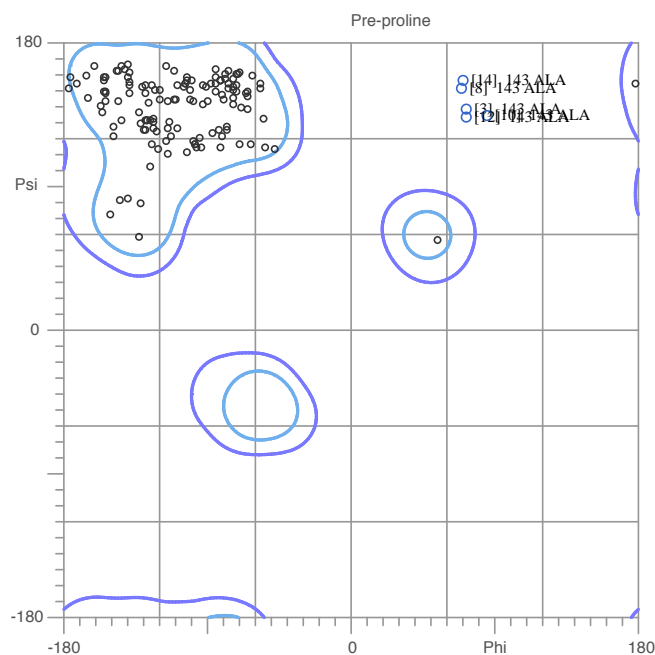
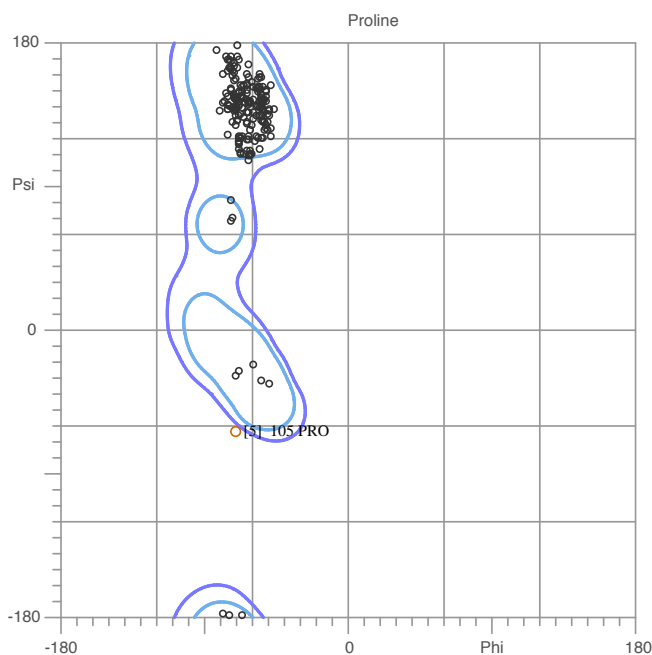
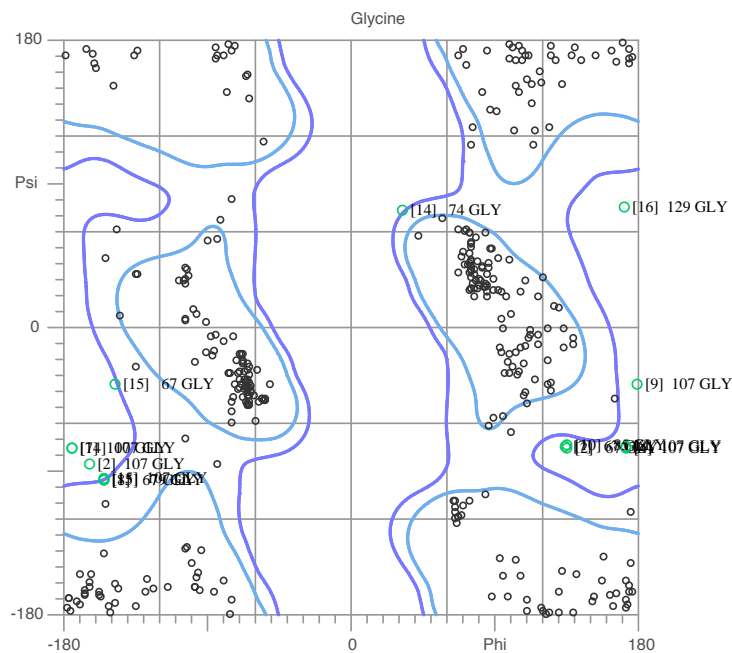
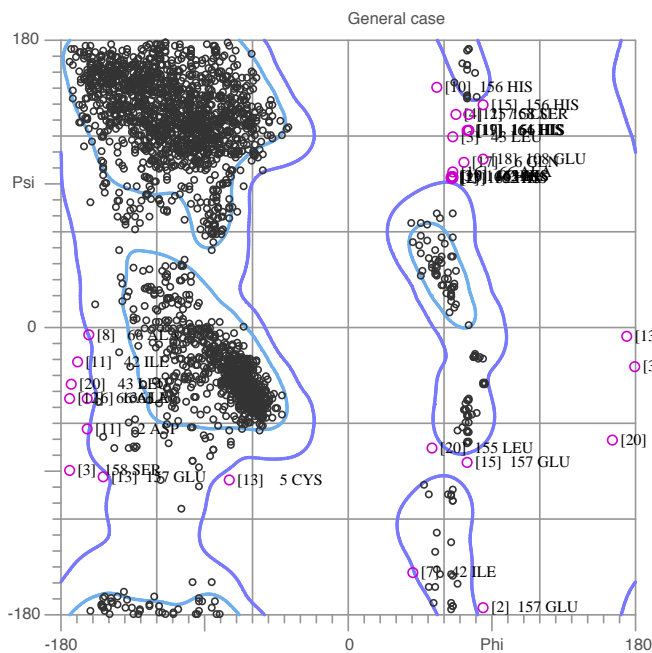


MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, all models



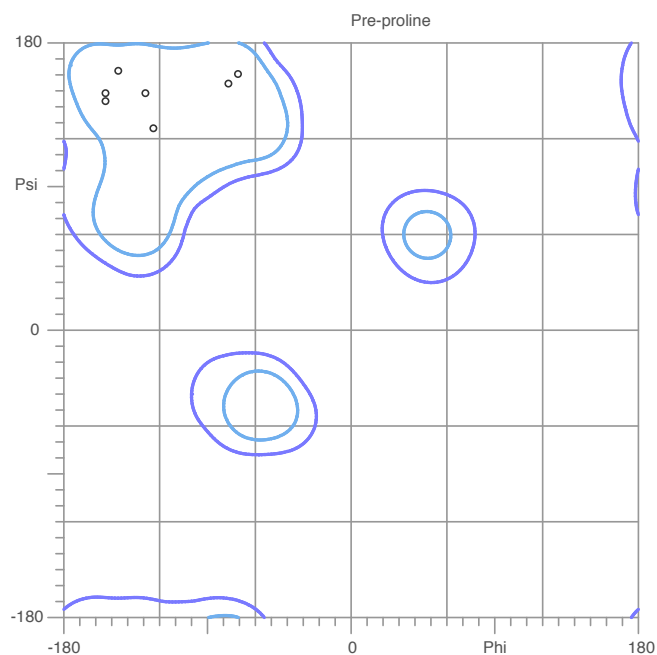
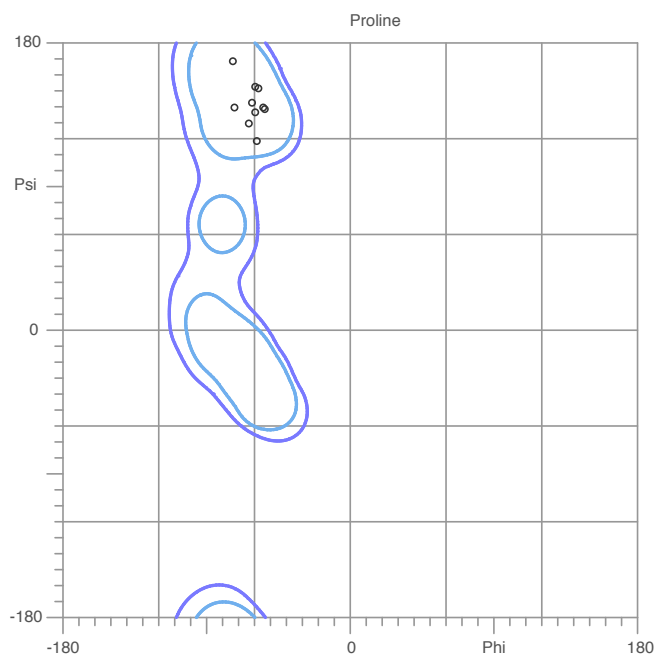
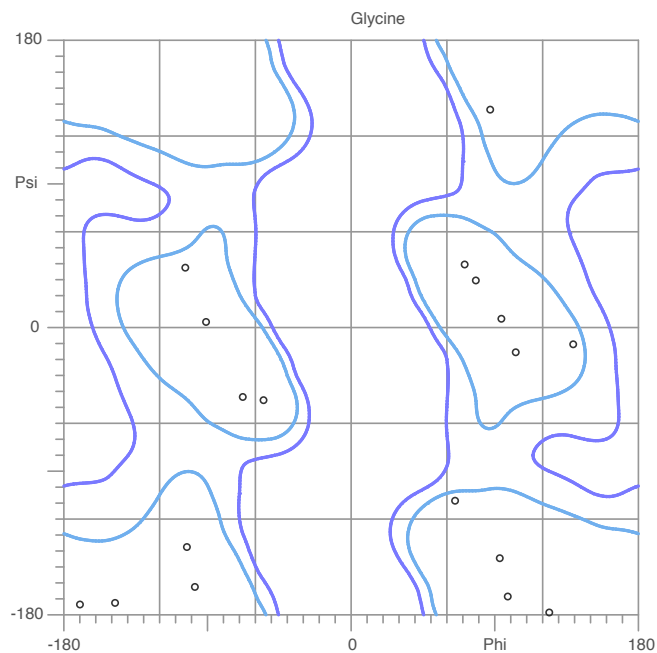
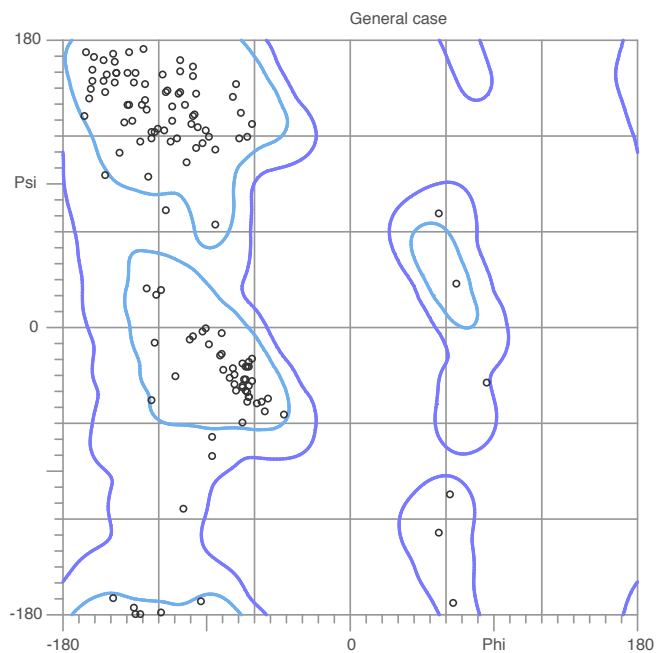
92.2% (3023/3280) of all residues were in favored (98%) regions.
98.4% (3227/3280) of all residues were in allowed (>99.8%) regions.

There were 53 outliers (phi, psi):

- | | |
|-----------------------------|------------------------------|
| [2] 67 GLY (135.1, -75.0) | [11] 2 ASP (-164.9, -63.8) |
| [2] 107 GLY (-165.0, 85.0) | [11] 42 ILE (-170.7, -21.8) |
| [2] 157 GLU (84.6, -175.1) | [11] 164 HIS (75.0, 125.0) |
| [2] 162 HIS (65.1, 95.0) | [12] 66 ALA (-175.0, -44.9) |
| [3] 30 GLU (179.5, -24.8) | [12] 143 ALA (72.9, 134.8) |
| [3] 43 LEU (65.0, 121.0) | [12] 158 SER (75.7, 135.0) |
| [3] 143 ALA (72.4, 139.5) | [13] 5 CYS (-75.0, 95.0) |
| [3] 158 SER (-175.9, -89.9) | [13] 66 ALA (174.9, -5.1) |
| [3] 164 HIS (65.0, 95.4) | [13] 157 GLU (-154.9, 93.0) |
| [7] 42 ILE (60.9, -153.6) | [13] 162 HIS (65.0, 95.0) |
| [7] 67 GLY (135.0, -75.0) | [14] 74 GLY (32.7, 75.0) |
| [7] 107 GLY (-175.0, -75.1) | [14] 107 GLY (-175.0, -75.1) |
| [8] 66 ALA (-163.5, -4.9) | [14] 143 ALA (70.4, 157.7) |
| [8] 67 GLY (-155.0, 95.1) | [15] 67 GLY (148.3, 35.0) |
| [8] 107 GLY (172.6, -75.0) | [15] 79 GLY (-155.0, -95.0) |
| [8] 143 ALA (70.0, 152.1) | [15] 107 GLY (-155.0, -94.9) |
| [9] 107 GLY (179.3, -35.0) | [15] 156 HIS (85.0, 140.0) |
| [10] 85 GLY (155.1, -74.0) | [15] 157 GLY (74.6, -84.9) |
| [10] 143 ALA (85.1, 135.1) | [16] 66 ALA (65.1, 98.5) |
| [10] 156 HIS (55.0, 151.5) | [16] 129 GLY (171.9, 76.4) |
| | [16] 163 HIS (65.1, 95.0) |
| | [17] 6 GLN (72.4, 105.0) |
| | [17] 156 HIS (75.0, 124.9) |
| | [18] 108 GLU (84.0, 106.8) |
| | [19] 161 HIS (75.0, 125.0) |
| | [19] 163 HIS (65.1, 95.1) |
| | [20] 43 LEU (-175.0, -35.0) |
| | [20] 155 LEU (52.7, -75.0) |
| | [20] 157 GLU (165.0, -70.4) |

