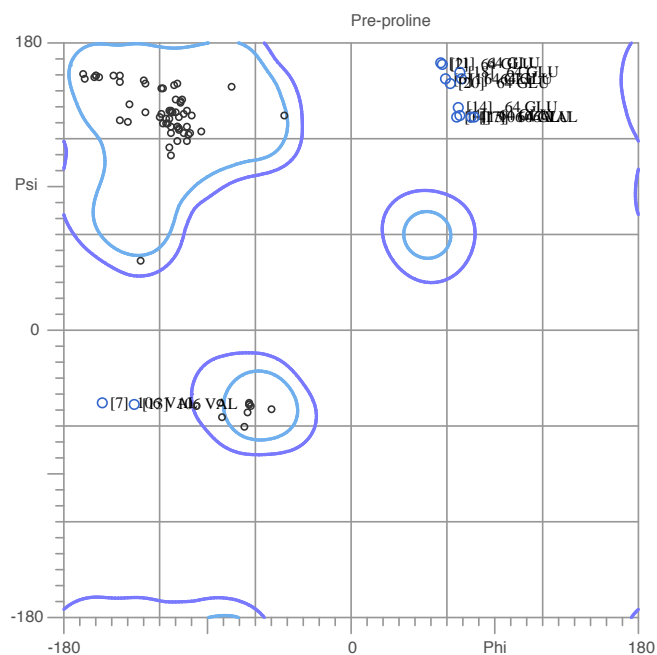
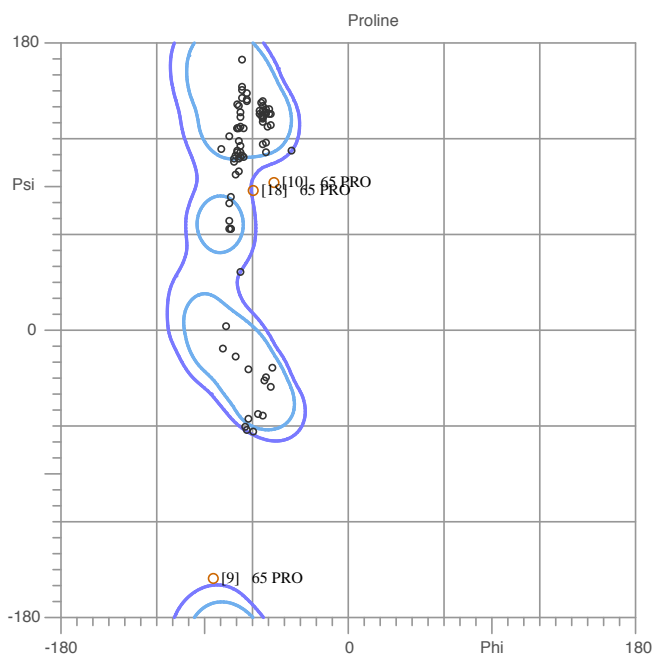
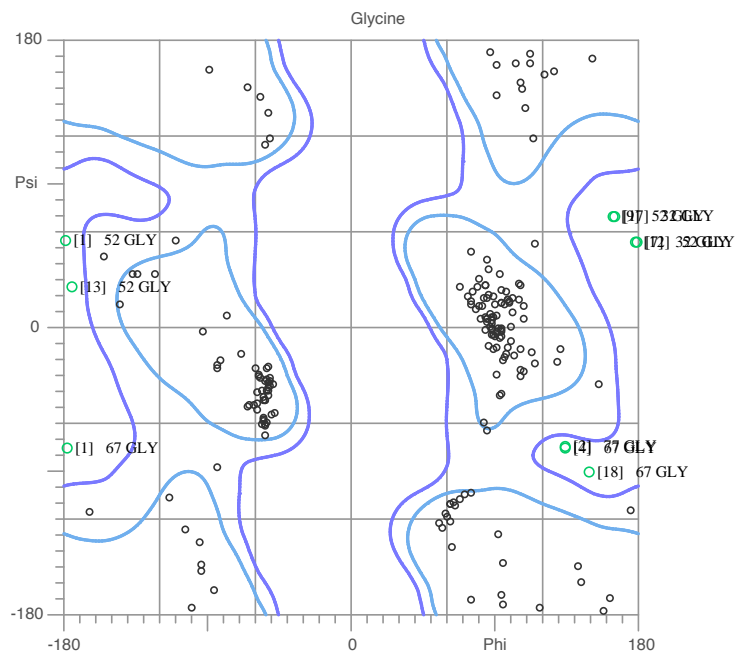
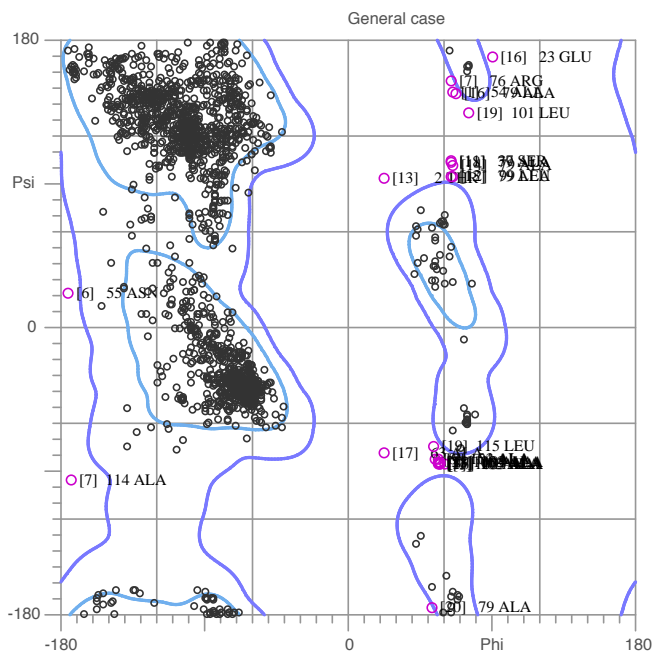


MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, all models



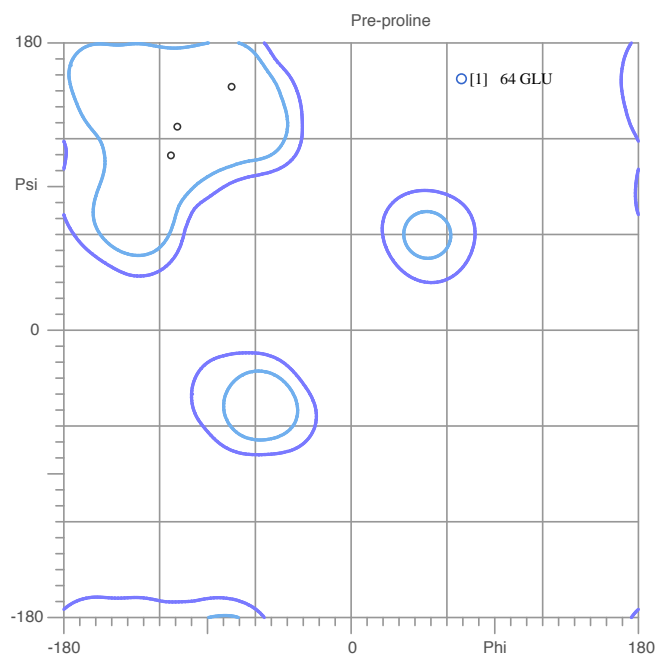
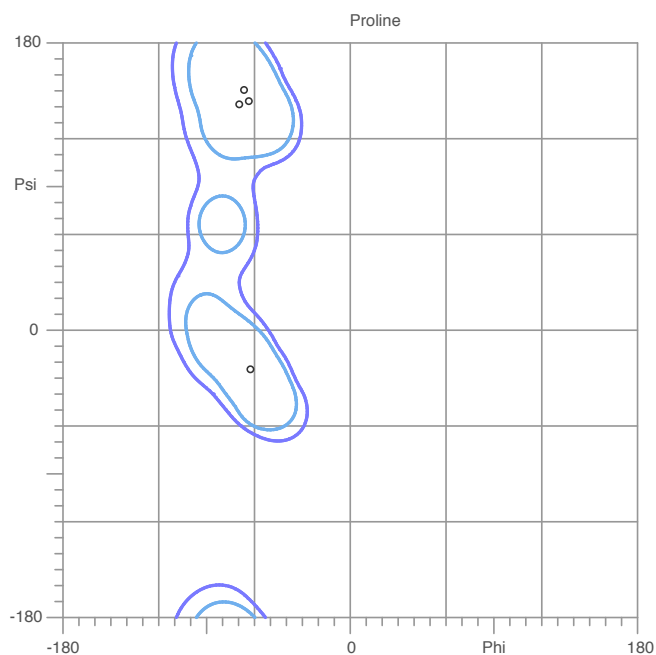
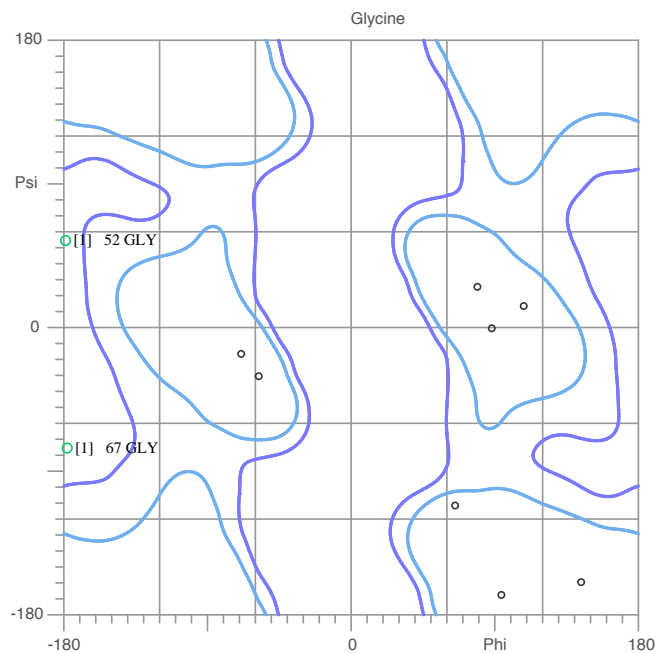
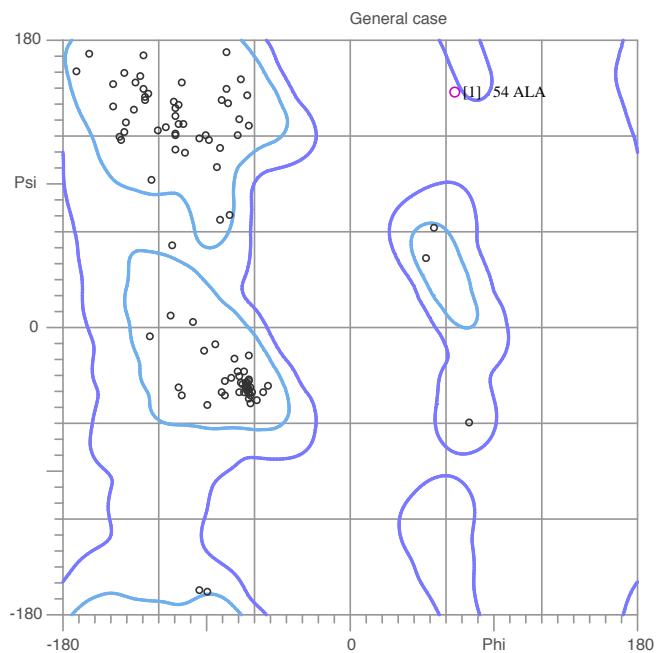
92.7% (2114/2280) of all residues were in favored (98%) regions.
97.8% (2229/2280) of all residues were in allowed (>99.8%) regions.

There were 51 outliers (phi, psi):

- | | |
|-----------------------------|----------------------------|
| [1] 52 GLY (-179.8, 55.0) | [11] 64 GLU (56.2, 168.4) |
| [1] 54 ALA (65.4, 148.1) | [12] 52 GLY (178.0, 55.0) |
| [1] 64 GLU (69.7, 158.9) | [13] 103 ALA (56.3, -85.2) |
| [1] 67 GLY (-179.0, -75.2) | [13] 2 THR (22.7, 95.0) |
| [2] 64 GLU (57.3, 167.2) | [13] 52 GLY (-175.0, 26.5) |
| [2] 77 GLY (134.9, -74.9) | [13] 79 ALA (65.0, 95.1) |
| [3] 103 ALA (57.3, -85.0) | [14] 103 ALA (56.3, -85.2) |
| [4] 64 GLU (68.2, 135.1) | [14] 106 VAL (66.2, 134.5) |
| [4] 67 GLY (135.0, -75.2) | [15] 106 VAL (77.1, 135.0) |
| [5] 103 ALA (56.2, -84.8) | [16] 23 GLU (90.2, 170.5) |
| [6] 55 ASN (-176.2, 22.6) | [16] 79 ALA (67.9, 147.8) |
| [6] 64 GLU (99.5, 158.5) | [16] 103 ALA (57.6, -85.2) |
| [7] 32 GLY (179.6, 55.0) | [17] 32 GLY (165.0, 70.5) |
| [7] 76 ARG (65.0, 155.0) | [17] 63 ALA (22.3, -78.1) |
| [7] 103 ALA (60.4, -85.6) | [17] 64 GLU (75.0, 135.0) |
| [7] 106 VAL (-156.9, -45.9) | [18] 64 GLU (68.3, 162.2) |
| [7] 114 ALA (-175.0, -95.0) | [18] 65 PRO (-60.2, 88.0) |
| [8] 103 ALA (54.1, -82.9) | [18] 67 GLY (150.0, -90.7) |
| [9] 52 GLY (165.0, 71.0) | [18] 79 ALA (65.0, 104.8) |
| [9] 54 ALA (56.9, -82.6) | [18] 103 ALA (56.7, -85.0) |
| [9] 65 PRO (-85.0, -155.6) | [19] 103 LEU (75.0, 135.1) |
| [10] 65 PRO (-47.9, 93.1) | [19] 103 ALA (57.2, -85.0) |
| [11] 37 SER (64.9, 105.0) | [19] 115 LEU (53.4, -75.0) |
| | [20] 64 GLU (62.6, 155.1) |
| | [20] 79 ALA (52.7, -175.1) |

