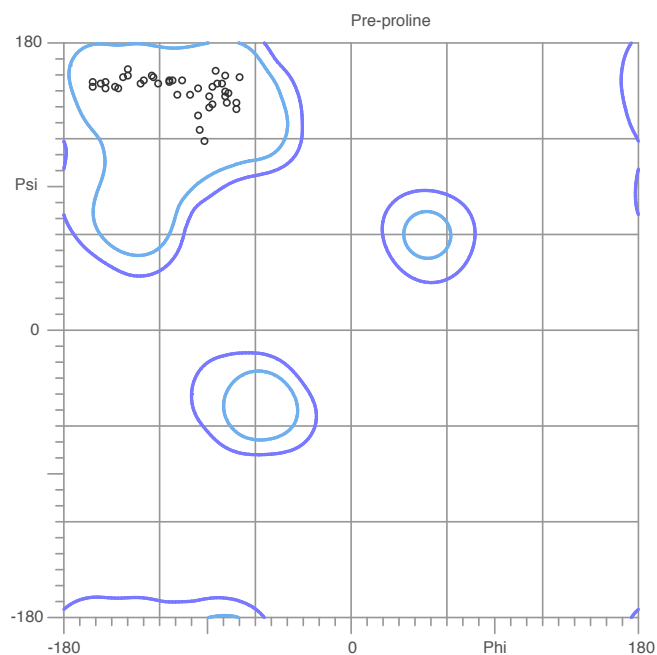
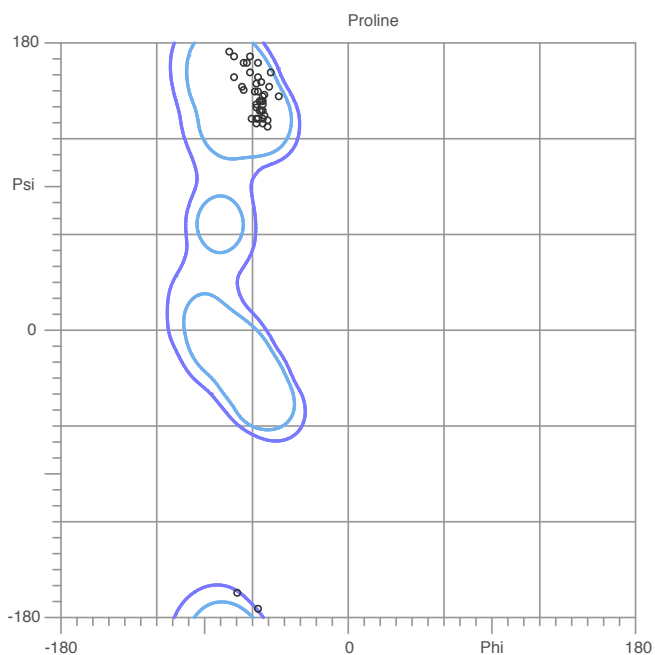
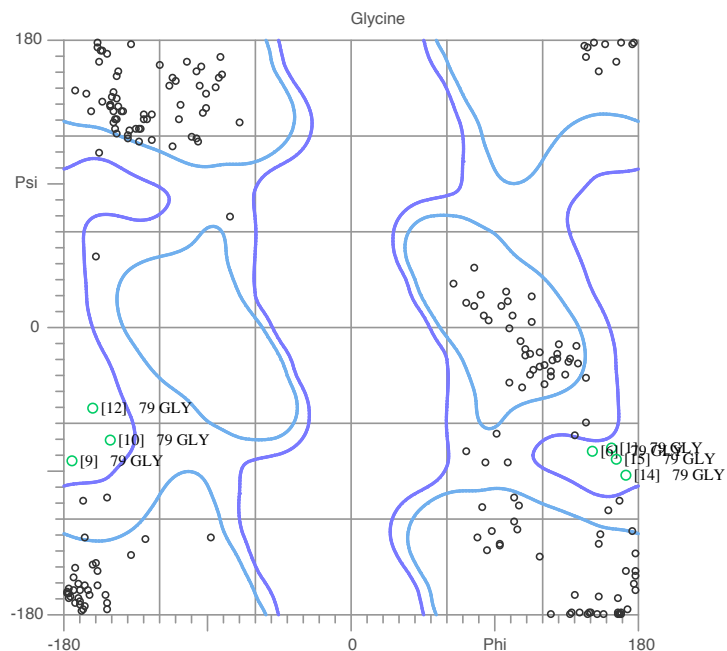
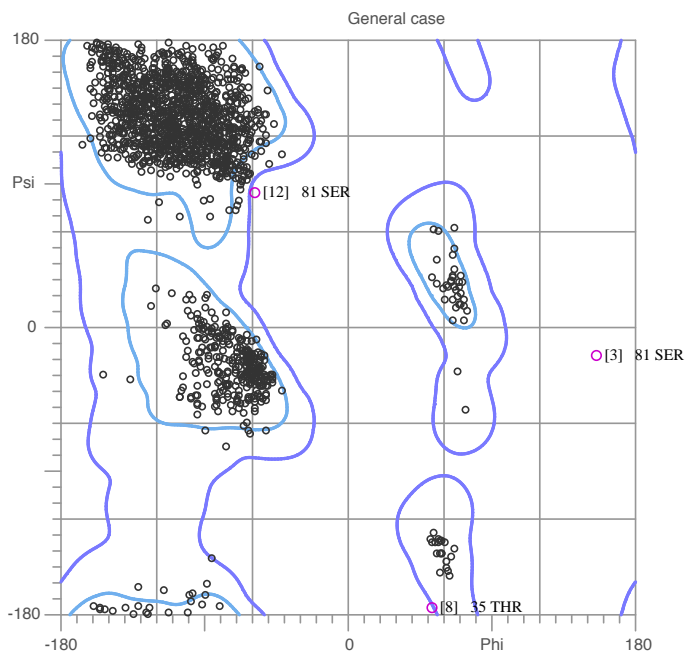


MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, all models



95.1% (1826/1920) of all residues were in favored (98%) regions.
99.5% (1910/1920) of all residues were in allowed (>99.8%) regions.

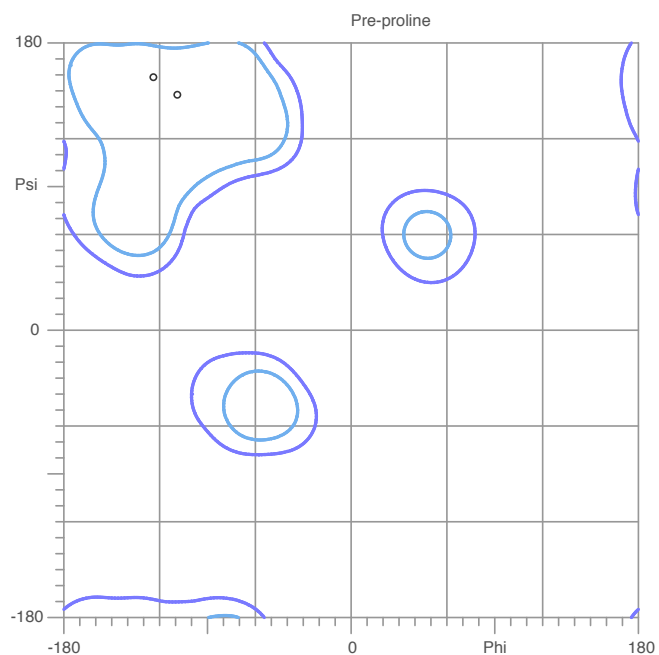
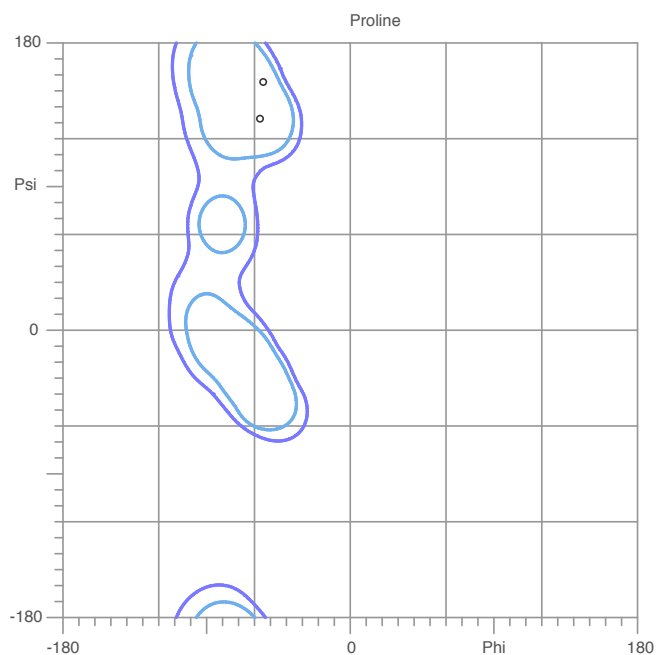
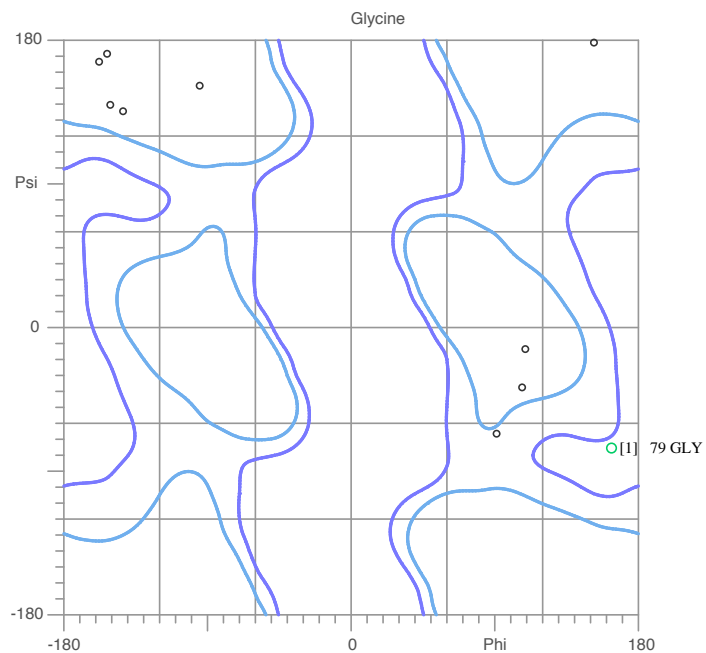
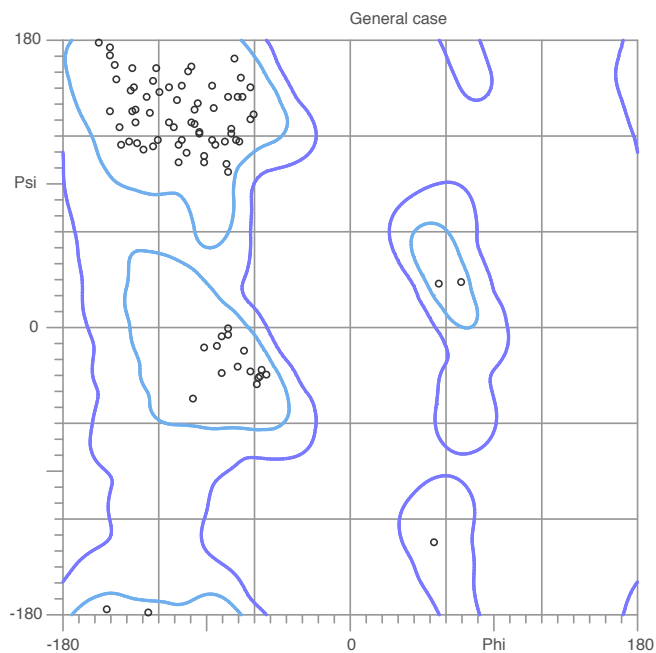
There were 10 outliers (phi, psi):

- [1] 79 GLY (163.3, -75.8)
- [3] 81 SER (155.8, -17.7)
- [6] 79 GLY (151.4, -77.8)

- [8] 35 THR (52.2, -175.9)
- [9] 79 GLY (-175.7, -83.6)
- [10] 79 GLY (-151.0, -70.8)
- [12] 81 SER (-59.8, 85.7)
- [14] 79 GLY (172.7, -92.1)
- [15] 79 GLY (166.1, -82.6)

MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 1



96.9% (93/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

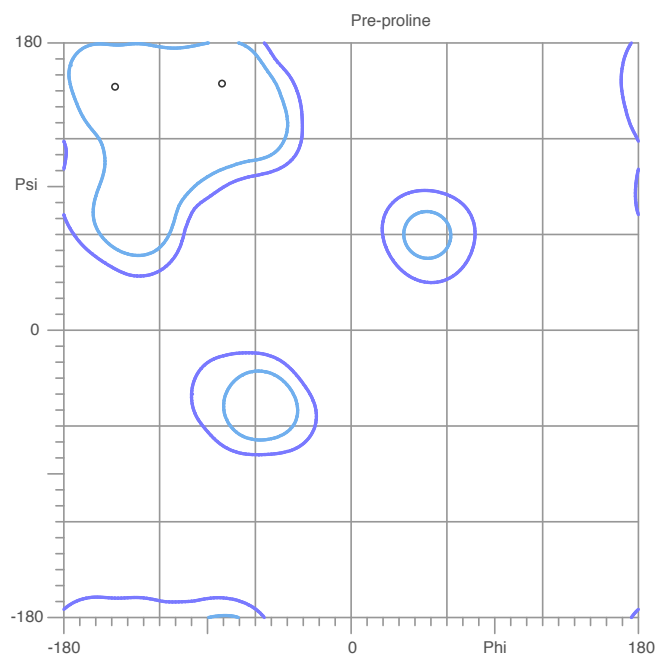
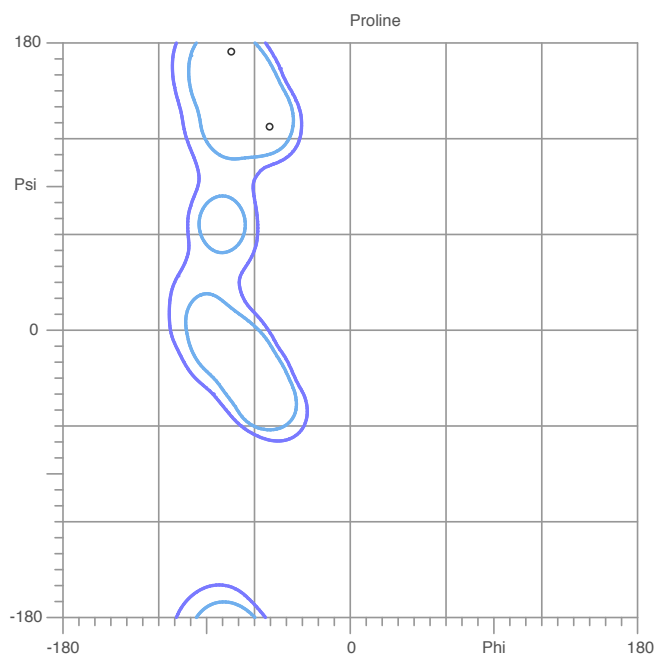
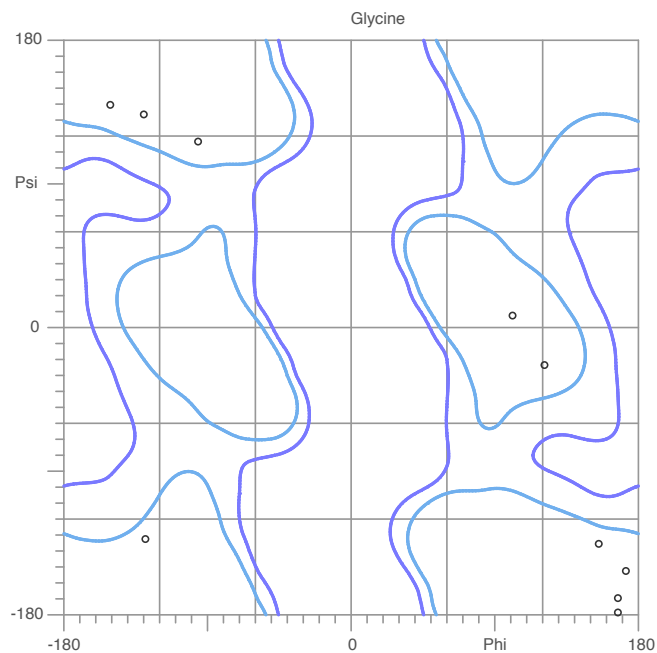
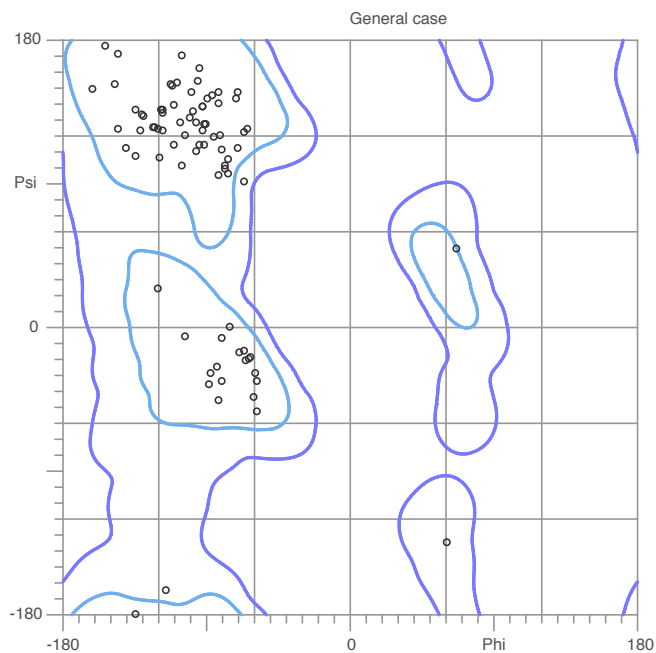
There were 1 outliers (phi, psi):
[1] 79 GLY (163.3, -75.8)

