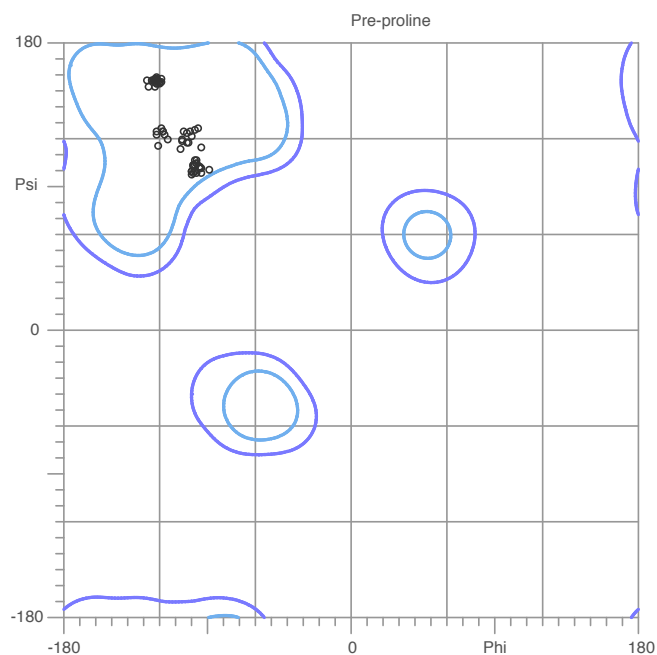
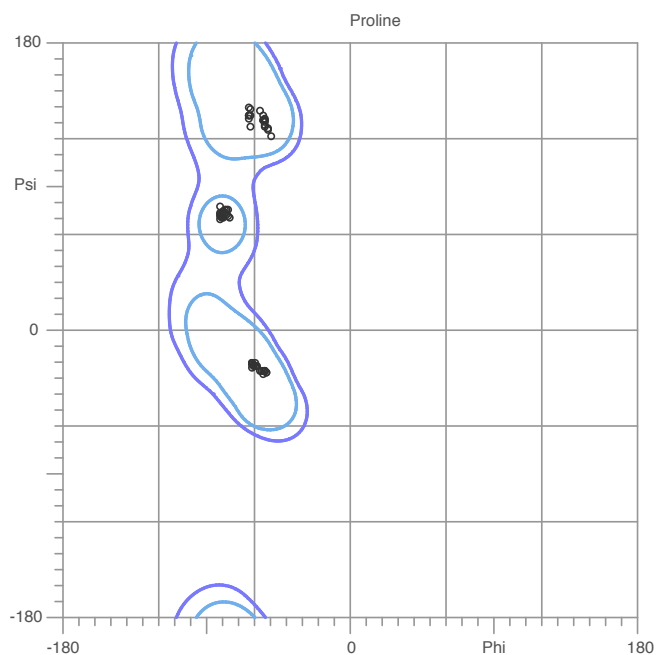
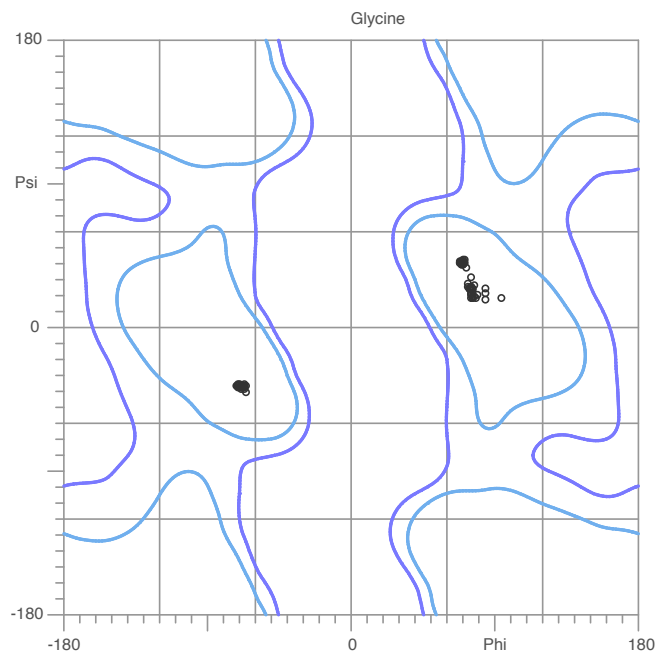
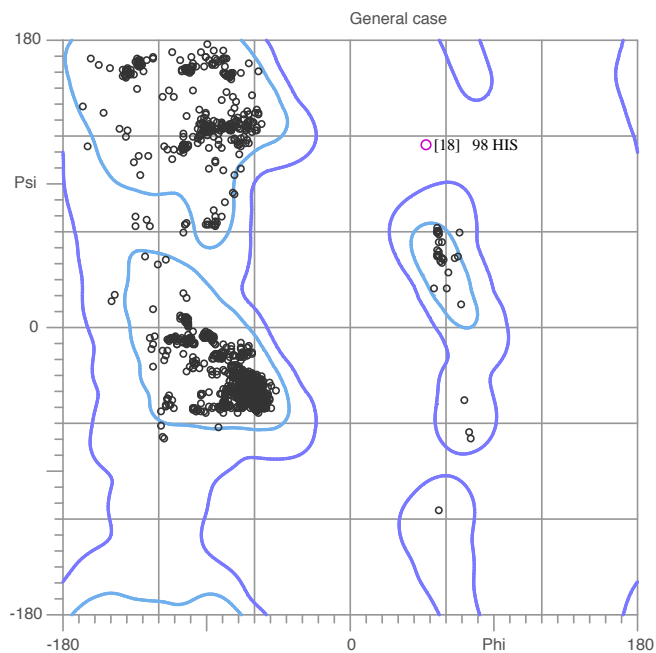


# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, all models



98.9% (1958/1980) of all residues were in favored (98%) regions.  
99.9% (1979/1980) of all residues were in allowed (>99.8%) regions.

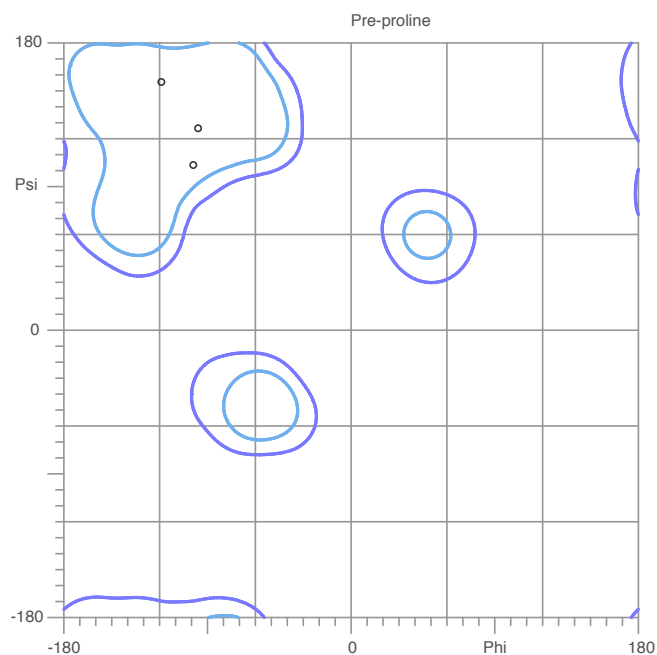
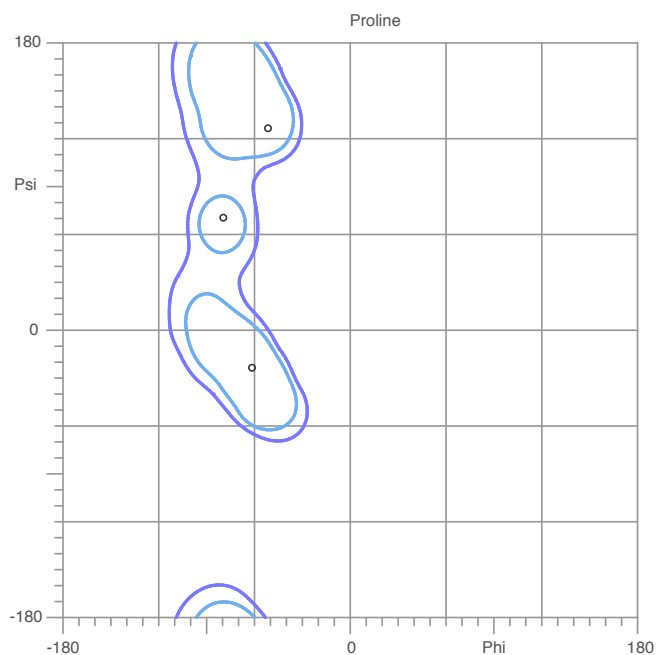
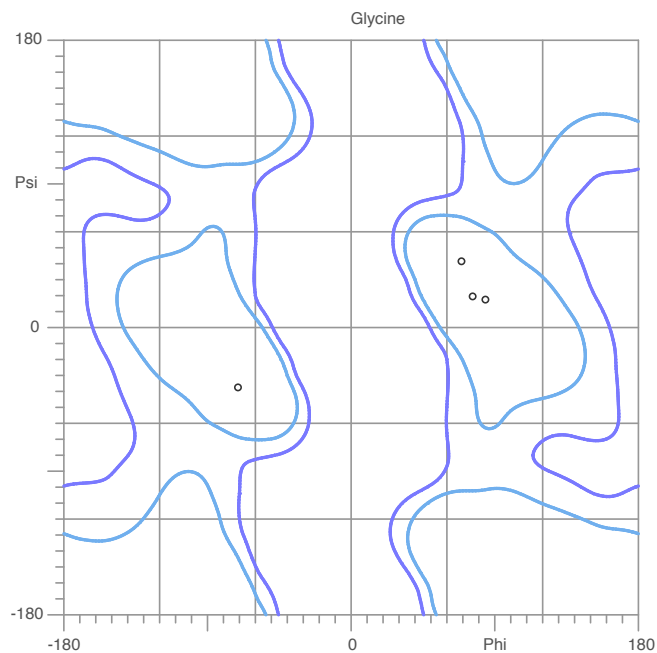
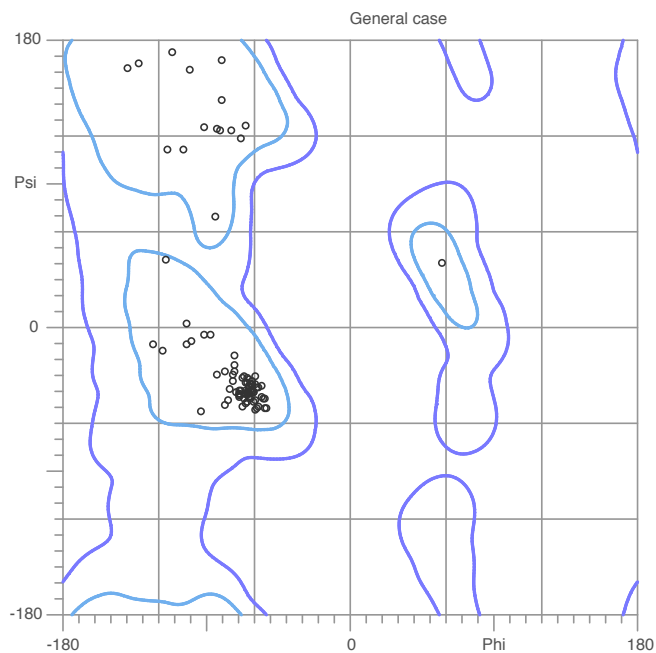
There were 1 outliers (phi, psi):  
[18] 98 HIS (47.4, 115.0)

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 1



100.0% (99/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

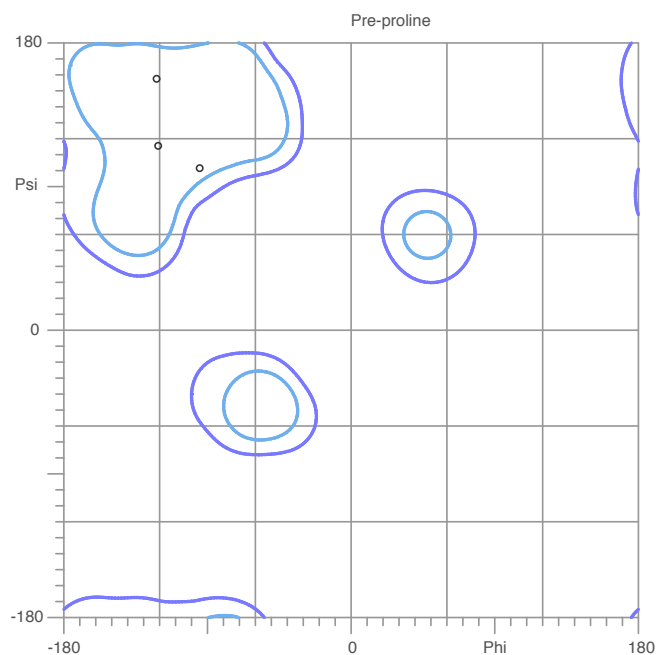
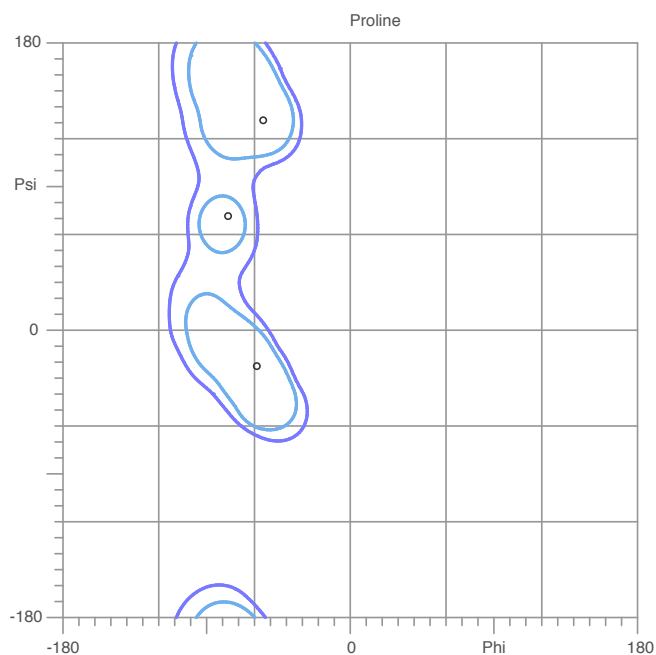
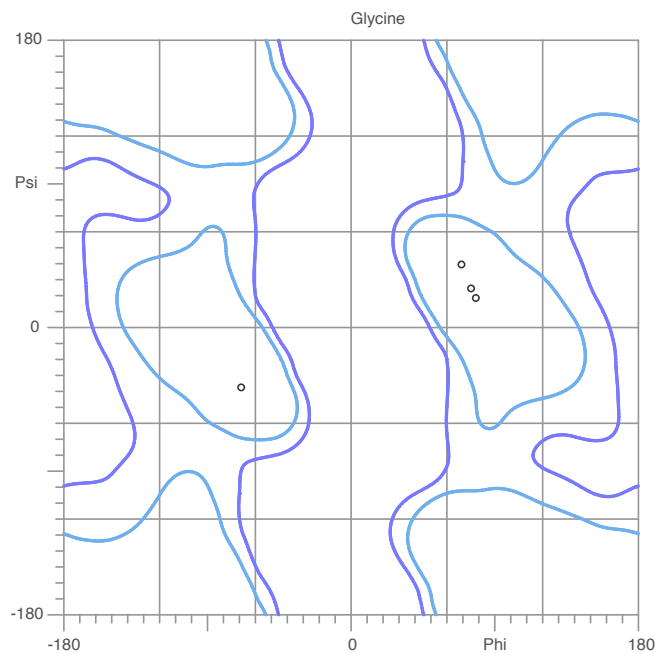
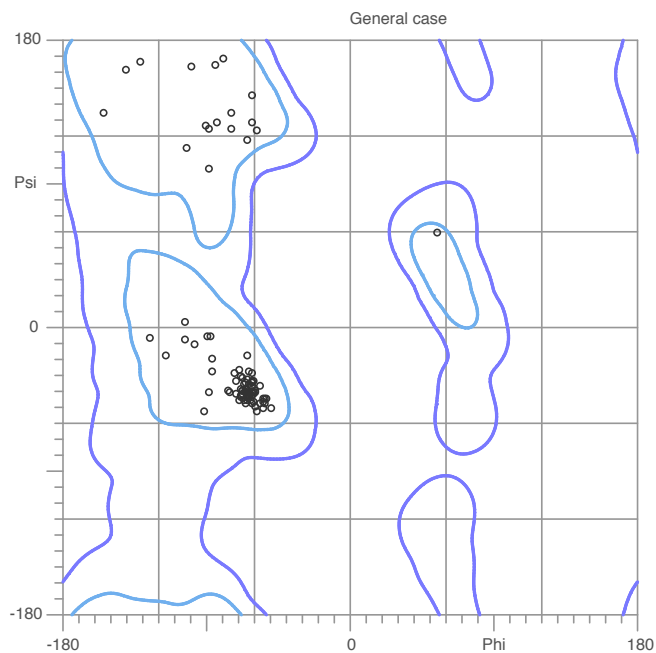
There were no outliers.

