MolProbity Ramachandran analysis

2KZV_NMR.pdb, all models

General case

Psi / Phi

Glycine

Psi / Phi

Proline

Psi / Phi

Pre-proline

Psi / Phi

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

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 1

General case

Glycine

Proline

Pre-proline

87.8% (79/90) of all residues were in favored (98%) regions.
93.3% (84/90) of all residues were in allowed (>99.8%) regions.
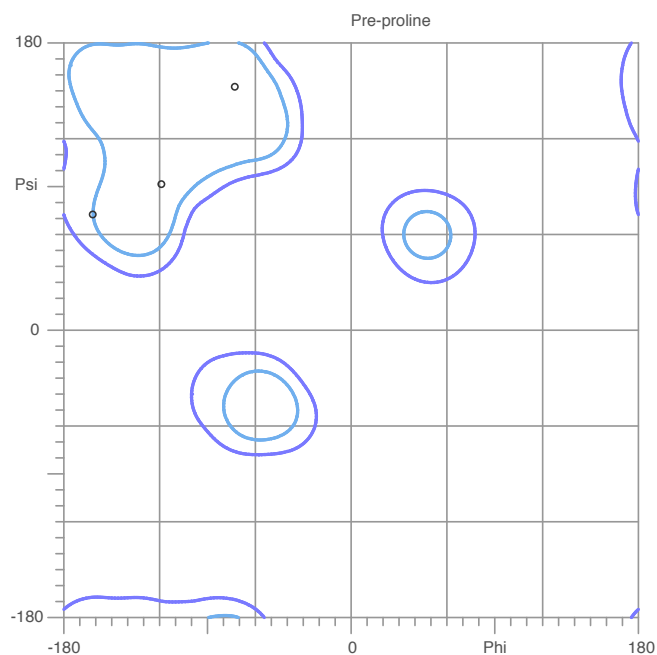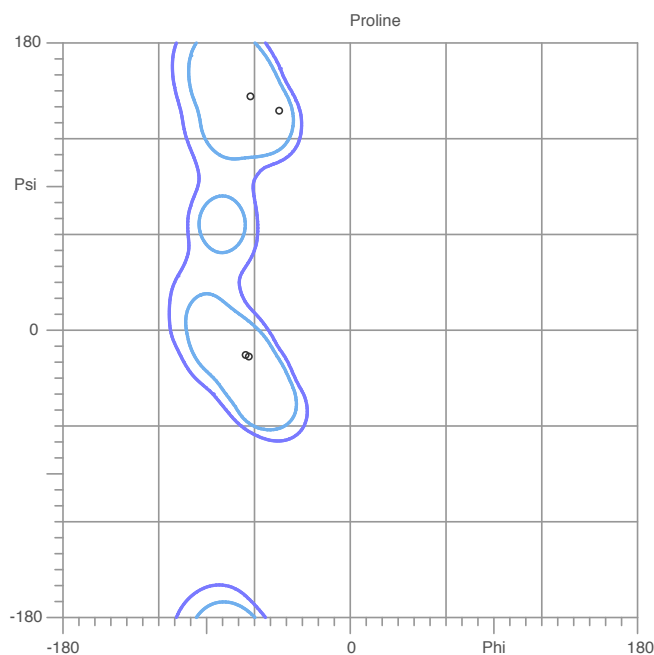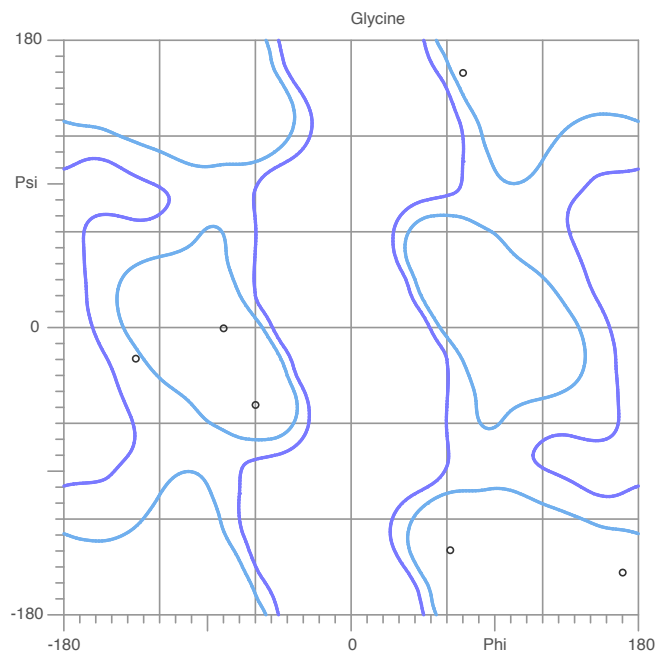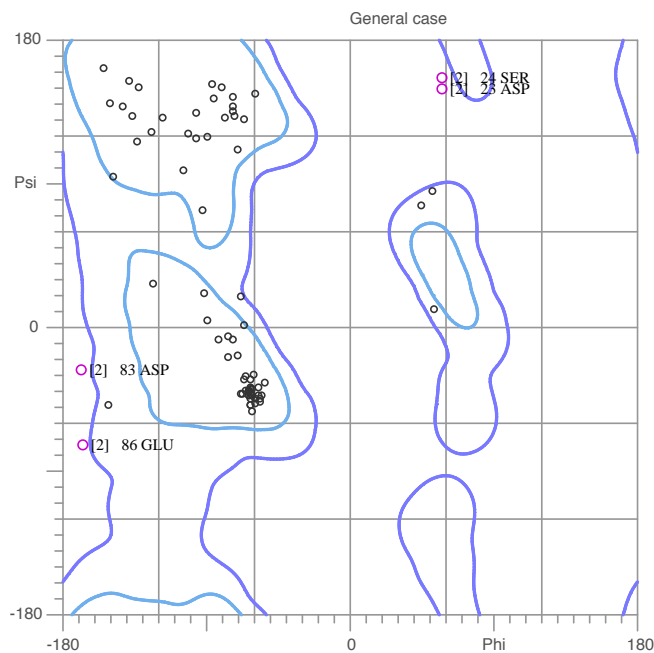
There were 6 outliers (phi, psi):
   [1]   4 LYS (54.2, -80.6)

[1]   6 LYS (54.1, 108.5)
[1]   24 SER (-179.8, 77.1)
[1]   25 GLY (56.0, -91.1)
[1]   26 TRP (-54.7, -174.1)
[1]   89 HIS (51.9, 179.6)

MolProbity Ramachandran analysis
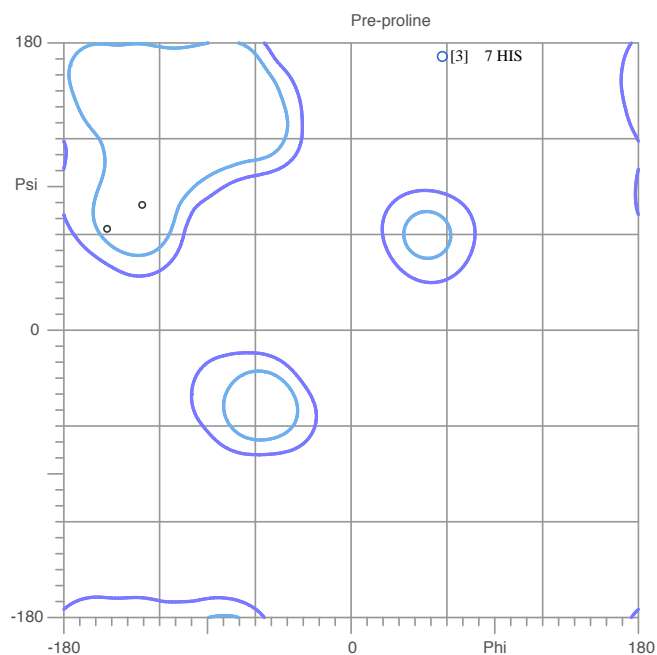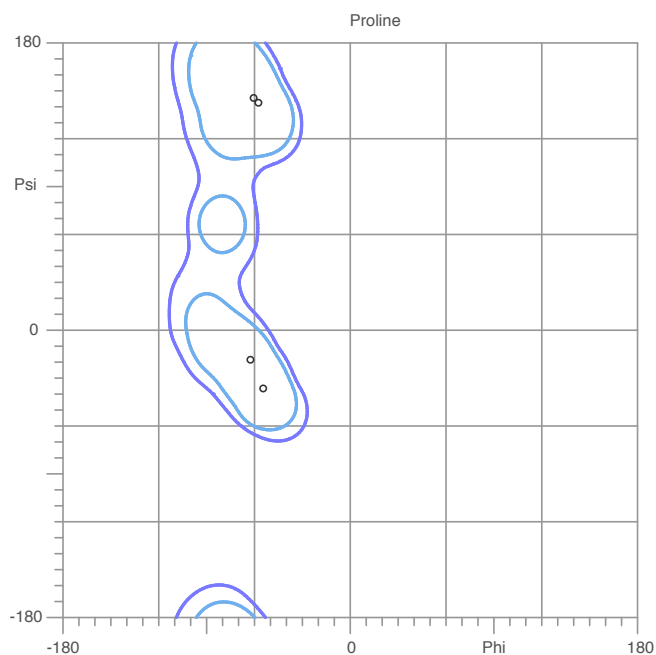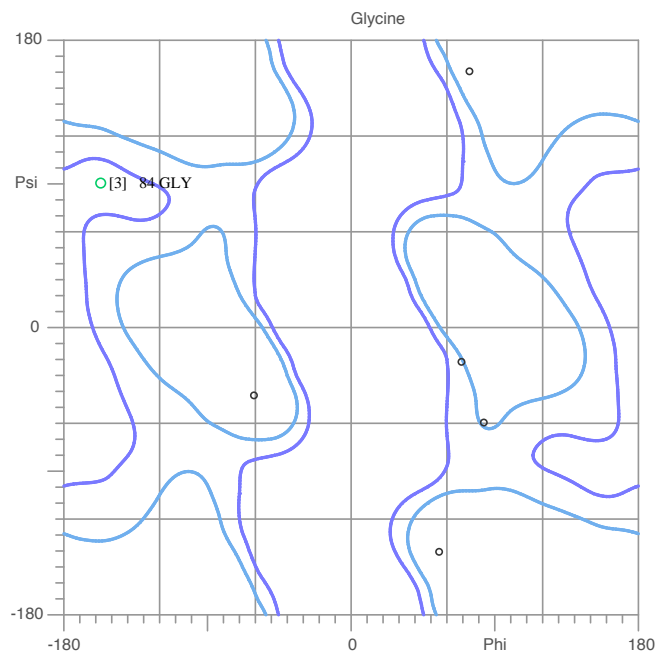
2KZV_NMR.pdb, model 2

87.8% (79/90) of all residues were in favored (98%) regions.
95.6% (86/90) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
  [2]   23 ASP (57.7, 150.4)
  [2]   24 SER (58.0, 157.9)
  [2]   83 ASP (-169.6, -26.7)
  [2]   86 GLU (-168.7, -73.0)

