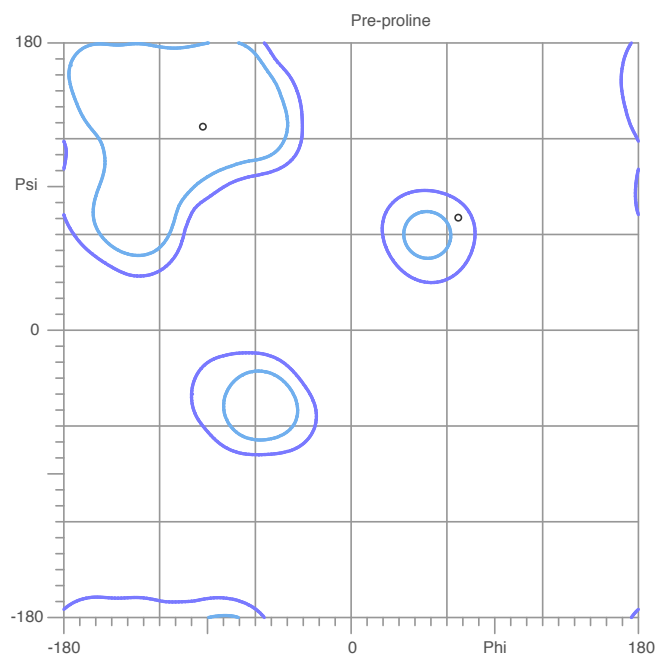
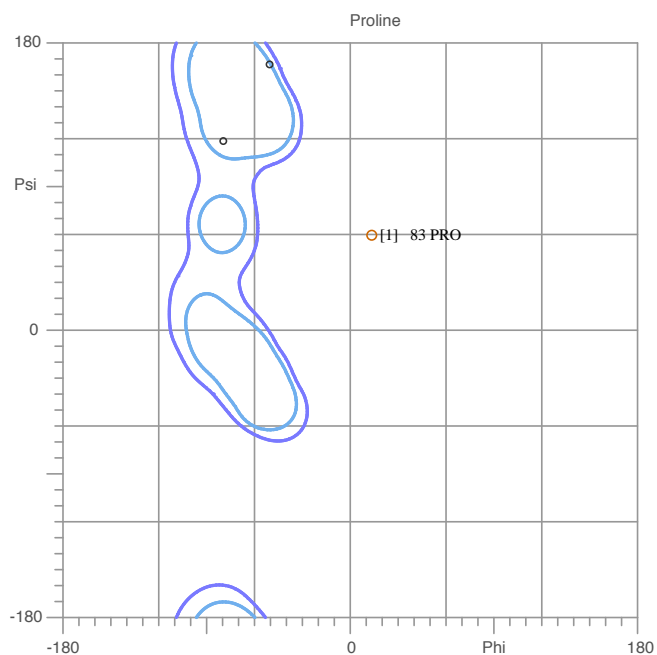
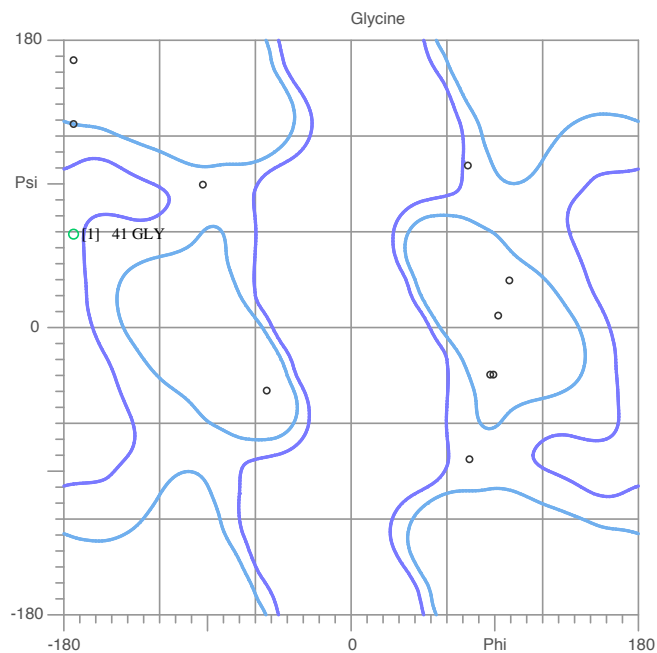
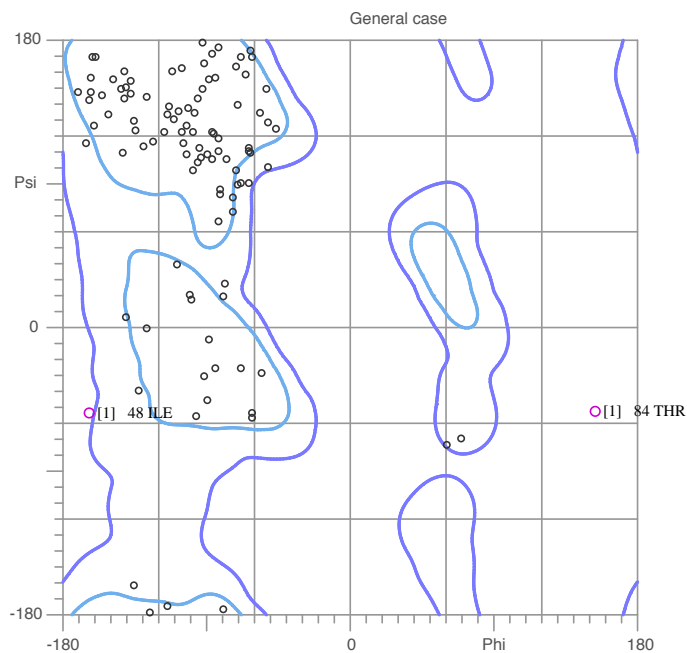


MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 1



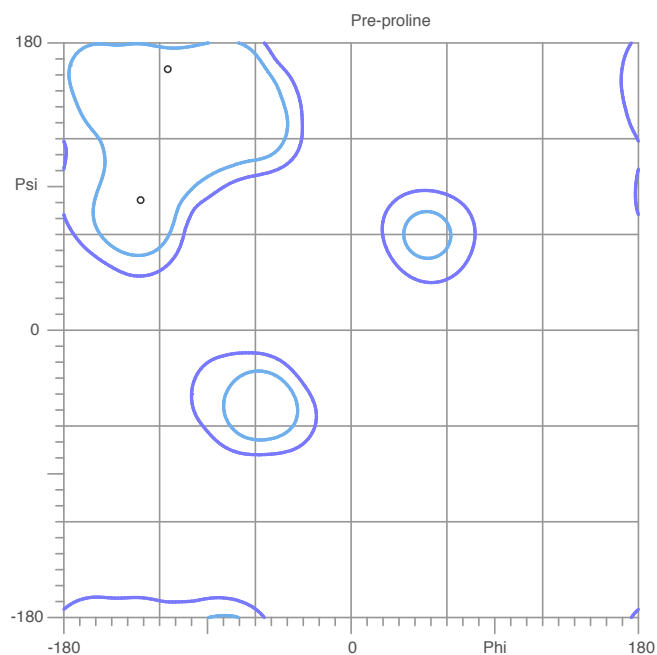
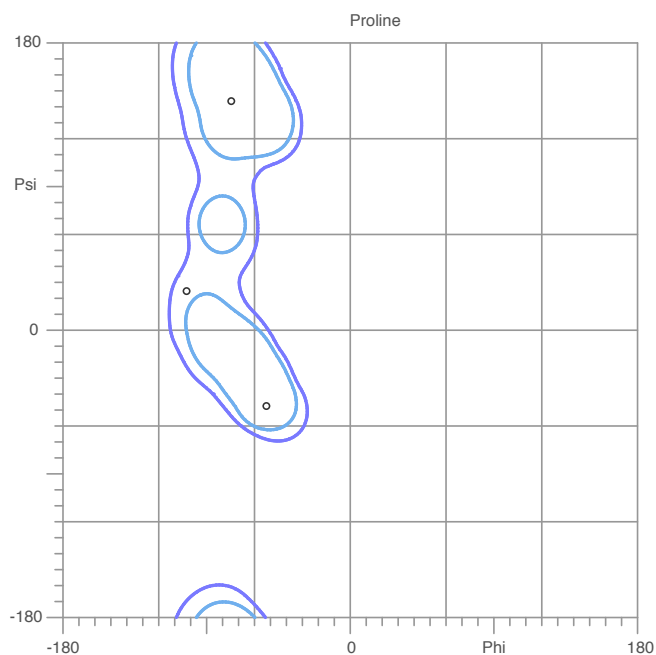
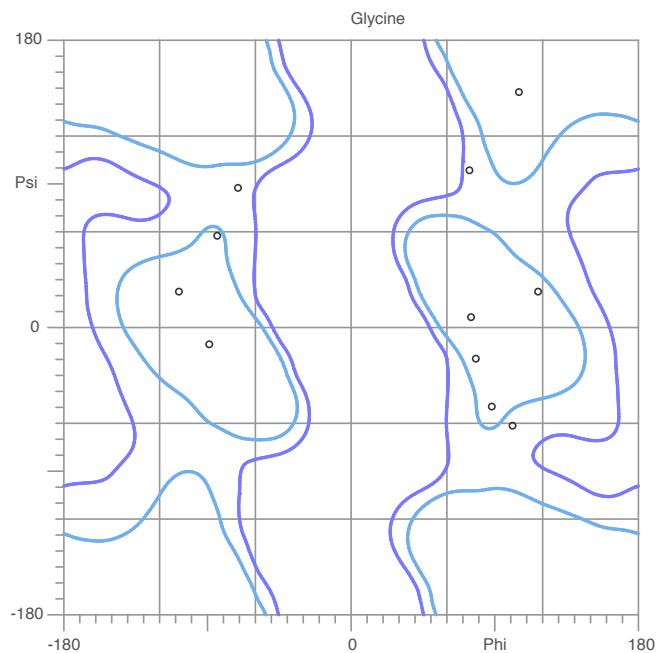
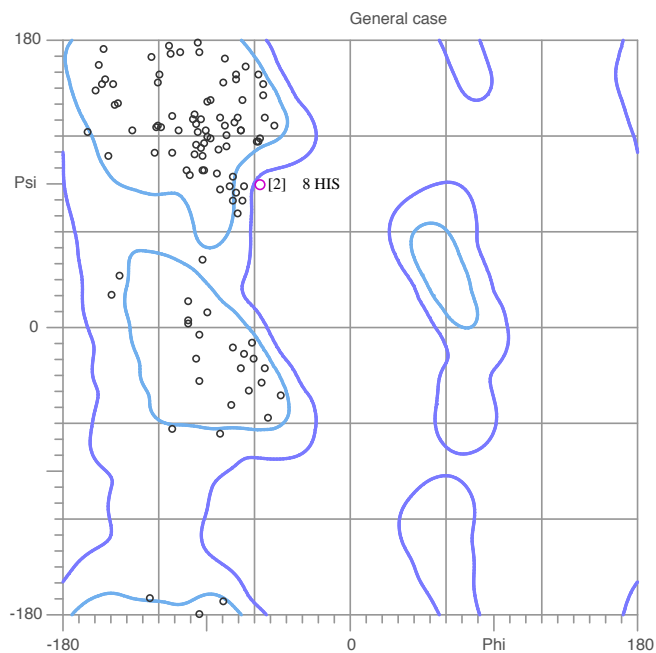
83.3% (100/120) of all residues were in favored (98%) regions.
96.7% (116/120) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [1] 41 GLY (-175.0, 59.5)
- [1] 48 ILE (-164.5, -53.8)
- [1] 83 PRO (13.4, 60.8)
- [1] 84 THR (153.7, -52.9)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 2



86.7% (104/120) of all residues were in favored (98%) regions.
99.2% (119/120) of all residues were in allowed (>99.8%) regions.

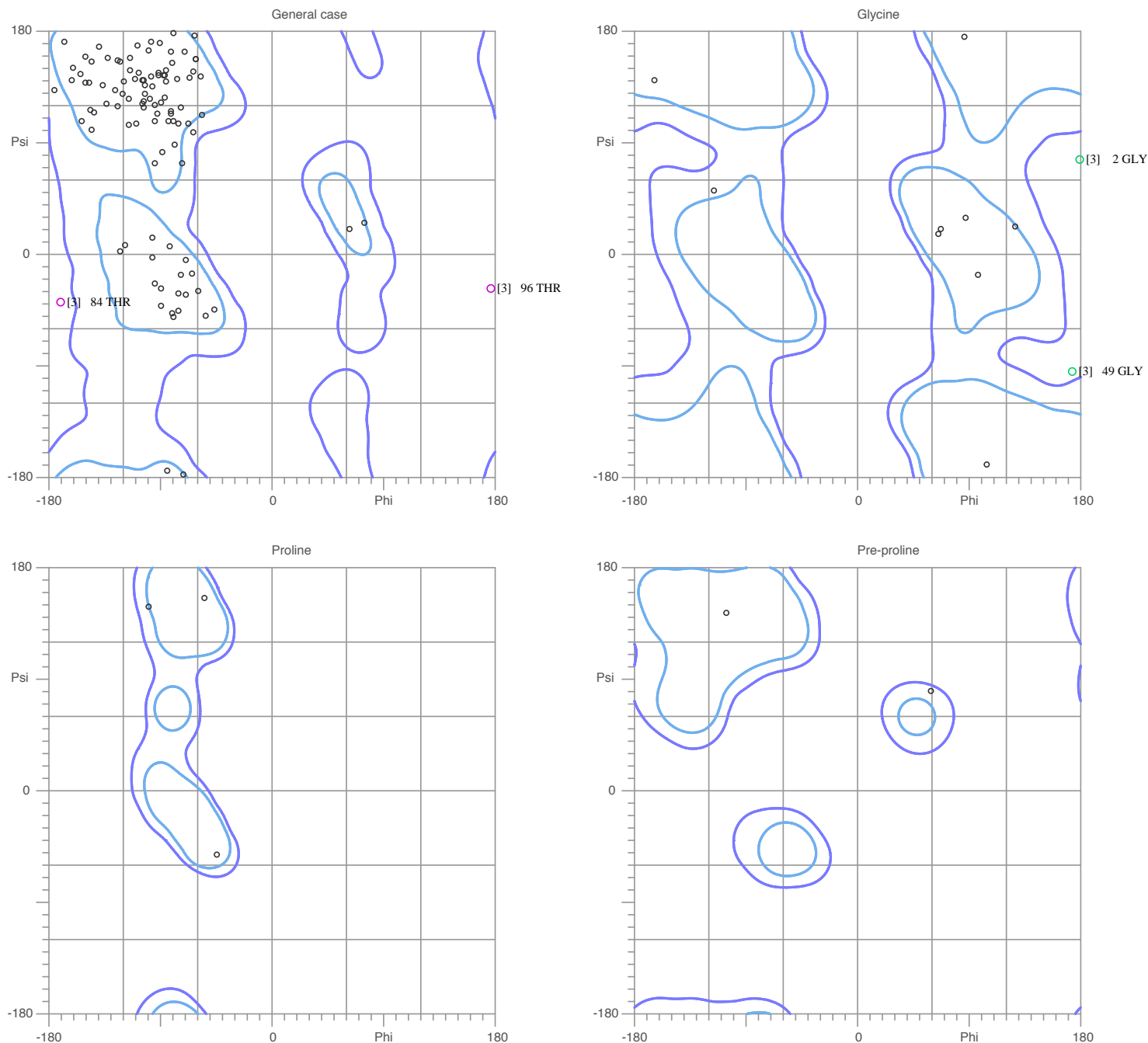
There were 1 outliers (phi, psi):
[2] 8 HIS (-57.5, 90.7)

