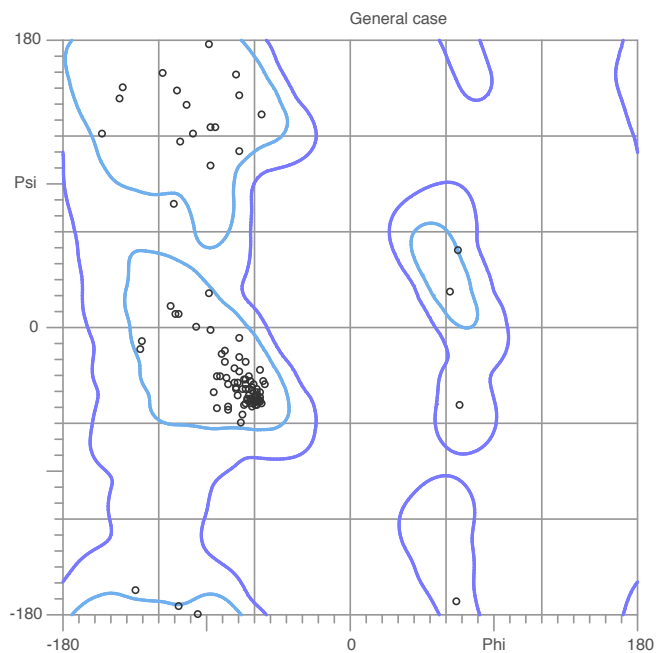
There were no outliers.

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MolProbity Ramachandran analysis

2KOB.pdb, model 2



94.3% (100/106) of all residues were in favored (98%) regions.
99.1% (105/106) of all residues were in allowed (>99.8%) regions.

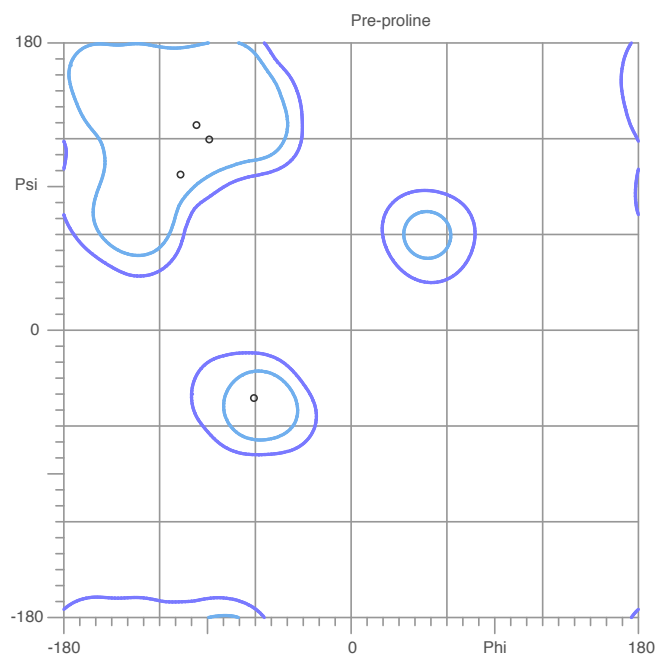
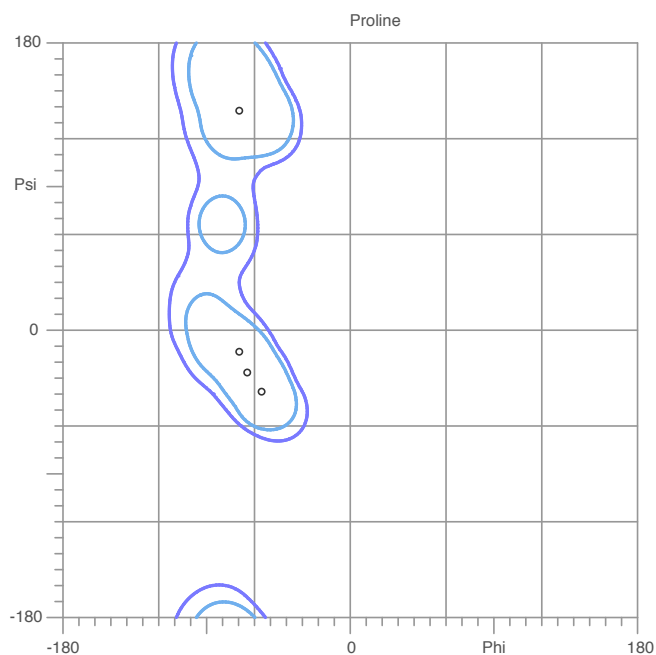
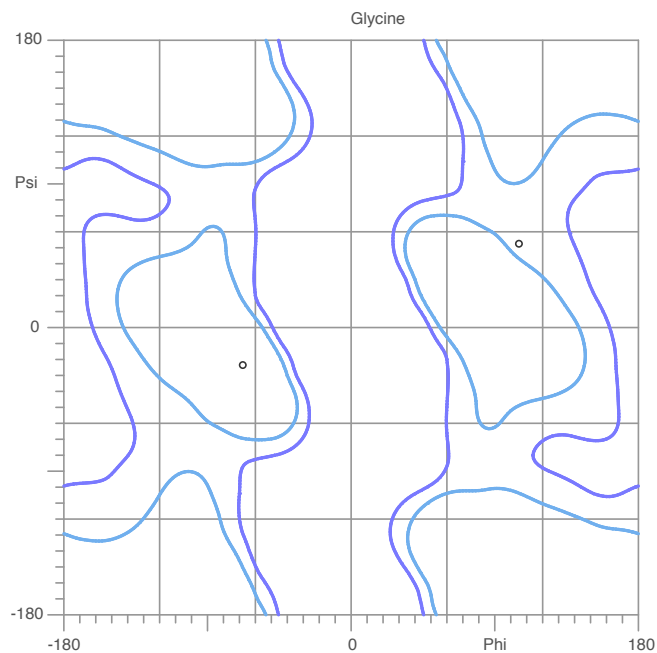
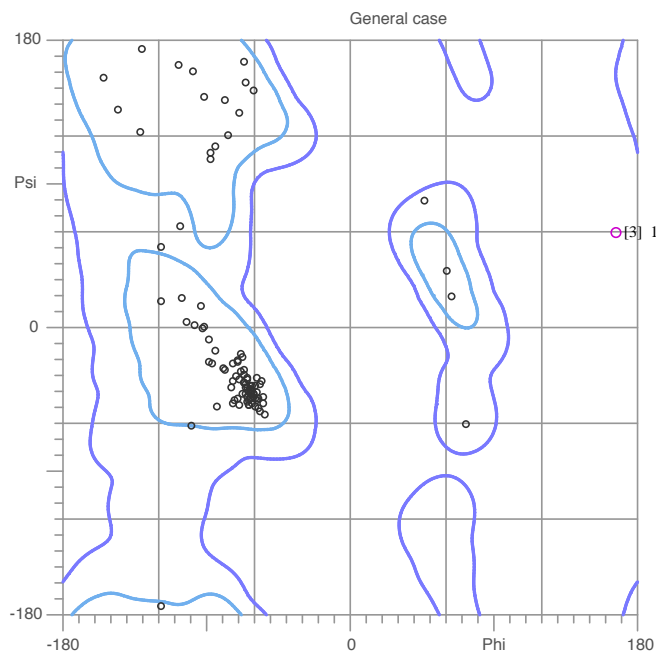
There were 1 outliers (phi, psi):
[2] 79 GLY (137.6, 65.2)

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MolProbity Ramachandran analysis

2KOB.pdb, model 3



94.3% (100/106) of all residues were in favored (98%) regions.
99.1% (105/106) of all residues were in allowed (>99.8%) regions.

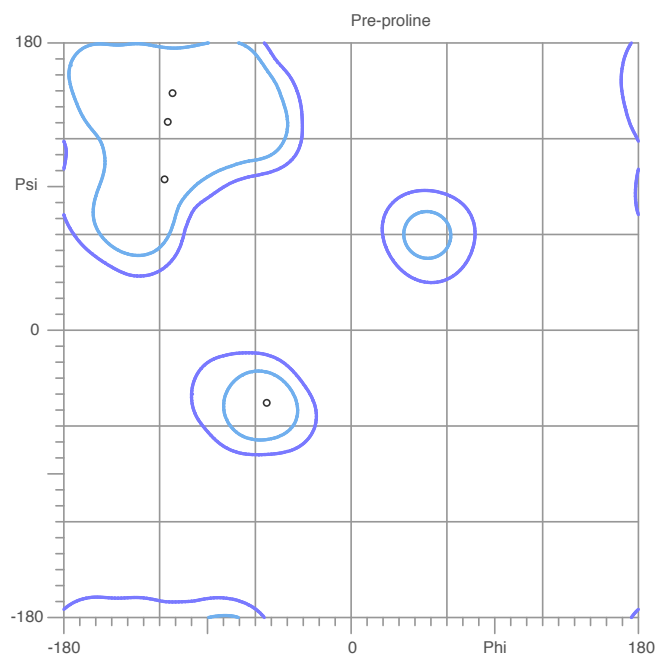
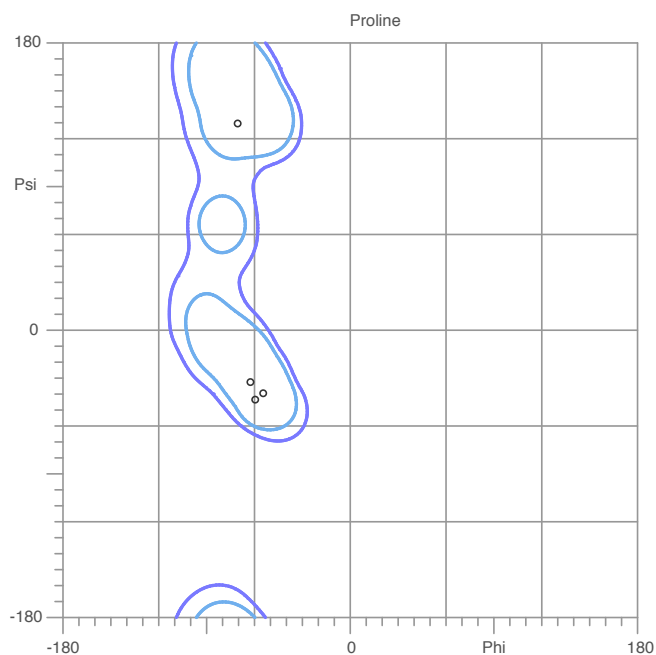
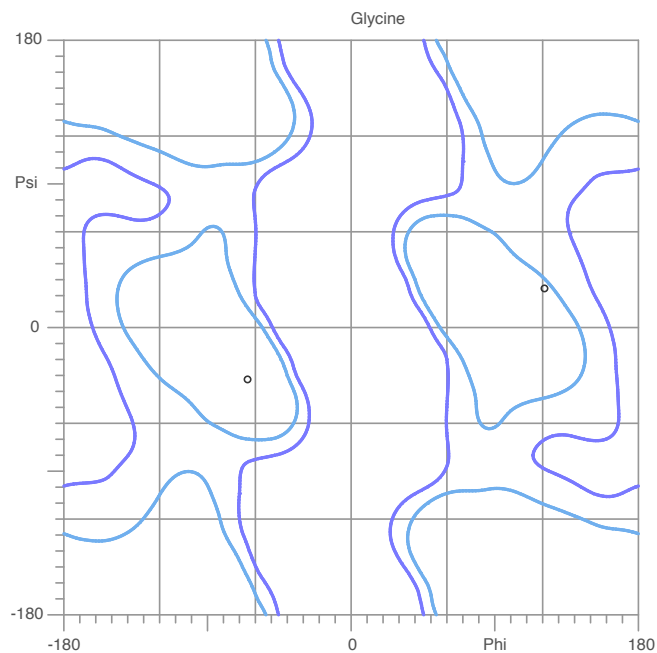
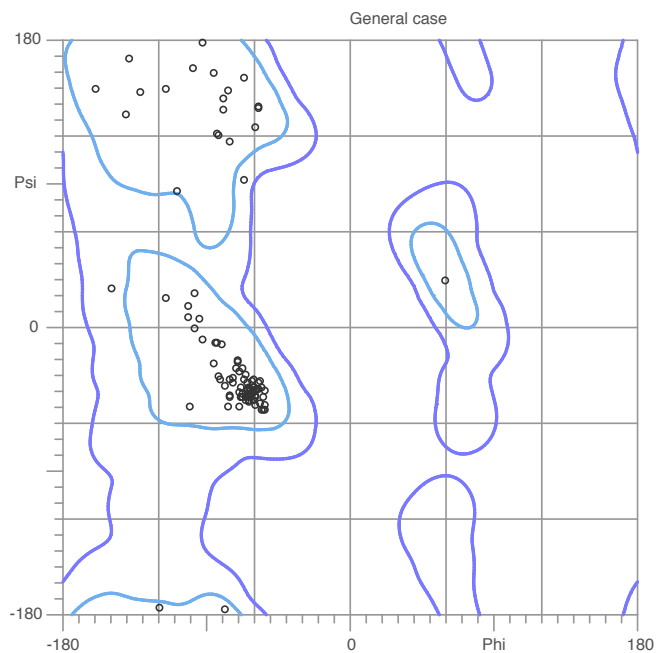
There were 1 outliers (phi, psi):
[3] 164 HIS (166.4, 60.8)

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MolProbity Ramachandran analysis

2KOB.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.