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

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

# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 2



100.0% (99/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

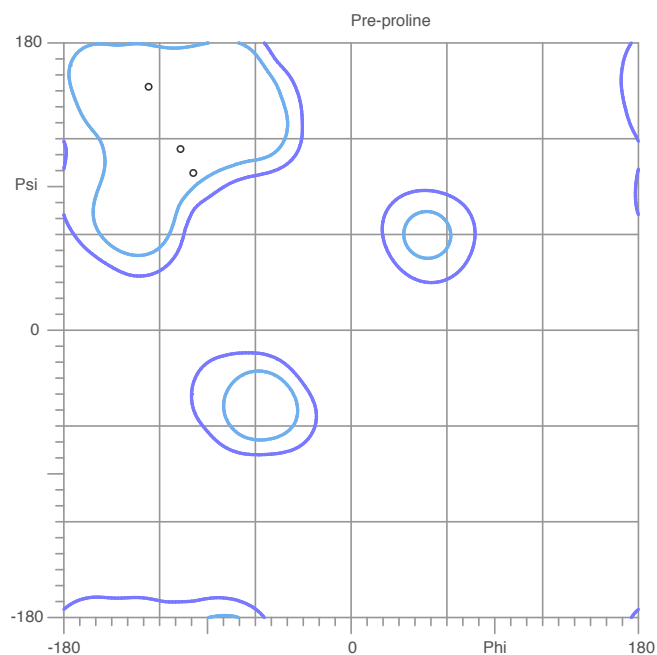
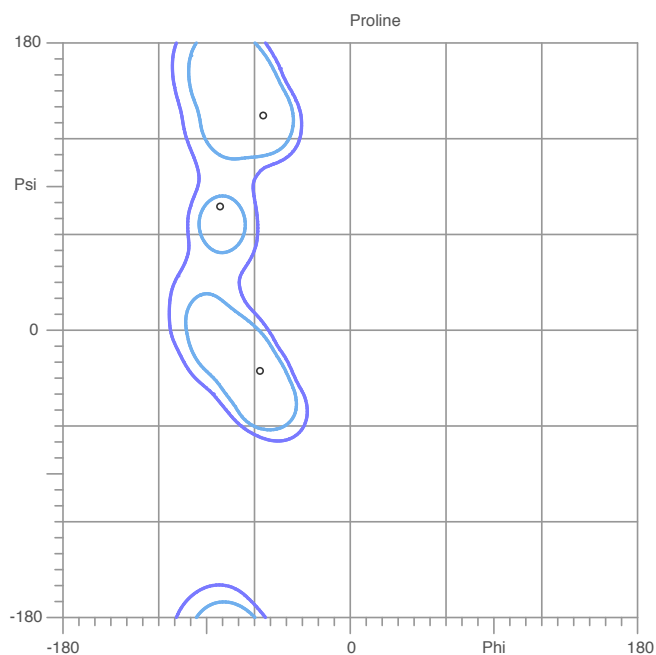
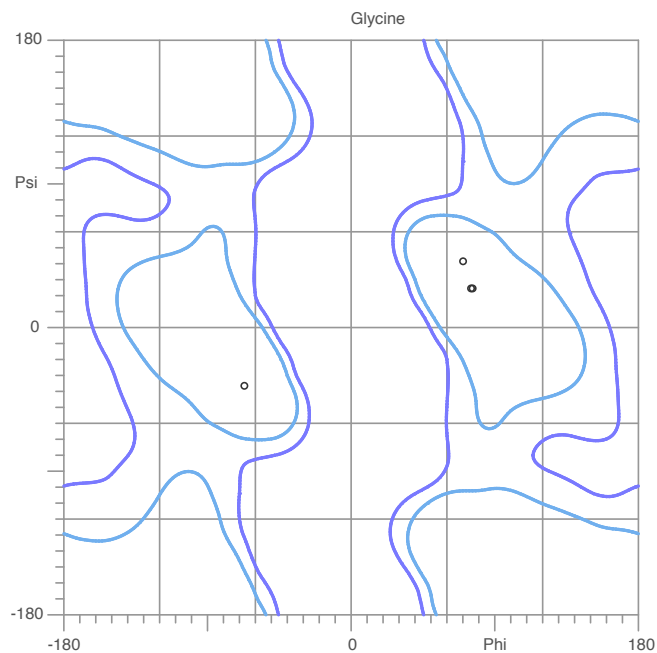
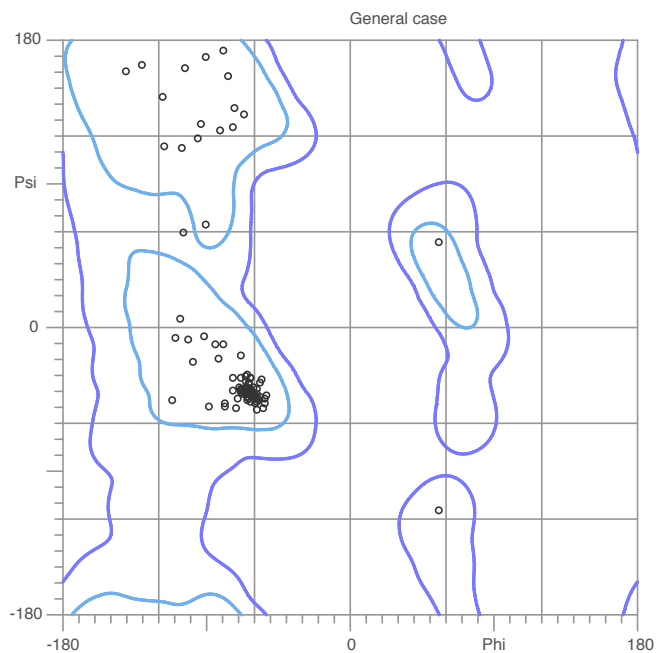
There were no outliers.

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

# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 3



98.0% (97/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

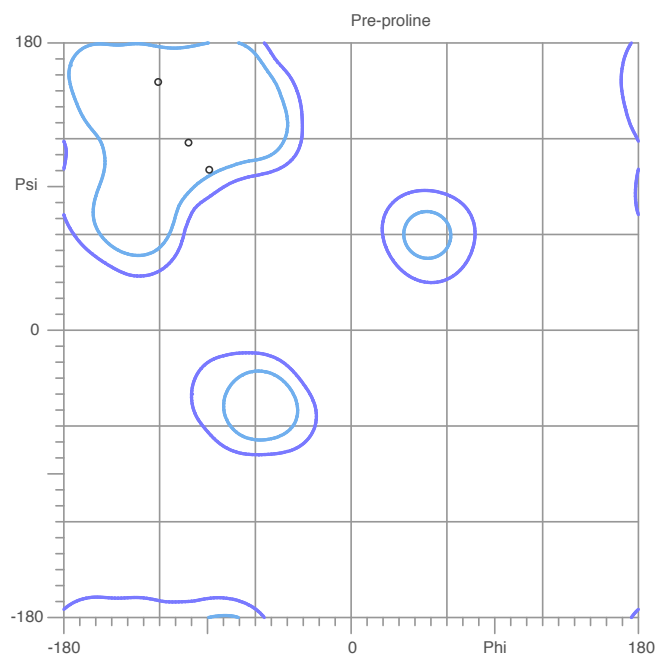
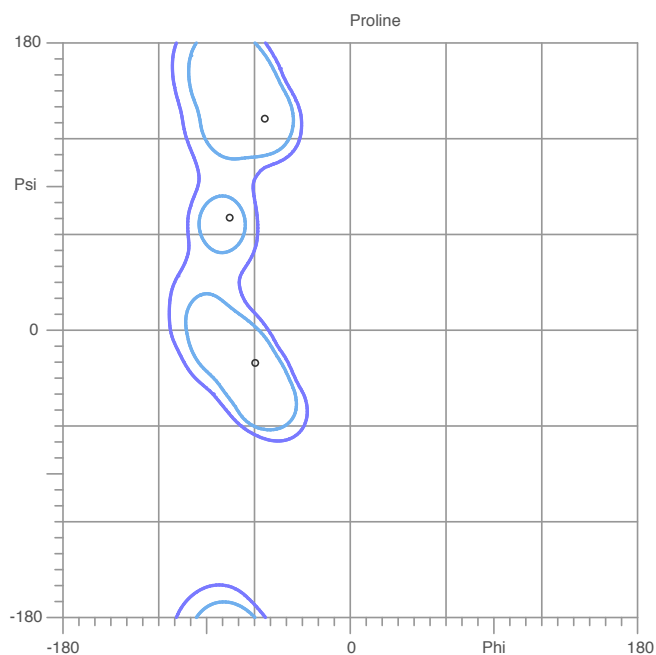
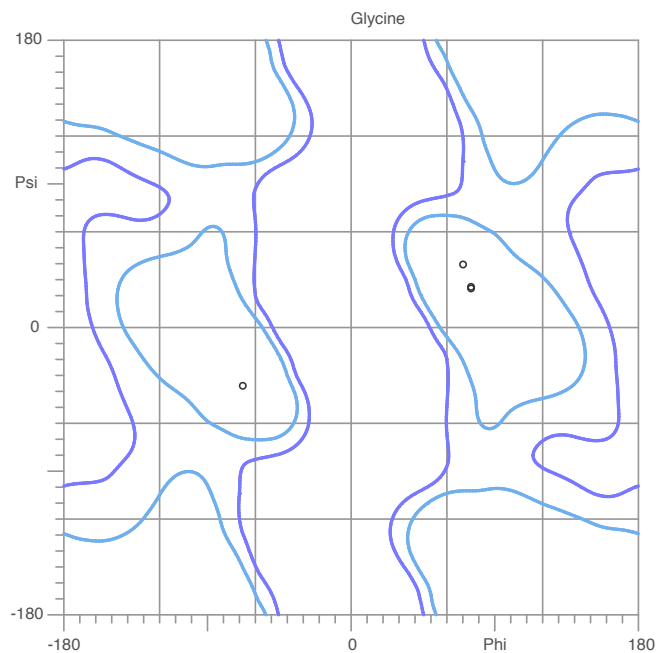
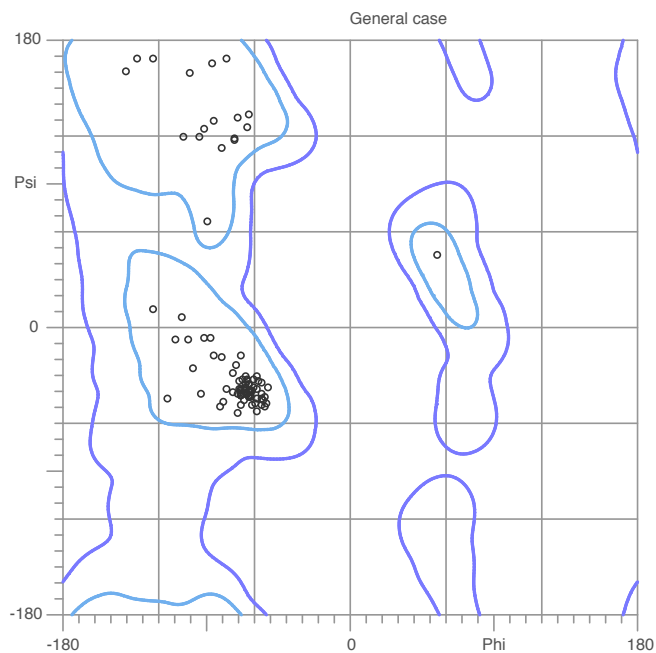
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 4



