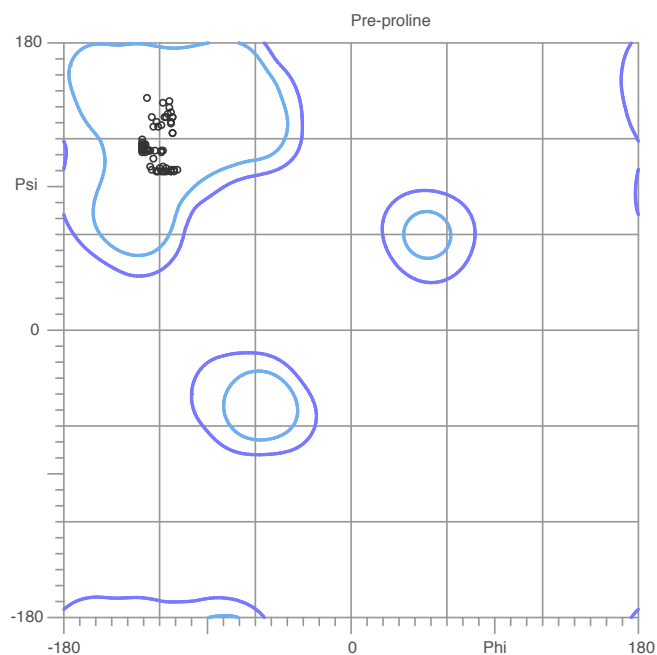
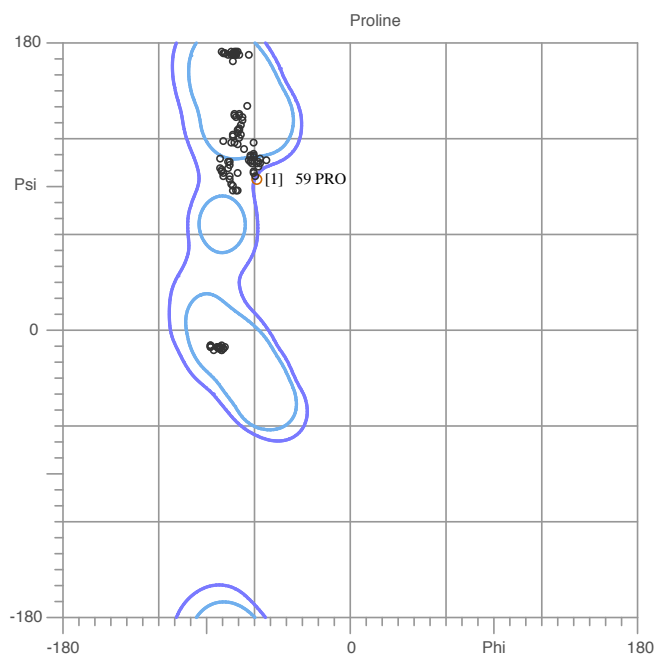
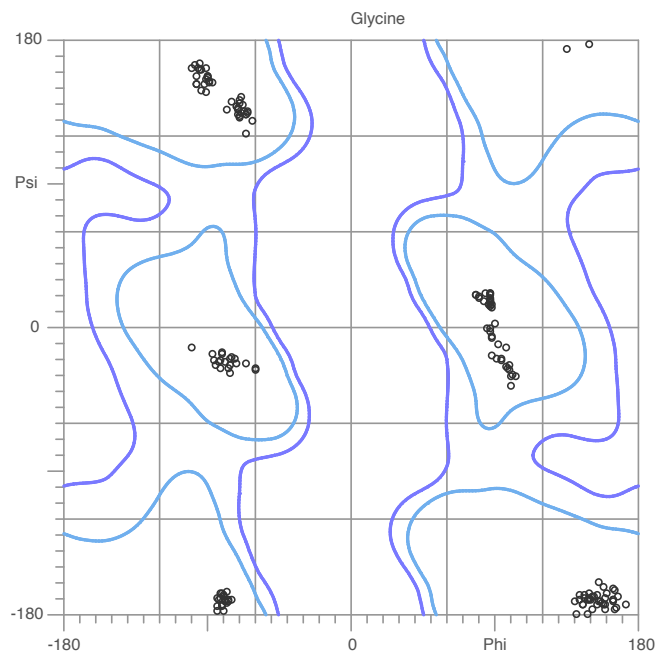
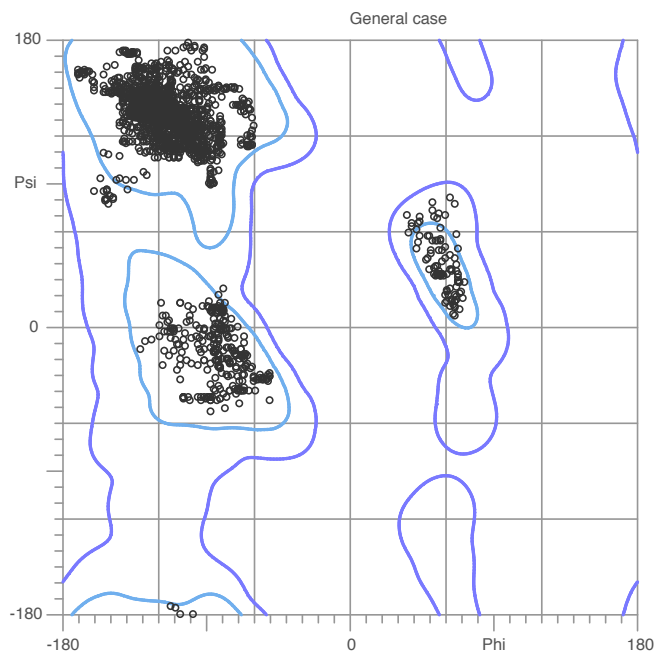


MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, all models



96.7% (2051/2120) of all residues were in favored (98%) regions.
100.0% (2119/2120) of all residues were in allowed (>99.8%) regions.

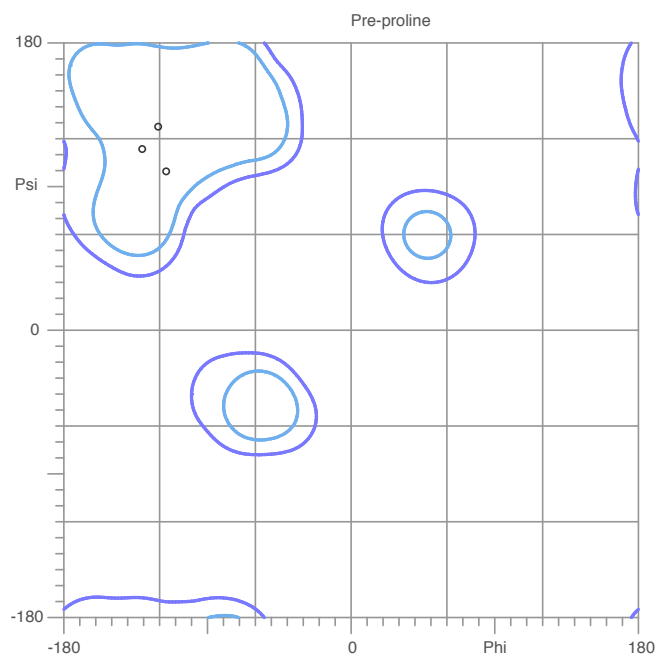
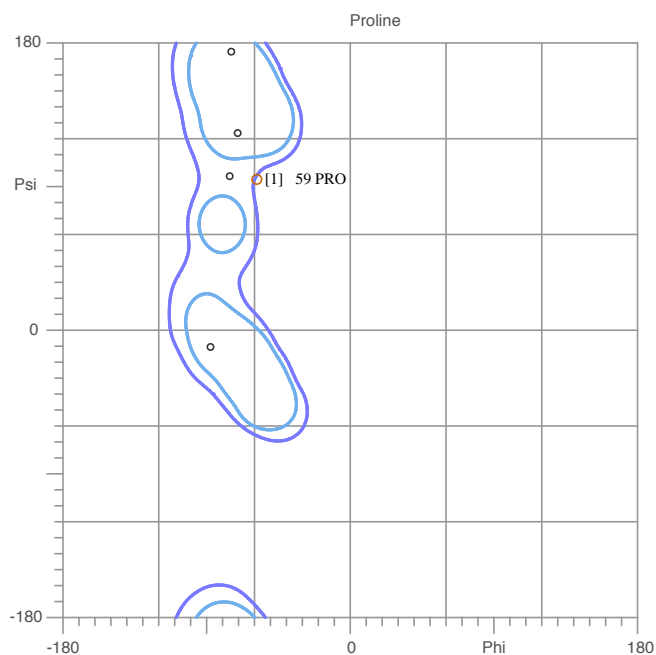
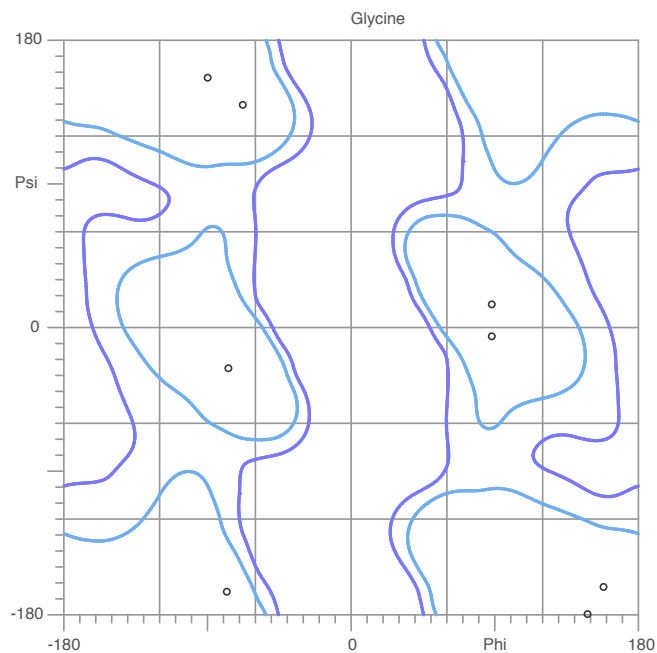
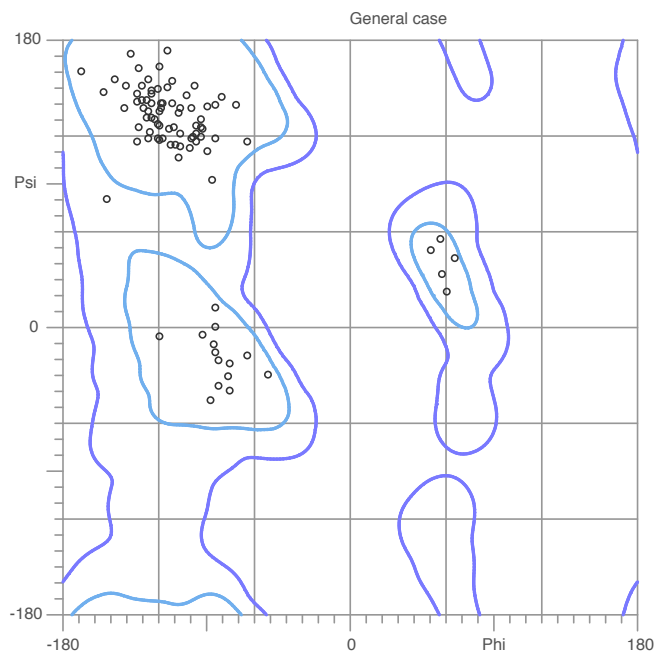
There were 1 outliers (phi, psi):
[1] 59 PRO (-59.2, 95.4)

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

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 1

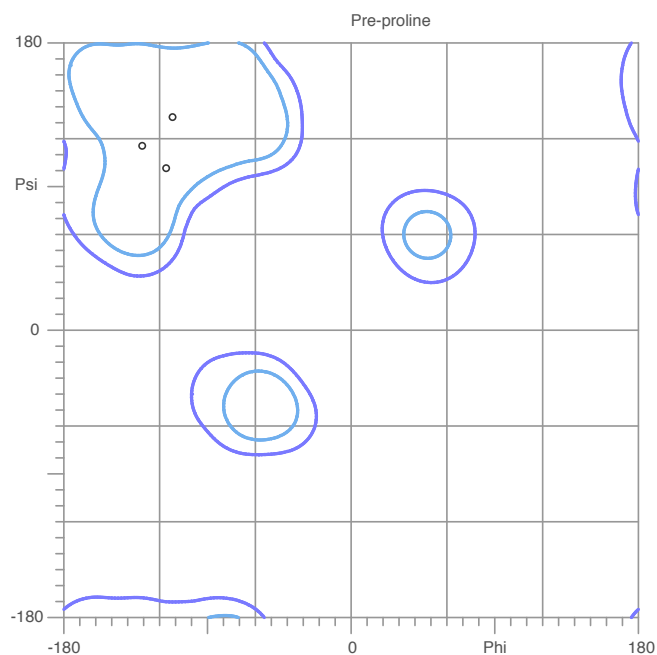
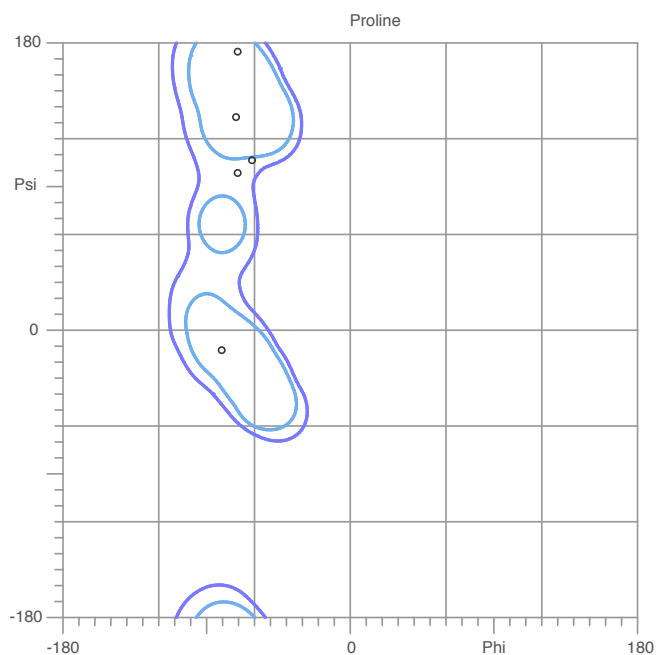
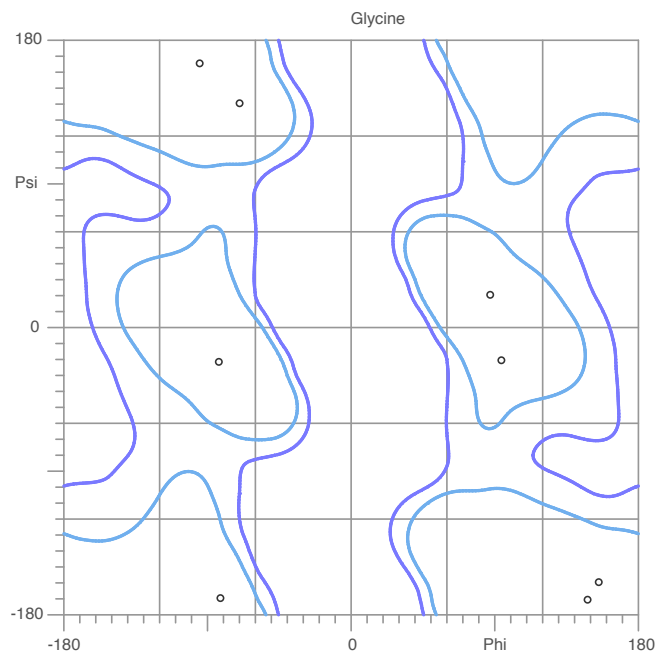
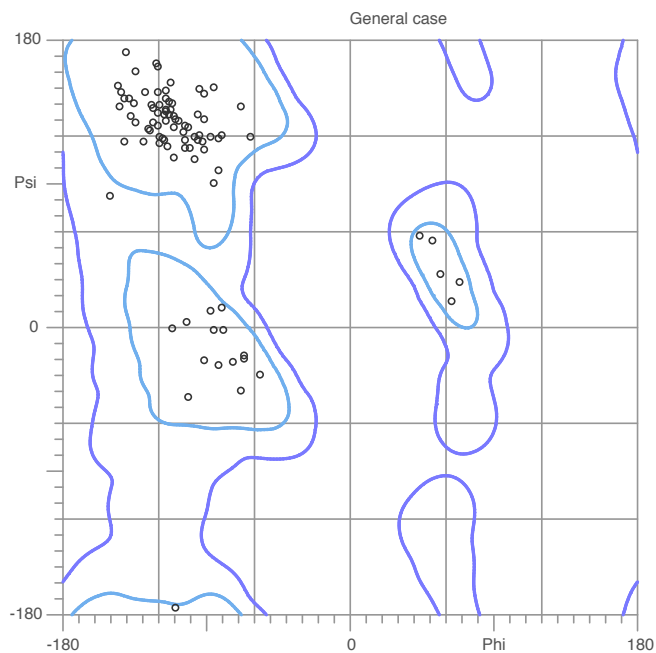


