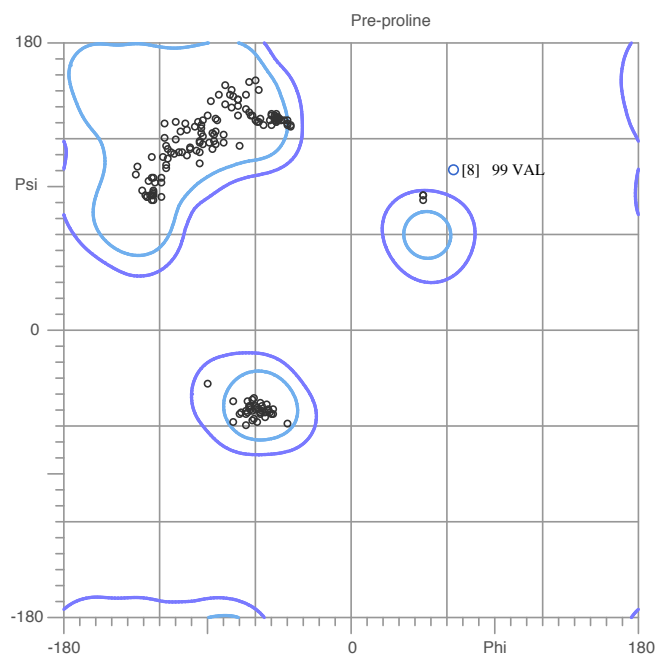
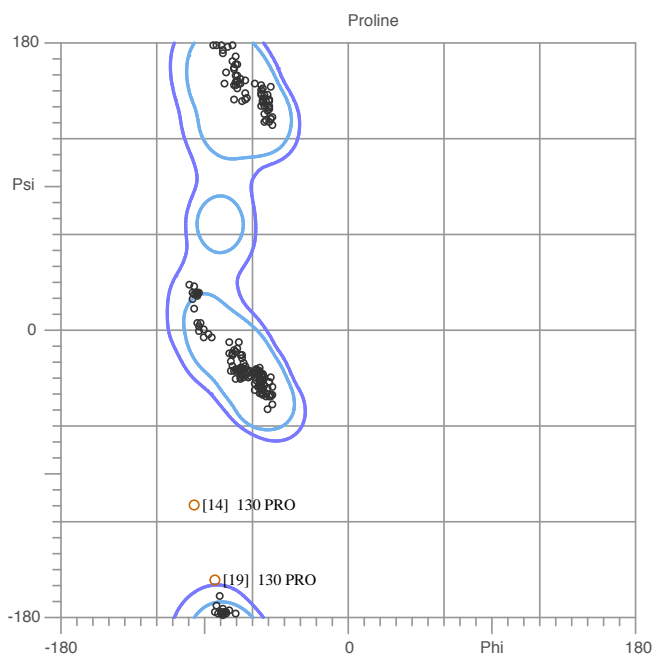
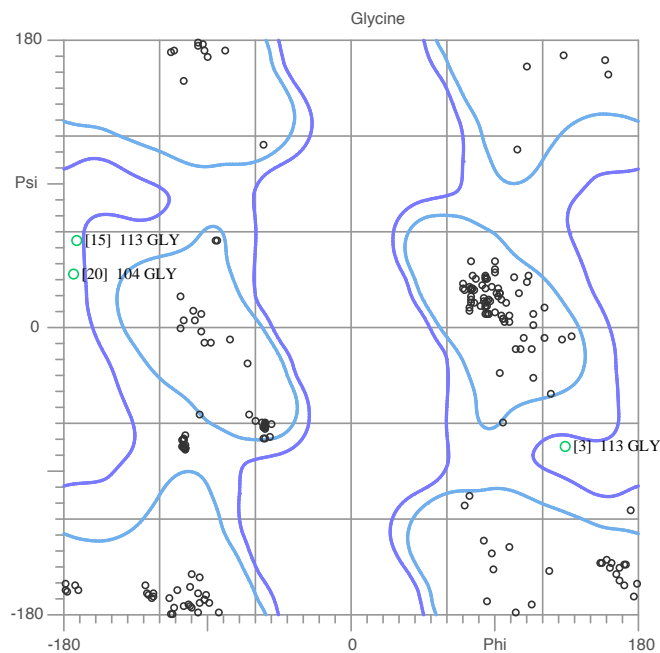
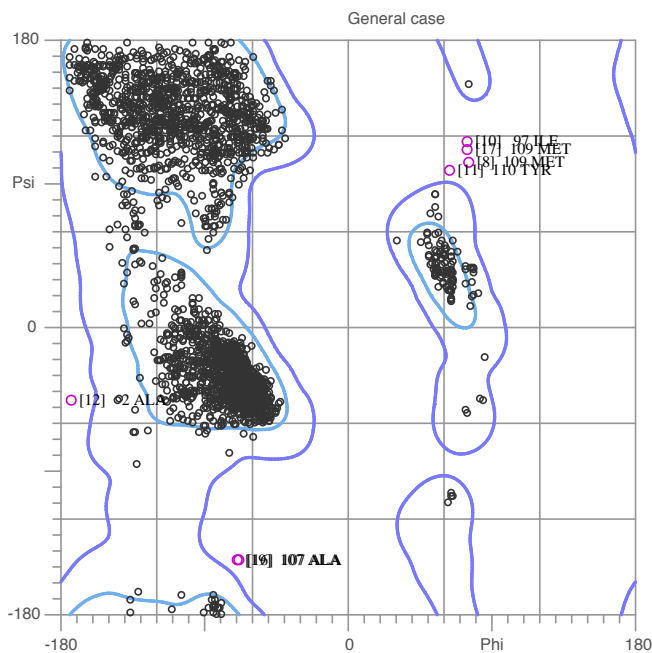


# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, all models



95.4% (3300/3460) of all residues were in favored (98%) regions.  
99.6% (3447/3460) of all residues were in allowed (>99.8%) regions.

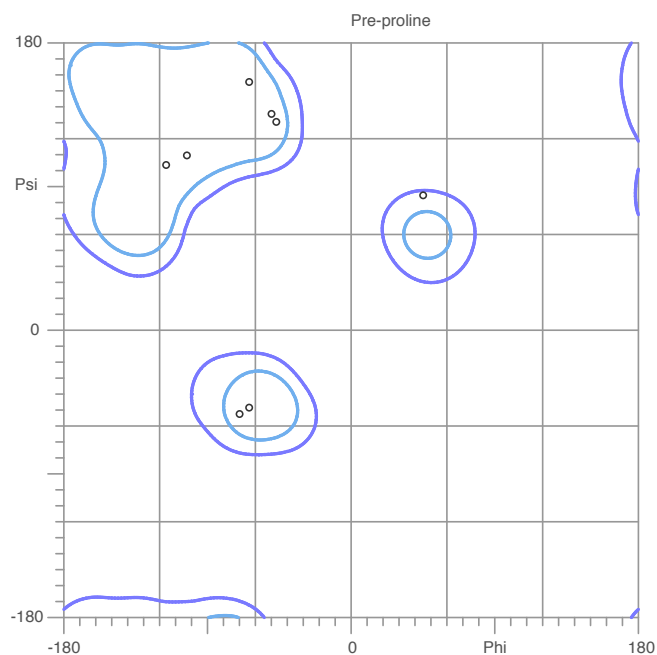
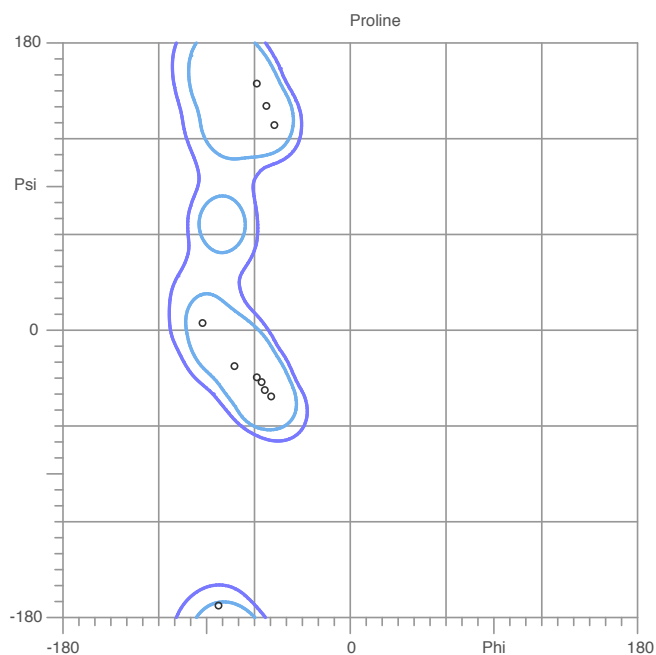
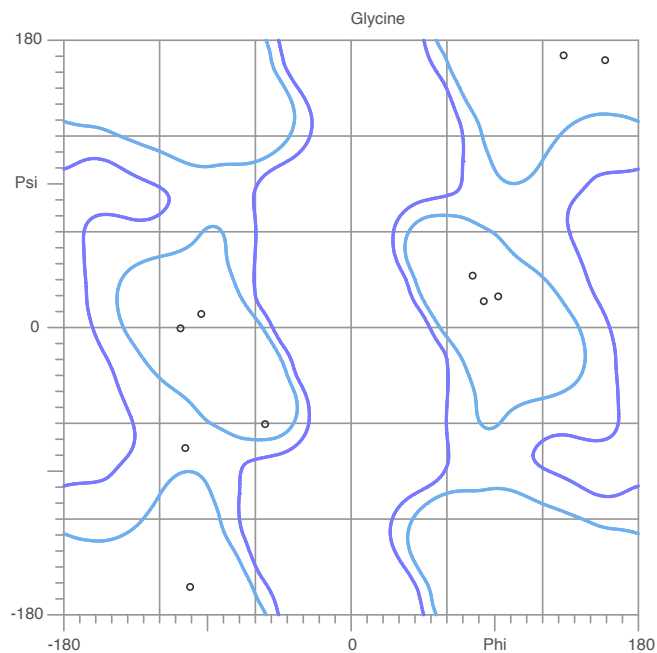
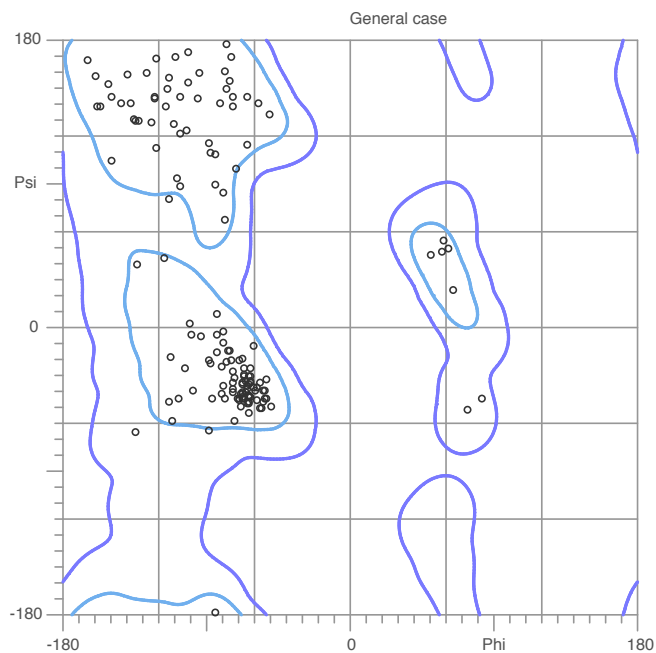
There were 13 outliers (phi, psi):

- [3] 113 GLY (135.0, -75.0)
- [8] 99 VAL (65.0, 101.3)
- [8] 109 MET (75.1, 105.0)
- [10] 97 ILE (74.9, 117.5)

- [11] 110 TYR (63.4, 99.4)
- [12] 2 ALA (-175.0, -45.0)
- [14] 130 PRO (-97.3, -109.5)
- [15] 113 GLY (-172.5, 55.1)
- [16] 107 ALA (-69.2, -145.0)
- [17] 109 MET (75.0, 112.1)
- [19] 107 ALA (-70.1, -145.0)
- [19] 130 PRO (-84.8, -156.8)
- [20] 104 GLY (-175.0, 34.8)

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 1

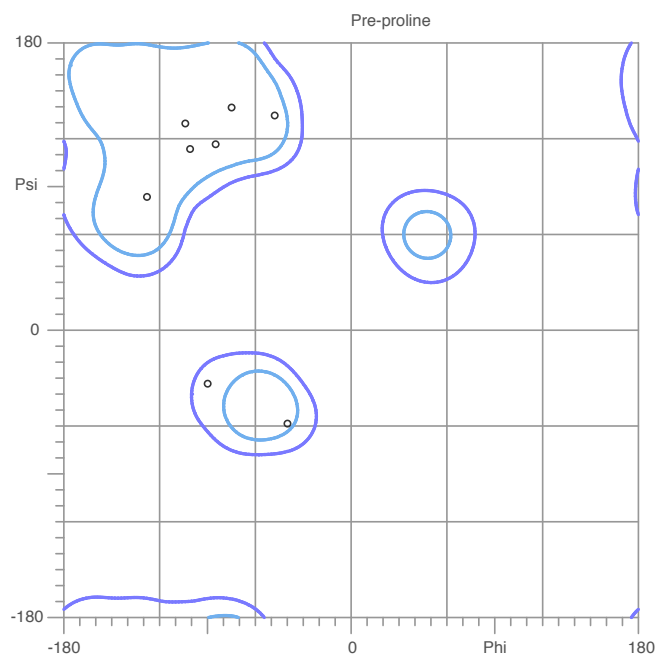
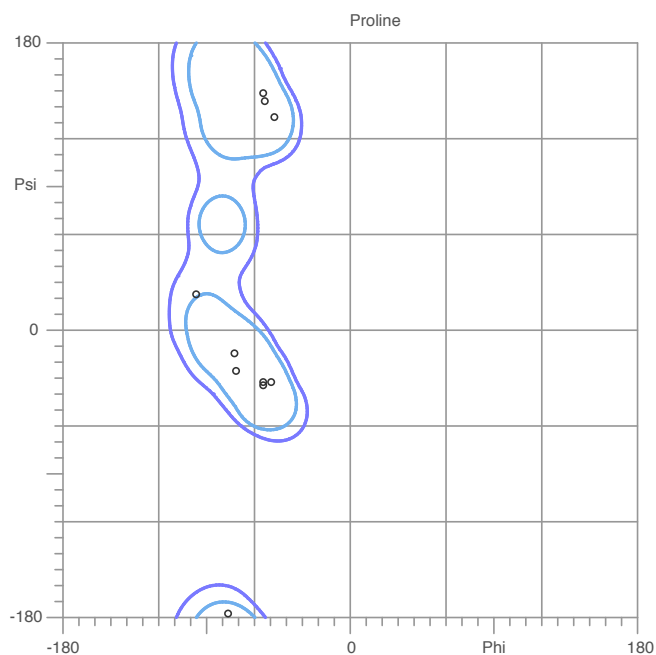
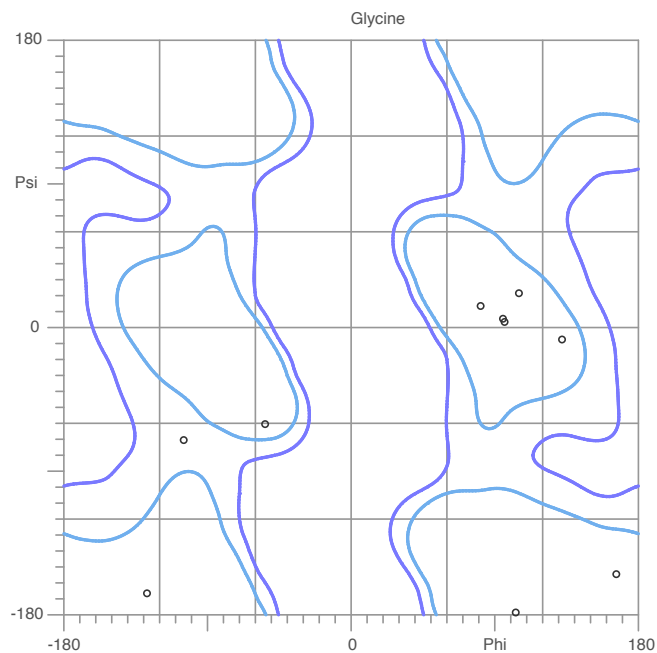
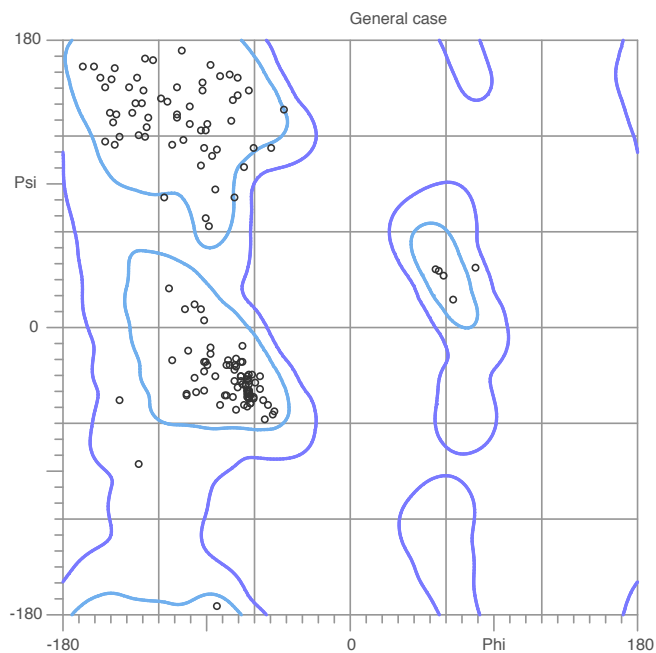