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 1



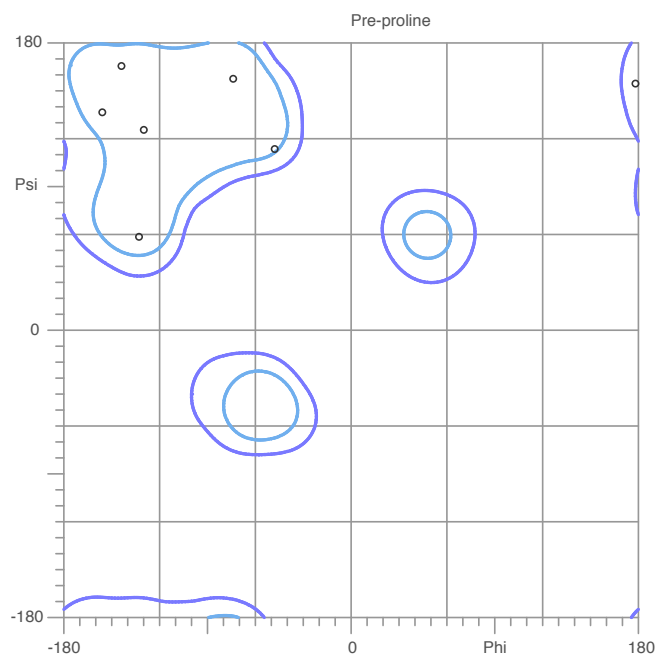
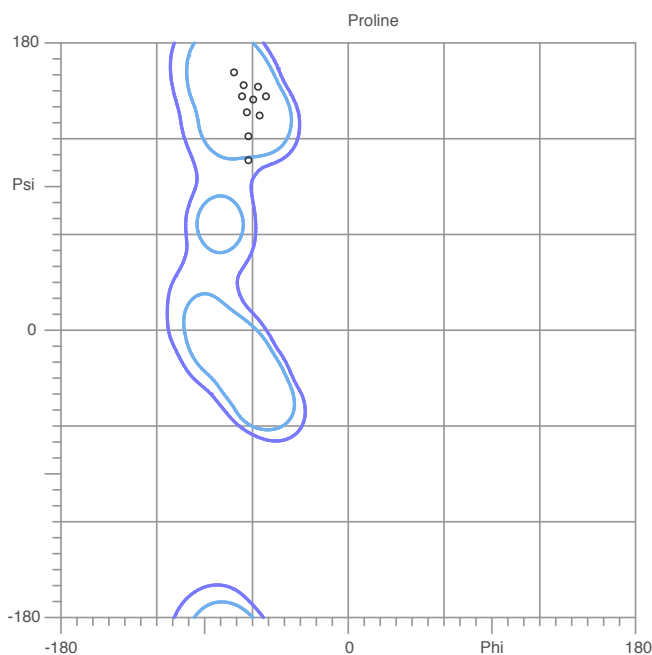
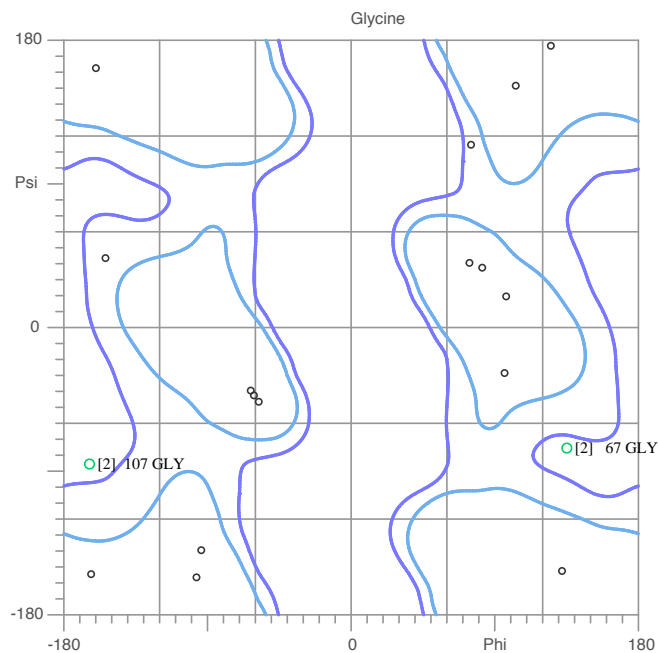
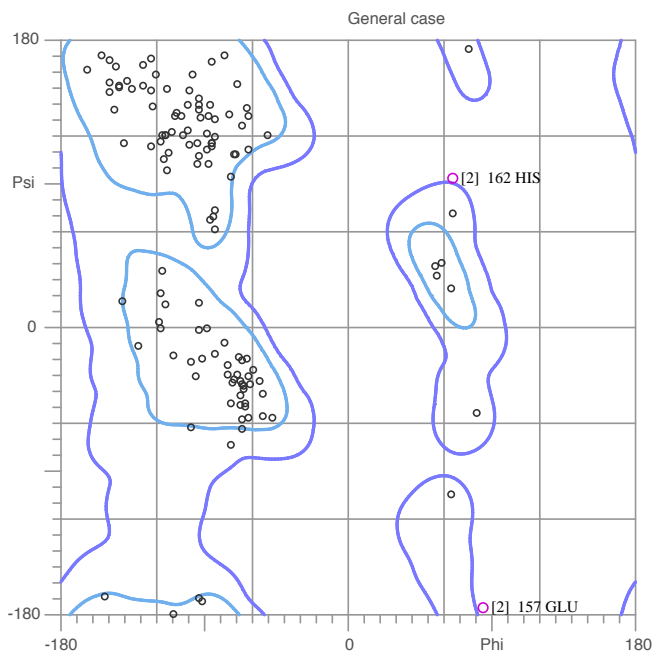
93.9% (154/164) of all residues were in favored (98%) regions.

100.0% (164/164) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 2



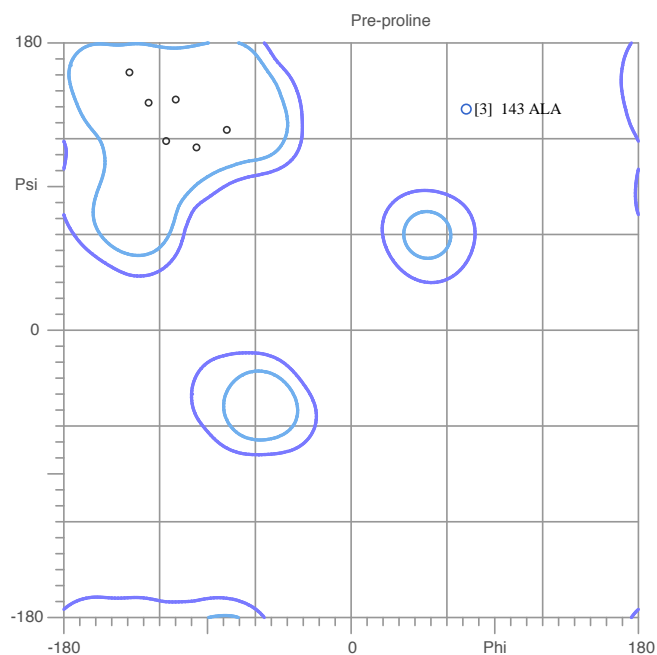
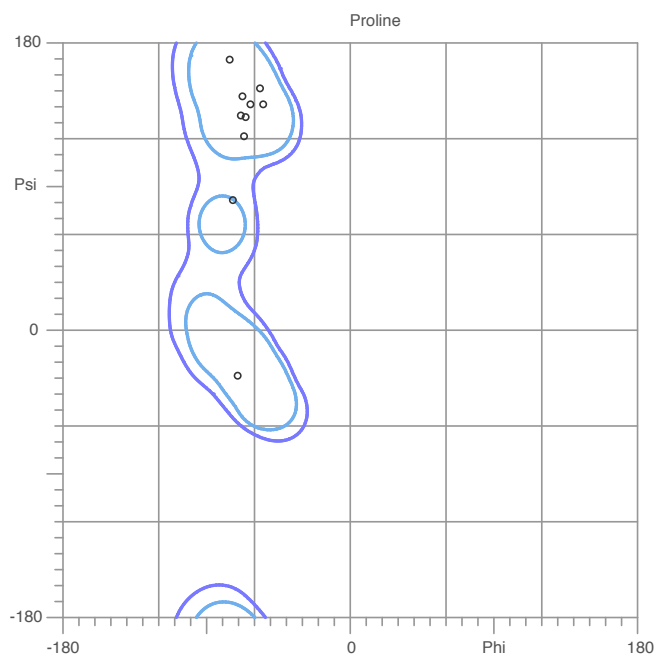
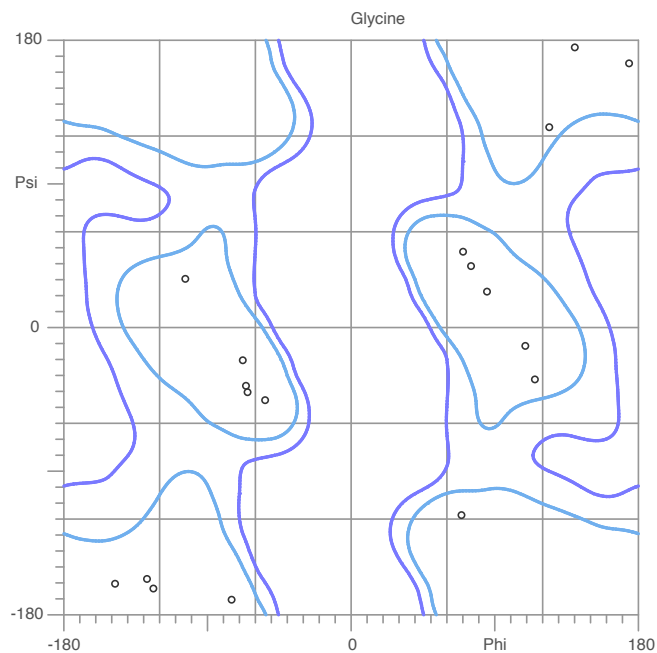
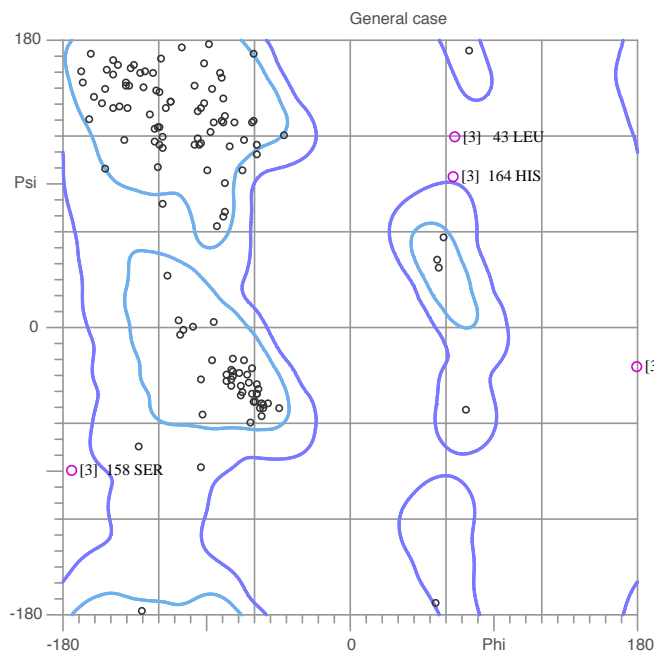
90.2% (148/164) of all residues were in favored (98%) regions.
97.6% (160/164) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [2] 67 GLY (135.1, -75.0)
- [2] 107 GLY (-165.0, -85.0)
- [2] 157 GLU (84.6, -175.1)
- [2] 162 HIS (65.1, 95.0)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 3



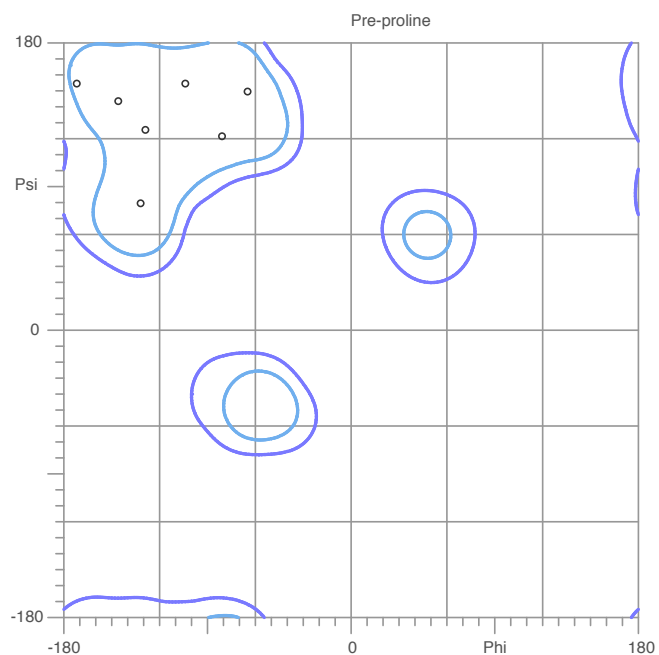
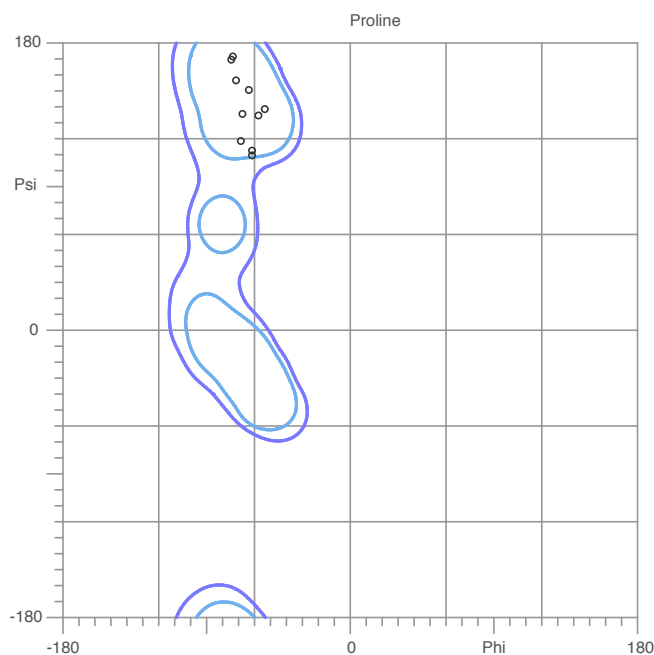
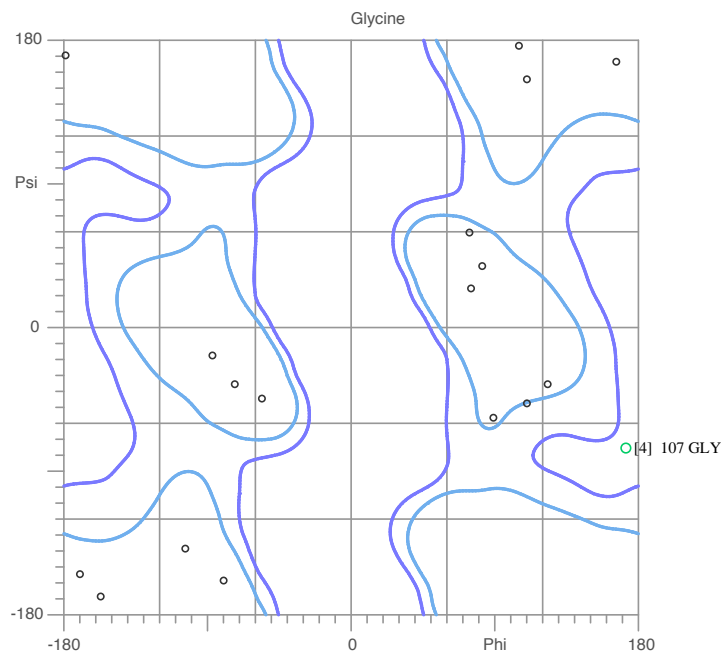
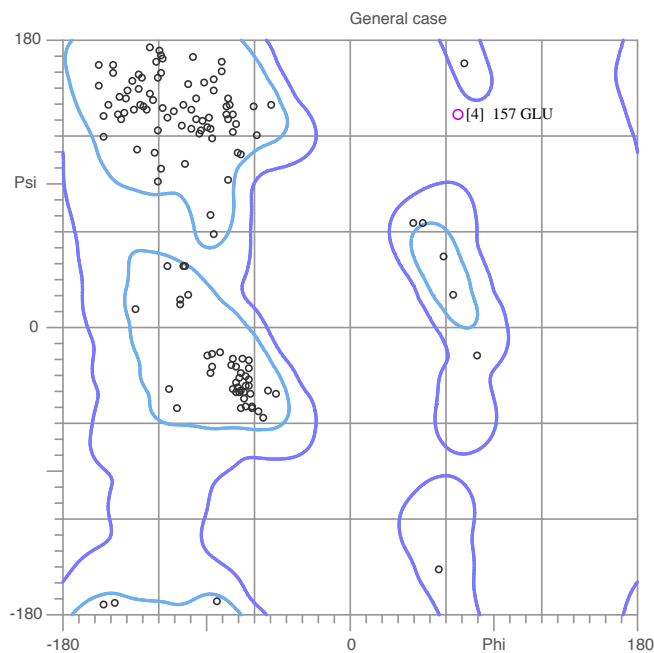
90.9% (149/164) of all residues were in favored (98%) regions.
97.0% (159/164) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[3] 30 GLU (179.5, -24.8)
[3] 43 LEU (65.0, 121.0)
[3] 143 ALA (72.4, 139.5)
[3] 158 SER (-175.9, -89.9)
[3] 164 HIS (65.0, 95.4)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 4

