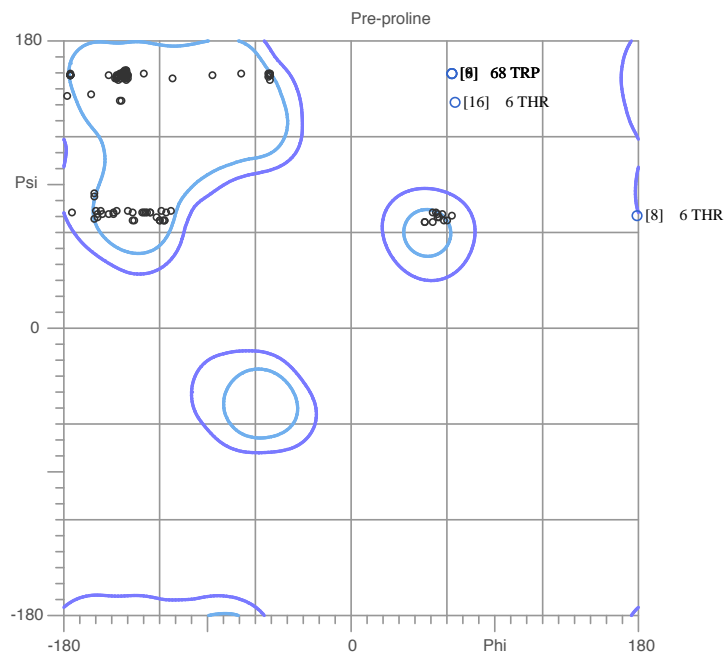
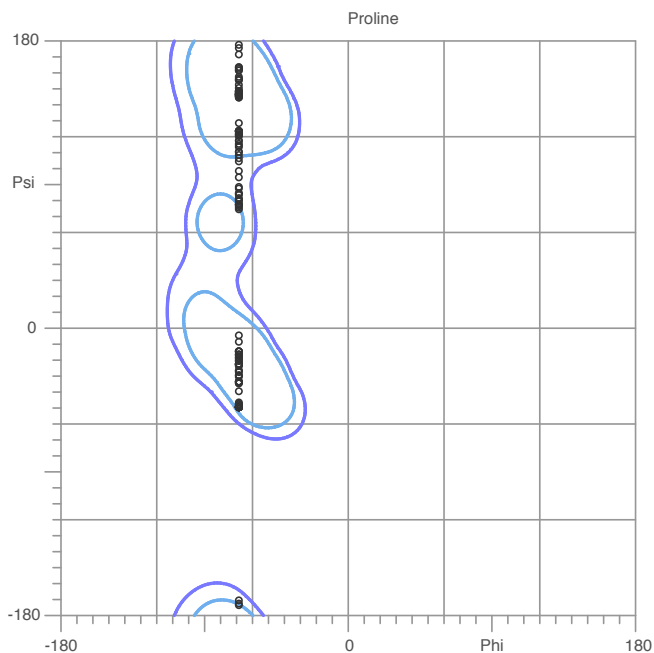
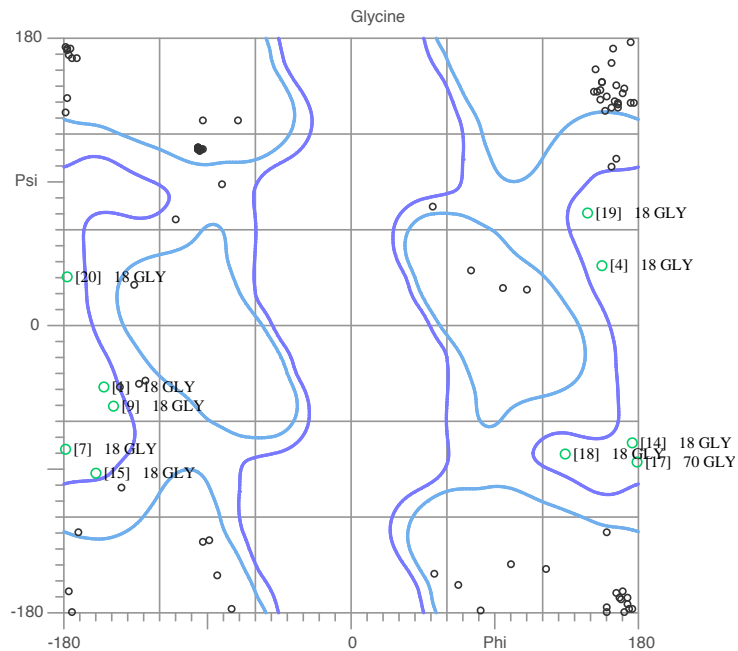
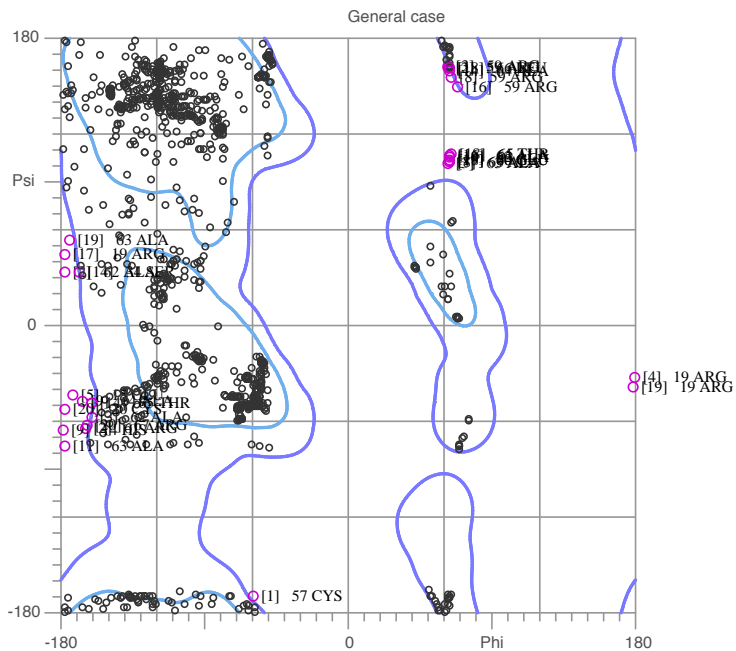


MolProbity Ramachandran analysis

2KSK.pdb, all models



80,1% (1105/1380) of all residues were in favored (98%) regions.
96,8% (1336/1380) of all residues were in allowed (>99.8%) regions.

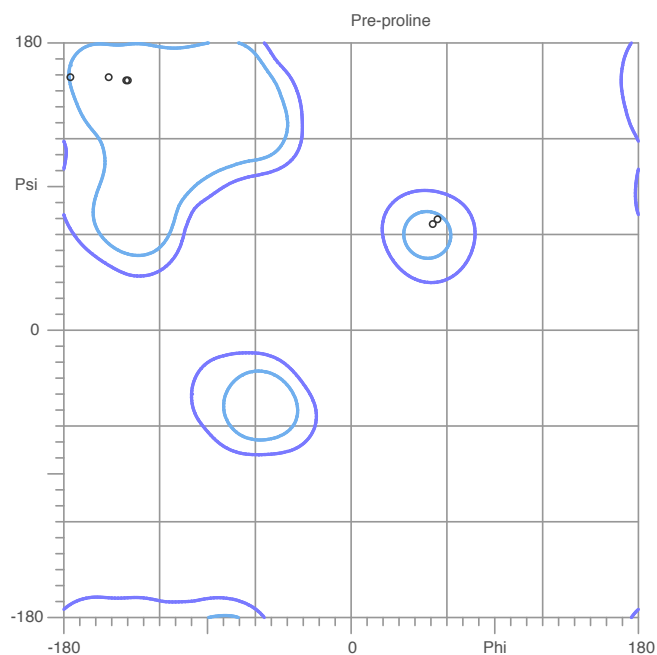
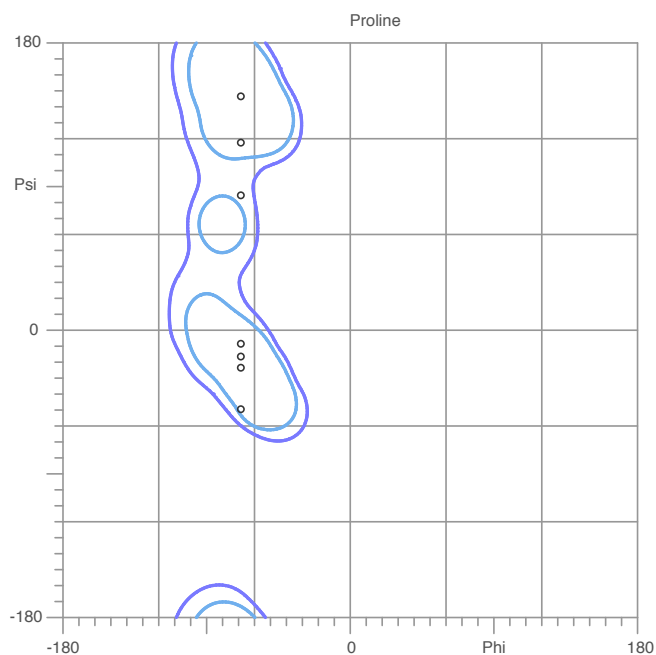
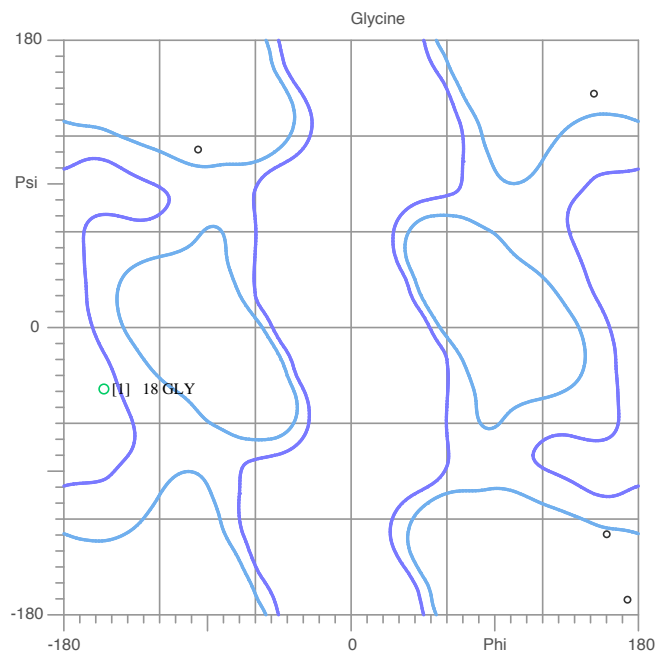
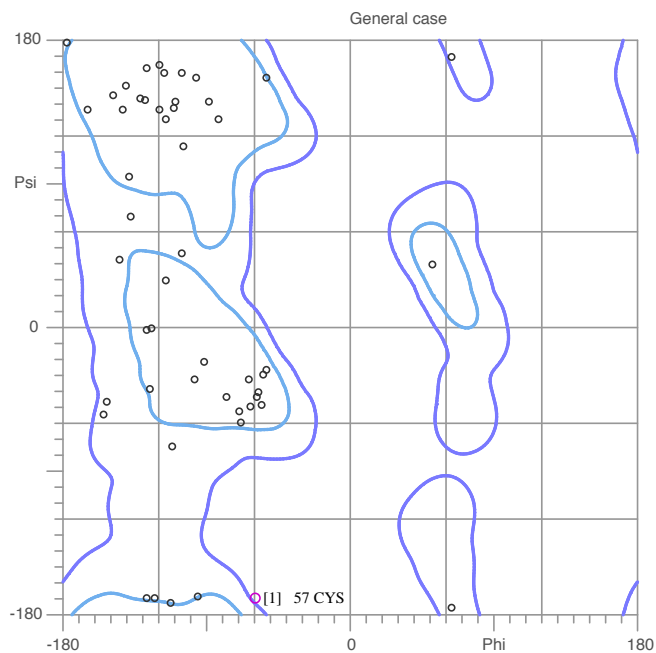
There were 44 outliers (phi, psi):

- [1] 18 GLY (-155.6, -38.8)
- [2] 57 CYS (-60.5, -169.4)
- [3] 59 ARG (63.0, 162.7)
- [2] 61 ARG (-165.4, -64.1)
- [2] 62 ALA (-178.3, 34.8)
- [3] 59 ARG (62.5, 163.8)
- [3] 62 ALA (-161.2, -57.7)
- [3] 63 ALA (63.0, 102.7)
- [4] 18 GLY (157.3, 38.6)
- [4] 19 ARG (179.3, -32.9)
- [5] 15 GLU (-174.0, -44.0)
- [6] 68 TRP (63.2, 160.6)
- [7] 18 GLY (179.3, -77.9)
- [8] 6 THR (179.6, 71.4)
- [9] 59 ARG (64.3, 156.3)
- [8] 63 ALA (63.3, 103.2)
- [8] 68 TRP (63.2, 160.6)
- [4] 14 HIS (-179.4, -65.2)
- [8] 18 GLY (-149.5, -50.3)
- [9] 64 ALA (-167.1, -47.1)

- [9] 68 TRP (63.3, 160.6)
- [11] 64 ALA (63.7, -75.4)
- [14] 18 GLY (176.9, 73.9)
- [14] 34 SER (-169.5, -34.6)
- [14] 64 ALA (63.7, 160.2)
- [15] 65 THR (-161.2, -82.6)
- [15] 18 GLY (-160.2, -92.6)
- [16] 6 THR (65.7, 142.3)
- [16] 59 ARG (68.2, 150.5)
- [16] 64 ALA (64.0, 107.5)
- [17] 19 ARG (-178.3, 46.0)
- [17] 70 GLY (179.6, -85.7)
- [17] 18 GLY (134.7, -80.8)
- [18] 60 GLU (63.2, 104.5)
- [18] 62 ALA (63.8, 106.8)
- [18] 65 THR (64.4, 108.3)
- [18] 66 LEU (63.1, 162.8)
- [19] 18 GLY (148.4, 71.9)
- [19] 19 ARG (178.5, -38.5)
- [19] 60 GLU (63.1, 104.1)
- [19] 63 ALA (-175.8, 54.8)
- [20] 18 GLY (-178.4, 31.8)
- [20] 20 CYS (-178.1, -62.9)
- [20] 67 ARG (-164.1, -52.8)

MolProbity Ramachandran analysis

2KSK.pdb, model 1



76,8% (53/69) of all residues were in favored (98%) regions.
97,1% (67/69) of all residues were in allowed (>99.8%) regions.