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 1



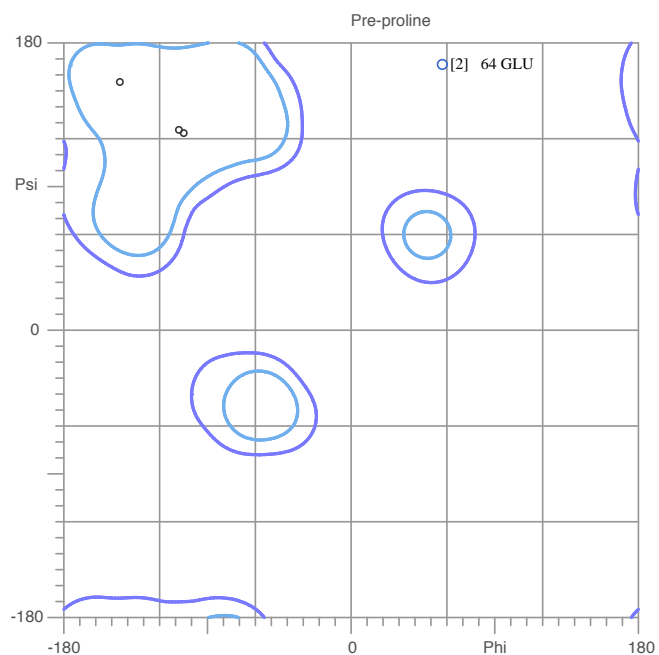
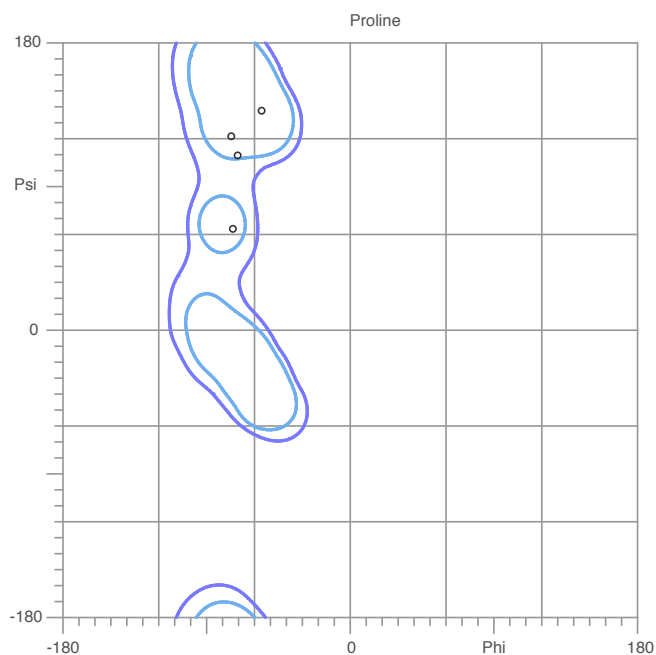
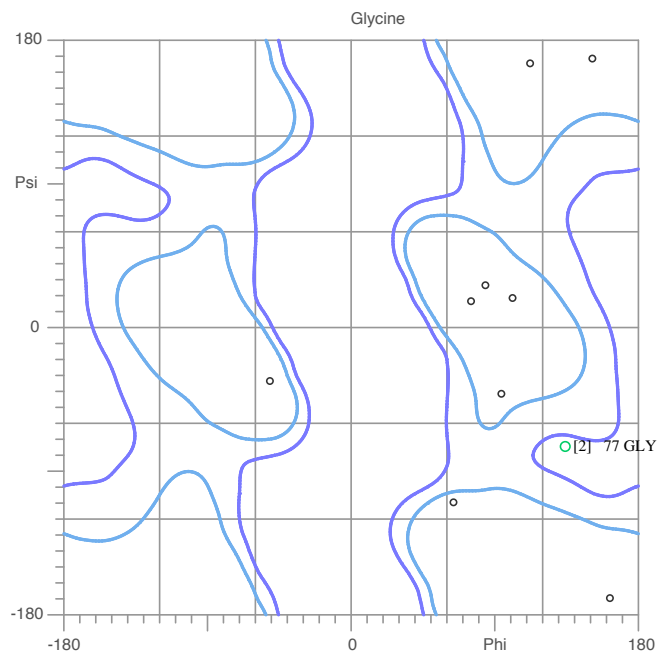
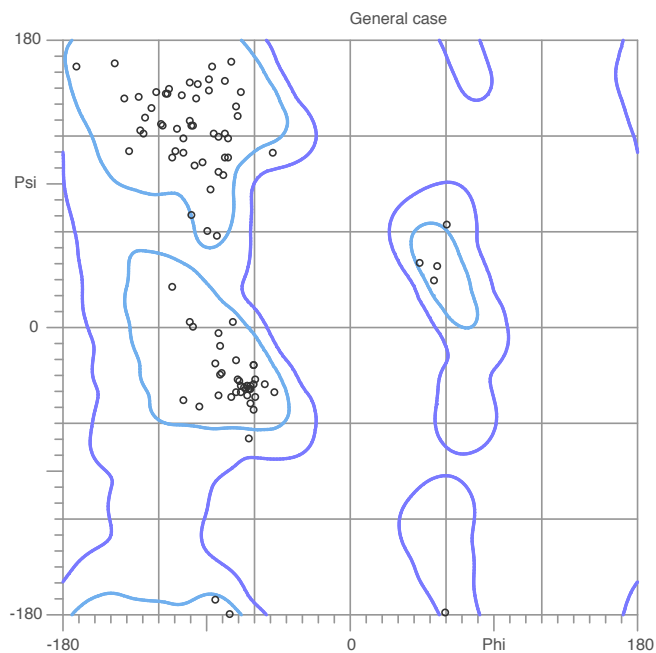
93.0% (106/114) of all residues were in favored (98%) regions.
96.5% (110/114) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [1] 52 GLY (-179.8, 55.0)
- [1] 54 ALA (65.4, 148.1)
- [1] 64 GLU (69.7, 158.9)
- [1] 67 GLY (-179.0, -75.2)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 2



93.9% (107/114) of all residues were in favored (98%) regions.
98.2% (112/114) of all residues were in allowed (>99.8%) regions.

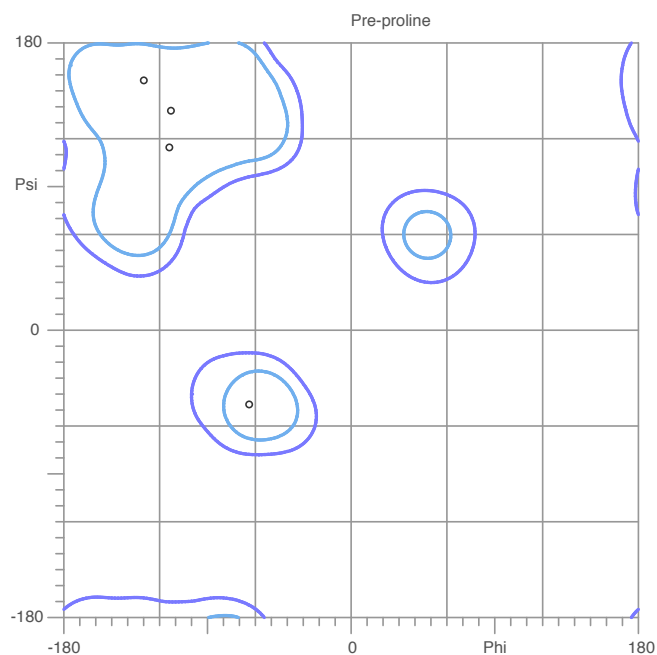
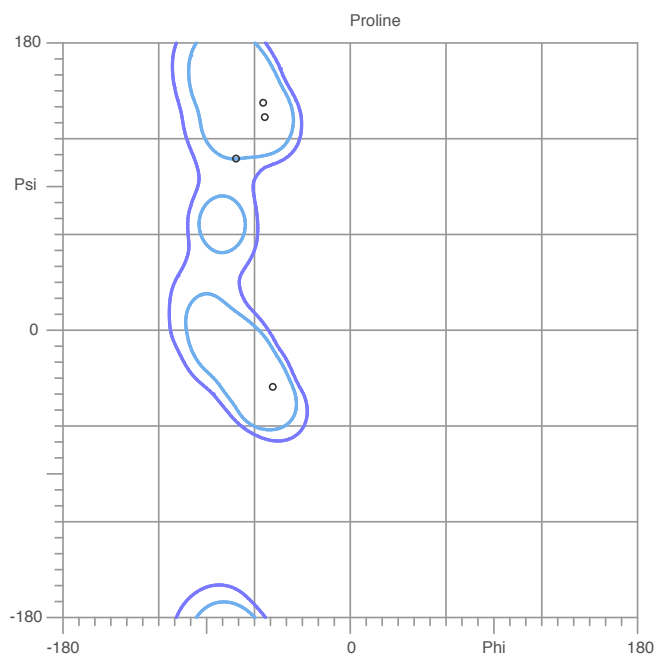
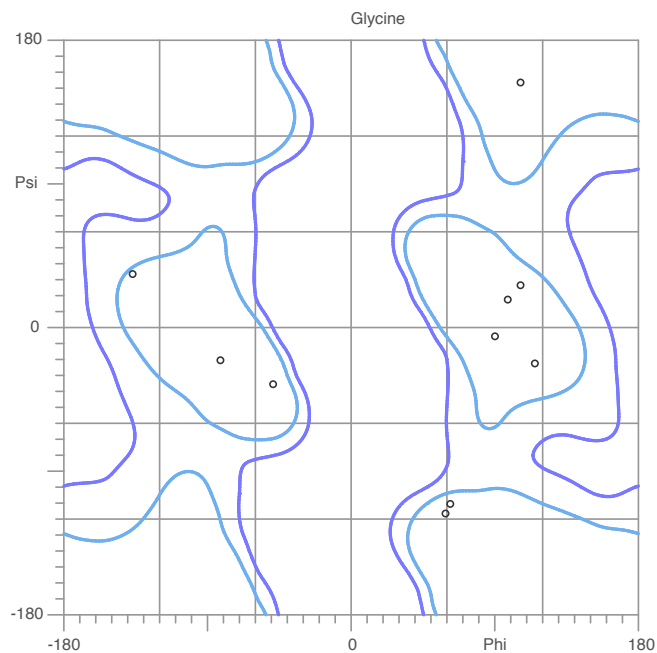
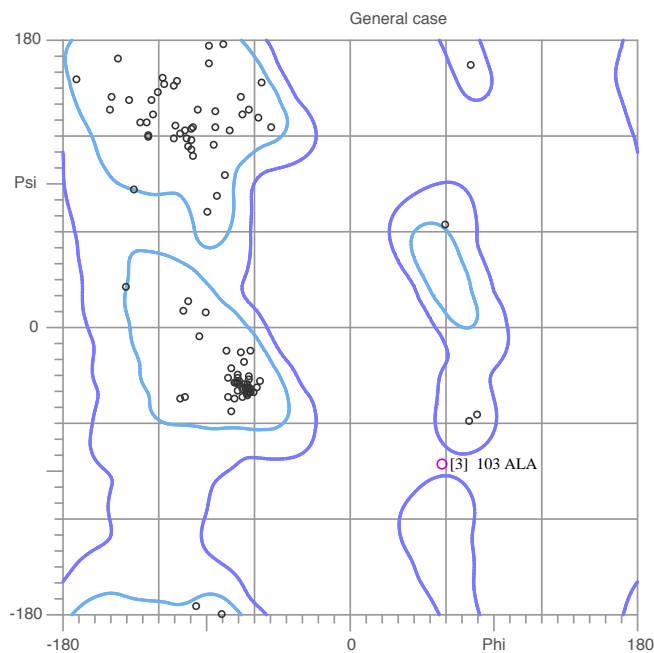
There were 2 outliers (phi, psi):

[2] 64 GLU (57.3, 167.2)

[2] 77 GLY (134.9, -74.9)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 3



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.

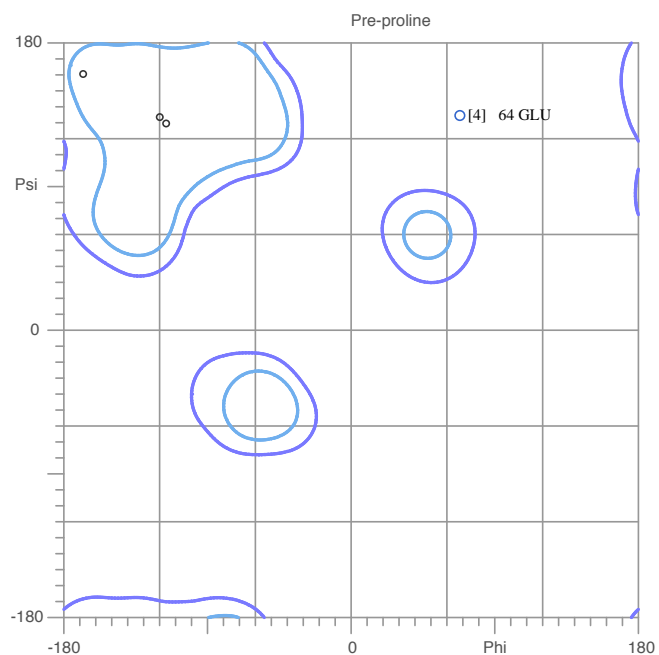
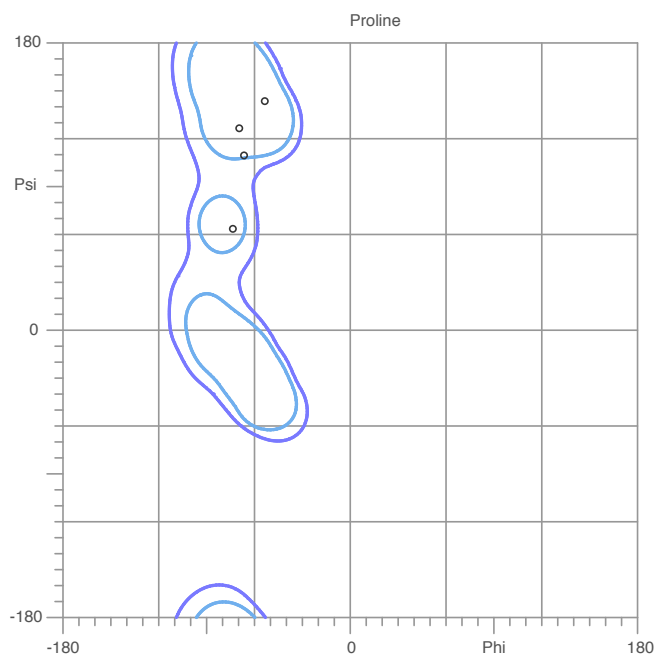
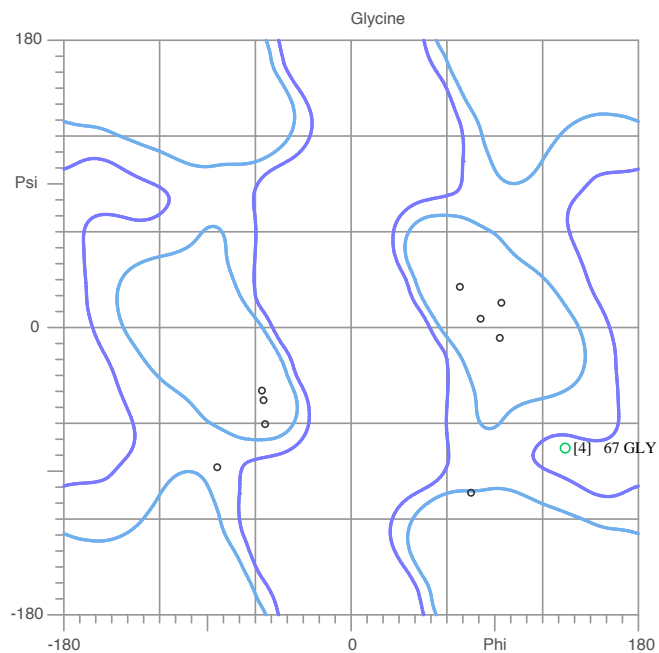
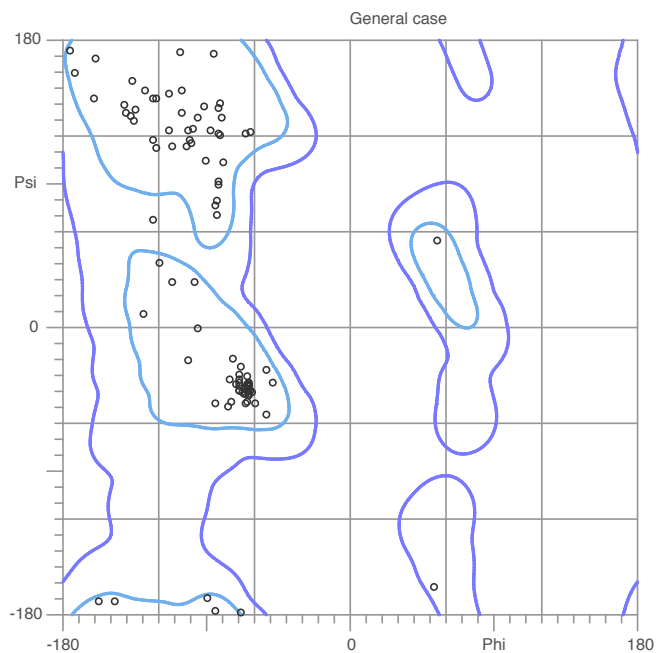
There were 1 outliers (phi, psi):
[3] 103 ALA (57.3, -85.0)

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MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 4



95.6% (109/114) of all residues were in favored (98%) regions.
98.2% (112/114) of all residues were in allowed (>99.8%) regions.