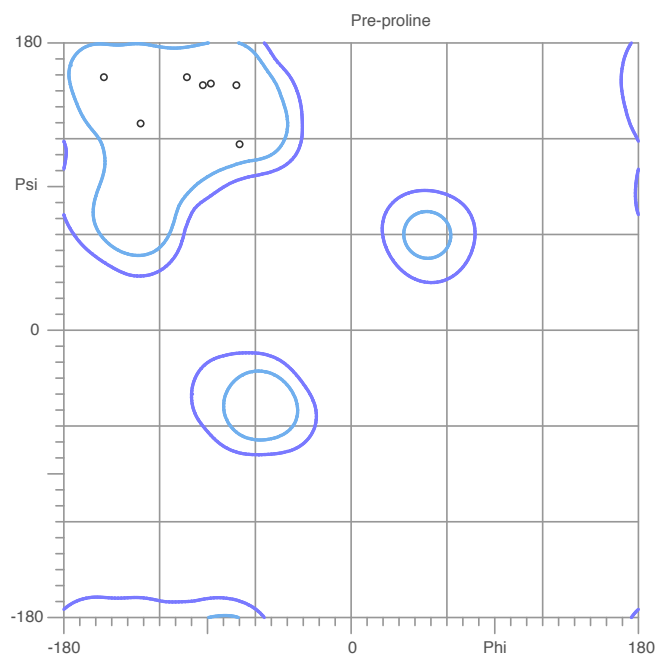
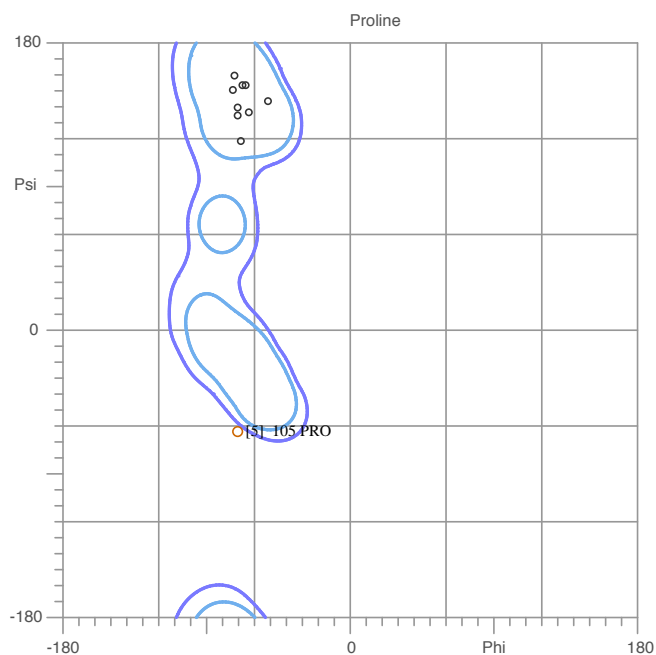
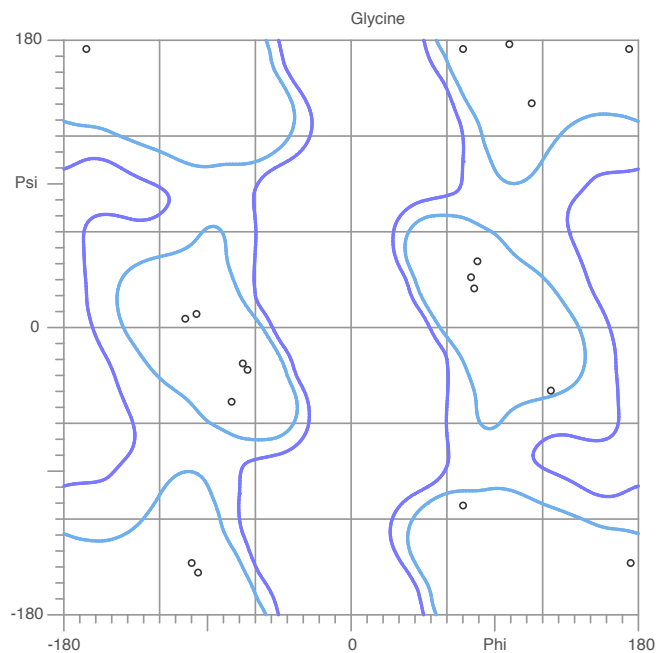
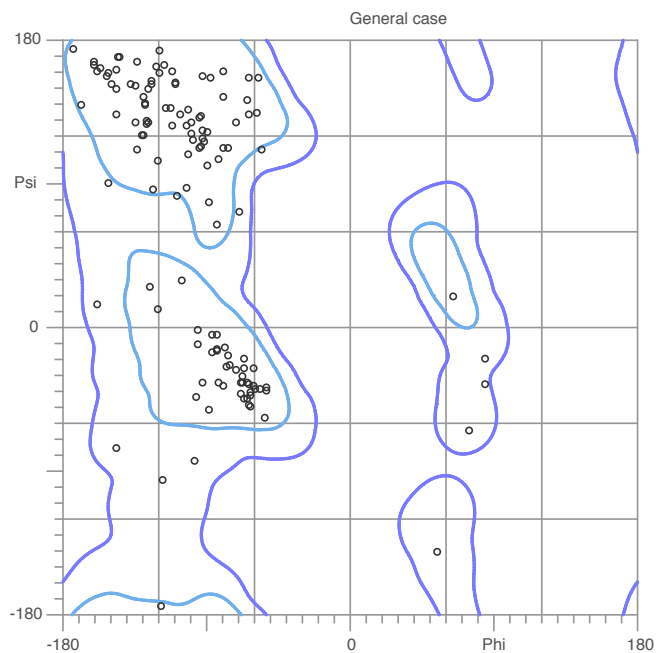


95.1% (156/164) of all residues were in favored (98%) regions.
98.8% (162/164) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[4] 107 GLY (172.7, -75.0)
[4] 157 GLU (67.6, 134.9)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 5



92.1% (151/164) of all residues were in favored (98%) regions.
99.4% (163/164) of all residues were in allowed (>99.8%) regions.

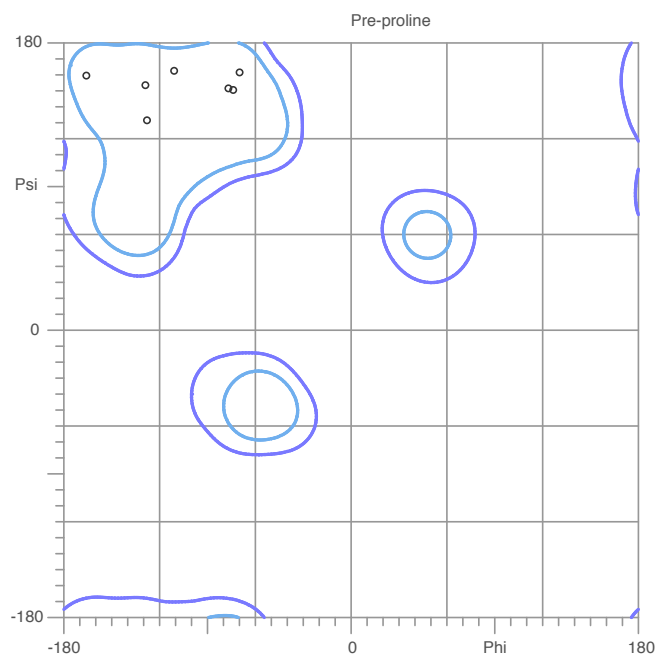
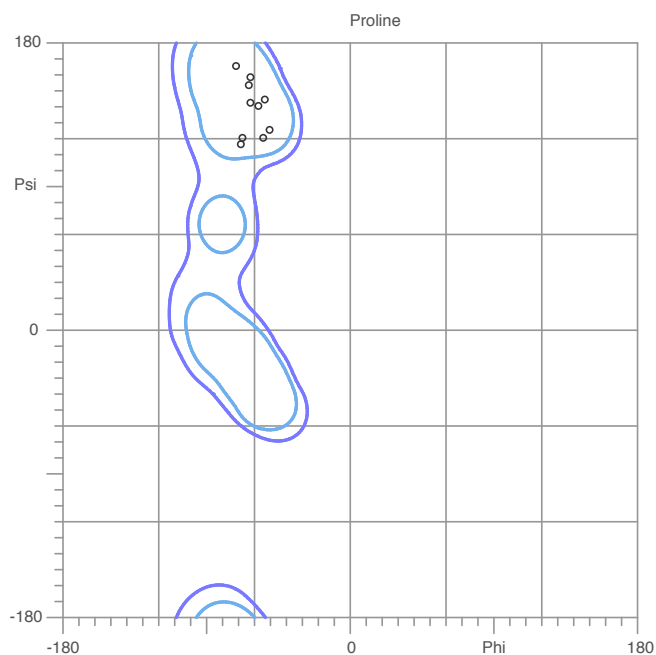
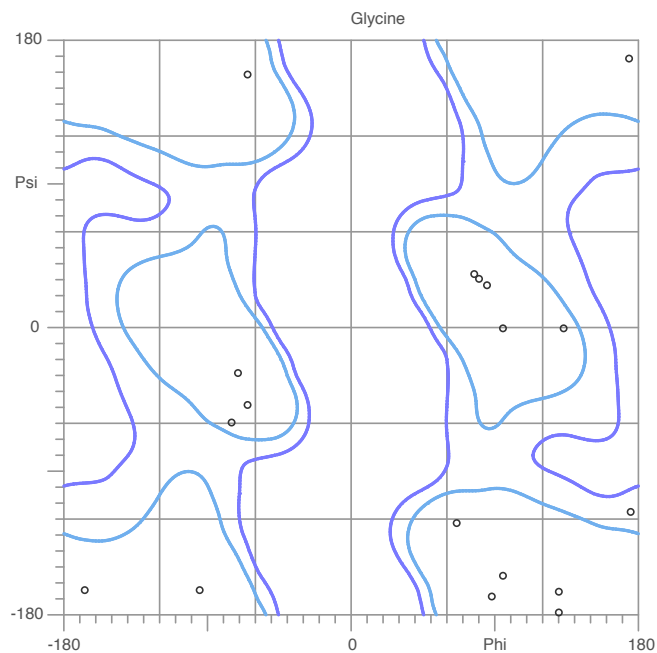
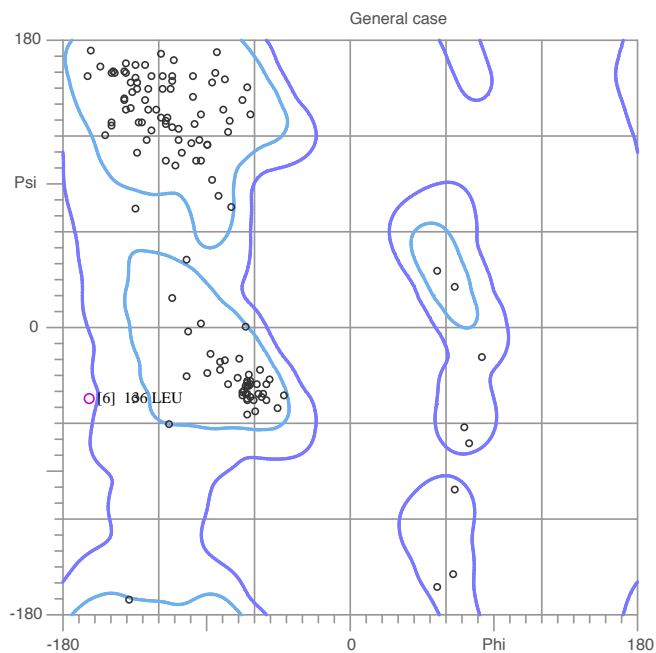
There were 1 outliers (phi, psi):
[5] 105 PRO (-71.0, -63.7)

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MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 6