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

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

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 3



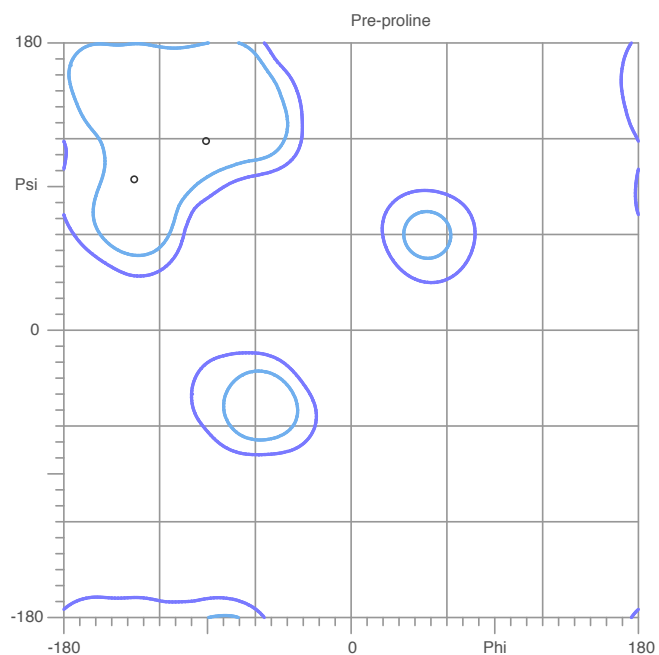
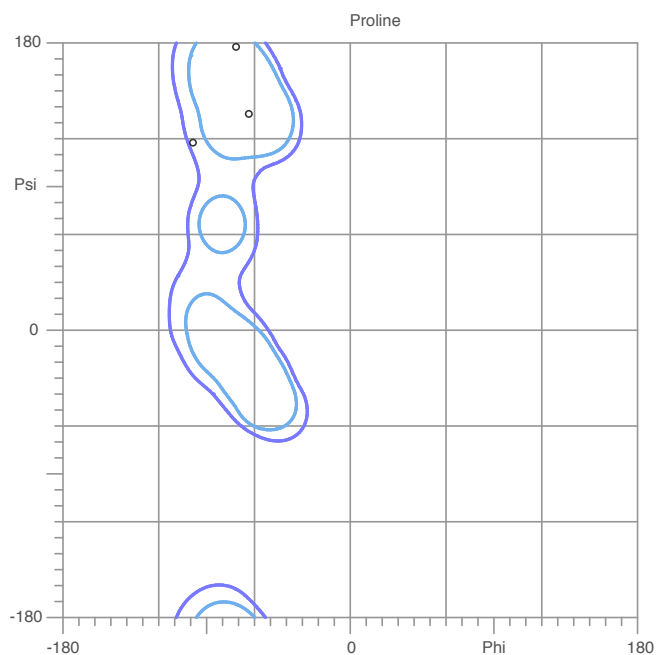
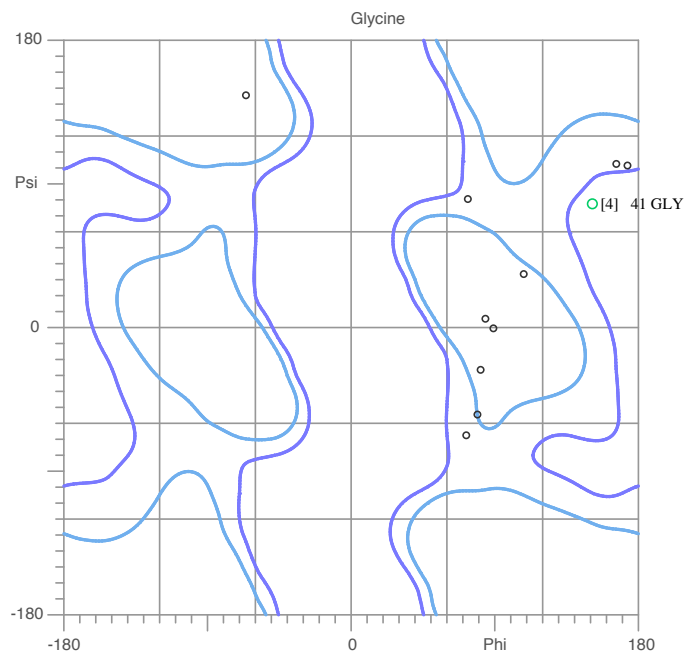
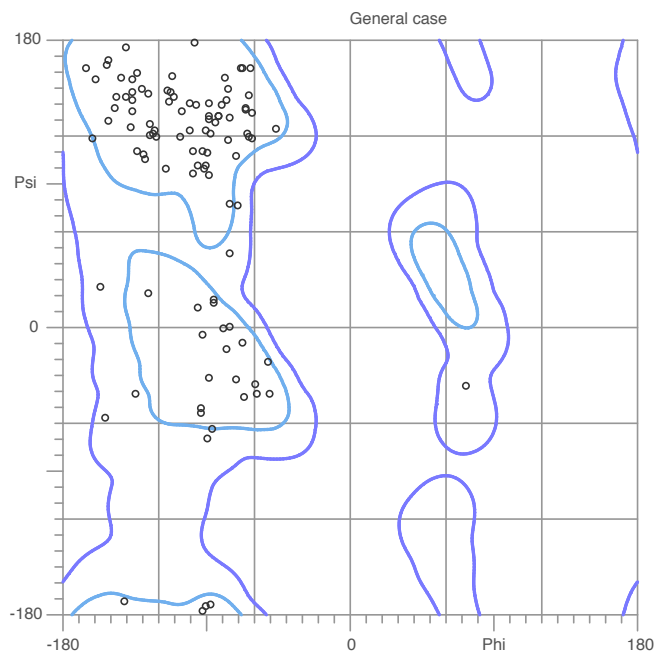
91.7% (110/120) of all residues were in favored (98%) regions.
96.7% (116/120) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [3] 2 GLY (179.1, 77.9)
- [3] 49 GLY (173.5, -94.8)
- [3] 84 THR (-171.0, -38.2)
- [3] 96 THR (176.5, -27.3)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 4



87.5% (105/120) of all residues were in favored (98%) regions.
99.2% (119/120) of all residues were in allowed (>99.8%) regions.

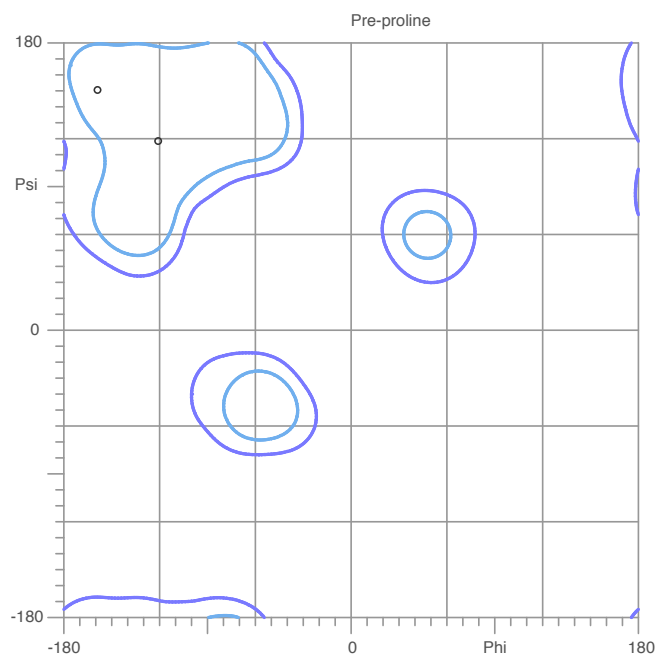
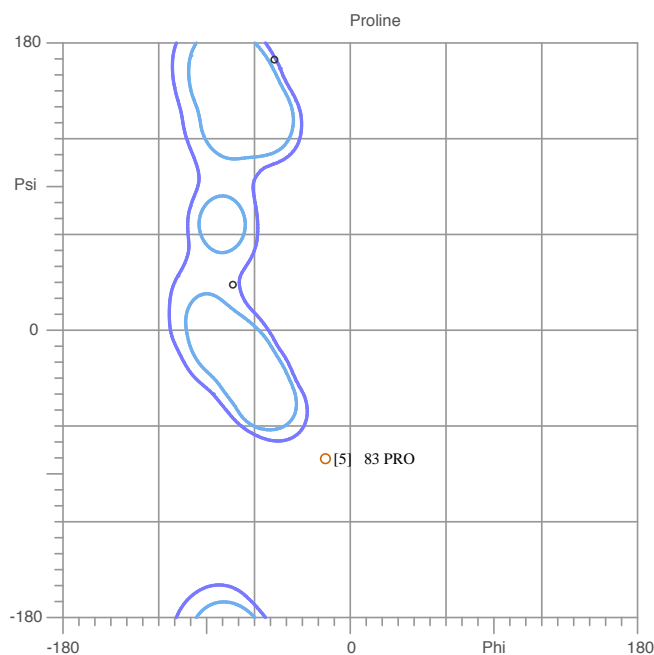
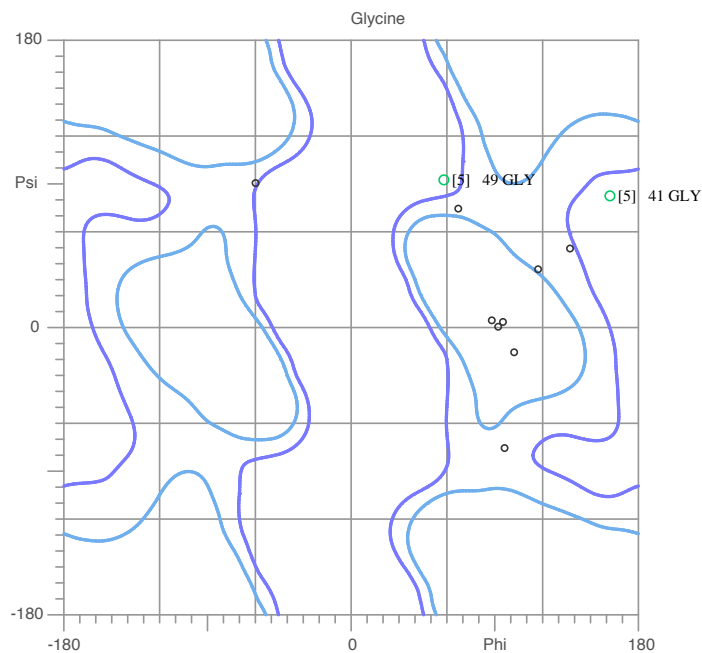
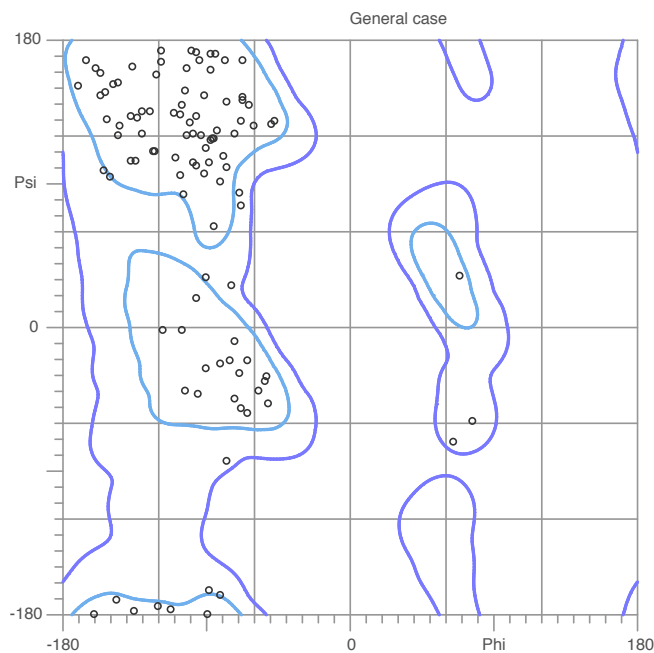
There were 1 outliers (phi, psi):
[4] 41 GLY (151.8, 78.5)

