MolProbity Ramachandran analysis

2KBN_NMR.pdb, all models

General case

Glycine

Proline

Pre-proline
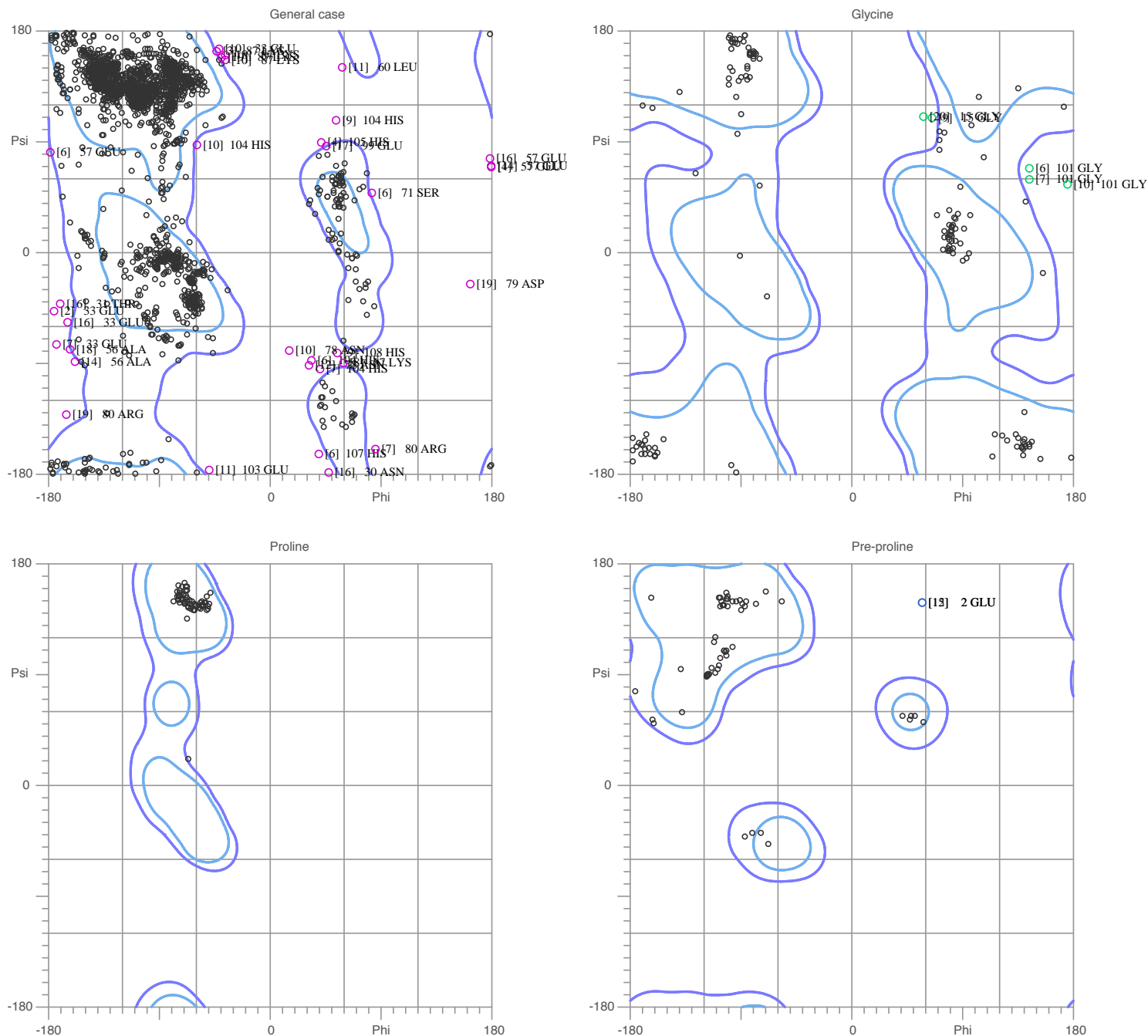
89.4% (1914/2140) of all residues were in favored (98%) regions.
98.1% (2100/2140) of all residues were in allowed (>99.8%) regions.

There were 40 outliers (phi, psi):
[2] 33 GLU (-176.7, -47.1)
[3] 87 LYS (-44.3, 164.8)
[4] 57 GLU (179.7, 70.6)
[4] 105 HIS (41.1, 90.5)
[6] 57 GLU (-179.6, 82.9)
[6] 71 SER (82.9, 49.9)
[6] 101 GLY (144.7, 69.1)
[6] 104 HIS (34.0, -87.3)
[6] 107 HIS (39.9, -163.2)
[7] 33 GLU (-174.1, -74.1)
[7] 80 ARG (85.6, -159.3)
[7] 101 GLY (144.3, 60.0)
[7] 104 HIS (40.8, -94.8)
[8] 87 LYS (59.3, -89.1)
[9] 15 GLY (66.0, 110.9)
[9] 104 HIS (53.6, 108.4)
[9] 108 HIS (54.7, -81.3)
[10] 33 GLU (-42.9, 166.2)

[10] 78 ASN (15.1, -79.8)
[10] 87 LYS (-37.8, 157.3)
[10] 101 GLY (175.6, 57.0)
[10] 104 HIS (-60.4, 88.7)
[11] 60 LEU (58.6, 151.9)
[11] 103 GLU (-50.6, -176.2)
[12] 2 GLU (57.3, 149.4)
[12] 78 ASN (31.1, -91.3)
[14] 56 ALA (-159.1, -88.6)
[14] 57 GLU (179.2, 71.6)
[15] 2 GLU (57.1, 149.3)
[16] 30 ASN (47.1, -178.5)
[16] 31 THR (-171.2, -42.0)
[16] 33 GLU (-165.9, -56.5)
[16] 57 GLU (178.9, 77.9)
[17] 99 GLU (45.1, 87.5)
[18] 56 ALA (-163.4, -78.7)
[18] 87 LYS (-37.9, 161.1)
[19] 79 ASP (162.4, -25.6)
[19] 80 ARG (-166.9, -131.7)
[19] 87 LYS (-40.9, 159.8)
[20] 15 GLY (58.0, 111.1)

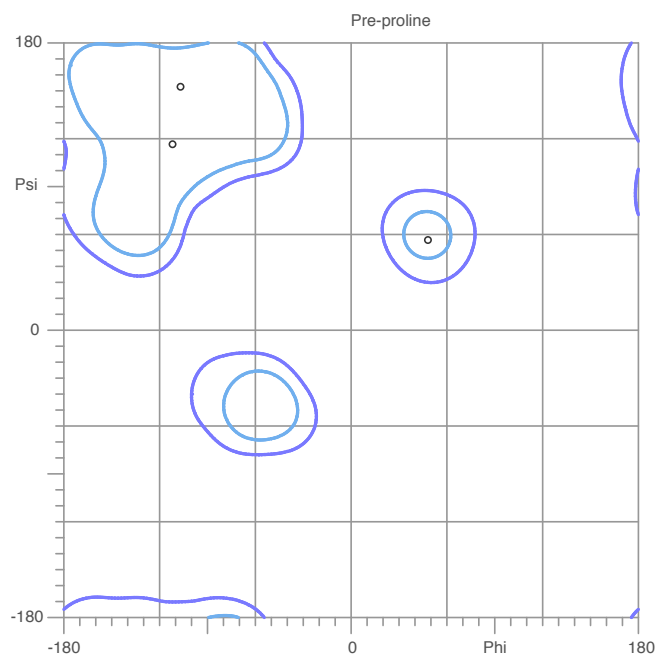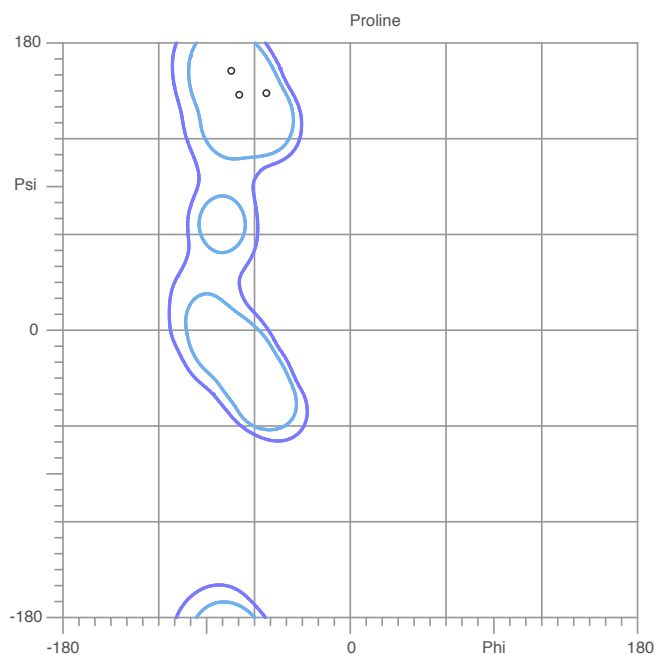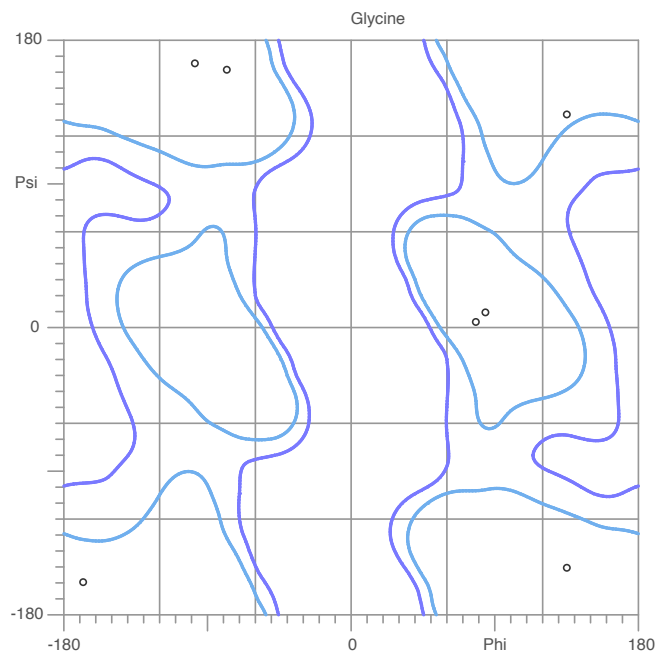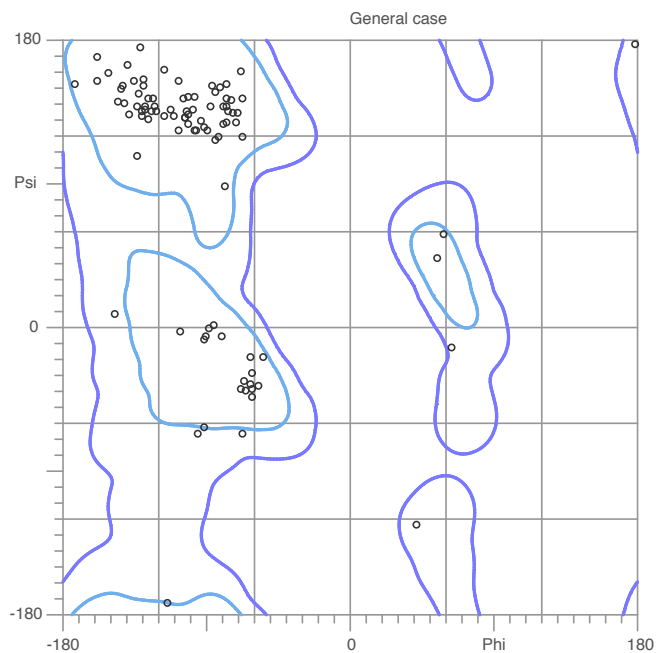# MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 1

94.4% (101/107) of all residues were in favored (98%) regions.
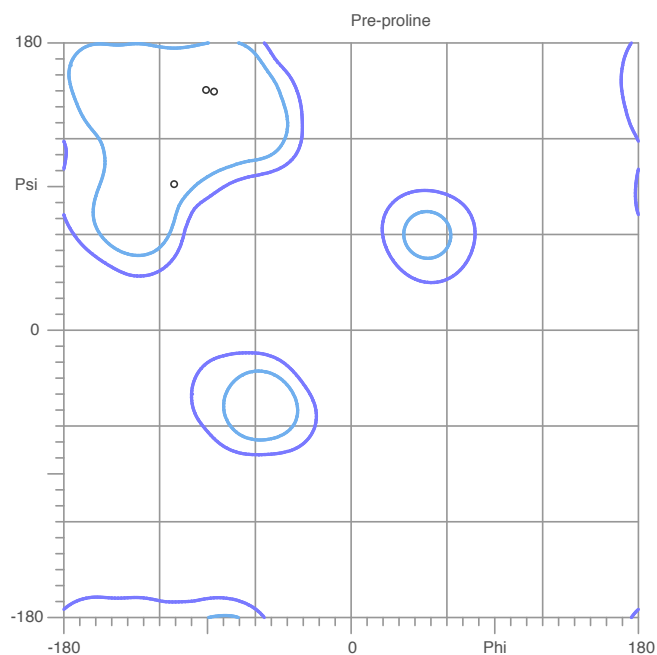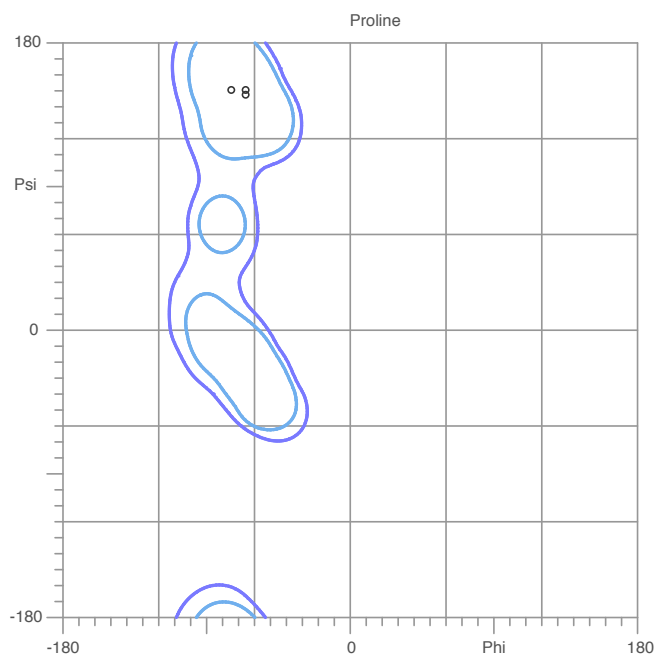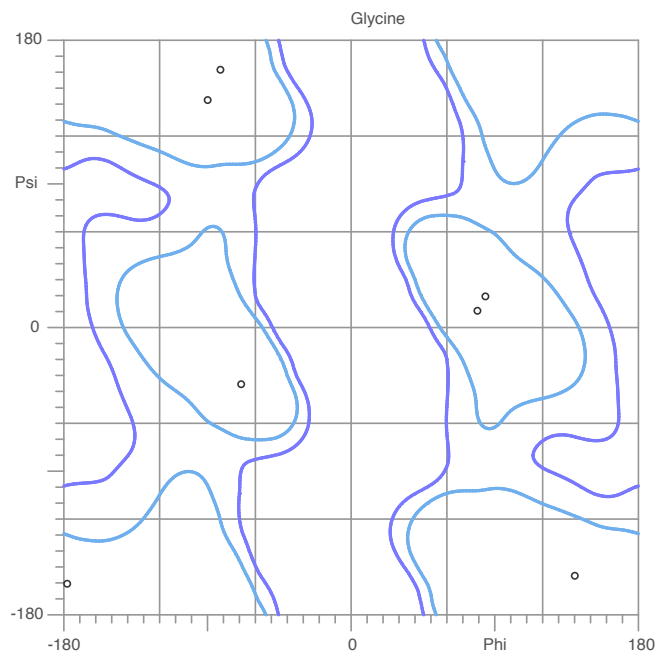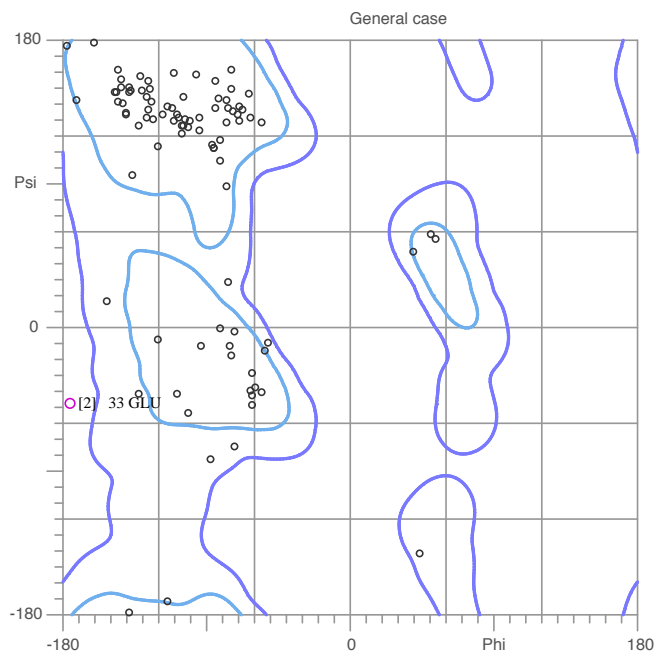100.0% (107/107) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 2