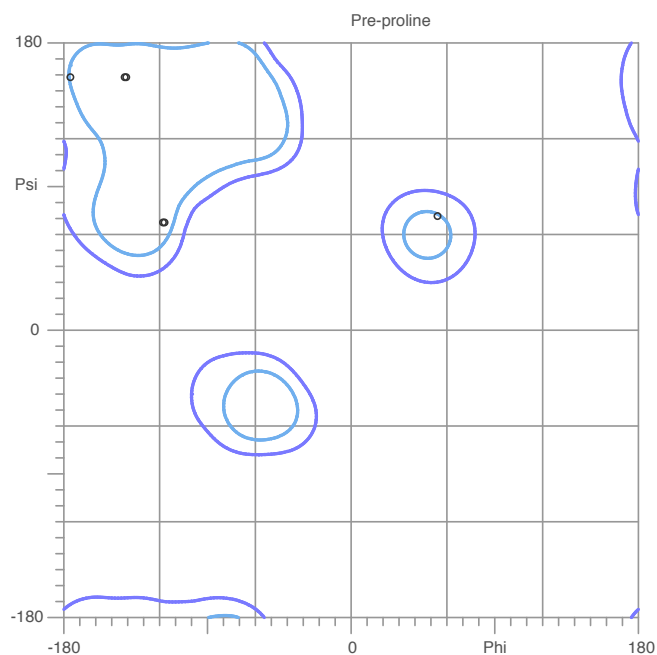
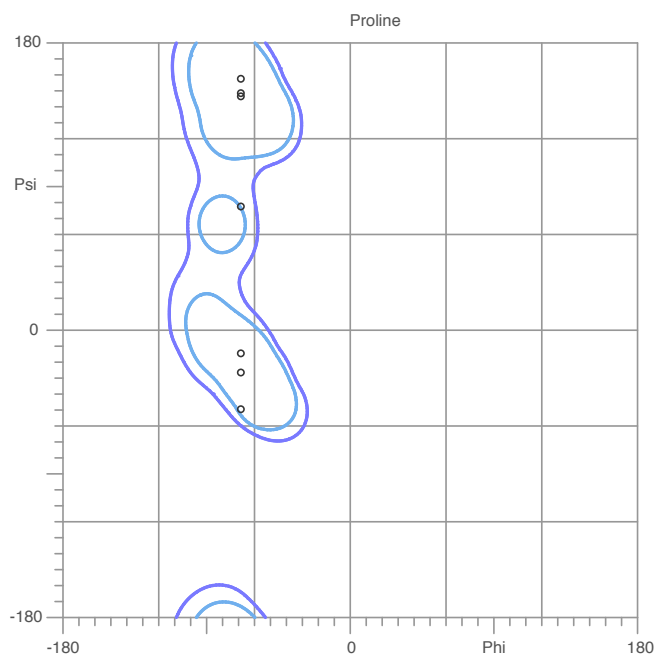
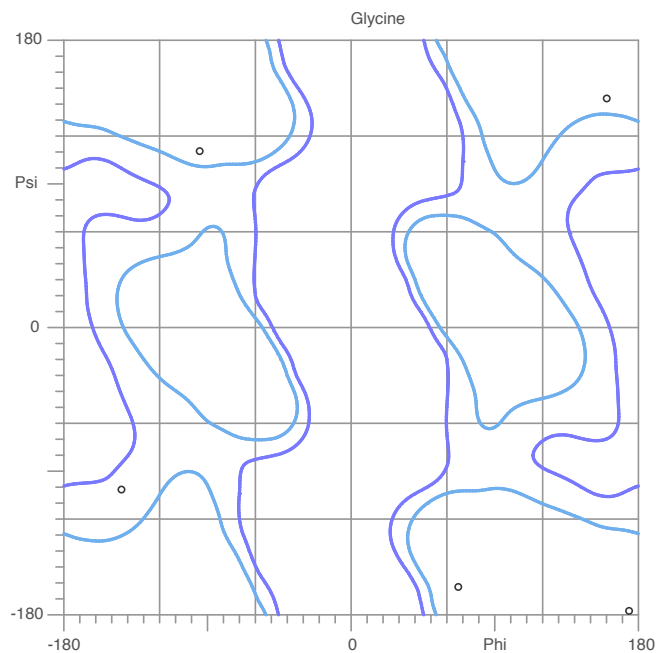
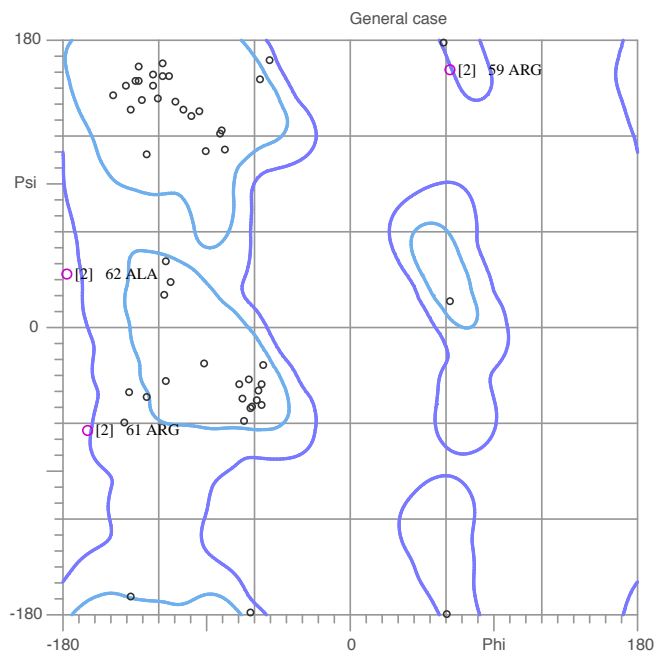
There were 2 outliers (phi, psi):

[1] 18 GLY (-155,6, -38,8)

[1] 57 CYS (-60,5, -169,4)

MolProbity Ramachandran analysis

2KSK.pdb, model 2



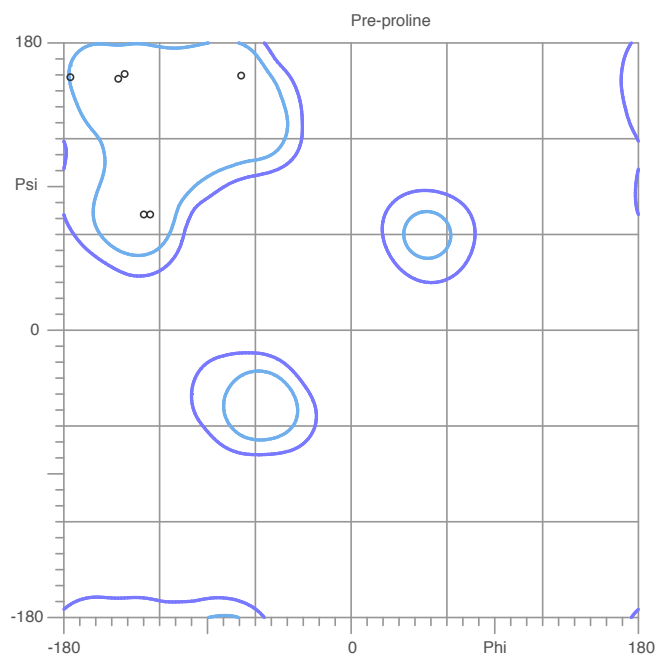
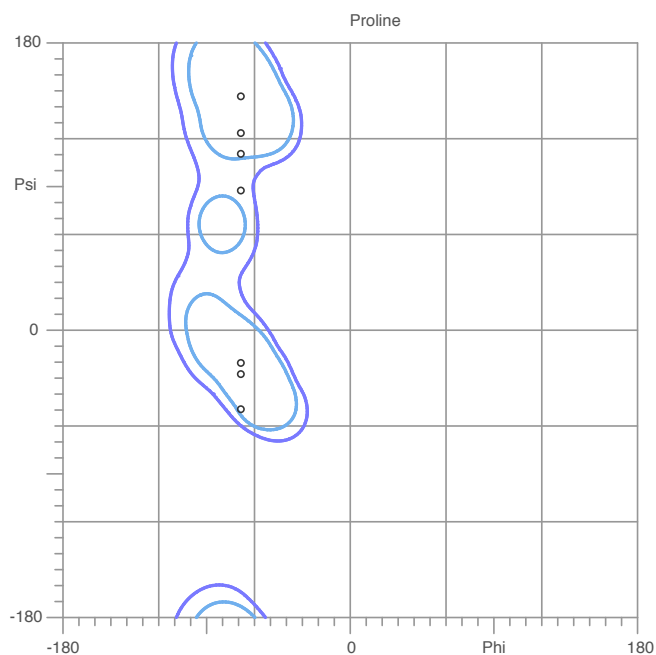
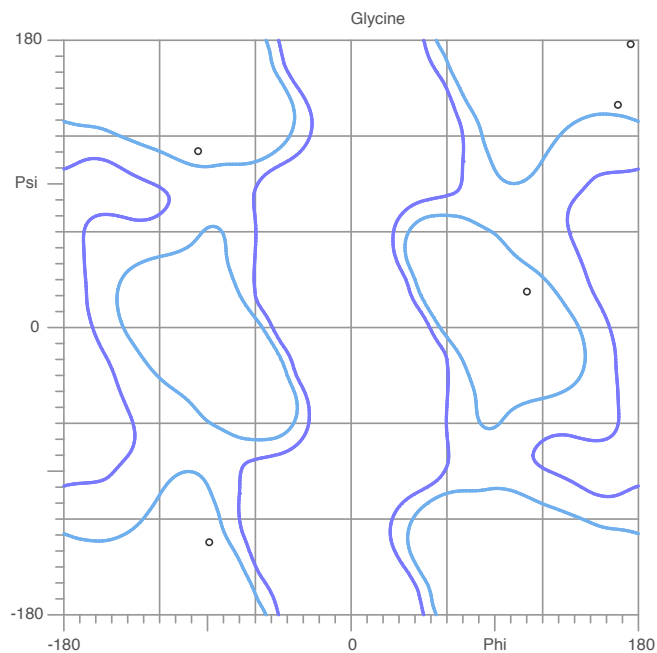
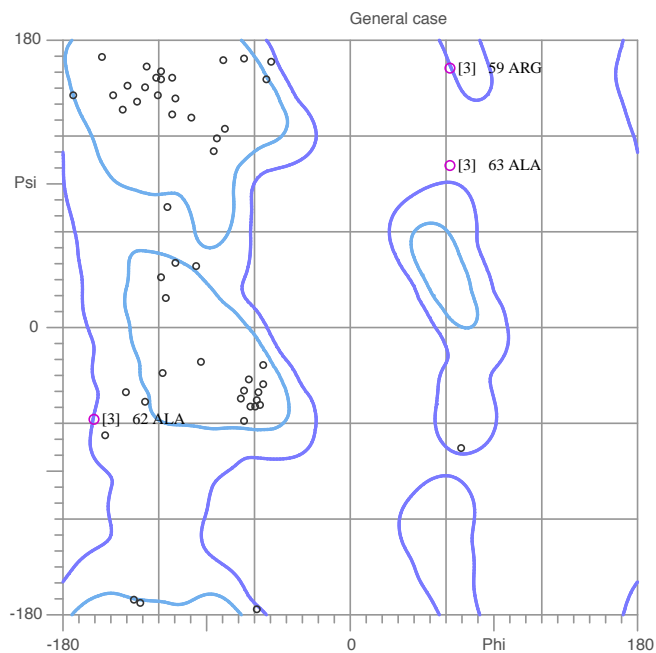
81,2% (56/69) of all residues were in favored (98%) regions.
95,7% (66/69) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 59 ARG (63,0, 162,7)
- [2] 61 ARG (-165,4, -64,1)
- [2] 62 ALA (-178,3, 34,8)

MolProbity Ramachandran analysis

2KSK.pdb, model 3



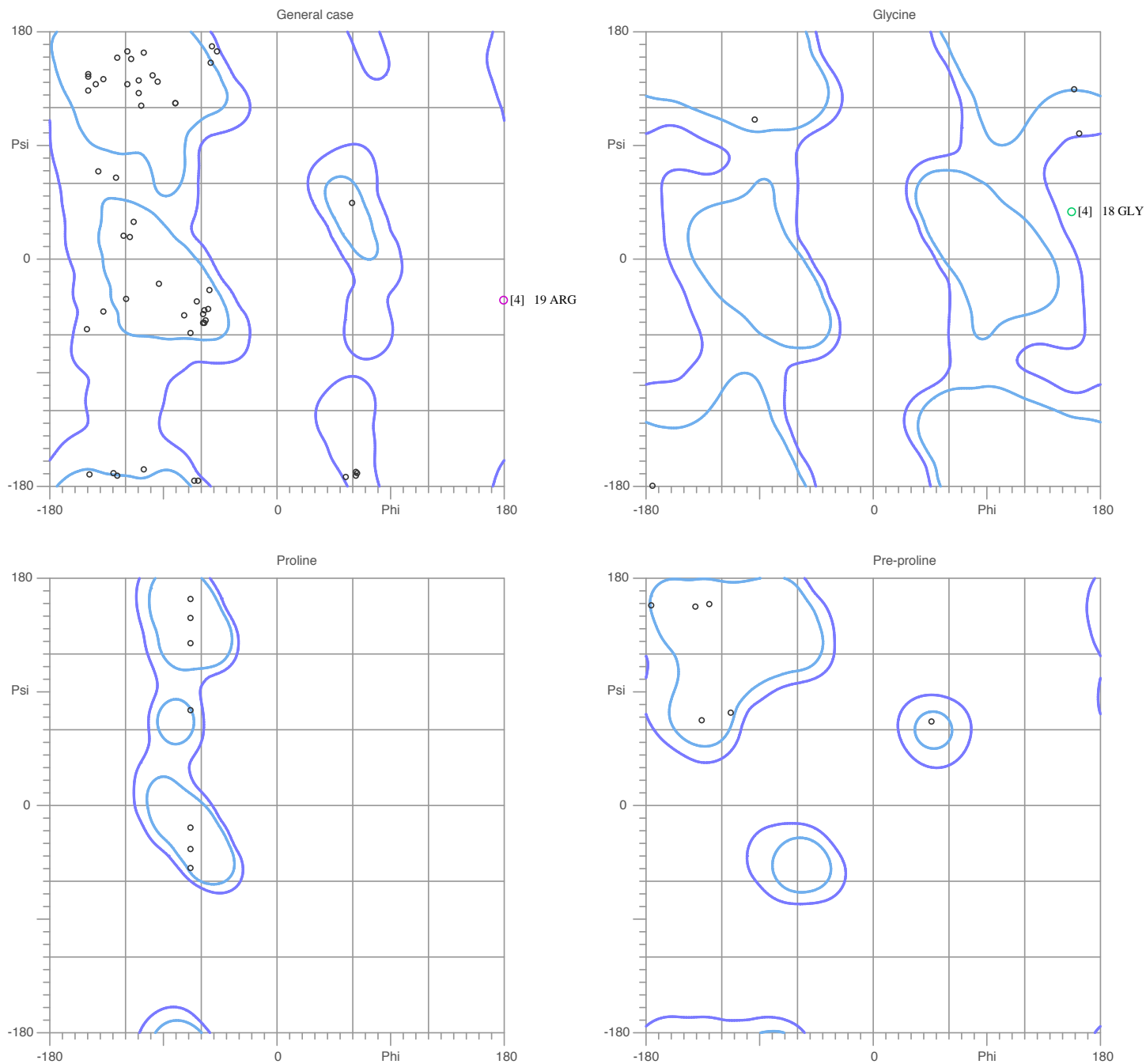
79,7% (55/69) of all residues were in favored (98%) regions.
95,7% (66/69) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 59 ARG (62,5, 163,8)
- [3] 62 ALA (-161,2, -57,7)
- [3] 63 ALA (63,0, 102,7)

MolProbity Ramachandran analysis

2KSK.pdb, model 4



75,4% (52/69) of all residues were in favored (98%) regions.
97,1% (67/69) of all residues were in allowed (>99.8%) regions.

