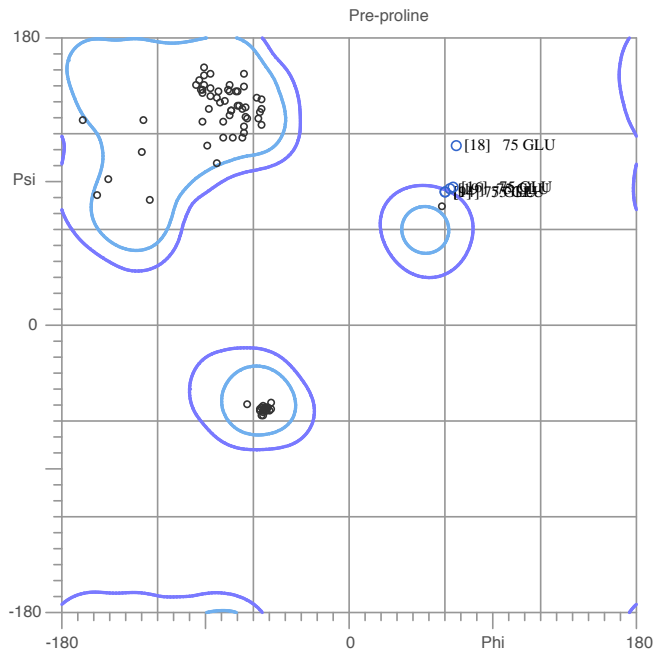
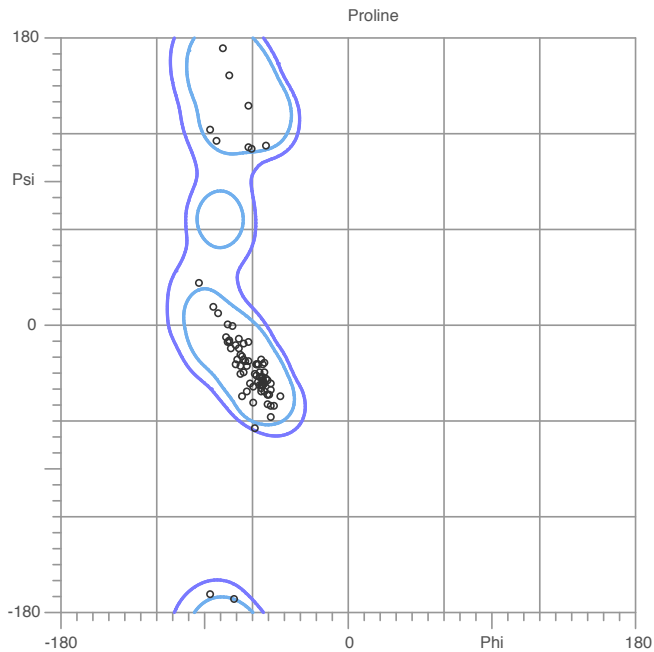
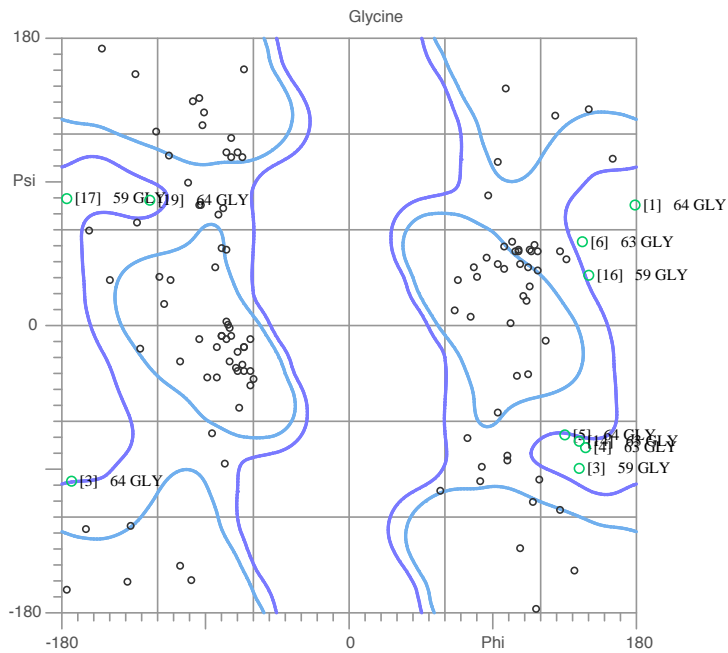
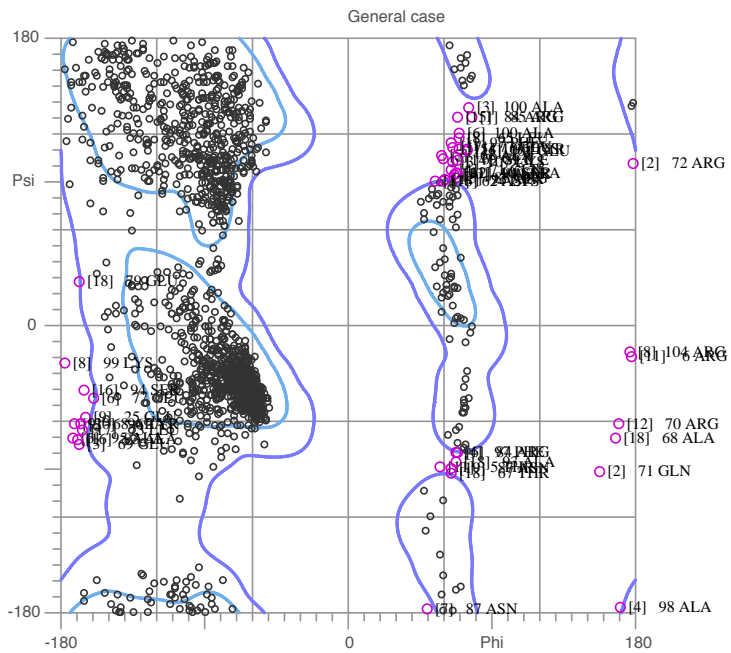


MolProbity Ramachandran analysis

2RN7_NMR.pdb, all models



85.8% (1820/2120) of all residues were in favored (98%) regions.
97.1% (2058/2120) of all residues were in allowed (>99.8%) regions.

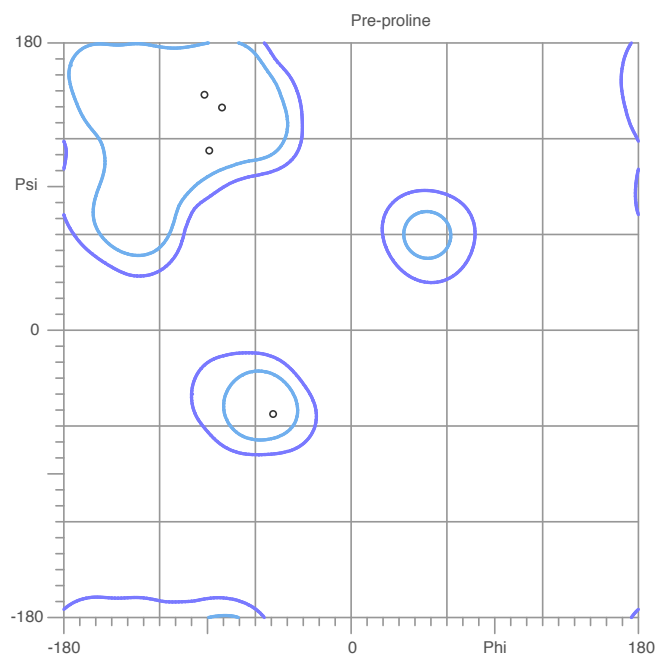
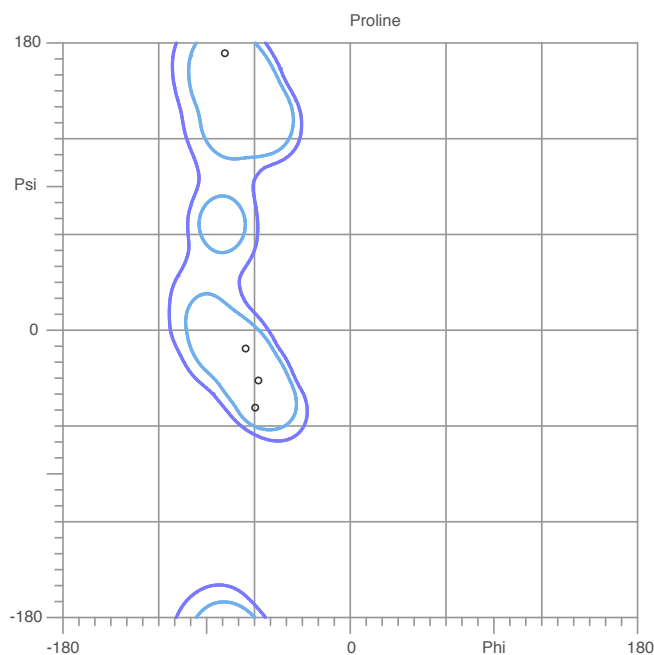
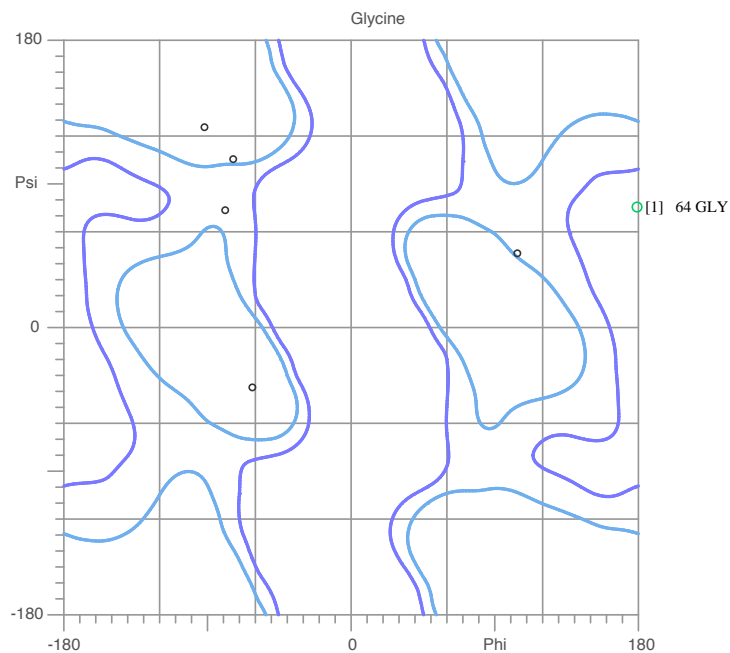
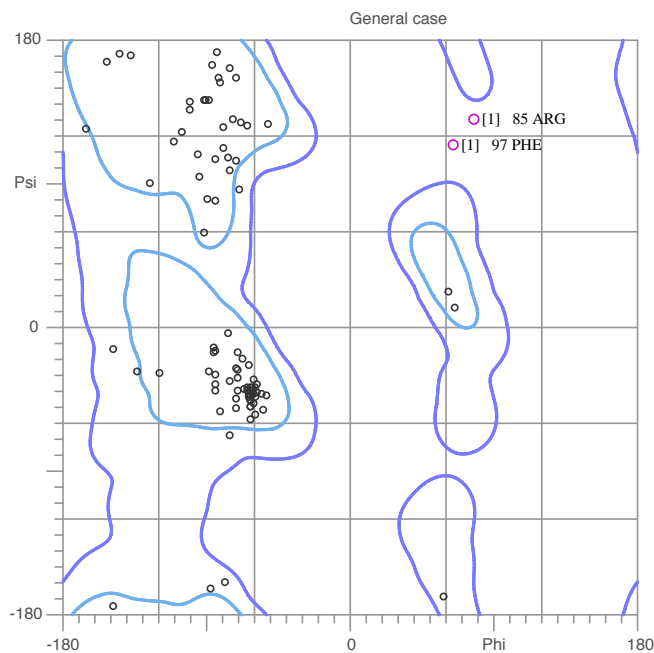
There were 62 outliers (phi, psi):

- [1] 85 GRL (1800, 76, 6)
- [2] 88 GRL (772, 131, 12)
- [3] 88 GRL (1782, 102, 6)
- [4] 71 GLN (1579, 91, 6)
- [5] 72 GRL (1782, 102, 6)
- [6] 59 GYL (1445, 89, 6)
- [7] 68 GYL (-1742, -97, 3)
- [8] 69 GYL (-169, -75, 10)
- [9] 100 ALA (753, 137, 0)
- [10] 107 LYS (654, 103, 2)
- [11] 63 GYL (1481, -76, 8)
- [12] 69 GYL (594, 105, 1)
- [13] 69 GYL (1732, 98, 2)
- [14] 97 PHE (78, -79, 2)
- [15] 98 ALA (1704, -176, 2)
- [16] 64 GYL (1353, -48, 6)
- [17] 88 ALA (581, 107, 2)
- [18] 85 GRL (607, 93, 7)
- [19] 63 GYL (1462, 53, 6)
- [20] 77 GYL (-160, -22, -45.5)
- [21] 84 GRL (682, -79, 6)
- [22] 84 GYL (773, -2, 98.2)
- [23] 100 ALA (698, 121, 1)
- [24] 87 ASN (495, -177, 4)
- [25] 85 LEU (595, 118, 9)
- [26] 39 PLYS (-1790, 23, 6)
- [27] 104 ARG (1762, -22, 6)
- [28] 25 GYL (-160, -67, 8)
- [29] 68 ALA (-172, -1, 51.3)

- [9] 75 GLU (0.64, 84.8)
- [10] 94 SER (0.64, 96.0)
- [11] 5 THR (57.2, -49.0)
- [12] 6 ARG (177.1, -89.8)
- [13] 93 ALA (0.60, 92.7)
- [14] 94 SER (67.9, 96.8)
- [15] 70 ARG (169.6, -61.5)
- [16] 100 ALA (109.9, -96.5)
- [17] 63 GLY (144.0, -72.5)
- [18] 75 GLU (60.0, 84.8)
- [19] 89 ILE (68.8, 104.9)
- [20] 96 TYR (74.1, 111.4)
- [21] 84 GLU (68.1, 131.3)
- [22] 101 GLU (74.4, 110.0)
- [23] 107 LYS (69.4, 111.5)
- [24] 59 GLY (150.5, 32.6)
- [25] 74 LYS (59.2, 91.6)
- [26] 94 SER (67.9, 96.8)
- [27] 94 SER (-170.5, -71.4)
- [28] 94 SER (-166.0, -82.0)
- [29] 59 GLY (-177.7, 80.9)
- [30] 62 ASP (54.0, 92.0)
- [31] 73 LEU (-167.0, -45.5)
- [32] 77 GLU (65.5, 112.9)
- [33] 67 THR (64.2, -92.5)
- [34] 68 ALA (167.1, -70.8)
- [35] 75 GLU (67.0, 113.7)
- [36] 93 GLU (-169.5, -29.0)
- [37] 59 ALA (67.4, -85.2)
- [38] 64 GLY (-125.0, 79.9)
- [39] 75 GLU (63.0, 86.6)
- [40] 87 ASN (64.3, -89.3)
- [41] 96 TYR (-168.7, -61.4)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 1