89.7% (96/107) of all residues were in favored (98%) regions.
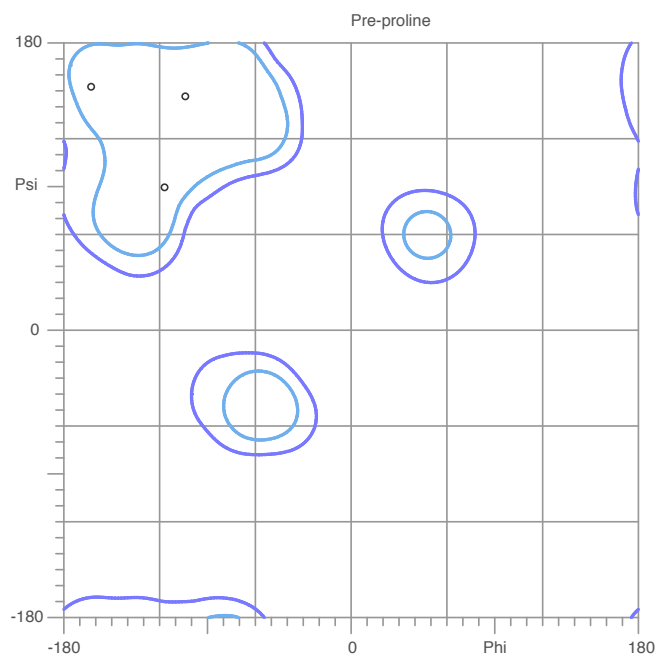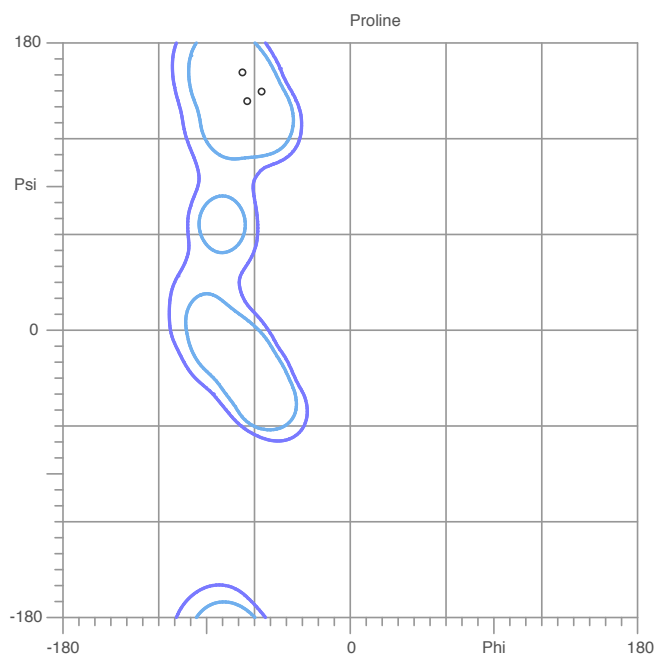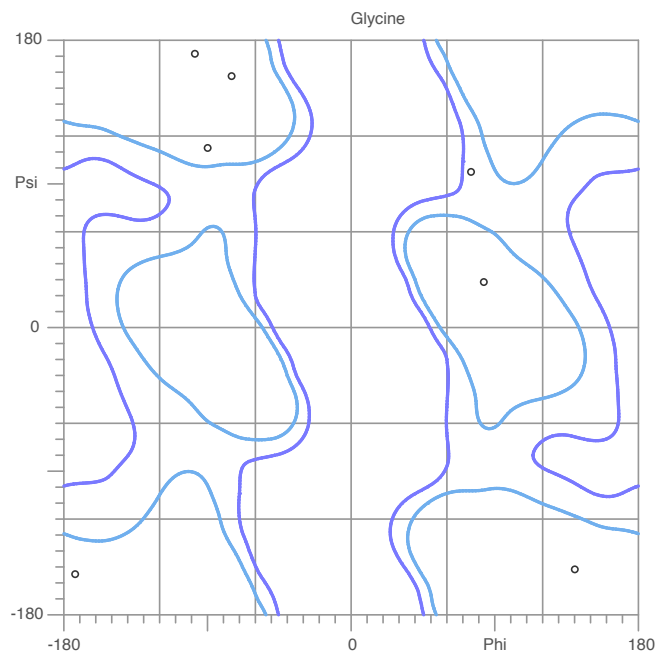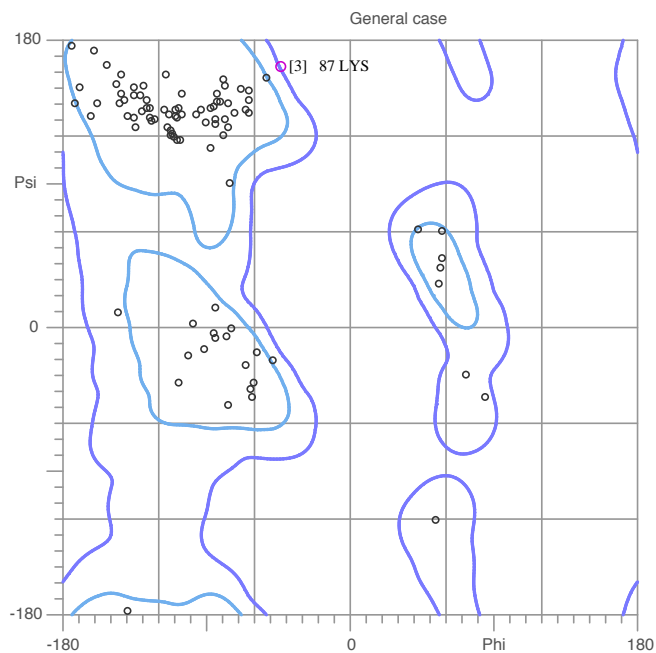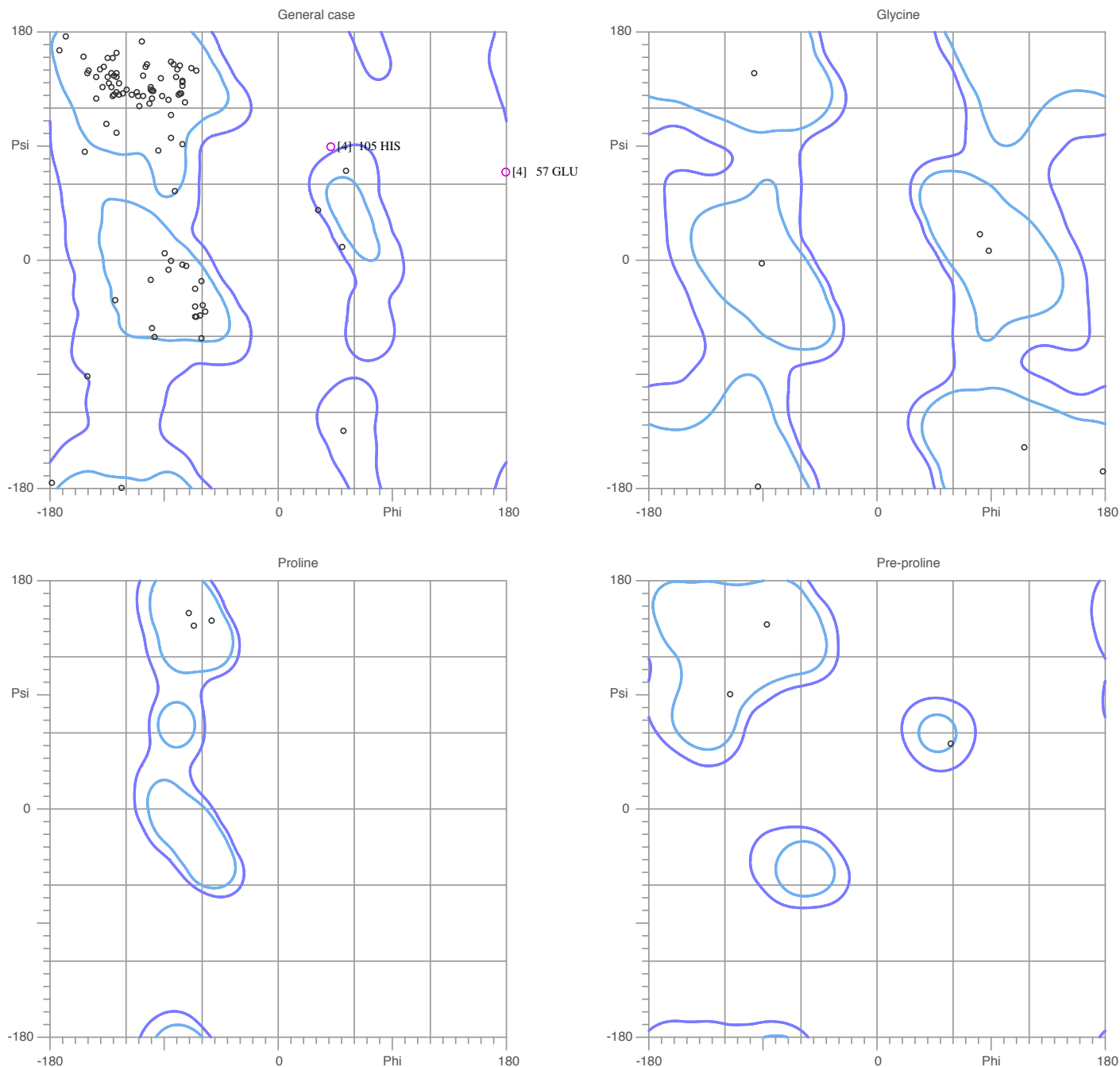99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
   [2] 33 GLU (-176.7, -47.1)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 3

92.5% (99/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
    [3]   87 LYS (-44.3, 164.8)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 4