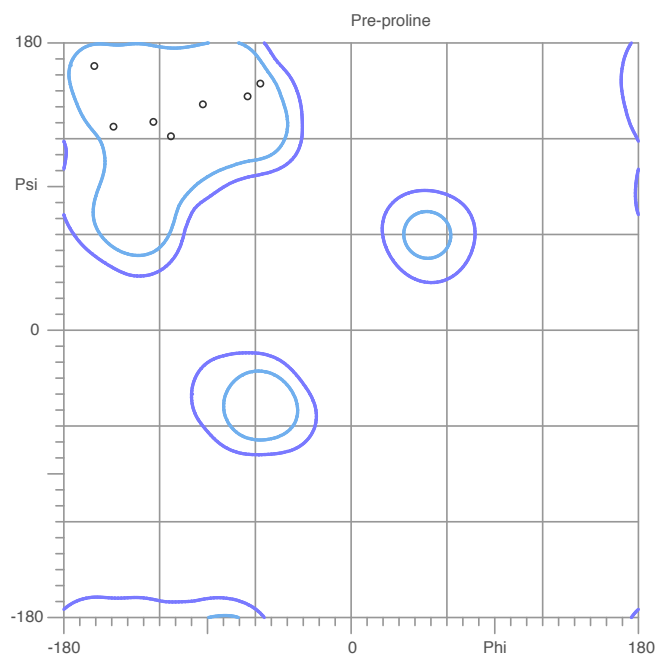
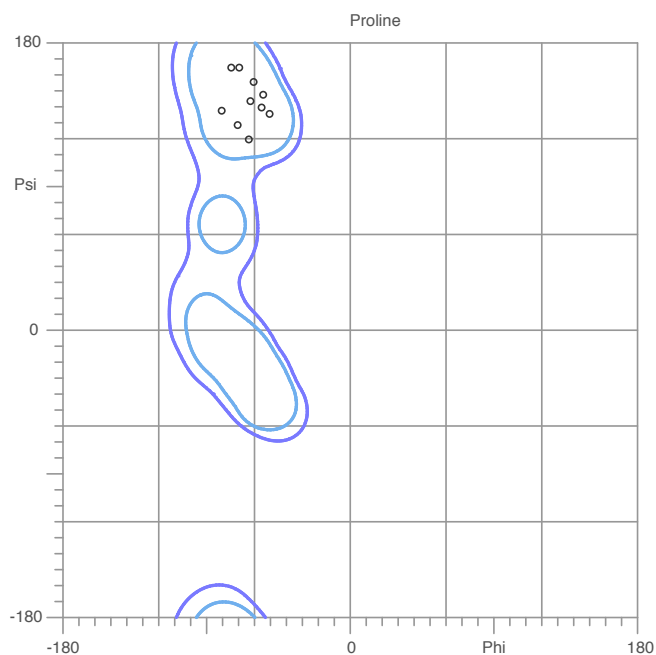
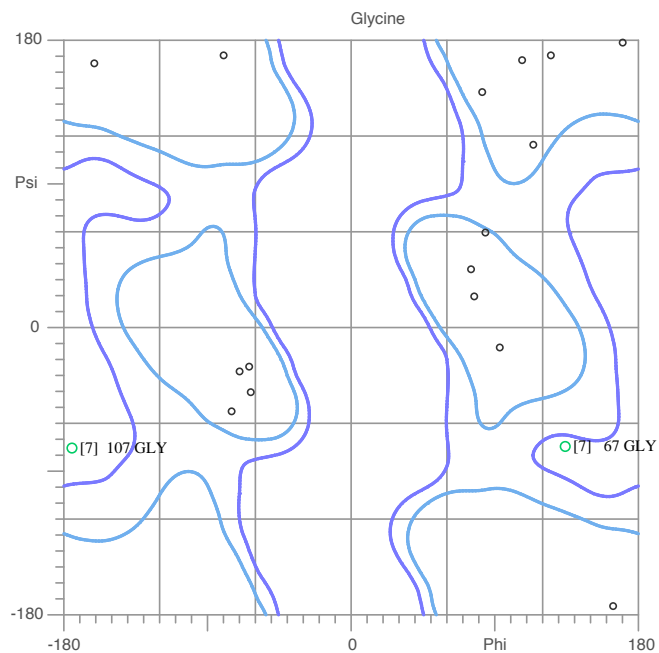
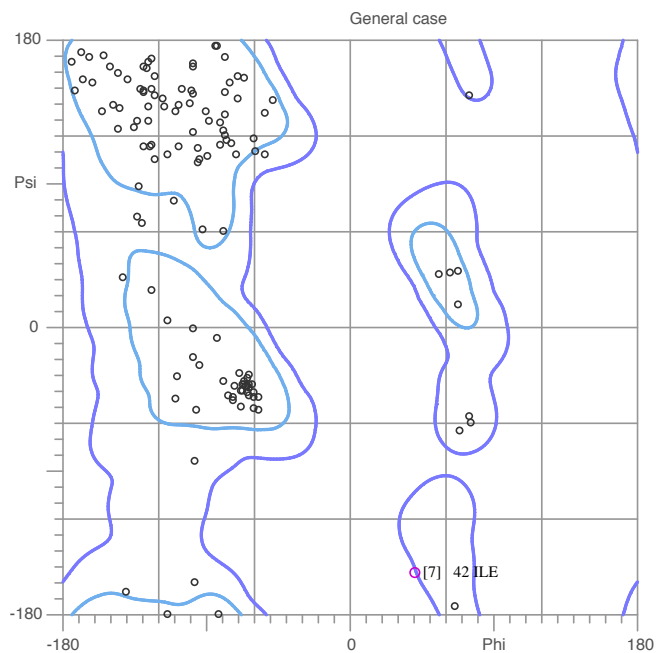


93.3% (153/164) of all residues were in favored (98%) regions.
99.4% (163/164) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[6] 136 LEU (-164.9, -44.5)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 7



90.2% (148/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

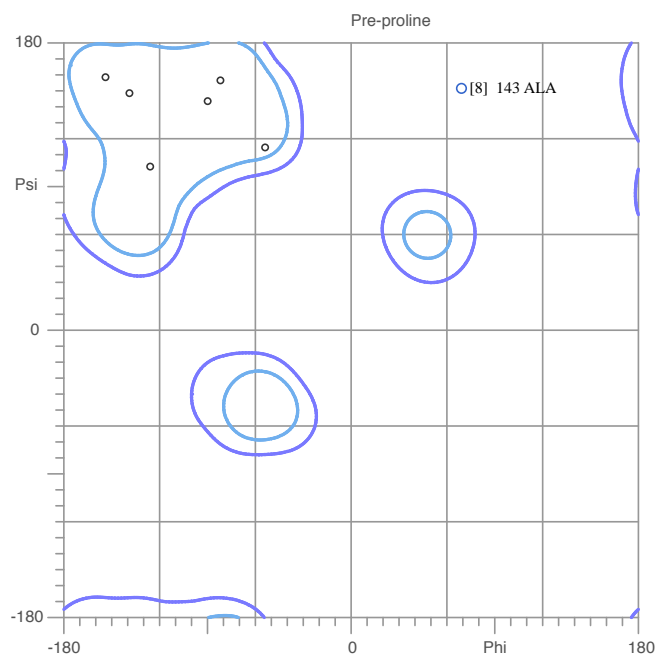
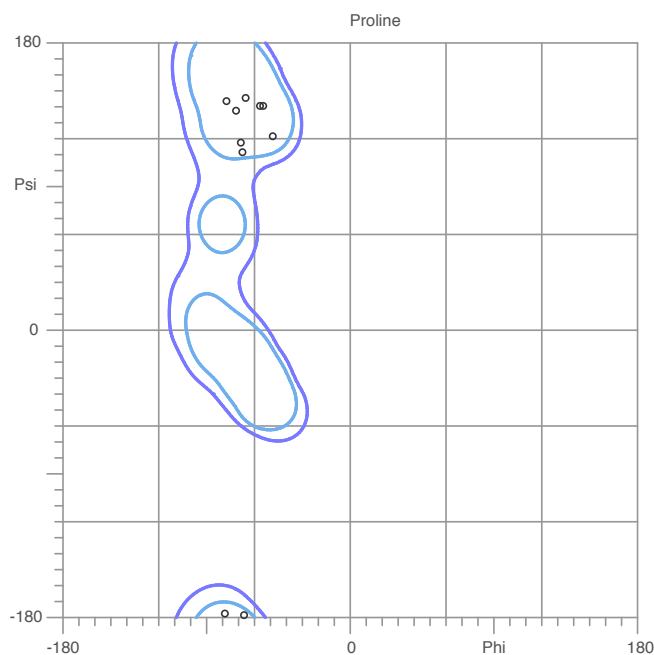
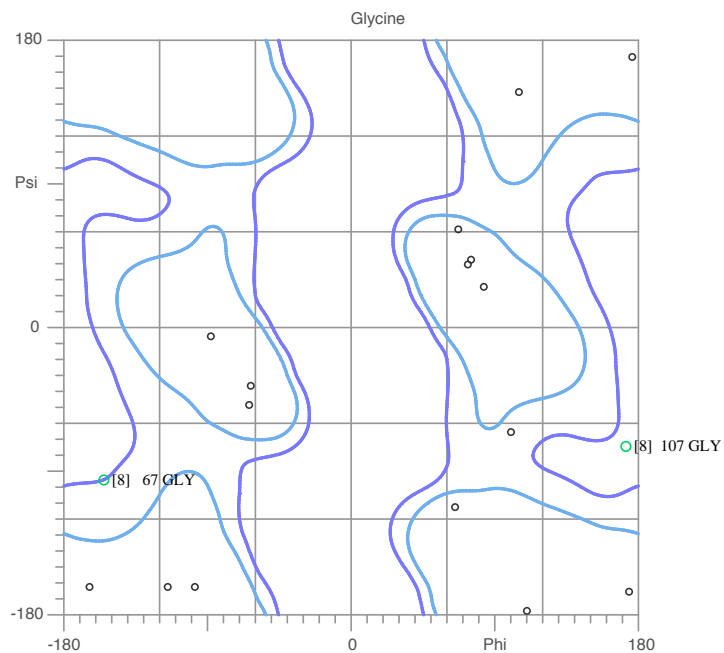
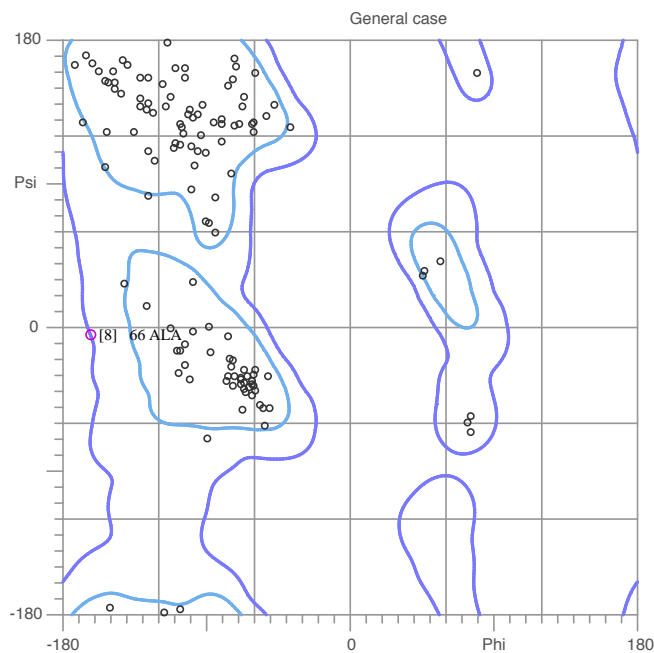
[7] 42 ILE (40.9, -153.6)

[7] 67 GLY (135.0, -75.0)

[7] 107 GLY (-175.0, -75.1)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 8



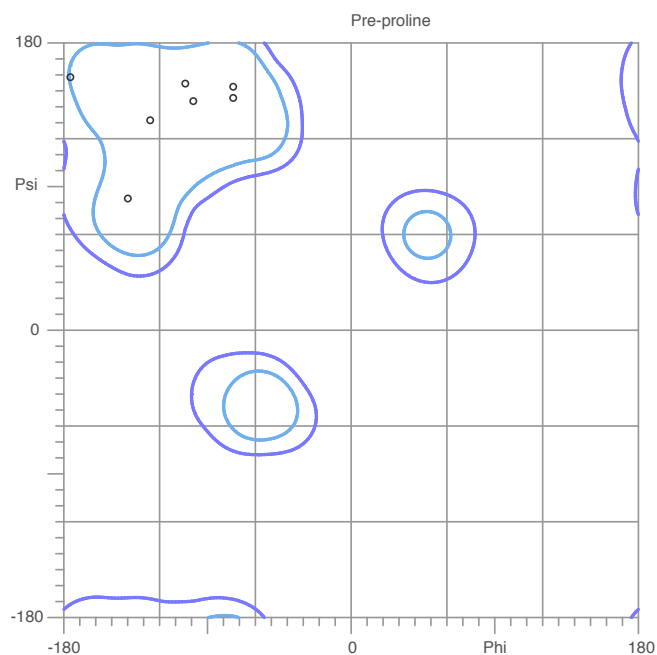
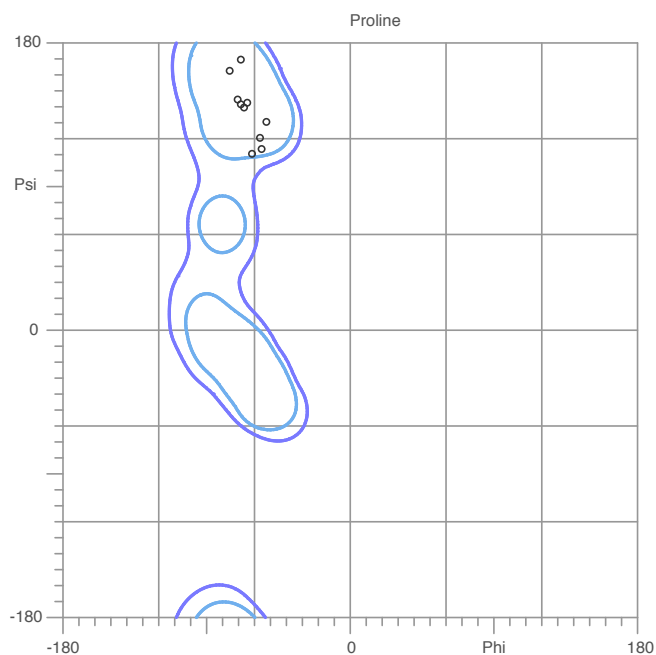
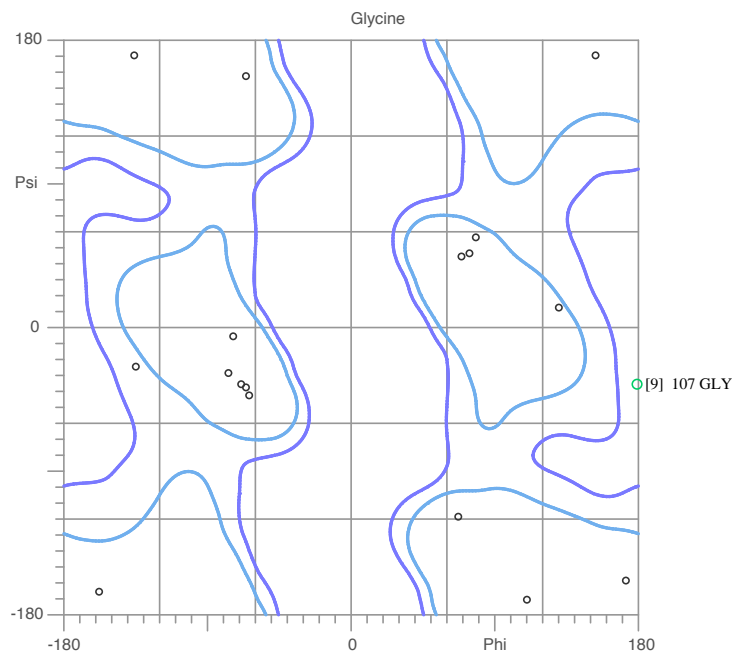
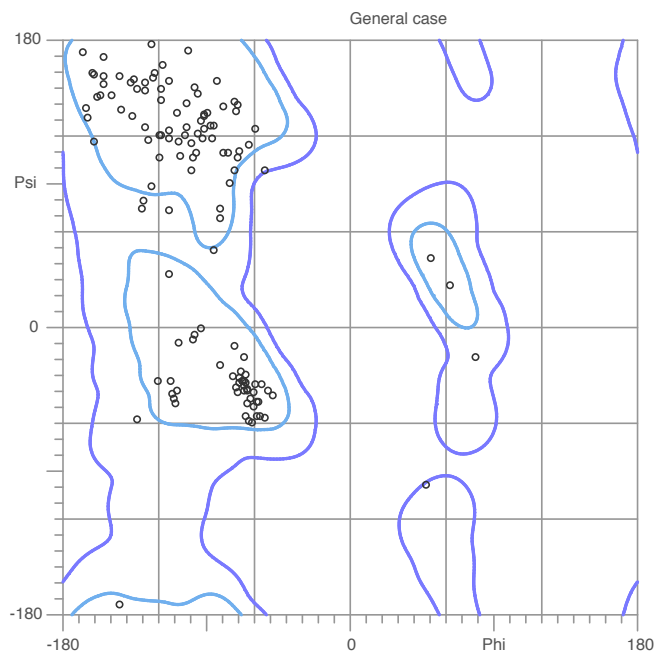
90.9% (149/164) of all residues were in favored (98%) regions.
97.6% (160/164) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [8] 66 ALA (-163.5, -4.9)
- [8] 67 GLY (-155.0, -95.1)
- [8] 107 GLY (172.6, -75.0)
- [8] 143 ALA (70.0, 152.1)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 9



93.3% (153/164) of all residues were in favored (98%) regions.
99.4% (163/164) of all residues were in allowed (>99.8%) regions.

