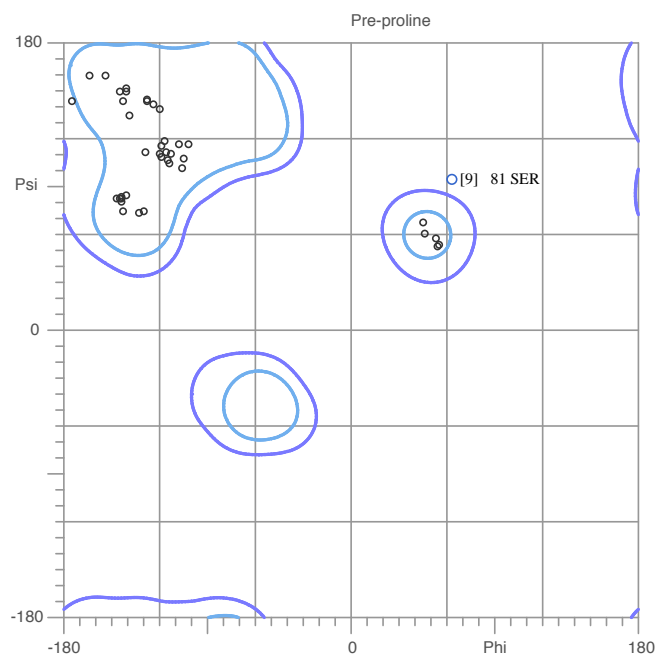
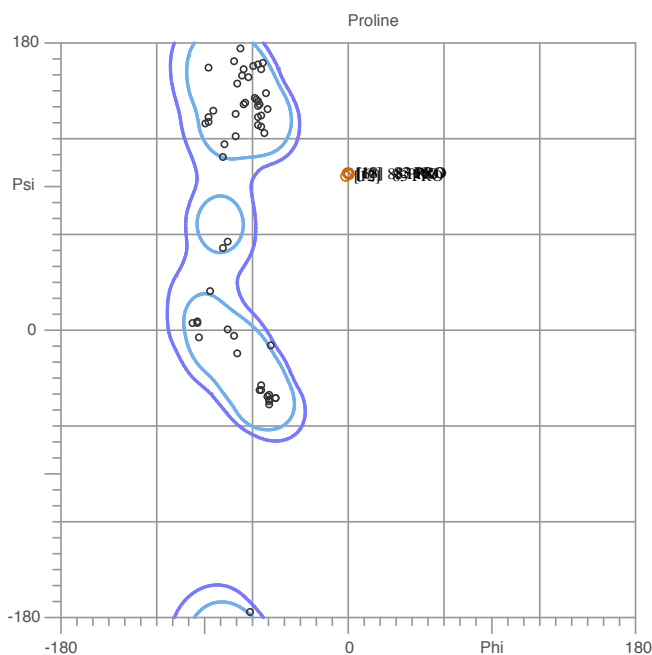
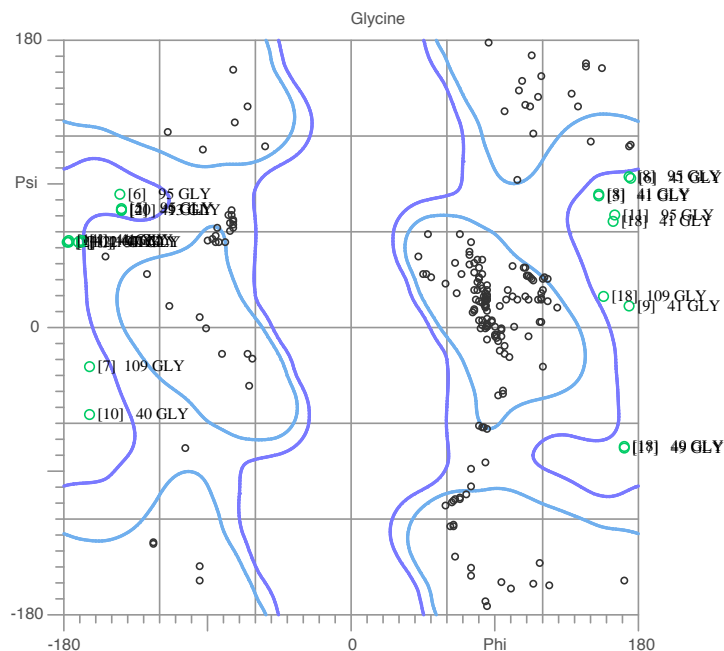
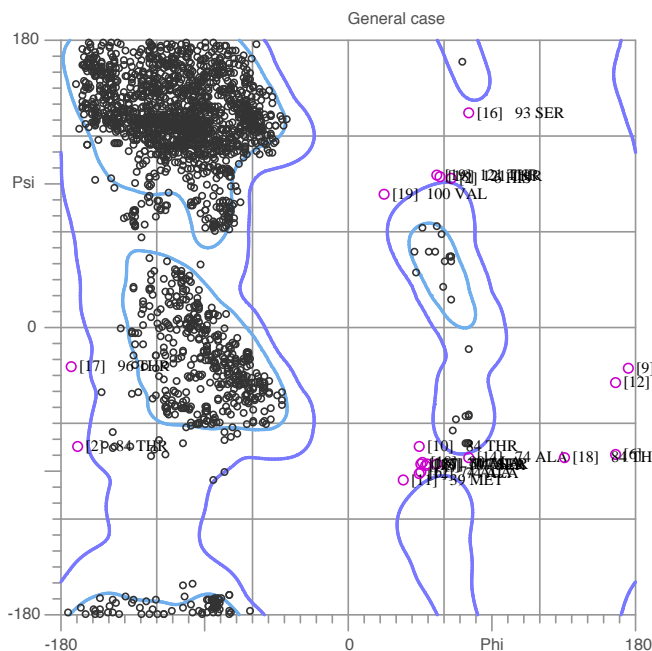


MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, all models



92.9% (2230/2400) of all residues were in favored (98%) regions.
98.0% (2352/2400) of all residues were in allowed (>99.8%) regions.

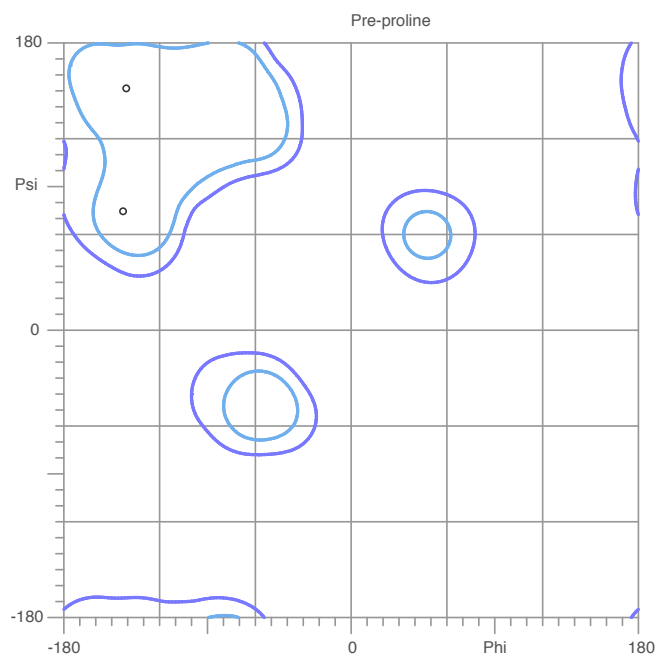
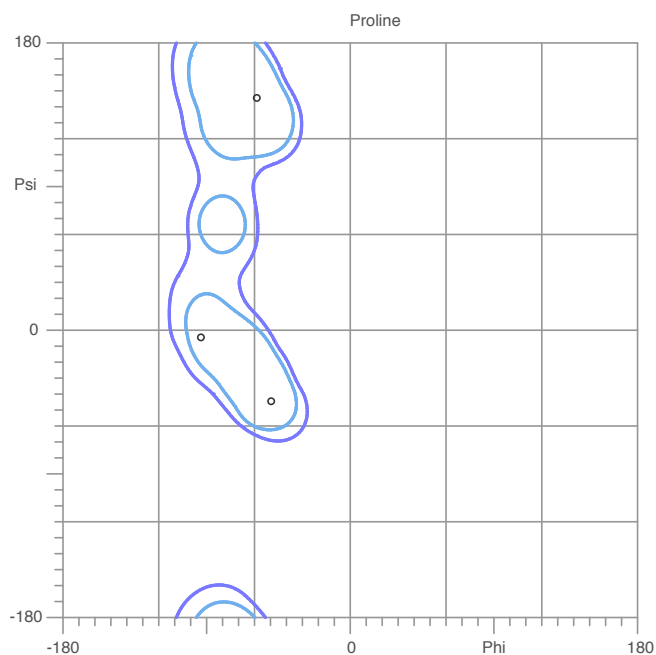
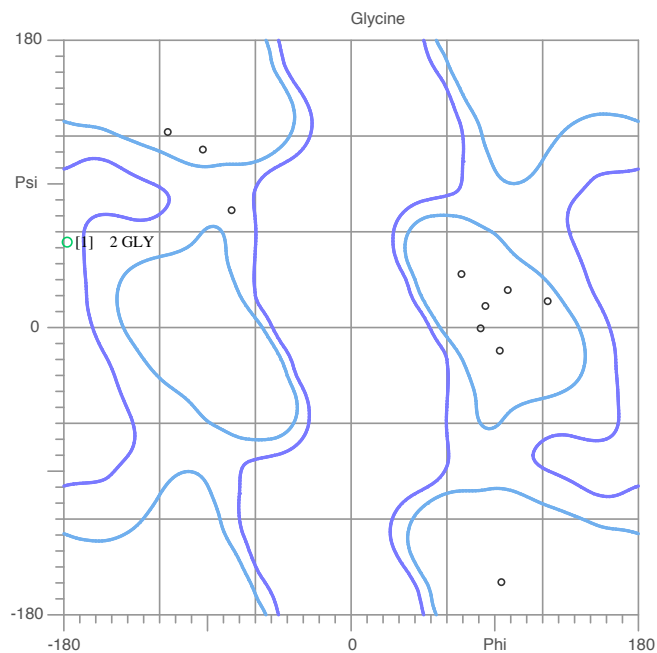
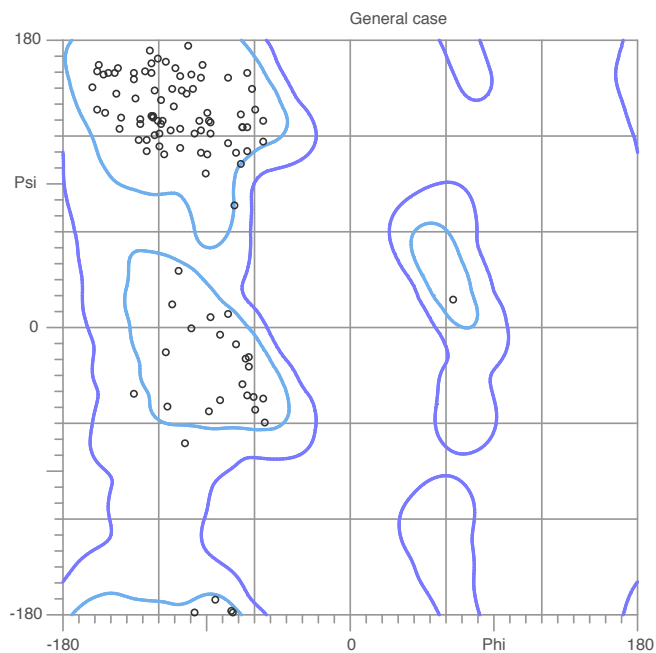
There were 48 outliers (phi, psi):

- [1] 2 GLY (-178.9, 55.0)
- [2] 6 HIS (64.9, 94.9)
- [2] 41 GLY (-177.4, 55.0)
- [2] 84 THR (-170.9, -75.0)
- [3] 41 GLY (155.0, 83.7)
- [4] 41 GLY (-169.4, 55.0)
- [4] 49 GLY (-145.0, 74.9)
- [5] 95 GLY (-145.0, 75.1)
- [6] 41 GLY (175.0, 94.9)
- [6] 74 ALA (45.2, -90.3)
- [6] 83 PRO (-61.1, 98.0)
- [6] 84 THR (167.4, -79.5)
- [6] 95 GLY (-145.2, 84.9)
- [7] 107 SER (55.5, -85.5)
- [7] 109 GLY (-165.0, -24.9)
- [8] 41 GLY (155.7, 84.1)
- [8] 95 GLY (175.0, 95.1)
- [9] 41 GLY (175.0, 15.0)
- [9] 81 SER (63.1, 95.3)
- [9] 84 THR (175.0, -25.0)
- [10] 40 GLY (-165.0, -55.0)
- [10] 83 PRO (-1.8, 99.1)

- [10] 84 THR (44.9, -74.9)
- [10] 97 GLY (-171.3, 55.0)
- [11] 39 MET (50.0, -95.1)
- [11] 95 GLY (165.1, 71.5)
- [12] 41 GLY (-169.8, 55.0)
- [12] 74 ALA (45.0, -91.8)
- [12] 83 PRO (-2.0, 97.2)
- [12] 84 THR (167.6, -34.6)
- [13] 107 SER (48.3, -86.9)
- [14] 41 GLY (-177.7, 55.0)
- [14] 74 ALA (75.1, -81.6)
- [16] 74 ALA (49.8, -85.0)
- [16] 93 SER (76.0, 135.2)
- [17] 49 GLY (171.2, -75.0)
- [17] 96 THR (-175.0, 24.9)
- [18] 41 GLY (164.9, 67.7)
- [18] 49 GLY (171.4, -75.0)
- [18] 74 ALA (45.0, -85.0)
- [18] 80 ALA (46.7, -85.0)
- [18] 83 PRO (0.0, 100.0)
- [18] 84 THR (135.6, -81.5)
- [18] 109 GLY (158.0, 20.6)
- [18] 121 THR (57.7, 95.5)
- [19] 100 VAL (22.6, 84.9)
- [19] 121 THR (55.2, 96.9)
- [20] 13 GLY (-144.9, 74.0)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 1



96.7% (116/120) of all residues were in favored (98%) regions.
99.2% (119/120) of all residues were in allowed (>99.8%) regions.

