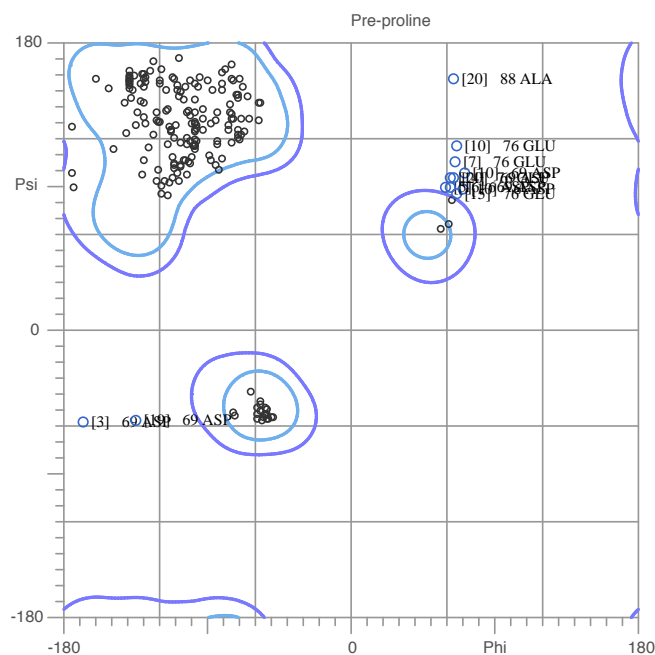
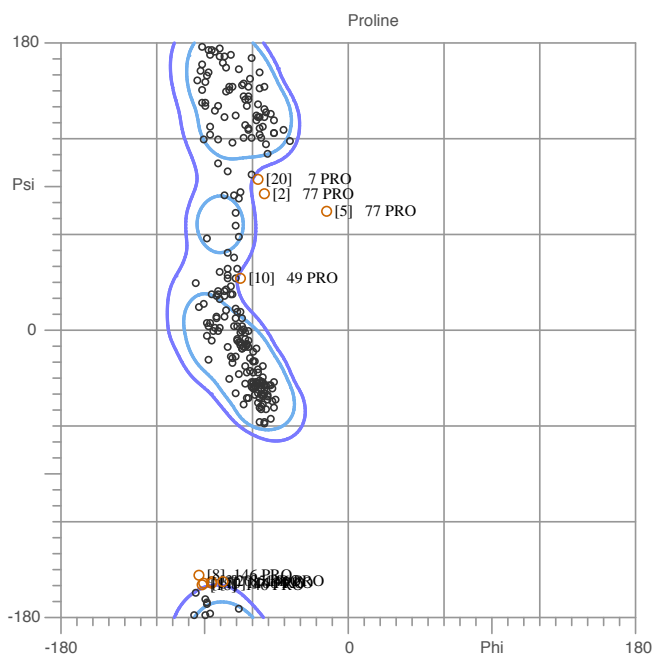
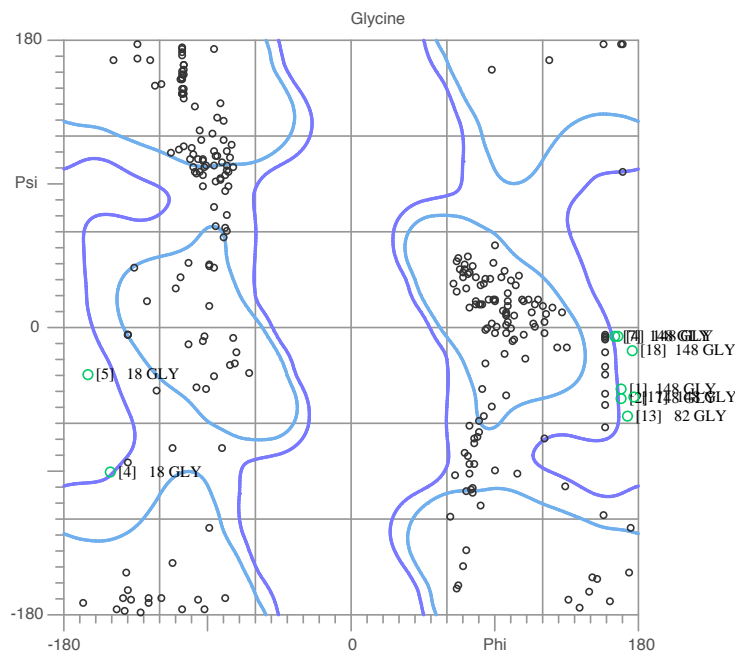
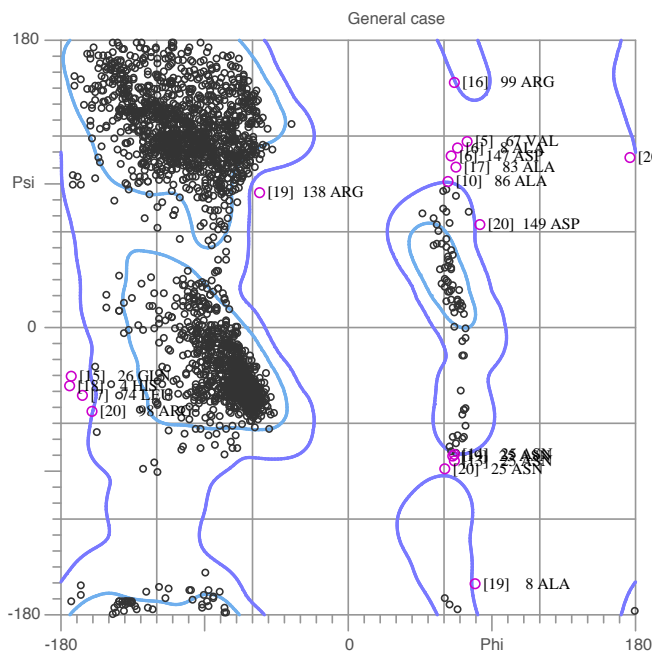


MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, all models



90.9% (2836/3120) of all residues were in favored (98%) regions.
98.4% (3071/3120) of all residues were in allowed (>99.8%) regions.

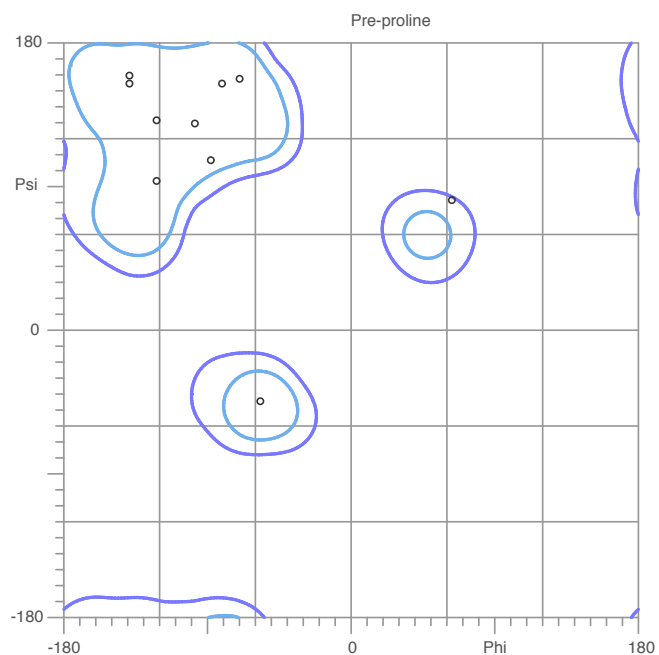
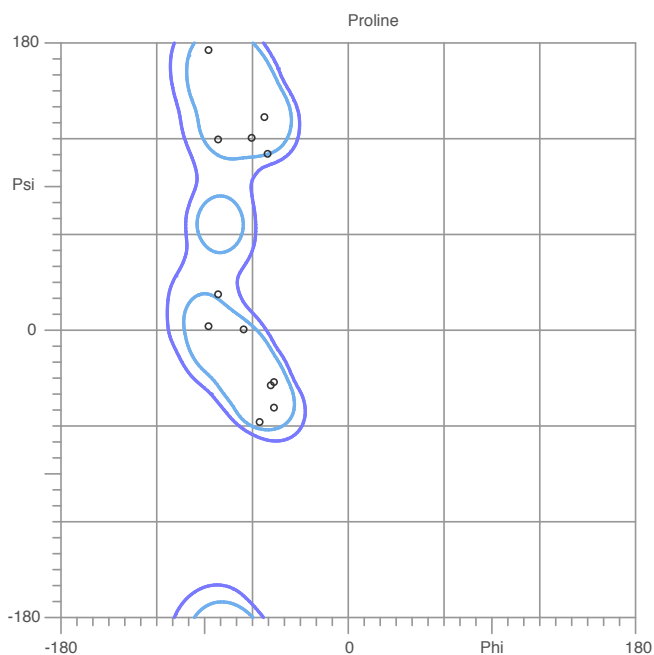
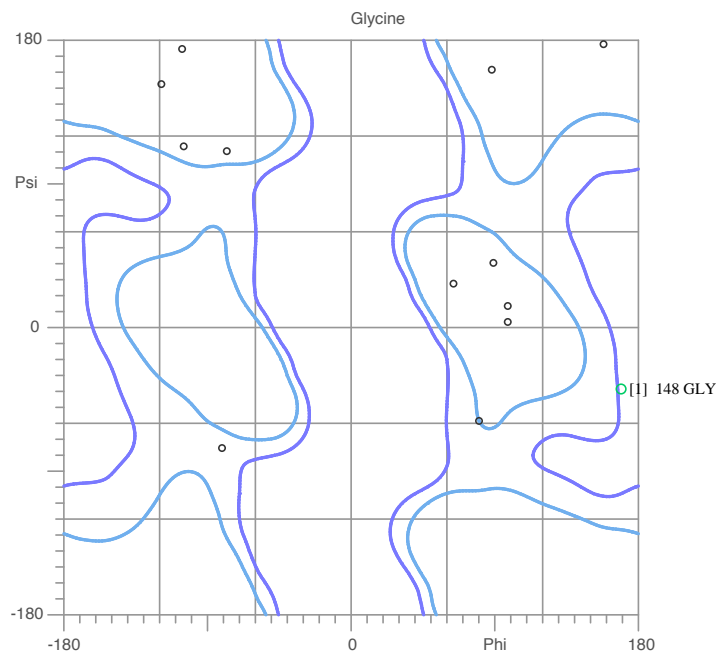
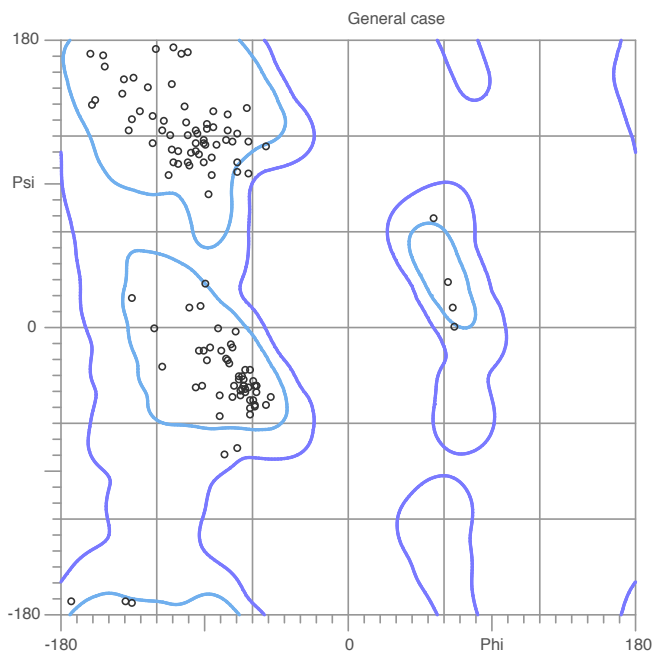
There were 49 outliers (phi, psi):

- [1] 148 GLY (169.1, -38.6)
- [2] 77 PRO (-53.8, 86.9)
- [3] 69 ASP (169.1, -44.8)
- [4] 69 ASP (-168.5, -57.6)
- [5] 85 PRO (-86.5, -157.4)
- [6] 18 GLY (-151.8, -90.0)
- [7] 148 GLY (167.4, -5.4)
- [8] 6 ASP (59.2, 90.7)
- [9] 18 GLY (-165.9, -29.6)
- [10] 67 VAL (74.2, 117.7)
- [11] 77 PRO (-14.1, 75.6)
- [12] 8 ALA (68.9, 113.7)
- [13] 147 ASP (64.6, 108.2)
- [14] 74 LEU (-167.8, -42.4)
- [15] 76 GLU (65.9, 106.7)
- [16] 148 GLY (165.4, -5.5)
- [17] 146 PRO (-94.1, -154.0)
- [18] 6 ASP (70.2, 89.6)
- [19] 49 PRO (-68.4, 33.9)
- [20] 69 ASP (71.6, 99.5)
- [21] 76 GLU (66.8, 116.7)
- [22] 86 ALA (62.4, 92.8)

- [10] 146 PRO (-86.3, -158.5)
- [11] 25 ASN (66.3, -83.8)
- [12] 82 GLY (173.6, -85.6)
- [13] 83 GLY (173.6, -85.6)
- [14] 25 ASN (66.7, -80.0)
- [15] 76 GLU (62.9, 96.0)
- [16] 26 GLN (-174.9, -30.9)
- [17] 76 GLU (66.1, 86.9)
- [18] 69 ASP (62.5, 90.6)
- [19] 99 ARG (66.3, 154.5)
- [20] 83 ALA (67.9, 101.4)
- [21] 146 PRO (-91.8, -158.1)
- [22] 148 GLY (177.6, -43.4)
- [23] 4 HIS (-175.9, -36.5)
- [24] 148 GLY (-92.4, -159.4)
- [25] 148 GLY (176.5, -14.5)
- [26] 8 ALA (79.2, -160.3)
- [27] 25 ASN (65.7, -80.5)
- [28] 69 ASP (-135.6, -86.8)
- [29] 138 ARG (-56.1, 85.3)
- [30] 7 PRO (-57.7, 95.5)
- [31] 25 ASN (60.0, -88.7)
- [32] 69 ASP (64.8, 96.8)
- [33] 74 LEU (176.9, 107.5)
- [34] 88 ALA (64.6, 158.8)
- [35] 98 ARG (-161.1, -52.6)
- [36] 146 PRO (-79.9, -157.9)
- [37] 149 ASP (82.9, 65.6)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 1



