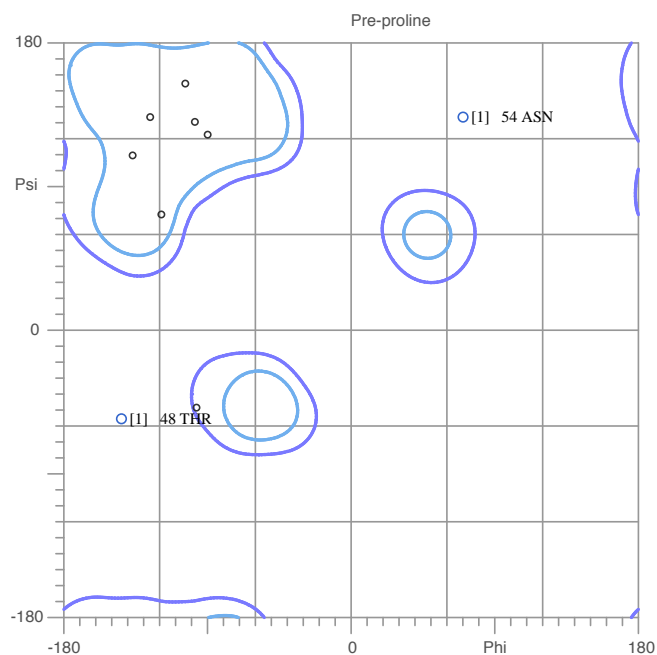
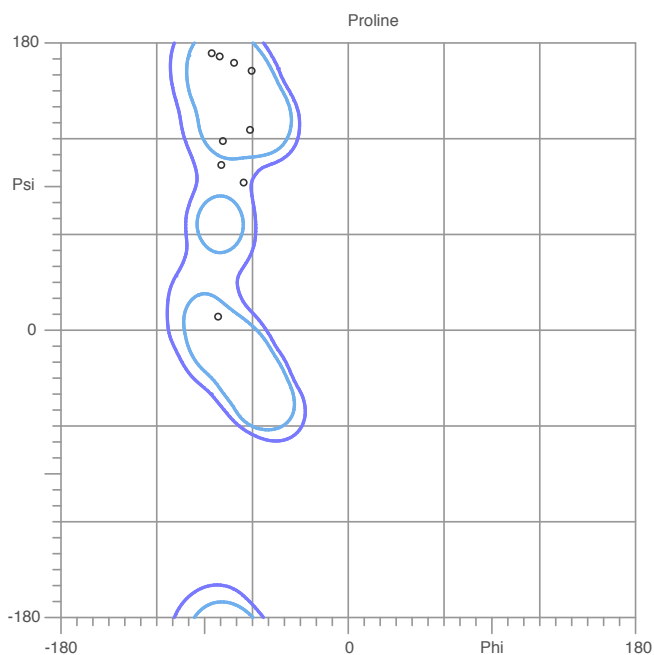
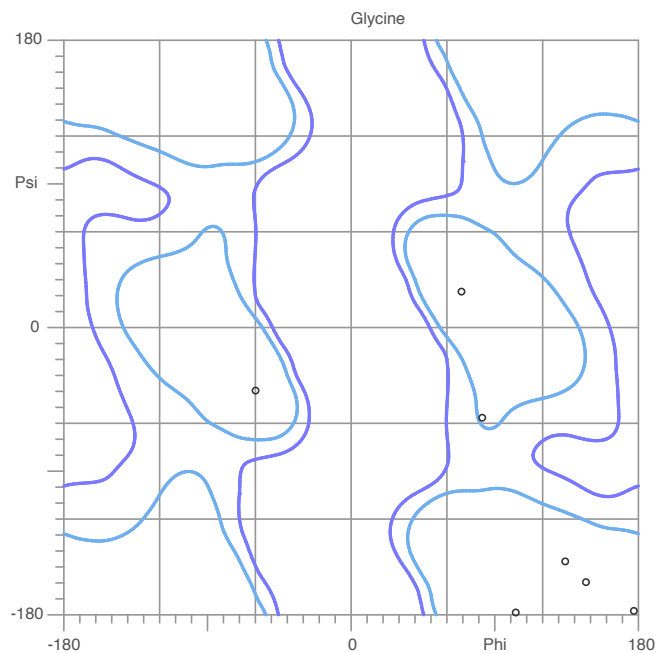
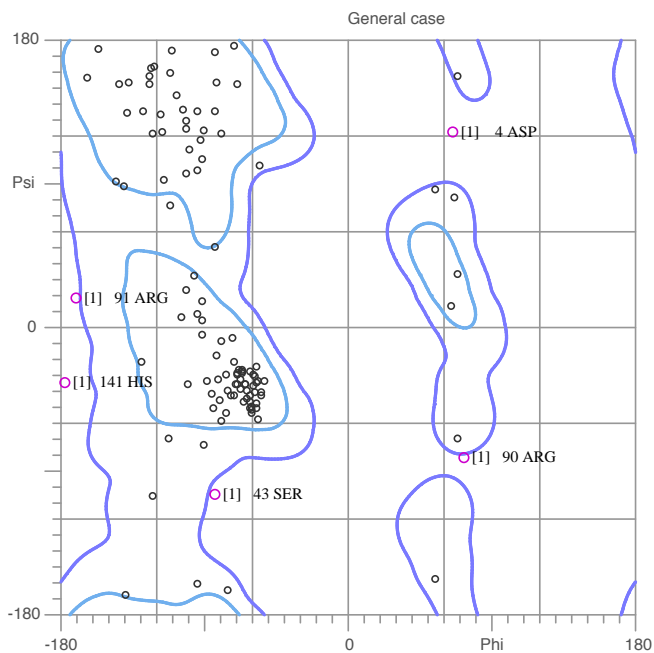




# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 1



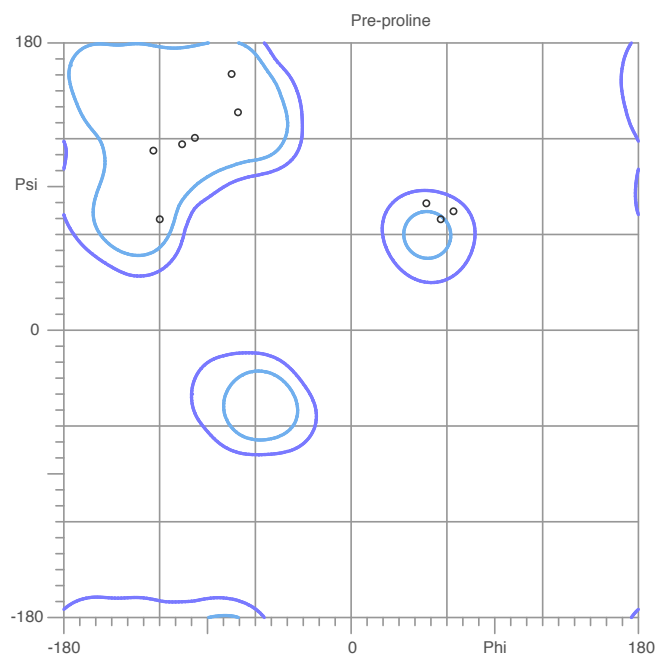
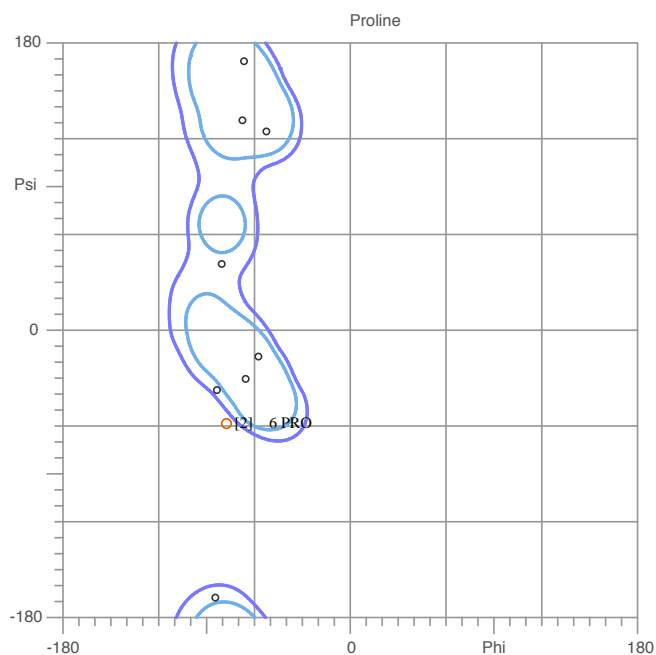
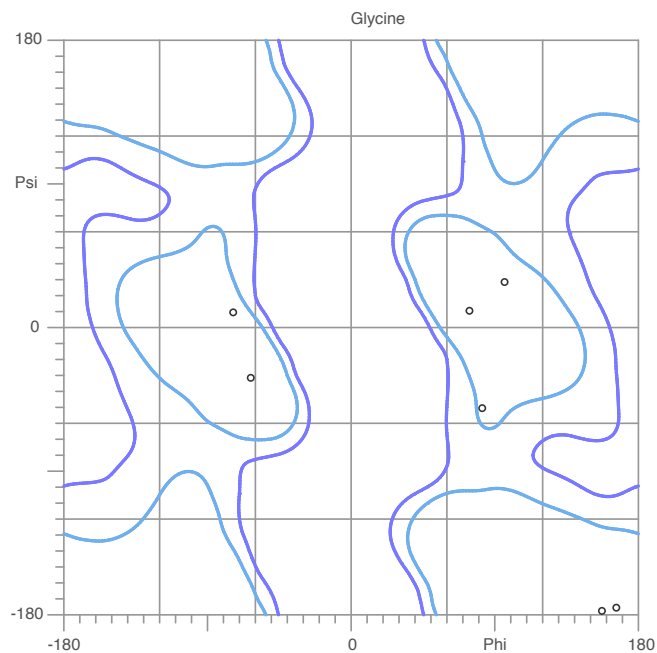
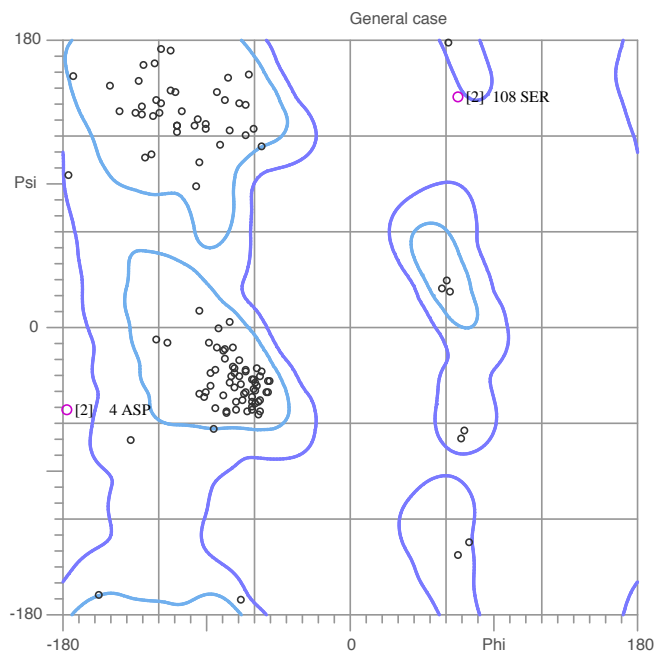
83.6% (117/140) of all residues were in favored (98%) regions.  
95.0% (133/140) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):  
[1] 4 ASP (65.9, 123.1)

[1] 43 SER (-84.0, -104.1)  
[1] 48 THR (-144.7, -55.9)  
[1] 54 ASN (70.0, 134.7)  
[1] 90 ARG (72.6, -81.8)  
[1] 91 ARG (-171.6, 19.7)  
[1] 141 HIS (-178.6, -34.2)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 2



87.1% (122/140) of all residues were in favored (98%) regions.  
97.9% (137/140) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

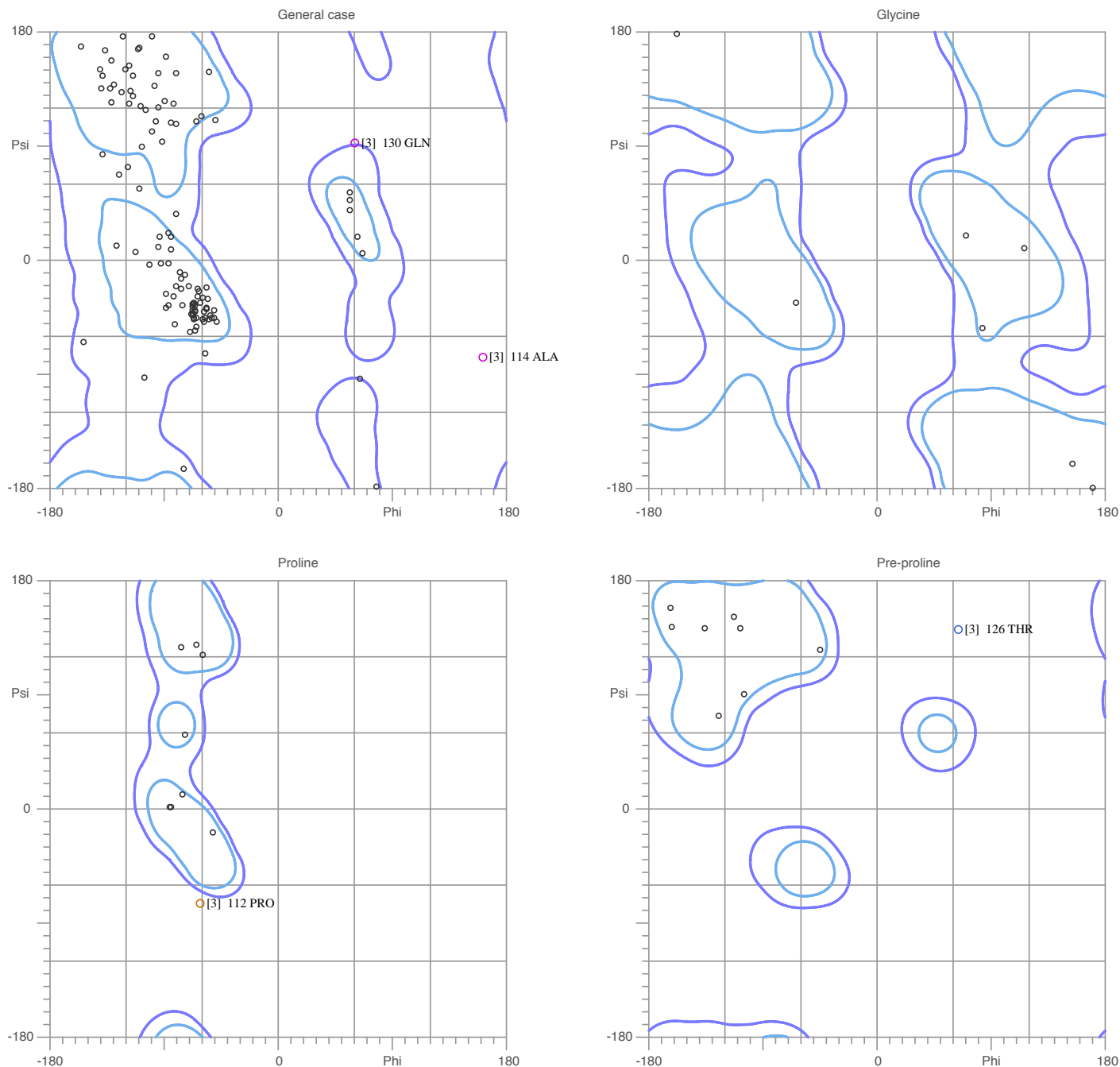
[2] 4 ASP (-178.8, -51.6)

