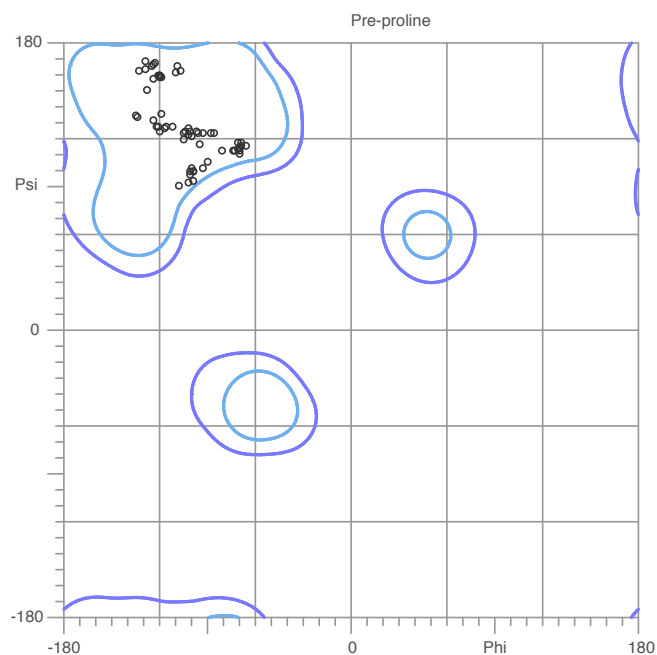
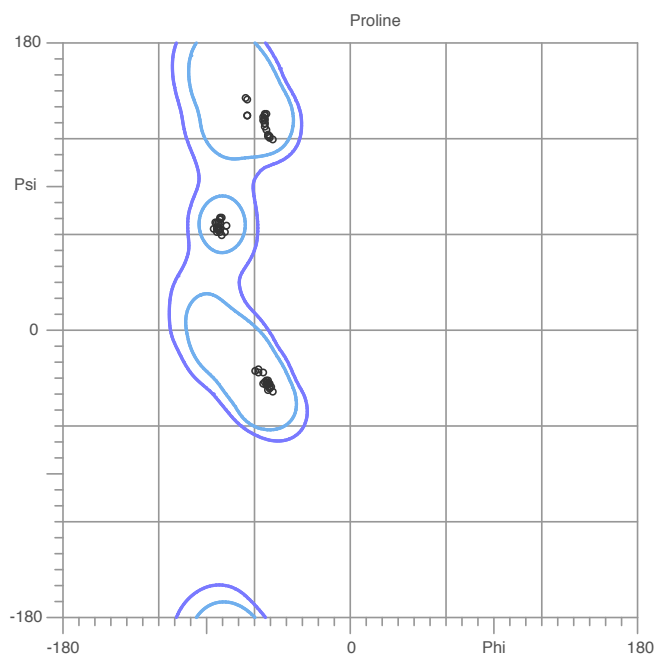
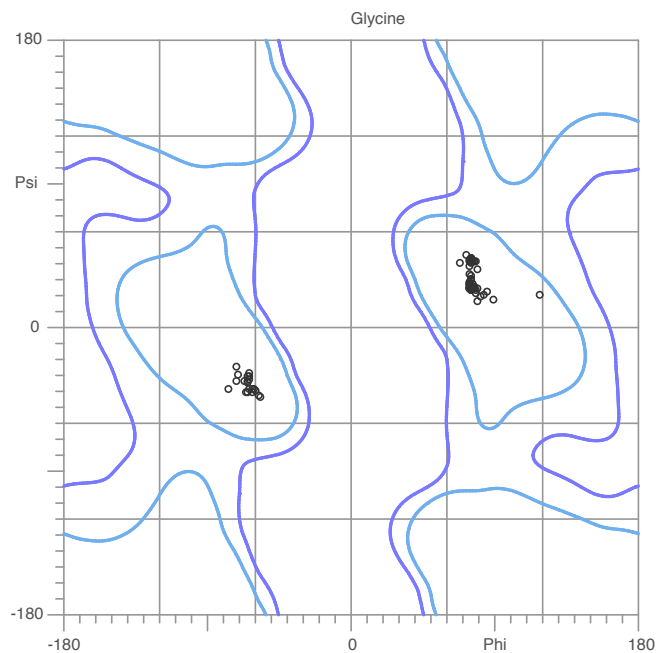
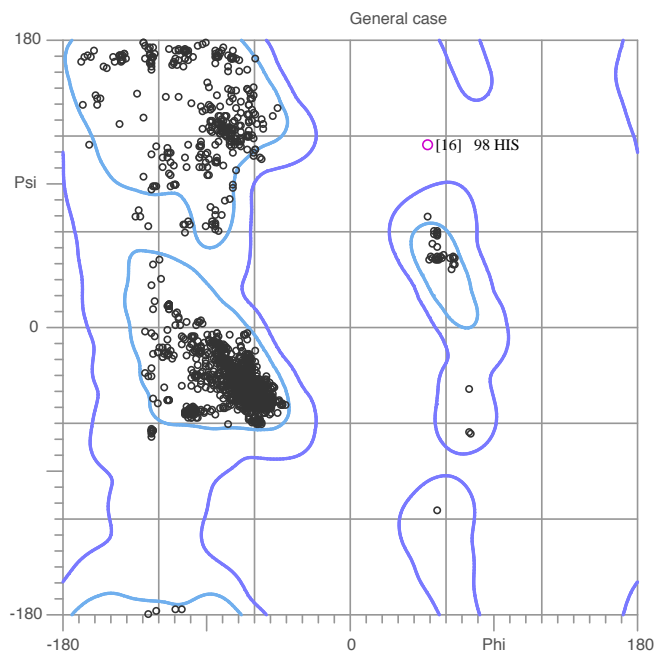


# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, all models



98.6% (1952/1980) of all residues were in favored (98%) regions.  
99.9% (1979/1980) of all residues were in allowed (>99.8%) regions.

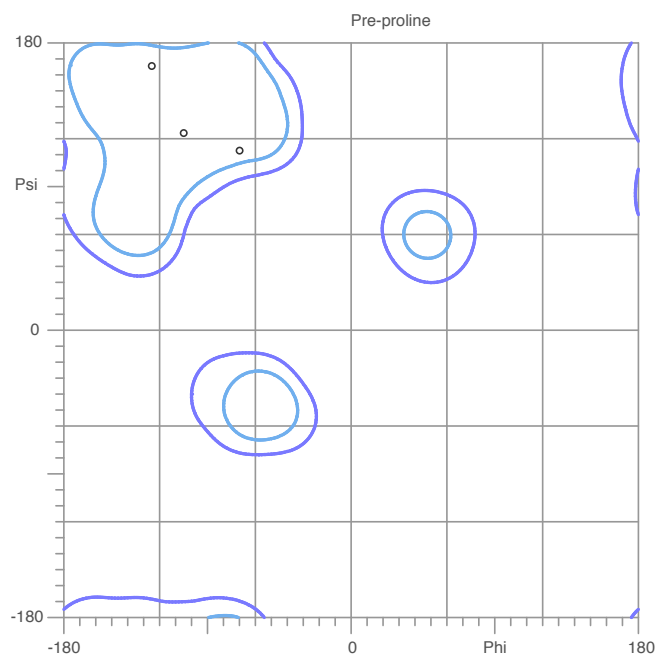
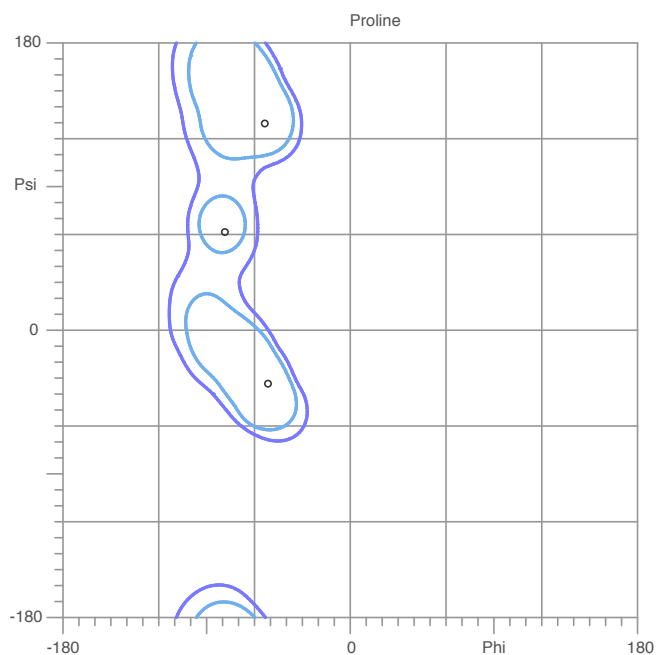
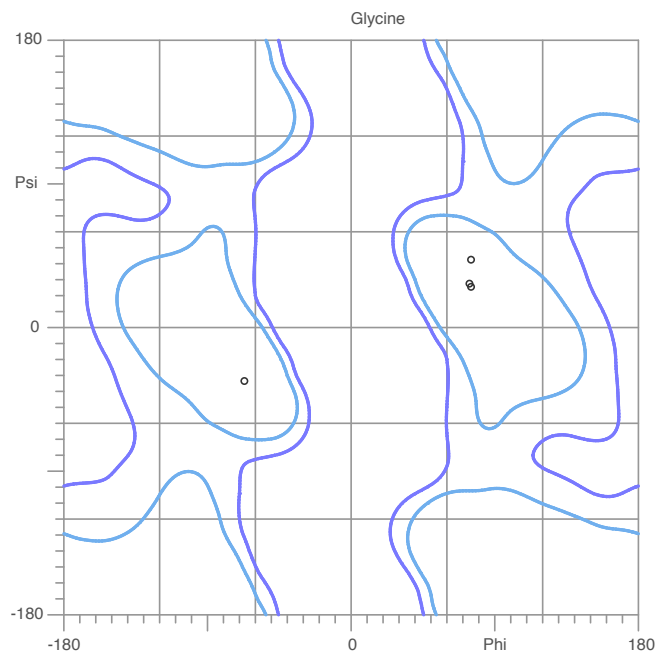
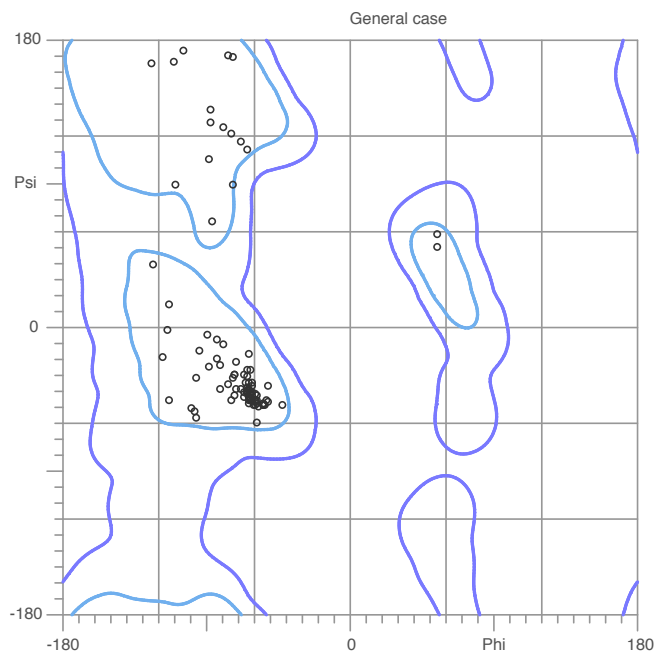
There were 1 outliers (phi, psi):  
[16] 98 HIS (48.5, 115.0)

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# MolProbity Ramachandran analysis

RPR324\_R3\_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.

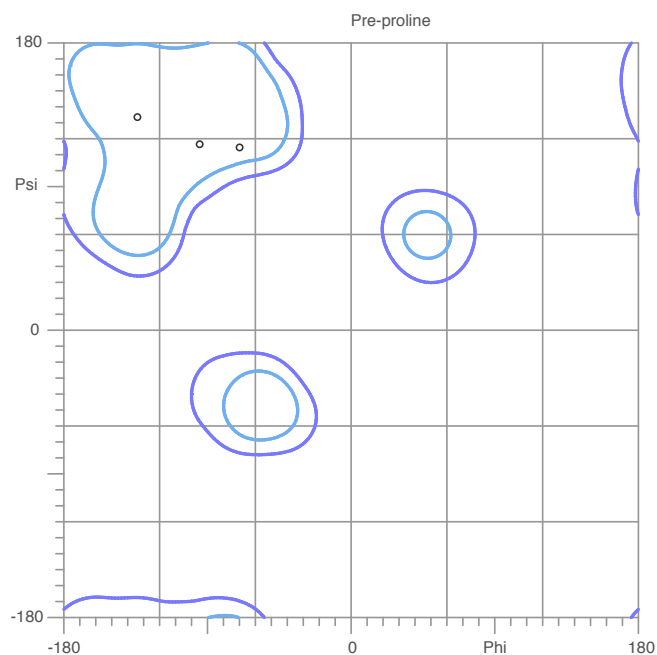
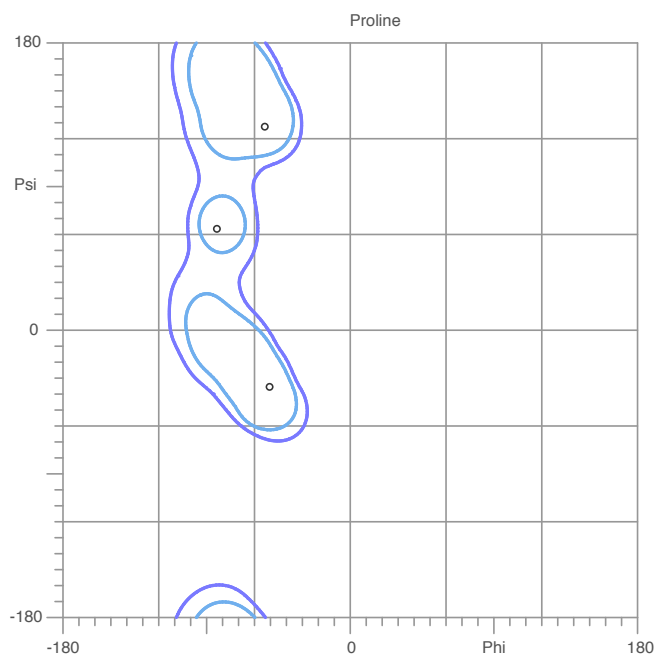
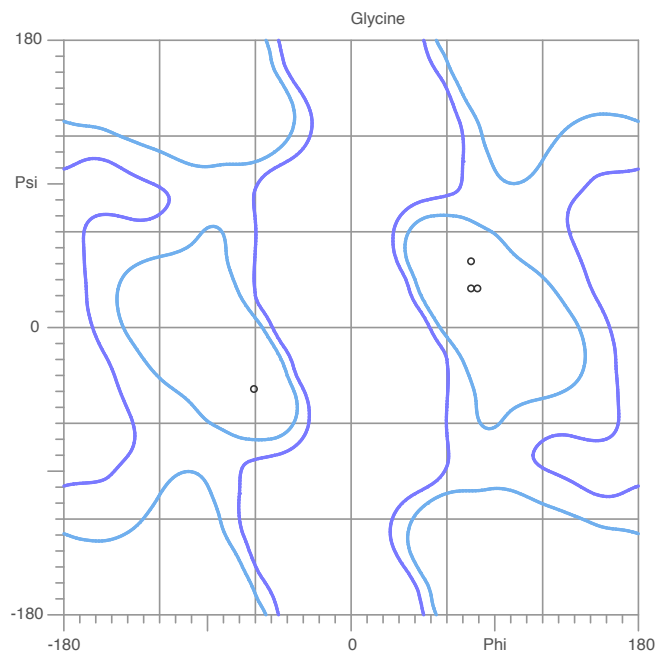
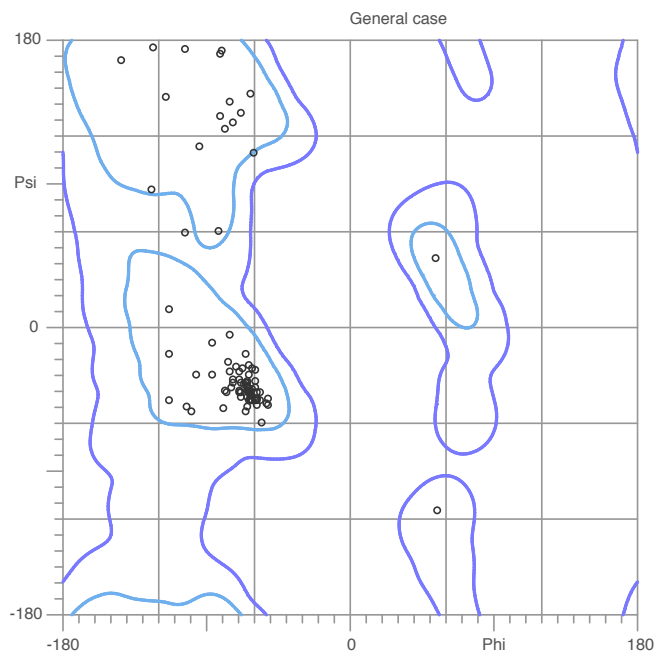
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 2



