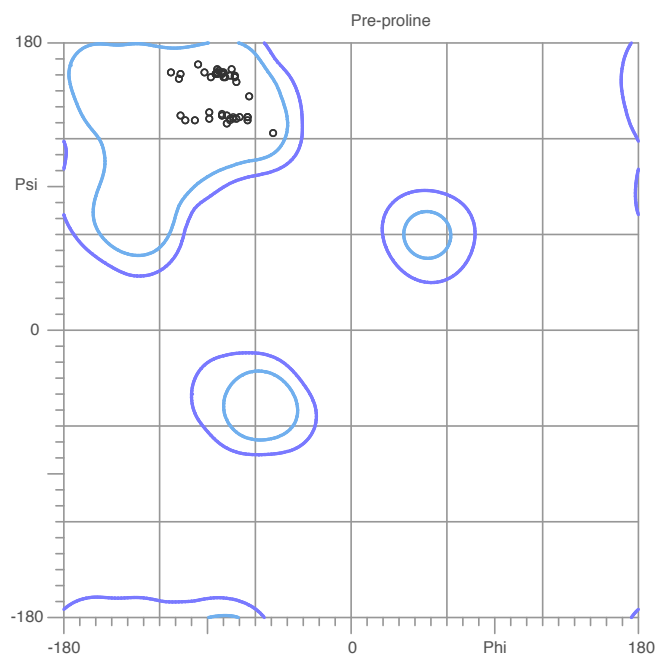
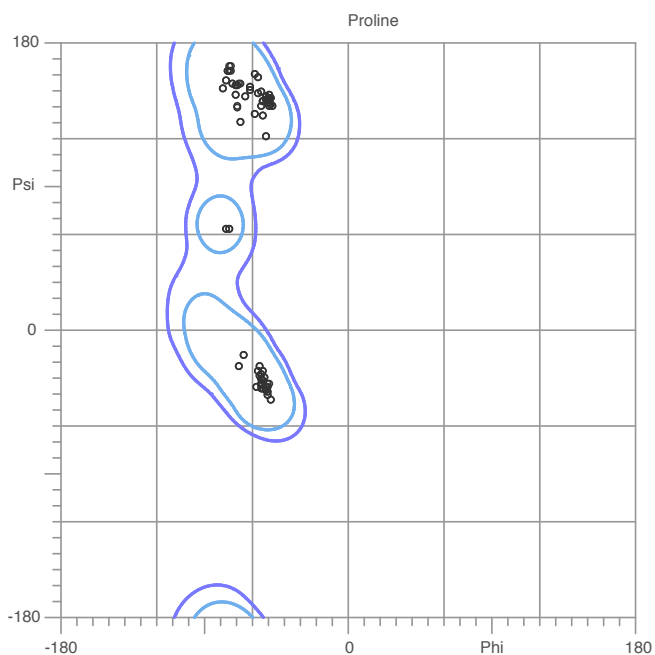
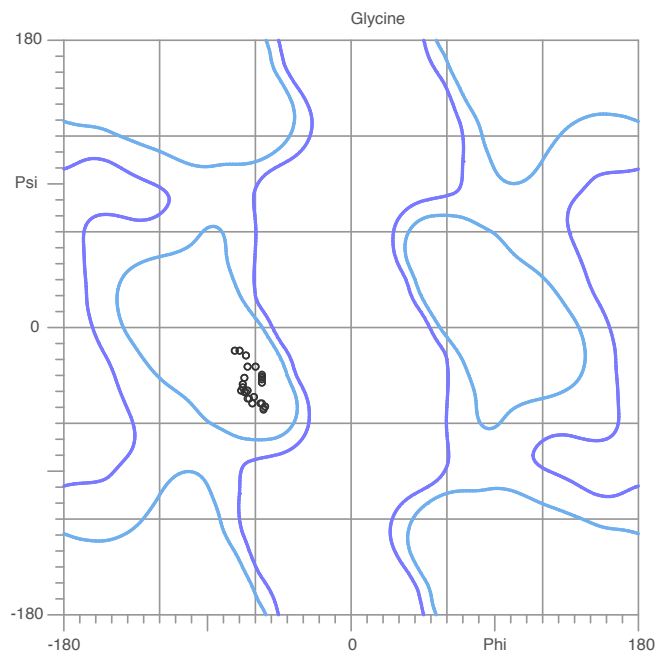
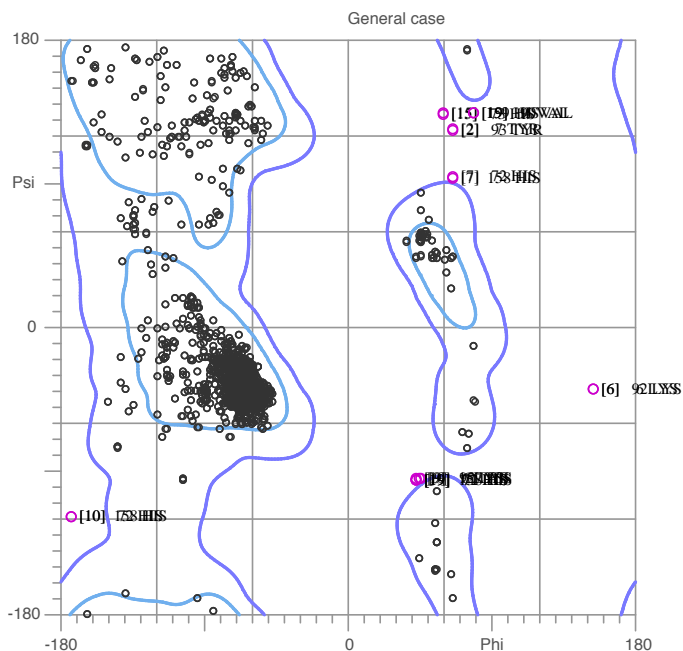


# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, all models



95.4% (2823/2960) of all residues were in favored (98%) regions.  
99.4% (2942/2960) of all residues were in allowed (>99.8%) regions.

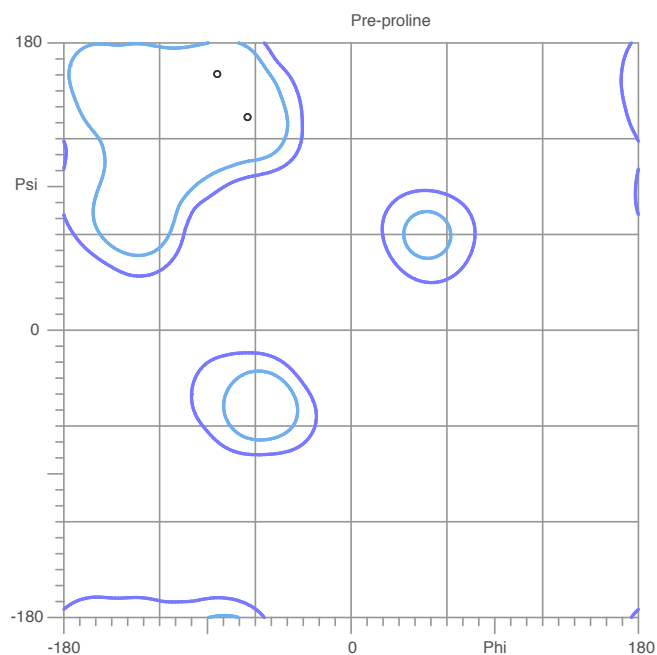
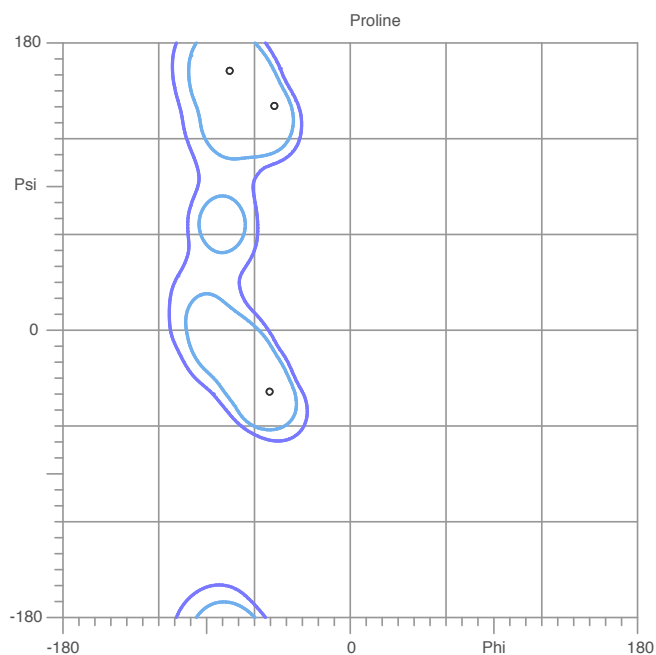
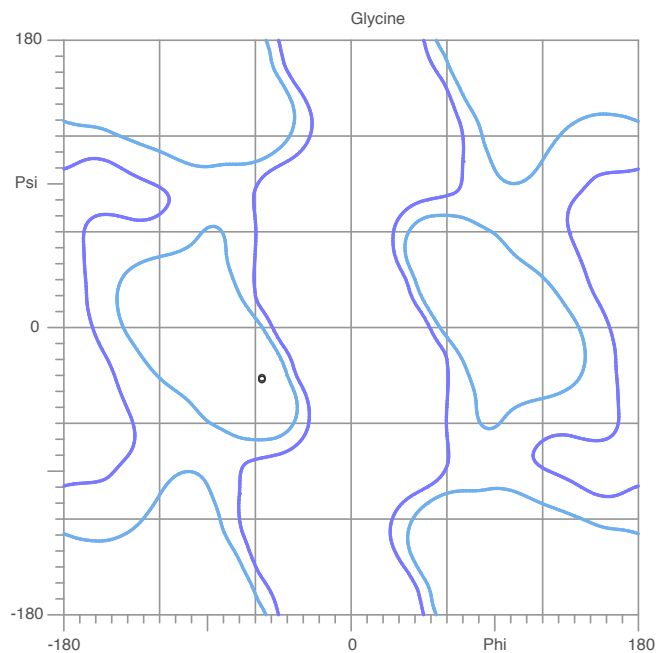
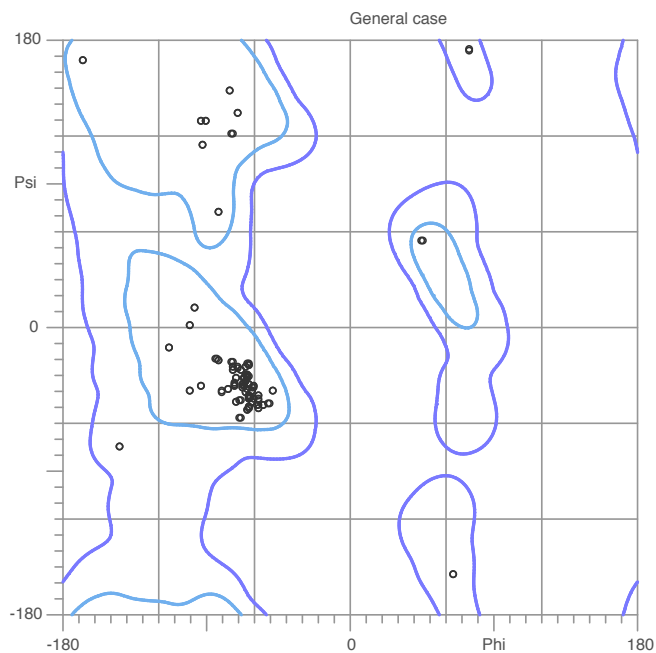
There were 18 outliers (phi, psi):

- [2] 7 TYR (65.0, 125.0)
- [2] 93 TYR (65.0, 125.0)
- [6] 6 LYS (153.9, -38.1)
- [6] 92 LYS (153.9, -38.2)
- [7] 72 HIS (65.1, 95.0)
- [7] 158 HIS (65.1, 95.0)
- [9] 6 LYS (44.9, -94.9)

- [9] 92 LYS (45.0, -94.9)
- [10] 72 HIS (-175.0, -118.8)
- [10] 158 HIS (-175.0, -118.8)
- [15] 73 HIS (59.7, 135.0)
- [15] 159 HIS (59.7, 135.1)
- [19] 4 VAL (78.5, 135.0)
- [19] 71 HIS (42.7, -95.0)
- [19] 72 HIS (42.8, -95.0)
- [19] 90 VAL (78.5, 135.0)
- [19] 157 HIS (42.6, -95.0)
- [19] 158 HIS (42.8, -95.1)

