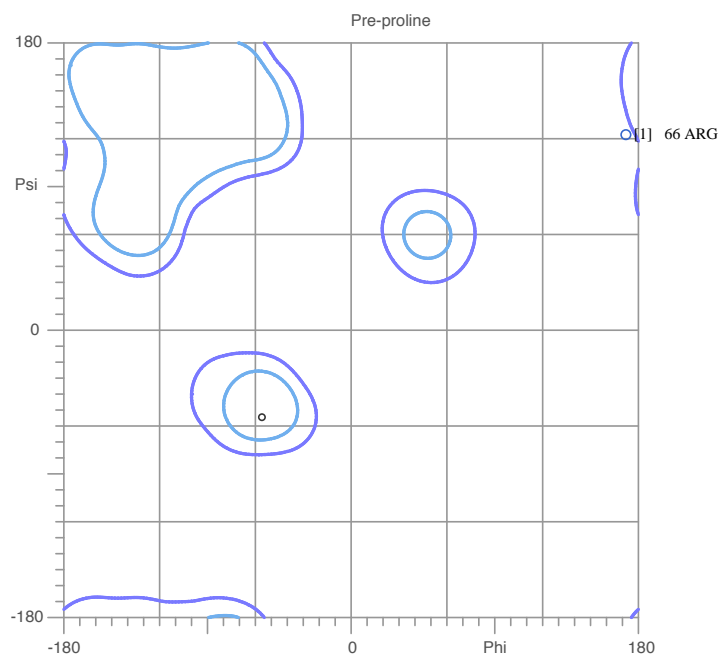
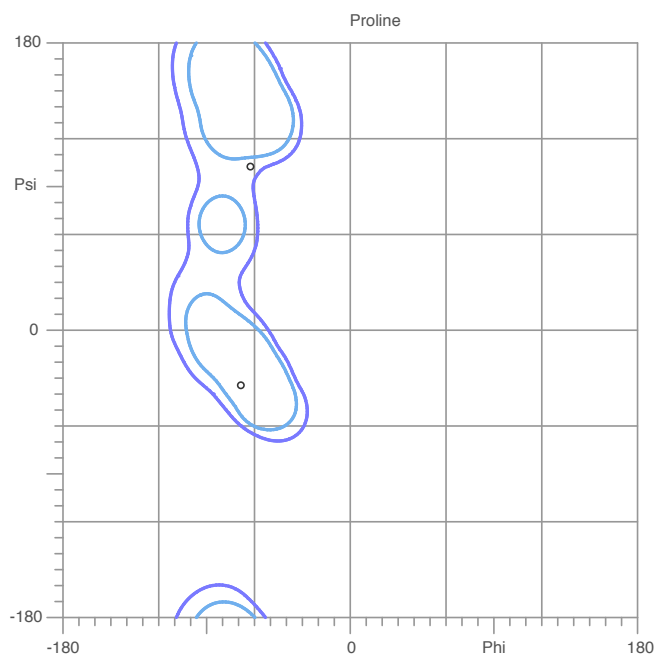
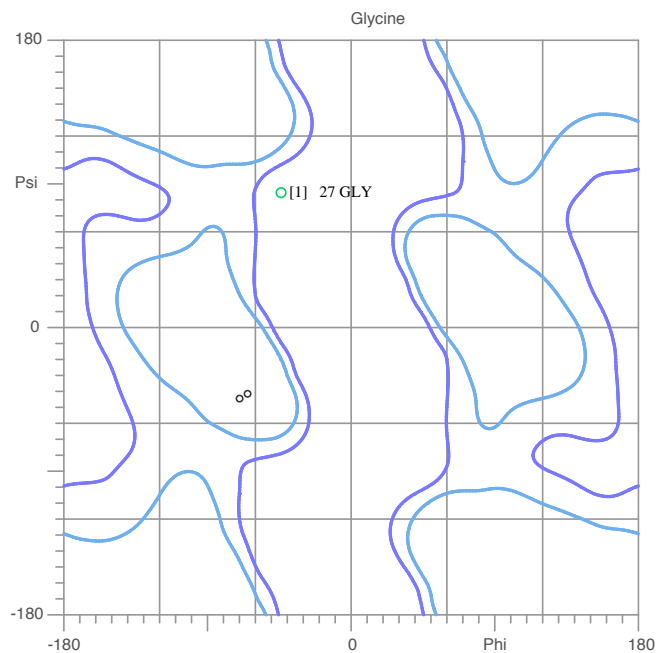
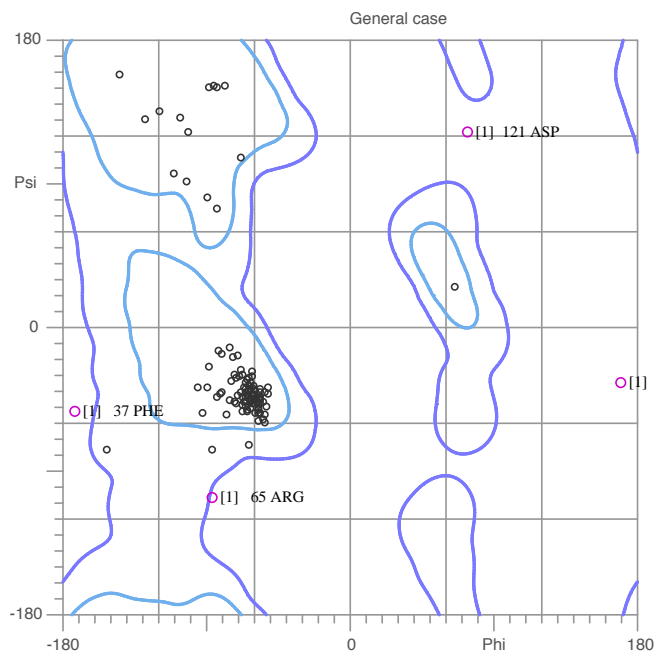




# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 1



91.7% (111/121) of all residues were in favored (98%) regions.  
95.0% (115/121) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[1] 27 GLY (-44.9, 85.1)

[1] 28 LYS (169.8, -34.2)

[1] 37 PHE (-173.3, -52.8)

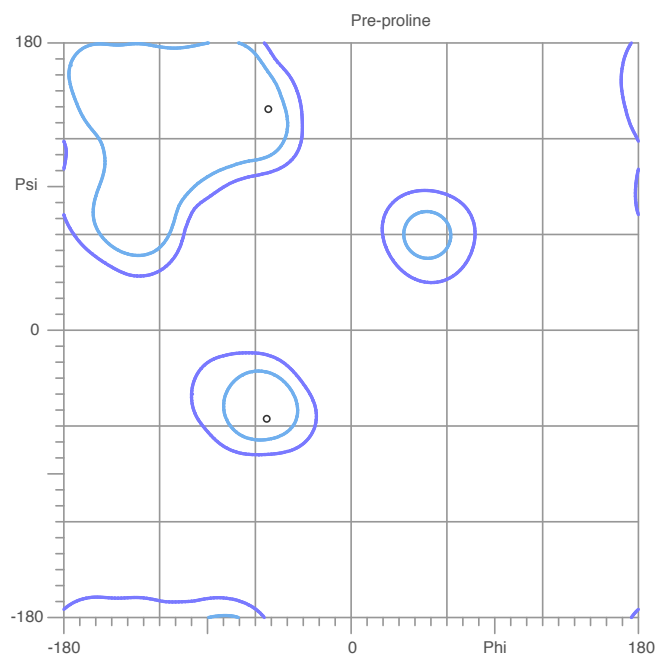
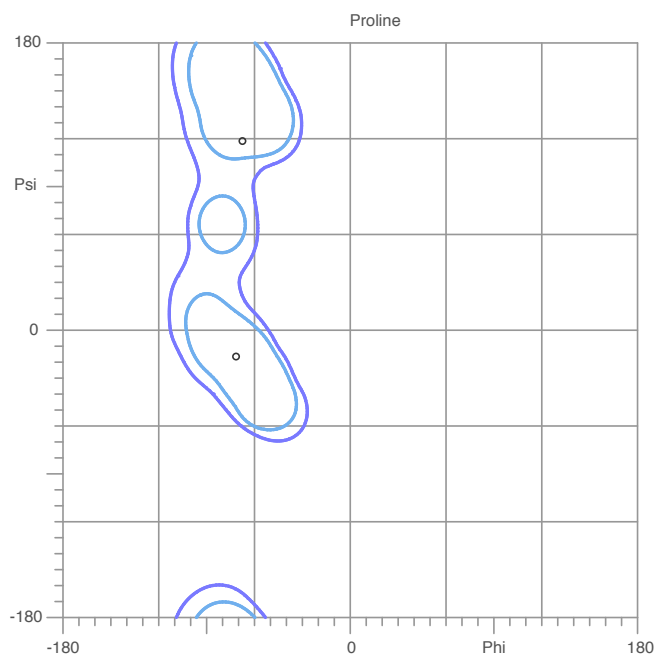
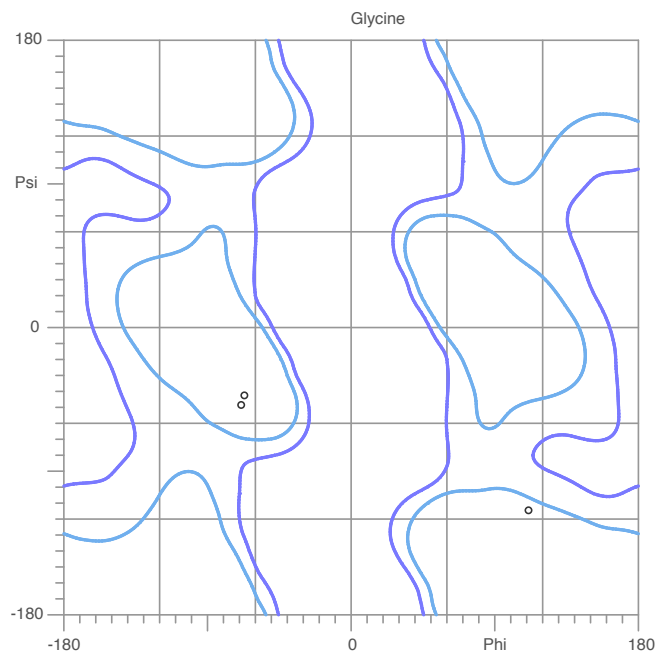
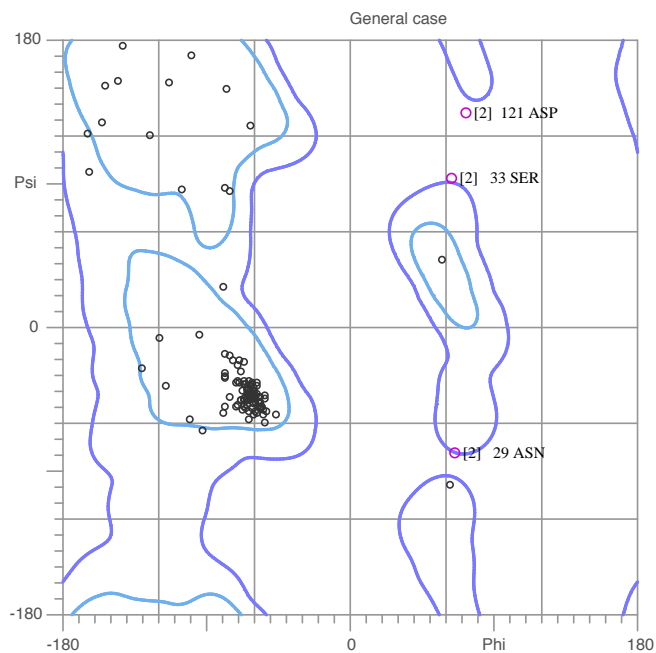
[1] 65 ARG (-87.3, -106.1)

[1] 66 ARG (172.9, 123.7)