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.

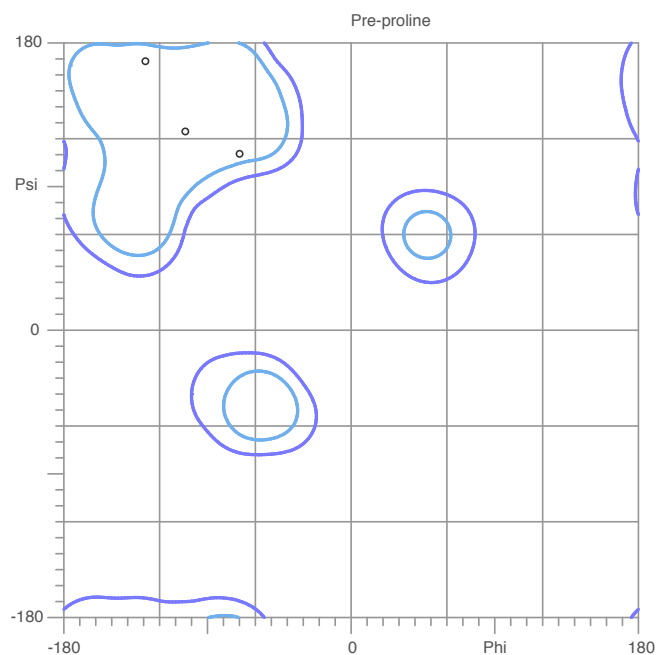
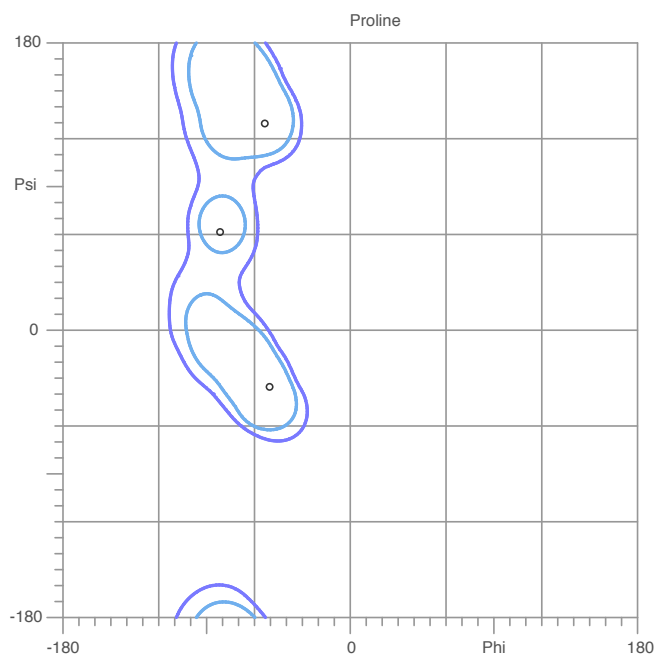
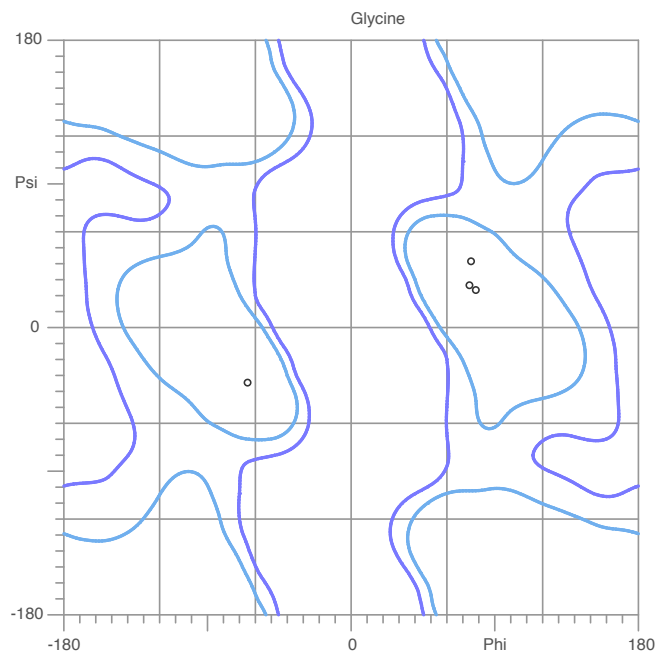
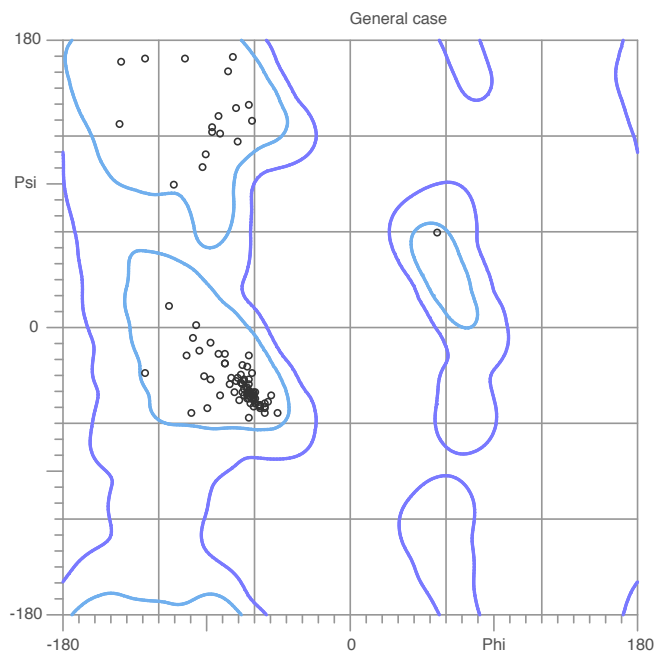
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 3



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.

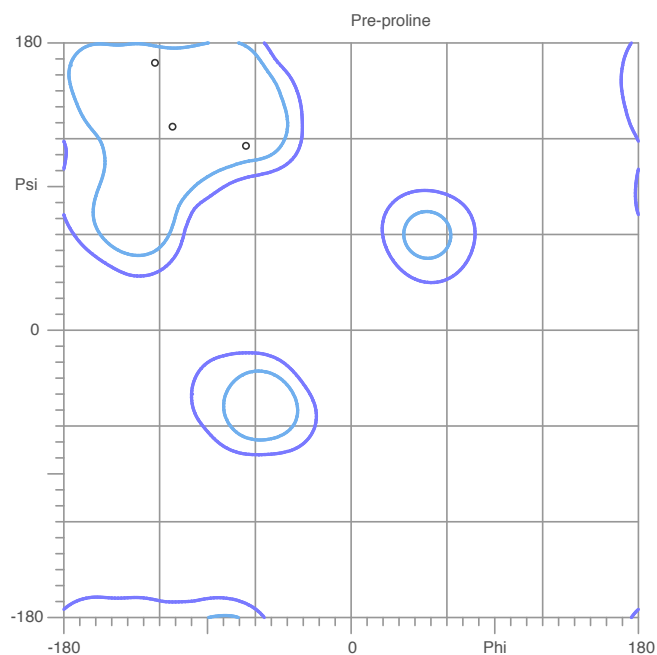
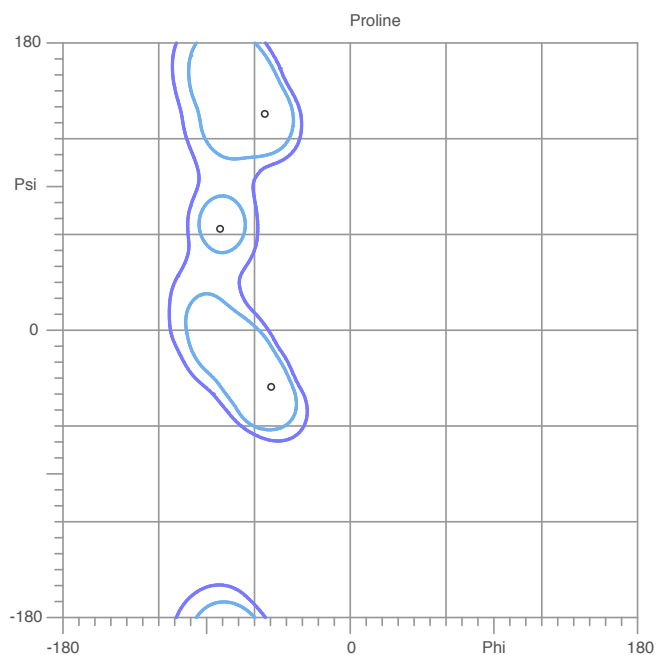
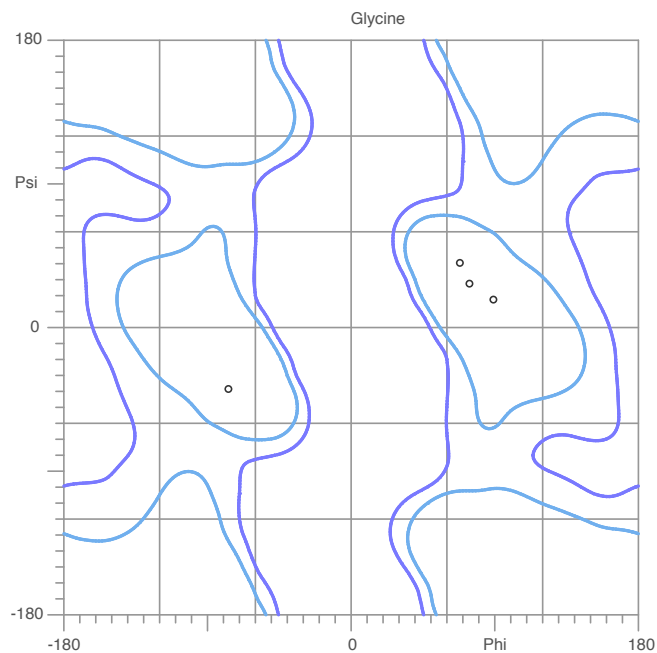
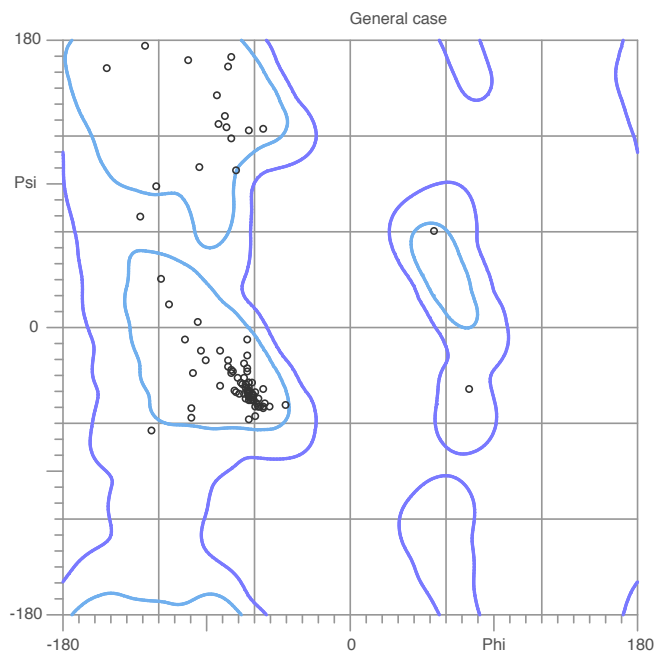
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 4



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.