96.0% (166/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 2

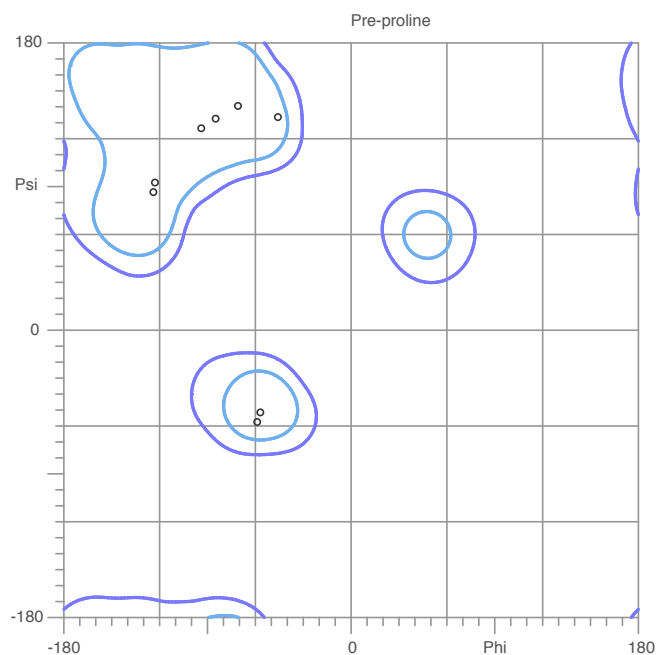
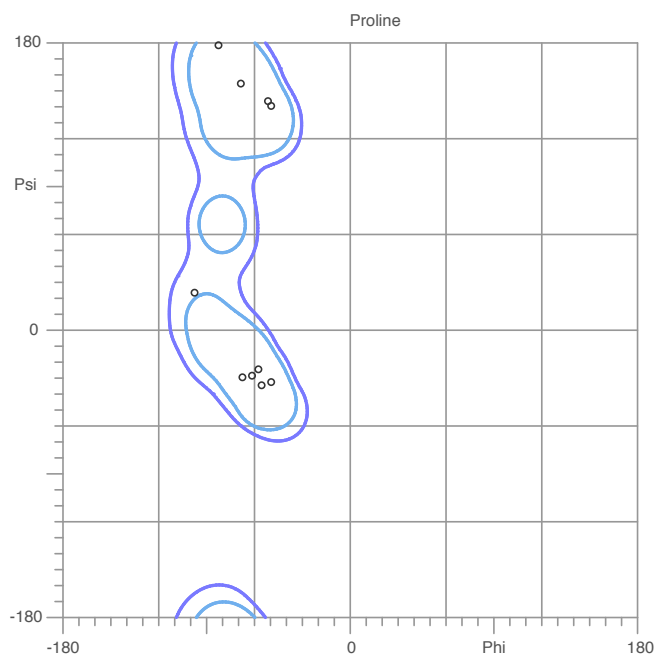
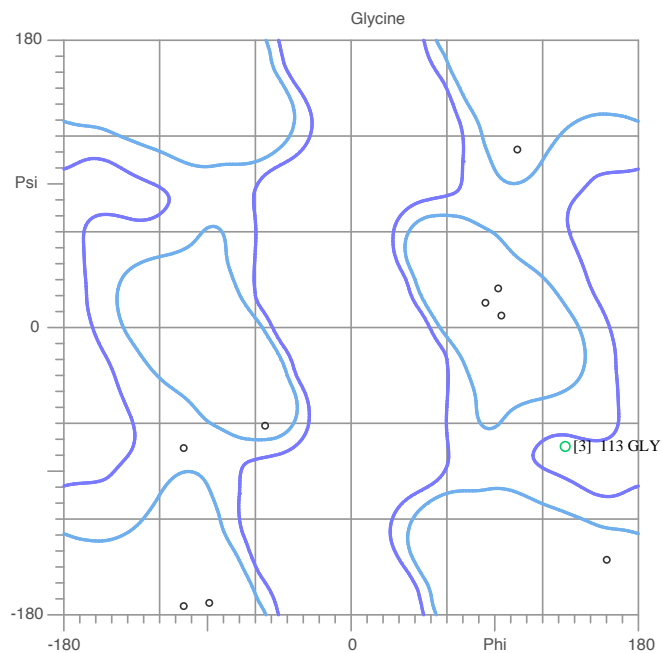
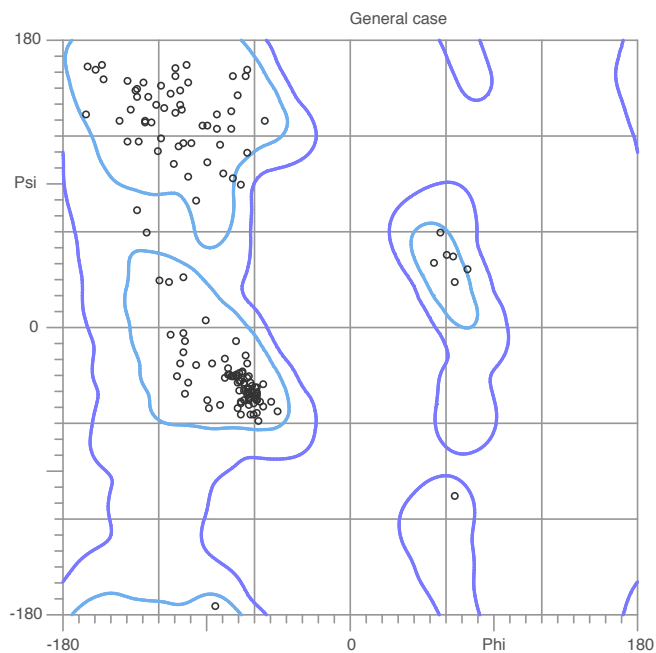


94.2% (163/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 3

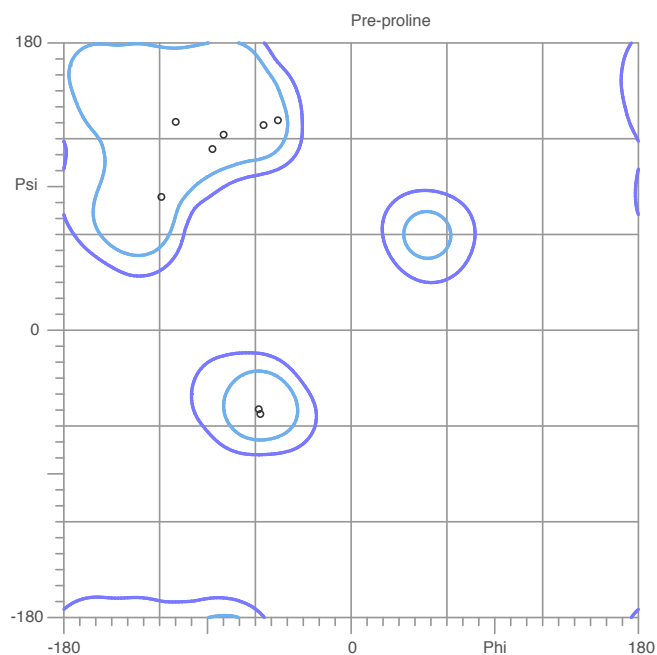
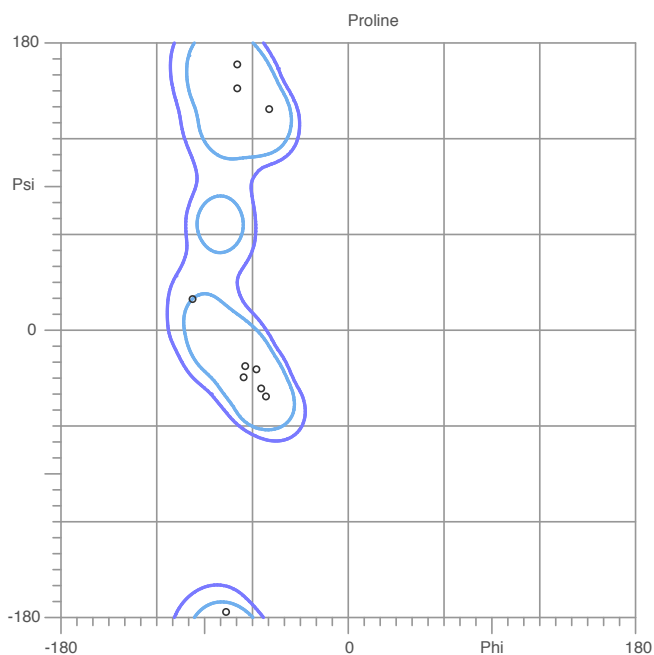
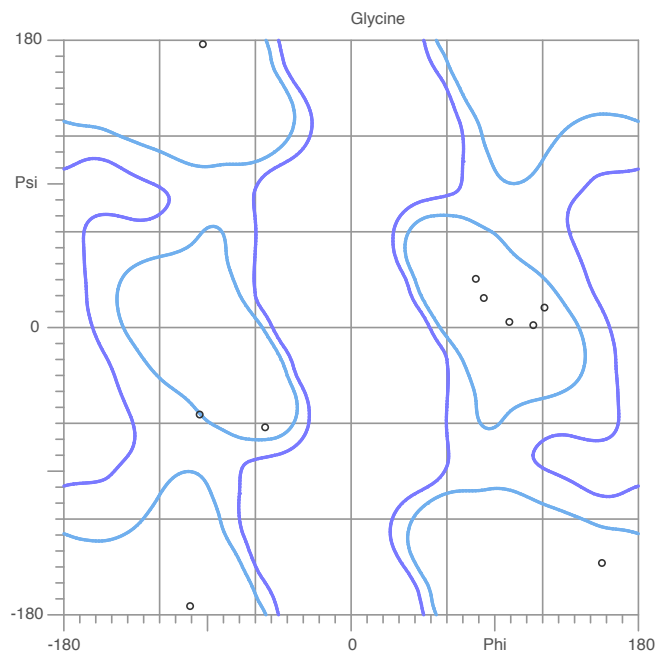
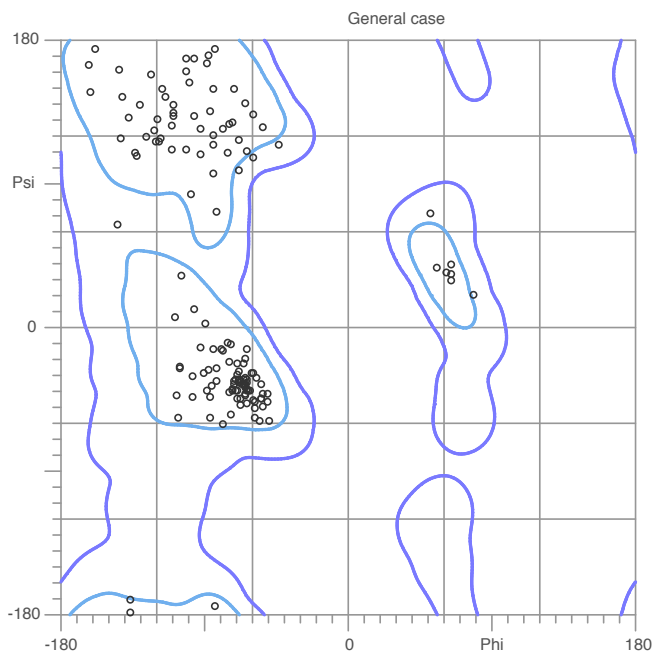


95.4% (165/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[3] 113 GLY (135.0, -75.0)

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 4



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.