91.6% (98/107) of all residues were in favored (98%) regions.
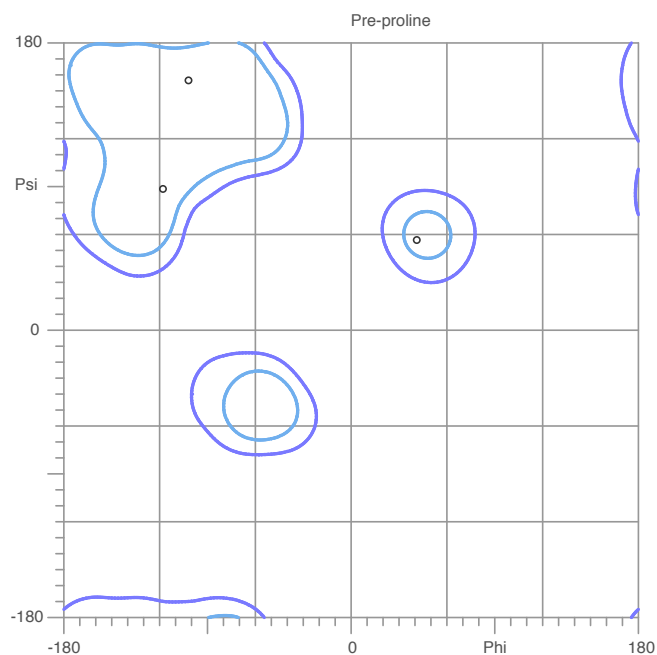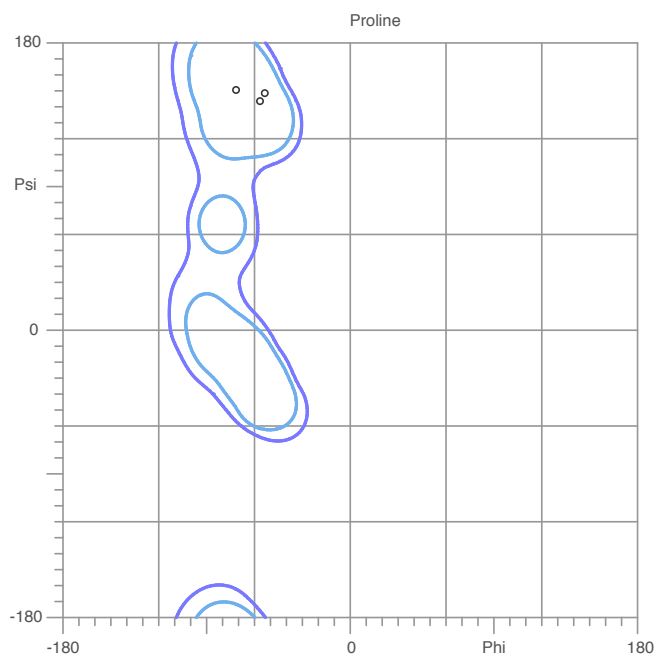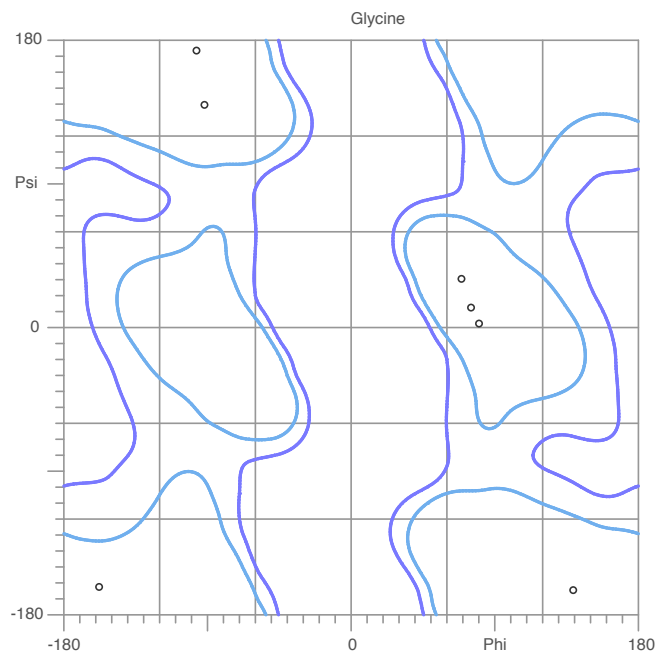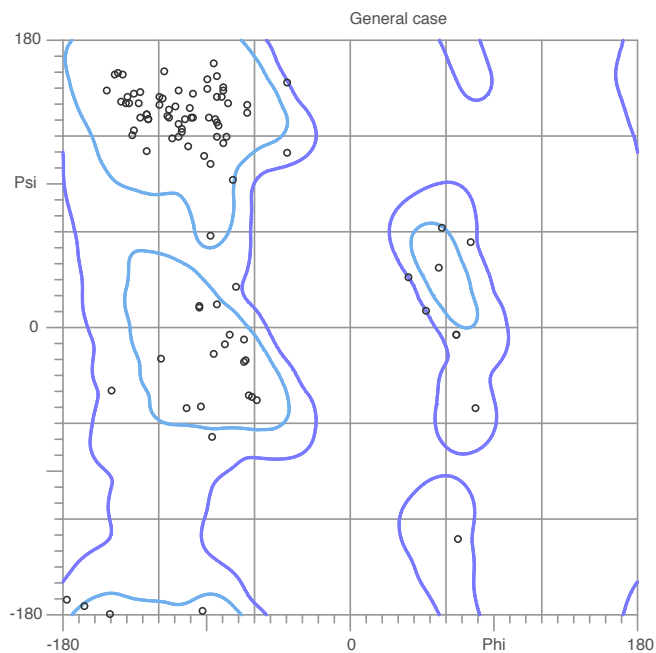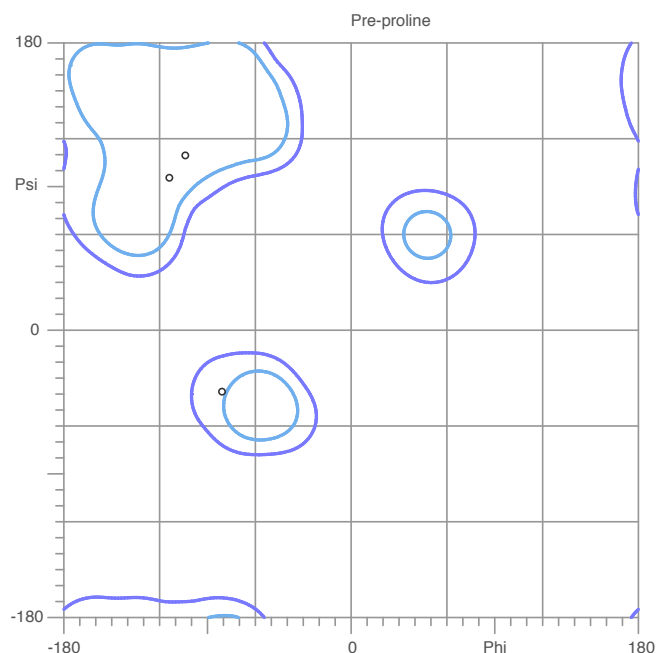98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
  [4]   57 GLU (179.7, 70.6)
  [4] 105 HIS (41.1, 90.5)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 5

86.9% (93/107) of all residues were in favored (98%) regions.

100.0% (107/107) of all residues were in allowed (>99.8%) regions.
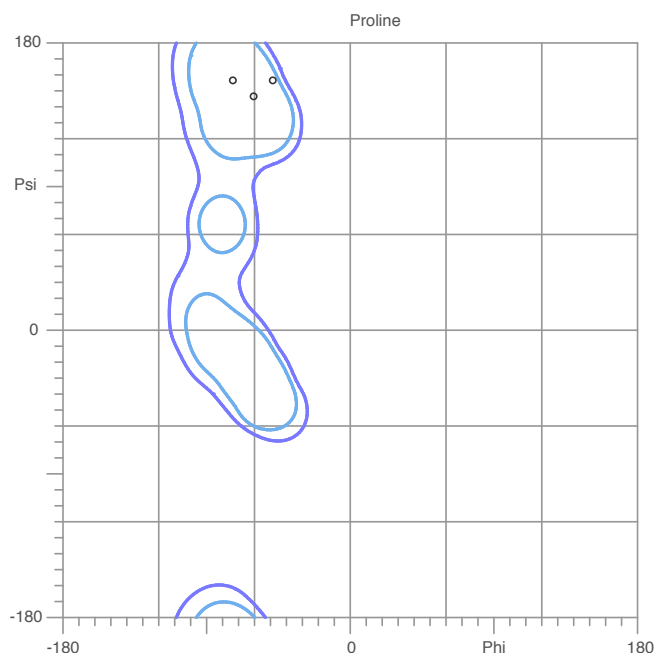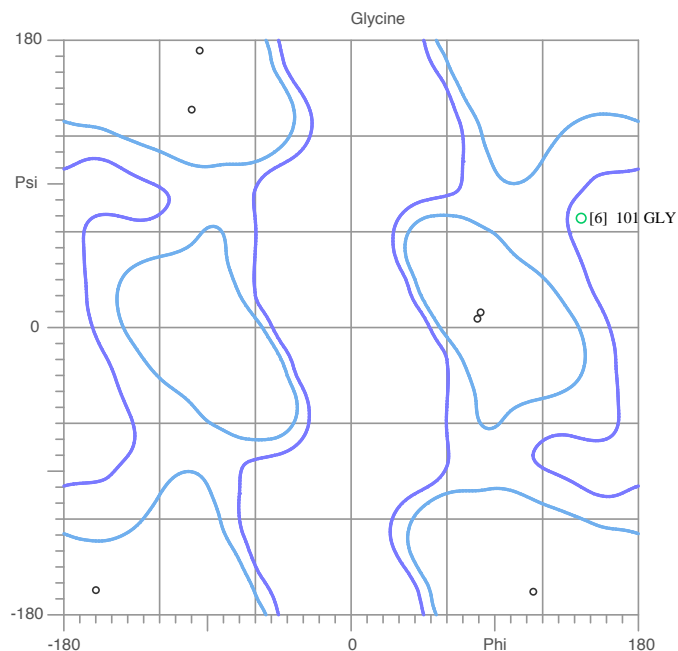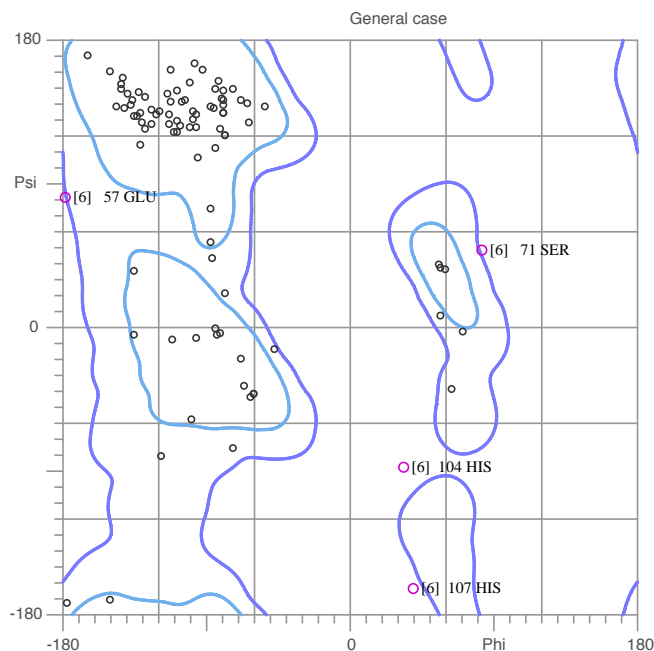
There were no outliers.

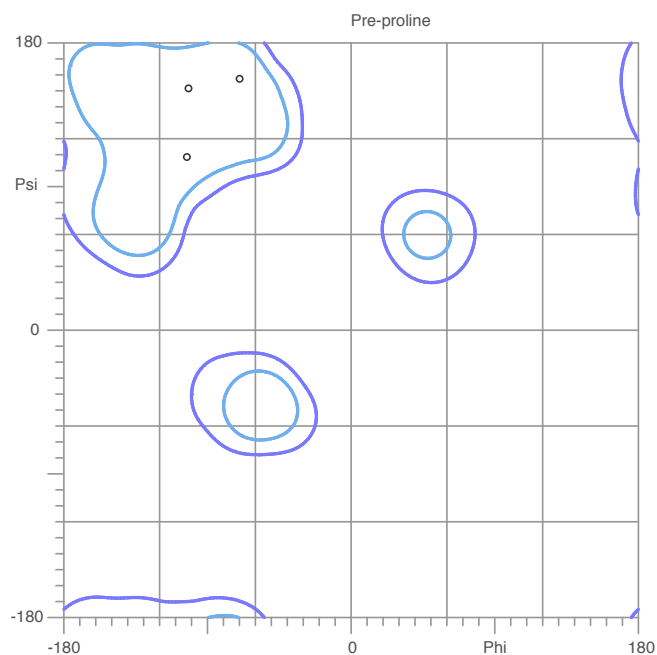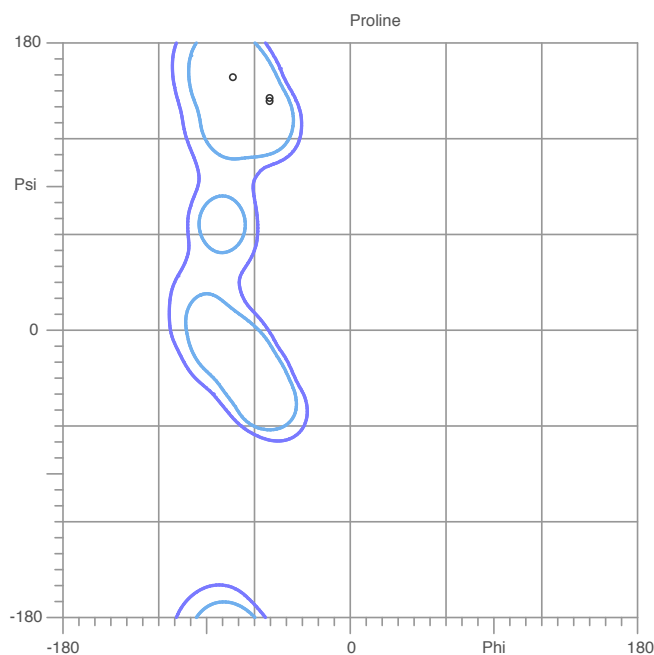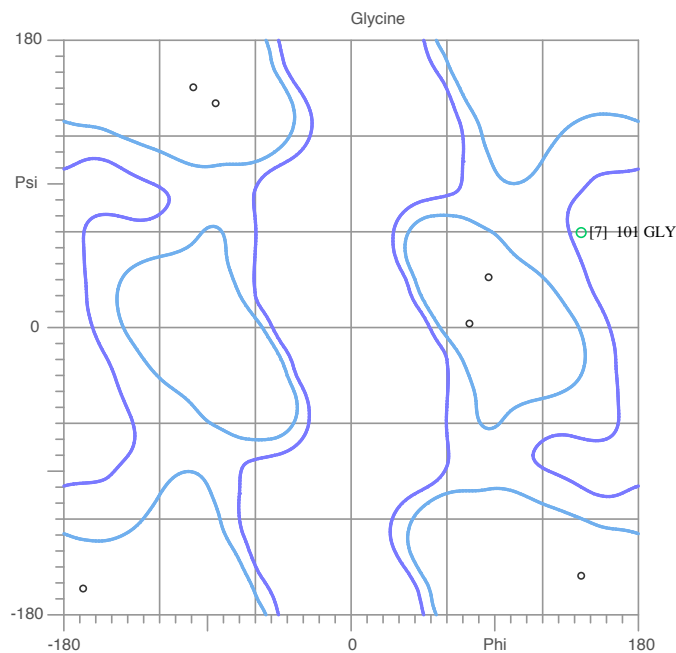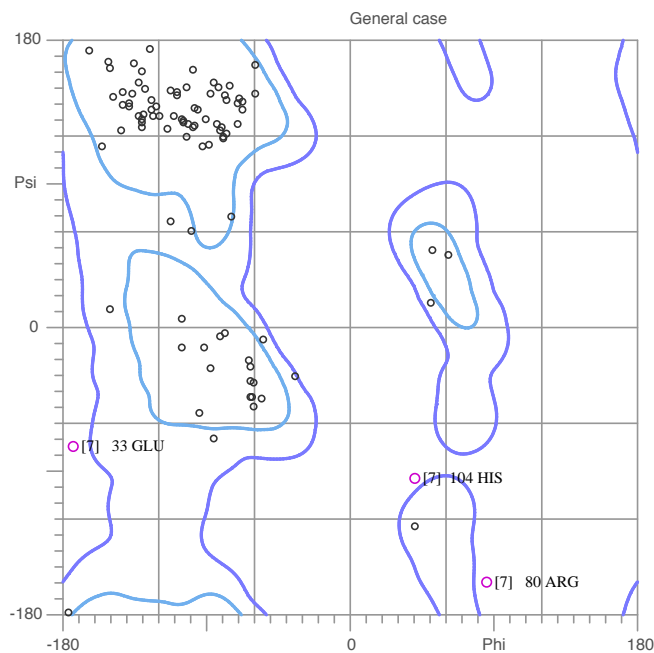# MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 6

86.0% (92/107) of all residues were in favored (98%) regions.
95.3% (102/107) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[6]   57 GLU (-179.6, 82.9)
[6]   71 SER (82.9, 49.9)
[6] 101 GLY (144.7, 69.1)
[6] 104 HIS (34.0, -87.3)
[6] 107 HIS (39.9, -163.2)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 7

87.9% (94/107) of all residues were in favored (98%) regions.
96.3% (103/107) of all residues were in allowed (>99.8%) regions.

