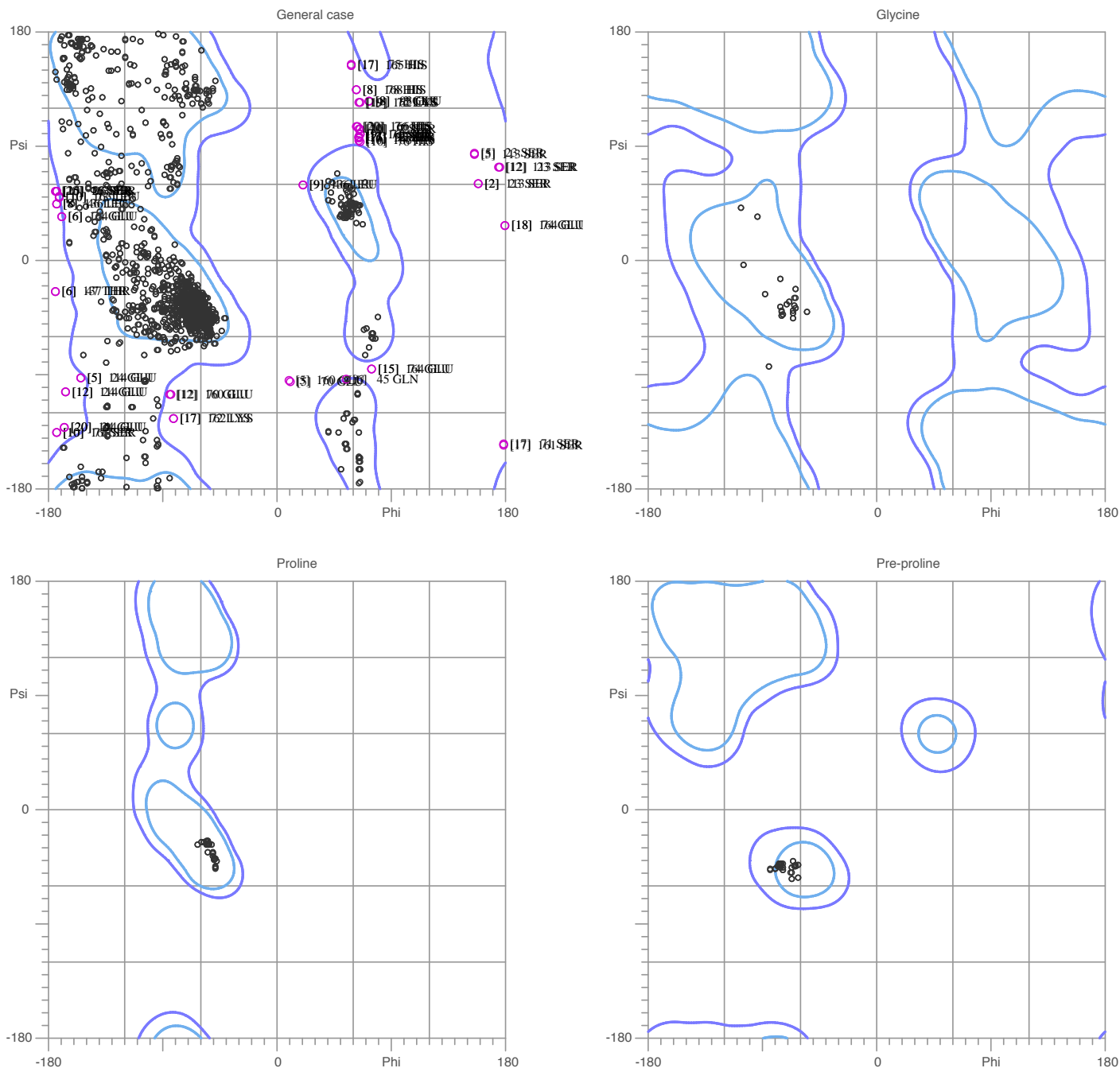


MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, all models



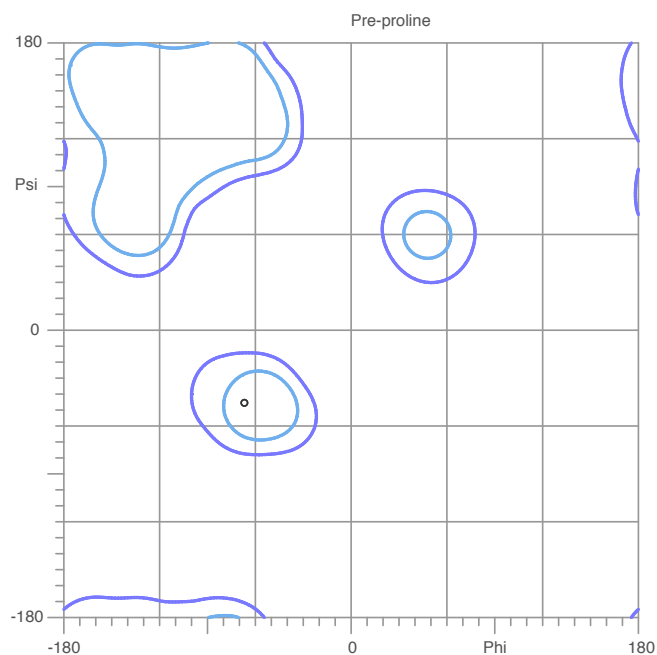
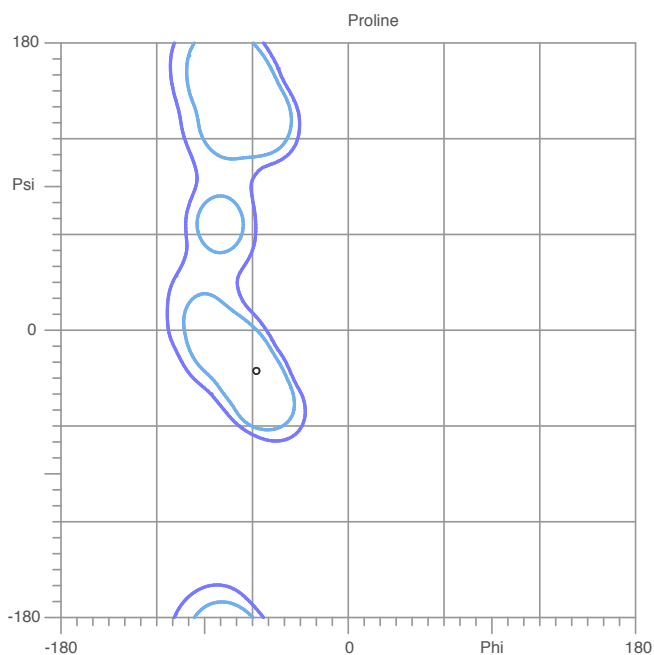
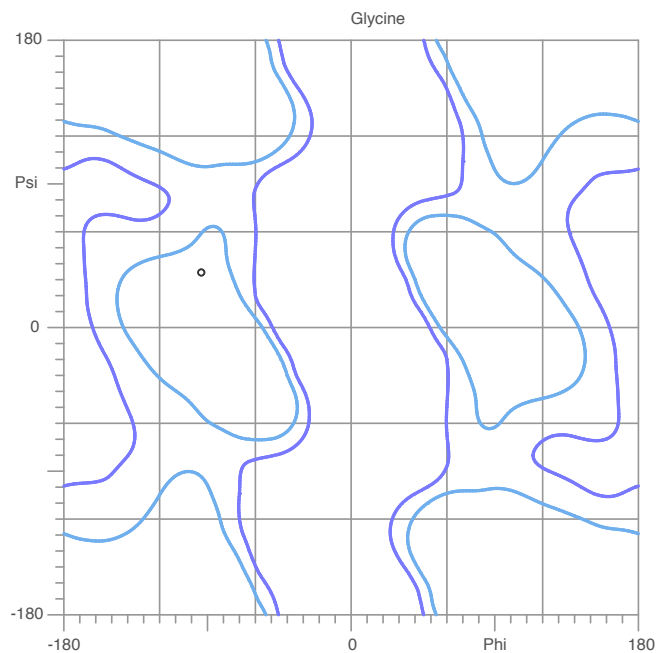
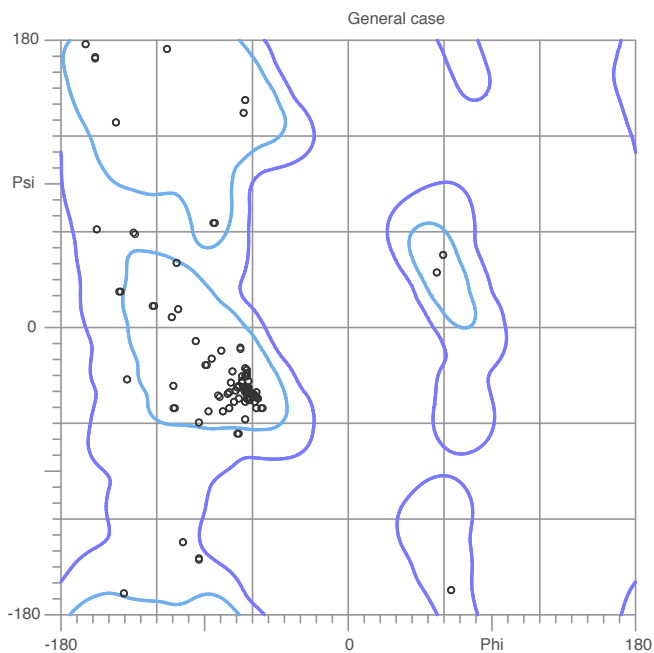
89.3% (2786/3120) of all residues were in favored (98%) regions.
98.0% (3059/3120) of all residues were in allowed (>99.8%) regions.

There were 61 outliers (phi, psi):

- | | |
|------------------------------|-------------------------------|
| (1) 23 SER (158.6, 61.1) | (10) 161 SER (-174.5, -135.1) |
| (2) 113 SER (158.6, 61.1) | (11) 163 LEU (-172.9, 51.1) |
| (3) 23 SER (155.1, 85.0) | (12) 23 SER (175.0, 75.0) |
| (4) 24 GLU (-155.0, 92.3) | (13) 24 GLU (-165.5, -103.3) |
| (5) 70 GLU (100.0, -95.0) | (14) 70 GLU (-85.1, -105.0) |
| (6) 113 SER (155.1, 85.0) | (15) 113 SER (175.0, 74.9) |
| (7) 114 GLU (-155.0, 92.3) | (16) 114 GLU (-165.5, -103.3) |
| (8) 160 GLU (100.0, -95.0) | (17) 160 GLU (-84.9, -105.1) |
| (9) 45 GLN (54.9, -93.2) | (18) 6 SER (-175.0, 55.1) |
| (10) 47 THR (-175.1, -25.0) | (19) 74 GLU (74.6, 85.2) |
| (11) 74 GLU (-170.6, 35.1) | (20) 96 SER (-175.0, 55.0) |
| (12) 157 THR (175.1, -24.9) | (21) 95 HIS (64.9, 97.4) |
| (13) 164 GLU (-170.7, 35.1) | (22) 2 SER (65.0, 98.9) |
| (14) 3 GLU (72.3, 126.5) | (23) 71 SER (179.0, -145.0) |
| (15) 46 LEU (-175.0, 45.1) | (24) 72 LYS (-82.9, -124.9) |
| (16) 78 HIS (62.3, 135.1) | (25) 75 HIS (68.4, 155.0) |
| (17) 93 GLU (72.3, 126.5) | (26) 92 SER (64.9, 98.9) |
| (18) 161 LEU (-175.0, 45.1) | (27) 161 SER (178.9, -145.1) |
| (19) 168 HIS (62.4, 135.0) | (28) 163 LYS (82.7, -124.9) |
| (20) 46 LEU (20.3, 60.6) | (29) 165 HIS (58.5, 155.0) |
| (21) 71 SER (65.0, 100.4) | (30) 74 GLU (179.7, 28.1) |
| (22) 136 LEU (20.3, 60.7) | (31) 164 GLU (179.8, 28.1) |
| (23) 161 SER (65.0, 100.3) | (32) 199 LYS (65.0, 125.2) |
| (24) 2 SER (64.9, 104.8) | (33) 23 SER (-175.1, 55.0) |
| (25) 71 SER (-174.6, -135.1) | (34) 24 GLU (-168.5, -131.1) |
| (26) 73 LEU (-172.8, 50.8) | (35) 76 HIS (63.0, 106.2) |
| (27) 76 HIS (65.0, 95.0) | (36) 113 SER (-174.9, 55.0) |
| (28) 92 SER (65.1, 104.8) | (37) 114 GLU (-168.5, -131.0) |
| | (38) 166 HIS (62.9, 106.1) |

