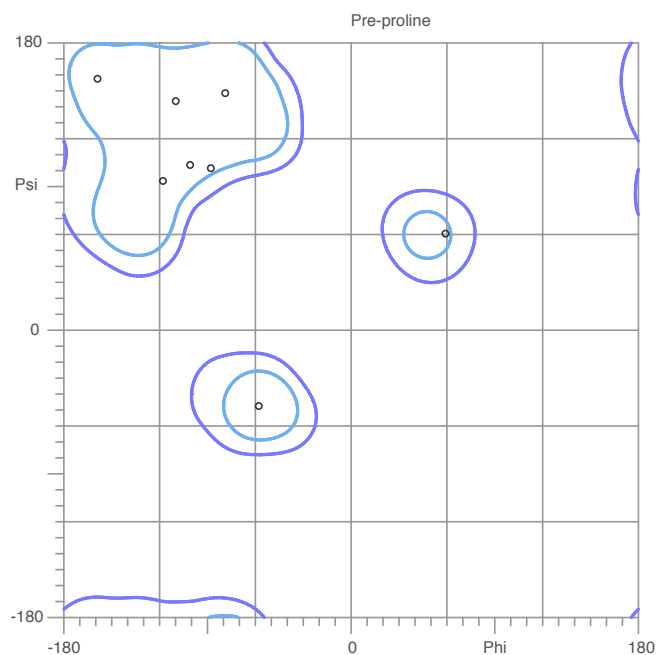
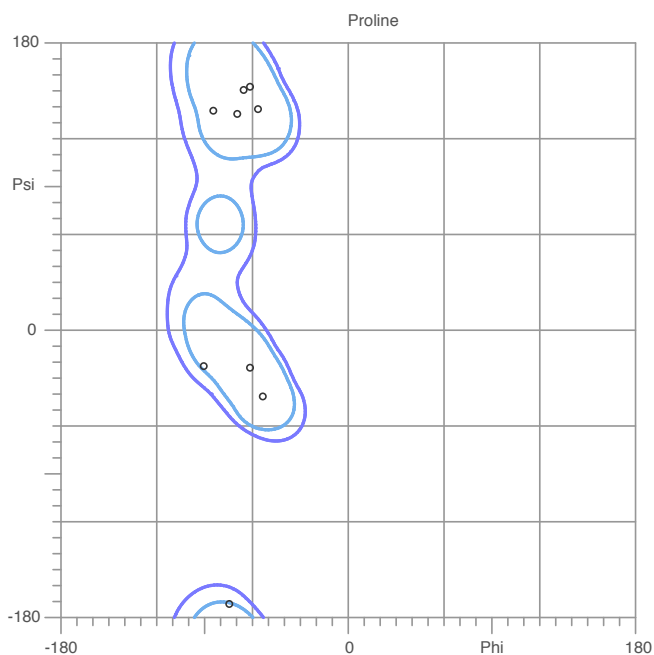
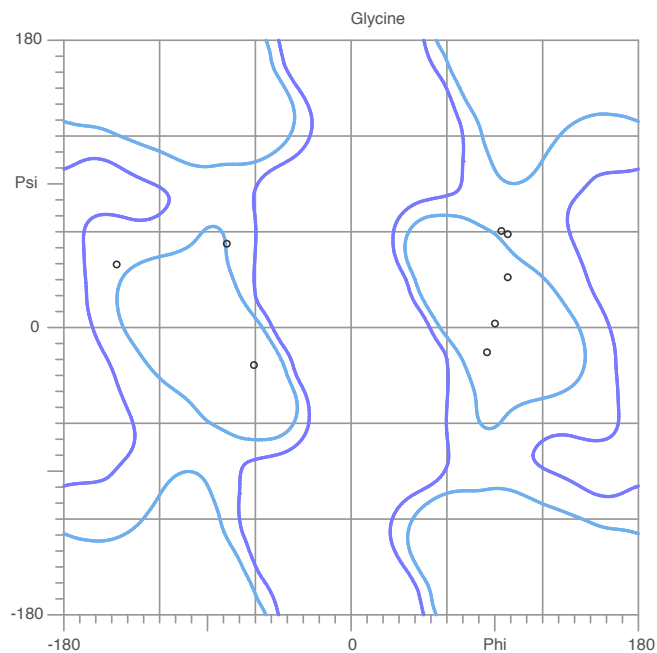
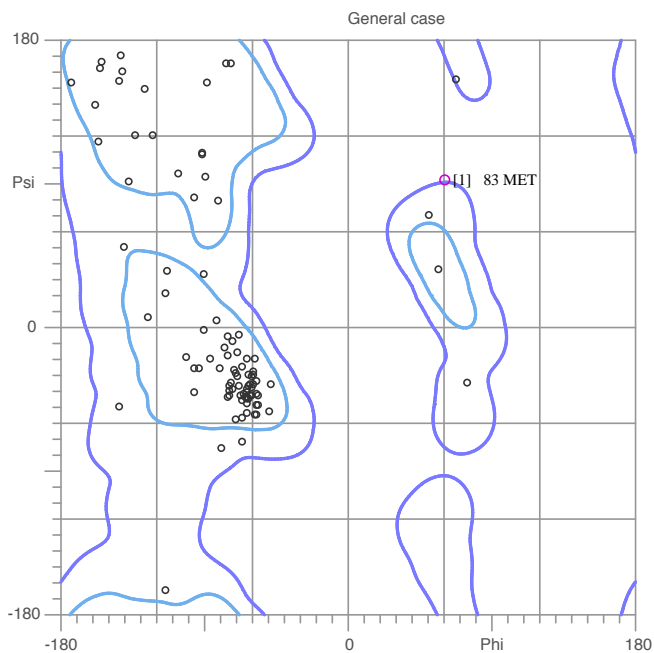




# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 1



88.2% (105/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

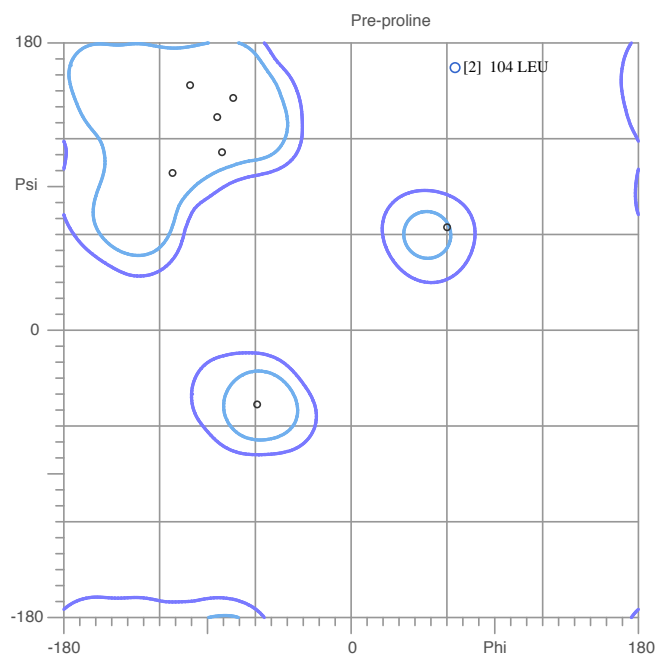
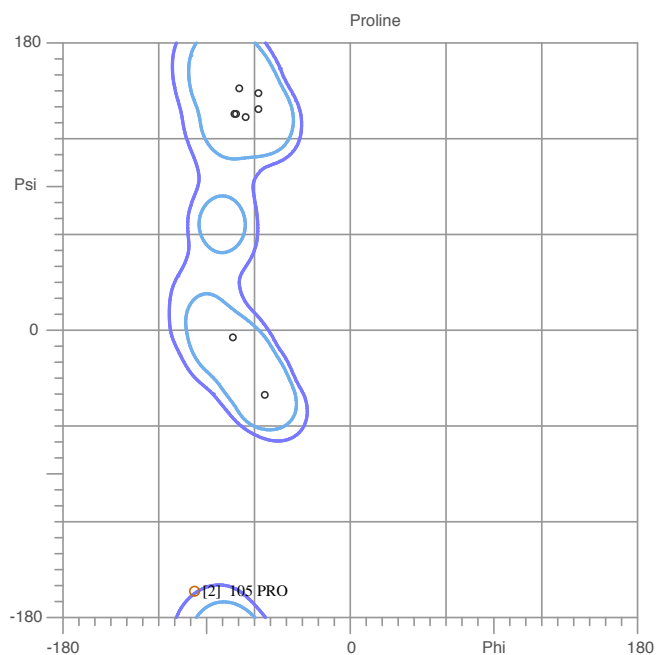
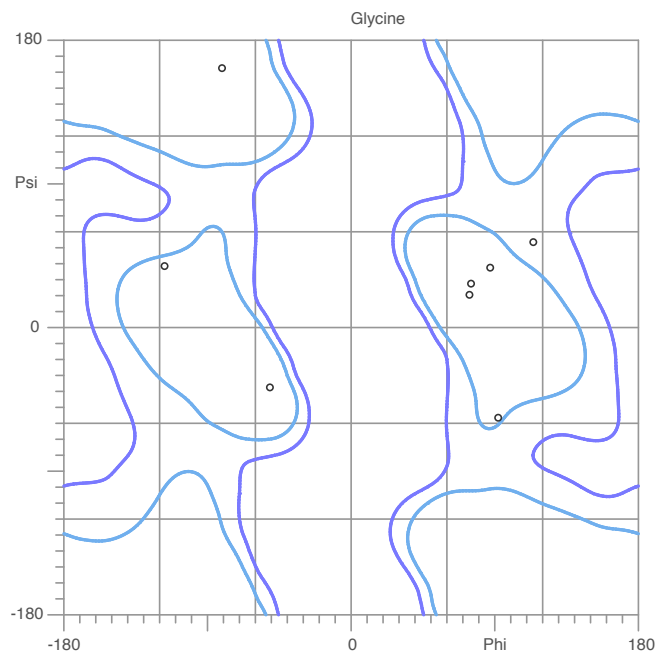
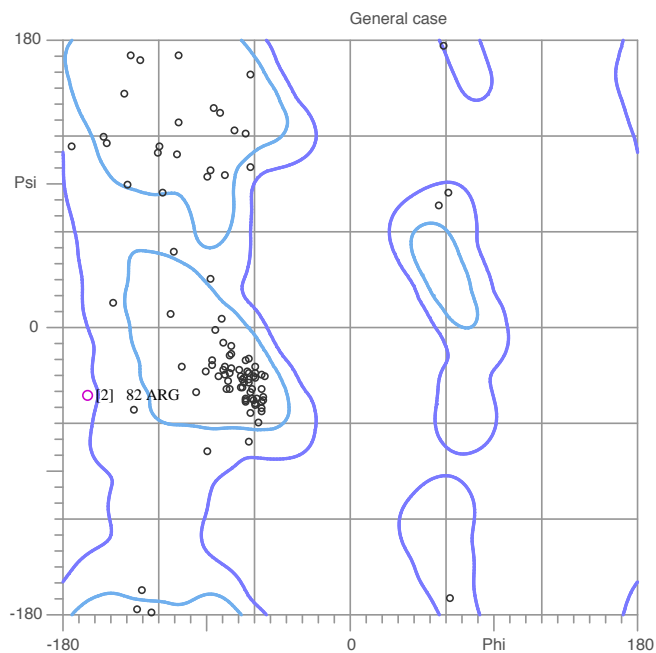
There were 1 outliers (phi, psi):  
[1] 83 MET (60.7, 93.0)

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# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 2



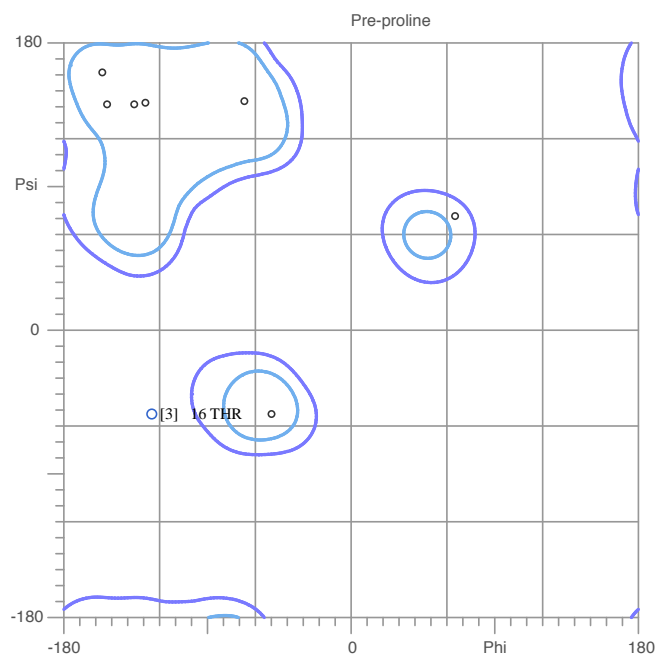
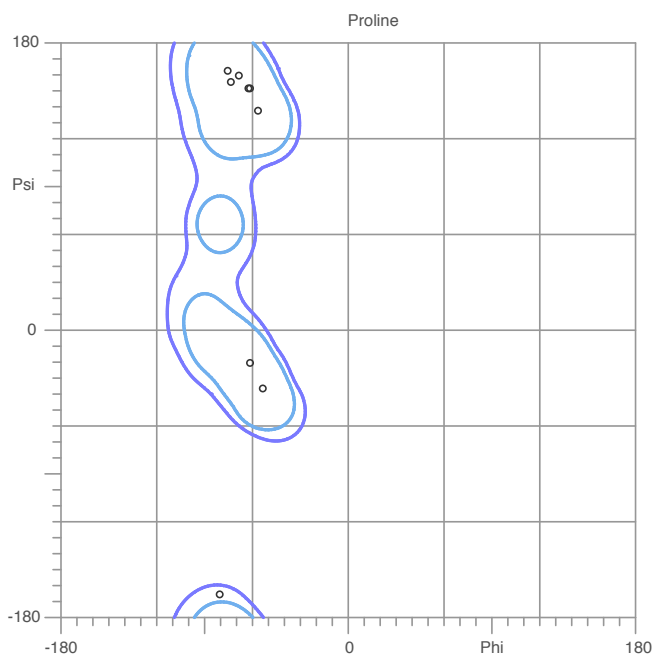
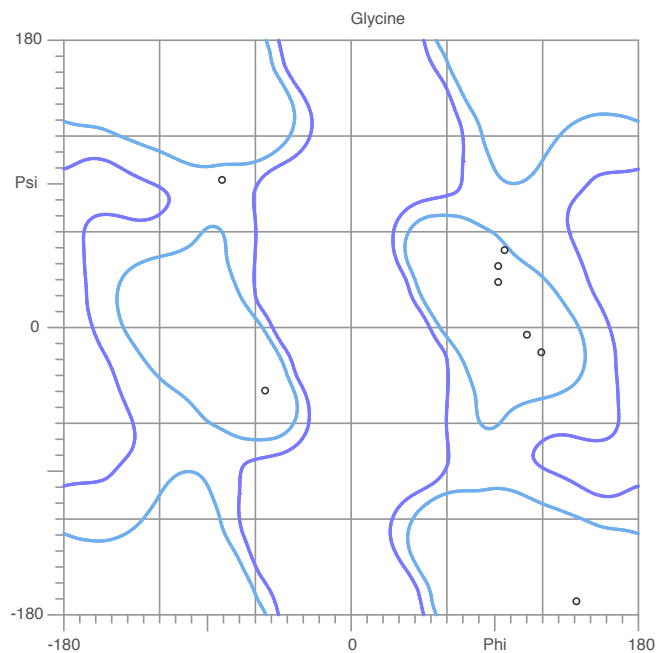
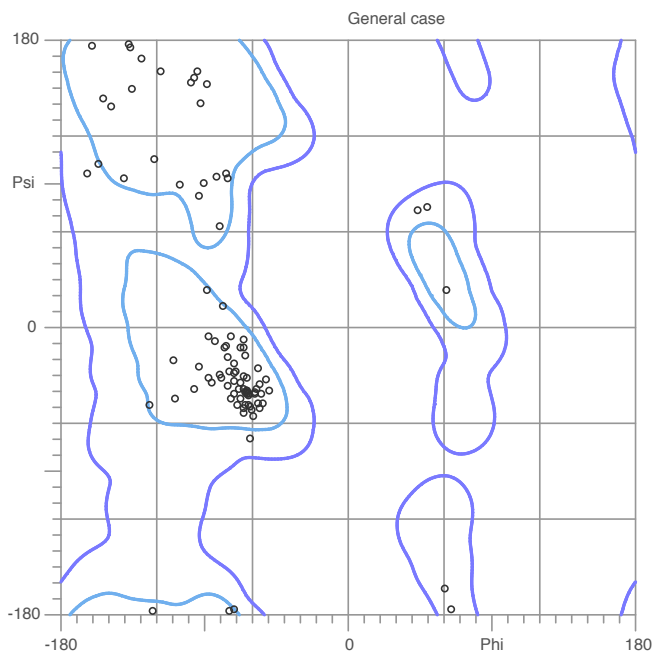
85.7% (102/119) of all residues were in favored (98%) regions.  
97.5% (116/119) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 82 ARG (-165.4, -42.2)
- [2] 104 LEU (65.7, 165.4)
- [2] 105 PRO (-98.4, -164.0)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 3

