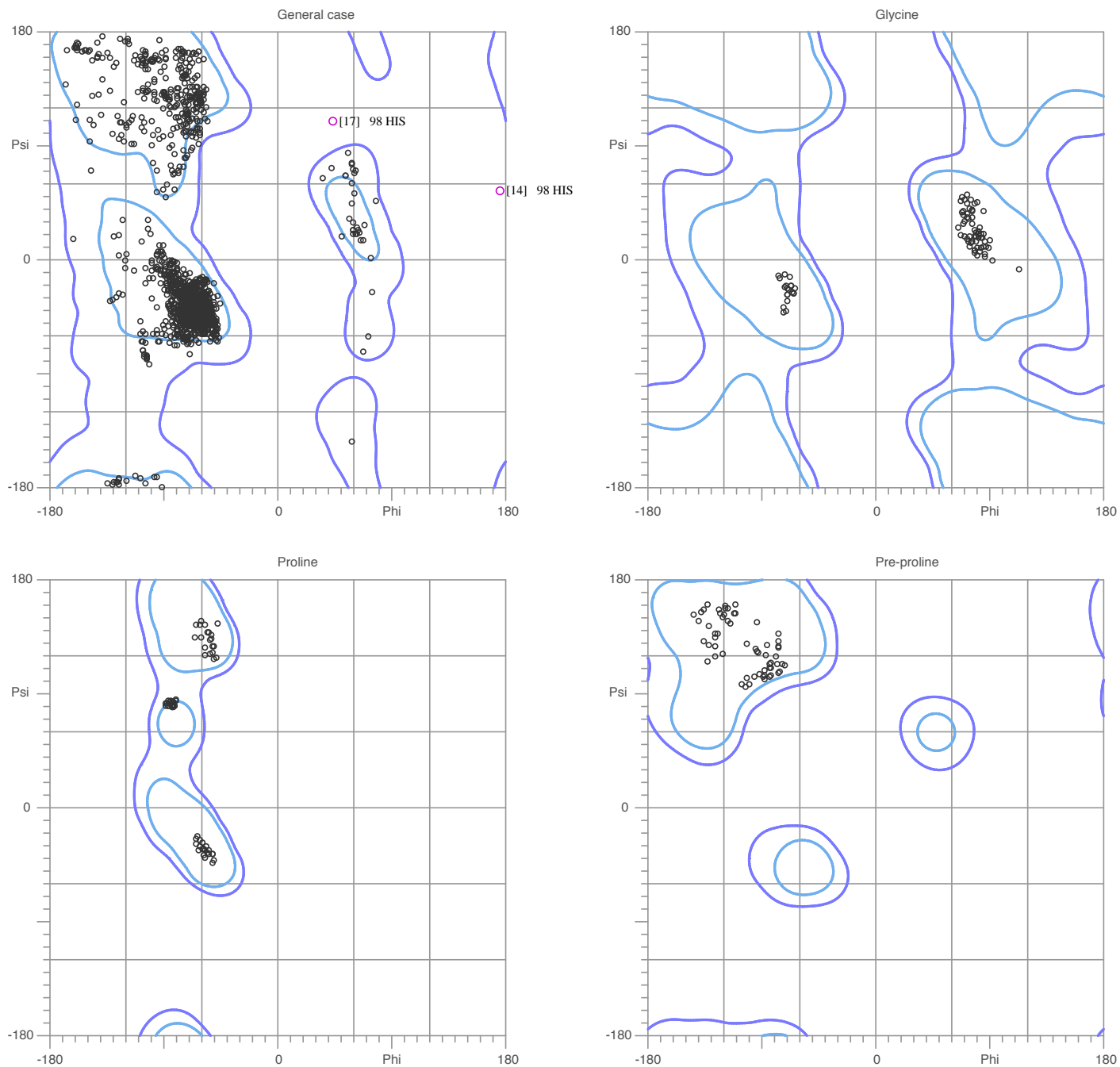


# MolProbity Ramachandran analysis

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



95.8% (1897/1980) of all residues were in favored (98%) regions.  
99.9% (1978/1980) of all residues were in allowed (>99.8%) regions.

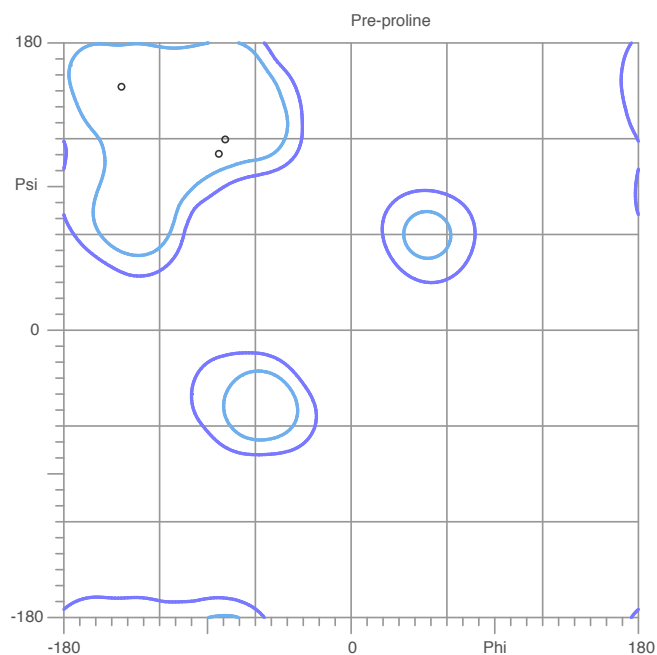
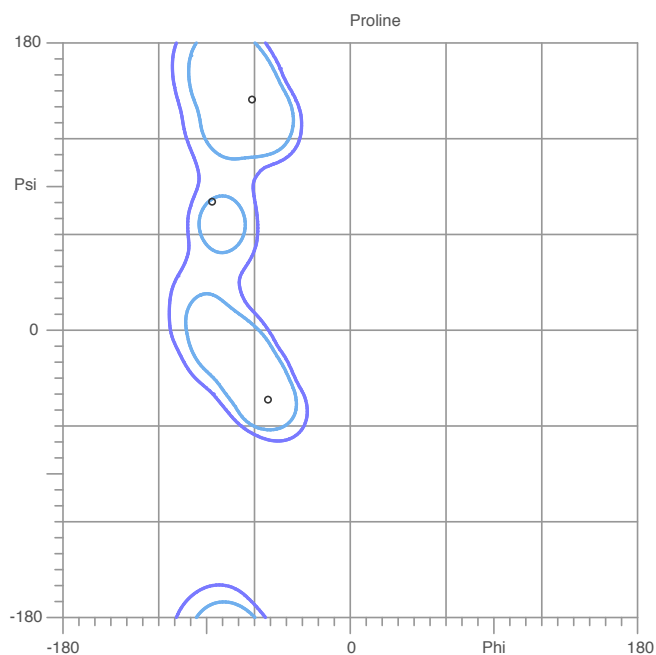
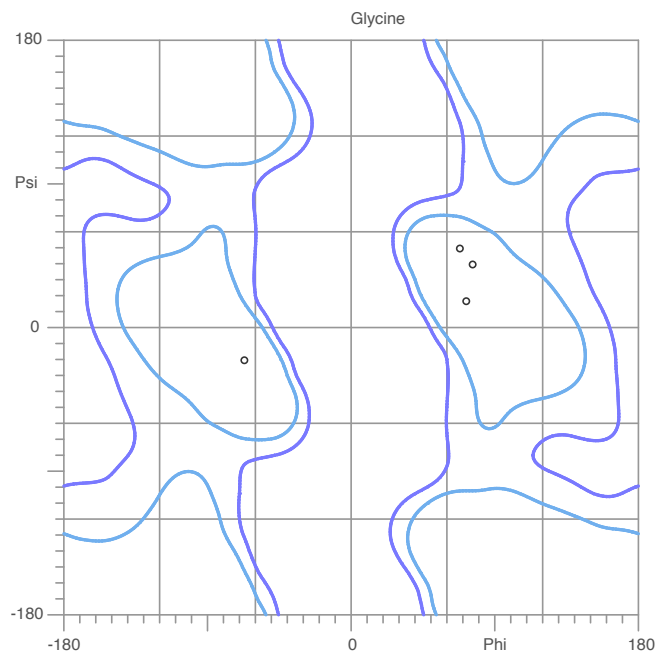
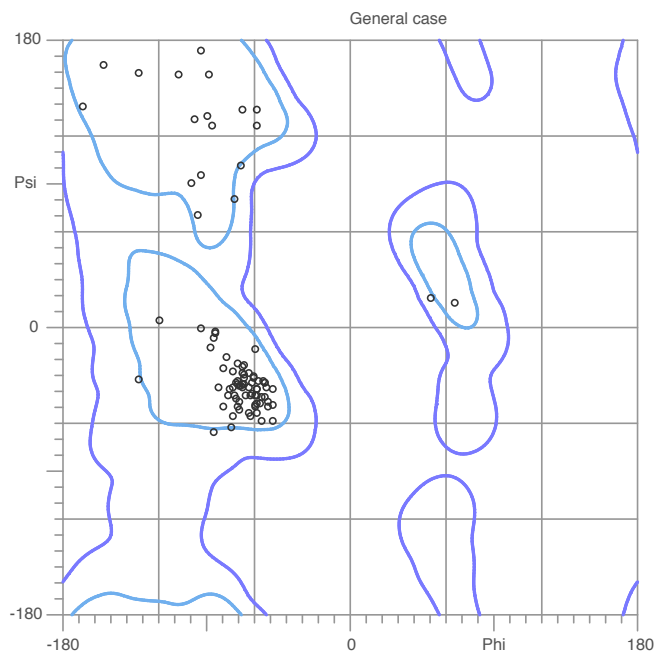
There were 2 outliers (phi, psi):

[14] 98 HIS (175.4, 55.6)

[17] 98 HIS (43.6, 110.0)

# MolProbity Ramachandran analysis

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



94.9% (94/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

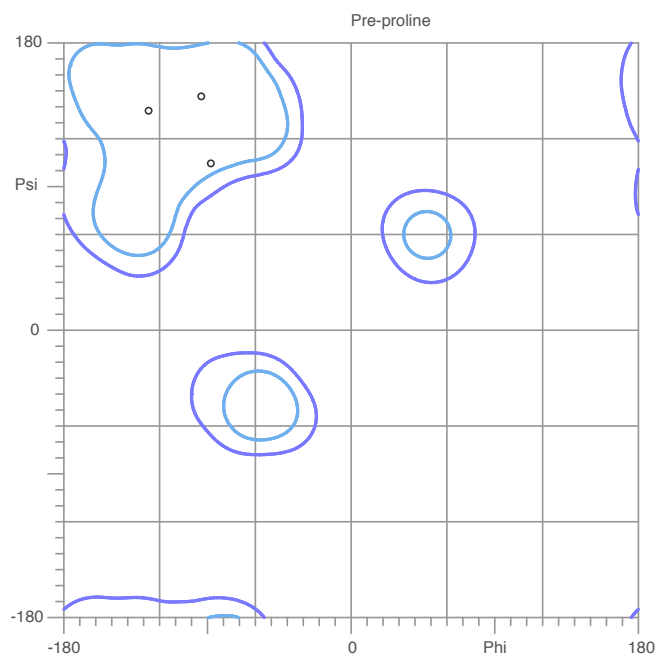
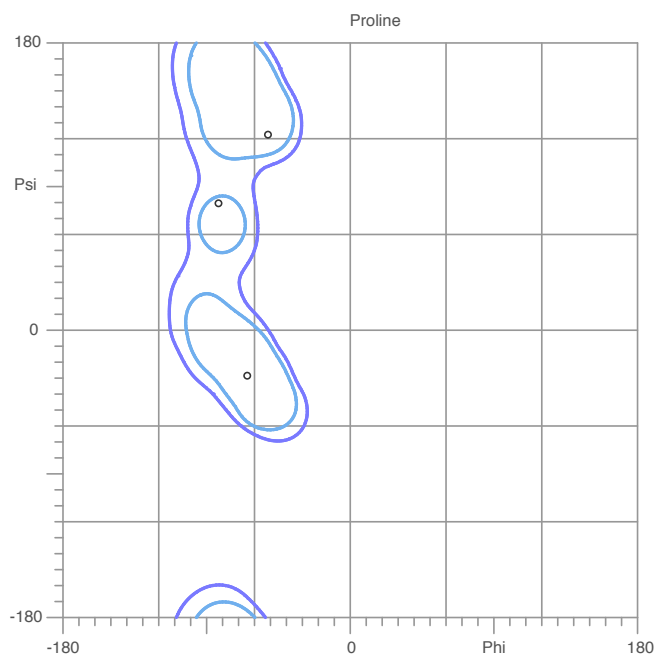
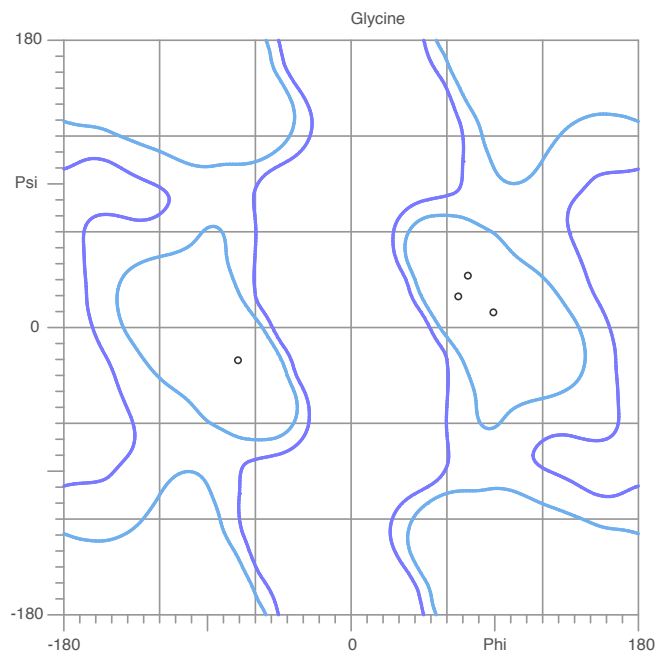
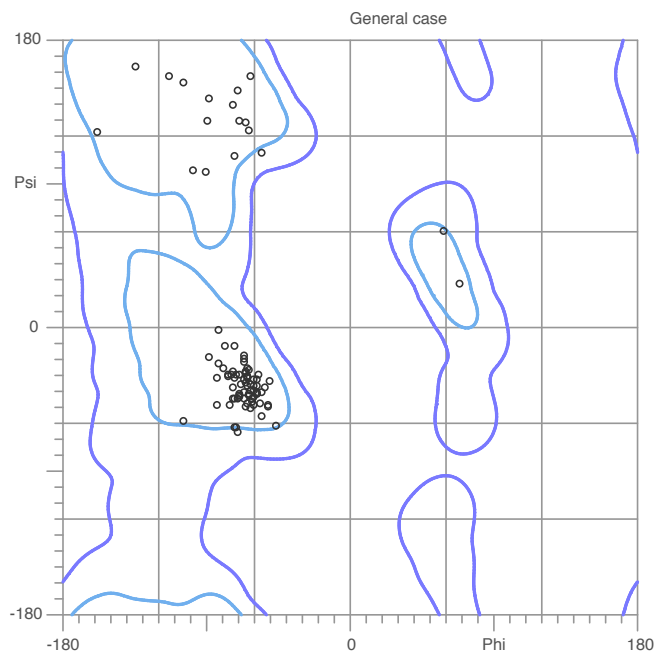
There were no outliers.