97.2% (103/106) of all residues were in favored (98%) regions.
99.1% (105/106) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[1] 59 PRO (-59.2, 95.4)

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 2



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.

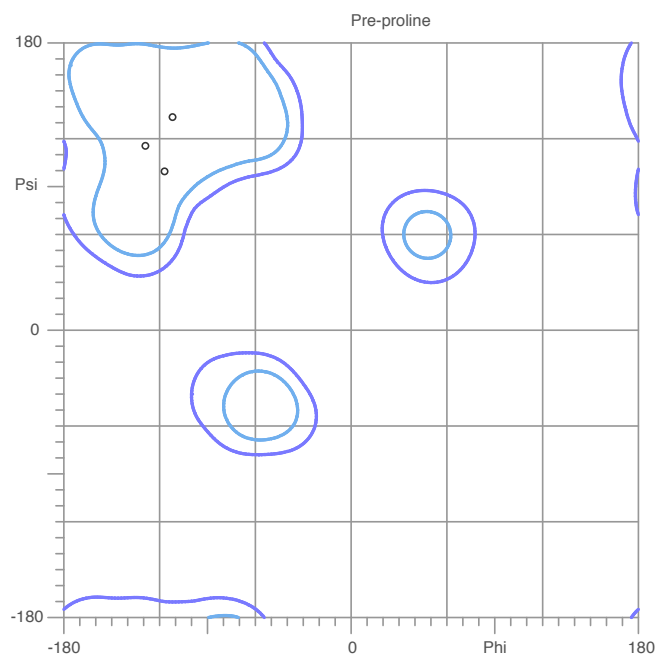
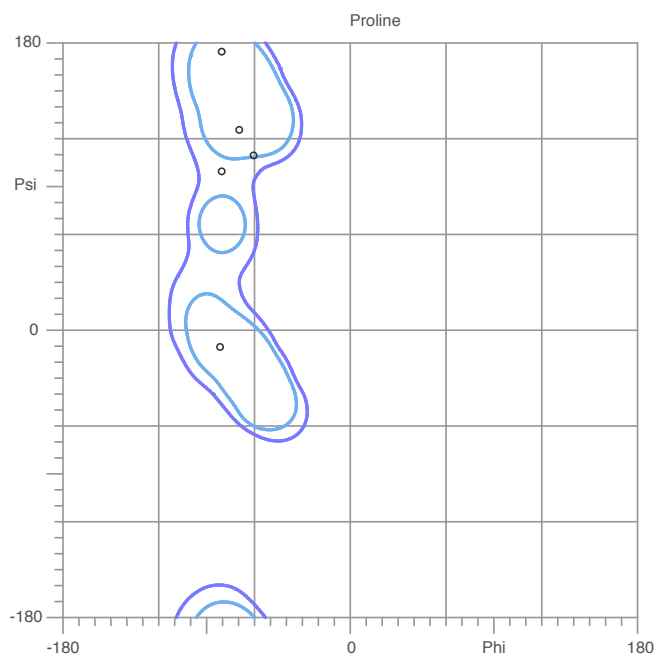
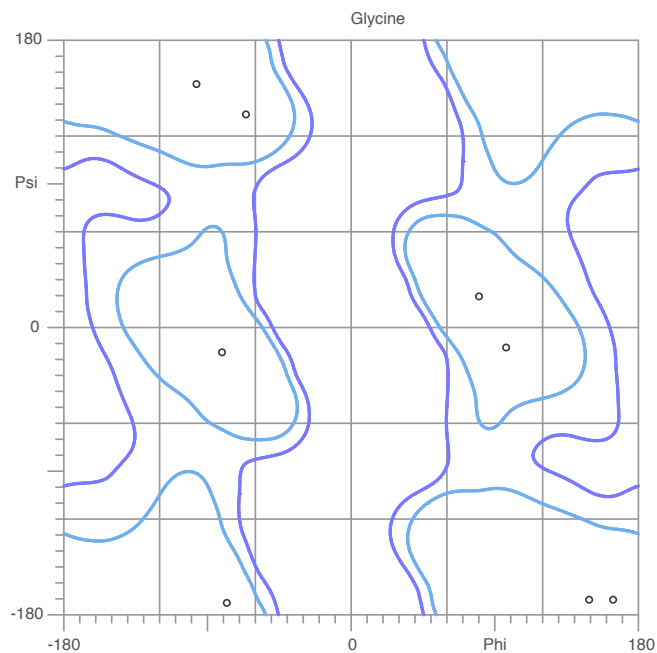
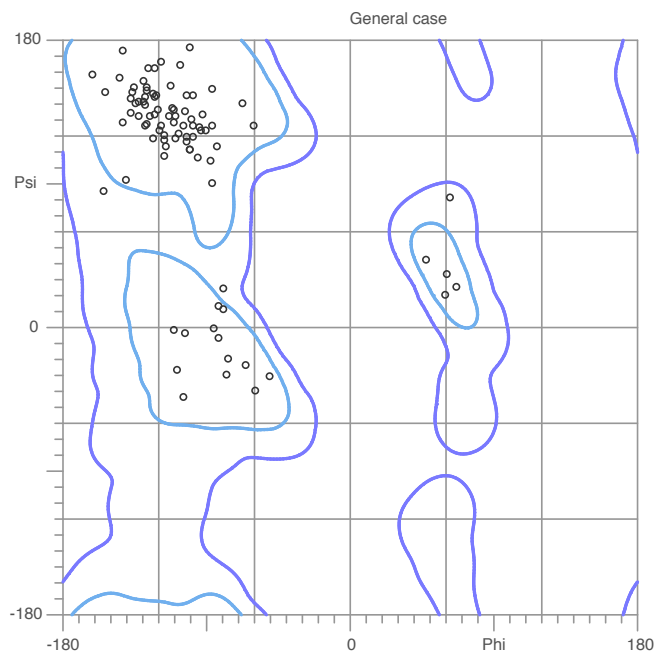
There were no outliers.

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

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

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 3



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.

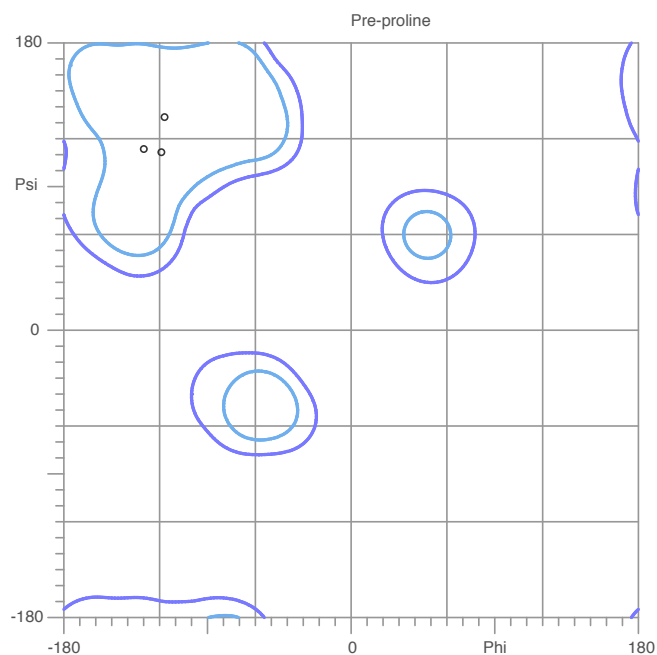
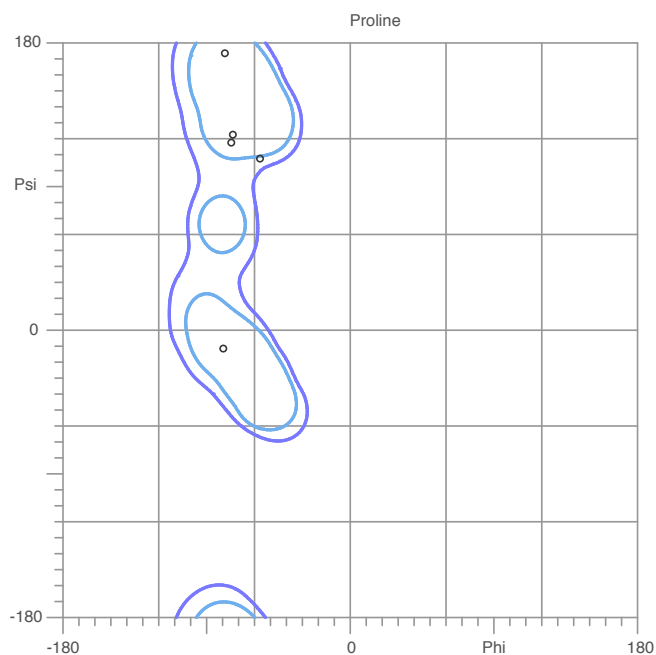
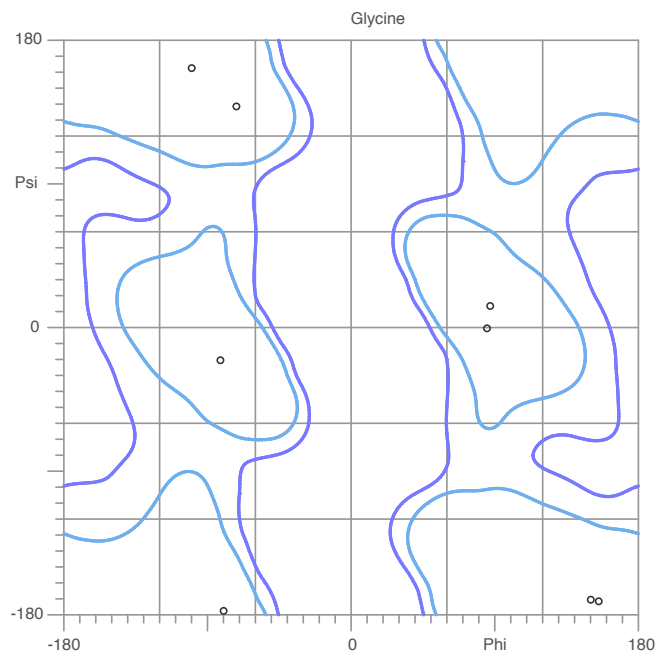
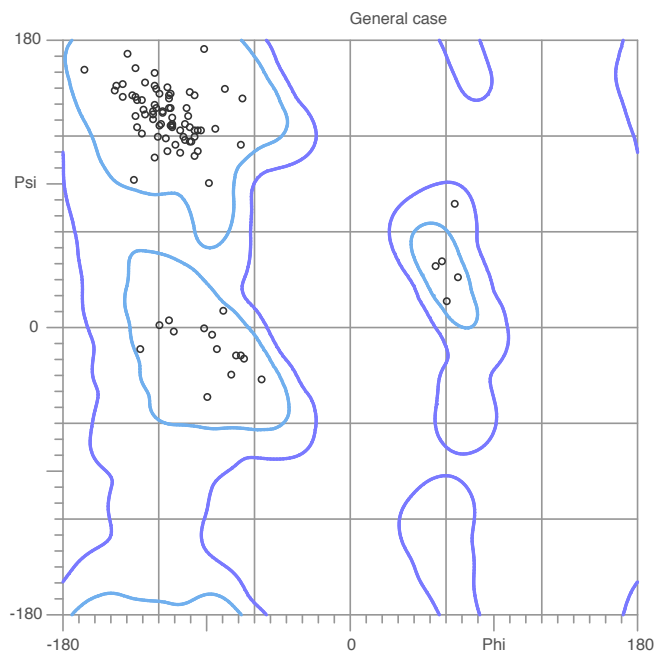
There were no outliers.