[2] 6 PRO (-79.0, -58.9)

[2] 108 SER (67.4, 145.1)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 3



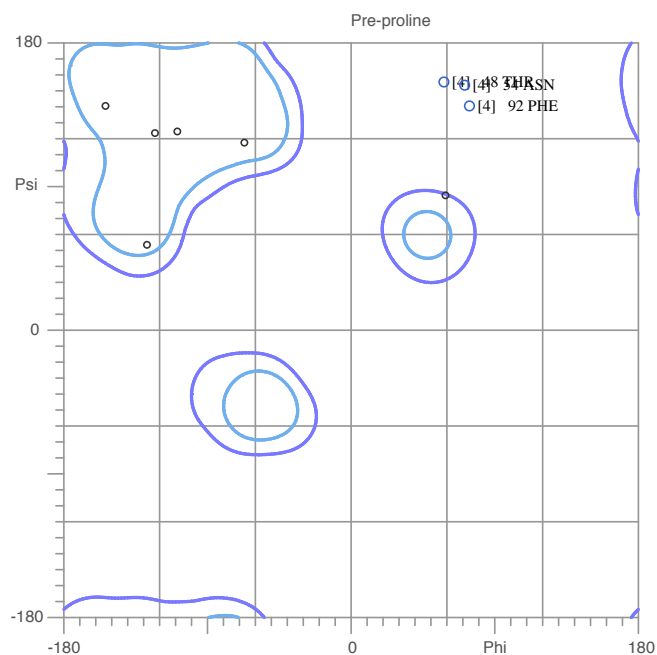
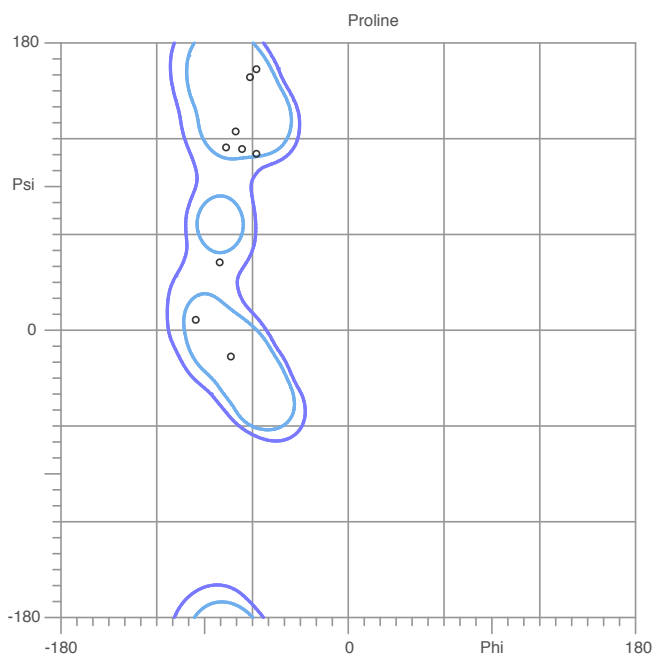
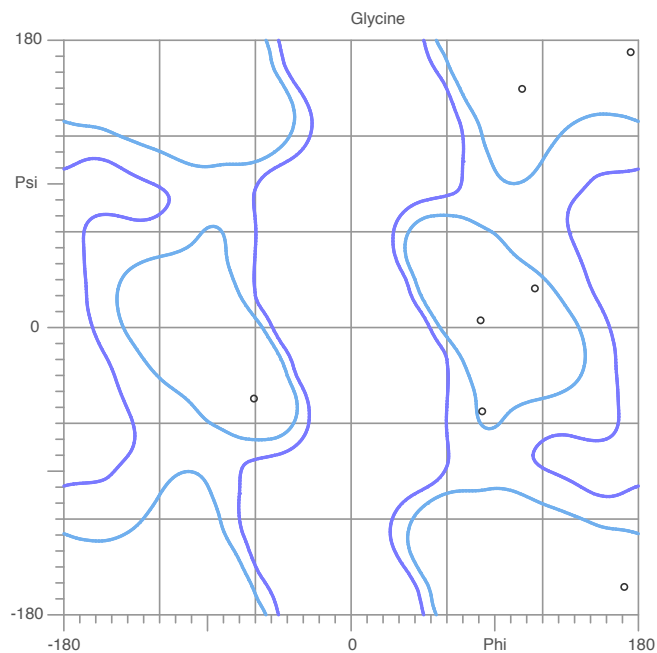
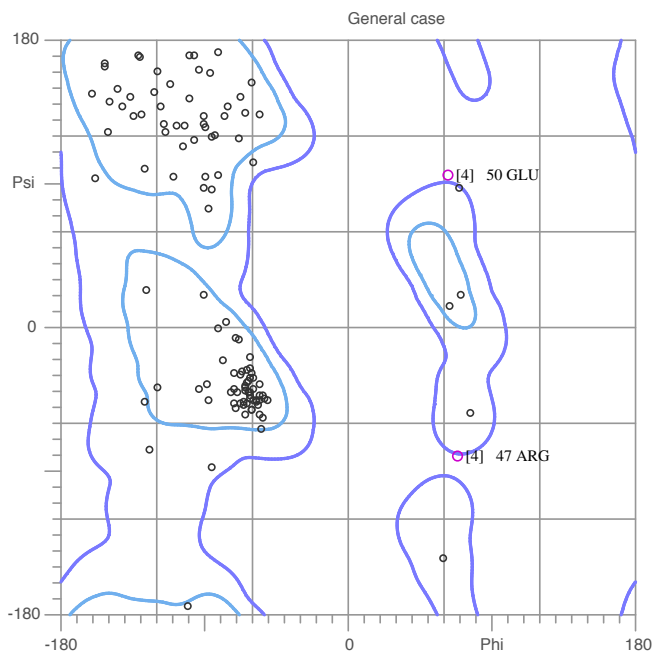
88.6% (124/140) of all residues were in favored (98%) regions.  
97.1% (136/140) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [3] 112 PRO (-63.0, -74.2)
- [3] 114 ALA (162.0, -76.8)
- [3] 126 THR (64.5, 142.2)
- [3] 130 GLN (60.7, 93.1)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 4



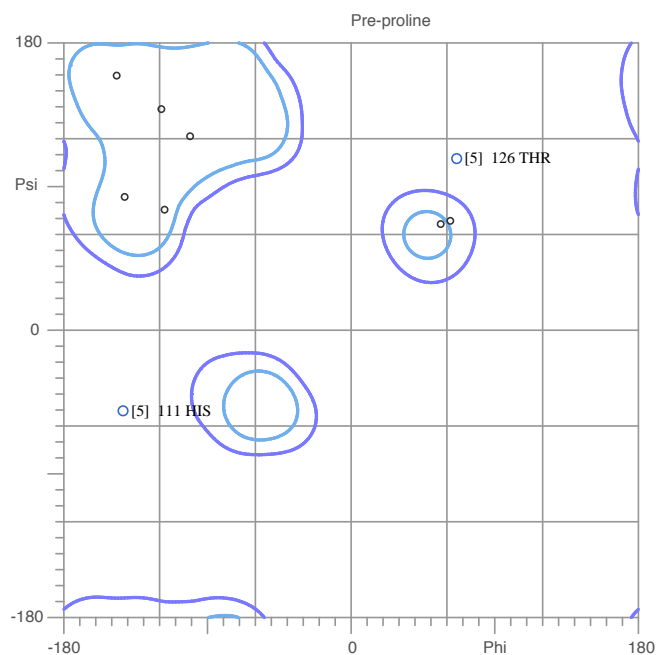
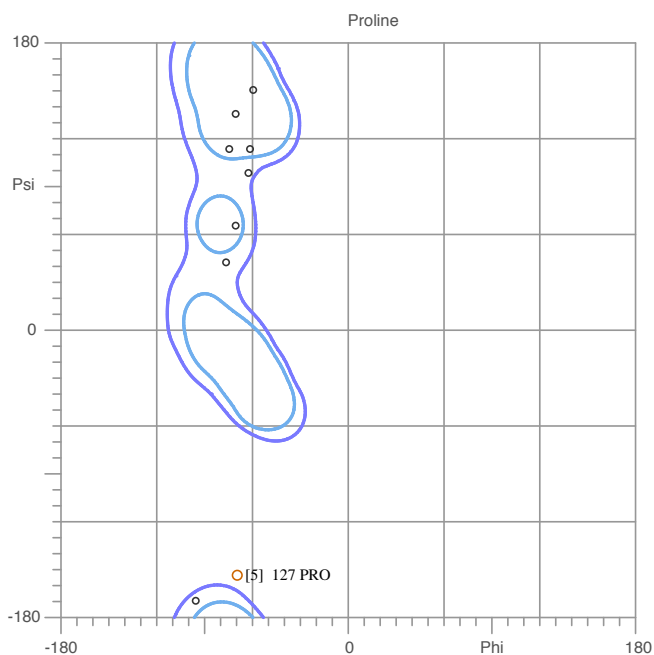
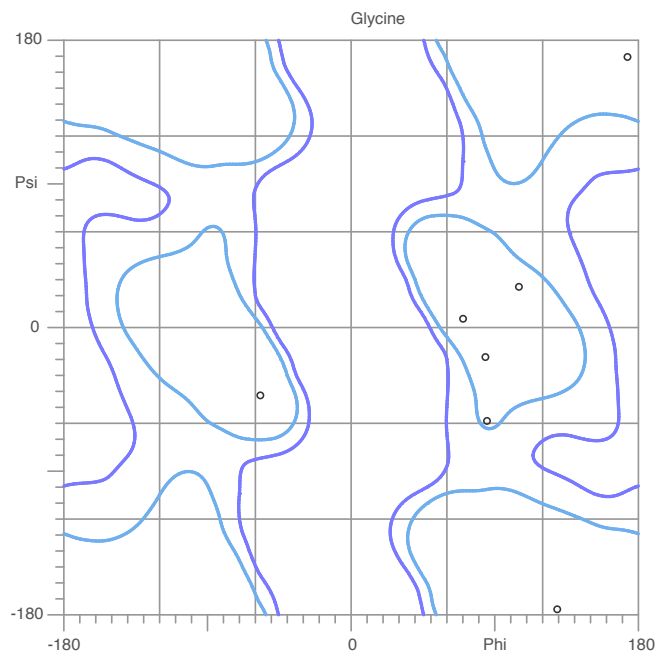
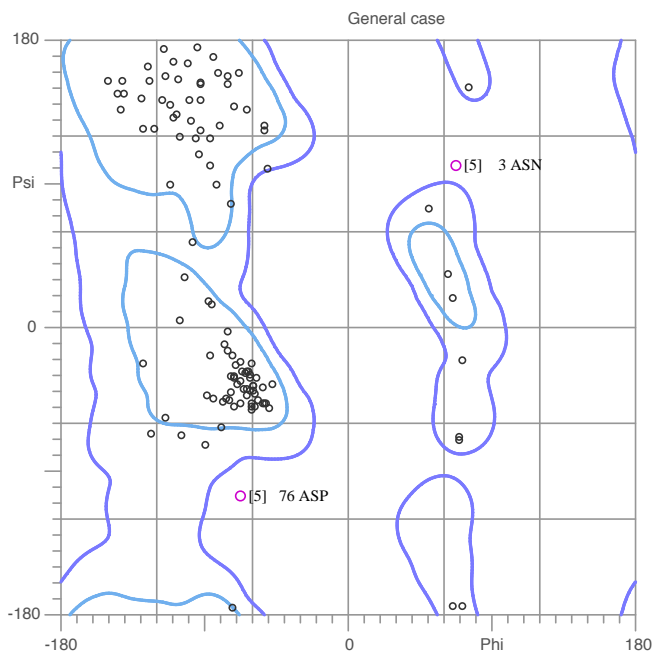
89.3% (125/140) of all residues were in favored (98%) regions.  
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[4] 47 ARG (68.1, -81.0)  
[4] 48 THR (58.4, 156.4)  
[4] 50 GLU (62.1, 96.8)  
[4] 54 ASN (71.8, 154.3)  
[4] 92 PHE (74.1, 141.9)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 5



