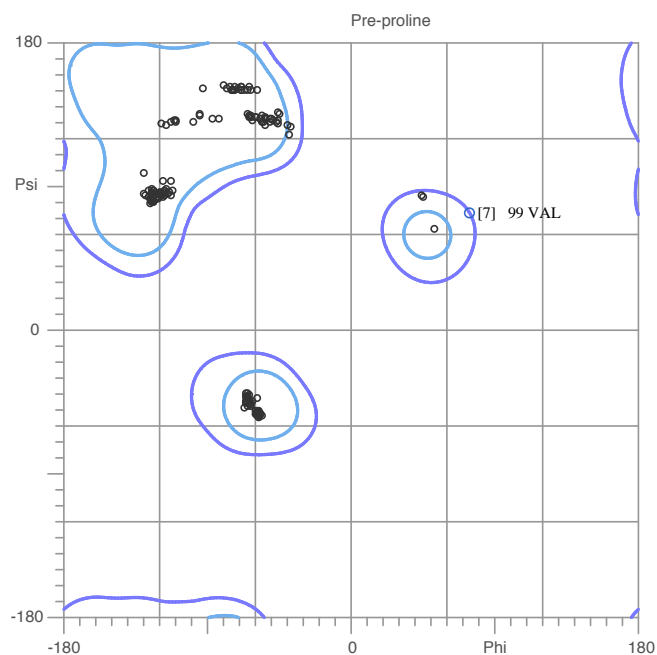
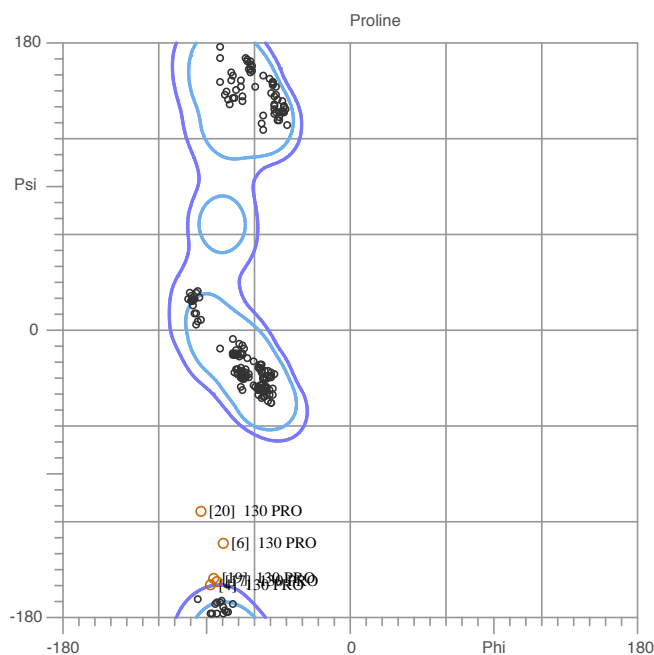
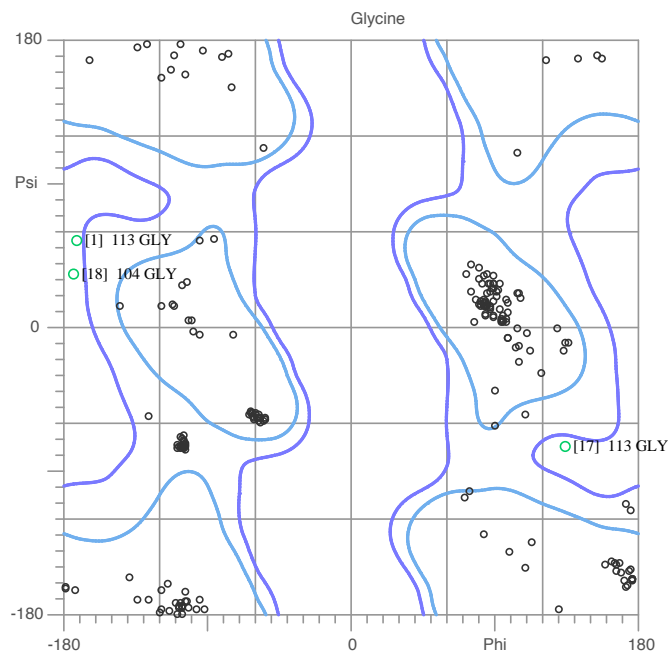
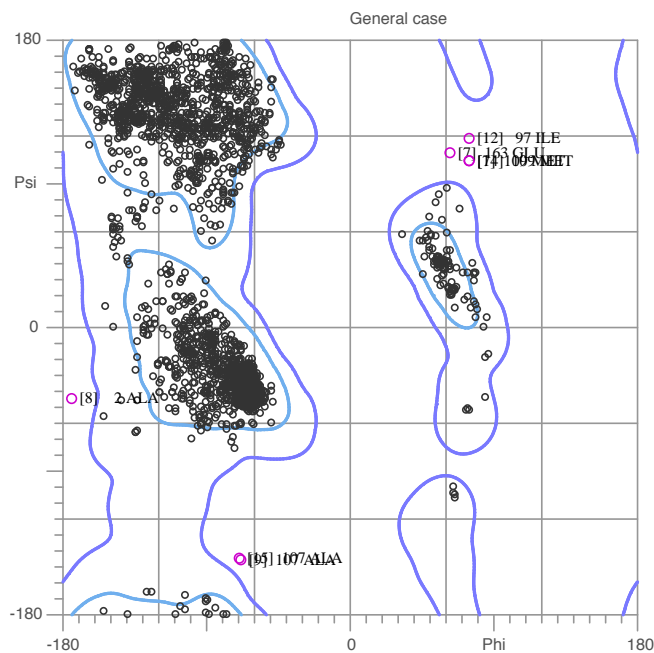


# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, all models



95.5% (3303/3460) of all residues were in favored (98%) regions.  
99.5% (3444/3460) of all residues were in allowed (>99.8%) regions.

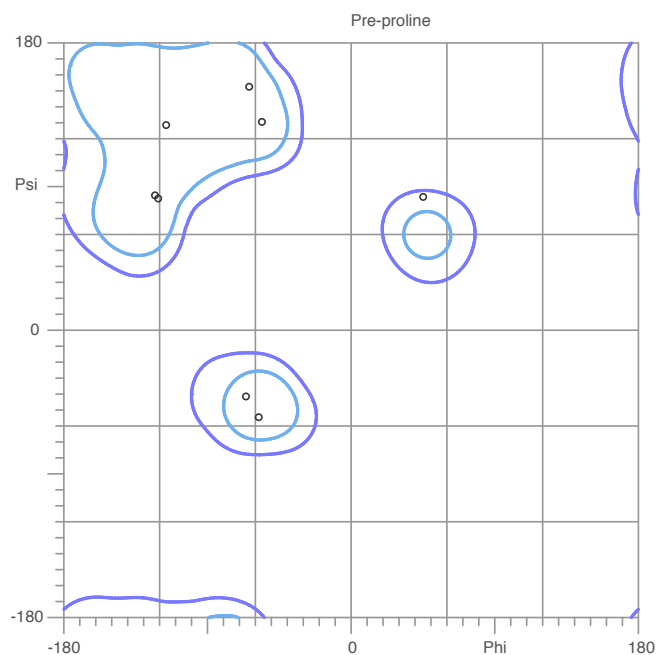
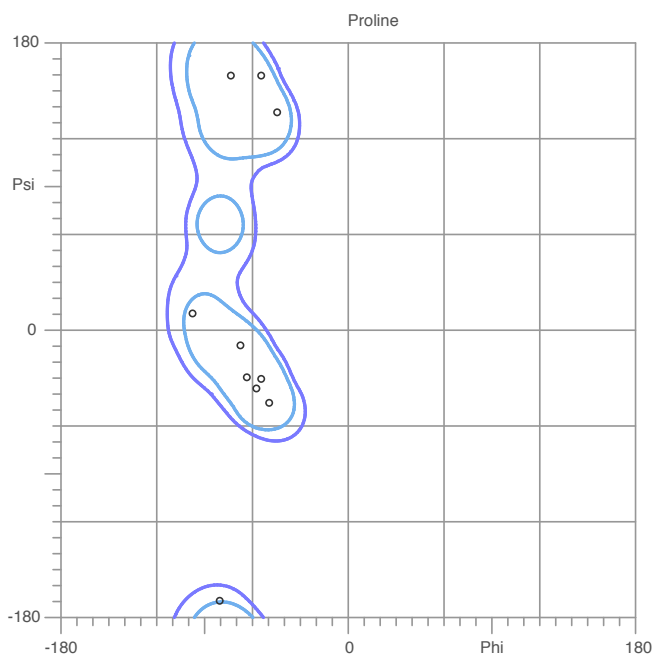
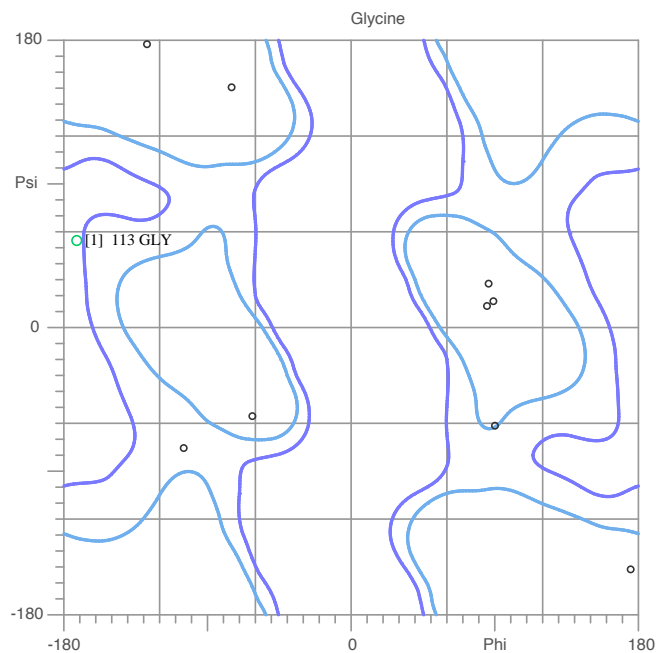
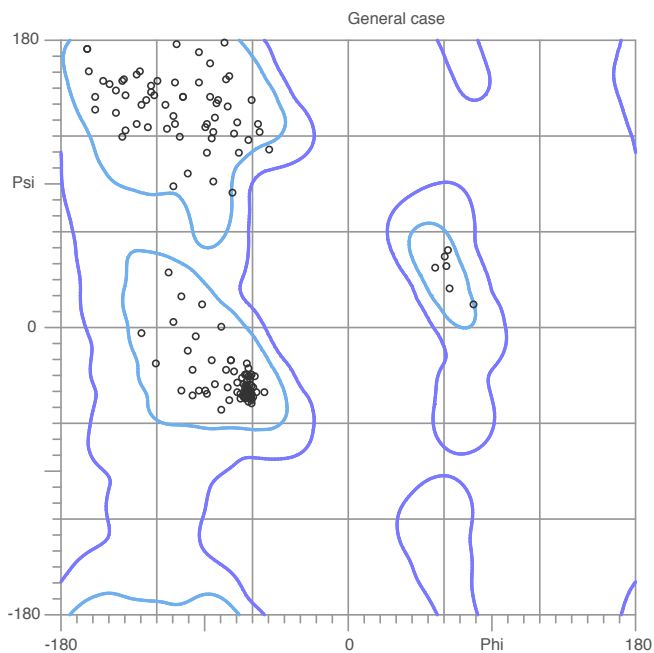
There were 16 outliers (phi, psi):

- [1] 113 GLY (-172.1, 55.0)
- [4] 130 PRO (-88.9, -159.5)
- [6] 130 PRO (-80.7, -133.6)
- [7] 99 VAL (75.0, 75.0)
- [7] 109 MET (74.9, 105.0)
- [7] 163 GLU (62.8, 110.1)

- [8] 2 ALA (-175.1, -45.0)
- [9] 107 ALA (-69.1, -145.0)
- [12] 97 ILE (74.9, 119.1)
- [14] 109 MET (74.9, 105.1)
- [15] 107 ALA (-70.7, -145.0)
- [17] 113 GLY (134.9, -75.0)
- [17] 130 PRO (-85.0, -158.0)
- [18] 104 GLY (-175.0, 34.0)
- [19] 130 PRO (-86.7, -155.8)
- [20] 130 PRO (-94.9, -113.1)