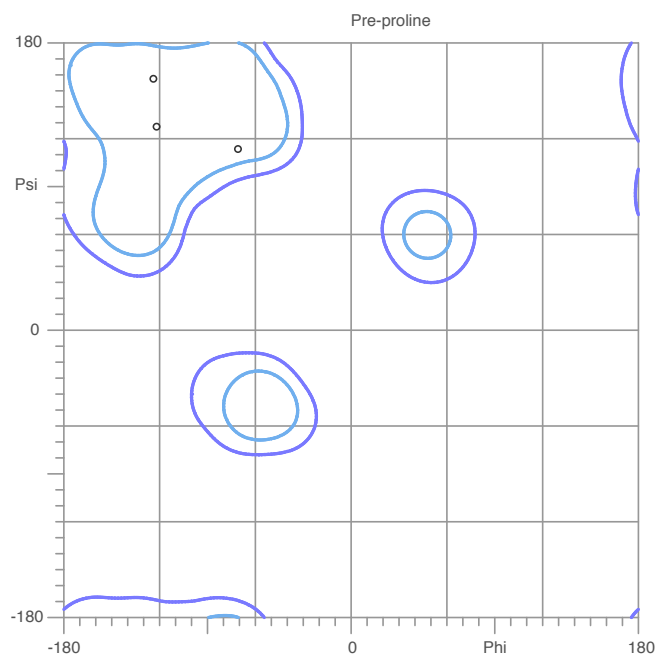
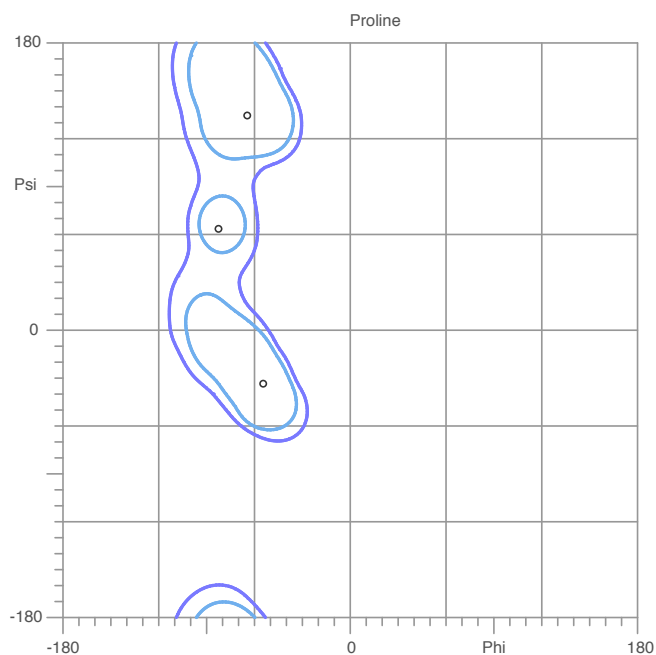
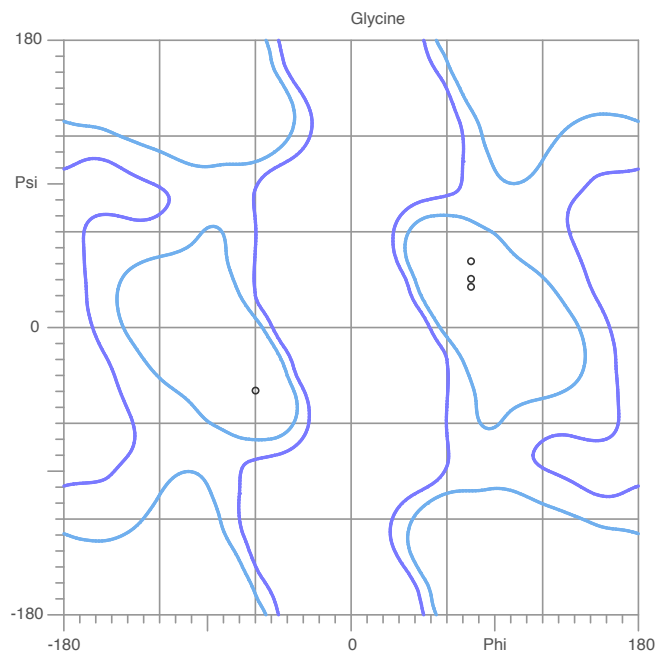
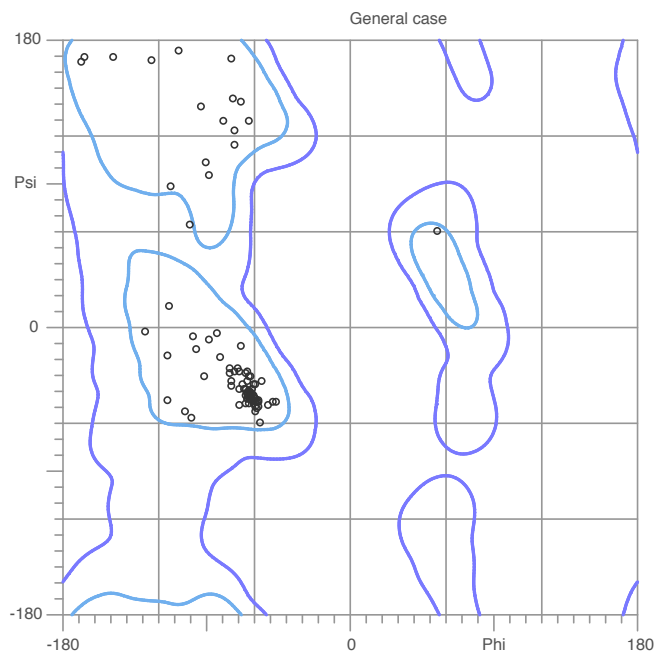
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 5



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.

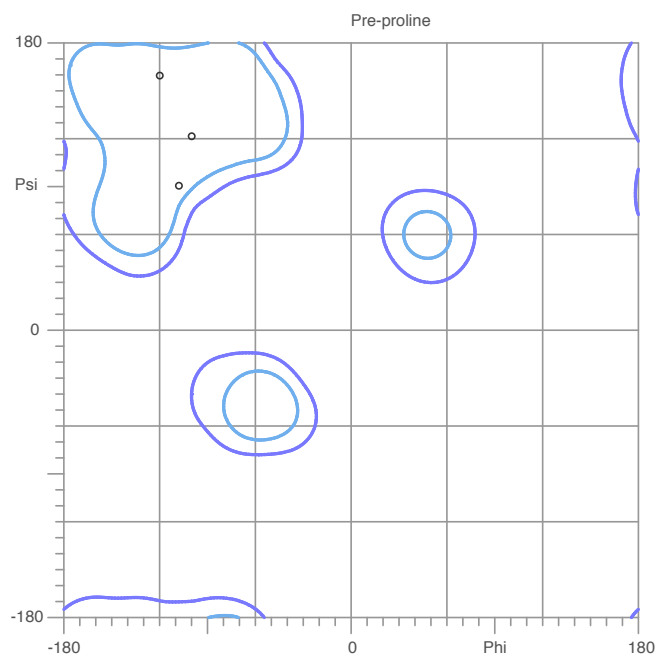
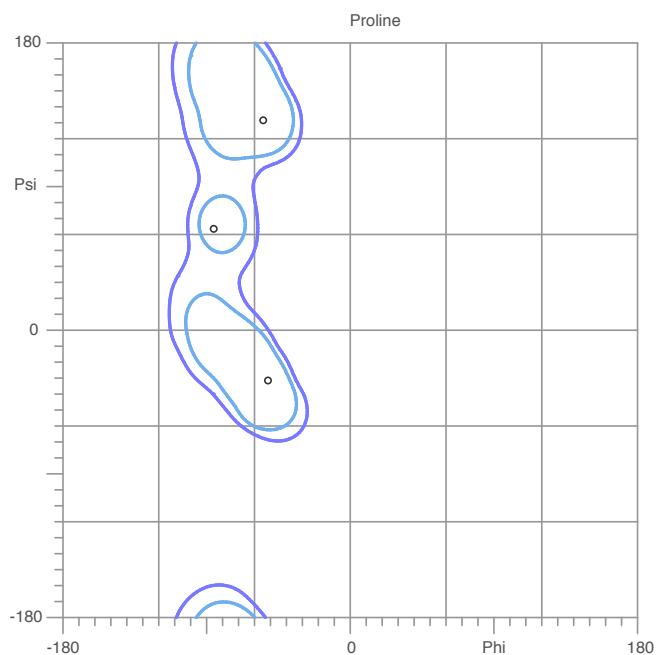
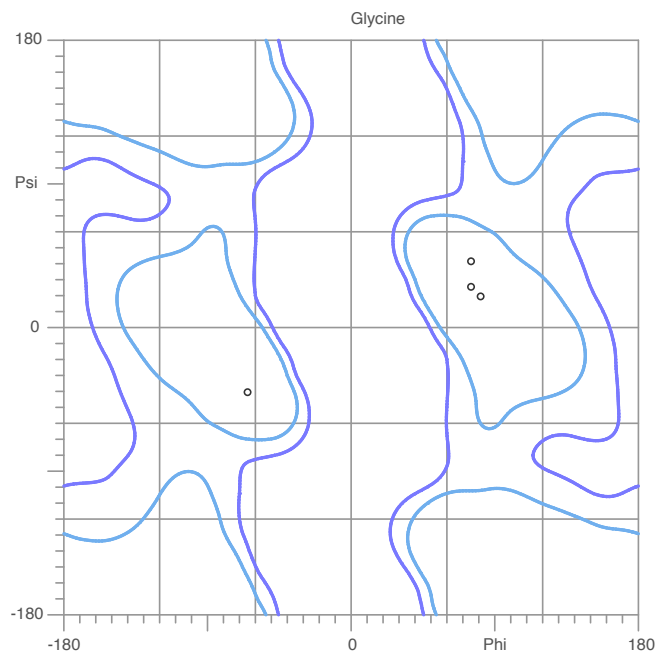
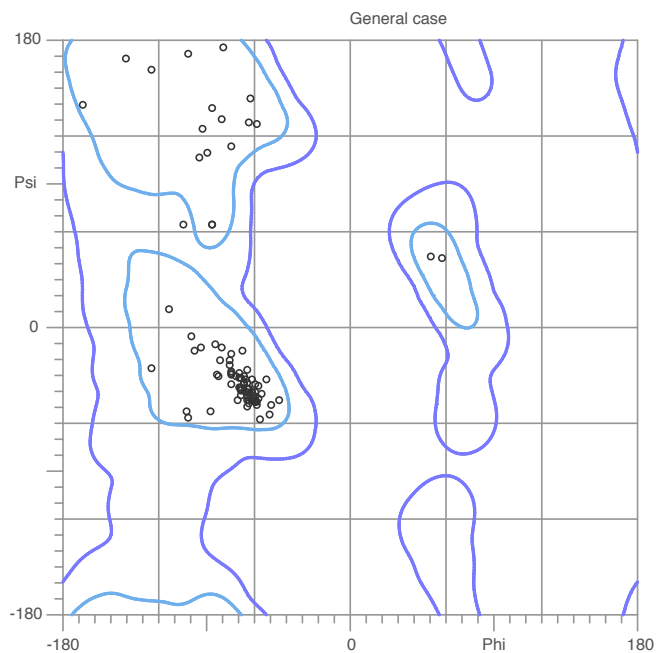
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 6



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.

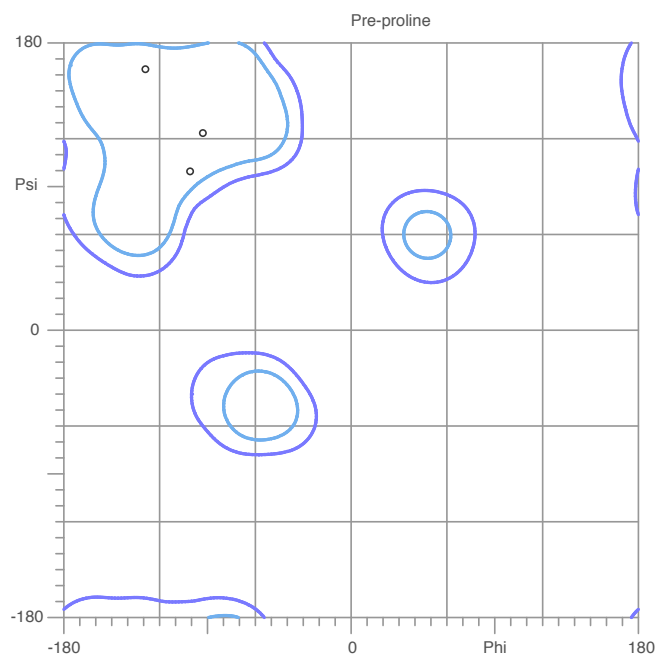
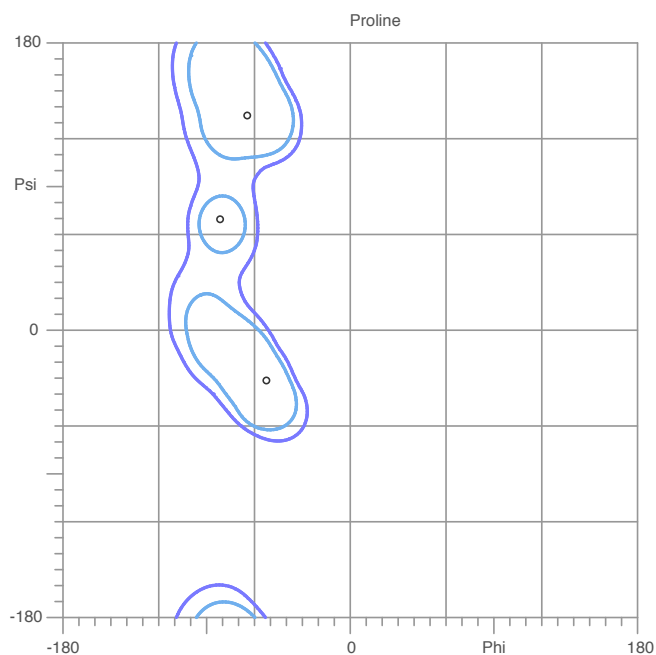
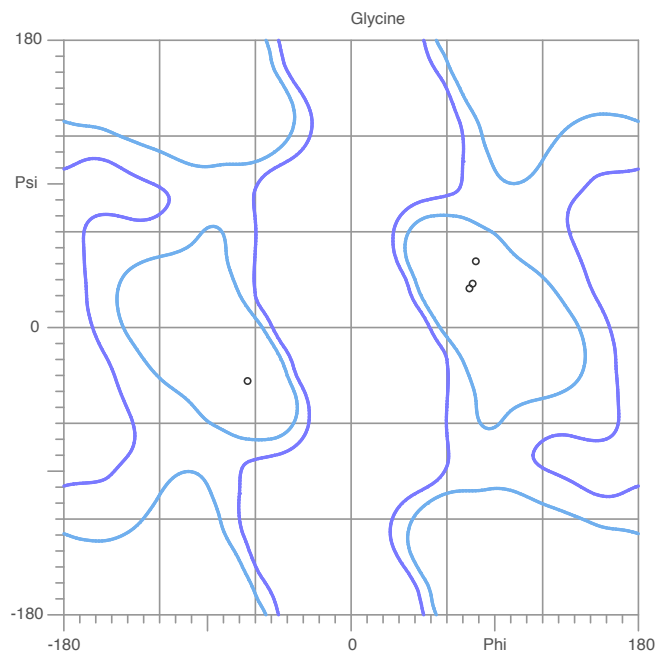
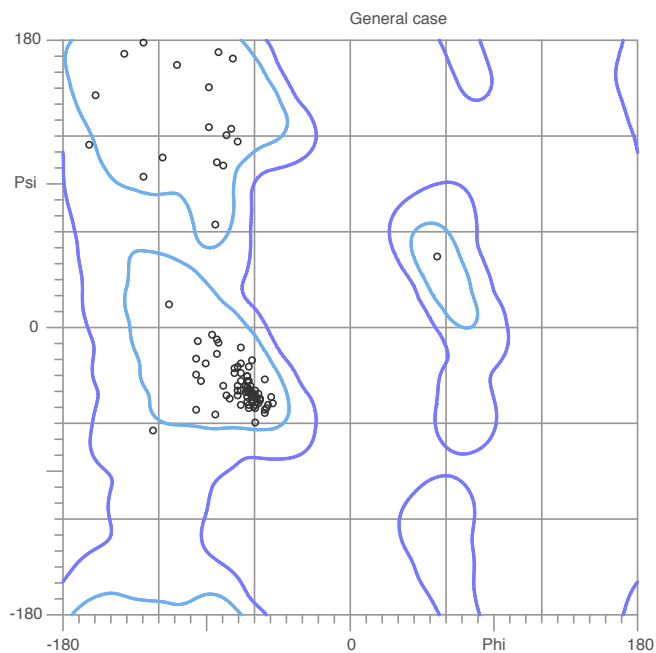
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 7



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.