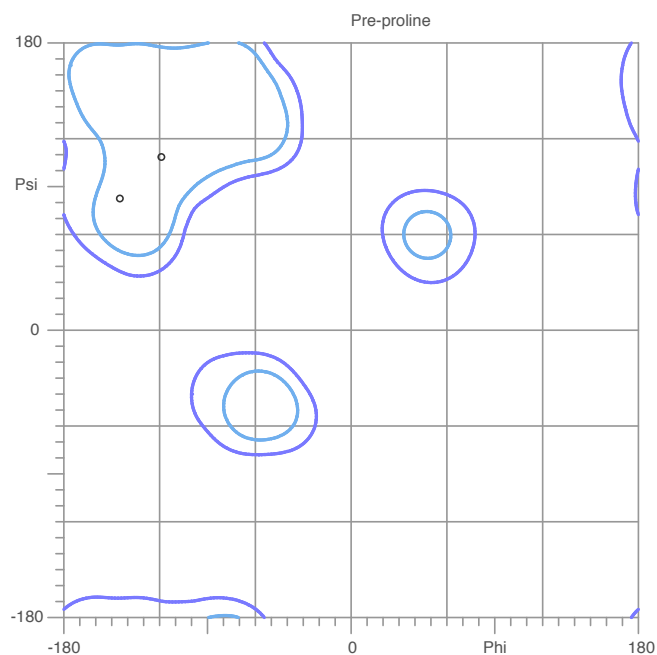
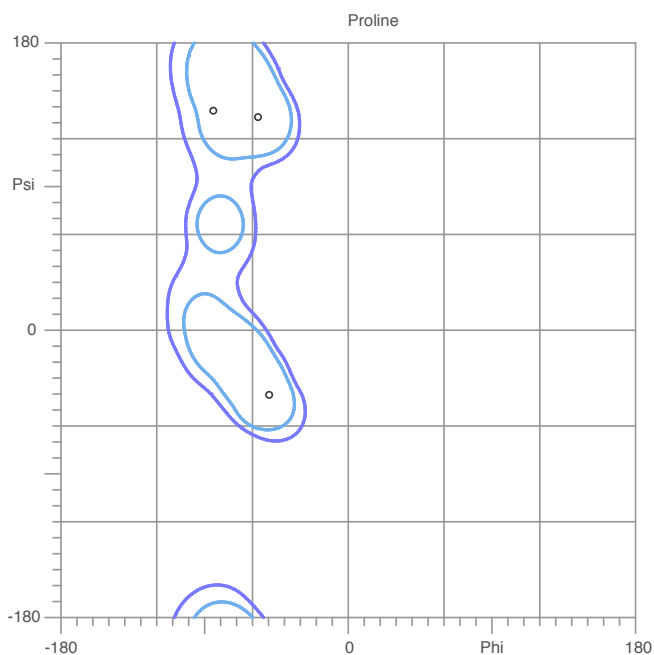
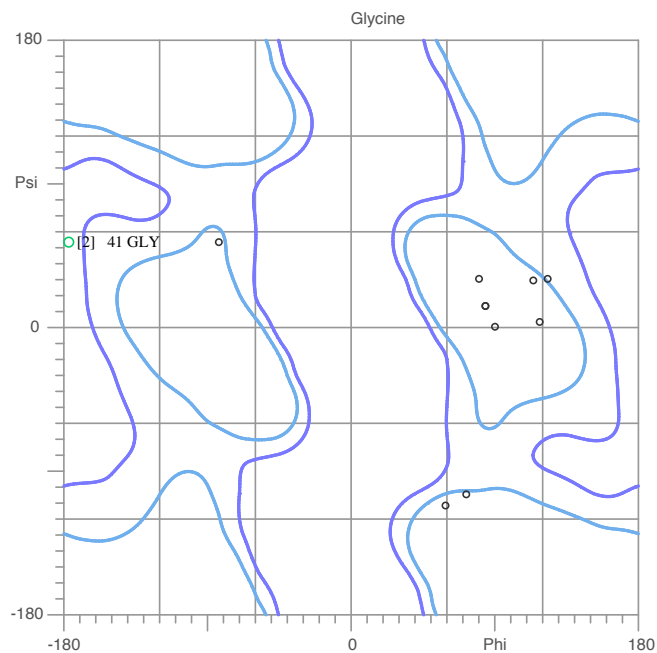
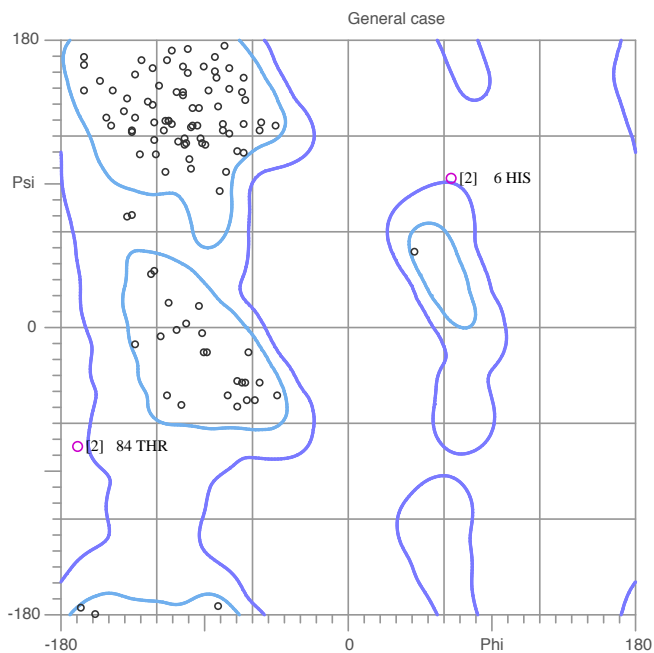
There were 1 outliers (phi, psi):
[1] 2 GLY (-178.9, 55.0)

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

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

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 2



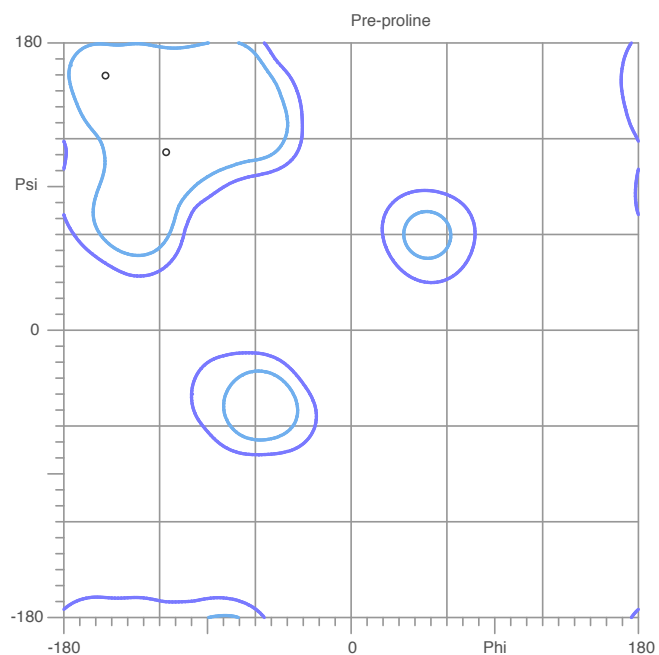
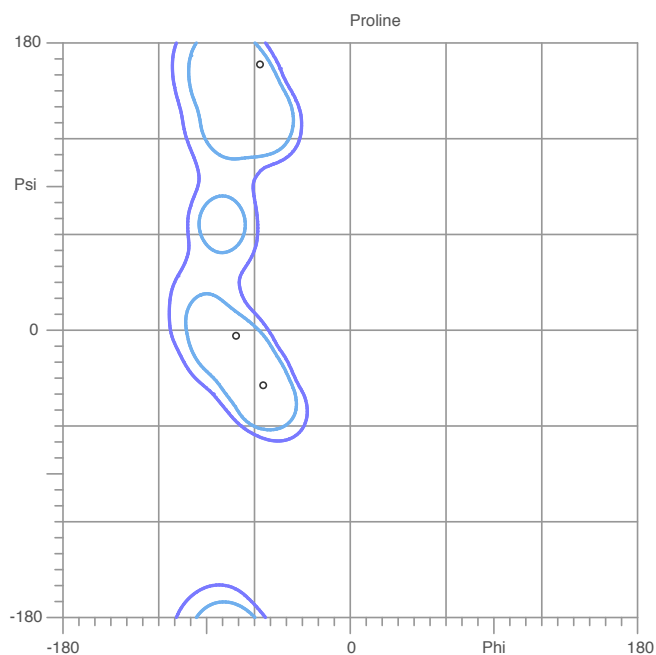
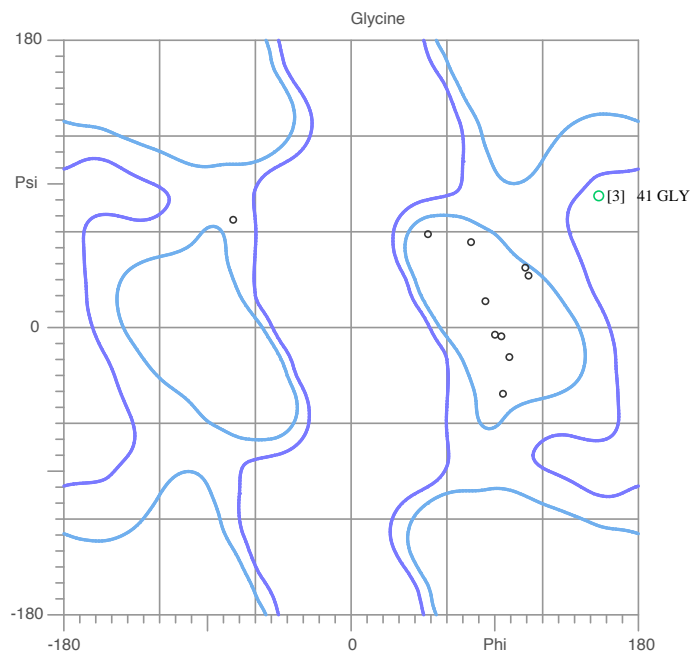
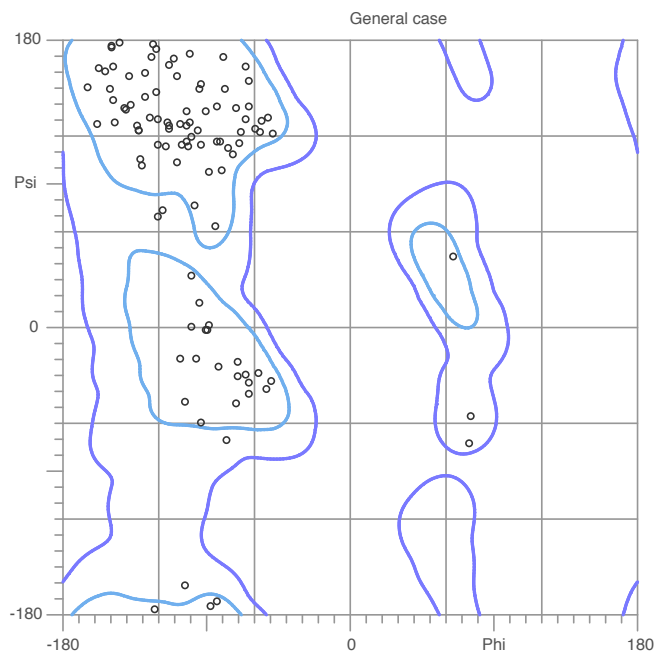
95.0% (114/120) of all residues were in favored (98%) regions.
97.5% (117/120) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 6 HIS (64.9, 94.9)
- [2] 41 GLY (-177.4, 55.0)
- [2] 84 THR (-170.9, -75.0)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 3

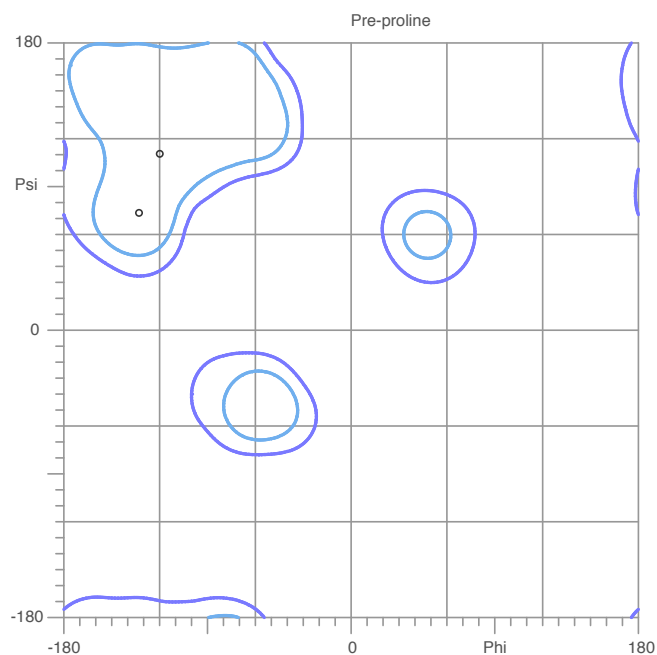
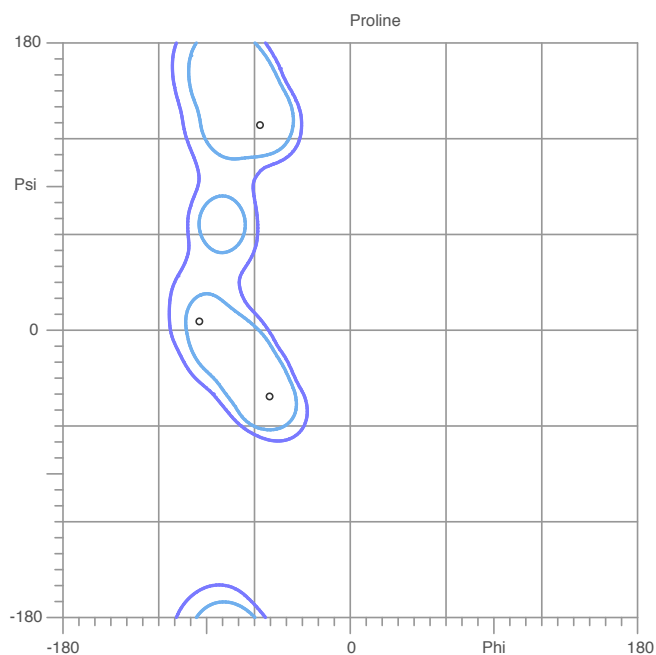
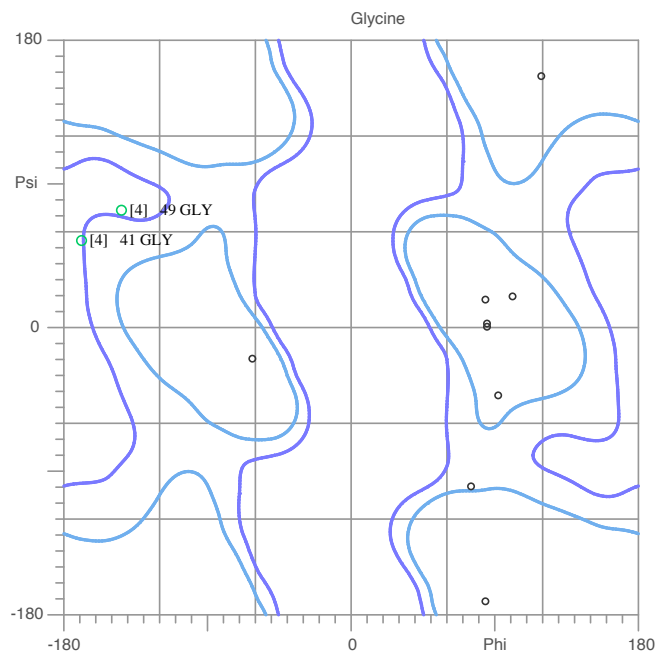
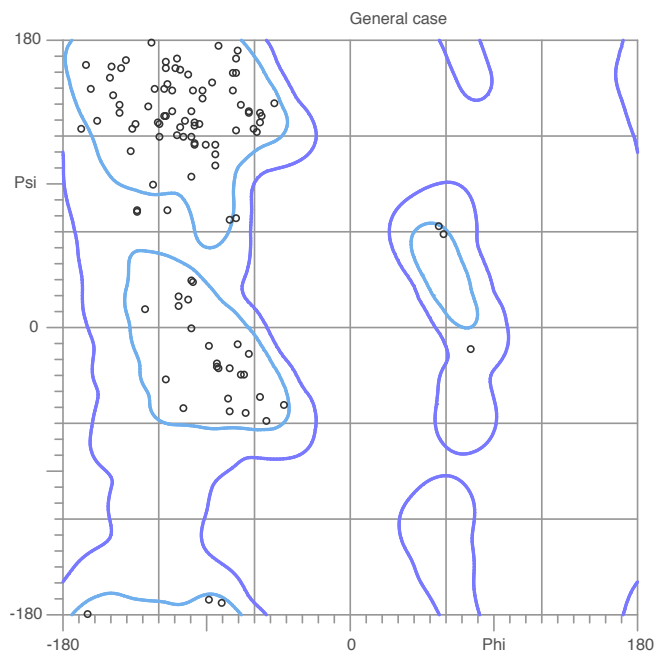


93.3% (112/120) of all residues were in favored (98%) regions.
99.2% (119/120) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 41 GLY (155.0, 83.7)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 4



91.7% (110/120) of all residues were in favored (98%) regions.
98.3% (118/120) of all residues were in allowed (>99.8%) regions.