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 1



88.5% (138/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

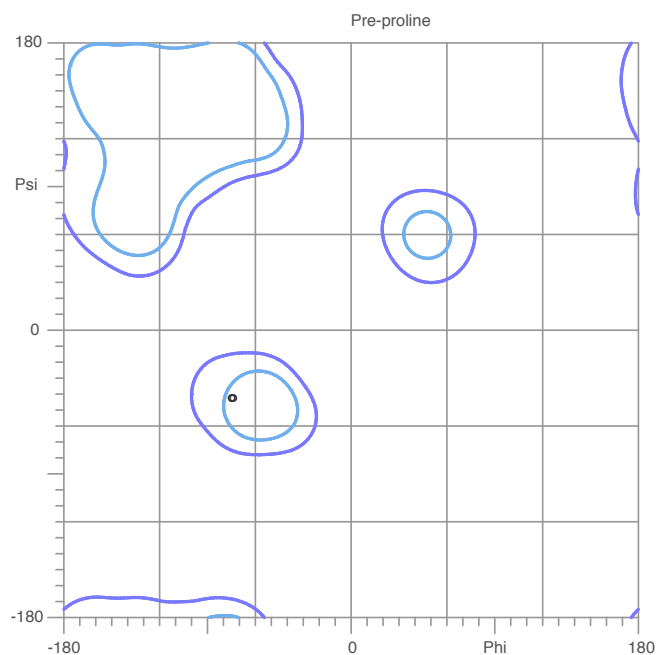
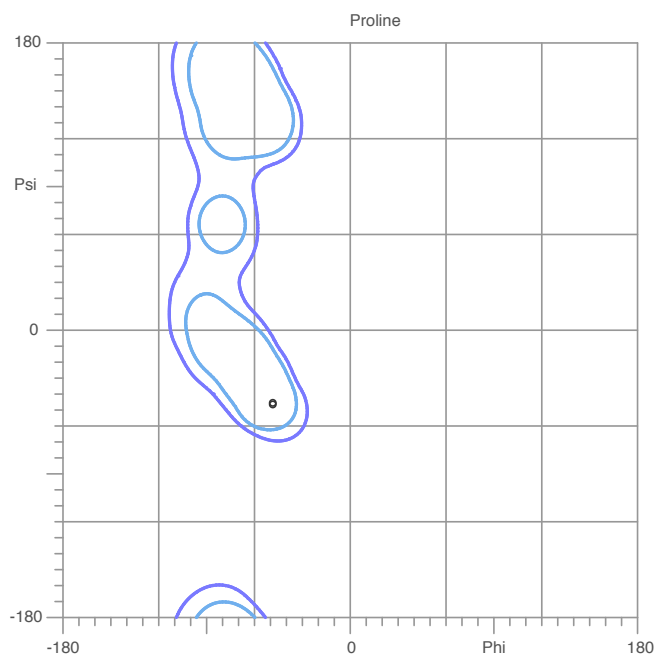
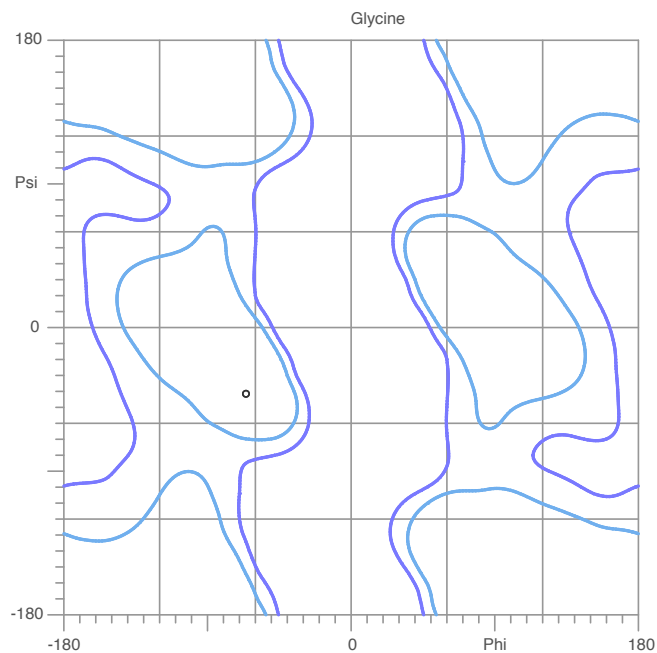
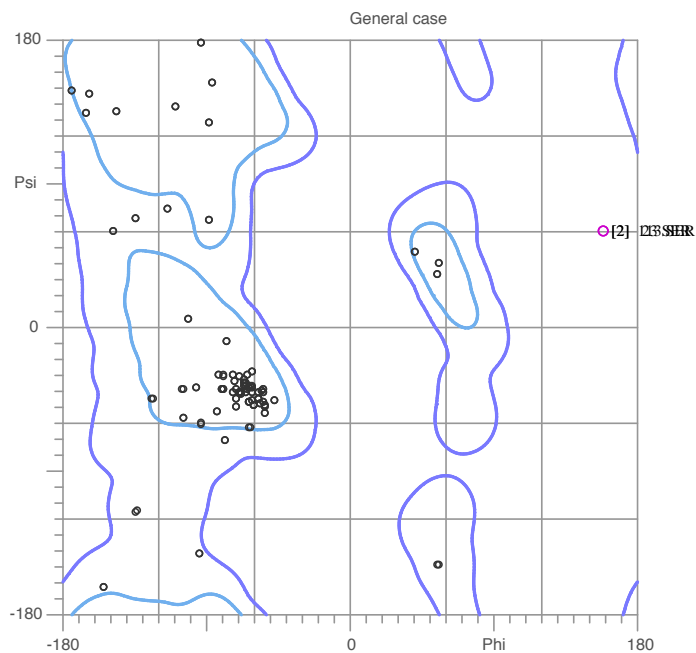
There were no outliers.

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

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MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 2



87.2% (136/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

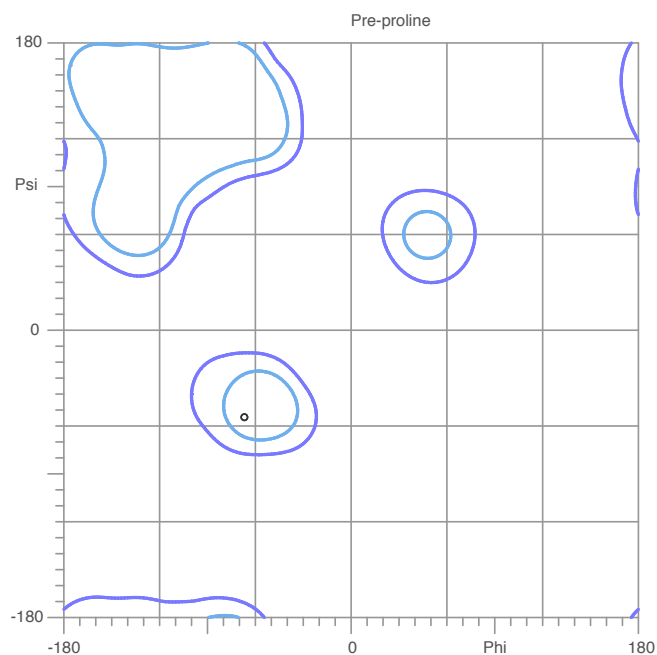
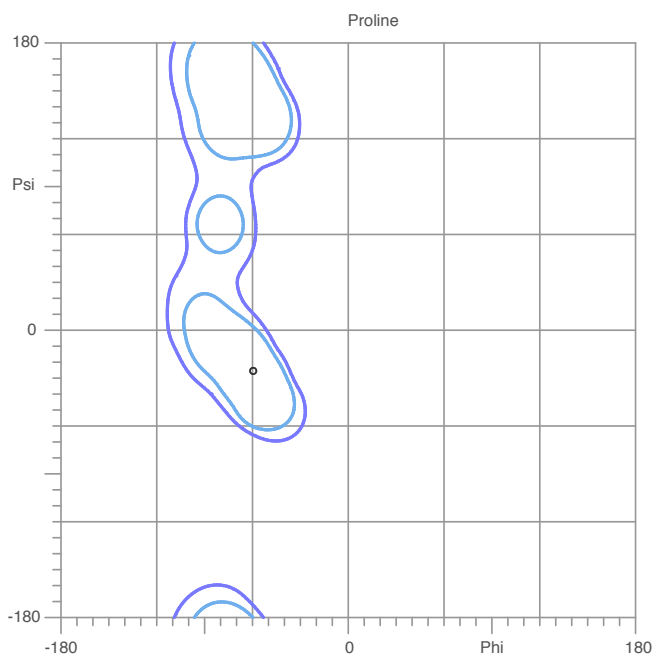
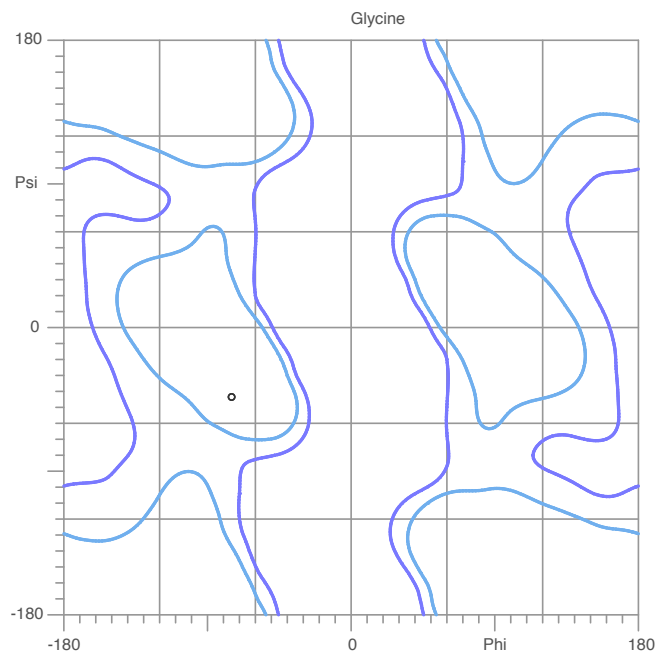
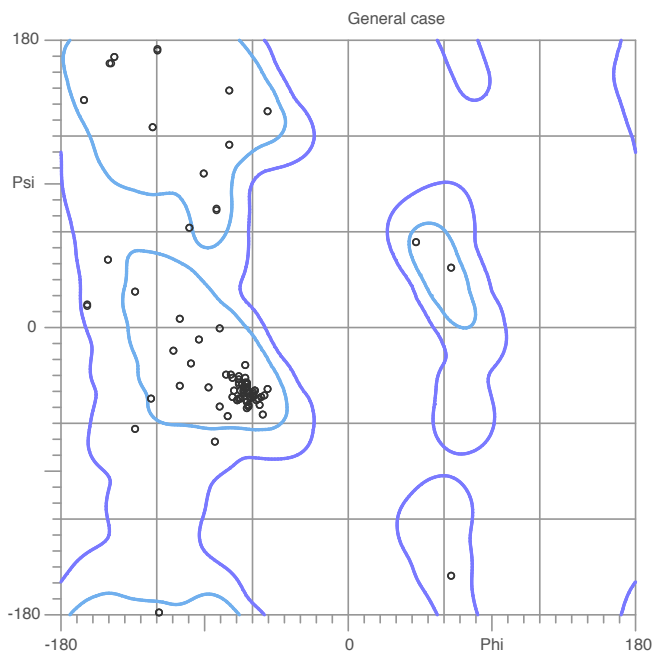
There were 2 outliers (phi, psi):

[2] 23 SER (158.6, 61.1)

[2] 113 SER (158.6, 61.1)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 3



92.3% (144/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

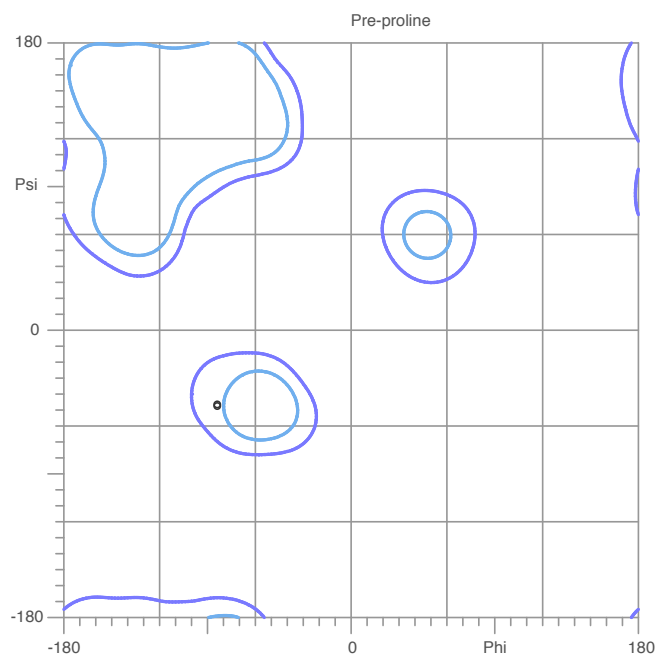
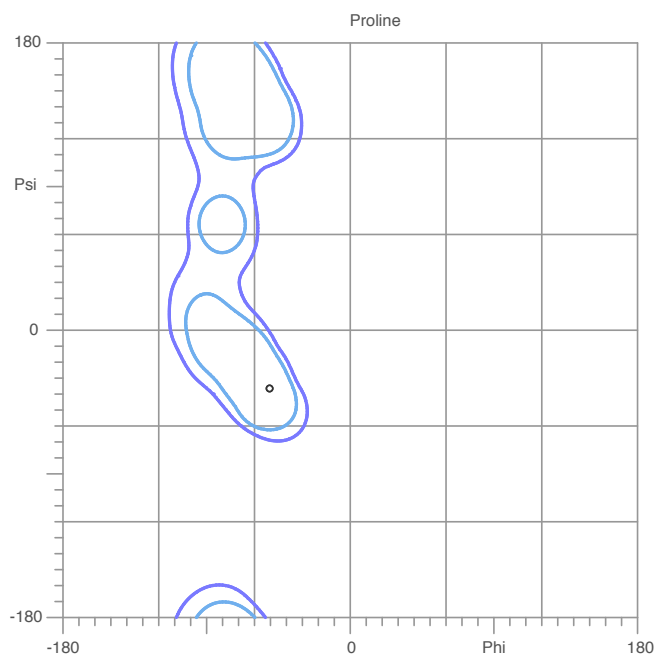
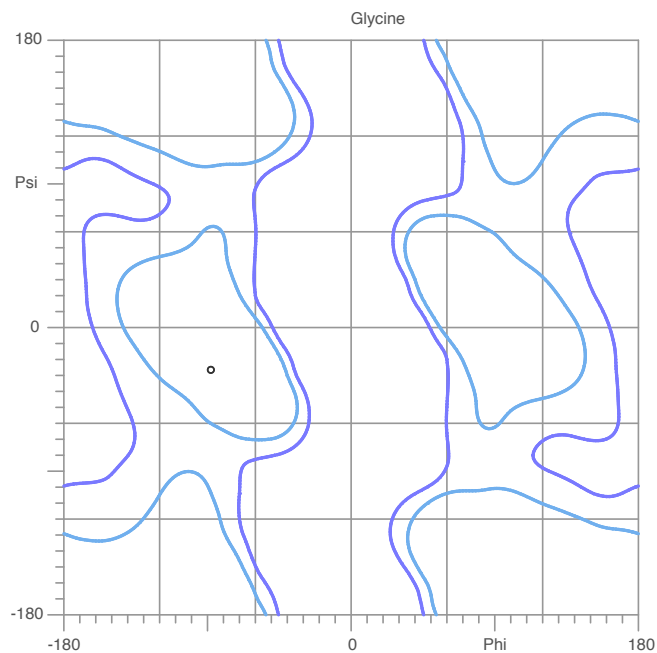
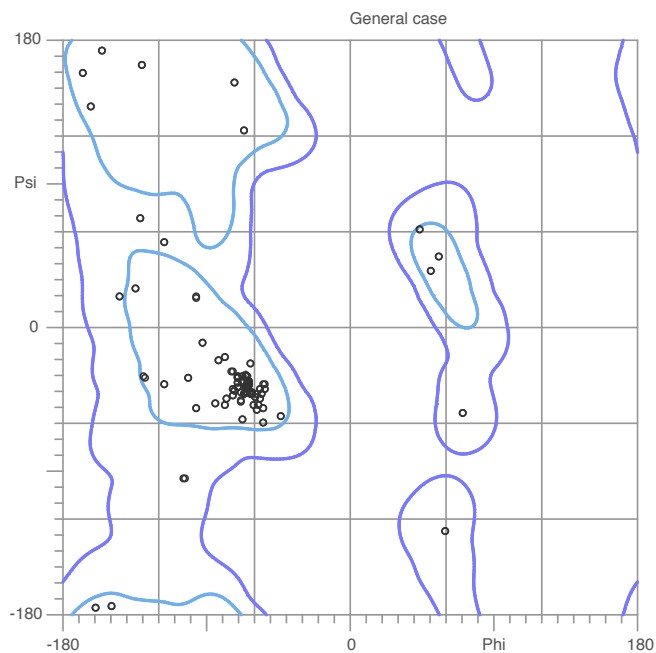
There were no outliers.