92.3% (144/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

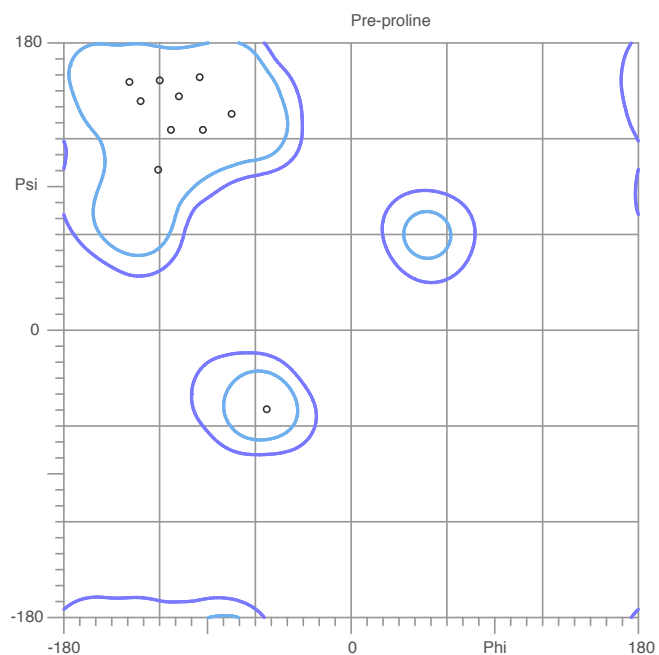
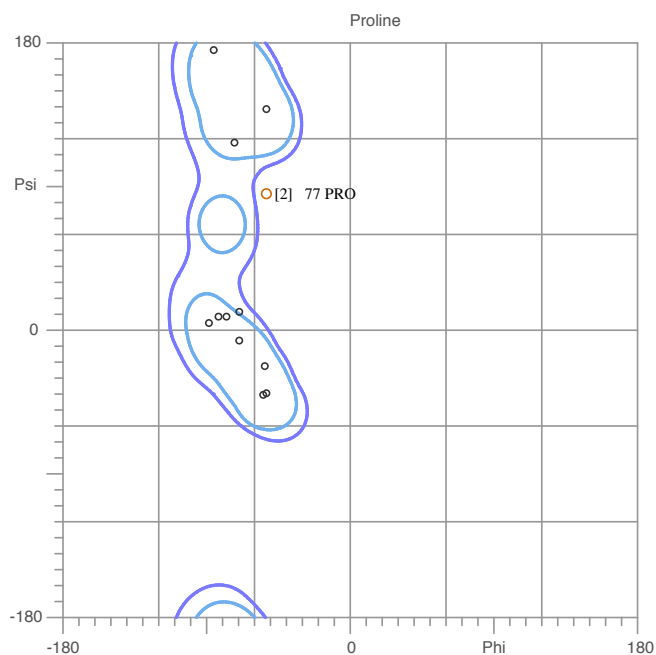
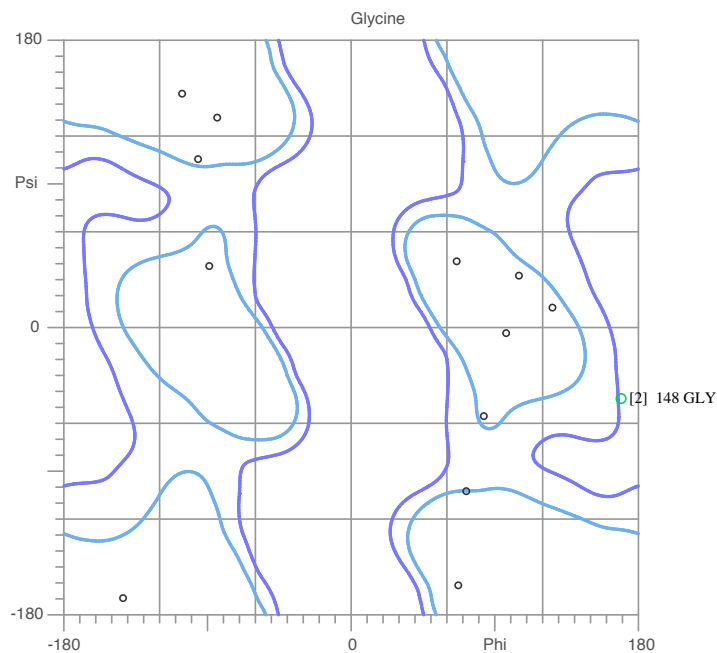
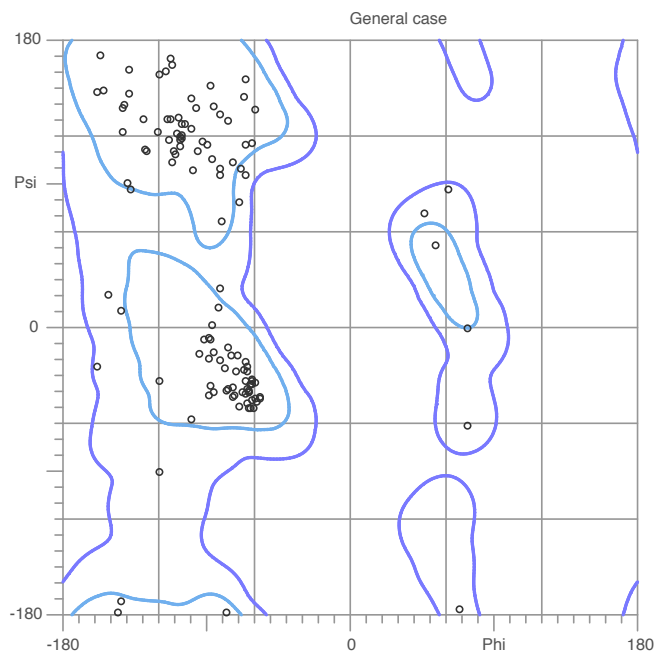
There were 1 outliers (phi, psi):
[1] 148 GLY (169.1, -38.6)

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MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 2



89.7% (140/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

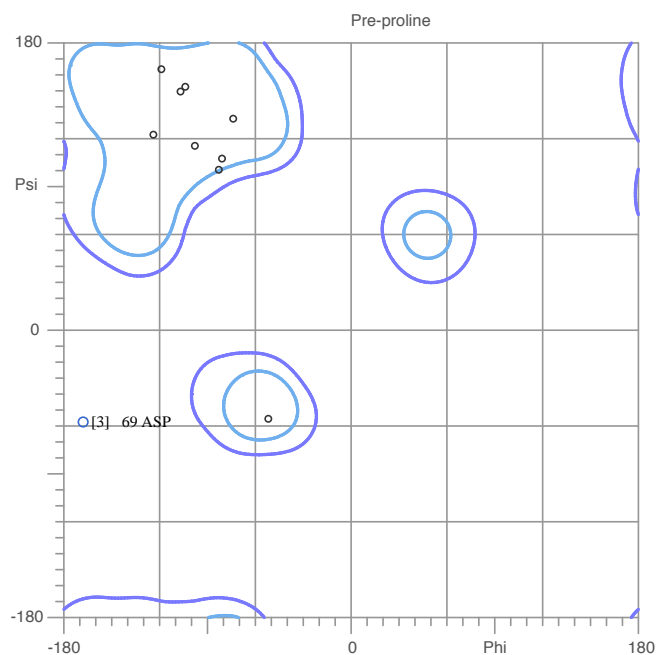
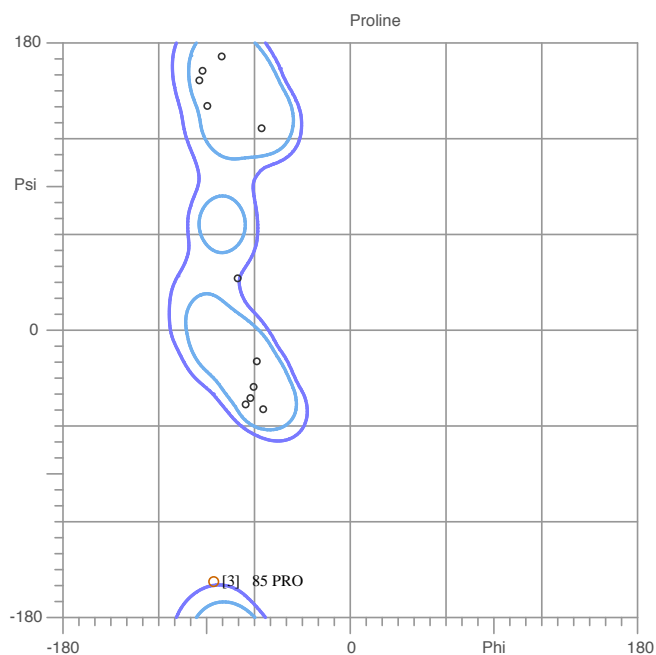
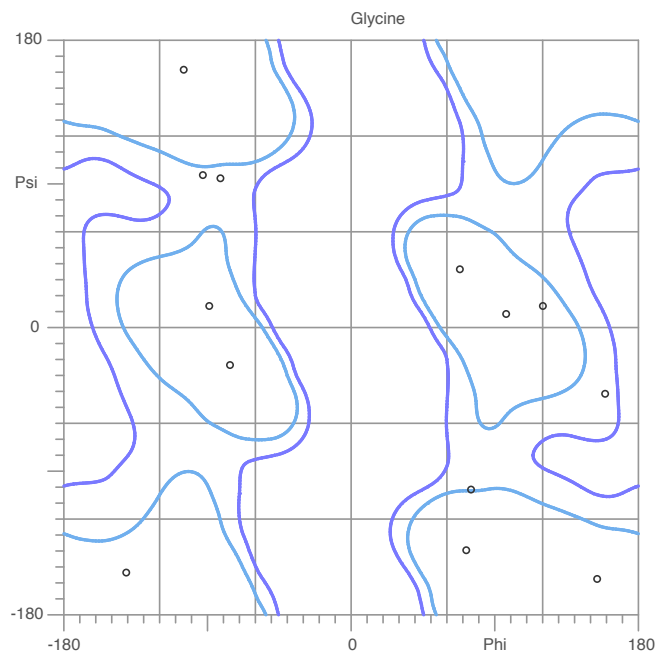
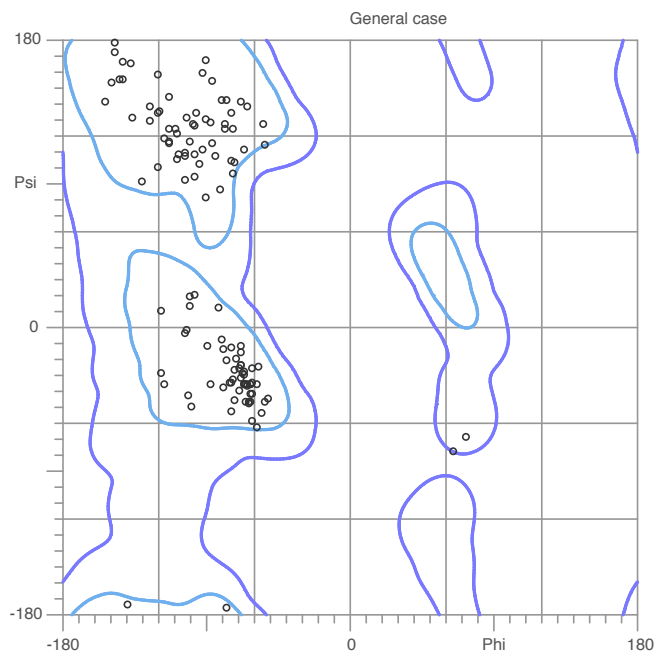
There were 2 outliers (phi, psi):

[2] 77 PRO (-53.8, 86.9)

[2] 148 GLY (169.1, -44.8)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 3



94.2% (147/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

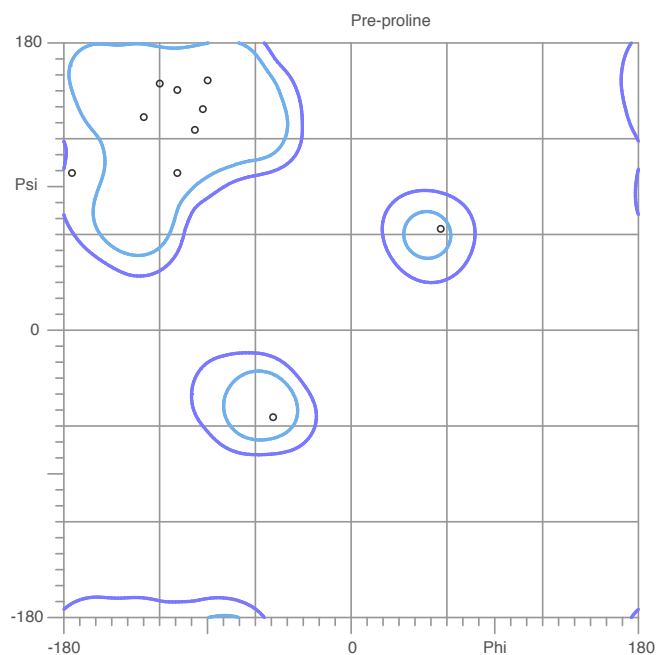
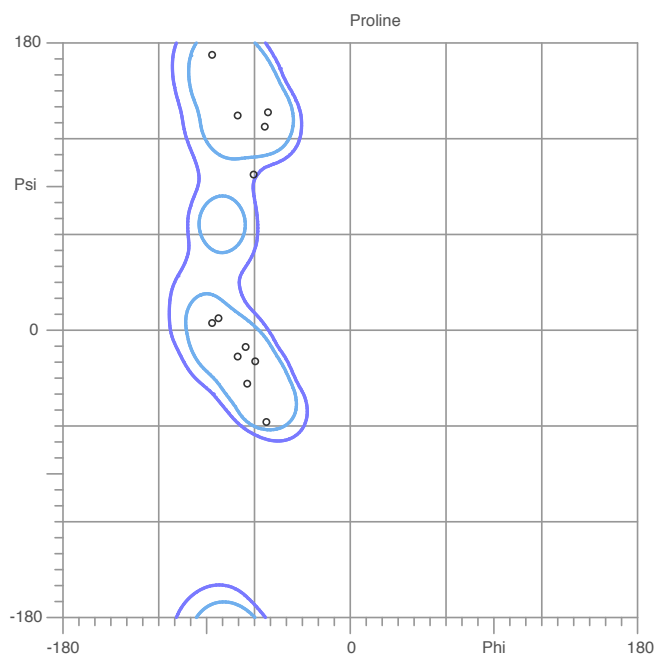
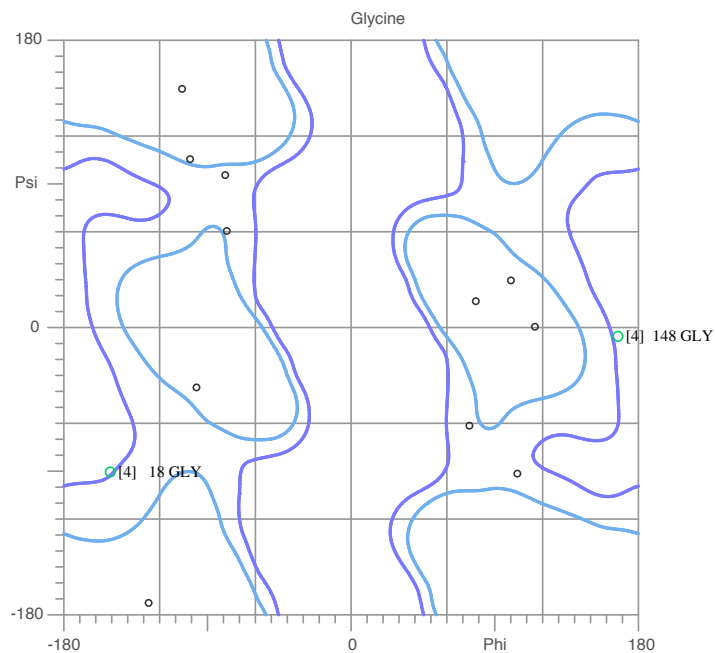
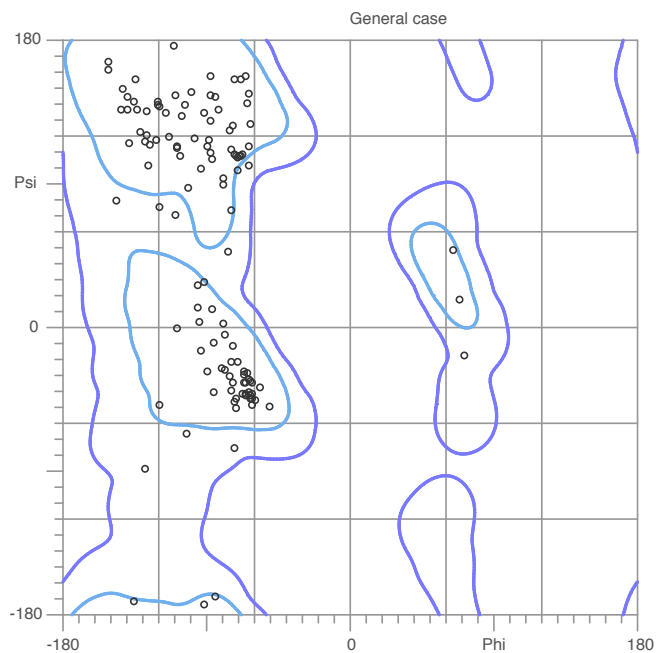
There were 2 outliers (phi, psi):