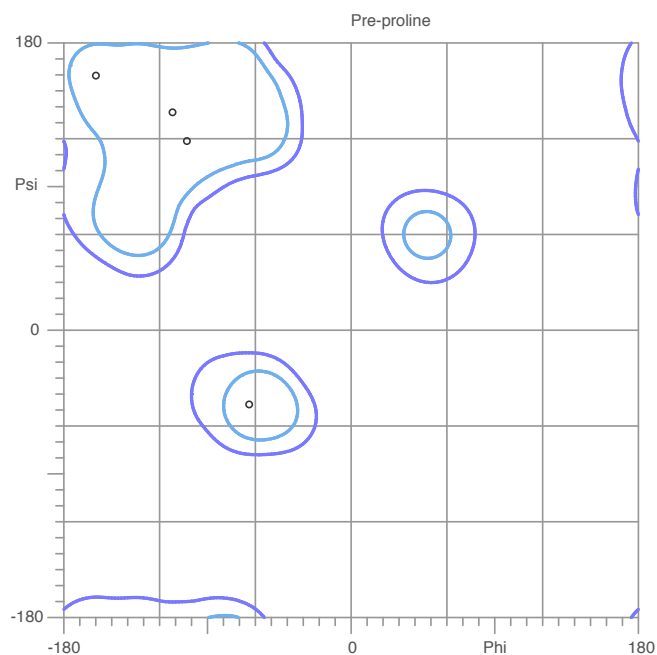
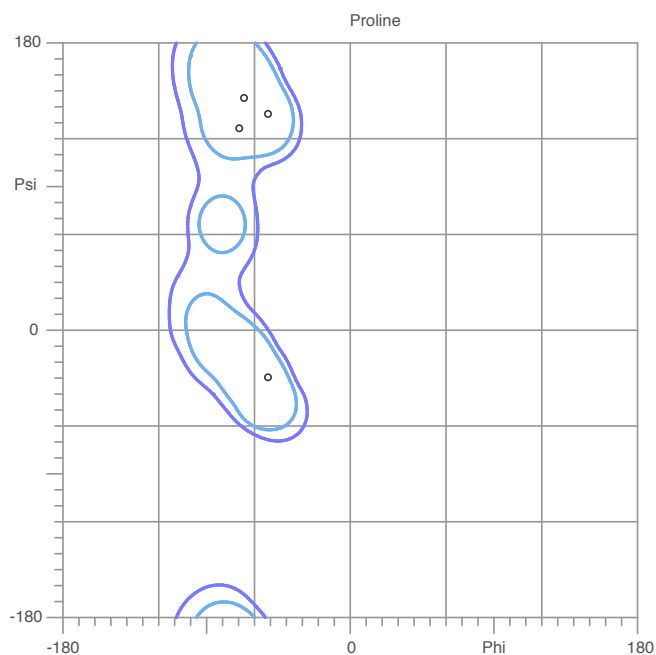
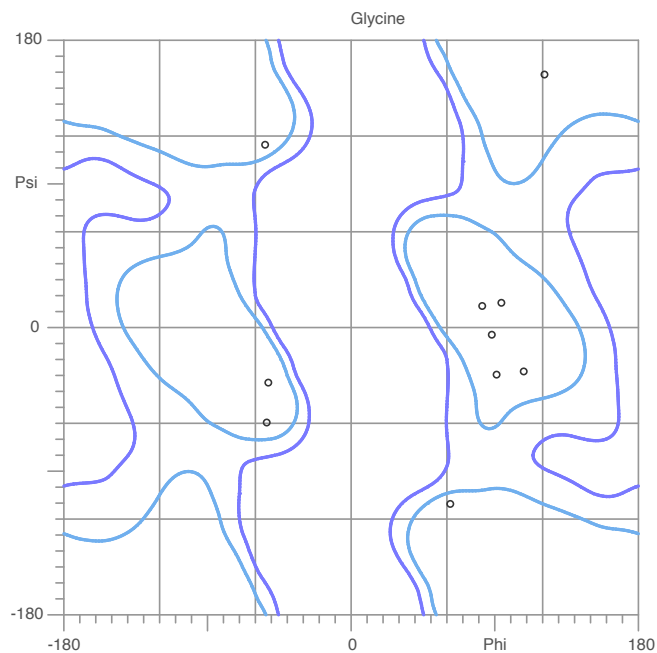
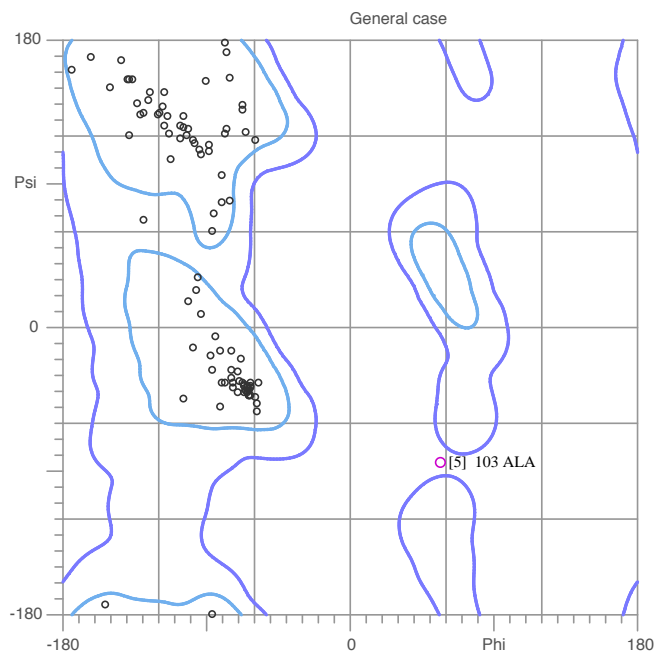
There were 2 outliers (phi, psi):

[4] 64 GLU (68.2, 135.1)

[4] 67 GLY (135.0, -75.2)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 5



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.

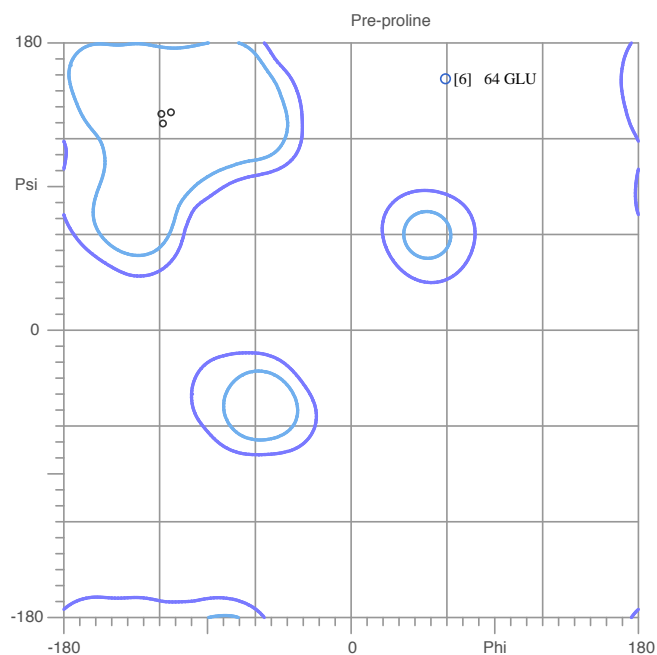
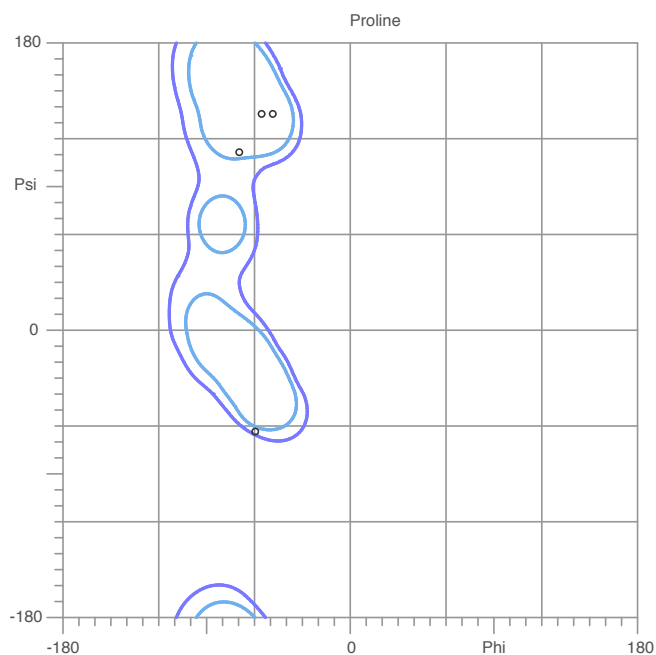
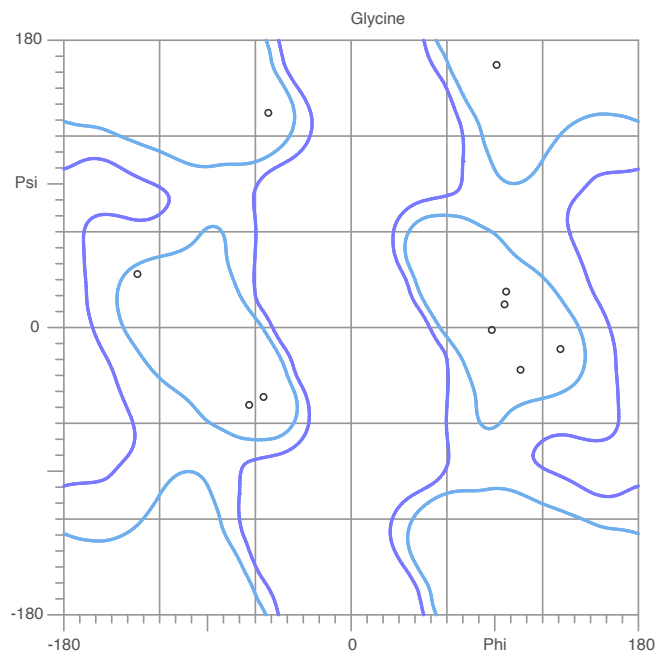
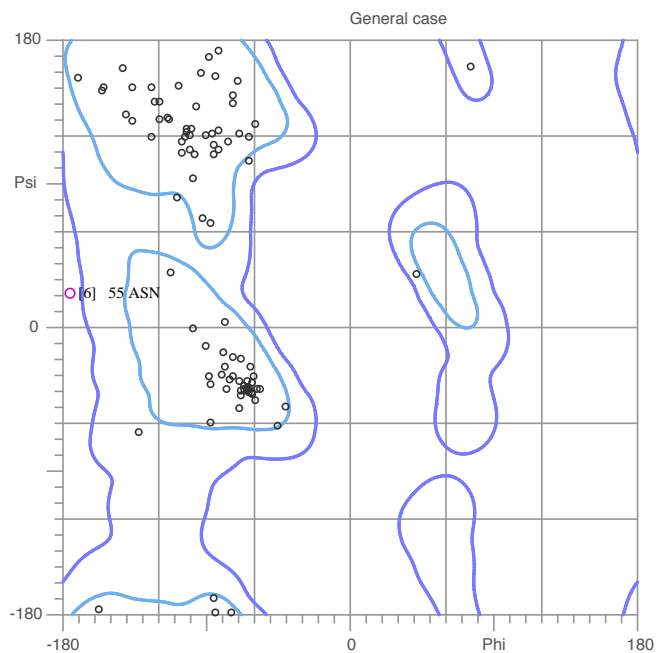
There were 1 outliers (phi, psi):
[5] 103 ALA (56.2, -84.8)

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MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 6



93.0% (106/114) of all residues were in favored (98%) regions.
98.2% (112/114) of all residues were in allowed (>99.8%) regions.

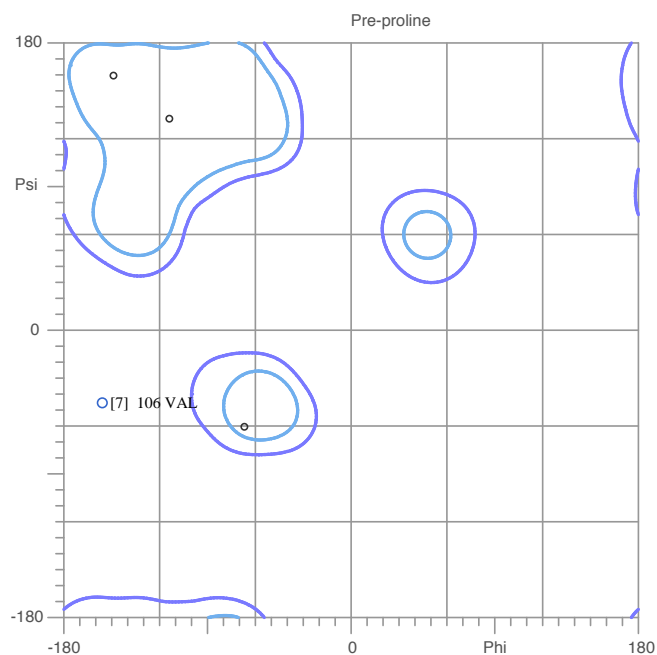
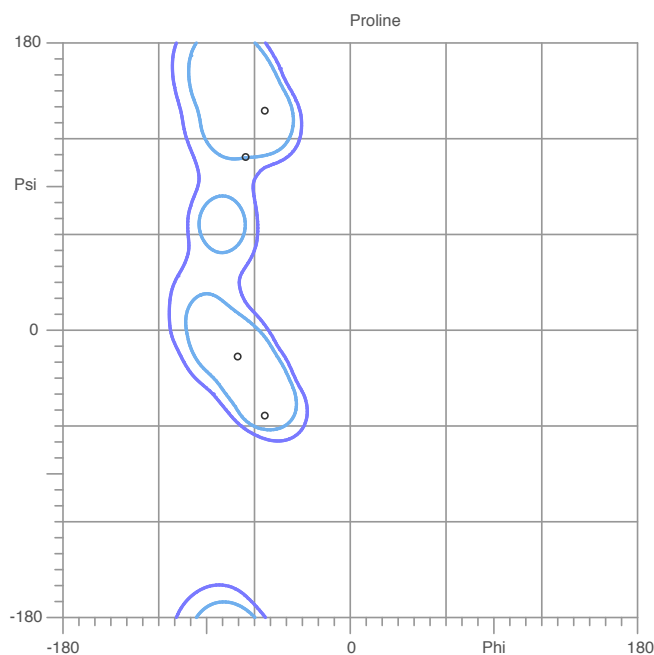
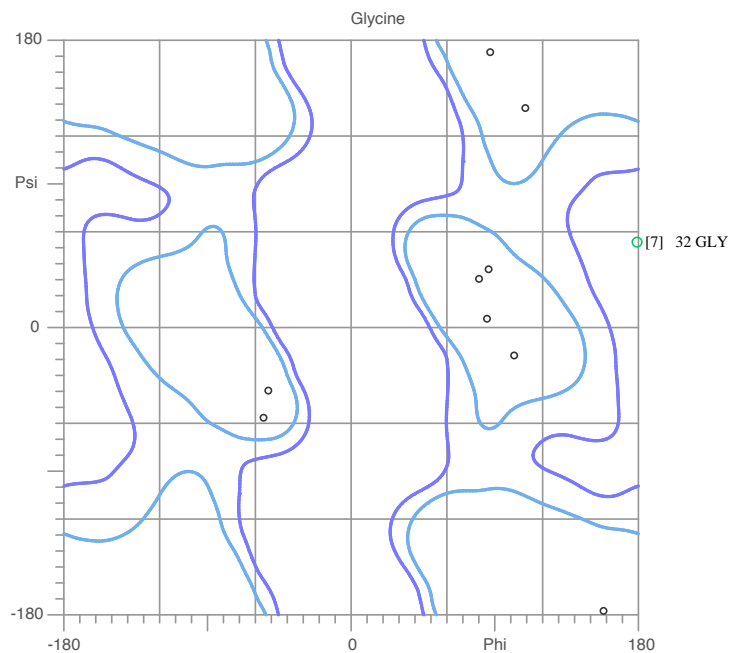
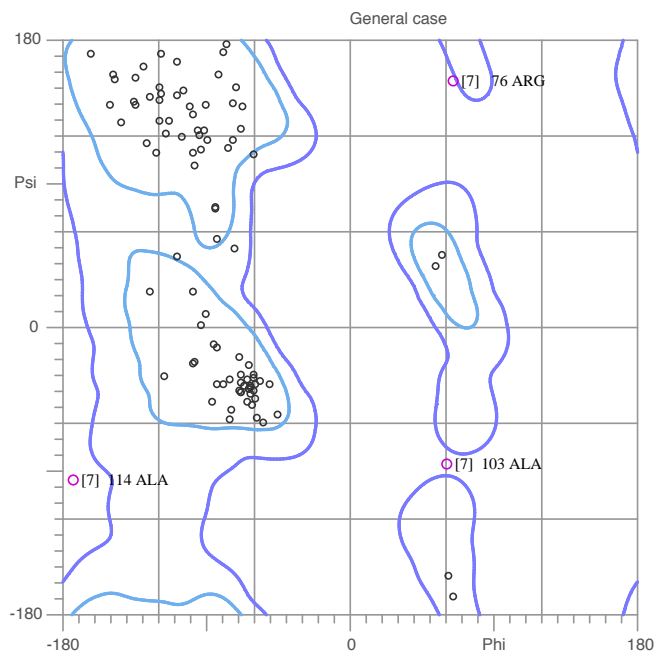
There were 2 outliers (phi, psi):