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 1



96.5% (167/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

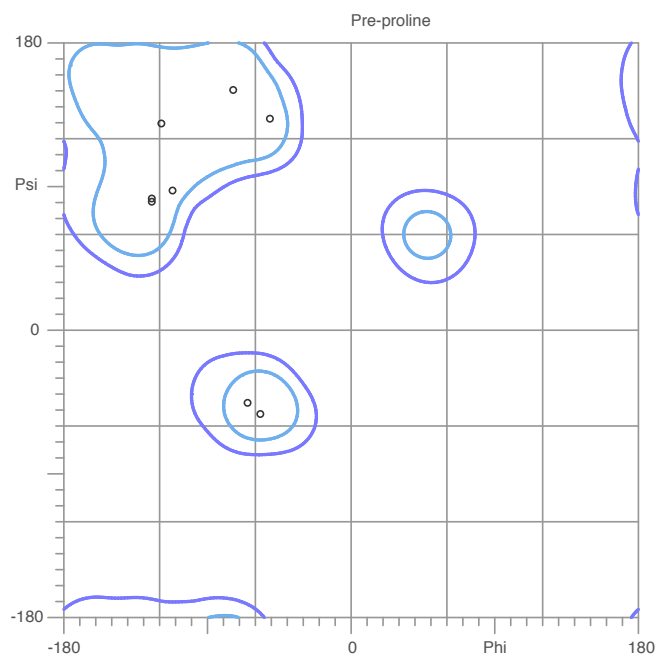
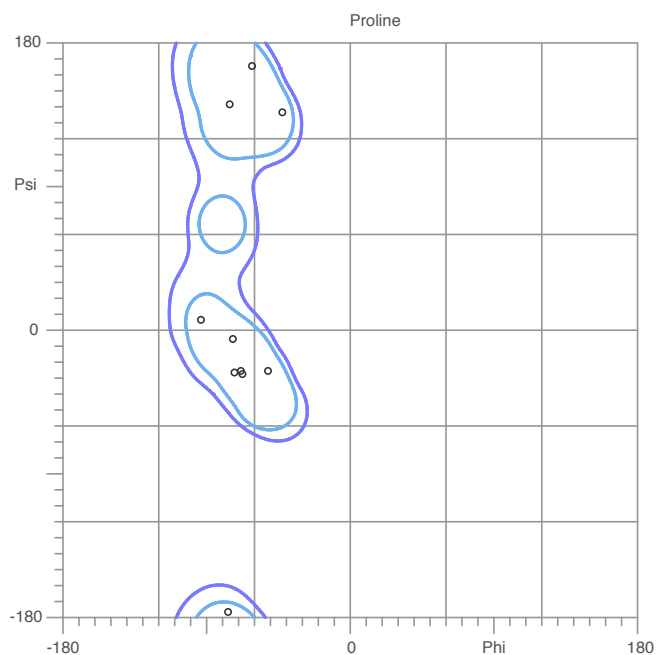
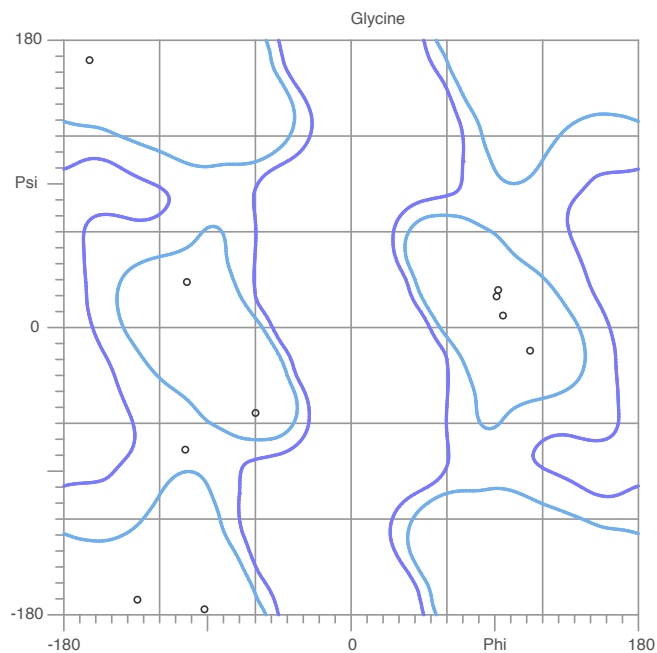
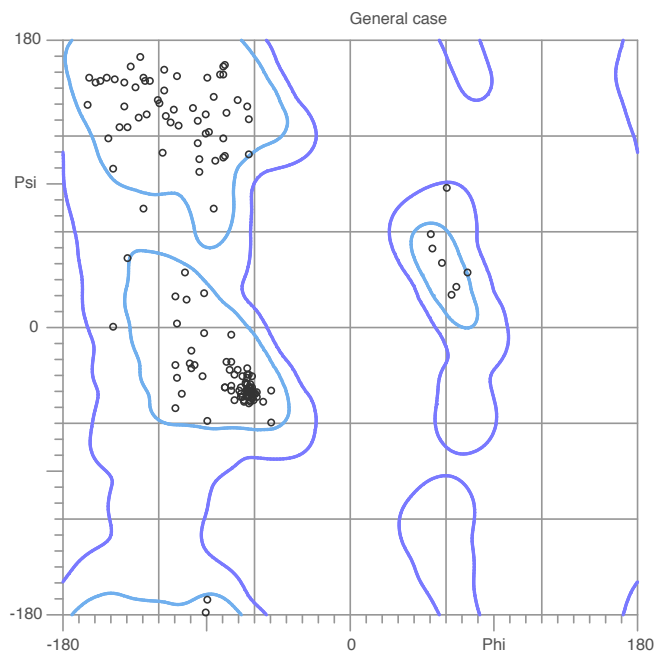
There were 1 outliers (phi, psi):  
[1] 113 GLY (-172.1, 55.0)

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 2



96.5% (167/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

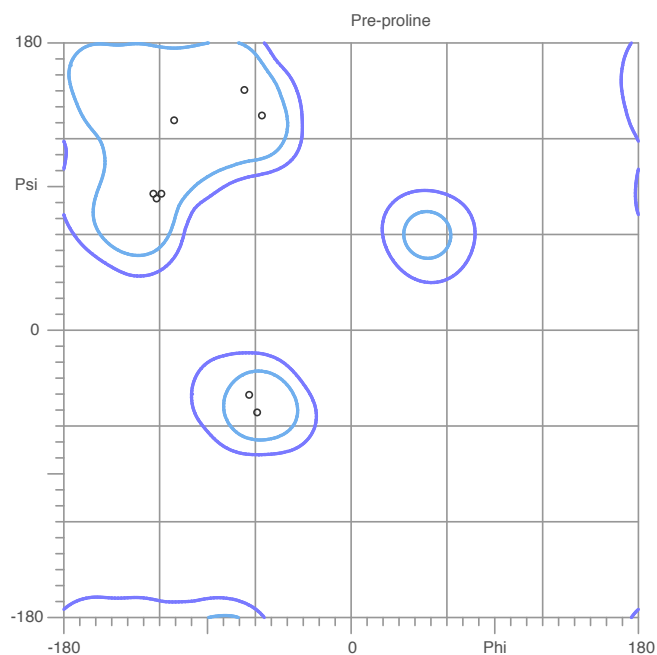
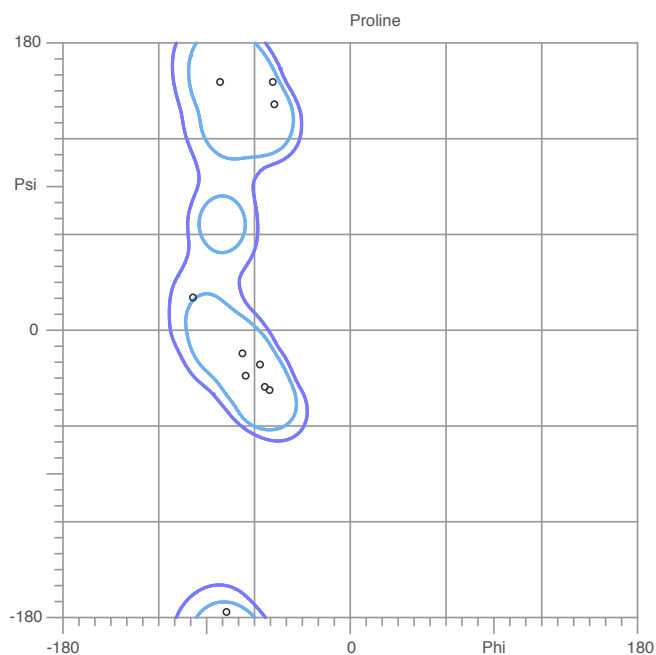
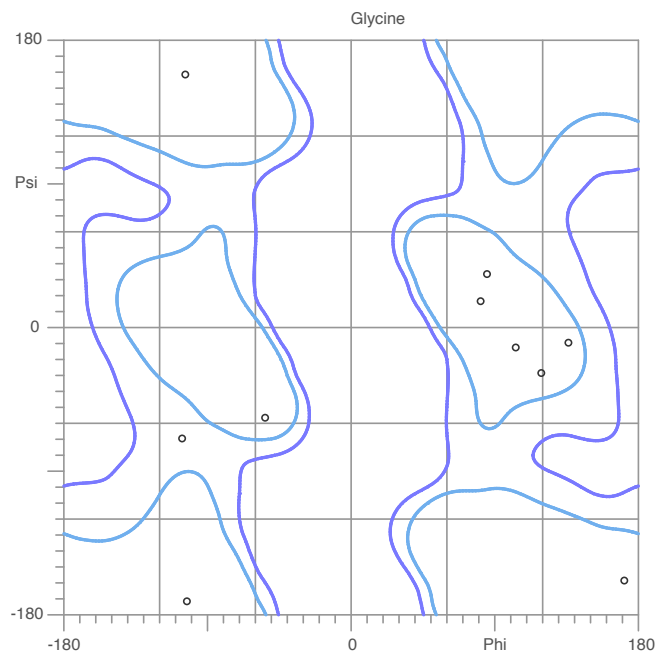
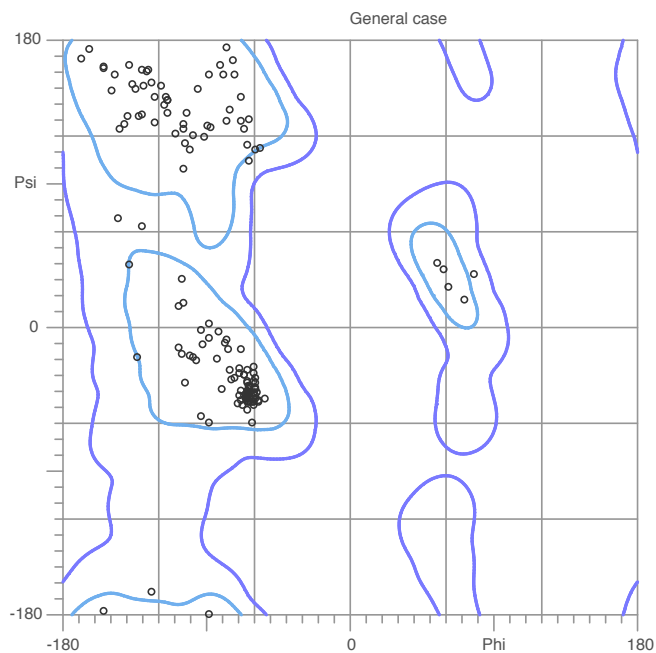
There were no outliers.

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 3

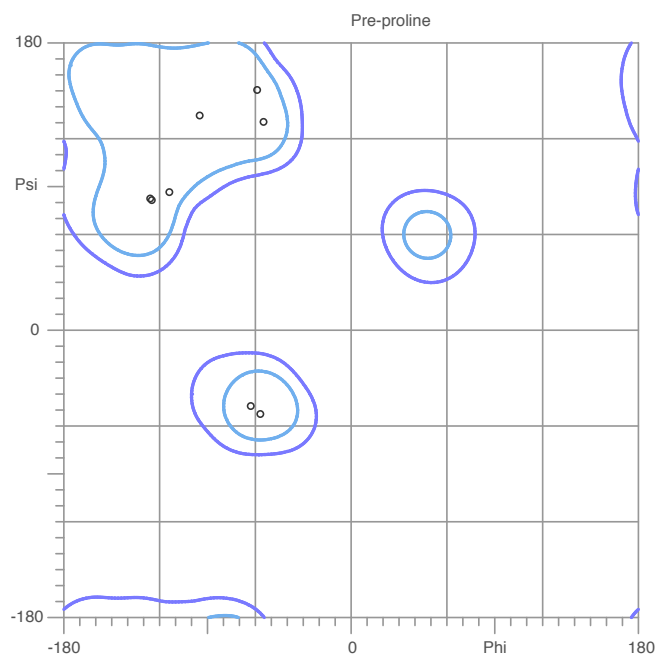
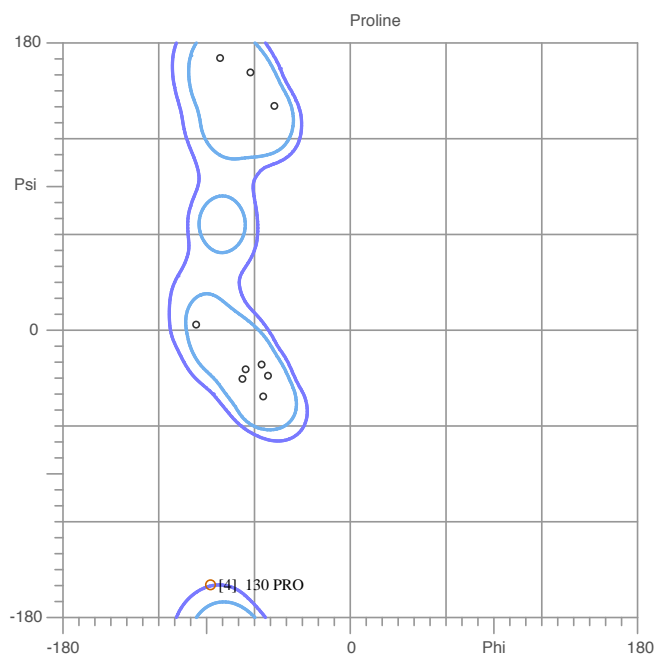
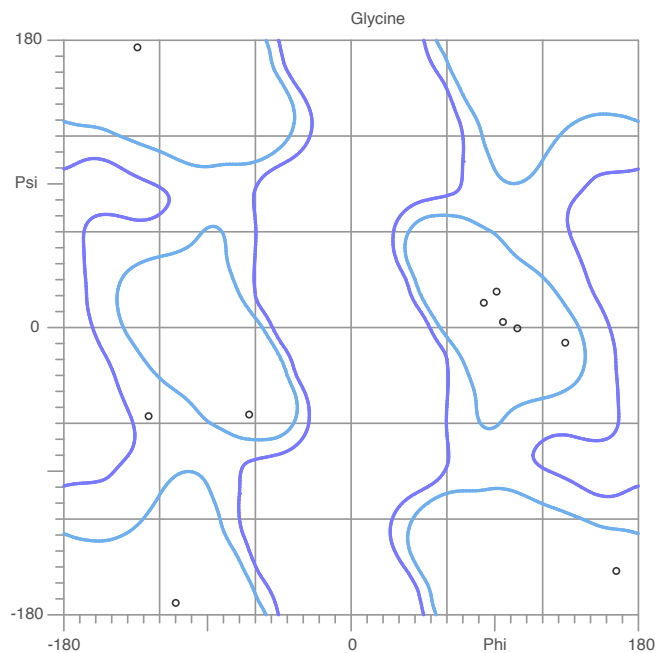
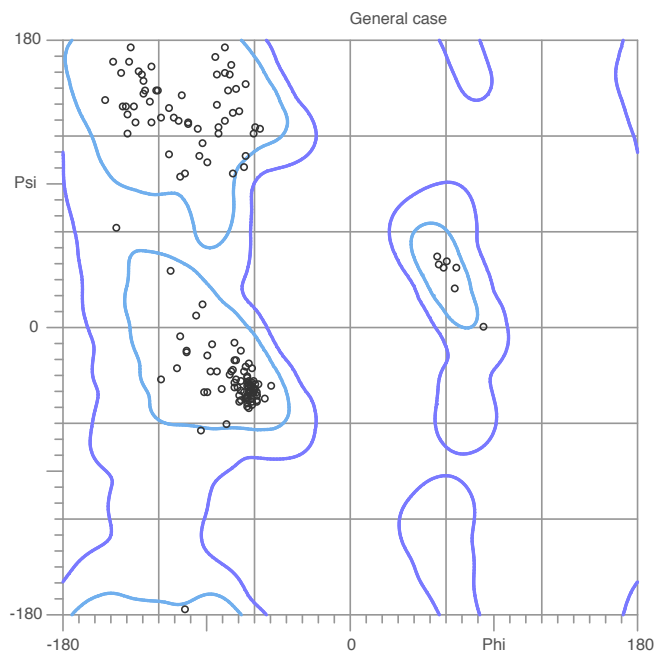