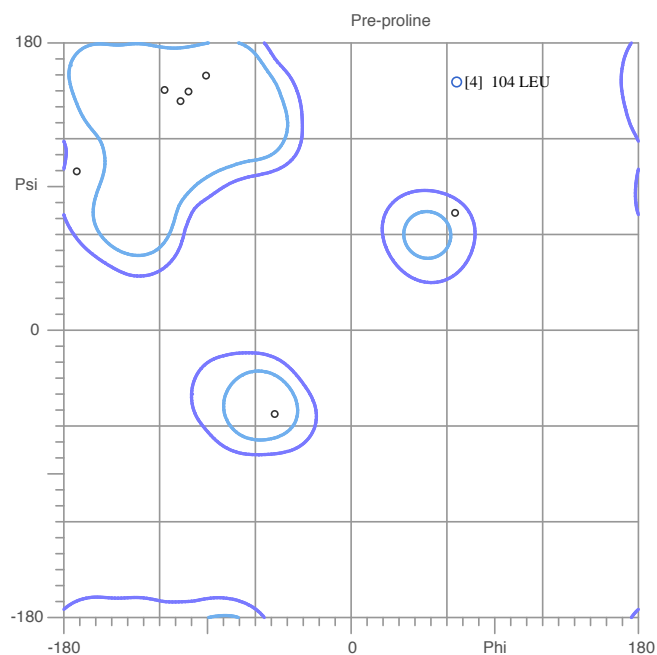
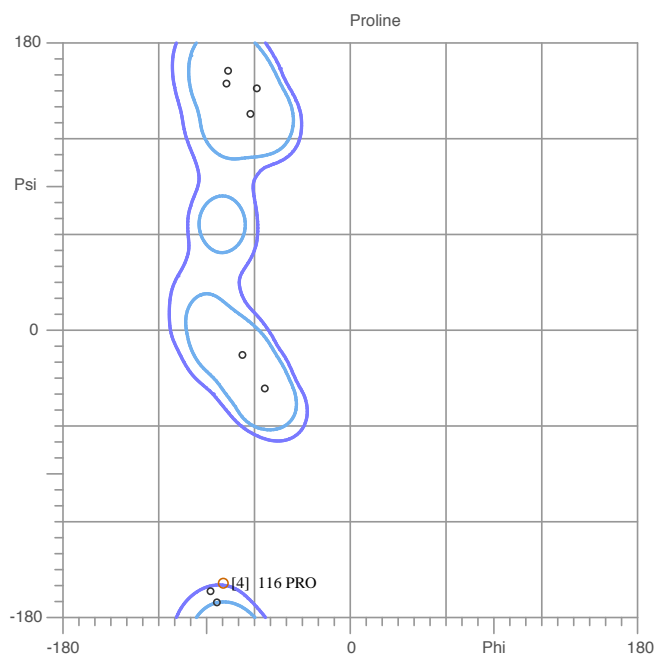
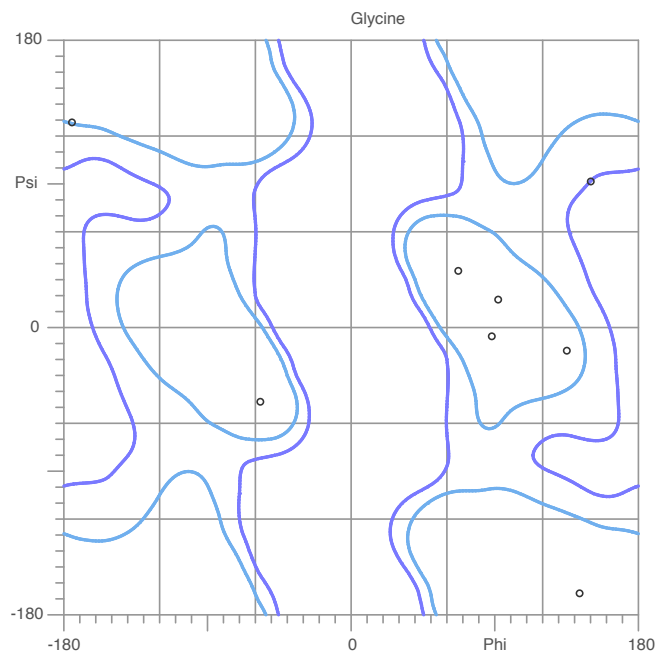
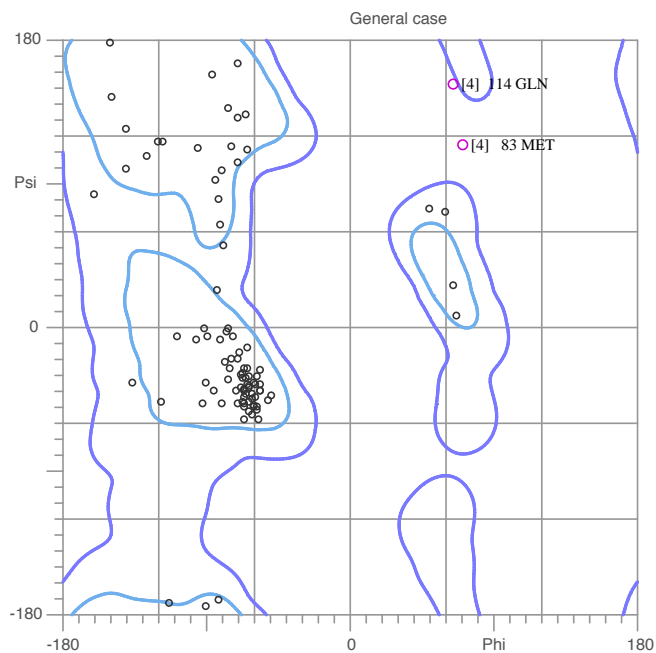


90.8% (108/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[3] 16 THR (-125.1, -52.1)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 4



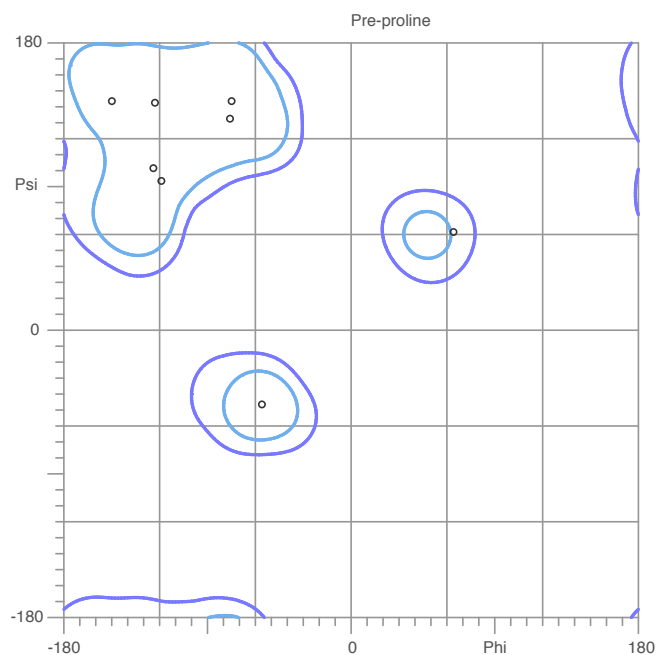
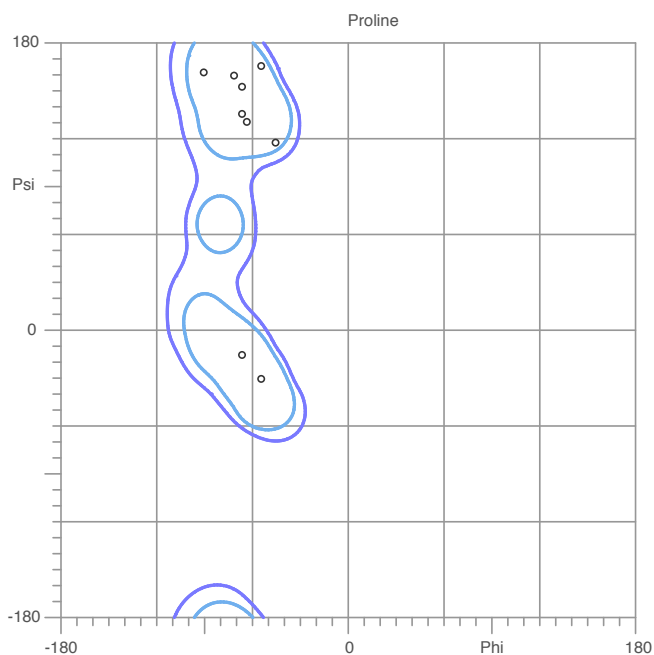
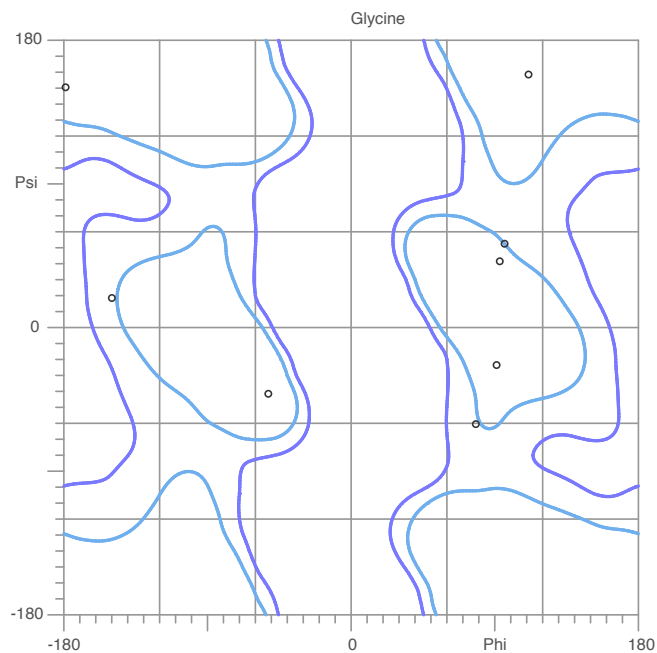
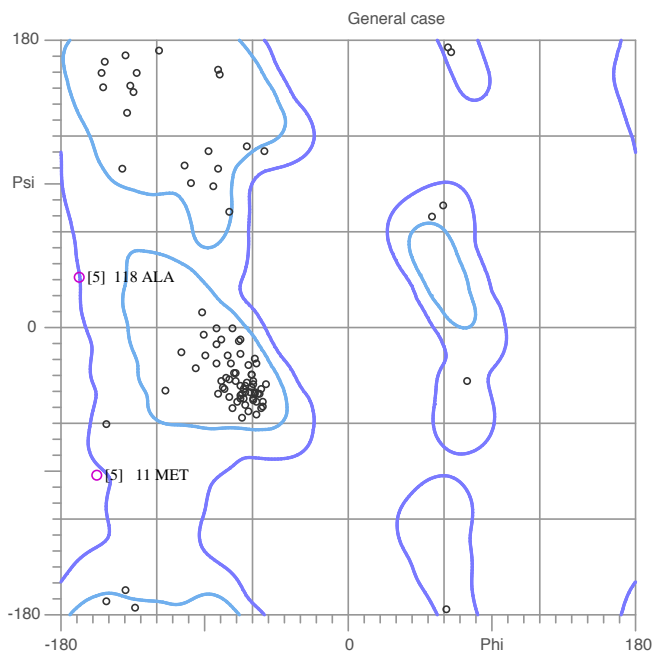
87.4% (104/119) of all residues were in favored (98%) regions.  
96.6% (115/119) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [4] 83 MET (70.4, 115.2)
- [4] 104 LEU (66.3, 156.1)
- [4] 114 GLN (64.1, 154.0)
- [4] 116 PRO (-80.9, -158.9)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 5



87.4% (104/119) of all residues were in favored (98%) regions.  
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

