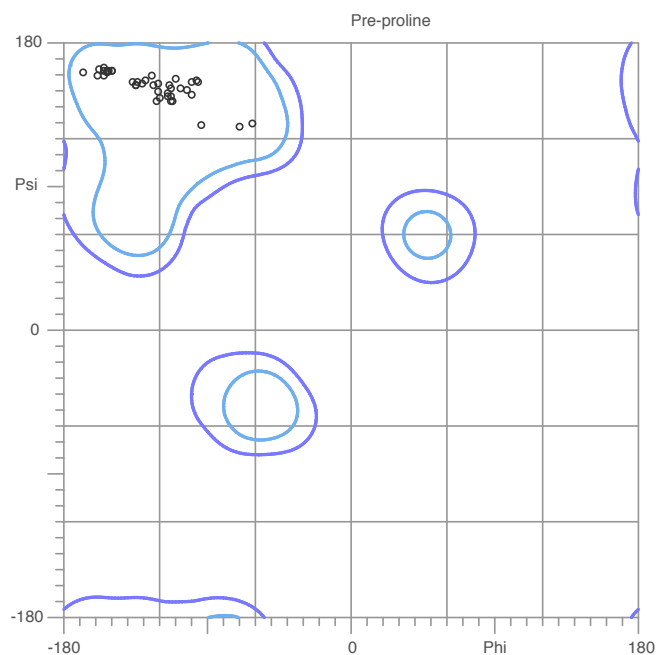
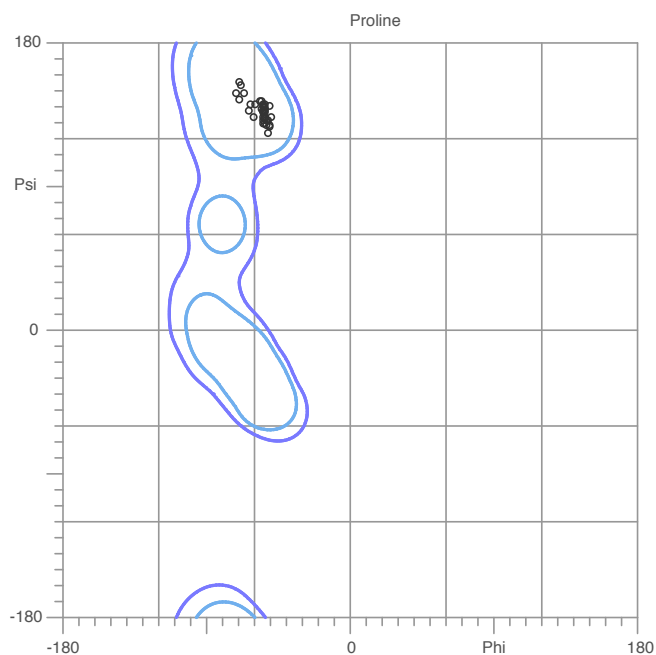
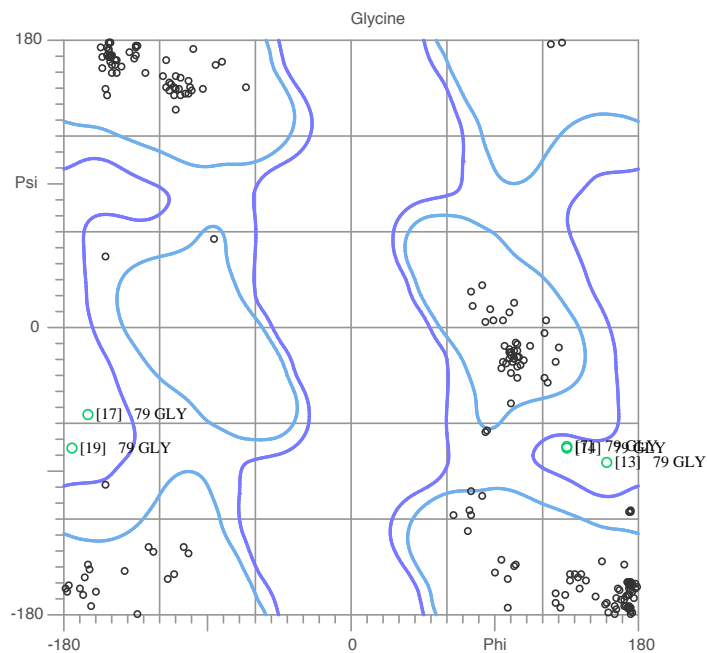
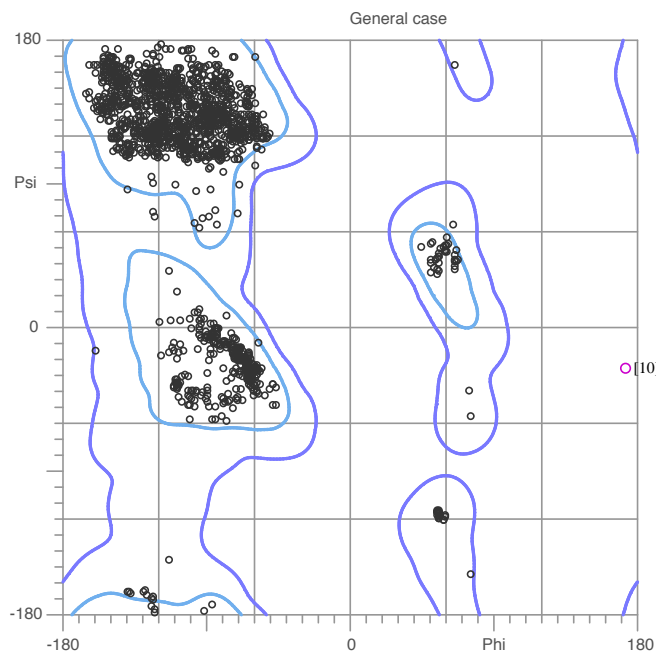


# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, all models



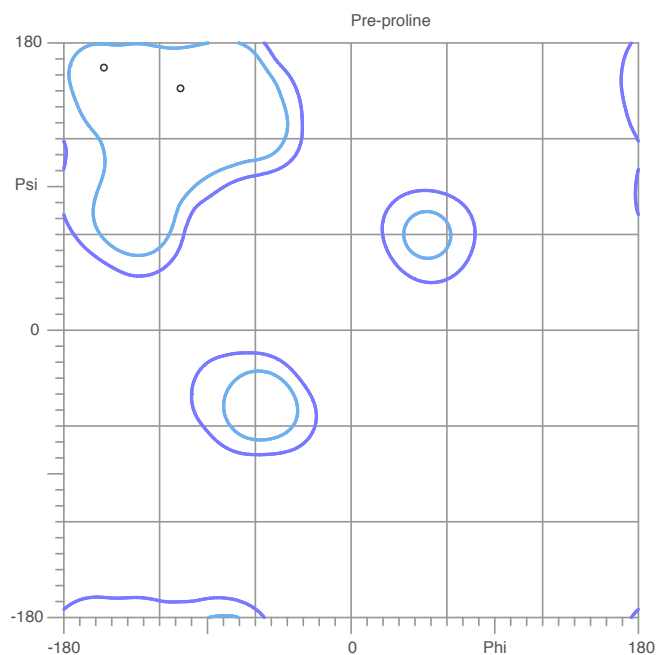
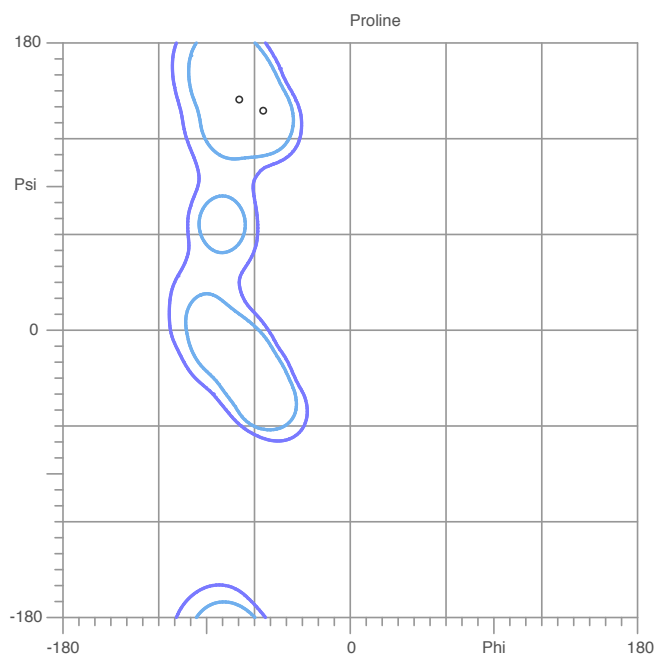
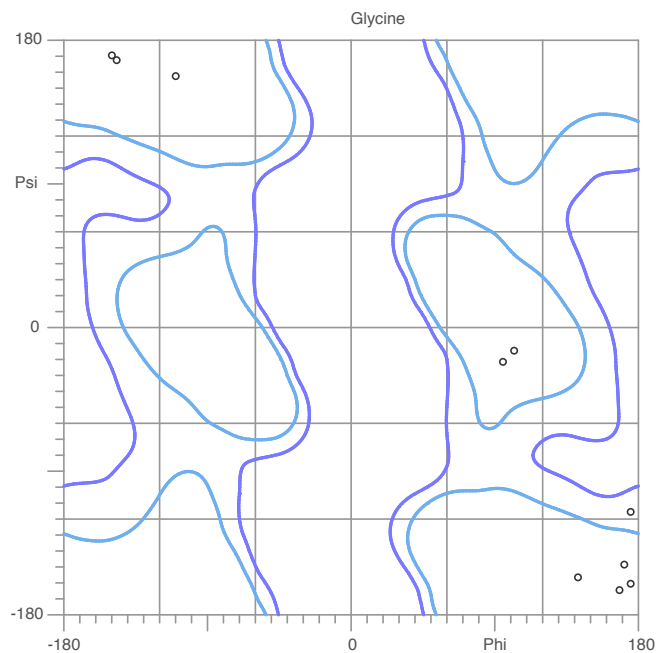
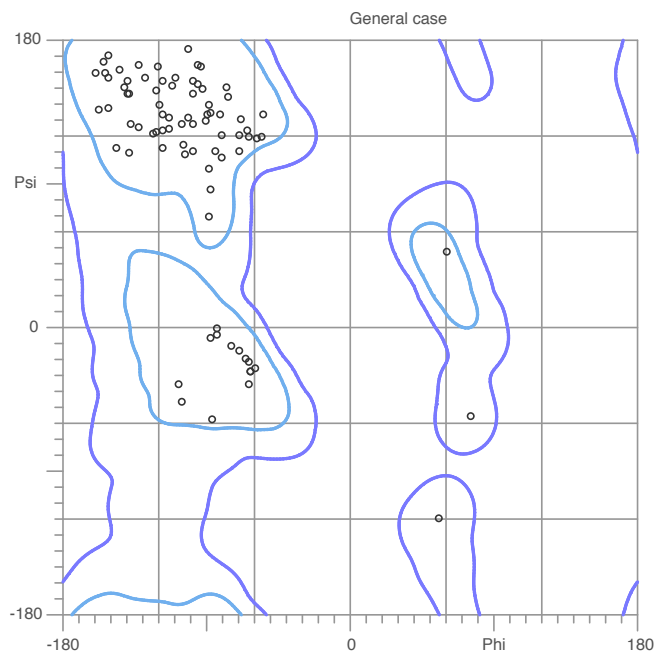
97.1% (1865/1920) of all residues were in favored (98%) regions.  
99.7% (1914/1920) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):  
[7] 79 GLY (135.0, -75.0)

[10] 81 SER (172.1, -25.0)  
[13] 79 GLY (160.6, -85.0)  
[14] 79 GLY (135.0, -75.0)  
[17] 79 GLY (-165.0, -54.9)  
[19] 79 GLY (-175.0, -75.0)

# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 1



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.

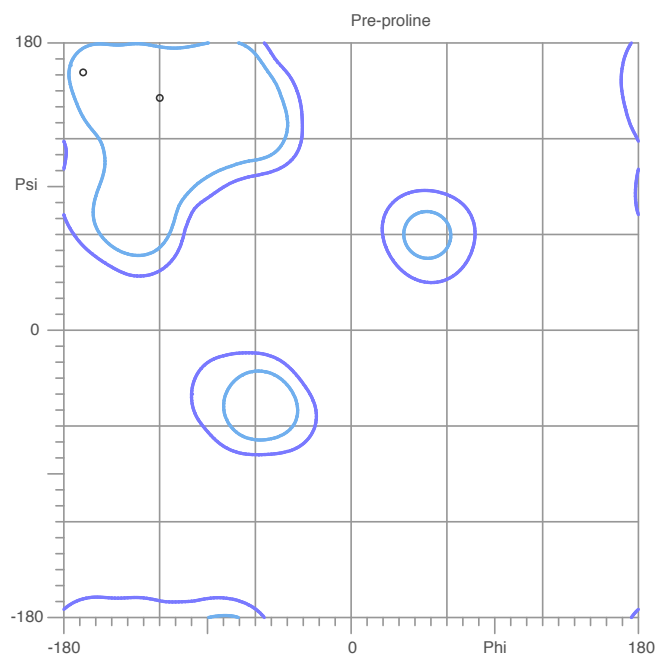
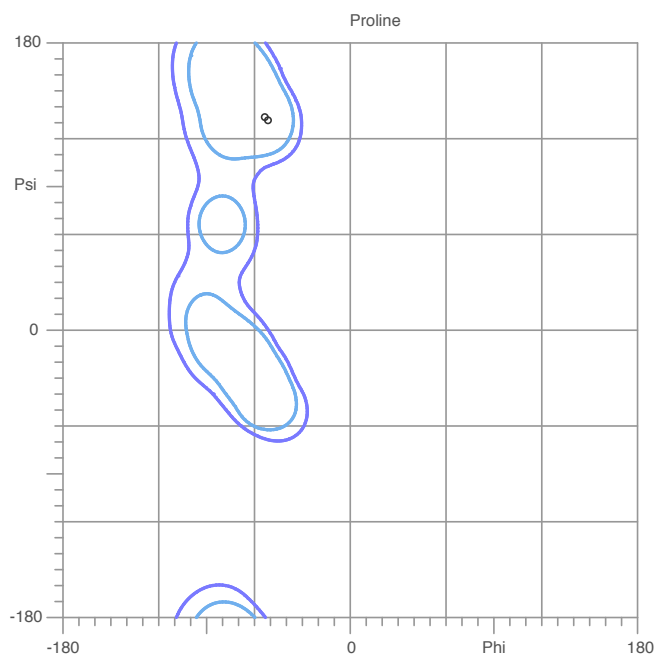
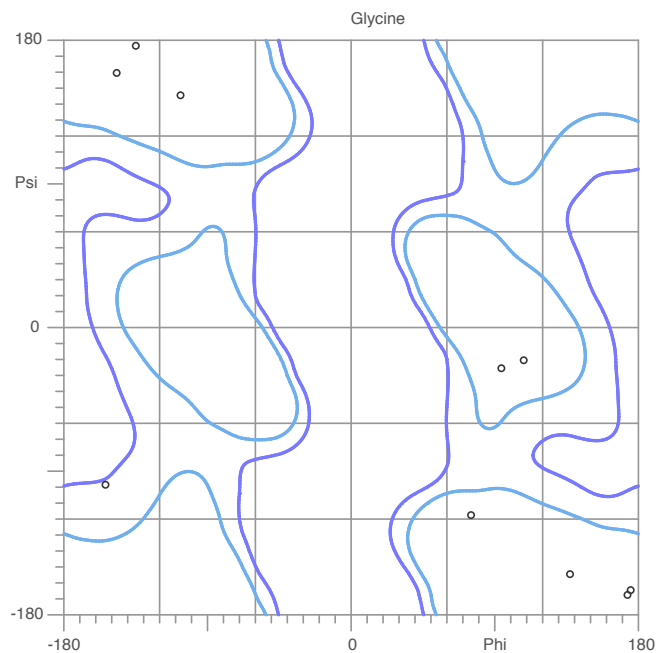
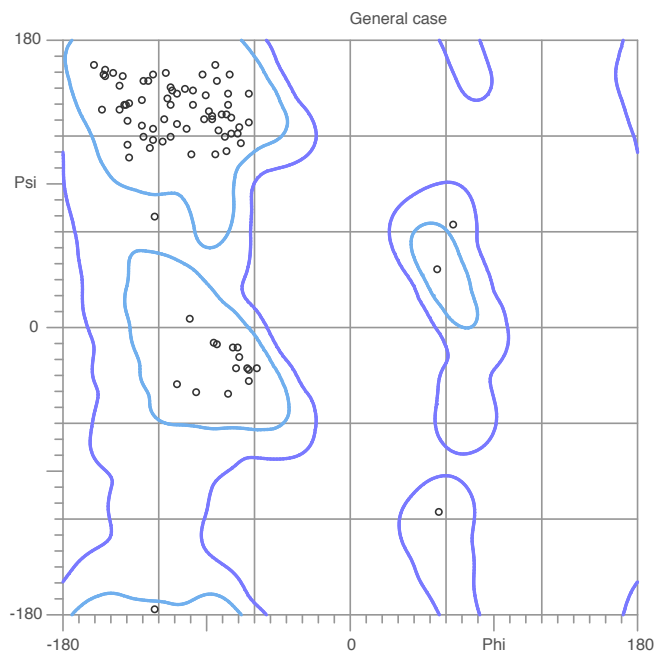
There were no outliers.