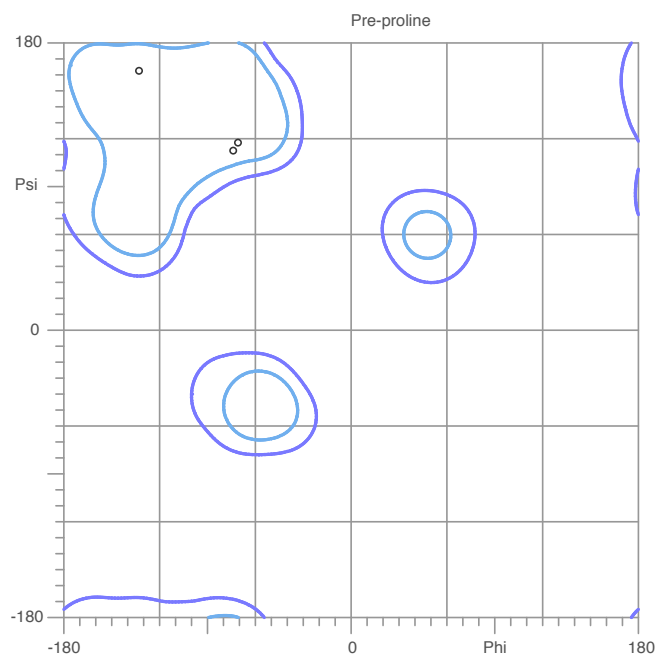
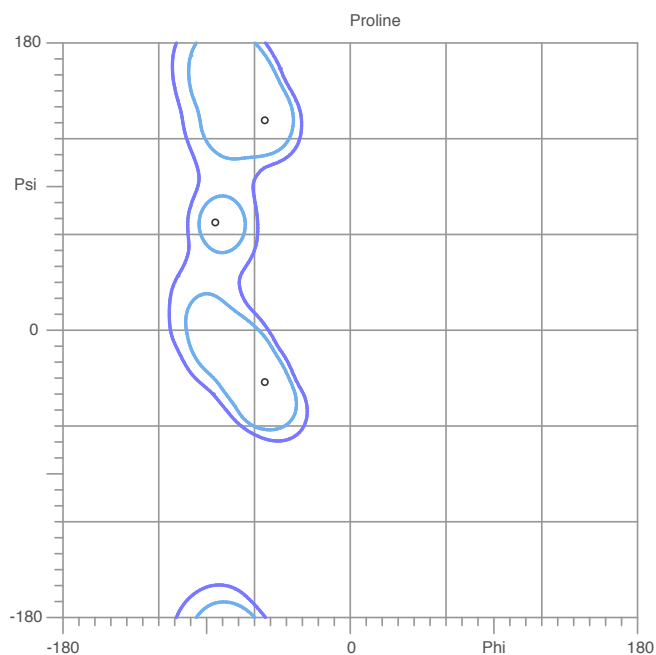
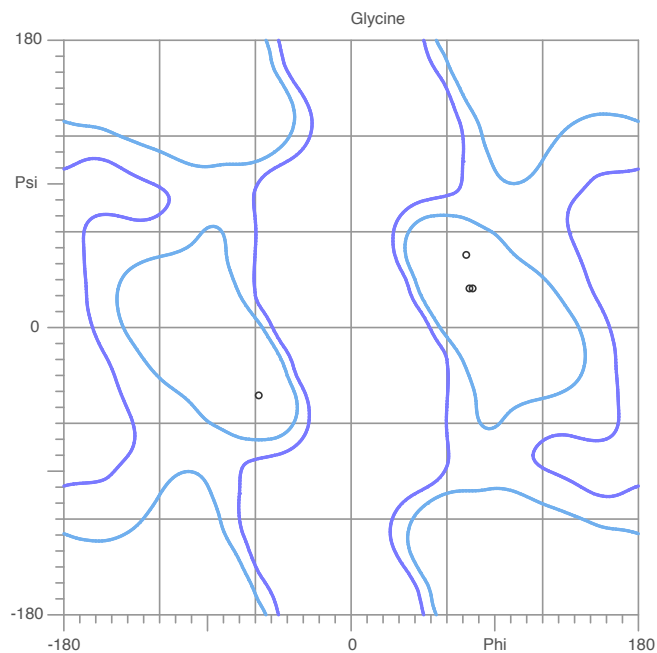
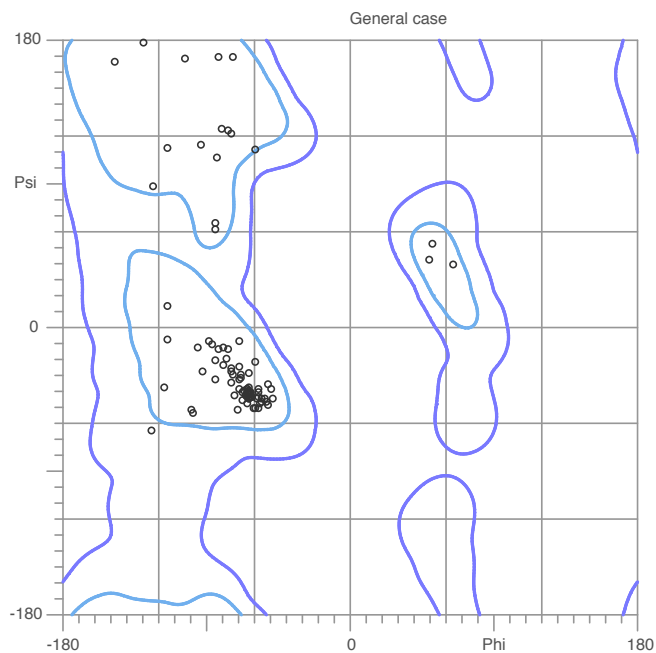
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_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.

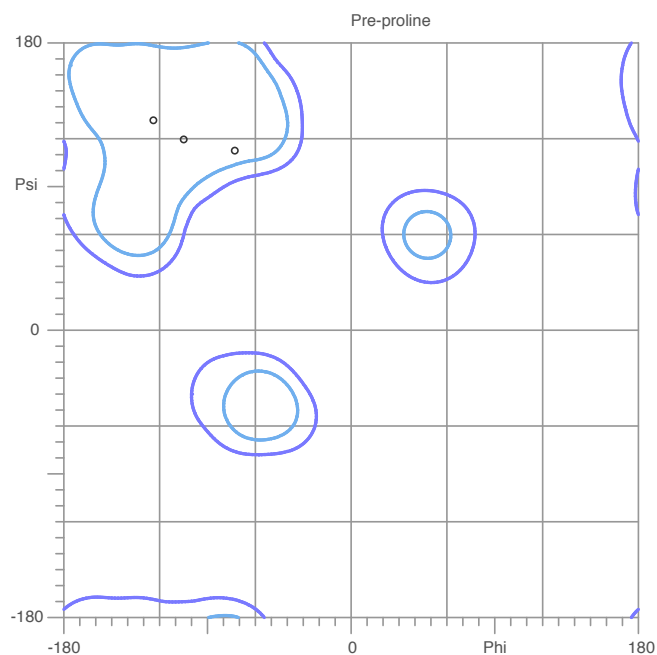
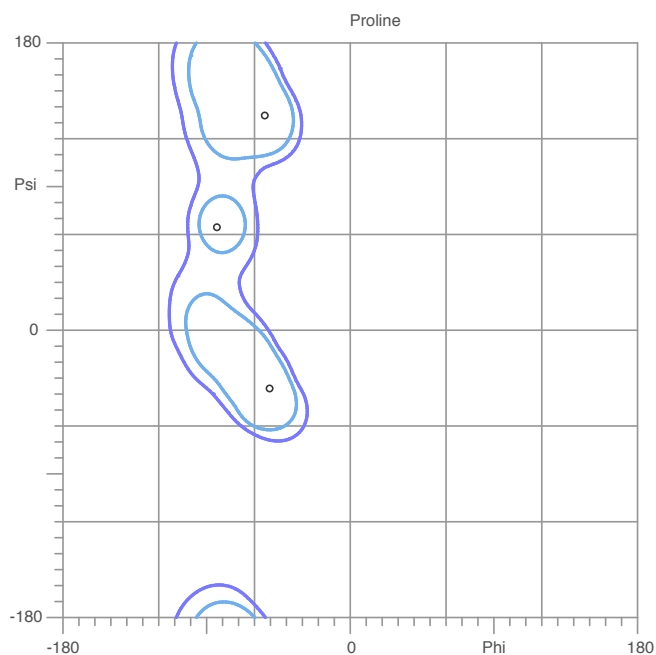
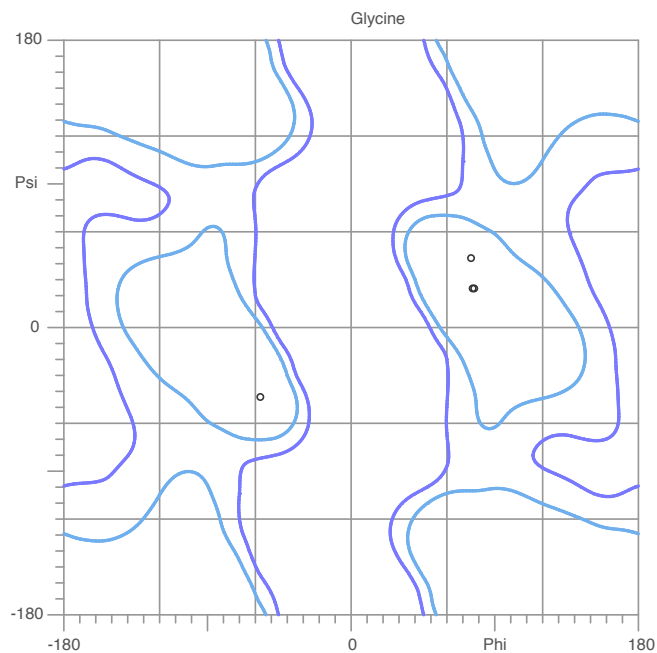
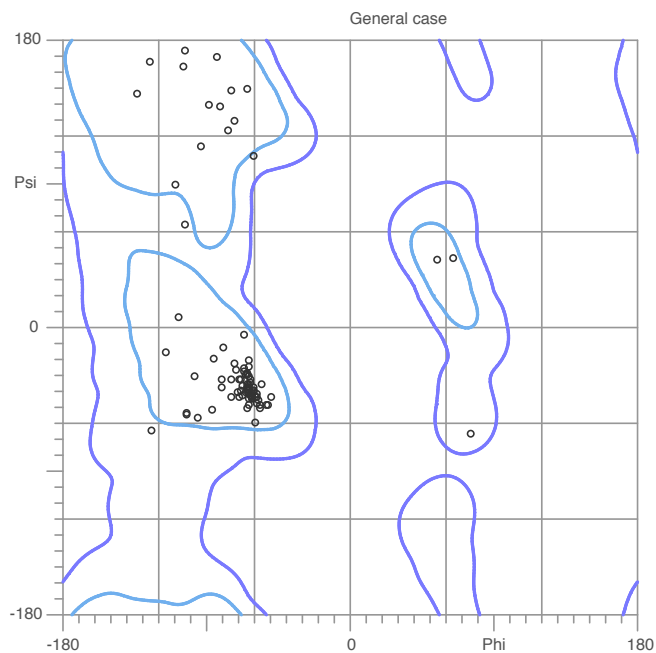
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 9



