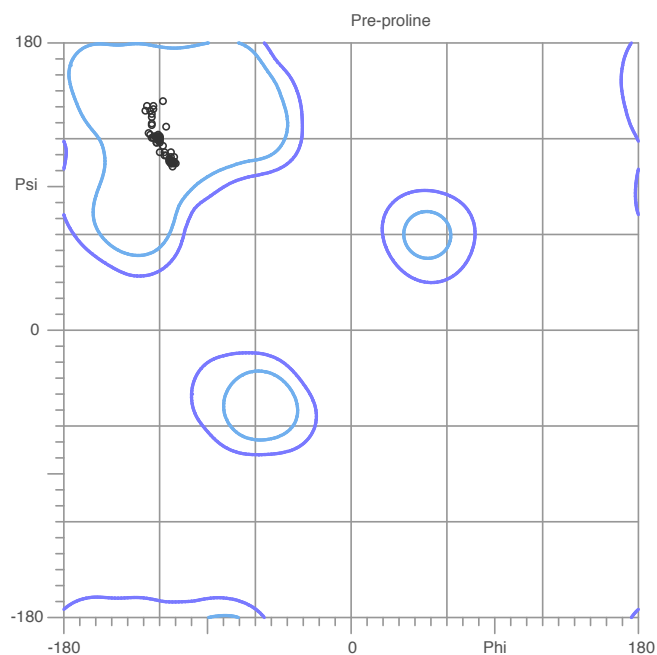
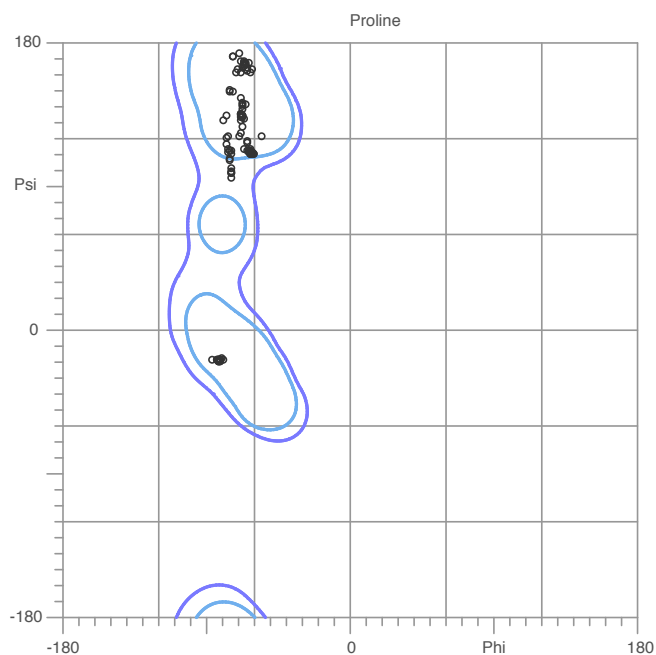
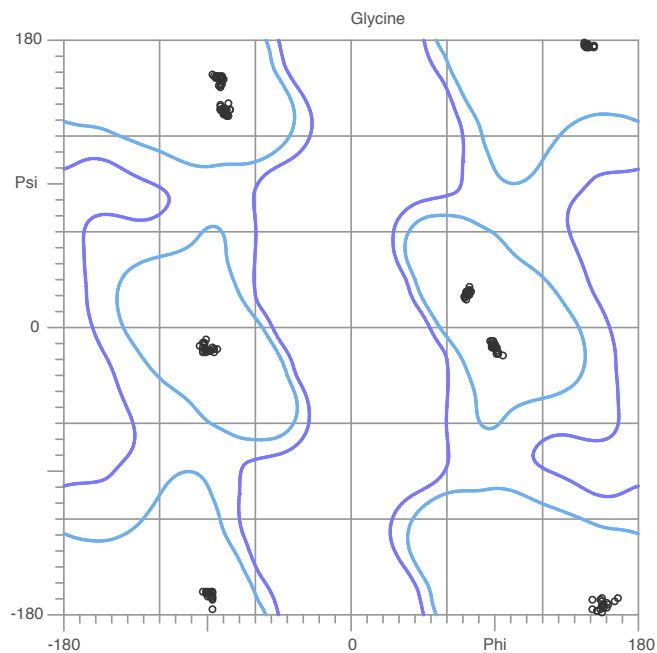
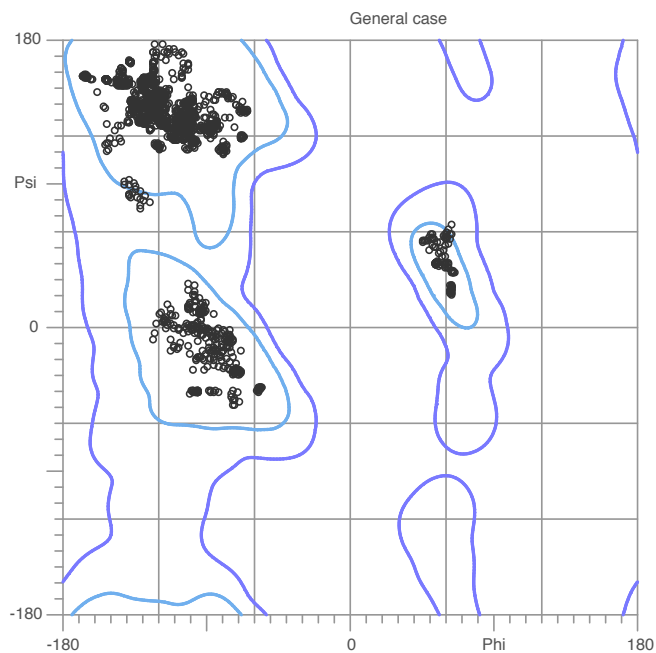


# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, all models



99.0% (2098/2120) of all residues were in favored (98%) regions.  
100.0% (2120/2120) of all residues were in allowed (>99.8%) regions.

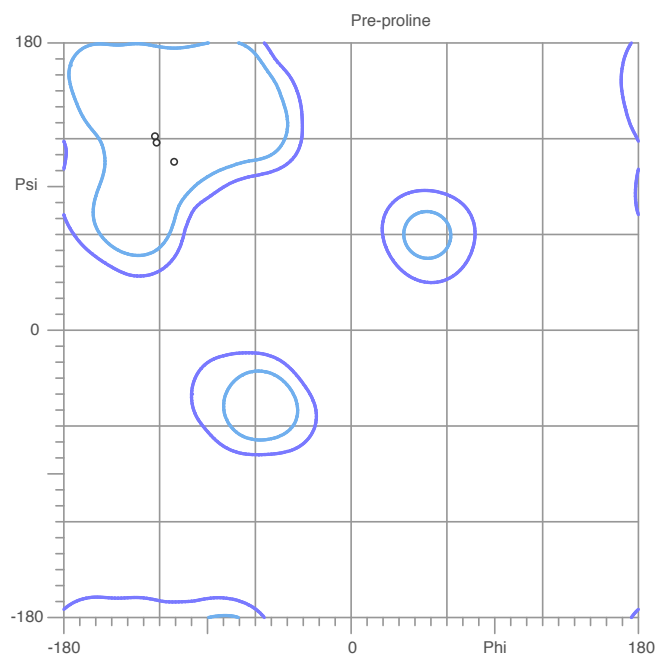
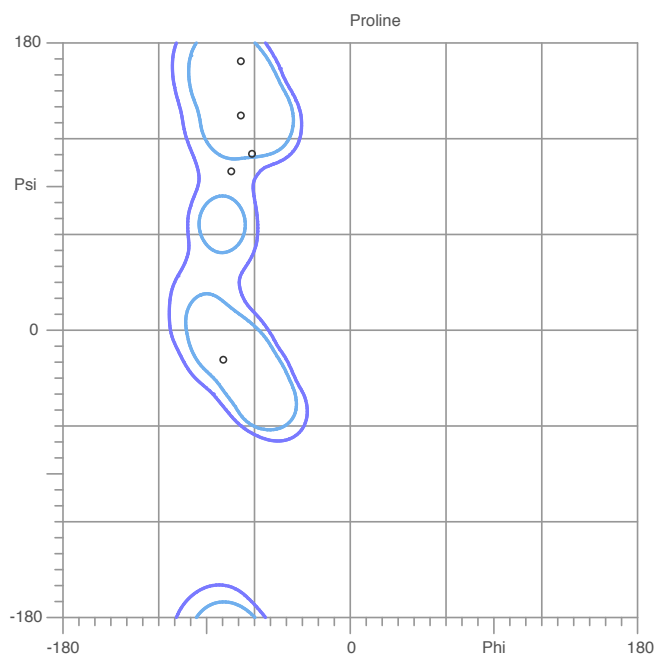
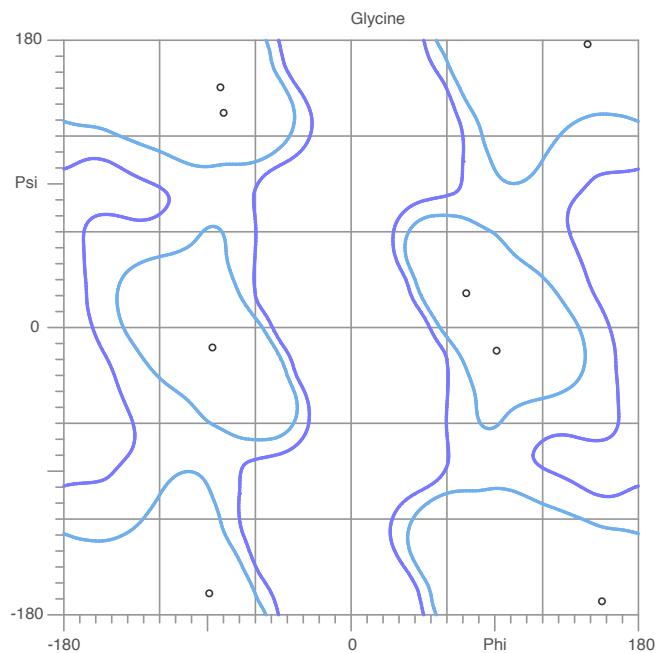
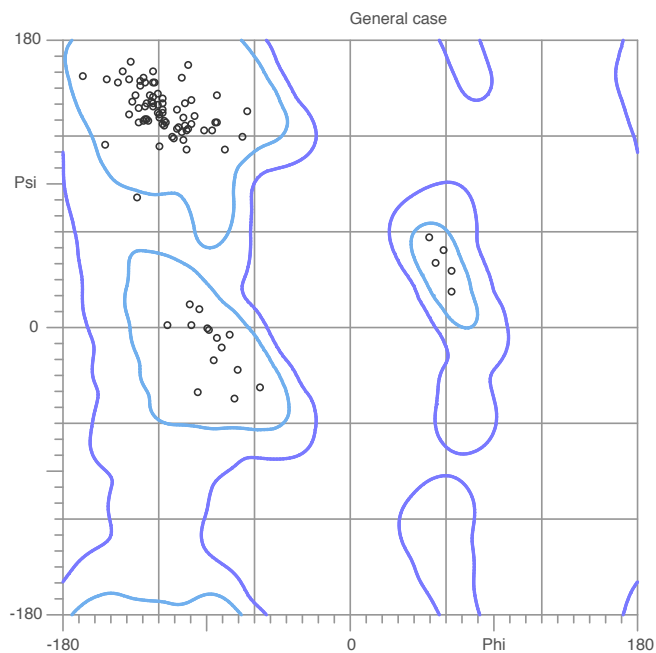
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 1

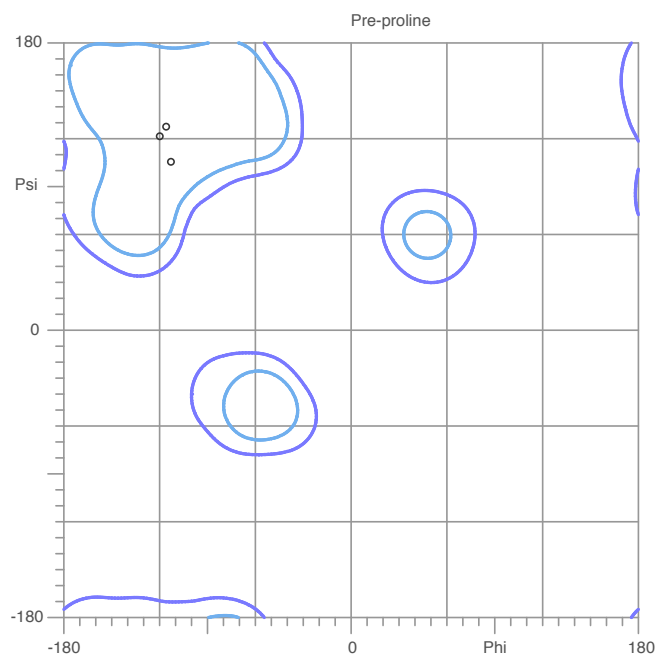
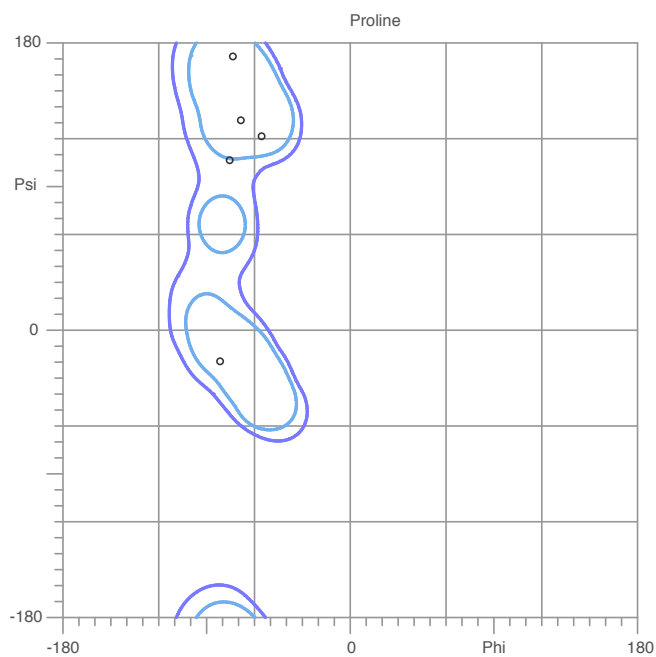
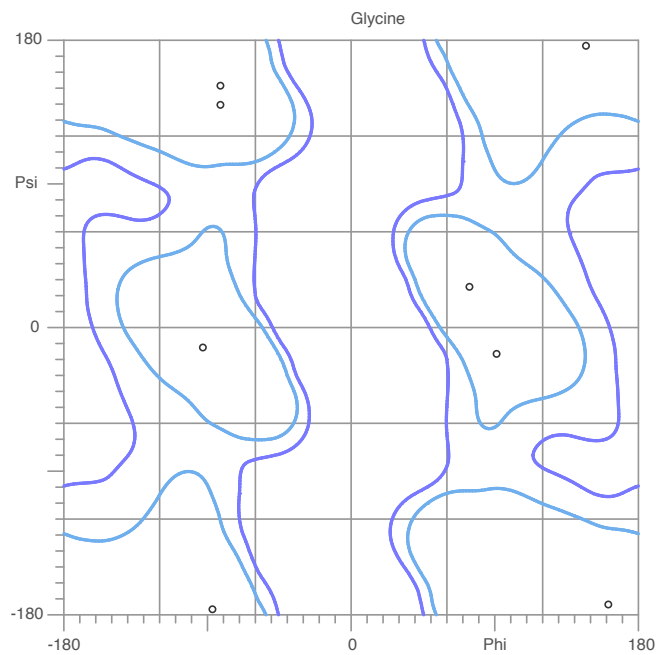
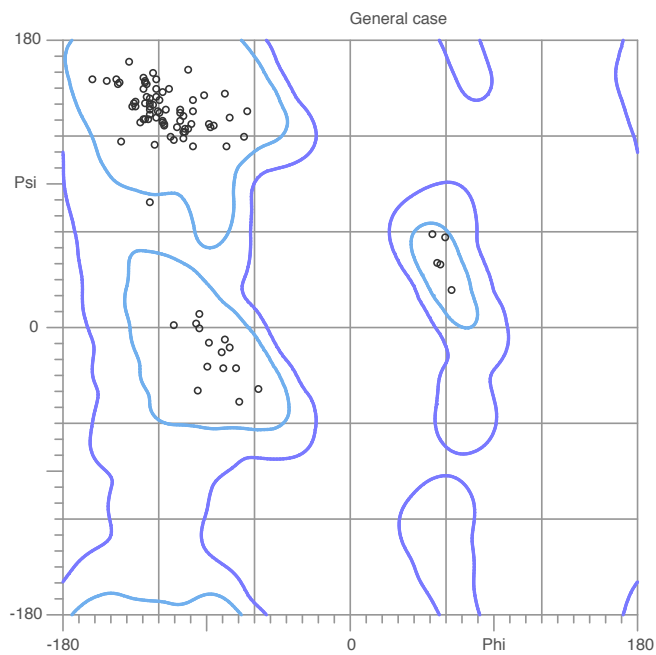


98.1% (104/106) of all residues were in favored (98%) regions.  
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 2



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.