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 1



95.9% (142/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

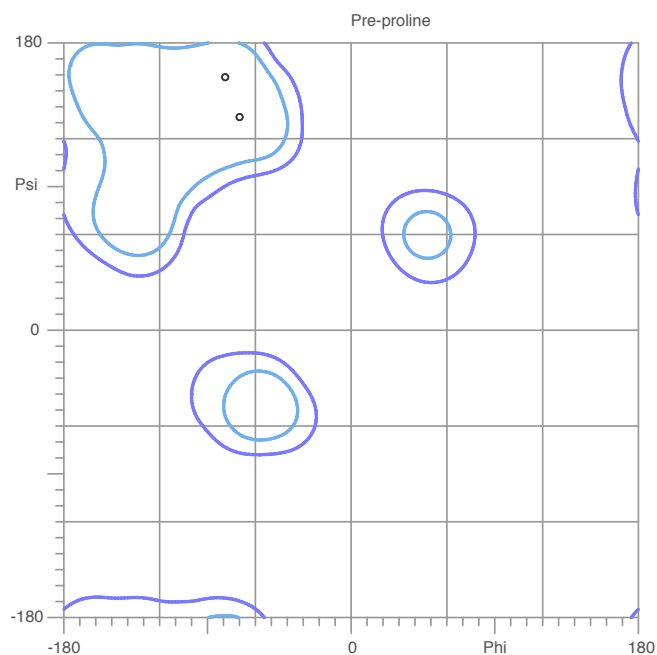
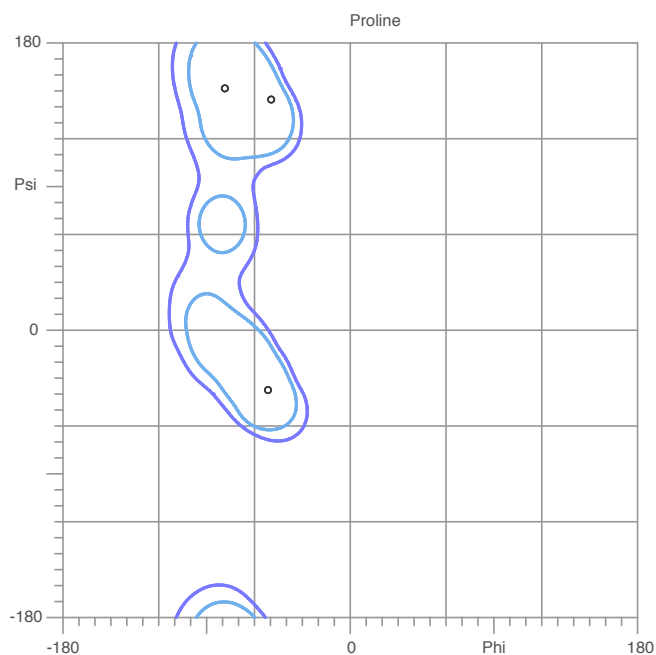
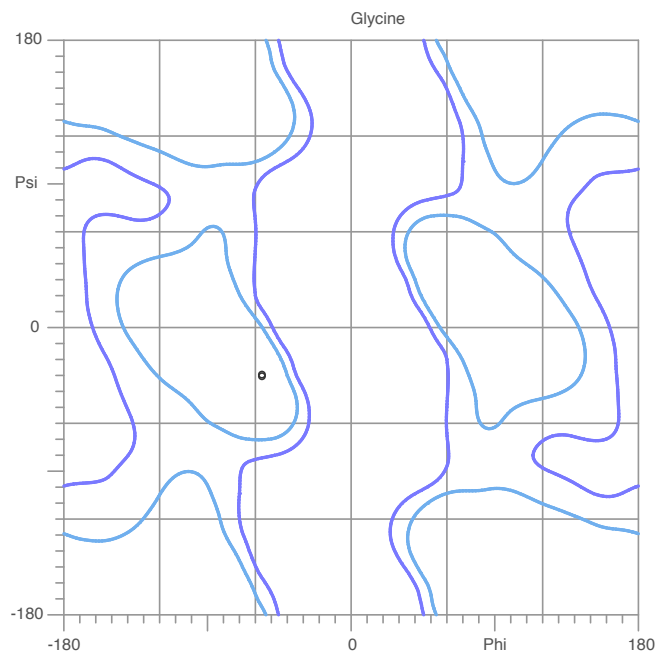
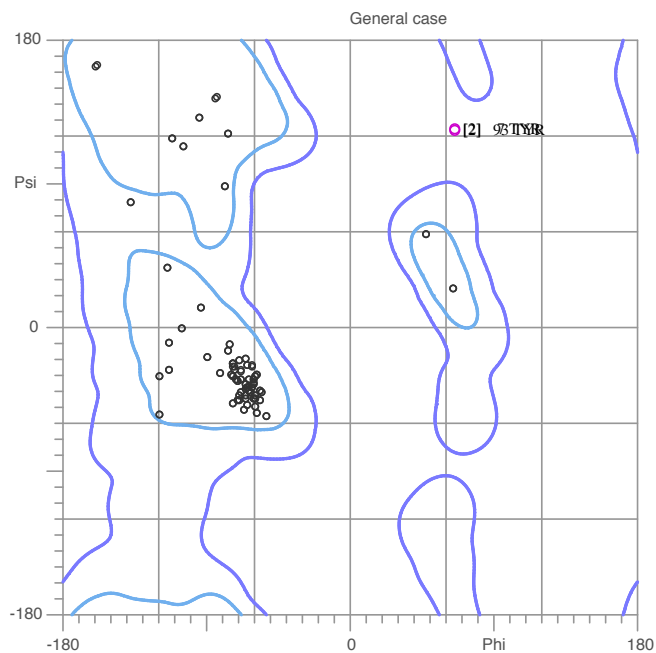
There were no outliers.

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

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 2



97.3% (144/148) of all residues were in favored (98%) regions.  
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

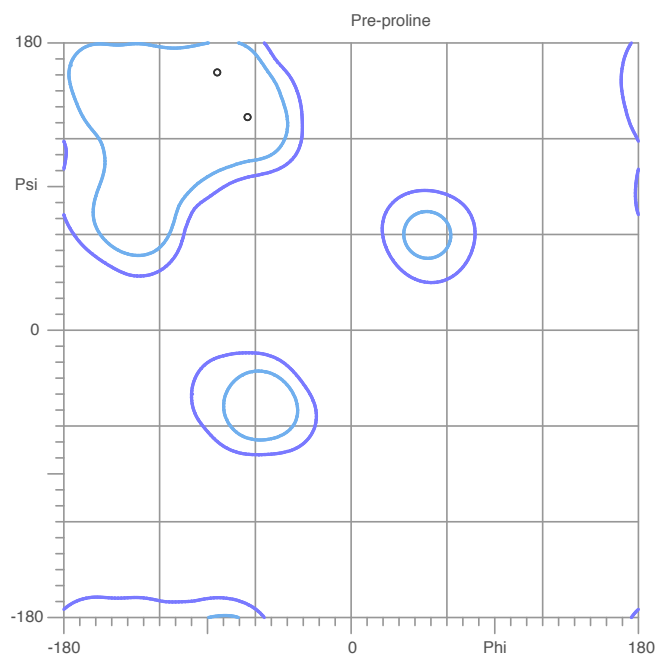
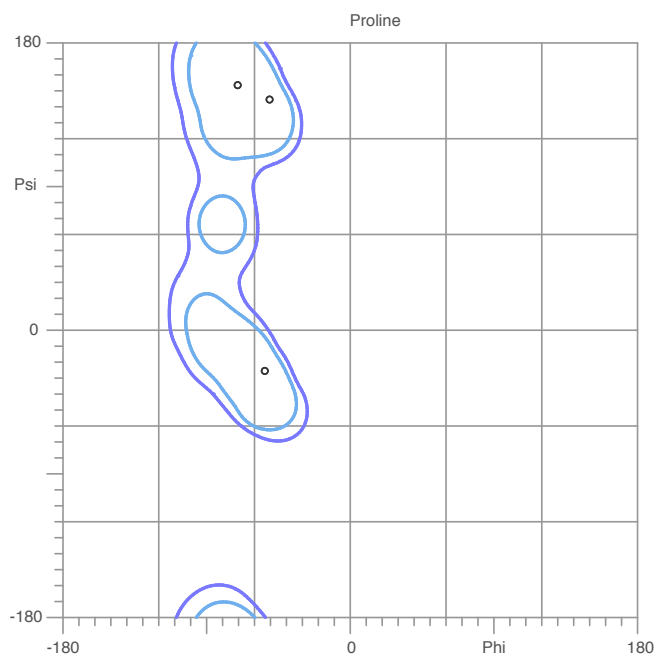
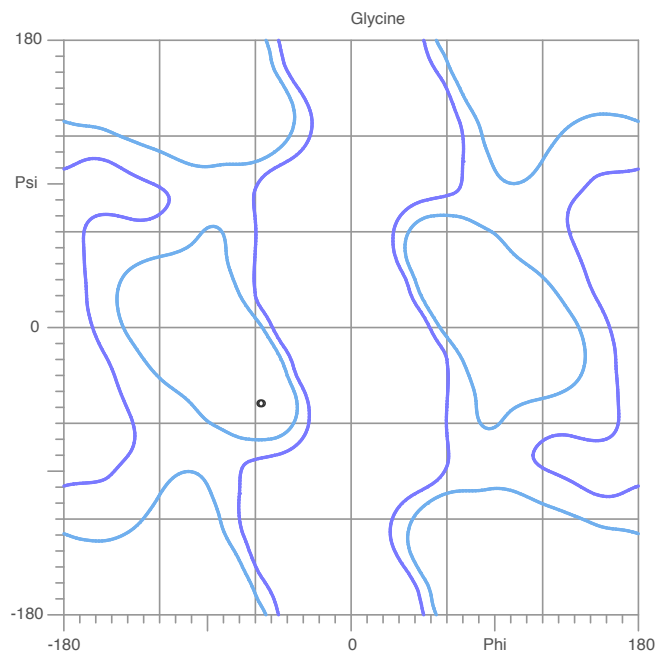
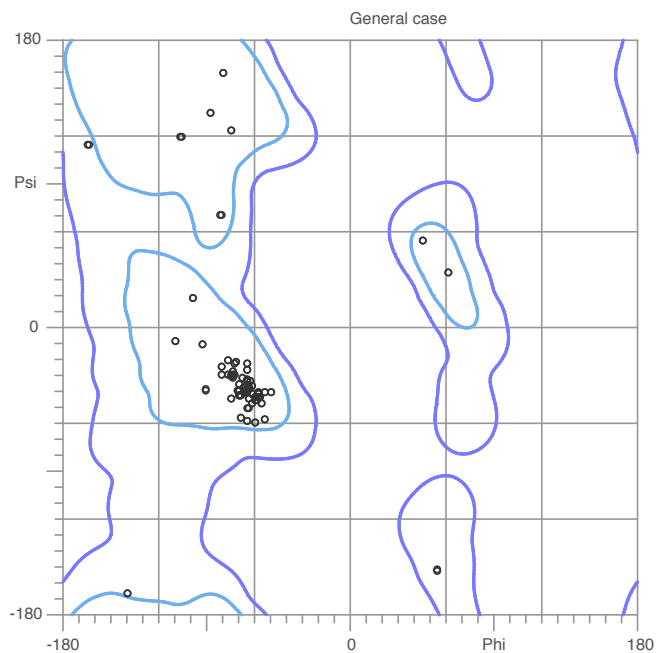
There were 2 outliers (phi, psi):

[2] 7 TYR (65.0, 125.0)

[2] 93 TYR (65.0, 125.0)

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 3

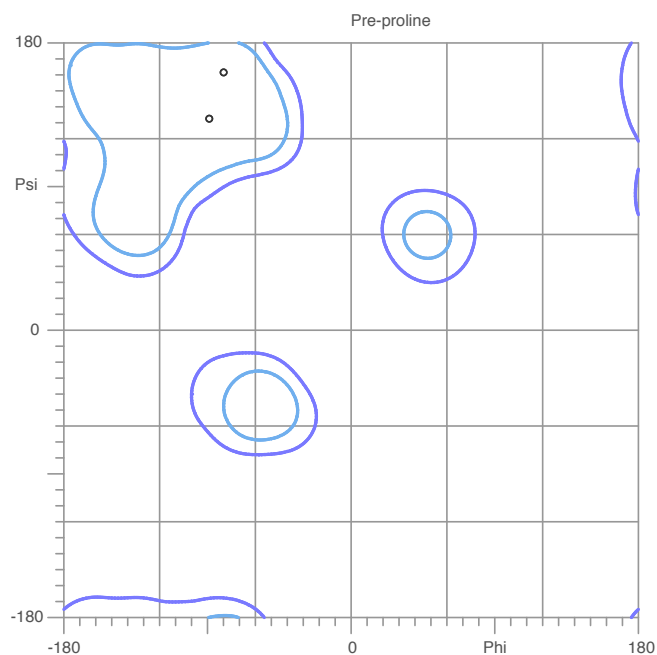
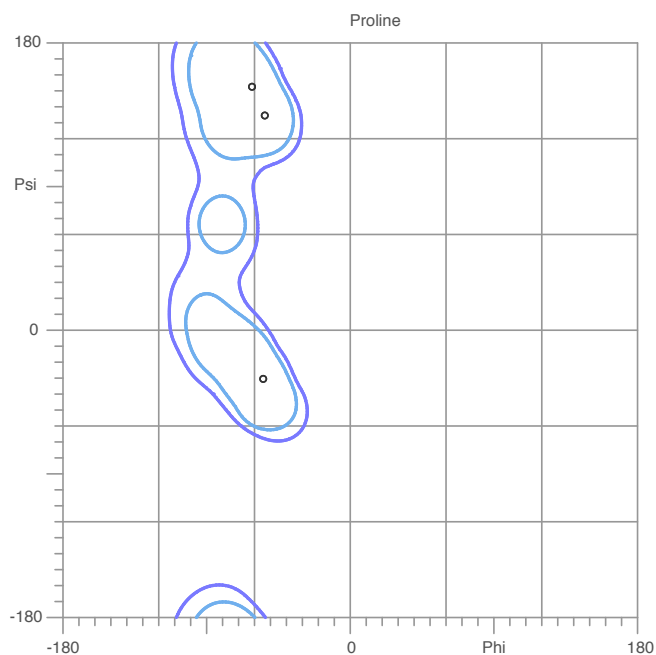
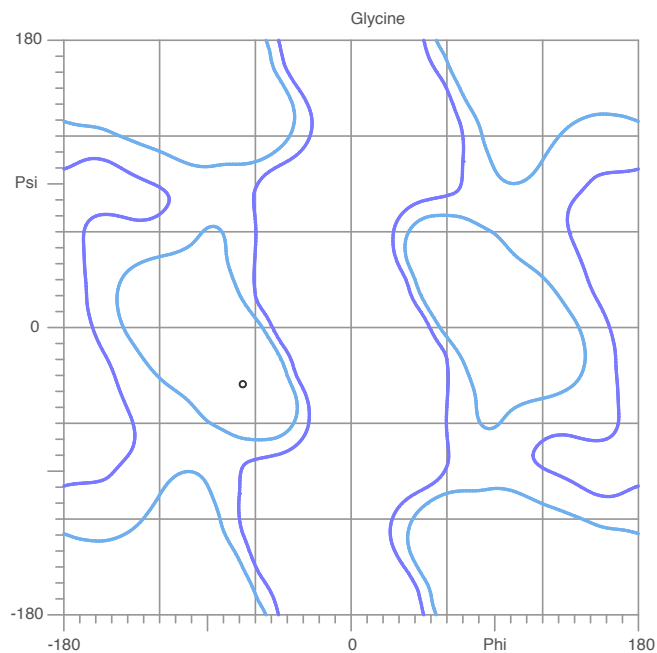
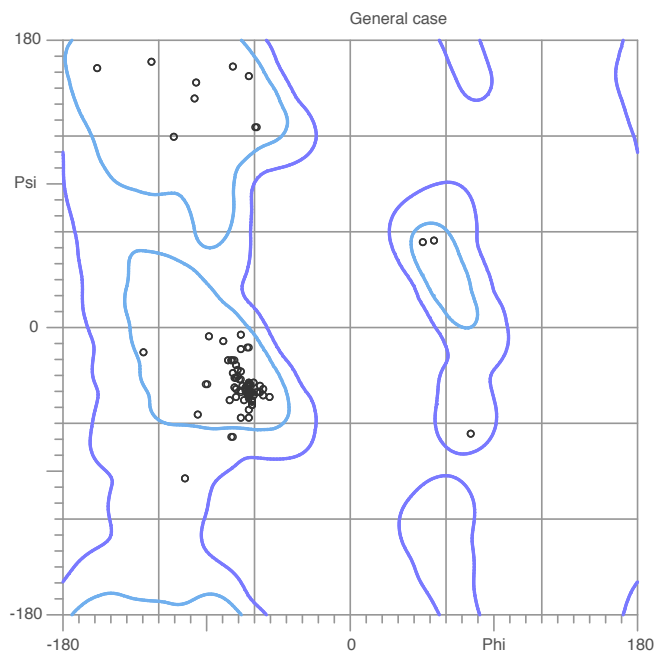