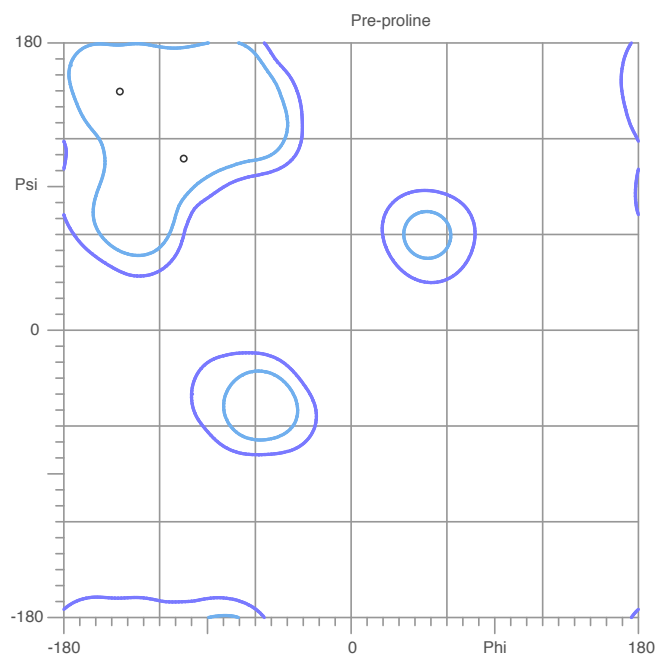
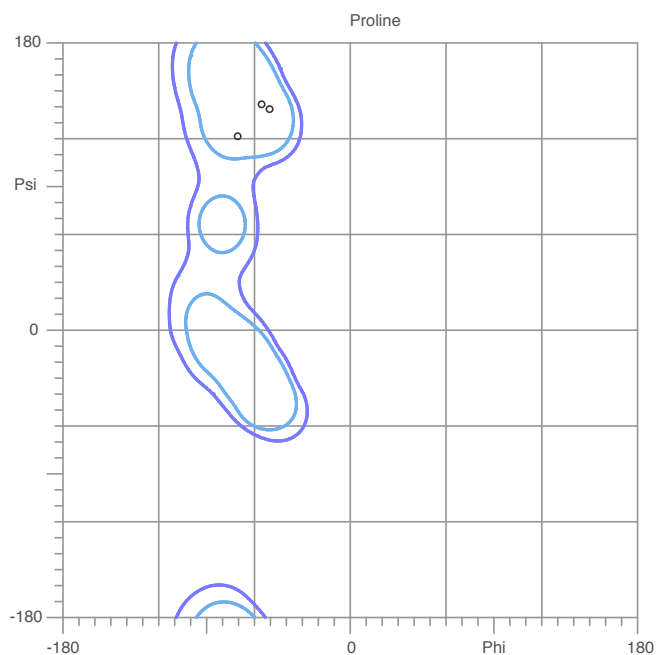
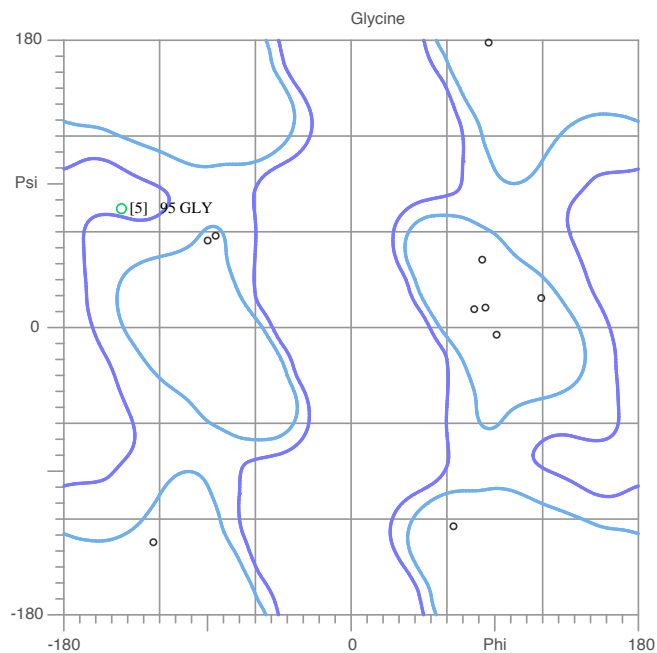
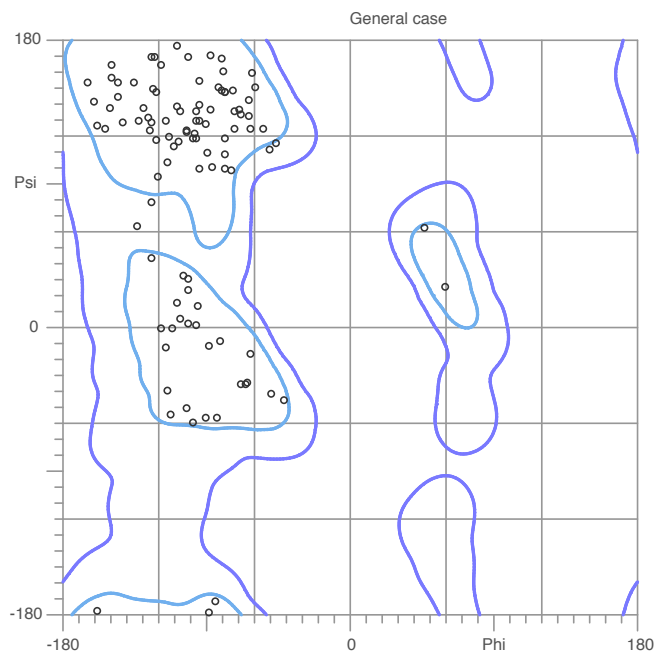
There were 2 outliers (phi, psi):

[4] 41 GLY (-169.4, 55.0)

[4] 49 GLY (-145.0, 74.9)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 5

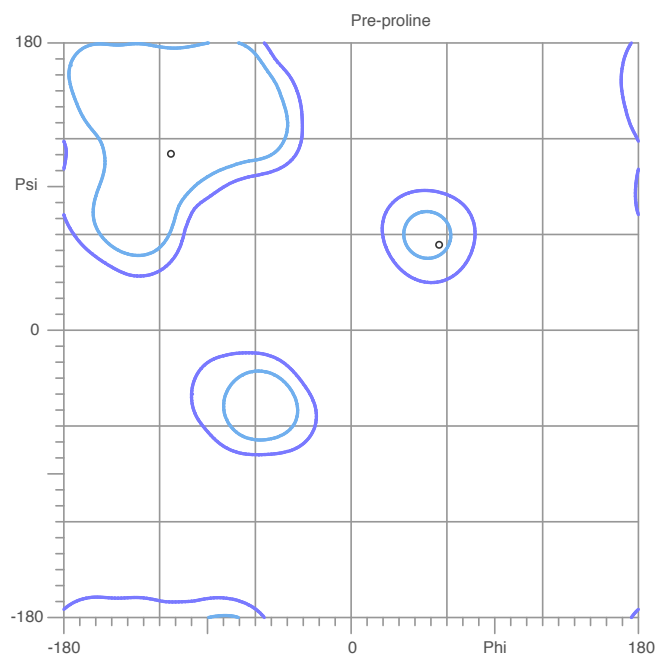
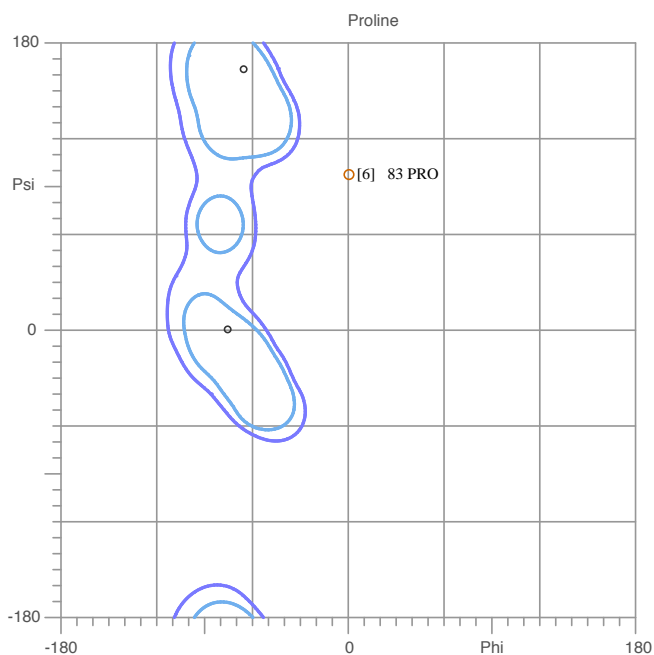
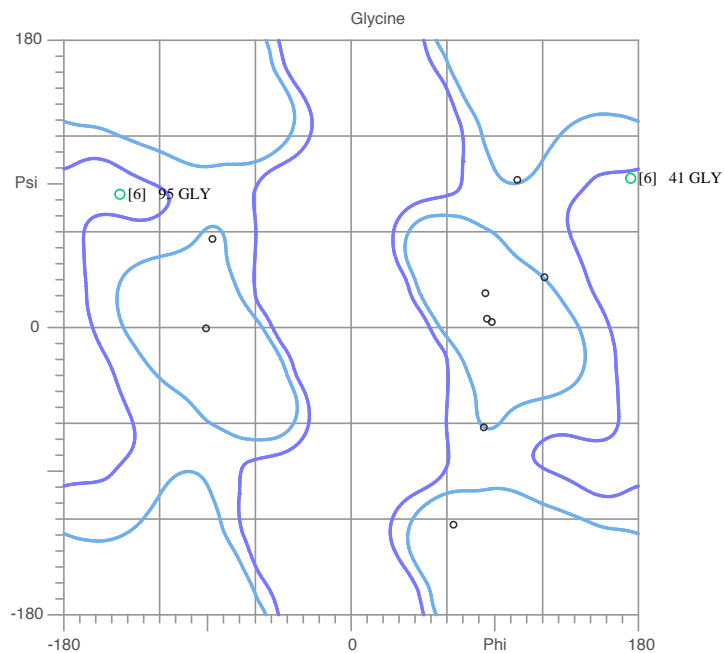
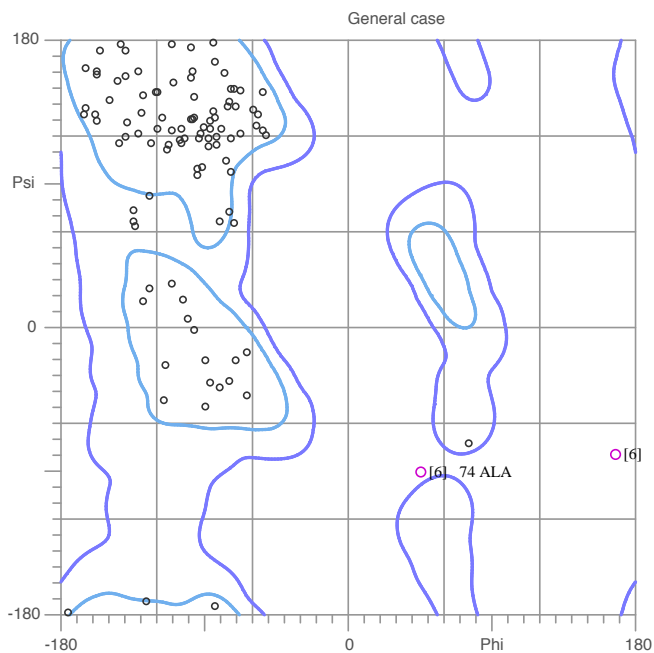


95.8% (115/120) of all residues were in favored (98%) regions.
99.2% (119/120) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 95 GLY (-145.0, 75.1)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 6



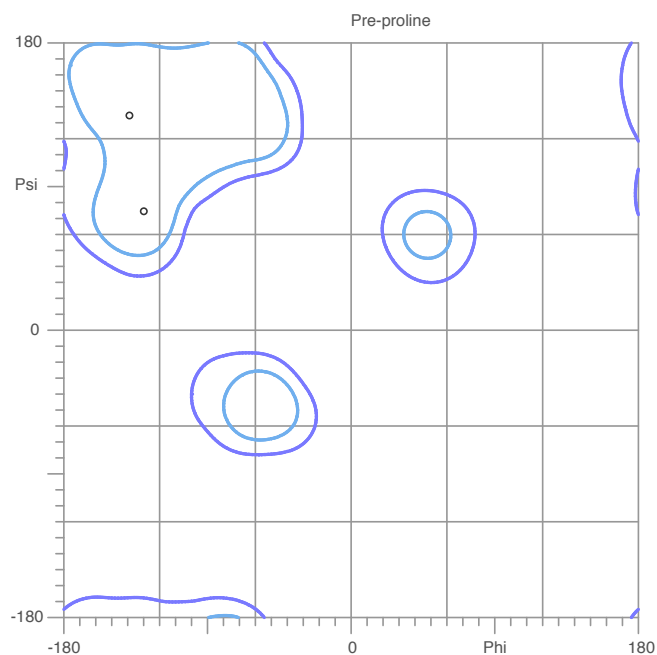
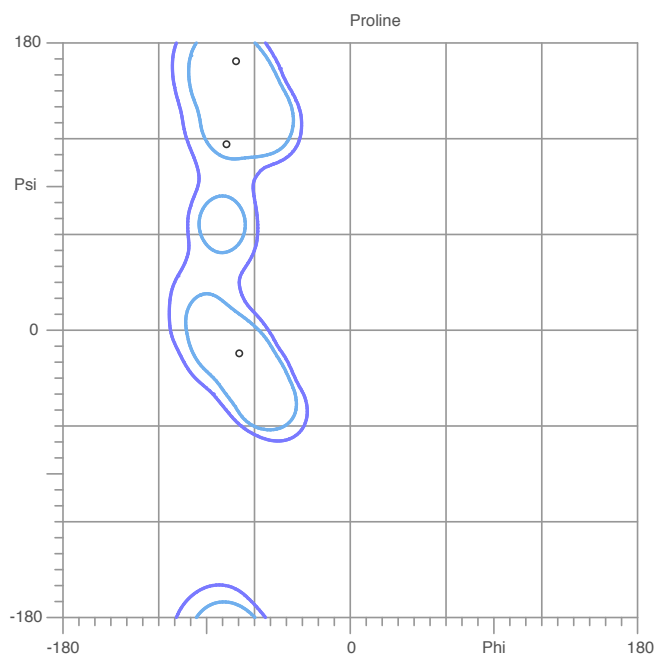
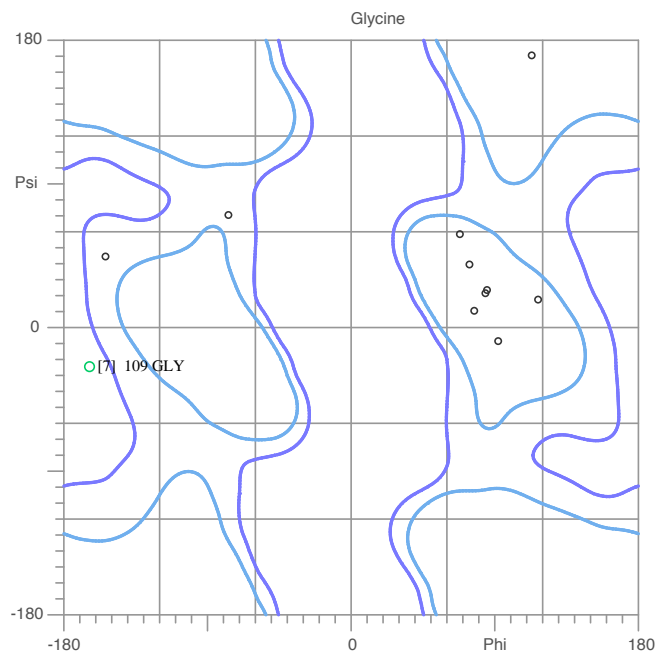
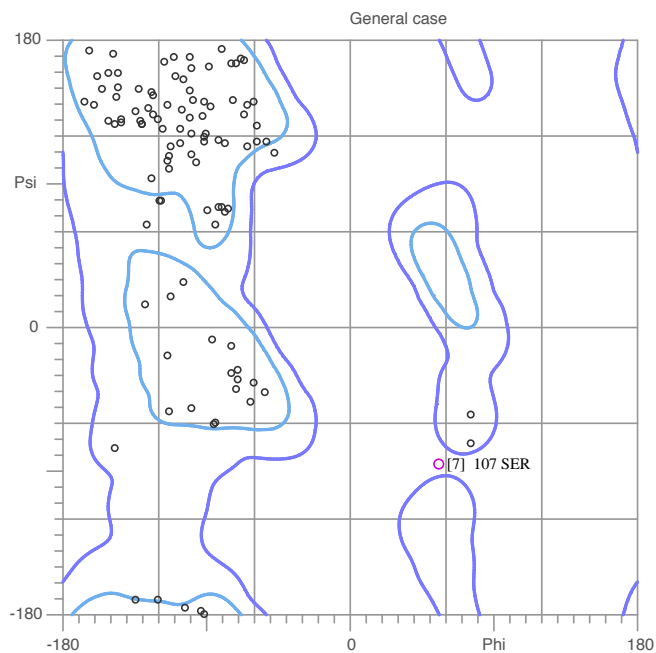
90.0% (108/120) of all residues were in favored (98%) regions.
95.8% (115/120) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[6] 41 GLY (175.0, 94.9)
[6] 74 ALA (45.2, -90.3)
[6] 83 PRO (-0.1, 98.0)
[6] 84 THR (167.4, -79.5)
[6] 95 GLY (-145.2, 84.9)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 7