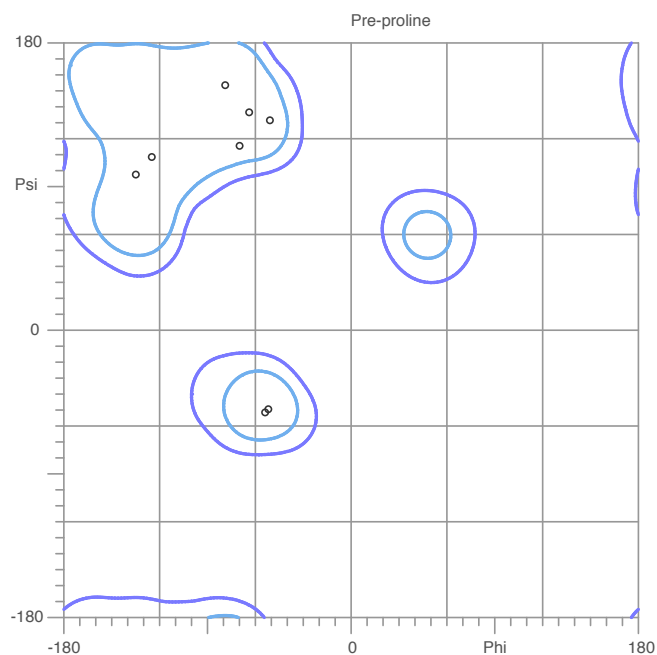
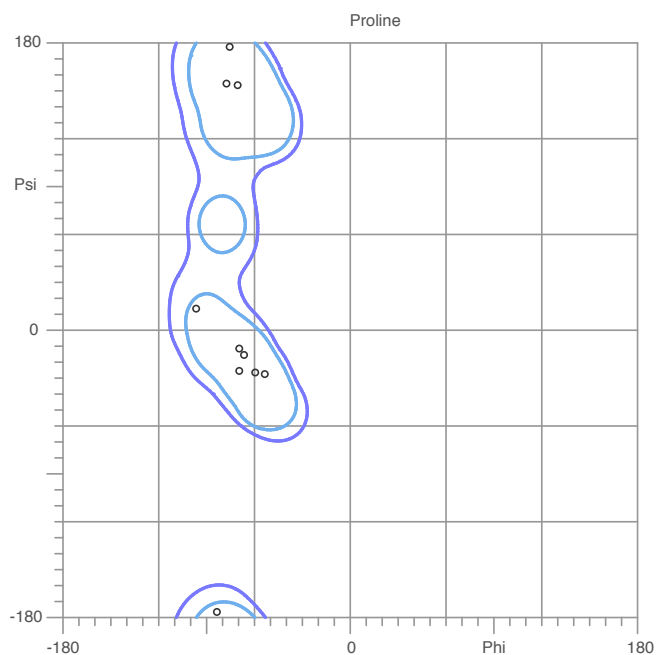
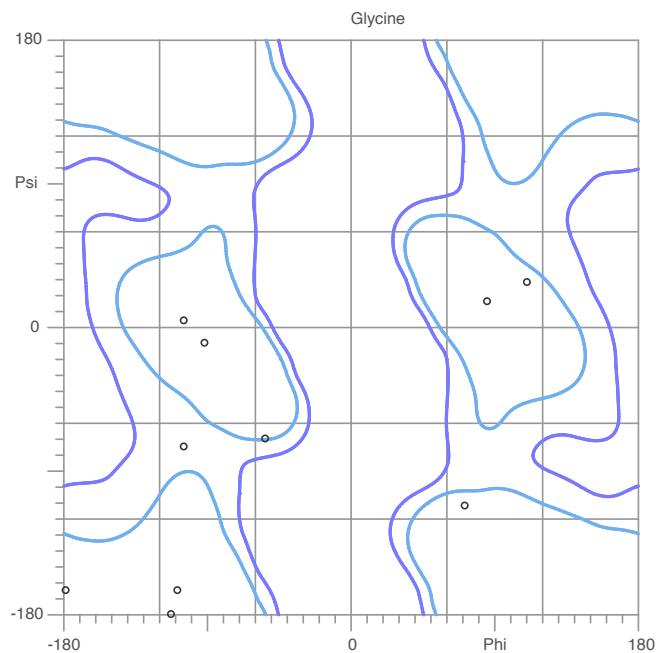
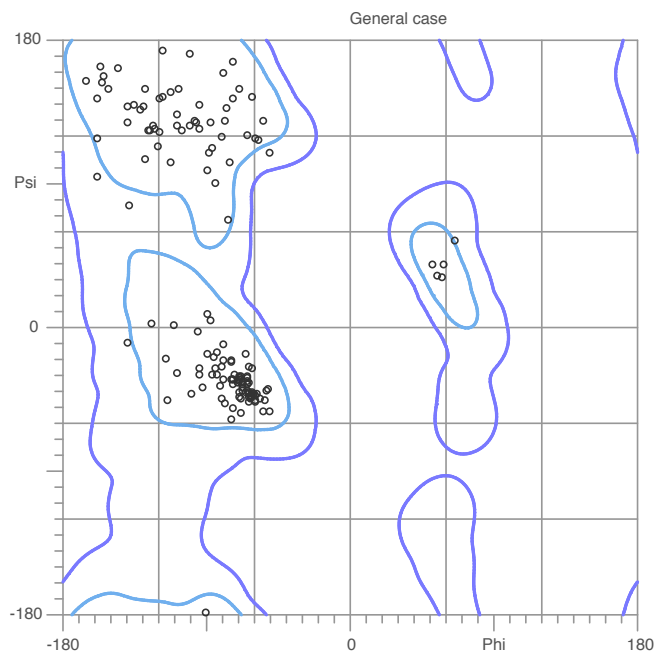
There were no outliers.

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

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# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 5



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.

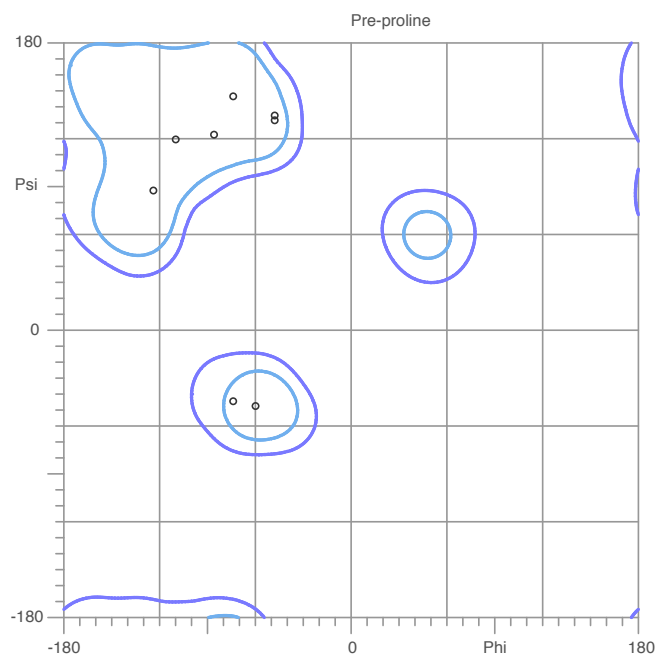
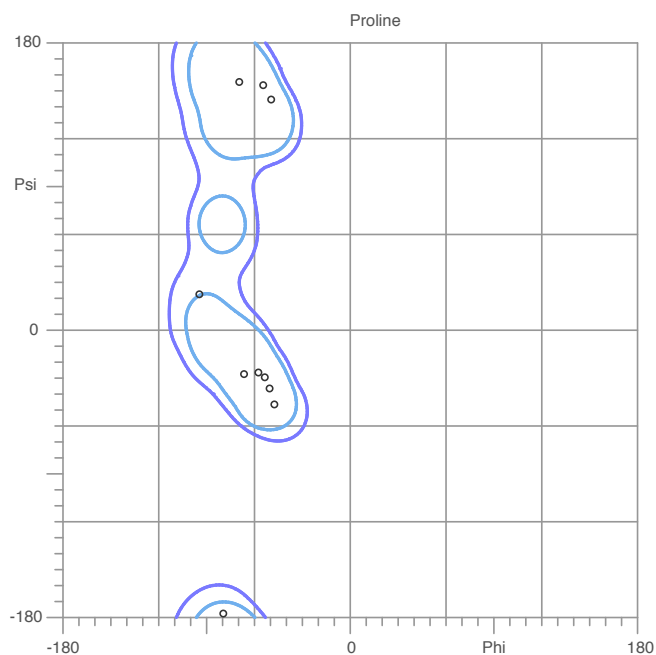
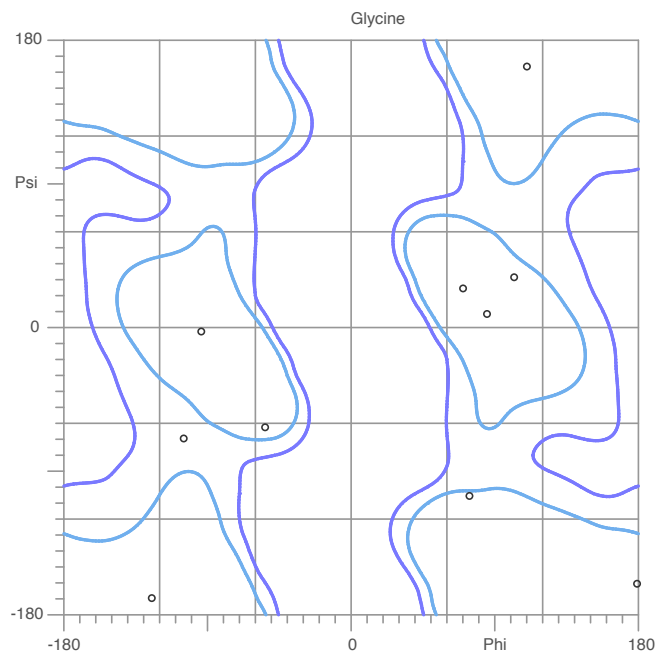
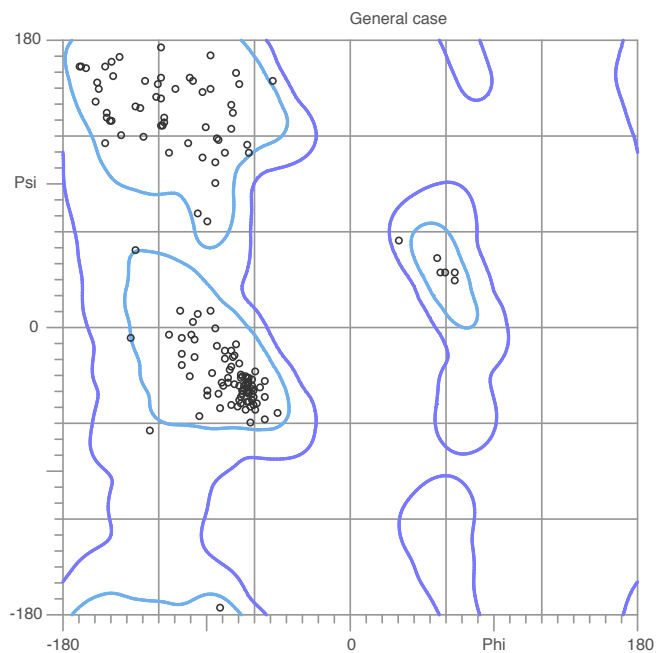
There were no outliers.

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

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# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 6



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.

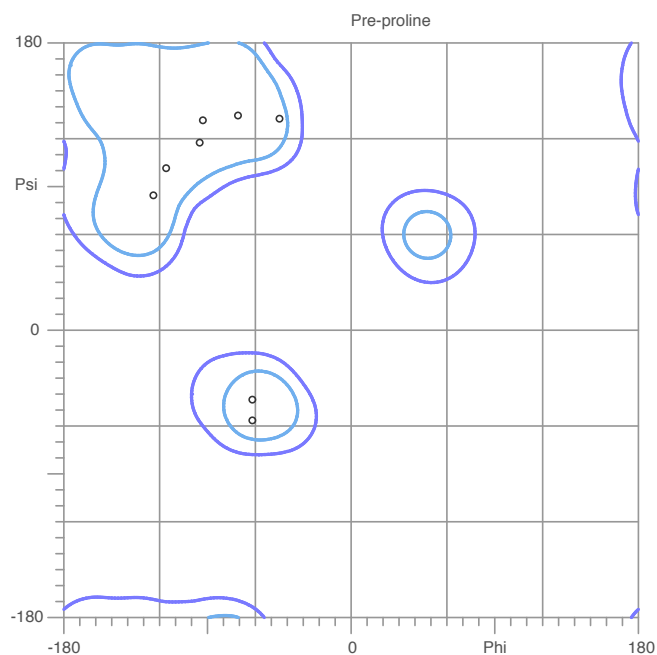
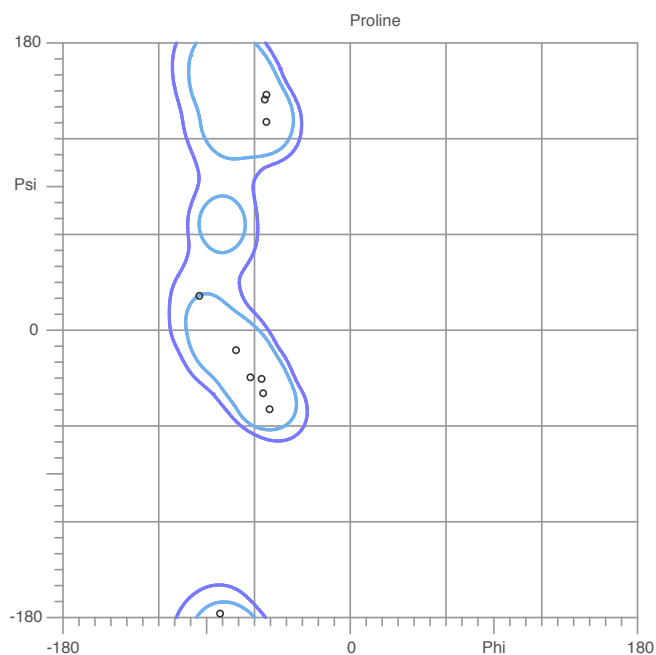
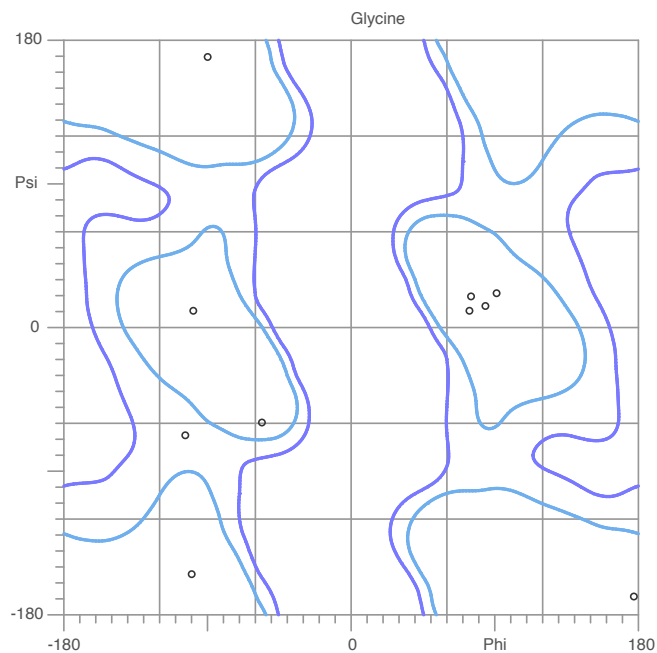
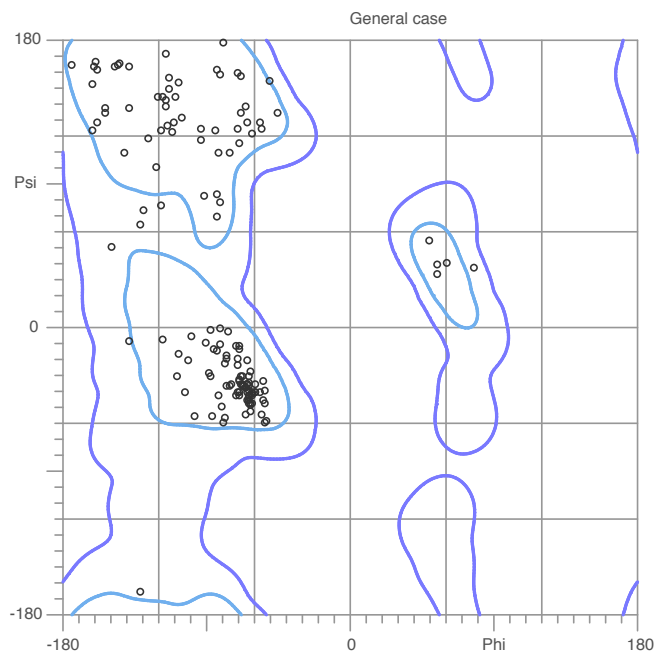
There were no outliers.

