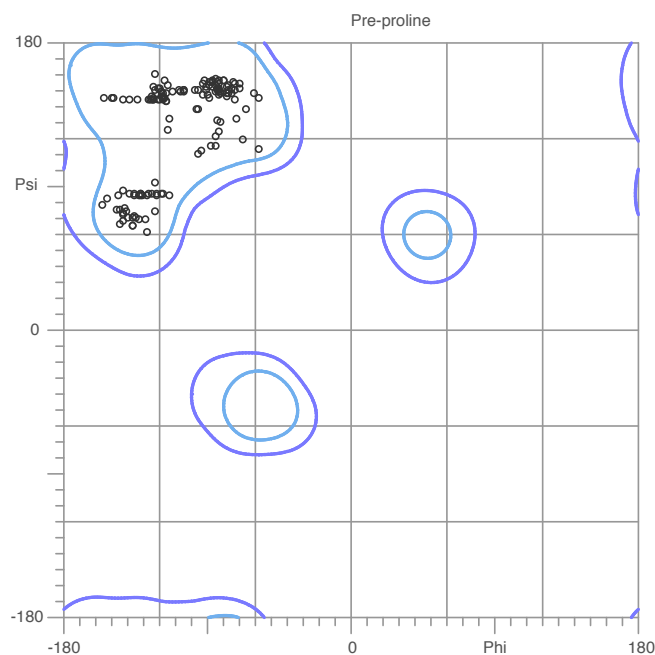
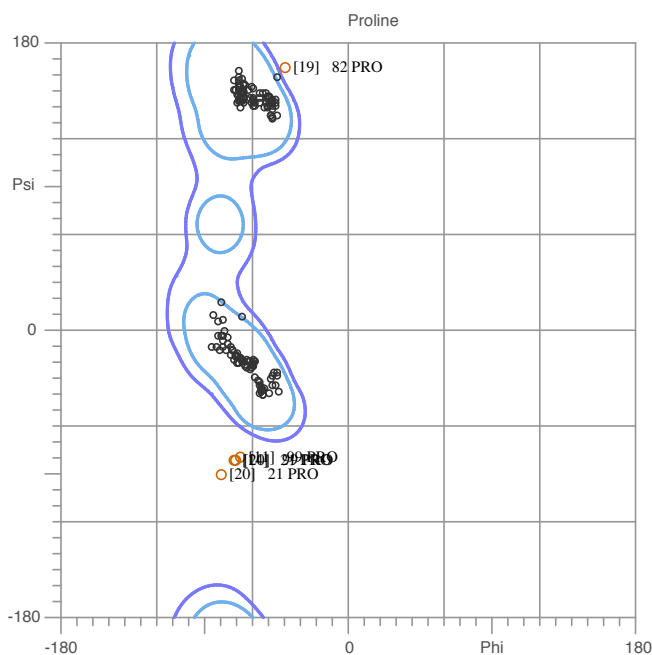
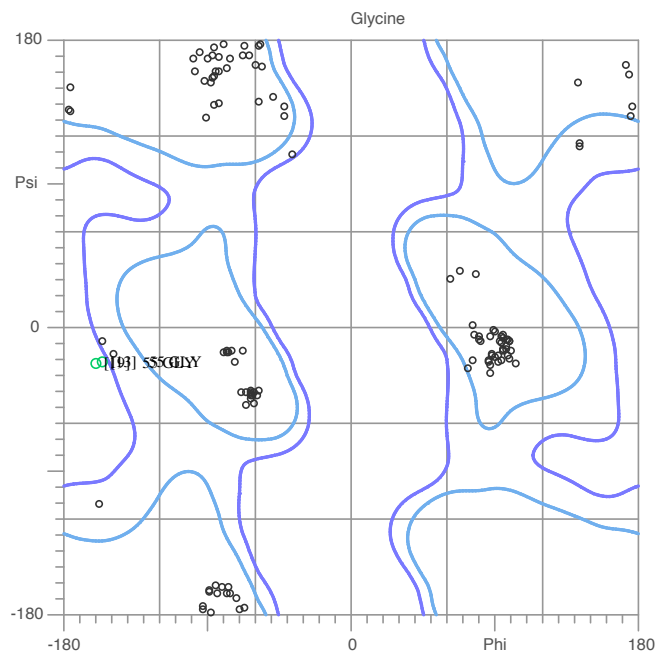
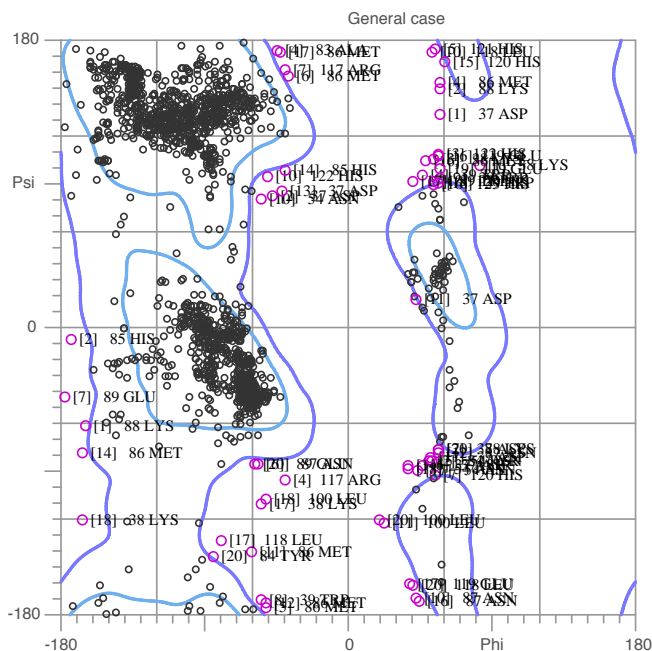


MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, all models



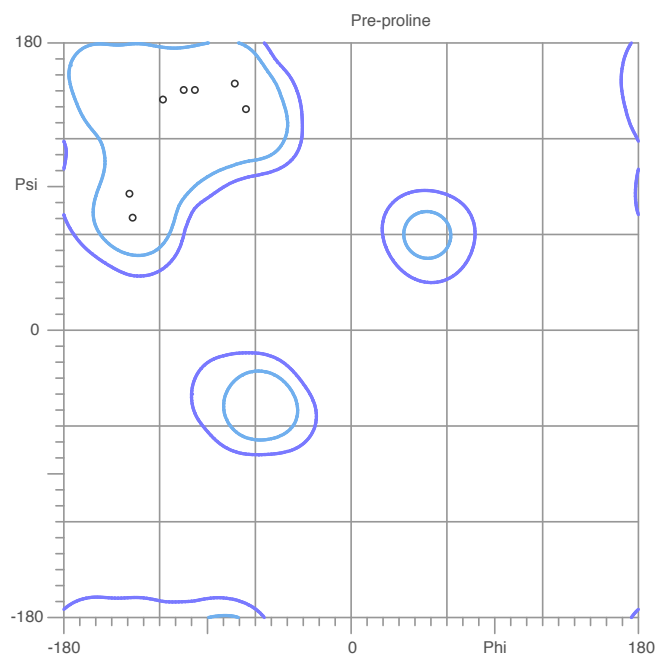
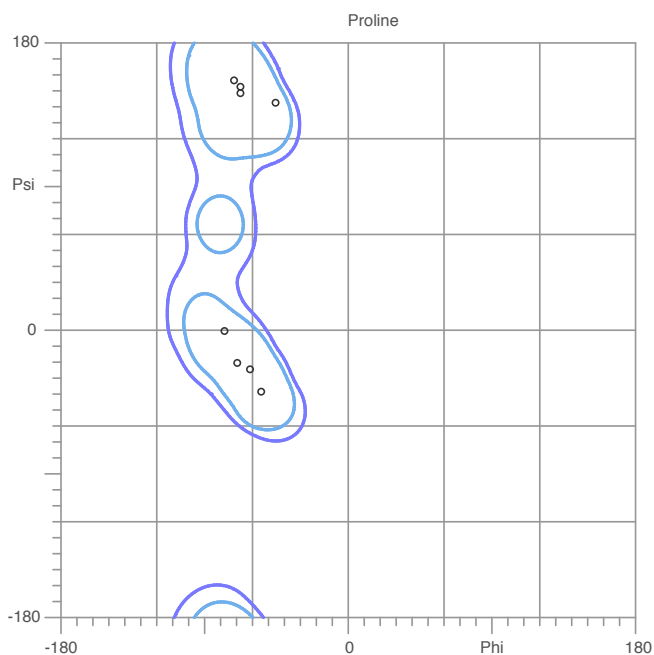
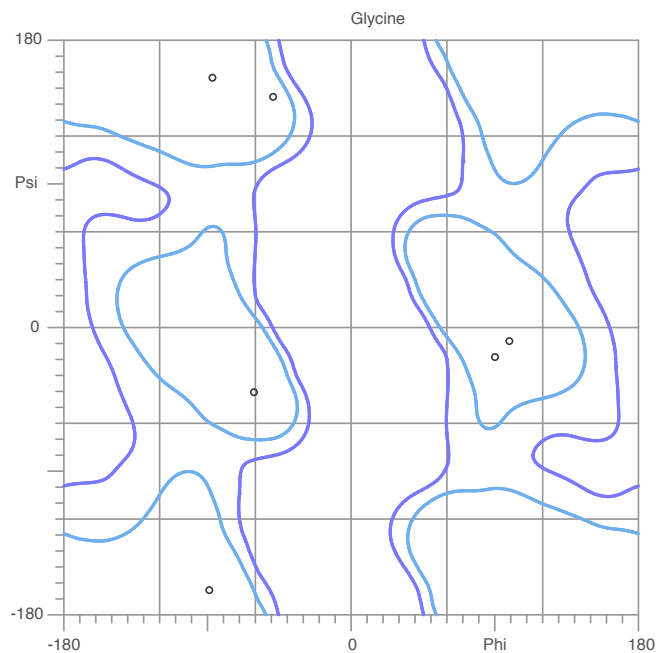
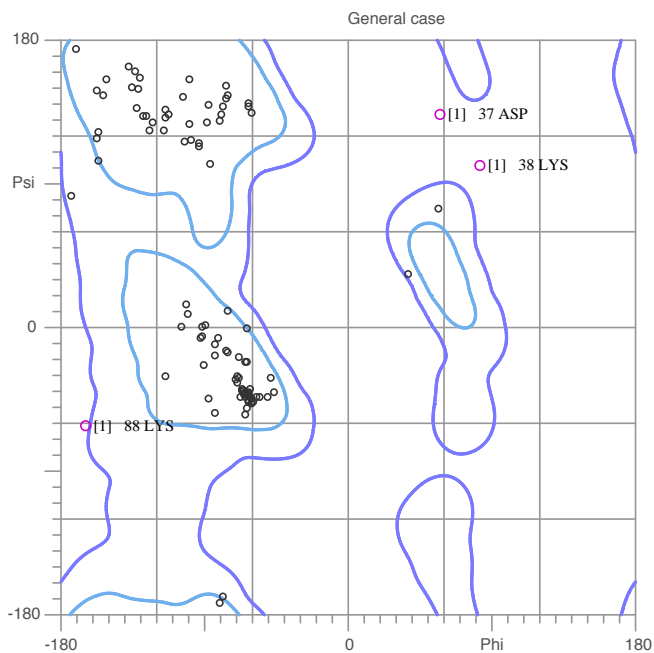
92.4% (2274/2460) of all residues were in favored (98%) regions.
97.2% (2392/2460) of all residues were in allowed (100%) regions.

There were 68 outliers (phi, psi):

- | | |
|-----------------------------|-------------------------------|
| (1) 37 ASP (57.7, 134.9) | (111) 99 PRO (-68.0, 79.9) |
| (2) 88 LYS (82.4, 102.2) | (112) 86 MET (-52.1, -172.9) |
| (3) 88 LYS (-165.3, -61.1) | (113) 87 ASN (-56.3, -78.7) |
| (4) 37 ASP (-48.4, 83.5) | (114) 21 PRO (72.3, -81.1) |
| (5) 86 TYR (55.8, -83.5) | (115) 37 ASP (37.2, -86.9) |
| (6) 85 HIS (-178.8, -7.7) | (116) 85 HIS (-40.8, 99.6) |
| (7) 88 LYS (57.9, 150.1) | (117) 86 MET (-167.7, -78.2) |
| (8) 88 LYS (53.2, 106.3) | (118) 120 HIS (60.3, 167.1) |
| (9) 122 HIS (56.3, 109.2) | (119) 86 MET (48.6, 105.7) |
| (10) 39 TRP (46.5, 96.3) | (120) 87 ASN (44.8, -171.3) |
| (11) 83 ALA (-66.8, 174.2) | (121) 119 GLY (56.9, 108.7) |
| (12) 86 MET (76.6, 154.1) | (122) 85 HIS (53.2, 90.7) |
| (13) 117 ARG (-40.8, -69.6) | (123) 37 ASP (51.3, -81.4) |
| (14) 54 ASN (52.8, -83.1) | (124) 38 LYS (55.8, -110.1) |
| (15) 86 MET (-5.8, -175.3) | (125) 39 TRP (40.8, 92.1) |
| (16) 121 HIS (54.5, 175.4) | (126) 54 ASN (43.8, -89.2) |
| (17) 37 ASP (46.7, -86.2) | (127) 86 MET (-43.7, 173.5) |
| (18) 86 MET (3.1, 139.9) | (128) 118 LEU (80.8, -133.5) |
| (19) 89 GLU (-57.8, -85.1) | (129) 119 GLY (58.6, -100.7) |
| (20) 37 ASP (56.7, -76.8) | (130) 38 LYS (-167.7, -120.1) |
| (21) 89 GLU (-178.8, -43.4) | (131) 39 TRP (56.2, 91.6) |
| (22) 117 ARG (-40.2, 162.1) | (132) 54 ASN (37.2, -88.9) |
| (23) 120 HIS (54.5, -92.7) | (133) 100 LEU (-52.6, -108.8) |
| (24) 39 TRP (-55.6, -170.5) | (134) 55 GLY (-160.1, -22.8) |
| (25) 39 TRP (57.2, -26.0) | (135) 82 PRO (-40.6, 163.2) |
| (26) 54 ASN (-55.9, 81.8) | (136) 119 GLY (57.2, 100.6) |
| (27) 87 ASN (-42.3, -109.9) | (137) 21 PRO (80.2, -90.2) |
| (28) 118 LEU (52.7, 173.7) | (138) 84 TYR (-85.1, -143.0) |
| (29) 120 HIS (53.3, 92.4) | (139) 88 LYS (56.9, -76.7) |
| (30) 122 HIS (53.5, 96.8) | (140) 99 PRO (-71.8, -81.2) |
| (31) 37 ASP (-27.7, 18.1) | (141) 103 LEU (19.2, -120.7) |
| (32) 86 MET (-61.6, -149.9) | (142) 118 LEU (40.0, -161.6) |