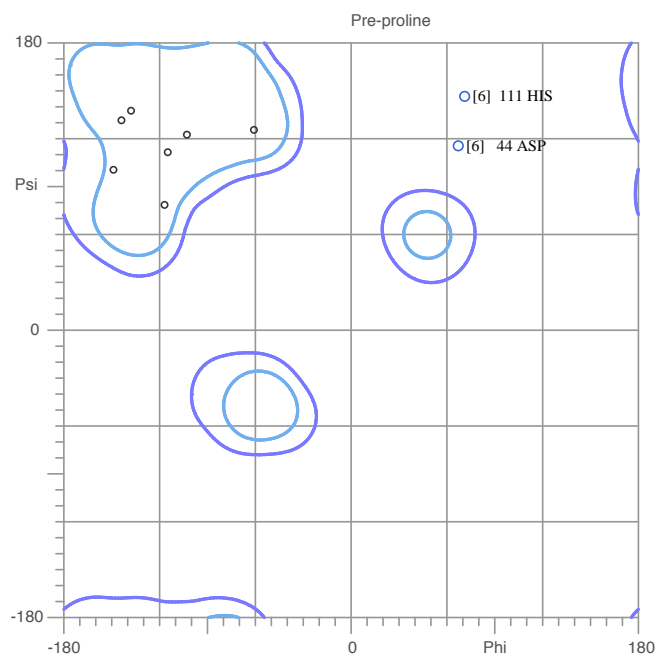
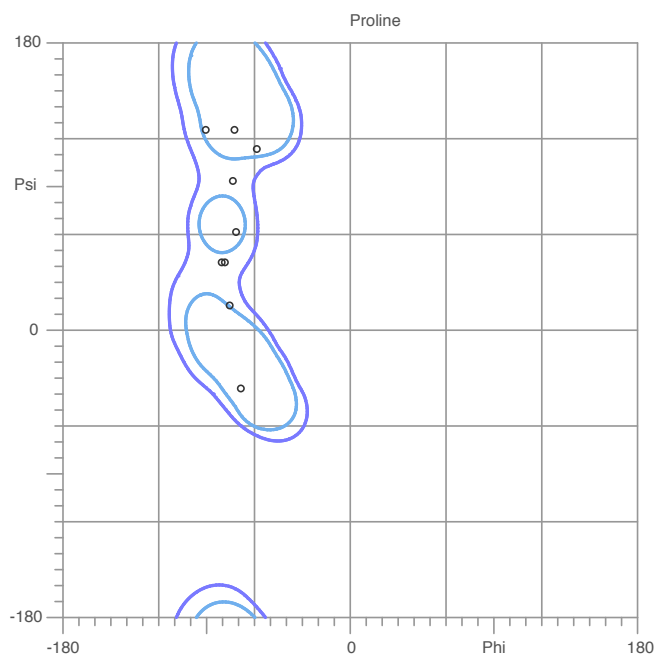
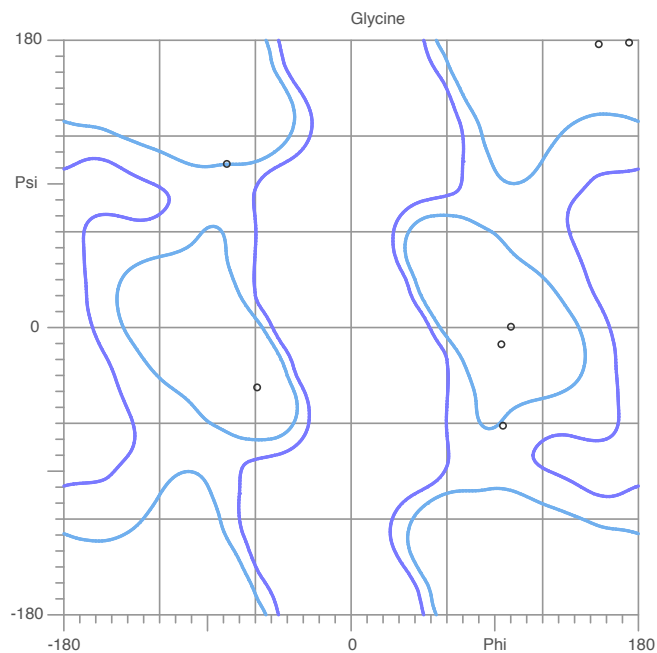
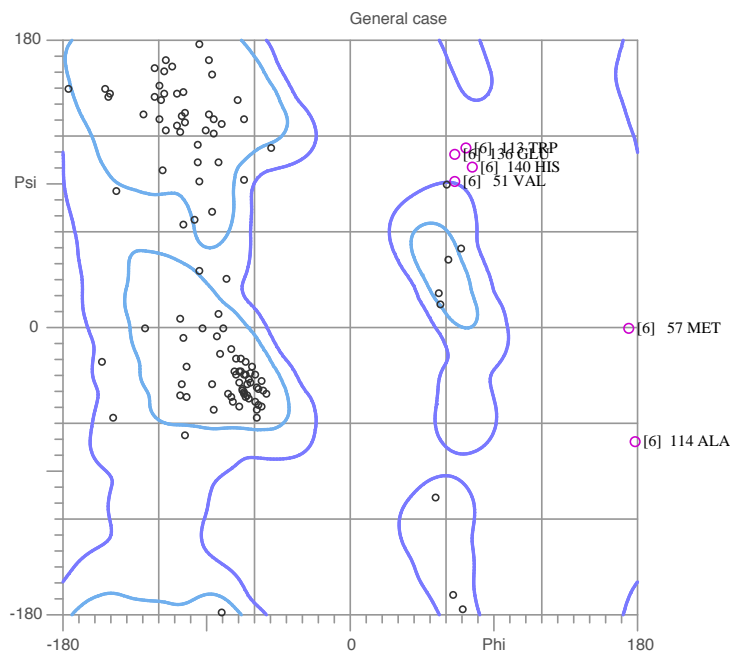
85.0% (119/140) of all residues were in favored (98%) regions.  
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[5] 3 ASN (67.4, 103.0)  
[5] 76 ASP (-68.1, -105.3)  
[5] 111 HIS (-143.7, -50.5)  
[5] 126 THR (66.1, 108.1)  
[5] 127 PRO (-71.0, -153.6)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 6



80.0% (112/140) of all residues were in favored (98%) regions.  
94.3% (132/140) of all residues were in allowed (>99.8%) regions.

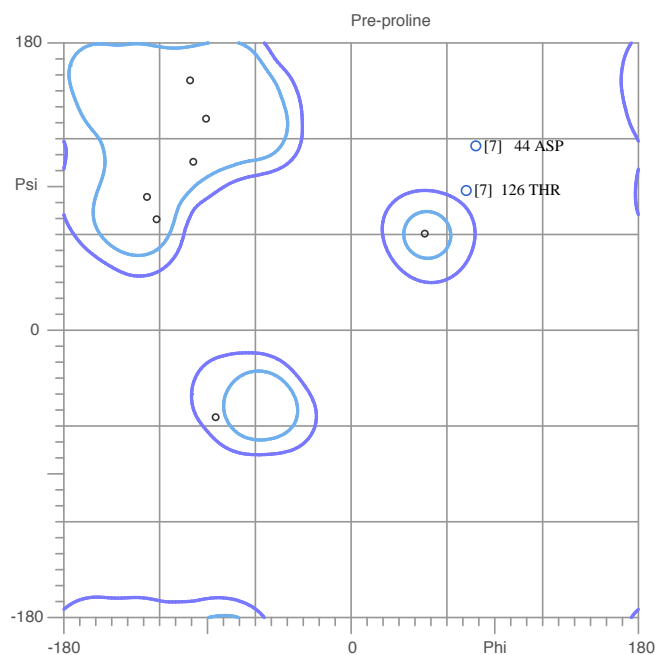
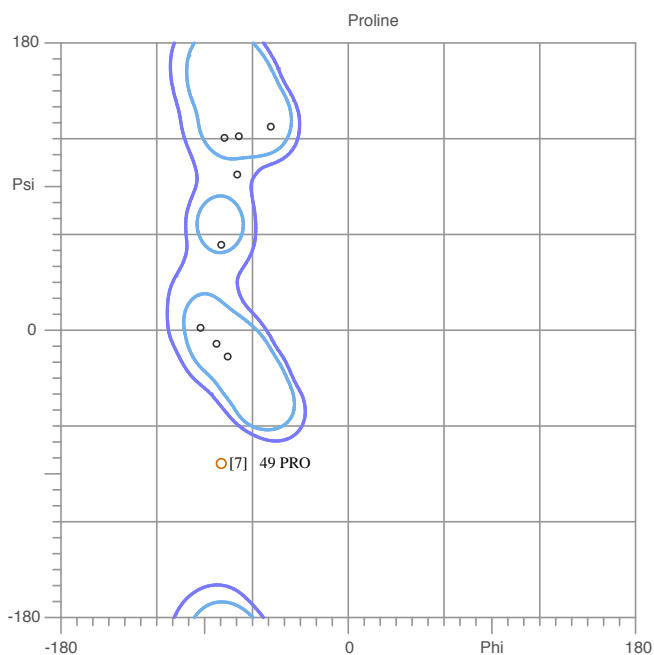
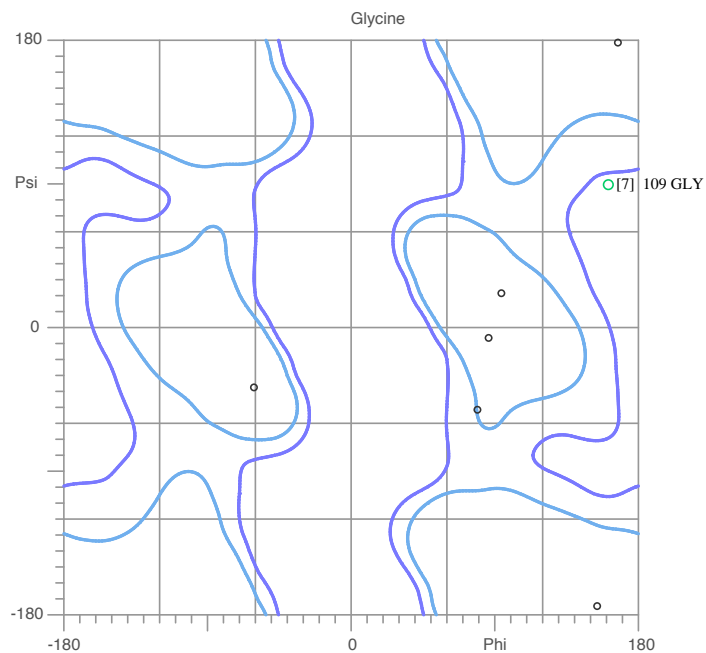
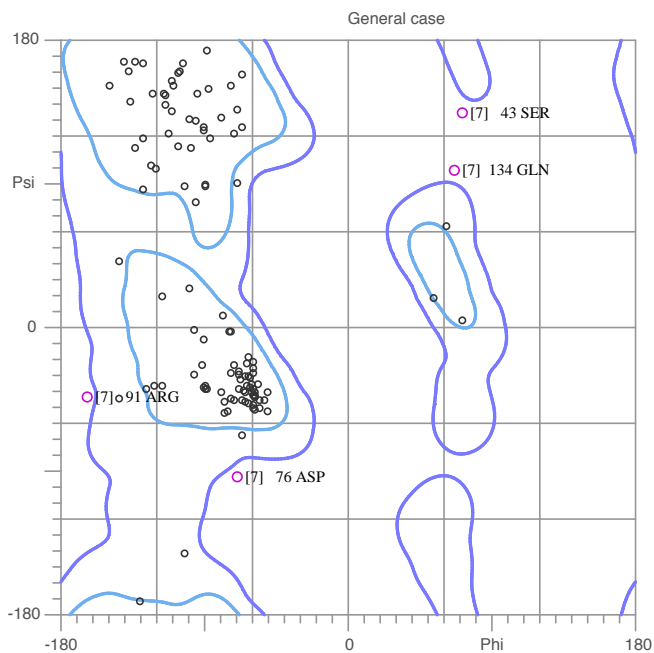
There were 8 outliers (phi, psi):

- [6] 44 ASP (67.1, 116.3)
- [6] 51 VAL (65.4, 92.5)

- [6] 57 MET (174.9, -0.4)
- [6] 111 HIS (71.5, 147.9)
- [6] 113 TRP (72.2, 113.7)
- [6] 114 ALA (178.9, -71.9)
- [6] 136 GLU (65.2, 109.1)
- [6] 140 HIS (76.0, 101.5)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 7



88.6% (124/140) of all residues were in favored (98%) regions.  
94.3% (132/140) of all residues were in allowed (>99.8%) regions.

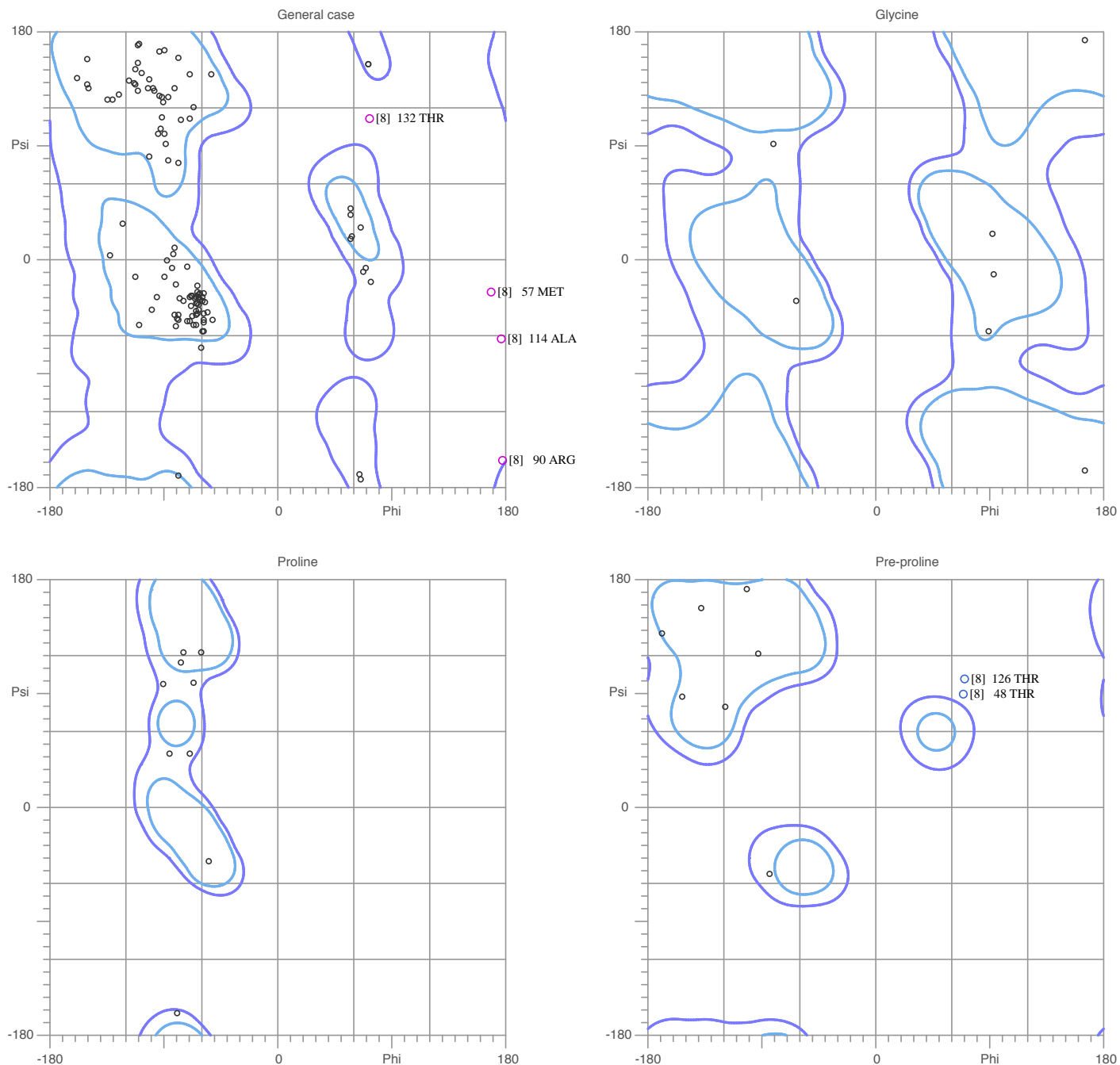
There were 8 outliers (phi, psi):