94.8% (164/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 4



96.5% (167/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

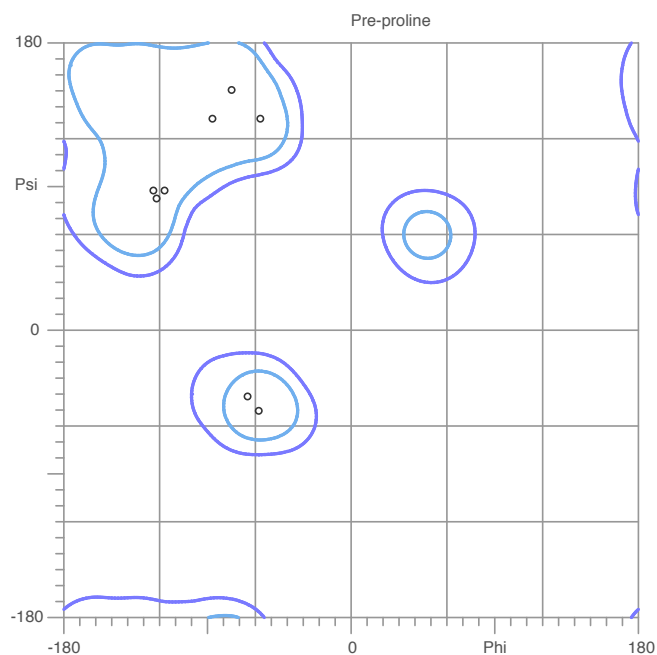
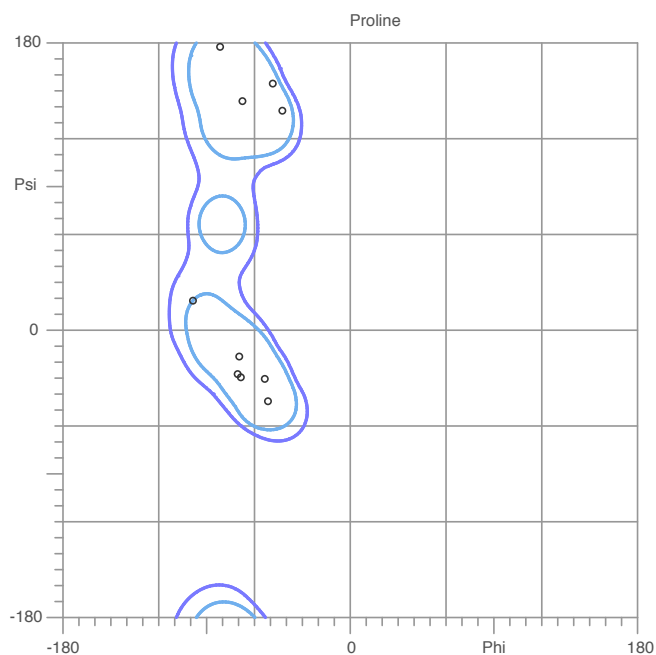
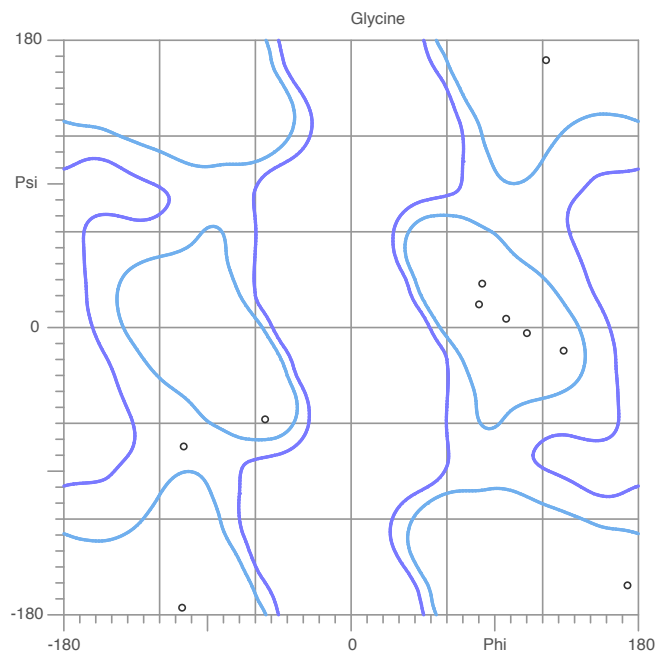
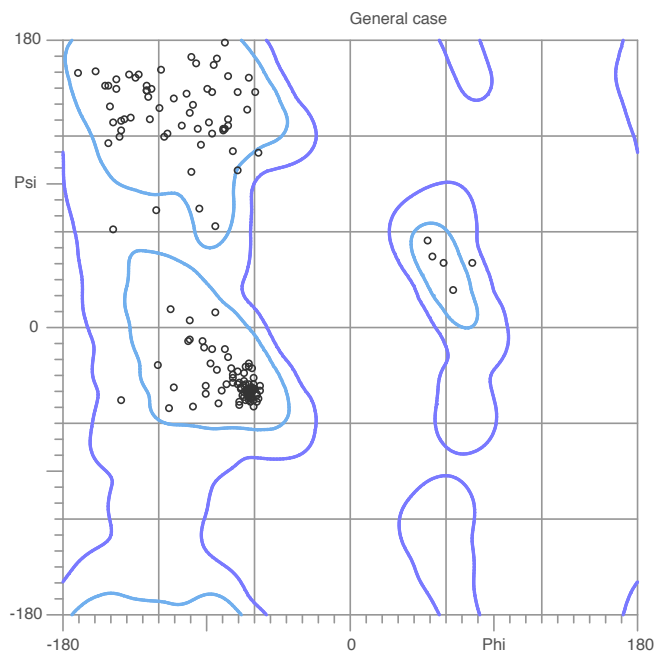
There were 1 outliers (phi, psi):  
[4] 130 PRO (-88.9, -159.5)

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 5



96.0% (166/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

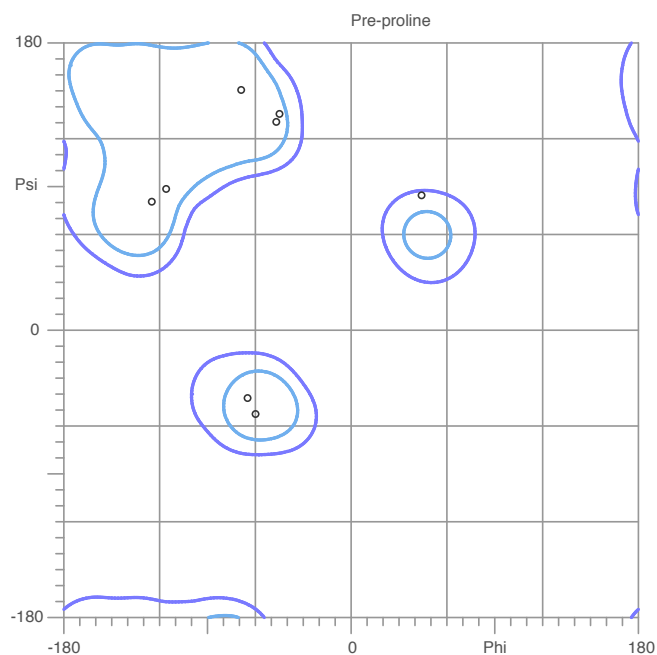
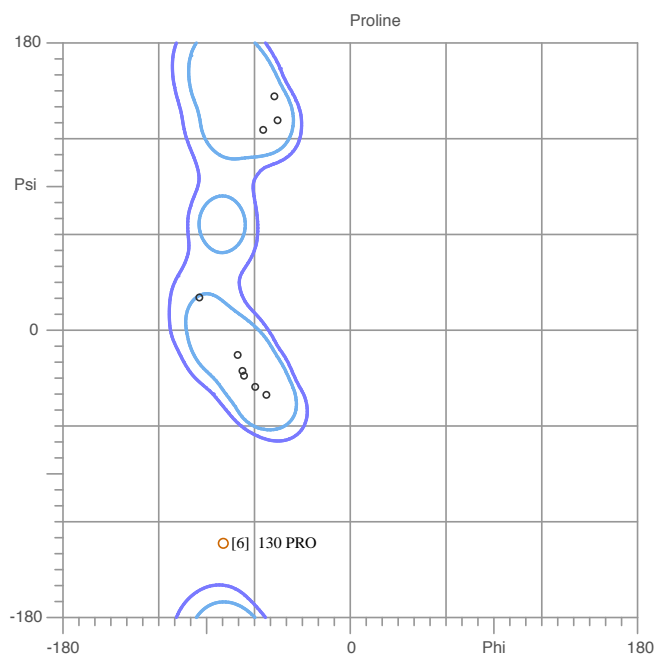
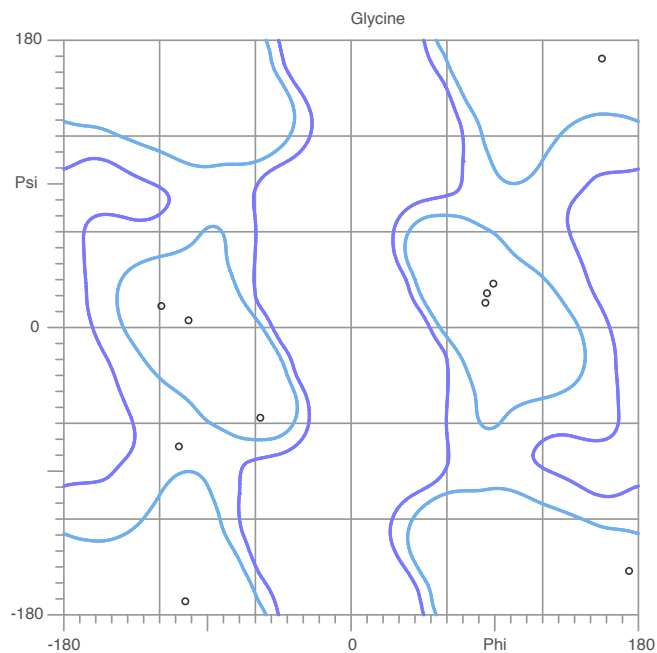
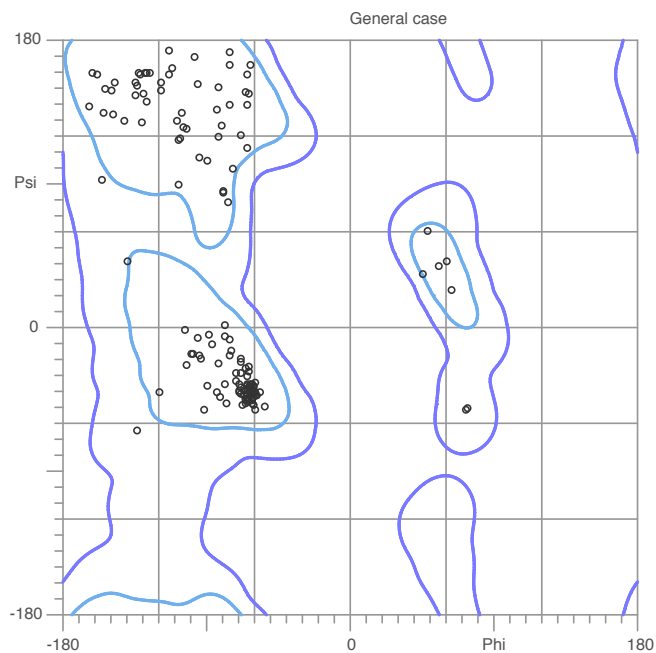
There were no outliers.

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 6

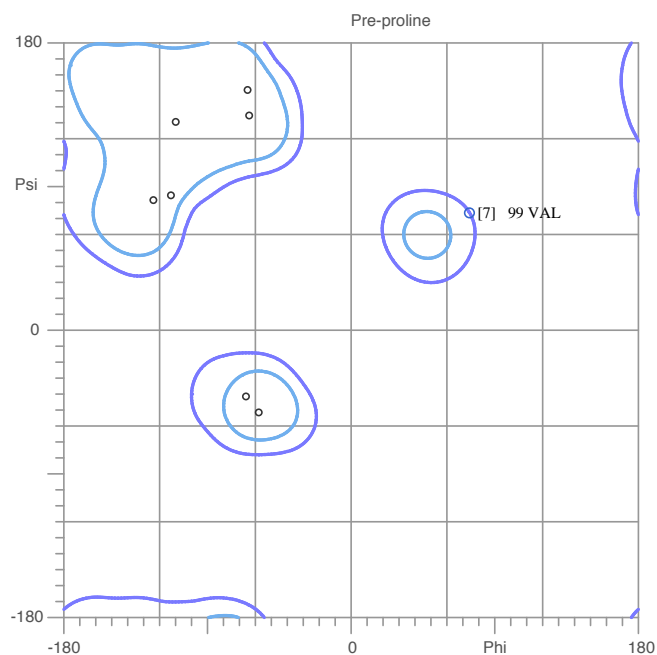
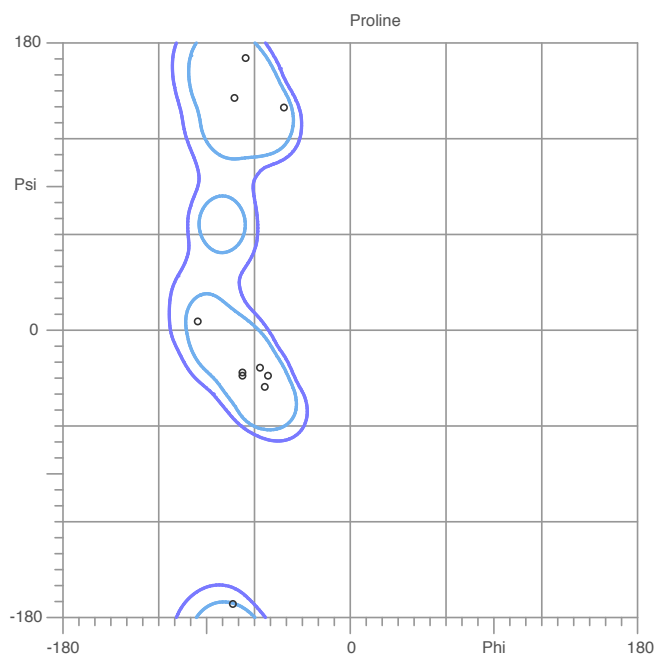
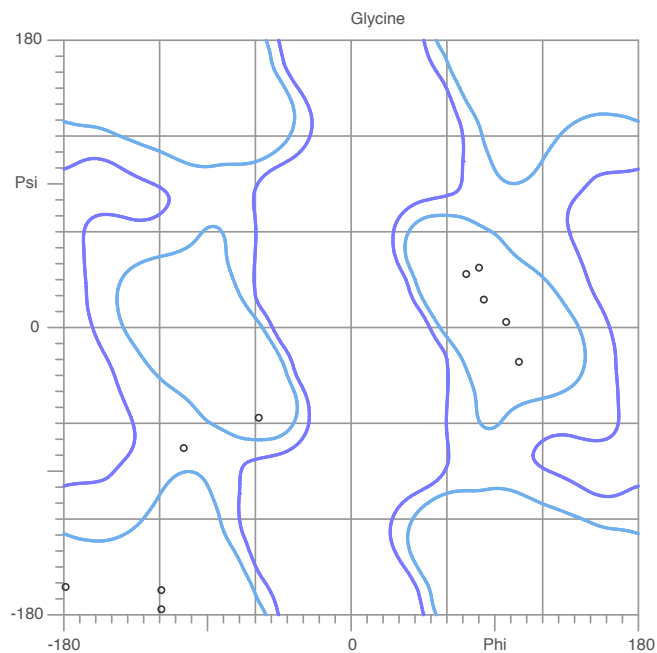
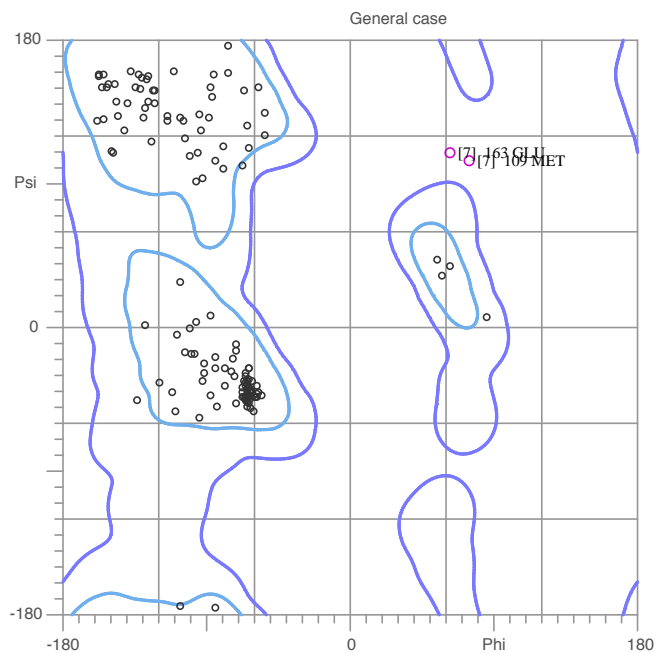