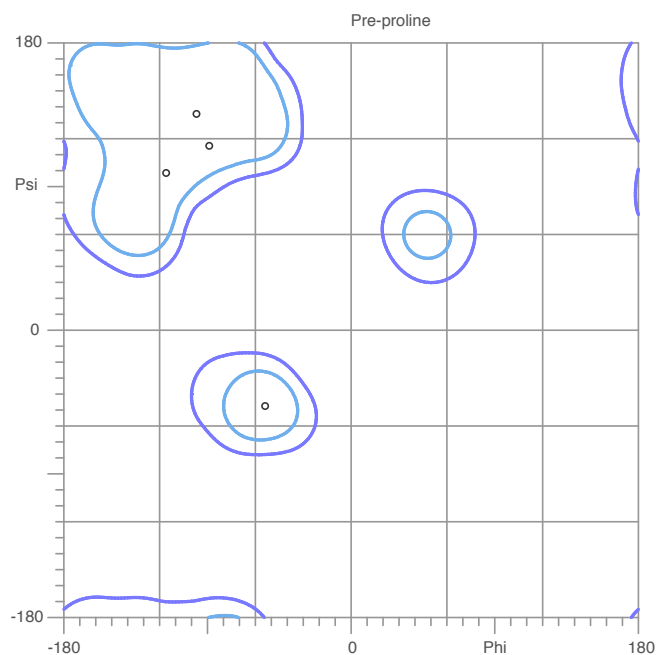
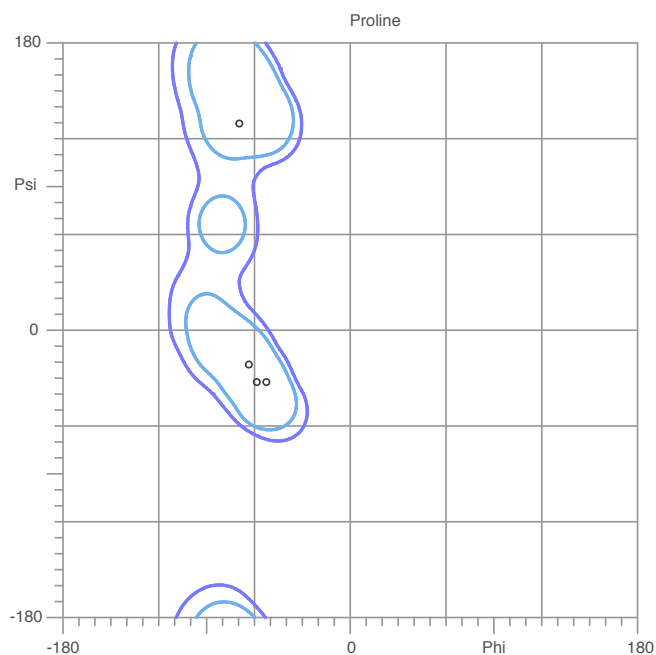
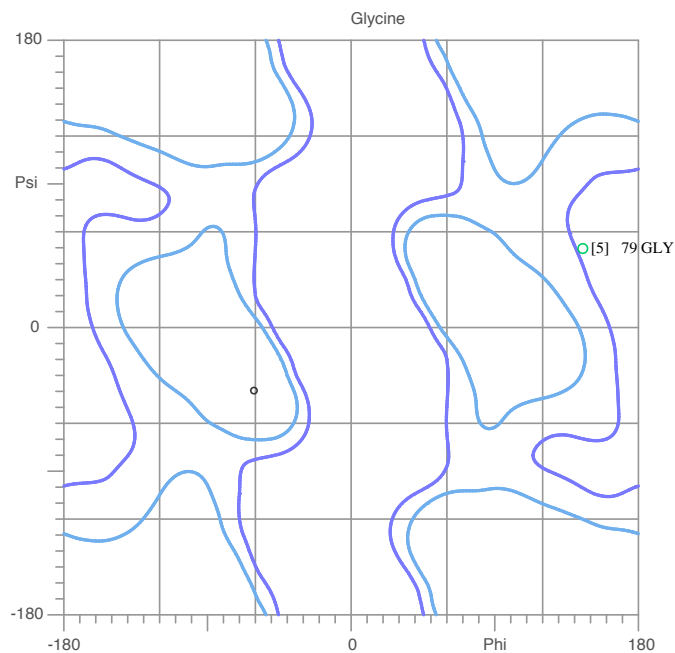
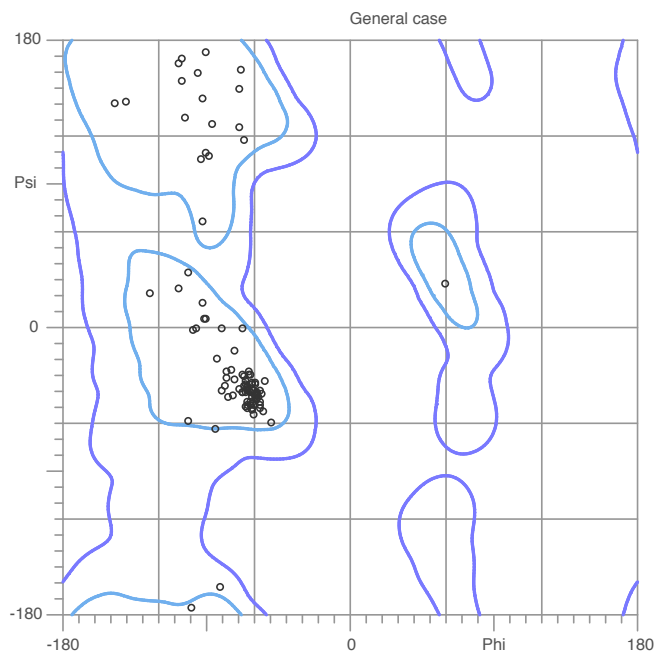
There were no outliers.

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MolProbity Ramachandran analysis

2KOB.pdb, model 5



97.2% (103/106) of all residues were in favored (98%) regions.
99.1% (105/106) of all residues were in allowed (>99.8%) regions.

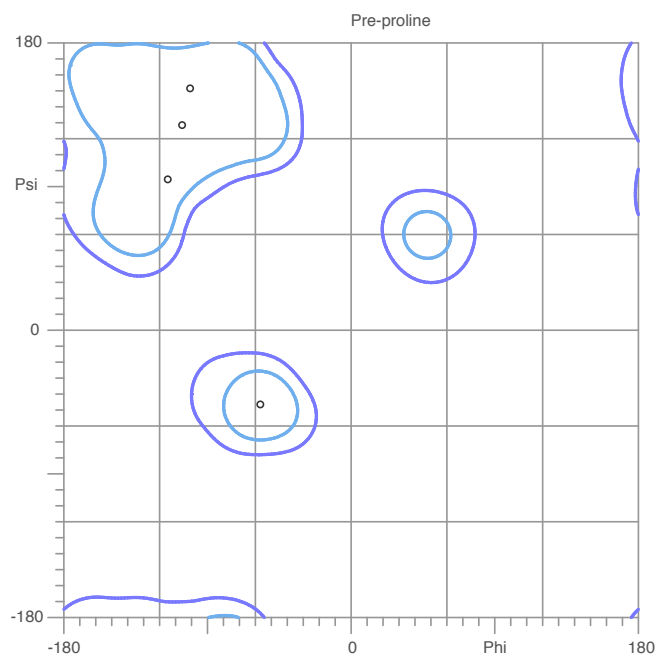
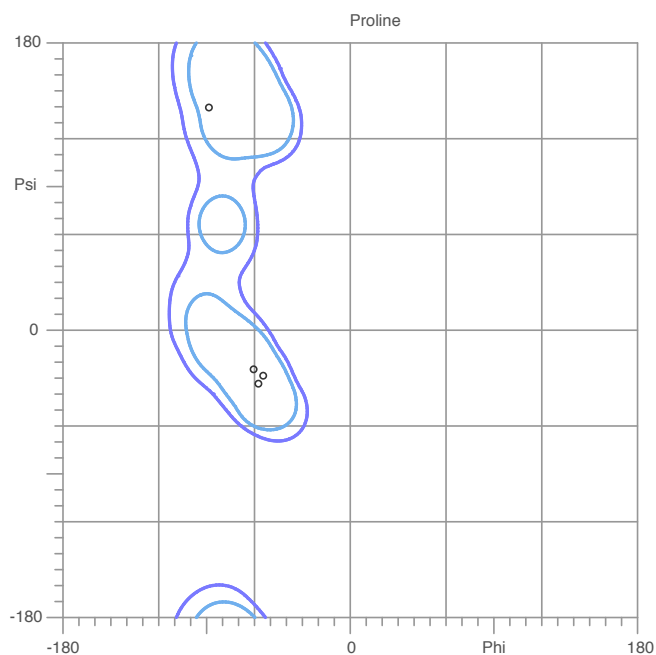
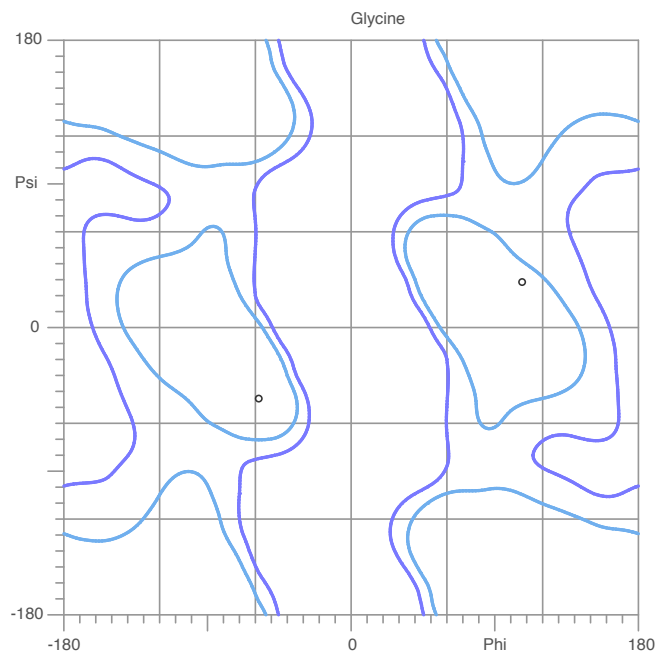
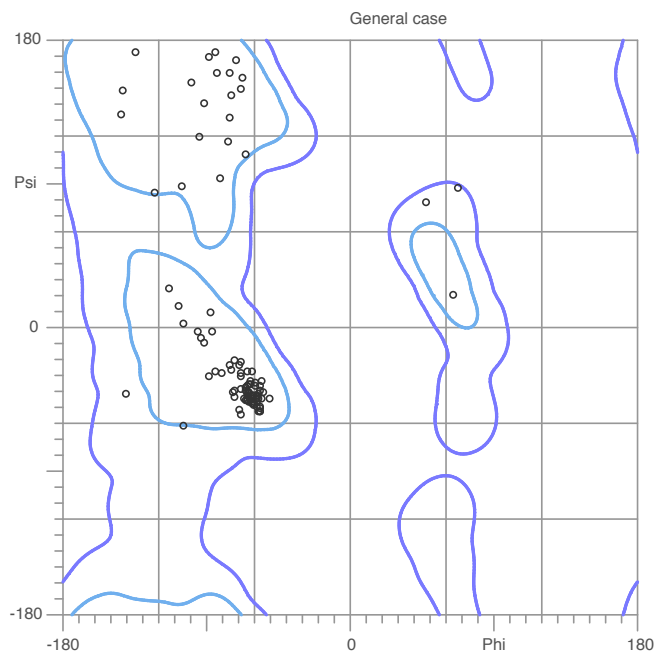
There were 1 outliers (phi, psi):
[5] 79 GLY (145.9, 50.4)

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MolProbity Ramachandran analysis

2KOB.pdb, model 6



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.