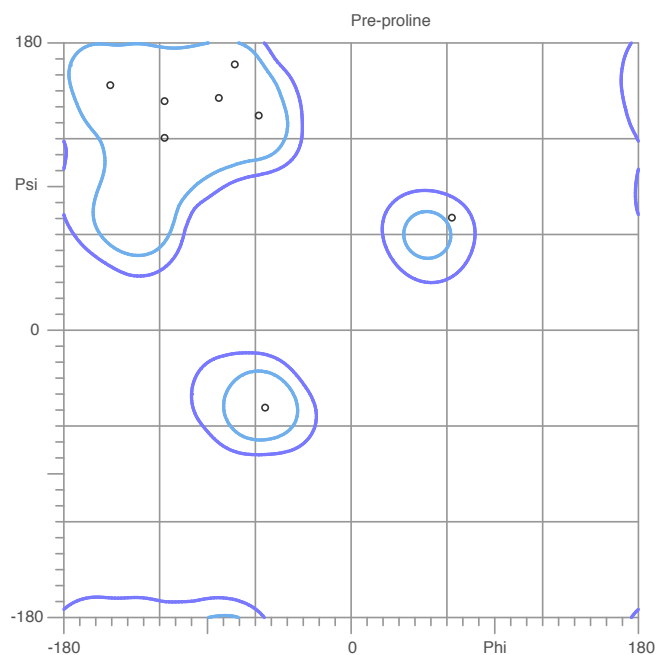
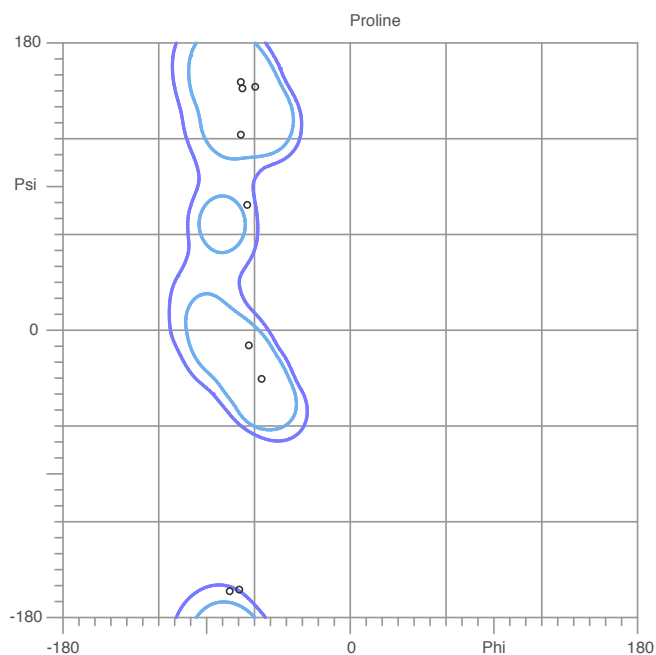
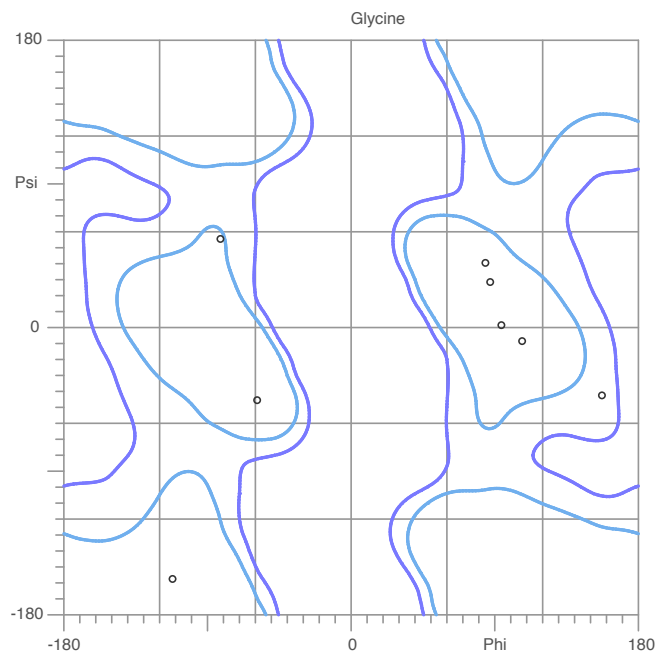
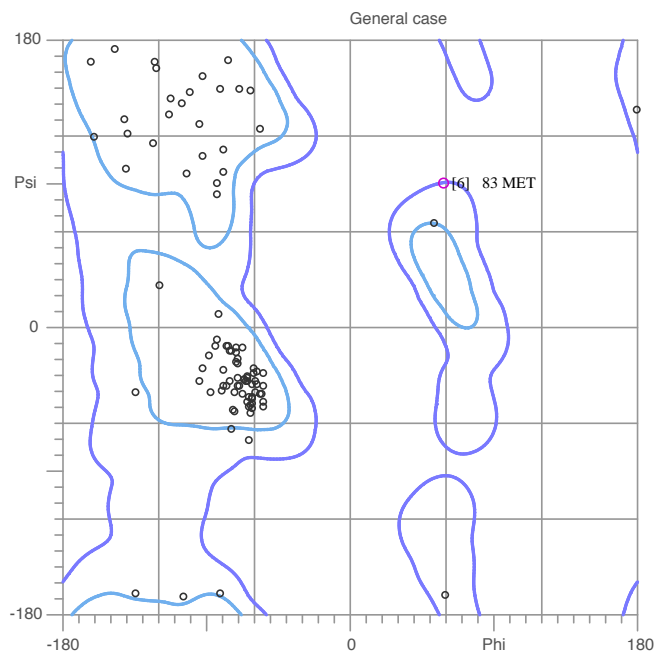
There were 2 outliers (phi, psi):

[5] 11 MET (-158.2, -92.1)

[5] 118 ALA (-169.6, 32.2)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 6

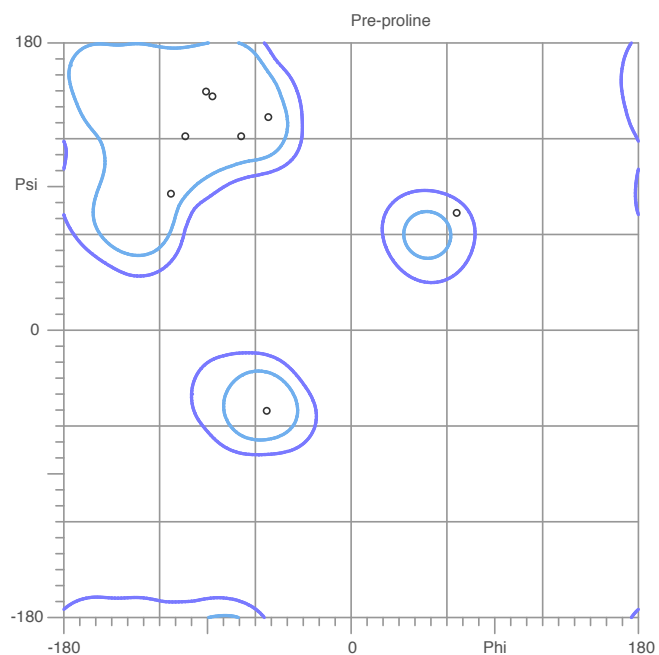
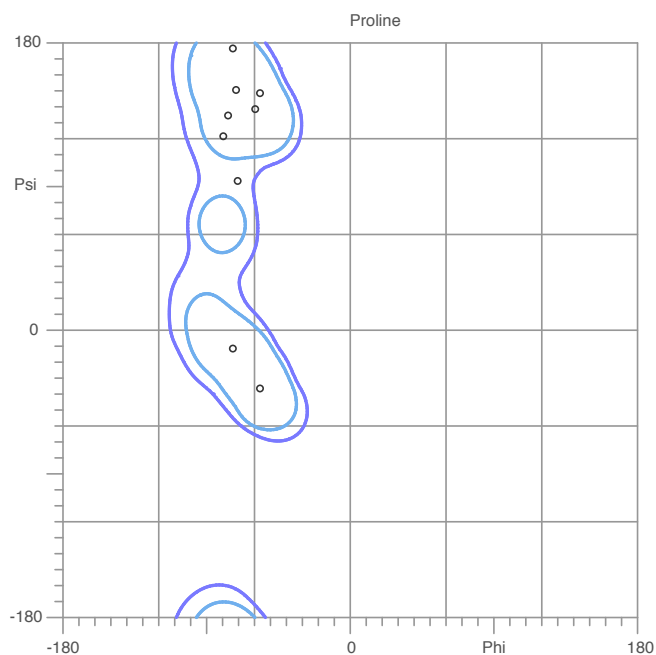
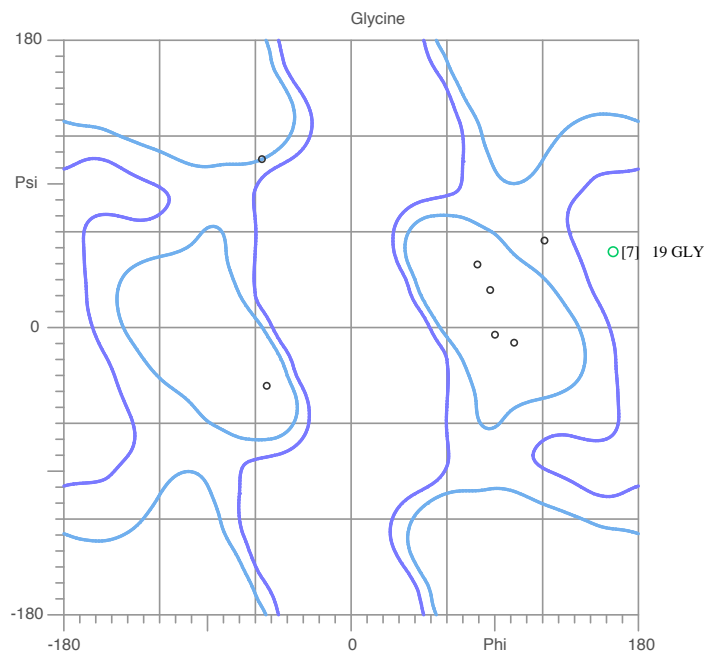
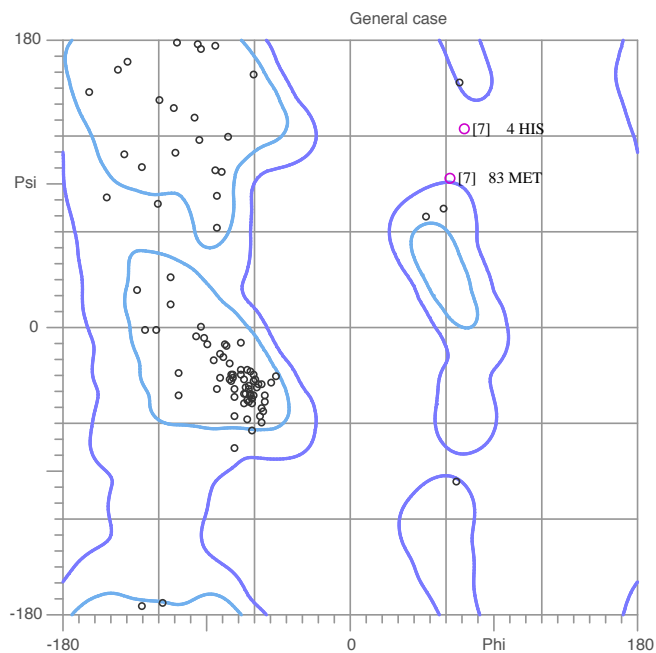


87.4% (104/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[6] 83 MET (58.6, 91.1)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 7



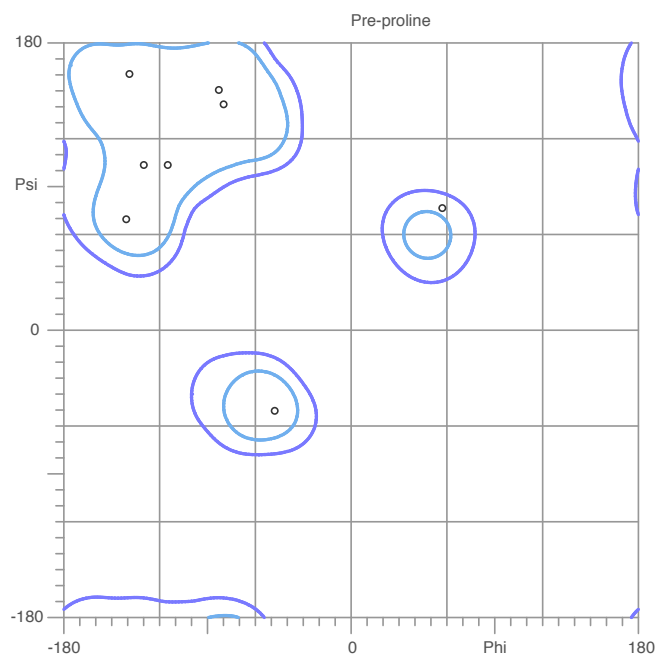
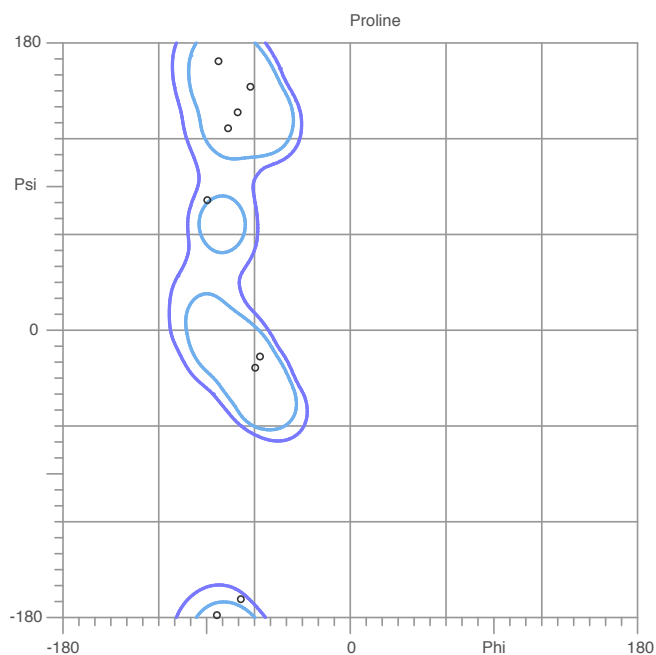
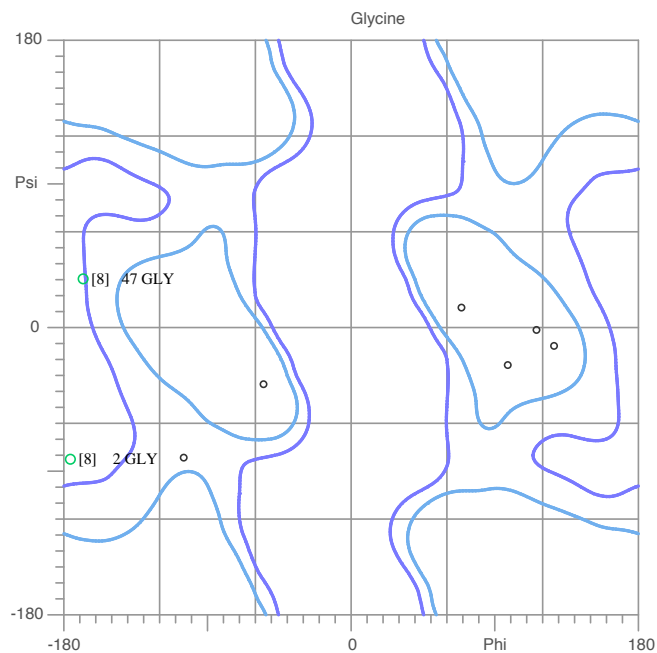
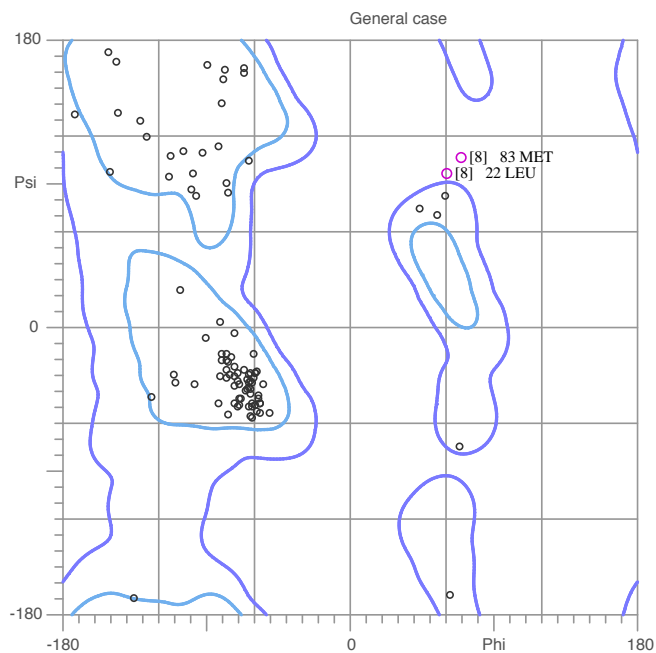
88.2% (105/119) of all residues were in favored (98%) regions.  
97.5% (116/119) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [7] 4 HIS (72.0, 125.3)
- [7] 19 GLY (164.5, 48.0)
- [7] 83 MET (62.6, 95.0)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 8