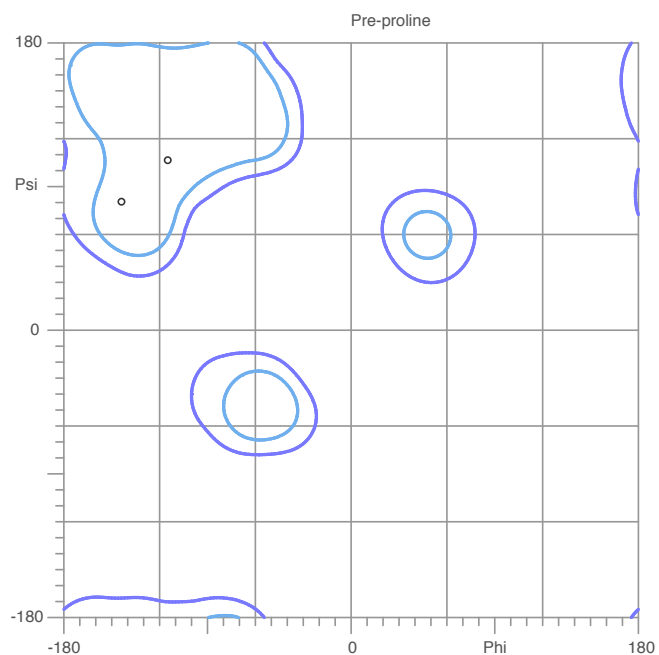
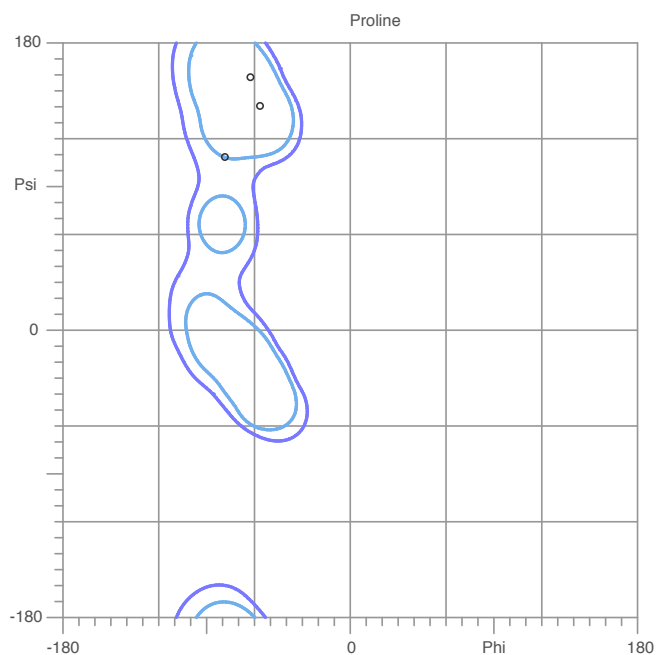
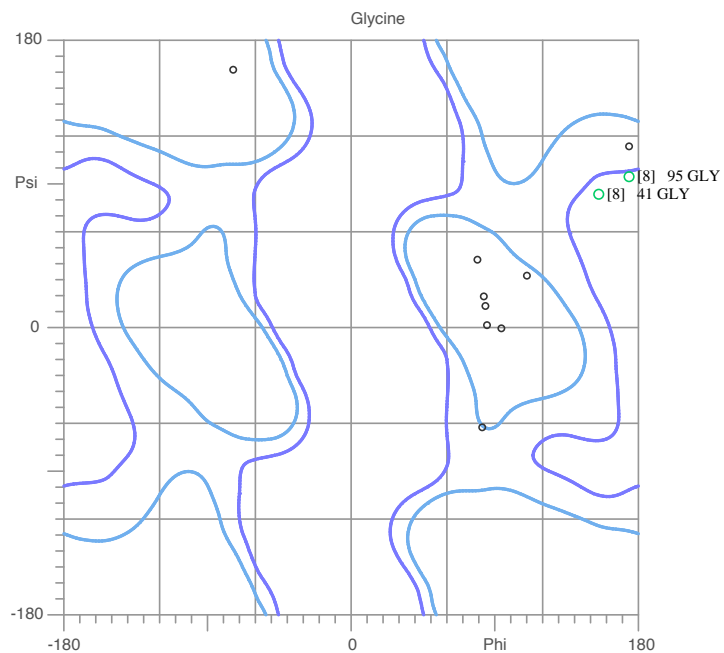
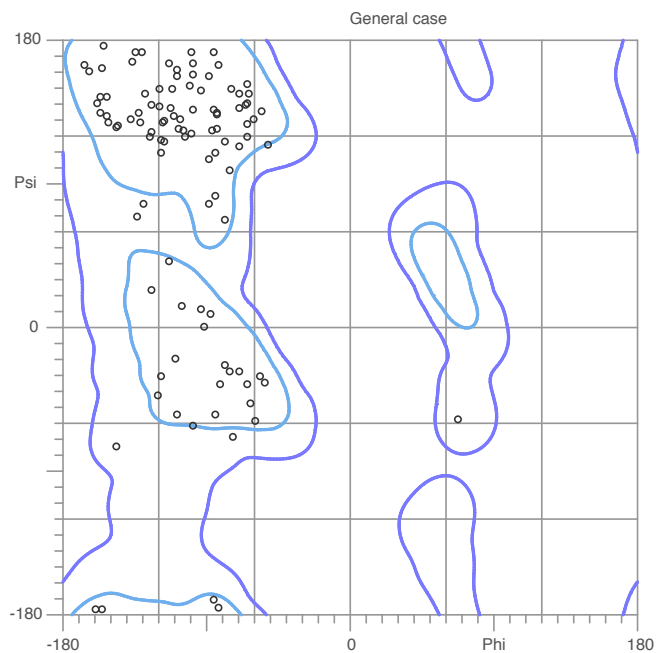


90.0% (108/120) of all residues were in favored (98%) regions.
98.3% (118/120) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[7] 107 SER (55.5, -85.5)
[7] 109 GLY (-165.0, -24.9)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 8



92.5% (111/120) of all residues were in favored (98%) regions.
98.3% (118/120) of all residues were in allowed (>99.8%) regions.

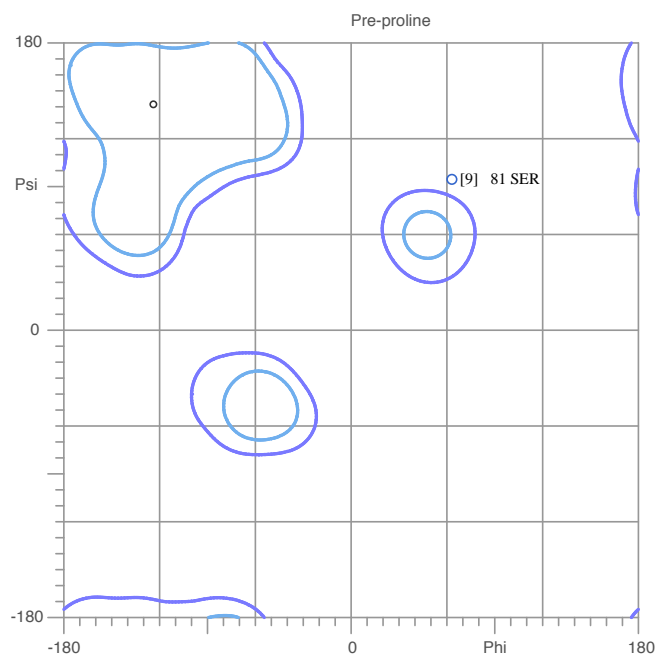
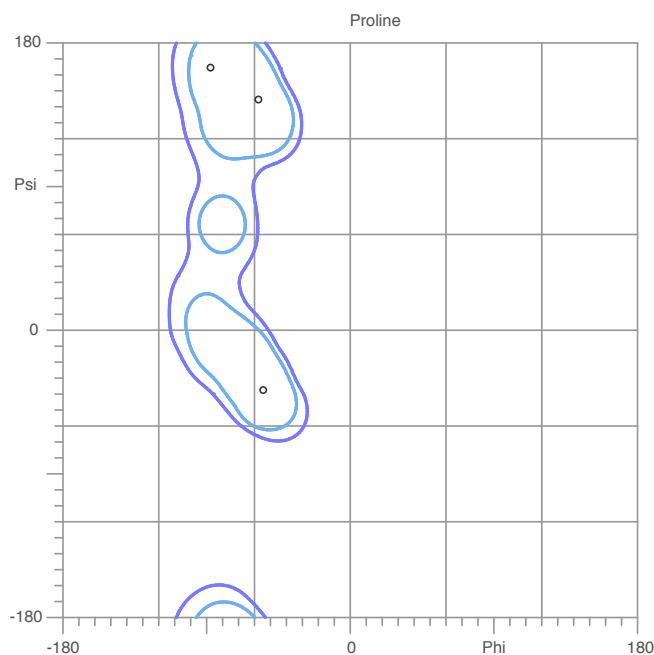
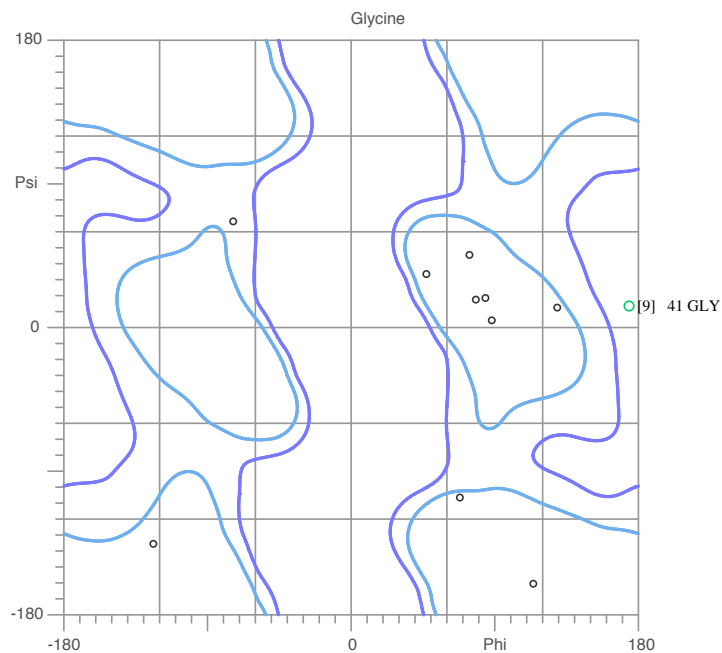
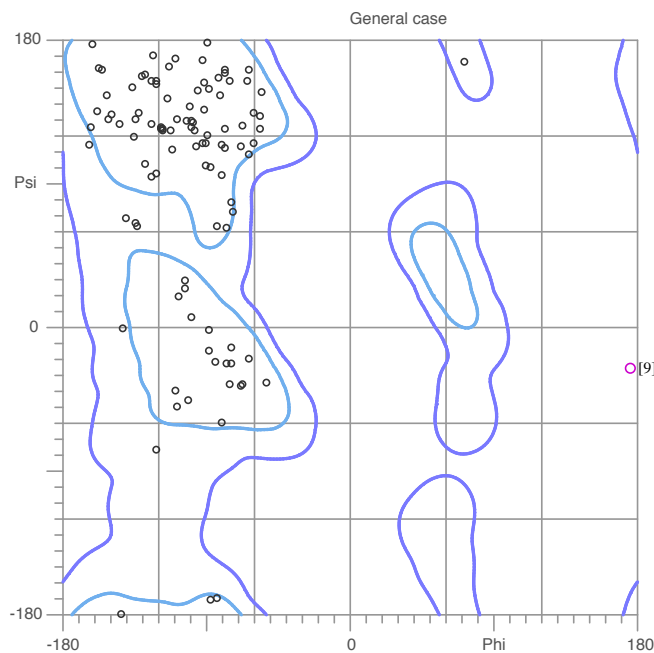
There were 2 outliers (phi, psi):

[8] 41 GLY (155.7, 84.1)