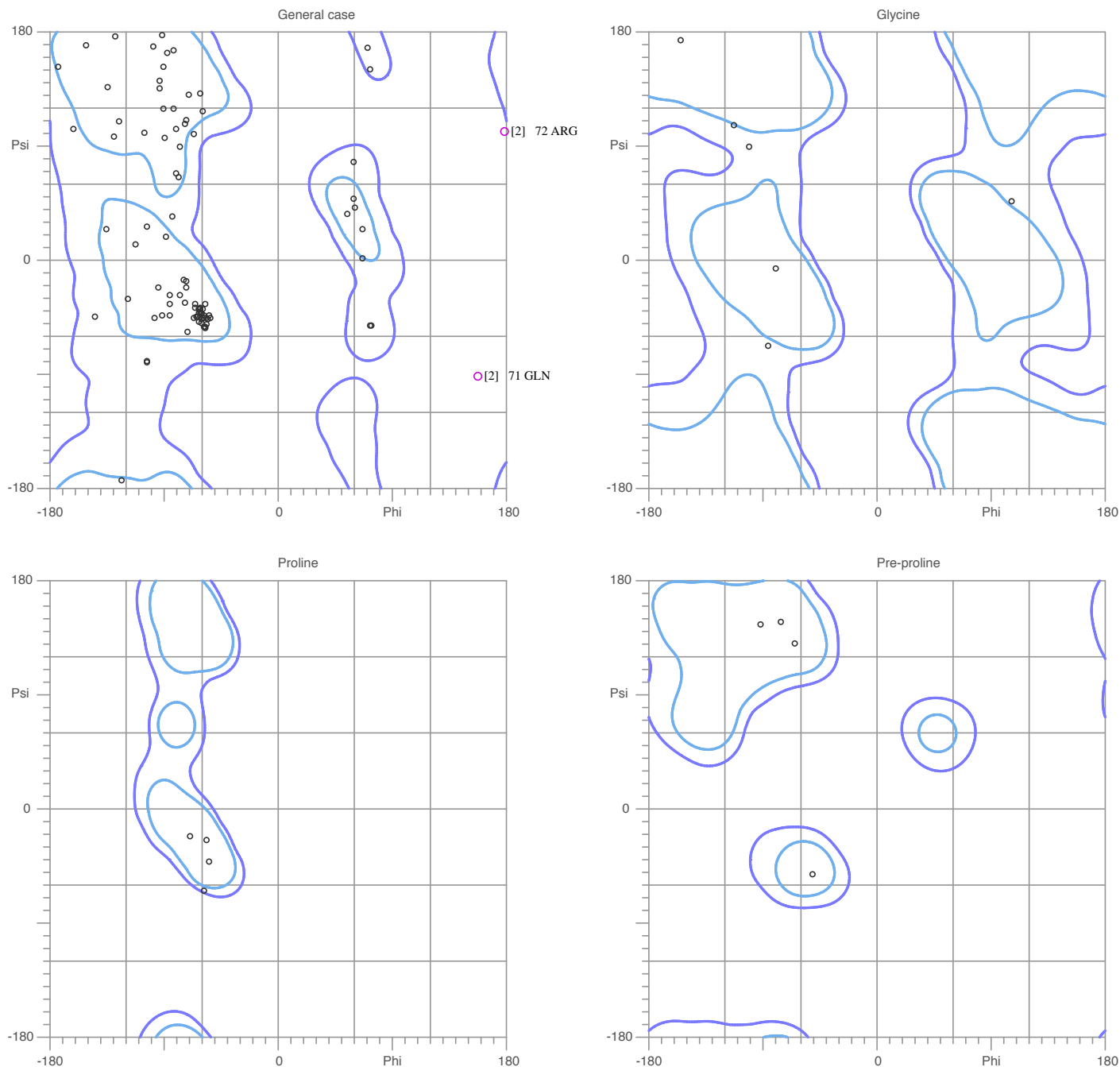
87.7% (93/106) of all residues were in favored (98%) regions.
97.2% (103/106) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 64 GLY (180.0, 76.3)
- [1] 85 ARG (77.2, 131.2)
- [1] 97 PHE (64.6, 115.1)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 2



83.0% (88/106) of all residues were in favored (98%) regions.
98.1% (104/106) of all residues were in allowed (>99.8%) regions.

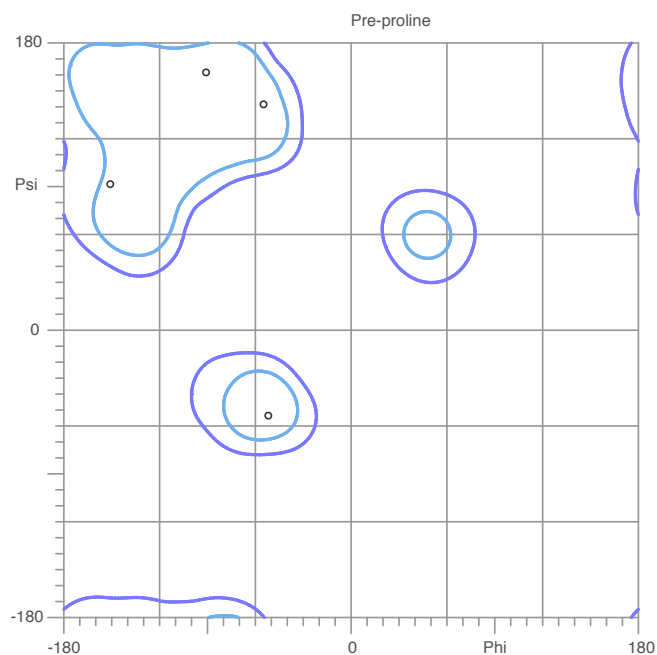
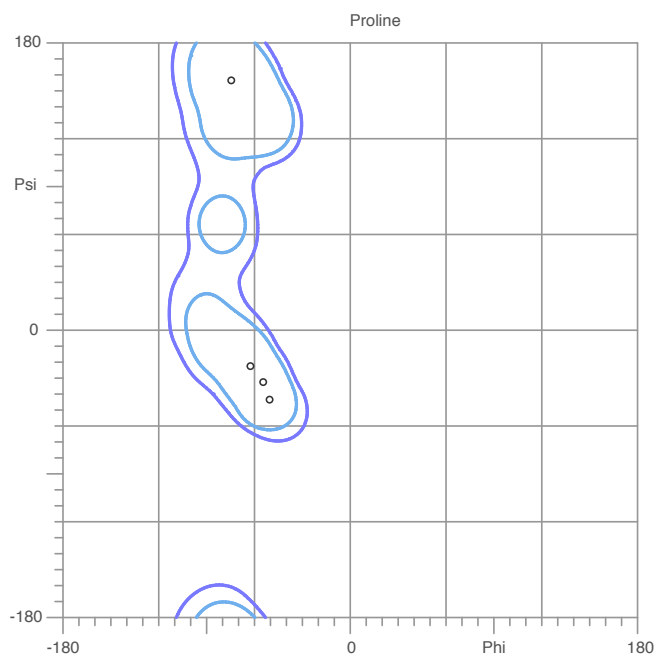
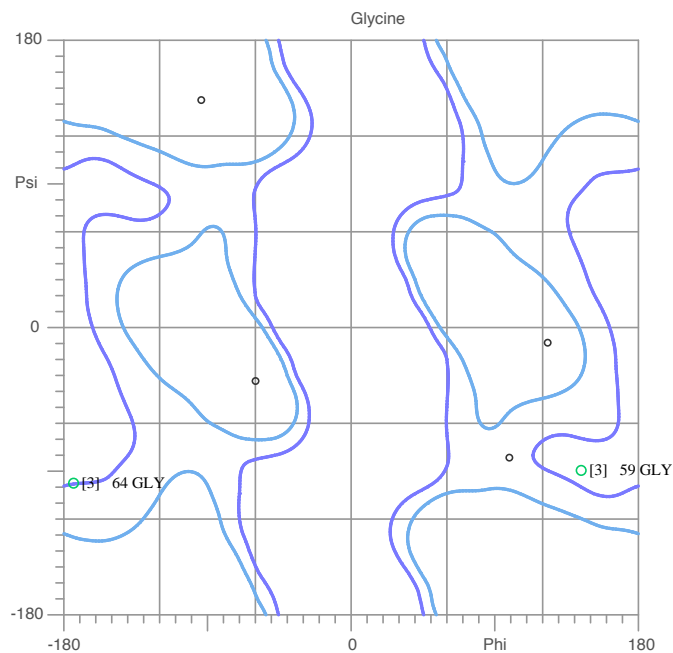
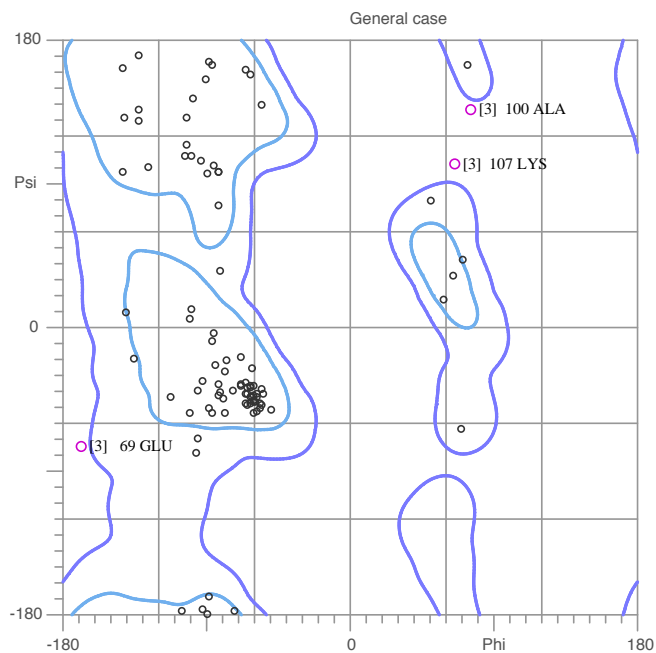
There were 2 outliers (phi, psi):

[2] 71 GLN (157.9, -91.6)

[2] 72 ARG (178.2, 102.6)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 3



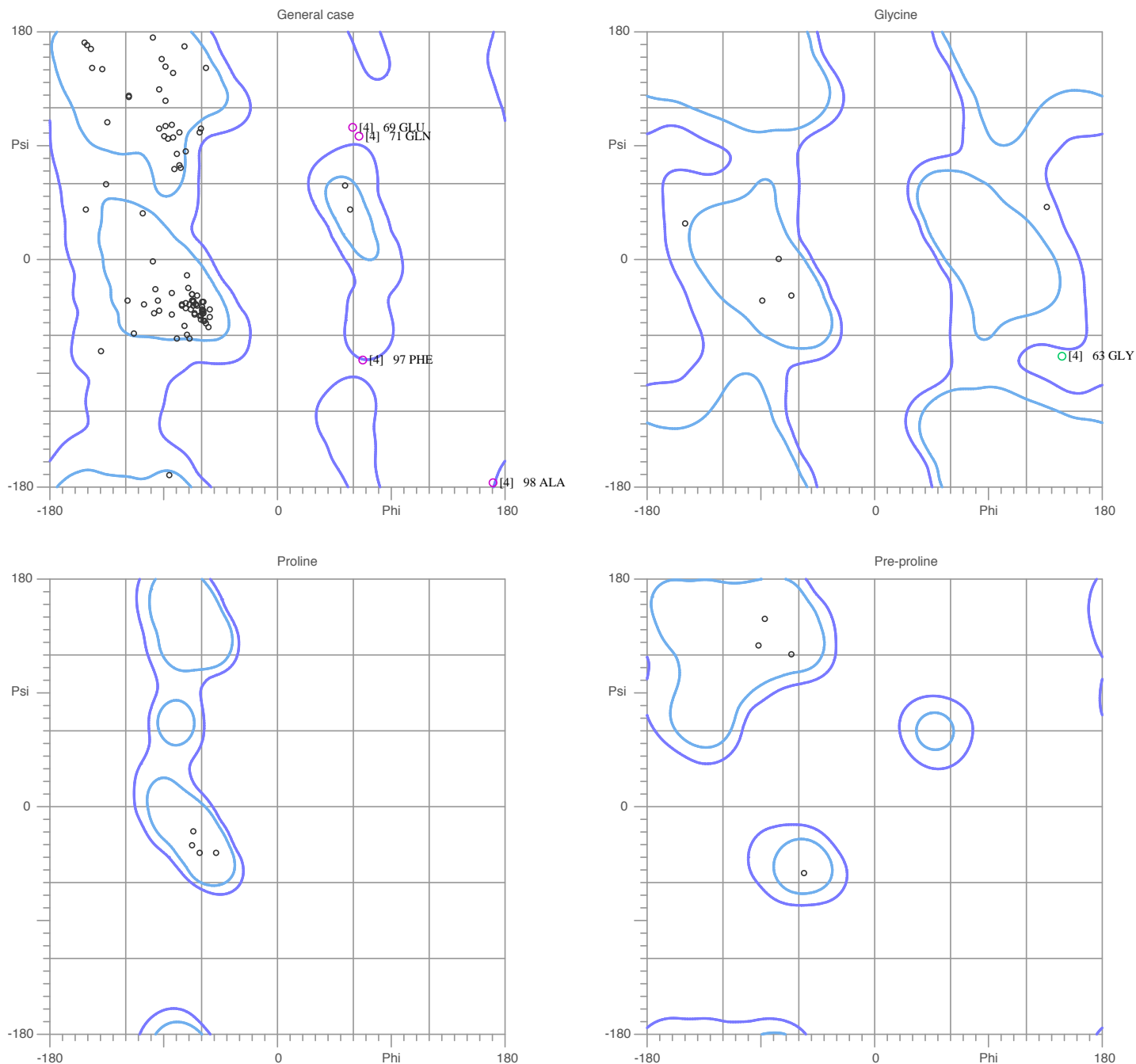
85.8% (91/106) of all residues were in favored (98%) regions.
95.3% (101/106) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[3] 59 GLY (144.5, -89.6)
[3] 64 GLY (-174.2, -97.3)
[3] 69 GLU (-169.1, -75.0)
[3] 100 ALA (75.3, 137.1)
[3] 107 LYS (65.4, 103.2)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 4