95.9% (142/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 4



95.9% (142/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

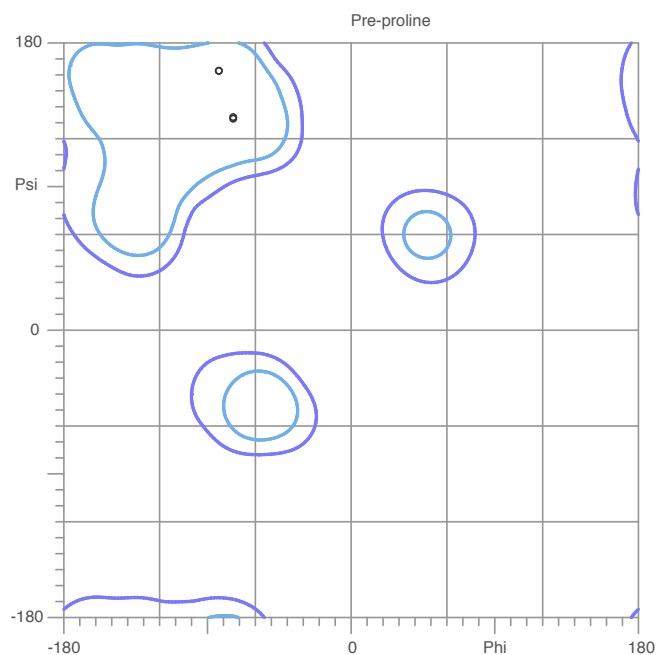
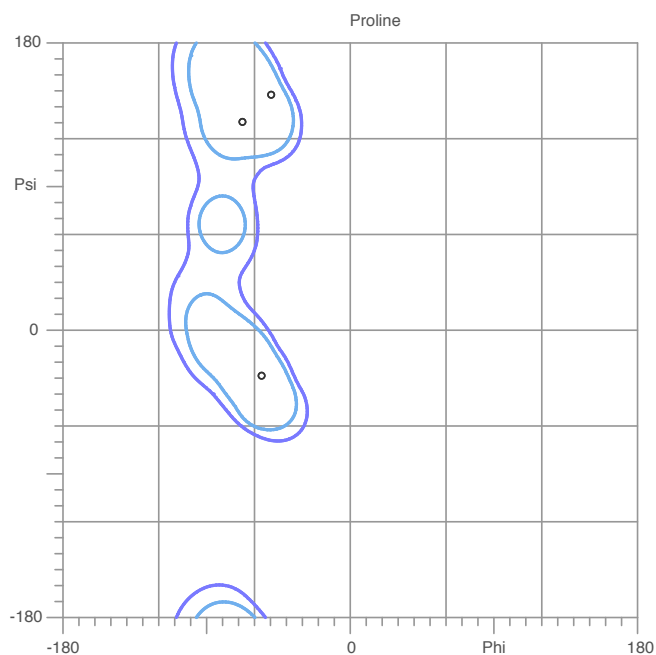
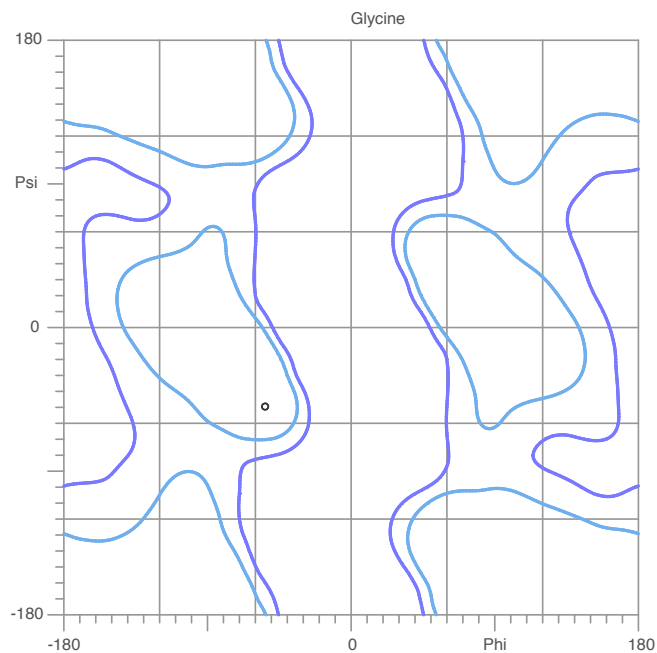
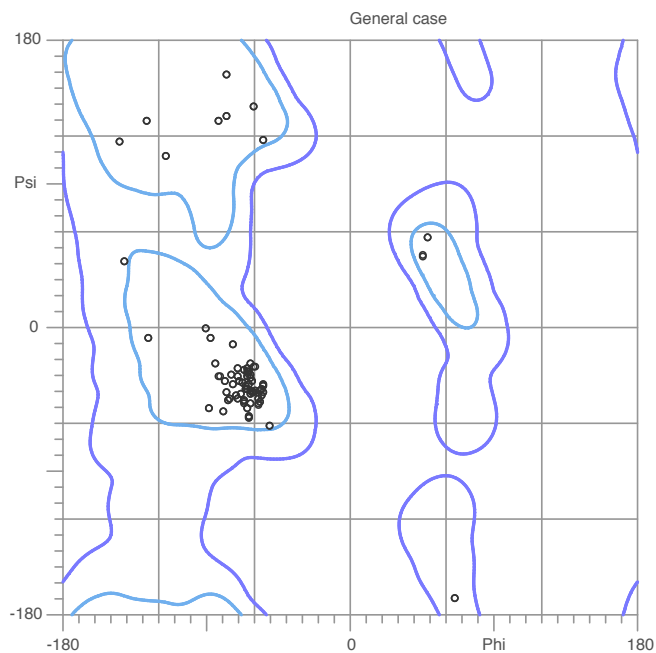
There were no outliers.

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

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 5



97.3% (144/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

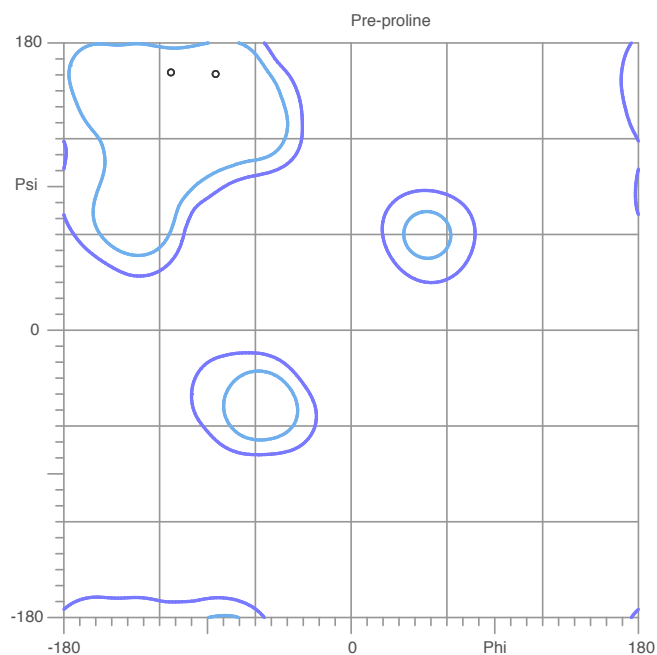
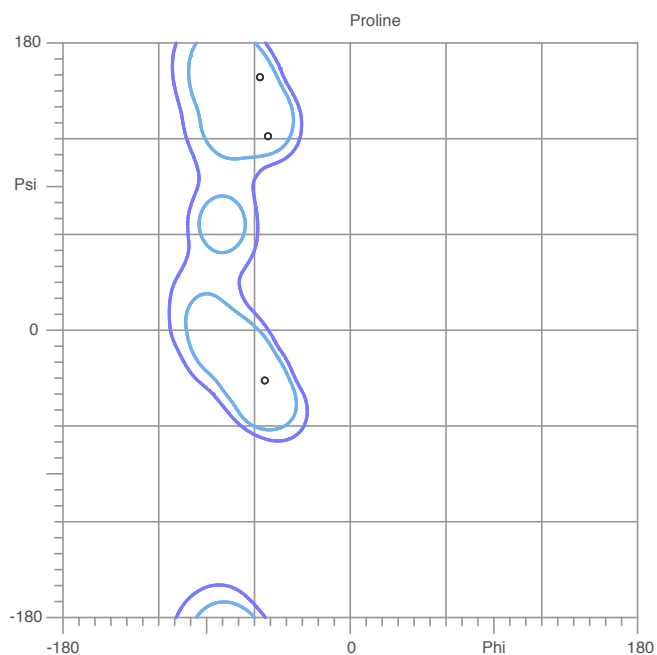
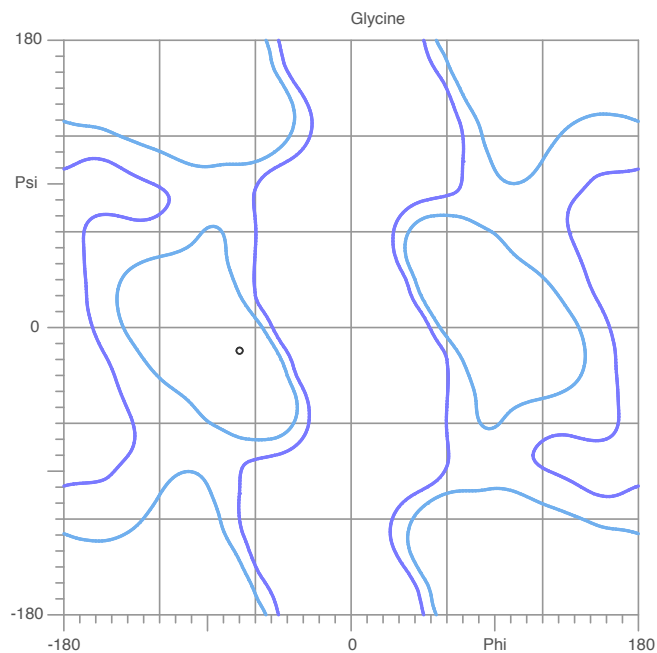
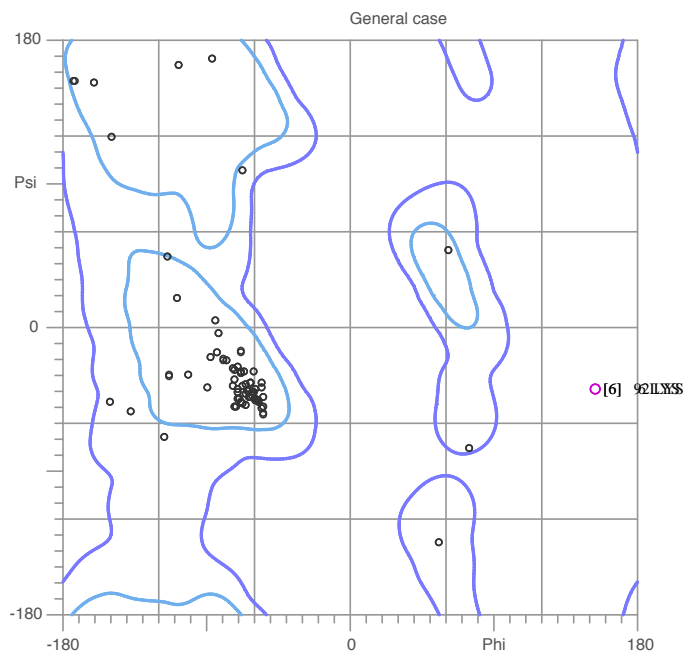
There were no outliers.

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

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 6



89.9% (133/148) of all residues were in favored (98%) regions.  
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

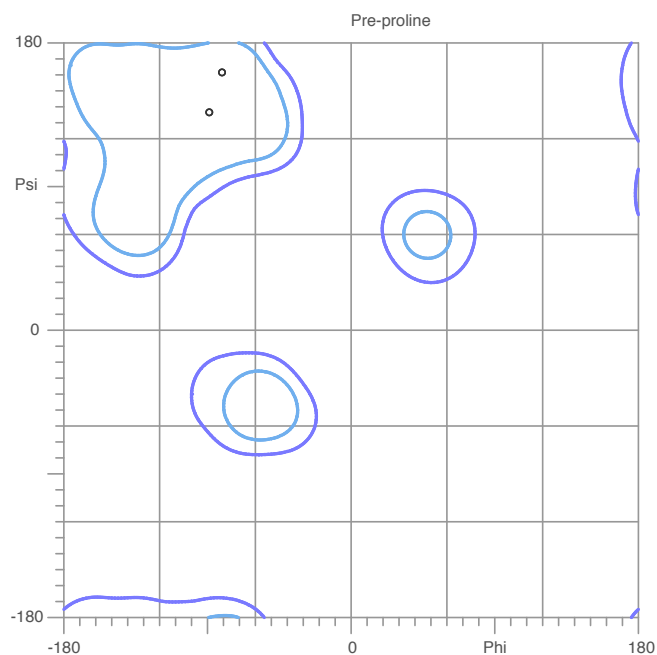
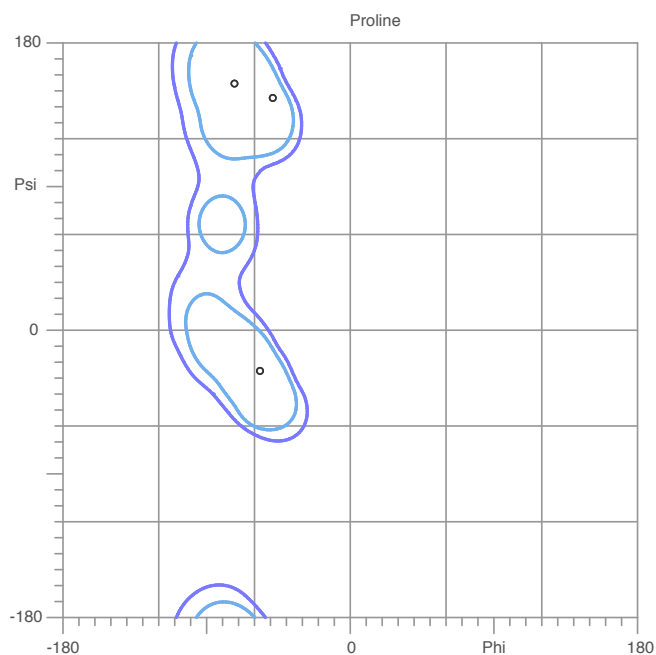
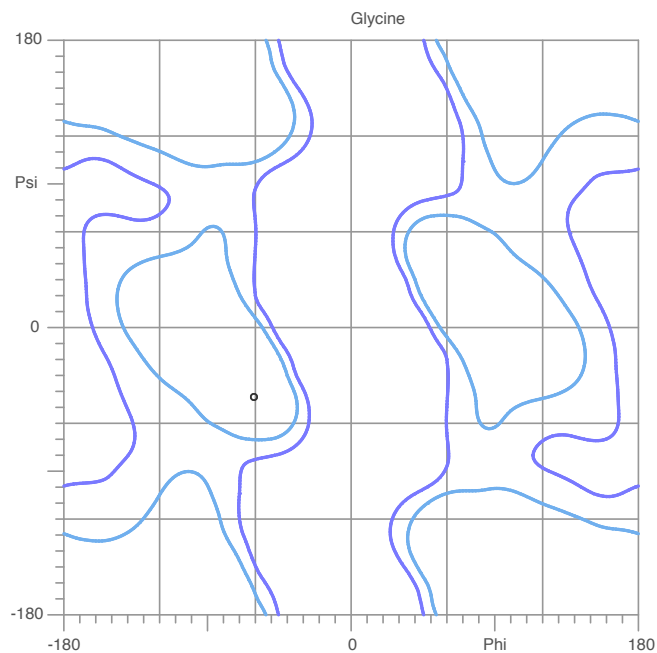
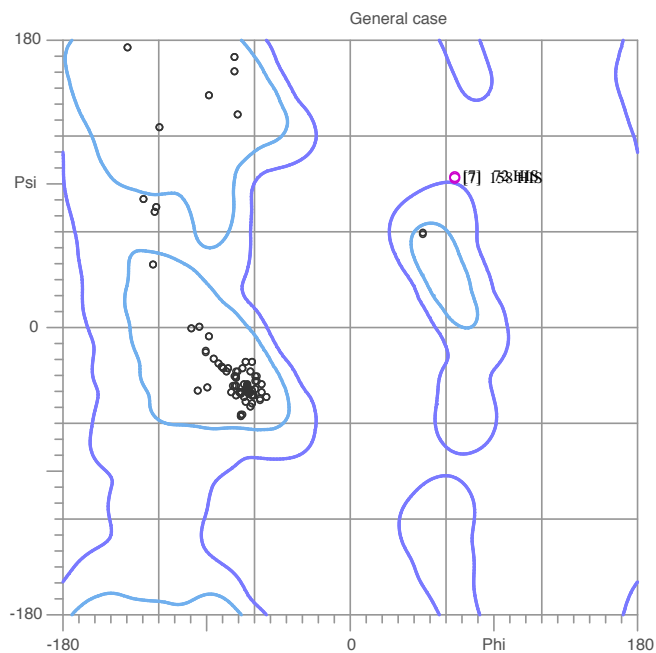
There were 2 outliers (phi, psi):