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 1



93.5% (115/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

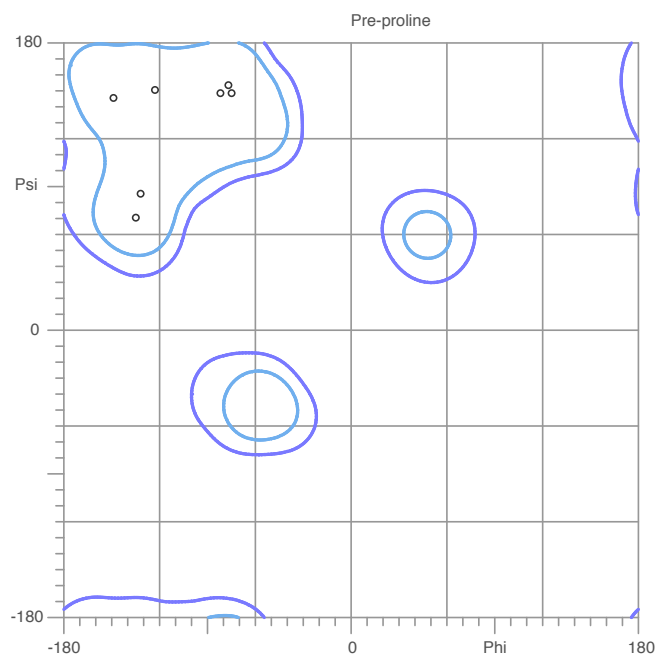
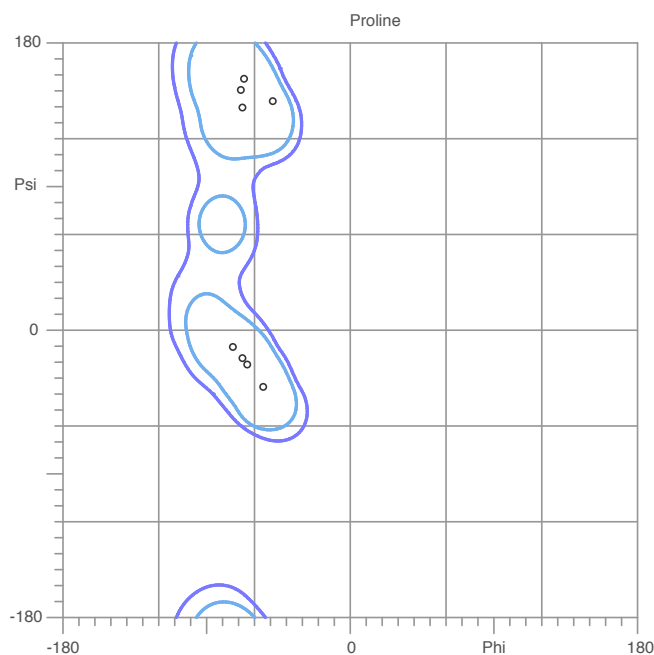
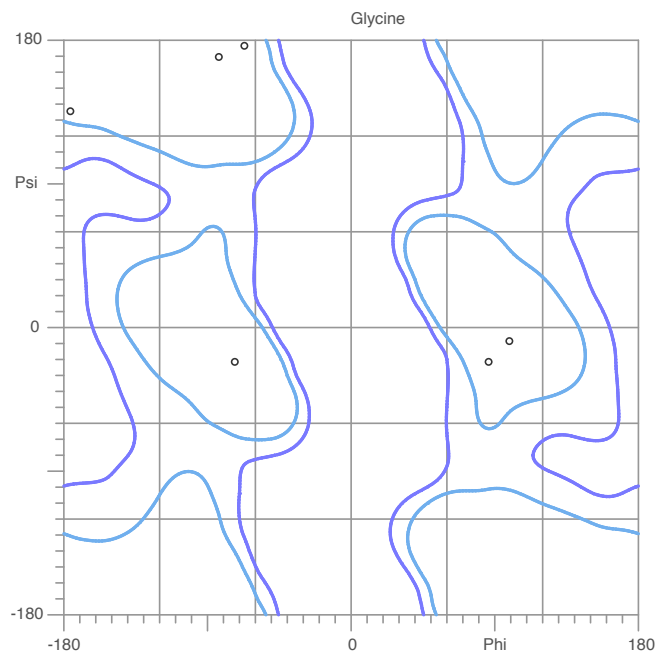
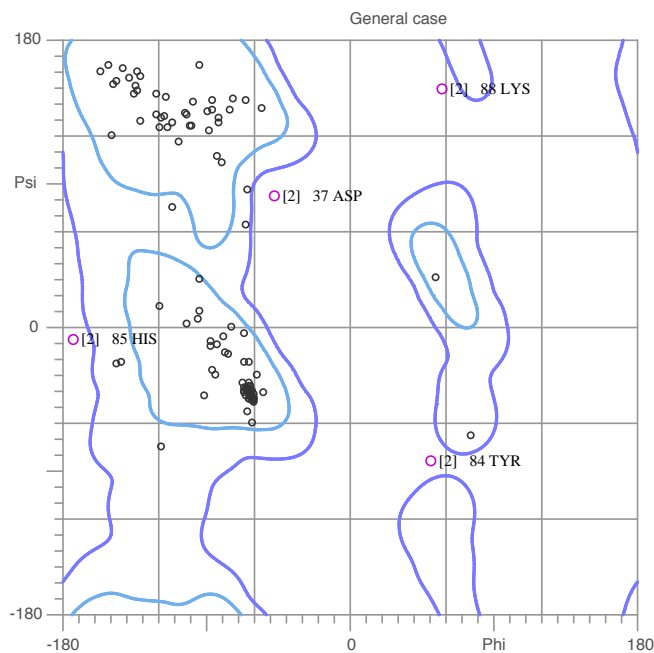
[1] 37 ASP (57.7, 134.9)

[1] 38 LYS (82.4, 102.2)

[1] 88 LYS (-165.3, -61.1)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 2



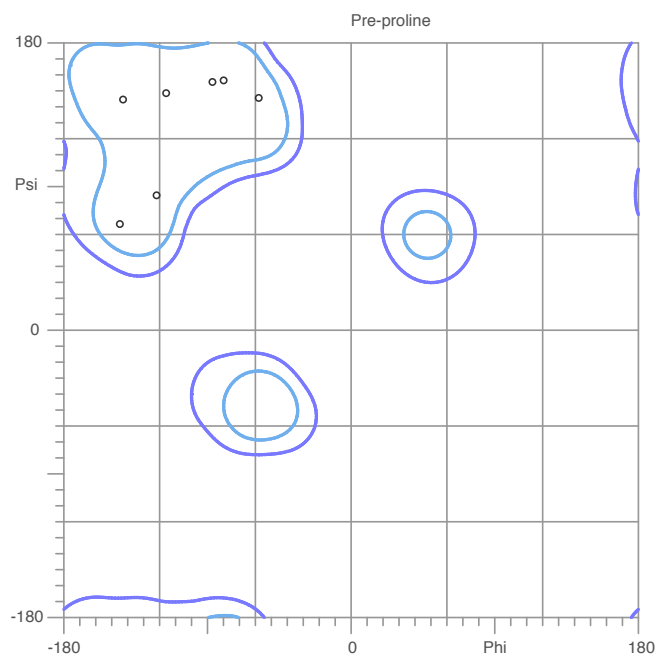
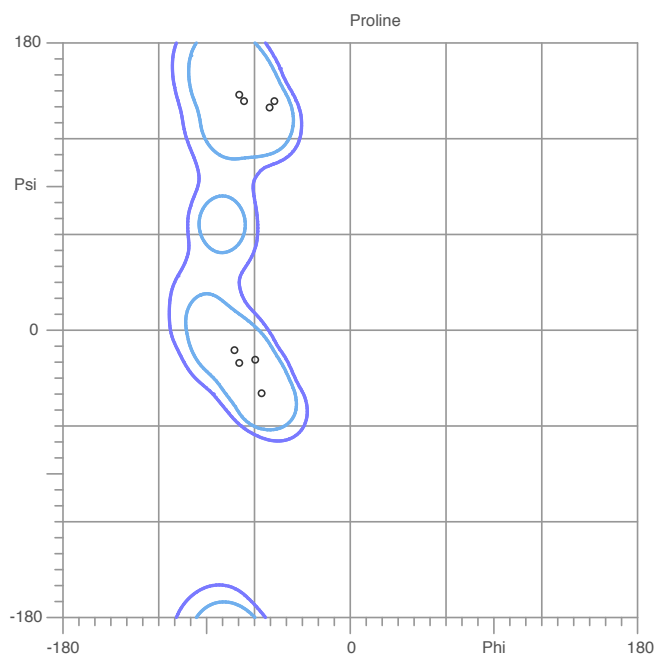
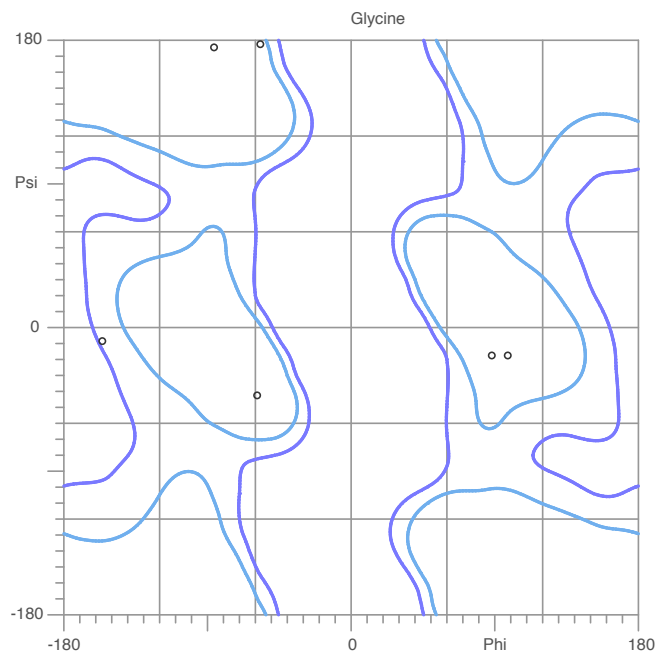
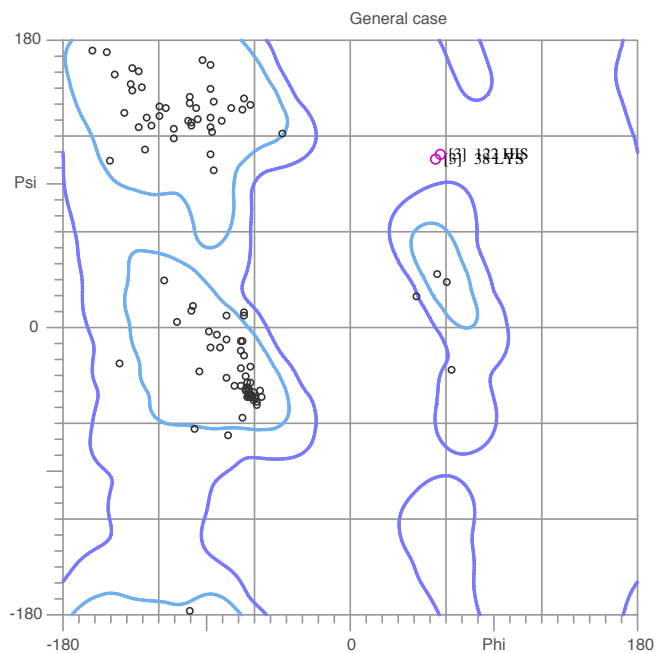
91.1% (112/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [2] 37 ASP (-48.4, 83.5)
- [2] 84 TYR (50.8, -83.5)
- [2] 85 HIS (-175.0, -7.7)
- [2] 88 LYS (57.9, 150.1)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 3



91.9% (113/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

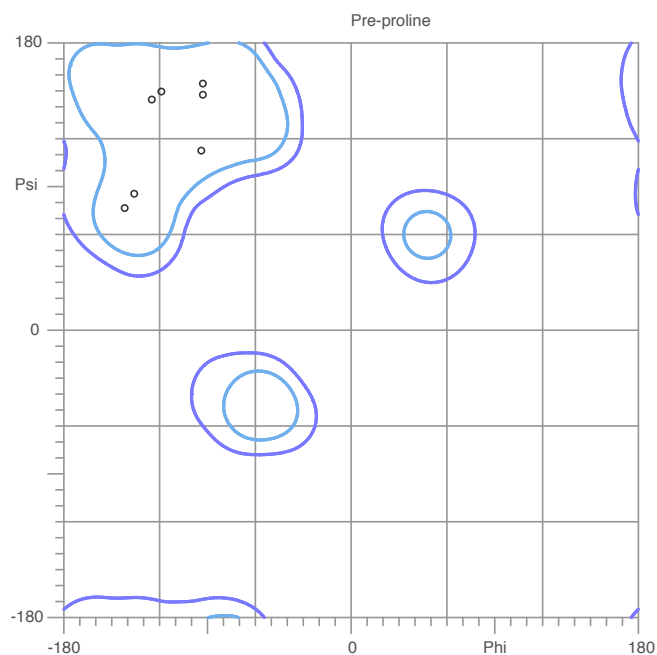
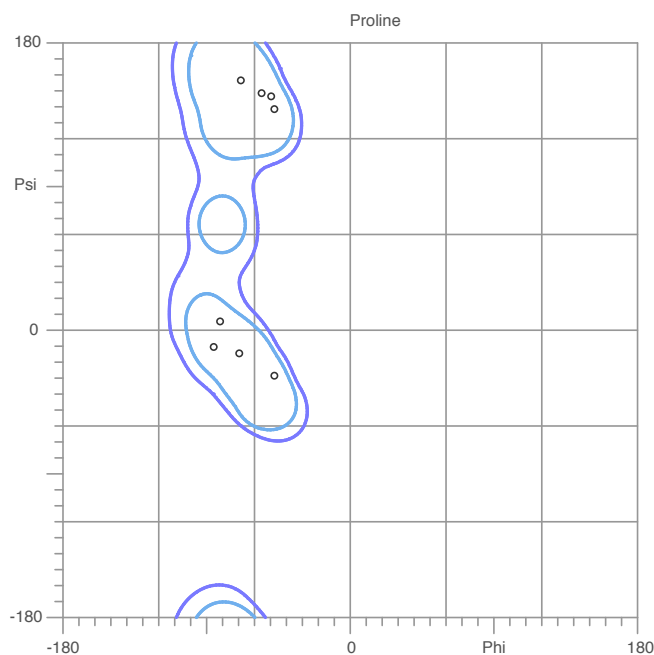
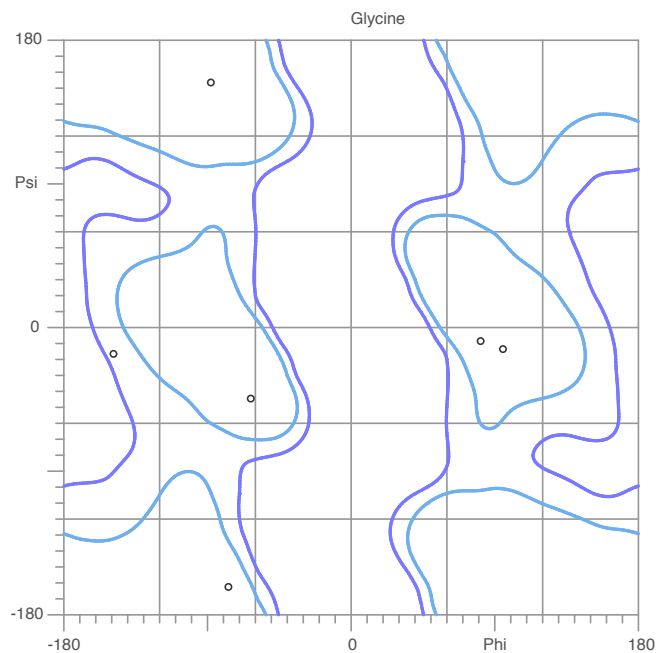
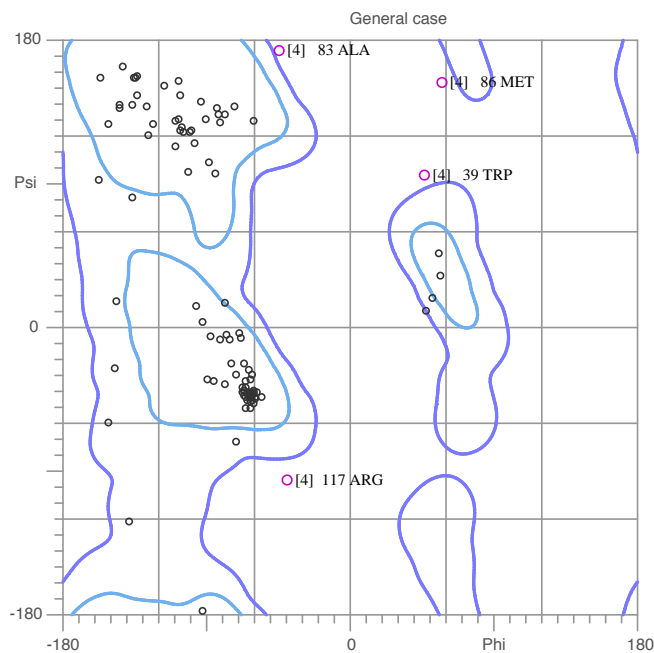
There were 2 outliers (phi, psi):

