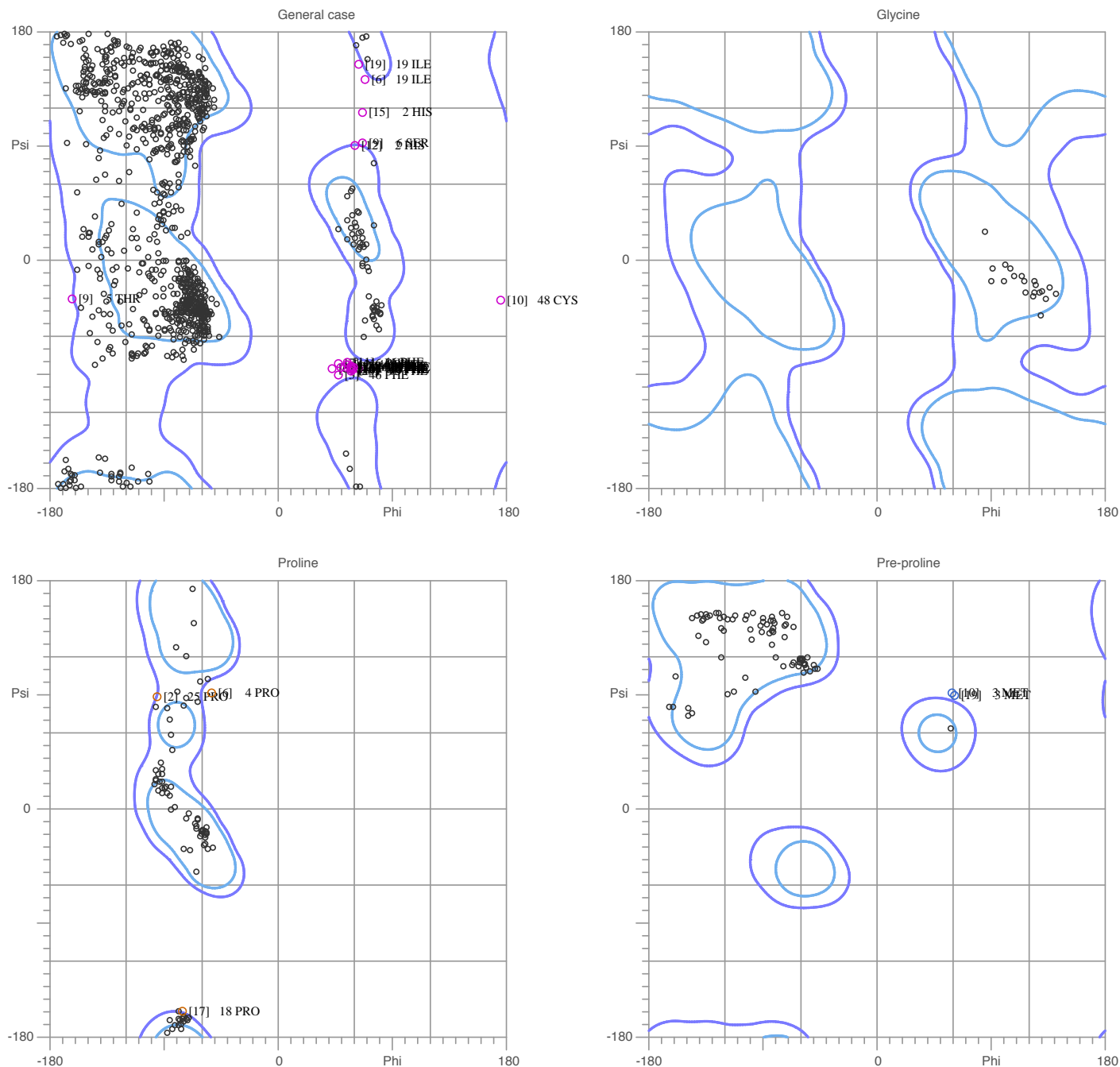# MolProbity Ramachandran analysis

2MA6_NMR.pdb, all models
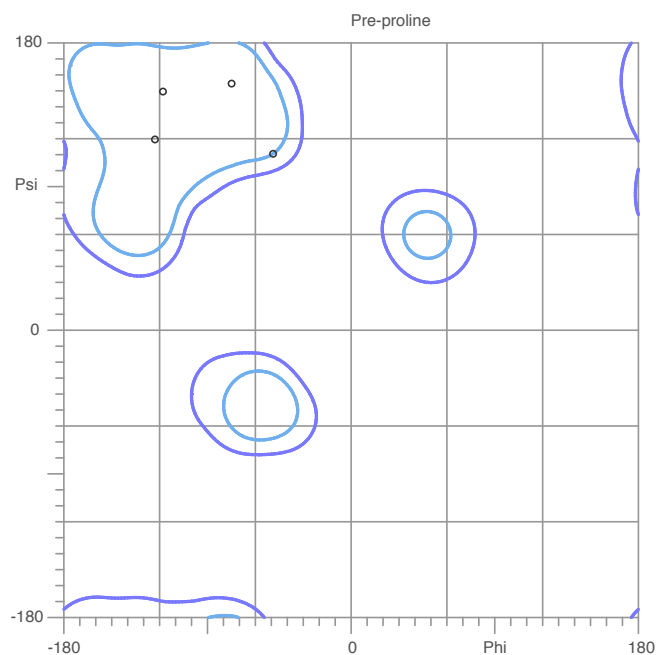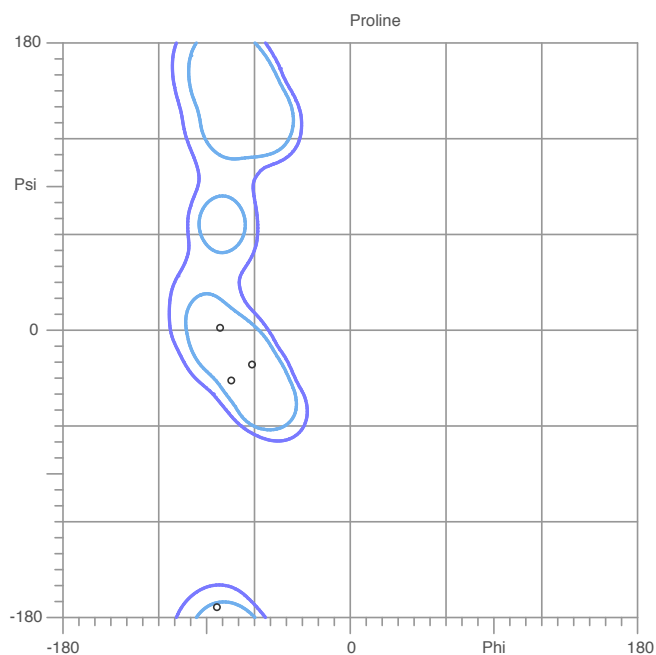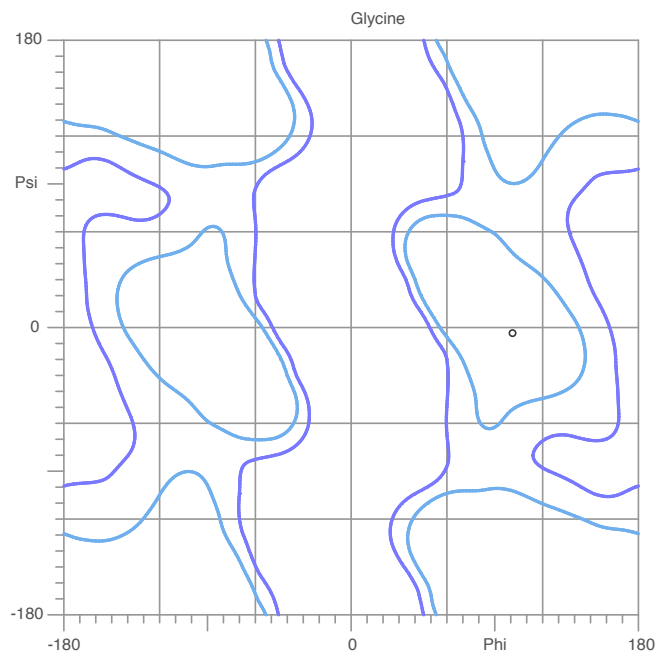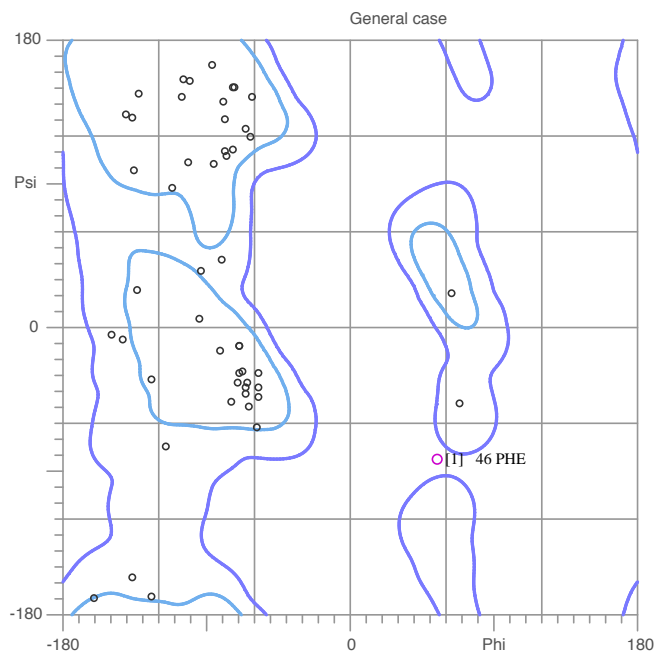

General case

Glycine

Proline

Pre-proline

81.9% (966/1180) of all residues were in favored (98%) regions.
97.5% (1151/1180) of all residues were in allowed (>99.8%) regions.

There were 29 outliers (phi, psi):

[1] 46 PHE (54.2, -82.4)	[9] 46 PHE (49.7, -84.6)	
[2] 25 PRO (-96.3, 89.9)	[10] 3 MET (59.3, 92.6)	
[2] 46 PHE (63.4, -85.7)	[10] 46 PHE (58.6, -86.3)	
[3] 46 PHE (47.7, -90.8)	[10] 48 CYS (175.8, -32.0)	
[4] 46 PHE (52.4, -84.0)	[11] 46 PHE (55.0, -80.3)	
[5] 46 PHE (57.1, -85.0)	[12] 2 HIS (60.3, 91.4)	
[6] 4 PRO (-53.9, 92.8)	[12] 46 PHE (54.2, -82.9)	
[6] 19 ILE (68.2, 143.6)	[13] 46 PHE (57.4, -84.7)	
[6] 46 PHE (43.0, -85.9)	[14] 46 PHE (58.9, -86.0)	
[7] 46 PHE (47.4, -81.5)	[15] 2 HIS (66.7, 117.4)	
[9] 5 THR (-163.8, -30.7)	[15] 46 PHE (57.6, -85.3)	
[9] 6 SER (66.6, 93.2)	[17] 18 PRO (-76.9, -159.6)	
	[17] 46 PHE (57.7, -83.5)	
	[18] 46 PHE (59.4, -84.4)	
	[19] 3 MET (62.0, 90.5)	
	[19] 19 ILE (63.1, 155.5)	
	[20] 46 PHE (57.4, -87.3)	