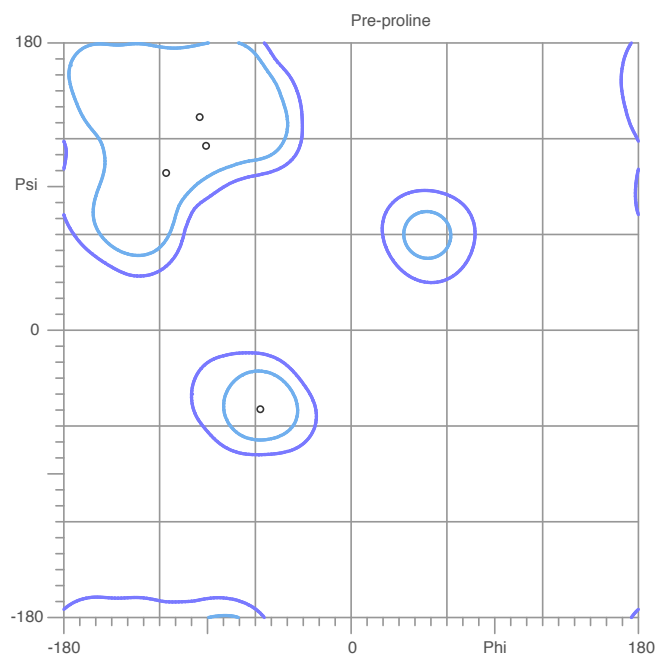
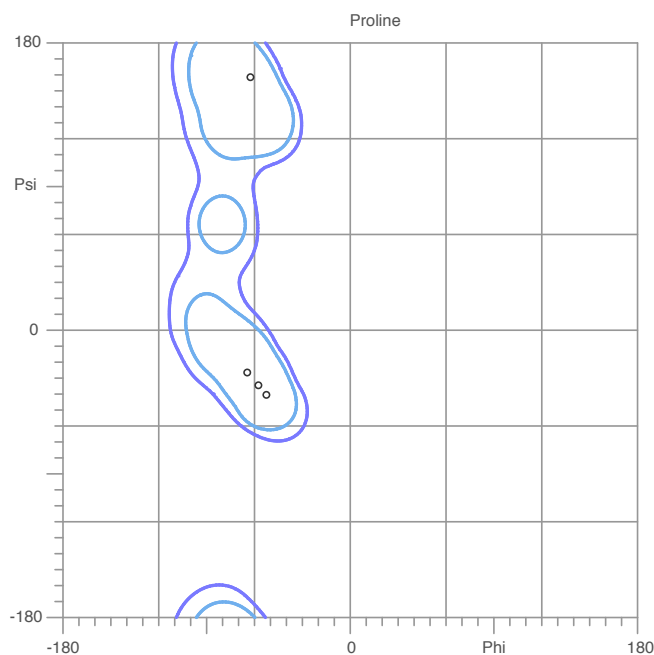
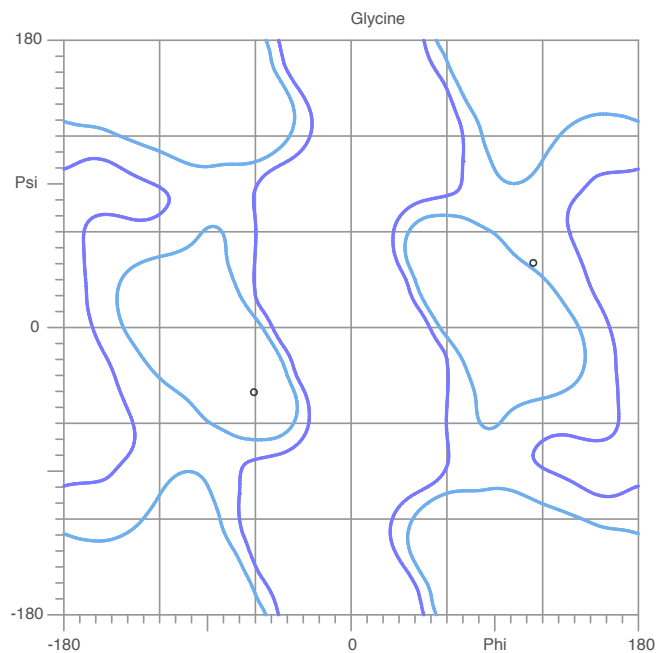
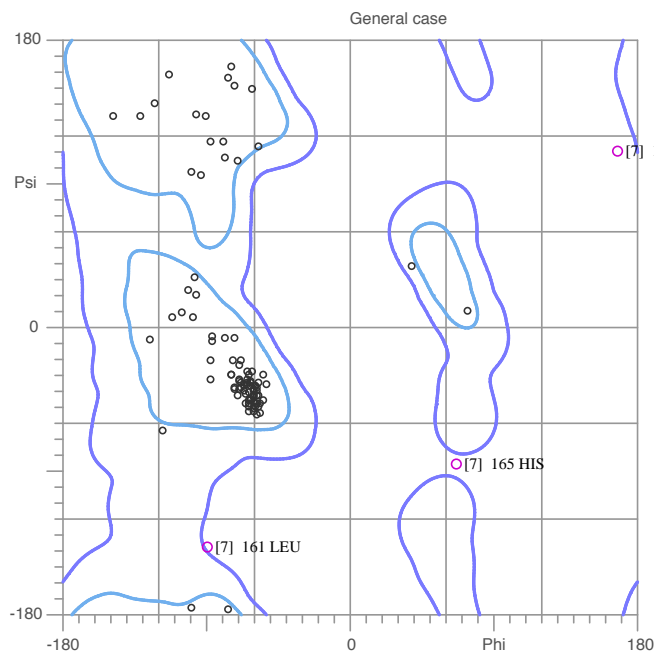
There were no outliers.

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MolProbity Ramachandran analysis

2KOB.pdb, model 7



94.3% (100/106) 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):

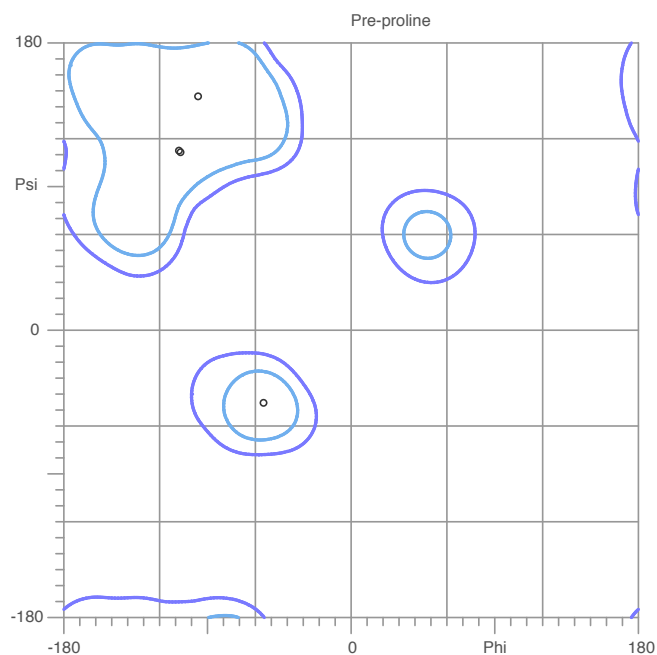
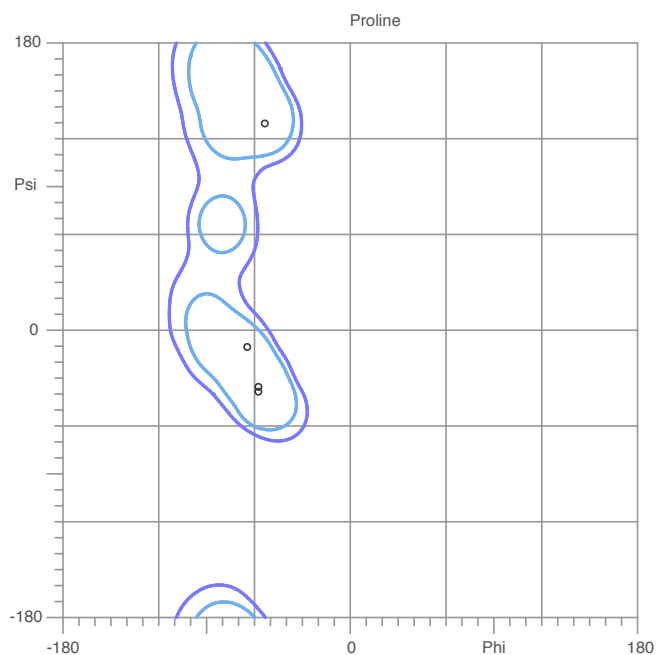
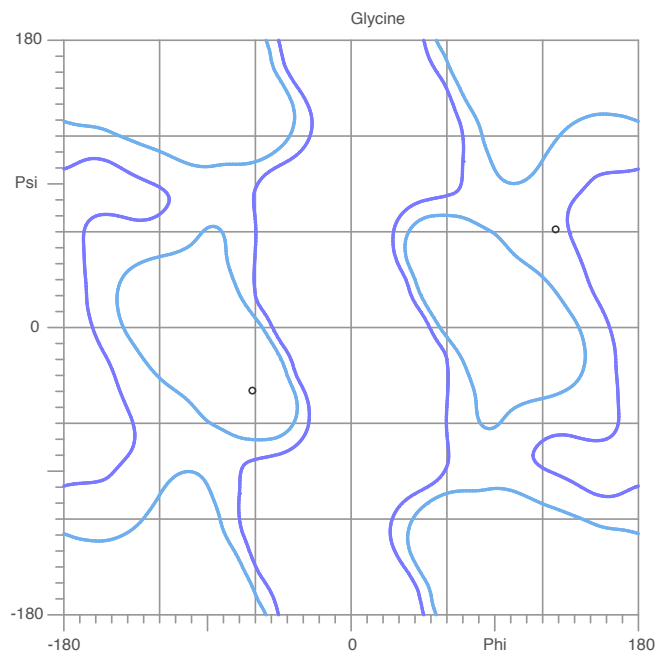
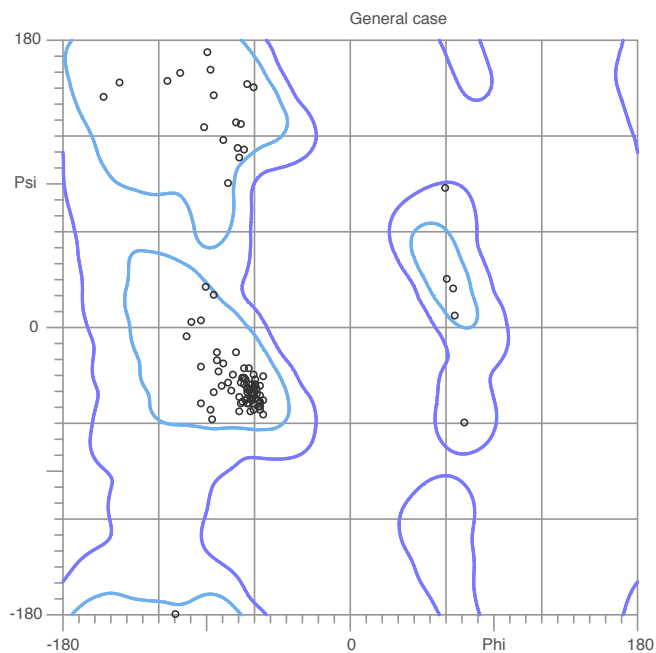
[7] 161 LEU (-90.8, -137.3)

[7] 165 HIS (66.7, -85.2)

[7] 166 HIS (167.1, 111.1)

MolProbity Ramachandran analysis

2KOB.pdb, model 8



97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

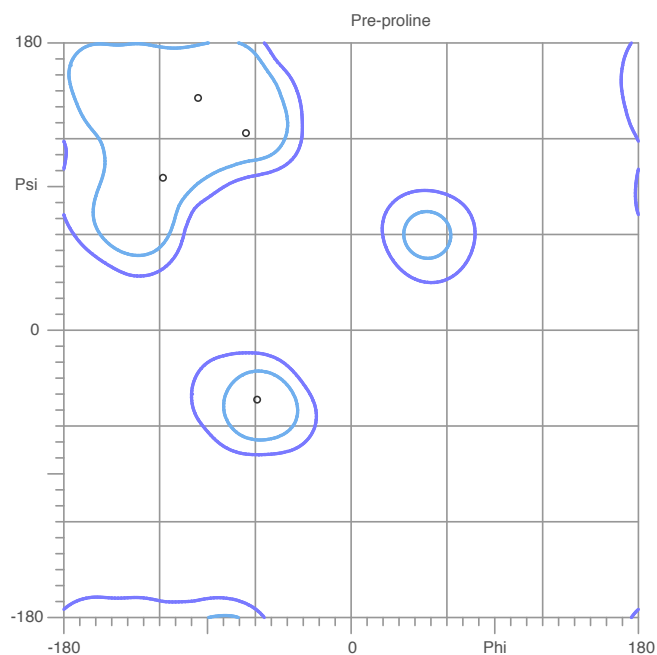
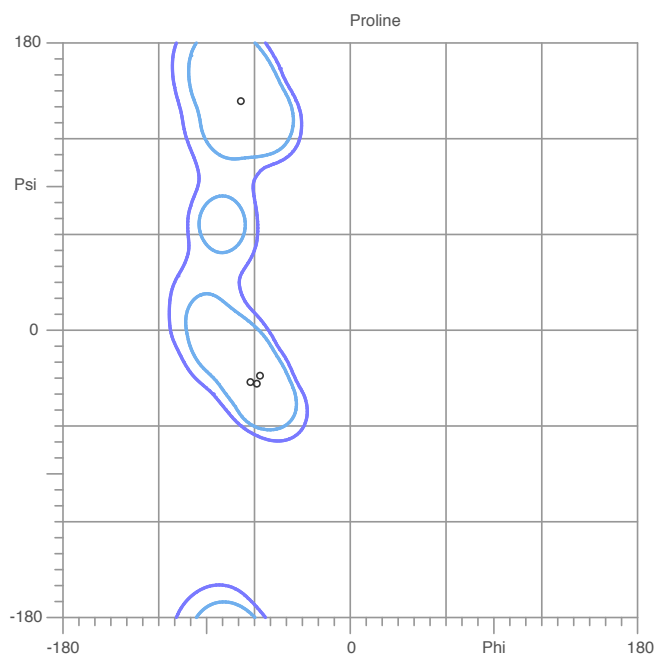
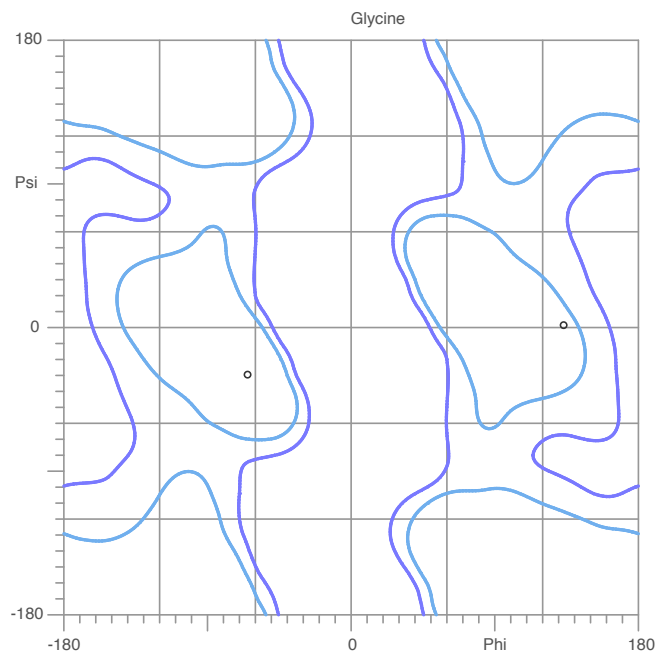
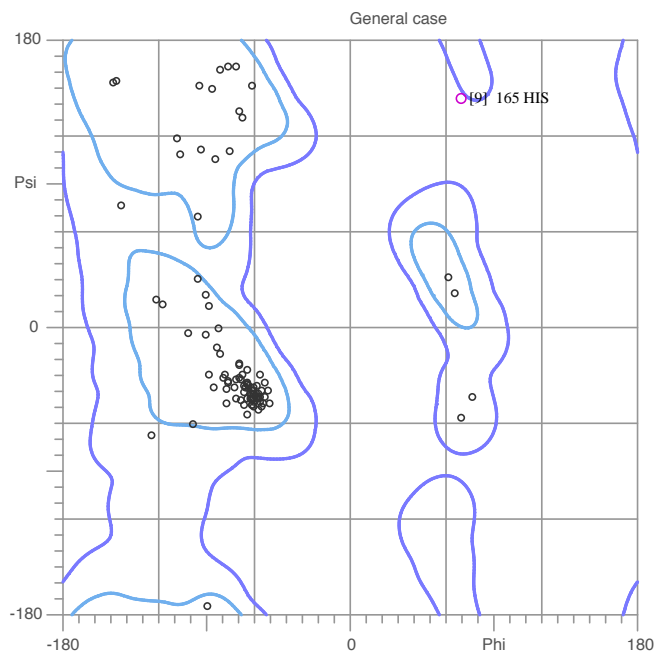
There were no outliers.