[1] 121 ASP (73.0, 124.0)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 2



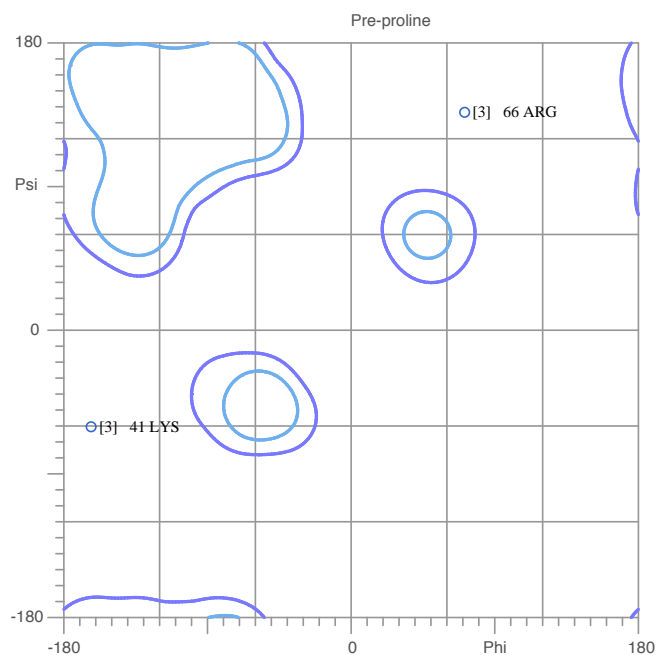
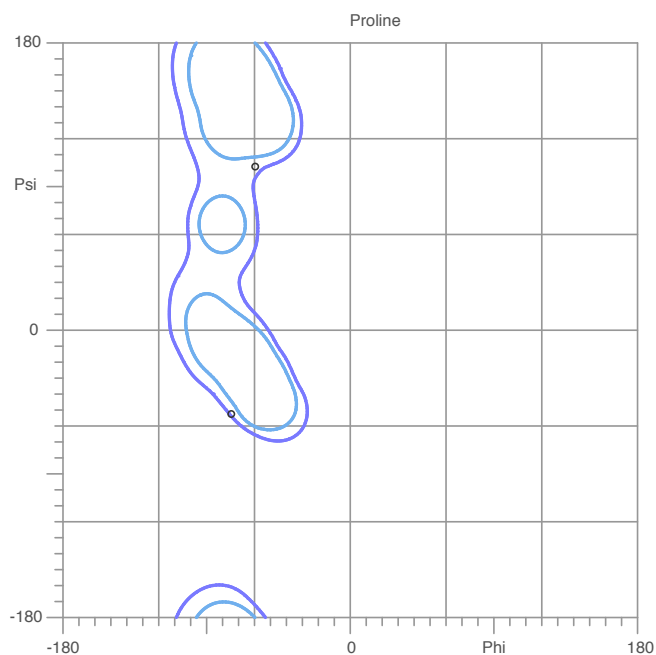
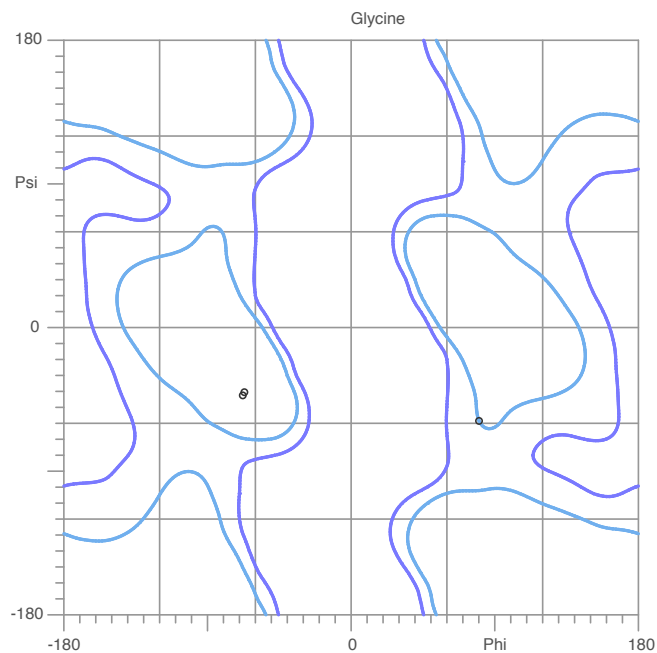
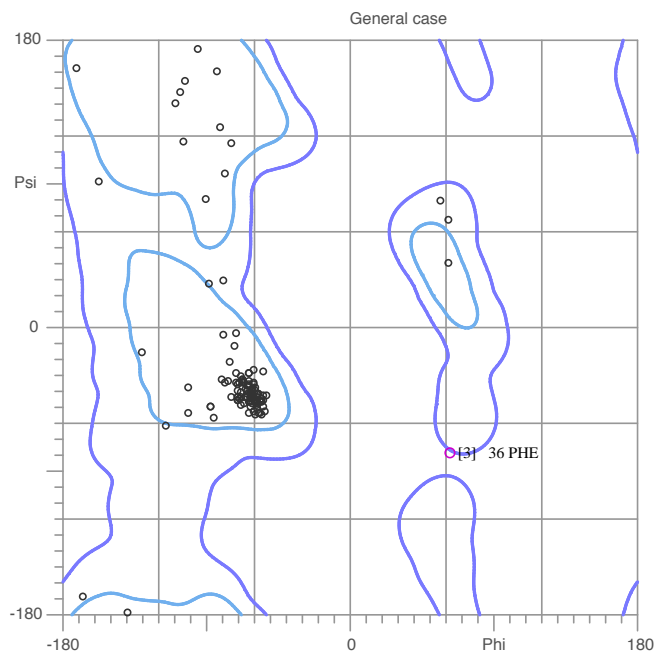
93.4% (113/121) of all residues were in favored (98%) regions.  
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 29 ASN (65.6, -79.0)
- [2] 33 SER (63.3, 94.3)
- [2] 121 ASP (72.4, 135.8)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 3



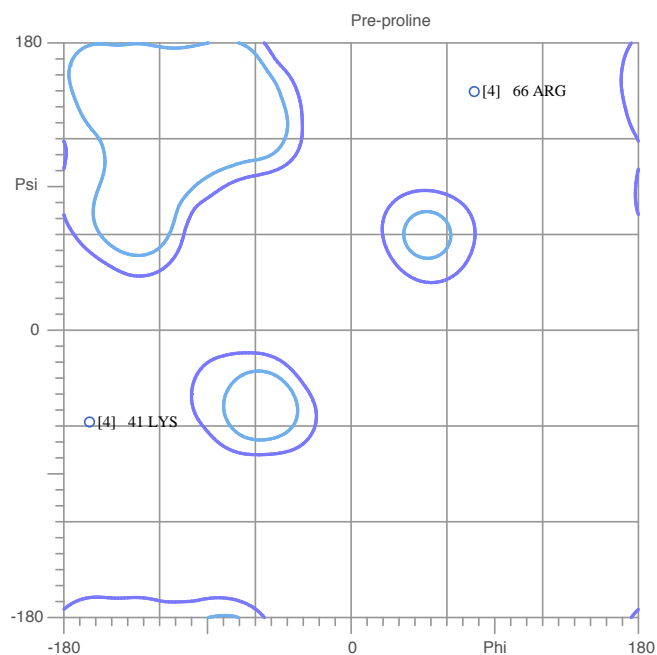
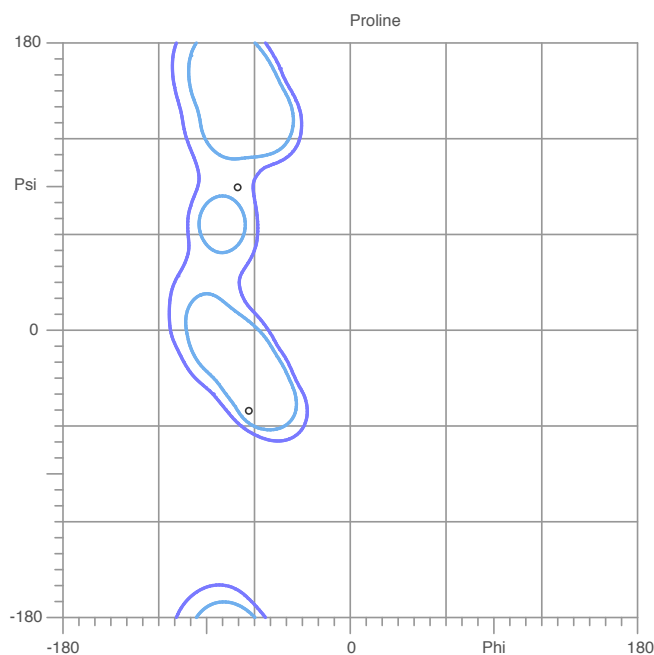
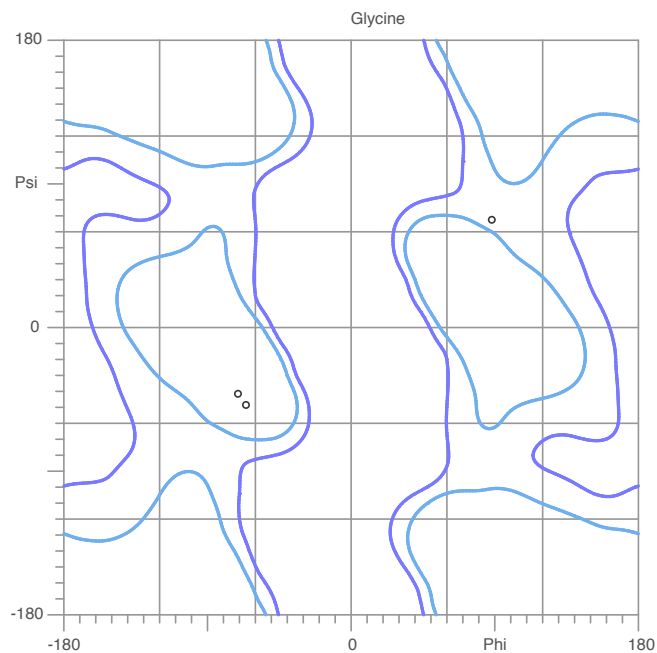
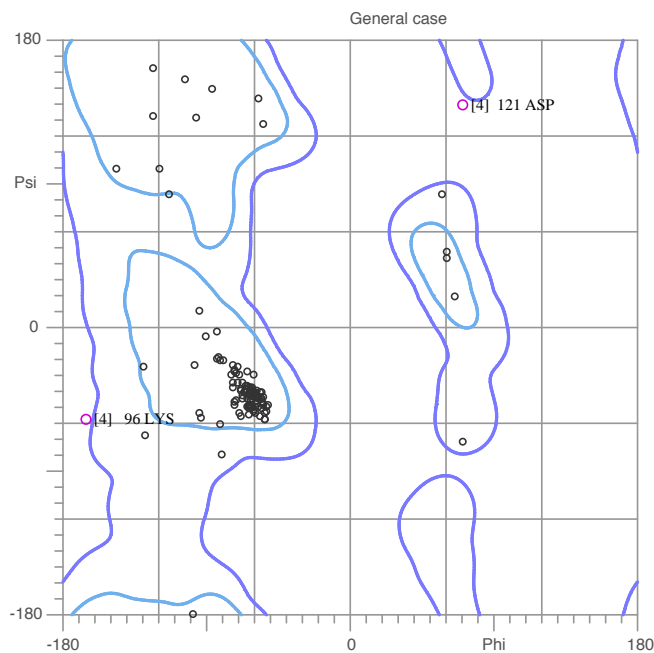
90.1% (109/121) of all residues were in favored (98%) regions.  
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 36 PHE (62.8, -78.9)
- [3] 41 LYS (-163.3, -60.2)
- [3] 66 ARG (71.8, 137.9)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 4



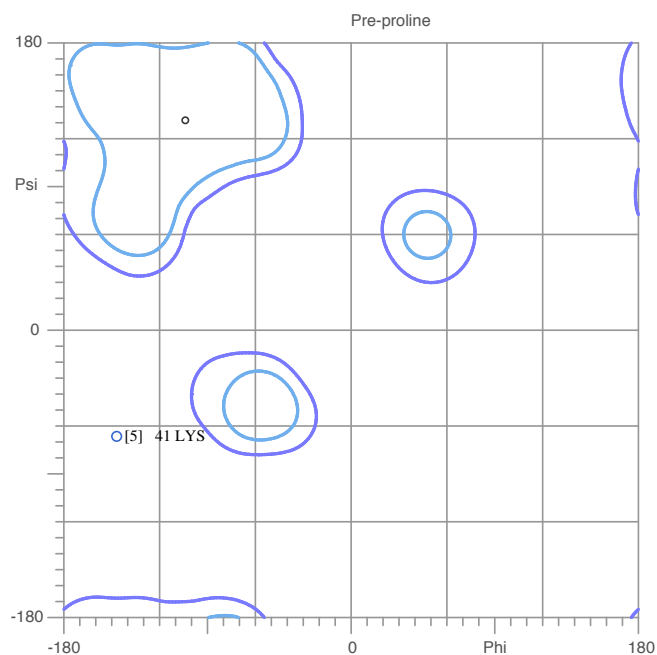
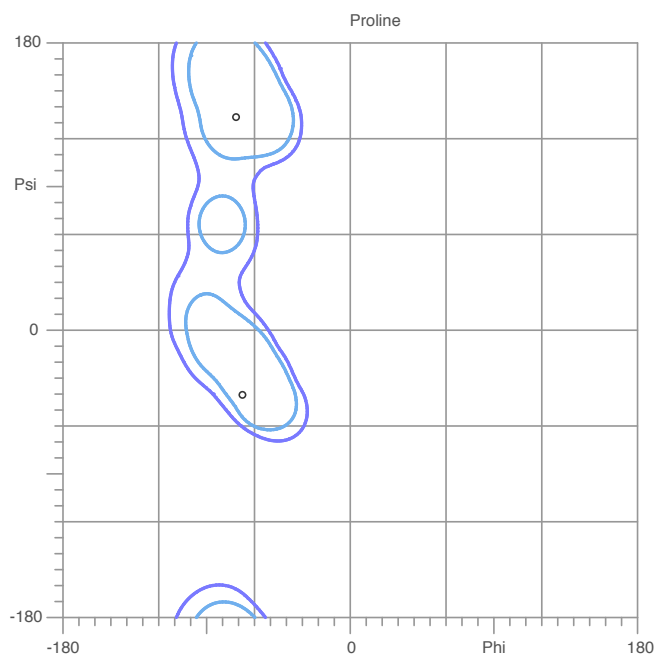
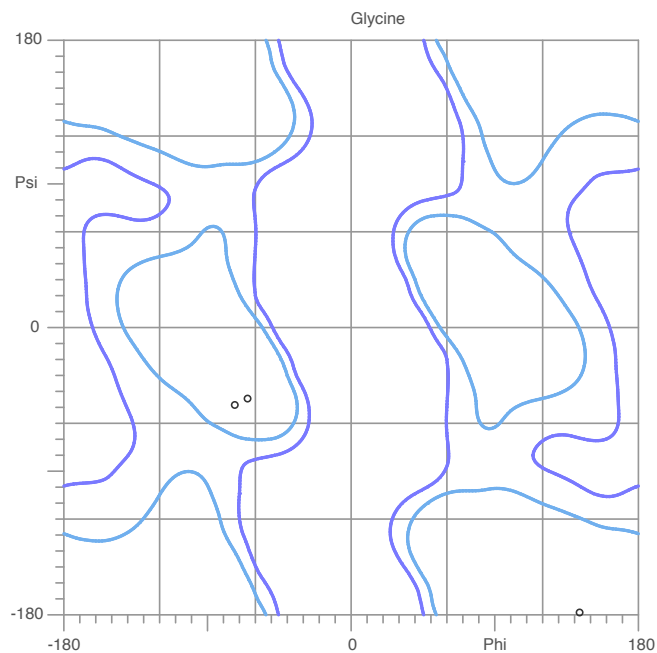
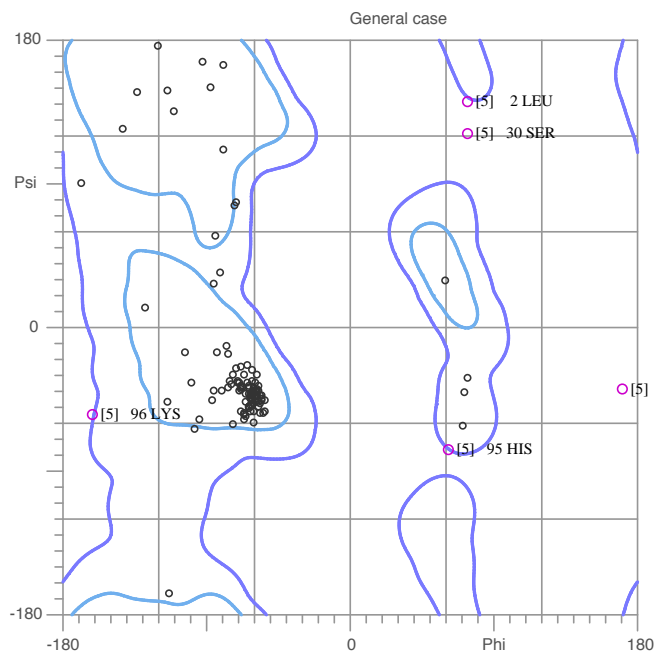
91.7% (111/121) of all residues were in favored (98%) regions.  
96.7% (117/121) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [4] 41 LYS (-164.8, -57.3)
- [4] 66 ARG (77.3, 150.2)
- [4] 96 LYS (-166.9, -57.9)
- [4] 121 ASP (70.5, 140.9)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 5