[3] 38 LYS (53.2, 106.1)

[3] 122 HIS (56.3, 109.2)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 4



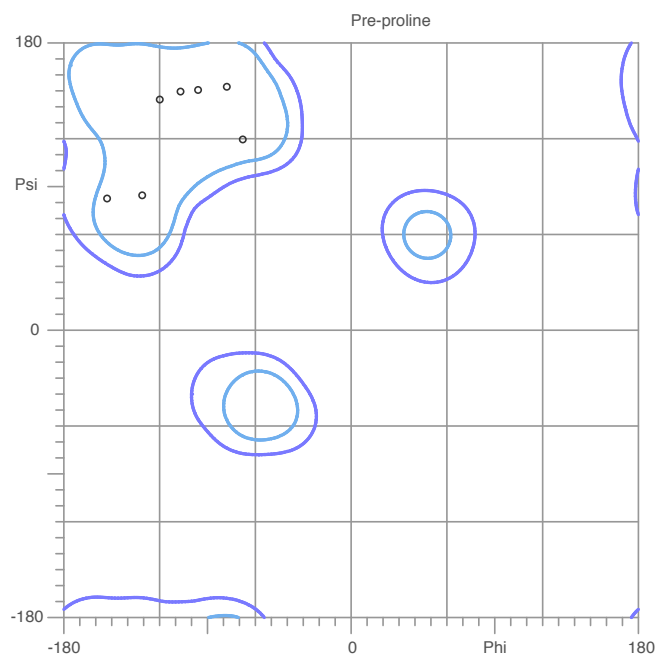
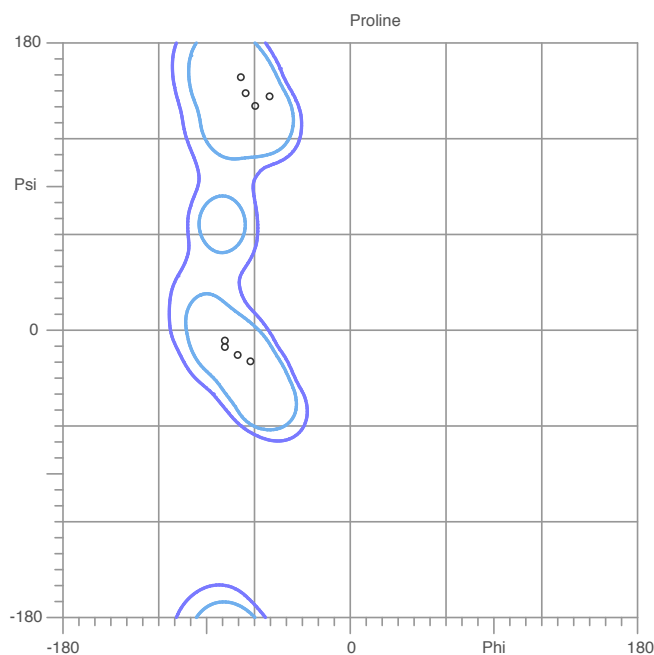
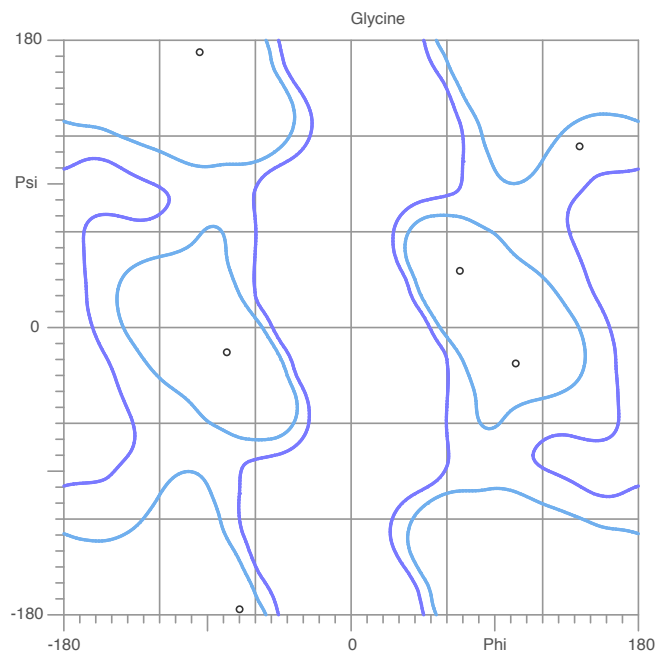
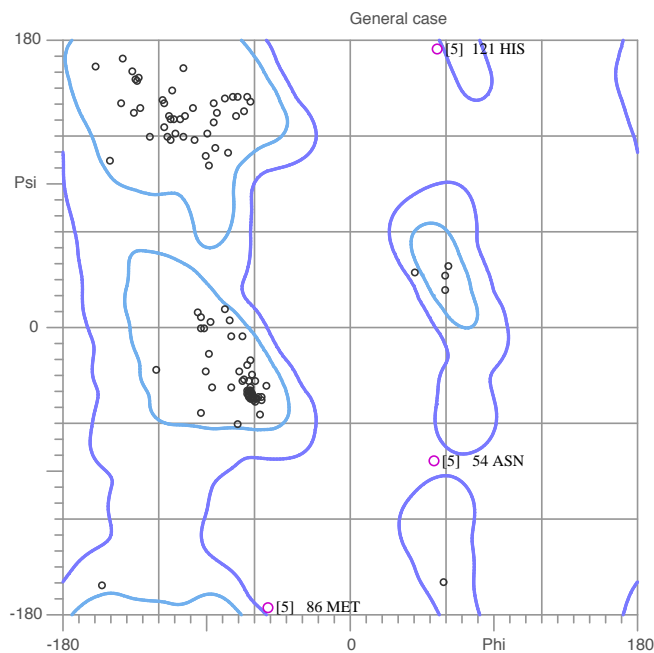
87.8% (108/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [4] 39 TRP (46.5, 96.2)
- [4] 83 ALA (-46.0, 174.2)
- [4] 86 MET (57.6, 154.1)
- [4] 117 ARG (-40.8, -95.6)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 5



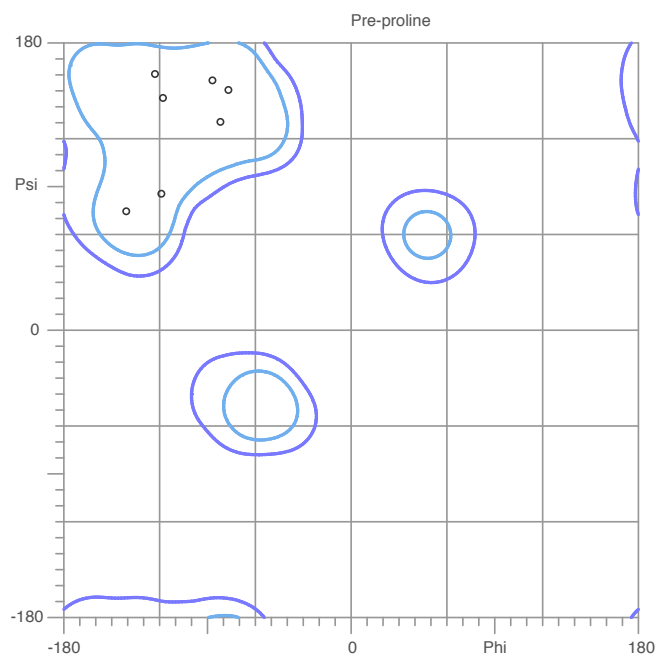
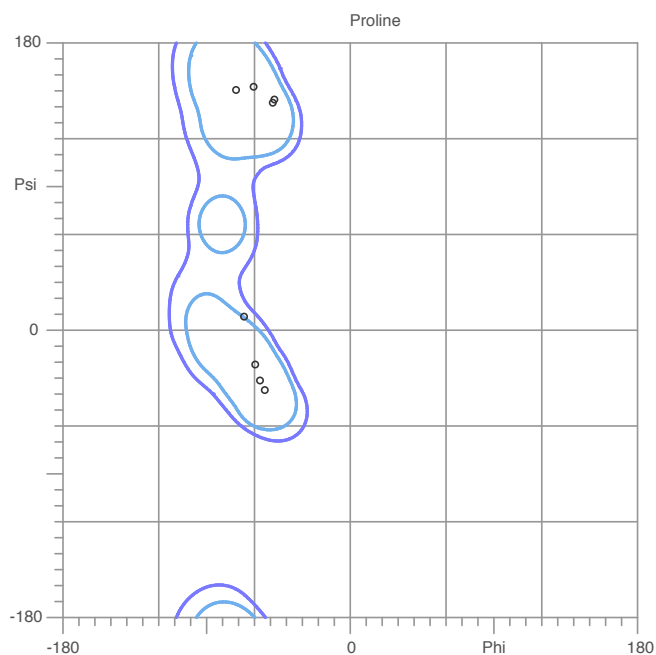
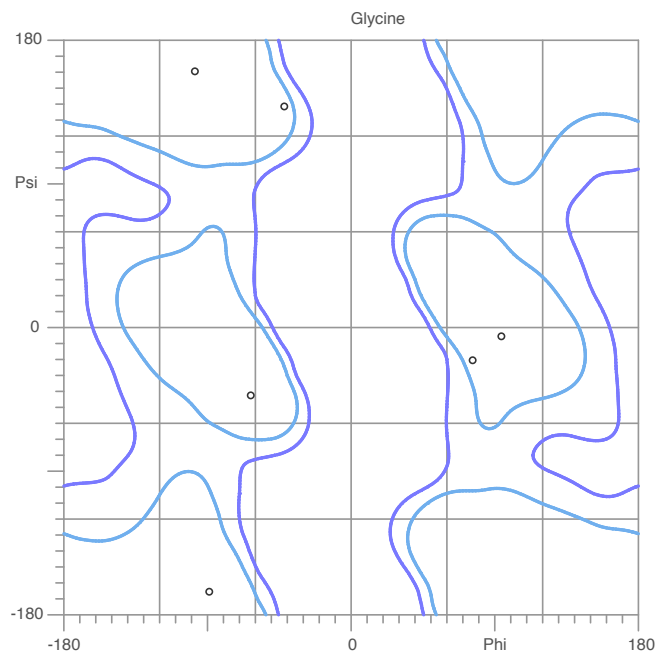
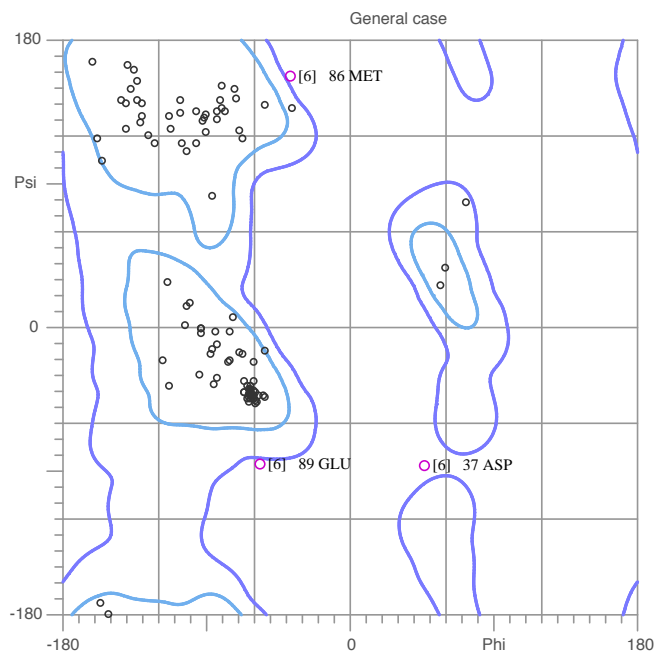
94.3% (116/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [5] 54 ASN (52.8, -83.1)
- [5] 86 MET (-52.8, -175.3)
- [5] 121 HIS (54.5, 175.4)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 6



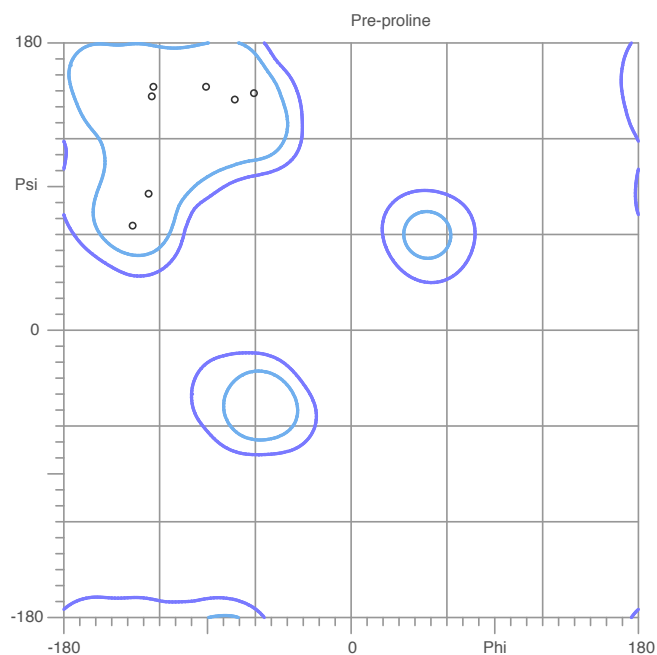
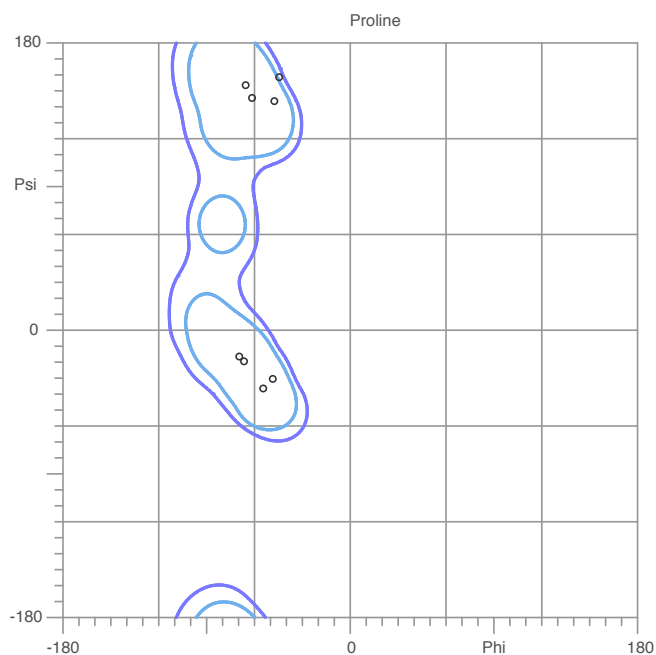
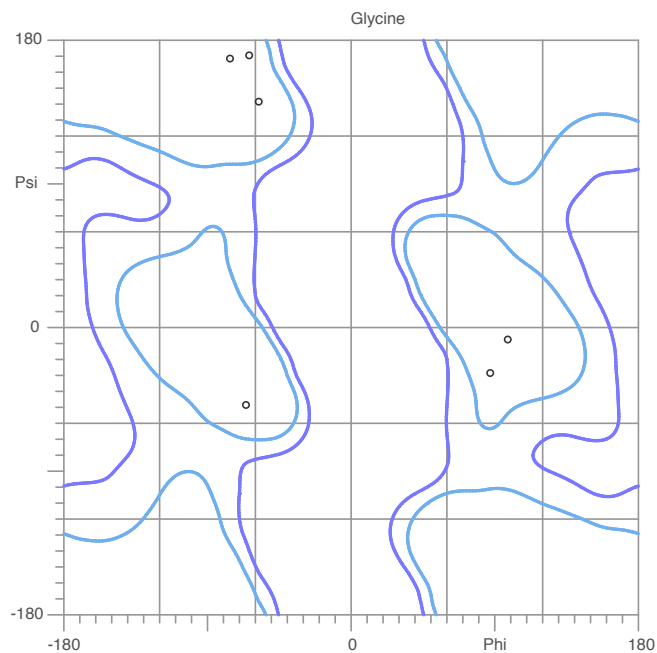
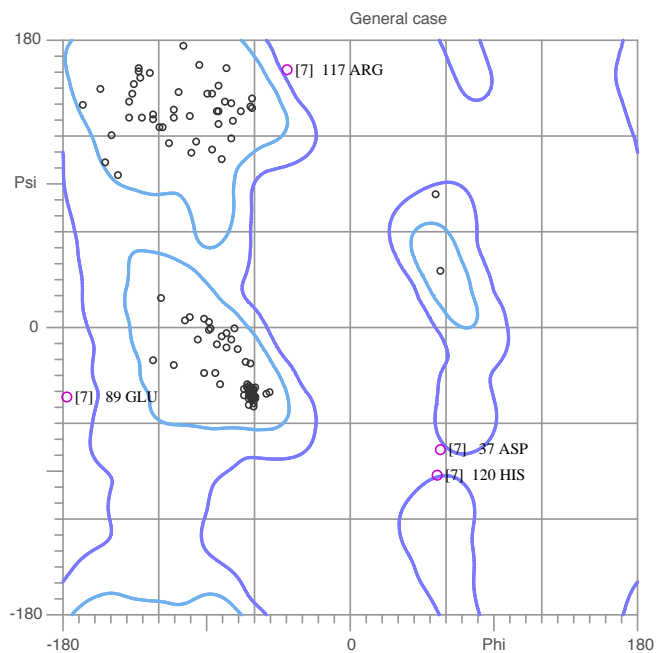
94.3% (116/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 37 ASP (46.7, -86.2)
- [6] 86 MET (-38.1, 158.9)
- [6] 89 GLU (-57.8, -85.1)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 7