[6] 6 LYS (153.9, -38.1)

[6] 92 LYS (153.9, -38.2)

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 7



94.6% (140/148) of all residues were in favored (98%) regions.  
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

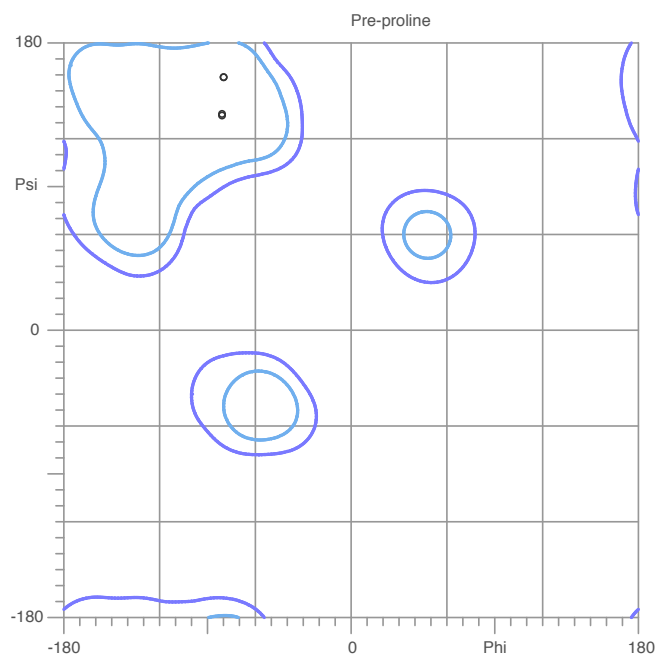
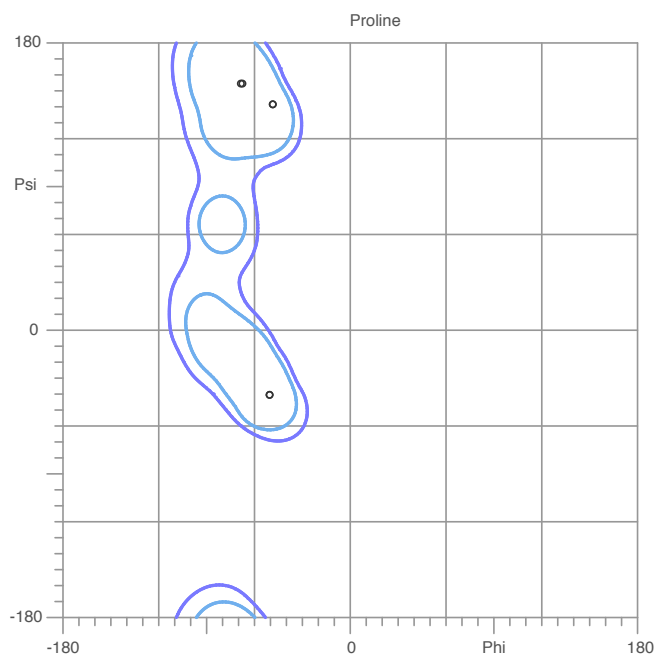
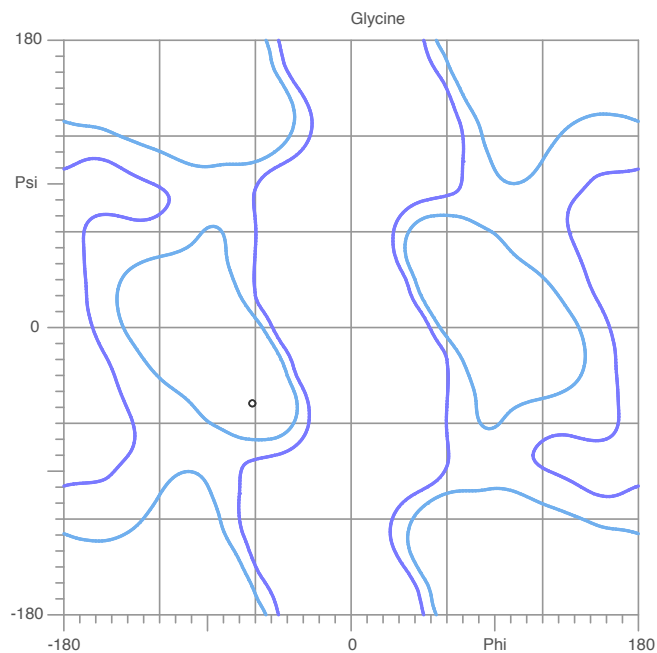
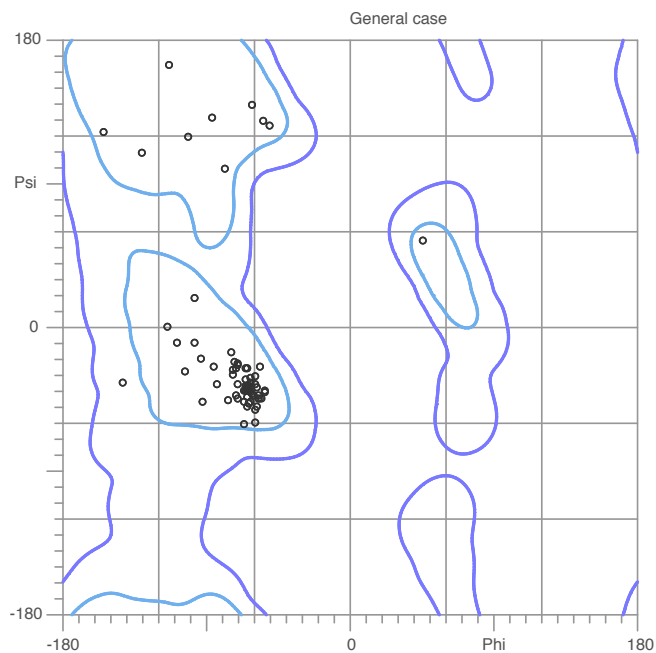
There were 2 outliers (phi, psi):

[7] 72 HIS (65.1, 95.0)

[7] 158 HIS (65.1, 95.0)

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 8



98.6% (146/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

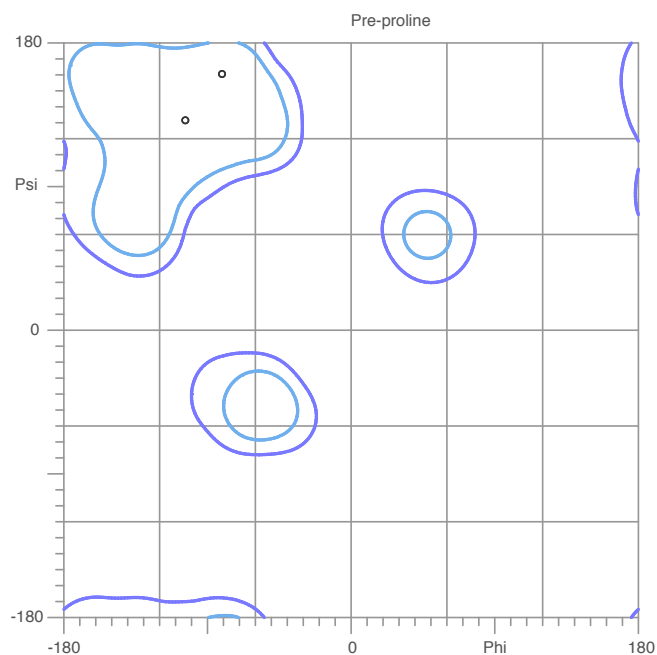
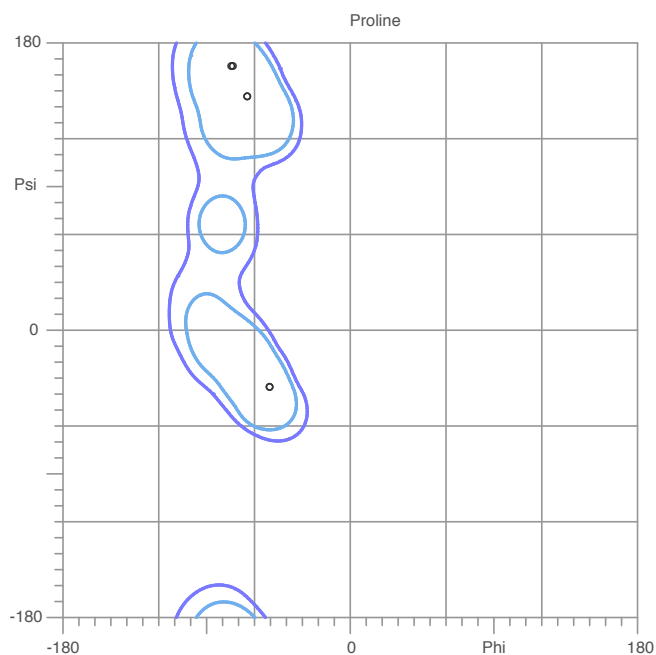
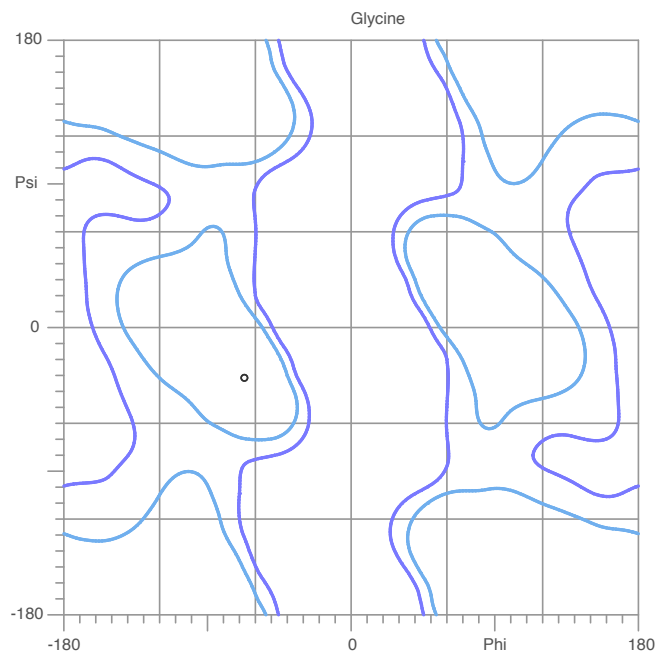
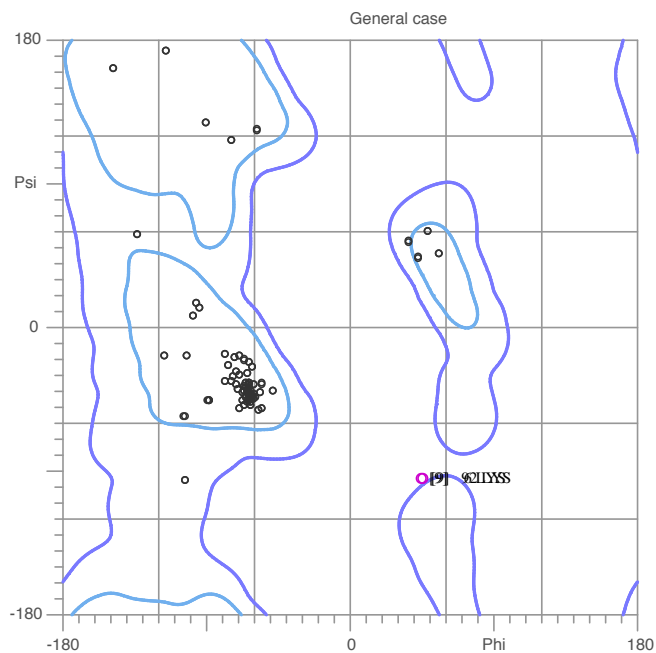
There were no outliers.

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 9



94.6% (140/148) of all residues were in favored (98%) regions.  
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