87.6% (106/121) of all residues were in favored (98%) regions.  
95.0% (115/121) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[5] 2 LEU (73.4, 142.5)

[5] 6 LEU (170.0, -38.9)

[5] 30 SER (73.2, 122.1)

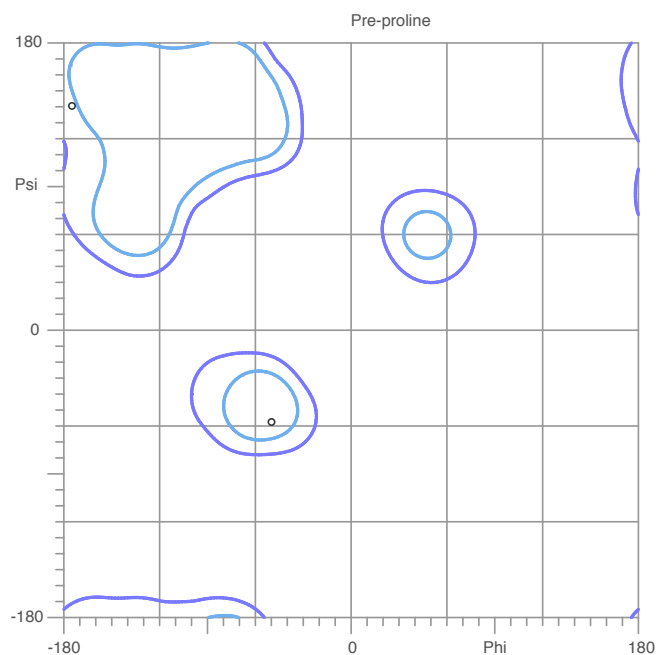
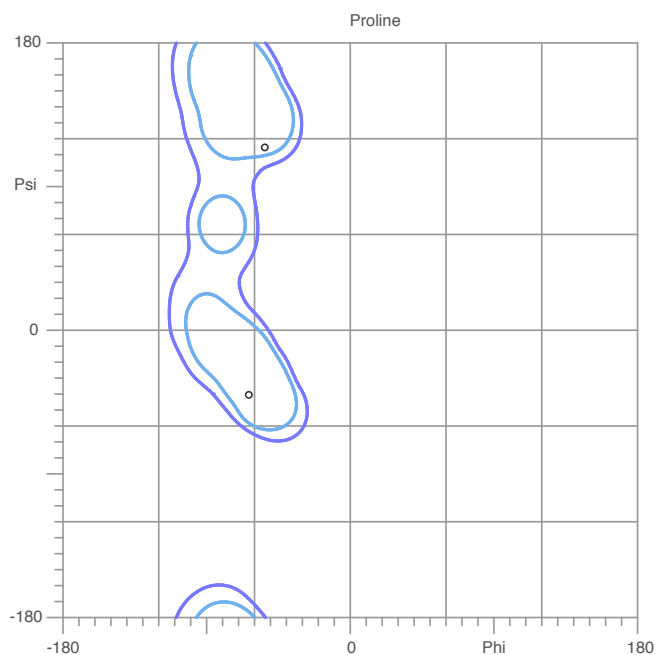
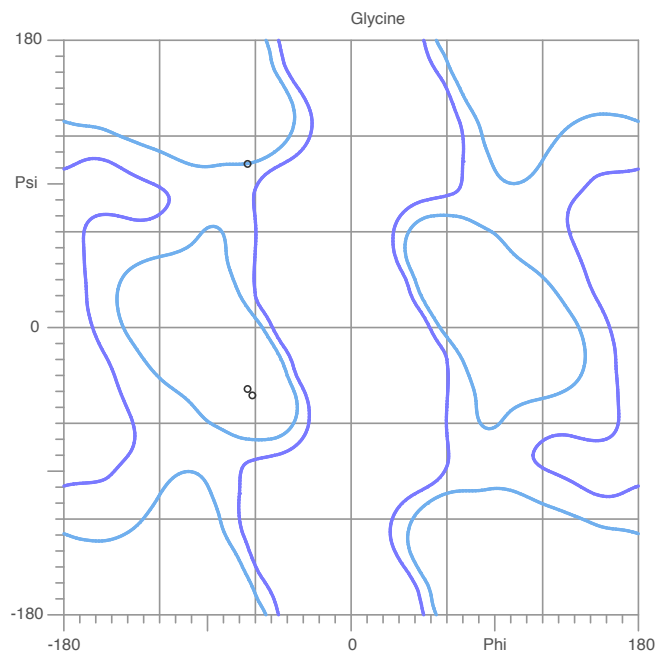
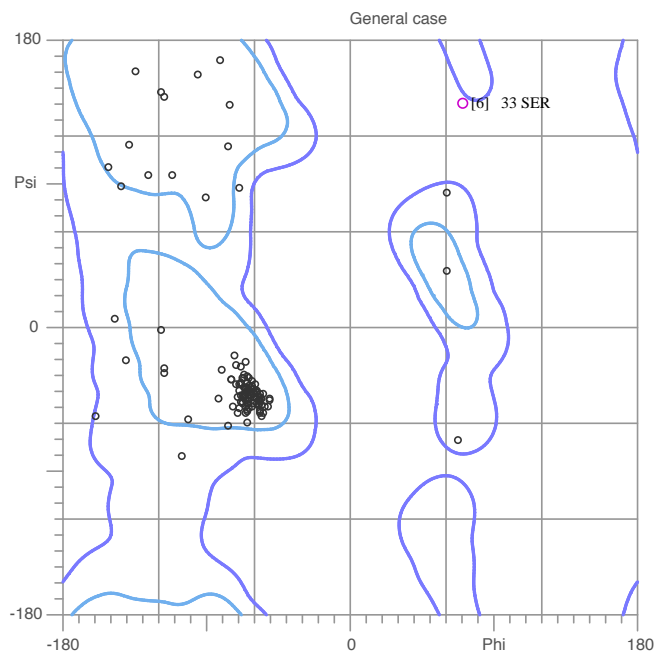
[5] 41 LYS (-147.3, -66.5)

[5] 95 HIS (61.5, -76.9)

[5] 96 LYS (-162.1, -54.9)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 6

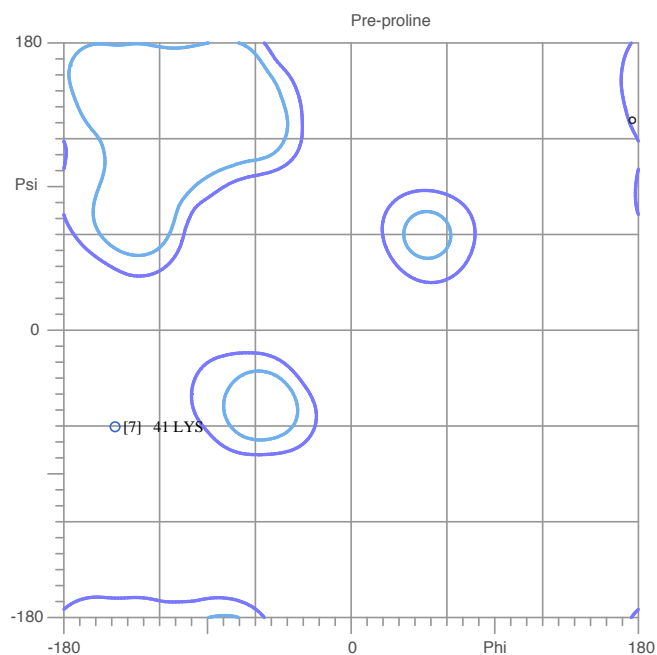
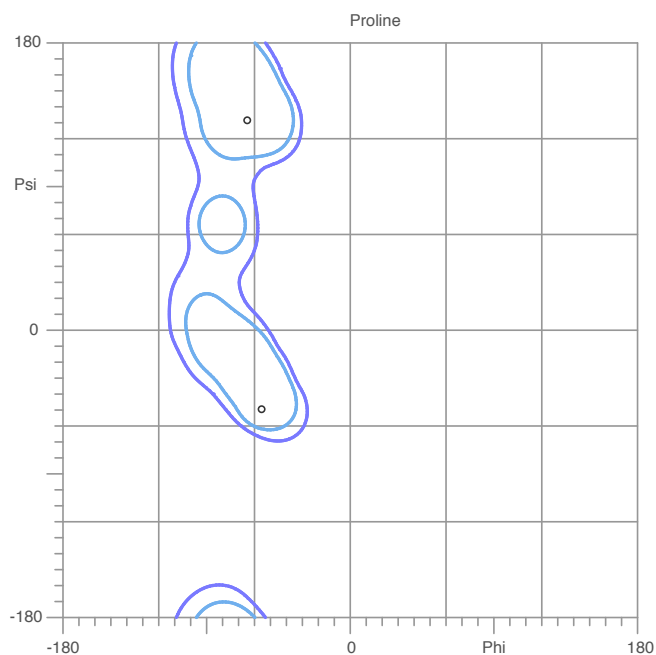
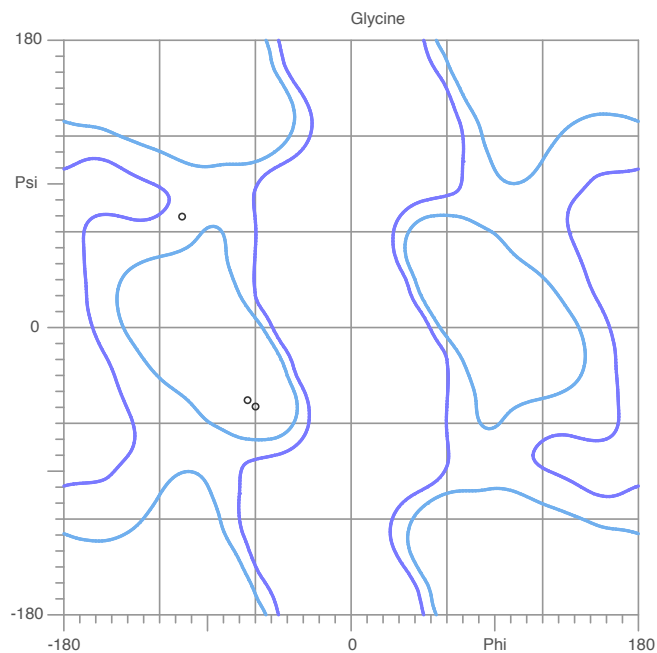
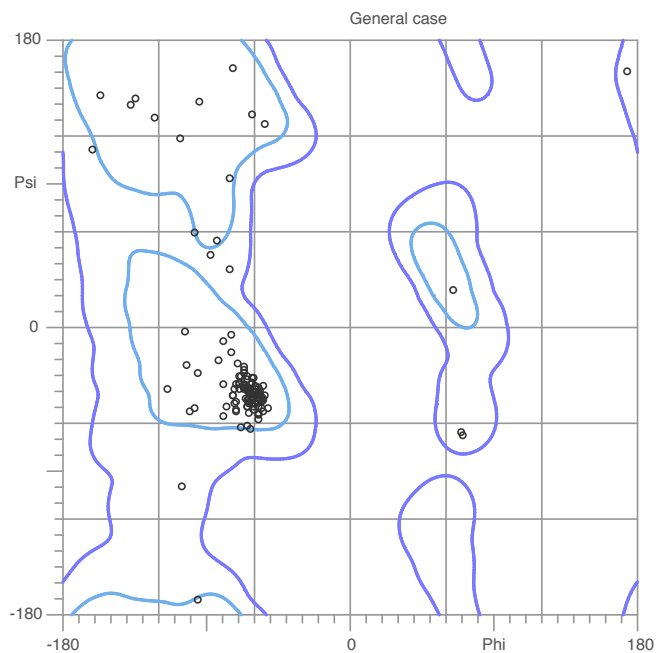


91.7% (111/121) of all residues were in favored (98%) regions.  
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[6] 33 SER (70.6, 141.3)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 7



90.1% (109/121) of all residues were in favored (98%) regions.  
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