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

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

# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 2



95.8% (92/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

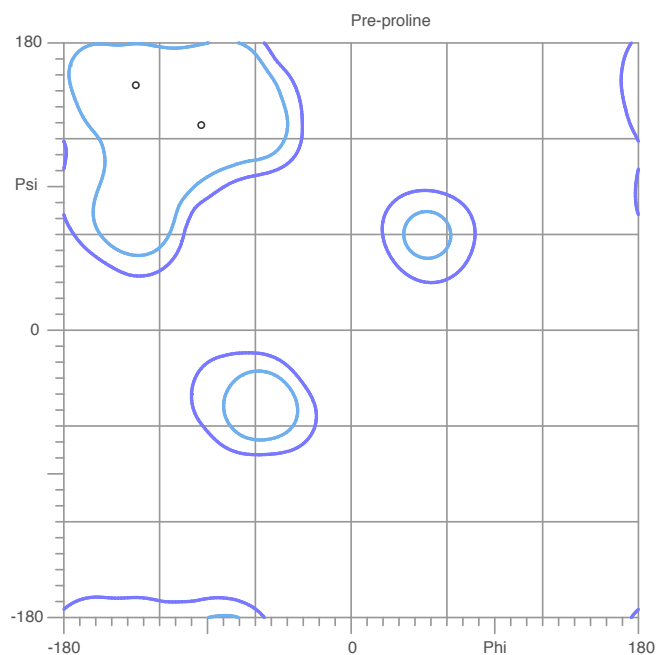
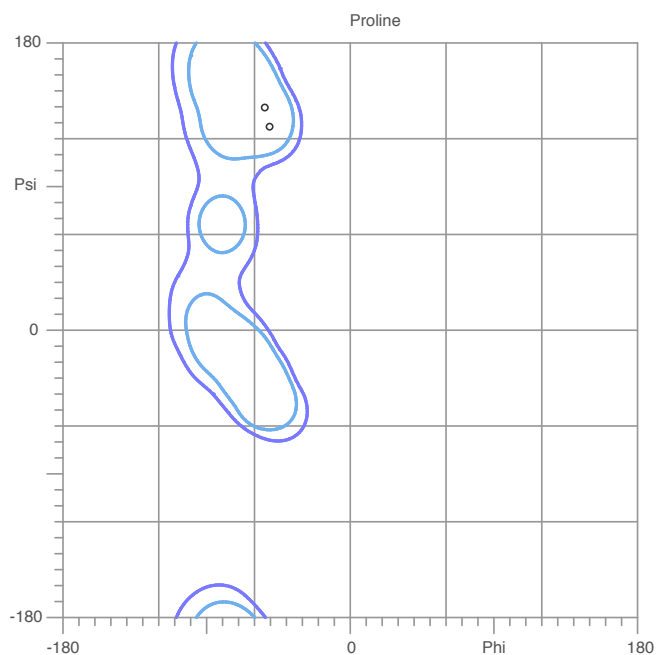
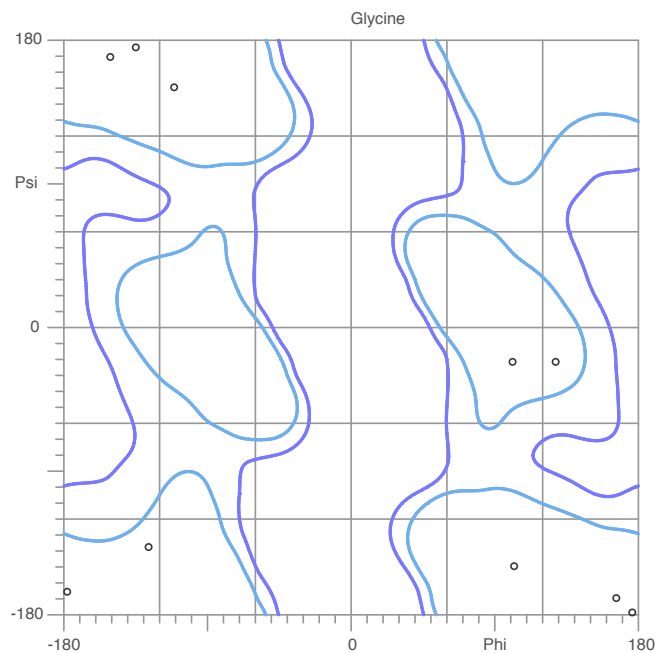
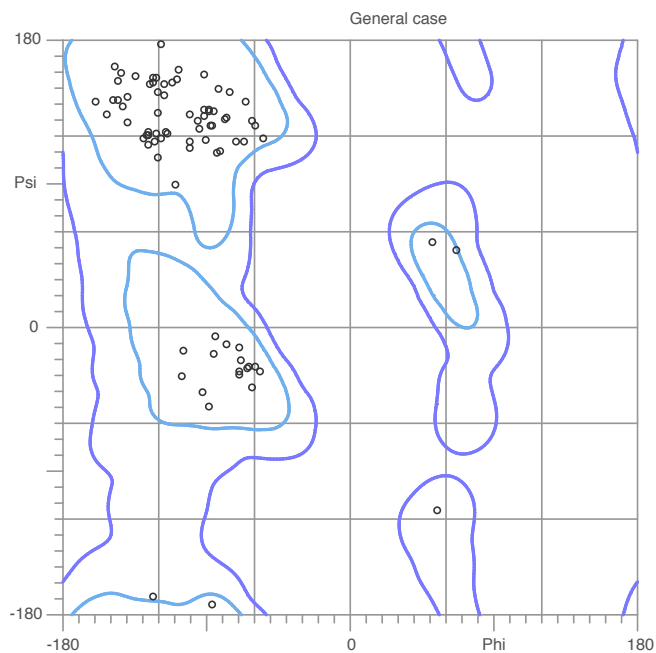
There were no outliers.

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

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 3



97.9% (94/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

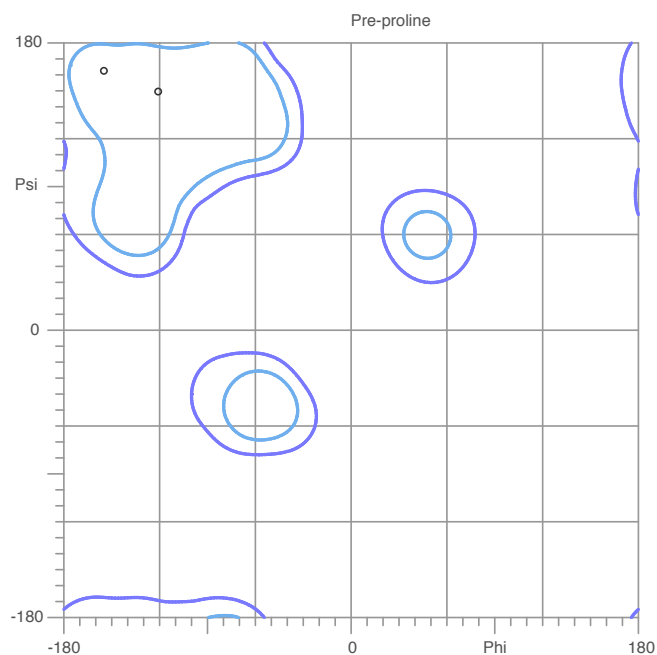
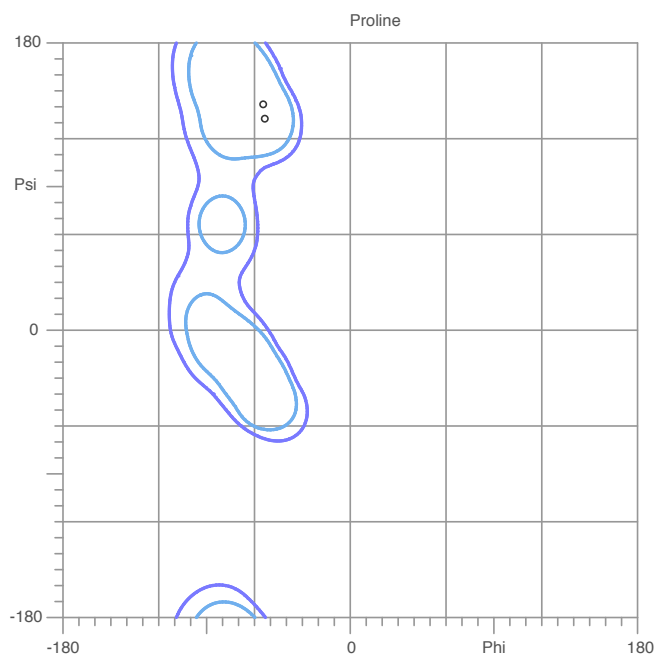
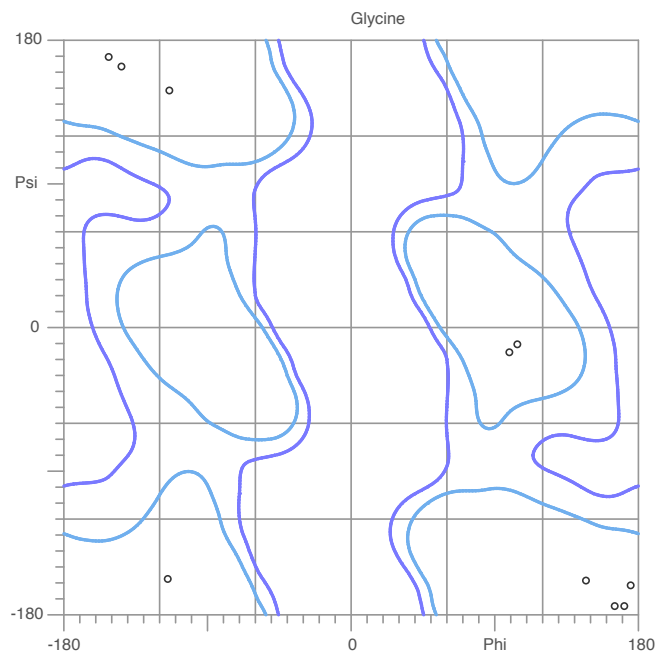
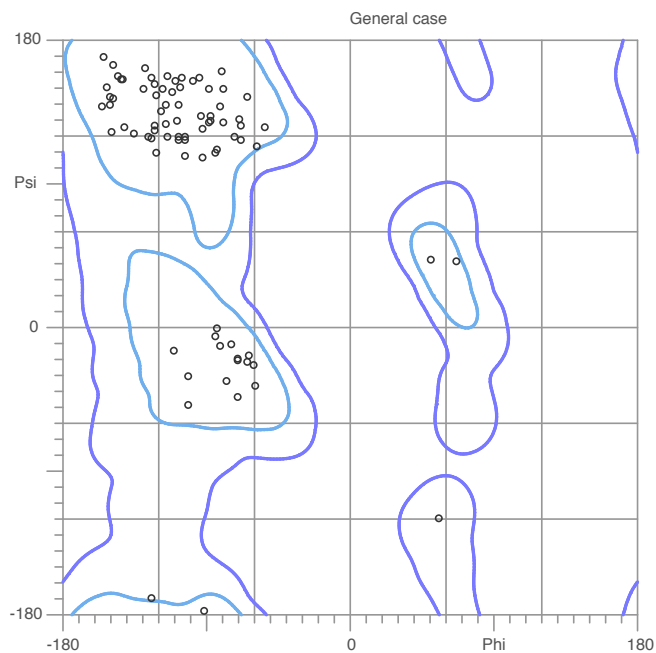
There were no outliers.