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

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 4

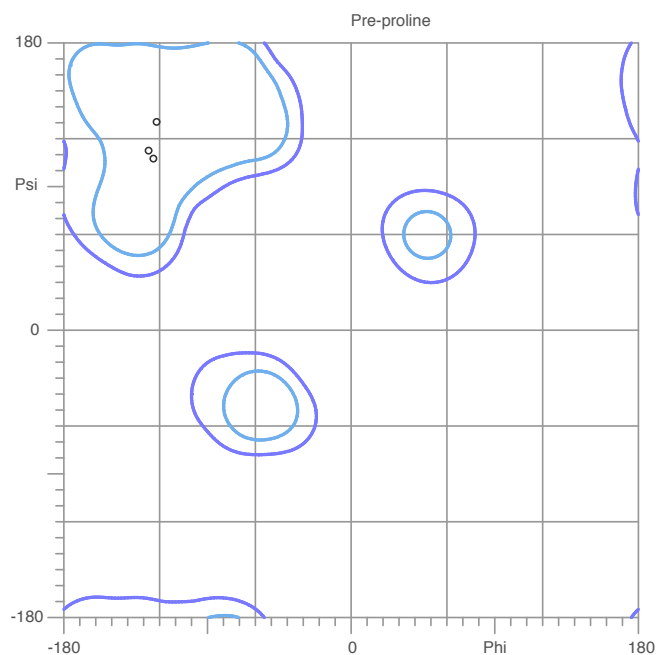
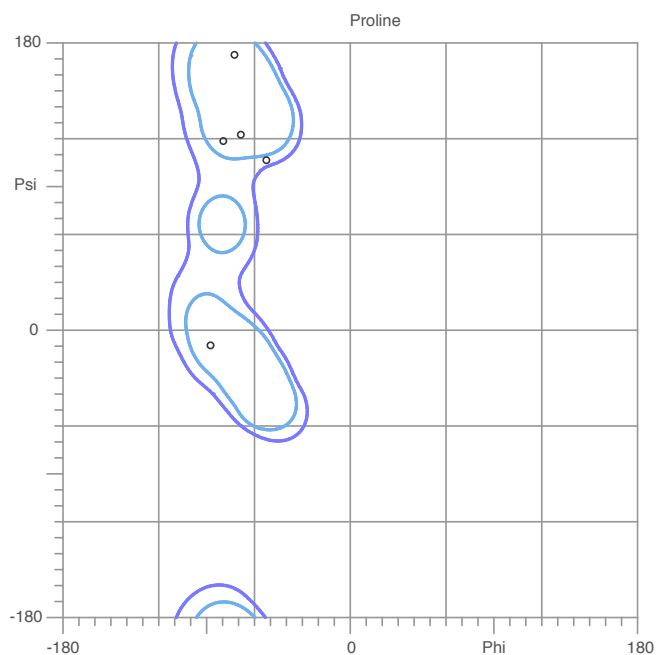
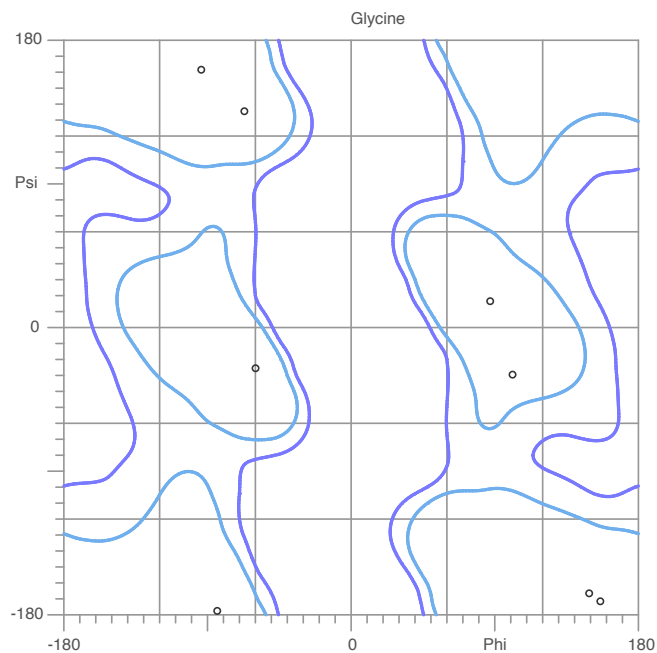
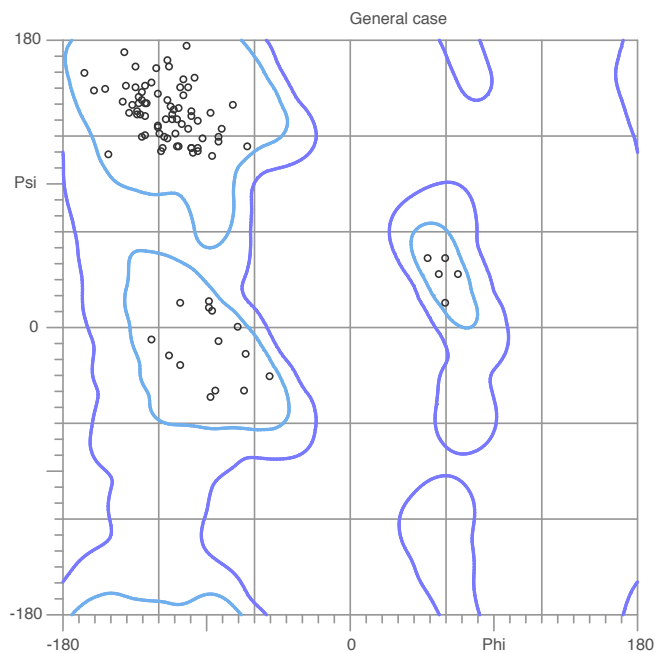


98.1% (104/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 5



99.1% (105/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

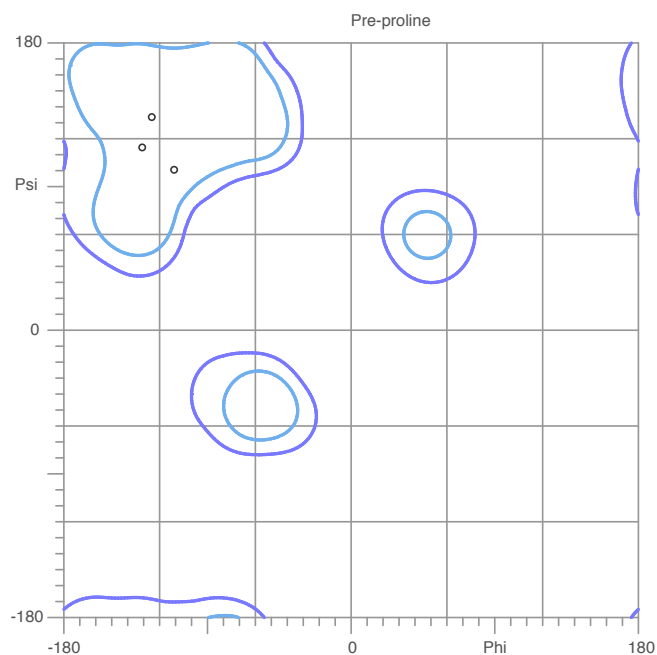
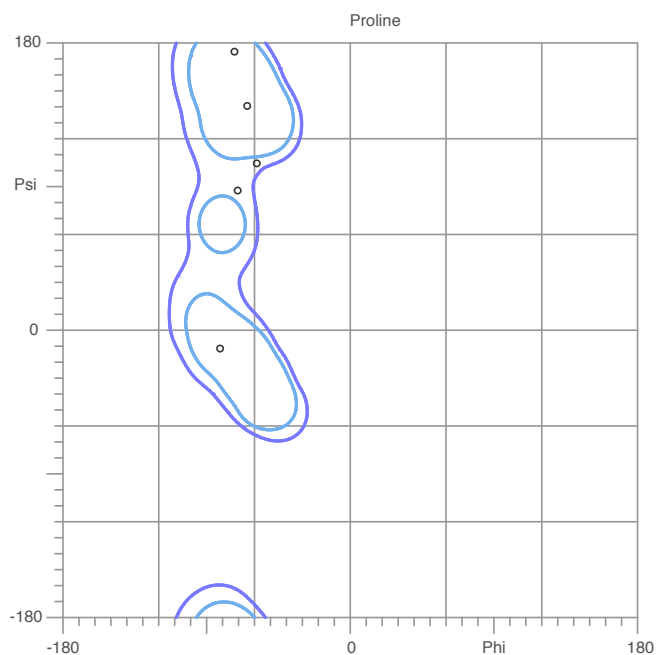
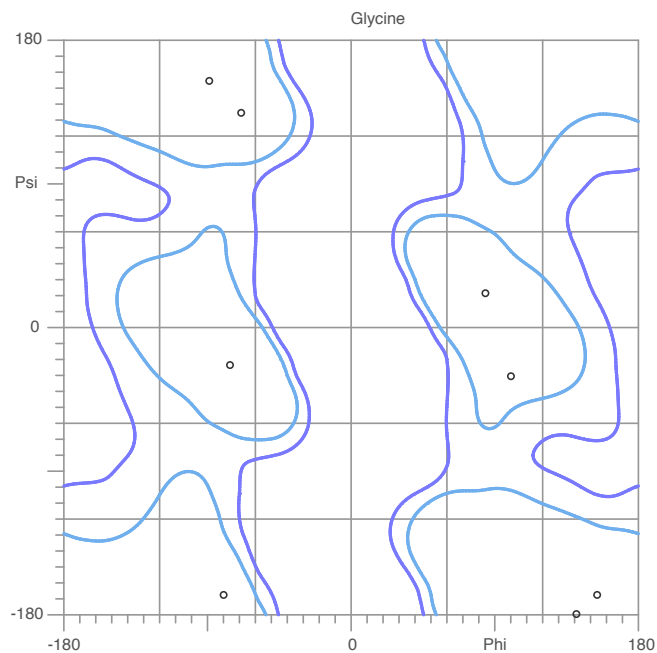
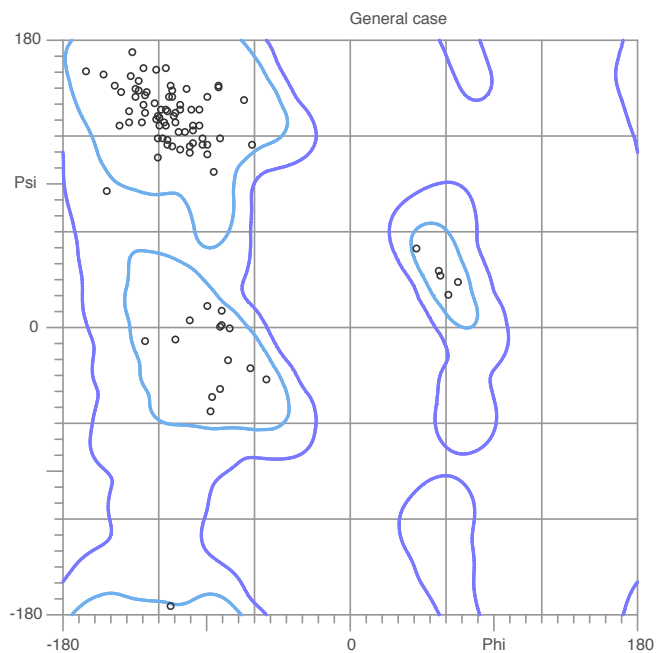
There were no outliers.

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 6



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.

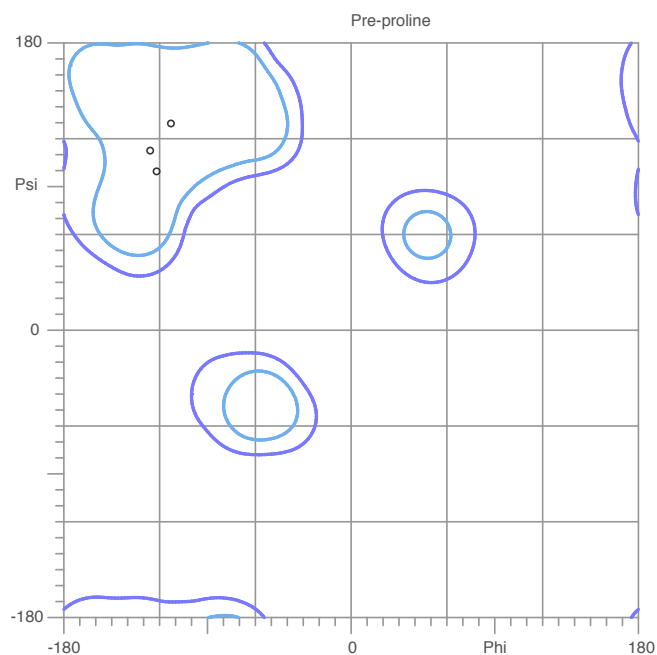
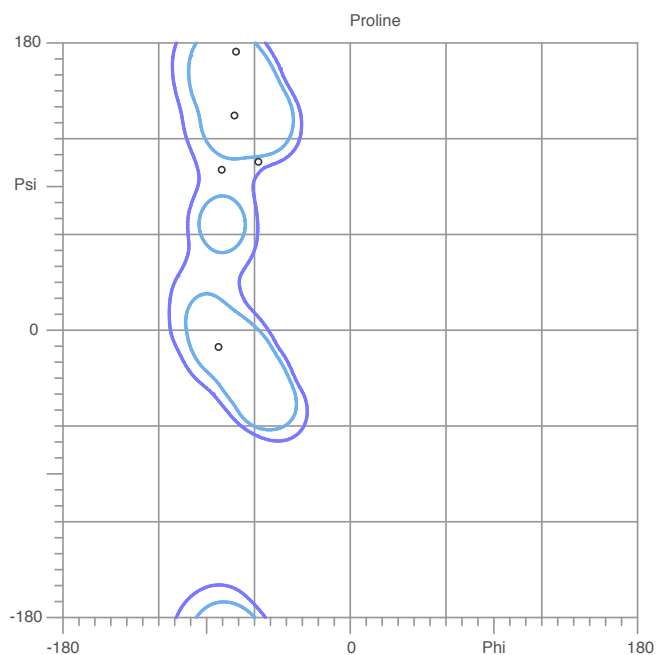
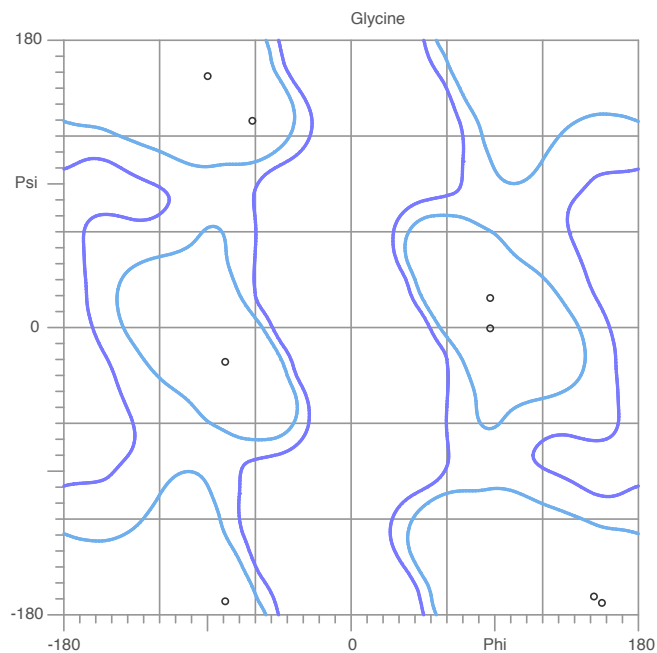
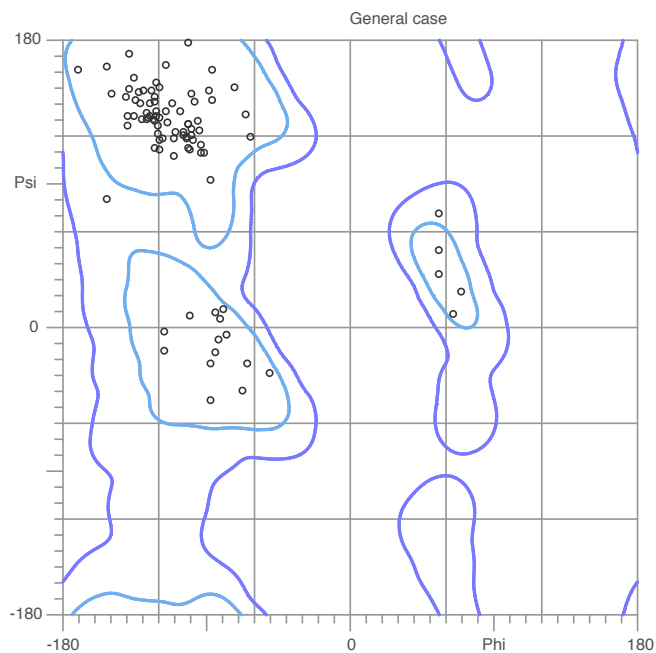
There were no outliers.