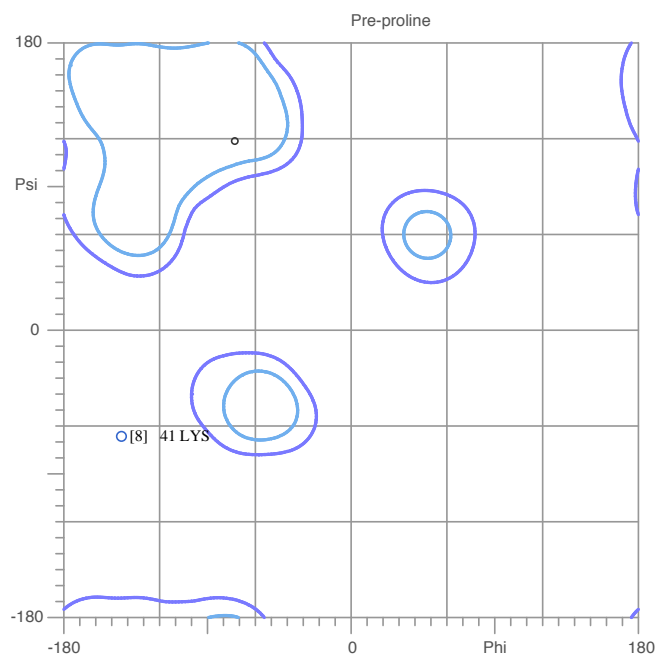
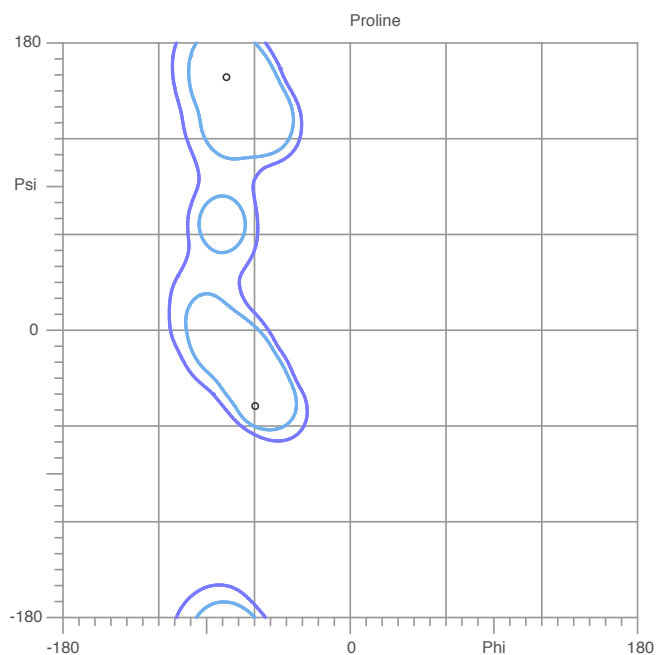
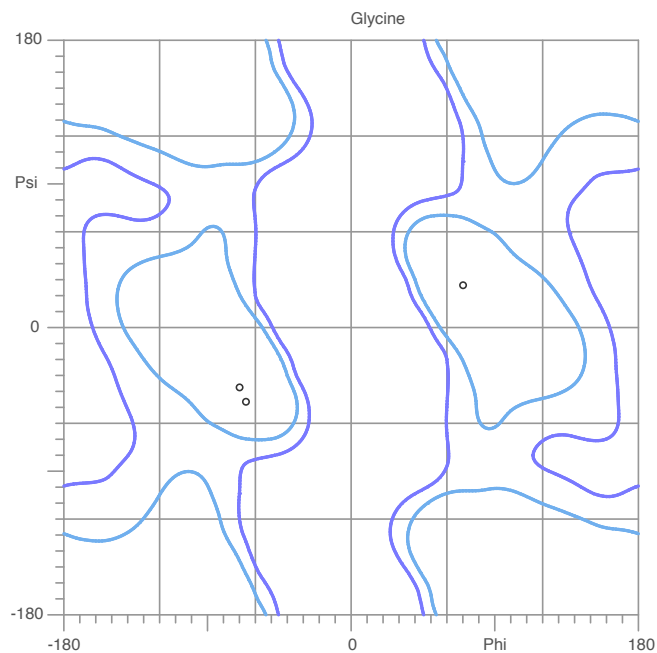
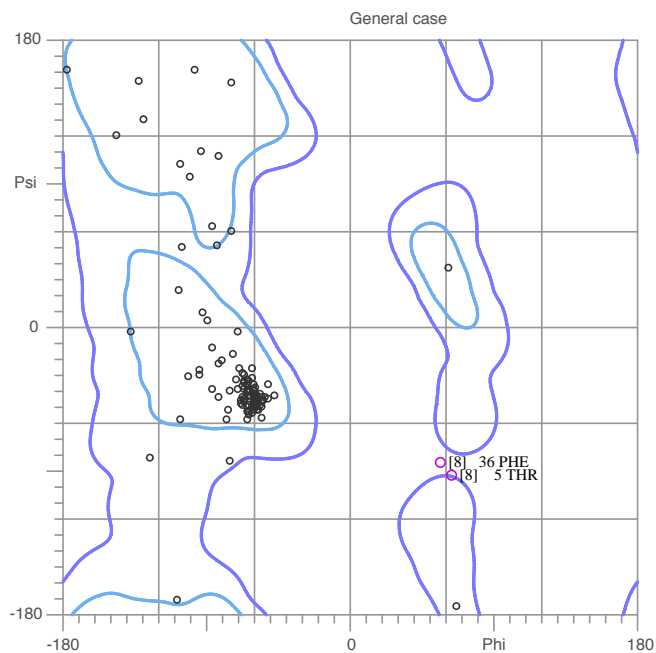
There were 1 outliers (phi, psi):  
[7] 41 LYS (-148.2, -60.9)

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

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

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 8



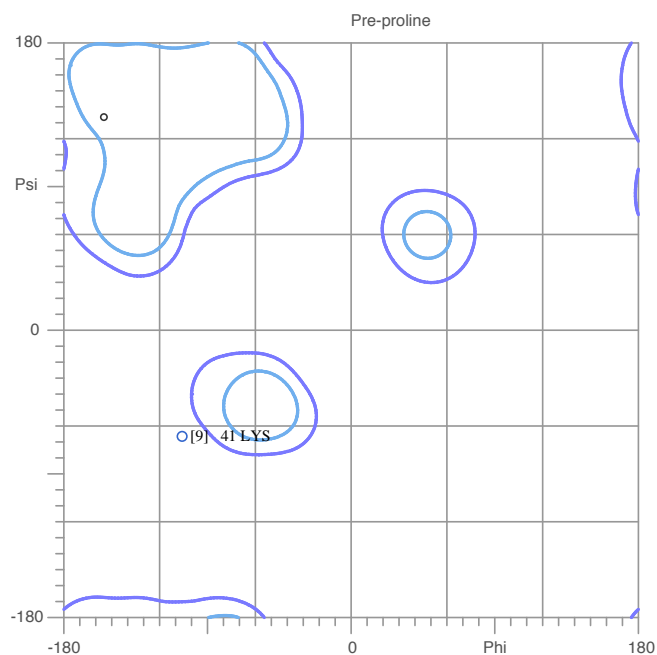
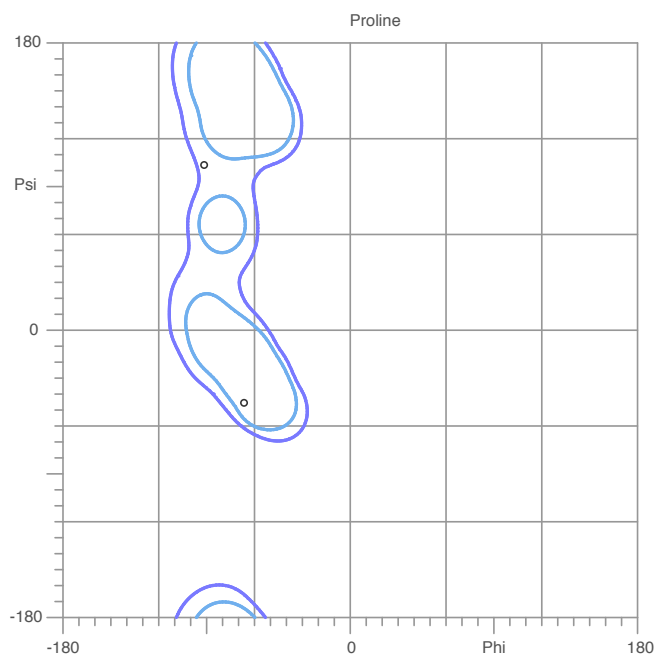
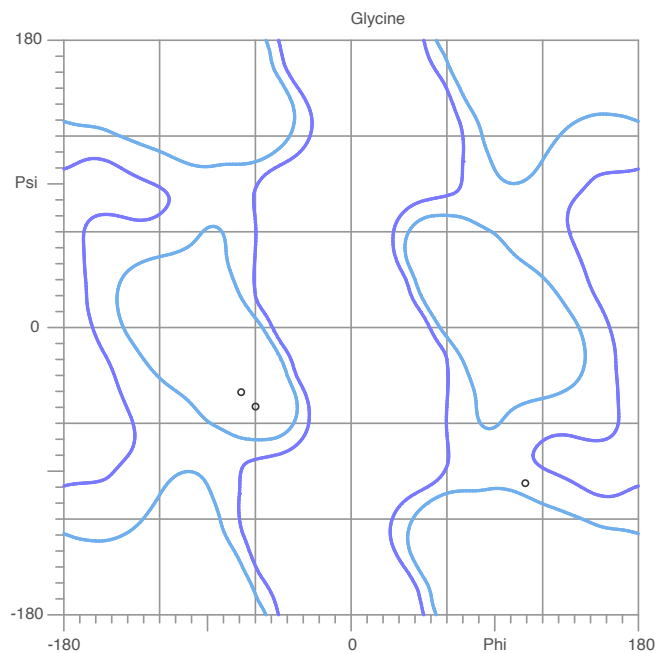
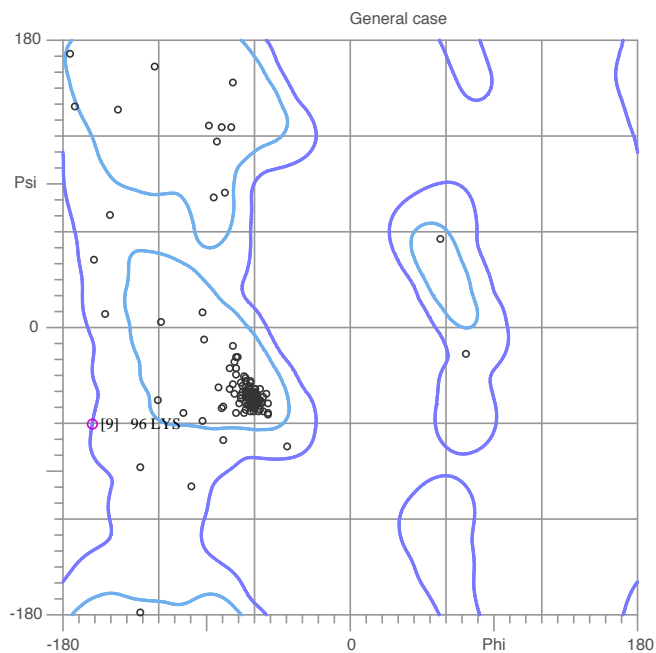
90.9% (110/121) of all residues were in favored (98%) regions.  
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 5 THR (63.0, -92.3)
- [8] 36 PHE (56.4, -84.5)
- [8] 41 LYS (-144.6, -66.2)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 9



89.3% (108/121) of all residues were in favored (98%) regions.  
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

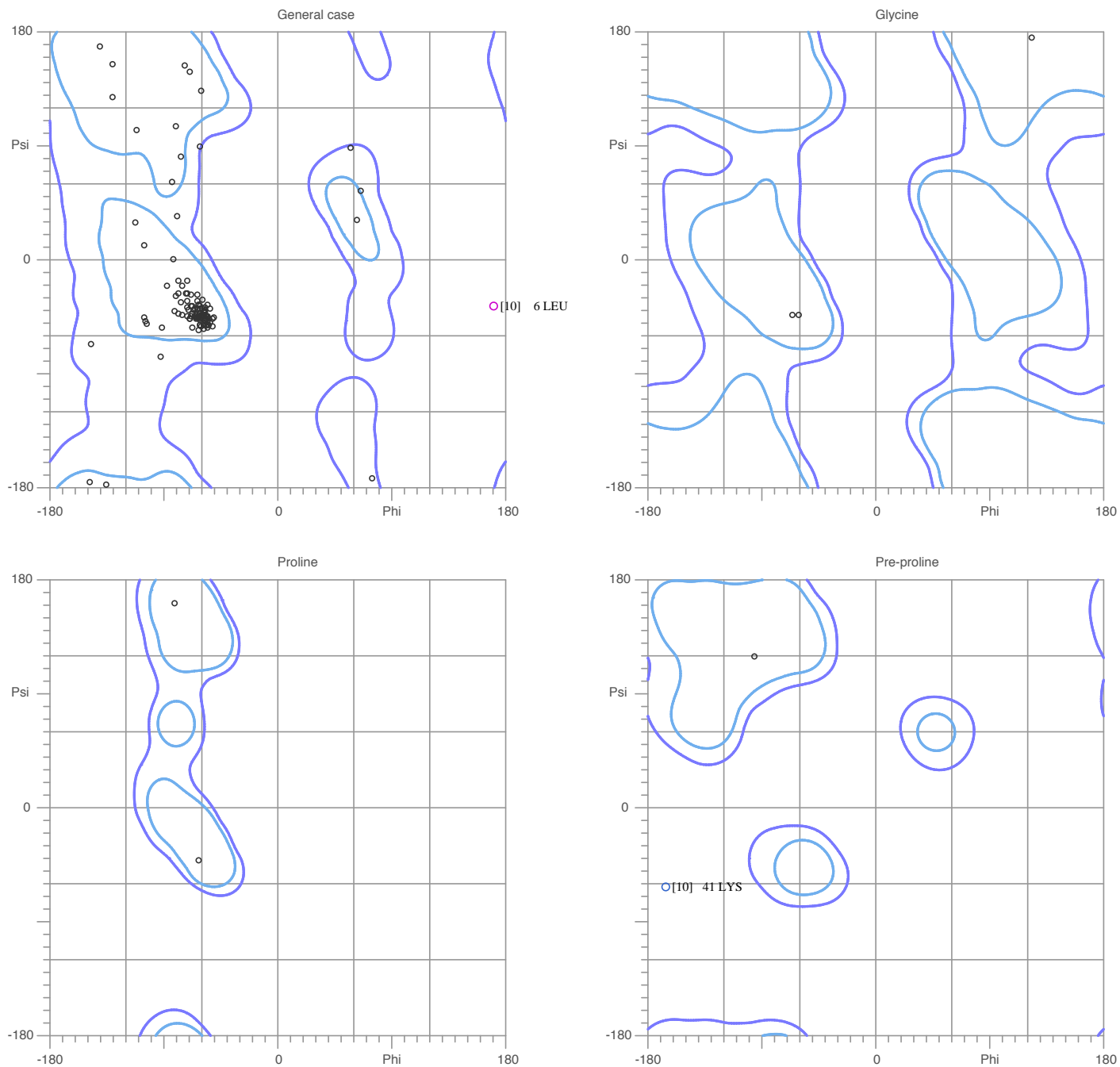
There were 2 outliers (phi, psi):

[9] 41 LYS (-106.5, -66.8)

[9] 96 LYS (-162.6, -60.5)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 10