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 1

General case

Glycine

Proline

Pre-proline

Psi

Phi

Psi

Phi

Psi

Phi

Psi

Phi

○[1]   46 PHE

84.7% (50/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
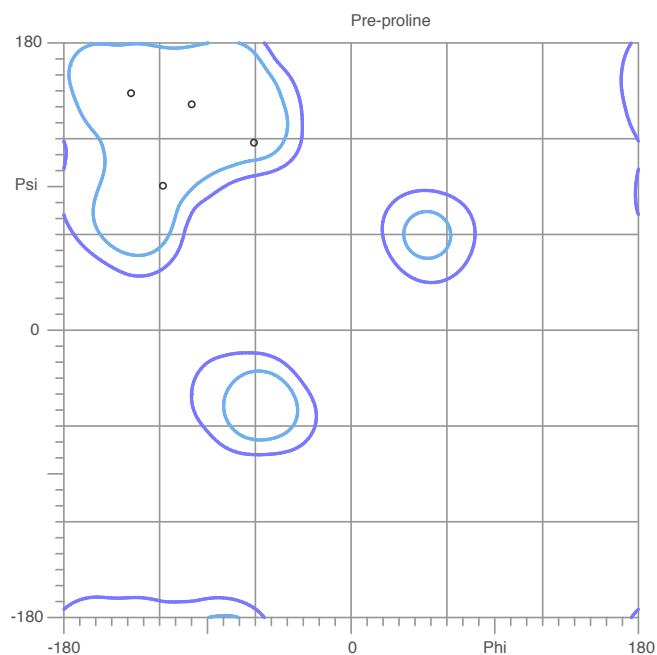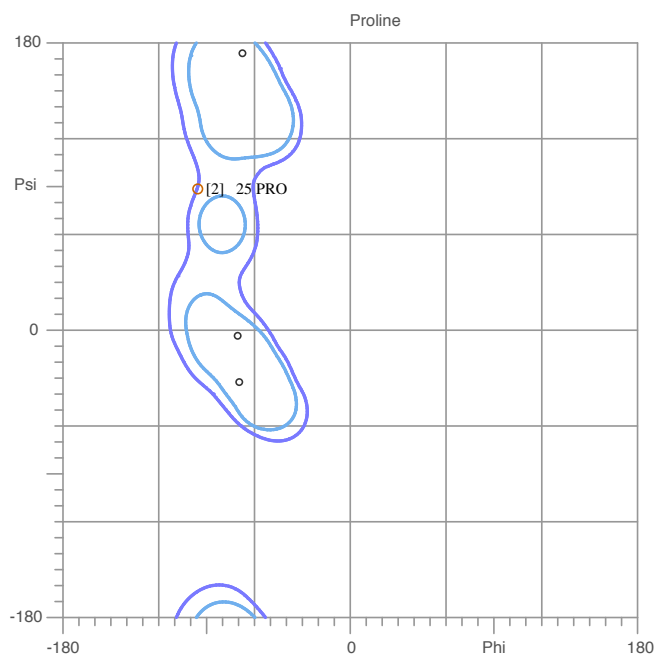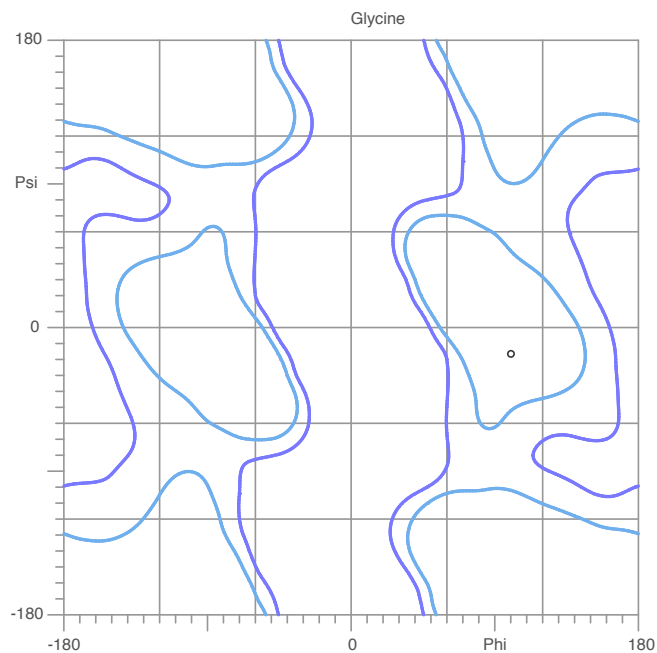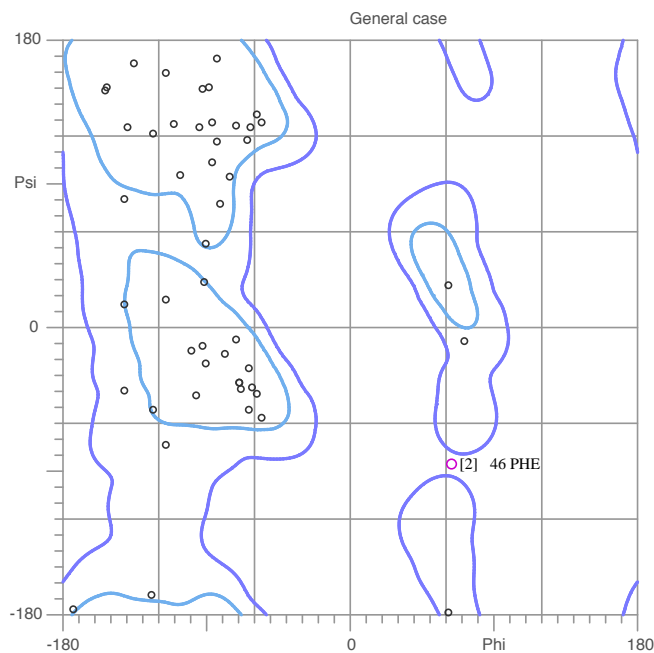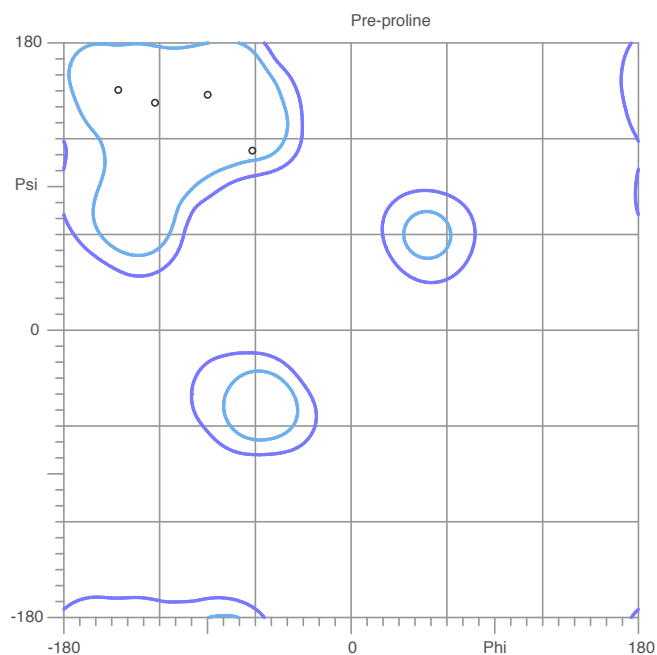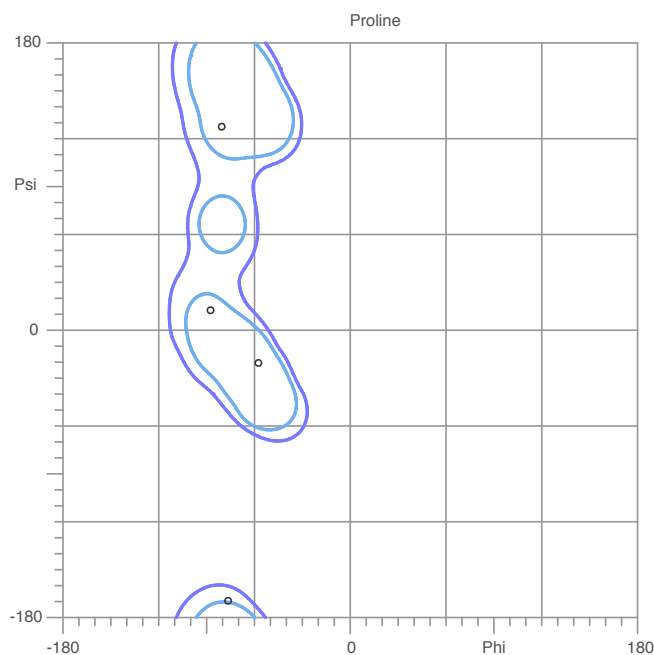   [1]   46 PHE (54.2, -82.4)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 2

83.1% (49/59) of all residues were in favored (98%) regions.
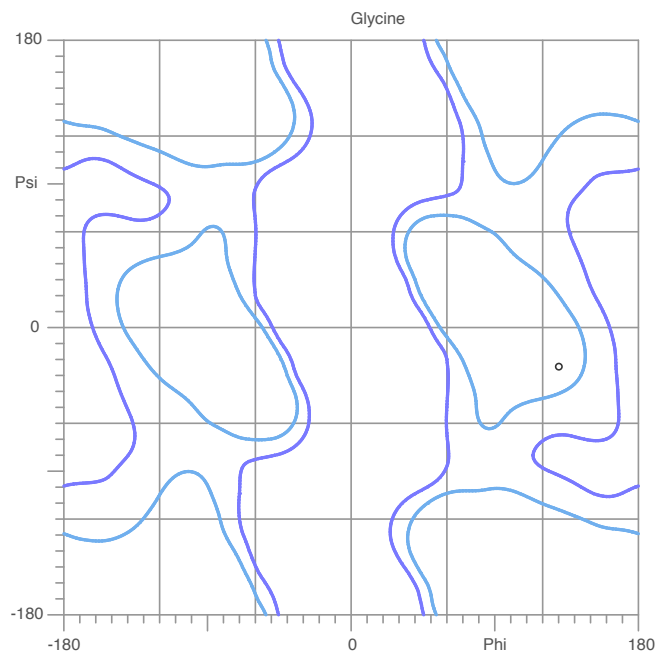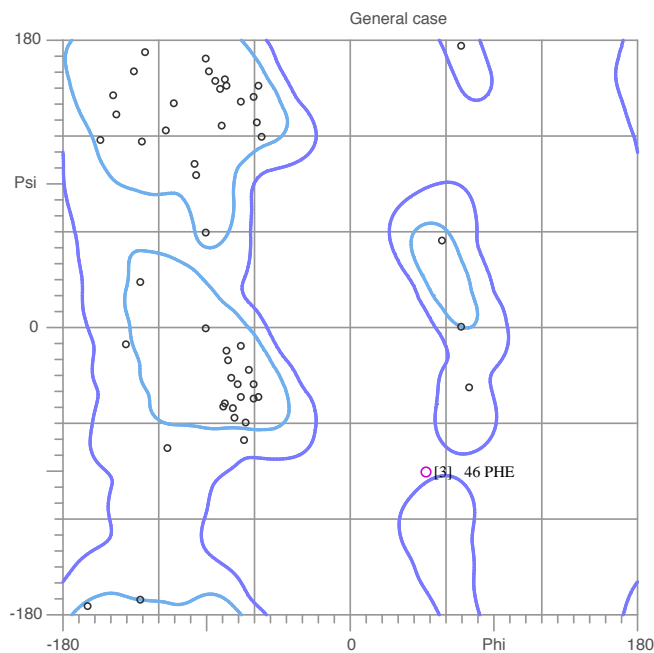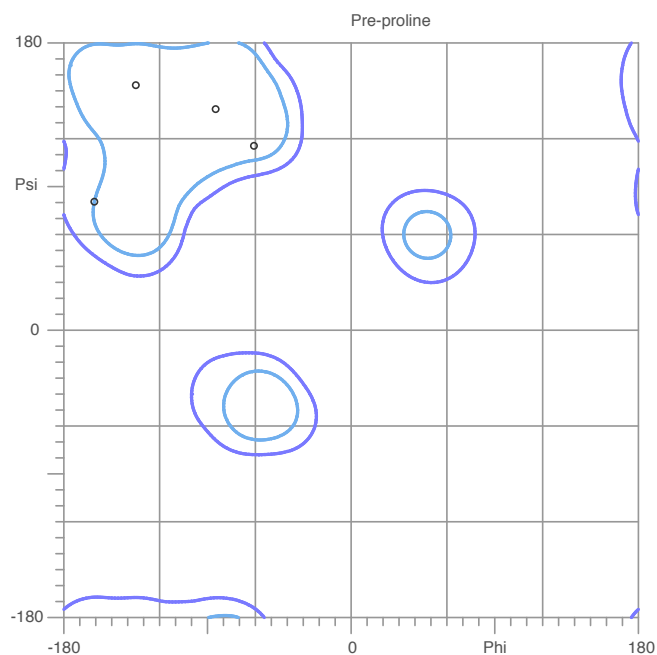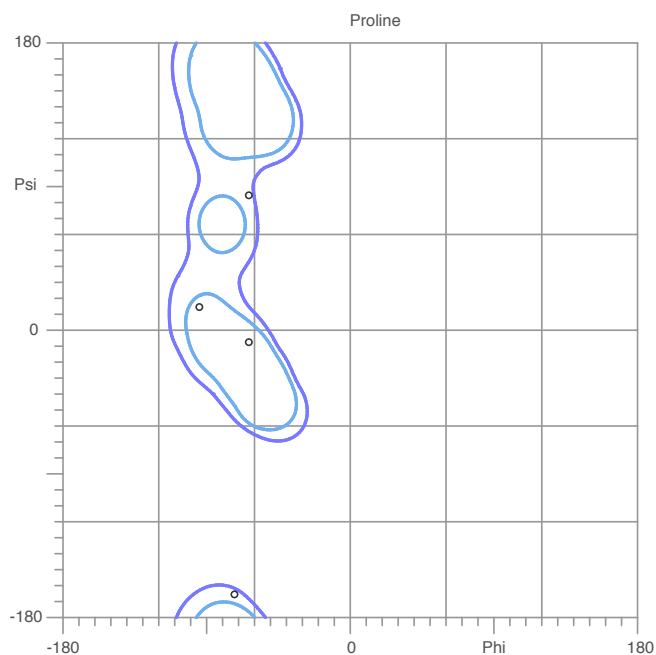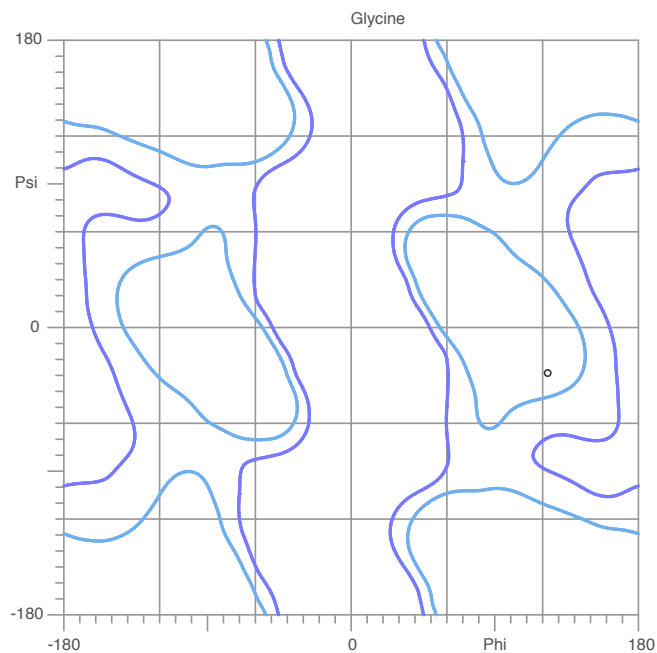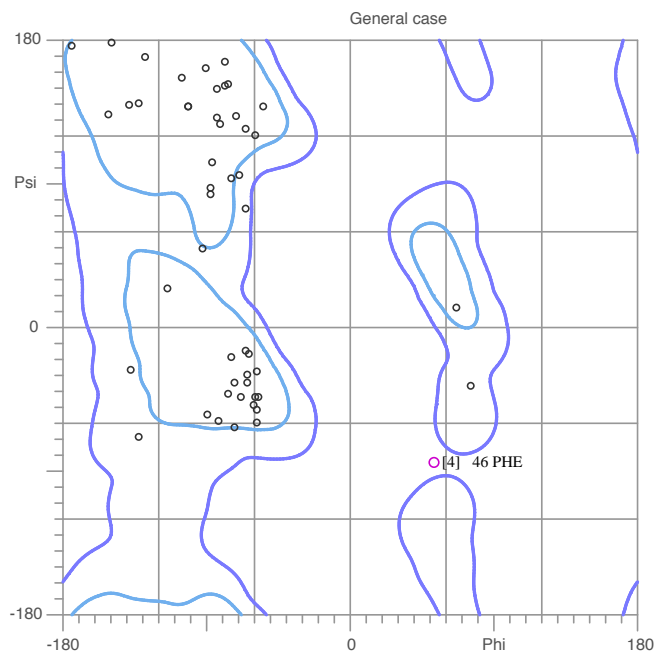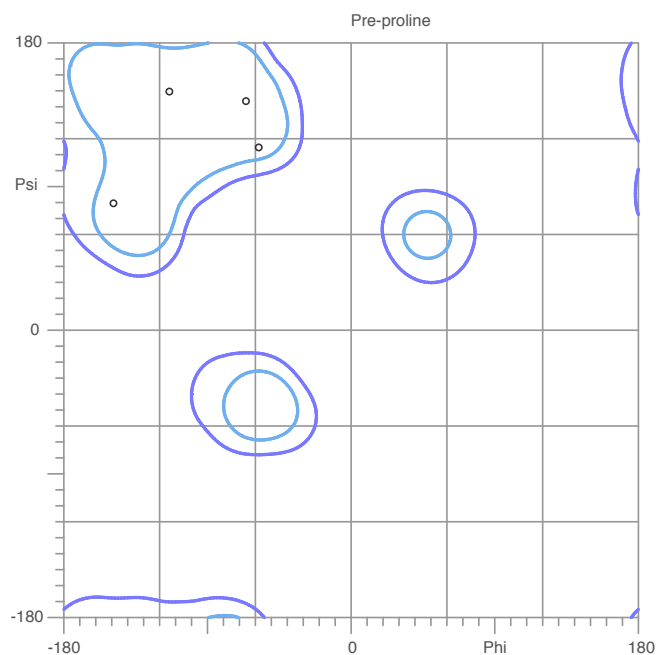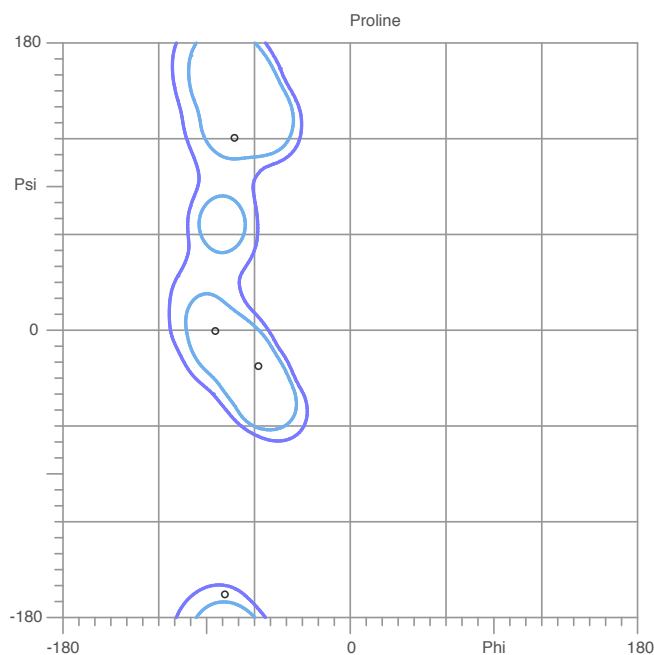96.6% (57/59) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
   [2]   25 PRO (-96.3, 89.9)
   [2]   46 PHE (63.4, -85.7)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 3