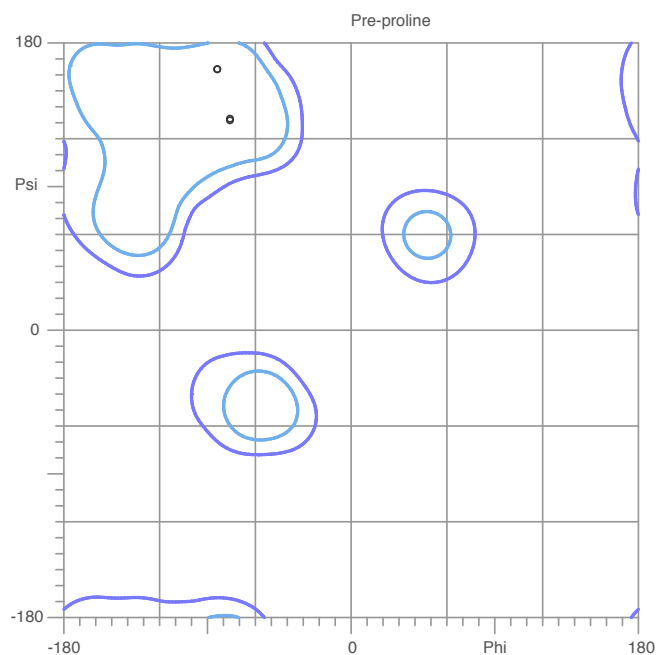
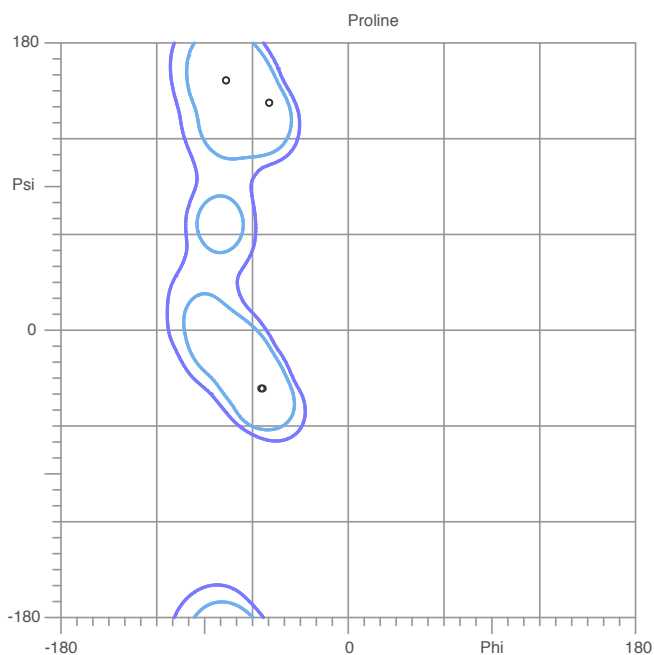
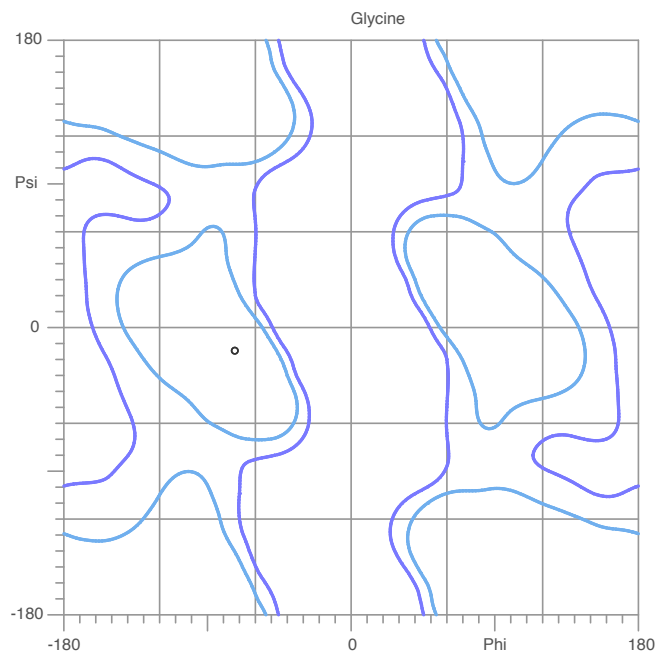
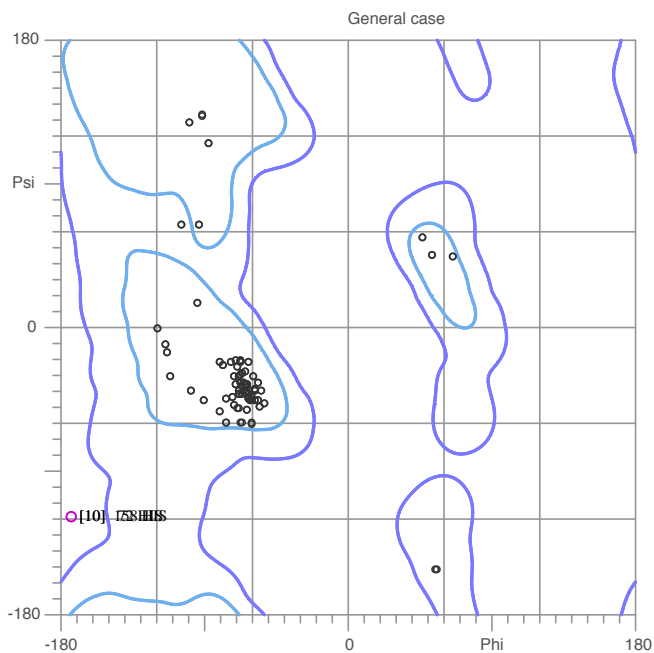
There were 2 outliers (phi, psi):

[9] 6 LYS (44.9, -94.9)

[9] 92 LYS (45.0, -94.9)

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 10



95.9% (142/148) of all residues were in favored (98%) regions.  
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

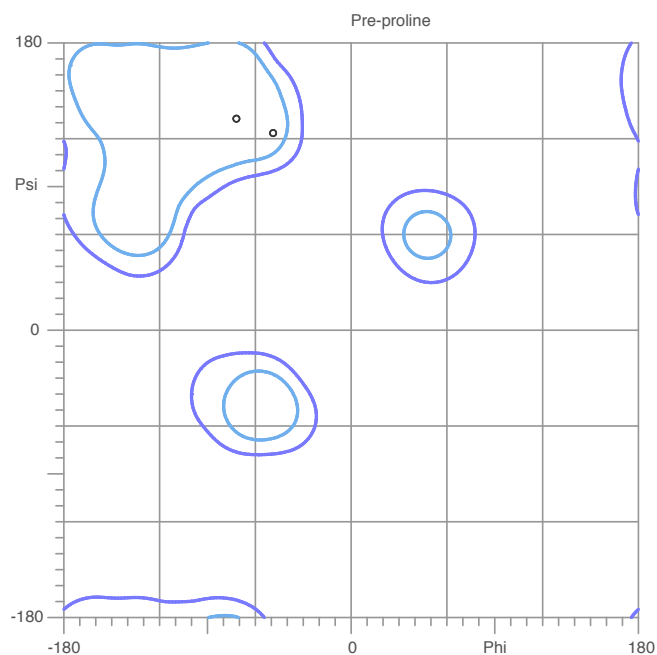
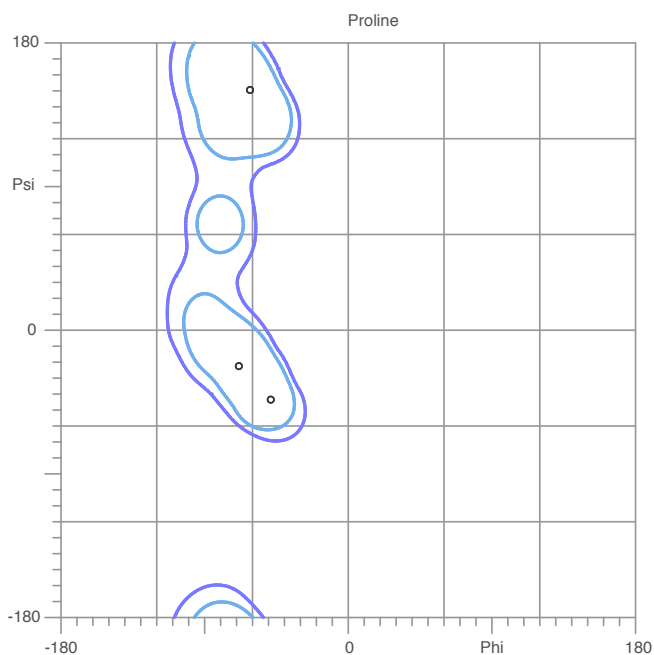
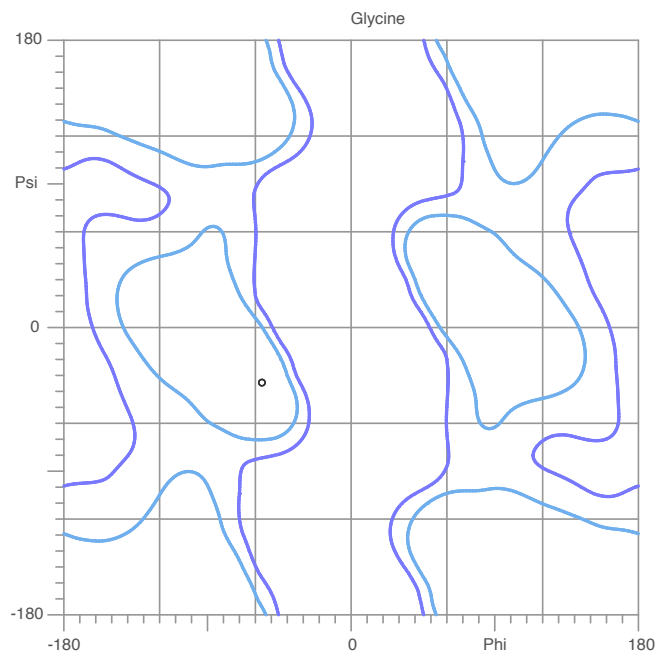
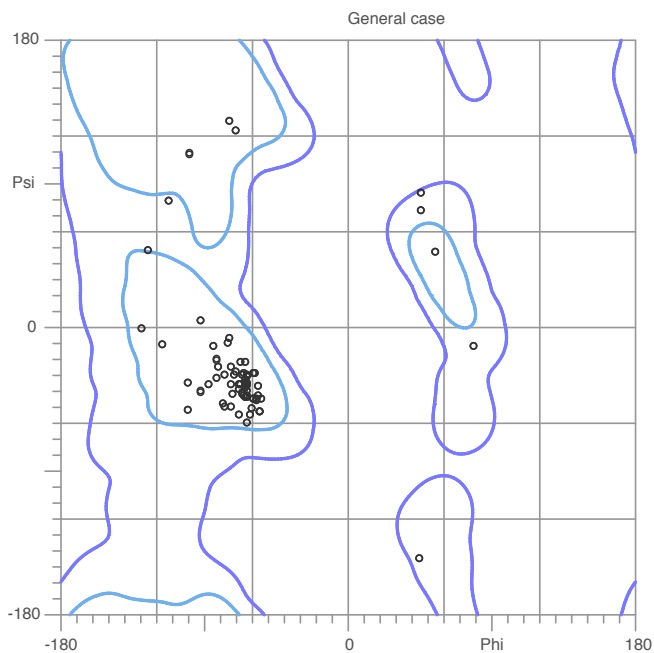
There were 2 outliers (phi, psi):

[10] 72 HIS (-175.0, -118.8)

[10] 158 HIS (-175.0, -118.8)

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 11



91.9% (136/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

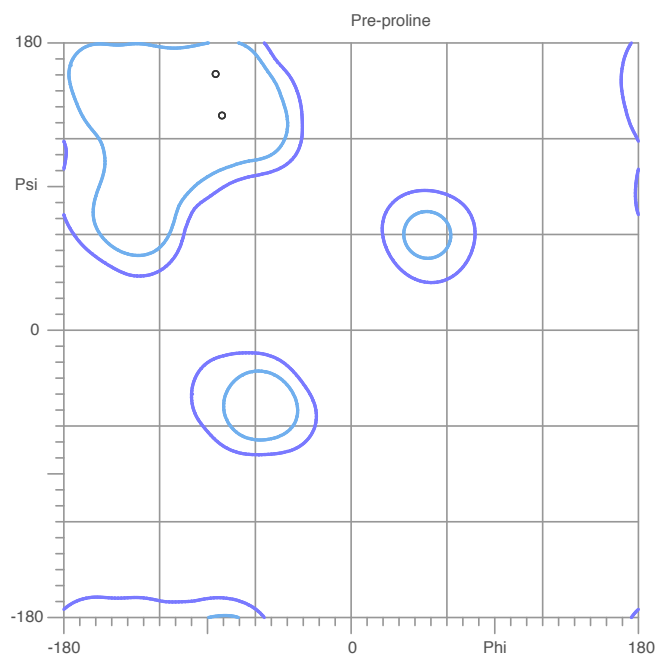
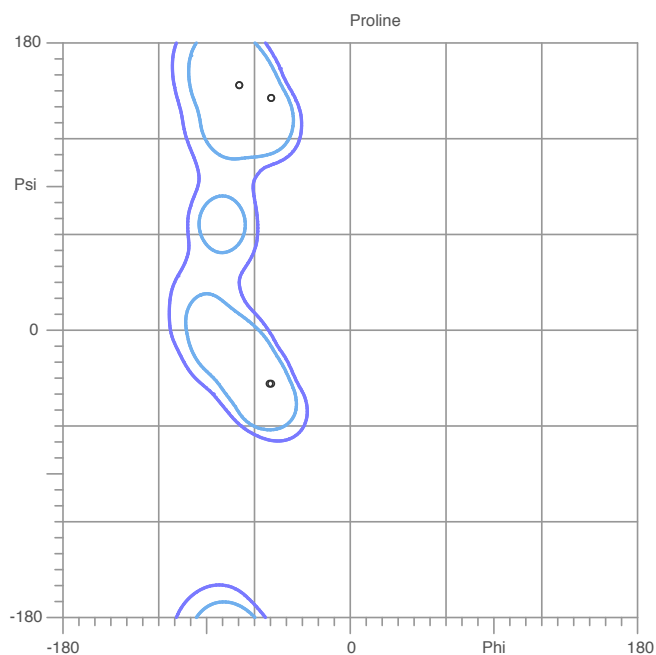
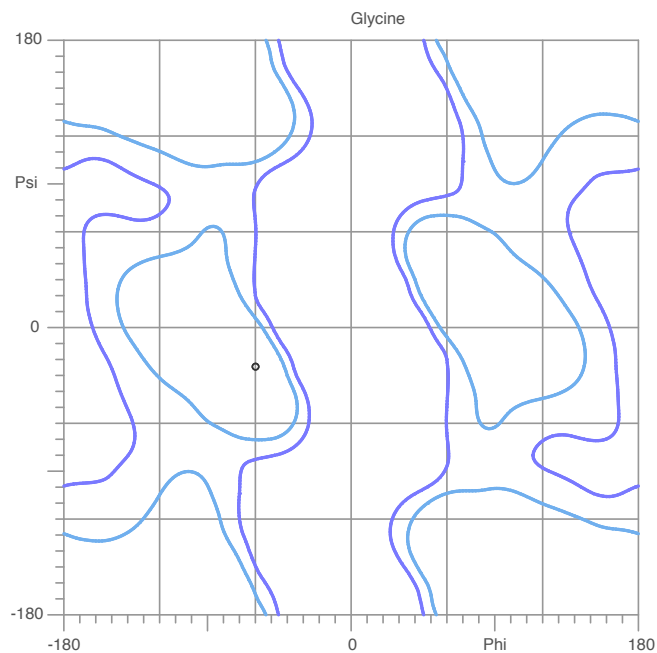
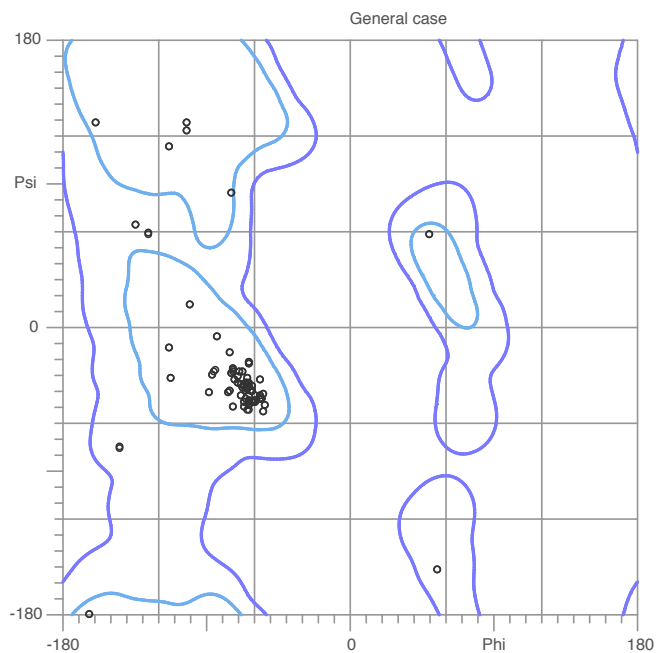
There were no outliers.