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

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

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 5



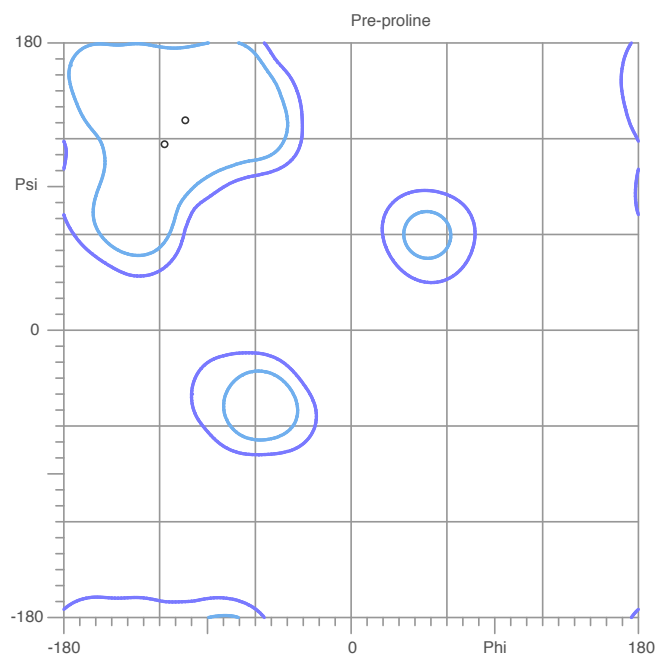
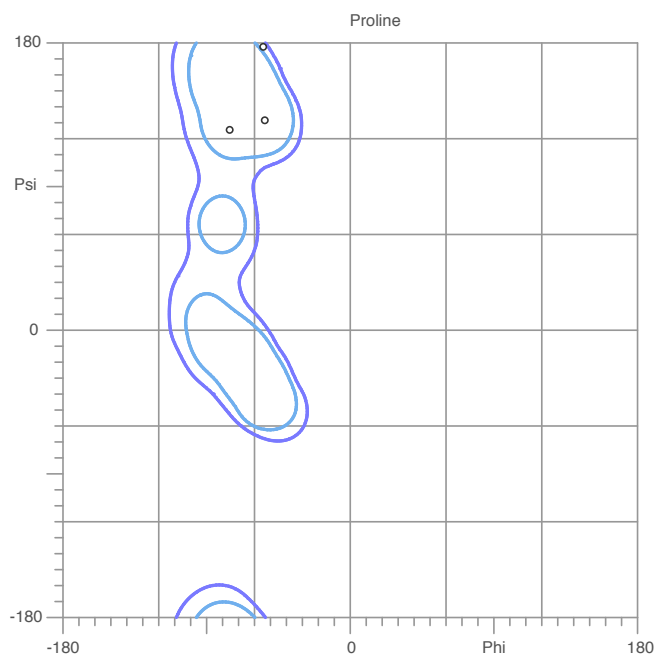
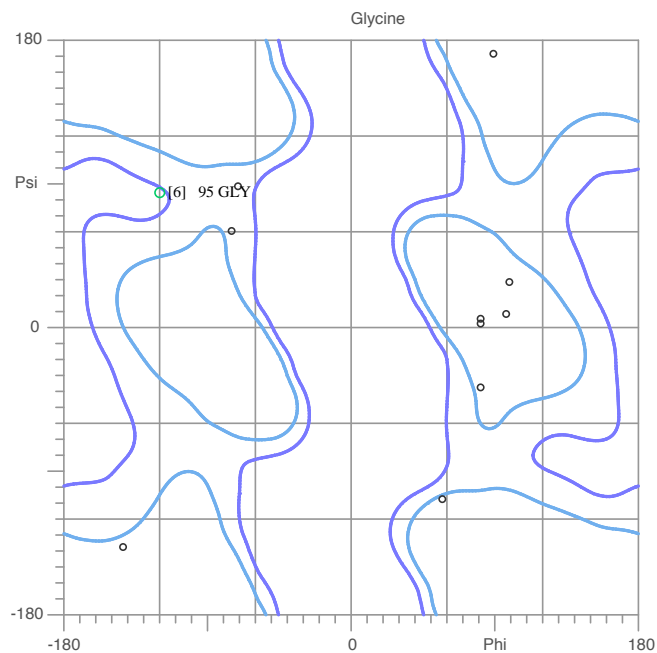
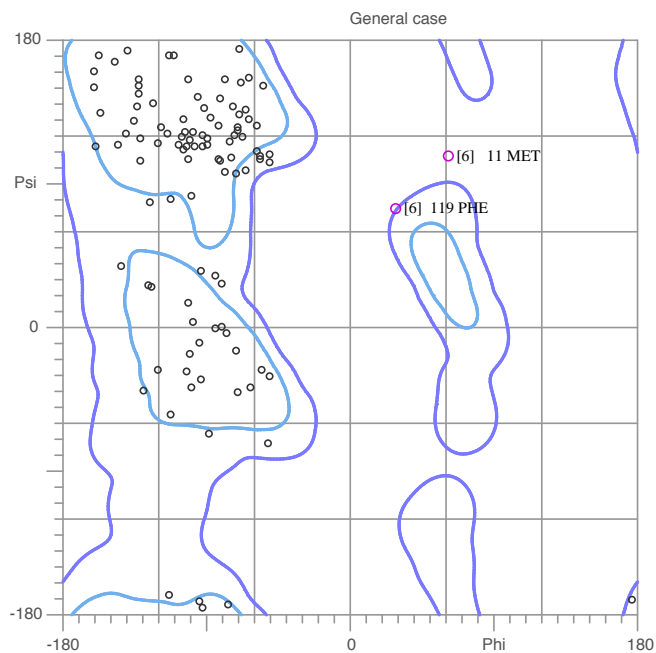
82.5% (99/120) of all residues were in favored (98%) regions.
97.5% (117/120) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [5] 41 GLY (162.5, 83.4)
- [5] 49 GLY (58.9, 93.7)
- [5] 83 PRO (-16.8, -80.5)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 6



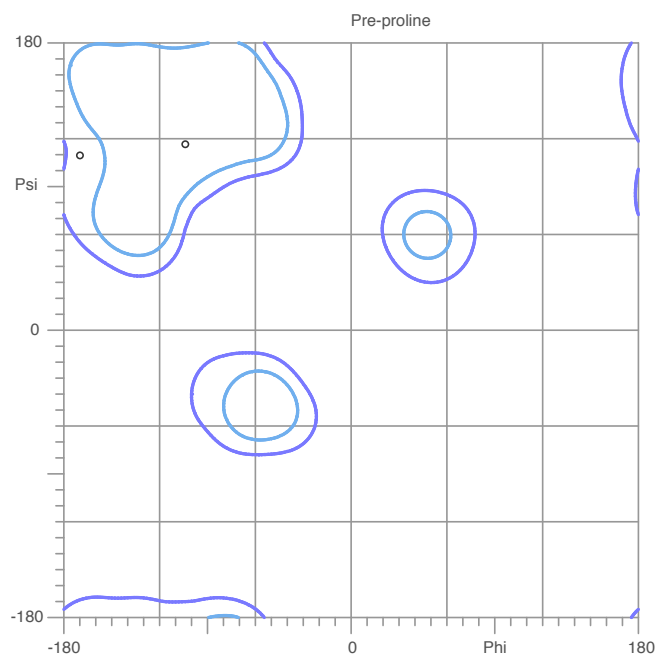
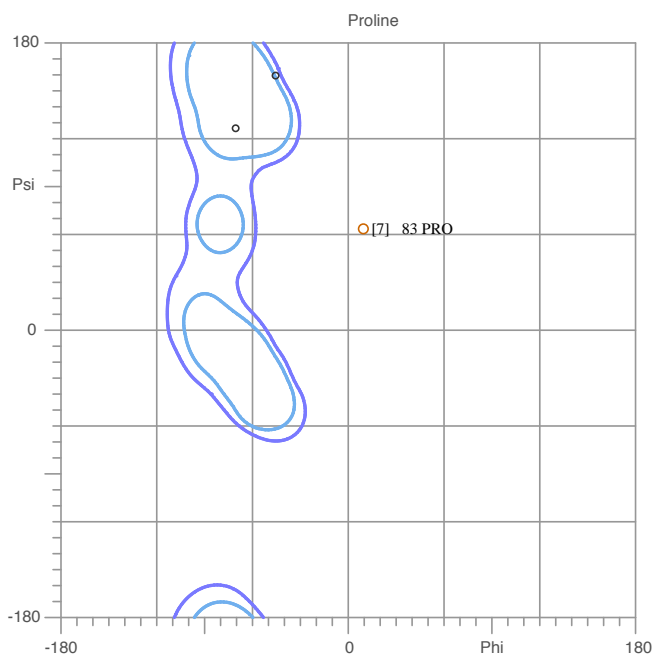
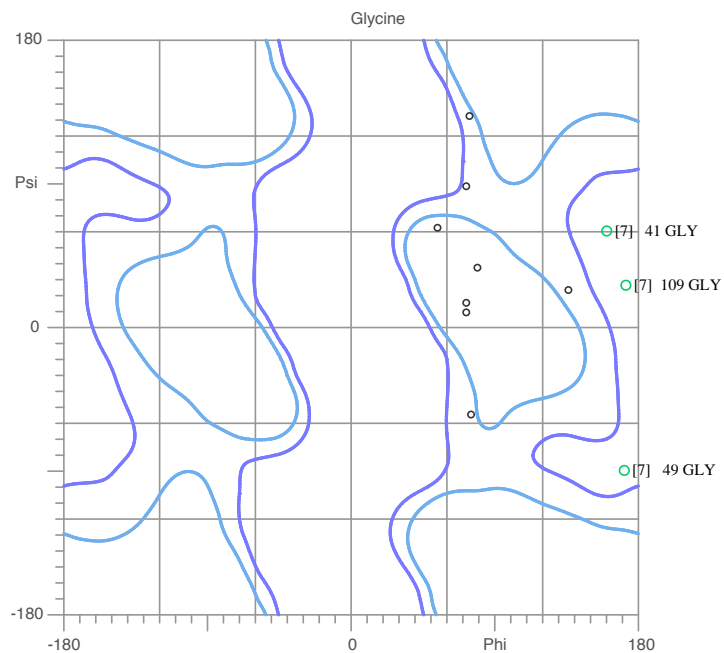
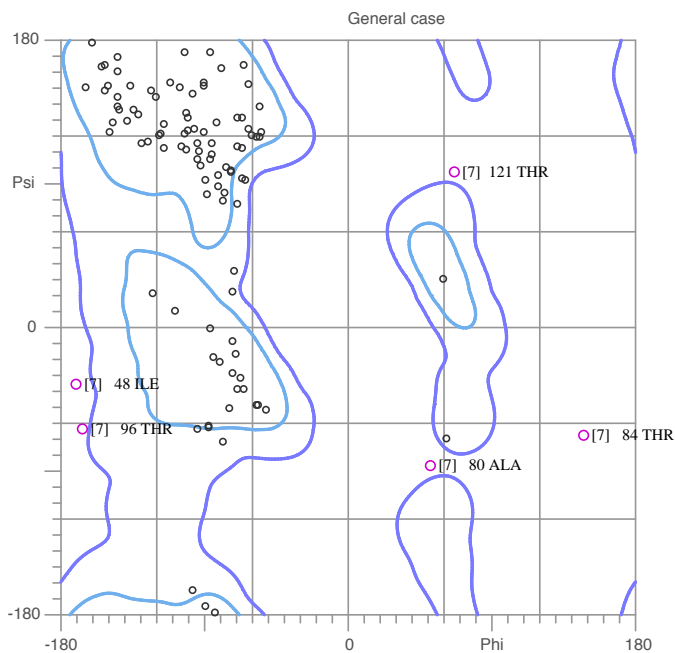
80.8% (97/120) of all residues were in favored (98%) regions.
97.5% (117/120) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 11 MET (61.6, 108.9)
- [6] 95 GLY (-120.9, 85.1)
- [6] 119 PHE (28.6, 76.0)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 7



80.0% (96/120) of all residues were in favored (98%) regions.
92.5% (111/120) of all residues were in allowed (>99.8%) regions.

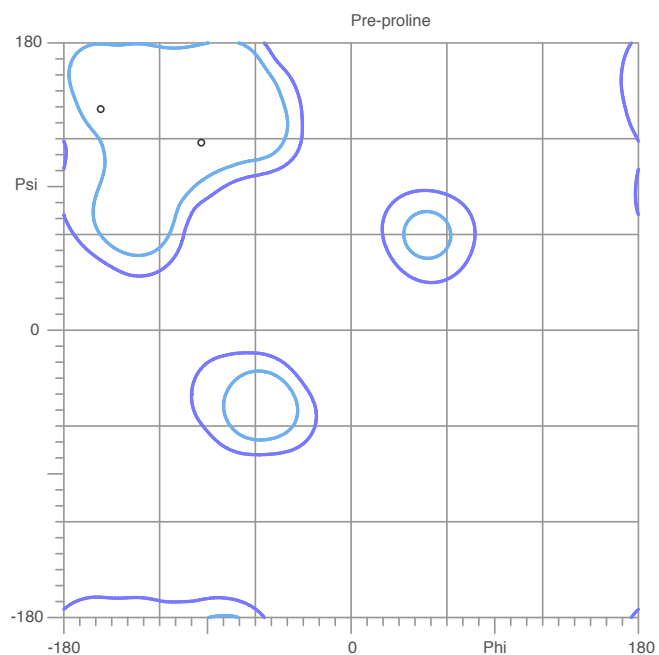
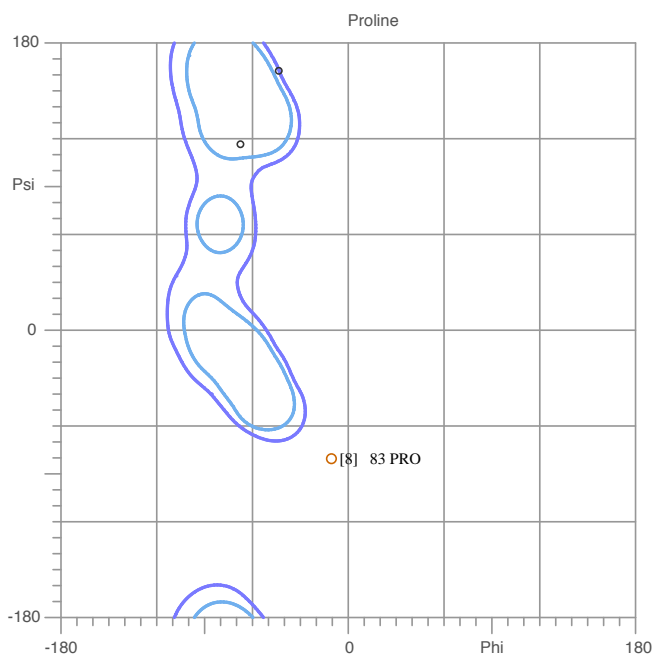
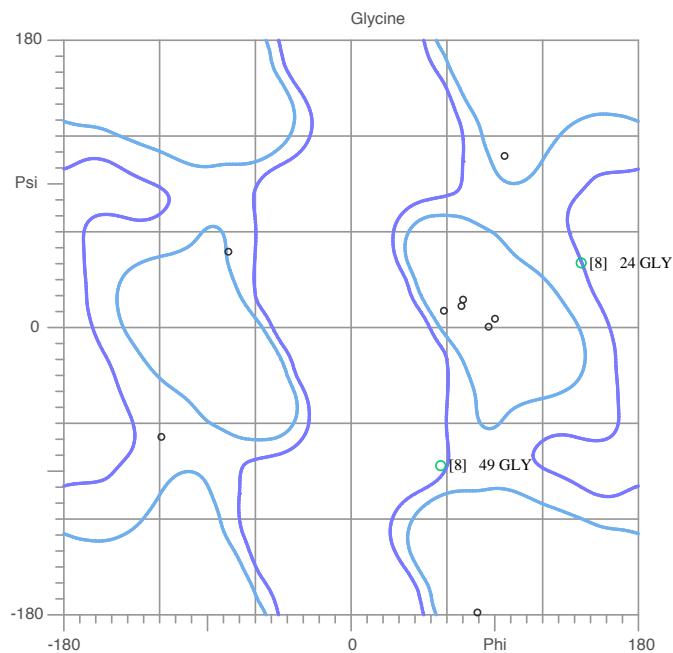
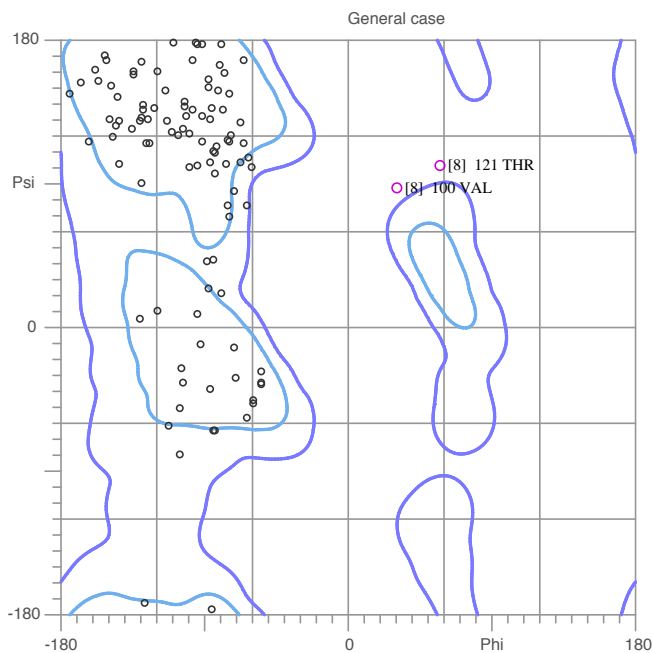
There were 9 outliers (phi, psi):