General case

Glycine

Proline

Pre-proline

88.1% (52/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
    [3]   46 PHE (47.7, -90.8)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 4

81.4% (48/59) of all residues were in favored (98%) regions.
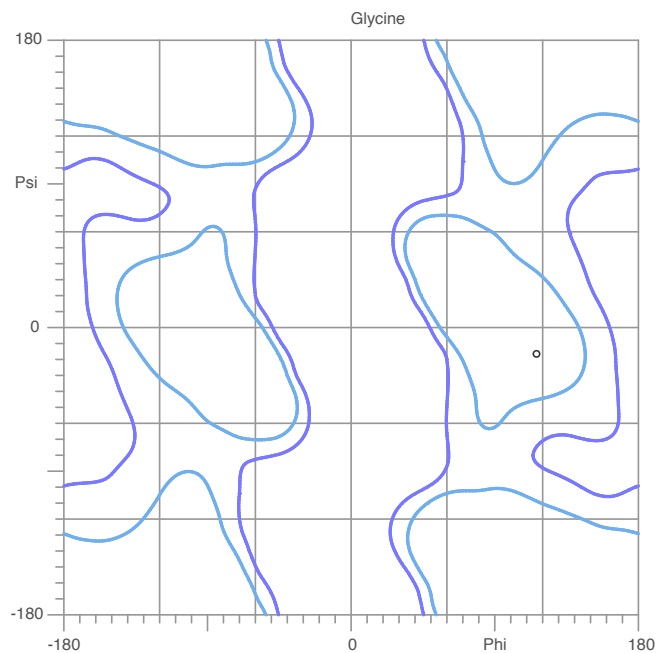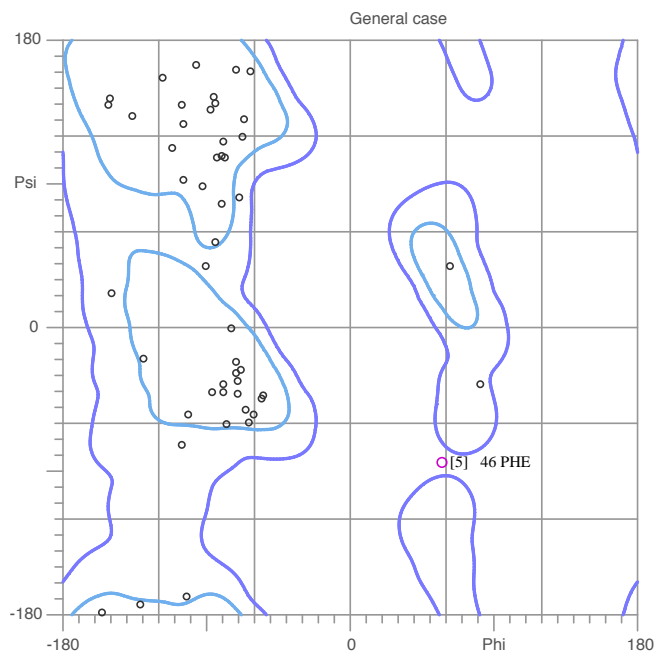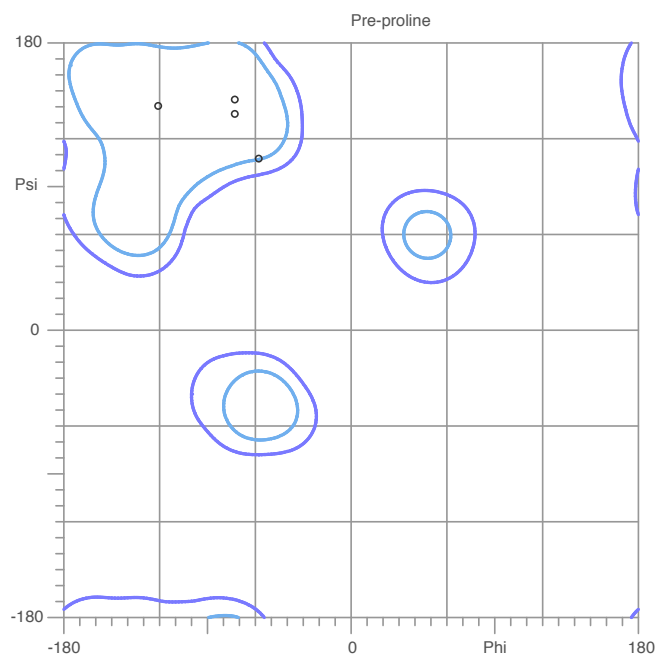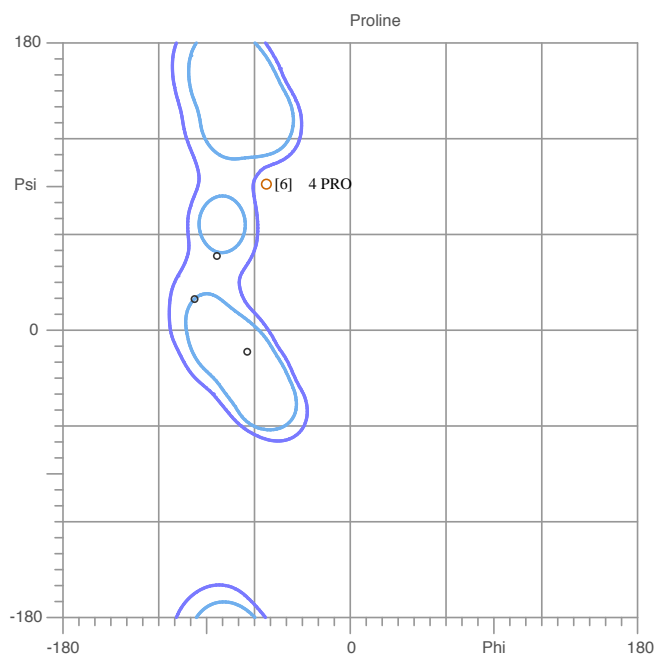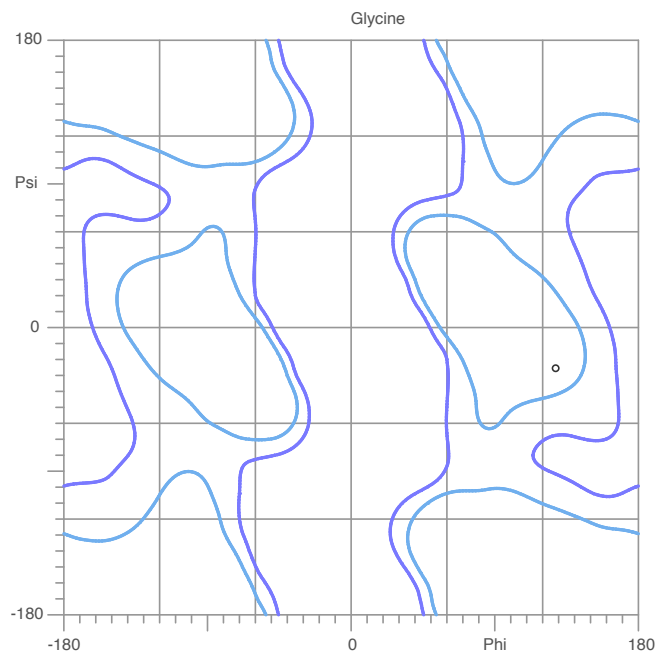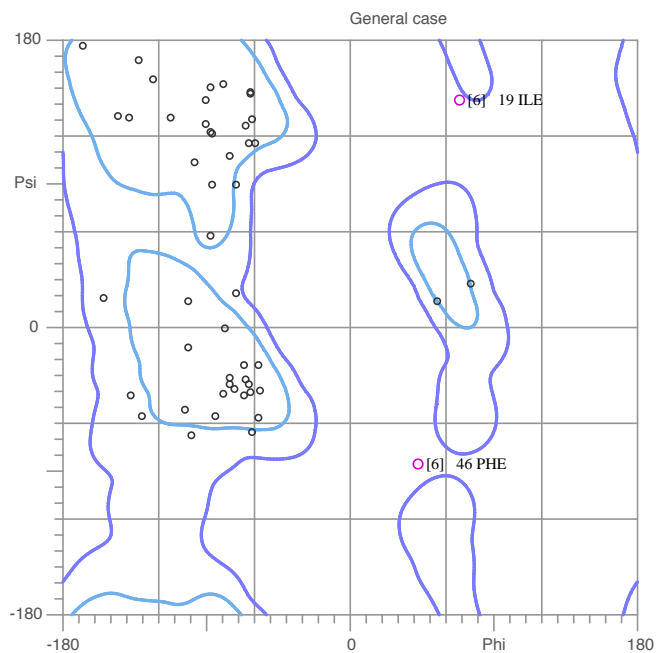98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
   [4]   46 PHE (52.4, -84.0)

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

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 5

86.4% (51/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
    [5]   46 PHE (57.1, -85.0)

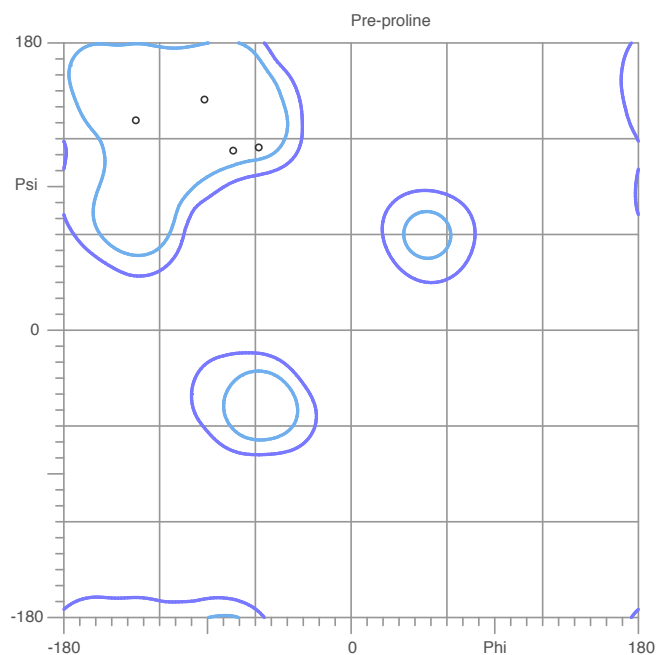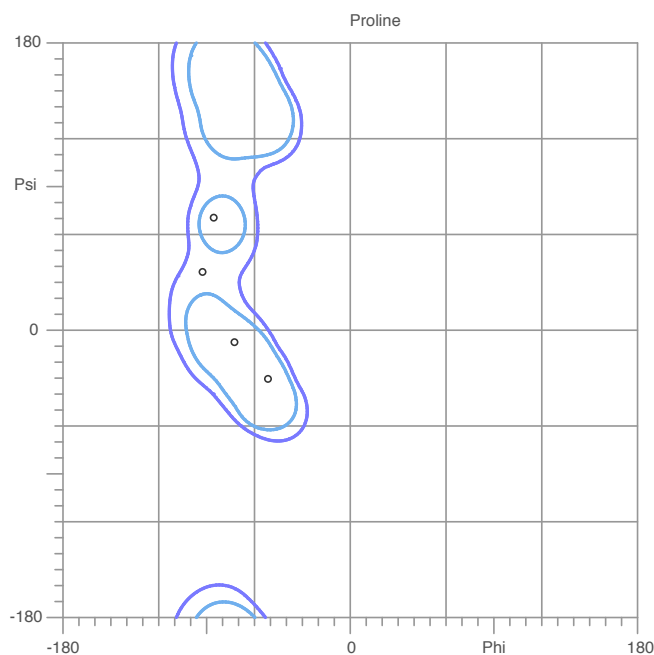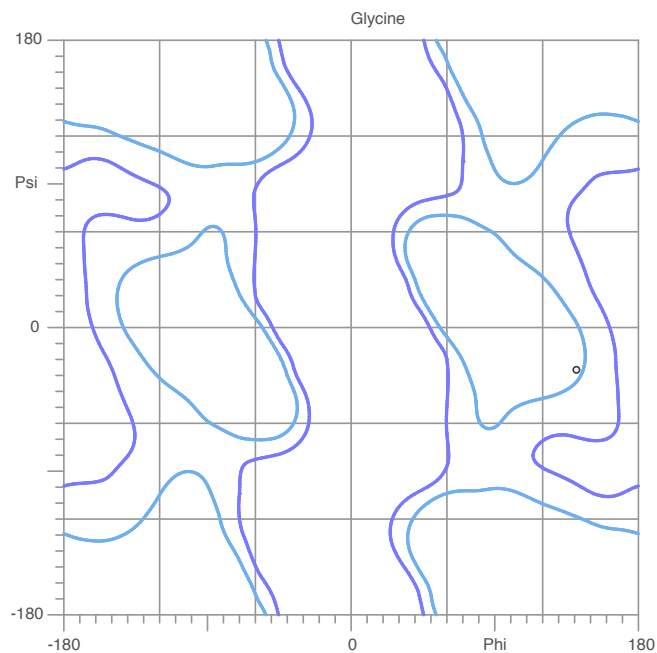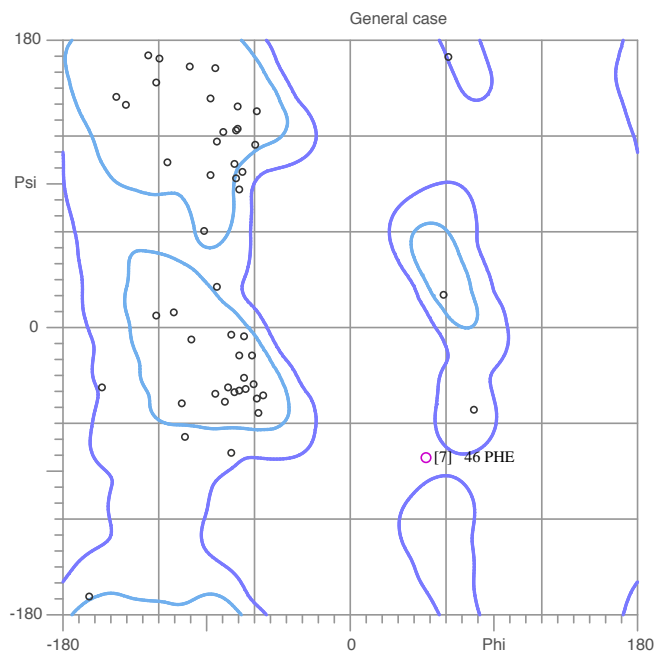# MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 6