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 2



96.9% (93/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

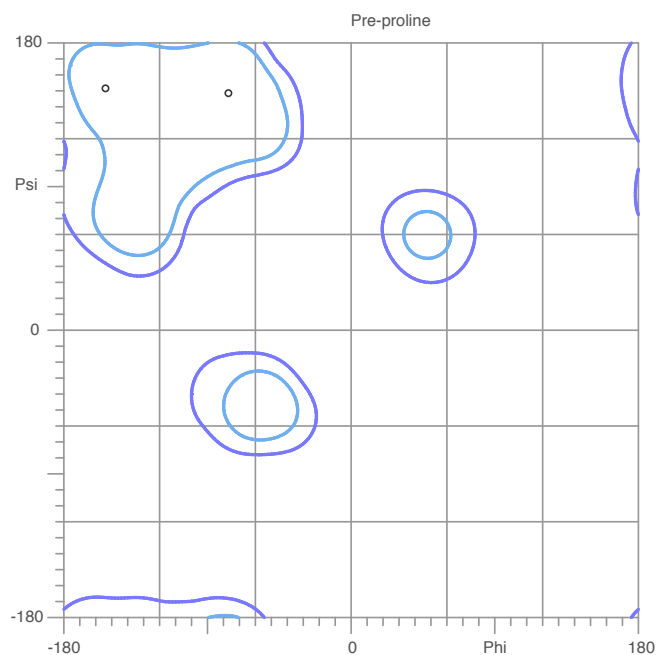
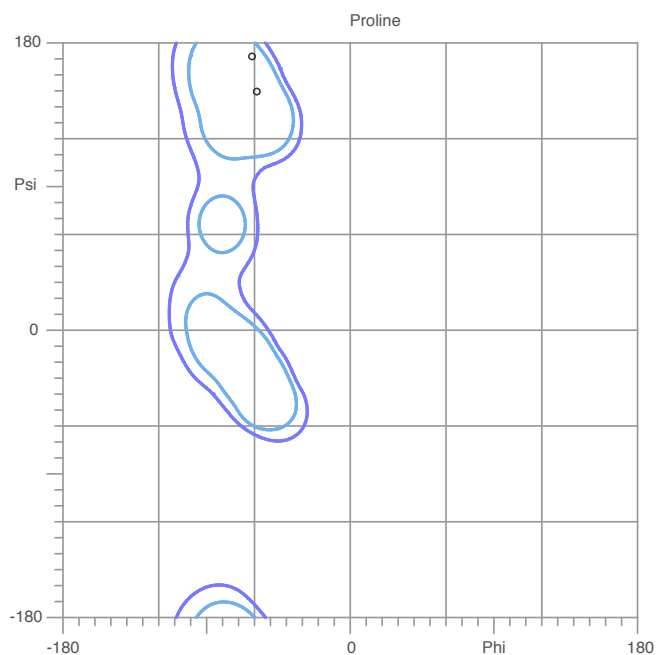
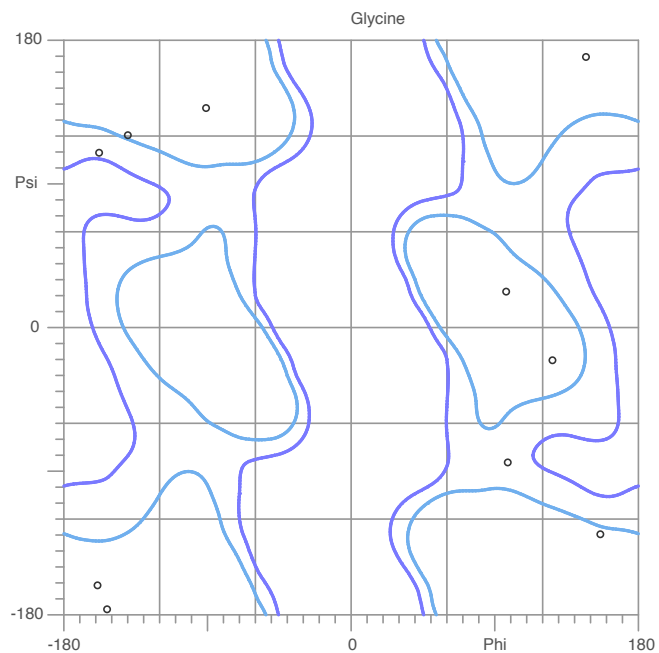
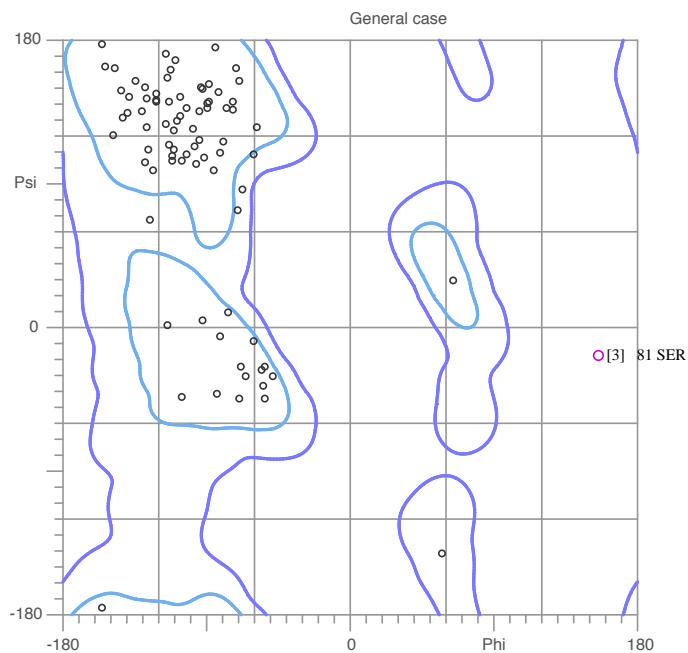
There were no outliers.

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

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 3

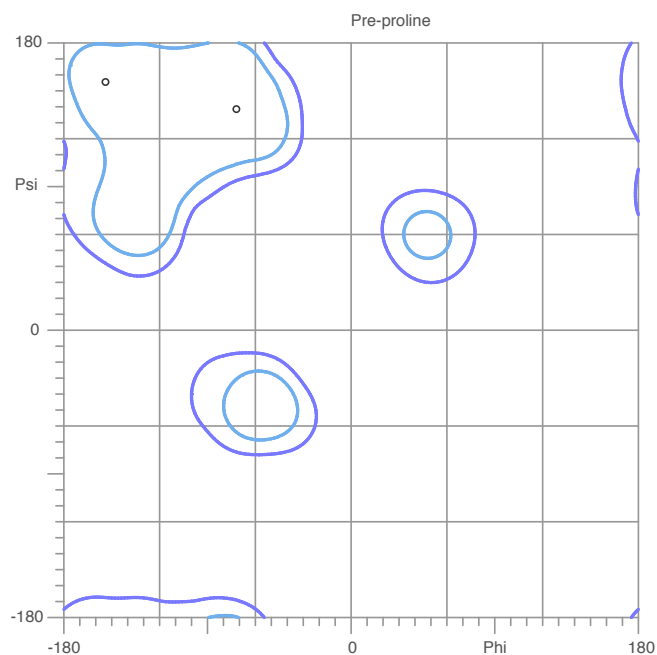
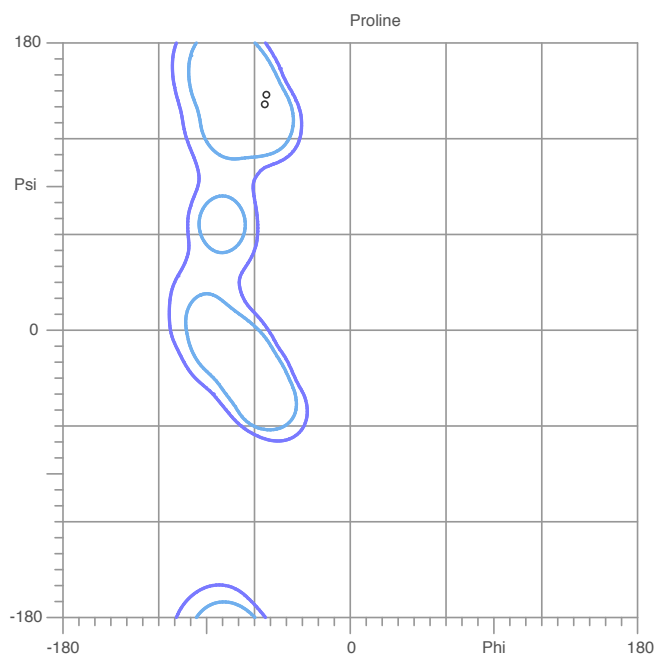
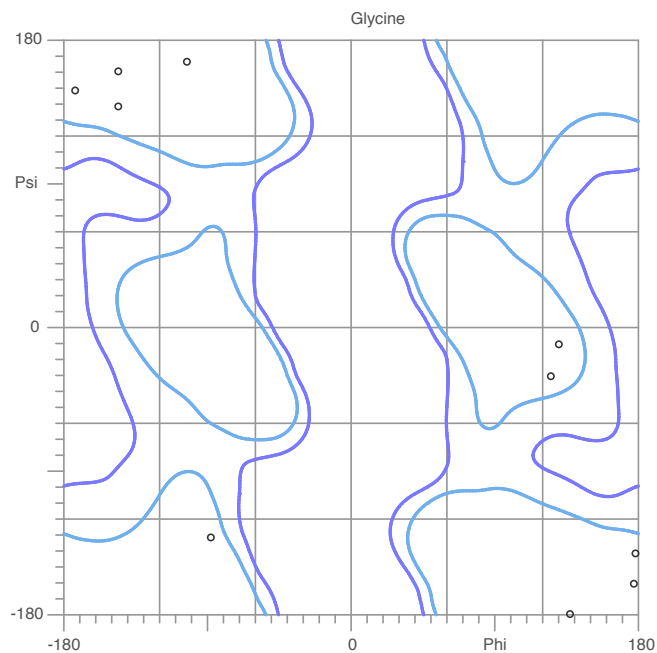
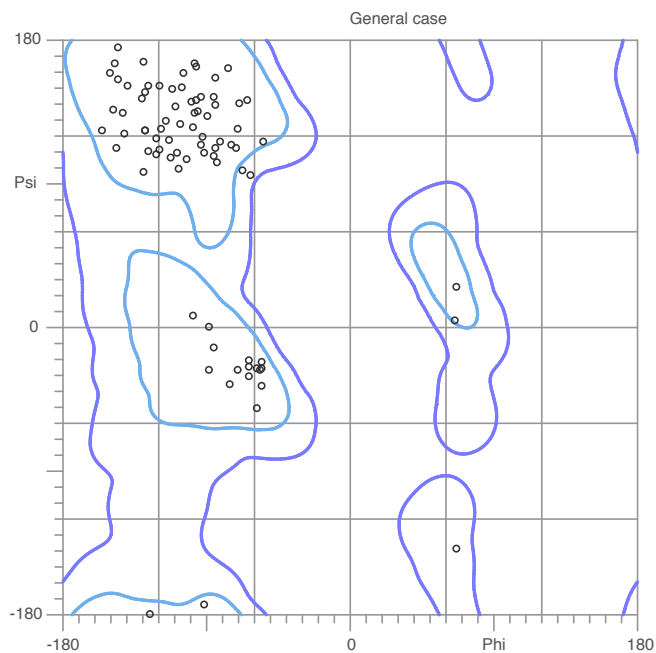


92.7% (89/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 81 SER (155.8, -17.7)

MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 4



96.9% (93/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

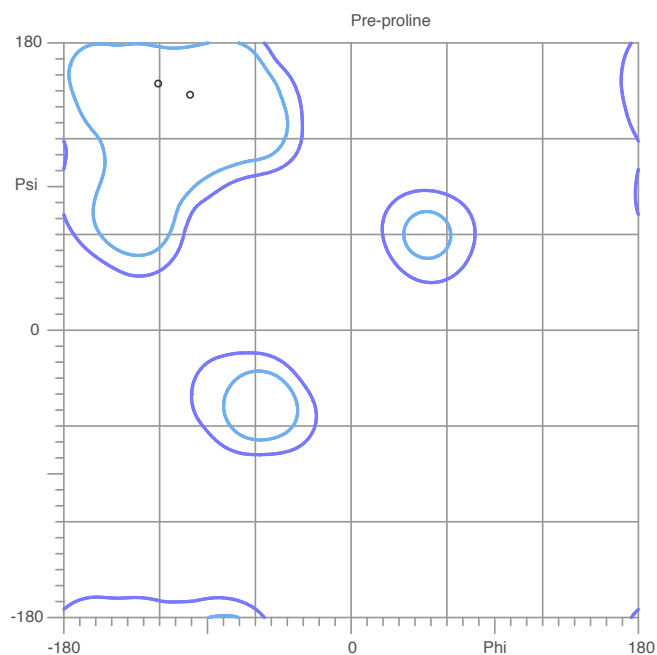
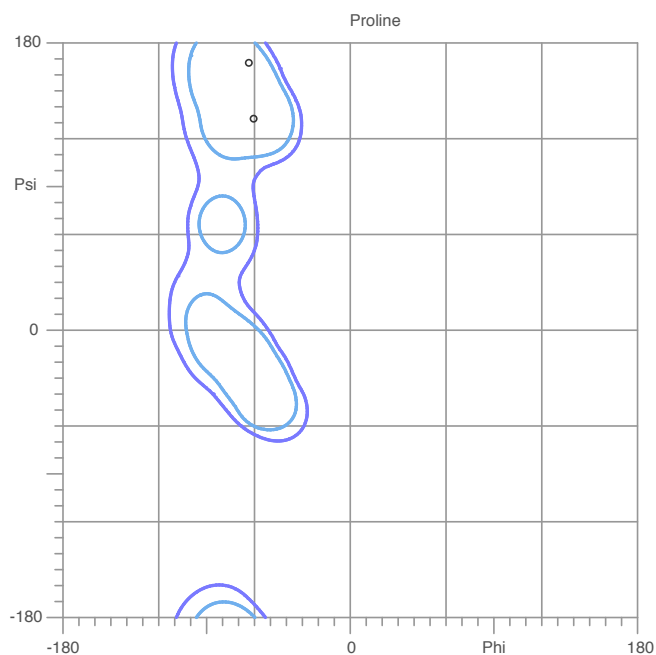
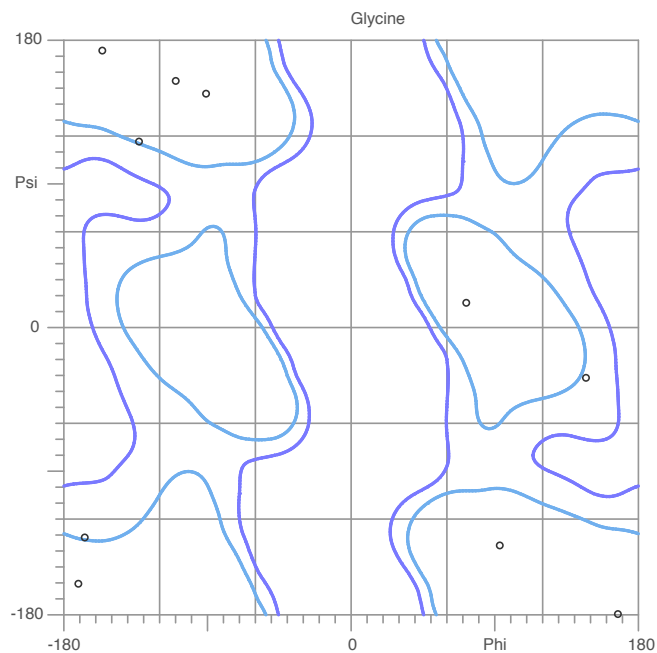
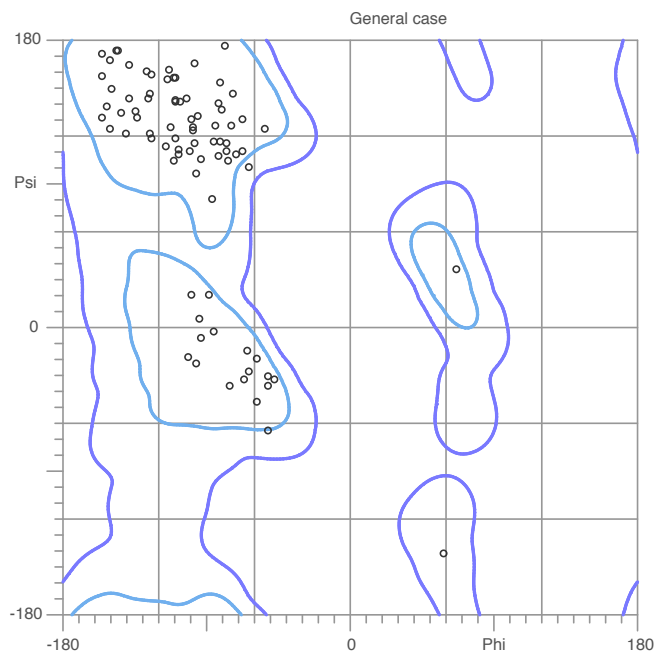
There were no outliers.

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 5



94.8% (91/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

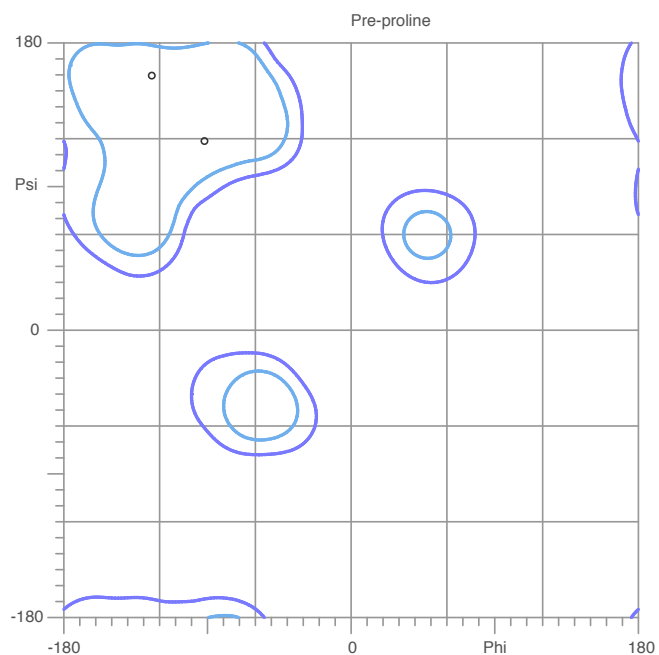
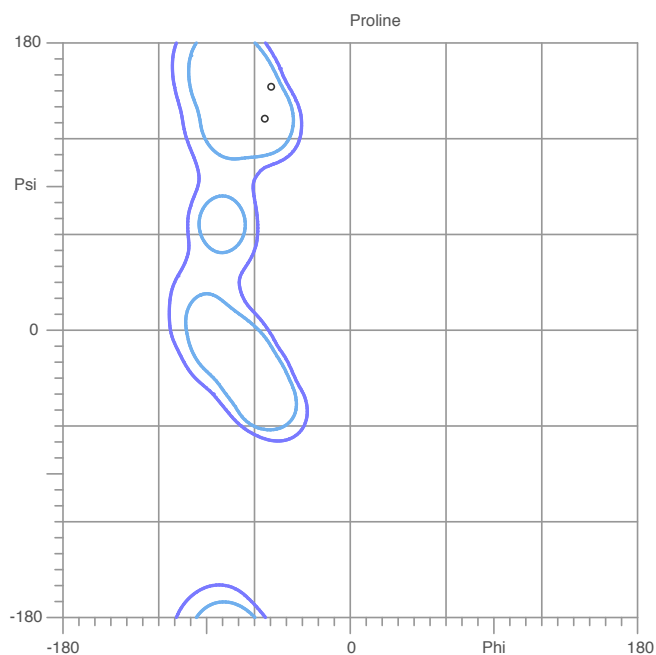
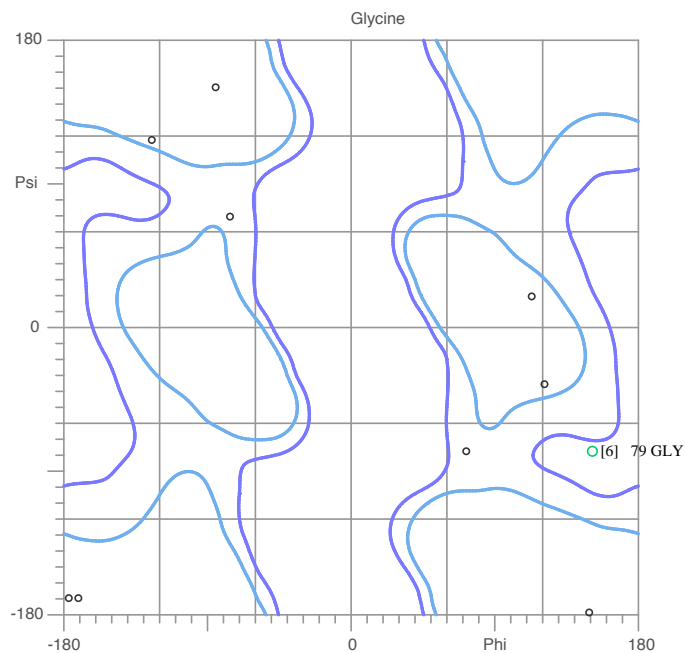
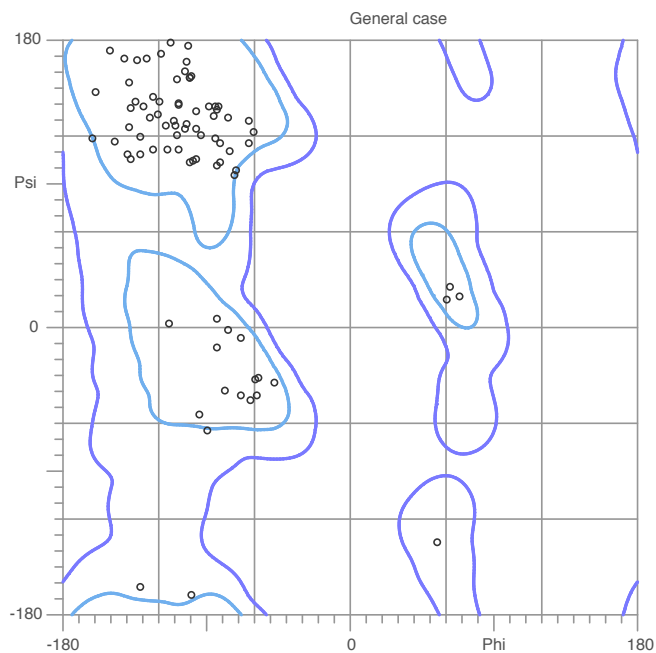
There were no outliers.

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

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 6



91.7% (88/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

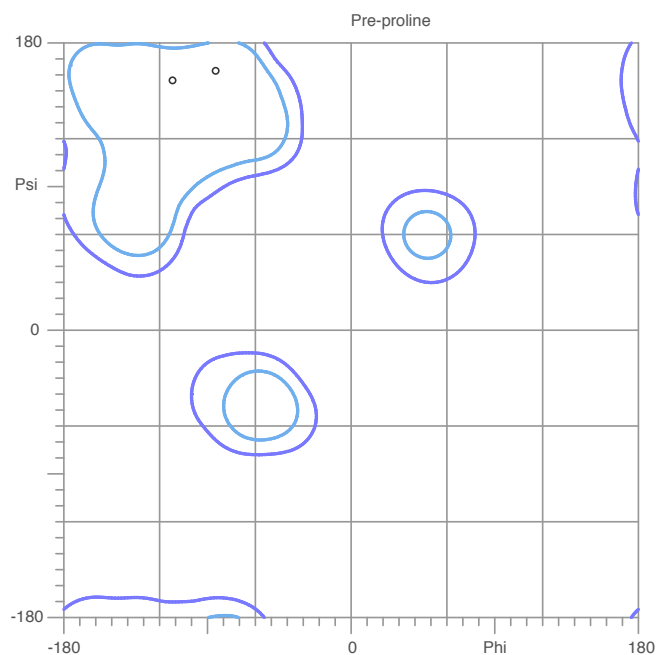
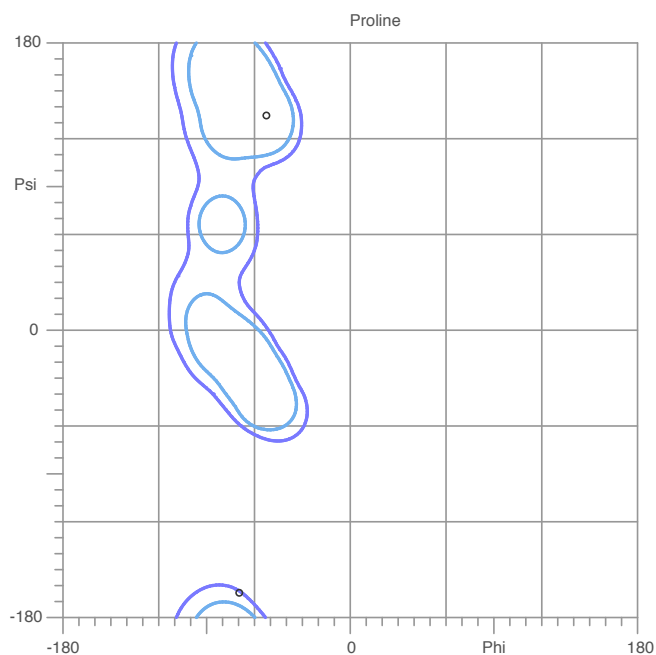
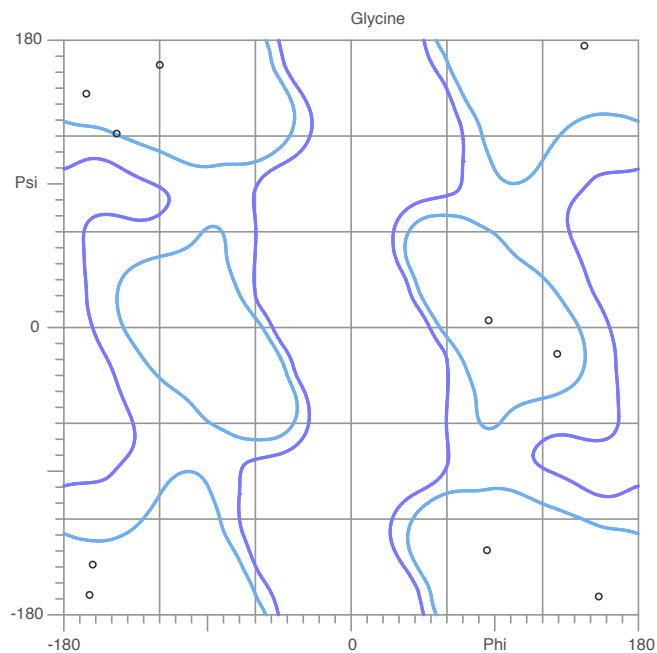
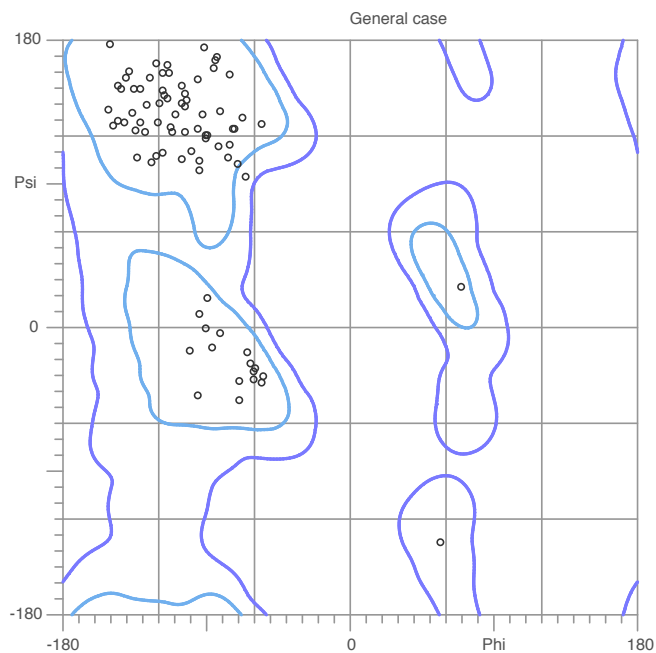
There were 1 outliers (phi, psi):
[6] 79 GLY (151.4, -77.8)

