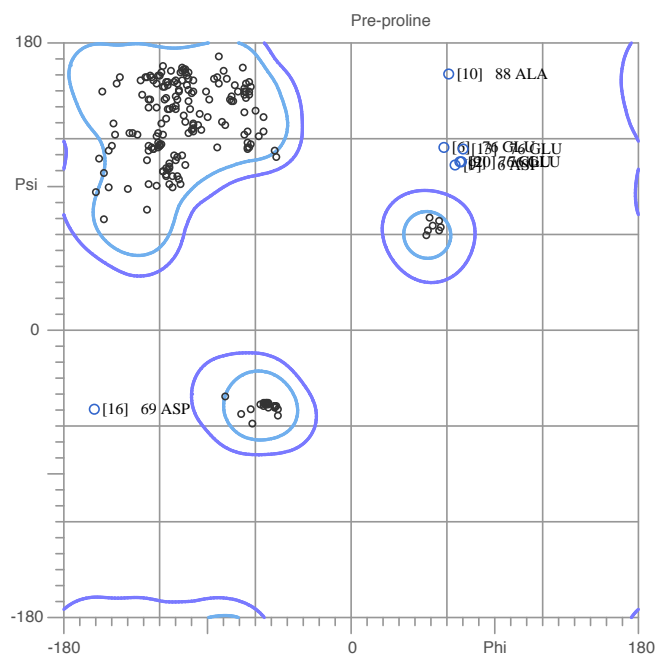
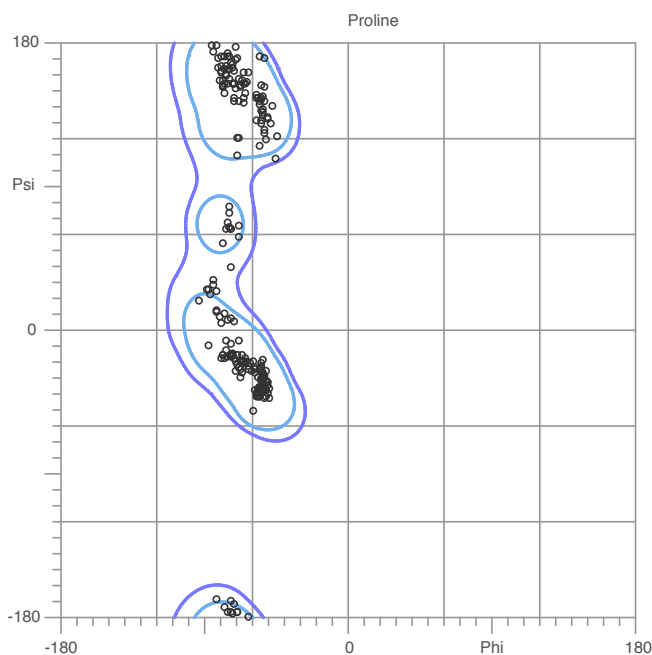
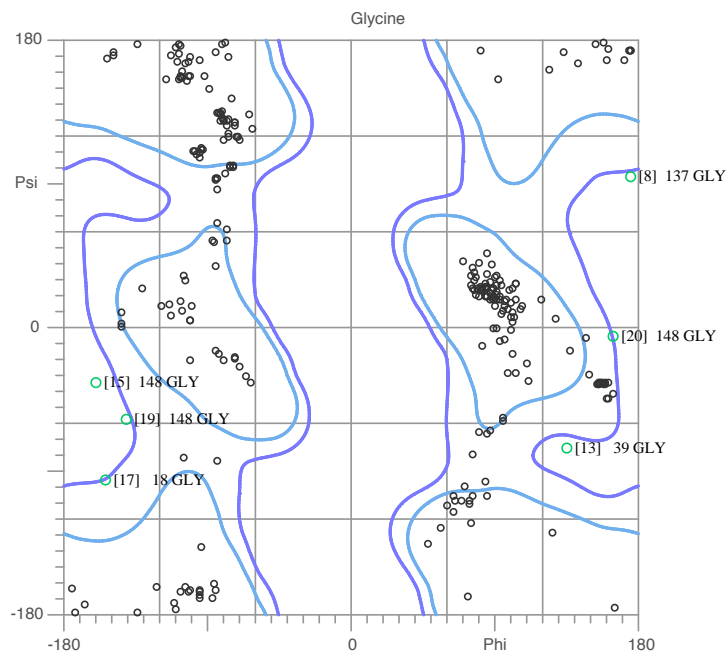
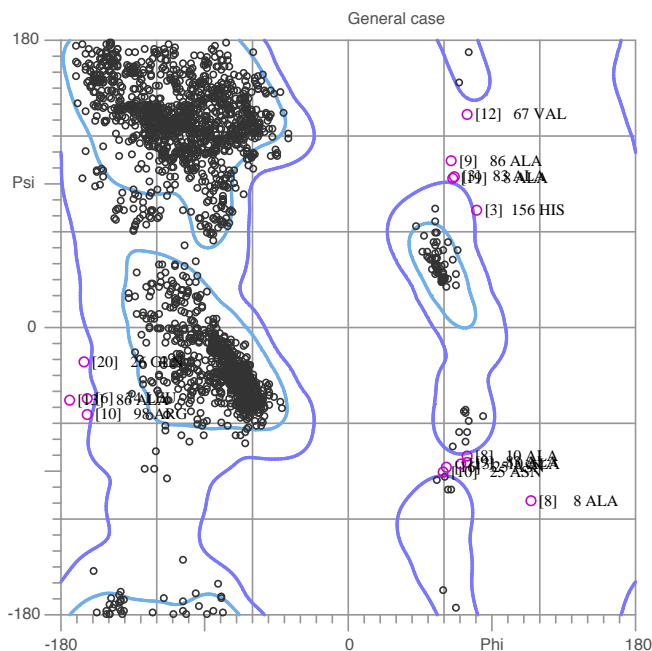


MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, all models



93.9% (2929/3120) of all residues were in favored (98%) regions.
99.1% (3092/3120) of all residues were in allowed (>99.8%) regions.

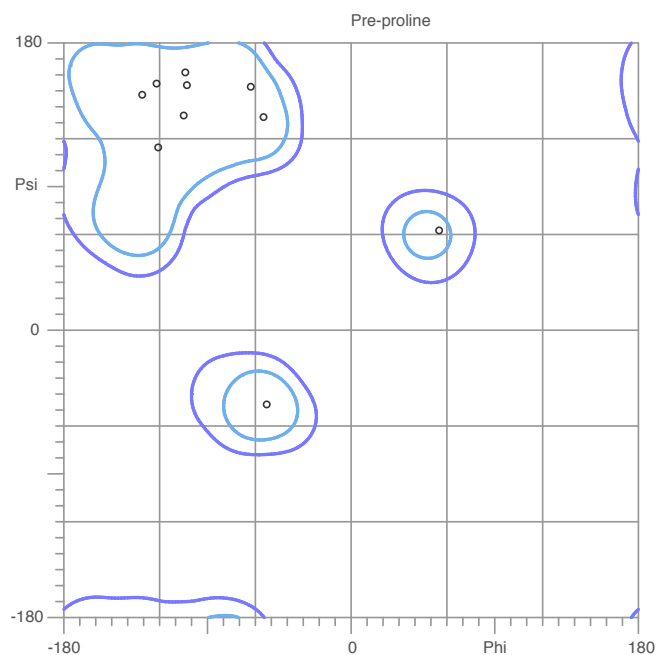
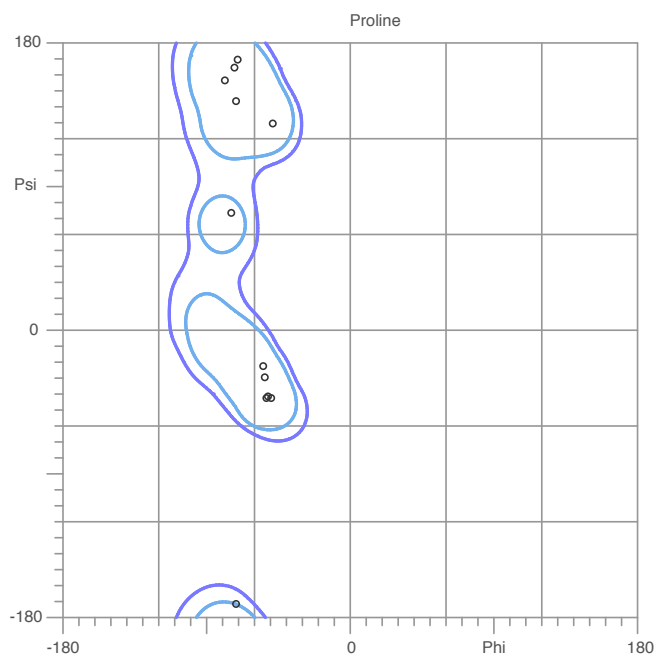
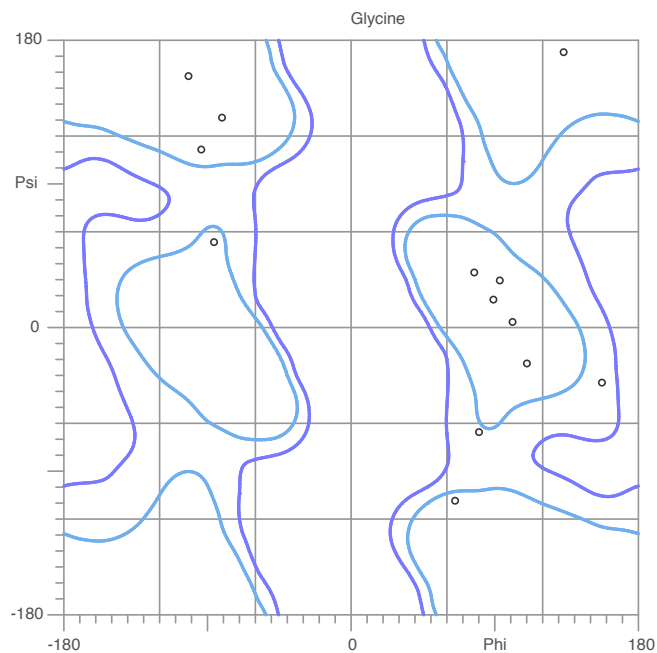
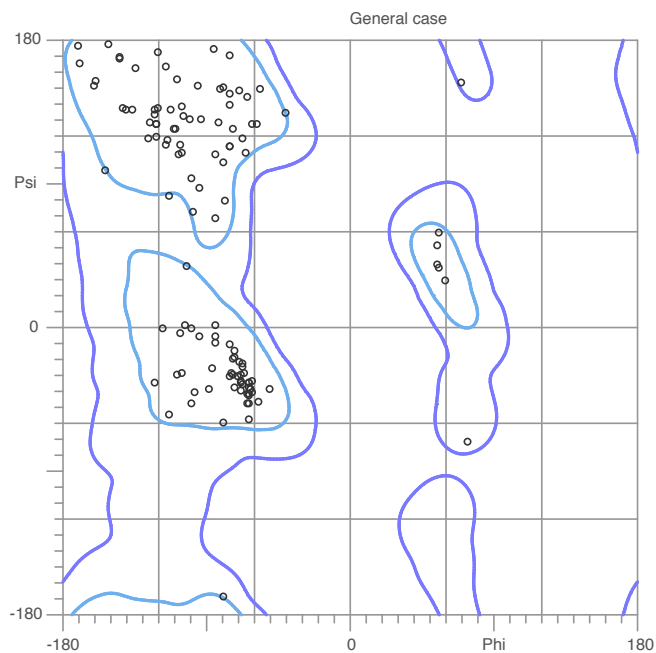
There were 28 outliers (phi, psi):

- [3] 83 ALA (66.1, 95.0)
- [3] 156 HIS (80.6, 74.9)
- [6] 74 LEU (-165.0, -45.0)
- [6] 76 GLU (58.9, 115.1)
- [8] 8 ALA (114.9, -108.6)
- [8] 10 ALA (74.3, -81.0)
- [8] 137 GLY (175.0, 95.0)
- [9] 6 ASP (65.0, 105.0)
- [9] 76 GLU (68.3, 106.6)
- [9] 83 ALA (74.0, -84.9)
- [9] 86 ALA (64.9, 105.0)
- [10] 25 ASN (59.9, -90.4)

- [10] 88 ALA (61.0, 161.2)
- [10] 98 ARG (-165.0, -55.0)
- [12] 67 VAL (74.8, 134.6)
- [13] 10 ALA (70.9, -85.1)
- [13] 39 GLY (135.1, -75.1)
- [13] 76 GLU (70.0, 115.0)
- [13] 86 ALA (-175.0, -45.0)
- [15] 148 GLY (-160.4, -35.0)
- [16] 25 ASN (61.0, -87.4)
- [16] 69 ASP (-161.2, -49.6)
- [17] 18 GLY (-155.0, -95.0)
- [19] 8 ALA (65.1, 95.0)
- [19] 148 GLY (-141.1, -57.7)
- [20] 26 GLN (-166.3, -21.4)
- [20] 76 GLU (69.0, 106.6)
- [20] 148 GLY (165.0, -5.0)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 1