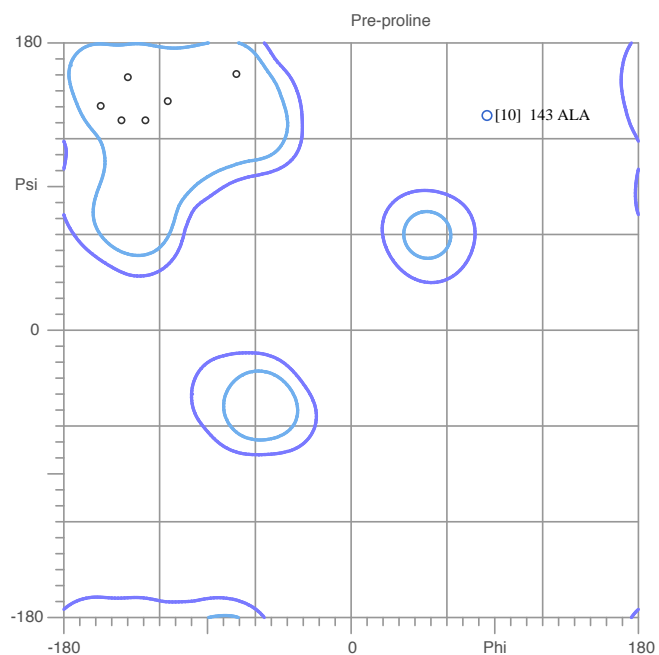
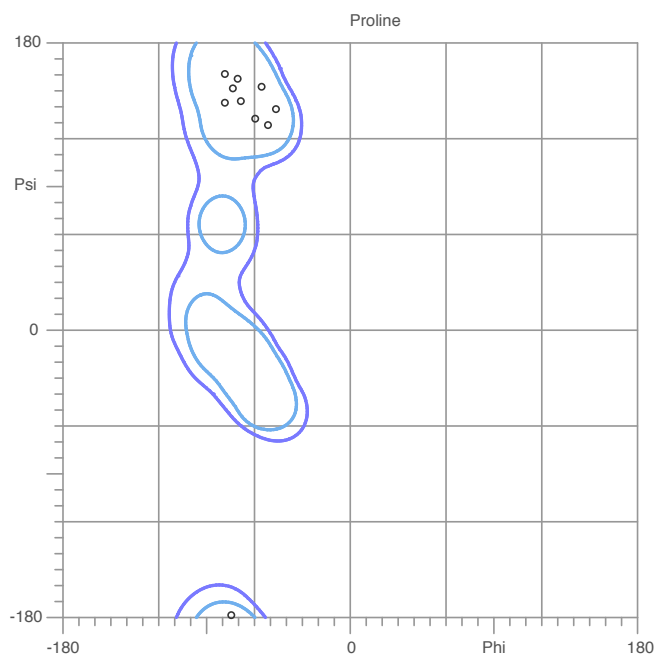
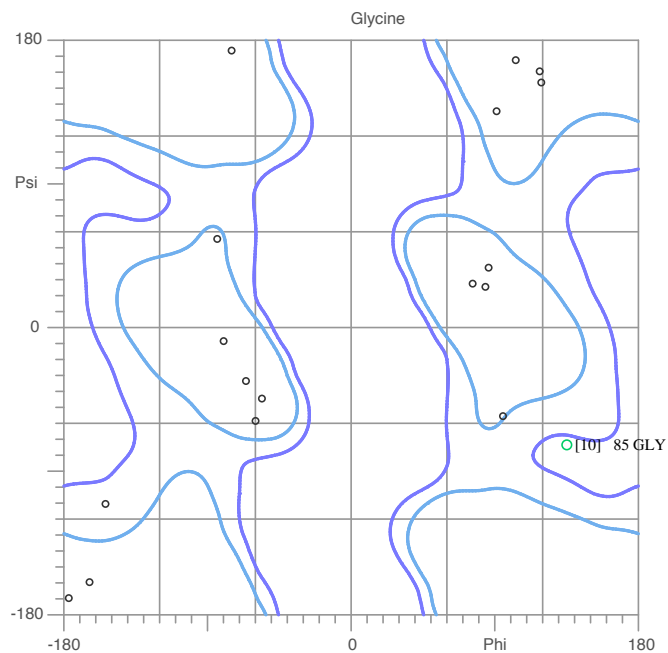
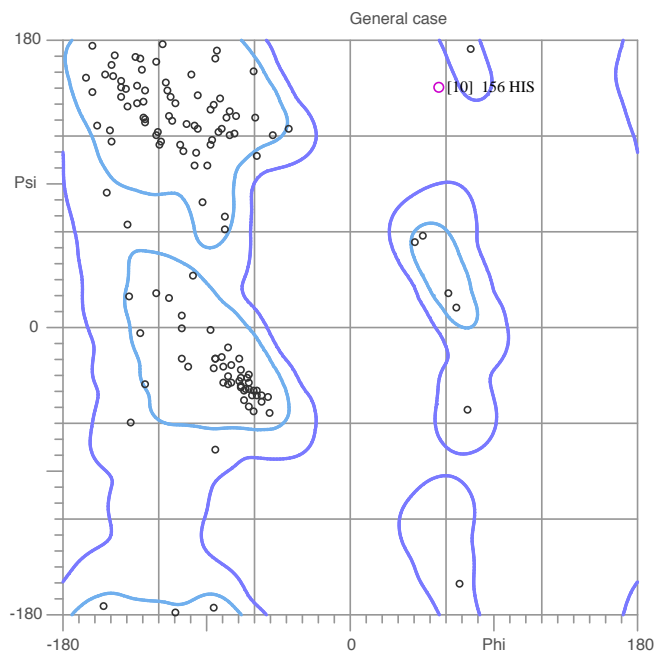
There were 1 outliers (phi, psi):
[9] 107 GLY (179.3, -35.0)

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MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 10



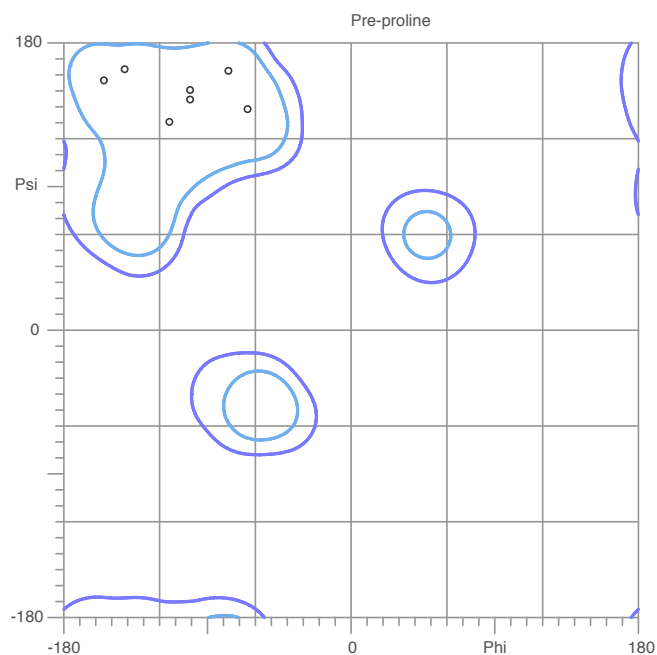
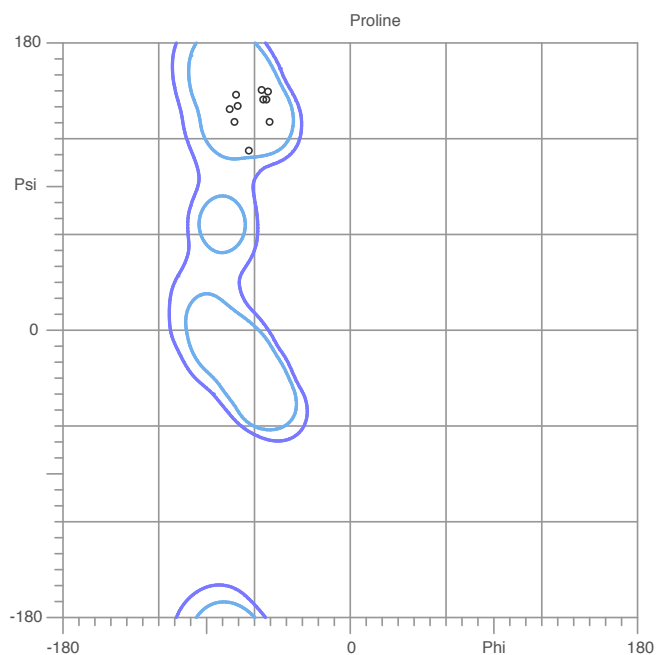
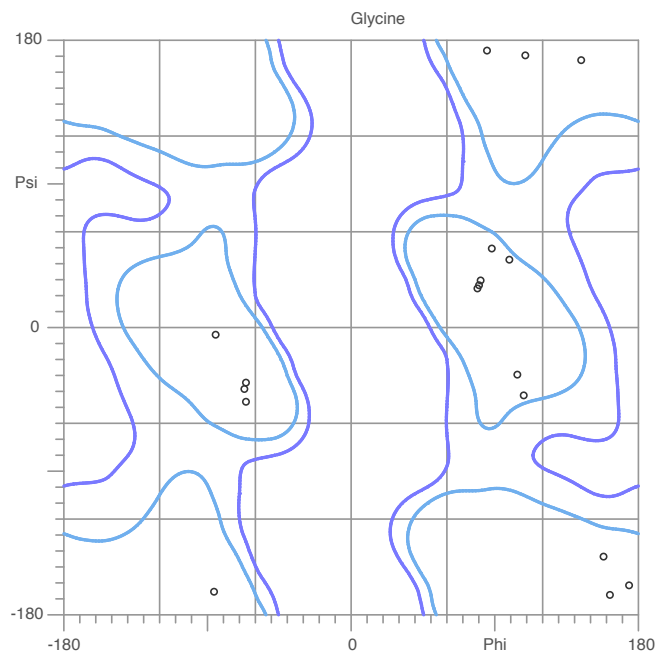
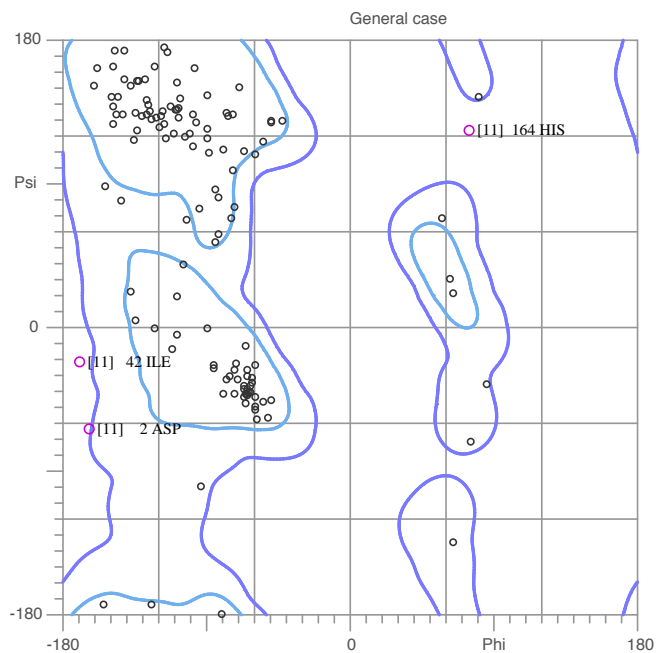
92.1% (151/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [10] 85 GLY (135.1, -74.0)
- [10] 143 ALA (85.1, 135.1)
- [10] 156 HIS (55.0, 151.5)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 11



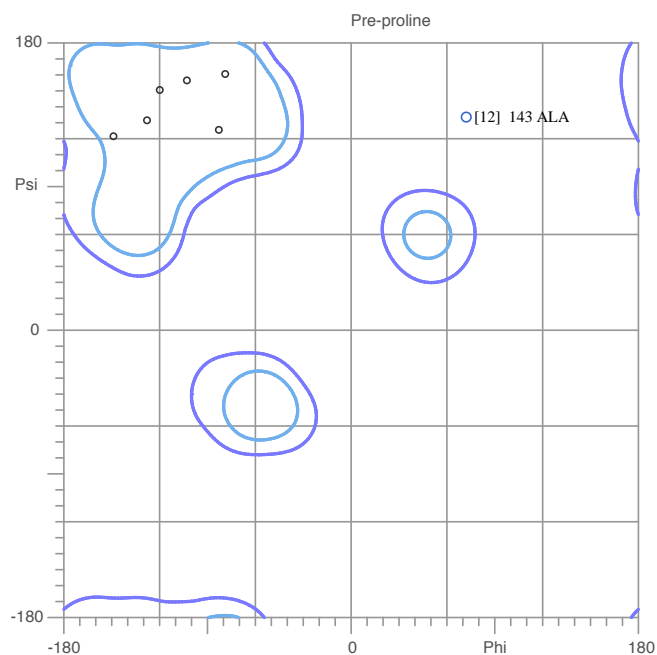
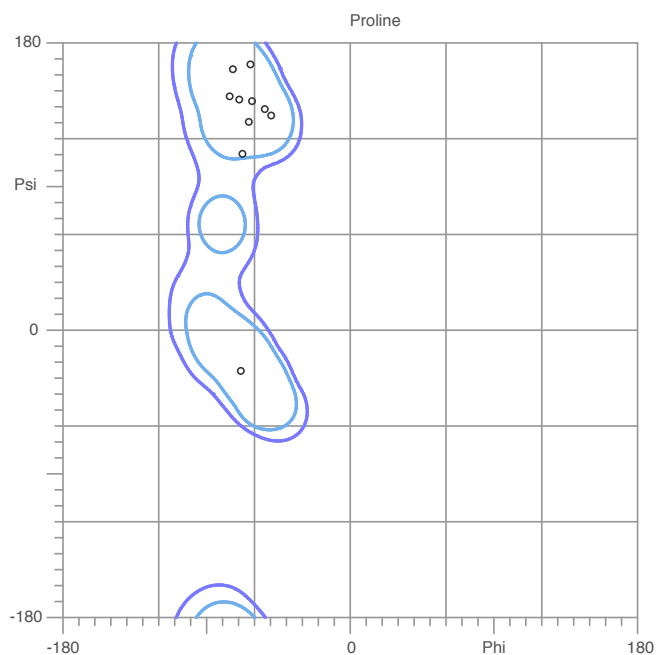
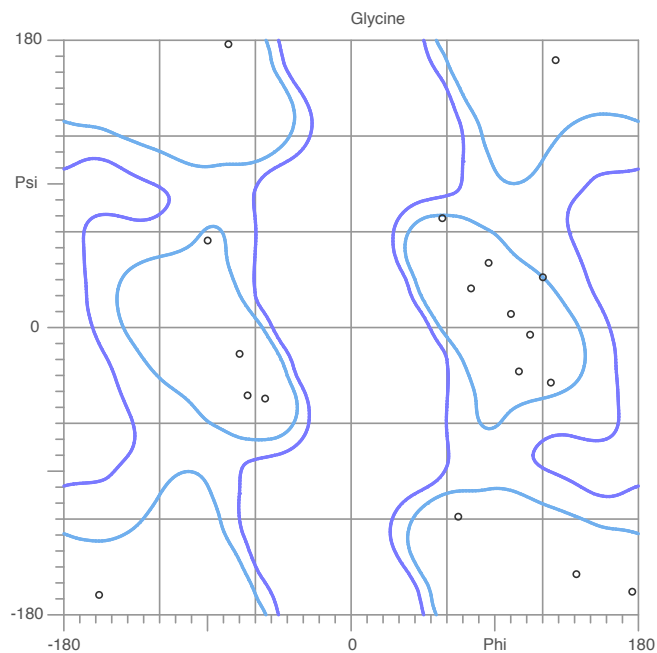
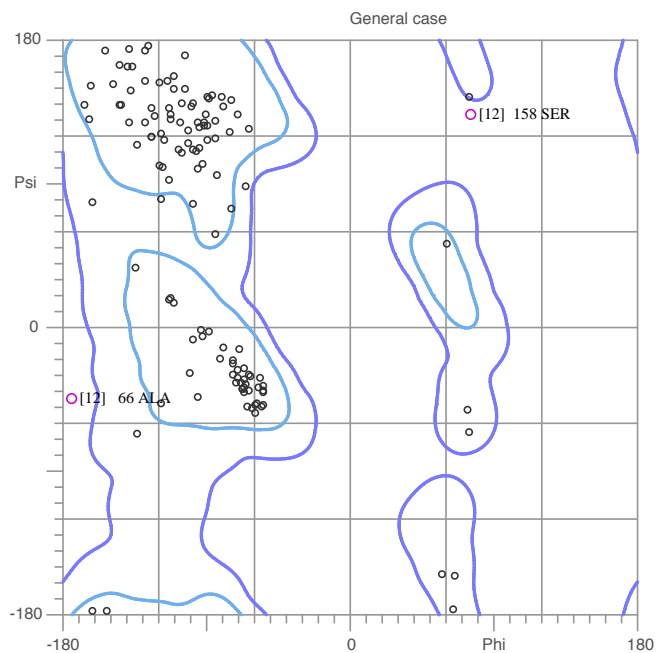
92.1% (151/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [11] 2 ASP (-164.9, -63.8)
- [11] 42 ILE (-170.7, -21.8)
- [11] 164 HIS (75.0, 125.0)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 12