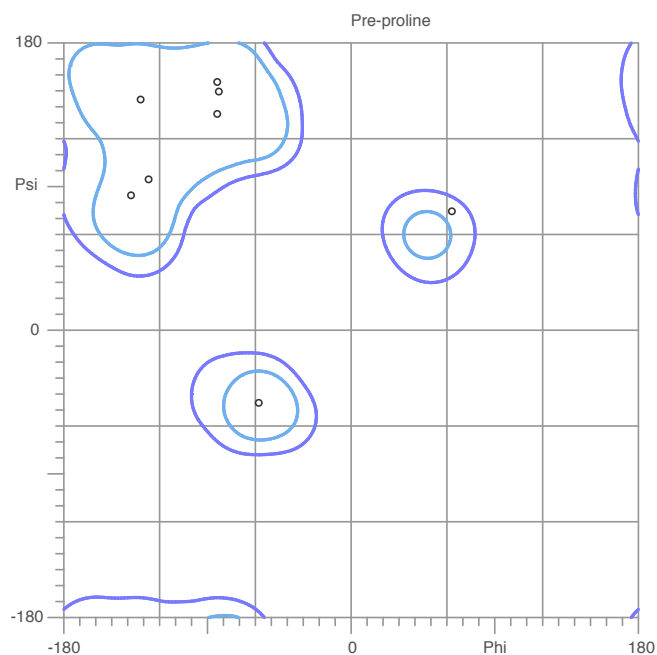
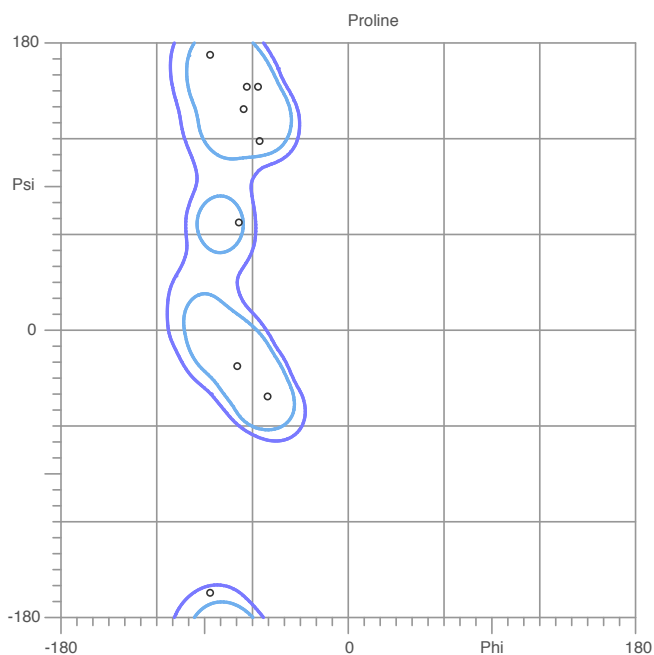
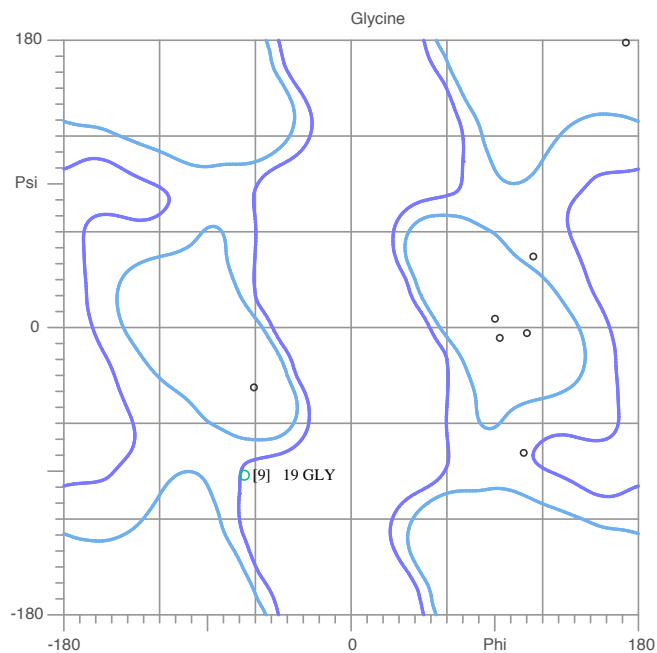
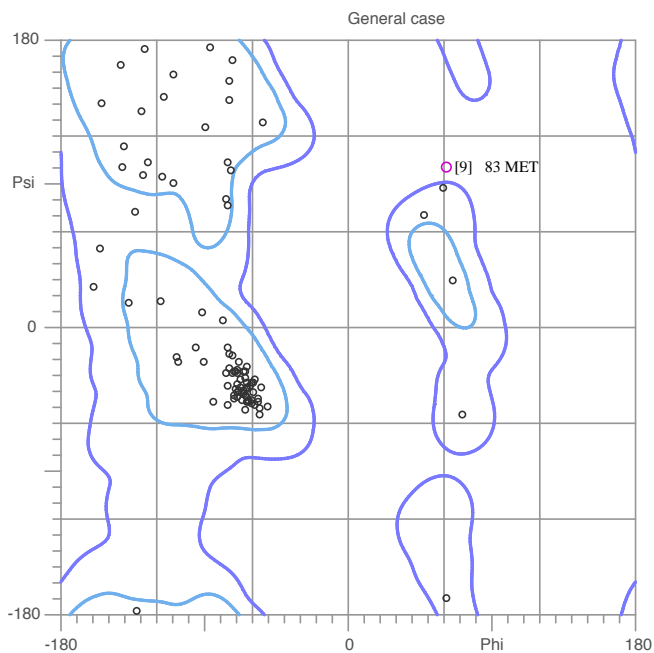
86.6% (103/119) of all residues were in favored (98%) regions.  
96.6% (115/119) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [8] 2 GLY (-176.3, -82.9)
- [8] 22 LEU (60.2, 97.6)
- [8] 47 GLY (-168.6, 31.7)
- [8] 83 MET (69.5, 108.0)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 9



89.1% (106/119) of all residues were in favored (98%) regions.  
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

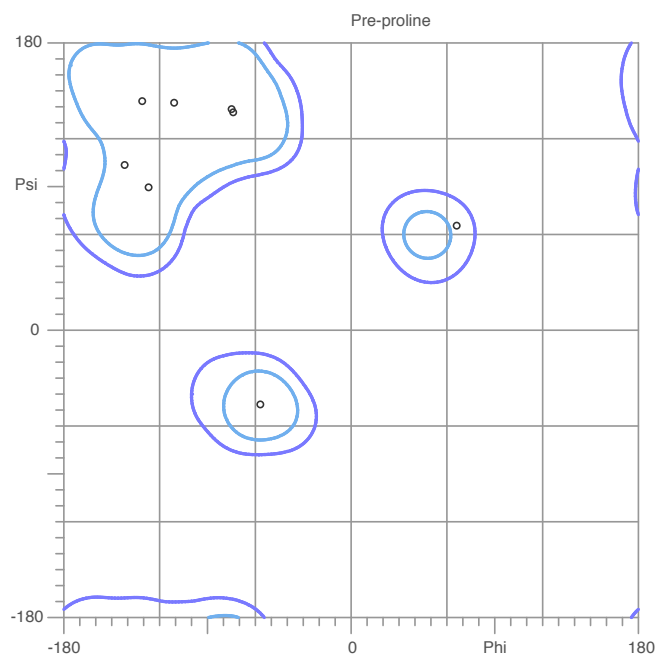
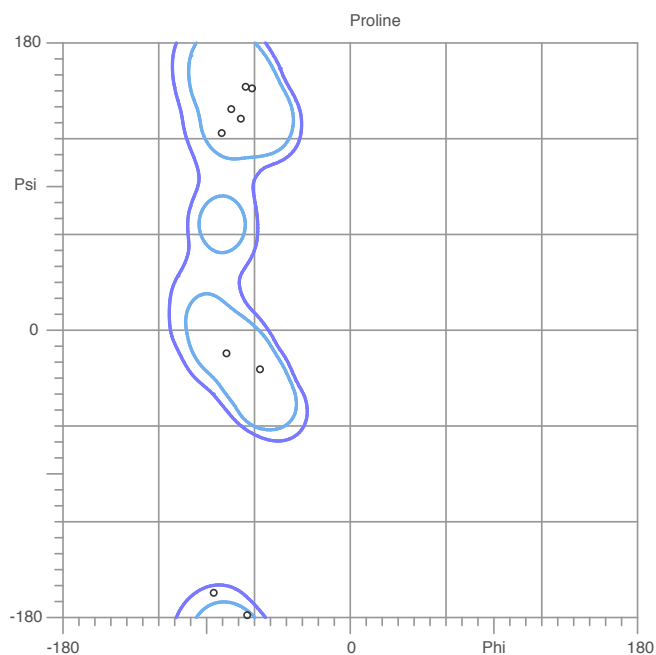
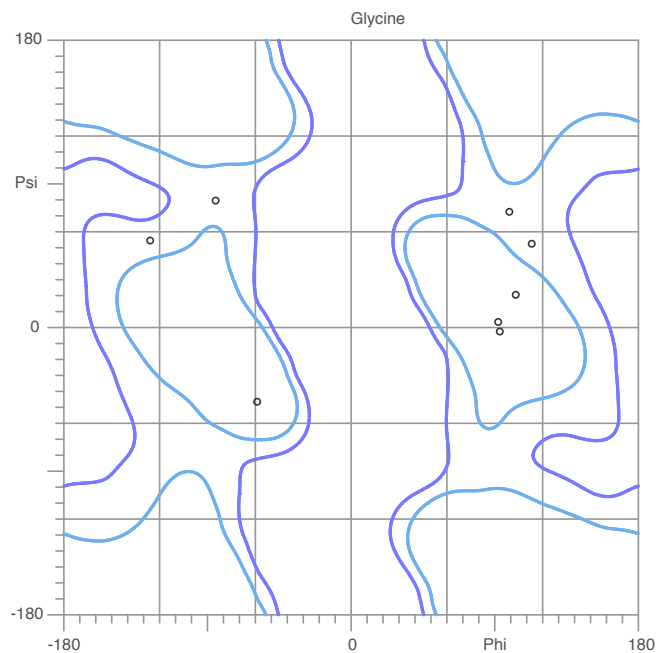
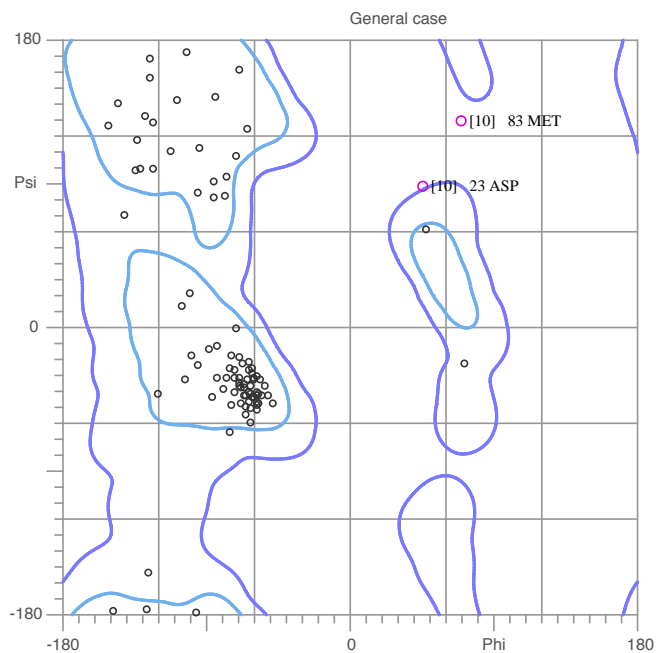
There were 2 outliers (phi, psi):

[9] 19 GLY (-67.7, -92.7)