[6] 55 ASN (-176.2, 22.6)

[6] 64 GLU (59.5, 158.5)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 7



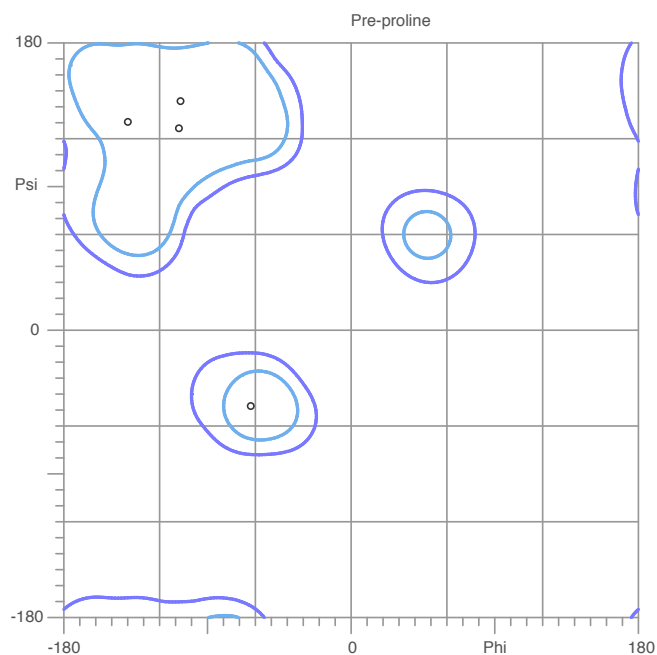
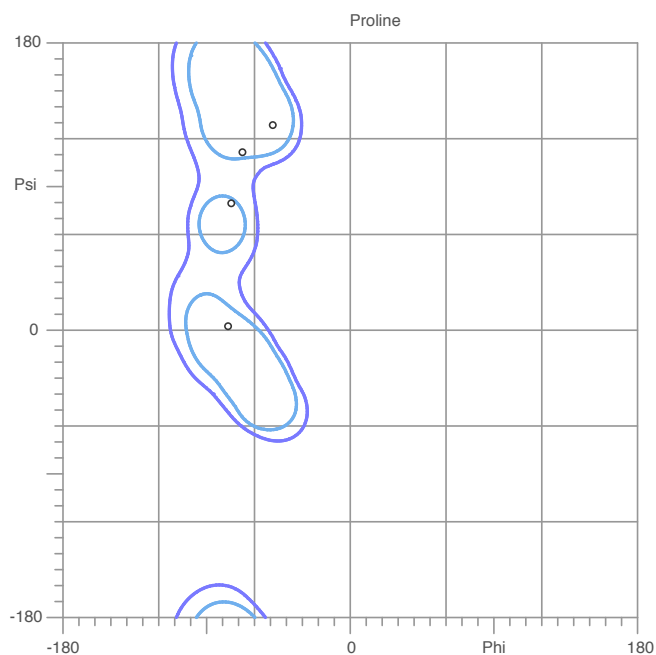
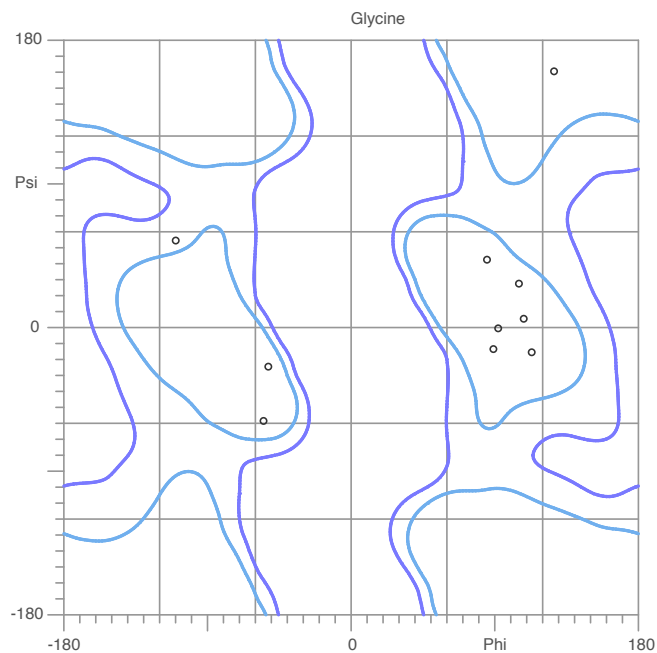
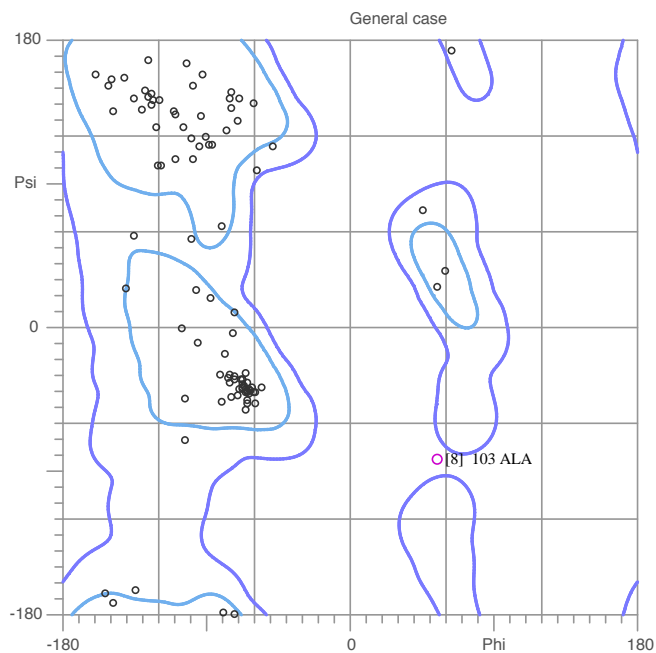
92.1% (105/114) of all residues were in favored (98%) regions.
95.6% (109/114) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[7] 32 GLY (179.6, 55.0)
[7] 76 ARG (65.0, 155.0)
[7] 103 ALA (60.4, -85.6)
[7] 106 VAL (-156.9, -45.9)
[7] 114 ALA (-175.0, -95.0)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 8



89.5% (102/114) of all residues were in favored (98%) regions.
99.1% (113/114) of all residues were in allowed (>99.8%) regions.

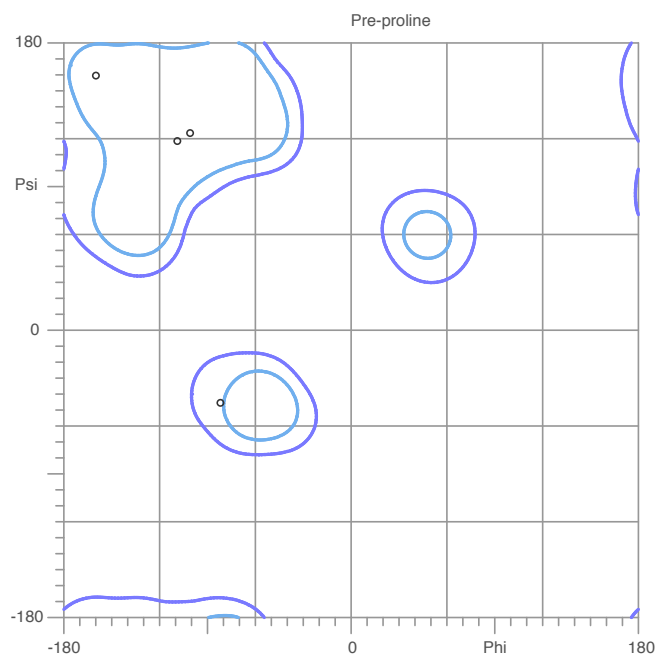
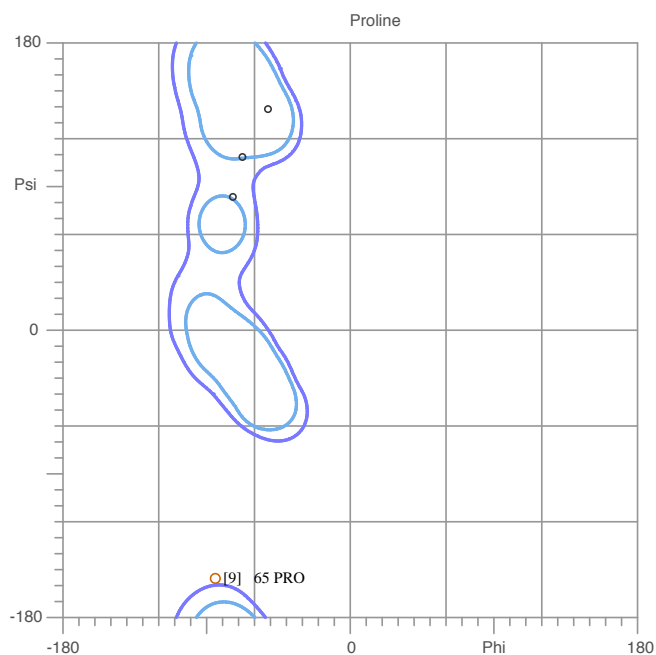
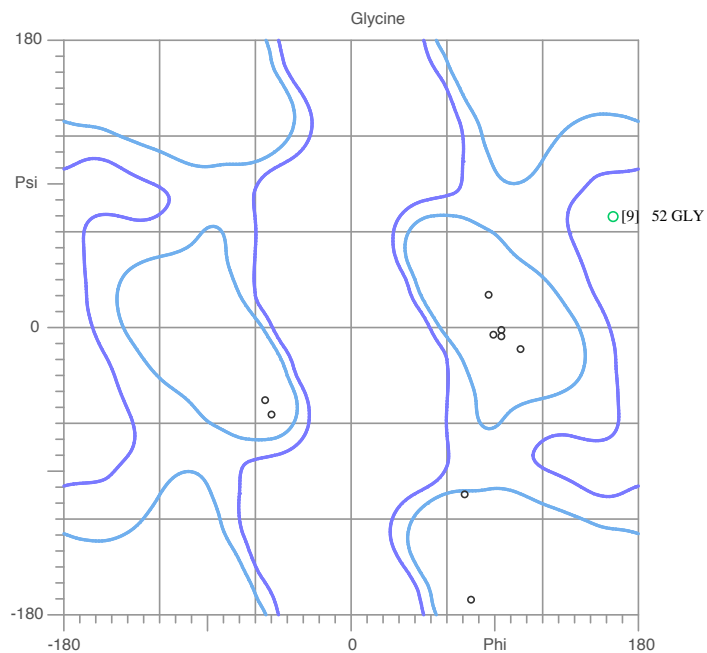
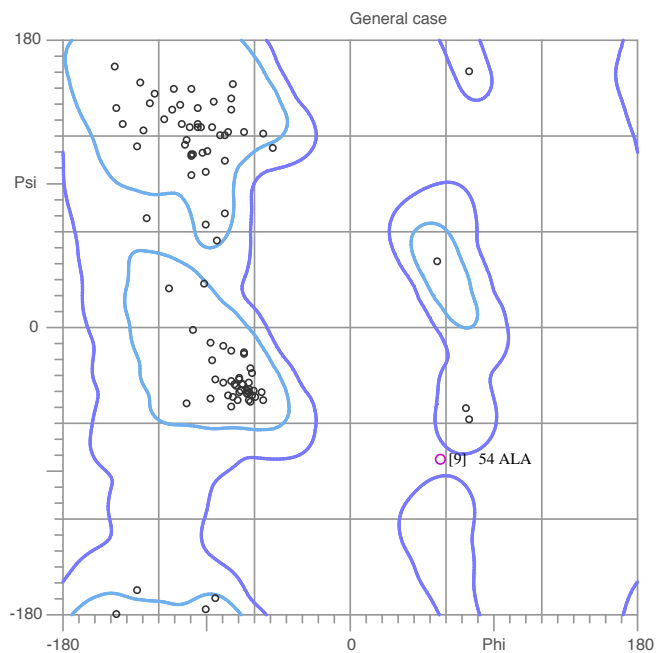
There were 1 outliers (phi, psi):
[8] 103 ALA (54.1, -82.9)

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MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 9



90.4% (103/114) 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):