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

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

# MolProbity Ramachandran analysis

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



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.

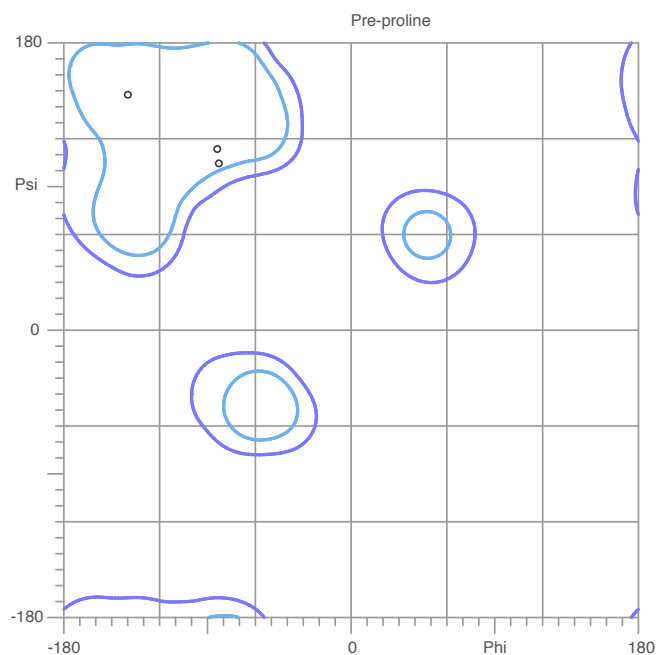
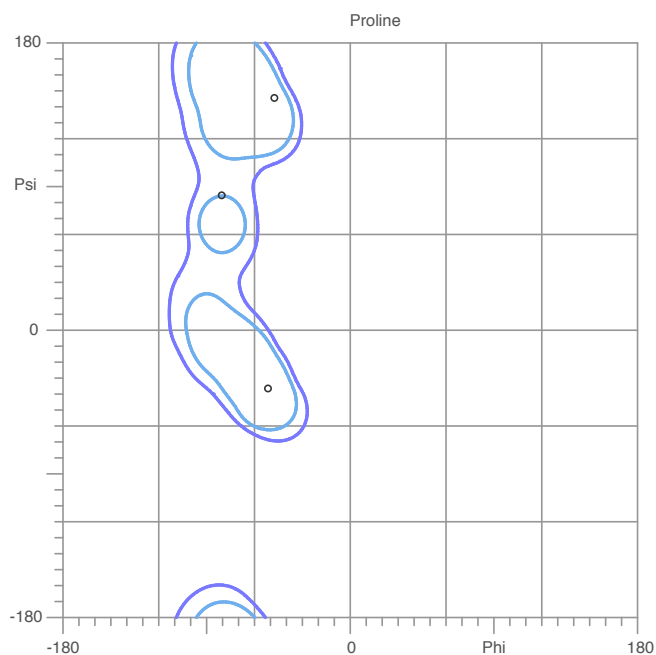
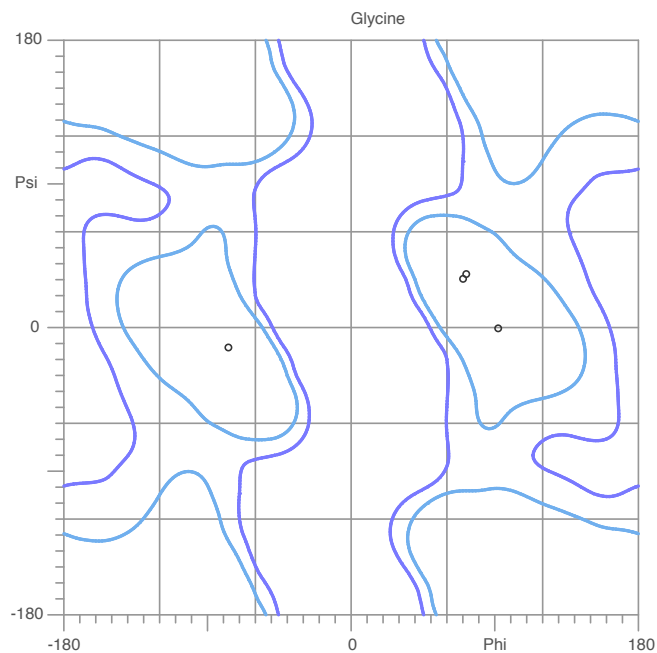
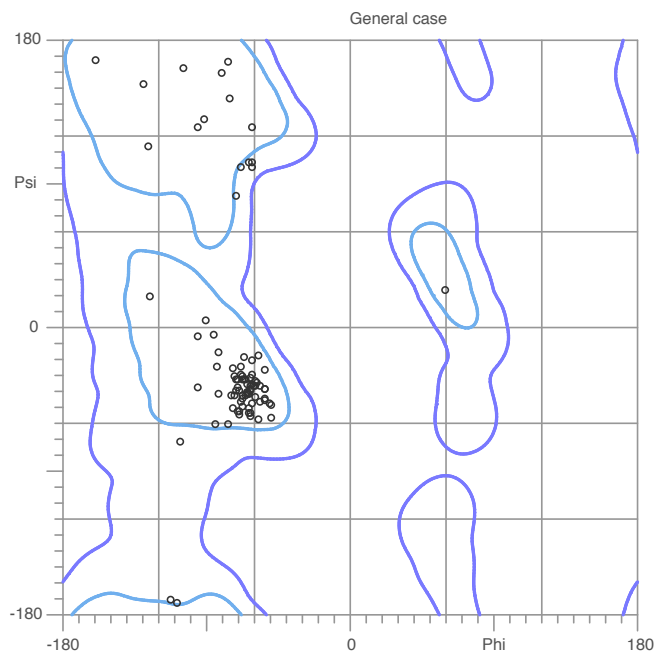
There were no outliers.

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

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

# MolProbity Ramachandran analysis

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



91.9% (91/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

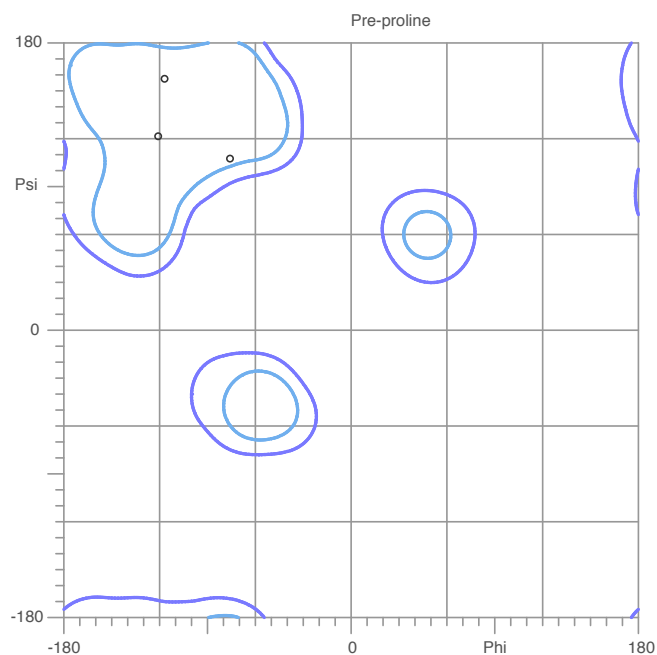
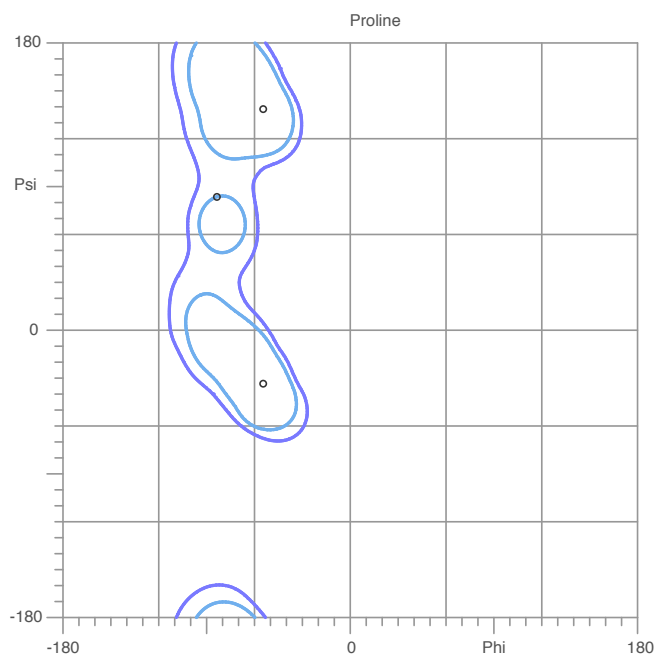
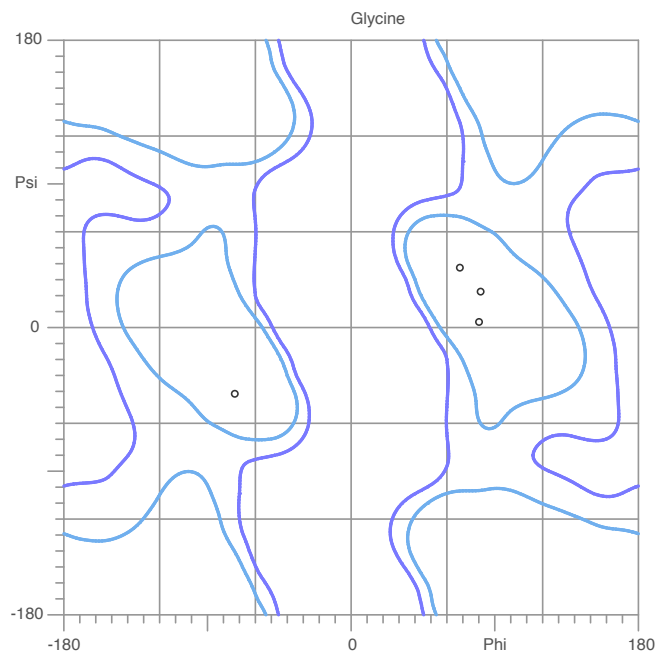
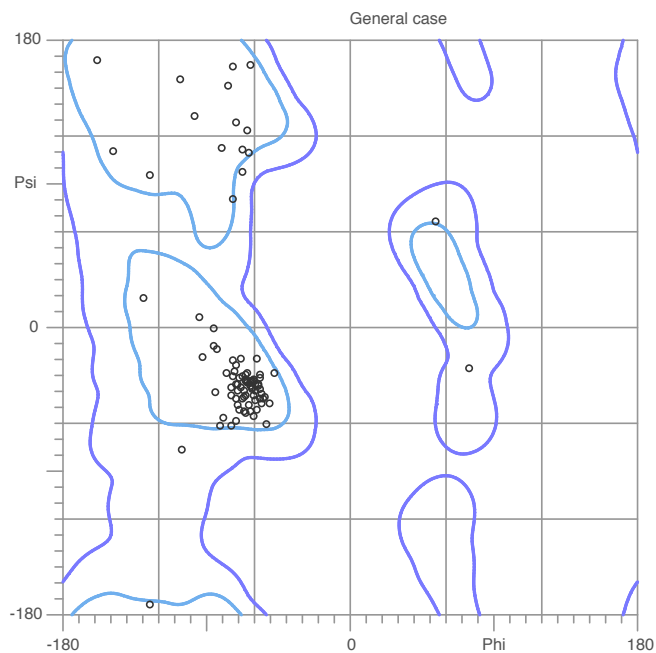
There were no outliers.