95.4% (165/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[6] 130 PRO (-80.7, -133.6)

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 7



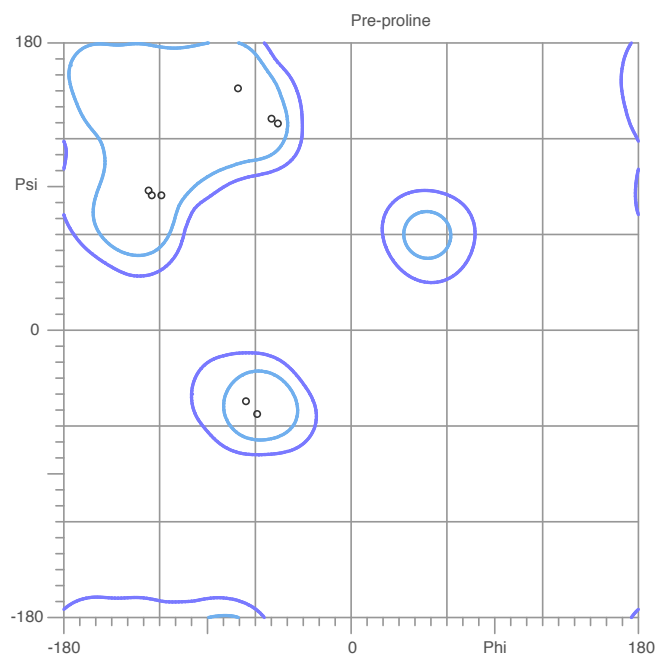
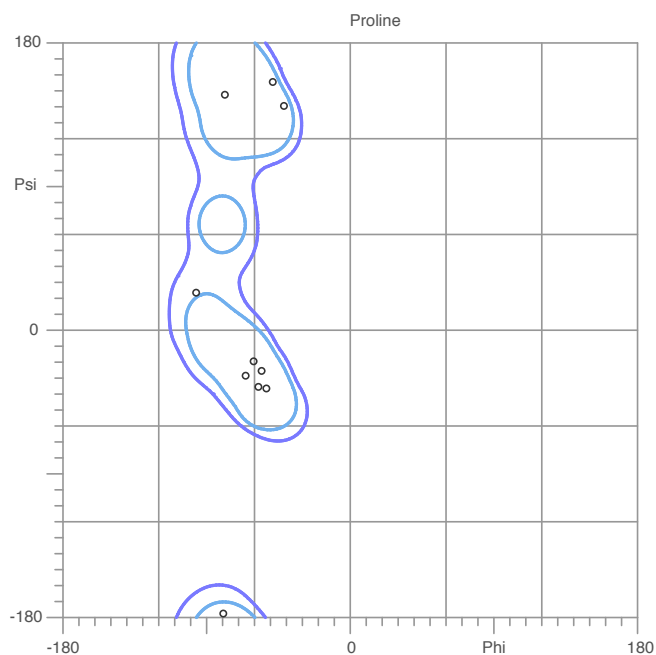
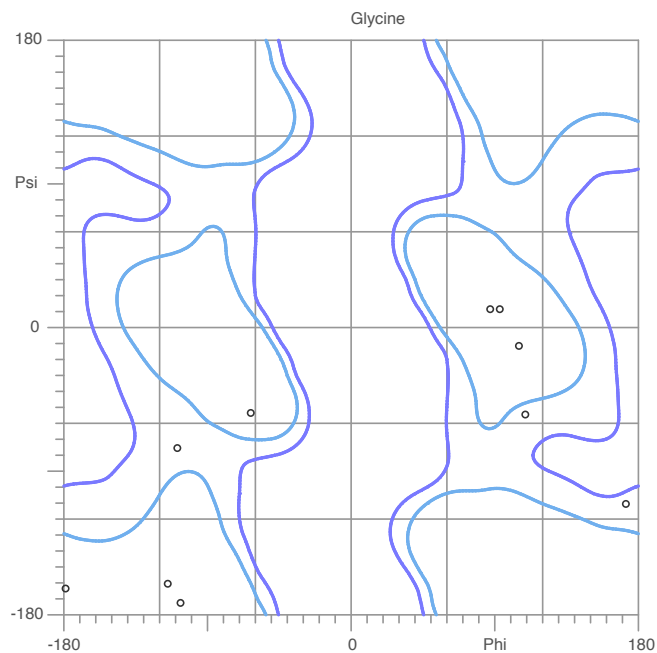
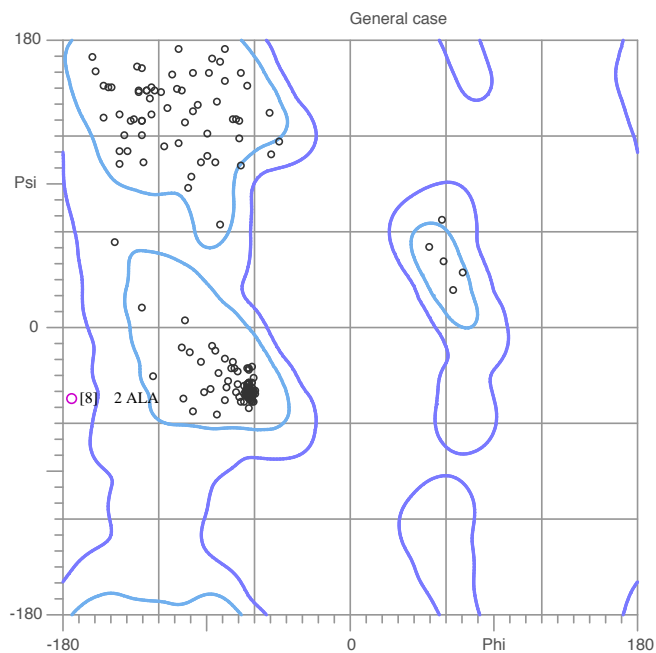
96.0% (166/173) of all residues were in favored (98%) regions.  
98.3% (170/173) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [7] 99 VAL (75.0, 75.0)
- [7] 109 MET (74.9, 105.0)
- [7] 163 GLU (62.8, 110.1)

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 8

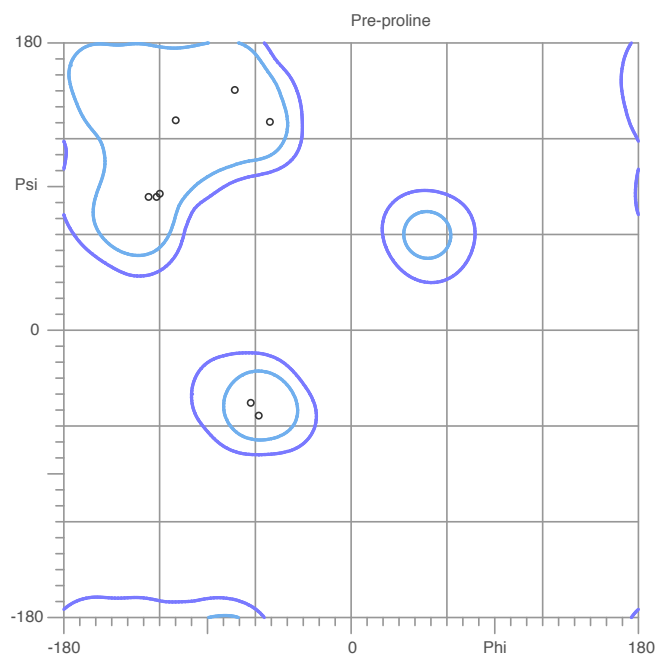
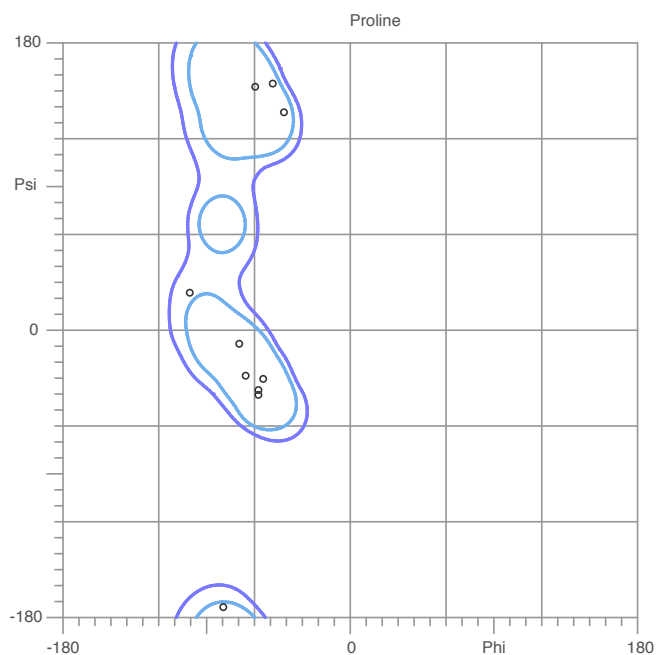
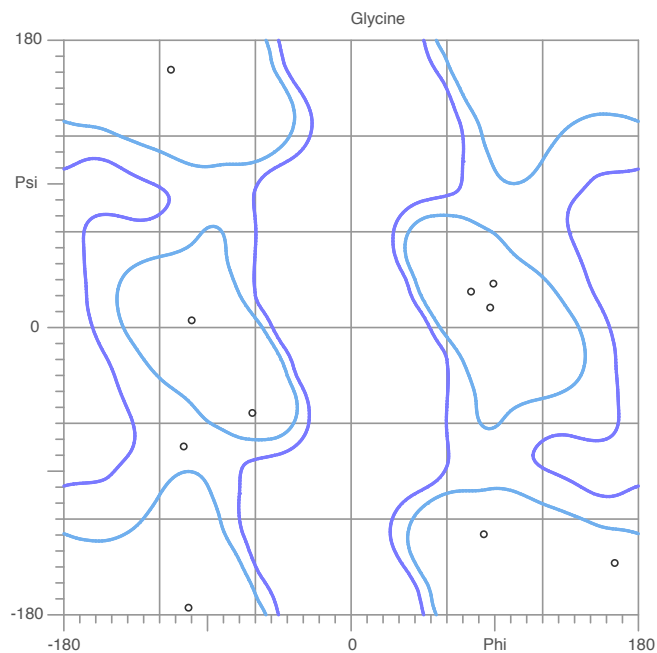
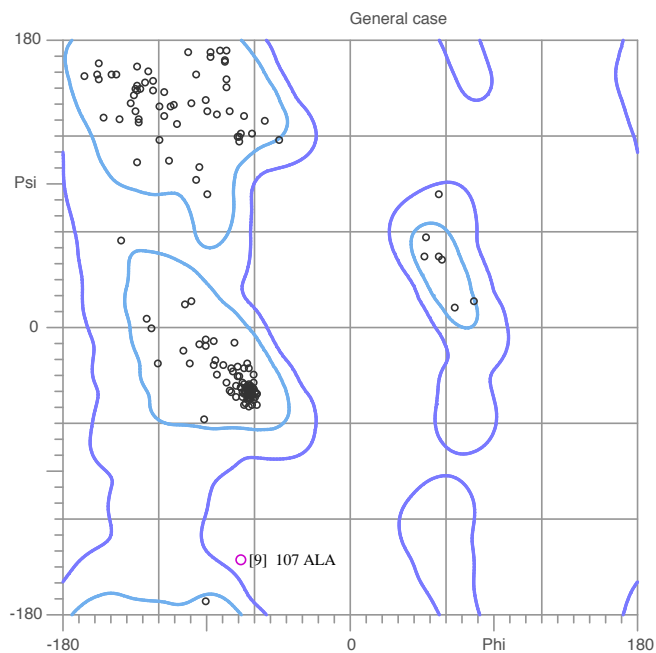


94.8% (164/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[8] 2 ALA (-175.1, -45.0)