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 7



96.9% (93/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

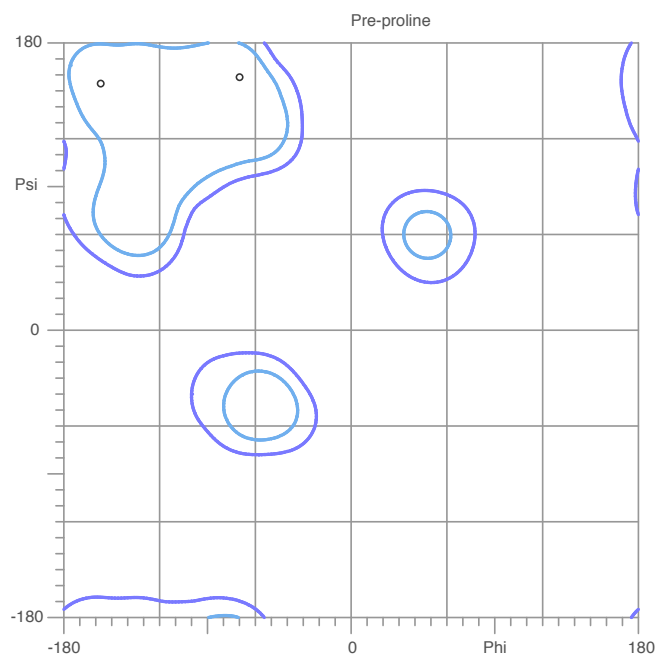
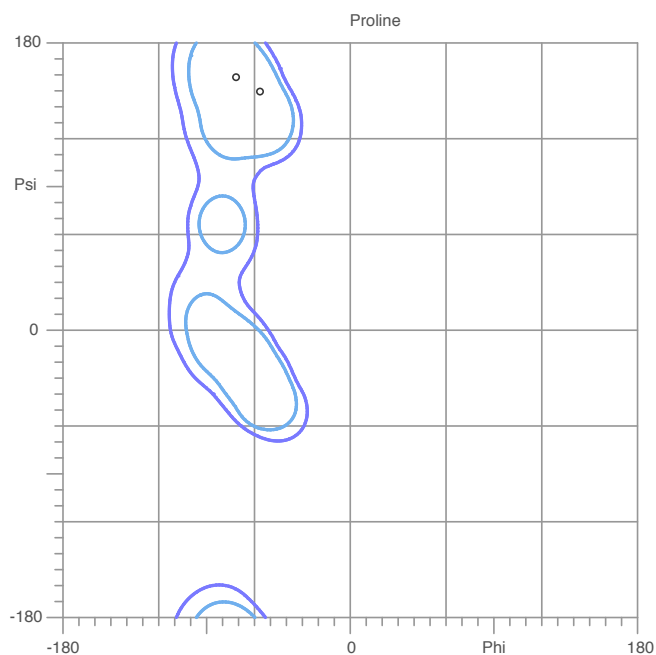
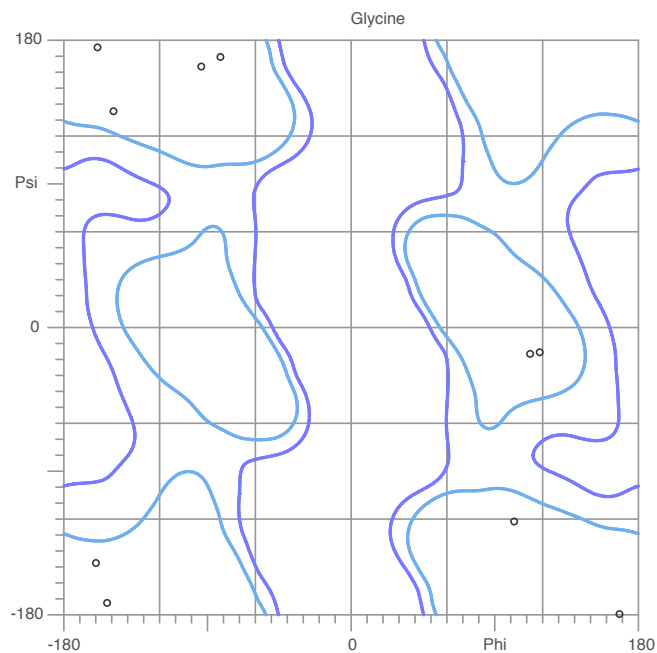
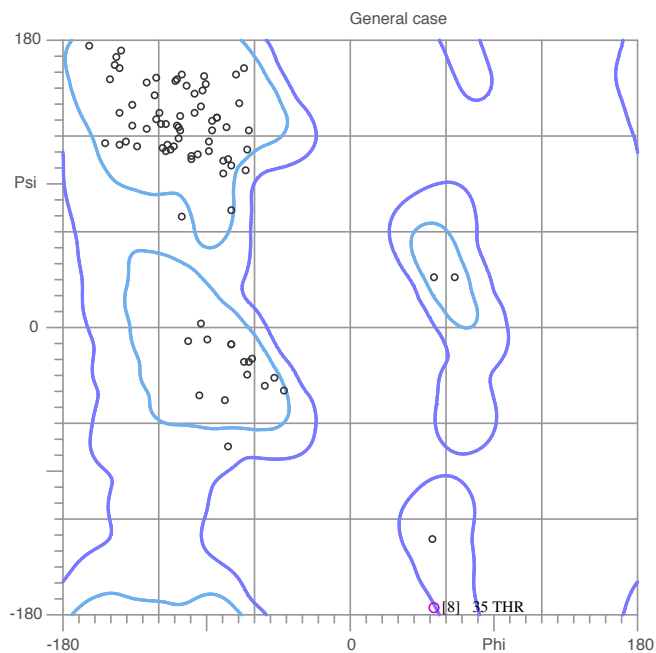
There were no outliers.

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

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 8



94.8% (91/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

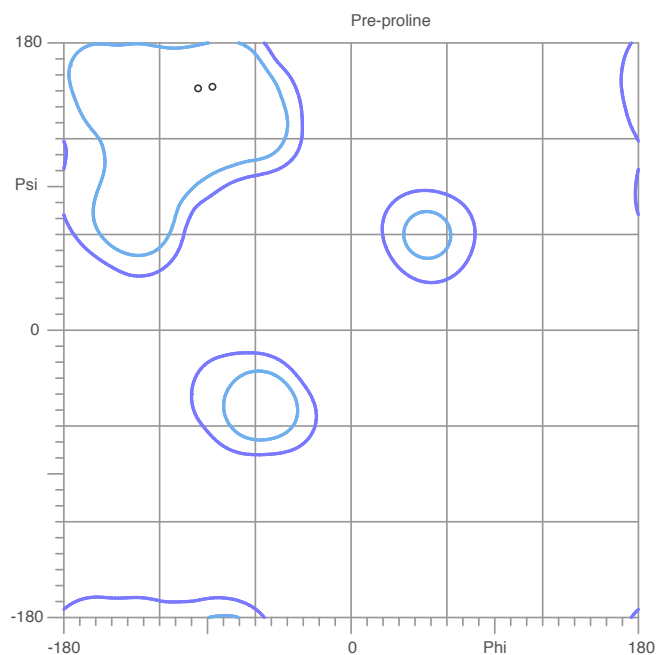
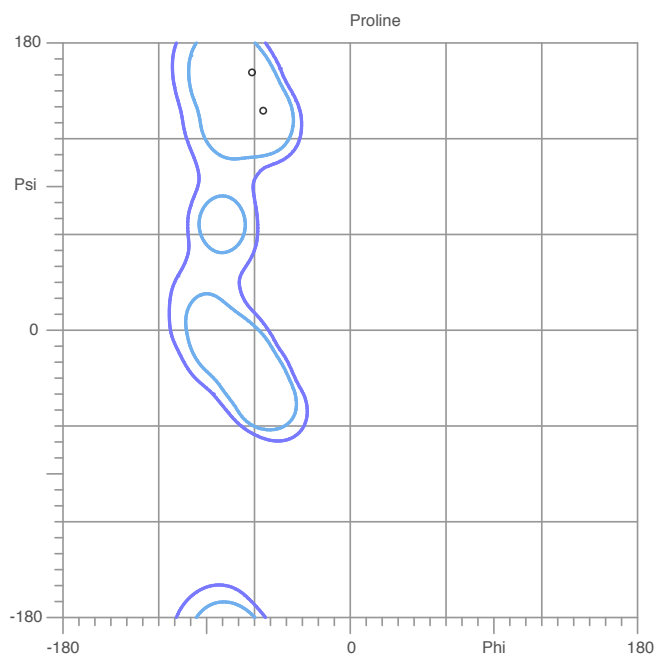
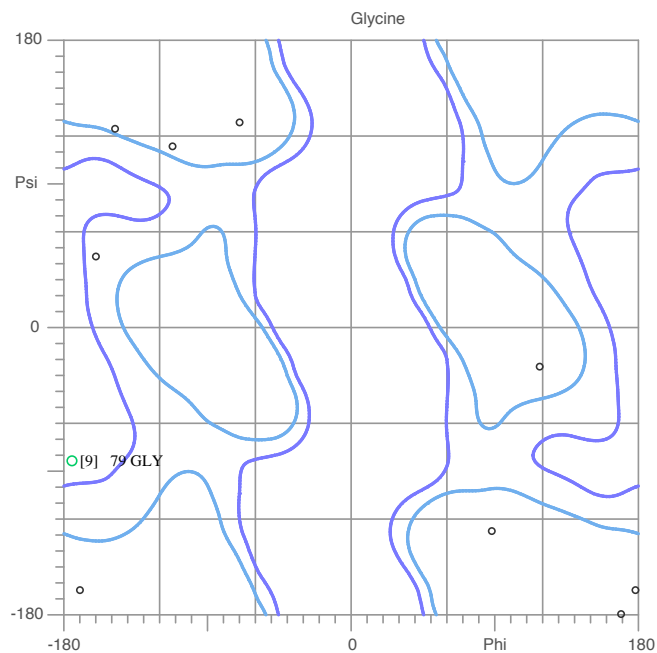
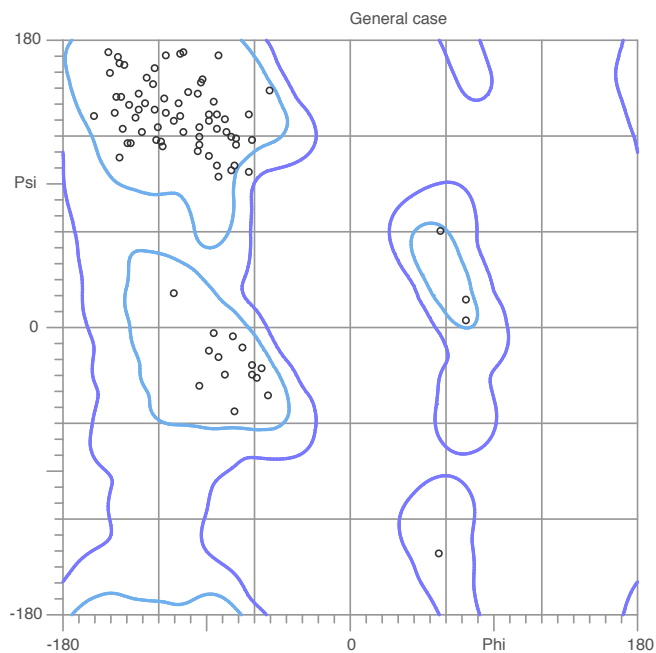
There were 1 outliers (phi, psi):
[8] 35 THR (52.2, -175.9)