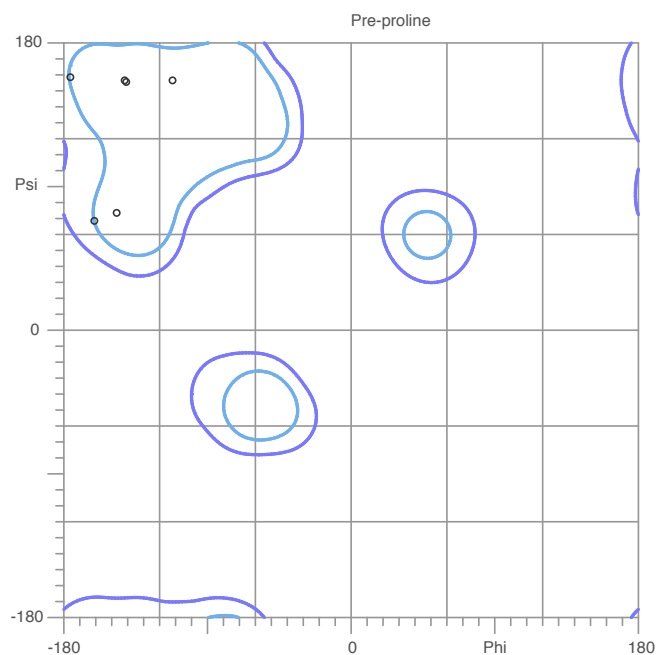
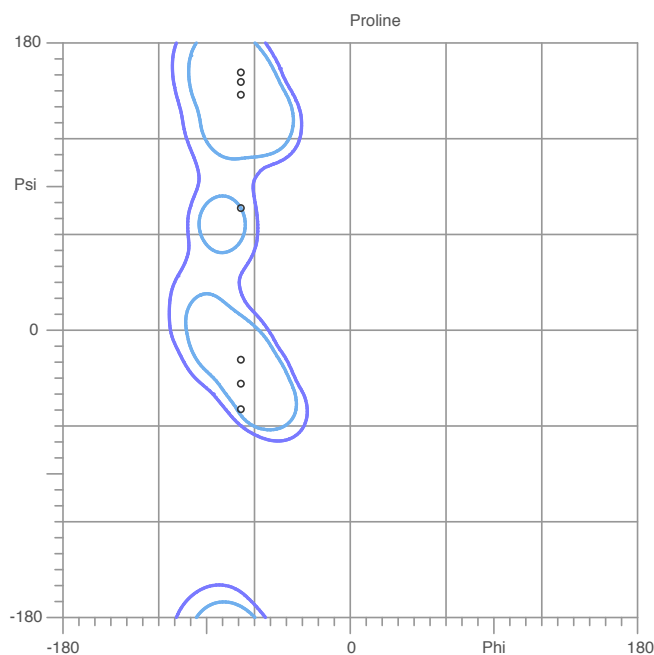
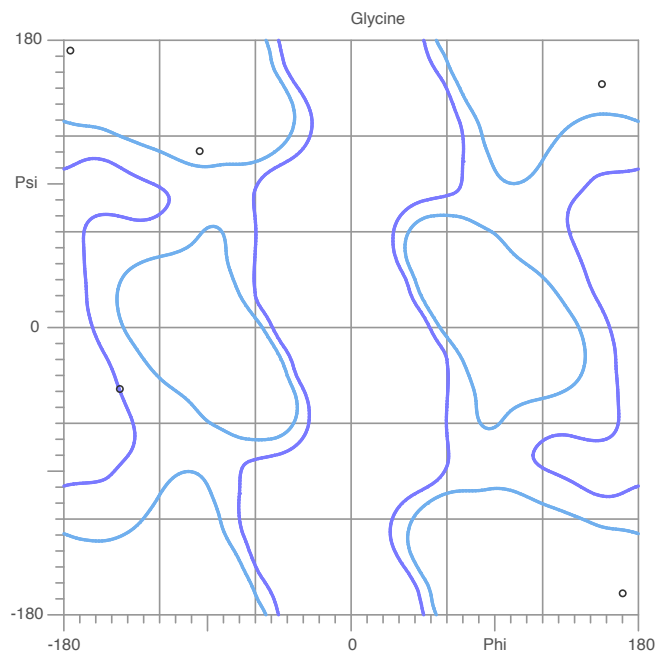
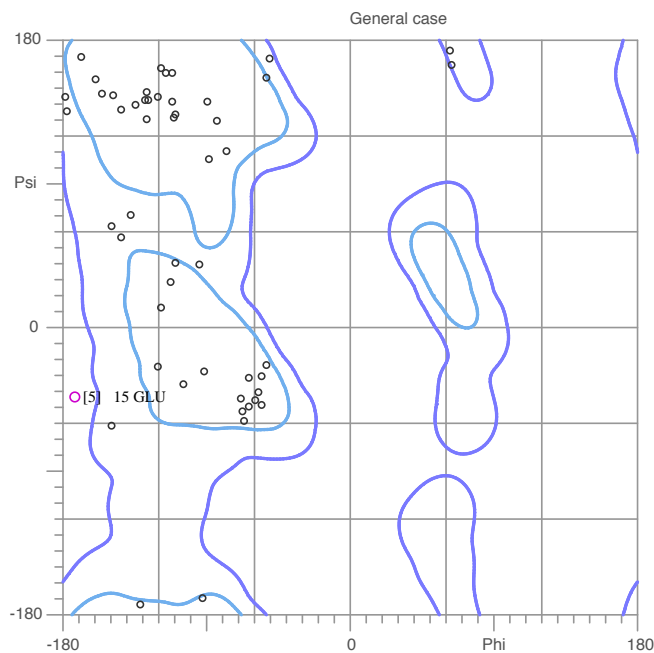
There were 2 outliers (phi, psi):

[4] 18 GLY (157,3, 38,6)

[4] 19 ARG (179,3, -32,9)

MolProbity Ramachandran analysis

2KSK.pdb, model 5



82,6% (57/69) of all residues were in favored (98%) regions.
98,6% (68/69) of all residues were in allowed (>99.8%) regions.

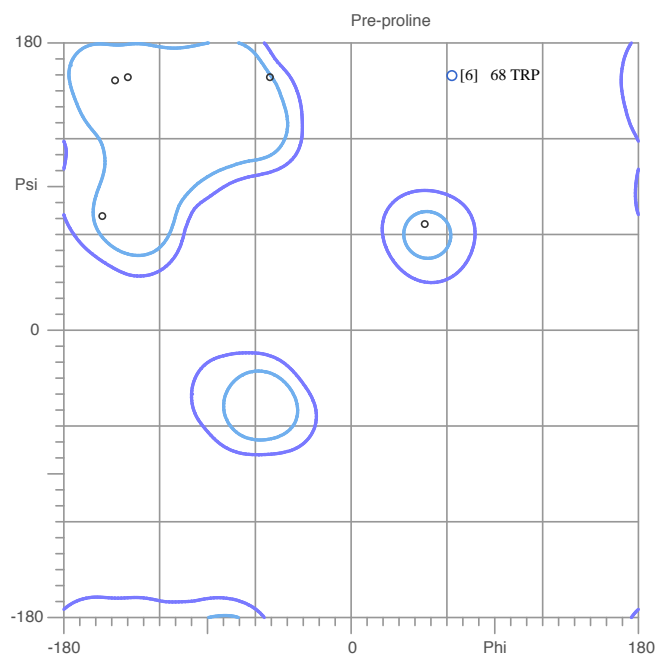
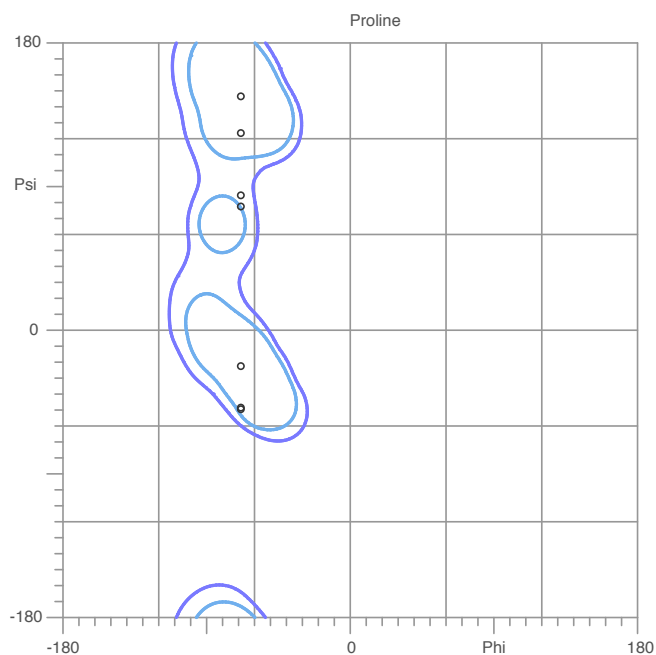
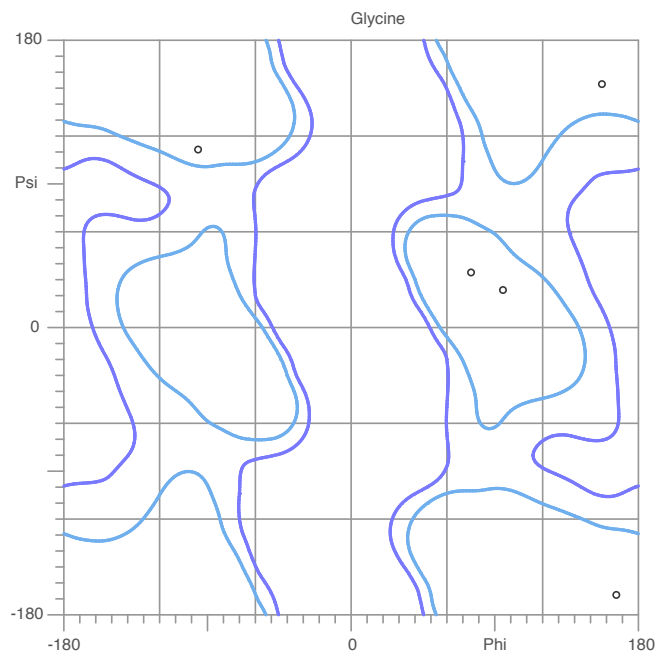
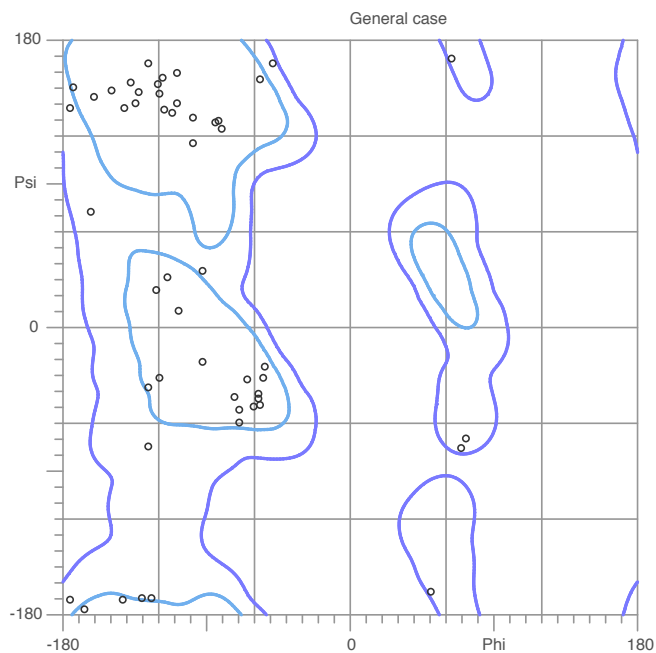
There were 1 outliers (phi, psi):
[5] 15 GLU (-174,0, -44,0)

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MolProbity Ramachandran analysis

2KSK.pdb, model 6



78,3% (54/69) of all residues were in favored (98%) regions.
98,6% (68/69) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

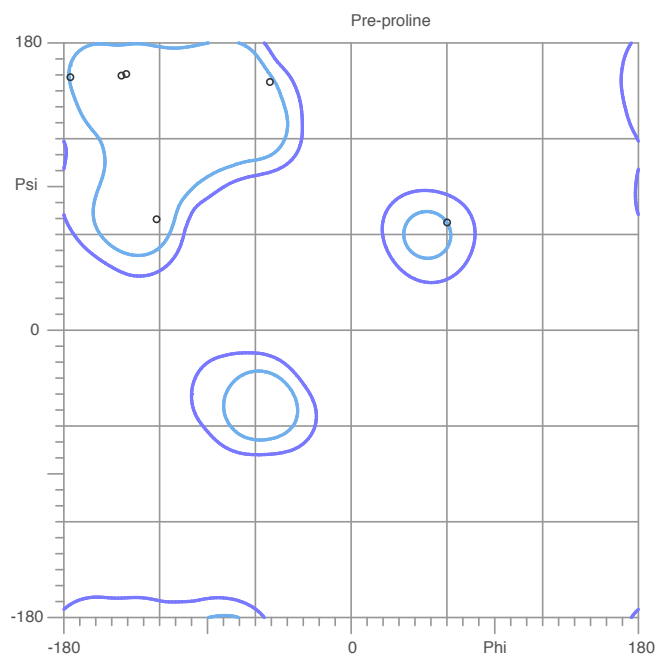
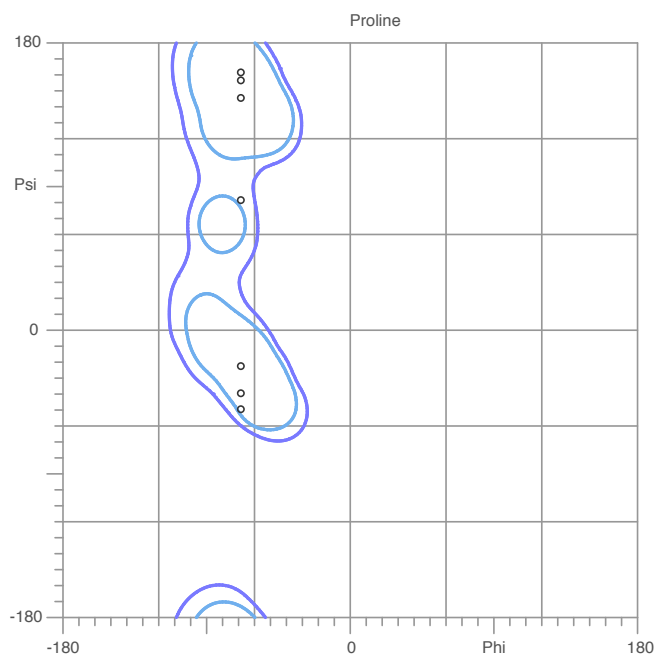
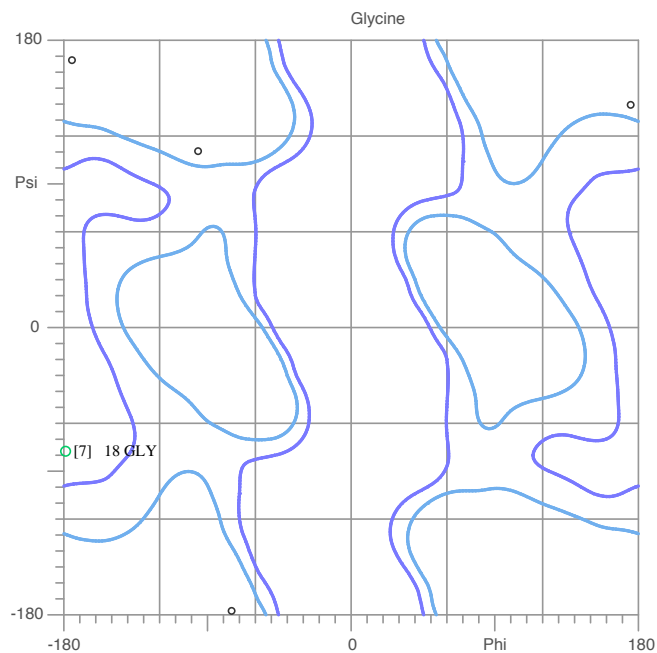
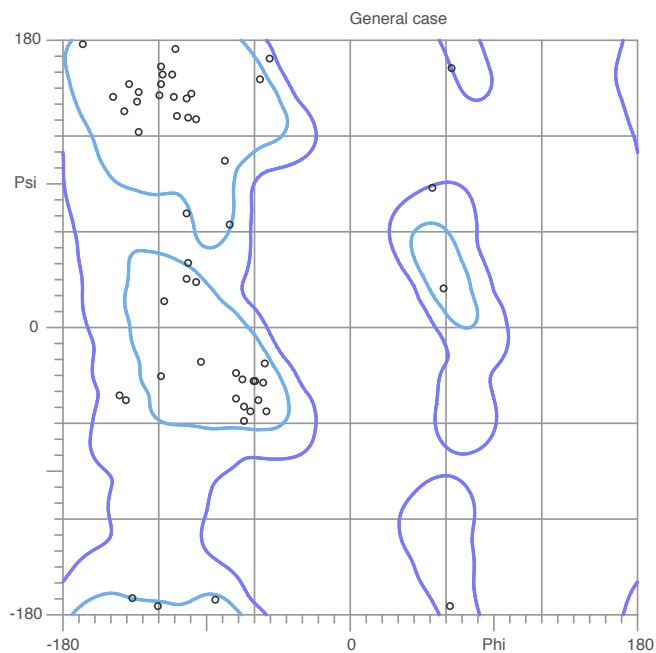
[6] 68 TRP (63,2, 160,6)

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MolProbity Ramachandran analysis

2KSK.pdb, model 7



82,6% (57/69) of all residues were in favored (98%) regions.
98,6% (68/69) of all residues were in allowed (>99.8%) regions.