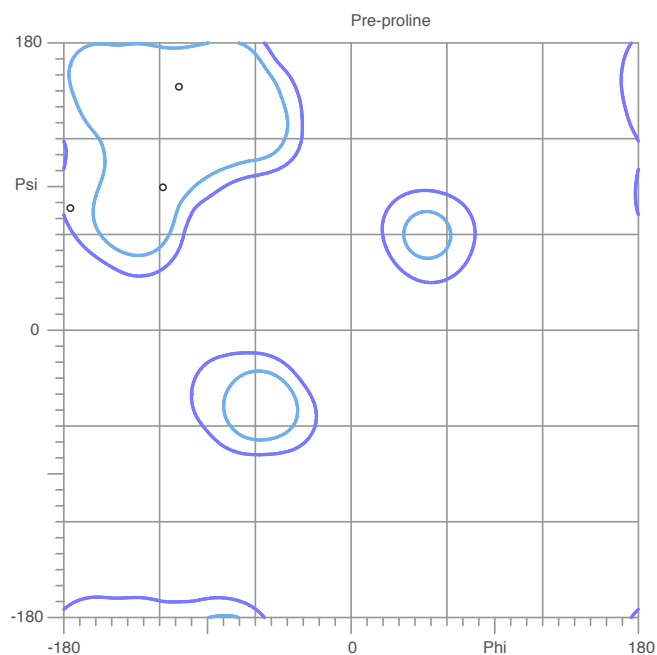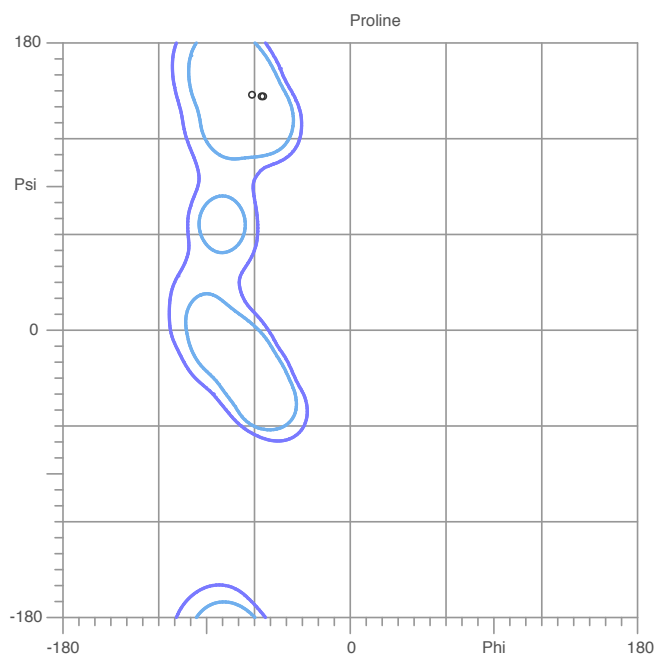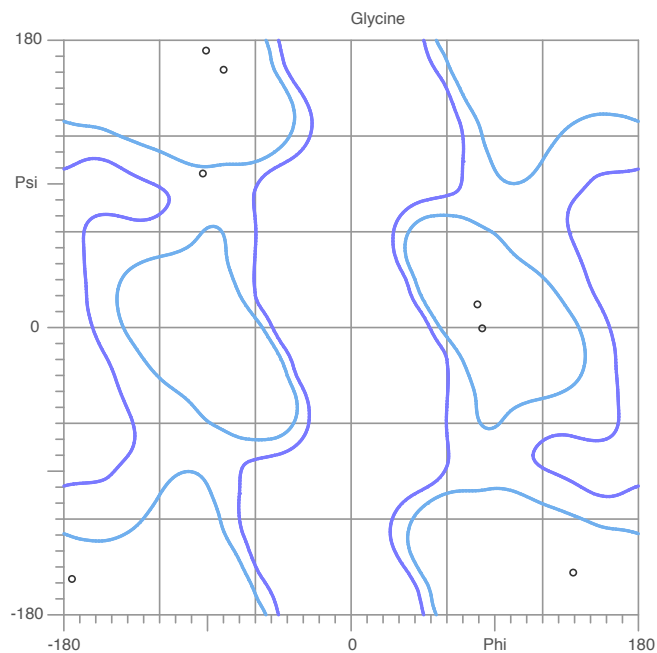There were 4 outliers (phi, psi):
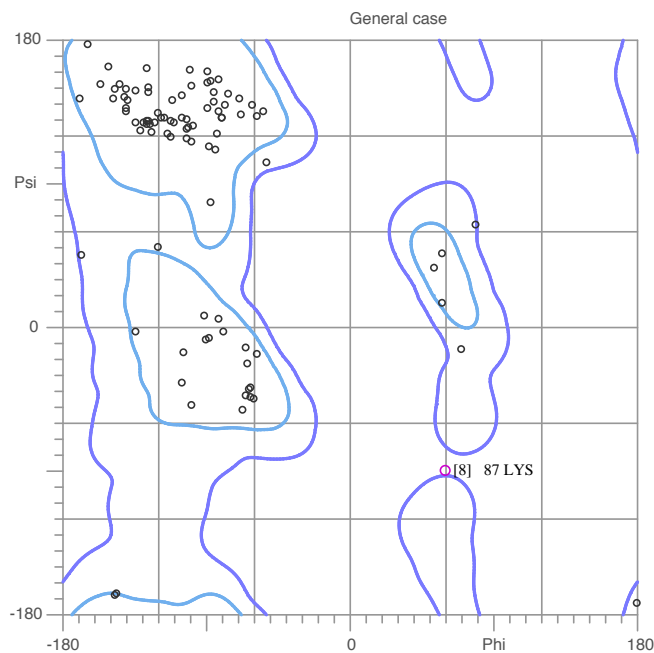   [7]   33 GLU (-174.1, -74.1)
    [7]   80 ARG (85.6, -159.3)
    [7] 101 GLY (144.3, 60.0)
    [7] 104 HIS (40.8, -94.8)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 8

General case

Glycine

[8]   87 LYS

Proline

Pre-proline

91.6% (98/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
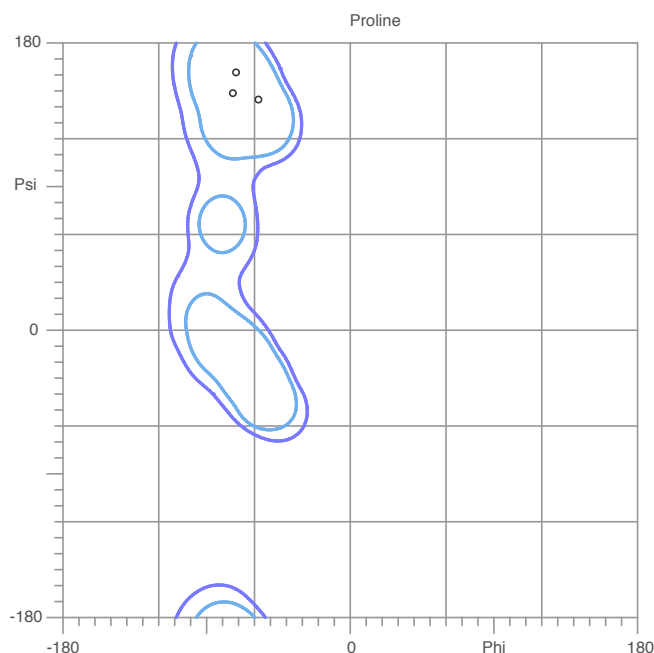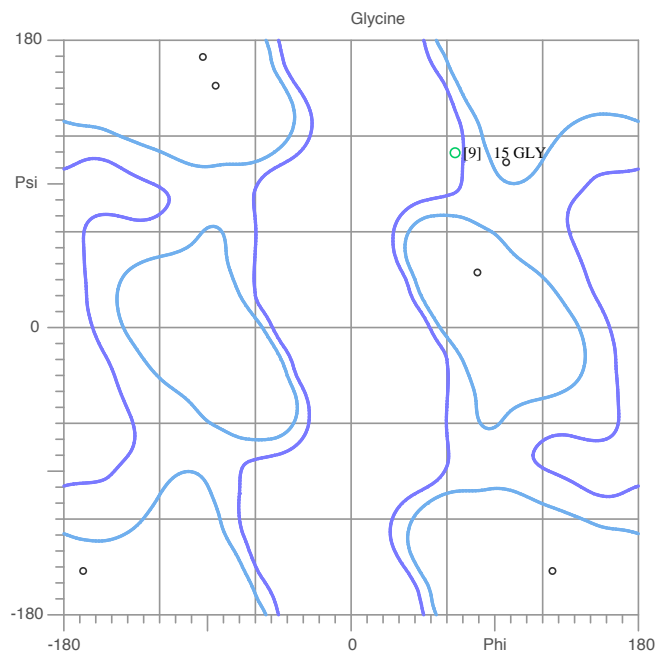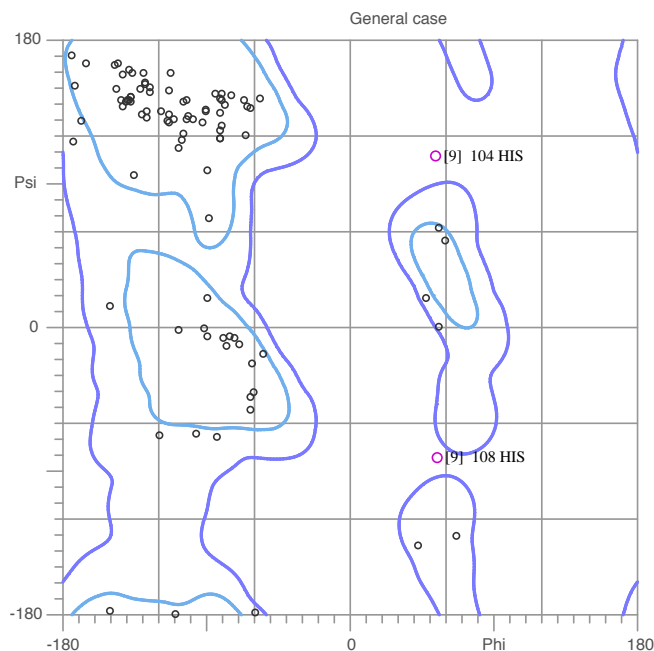   [8]   87 LYS (59.3, -89.1)