78.0% (46/59) of all residues were in favored (98%) regions.
94.9% (56/59) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
    [6]   4 PRO (-53.9, 92.8)
    [6]   19 ILE (68.2, 143.6)
    [6]   46 PHE (43.0, -85.9)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 7

81.4% (48/59) of all residues were in favored (98%) regions.
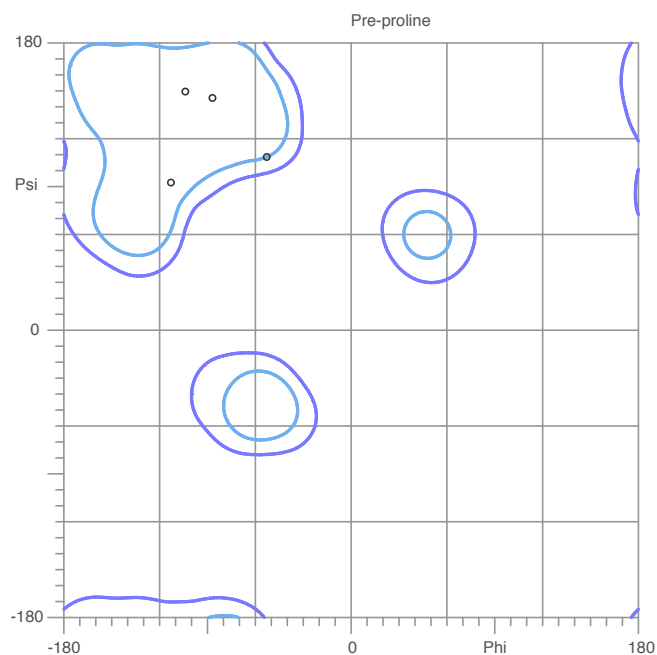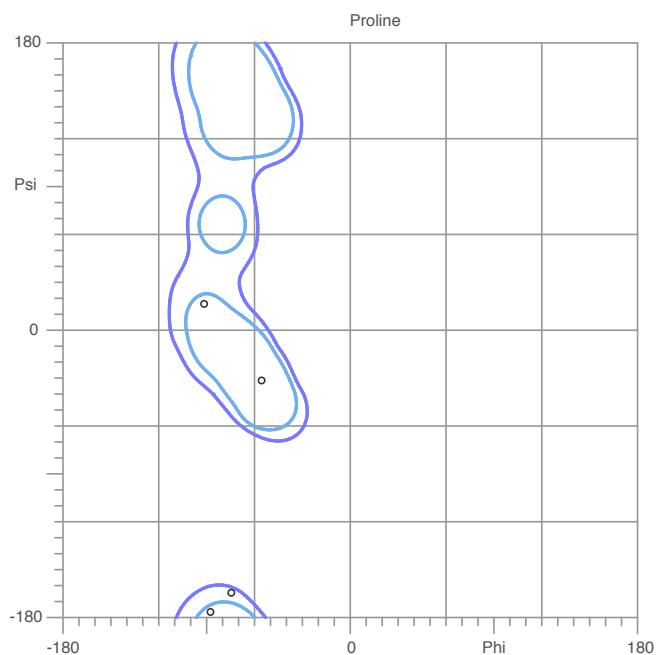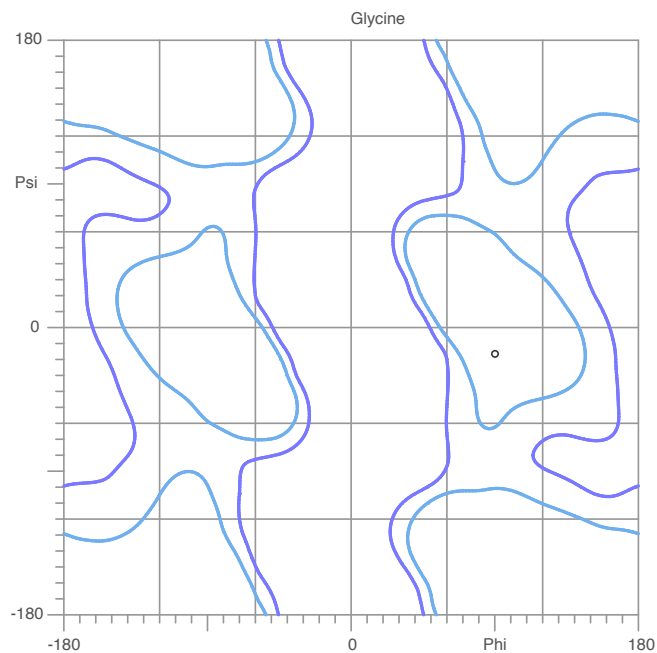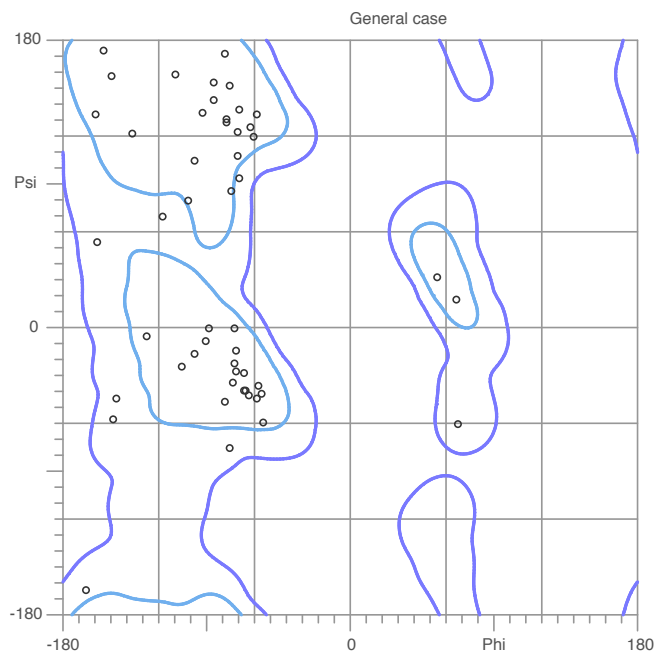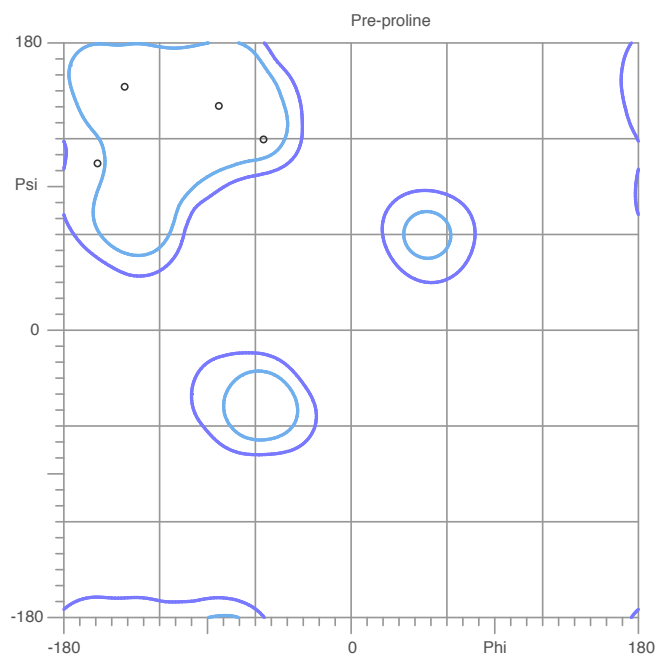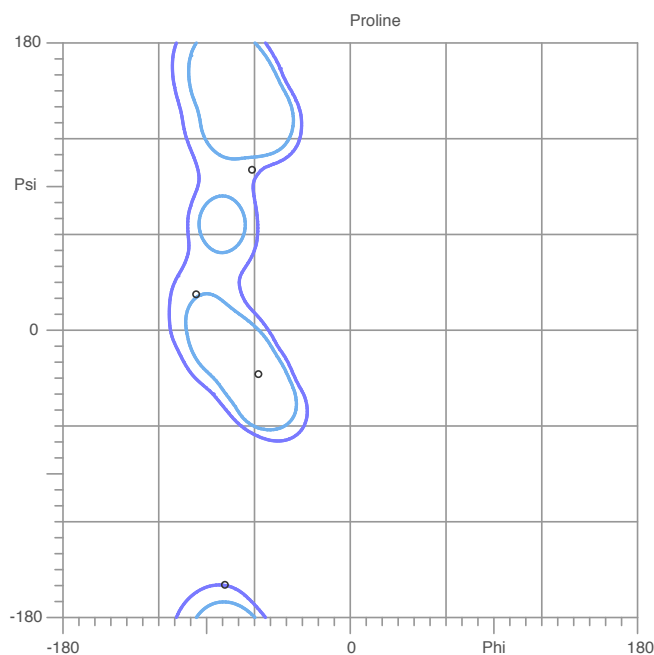98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
    [7]   46 PHE (47.4, -81.5)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 8

General case

Glycine

Proline

Pre-proline

84.7% (50/59) of all residues were in favored (98%) regions.
100.0% (59/59) of all residues were in allowed (>99.8%) regions.