[9] 83 MET (61.2, 101.1)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 10

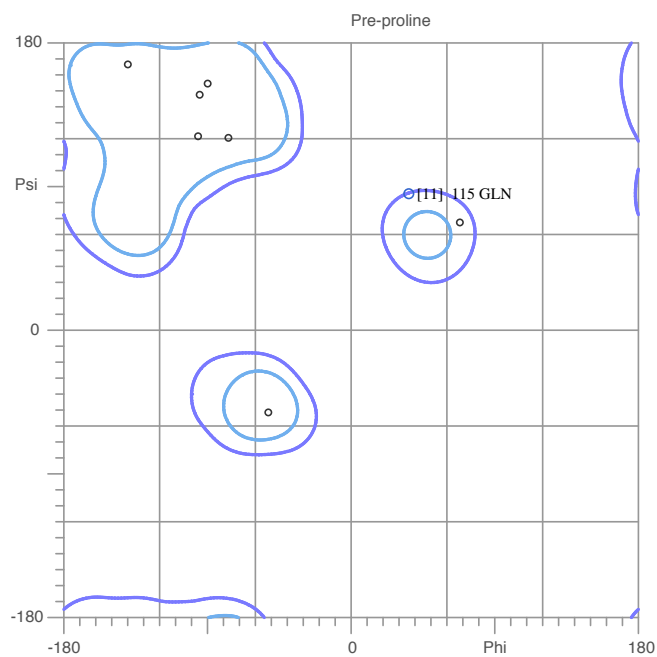
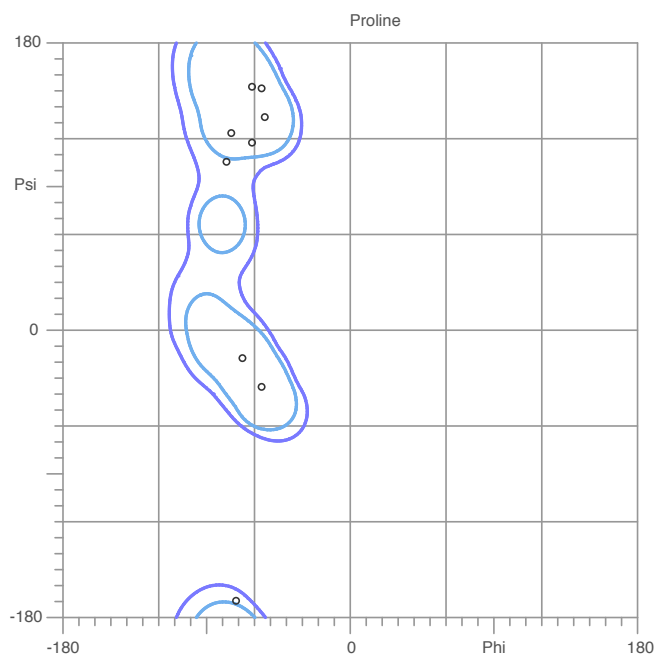
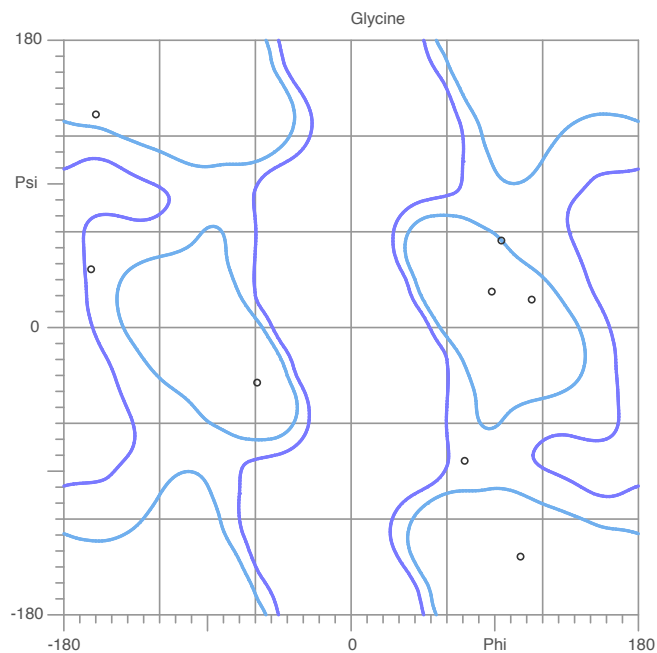
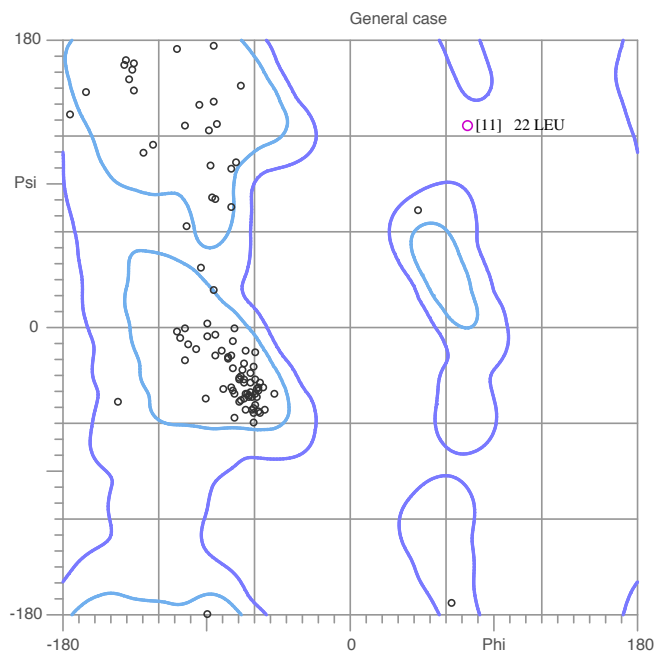


89.9% (107/119) of all residues were in favored (98%) regions.  
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[10] 23 ASP (45.2, 89.2)  
[10] 83 MET (69.7, 130.7)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 11

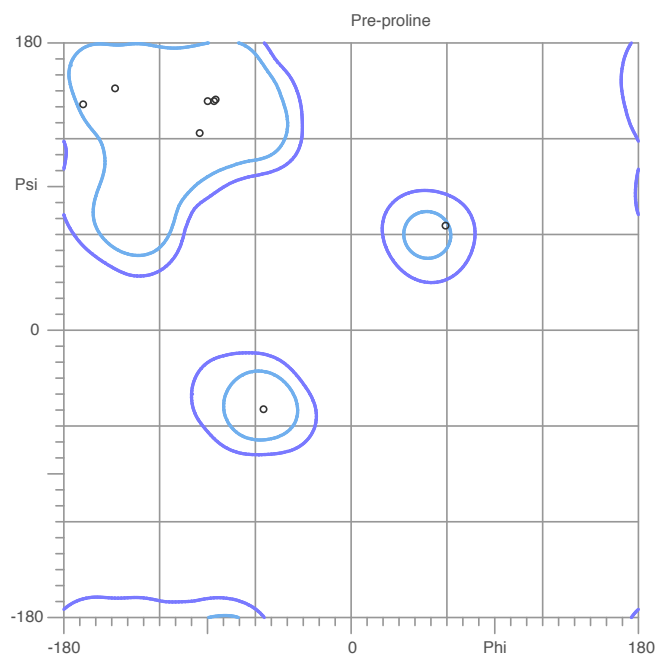
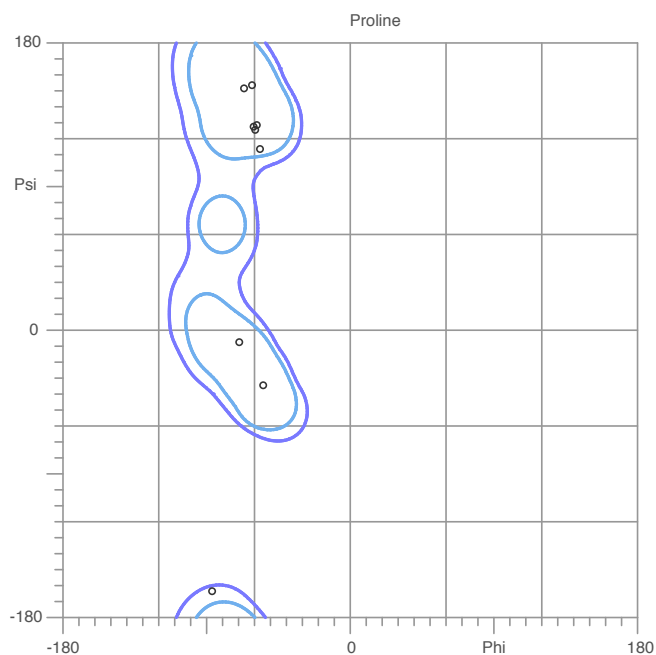
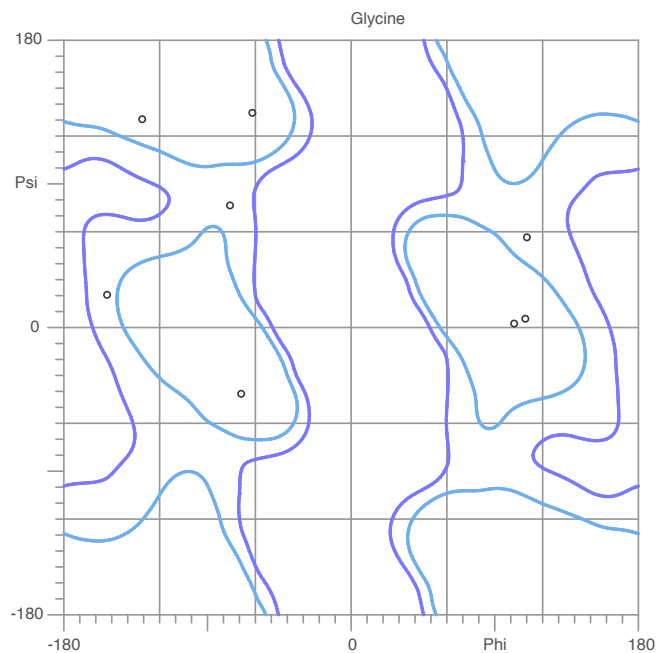
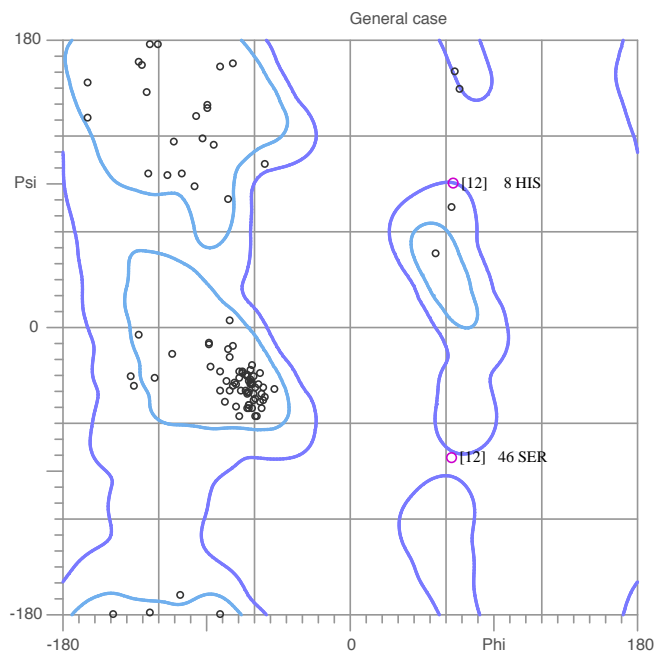


88.2% (105/119) of all residues were in favored (98%) regions.  
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[11] 22 LEU (73.1, 127.7)  
[11] 115 GLN (36.5, 87.0)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 12



89.1% (106/119) of all residues were in favored (98%) regions.  
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

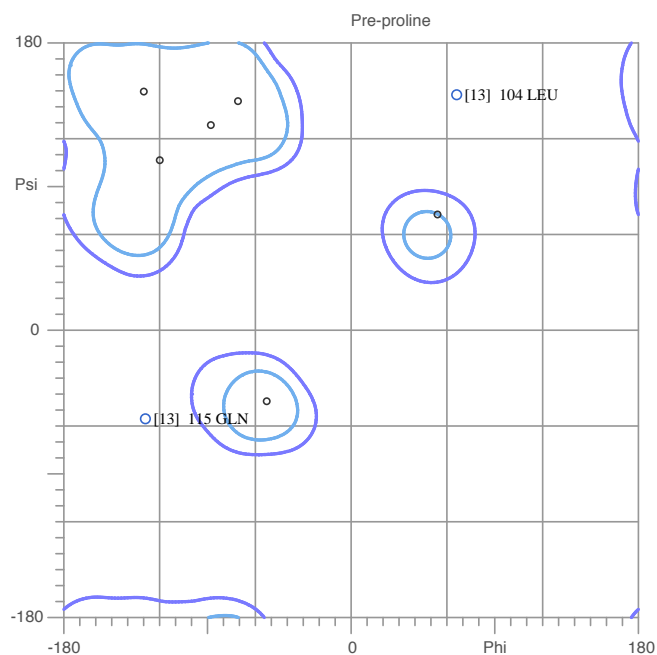
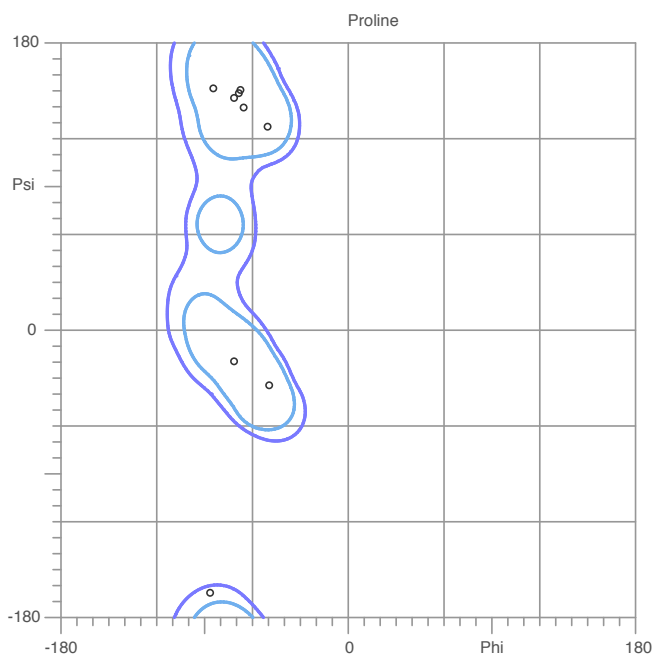
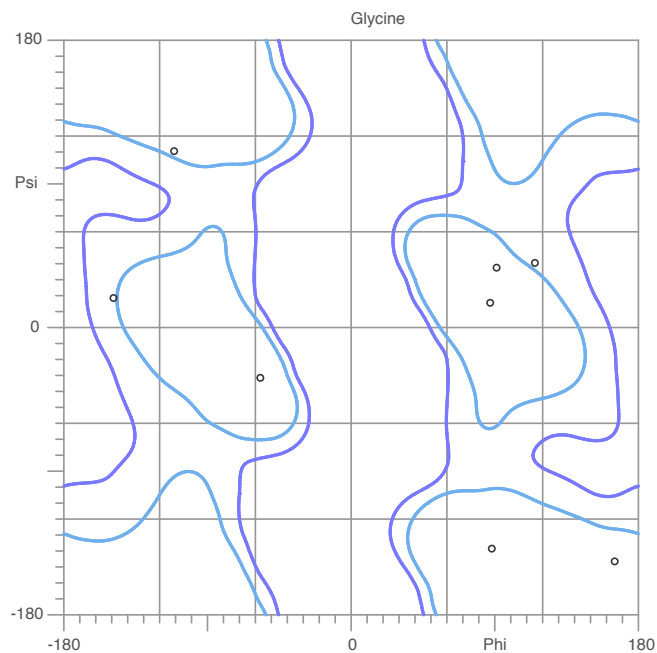
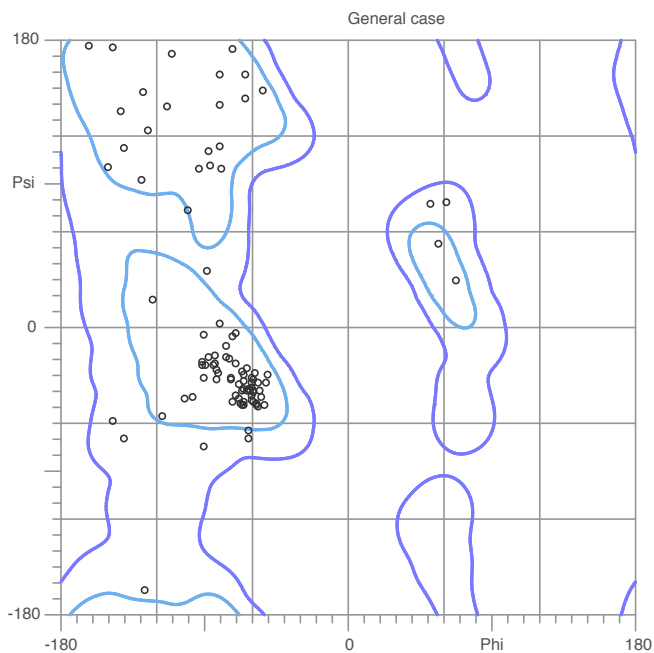
There were 2 outliers (phi, psi):