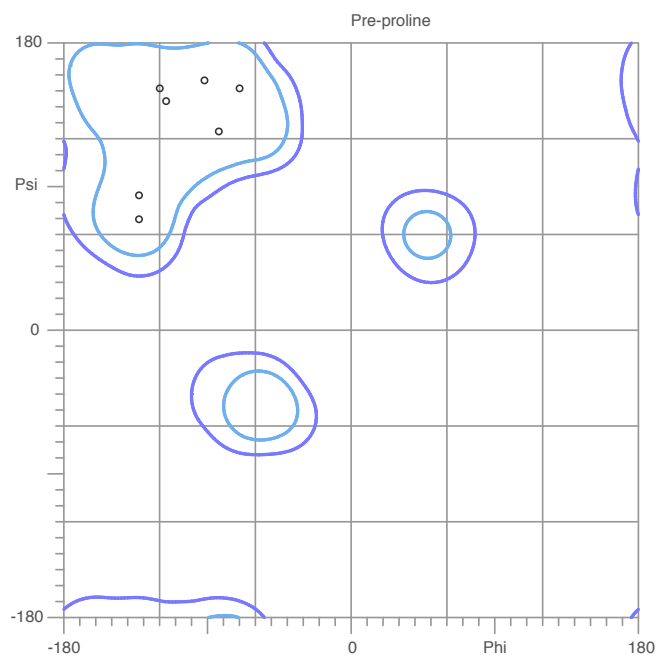
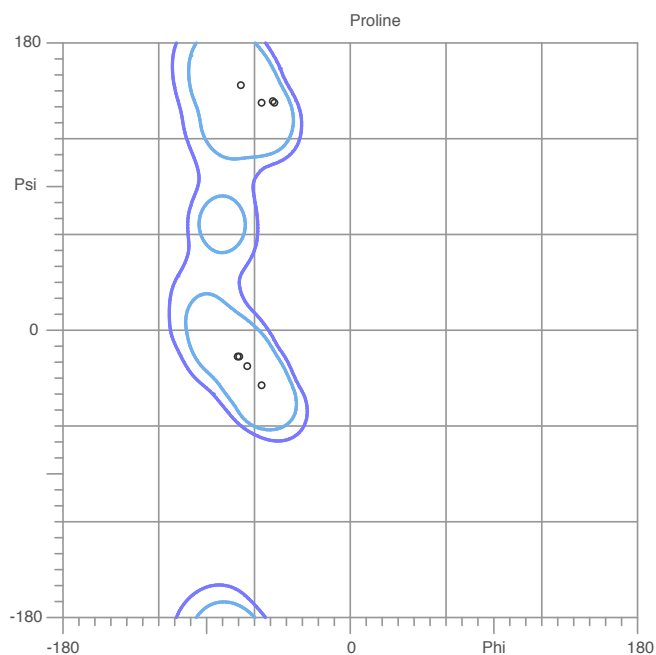
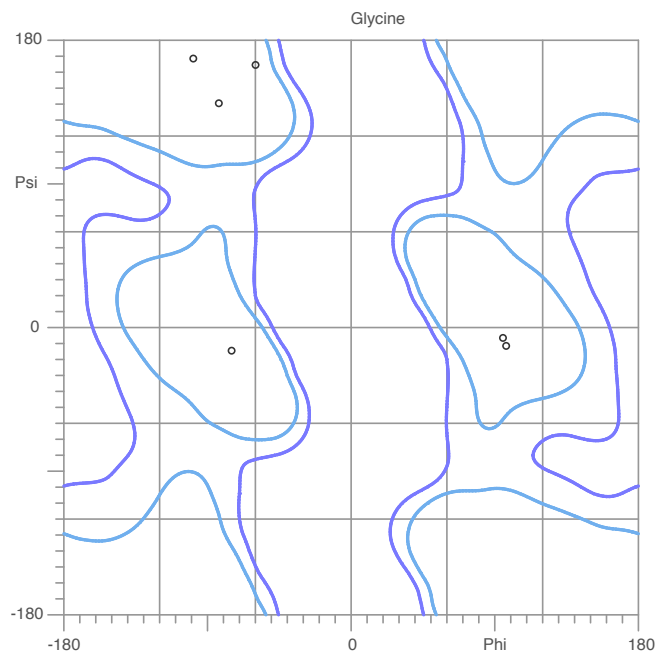
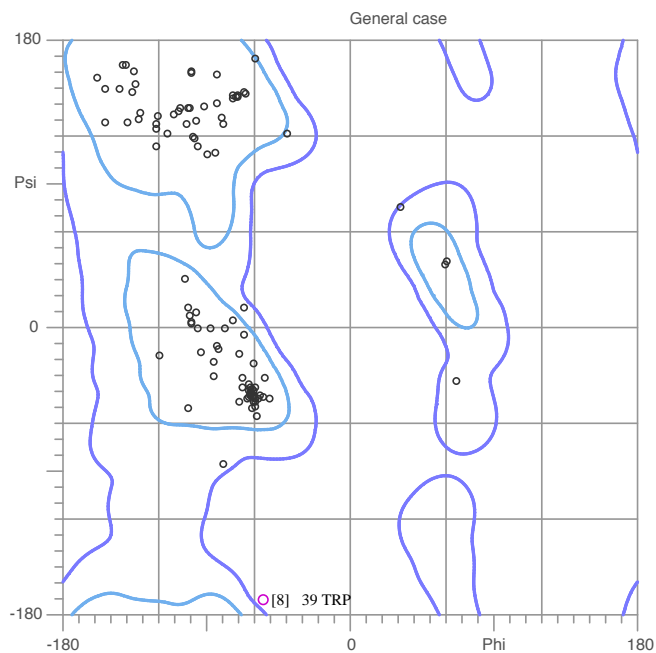
95.1% (117/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [7] 37 ASP (56.8, -76.8)
- [7] 89 GLU (-178.8, -43.4)
- [7] 117 ARG (-40.2, 162.1)
- [7] 120 HIS (54.3, -92.7)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 8

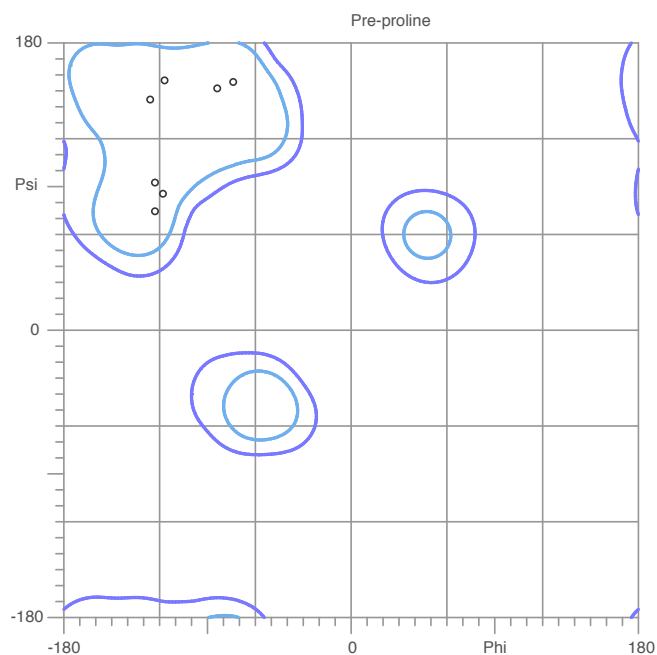
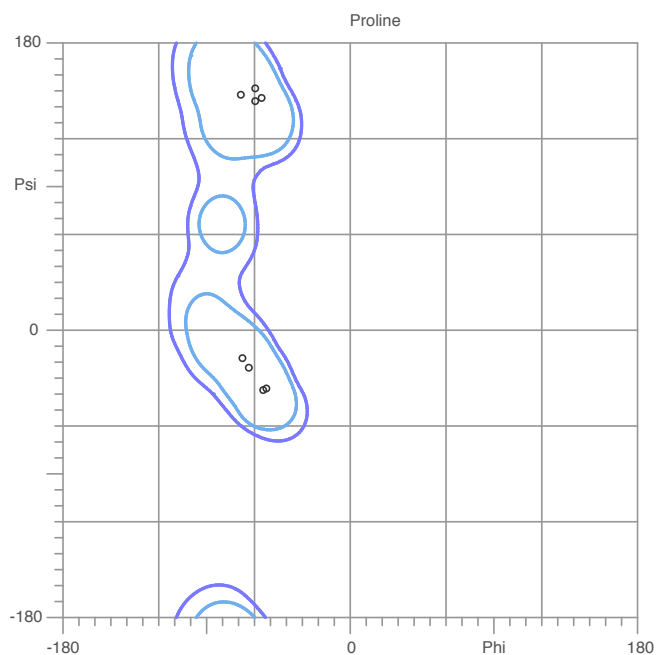
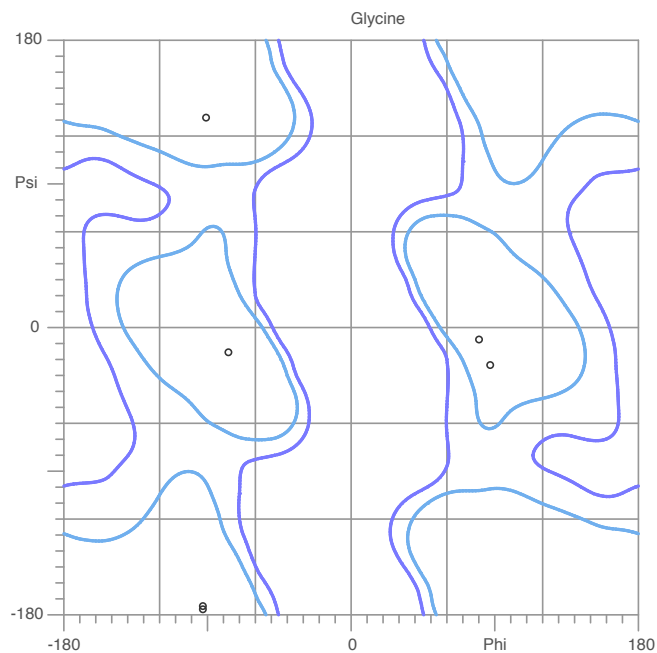
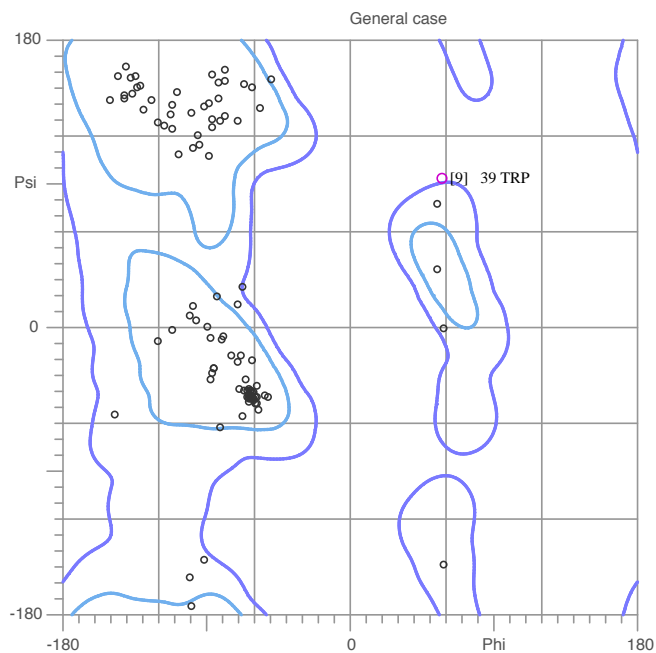


95.1% (117/123) of all residues were in favored (98%) regions.
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 39 TRP (-55.6, -170.5)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 9



91.9% (113/123) of all residues were in favored (98%) regions.
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