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MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 4



91.0% (142/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

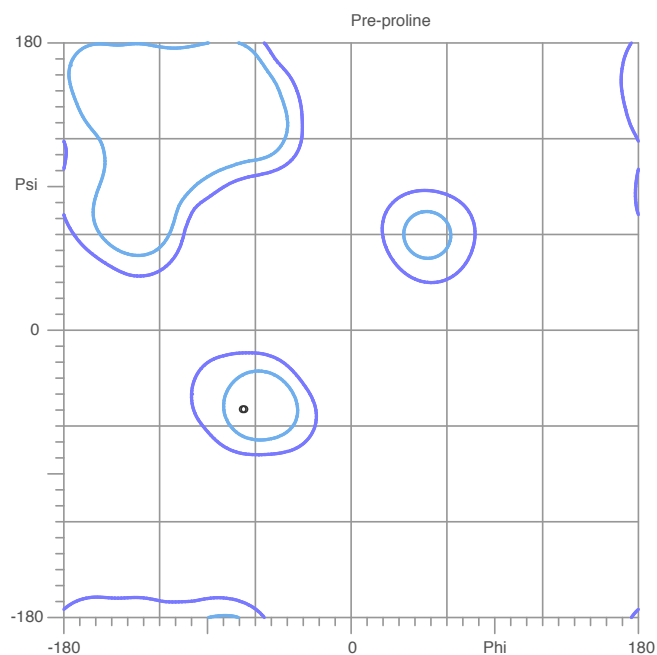
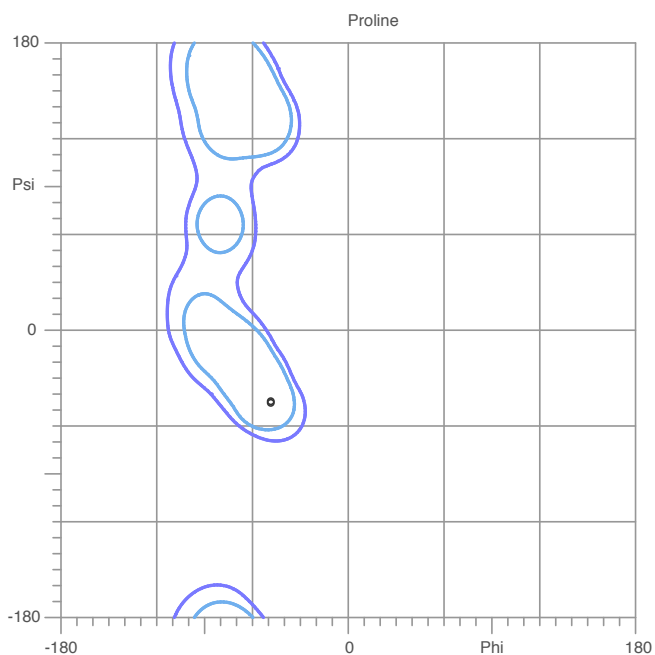
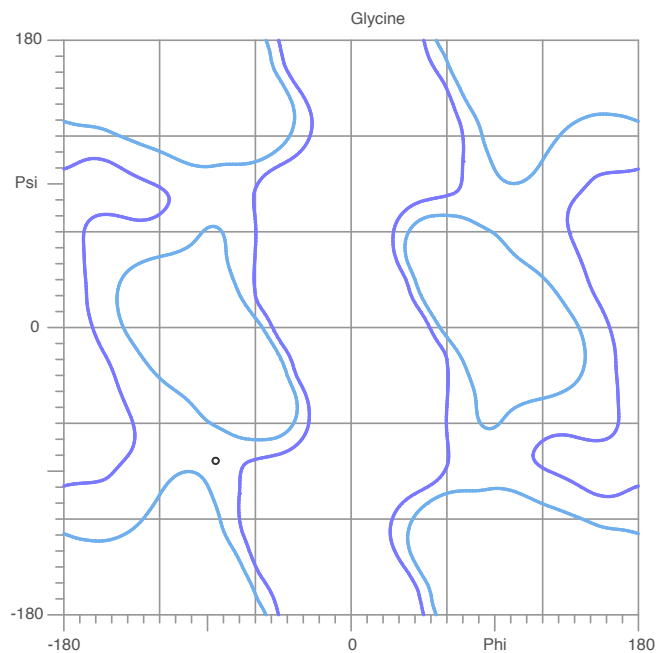
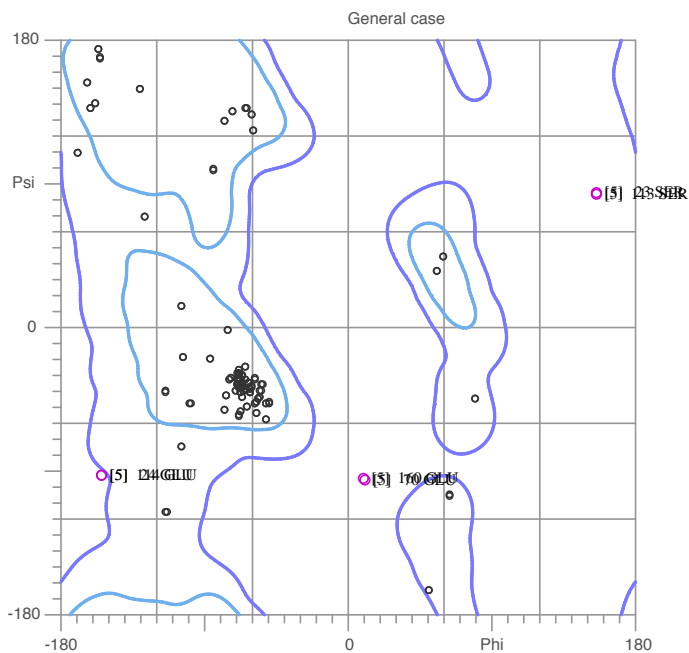
There were no outliers.

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MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 5



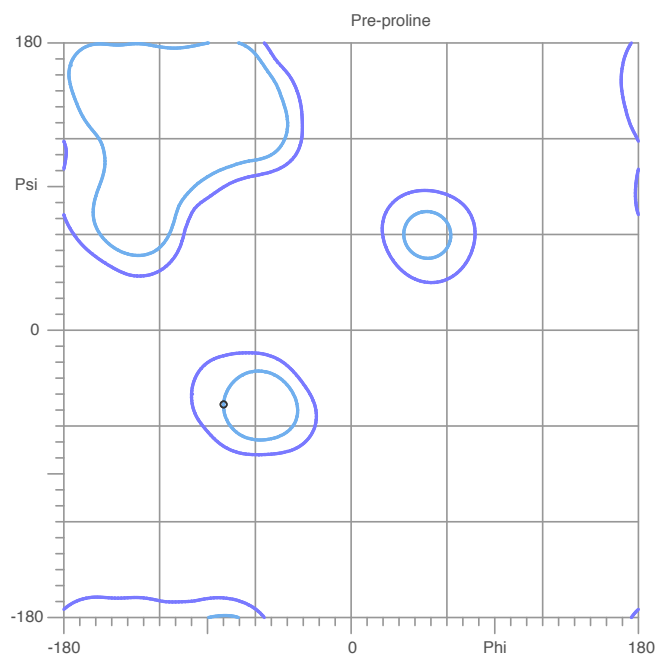
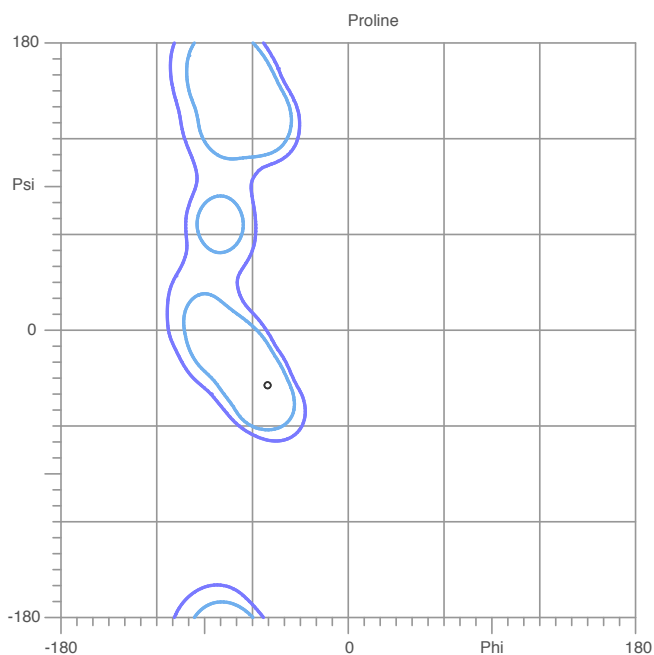
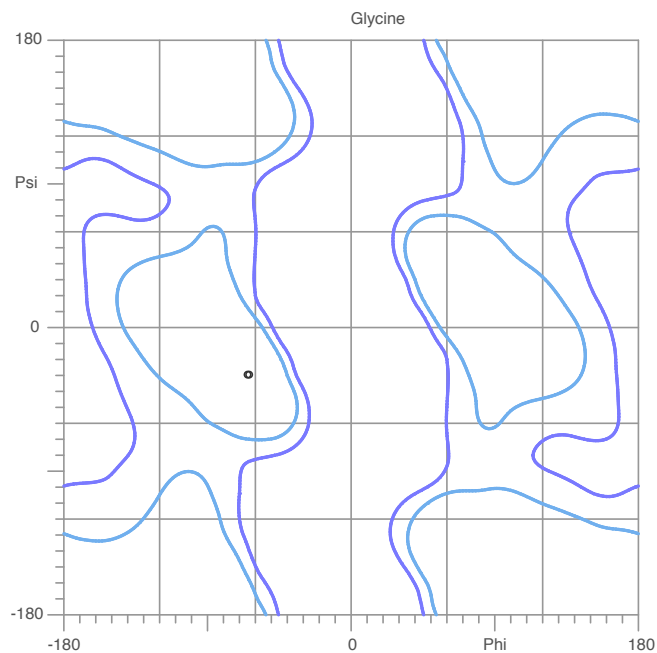
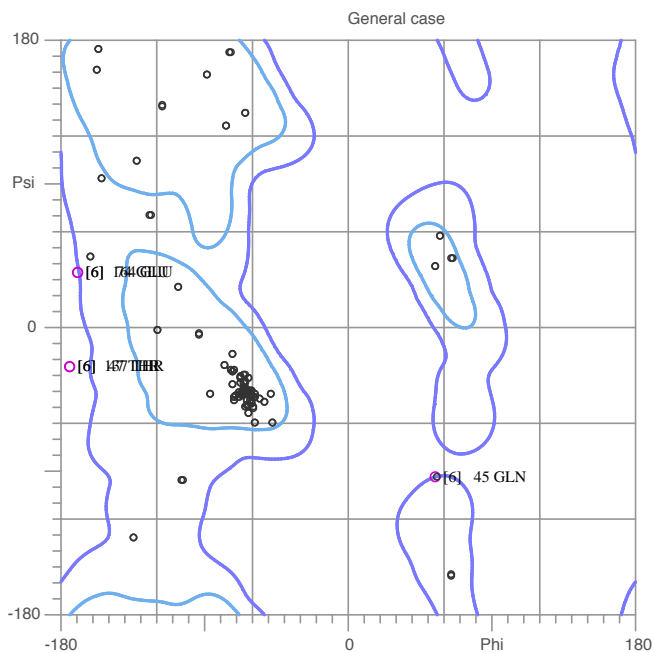
85.9% (134/156) of all residues were in favored (98%) regions.
96.2% (150/156) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[5] 23 SER (155.1, 85.0)

[5] 24 GLU (-155.0, -92.3)
[5] 70 GLU (10.0, -95.0)
[5] 113 SER (155.1, 85.0)
[5] 114 GLU (-155.0, -92.3)
[5] 160 GLU (10.0, -95.0)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 6



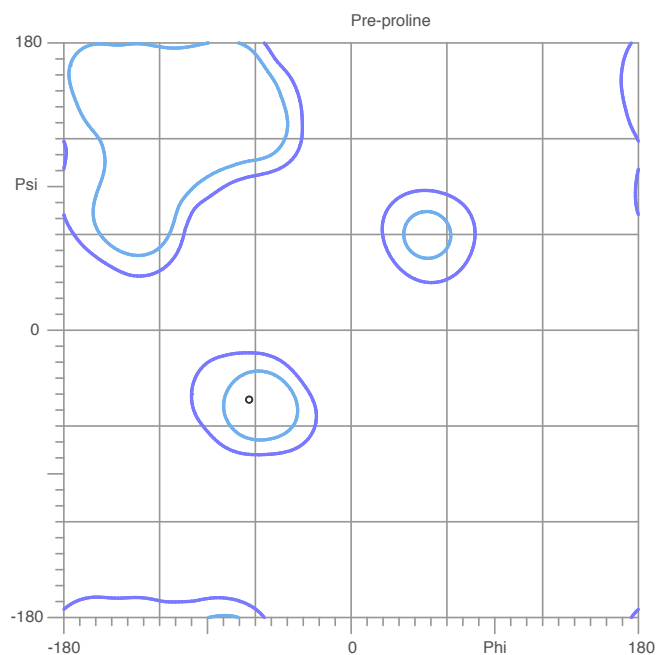
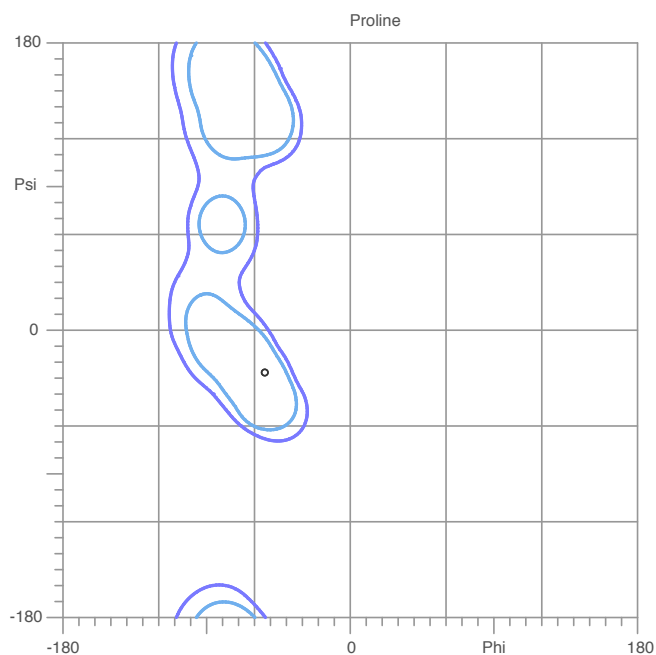
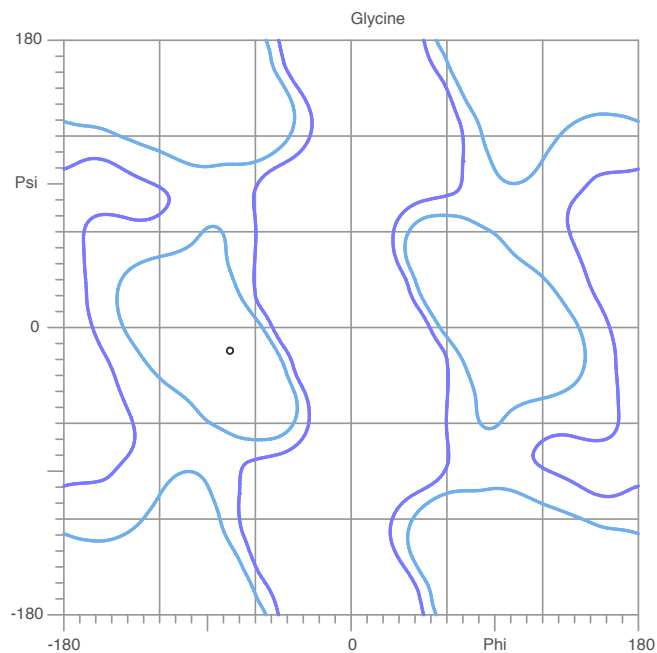
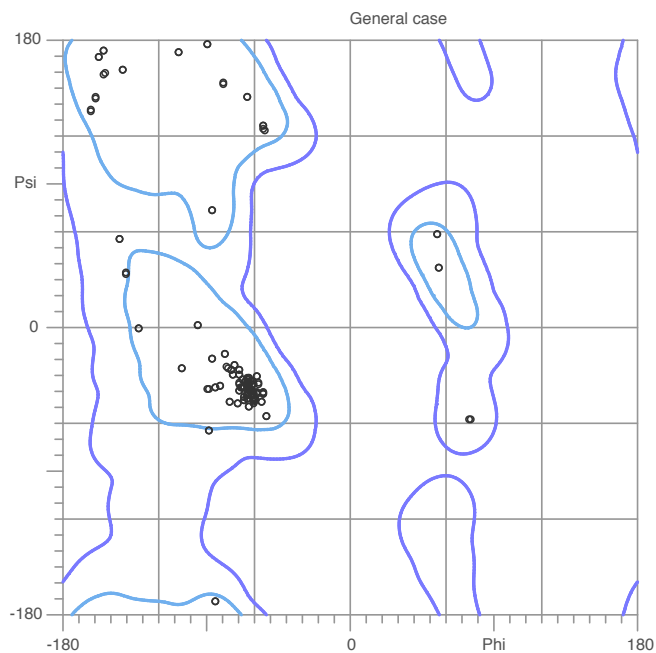
87.2% (136/156) of all residues were in favored (98%) regions.
96.8% (151/156) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [6] 45 GLN (54.9, -93.2)
- [6] 47 THR (-175.1, -25.0)
- [6] 74 GLU (-170.6, 35.1)
- [6] 137 THR (-175.0, -24.9)
- [6] 164 GLU (-170.7, 35.1)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 7