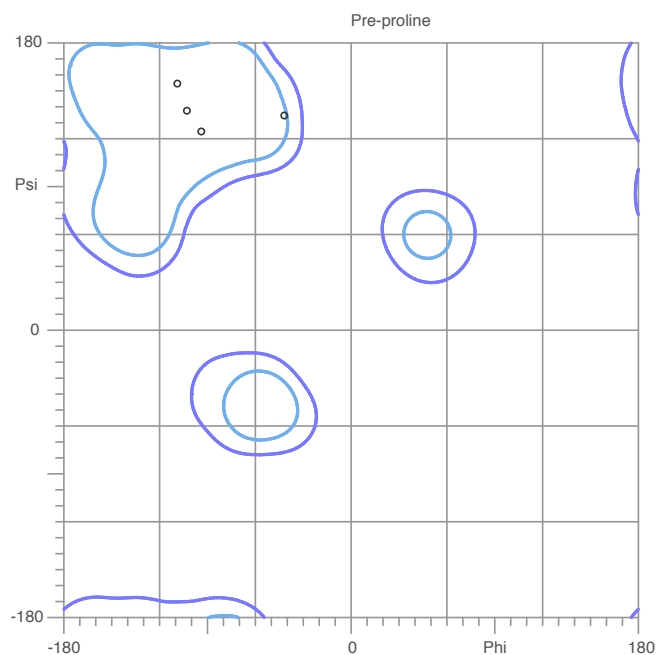
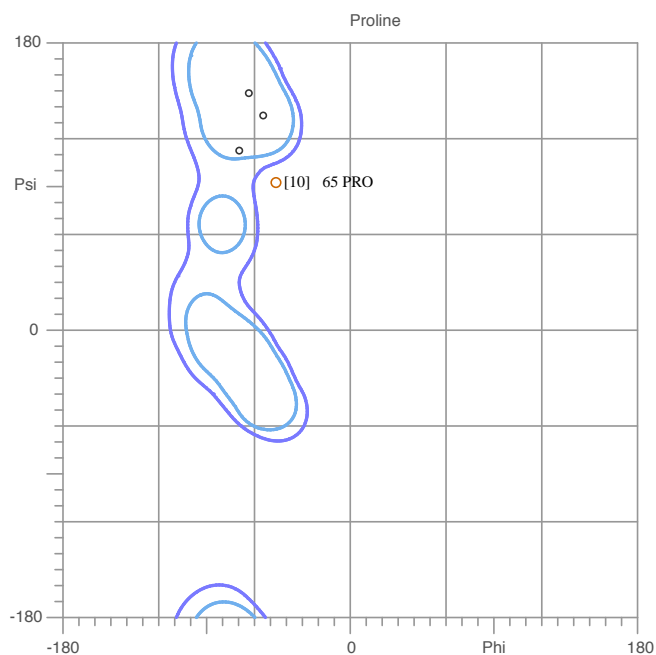
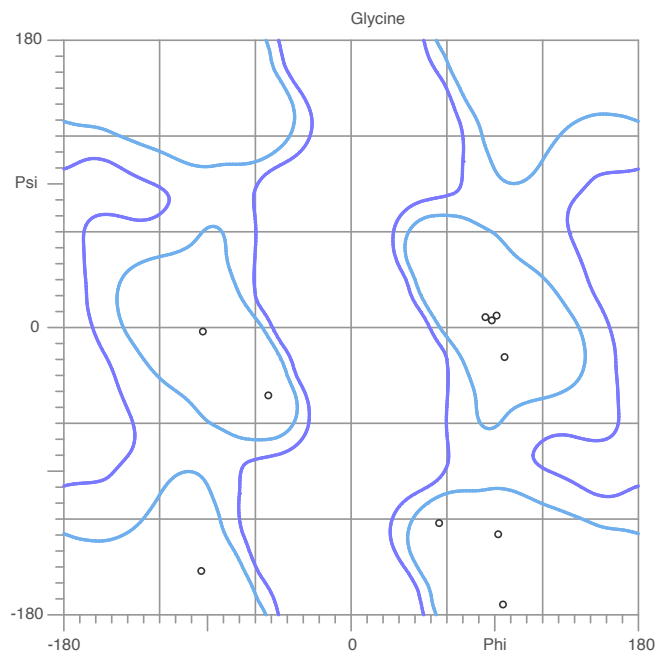
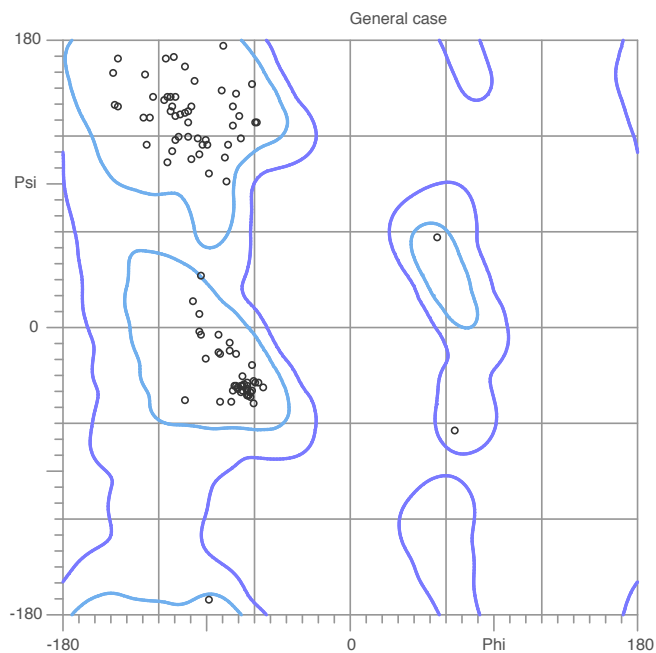
[9] 52 GLY (165.0, 71.0)

[9] 54 ALA (56.9, -82.6)

[9] 65 PRO (-85.0, -155.6)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 10



97.4% (111/114) of all residues were in favored (98%) regions.
99.1% (113/114) of all residues were in allowed (>99.8%) regions.

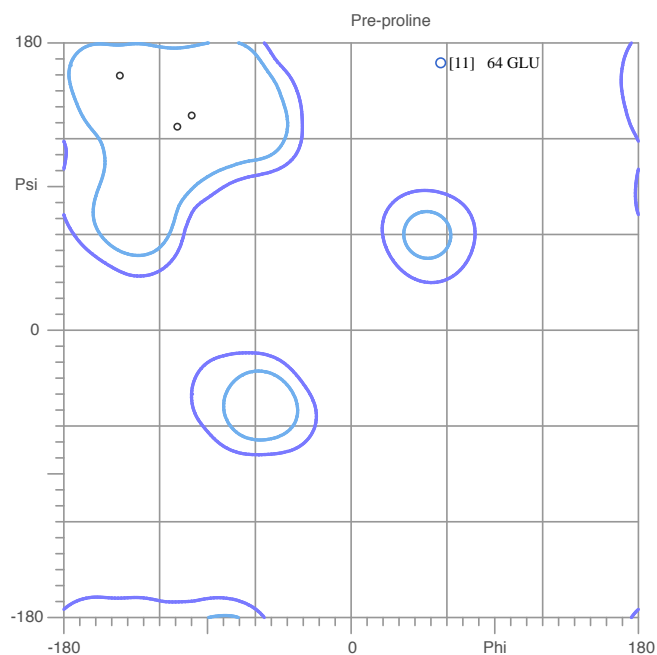
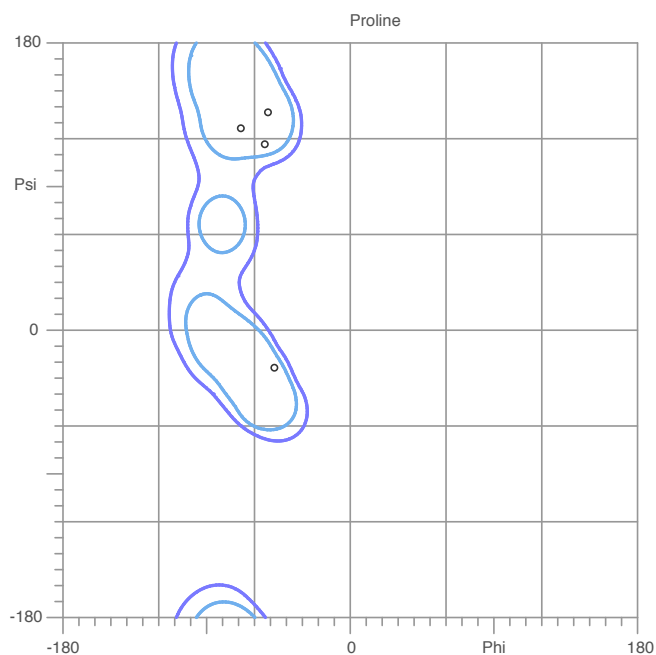
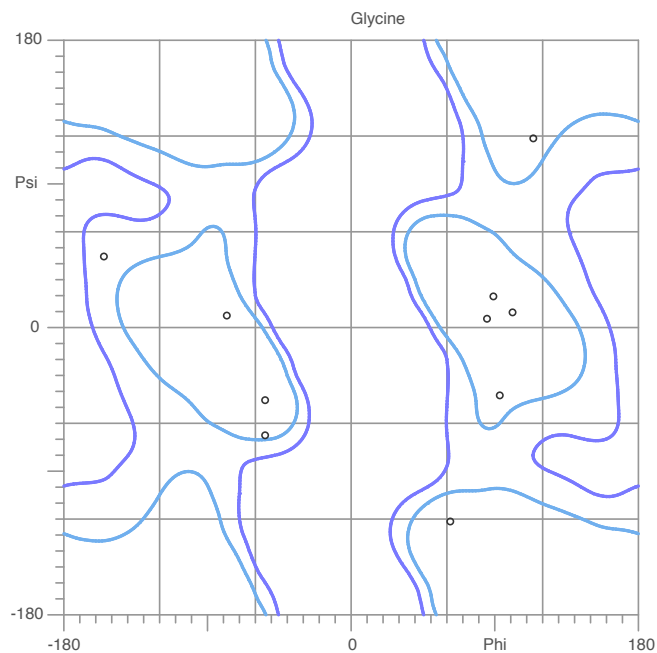
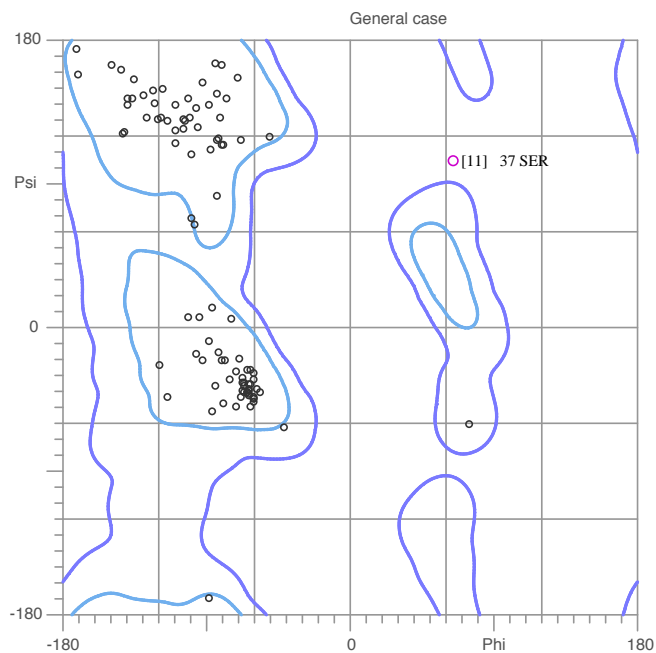
There were 1 outliers (phi, psi):
[10] 65 PRO (-47.9, 93.1)

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MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 11

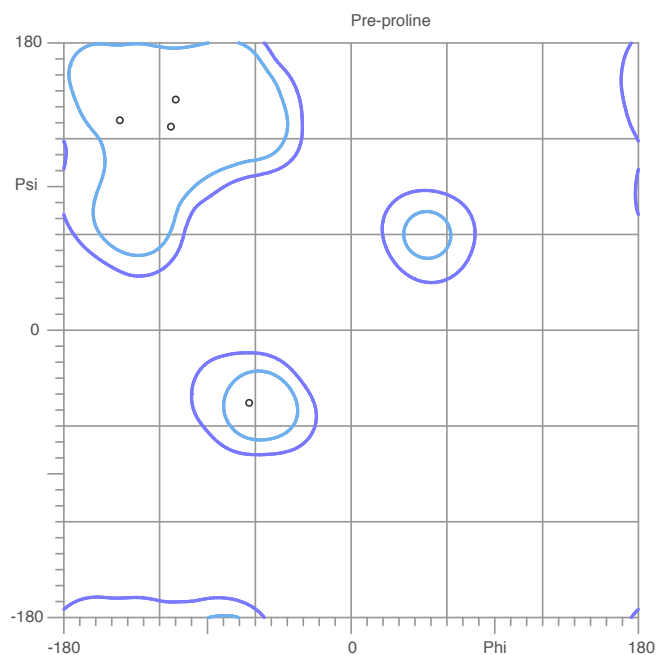
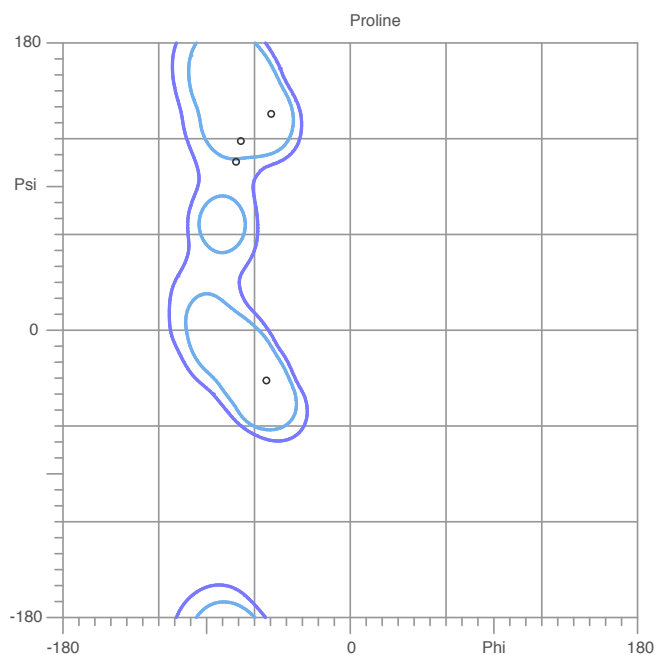
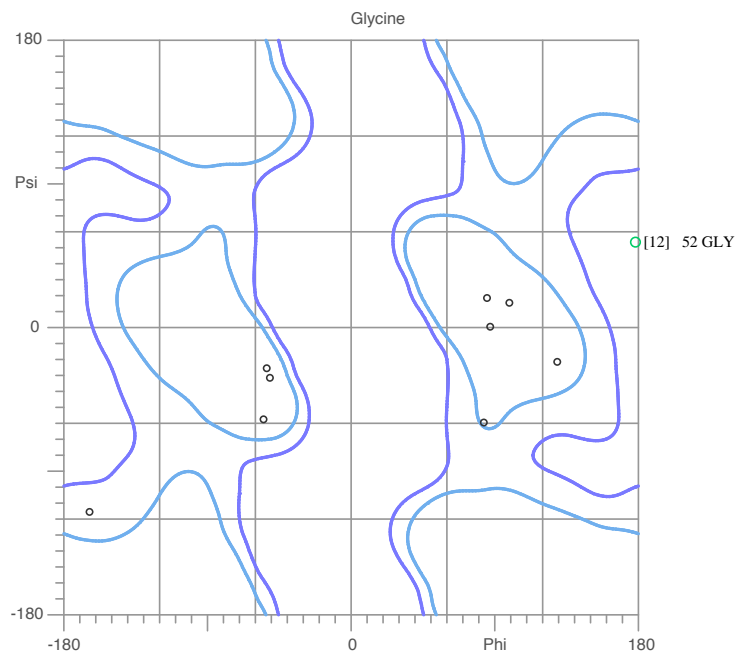
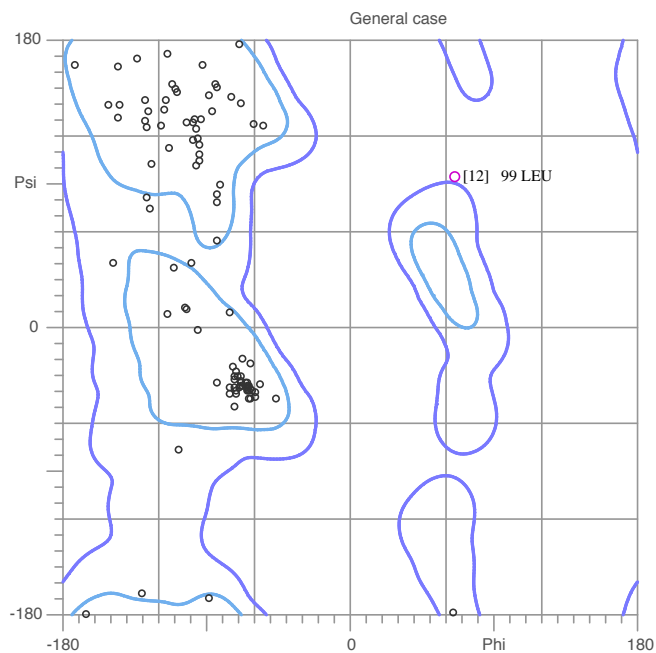


93.9% (107/114) of all residues were in favored (98%) regions.
98.2% (112/114) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[11] 37 SER (64.9, 105.0)
[11] 64 GLU (56.2, 168.4)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 12