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 9

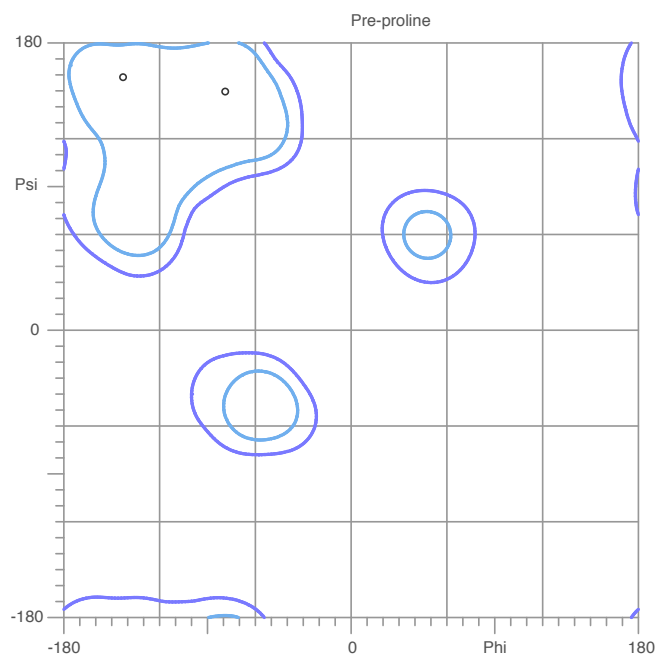
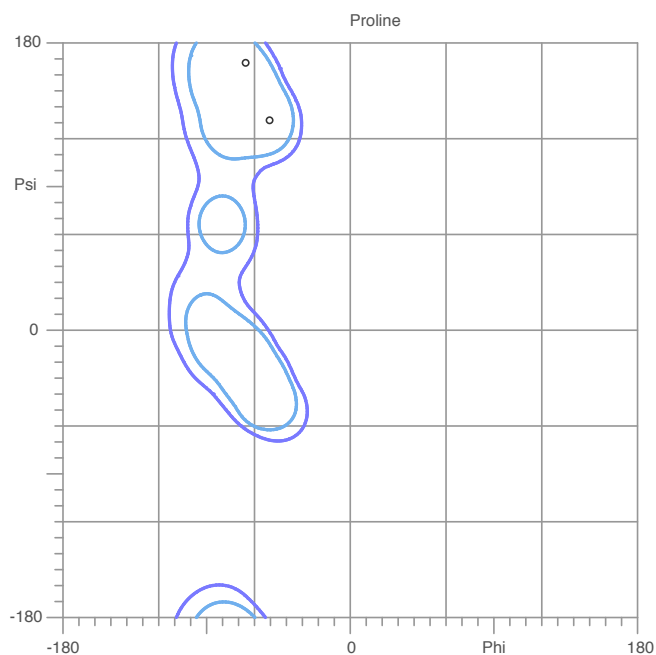
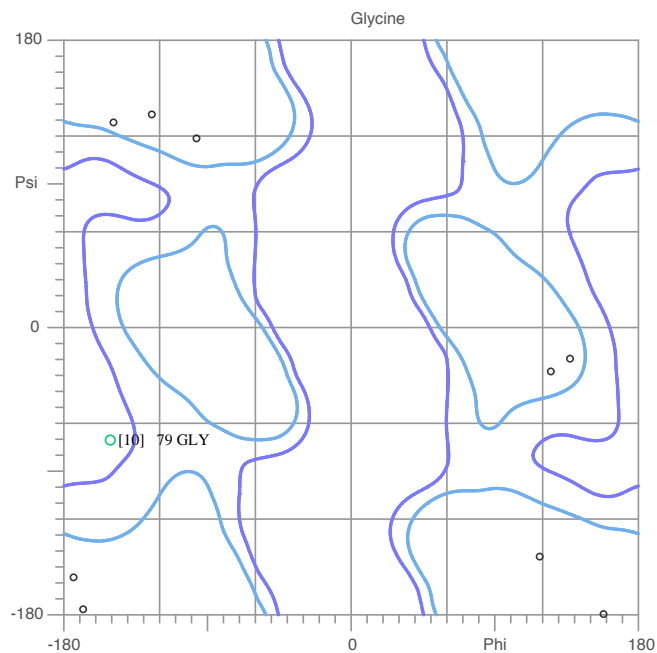
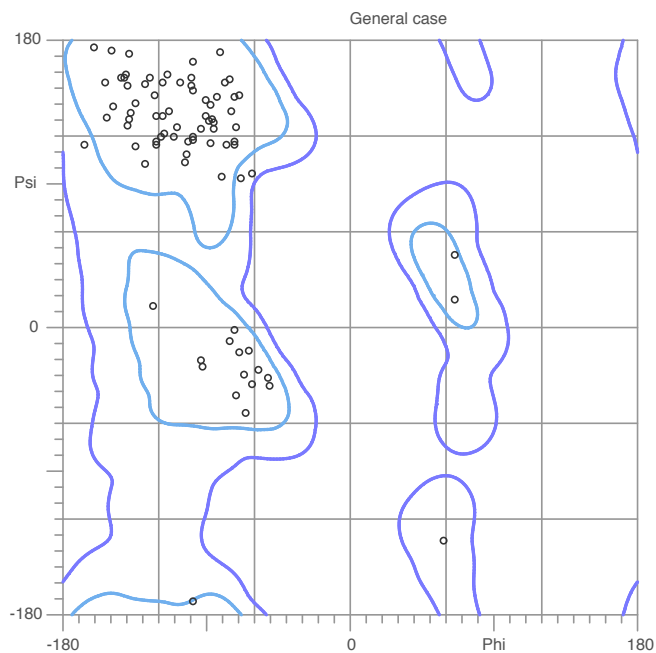


95.8% (92/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 79 GLY (-175.7, -83.6)

MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 10



93.8% (90/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

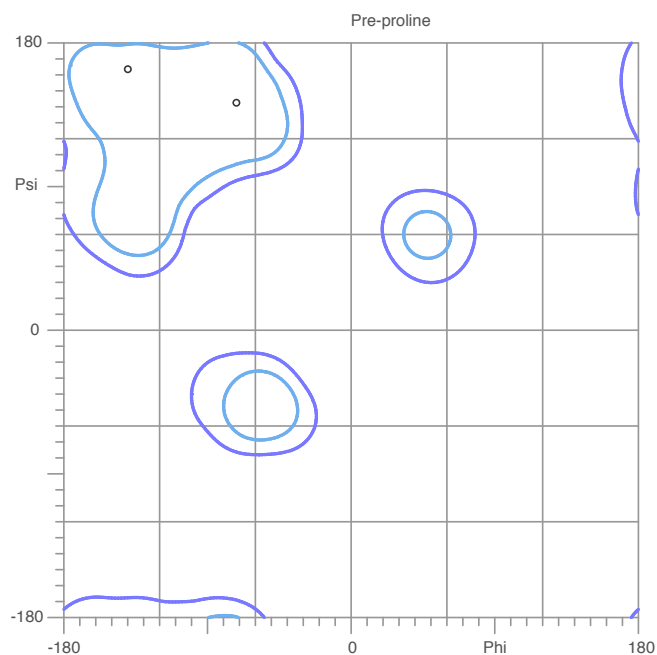
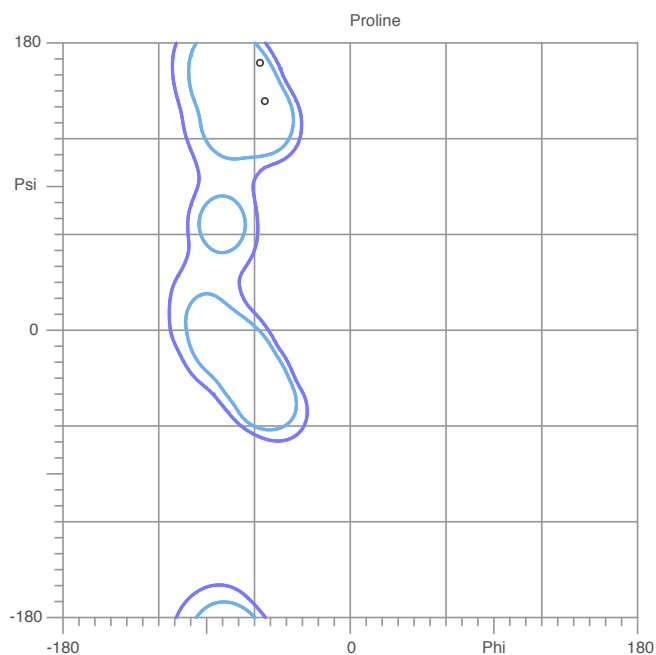
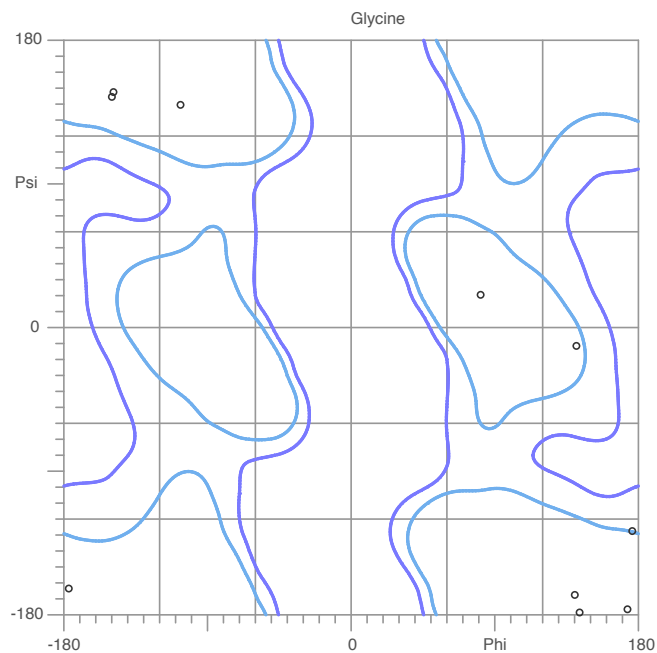
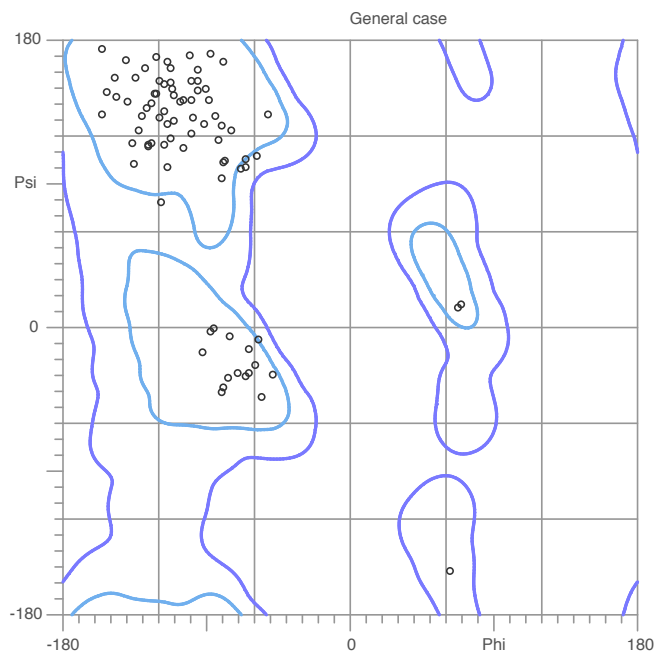
There were 1 outliers (phi, psi):
[10] 79 GLY (-151.0, -70.8)

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 11



93.8% (90/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

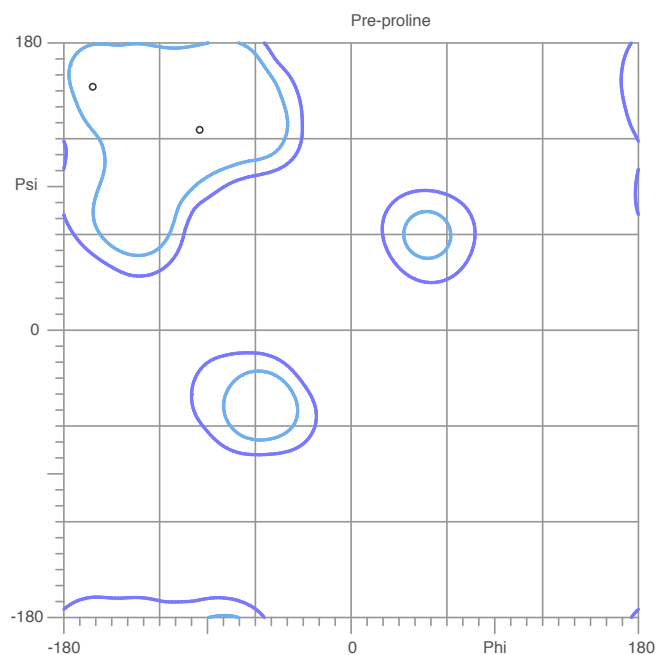
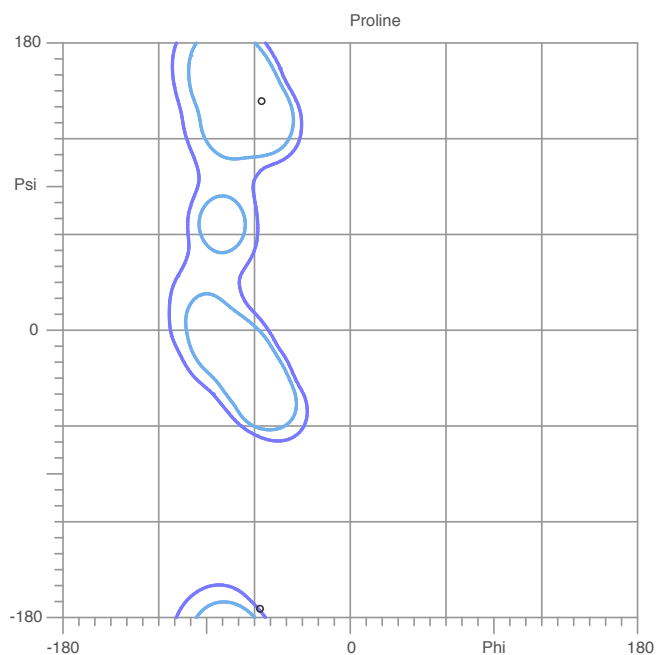
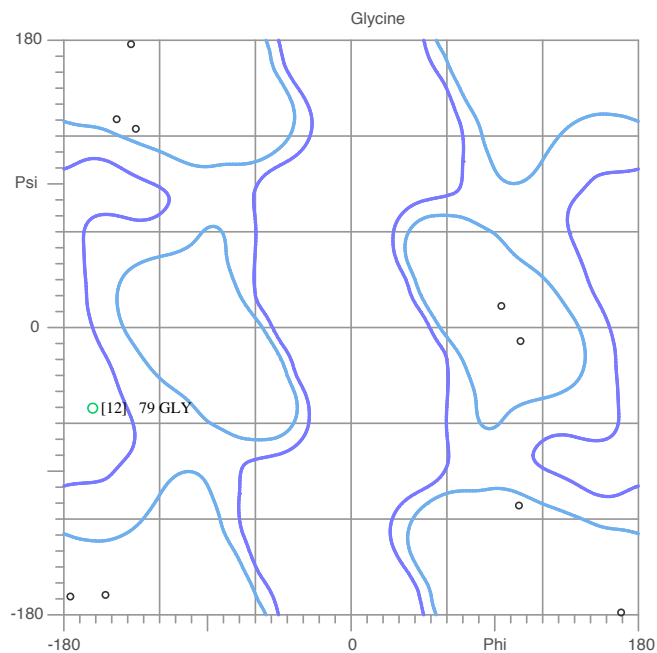
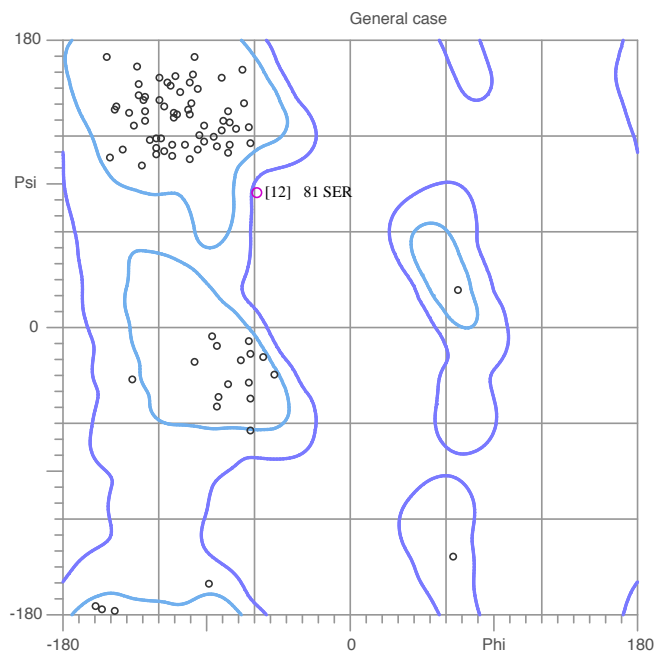
There were no outliers.