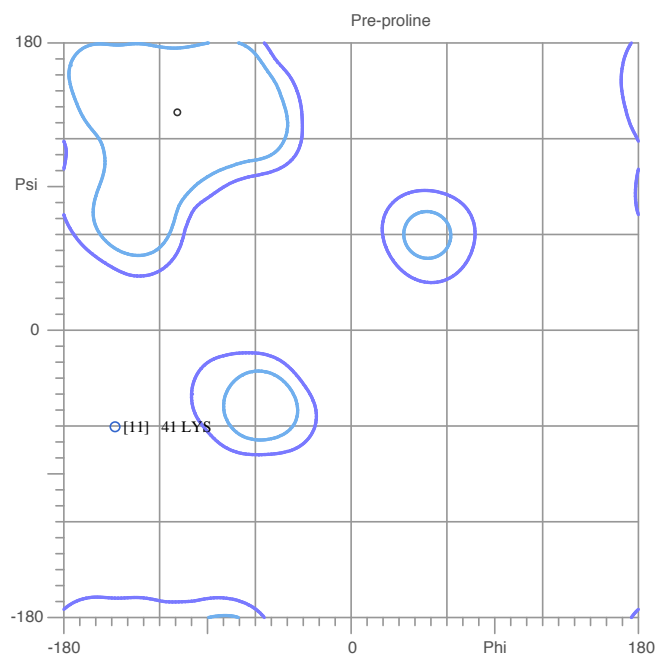
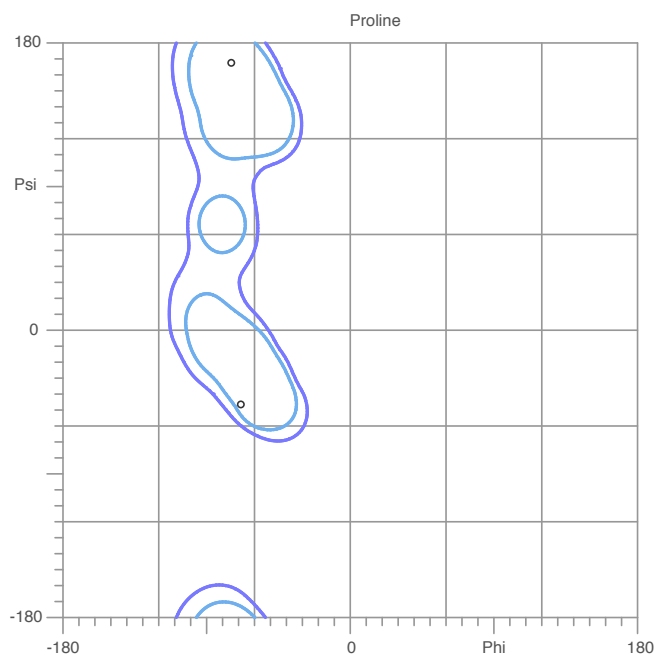
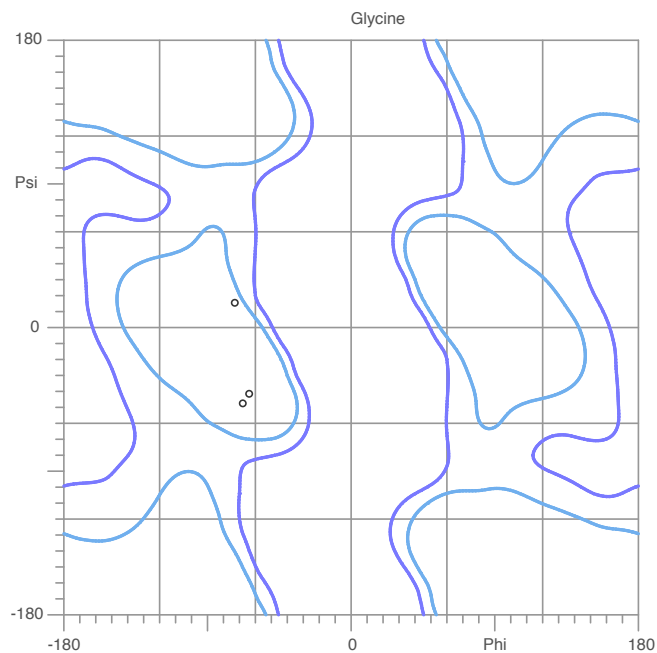
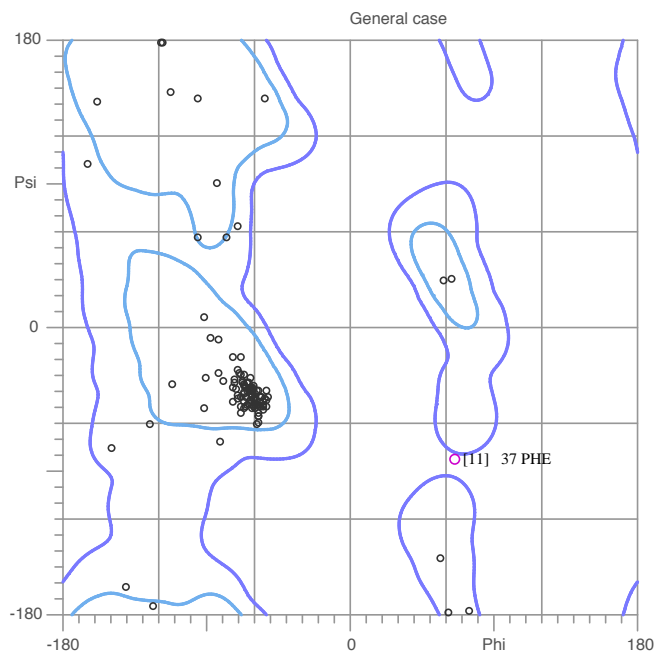


92.6% (112/121) of all residues were in favored (98%) regions.  
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[10] 6 LEU (170.5, -36.4)  
[10] 41 LYS (-166.8, -62.1)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 11

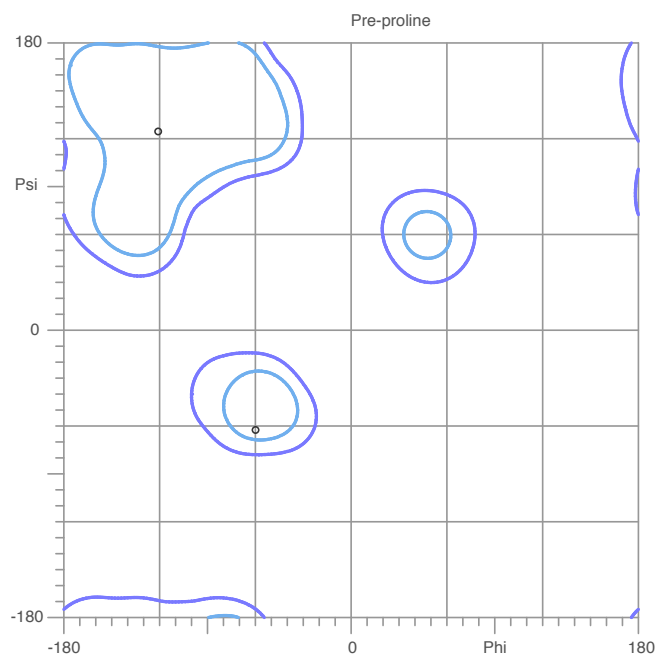
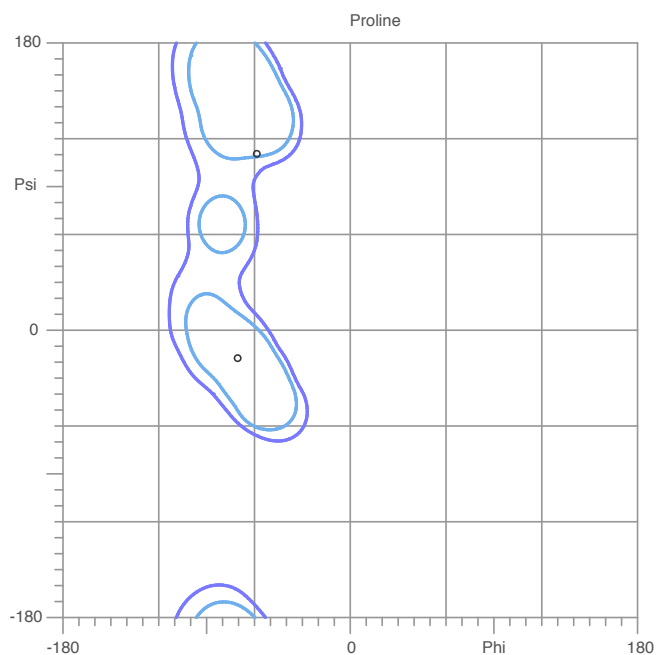
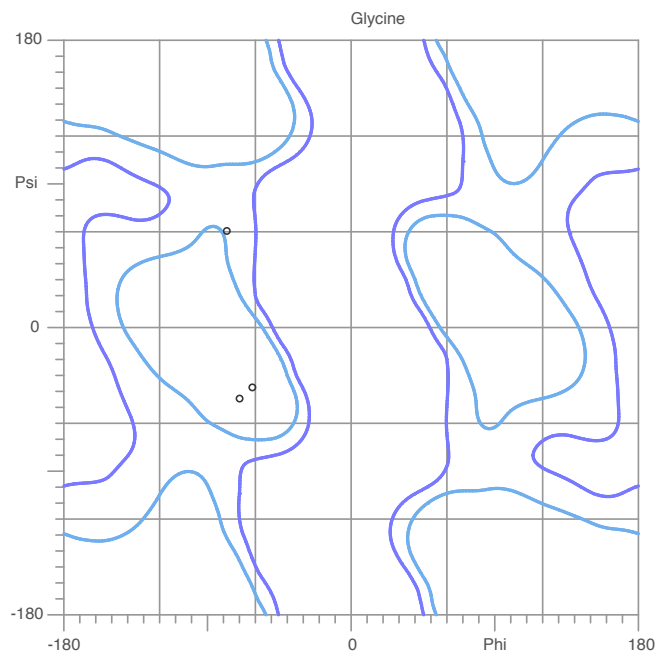
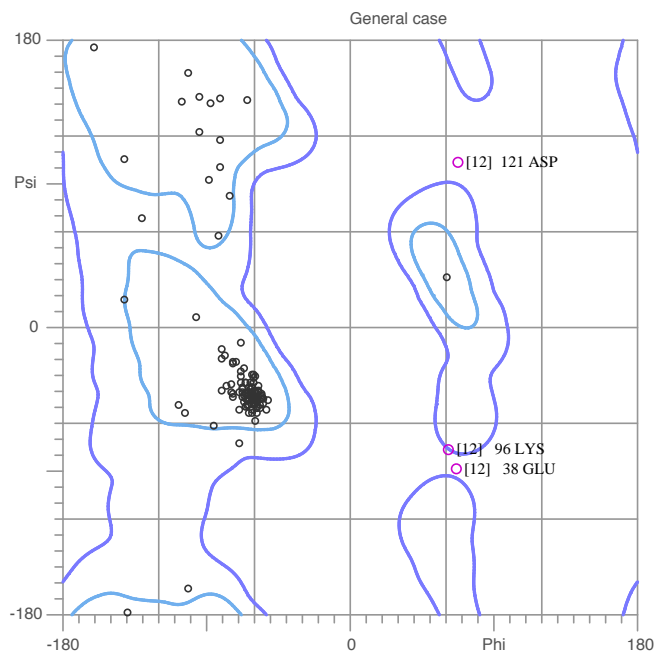


90.9% (110/121) of all residues were in favored (98%) regions.  
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[11] 37 PHE (65.3, -82.3)  
[11] 41 LYS (-148.6, -61.0)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 12



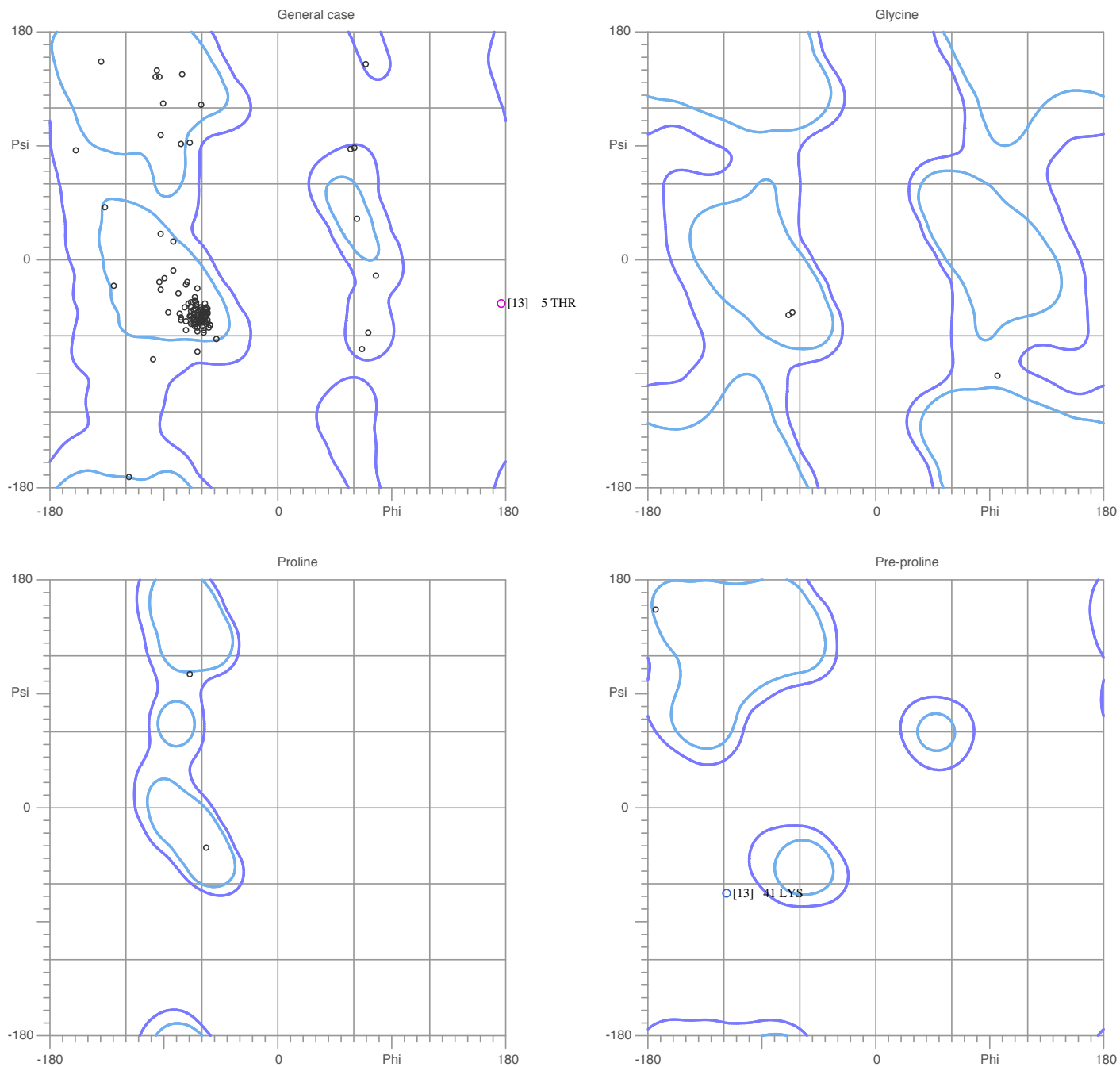
93.4% (113/121) of all residues were in favored (98%) regions.  
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [12] 38 GLU (66.6, -88.3)
- [12] 96 LYS (61.4, -76.5)
- [12] 121 ASP (67.4, 104.5)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 13