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# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 7

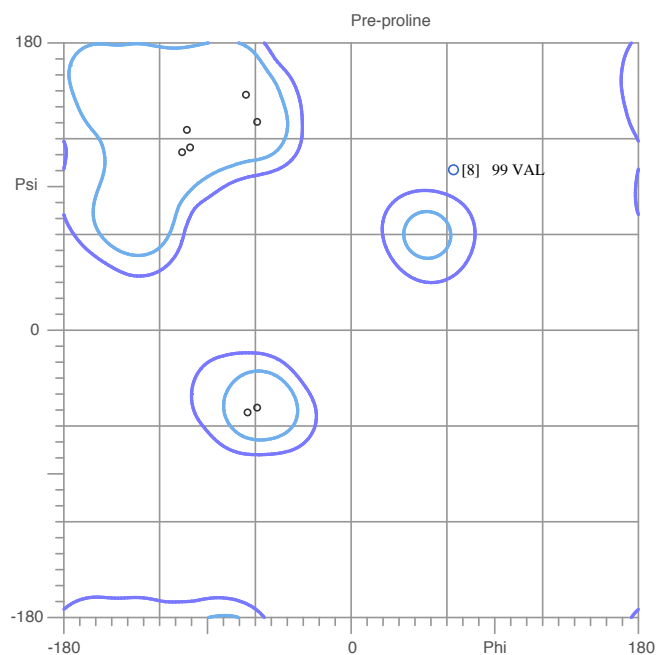
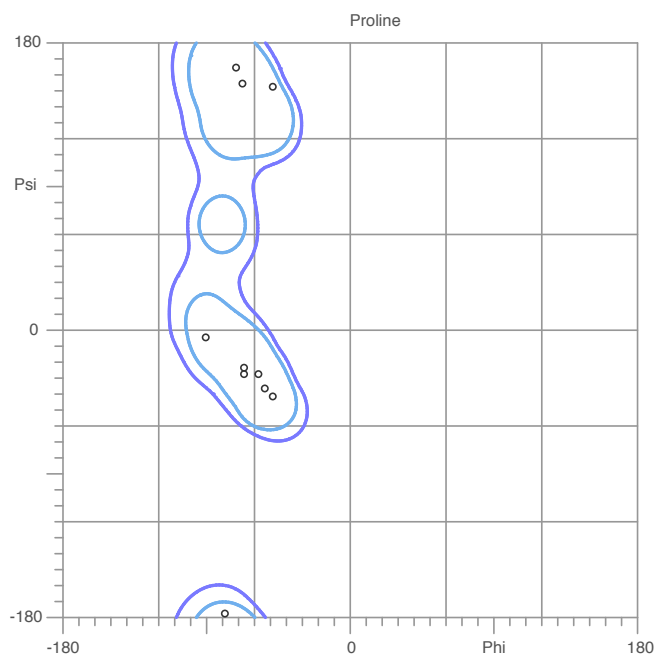
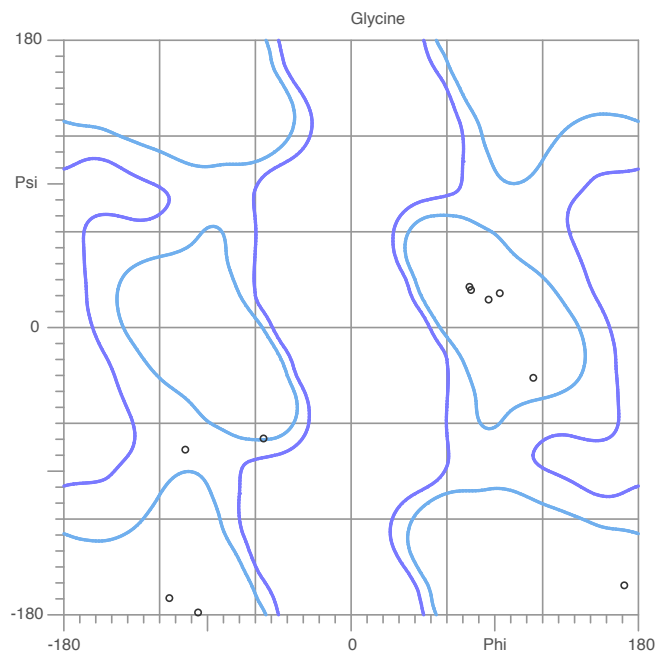
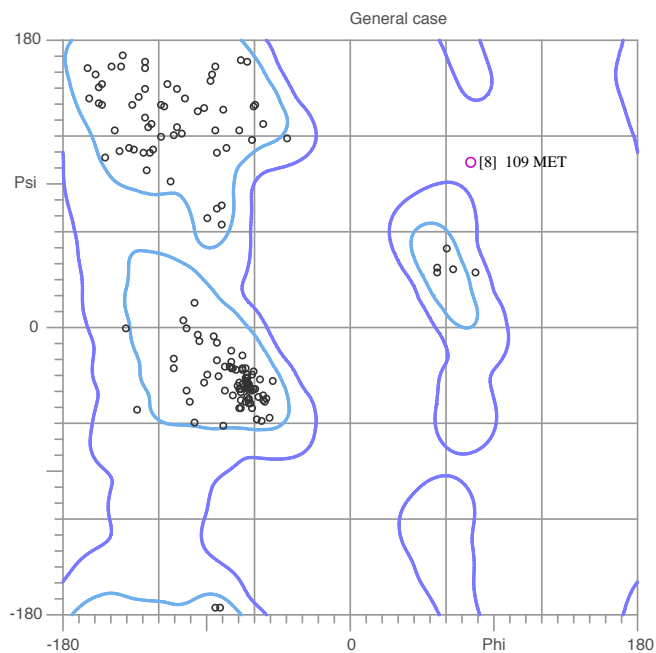


94.2% (163/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 8



96.0% (166/173) of all residues were in favored (98%) regions.  
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

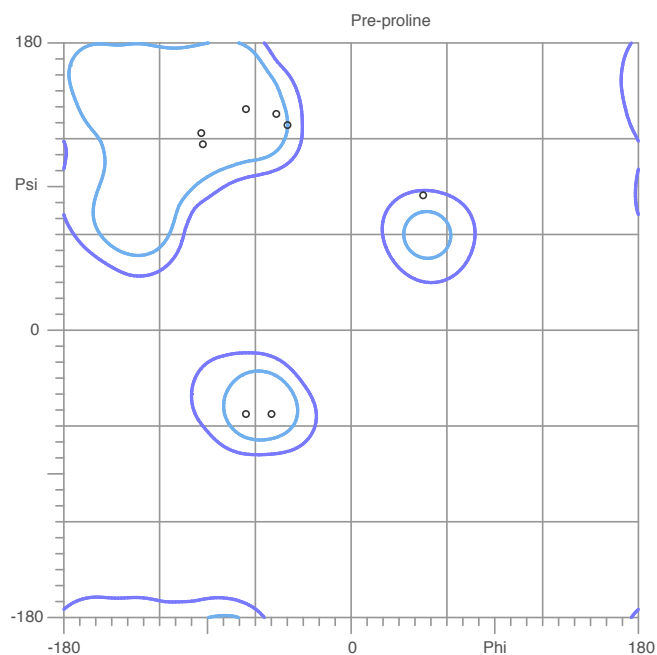
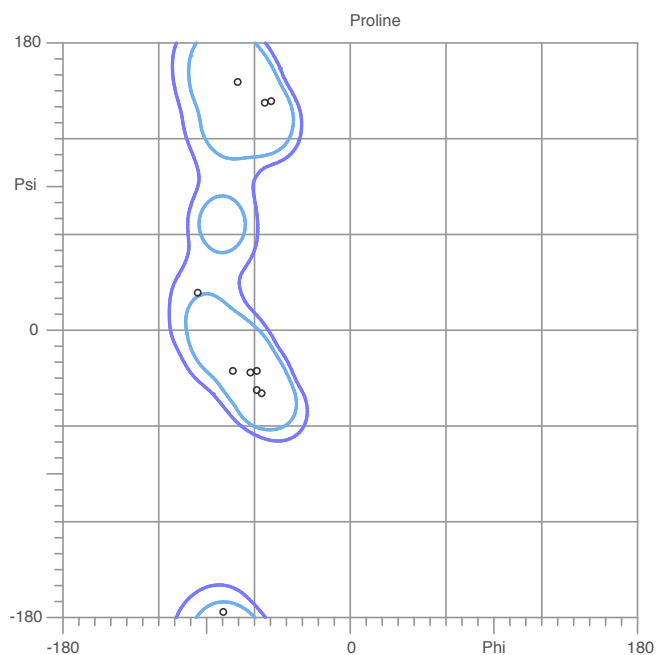
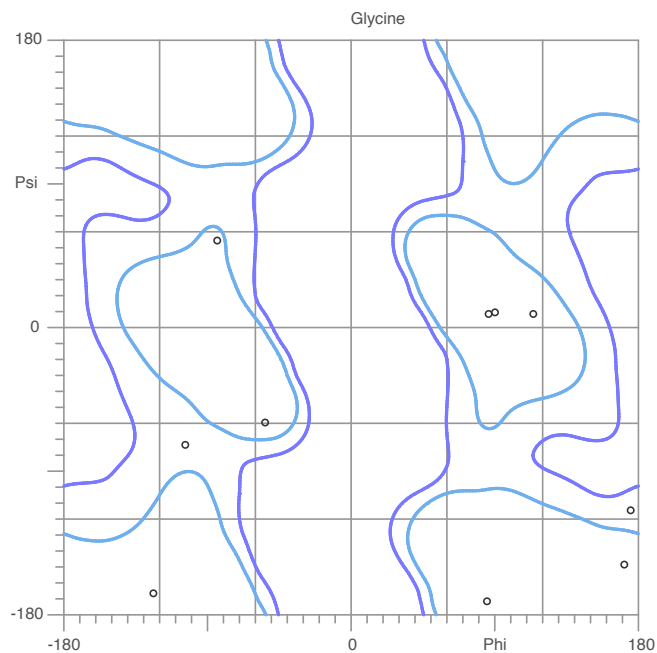
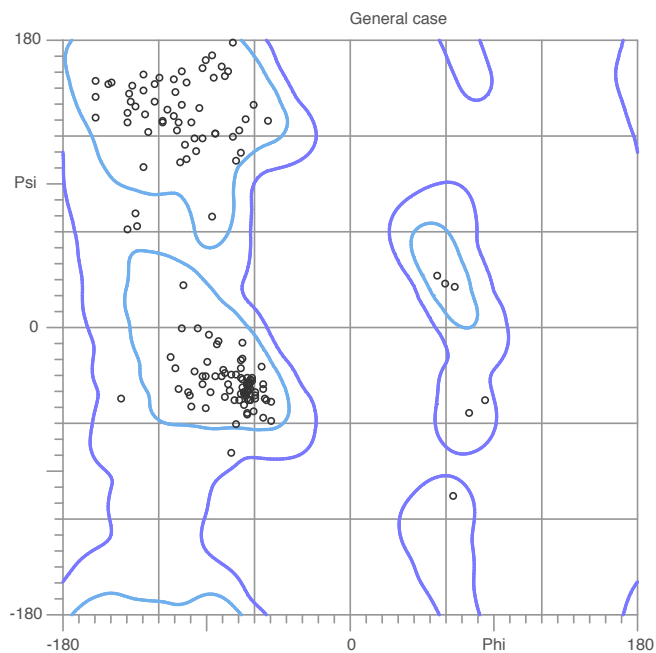
There were 2 outliers (phi, psi):

[8] 99 VAL (65.0, 101.3)

[8] 109 MET (75.1, 105.0)

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 9



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.