91.5% (150/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

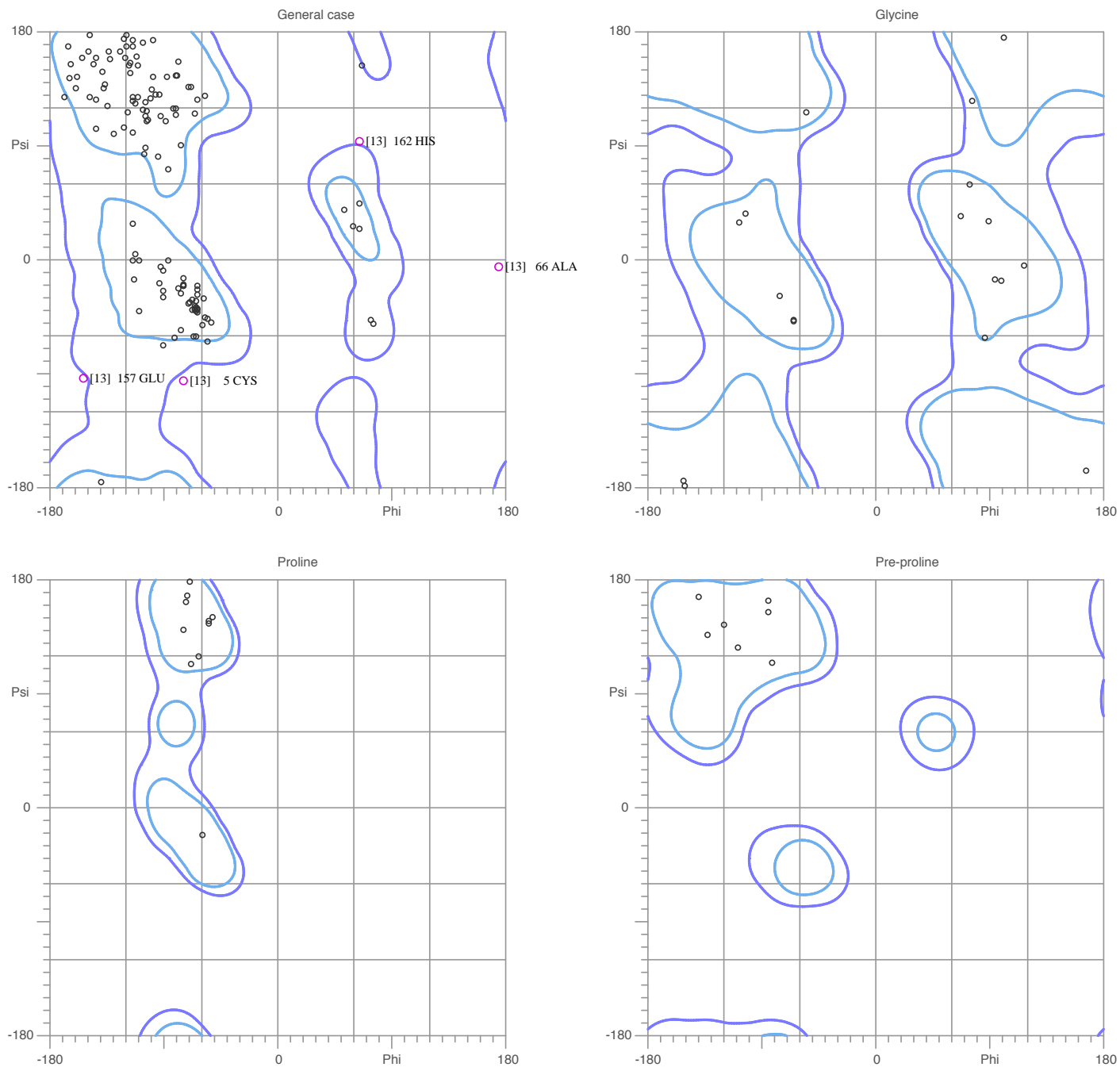
[12] 66 ALA (-175.0, -44.9)

[12] 143 ALA (72.9, 134.8)

[12] 158 SER (75.7, 135.0)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 13



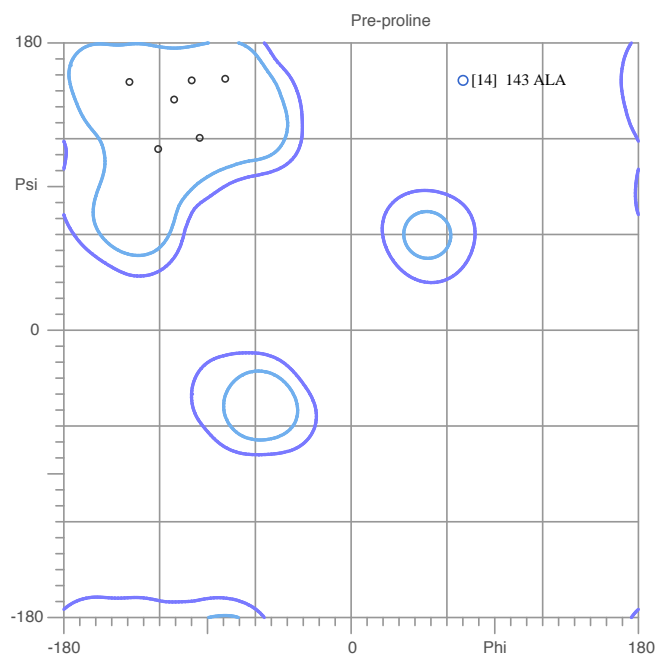
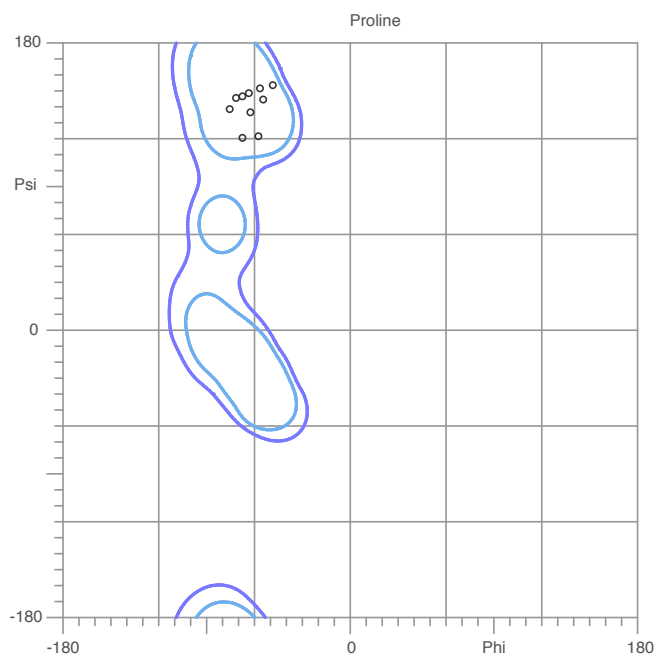
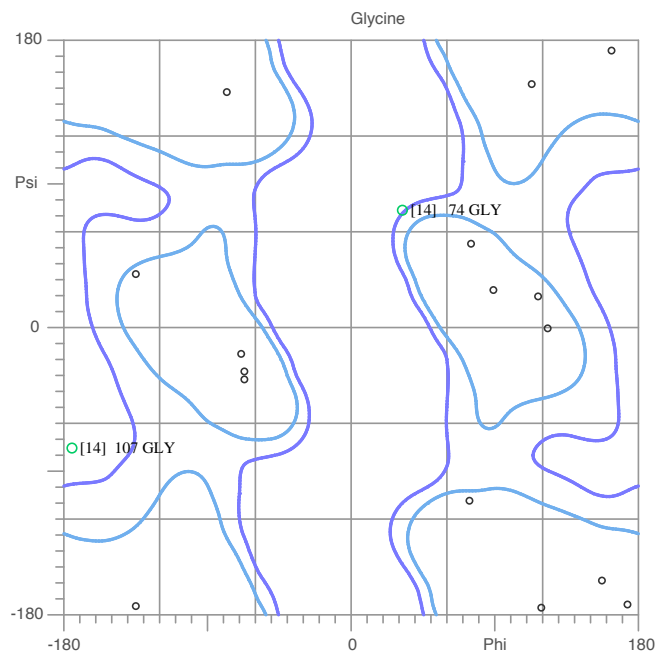
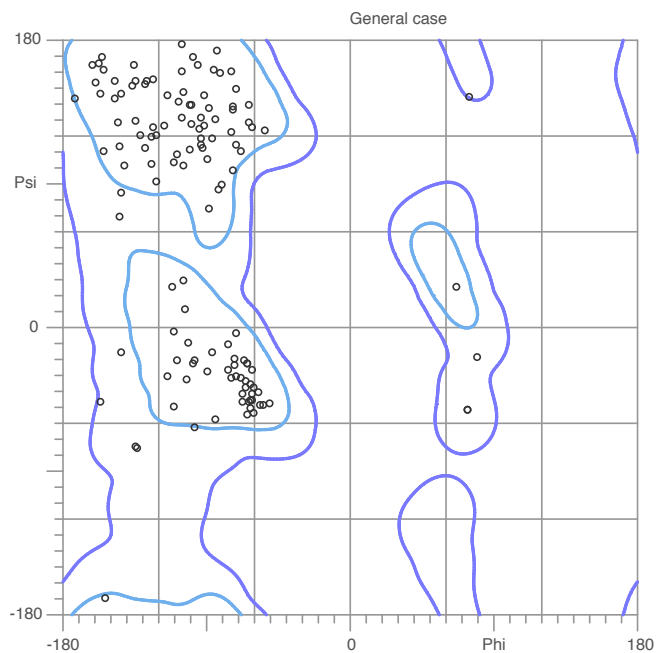
93.3% (153/164) of all residues were in favored (98%) regions.
97.6% (160/164) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [13] 5 CYS (-75.0, -95.0)
- [13] 66 ALA (174.9, -5.1)
- [13] 157 GLU (-154.9, -93.0)
- [13] 162 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 14



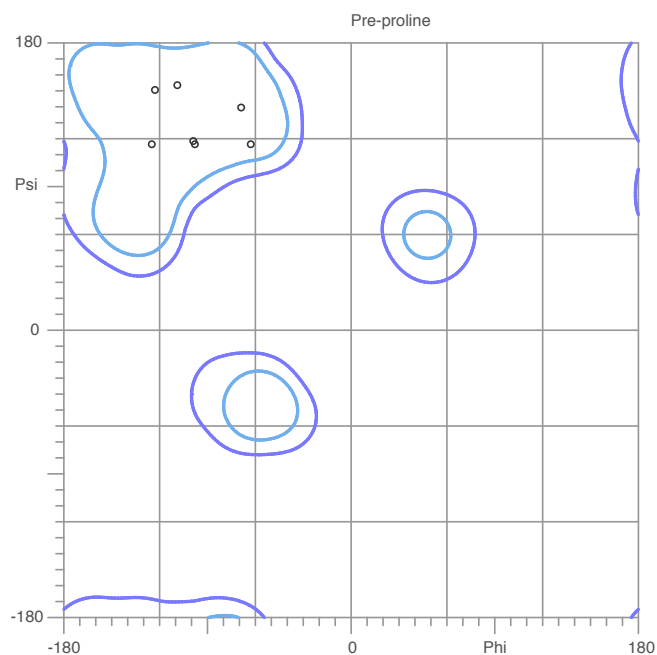
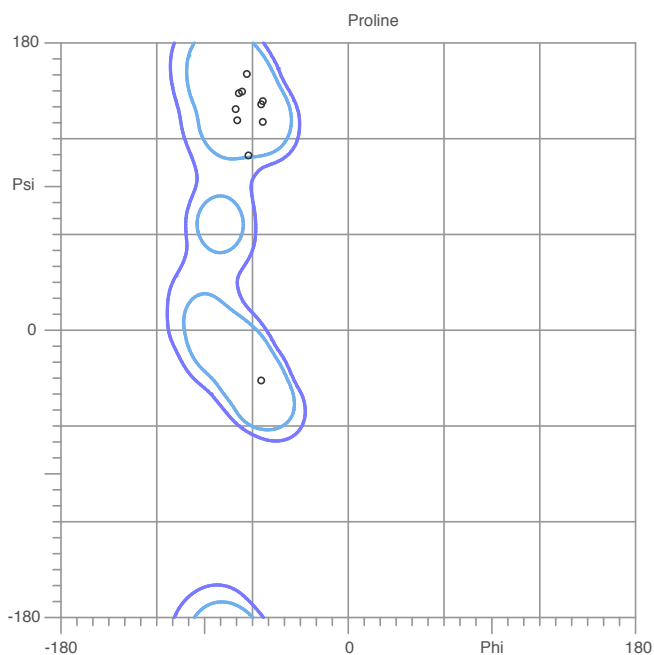
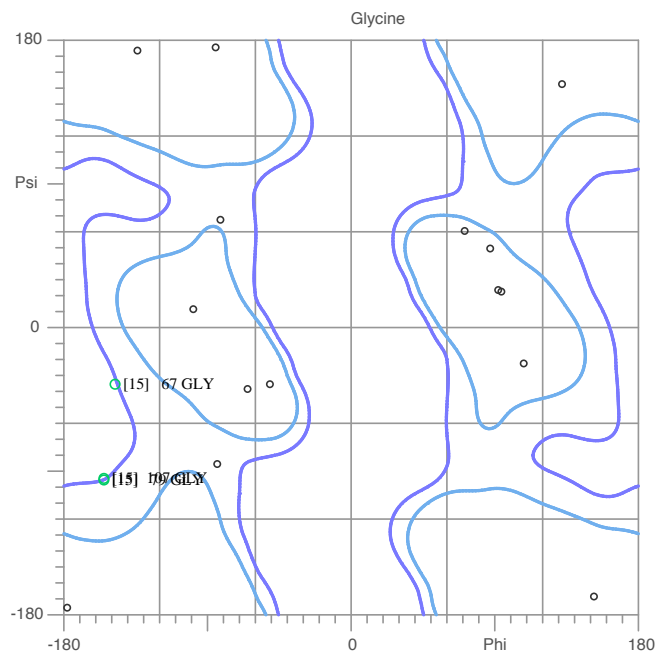
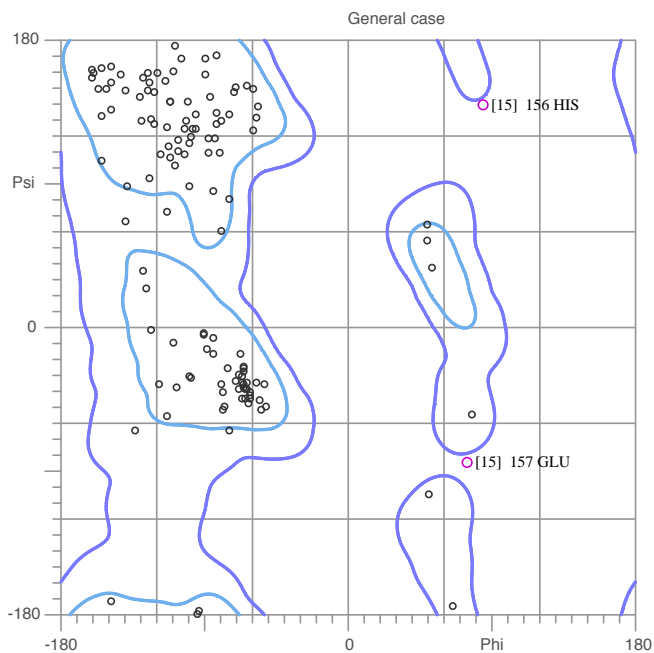
90.9% (149/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [14] 74 GLY (32.7, 75.0)
- [14] 107 GLY (-175.0, -75.1)
- [14] 143 ALA (70.4, 157.7)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 15