There were no outliers.
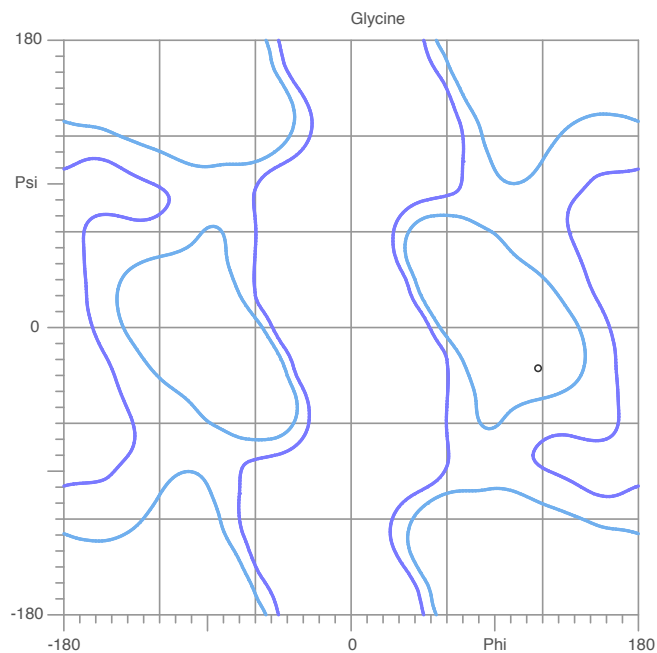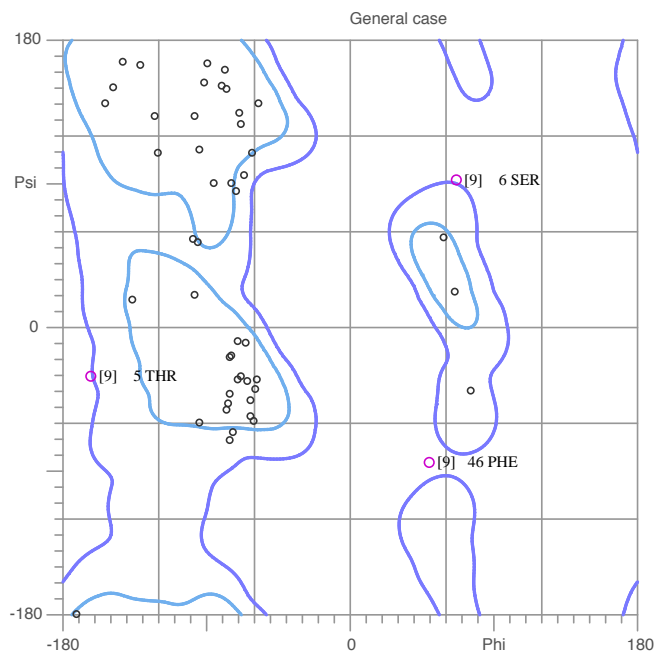
http://kinemage.biochem.duke.edu   Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis
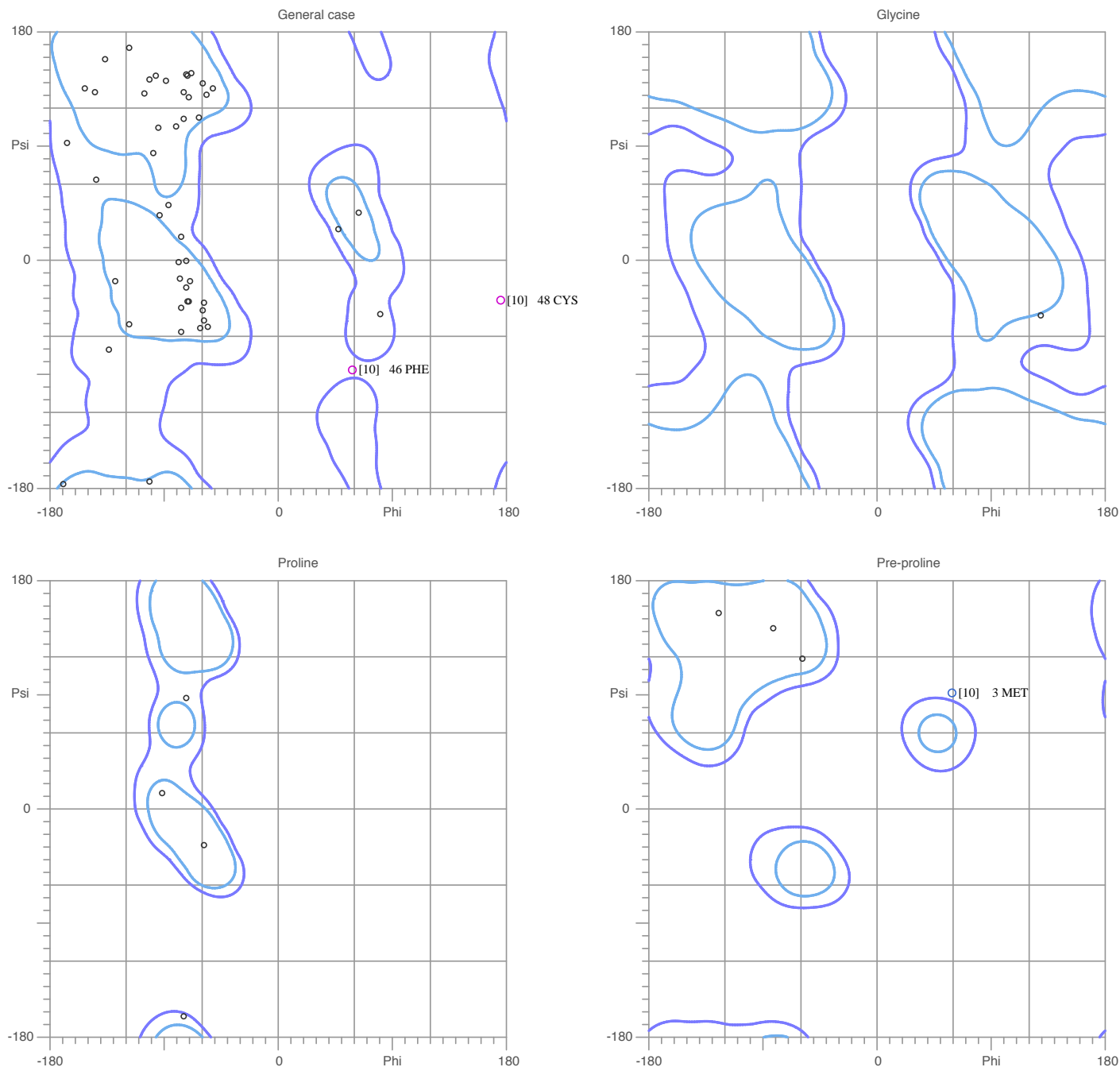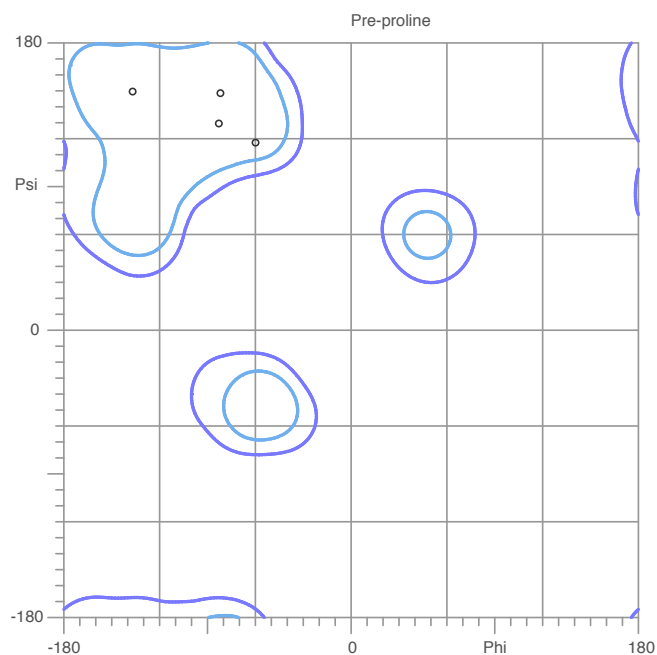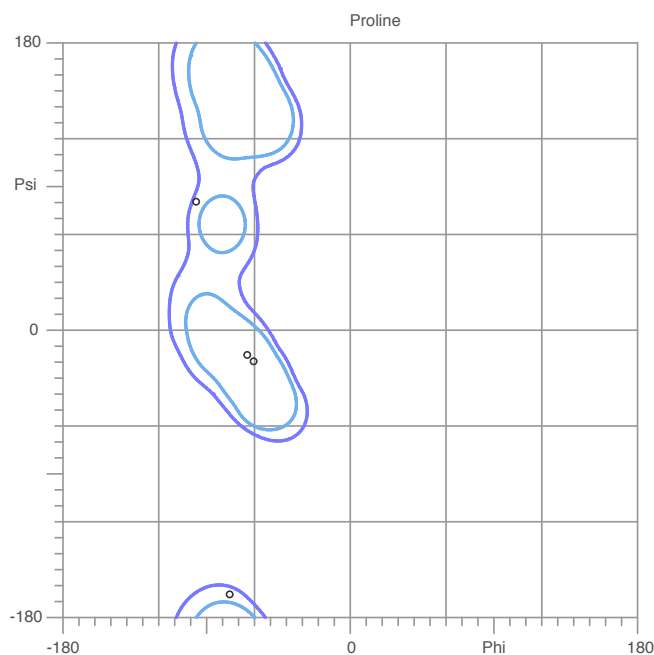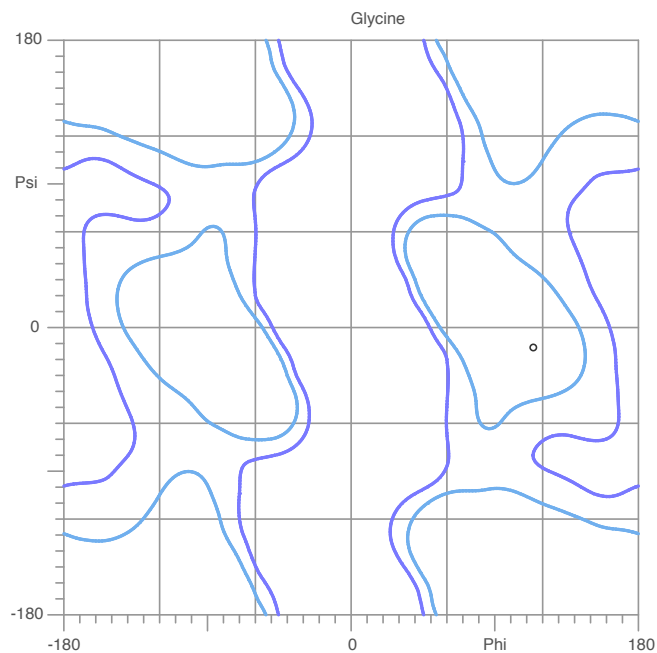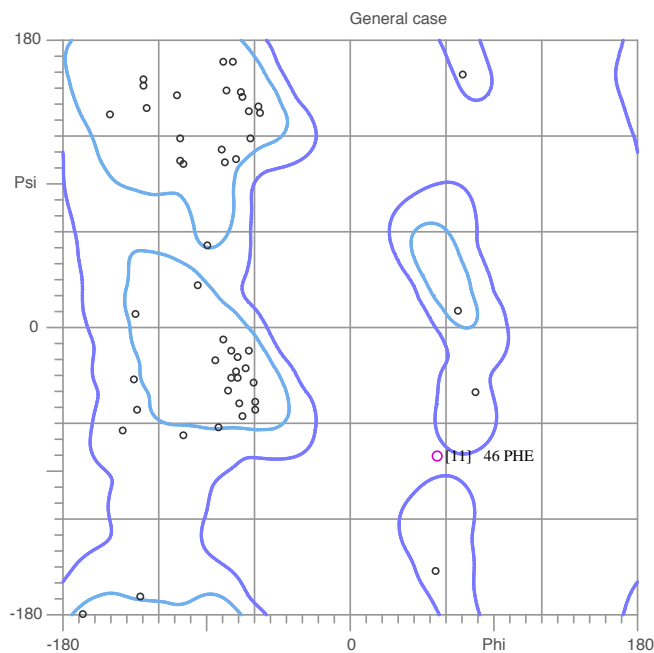
2MA6_NMR.pdb, model 9

76.3% (45/59) of all residues were in favored (98%) regions.
94.9% (56/59) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
- [9] 5 THR (-163.8, -30.7)
- [9] 6 SER (66.6, 93.2)
- [9] 46 PHE (49.7, -84.6)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 10

76.3% (45/59) of all residues were in favored (98%) regions.
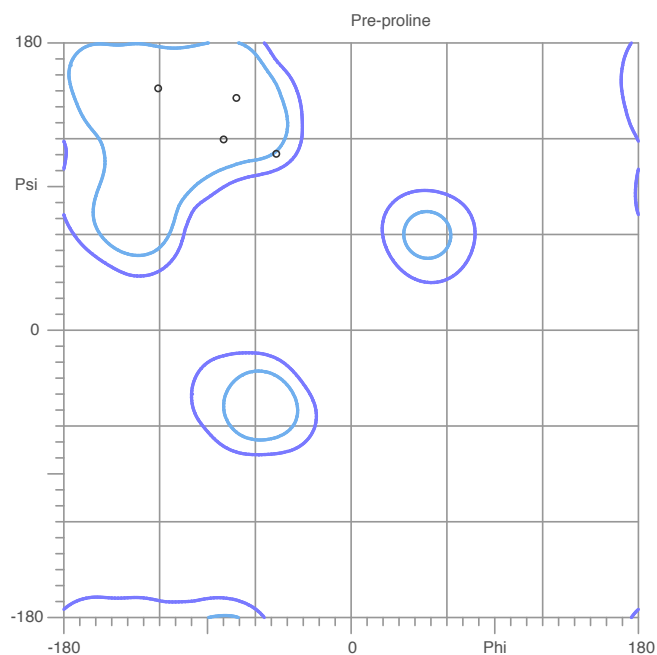94.9% (56/59) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
    [10]   3 MET (59.3, 92.6)
    [10]   46 PHE (58.6, -86.3)
    [10]   48 CYS (175.8, -32.0)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 11

81.4% (48/59) of all residues were in favored (98%) regions.
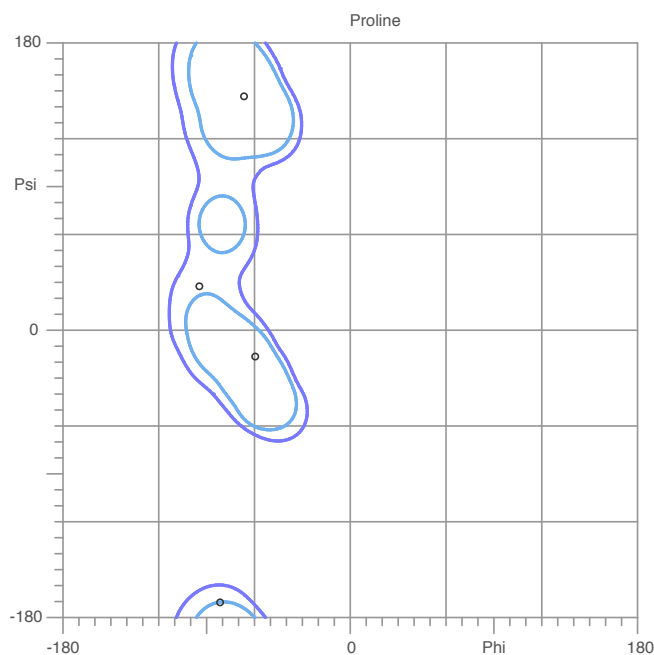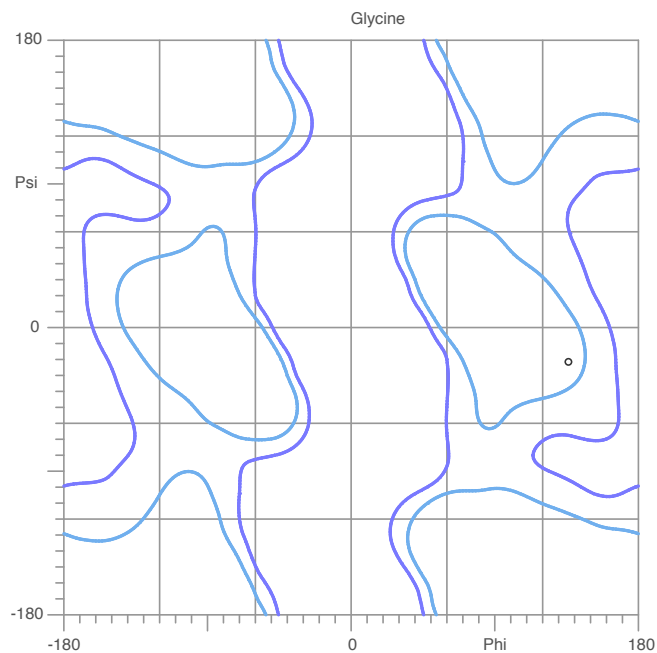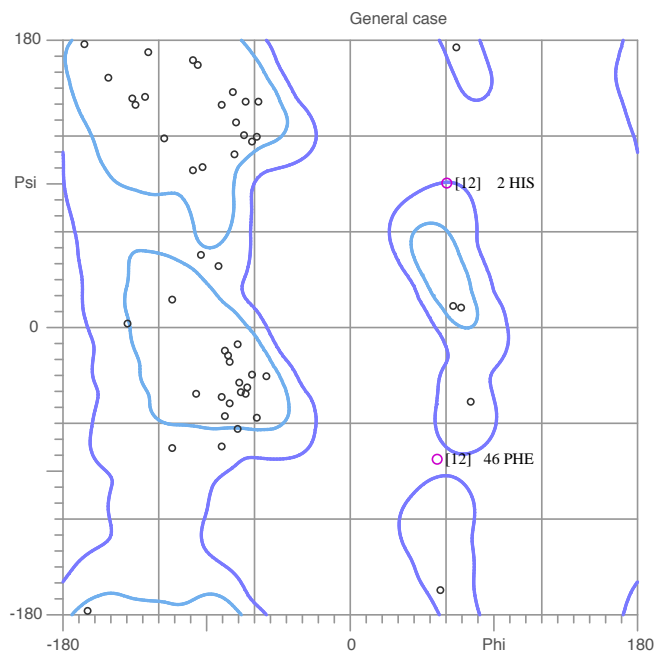98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[11]   46 PHE (55.0, -80.3)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 12

