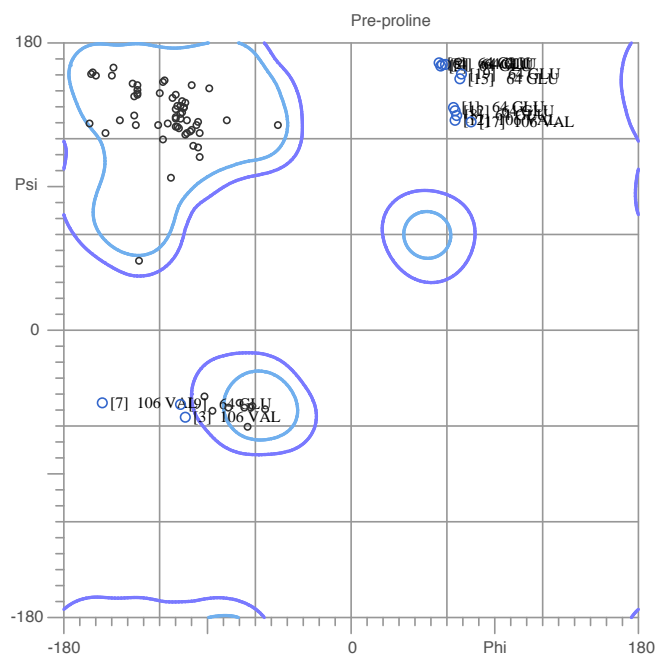
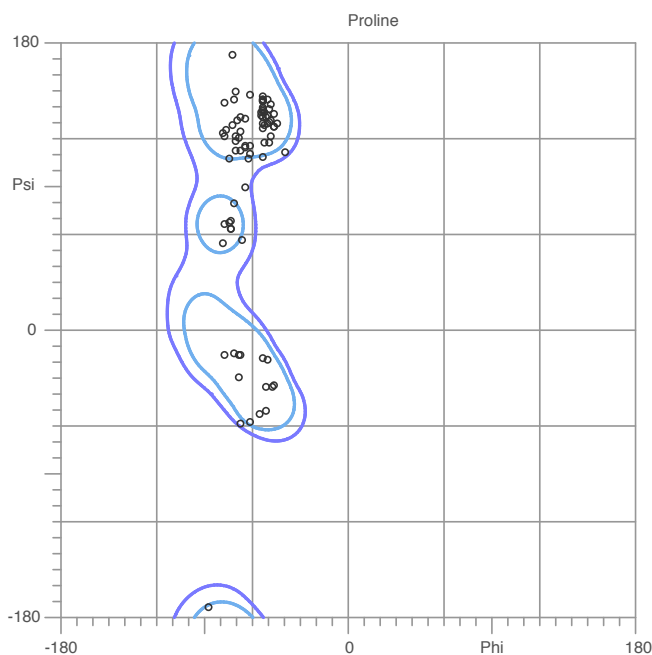
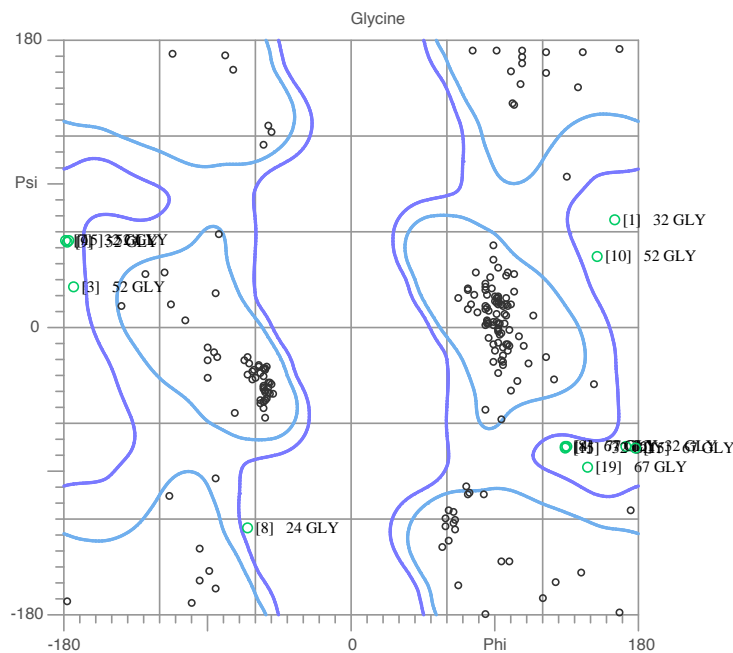
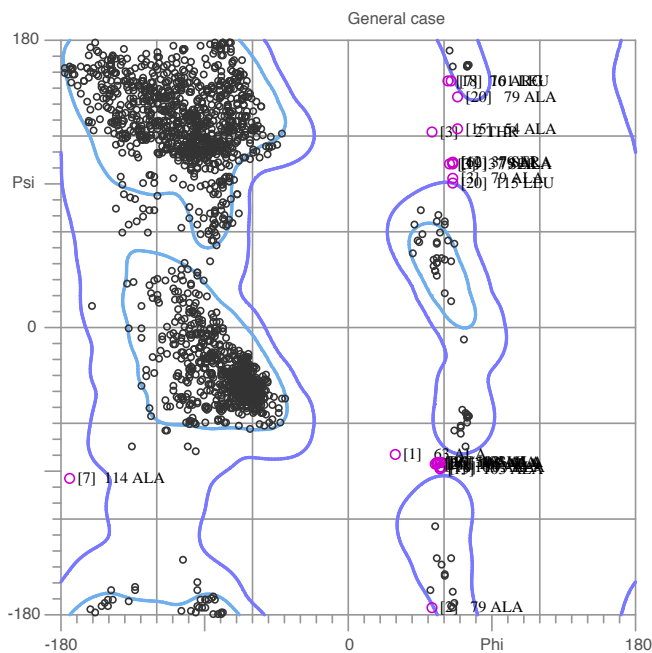


# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, all models



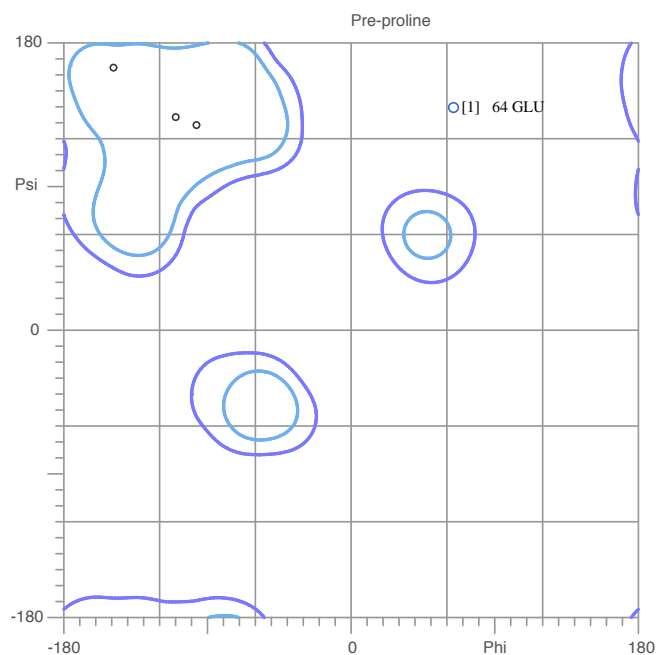
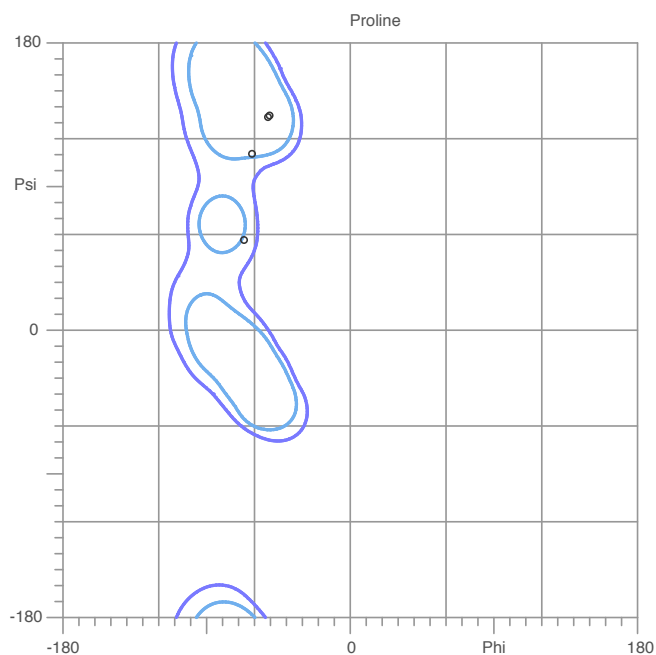
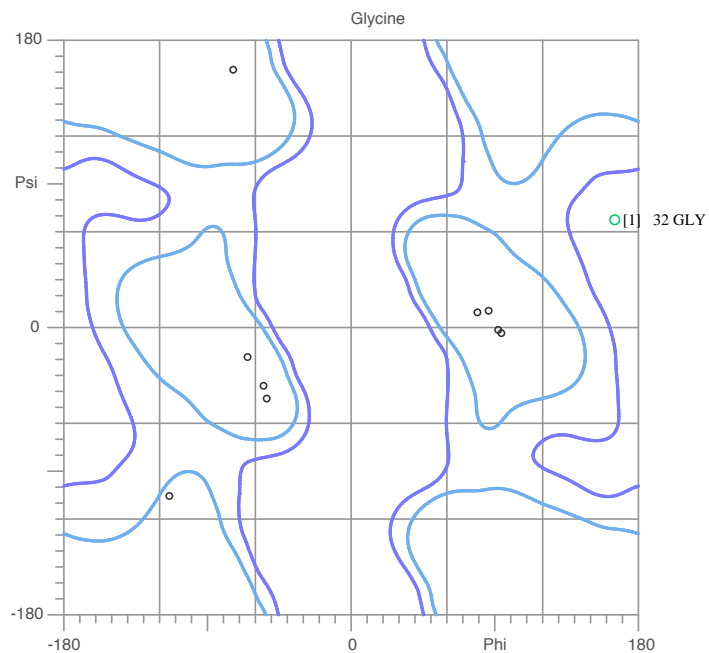
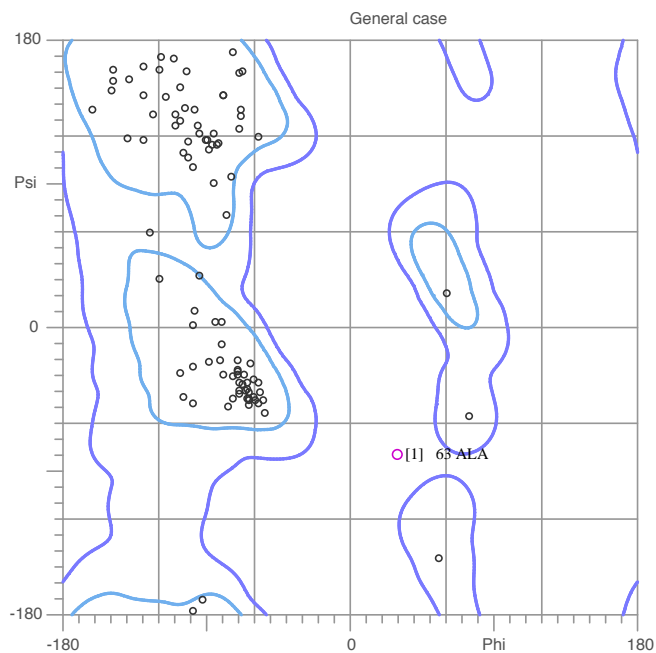
93.3% (2128/2280) of all residues were in favored (98%) regions.  
97.8% (2230/2280) of all residues were in allowed (>99.8%) regions.

There were 50 outliers (phi, psi):

- |                             |                            |
|-----------------------------|----------------------------|
| [1] 32 GLY (165.0, 68.5)    | [8] 64 GLU (66.3, 135.8)   |
| [1] 63 ALA (29.8, -79.1)    | [8] 67 GLY (134.9, -75.0)  |
| [1] 64 GLU (64.7, 140.4)    | [9] 52 GLY (-178.2, 55.0)  |
| [2] 64 GLU (57.6, 167.2)    | [9] 54 ALA (55.3, -85.0)   |
| [2] 79 ALA (52.2, -175.0)   | [9] 64 GLU (-107.6, -47.0) |
| [3] 2 THR (52.2, 124.0)     | [10] 52 GLY (155.0, 45.7)  |
| [3] 37 SER (63.3, 103.0)    | [12] 64 GLU (65.0, 138.2)  |
| [3] 52 GLY (-174.9, 26.9)   | [12] 79 ALA (65.0, 104.7)  |
| [3] 79 ALA (65.1, 94.9)     | [12] 106 VAL (65.2, 132.9) |
| [3] 103 ALA (58.7, -84.3)   | [13] 103 ALA (57.1, -88.2) |
| [3] 106 VAL (-104.5, -54.9) | [14] 103 ALA (54.4, -85.0) |
| [4] 64 GLU (60.0, 167.3)    | [15] 32 GLY (135.0, -75.0) |
| [4] 77 GLY (135.0, -74.9)   | [15] 52 GLY (-177.7, 55.1) |
| [5] 64 GLU (56.6, 166.4)    | [15] 54 ALA (68.0, 125.1)  |
| [6] 32 GLY (172.2, -75.0)   | [15] 64 GLU (68.0, 158.4)  |
| [6] 37 SER (65.0, 105.0)    | [15] 67 GLY (178.9, -75.0) |
| [6] 64 GLU (55.7, 168.7)    | [16] 103 ALA (56.7, -84.9) |
| [7] 32 GLY (-179.4, 55.1)   | [17] 106 VAL (75.1, 131.3) |
| [7] 76 ARG (64.9, 155.0)    | [18] 101 LEU (62.8, 155.0) |
| [7] 103 ALA (57.5, -87.5)   | [18] 103 ALA (58.7, -87.7) |
| [7] 106 VAL (-156.6, -45.1) | [19] 64 GLU (69.7, 161.6)  |
| [7] 114 ALA (-175.0, -95.0) | [19] 67 GLY (148.9, -87.8) |
| [8] 24 GLY (-65.9, -125.1)  | [19] 79 ALA (65.1, 105.1)  |
|                             | [19] 103 ALA (57.9, -84.9) |
|                             | [20] 79 ALA (68.8, 145.3)  |
|                             | [20] 103 ALA (55.7, -85.1) |
|                             | [20] 115 LEU (65.2, 91.3)  |