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MolProbity Ramachandran analysis

2KOB.pdb, model 9



95.3% (101/106) of all residues were in favored (98%) regions.
99.1% (105/106) of all residues were in allowed (>99.8%) regions.

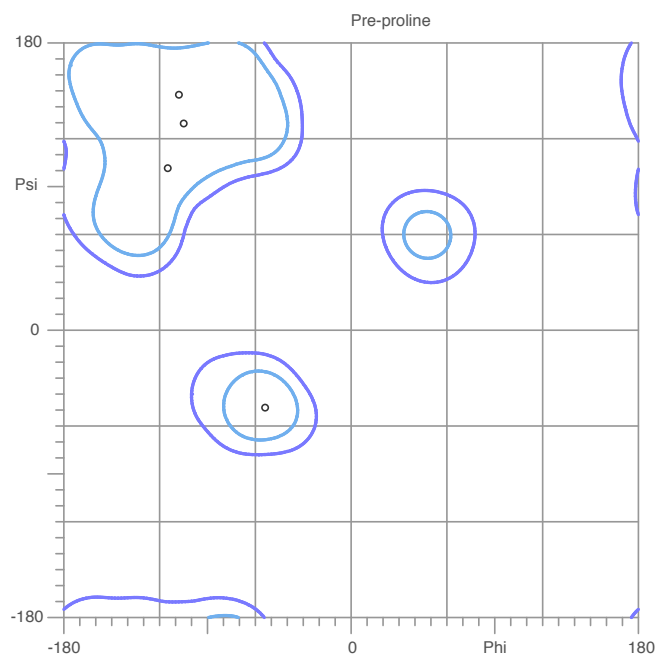
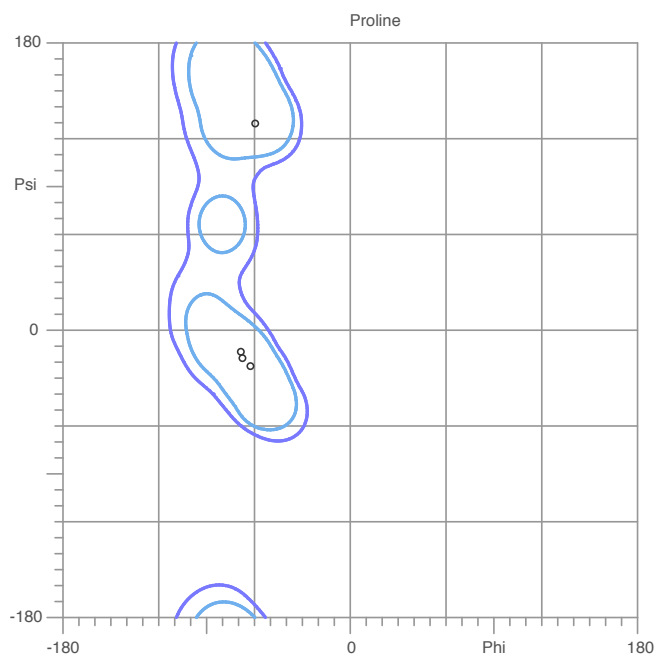
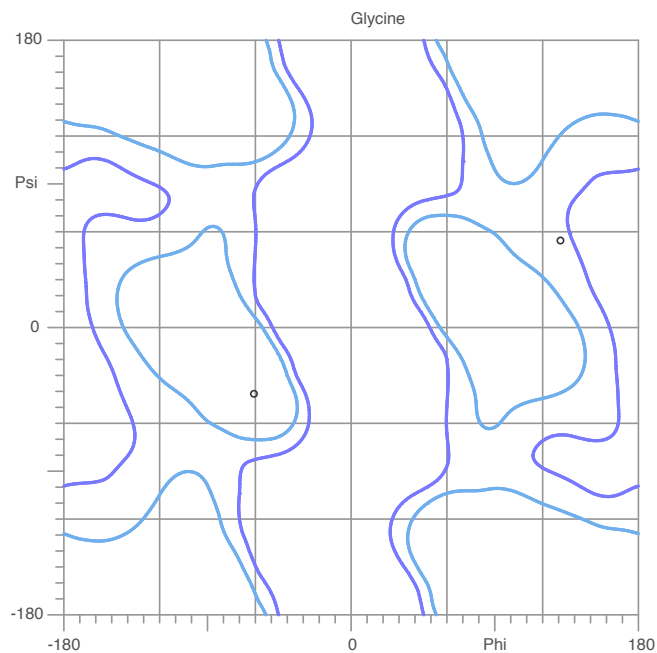
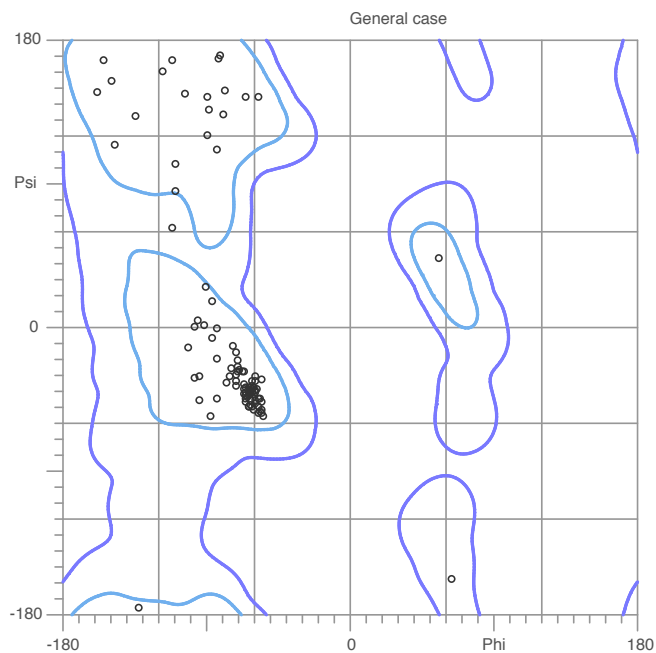
There were 1 outliers (phi, psi):
[9] 165 HIS (69.3, 144.7)

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MolProbity Ramachandran analysis

2KOB.pdb, model 10



97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

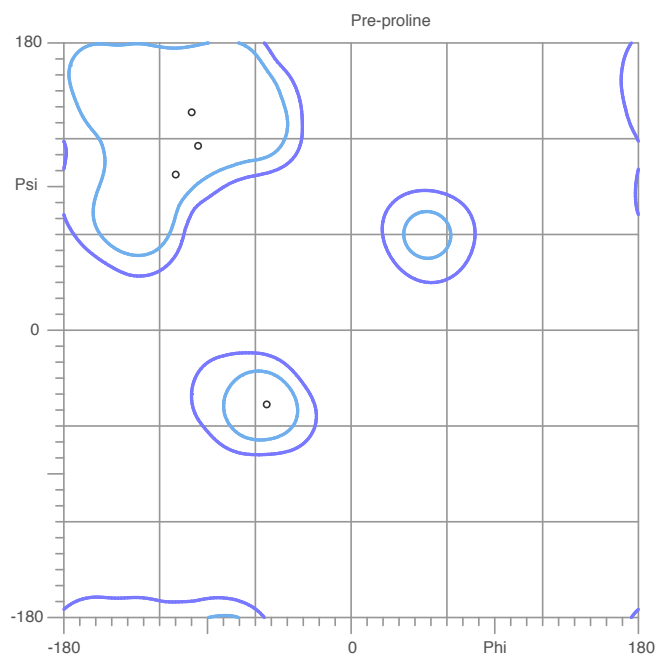
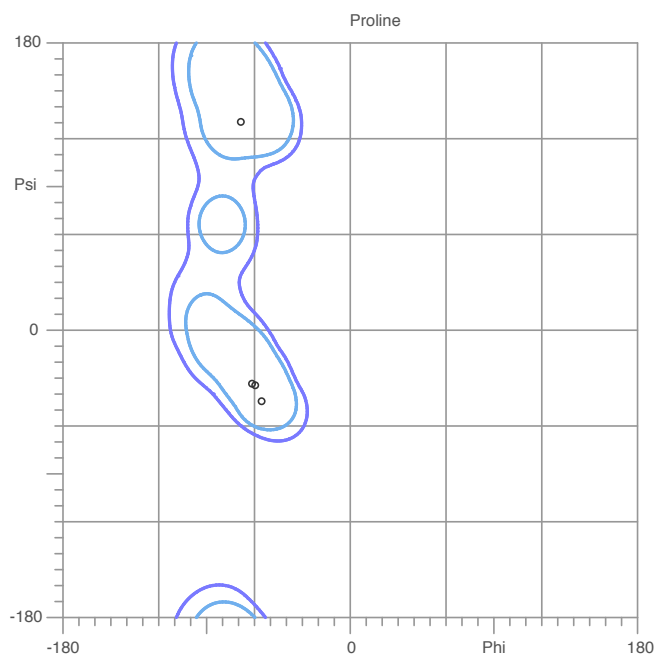
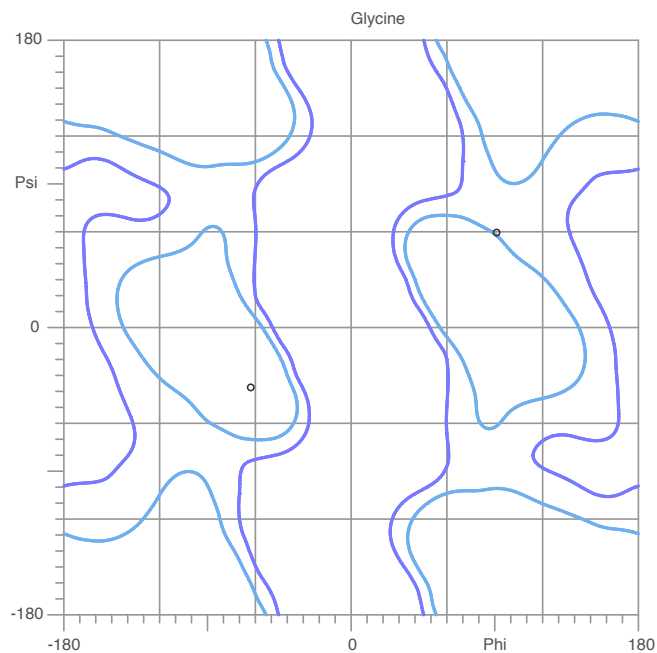
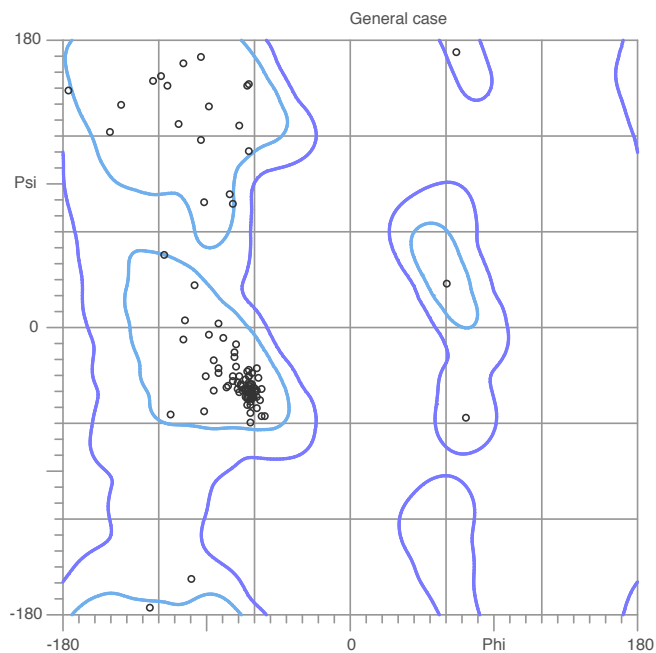
There were no outliers.