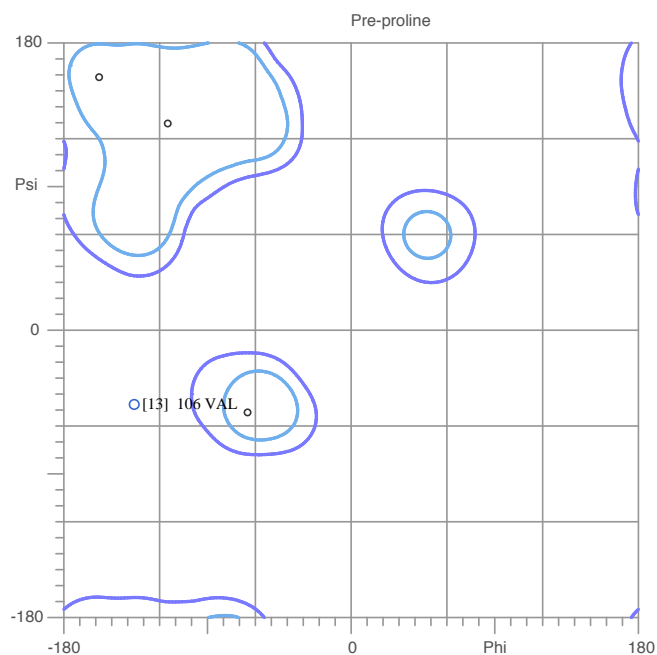
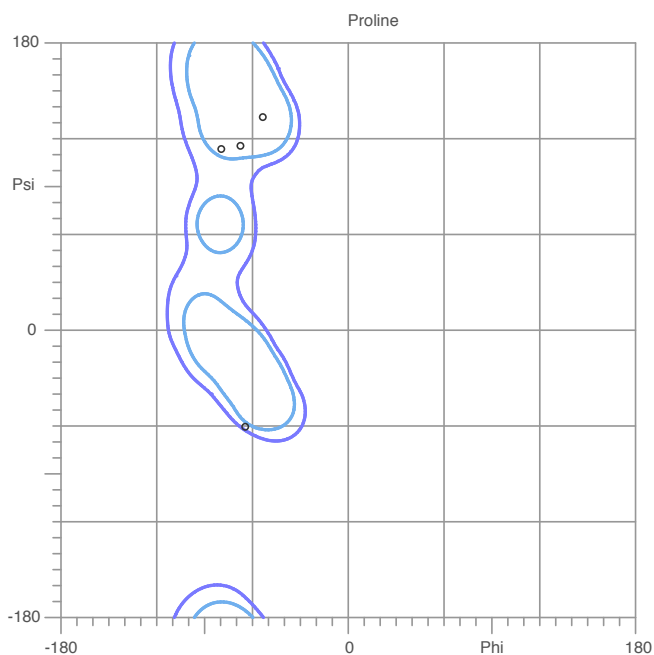
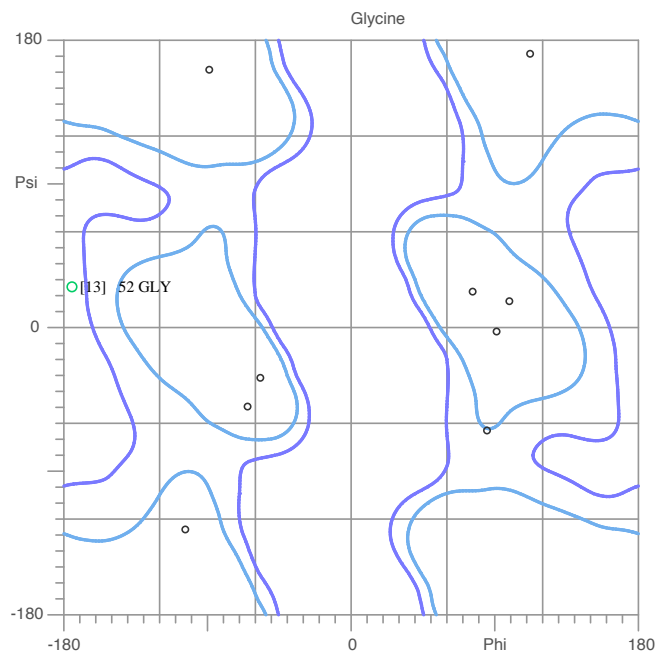
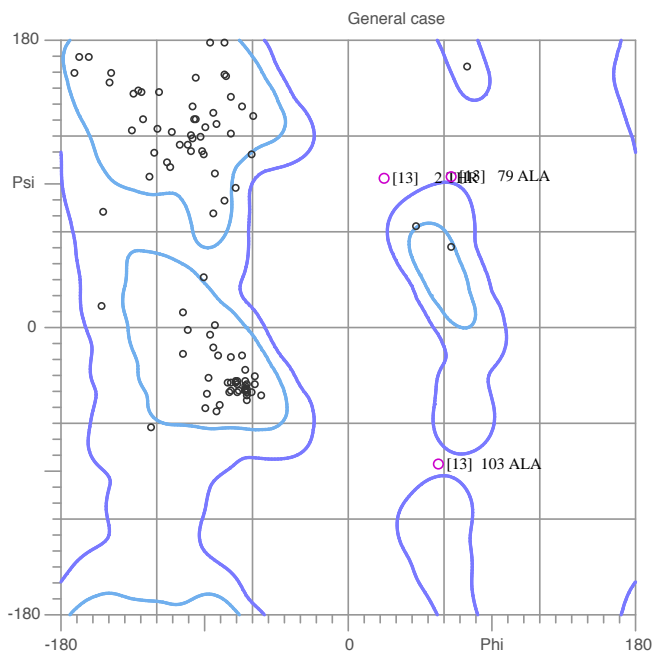


90.4% (103/114) of all residues were in favored (98%) regions.
98.2% (112/114) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 52 GLY (178.0, 55.0)
[12] 99 LEU (65.0, 95.0)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 13



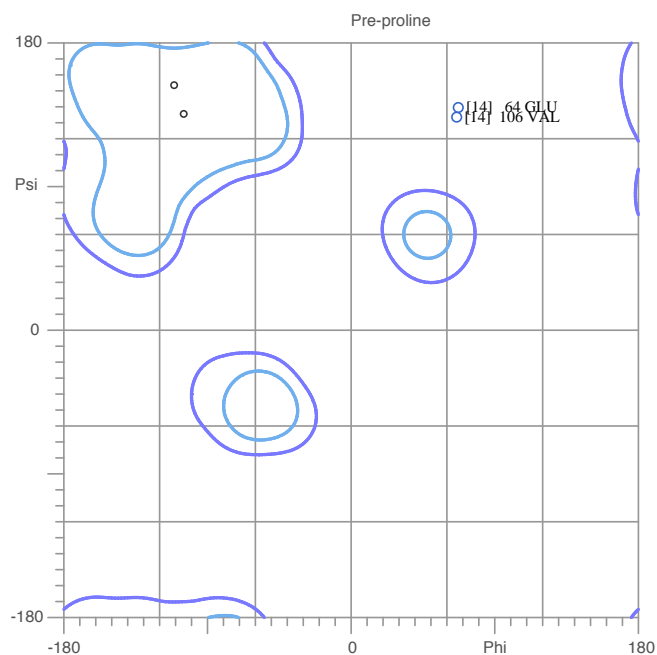
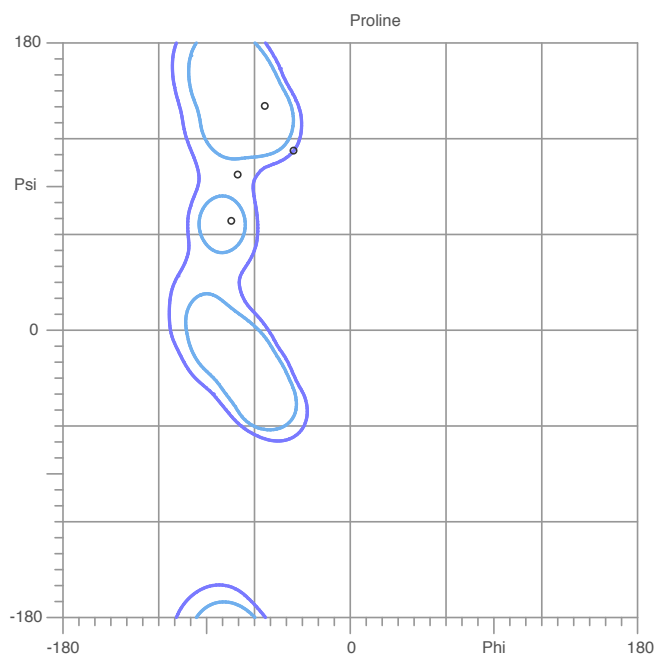
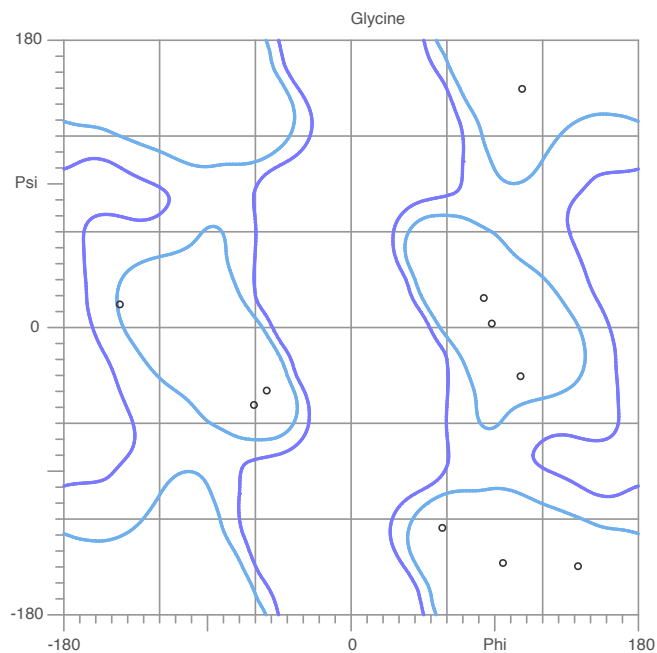
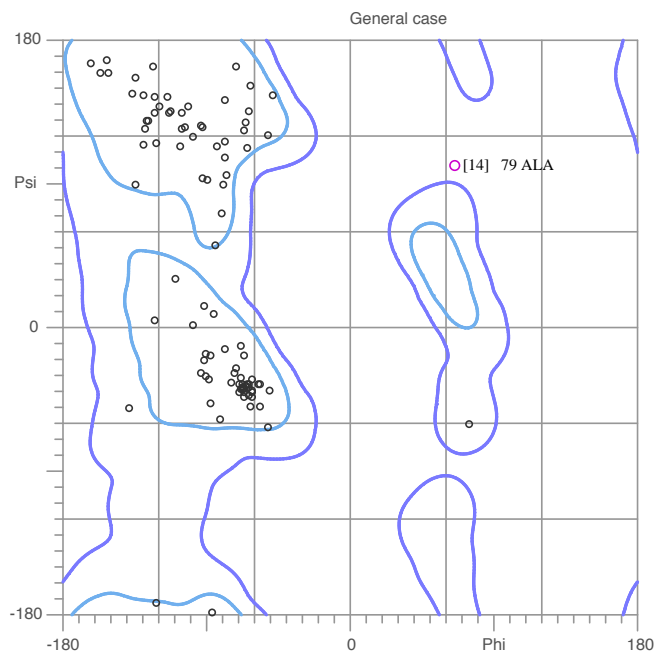
87.7% (100/114) of all residues were in favored (98%) regions.
95.6% (109/114) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [13] 2 THR (22.7, 95.0)
- [13] 52 GLY (-175.0, 26.5)
- [13] 79 ALA (65.0, 95.1)
- [13] 103 ALA (56.3, -85.2)
- [13] 106 VAL (-137.0, -46.5)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 14



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):

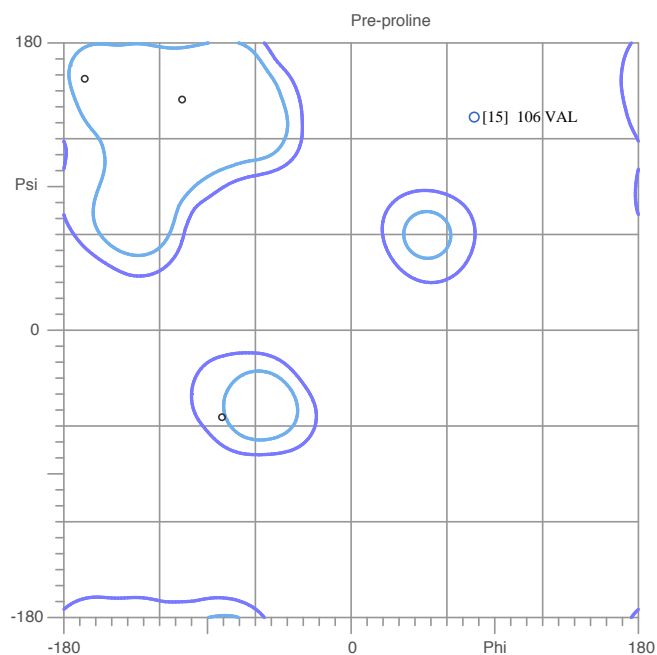
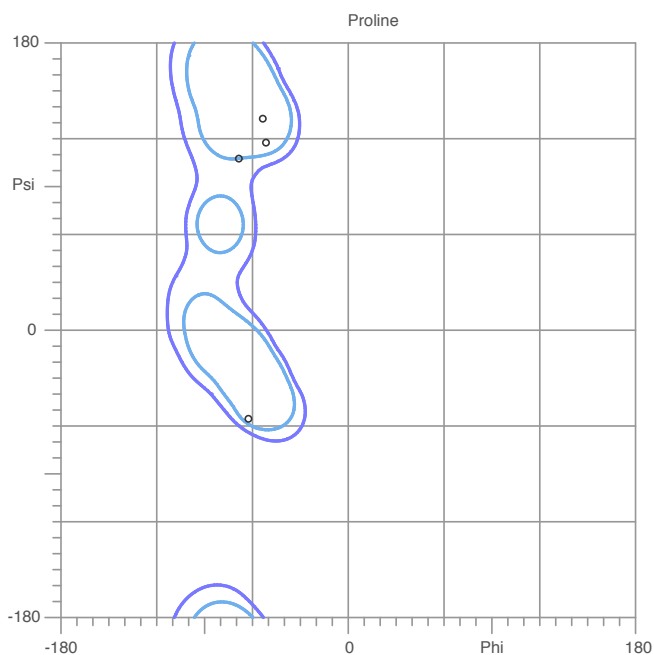
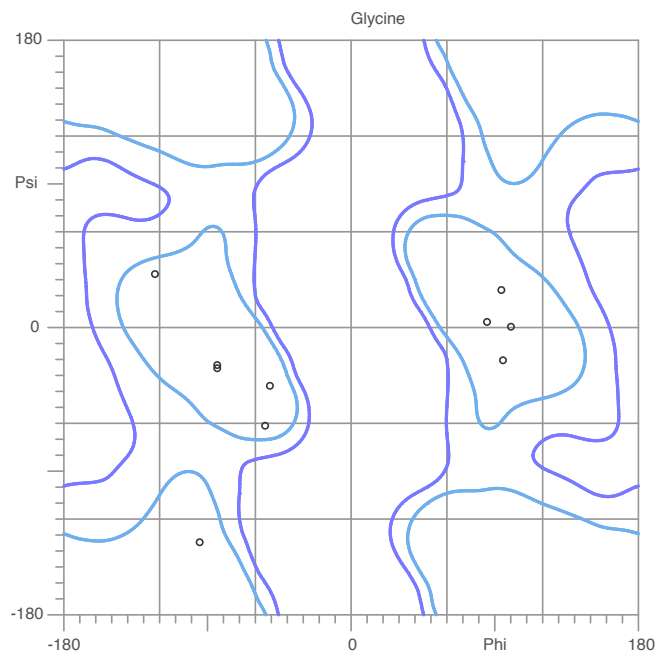
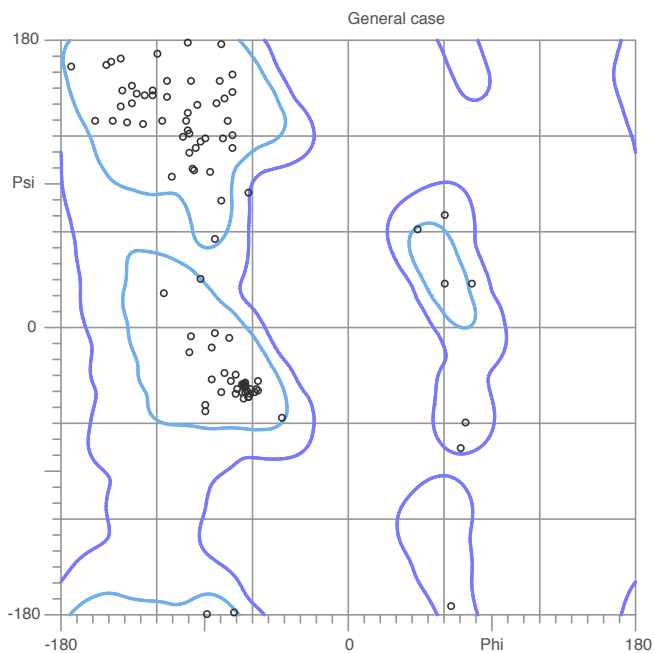
[14] 64 GLU (67.1, 140.8)

[14] 79 ALA (65.2, 102.0)

[14] 106 VAL (66.2, 134.5)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 15



92.1% (105/114) of all residues were in favored (98%) regions.
99.1% (113/114) of all residues were in allowed (>99.8%) regions.