78.0% (46/59) of all residues were in favored (98%) regions.
96.6% (57/59) of all residues were in allowed (>99.8%) regions.
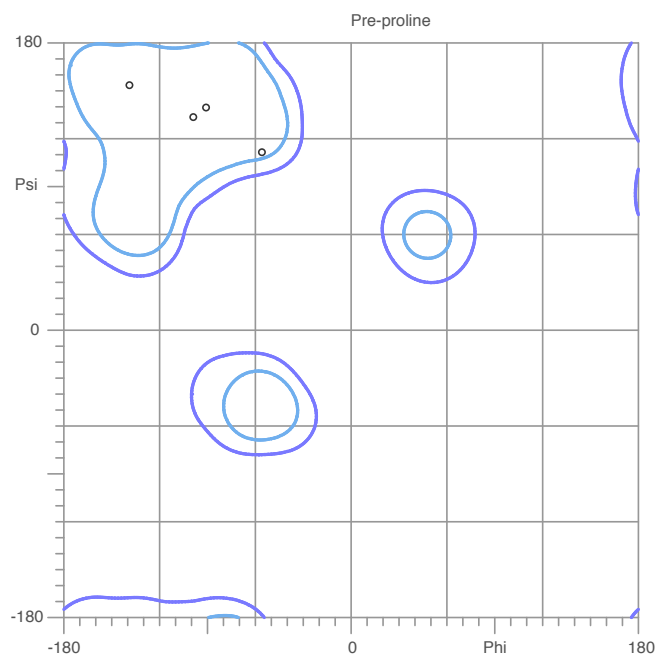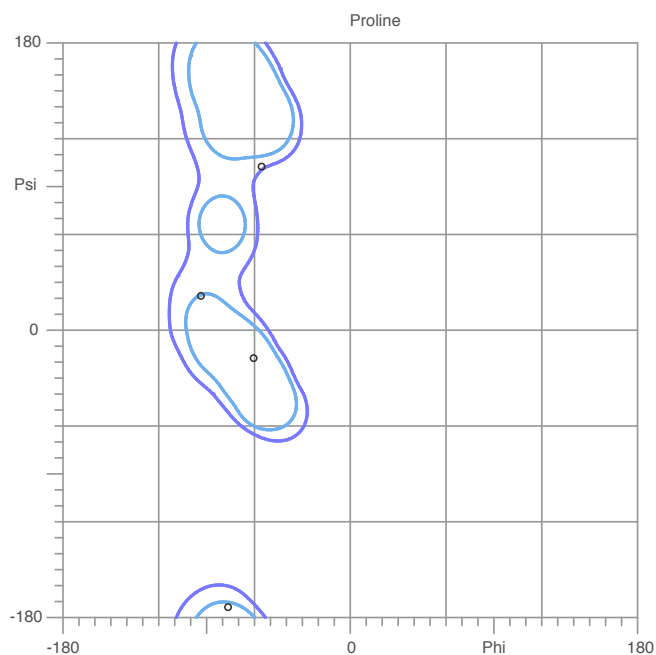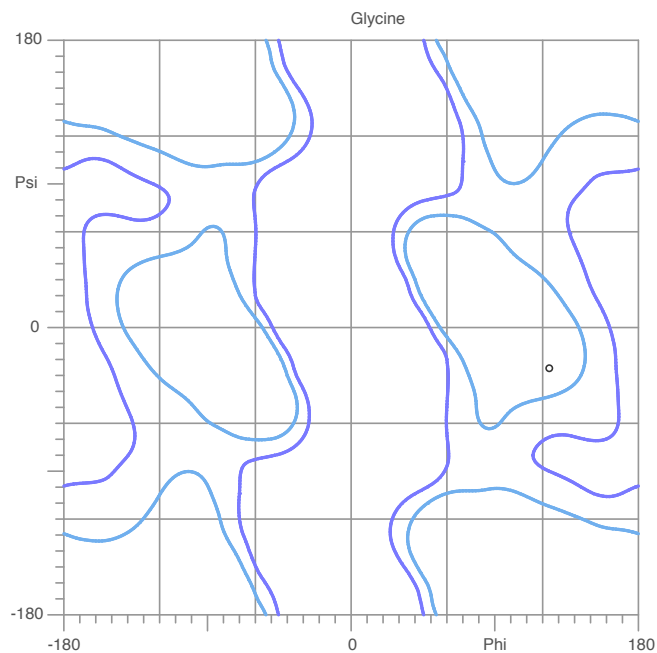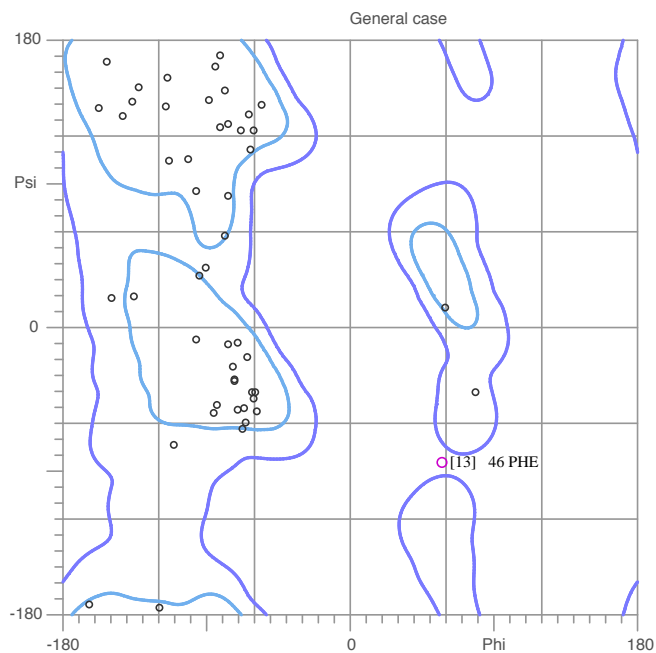
There were 2 outliers (phi, psi):
    [12]   2 HIS (60.3, 91.4)
    [12]   46 PHE (54.2, -82.9)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 13

86.4% (51/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.
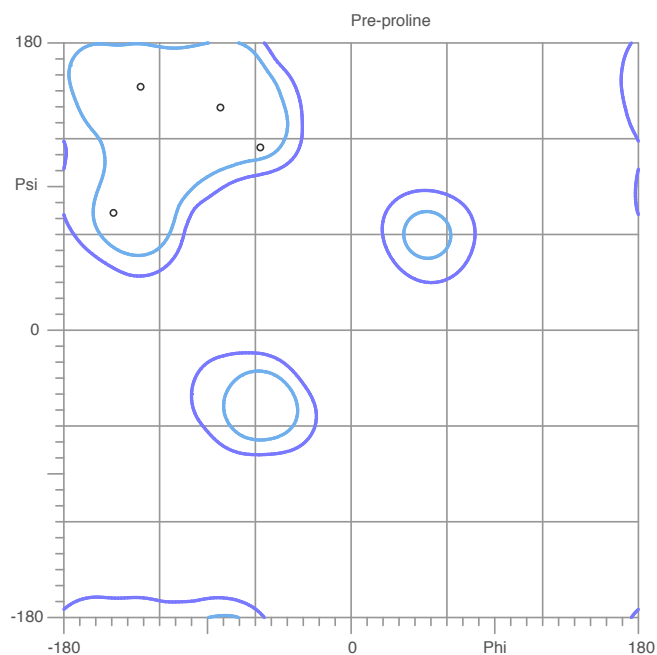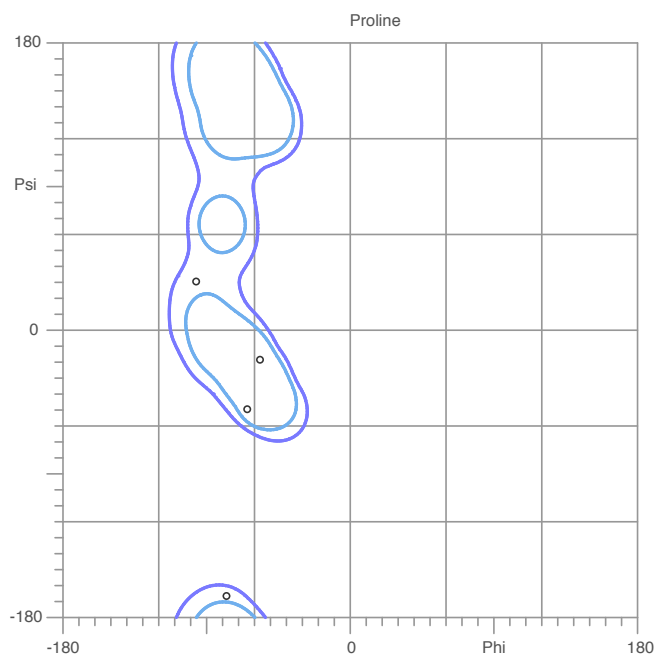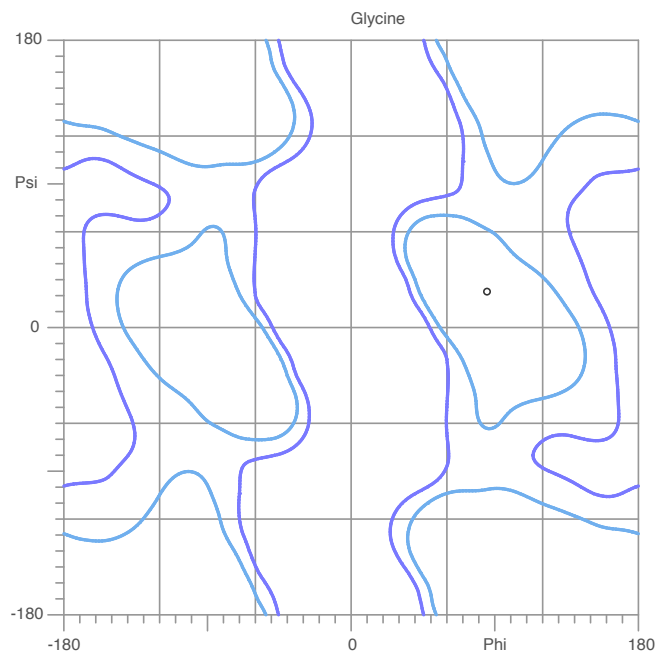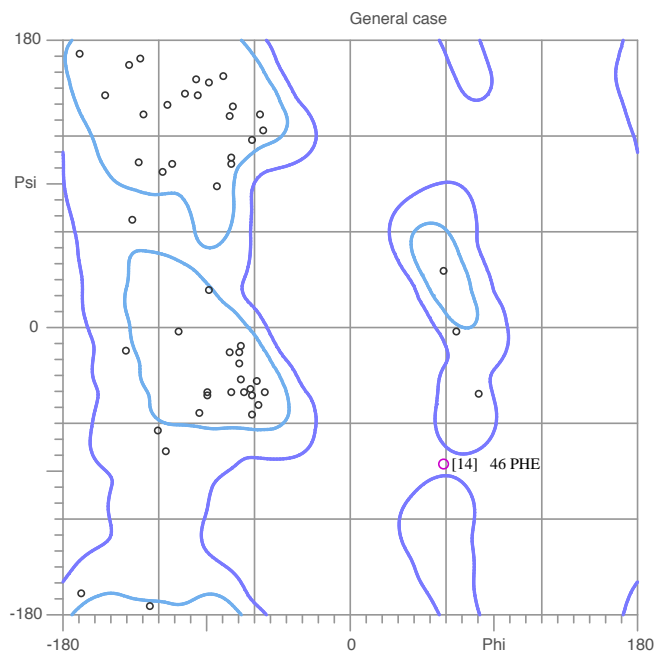
There were 1 outliers (phi, psi):
    [13]   46 PHE (57.4, -84.7)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 14

83.1% (49/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.
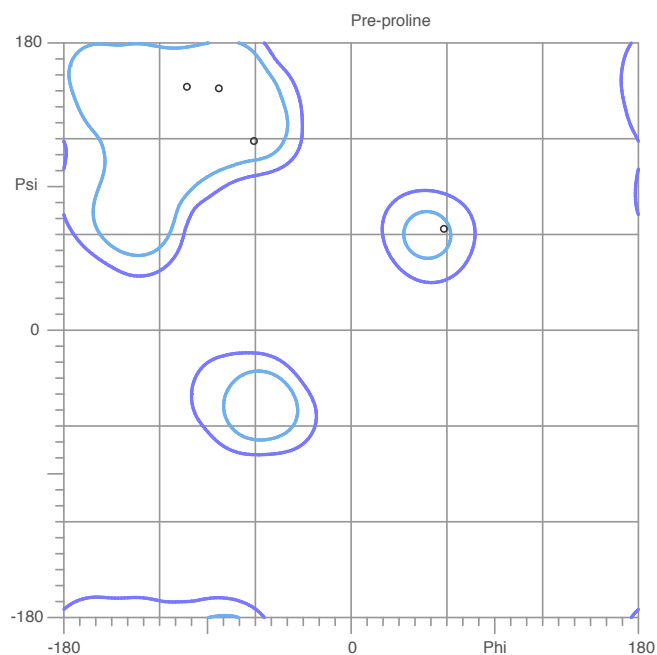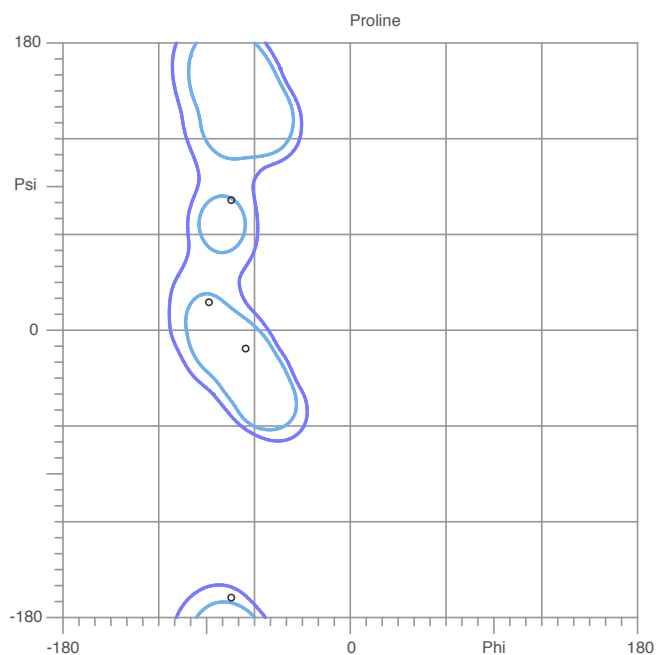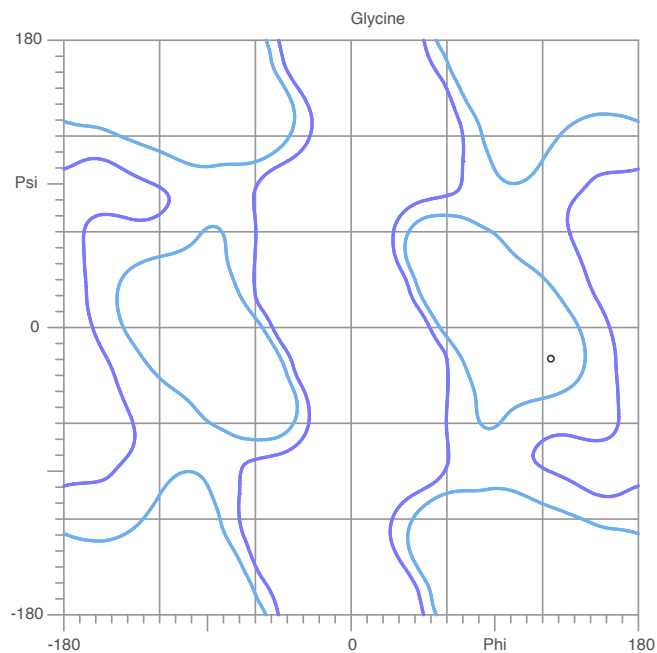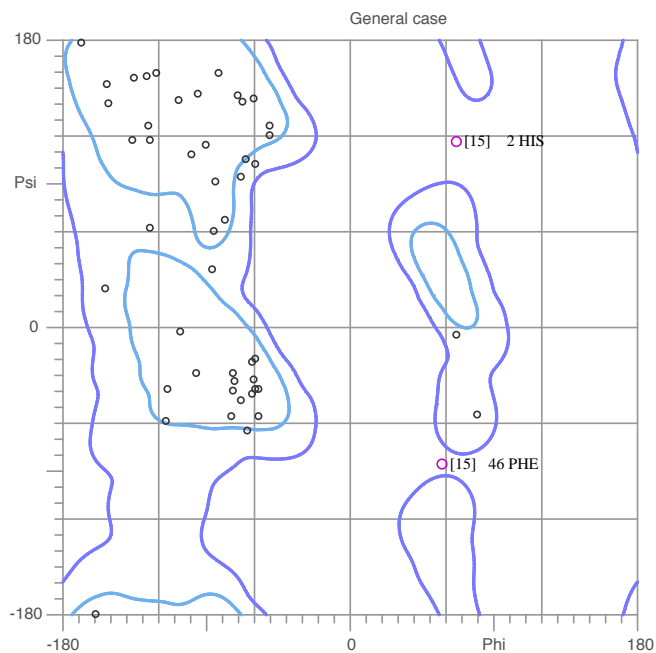
There were 1 outliers (phi, psi):
   [14]   46 PHE (58.9, -86.0)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 15