94.9% (148/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

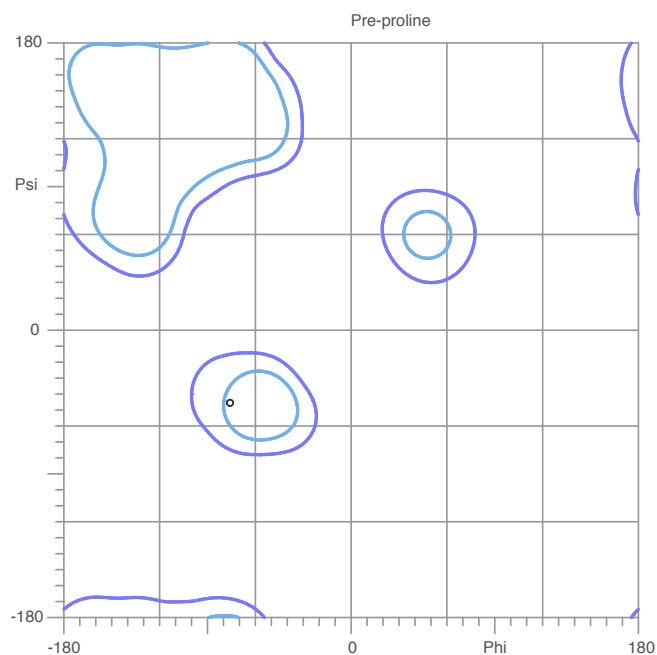
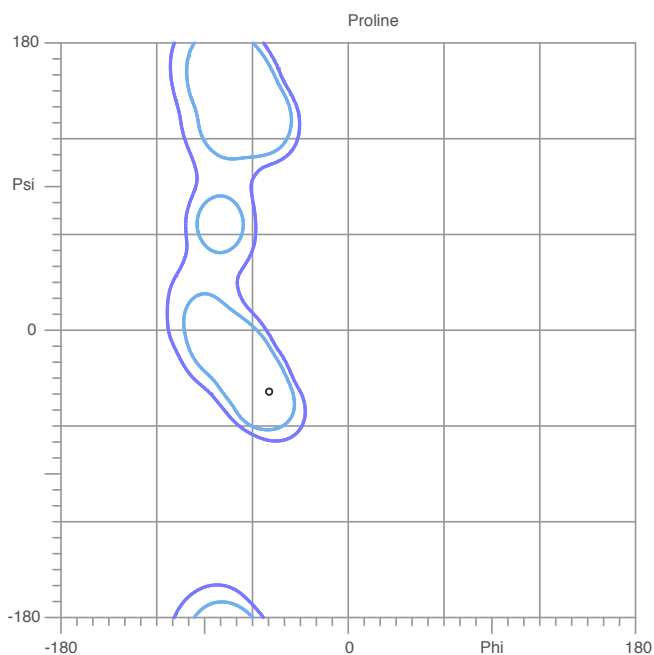
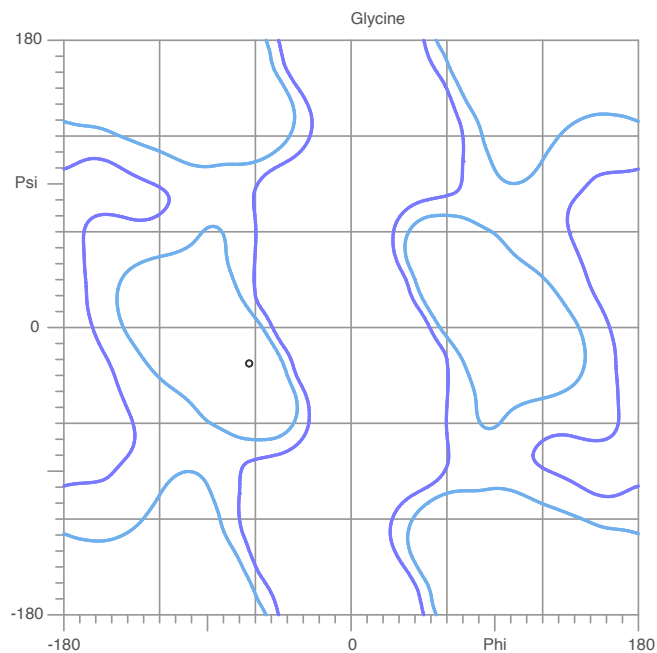
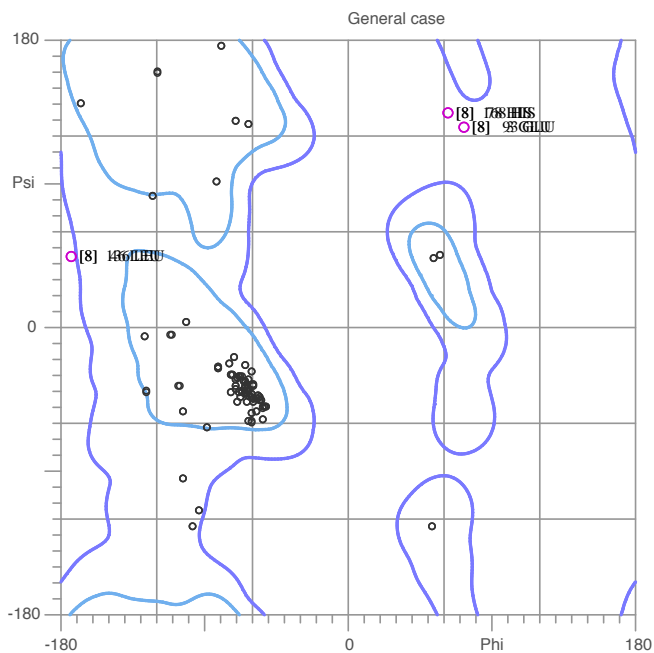
There were no outliers.

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MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 8



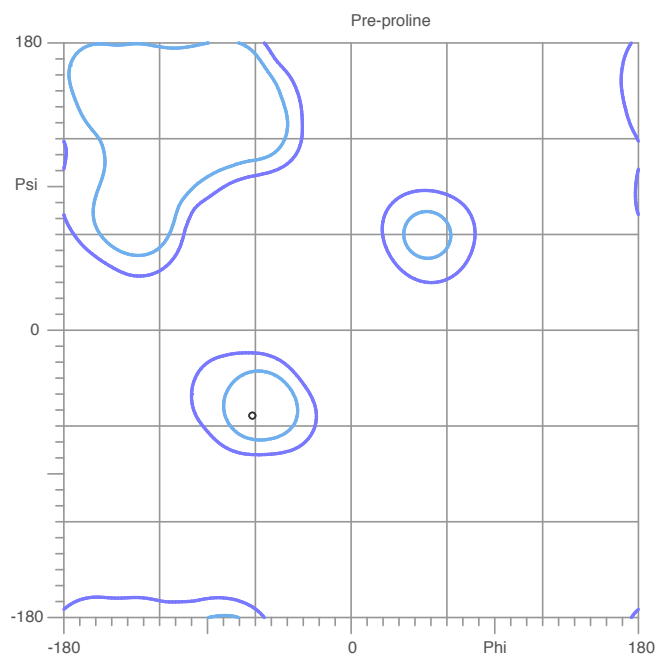
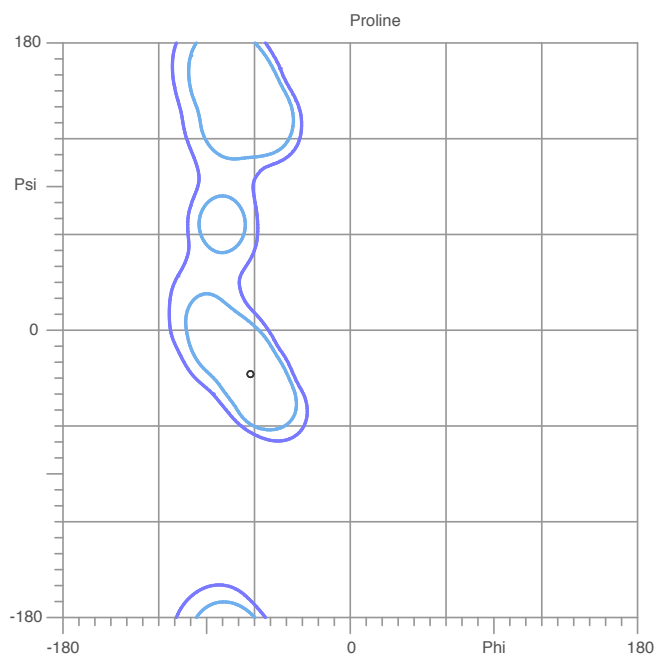
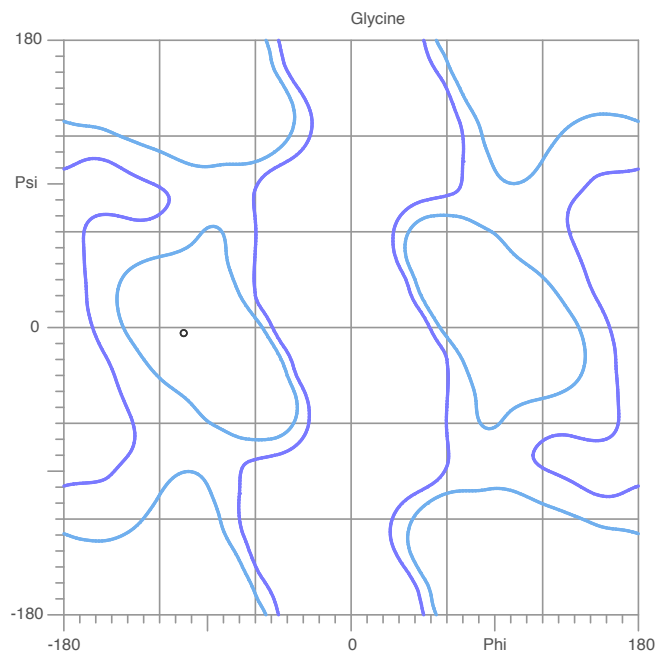
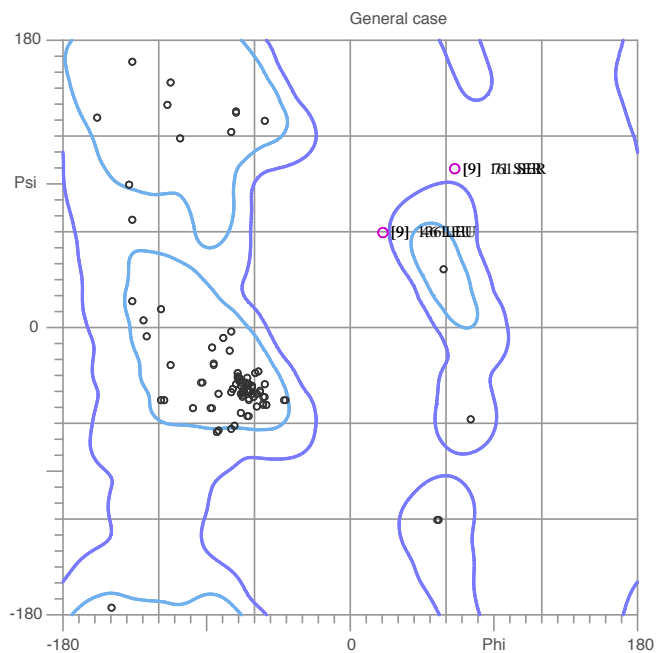
89.7% (140/156) of all residues were in favored (98%) regions.
96.2% (150/156) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[8] 3 GLU (72.3, 126.5)

[8] 46 LEU (-175.0, 45.1)
[8] 78 HIS (62.3, 135.1)
[8] 93 GLU (72.3, 126.5)
[8] 136 LEU (-175.0, 45.1)
[8] 168 HIS (62.4, 135.0)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 9