[7] 43 SER (71.6, 136.0)  
[7] 44 ASP (78.1, 116.2)

[7] 49 PRO (-80.5, -83.3)  
[7] 76 ASP (-70.6, -93.7)  
[7] 91 ARG (-164.7, -43.4)  
[7] 109 GLY (161.1, 90.1)  
[7] 126 THR (72.1, 88.5)  
[7] 134 GLN (67.0, 99.9)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 8



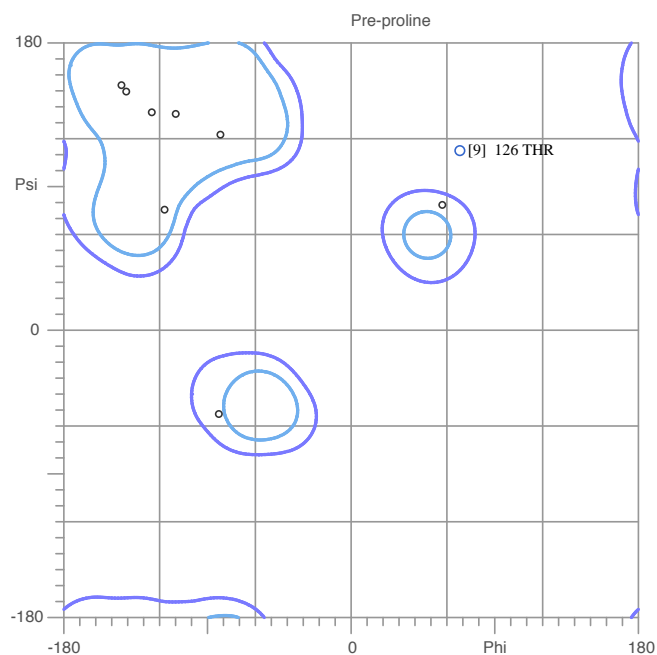
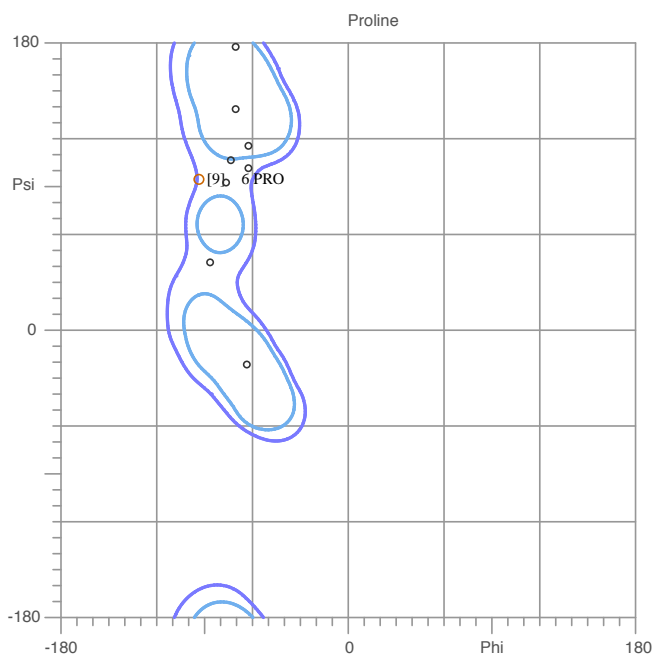
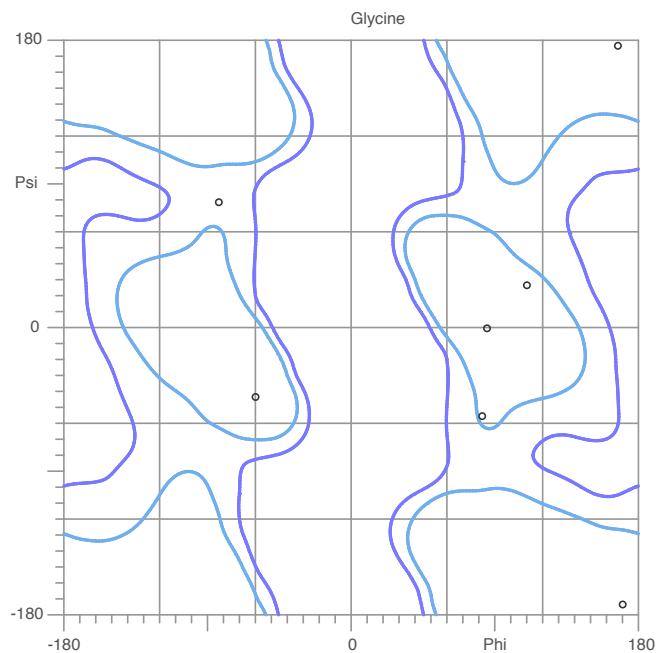
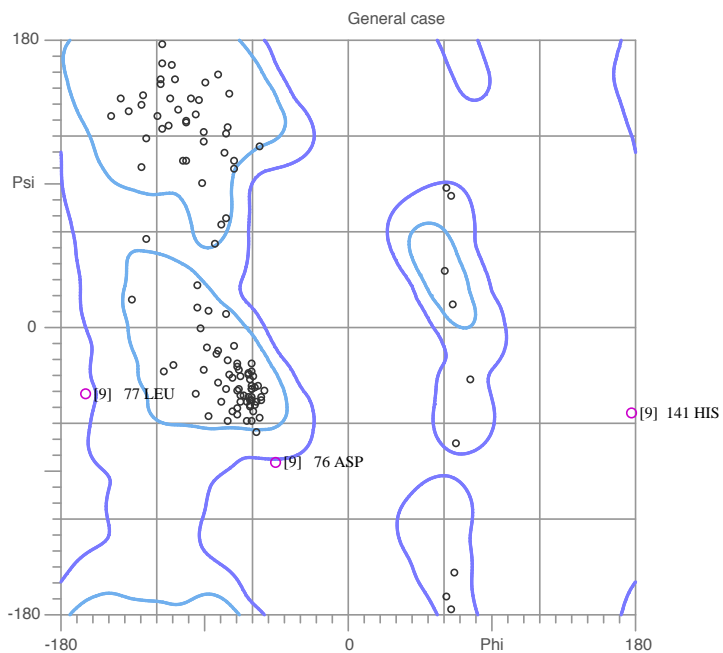
85.0% (119/140) of all residues were in favored (98%) regions.  
95.7% (134/140) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):  
[8] 48 THR (69.9, 90.1)

[8] 57 MET (169.0, -25.6)  
[8] 90 ARG (177.9, -158.5)  
[8] 114 ALA (176.7, -62.9)  
[8] 126 THR (70.5, 102.1)  
[8] 132 THR (72.4, 112.6)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 9



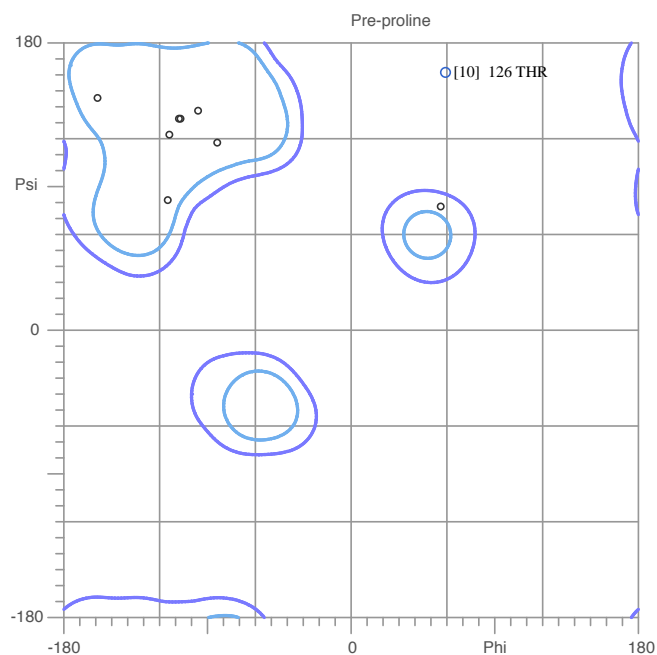
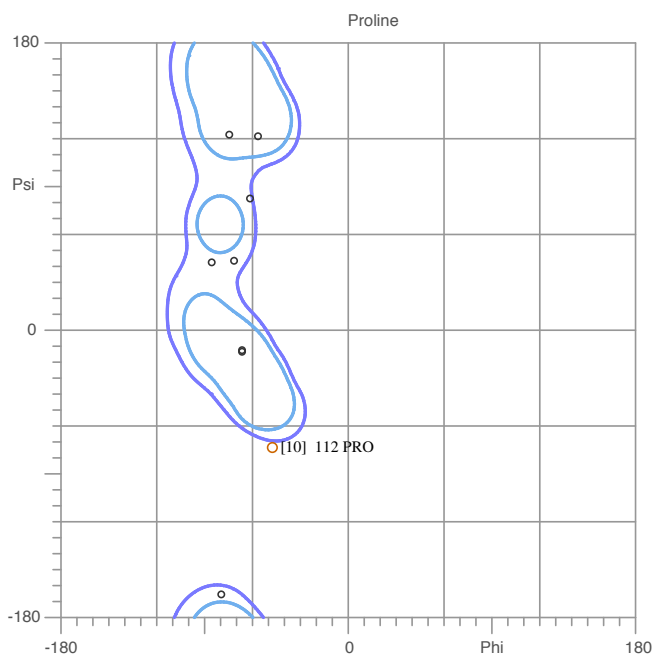
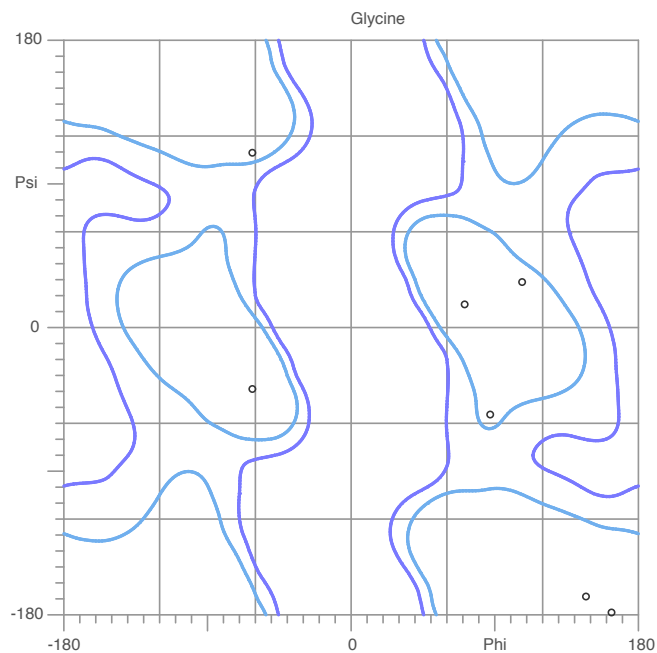
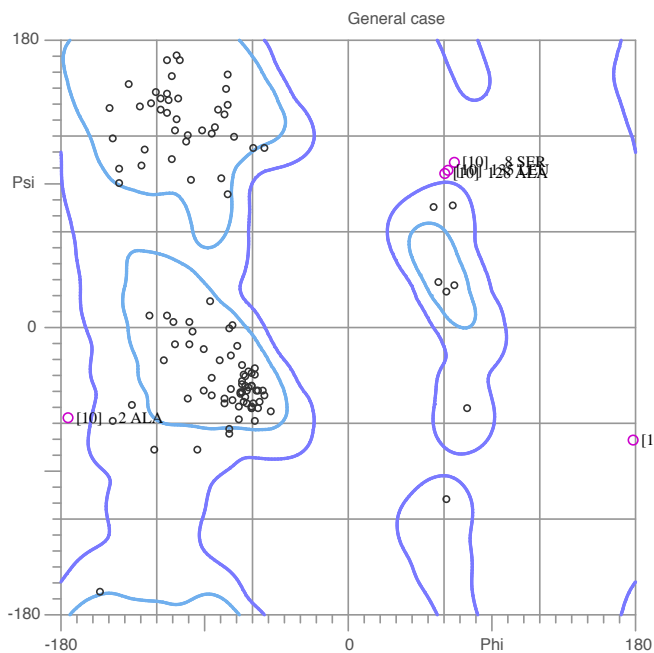
85.7% (120/140) of all residues were in favored (98%) regions.  
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[9] 6 PRO (-94.6, 95.5)  
[9] 76 ASP (-47.0, -84.9)  
[9] 77 LEU (-165.0, -41.0)  
[9] 126 THR (69.0, 113.3)  
[9] 141 HIS (177.5, -53.4)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 10