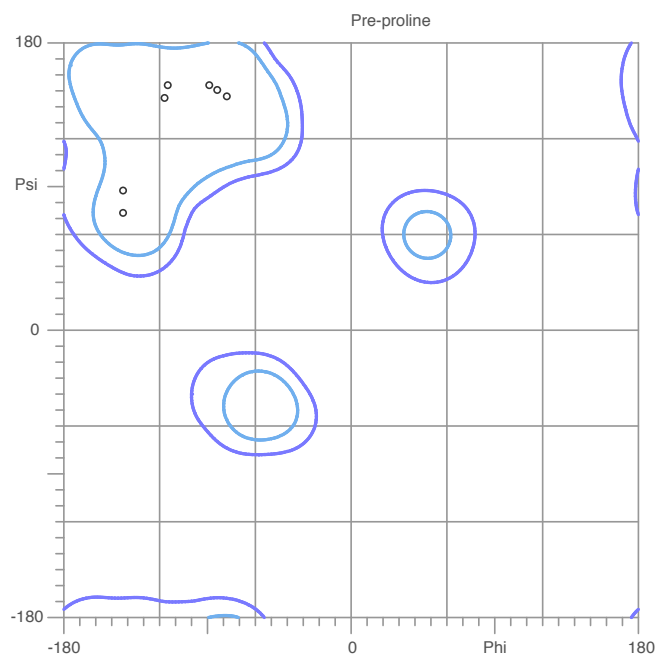
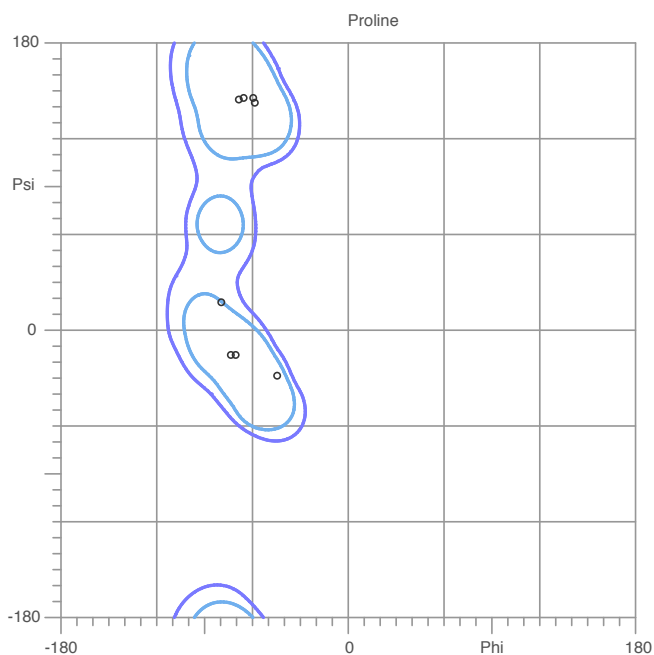
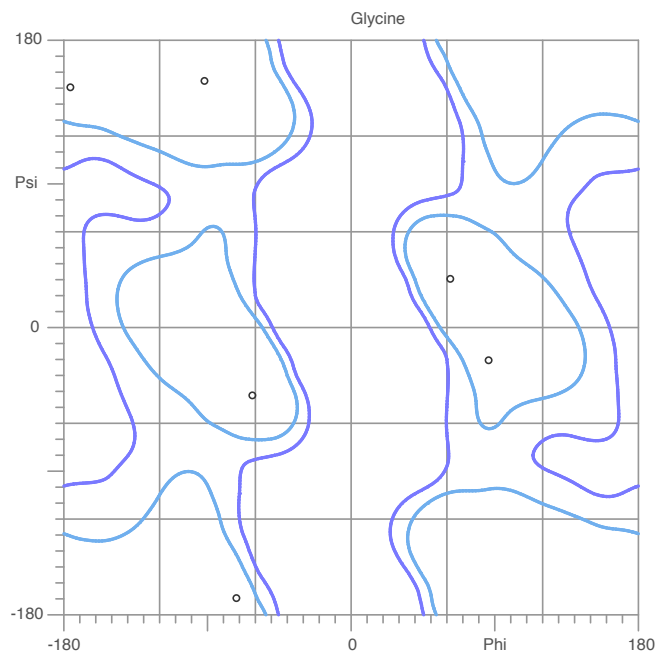
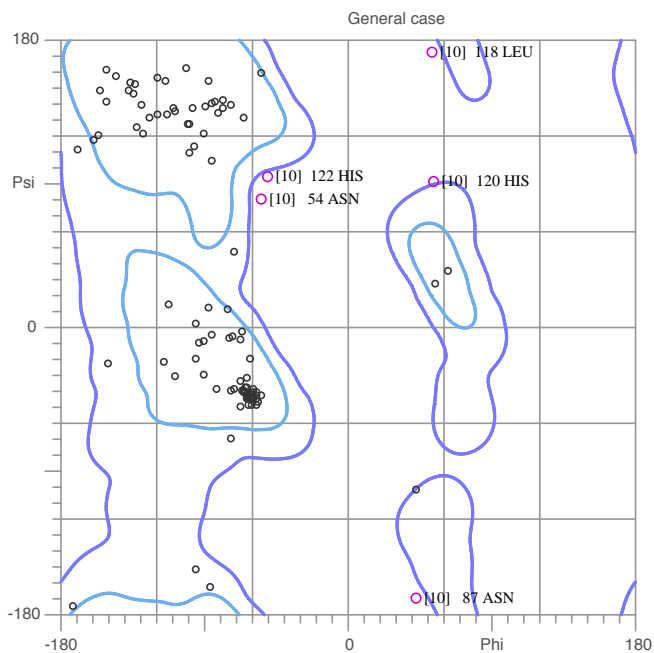
There were 1 outliers (phi, psi):
[9] 39 TRP (57.2, 95.0)

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

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

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 10



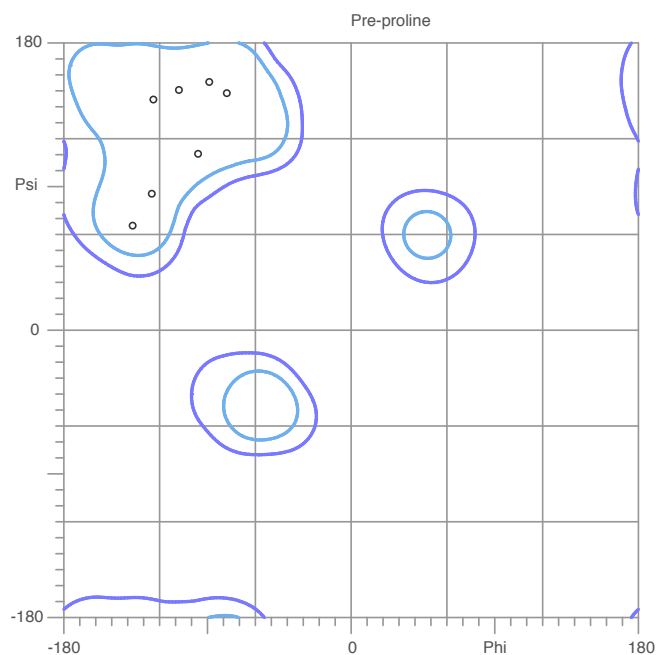
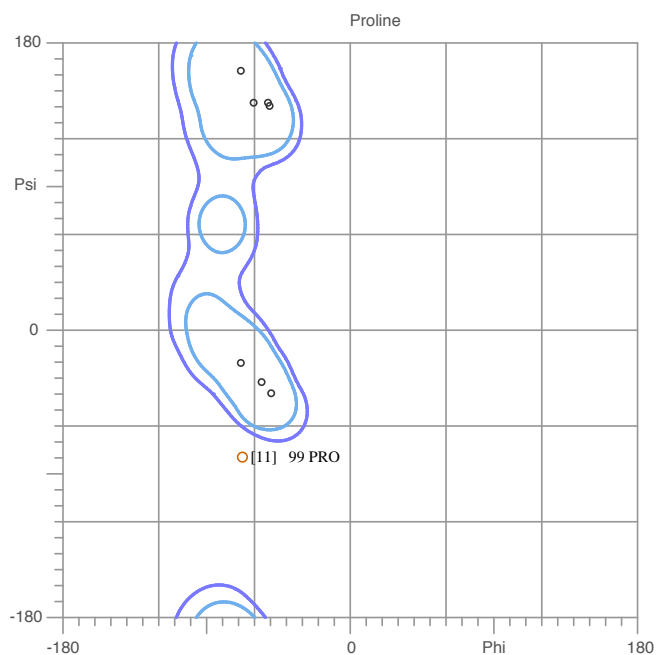
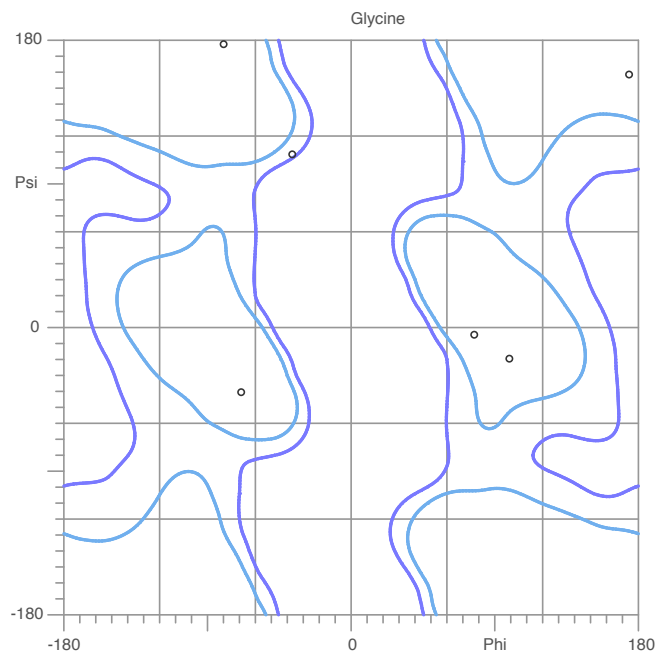
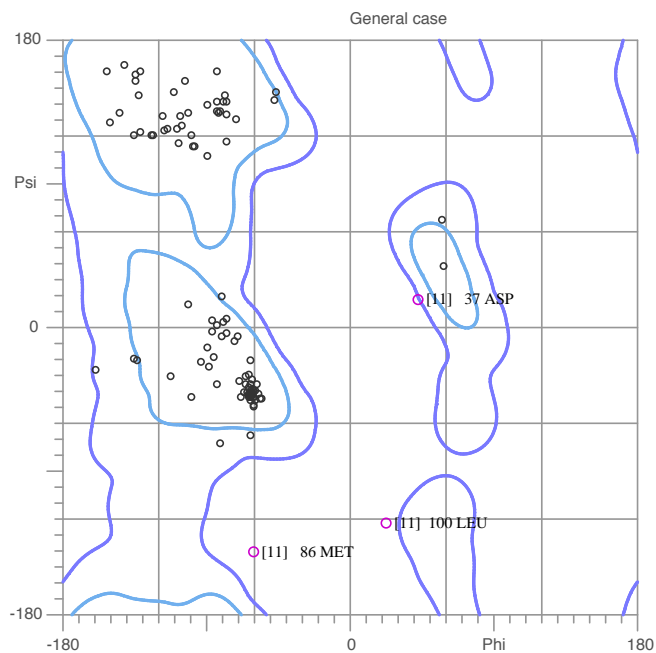
89.4% (110/123) of all residues were in favored (98%) regions.
95.9% (118/123) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[10] 54 ASN (-55.9, 81.8)
[10] 87 ASN (42.3, -169.9)
[10] 118 LEU (52.7, 173.7)
[10] 120 HIS (53.3, 92.4)
[10] 122 HIS (-51.5, 95.0)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 11



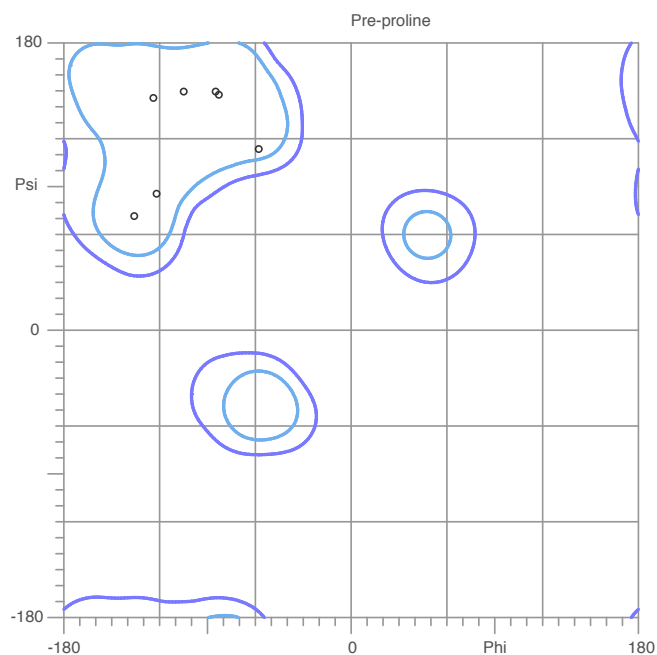
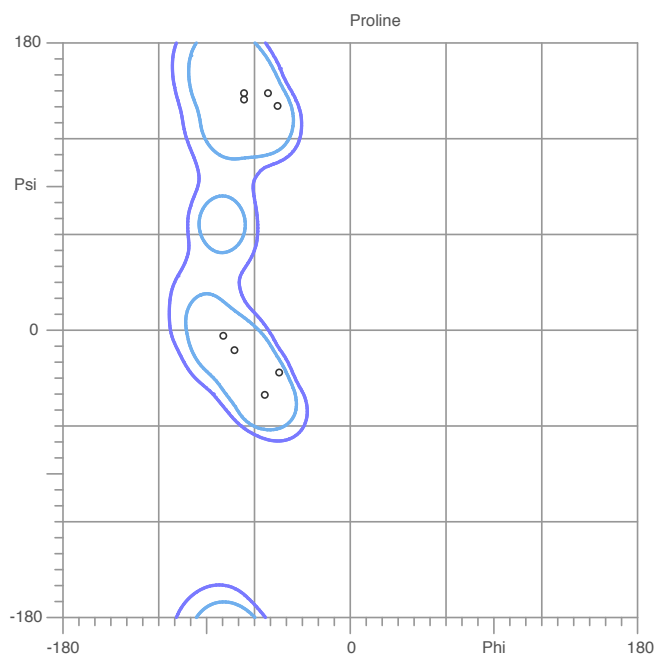
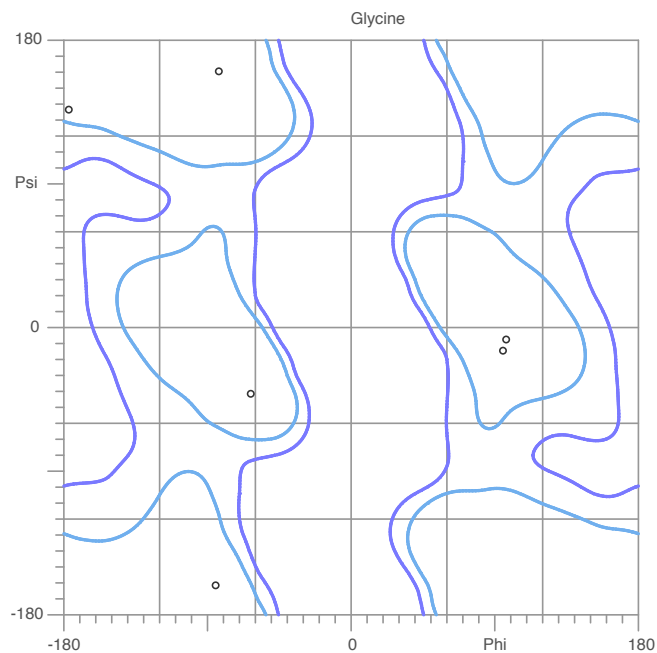
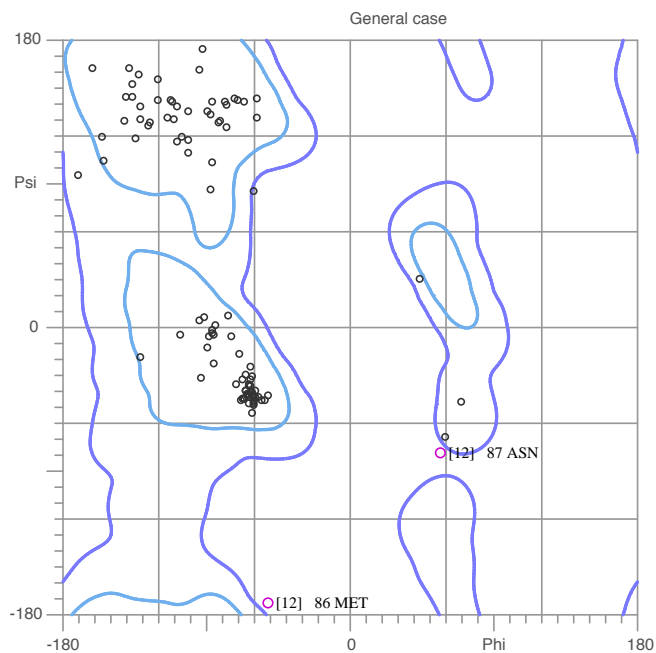
90.2% (111/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [11] 37 ASP (42.7, 18.1)
- [11] 86 MET (-61.6, -140.9)
- [11] 99 PRO (-68.0, -79.9)
- [11] 100 LEU (22.9, -122.0)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 12