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

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MolProbity Ramachandran analysis

2KOB.pdb, model 11



94.3% (100/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

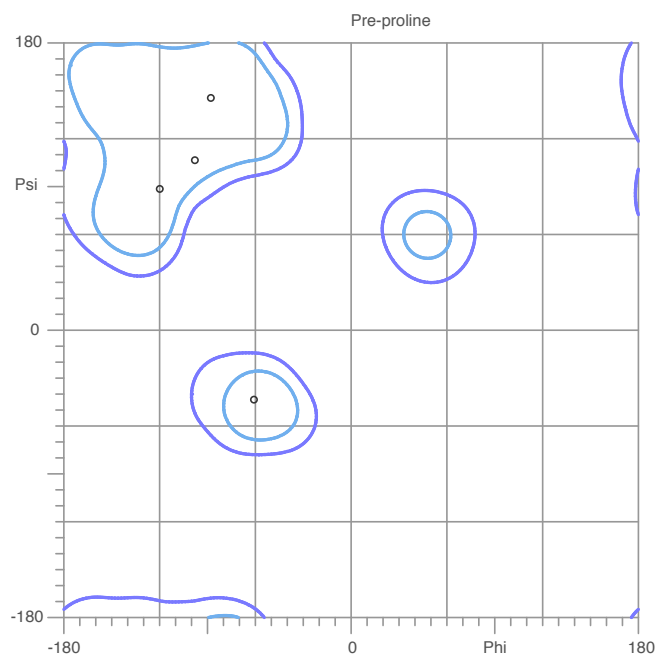
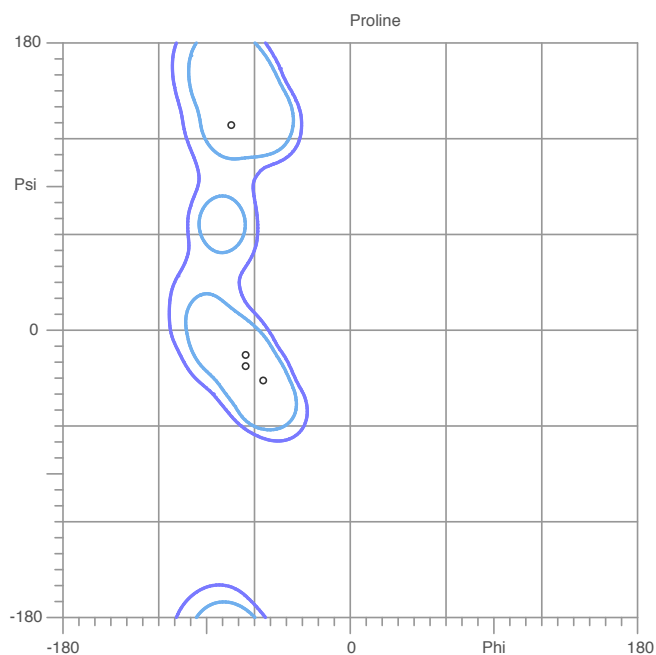
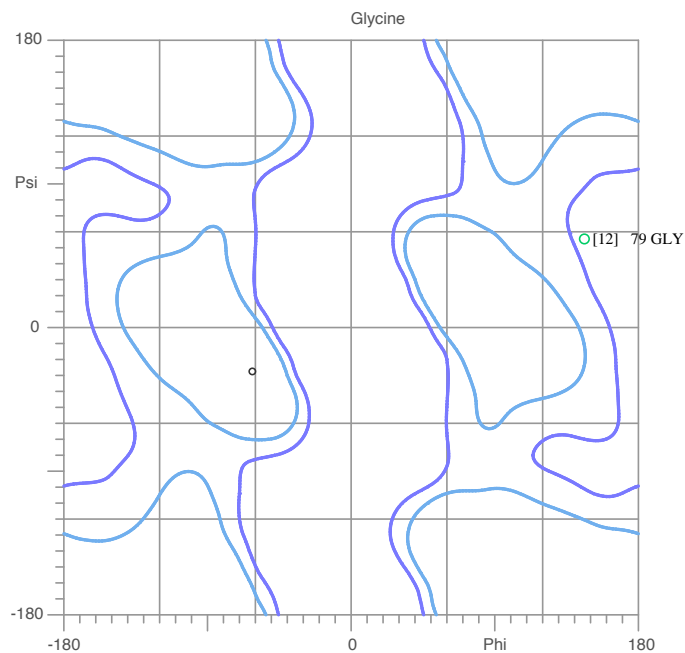
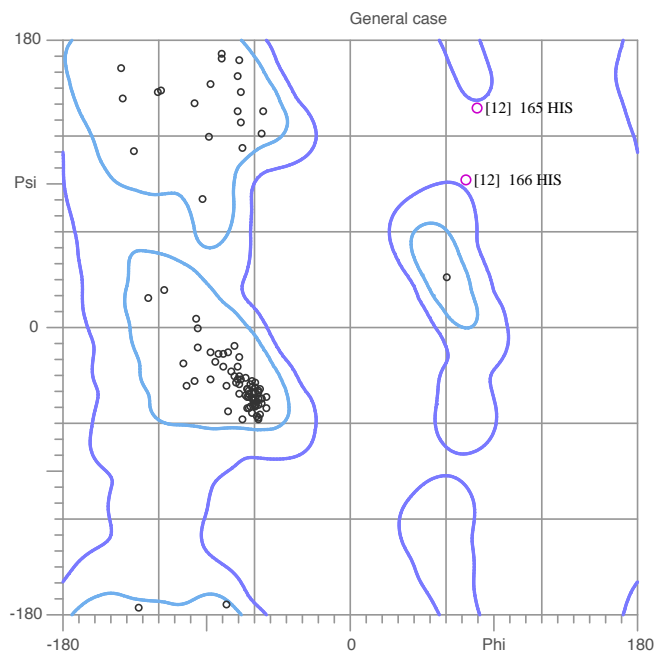
There were no outliers.

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MolProbity Ramachandran analysis

2KOB.pdb, model 12



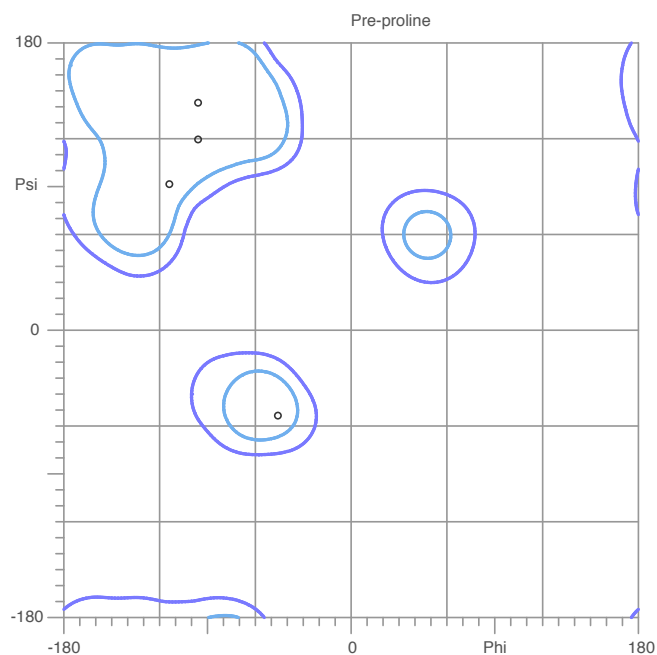
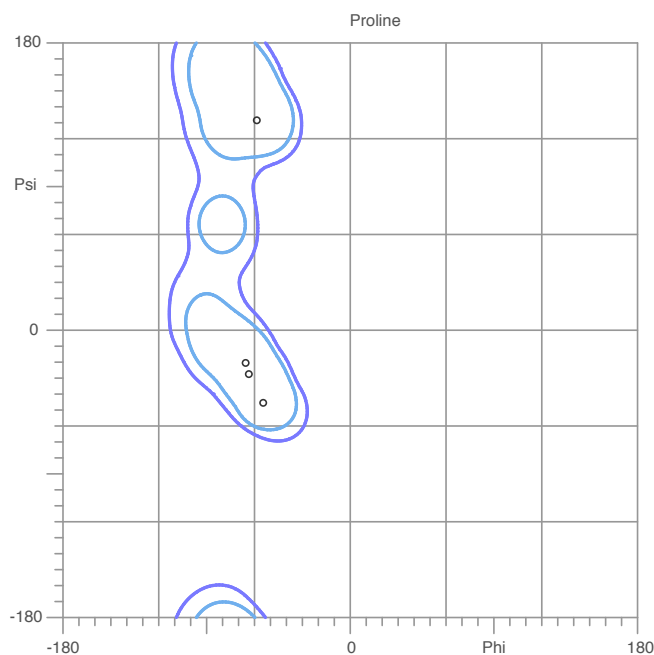
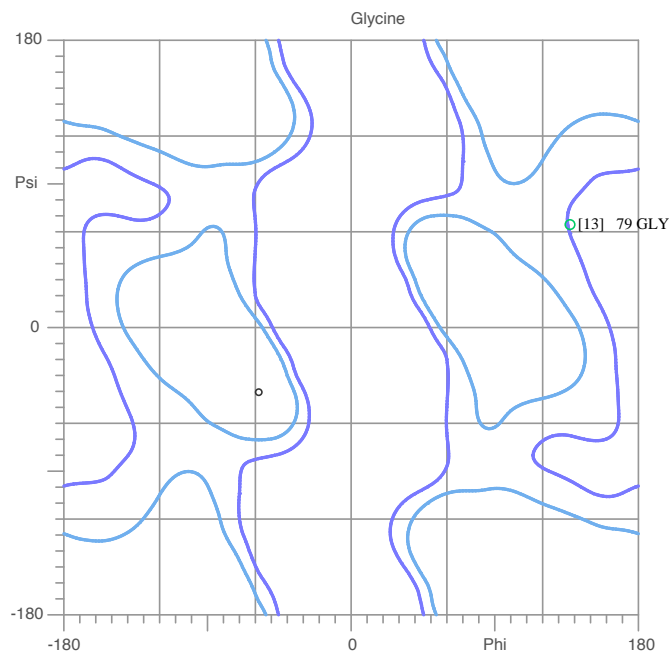
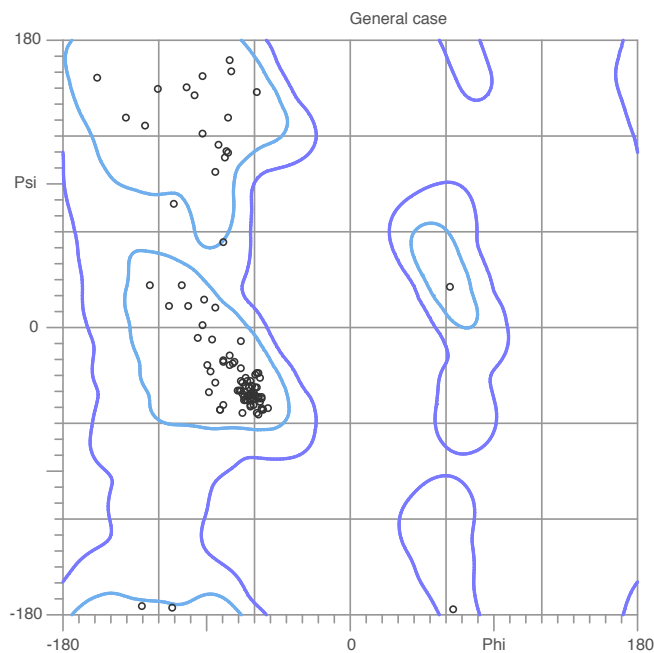
97.2% (103/106) of all residues were in favored (98%) regions.
97.2% (103/106) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[12] 79 GLY (146.5, 56.4)
[12] 165 HIS (79.6, 138.7)
[12] 166 HIS (72.2, 93.0)

MolProbity Ramachandran analysis

2KOB.pdb, model 13



97.2% (103/106) of all residues were in favored (98%) regions.
99.1% (105/106) of all residues were in allowed (>99.8%) regions.