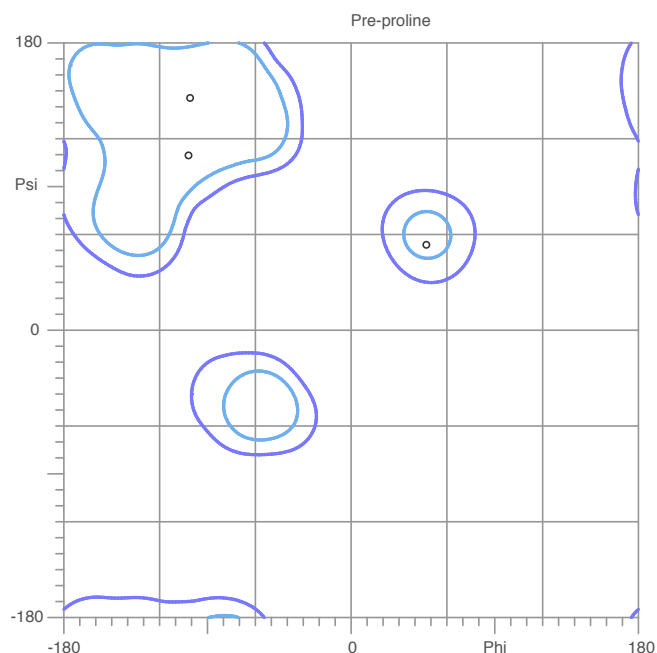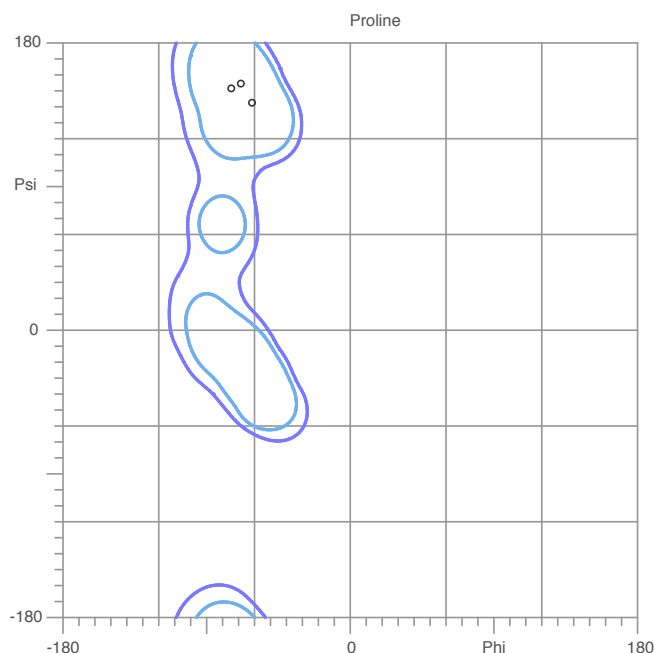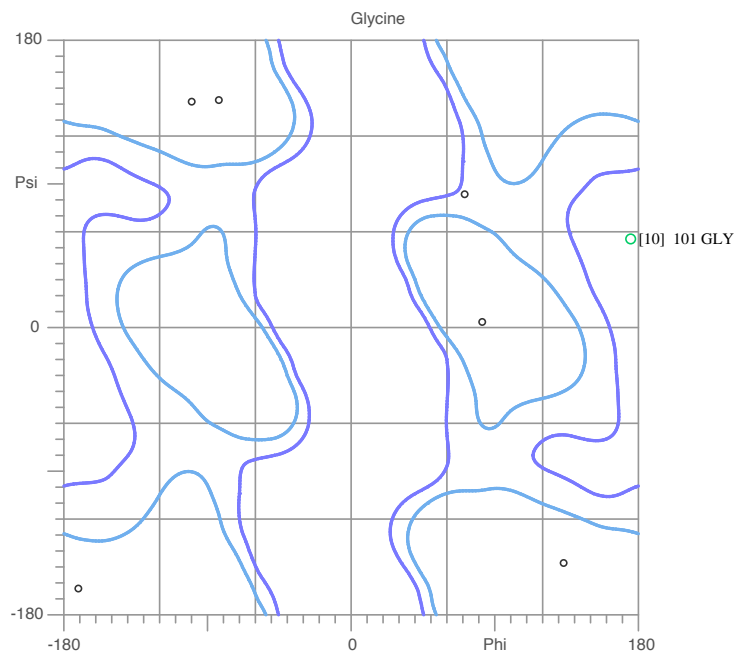# MolProbity Ramachandran analysis
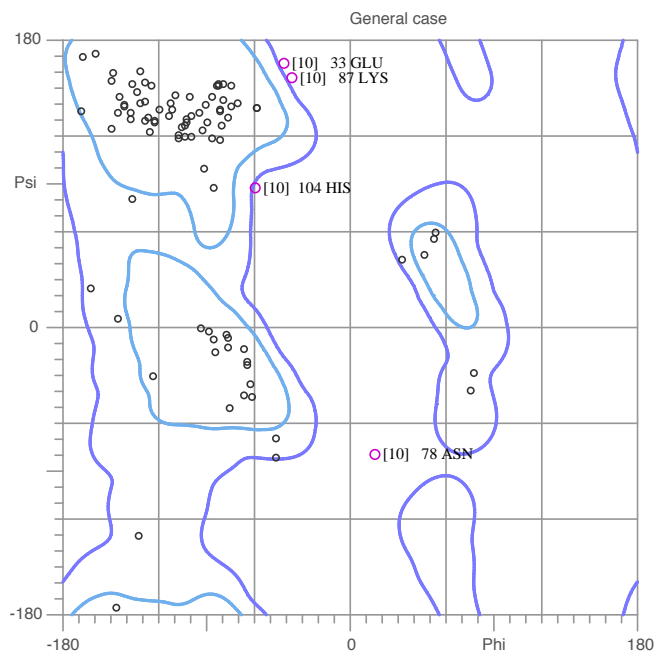
2KBN_NMR.pdb, model 9
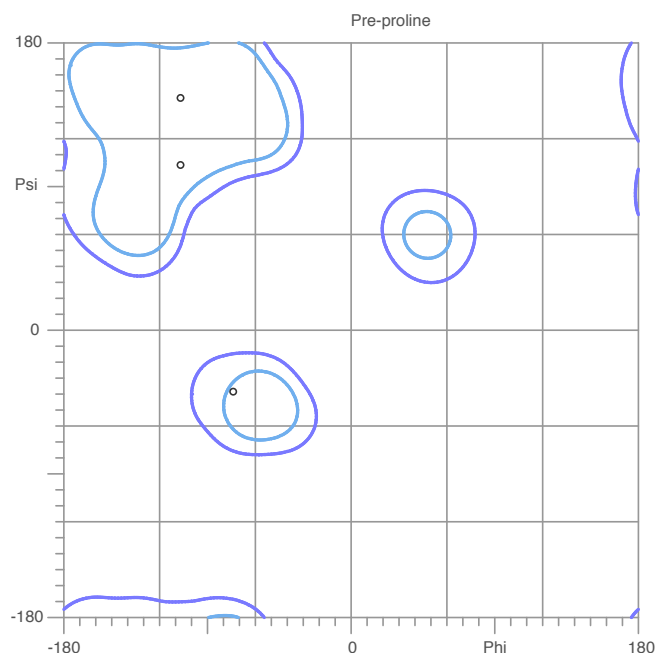
86.9% (93/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
   [9]   15 GLY (66.0, 110.9)
   [9] 104 HIS (53.6, 108.4)
   [9] 108 HIS (54.7, -81.3)

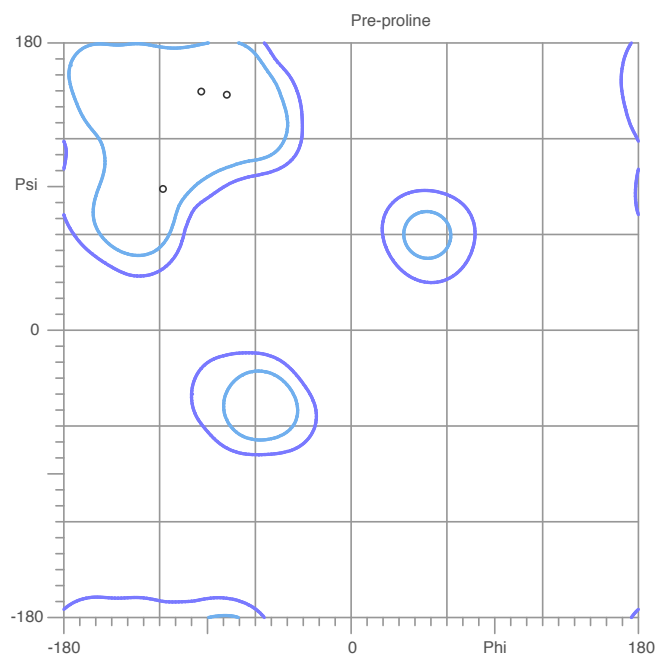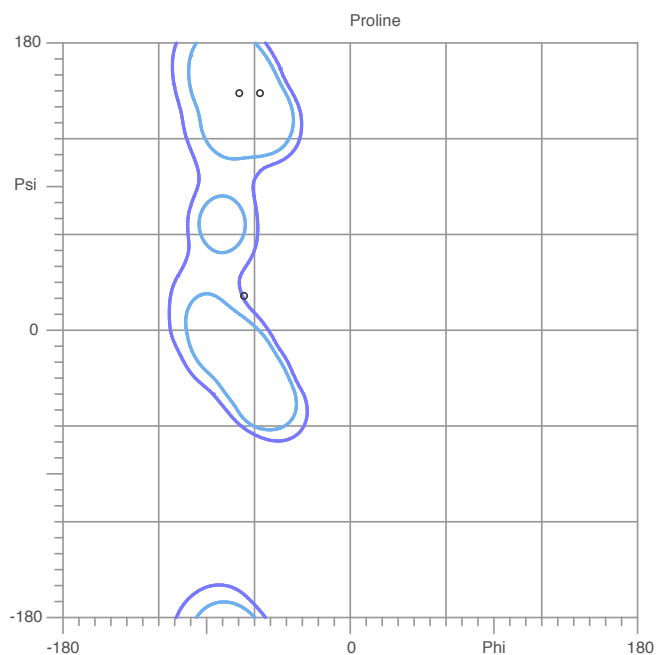# MolProbity Ramachandran analysis
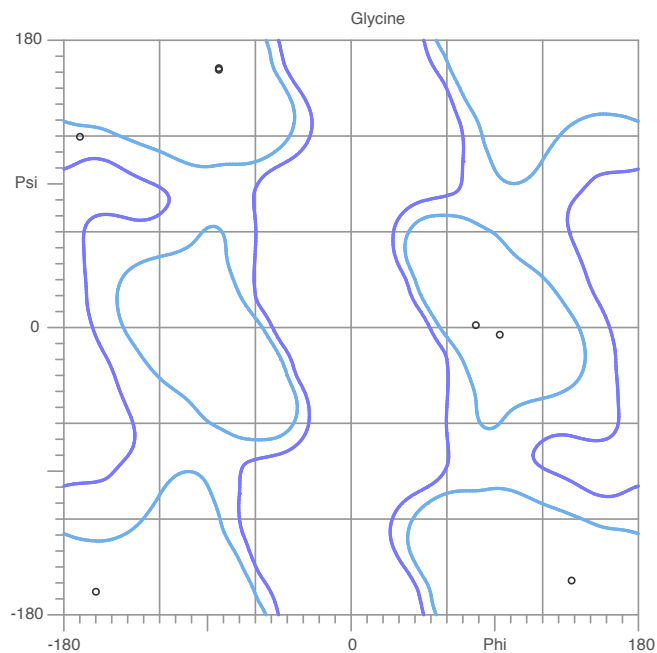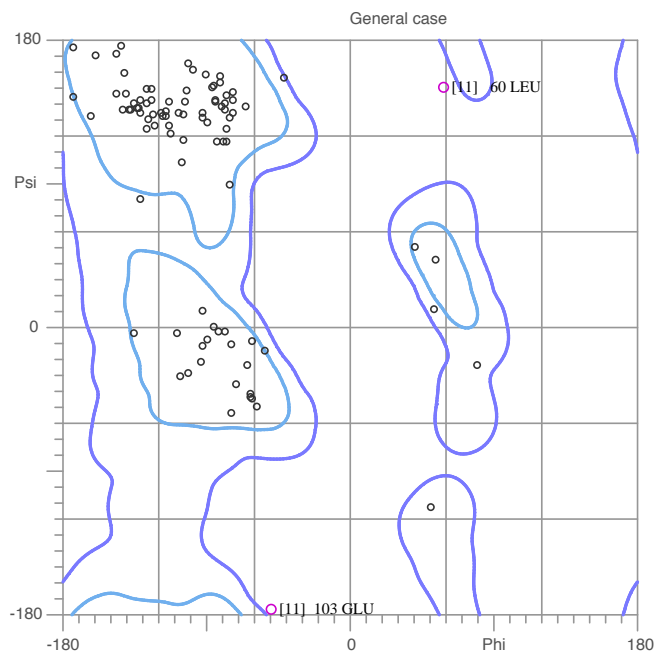
2KBN_NMR.pdb, model 10

86.0% (92/107) of all residues were in favored (98%) regions.
95.3% (102/107) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[10] 33 GLU (-42.9, 166.2)
[10] 78 ASN (15.1, -79.8)
[10] 87 LYS (-37.8, 157.3)
[10] 101 GLY (175.6, 57.0)
[10] 104 HIS (-60.4, 88.7)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 11

90.7% (97/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.
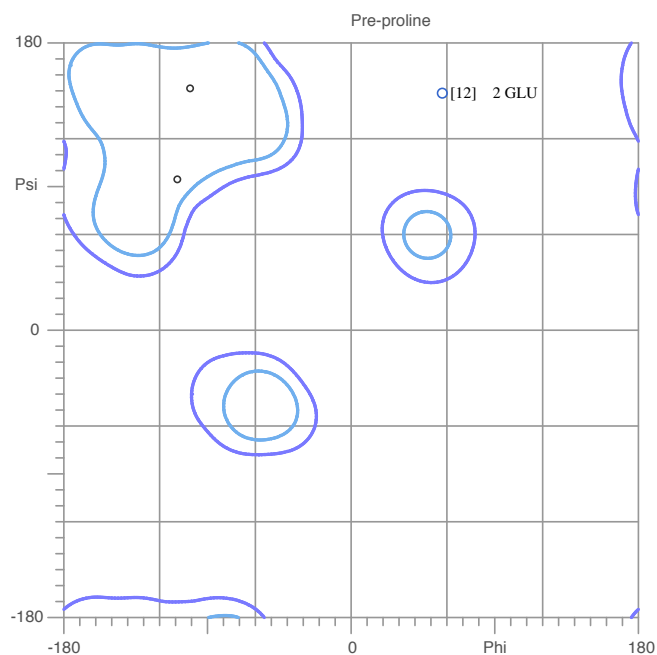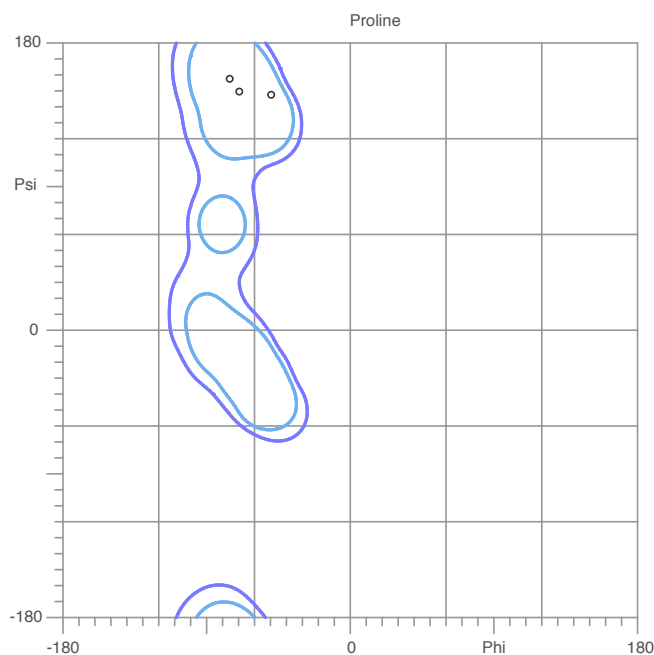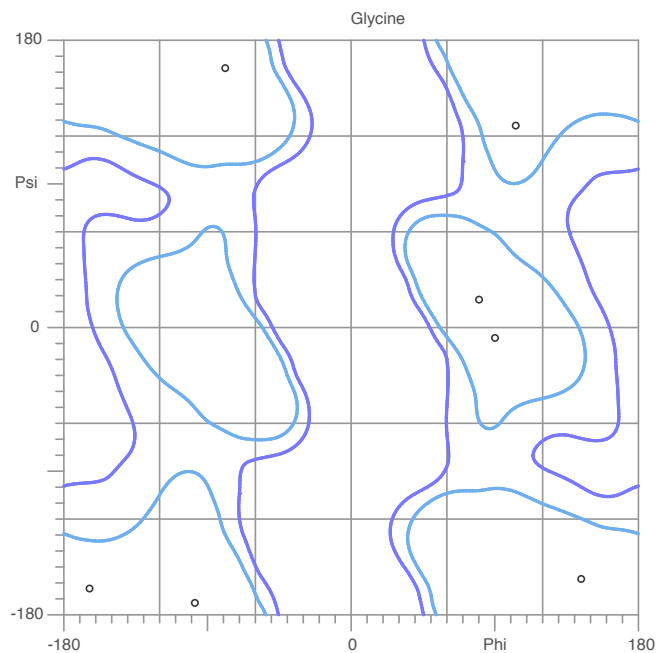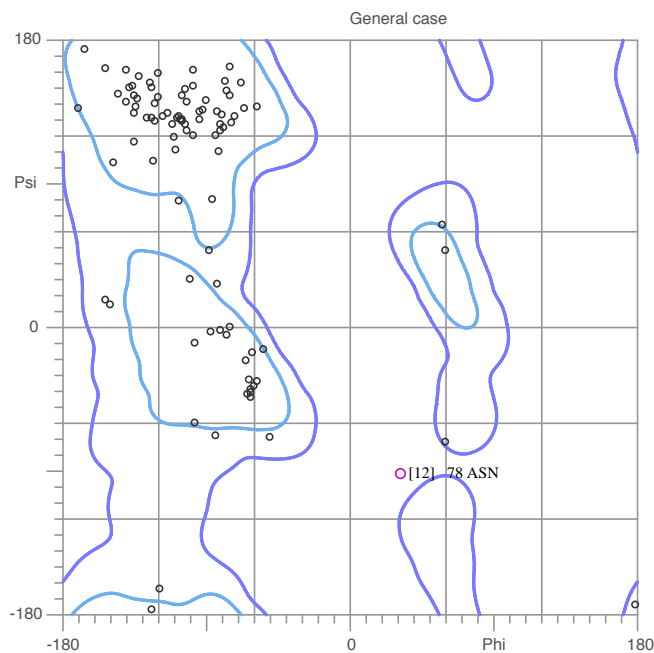
There were 2 outliers (phi, psi):
    [11]   60 LEU (58.6, 151.9)
    [11]   103 GLU (-50.6, -176.2)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 12