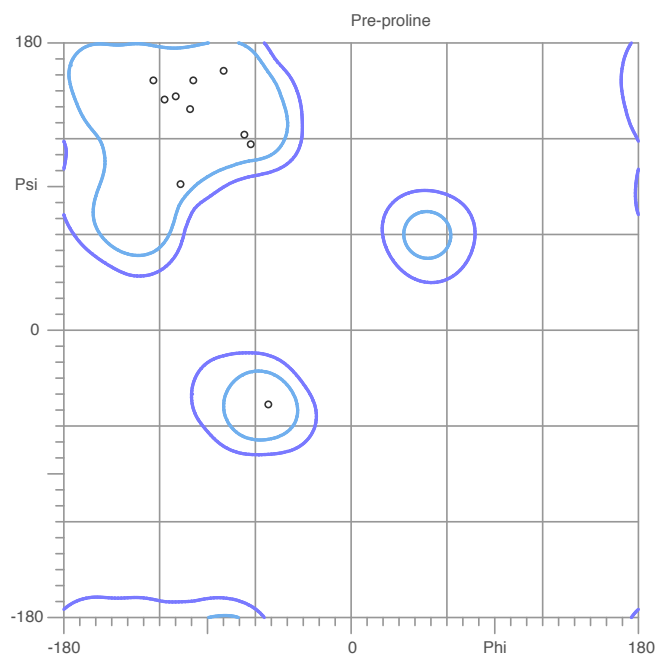
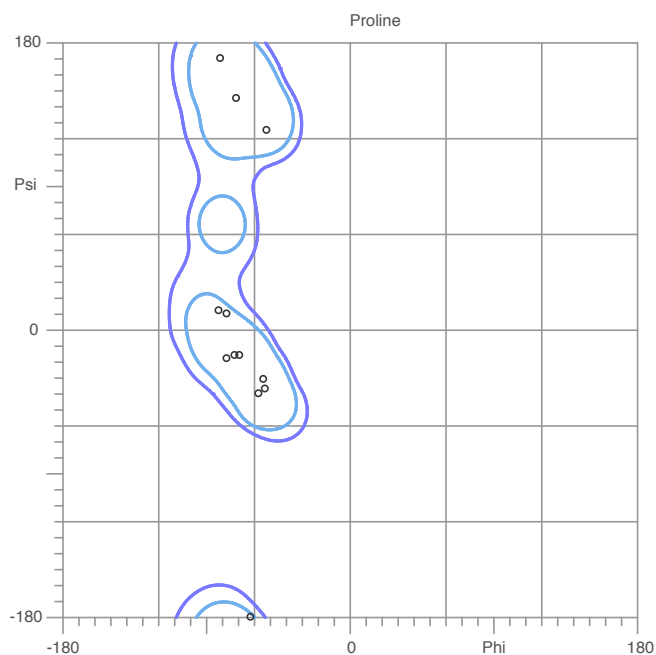
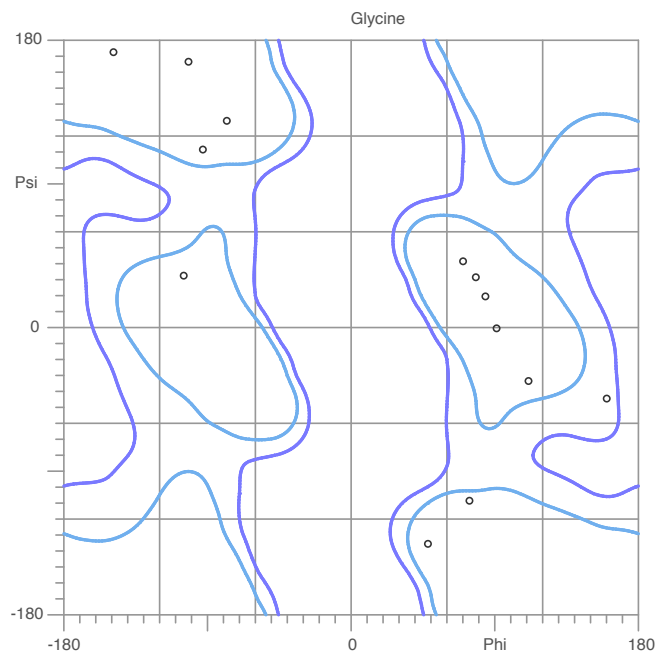
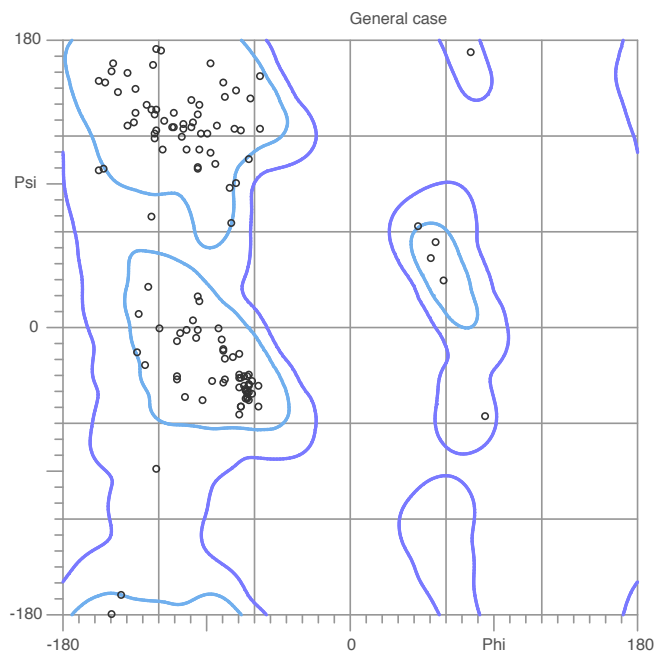
94.2% (147/156) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 2



92.9% (145/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

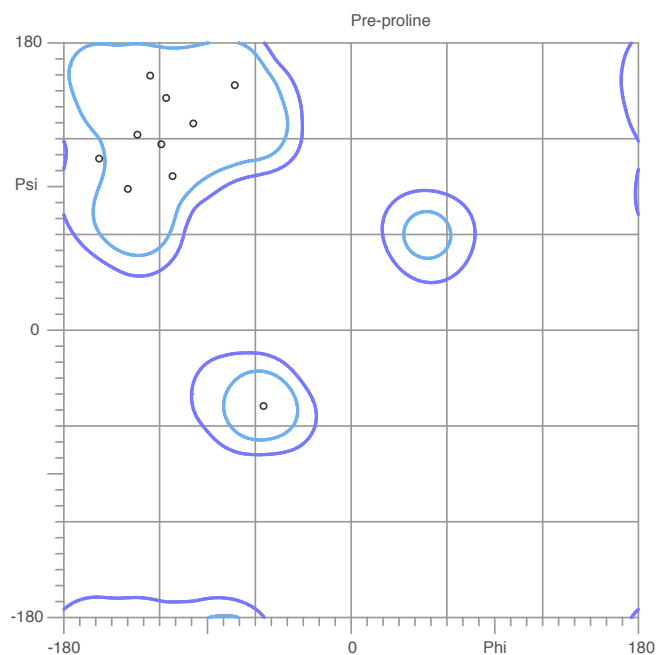
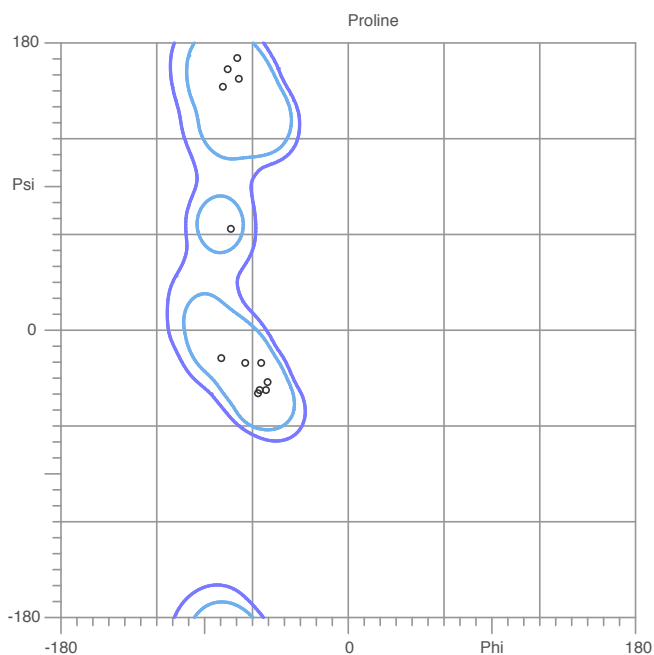
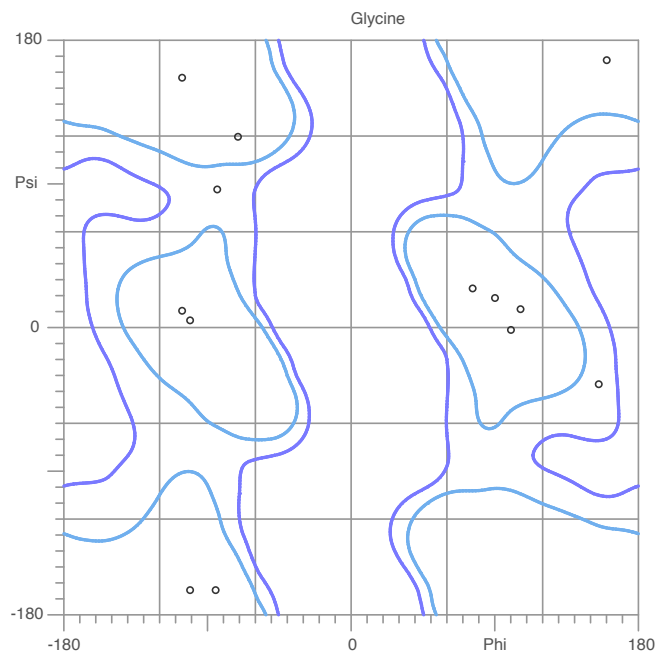
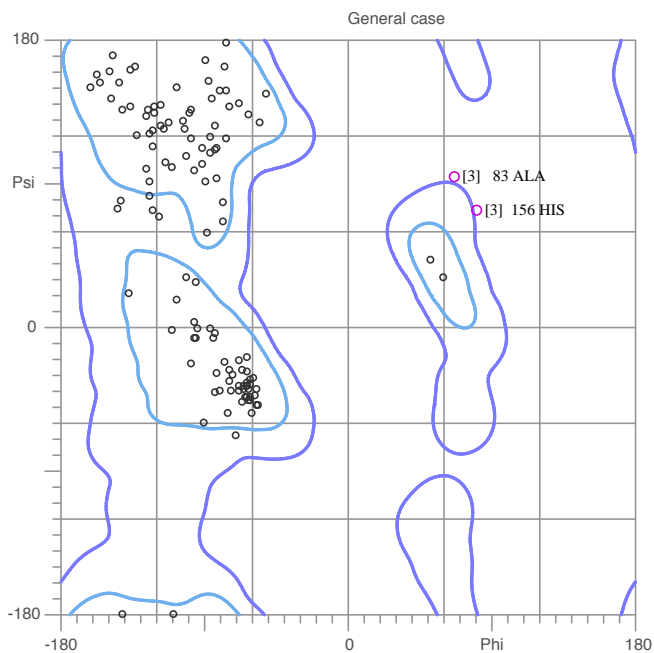
There were no outliers.

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

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MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 3