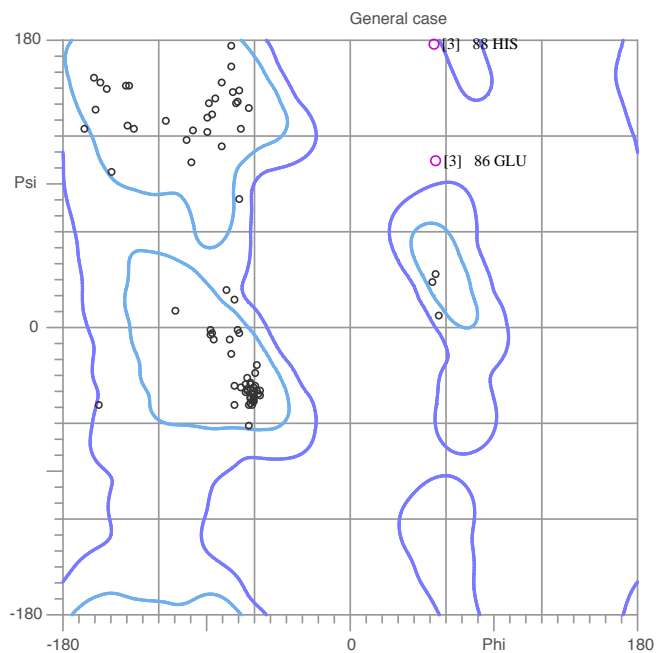# MolProbity Ramachandran analysis
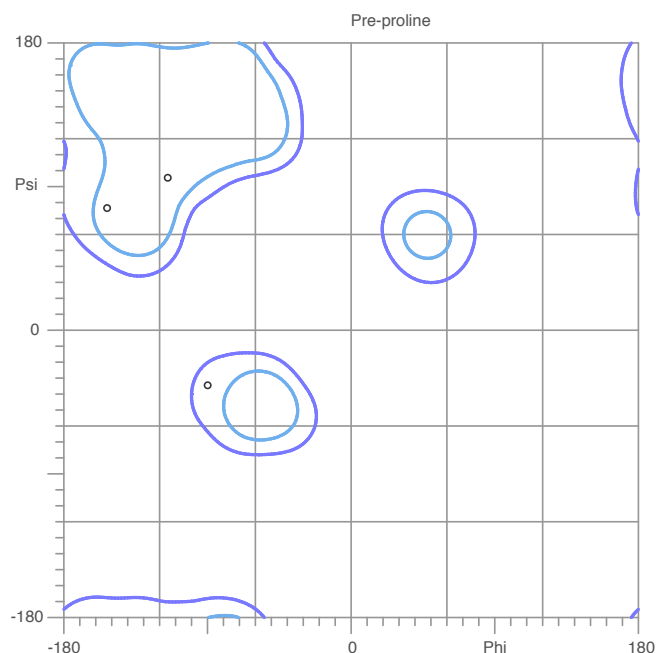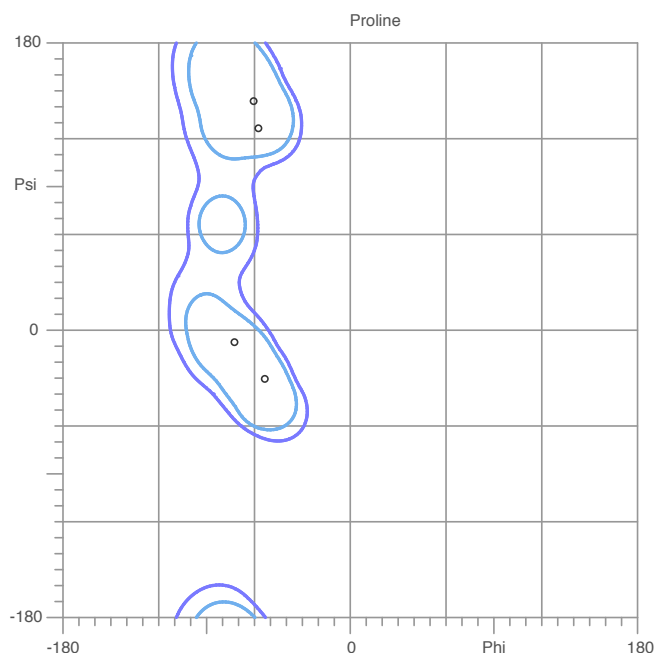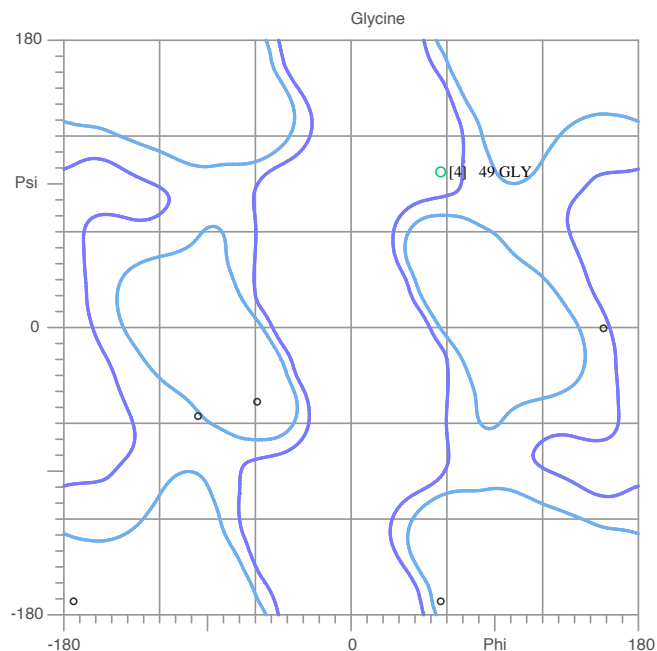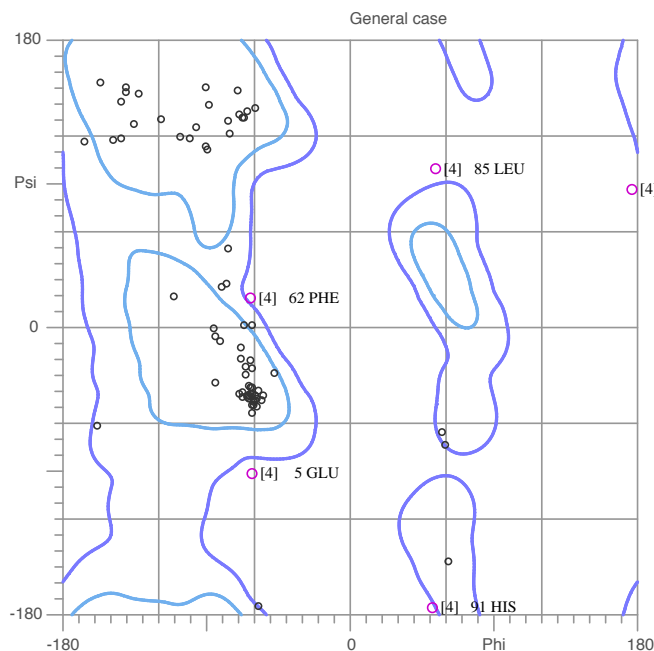
2KZV_NMR.pdb, model 3

87.8% (79/90) of all residues were in favored (98%) regions.
95.6% (86/90) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
    [3]   7 HIS (57.7, 172.3)
    [3] 84 GLY (-157.3, 91.3)
    [3] 86 GLU (53.6, 105.9)
    [3] 88 HIS (52.2, 178.4)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 4

78.9% (71/90) of all residues were in favored (98%) regions.
93.3% (84/90) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
   [4]   5 GLU (-62.5, -91.5)

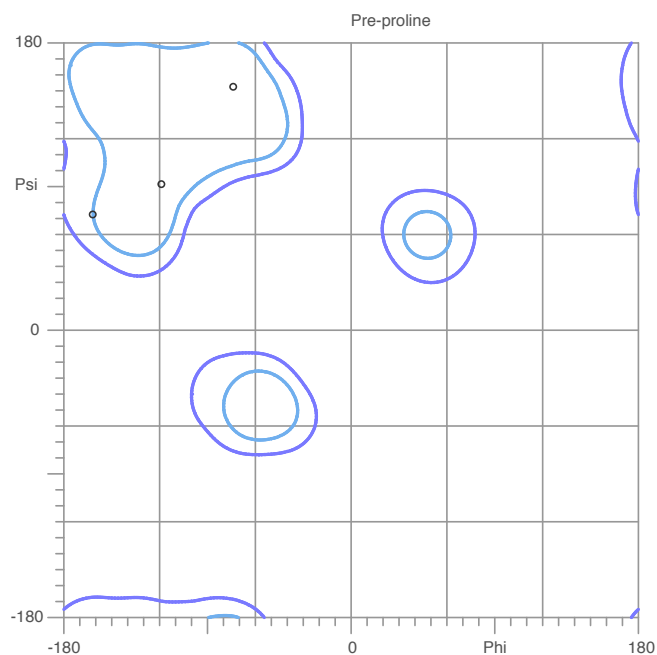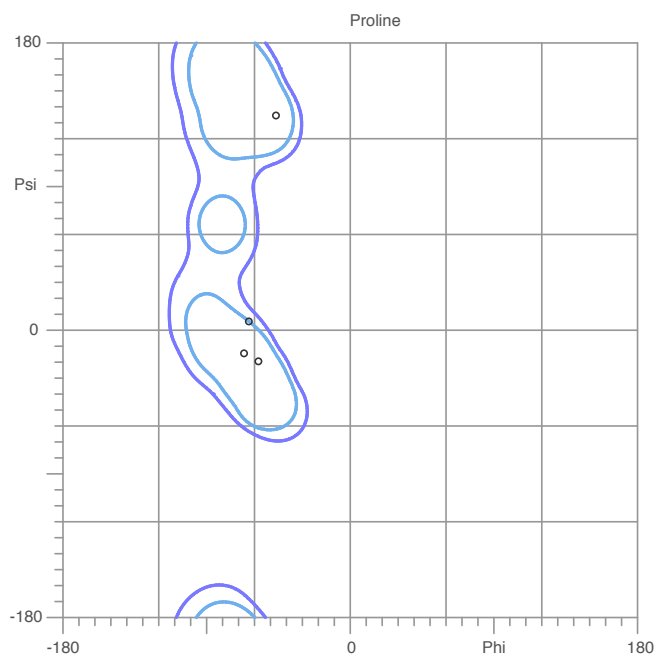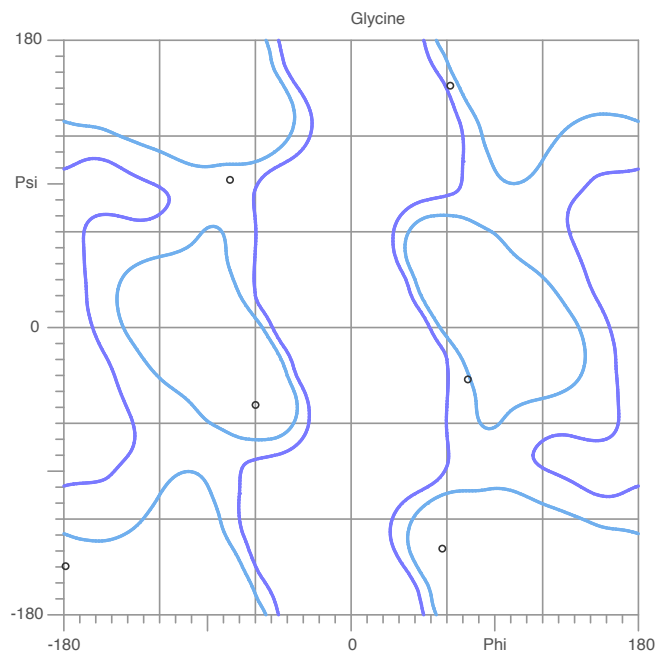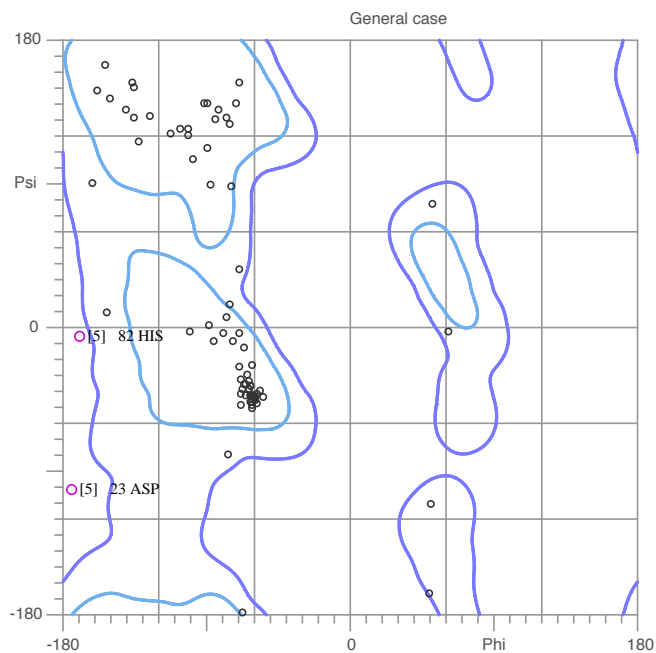[4]   24 SER (176.8, 87.7)
[4]   49 GLY (56.8, 98.9)
[4]   62 PHE (-63.2, 19.1)
[4]   85 LEU (53.7, 100.2)
[4]   91 HIS (51.3, -175.5)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 5

82.2% (74/90) of all residues were in favored (98%) regions.
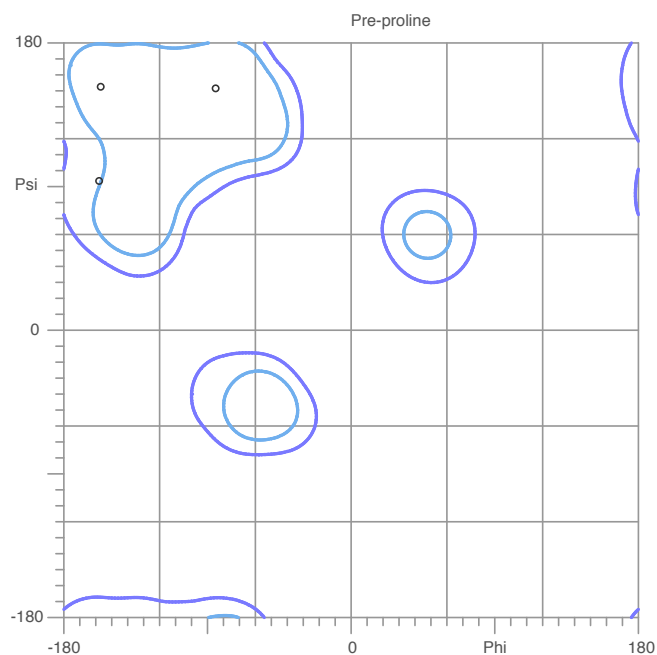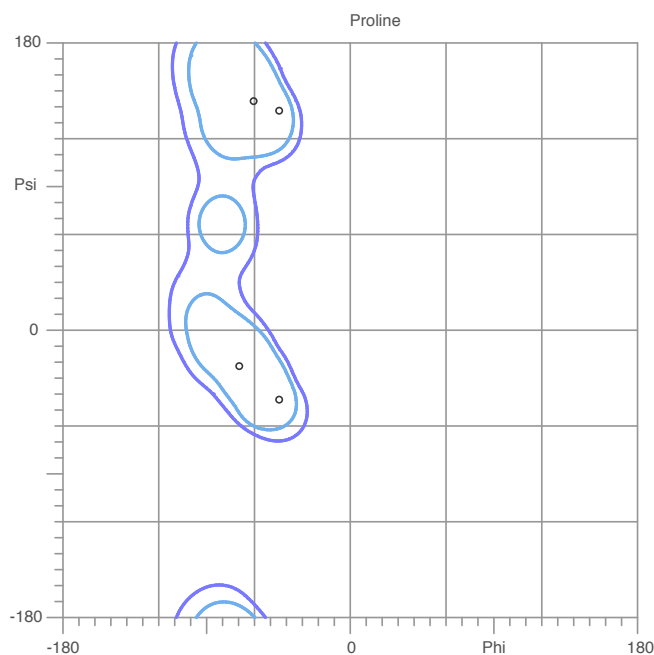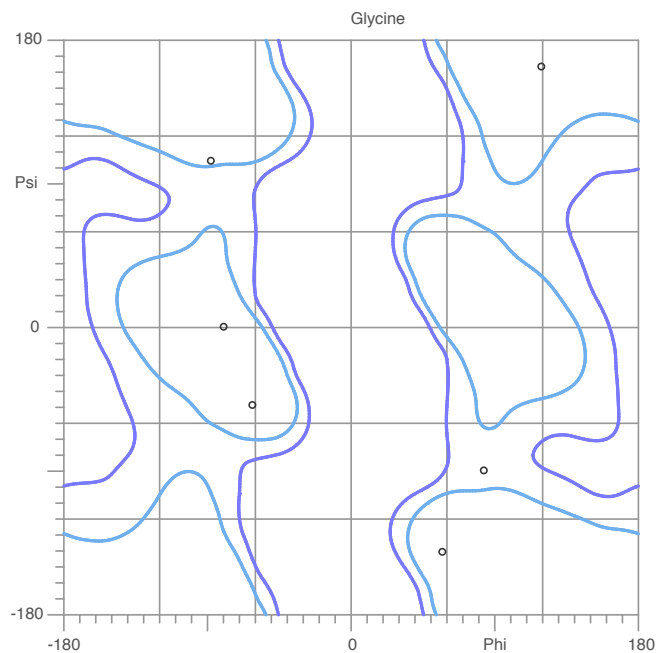97.8% (88/90) of all residues were in allowed (>99.8%) regions.
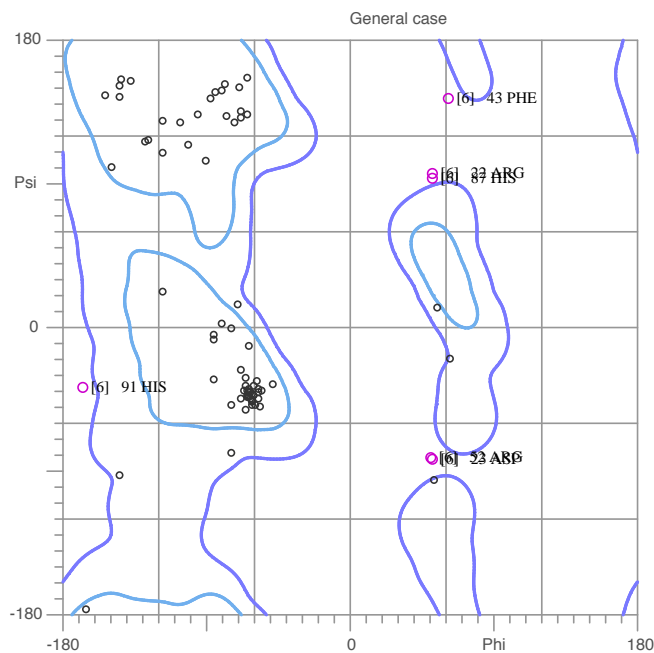
There were 2 outliers (phi, psi):
    [5]   23 ASP (-175.1, -101.4)
    [5]   82 HIS (-170.9, -5.9)

