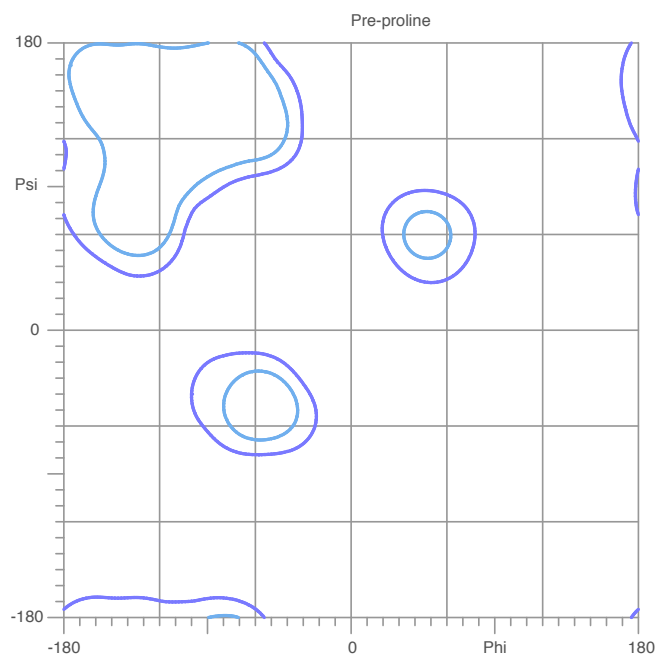
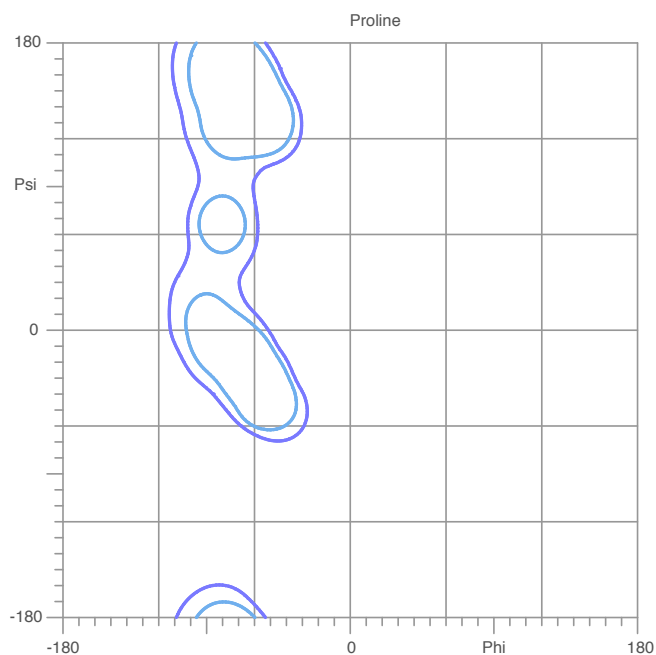
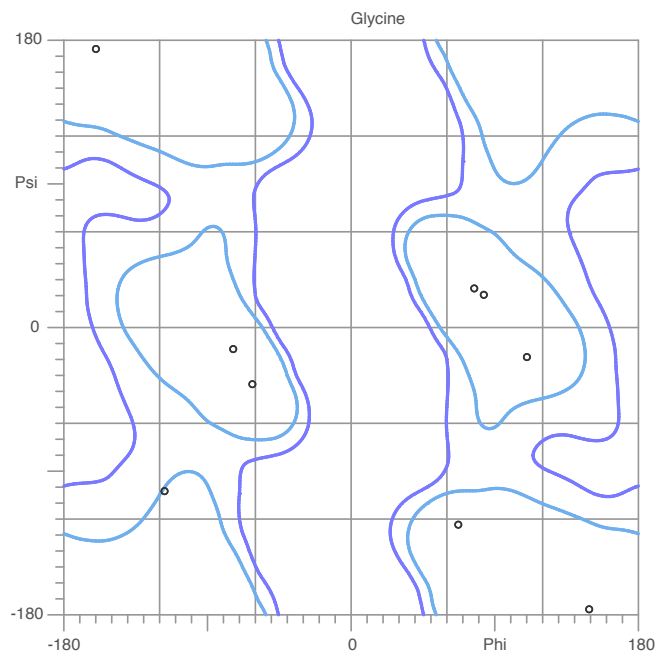
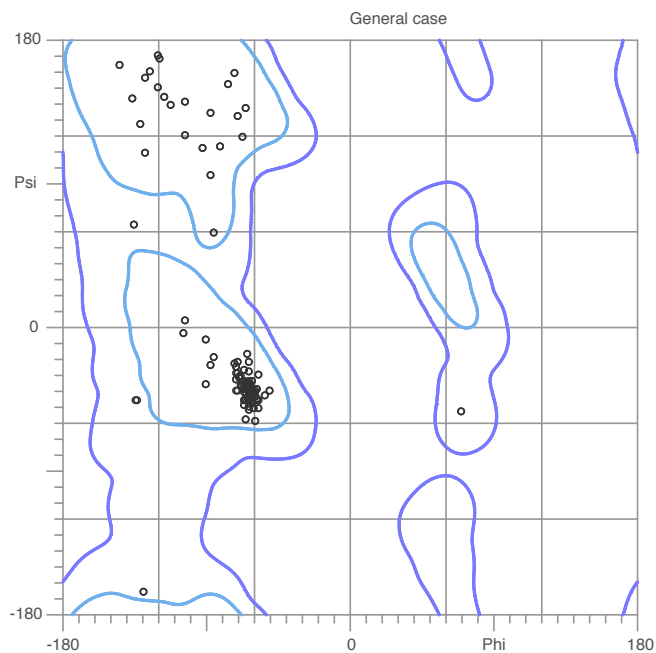




# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 1



96.2% (204/212) of all residues were in favored (98%) regions.  
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

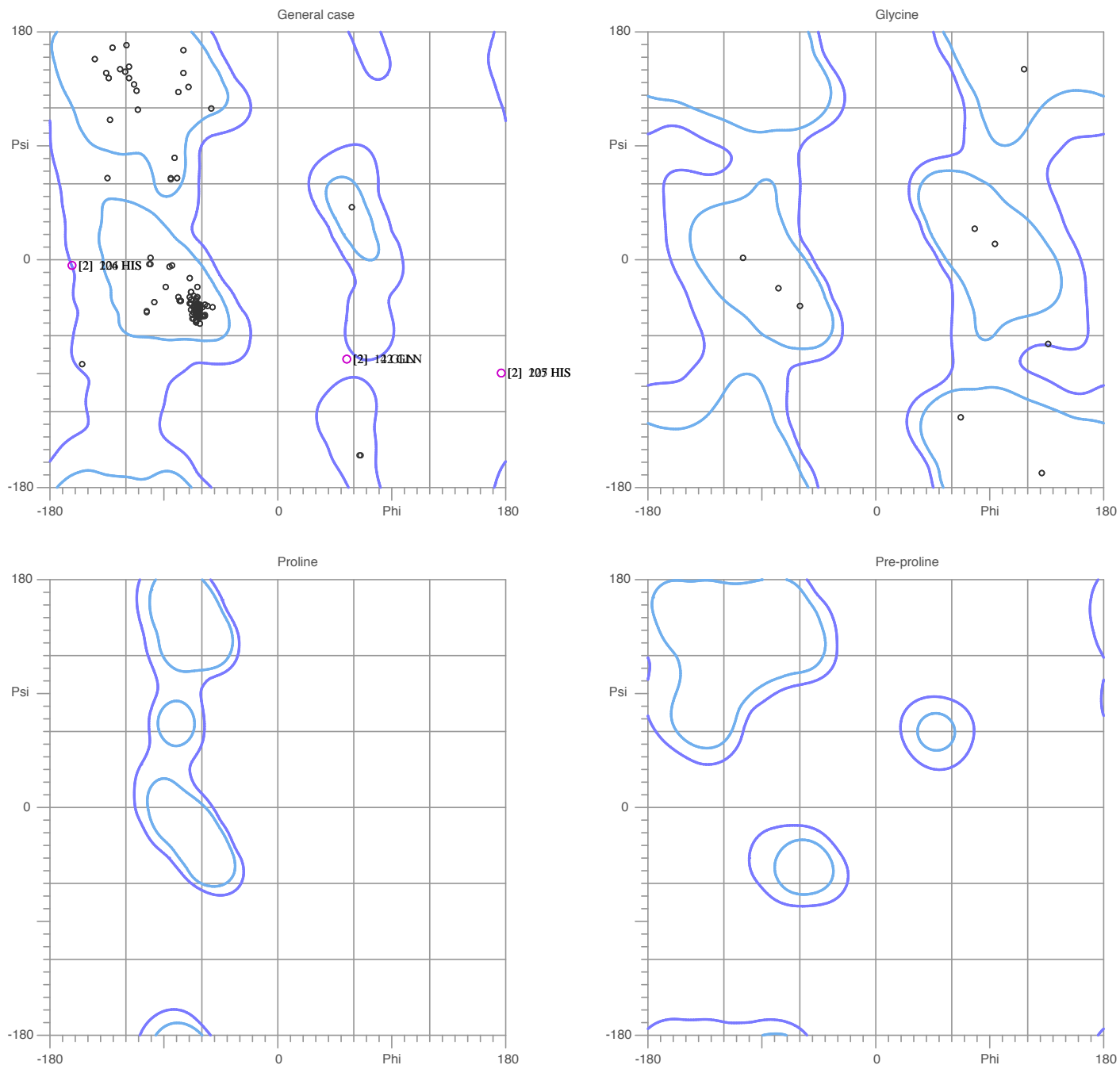
There were no outliers.

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

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# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 2



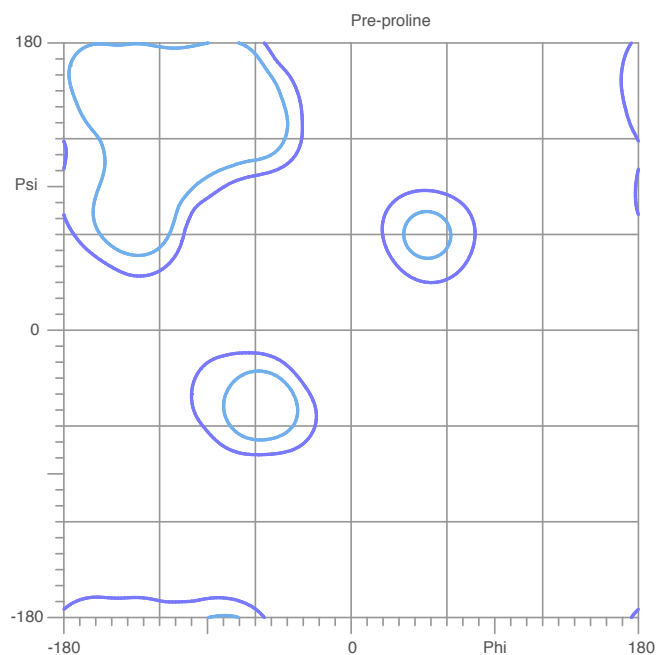
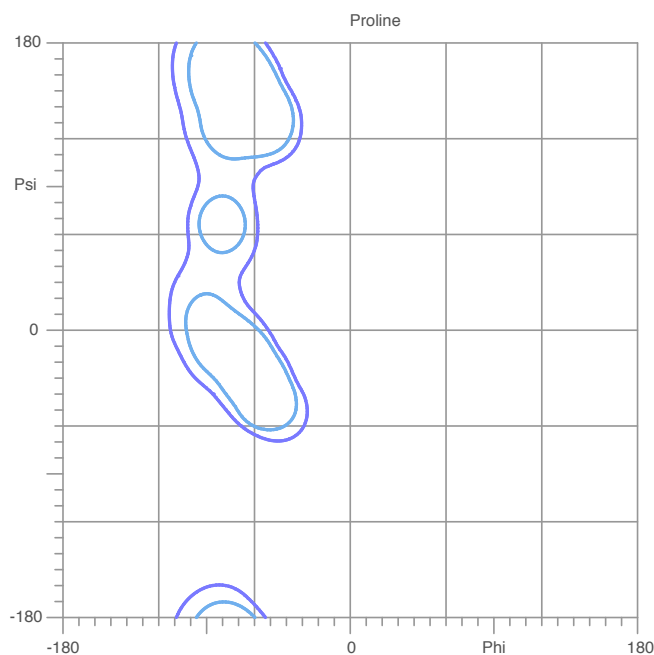
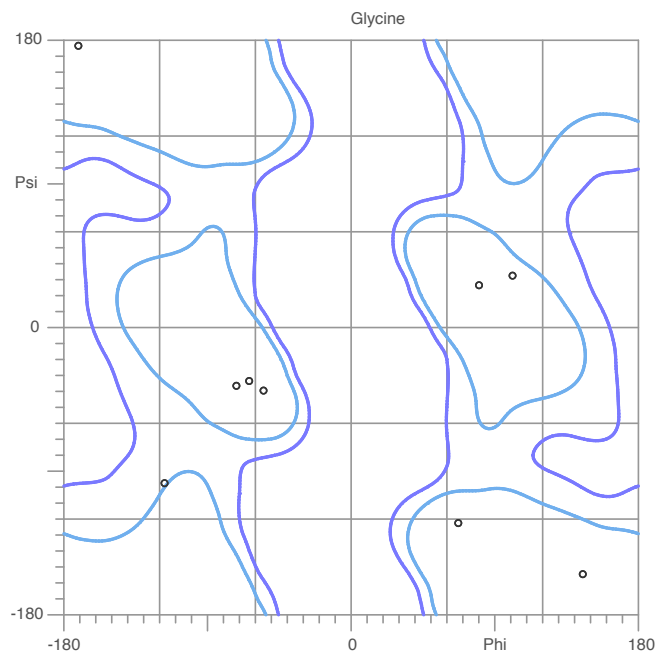
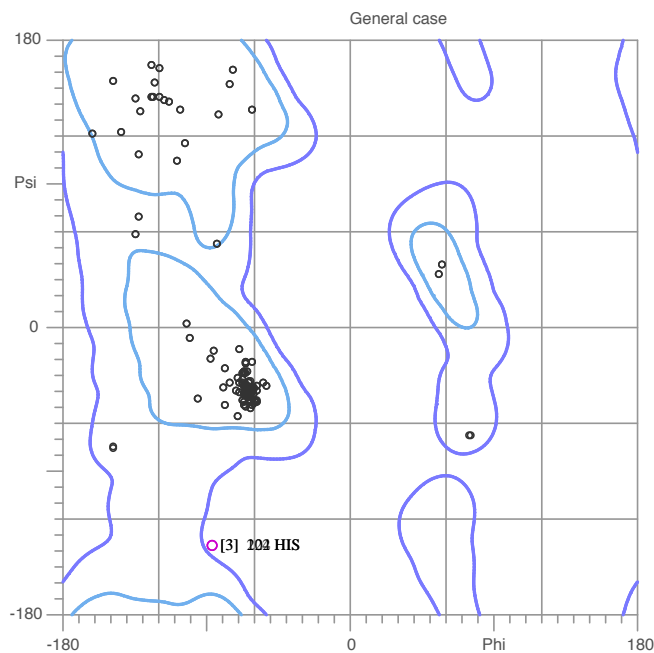
93.4% (198/212) of all residues were in favored (98%) regions.  
97.2% (206/212) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):  
[2] 4 GLN (54.9, -78.5)