[7] 41 GLY (160.7, 61.8)
[7] 48 ILE (-171.2, -35.7)

[7] 49 GLY (171.5, -89.2)
[7] 80 ALA (51.6, -86.1)
[7] 83 PRO (9.0, 64.5)
[7] 84 THR (147.8, -67.6)
[7] 96 THR (-167.5, -63.3)
[7] 109 GLY (172.6, 27.7)
[7] 121 THR (66.4, 98.4)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 8



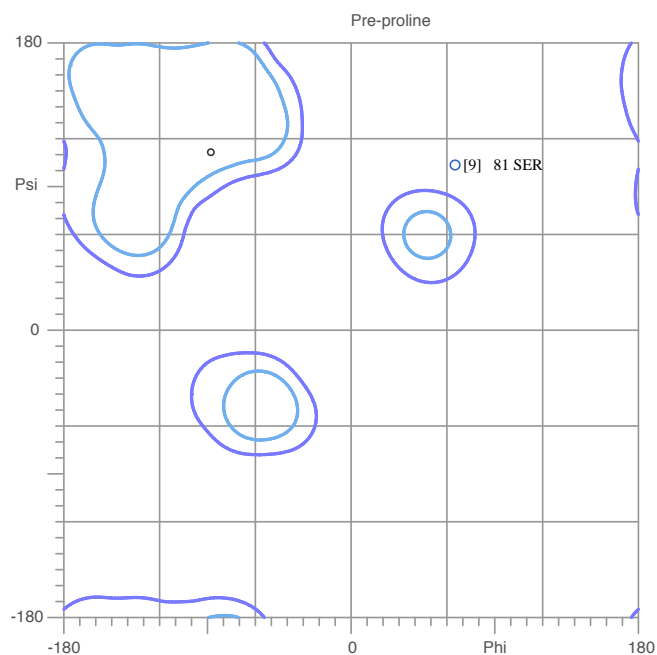
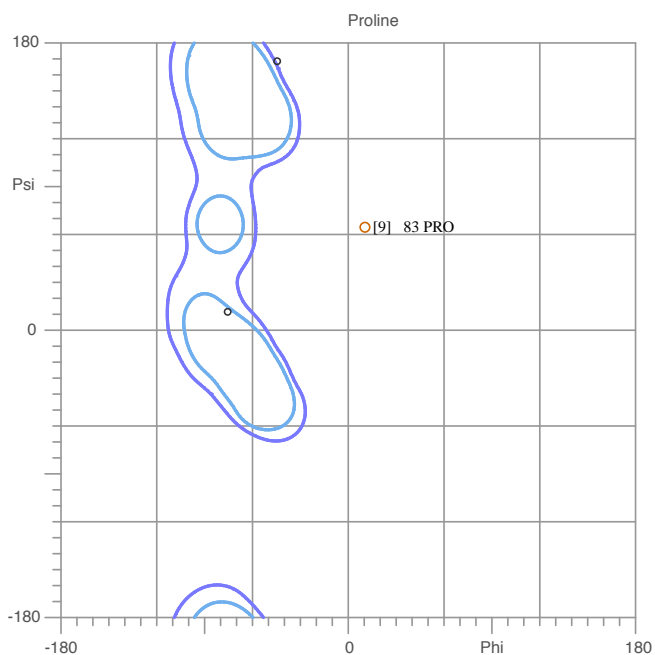
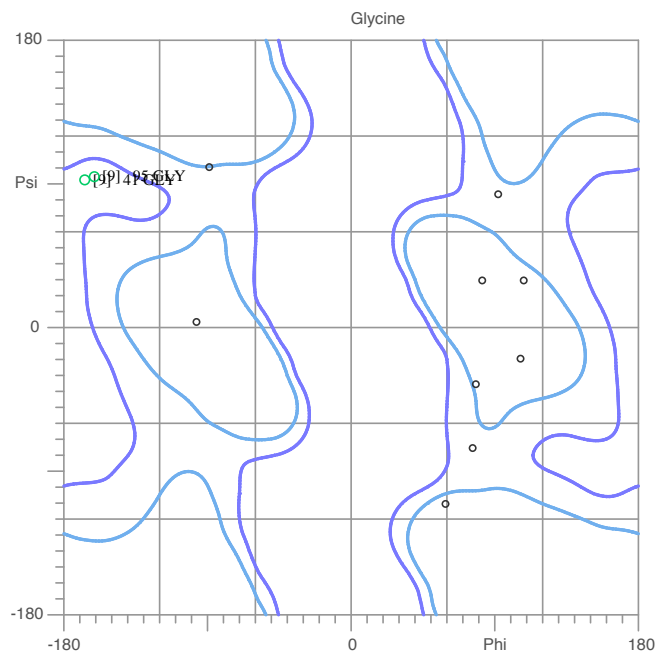
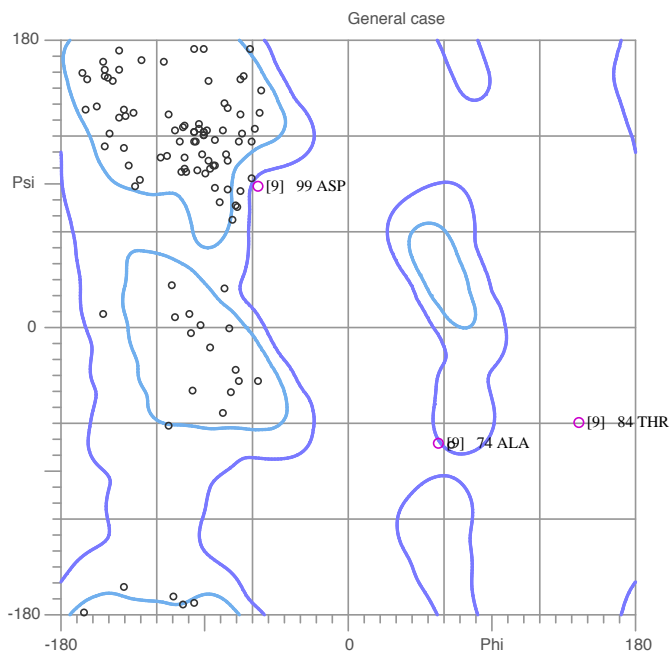
82.5% (99/120) of all residues were in favored (98%) regions.
95.8% (115/120) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[8] 24 GLY (144.3, 41.9)
[8] 49 GLY (56.5, -86.8)
[8] 83 PRO (-11.0, -80.7)
[8] 100 VAL (30.7, 88.6)
[8] 121 THR (57.9, 102.3)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 9



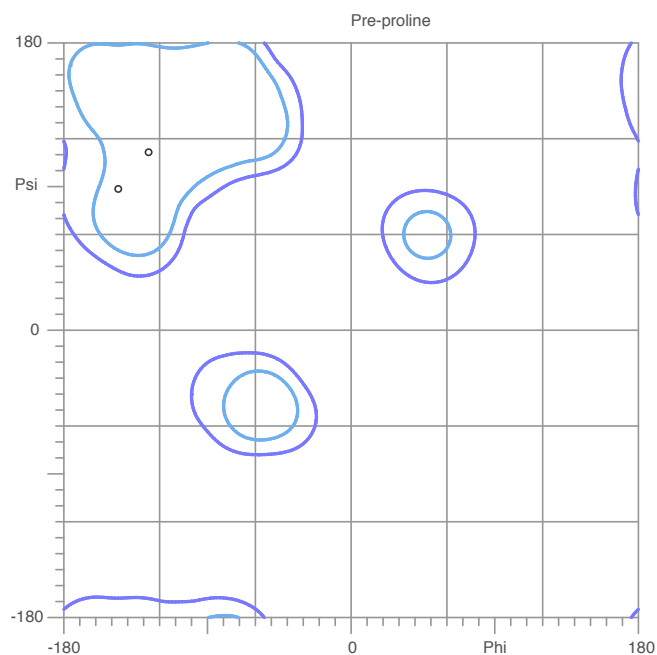
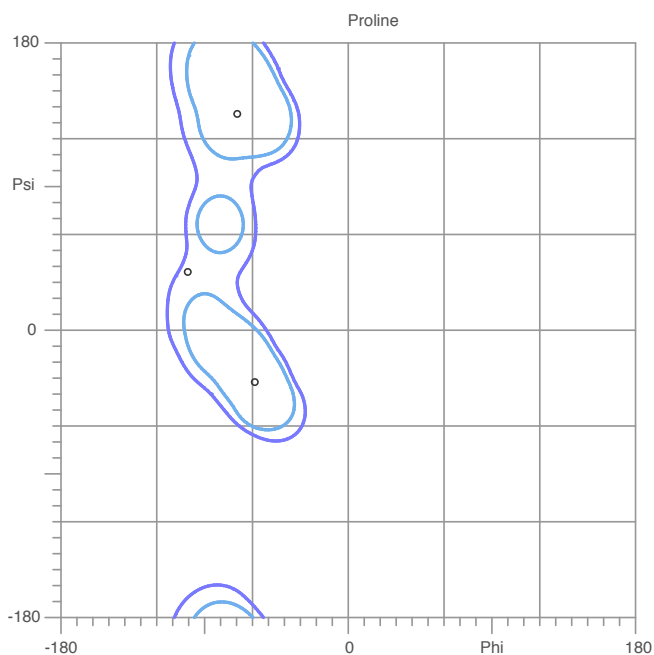
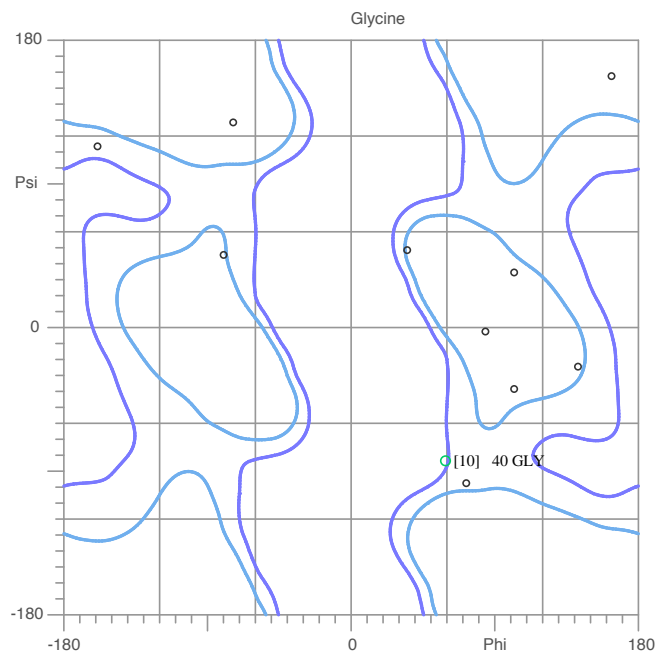
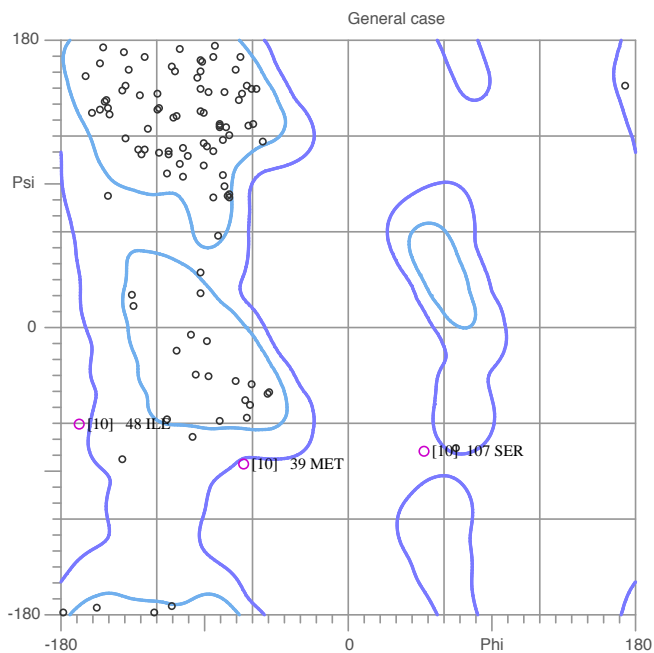
81.7% (98/120) of all residues were in favored (98%) regions.
94.2% (113/120) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[9] 41 GLY (-167.7, 93.7)

[9] 74 ALA (56.5, -72.8)
[9] 81 SER (65.2, 104.2)
[9] 83 PRO (10.8, 65.4)
[9] 84 THR (144.7, -59.6)
[9] 95 GLY (-161.8, 95.9)
[9] 99 ASP (-57.9, 89.9)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 10



88.3% (106/120) of all residues were in favored (98%) regions.
96.7% (116/120) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[10] 39 MET (-66.3, -85.6)