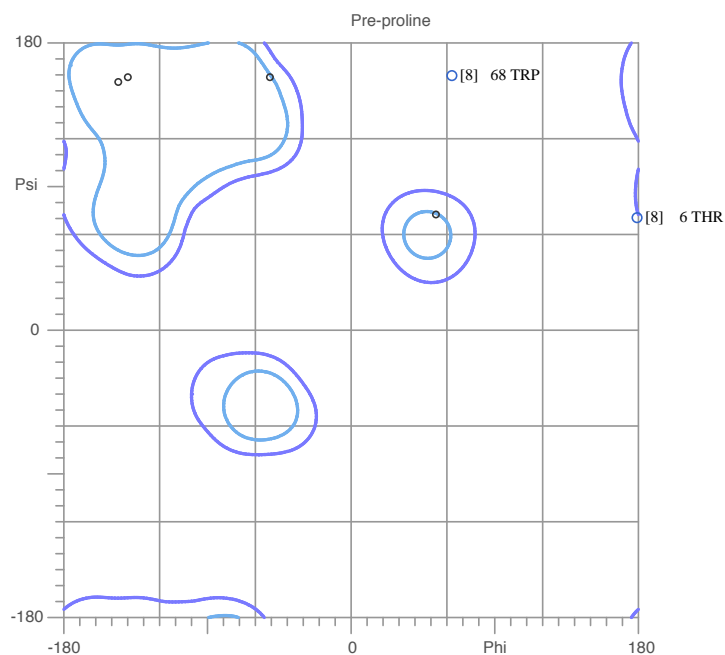
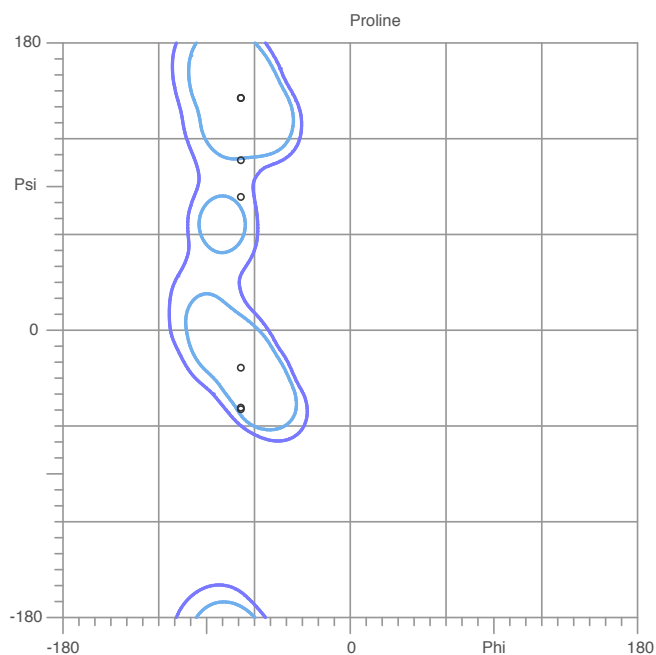
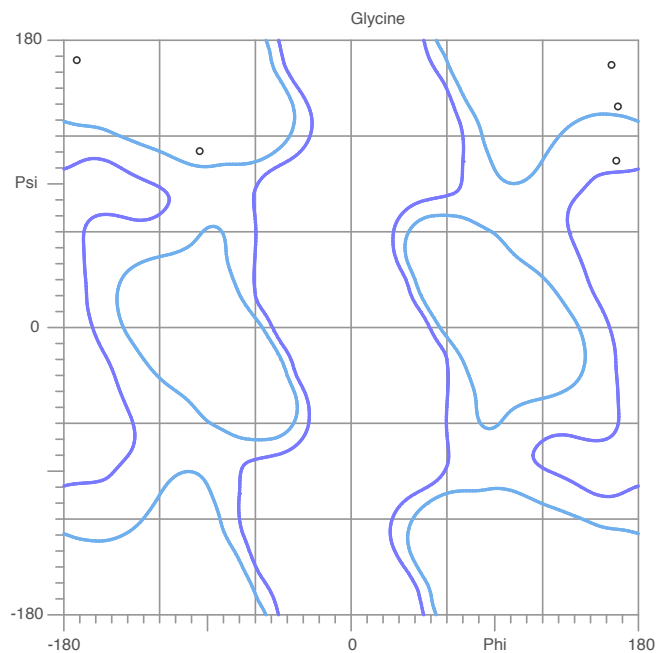
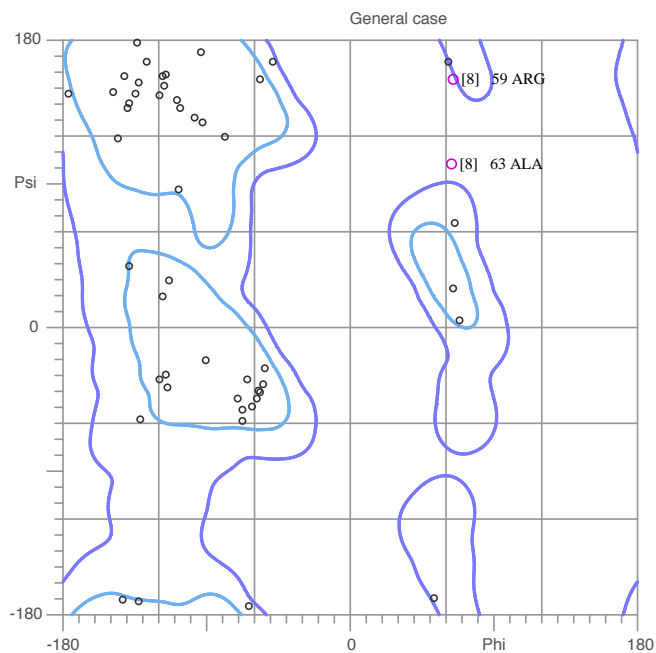
There were 1 outliers (phi, psi):
[7] 18 GLY (-179,3, -77,9)

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MolProbity Ramachandran analysis

2KSK.pdb, model 8



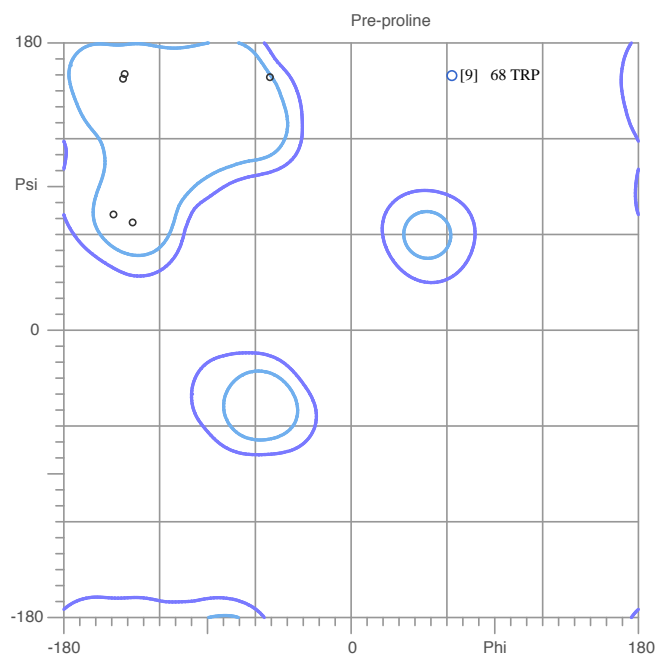
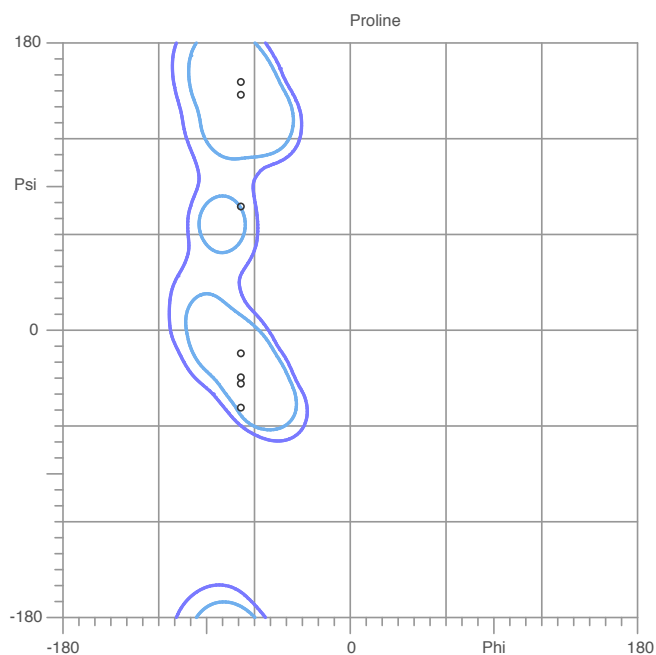
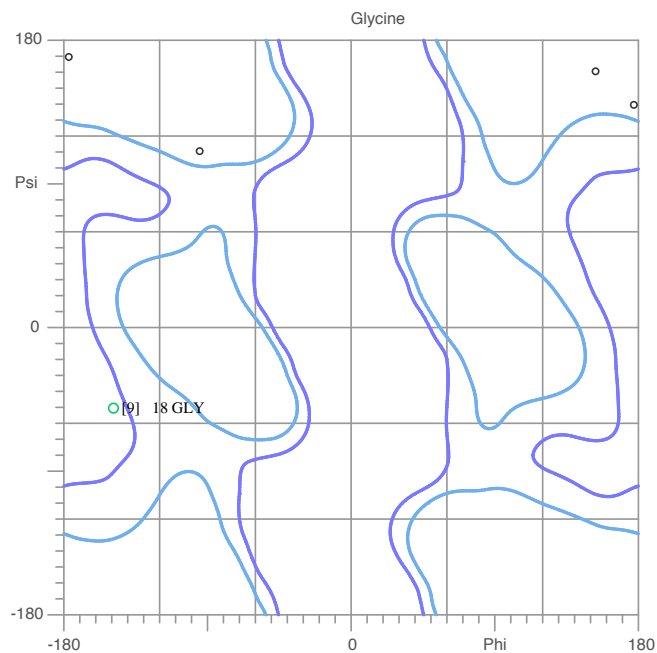
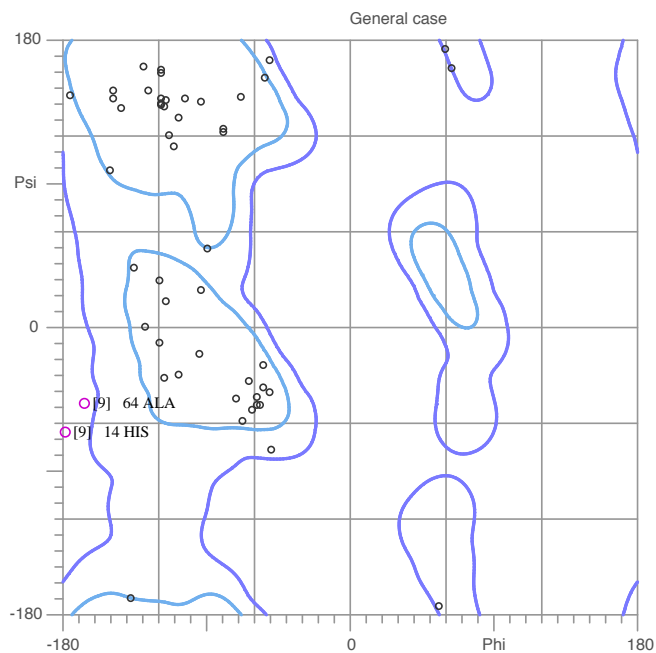
76,8% (53/69) of all residues were in favored (98%) regions.
94,2% (65/69) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [8] 6 THR (179,6, 71,4)
- [8] 59 ARG (64,3, 156,3)
- [8] 63 ALA (63,3, 103,2)
- [8] 68 TRP (63,2, 160,6)