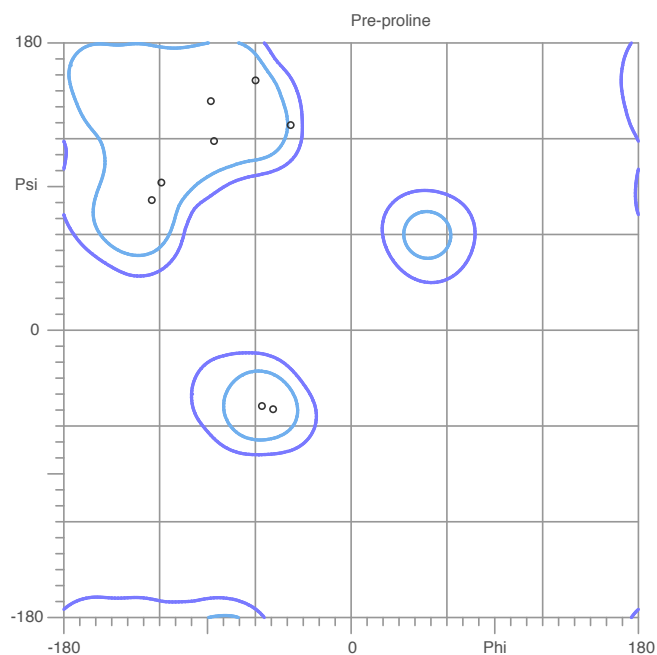
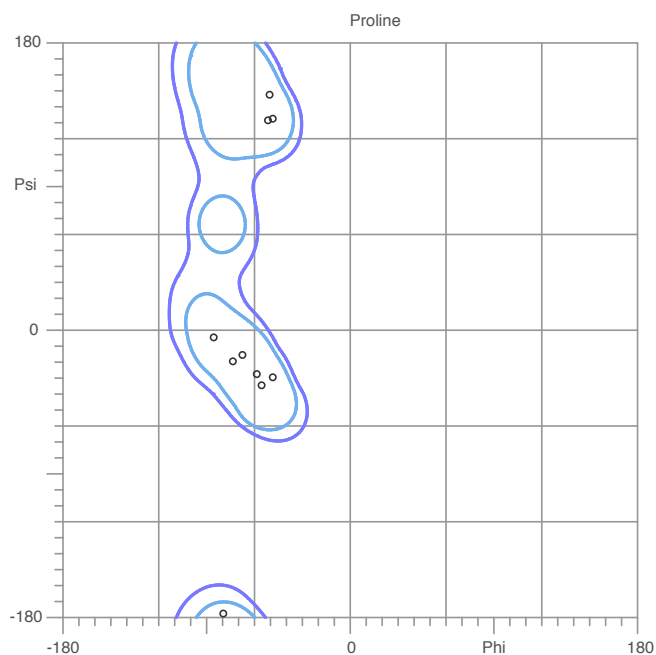
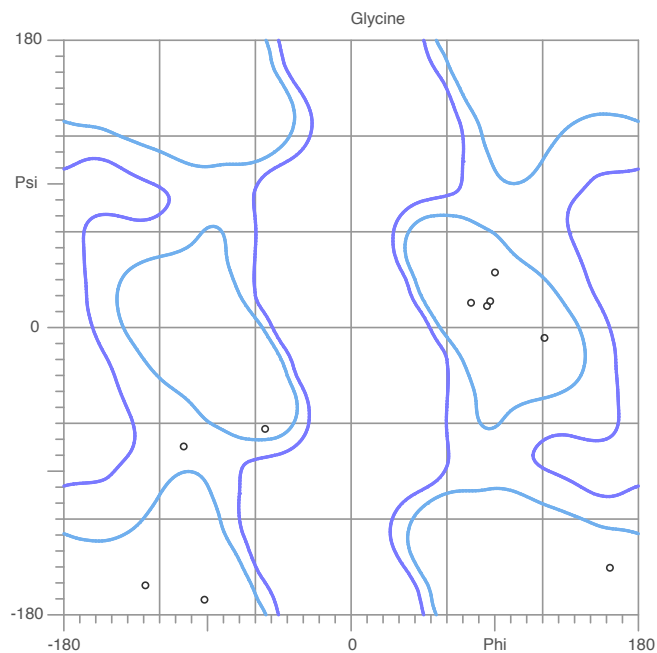
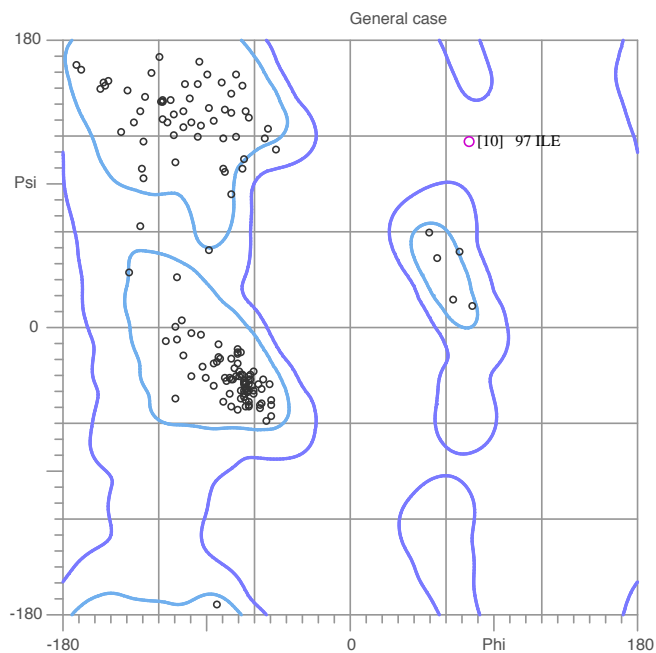
There were no outliers.

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# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 10



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.

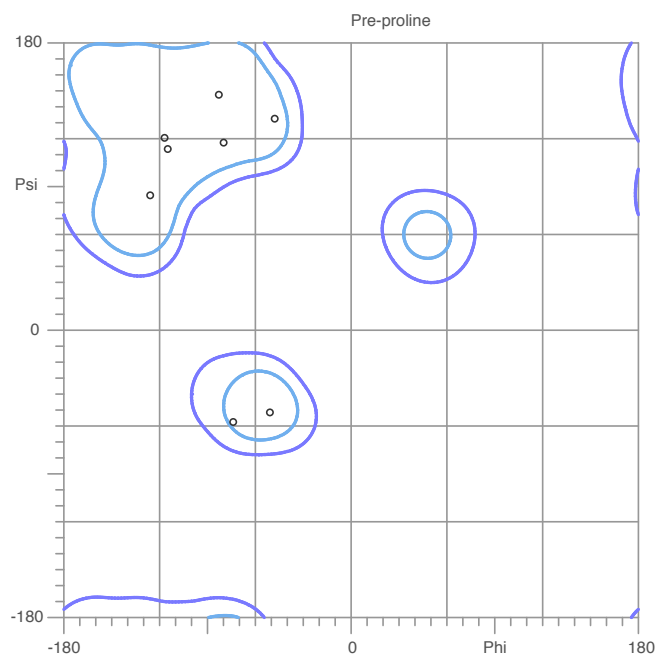
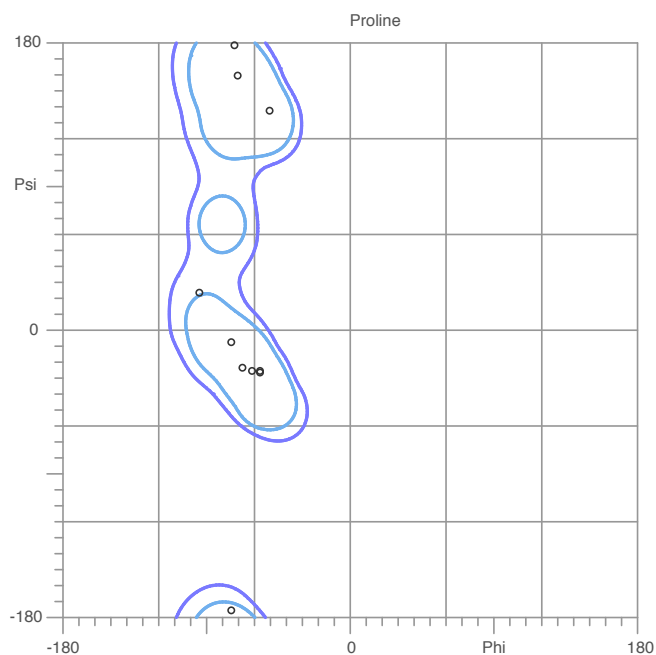
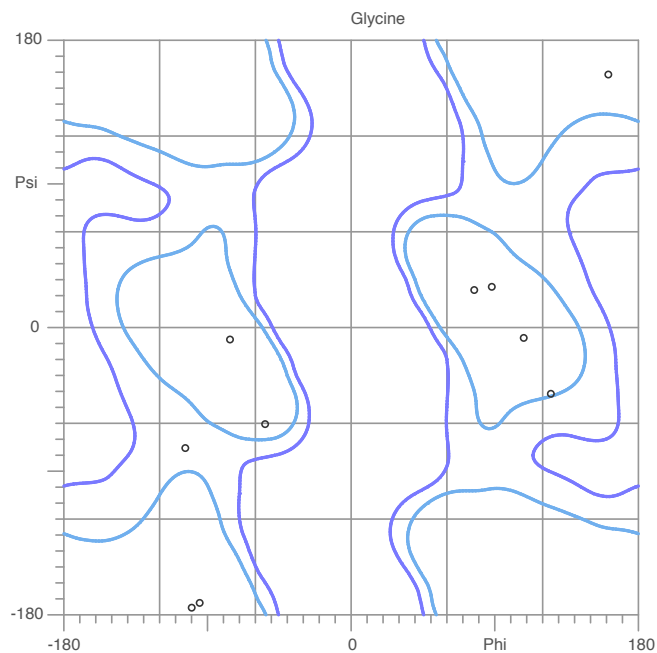
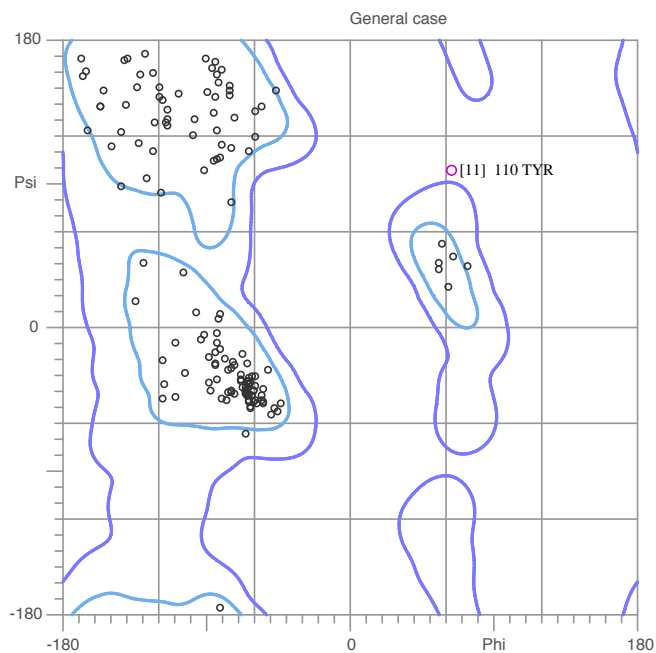
There were 1 outliers (phi, psi):  
[10] 97 ILE (74.9, 117.5)

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# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 11



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.

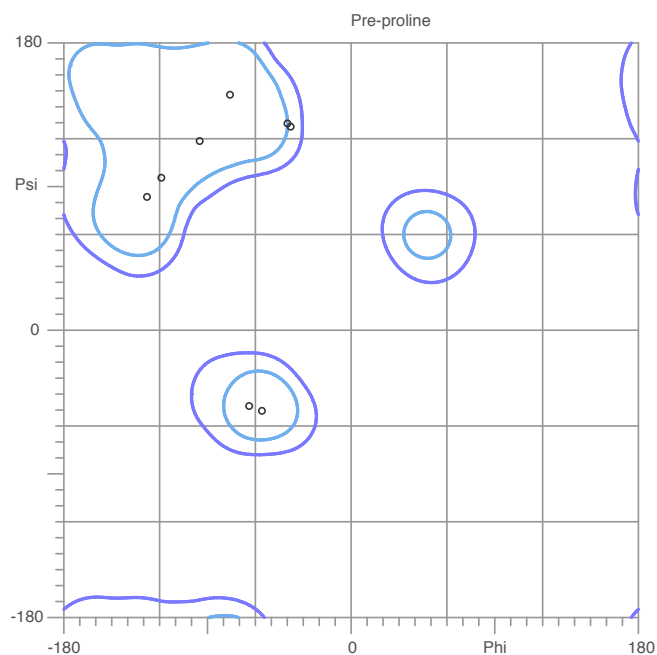
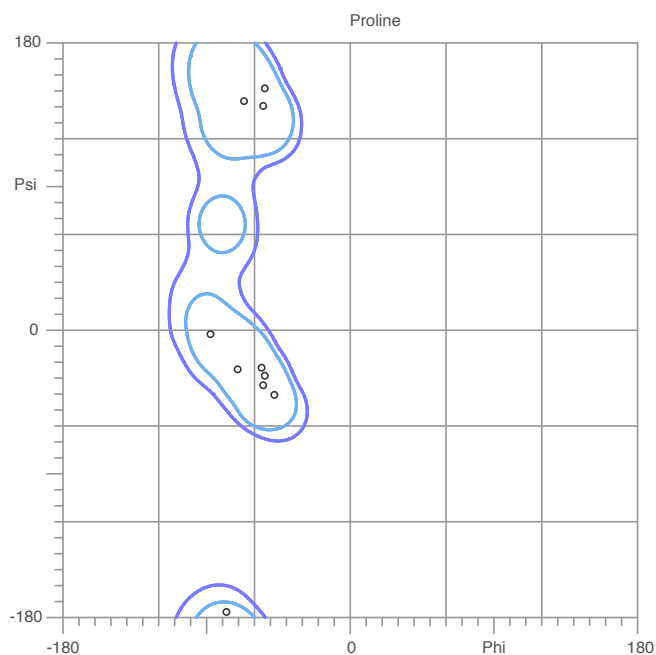
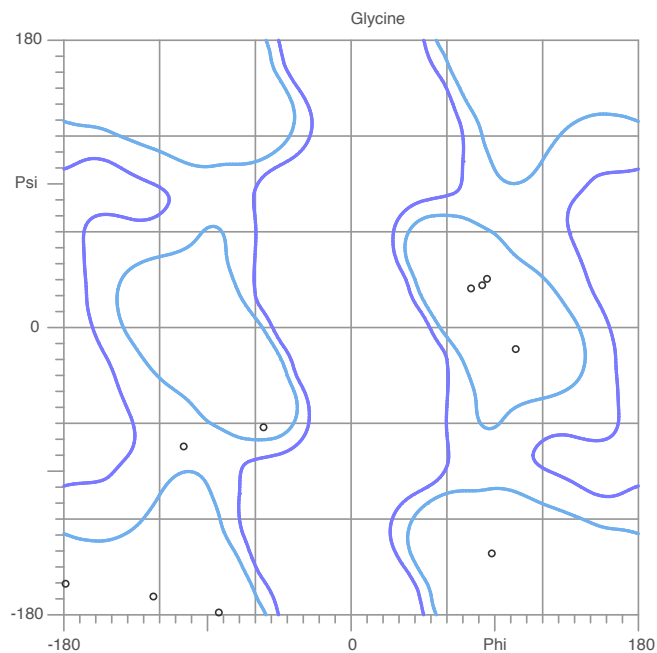
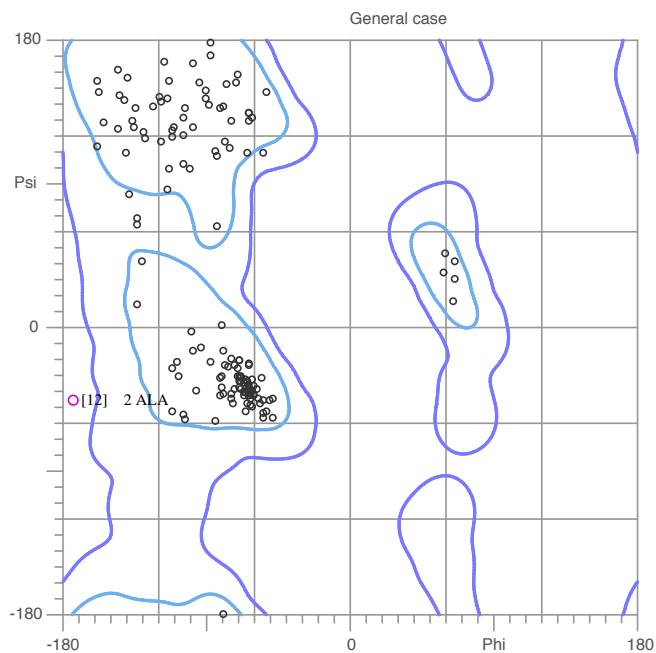
There were 1 outliers (phi, psi):  
[11] 110 TYR (63.4, 99.4)

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# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 12