[12] 8 HIS (64.4, 91.9)

[12] 46 SER (63.8, -81.5)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 13



87.4% (104/119) of all residues were in favored (98%) regions.  
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[13] 104 LEU (66.5, 148.5)

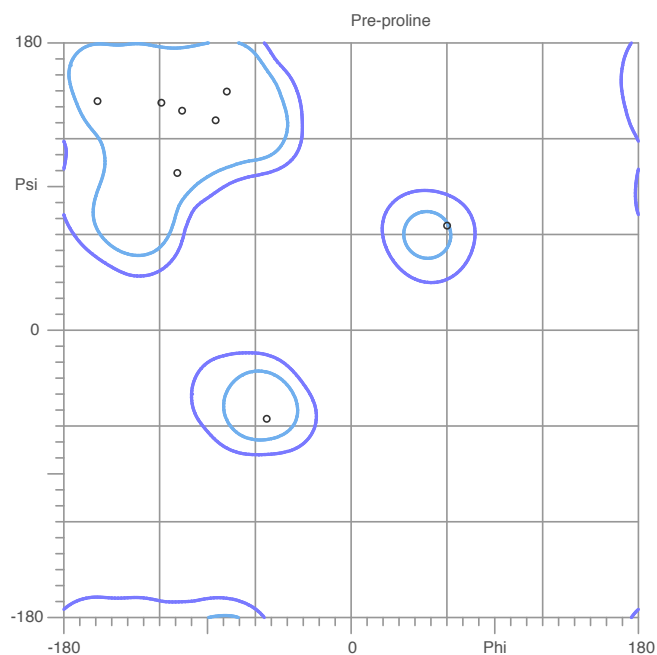
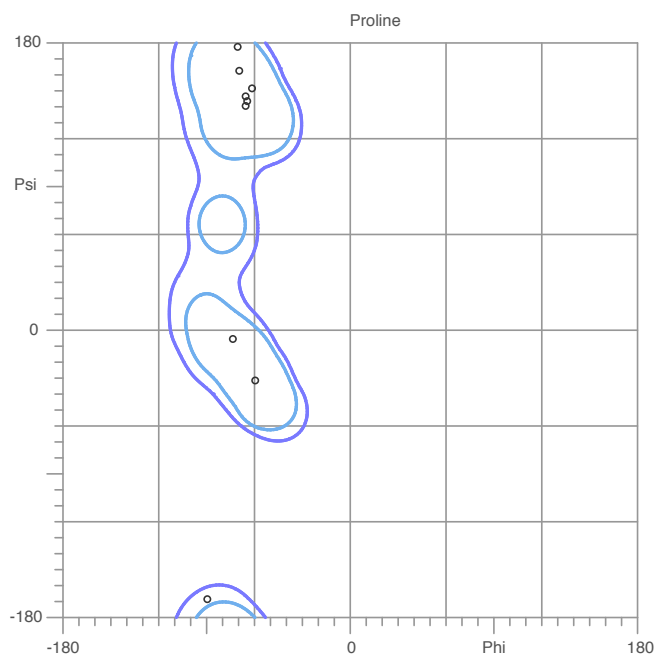
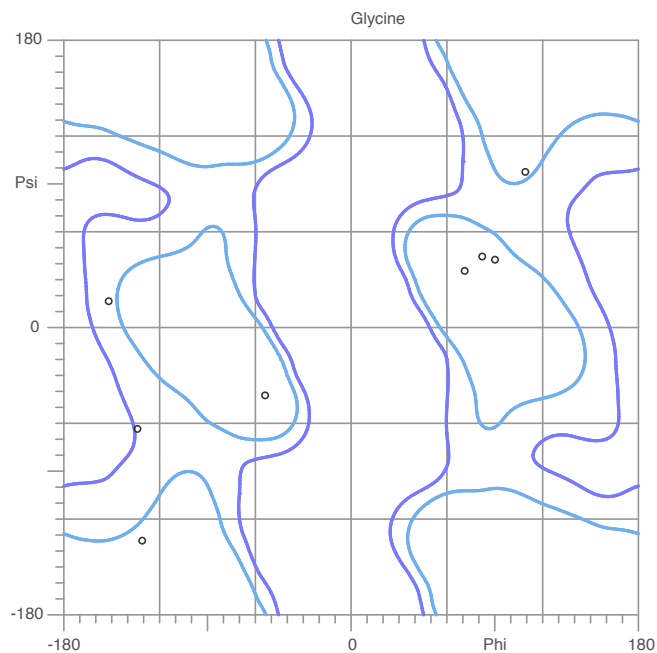
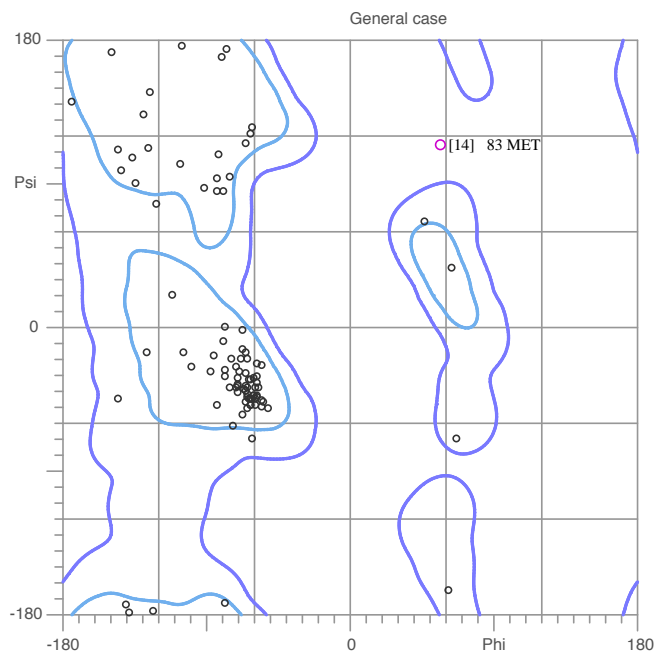
[13] 115 GLN (-129.3, -55.5)

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# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 14



90.8% (108/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

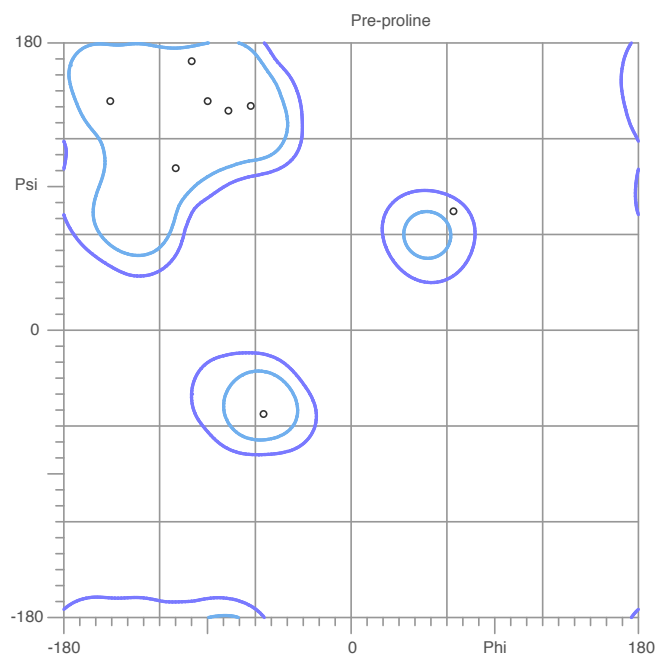
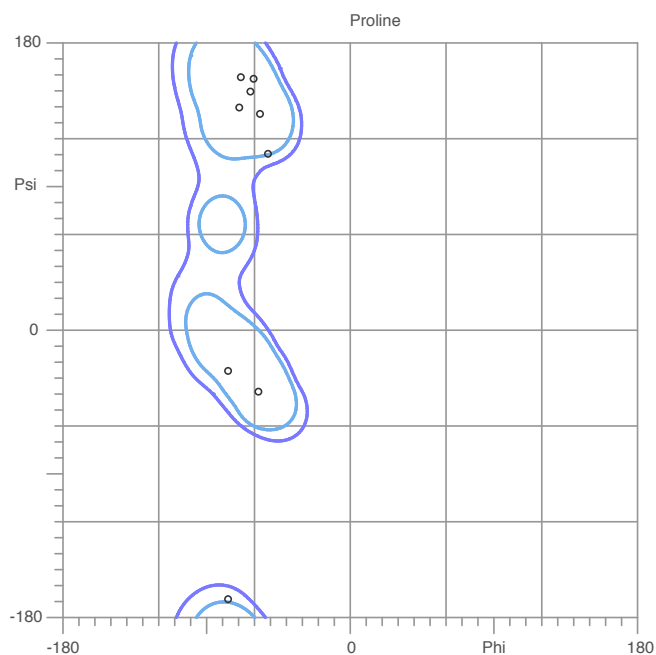
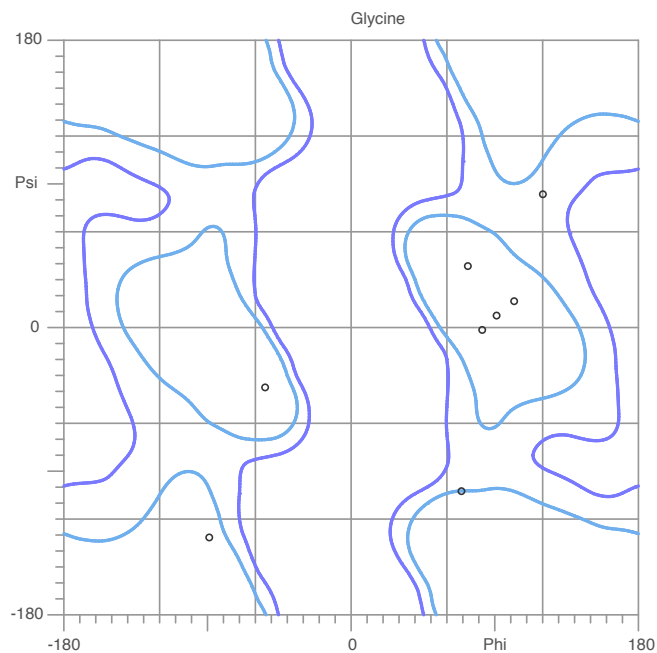
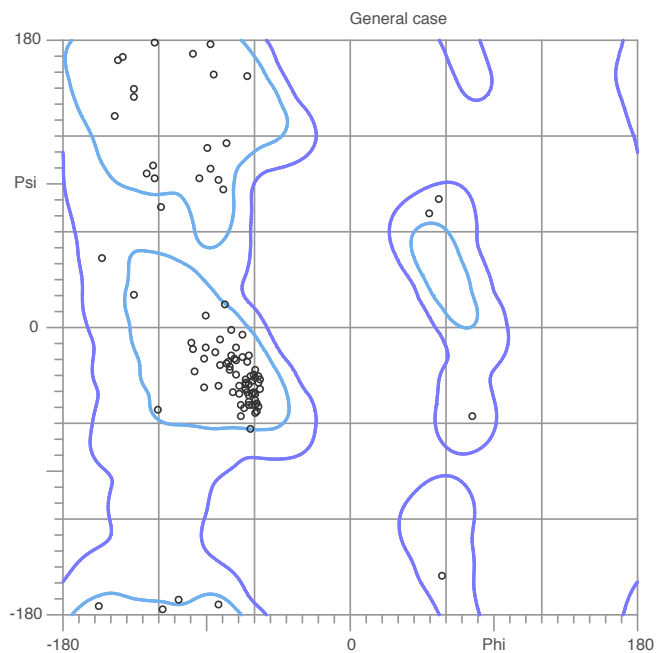
There were 1 outliers (phi, psi):  
[14] 83 MET (56.1, 116.0)

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# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 15