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 1



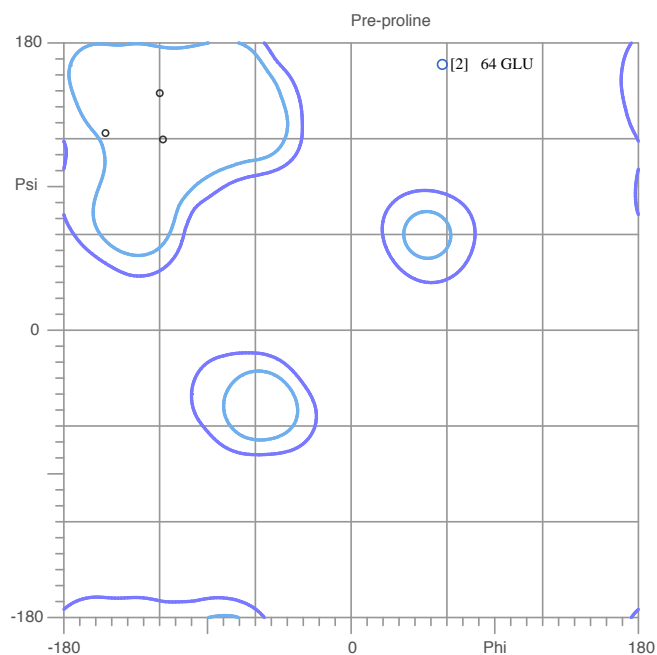
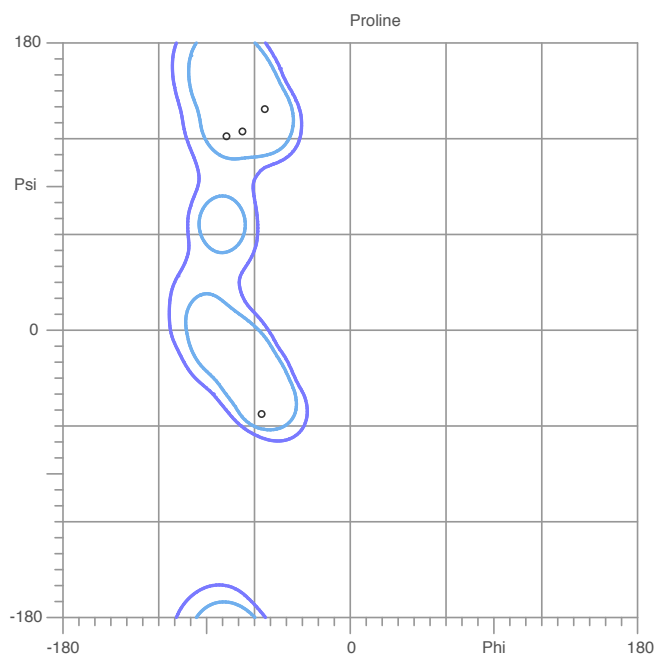
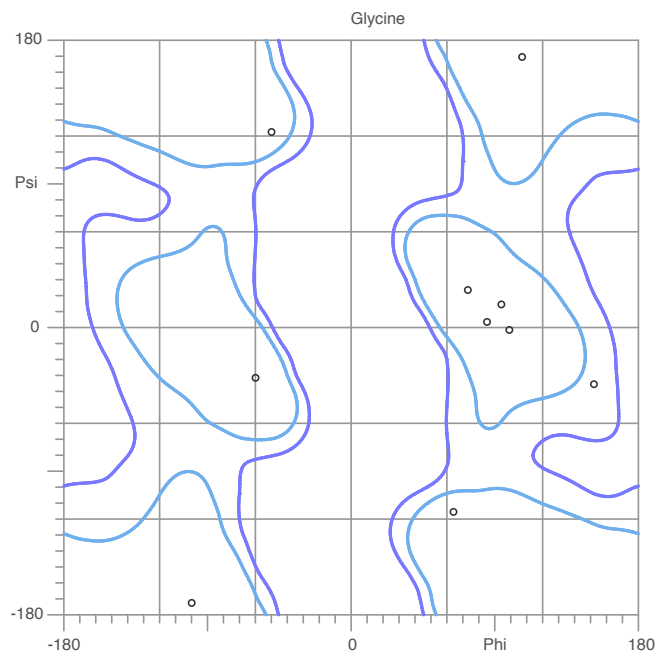
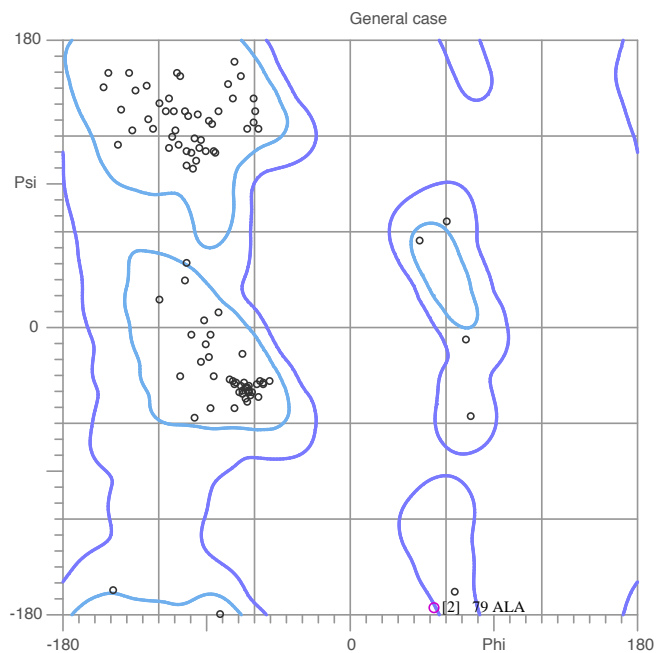
93.9% (107/114) of all residues were in favored (98%) regions.  
97.4% (111/114) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 32 GLY (165.0, 68.5)
- [1] 63 ALA (29.8, -79.1)
- [1] 64 GLU (64.7, 140.4)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 2



92.1% (105/114) of all residues were in favored (98%) regions.  
98.2% (112/114) of all residues were in allowed (>99.8%) regions.

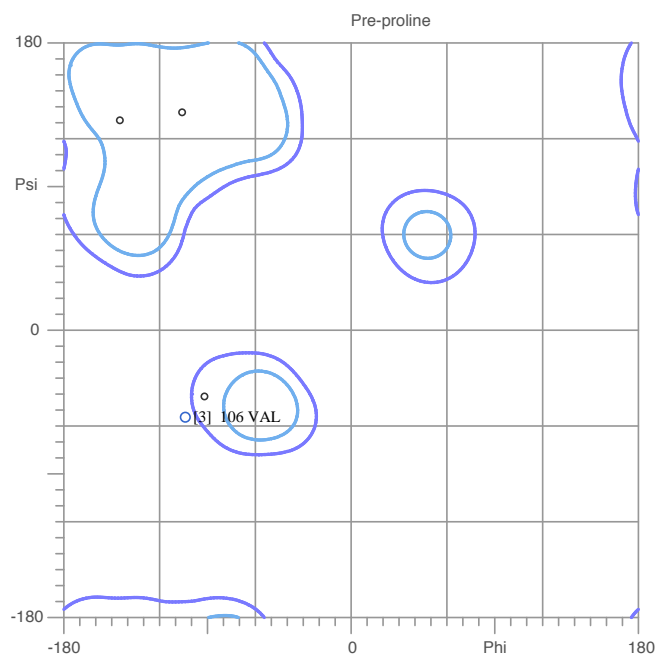
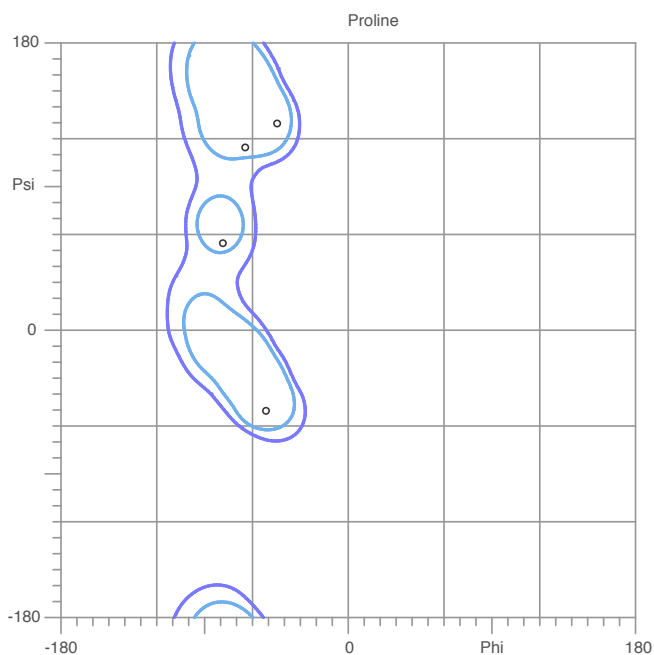
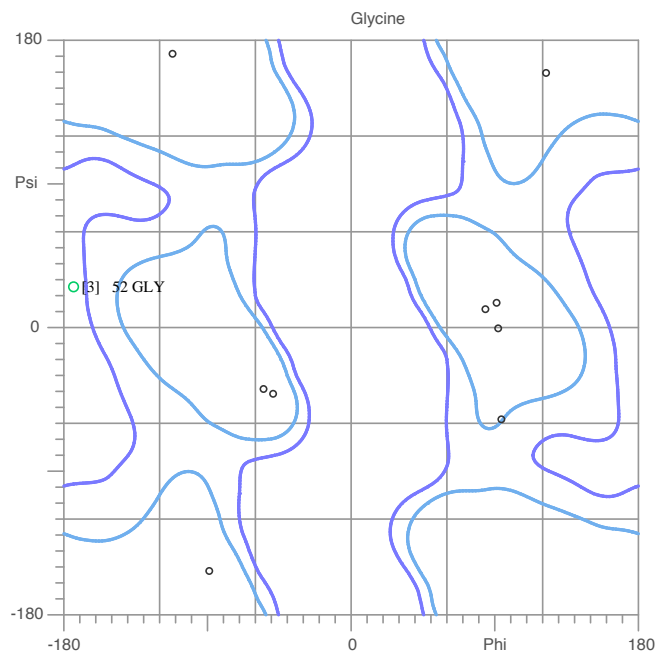
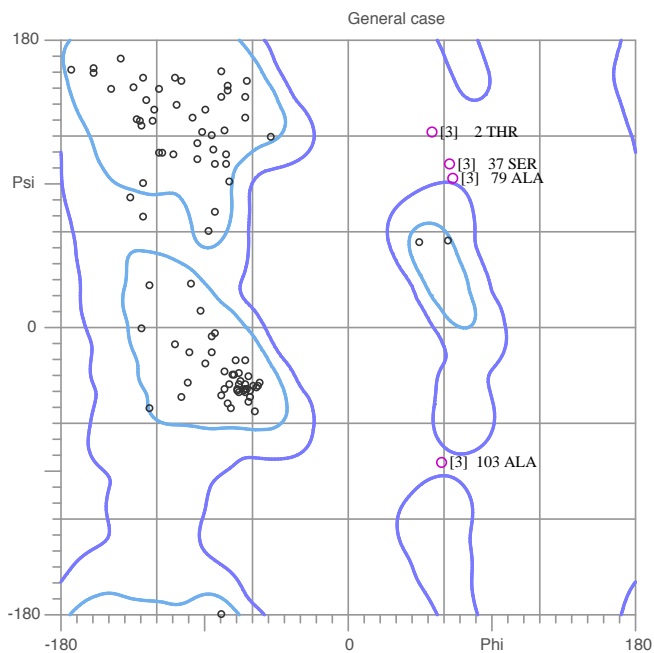
There were 2 outliers (phi, psi):

[2] 64 GLU (57.6, 167.2)

[2] 79 ALA (52.2, -175.0)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 3



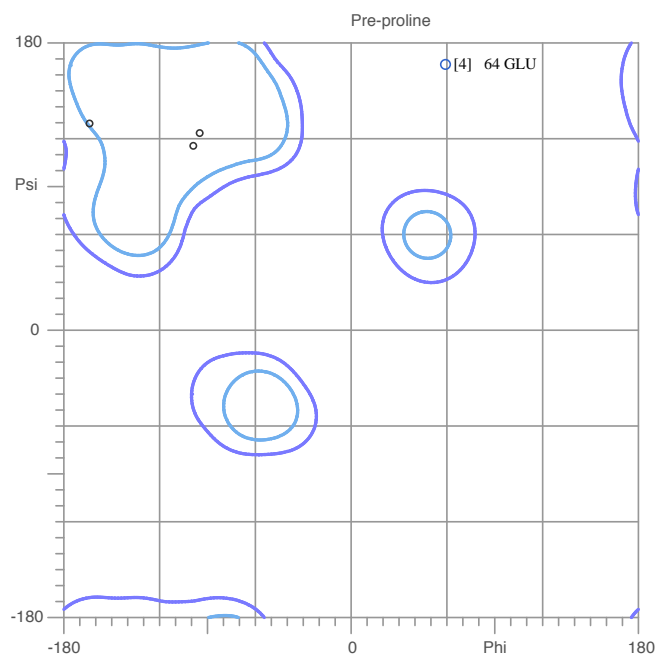
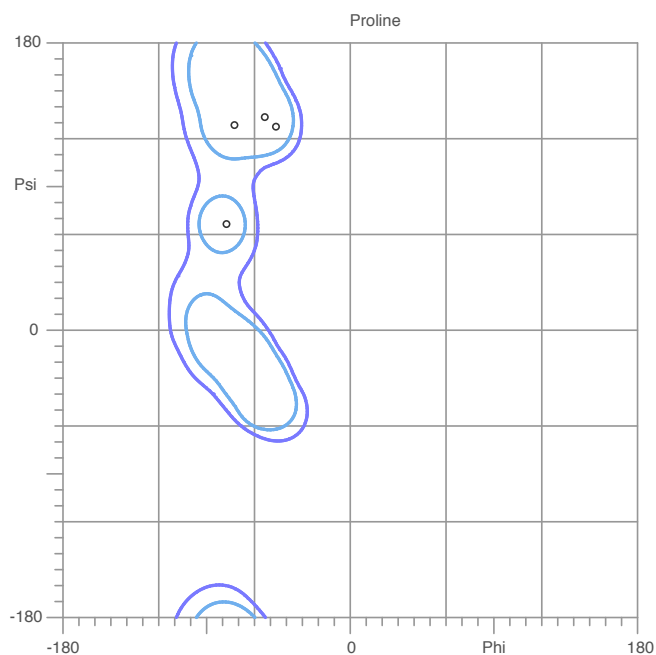
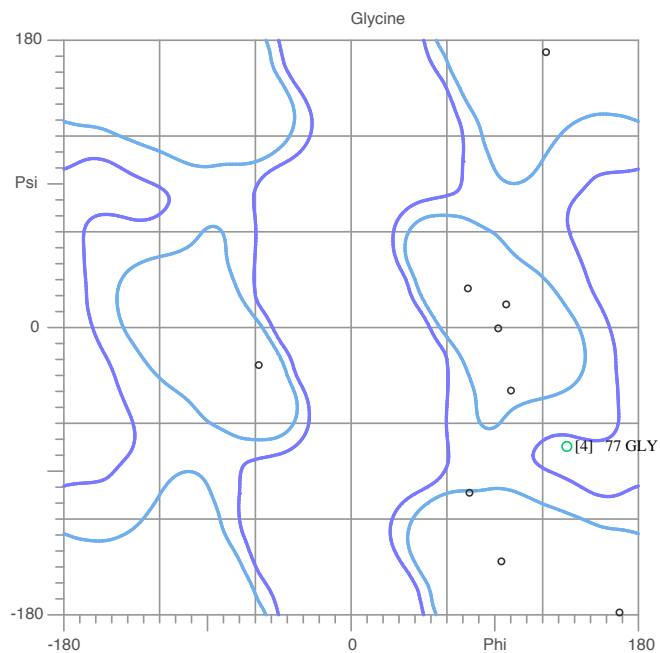
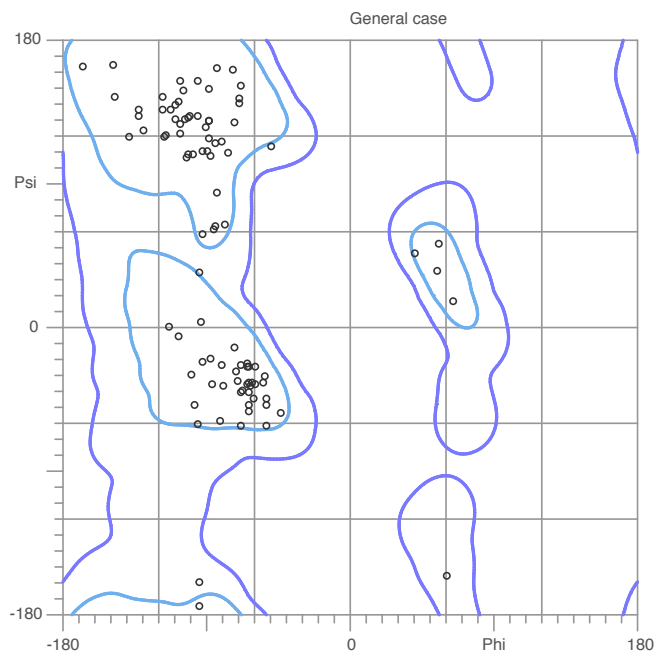
91.2% (104/114) of all residues were in favored (98%) regions.  
94.7% (108/114) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):  
[3] 2 THR (52.2, 124.0)

[3] 37 SER (63.3, 103.0)  
[3] 52 GLY (-174.9, 26.9)  
[3] 79 ALA (65.1, 94.9)  
[3] 103 ALA (58.7, -84.3)  
[3] 106 VAL (-104.5, -54.9)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 4



94.7% (108/114) of all residues were in favored (98%) regions.  
98.2% (112/114) of all residues were in allowed (>99.8%) regions.