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 7



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.

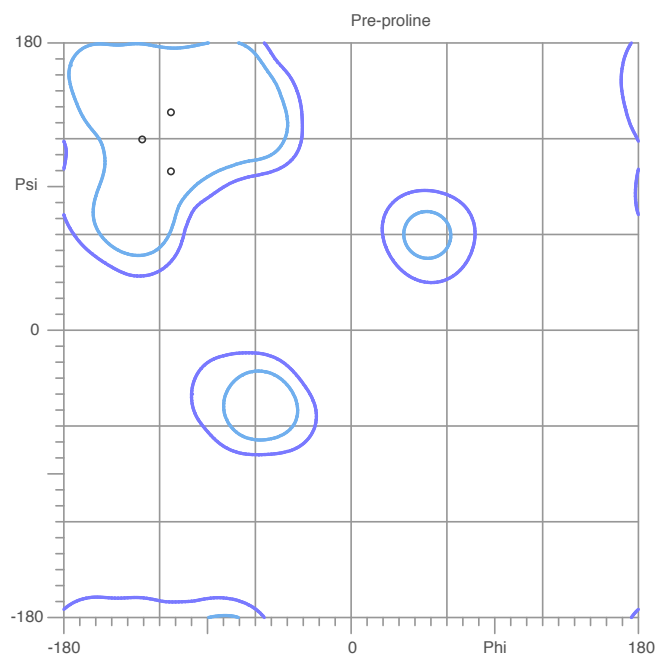
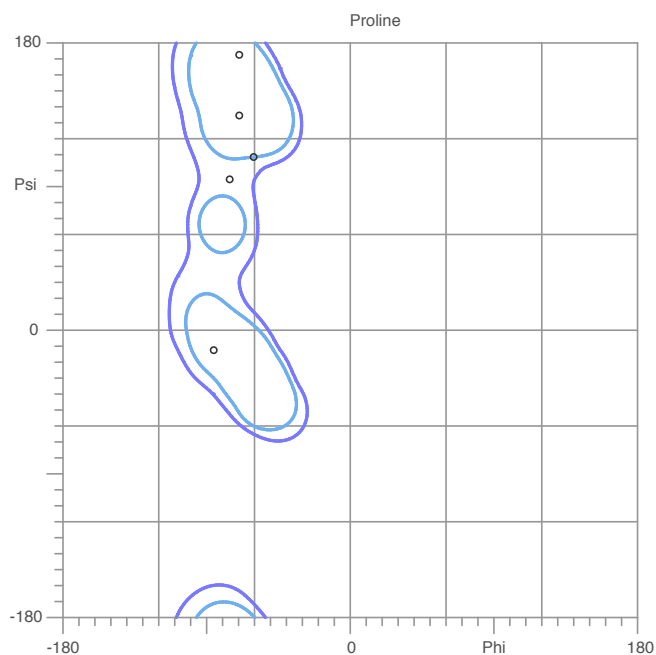
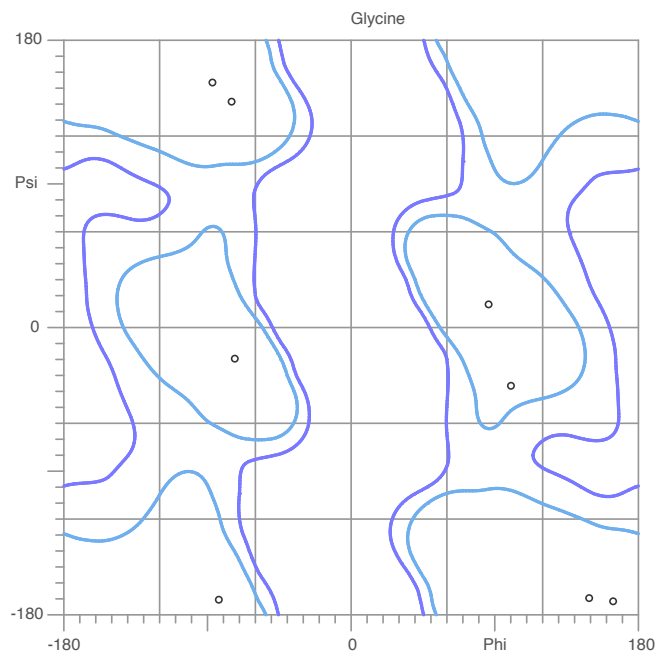
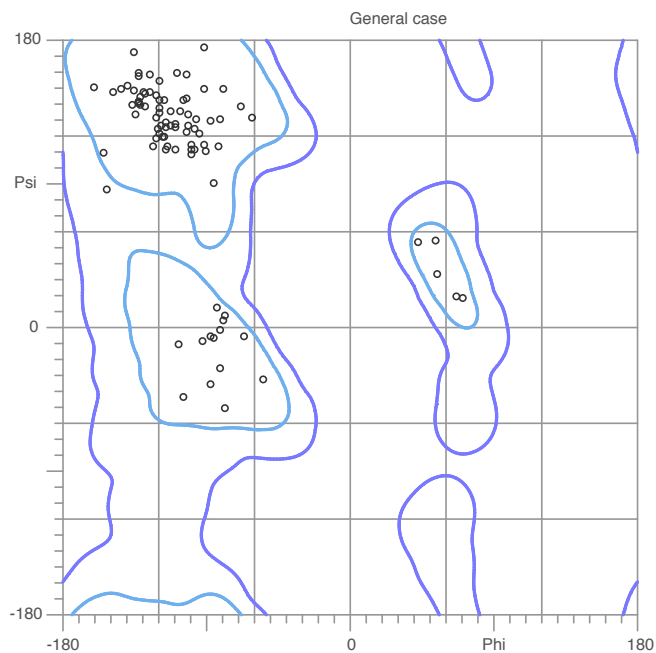
There were no outliers.

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

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 8



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.

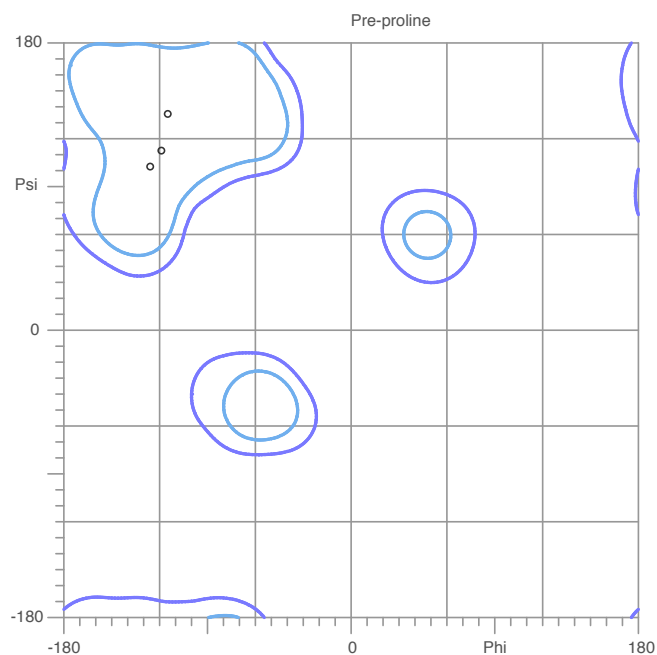
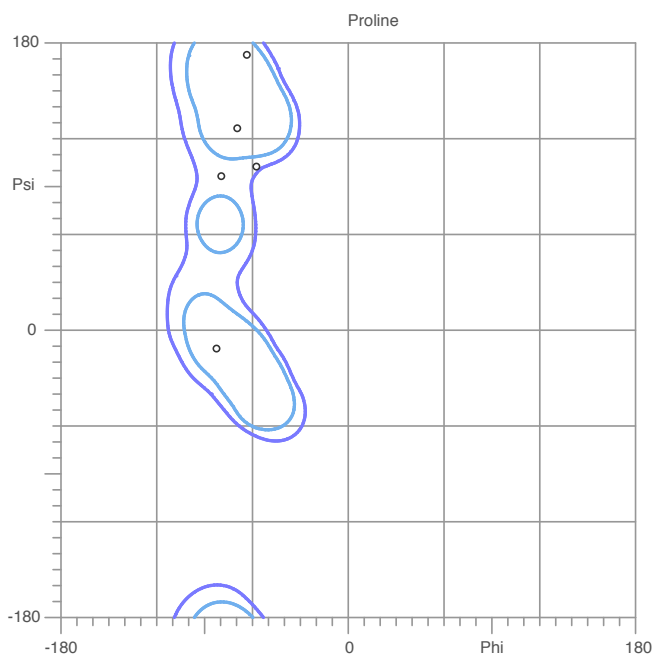
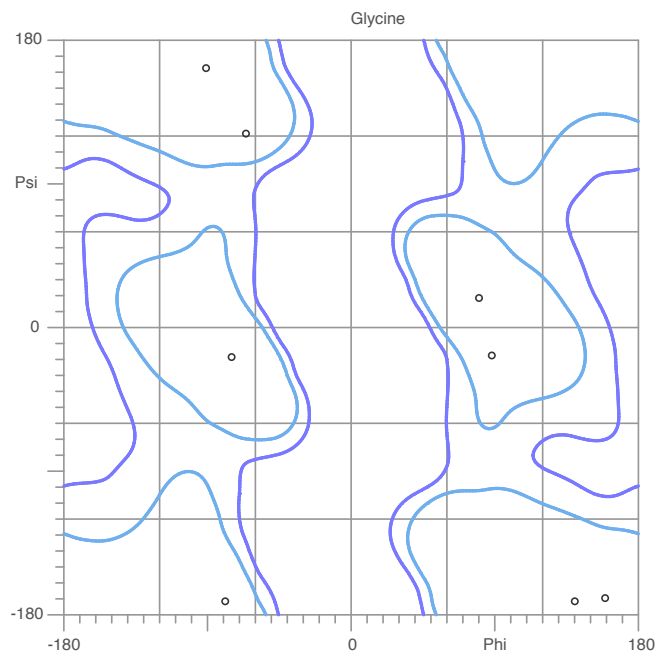
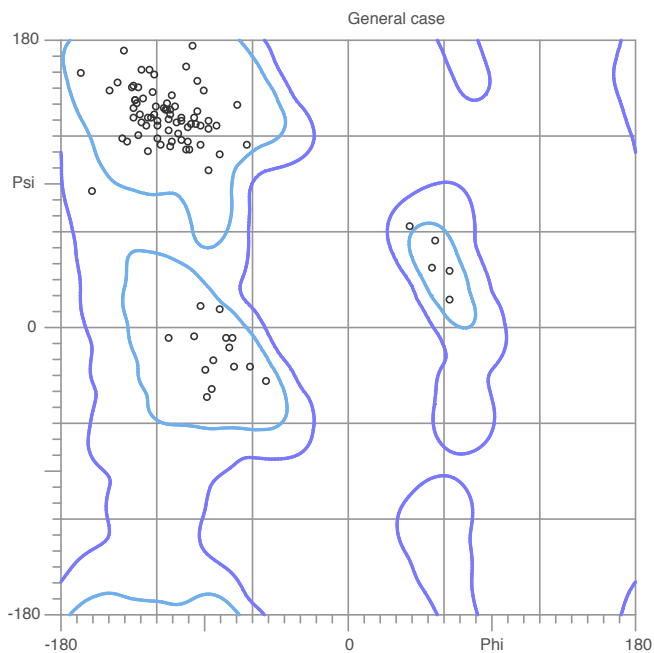
There were no outliers.