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 12



94.6% (140/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

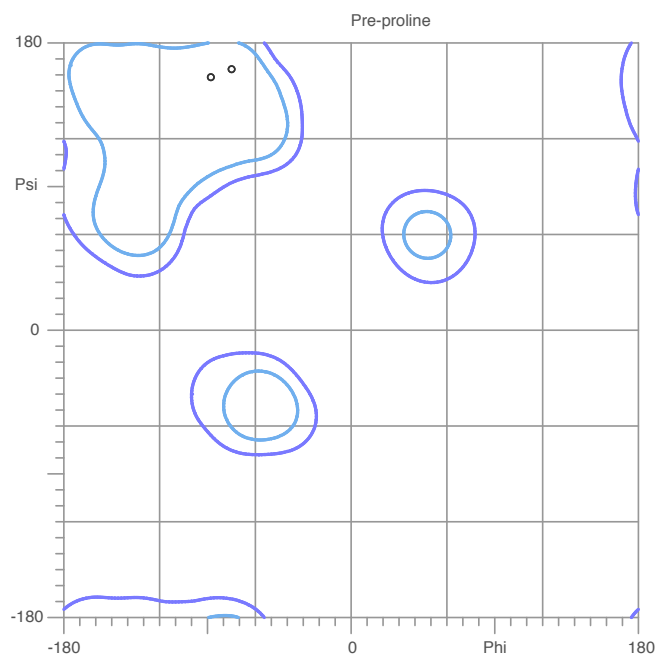
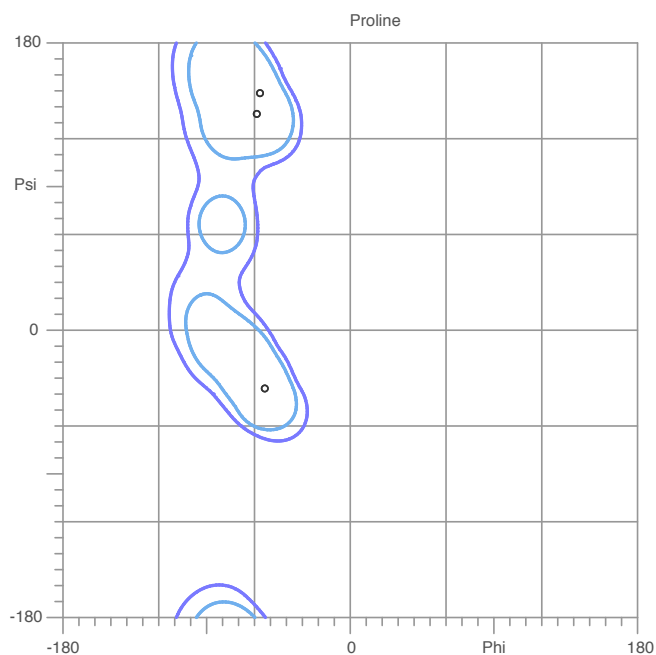
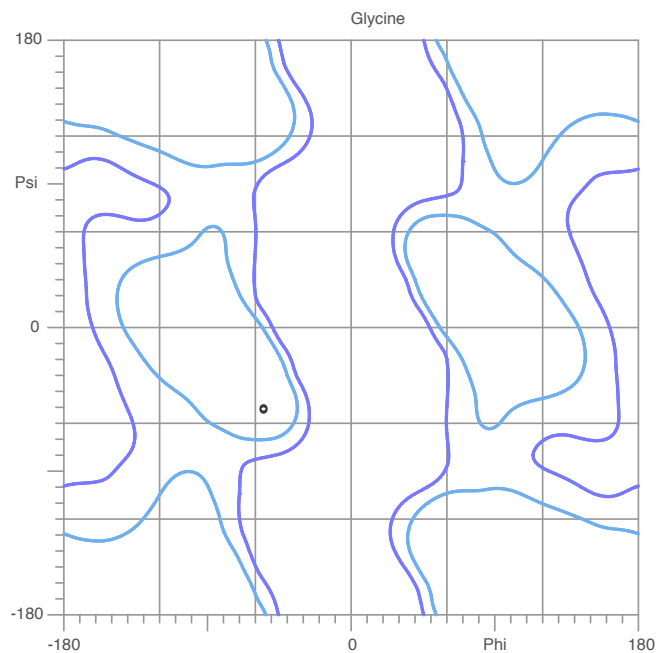
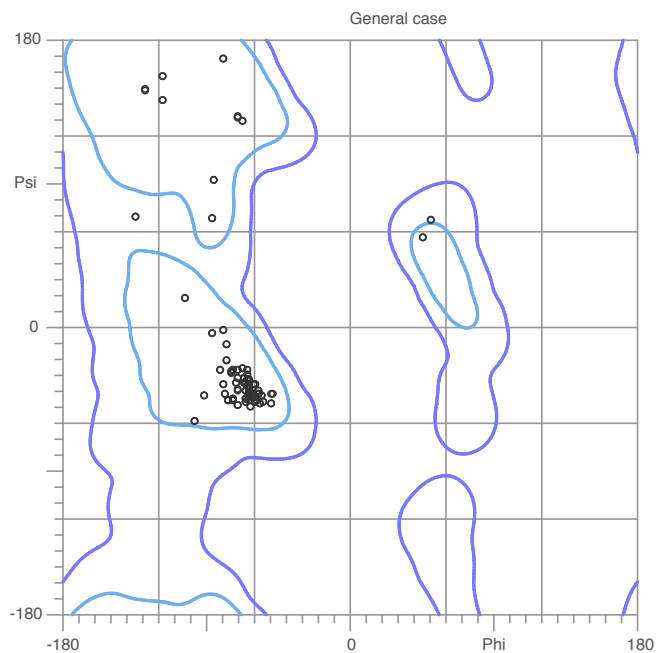
There were no outliers.

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

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 13



97.3% (144/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

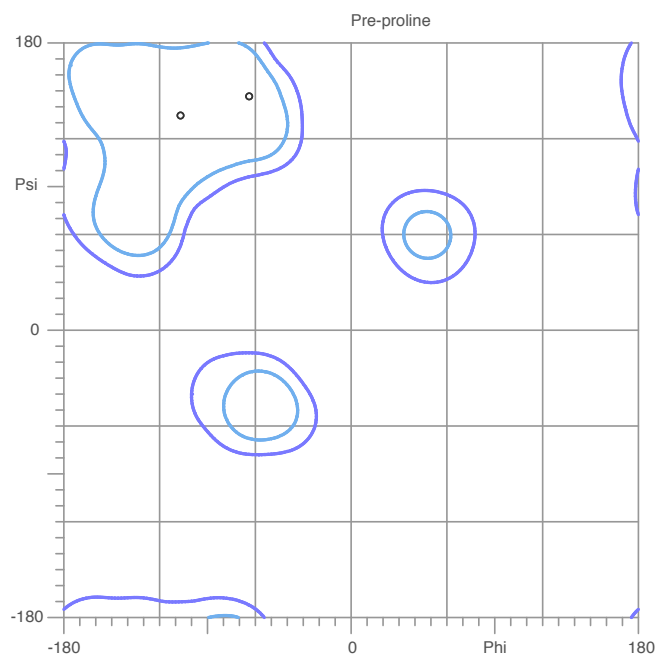
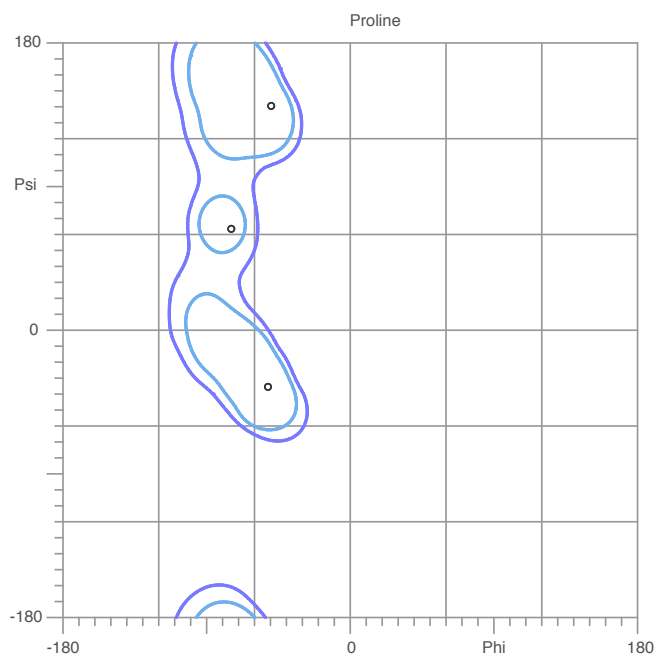
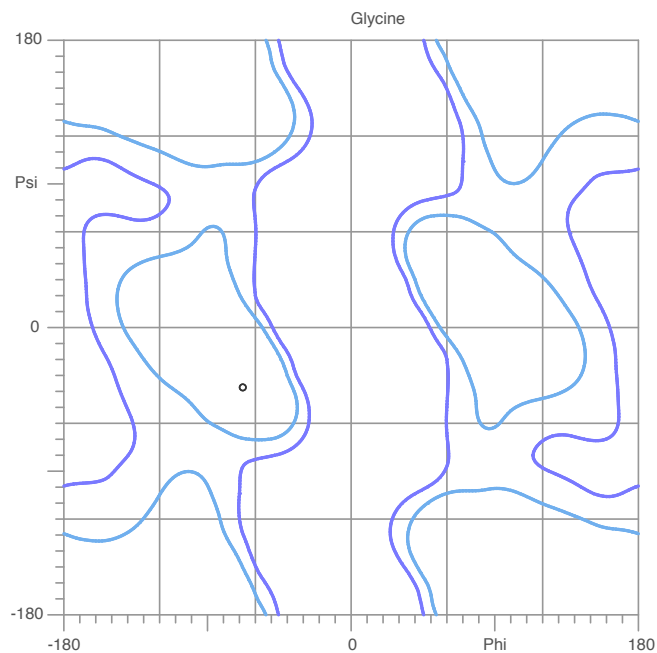
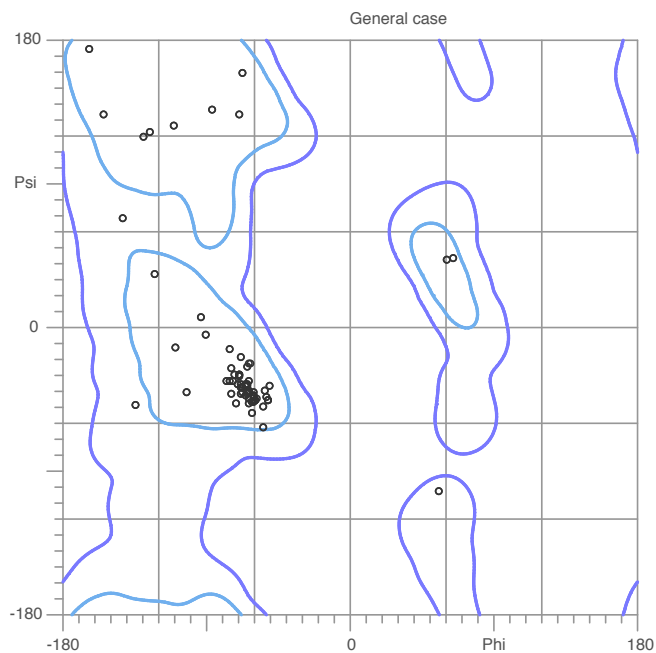
There were no outliers.

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

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 14

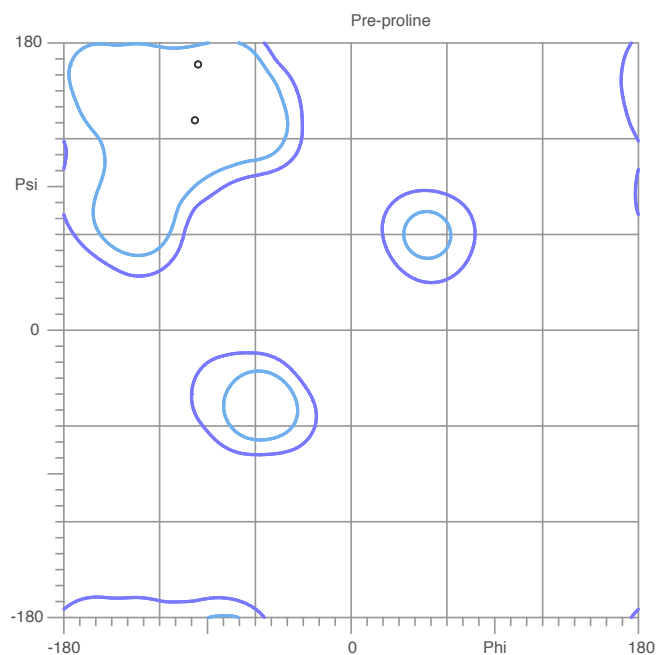
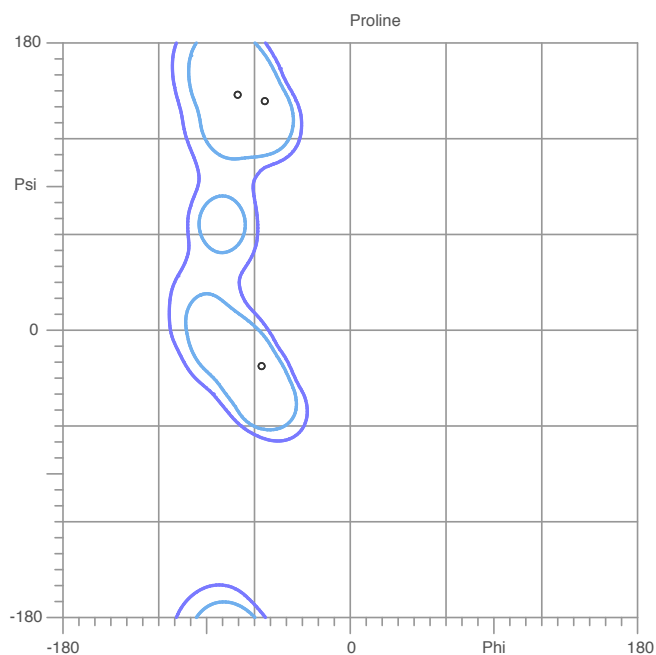
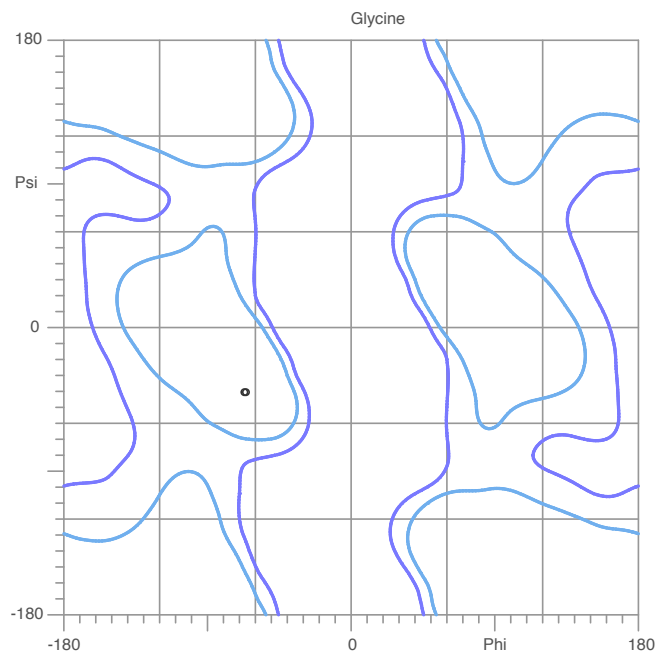
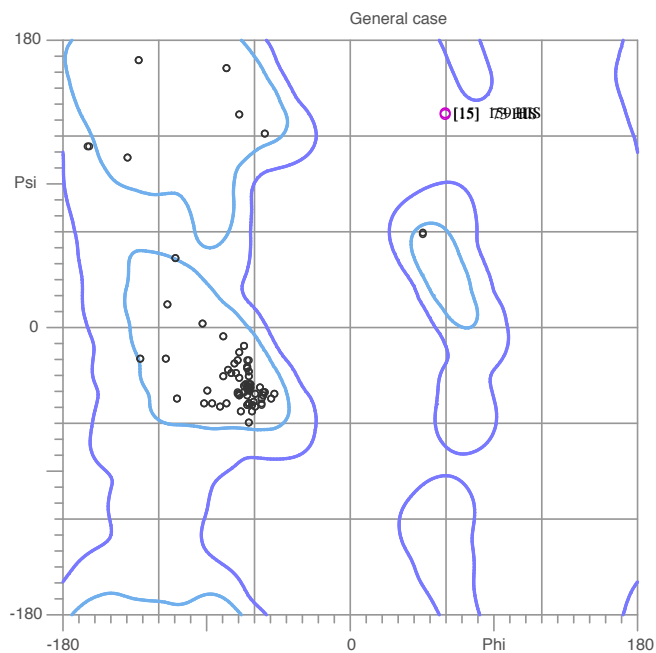