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

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 4



97.9% (94/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

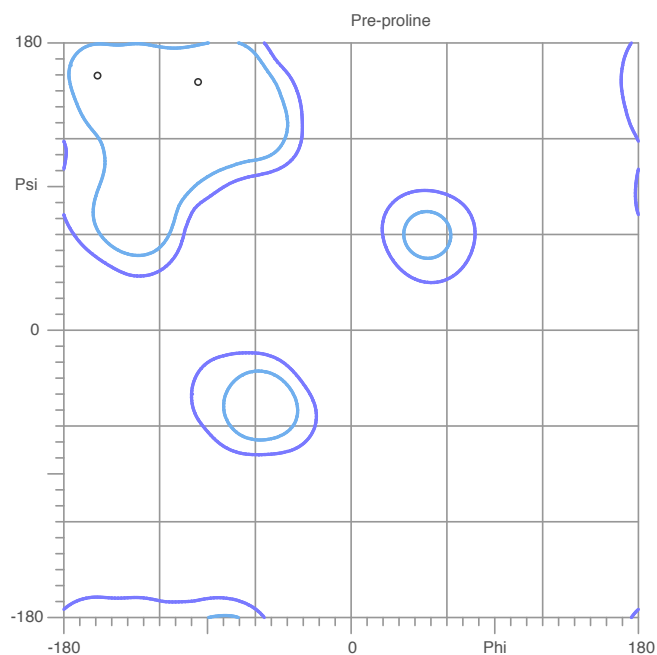
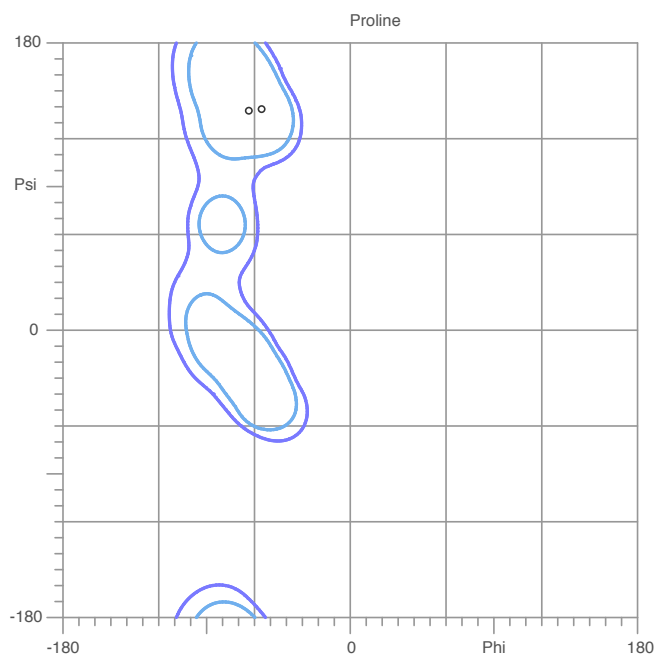
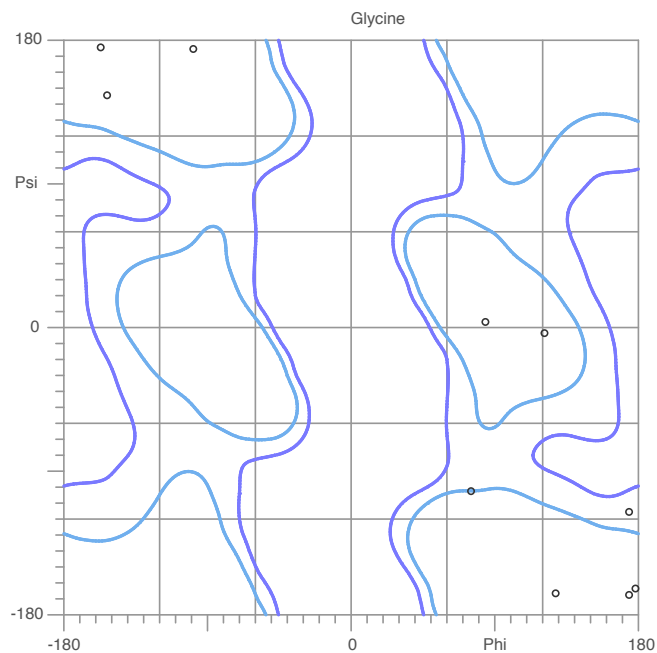
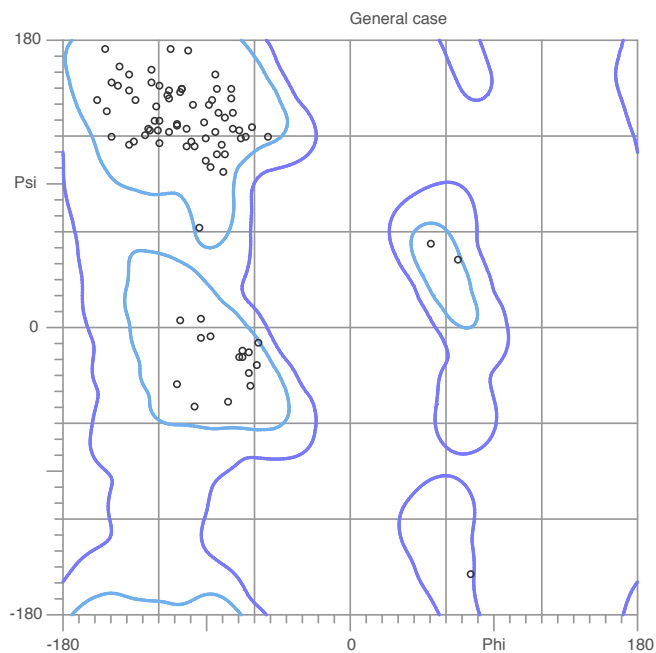
There were no outliers.

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 5

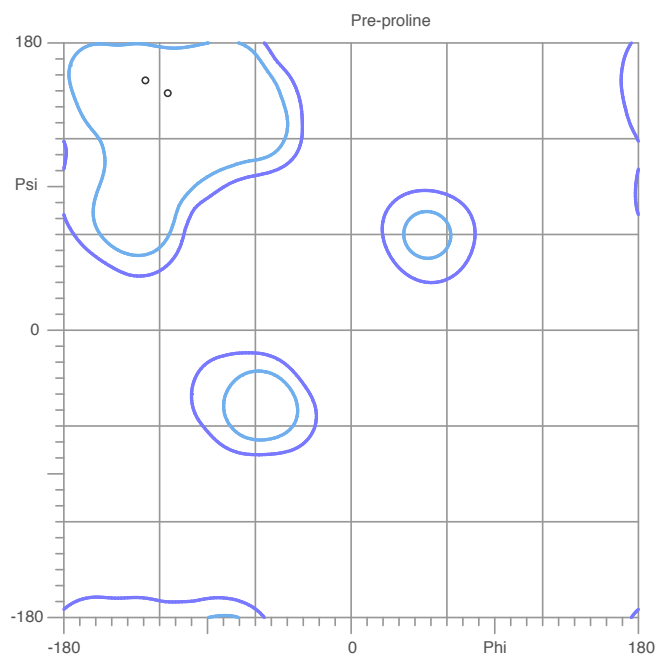
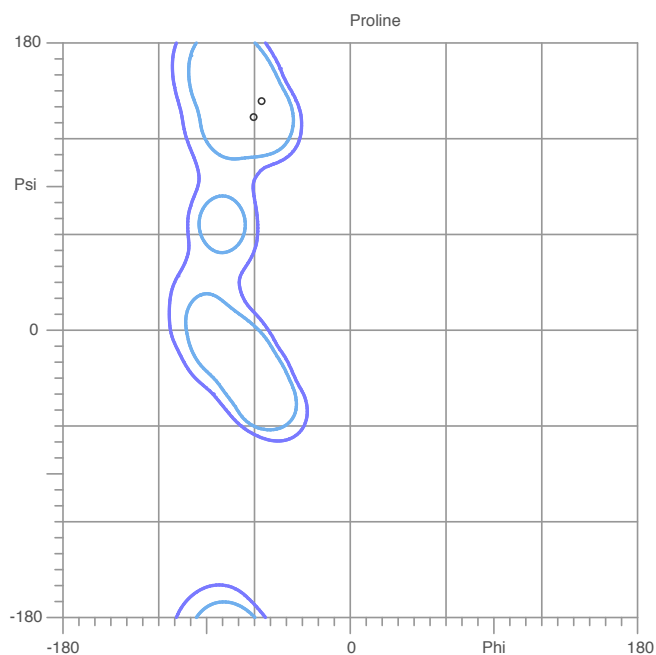
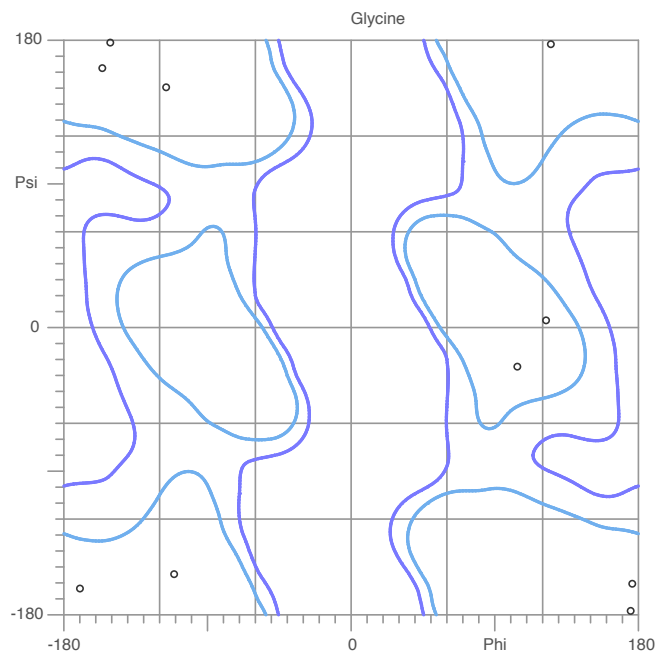
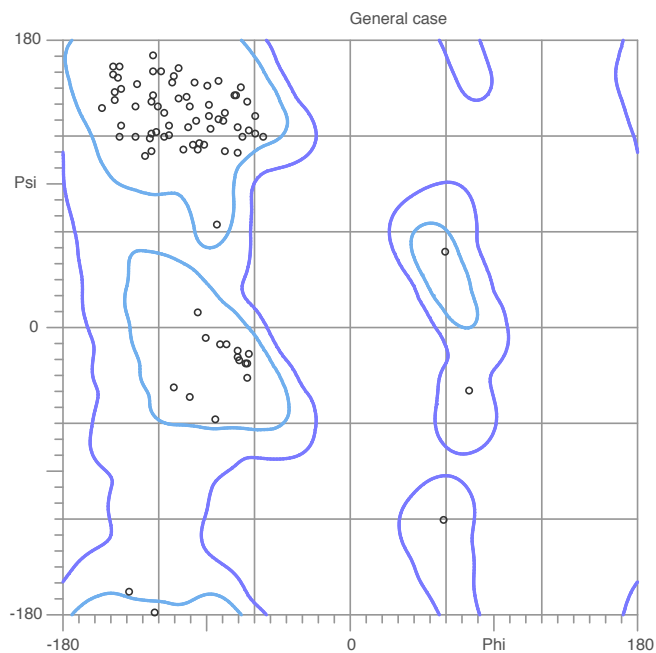


97.9% (94/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 6



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.

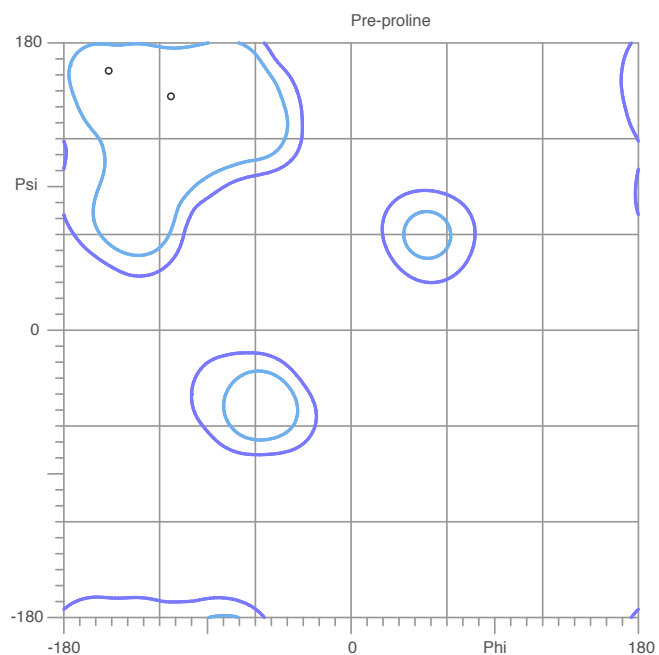
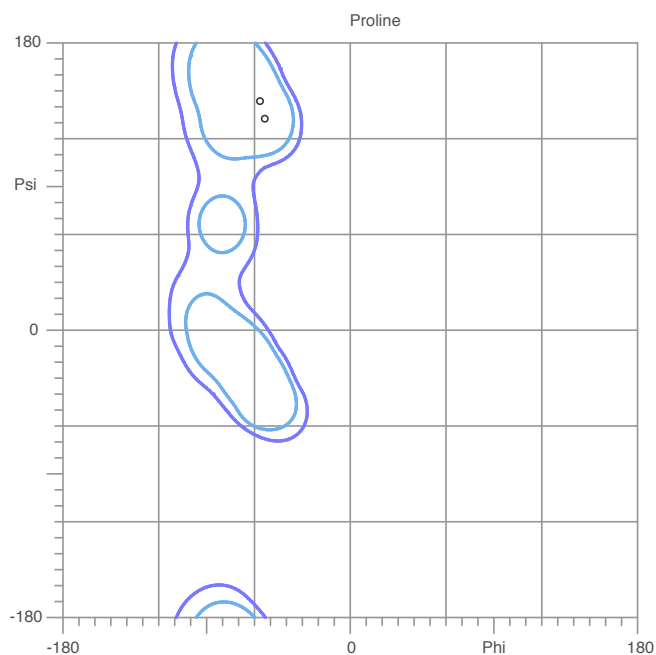
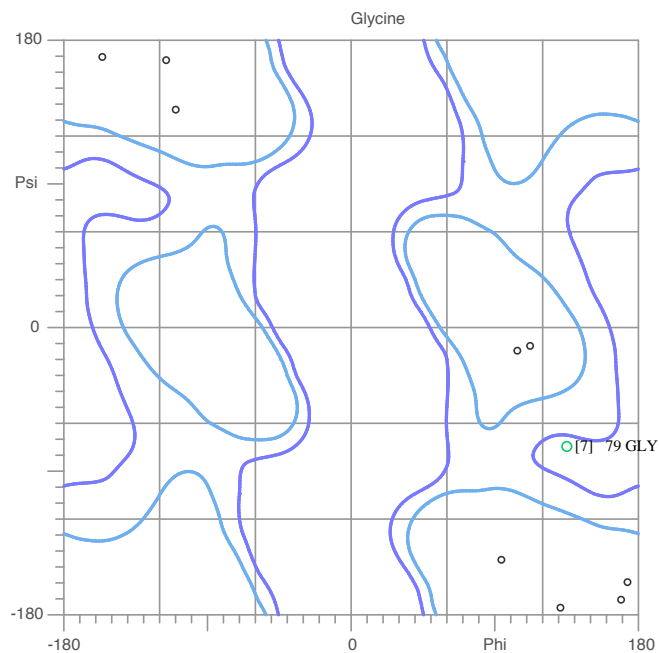
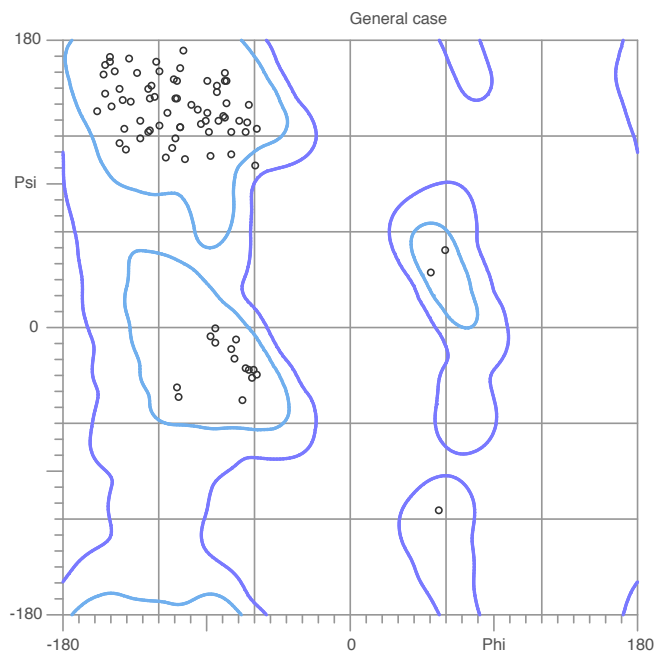
There were no outliers.