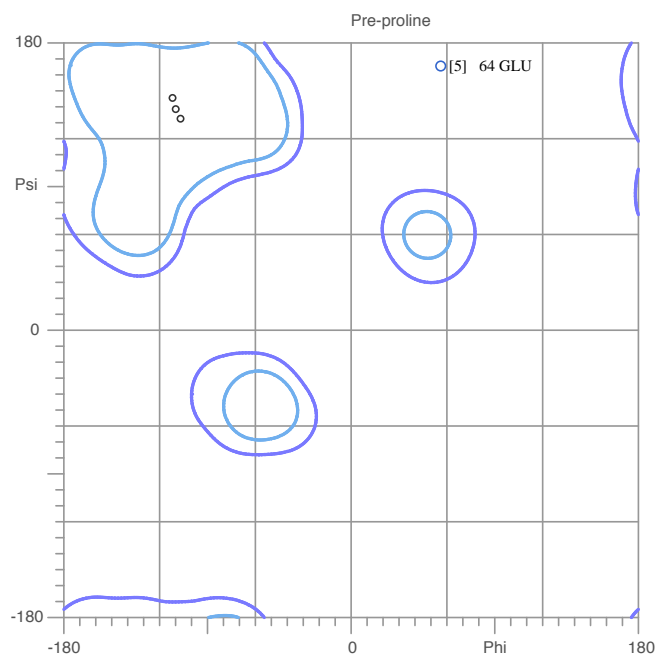
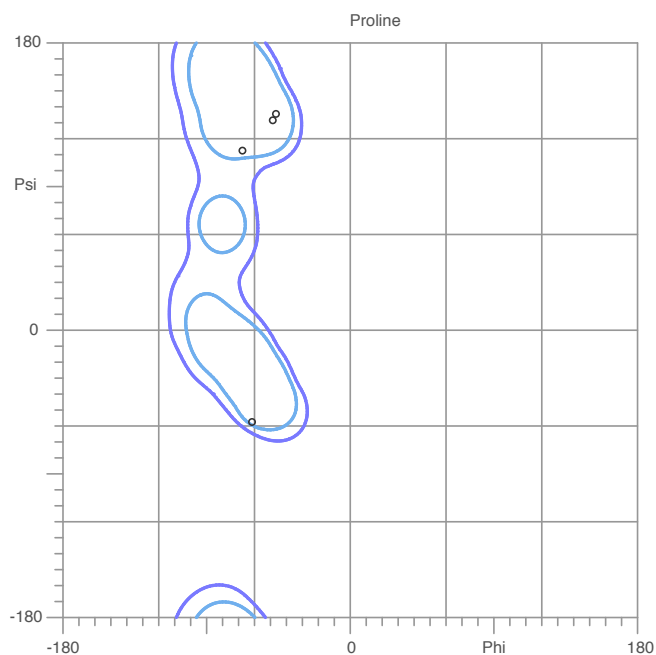
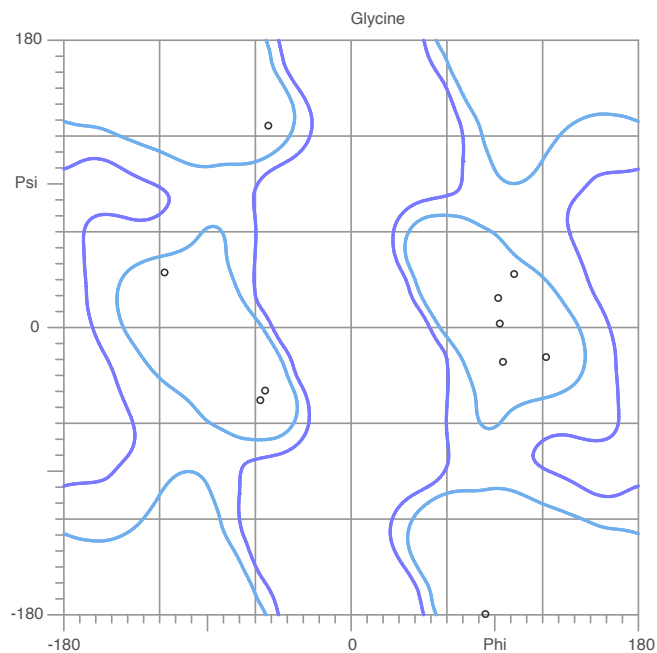
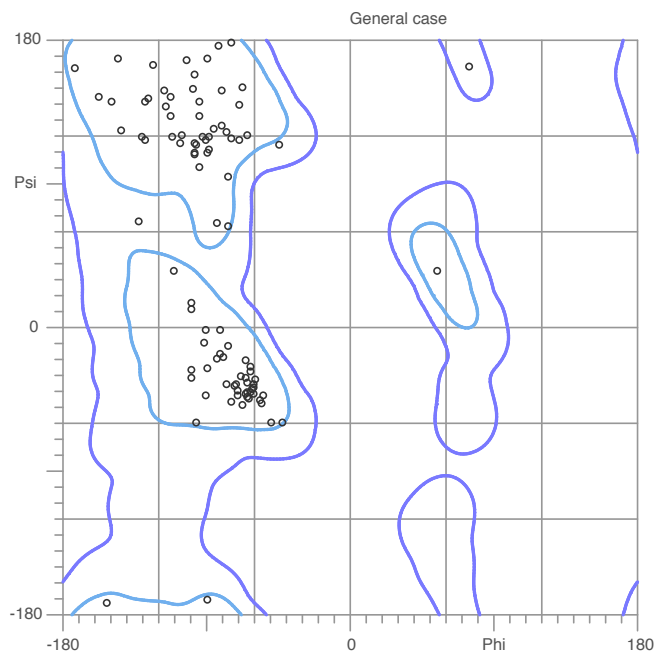
There were 2 outliers (phi, psi):

[4] 64 GLU (60.0, 167.3)

[4] 77 GLY (135.0, -74.9)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 5



96.5% (110/114) of all residues were in favored (98%) regions.  
99.1% (113/114) of all residues were in allowed (>99.8%) regions.

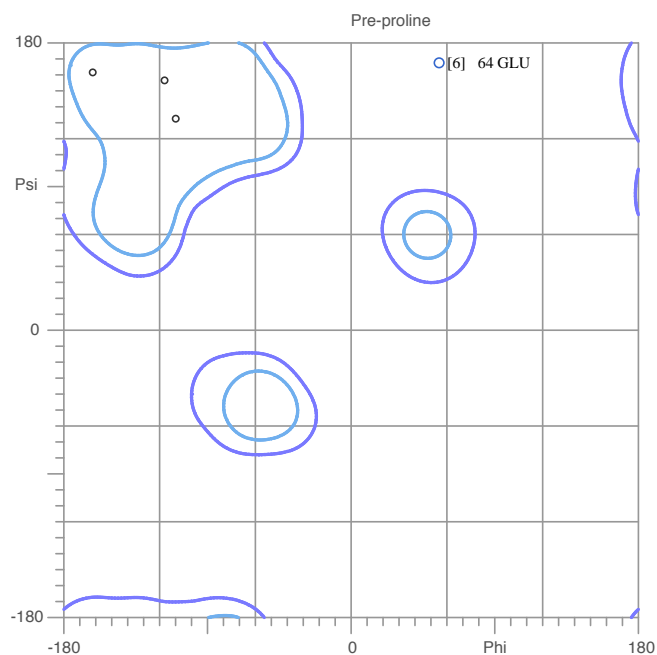
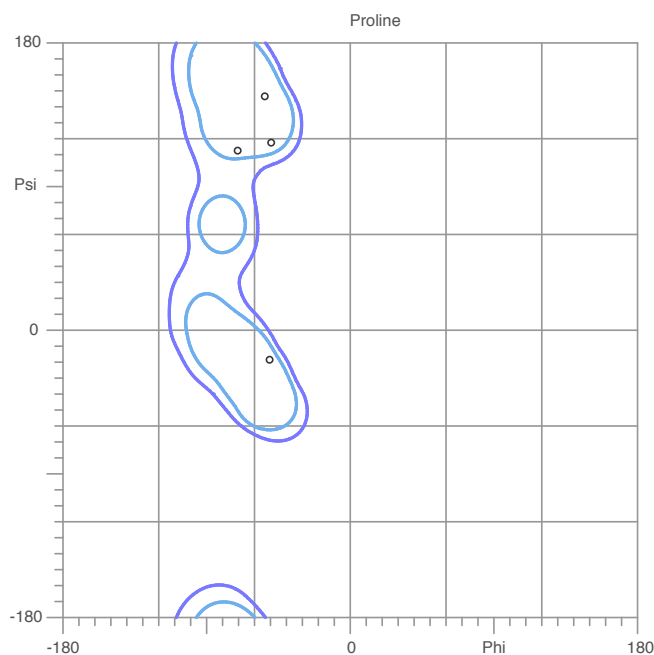
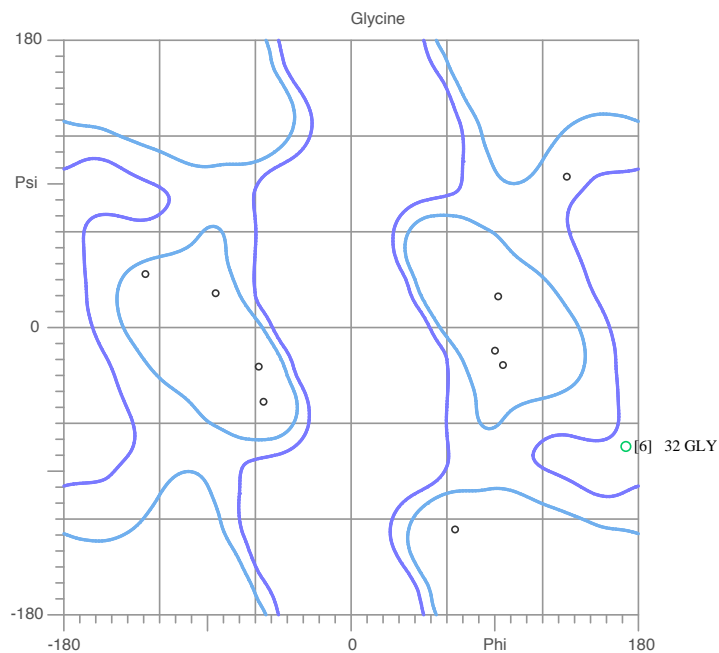
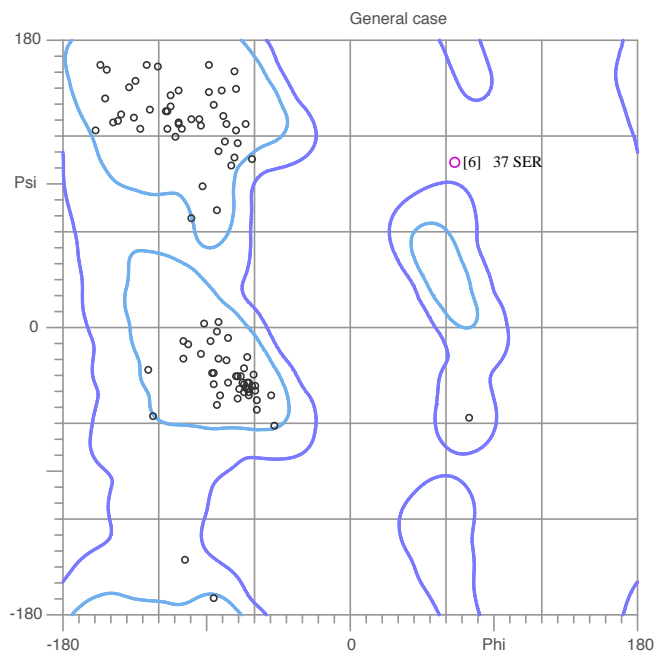
There were 1 outliers (phi, psi):  
[5] 64 GLU (56.6, 166.4)

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# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 6



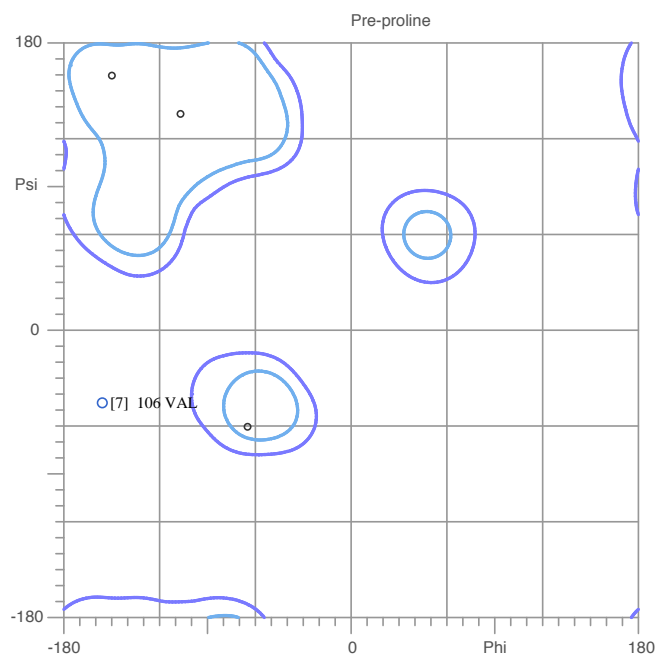
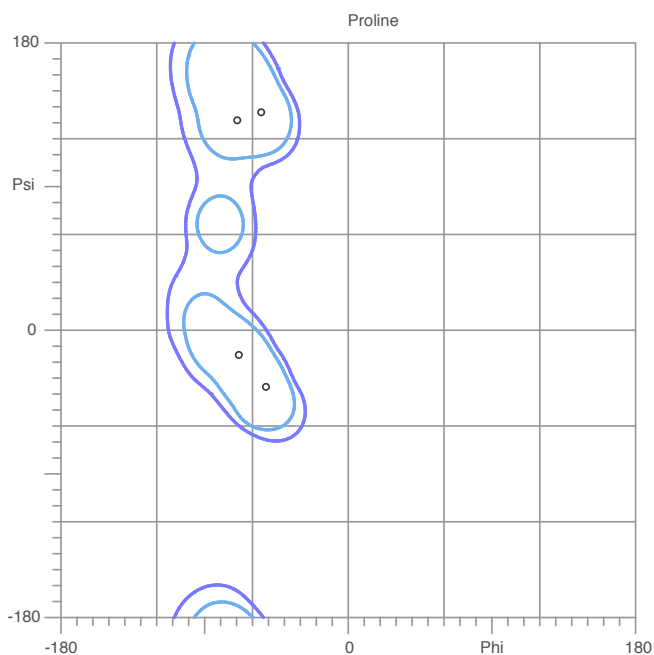
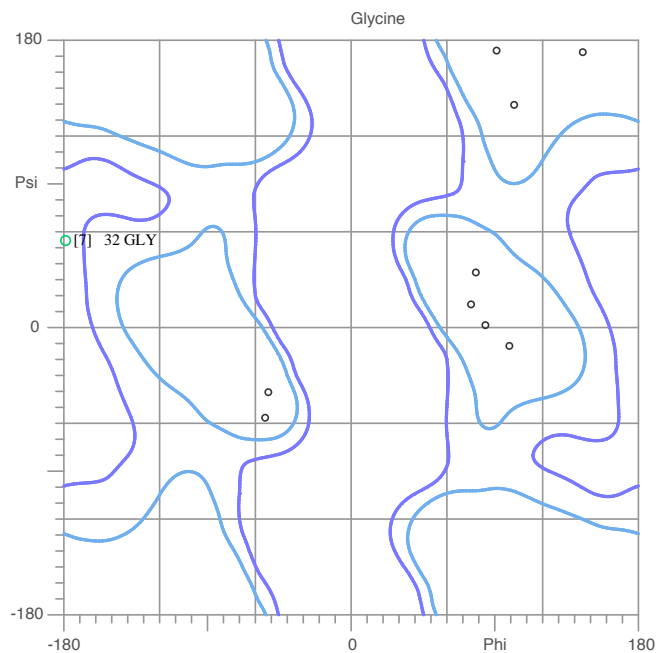
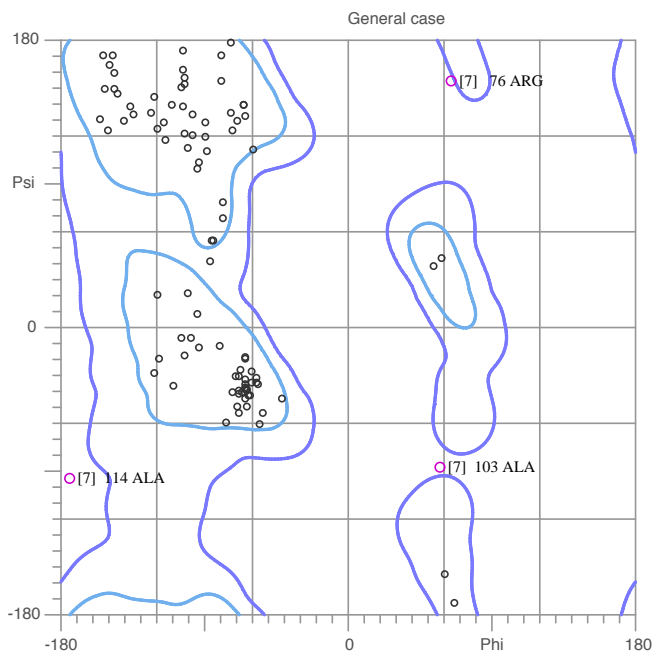
92.1% (105/114) of all residues were in favored (98%) regions.  
97.4% (111/114) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 32 GLY (172.2, -75.0)
- [6] 37 SER (65.0, 105.0)
- [6] 64 GLU (55.7, 168.7)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 7