[8] 95 GLY (175.0, 95.1)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 9



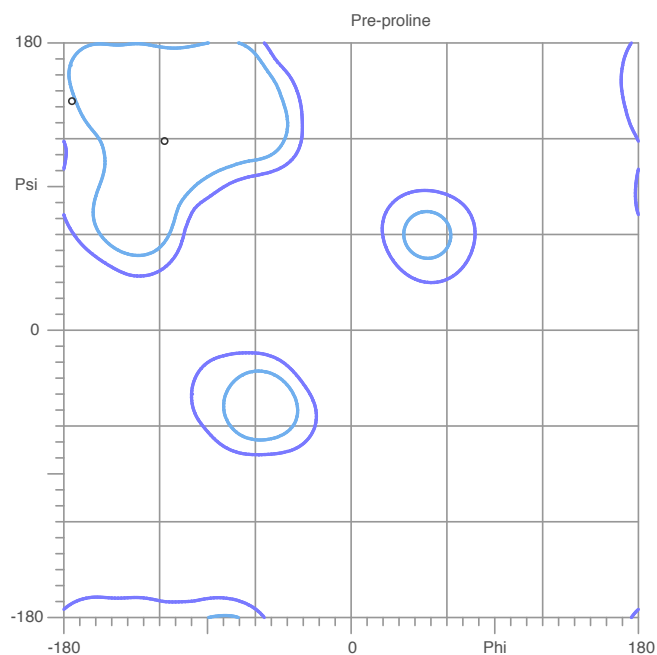
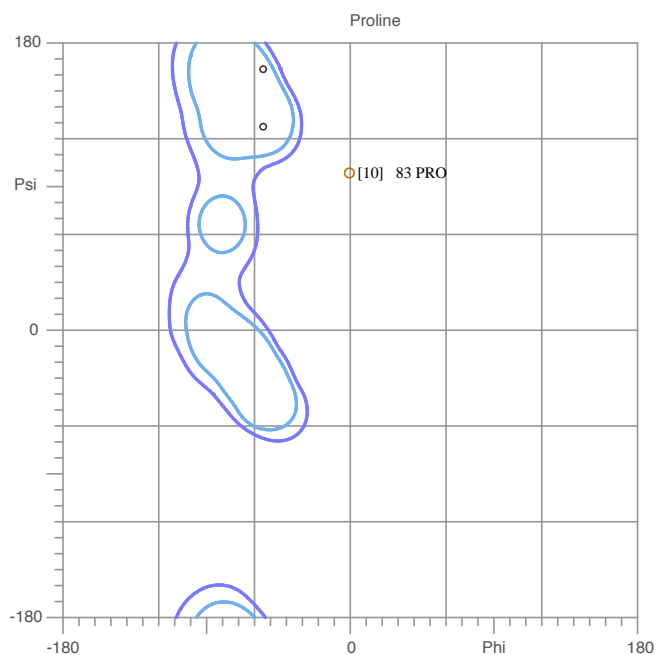
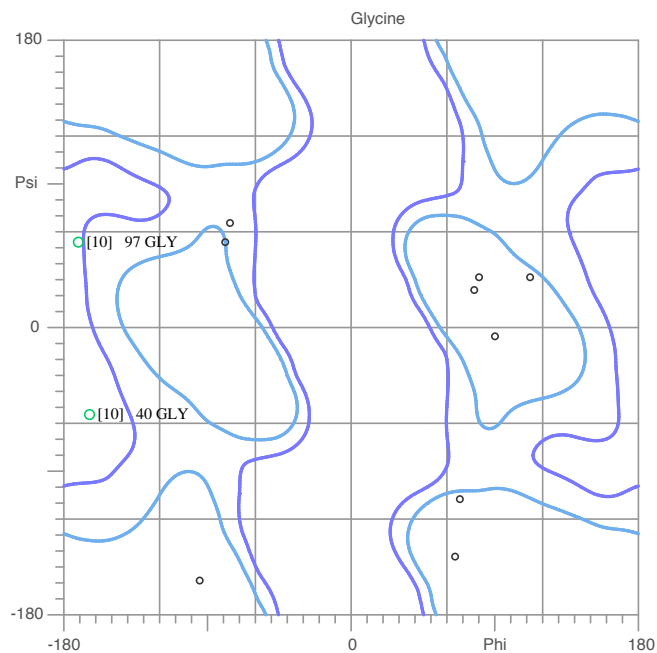
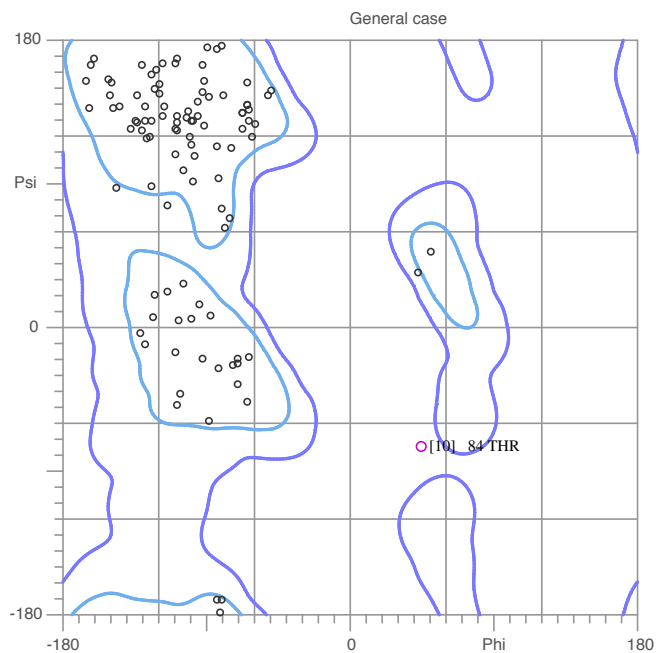
90.8% (109/120) of all residues were in favored (98%) regions.
97.5% (117/120) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [9] 41 GLY (175.0, 15.0)
- [9] 81 SER (63.1, 95.3)
- [9] 84 THR (175.0, -25.0)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 10



92.5% (111/120) of all residues were in favored (98%) regions.
96.7% (116/120) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[10] 40 GLY (-165.0, -55.0)

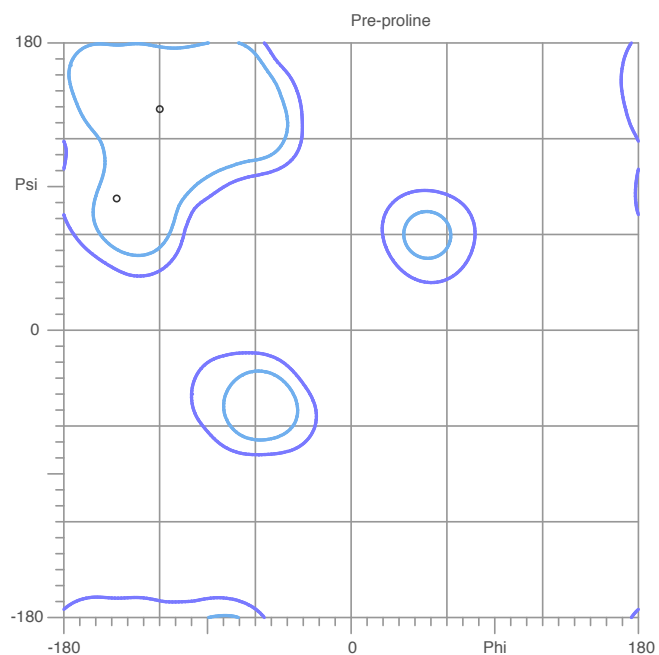
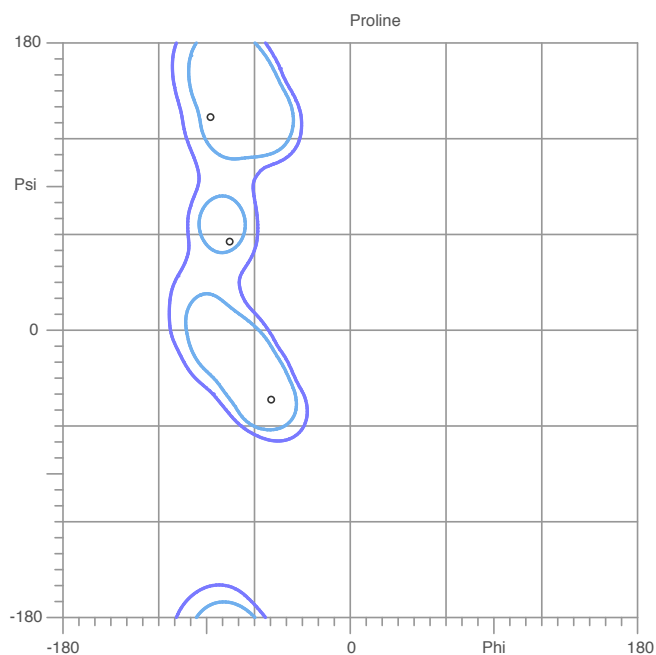
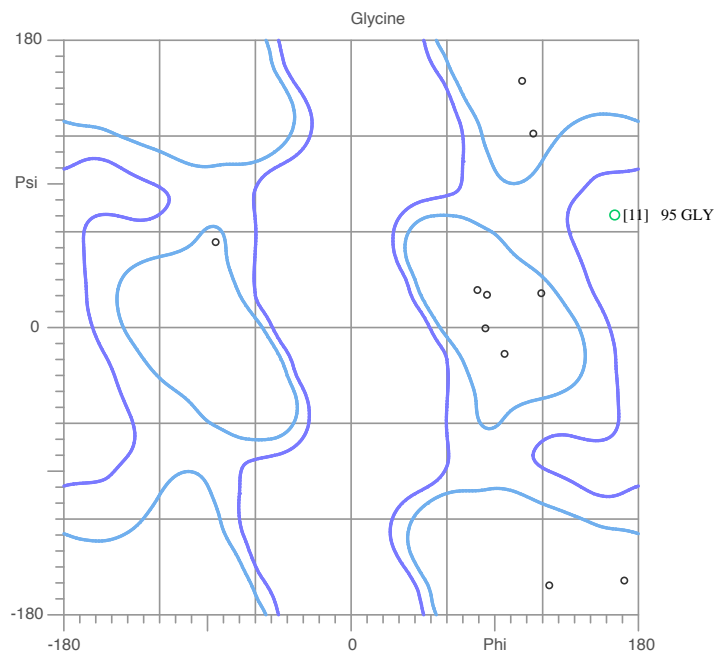
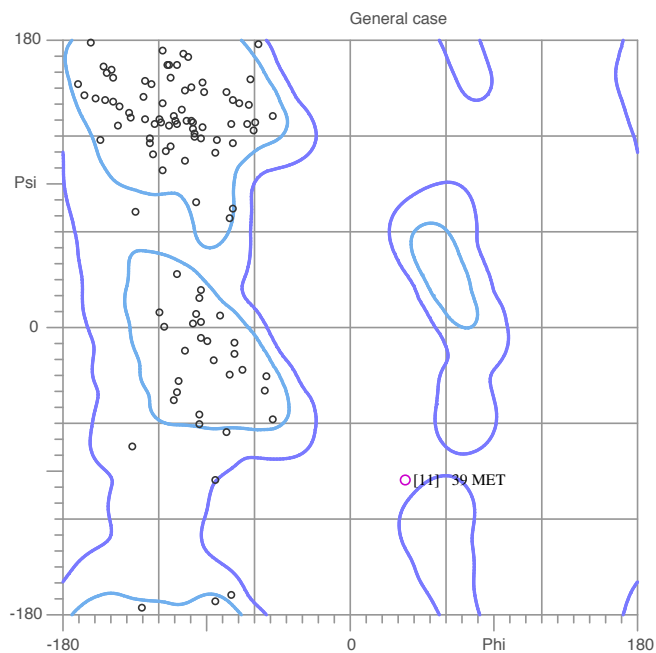
[10] 83 PRO (-1.8, 99.1)

[10] 84 THR (44.9, -74.9)

[10] 97 GLY (-171.3, 55.0)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 11



93.3% (112/120) of all residues were in favored (98%) regions.
98.3% (118/120) of all residues were in allowed (>99.8%) regions.

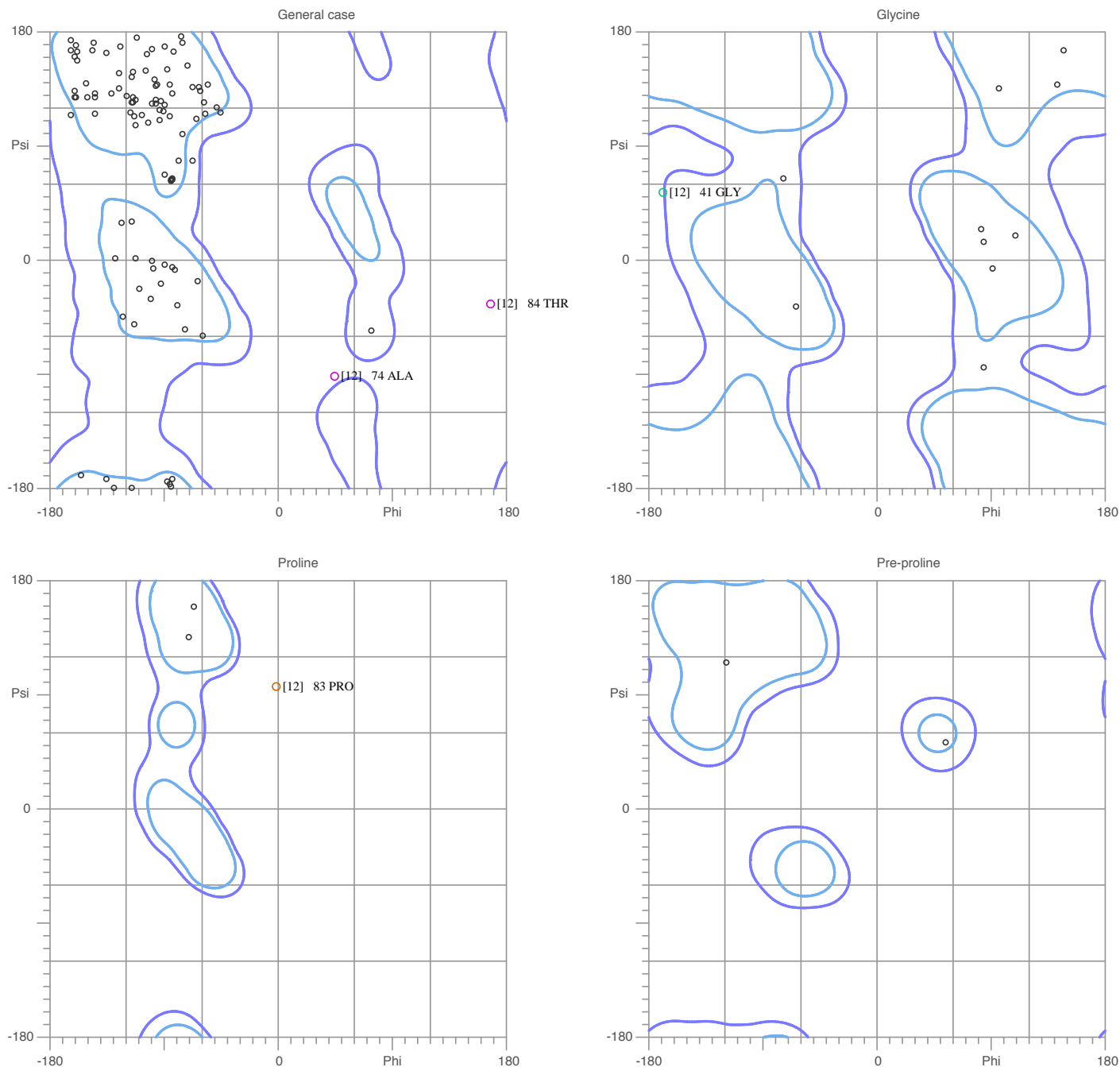
There were 2 outliers (phi, psi):

[11] 39 MET (35.0, -95.1)

[11] 95 GLY (165.1, 71.5)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 12