100.0% (99/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

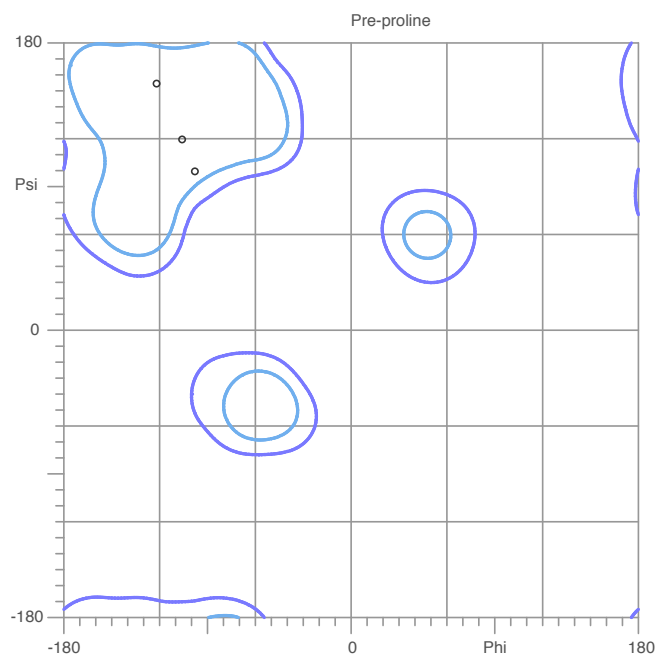
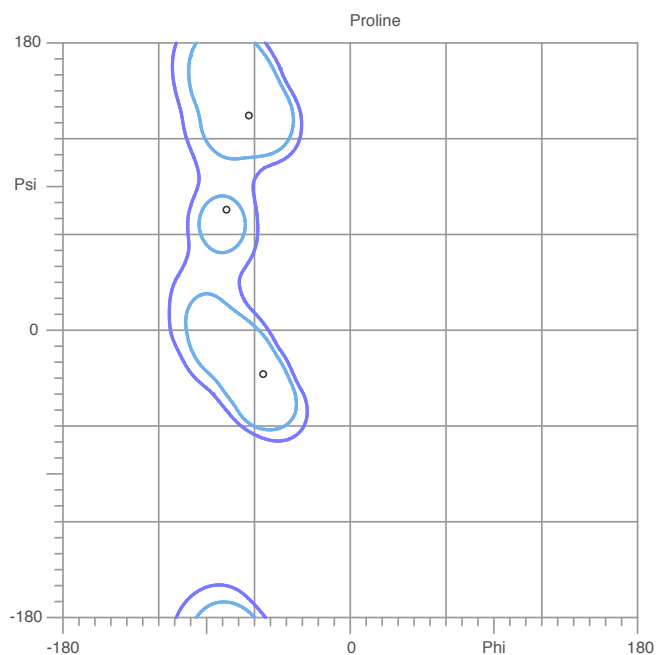
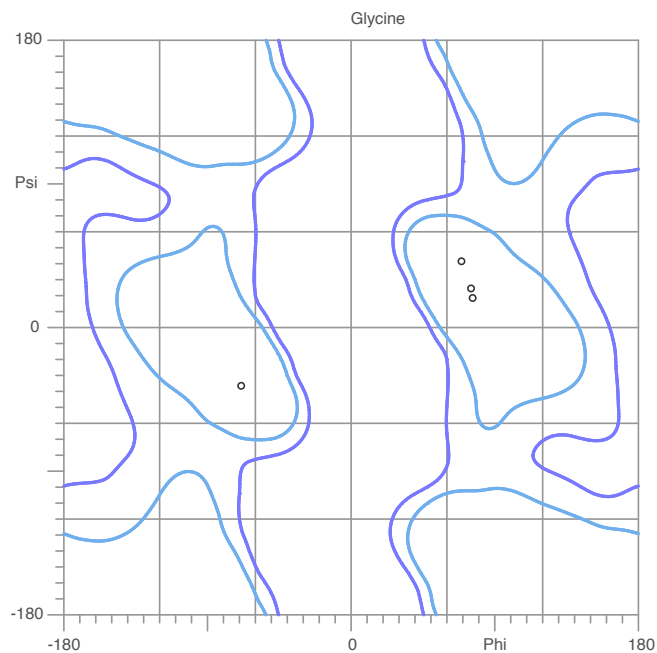
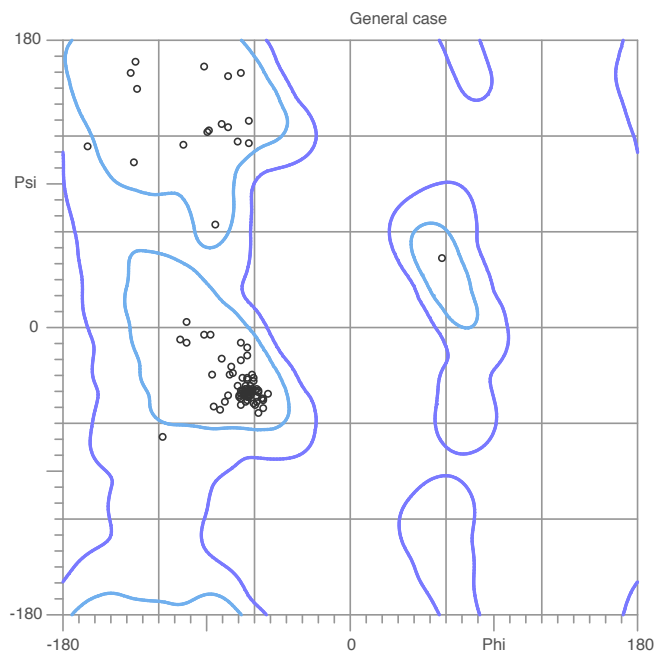
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 5



98.0% (97/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

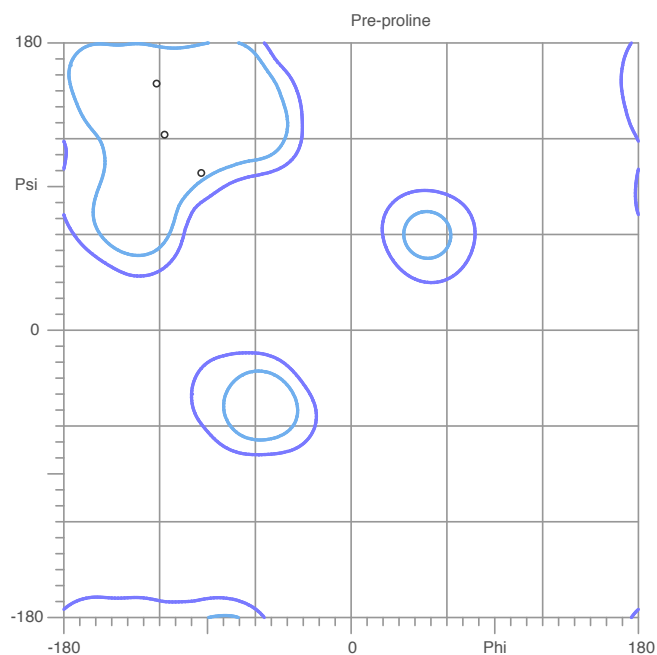
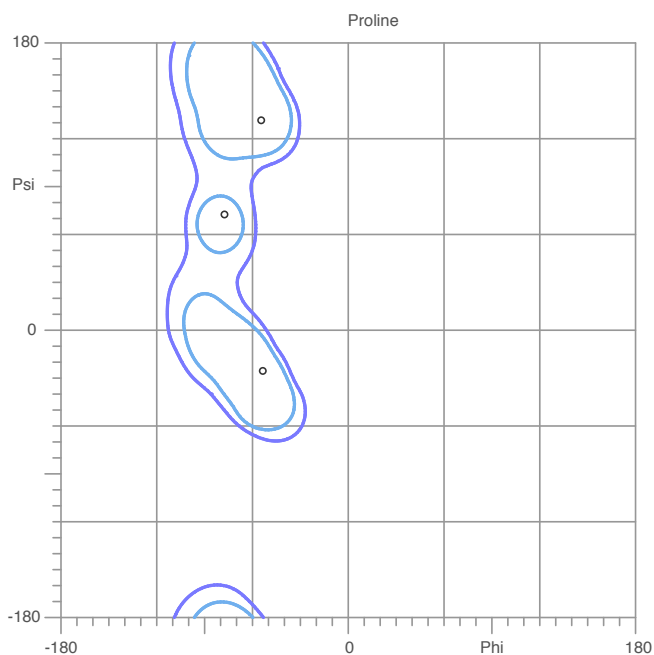
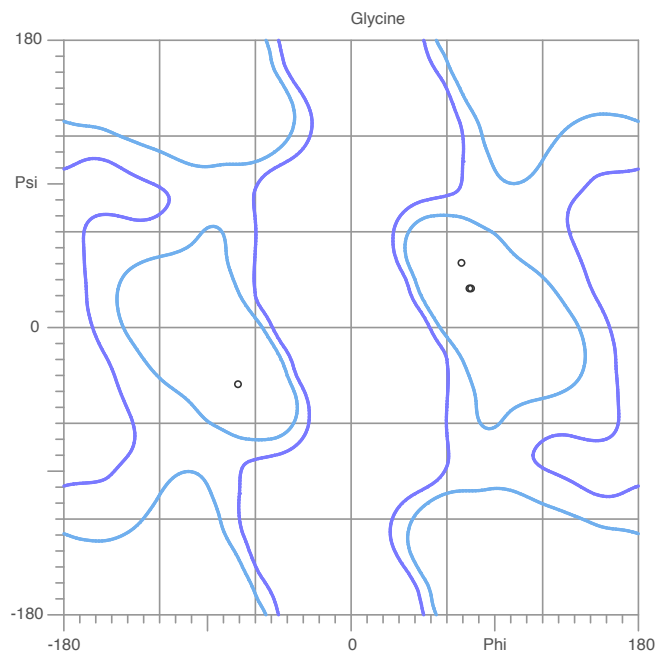
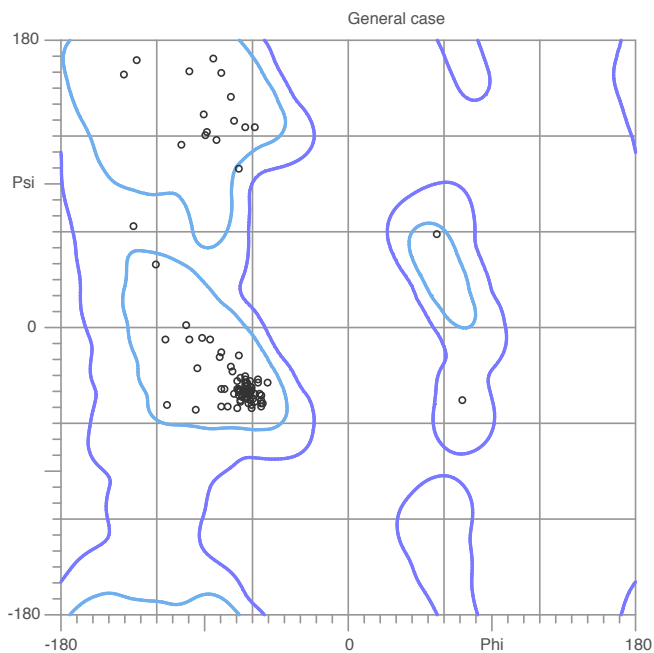
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 6



97.0% (96/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

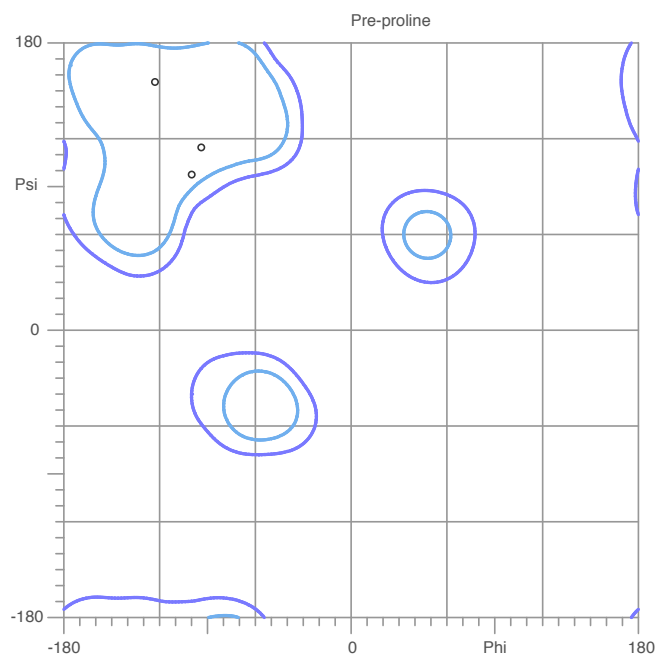
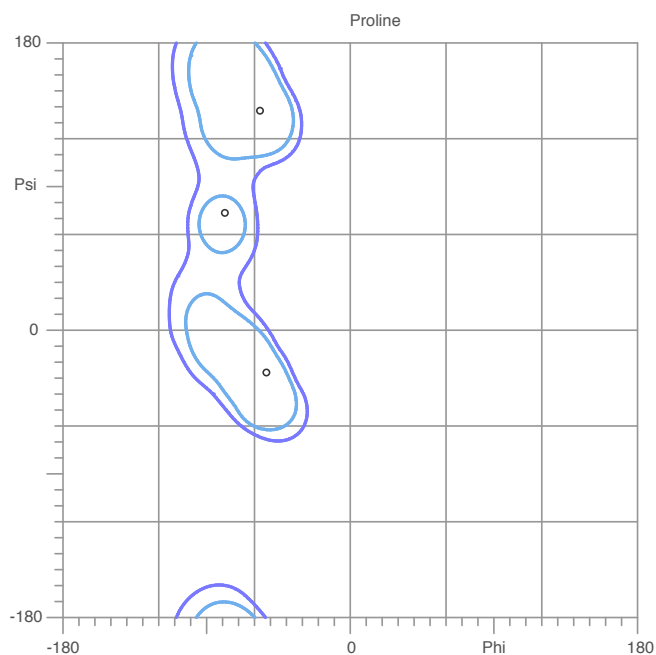
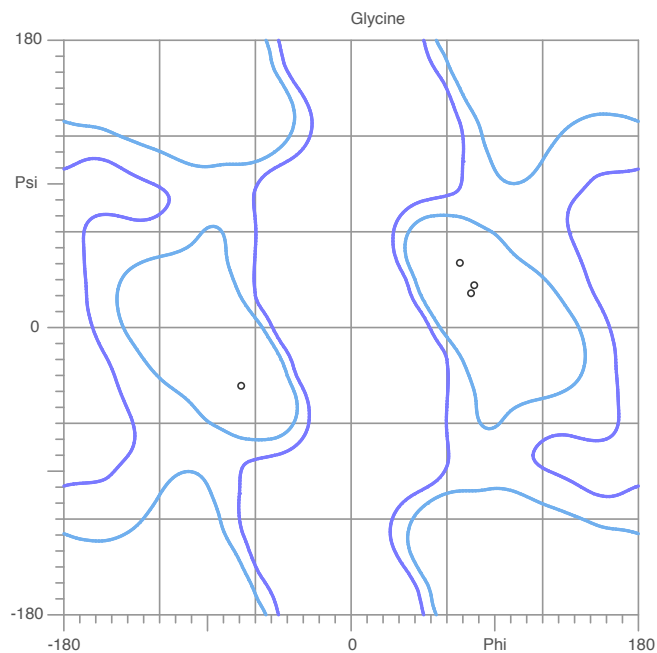
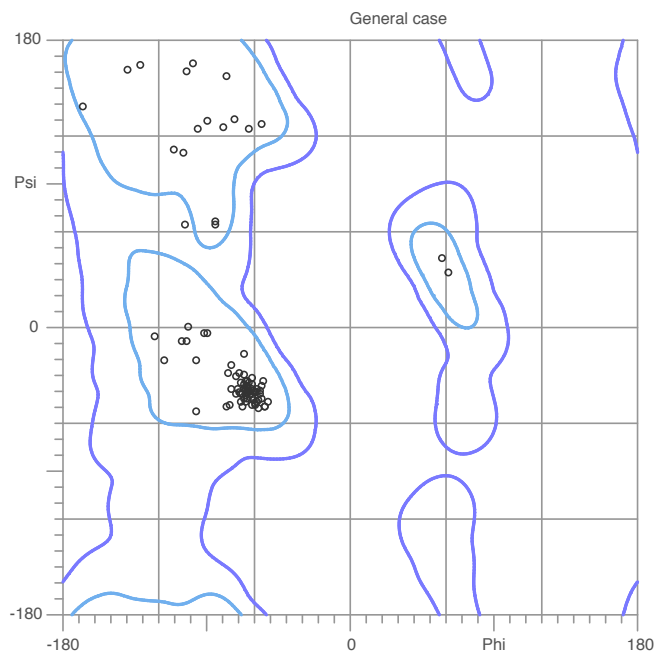
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 7