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

# MolProbity Ramachandran analysis

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



94.9% (94/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

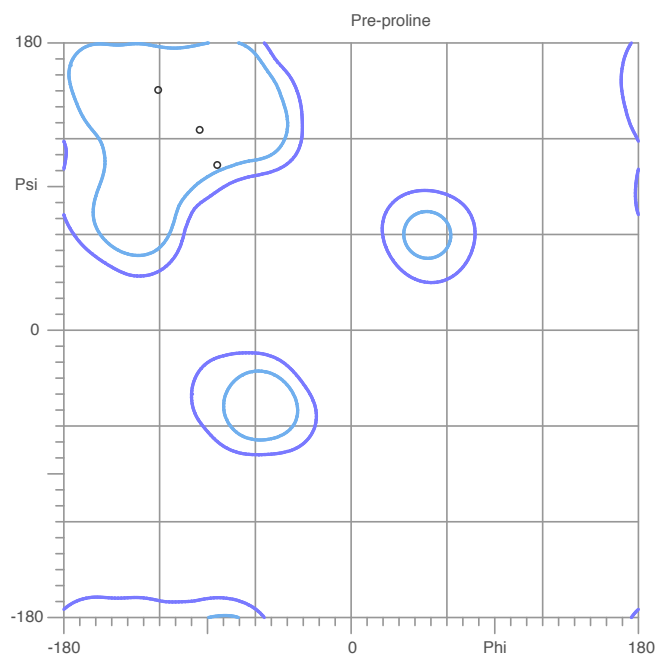
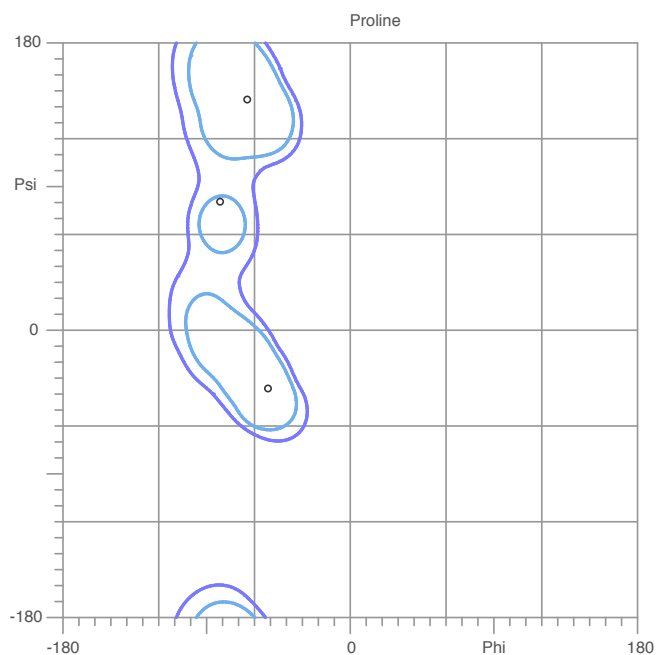
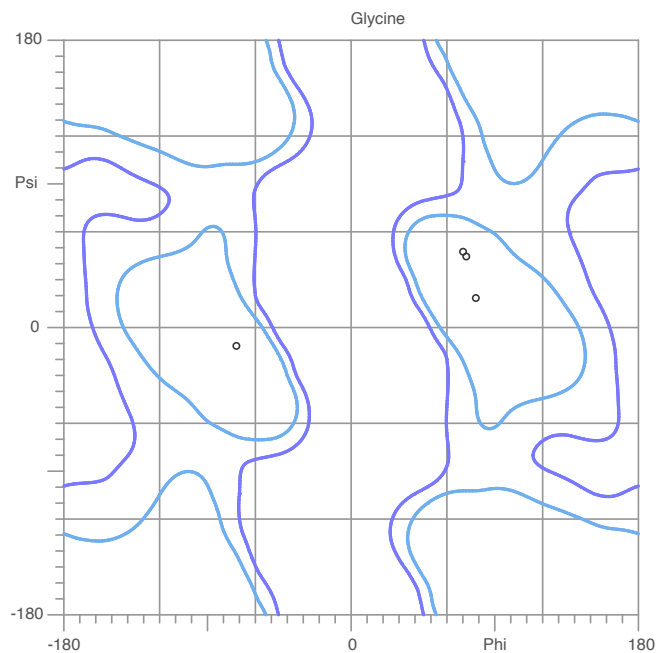
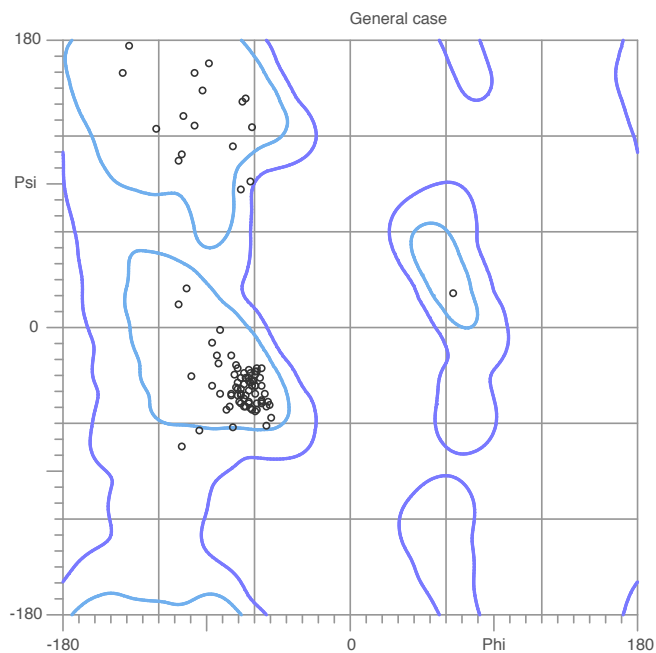
There were no outliers.

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

# MolProbity Ramachandran analysis

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



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.

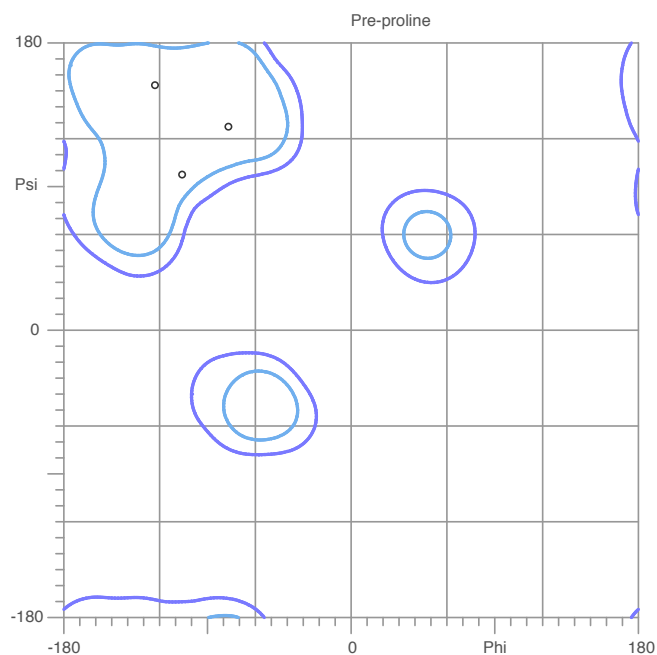
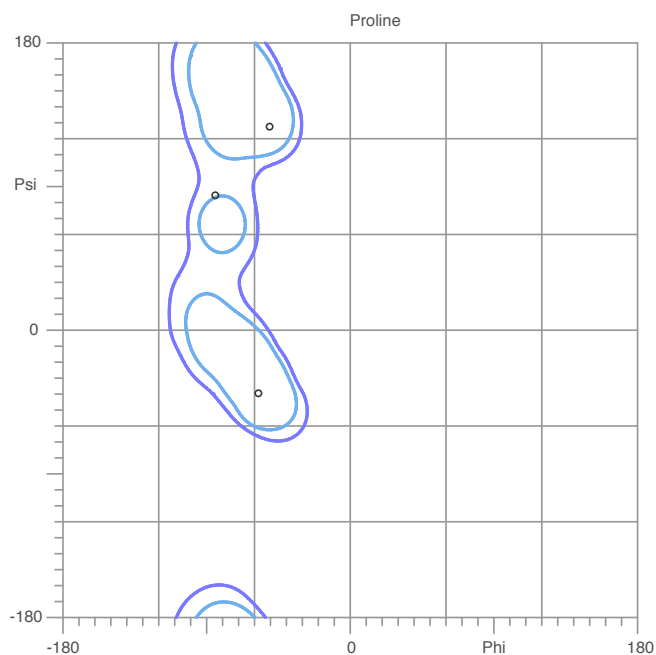
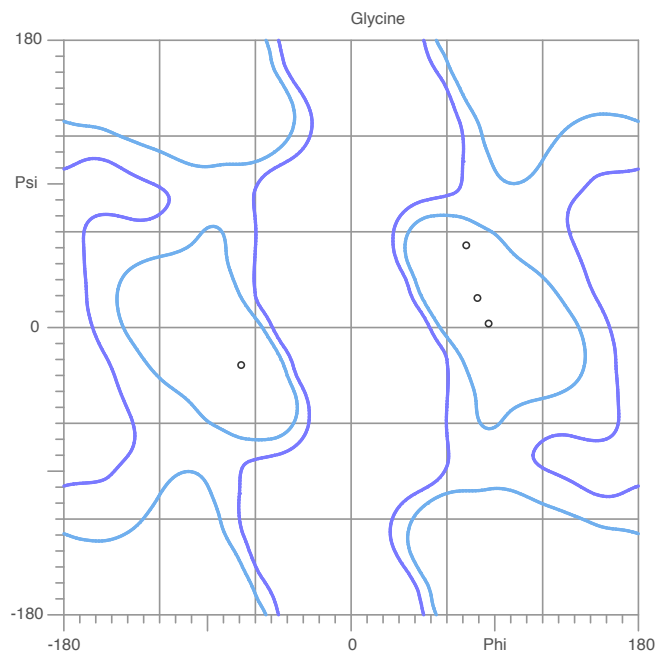
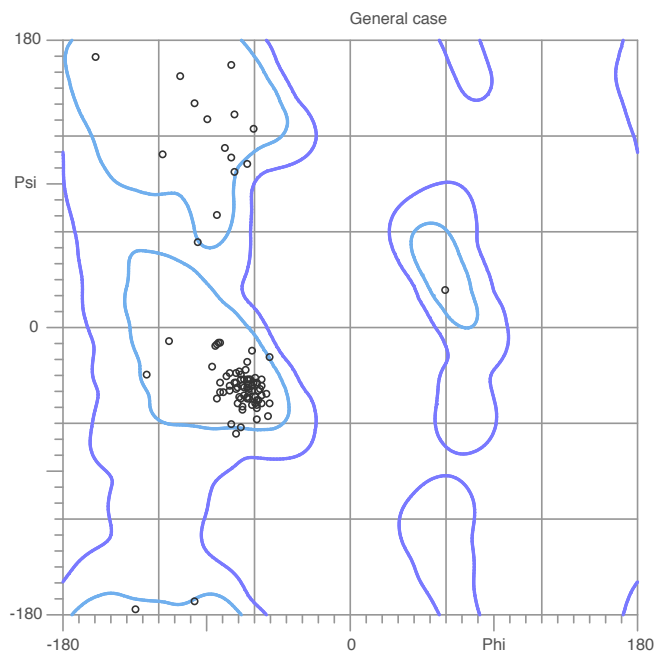
There were no outliers.

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

# MolProbity Ramachandran analysis

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



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.

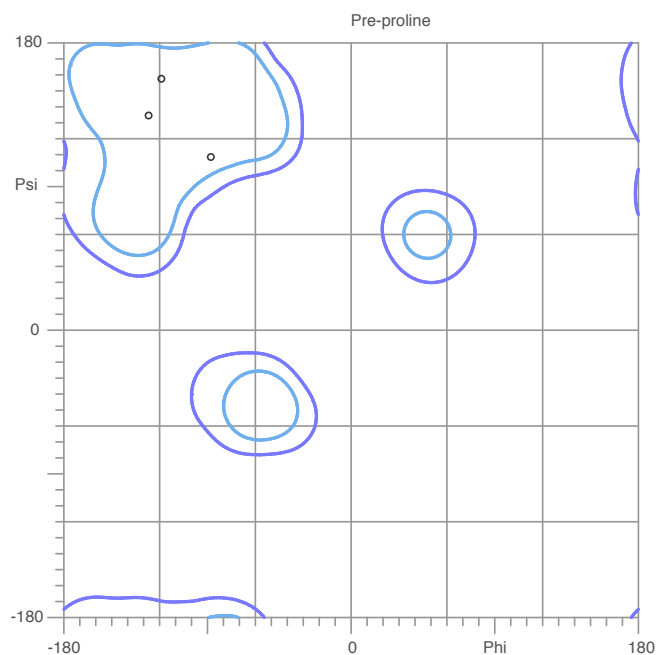
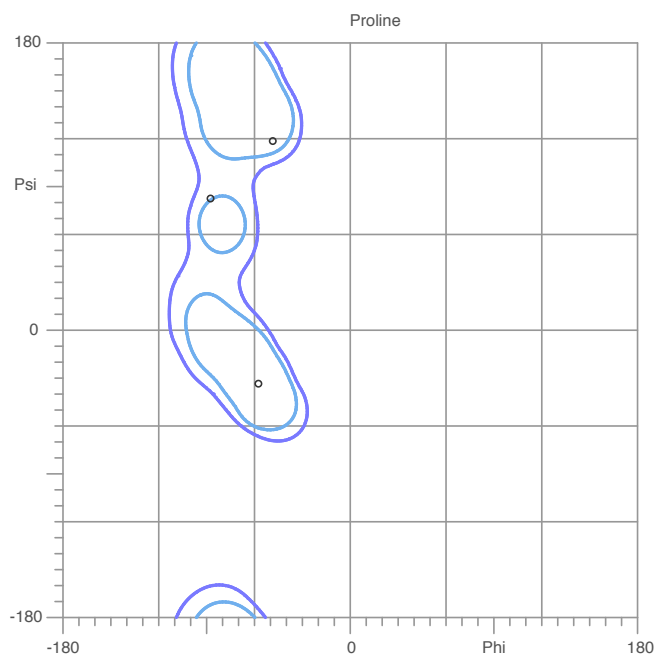
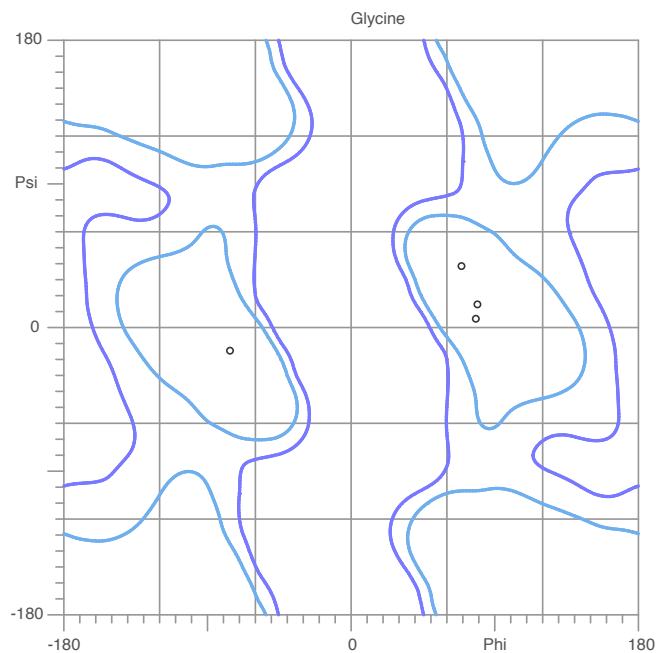
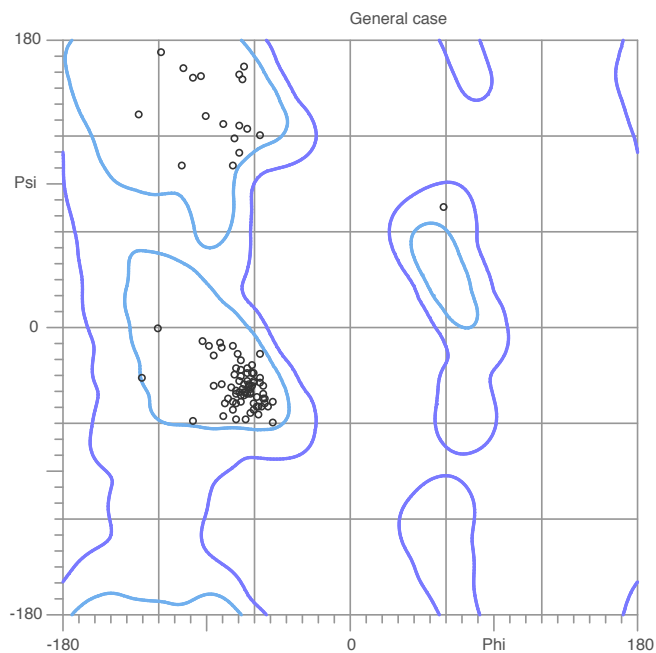
There were no outliers.