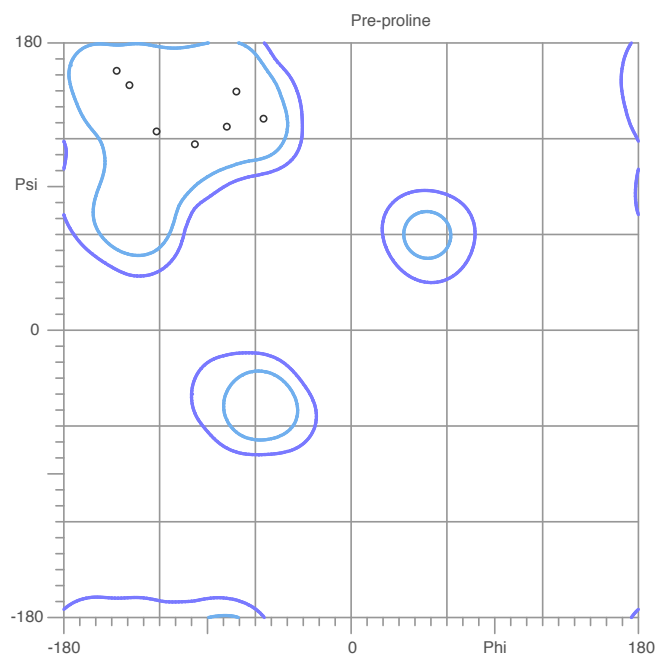
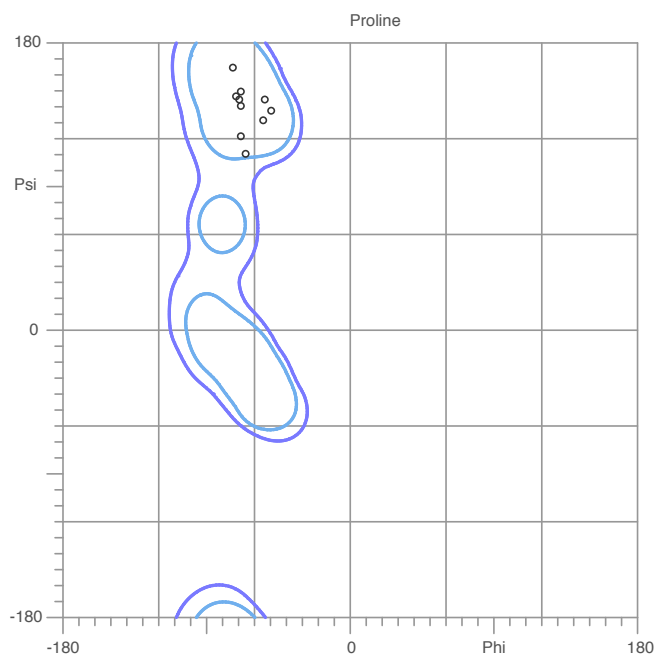
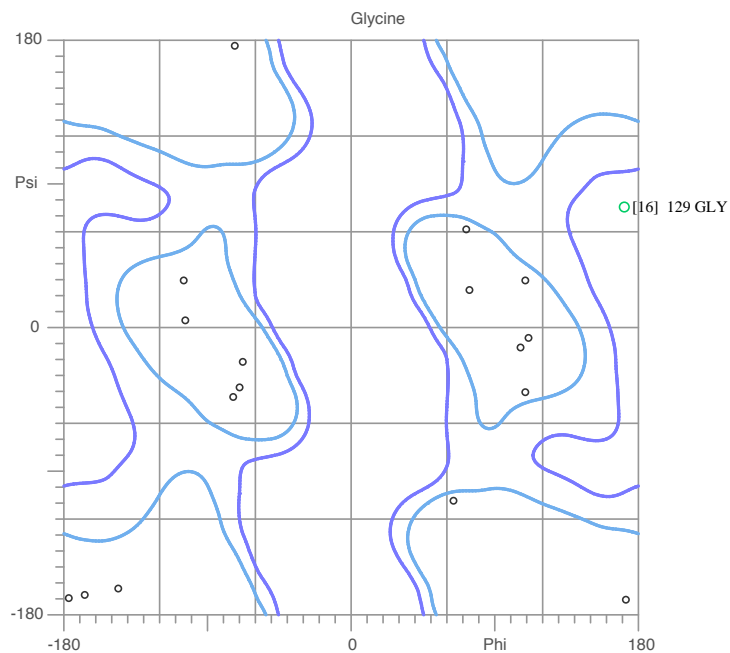
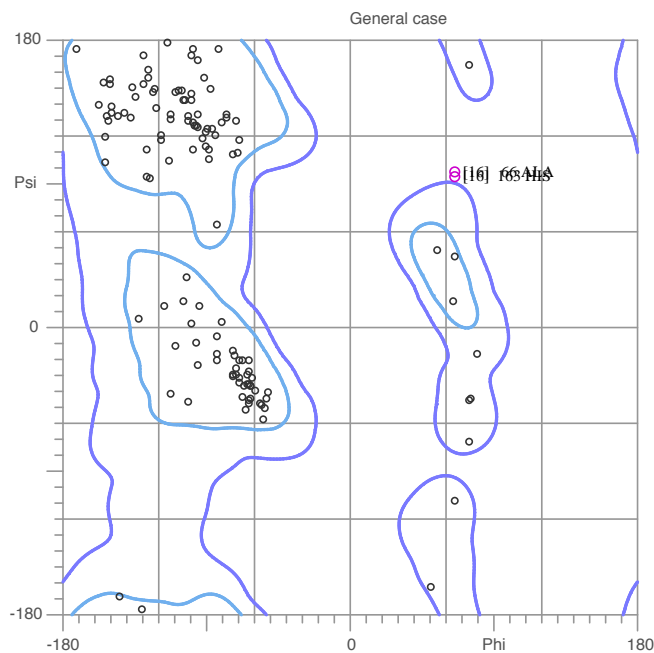
90.9% (149/164) of all residues were in favored (98%) regions.
97.0% (159/164) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [15] 67 GLY (-148.3, -35.0)
- [15] 79 GLY (-155.0, -95.0)
- [15] 107 GLY (-155.0, -94.9)
- [15] 156 HIS (85.0, 140.0)
- [15] 157 GLU (74.6, -84.9)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 16



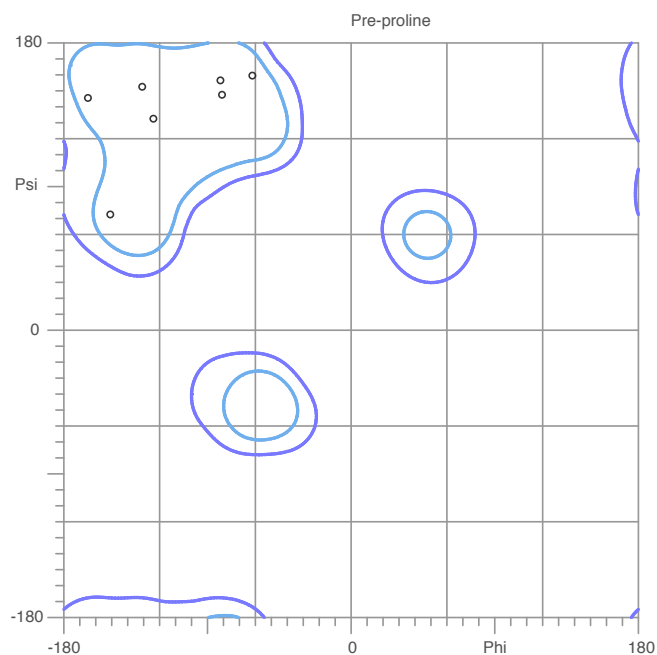
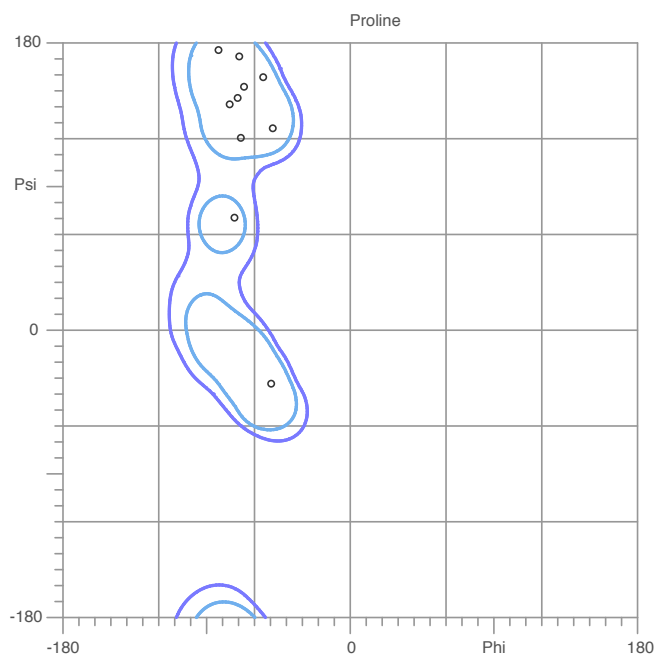
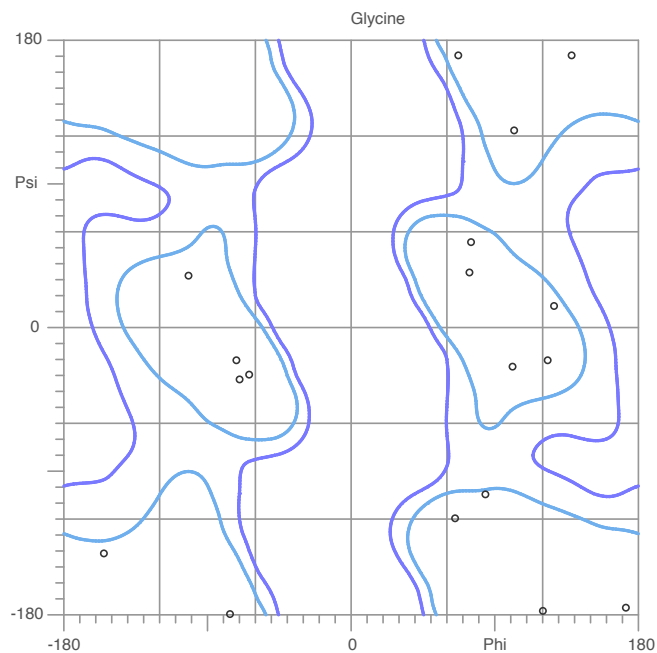
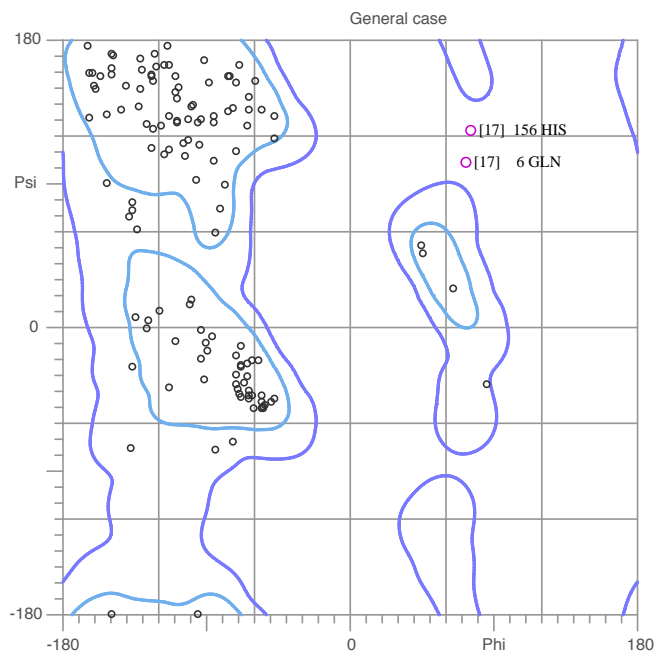
93.9% (154/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [16] 66 ALA (65.1, 98.5)
- [16] 129 GLY (171.9, 76.4)
- [16] 163 HIS (65.1, 95.0)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 17