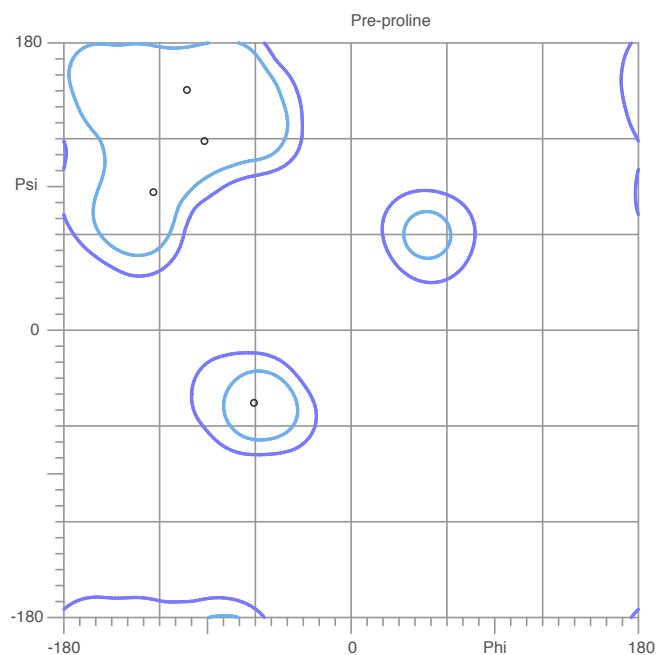
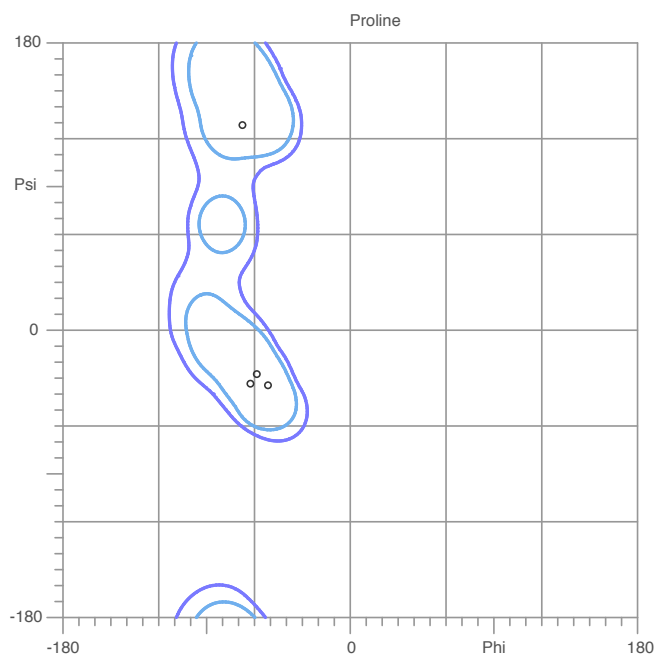
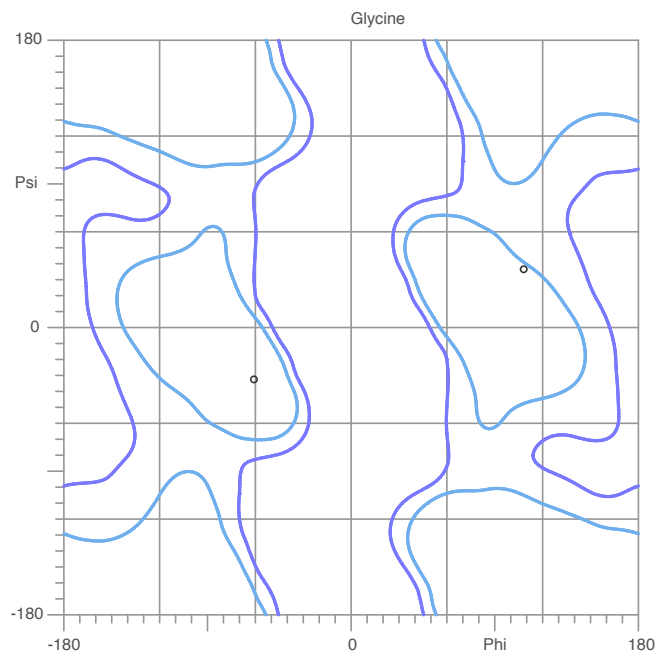
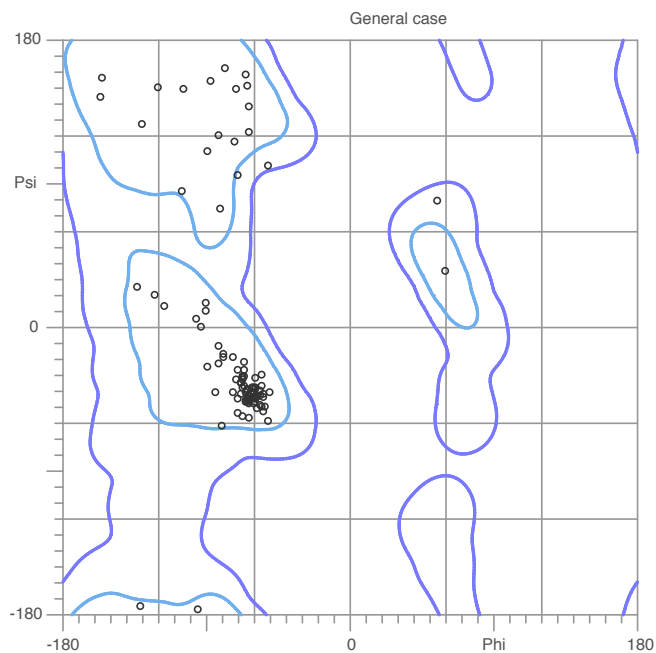
There were 1 outliers (phi, psi):
[13] 79 GLY (137.5, 65.8)

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MolProbity Ramachandran analysis

2KOB.pdb, model 14



97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

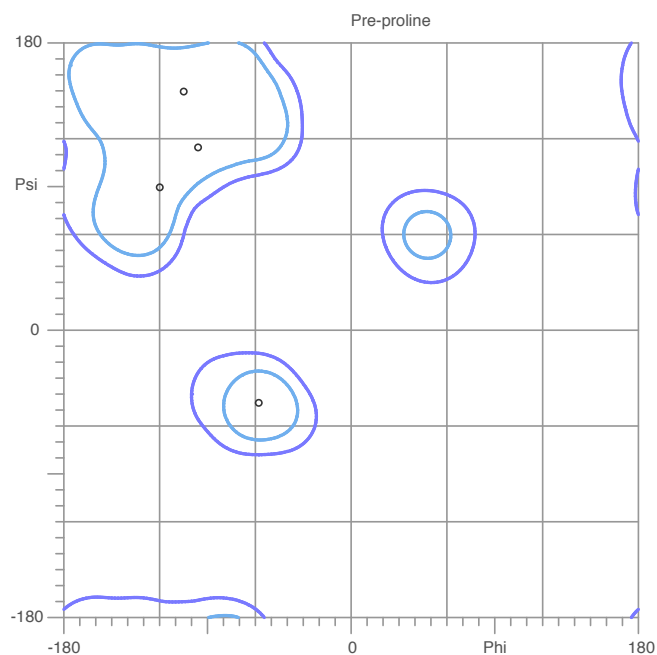
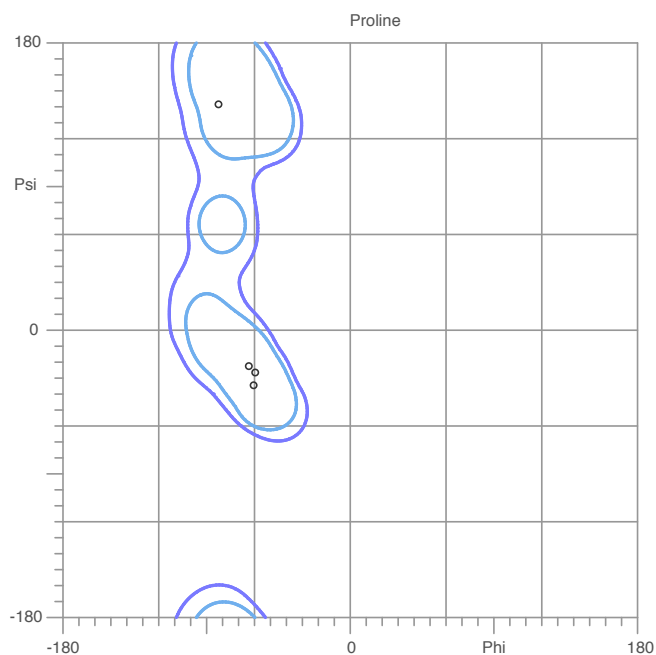
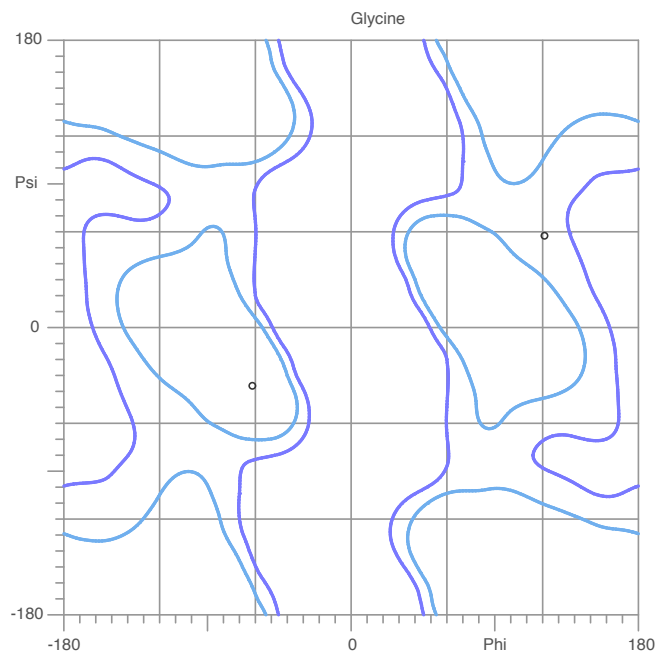
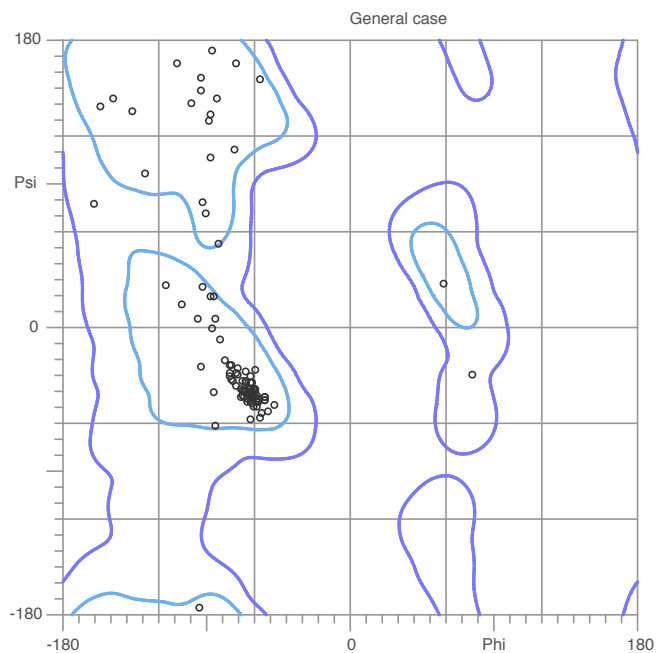
There were no outliers.

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

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MolProbity Ramachandran analysis