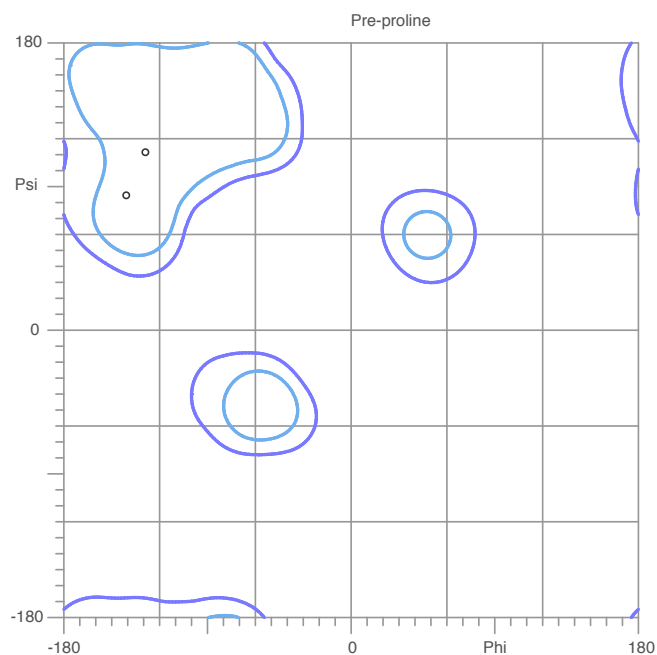
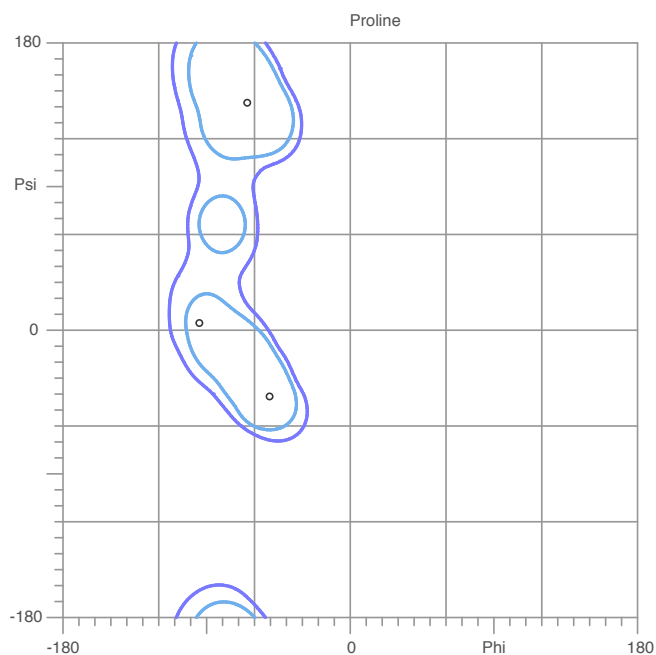
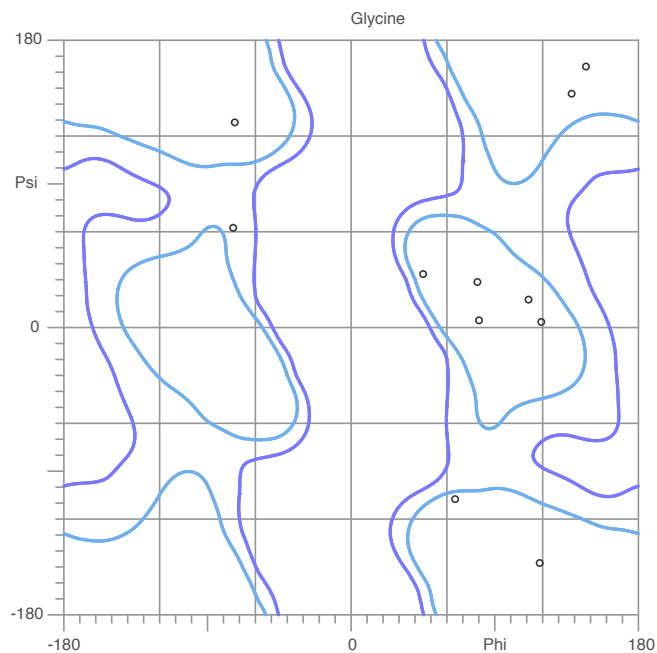
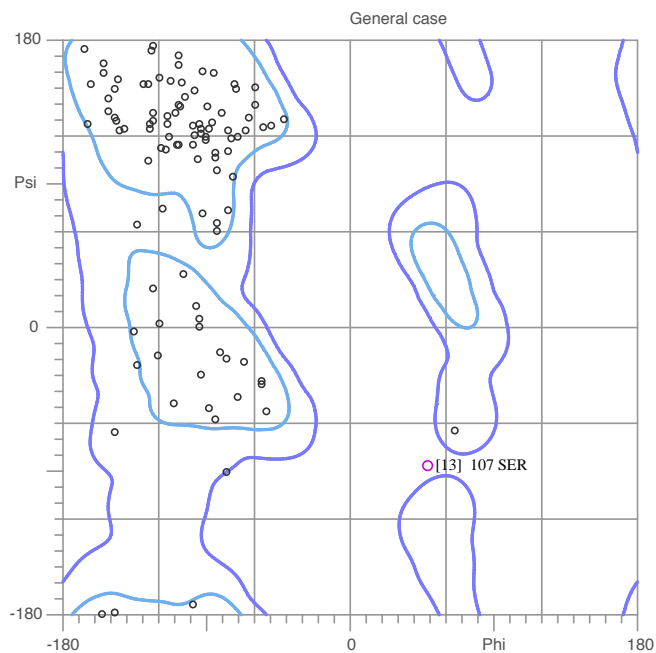
92.5% (111/120) of all residues were in favored (98%) regions.
96.7% (116/120) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [12] 41 GLY (-169.8, 55.0)
- [12] 74 ALA (45.0, -91.8)
- [12] 83 PRO (-2.0, 97.2)
- [12] 84 THR (167.6, -34.6)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 13



93.3% (112/120) of all residues were in favored (98%) regions.
99.2% (119/120) of all residues were in allowed (>99.8%) regions.

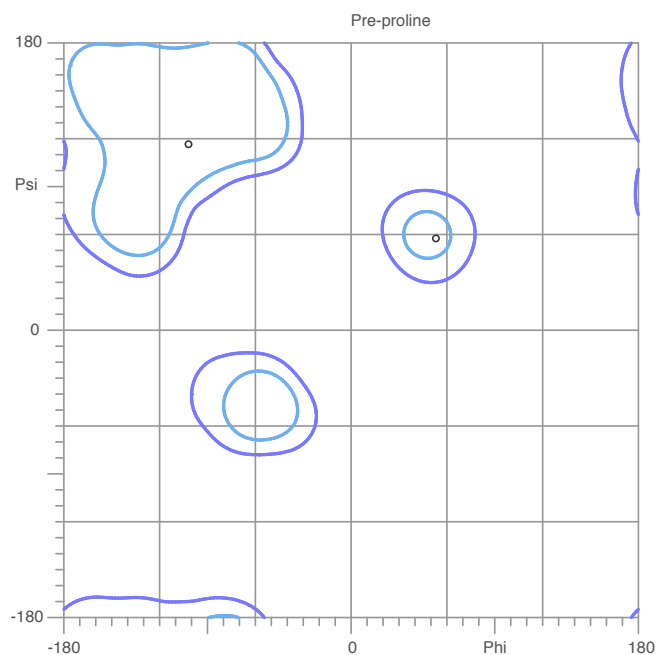
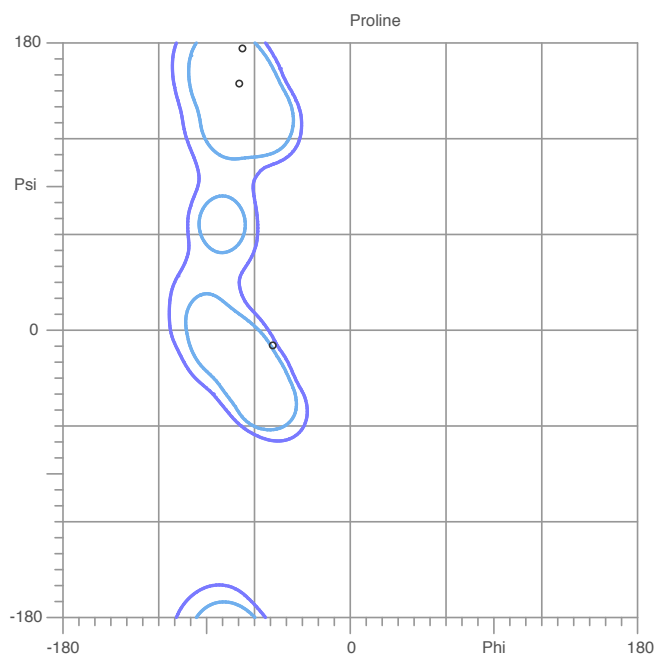
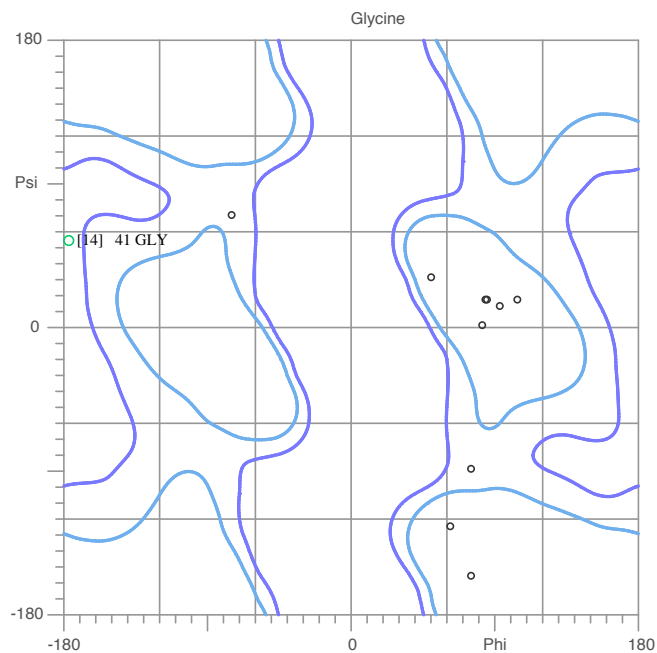
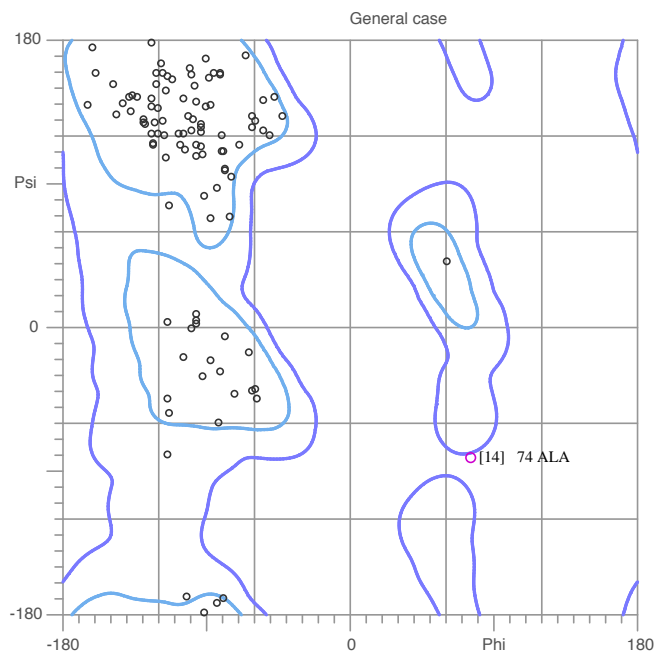
There were 1 outliers (phi, psi):
[13] 107 SER (48.3, -86.9)

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

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

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 14

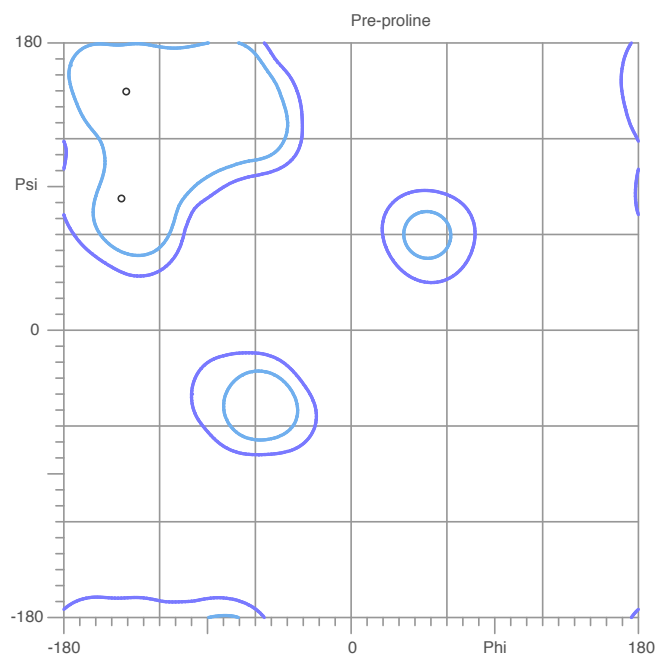
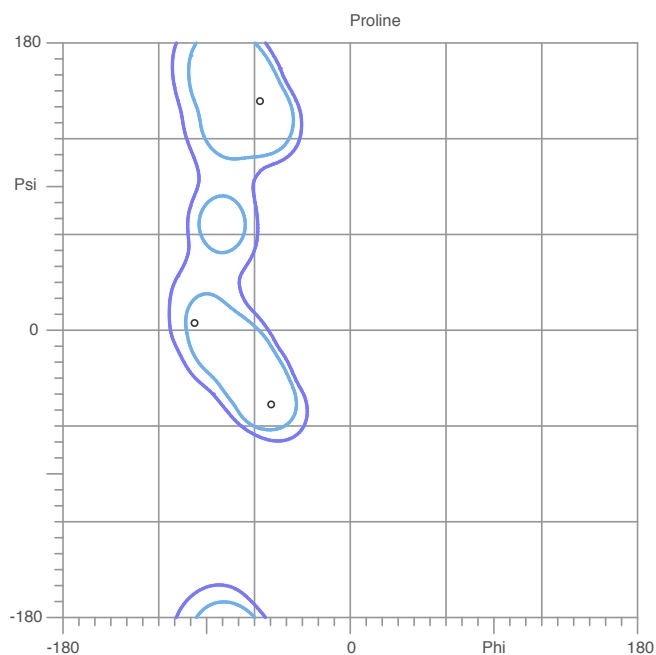
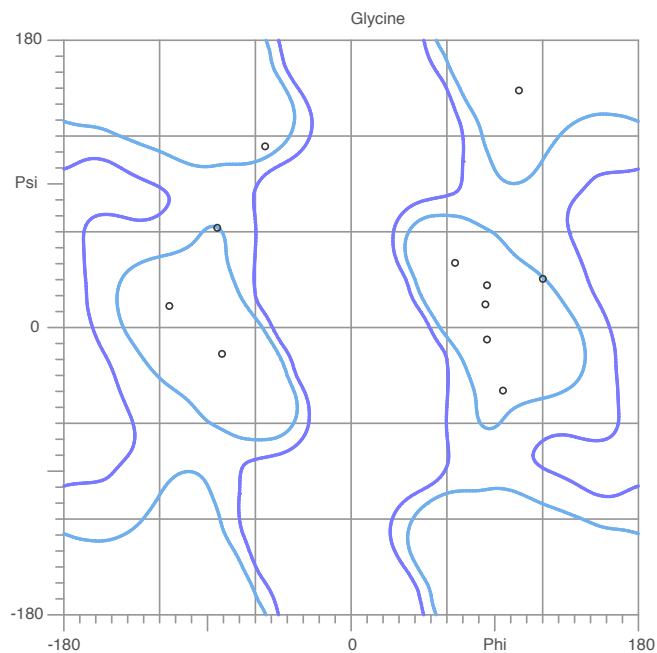
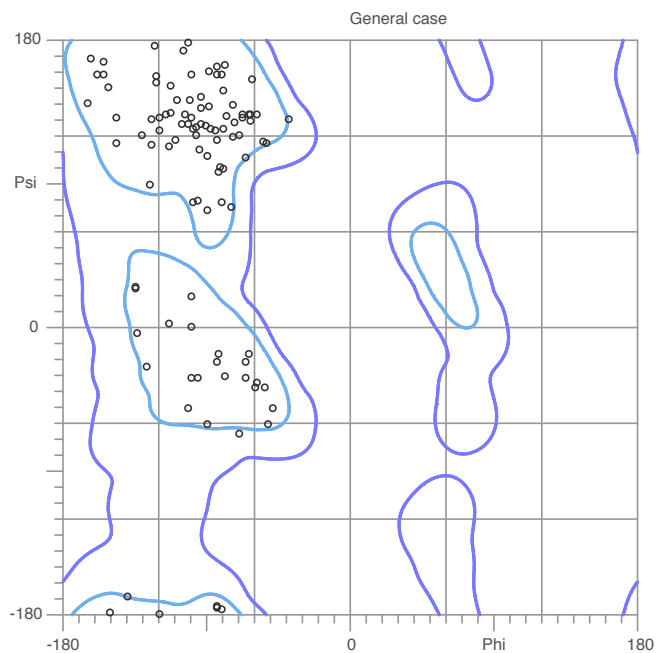


93.3% (112/120) of all residues were in favored (98%) regions.
98.3% (118/120) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[14] 41 GLY (-177.7, 55.0)
[14] 74 ALA (75.1, -81.6)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 15



95.8% (115/120) of all residues were in favored (98%) regions.
100.0% (120/120) of all residues were in allowed (>99.8%) regions.