93.0% (106/114) of all residues were in favored (98%) regions.  
95.6% (109/114) of all residues were in allowed (>99.8%) regions.

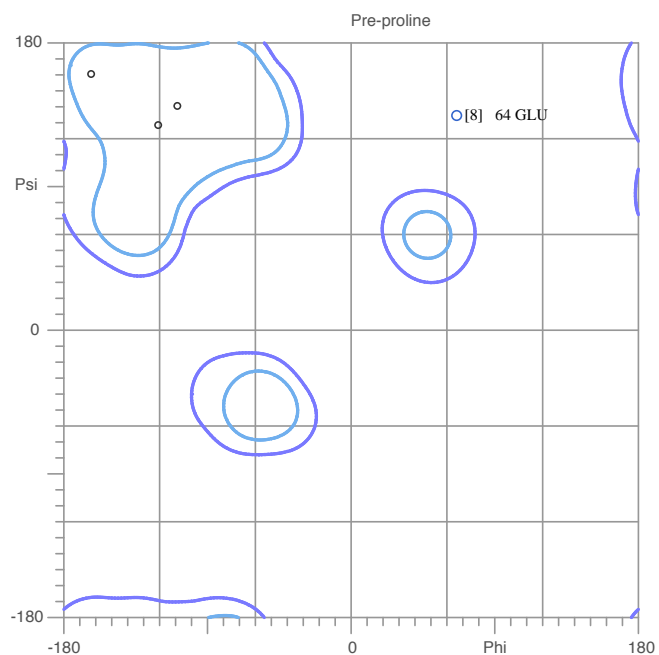
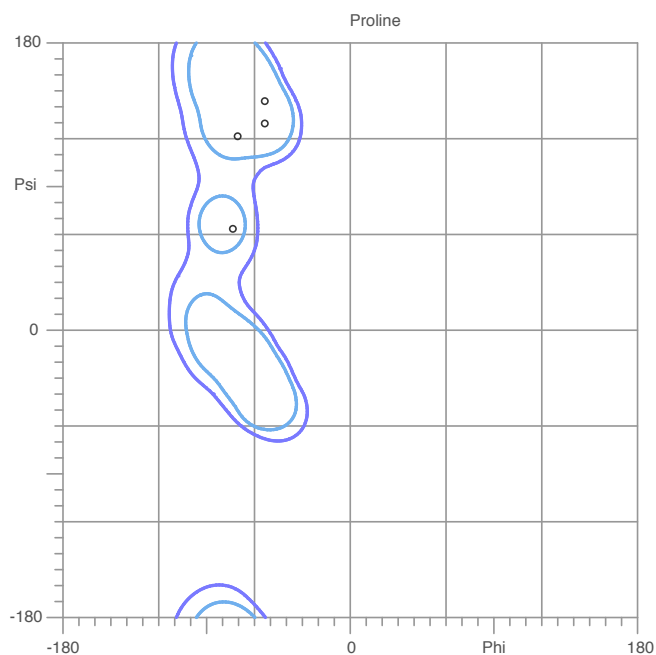
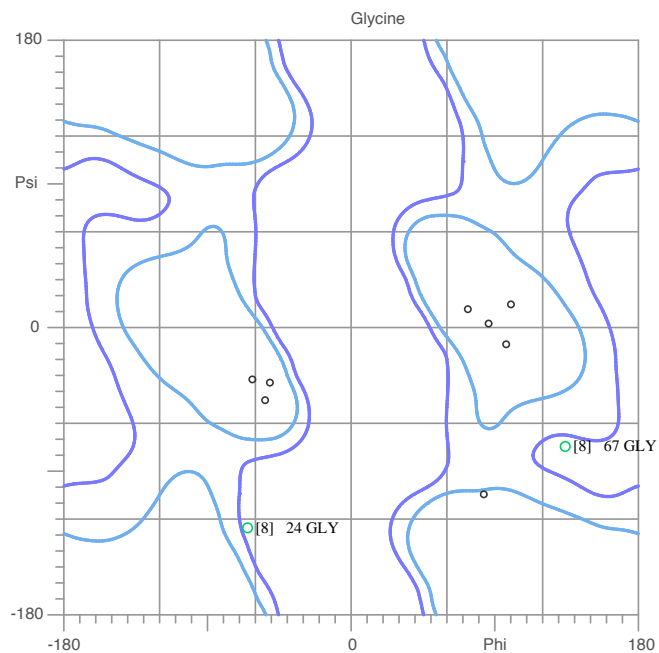
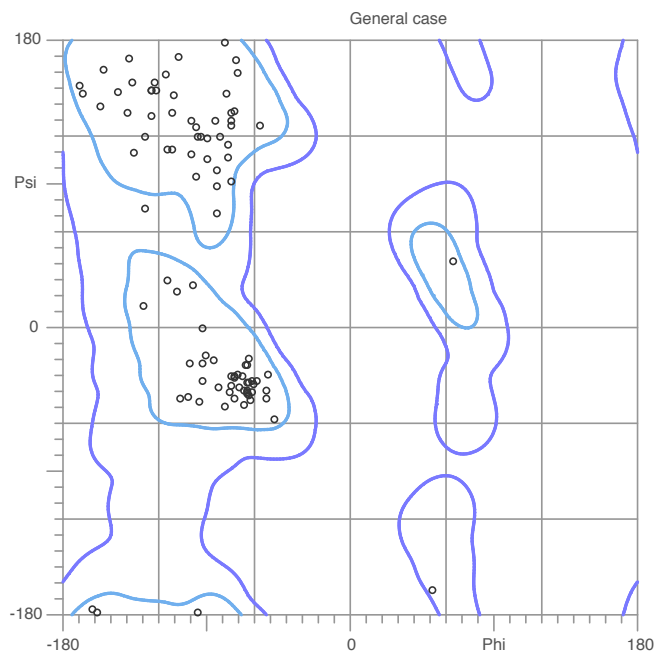
There were 5 outliers (phi, psi):

[7] 32 GLY (-179.4, 55.1)  
[7] 76 ARG (64.9, 155.0)  
[7] 103 ALA (57.5, -87.5)  
[7] 106 VAL (-156.6, -45.1)  
[7] 114 ALA (-175.0, -95.0)



# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 8



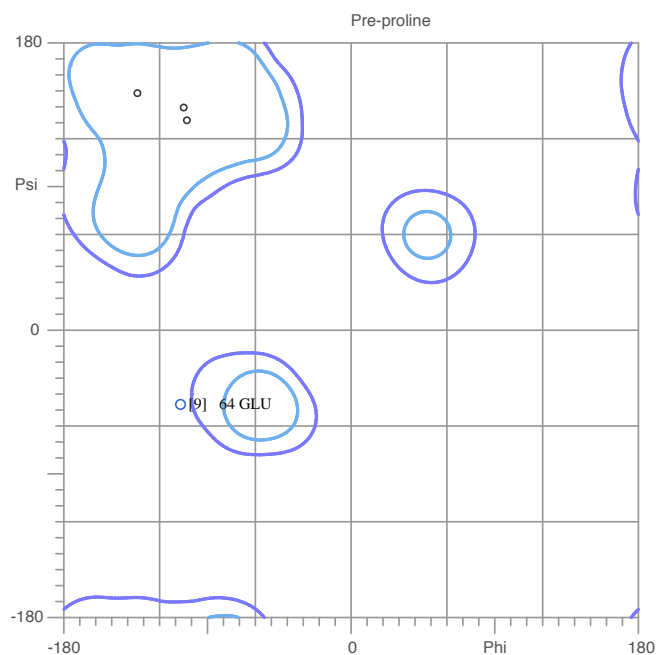
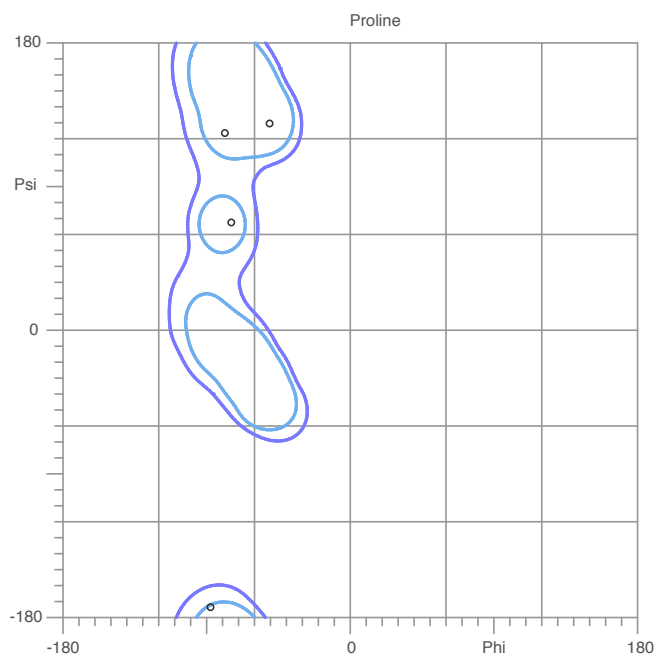
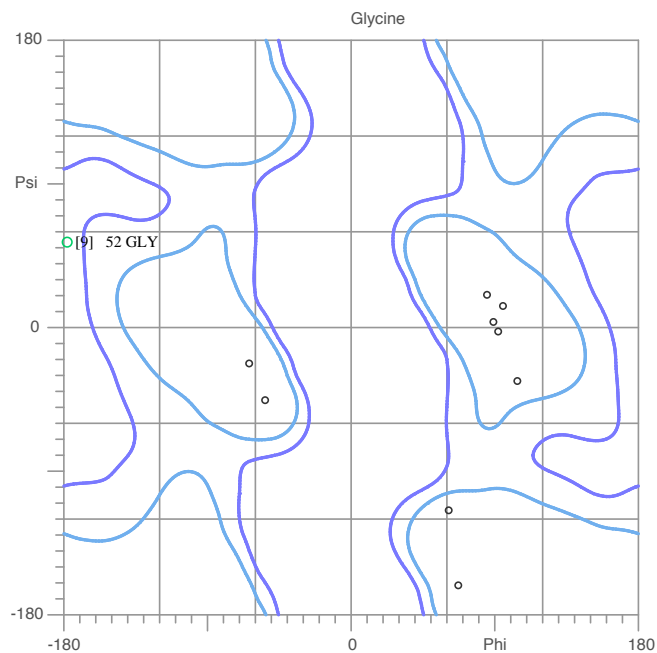
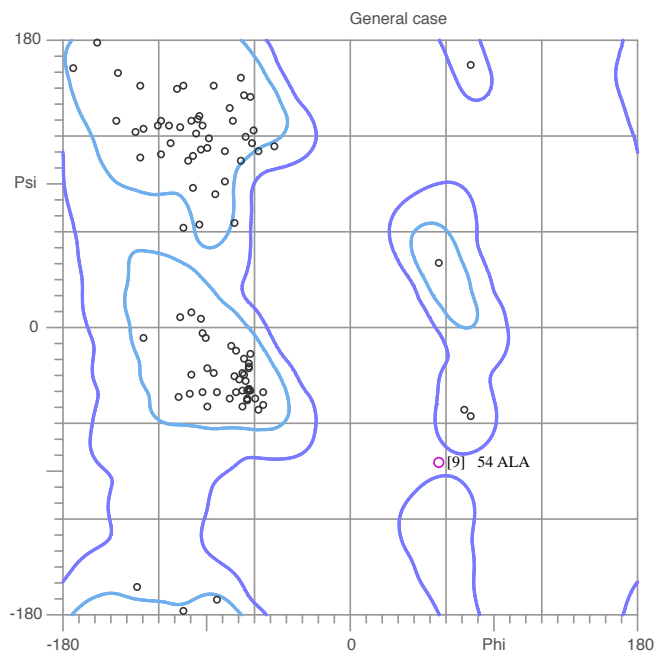
95.6% (109/114) of all residues were in favored (98%) regions.  
97.4% (111/114) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 24 GLY (-65.9, -125.1)
- [8] 64 GLU (66.3, 135.8)
- [8] 67 GLY (134.9, -75.0)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 9