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

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 9

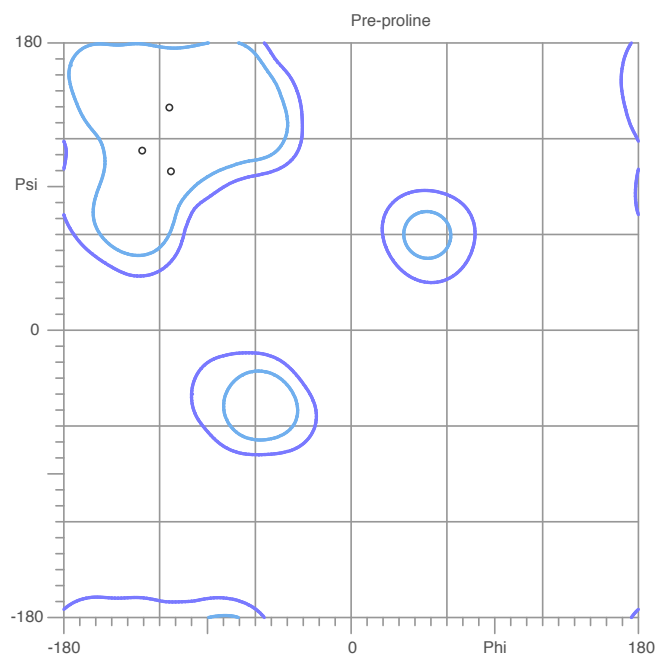
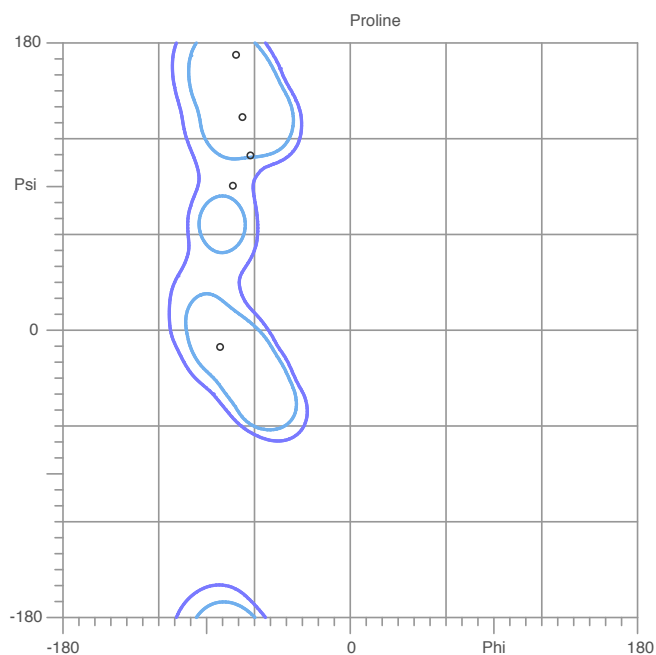
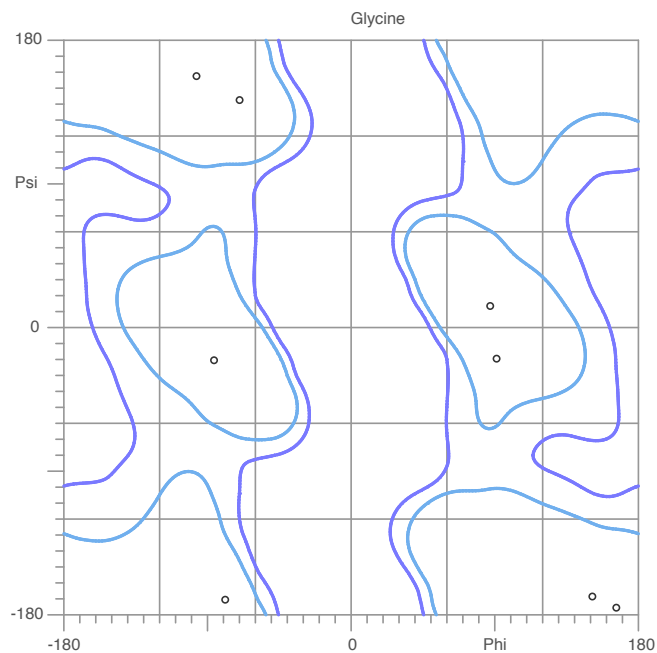
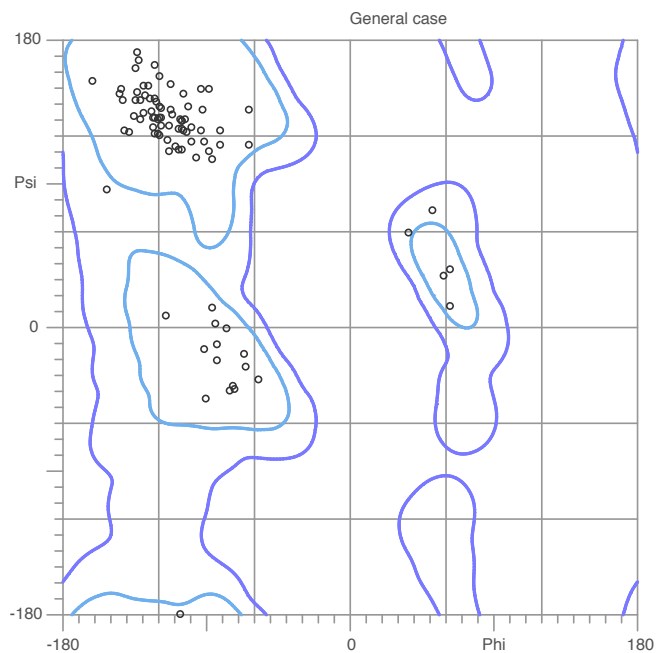


96.2% (102/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 10



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.

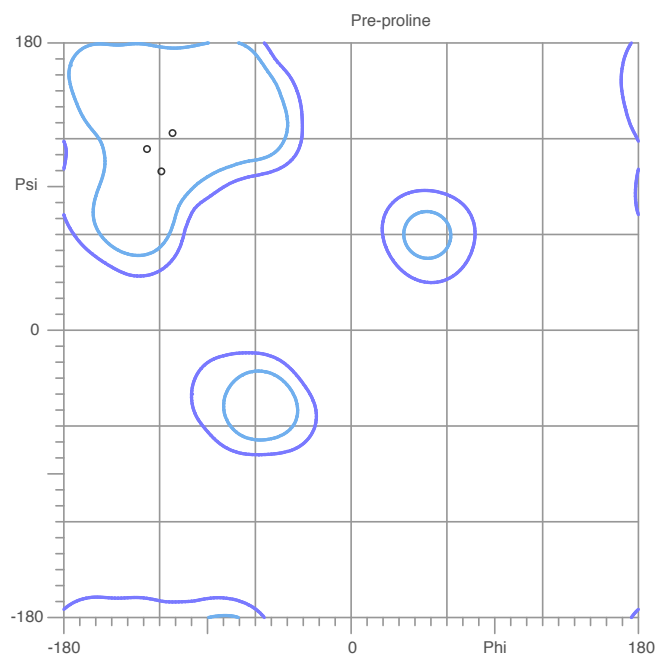
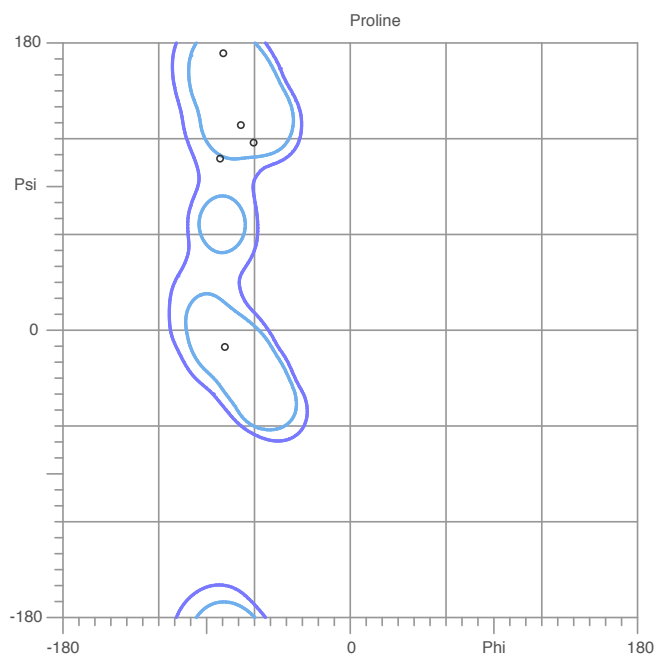
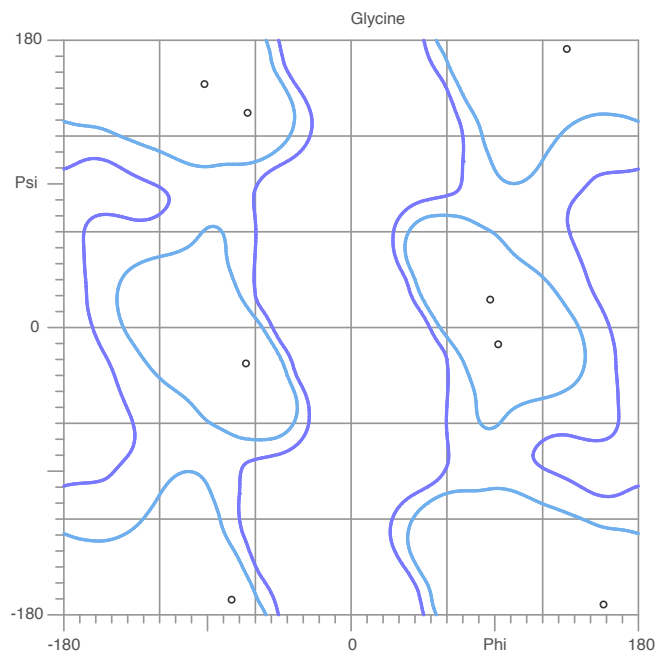
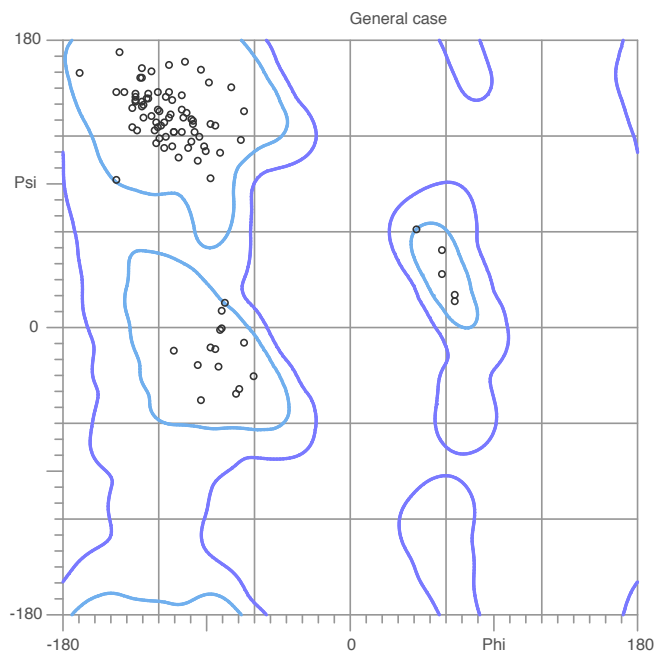
There were no outliers.

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 11



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.

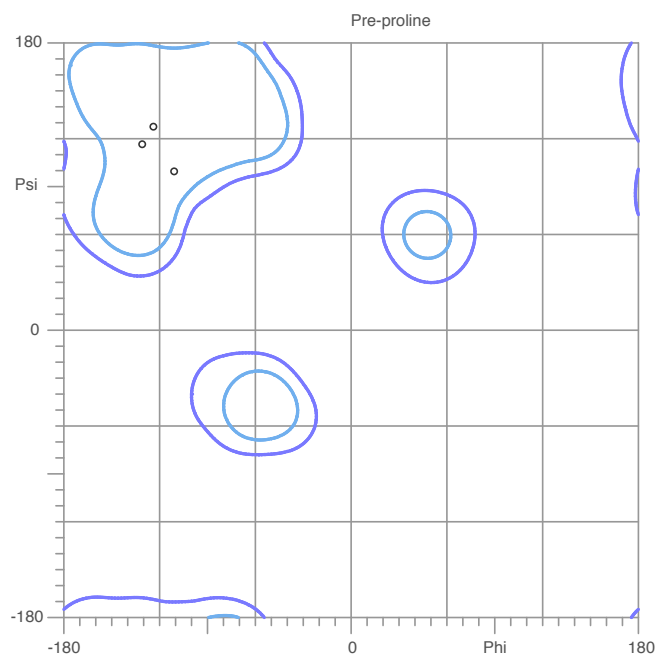
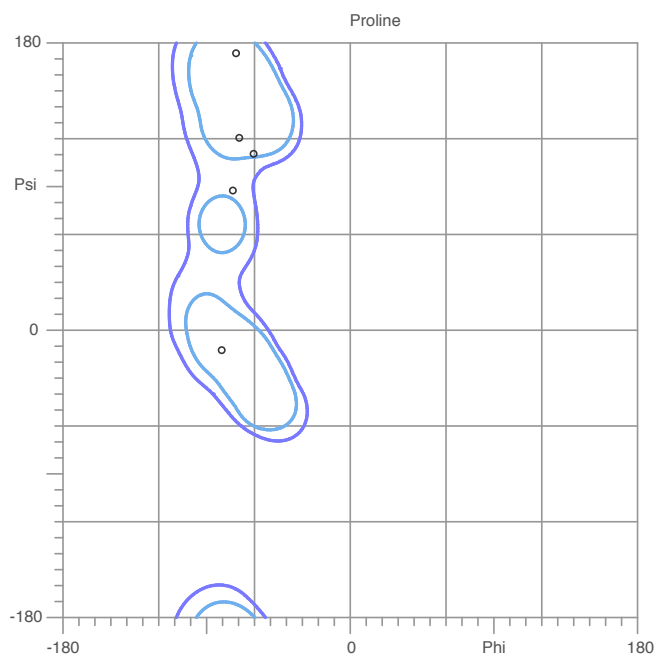
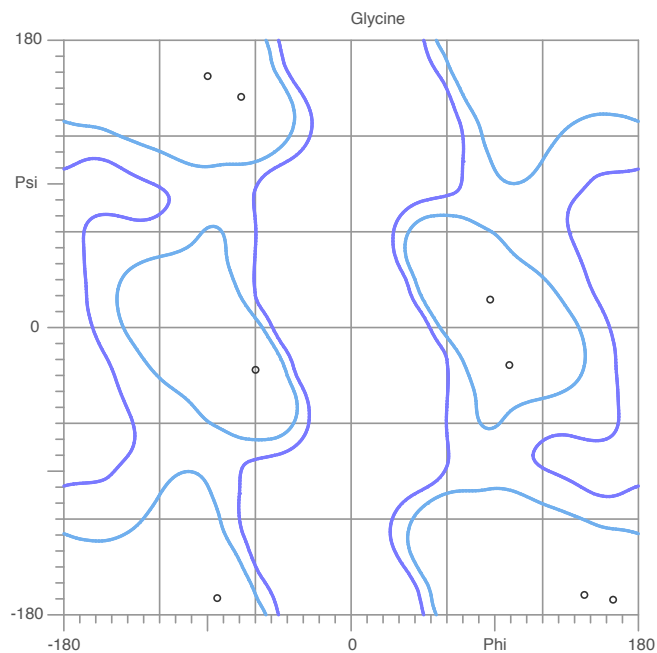
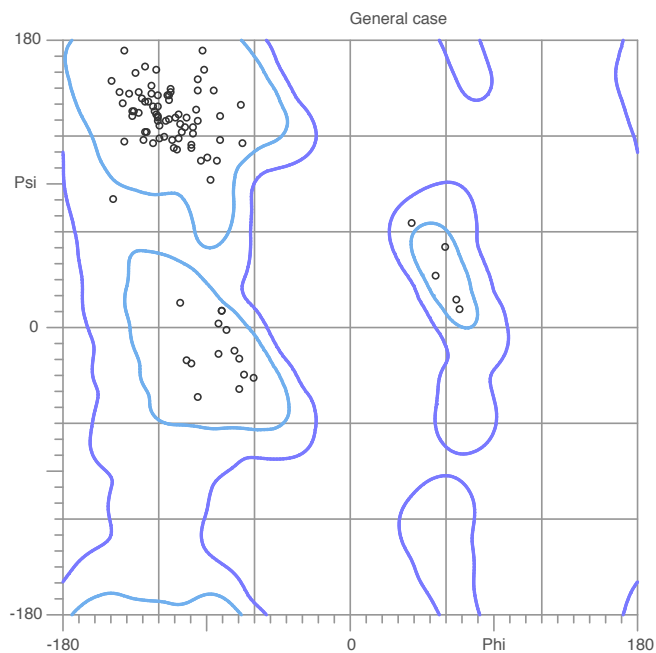
There were no outliers.

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 12



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.