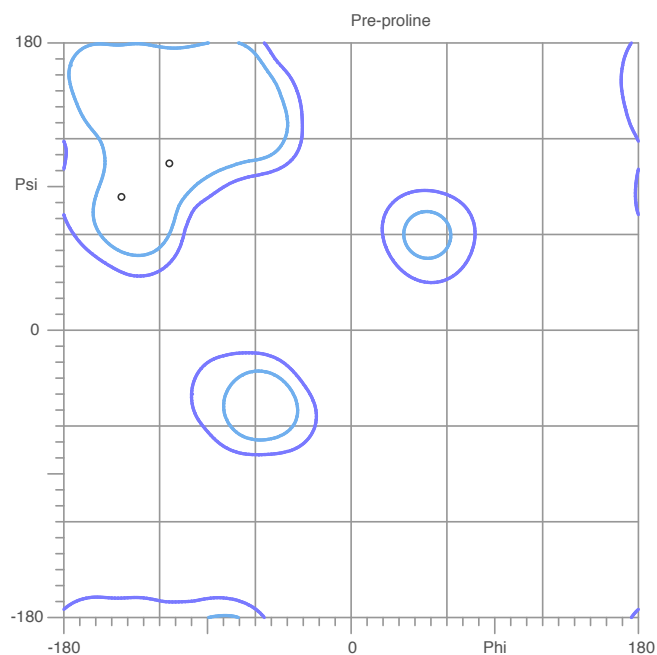
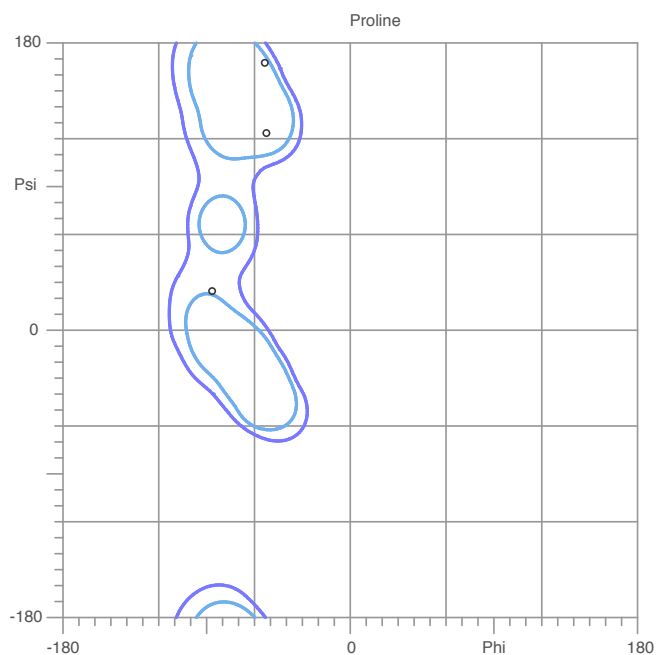
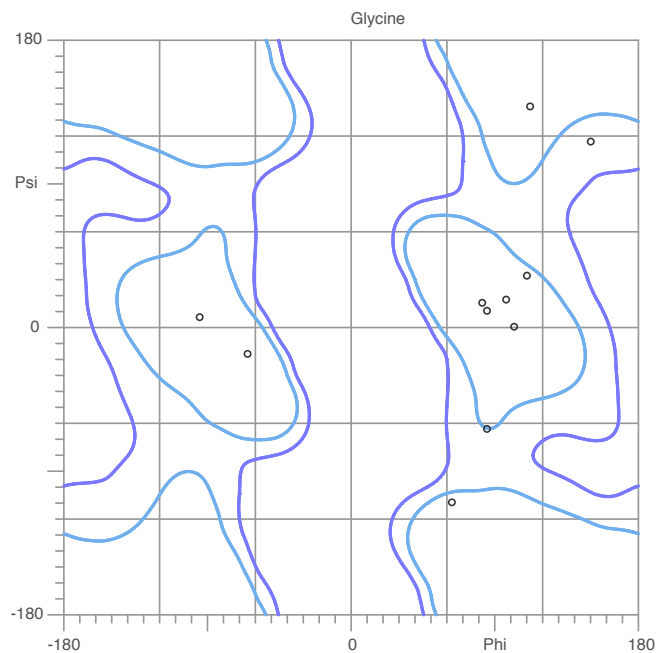
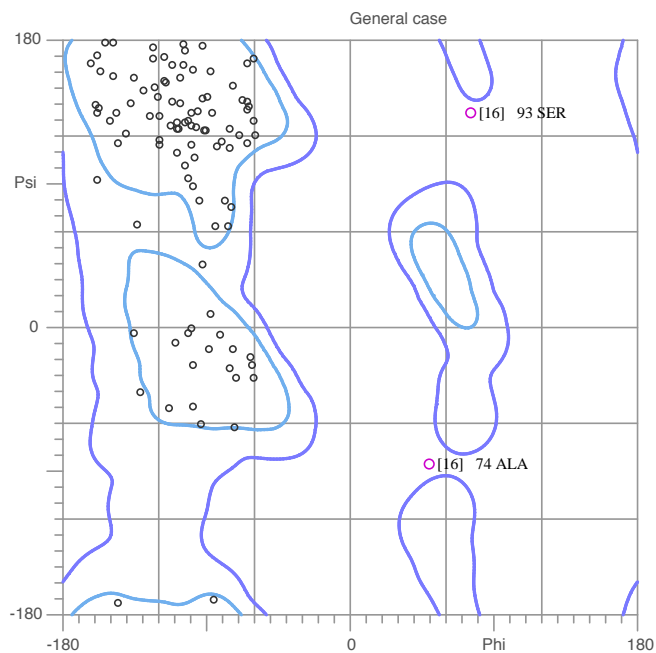
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 16

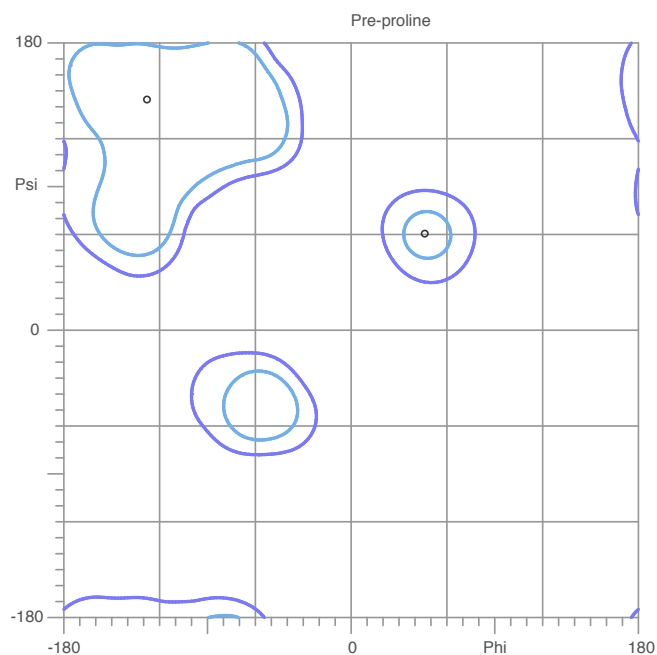
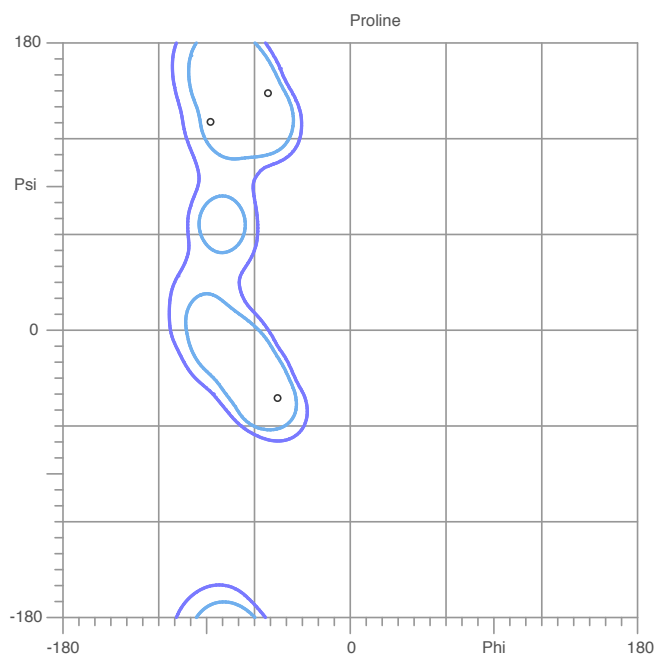
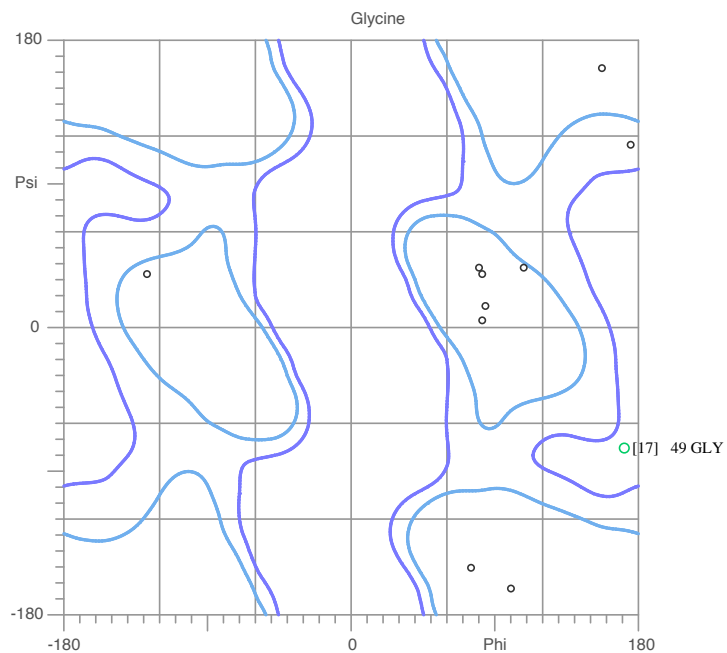
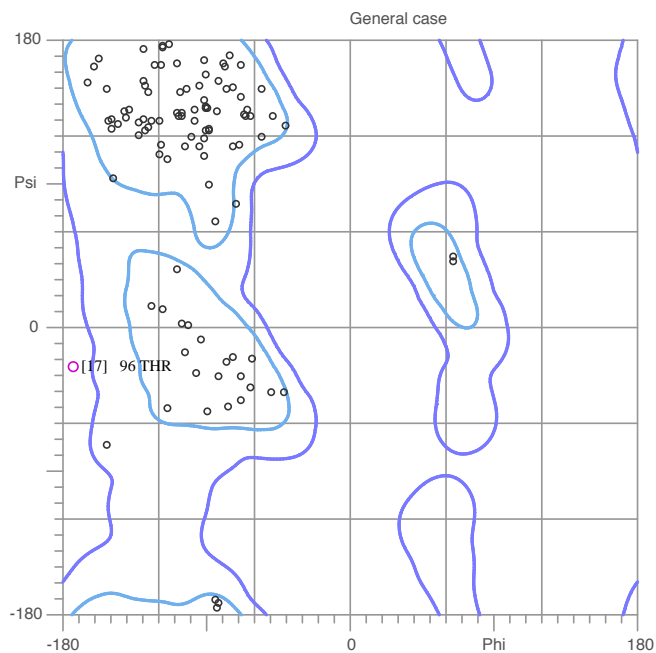


92.5% (111/120) of all residues were in favored (98%) regions.
98.3% (118/120) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[16] 74 ALA (49.8, -85.0)
[16] 93 SER (76.0, 135.2)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 17