86.9% (93/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.
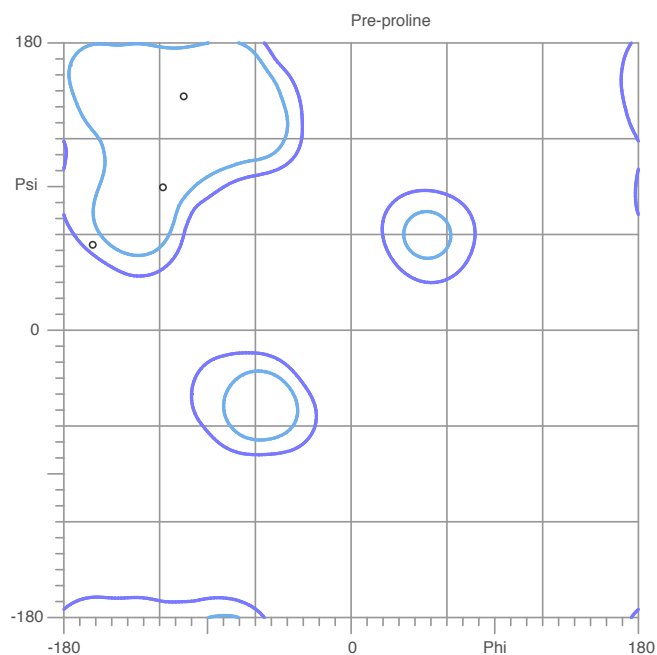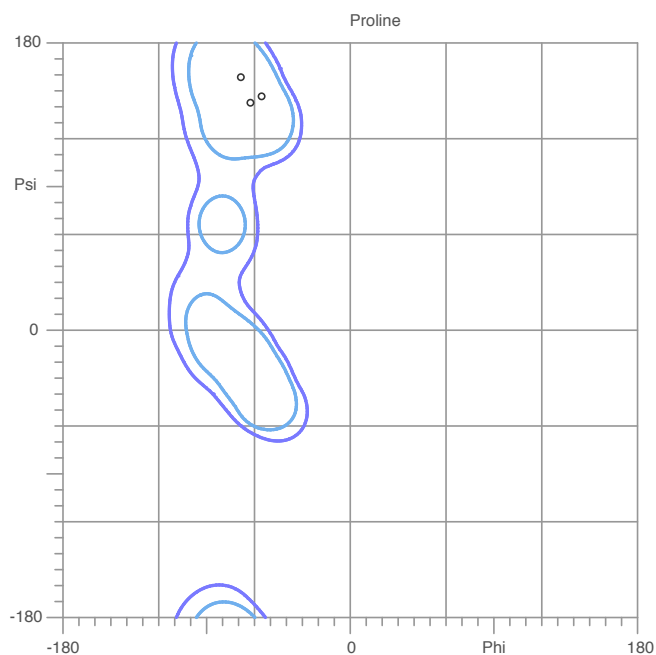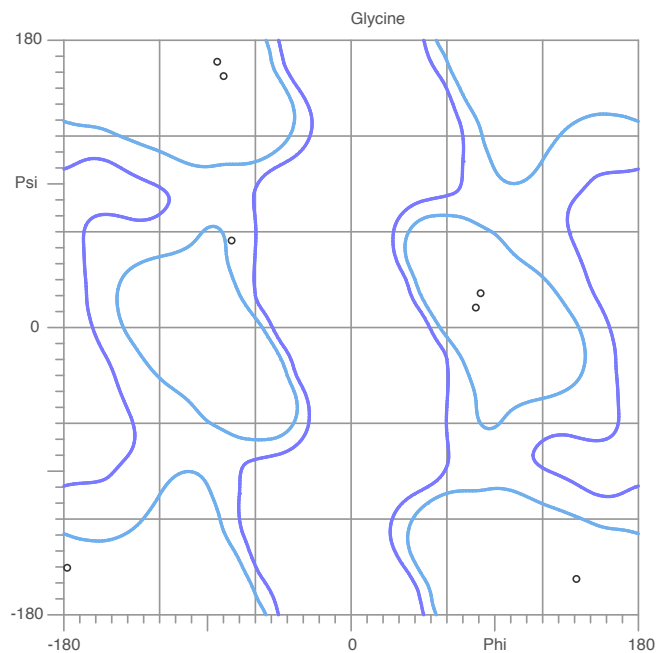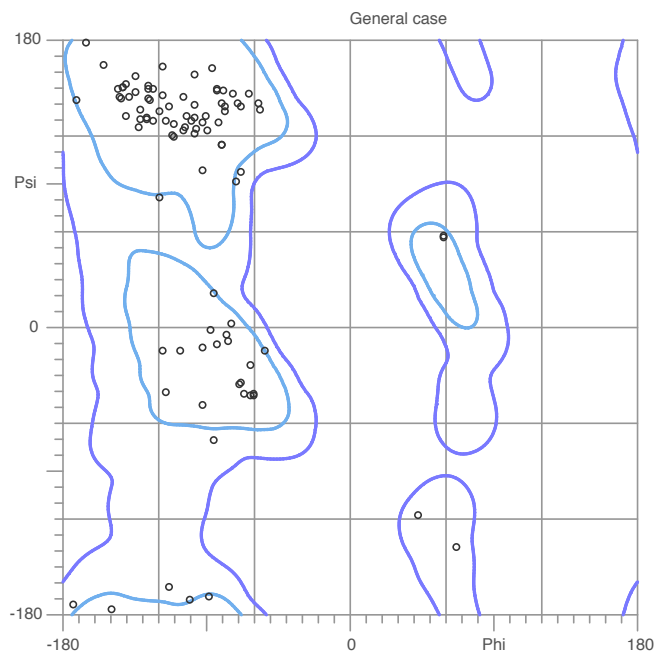
There were 2 outliers (phi, psi):
    [12]   2 GLU (57.3, 149.4)
    [12]   78 ASN (31.1, -91.3)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 13

90.7% (97/107) of all residues were in favored (98%) regions.
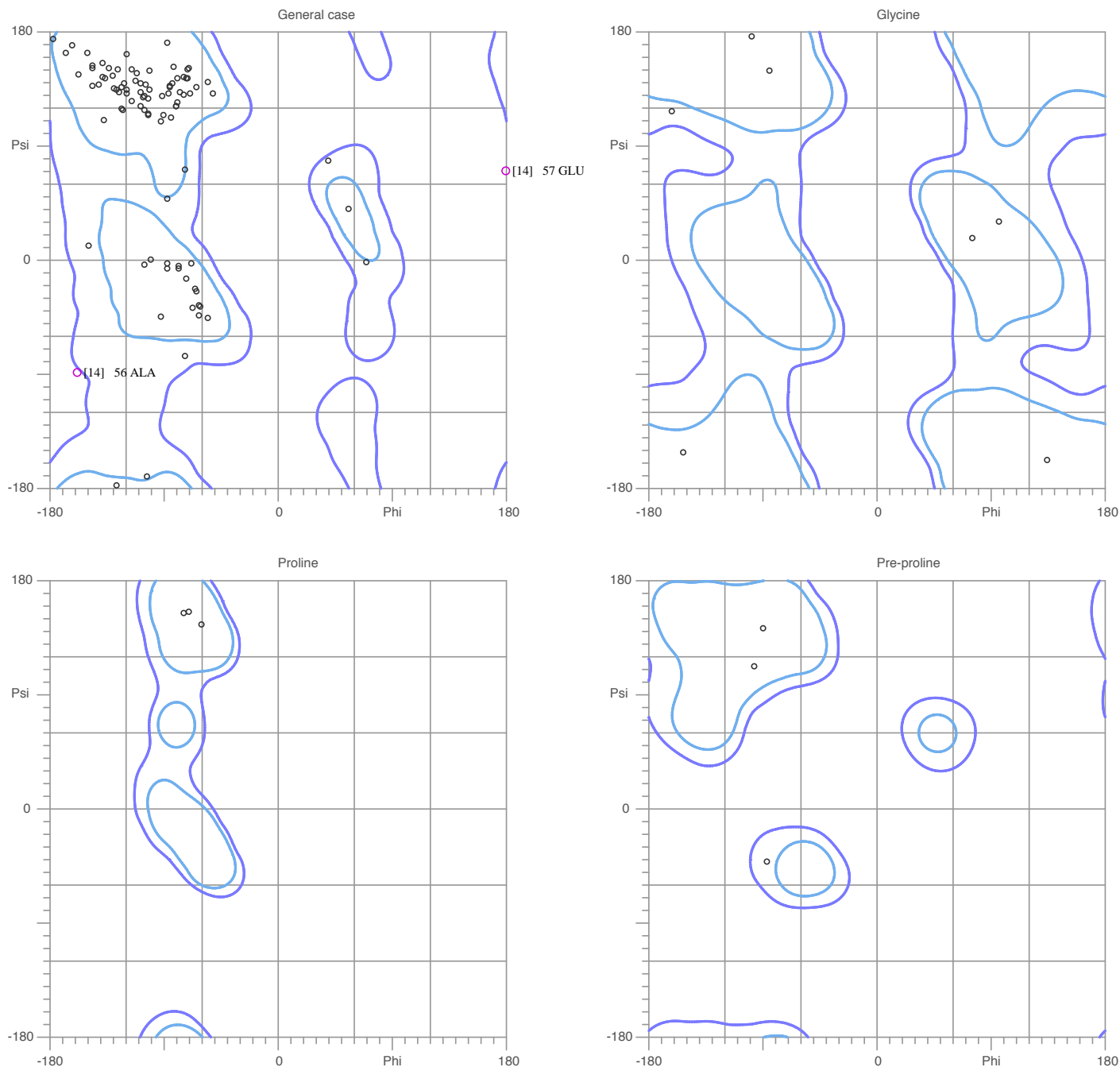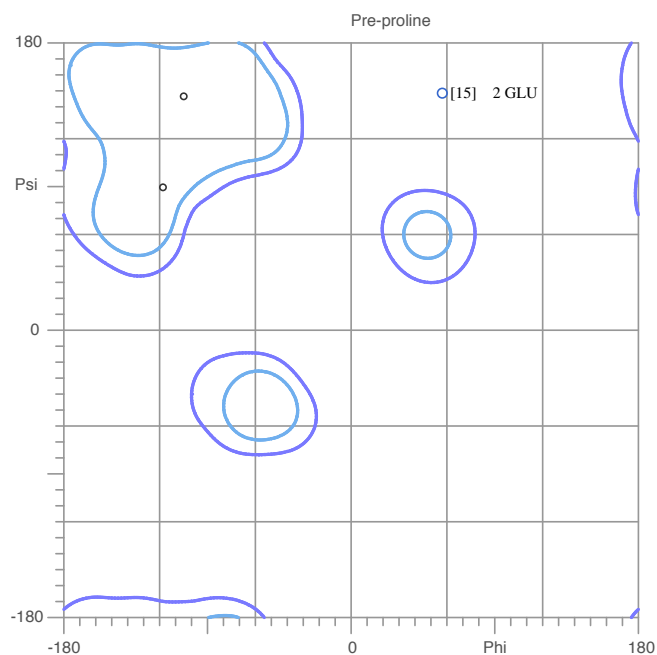100.0% (107/107) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

General case

Glycine

Proline

Pre-proline

89.7% (96/107) of all residues were in favored (98%) regions.

98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

    [14]   56 ALA (-159.1, -88.6)

    [14]   57 GLU (179.2, 71.6)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 15