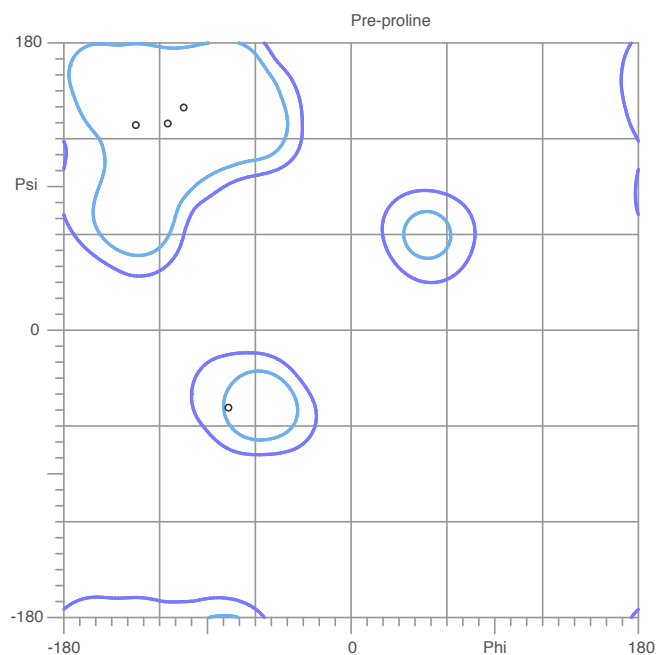
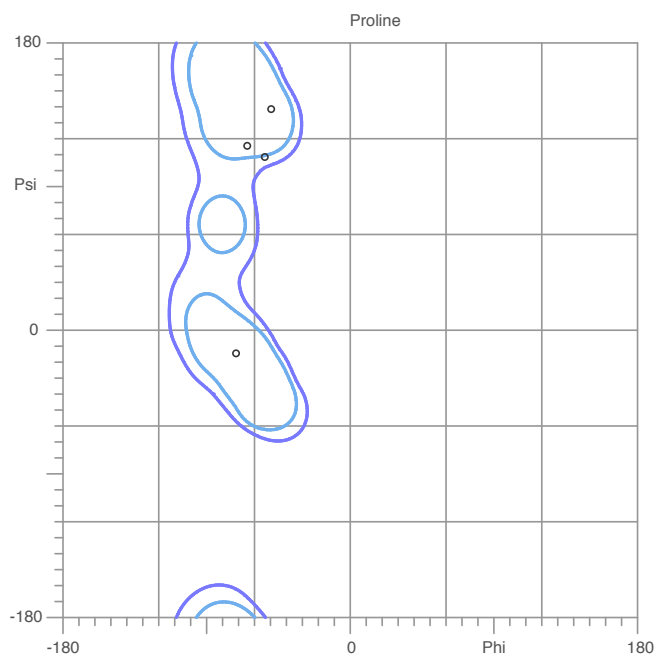
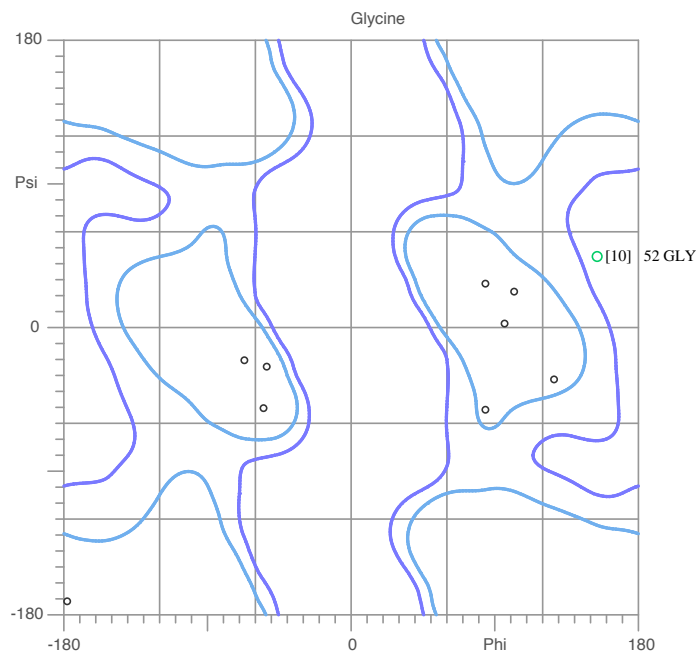
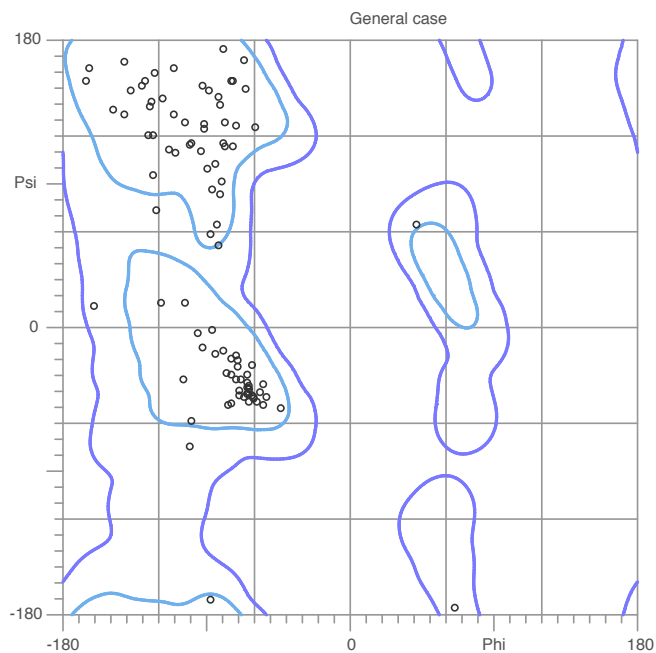
91.2% (104/114) of all residues were in favored (98%) regions.  
97.4% (111/114) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [9] 52 GLY (-178.2, 55.0)
- [9] 54 ALA (55.3, -85.0)
- [9] 64 GLU (-107.6, -47.0)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 10



94.7% (108/114) of all residues were in favored (98%) regions.  
99.1% (113/114) of all residues were in allowed (>99.8%) regions.

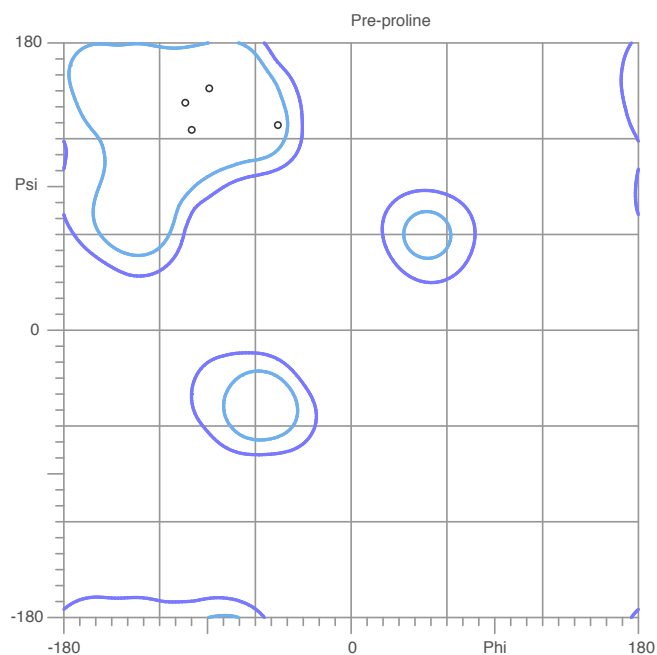
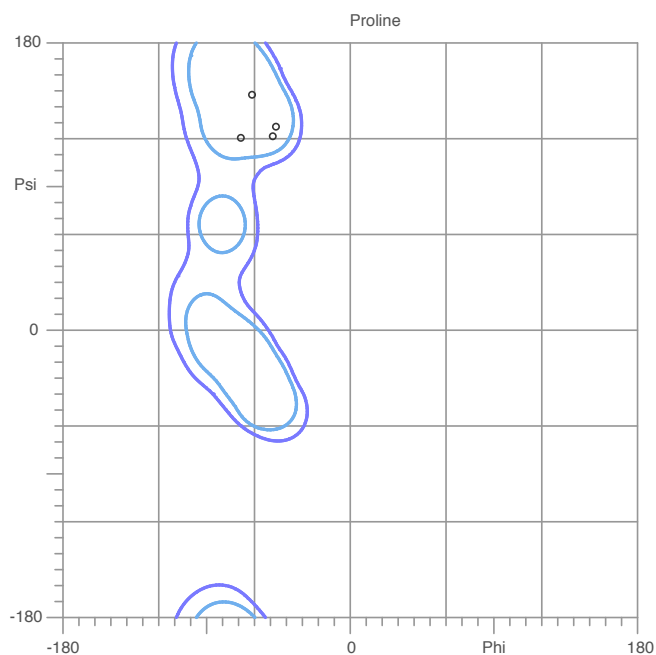
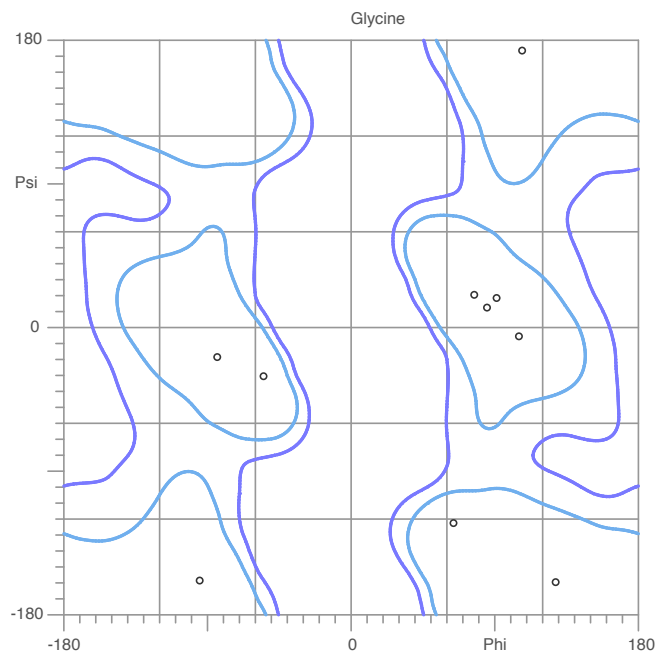
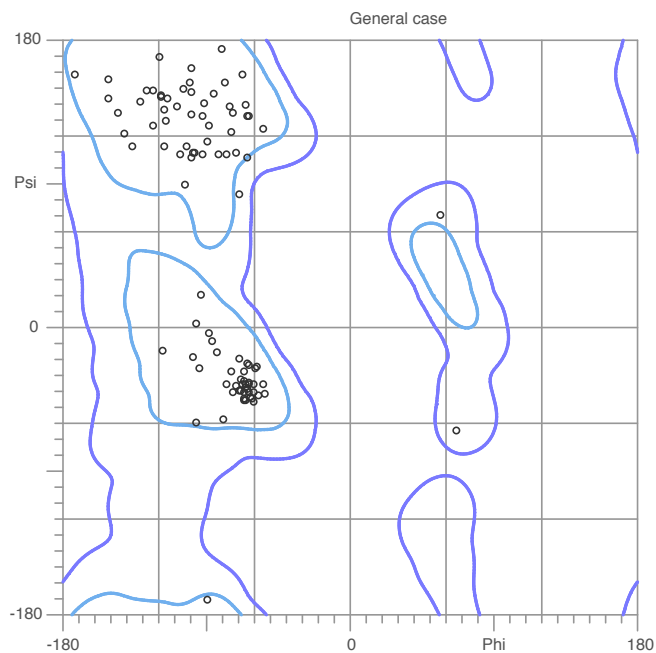
There were 1 outliers (phi, psi):  
[10] 52 GLY (155.0, 45.7)

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# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 11

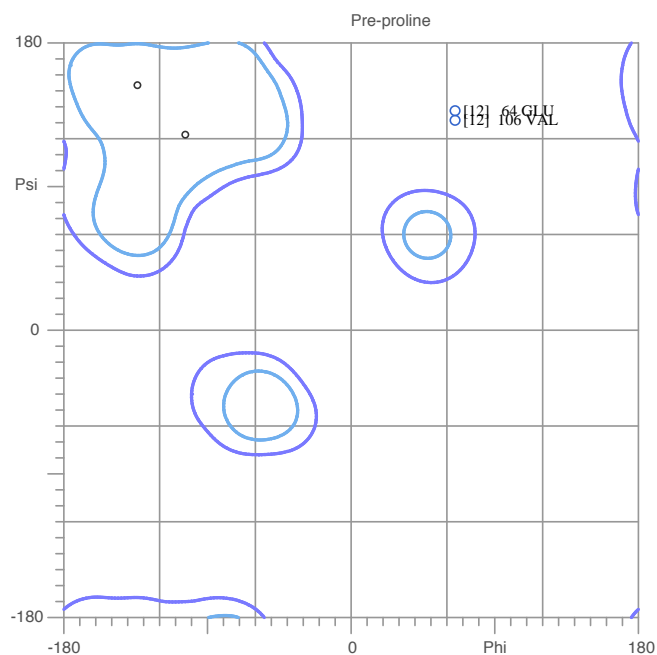
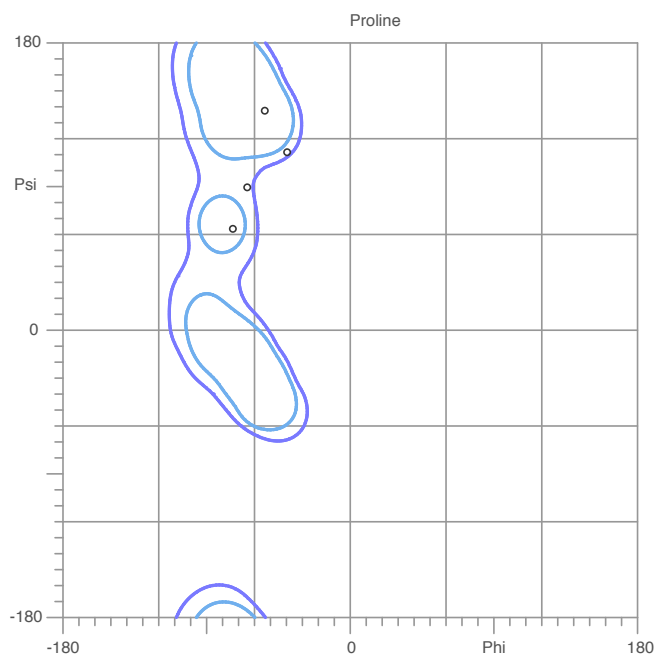
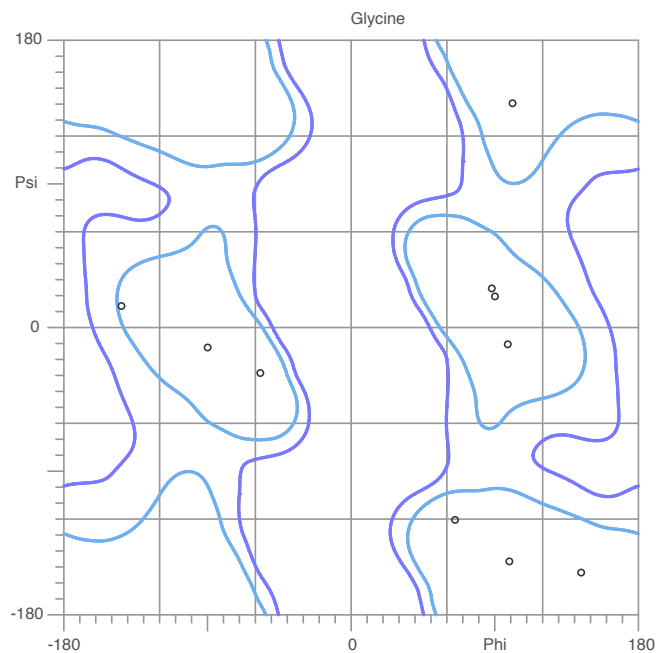
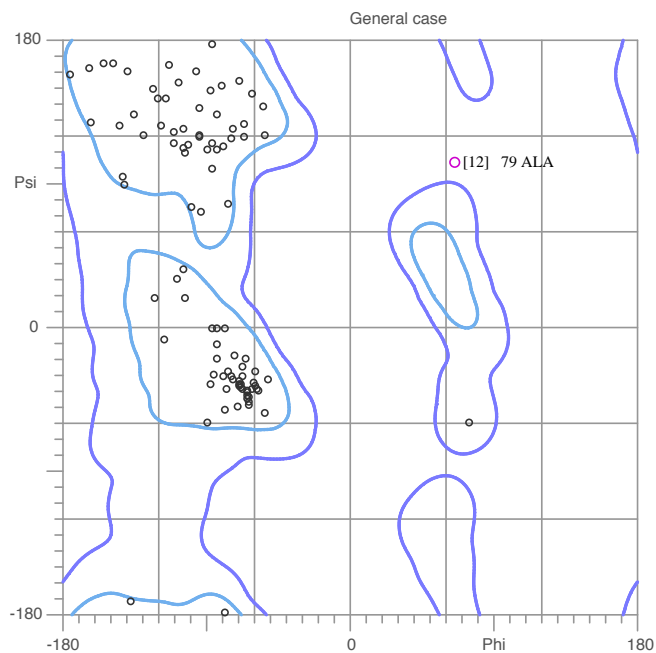


97.4% (111/114) of all residues were in favored (98%) regions.  
100.0% (114/114) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 12