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

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 12

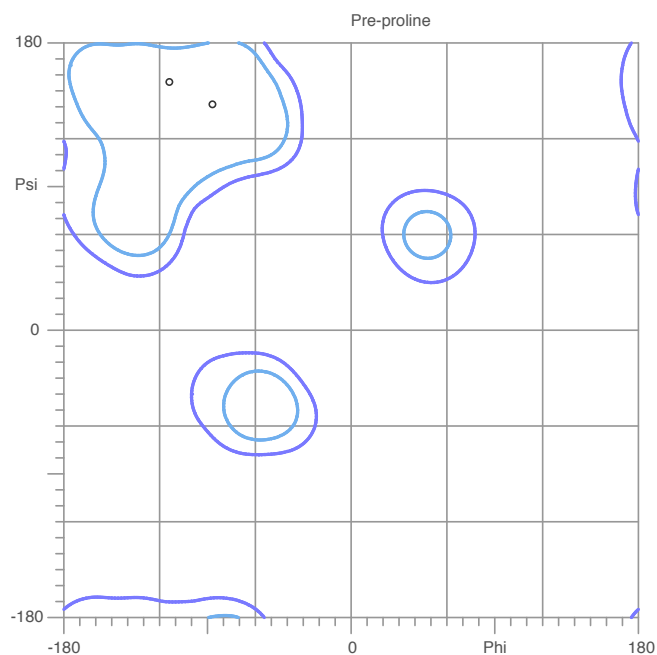
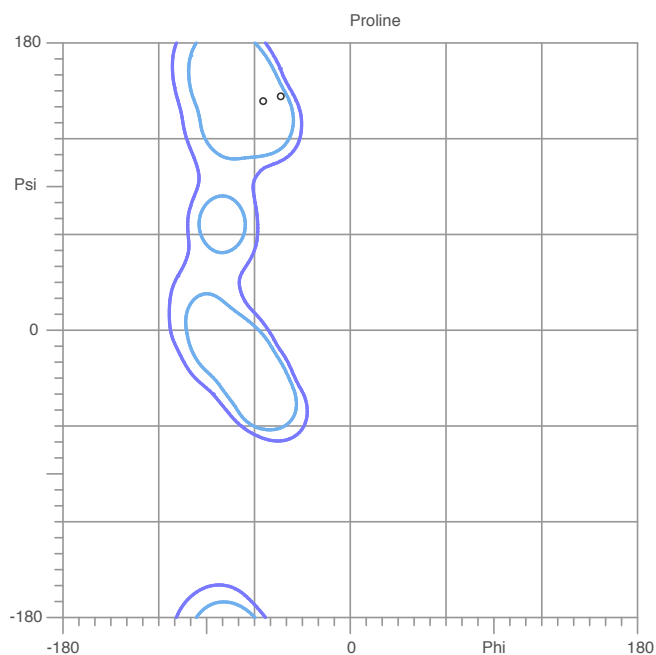
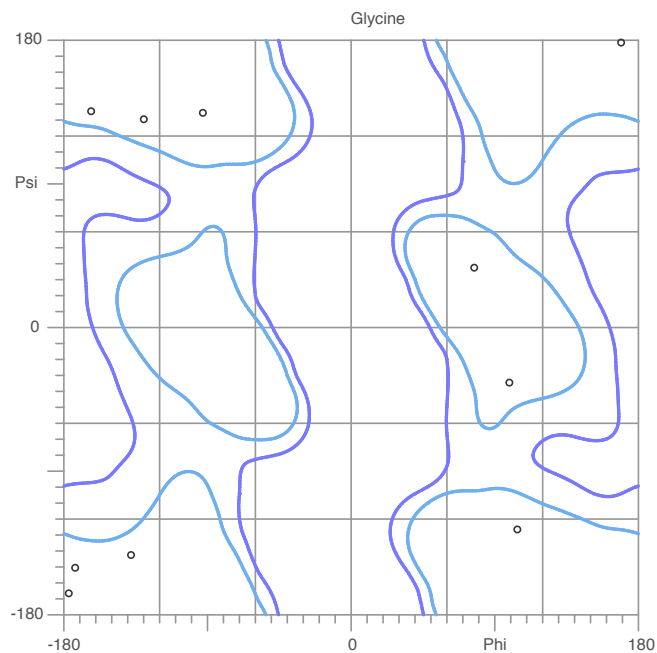
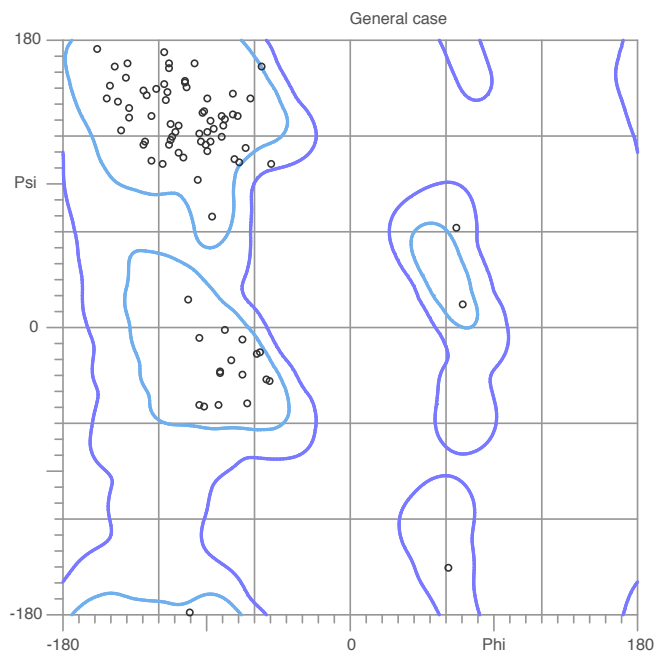


92.7% (89/96) of all residues were in favored (98%) regions.
97.9% (94/96) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 79 GLY (-162.7, -50.1)
[12] 81 SER (-59.8, 85.7)

MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 13



96.9% (93/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

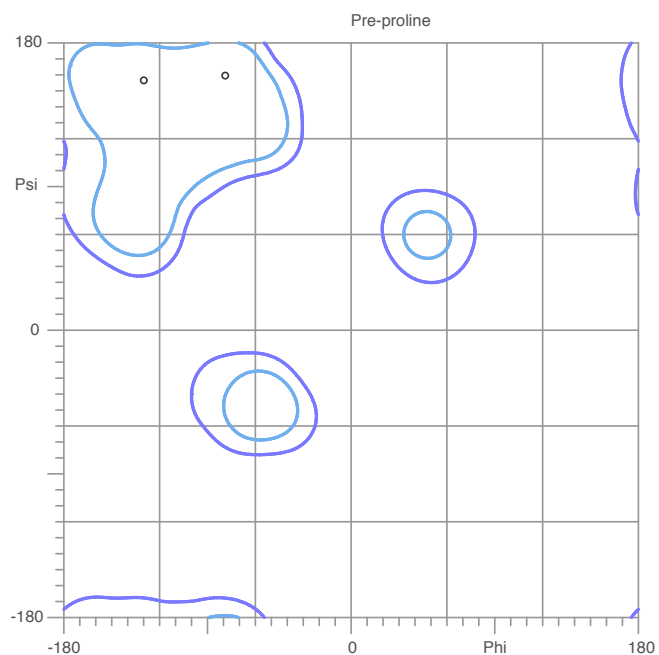
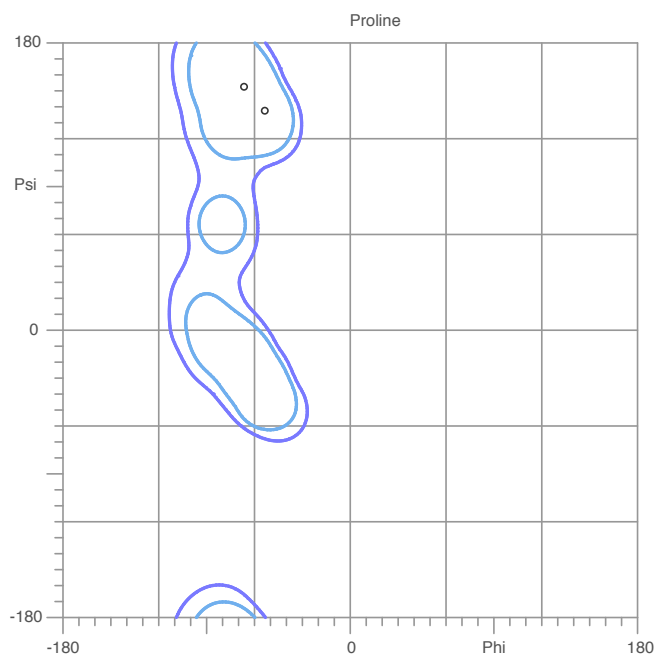
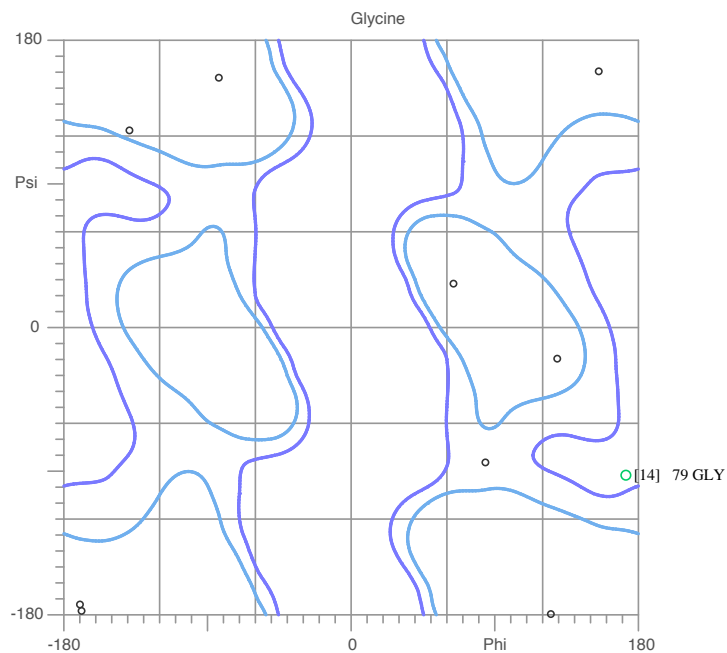
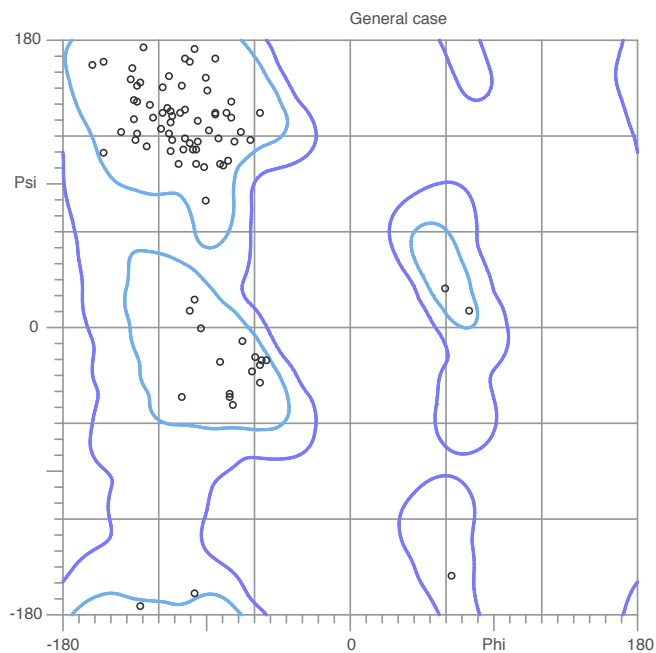
There were no outliers.

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

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 14

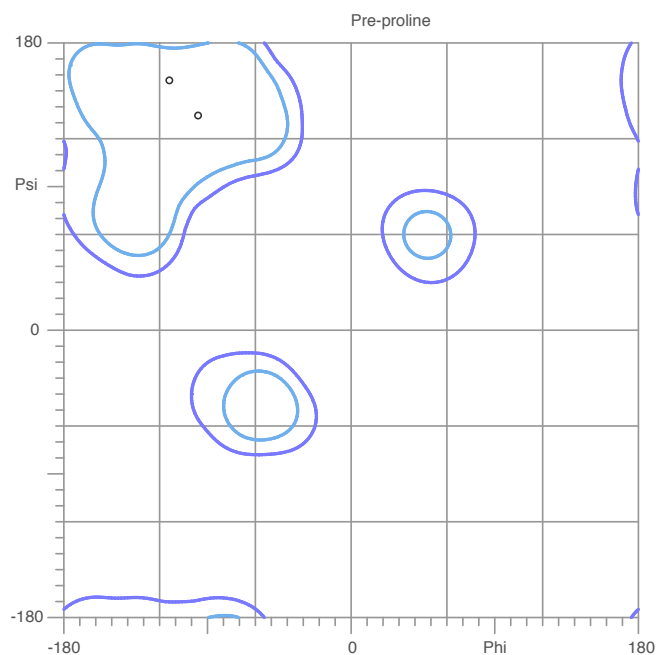
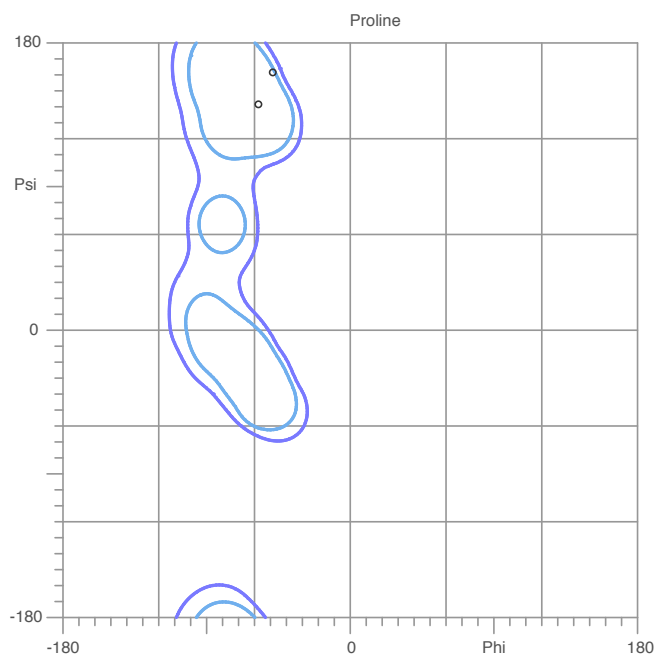
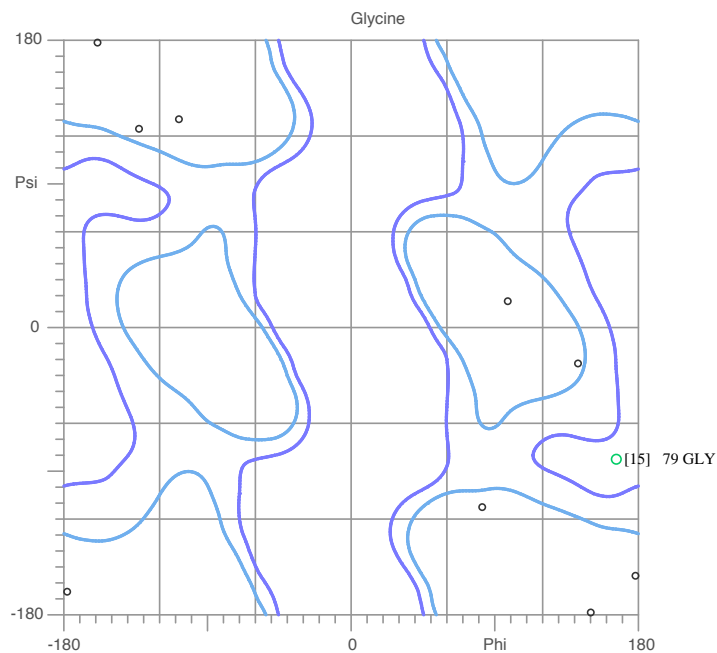
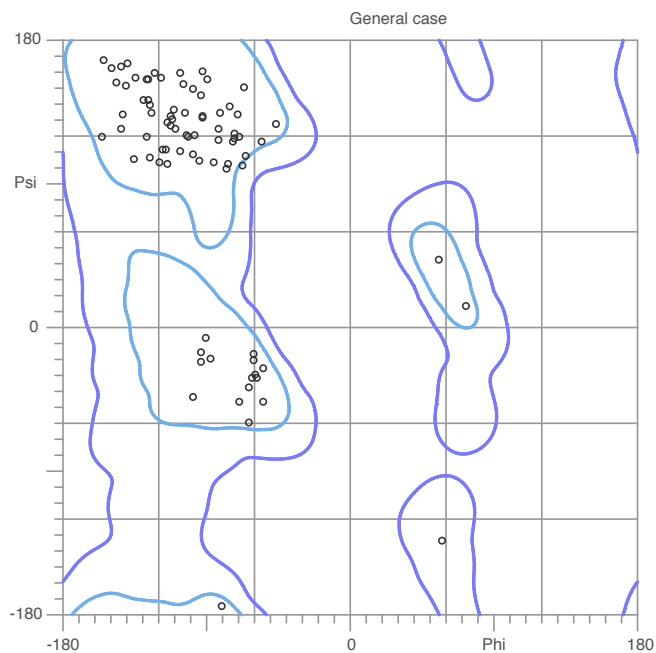