[2] 106 HIS (-163.8, -4.9)  
[2] 107 HIS (176.9, -89.3)  
[2] 122 GLN (54.9, -78.5)  
[2] 224 HIS (-163.8, -4.9)  
[2] 225 HIS (176.9, -89.3)

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 3



94.3% (200/212) of all residues were in favored (98%) regions.  
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

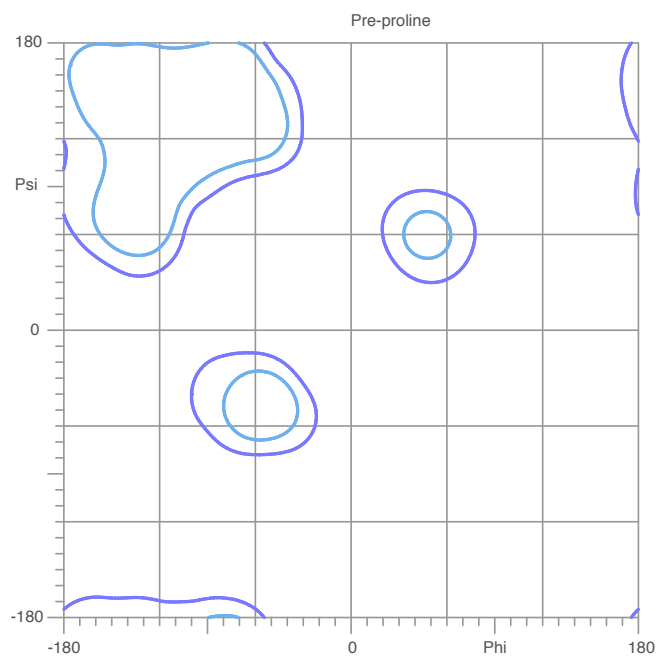
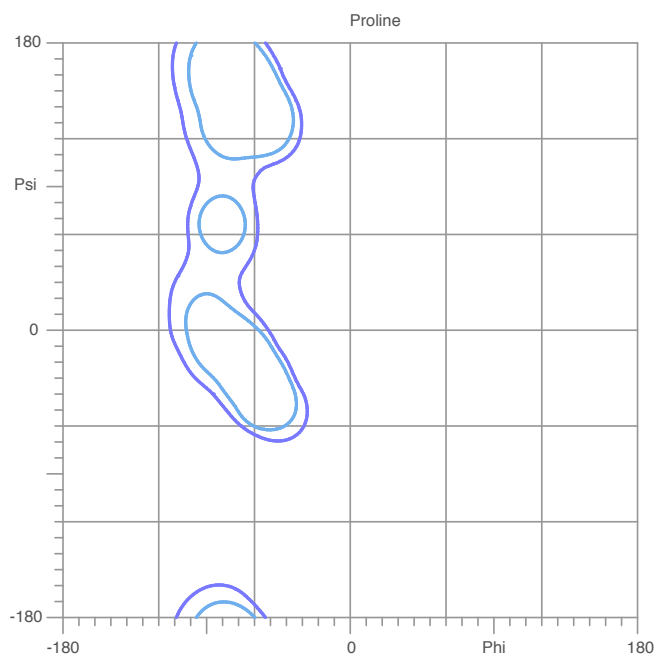
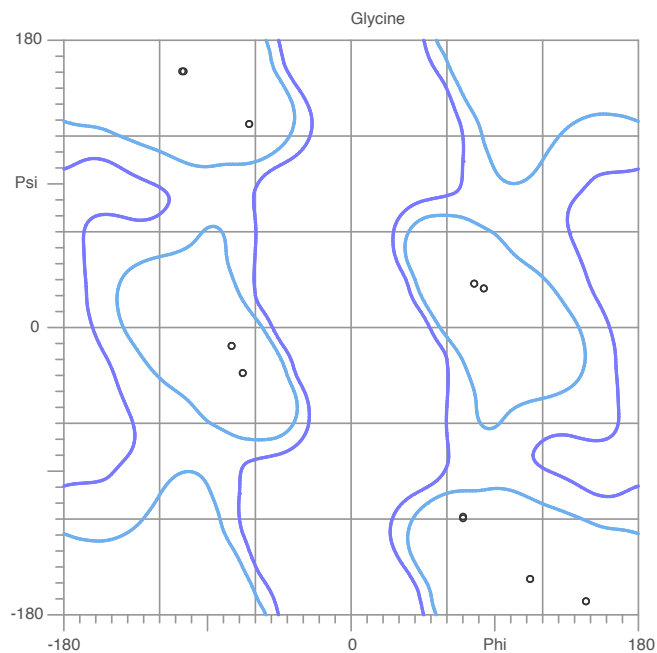
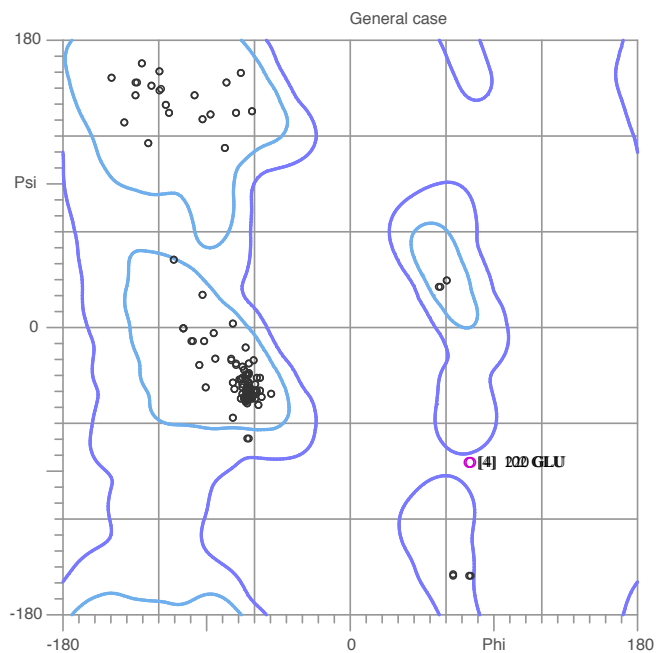
There were 2 outliers (phi, psi):

[3] 104 HIS (-87.3, -136.7)

[3] 222 HIS (-87.2, -136.8)

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 4



96.2% (204/212) of all residues were in favored (98%) regions.  
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

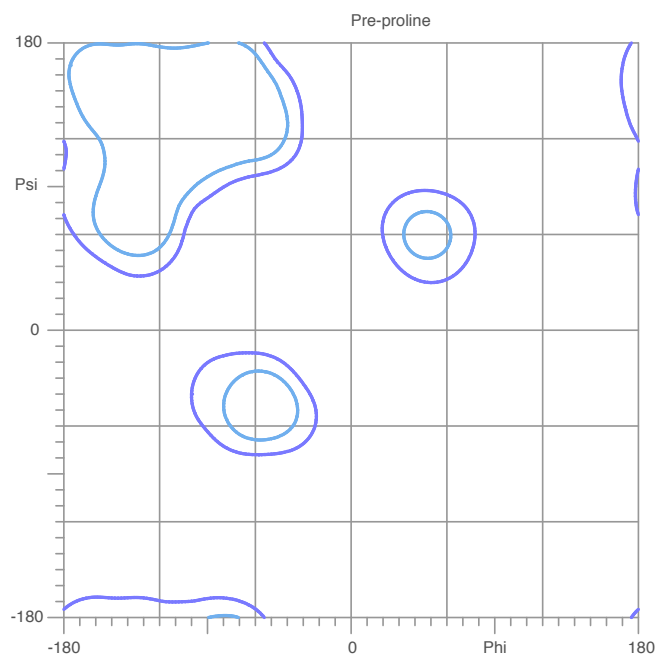
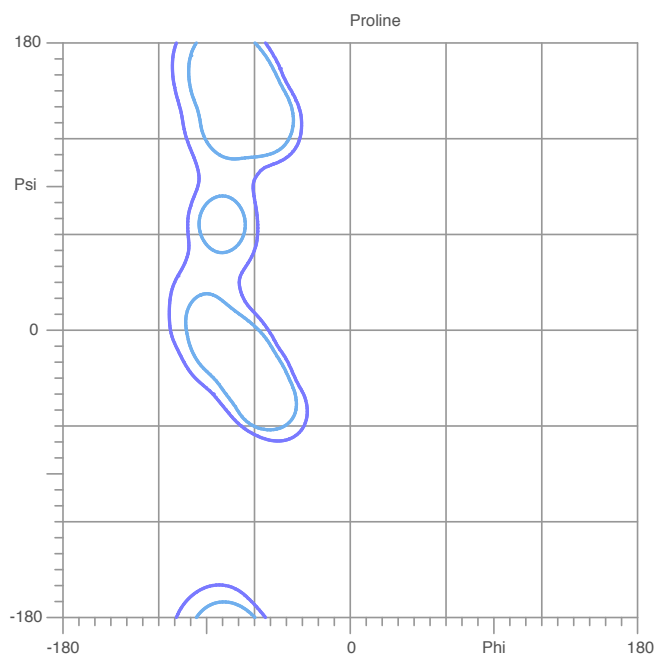
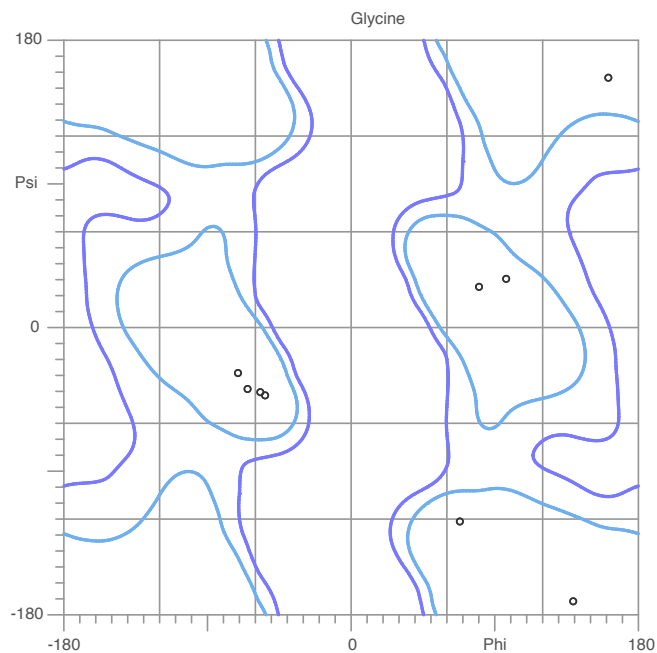
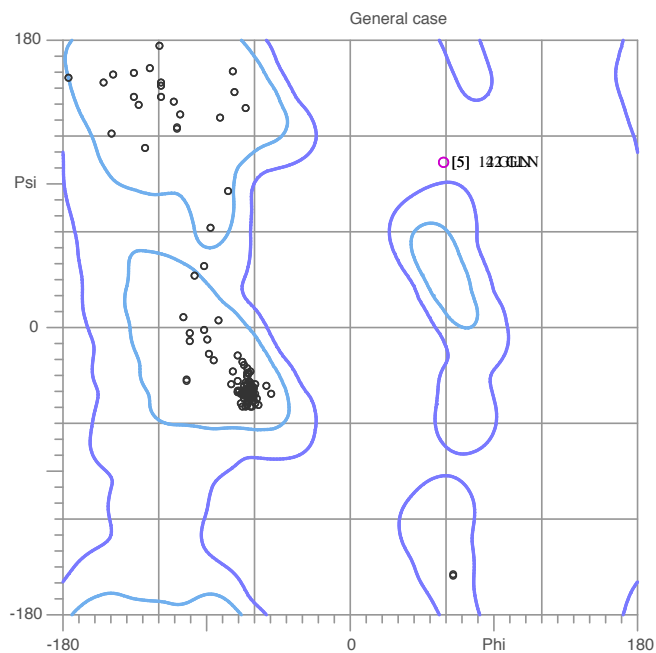
There were 2 outliers (phi, psi):