MolProbity Ramachandran analysis
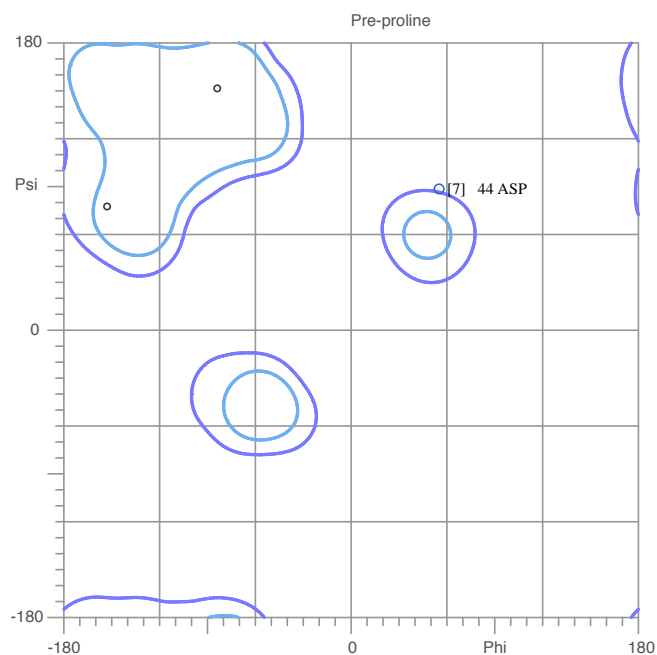
2KZV_NMR.pdb, model 6

84.4% (76/90) of all residues were in favored (98%) regions.
93.3% (84/90) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
   [6]   22 ARG (51.8, 97.5)

[6]   23 ASP (51.1, -82.7)
[6]   43 PHE (61.8, 144.7)
[6]   52 ARG (50.1, -81.9)
[6]   87 HIS (51.0, 94.8)
[6]   91 HIS (-168.5, -37.5)

MolProbity Ramachandran analysis
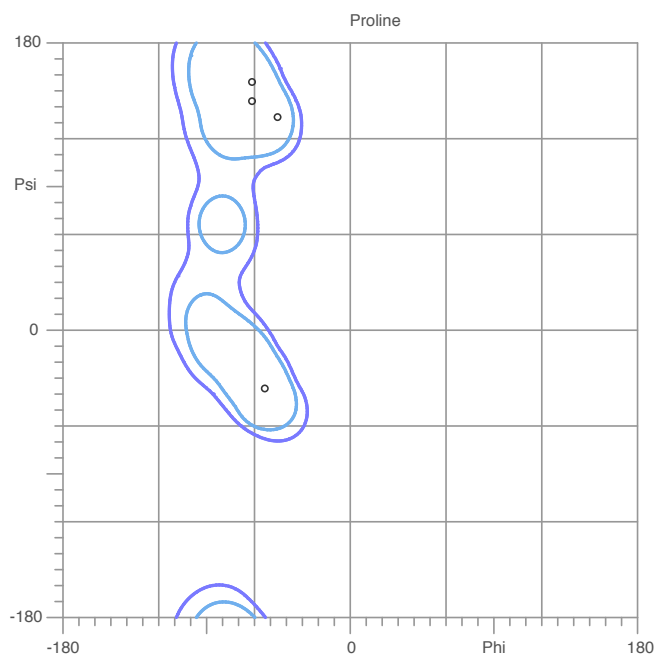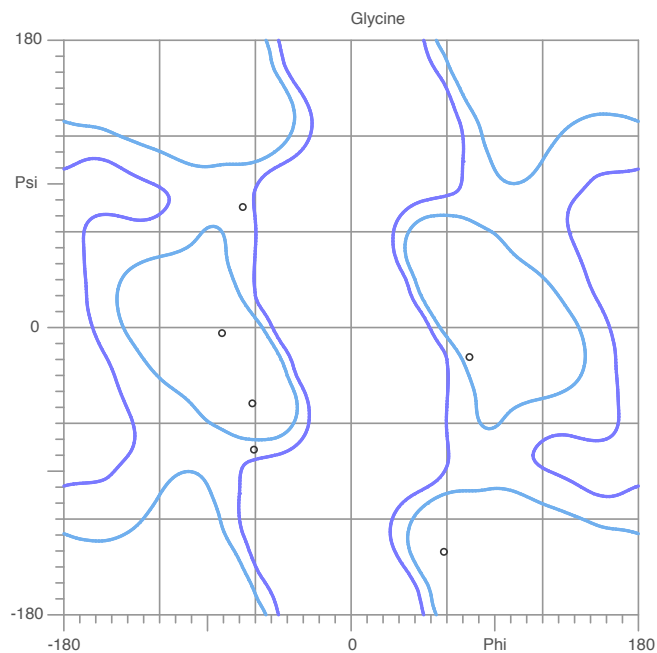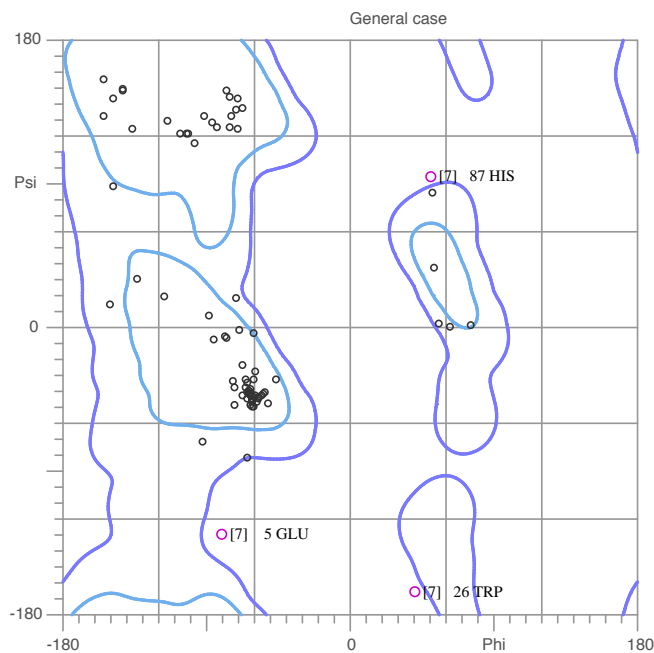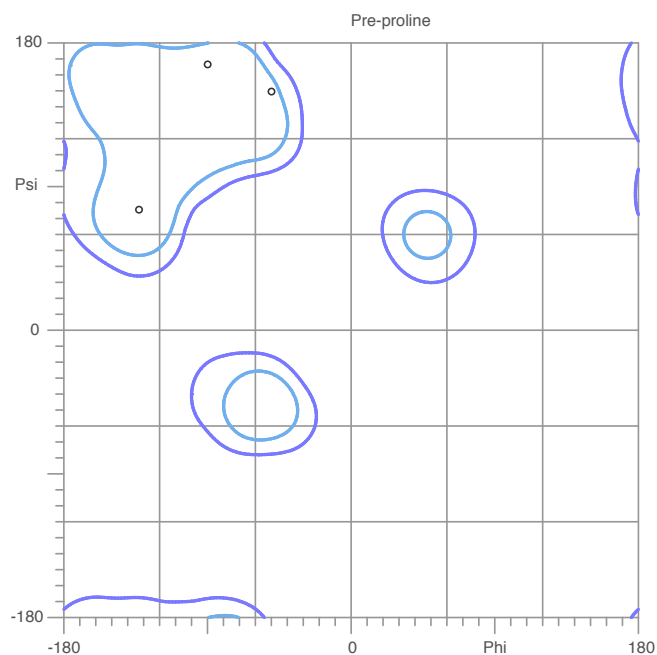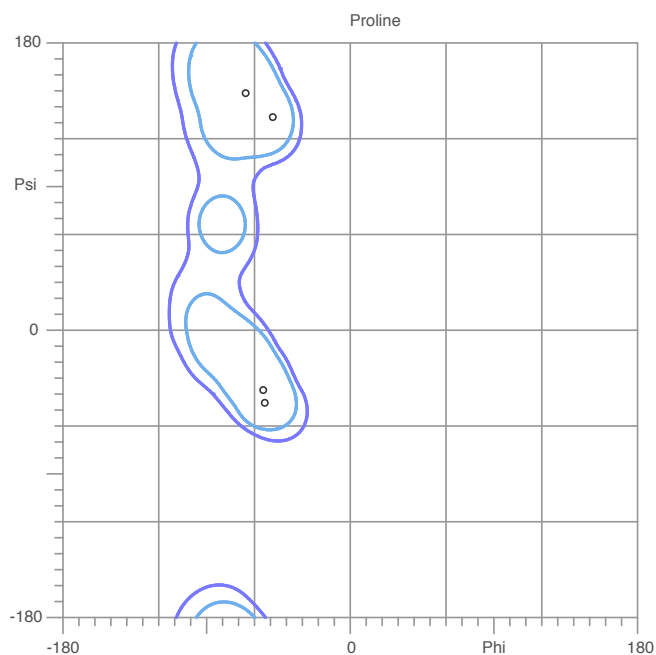
2KZV_NMR.pdb, model 7

84.4% (76/90) of all residues were in favored (98%) regions.
95.6% (86/90) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
    [7]   5 GLU (-81.4, -129.3)
    [7] 26 TRP (40.7, -165.7)
    [7] 44 ASP (55.2, 89.4)
    [7] 87 HIS (50.2, 95.5)