95.8% (92/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[14] 79 GLY (172.7, -92.1)

MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 15



97.9% (94/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

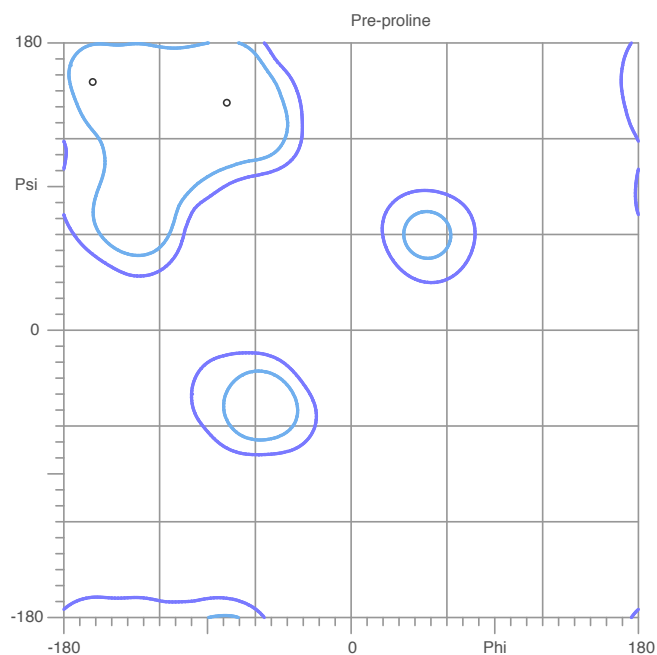
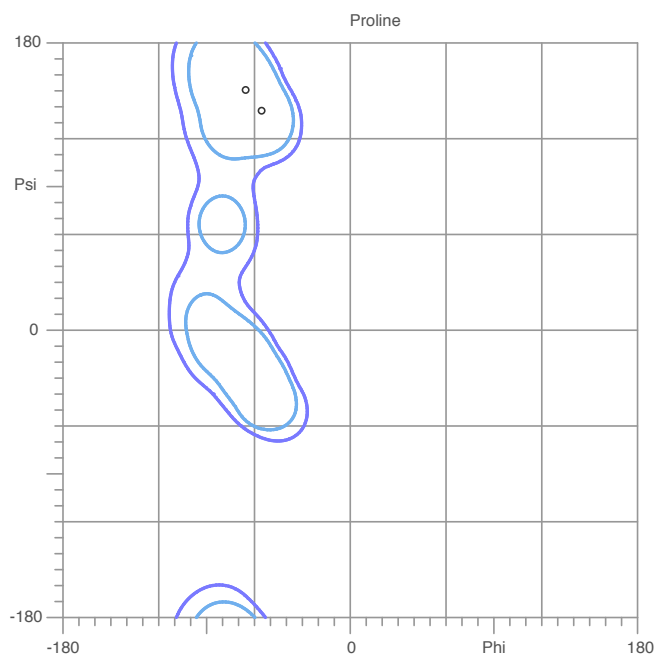
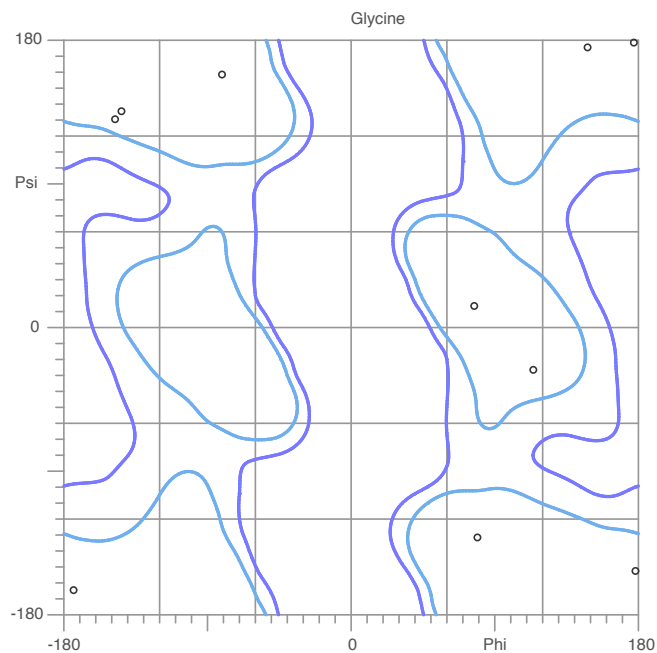
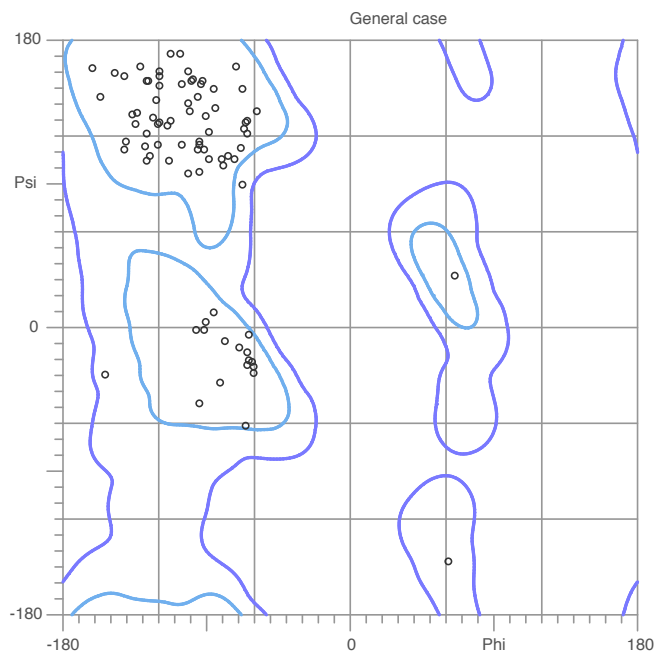
There were 1 outliers (phi, psi):
[15] 79 GLY (166.1, -82.6)

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

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 16



96.9% (93/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

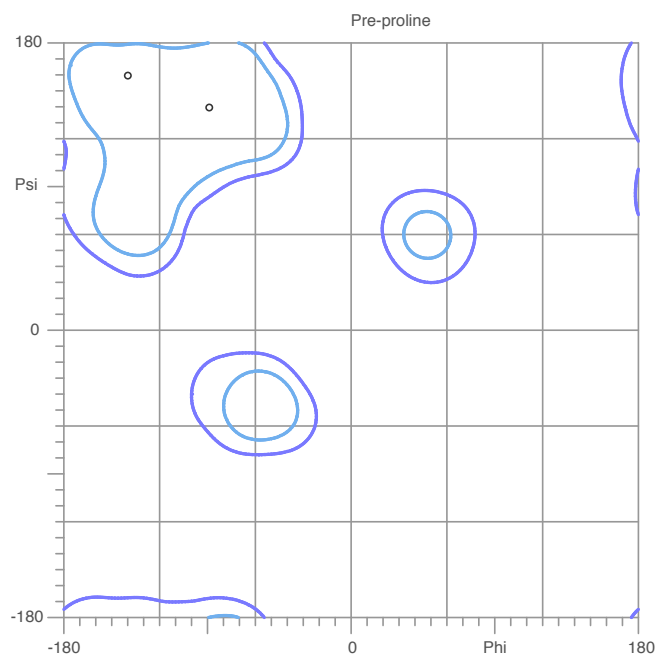
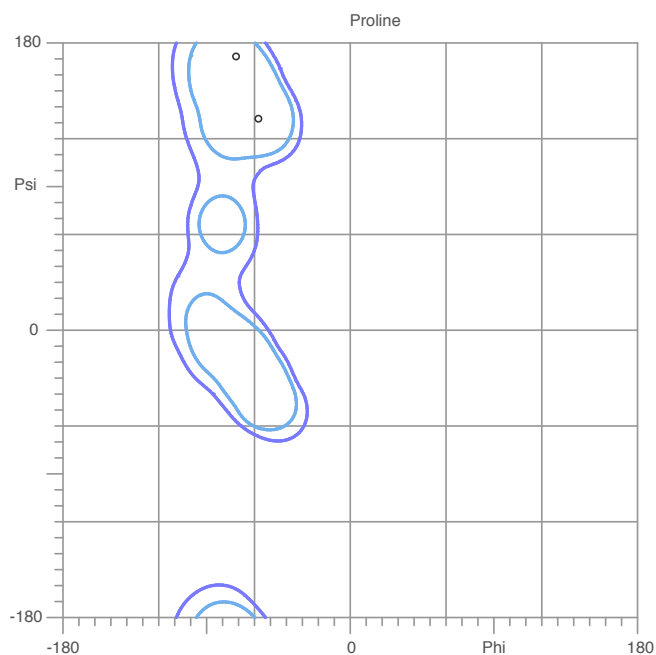
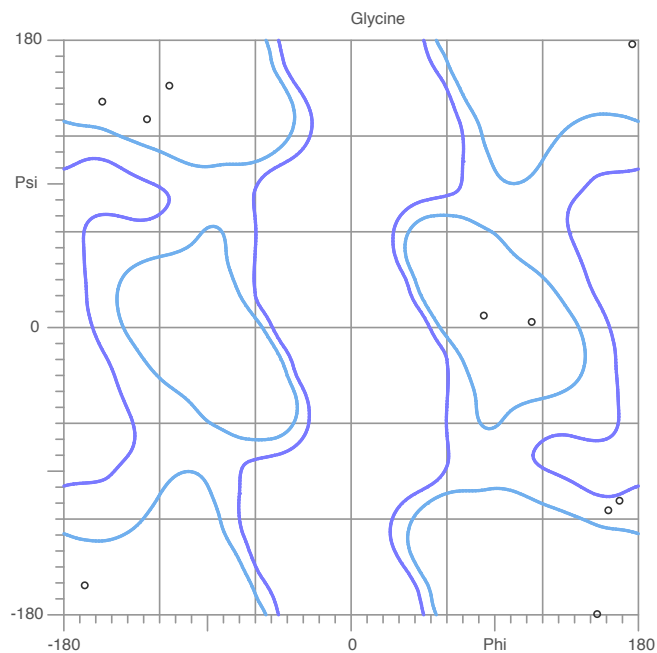
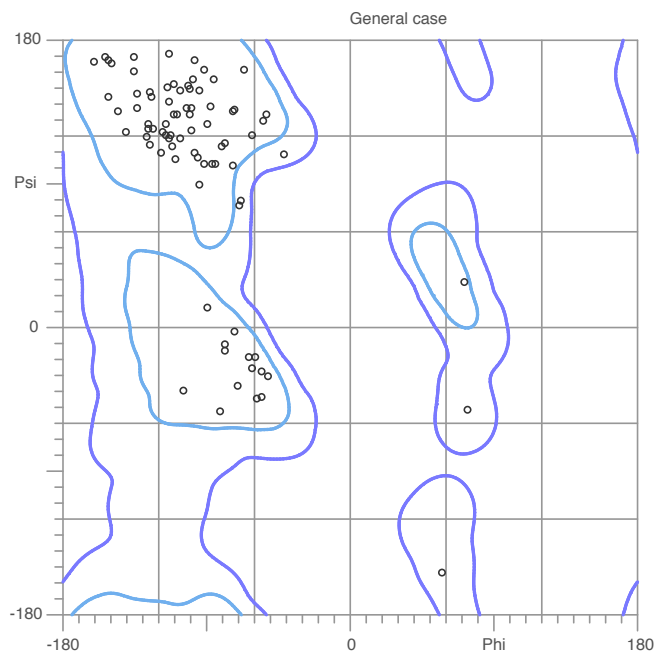
There were no outliers.