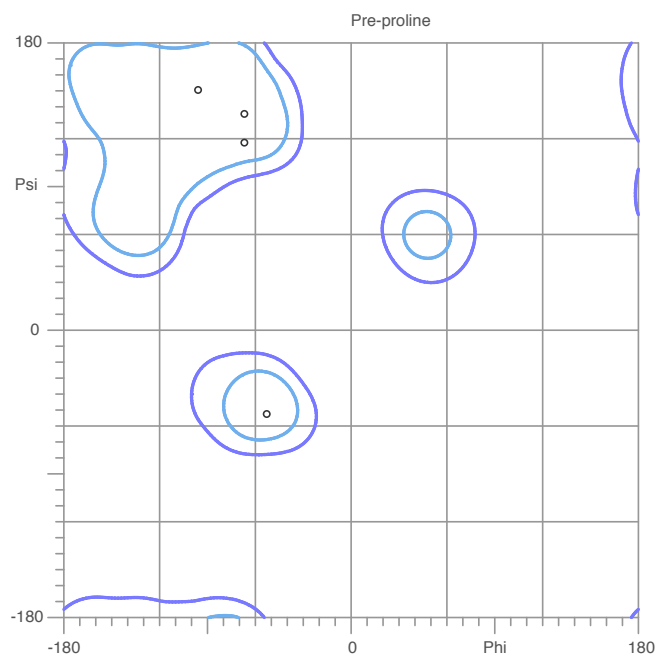
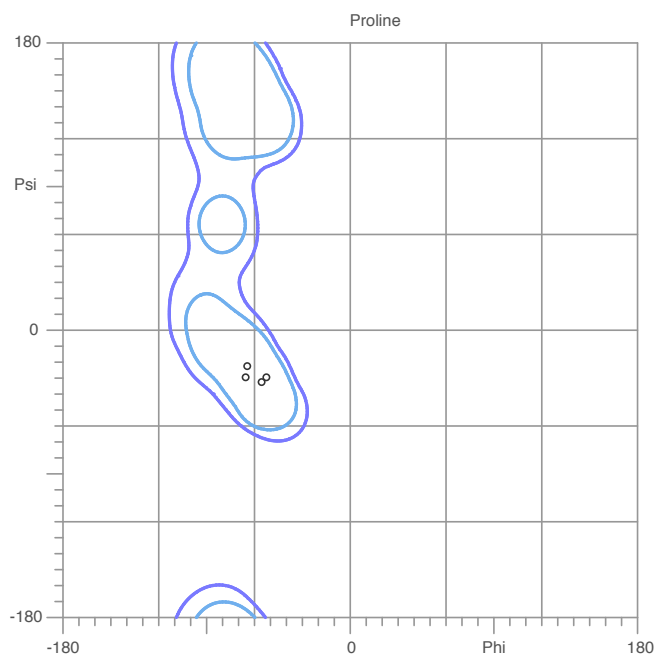
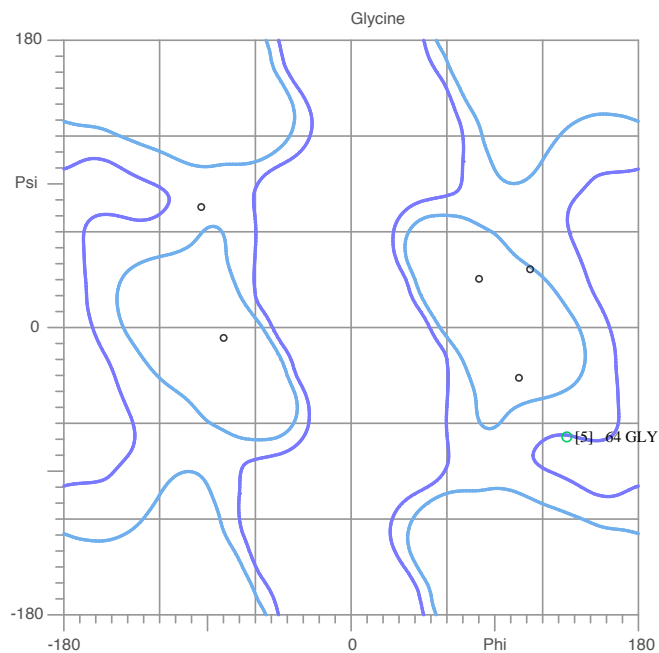
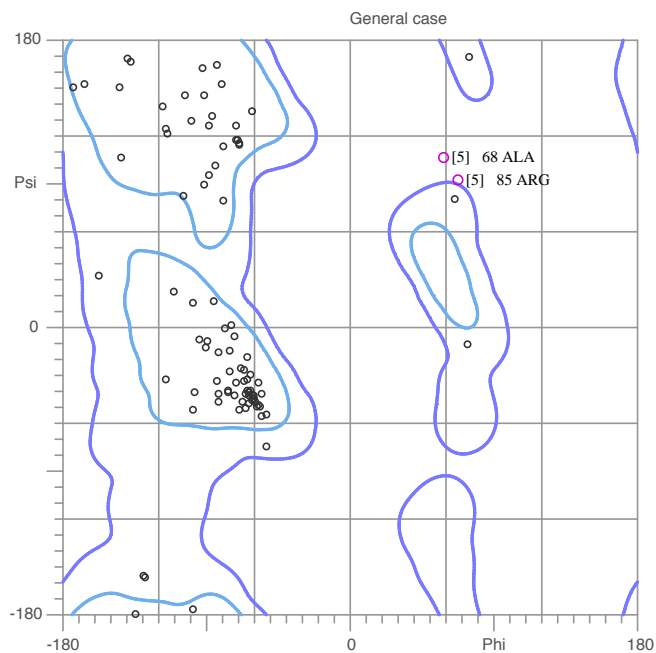
88.7% (94/106) of all residues were in favored (98%) regions.
95.3% (101/106) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (ϕ , ψ):

[4] 63 GLY (148.1, -76.8)
[4] 69 GLU (59.4, 105.1)
[4] 71 GLN (64.2, 98.2)
[4] 97 PHE (67.8, -79.2)
[4] 98 ALA (170.4, -176.2)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 5



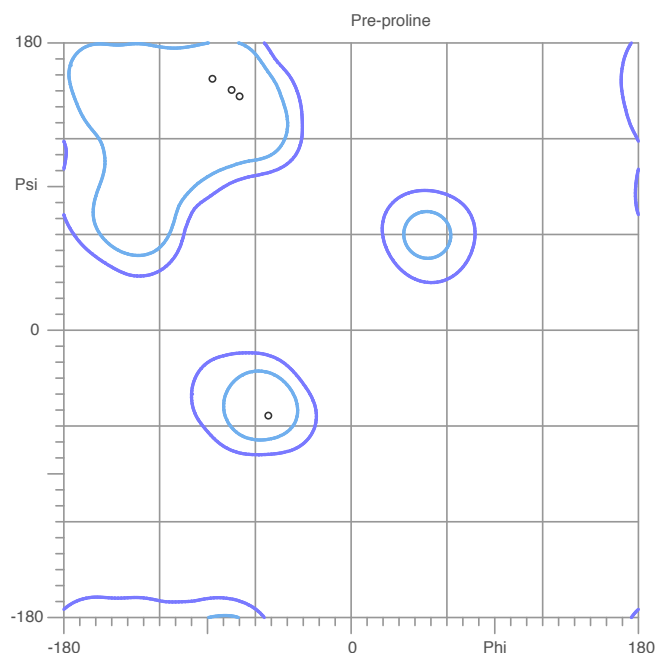
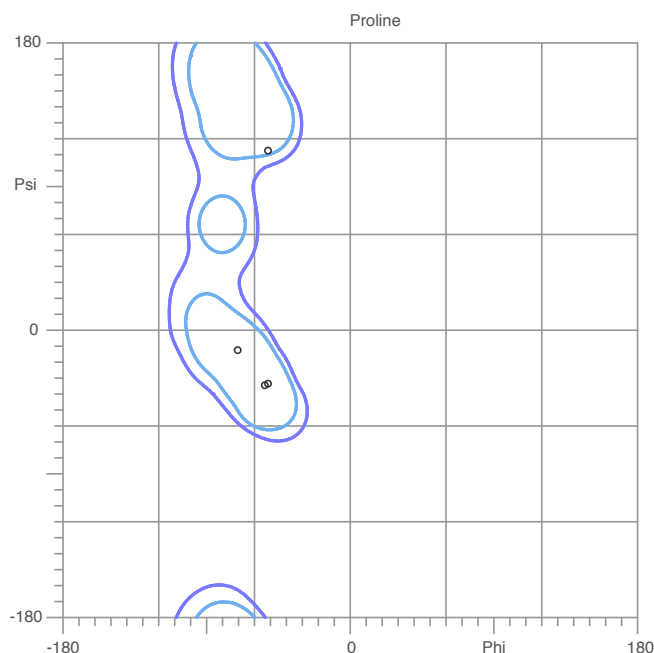
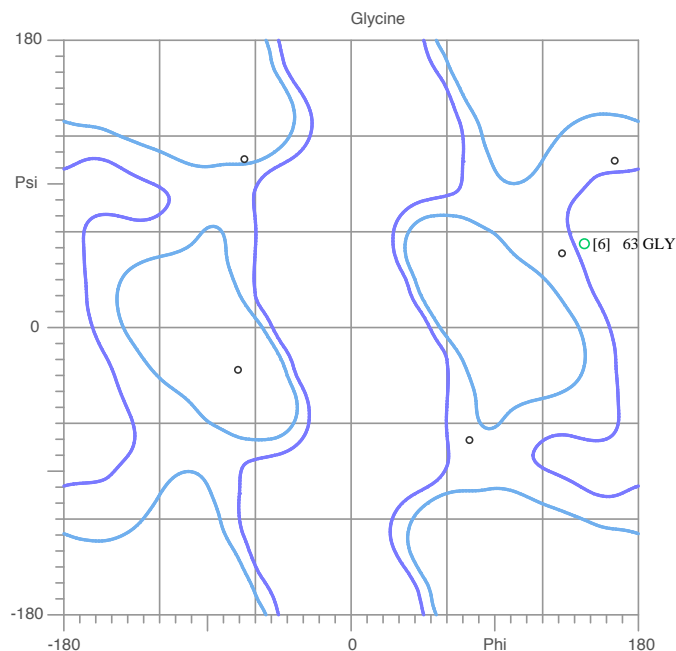
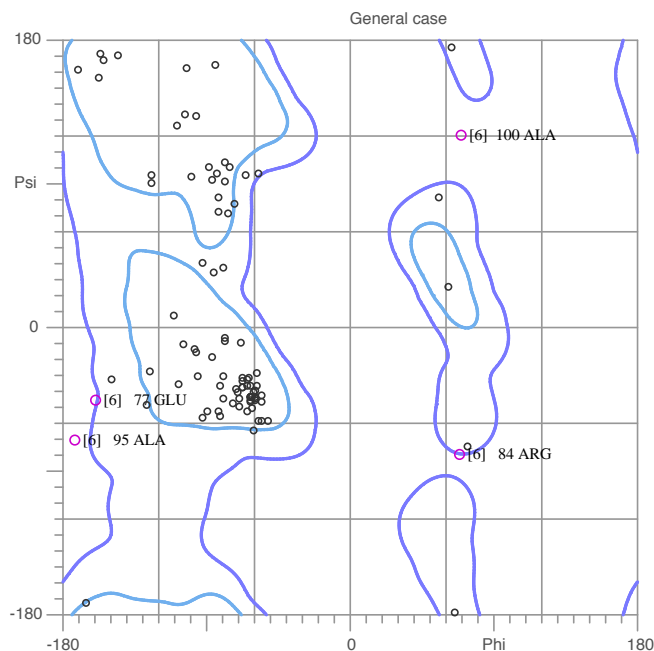
89.6% (95/106) of all residues were in favored (98%) regions.
97.2% (103/106) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [5] 64 GLY (135.3, -68.4)
- [5] 68 ALA (58.1, 107.2)
- [5] 85 ARG (67.0, 93.7)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 6