2KOB.pdb, model 15



97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

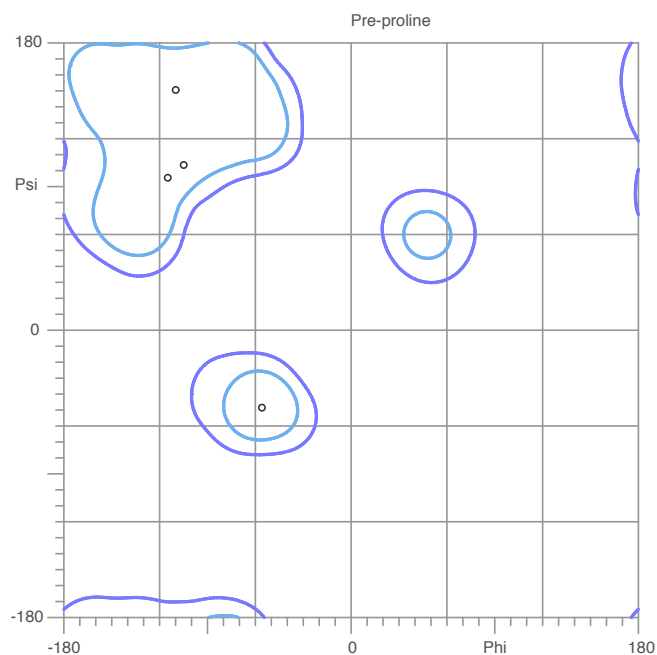
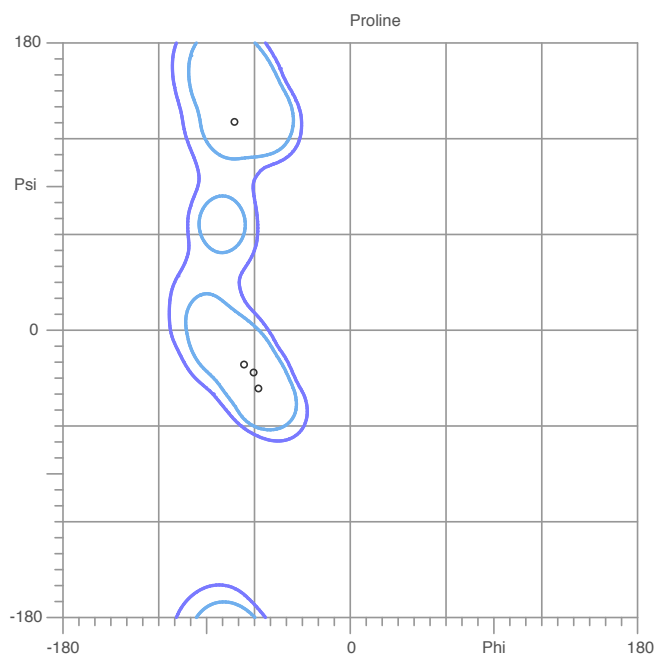
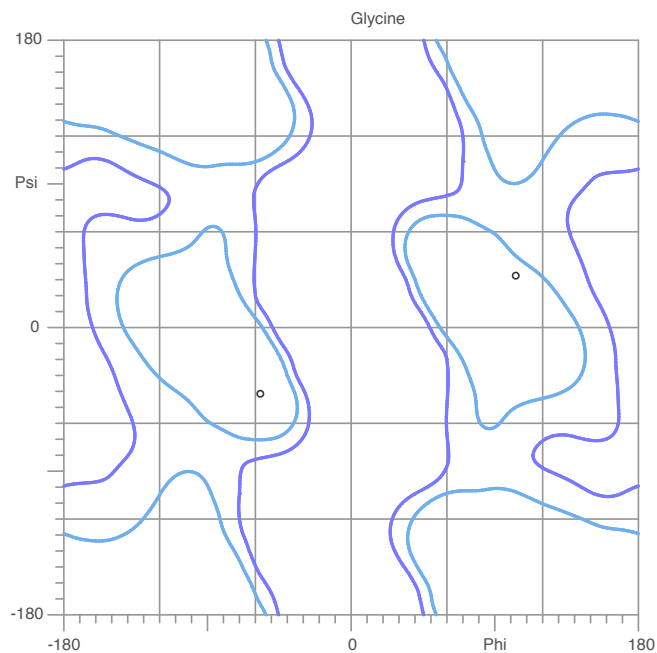
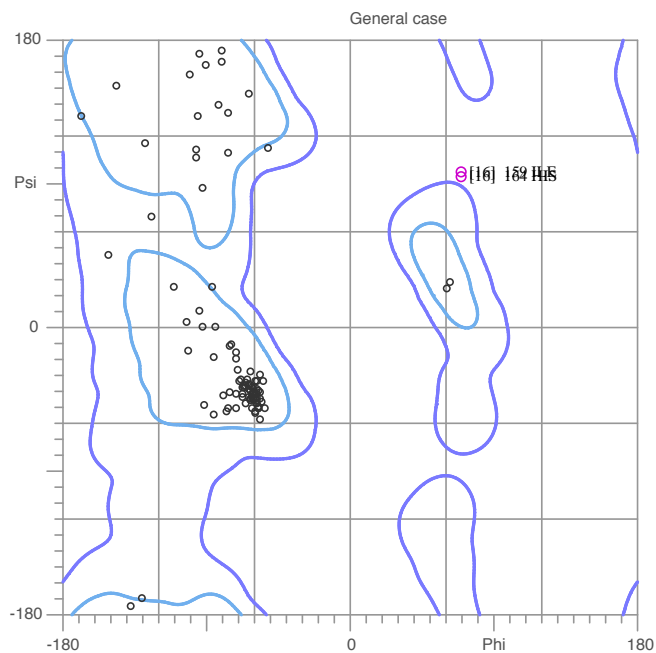
There were no outliers.

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

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MolProbity Ramachandran analysis

2KOB.pdb, model 16



92.5% (98/106) of all residues were in favored (98%) regions.
98.1% (104/106) of all residues were in allowed (>99.8%) regions.

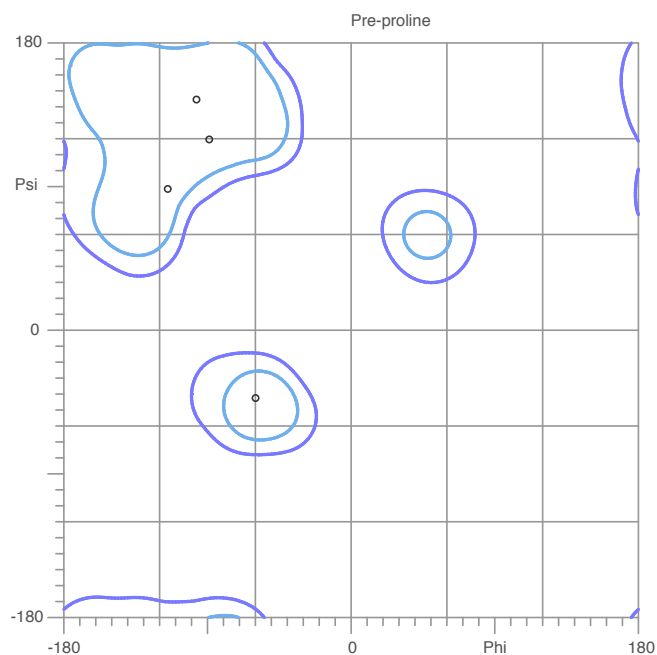
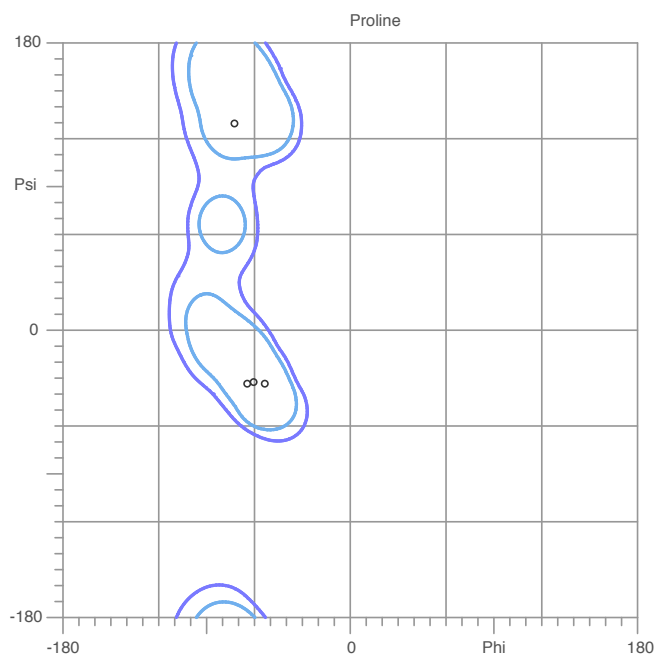
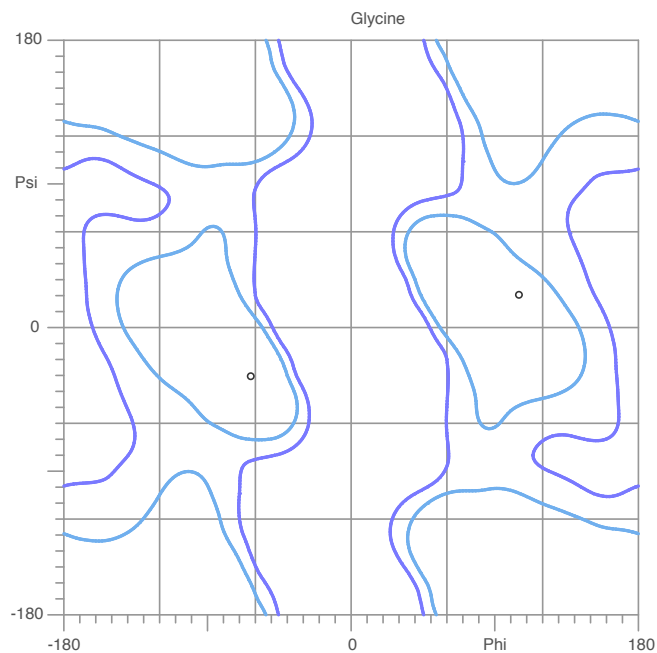
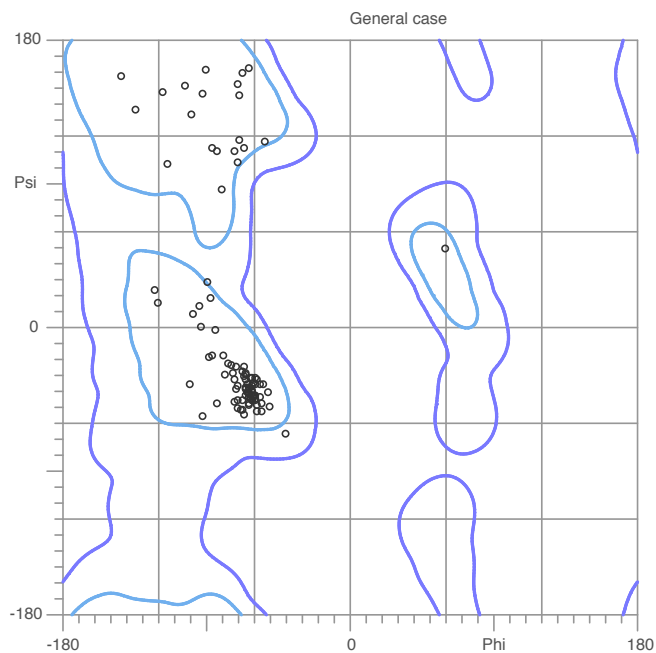
There were 2 outliers (phi, psi):

[16] 159 ILE (69.0, 98.7)

[16] 164 HIS (69.1, 95.1)

MolProbity Ramachandran analysis

2KOB.pdb, model 17



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.

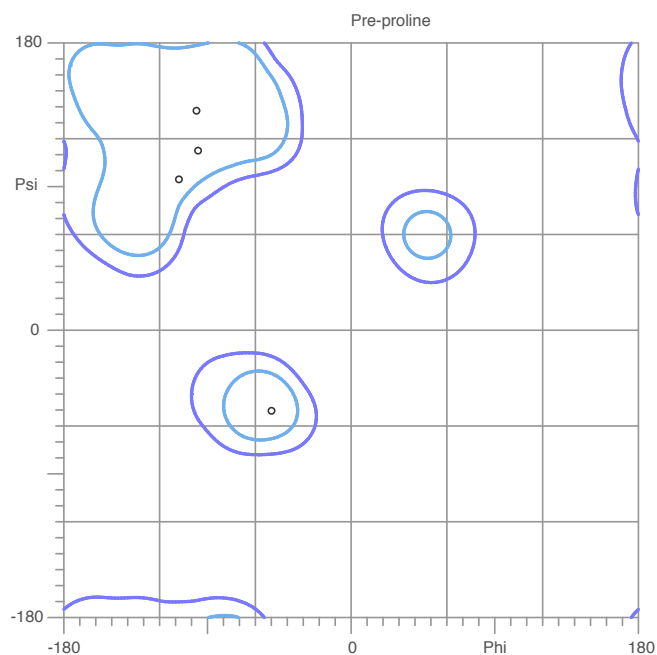
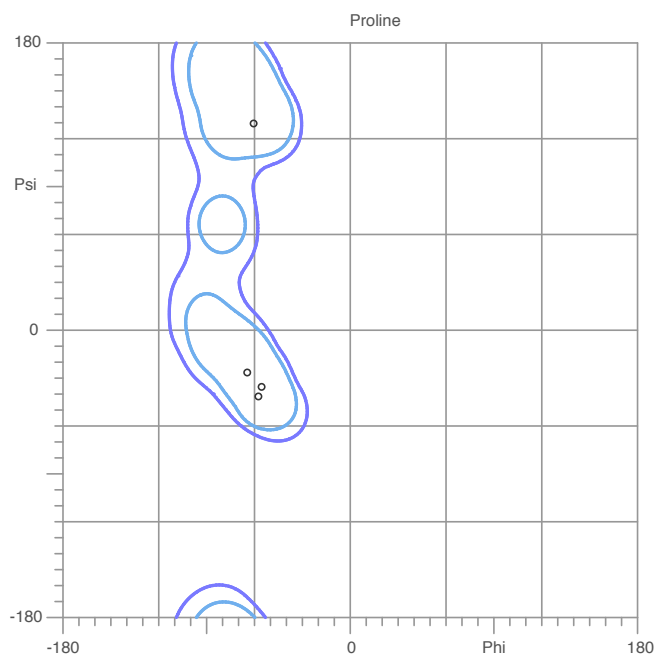
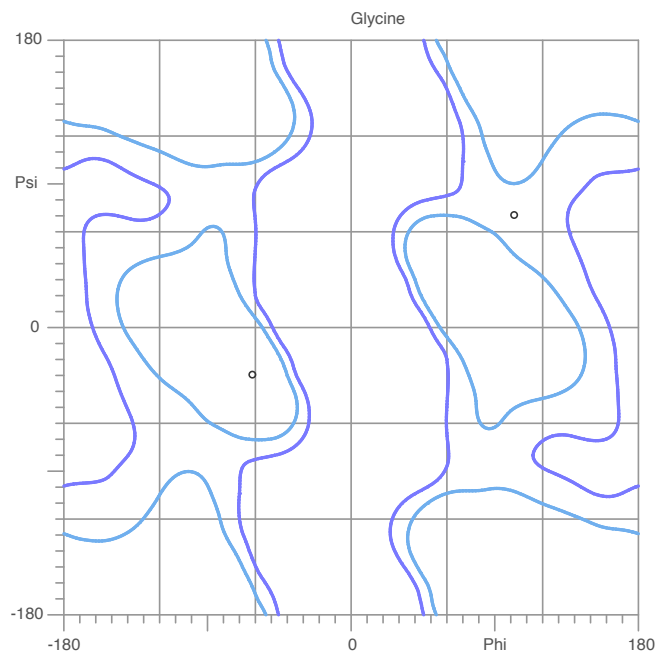
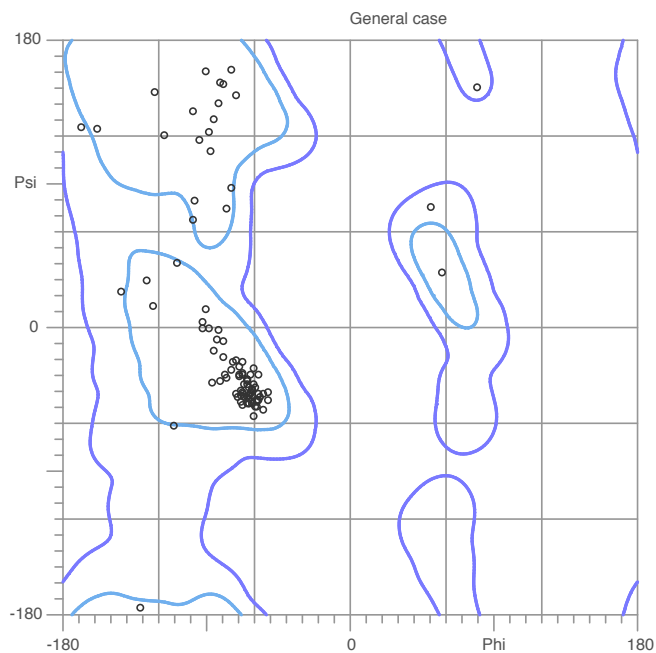
There were no outliers.