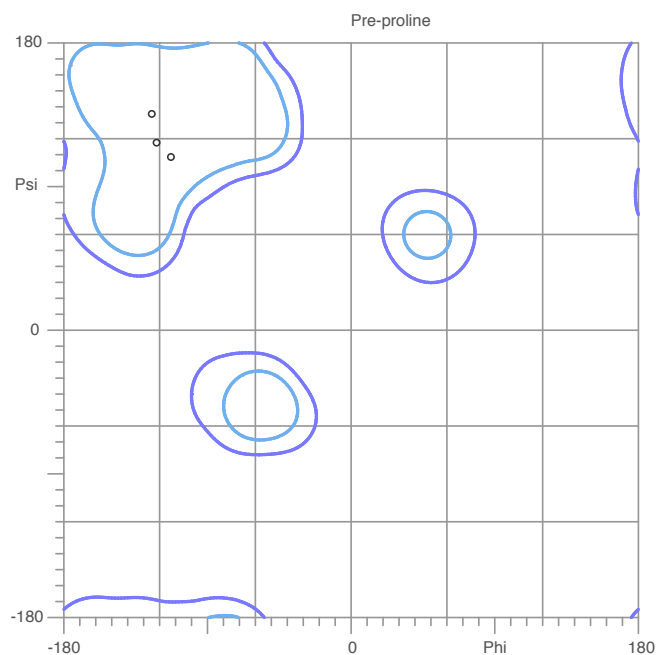
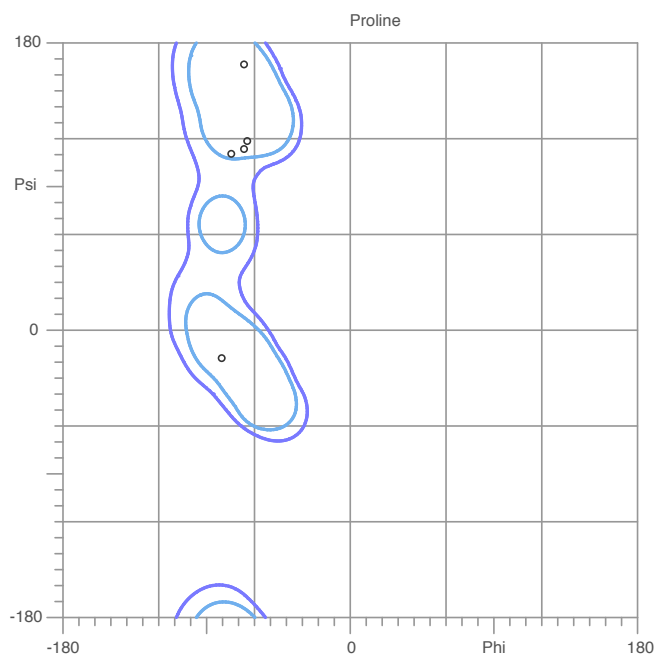
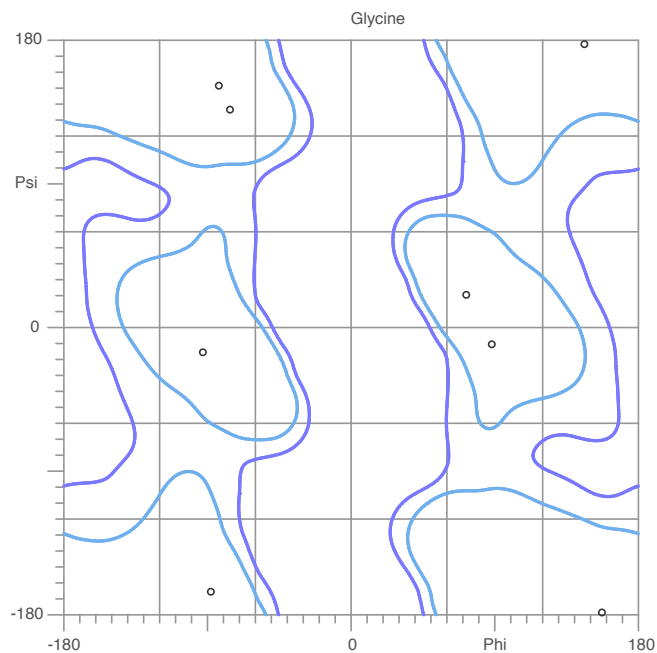
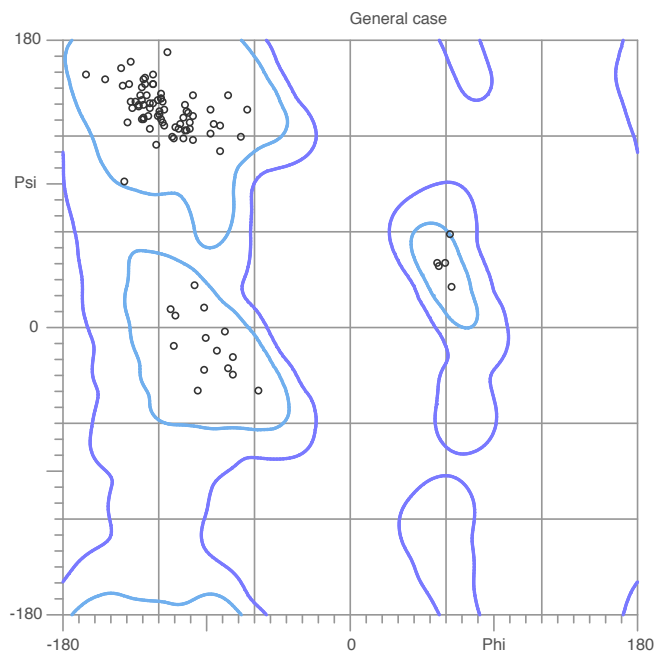
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 3



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.

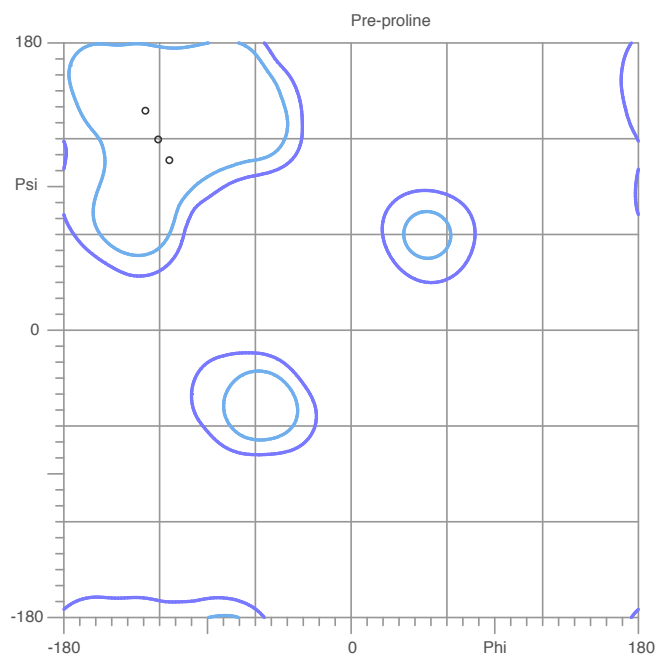
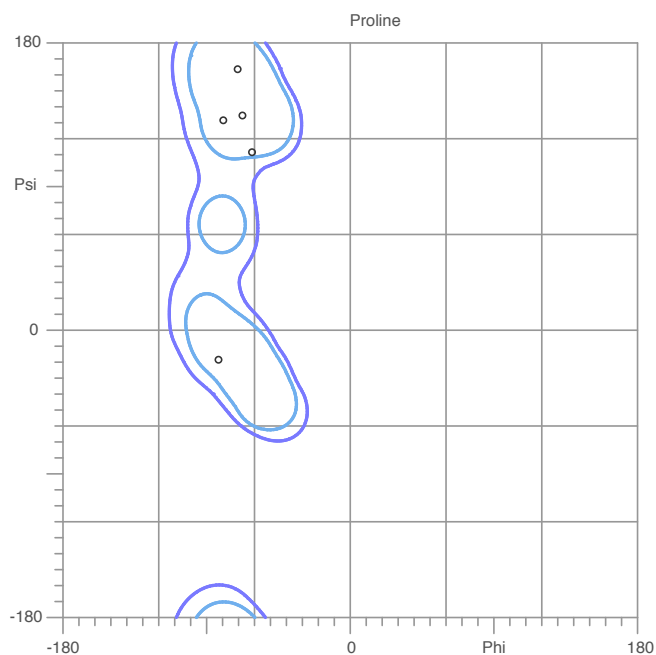
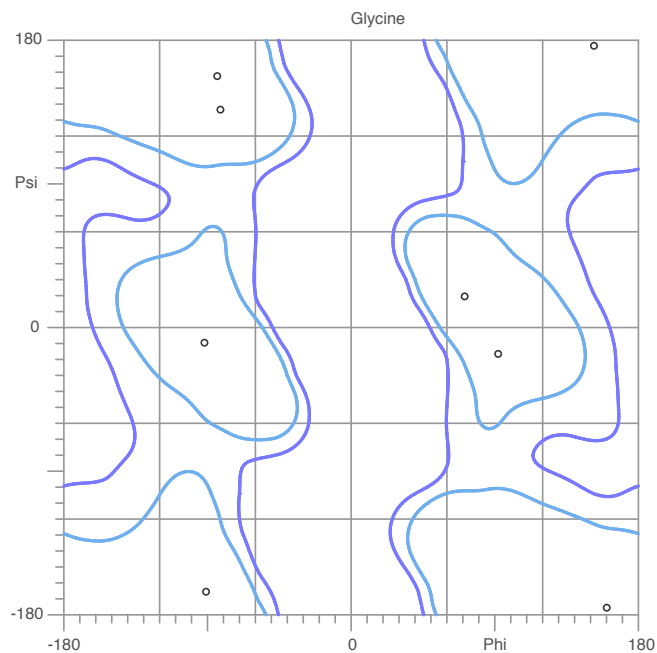
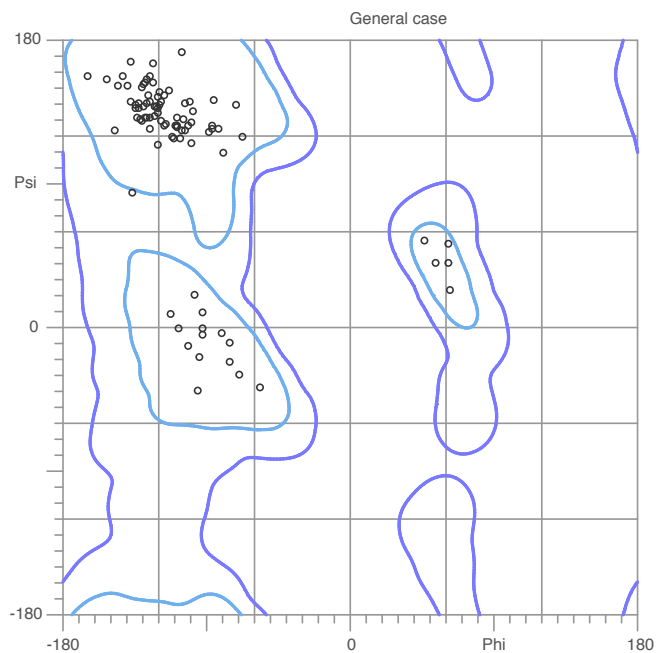
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 4



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.