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

# MolProbity Ramachandran analysis

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

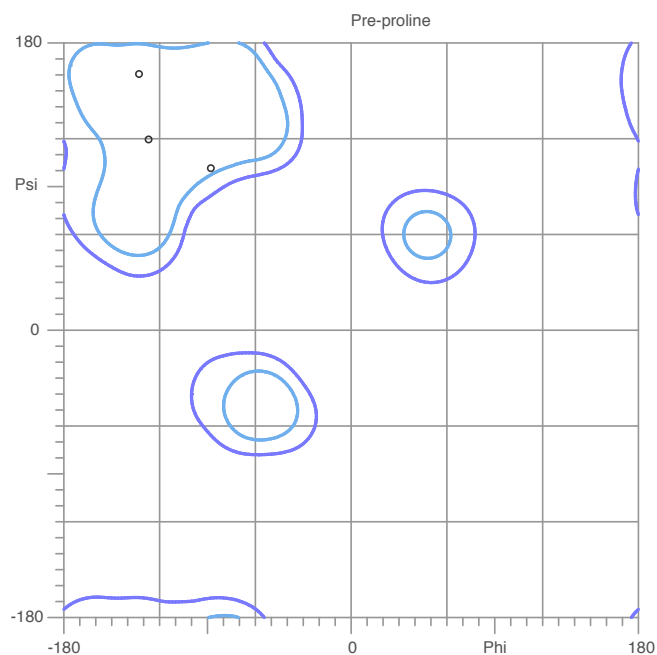
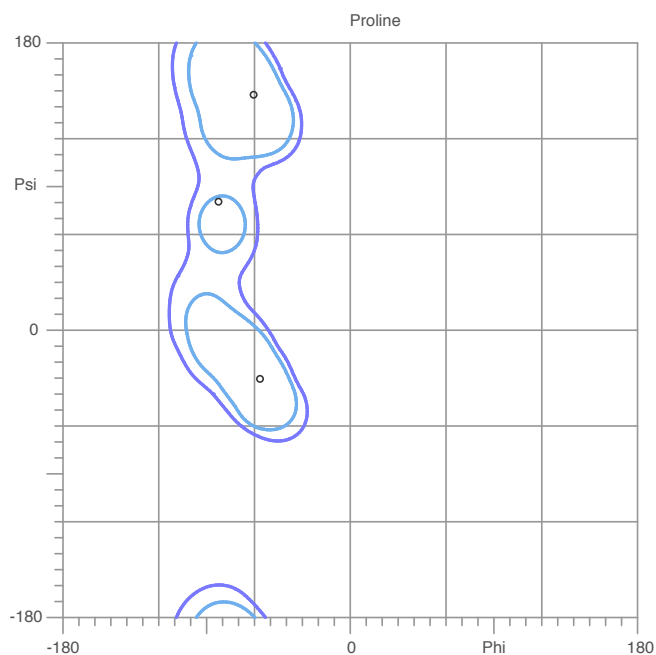
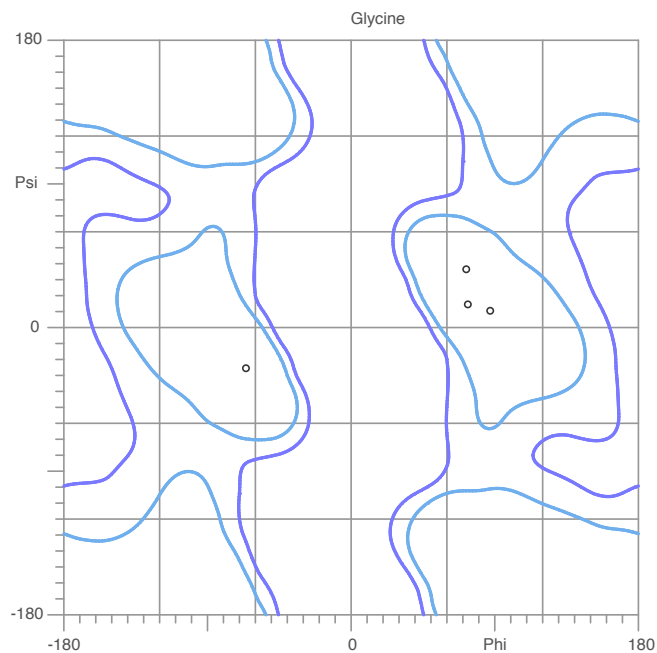
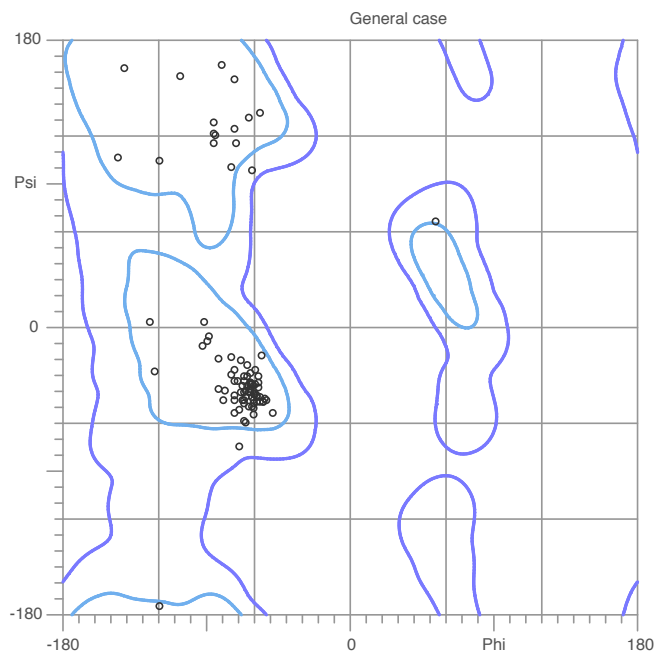


97.0% (96/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

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



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.

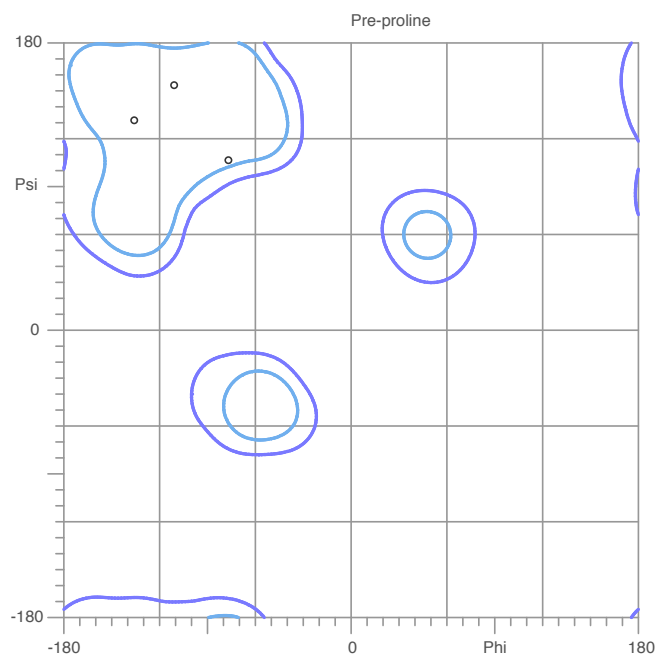
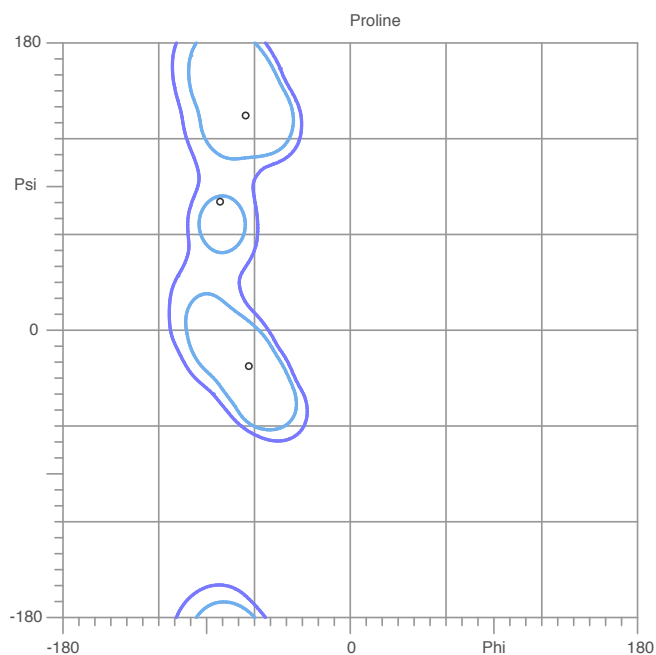
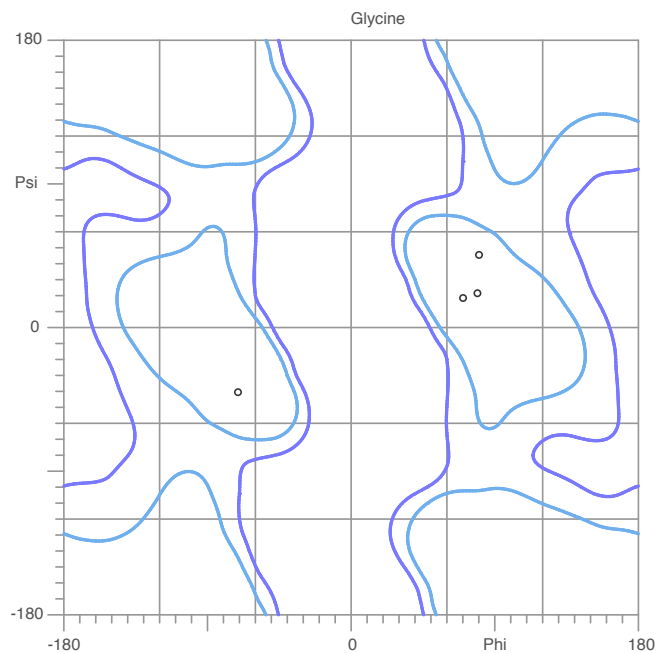
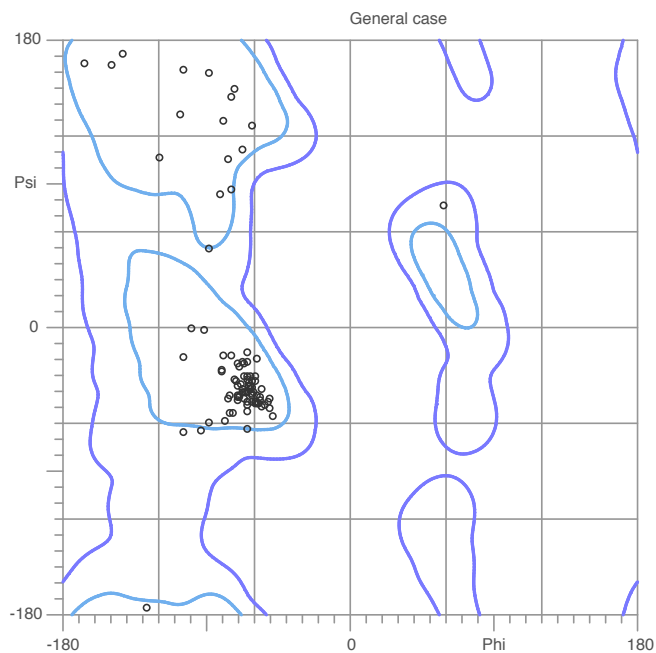
There were no outliers.

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

# MolProbity Ramachandran analysis

RPR324\_NMR\_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.

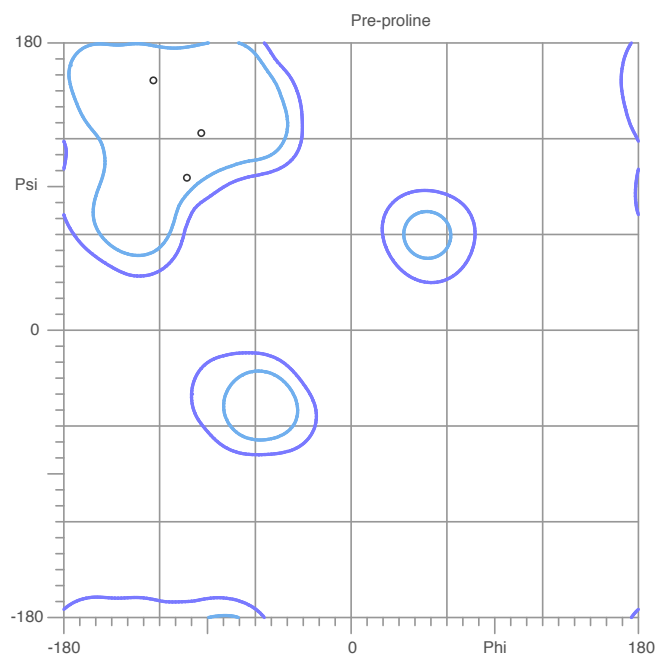
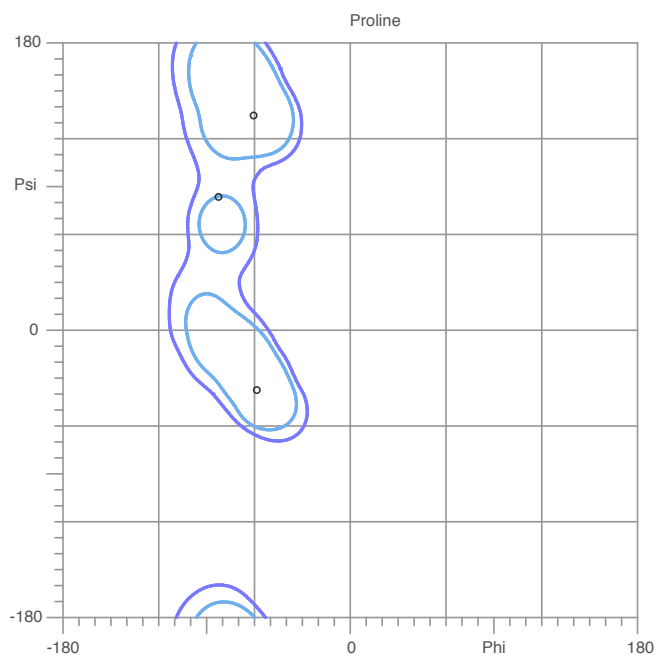
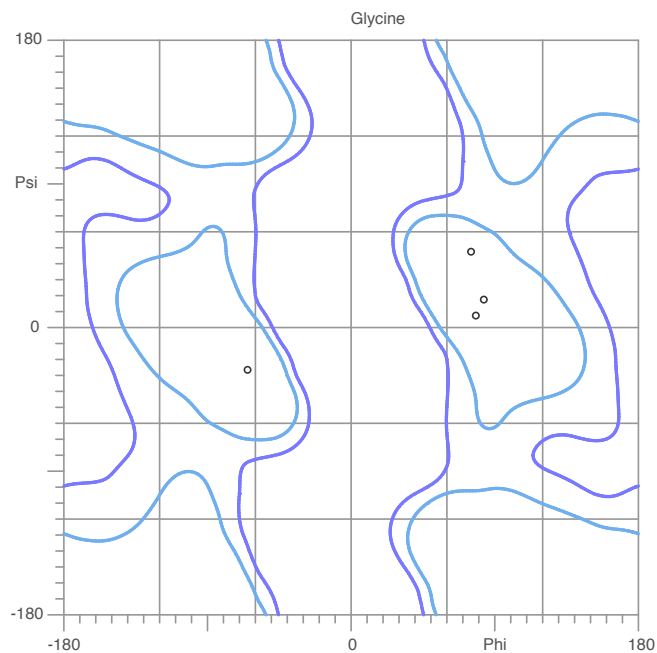
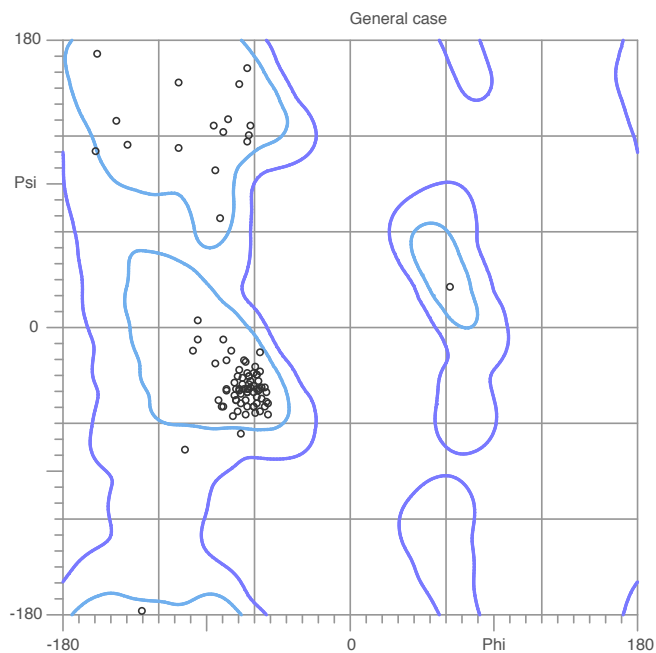
There were no outliers.