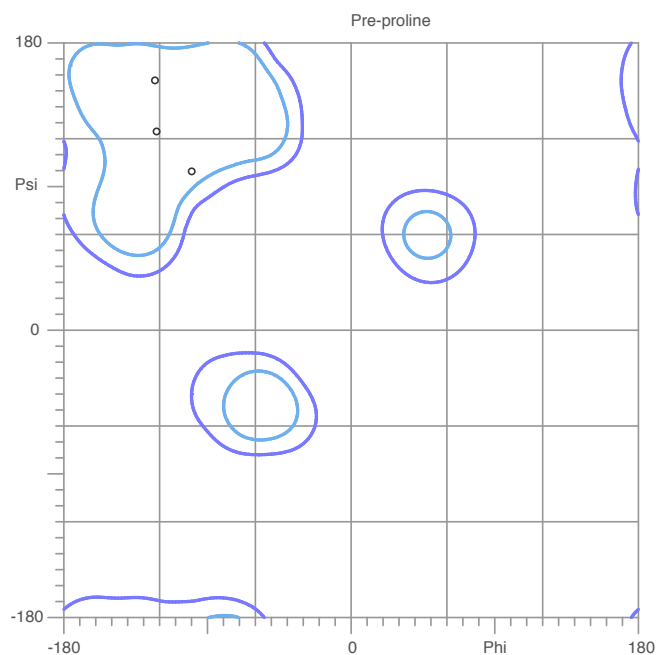
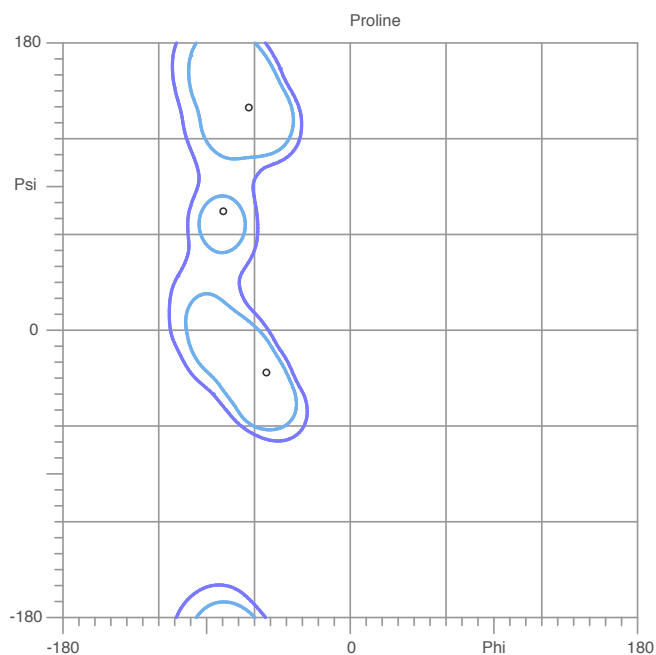
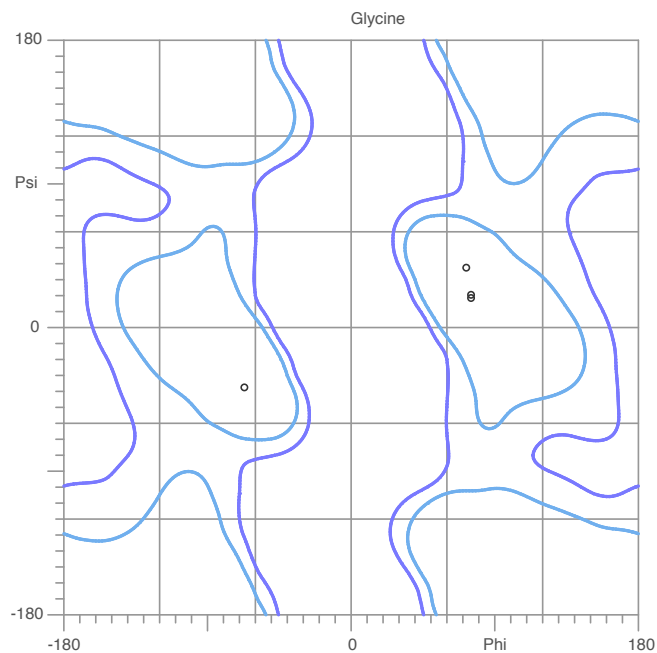
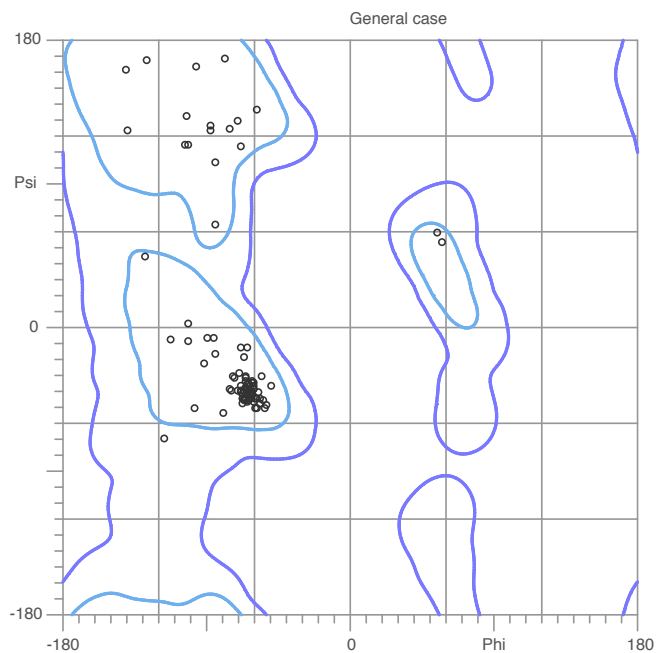


99.0% (98/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 8



99.0% (98/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

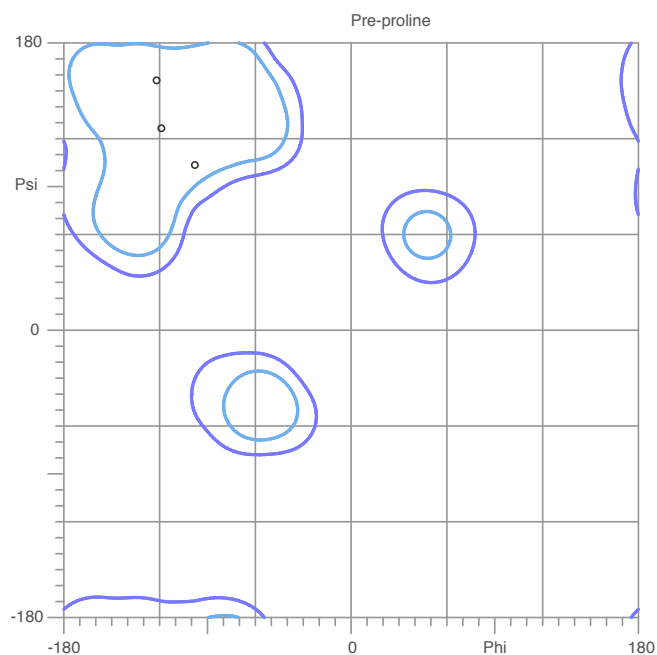
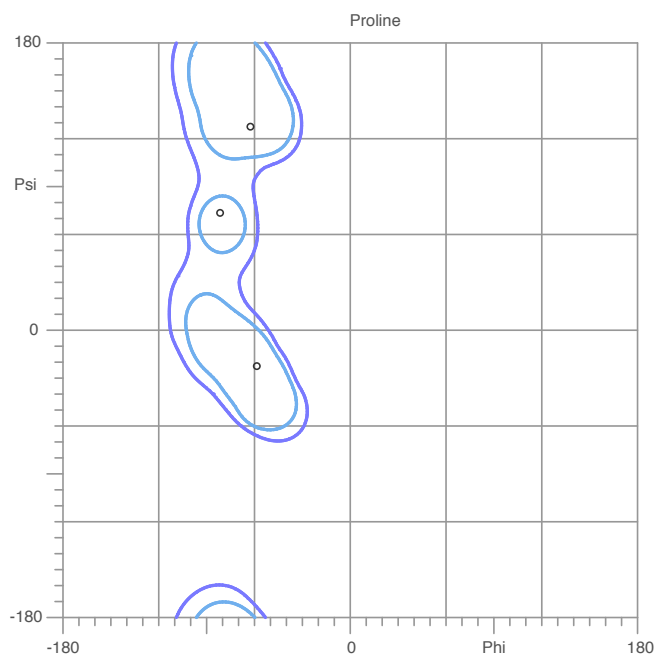
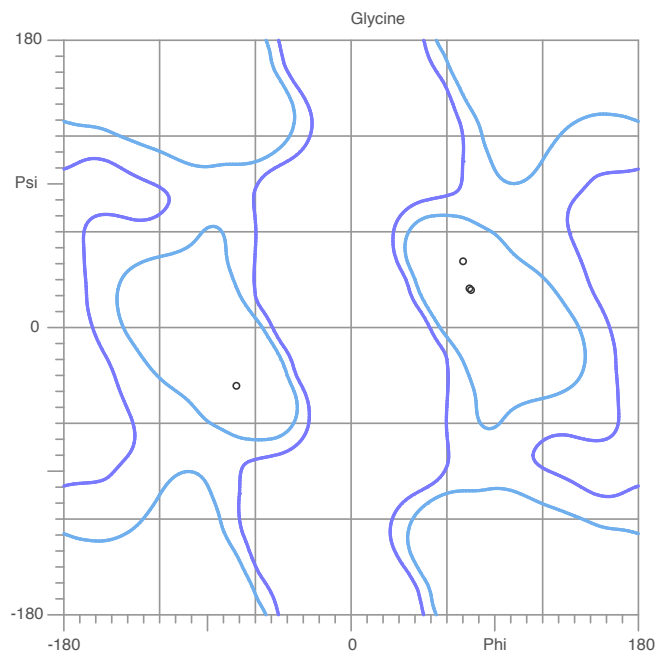
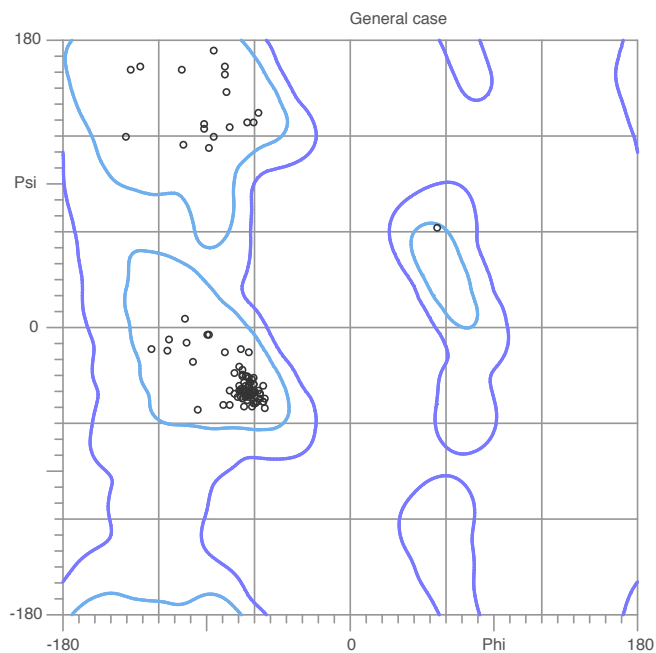
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 9