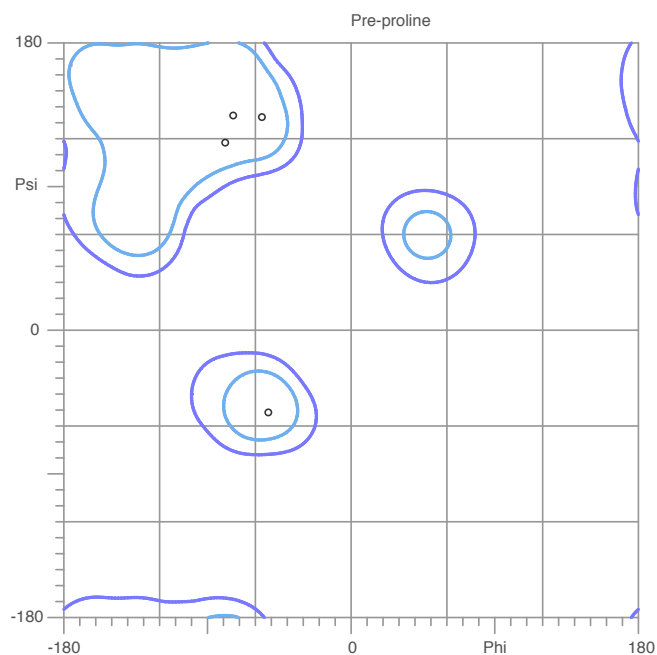
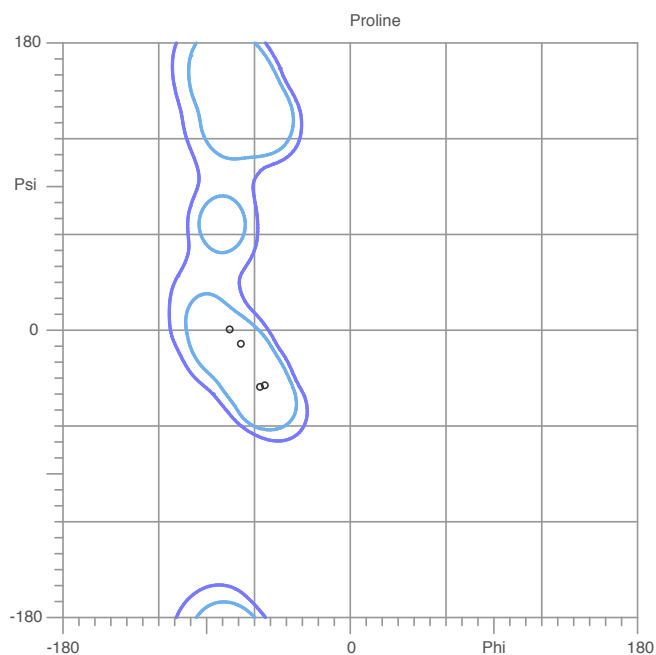
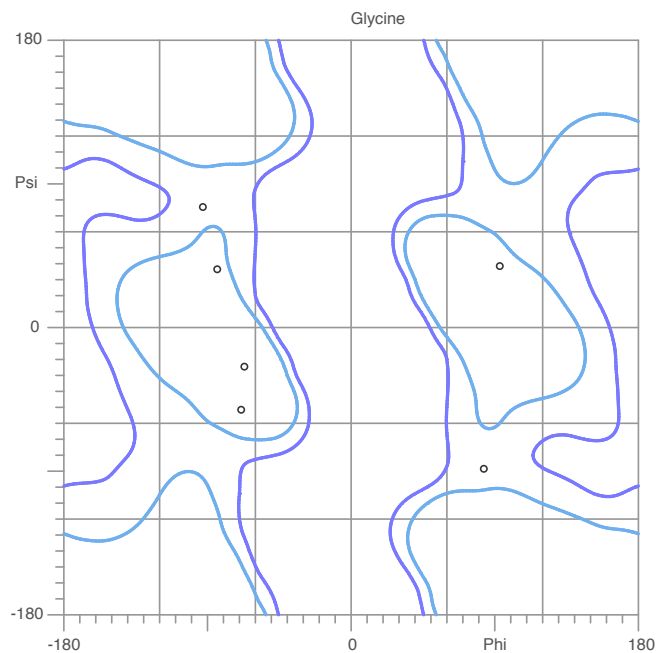
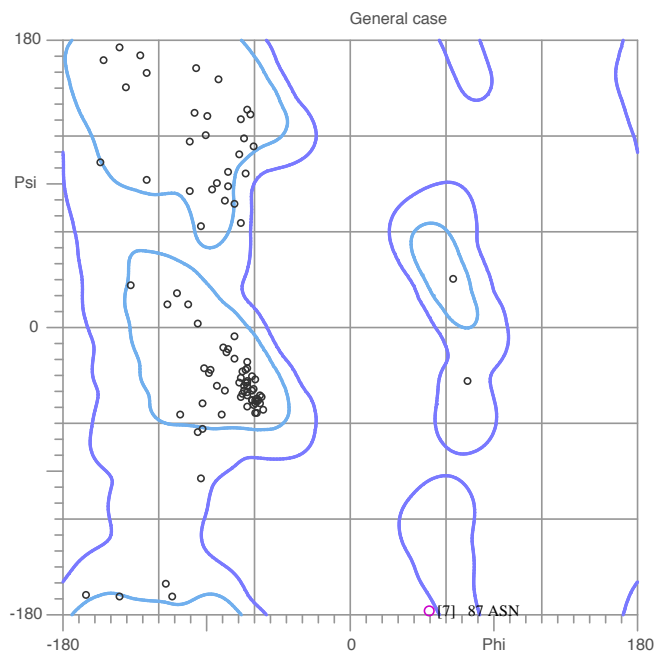
81.1% (86/106) of all residues were in favored (98%) regions.
95.3% (101/106) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[6] 63 GLY (146.2, 53.9)
[6] 77 GLU (-160.2, -45.5)
[6] 84 ARG (68.2, -79.6)
[6] 95 ALA (-173.3, -70.3)
[6] 100 ALA (69.8, 121.1)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 7



87.7% (93/106) of all residues were in favored (98%) regions.
99.1% (105/106) of all residues were in allowed (>99.8%) regions.

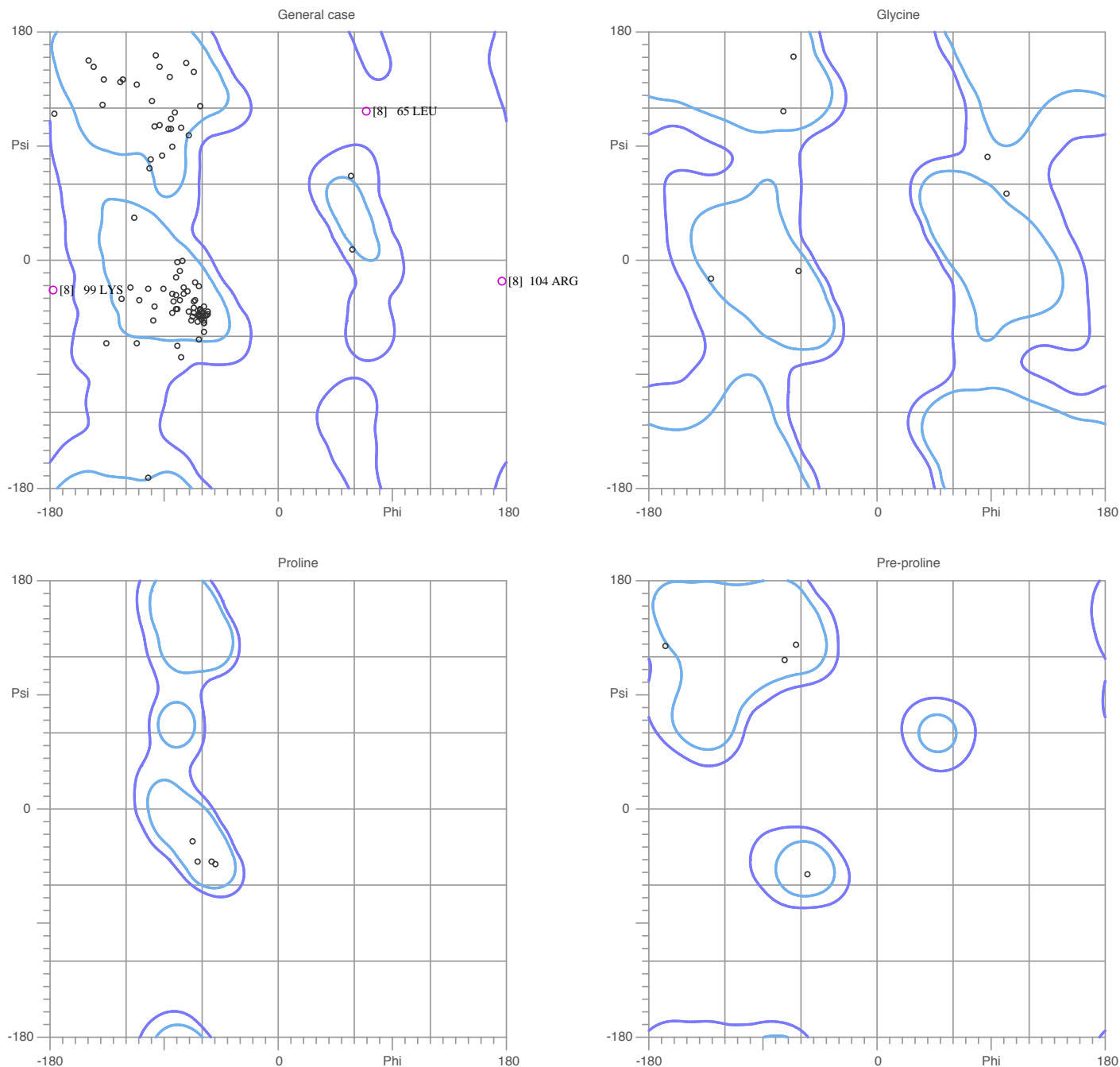
There were 1 outliers (phi, psi):
[7] 87 ASN (49.5, -177.4)

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MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 8



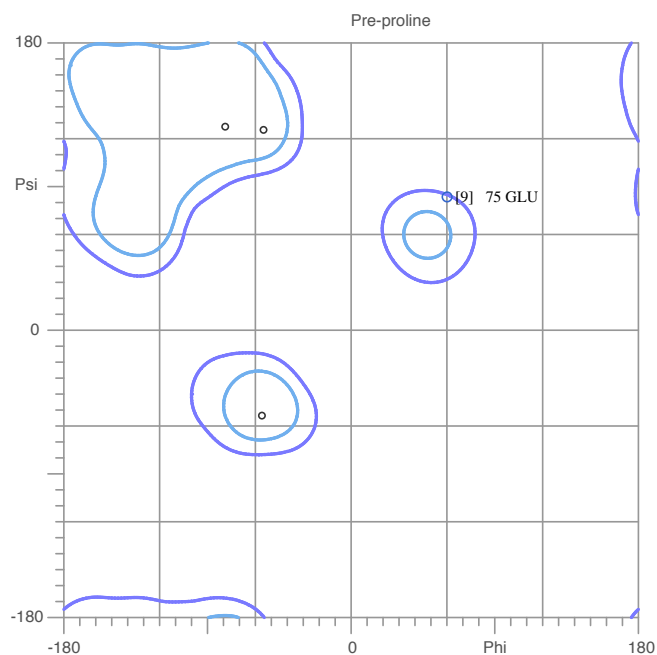
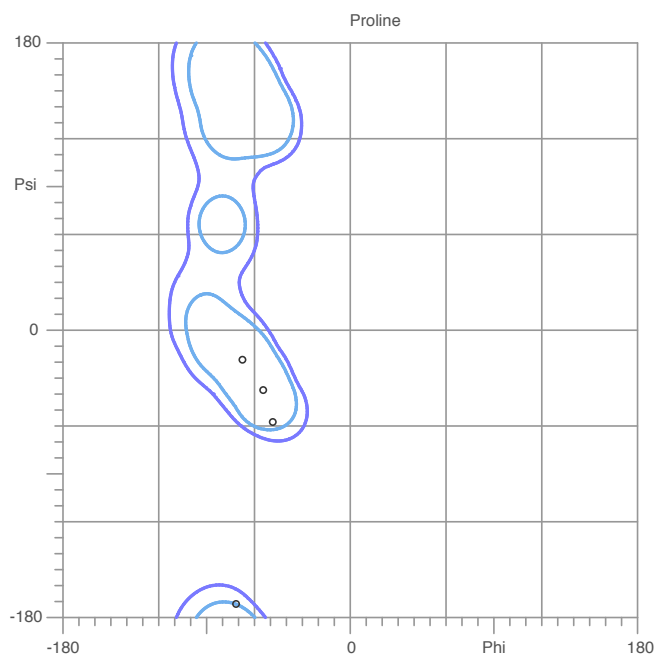
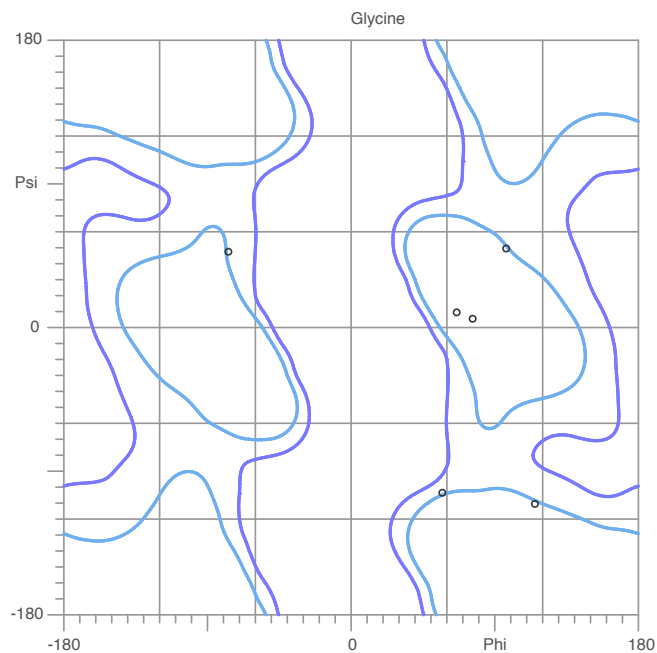
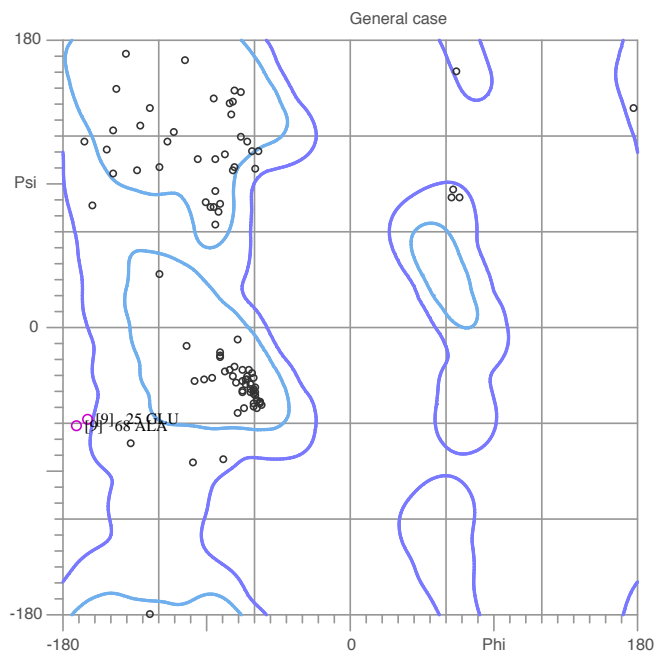
85.8% (91/106) of all residues were in favored (98%) regions.
97.2% (103/106) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 65 LEU (69.5, 118.9)
- [8] 99 LYS (-179.0, -23.6)
- [8] 104 ARG (176.2, -16.3)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 9