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

# MolProbity Ramachandran analysis

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



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.

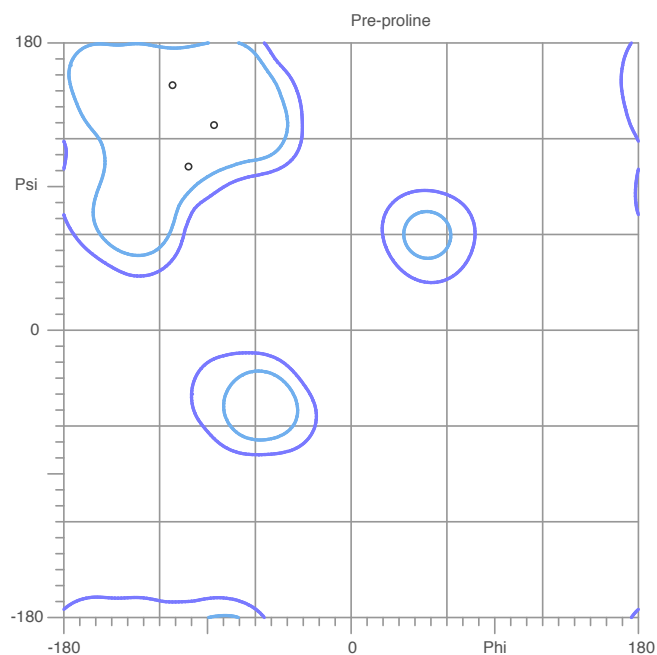
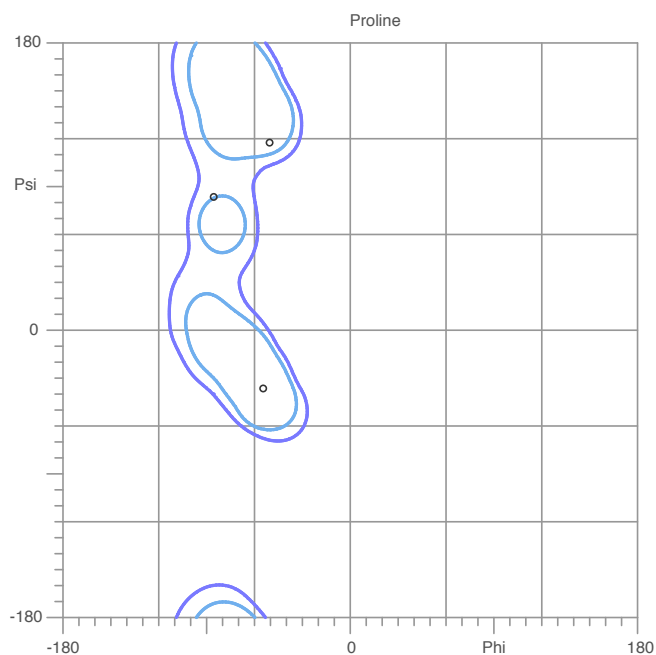
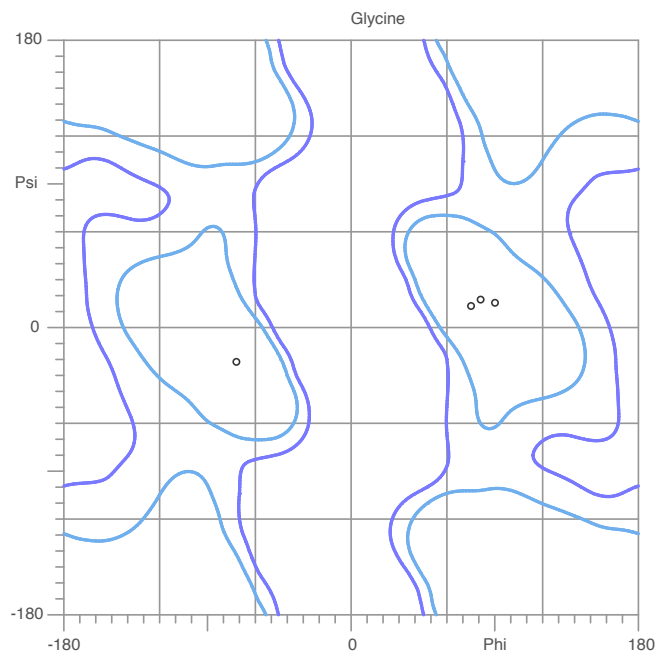
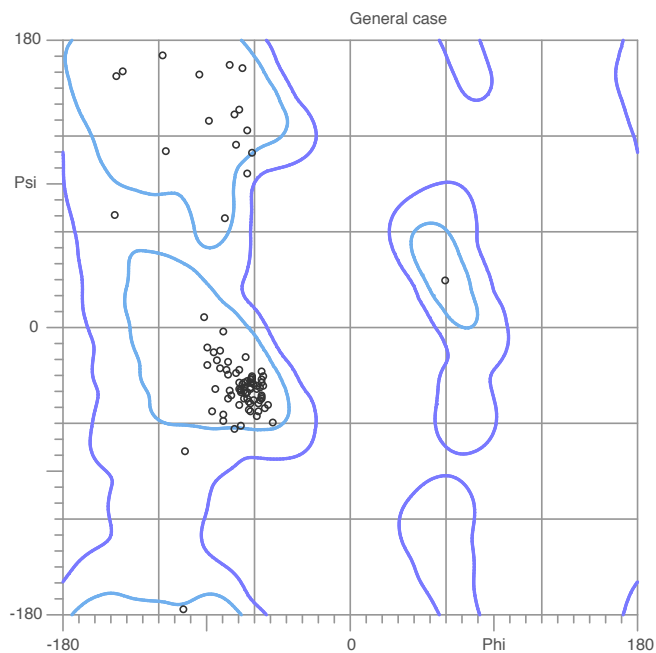
There were no outliers.

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

# MolProbity Ramachandran analysis

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



94.9% (94/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

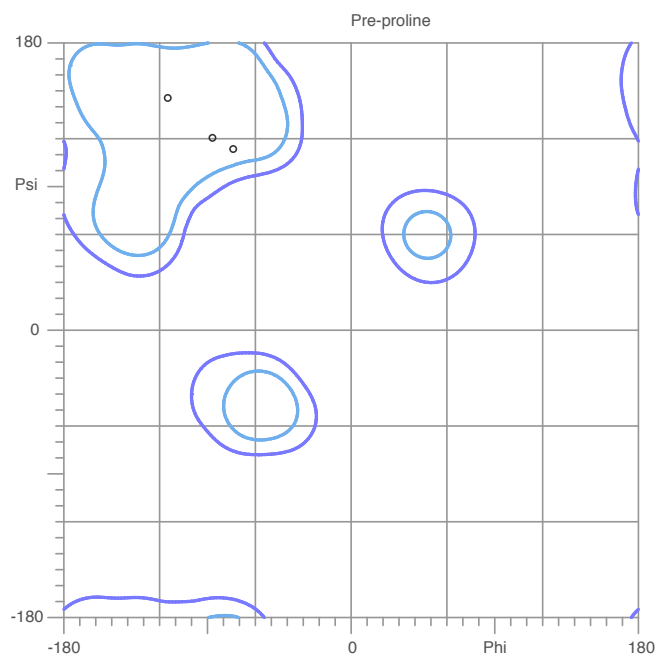
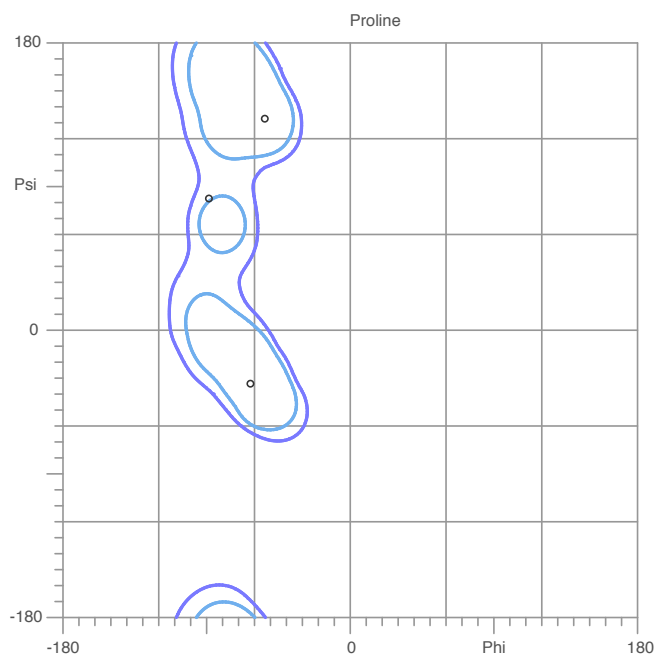
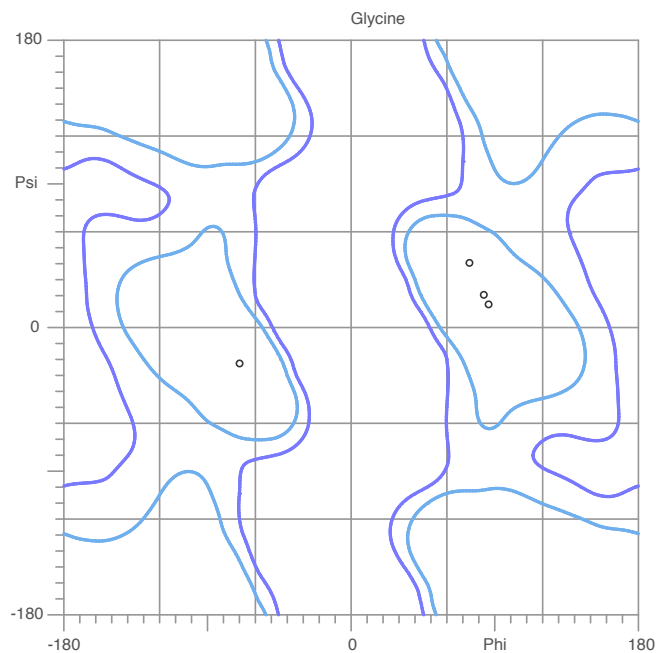
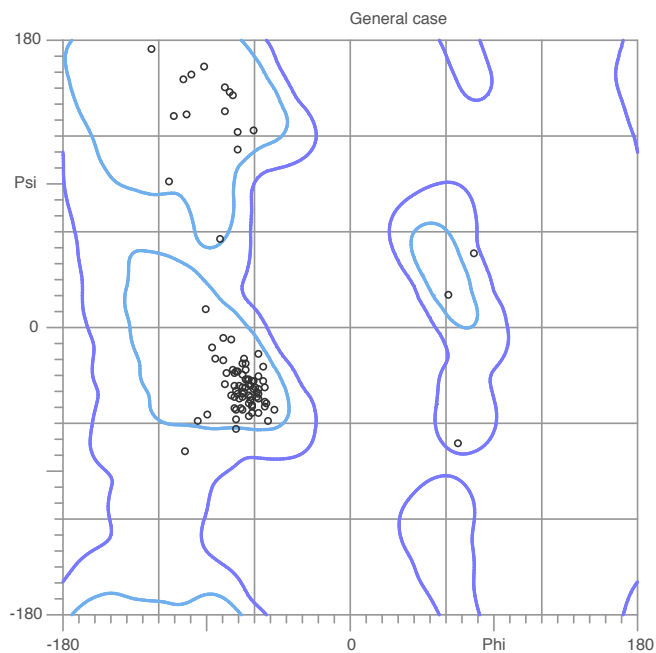
There were no outliers.