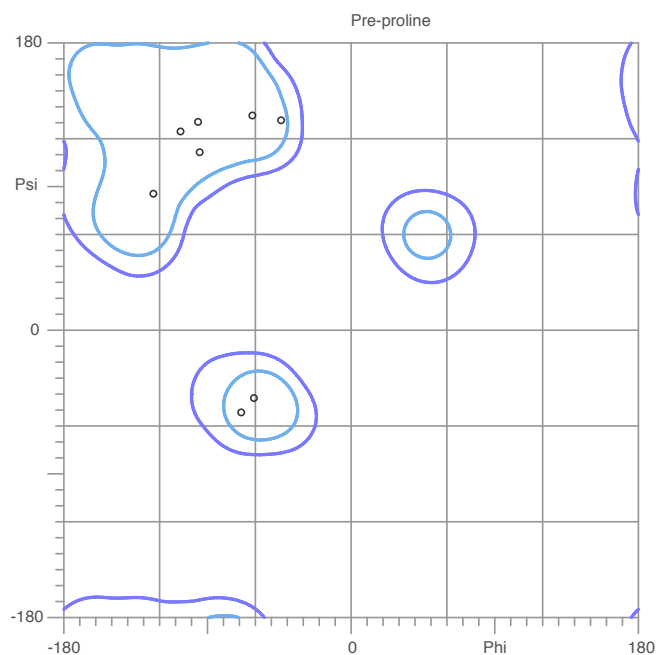
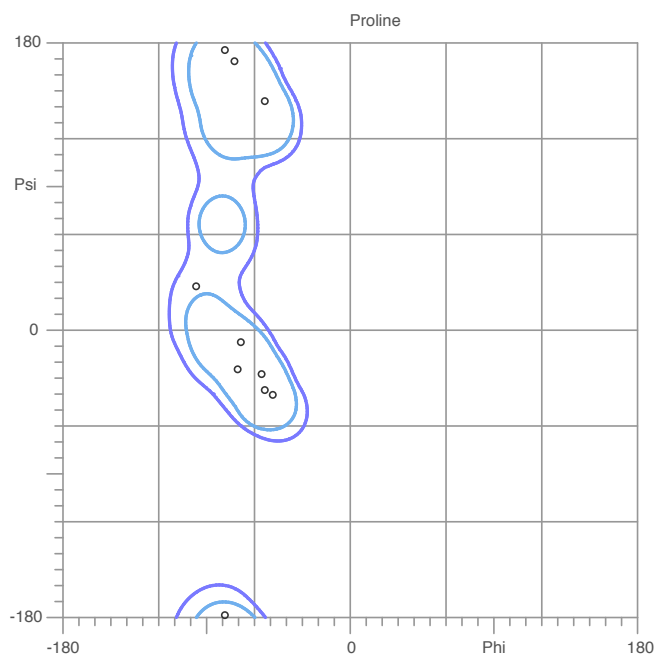
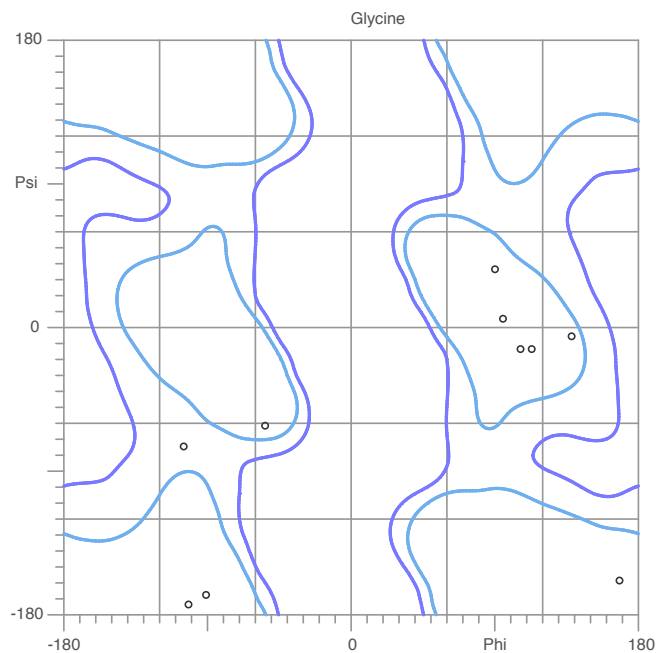
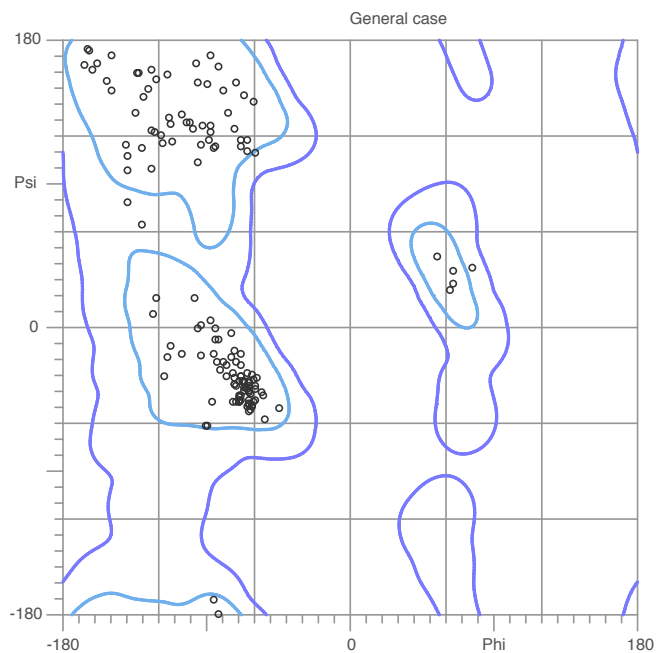


96.0% (166/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[12] 2 ALA (-175.0, -45.0)

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 13



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.

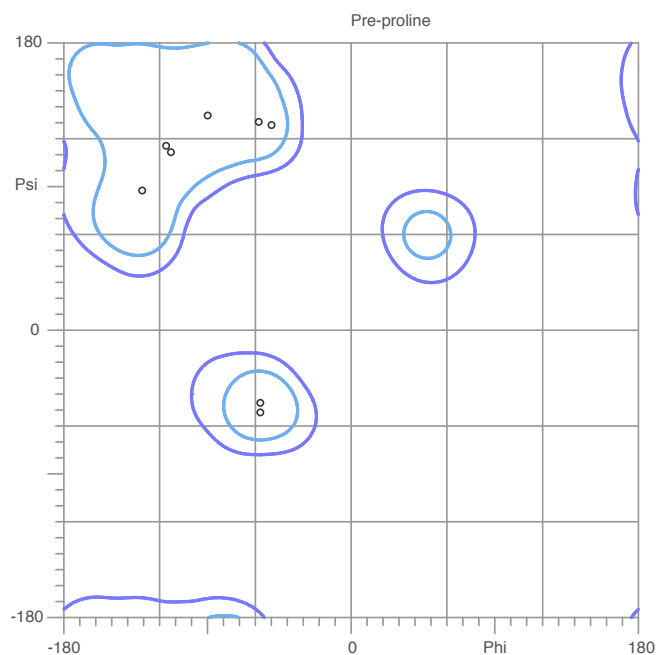
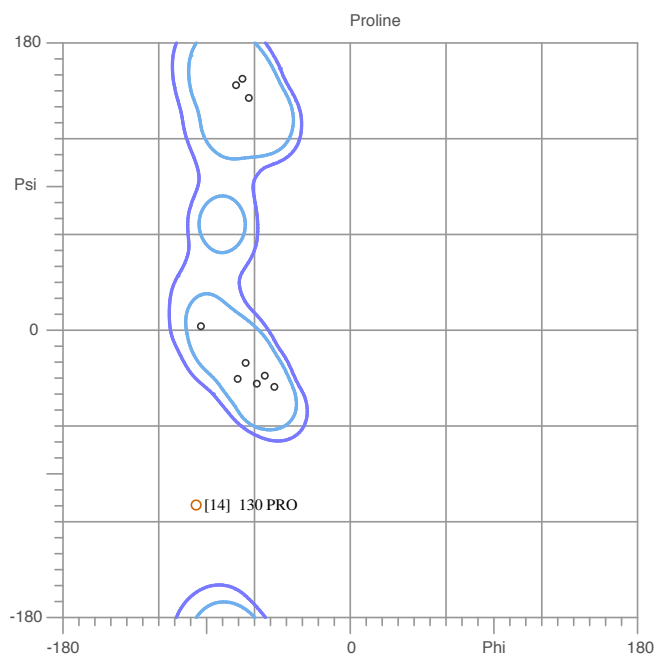
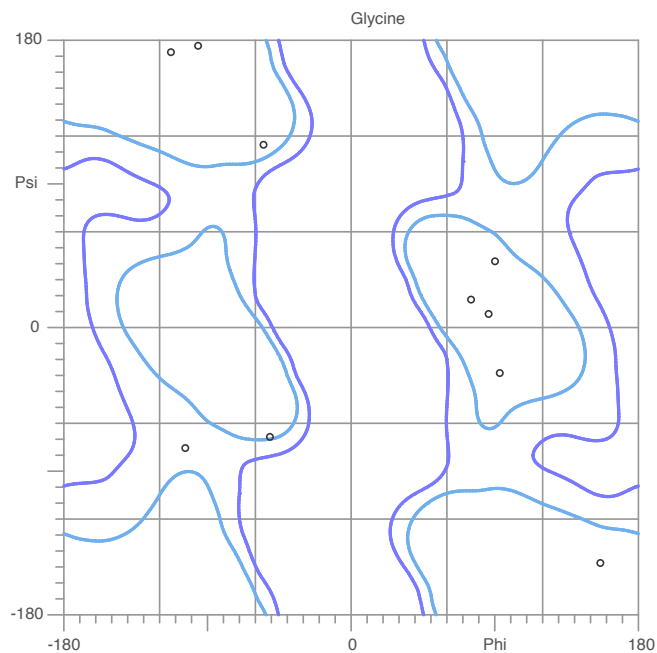
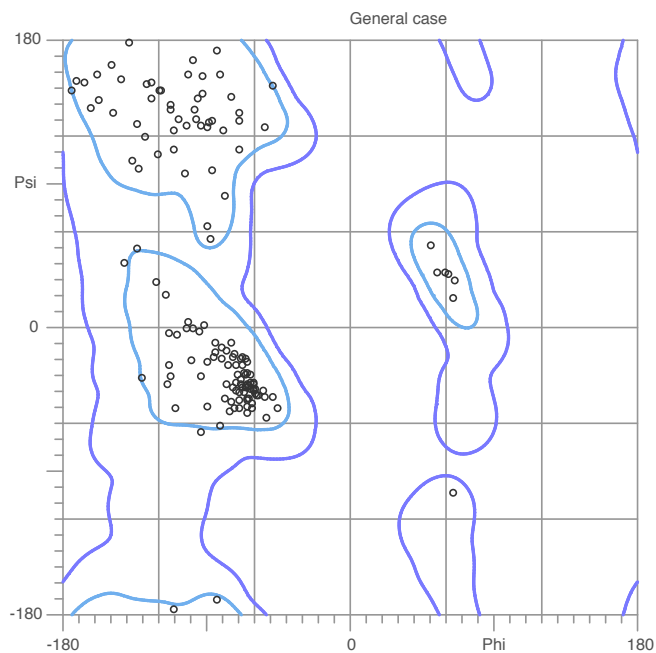
There were no outliers.

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# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 14

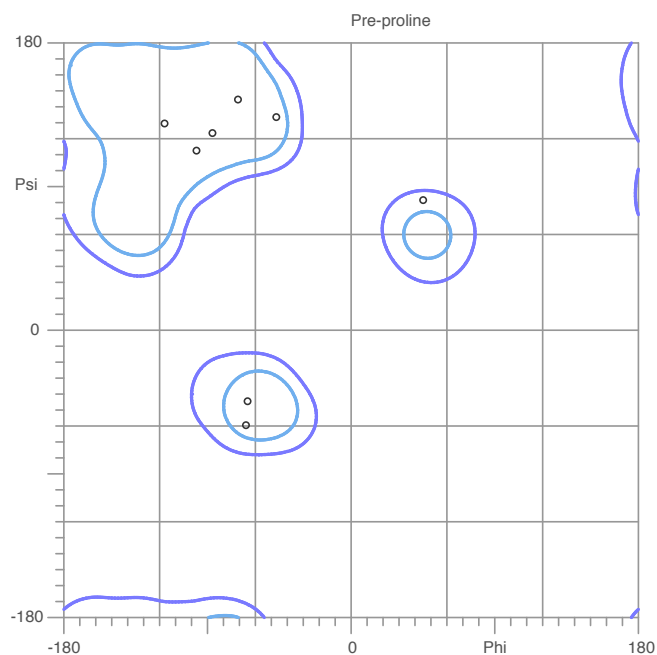
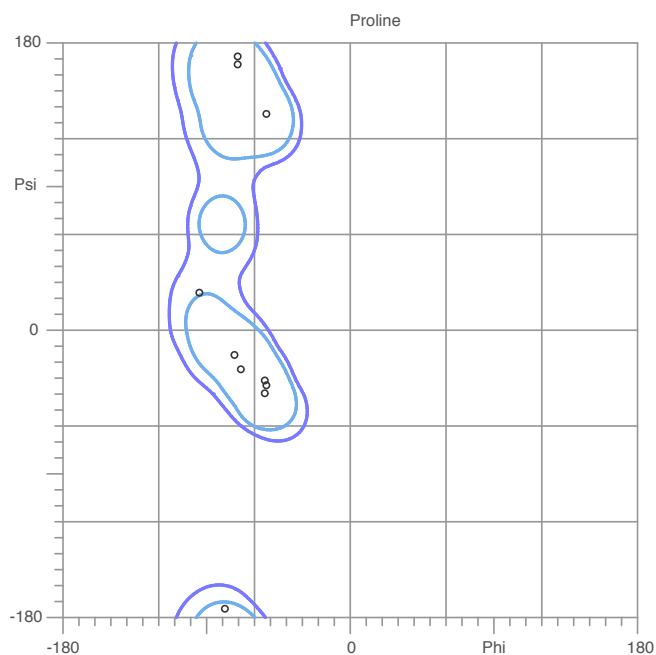
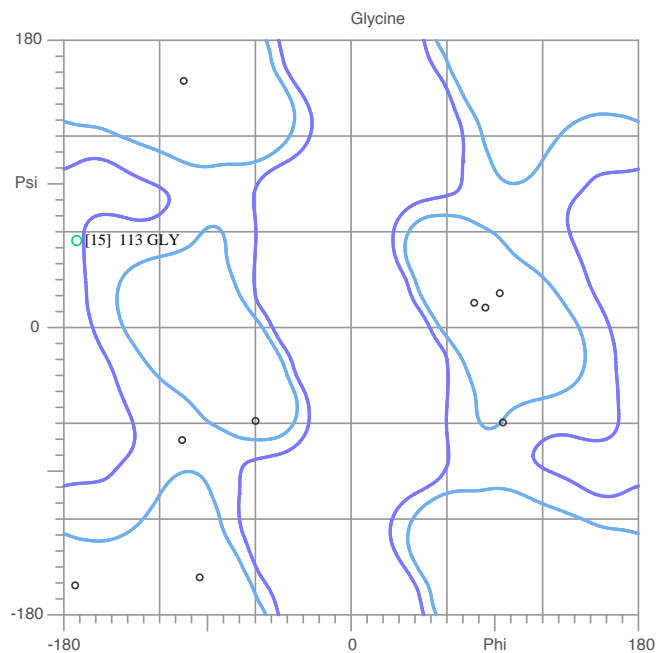
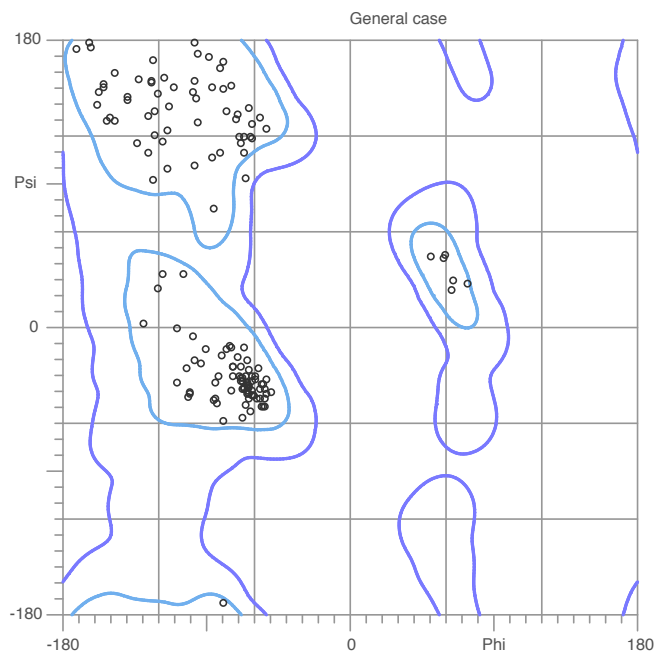


95.4% (165/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[14] 130 PRO (-97.3, -109.5)

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 15



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.