93.6% (146/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

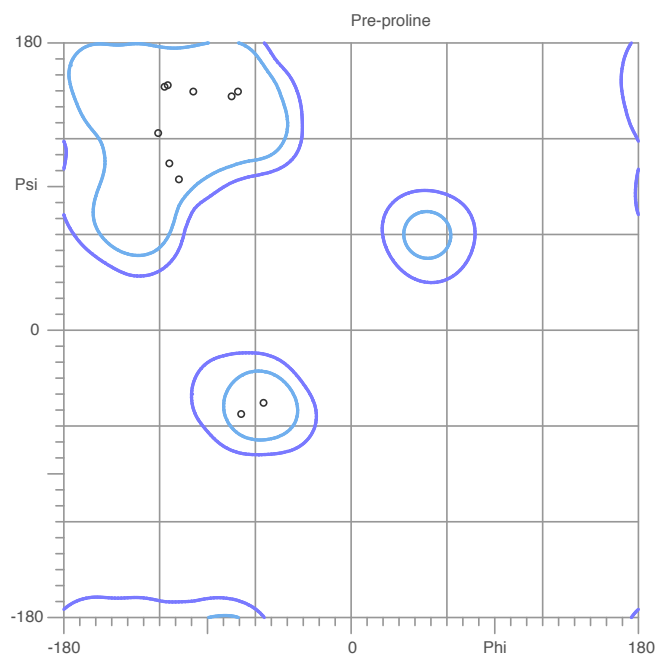
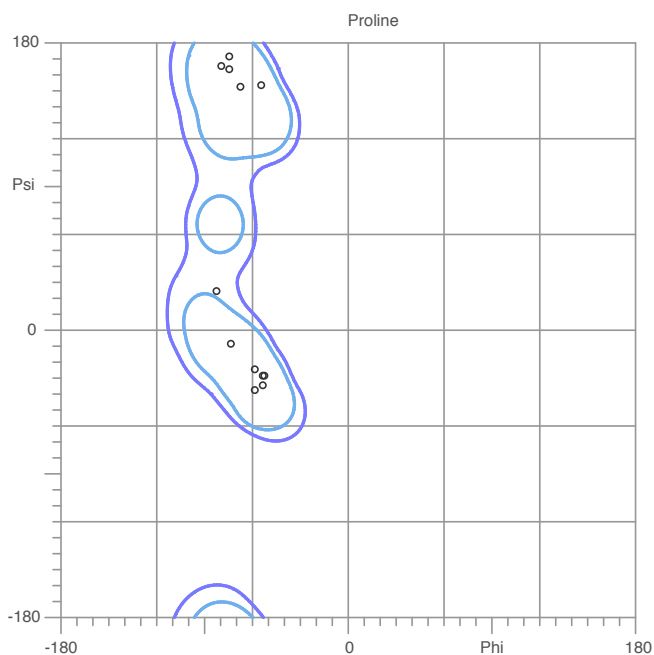
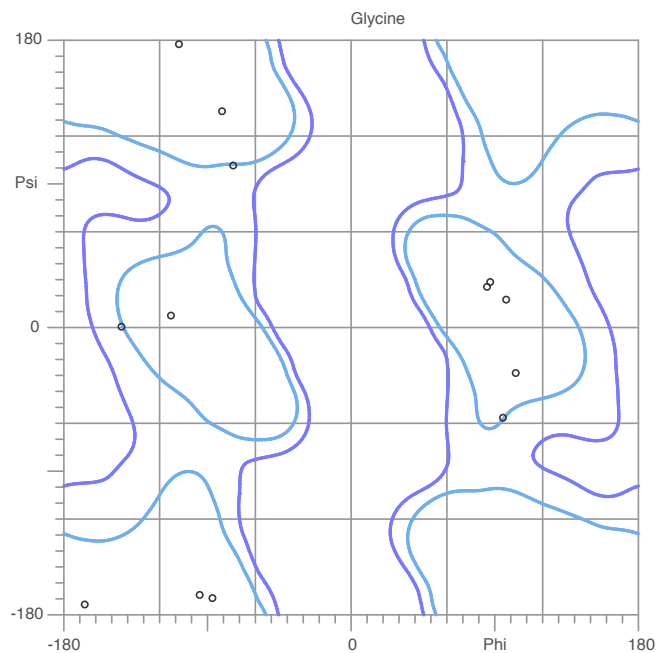
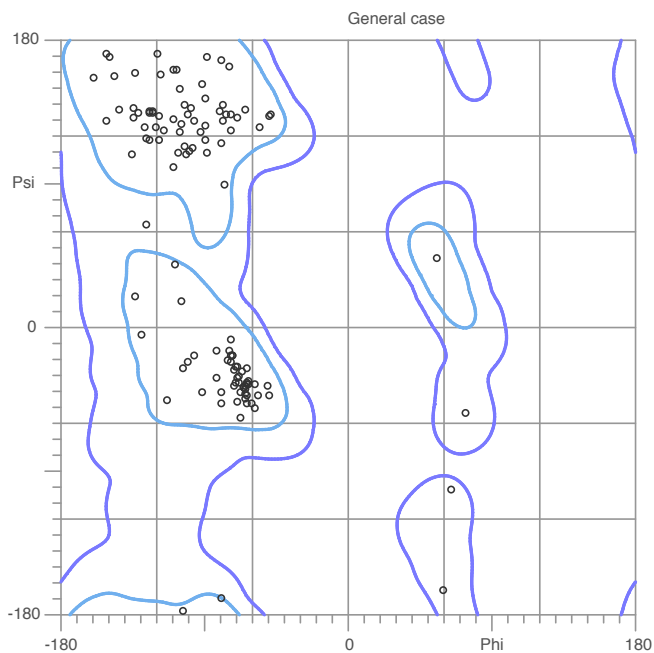
There were 2 outliers (phi, psi):

[3] 83 ALA (66.1, 95.0)

[3] 156 HIS (80.6, 74.9)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 4

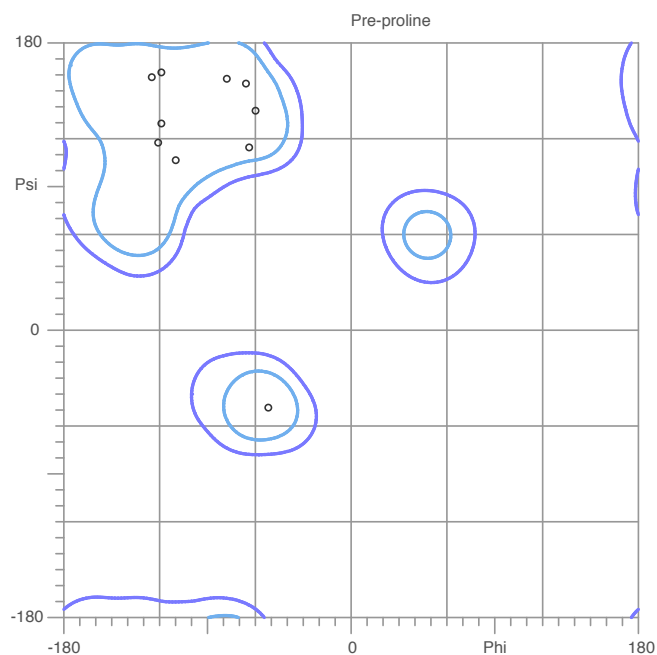
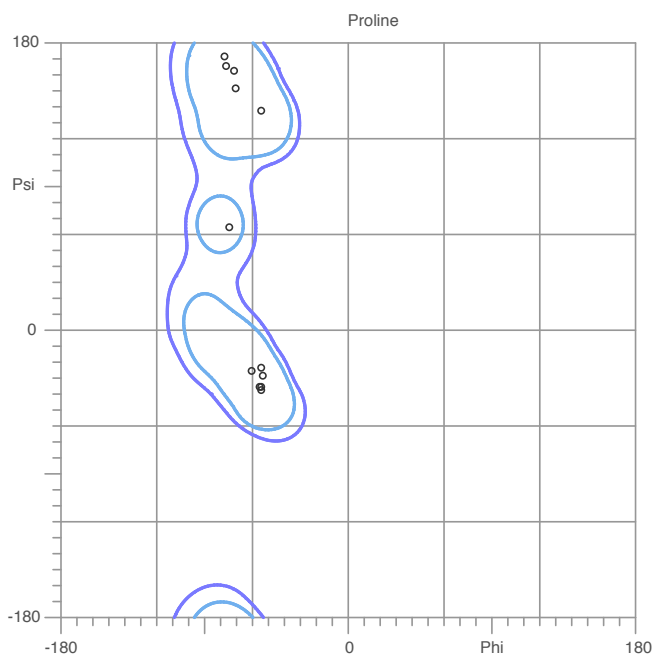
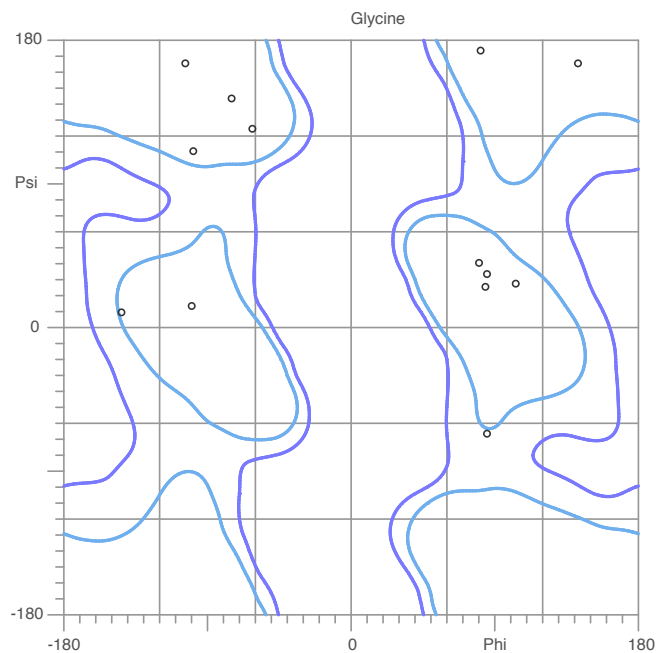
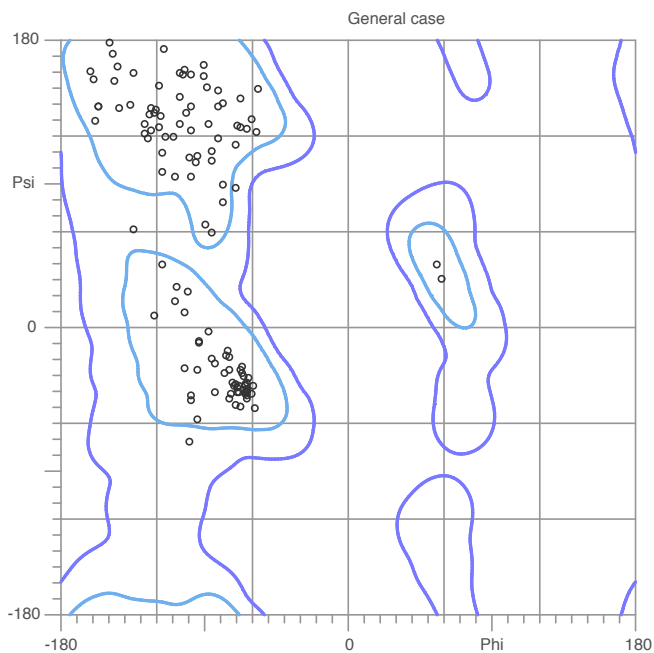


96.2% (150/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 5



97.4% (152/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

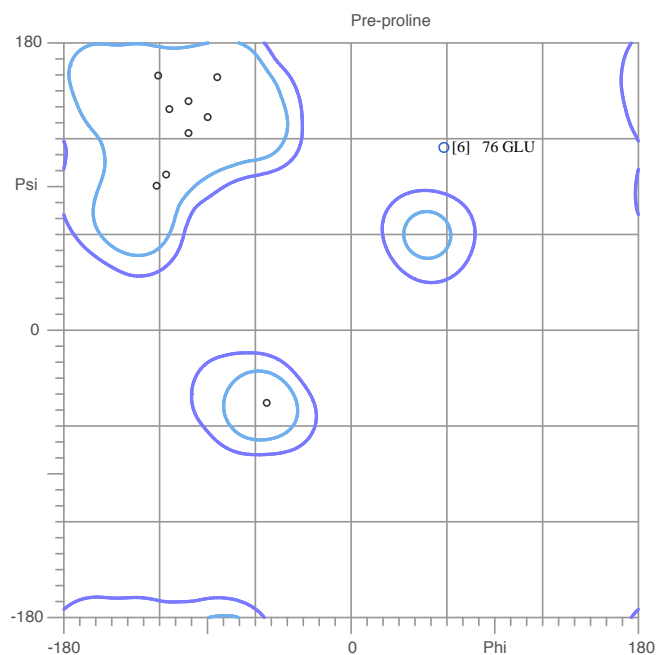
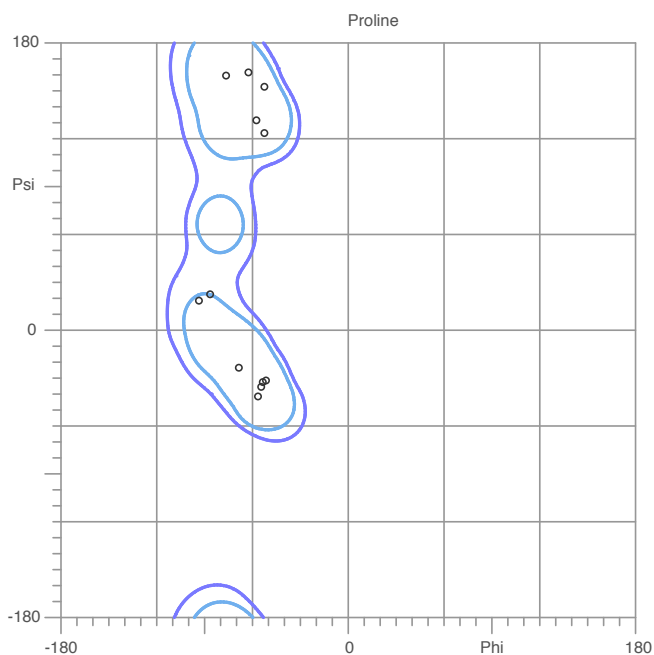
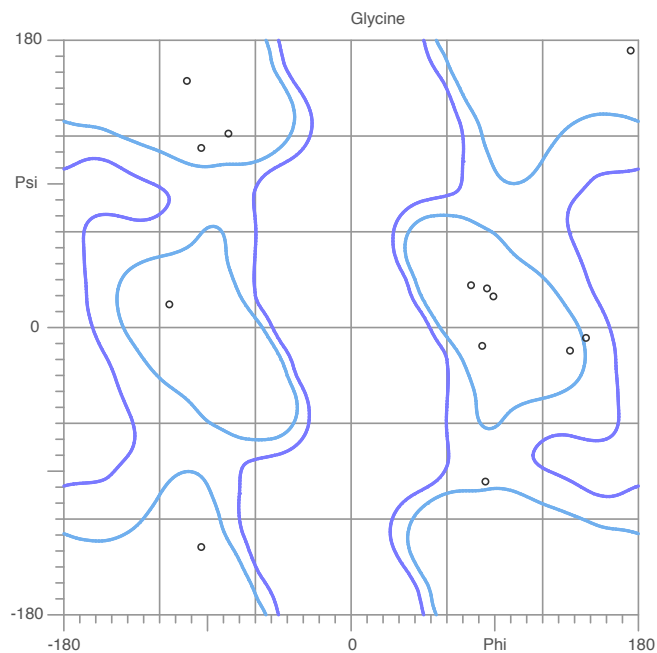
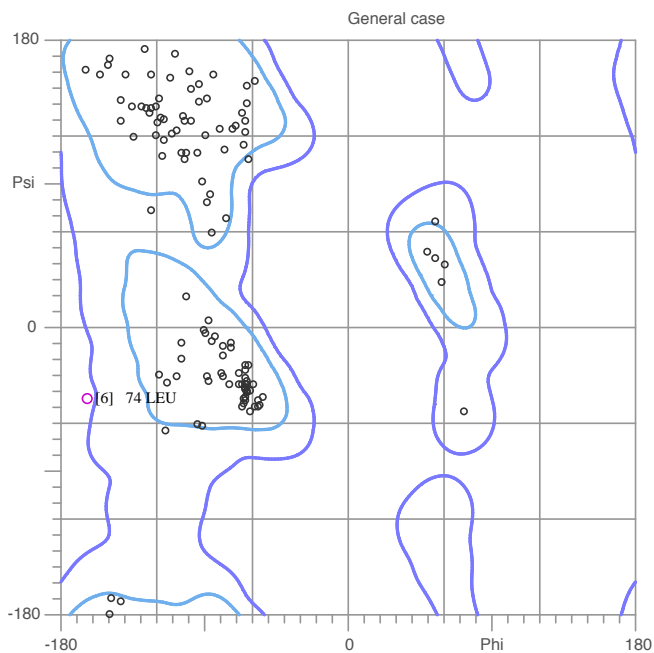
There were no outliers.