MolProbity Ramachandran analysis
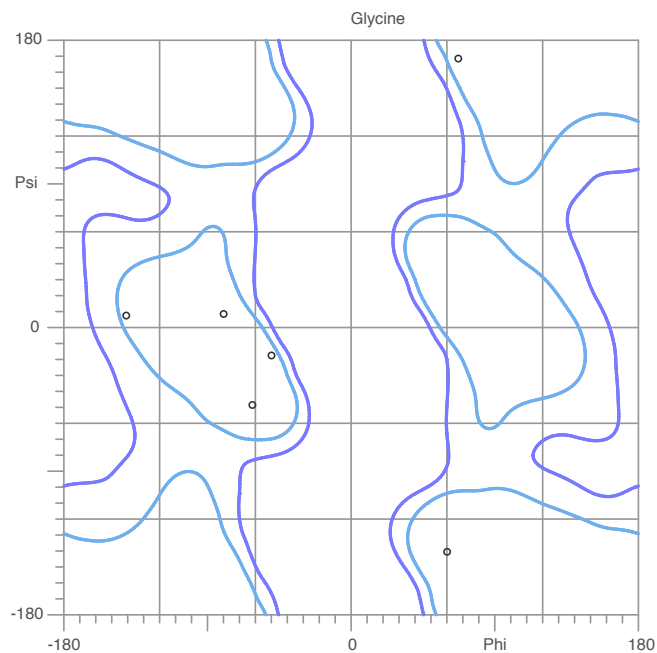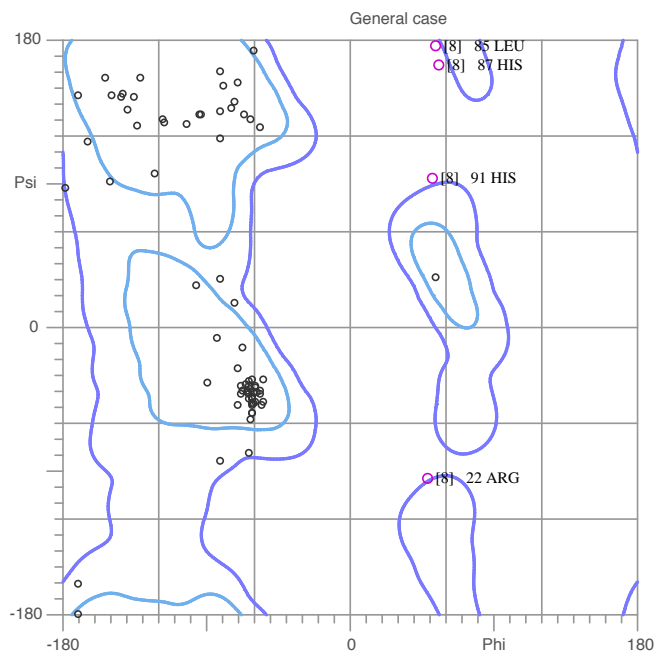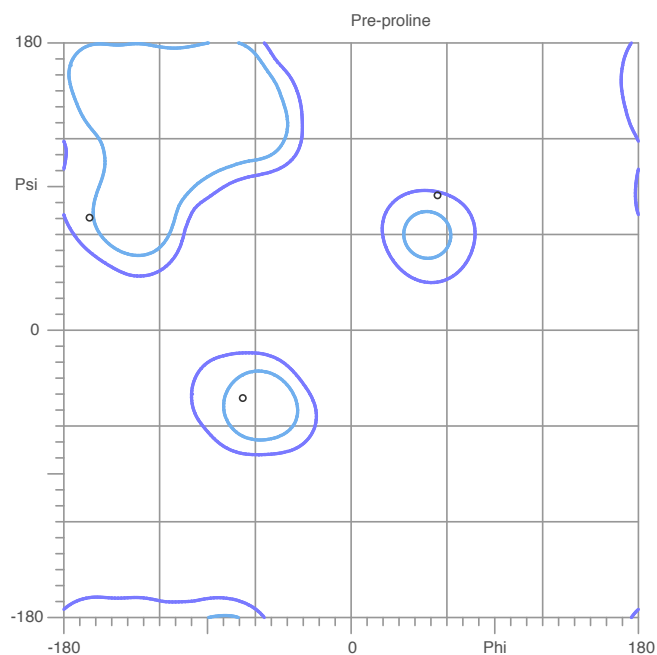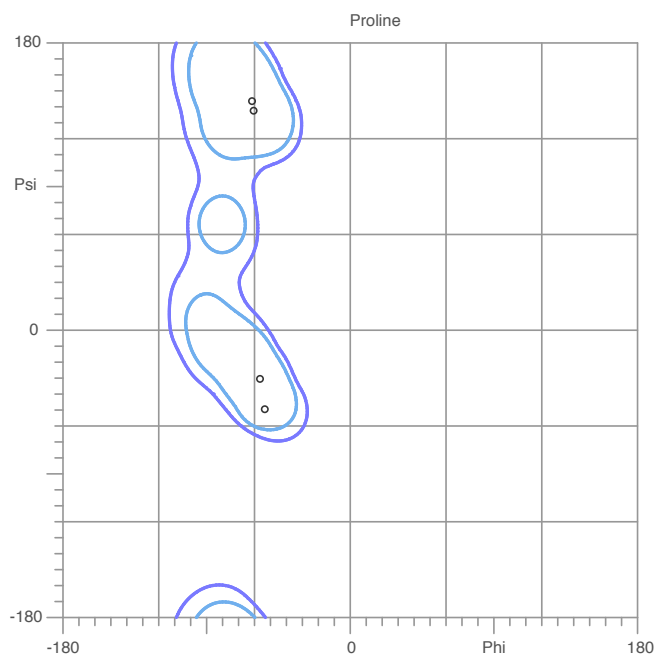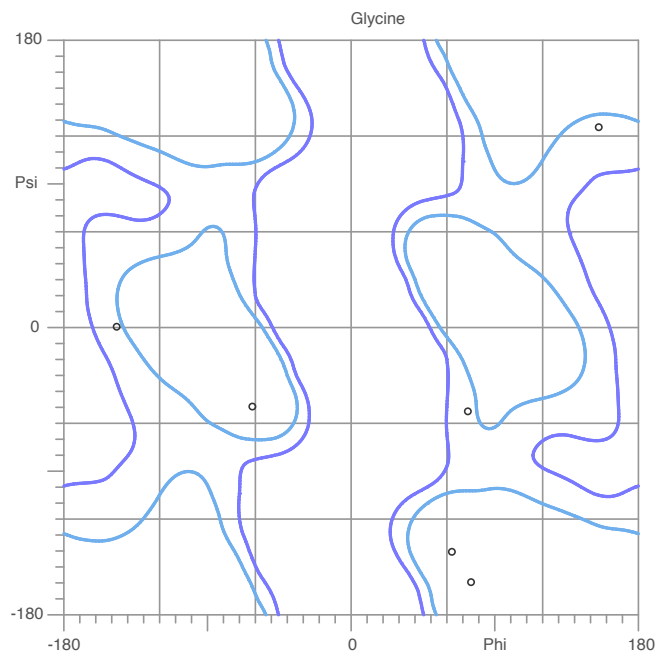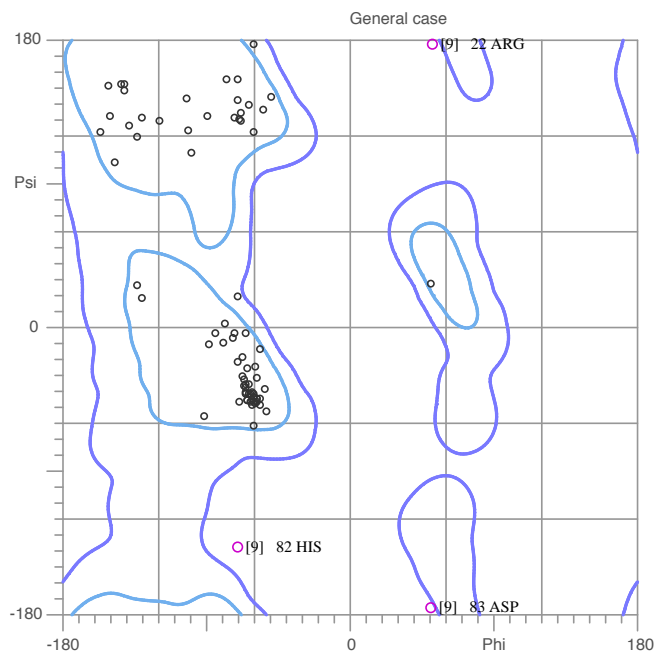
2KZV_NMR.pdb, model 8

85.6% (77/90) of all residues were in favored (98%) regions.
95.6% (86/90) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
    [8] 22 ARG (48.7, -94.9)
    [8] 85 LEU (53.7, 177.9)
    [8] 87 HIS (55.7, 165.9)
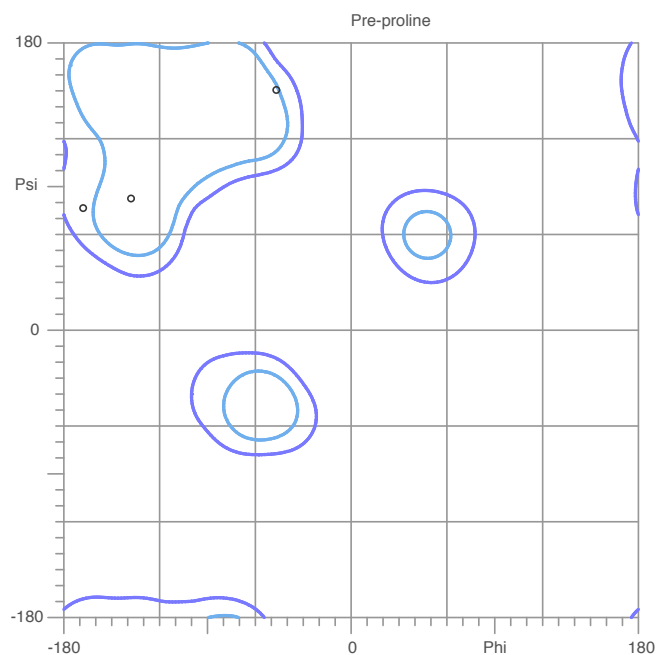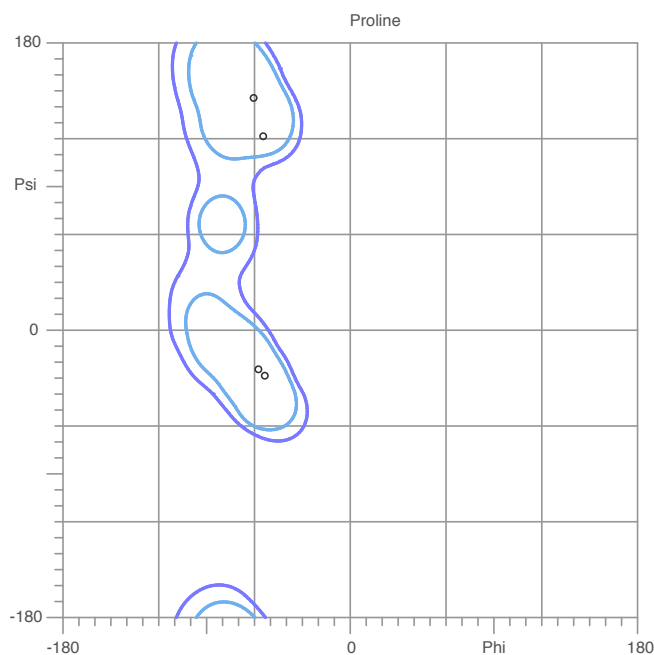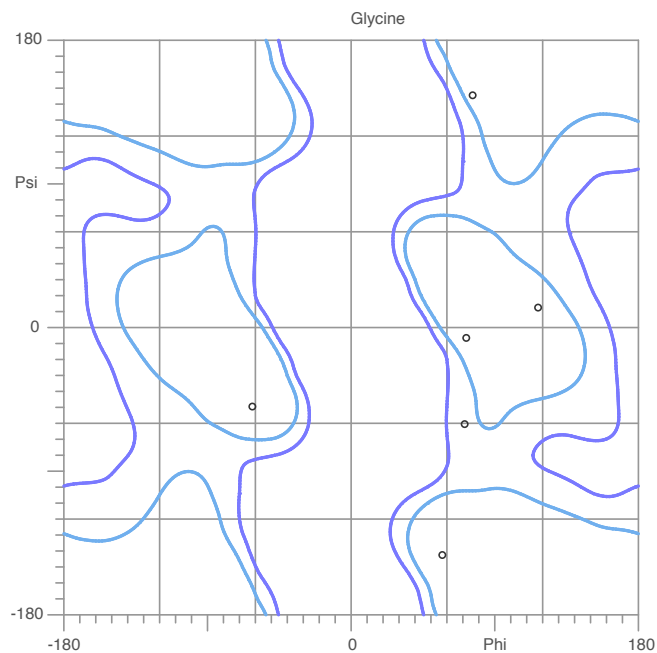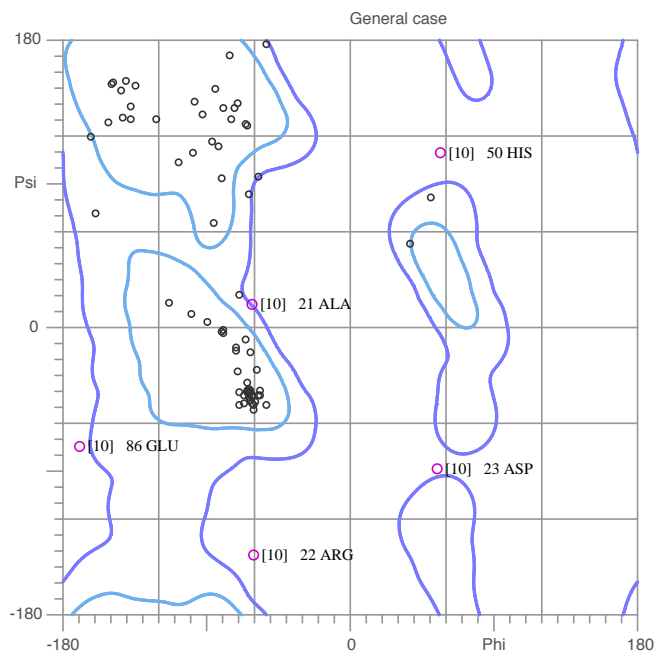   [8] 91 HIS (52.0, 94.8)

MolProbity Ramachandran analysis

88.9% (80/90) of all residues were in favored (98%) regions.
96.7% (87/90) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
- [9]   22 ARG (51.8, 178.8)
- [9]   82 HIS (-71.5, -137.6)
- [9]   83 ASP (50.8, -175.5)

MolProbity Ramachandran analysis
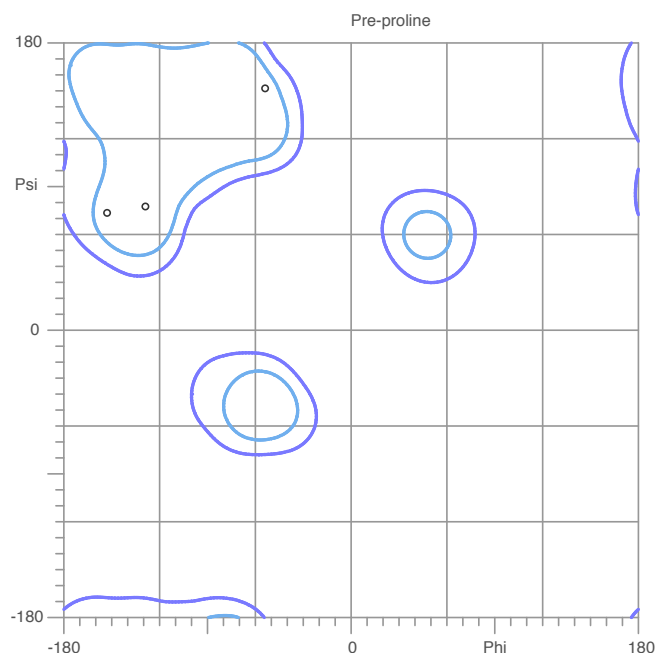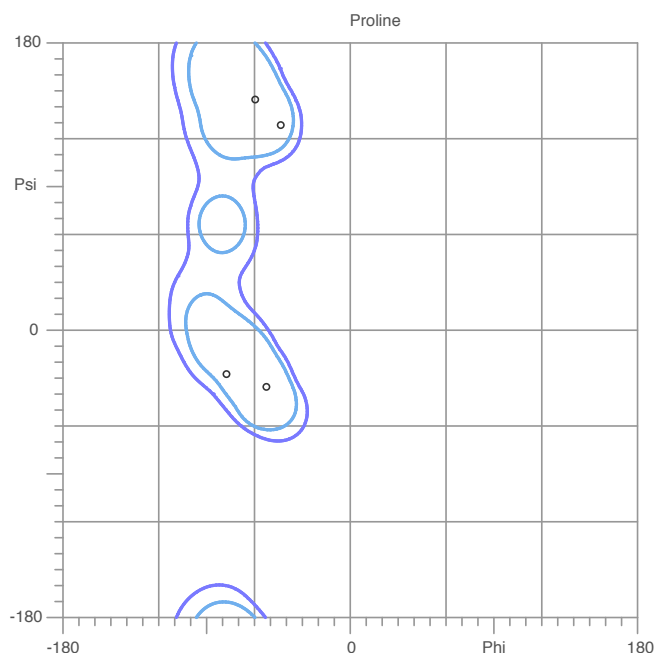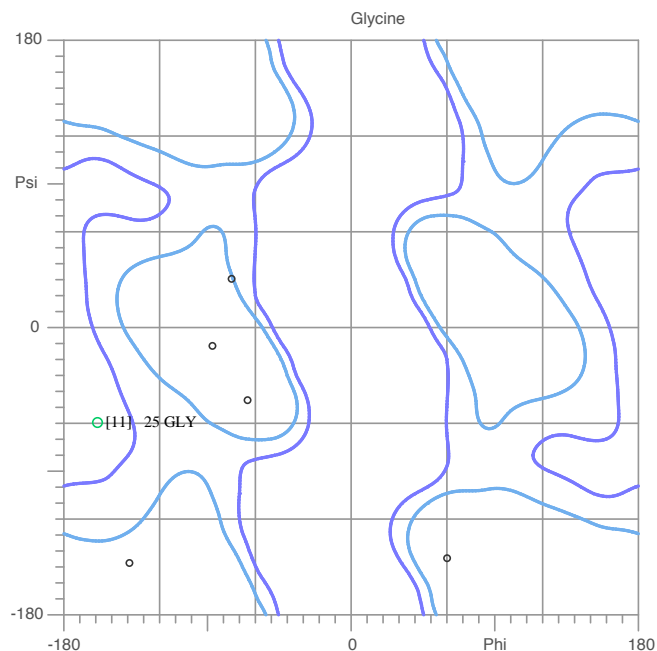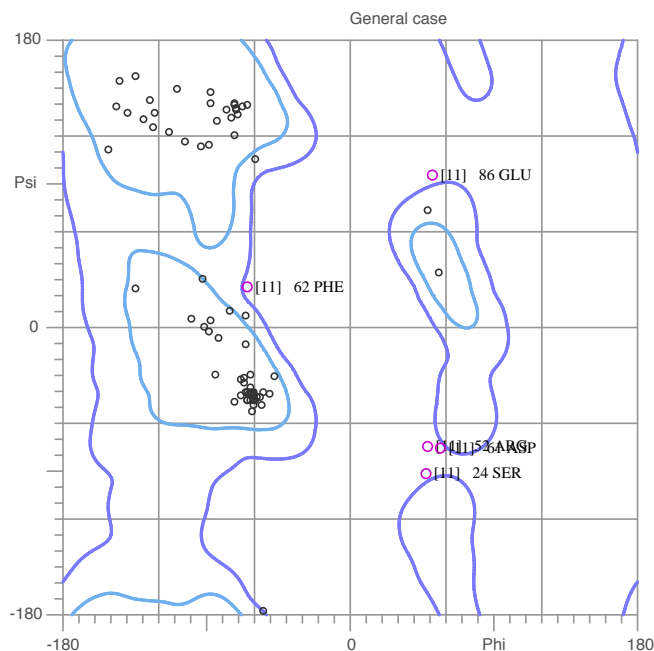
2KZV_NMR.pdb, model 10