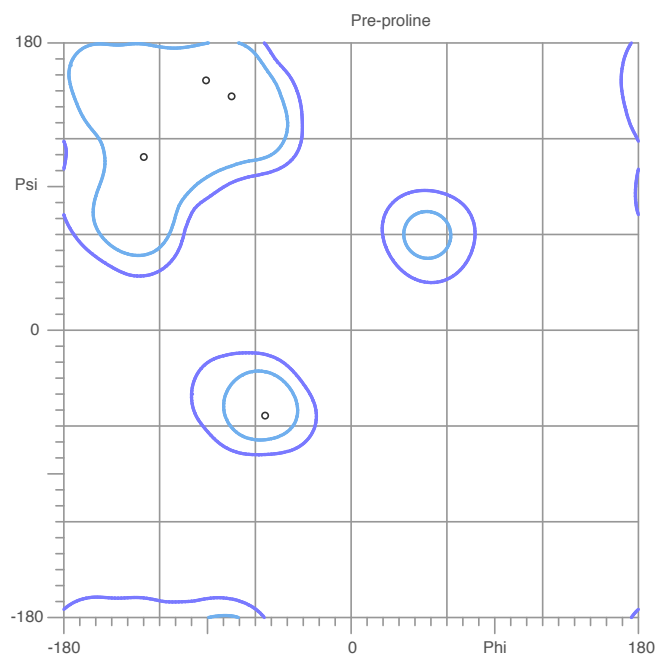
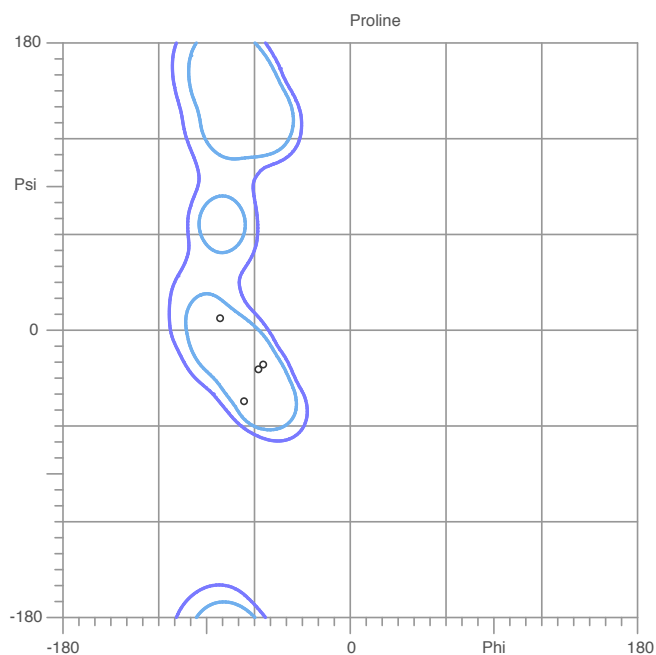
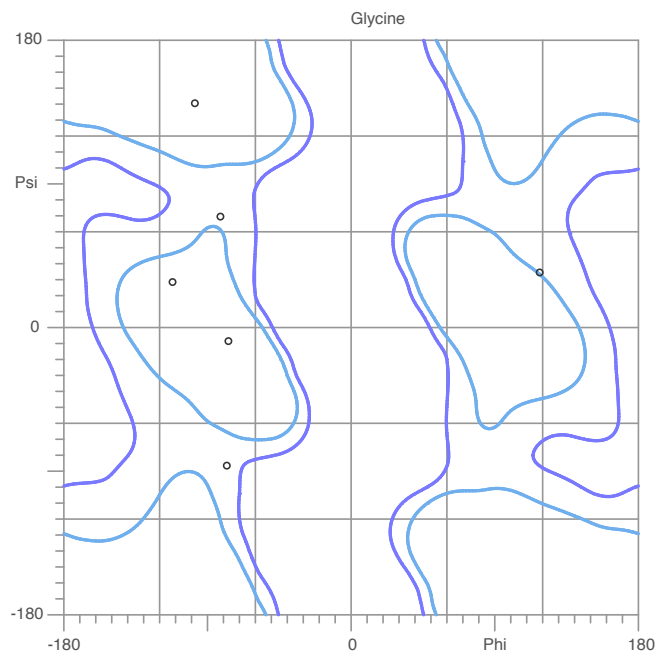
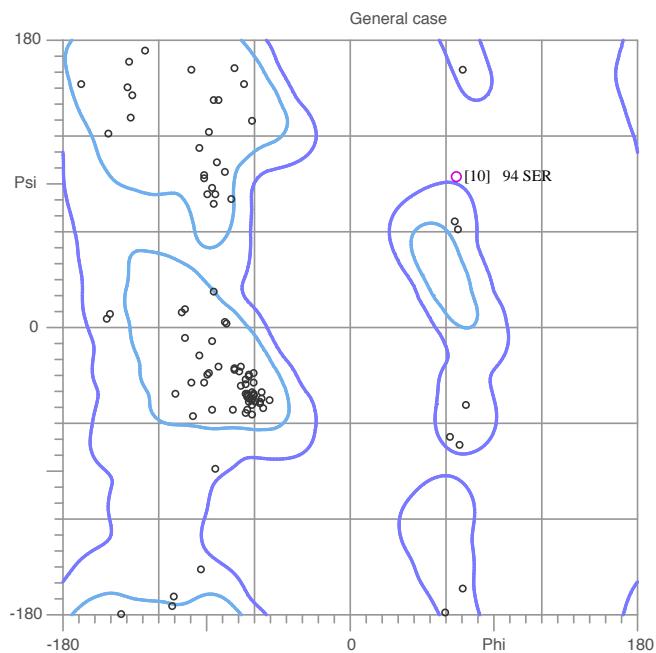
84.0% (89/106) of all residues were in favored (98%) regions.
97.2% (103/106) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [9] 25 GLU (-166.0, -57.3)
- [9] 68 ALA (-172.1, -61.8)
- [9] 75 GLU (60.6, 84.8)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 10



84.0% (89/106) of all residues were in favored (98%) regions.
99.1% (105/106) of all residues were in allowed (>99.8%) regions.

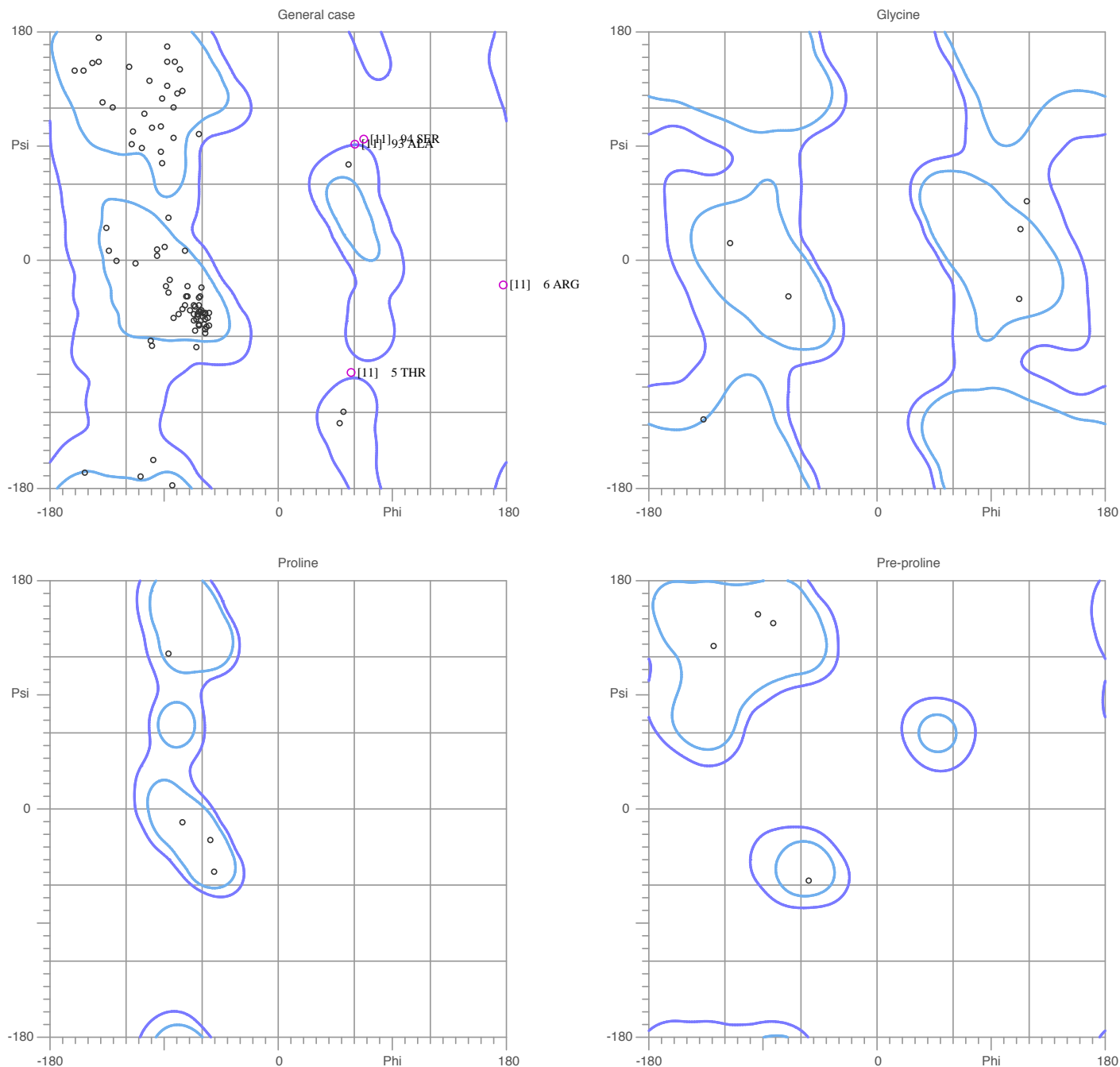
There were 1 outliers (phi, psi):
[10] 94 SER (66.4, 96.0)

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MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 11



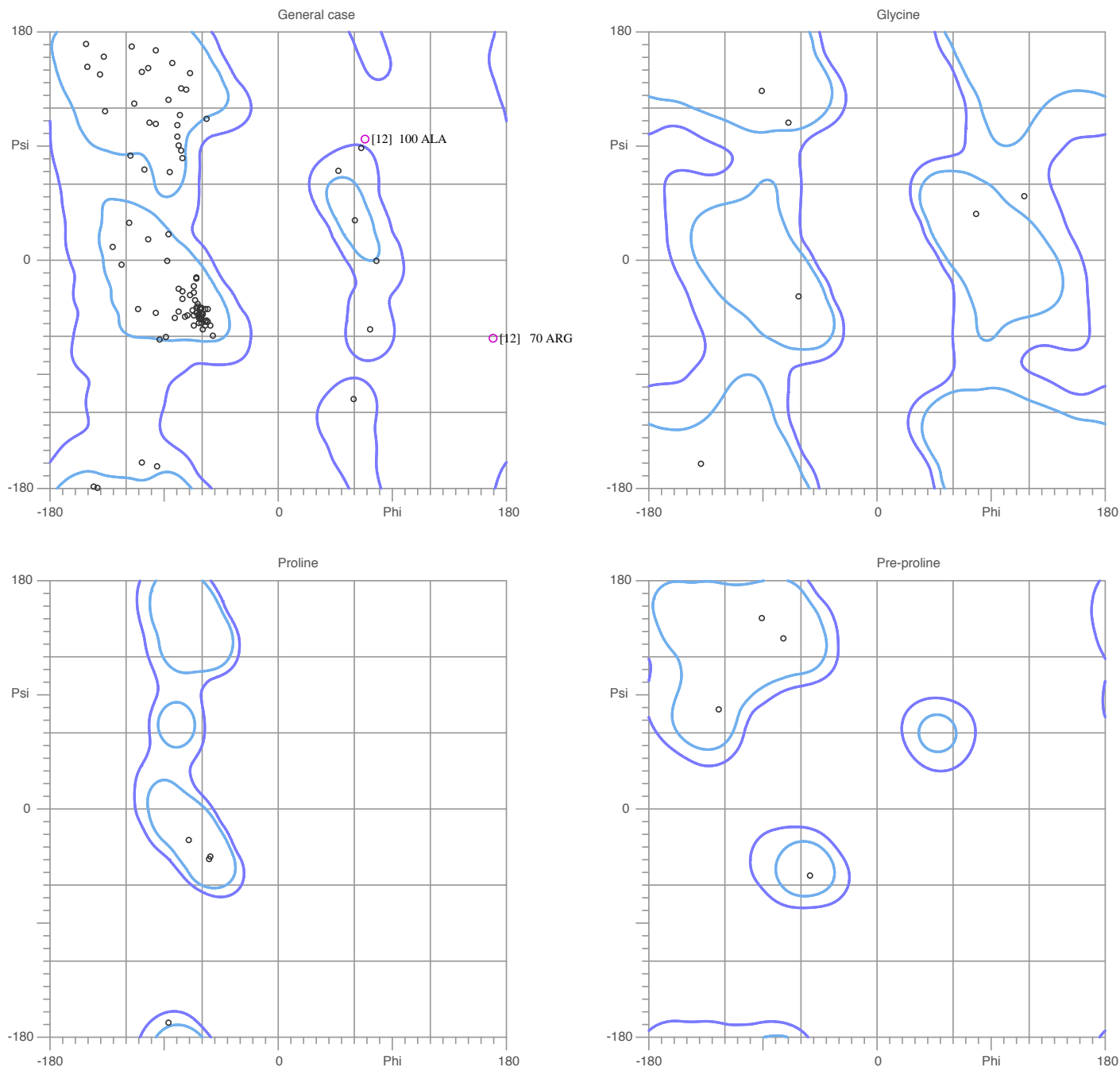
84.9% (90/106) of all residues were in favored (98%) regions.
96.2% (102/106) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (ϕ , ψ):

- [11] 5 THR (57.2, -89.0)
- [11] 6 ARG (177.1, -19.8)
- [11] 93 ALA (60.7, 92.7)
- [11] 94 SER (67.9, 96.8)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 12



87.7% (93/106) of all residues were in favored (98%) regions.
98.1% (104/106) of all residues were in allowed (>99.8%) regions.