General case

Glycine

Proline

Pre-proline

81.4% (48/59) of all residues were in favored (98%) regions.
96.6% (57/59) of all residues were in allowed (>99.8%) regions.
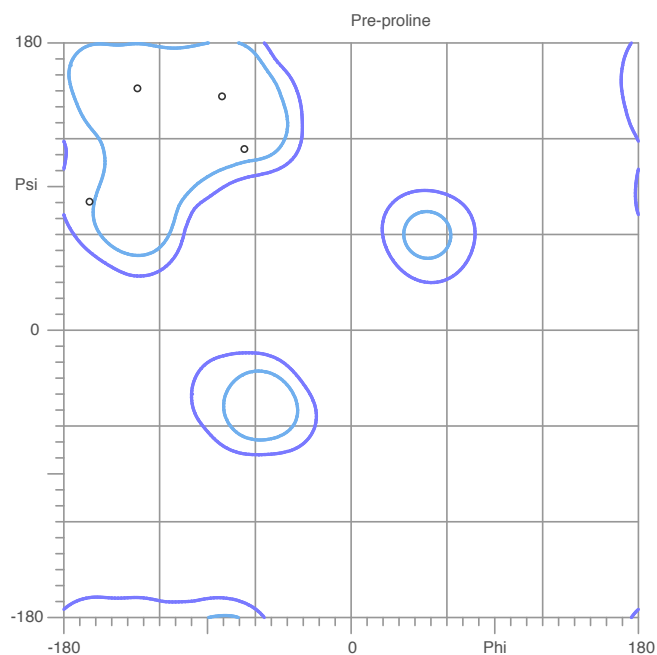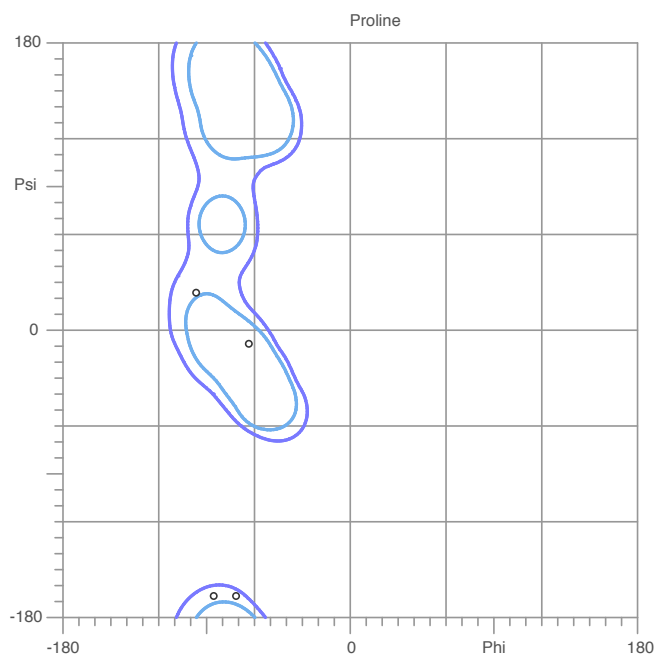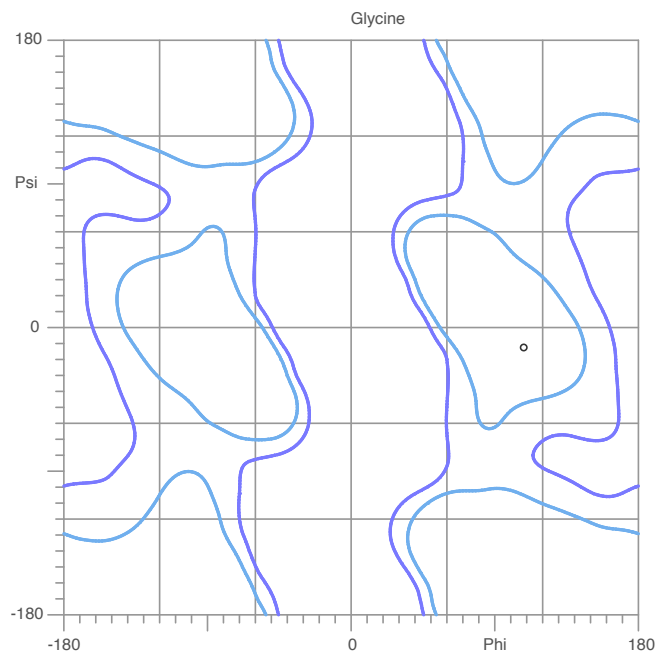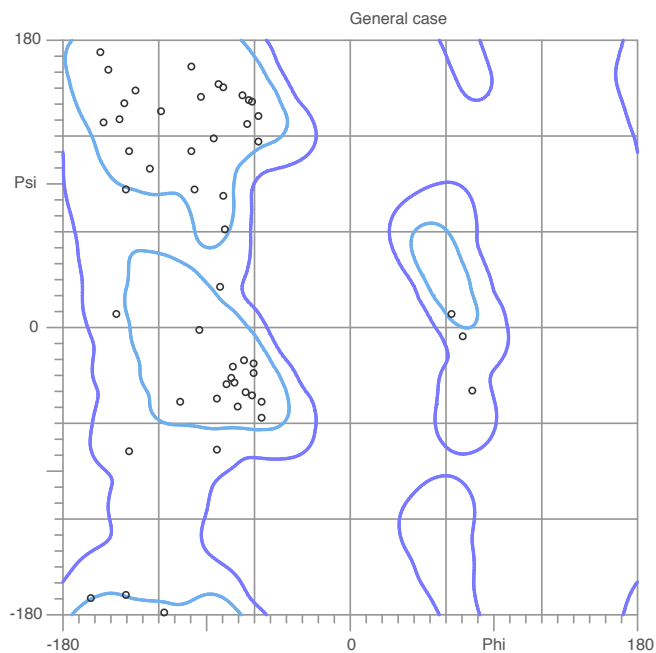
There were 2 outliers (phi, psi):
    [15]   2 HIS (66.7, 117.4)
    [15]   46 PHE (57.6, -85.3)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 16

78.0% (46/59) of all residues were in favored (98%) regions.
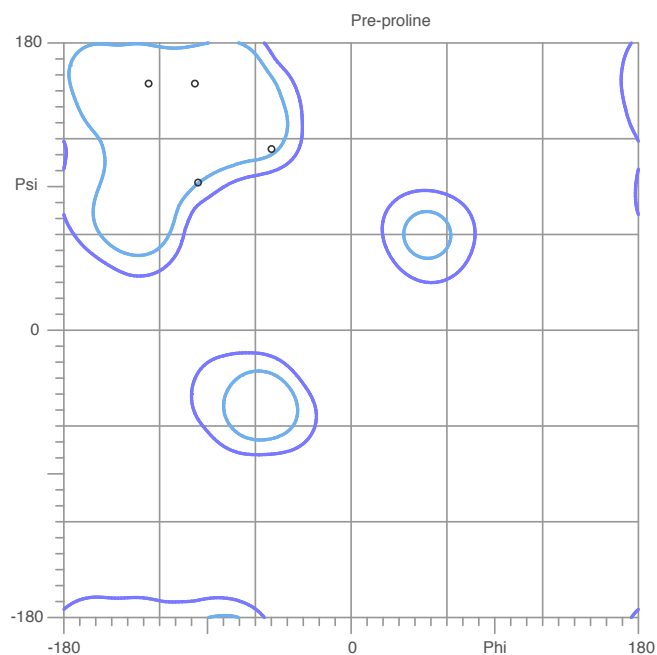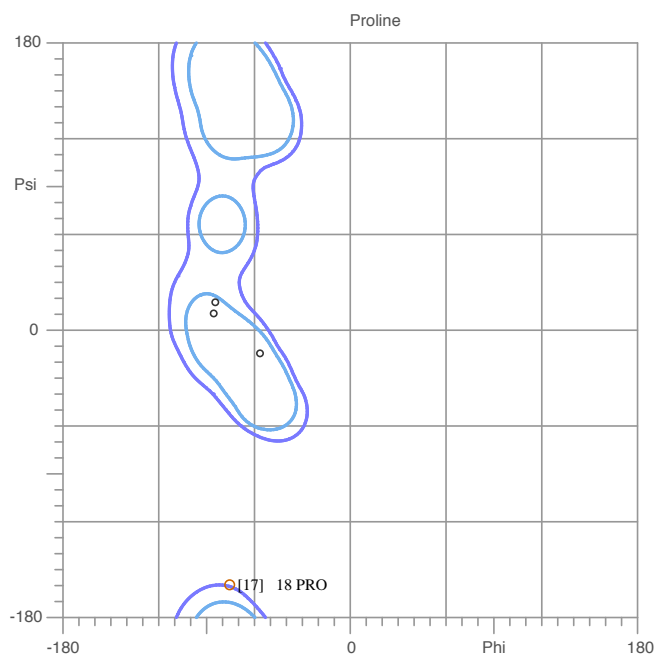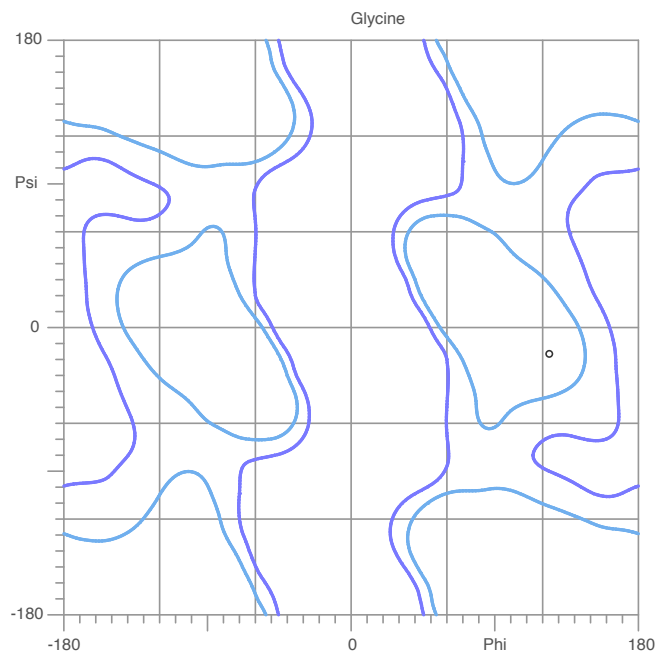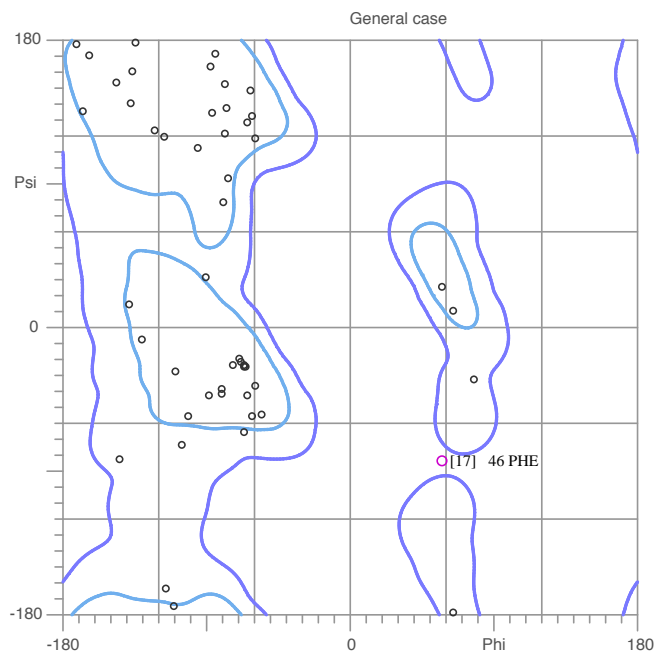100.0% (59/59) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

84.7% (50/59) of all residues were in favored (98%) regions.
96.6% (57/59) of all residues were in allowed (>99.8%) regions.
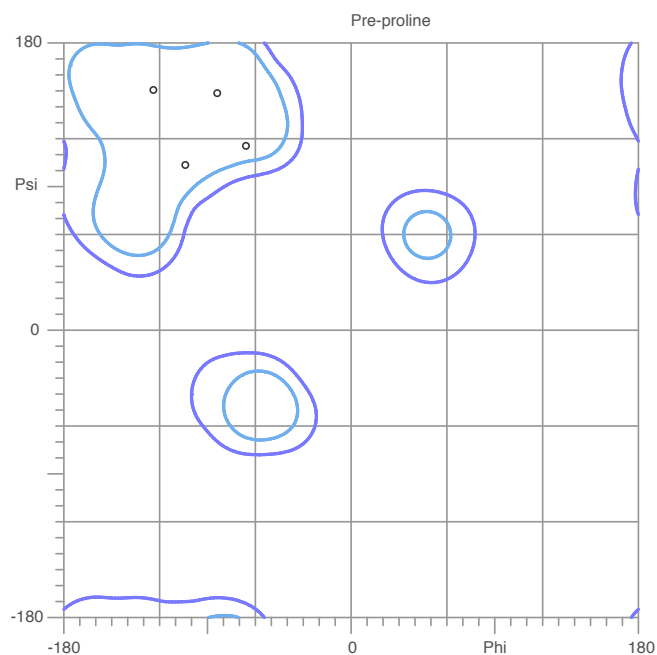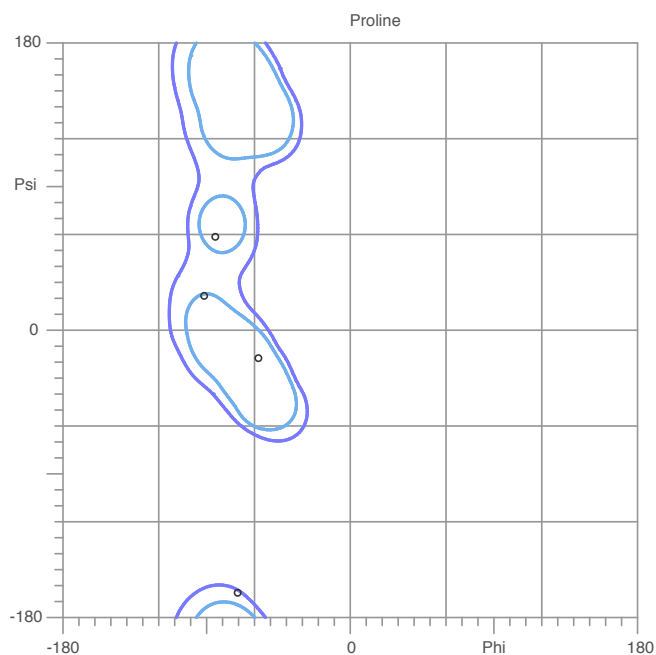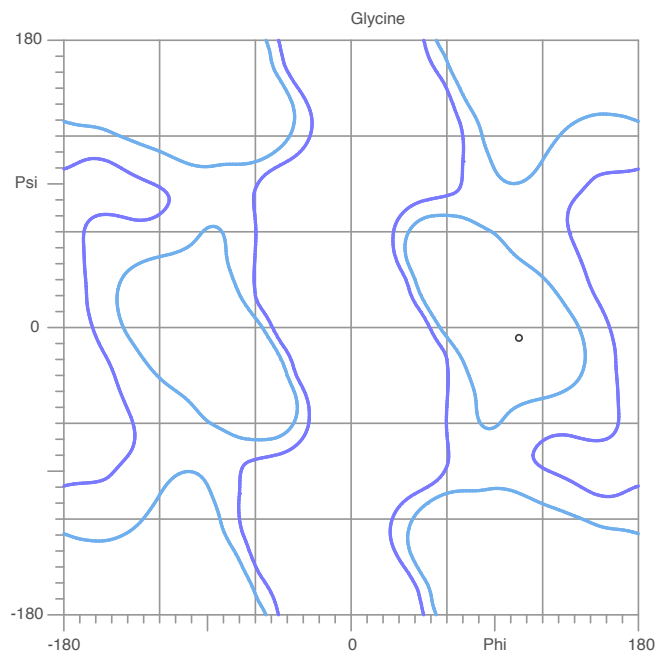
There were 2 outliers (phi, psi):
    [17]   18 PRO (-76.9, -159.6)
    [17]   46 PHE (57.7, -83.5)