92.5% (99/107) of all residues were in favored (98%) regions.
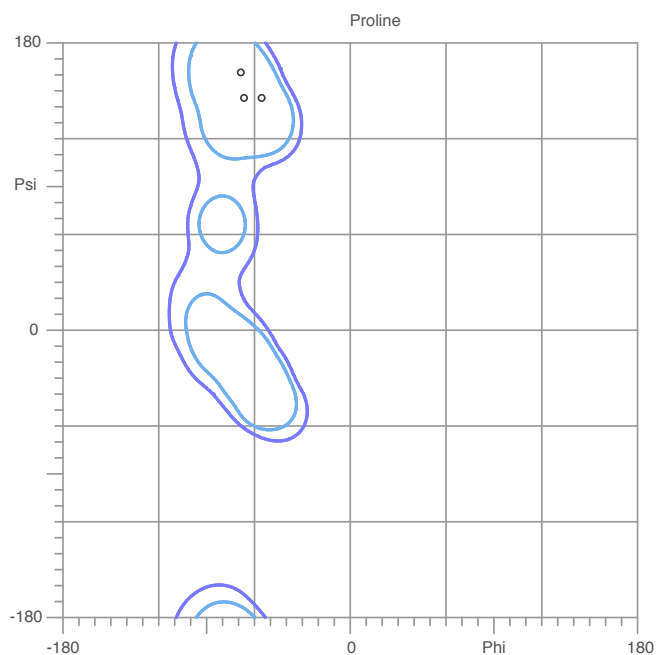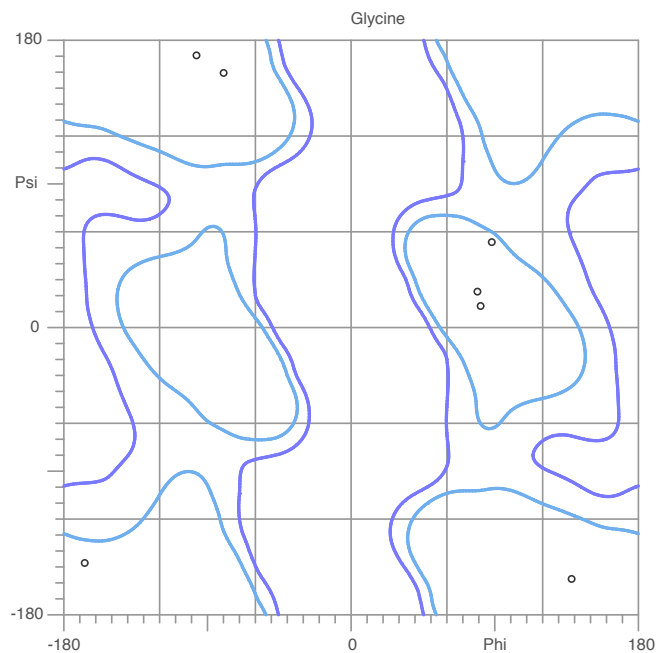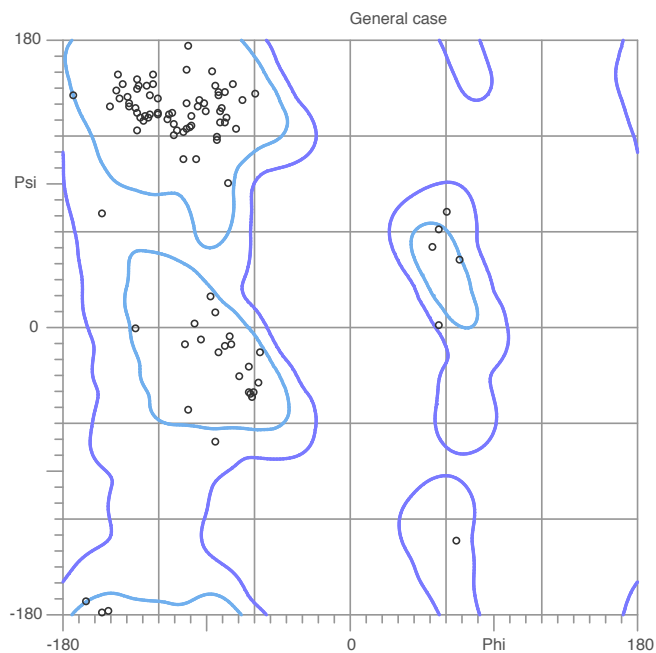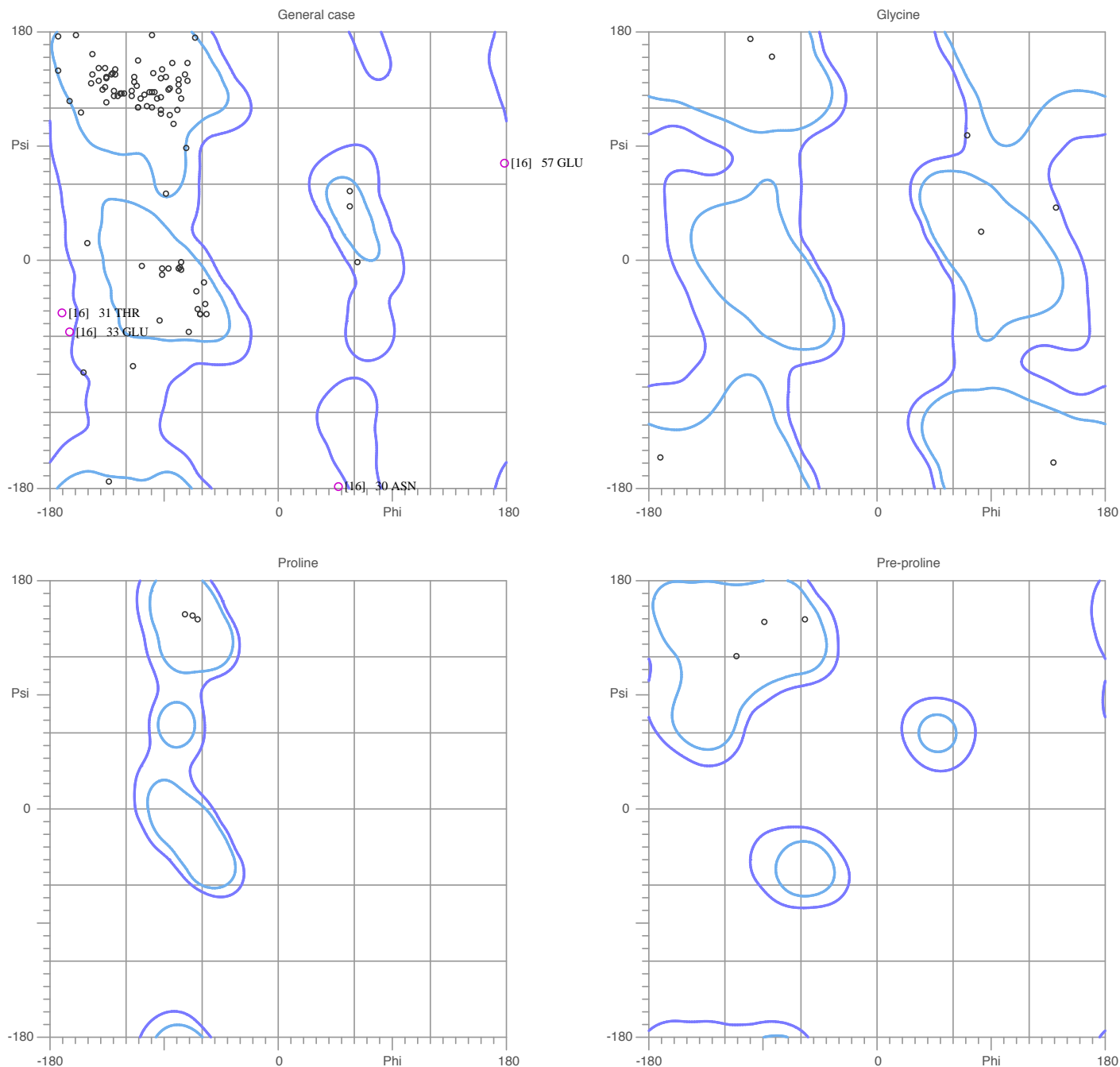99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
    [15]   2 GLU (57.1, 149.3)

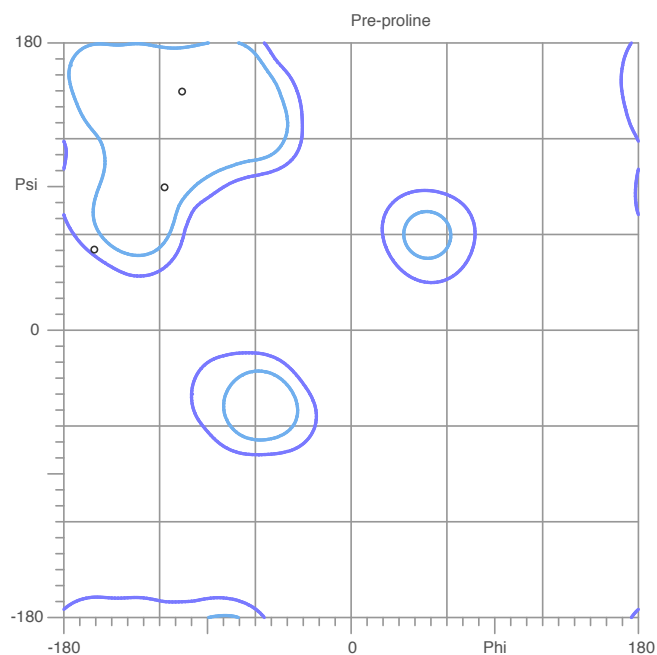# MolProbity Ramachandran analysis
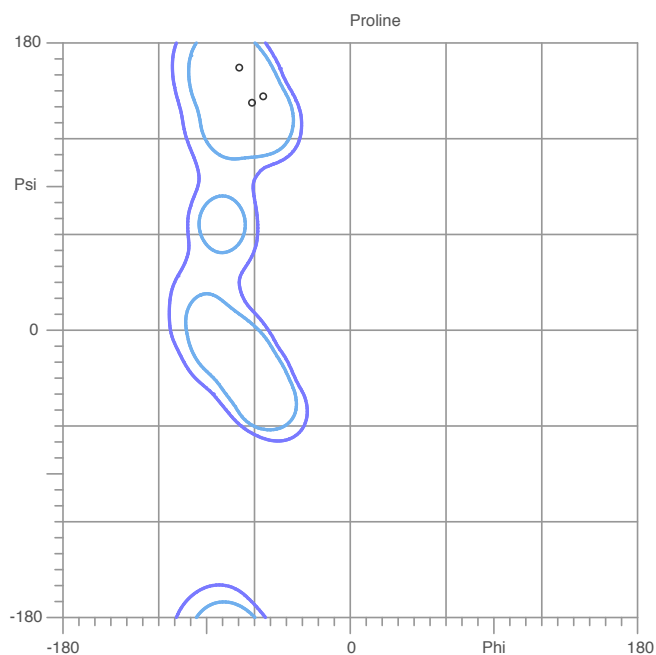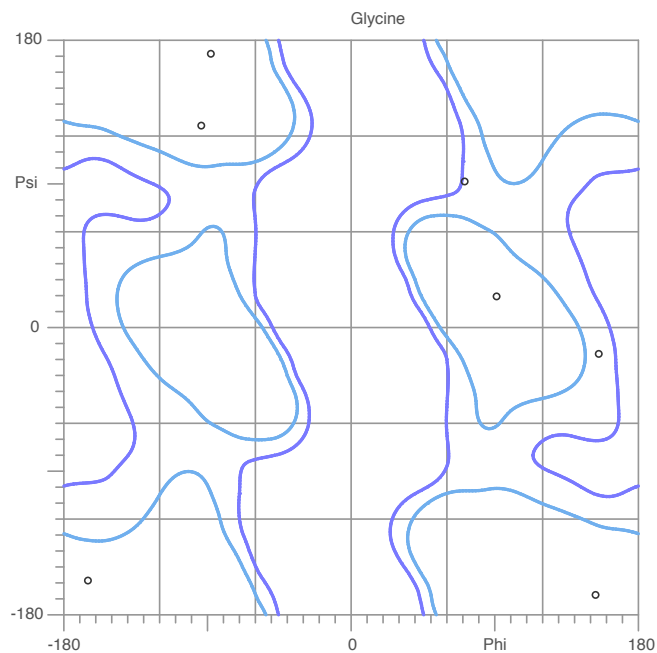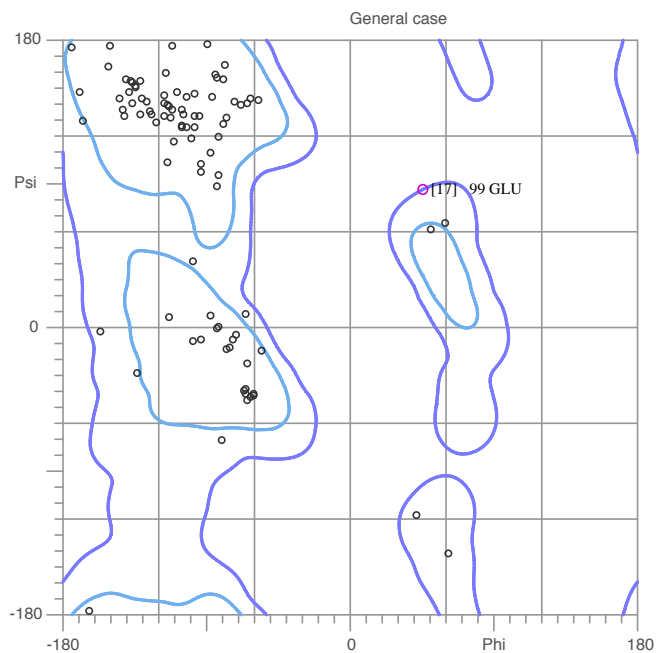
2KBN_NMR.pdb, model 16

90.7% (97/107) of all residues were in favored (98%) regions.
96.3% (103/107) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
    [16]   30 ASN (47.1, -178.5)
    [16]   31 THR (-171.2, -42.0)
    [16]   33 GLU (-165.9, -56.5)
    [16]   57 GLU (178.9, 77.9)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 17

87.9% (94/107) of all residues were in favored (98%) regions.
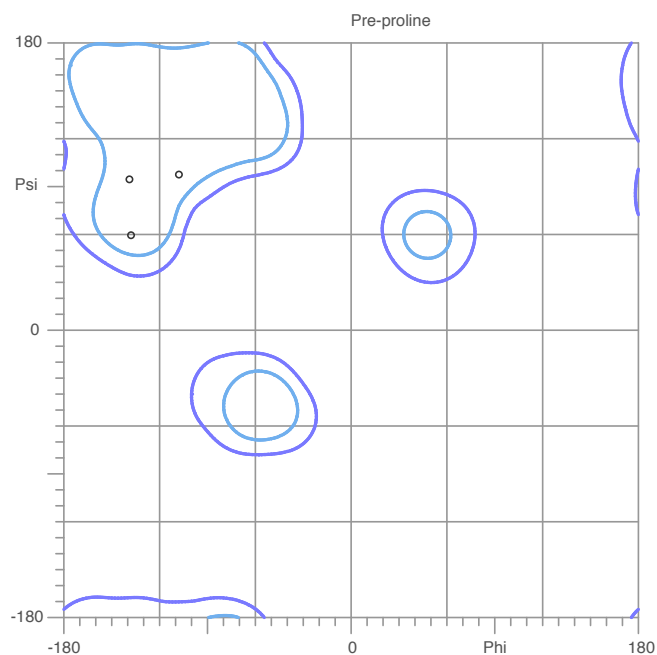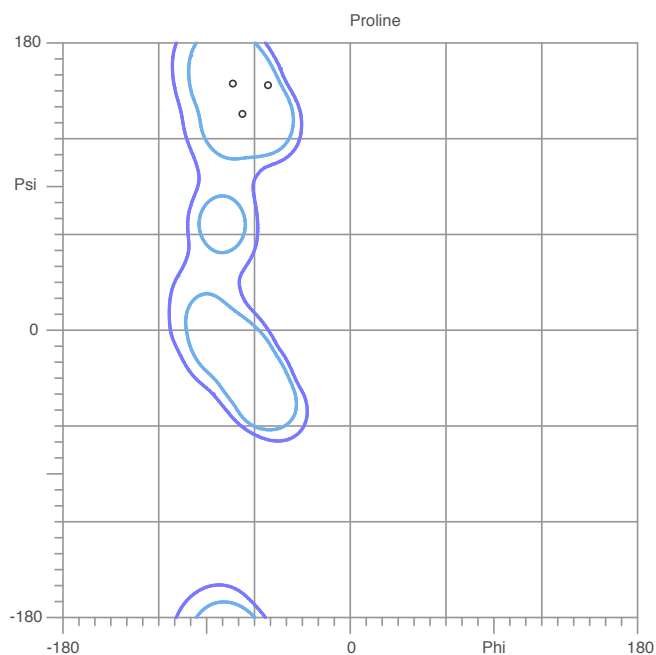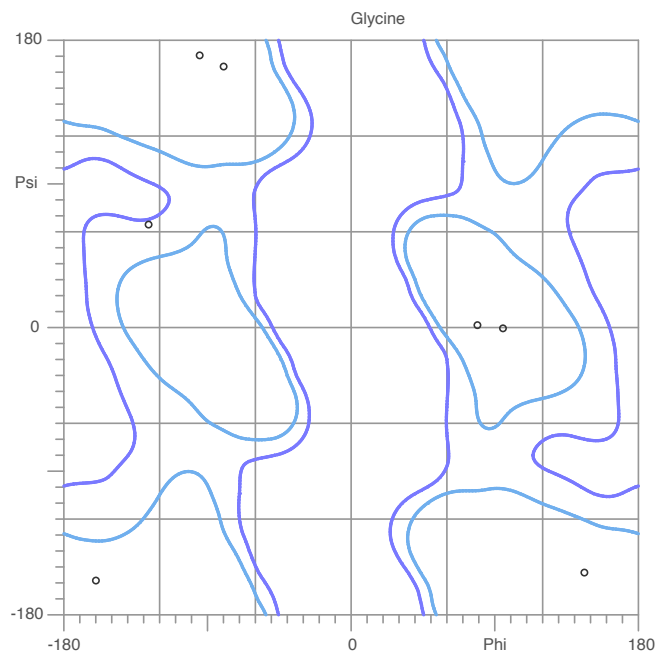99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
    [17] 99 GLU (45.1, 87.5)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 18