83.3% (75/90) of all residues were in favored (98%) regions.
94.4% (85/90) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[10]   21 ALA (-63.0, 15.5)
[10]   22 ARG (-61.1, -142.3)
[10]   23 ASP (54.1, -88.5)
[10]   50 HIS (56.2, 110.7)
[10]   86 GLU (-170.7, -74.8)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 11

General case

Glycine

Proline

Pre-proline

87.8% (79/90) of all residues were in favored (98%) regions.
93.3% (84/90) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
  [11] 24 SER (47.4, -91.8)

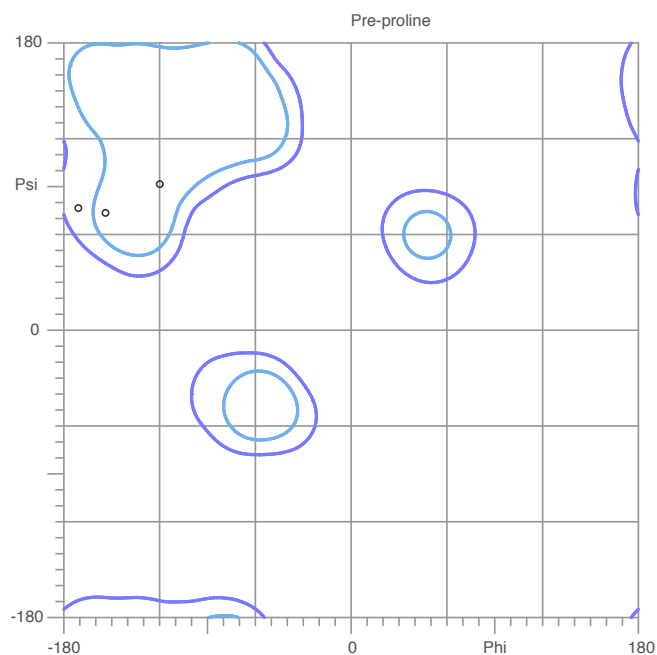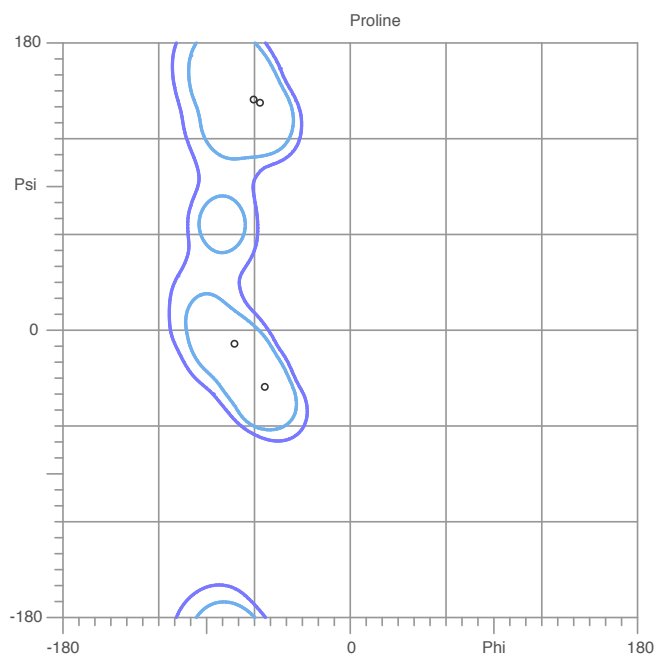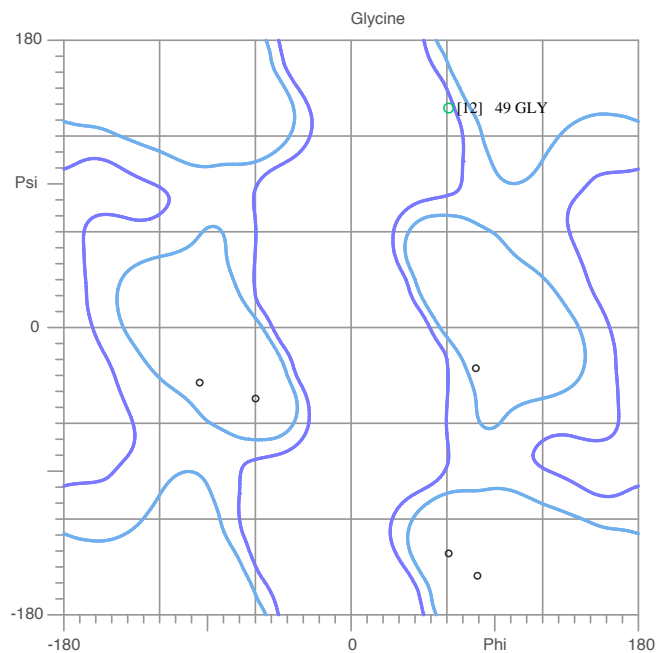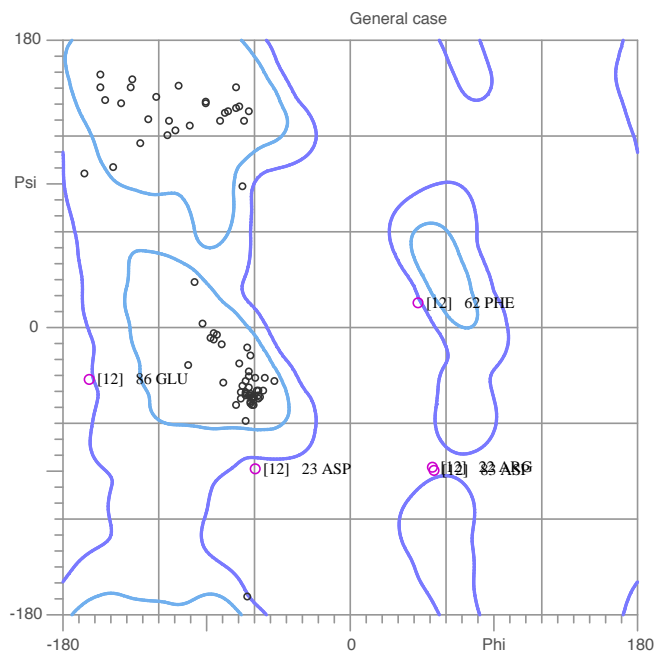[11] 25 GLY (-159.4, -59.0)
[11] 52 ARG (49.0, -74.8)
[11] 61 ASP (56.6, -75.8)
[11] 62 PHE (-65.5, 26.9)
[11] 86 GLU (51.5, 96.9)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 12

General case

Glycine

Proline

Pre-proline

88.9% (80/90) of all residues were in favored (98%) regions.
93.3% (84/90) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
  [12]   22 ARG (51.9, -87.5)

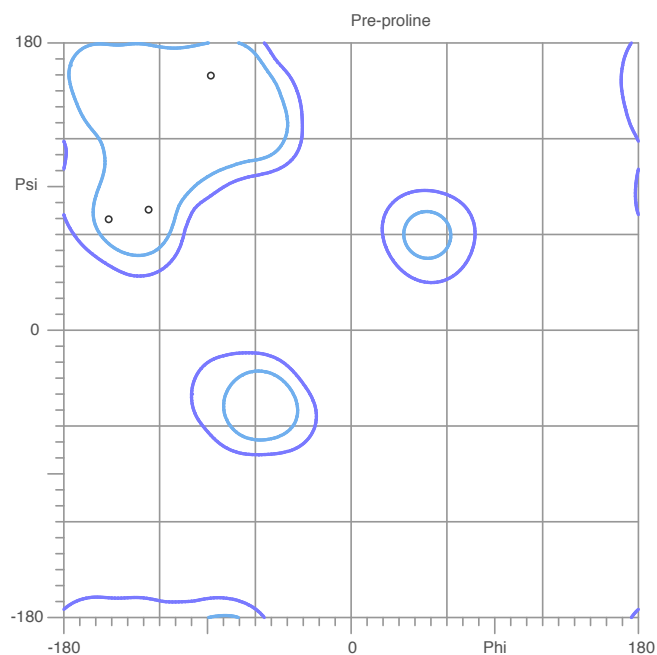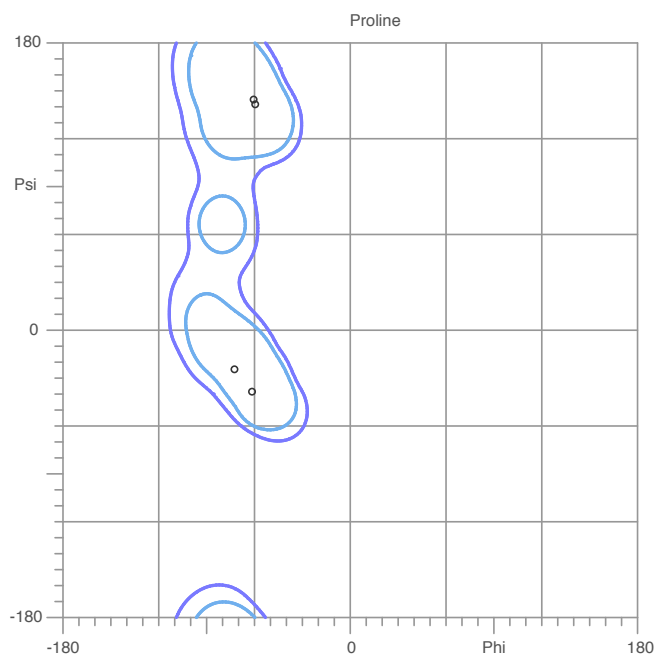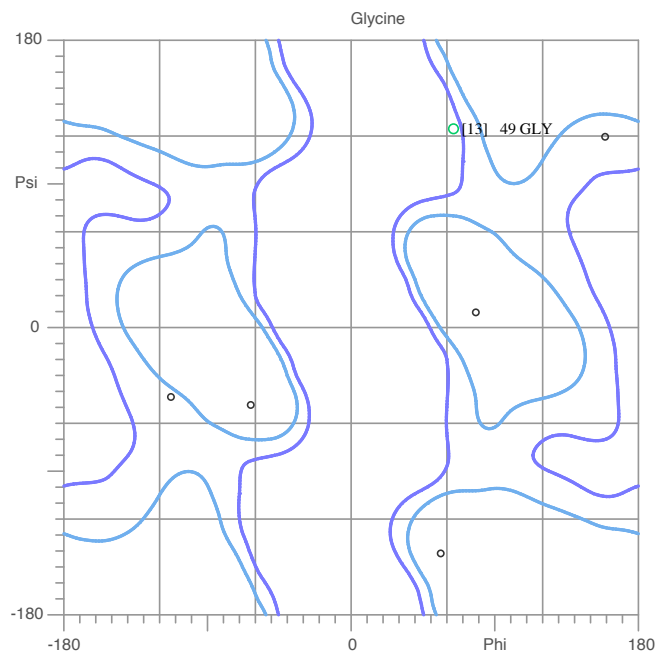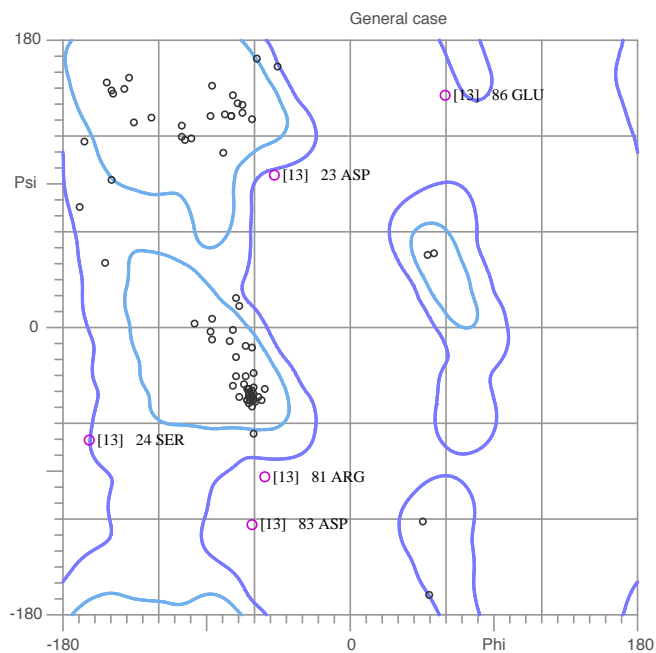[12]   23 ASP (-60.7, -88.4)
[12]   49 GLY (61.4, 138.7)
[12]   62 PHE (42.9, 16.5)
[12]   83 ASP (52.2, -89.2)
[12]   86 GLU (-164.6, -32.1)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 13