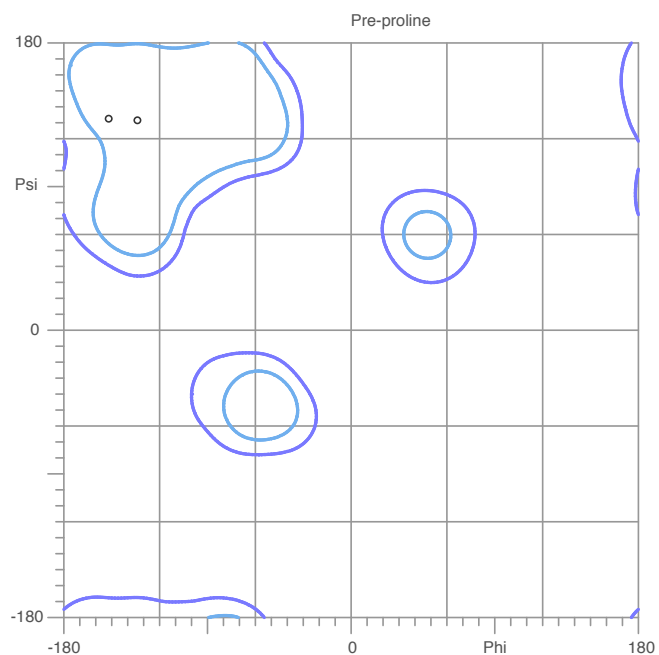
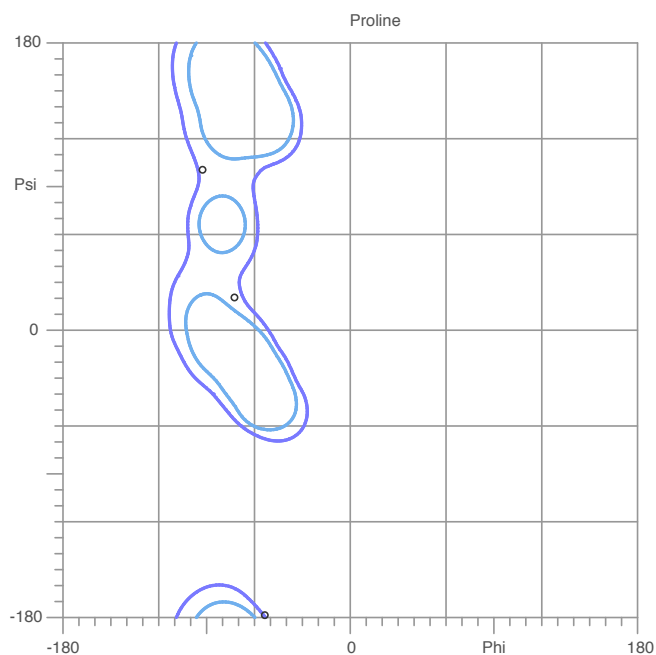
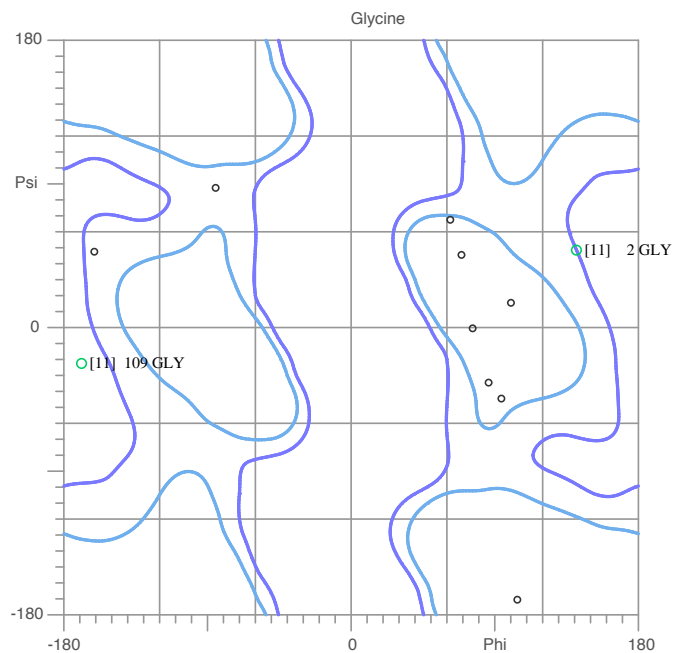
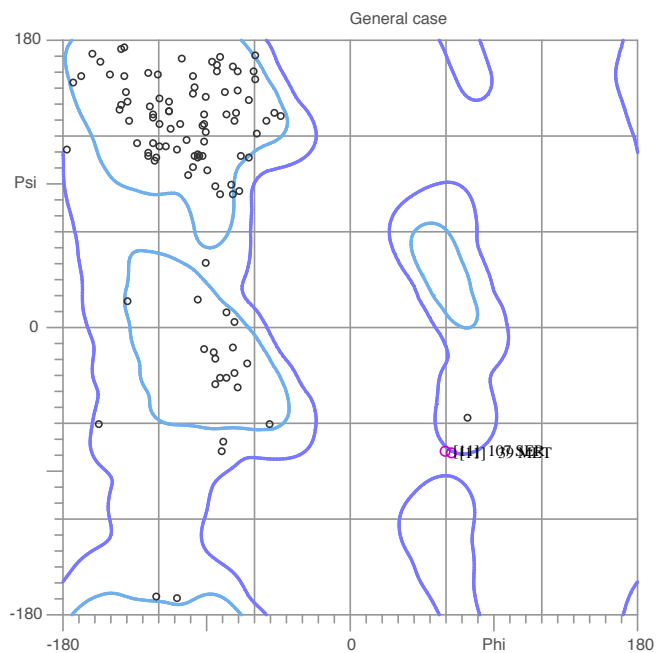
[10] 40 GLY (59.9, -83.1)

[10] 48 ILE (-169.7, -60.3)

[10] 107 SER (47.7, -77.5)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 11



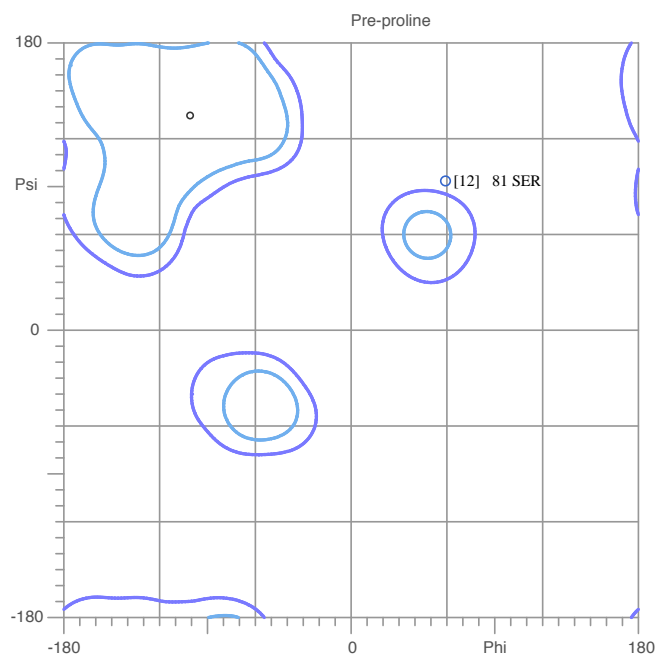
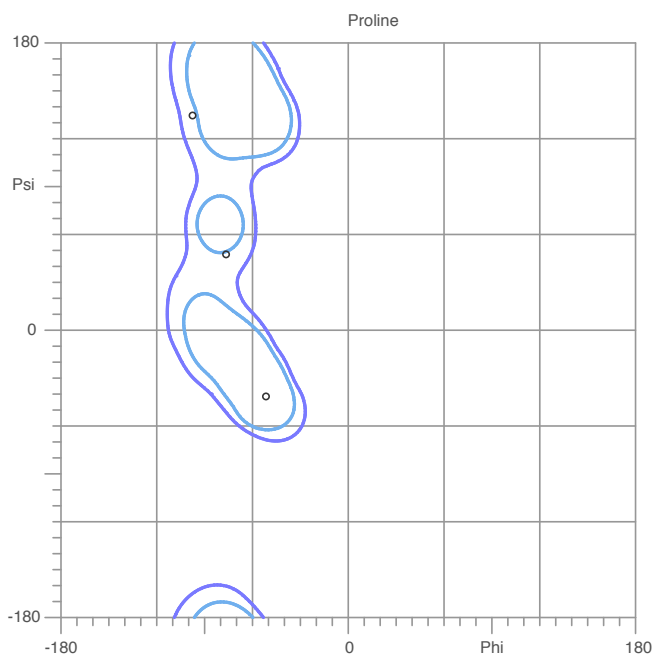
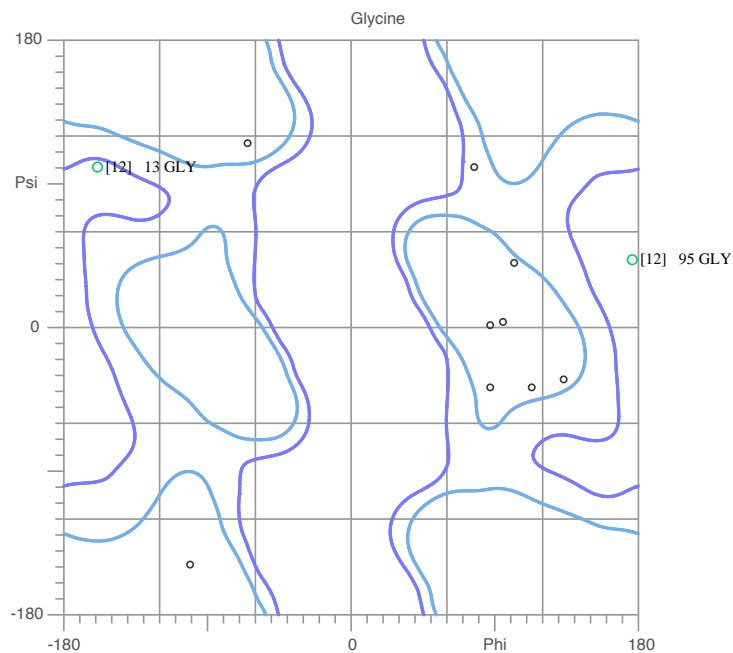
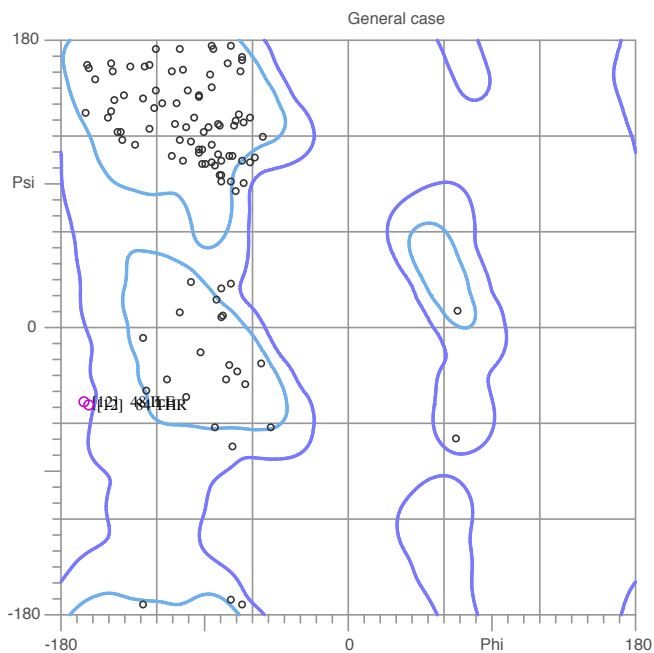
84.2% (101/120) of all residues were in favored (98%) regions.
96.7% (116/120) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [11] 2 GLY (141.3, 49.0)
- [11] 39 MET (63.5, -78.8)
- [11] 107 SER (59.9, -77.5)
- [11] 109 GLY (-169.6, -22.8)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 12



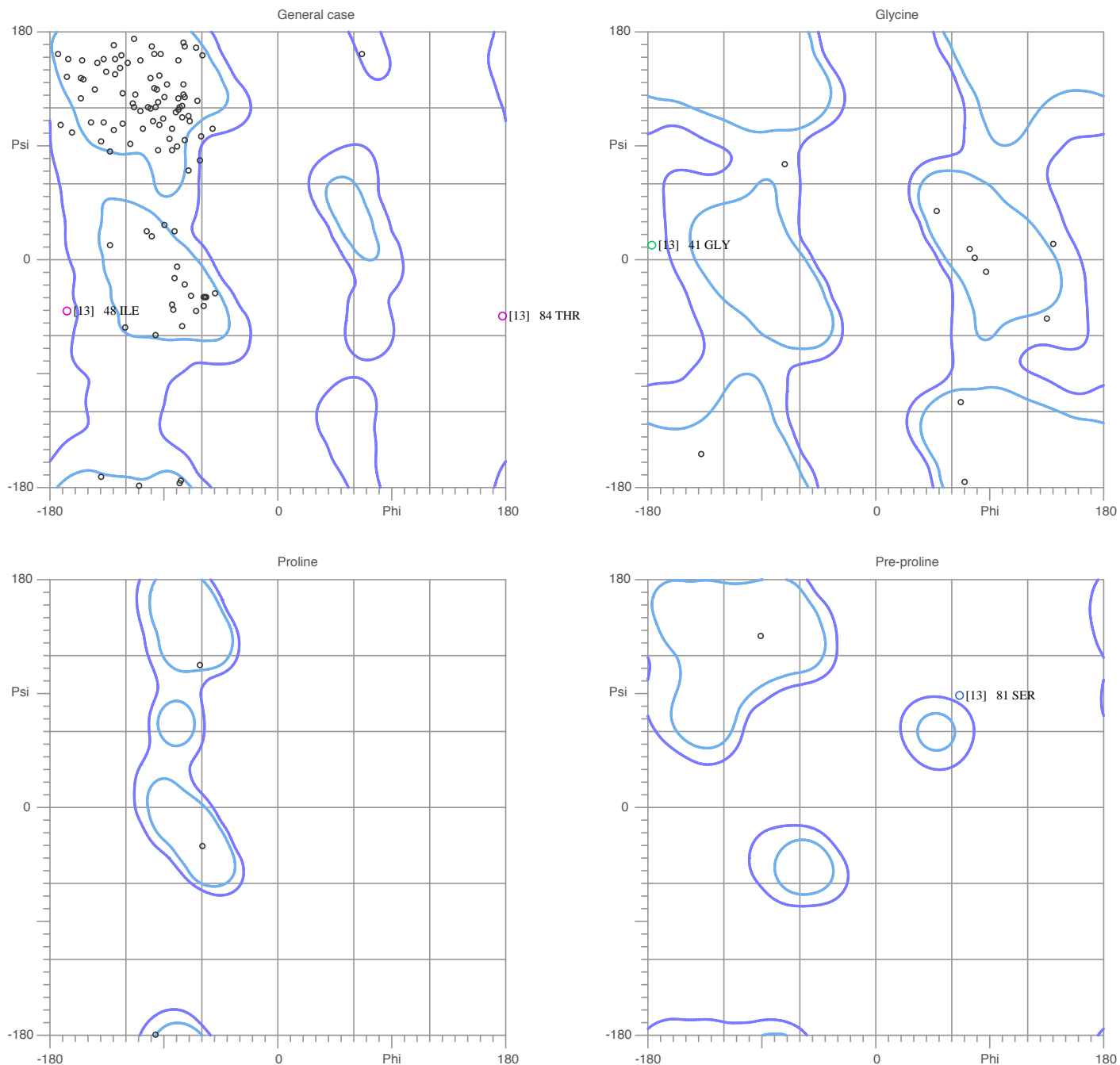
85.0% (102/120) of all residues were in favored (98%) regions.
95.8% (115/120) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [12] 13 GLY (-159.3, 101.8)
- [12] 48 ILE (-166.1, -46.5)
- [12] 81 SER (60.0, 94.5)
- [12] 84 THR (-163.8, -48.3)
- [12] 95 GLY (176.7, 43.5)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 13