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 9



97.1% (168/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

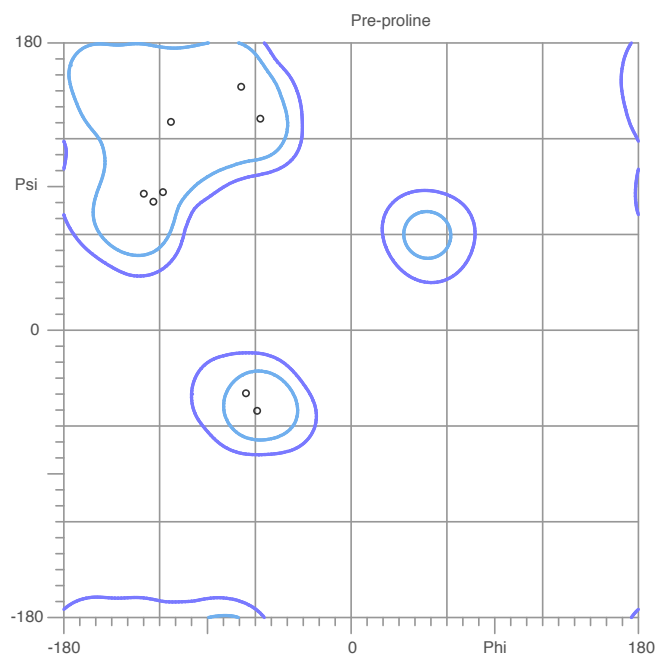
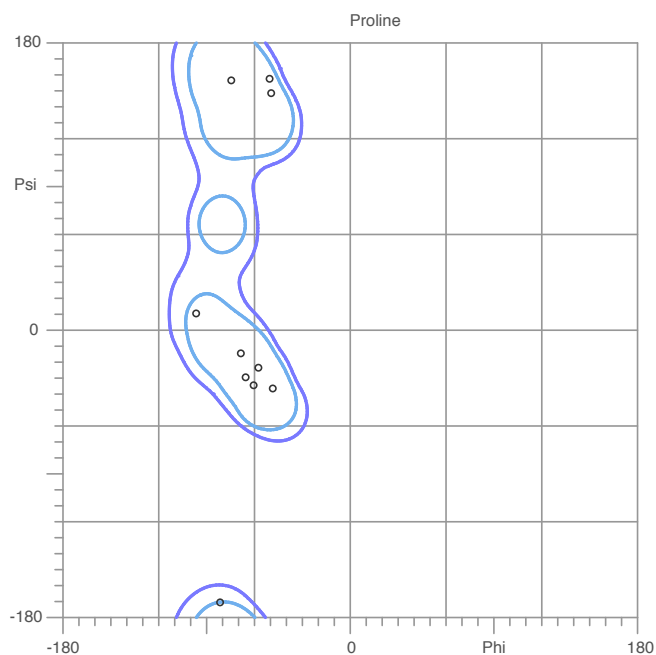
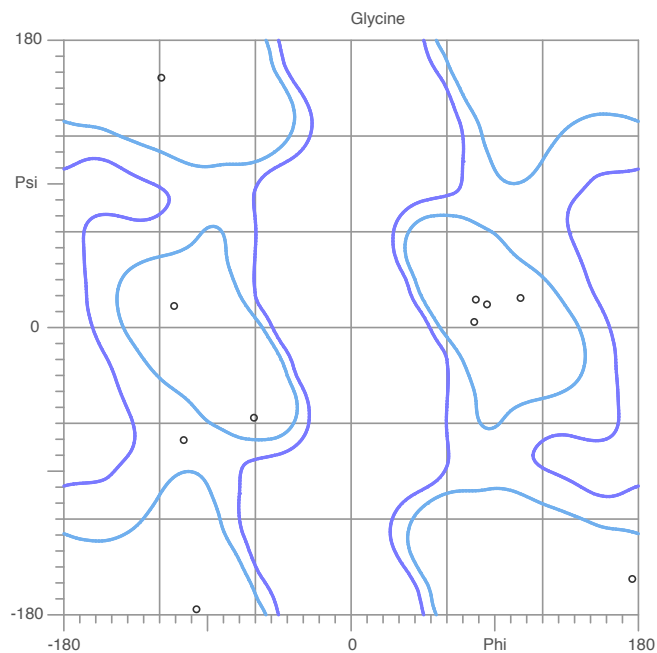
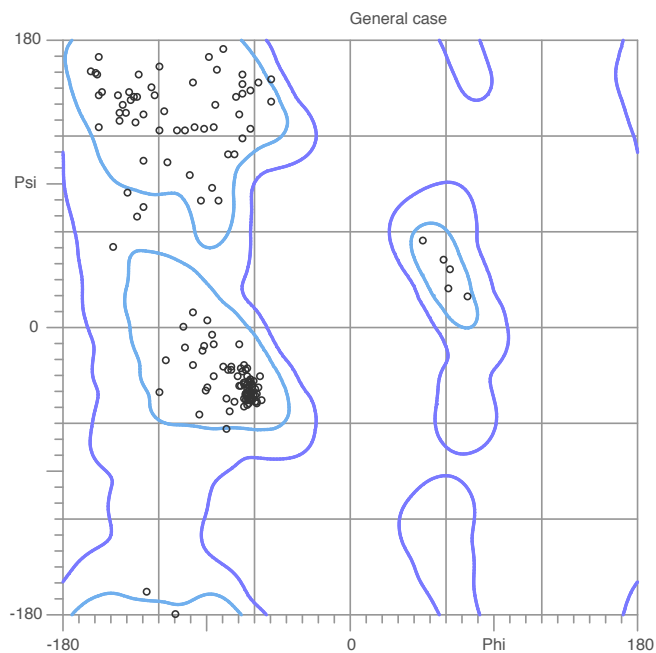
There were 1 outliers (phi, psi):  
[9] 107 ALA (-69.1, -145.0)

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 10



95.4% (165/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

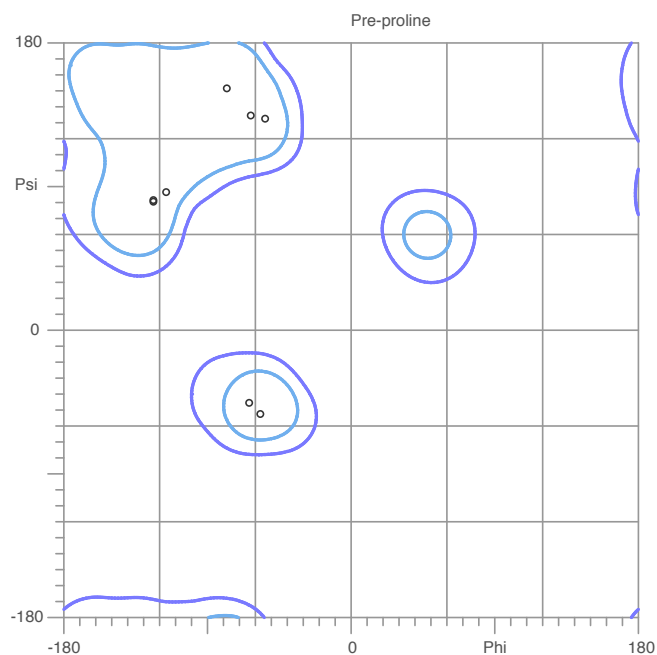
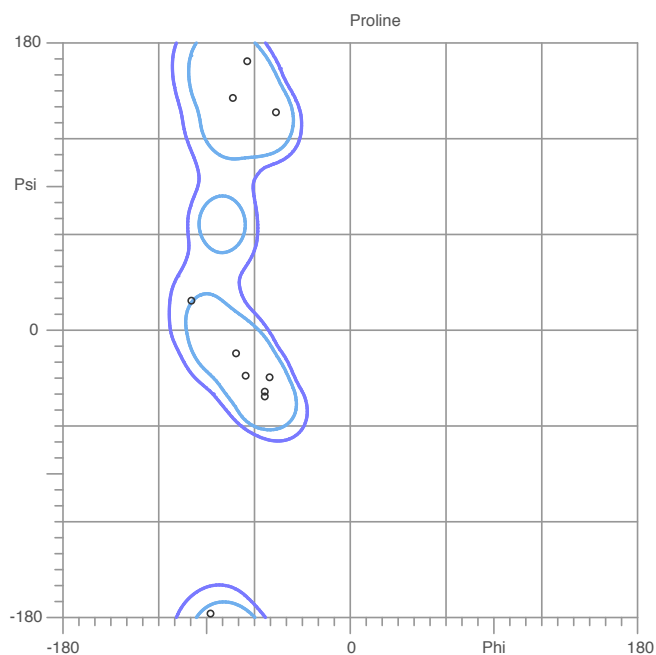
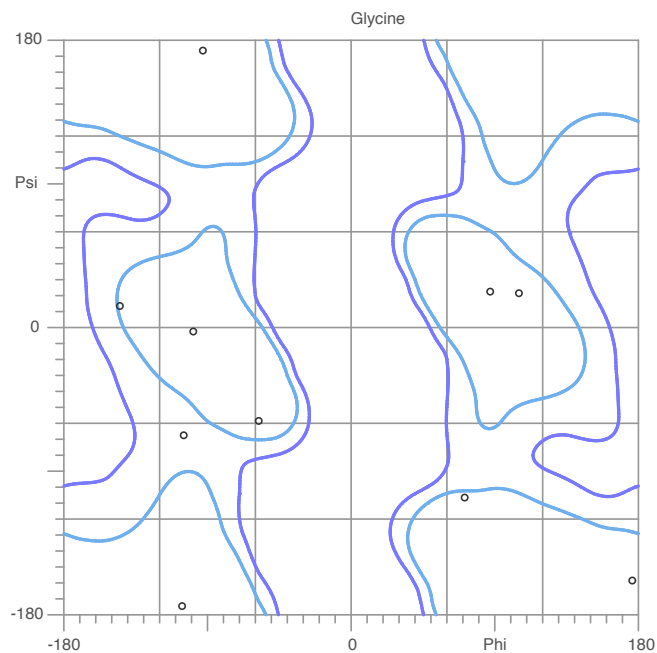
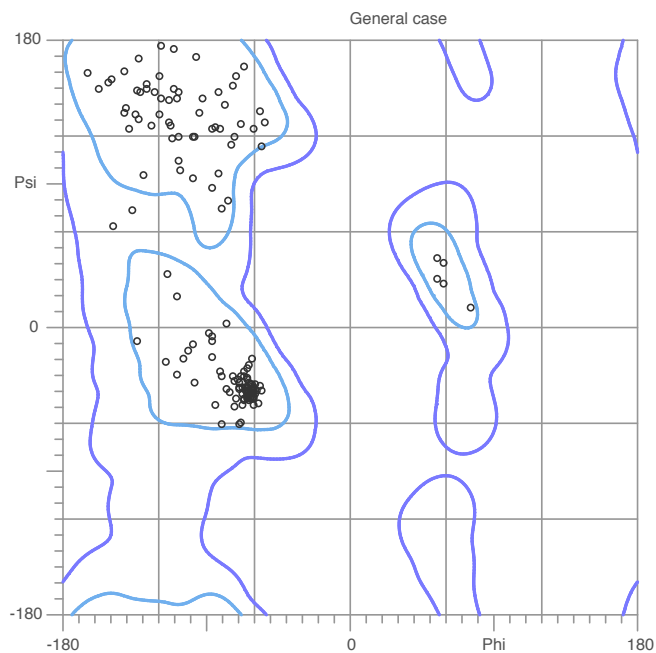
There were no outliers.

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 11



97.7% (169/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

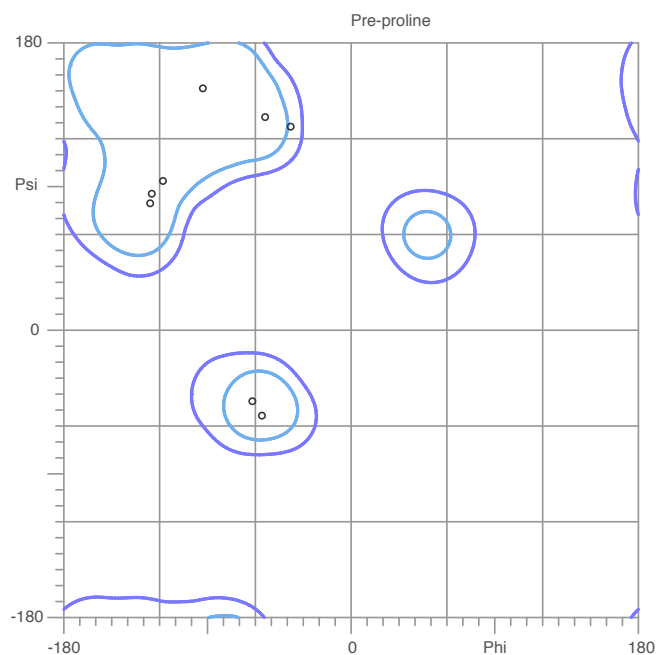
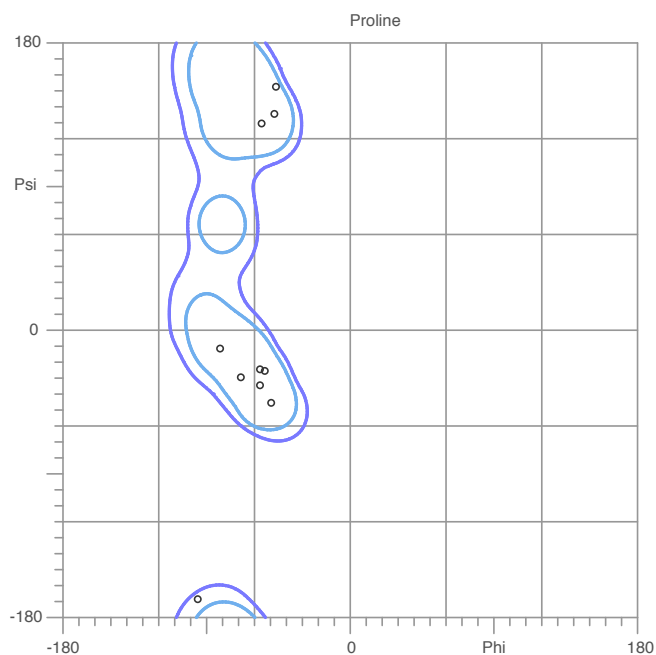
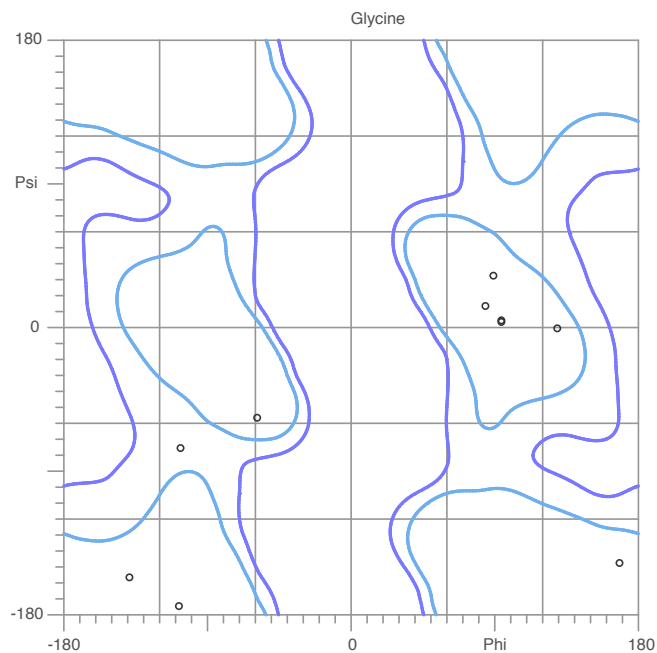
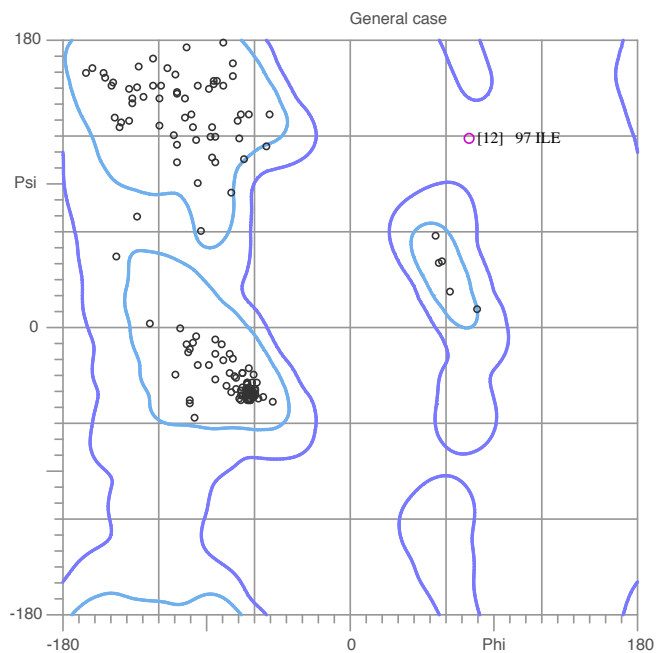
There were no outliers.