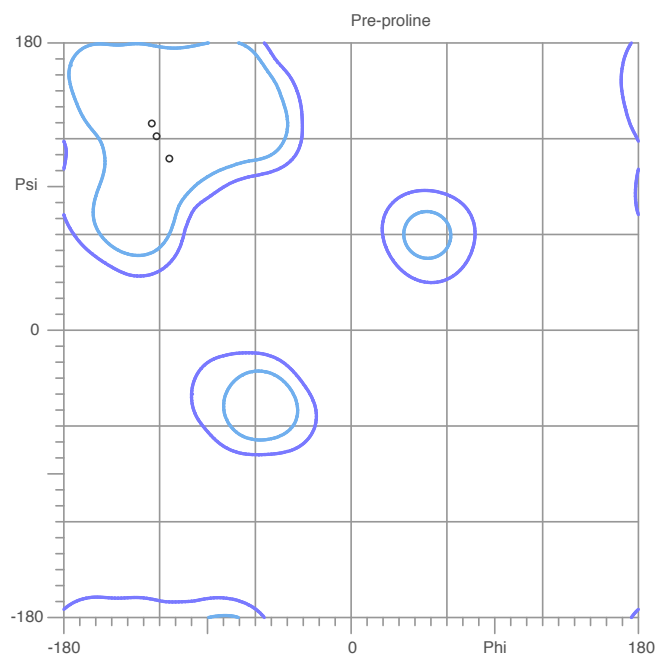
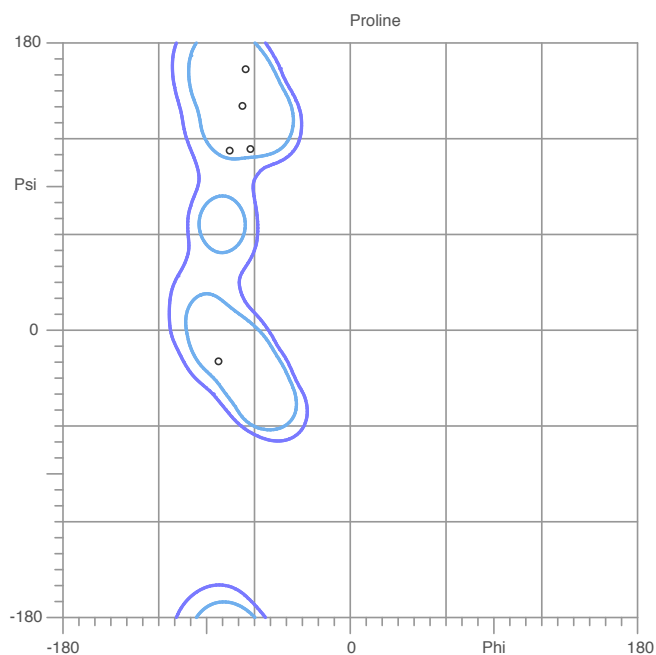
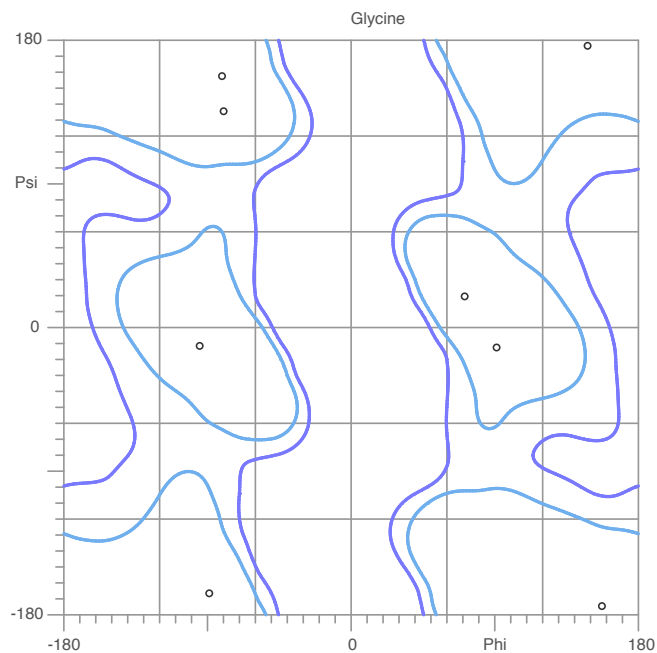
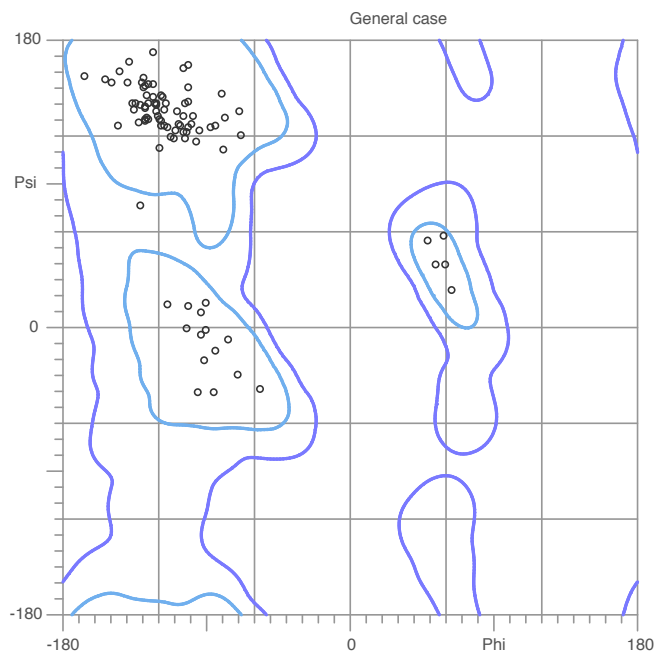
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 5

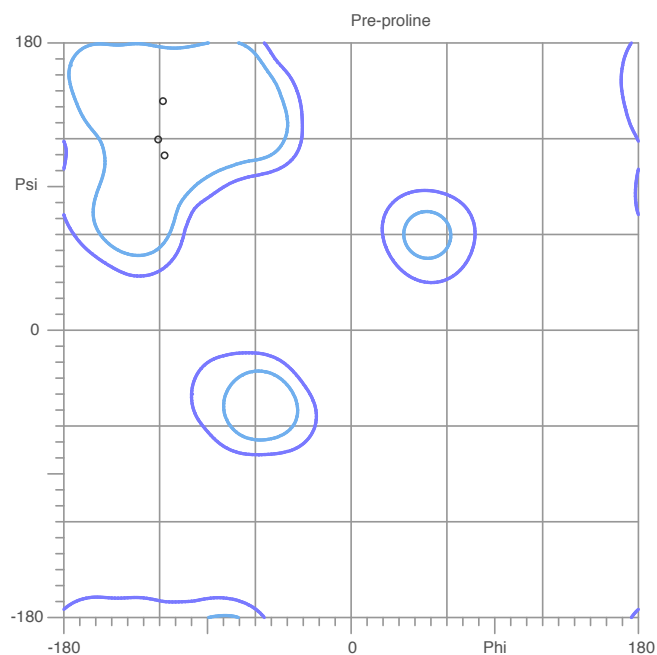
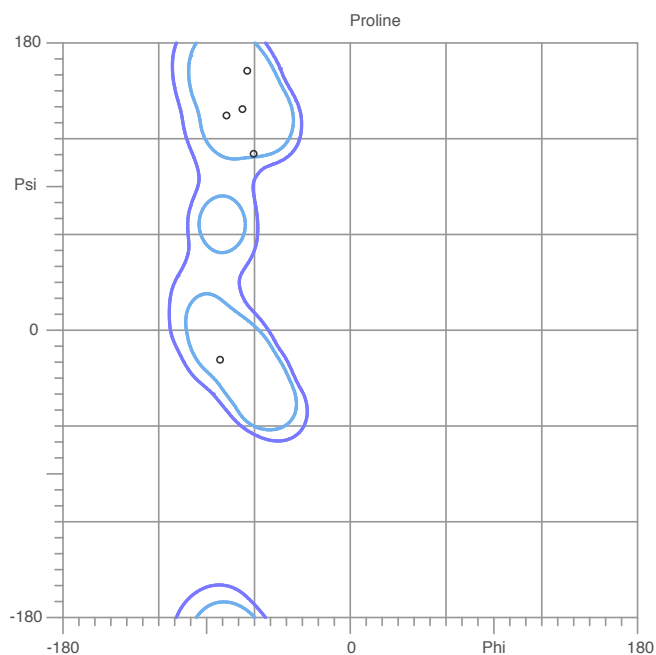
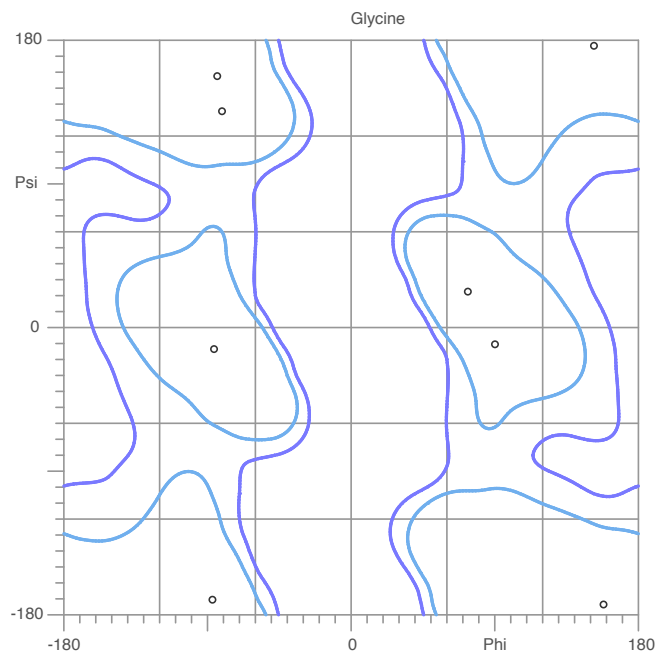
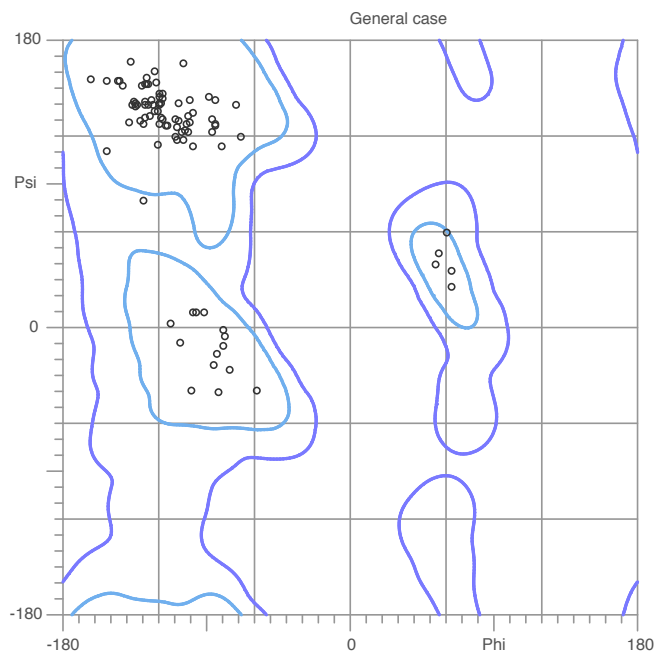


99.1% (105/106) of all residues were in favored (98%) regions.  
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 6



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.

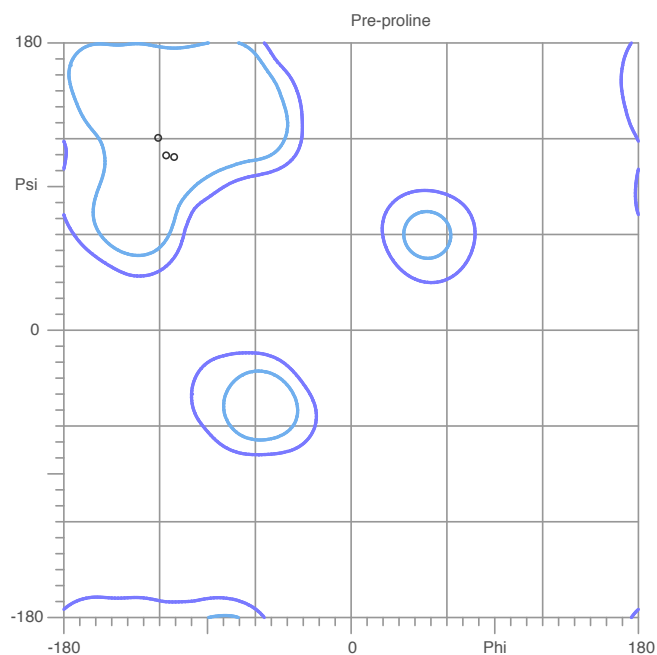
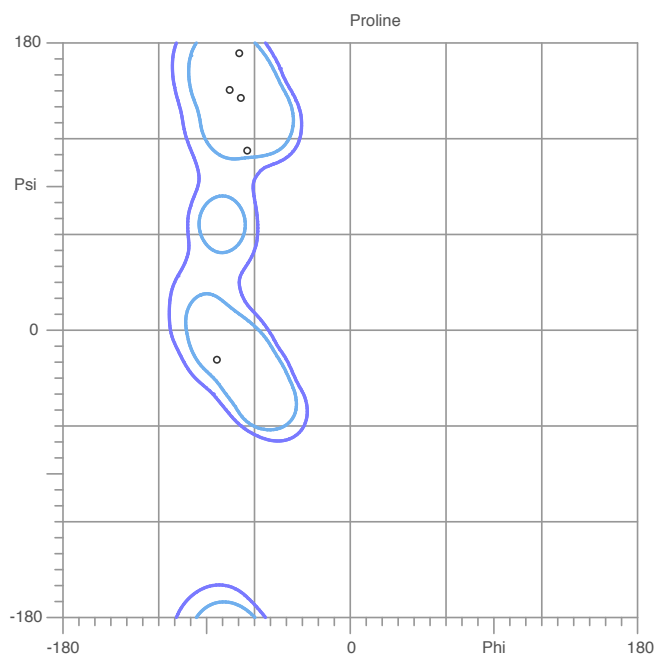
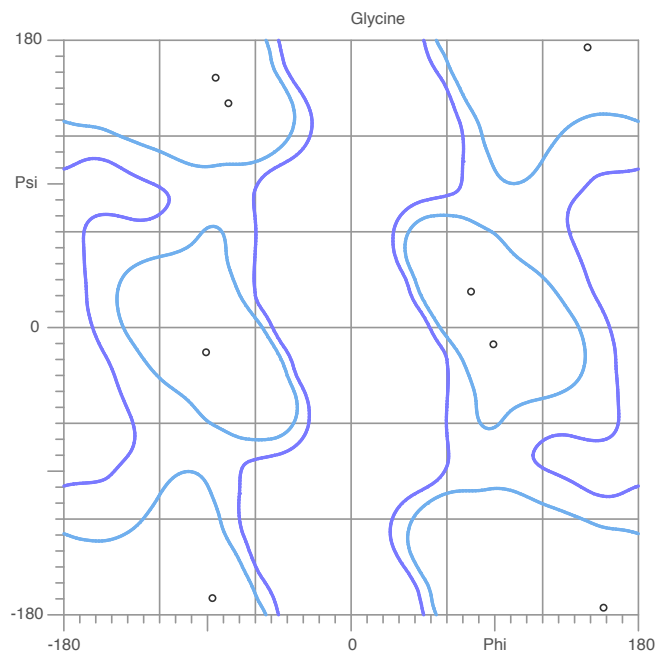
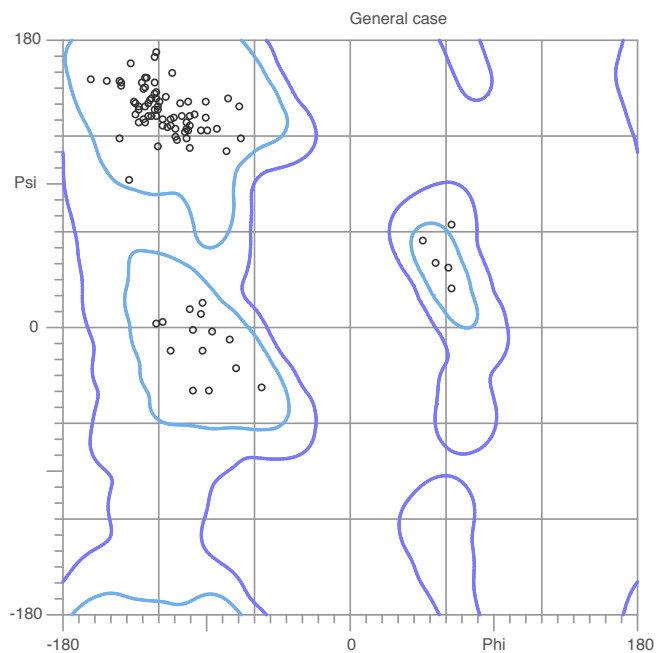
There were no outliers.