89.9% (107/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

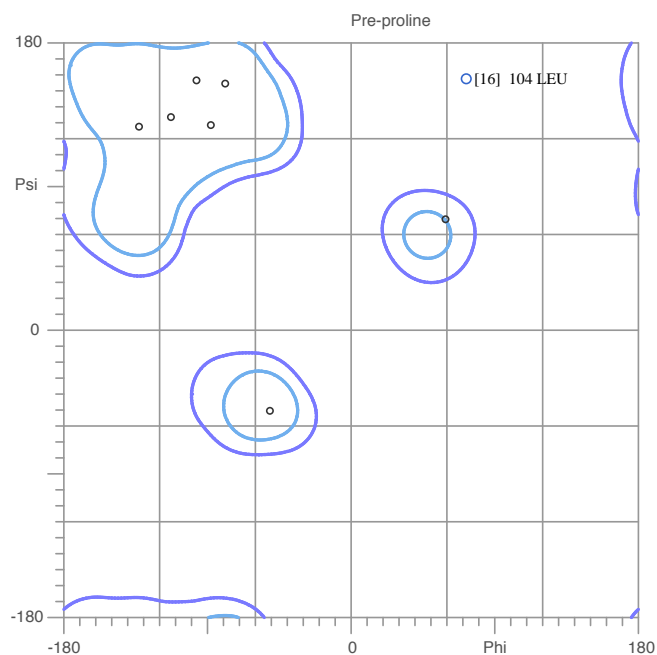
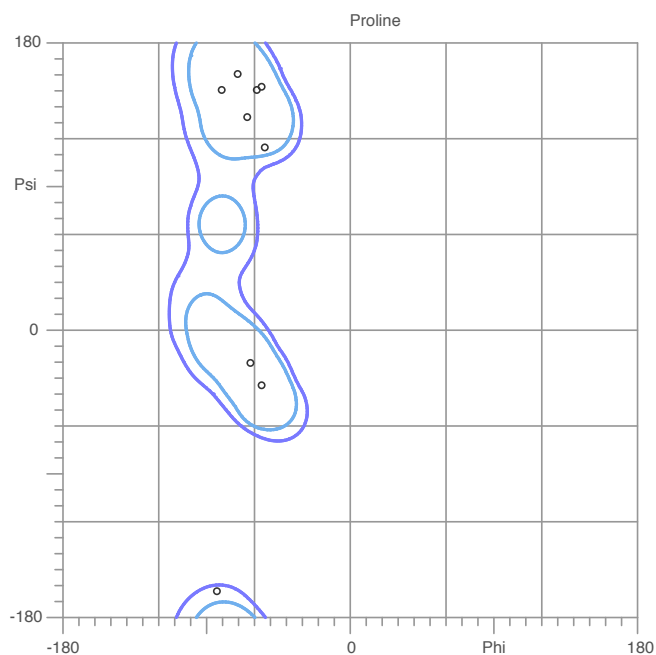
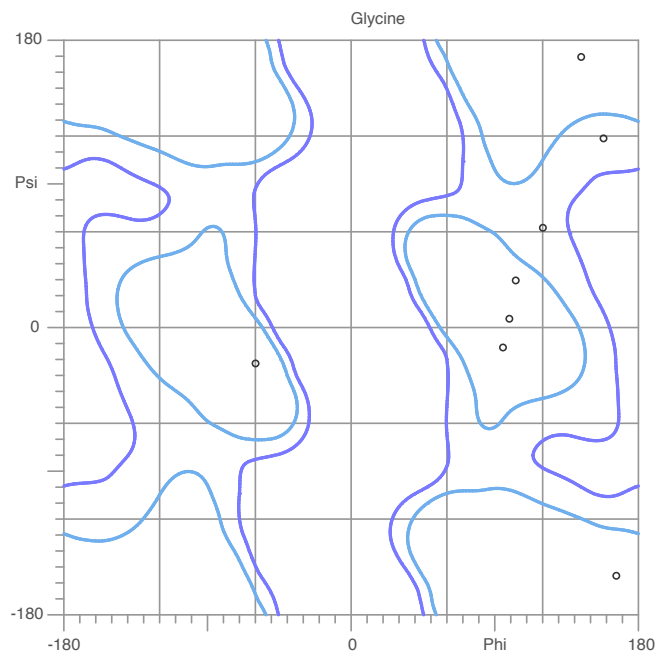
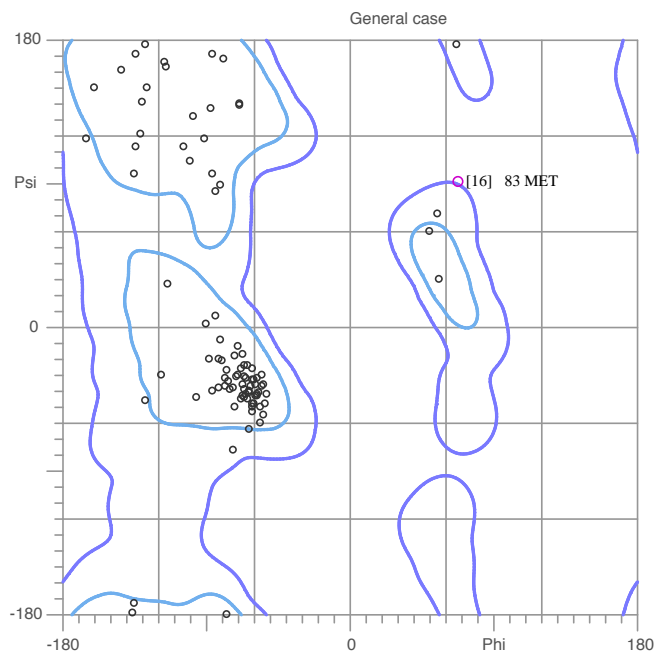
There were no outliers.

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# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 16

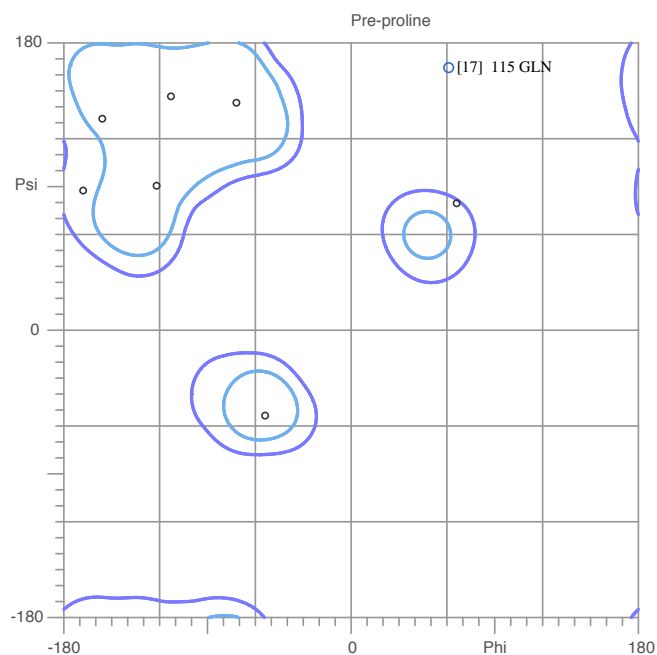
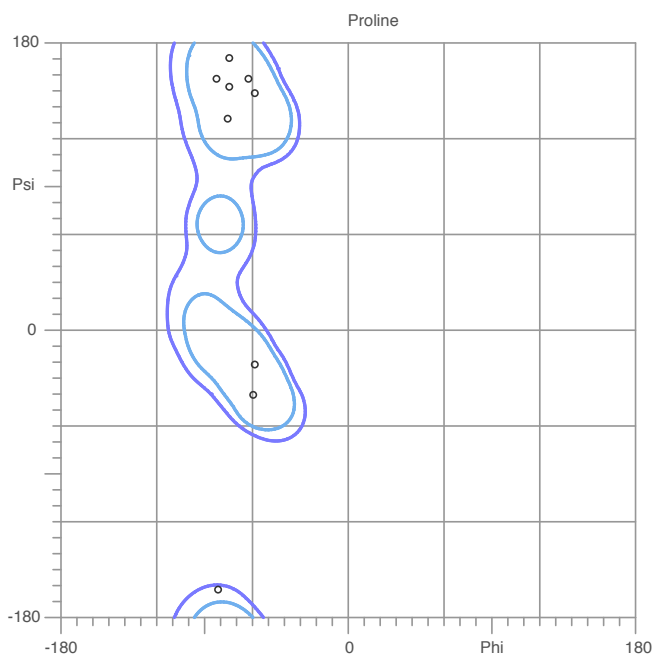
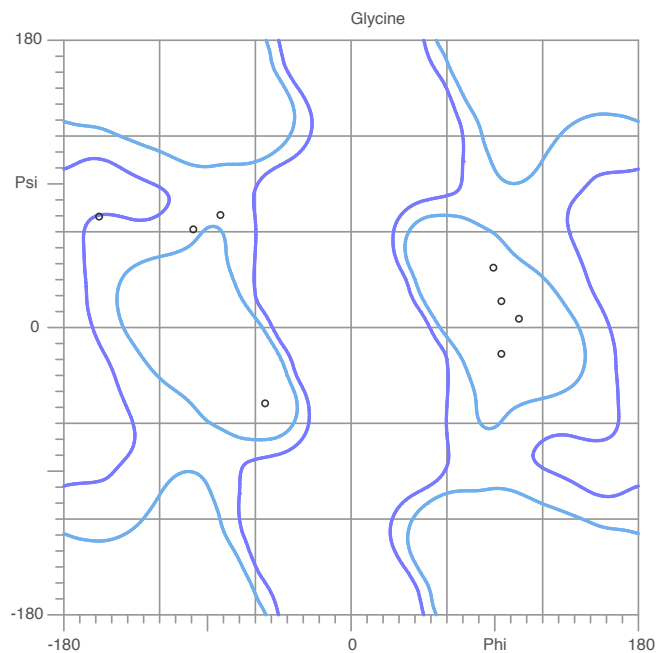
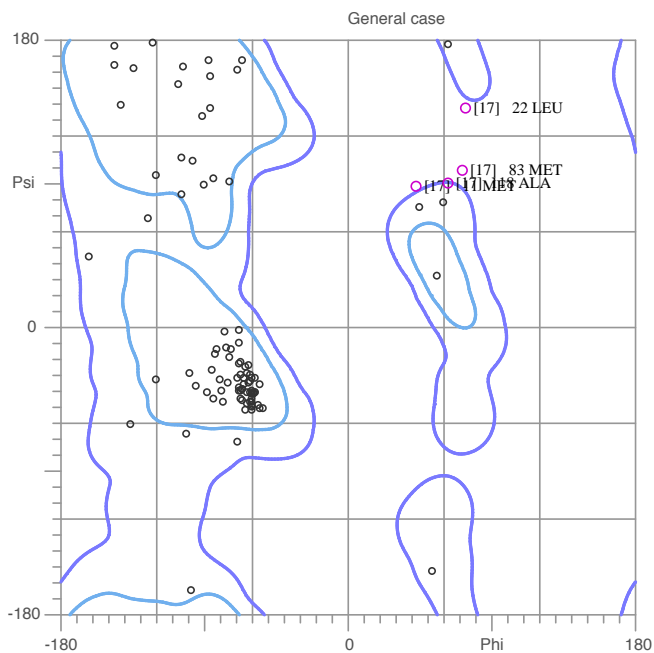


89.9% (107/119) of all residues were in favored (98%) regions.  
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[16] 83 MET (67.6, 92.7)  
[16] 104 LEU (72.8, 158.6)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 17



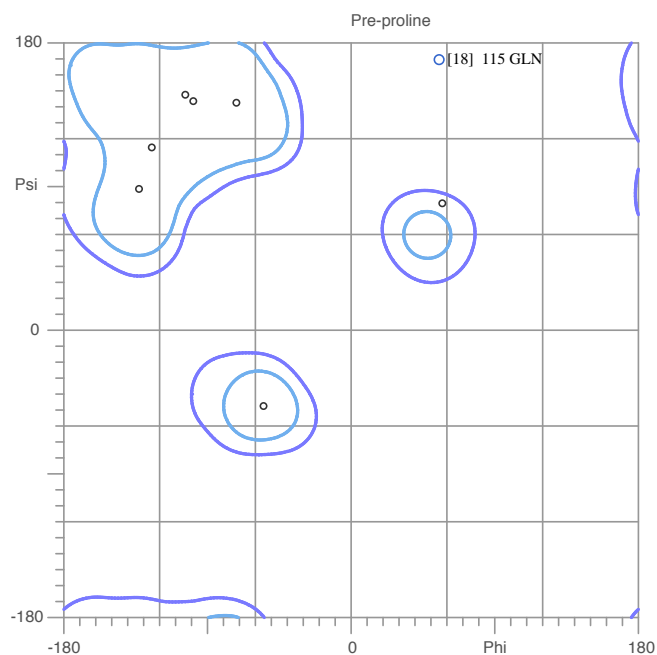
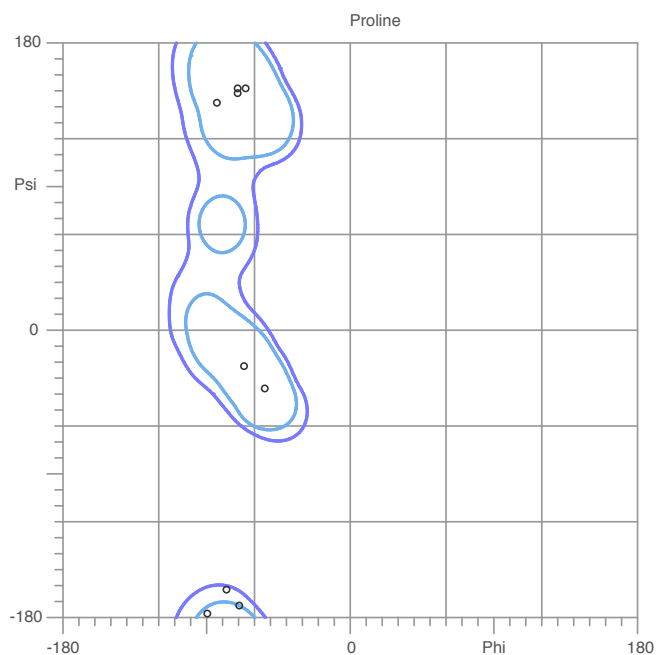
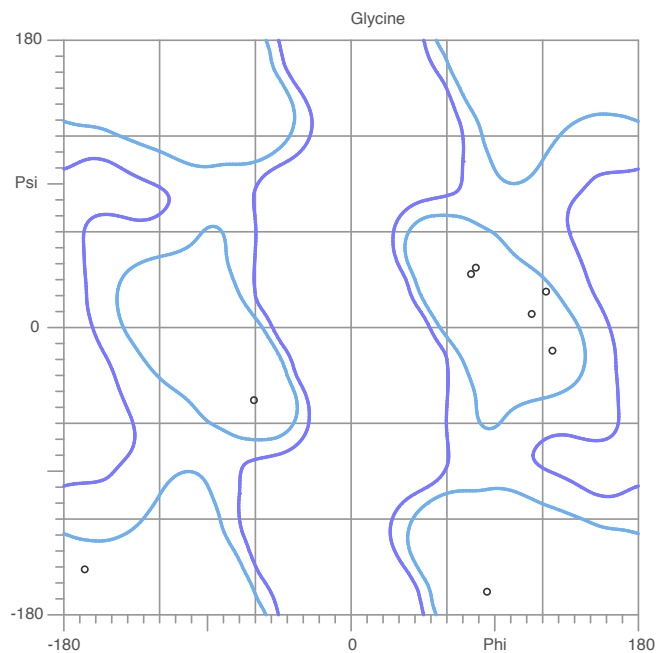
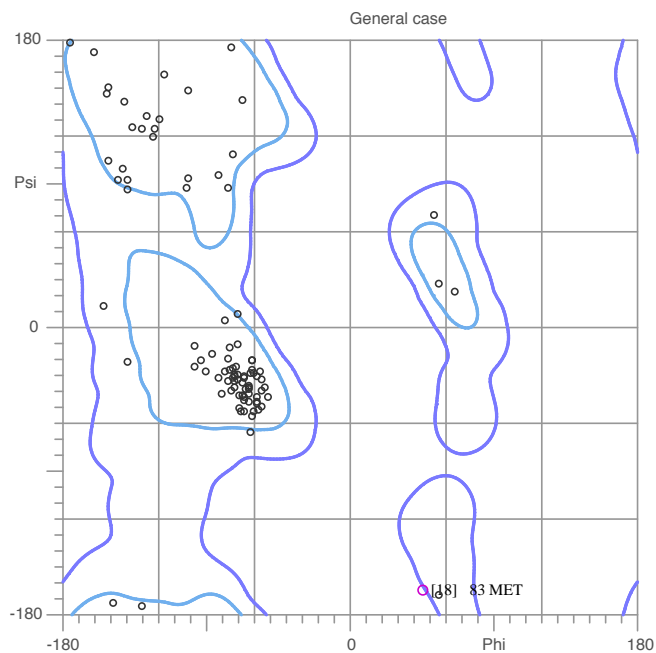
82.4% (98/119) of all residues were in favored (98%) regions.  
95.8% (114/119) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[17] 11 MET (42.3, 89.4)  
[17] 22 LEU (73.7, 138.9)  
[17] 83 MET (71.6, 99.4)  
[17] 115 GLN (61.5, 165.8)  
[17] 118 ALA (62.0, 91.6)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 18