95.9% (142/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 15



95.9% (142/148) of all residues were in favored (98%) regions.  
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

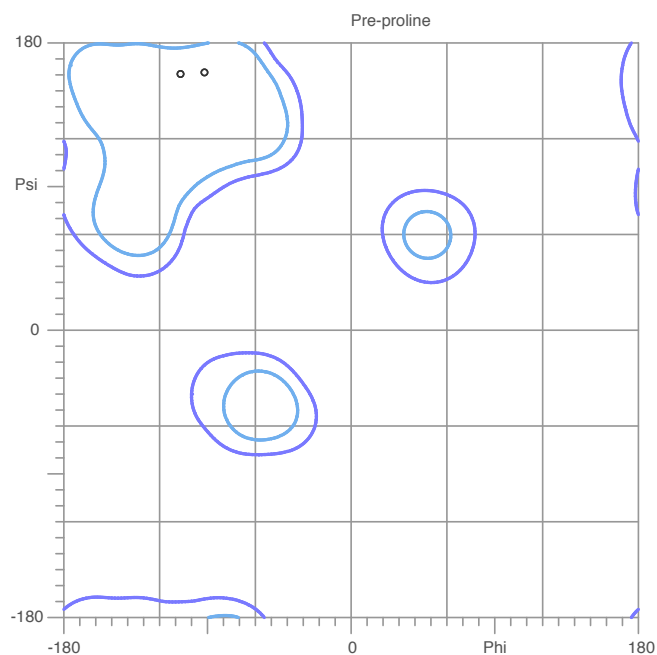
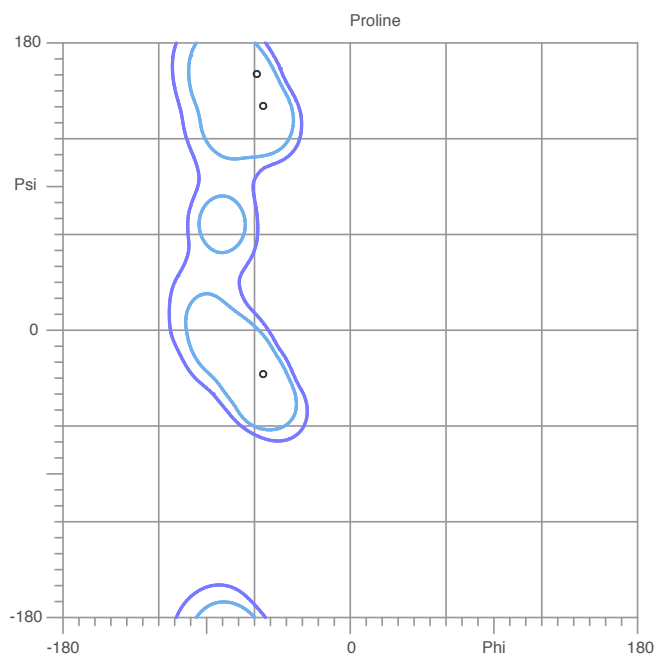
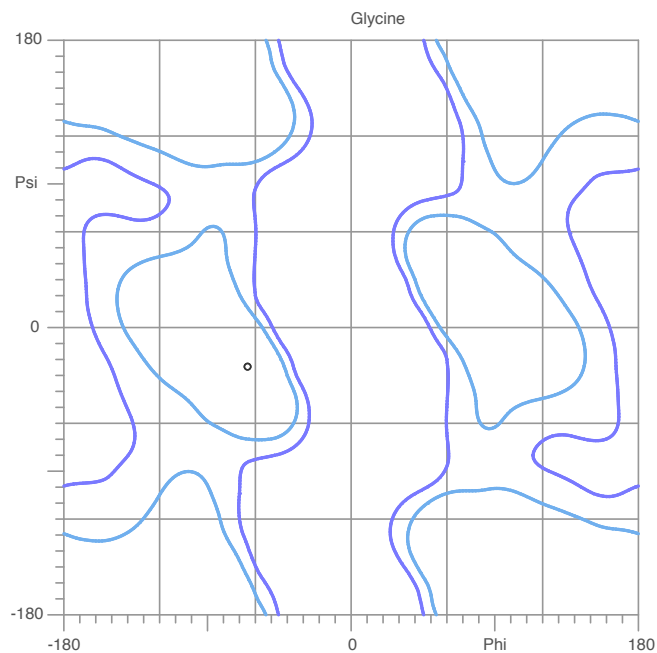
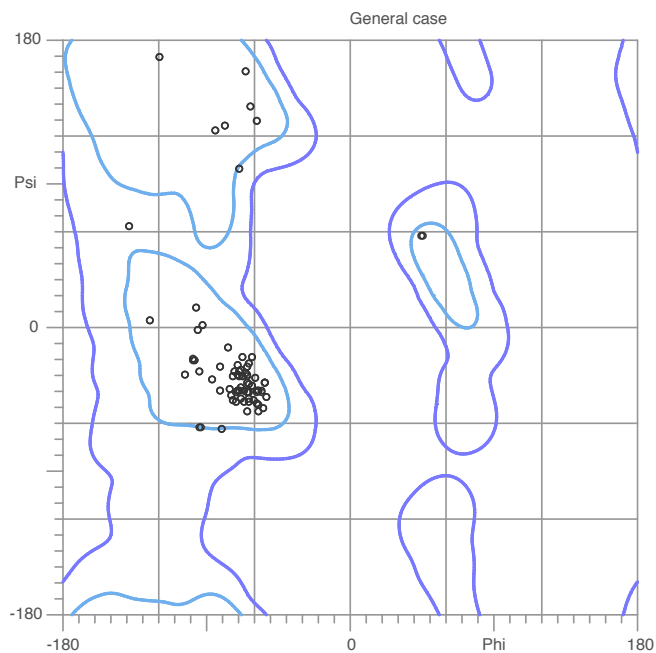
There were 2 outliers (phi, psi):

[15] 73 HIS (59.7, 135.0)

[15] 159 HIS (59.7, 135.1)

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 16



94.6% (140/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

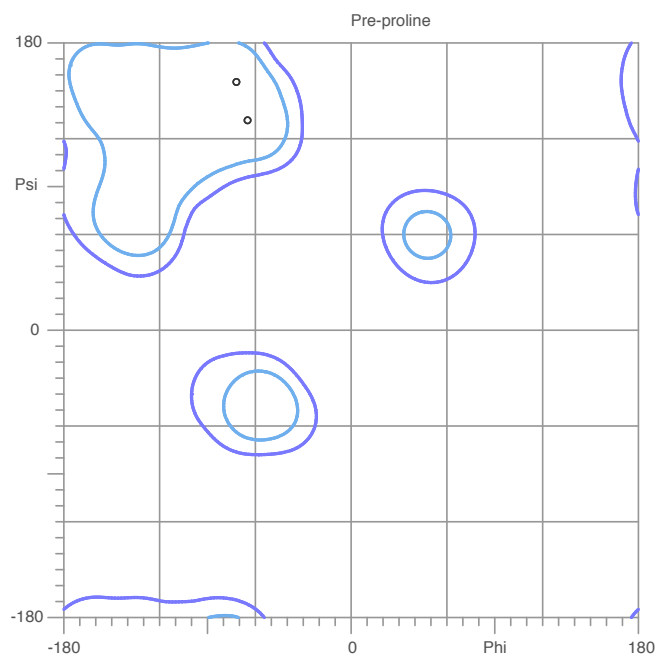
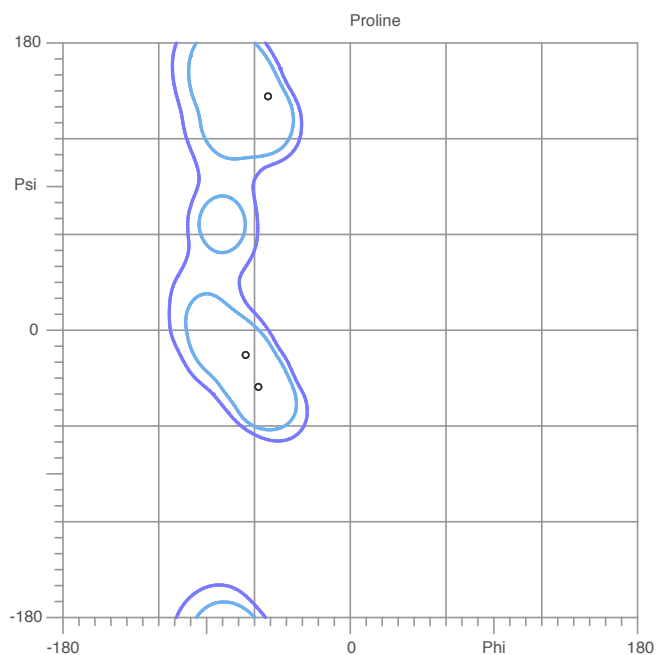
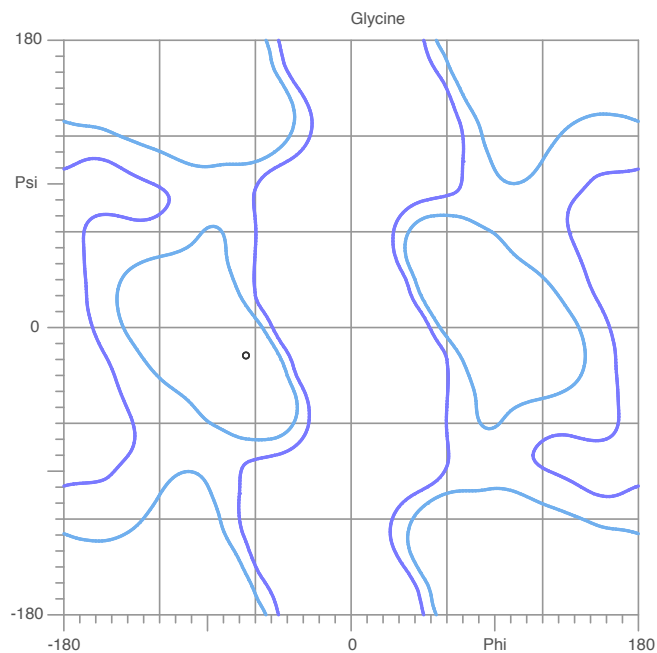
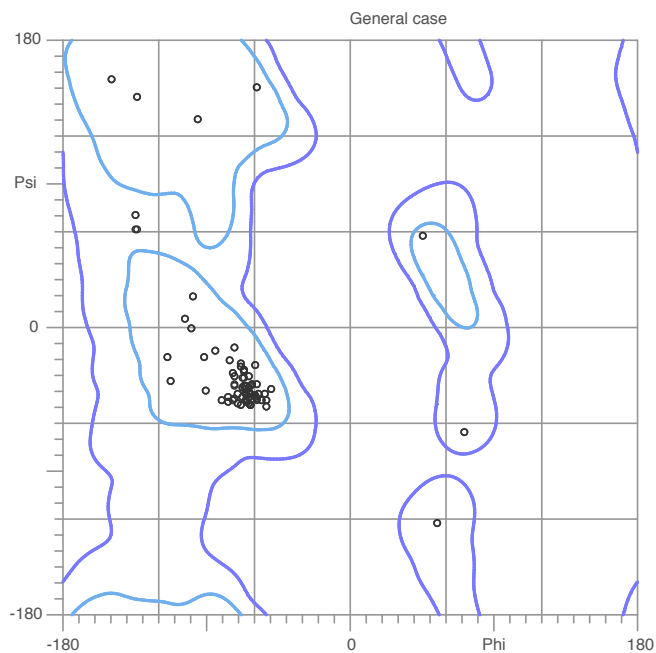
There were no outliers.