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 7



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.

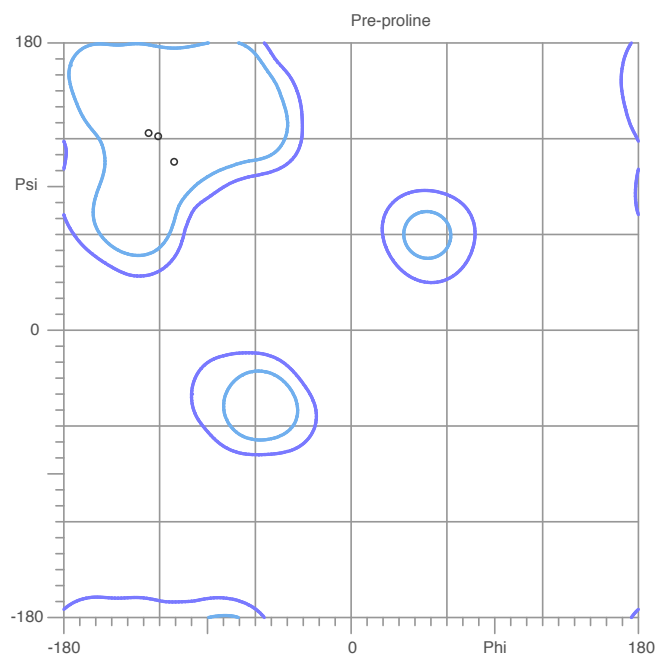
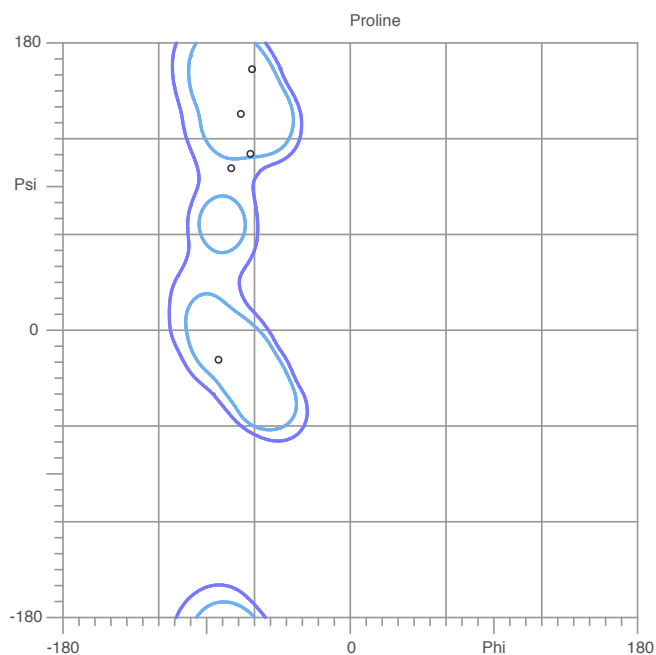
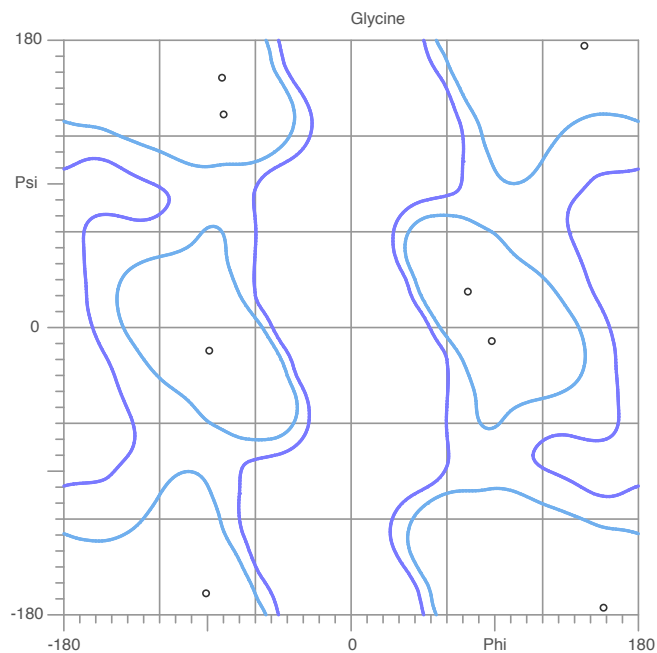
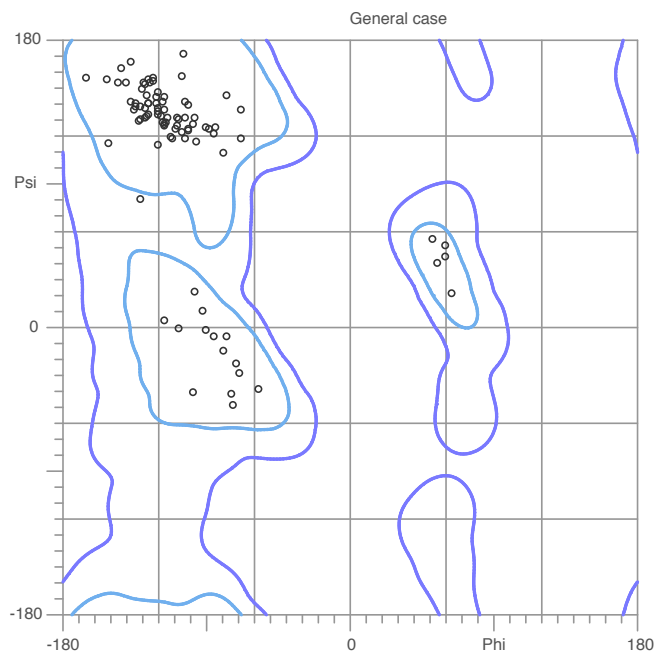
There were no outliers.

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_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.

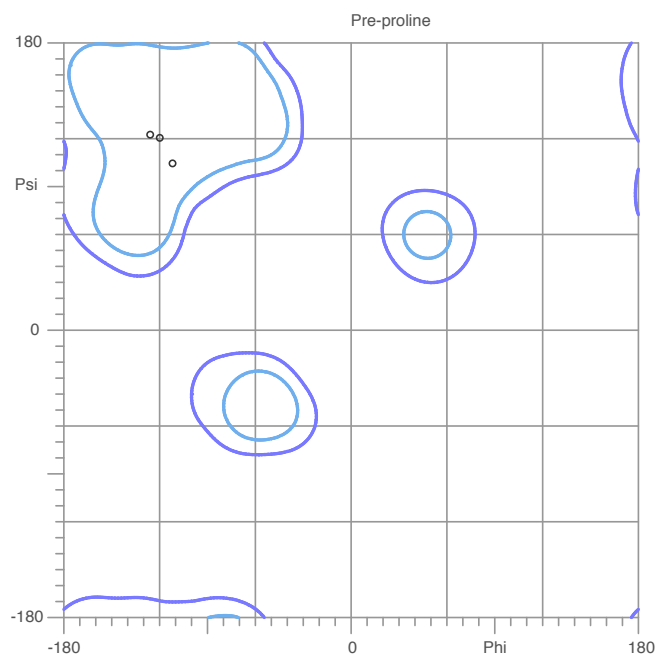
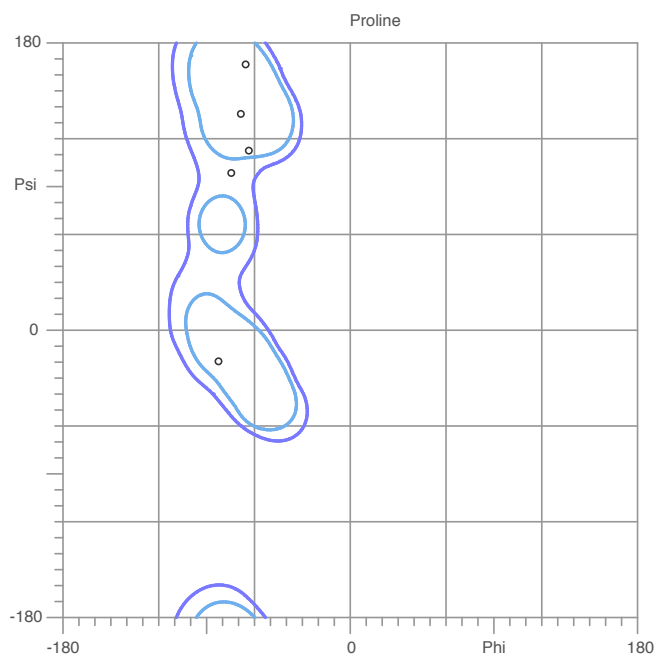
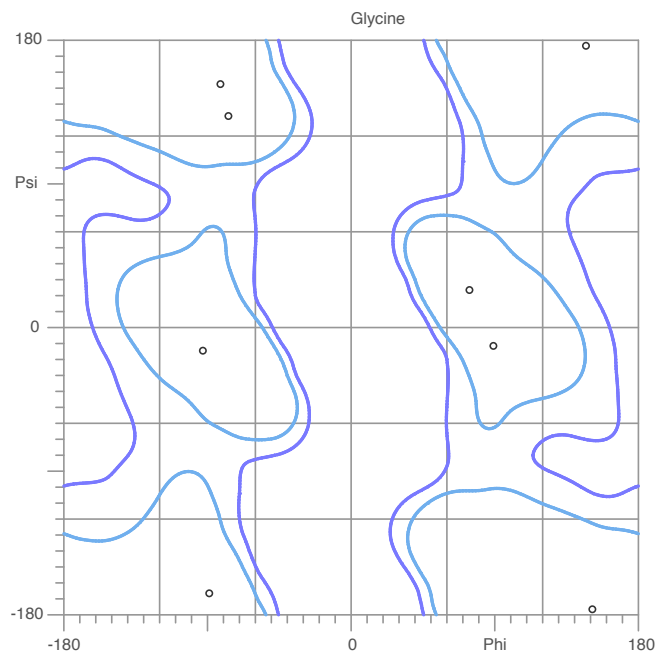
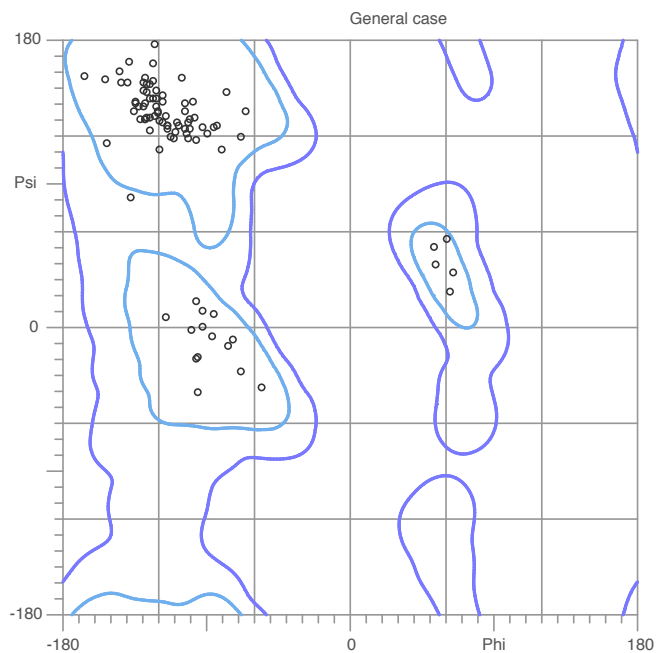
There were no outliers.

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 9



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.

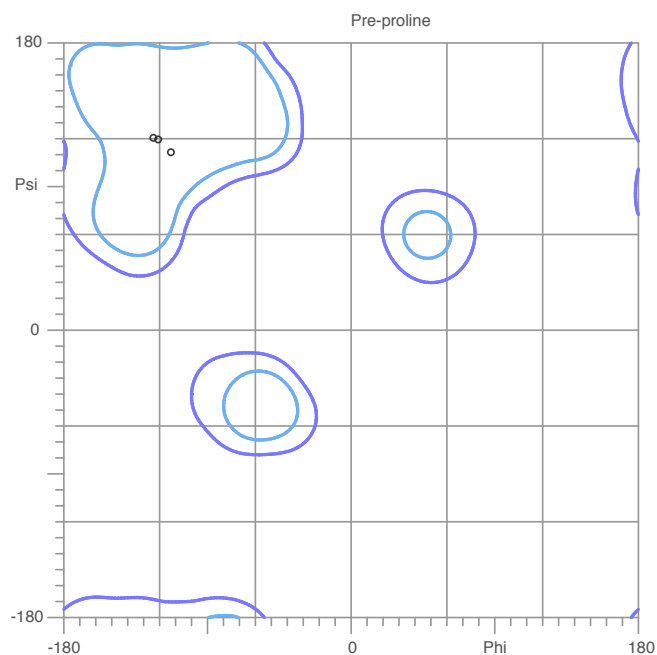
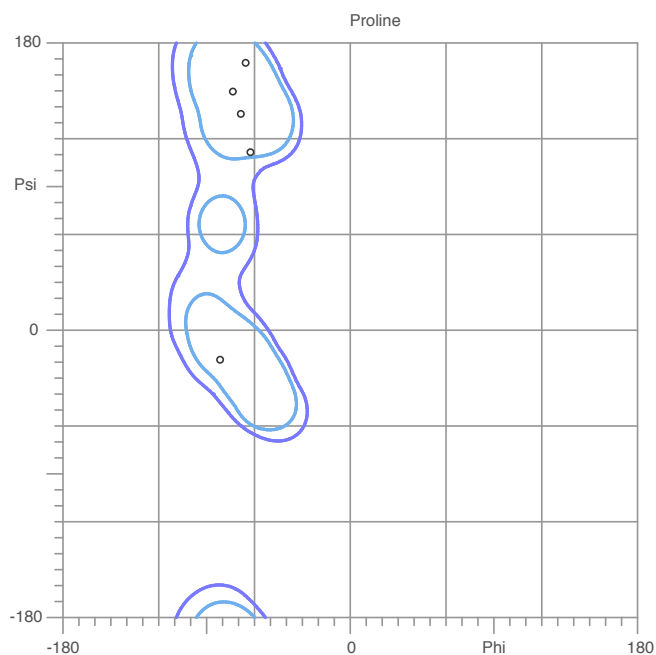
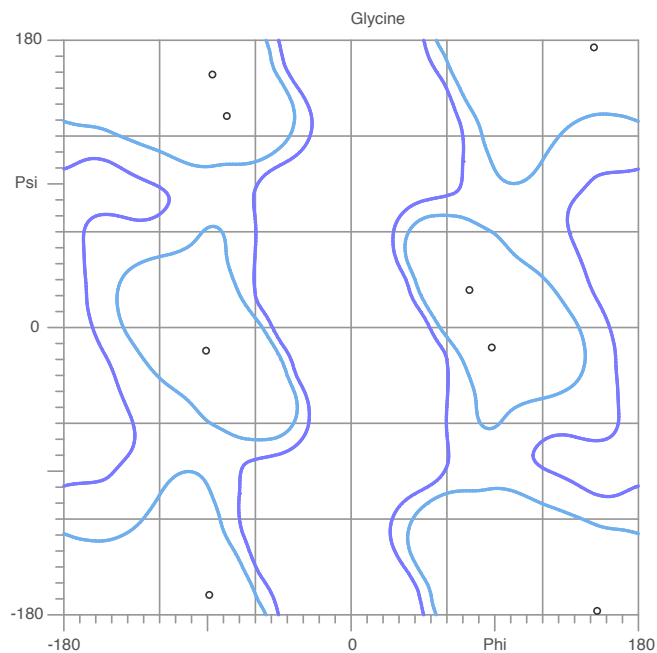
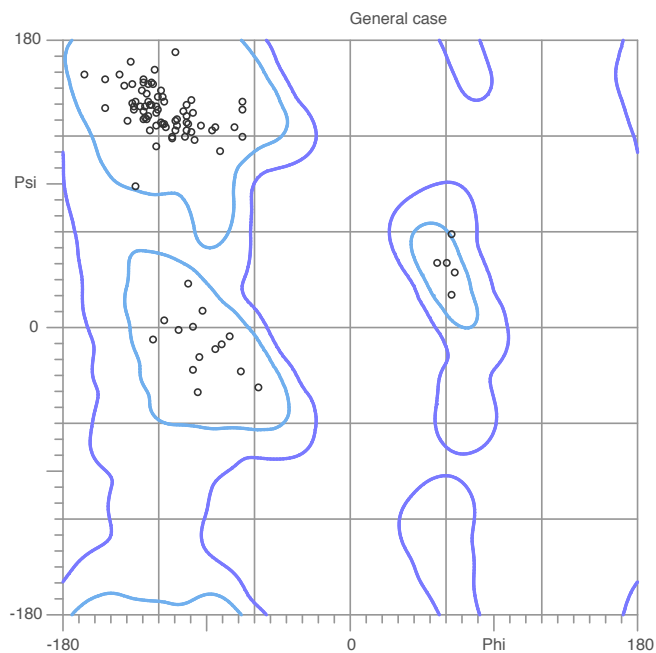
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 10