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

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

MolProbity Ramachandran analysis

2KOB.pdb, model 18



94.3% (100/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

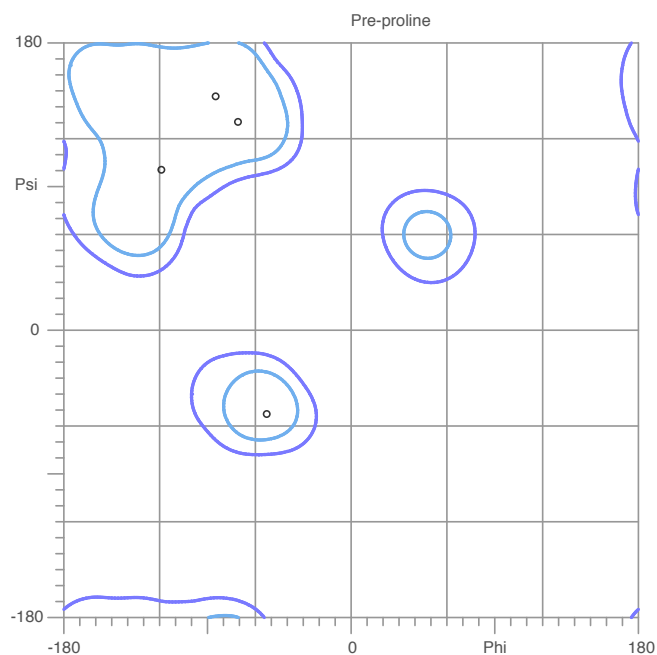
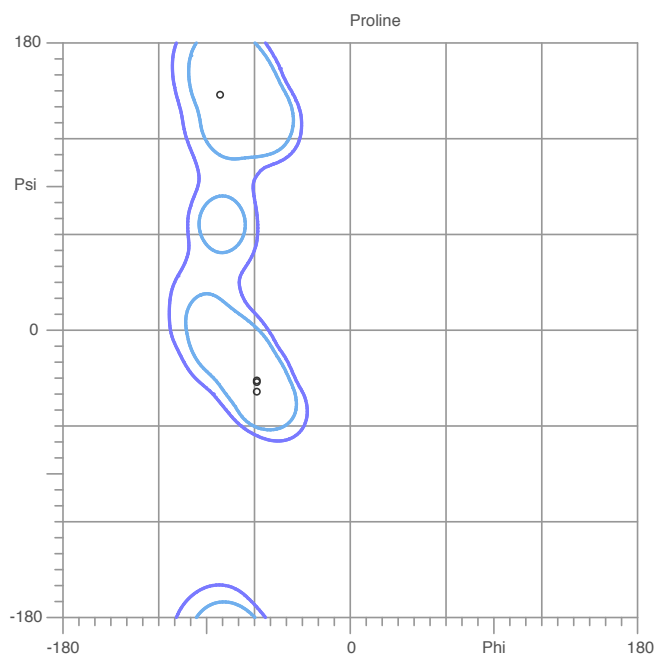
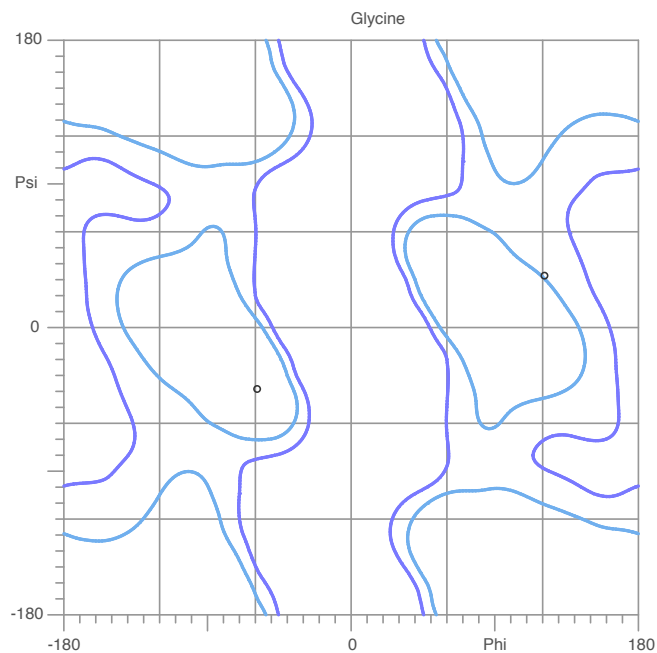
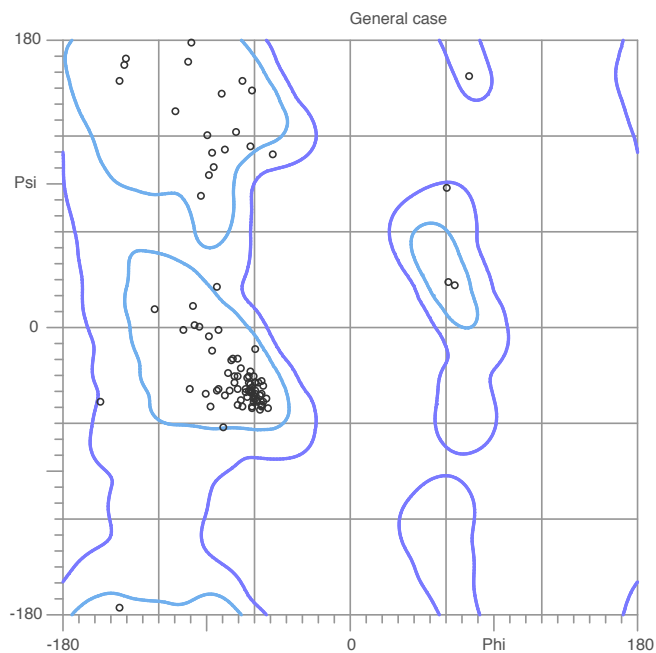
There were no outliers.

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

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

MolProbity Ramachandran analysis

2KOB.pdb, model 19



94.3% (100/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

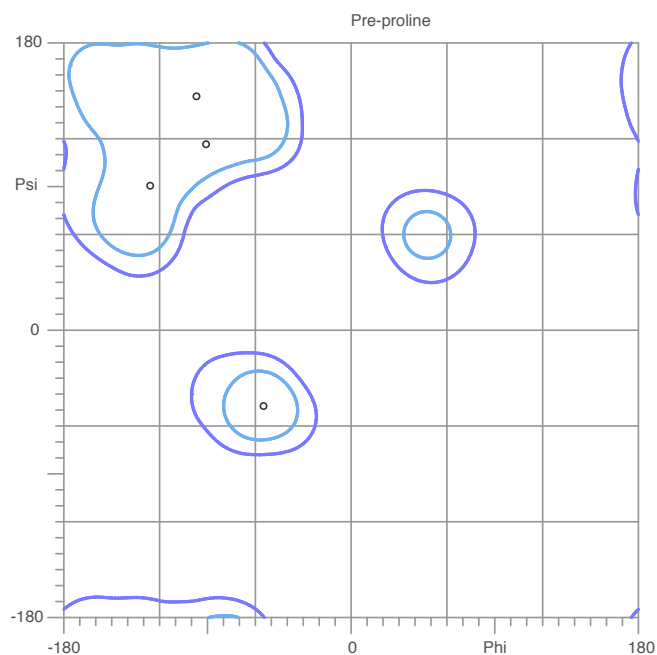
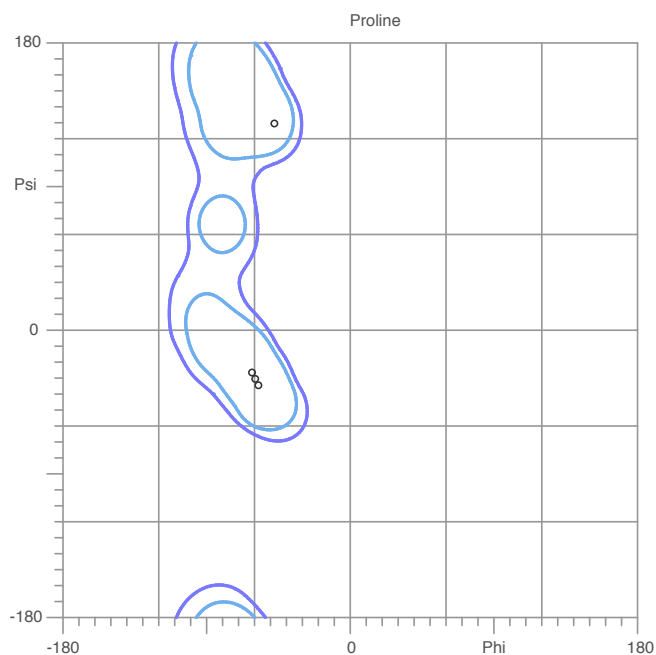
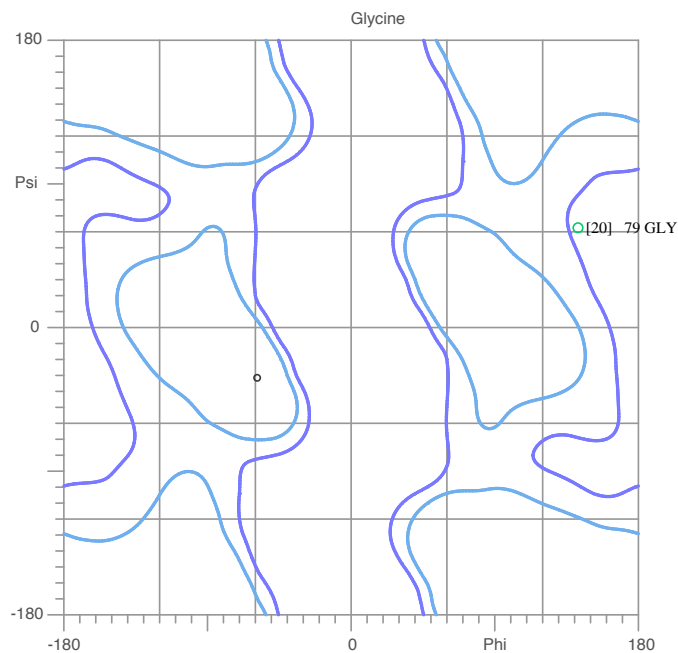
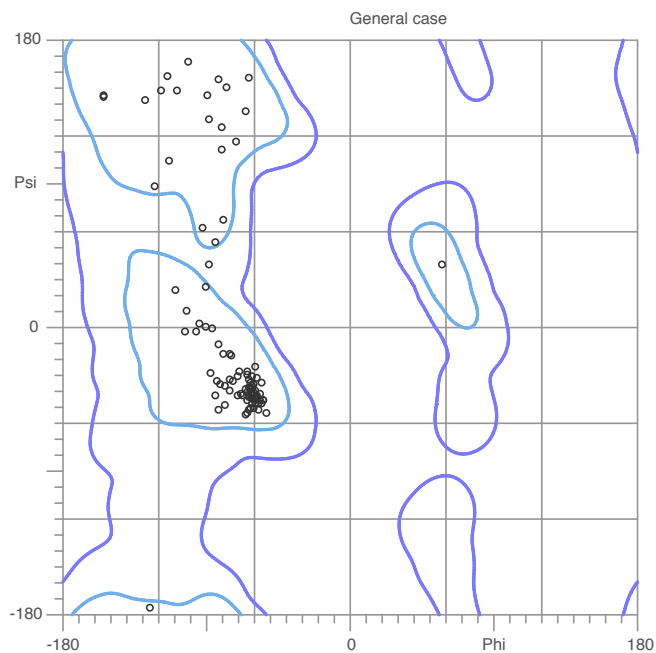
There were no outliers.

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

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MolProbity Ramachandran analysis

2KOB.pdb, model 20



98.1% (104/106) 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):
[20] 79 GLY (142.3, 64.0)

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

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