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

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MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 6



93.6% (146/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

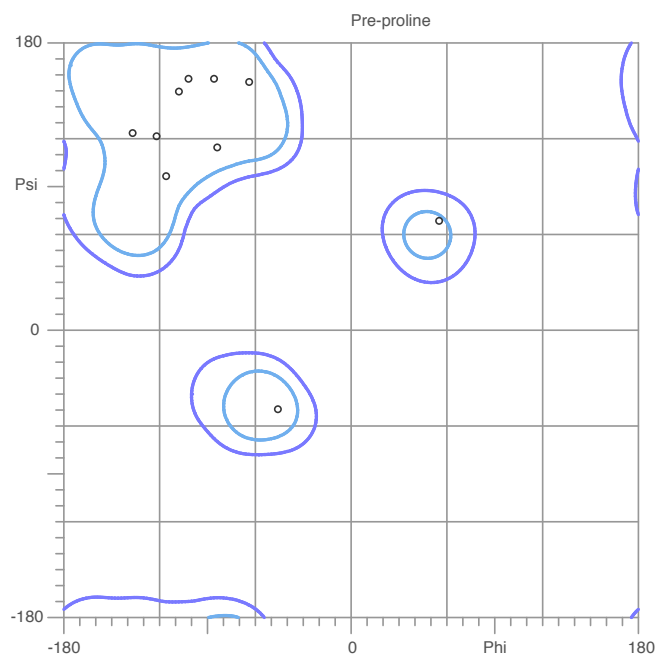
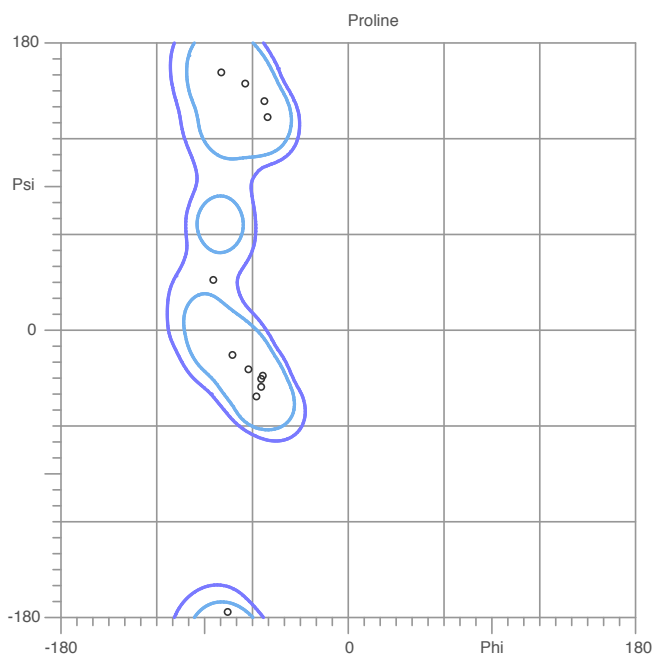
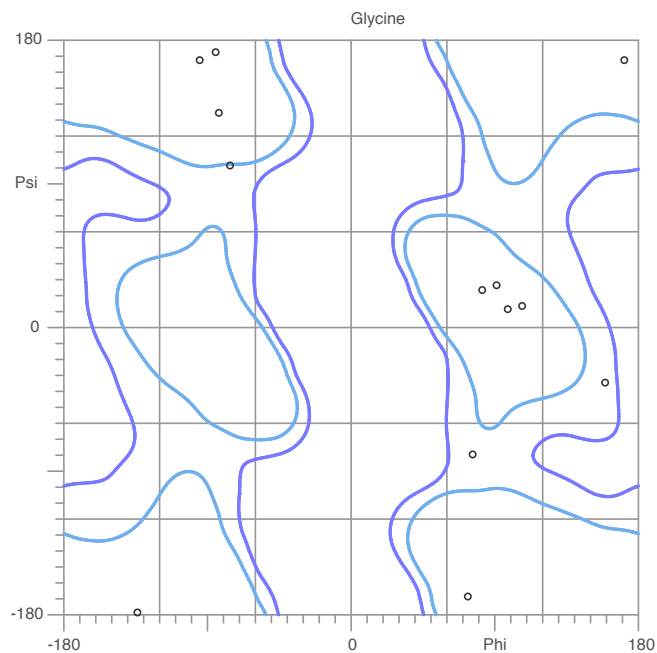
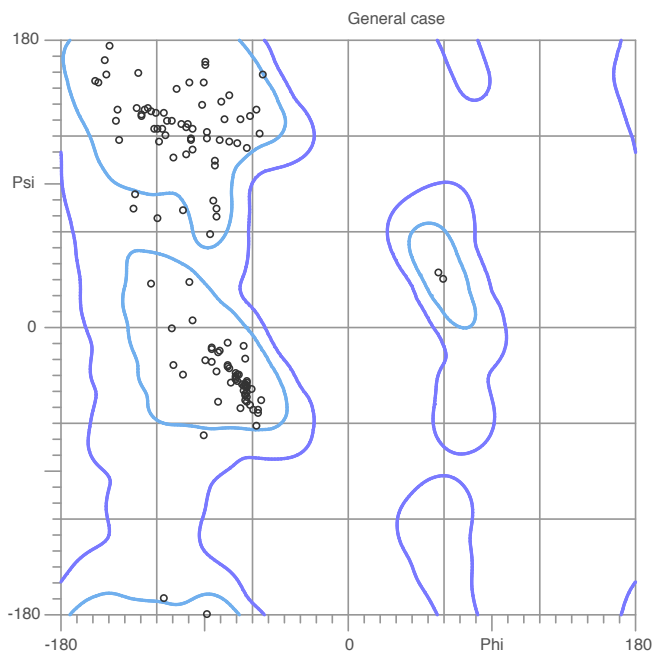
There were 2 outliers (phi, psi):

[6] 74 LEU (-165.0, -45.0)

[6] 76 GLU (58.9, 115.1)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 7

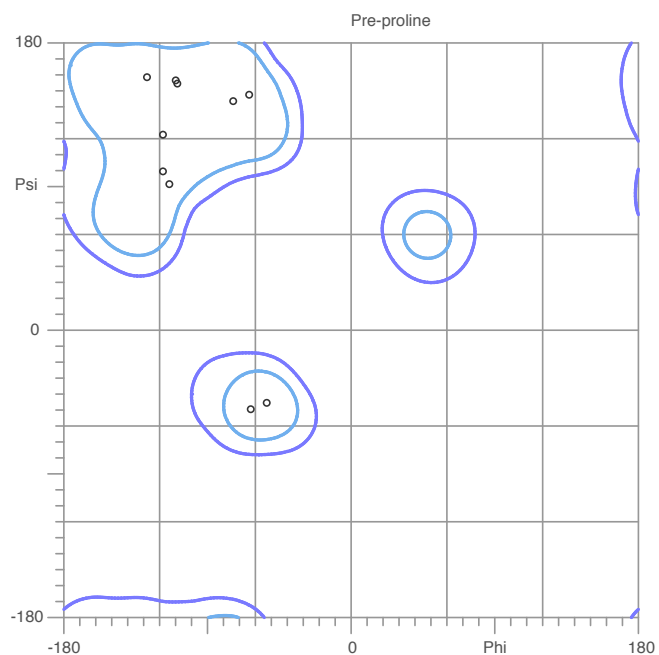
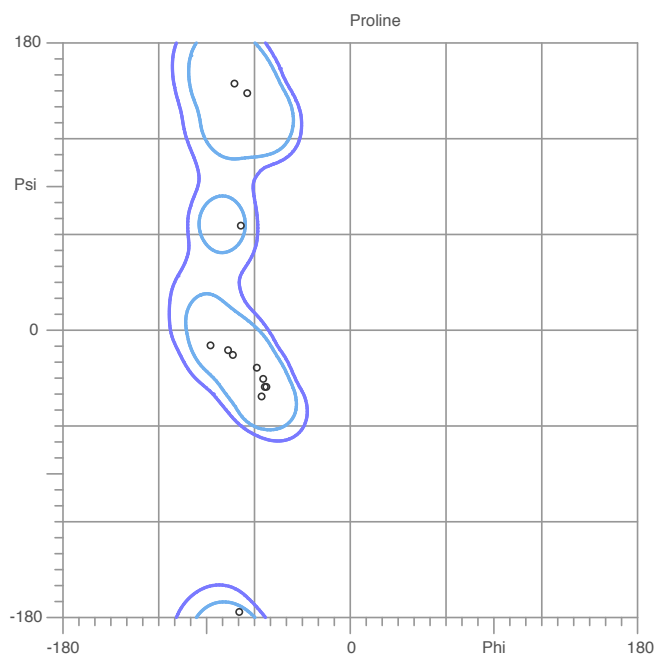
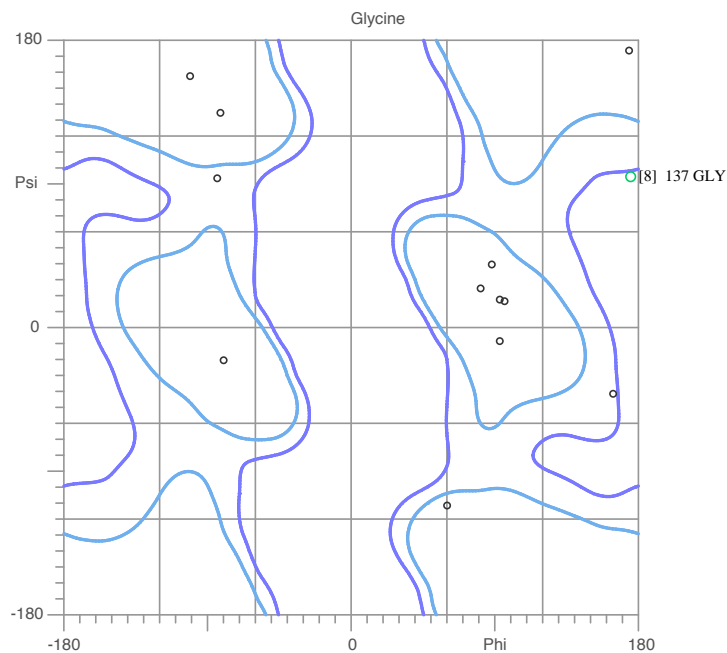
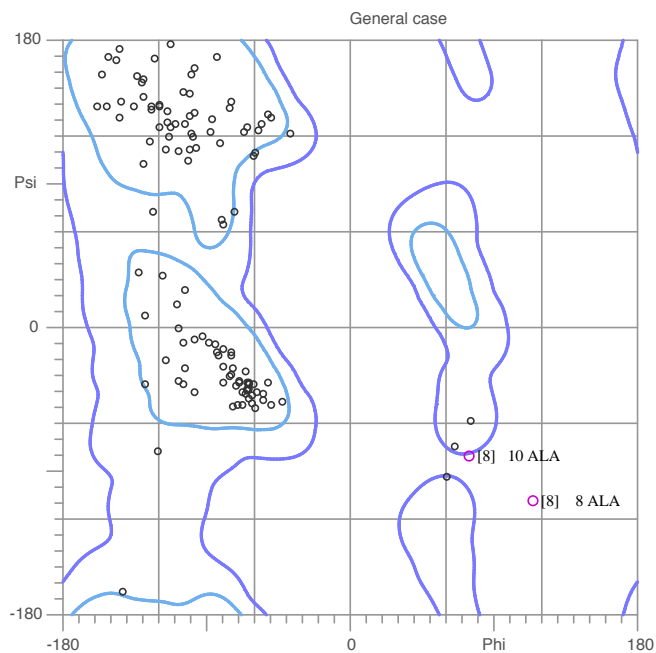