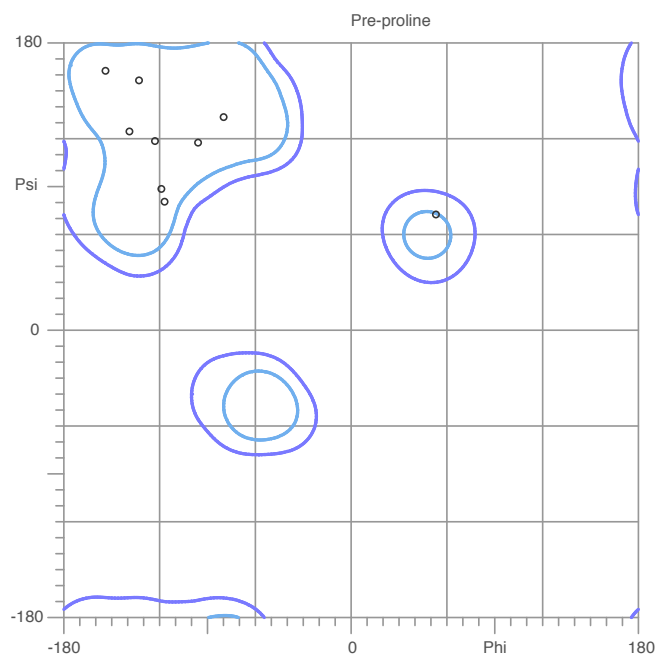
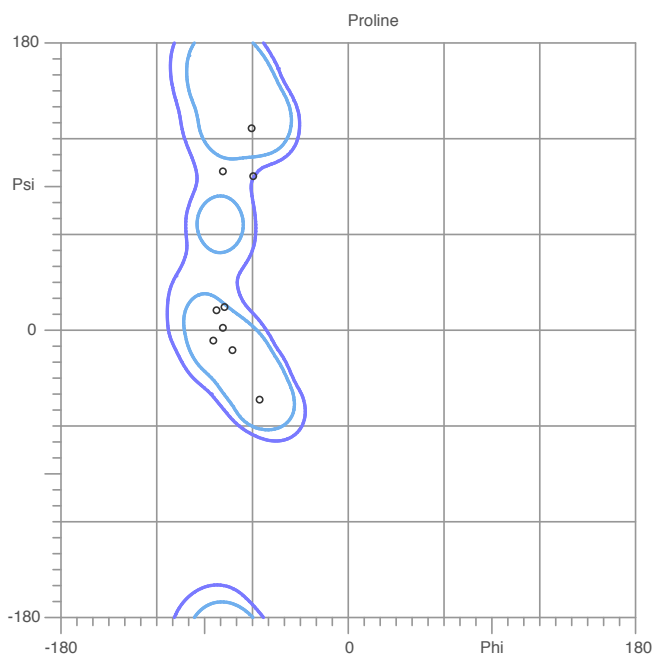
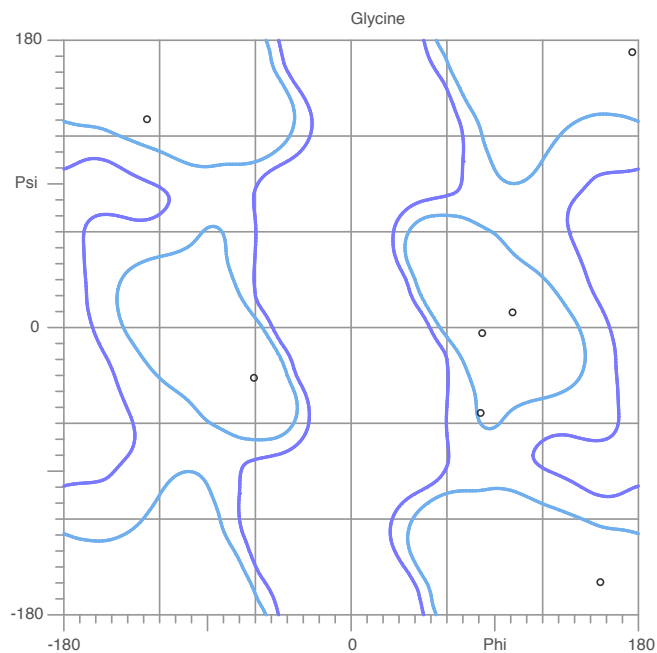
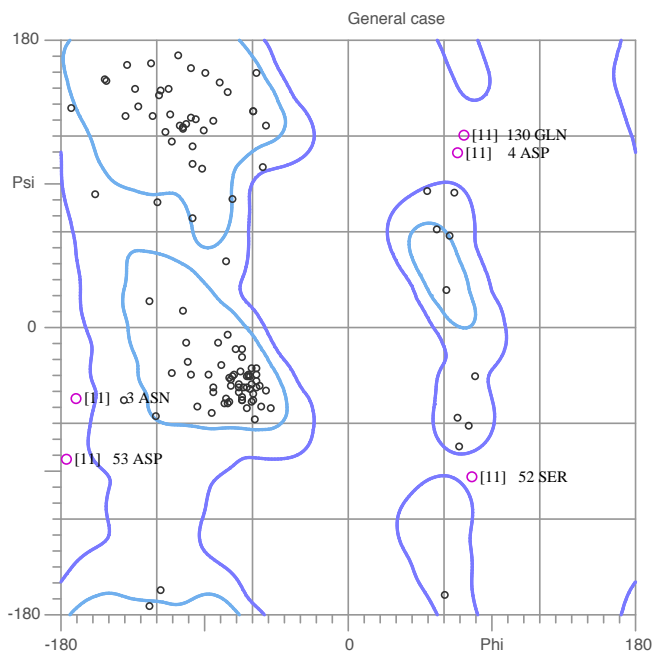
82.9% (116/140) of all residues were in favored (98%) regions.  
95.0% (133/140) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):  
[10] 2 ALA (-176.3, -56.7)

[10] 8 SER (66.7, 104.1)  
[10] 112 PRO (-48.8, -73.7)  
[10] 114 ALA (178.6, -70.3)  
[10] 126 THR (59.8, 162.3)  
[10] 128 ALA (60.3, 97.1)  
[10] 135 LEU (62.6, 99.7)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 11



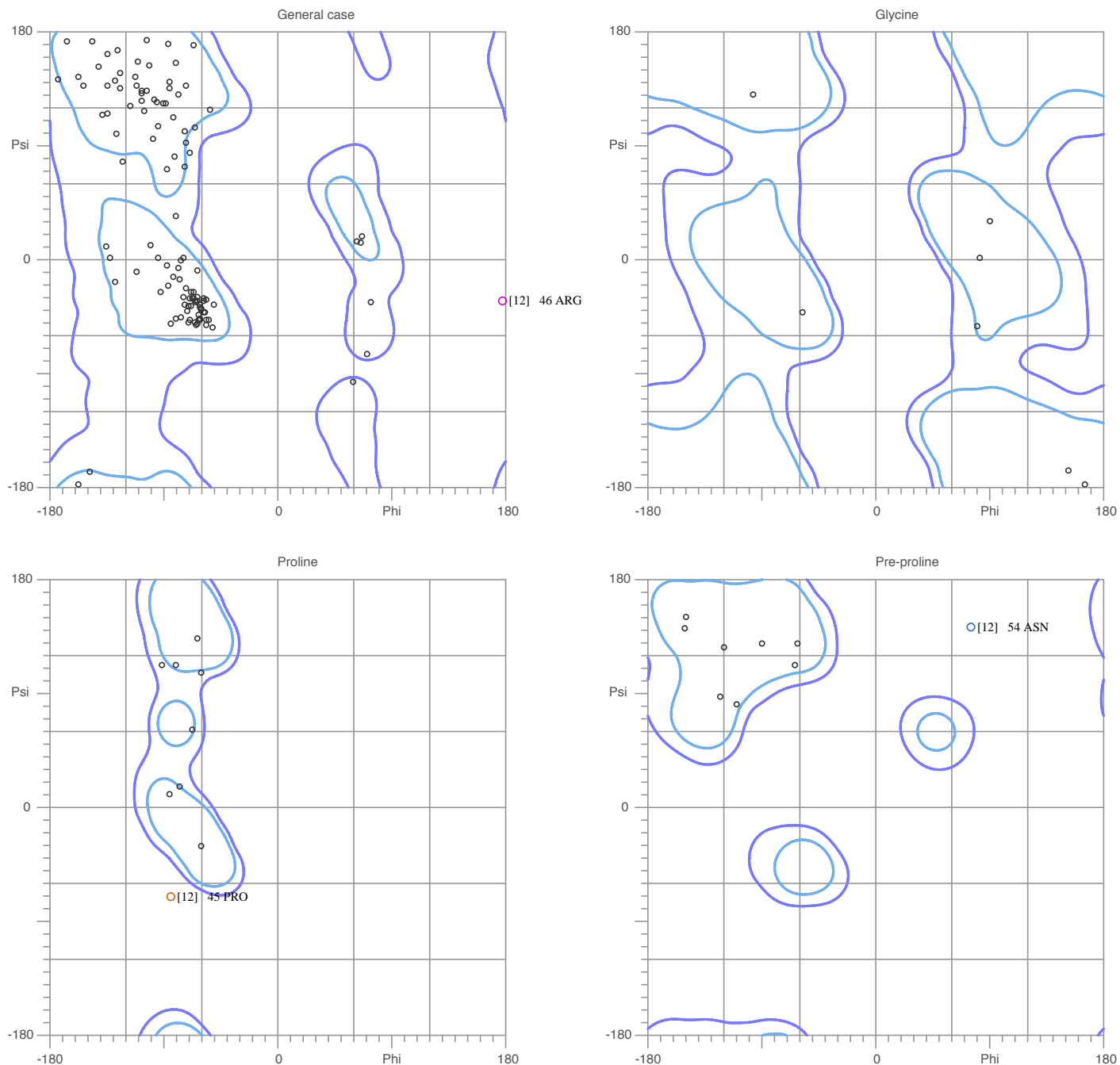
83.6% (117/140) of all residues were in favored (98%) regions.  
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[11] 3 ASN (-171.4, -44.9)  
[11] 4 ASP (68.4, 110.4)  
[11] 52 SER (77.4, -93.7)  
[11] 53 ASP (-177.4, -82.8)  
[11] 130 GLN (72.2, 121.1)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 12



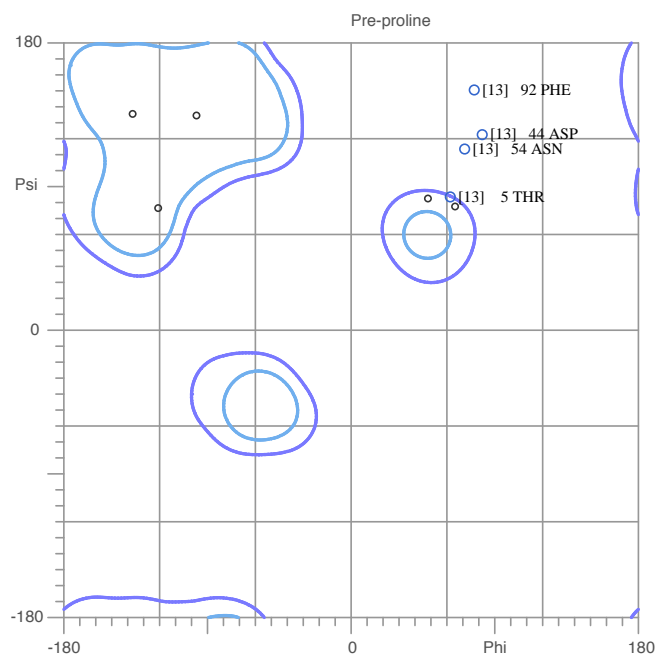
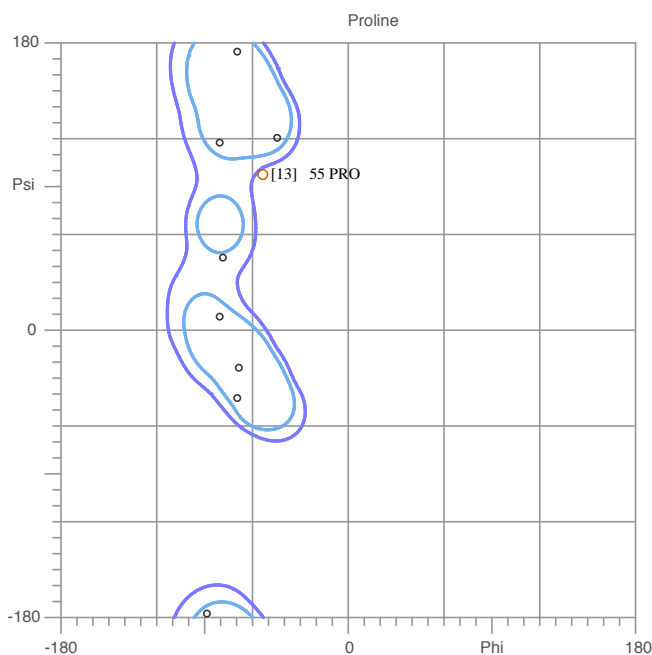
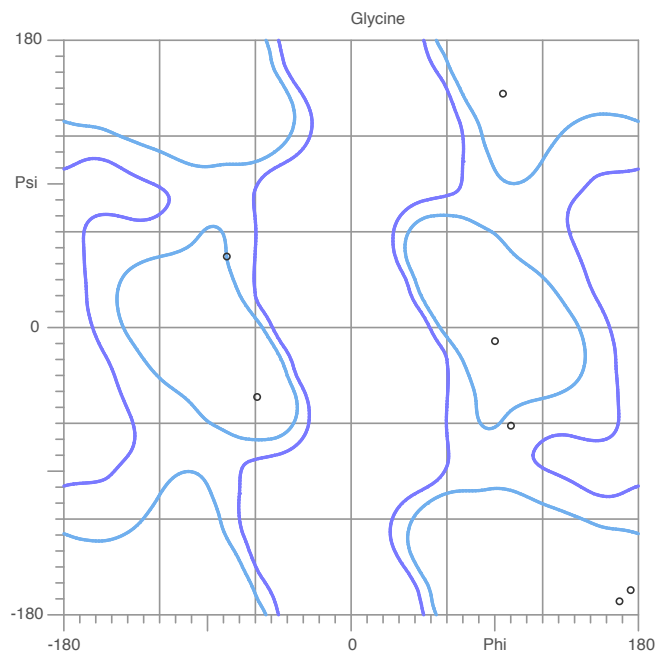
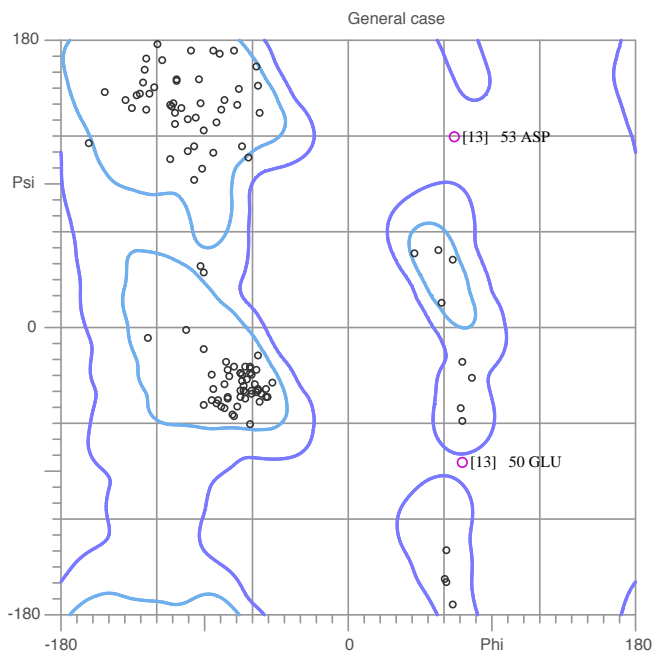
90.7% (127/140) of all residues were in favored (98%) regions.  
97.9% (137/140) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [12] 45 PRO (-85.7, -70.4)
- [12] 46 ARG (178.0, -32.3)
- [12] 54 ASN (75.3, 143.8)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 13