100.0% (99/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

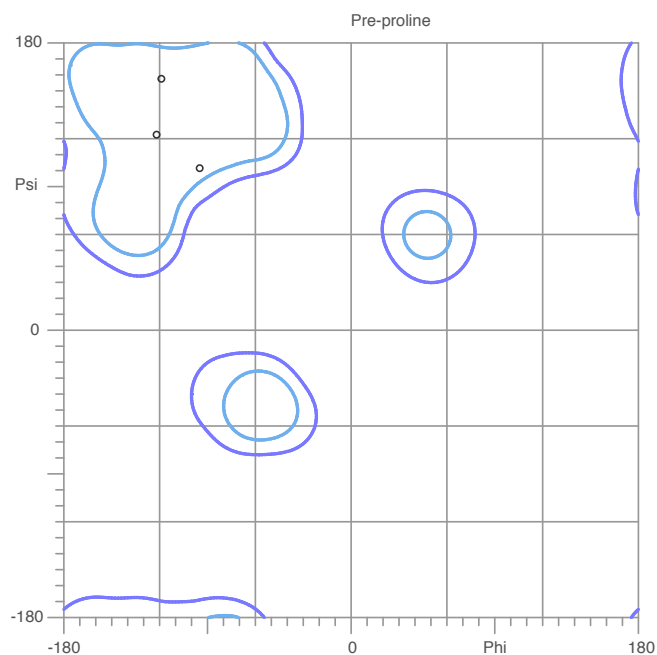
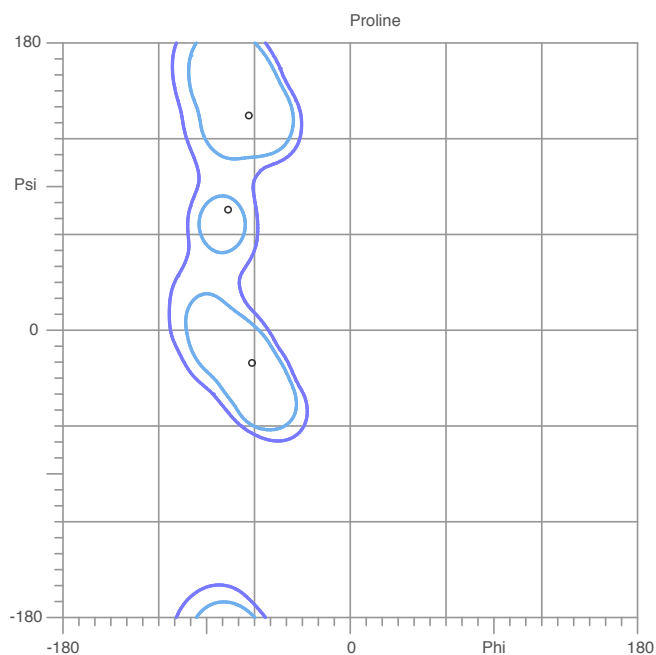
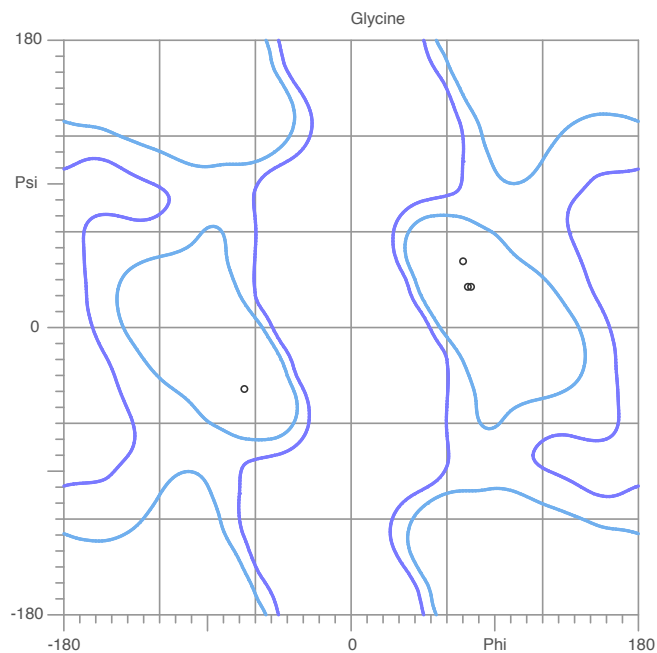
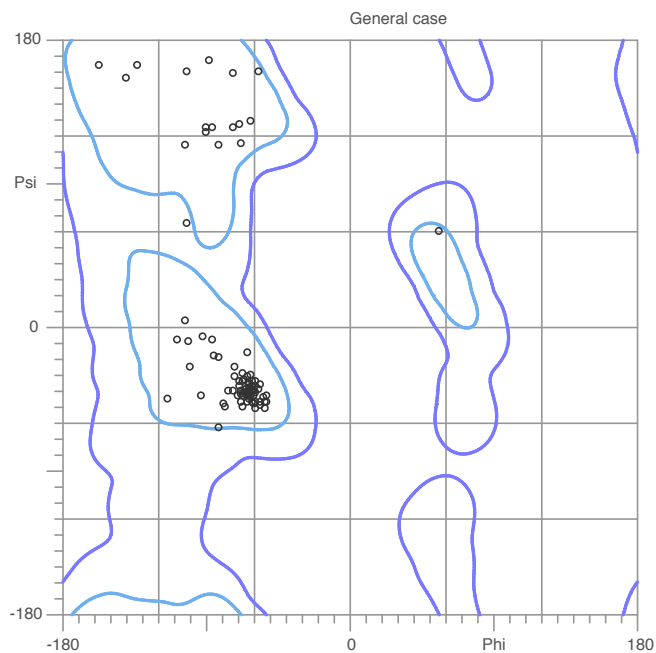
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 10



99.0% (98/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

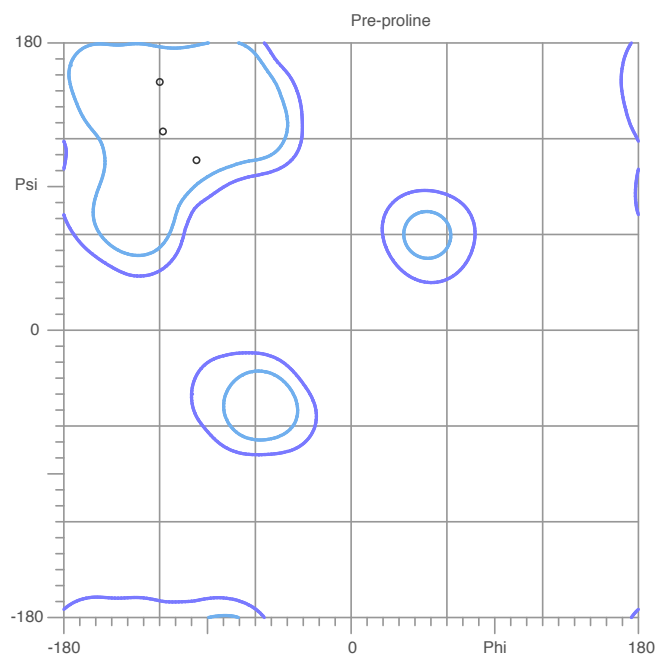
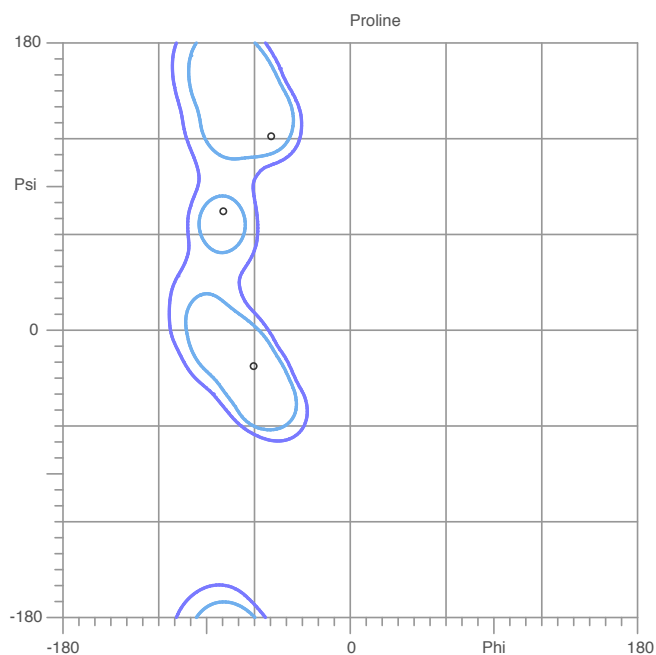
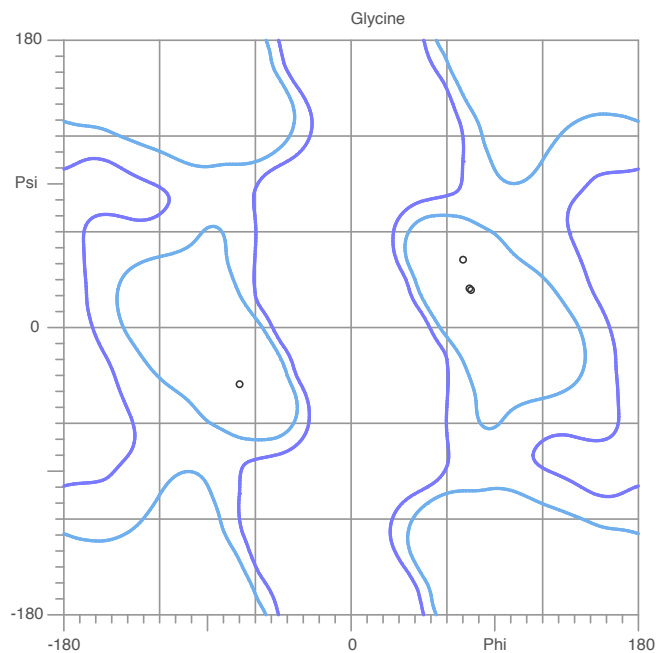
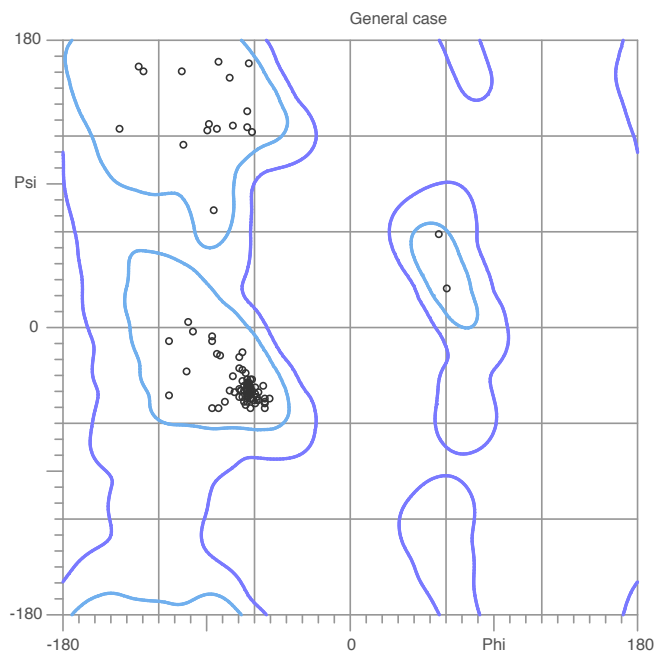
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 11



100.0% (99/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

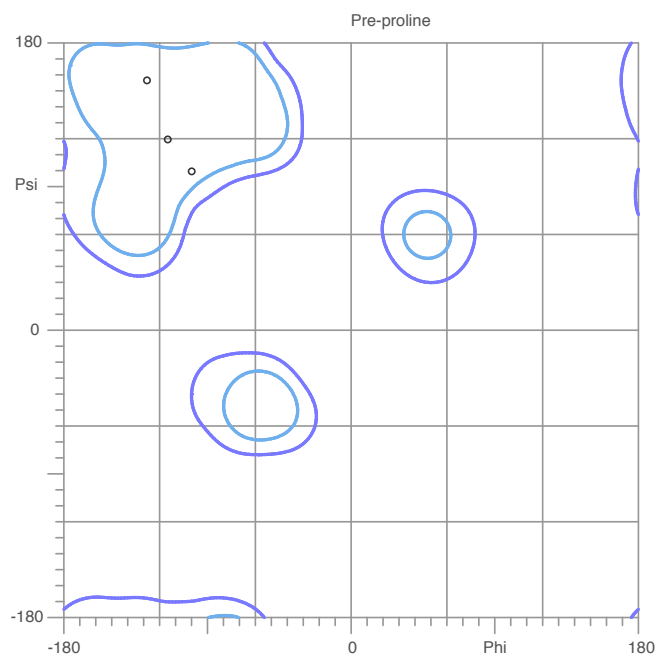
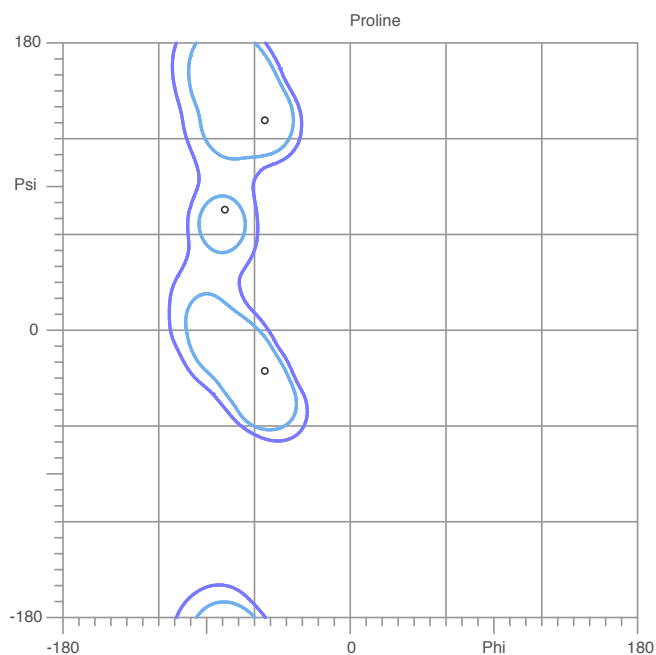
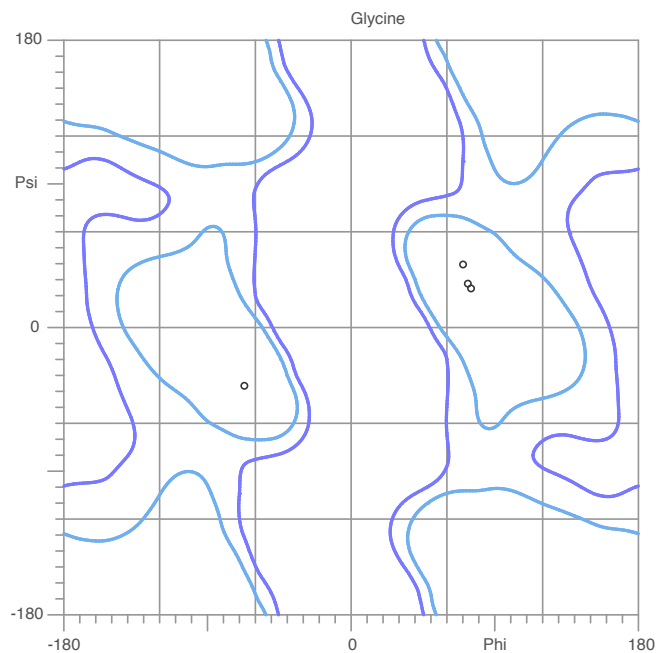
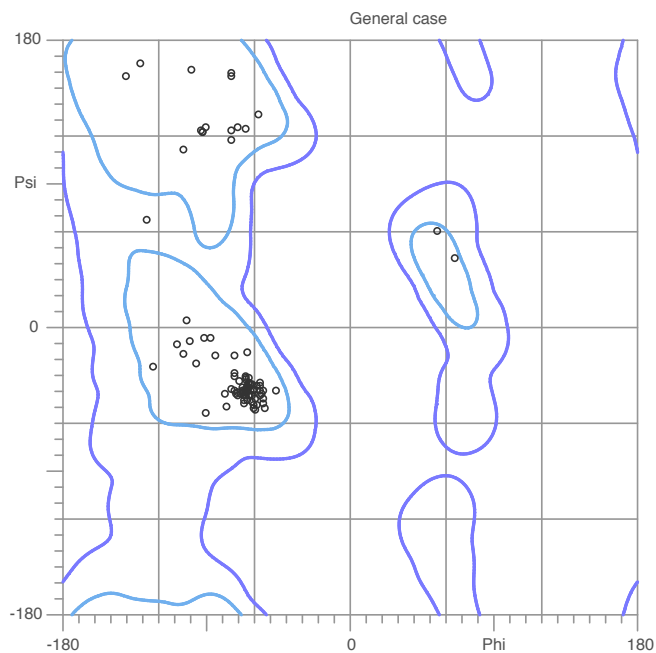
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 12