94.2% (147/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 8



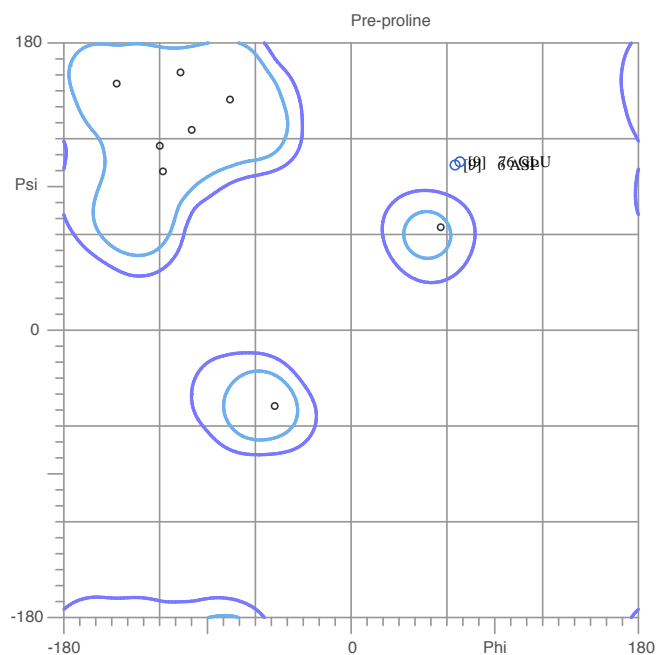
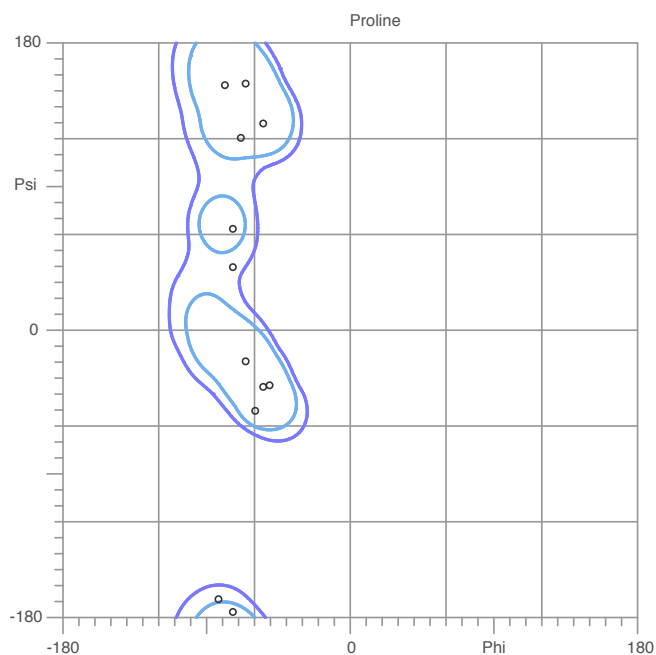
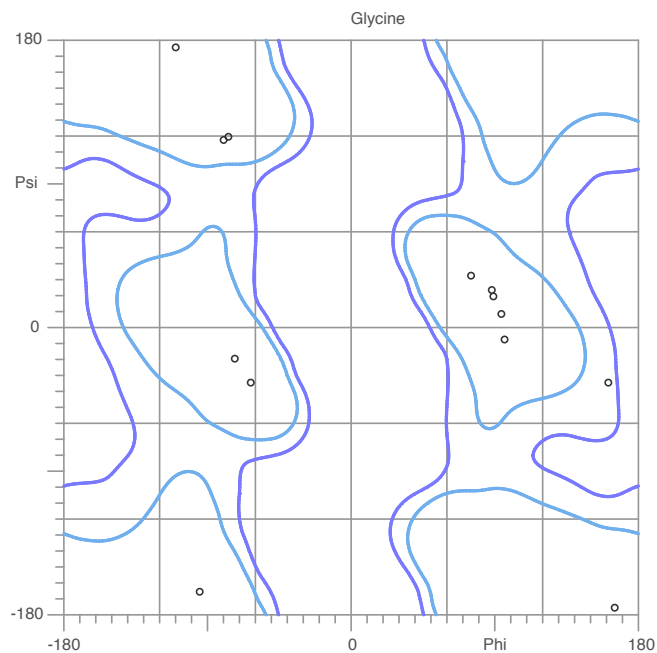
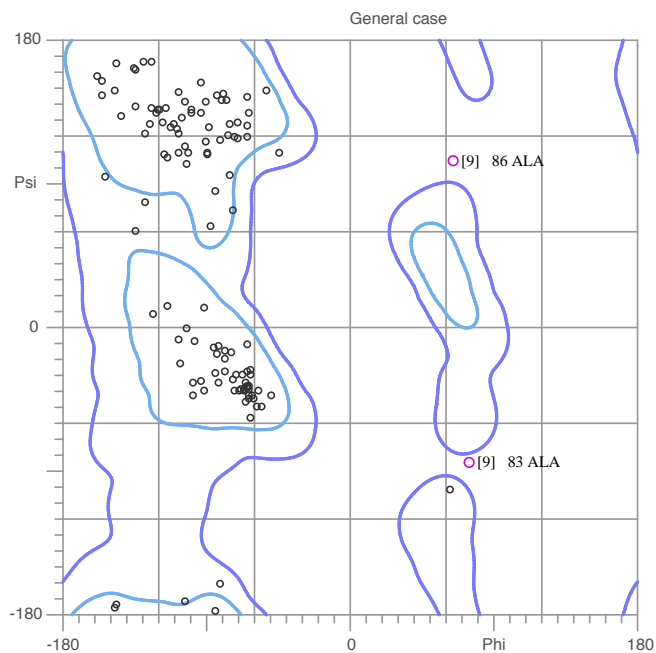
91.7% (143/156) of all residues were in favored (98%) regions.
98.1% (153/156) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 8 ALA (114.9, -108.6)
- [8] 10 ALA (74.3, -81.0)
- [8] 137 GLY (175.0, 95.0)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 9



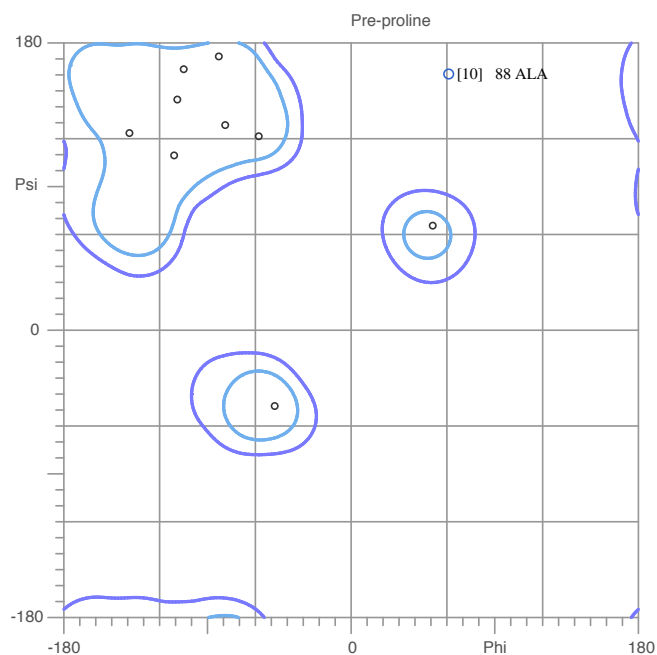
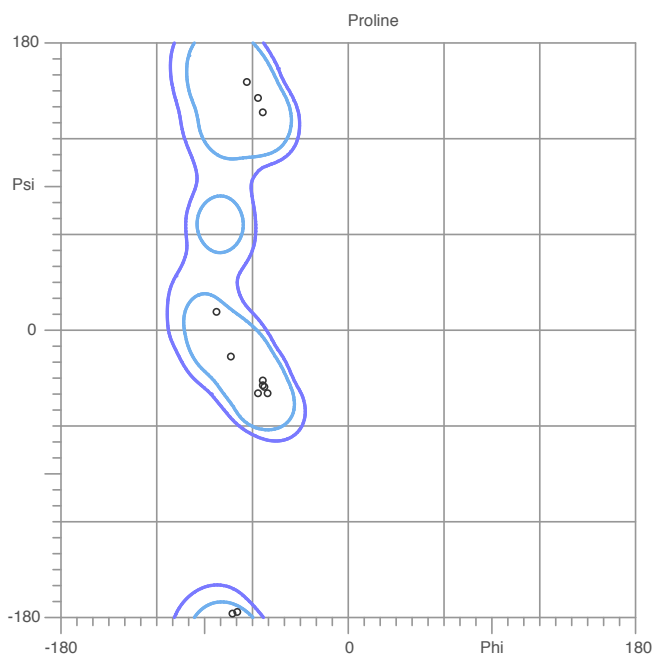
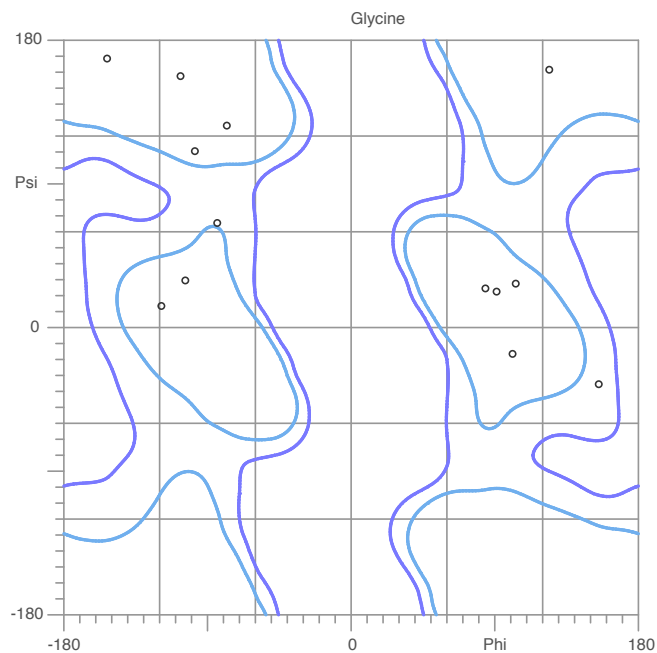
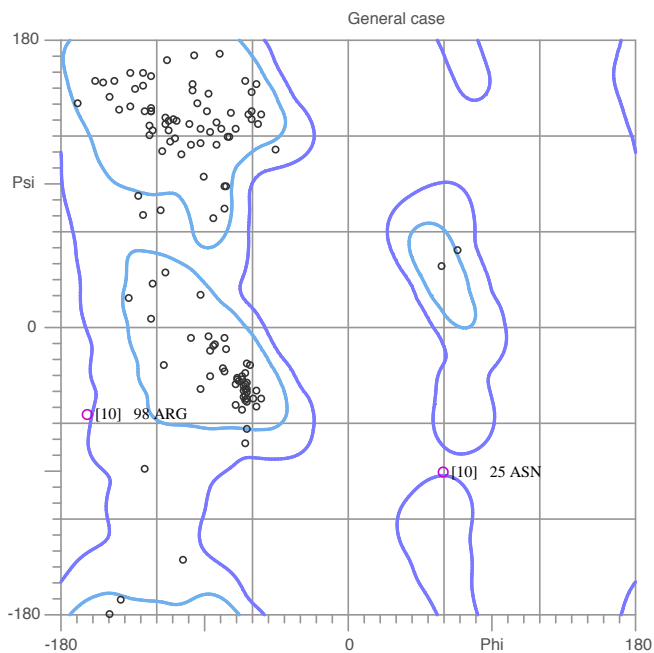
91.0% (142/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [9] 6 ASP (65.0, 105.0)
- [9] 76 GLU (68.3, 106.6)
- [9] 83 ALA (74.0, -84.9)
- [9] 86 ALA (64.9, 105.0)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 10