90.7% (97/107) of all residues were in favored (98%) regions.
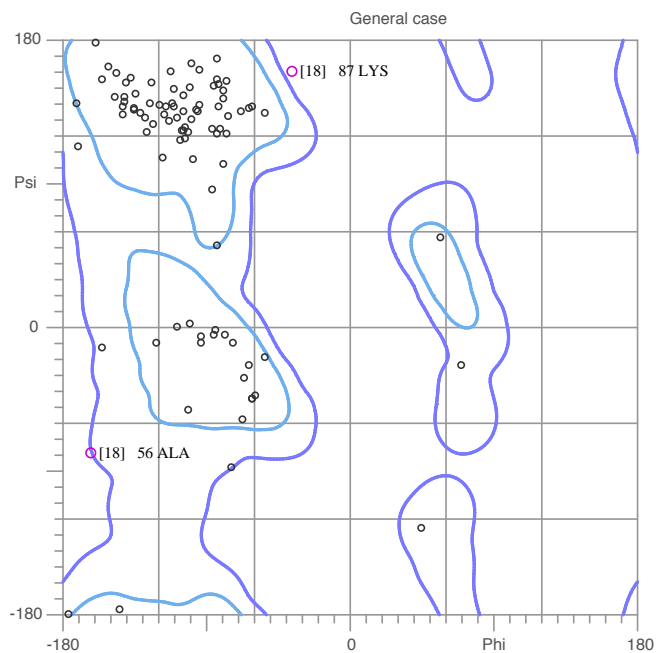98.1% (105/107) of all residues were in allowed (>99.8%) regions.
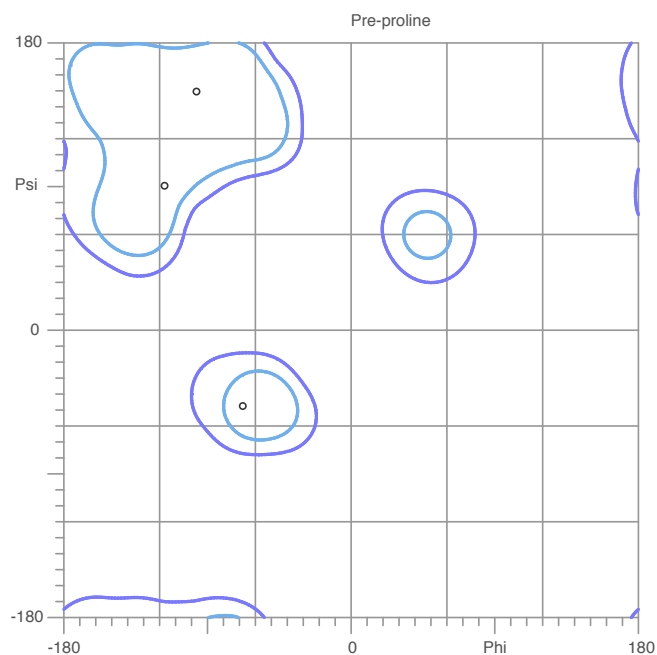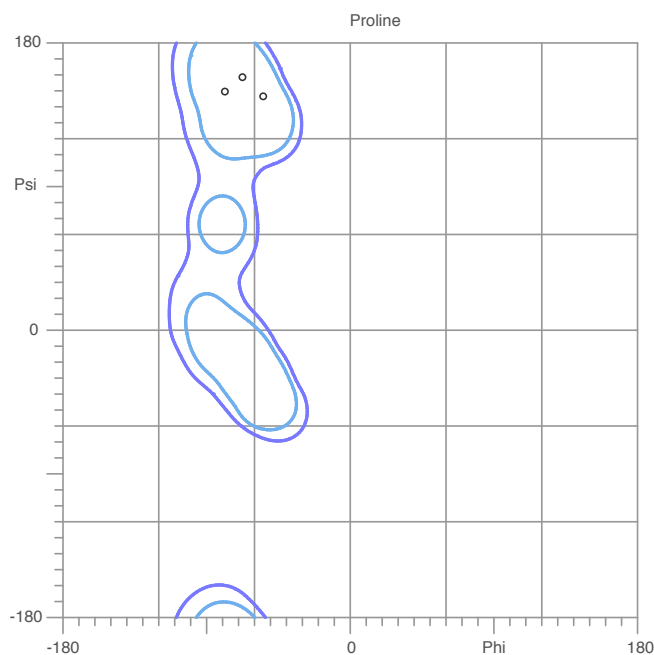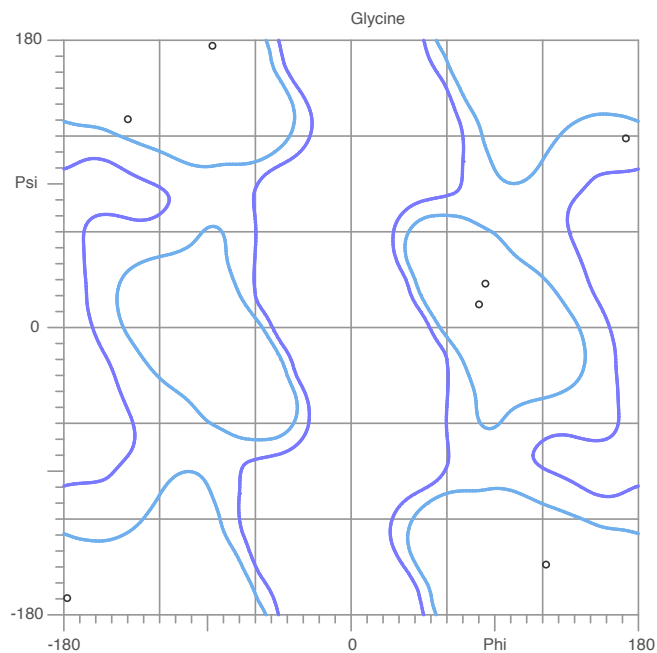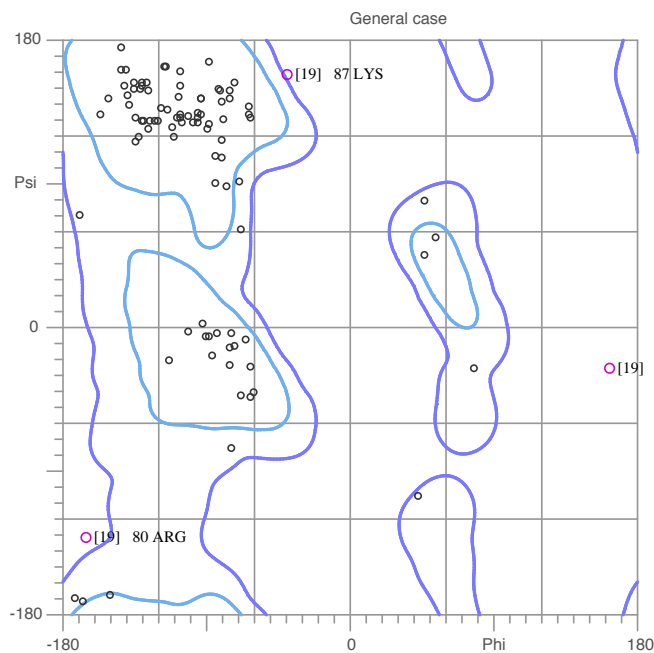
There were 2 outliers (phi, psi):
    [18]   56 ALA (-163.4, -78.7)
    [18]   87 LYS (-37.9, 161.1)

MolProbity Ramachandran analysis
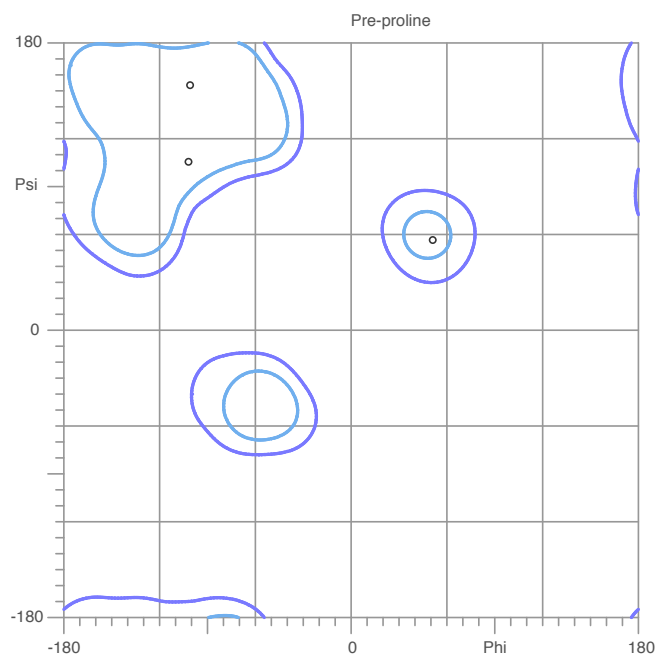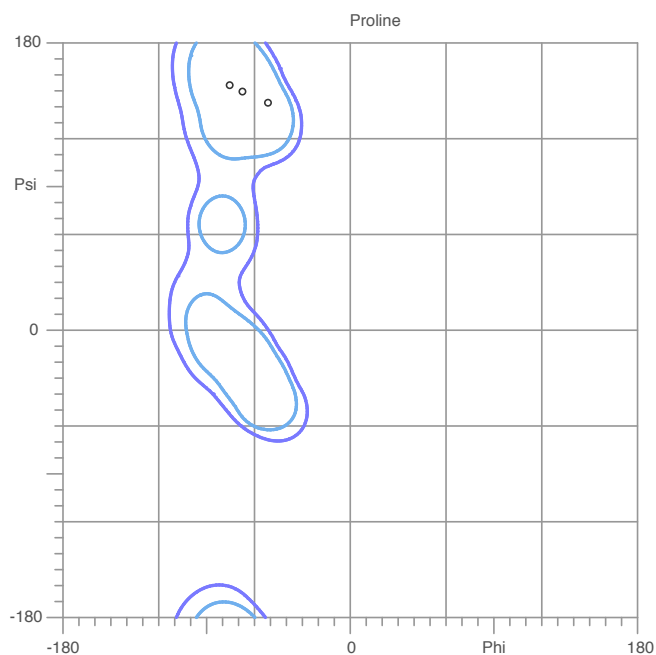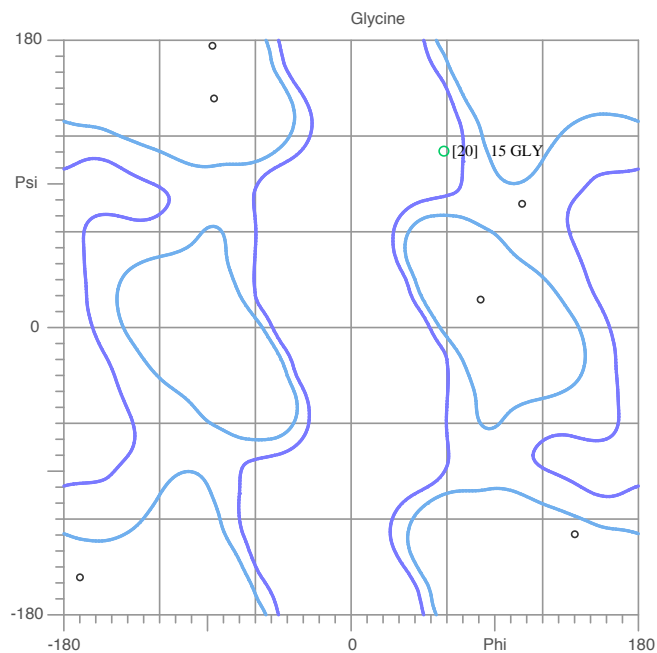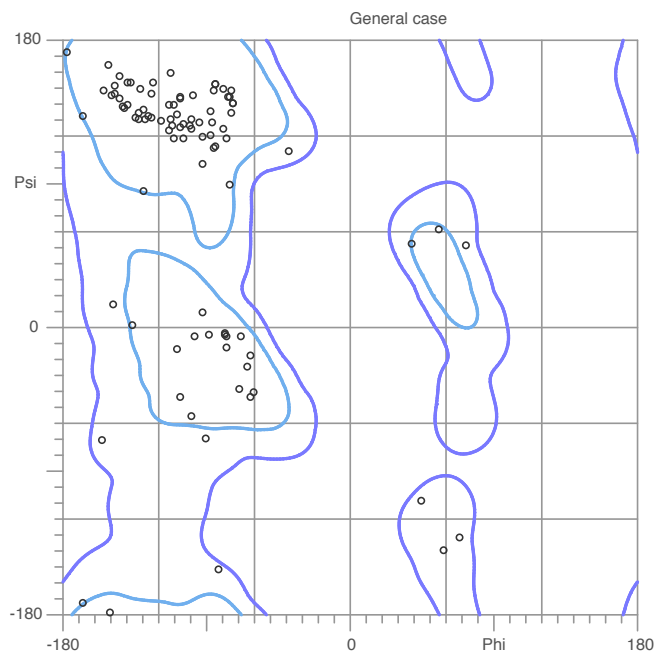
2KBN_NMR.pdb, model 19

87.9% (94/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
    [19] 79 ASP (162.4, -25.6)
    [19] 80 ARG (-166.9, -131.7)
    [19] 87 LYS (-40.9, 159.8)

MolProbity Ramachandran analysis

2KBN_NMR.pdb, model 20

87.9% (94/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
    [20]   15 GLY (58.0, 111.1)