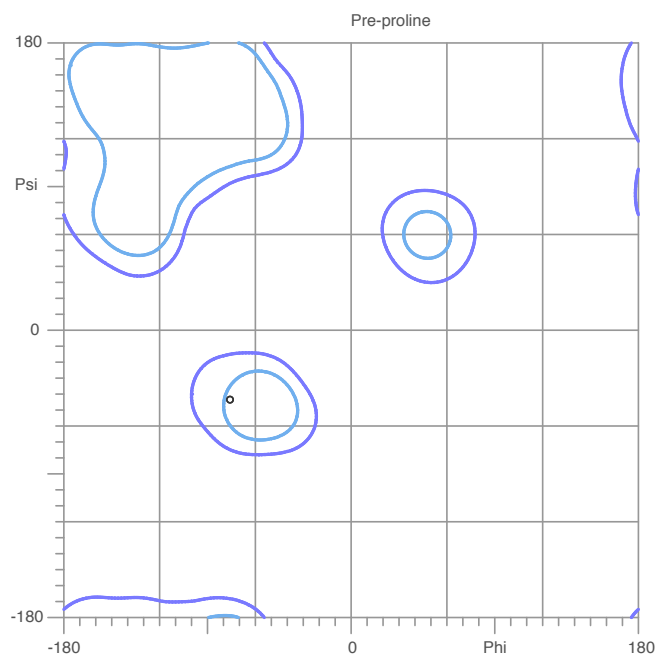
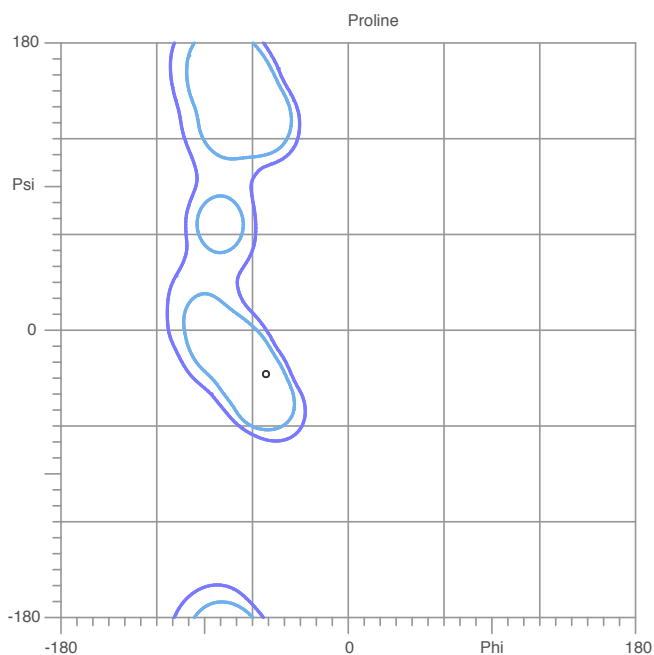
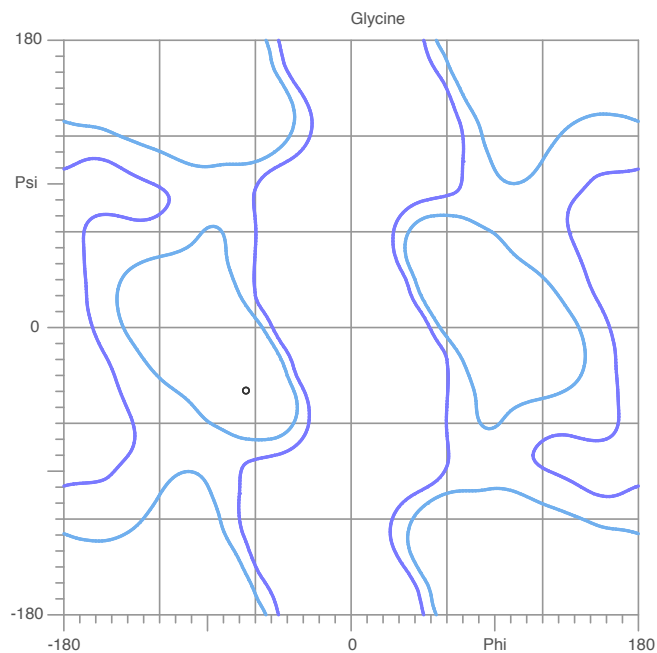
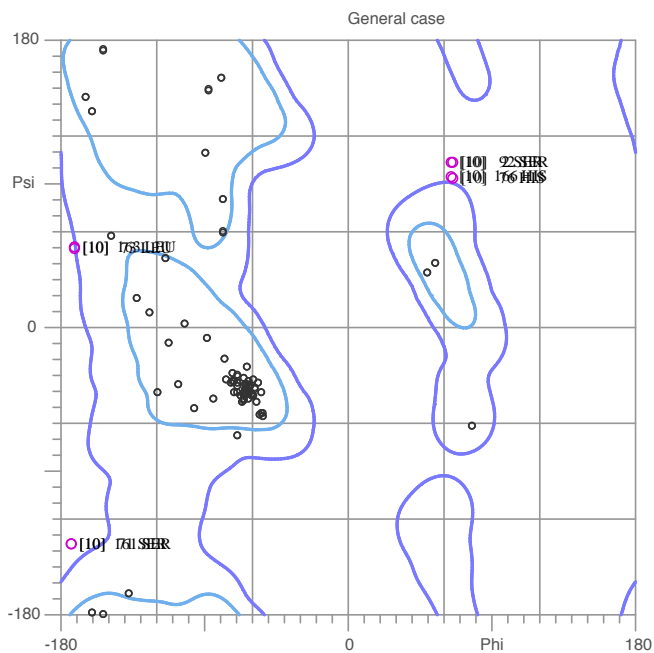
89.7% (140/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [9] 46 LEU (20.3, 60.6)
- [9] 71 SER (65.0, 100.4)
- [9] 136 LEU (20.3, 60.7)
- [9] 161 SER (65.0, 100.3)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 10



89.7% (140/156) of all residues were in favored (98%) regions.
94.9% (148/156) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[10] 2 SER (64.9, 104.8)

[10] 71 SER (-174.6, -135.1)

[10] 73 LEU (-172.8, 50.8)

[10] 76 HIS (65.0, 95.0)

[10] 92 SER (65.1, 104.8)

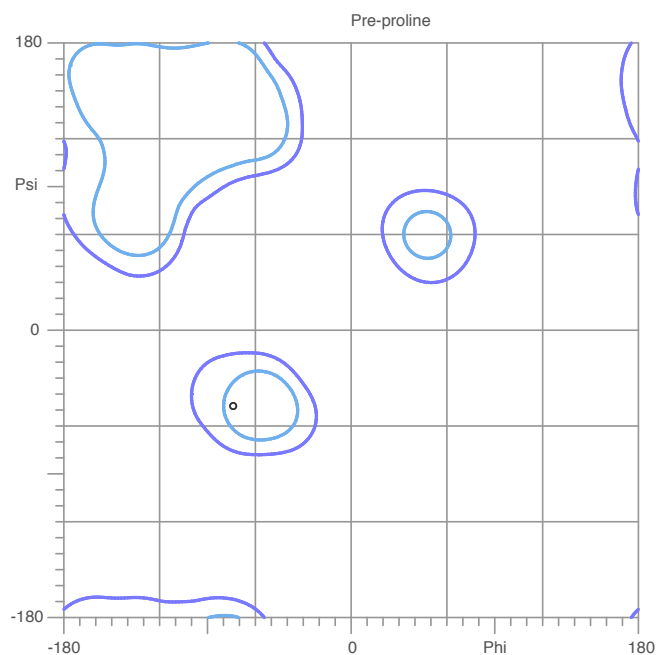
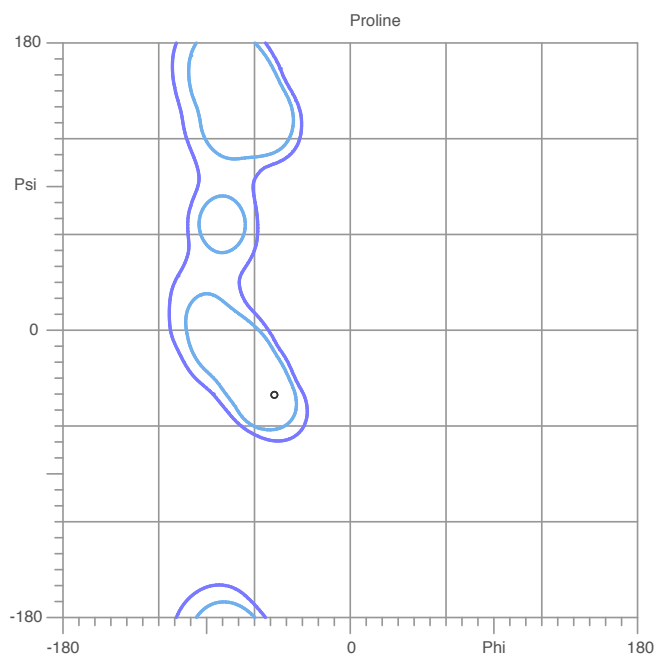
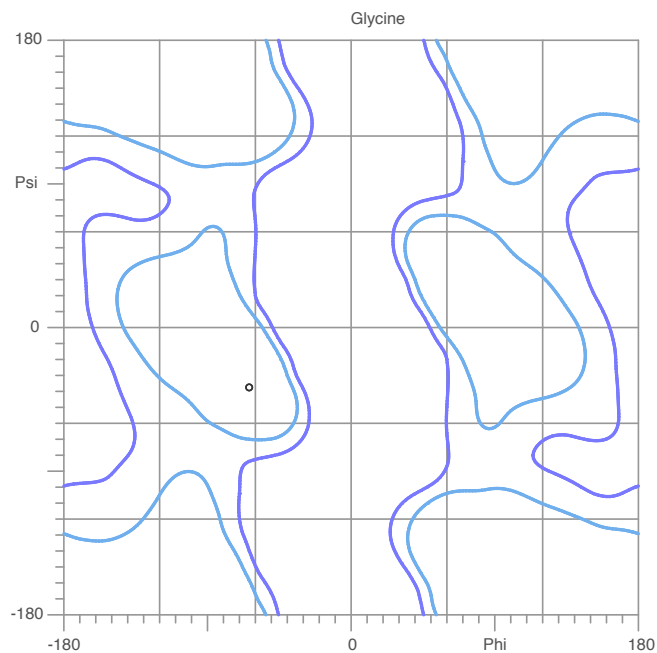
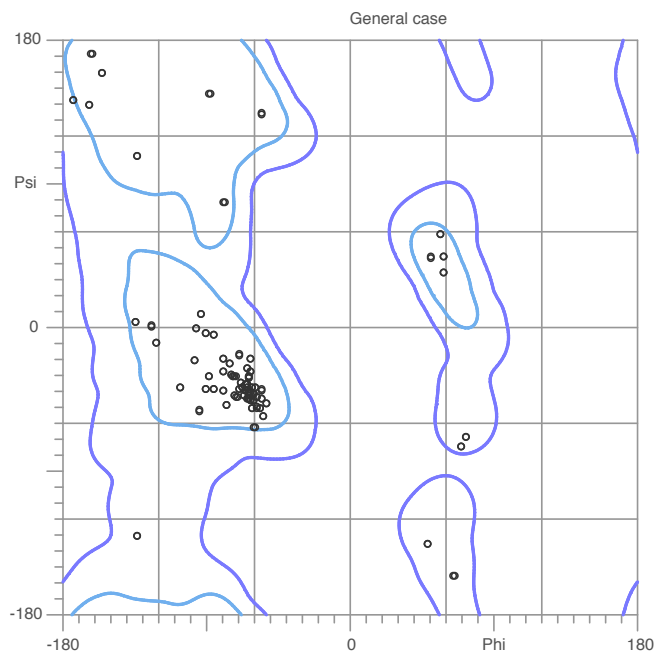
[10] 161 SER (-174.5, -135.1)

[10] 163 LEU (-172.9, 51.1)

[10] 166 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 11



92.3% (144/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

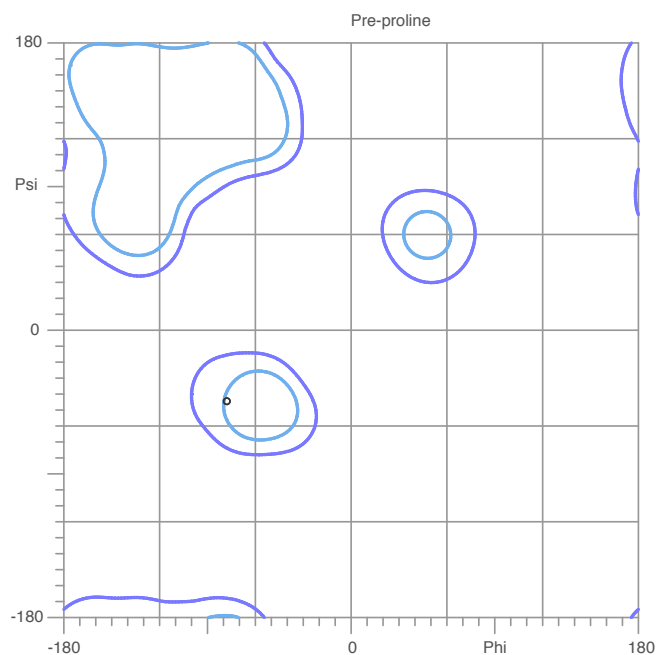
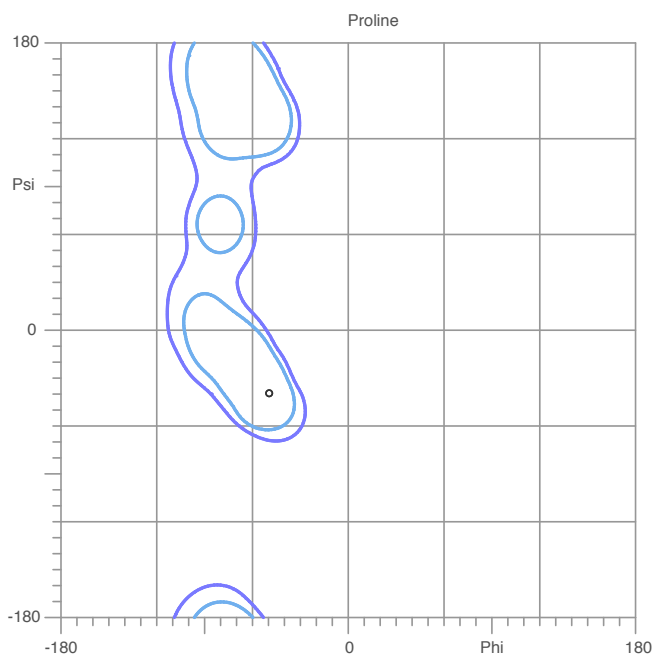
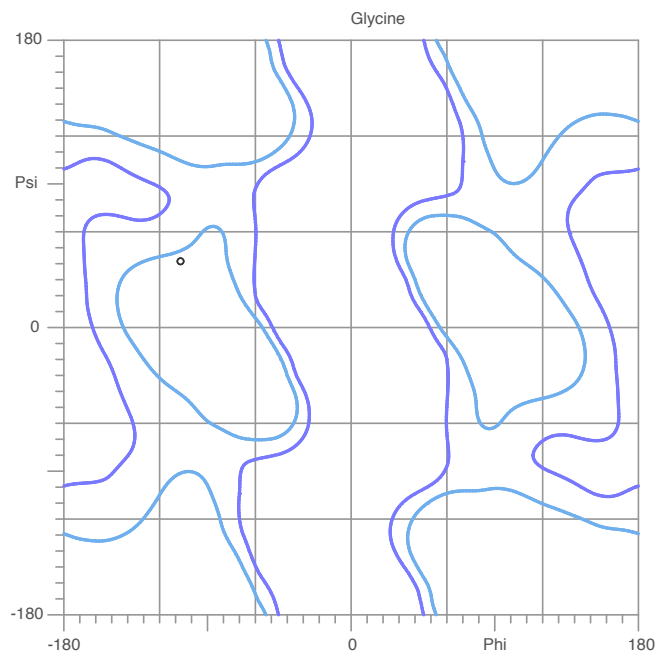
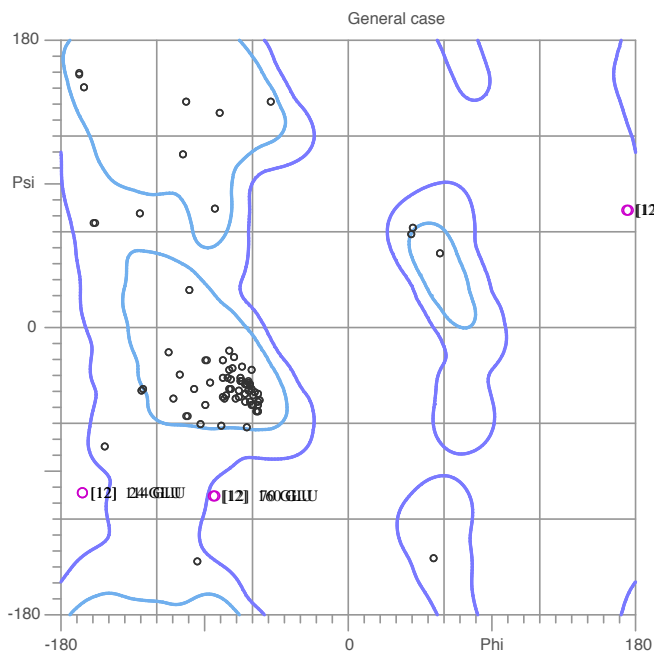
There were no outliers.