[4] 102 GLU (75.0, -84.8)

[4] 220 GLU (75.0, -84.8)

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 5



96.2% (204/212) of all residues were in favored (98%) regions.  
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

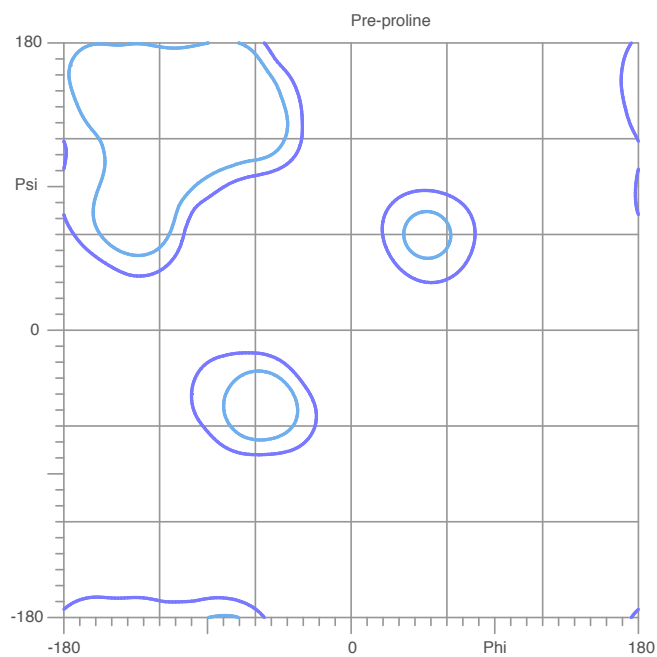
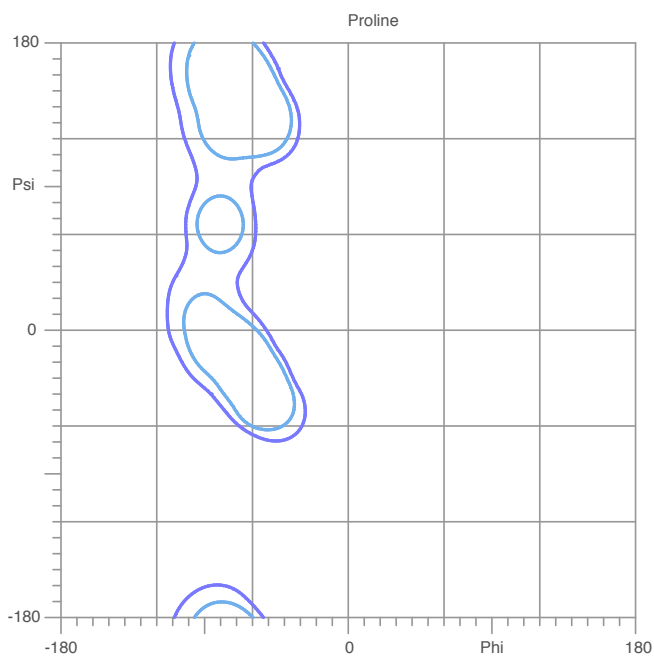
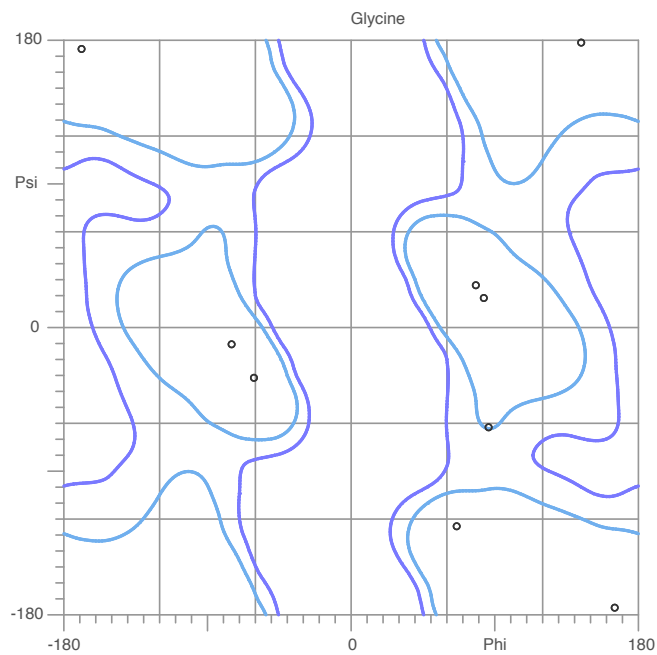
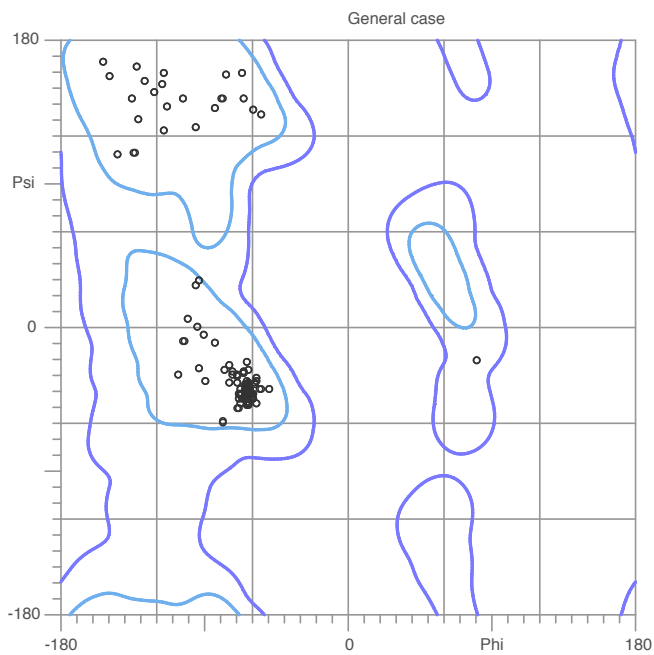
There were 2 outliers (phi, psi):

[5] 4 GLN (58.3, 104.9)

[5] 122 GLN (58.3, 104.9)

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 6

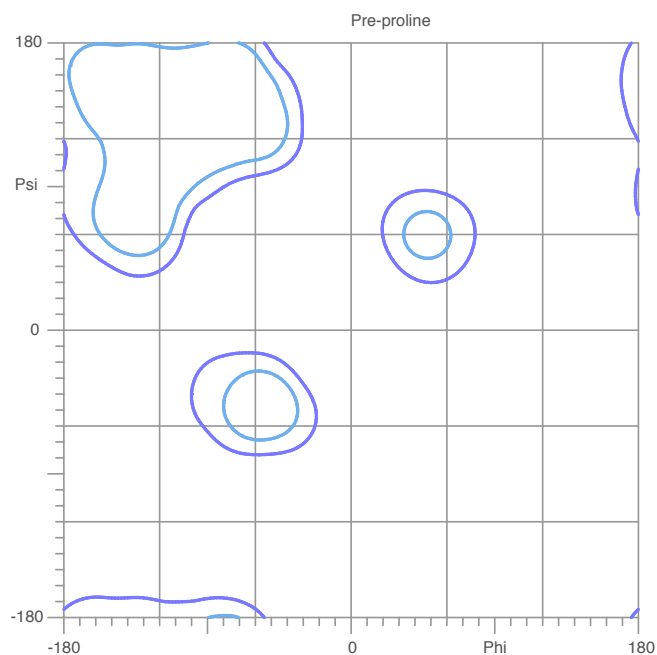
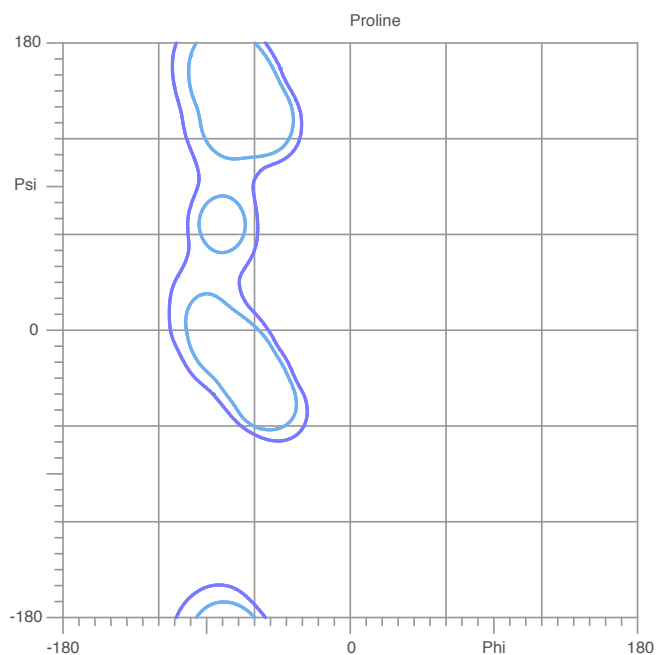
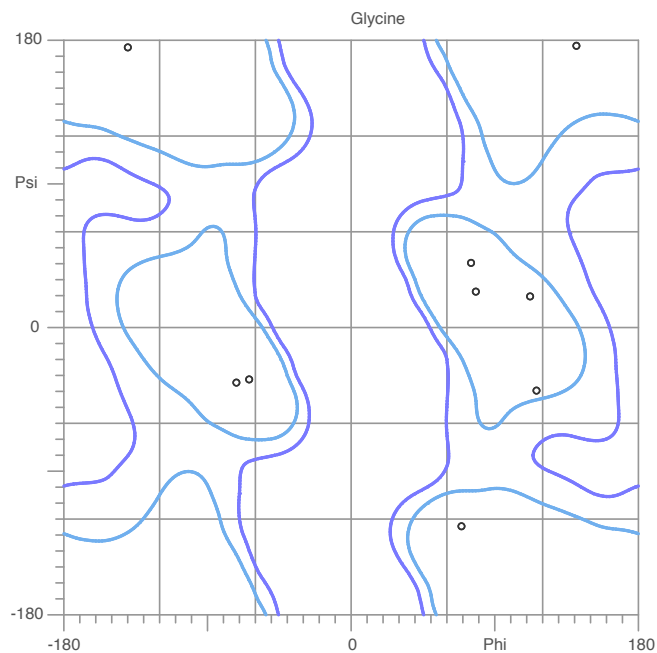
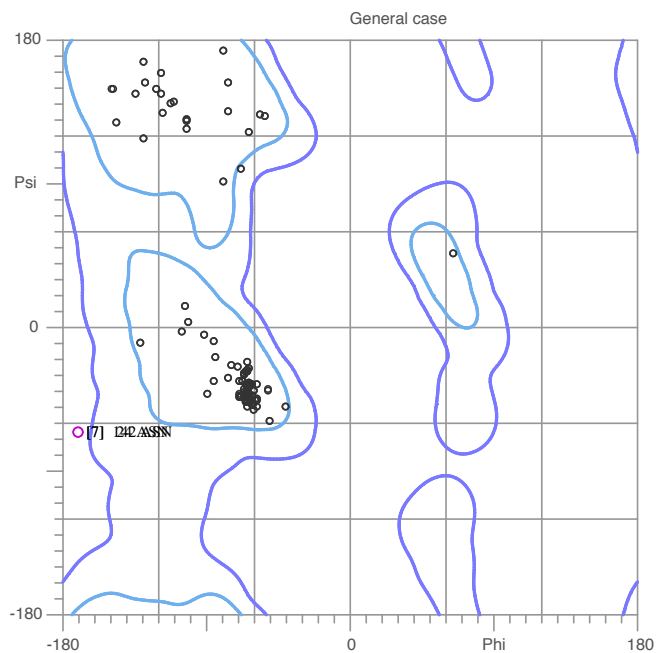