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 12



96.0% (166/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

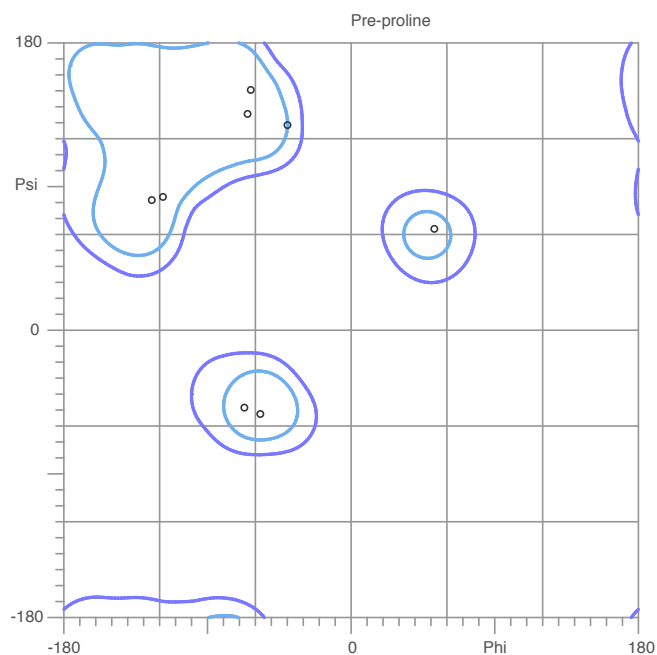
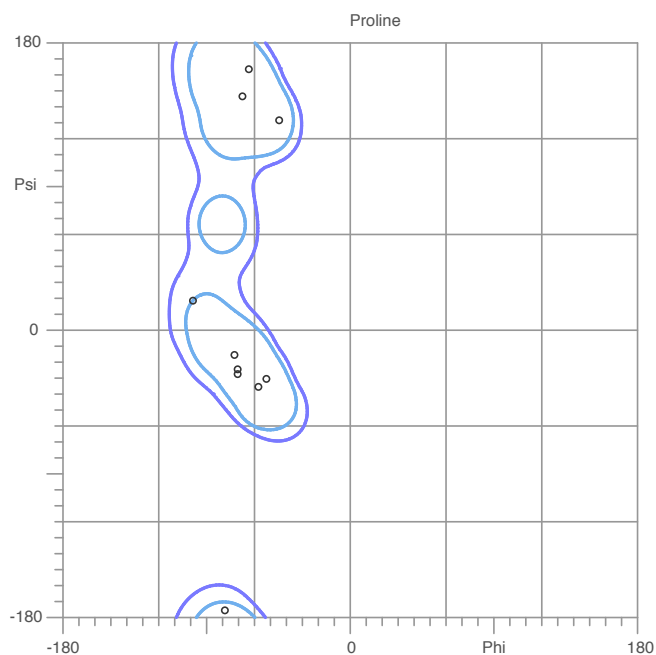
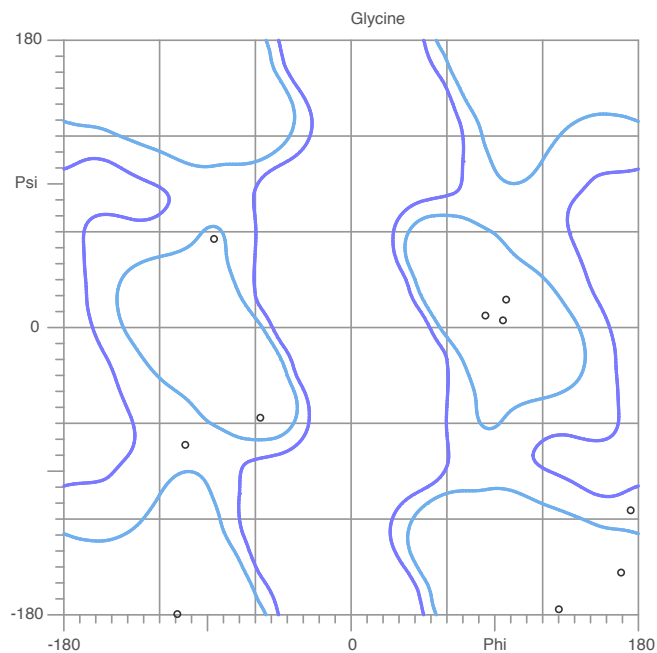
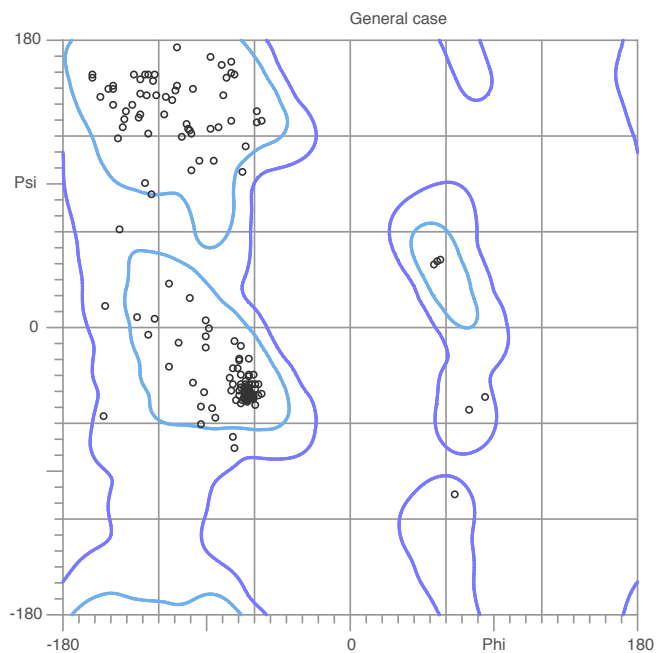
There were 1 outliers (phi, psi):  
[12] 97 ILE (74.9, 119.1)

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 13

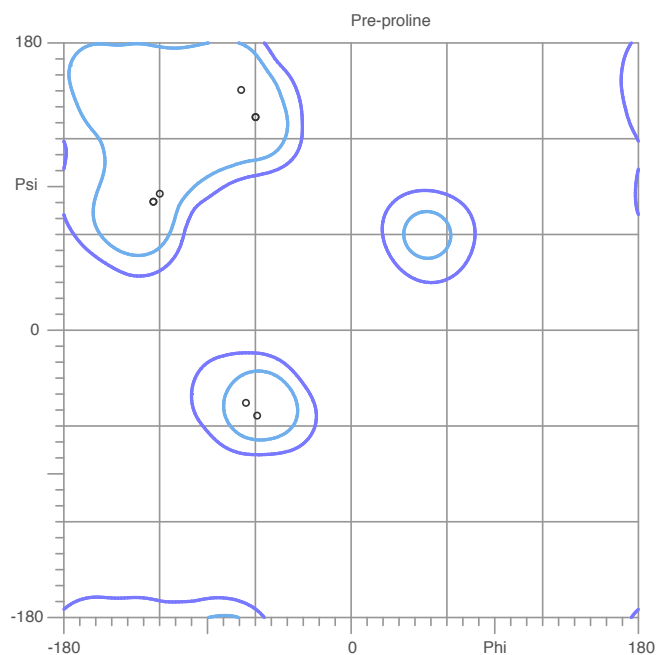
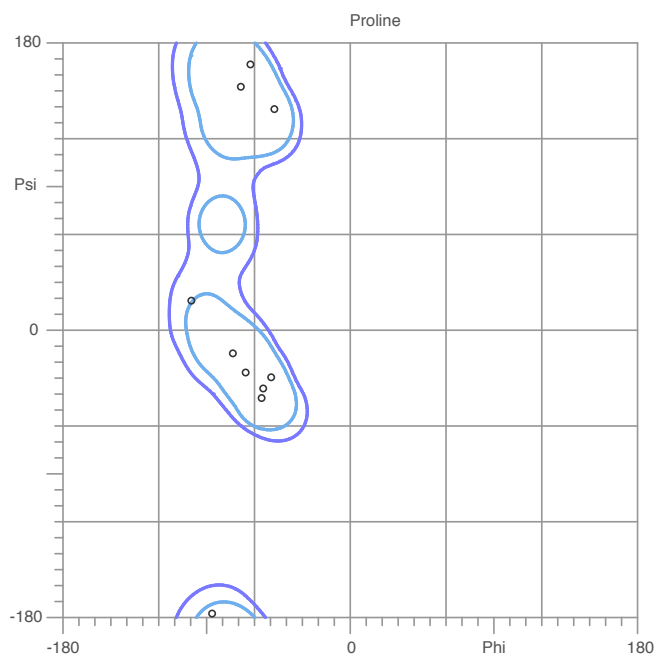
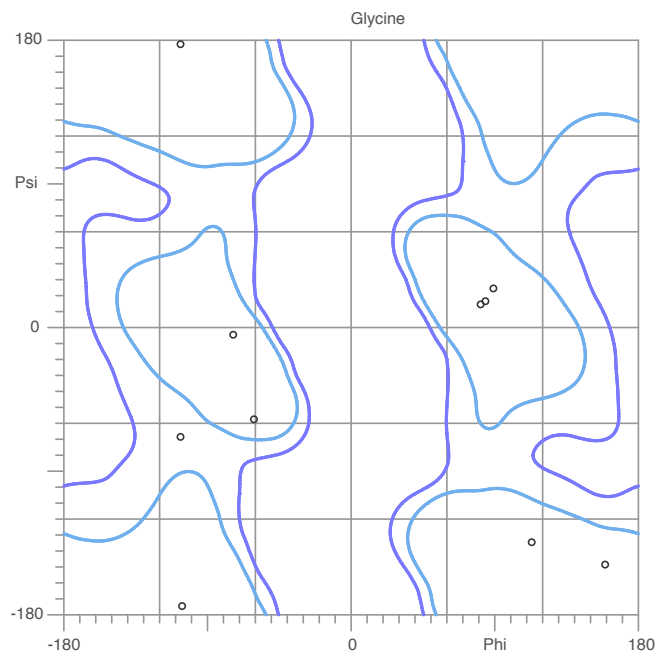
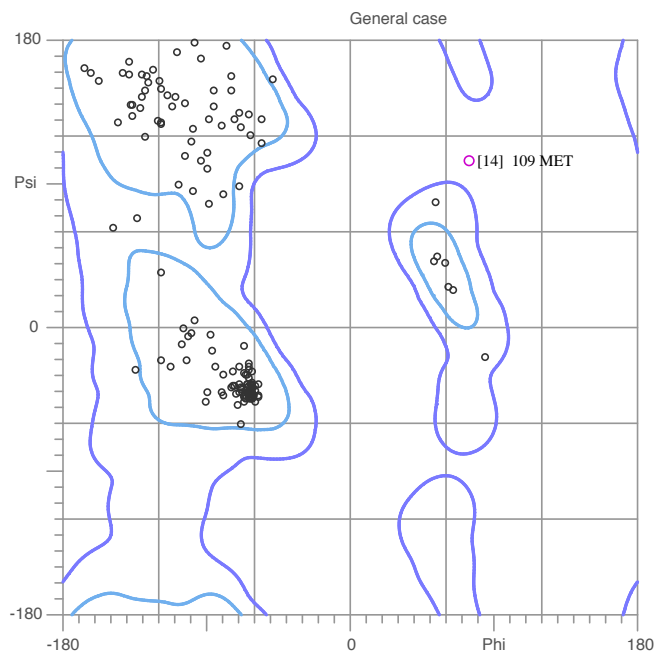


93.1% (161/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 14

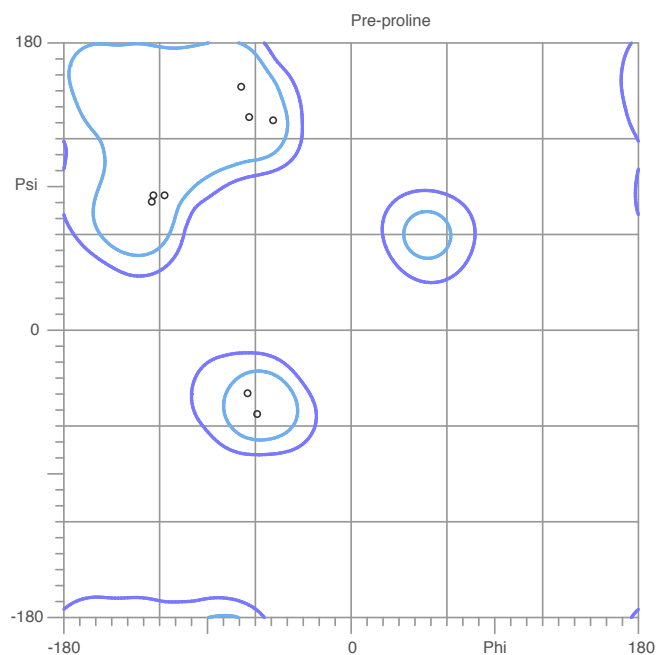
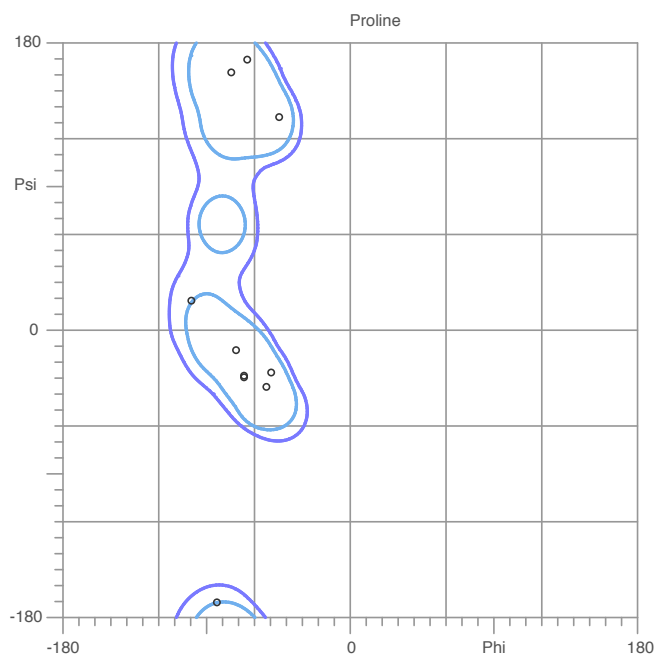
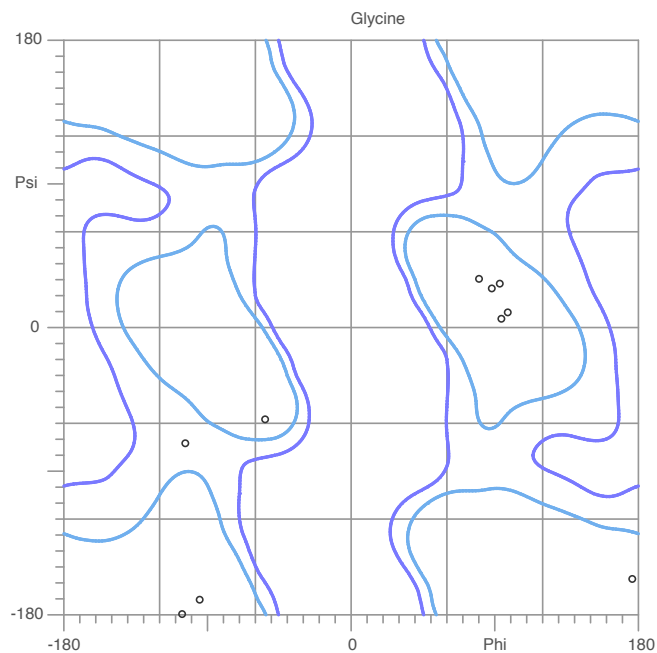
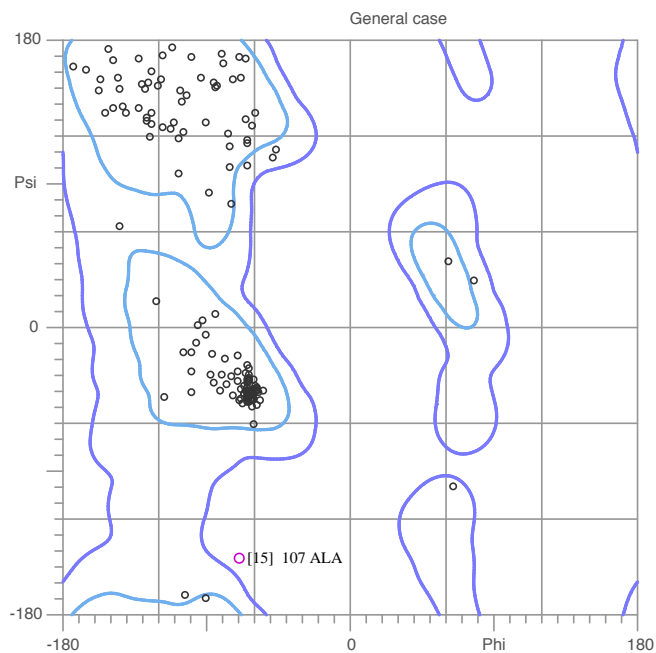