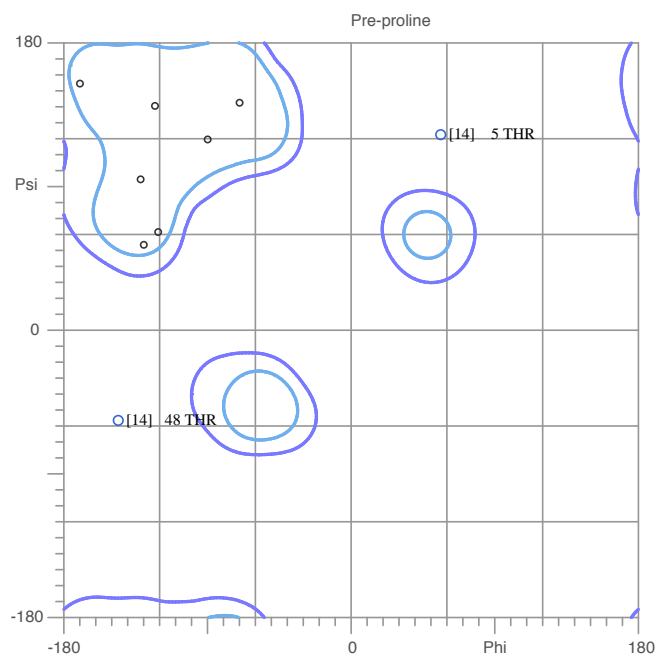
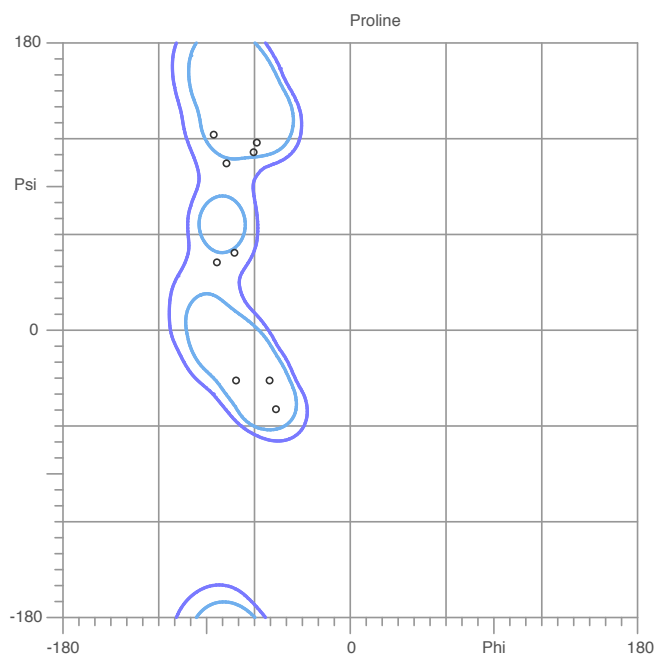
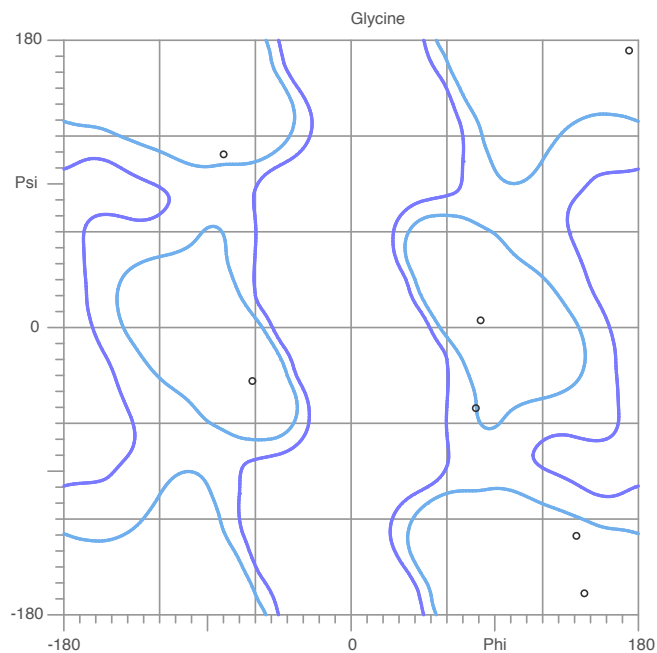
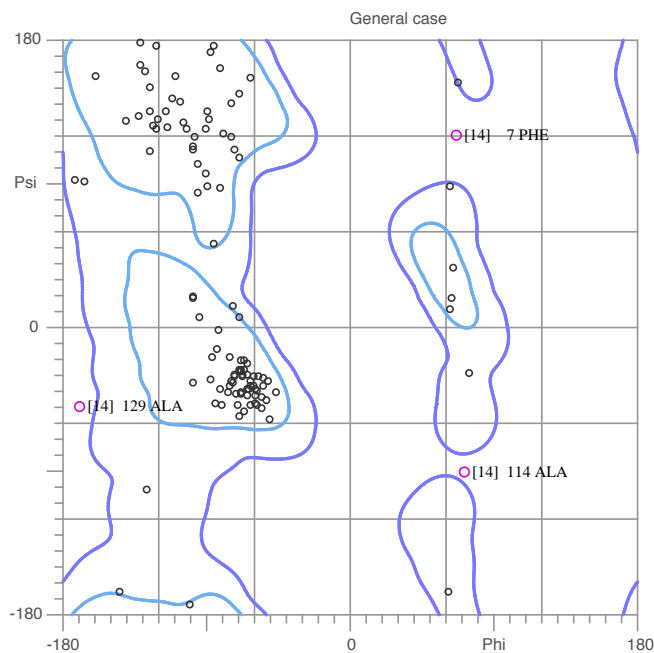
83.6% (117/140) of all residues were in favored (98%) regions.  
95.0% (133/140) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):  
[13] 5 THR (62.9, 84.7)

[13] 44 ASP (82.9, 123.4)  
[13] 50 GLU (71.4, -84.8)  
[13] 53 ASP (66.2, 120.5)  
[13] 54 ASN (71.7, 114.5)  
[13] 55 PRO (-54.8, 98.8)  
[13] 92 PHE (78.0, 151.9)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 14



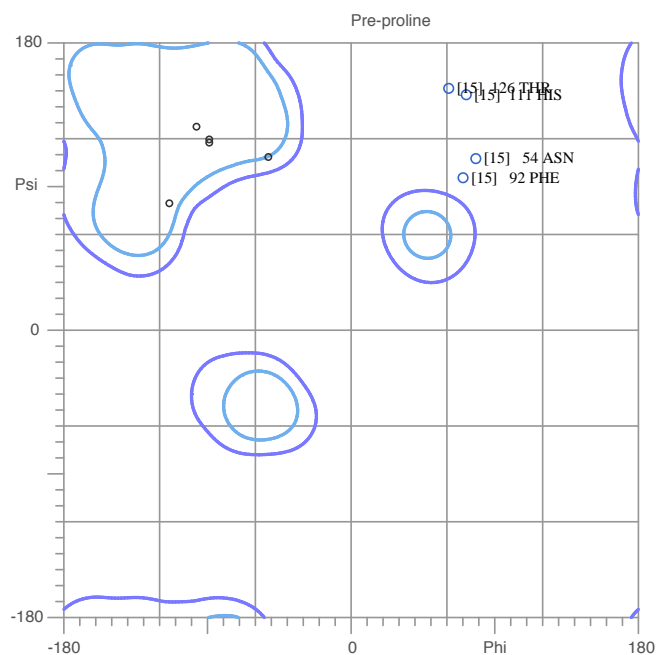
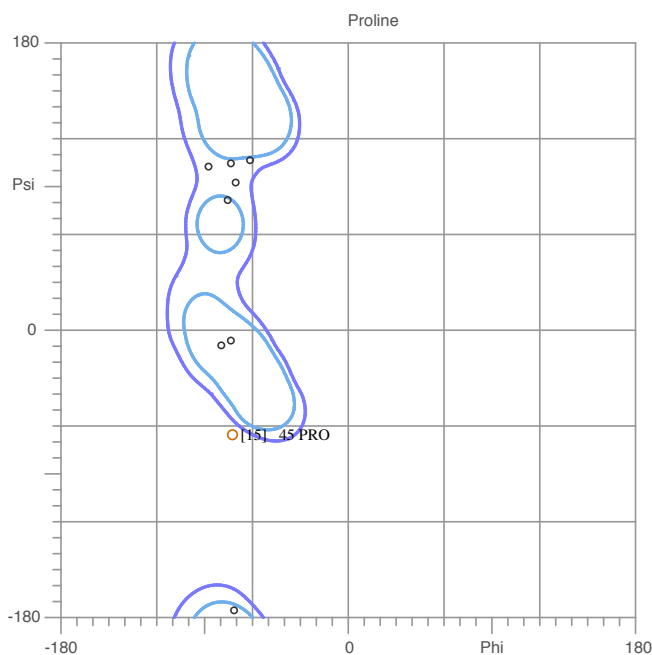
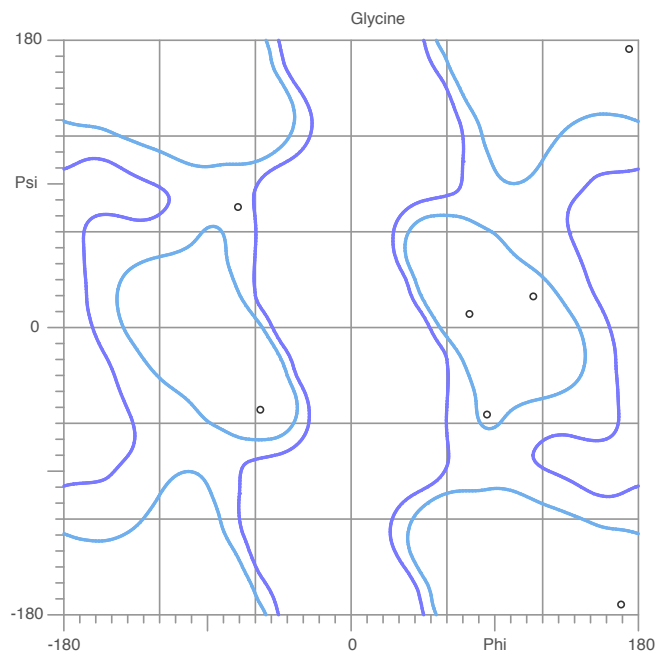
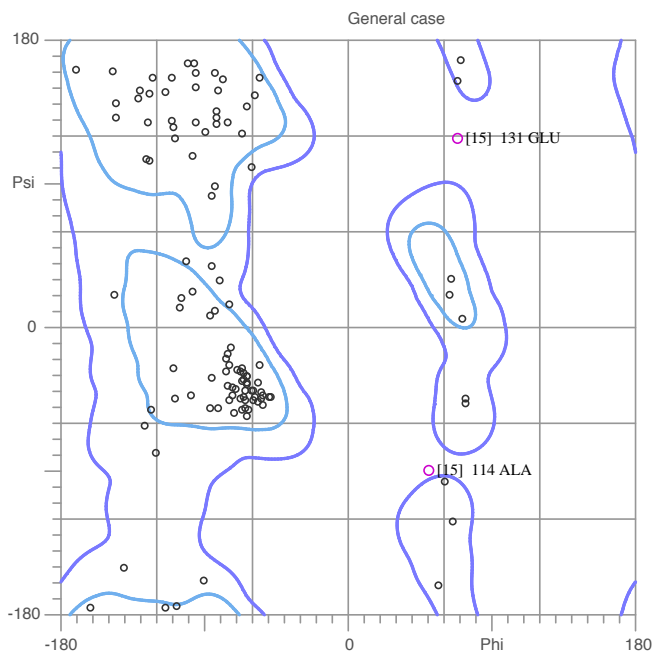
87.1% (122/140) of all residues were in favored (98%) regions.  
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[14] 5 THR (56.9, 123.7)  
[14] 7 PHE (66.7, 121.5)  
[14] 48 THR (-146.9, -56.6)  
[14] 114 ALA (71.9, -90.0)  
[14] 129 ALA (-170.1, -49.7)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 15