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 7



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.

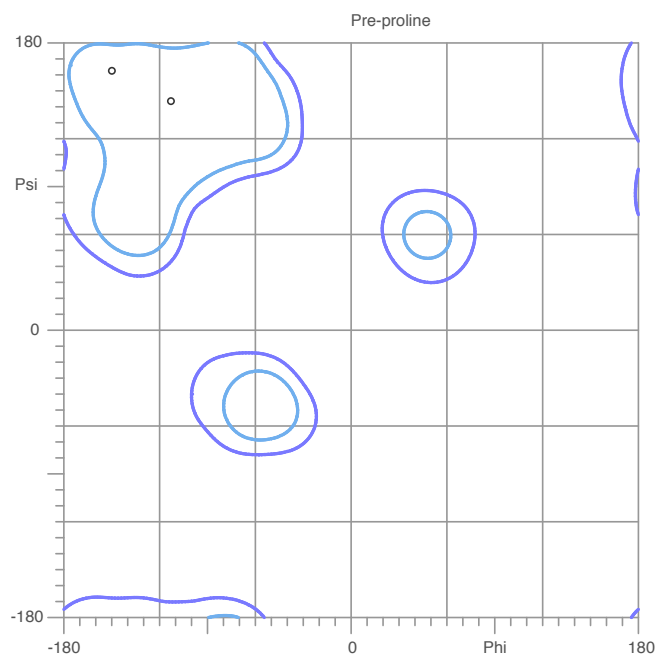
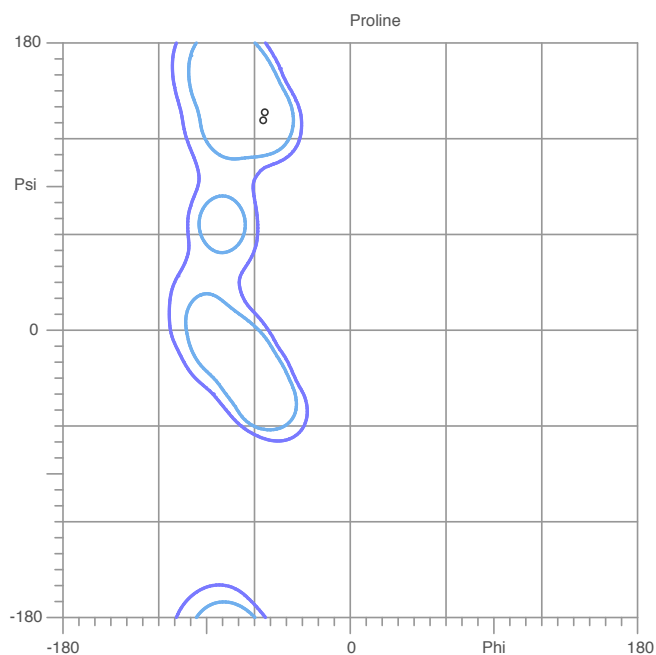
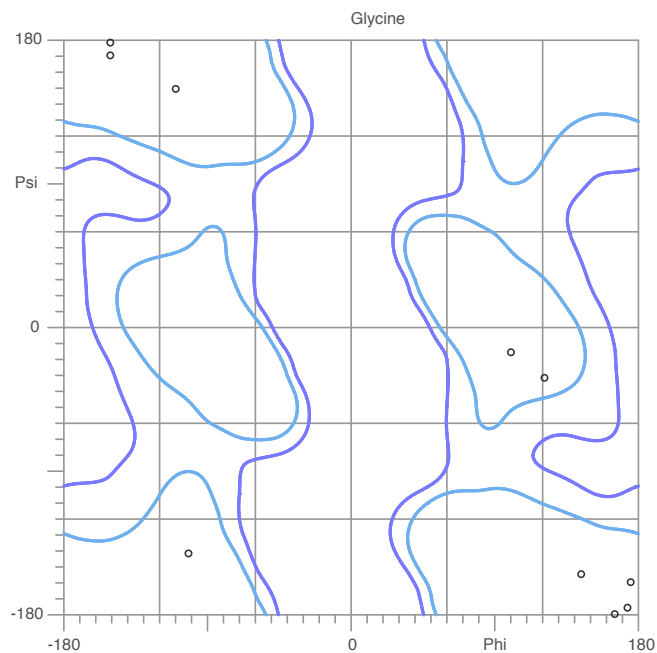
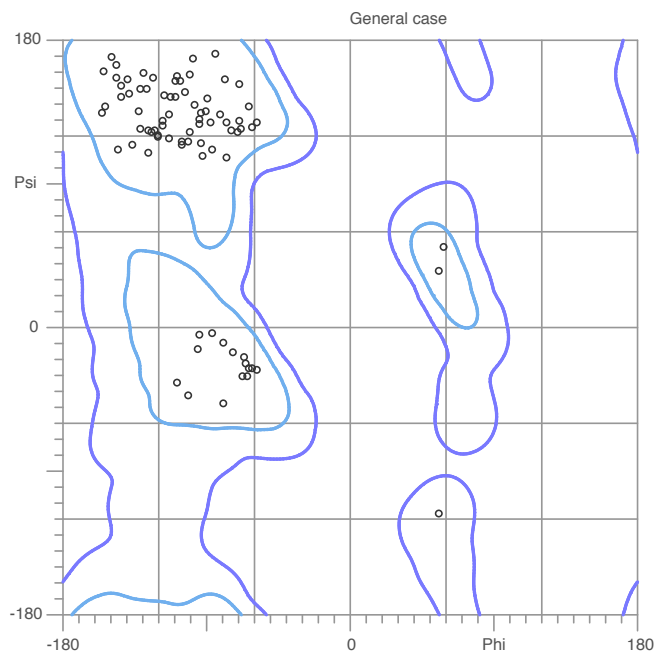
There were 1 outliers (phi, psi):  
[7] 79 GLY (135.0, -75.0)

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 8



99.0% (95/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

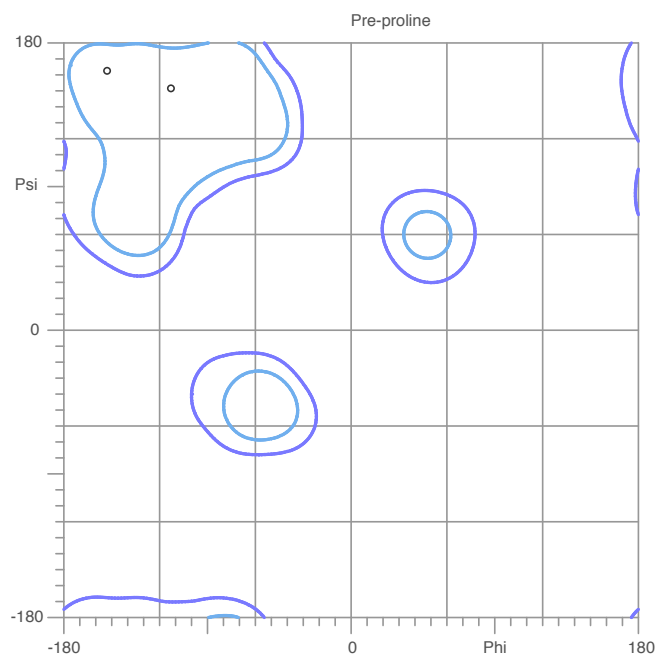
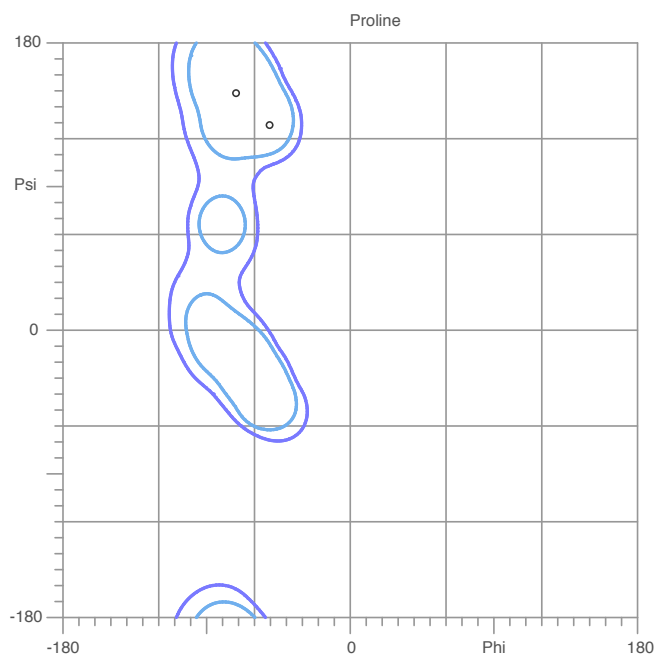
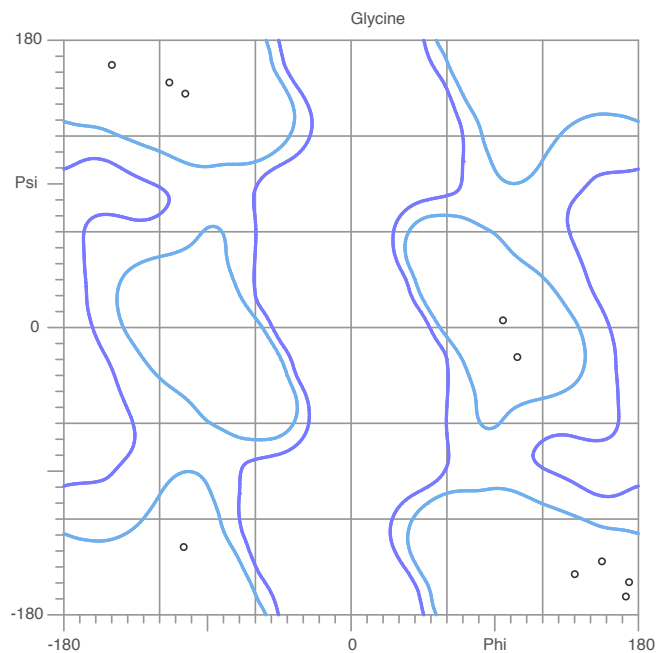
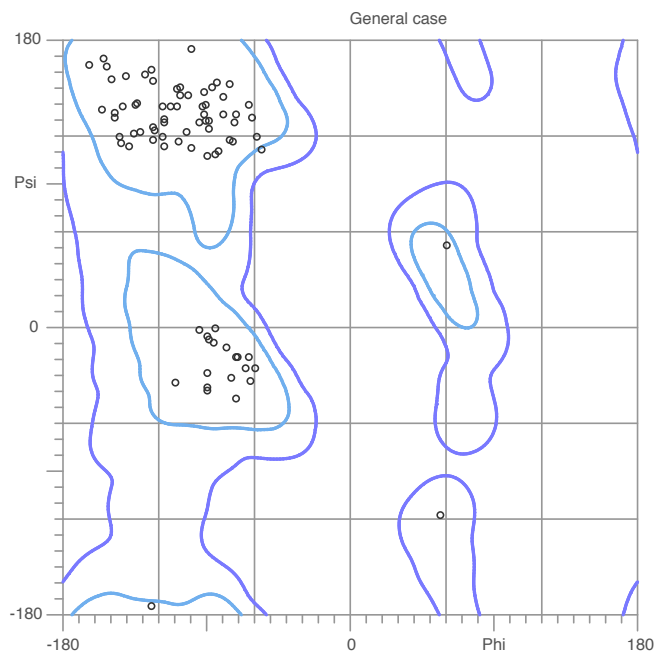
There were no outliers.

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 9



99.0% (95/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

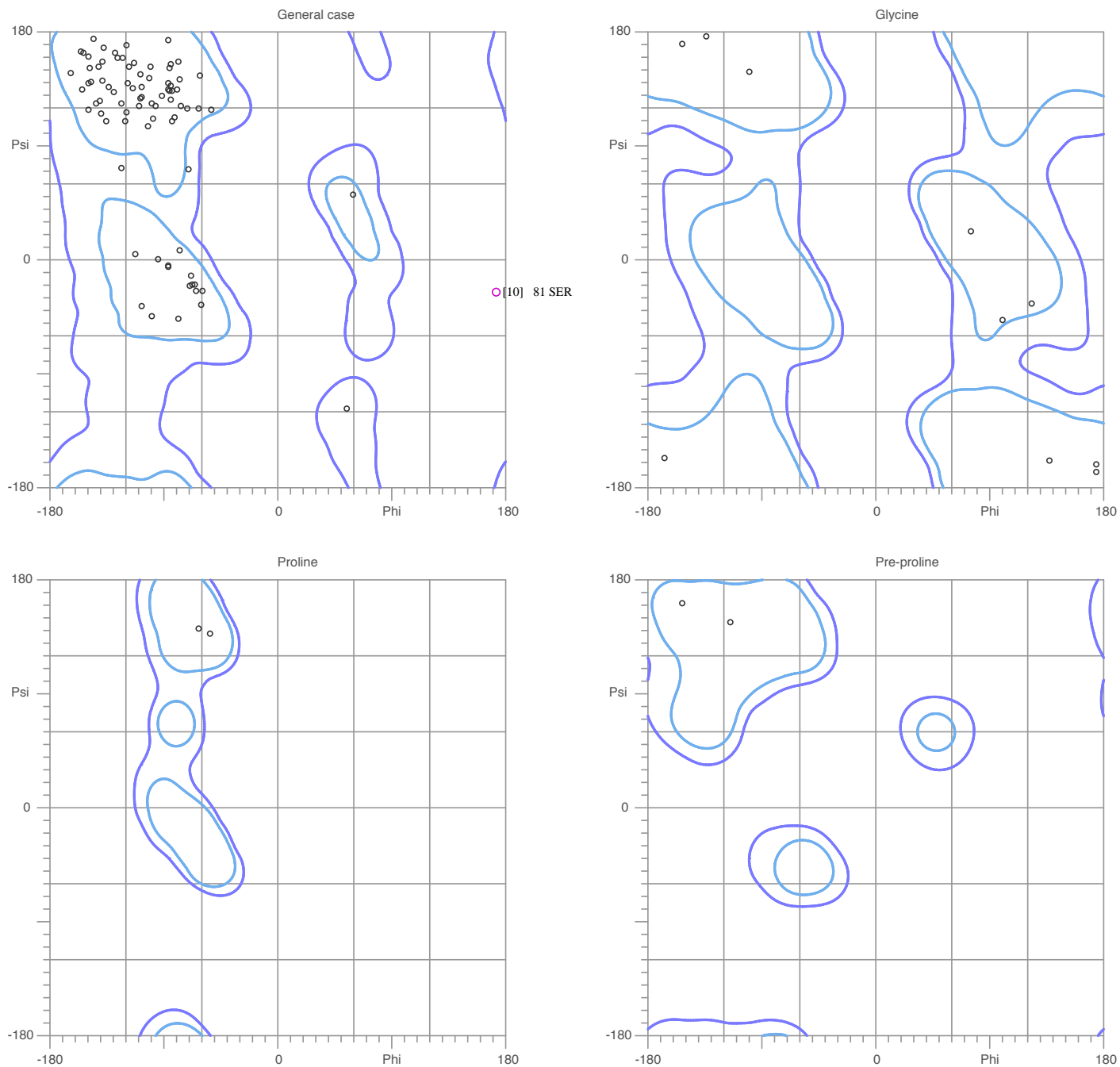
There were no outliers.