94.2% (163/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[14] 109 MET (74.9, 105.1)

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 15

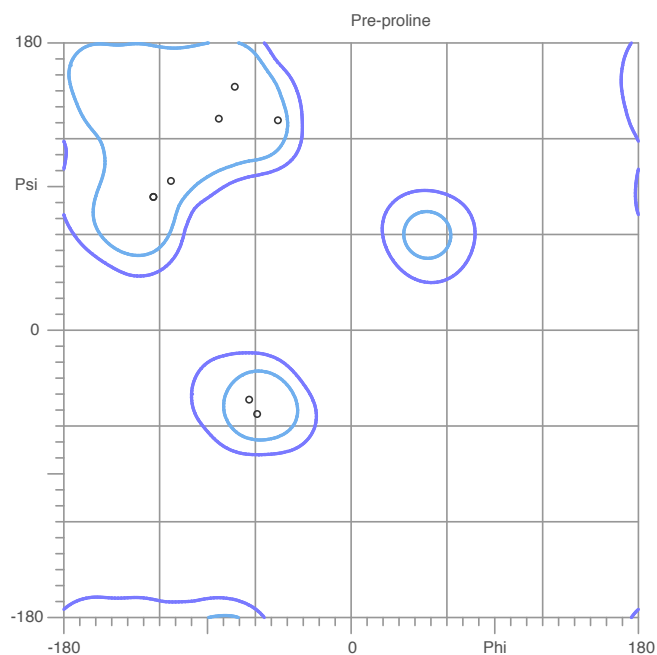
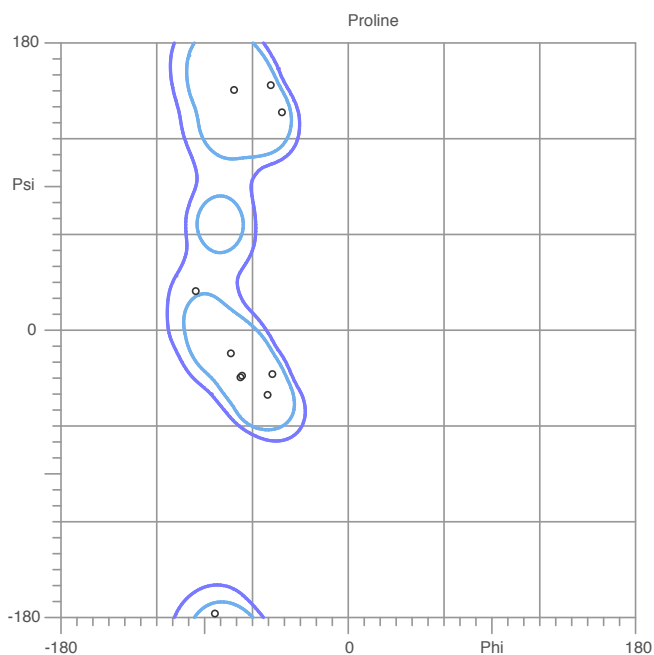
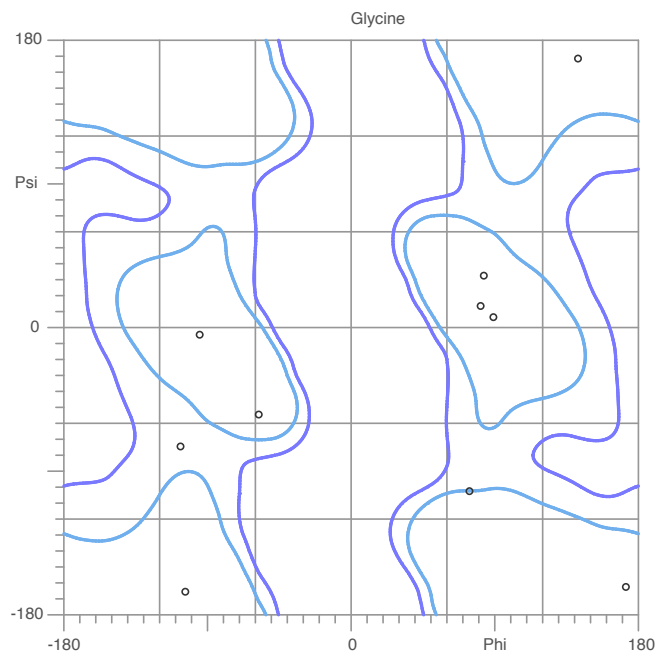
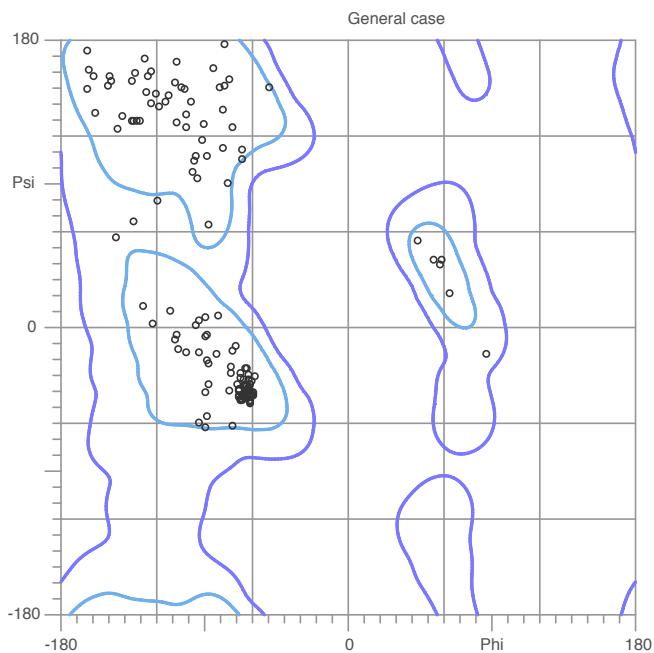


93.6% (162/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[15] 107 ALA (-70.7, -145.0)

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 16



96.5% (167/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

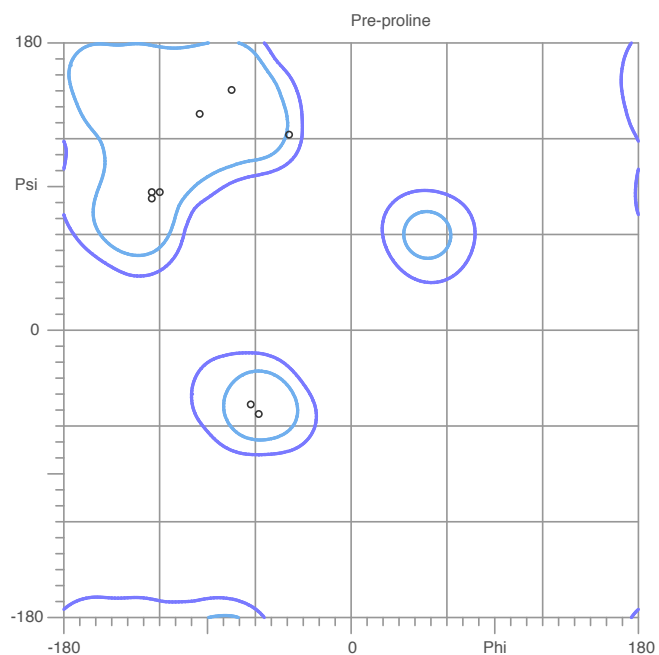
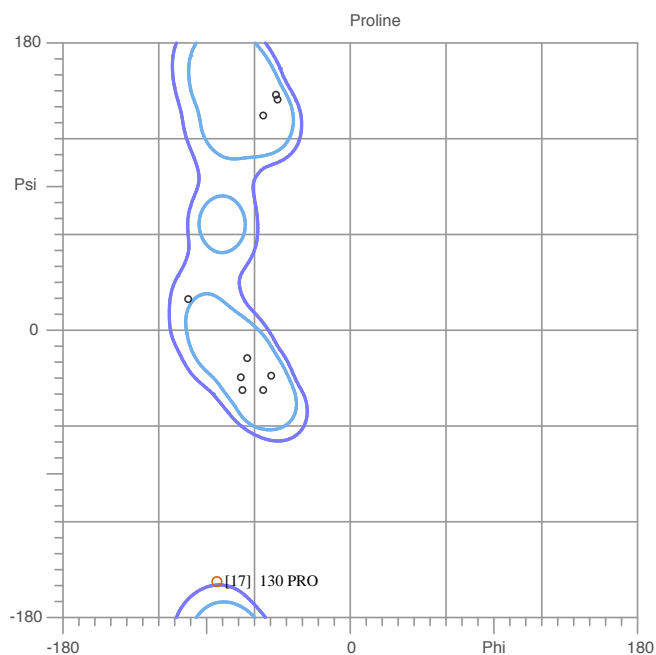
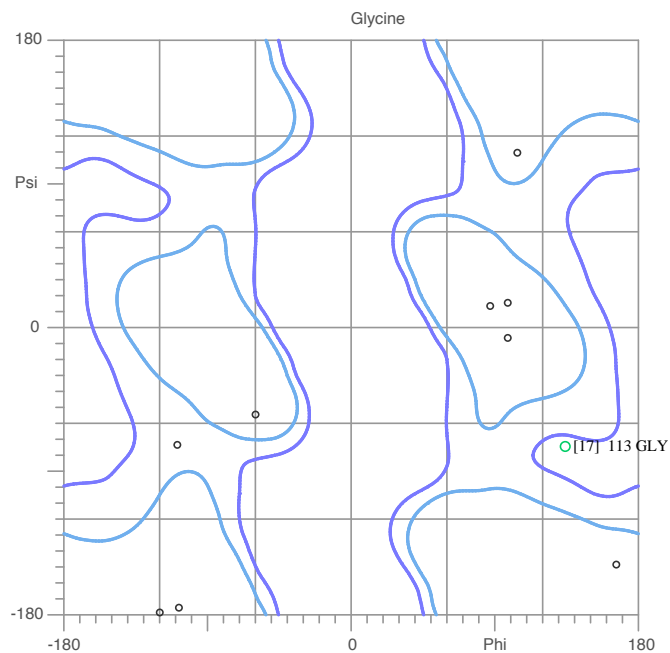
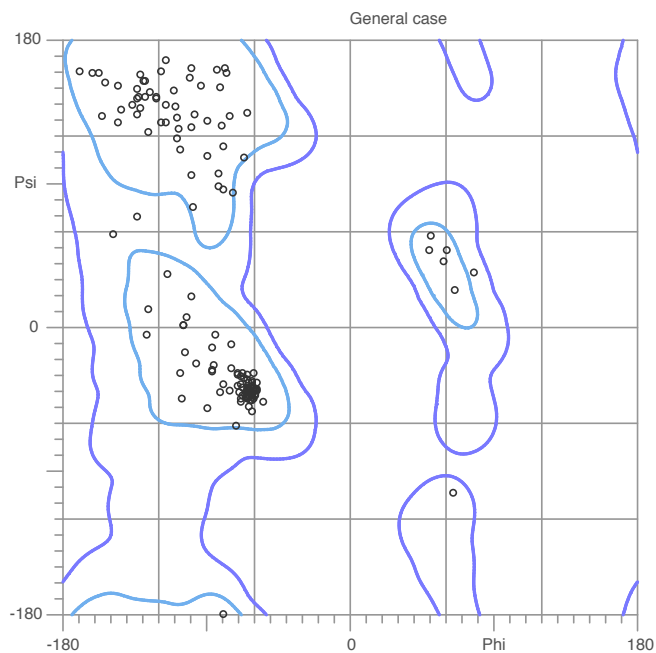
There were no outliers.