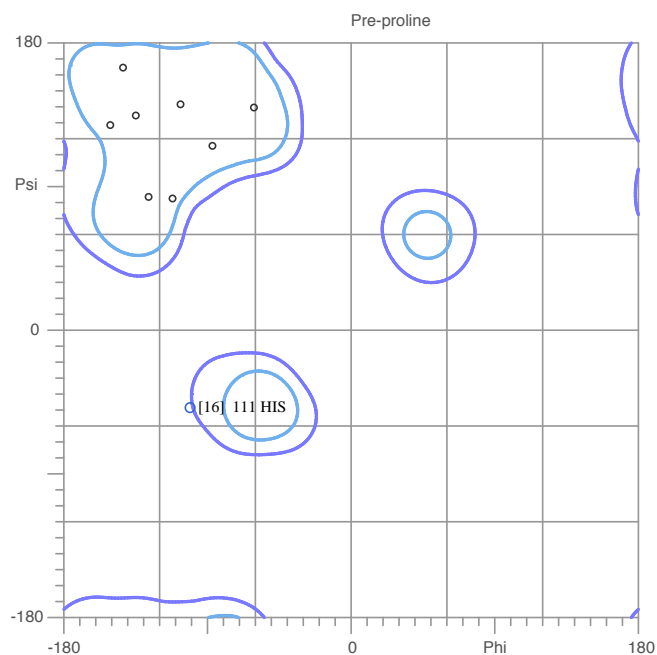
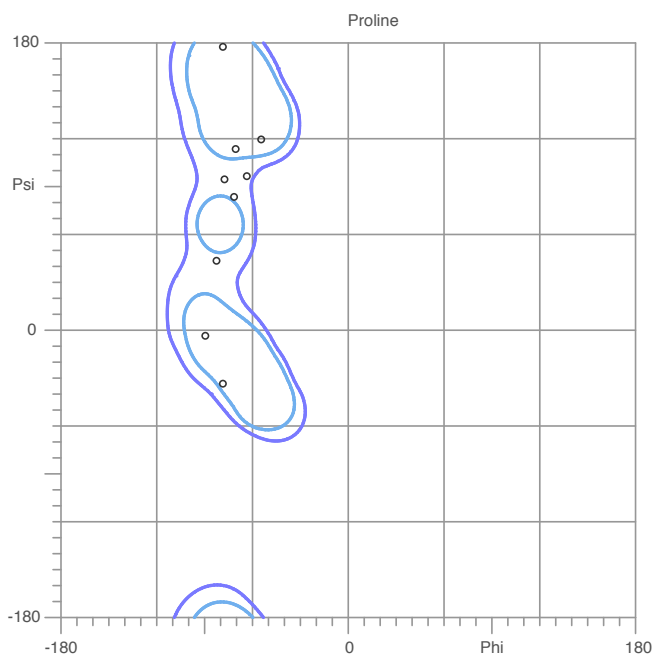
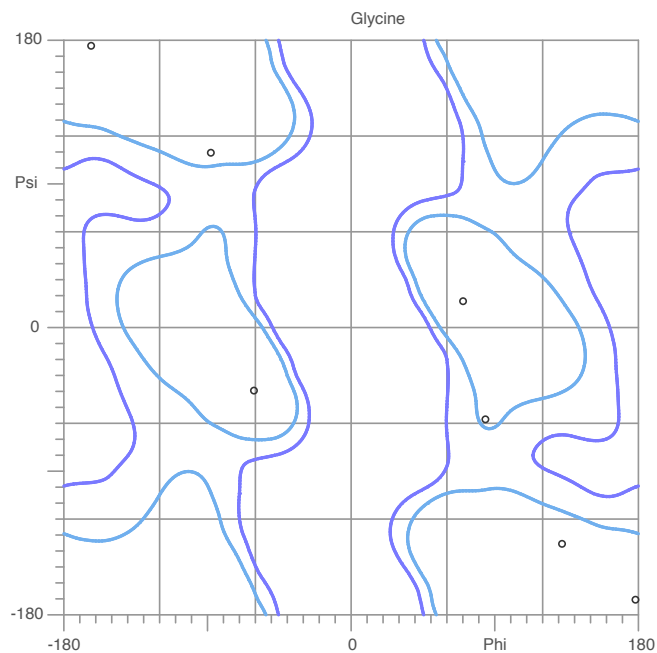
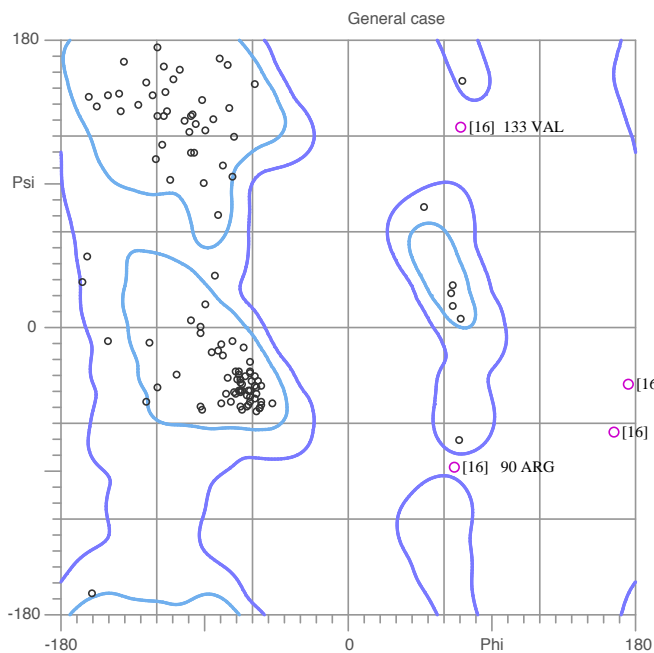
79.3% (111/140) of all residues were in favored (98%) regions.  
95.0% (133/140) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):  
[15] 45 PRO (-73.6, -65.1)

[15] 54 ASN (78.7, 108.5)  
[15] 92 PHE (70.5, 96.6)  
[15] 111 HIS (72.1, 148.9)  
[15] 114 ALA (50.7, -89.1)  
[15] 126 THR (61.6, 152.3)  
[15] 131 GLU (68.2, 119.7)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 16



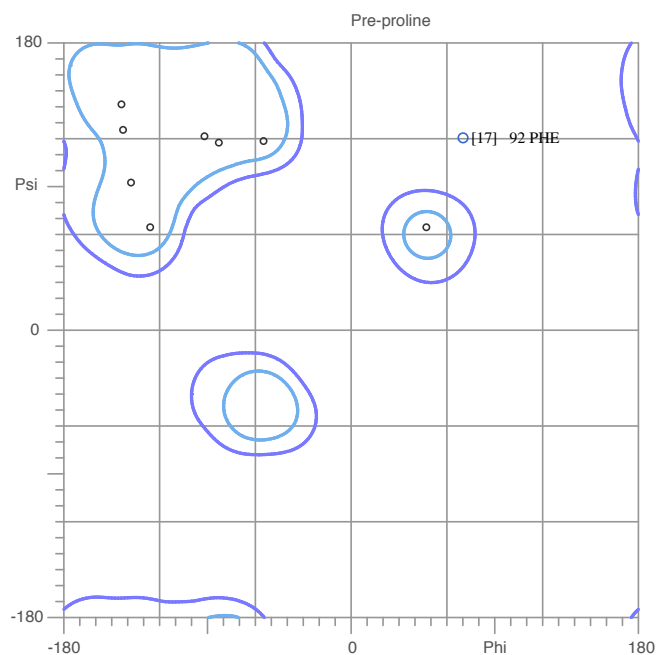
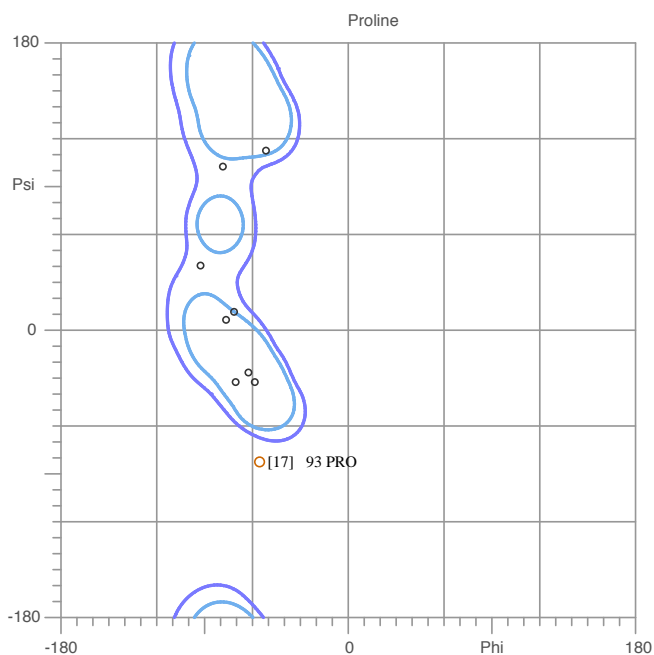
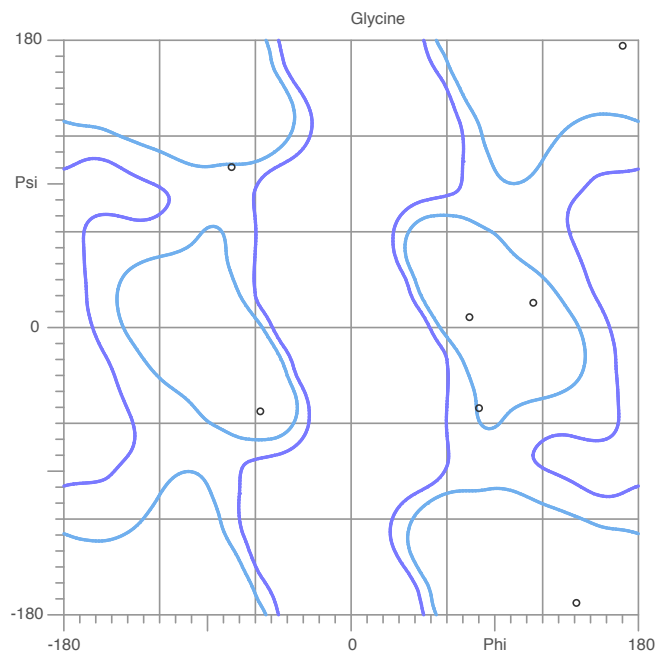
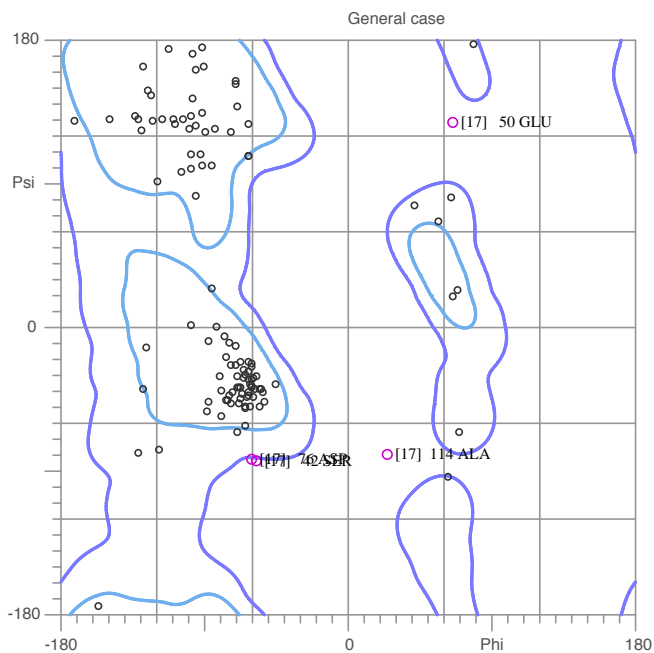
87.1% (122/140) of all residues were in favored (98%) regions.  
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[16] 46 ARG (175.5, -35.3)  
[16] 90 ARG (66.1, -87.7)  
[16] 111 HIS (-101.1, -48.6)  
[16] 114 ALA (166.9, -65.0)  
[16] 133 VAL (70.1, 126.6)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 17



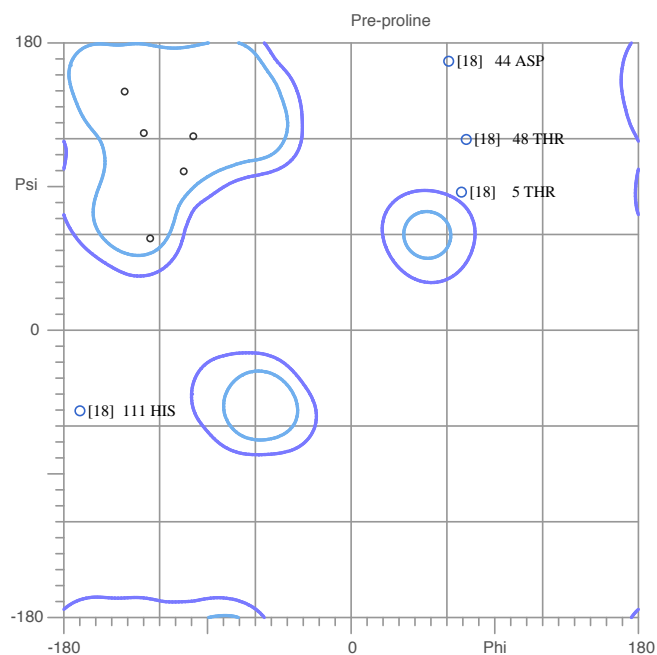
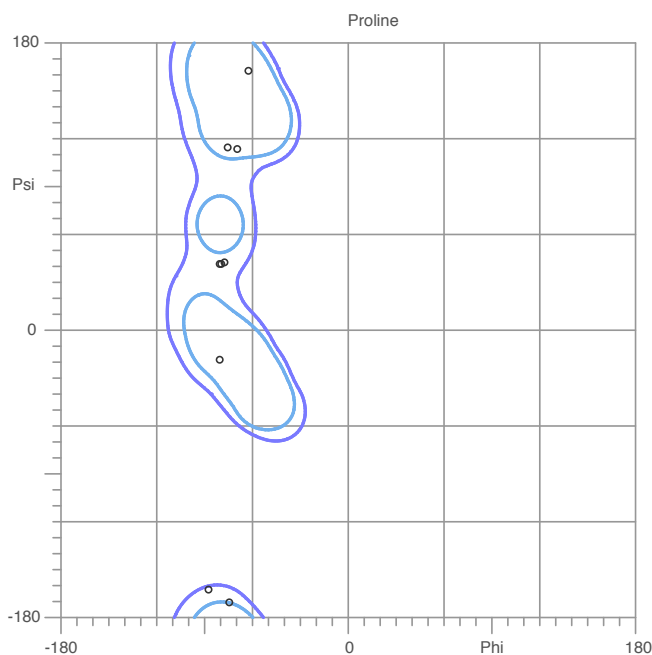
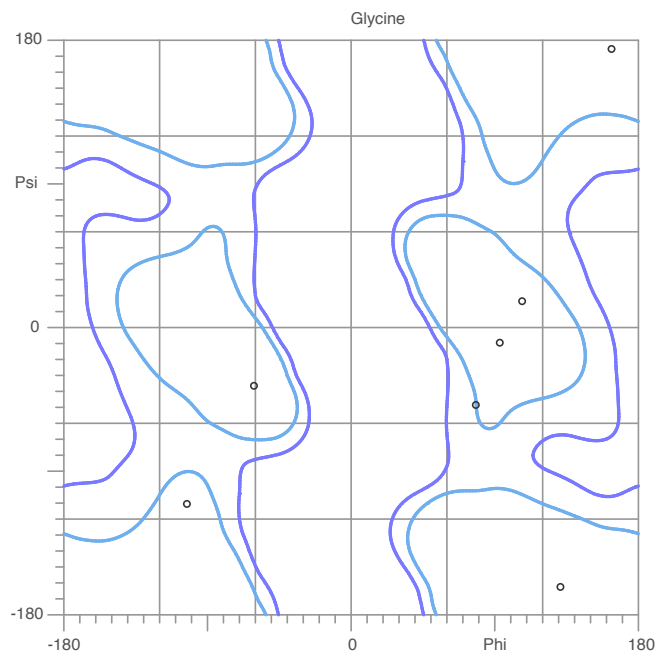
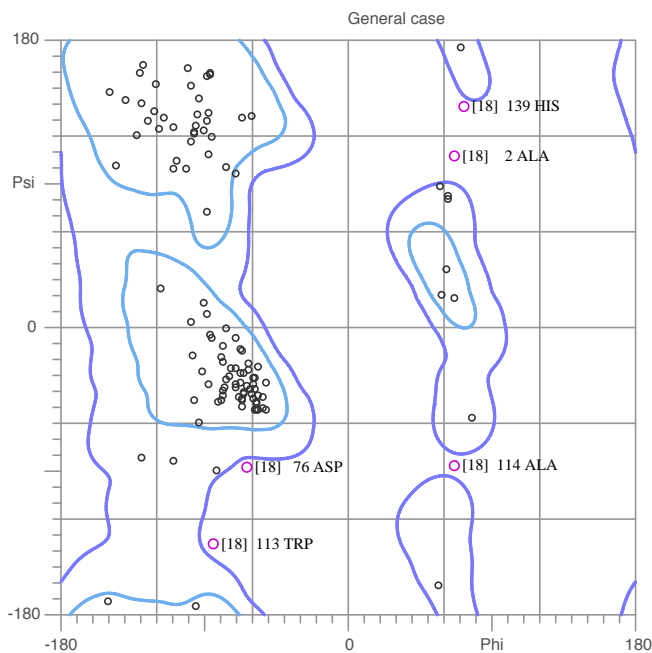
84.3% (118/140) of all residues were in favored (98%) regions.  
95.7% (134/140) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):  
[17] 42 SER (-58.7, -83.5)

[17] 50 GLU (65.5, 129.4)  
[17] 76 ASP (-61.1, -82.0)  
[17] 92 PHE (70.5, 121.8)  
[17] 93 PRO (-56.5, -82.6)  
[17] 114 ALA (24.4, -79.2)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 18



82.9% (116/140) of all residues were in favored (98%) regions.  
93.6% (131/140) of all residues were in allowed (>99.8%) regions.