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# MolProbity Ramachandran analysis

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



94.9% (94/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

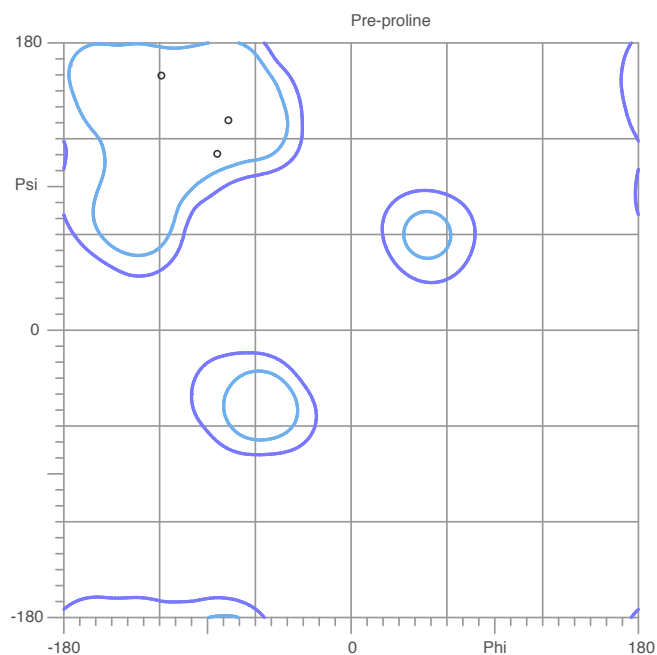
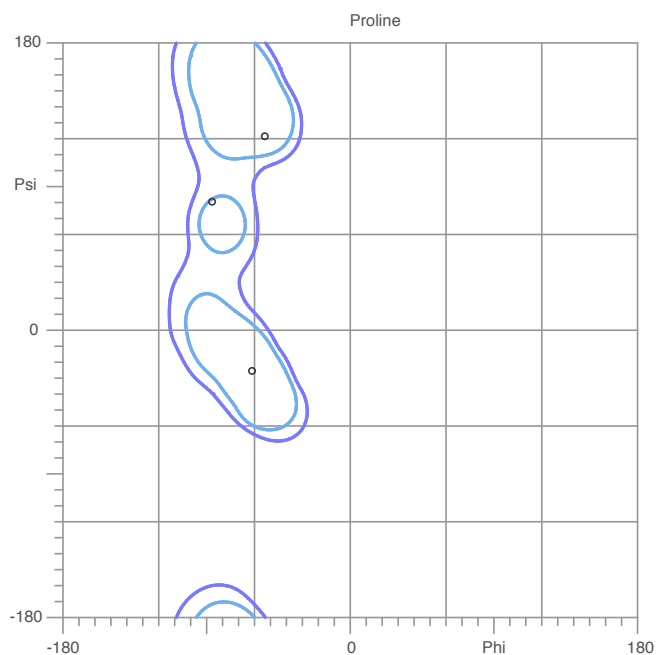
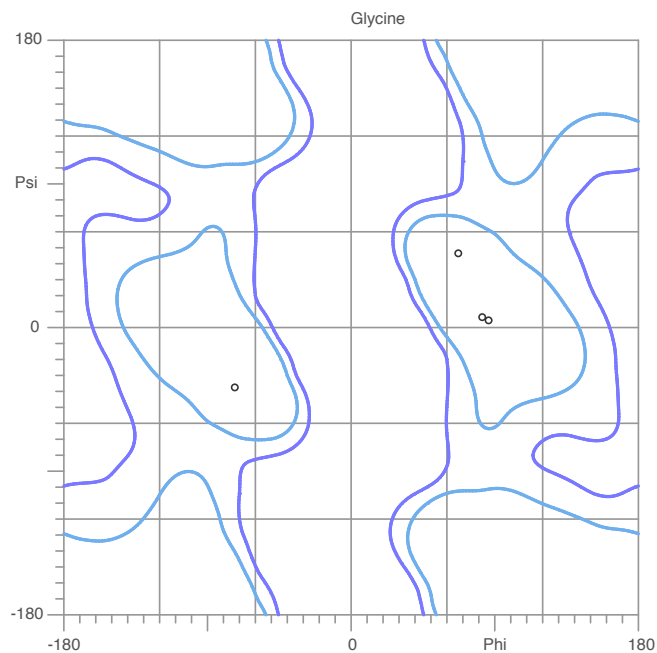
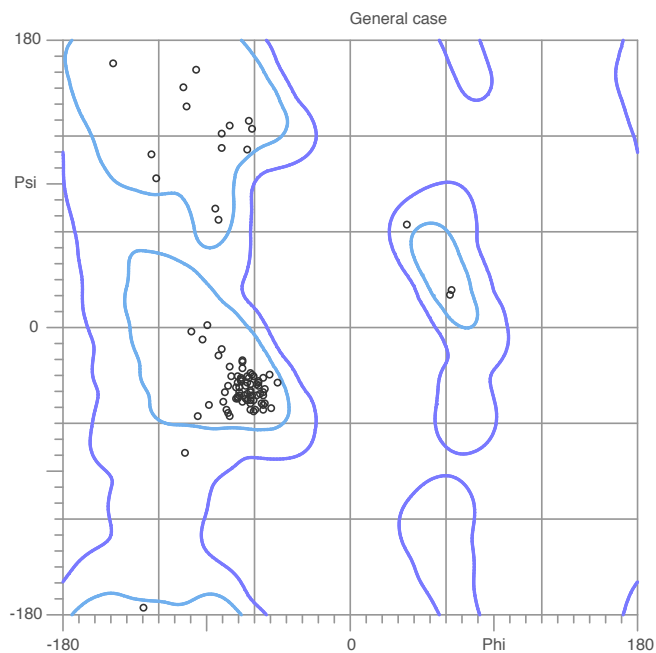
There were no outliers.

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# MolProbity Ramachandran analysis

RPR324\_NMR\_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.

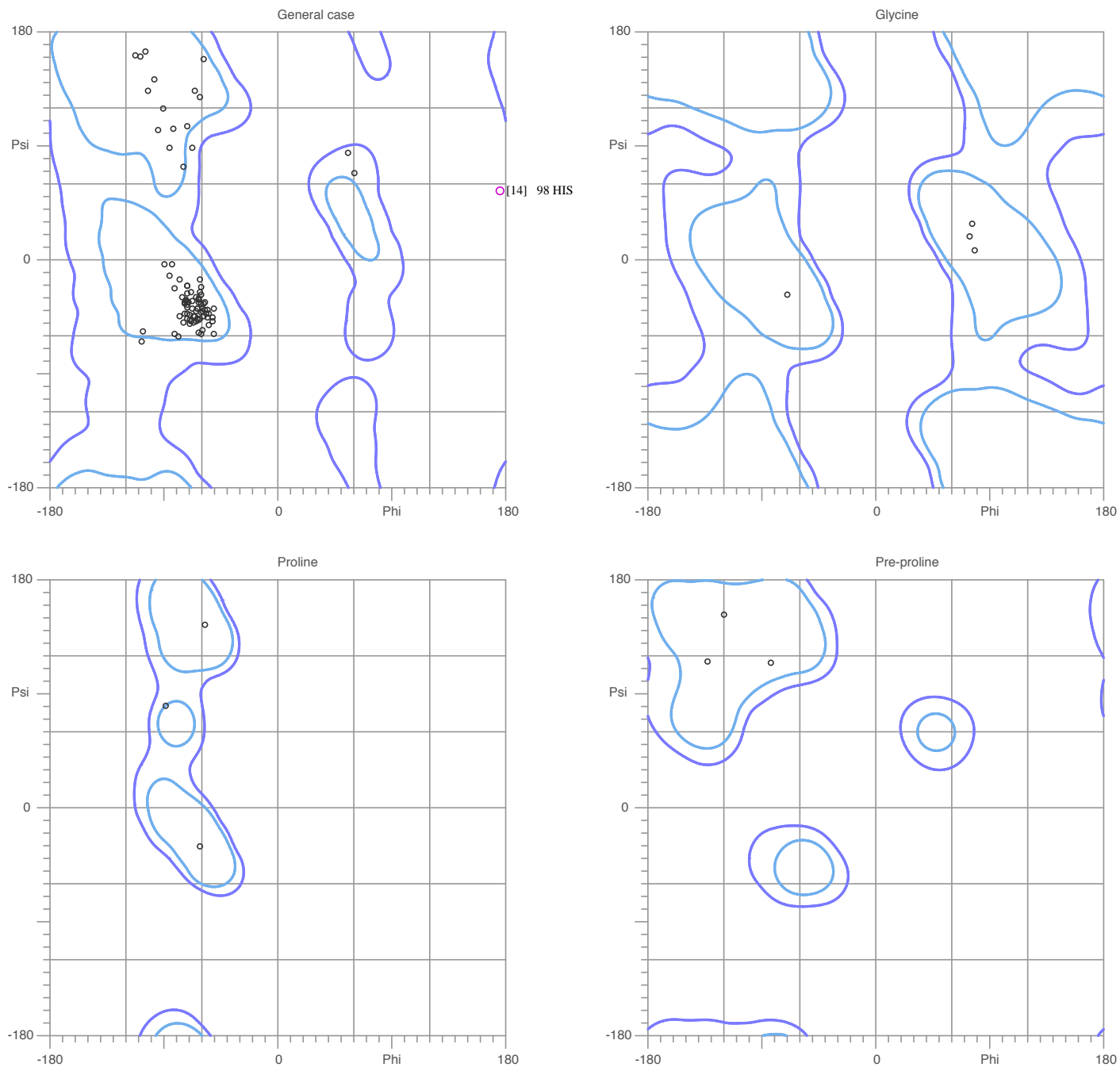
There were no outliers.

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# MolProbity Ramachandran analysis

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



93.9% (93/99) of all residues were in favored (98%) regions.  
99.0% (98/99) of all residues were in allowed (>99.8%) regions.

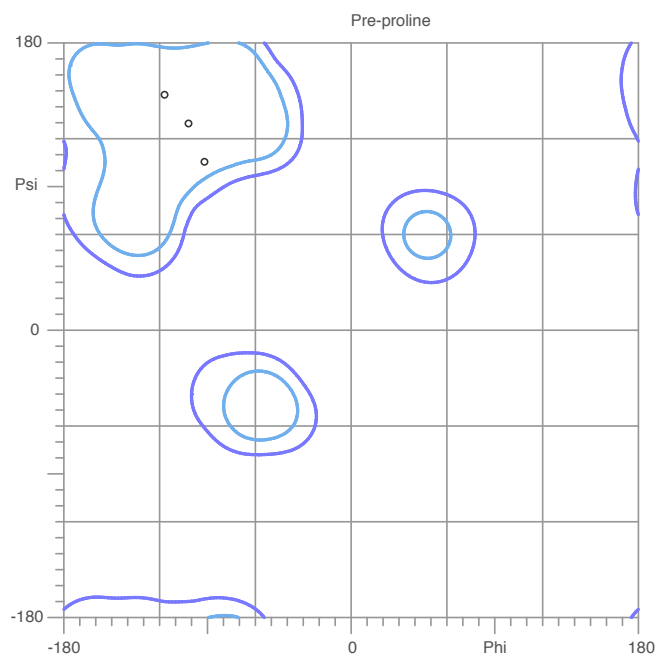
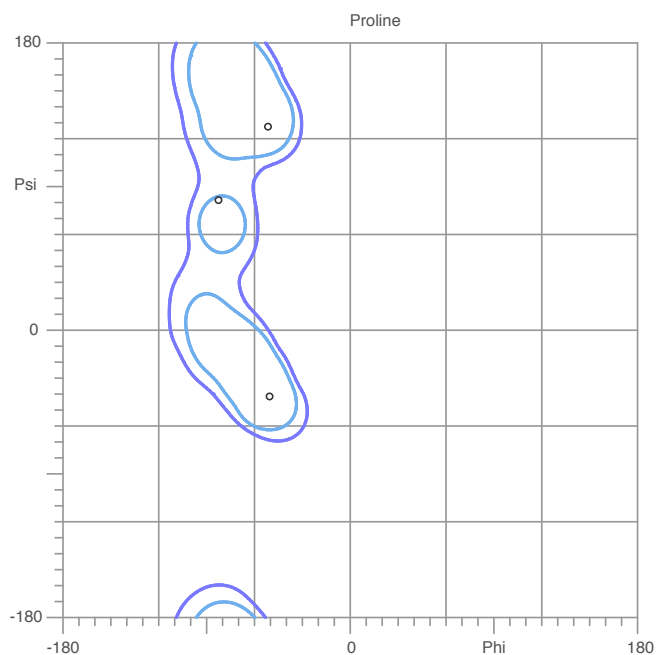
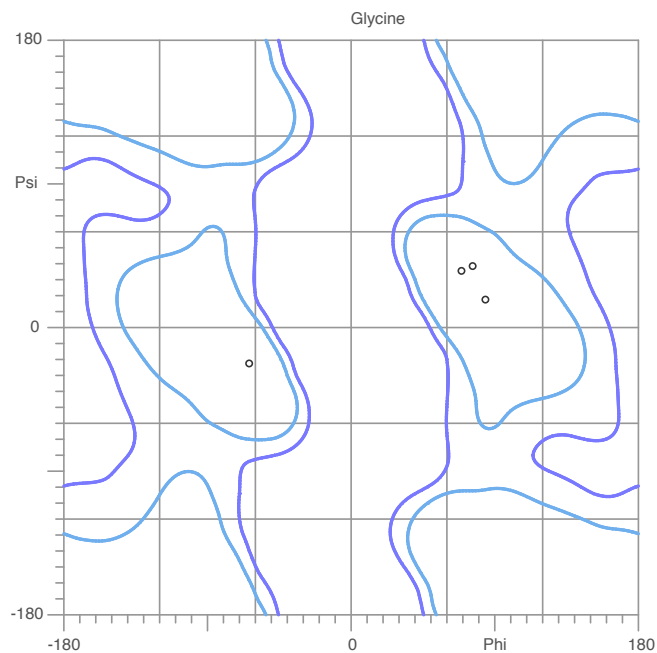
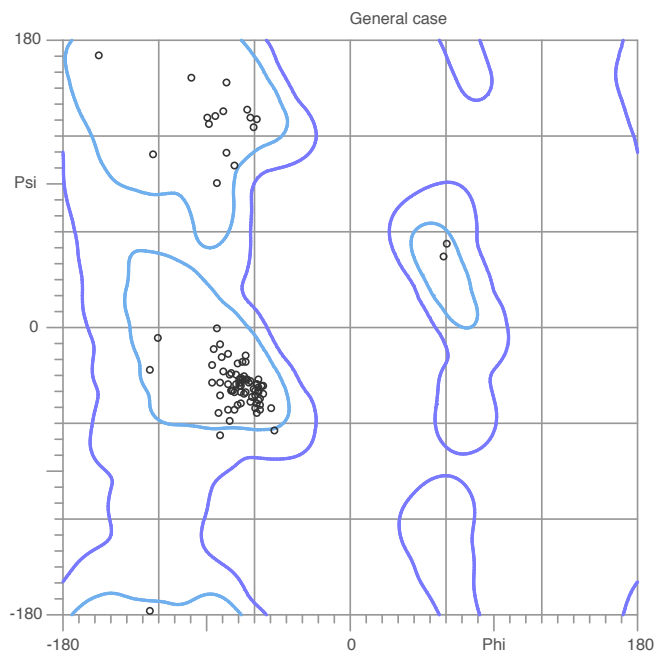
There were 1 outliers (phi, psi):  
[14] 98 HIS (175.4, 55.6)

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

# MolProbity Ramachandran analysis

RPR324\_NMR\_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.