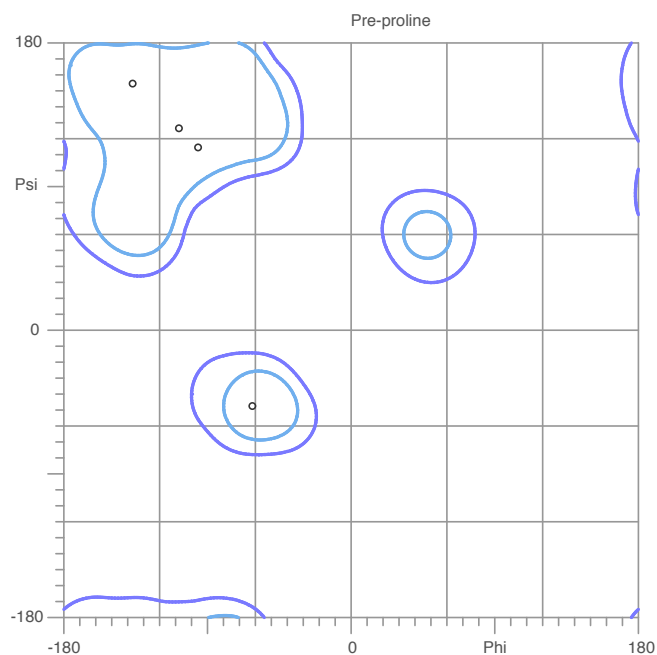
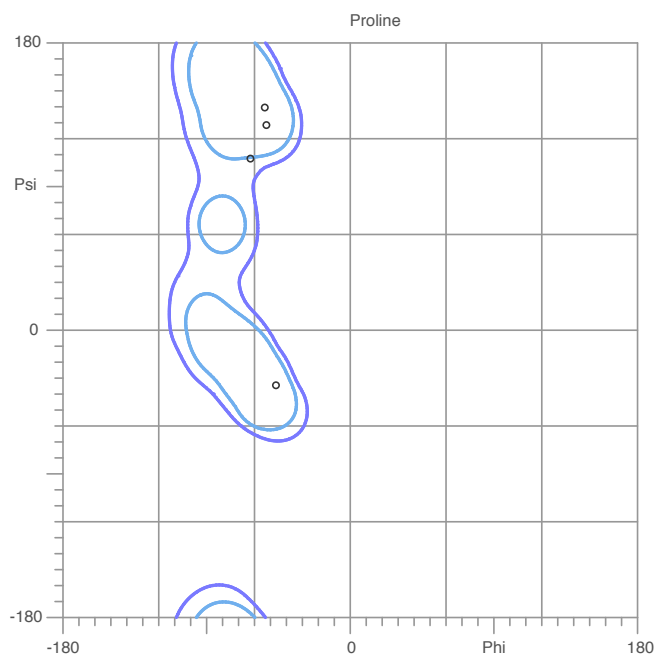
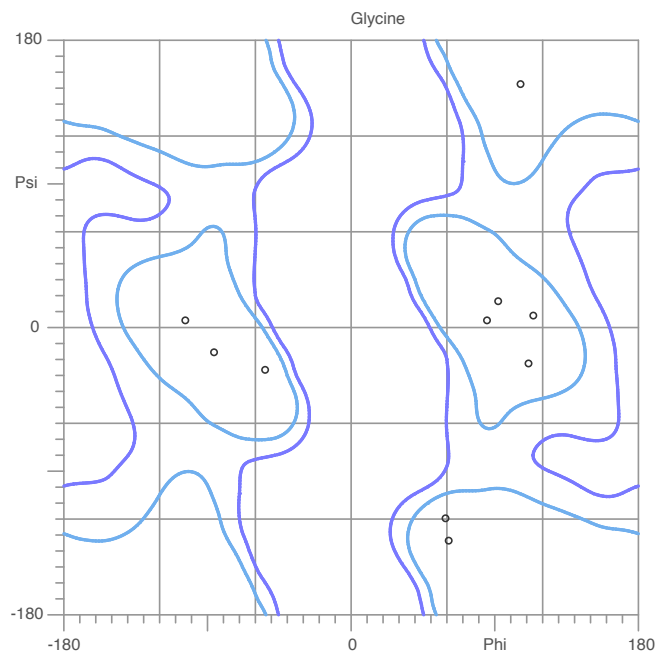
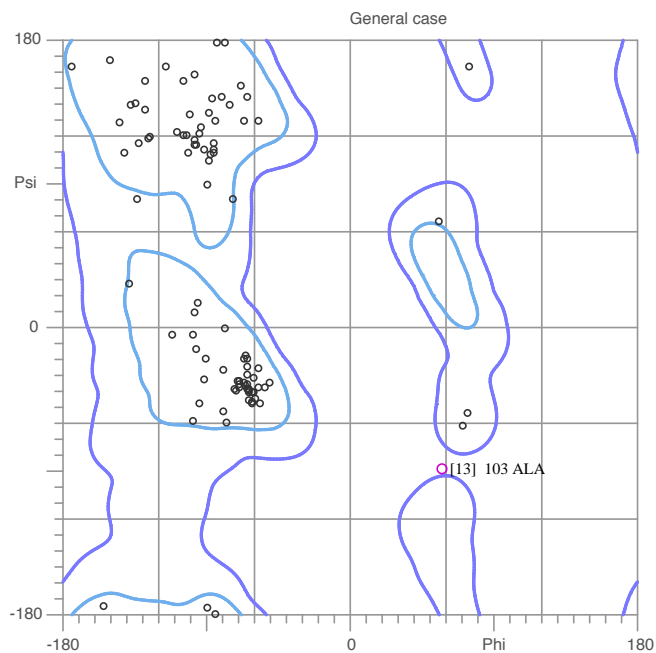
94.7% (108/114) of all residues were in favored (98%) regions.  
97.4% (111/114) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [12] 64 GLU (65.0, 138.2)
- [12] 79 ALA (65.0, 104.7)
- [12] 106 VAL (65.2, 132.9)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 13



93.9% (107/114) of all residues were in favored (98%) regions.  
99.1% (113/114) of all residues were in allowed (>99.8%) regions.

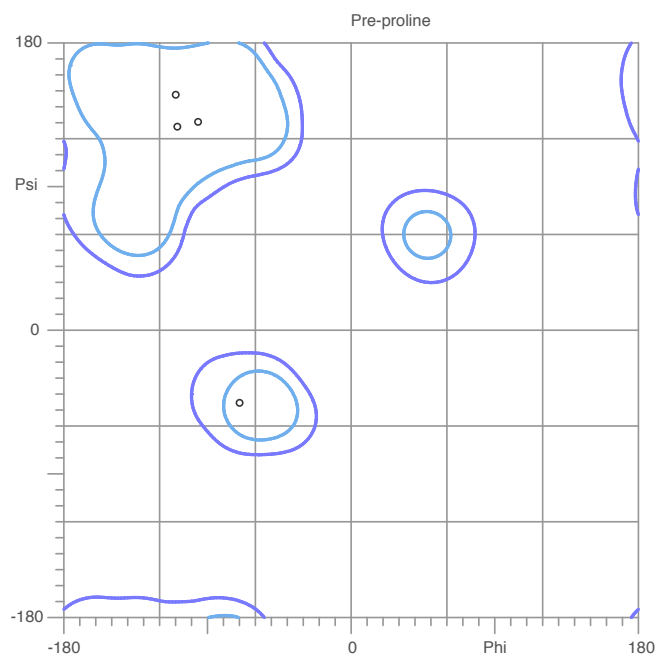
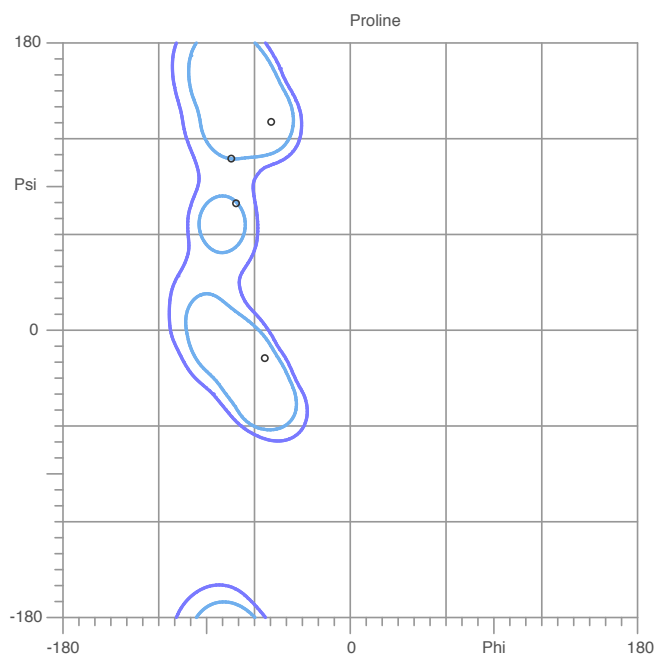
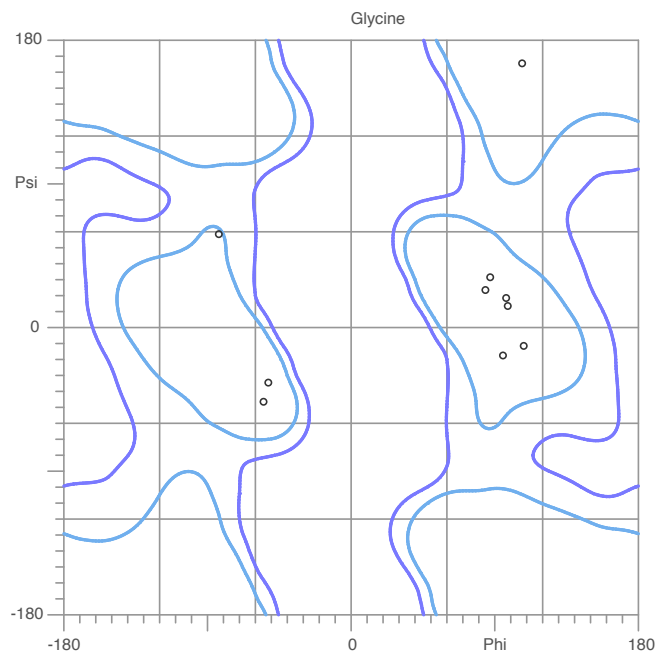
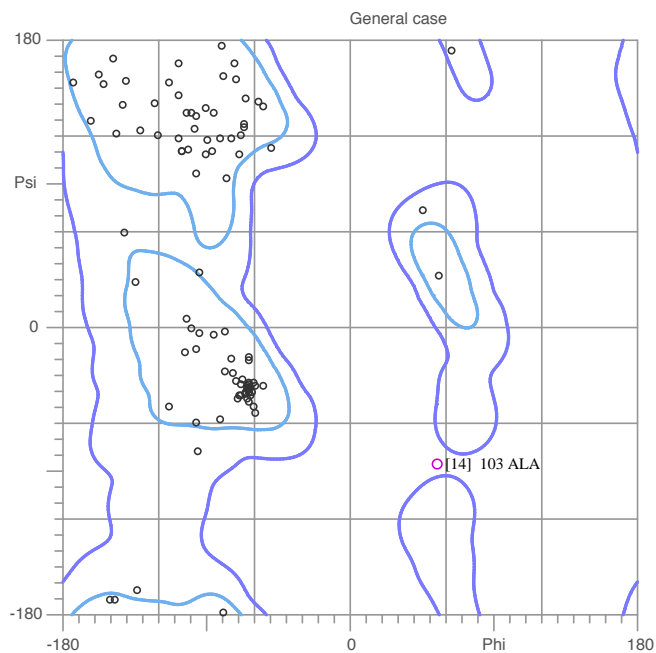
There were 1 outliers (phi, psi):  
[13] 103 ALA (57.1, -88.2)

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# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 14



93.0% (106/114) of all residues were in favored (98%) regions.  
99.1% (113/114) of all residues were in allowed (>99.8%) regions.

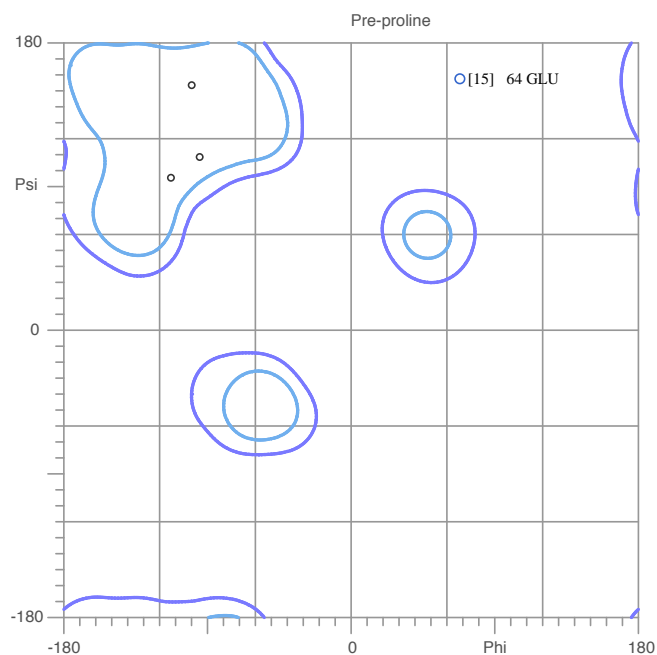
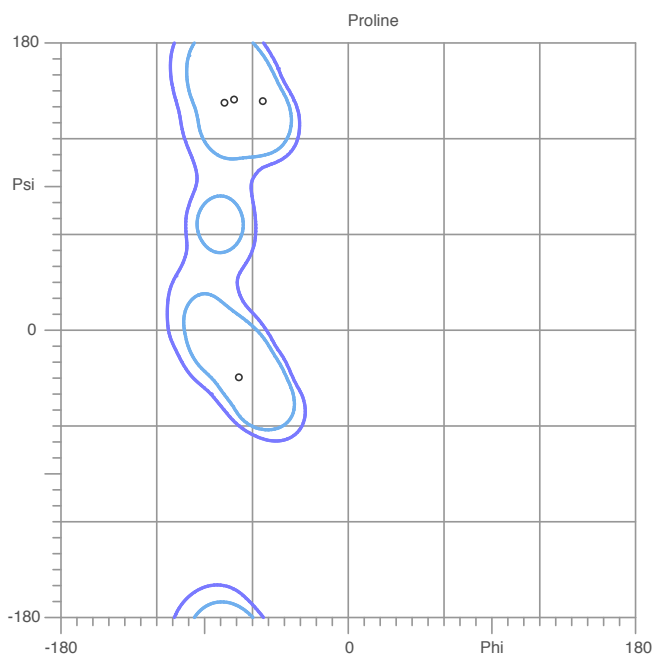
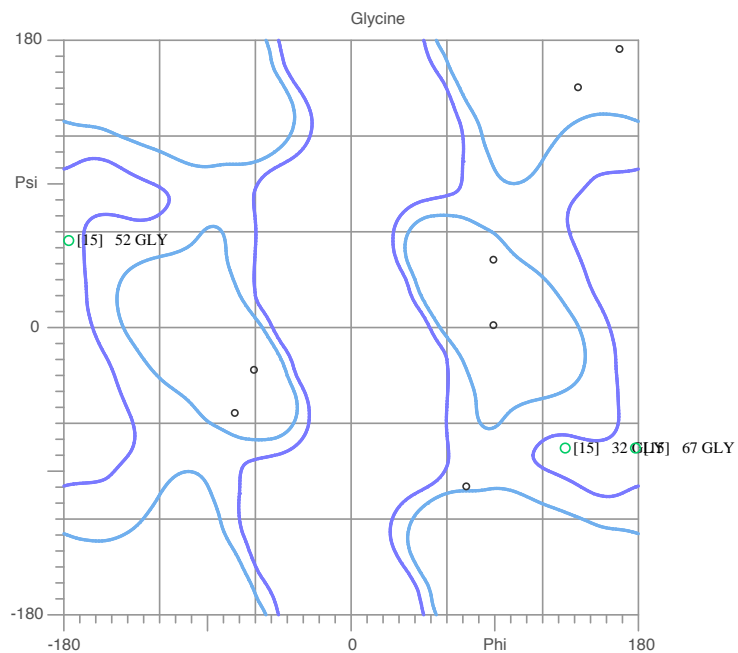
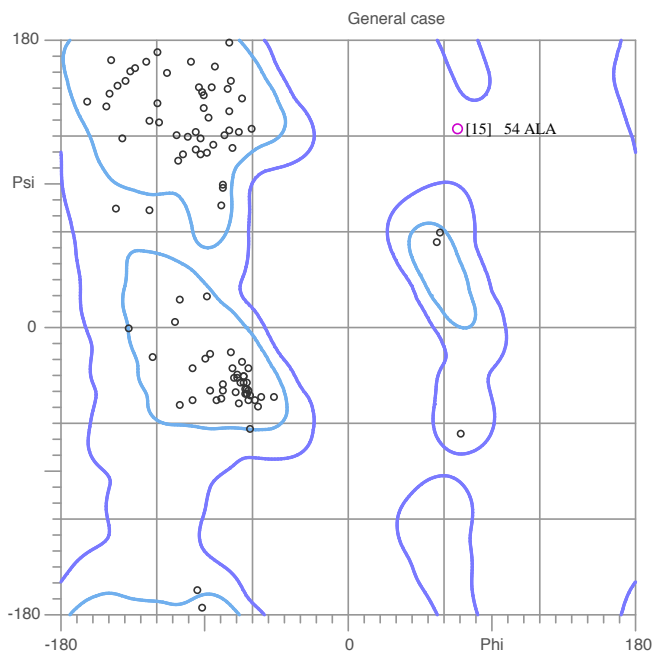
There were 1 outliers (phi, psi):  
[14] 103 ALA (54.4, -85.0)

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# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 15



89.5% (102/114) of all residues were in favored (98%) regions.  
95.6% (109/114) of all residues were in allowed (>99.8%) regions.