99.0% (98/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

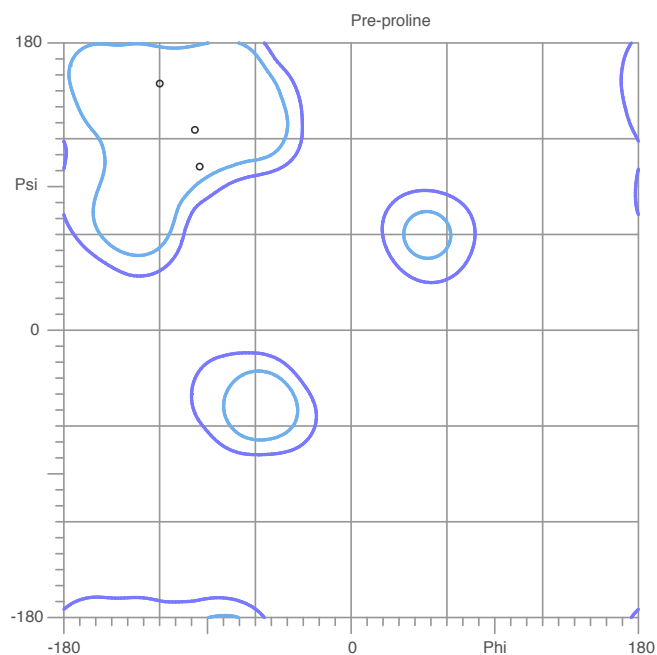
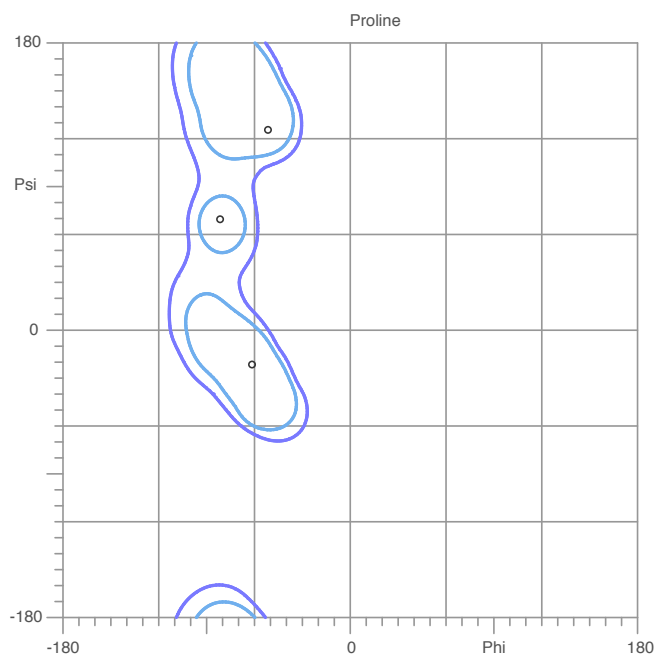
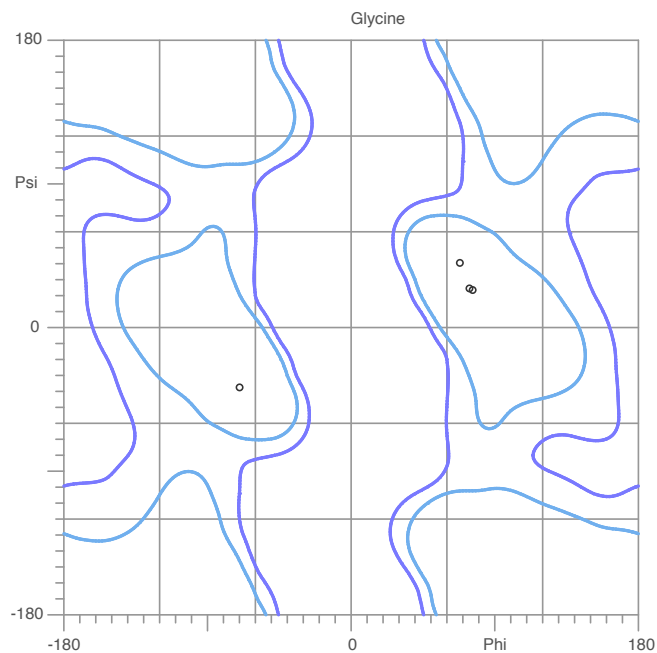
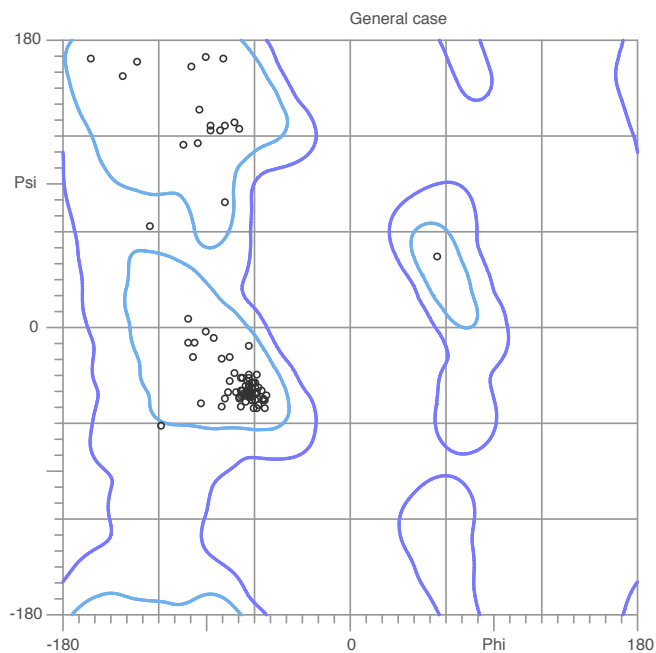
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 13



98.0% (97/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

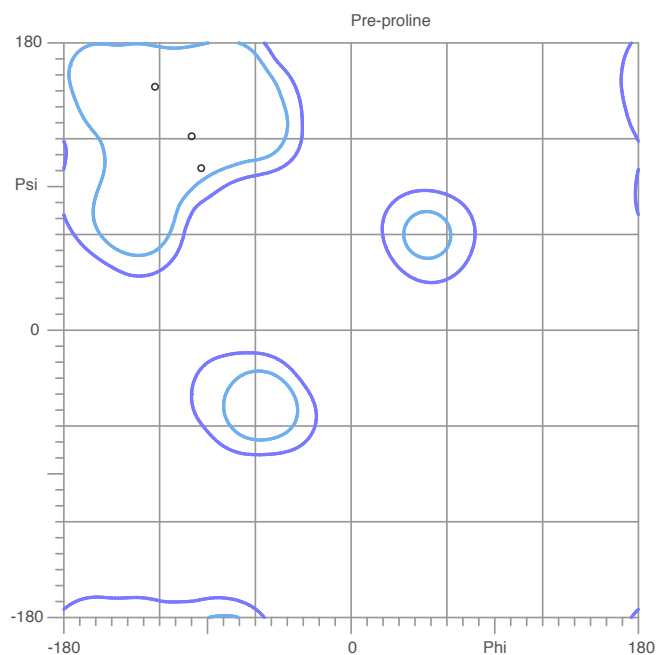
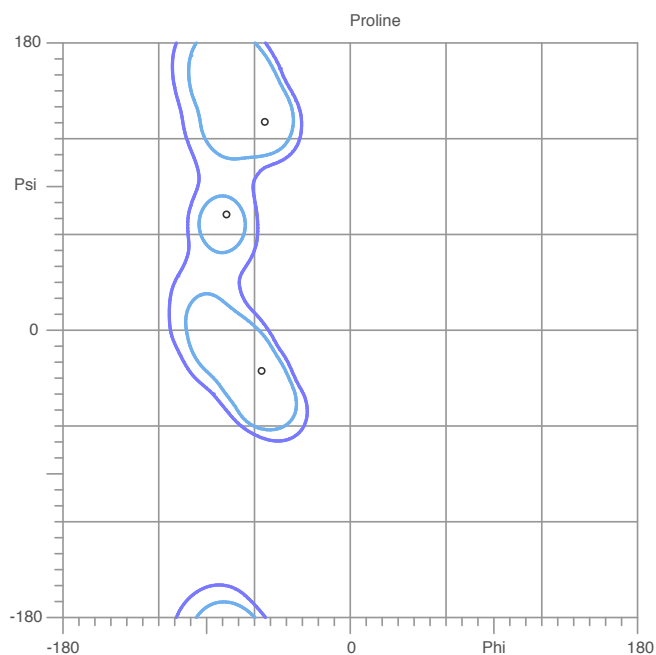
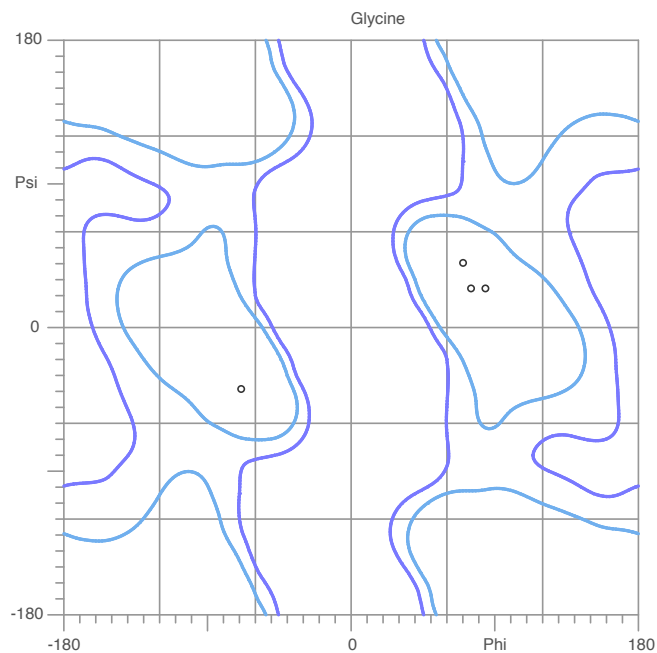
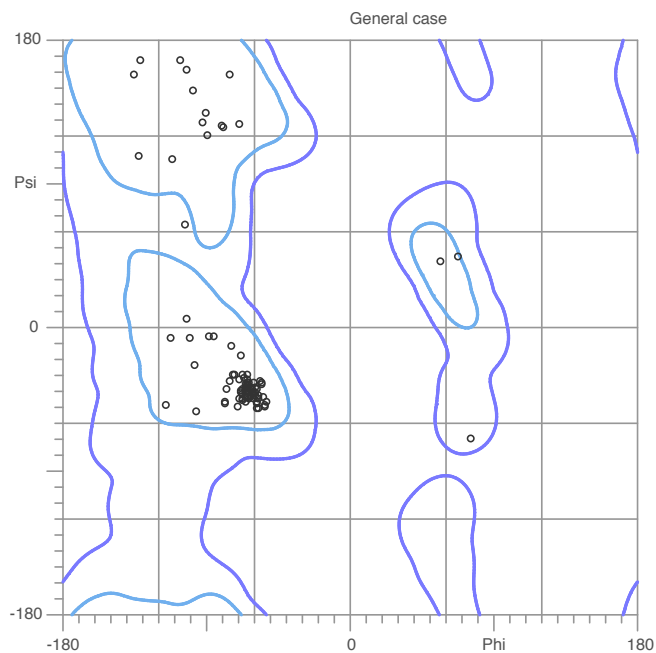
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 14



98.0% (97/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

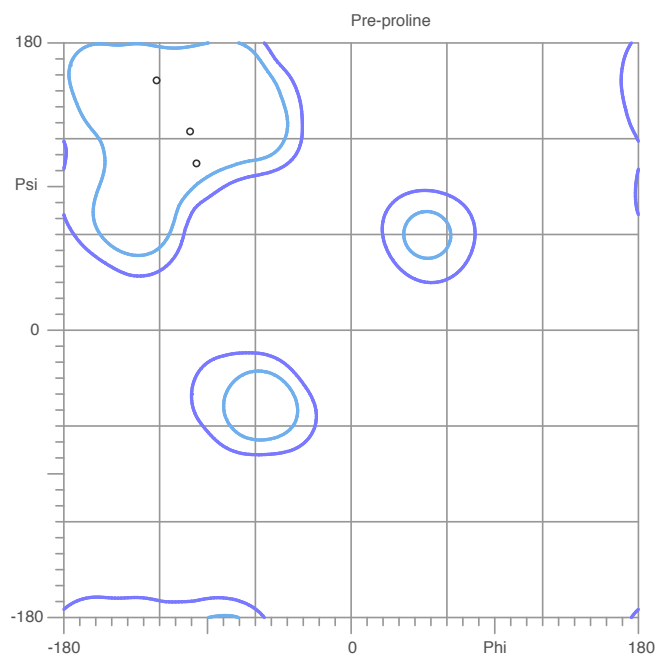
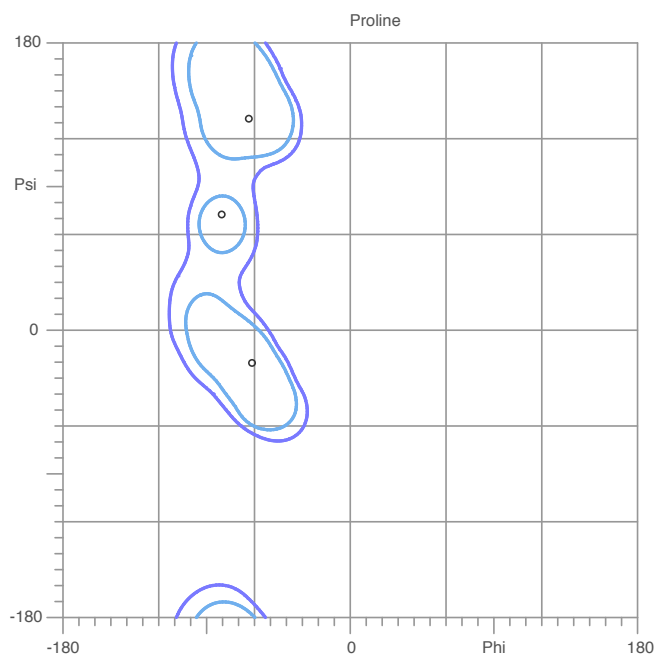
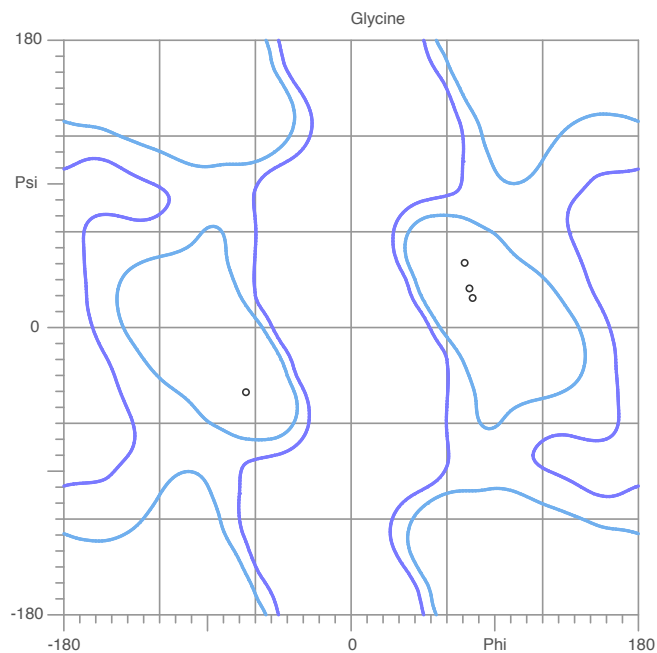
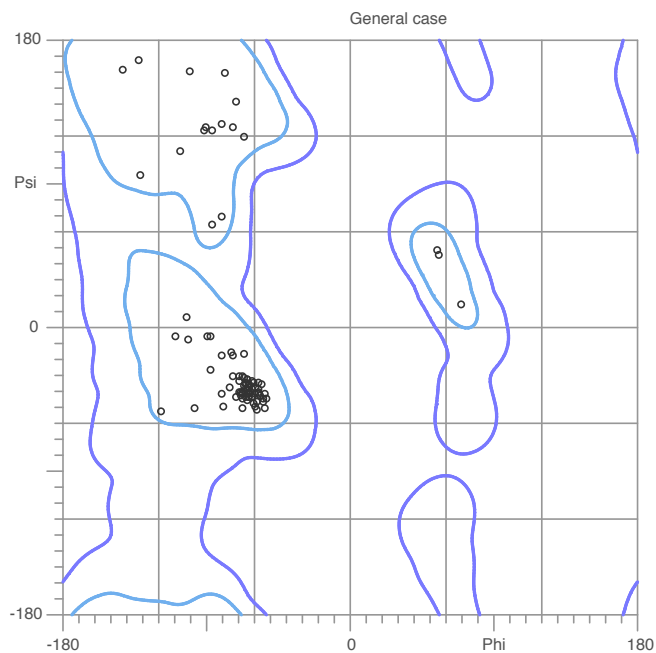
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 15