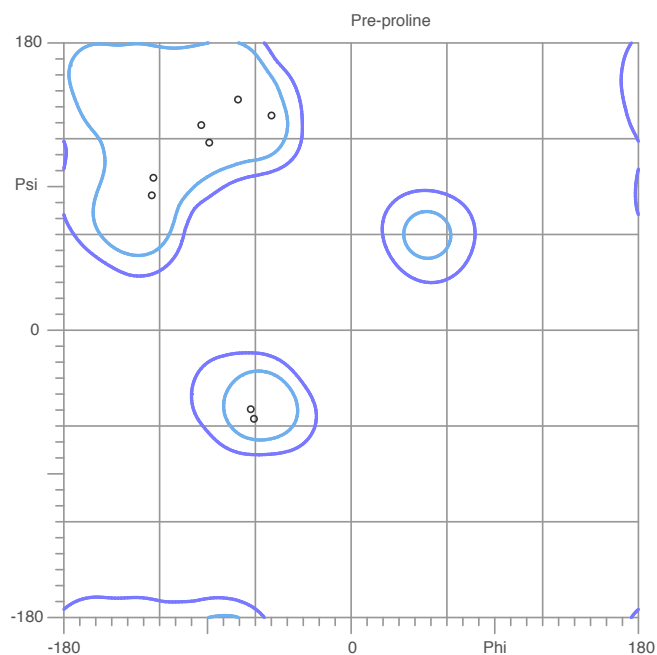
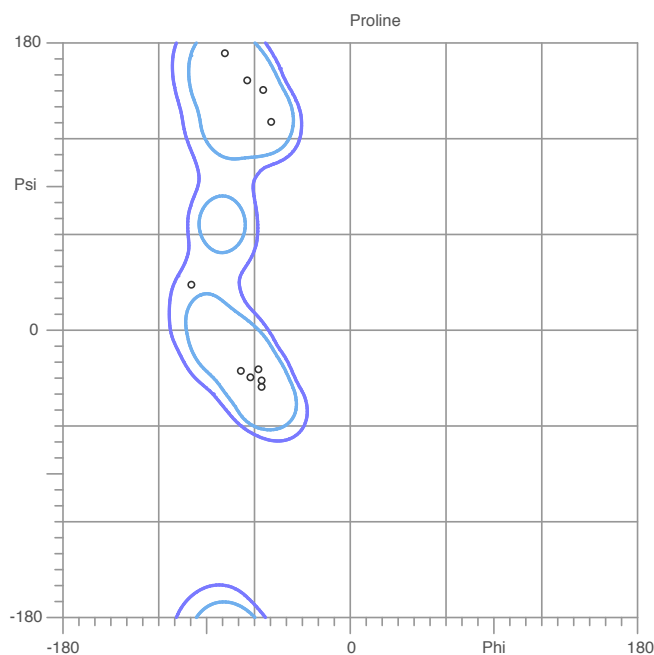
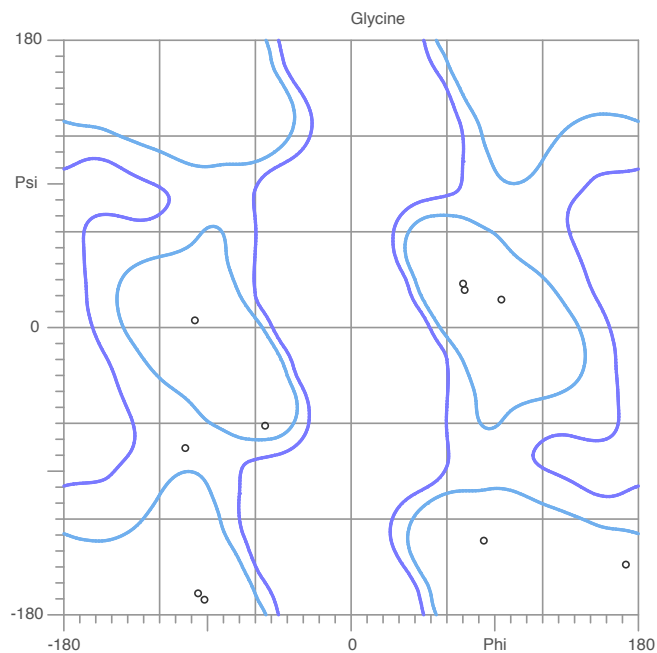
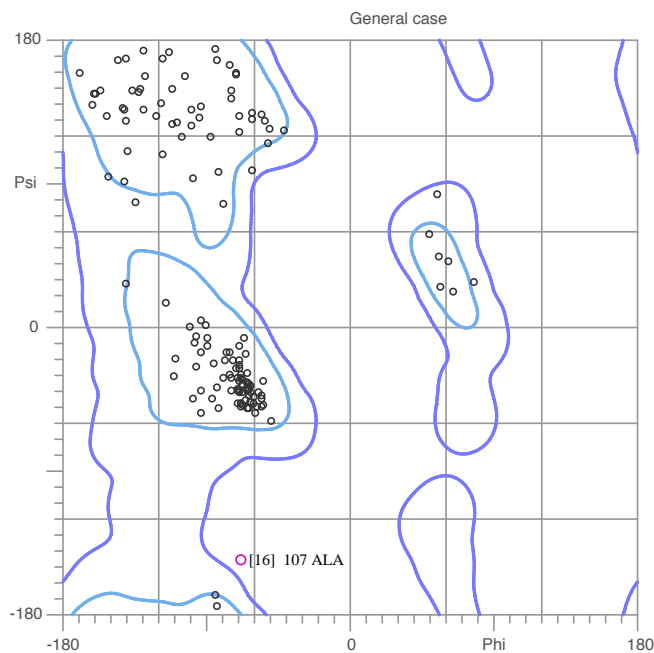
There were 1 outliers (phi, psi):  
[15] 113 GLY (-172.5, 55.1)

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# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 16

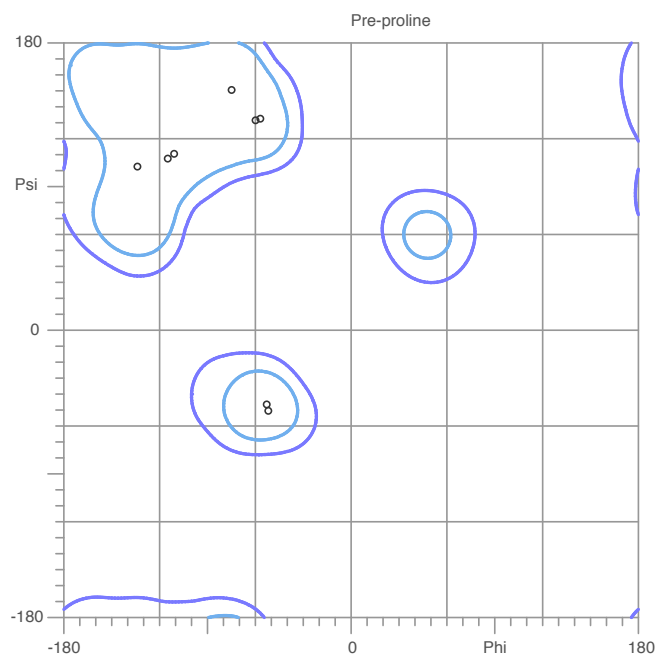
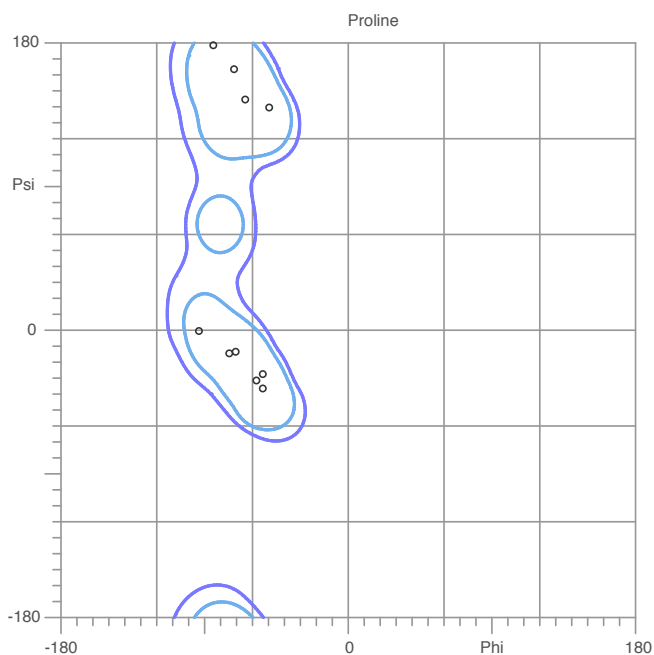
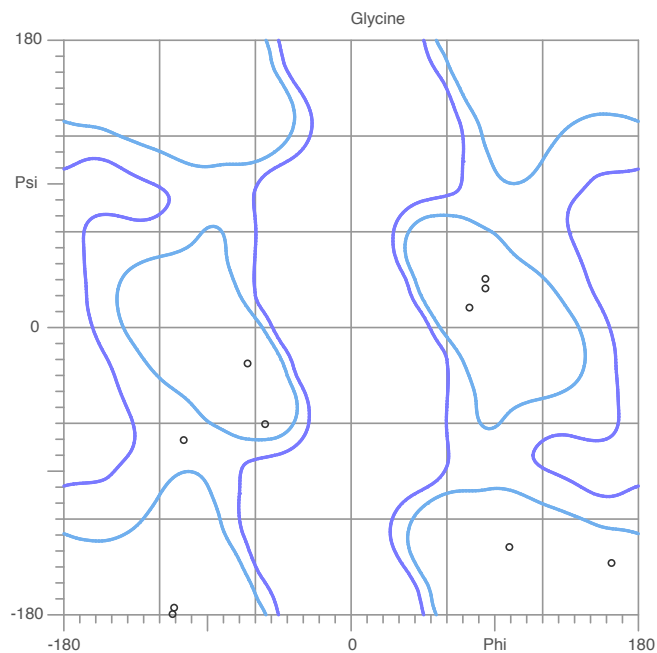
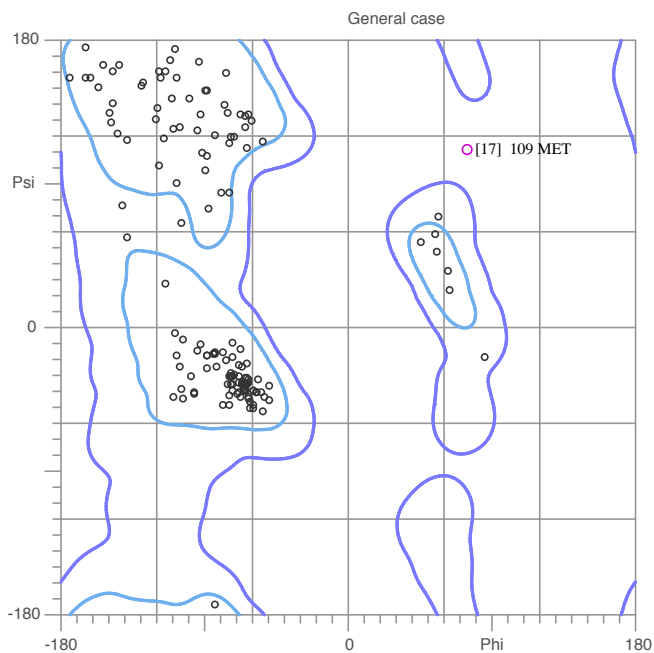


94.8% (164/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[16] 107 ALA (-69.2, -145.0)