[3] 69 ASP (-168.5, -57.6)

[3] 85 PRO (-86.5, -157.4)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 4



89.1% (139/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

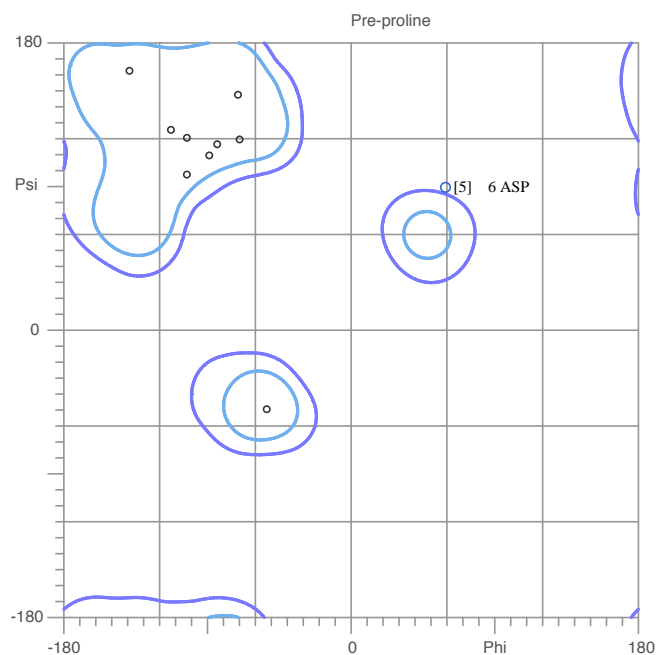
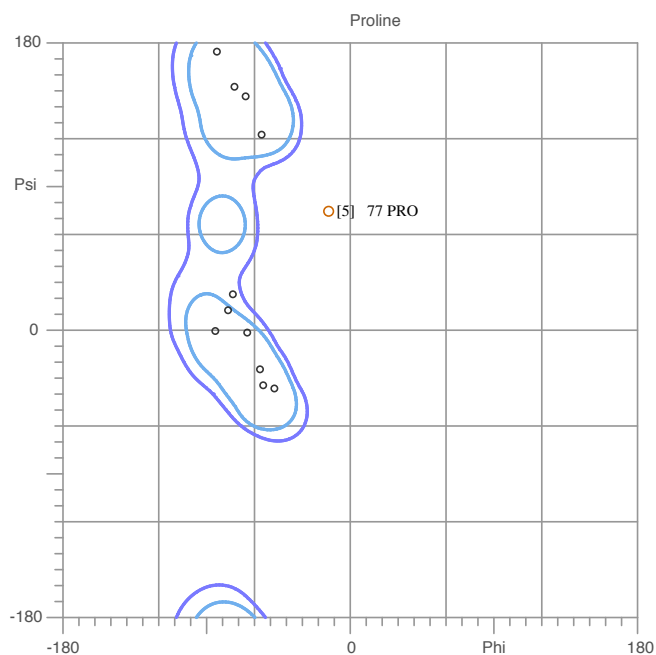
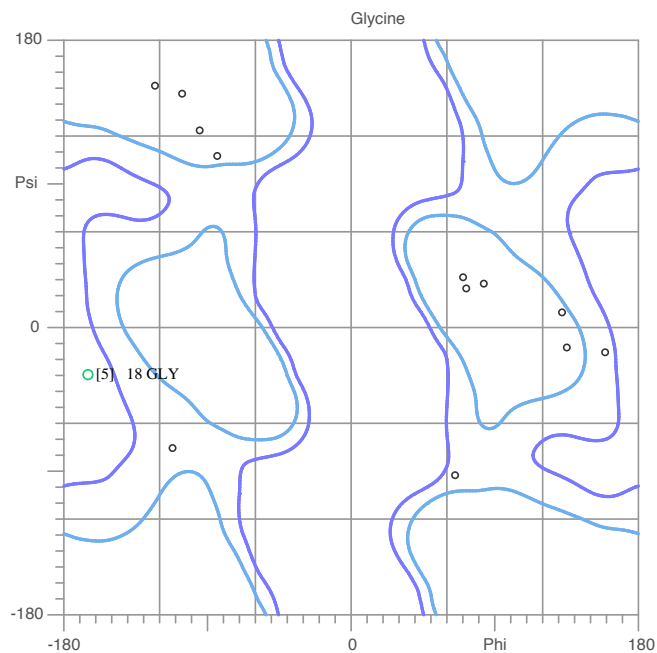
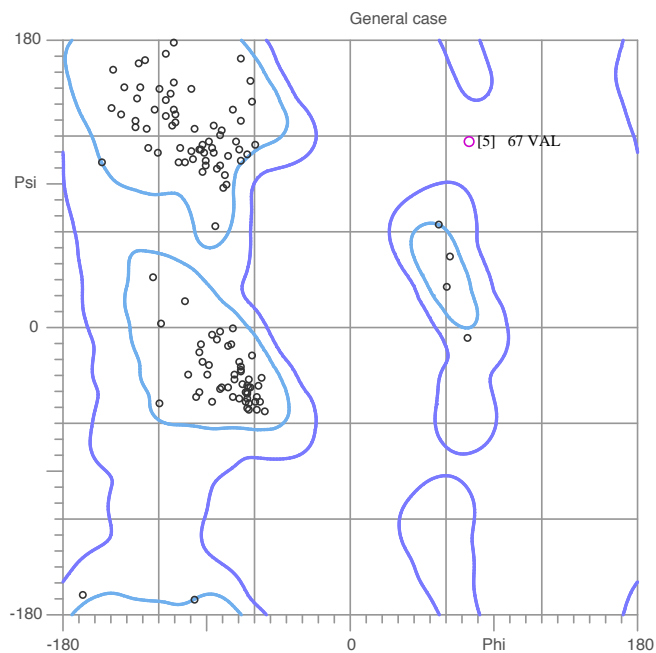
There were 2 outliers (phi, psi):

[4] 18 GLY (-151.8, -90.0)

[4] 148 GLY (167.4, -5.4)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 5



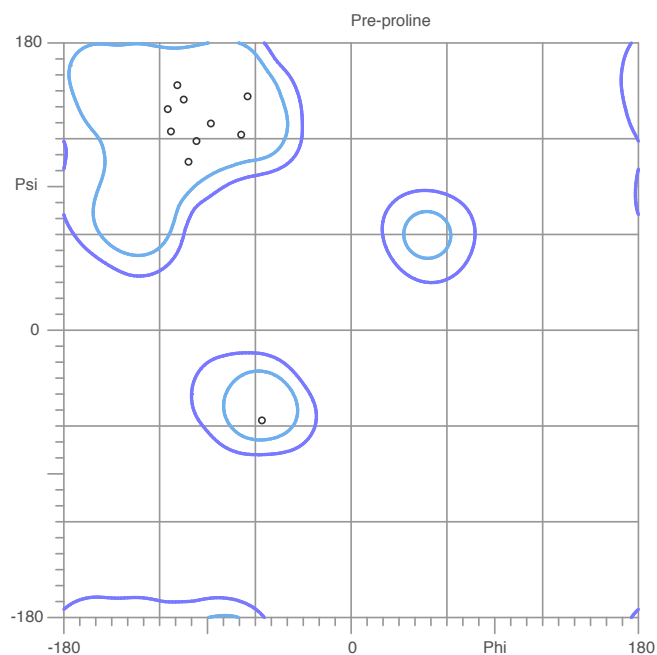
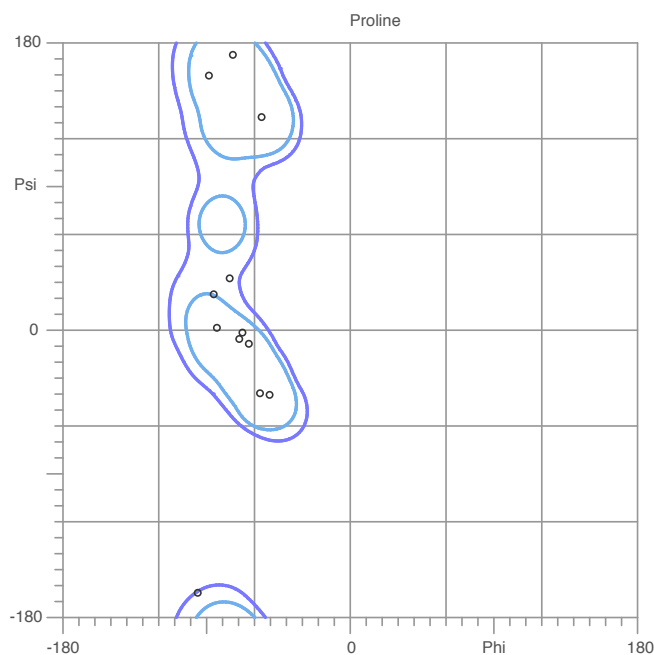
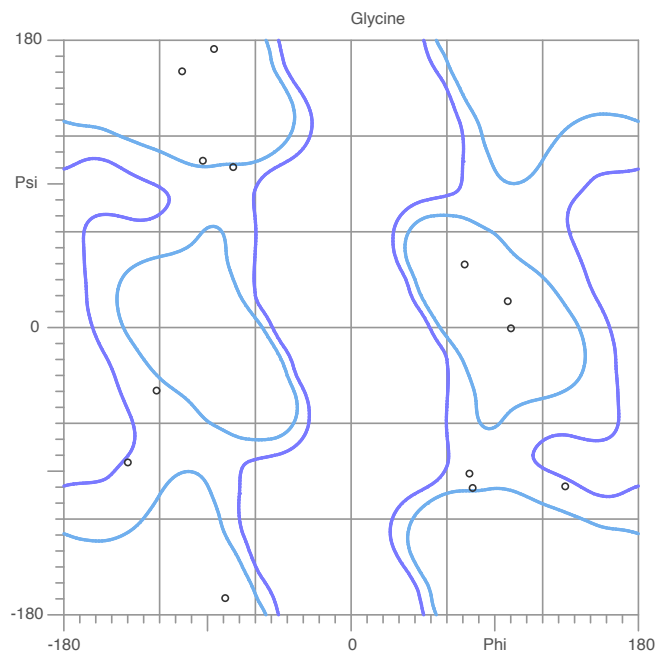
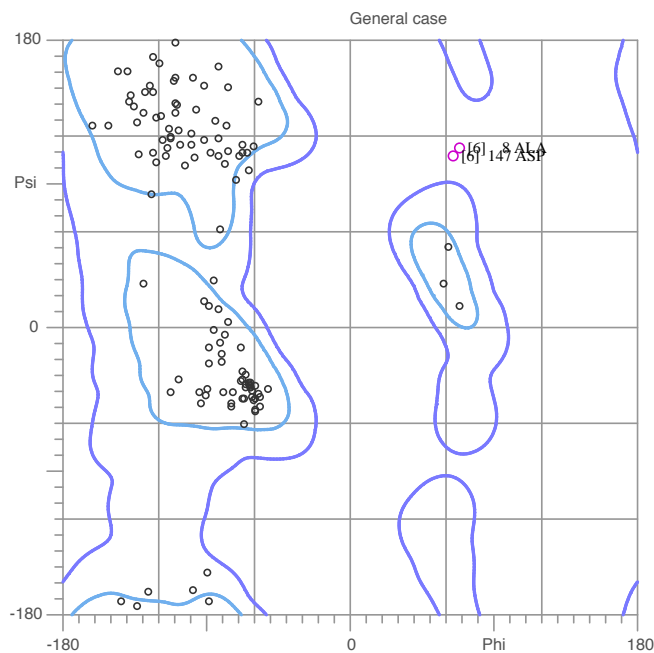
92.3% (144/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [5] 6 ASP (59.2, 90.7)
- [5] 18 GLY (-165.9, -29.6)
- [5] 67 VAL (74.2, 117.7)
- [5] 77 PRO (-14.1, 75.6)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 6



89.7% (140/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

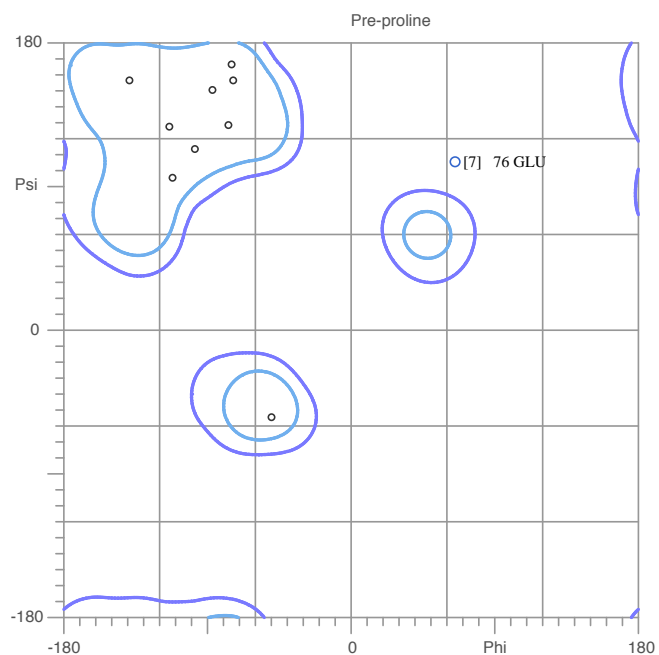
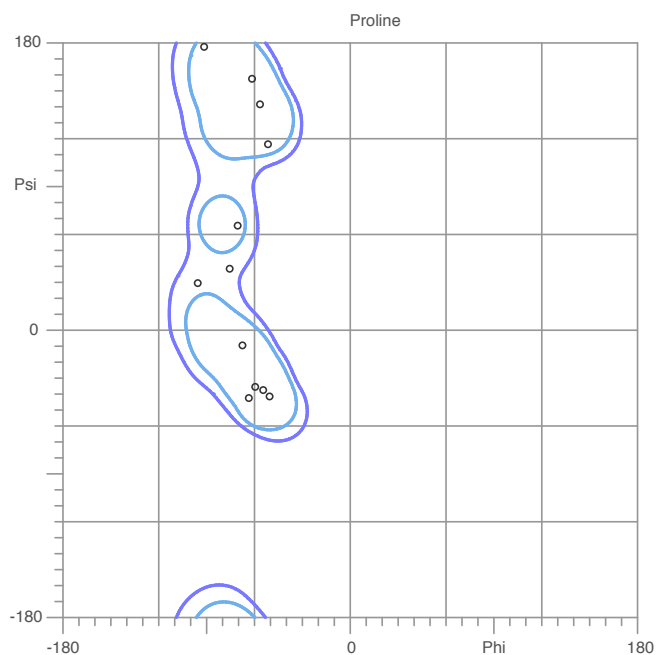
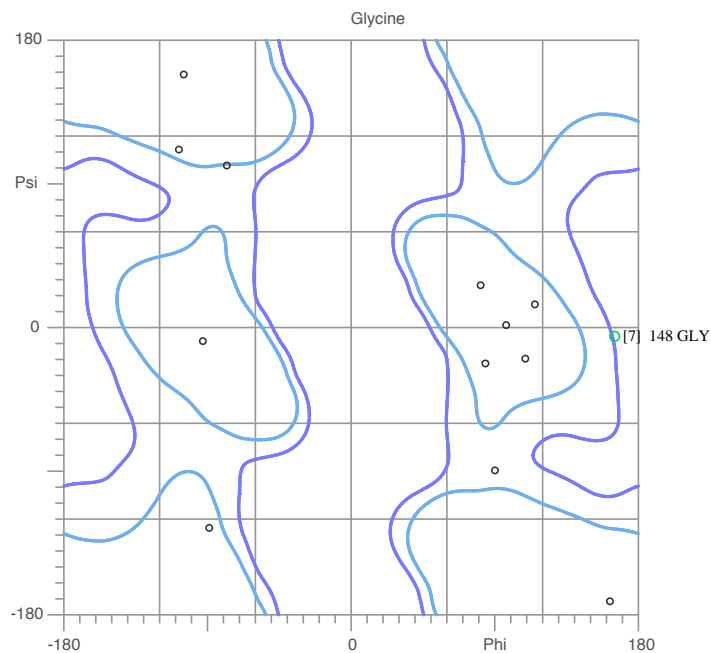
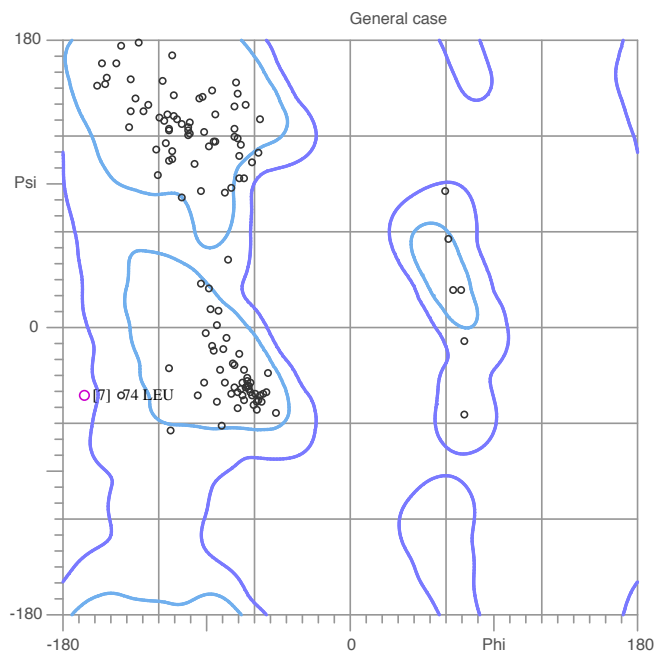
There were 2 outliers (phi, psi):