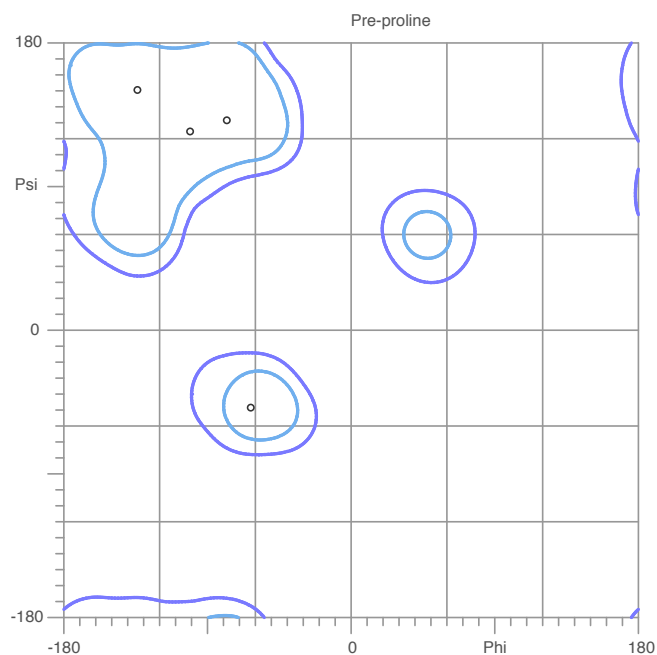
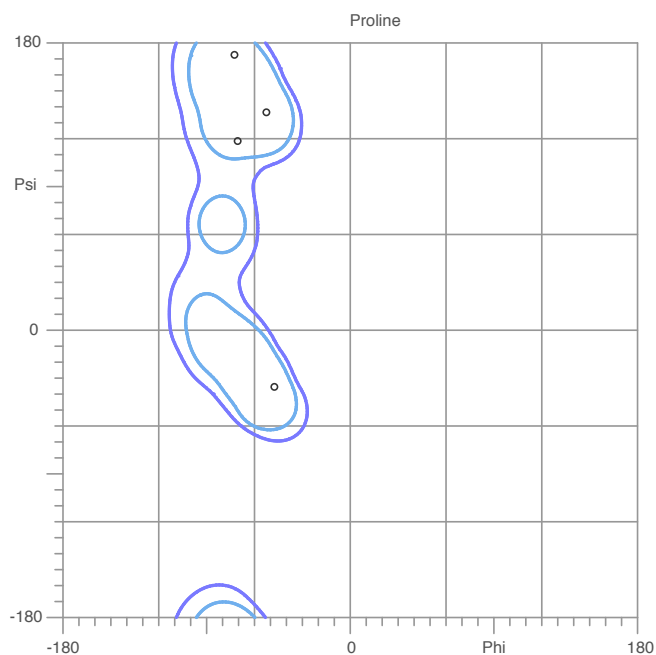
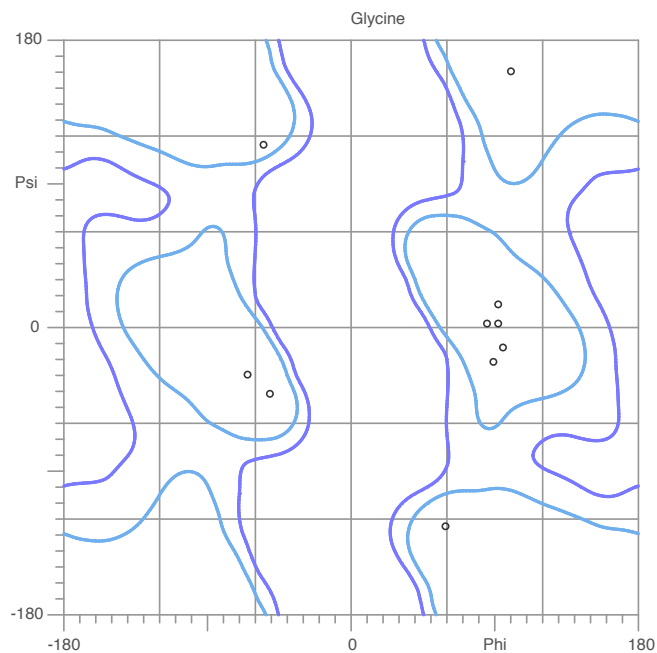
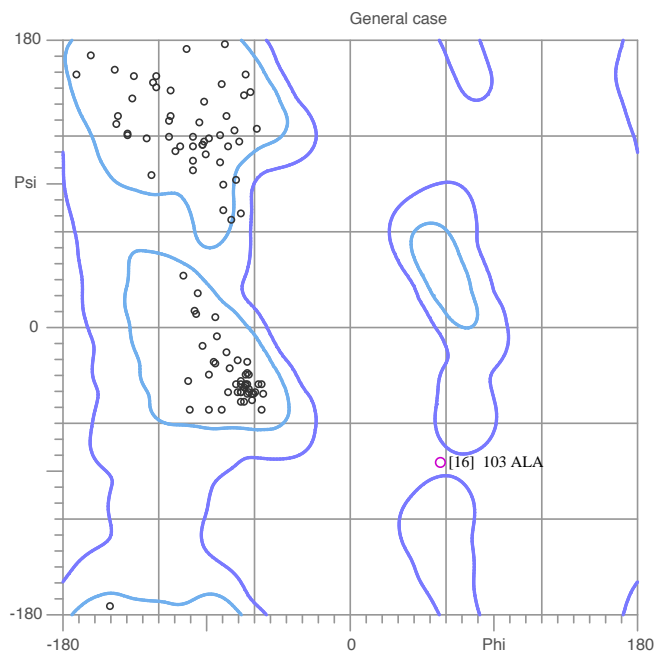
There were 5 outliers (phi, psi):

[15] 32 GLY (135.0, -75.0)  
[15] 52 GLY (-177.7, 55.1)  
[15] 54 ALA (68.0, 125.1)  
[15] 64 GLU (68.0, 158.4)  
[15] 67 GLY (178.9, -75.0)



# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 16



98.2% (112/114) of all residues were in favored (98%) regions.  
99.1% (113/114) of all residues were in allowed (>99.8%) regions.

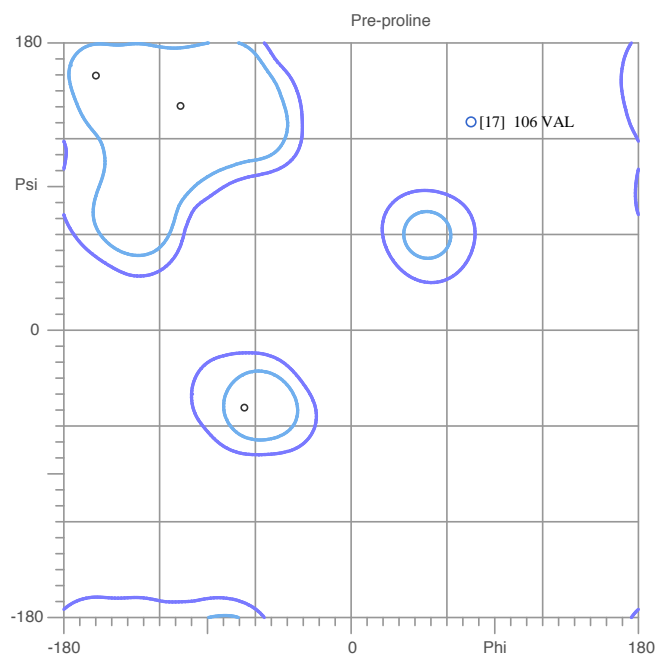
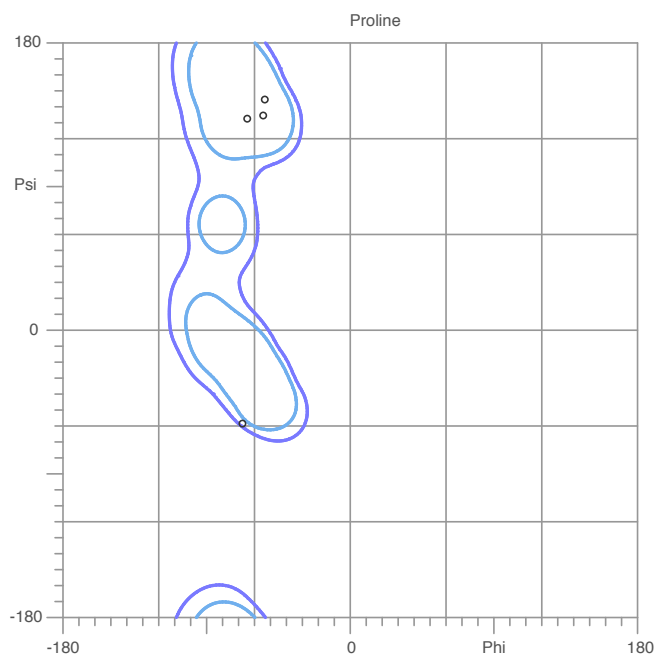
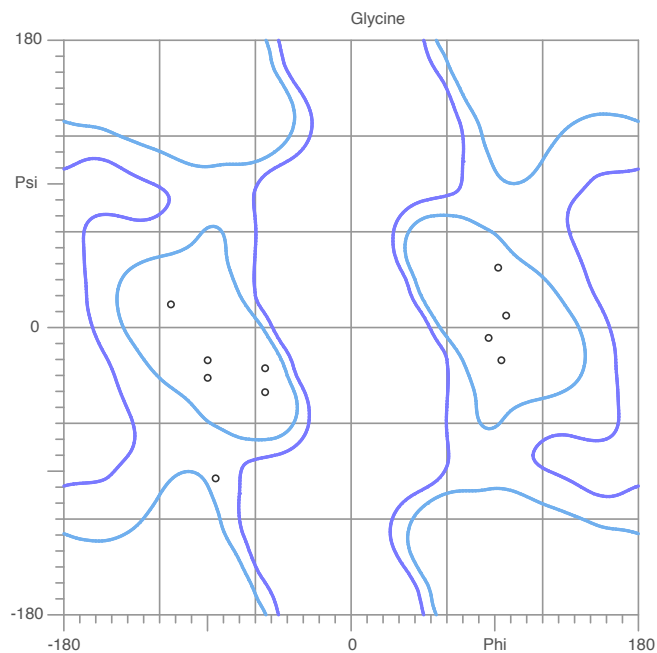
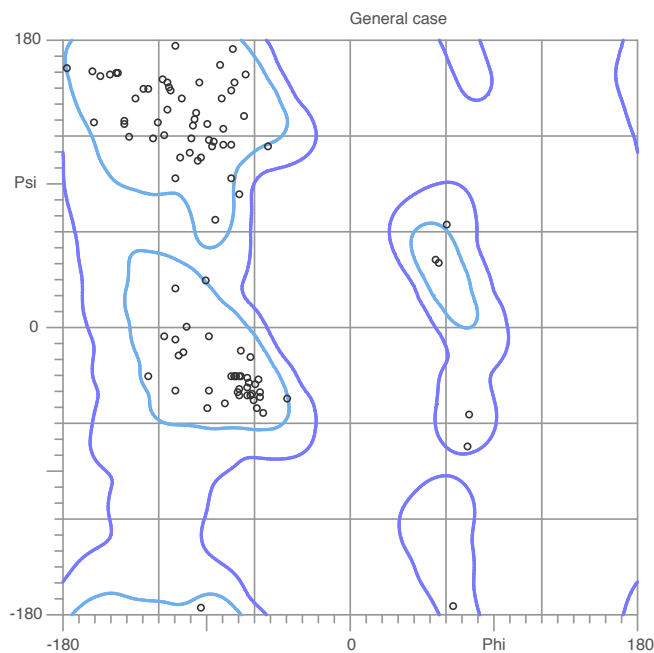
There were 1 outliers (phi, psi):  
[16] 103 ALA (56.7, -84.9)

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# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 17



91.2% (104/114) of all residues were in favored (98%) regions.  
99.1% (113/114) of all residues were in allowed (>99.8%) regions.