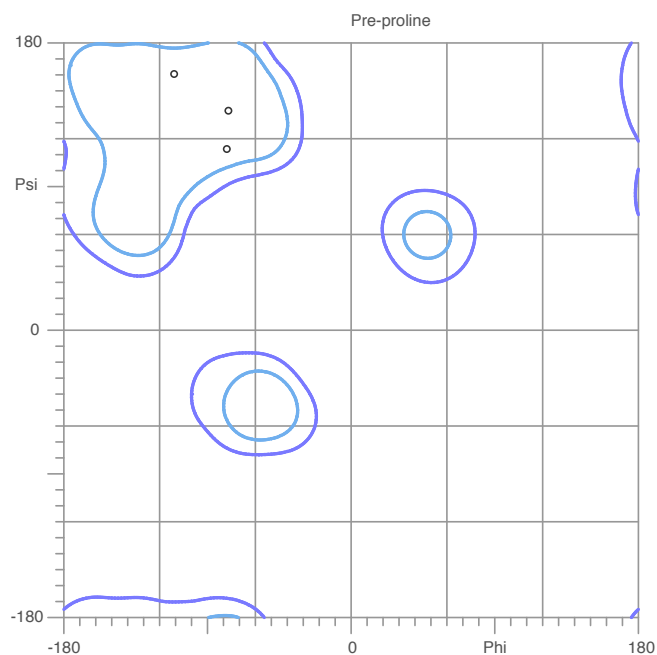
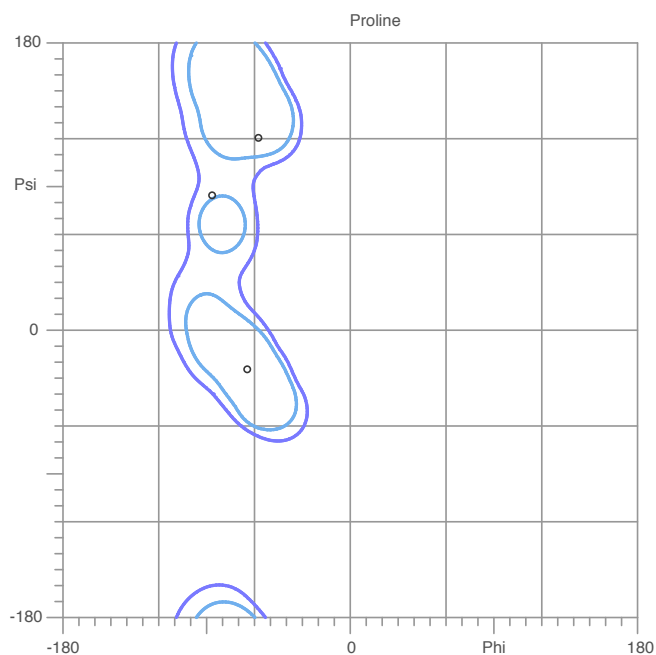
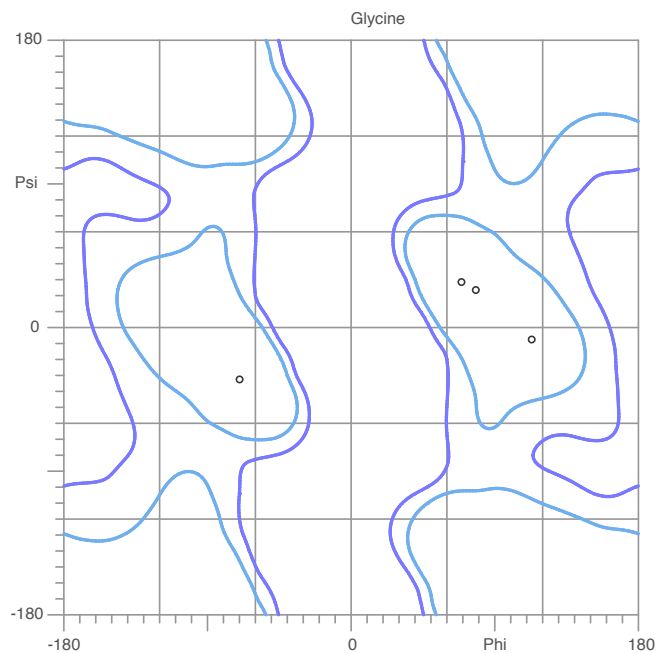
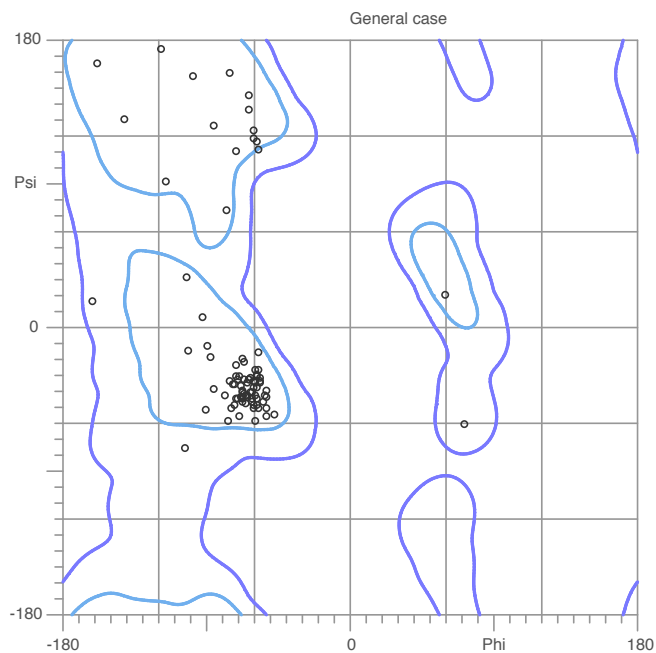
There were no outliers.

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

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

# MolProbity Ramachandran analysis

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



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.

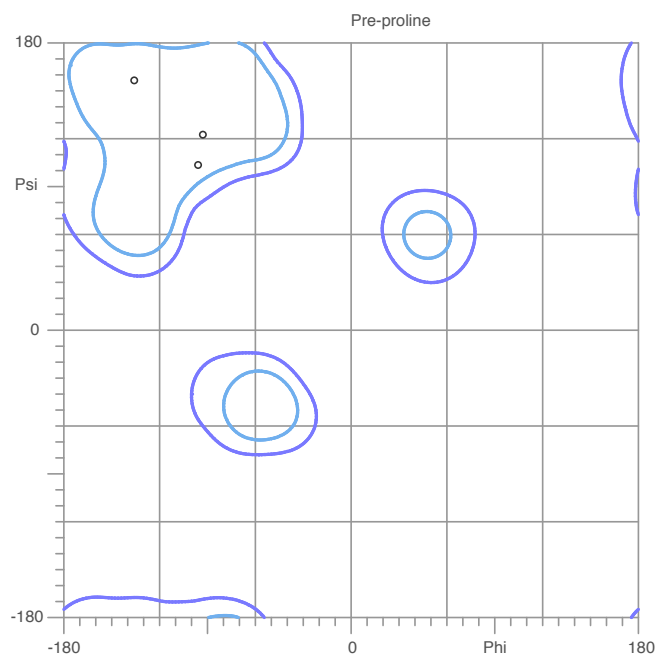
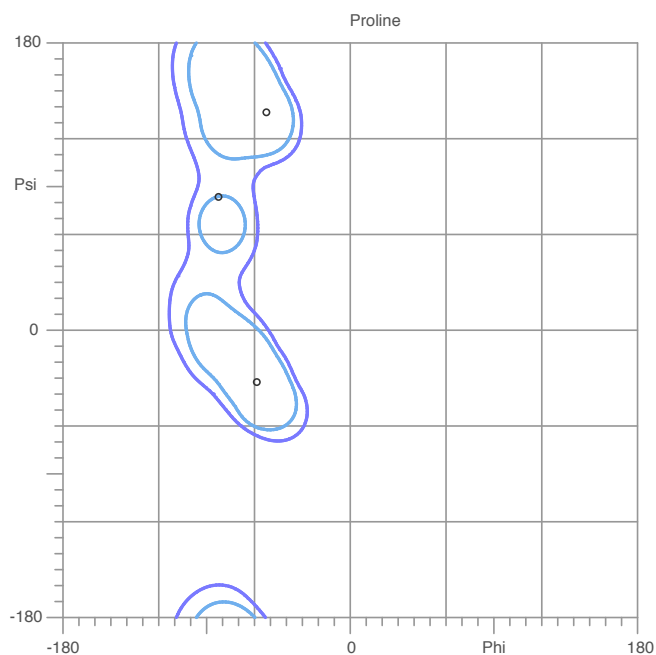
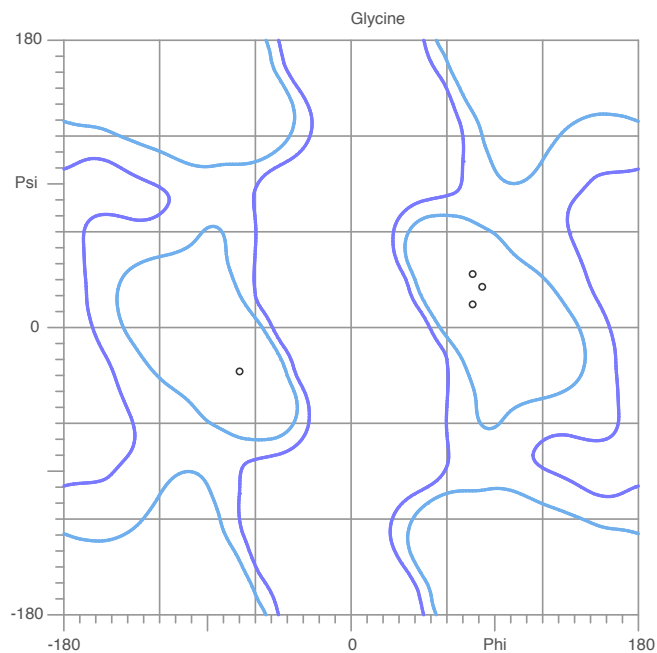
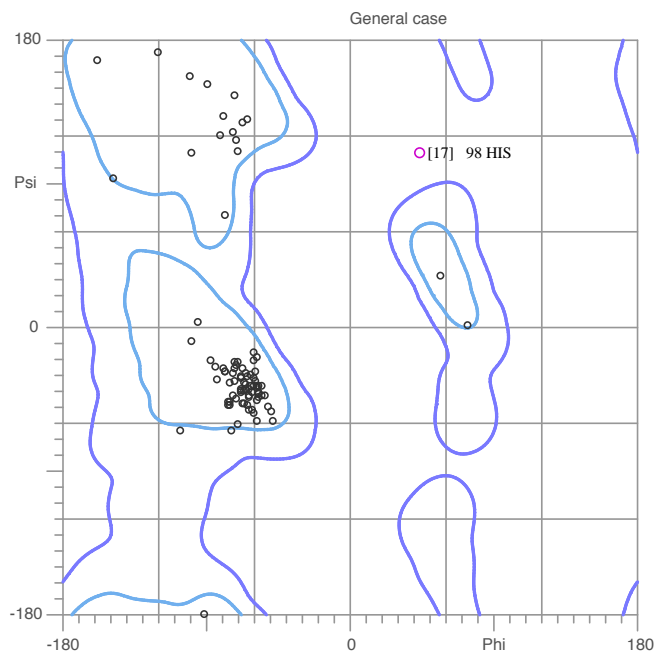
There were no outliers.

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

# MolProbity Ramachandran analysis

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



96.0% (95/99) of all residues were in favored (98%) regions.  
99.0% (98/99) of all residues were in allowed (>99.8%) regions.