MolProbity Ramachandran analysis

2KSK.pdb, model 9



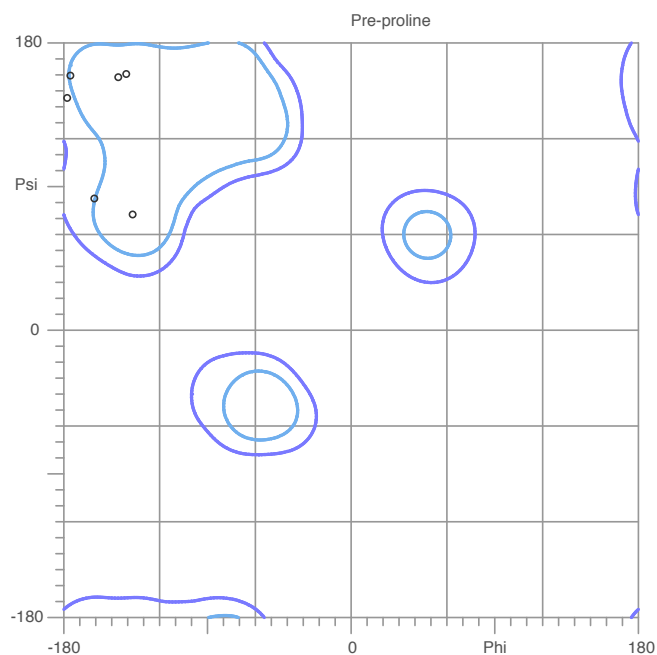
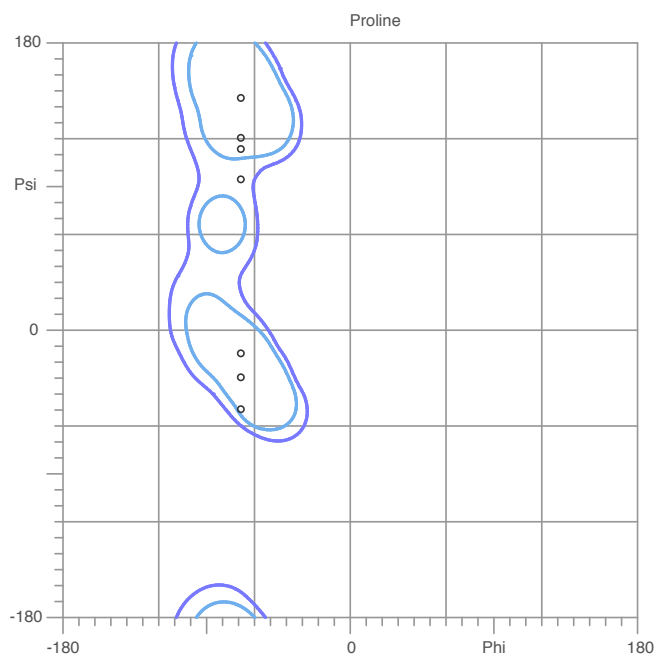
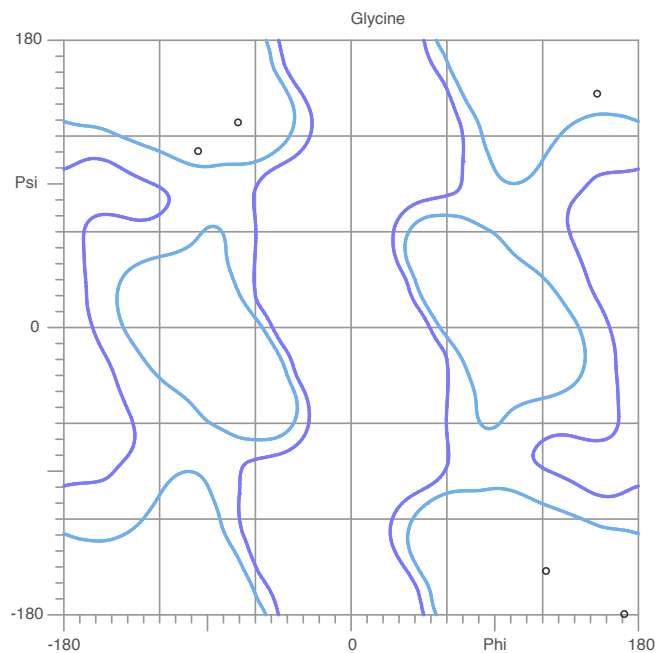
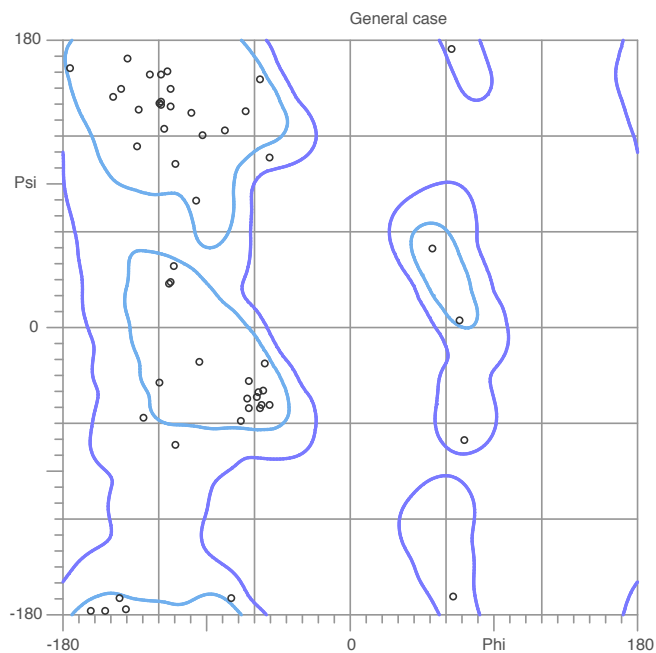
84,1% (58/69) of all residues were in favored (98%) regions.
94,2% (65/69) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [9] 14 HIS (-179,4, -65,2)
- [9] 18 GLY (-149,5, -50,3)
- [9] 64 ALA (-167,1, -47,1)
- [9] 68 TRP (63,3, 160,6)

MolProbity Ramachandran analysis

2KSK.pdb, model 10



85,5% (59/69) of all residues were in favored (98%) regions.
100,0% (69/69) of all residues were in allowed (>99.8%) regions.

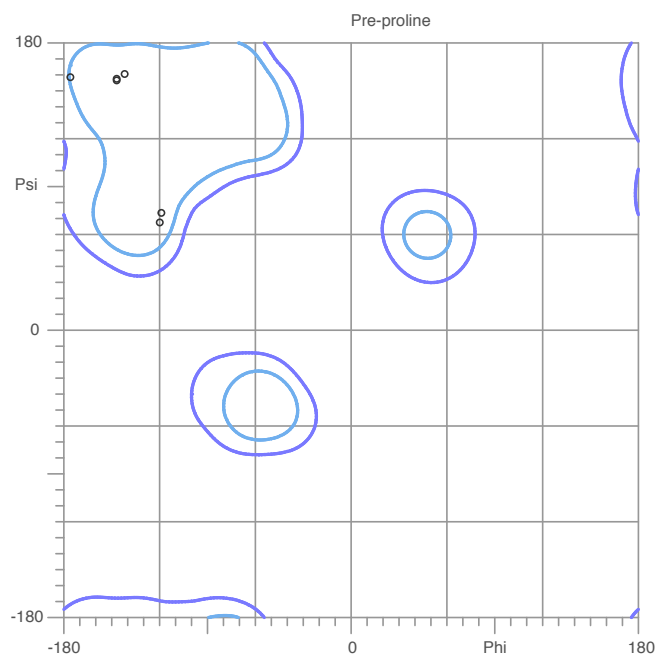
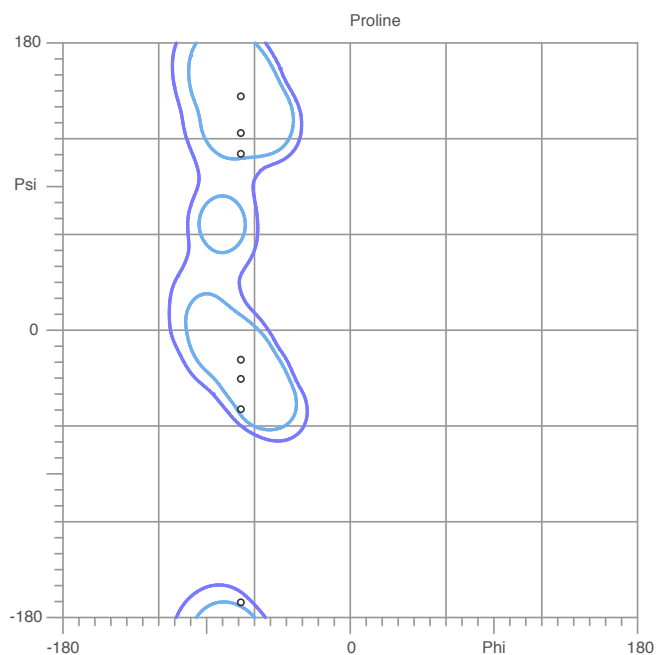
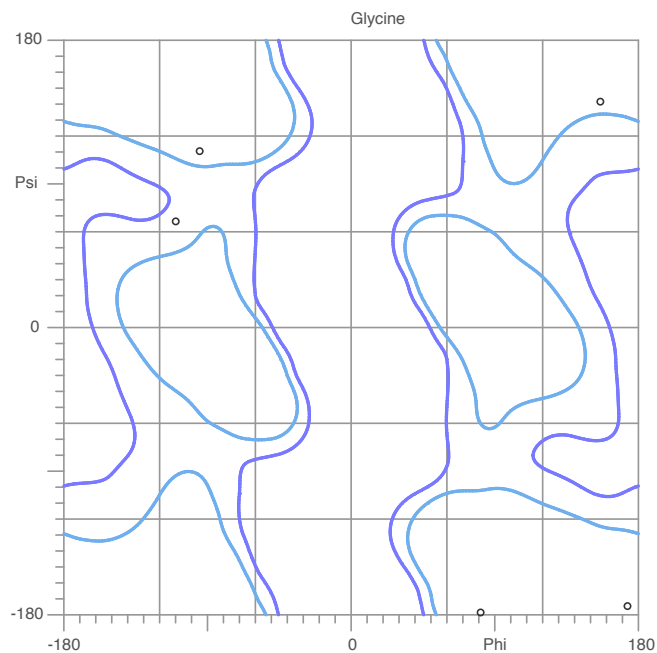
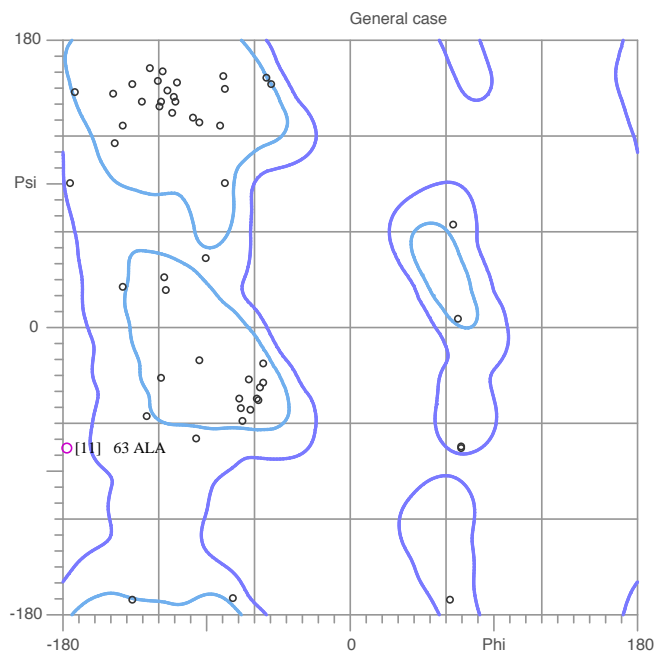
There were no outliers.

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MolProbity Ramachandran analysis

2KSK.pdb, model 11



81,2% (56/69) of all residues were in favored (98%) regions.
98,6% (68/69) of all residues were in allowed (>99.8%) regions.

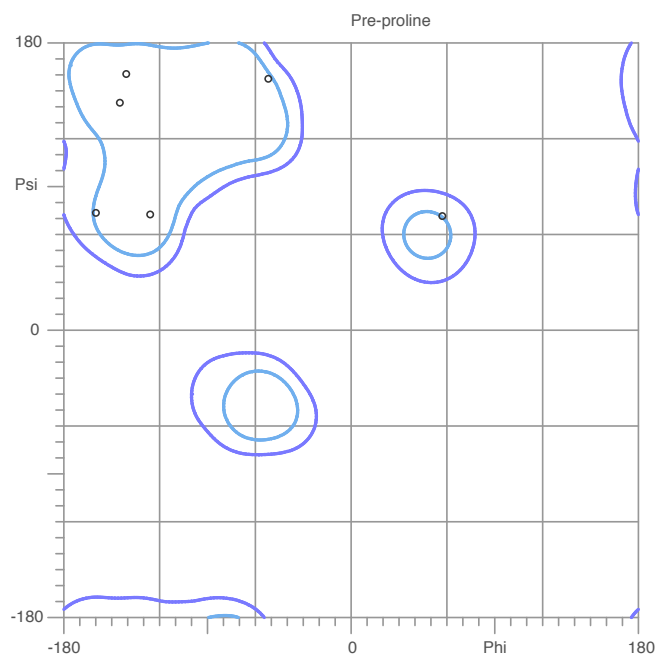
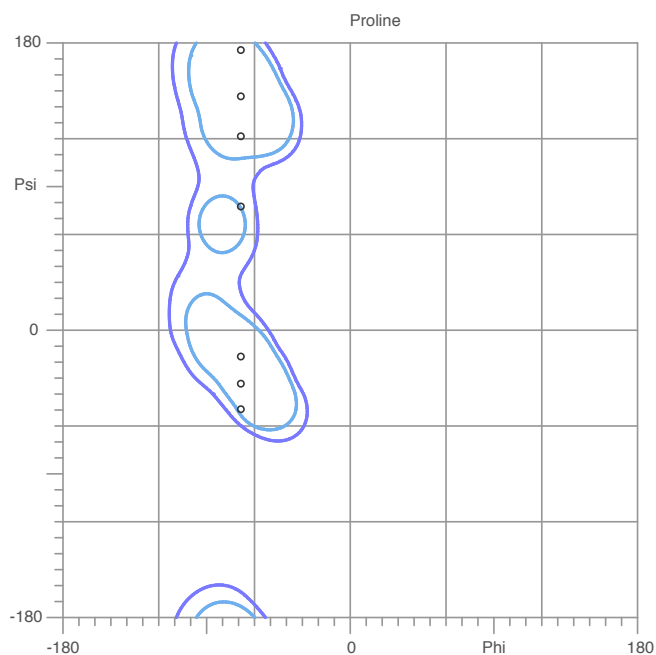
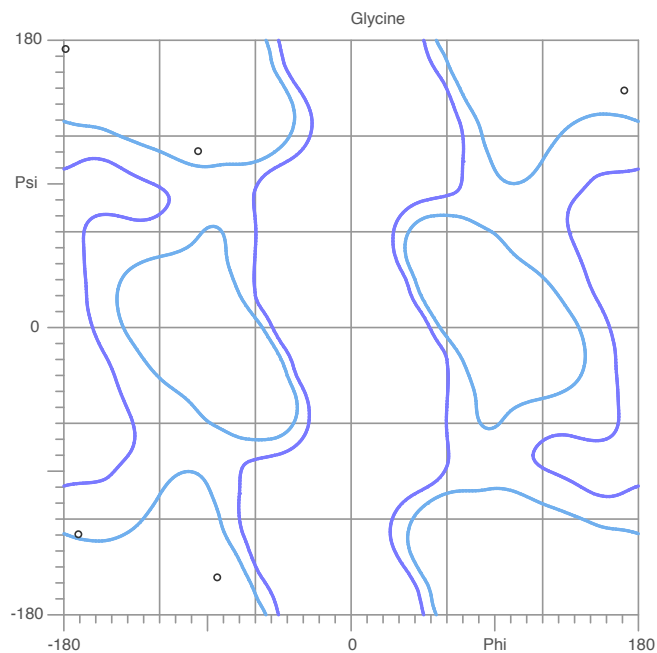
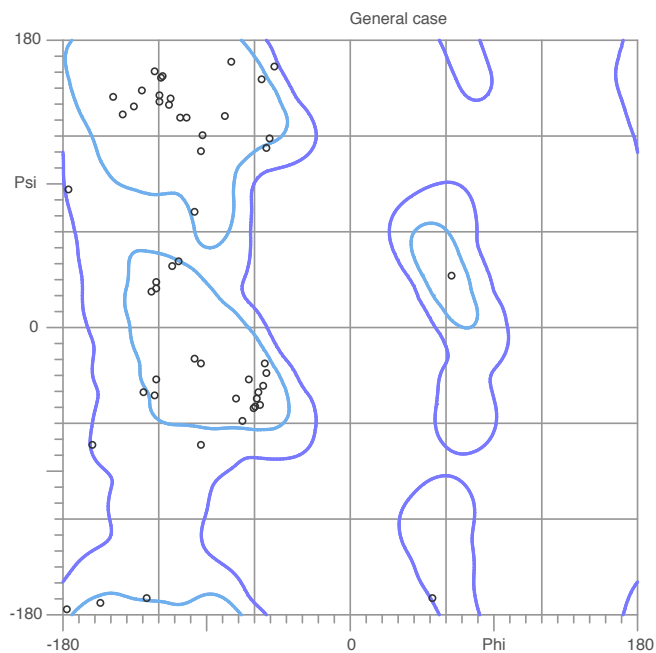
There were 1 outliers (phi, psi):
[11] 63 ALA (-178,2, -75,4)

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MolProbity Ramachandran analysis

2KSK.pdb, model 12



81,2% (56/69) of all residues were in favored (98%) regions.
100,0% (69/69) of all residues were in allowed (>99.8%) regions.