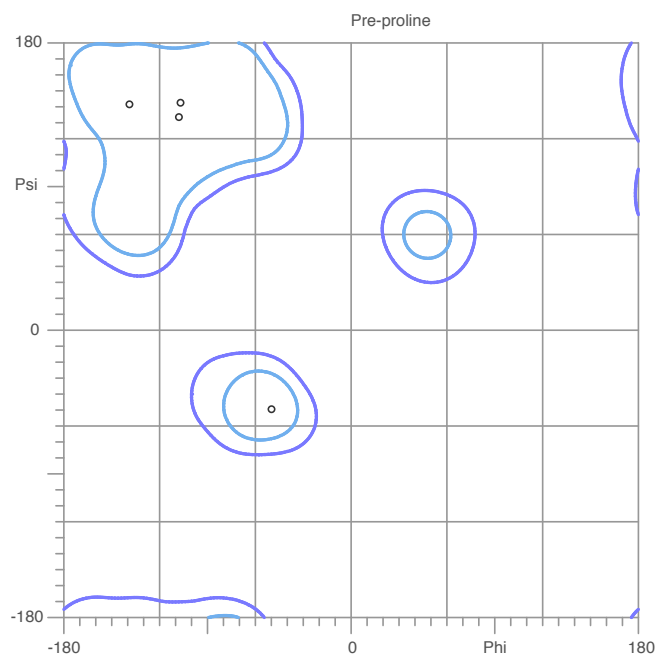
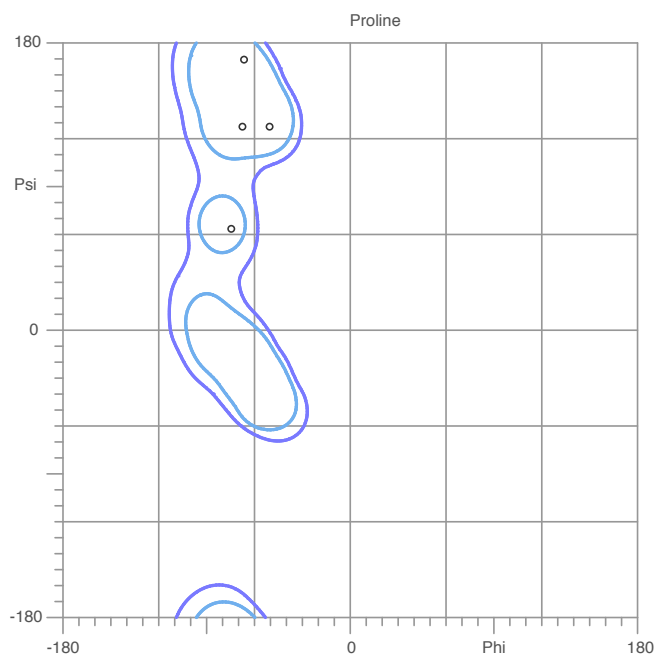
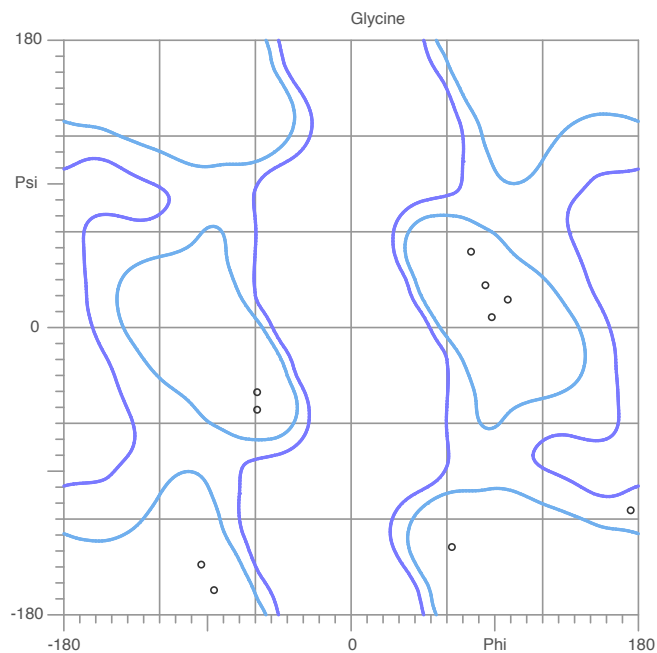
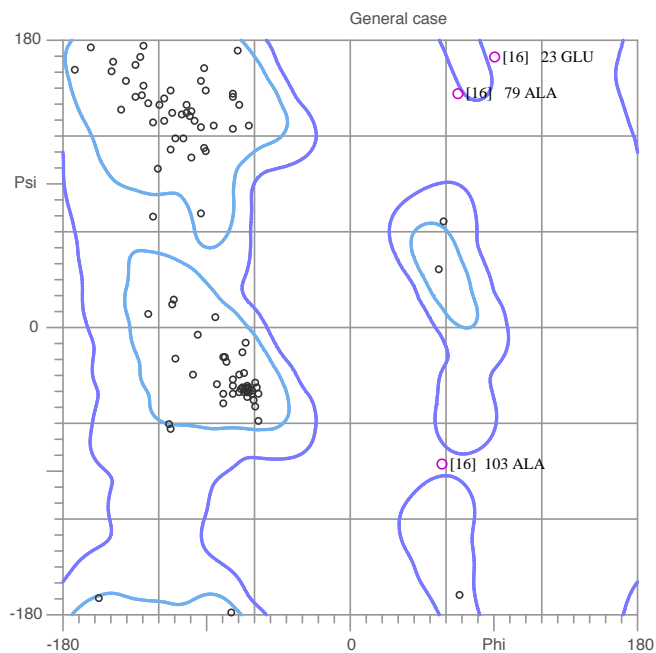
There were 1 outliers (phi, psi):
[15] 106 VAL (77.1, 135.0)

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

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

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 16



93.0% (106/114) 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):

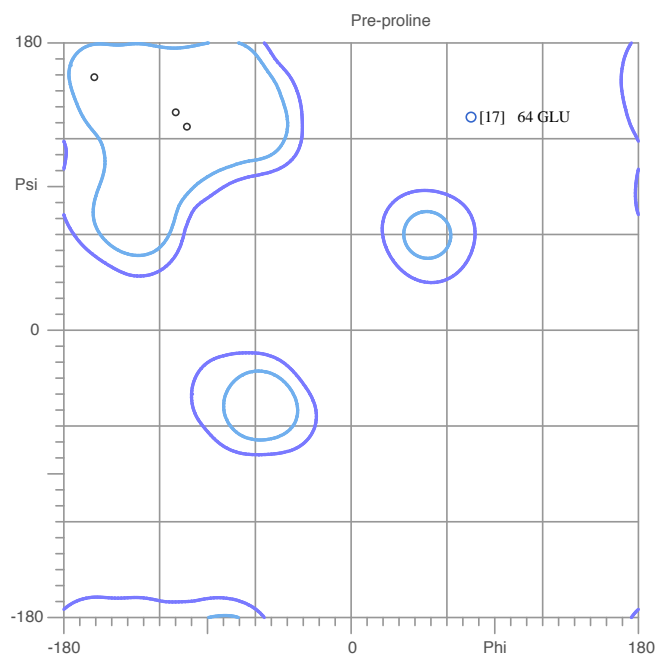
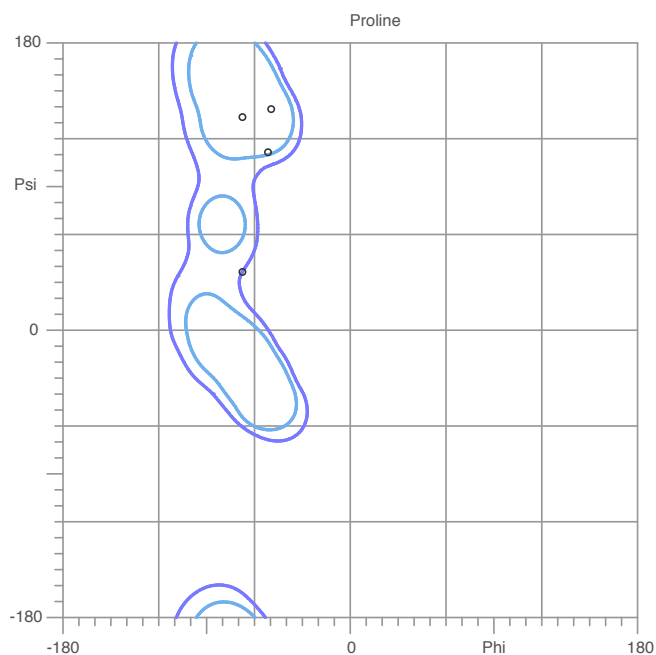
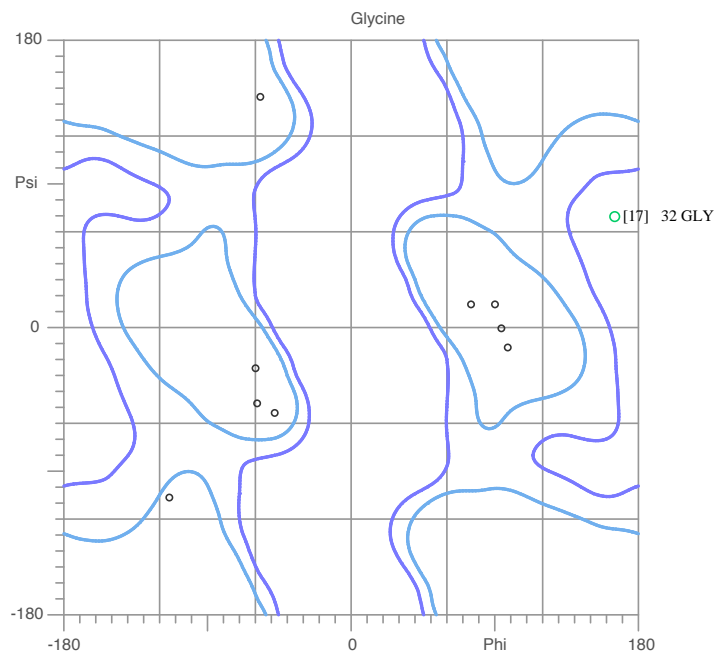
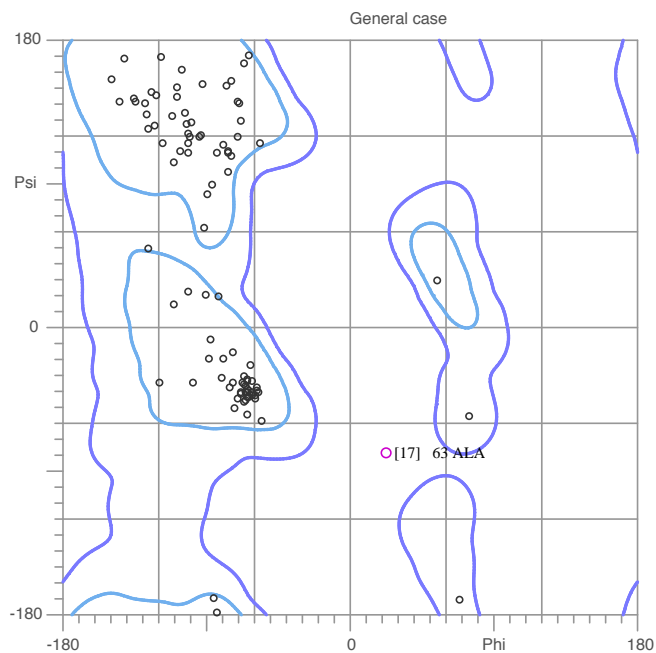
[16] 23 GLU (90.2, 170.5)

[16] 79 ALA (67.9, 147.8)

[16] 103 ALA (57.6, -85.2)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 17