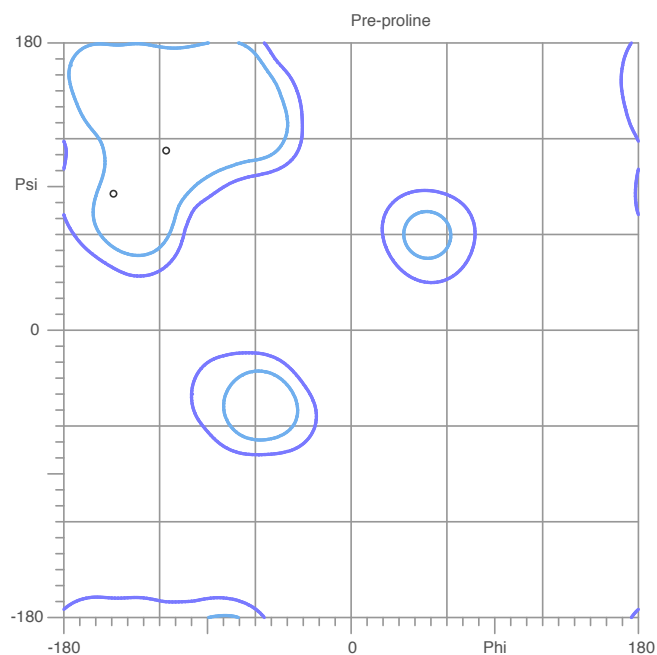
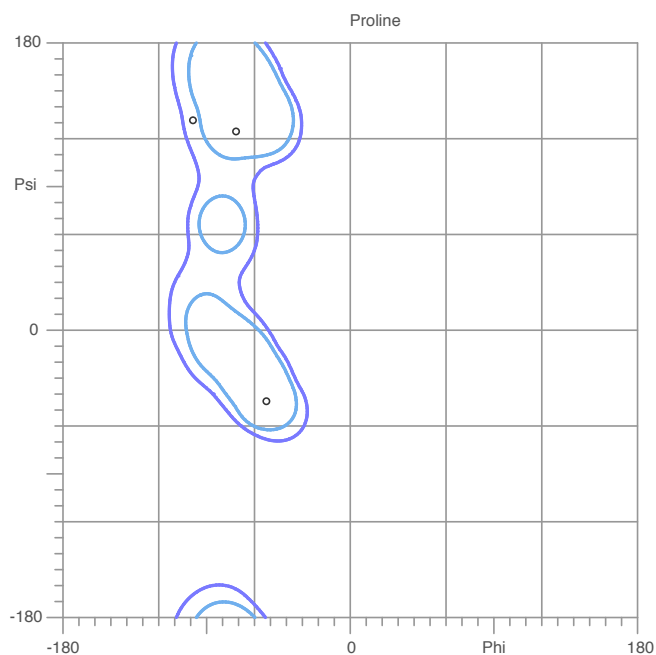
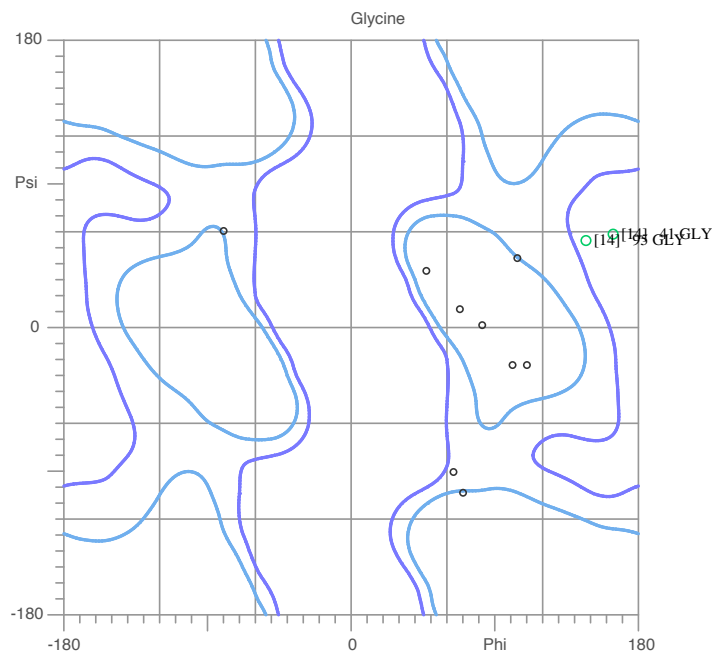
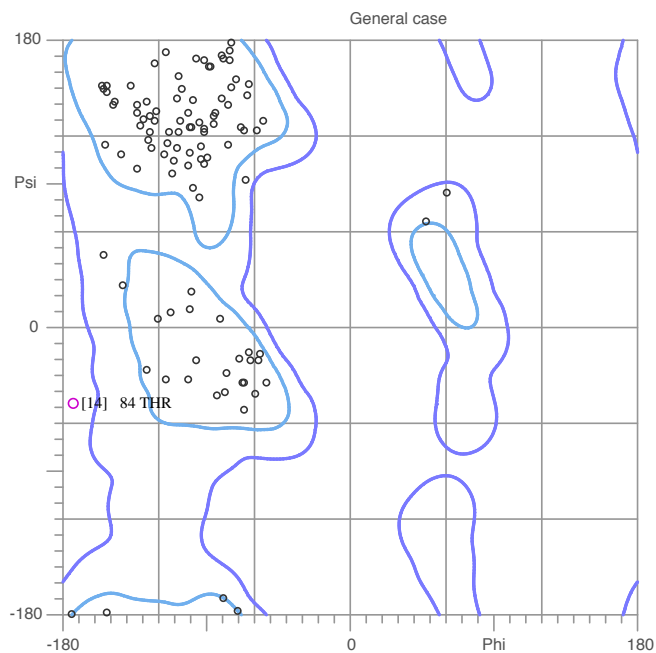
86.7% (104/120) of all residues were in favored (98%) regions.
96.7% (116/120) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [13] 41 GLY (-177.1, 12.6)
- [13] 48 ILE (-167.8, -40.6)
- [13] 81 SER (66.1, 89.9)
- [13] 84 THR (177.0, -44.8)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 14



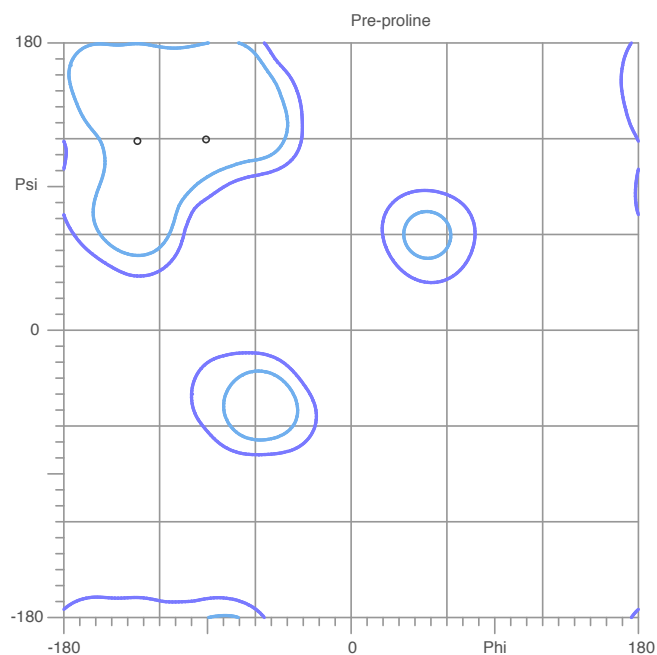
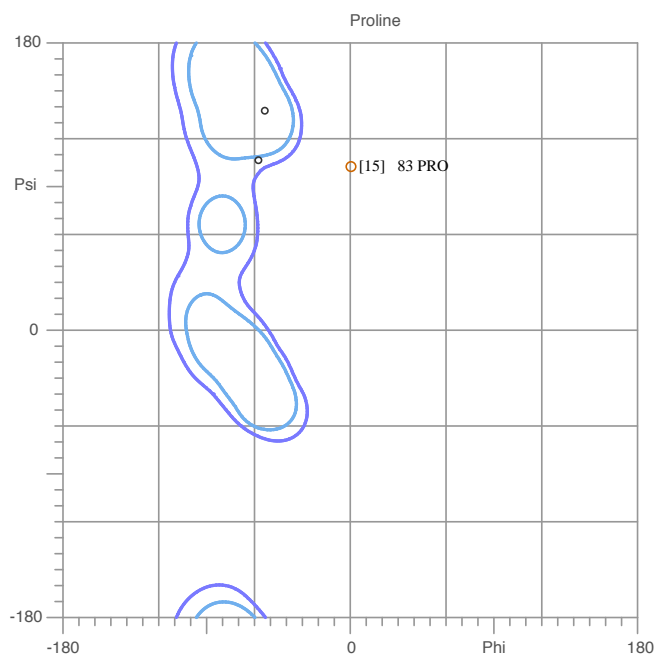
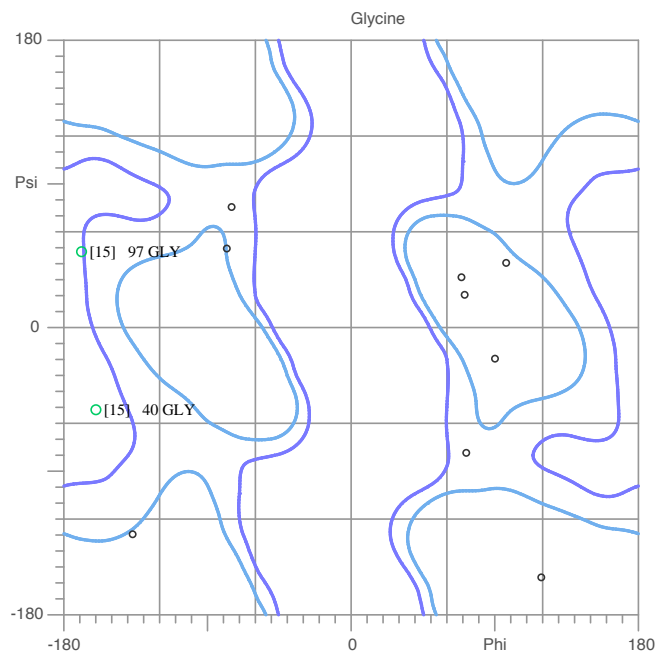
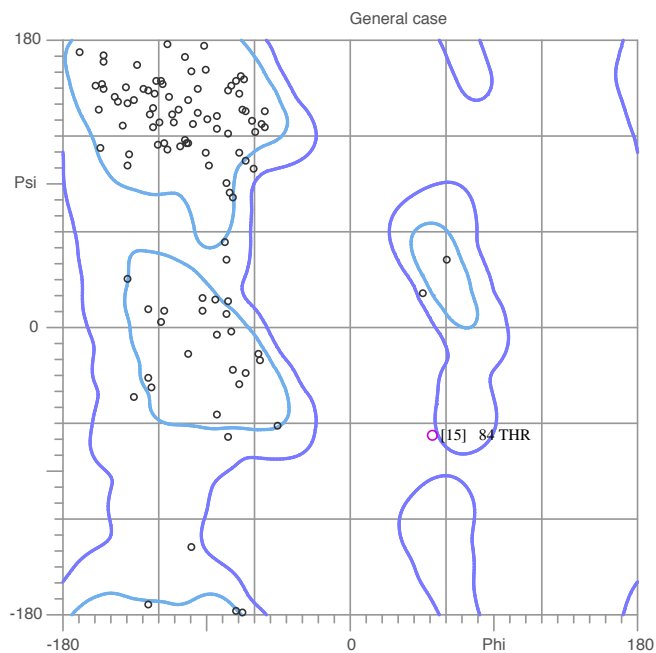
89.2% (107/120) of all residues were in favored (98%) regions.
97.5% (117/120) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [14] 41 GLY (164.1, 59.7)
- [14] 84 THR (-174.7, -47.2)
- [14] 95 GLY (147.2, 55.2)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 15



86.7% (104/120) of all residues were in favored (98%) regions.
96.7% (116/120) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[15] 40 GLY (-160.0, -51.7)