100.0% (99/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

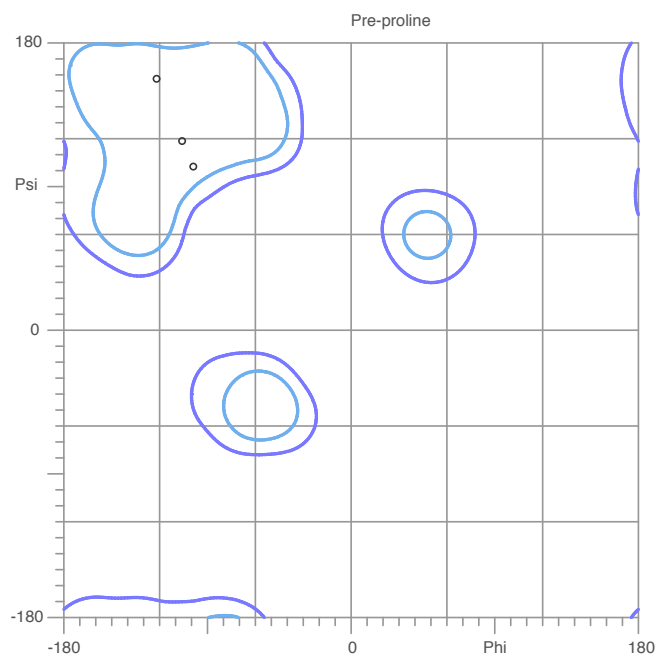
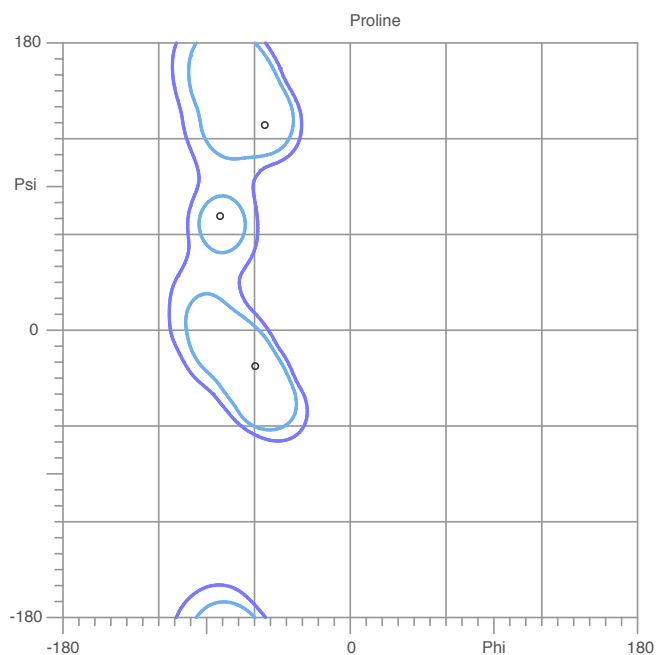
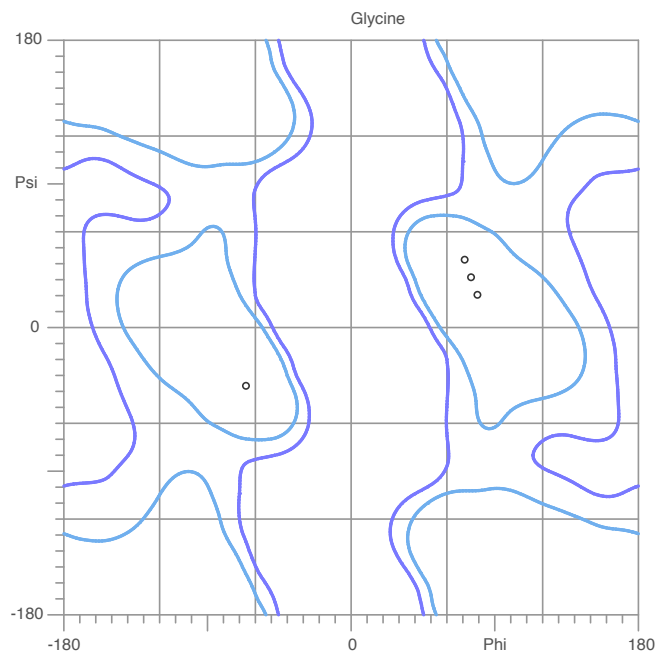
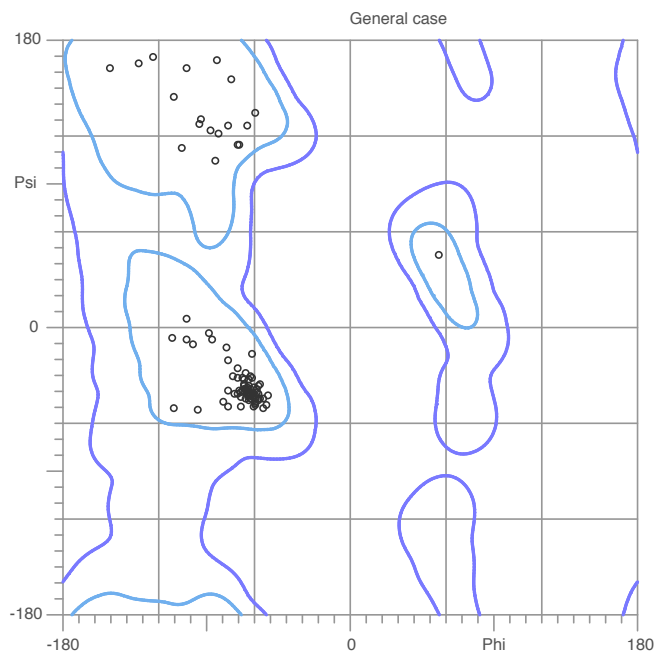
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 16



100.0% (99/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

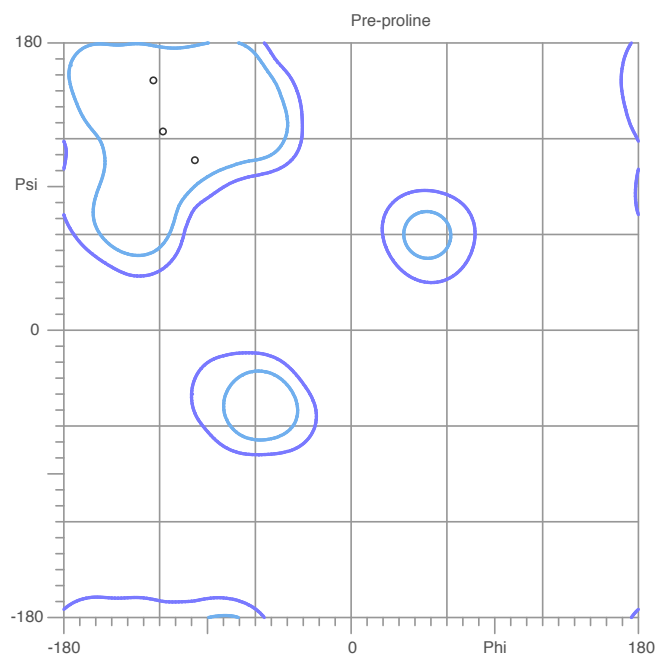
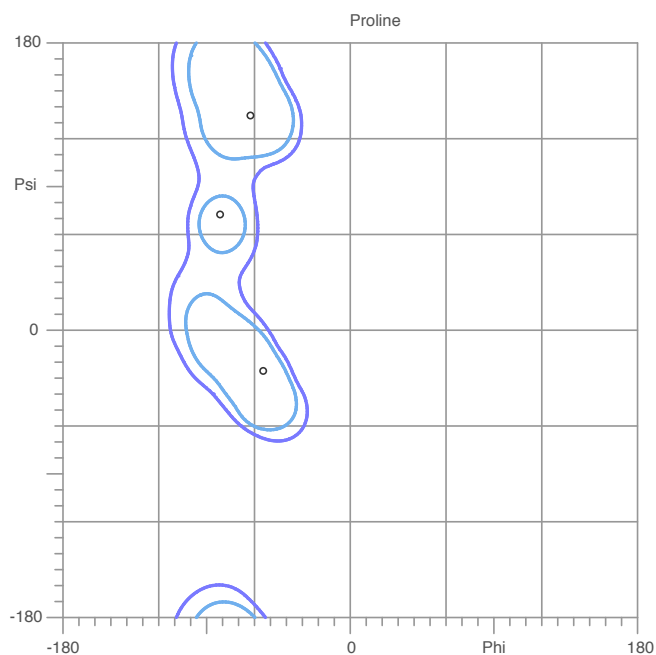
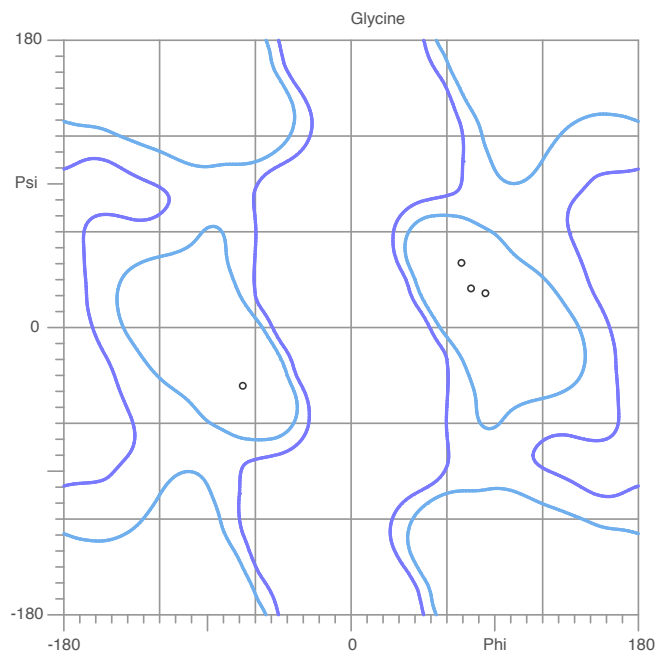
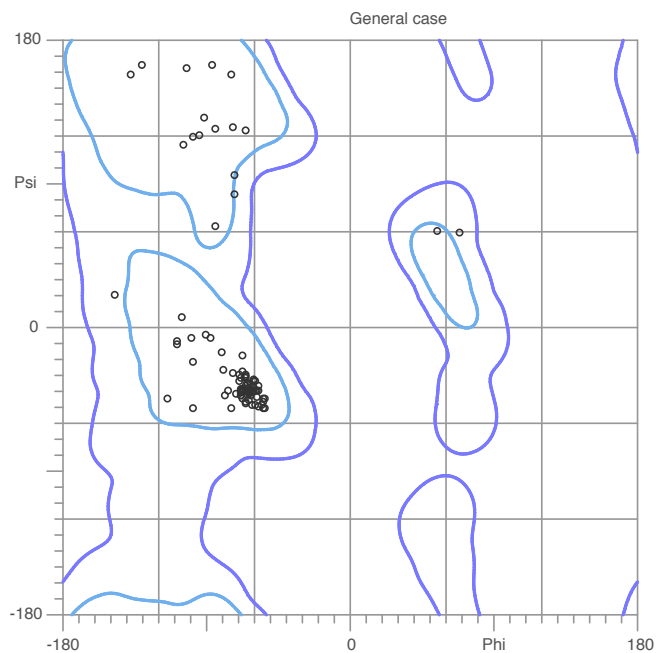
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 17