[6] 8 ALA (68.9, 113.7)

[6] 147 ASP (64.6, 108.2)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 7



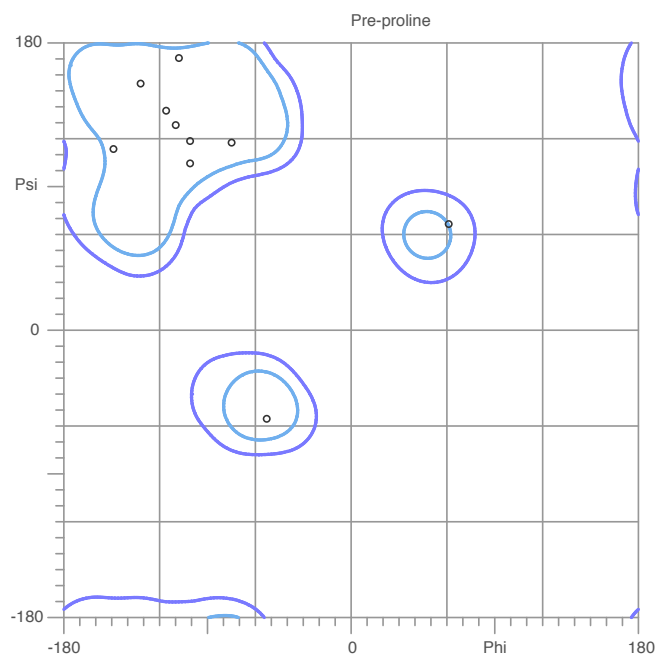
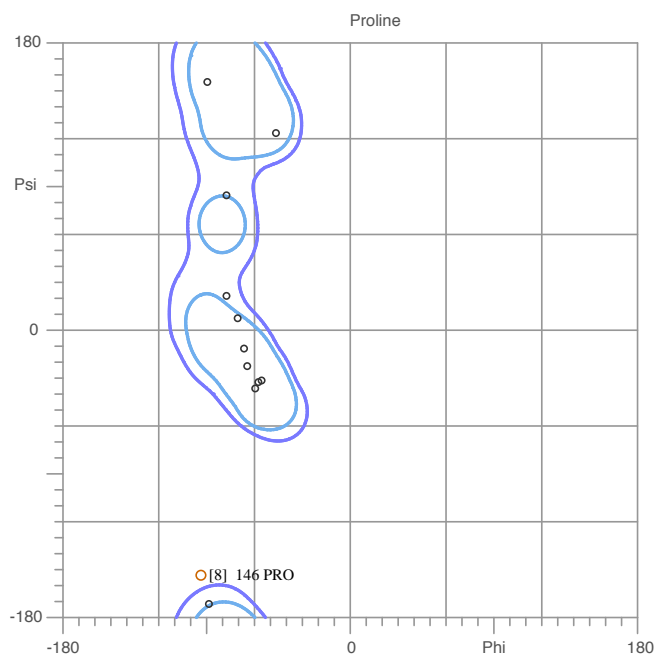
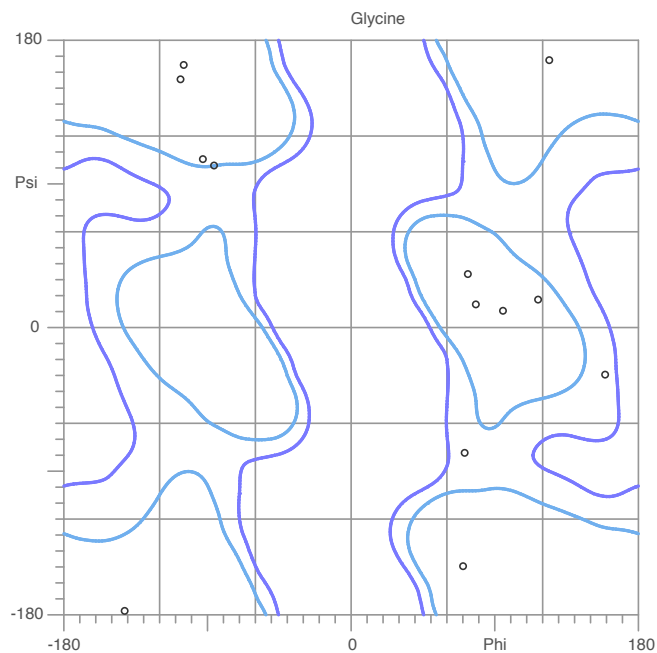
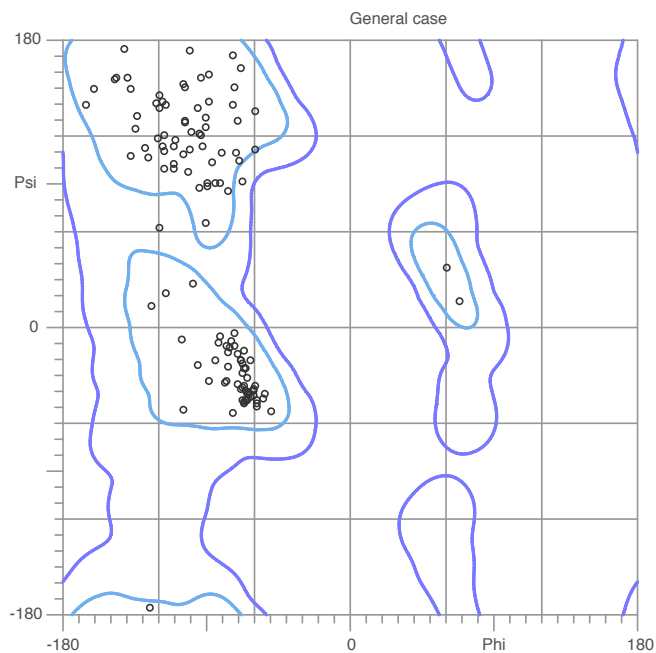
89.1% (139/156) of all residues were in favored (98%) regions.
98.1% (153/156) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [7] 74 LEU (-167.8, -42.4)
- [7] 76 GLU (65.9, 106.7)
- [7] 148 GLY (165.4, -5.5)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 8

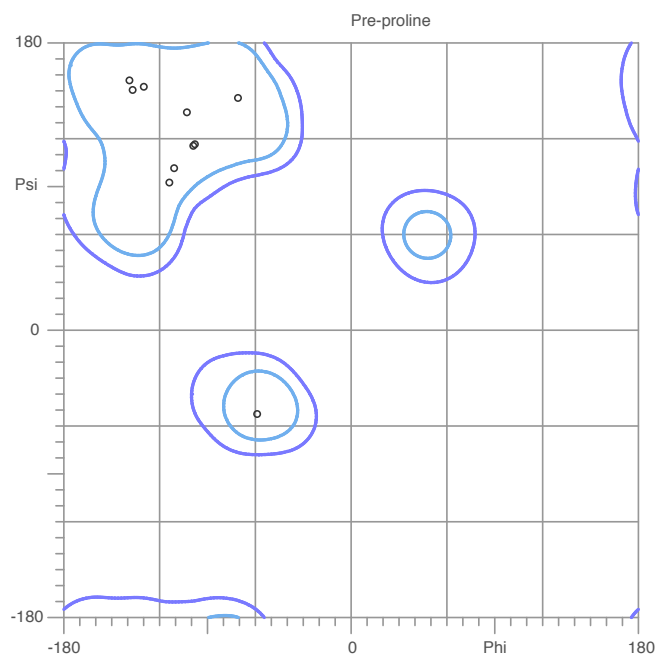
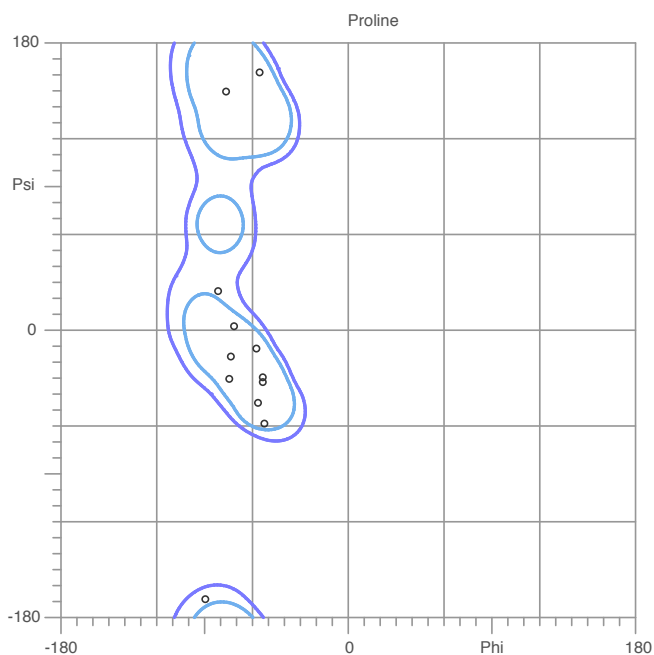
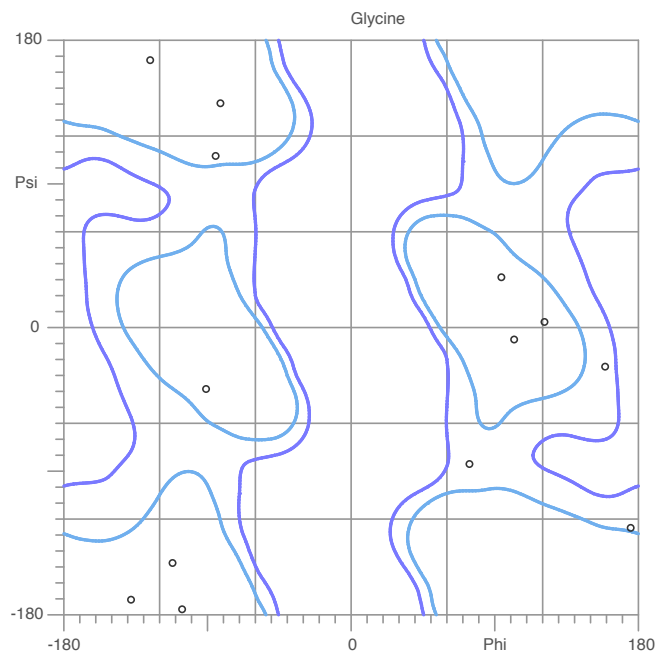
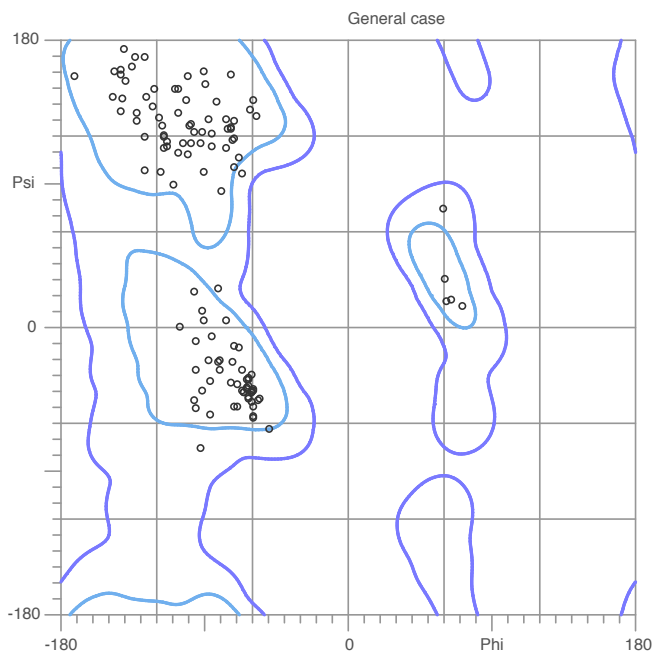


94.2% (147/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 146 PRO (-94.1, -154.0)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 9