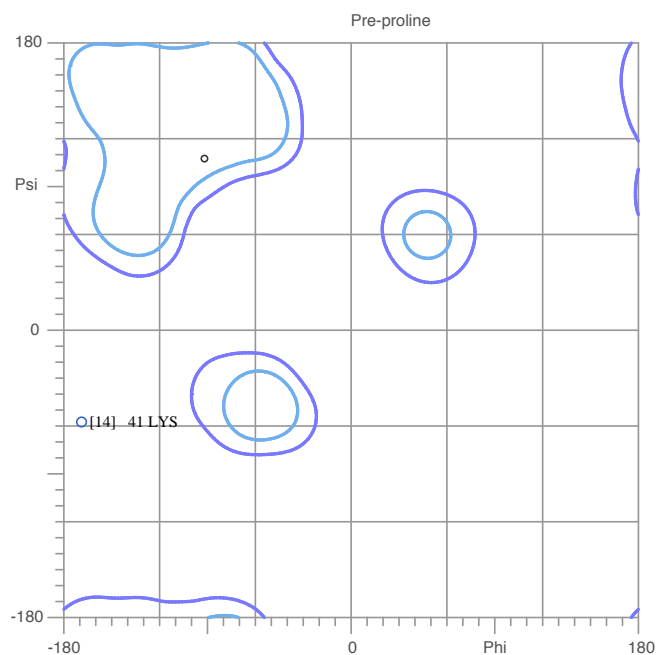
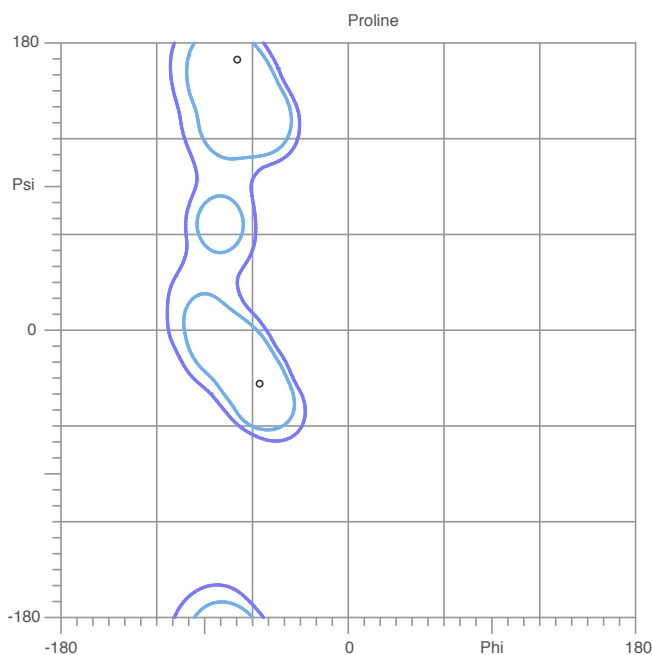
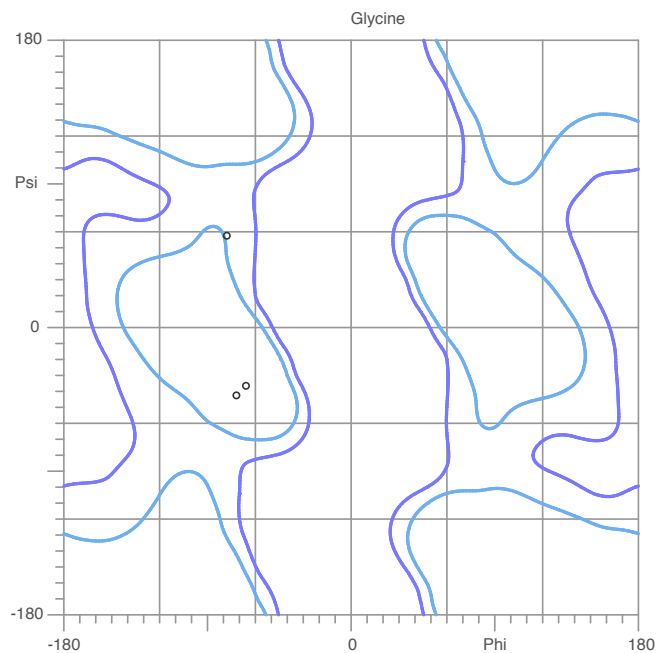
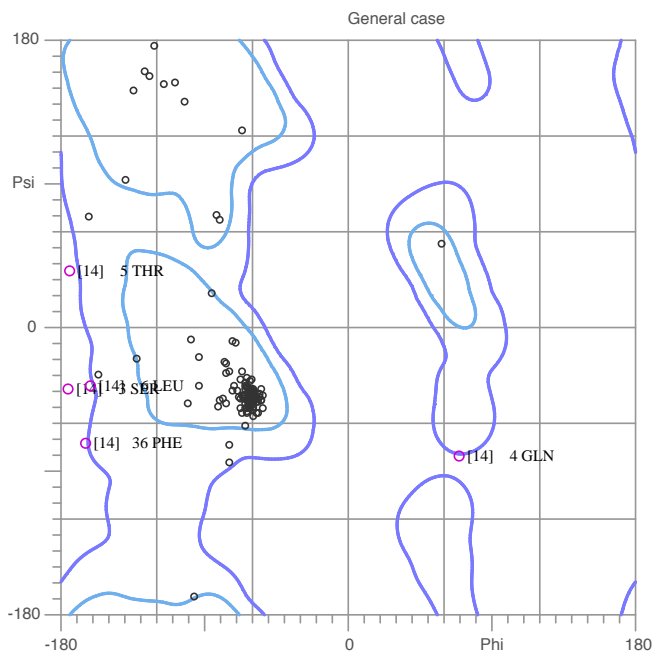


87.6% (106/121) of all residues were in favored (98%) regions.  
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[13] 5 THR (176.6, -34.7)  
[13] 41 LYS (-118.4, -67.2)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 14



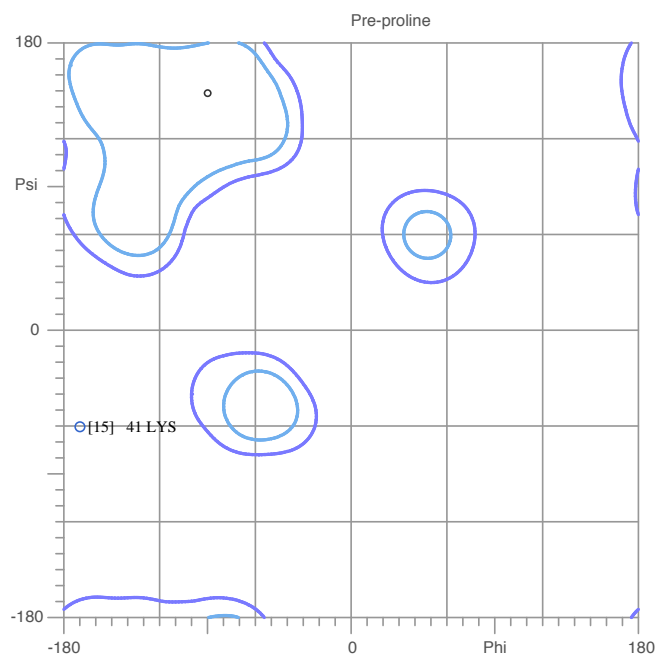
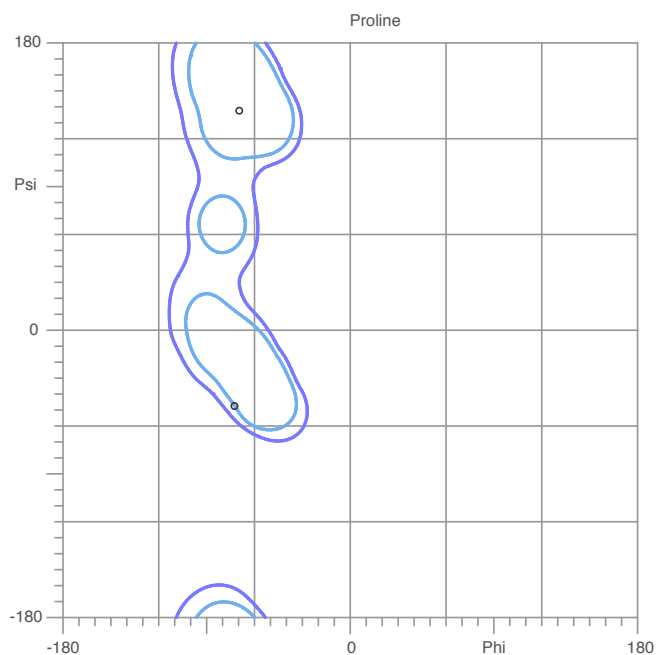
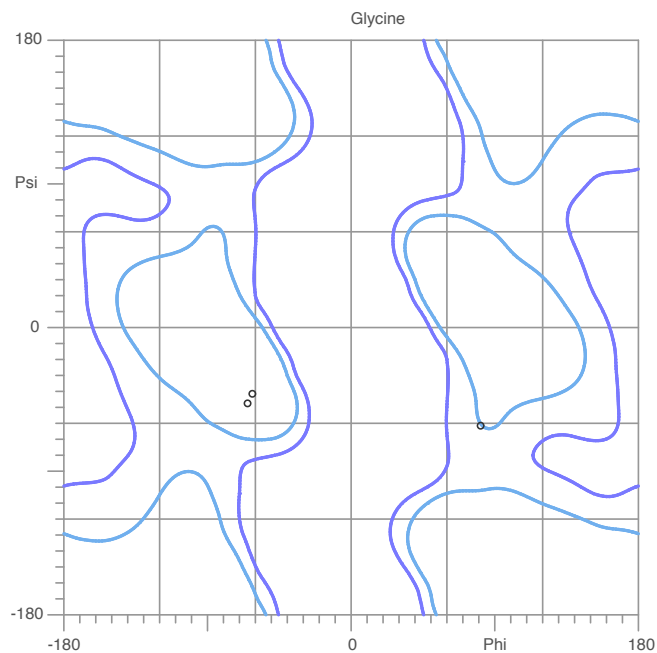
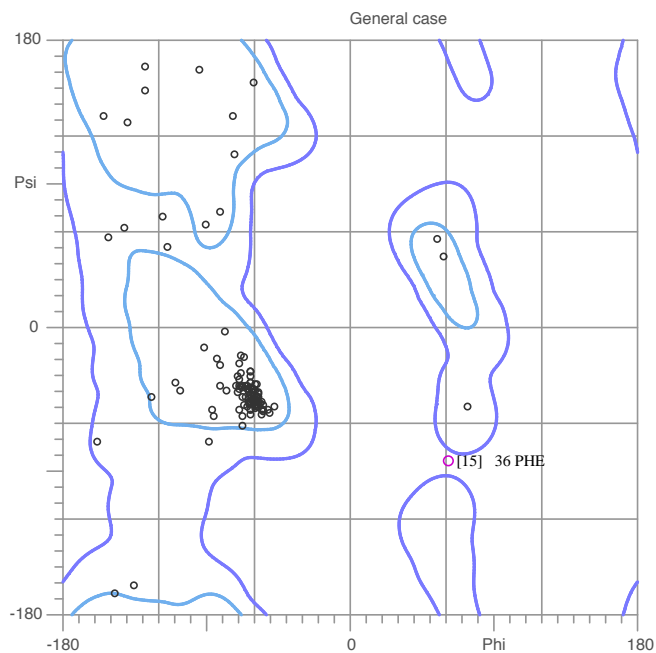
89.3% (108/121) of all residues were in favored (98%) regions.  
95.0% (115/121) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):  
[14] 3 SER (-176.5, -38.8)

[14] 4 GLN (69.1, -80.1)  
[14] 5 THR (-175.6, 36.4)  
[14] 6 LEU (-162.5, -36.2)  
[14] 36 PHE (-165.2, -72.1)  
[14] 41 LYS (-169.5, -57.6)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 15