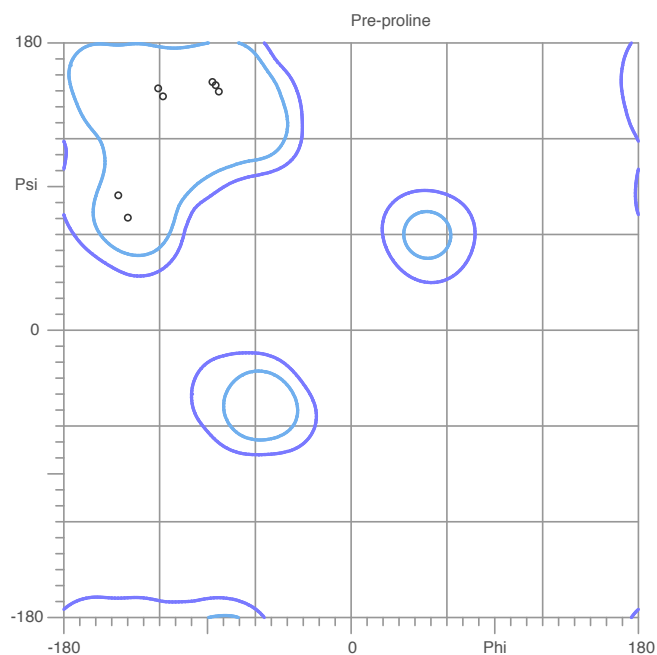
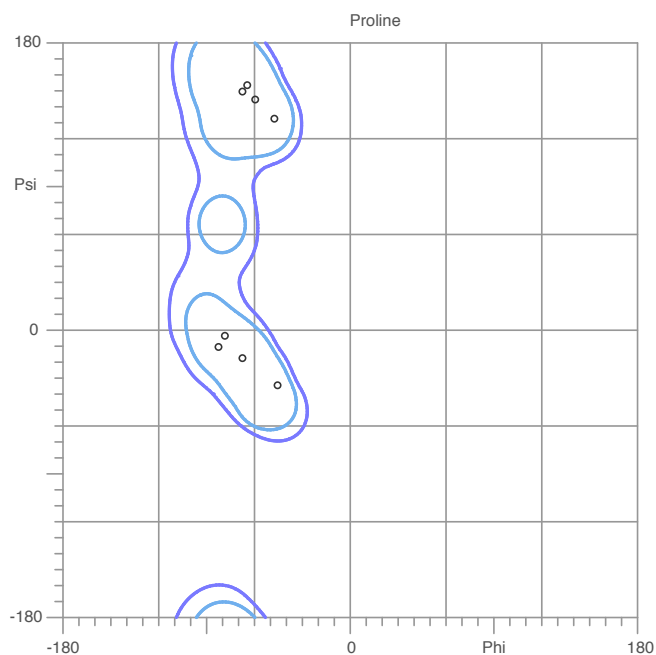
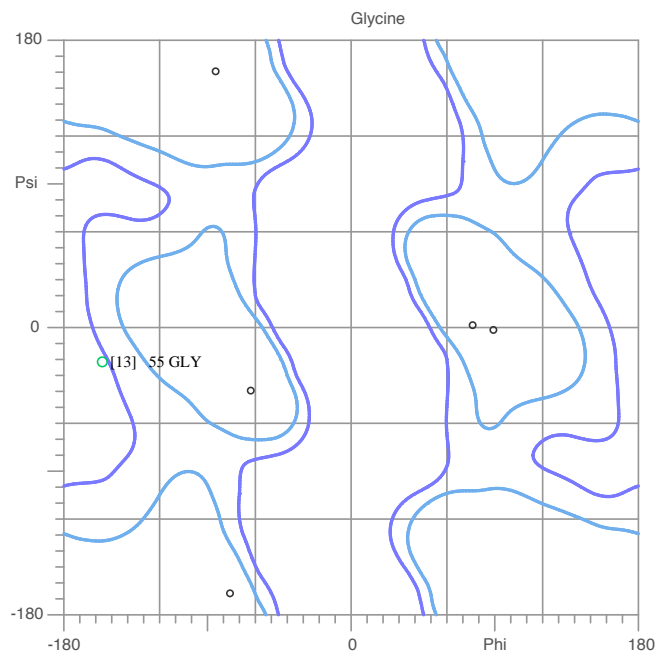
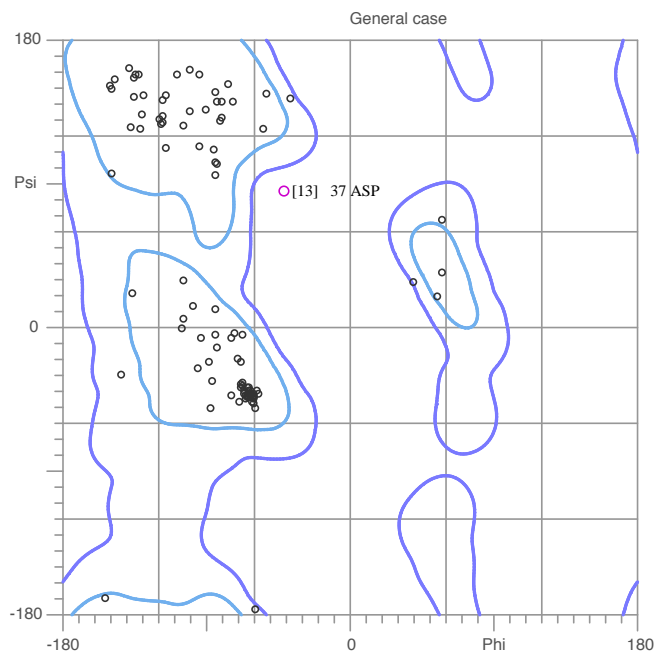


94.3% (116/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 86 MET (-52.1, -172.9)
[12] 87 ASN (56.3, -78.7)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 13

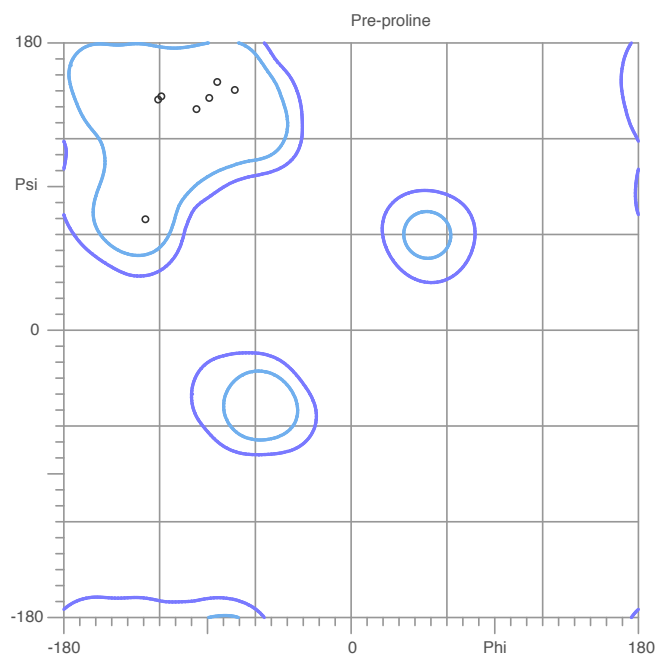
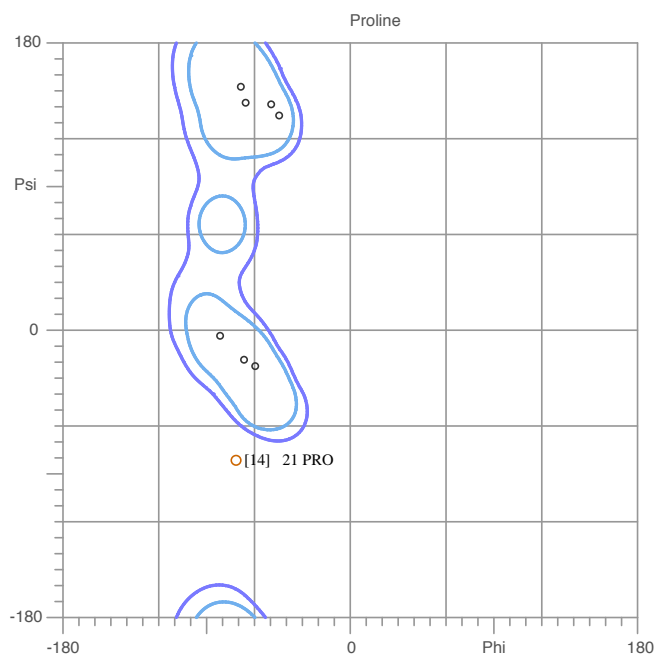
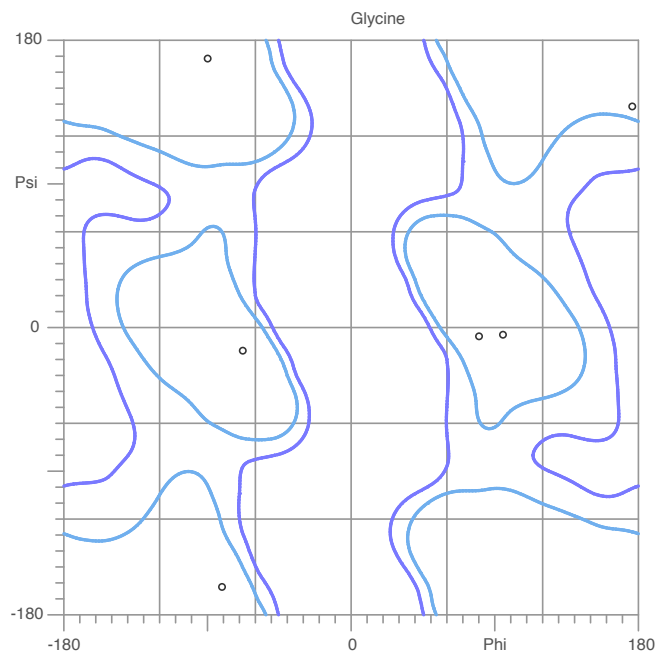
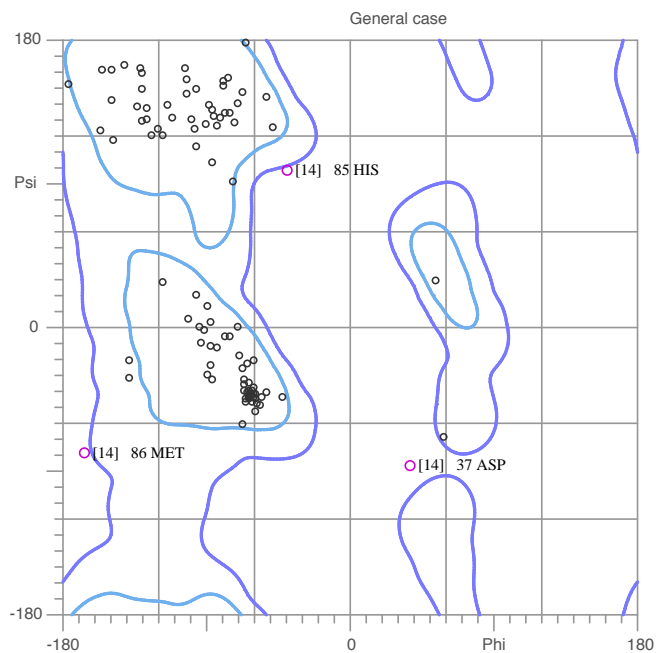


94.3% (116/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[13] 37 ASP (-42.5, 87.0)
[13] 55 GLY (-156.9, -21.9)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 14



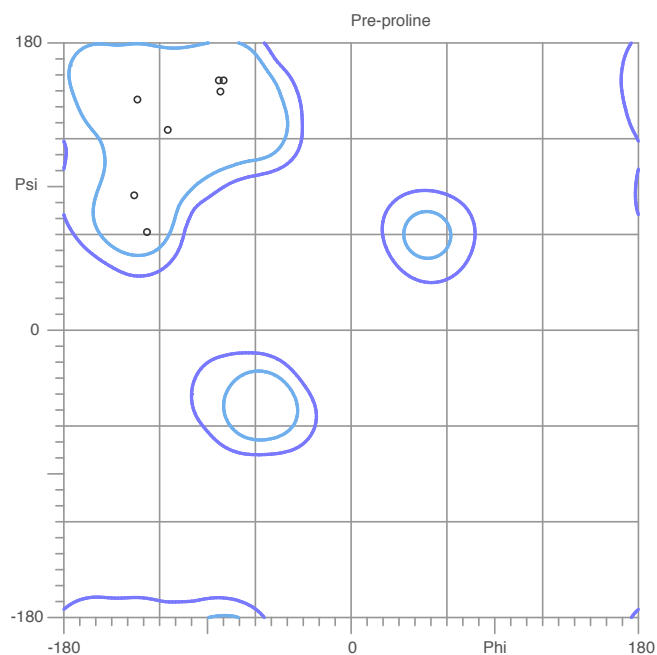
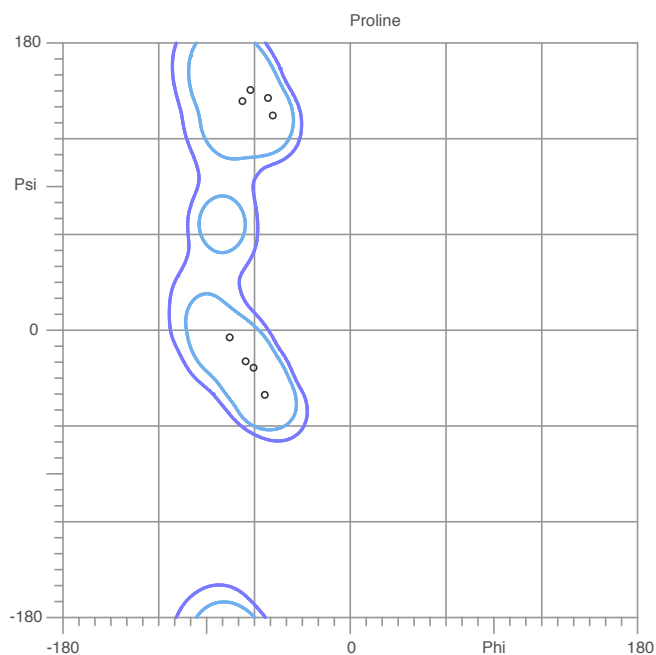
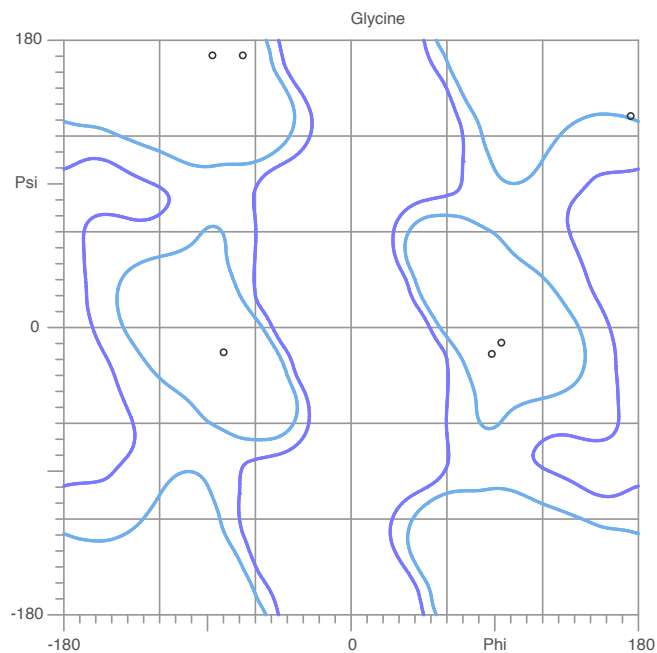
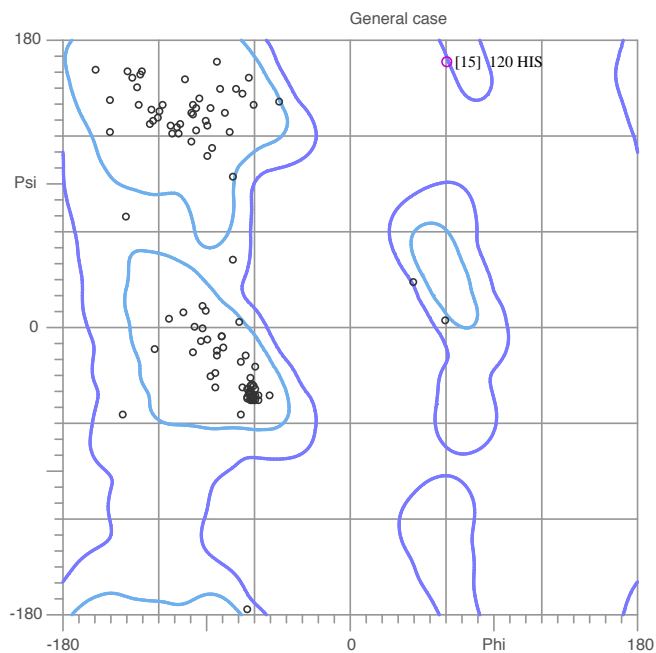
92.7% (114/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [14] 21 PRO (-72.3, -81.1)
- [14] 37 ASP (37.2, -86.9)
- [14] 85 HIS (-40.8, 99.4)
- [14] 86 MET (-167.7, -78.2)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 15