99.1% (210/212) of all residues were in favored (98%) regions.  
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 7



98.1% (208/212) of all residues were in favored (98%) regions.  
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

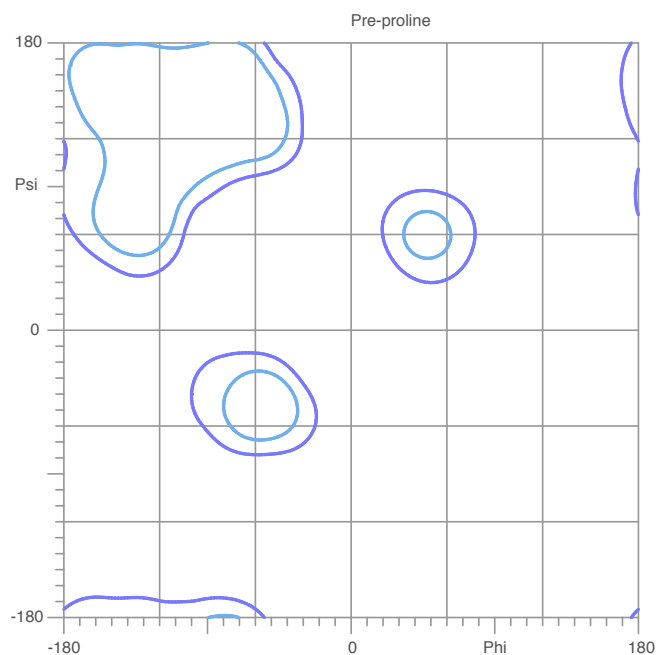
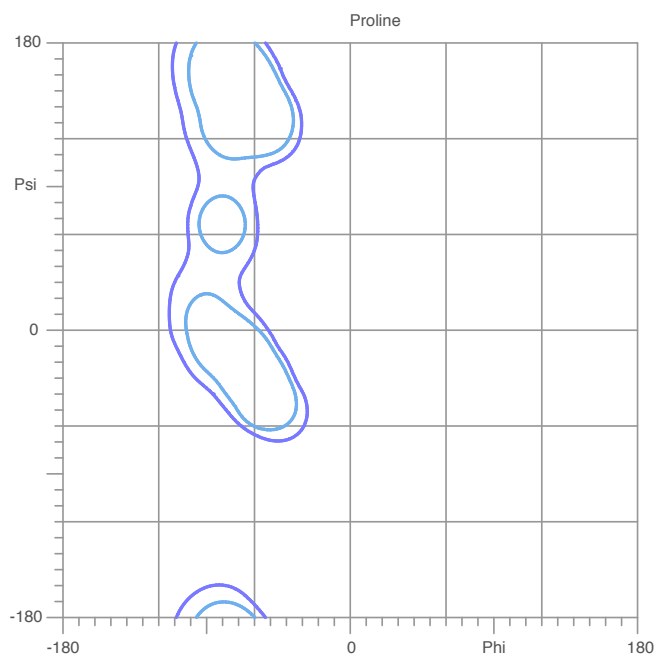
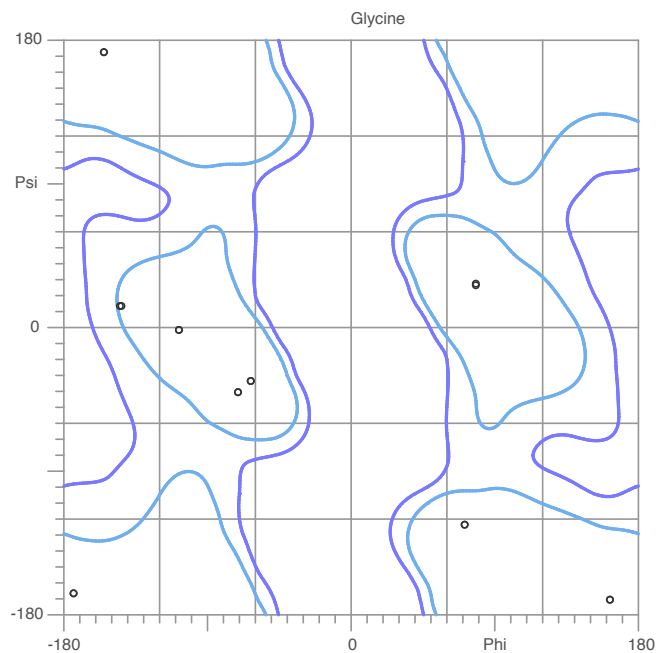
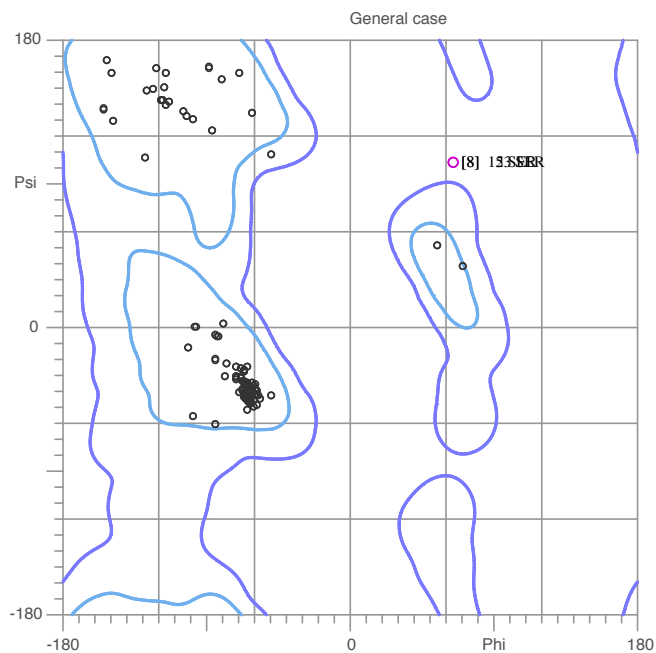
There were 2 outliers (phi, psi):

[7] 24 ASN (-171.7, -65.0)

[7] 142 ASN (-171.7, -65.1)

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 8



98.1% (208/212) of all residues were in favored (98%) regions.  
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

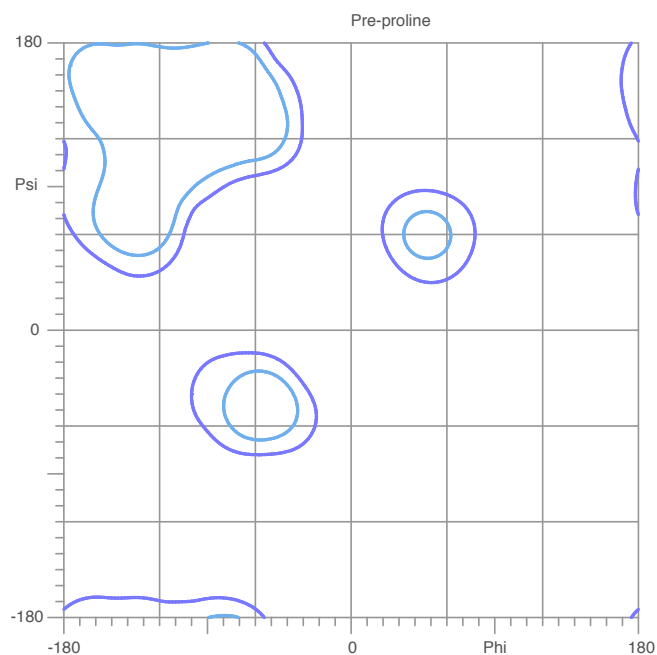
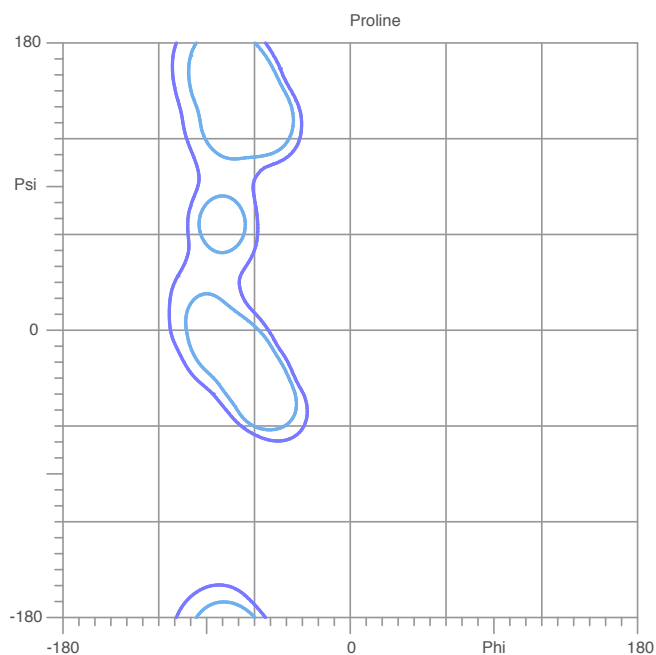
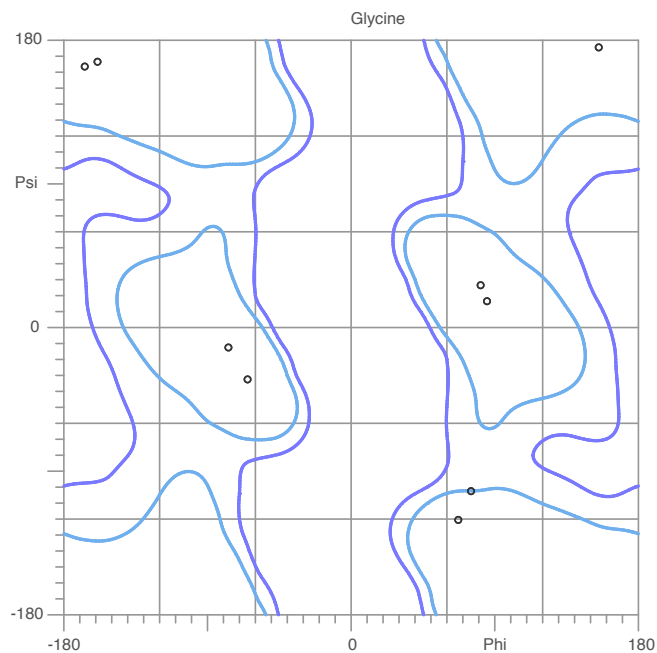
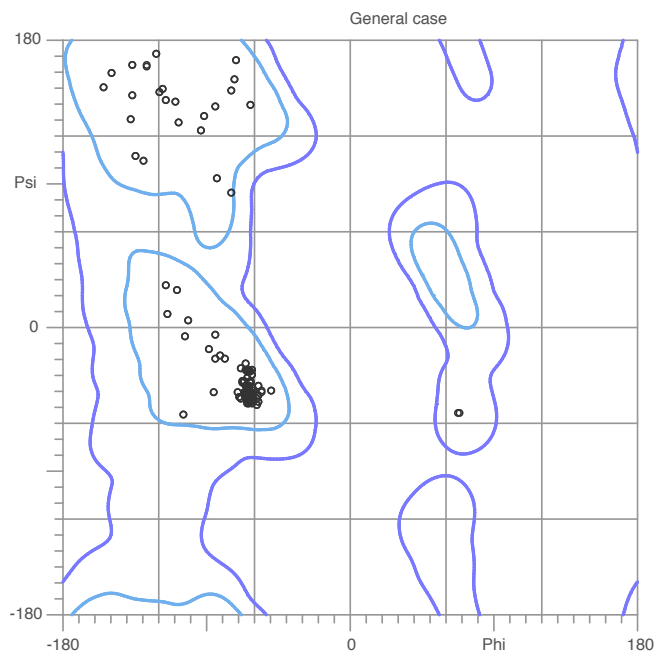
There were 2 outliers (phi, psi):

[8] 5 SER (65.0, 105.0)

[8] 123 SER (64.9, 105.0)

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 9



99.1% (210/212) of all residues were in favored (98%) regions.  
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