96.0% (95/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

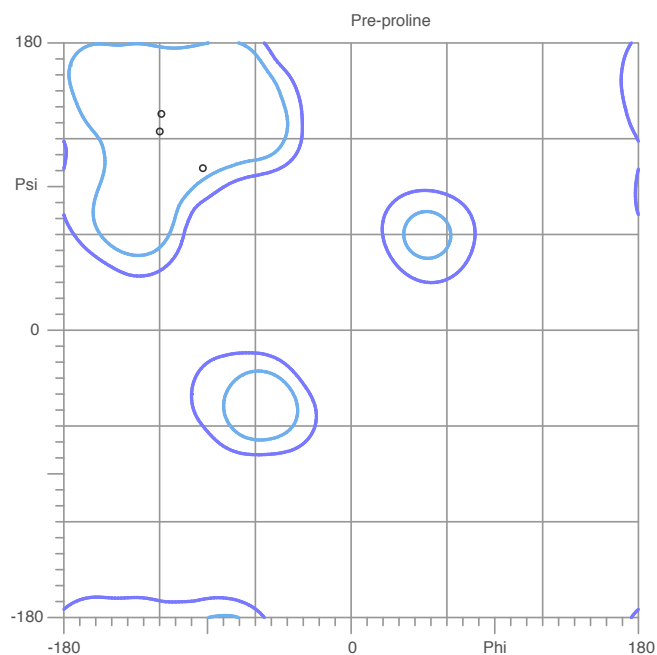
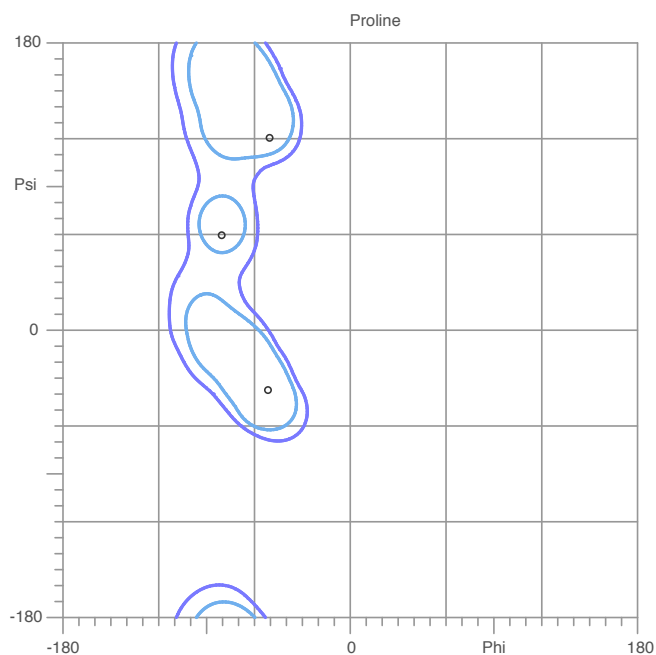
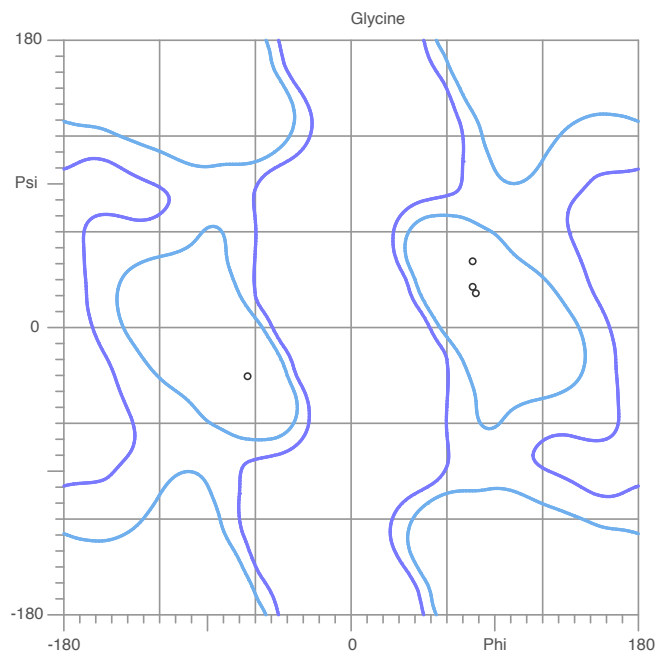
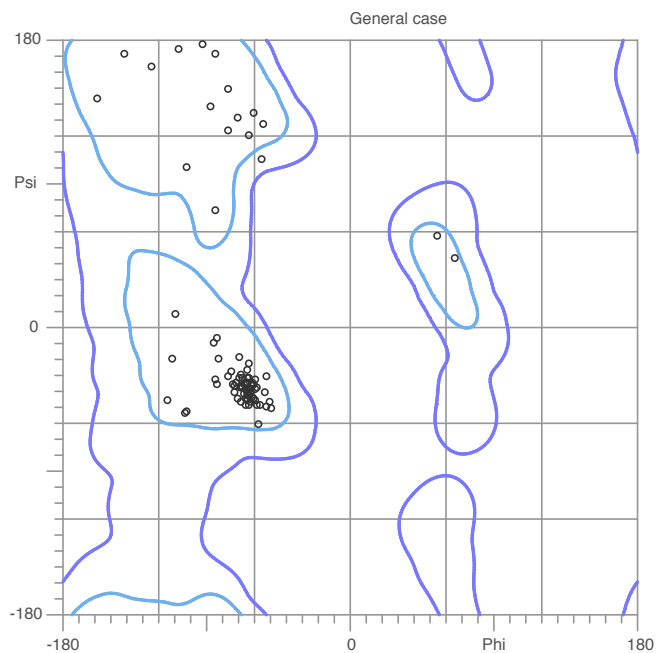
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_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.

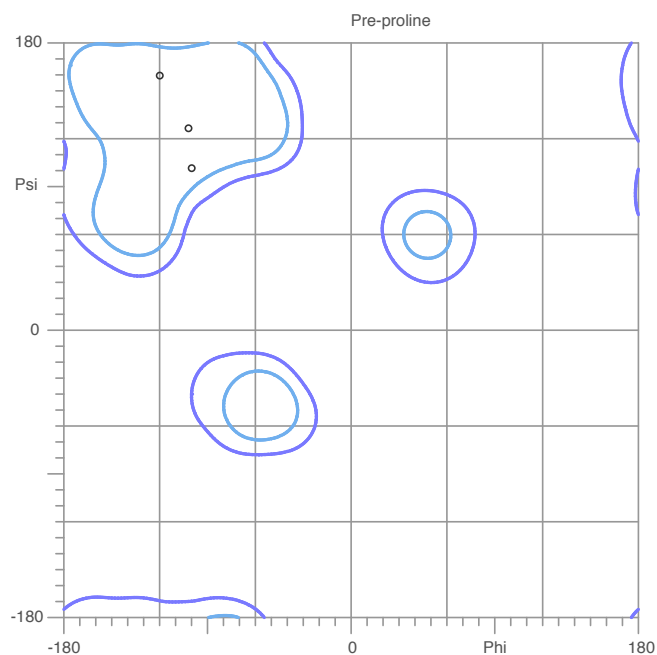
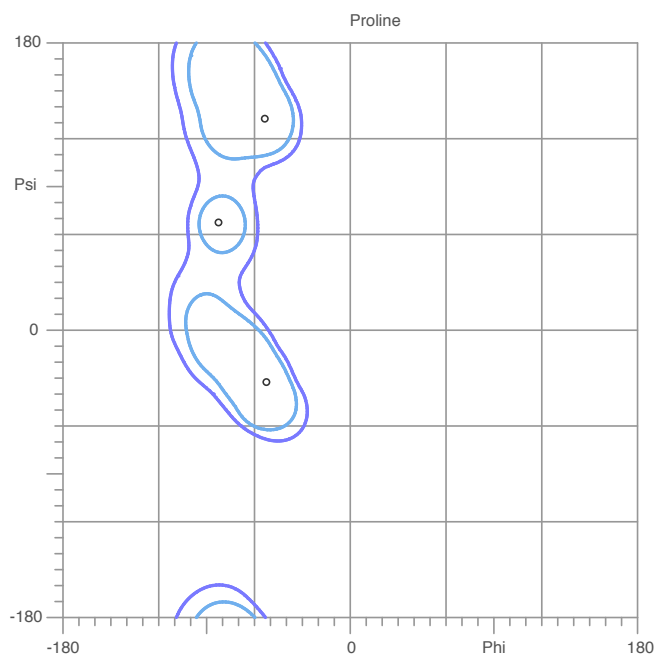
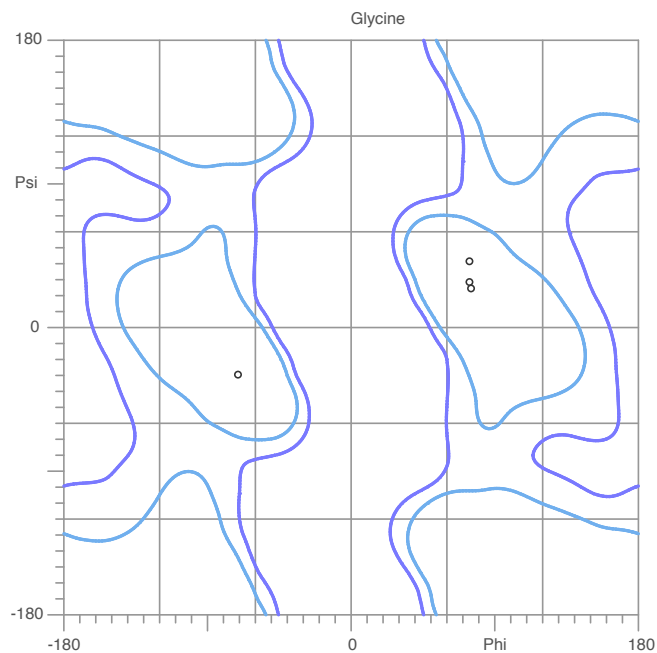
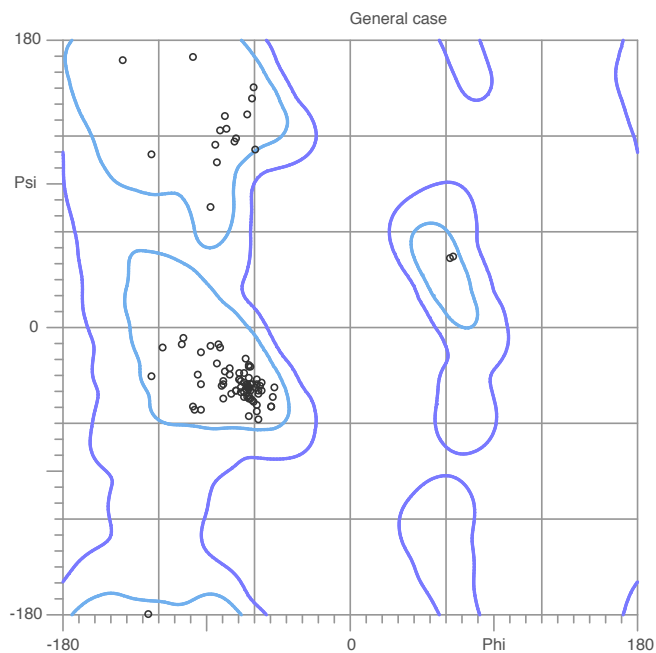
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_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.

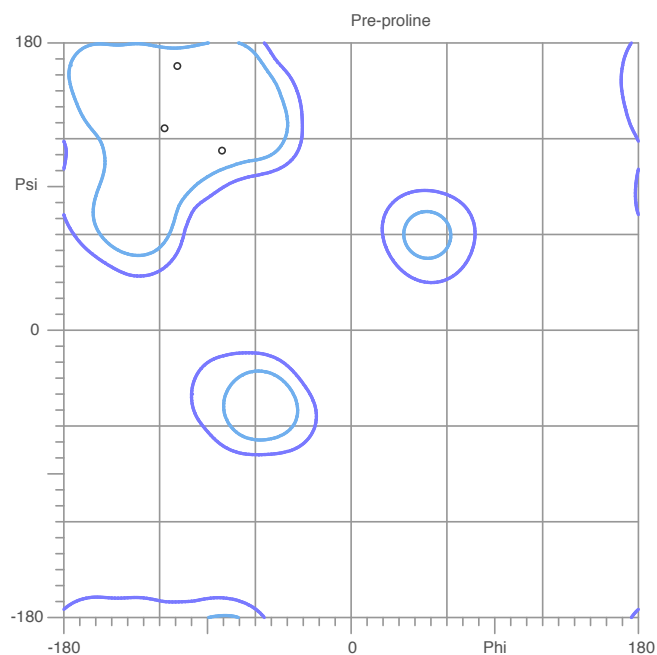
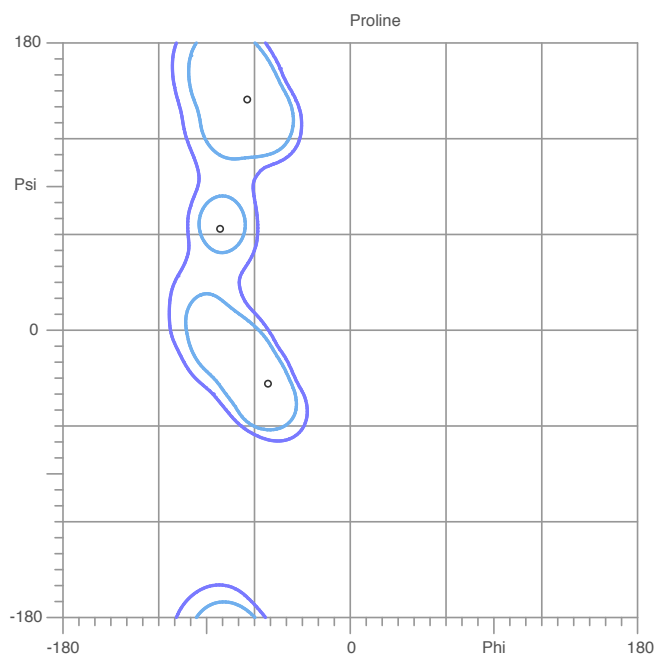
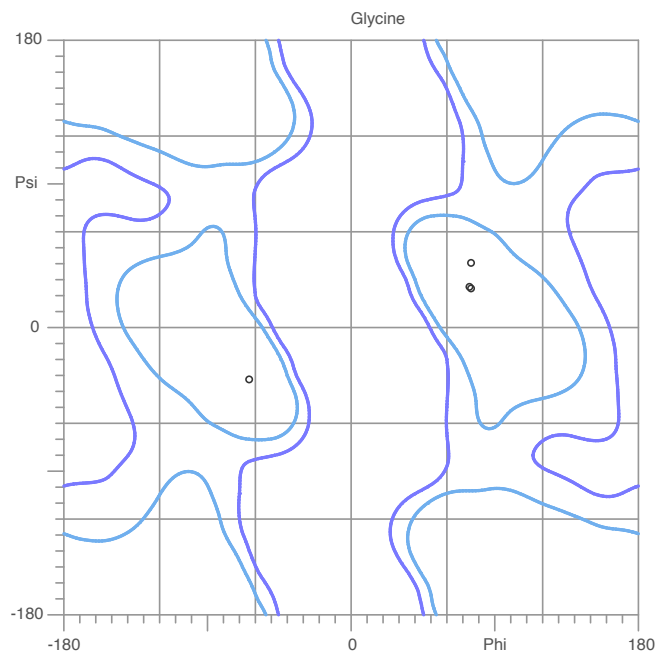
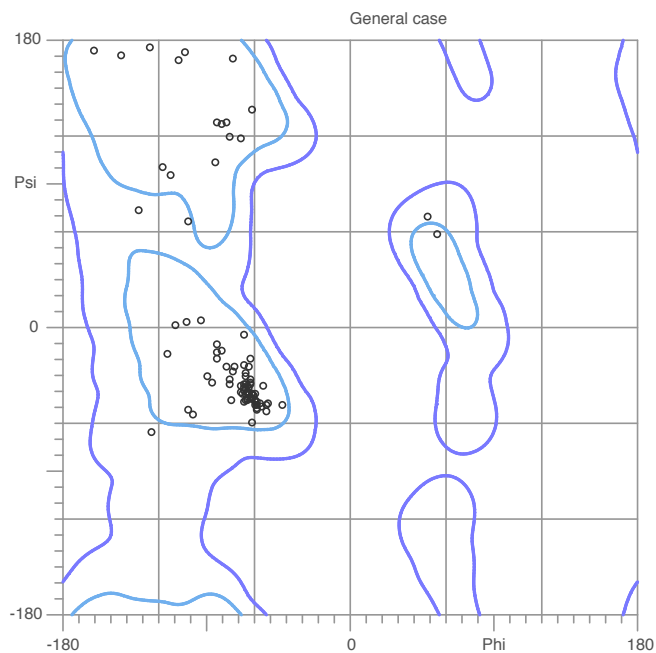
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 12