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 17

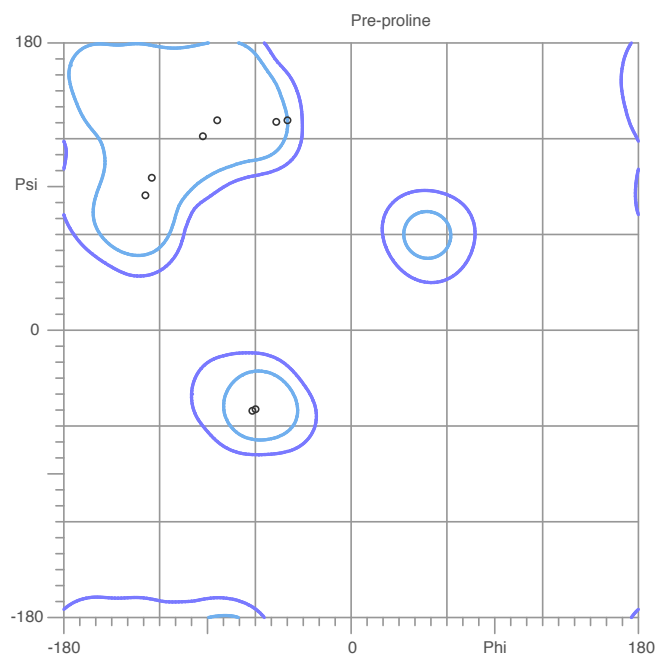
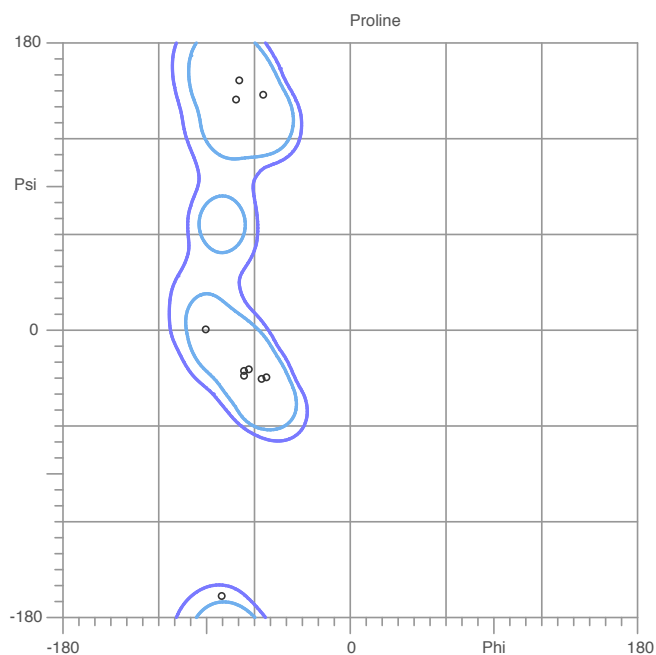
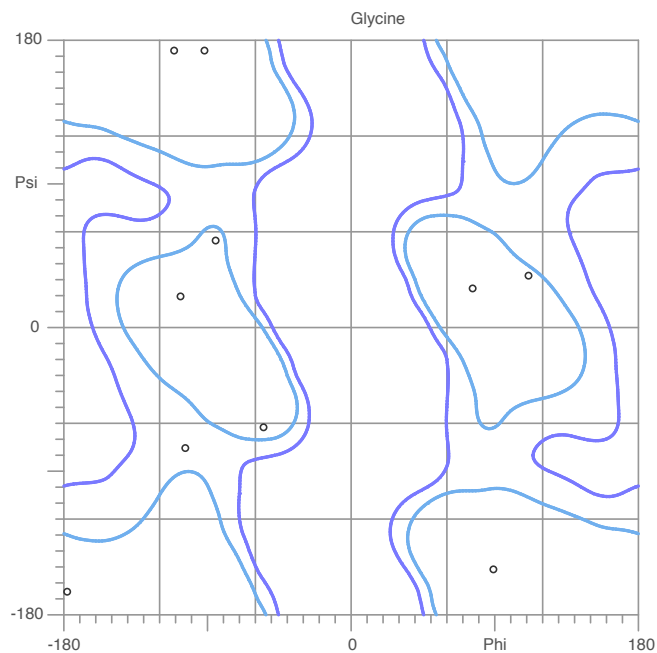
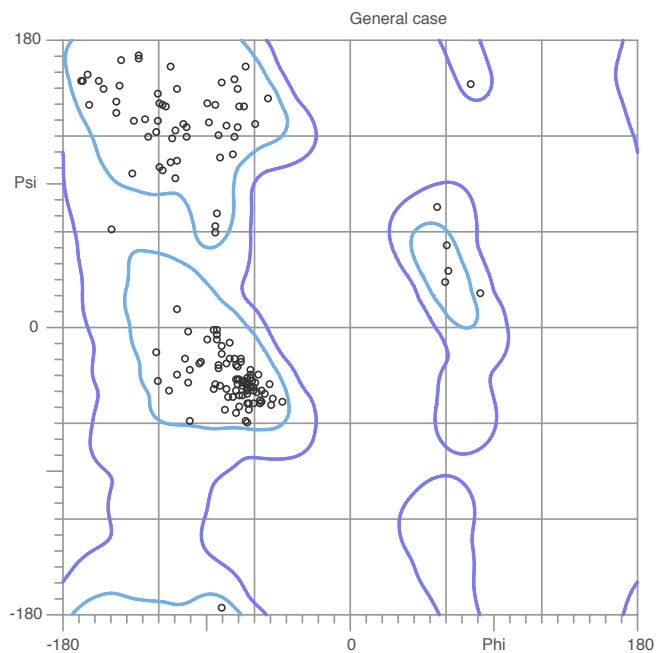


96.0% (166/173) of all residues were in favored (98%) regions.  
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[17] 109 MET (75.0, 112.1)

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 18

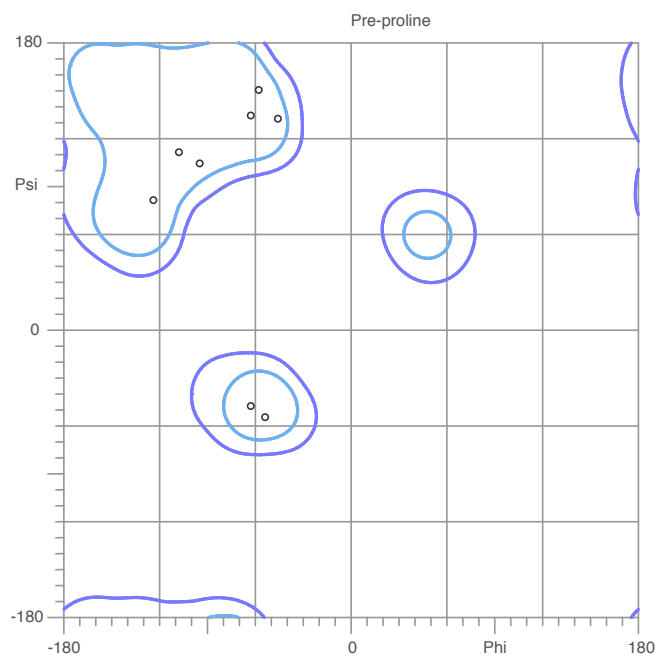
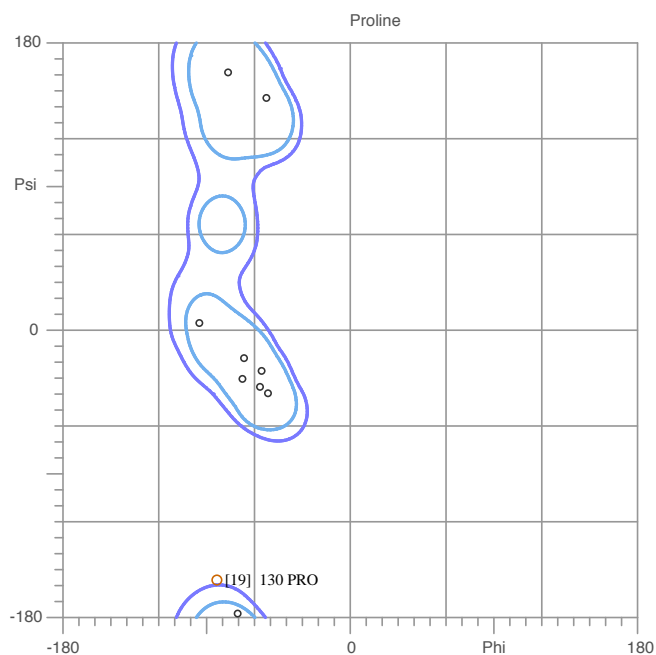
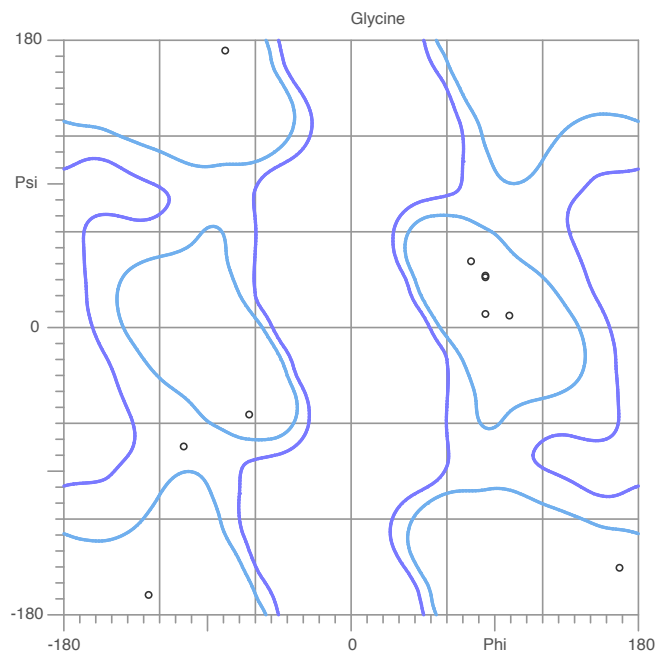
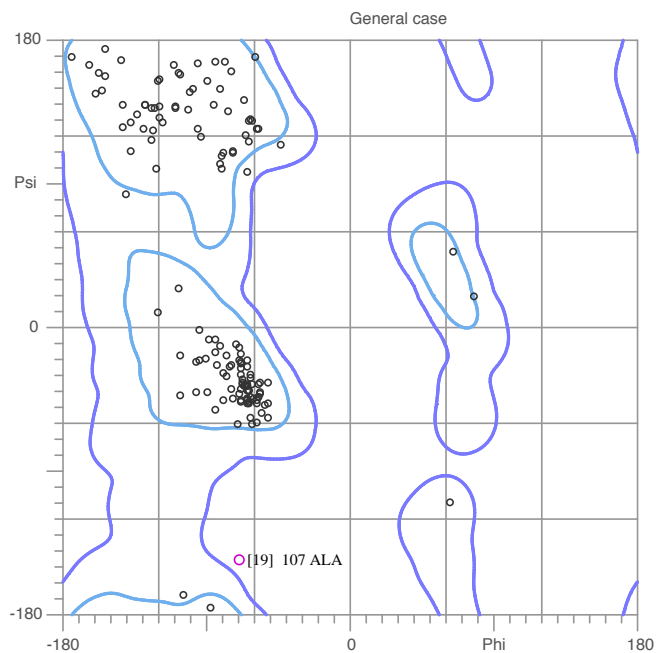


96.5% (167/173) of all residues were in favored (98%) regions.  
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 19

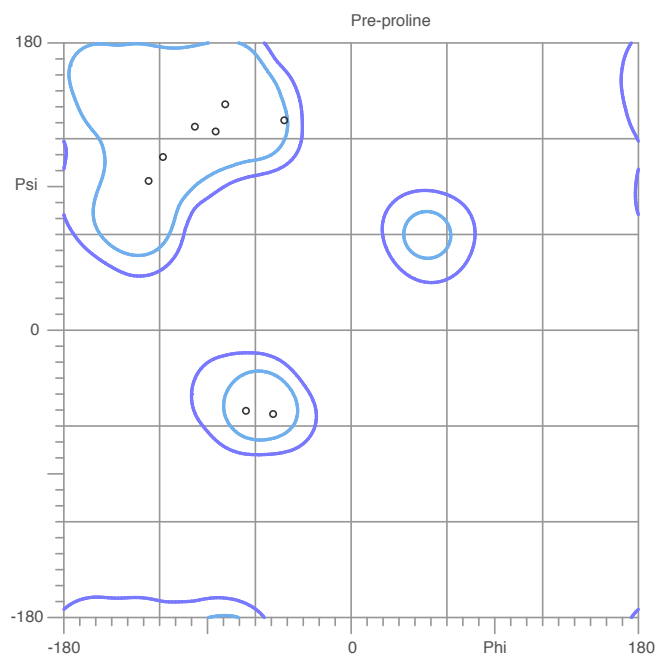
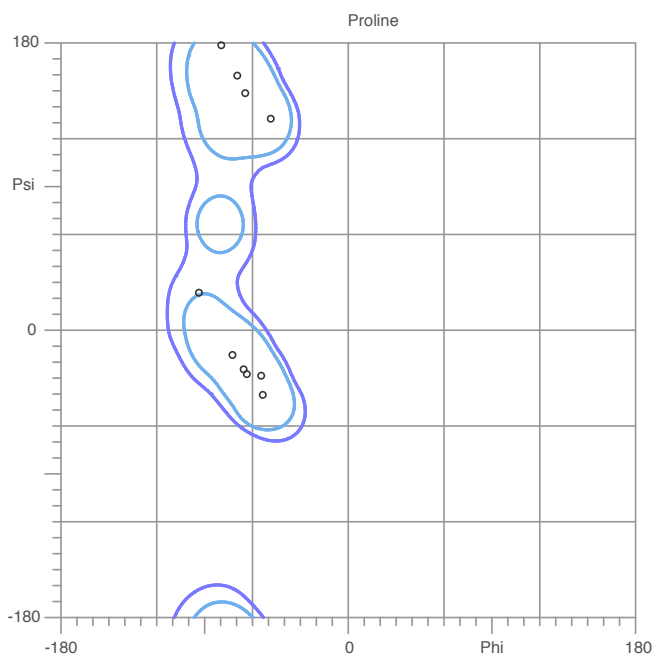
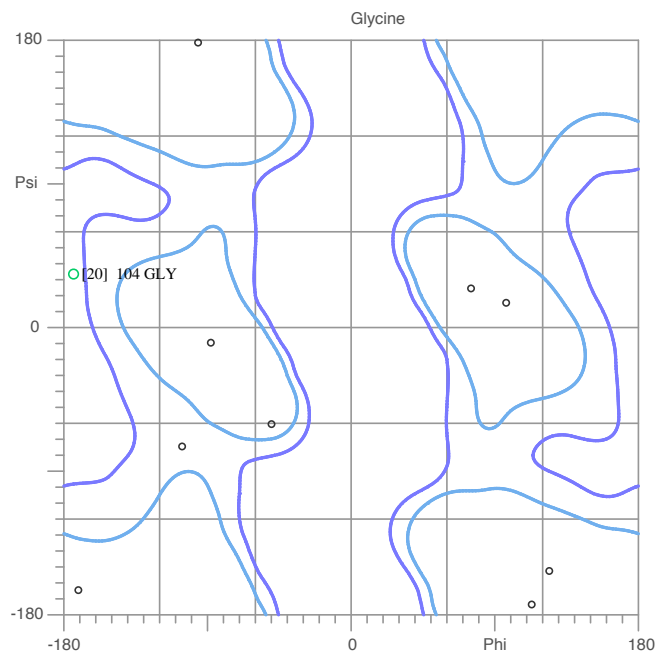
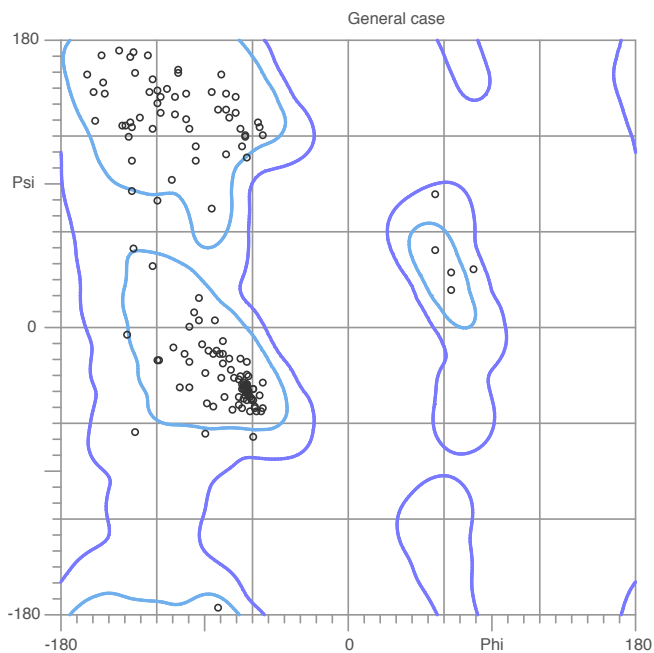


94.8% (164/173) of all residues were in favored (98%) regions.  
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[19] 107 ALA (-70.1, -145.0)  
[19] 130 PRO (-84.8, -156.8)

# MolProbity Ramachandran analysis

HR41\_R3\_em\_bcr3.pdb, model 20



93.1% (161/173) 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] 104 GLY (-175.0, 34.8)