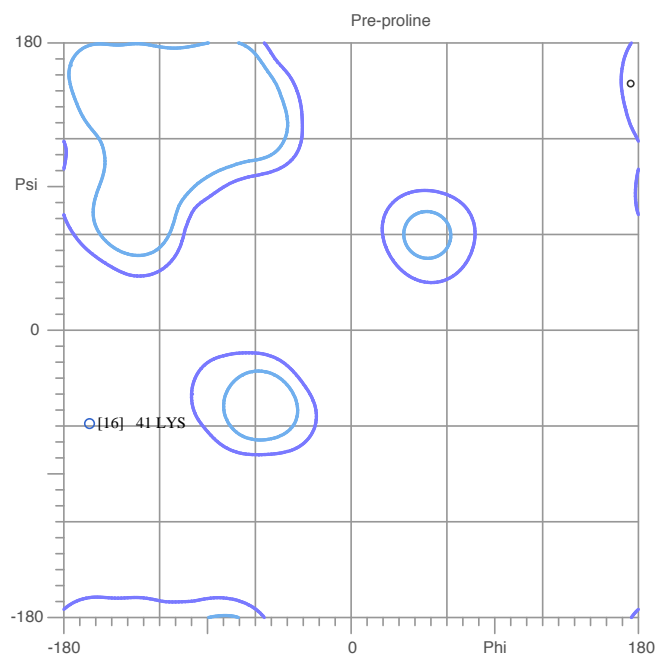
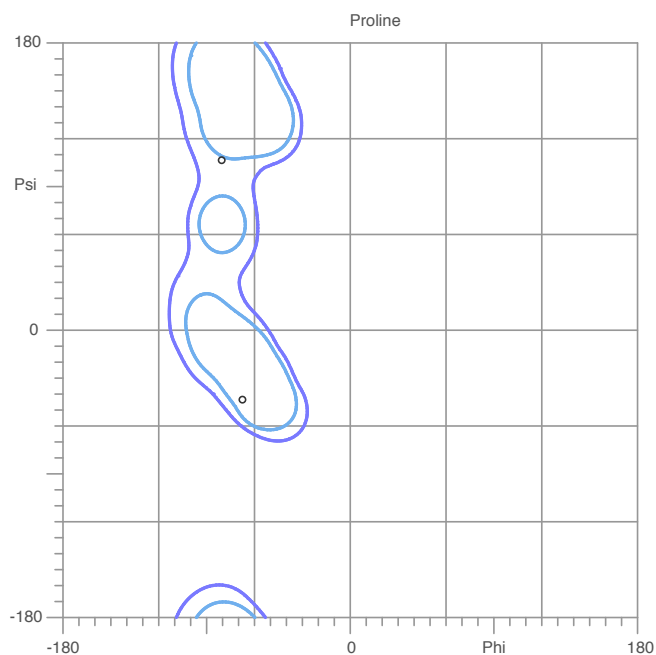
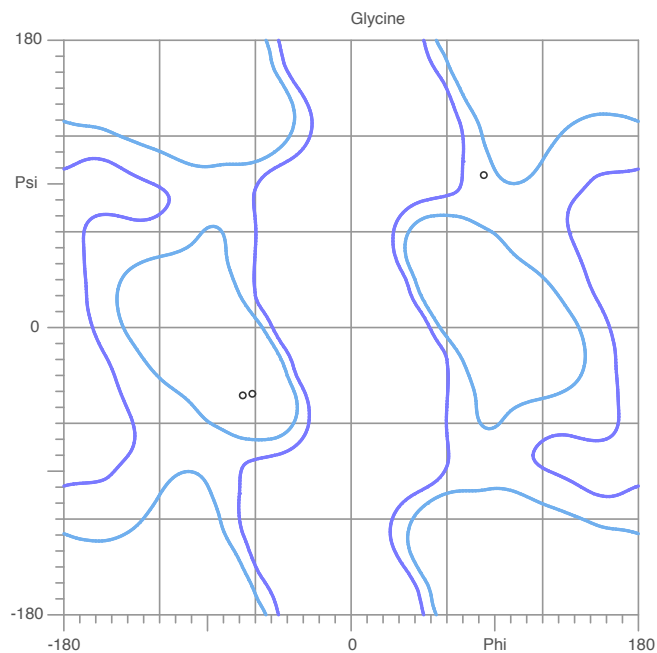
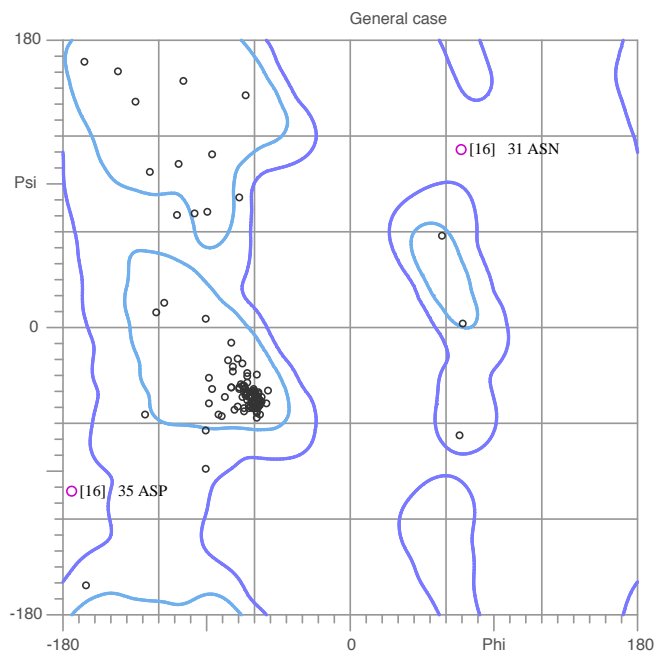


89.3% (108/121) of all residues were in favored (98%) regions.  
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[15] 36 PHE (61.8, -83.7)  
[15] 41 LYS (-170.1, -60.8)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 16



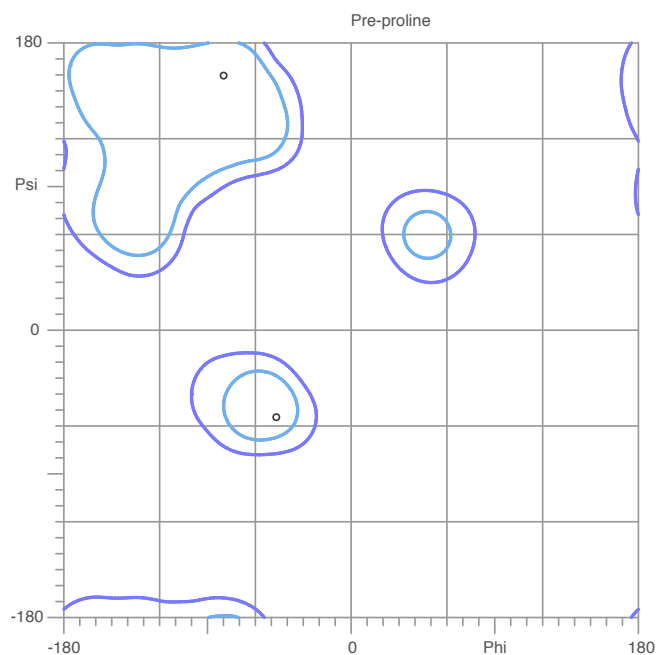
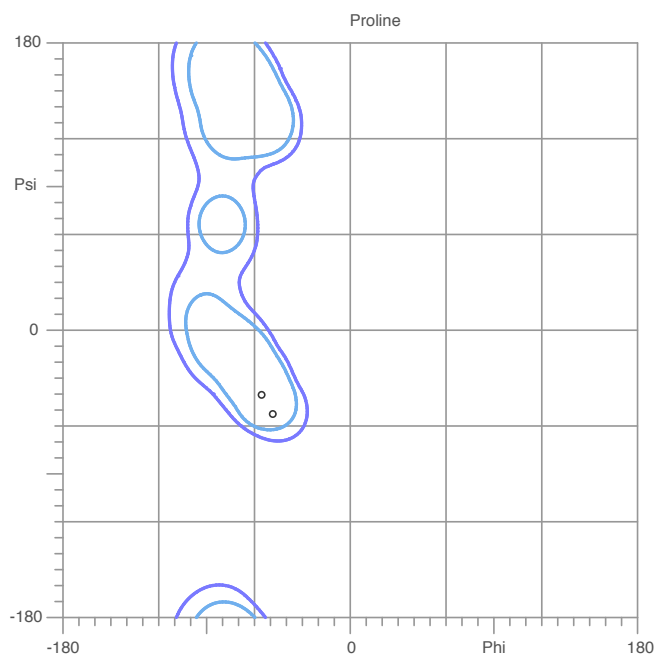
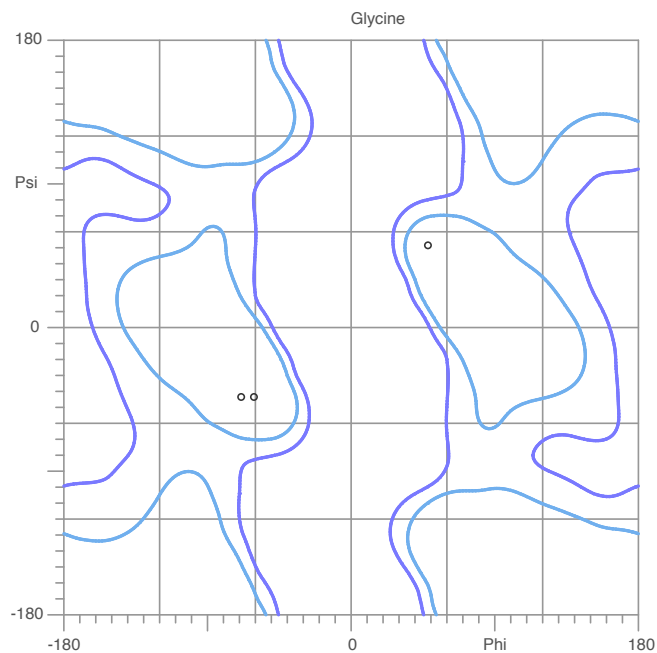
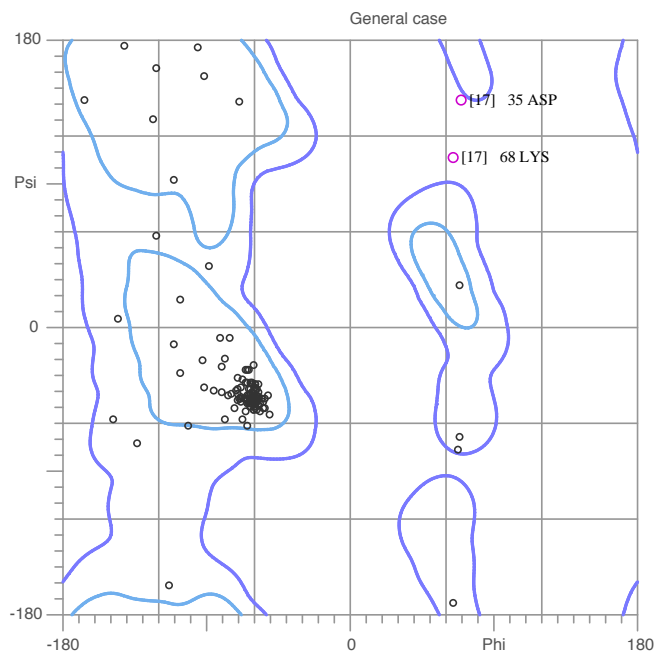
89.3% (108/121) of all residues were in favored (98%) regions.  
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [16] 31 ASN (69.2, 113.0)
- [16] 35 ASP (-175.7, -102.6)
- [16] 41 LYS (-164.5, -58.1)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 17



90.9% (110/121) of all residues were in favored (98%) regions.  
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

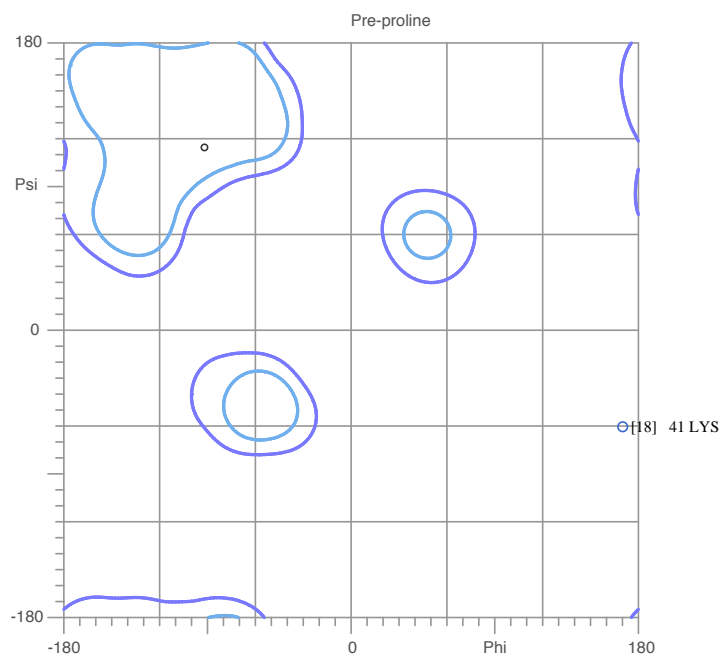
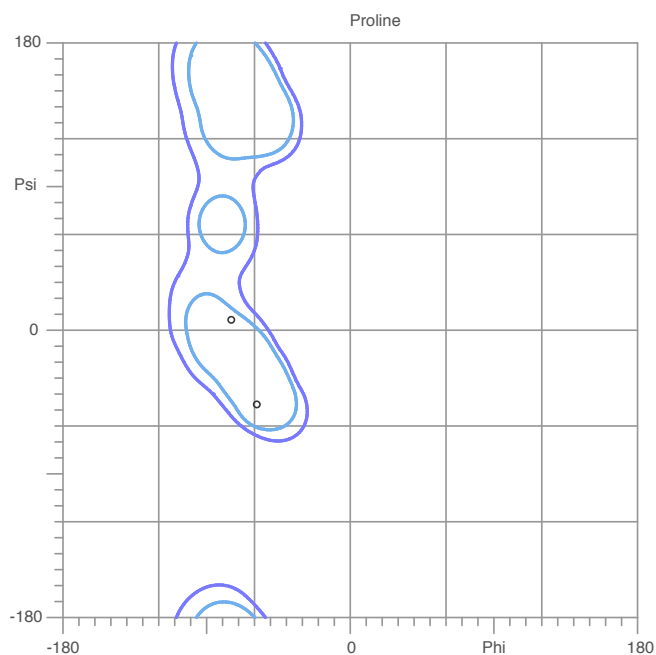
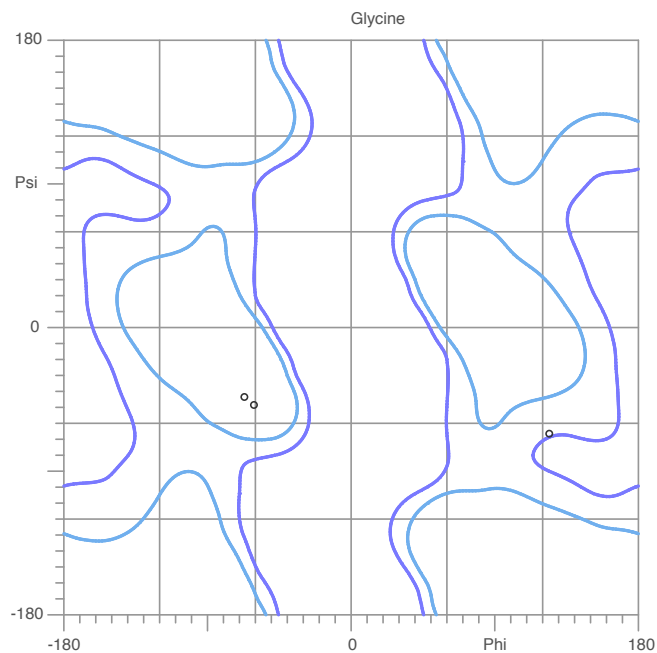
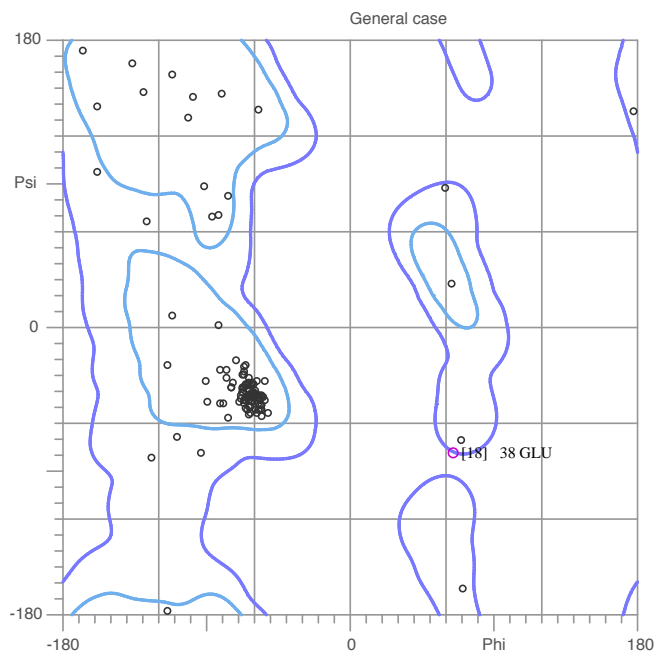
There were 2 outliers (phi, psi):