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

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 10



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.

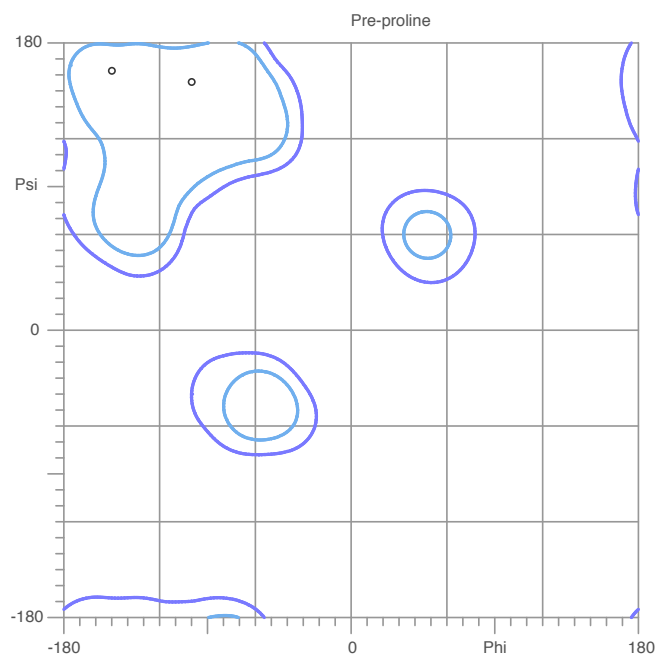
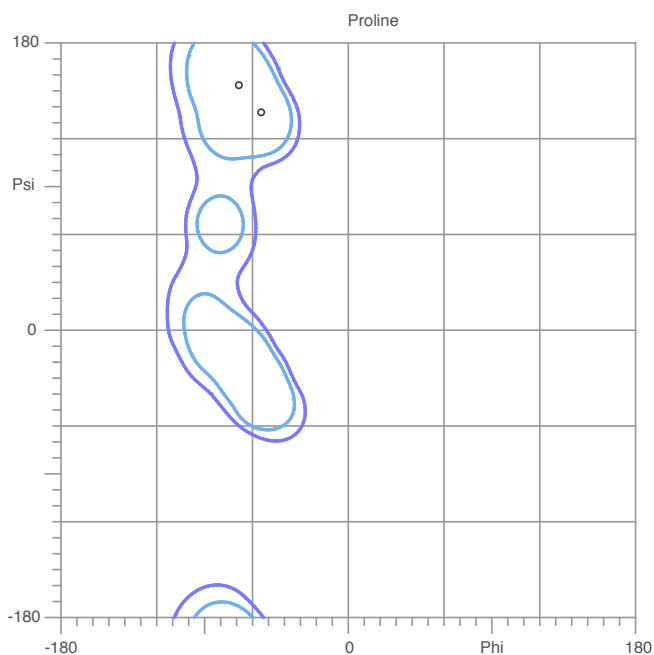
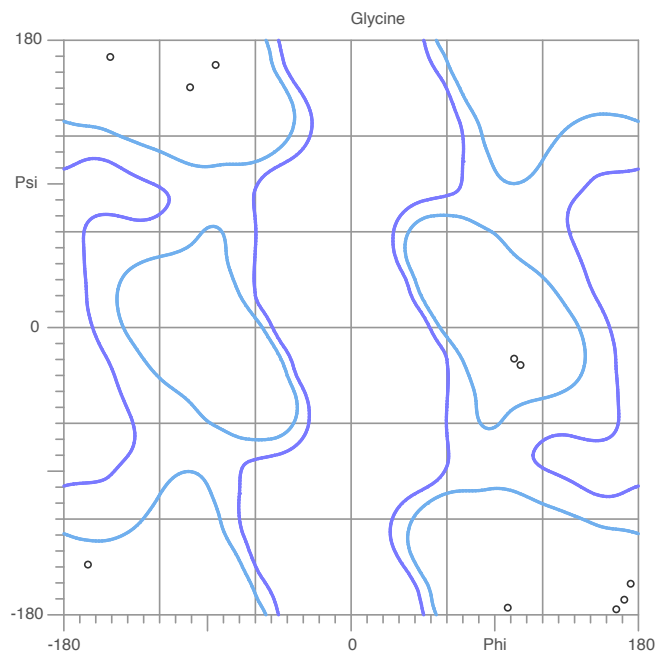
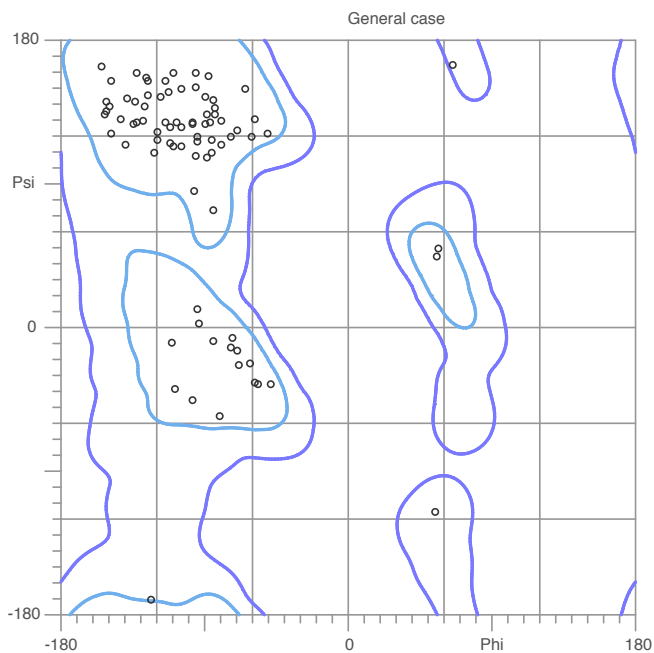
There were 1 outliers (phi, psi):  
[10] 81 SER (172.1, -25.0)

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

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 11



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.

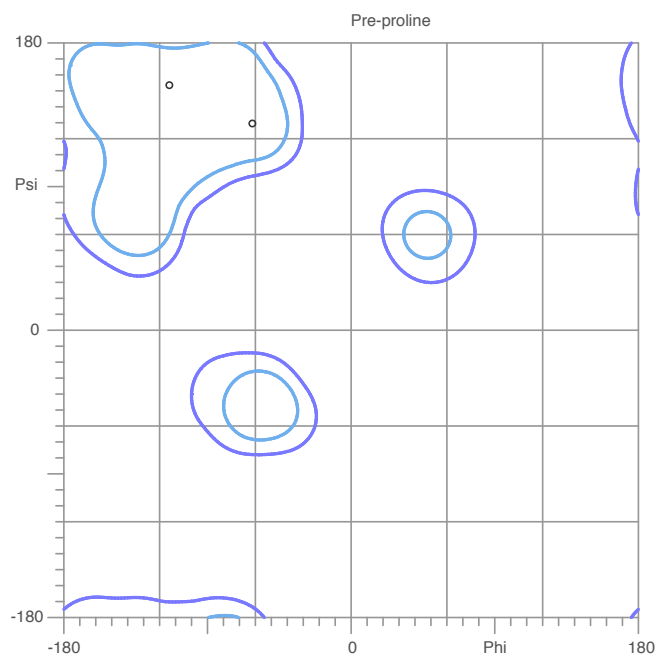
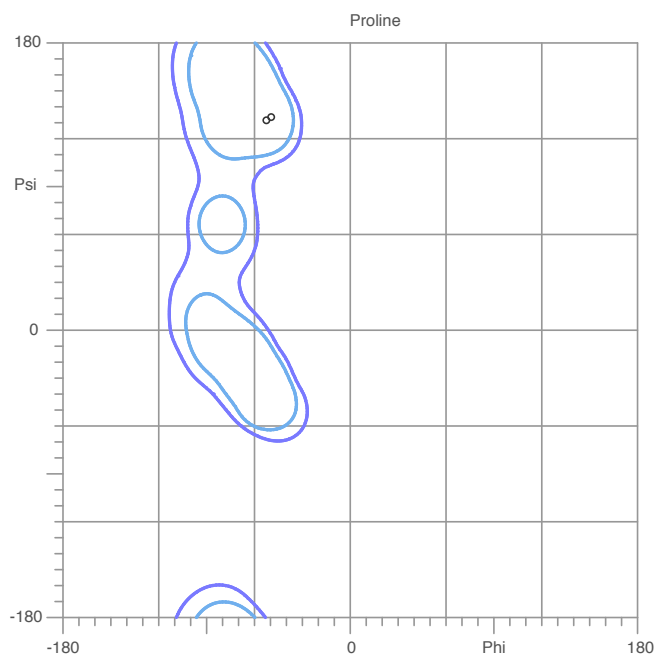
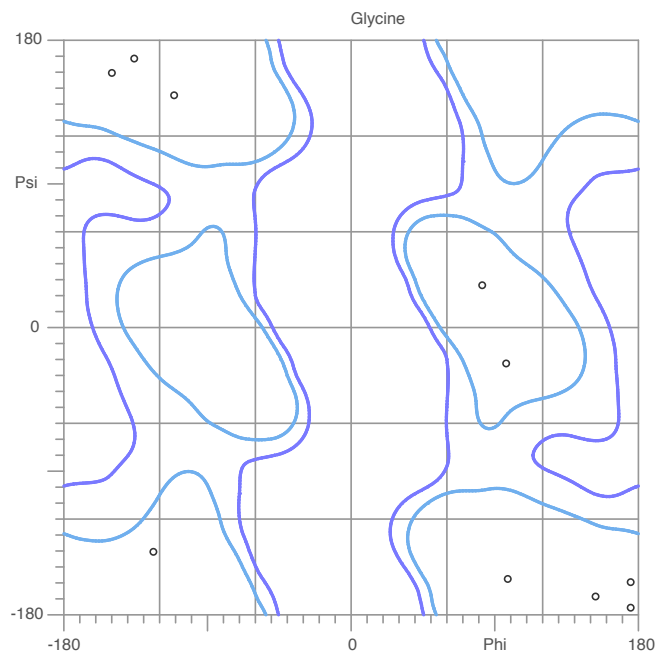
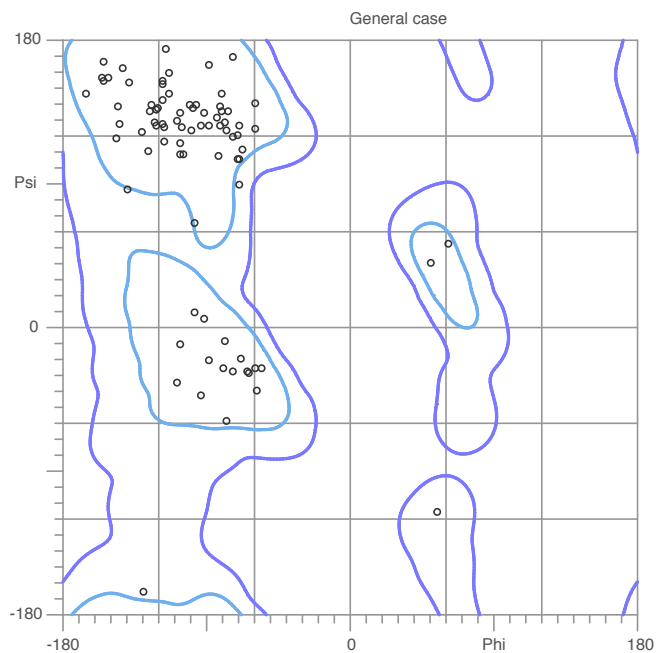
There were no outliers.