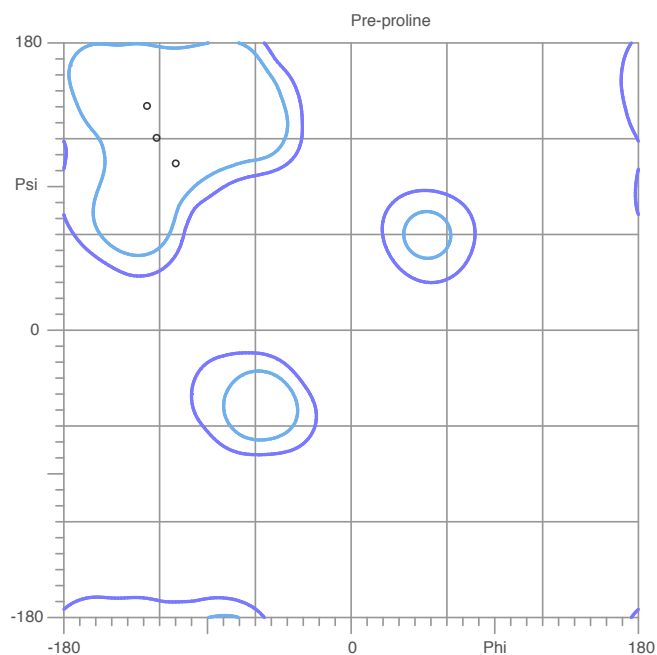
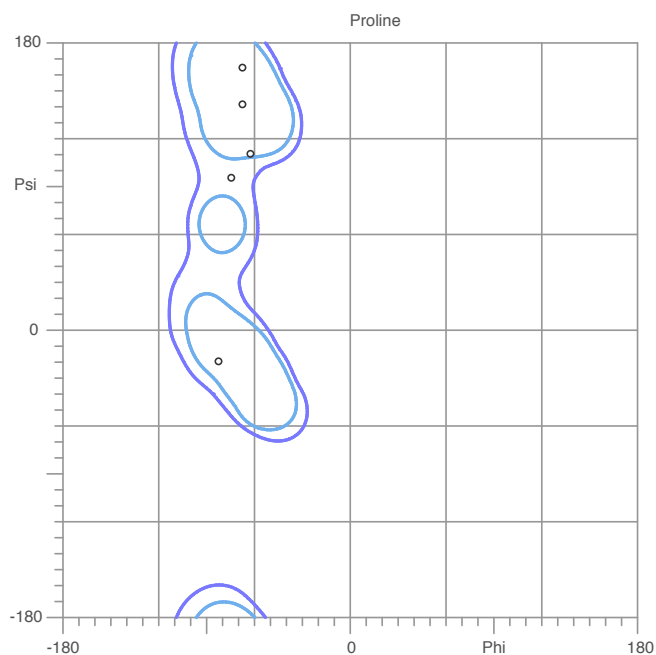
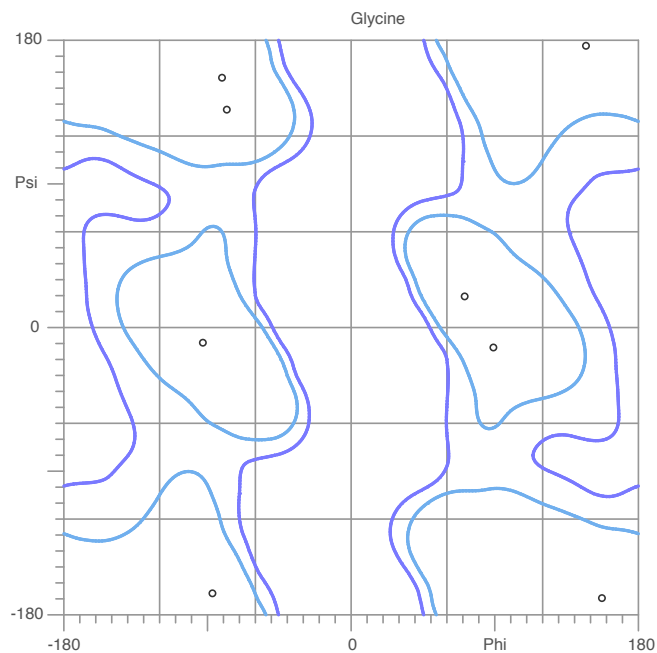
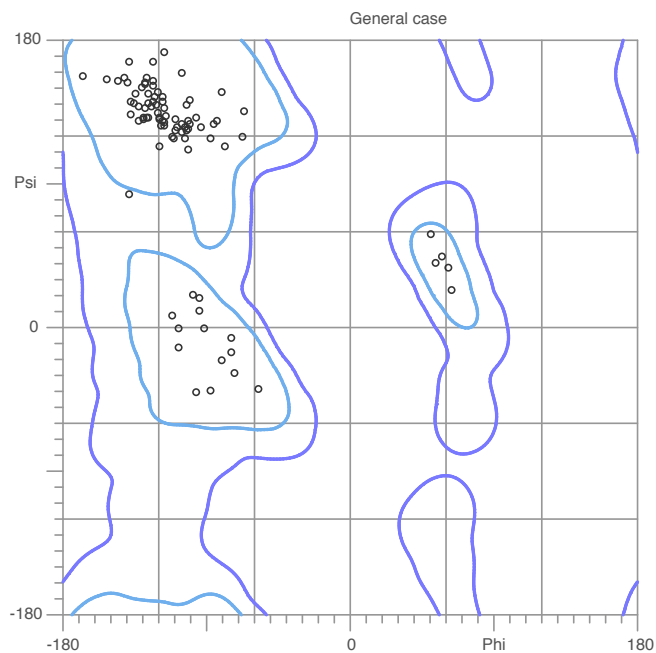


99.1% (105/106) of all residues were in favored (98%) regions.  
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 11



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.

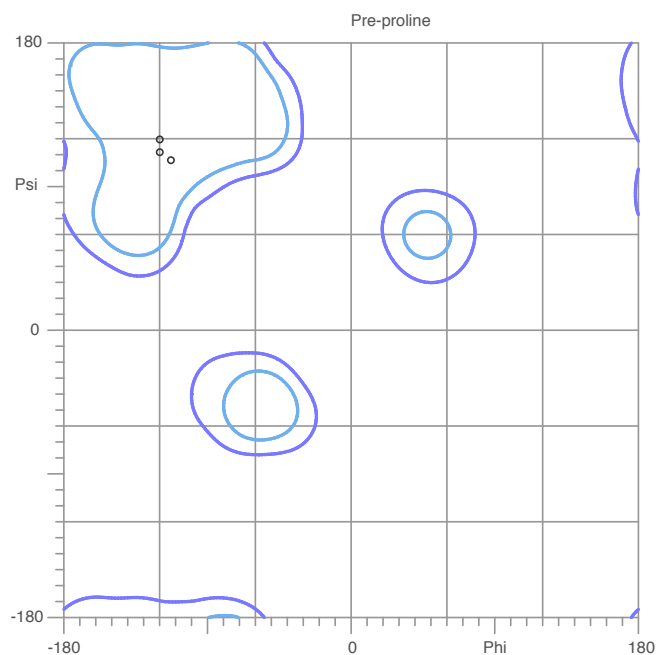
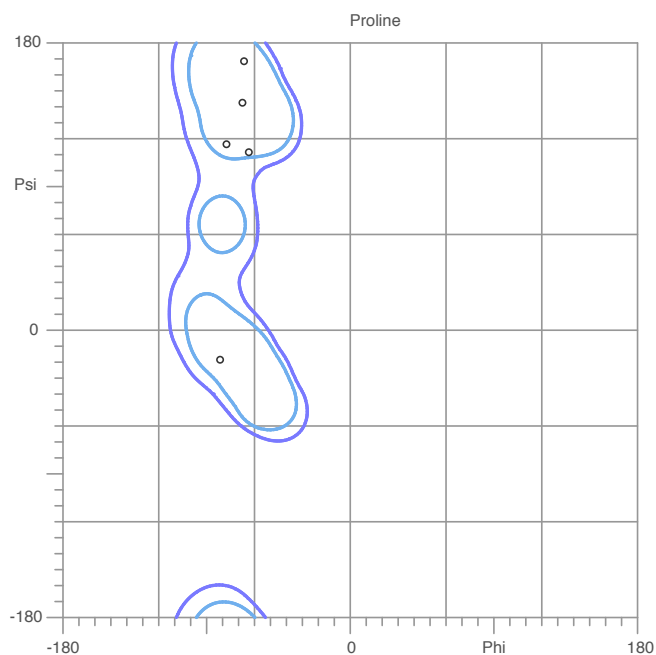
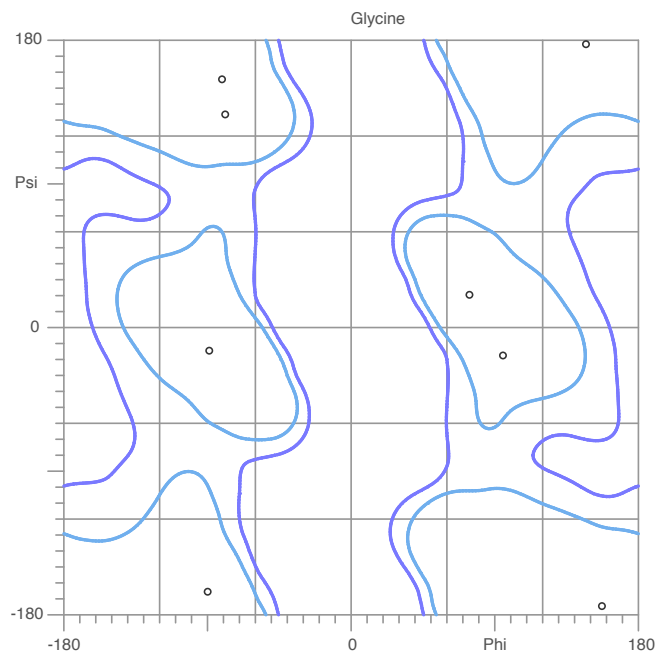
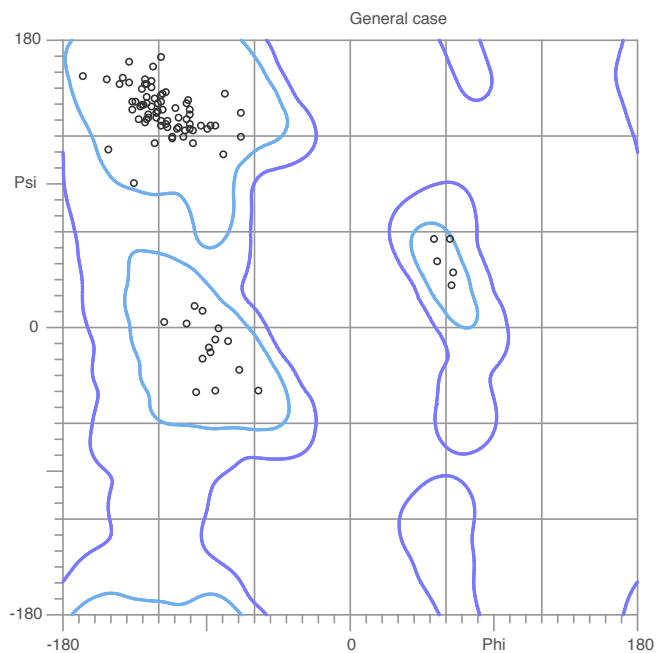
There were no outliers.