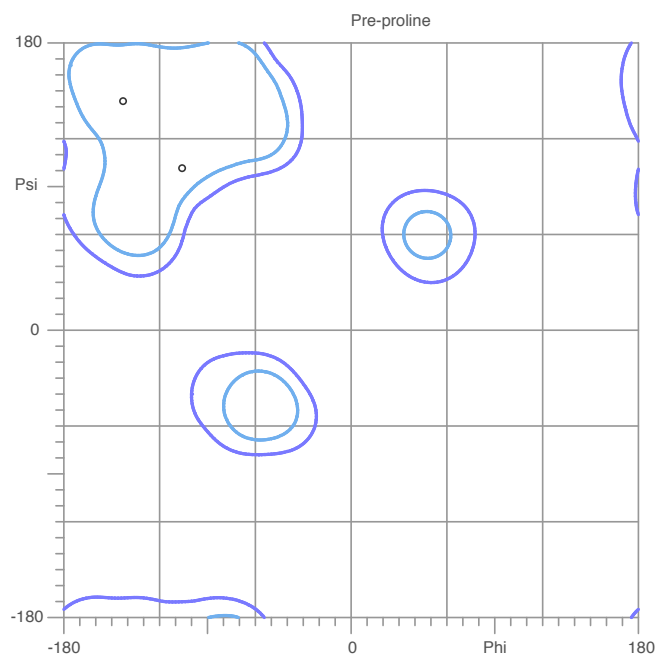
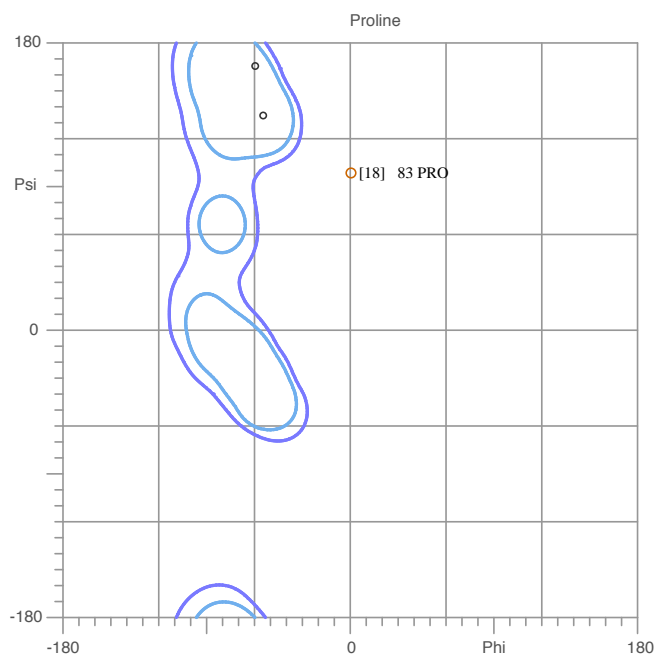
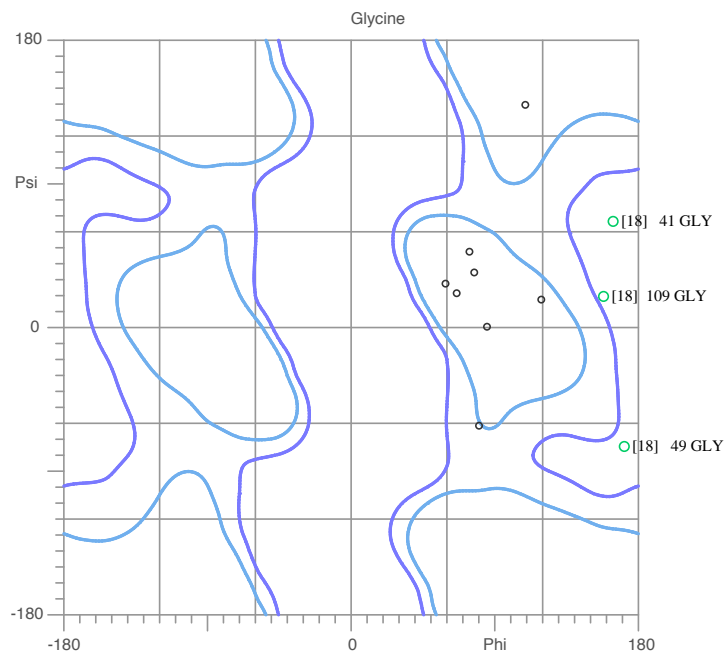
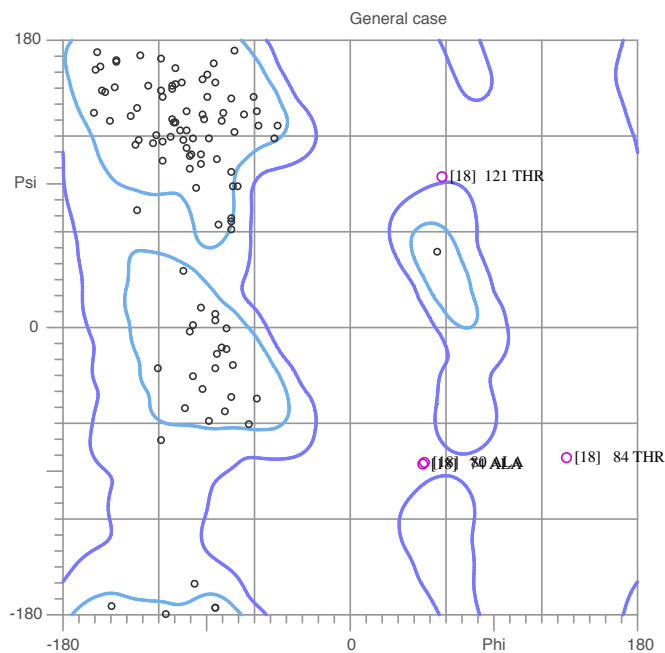


95.8% (115/120) of all residues were in favored (98%) regions.
98.3% (118/120) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[17] 49 GLY (171.2, -75.0)
[17] 96 THR (-175.0, -24.9)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 18



89.2% (107/120) of all residues were in favored (98%) regions.
93.3% (112/120) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[18] 41 GLY (164.9, 67.7)

[18] 49 GLY (171.4, -75.0)

[18] 74 ALA (45.0, -85.0)

[18] 80 ALA (46.7, -85.0)

[18] 83 PRO (0.0, 100.0)

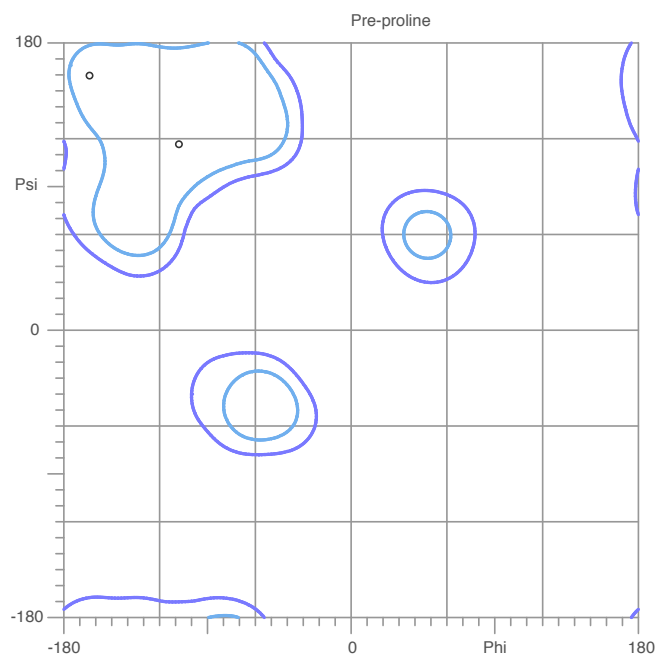
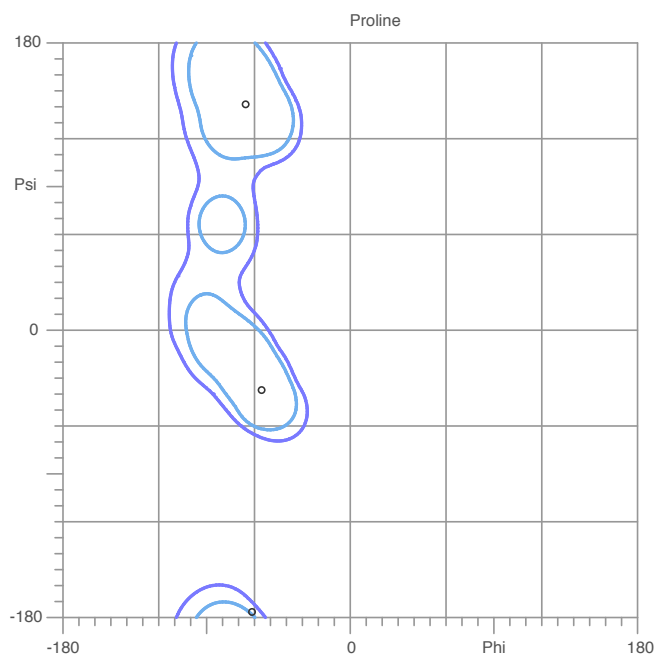
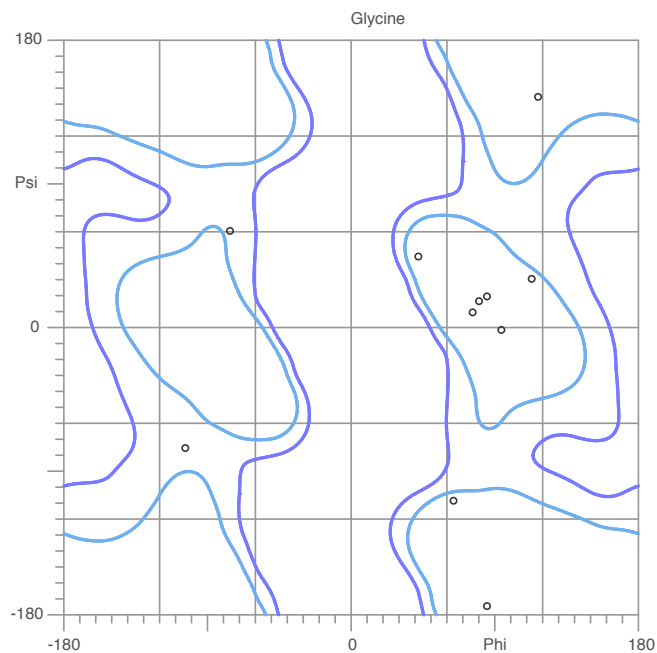
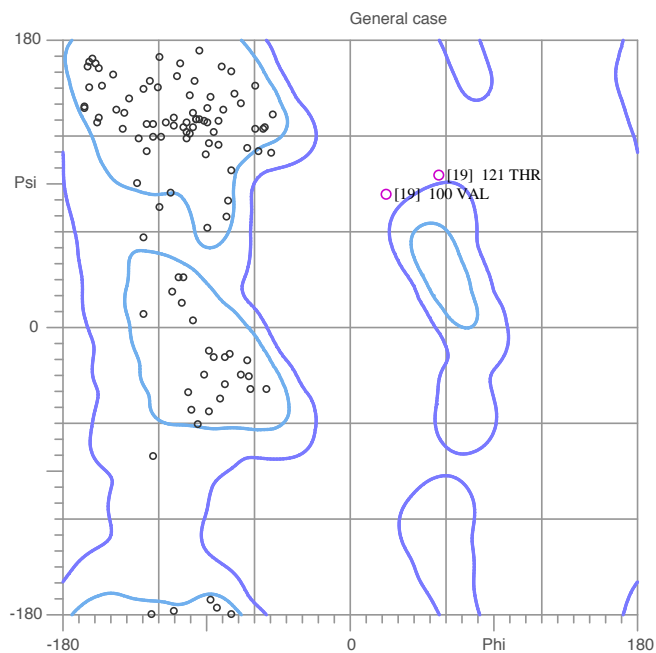
[18] 84 THR (135.6, -81.5)

[18] 109 GLY (158.0, 20.6)

[18] 121 THR (57.7, 95.5)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 19



92.5% (111/120) of all residues were in favored (98%) regions.
98.3% (118/120) of all residues were in allowed (>99.8%) regions.

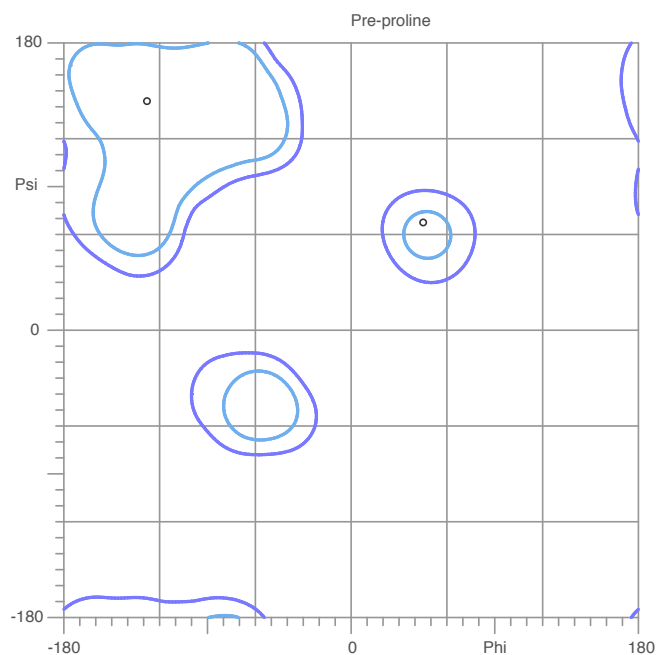
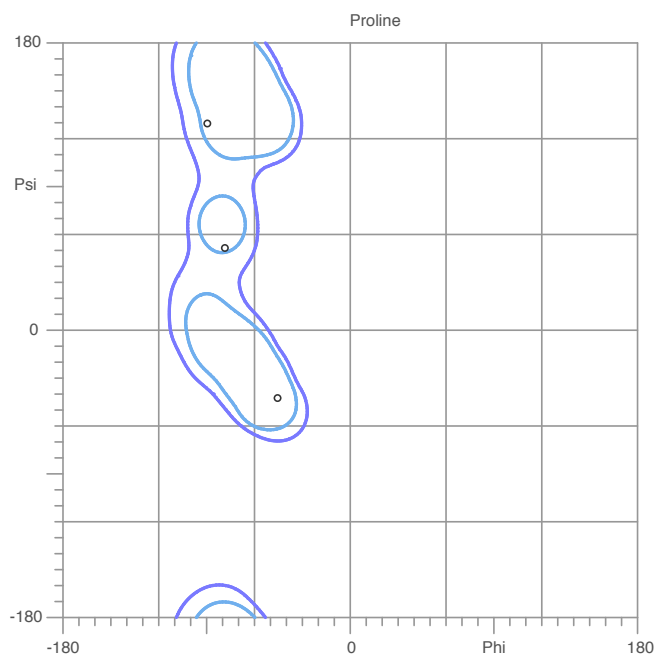
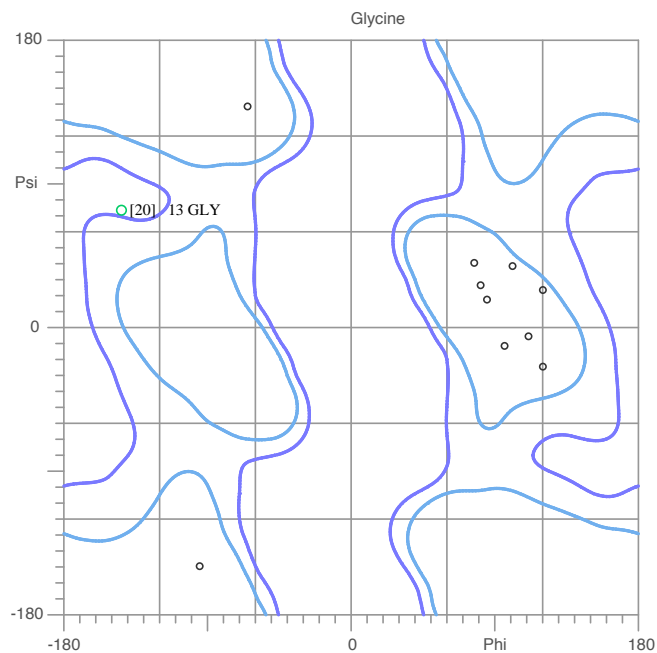
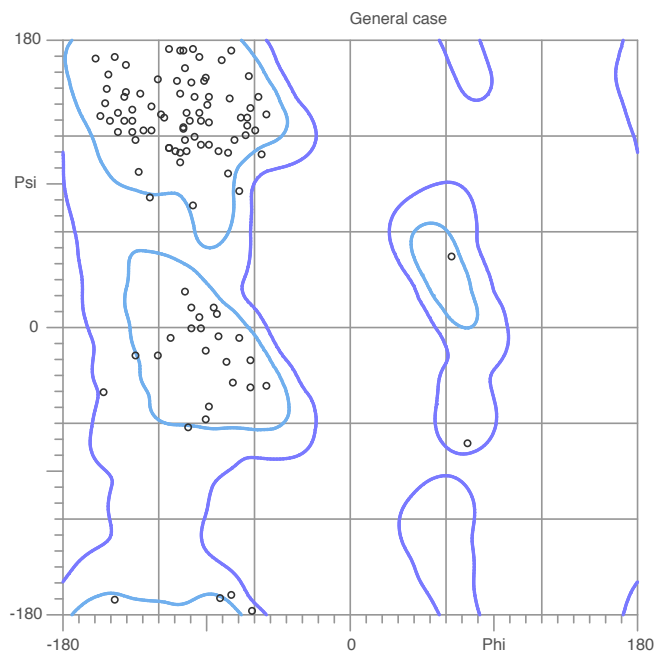
There were 2 outliers (phi, psi):

[19] 100 VAL (22.6, 84.9)

[19] 121 THR (55.2, 96.9)

MolProbity Ramachandran analysis

HR5546A_R3Cons_em_bcr3.pdb, model 20



91.7% (110/120) of all residues were in favored (98%) regions.
99.2% (119/120) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 13 GLY (-144.9, 74.0)

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

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