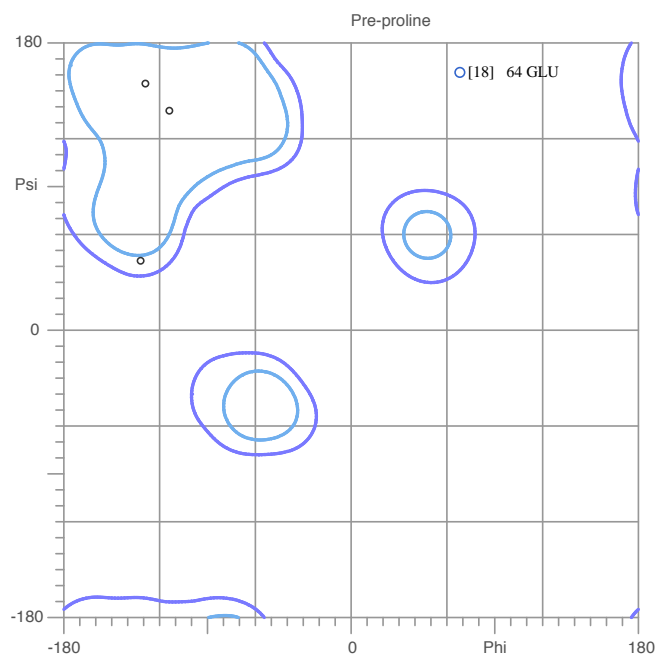
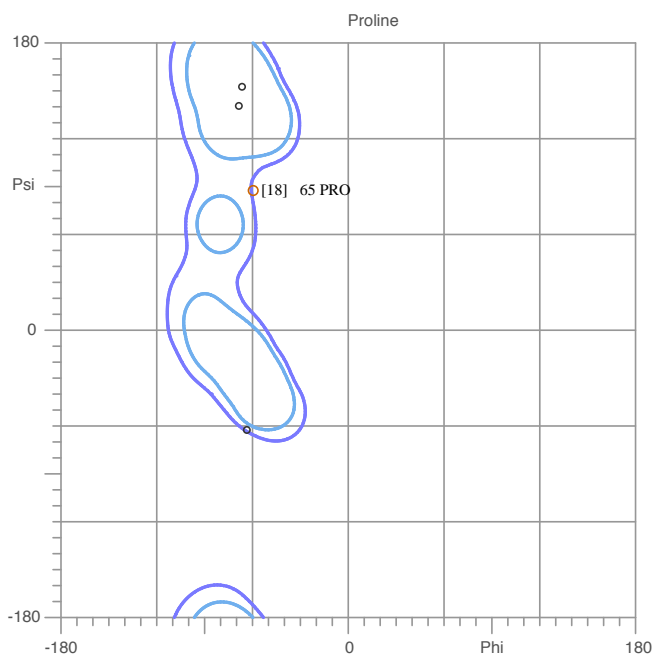
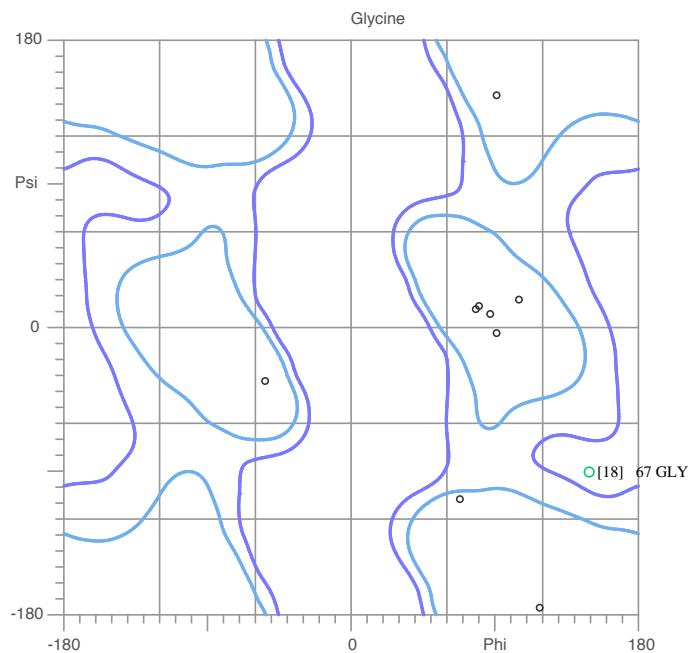
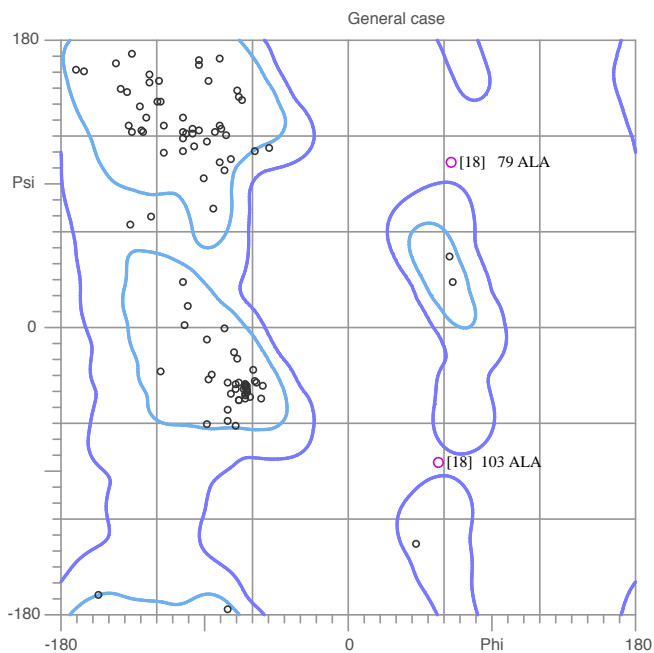
93.0% (106/114) of all residues were in favored (98%) regions.
97.4% (111/114) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [17] 32 GLY (165.0, 70.5)
- [17] 63 ALA (22.3, -78.1)
- [17] 64 GLU (75.0, 135.0)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 18



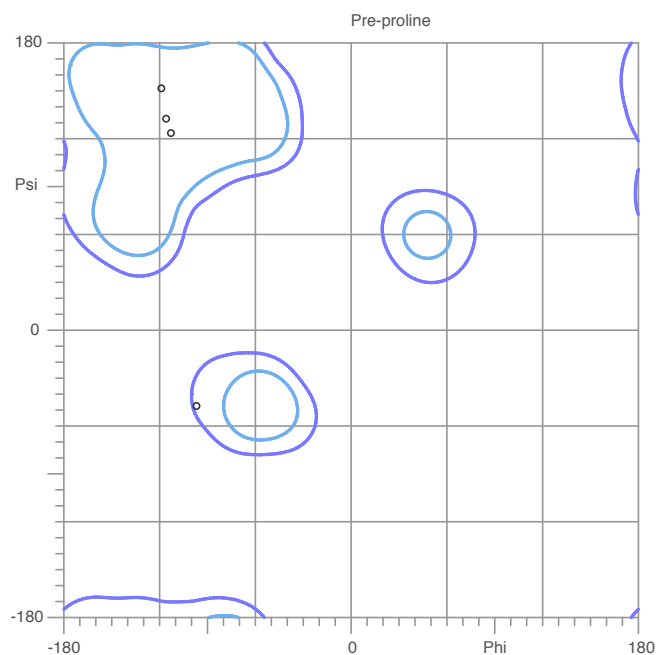
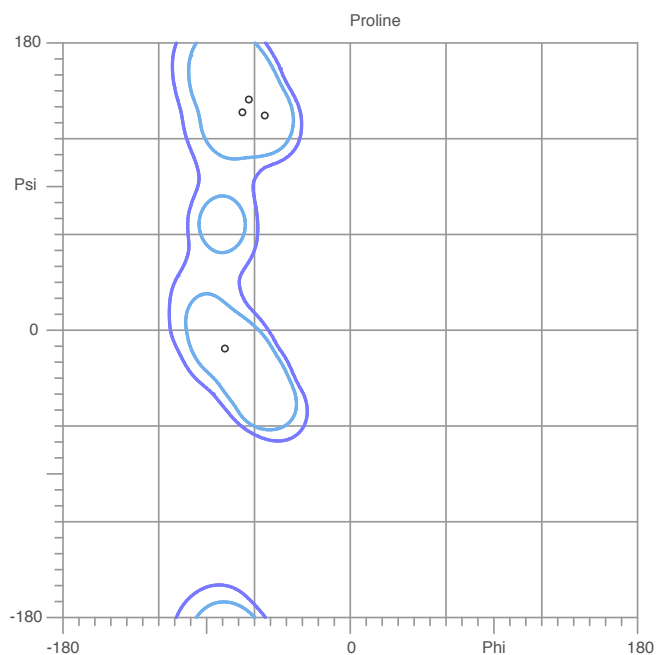
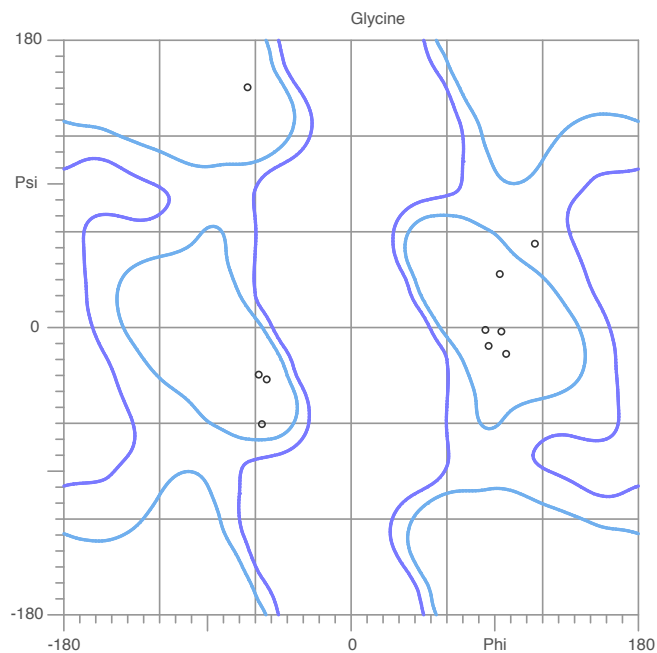
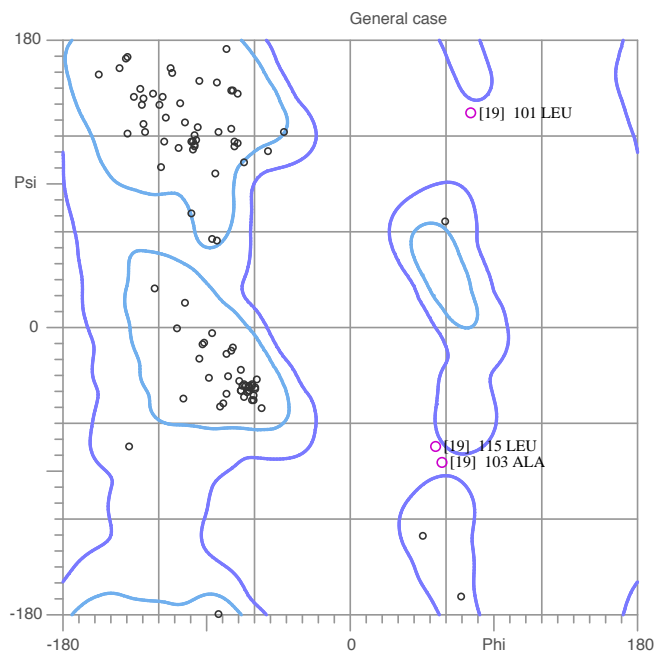
89.5% (102/114) of all residues were in favored (98%) regions.
95.6% (109/114) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [18] 64 GLU (68.3, 162.2)
- [18] 65 PRO (-60.2, 88.0)
- [18] 67 GLY (150.0, -90.7)
- [18] 79 ALA (65.0, 104.8)
- [18] 103 ALA (56.7, -85.0)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 19



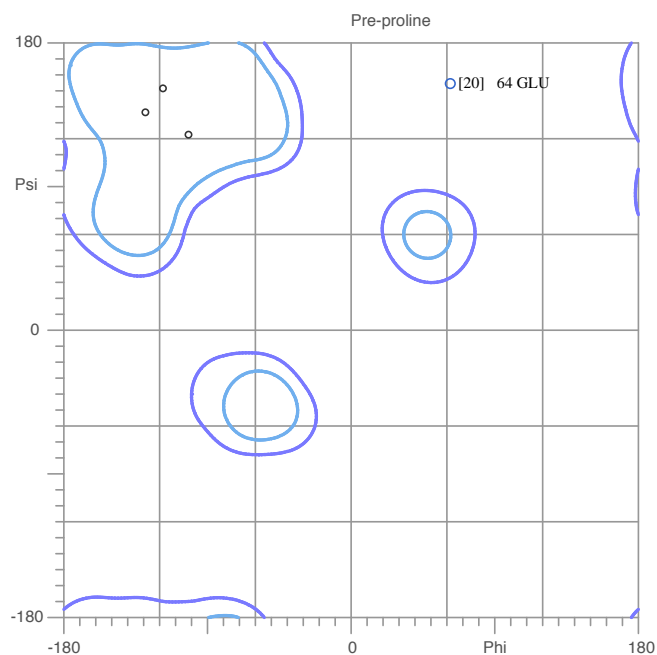
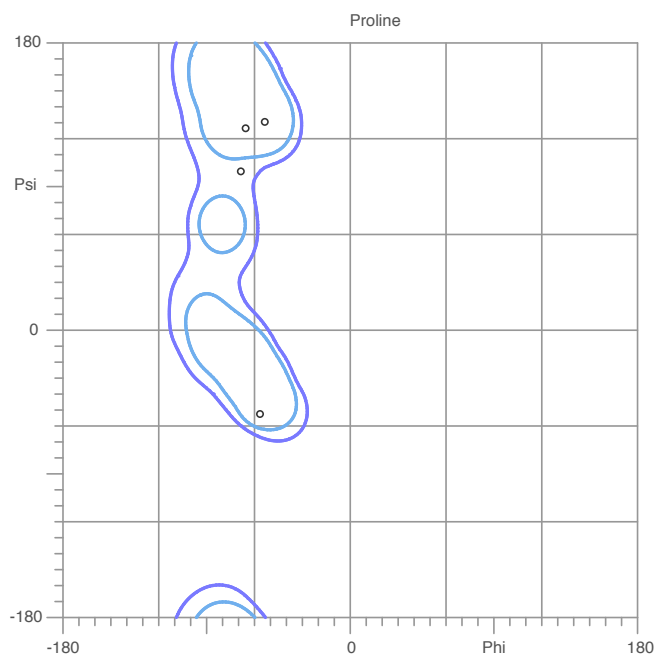
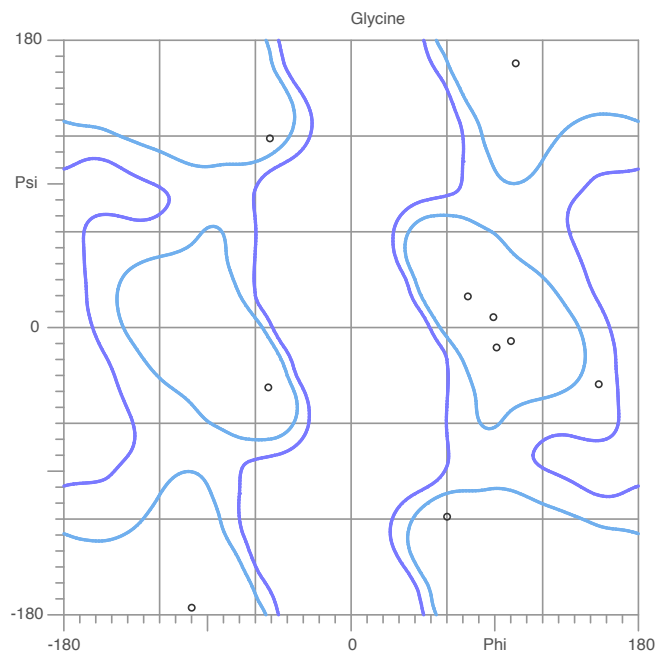
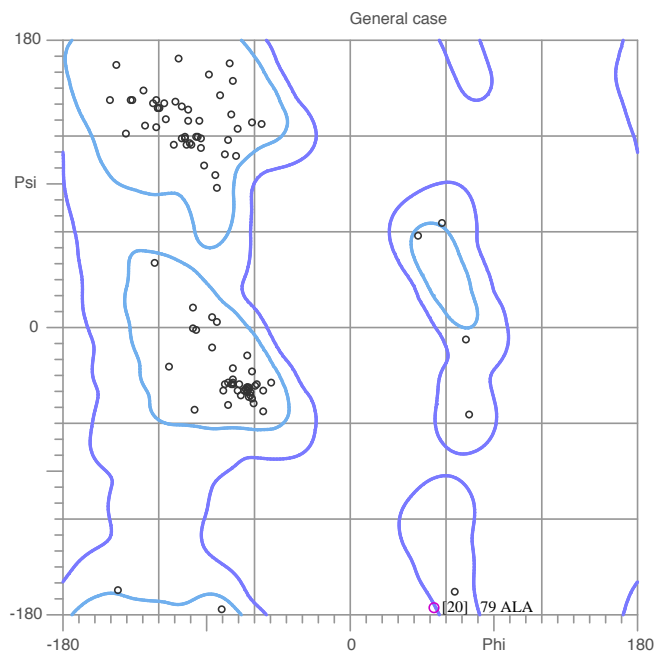
91.2% (104/114) of all residues were in favored (98%) regions.
97.4% (111/114) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [19] 101 LEU (75.0, 135.1)
- [19] 103 ALA (57.2, -85.0)
- [19] 115 LEU (53.4, -75.0)

MolProbity Ramachandran analysis

CCR55_R3Cons_em_bcr3.pdb, model 20



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):
[20] 64 GLU (62.6, 155.1)
[20] 79 ALA (52.7, -175.1)