97.0% (96/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

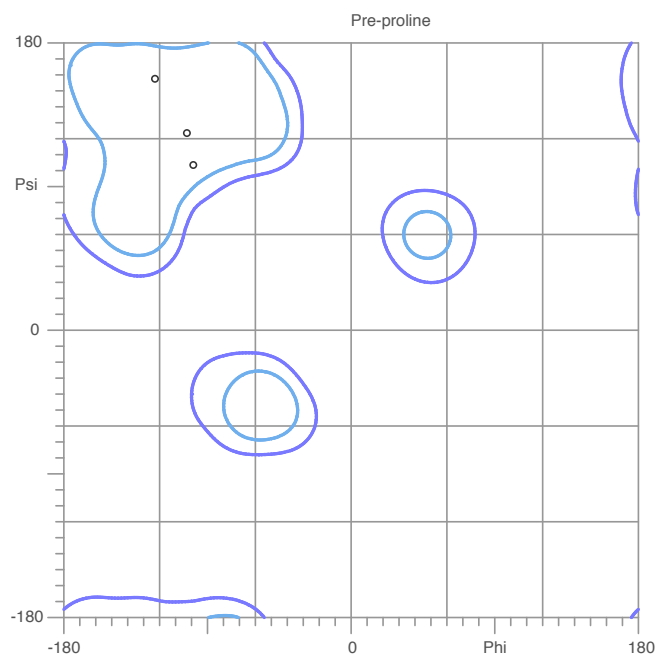
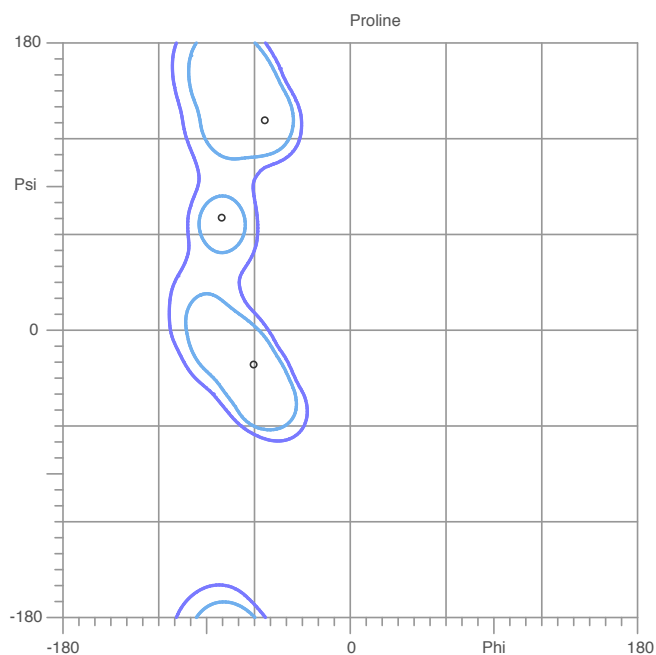
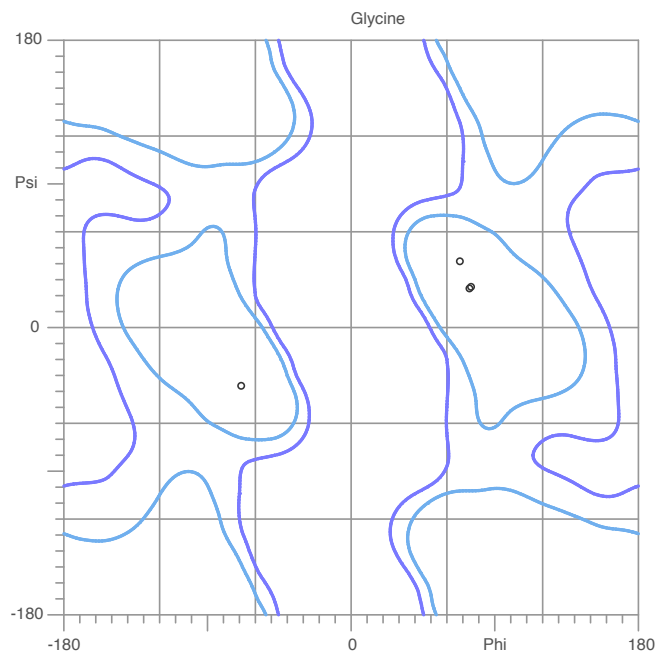
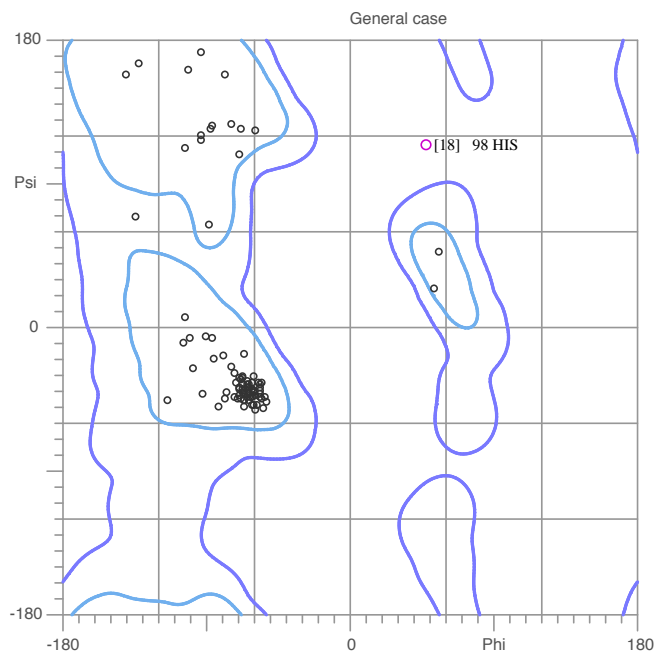
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 18



98.0% (97/99) of all residues were in favored (98%) regions.  
99.0% (98/99) of all residues were in allowed (>99.8%) regions.

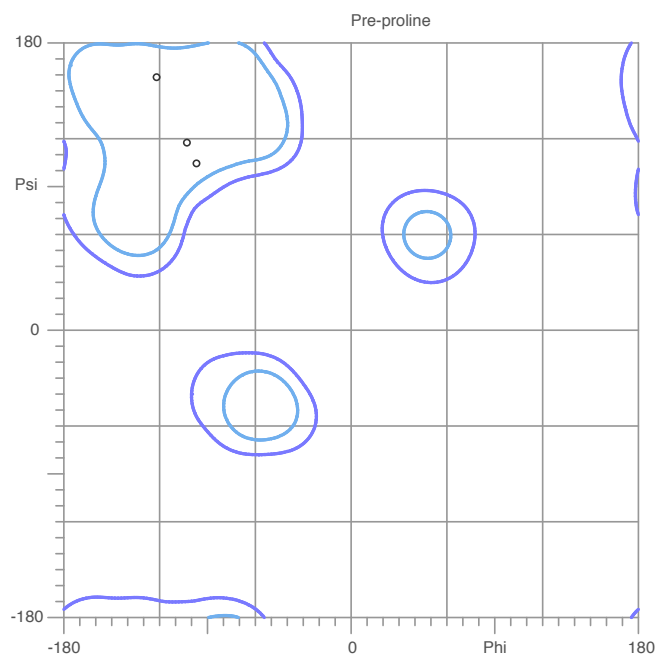
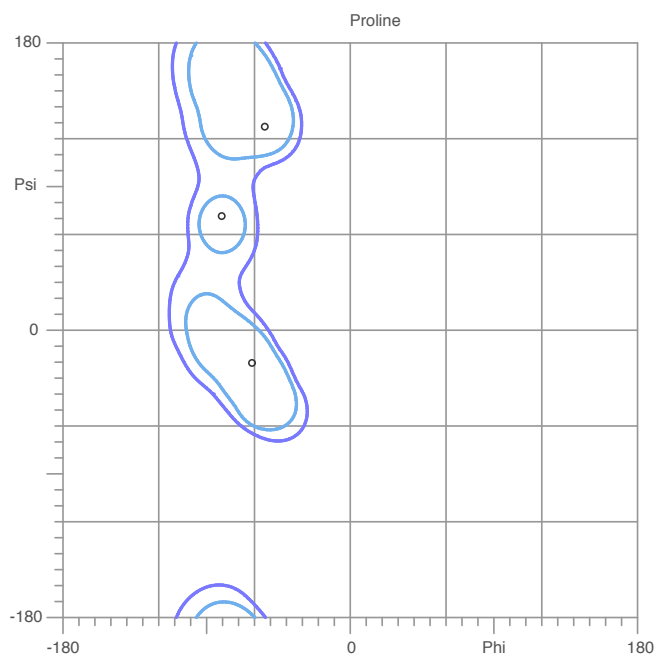
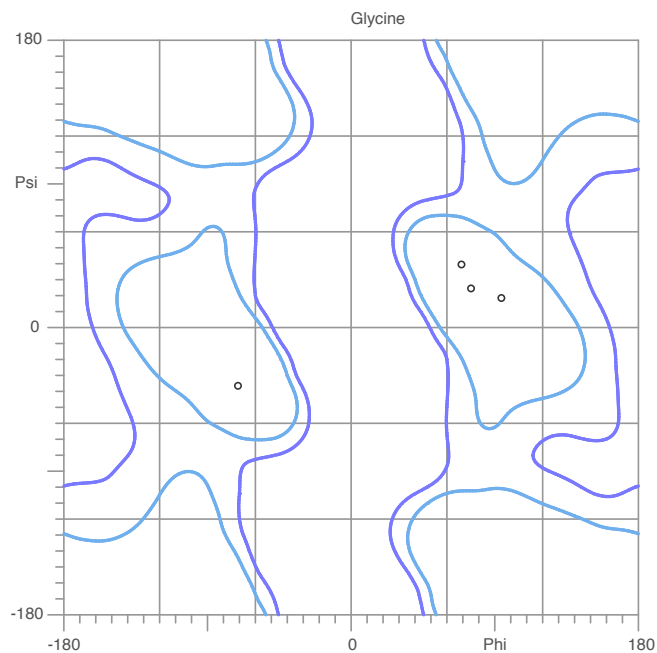
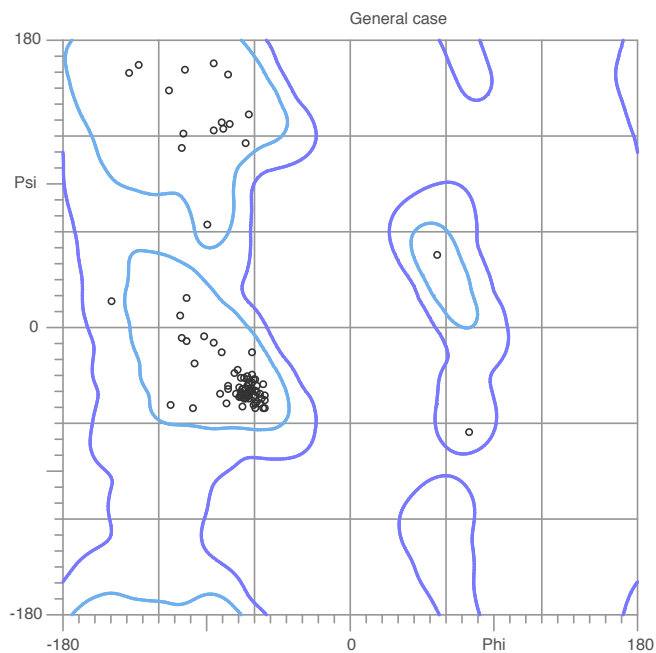
There were 1 outliers (phi, psi):  
[18] 98 HIS (47.4, 115.0)

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 19



98.0% (97/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

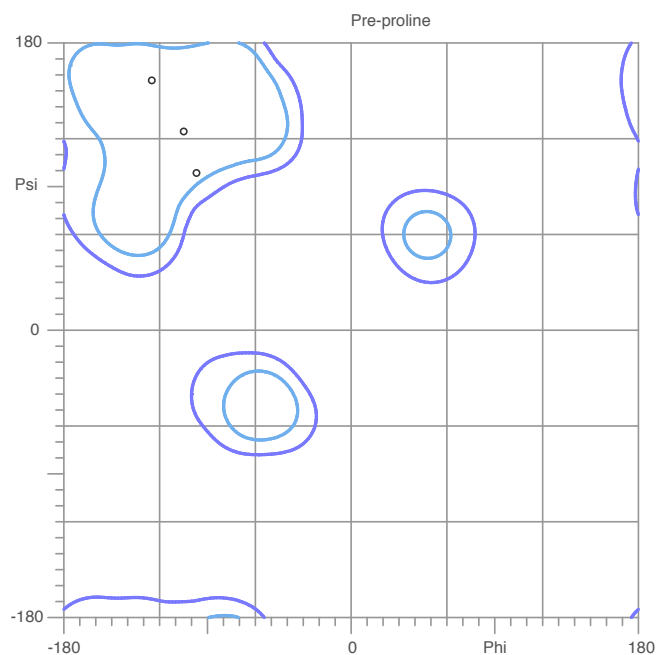
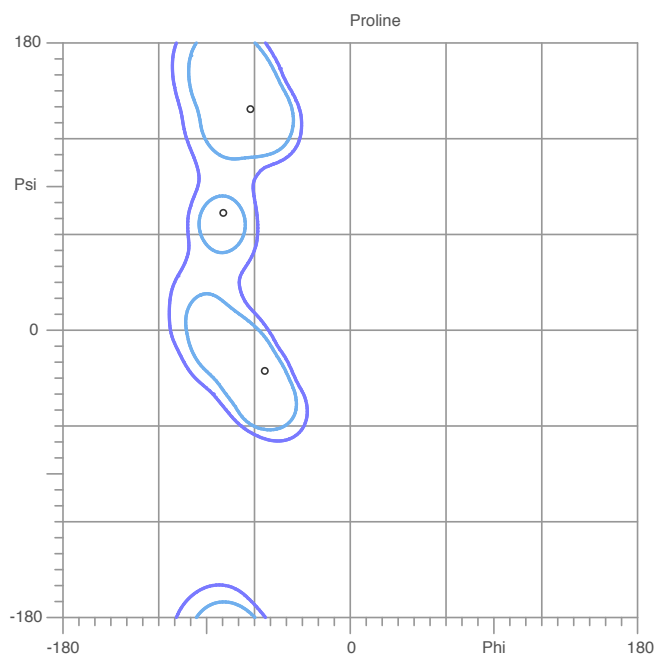
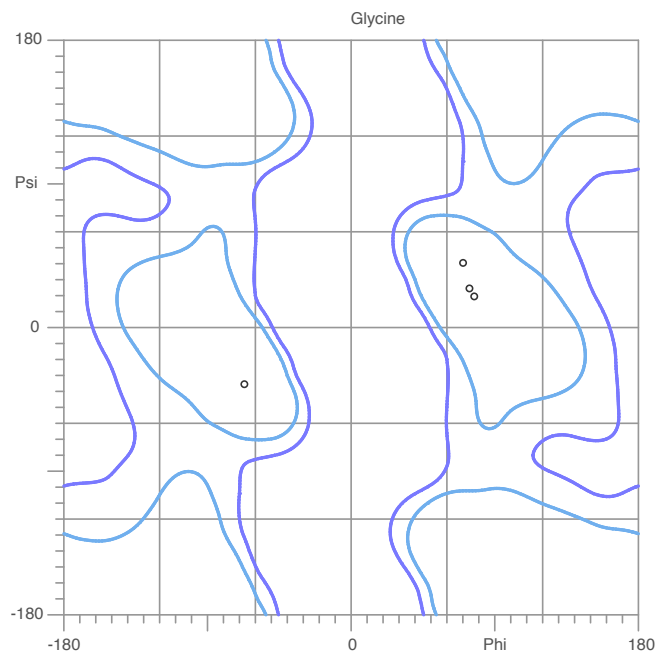
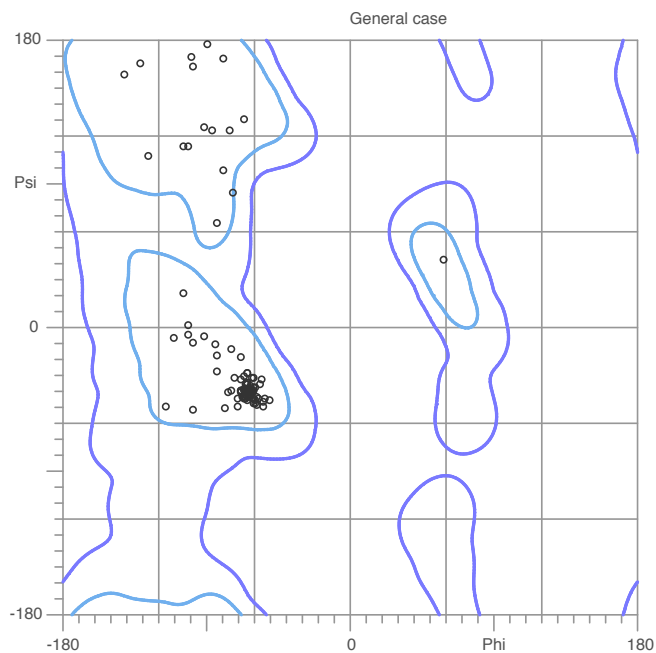
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3Cons\_em\_bcr3.pdb, model 20



100.0% (99/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

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