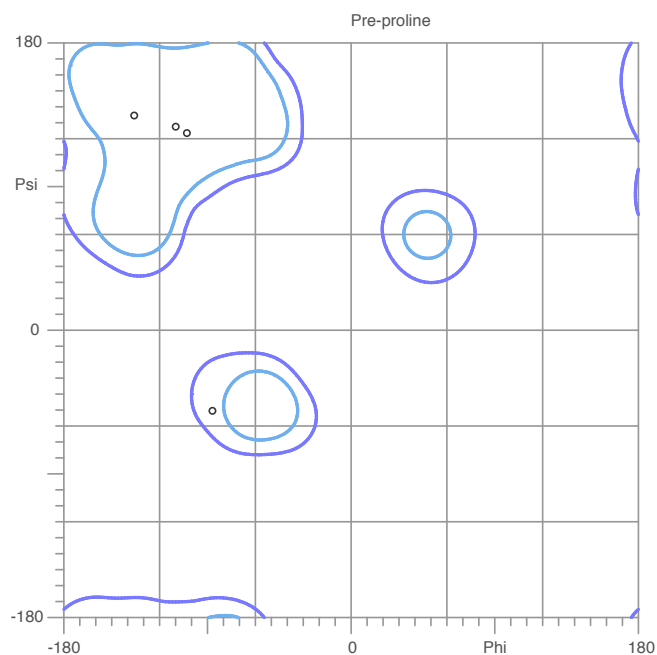
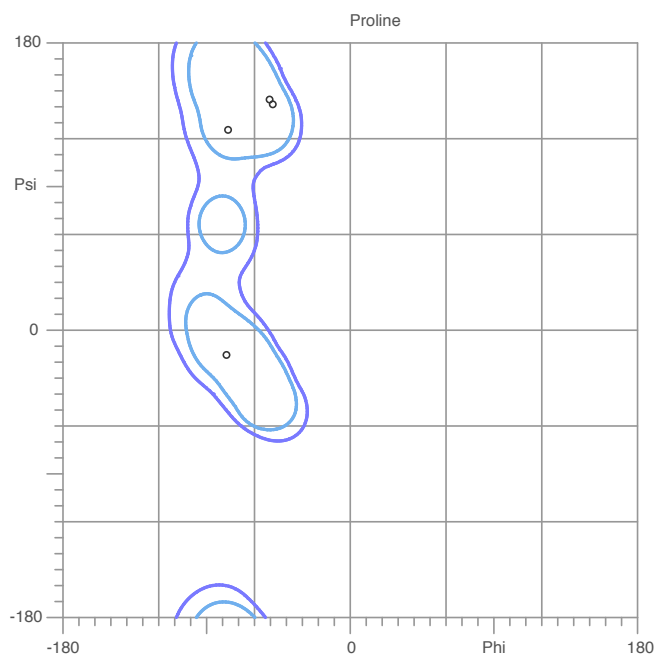
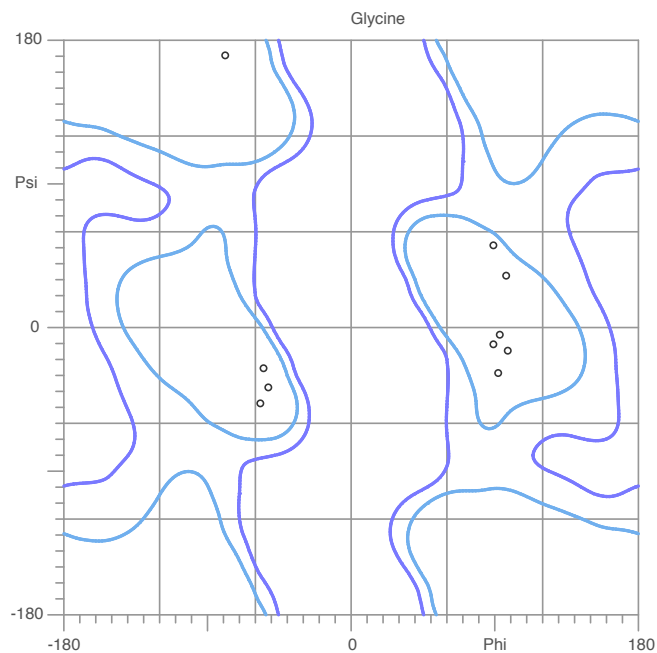
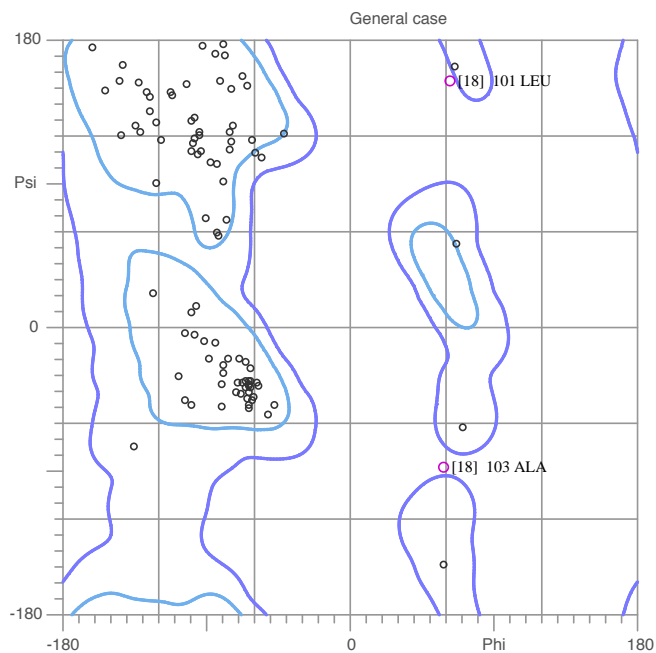
There were 1 outliers (phi, psi):  
[17] 106 VAL (75.1, 131.3)

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# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 18

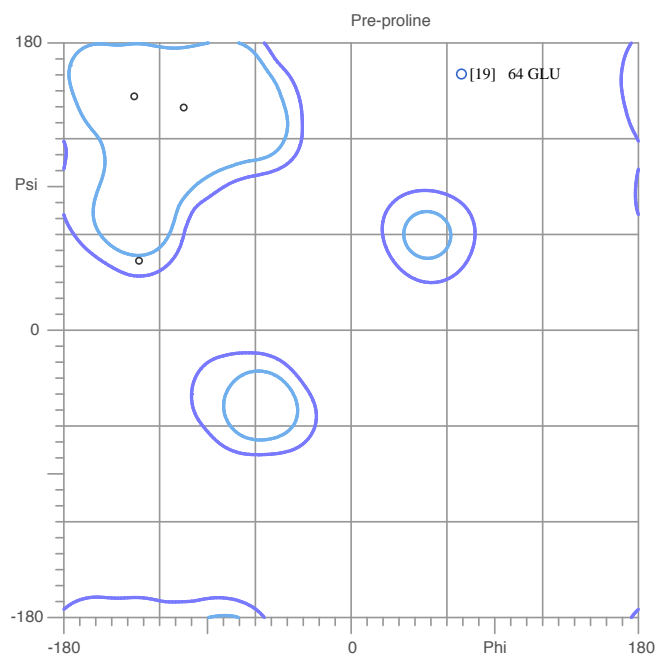
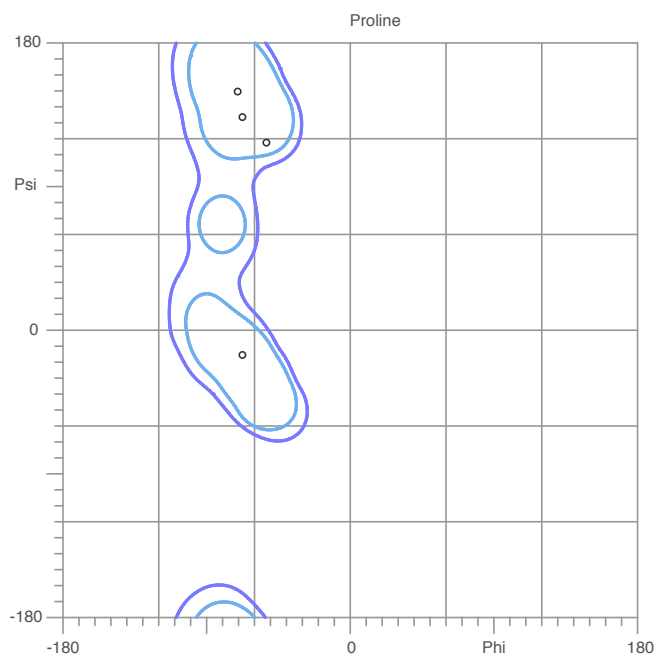
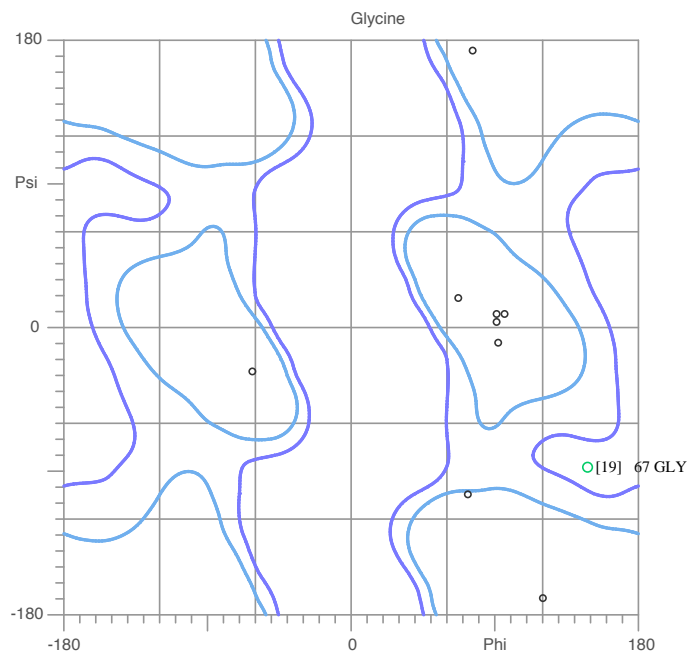
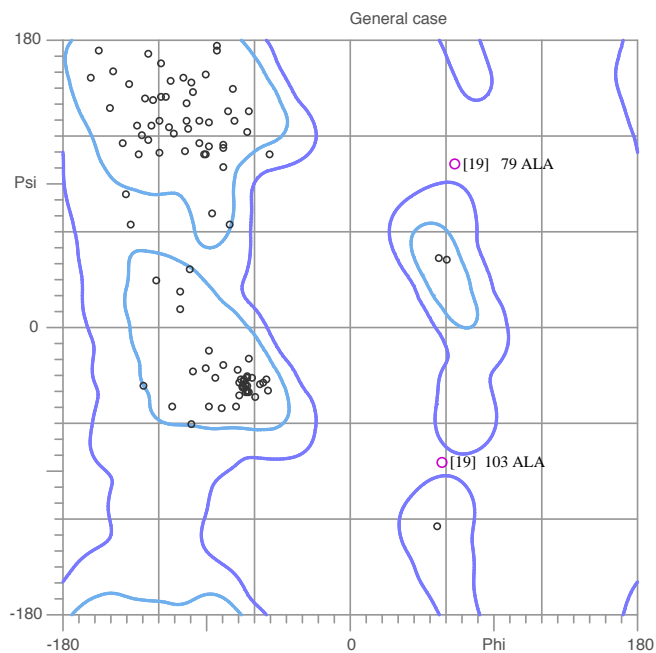


91.2% (104/114) of all residues were in favored (98%) regions.  
98.2% (112/114) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[18] 101 LEU (62.8, 155.0)  
[18] 103 ALA (58.7, -87.7)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 19



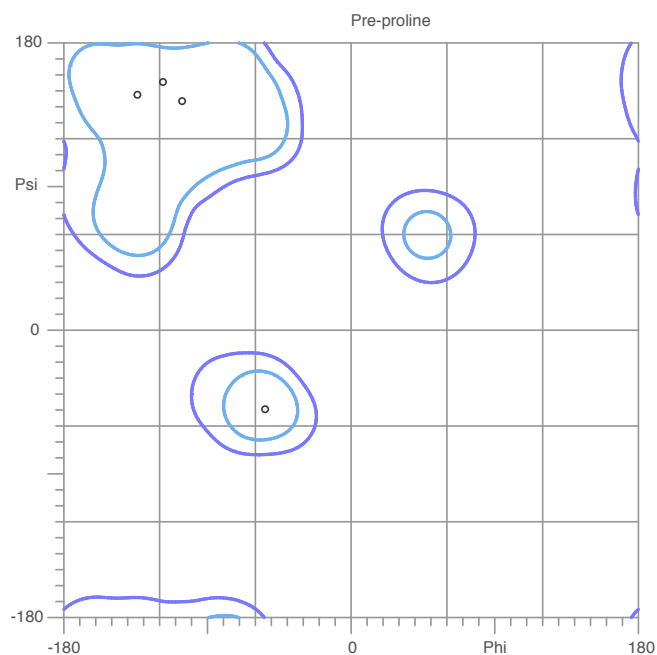
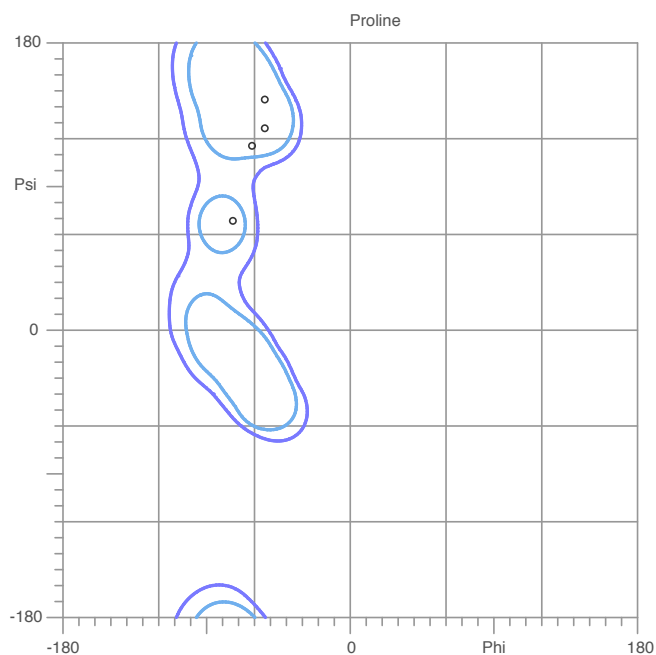
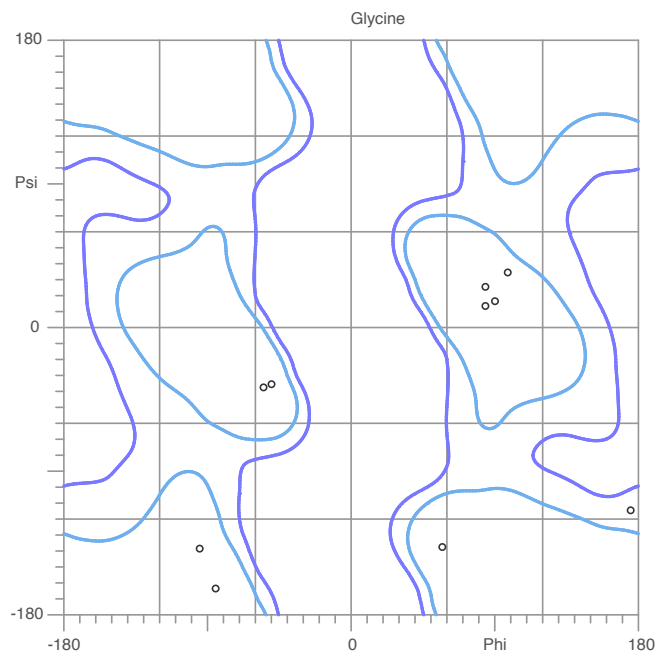
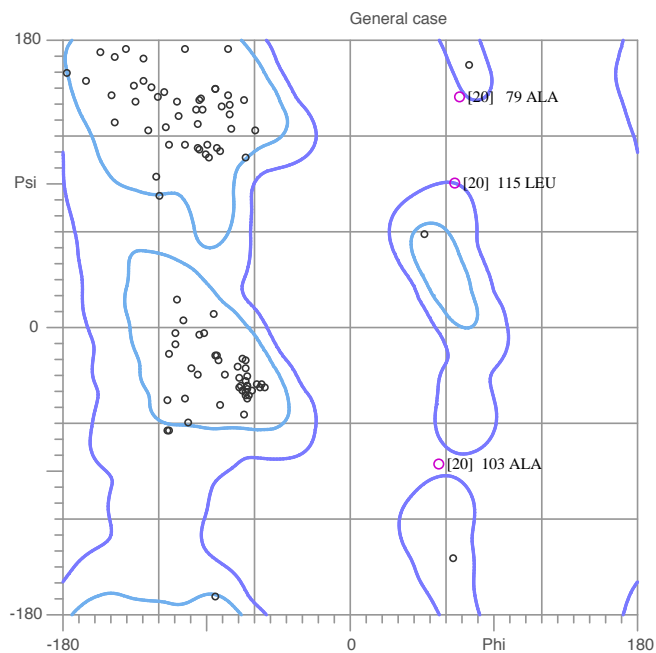
91.2% (104/114) of all residues were in favored (98%) regions.  
96.5% (110/114) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [19] 64 GLU (69.7, 161.6)
- [19] 67 GLY (148.9, -87.8)
- [19] 79 ALA (65.1, 103.1)
- [19] 103 ALA (57.9, -84.9)

# MolProbity Ramachandran analysis

CCR55\_R3\_em\_bcr3.pdb, model 20



91.2% (104/114) of all residues were in favored (98%) regions.  
97.4% (111/114) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[20] 79 ALA (68.8, 145.3)

[20] 103 ALA (55.7, -85.1)

[20] 115 LEU (65.2, 91.3)