94.2% (147/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

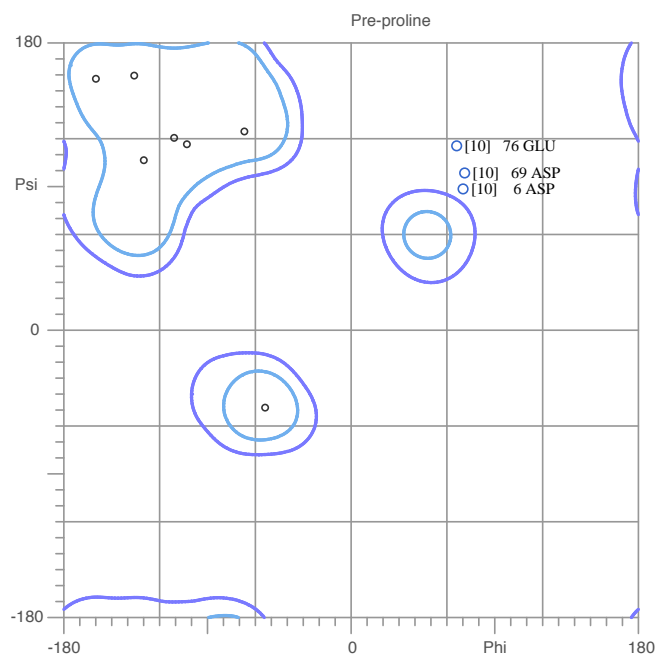
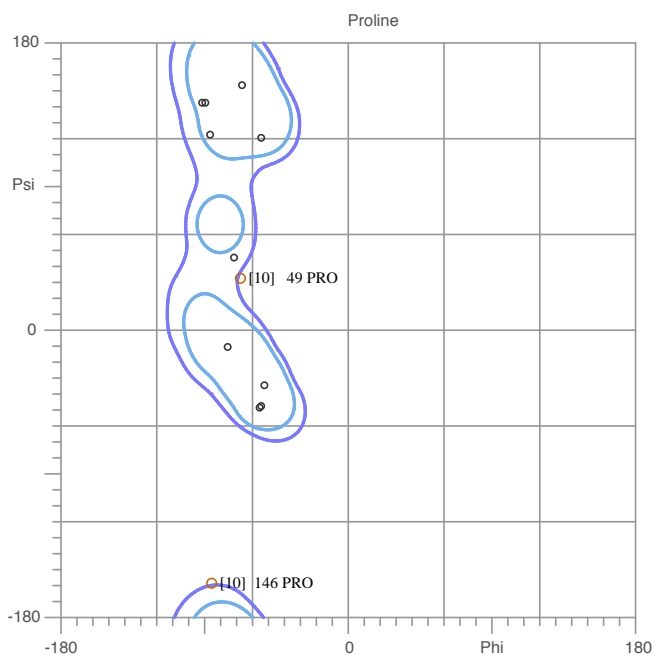
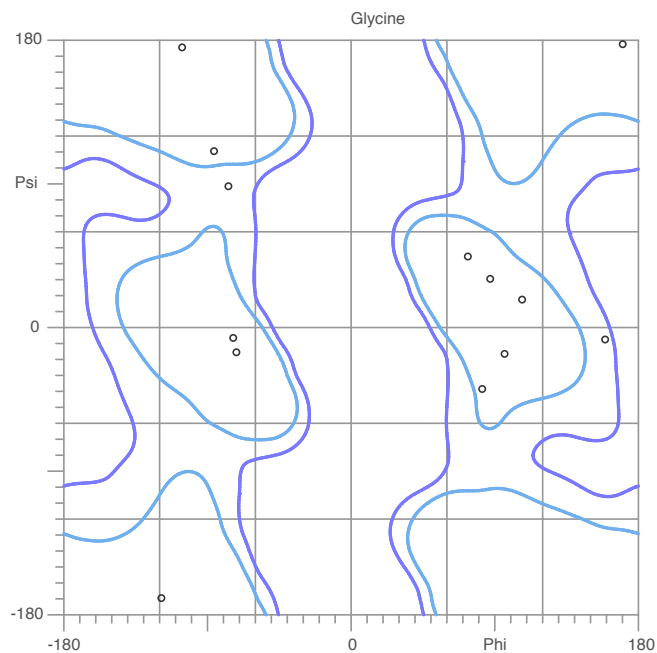
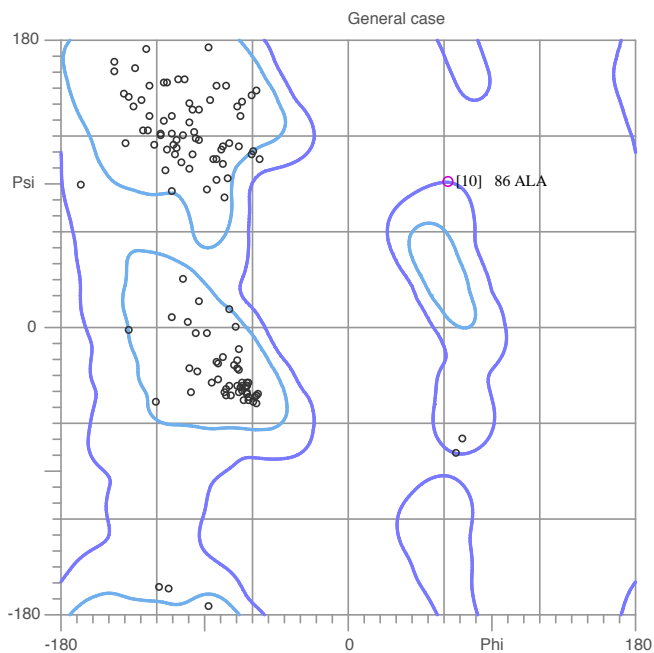
There were no outliers.

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BER31_NMR_em_bcr3.pdb, model 10



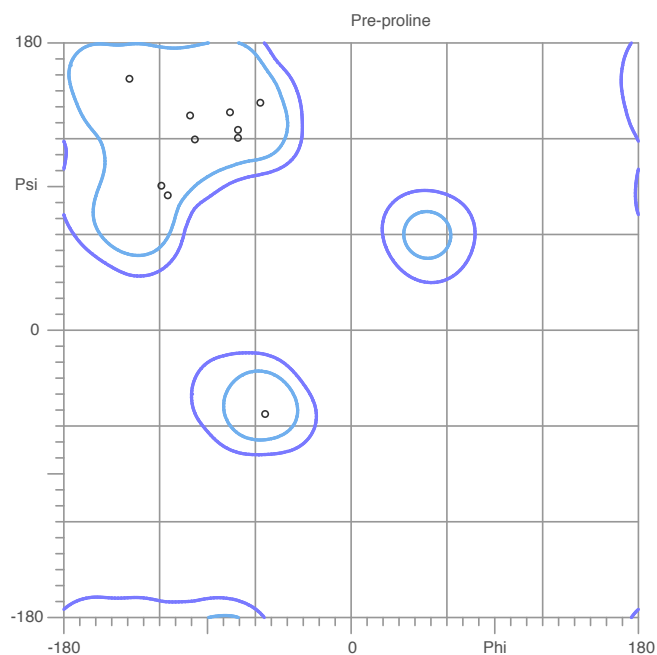
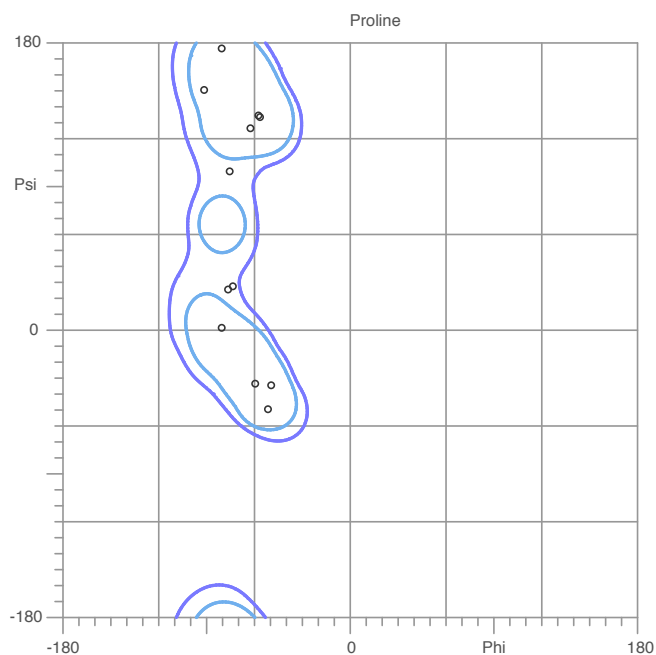
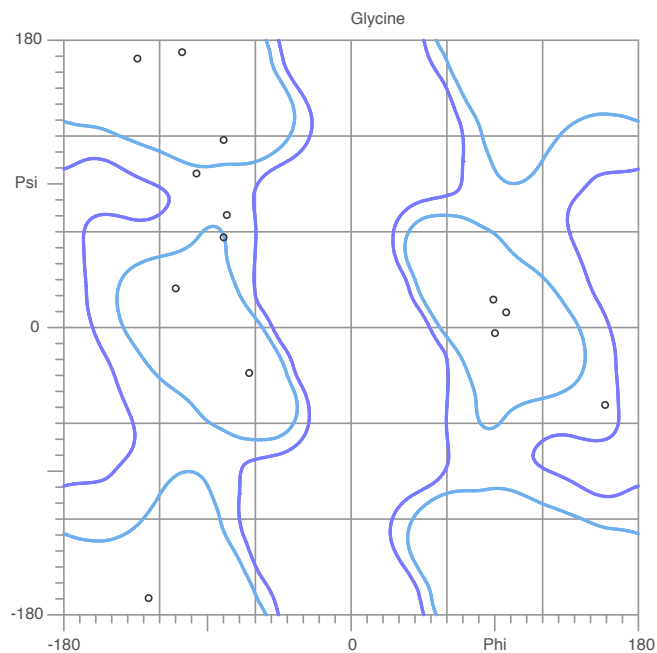
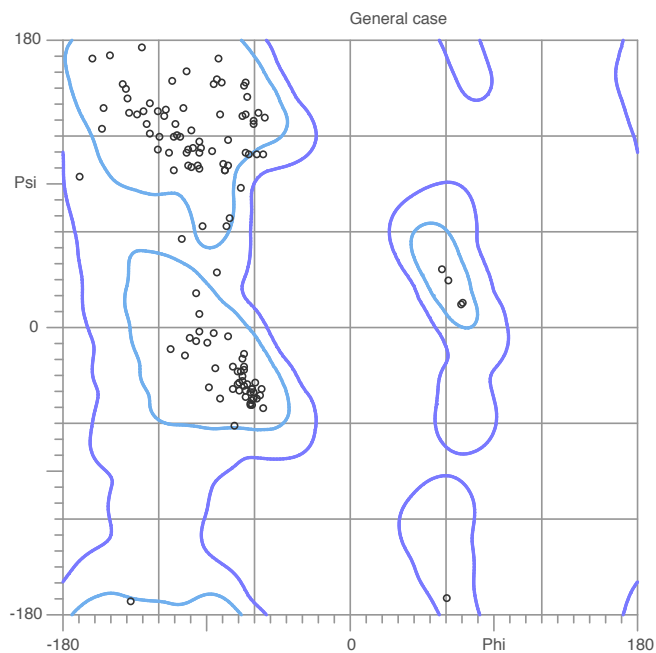
89.7% (140/156) of all residues were in favored (98%) regions.
96.2% (150/156) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[10] 6 ASP (70.2, 89.6)

[10] 49 PRO (-68.4, 33.9)
[10] 69 ASP (71.6, 99.5)
[10] 76 GLU (66.8, 116.7)
[10] 86 ALA (62.4, 92.8)
[10] 146 PRO (-86.3, -158.5)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 11



91.7% (143/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

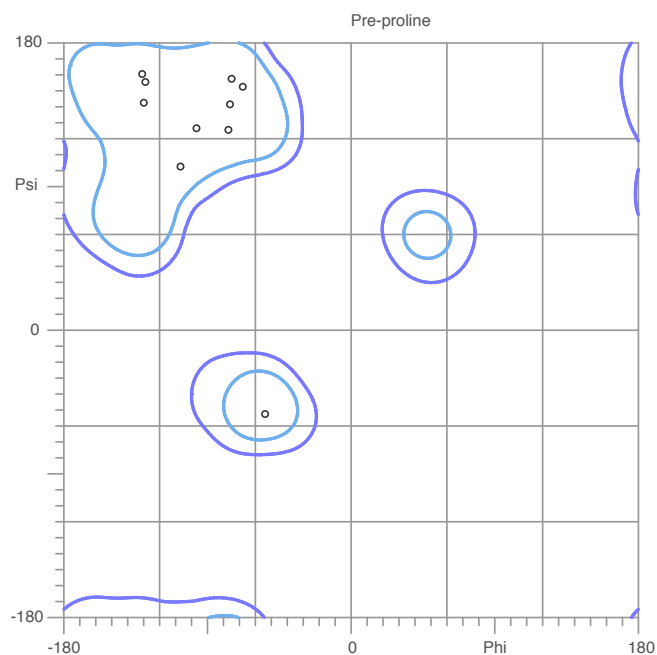
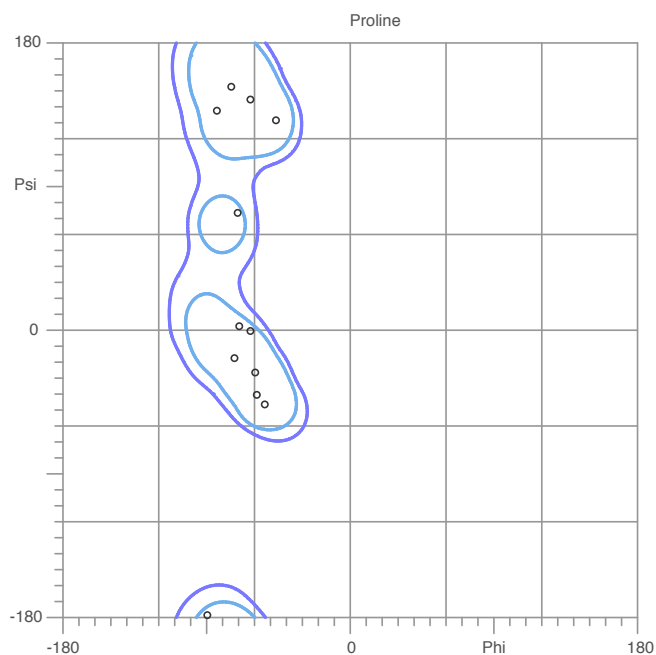
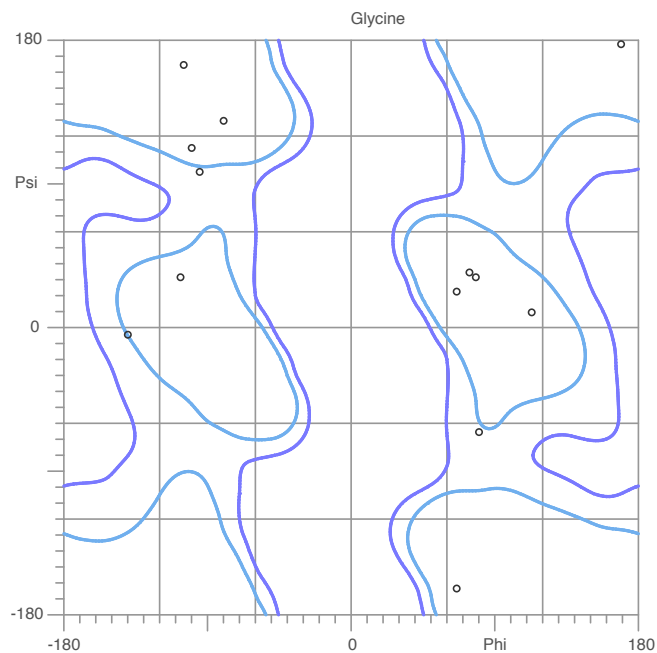
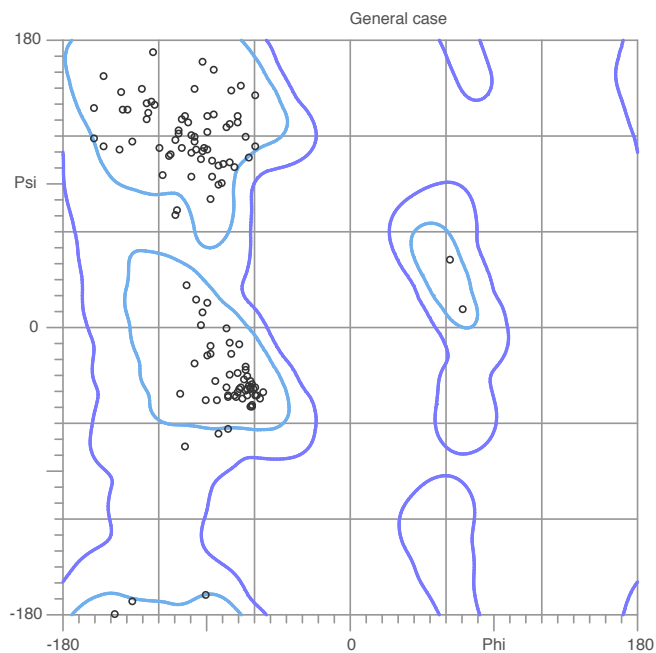
There were no outliers.

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MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 12



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.