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 12



95.8% (92/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

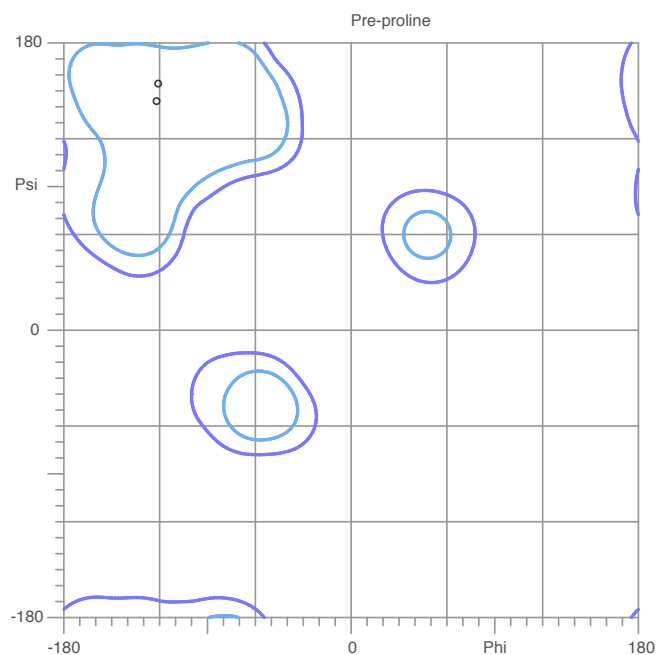
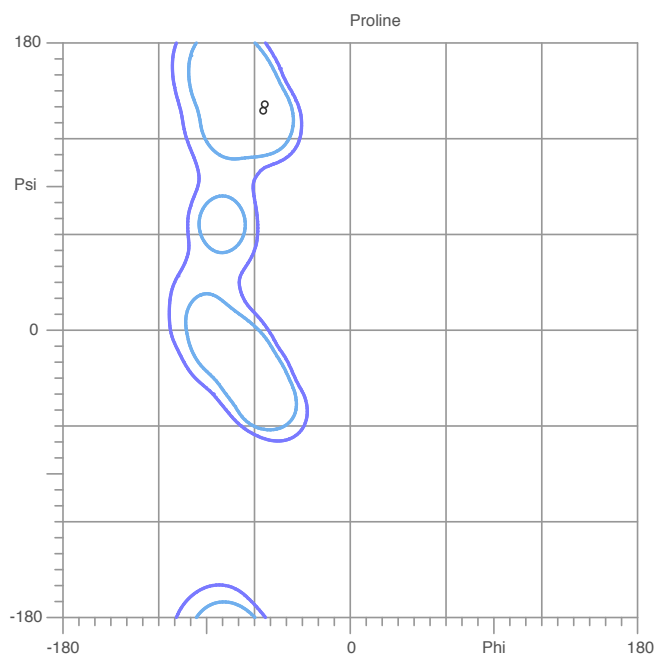
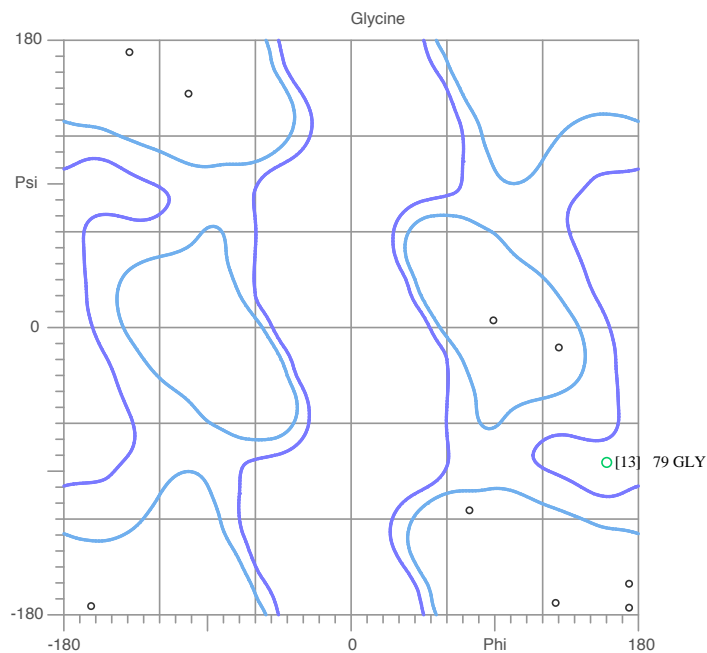
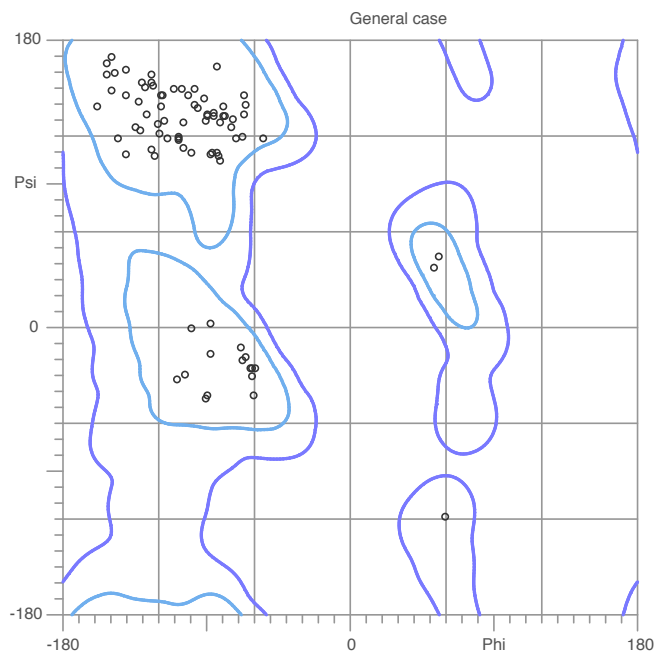
There were no outliers.

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 13

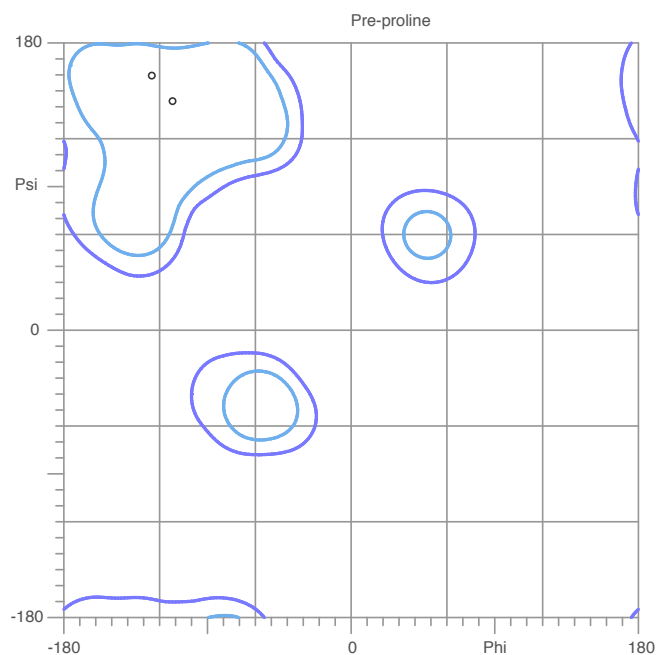
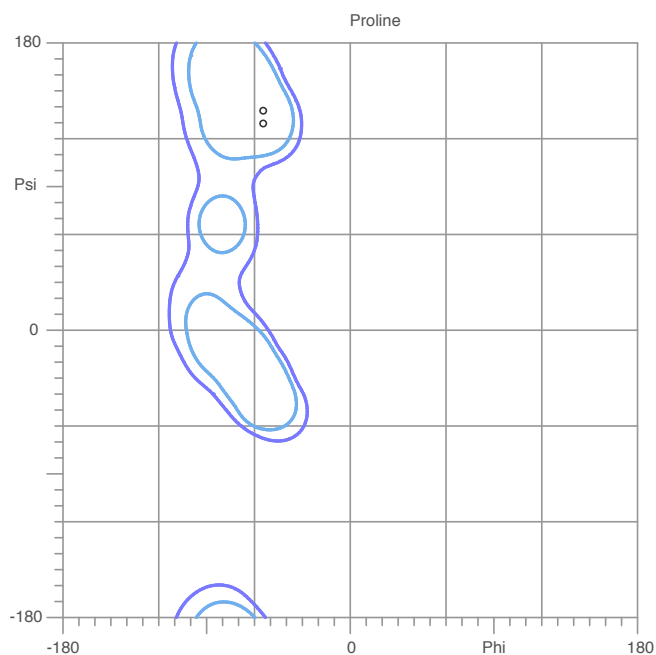
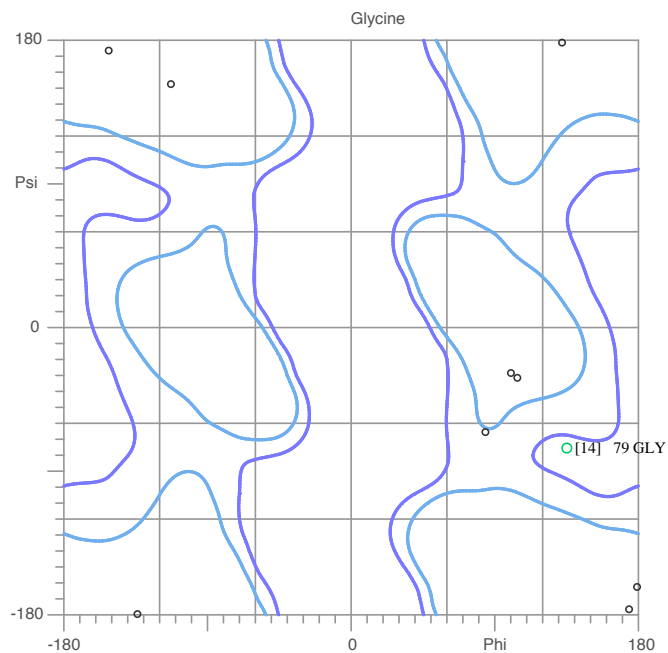
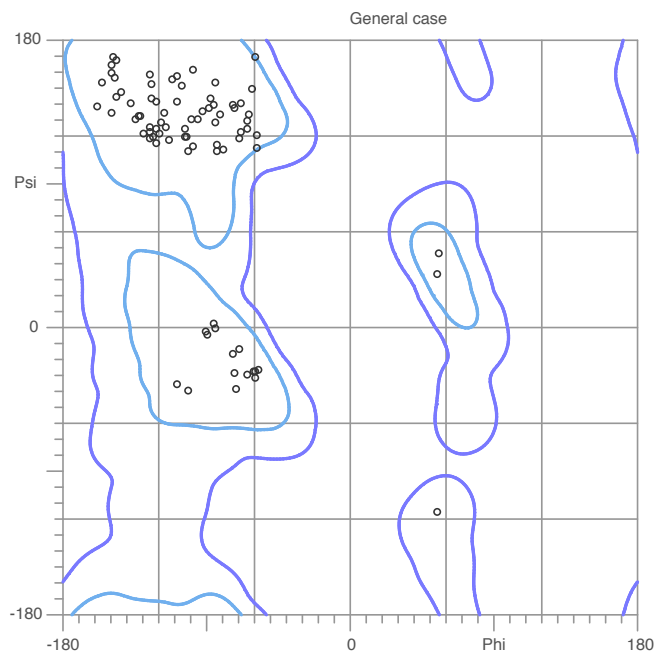


97.9% (94/96) of all residues were in favored (98%) regions.  
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[13] 79 GLY (160.6, -85.0)

# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 14

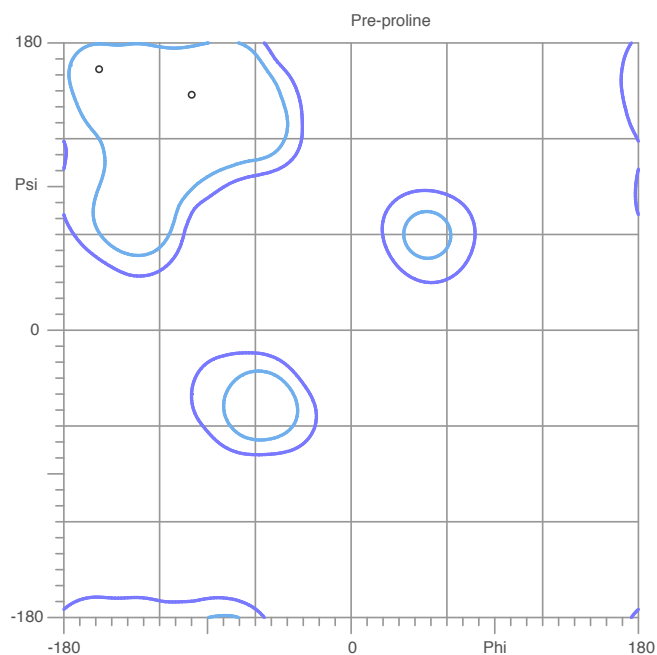
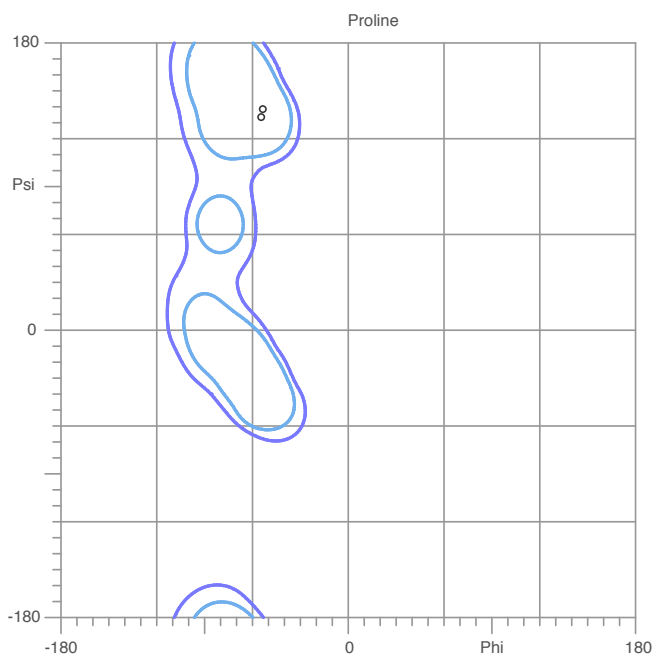
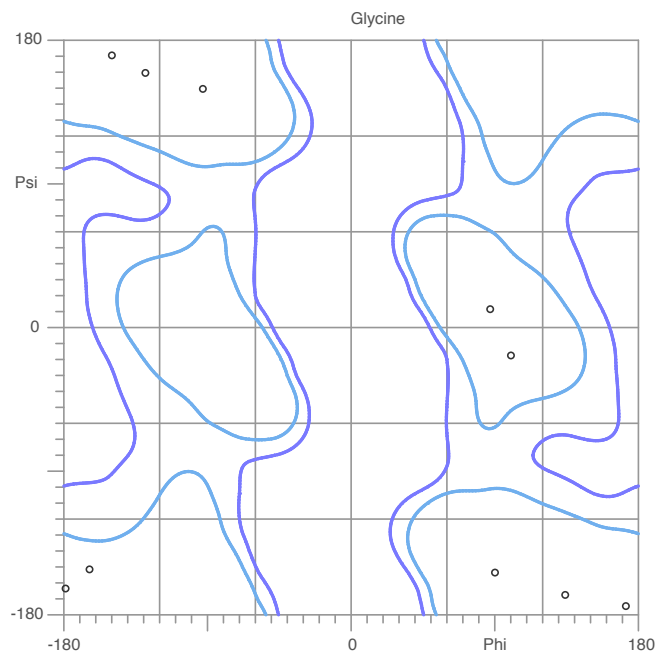
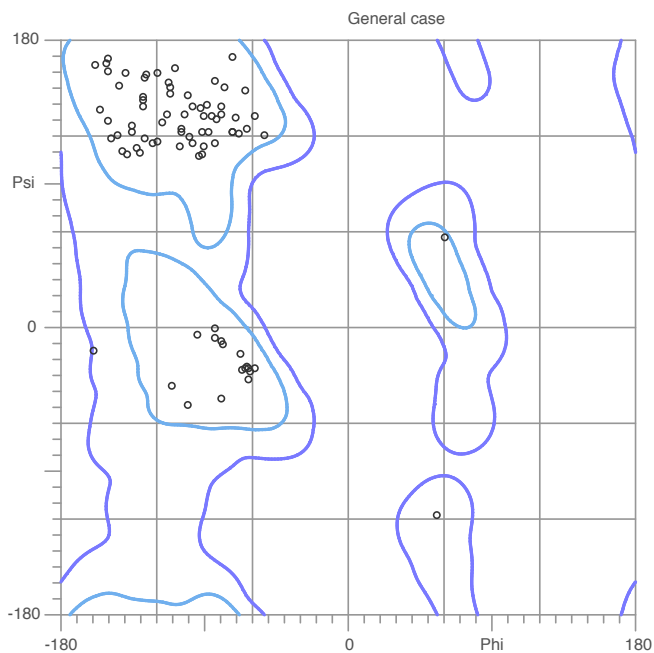