[17] 35 ASP (69.8, 143.9)

[17] 68 LYS (64.5, 107.0)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 18

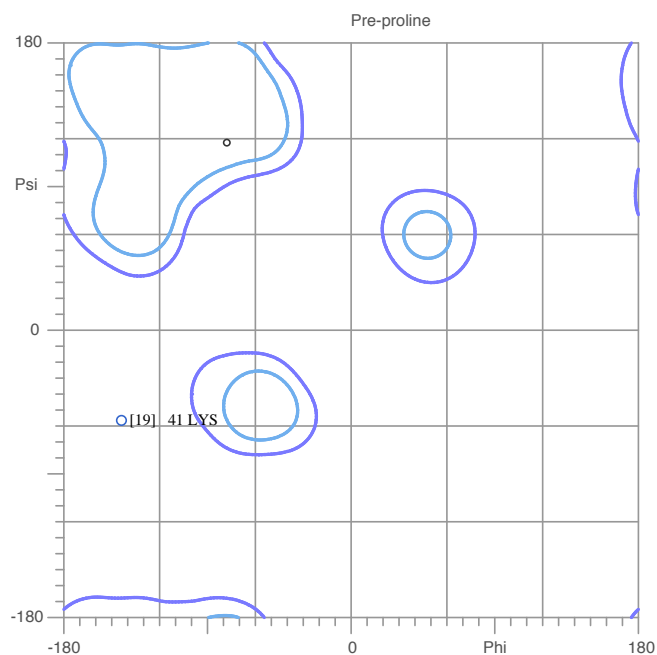
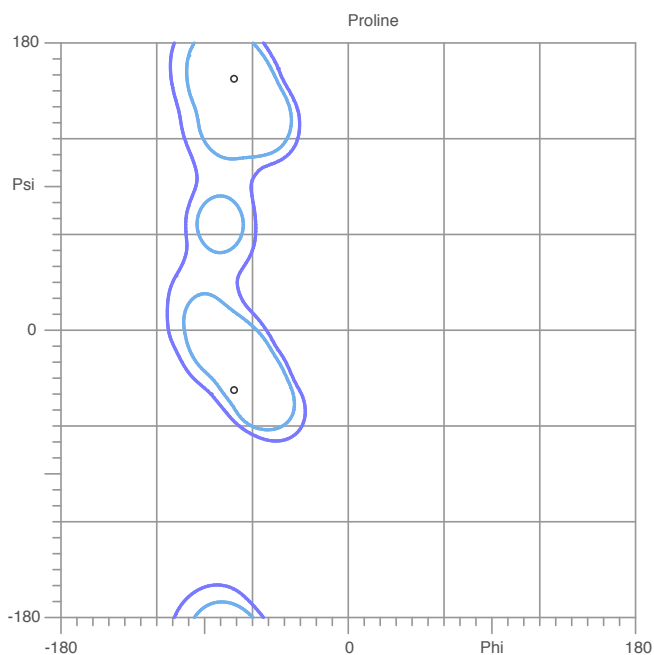
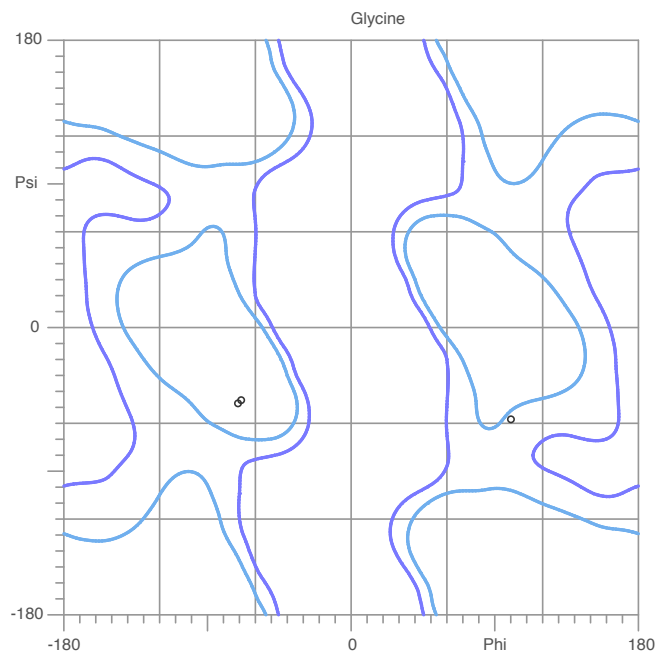
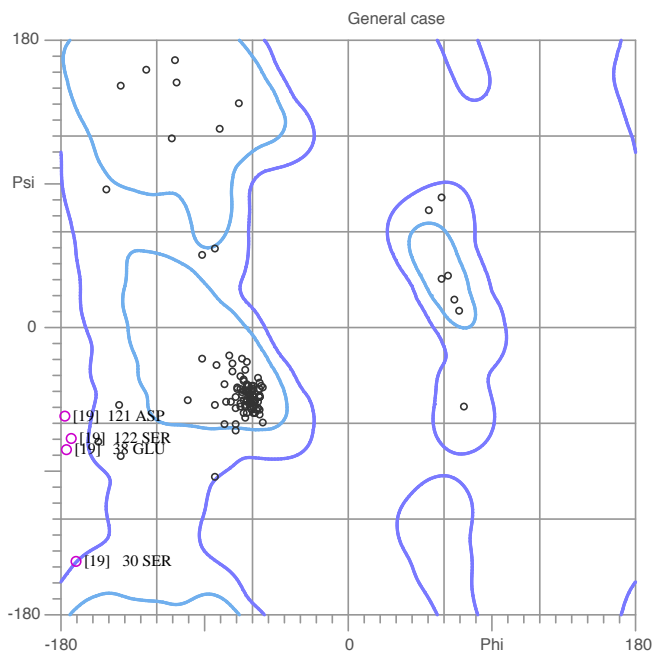


90.1% (109/121) of all residues were in favored (98%) regions.  
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[18] 38 GLU (64.9, -78.9)  
[18] 41 LYS (170.6, -60.8)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 19



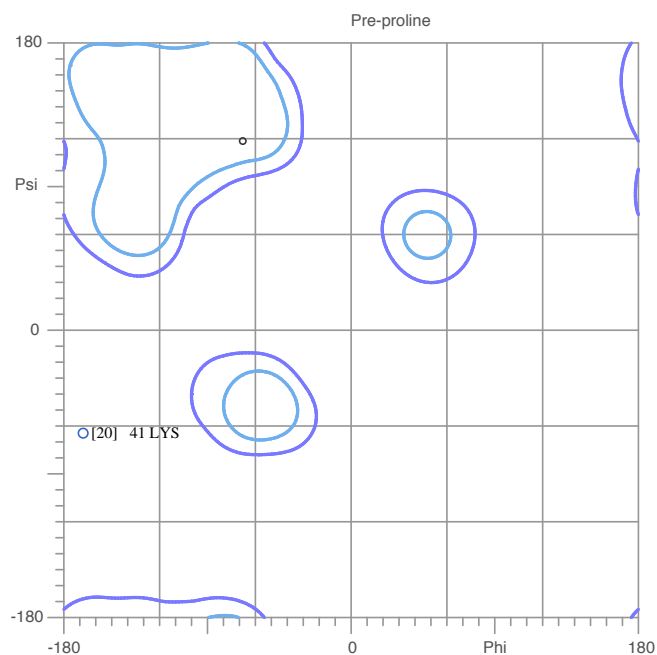
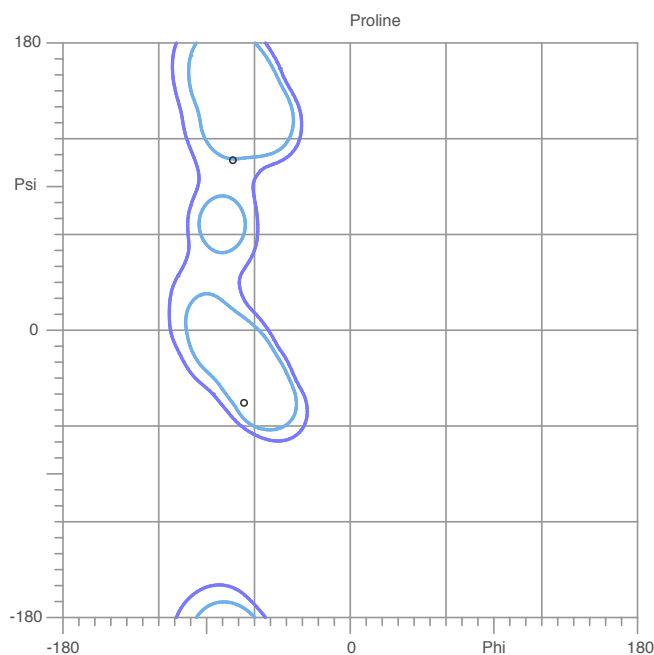
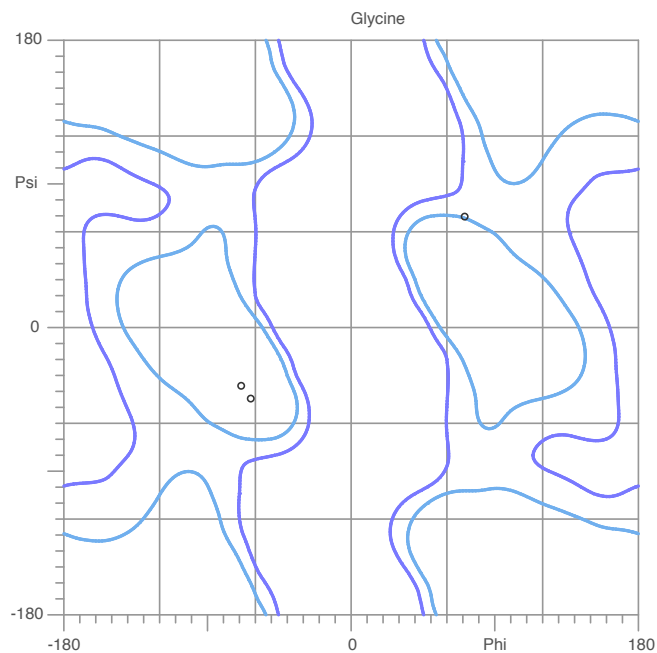
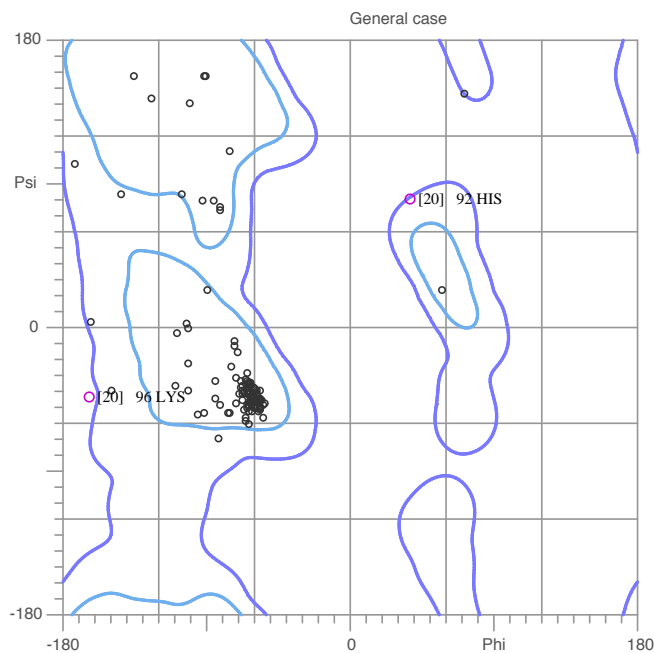
86.8% (105/121) of all residues were in favored (98%) regions.  
95.9% (116/121) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[19] 30 SER (-171.2, -146.1)  
[19] 38 GLU (-177.9, -76.1)  
[19] 41 LYS (-144.9, -56.3)  
[19] 121 ASP (-178.9, -55.1)  
[19] 122 SER (-174.7, -69.0)

# MolProbity Ramachandran analysis

SR213\_NMR\_em\_bcr3.pdb, model 20



91.7% (111/121) of all residues were in favored (98%) regions.  
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[20] 41 LYS (-168.3, -64.9)

[20] 92 HIS (37.0, 81.5)

[20] 96 LYS (-164.8, -43.6)