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 17



92.7% (89/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

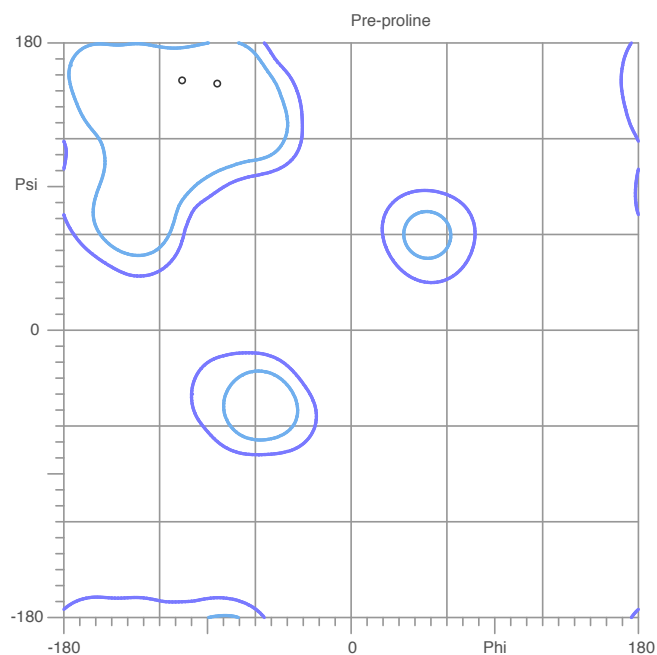
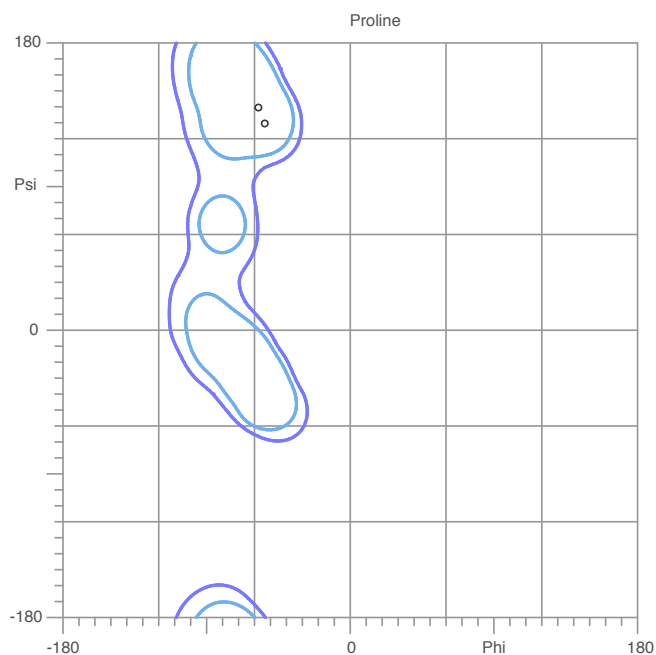
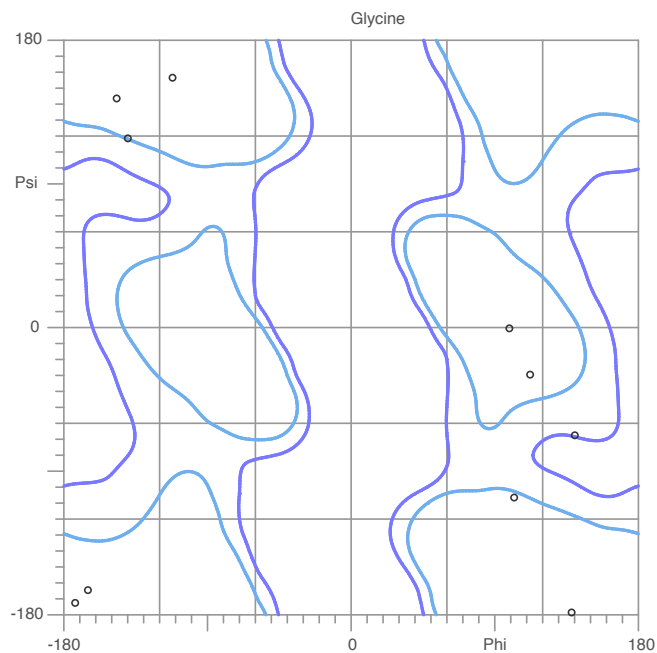
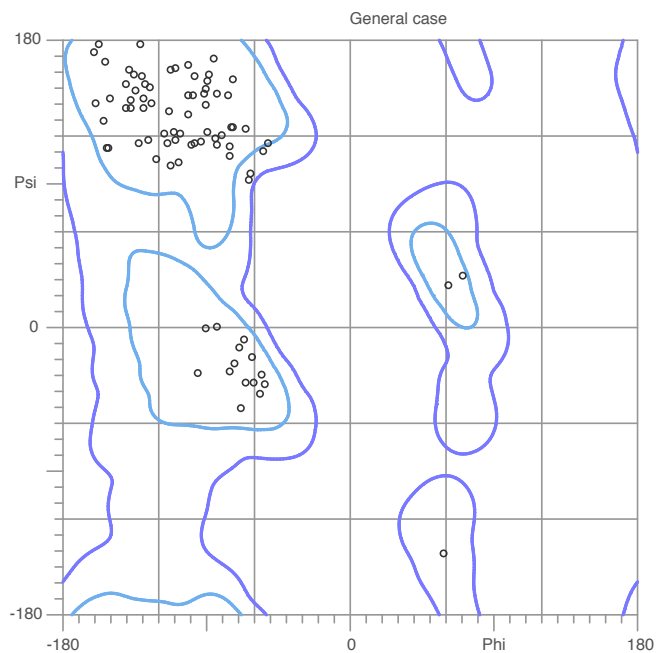
There were no outliers.

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 18



94.8% (91/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

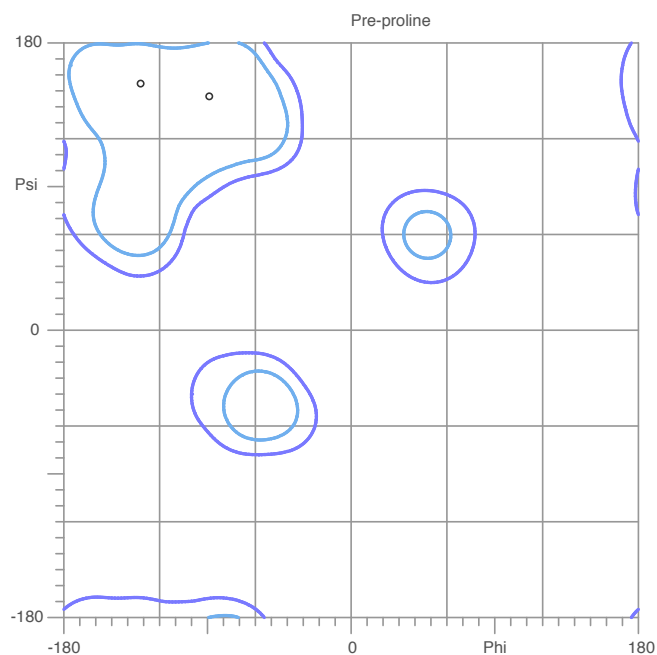
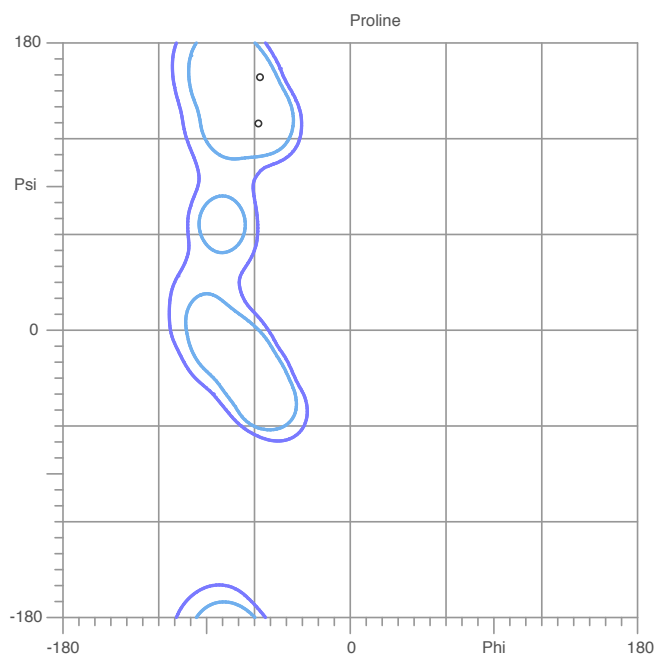
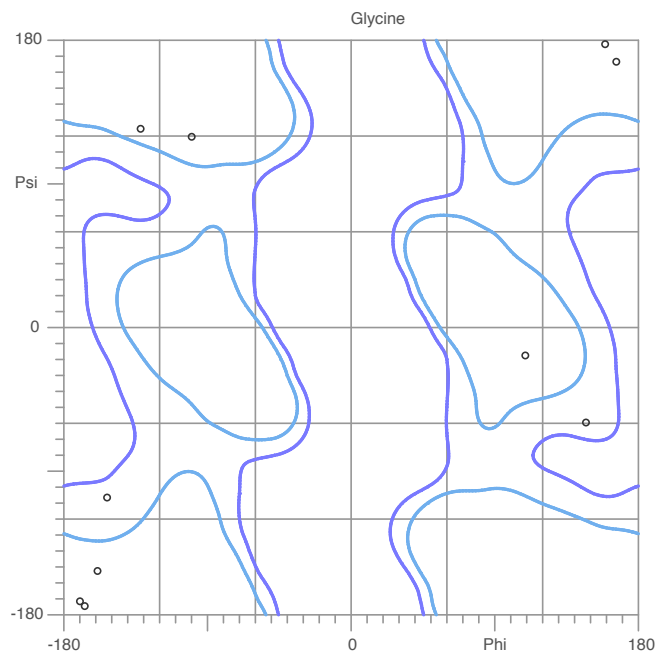
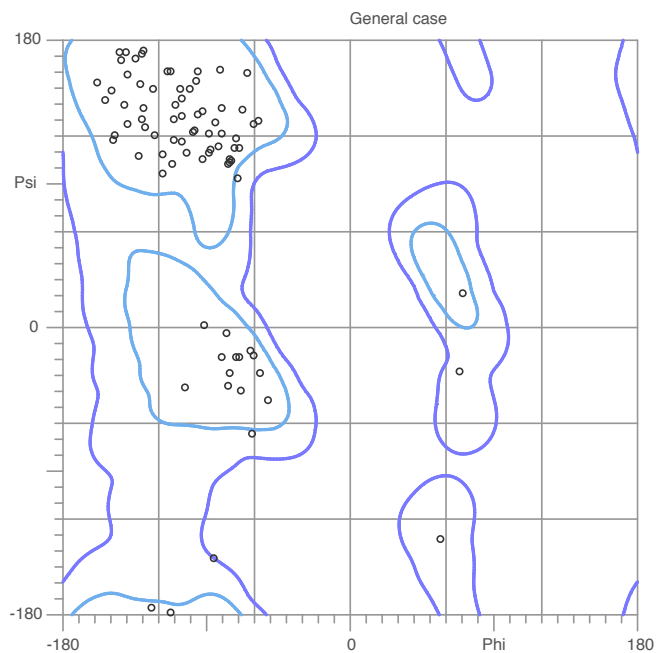
There were no outliers.

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 19



92.7% (89/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

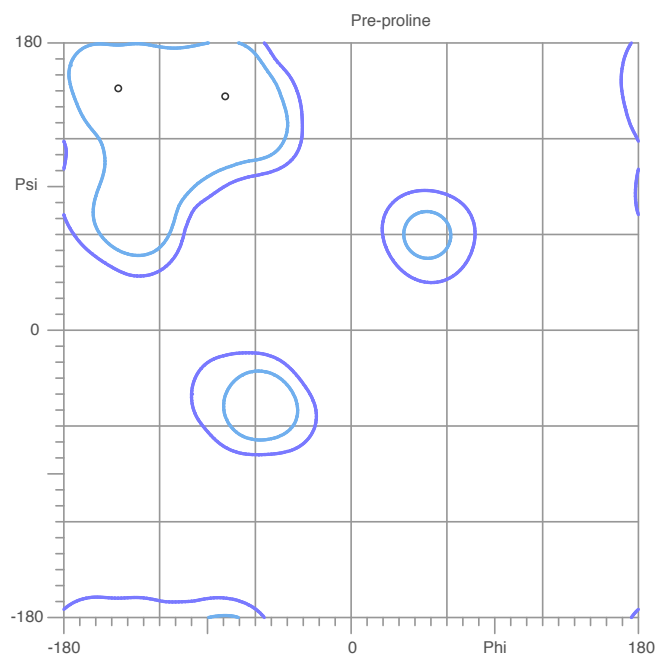
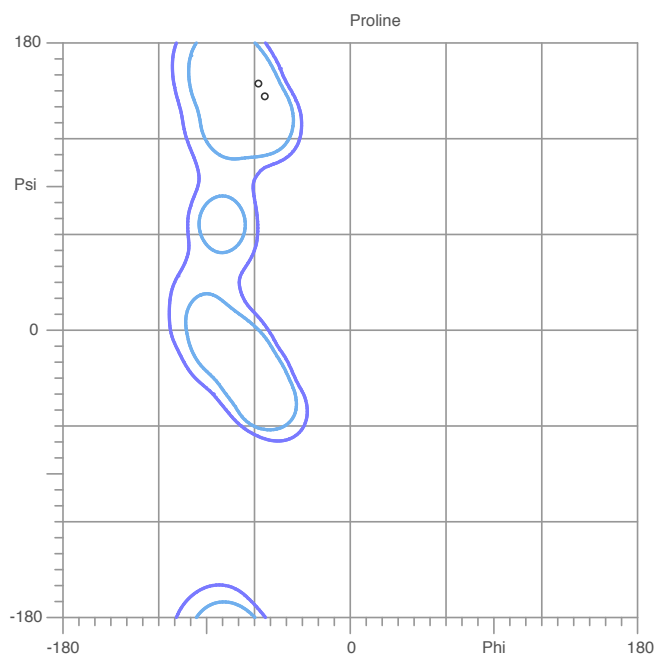
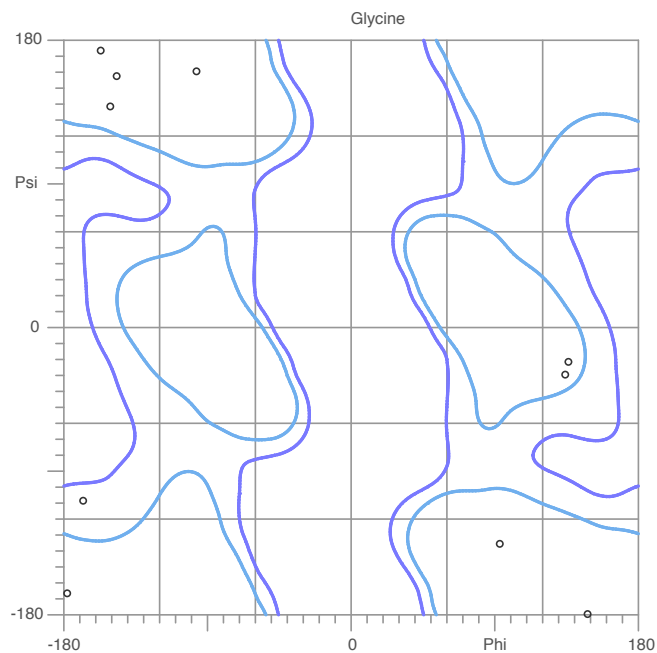
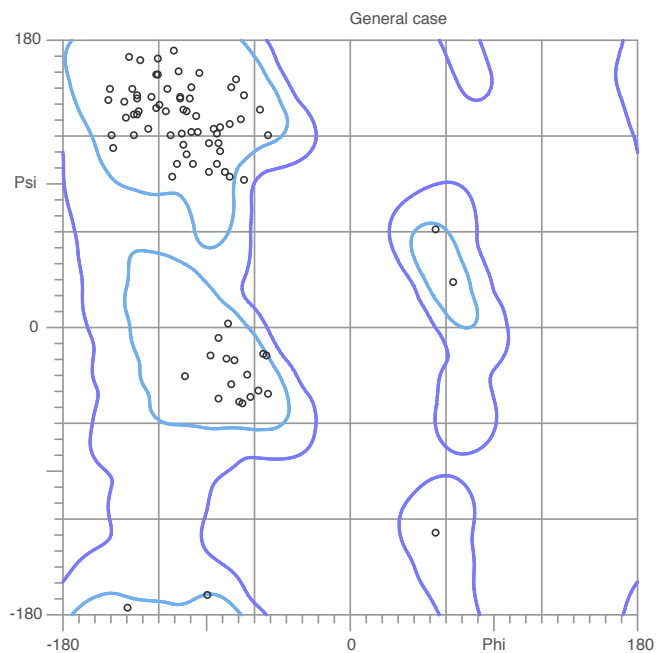
There were no outliers.

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

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MolProbity Ramachandran analysis

MRR110B_NMR_em_bcr3.pdb, model 20



96.9% (93/96) of all residues were in favored (98%) regions.
100.0% (96/96) 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)