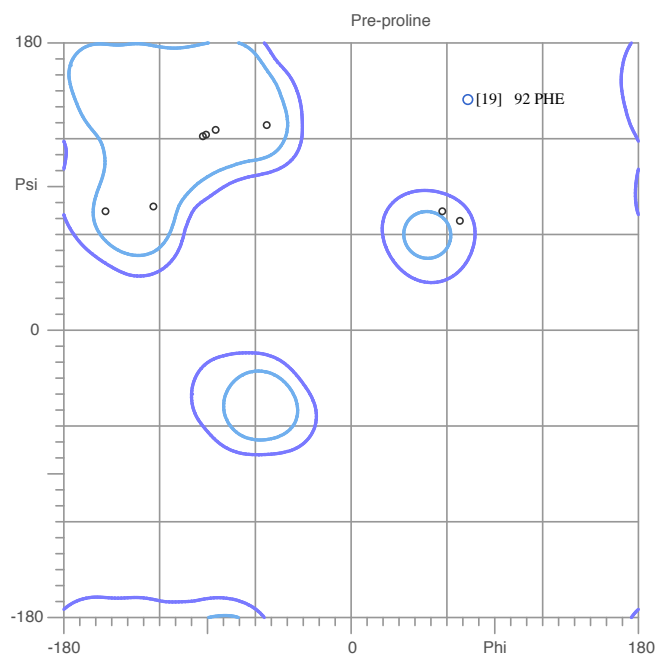
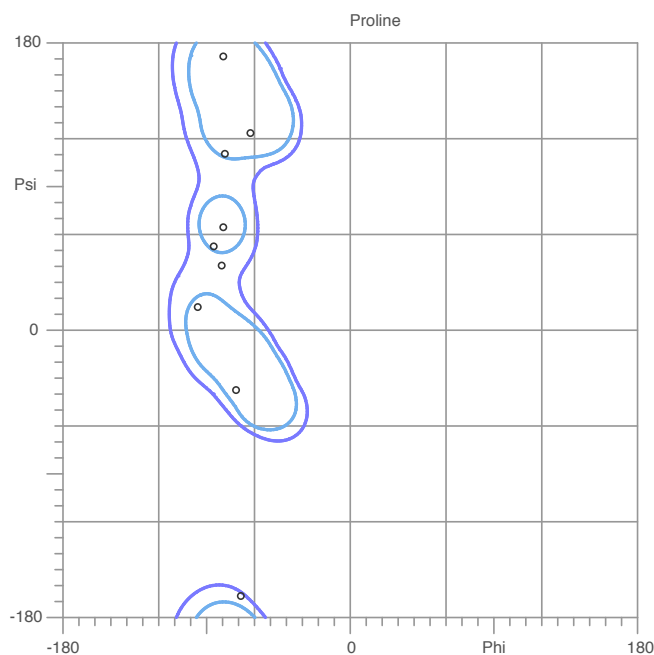
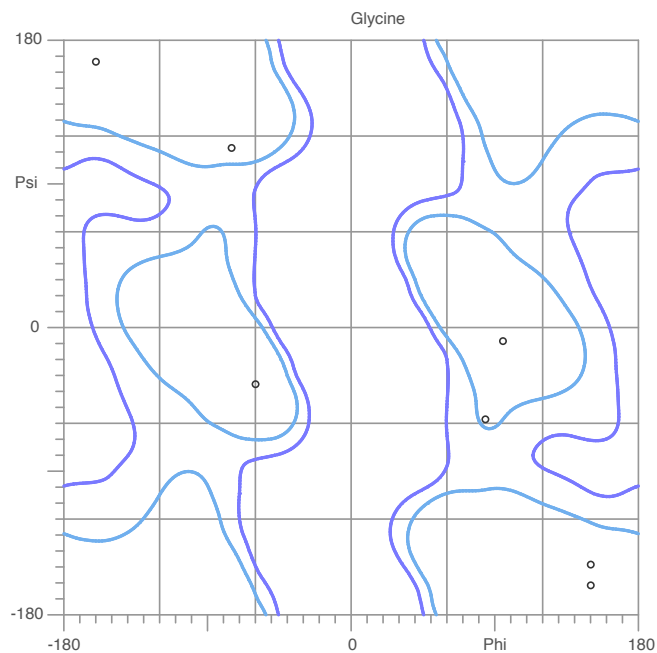
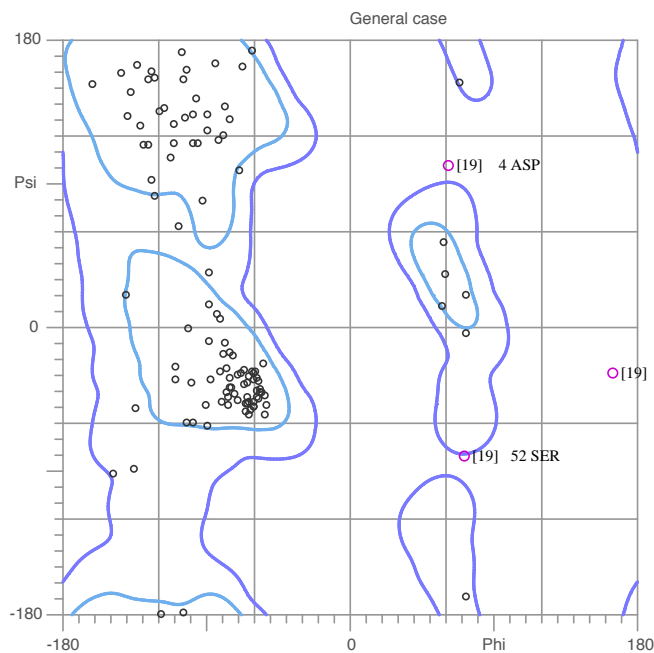
There were 9 outliers (phi, psi):

[18] 2 ALA (66.3, 108.8)  
[18] 5 THR (69.3, 87.4)

[18] 44 ASP (61.8, 169.3)  
[18] 48 THR (72.2, 120.9)  
[18] 76 ASP (-64.4, -87.6)  
[18] 111 HIS (-170.2, -50.3)  
[18] 113 TRP (-85.8, -135.2)  
[18] 114 ALA (66.4, -86.4)  
[18] 139 HIS (72.9, 139.9)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 19



85.7% (120/140) of all residues were in favored (98%) regions.  
97.1% (136/140) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[19] 4 ASP (61.8, 102.9)

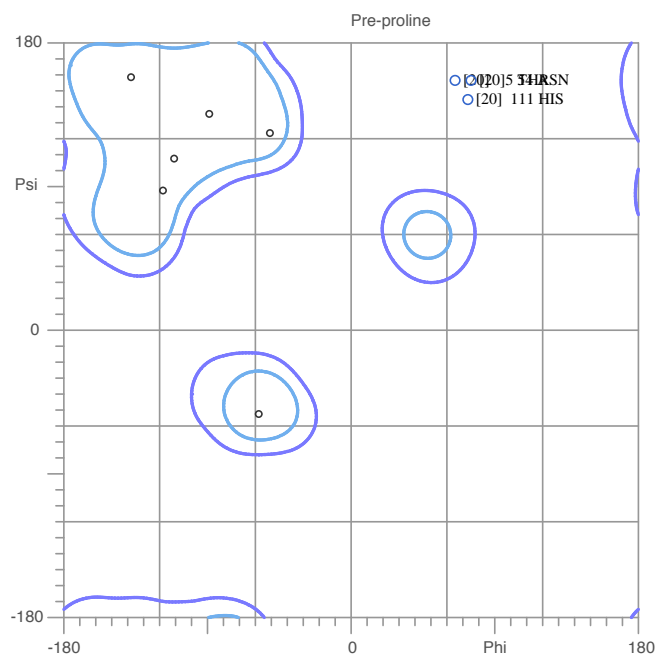
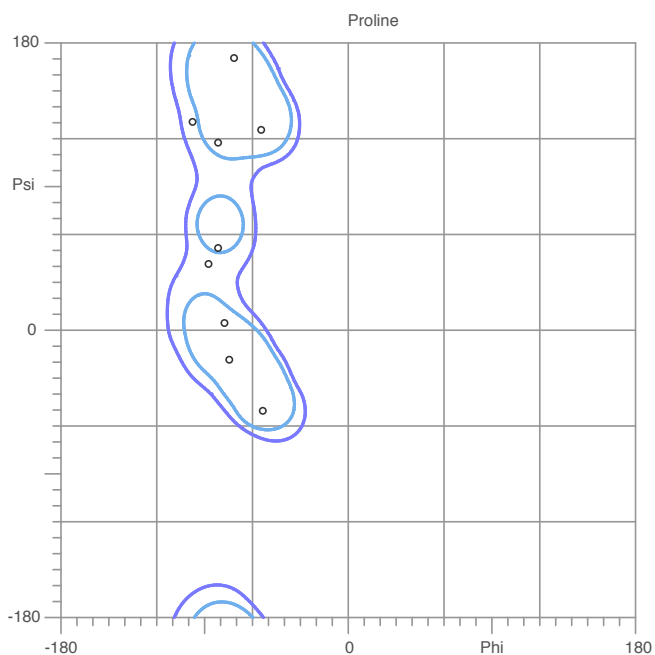
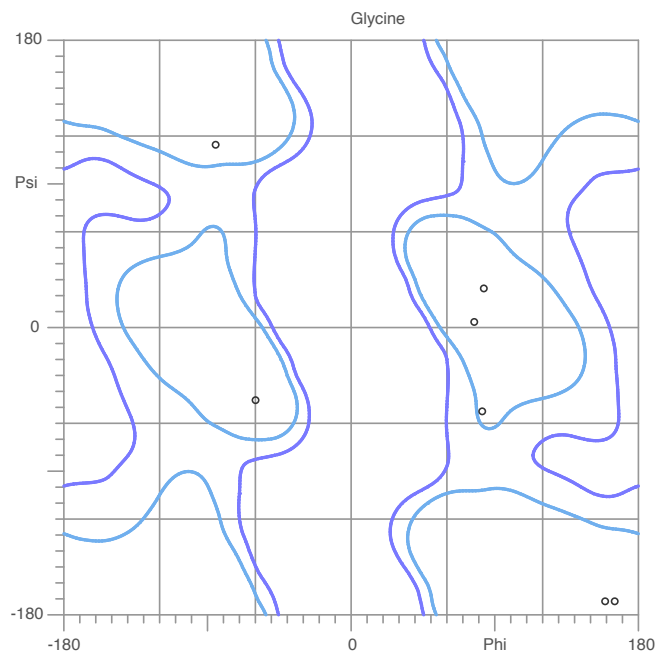
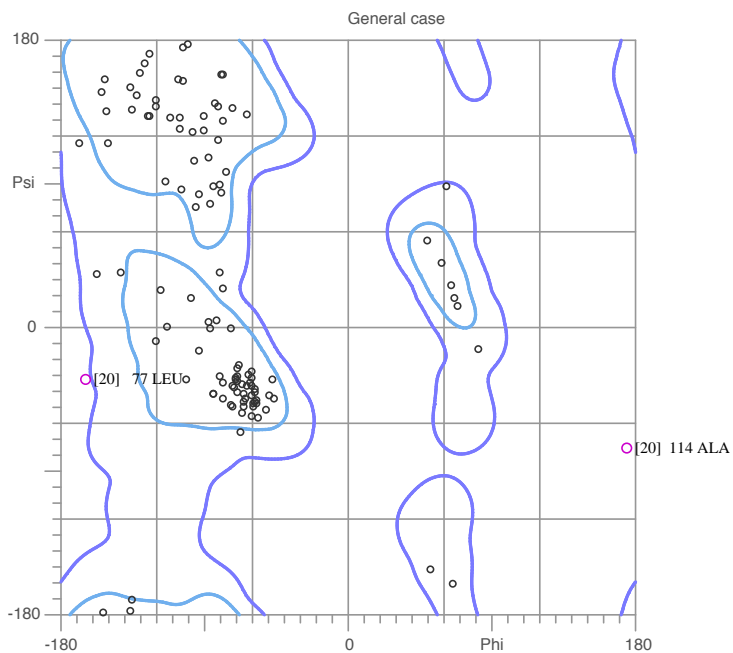
[19] 52 SER (71.5, -80.9)

[19] 92 PHE (73.3, 145.3)

[19] 114 ALA (164.0, -28.7)

# MolProbity Ramachandran analysis

STR70\_NMR\_em\_bcr3.pdb, model 20



87.9% (123/140) of all residues were in favored (98%) regions.  
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[20] 5 THR (65.8, 157.7)  
[20] 54 ASN (75.2, 157.5)  
[20] 77 LEU (-165.7, -32.5)  
[20] 111 HIS (73.0, 145.4)  
[20] 114 ALA (174.6, -75.6)