General case

Glycine

Proline

Pre-proline

78.9% (71/90) of all residues were in favored (98%) regions.
93.3% (84/90) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
   [13] 23 ASP (-48.7, 96.8)

[13] 24 SER (-164.8, -70.7)
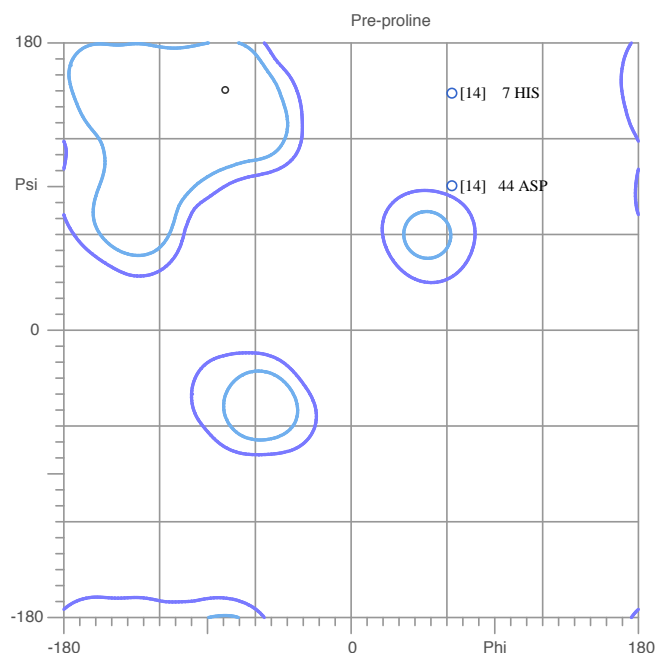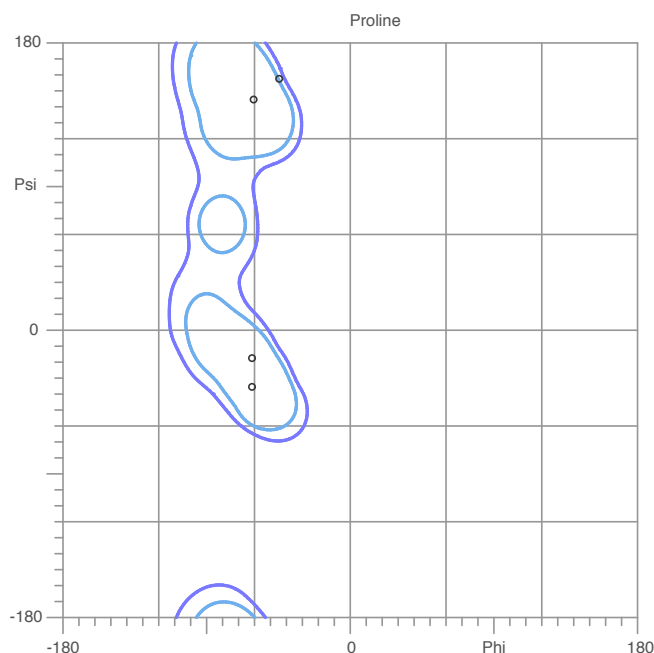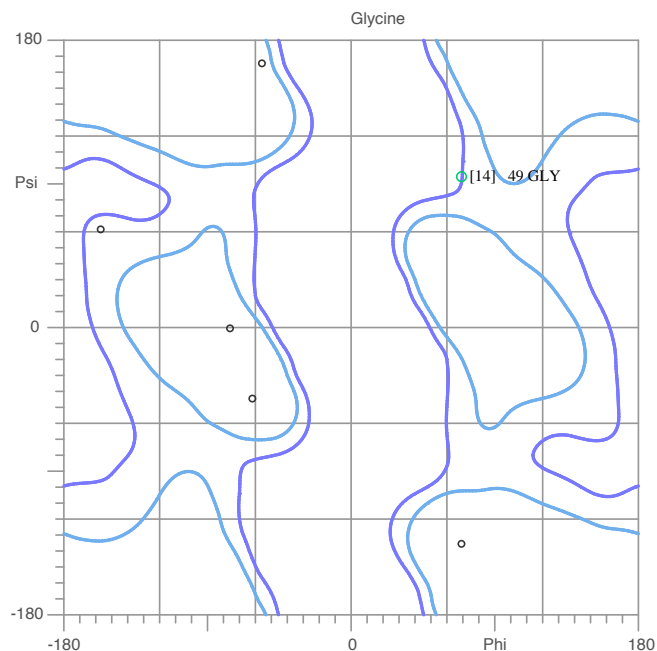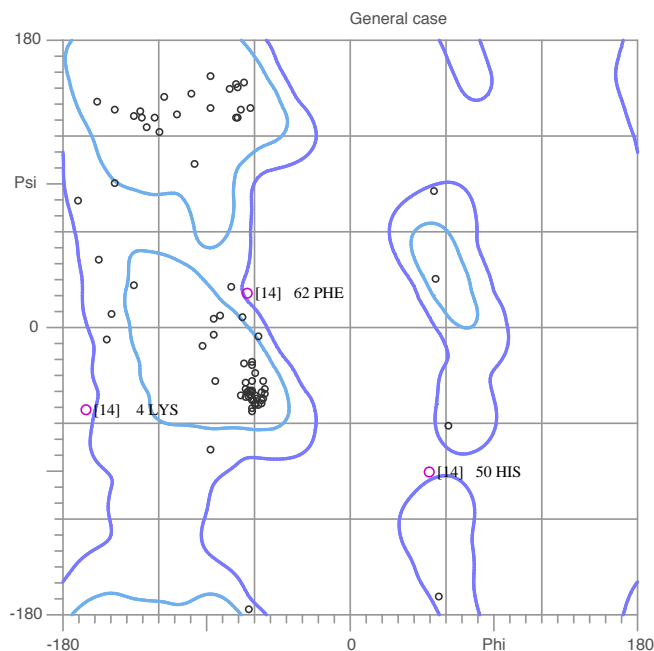[13] 49 GLY (64.4, 125.0)
[13] 81 ARG (-54.8, -93.2)
[13] 83 ASP (-62.6, -123.8)
[13] 86 GLU (59.5, 146.7)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 14

General case

Glycine

Proline

Pre-proline

77.8% (70/90) of all residues were in favored (98%) regions.
93.3% (84/90) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
  [14]   4 LYS (-166.9, -51.6)

[14]   7 HIS (63.7, 149.6)
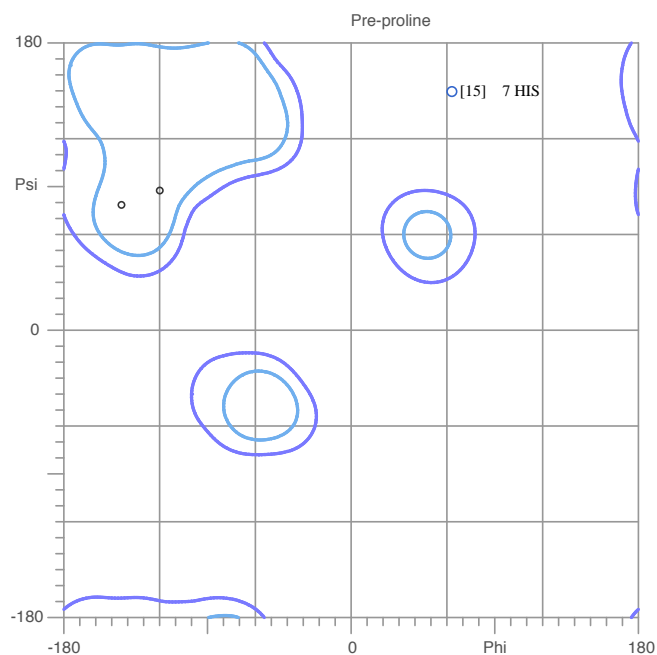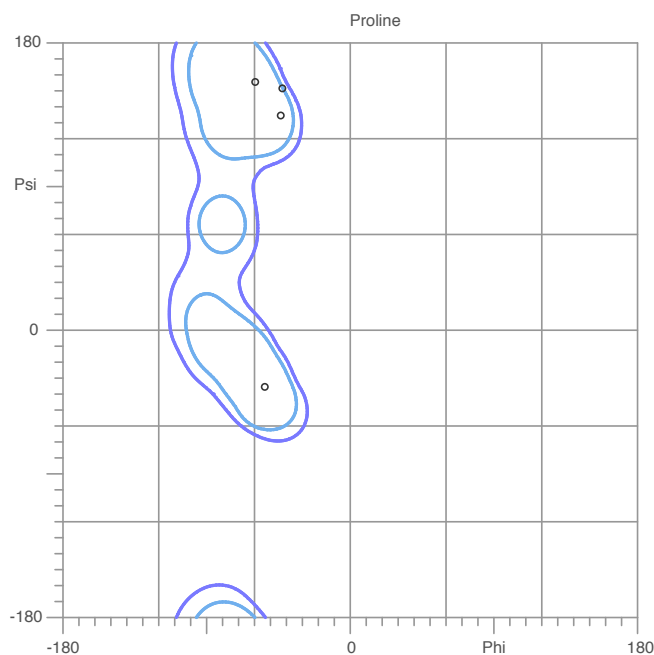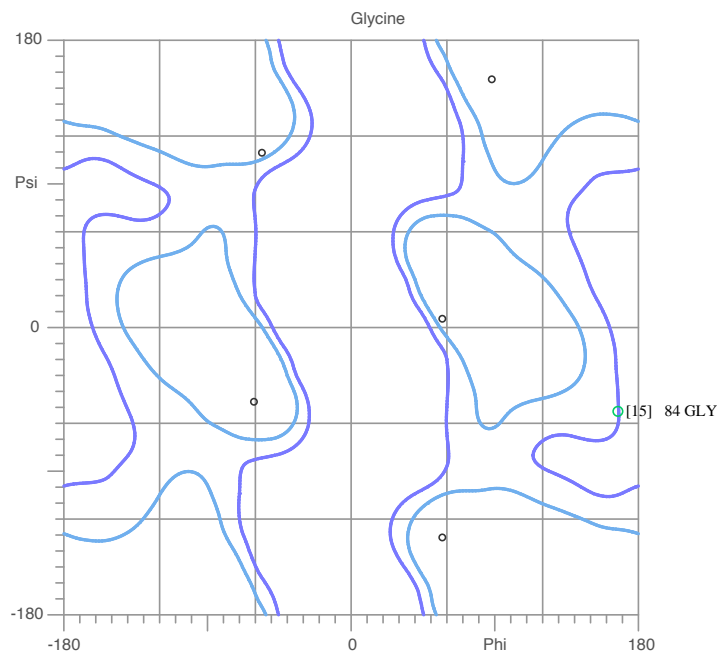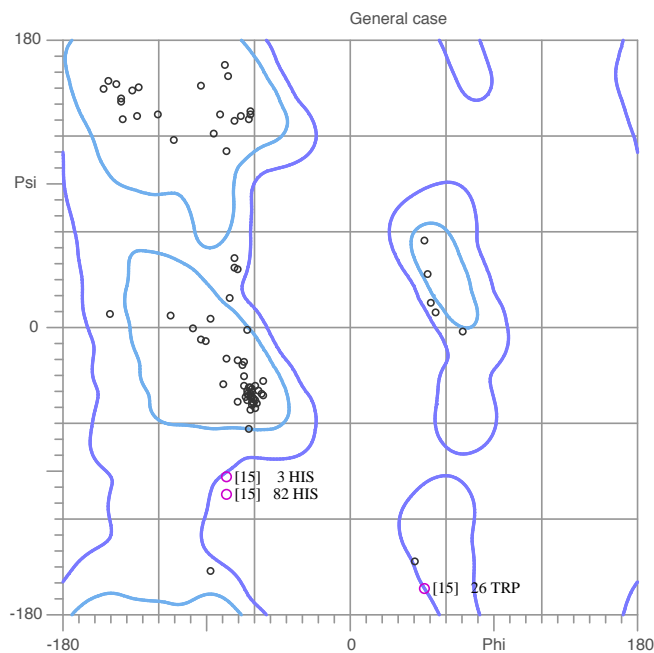[14] 44 ASP (63.2, 91.1)
[14] 49 GLY (69.4, 95.8)
[14] 50 HIS (49.3, -90.8)
[14] 62 PHE (-65.8, 22.0)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 15