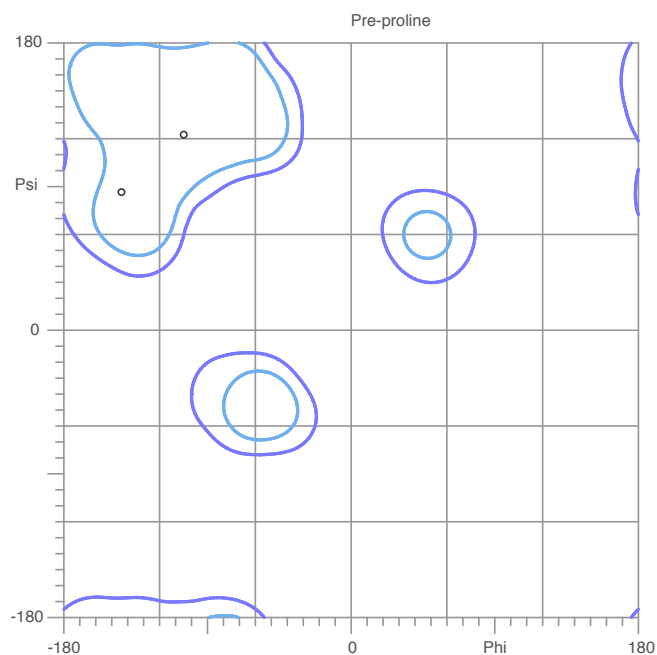
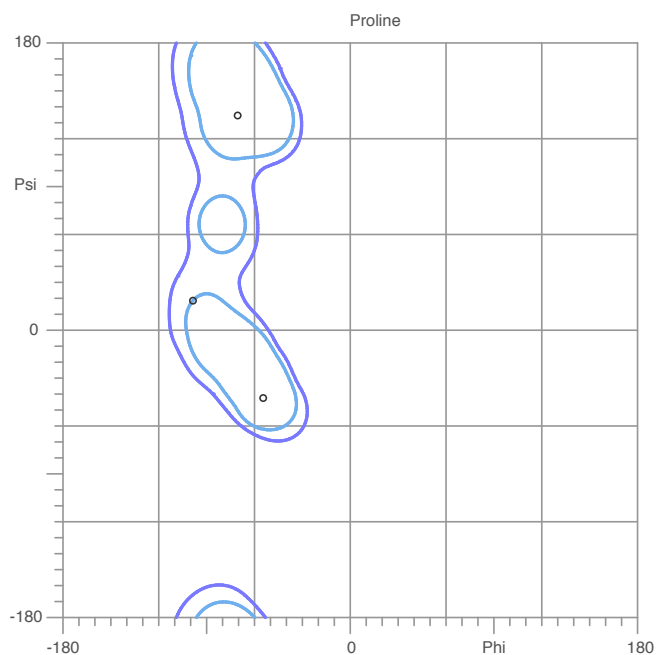
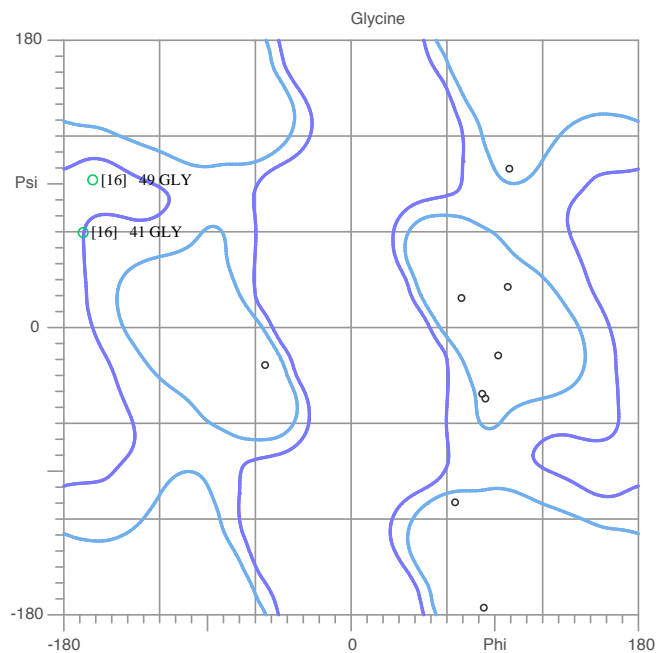
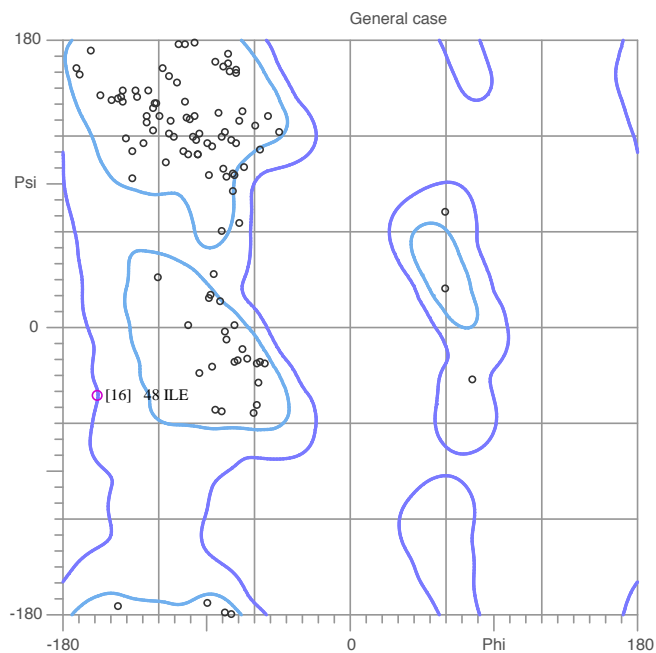
[15] 83 PRO (0.3, 103.6)

[15] 84 THR (51.3, -67.2)

[15] 97 GLY (-169.8, 48.4)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 16



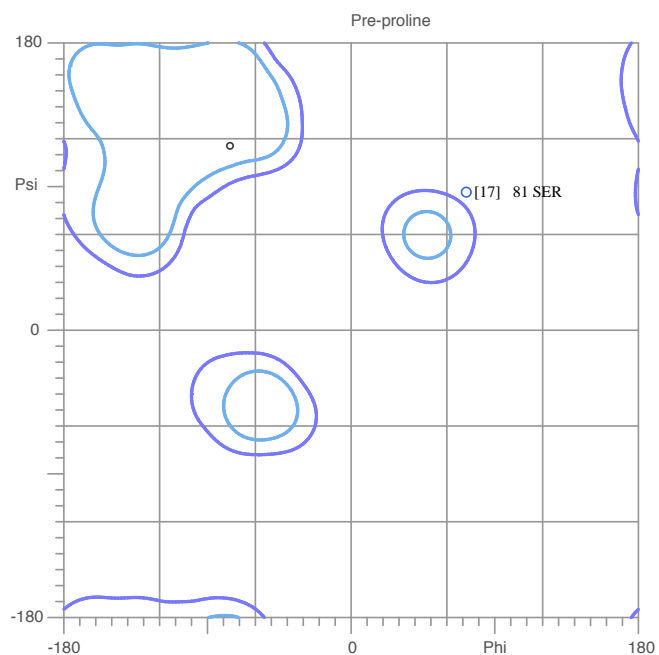
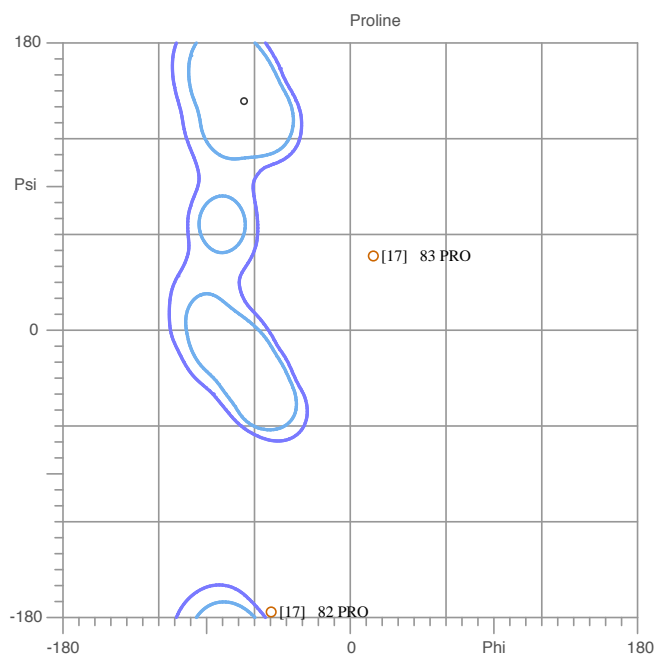
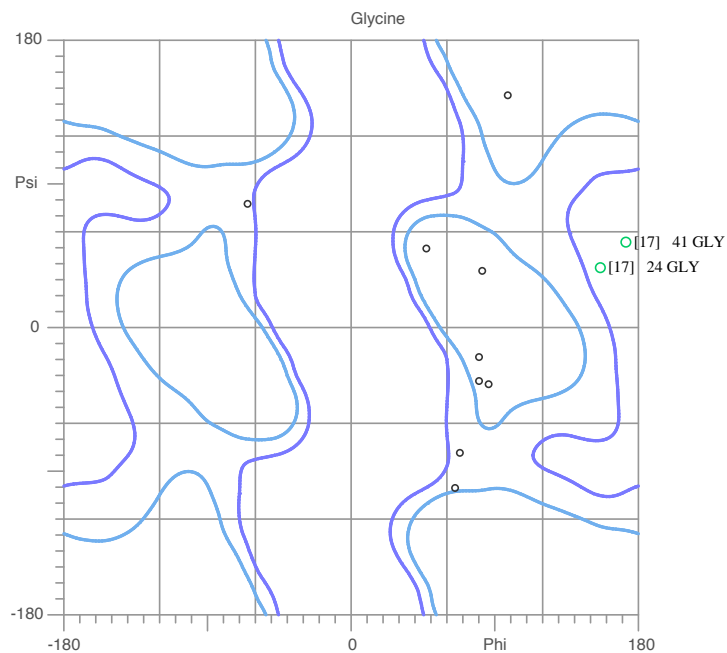
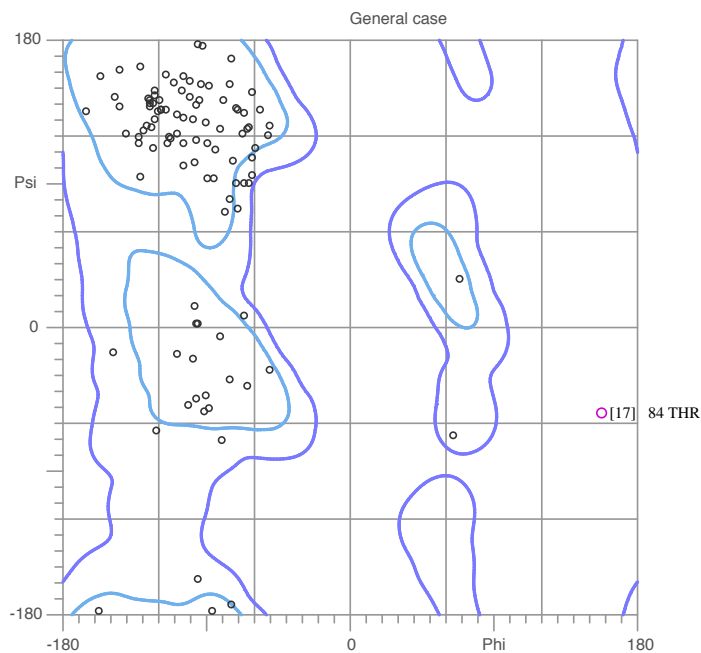
92.5% (111/120) of all residues were in favored (98%) regions.
97.5% (117/120) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [16] 41 GLY (-168.8, 60.1)
- [16] 48 ILE (-159.2, -42.6)
- [16] 49 GLY (-162.6, 93.9)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 17



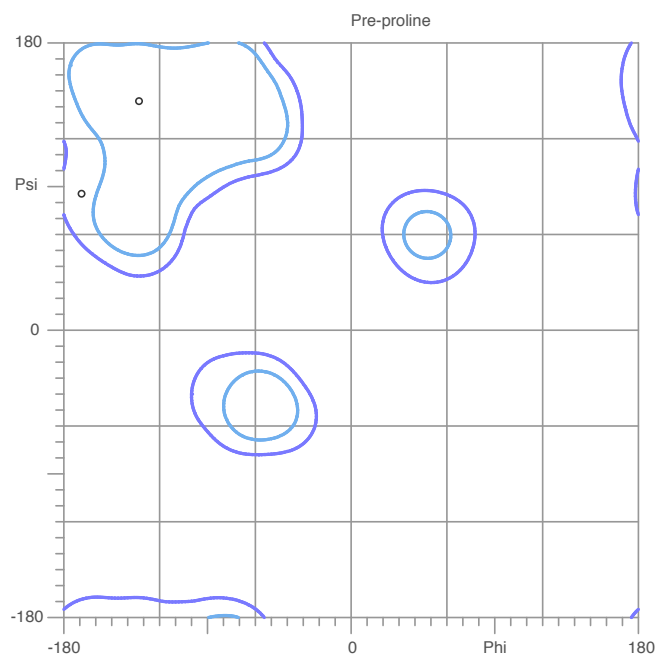
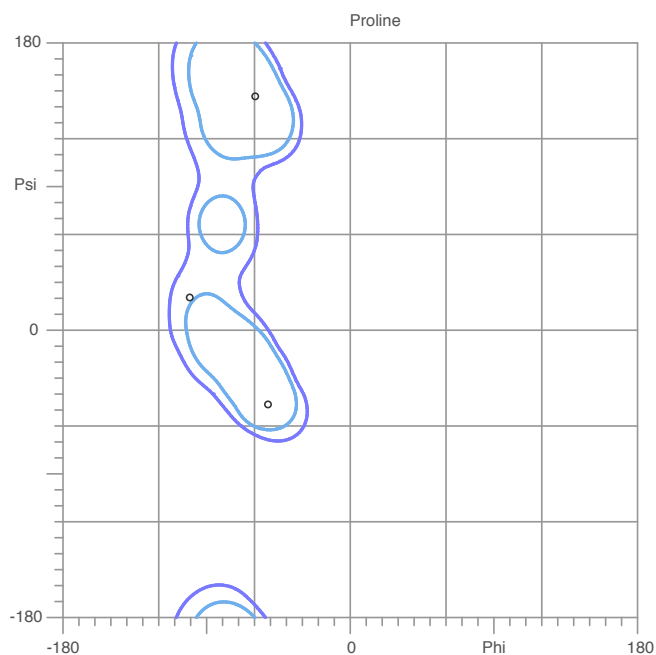
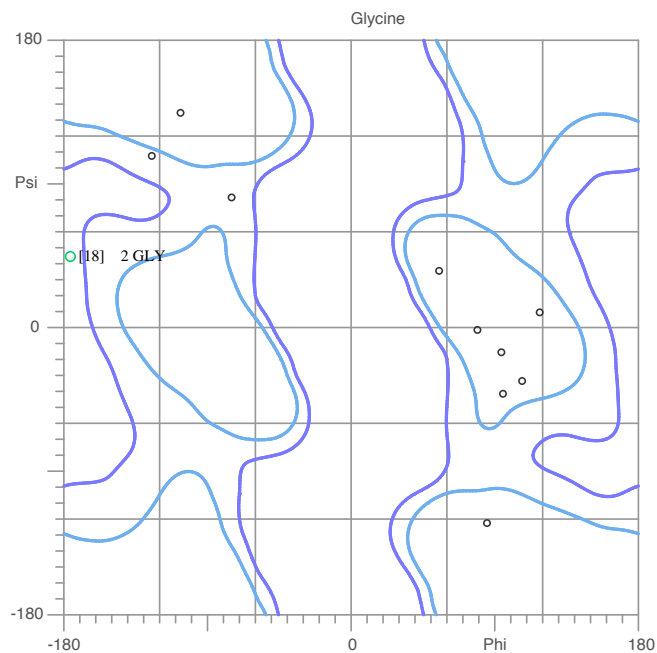
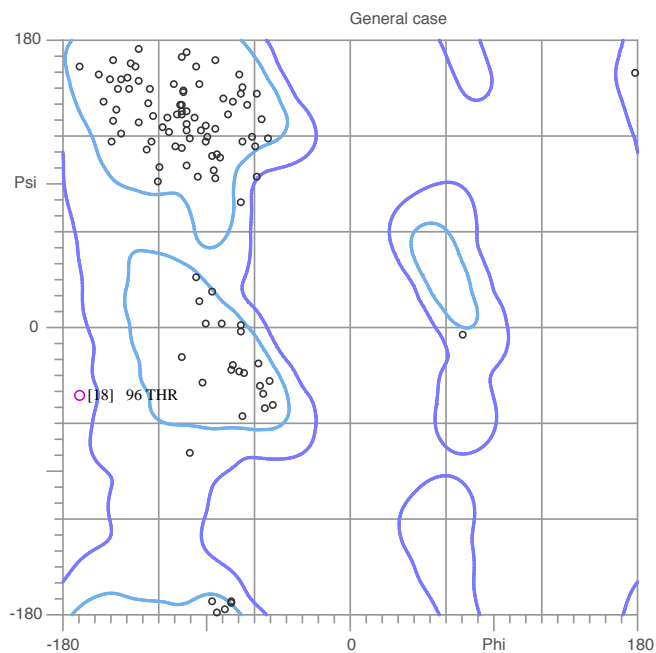
82.5% (99/120) of all residues were in favored (98%) regions.
95.0% (114/120) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[17] 24 GLY (156.4, 38.8)