96.0% (95/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

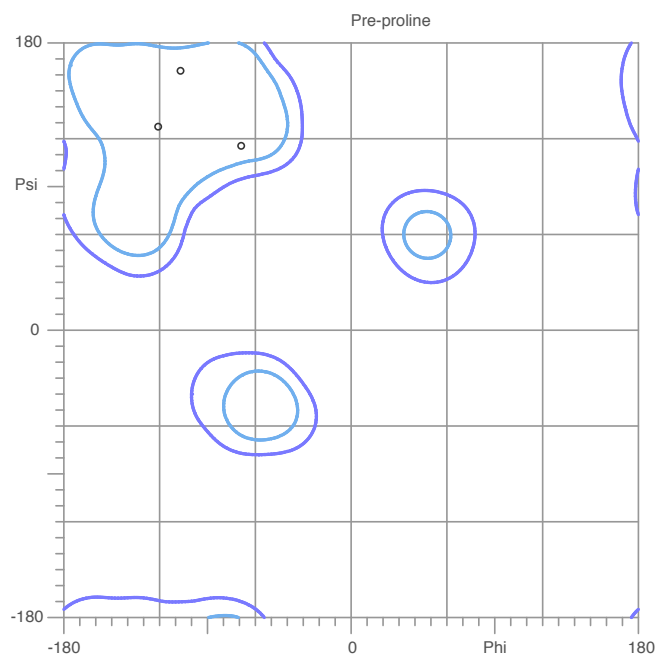
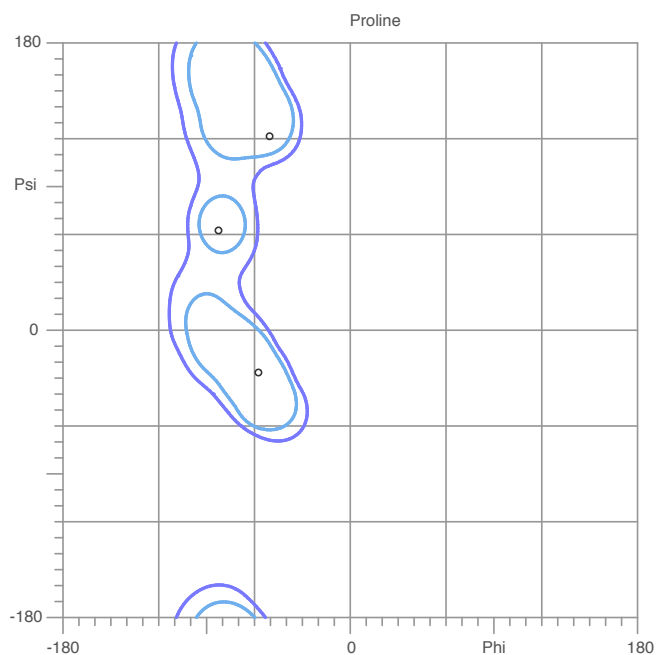
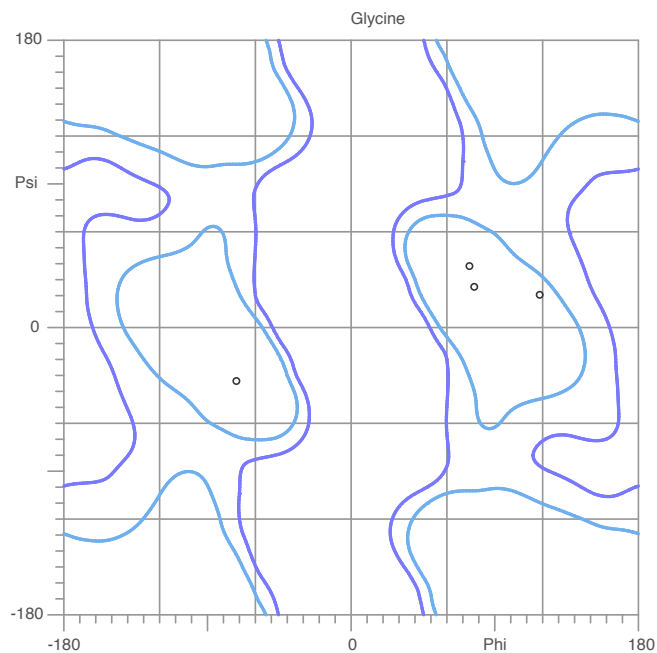
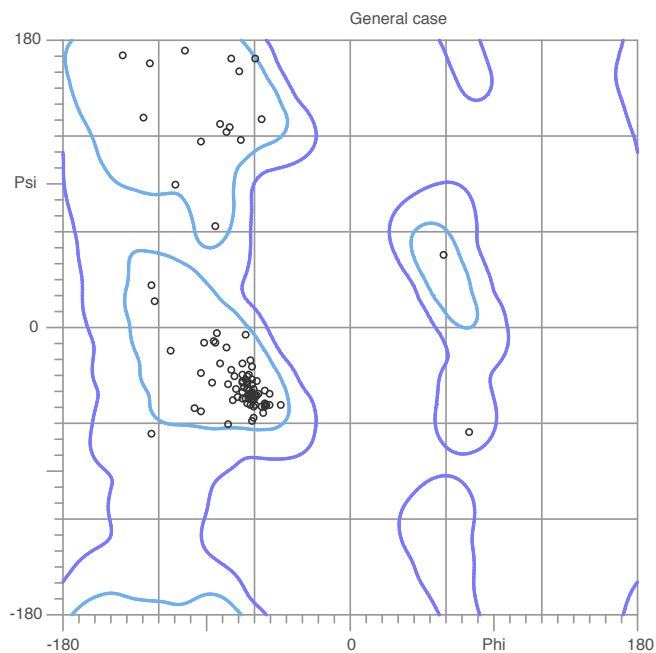
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_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.

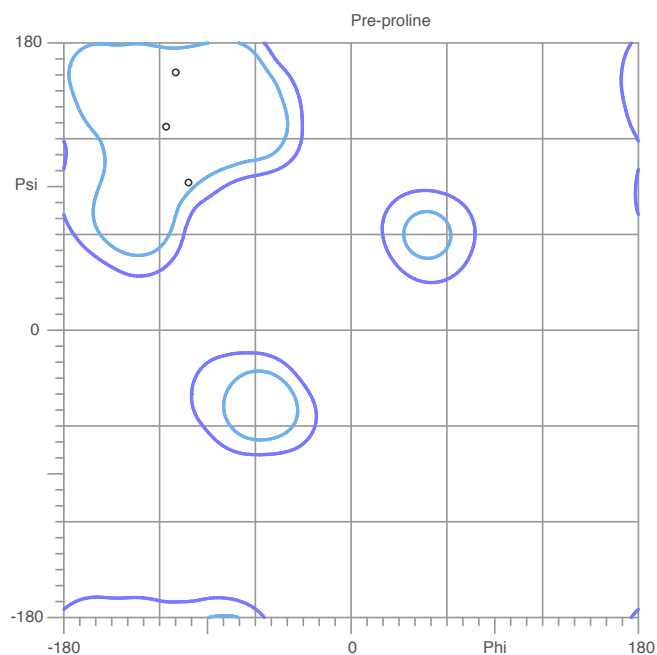
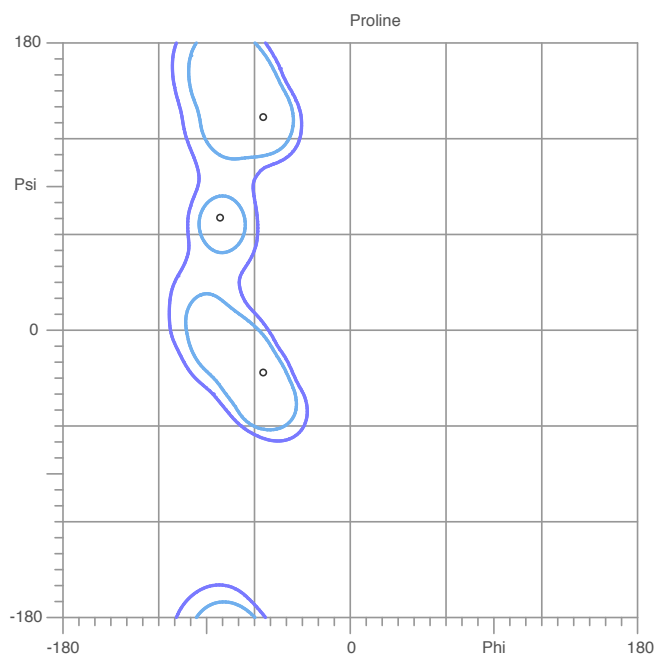
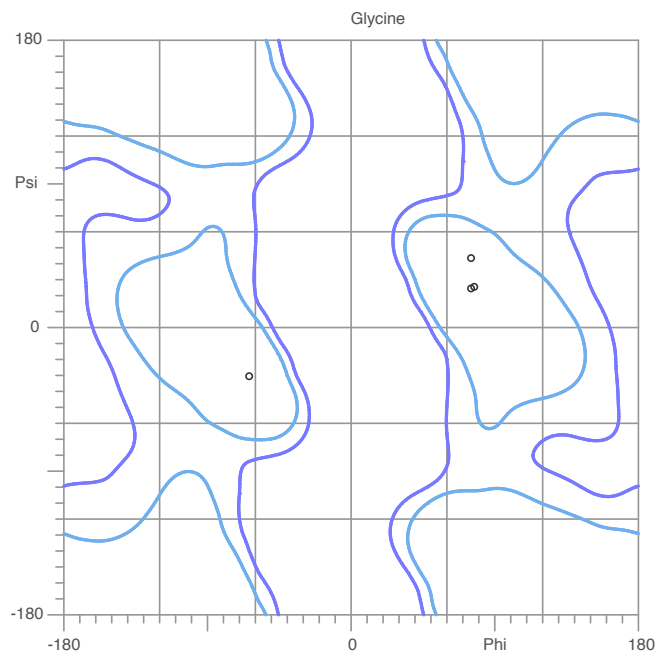
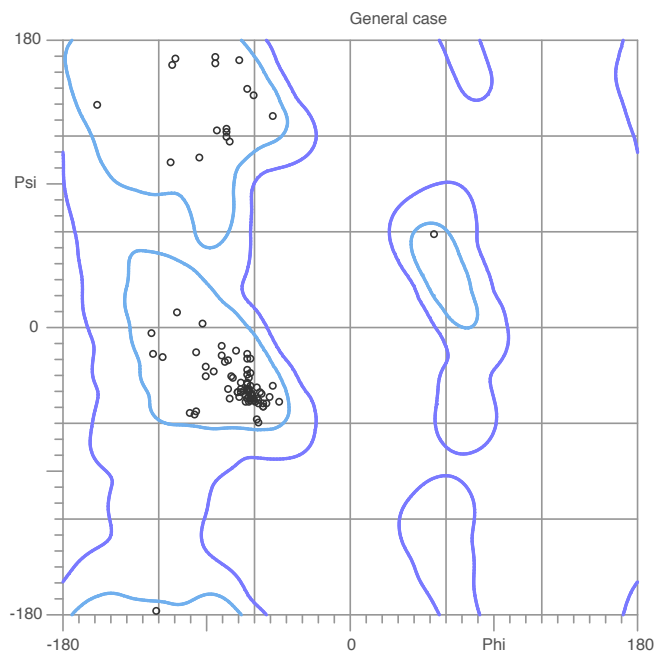
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 14



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.

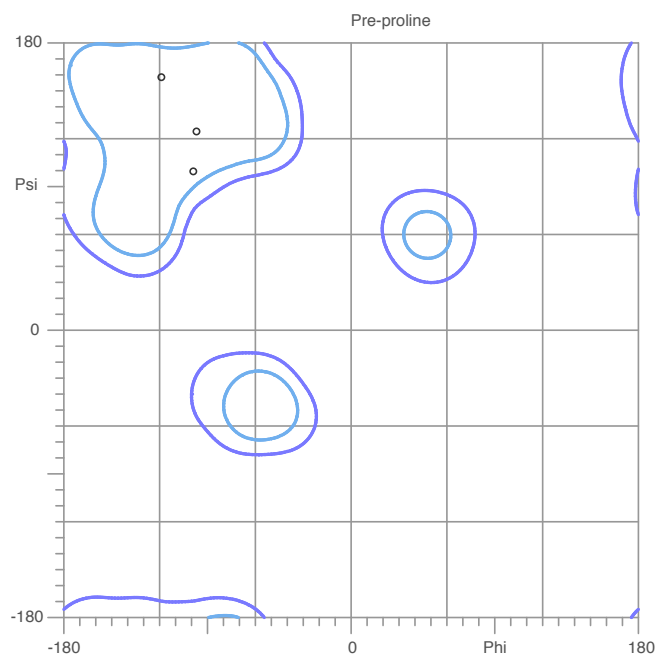
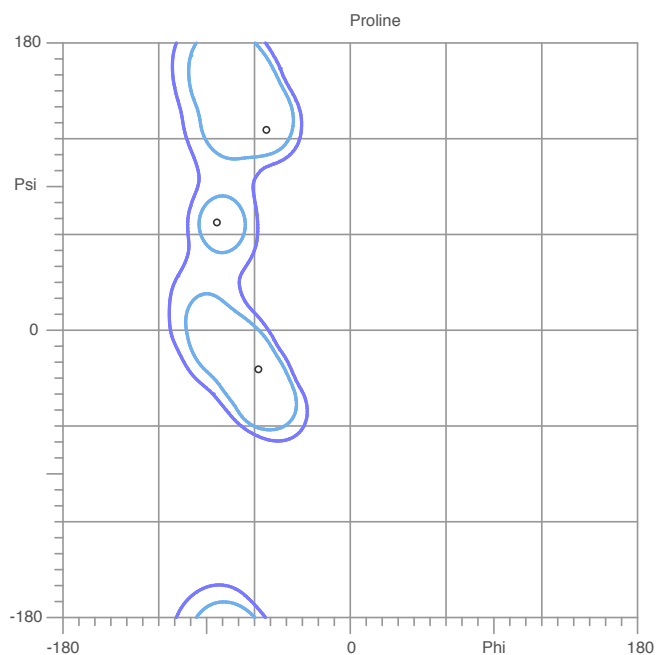
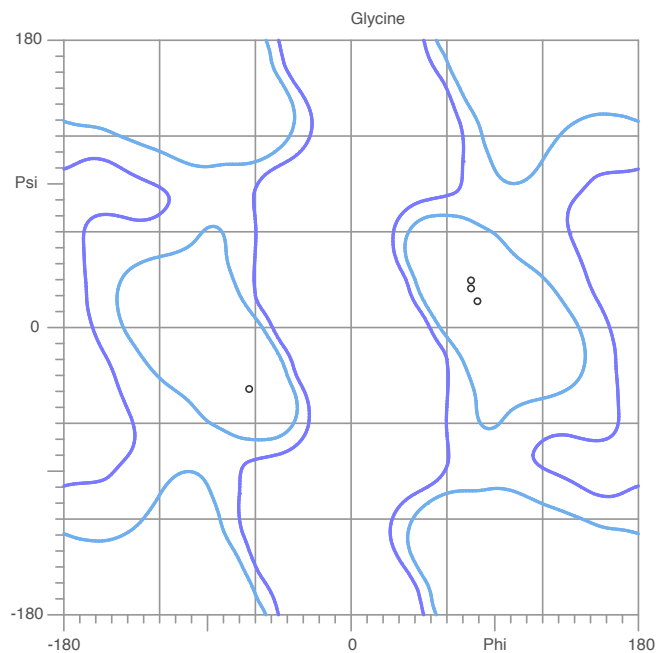
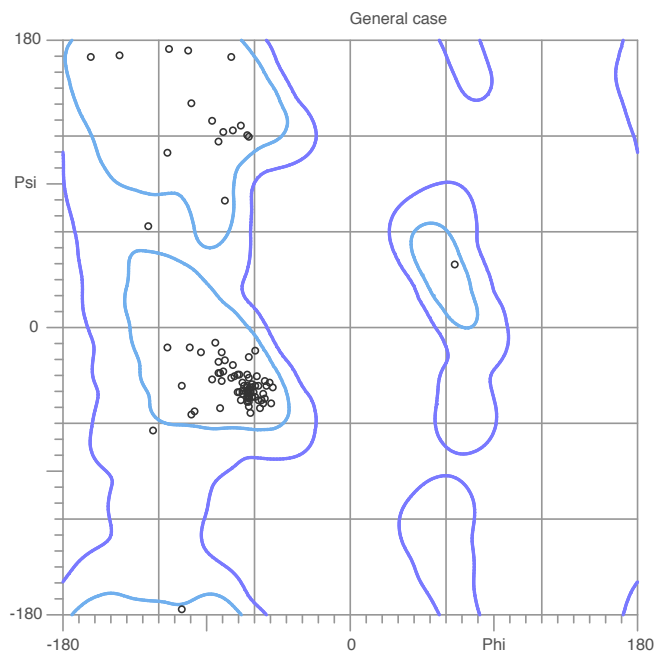
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 15



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.