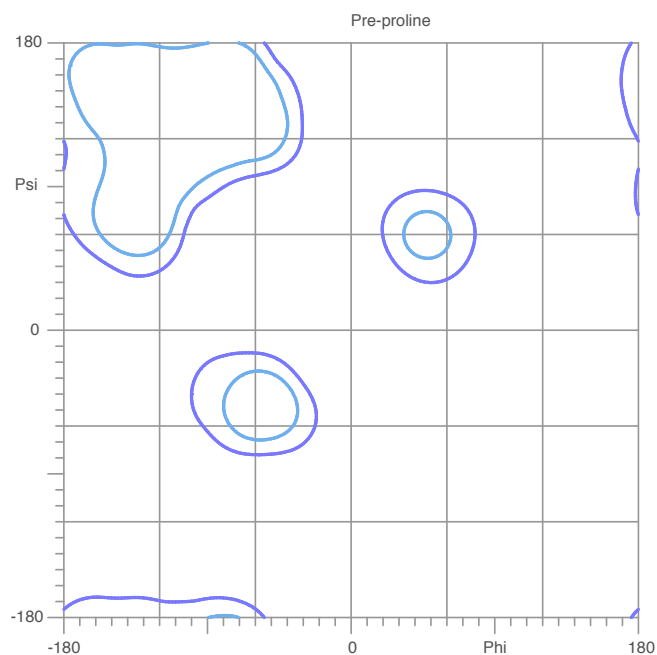
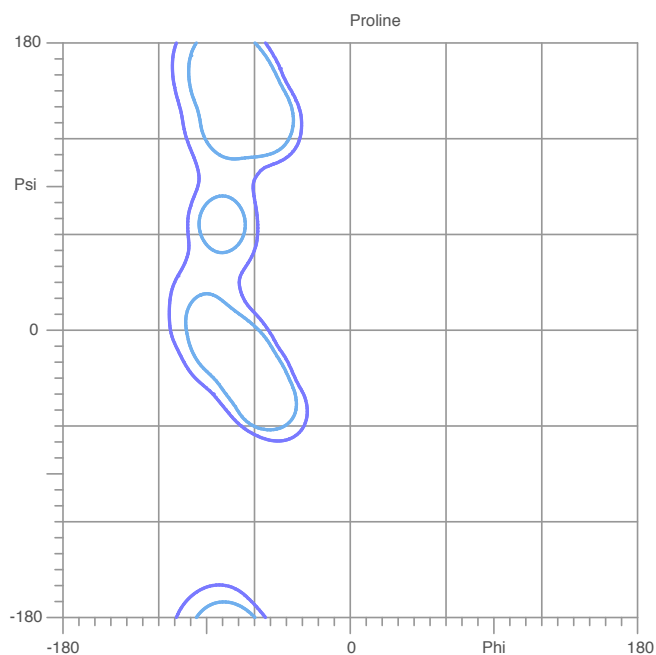
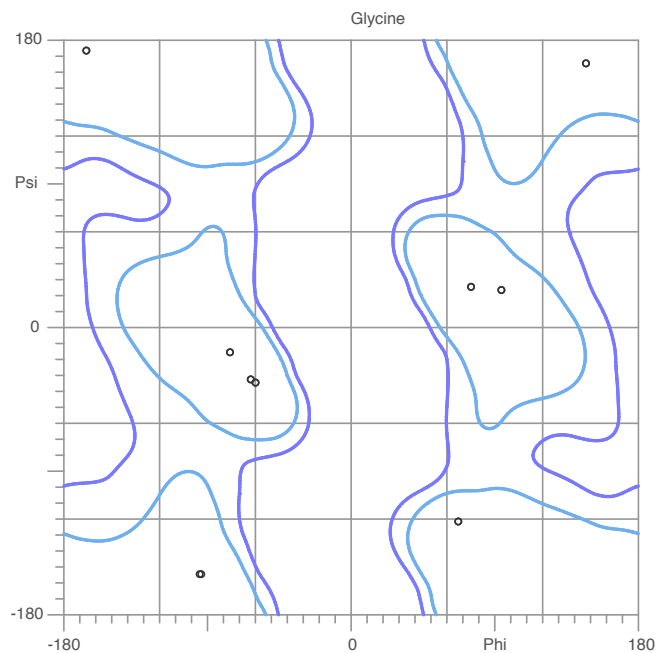
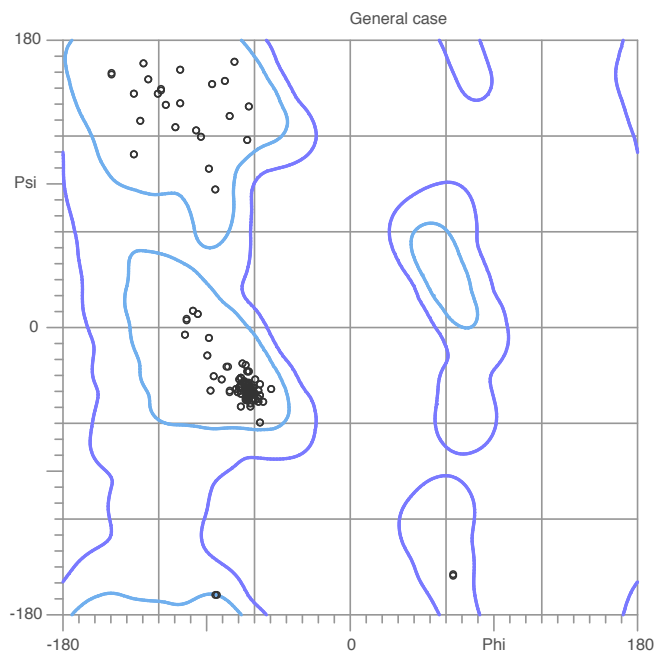
There were no outliers.

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# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 10

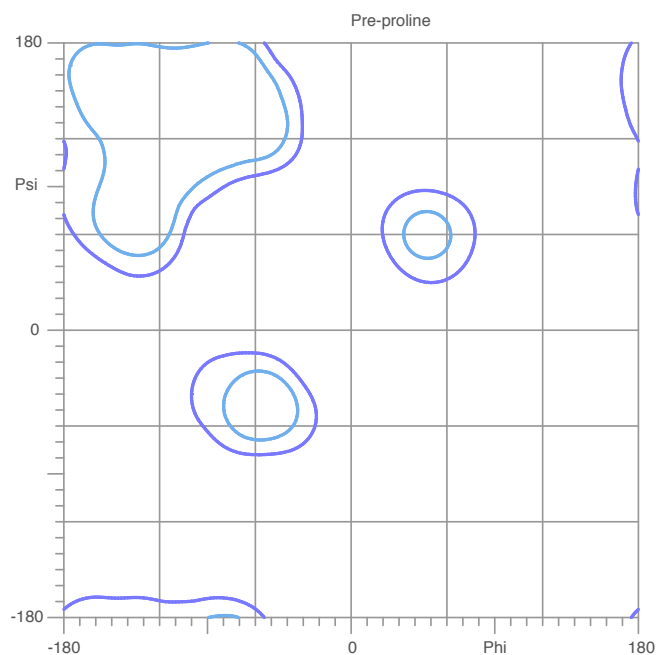
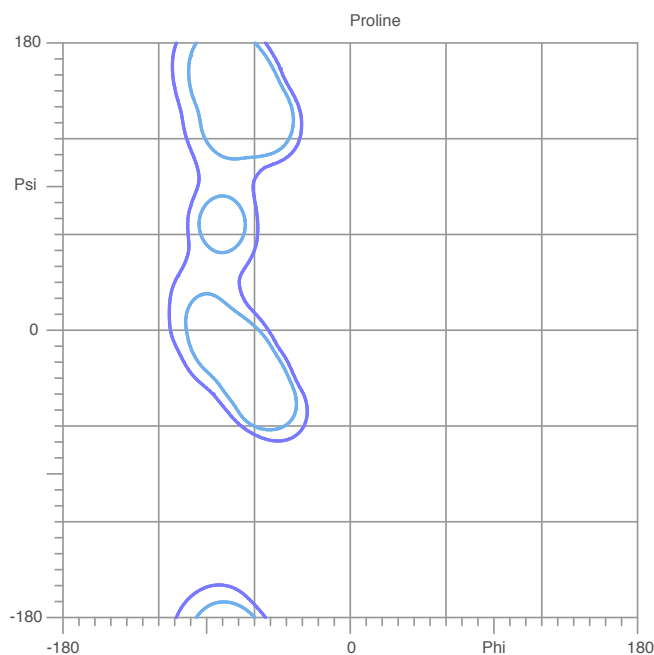
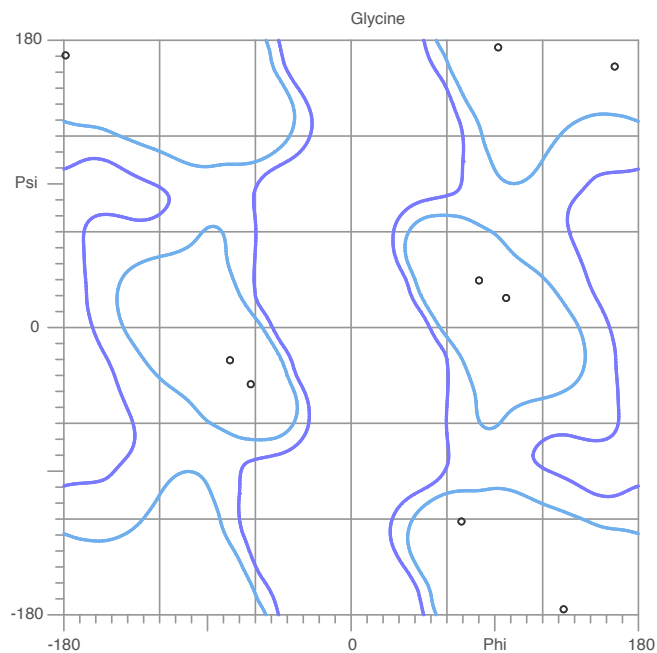
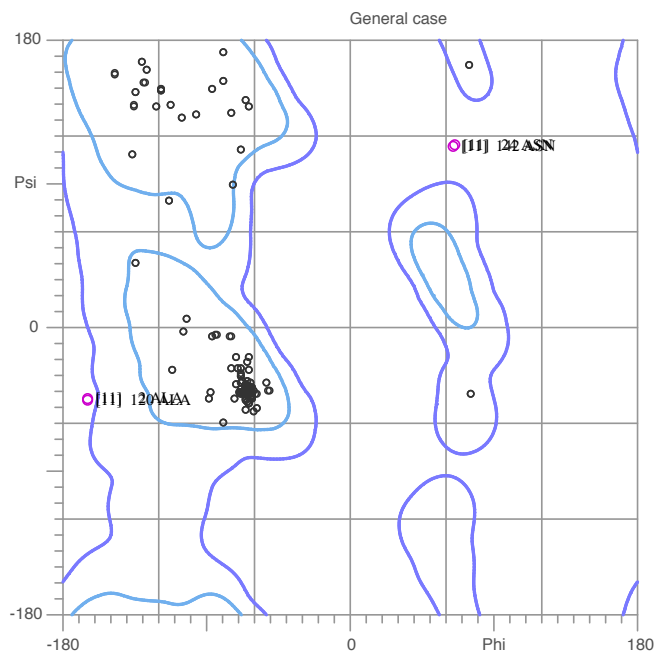


99.1% (210/212) of all residues were in favored (98%) regions.  
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 11