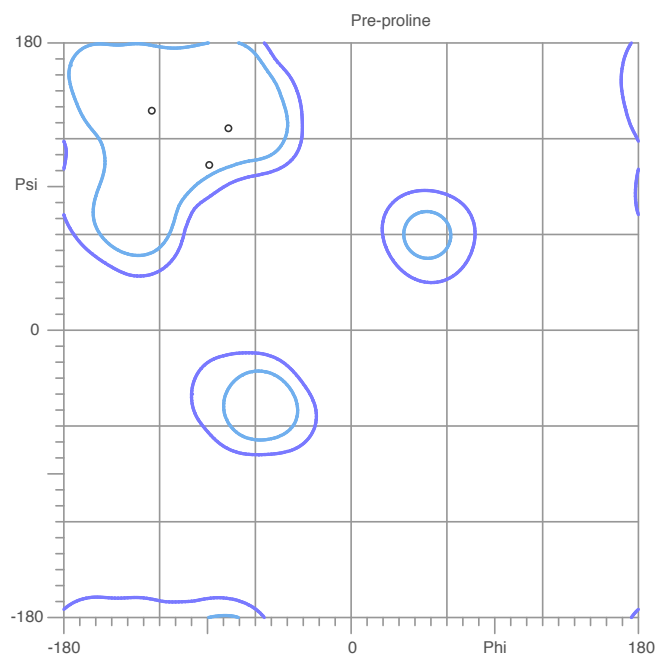
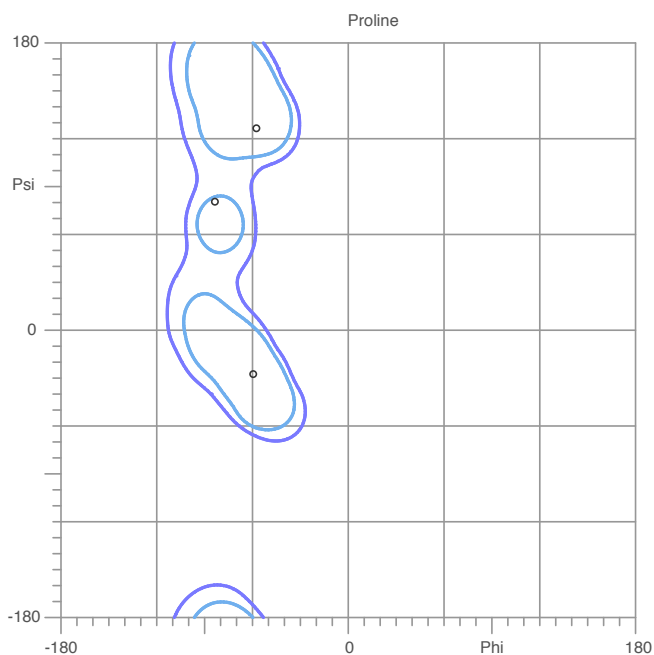
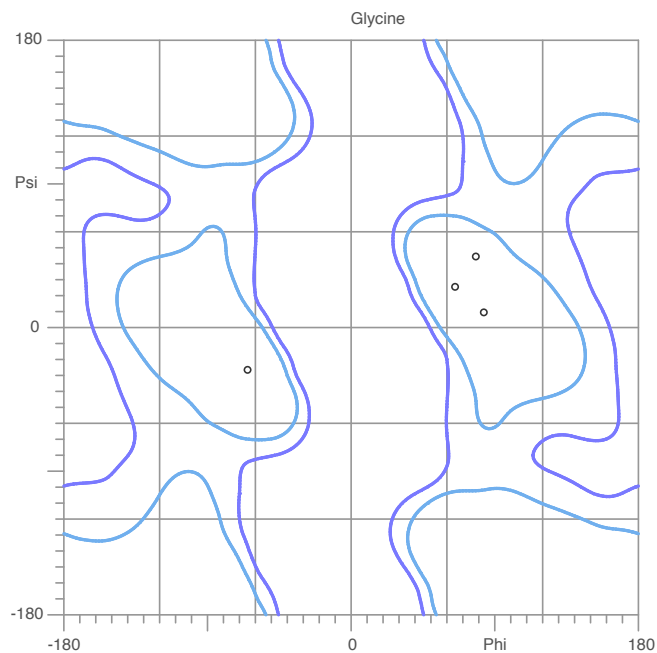
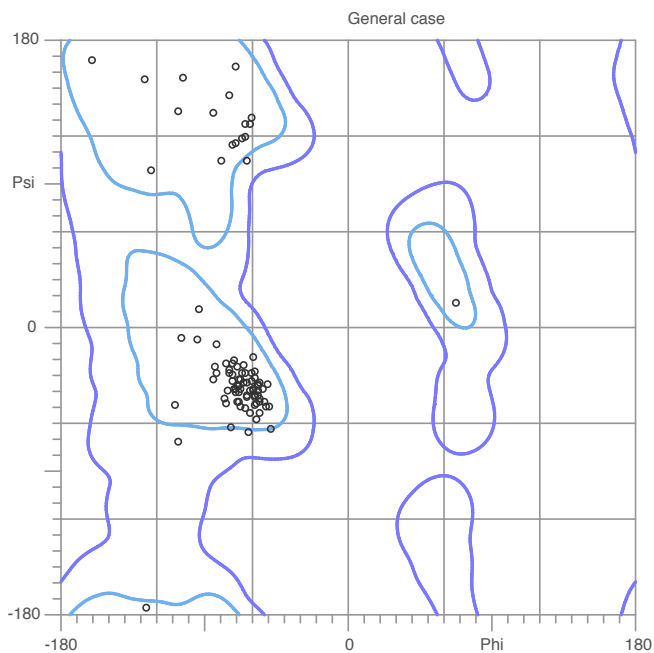
There were 1 outliers (phi, psi):  
[17] 98 HIS (43.6, 110.0)

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

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

# MolProbity Ramachandran analysis

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



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.

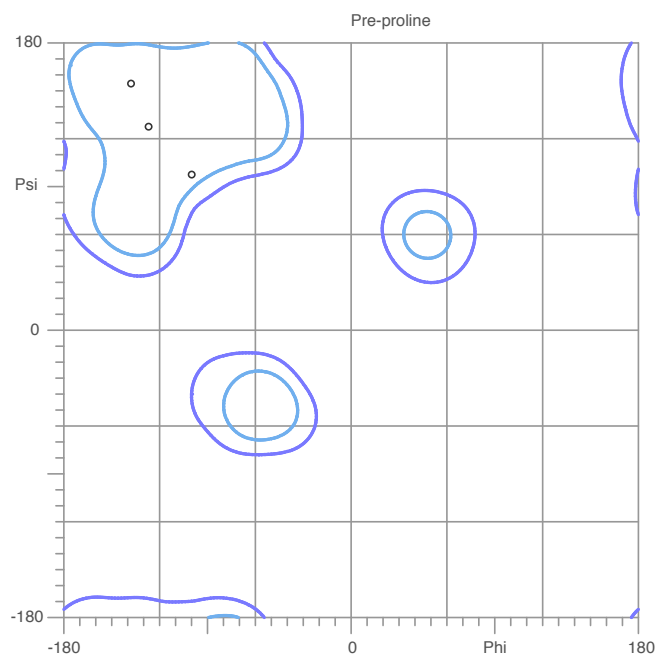
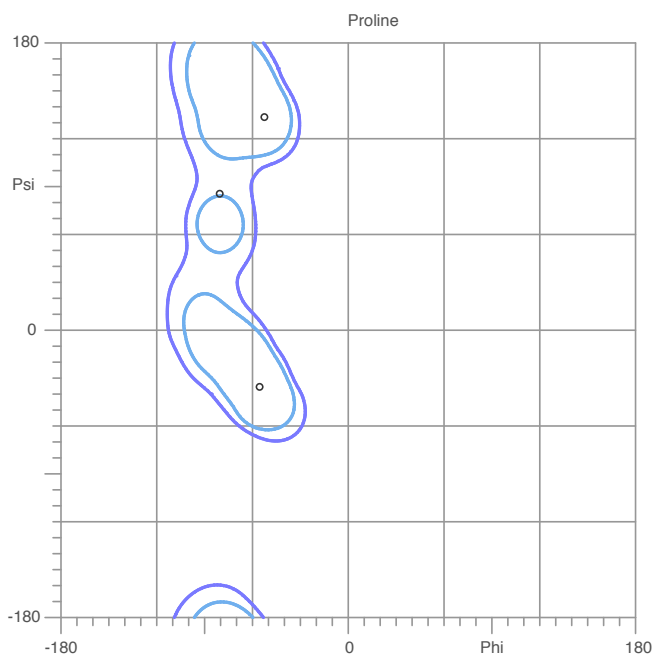
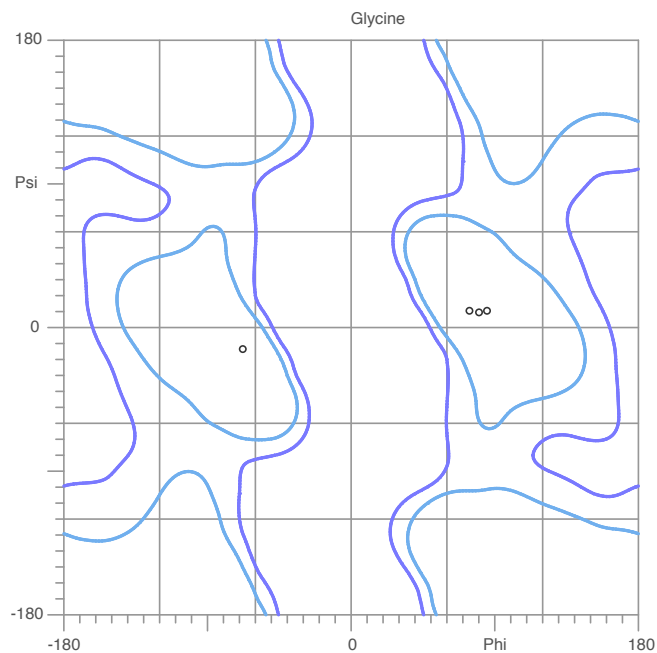
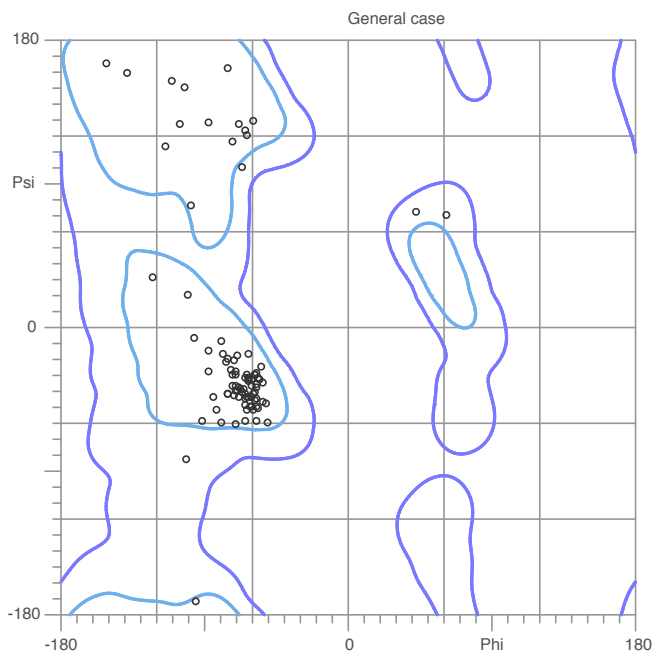
There were no outliers.

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

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

# MolProbity Ramachandran analysis

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



94.9% (94/99) of all residues were in favored (98%) regions.  
100.0% (99/99) of all residues were in allowed (>99.8%) regions.

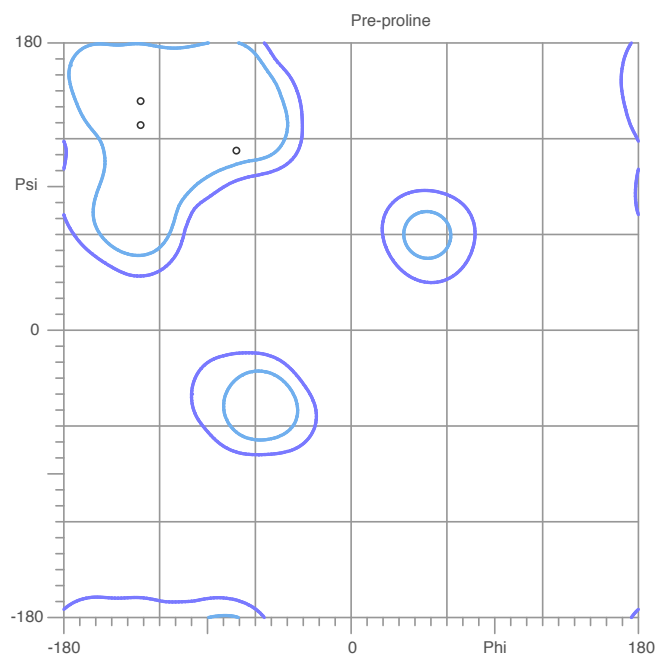
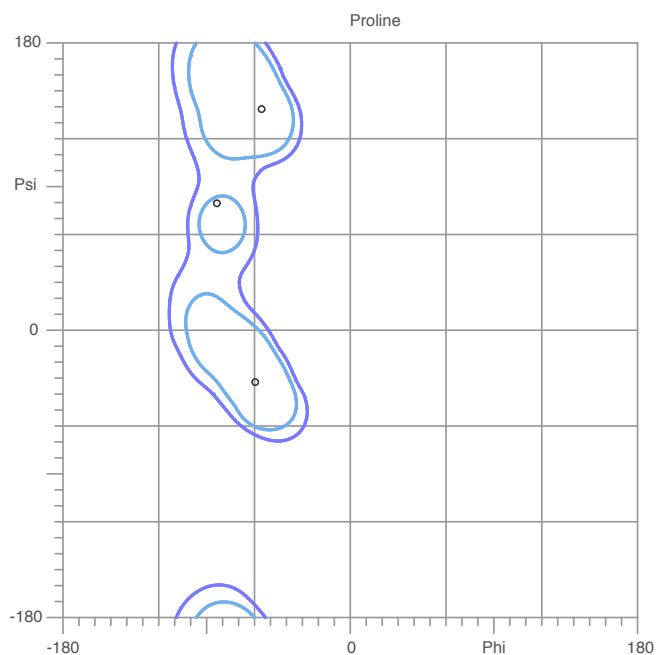
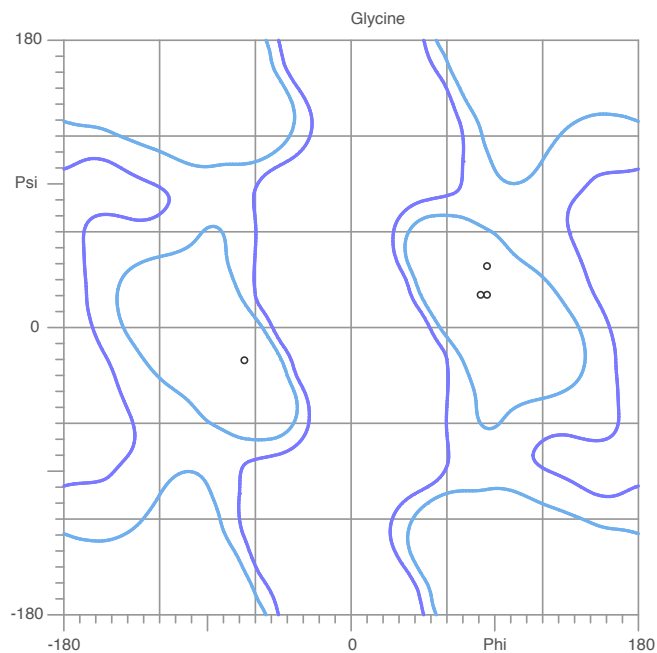
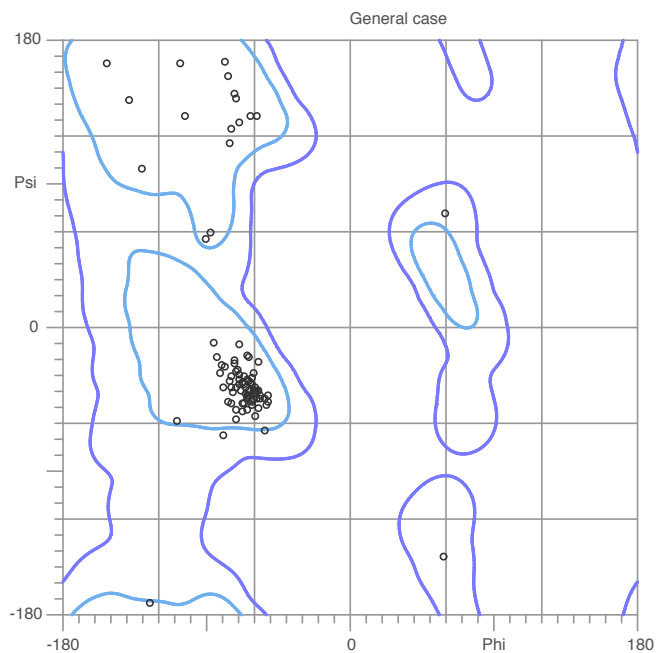
There were no outliers.

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

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

# MolProbity Ramachandran analysis

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



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.

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

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