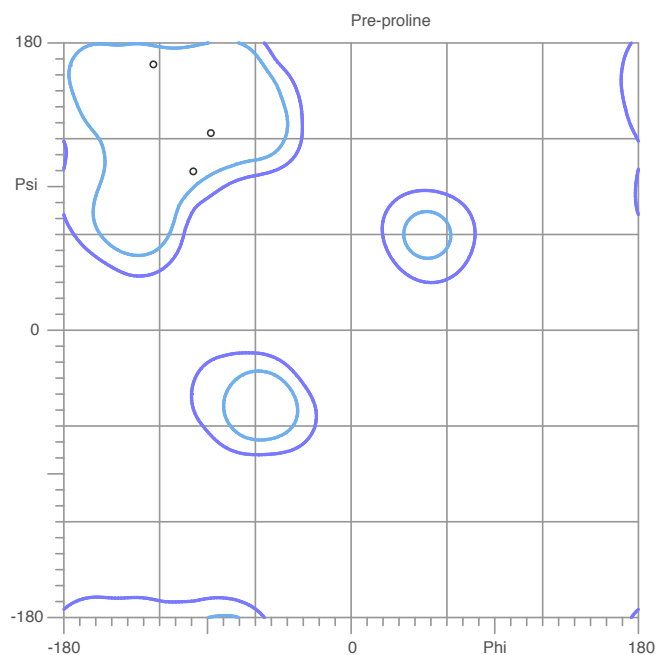
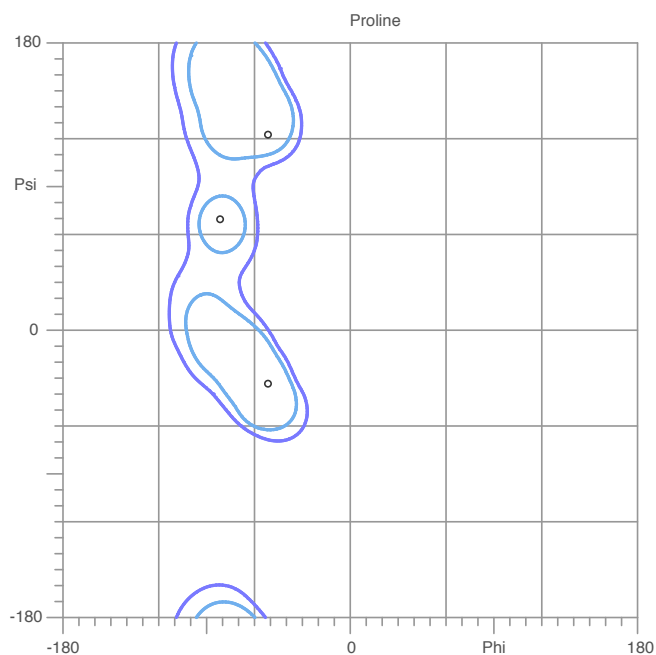
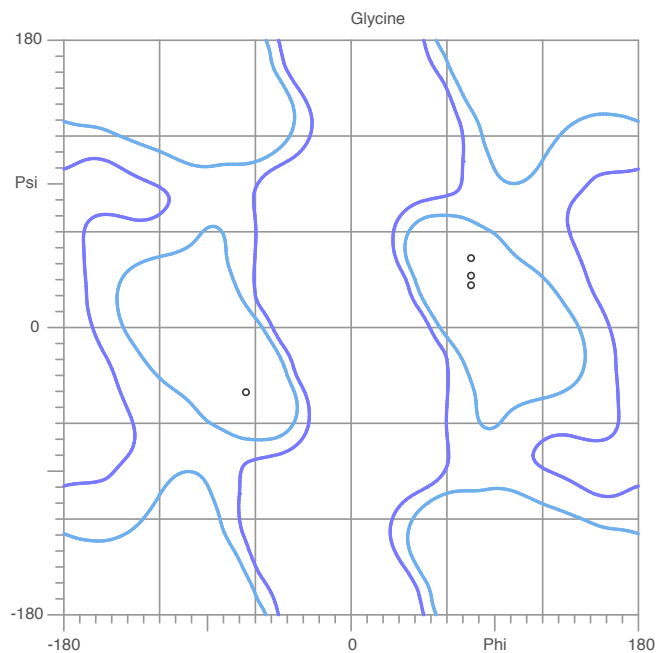
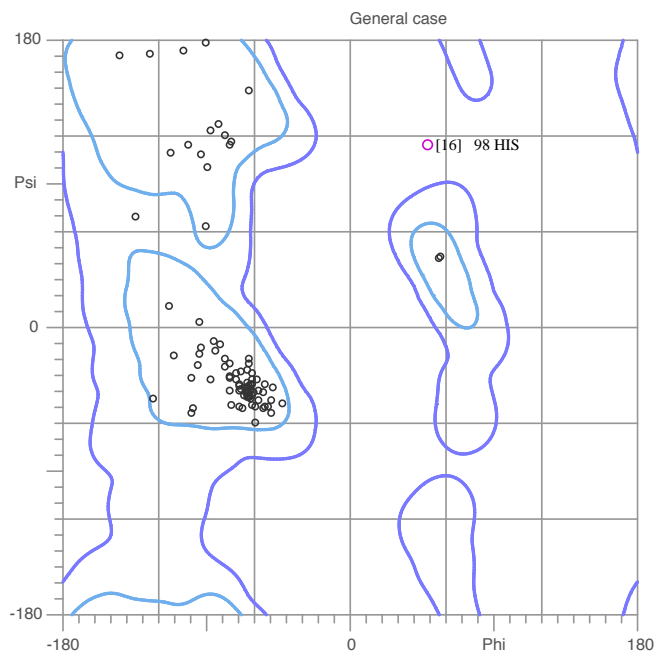
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 16



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.

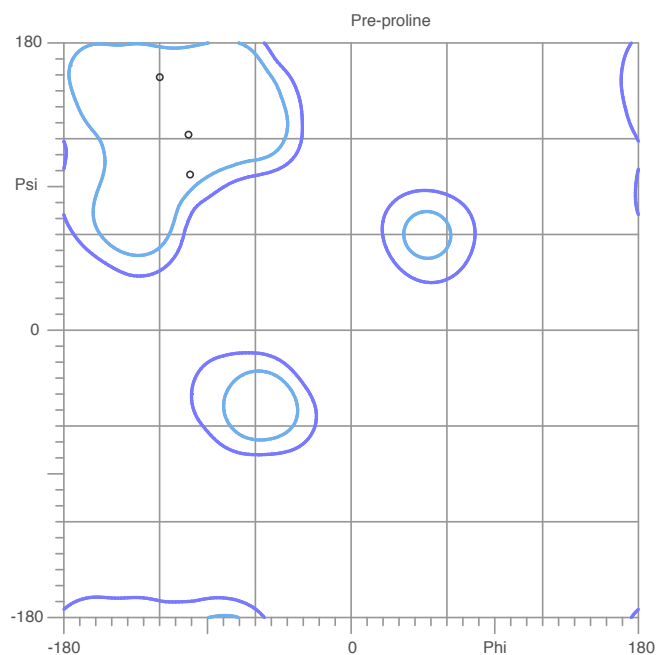
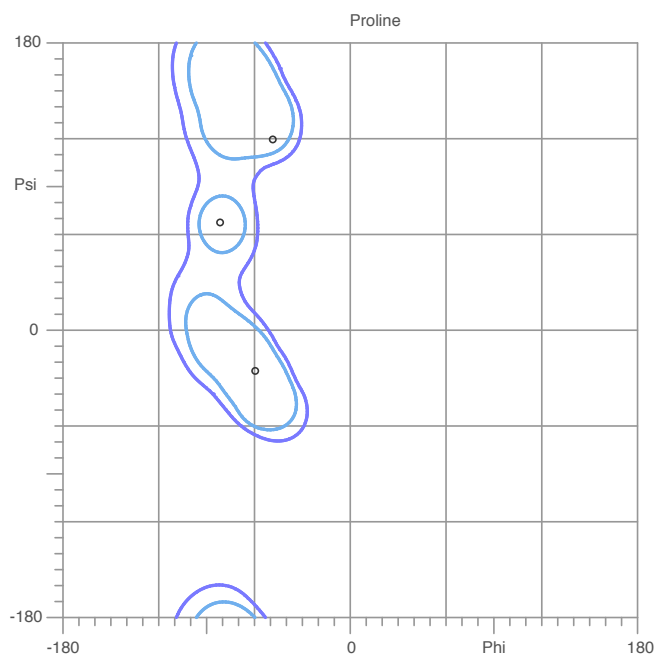
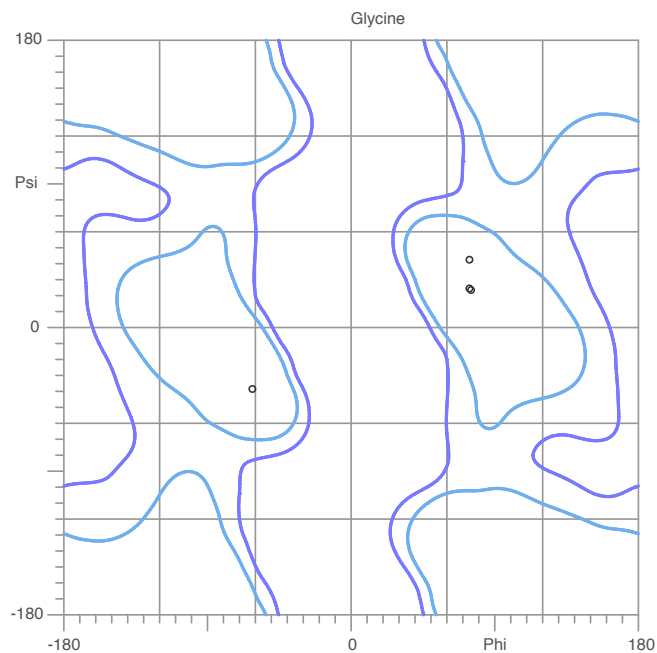
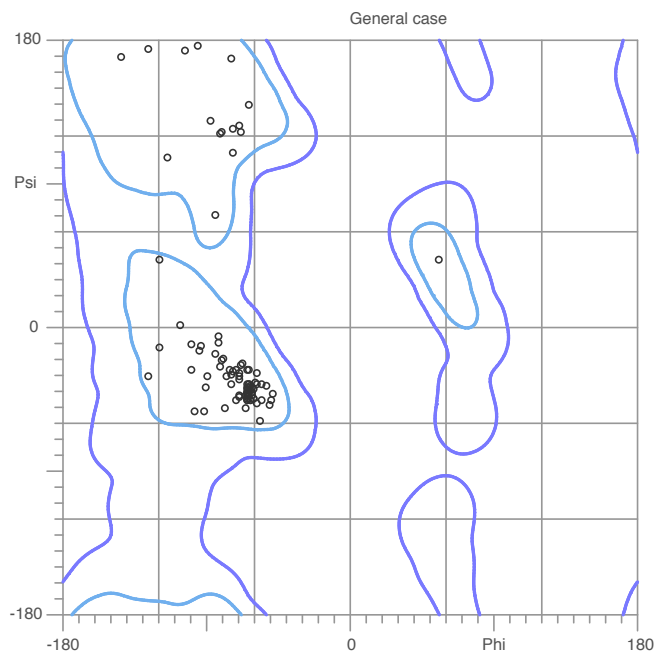
There were 1 outliers (phi, psi):  
[16] 98 HIS (48.5, 115.0)

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 17



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.