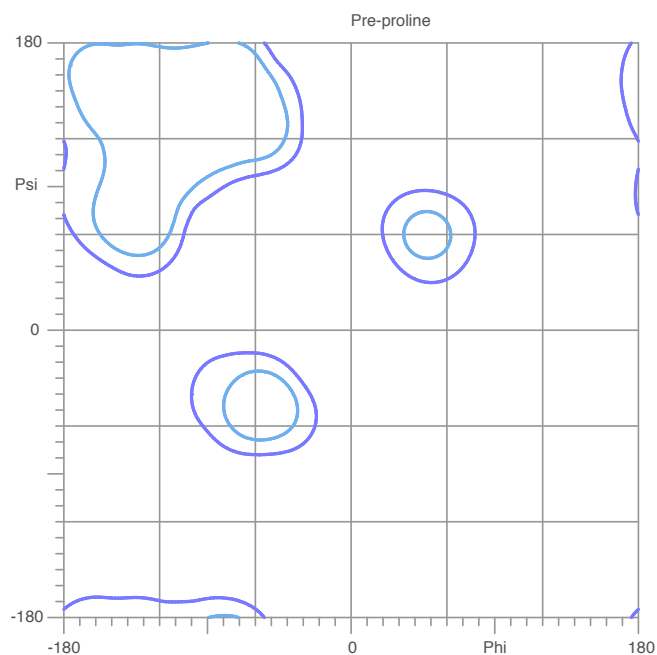
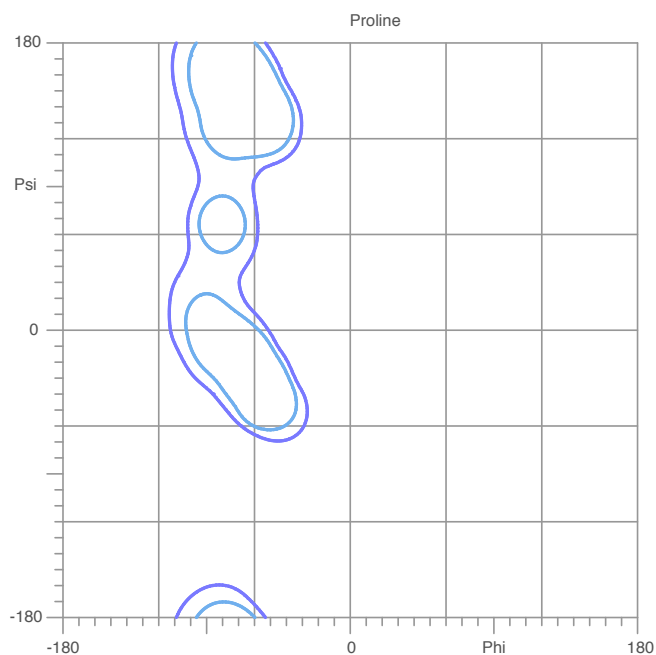
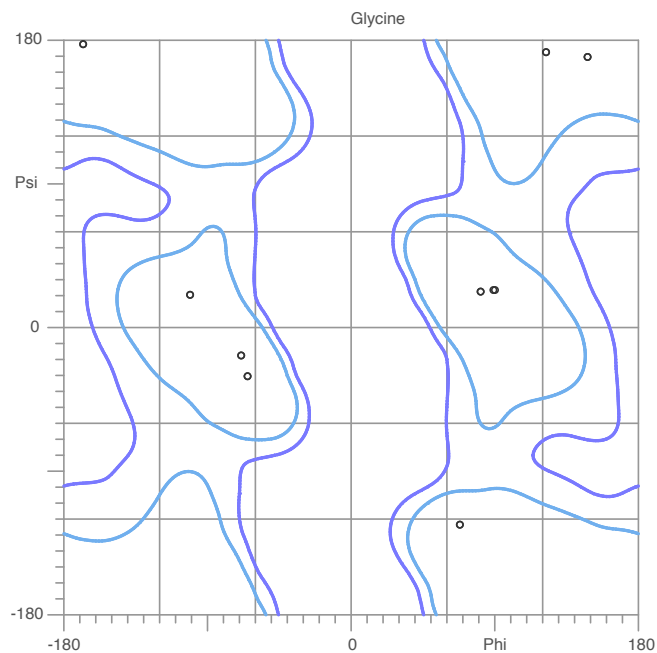
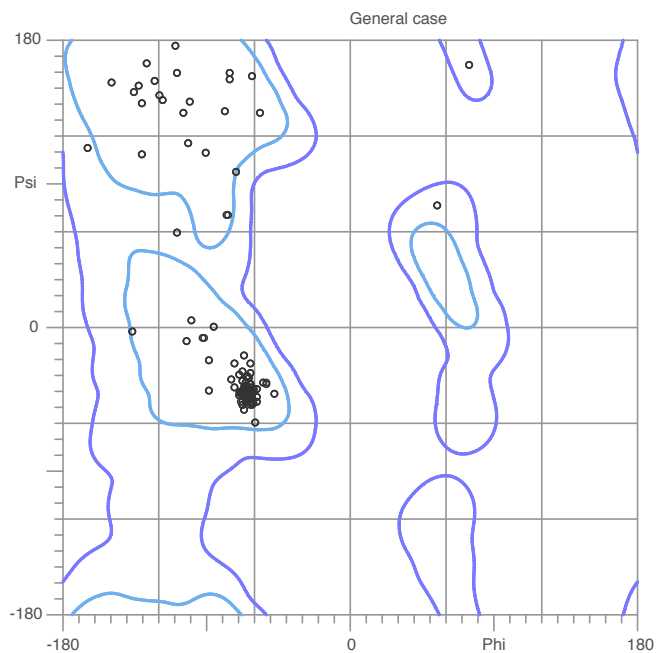
95.3% (202/212) of all residues were in favored (98%) regions.  
98.1% (208/212) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [11] 2 ALA (-165.0, -45.0)
- [11] 24 ASN (65.0, 115.1)
- [11] 120 ALA (-165.0, -45.1)
- [11] 142 ASN (65.0, 115.0)

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 12

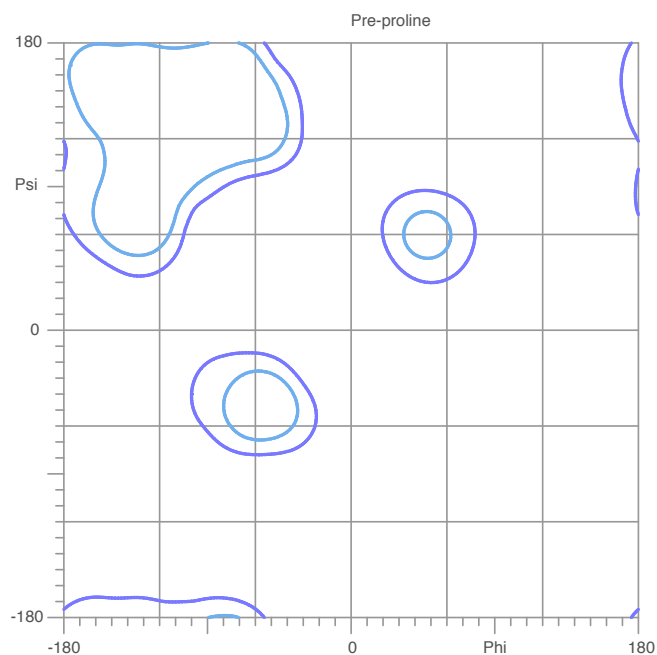
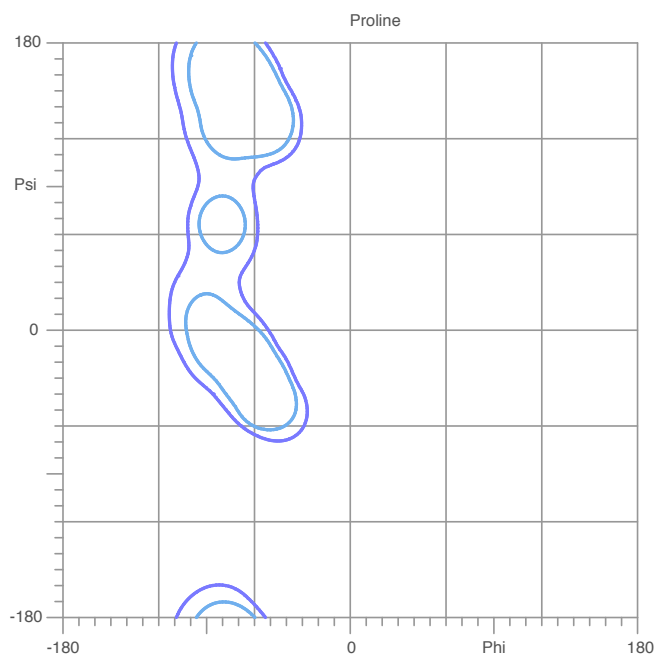
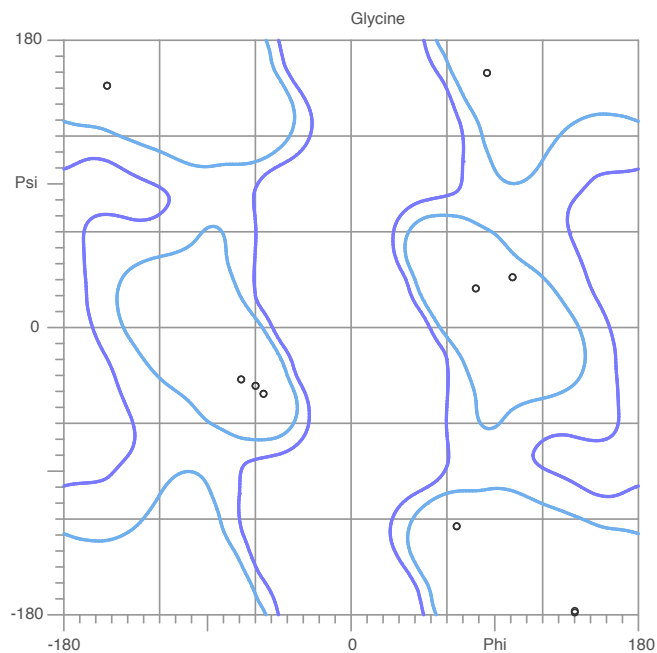
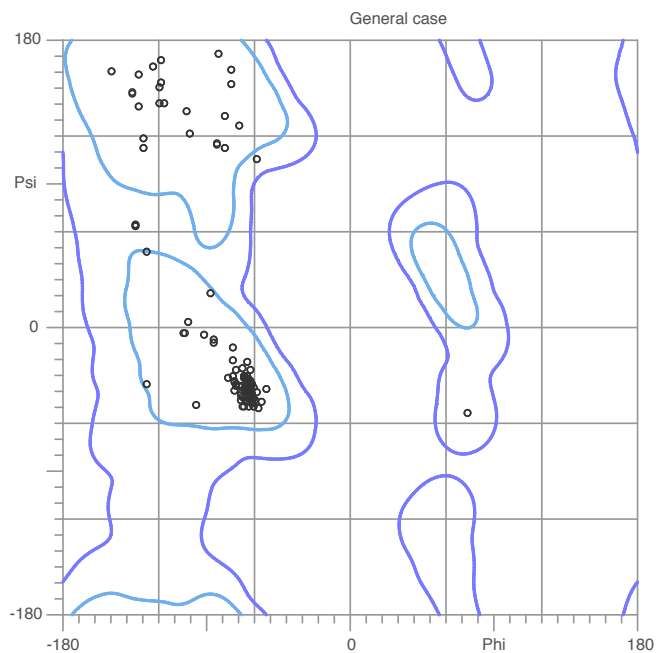


96.2% (204/212) of all residues were in favored (98%) regions.  
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 13



95.3% (202/212) of all residues were in favored (98%) regions.  
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

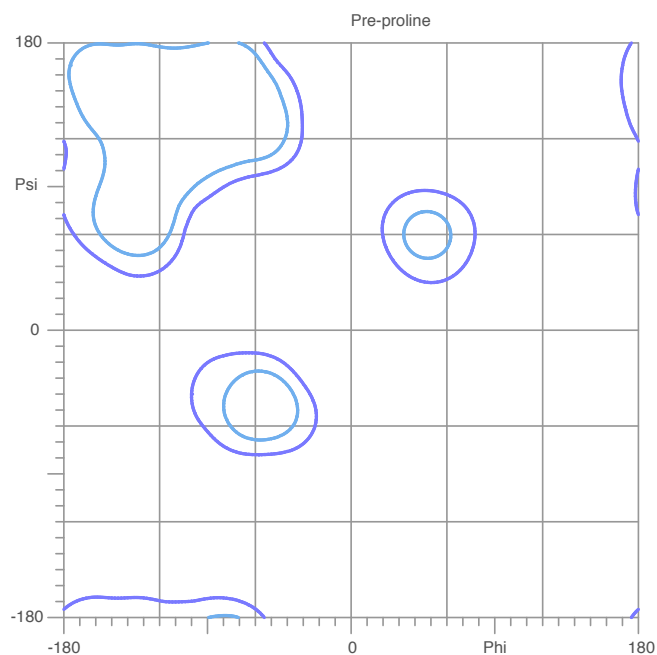
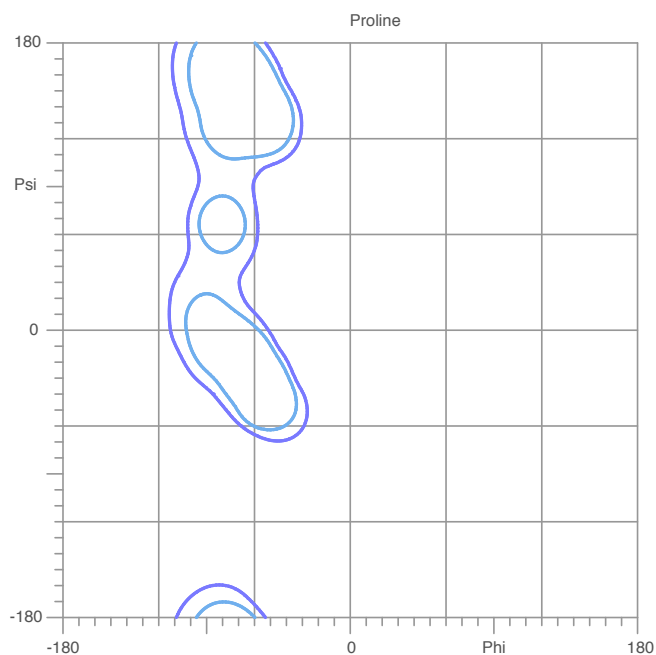
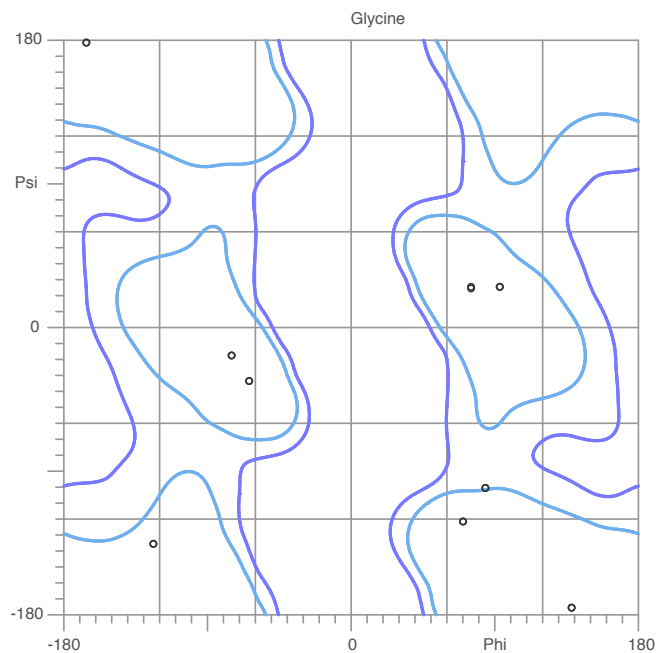
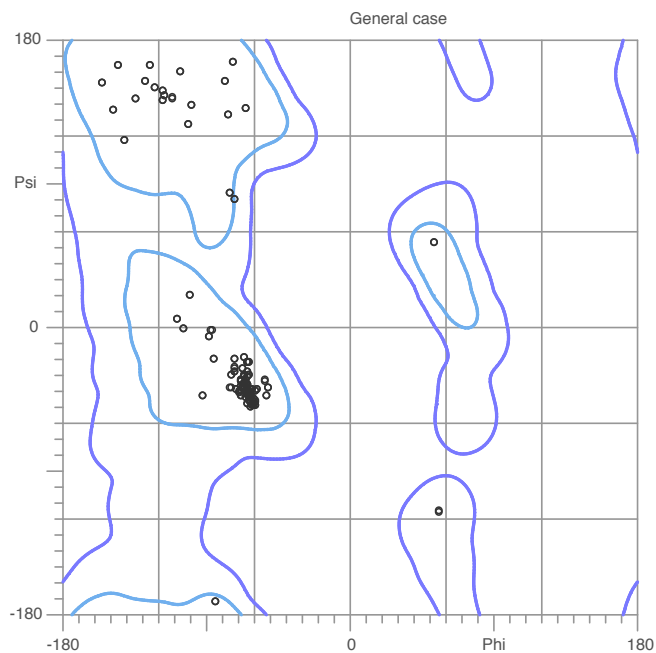
There were no outliers.