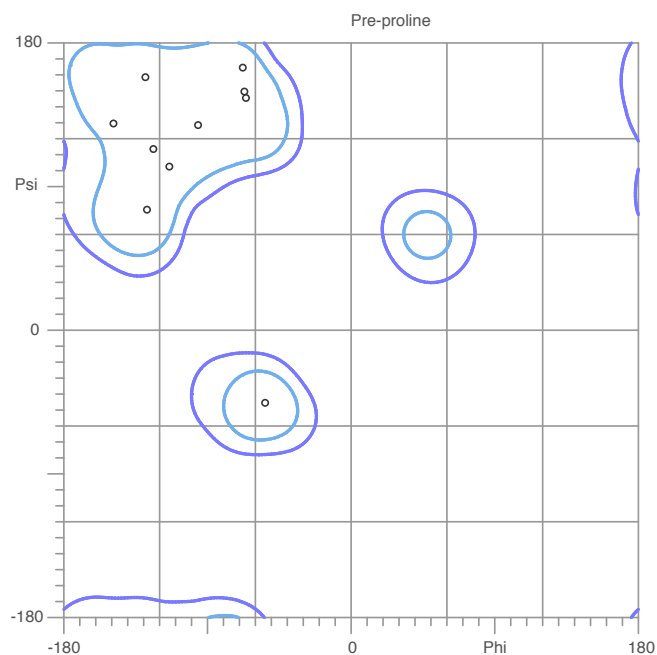
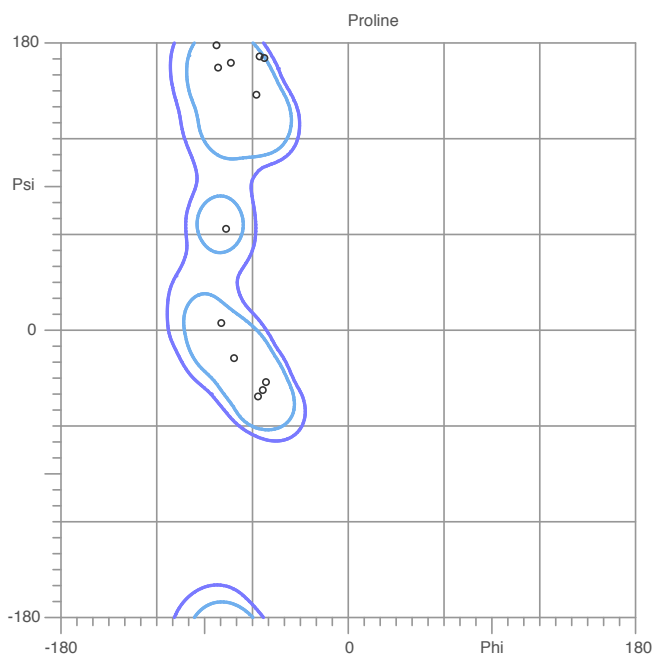
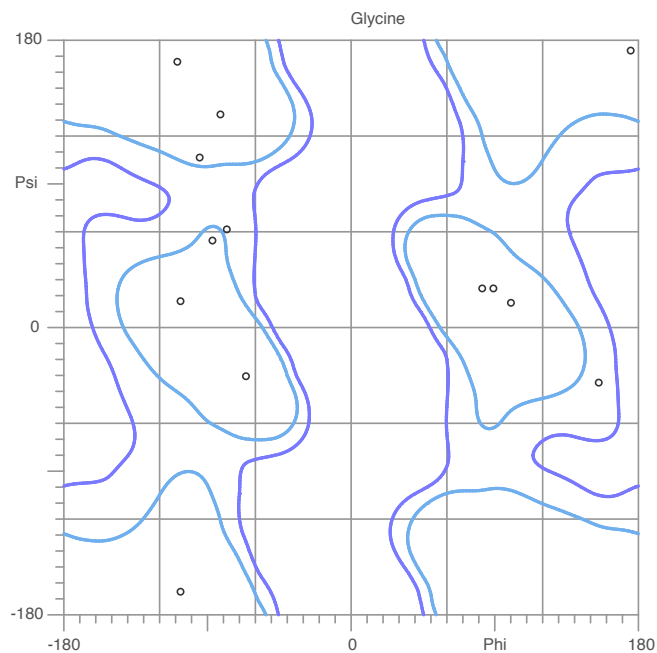
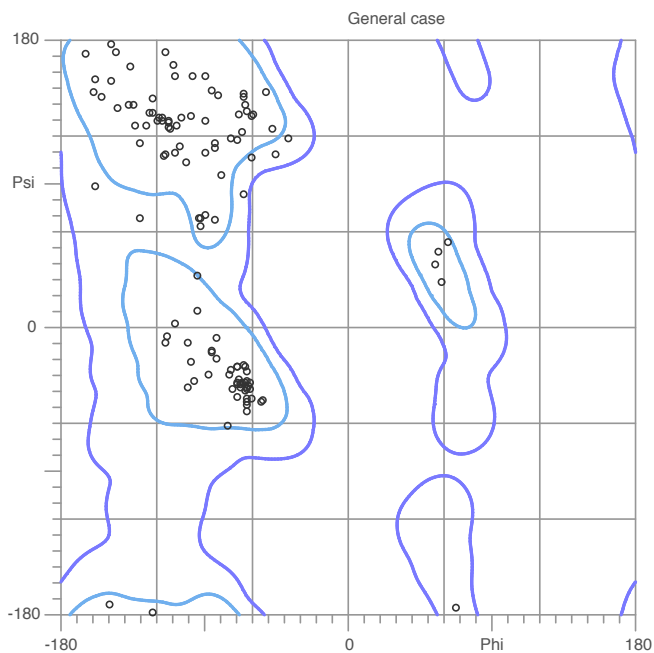
91.0% (142/156) of all residues were in favored (98%) regions.
98.1% (153/156) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [10] 25 ASN (59.9, -90.4)
- [10] 88 ALA (61.0, 161.2)
- [10] 98 ARG (-165.0, -55.0)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 11



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.

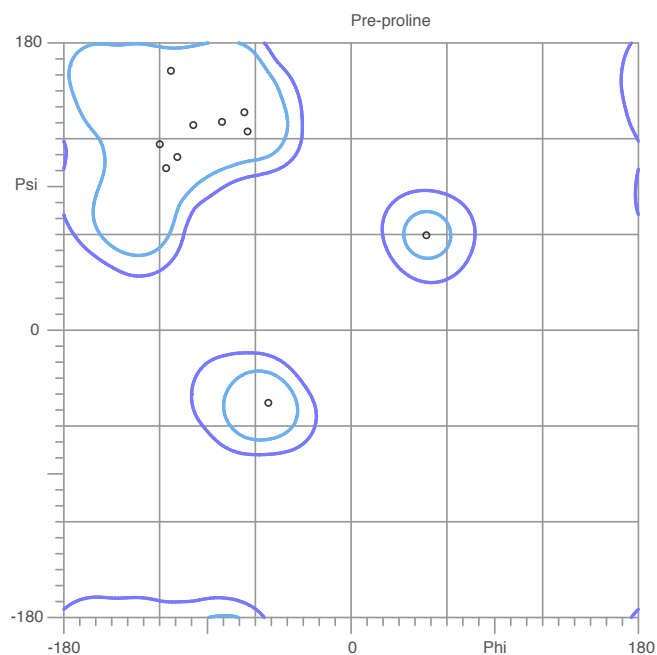
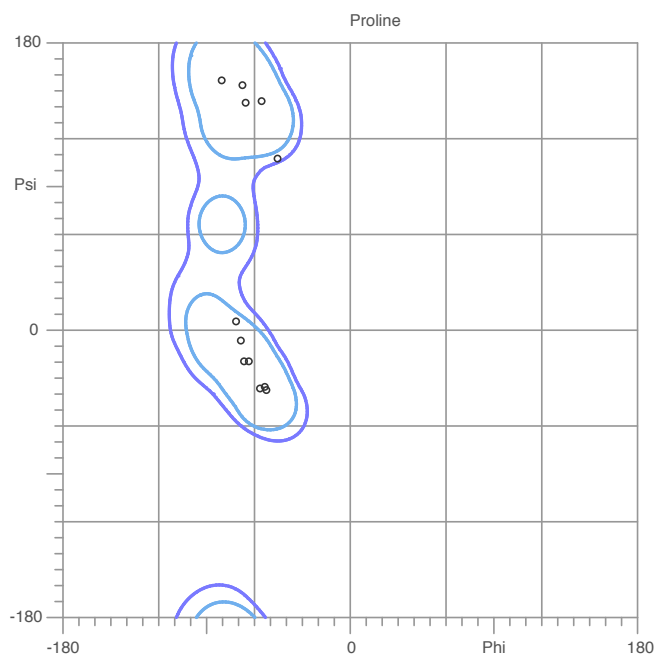
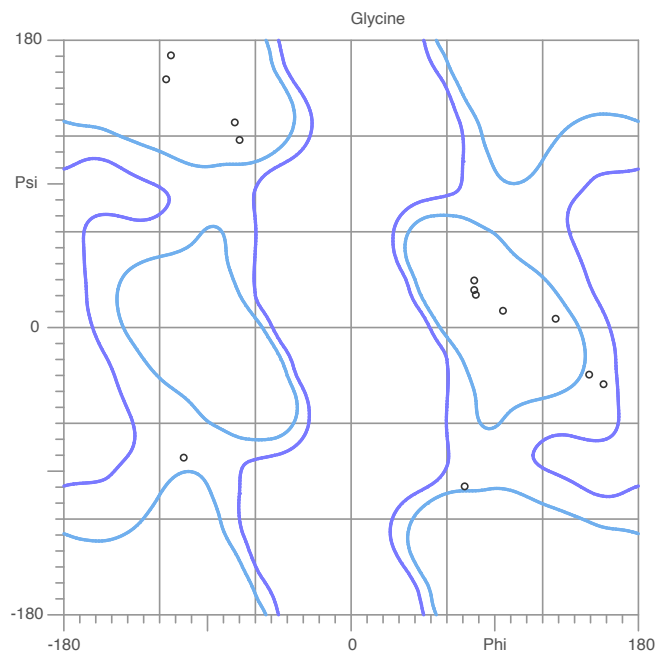
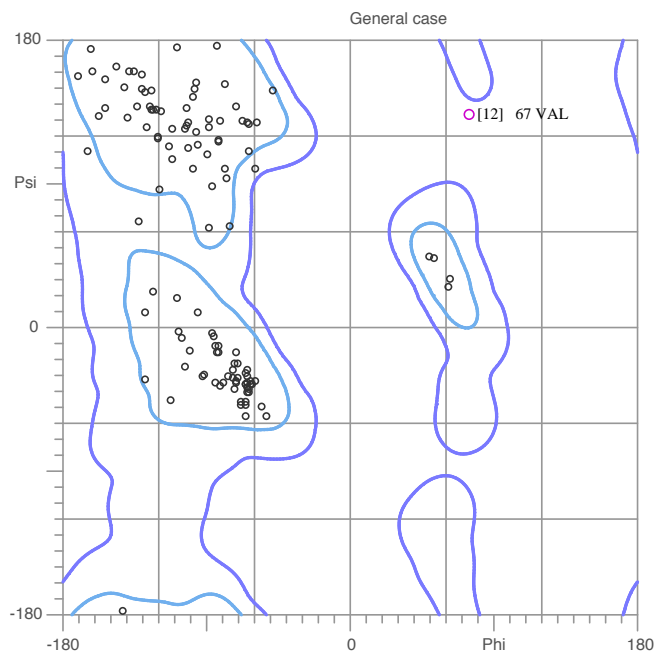
There were no outliers.

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

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MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 12



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.

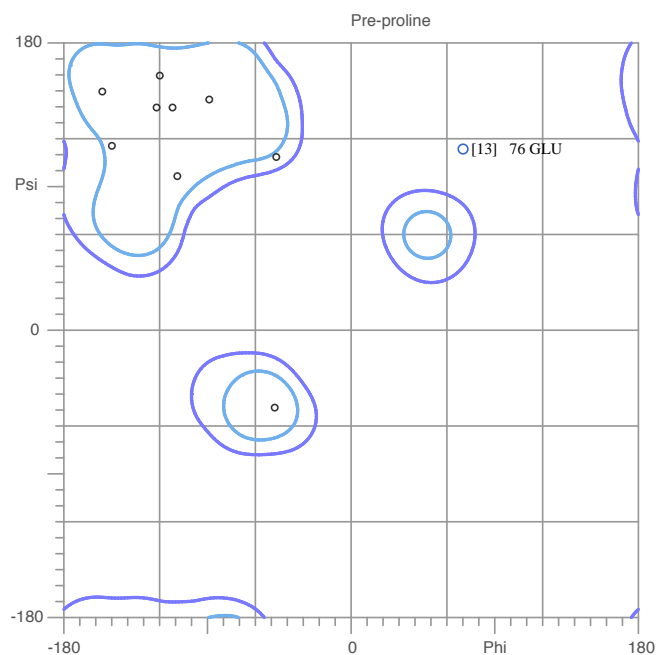
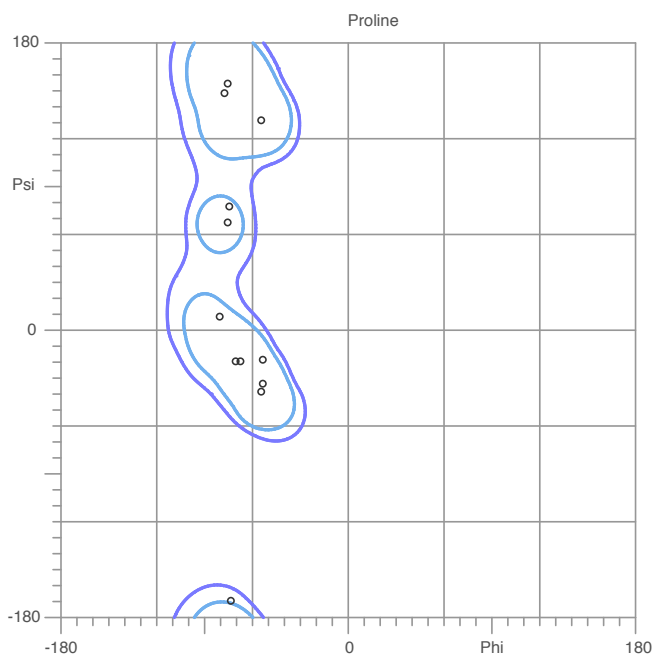
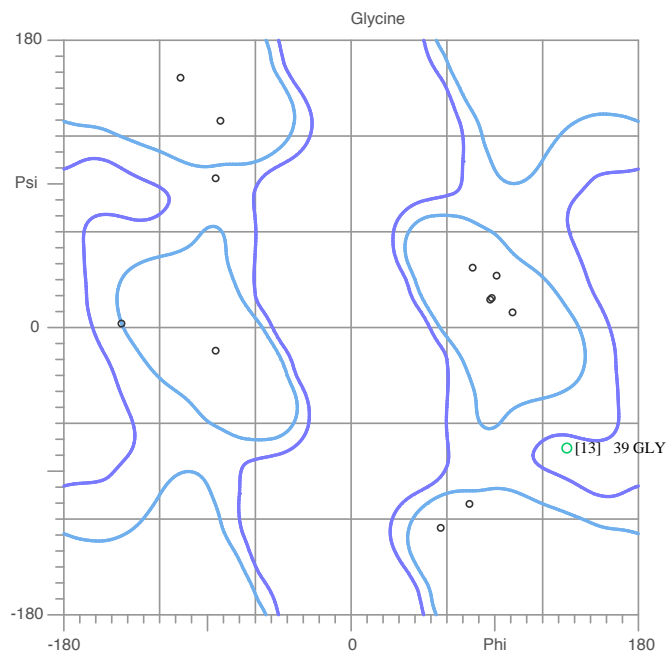
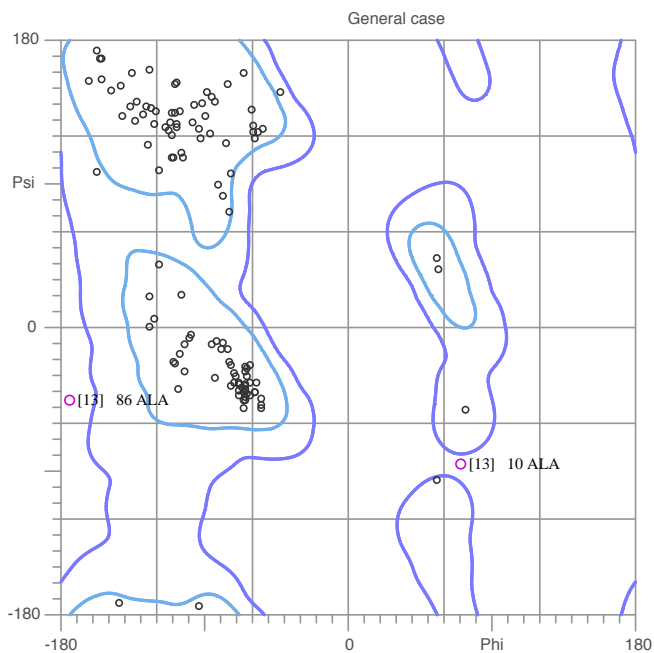
There were 1 outliers (phi, psi):
[12] 67 VAL (74.8, 134.6)