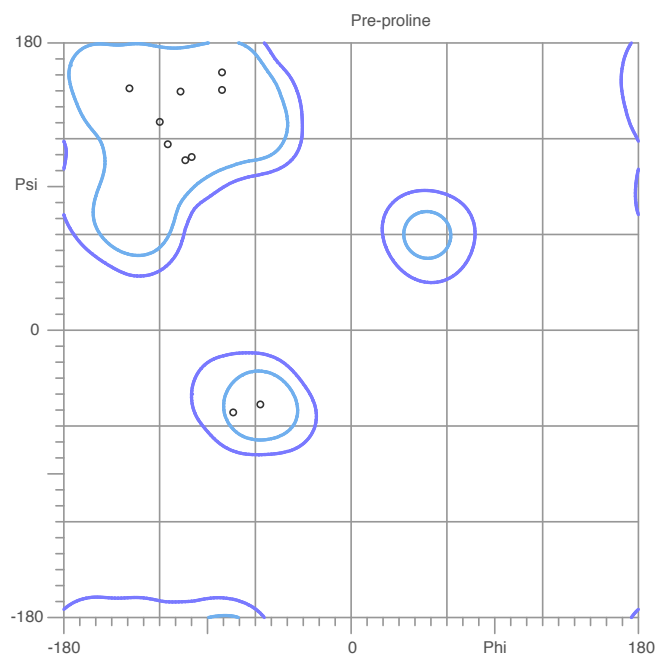
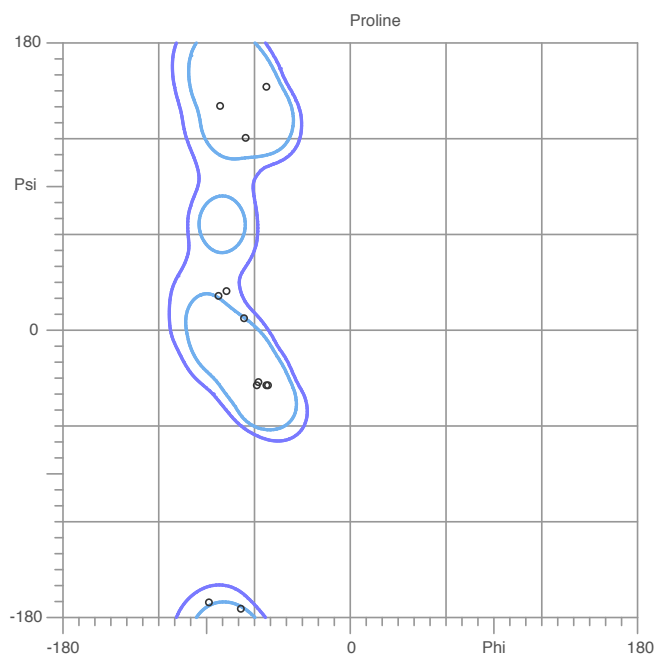
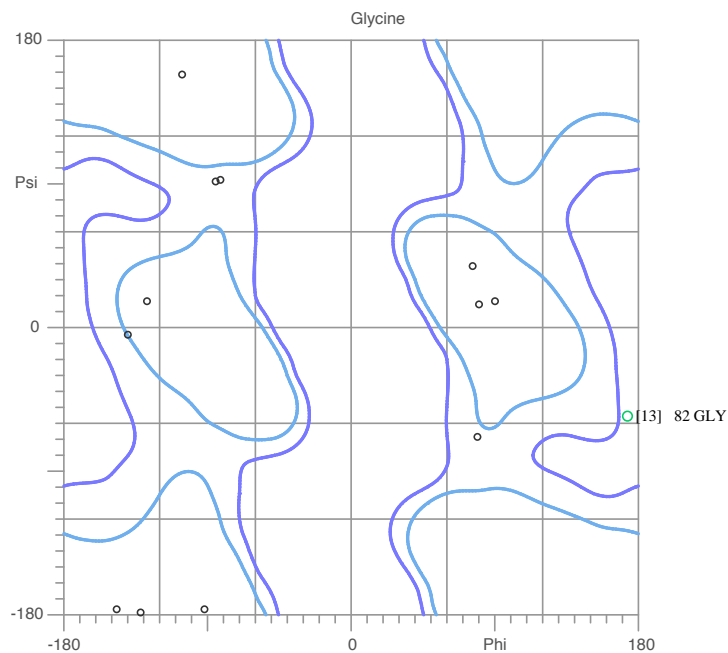
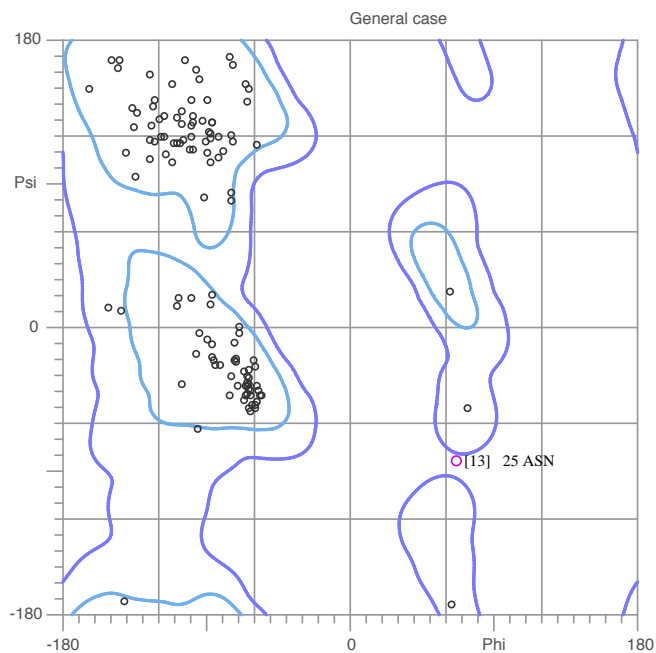
There were no outliers.

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

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MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 13

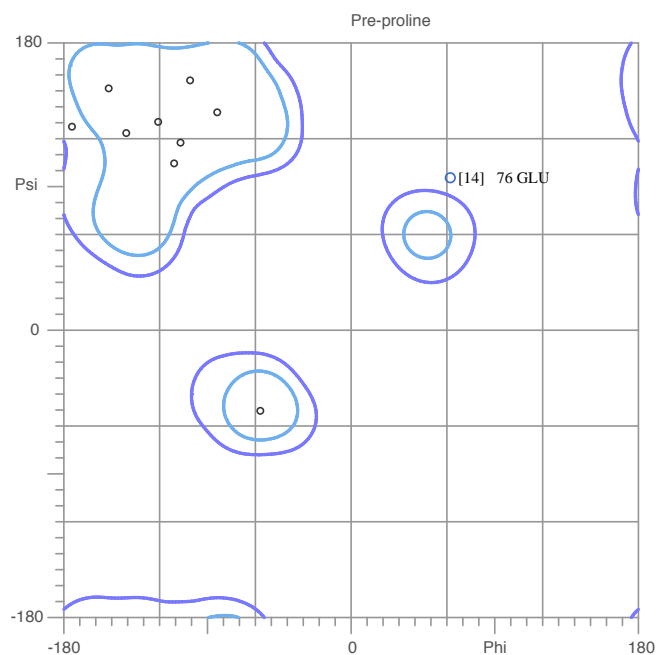
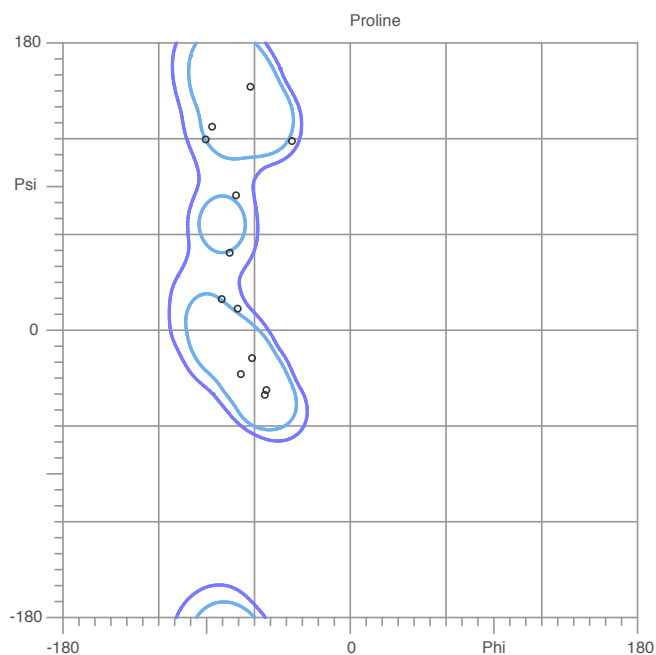
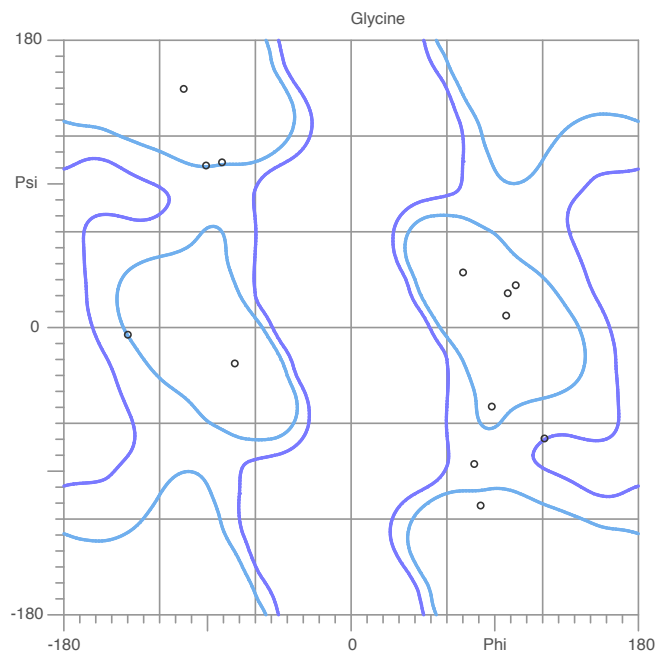
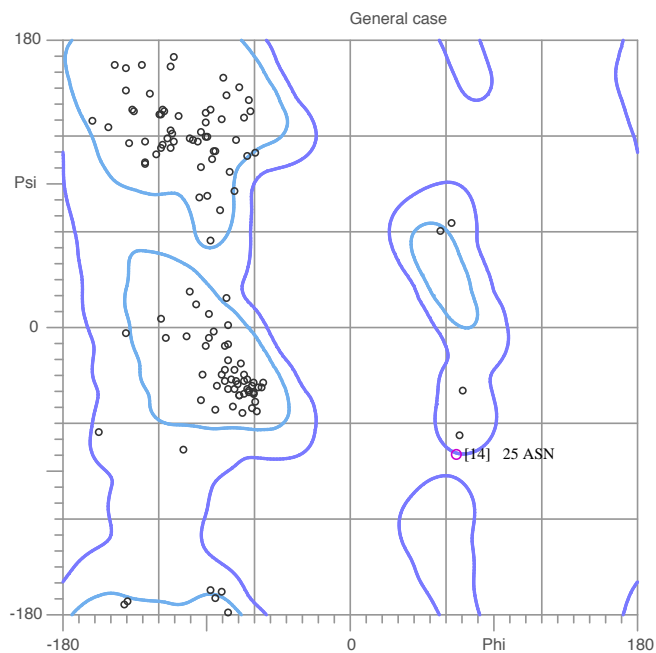


91.7% (143/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[13] 25 ASN (66.3, -83.8)
[13] 82 GLY (173.6, -55.6)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 14



87.8% (137/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

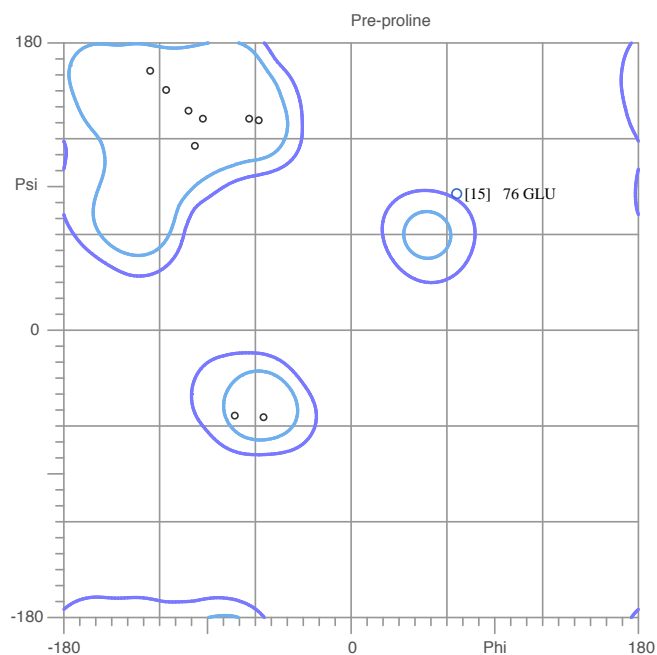
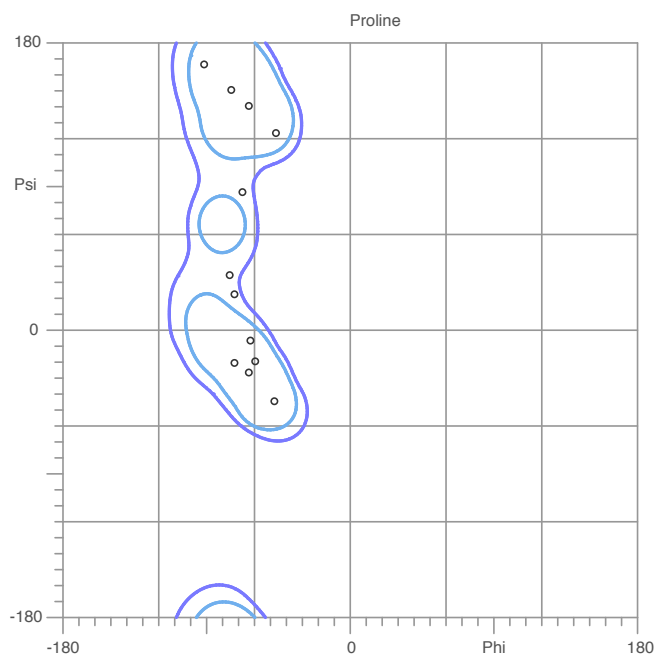
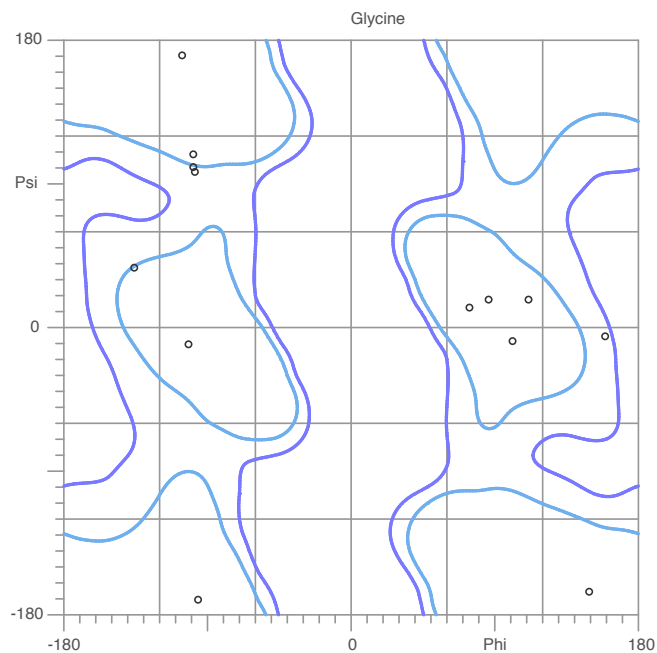
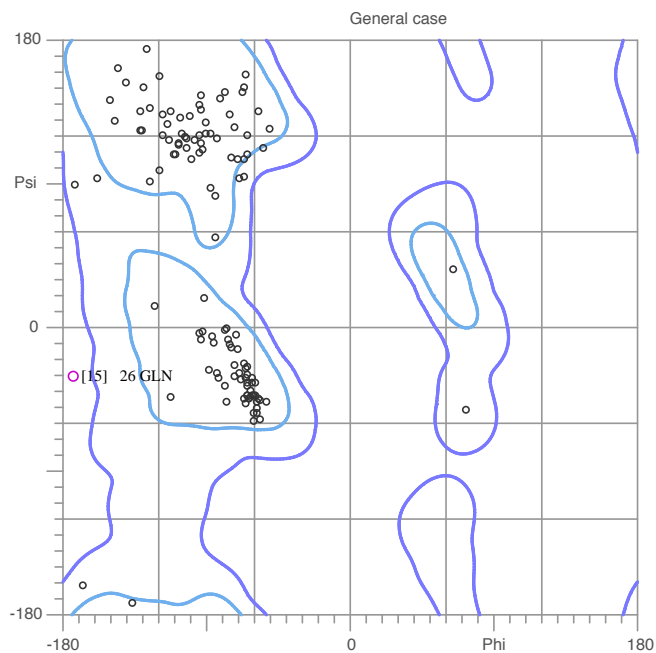
There were 2 outliers (phi, psi):