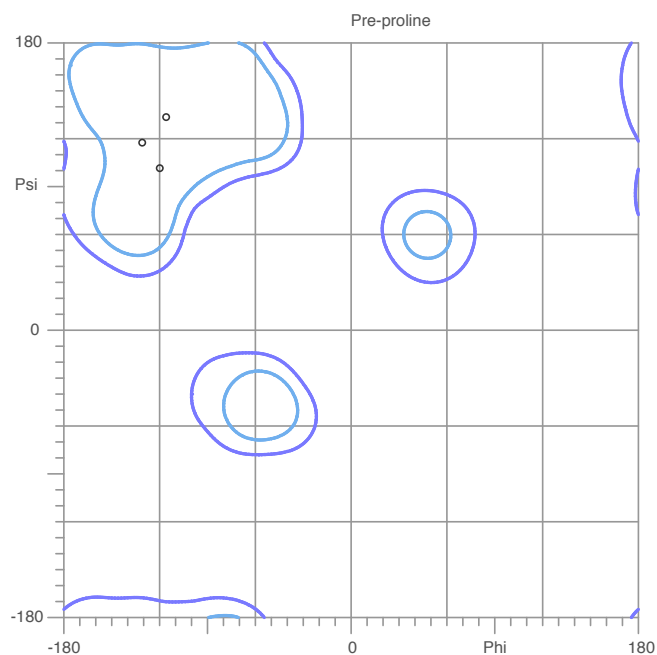
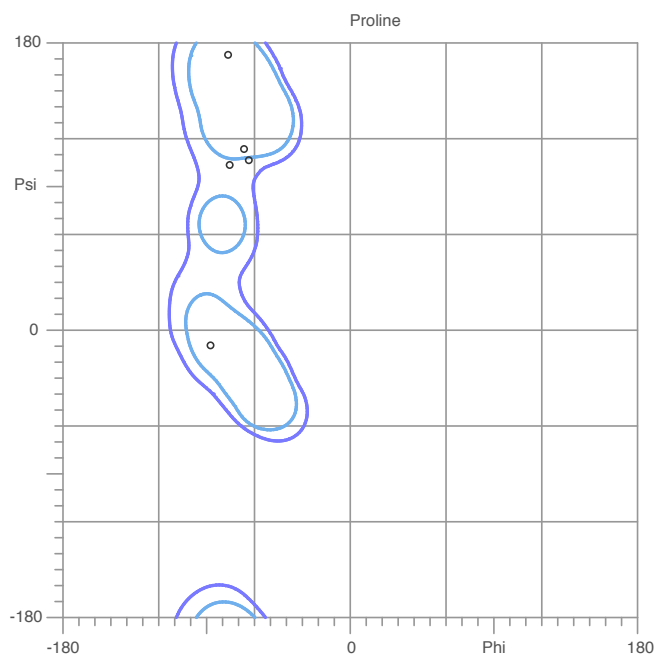
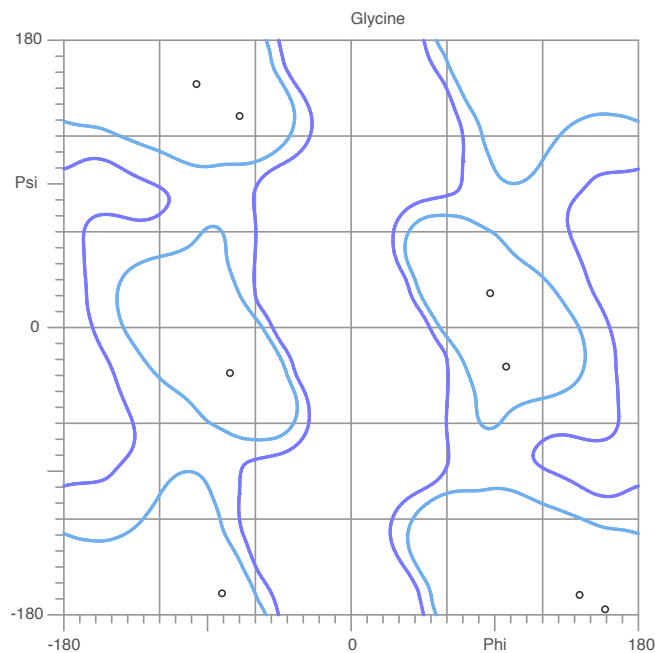
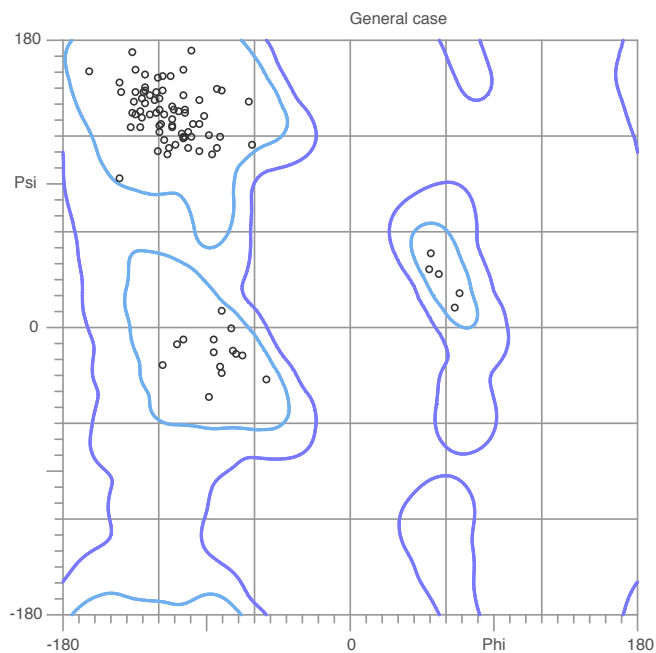
There were no outliers.

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

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

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 13



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.

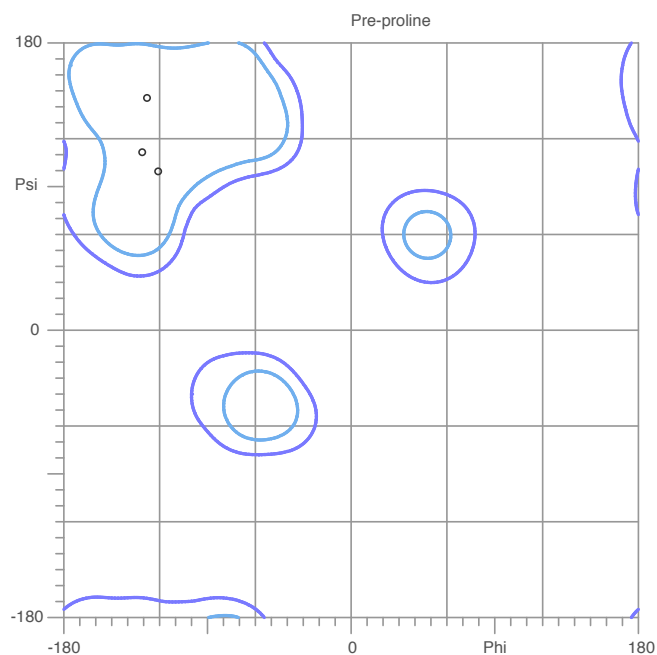
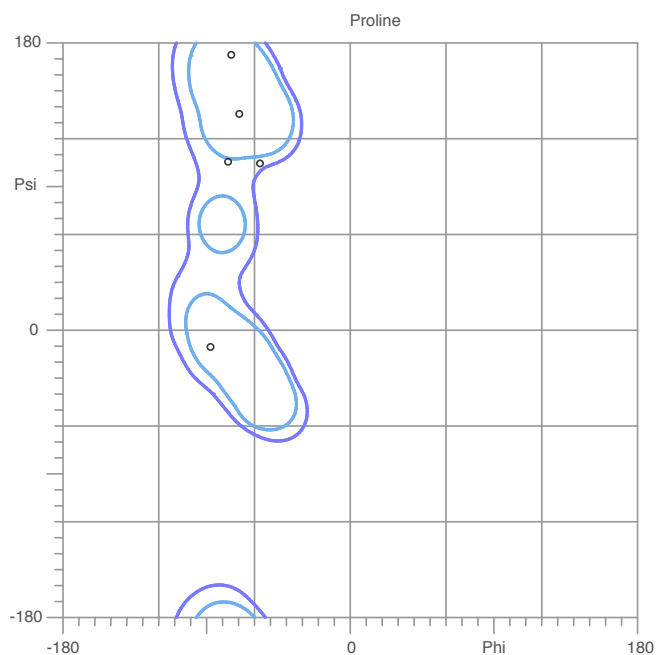
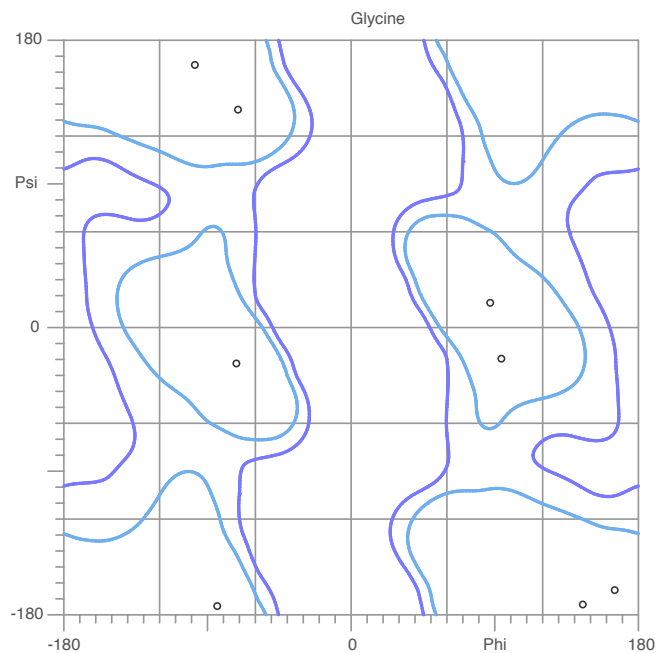
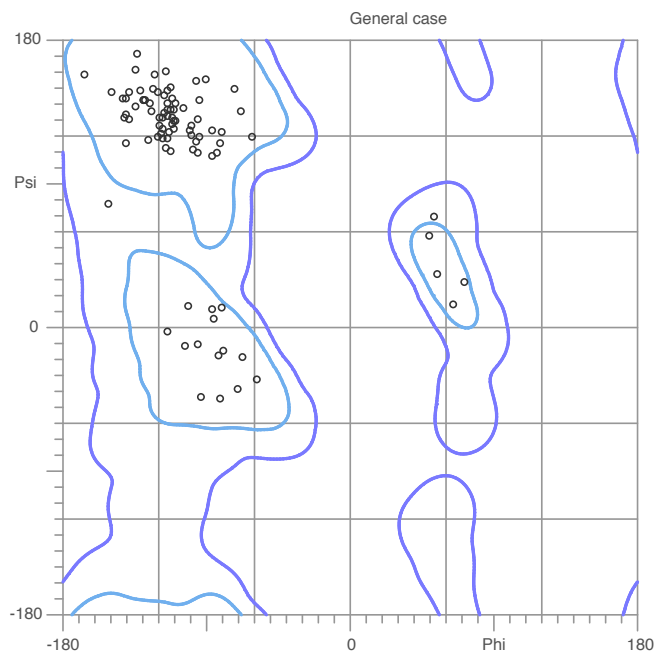
There were no outliers.

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

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 14



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.

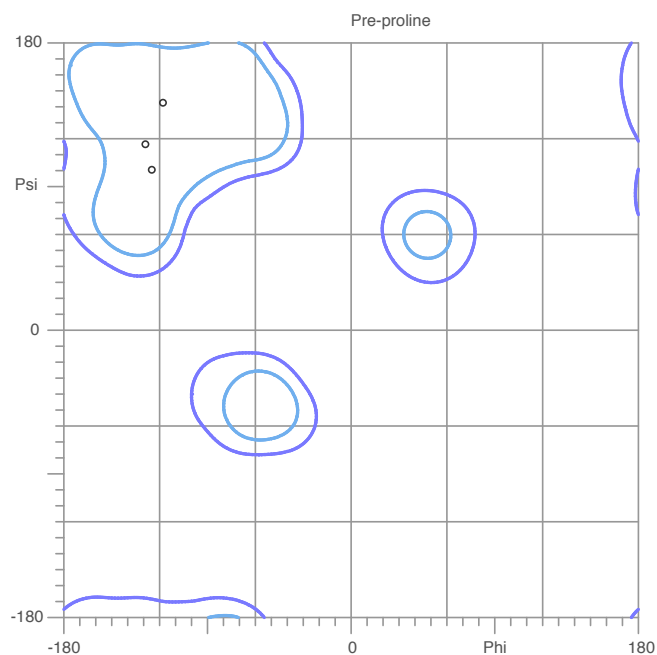
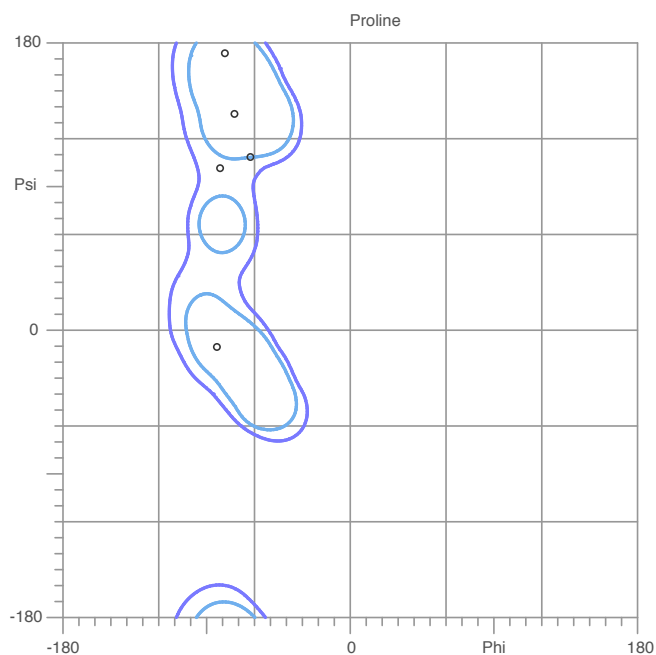
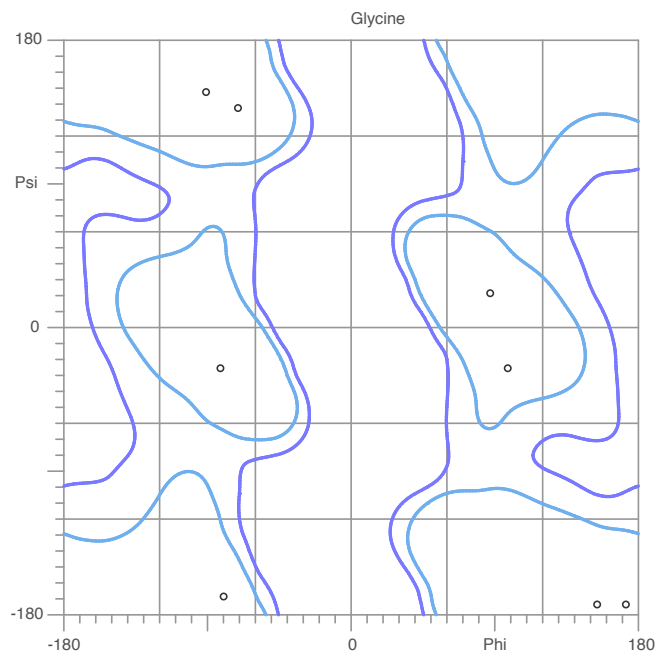
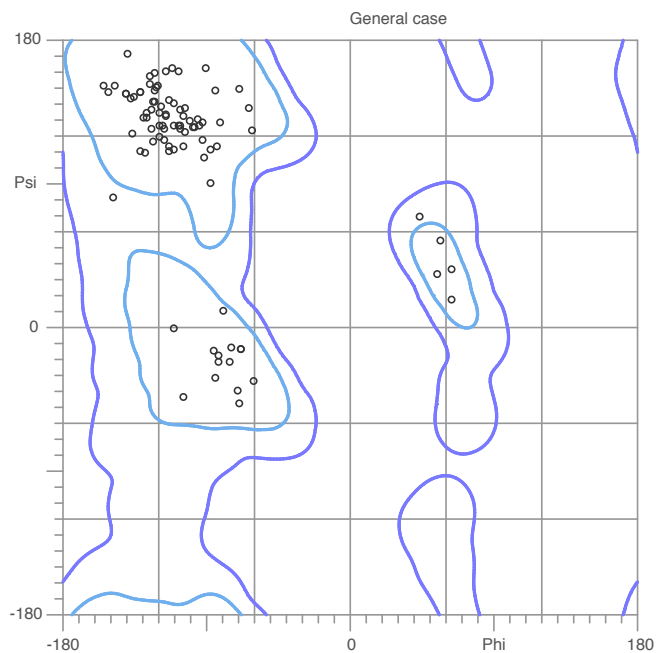
There were no outliers.