94.3% (116/123) of all residues were in favored (98%) regions.
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

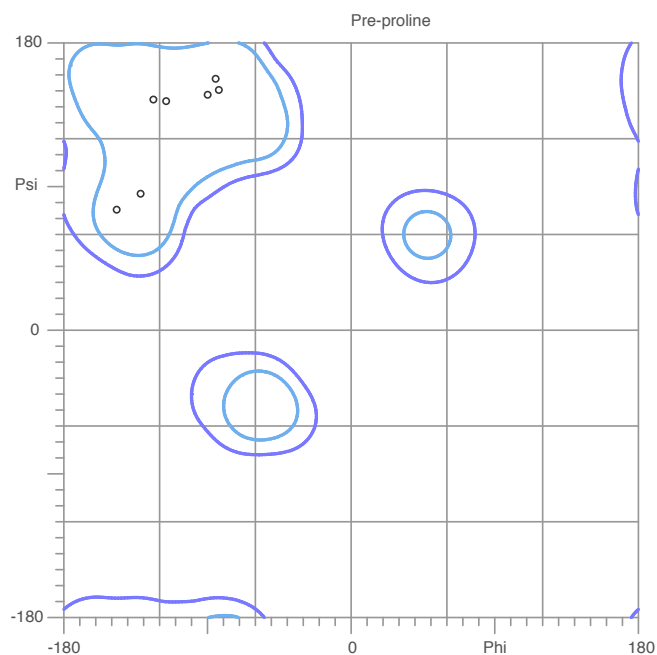
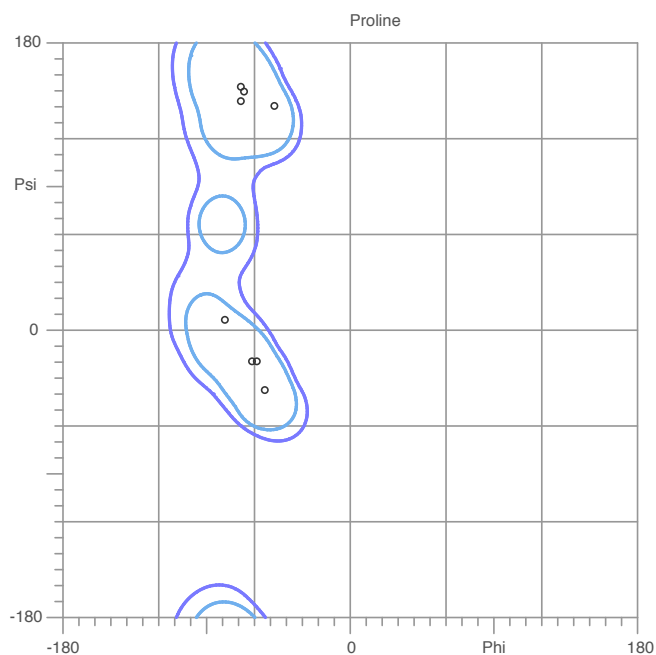
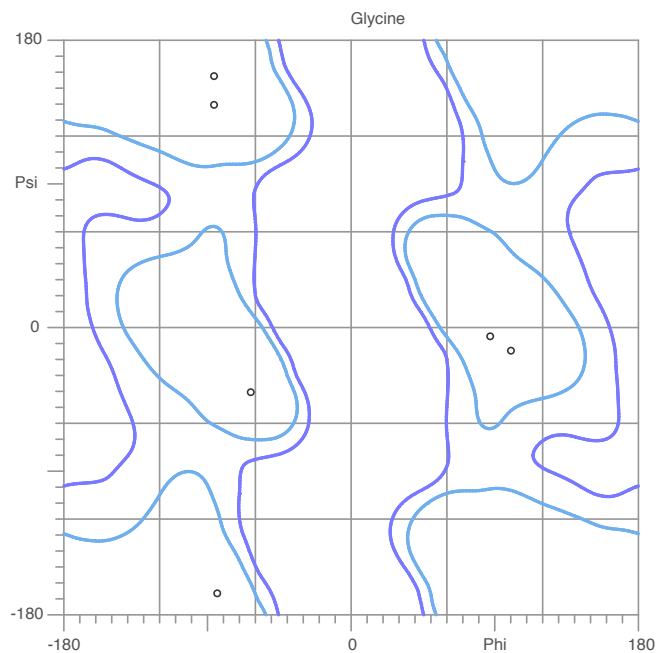
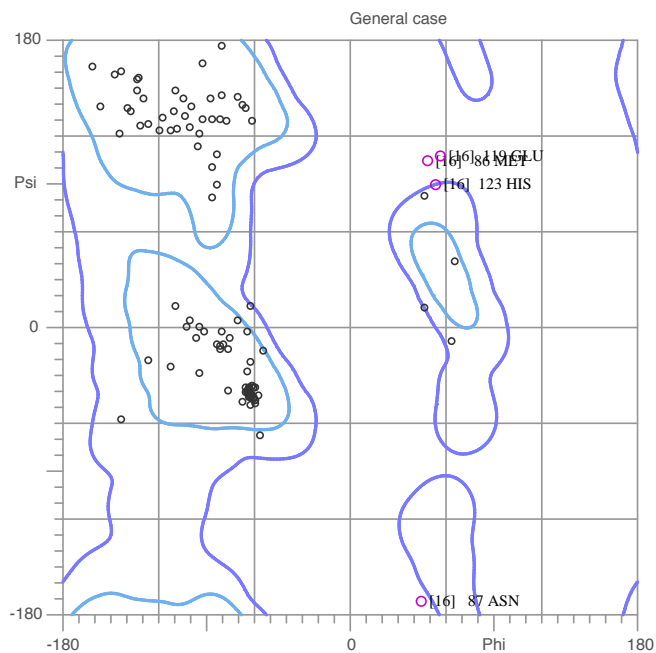
There were 1 outliers (phi, psi):
[15] 120 HIS (60.3, 167.1)

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

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

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 16



91.9% (113/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[16] 86 MET (48.6, 105.7)

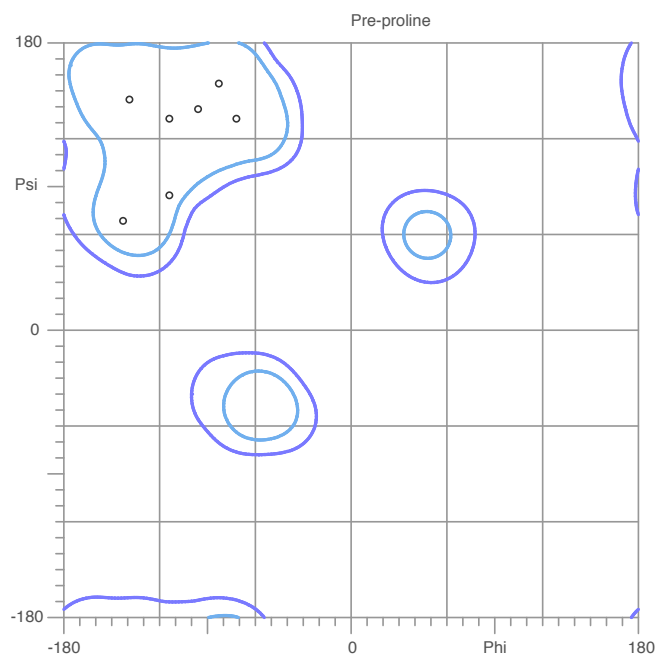
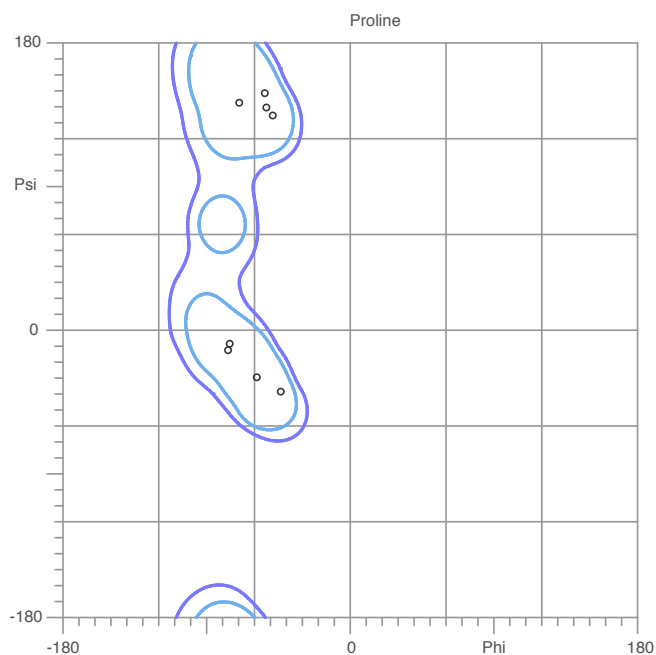
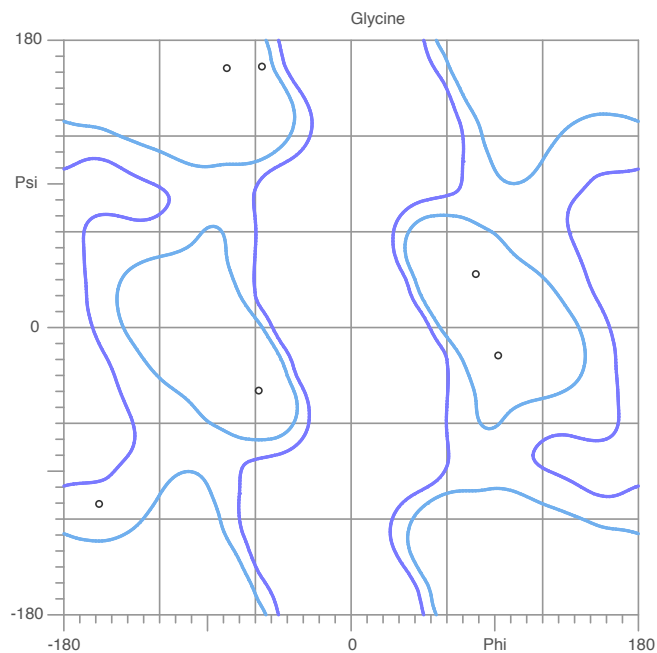
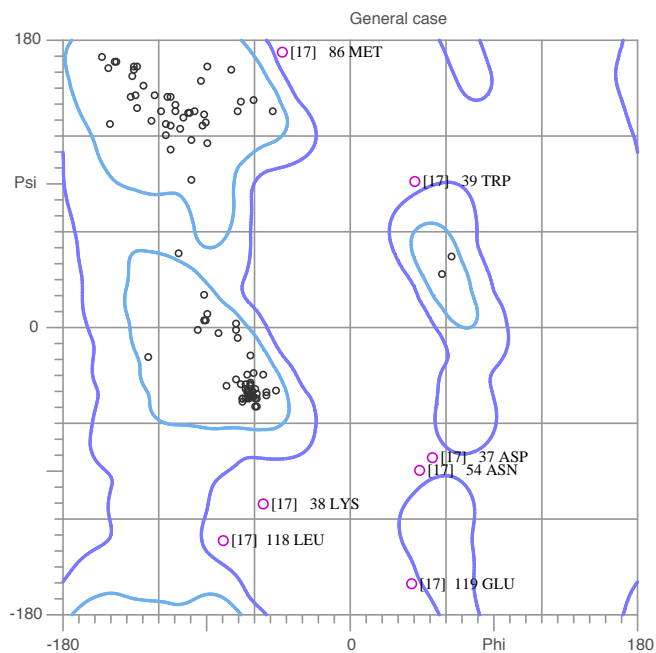
[16] 87 ASN (44.0, -171.3)

[16] 119 GLU (56.9, 108.7)

[16] 123 HIS (53.2, 90.7)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 17