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 12



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

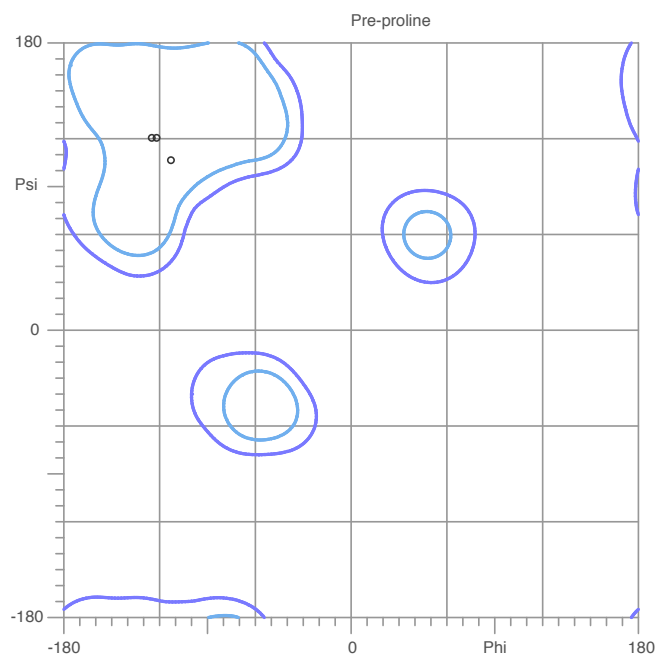
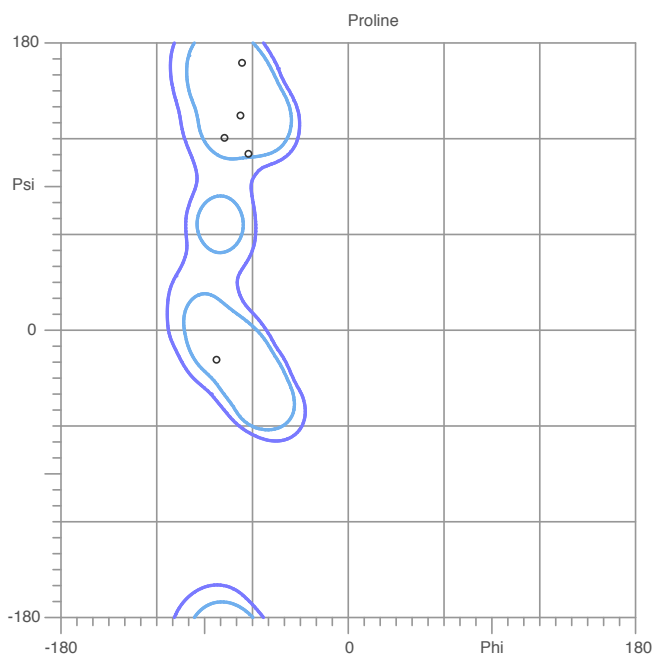
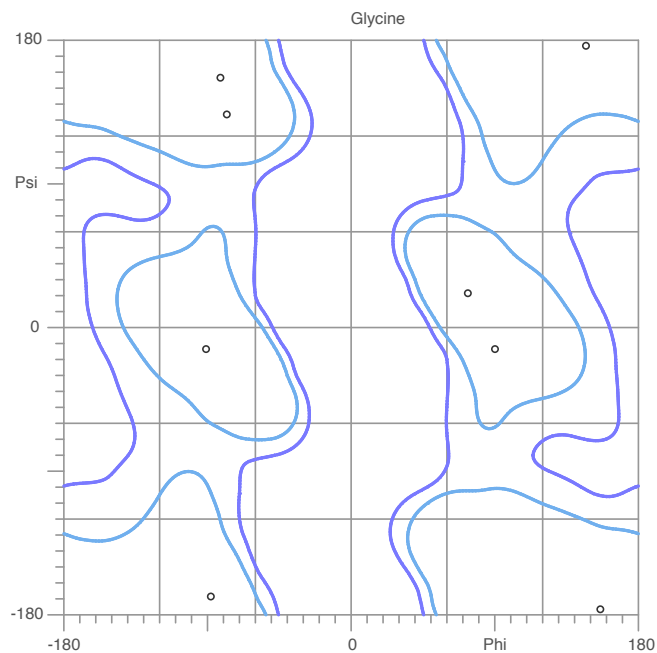
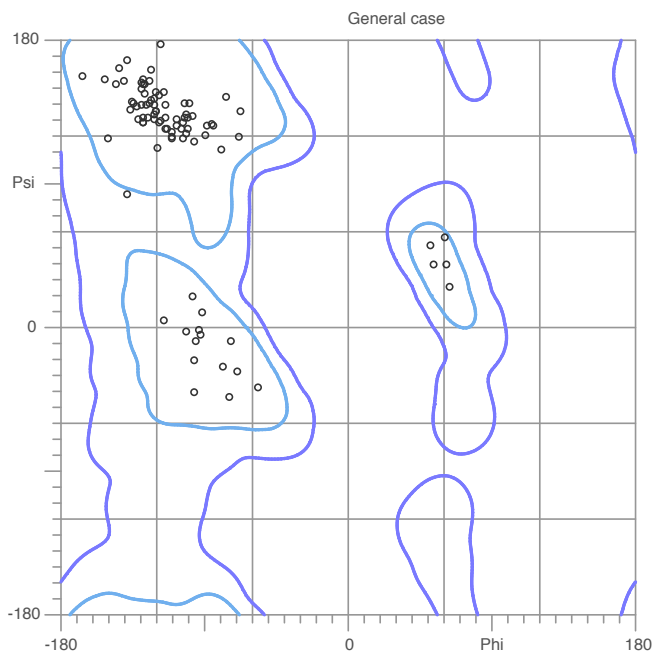
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 13



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.

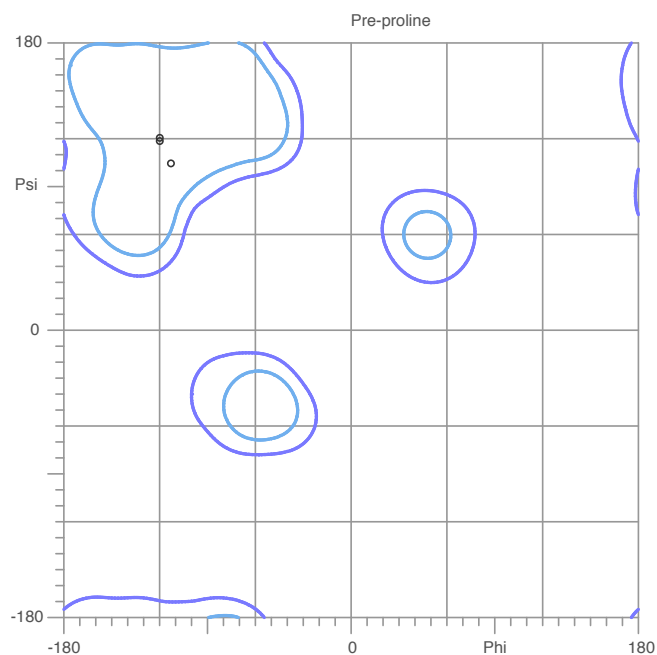
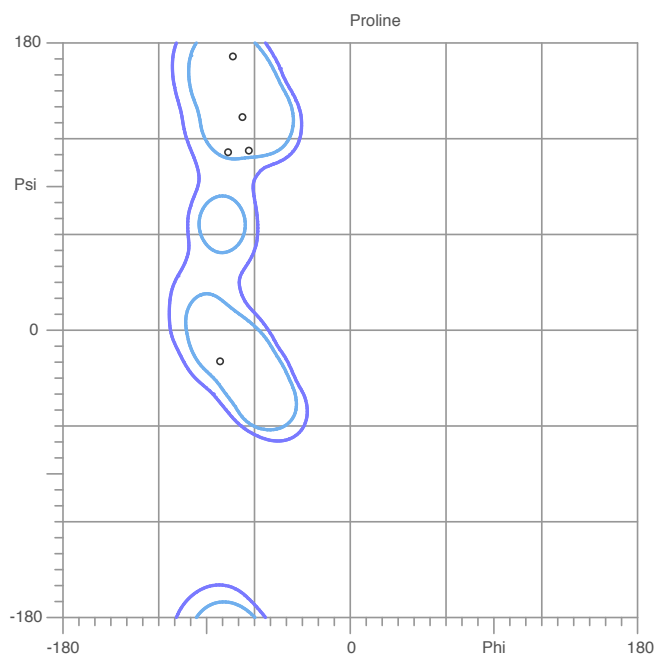
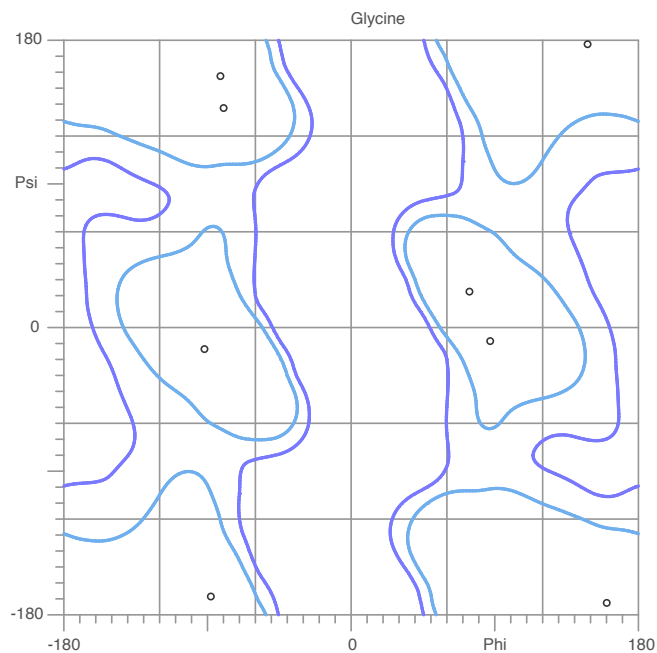
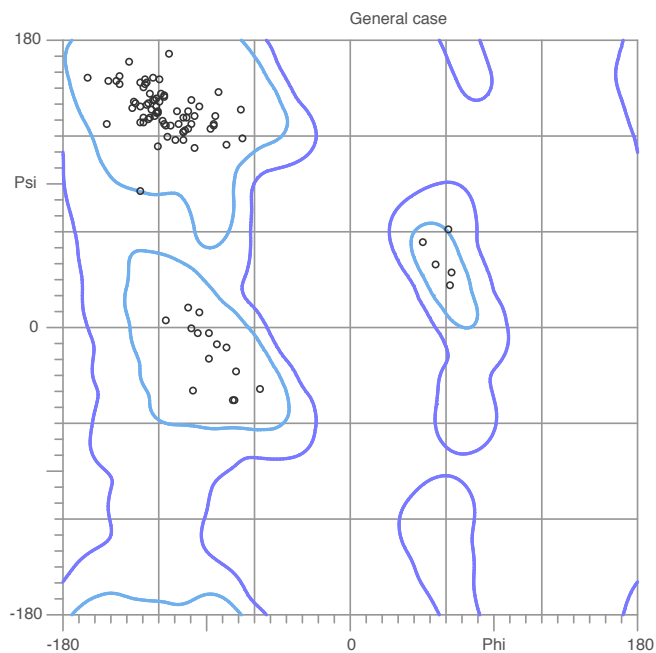
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 14

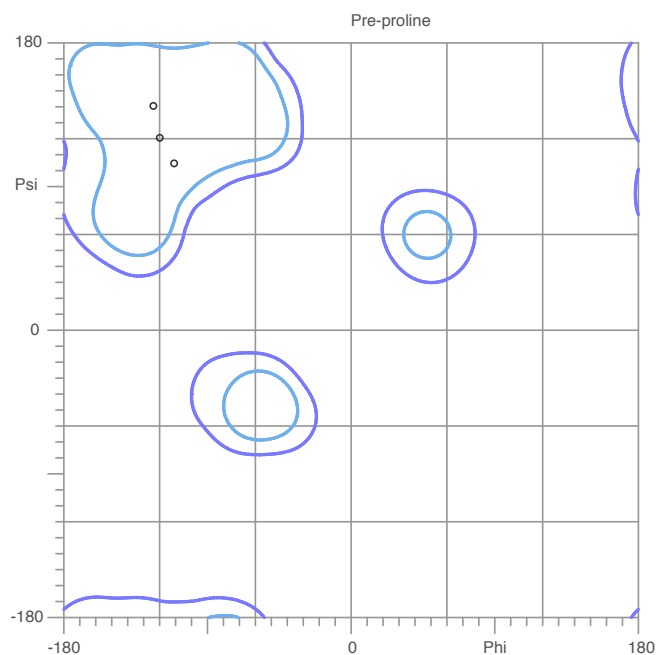
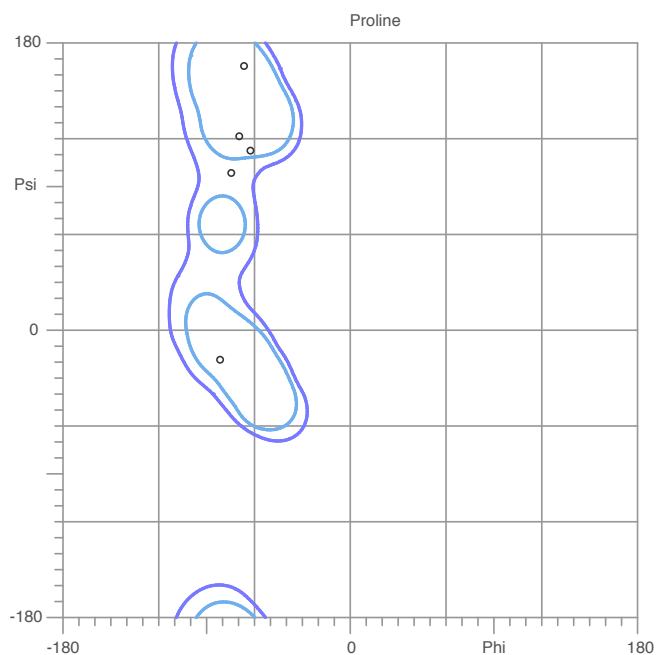
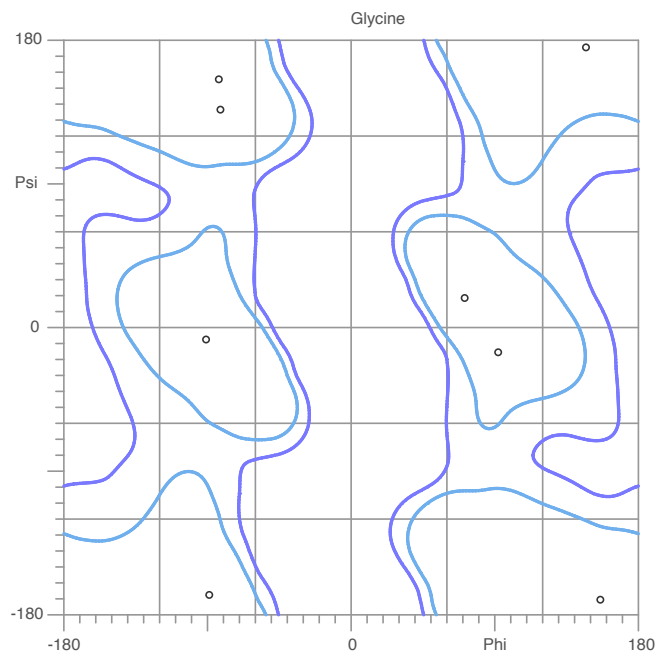
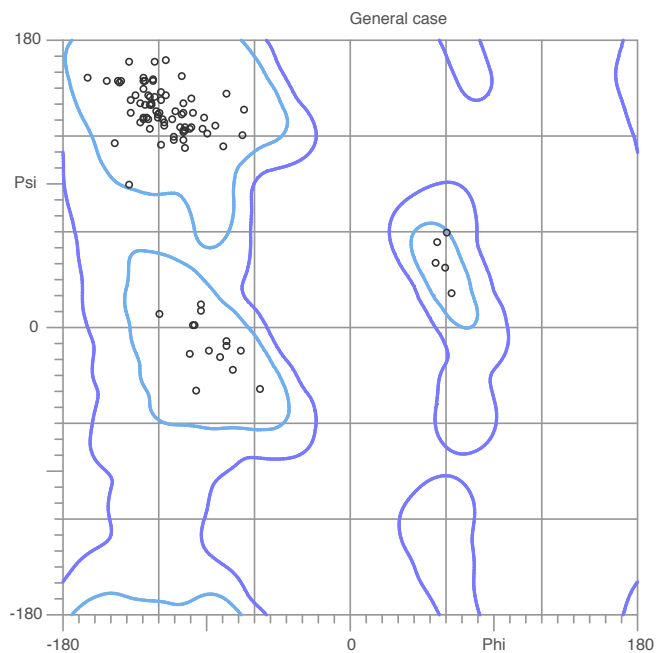


99.1% (105/106) of all residues were in favored (98%) regions.  
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 15



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.