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

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.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.

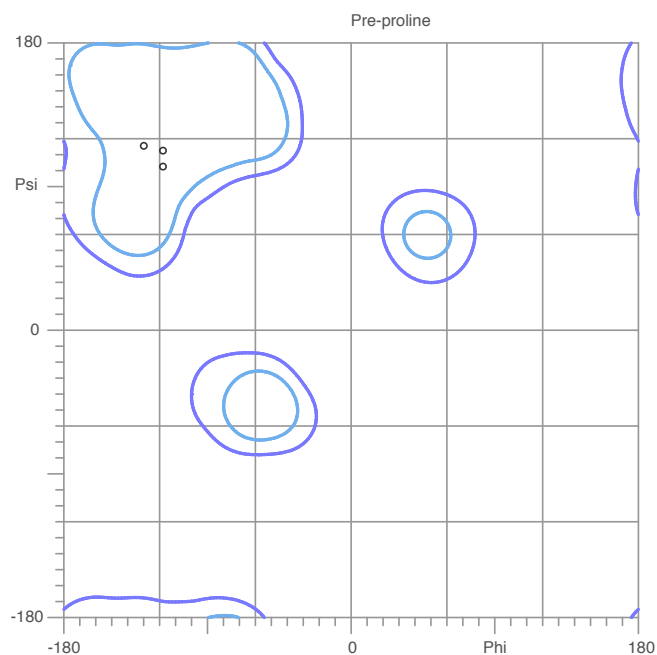
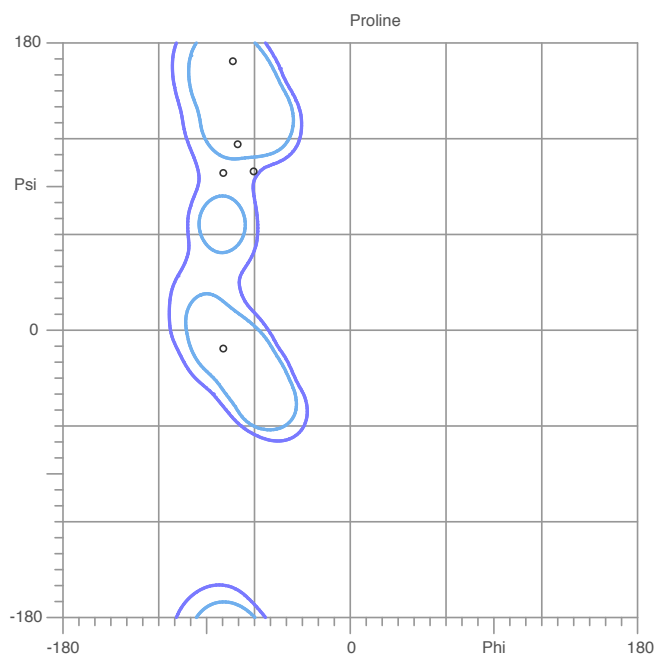
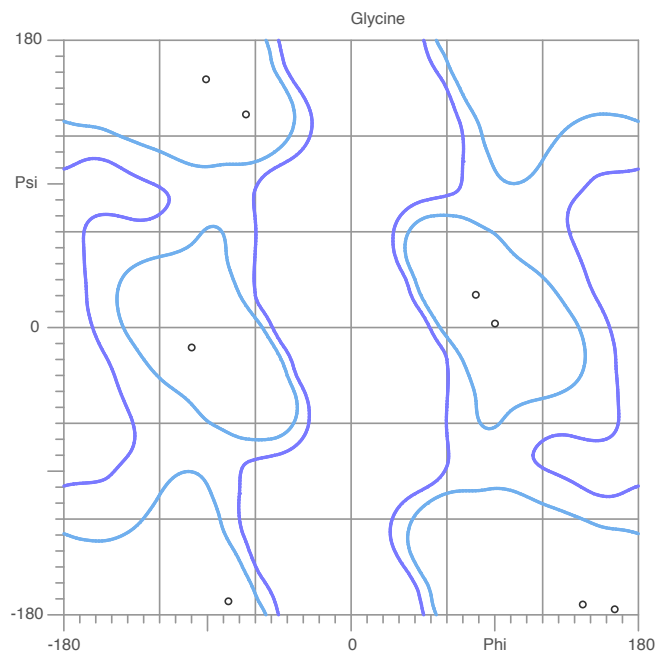
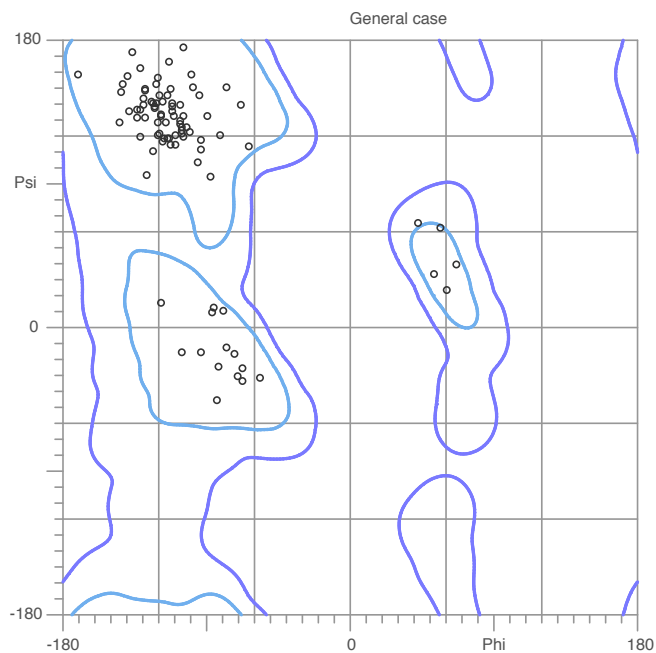
There were no outliers.

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

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

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 16



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.

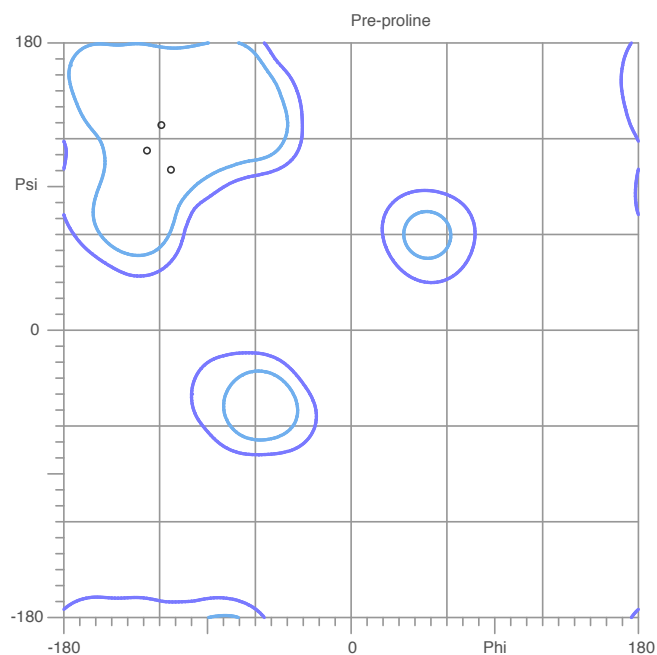
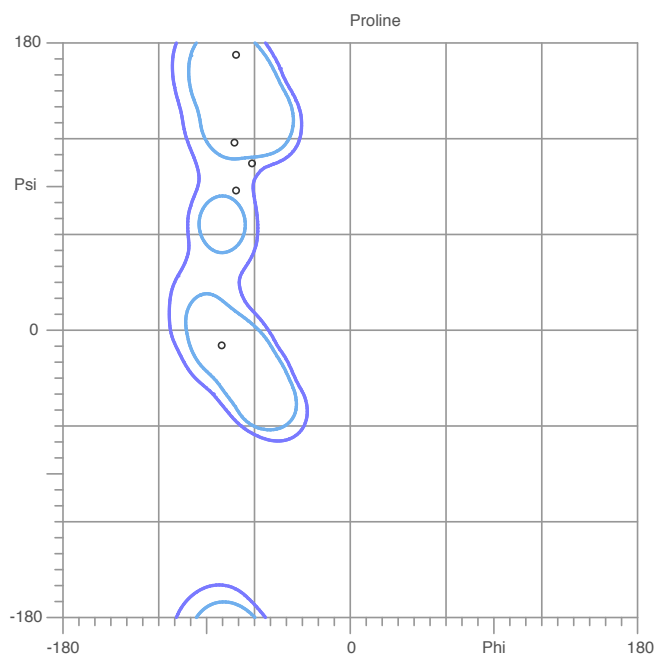
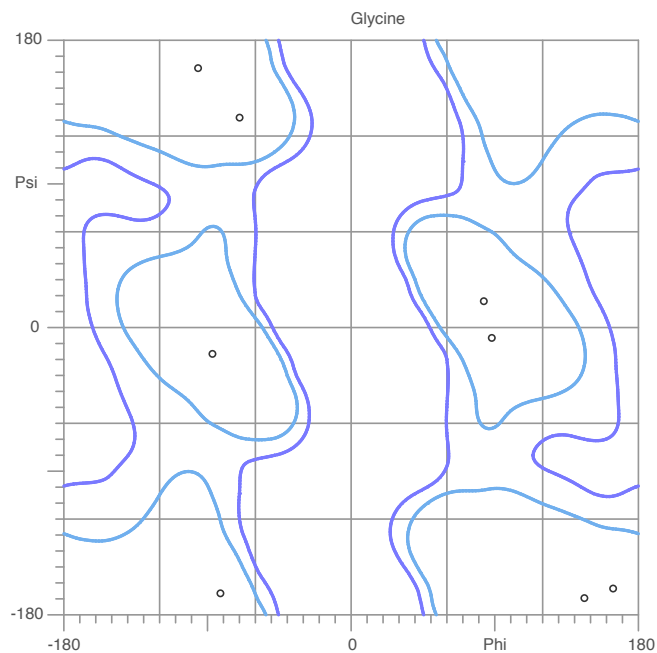
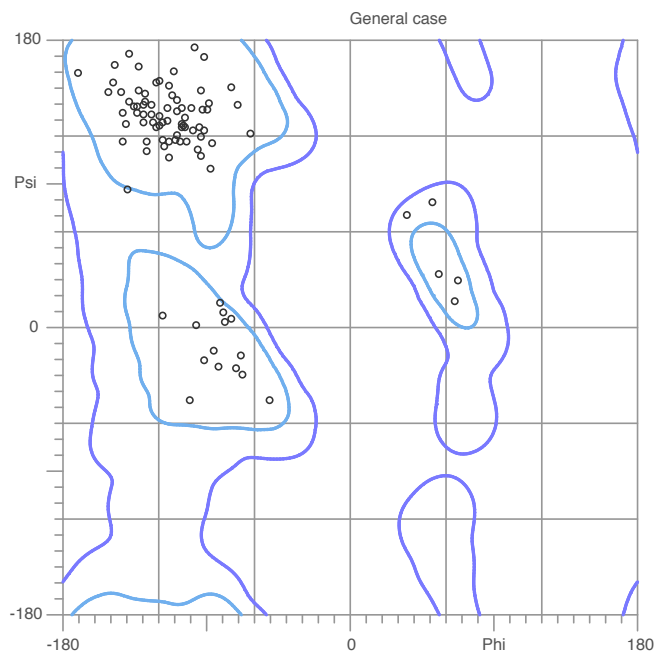
There were no outliers.

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

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MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 17