95.8% (92/96) of all residues were in favored (98%) regions.  
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[14] 79 GLY (135.0, -75.0)

# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 15



97.9% (94/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

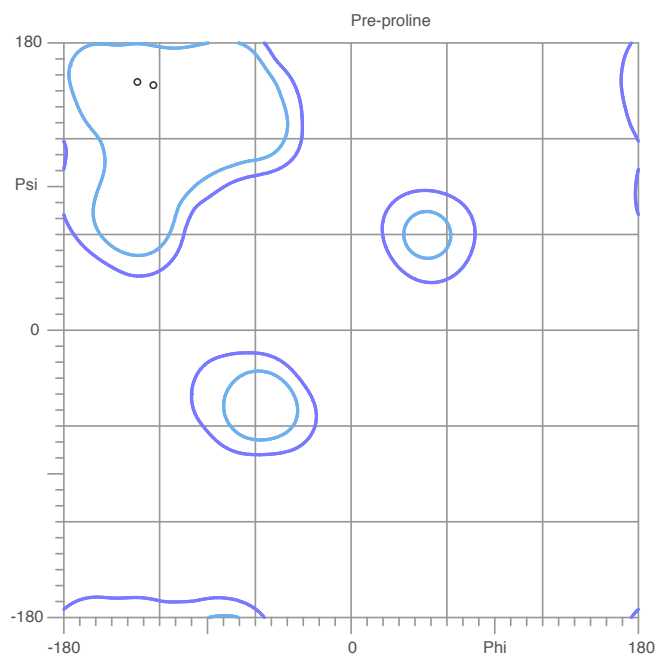
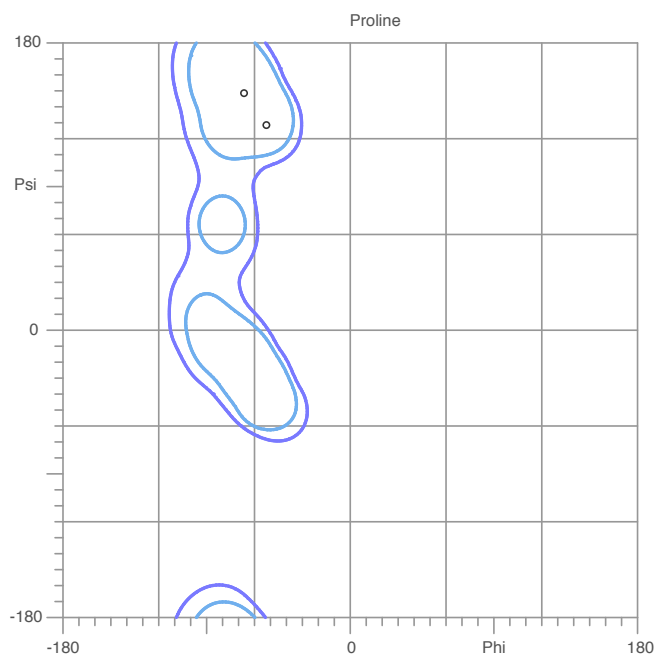
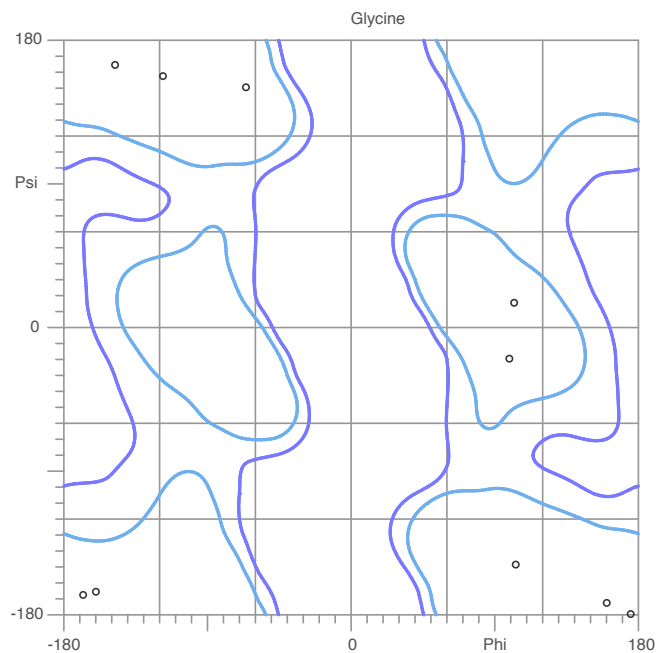
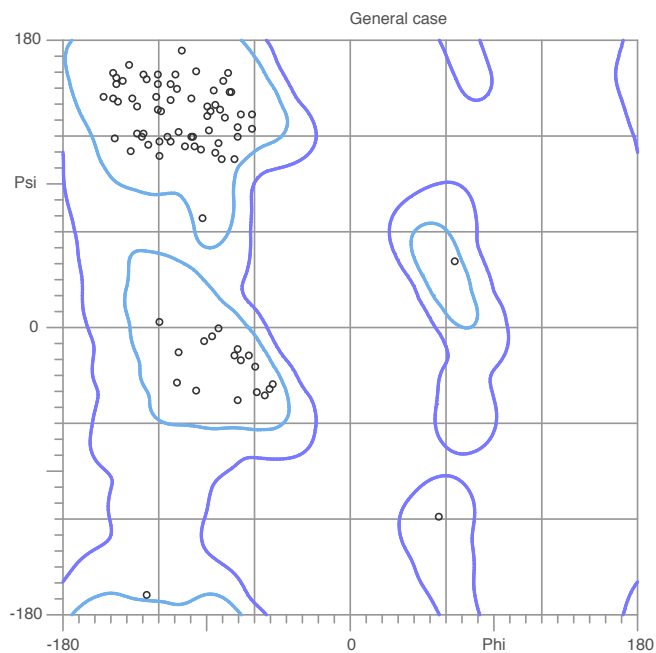
There were no outliers.

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 16



97.9% (94/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

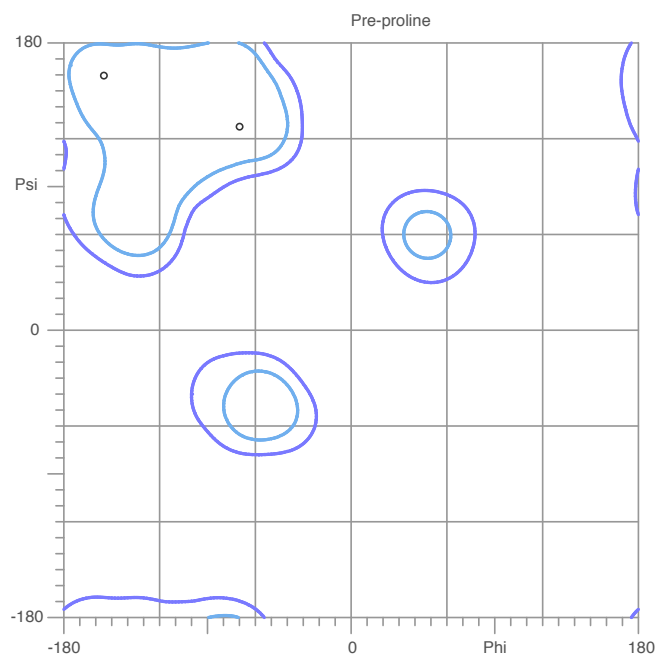
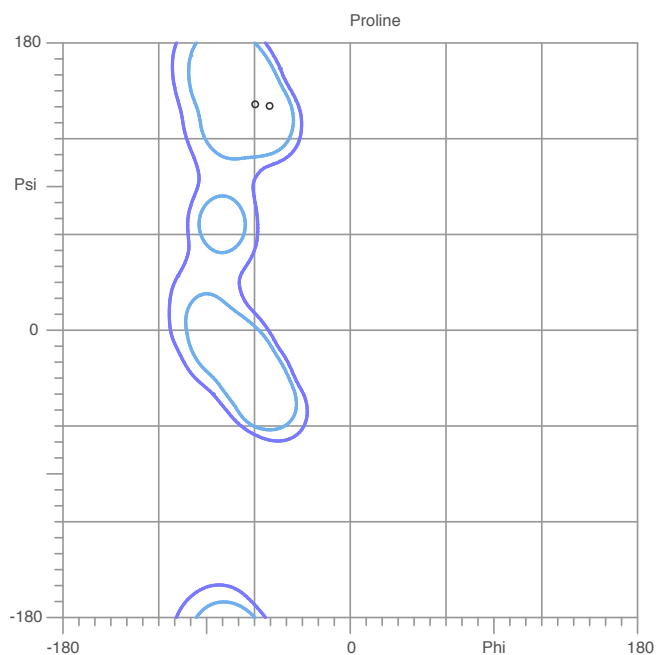
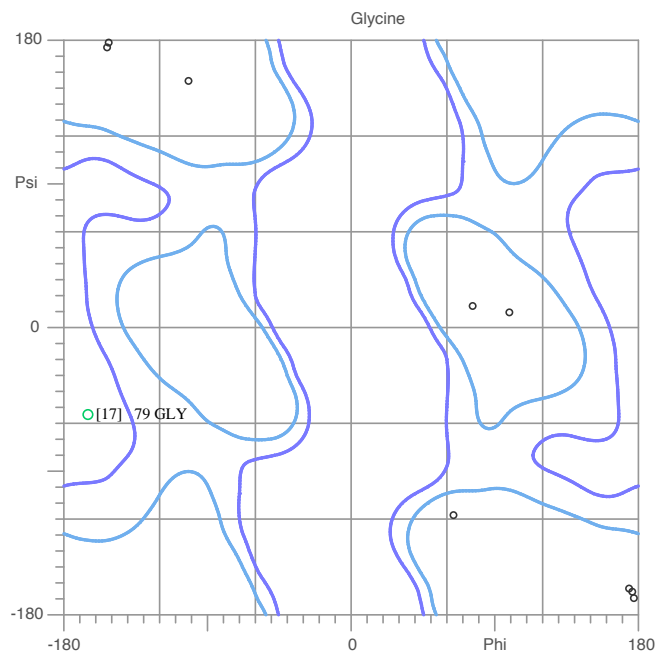
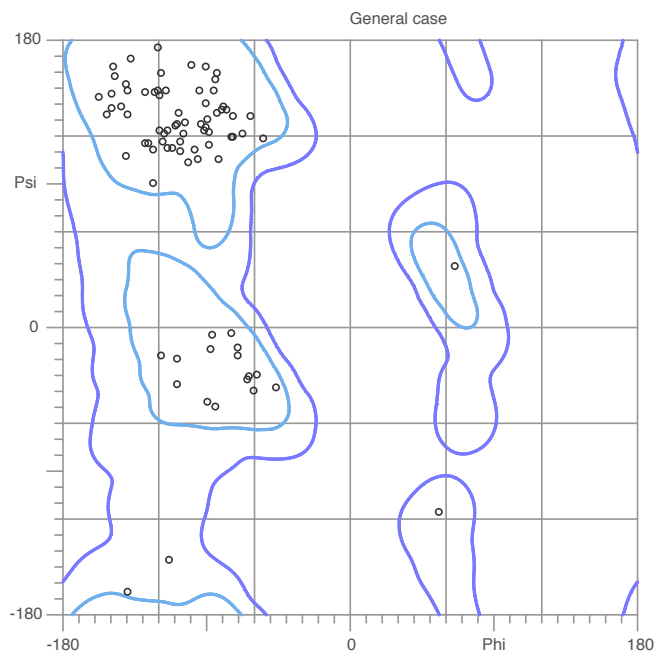
There were no outliers.

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

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# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 17



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.