MolProbity Ramachandran analysis

84.7% (50/59) of all residues were in favored (98%) regions.
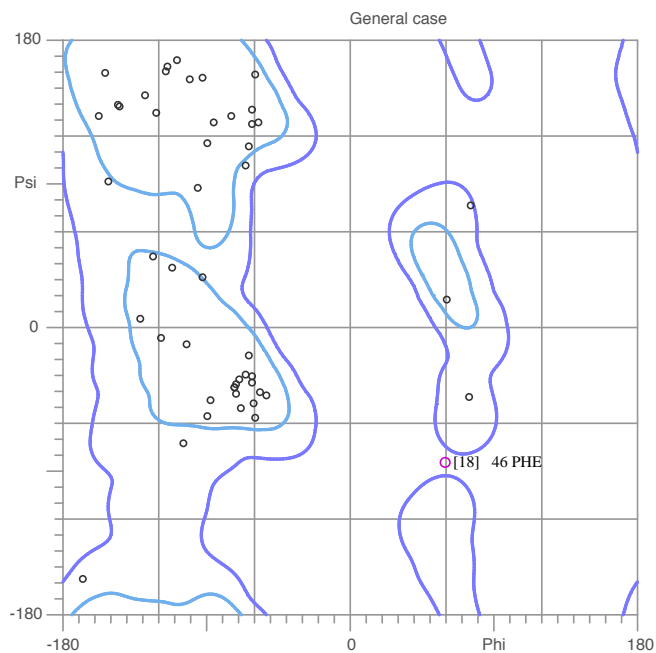98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
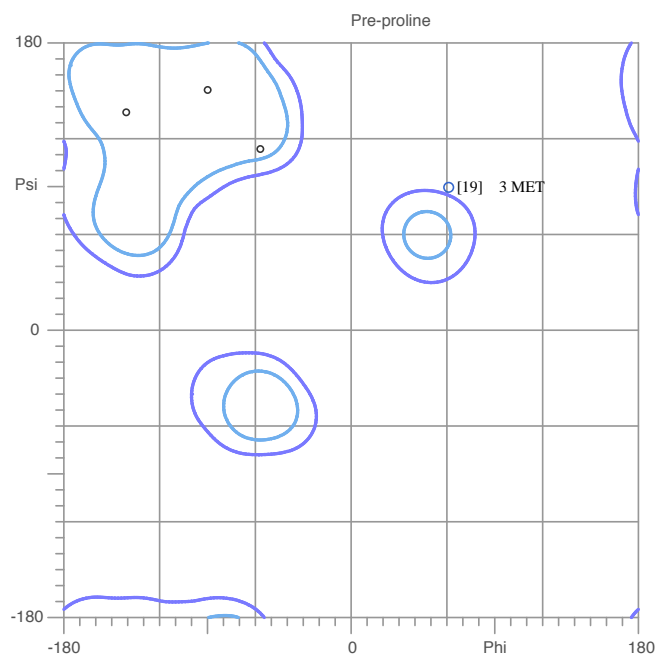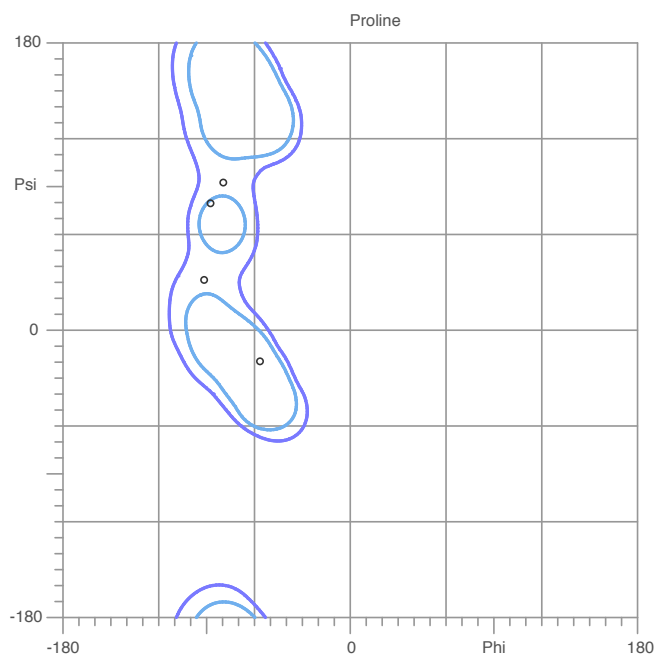   [18]   46 PHE (59.4, -84.4)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 19

General case

Glycine

Proline

Pre-proline

[19] 19 ILE

[19] 3 MET

72.9% (43/59) of all residues were in favored (98%) regions.
96.6% (57/59) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
   [19] 3 MET (62.0, 90.5)
   [19] 19 ILE (63.1, 155.5)

MolProbity Ramachandran analysis

2MA6_NMR.pdb, model 20

86.4% (51/59) of all residues were in favored (98%) regions.
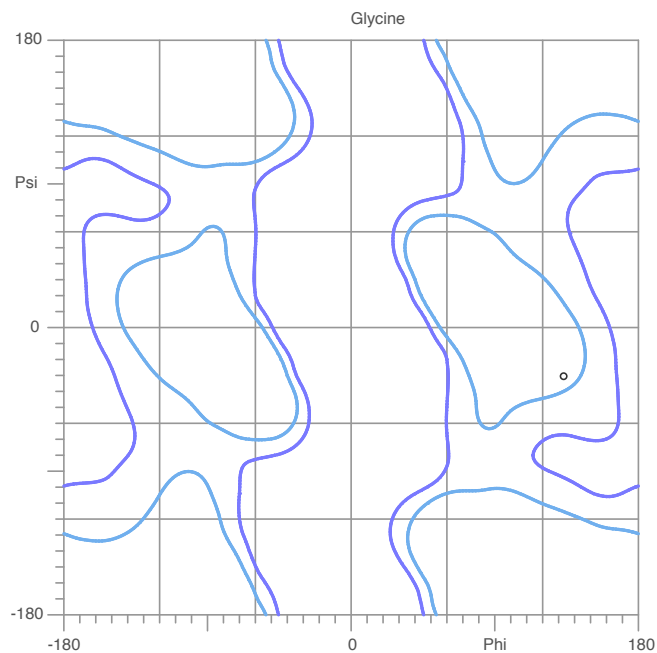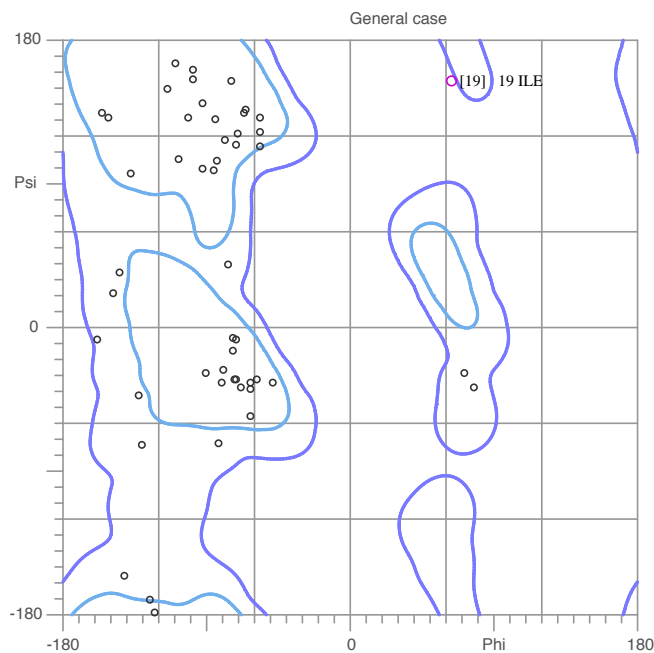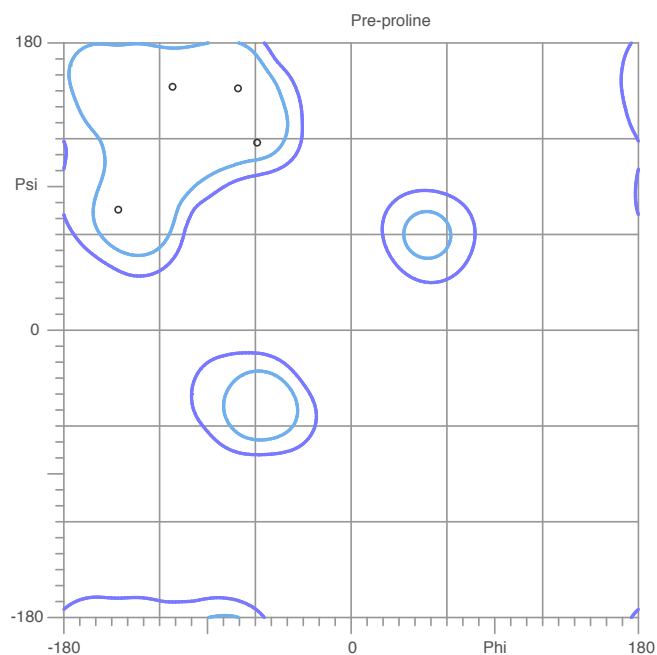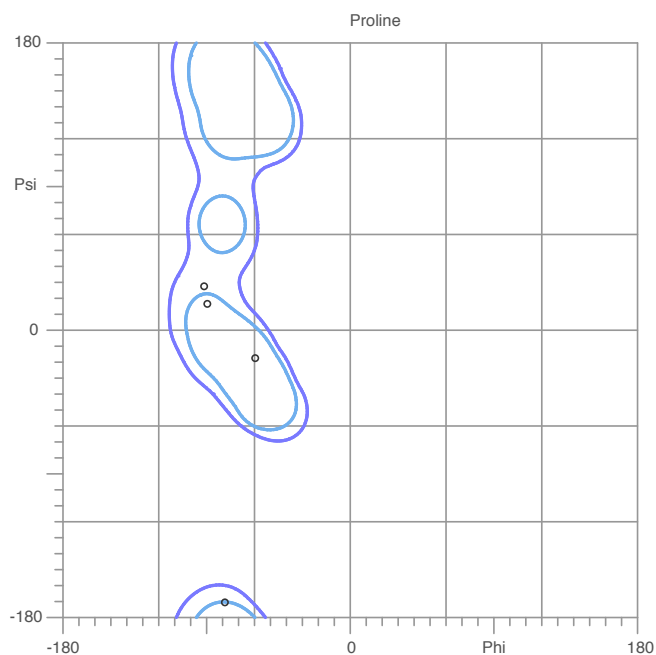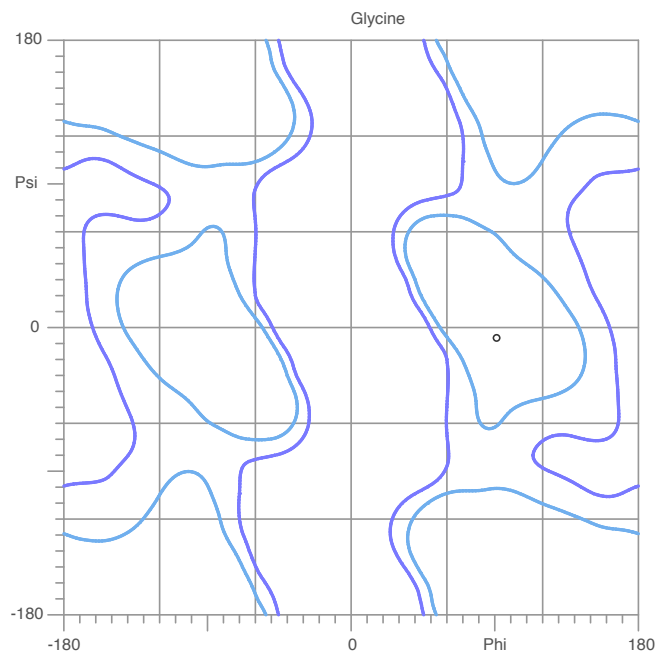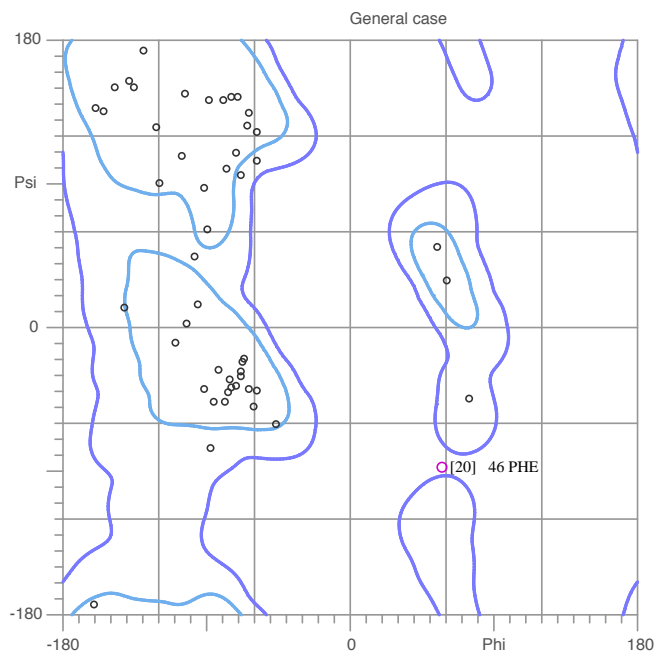98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20]   46 PHE (57.4, -87.3)