[17] 41 GLY (172.3, 55.0)
[17] 81 SER (72.8, 87.1)
[17] 82 PRO (-50.7, -176.2)
[17] 83 PRO (14.8, 47.9)
[17] 84 THR (157.7, -53.4)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 18

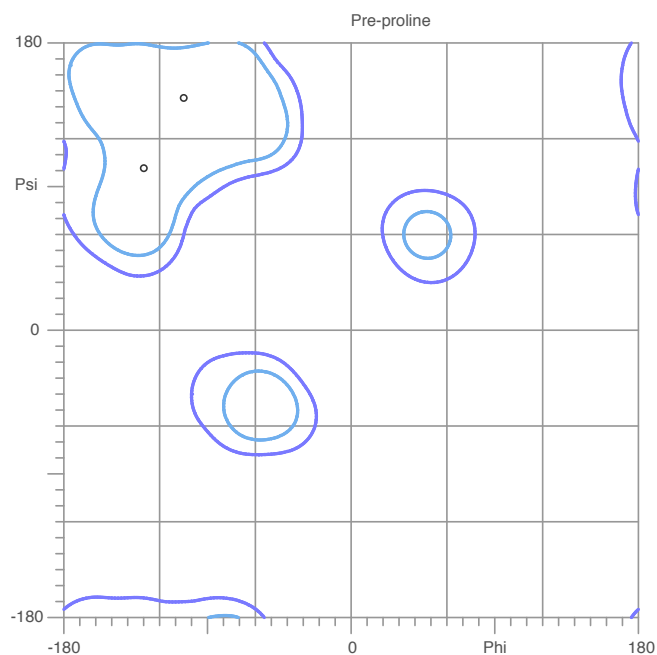
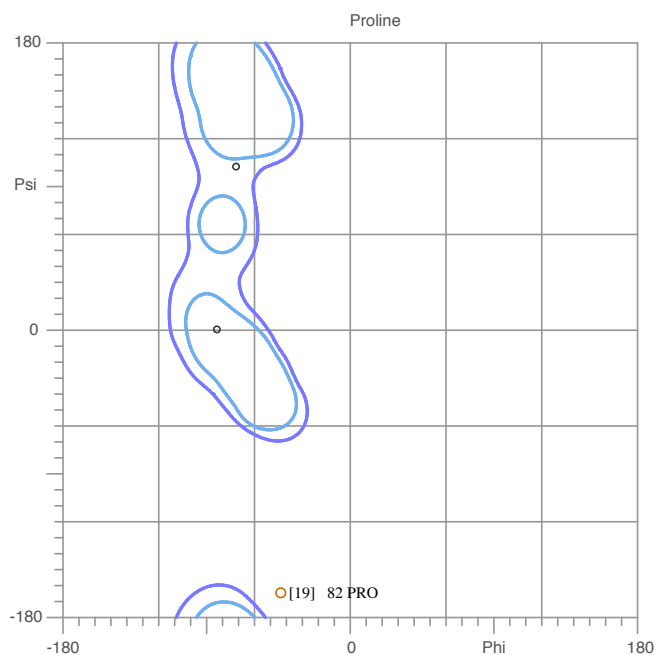
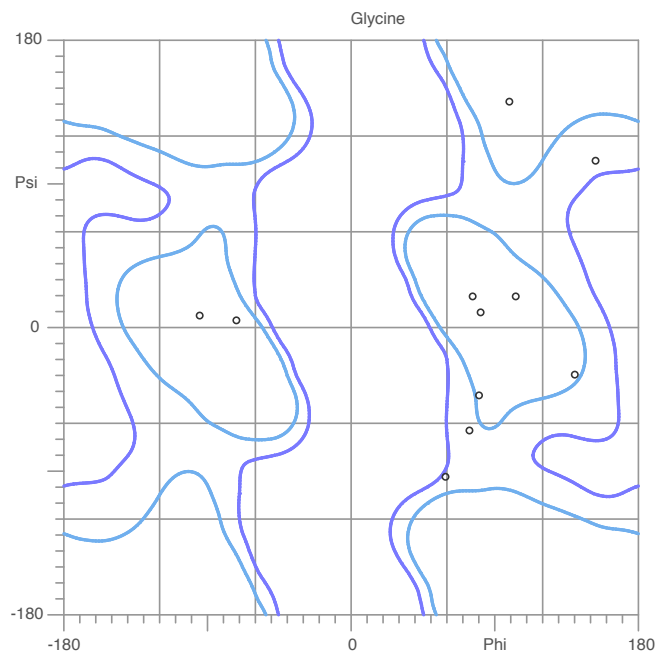
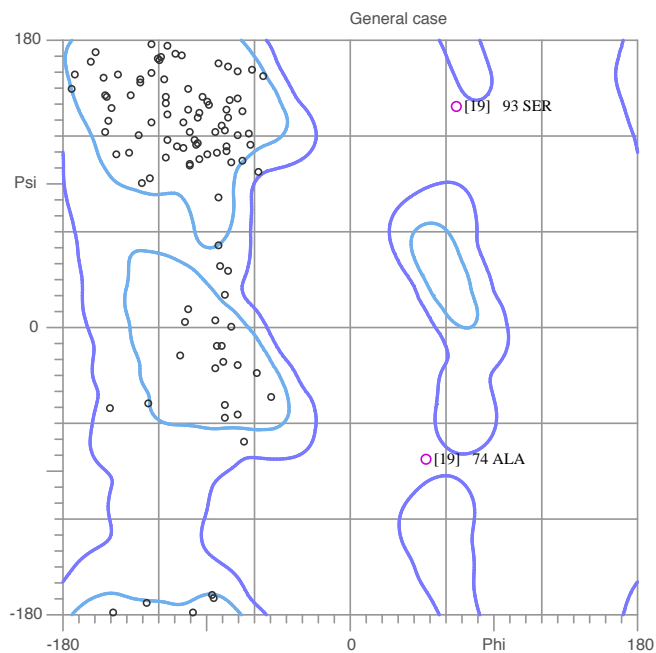


89.2% (107/120) of all residues were in favored (98%) regions.
98.3% (118/120) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 2 GLY (-176.9, 46.0)
[18] 96 THR (-170.9, -42.7)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 19



87.5% (105/120) of all residues were in favored (98%) regions.
97.5% (117/120) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

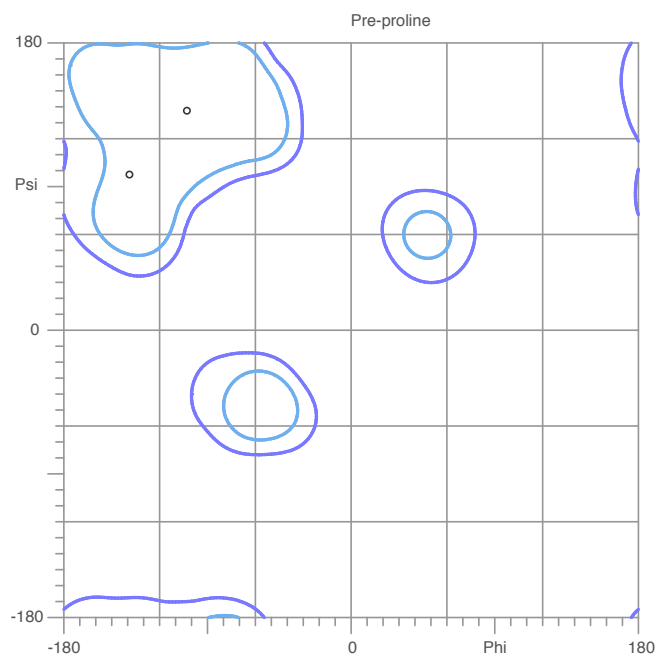
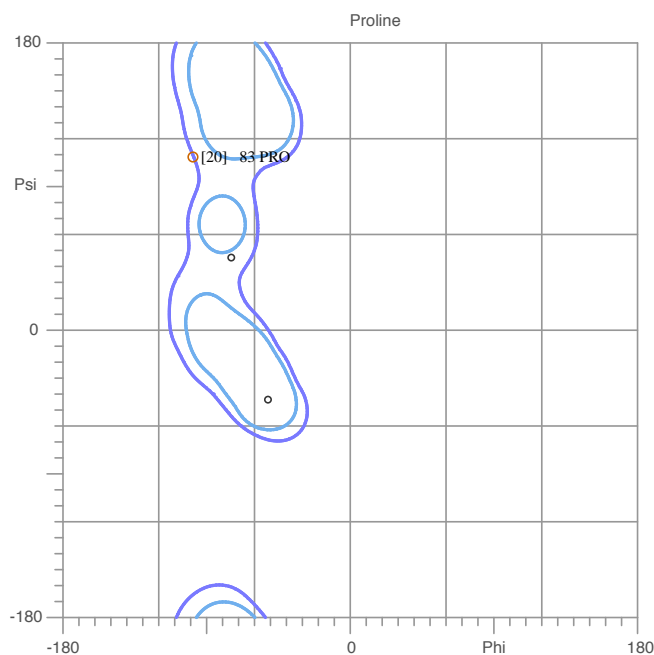
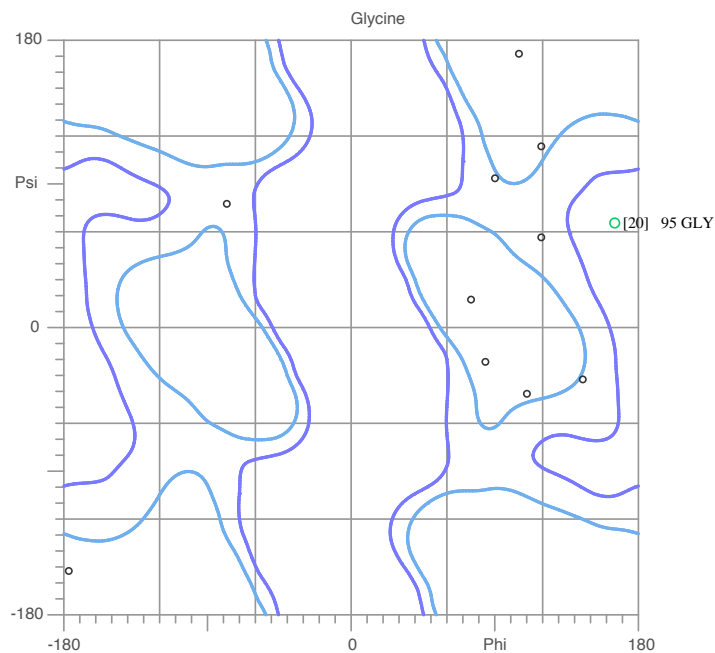
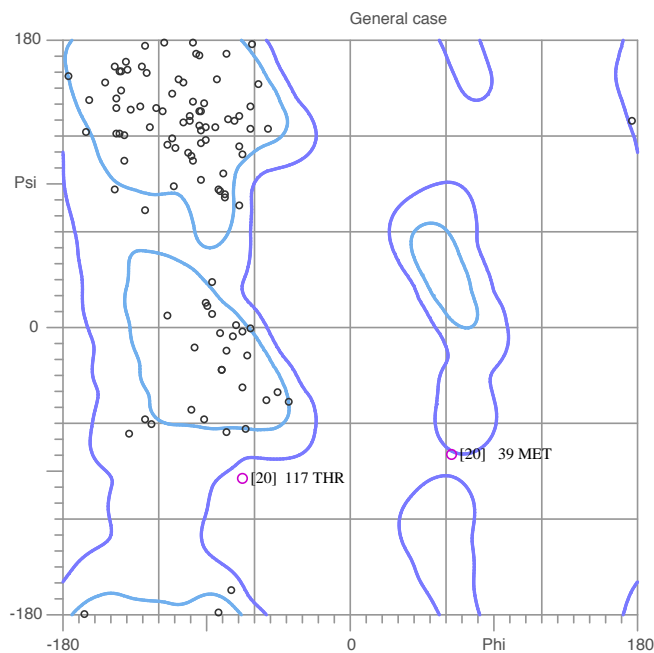
[19] 74 ALA (47.5, -82.6)

[19] 82 PRO (-44.5, -164.1)

[19] 93 SER (66.6, 139.3)

MolProbity Ramachandran analysis

HR5546A_NMR_em_bcr3.pdb, model 20



80.0% (96/120) of all residues were in favored (98%) regions.
96.7% (116/120) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[20] 39 MET (63.1, -79.9)

[20] 83 PRO (-99.3, 109.9)

[20] 95 GLY (165.2, 66.3)

[20] 117 THR (-68.4, -94.4)