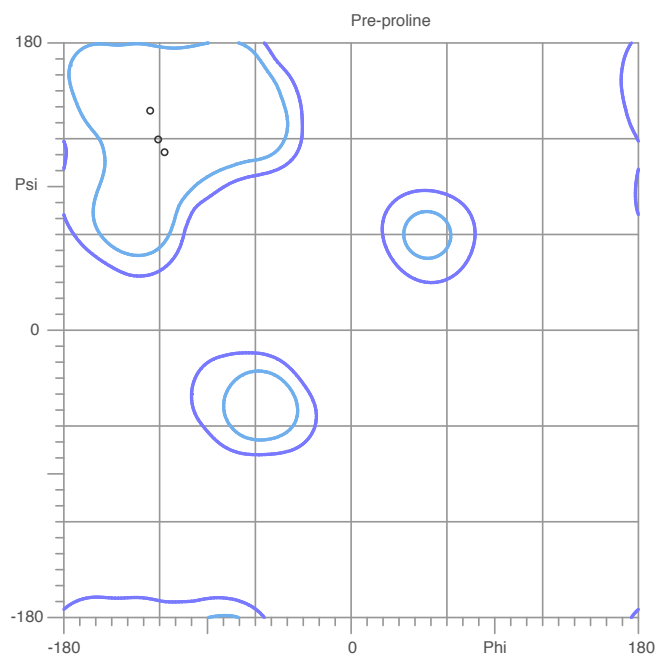
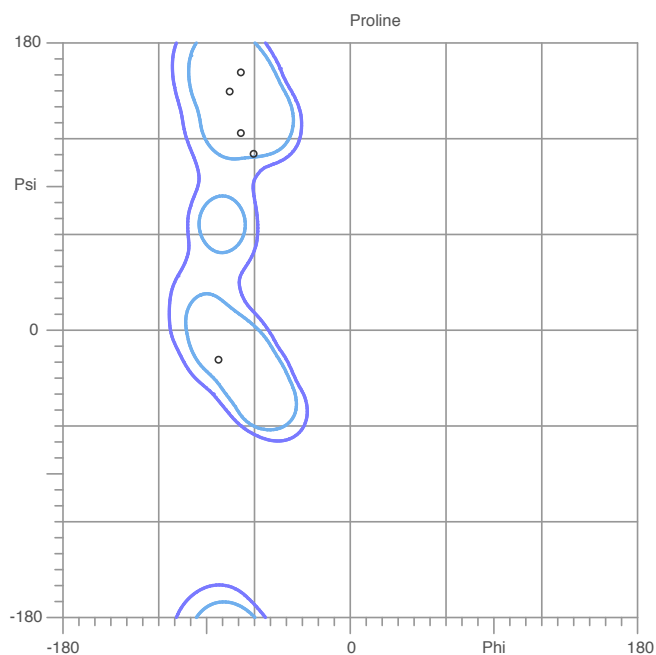
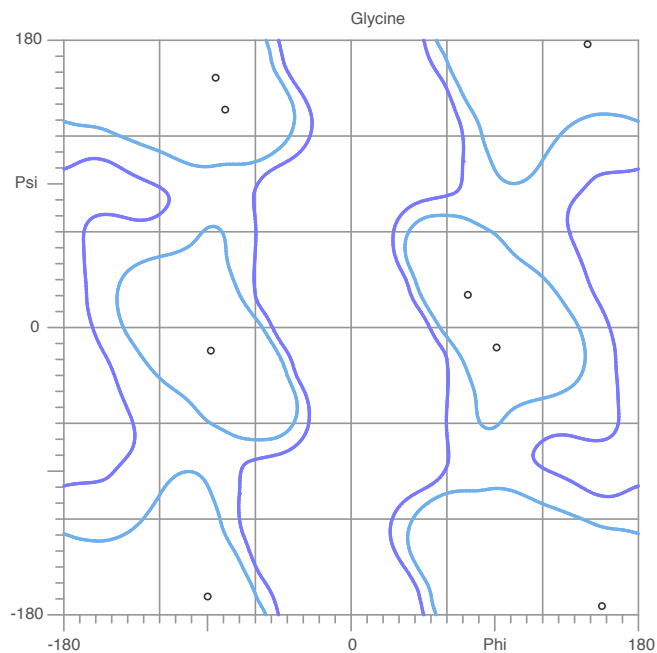
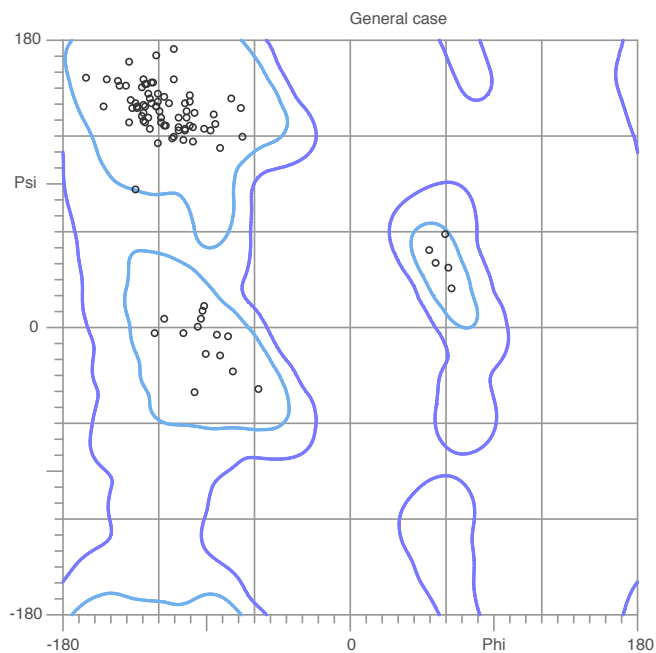
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 16



100.0% (106/106) of all residues were in favored (98%) regions.

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

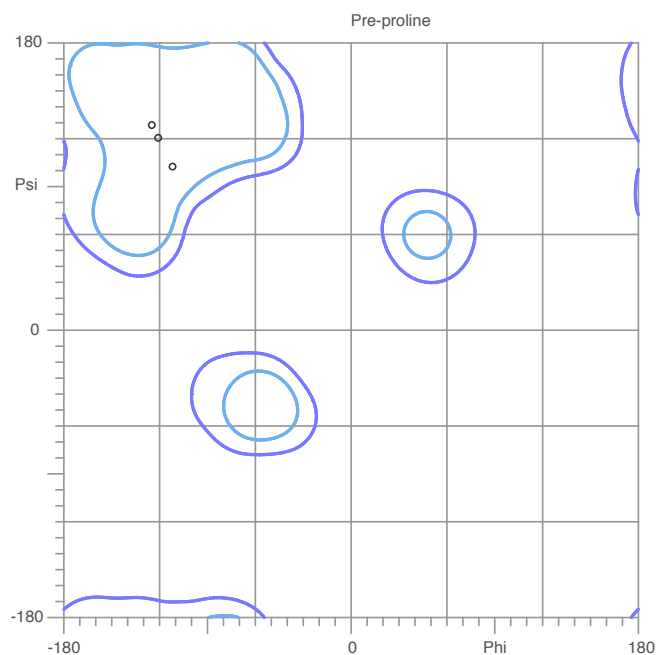
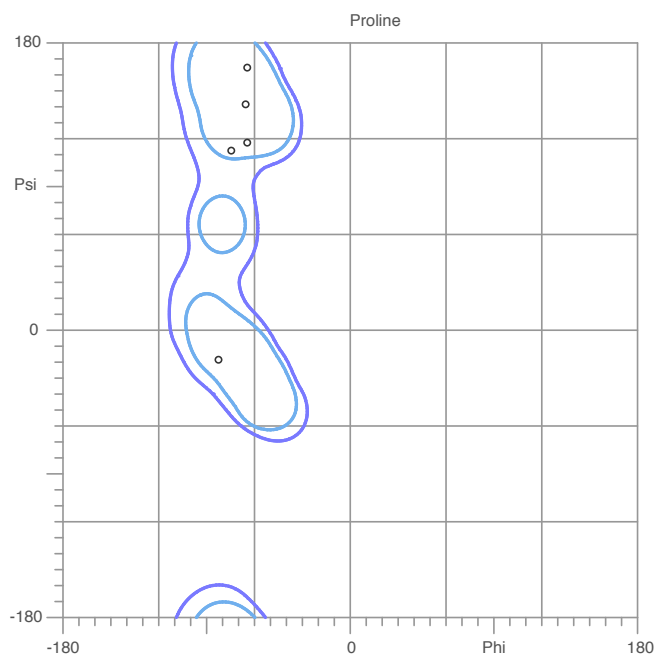
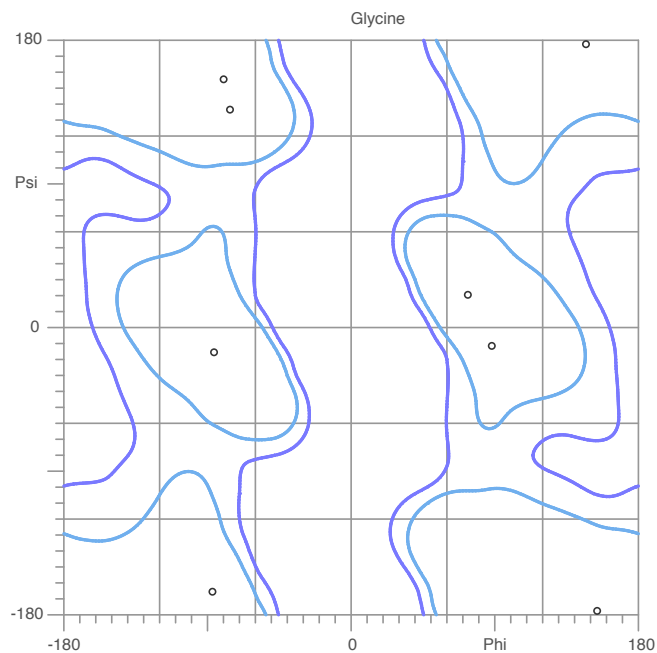
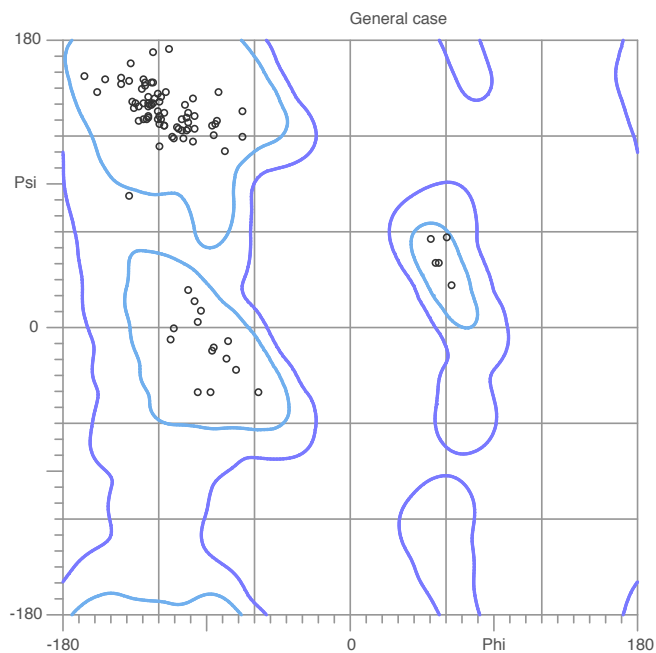
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 17



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.