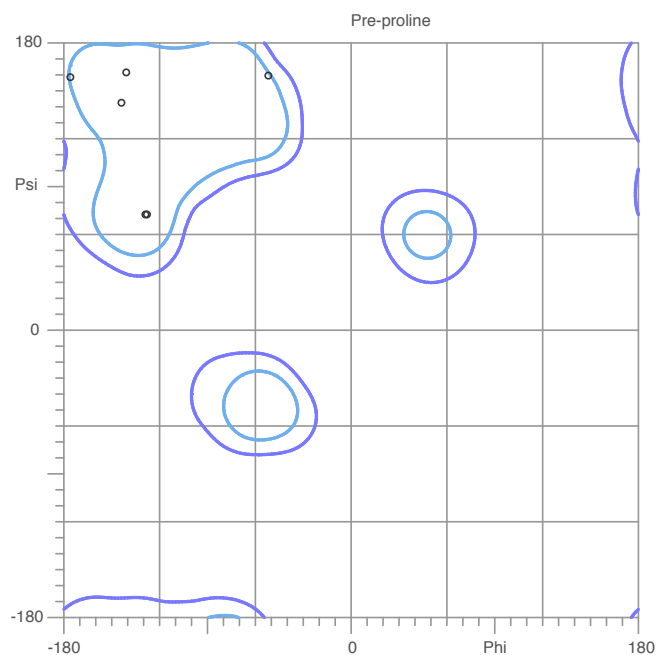
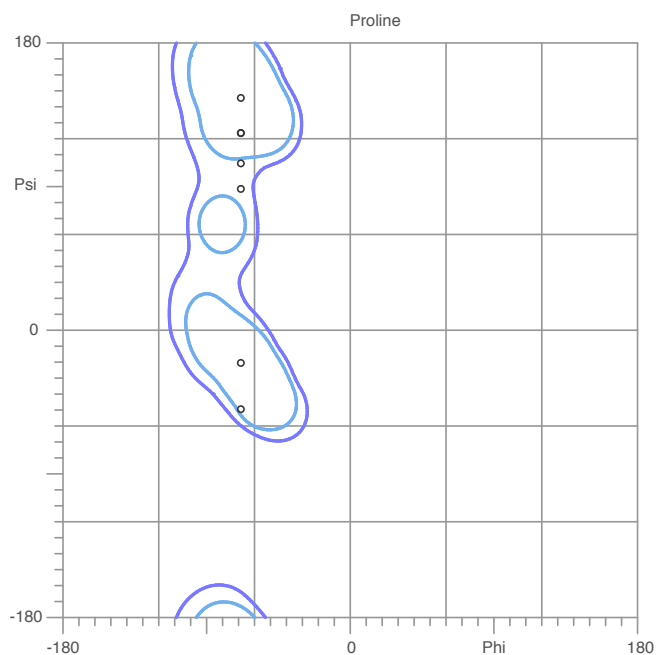
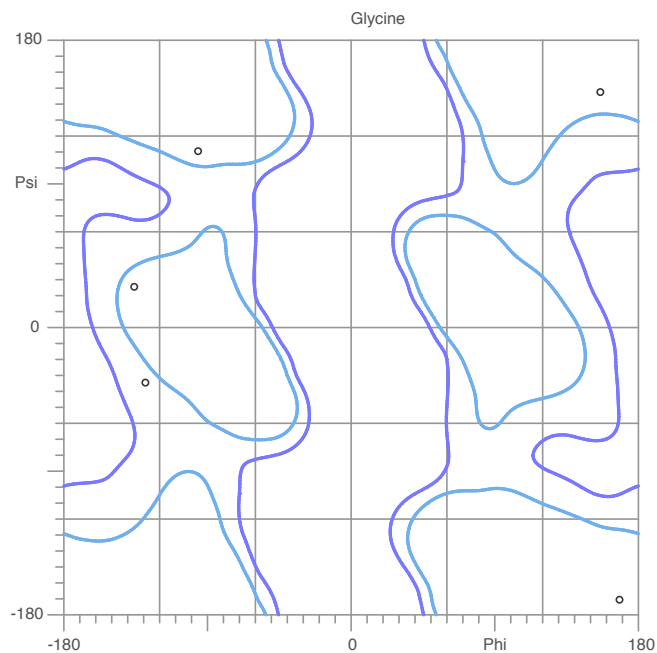
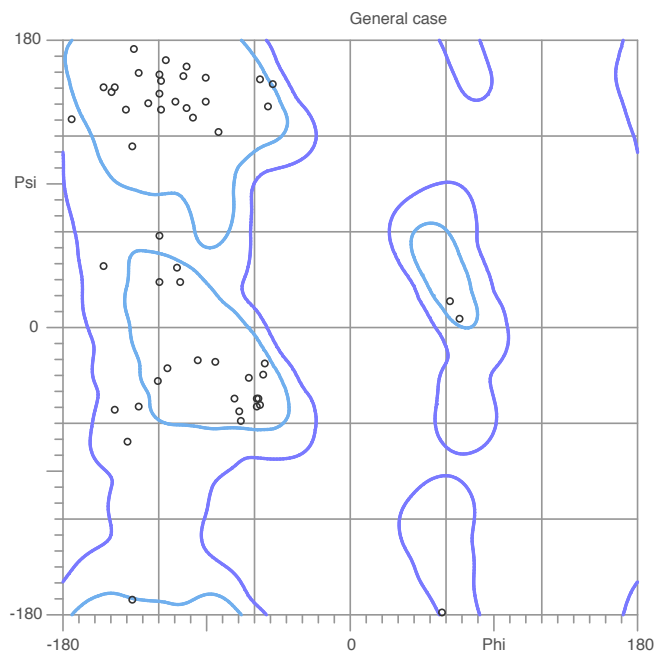
There were no outliers.

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MolProbity Ramachandran analysis

2KSK.pdb, model 13



82,6% (57/69) of all residues were in favored (98%) regions.
100,0% (69/69) of all residues were in allowed (>99.8%) regions.

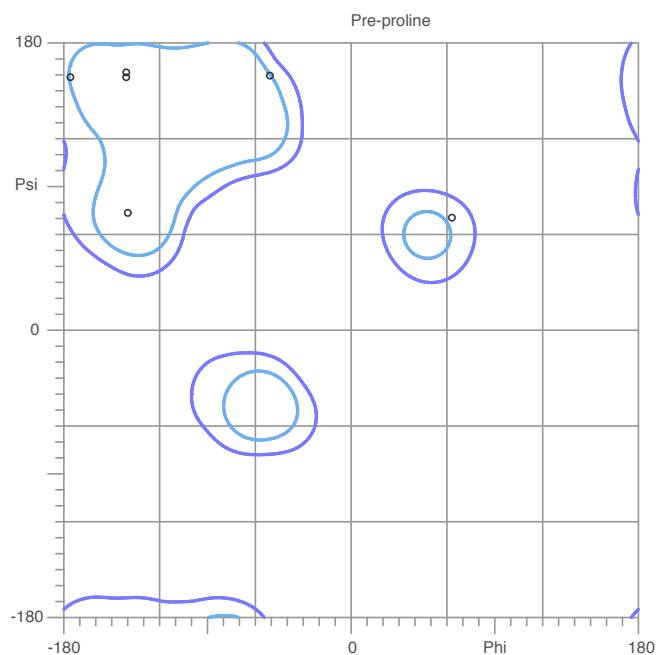
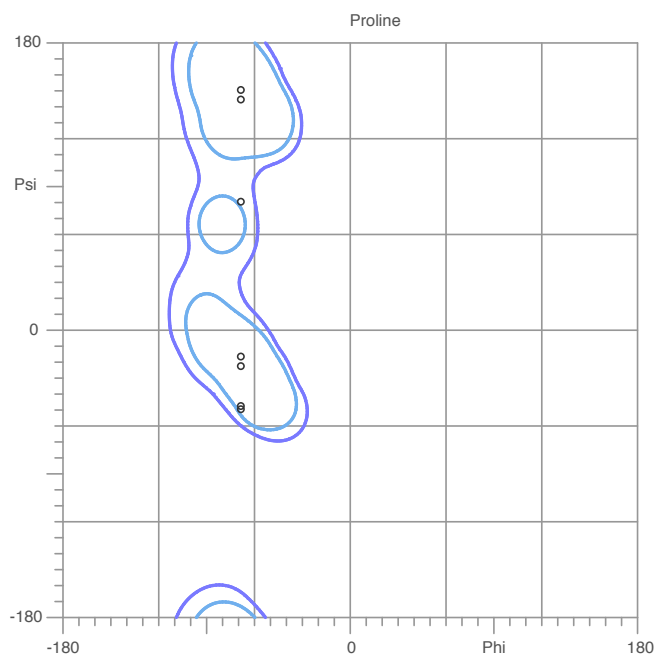
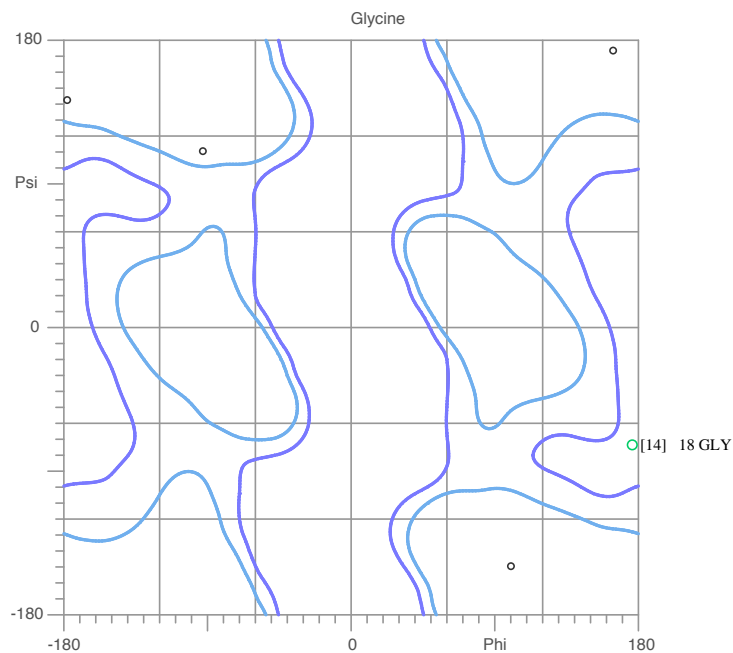
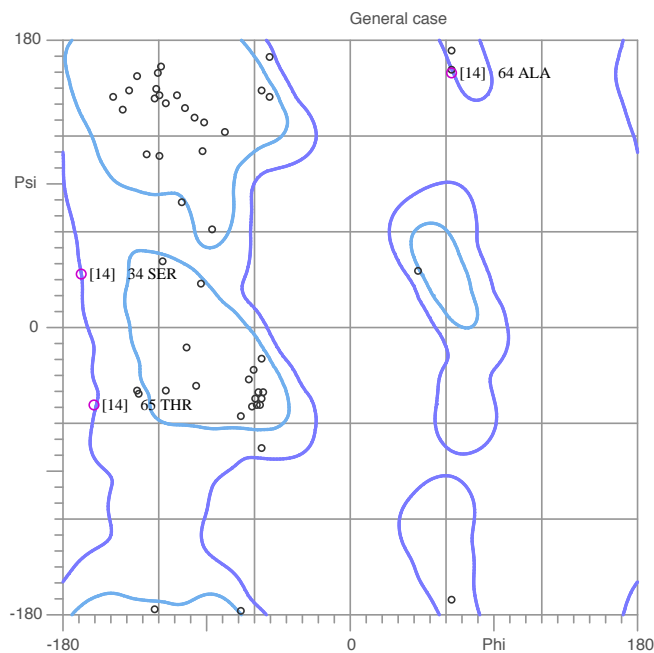
There were no outliers.

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MolProbity Ramachandran analysis

2KSK.pdb, model 14



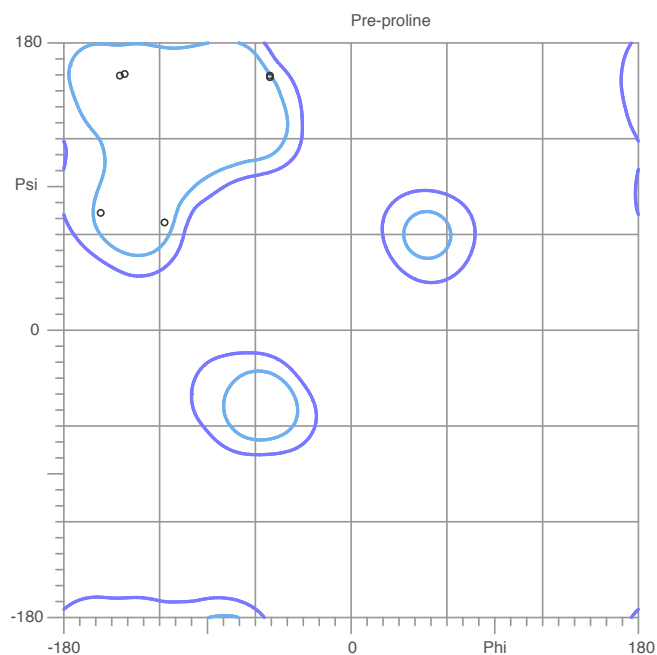
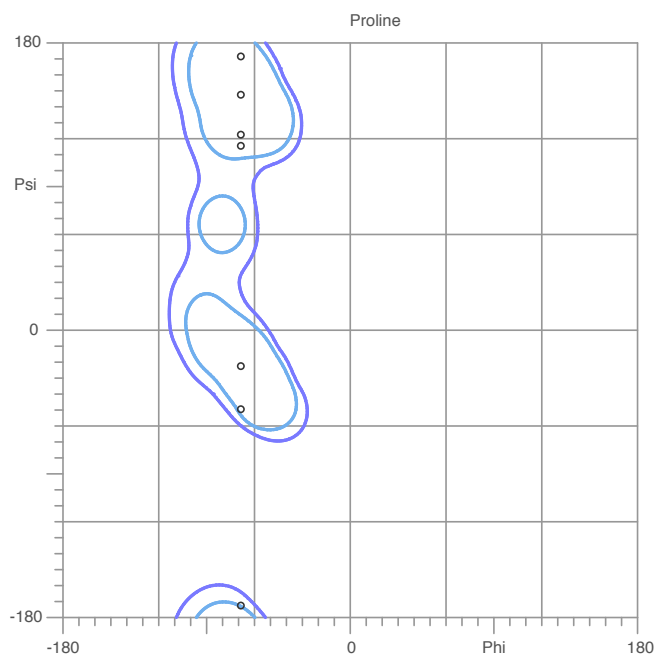
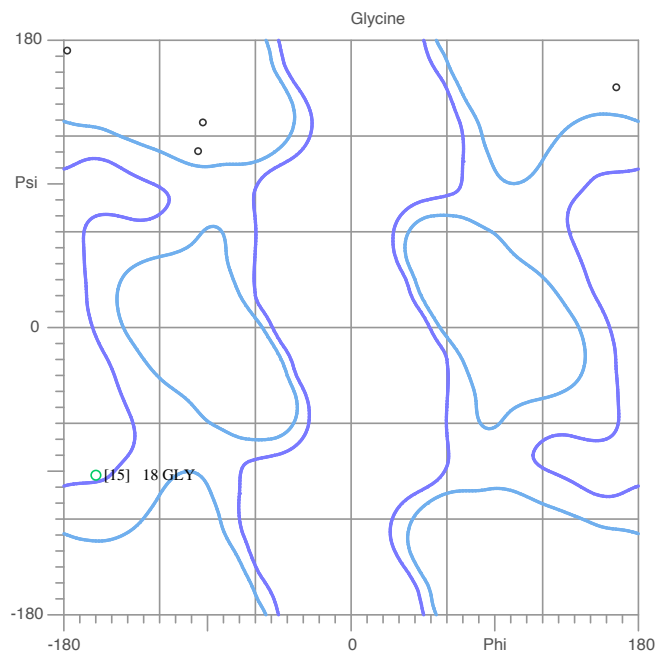
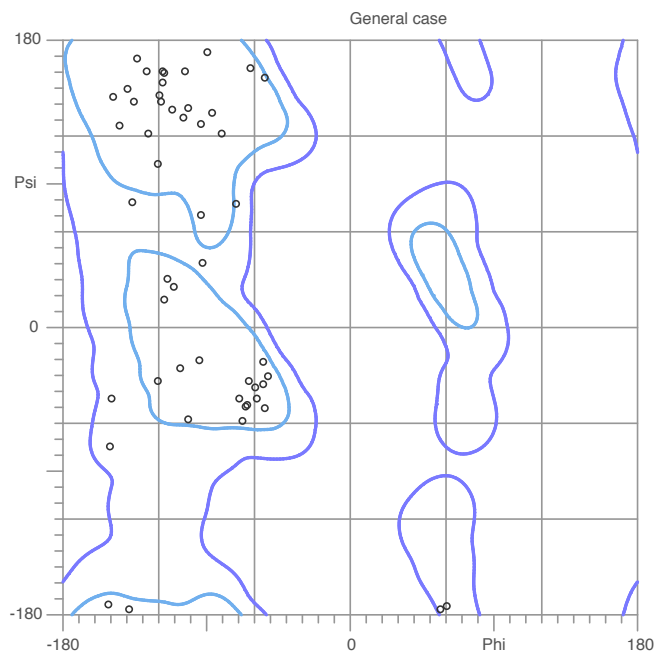
75,4% (52/69) of all residues were in favored (98%) regions.
94,2% (65/69) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [14] 18 GLY (176,9, -73,6)
- [14] 34 SER (-169,5, 34,9)
- [14] 64 ALA (63,7, 160,2)
- [14] 65 THR (-161,2, -48,6)