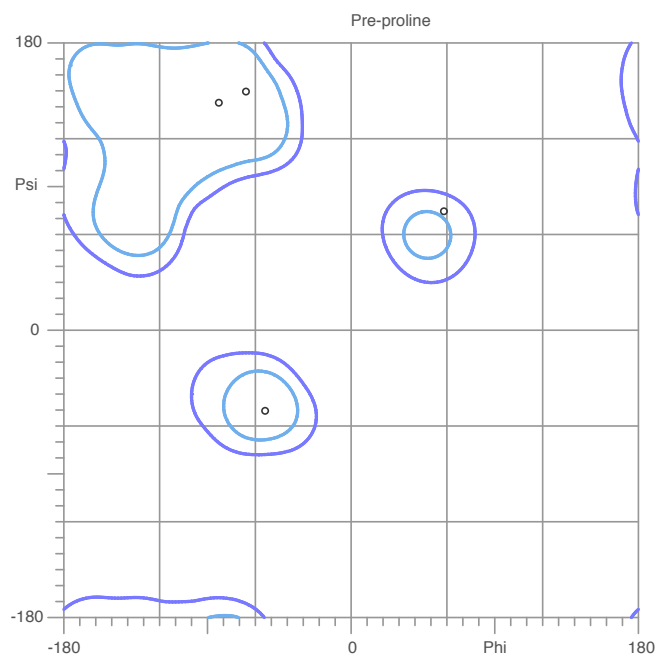
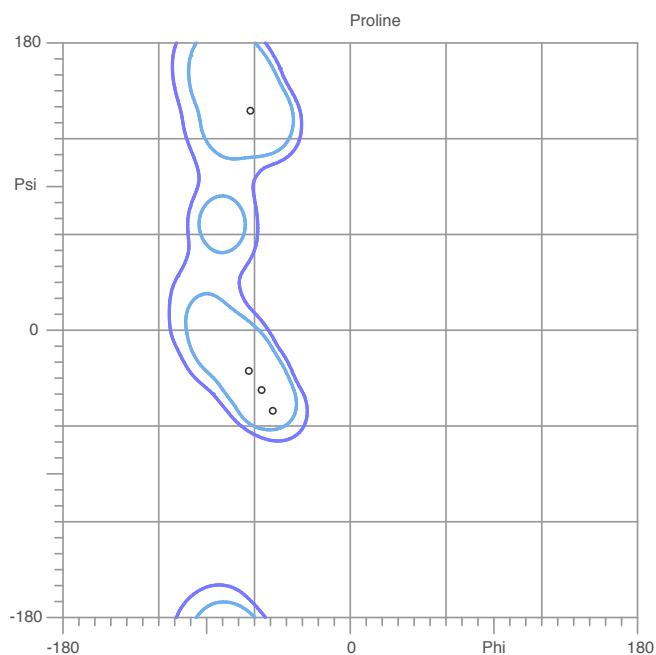
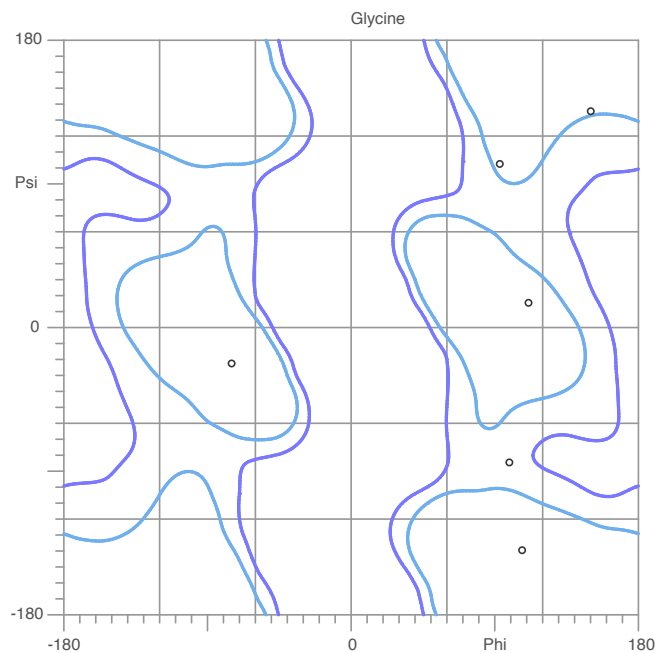
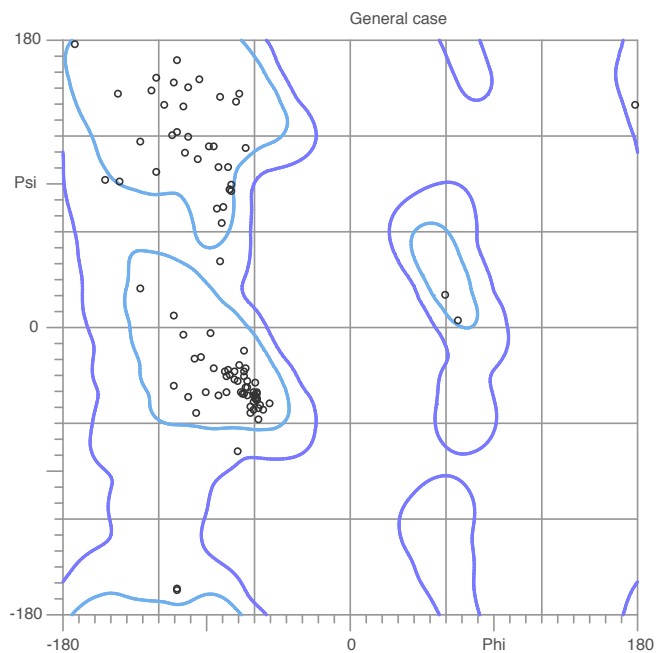
There were 2 outliers (phi, psi):
[12] 70 ARG (169.6, -61.5)
[12] 100 ALA (68.9, 96.9)

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MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 13



92.5% (98/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

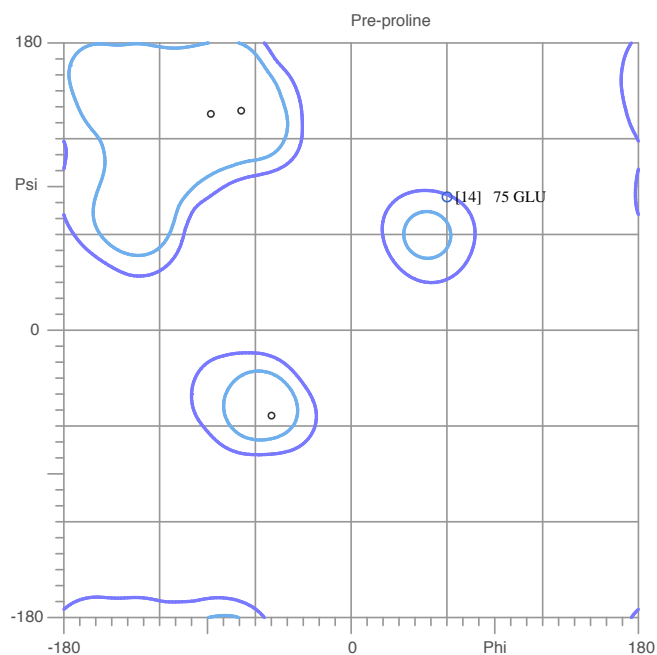
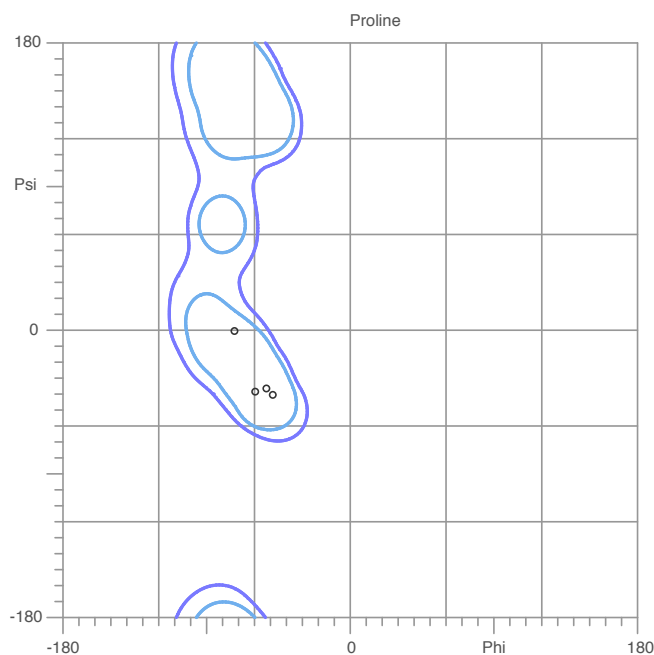
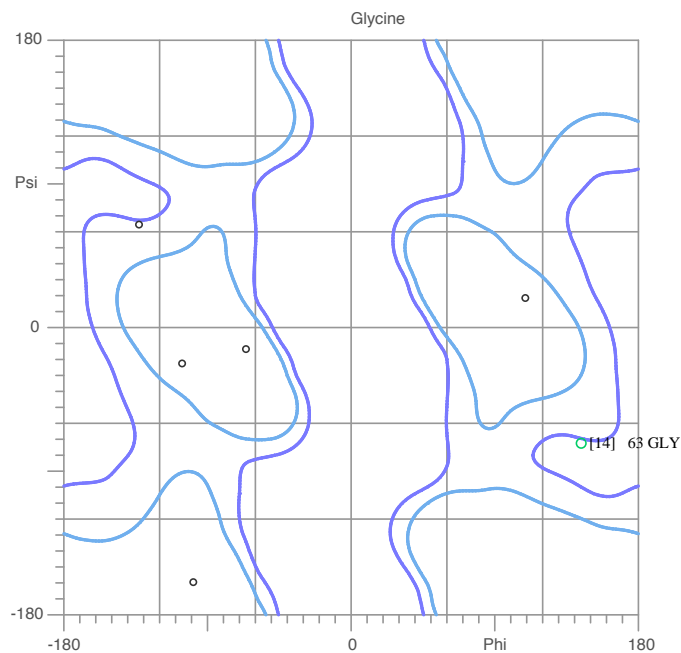
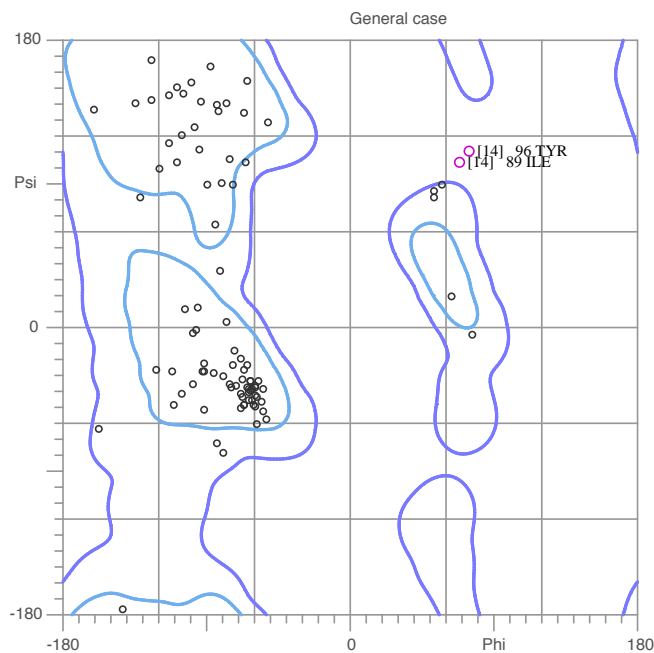
There were no outliers.

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MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 14



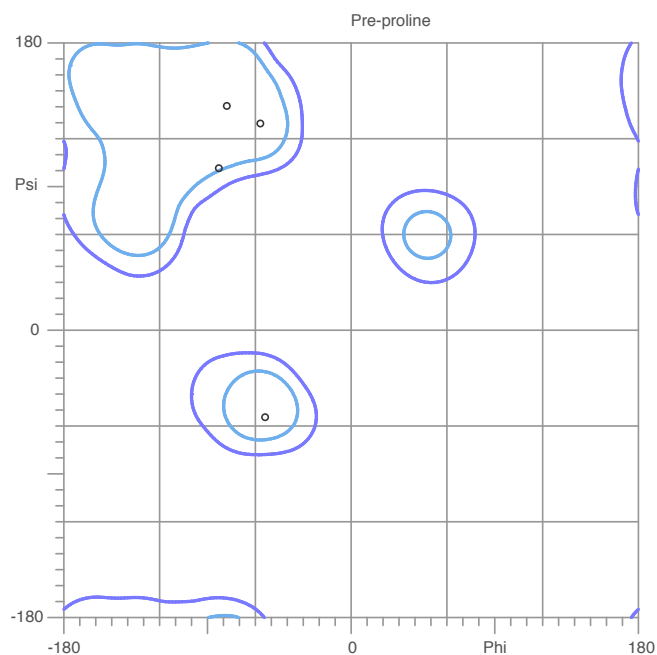
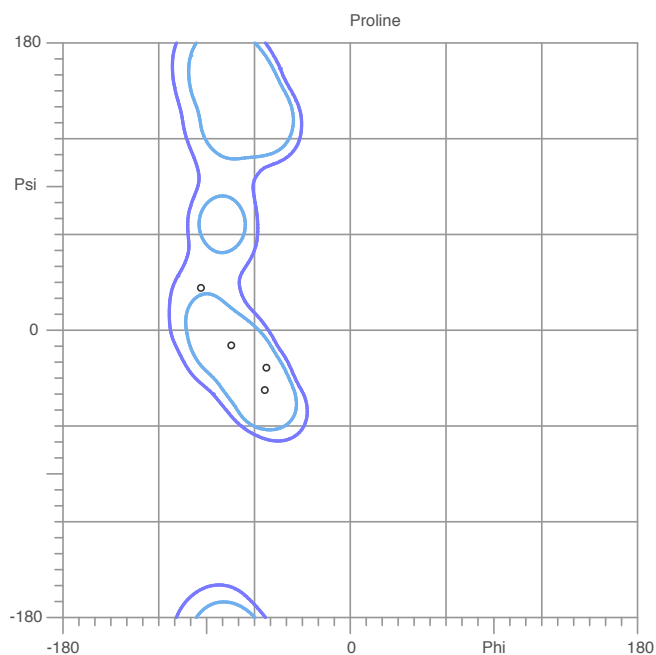
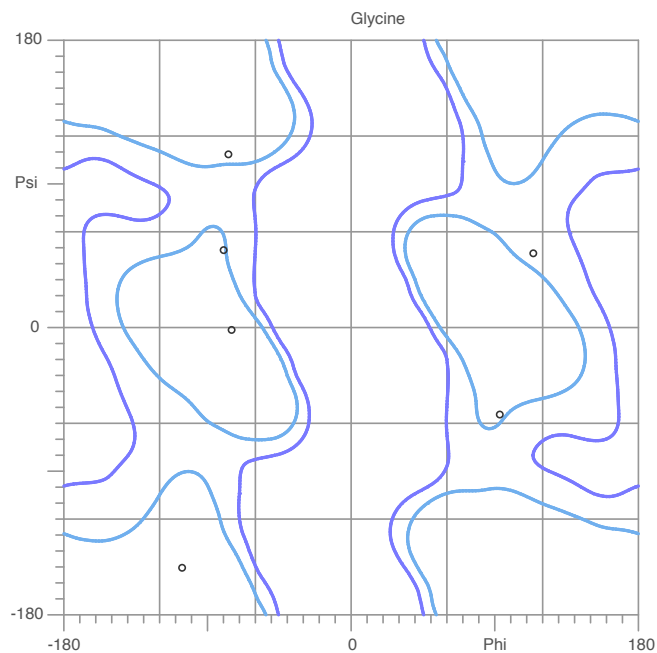
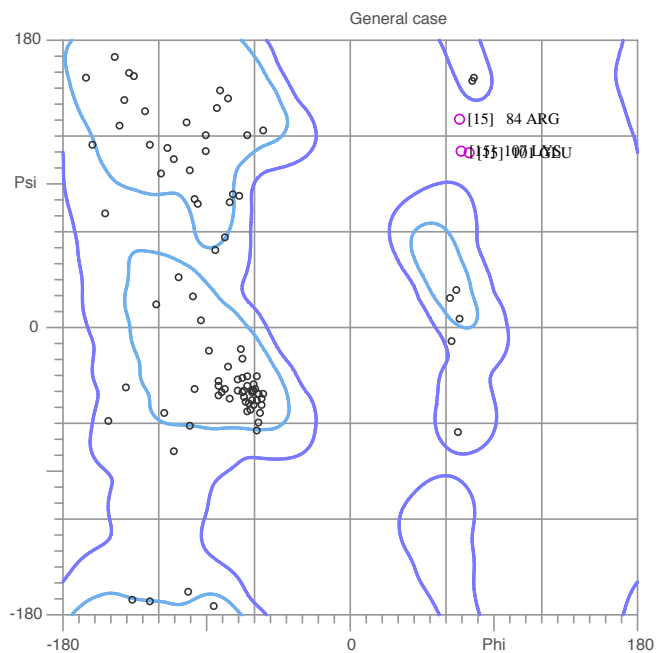
85.8% (91/106) of all residues were in favored (98%) regions.
96.2% (102/106) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [14] 63 GLY (144.0, -72.5)
- [14] 75 GLU (60.0, 84.6)
- [14] 89 ILE (68.4, 104.9)
- [14] 96 TYR (74.1, 111.4)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 15