General case

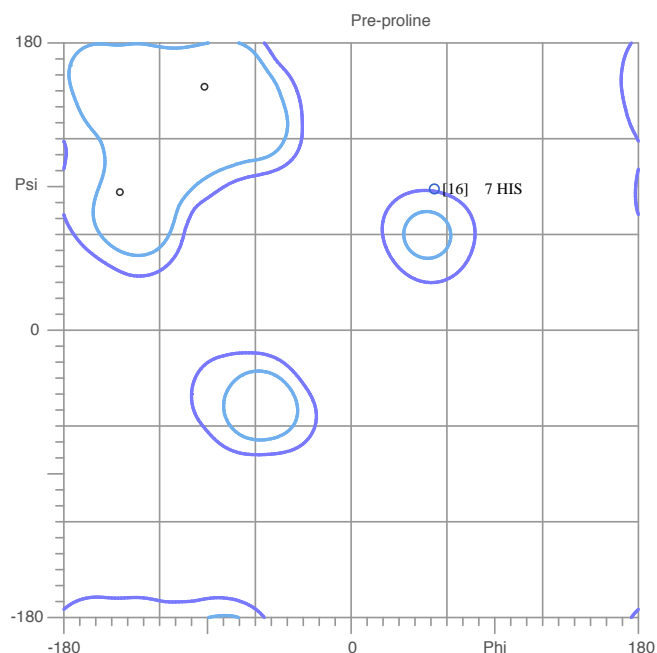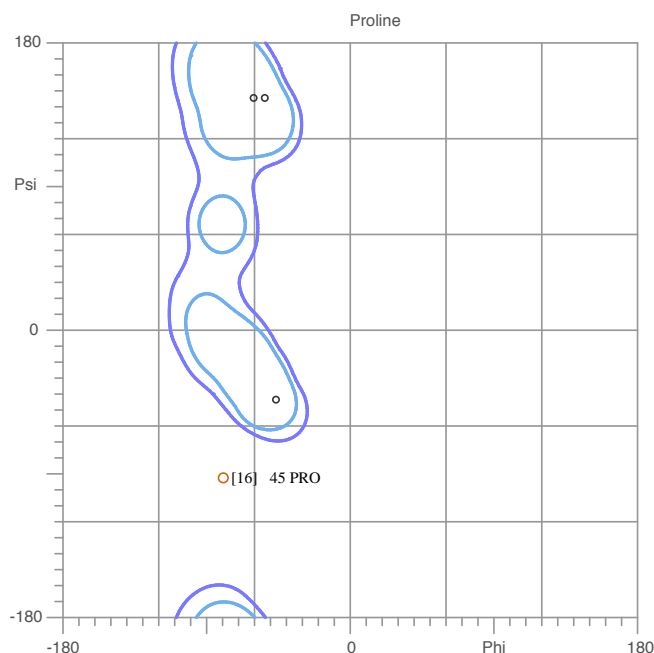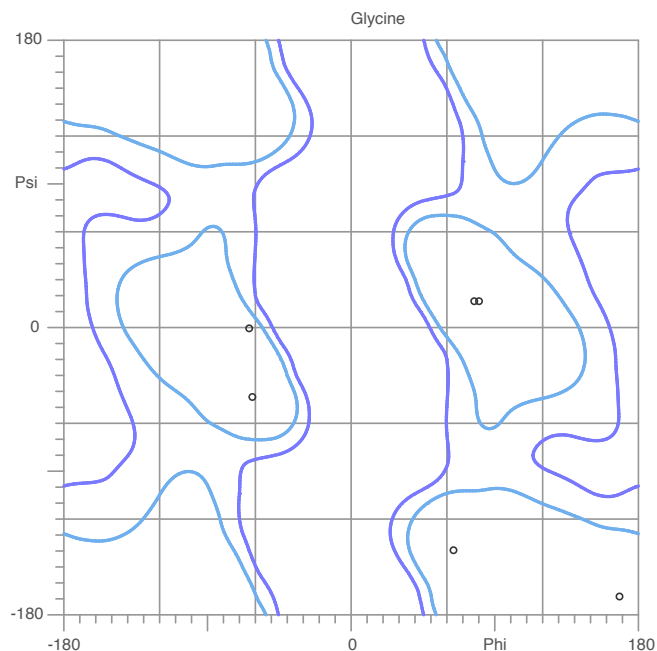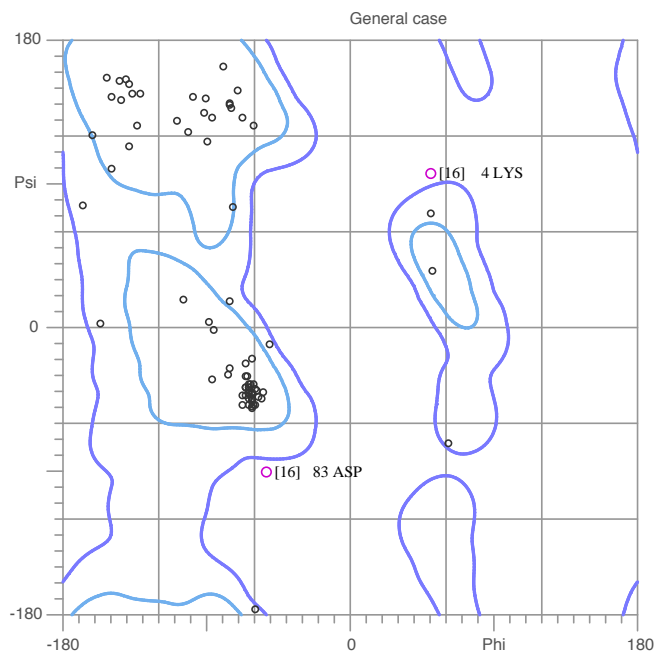Glycine

Proline

Pre-proline

82.2% (74/90) of all residues were in favored (98%) regions.
94.4% (85/90) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[15]   3 HIS (-78.2, -93.2)
[15]   7 HIS (63.7, 150.5)
[15]   26 TRP (46.3, -163.6)
[15]   82 HIS (-78.3, -104.8)
[15]   84 GLY (167.5, -52.9)

MolProbity Ramachandran analysis
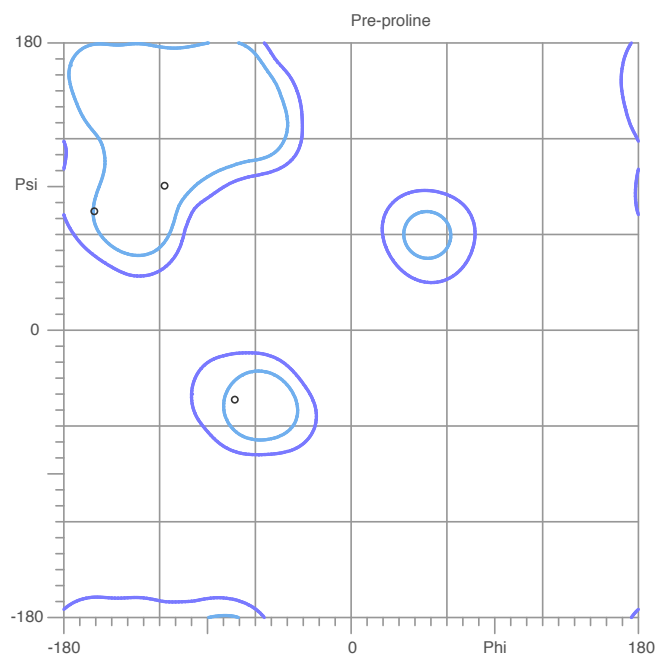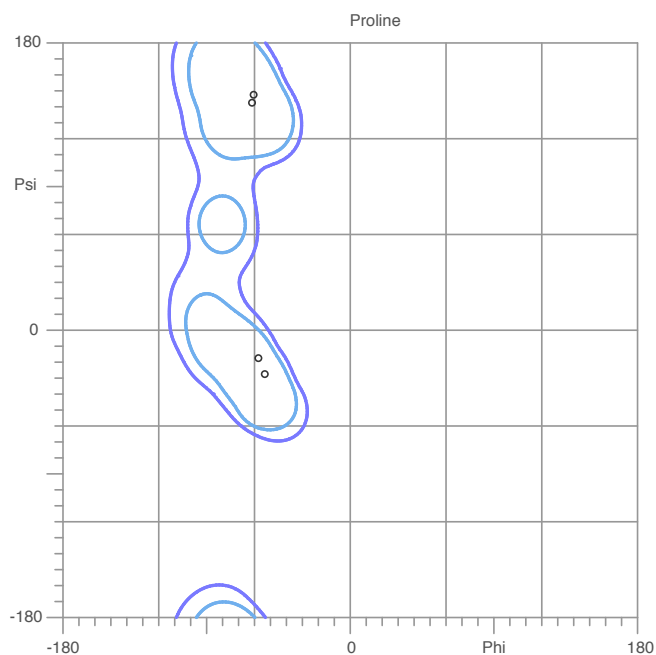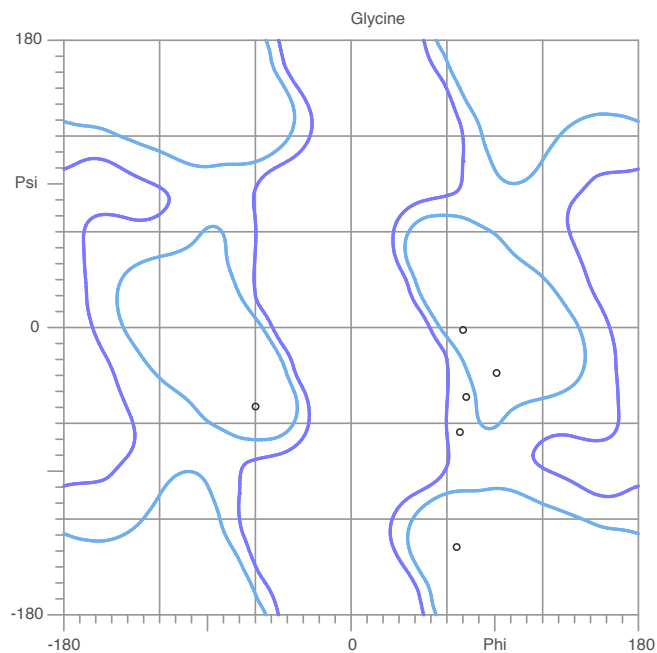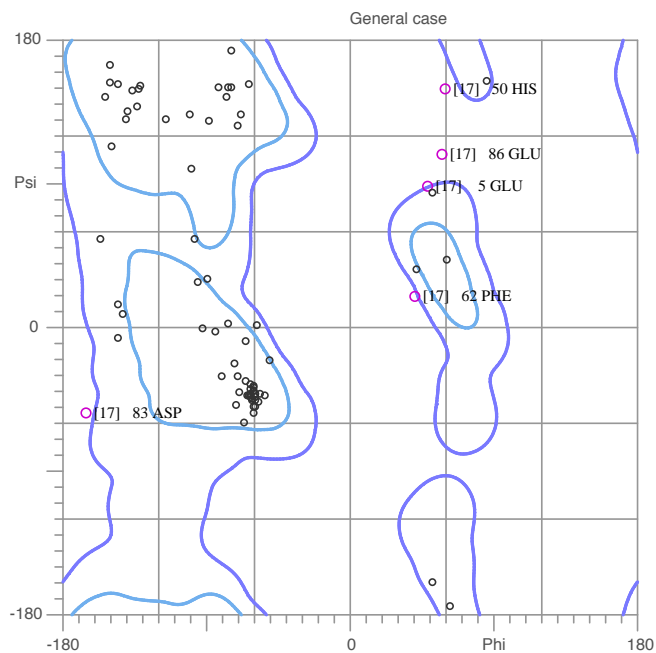
2KZV_NMR.pdb, model 16

87.8% (79/90) of all residues were in favored (98%) regions.
95.6% (86/90) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
    [16]   4 LYS (50.9, 97.4)
    [16]   7 HIS (52.2, 89.1)
    [16]   45 PRO (-80.7, -92.2)
    [16]   83 ASP (-53.6, -90.3)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 17

General case

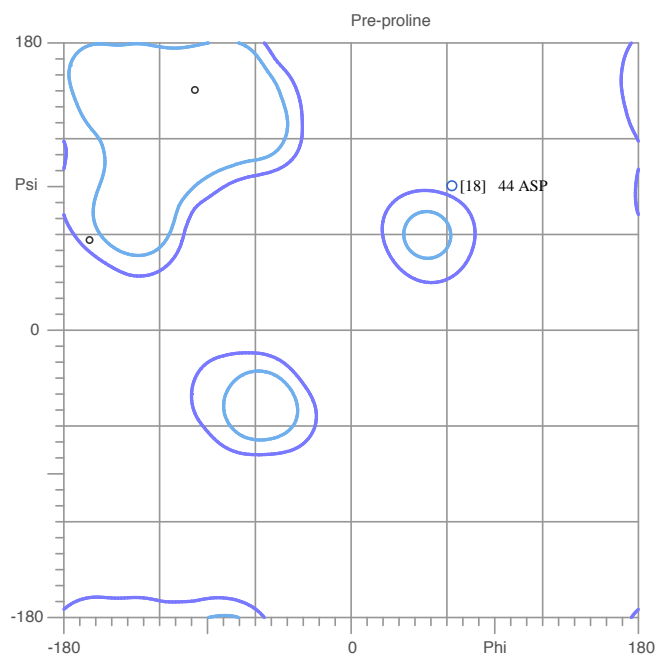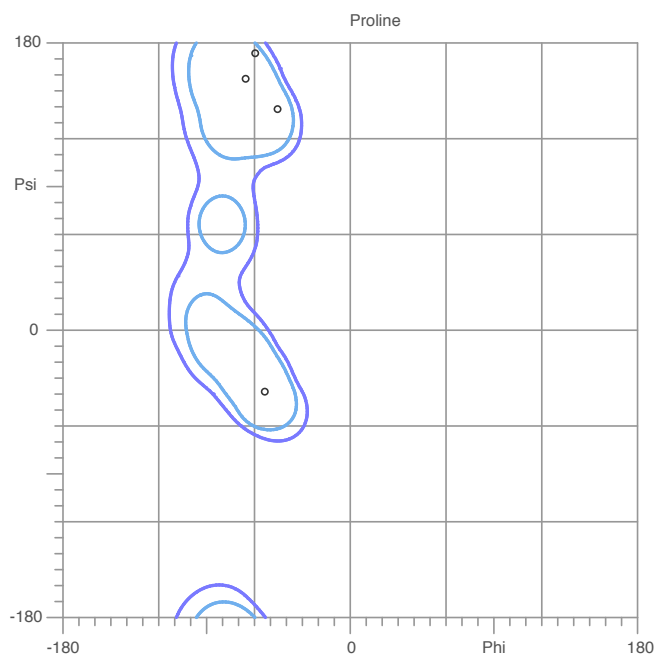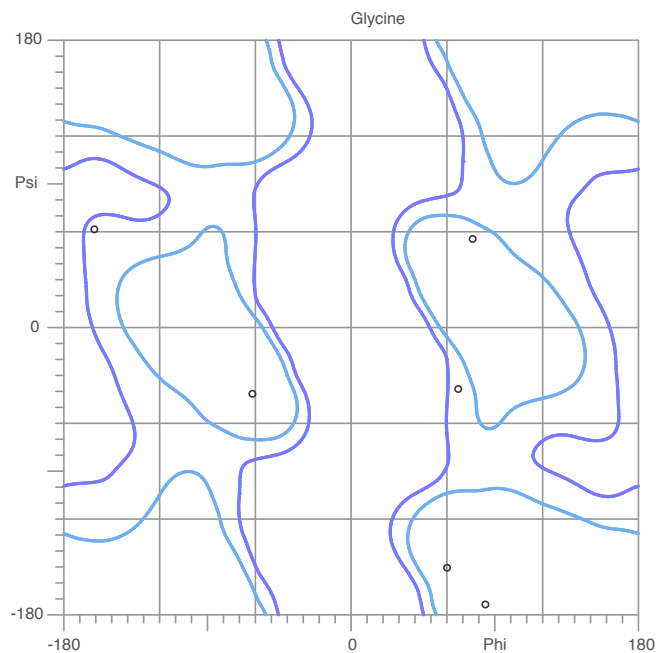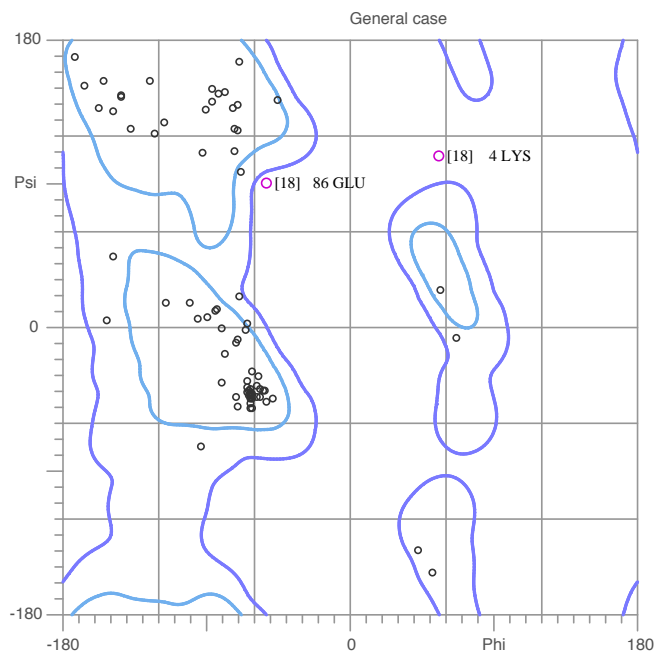Glycine

Proline

Pre-proline

78.9% (71/90) of all residues were in favored (98%) regions.
94.4% (85/90) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[17]   5 GLU (48.6, 89.3)
[17]   50 HIS (59.1, 151.0)
[17]   62 PHE (40.7, 20.0)
[17]   83 ASP (-167.0, -54.0)
[17]   86 GLU (57.4, 109.5)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 18

83.3% (75/90) of all residues were in favored (98%) regions.
96.7% (87/90) of all residues were in allowed (>99.8%) regions.