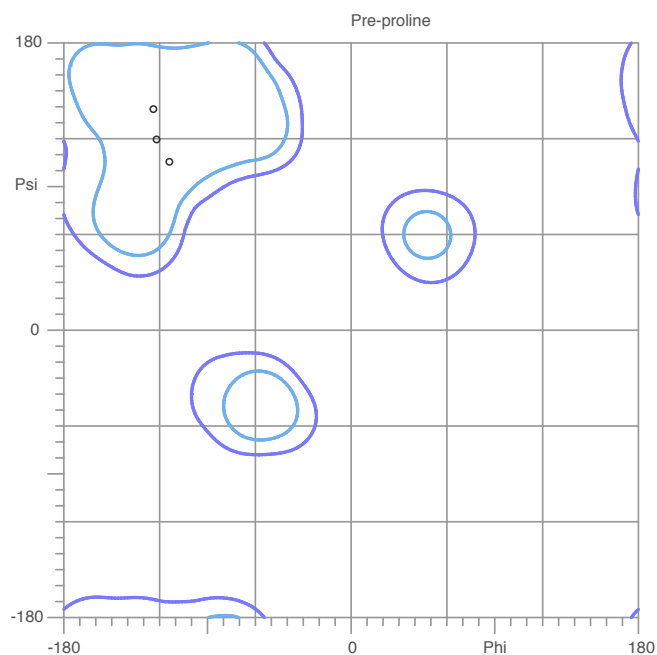
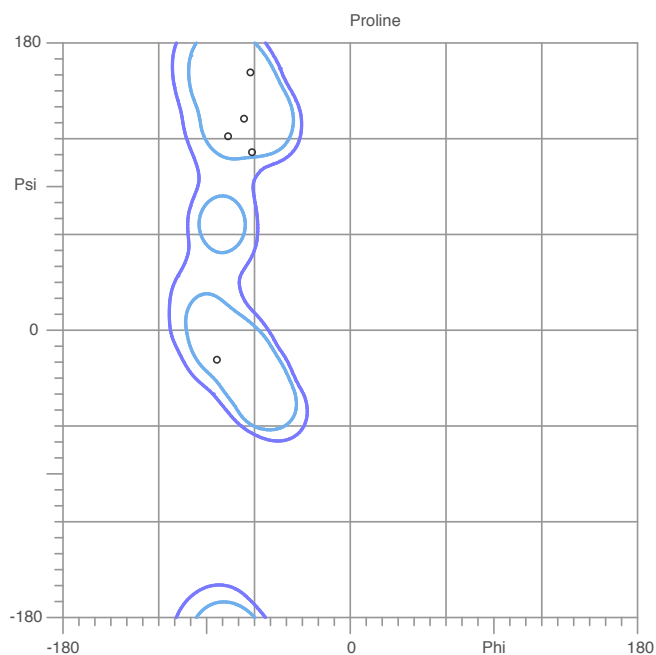
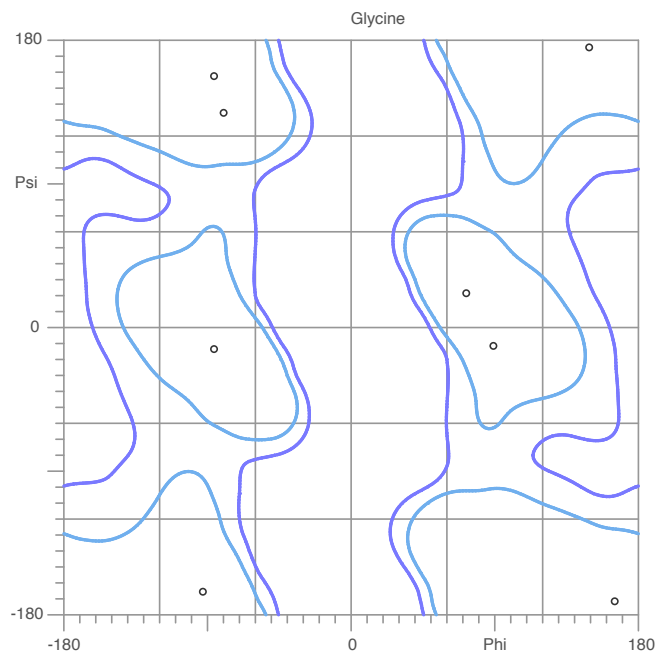
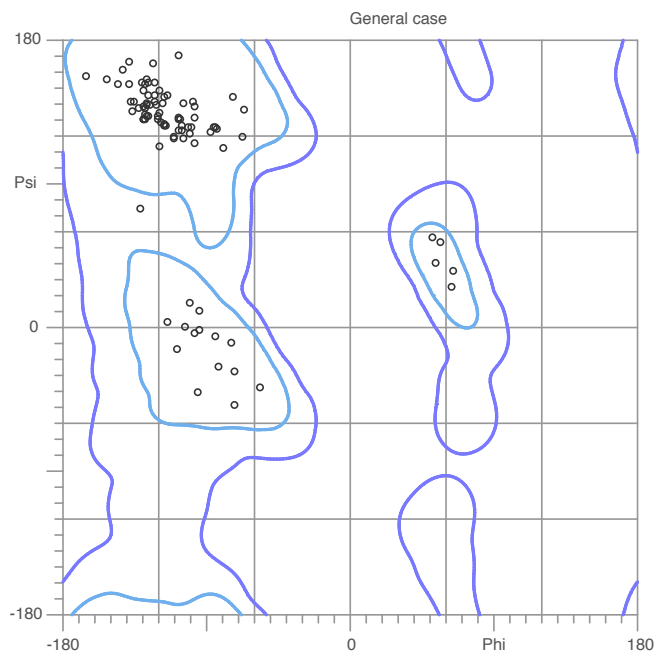
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 18

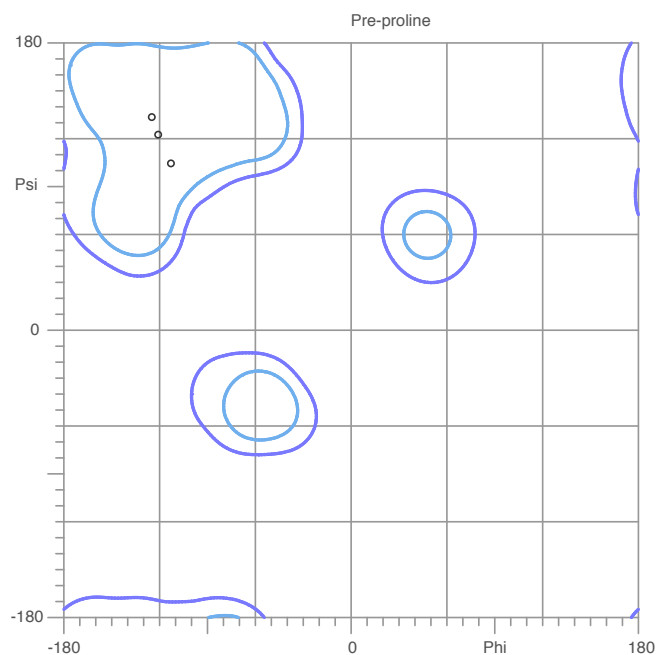
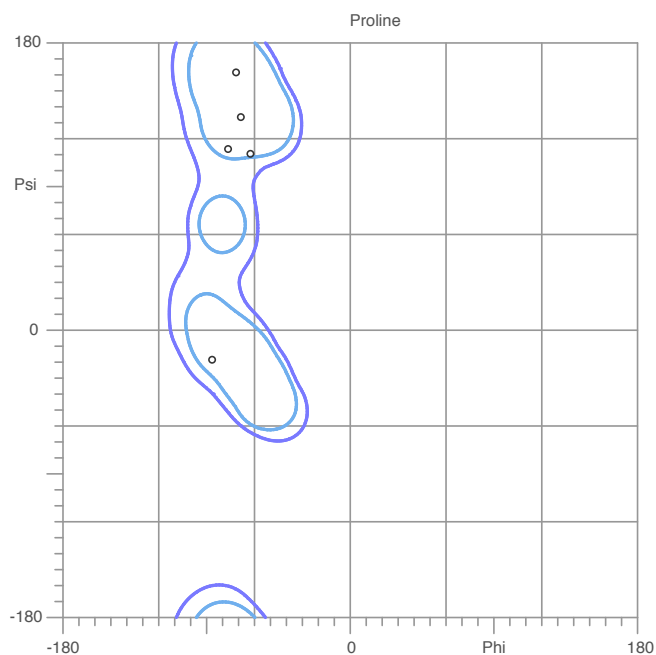
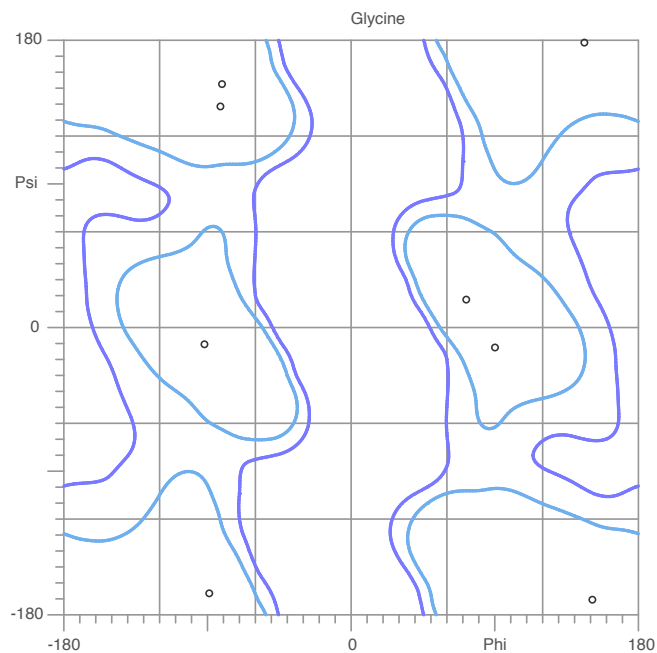
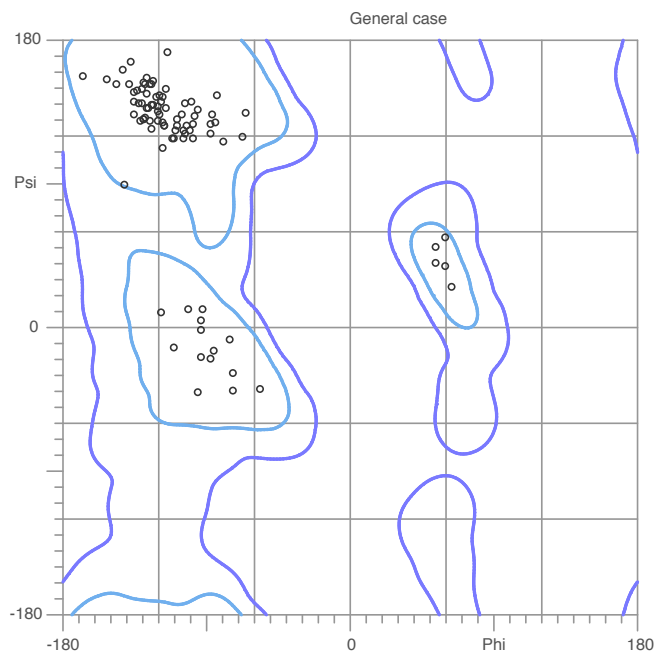


99.1% (105/106) of all residues were in favored (98%) regions.  
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 19



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

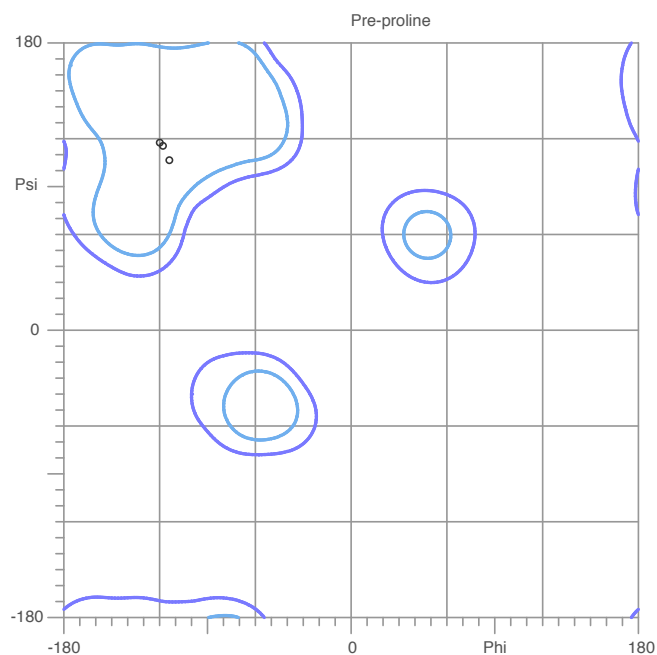
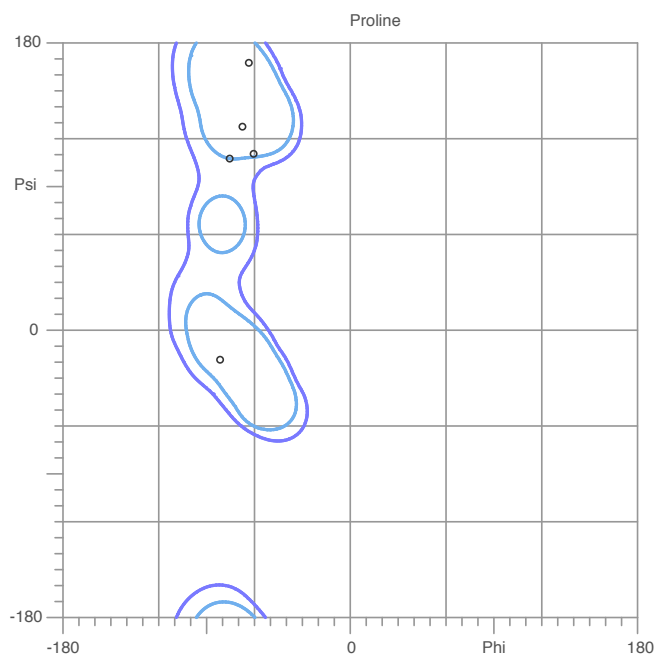
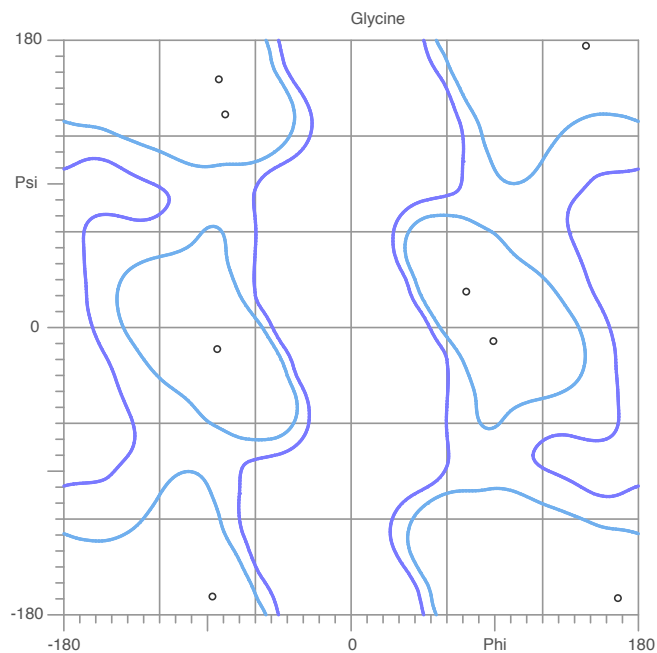
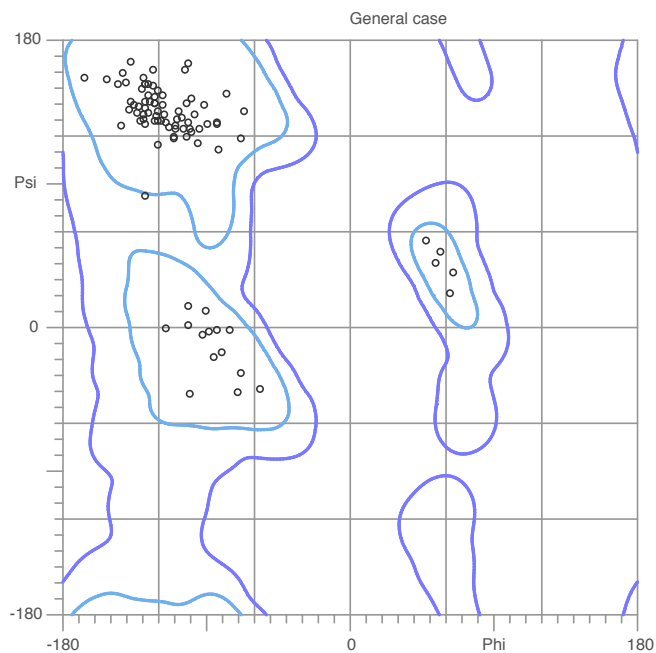
There were no outliers.

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

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# MolProbity Ramachandran analysis

PFR193A\_R3Cons\_em\_bcr3.pdb, model 20



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.

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

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