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MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 12



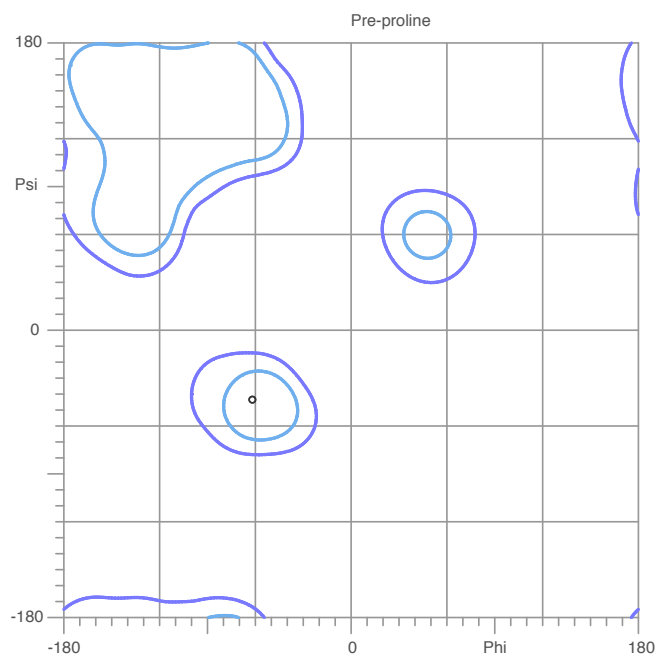
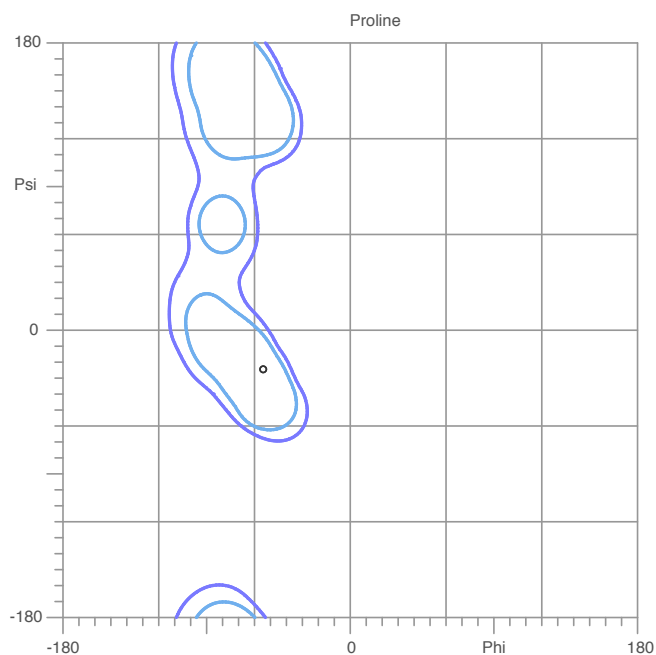
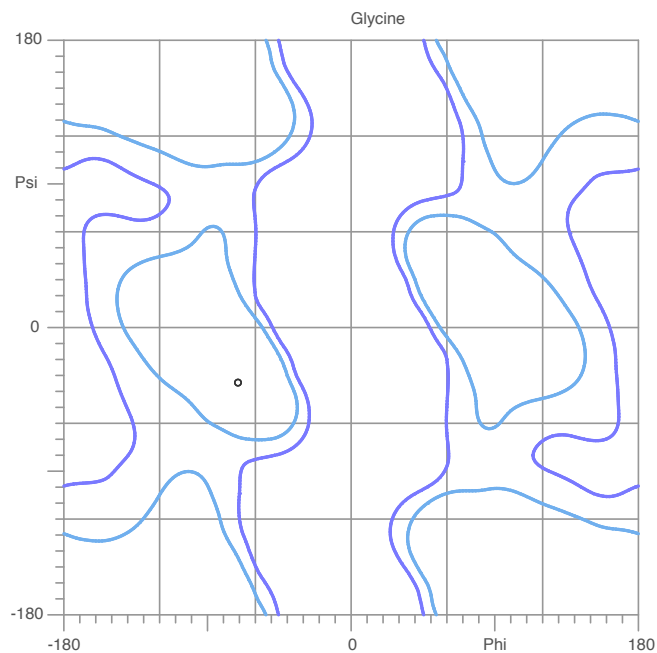
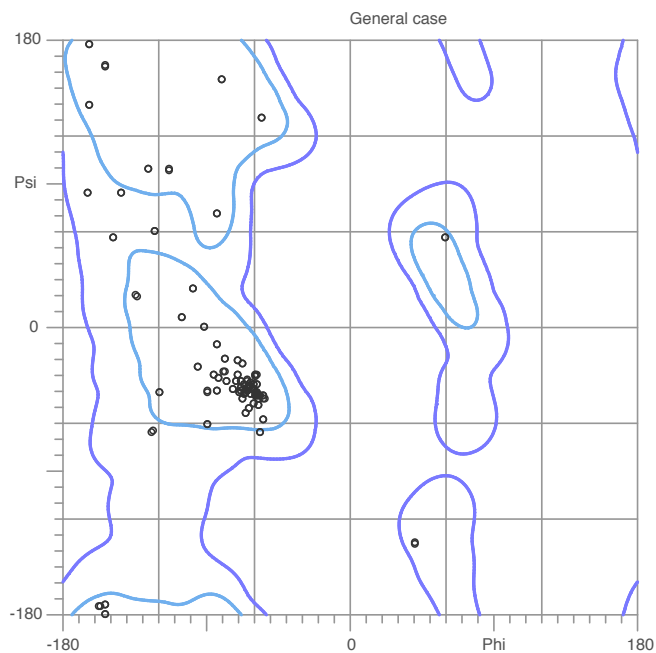
84.6% (132/156) of all residues were in favored (98%) regions.
96.2% (150/156) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[12] 23 SER (175.0, 75.0)

[12] 24 GLU (-167.5, -103.3)
[12] 70 GLU (-85.1, -105.0)
[12] 113 SER (175.0, 74.9)
[12] 114 GLU (-167.5, -103.3)
[12] 160 GLU (-84.9, -105.1)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 13



91.0% (142/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

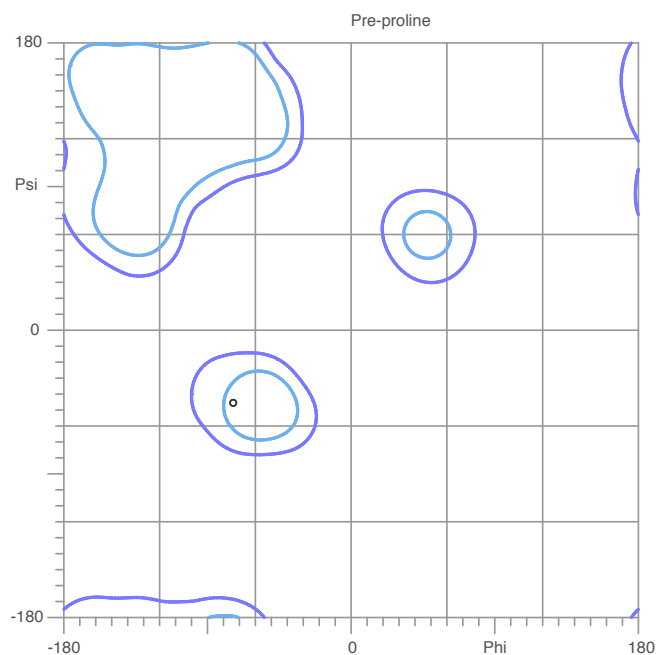
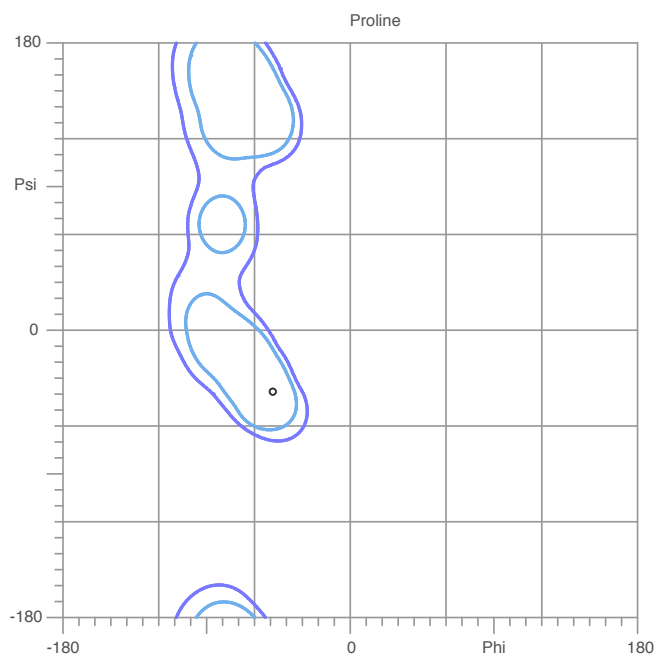
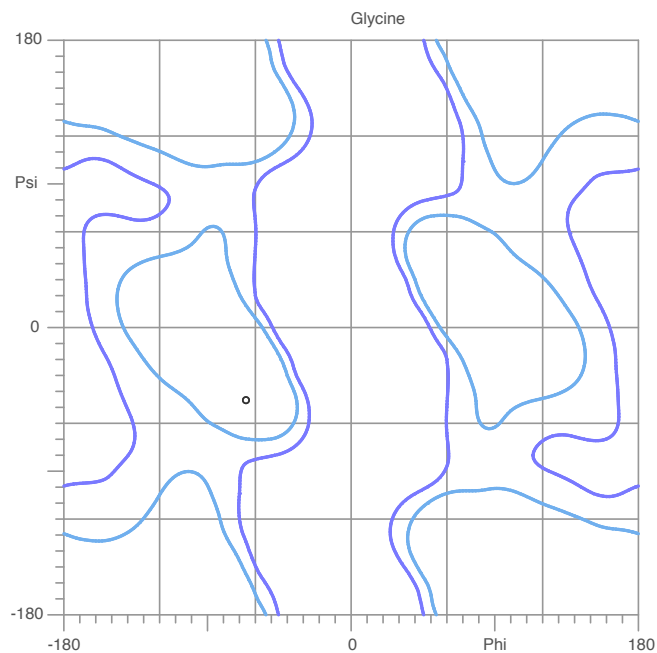
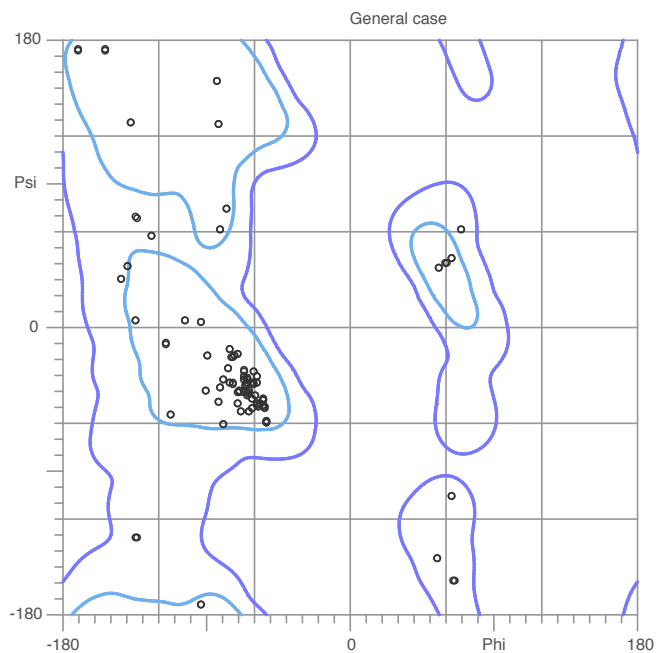
There were no outliers.

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MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 14



88.5% (138/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

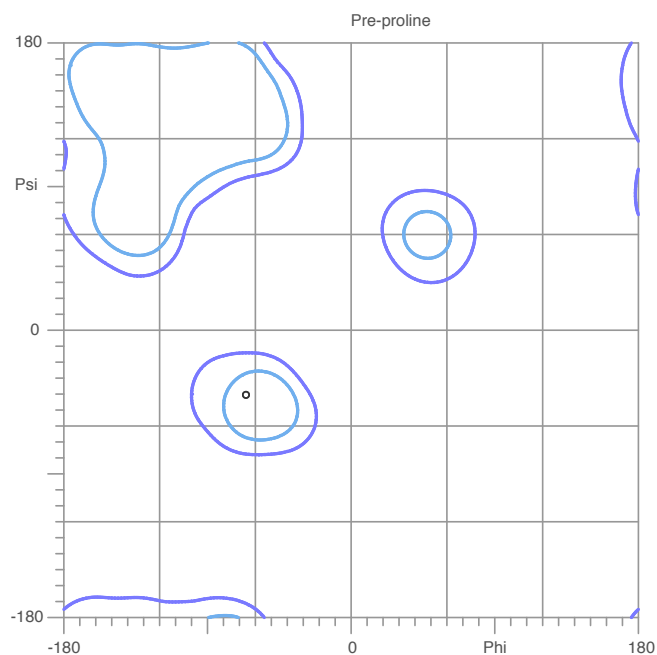
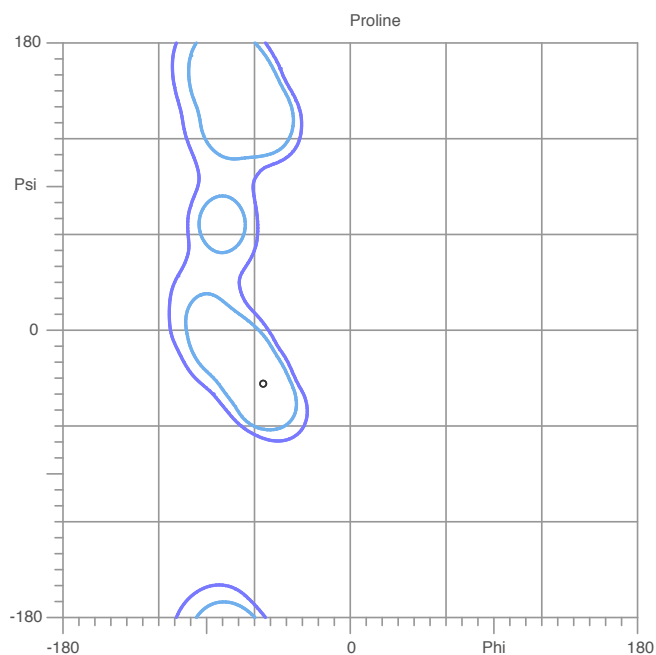
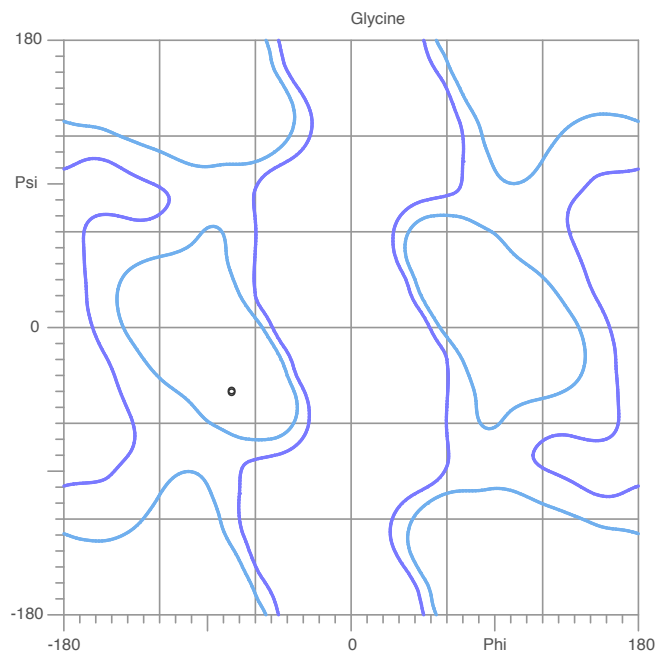
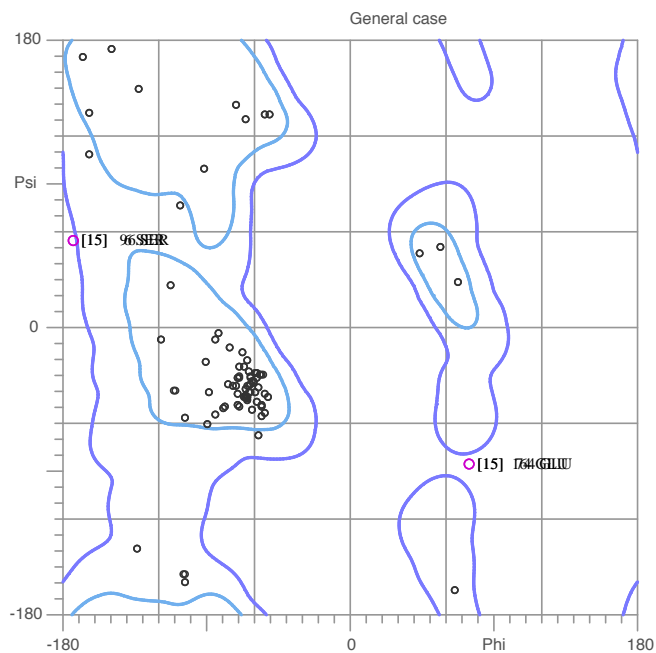
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 15