[14] 25 ASN (66.7, -80.0)

[14] 76 GLU (62.9, 96.0)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 15

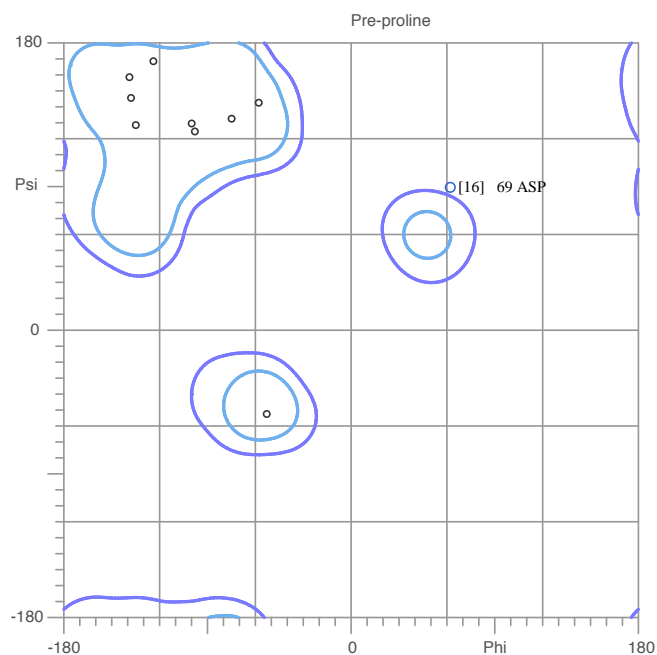
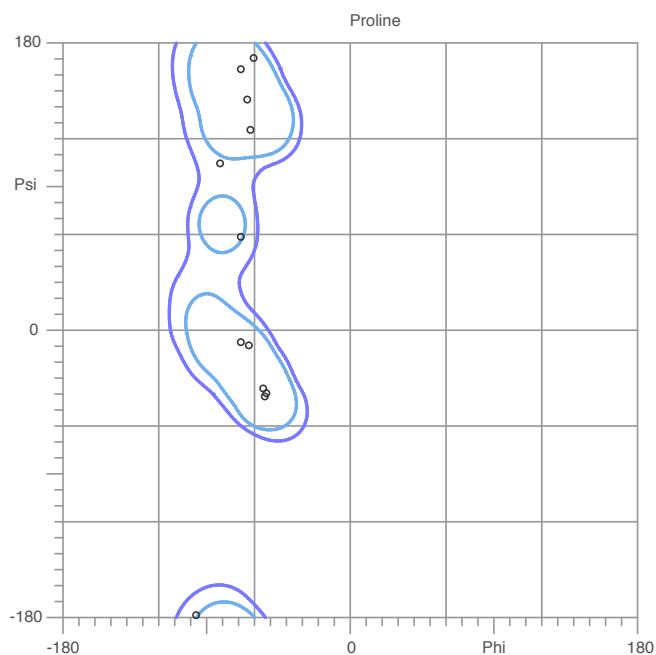
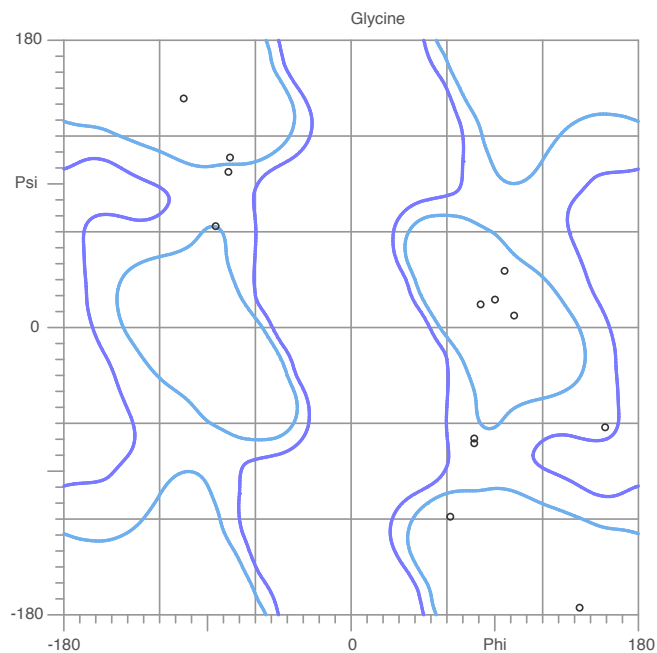
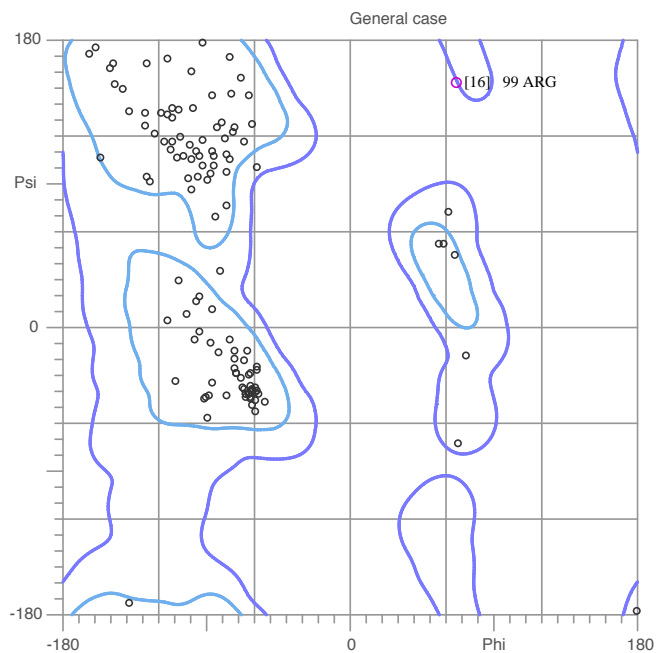


91.0% (142/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[15] 26 GLN (-174.9, -30.9)
[15] 76 GLU (66.1, 86.9)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 16



90.4% (141/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

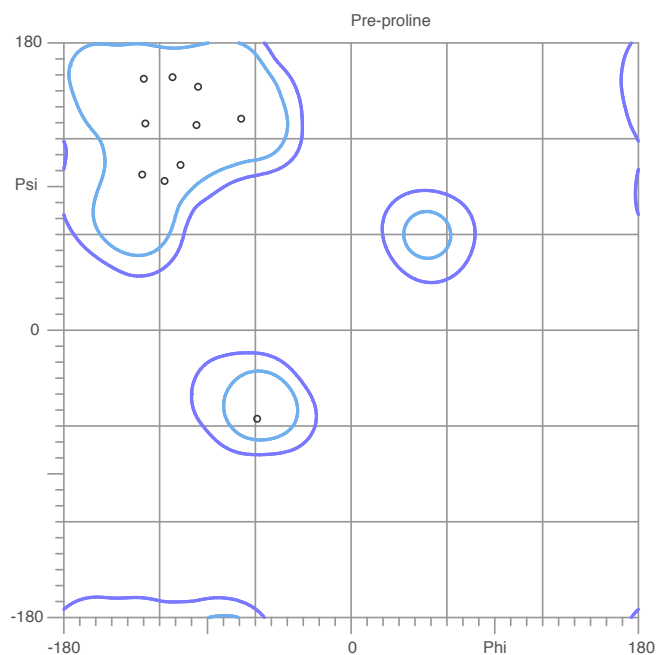
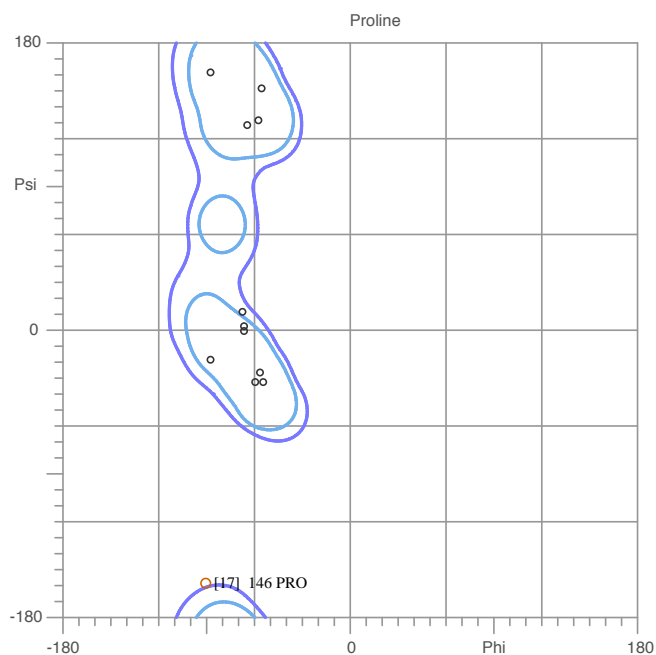
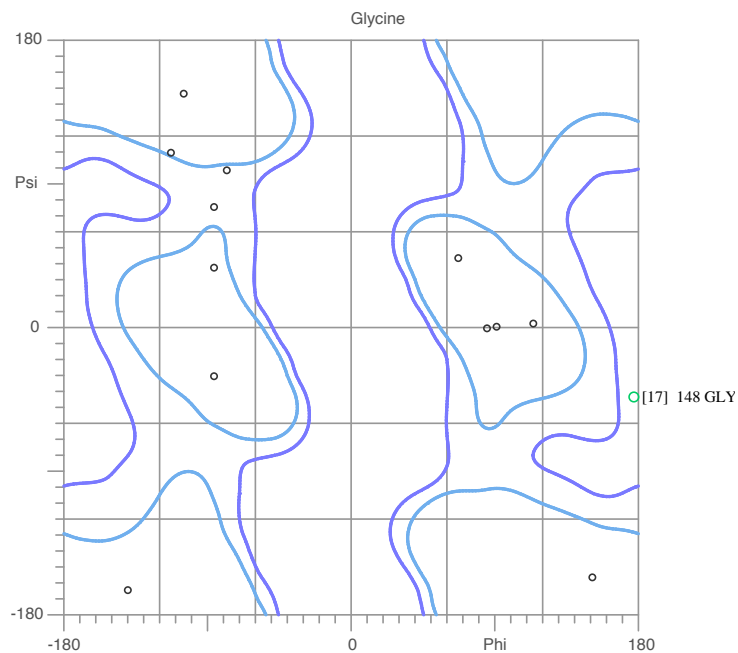
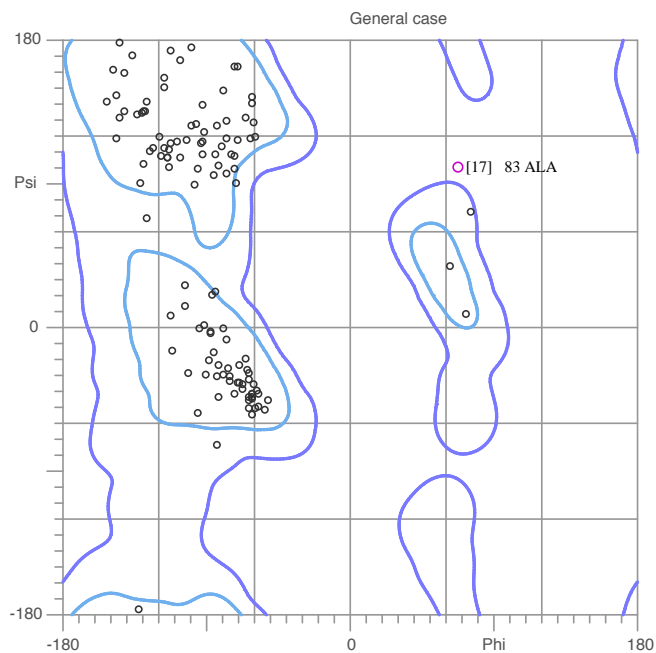
There were 2 outliers (phi, psi):

[16] 69 ASP (62.5, 90.6)

[16] 99 ARG (66.3, 154.5)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 17



92.9% (145/156) of all residues were in favored (98%) regions.
98.1% (153/156) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