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

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MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 13



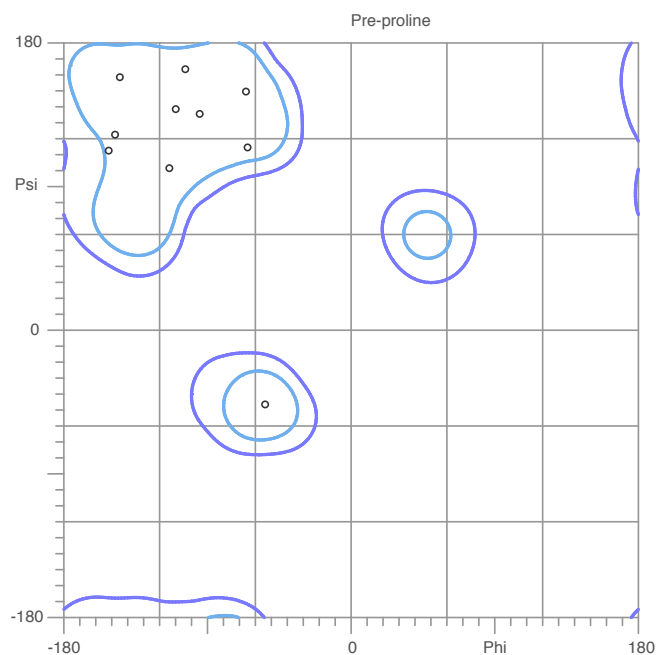
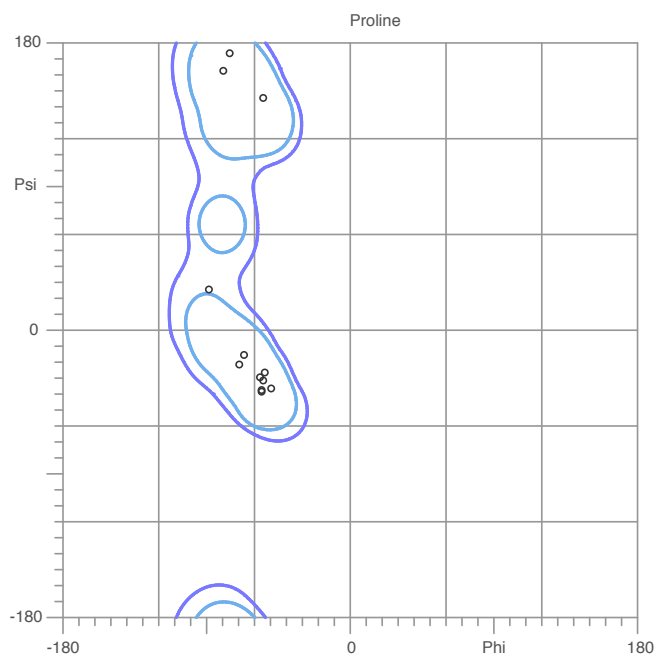
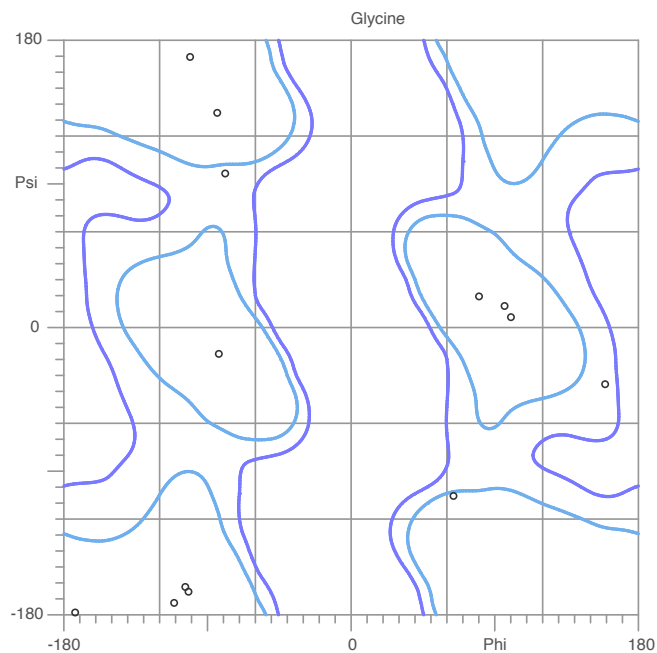
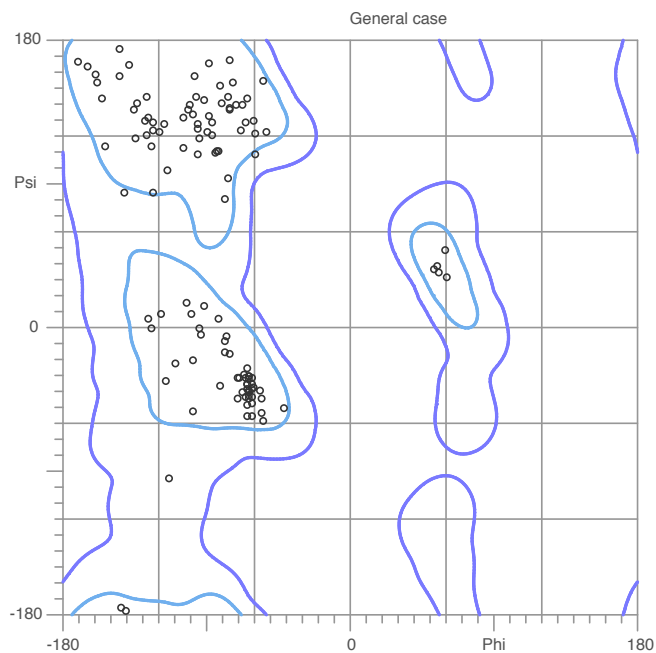
92.3% (144/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [13] 10 ALA (70.9, -85.1)
- [13] 39 GLY (135.1, -75.1)
- [13] 76 GLU (70.0, 115.0)
- [13] 86 ALA (-175.0, -45.0)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 14



96.2% (150/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

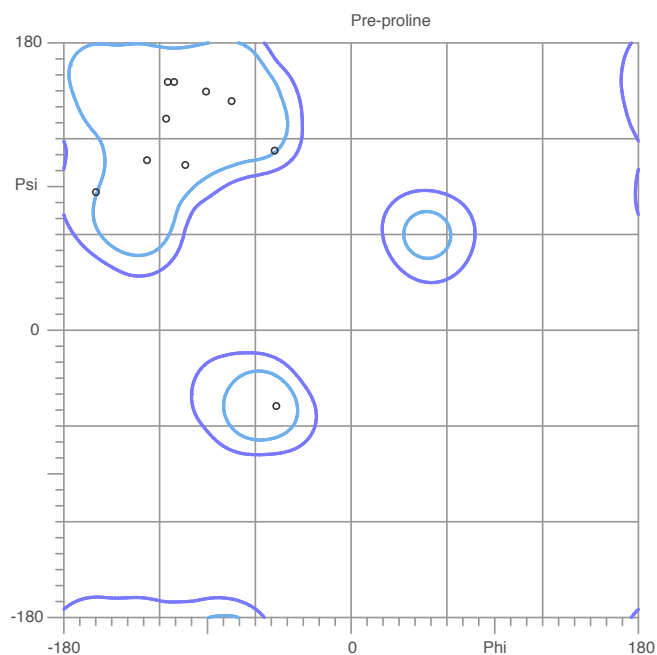
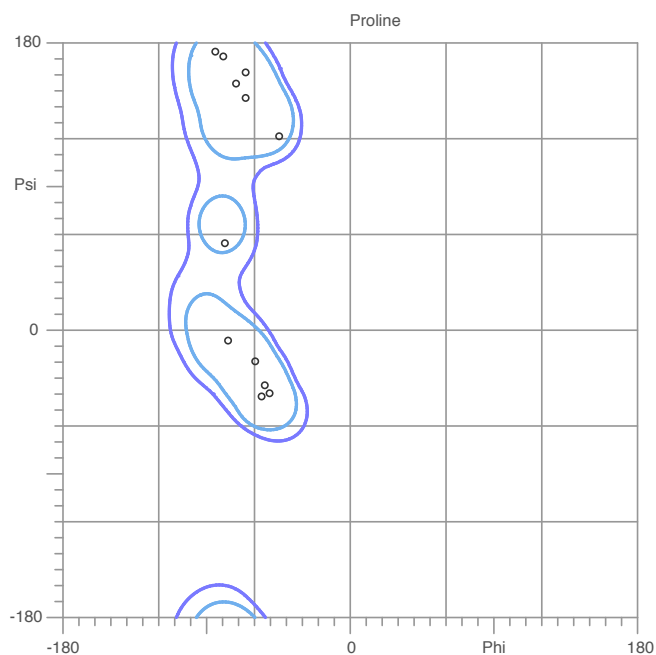
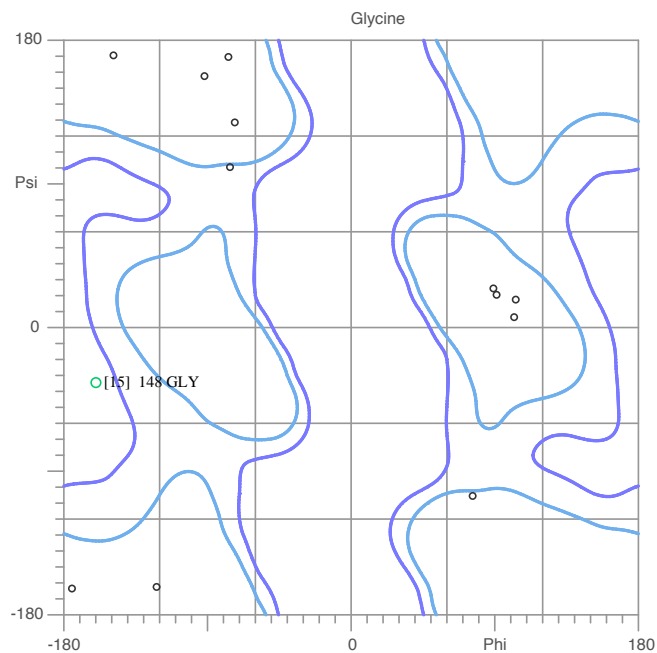
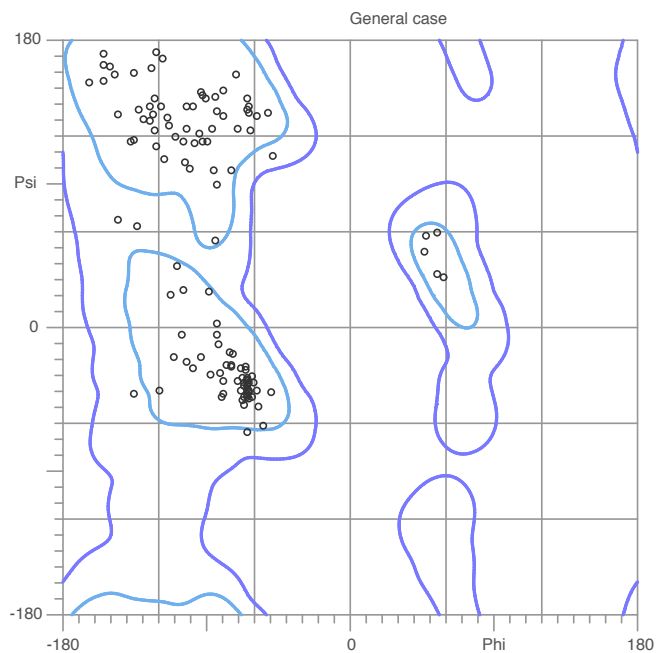
There were no outliers.