82.1% (87/106) of all residues were in favored (98%) regions.
97.2% (103/106) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

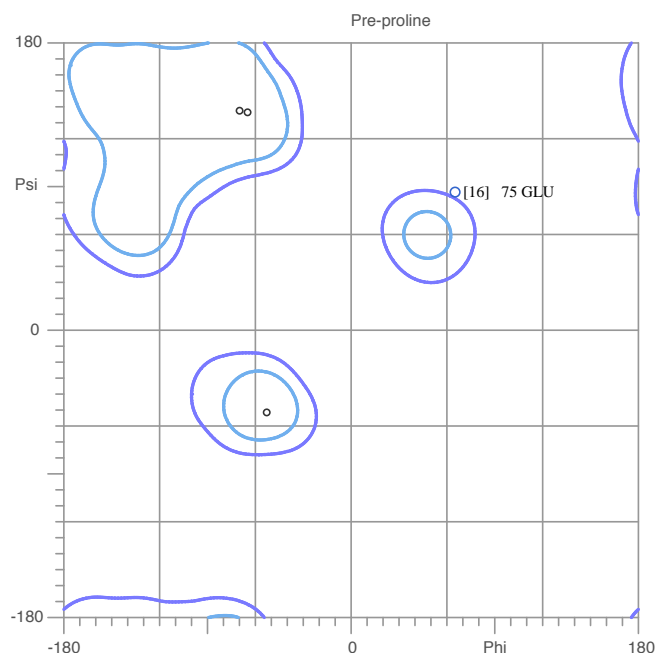
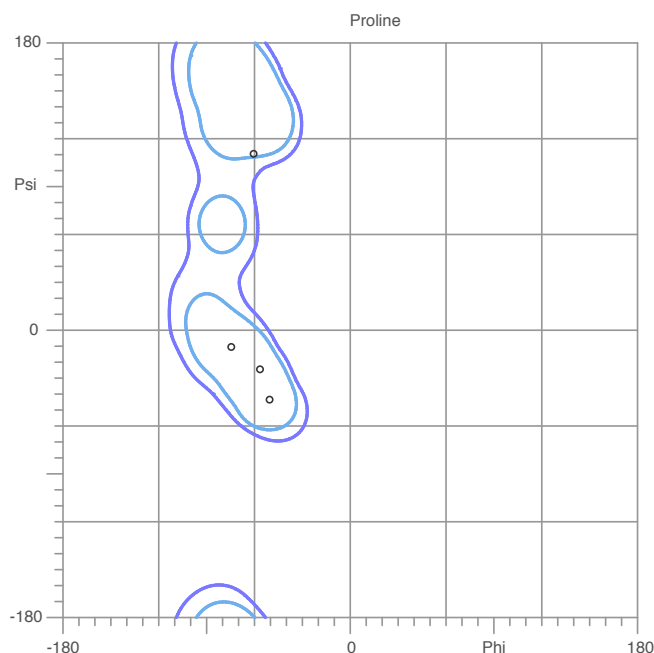
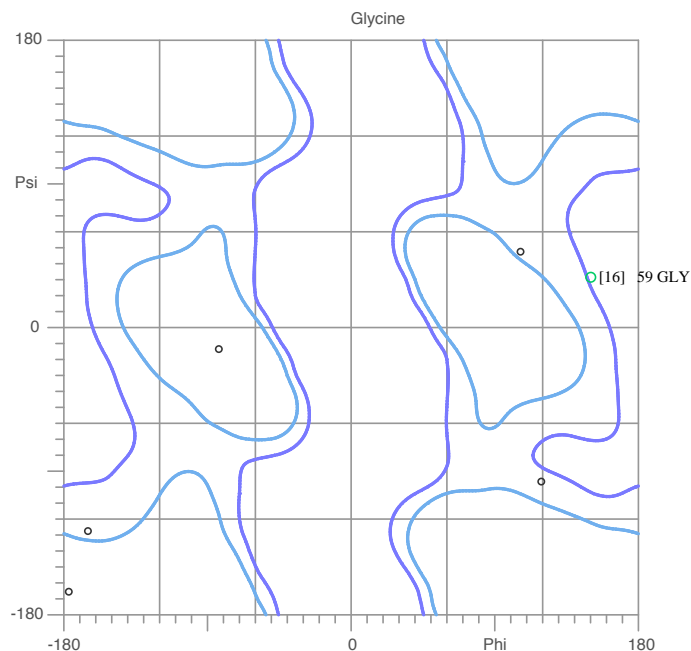
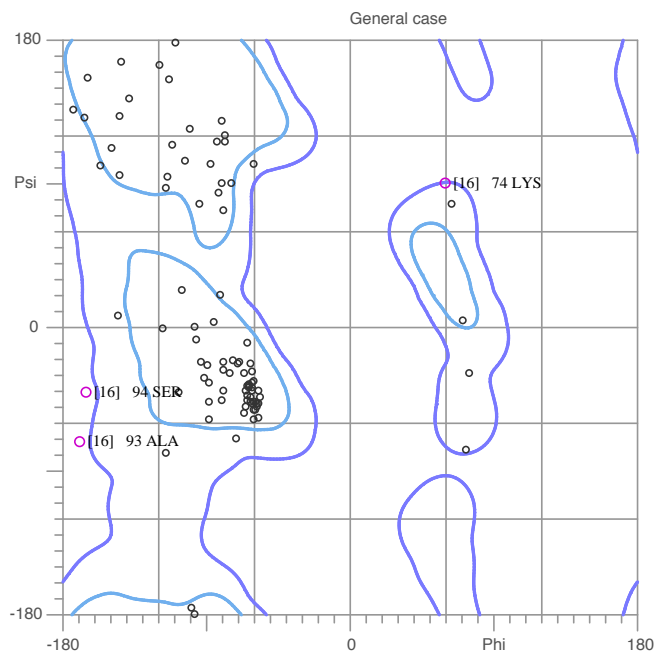
[15] 84 ARG (68.1, 131.3)

[15] 101 GLU (74.4, 110.7)

[15] 107 LYS (69.4, 111.5)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 16



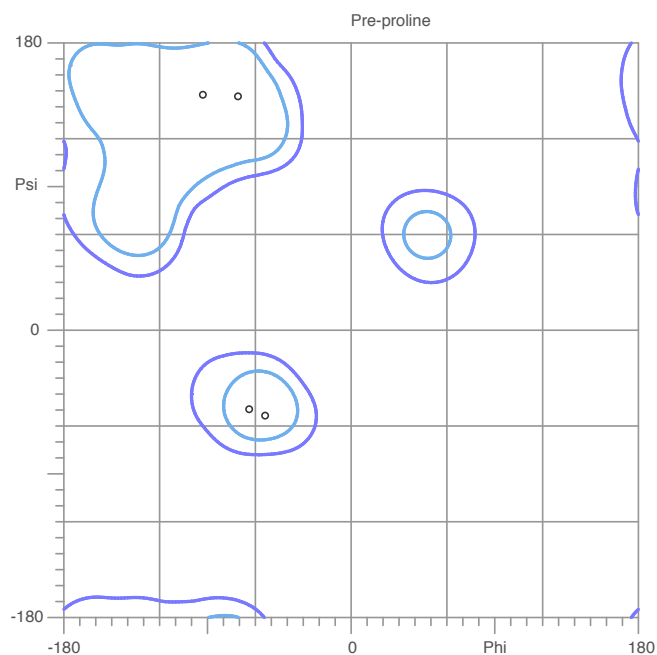
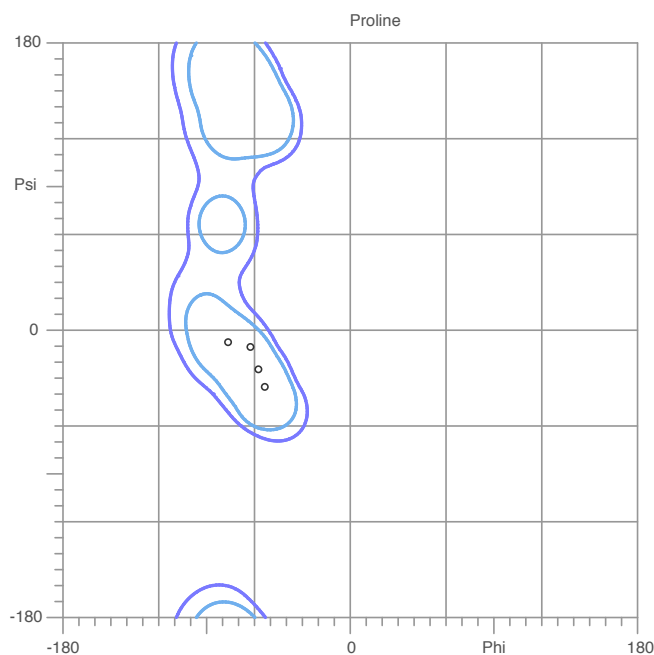
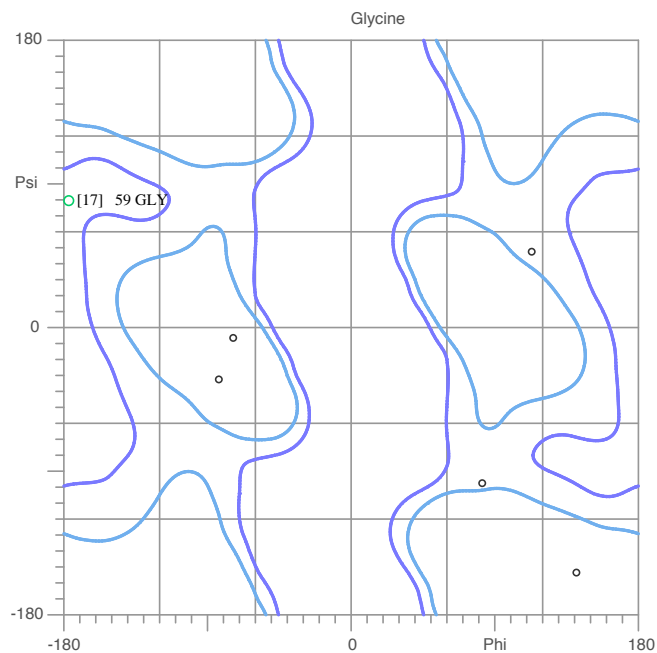
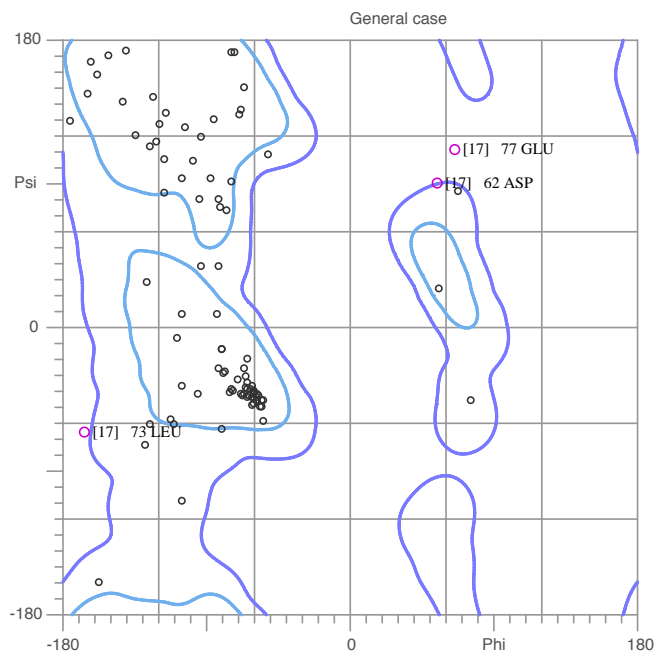
83.0% (88/106) of all residues were in favored (98%) regions.
95.3% (101/106) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[16] 59 GLY (150.5, 32.6)
[16] 74 LYS (59.2, 91.6)
[16] 75 GLU (65.2, 87.9)
[16] 93 ALA (-170.5, -71.3)
[16] 94 SER (-166.0, -40.2)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 17