MolProbity Ramachandran analysis

2KSK.pdb, model 15



88,4% (61/69) of all residues were in favored (98%) regions.
98,6% (68/69) of all residues were in allowed (>99.8%) regions.

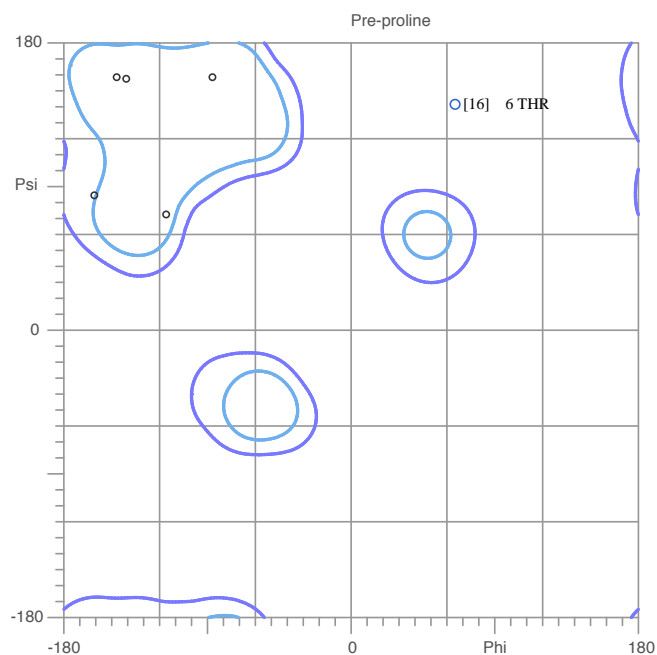
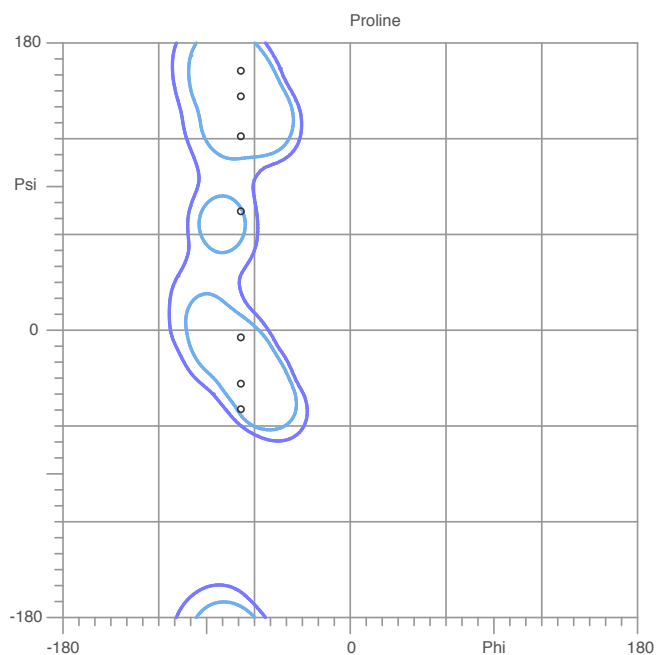
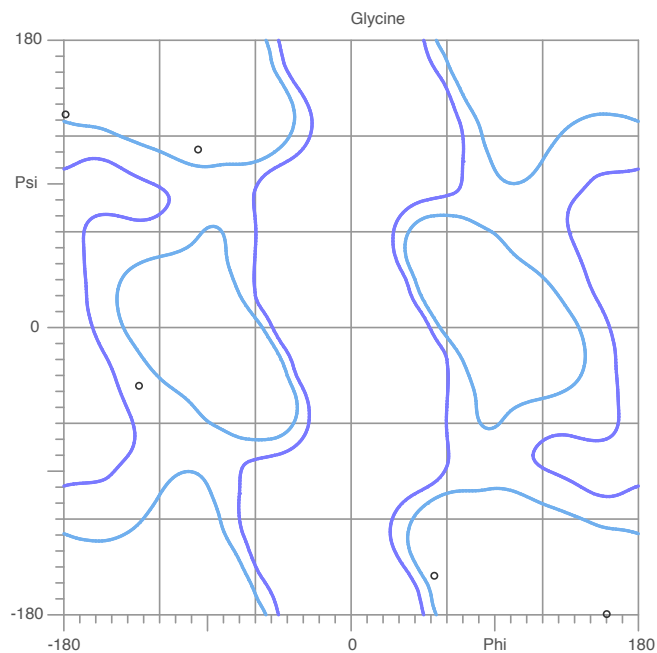
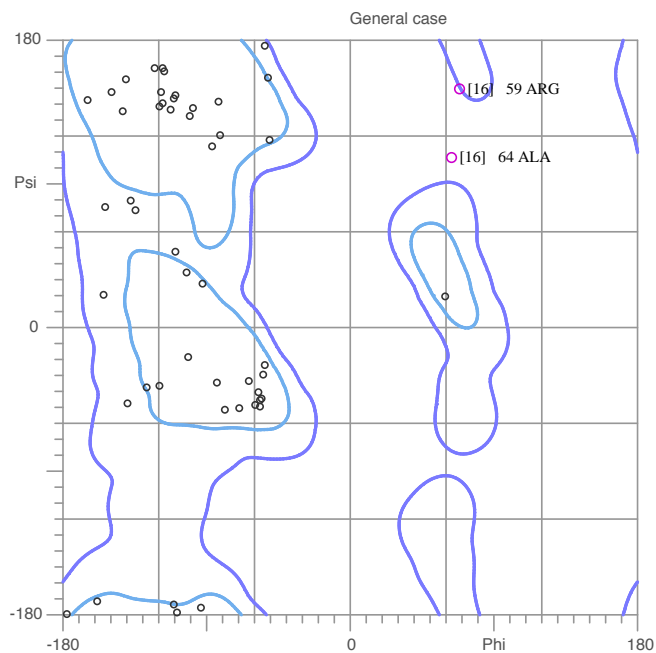
There were 1 outliers (phi, psi):
[15] 18 GLY (-160,3, -92,6)

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MolProbity Ramachandran analysis

2KSK.pdb, model 16



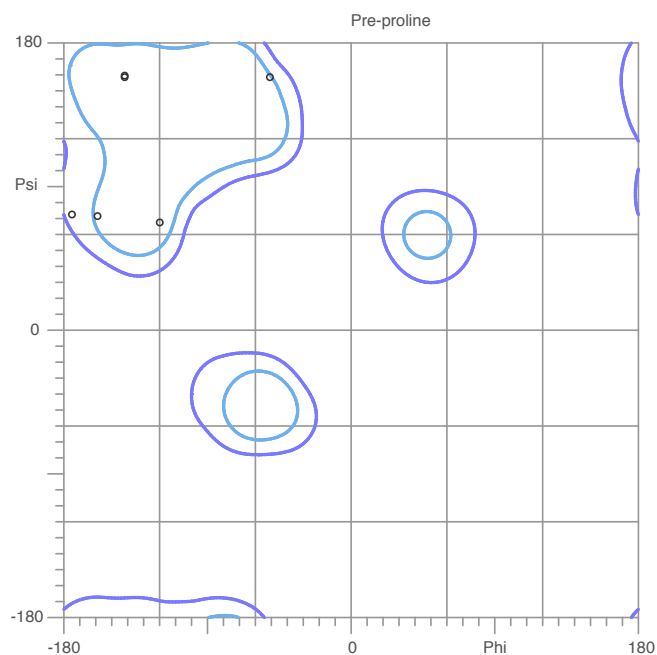
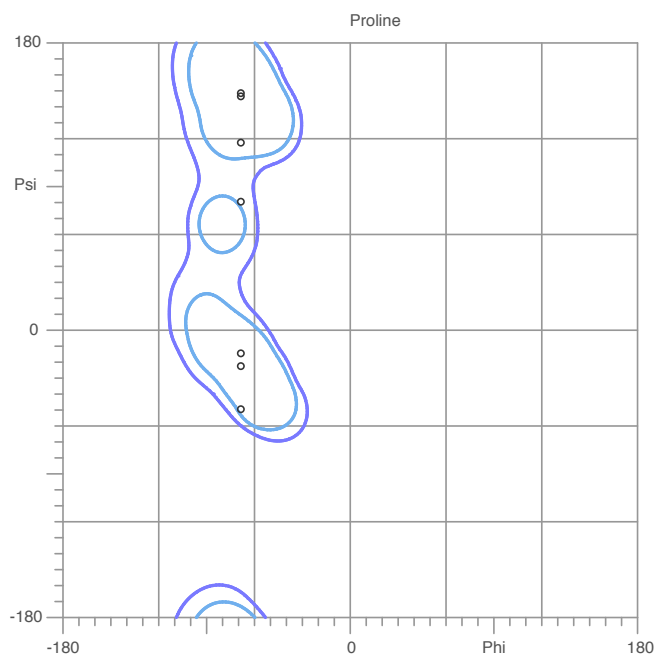
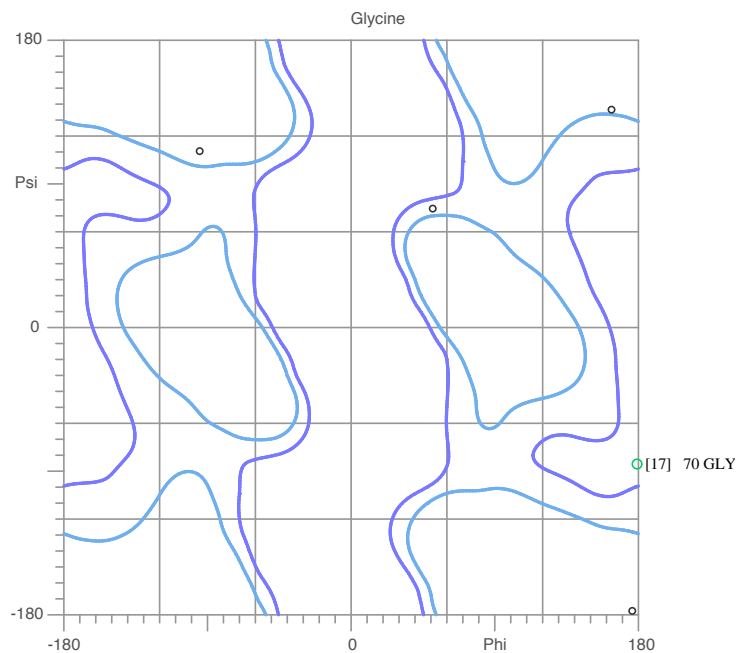
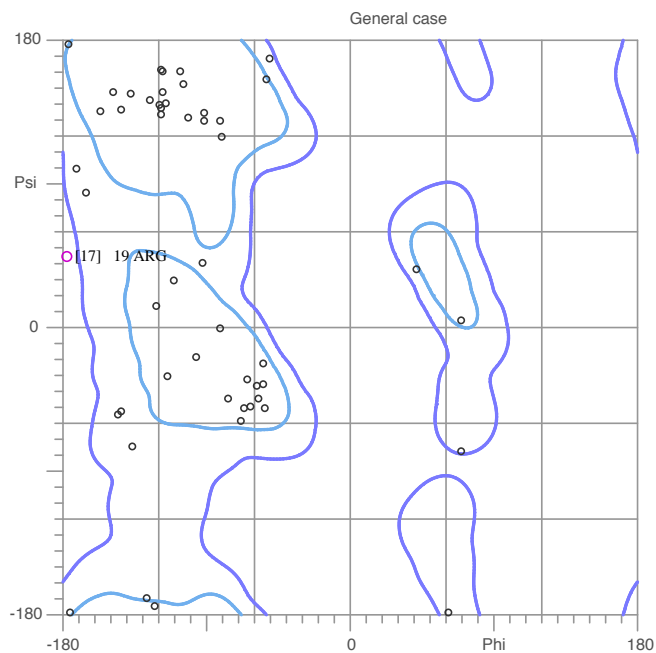
79,7% (55/69) of all residues were in favored (98%) regions.
95,7% (66/69) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [16] 6 THR (65,7, 142,3)
- [16] 59 ARG (68,2, 150,1)
- [16] 64 ALA (64,0, 107,5)

MolProbity Ramachandran analysis

2KSK.pdb, model 17



73,9% (51/69) of all residues were in favored (98%) regions.
97,1% (67/69) of all residues were in allowed (>99.8%) regions.