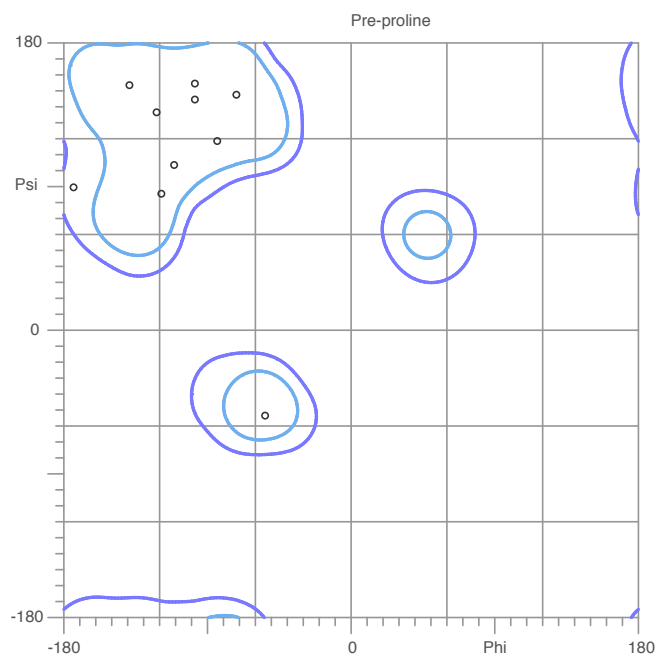
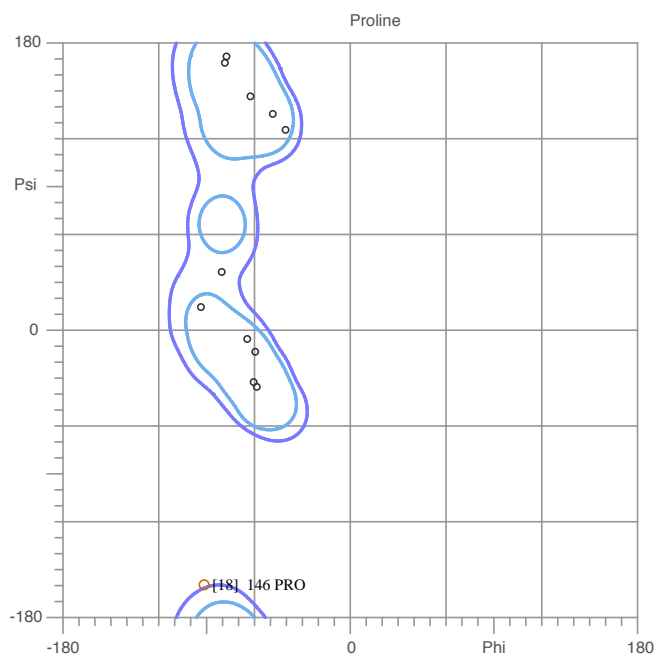
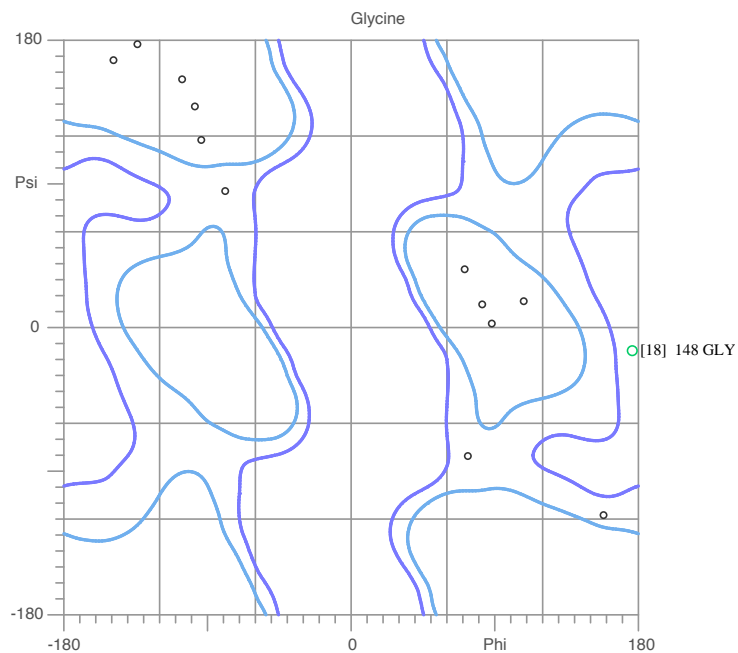
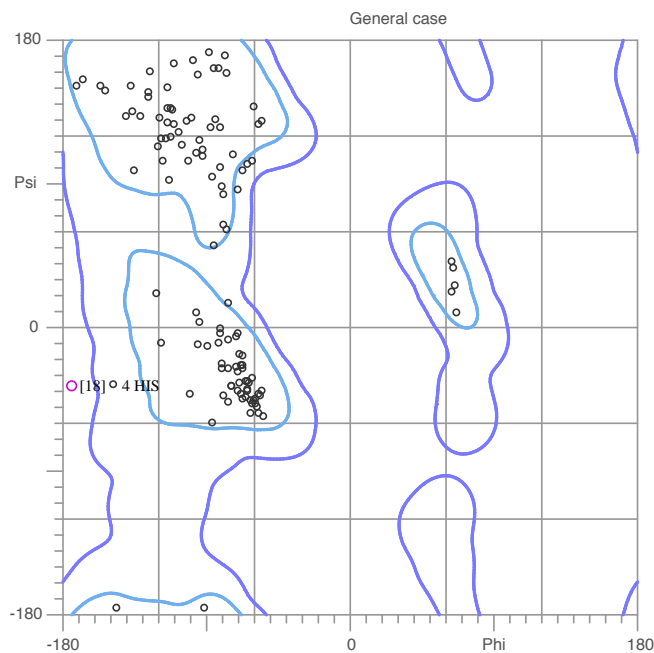
[17] 83 ALA (67.9, 101.4)

[17] 146 PRO (-91.8, -158.1)

[17] 148 GLY (177.6, -43.4)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 18



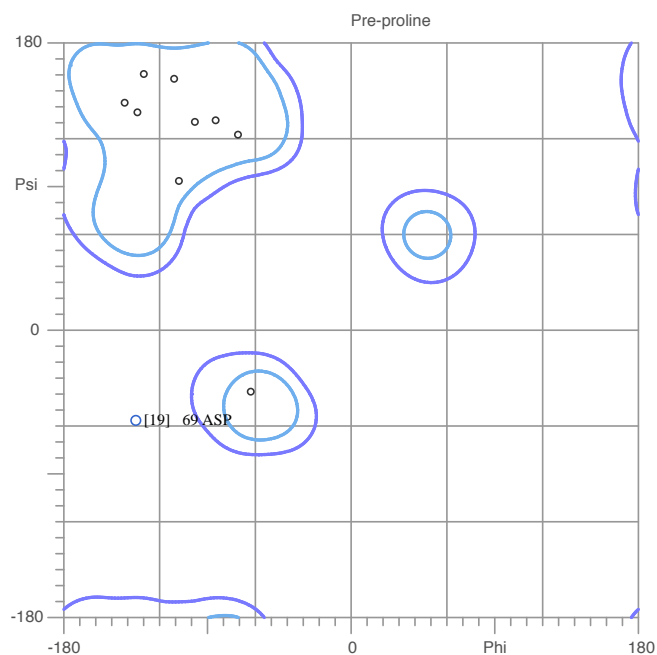
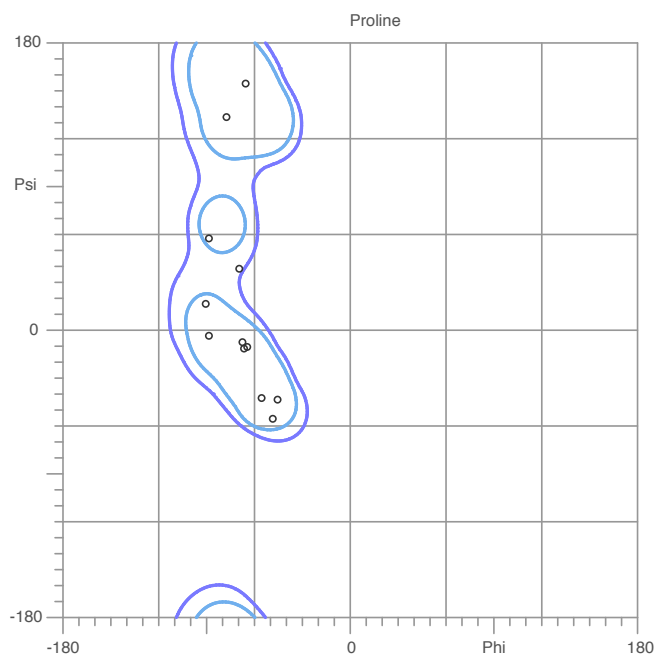
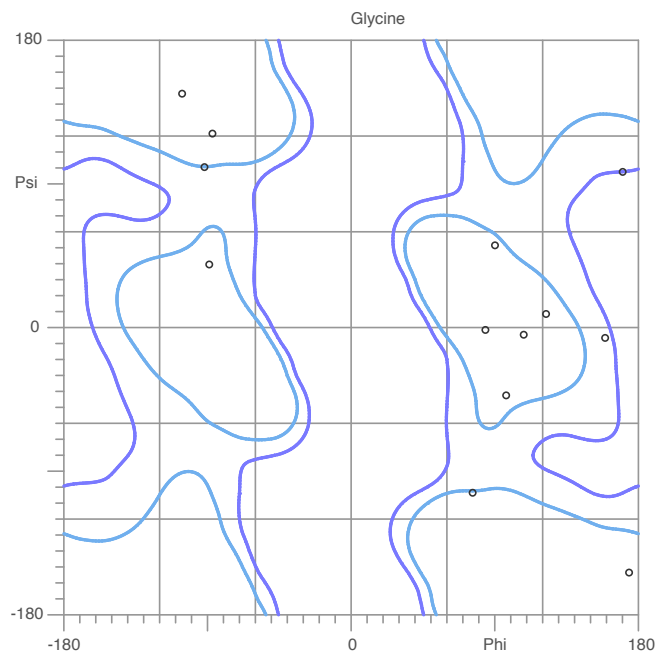
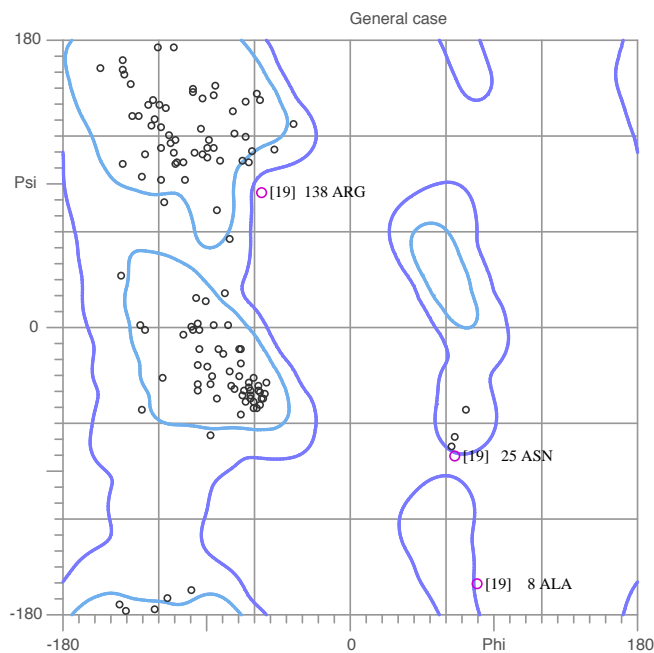
91.0% (142/156) of all residues were in favored (98%) regions.
98.1% (153/156) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [18] 4 HIS (-175.9, -36.5)
- [18] 146 PRO (-92.4, -159.4)
- [18] 148 GLY (176.5, -14.5)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 19



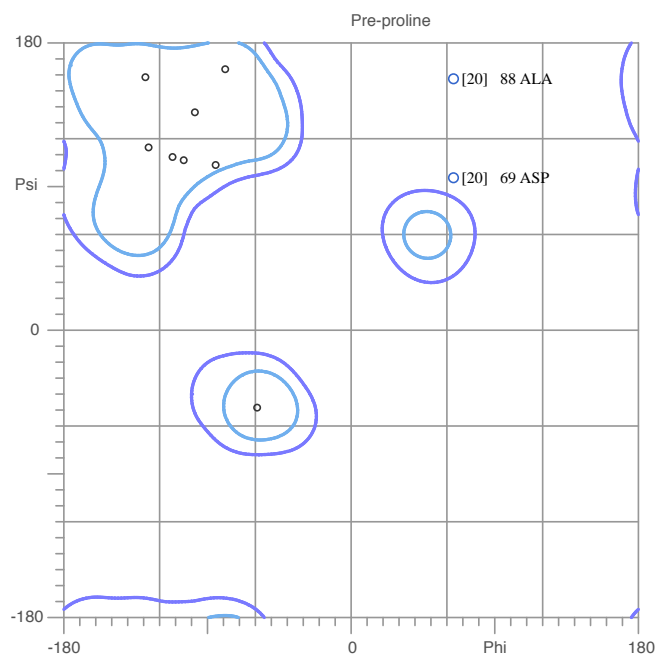
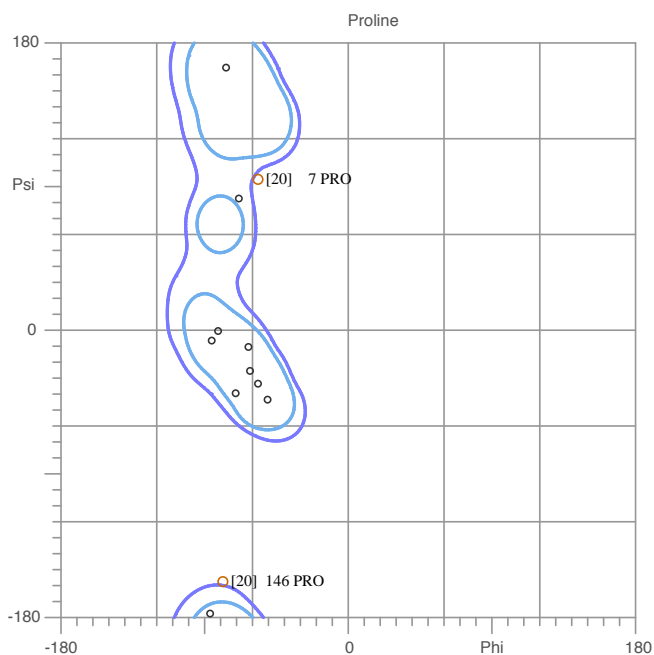
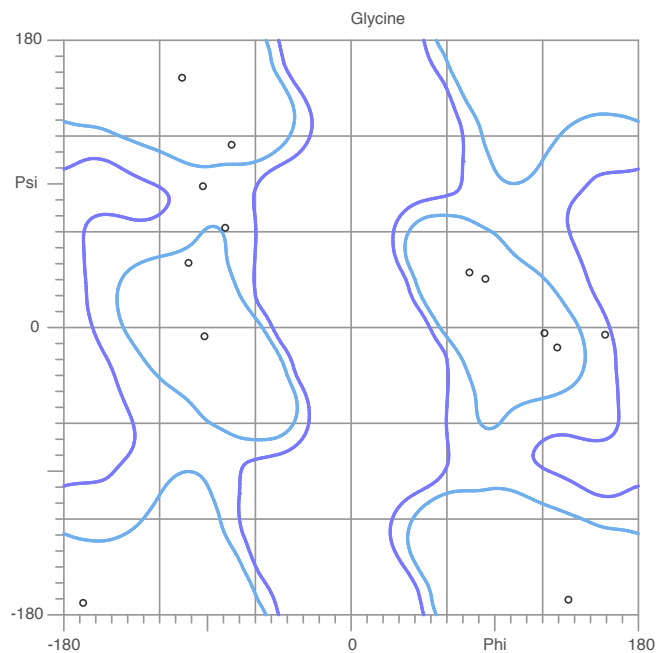
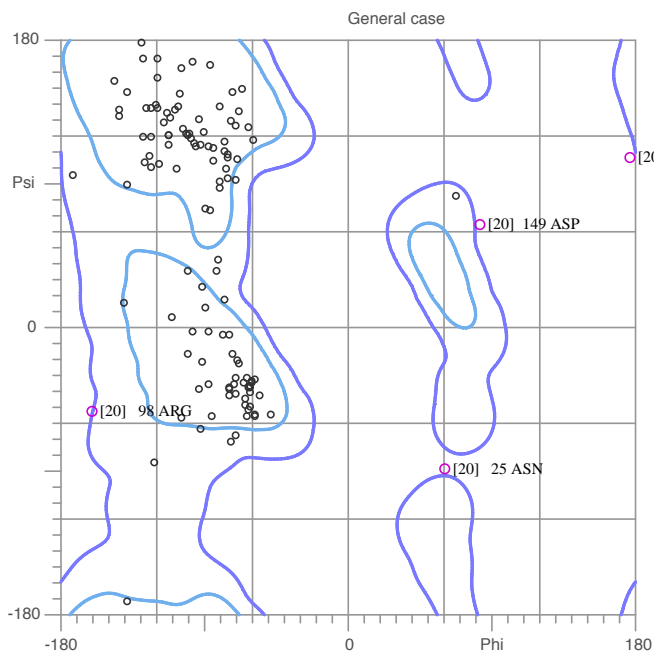
86.5% (135/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [19] 8 ALA (79.2, -160.3)
- [19] 25 ASN (65.7, -80.5)
- [19] 69 ASP (-135.6, -56.8)
- [19] 138 ARG (-56.1, 85.3)

MolProbity Ramachandran analysis

BER31_NMR_em_bcr3.pdb, model 20



85.3% (133/156) 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):

[20] 7 PRO (-57.7, 95.5)

[20] 25 ASN (60.0, -88.7)

[20] 69 ASP (64.8, 96.8)

[20] 74 LEU (176.9, 107.5)

[20] 88 ALA (64.6, 158.8)

[20] 98 ARG (-161.1, -52.6)

[20] 146 PRO (-79.9, -157.9)

[20] 149 ASP (82.9, 65.6)