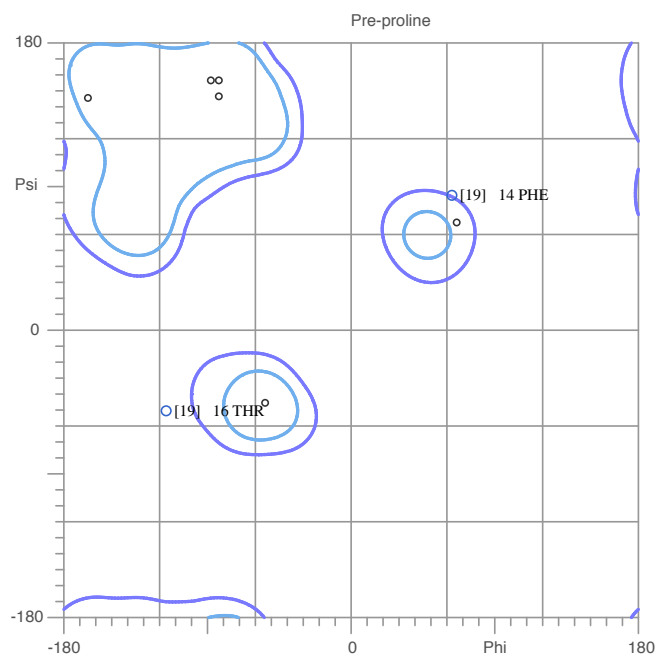
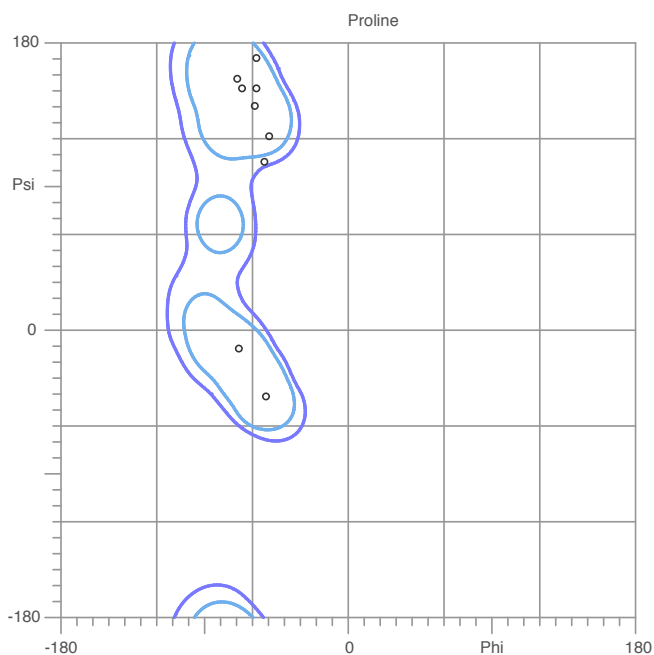
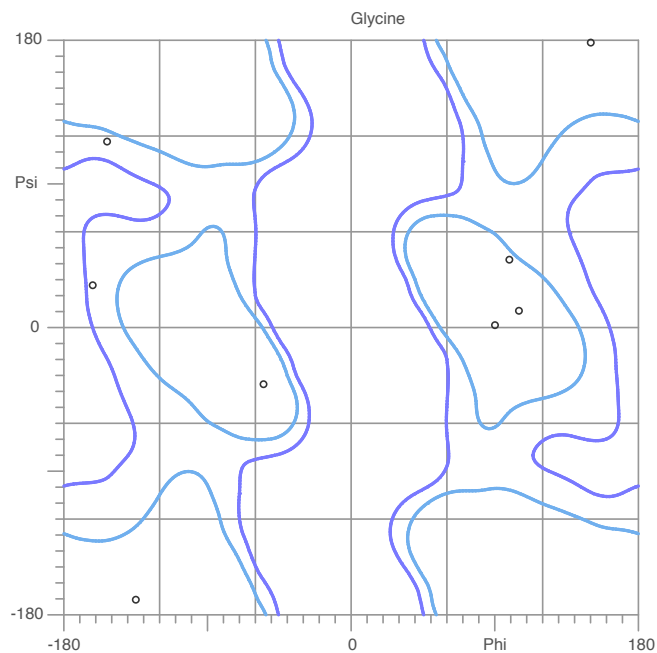
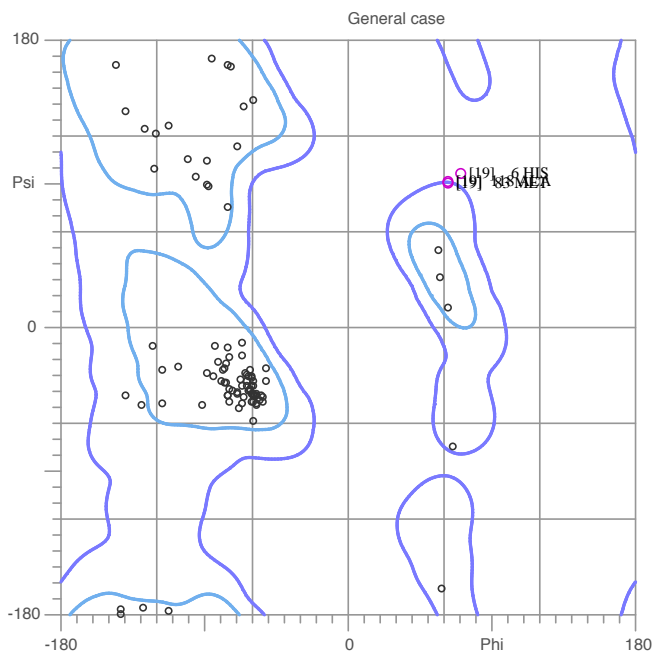


90.8% (108/119) of all residues were in favored (98%) regions.  
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[18] 83 MET (45.8, -164.7)  
[18] 115 GLN (55.1, 170.7)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 19



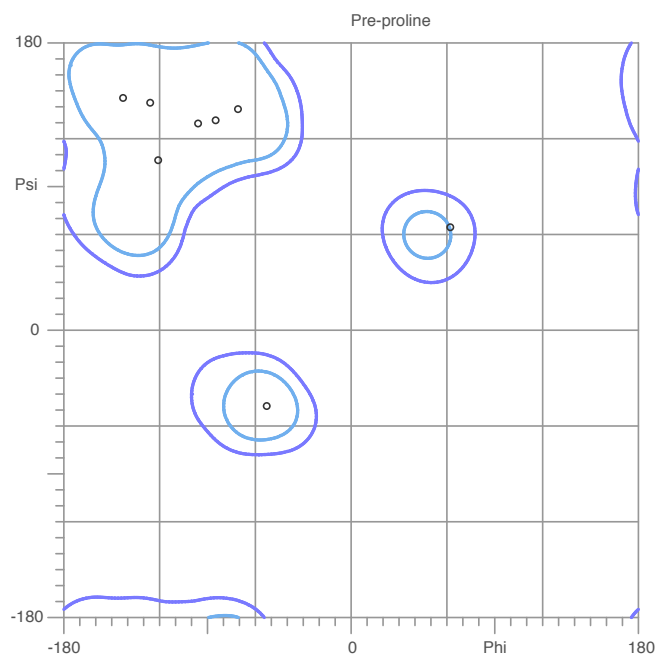
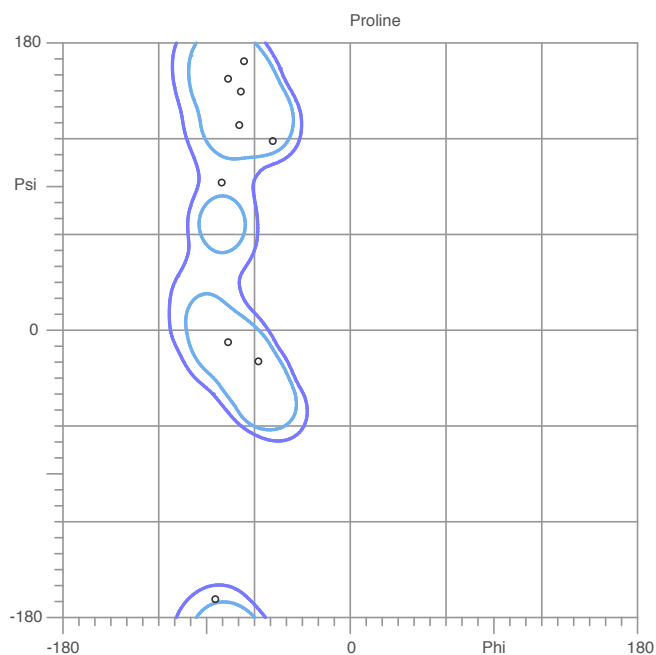
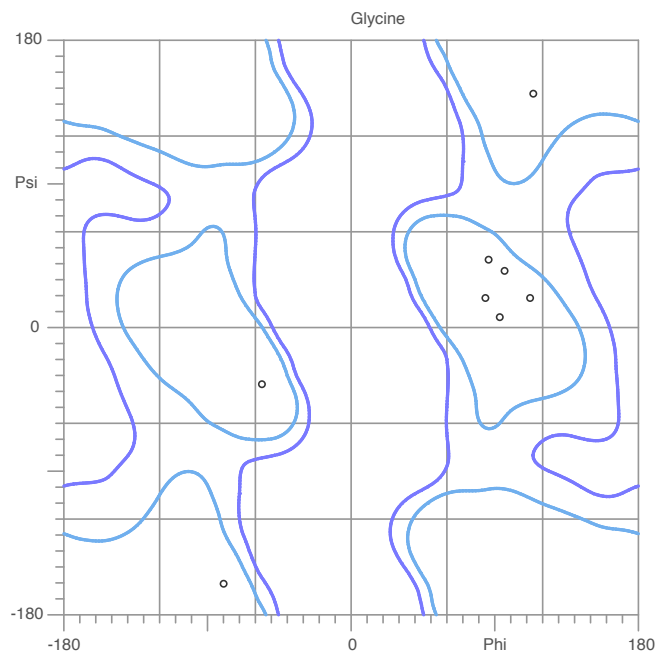
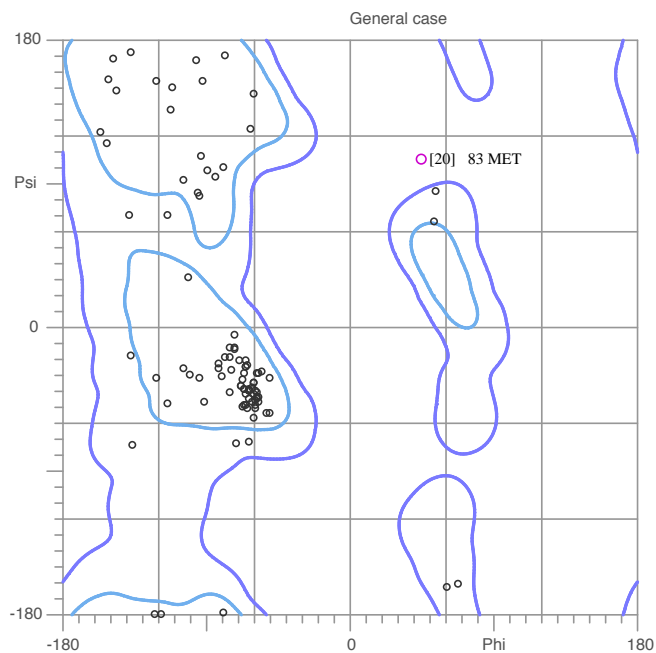
89.1% (106/119) of all residues were in favored (98%) regions.  
95.8% (114/119) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[19] 6 HIS (70.5, 97.5)  
[19] 14 PHE (63.7, 85.7)  
[19] 16 THR (-116.6, -50.2)  
[19] 83 MET (62.5, 91.7)  
[19] 118 ALA (62.3, 92.6)

# MolProbity Ramachandran analysis

HR3646E\_NMR\_em\_bcr3.pdb, model 20



88.2% (105/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[20] 83 MET (44.9, 106.3)

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

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