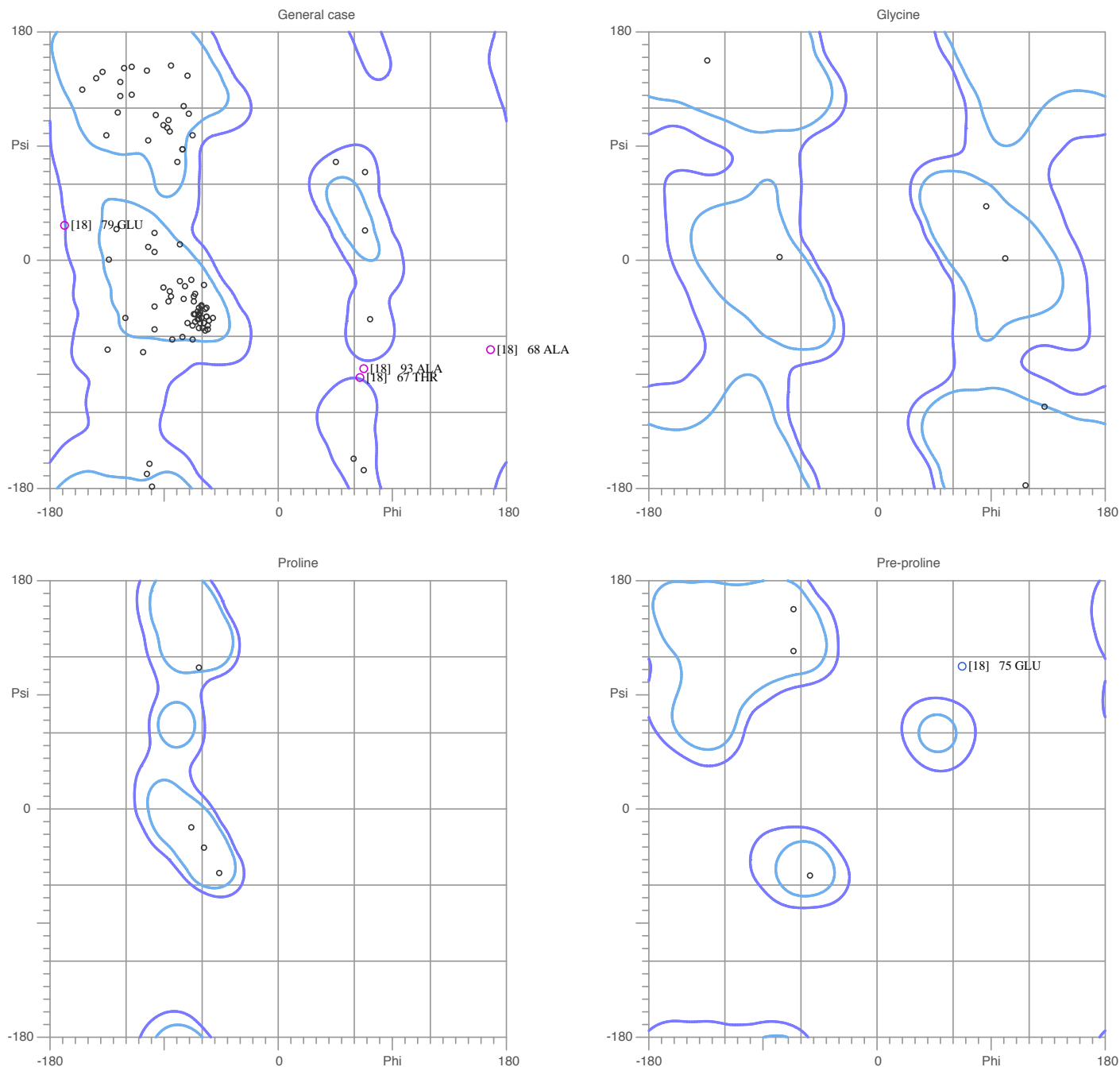
84.0% (89/106) of all residues were in favored (98%) regions.
96.2% (102/106) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [17] 59 GLY (-177.7, 80.9)
- [17] 62 ASP (54.0, 92.0)
- [17] 73 LEU (-167.0, -65.6)
- [17] 77 GLU (65.5, 112.5)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 18



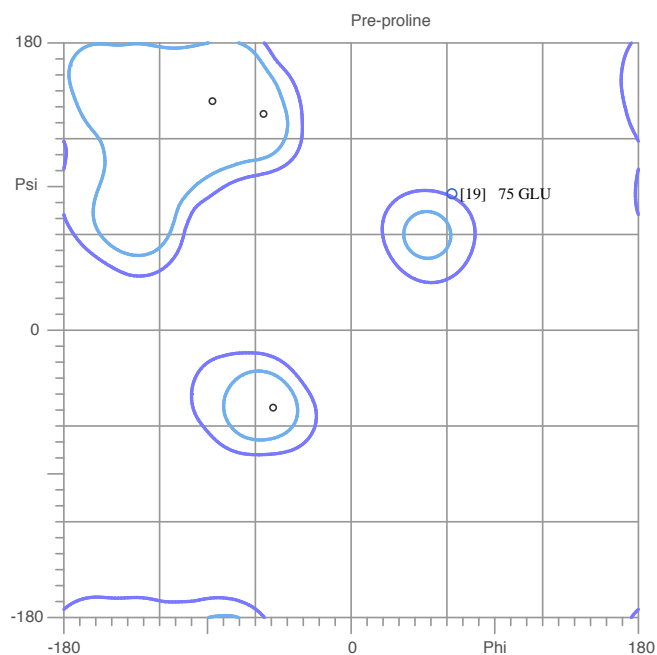
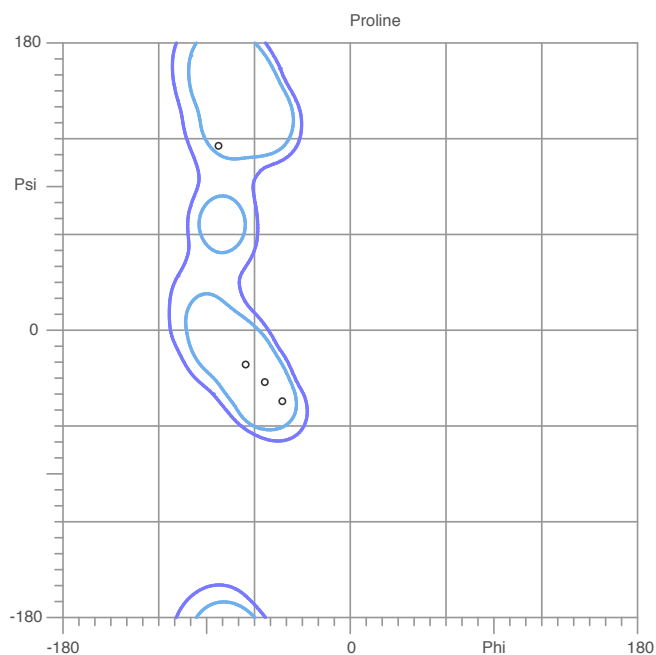
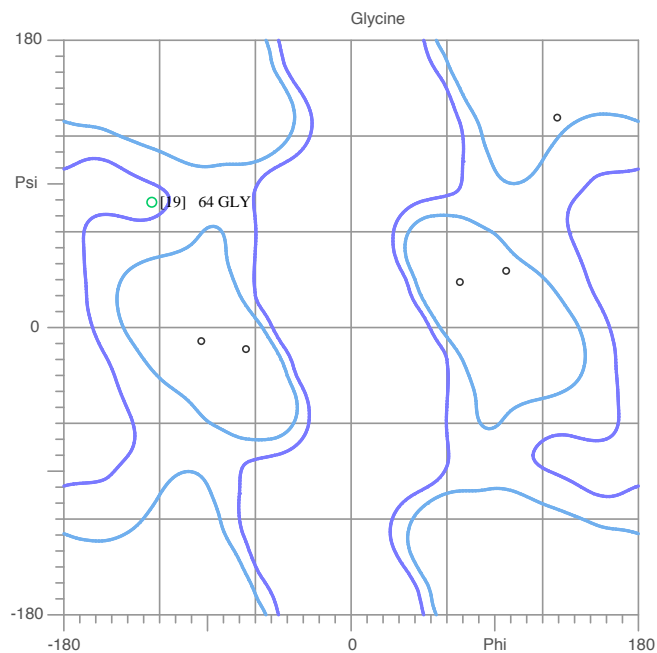
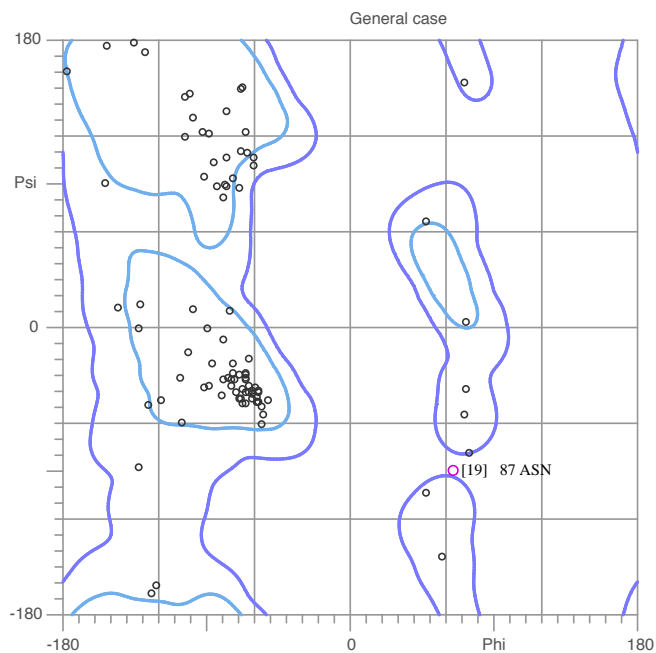
85.8% (91/106) of all residues were in favored (98%) regions.
95.3% (101/106) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[18] 67 THR (64.2, -92.9)
[18] 68 ALA (167.1, -70.8)
[18] 75 GLU (67.0, 113.7)
[18] 79 GLU (-169.5, 29.0)
[18] 93 ALA (67.4, -85.2)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 19



81.1% (86/106) of all residues were in favored (98%) regions.
97.2% (103/106) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

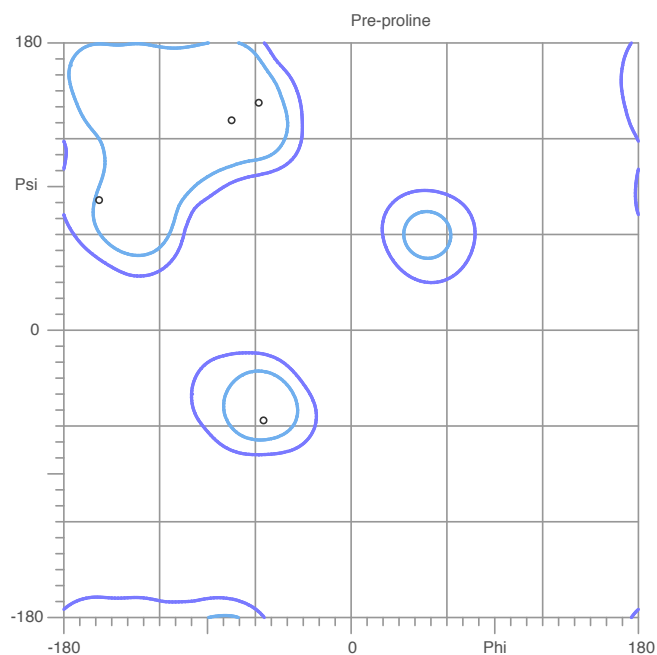
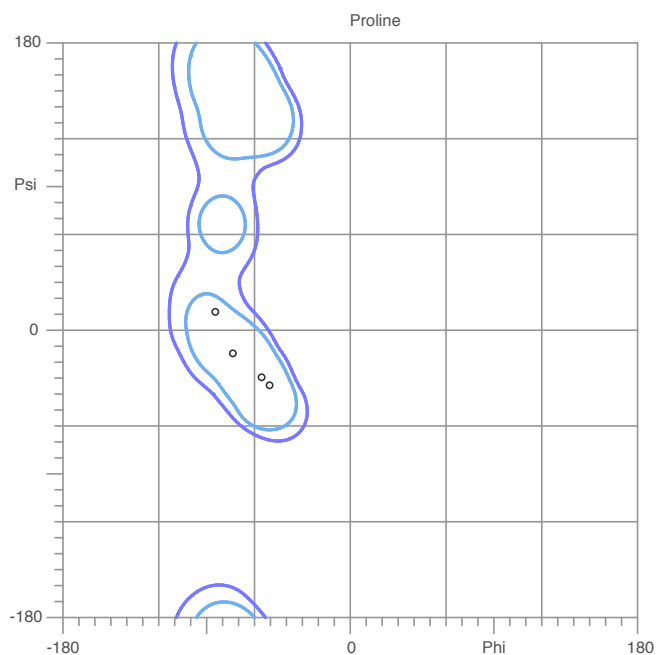
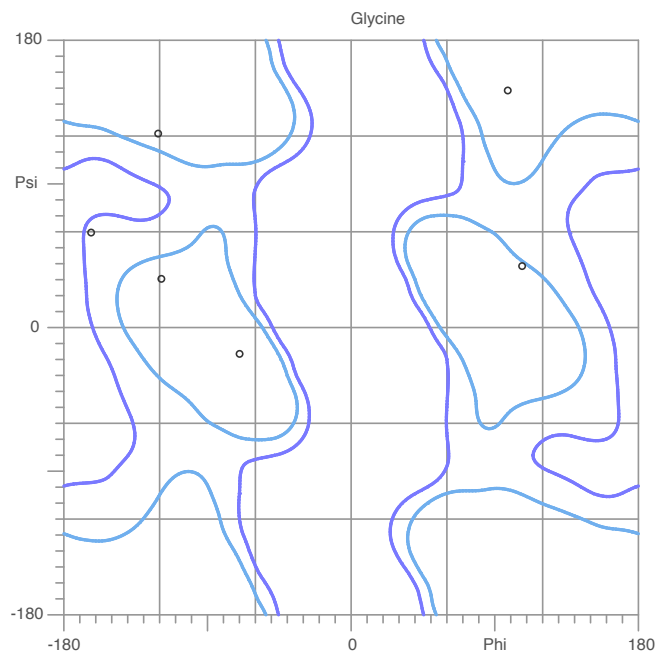
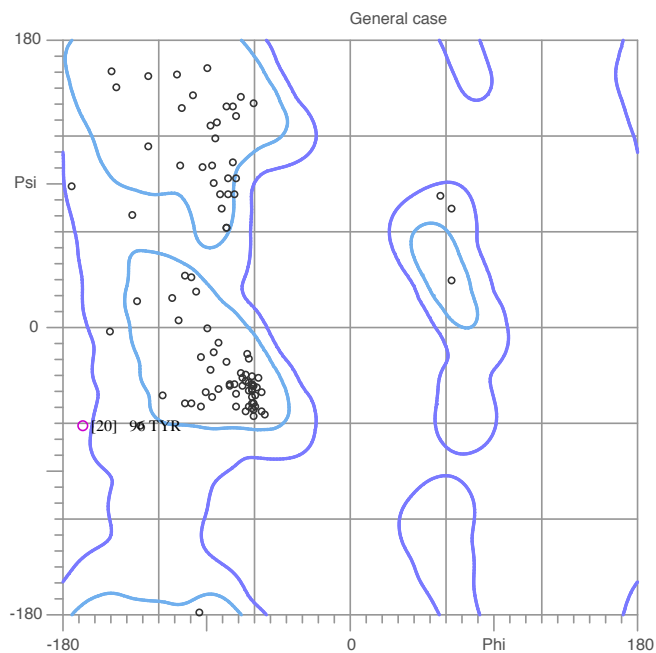
[19] 64 GLY (-125.0, 79.6)

[19] 75 GLU (63.0, 86.6)

[19] 87 ASN (64.3, -89.3)

MolProbity Ramachandran analysis

2RN7_NMR.pdb, model 20



92.5% (98/106) of all residues were in favored (98%) regions.
99.1% (105/106) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 96 TYR (-168.7, -61.4)

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

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