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# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 14



98.1% (208/212) of all residues were in favored (98%) regions.  
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

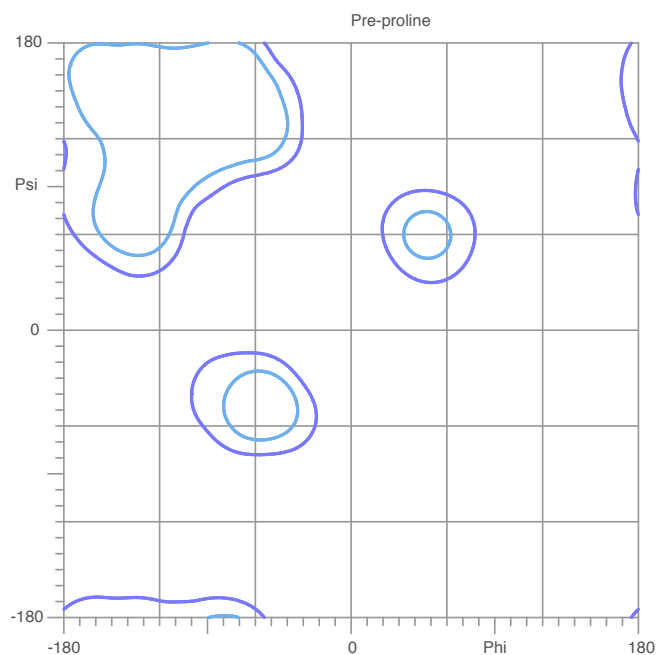
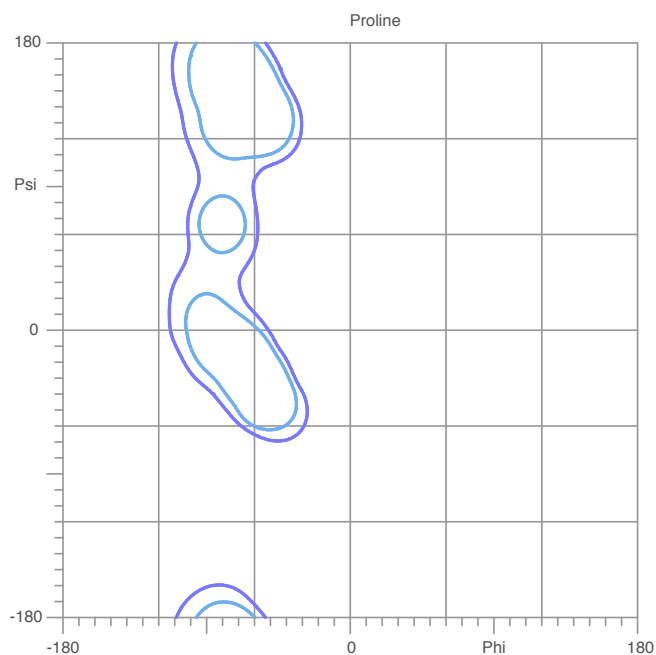
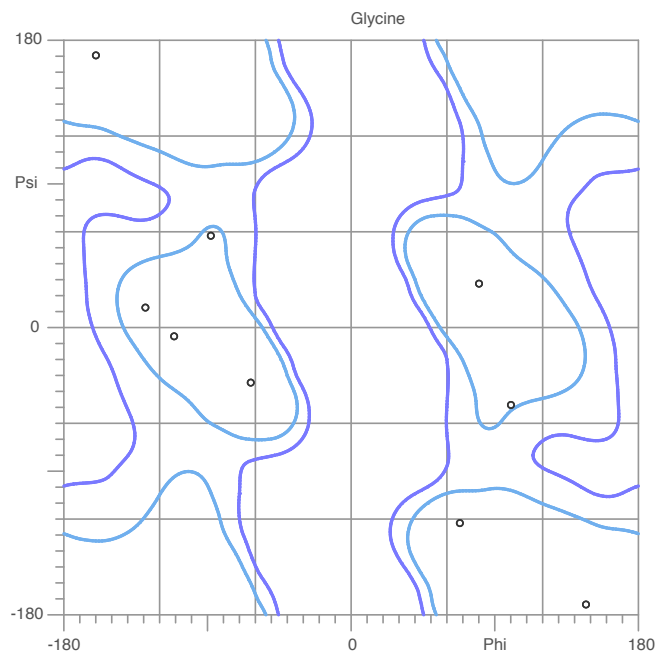
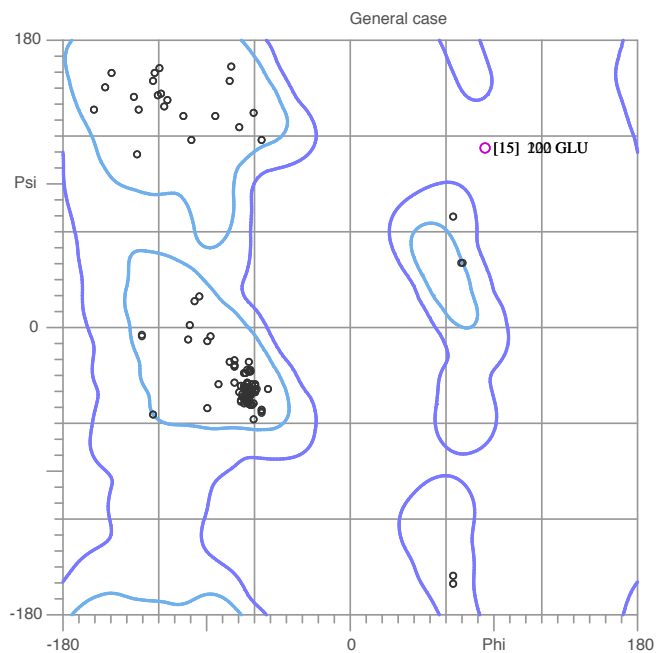
There were no outliers.

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

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# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 15

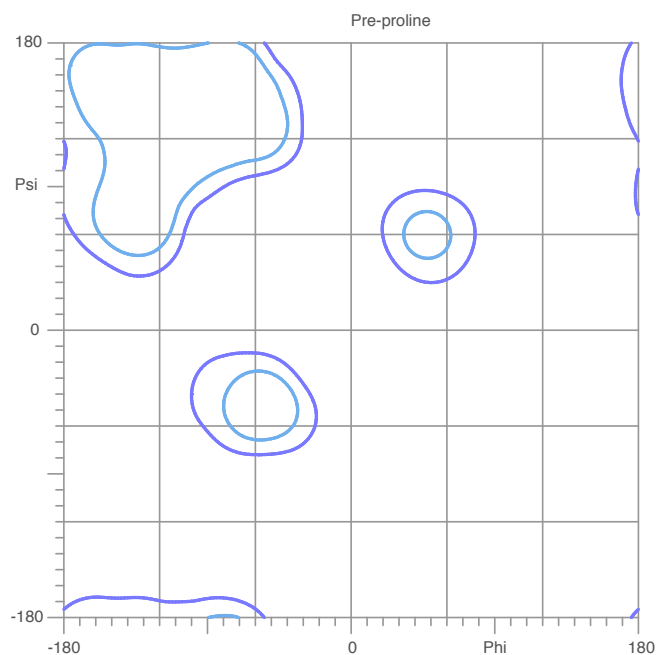
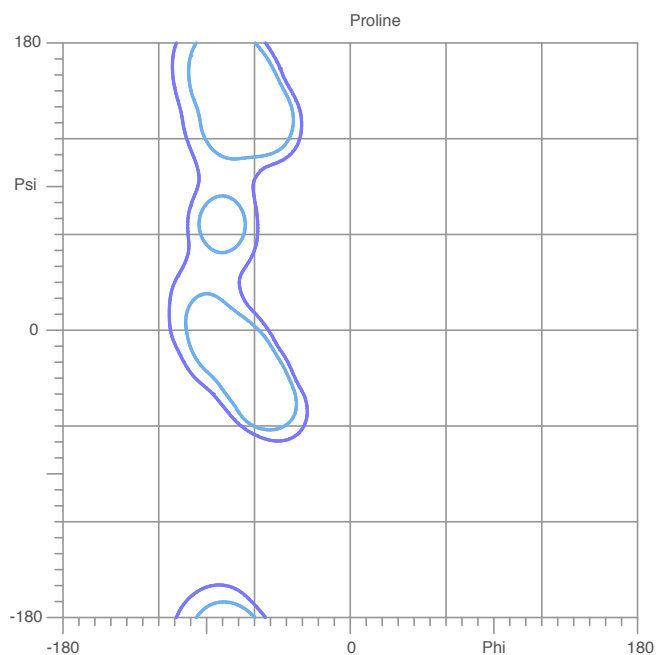
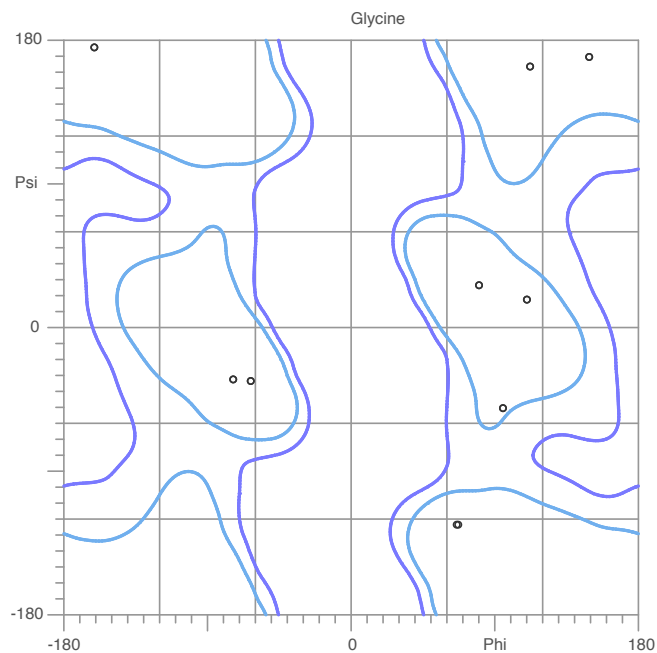
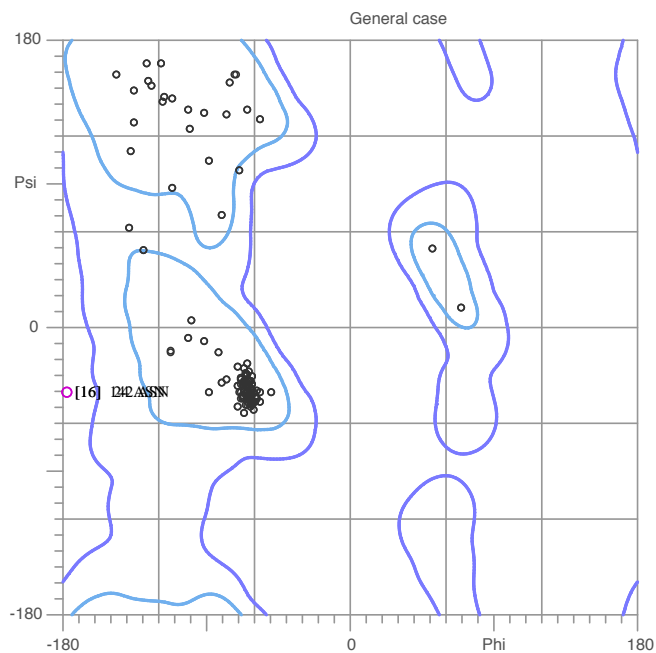