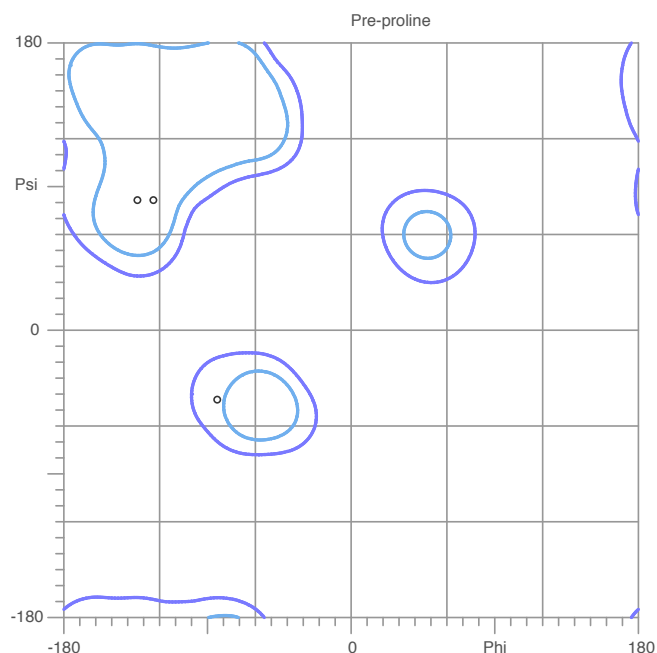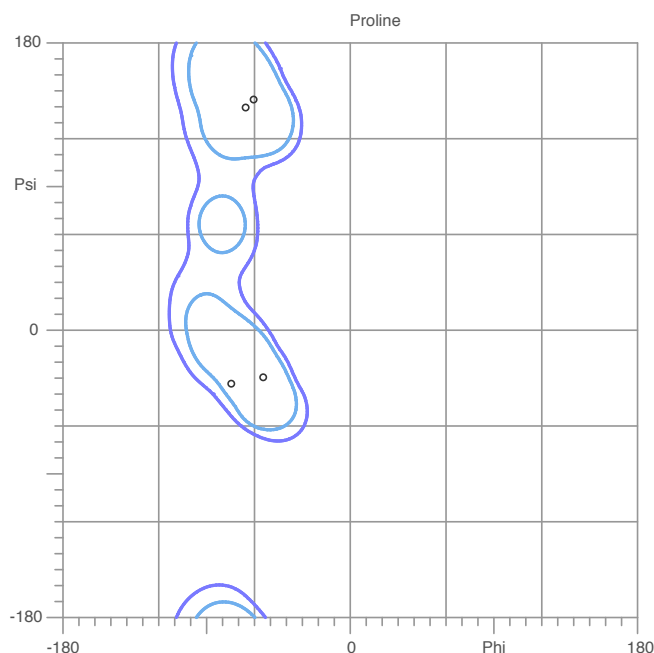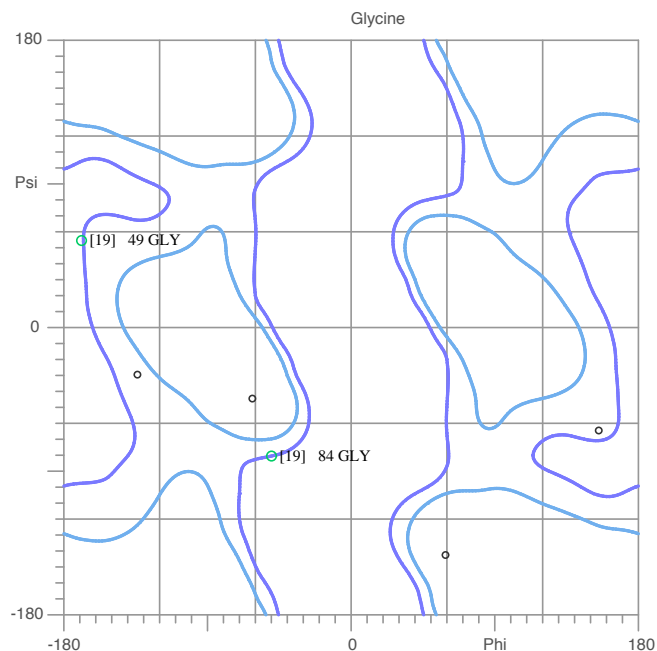There were 3 outliers (phi, psi):
    [18]   4 LYS (55.4, 108.8)
    [18]   44 ASP (63.9, 91.5)
    [18]   86 GLU (-53.4, 91.3)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 19

81.1% (73/90) of all residues were in favored (98%) regions.
92.2% (83/90) of all residues were in allowed (>99.8%) regions.
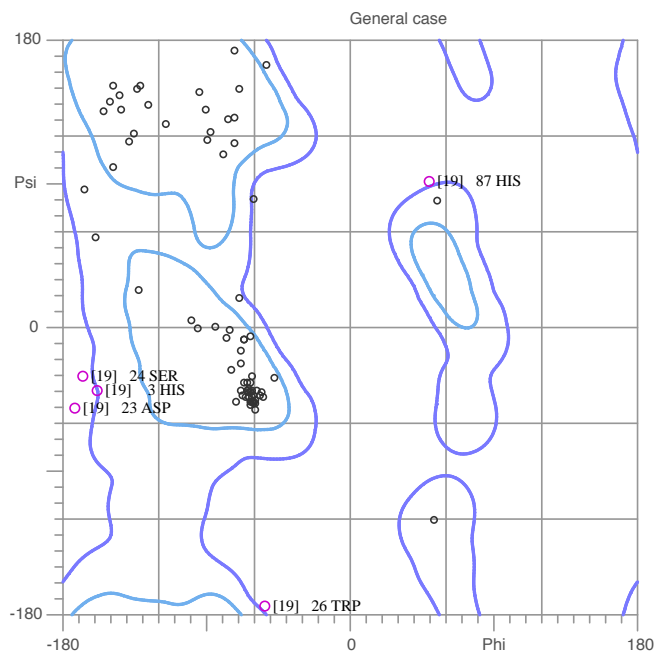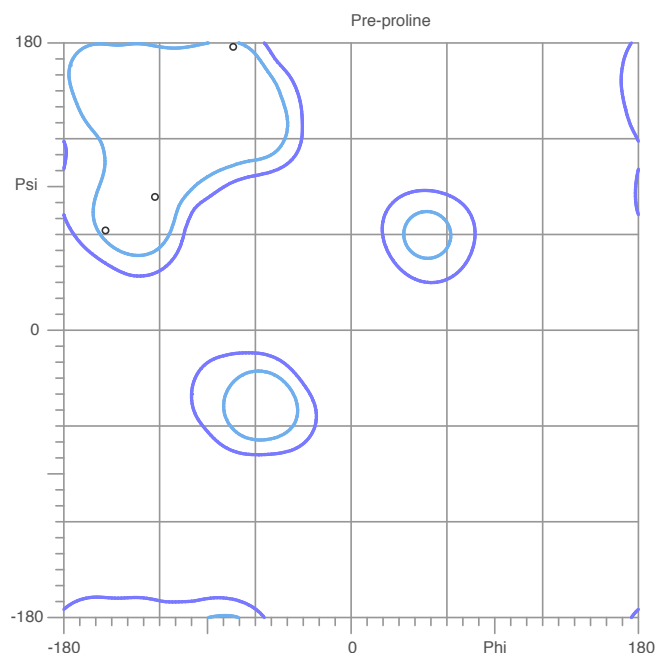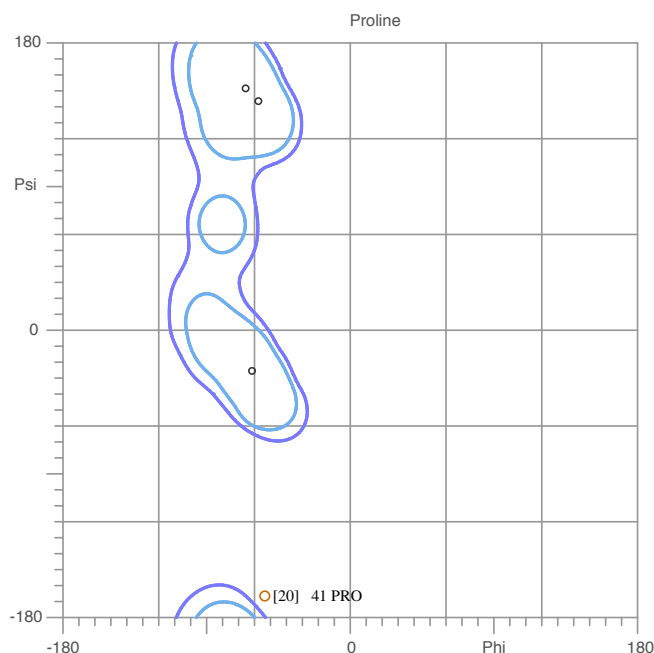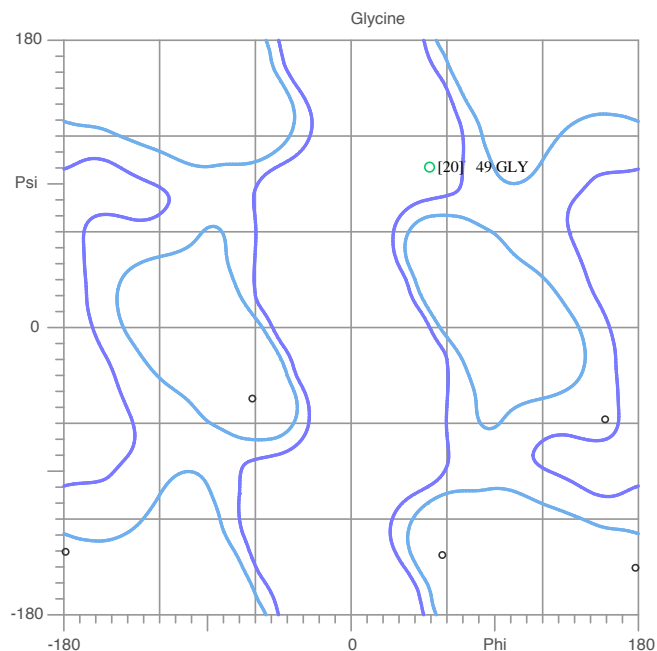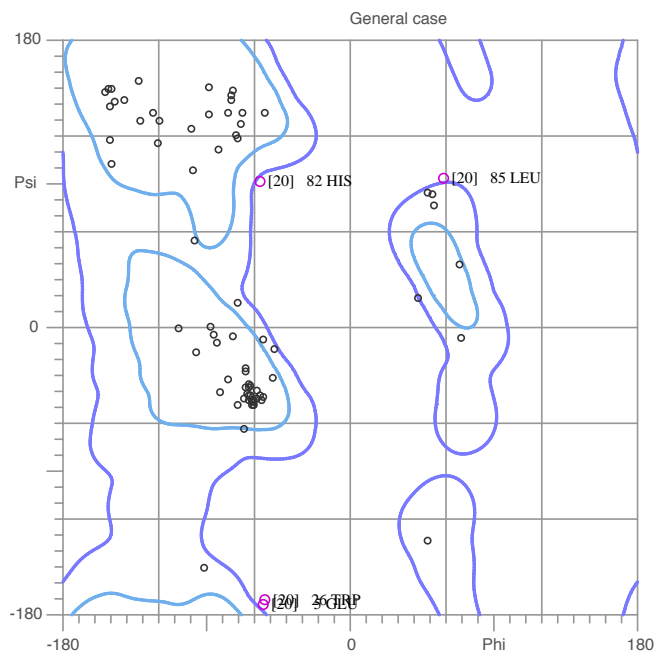
There were 7 outliers (phi, psi):
   [19]   3 HIS (-159.9, -39.9)

[19]   23 ASP (-173.5, -50.8)
[19]   24 SER (-168.9, -30.7)
[19]   26 TRP (-54.3, -174.9)
[19]   49 GLY (-169.9, 55.9)
[19]   84 GLY (-50.5, -80.4)
[19]   87 HIS (49.7, 92.4)

MolProbity Ramachandran analysis

2KZV_NMR.pdb, model 20

78.9% (71/90) of all residues were in favored (98%) regions.
93.3% (84/90) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
   [20]   5 GLU (-55.8, -173.5)

[20]   26 TRP (-54.6, -170.3)
[20]   41 PRO (-54.8, -166.8)
[20]   49 GLY (49.8, 101.3)
[20]   82 HIS (-57.1, 92.0)
[20]   85 LEU (58.2, 94.9)