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 17

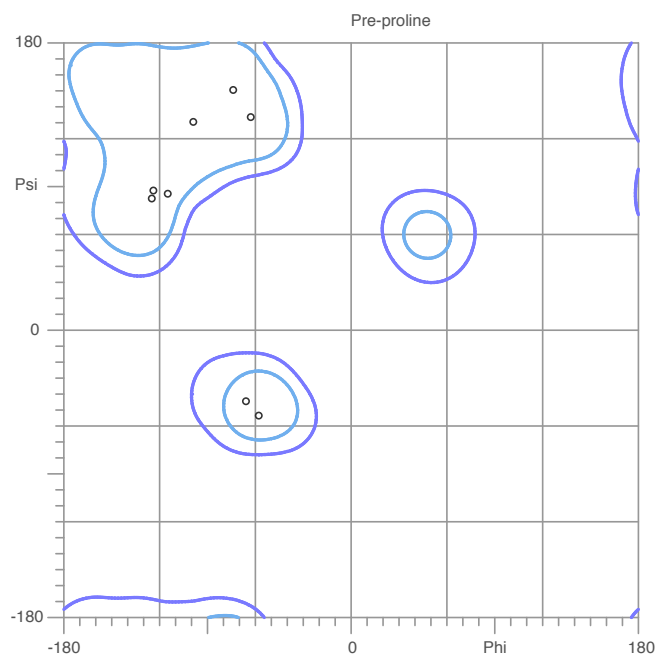
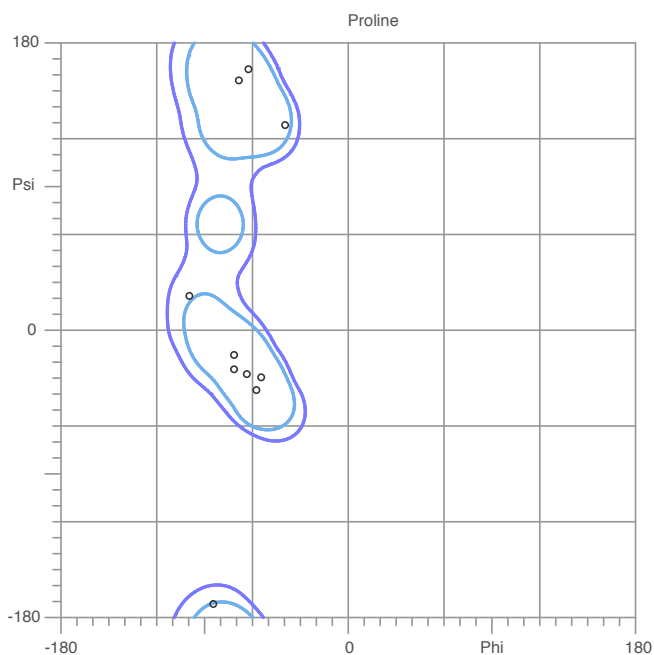
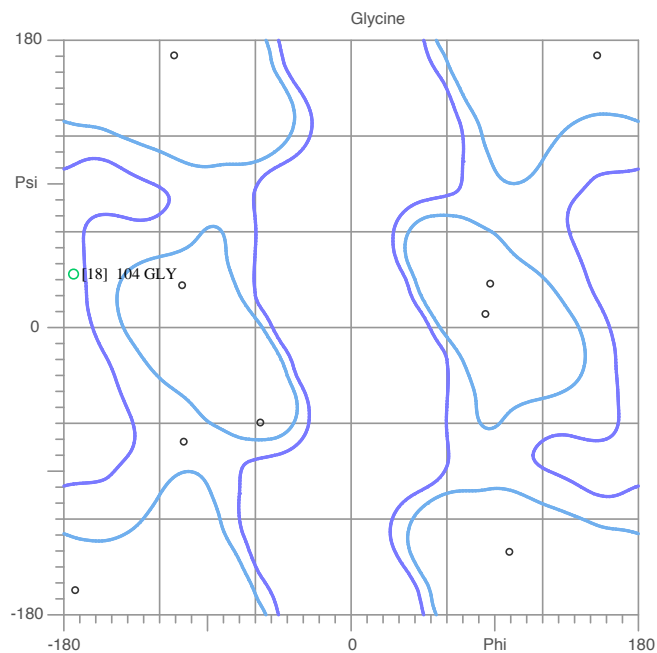
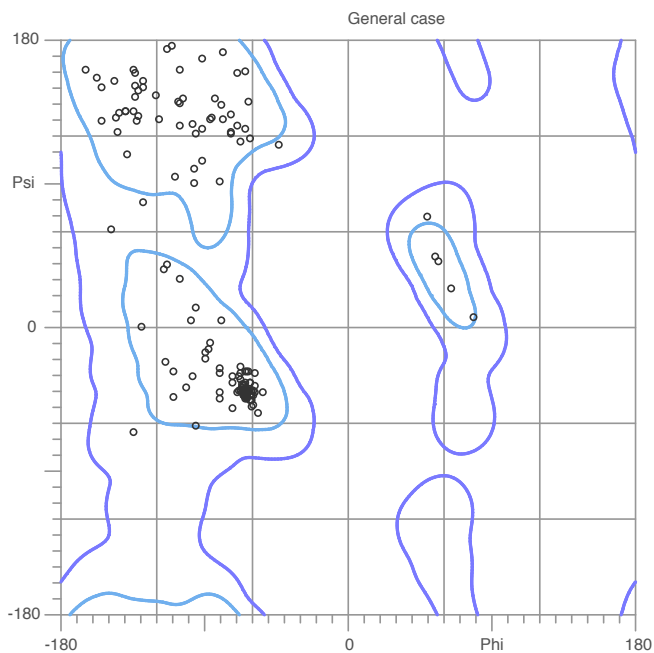


94.8% (164/173) of all residues were in favored (98%) regions.  
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[17] 113 GLY (134.9, -75.0)  
[17] 130 PRO (-85.0, -158.0)

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 18

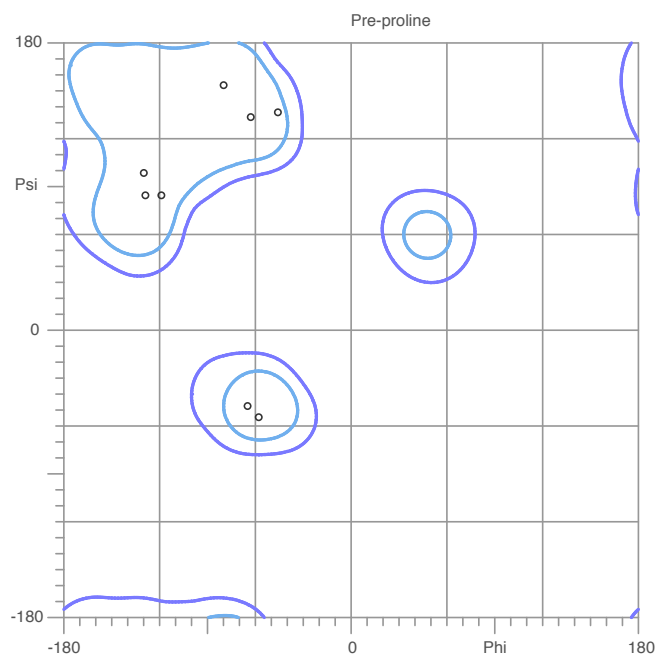
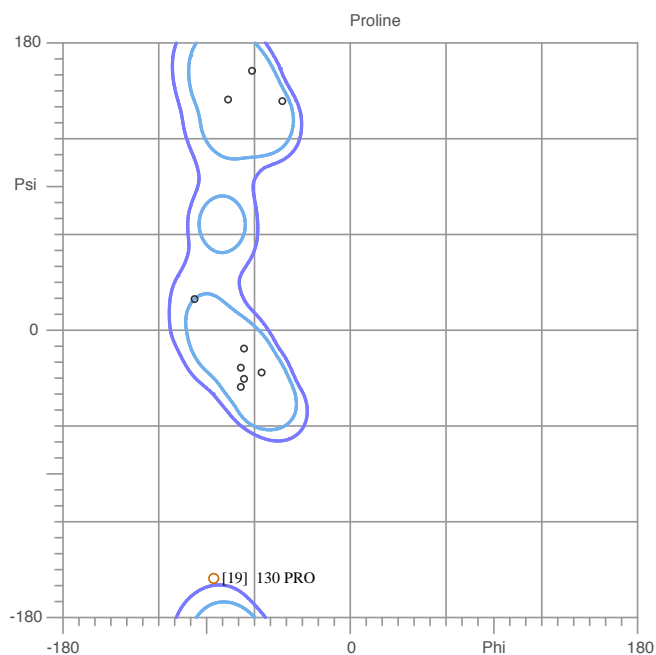
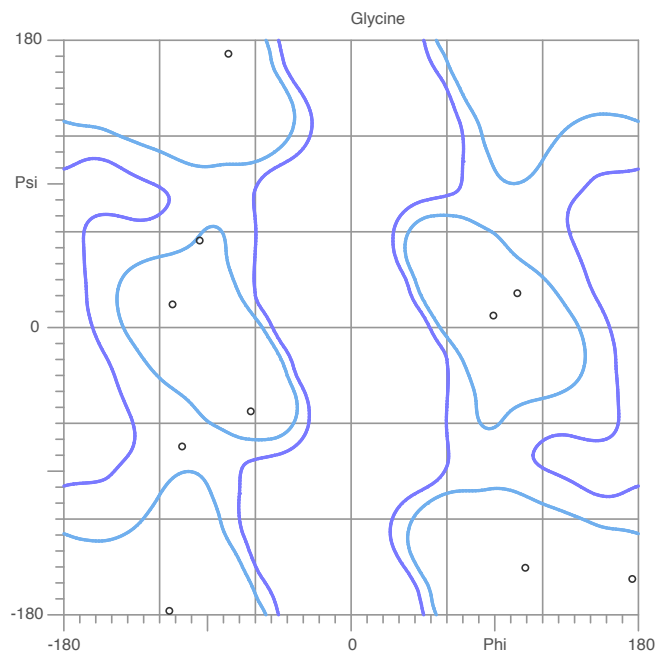
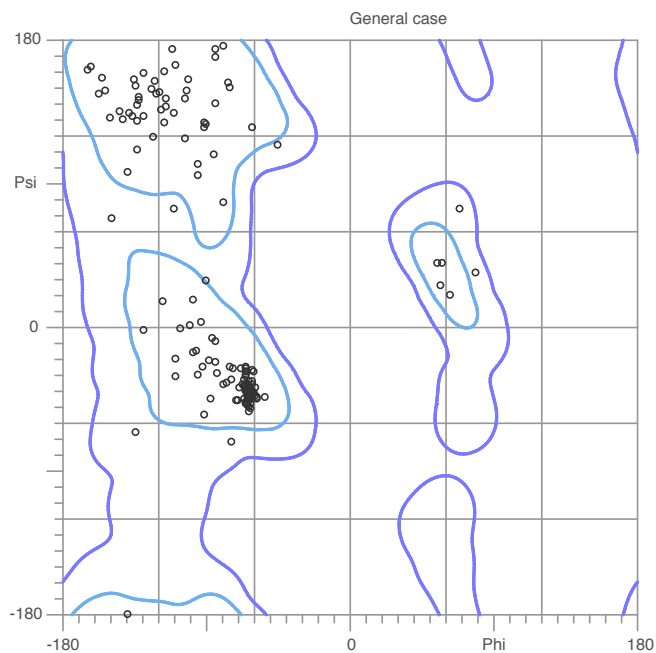


95.4% (165/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[18] 104 GLY (-175.0, 34.0)

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 19



93.6% (162/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

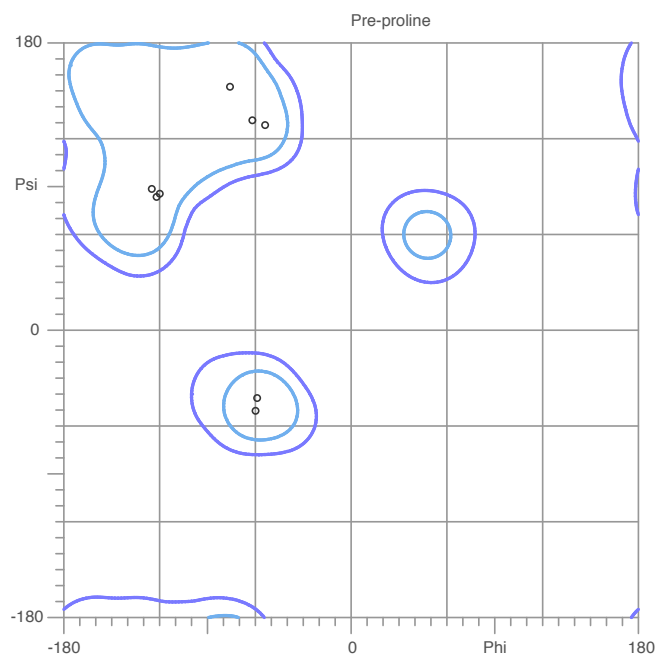
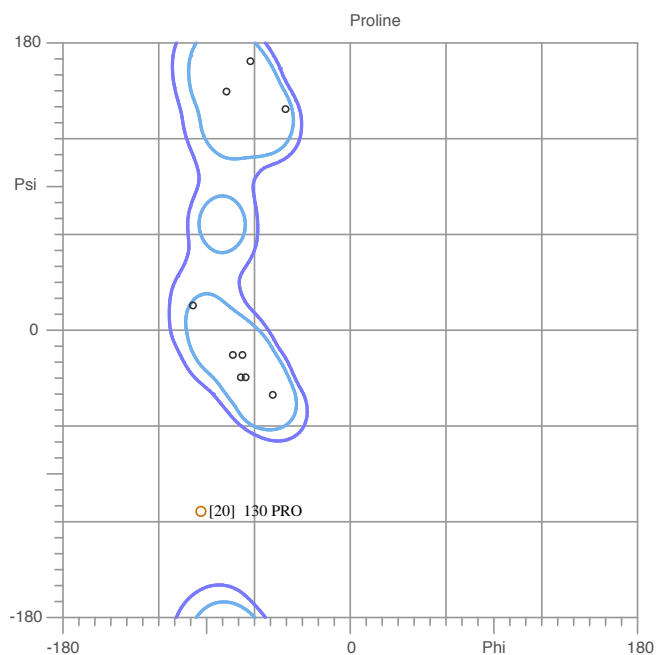
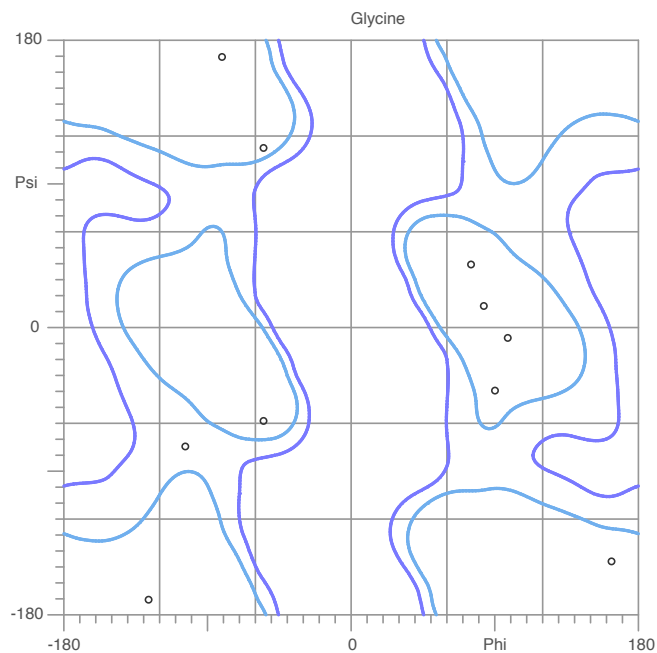
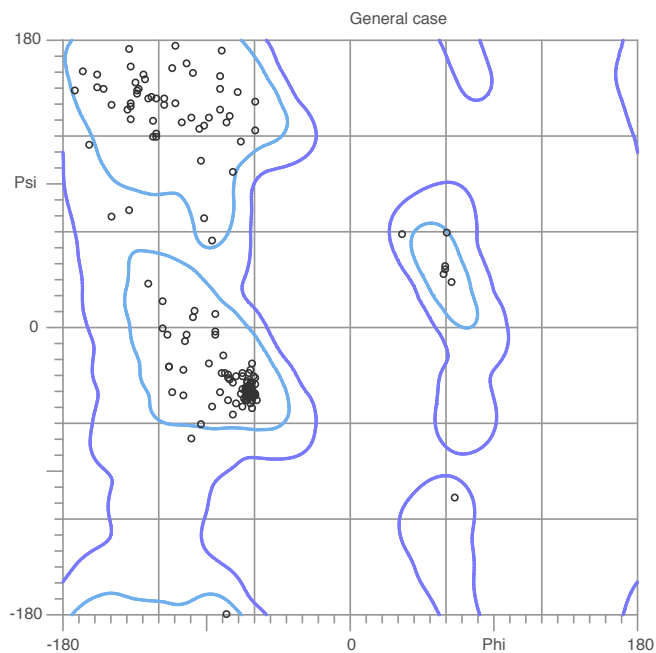
There were 1 outliers (phi, psi):  
[19] 130 PRO (-86.7, -155.8)

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

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

# MolProbity Ramachandran analysis

HR41\_R3Cons\_em\_bcr3.pdb, model 20



95.4% (165/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[20] 130 PRO (-94.9, -113.1)

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

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