95.3% (202/212) of all residues were in favored (98%) regions.  
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[15] 102 GLU (84.5, 113.6)  
[15] 220 GLU (84.5, 113.5)

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 16



97.2% (206/212) of all residues were in favored (98%) regions.  
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

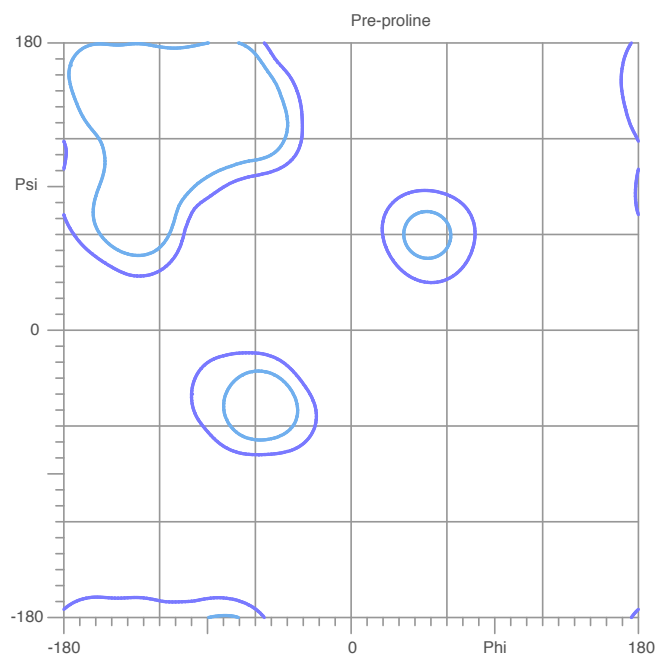
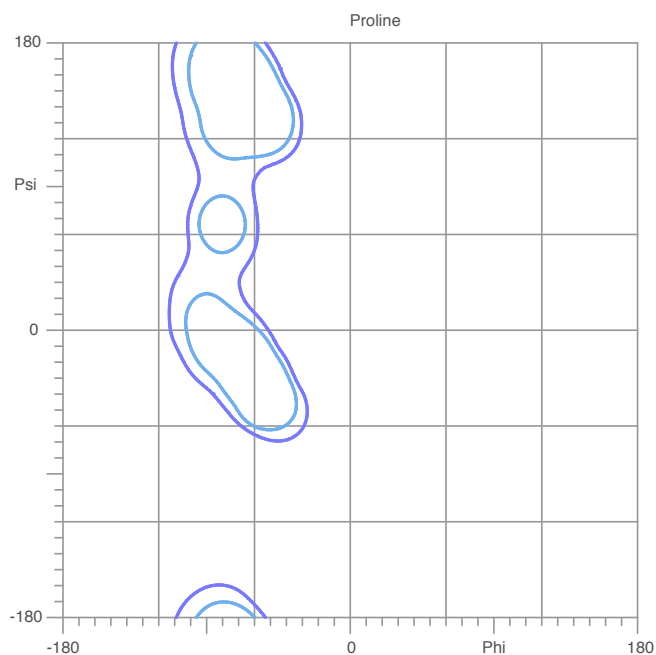
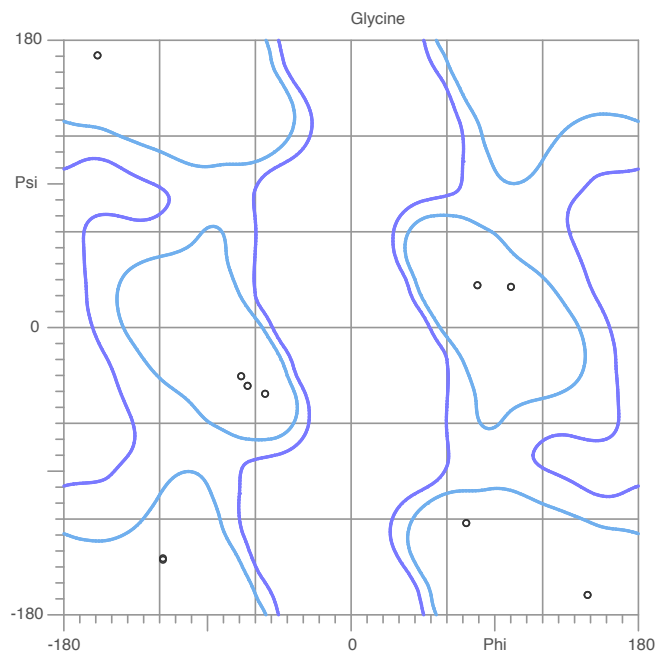
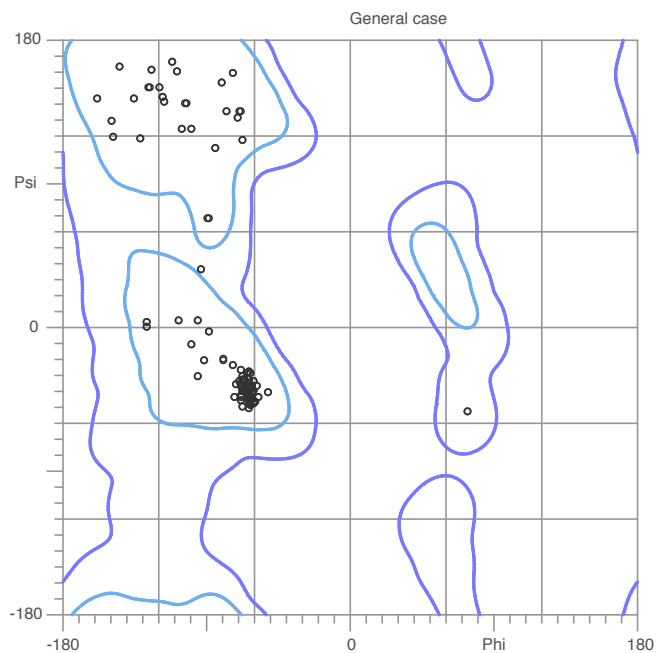
There were 2 outliers (phi, psi):

[16] 24 ASN (-178.3, -40.9)

[16] 142 ASN (-178.2, -40.9)

# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 17



98.1% (208/212) of all residues were in favored (98%) regions.  
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

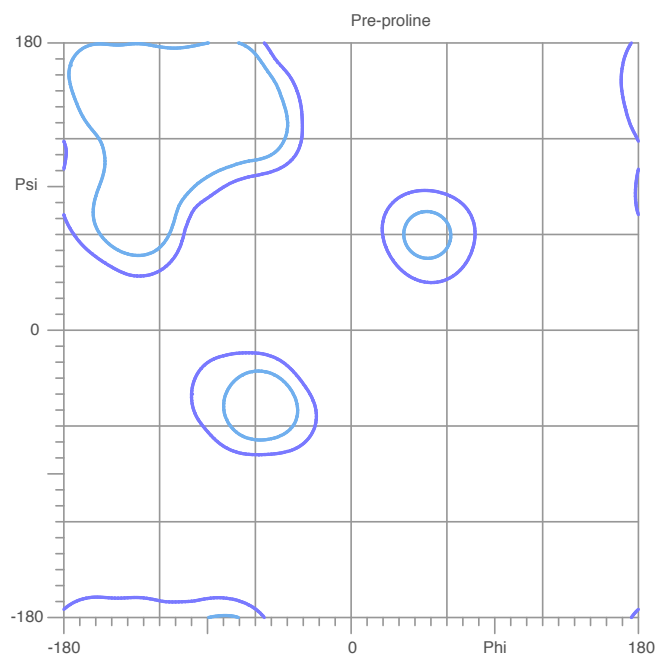
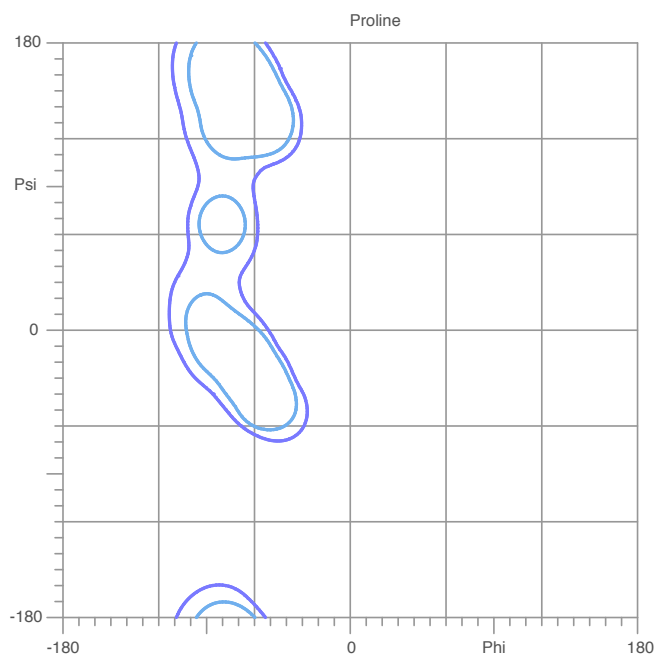
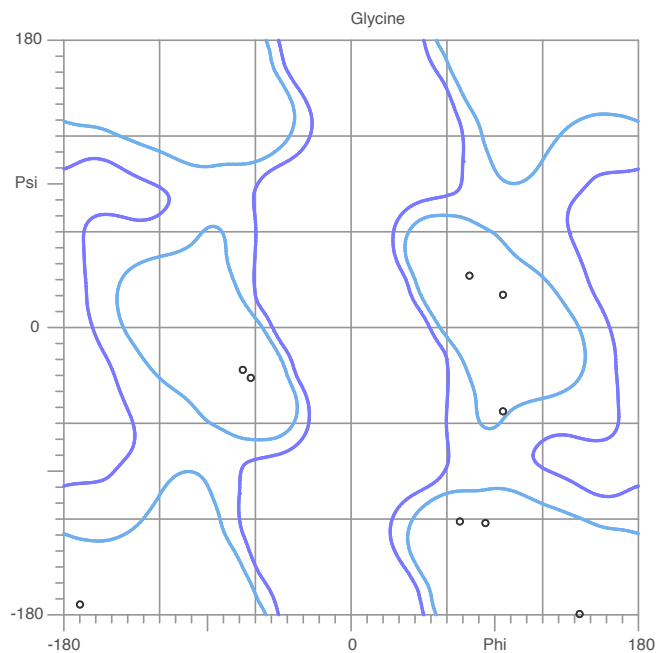
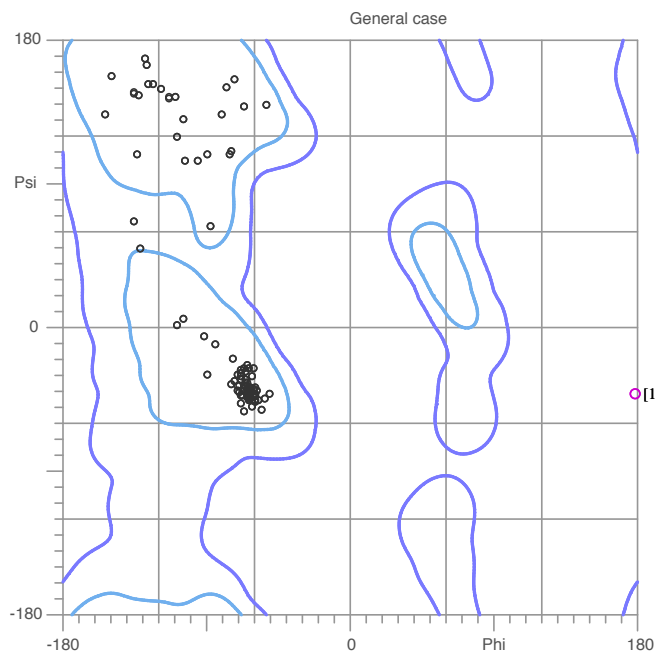
There were no outliers.

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

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# MolProbity Ramachandran analysis

MBR242E\_R3Cons\_em\_bcr3.pdb, model 18



97.2% (206/212) of all residues were in favored (98%) regions.  
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[18] 24 ASN (178.2, -41.3)

[18] 142 ASN (178.3, -41.3)