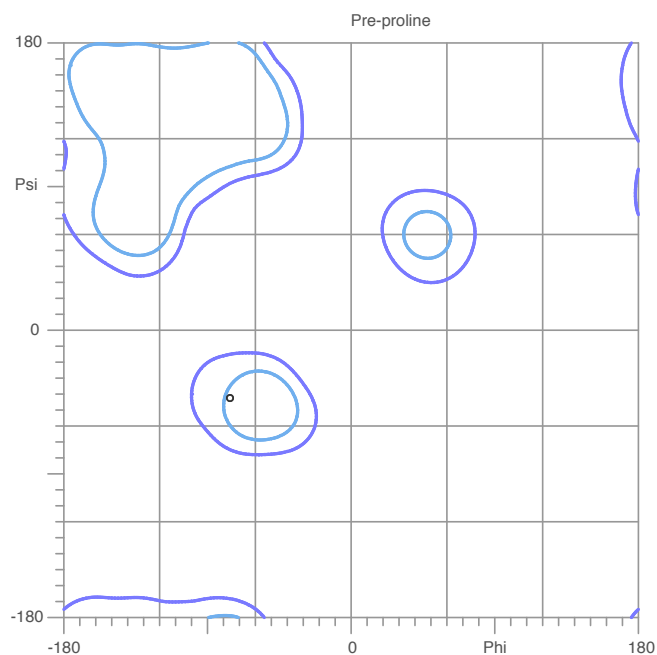
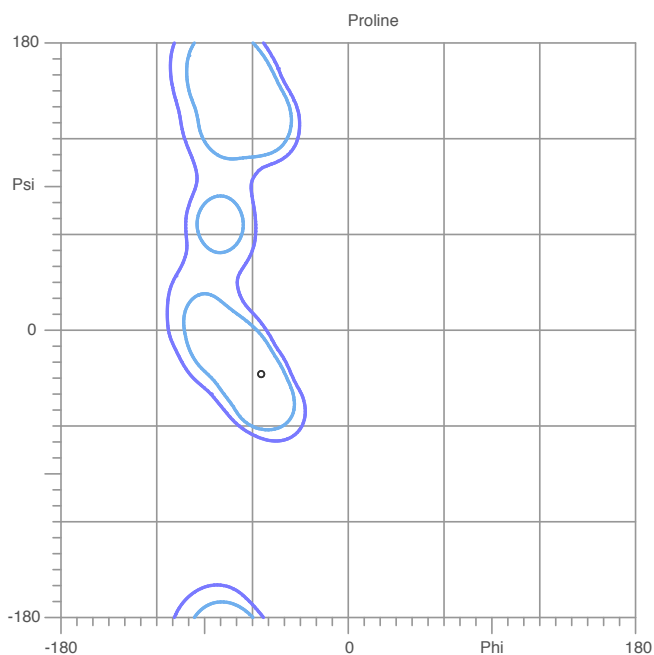
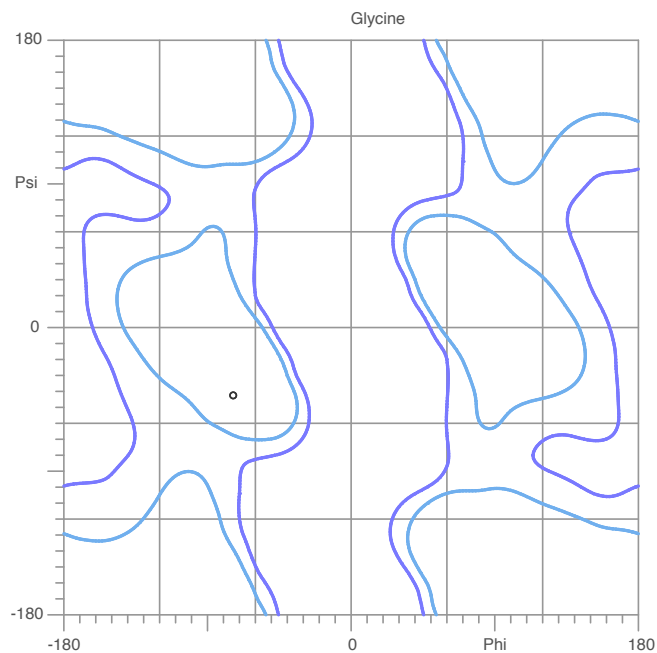
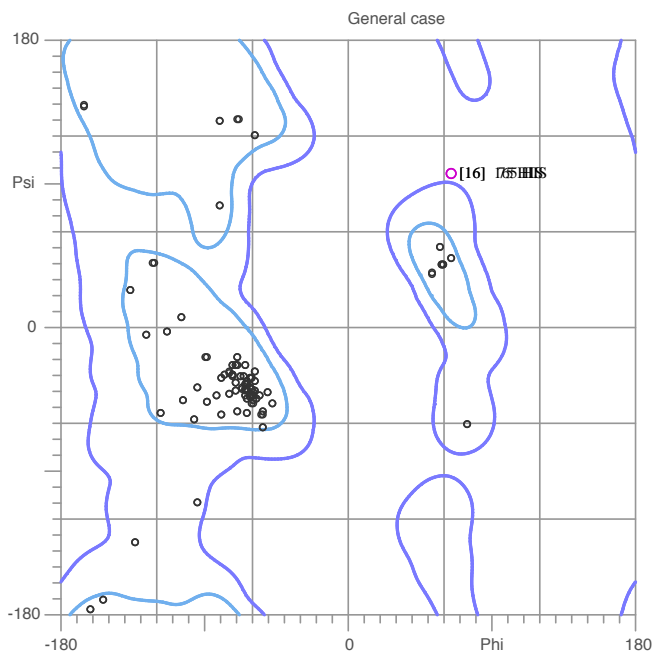
88.5% (138/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [15] 6 SER (-175.0, 55.1)
- [15] 74 GLU (74.6, -85.2)
- [15] 96 SER (-175.0, 55.0)
- [15] 164 GLU (74.5, -85.1)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 16



94.9% (148/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

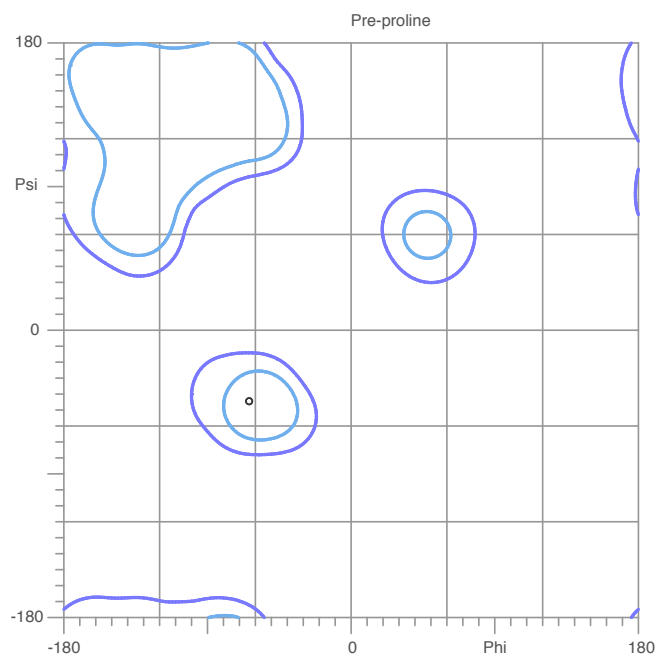
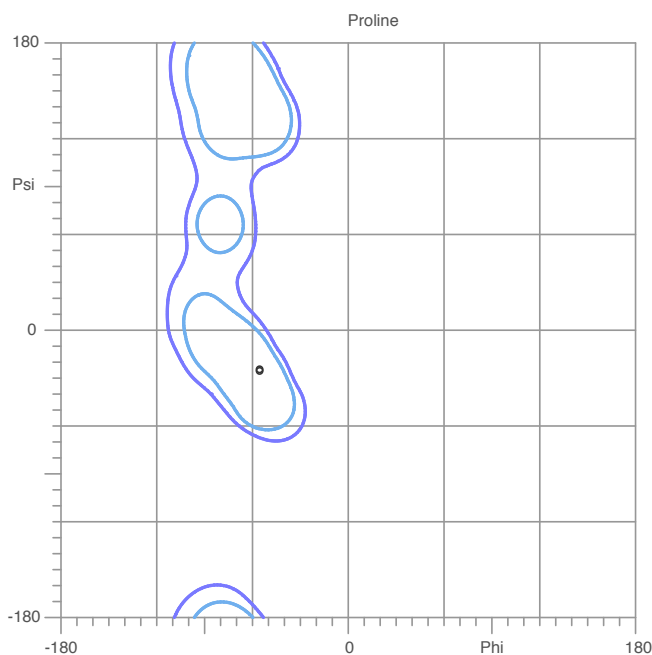
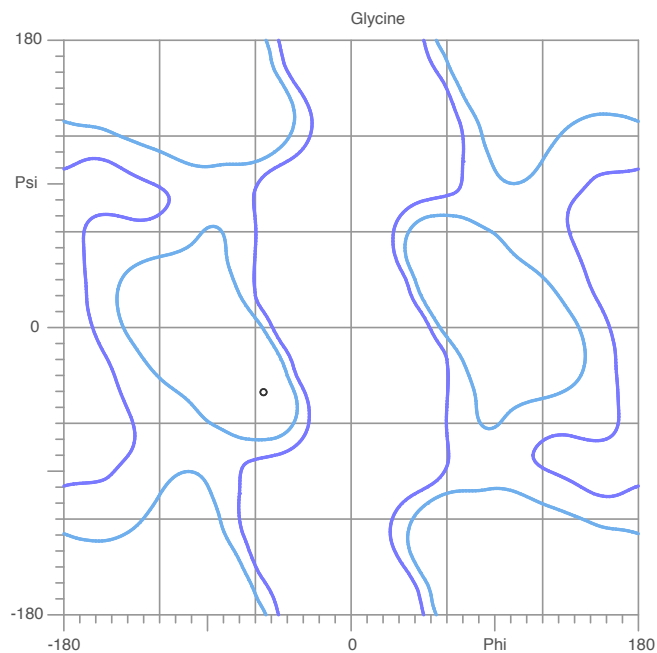
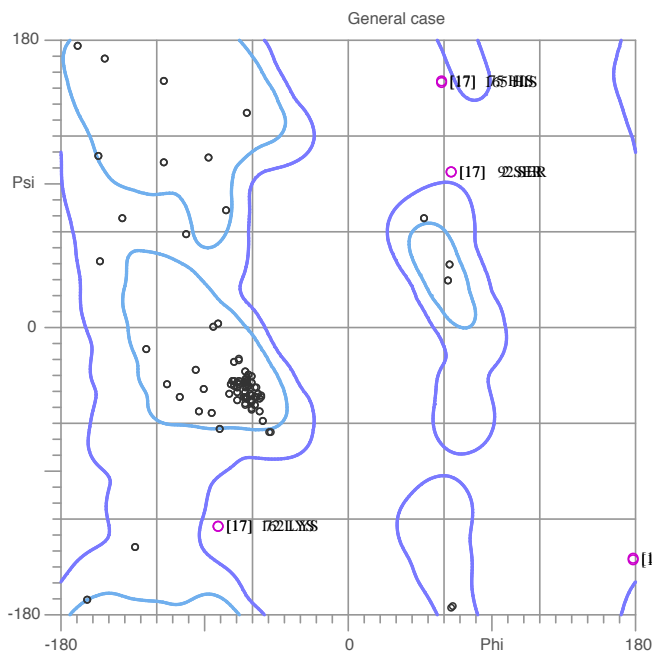
There were 2 outliers (phi, psi):

[16] 75 HIS (64.9, 97.4)

[16] 165 HIS (64.9, 97.4)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 17



83.3% (130/156) of all residues were in favored (98%) regions.
94.9% (148/156) of all residues were in allowed (>99.8%) regions.