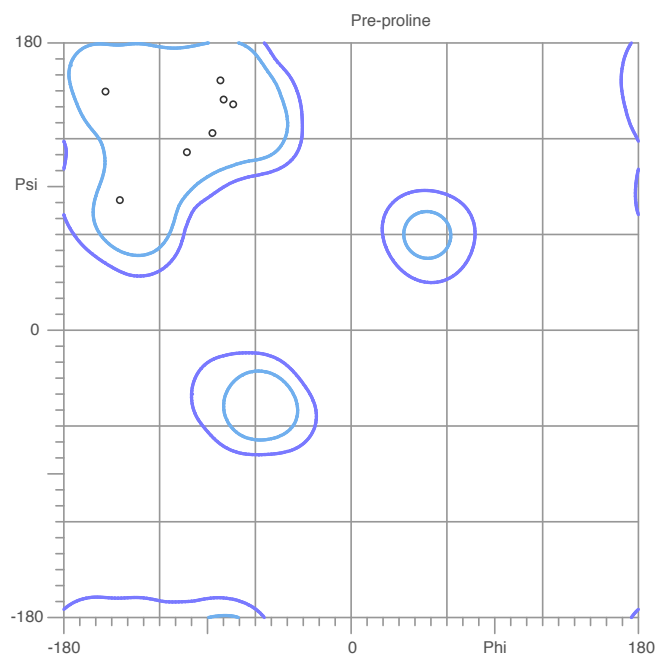
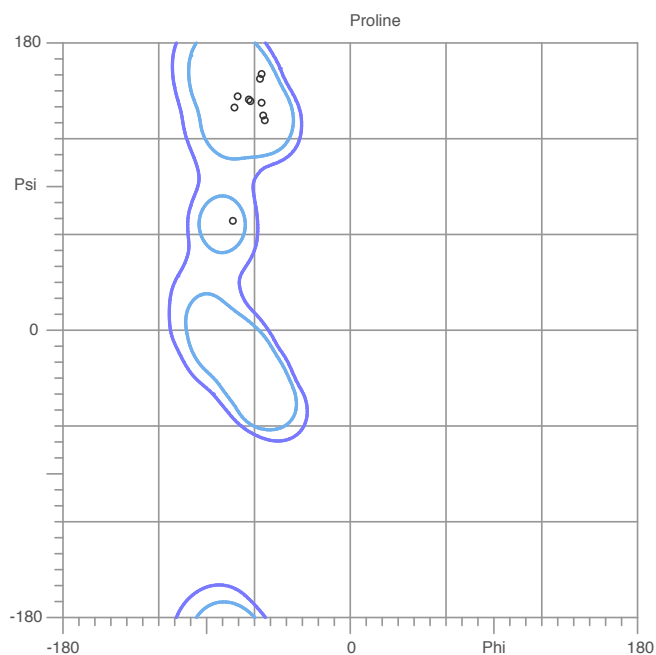
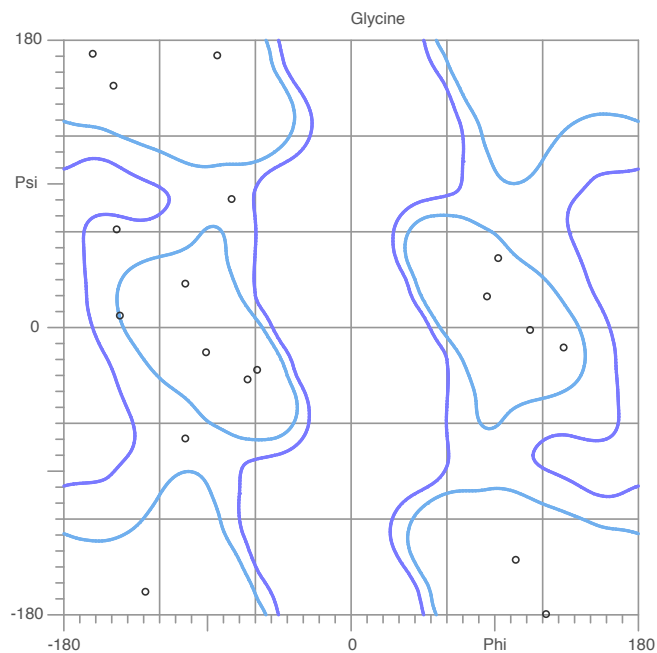
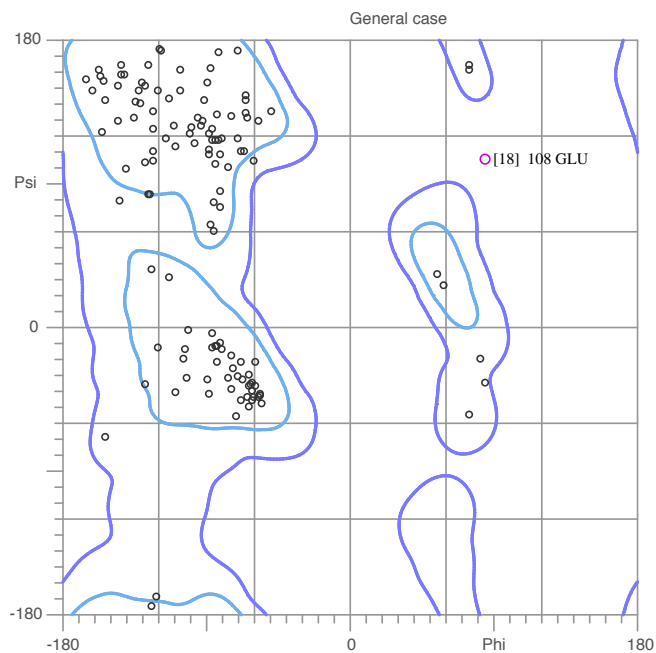


92.7% (152/164) of all residues were in favored (98%) regions.
98.8% (162/164) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[17] 6 GLN (72.4, 105.0)
[17] 156 HIS (75.0, 124.9)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 18

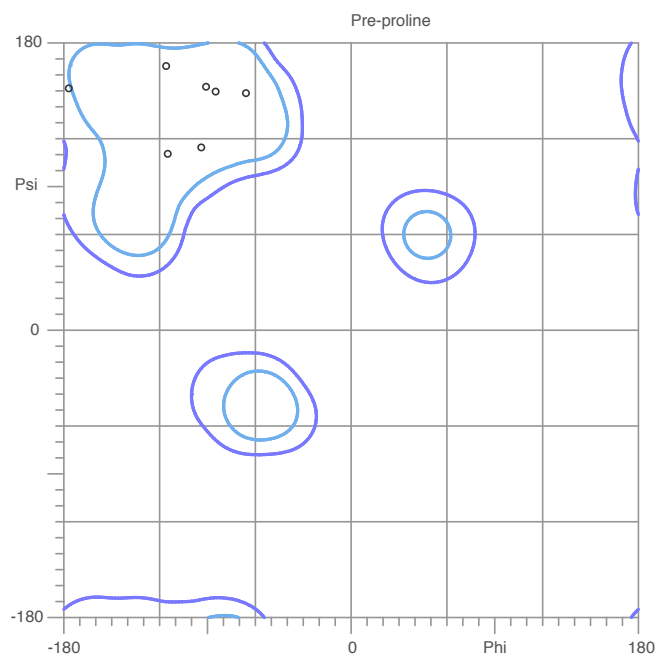
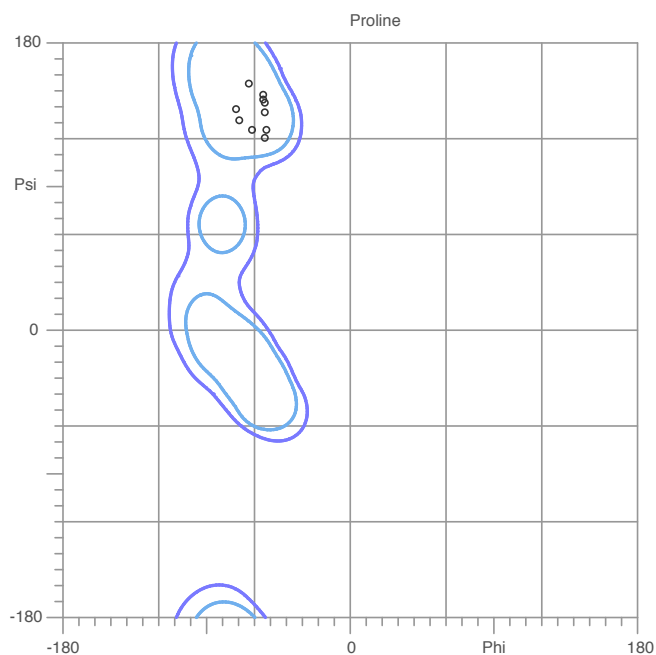
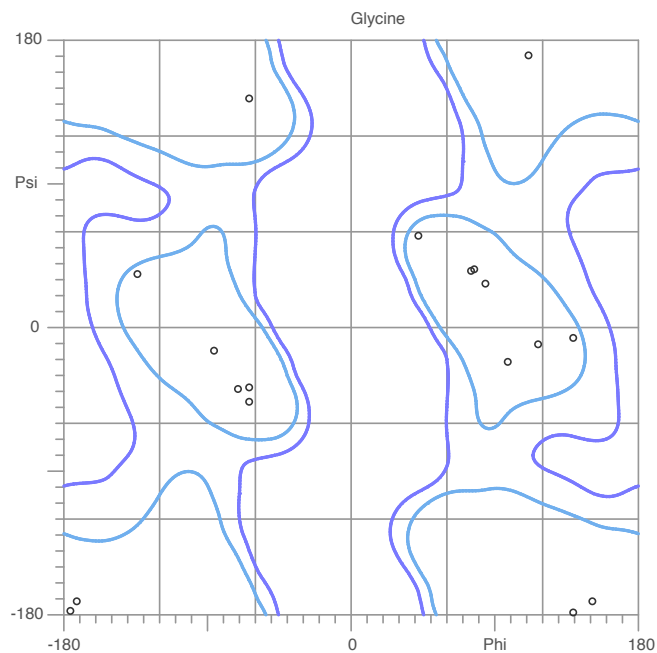
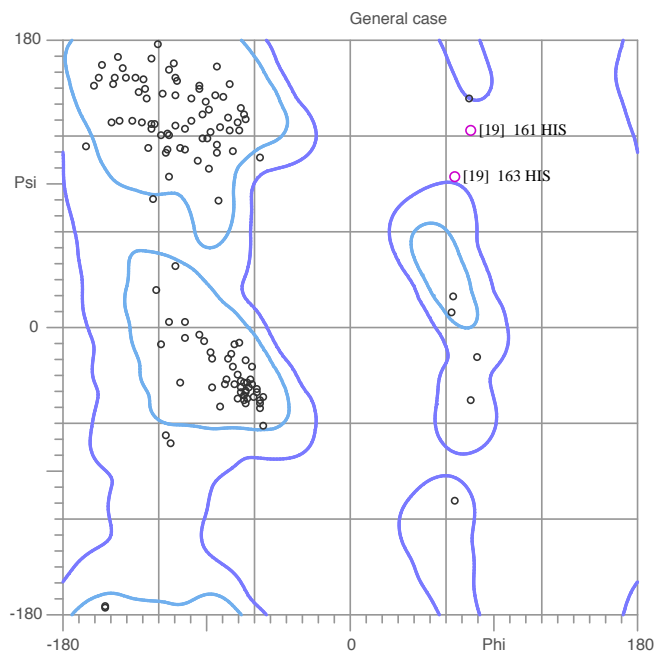


92.1% (151/164) of all residues were in favored (98%) regions.
99.4% (163/164) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[18] 108 GLU (84.0, 106.8)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 19

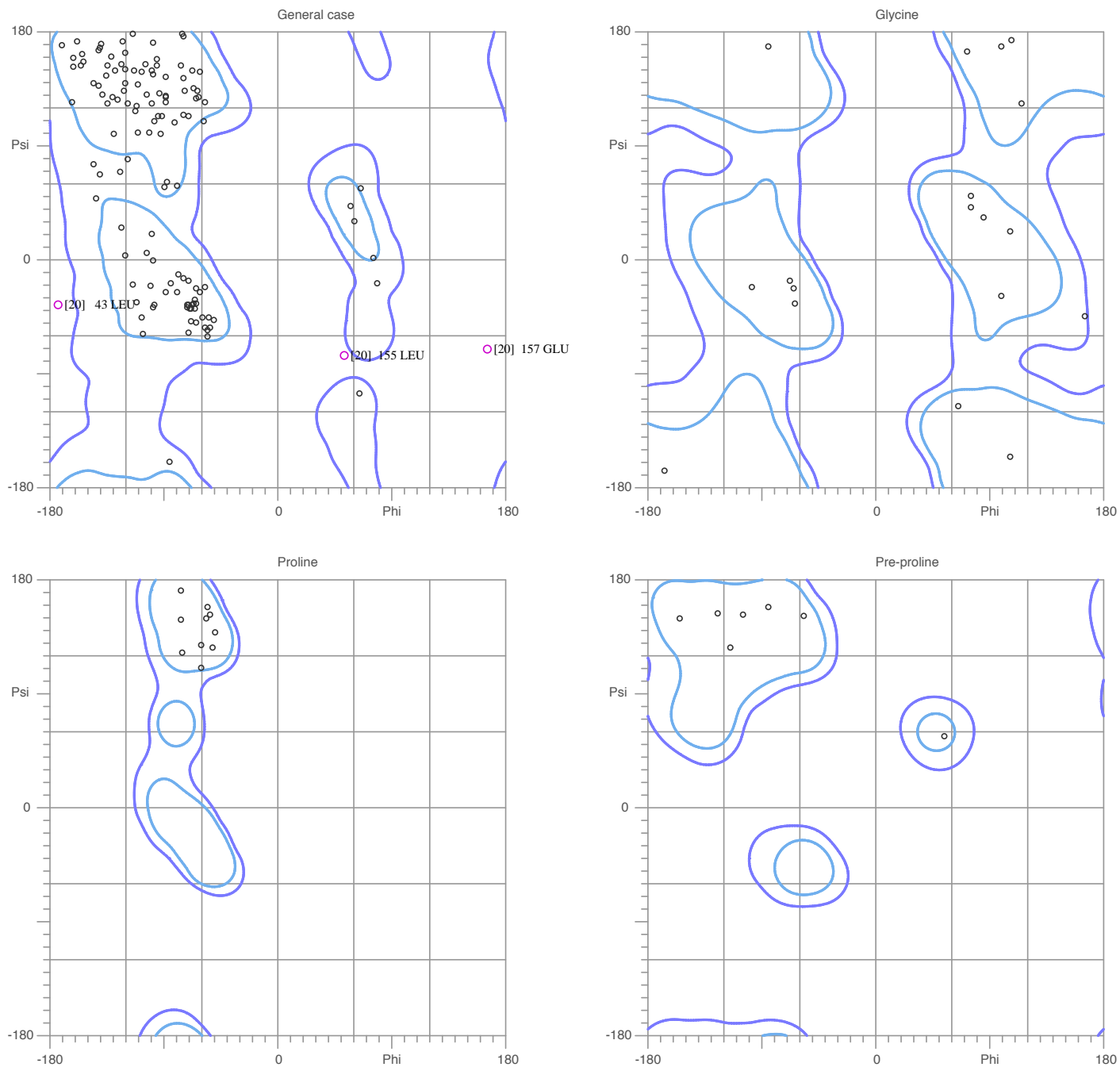


92.7% (152/164) of all residues were in favored (98%) regions.
98.8% (162/164) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 161 HIS (75.0, 125.0)
[19] 163 HIS (65.1, 95.1)

MolProbity Ramachandran analysis

CTR107_R3_em_bcr3.pdb, model 20



91.5% (150/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[20] 43 LEU (-175.0, -35.0)

[20] 155 LEU (52.7, -75.0)

[20] 157 GLU (165.0, -70.4)