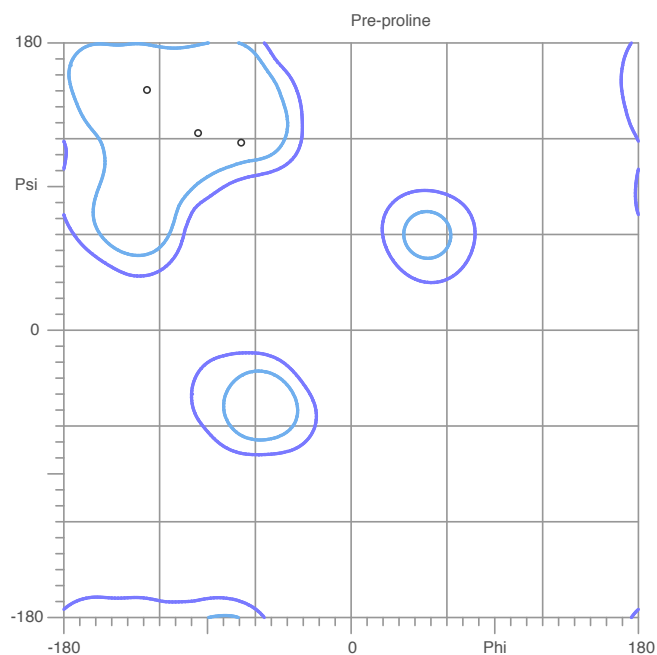
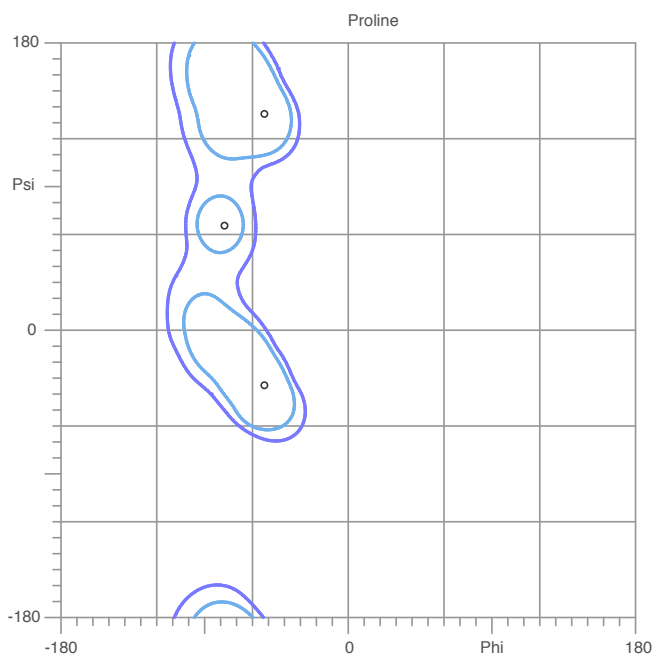
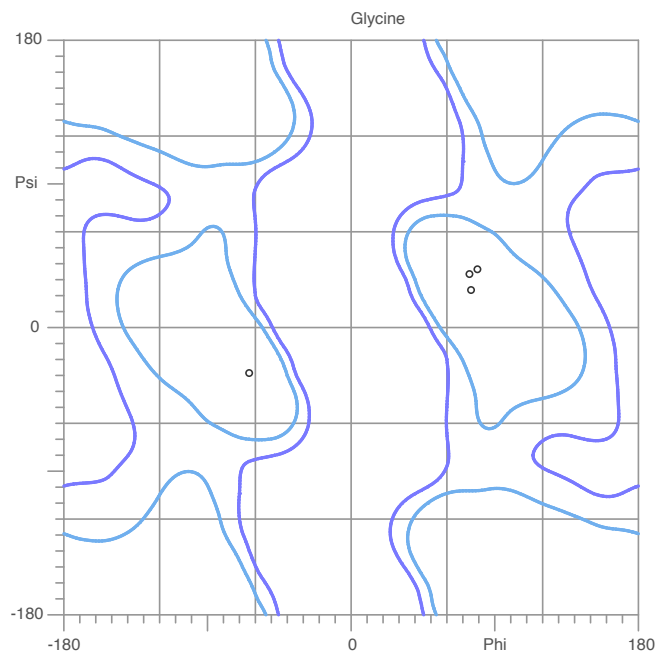
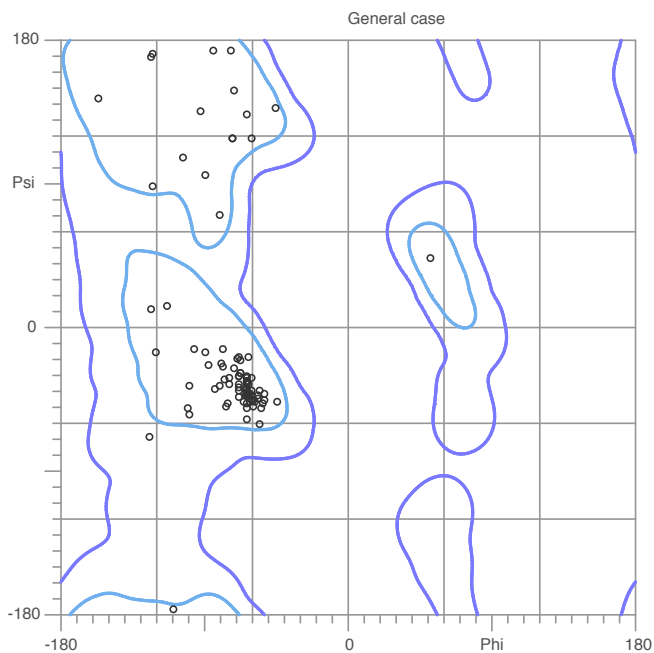
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_em\_bcr3.pdb, model 18



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.

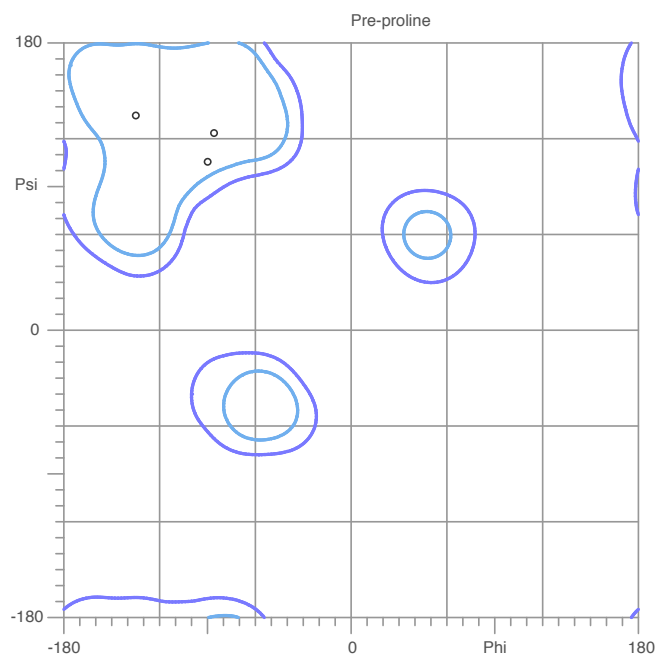
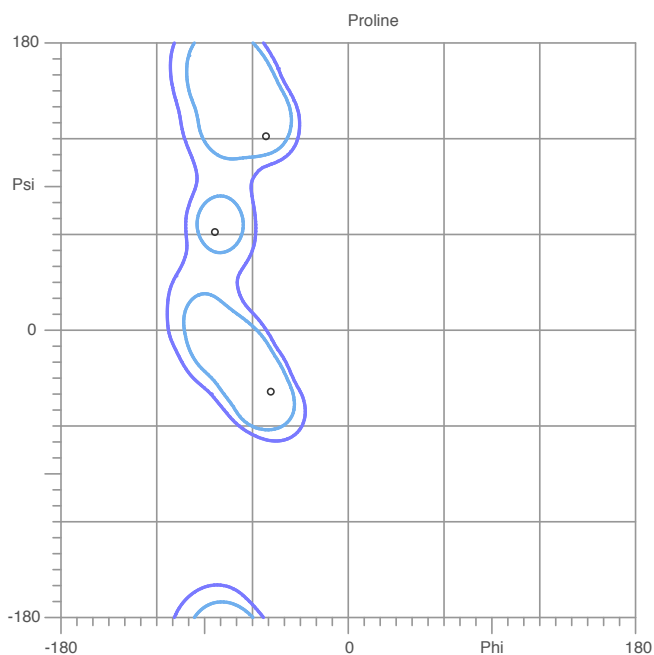
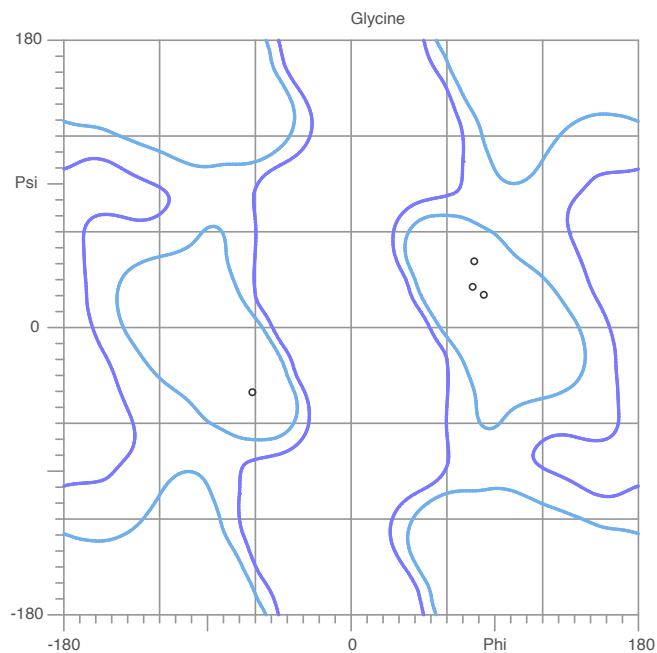
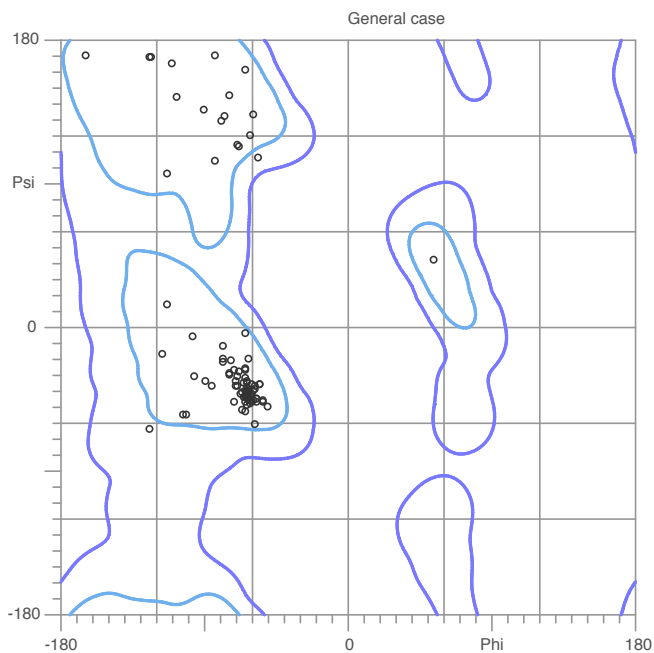
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_R3\_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.

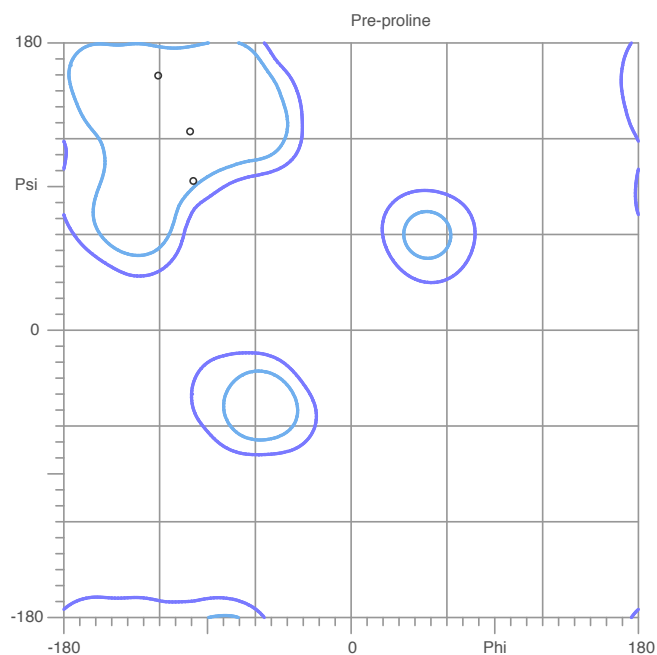
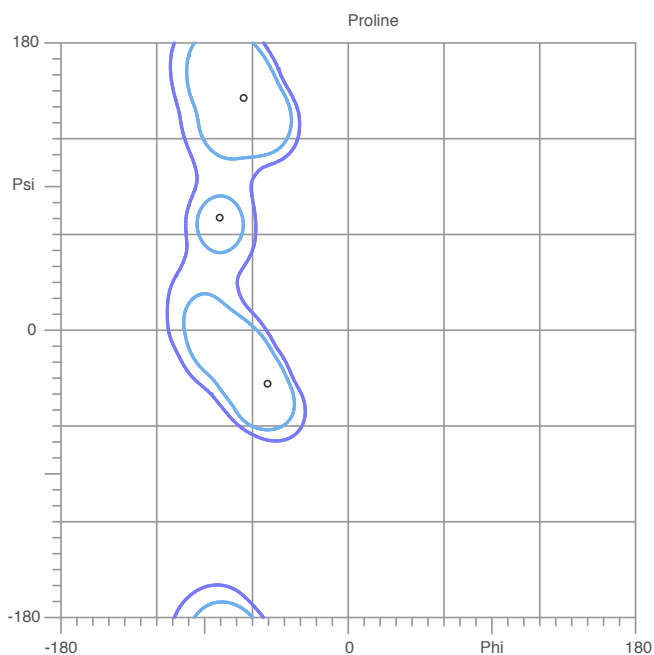
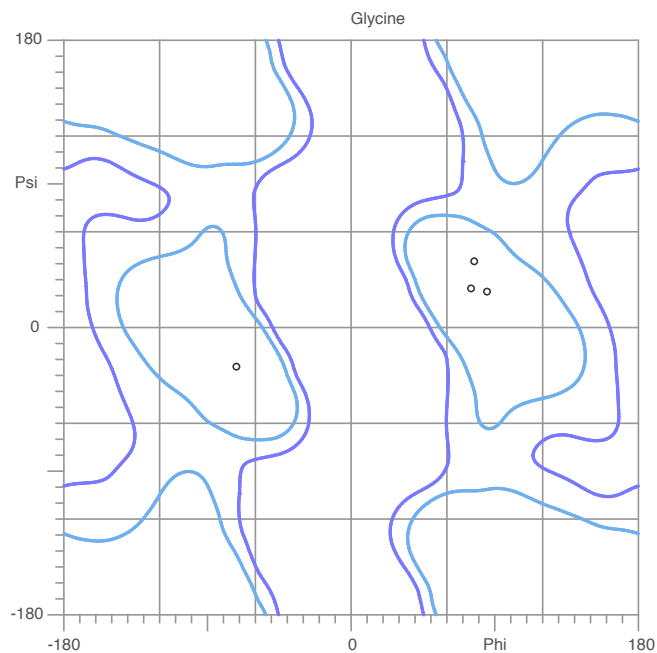
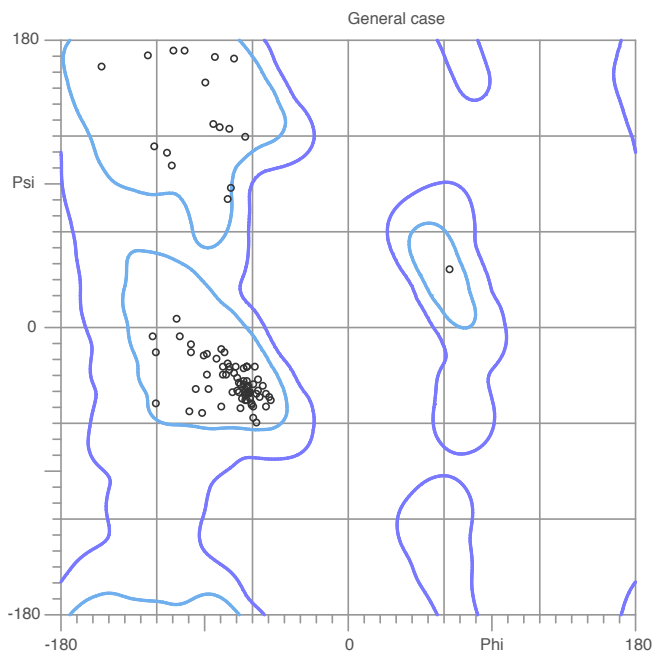
There were no outliers.

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

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# MolProbity Ramachandran analysis

RPR324\_R3\_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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