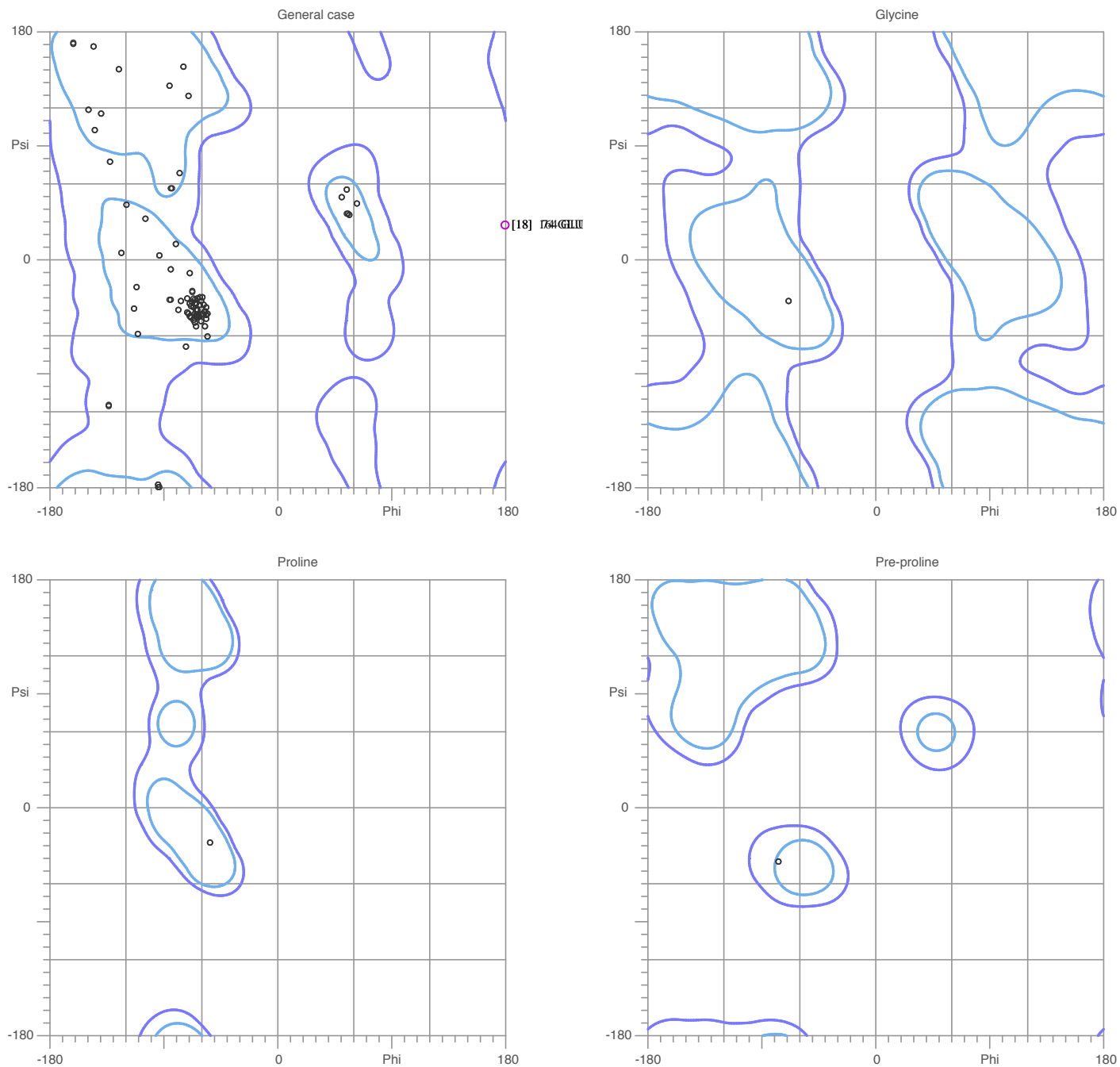
There were 8 outliers (phi, psi):

[17] 2 SER (65.0, 98.9)
[17] 71 SER (179.0, -145.0)

[17] 72 LYS (-82.9, -124.9)
[17] 75 HIS (58.3, 155.0)
[17] 92 SER (64.9, 98.9)
[17] 161 SER (178.9, -145.1)
[17] 162 LYS (-82.7, -124.9)
[17] 165 HIS (58.5, 155.0)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 18

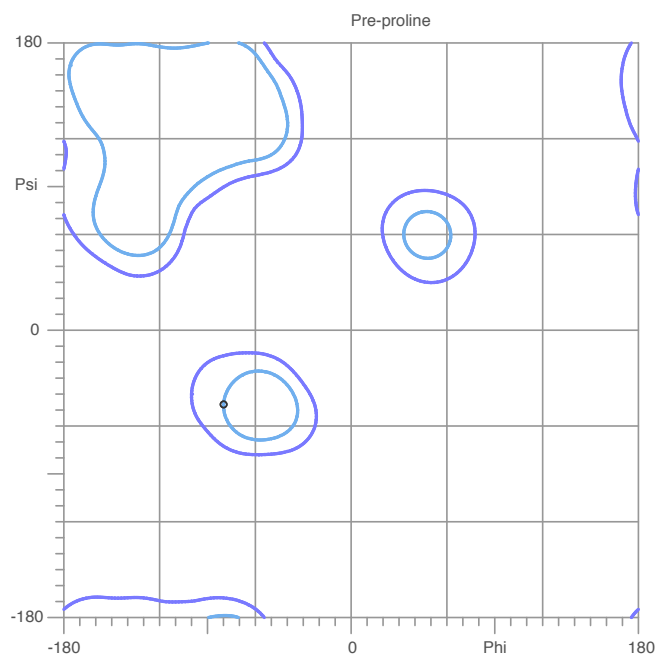
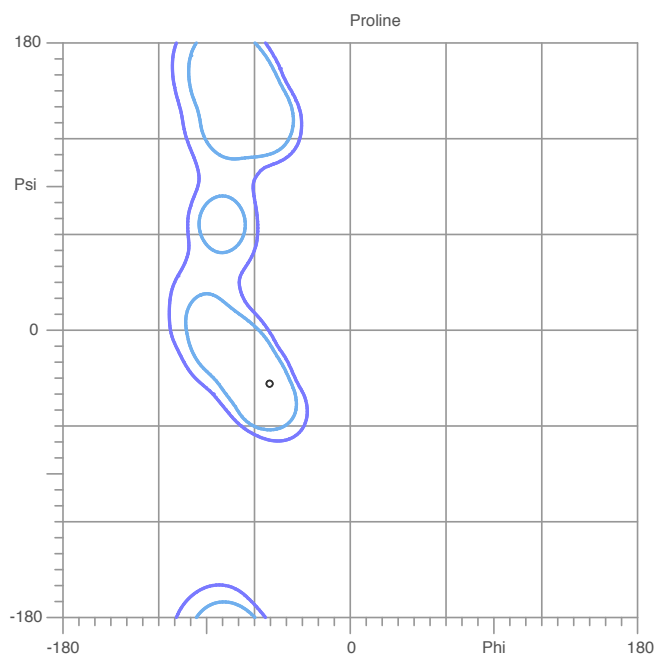
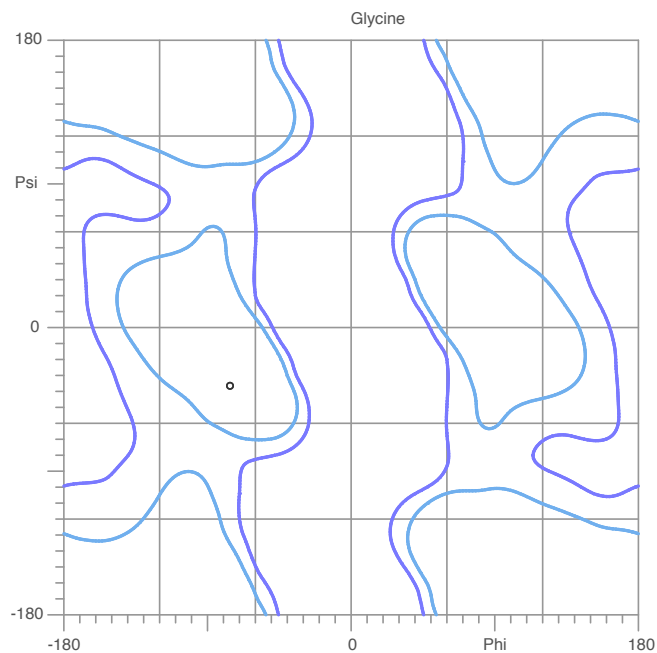
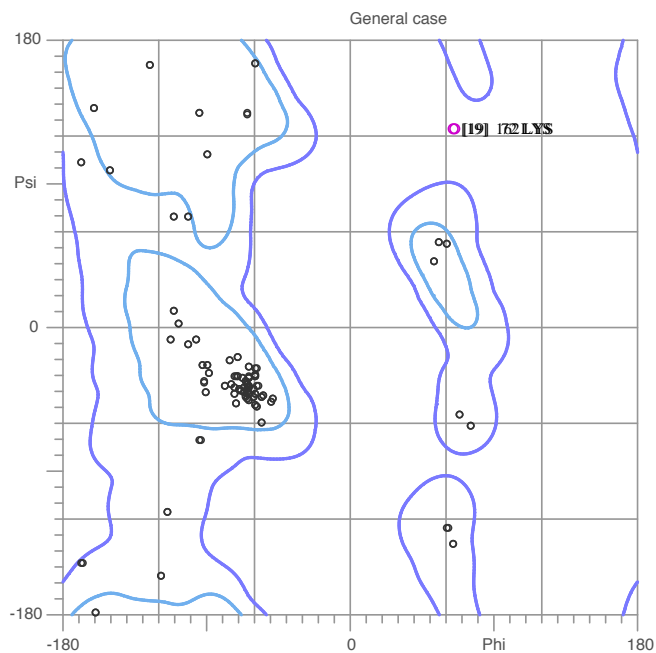


94.9% (148/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 74 GLU (179.7, 28.1)
[18] 164 GLU (179.8, 28.1)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 19

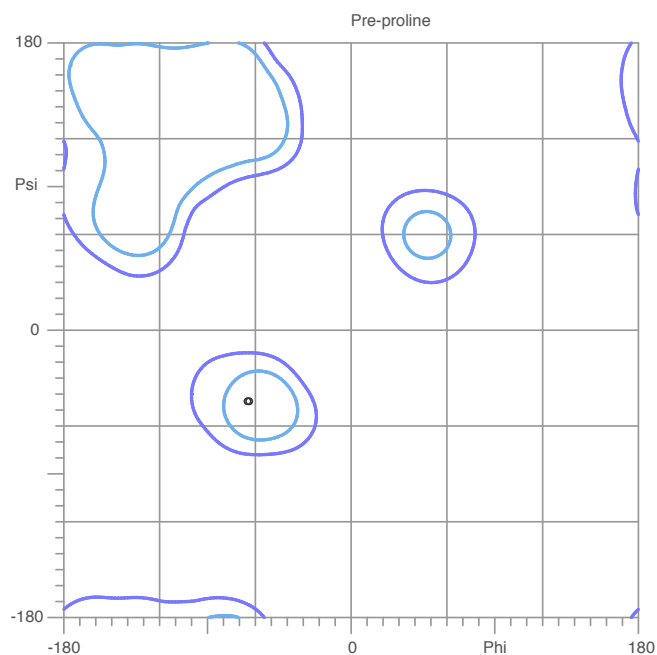
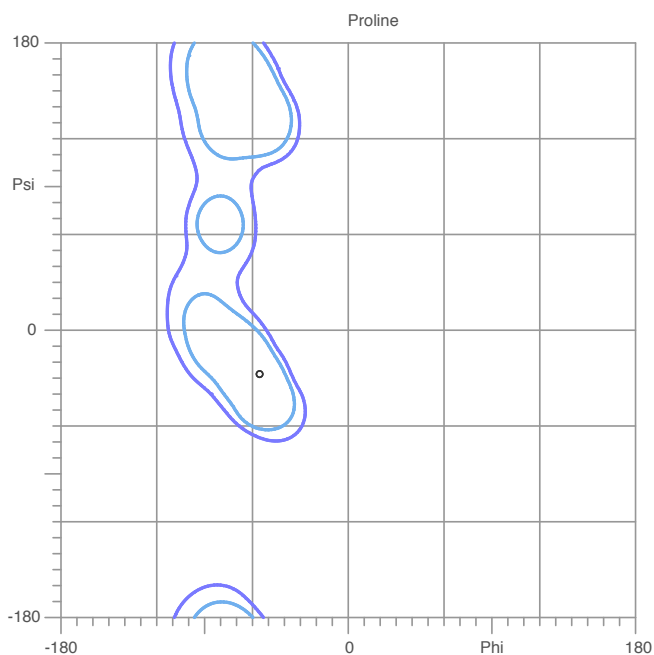
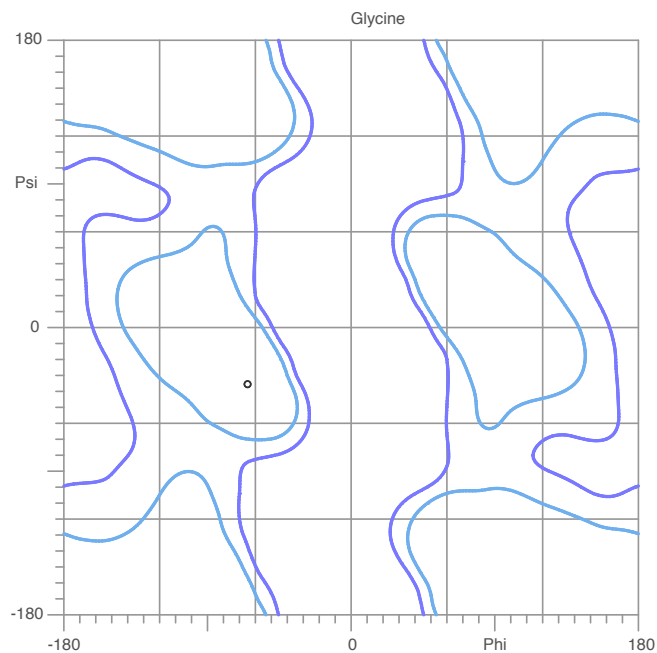
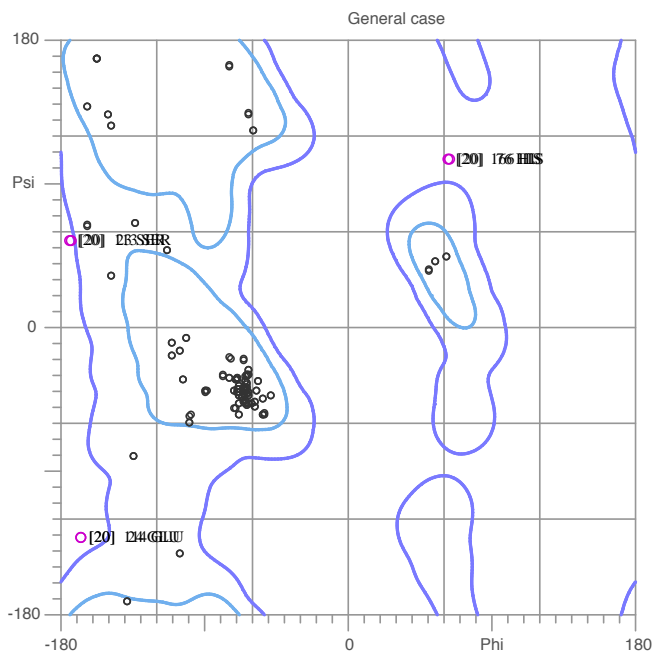


83.3% (130/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 72 LYS (65.0, 125.1)
[19] 162 LYS (65.0, 125.2)

MolProbity Ramachandran analysis

SR478_R3_em_bcr3.pdb, model 20



88.5% (138/156) of all residues were in favored (98%) regions.
96.2% (150/156) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[20] 23 SER (-175.1, 55.0)

[20] 24 GLU (-168.5, -131.1)
[20] 76 HIS (63.0, 106.2)
[20] 113 SER (-174.9, 55.0)
[20] 114 GLU (-168.5, -131.0)
[20] 166 HIS (62.9, 106.1)