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

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 17



94.6% (140/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

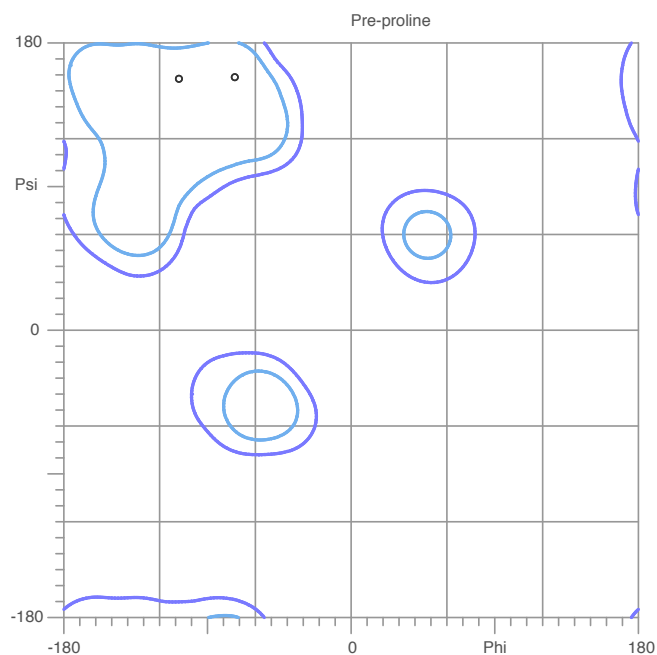
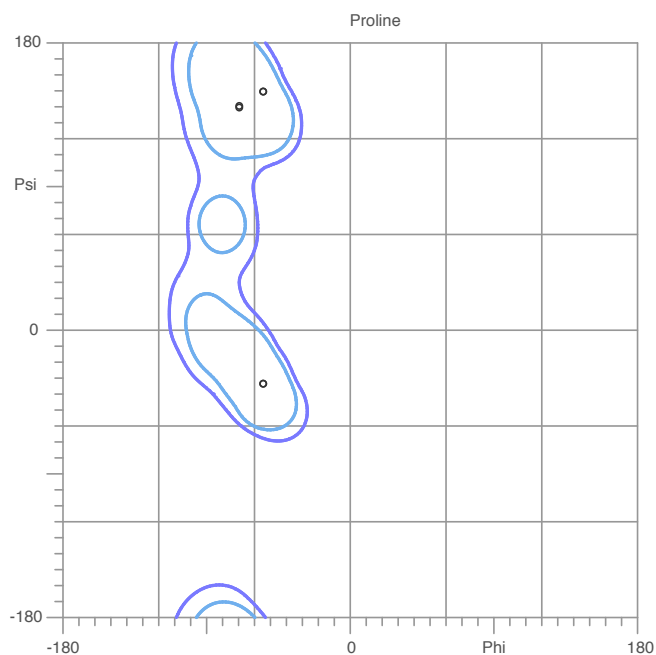
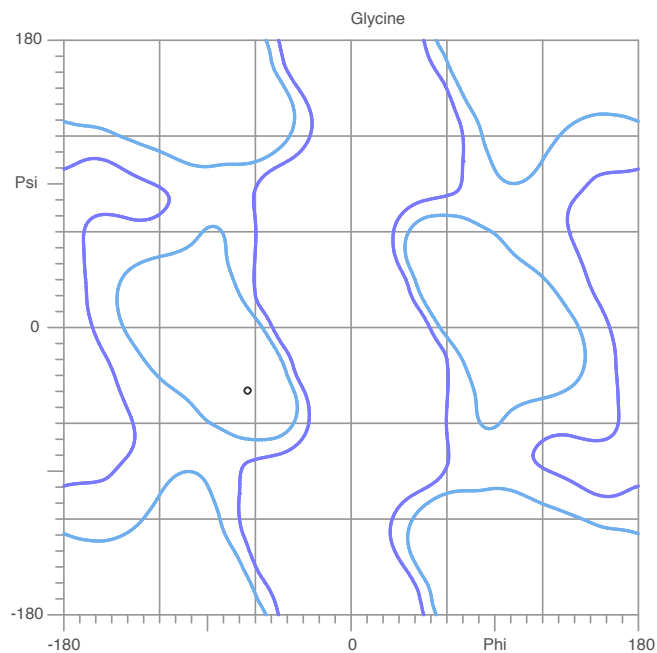
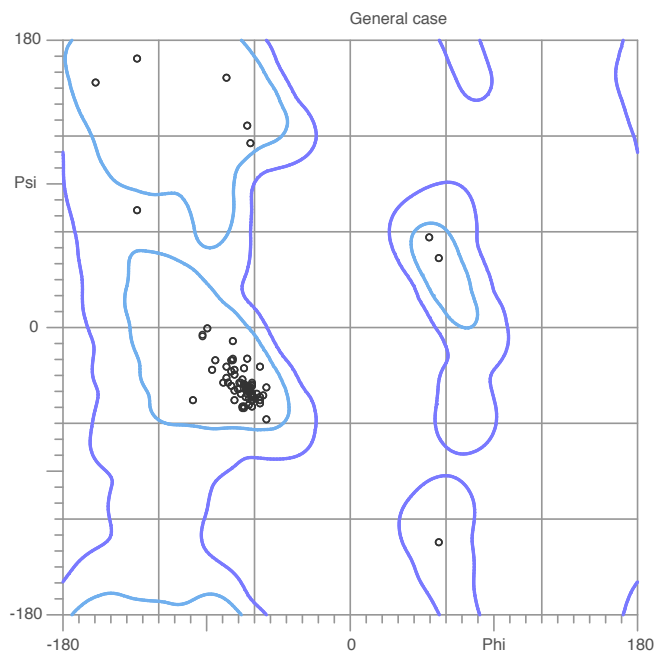
There were no outliers.

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

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 18



97.3% (144/148) of all residues were in favored (98%) regions.  
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

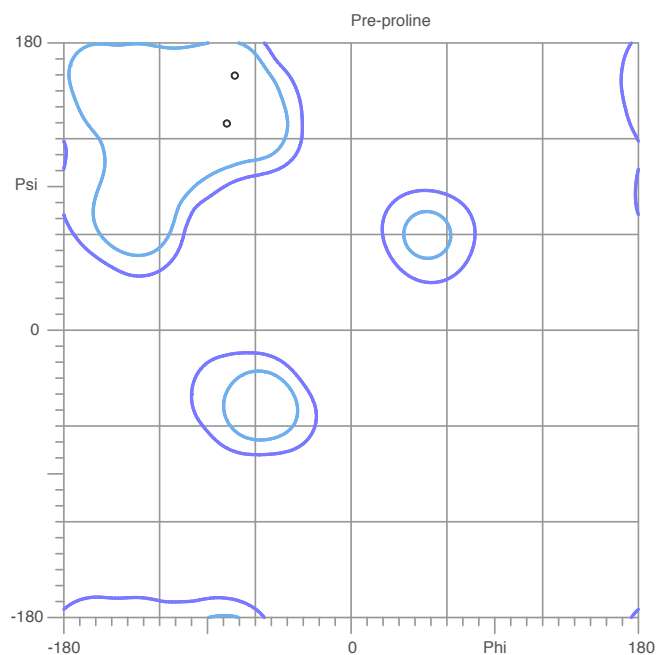
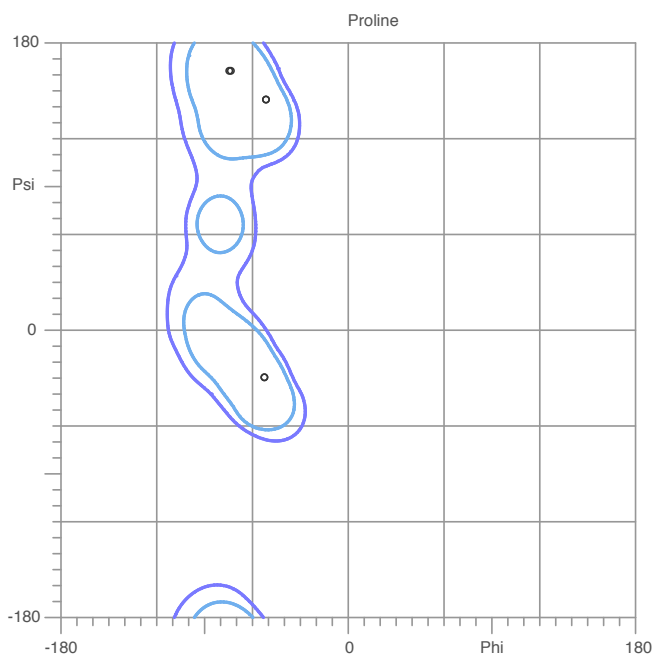
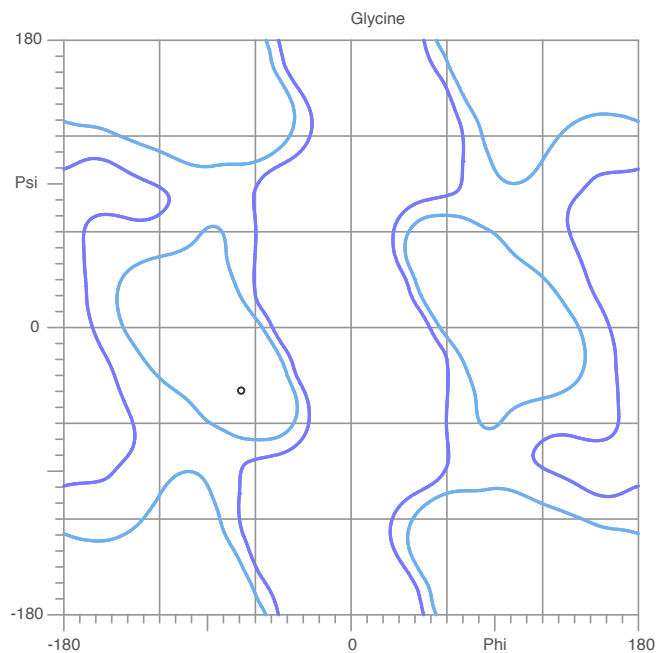
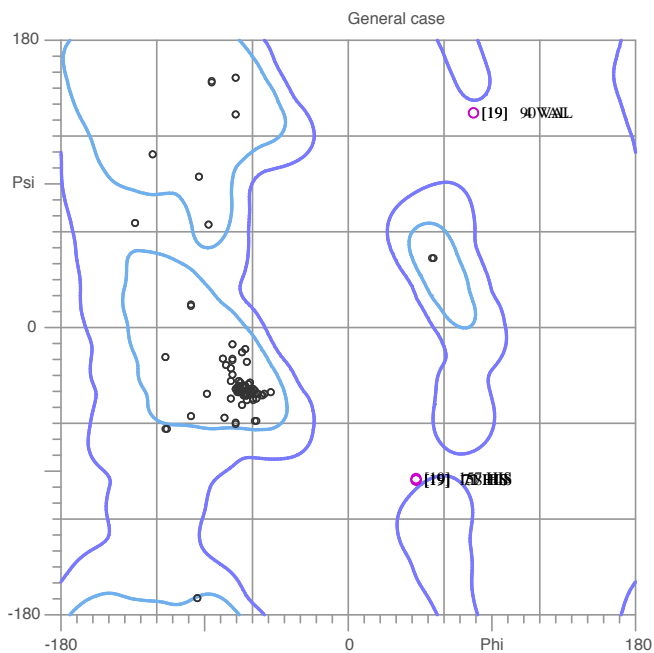
There were no outliers.

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

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 19



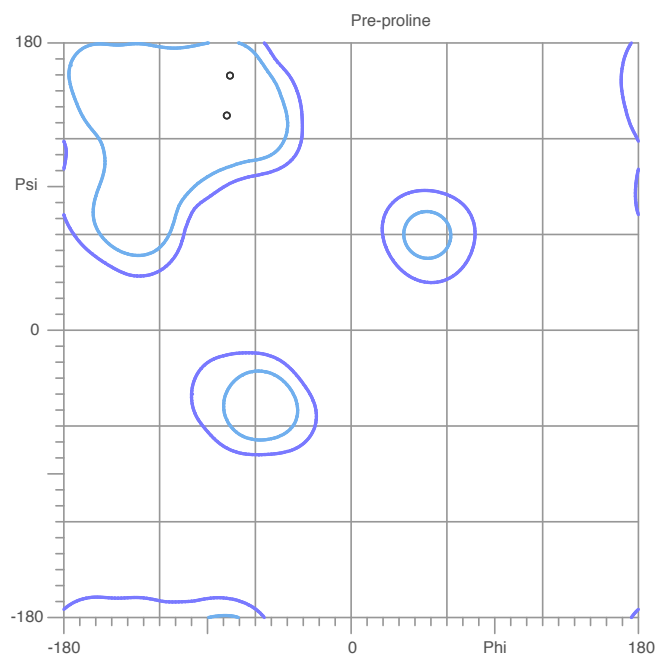
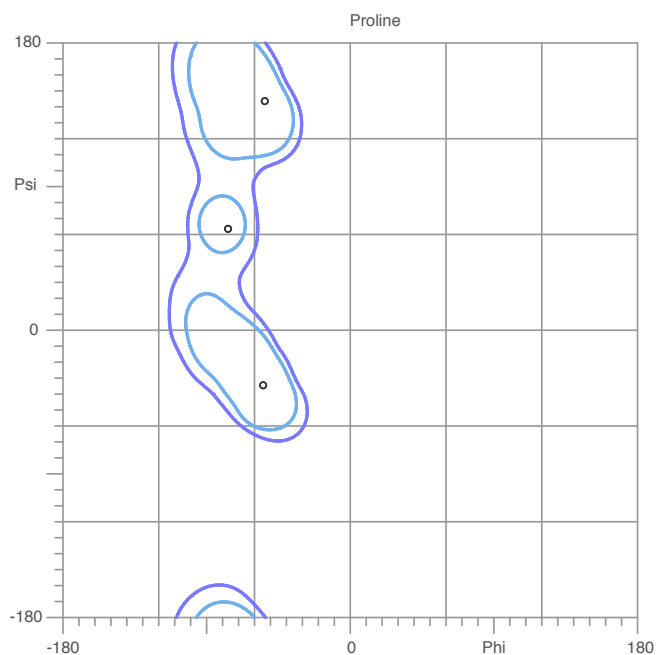
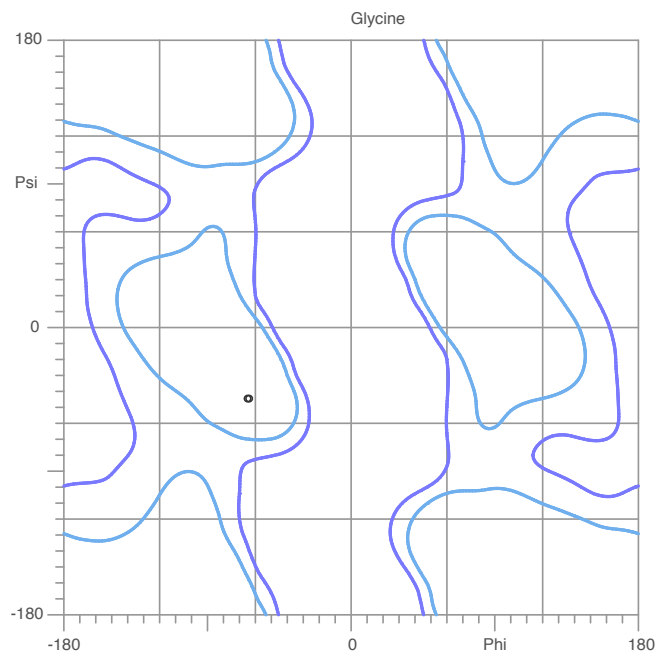
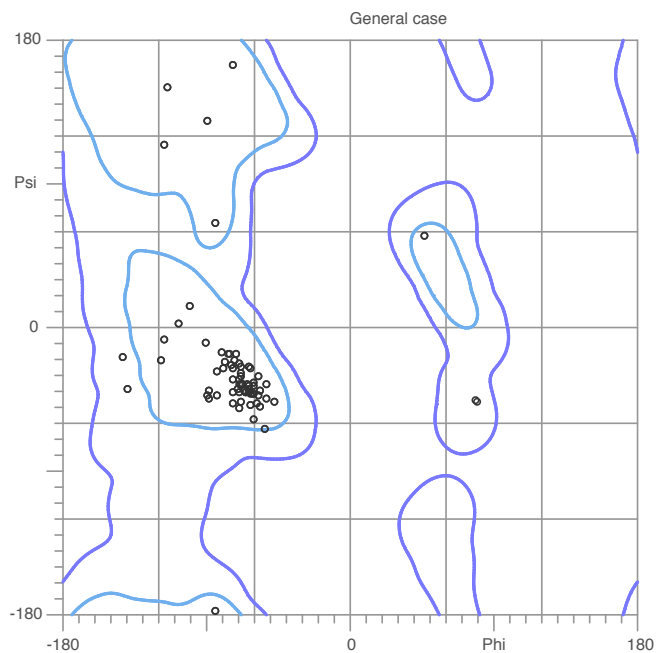
93.2% (138/148) of all residues were in favored (98%) regions.  
95.9% (142/148) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):  
[19] 4 VAL (78.5, 135.0)

[19] 71 HIS (42.7, -95.0)  
[19] 72 HIS (42.8, -95.0)  
[19] 90 VAL (78.5, 135.0)  
[19] 157 HIS (42.6, -95.0)  
[19] 158 HIS (42.8, -95.1)

# MolProbity Ramachandran analysis

CSR4\_R3\_em\_bcr3.pdb, model 20



95.9% (142/148) of all residues were in favored (98%) regions.  
100.0% (148/148) 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)