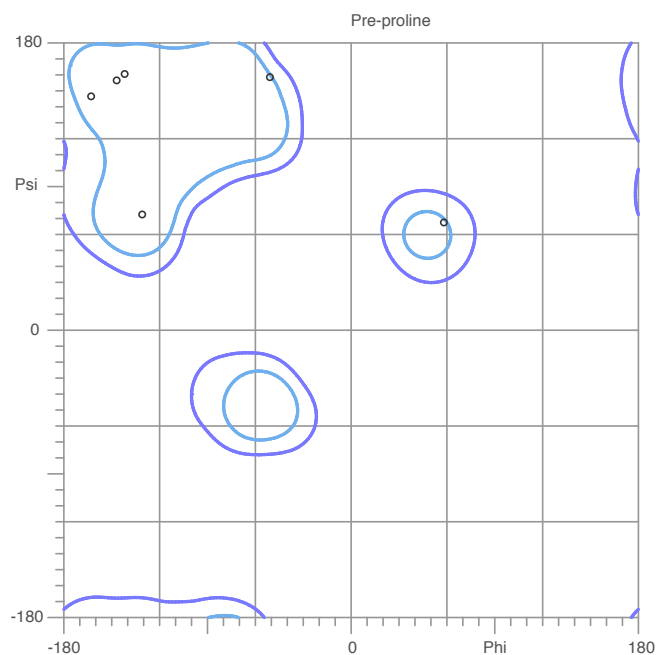
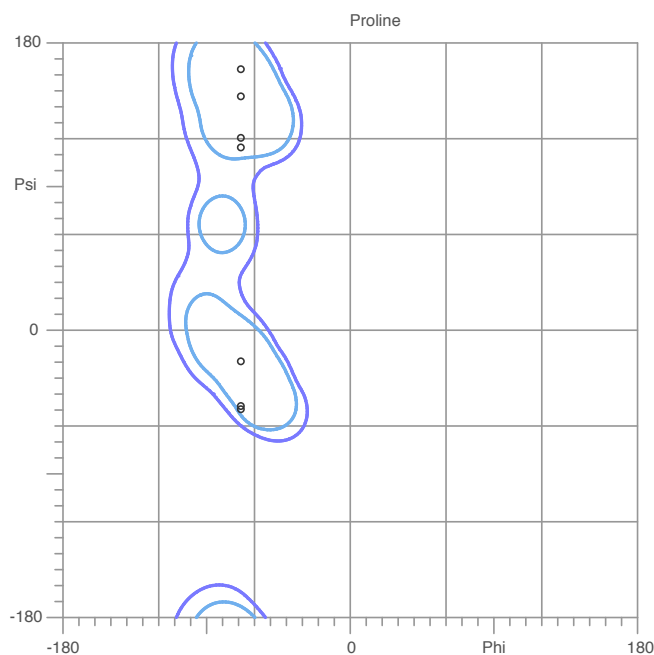
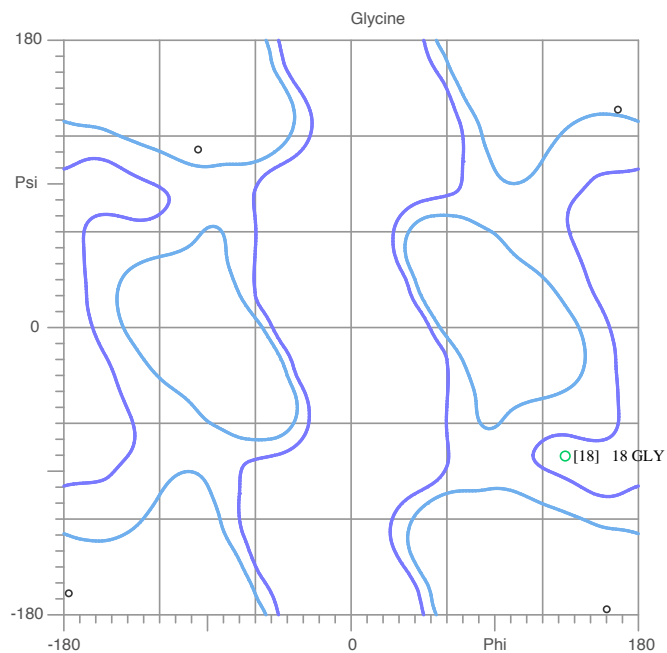
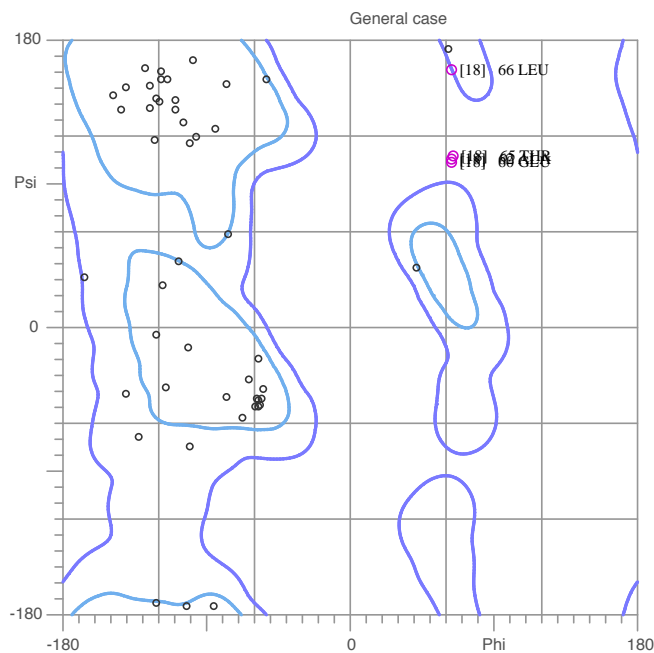
There were 2 outliers (phi, psi):

[17] 19 ARG (-178,3, 46,0)

[17] 70 GLY (179,6, -85,7)

MolProbity Ramachandran analysis

2KSK.pdb, model 18



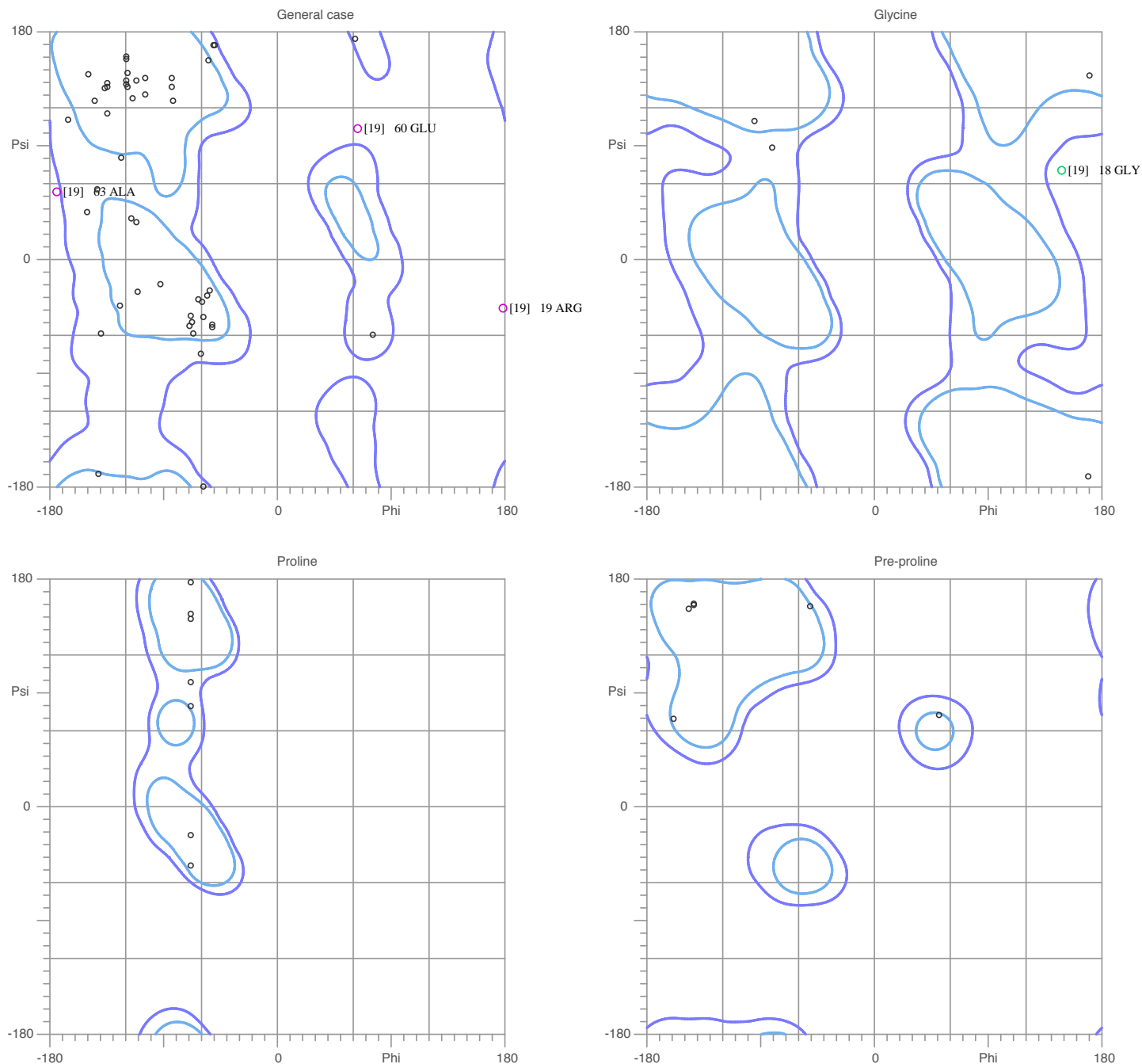
82,6% (57/69) of all residues were in favored (98%) regions.
92,8% (64/69) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[18] 18 GLY (134,7, -80,8)
[18] 60 GLU (63,2, 104,5)
[18] 62 ALA (63,8, 106,8)
[18] 65 THR (64,4, 108,3)
[18] 66 LEU (63,1, 162,8)

MolProbity Ramachandran analysis

2KSK.pdb, model 19



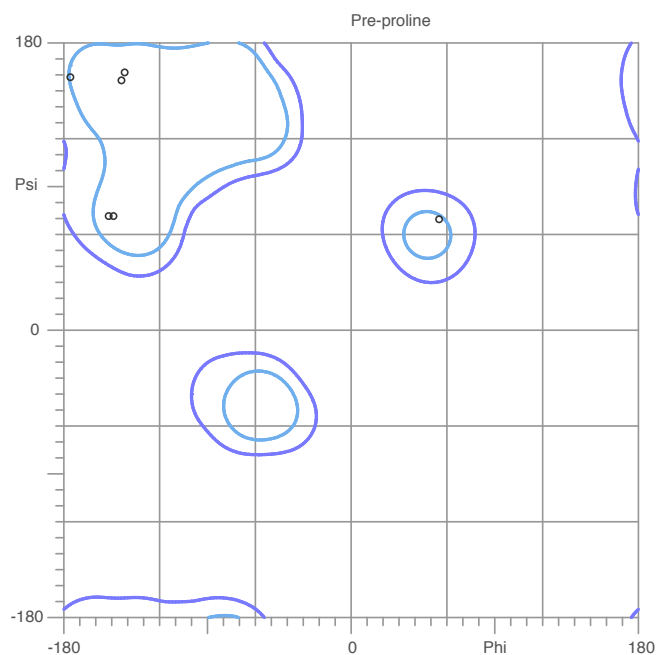
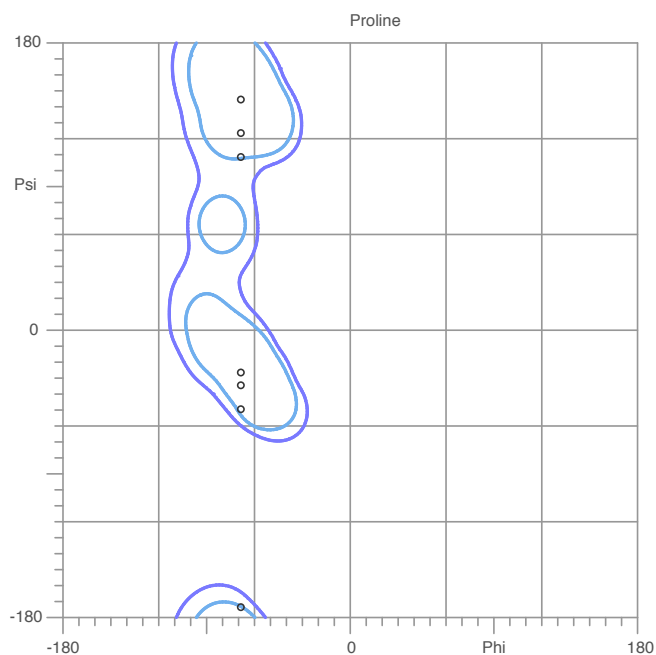
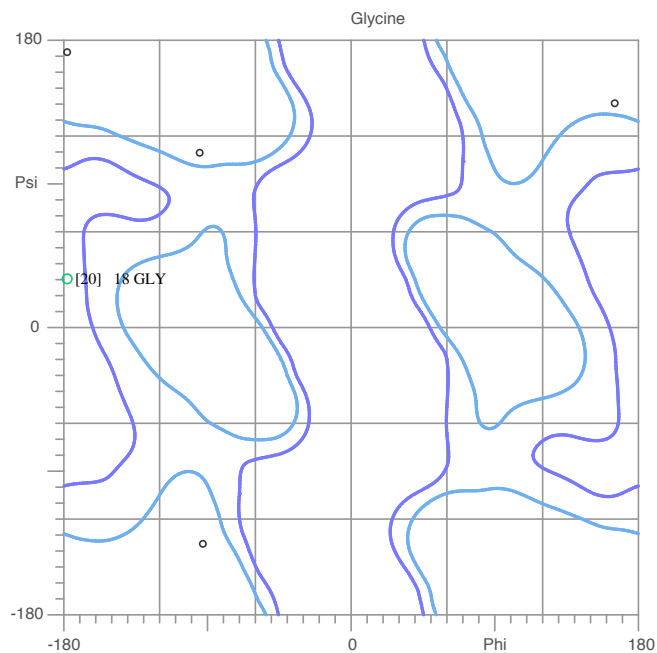
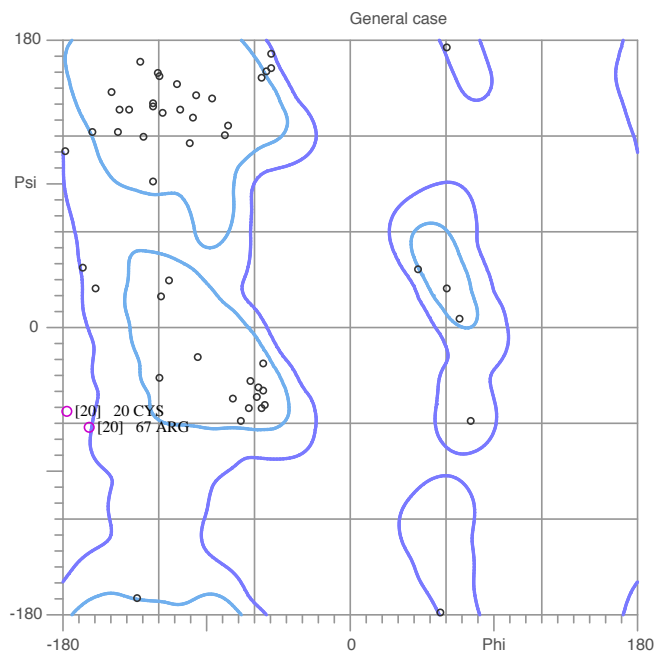
73,9% (51/69) of all residues were in favored (98%) regions.
94,2% (65/69) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [19] 18 GLY (148,4, 71,9)
- [19] 19 ARG (178,5, -38,5)
- [19] 60 GLU (63,1, 104,1)
- [19] 63 ALA (-175,8, 54,8)

MolProbity Ramachandran analysis

2KSK.pdb, model 20



79,7% (55/69) of all residues were in favored (98%) regions.
95,7% (66/69) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [20] 18 GLY (-178,4, 31,5)
- [20] 20 CYS (-178,3, -52,8)
- [20] 67 ARG (-164,1, -62,9)