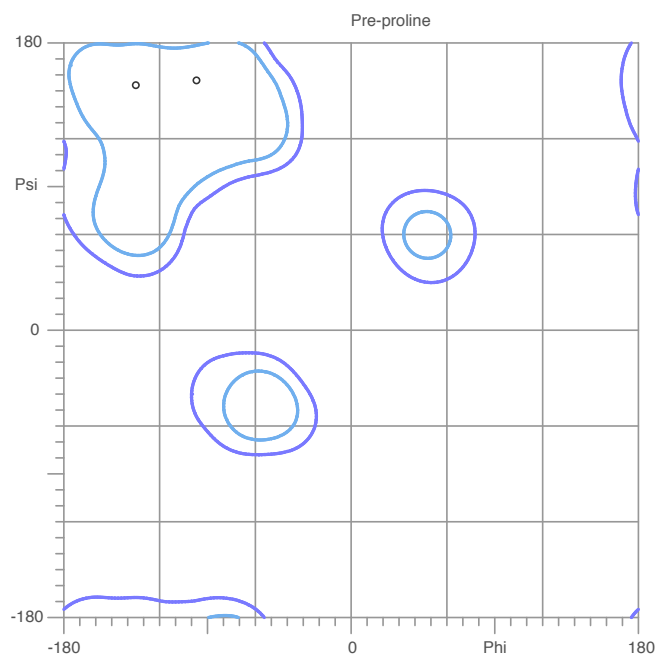
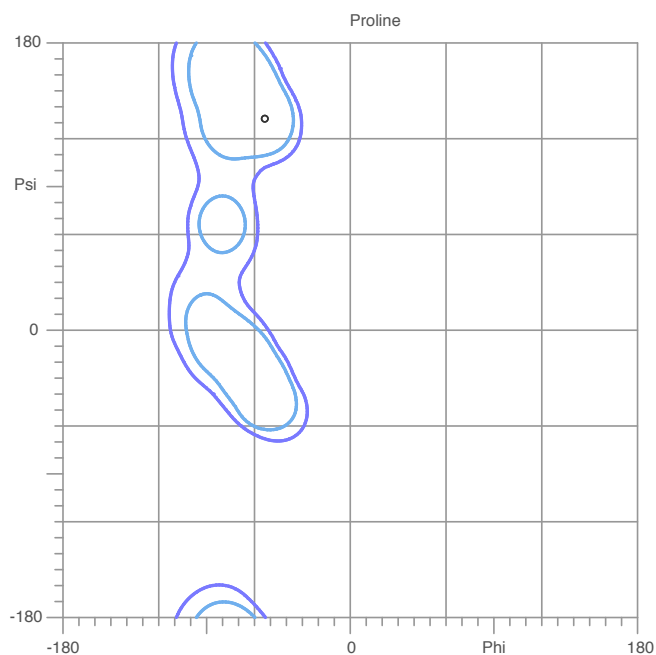
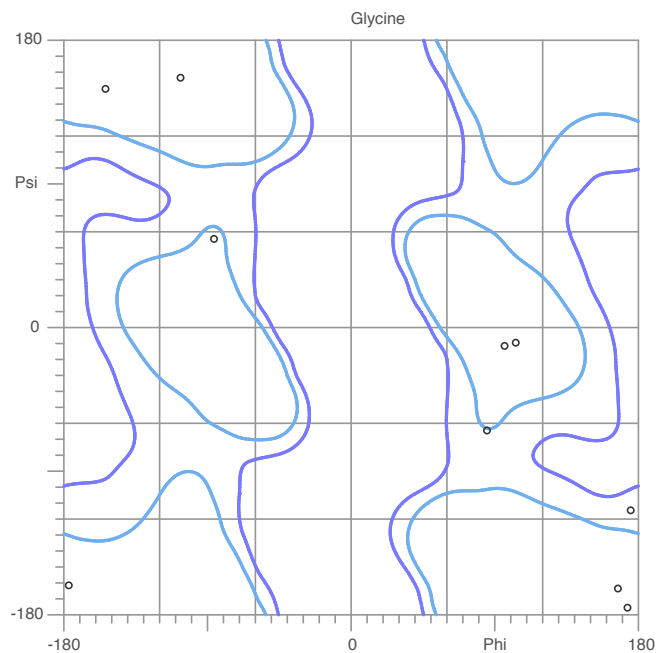
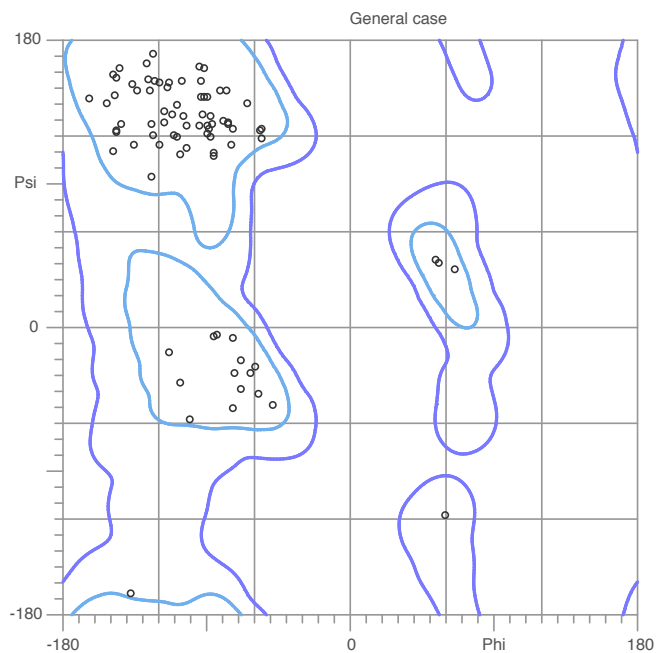
There were 1 outliers (phi, psi):  
[17] 79 GLY (-165.0, -54.9)

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

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

# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 18

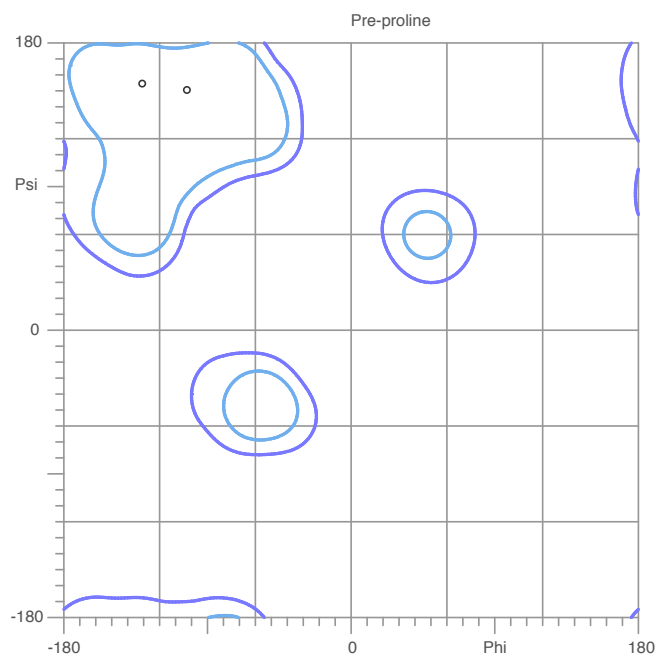
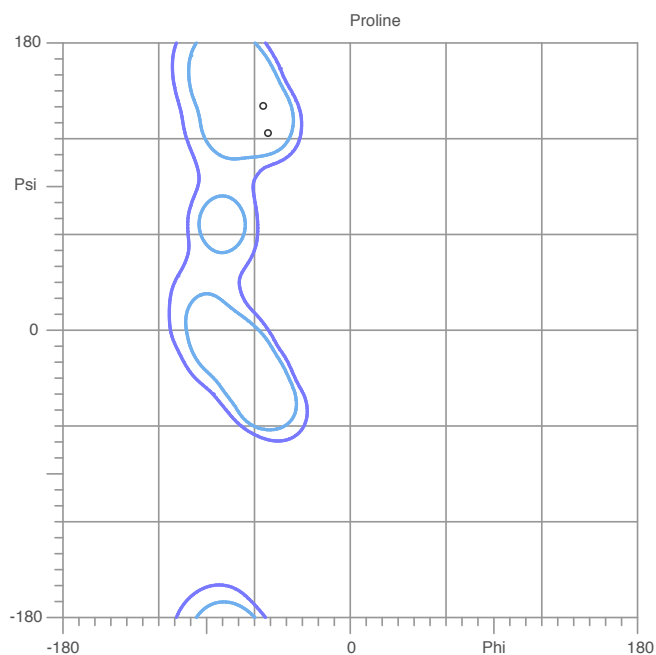
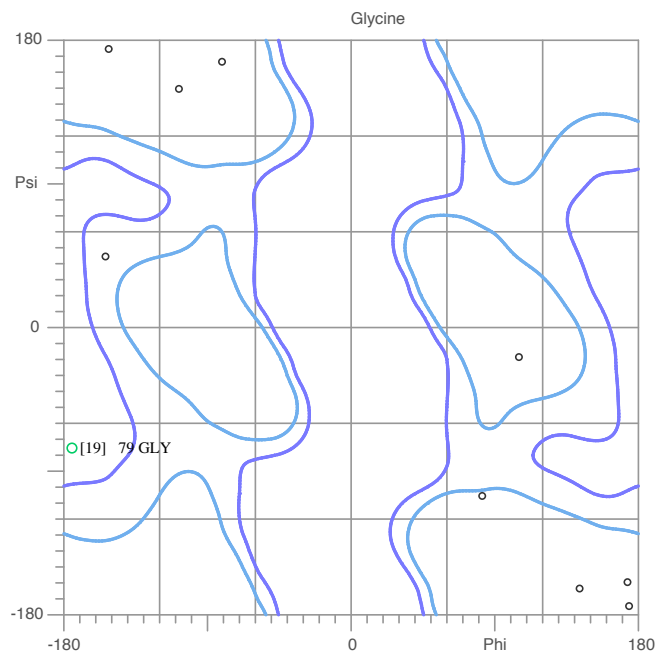
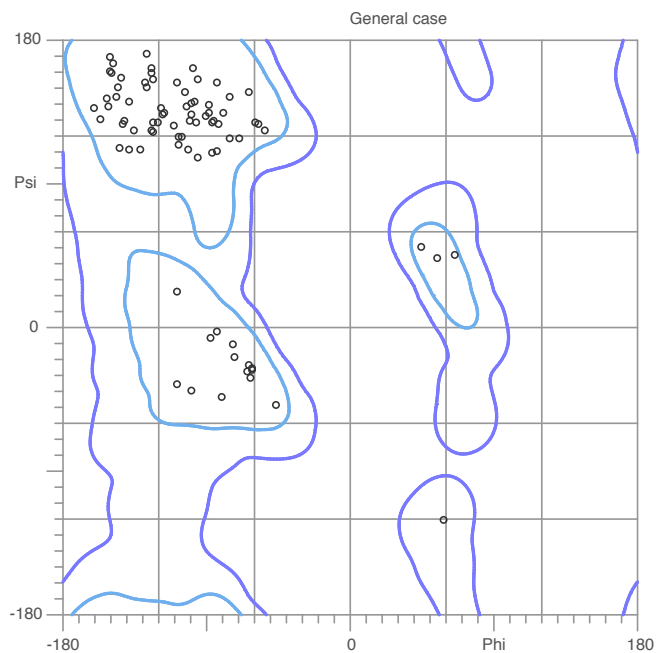


95.8% (92/96) of all residues were in favored (98%) regions.  
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 19

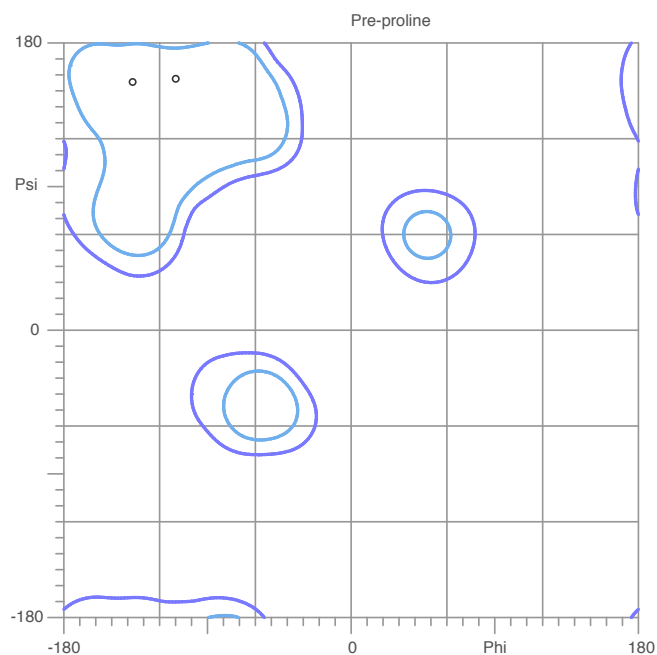
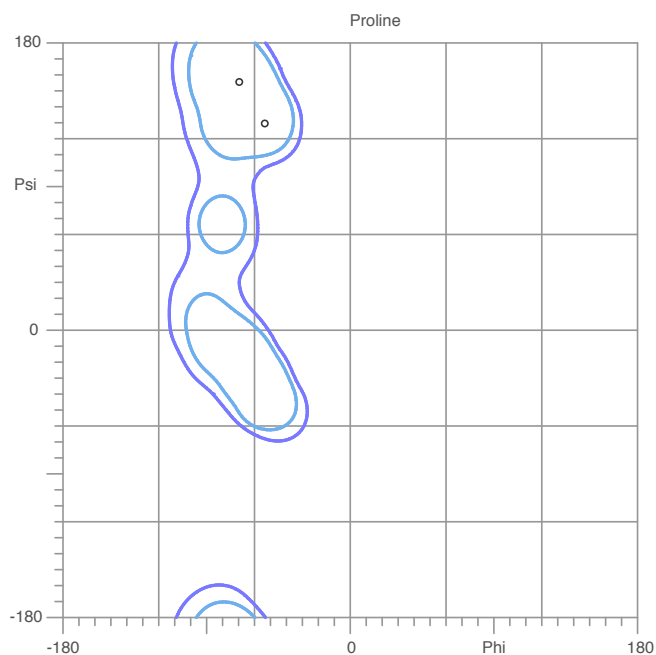
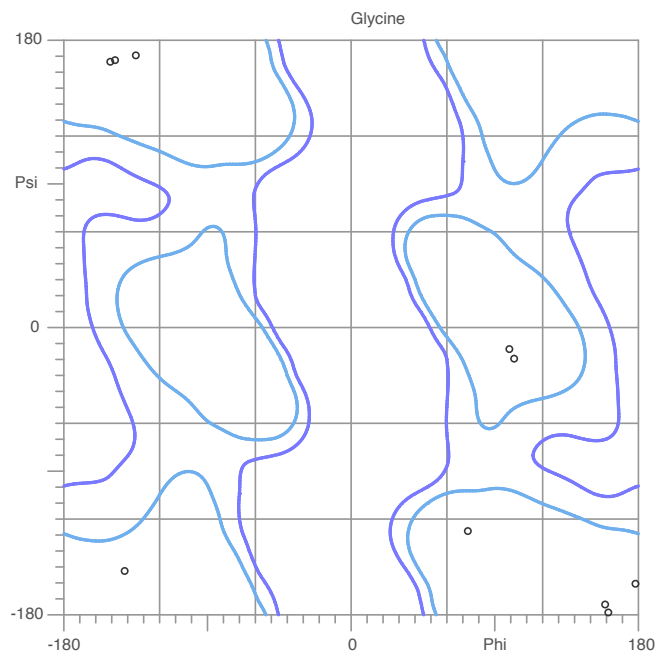
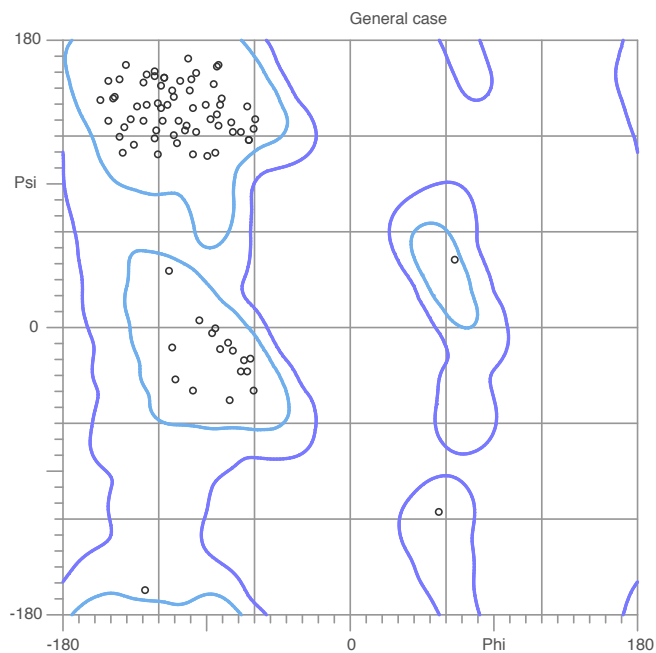


96.9% (93/96) of all residues were in favored (98%) regions.  
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[19] 79 GLY (-175.0, -75.0)

# MolProbity Ramachandran analysis

MRR110B\_R3\_em\_bcr3.pdb, model 20



97.9% (94/96) 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.