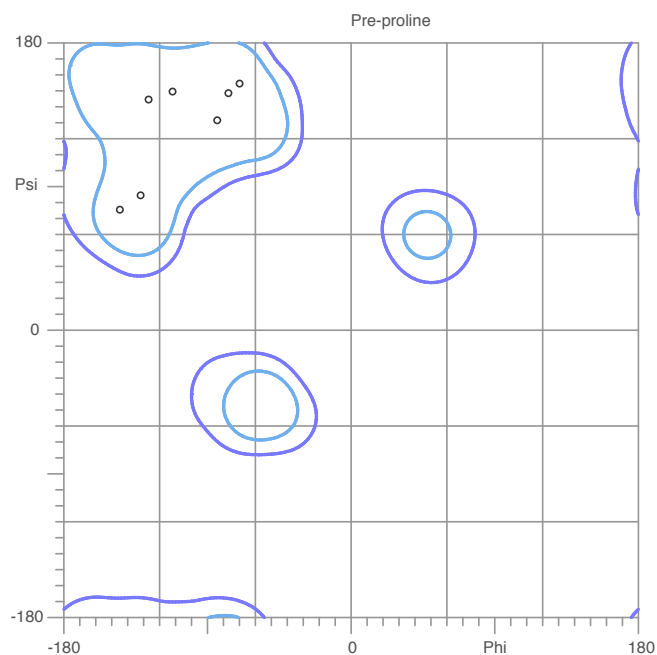
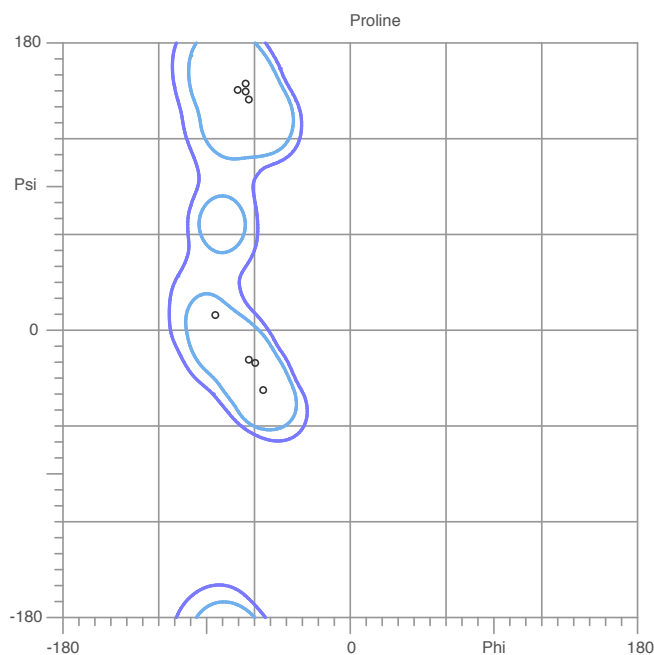
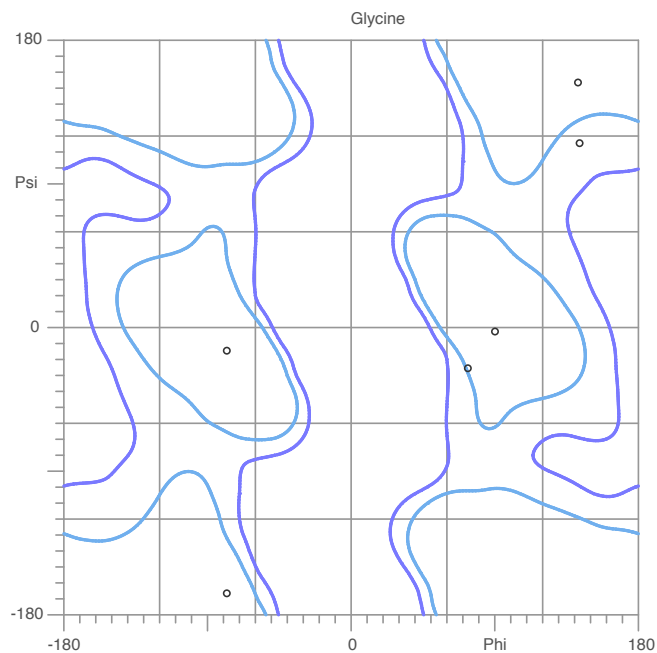
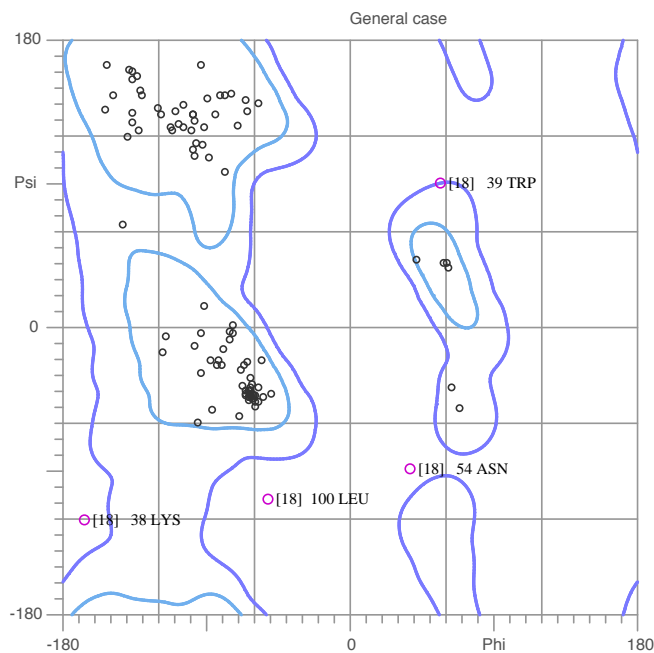
92.7% (114/123) of all residues were in favored (98%) regions.
94.3% (116/123) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[17] 37 ASP (51.3, -81.4)

[17] 38 LYS (-55.9, -110.1)
[17] 39 TRP (40.8, 92.1)
[17] 54 ASN (43.0, -89.2)
[17] 86 MET (-43.7, 173.5)
[17] 118 LEU (-80.8, -133.5)
[17] 119 GLU (38.8, -160.7)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 18



93.5% (115/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[18] 38 LYS (-167.7, -120.3)

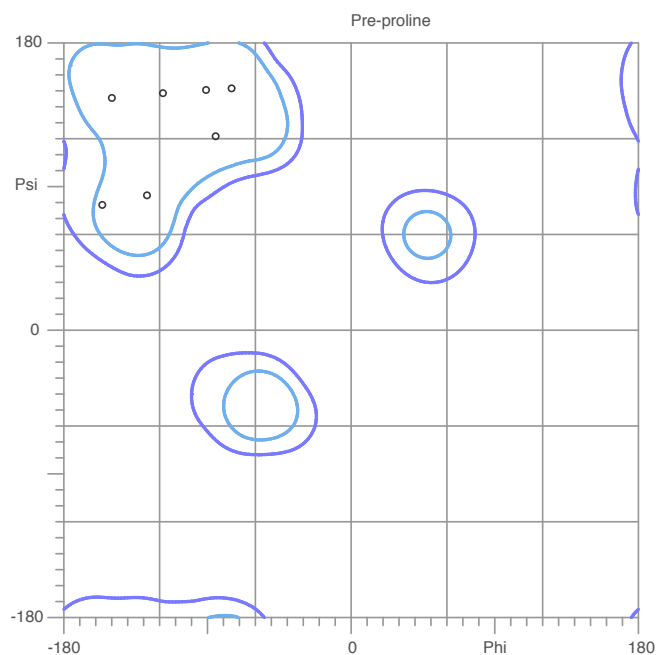
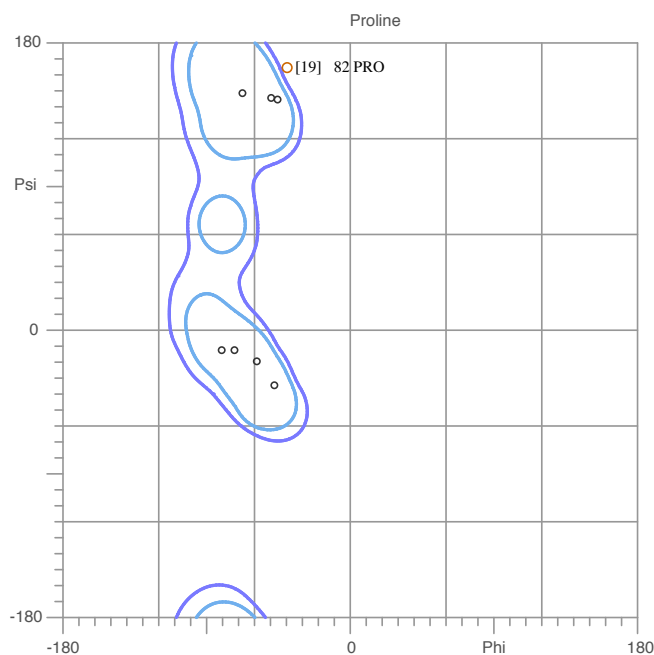
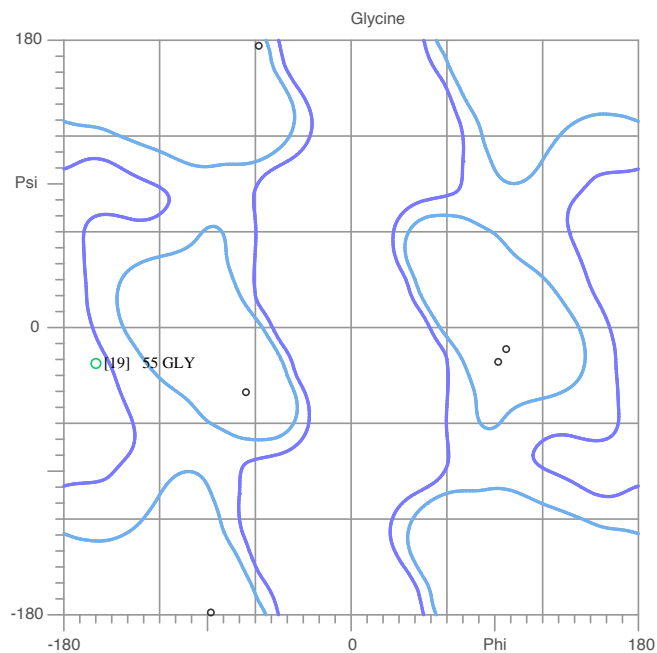
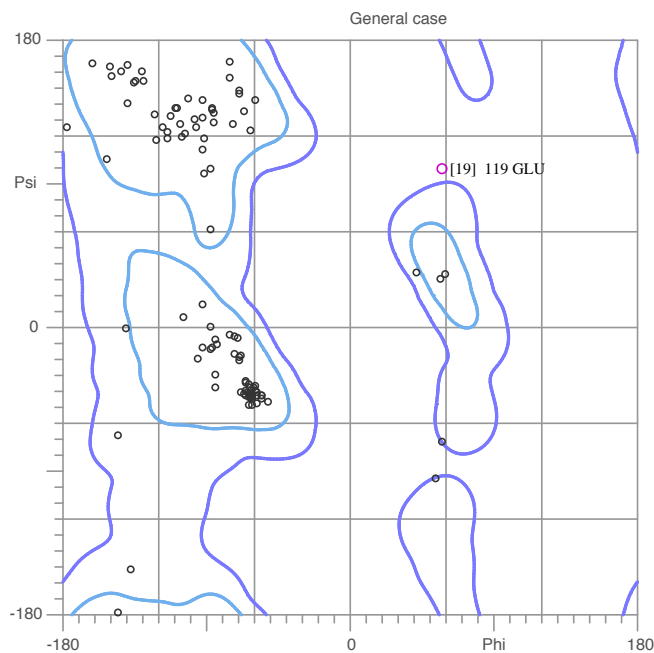
[18] 39 TRP (56.2, 91.6)

[18] 54 ASN (37.2, -88.9)

[18] 100 LEU (-52.6, -108.0)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 19



91.9% (113/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

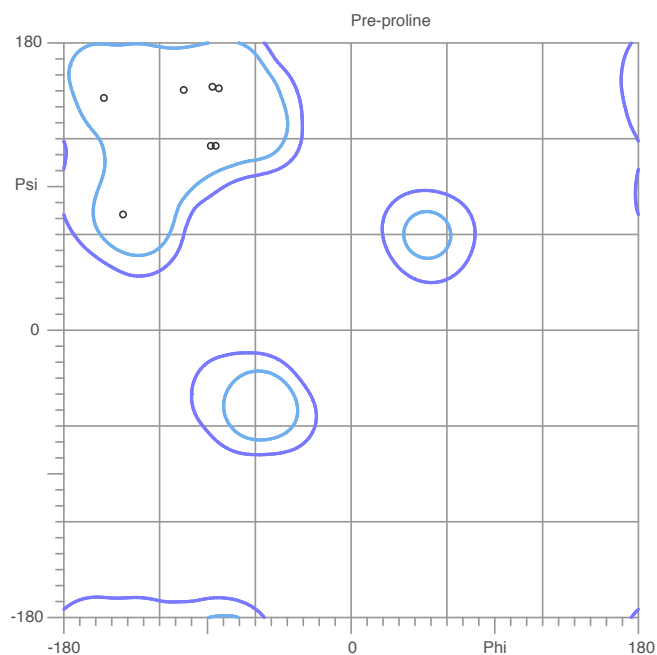
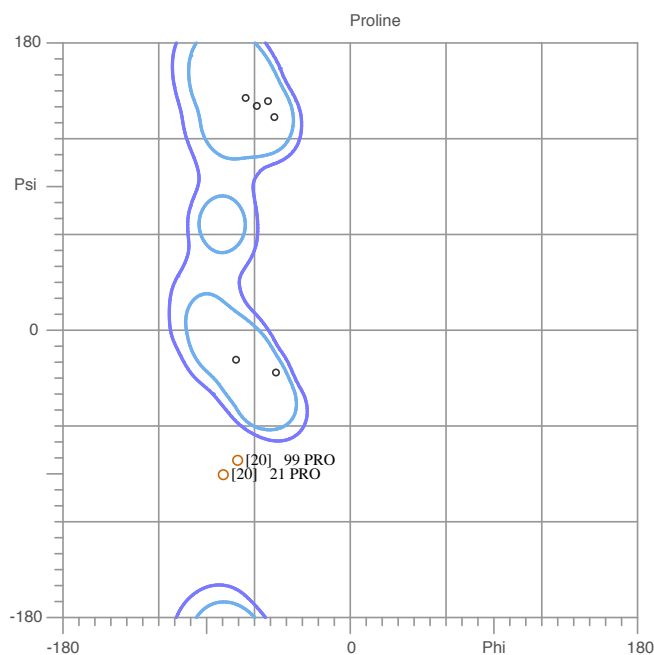
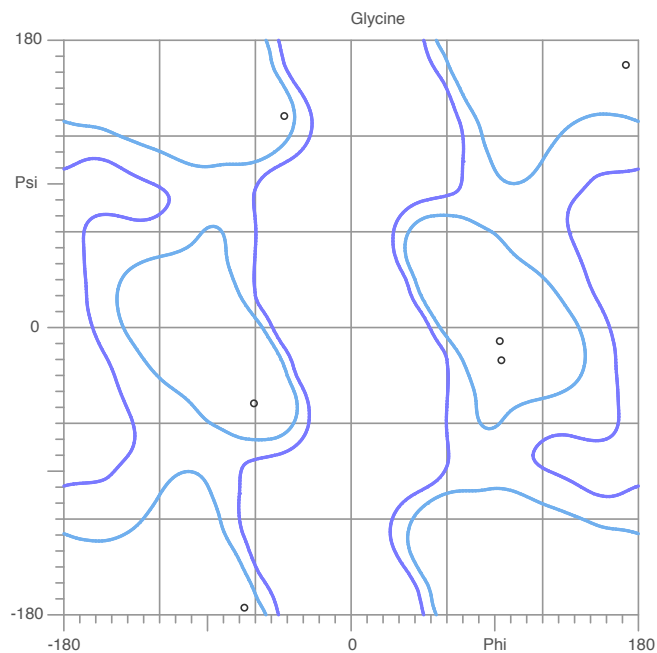
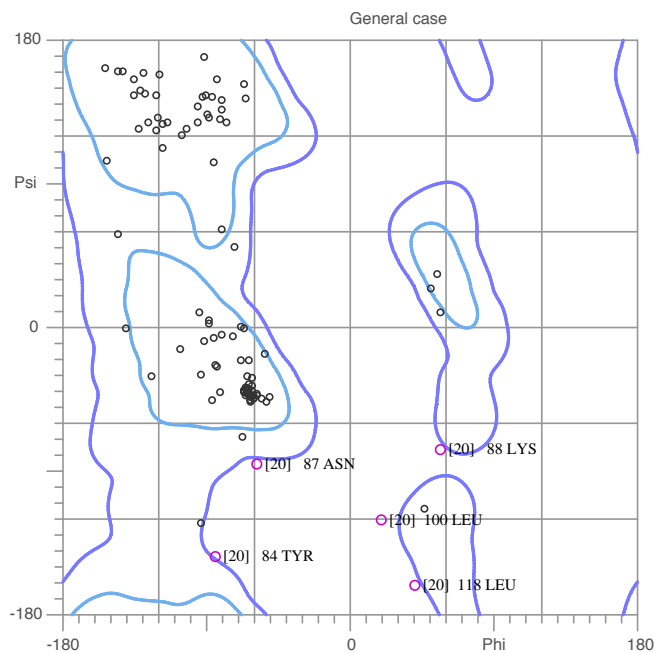
[19] 55 GLY (-160.1, -22.5)

[19] 82 PRO (-40.6, 165.2)

[19] 119 GLU (57.2, 100.6)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 20



88.6% (109/123) of all residues were in favored (98%) regions.
94.3% (116/123) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[20] 21 PRO (-80.2, -90.2)

[20] 84 TYR (-85.1, -143.0)
[20] 87 ASN (-59.6, -85.9)
[20] 88 LYS (56.9, -76.7)
[20] 99 PRO (-71.6, -81.2)
[20] 100 LEU (19.2, -120.7)
[20] 118 LEU (40.0, -161.6)