95.3% (101/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

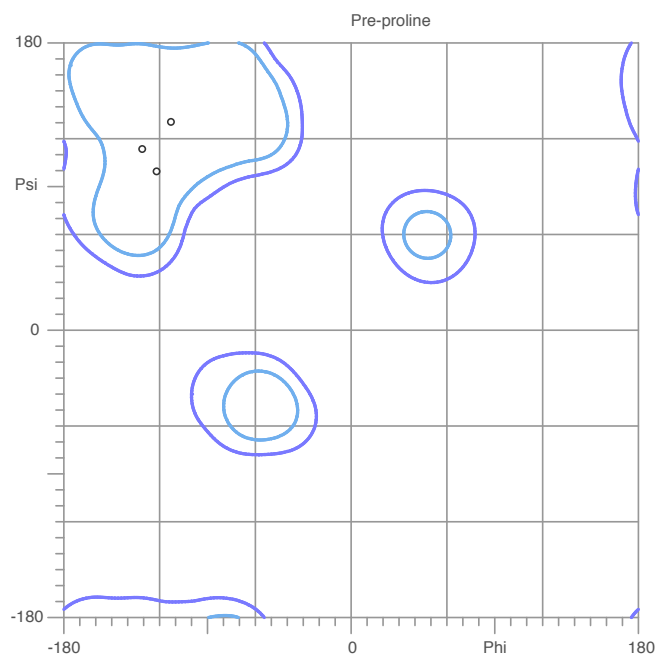
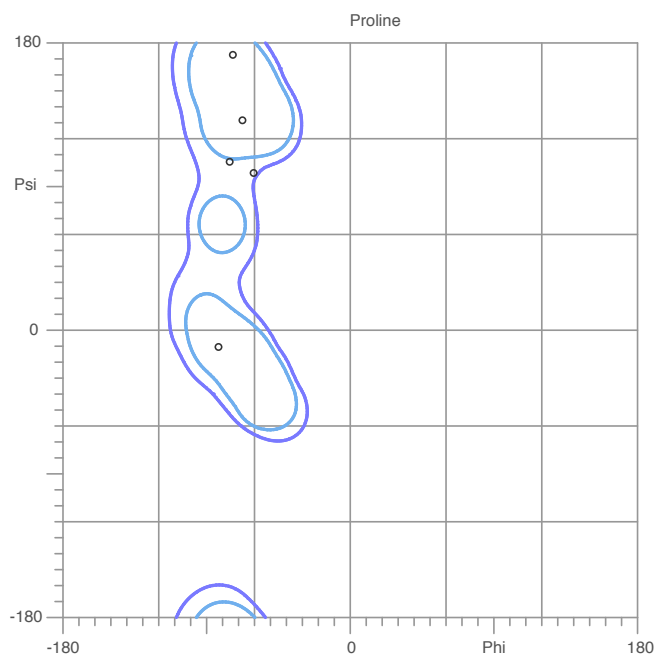
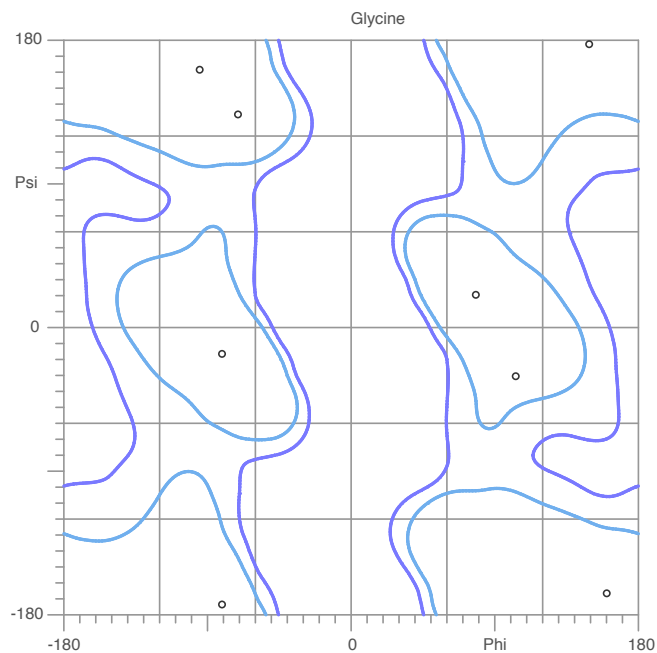
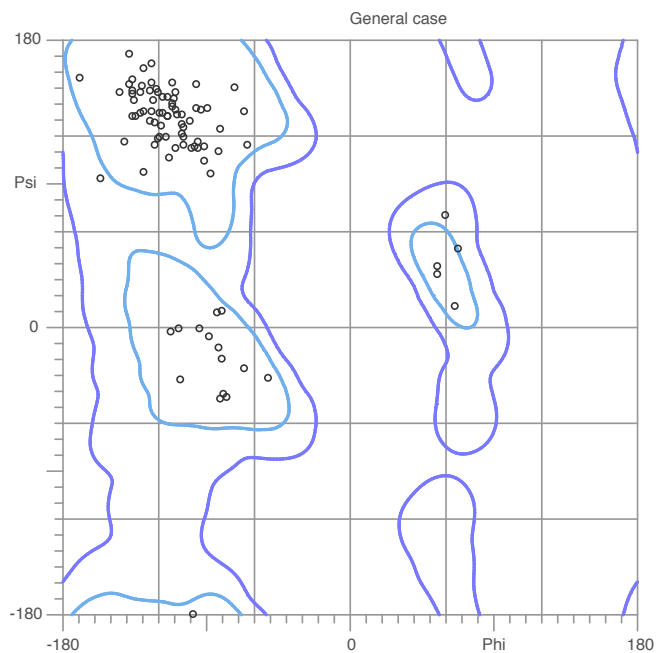
There were no outliers.

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

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

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 18



95.3% (101/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

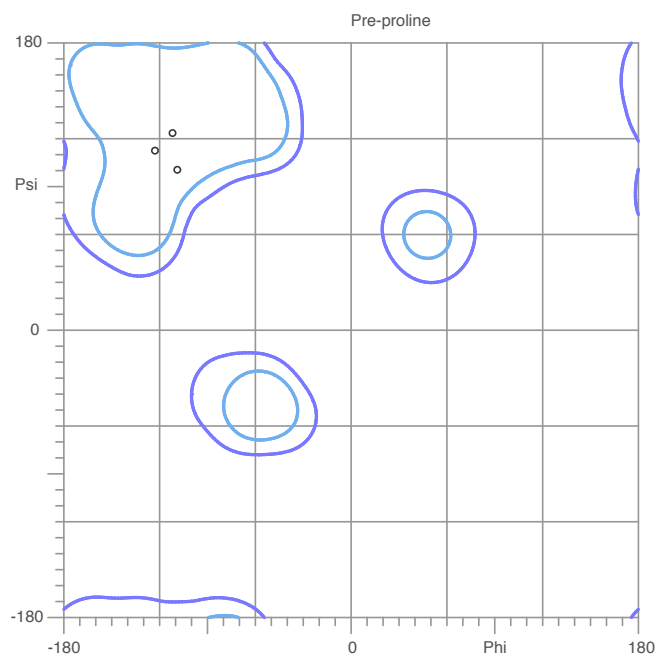
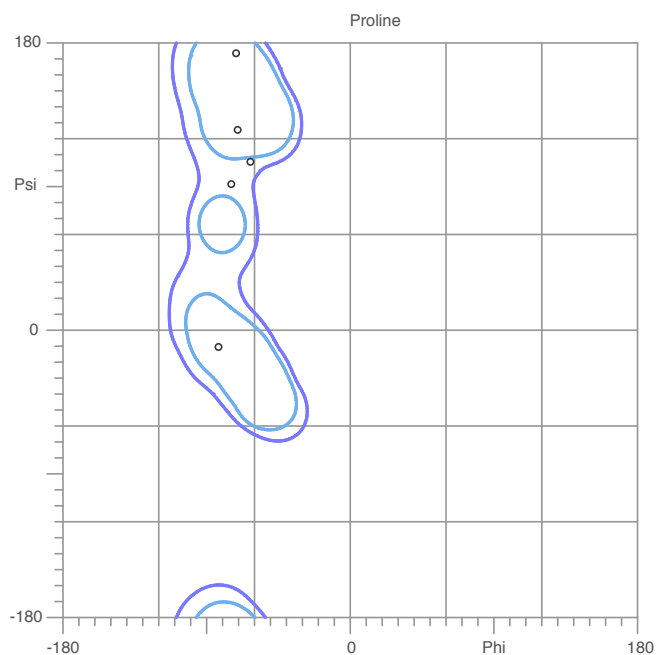
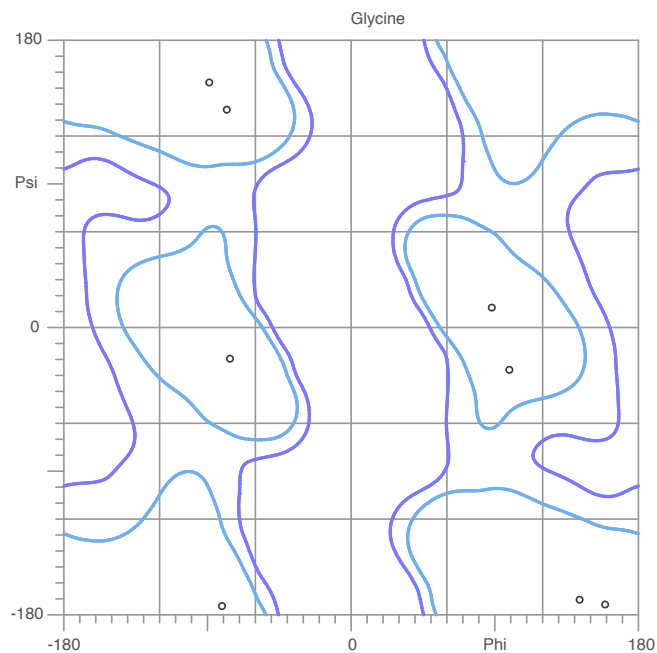
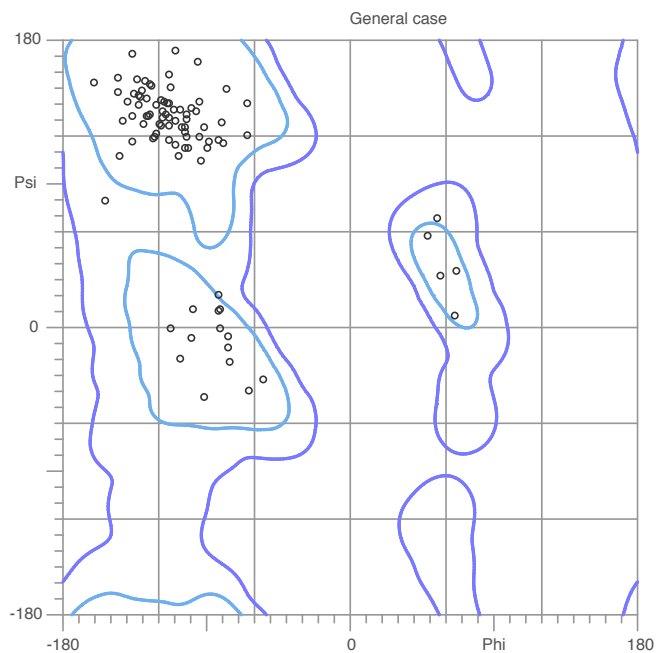
There were no outliers.

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

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

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 19



95.3% (101/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

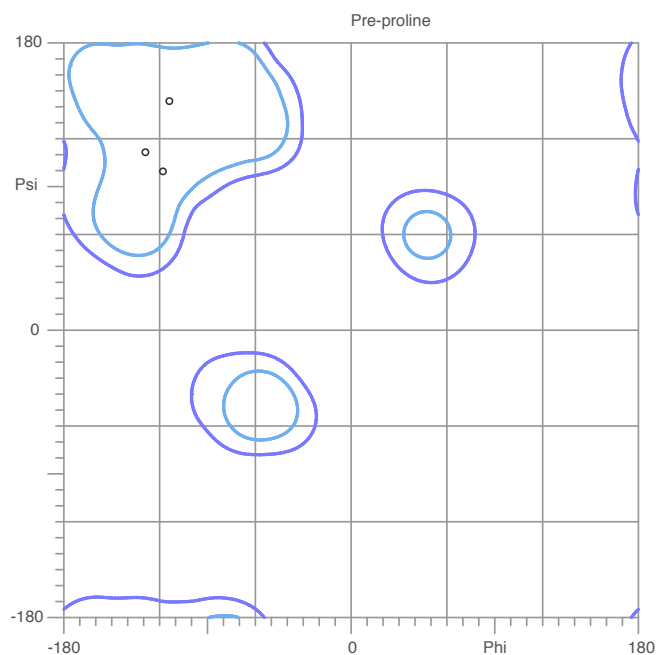
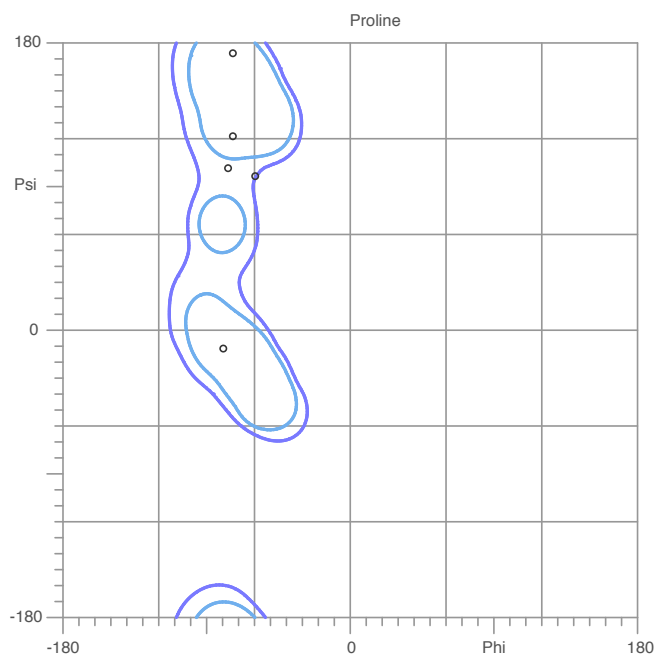
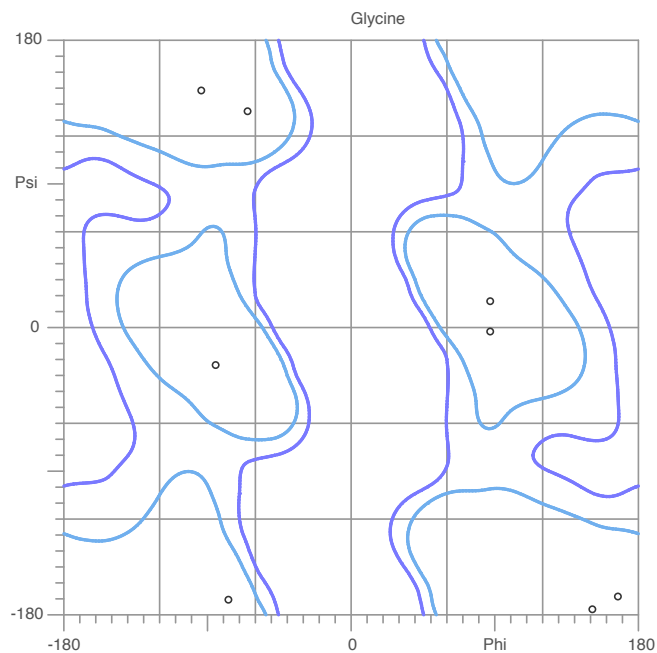
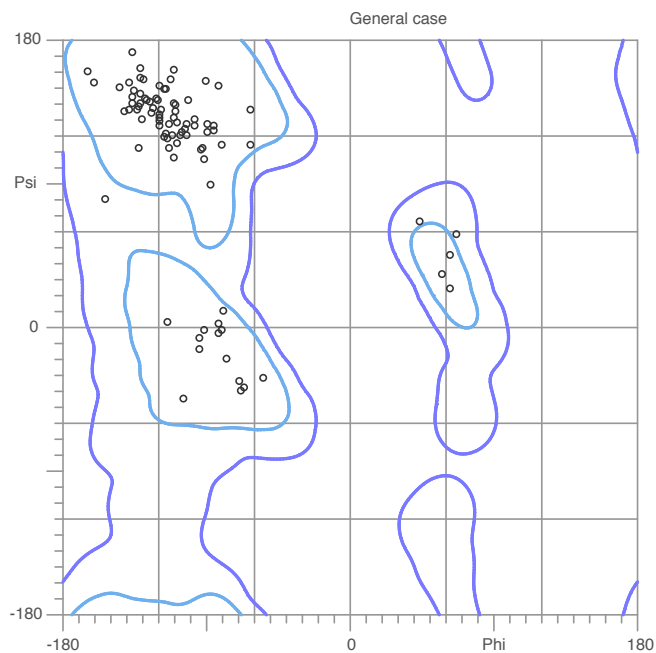
There were no outliers.

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

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

MolProbity Ramachandran analysis

PFR193A_NMR_em_bcr3.pdb, model 20



95.3% (101/106) 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)