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

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MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 15



94.9% (148/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

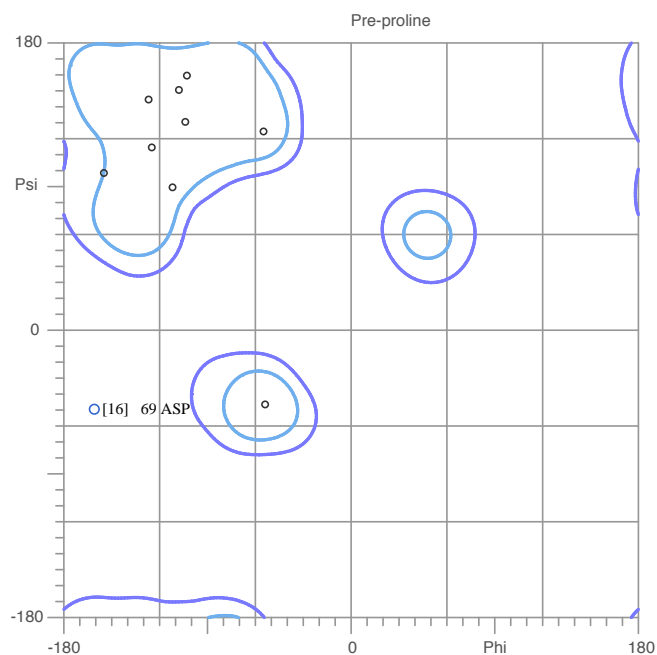
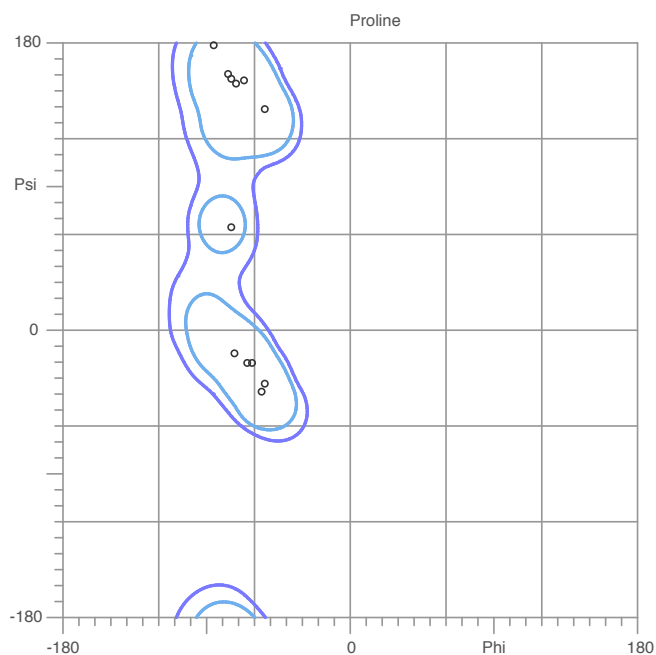
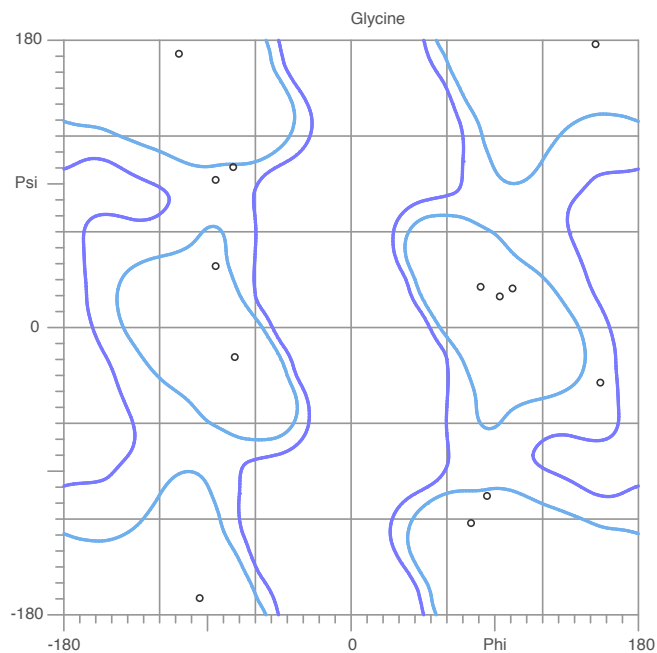
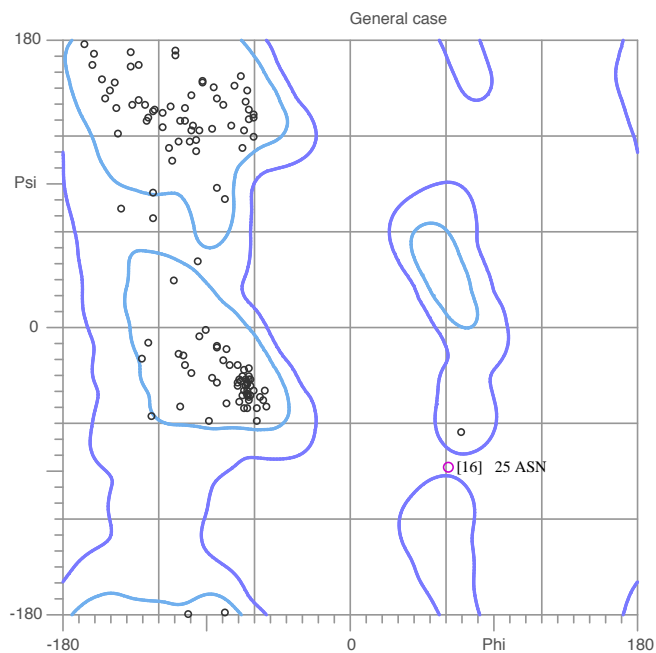
There were 1 outliers (phi, psi):
[15] 148 GLY (-160.4, -35.0)

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MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 16

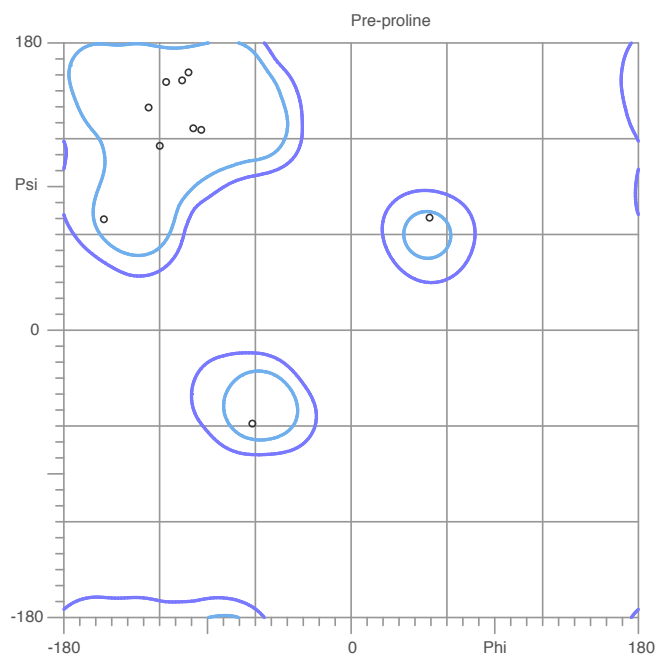
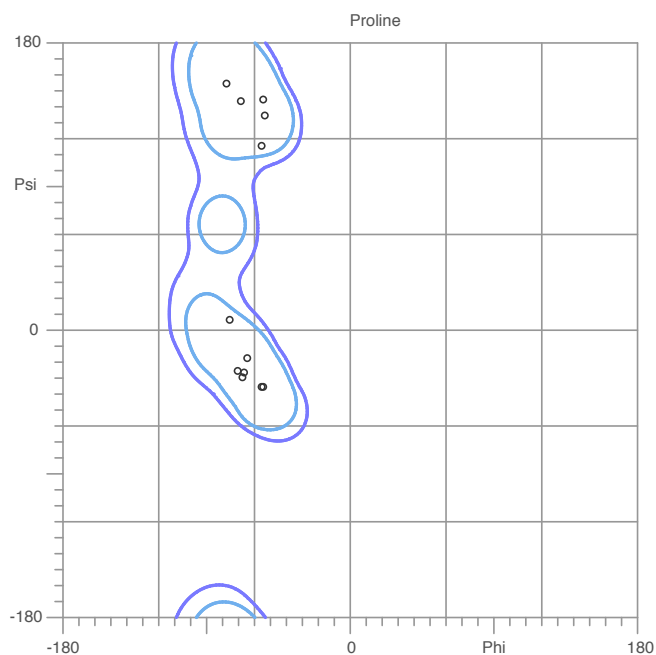
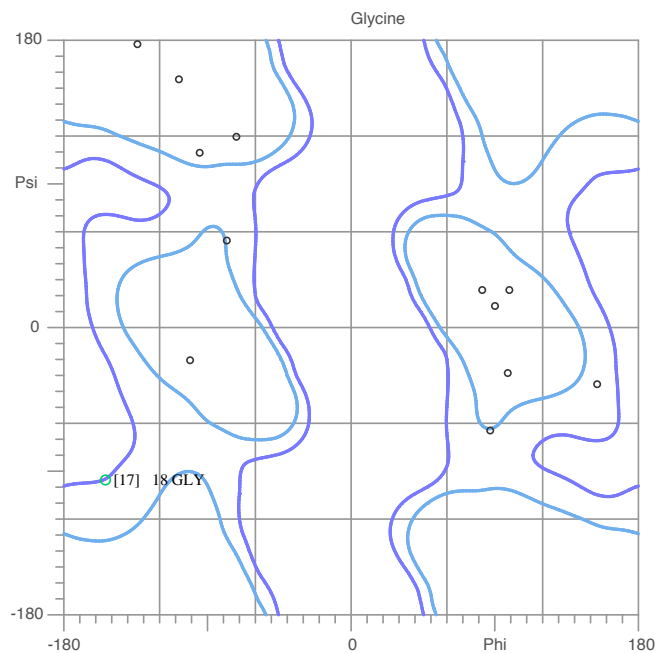
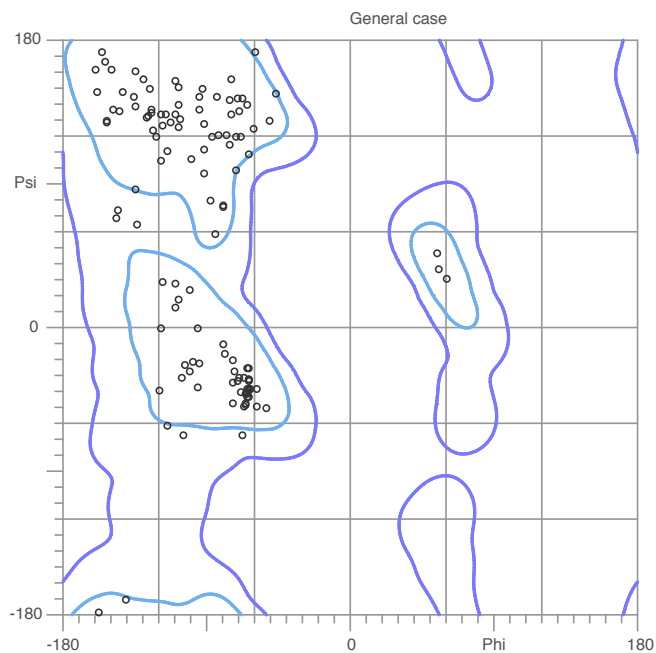


92.9% (145/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[16] 25 ASN (61.0, -87.4)
[16] 69 ASP (-161.2, -49.6)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 17

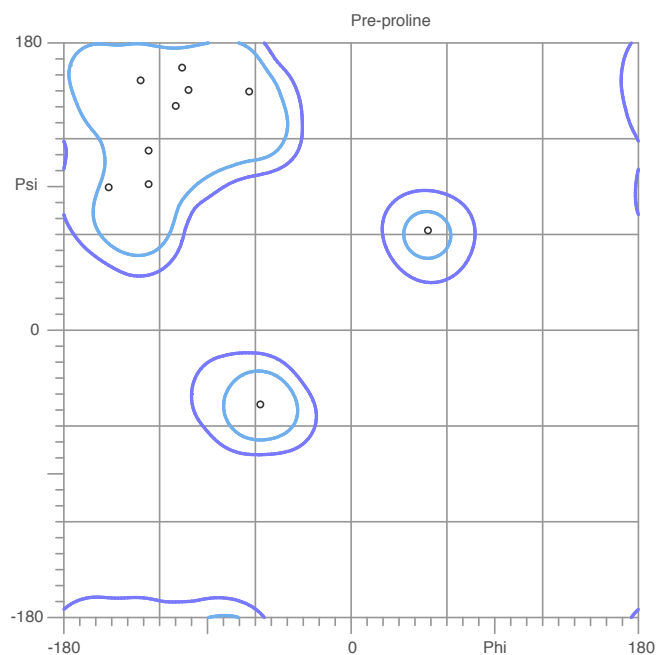
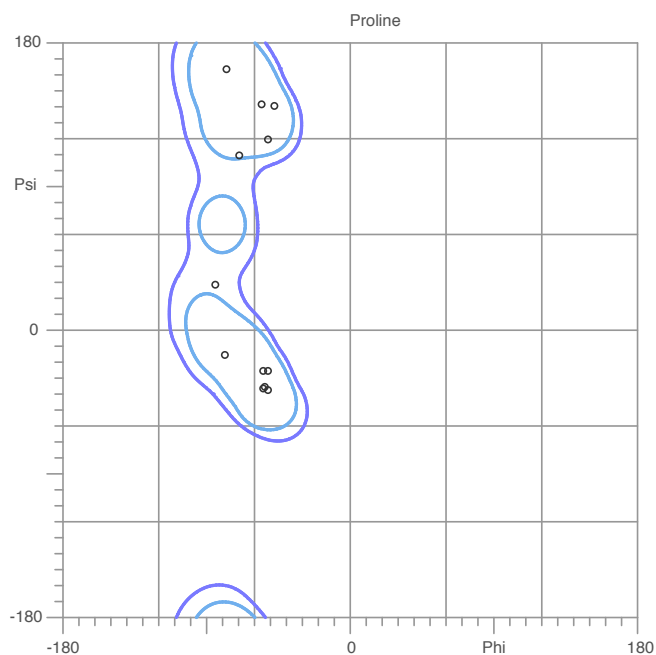
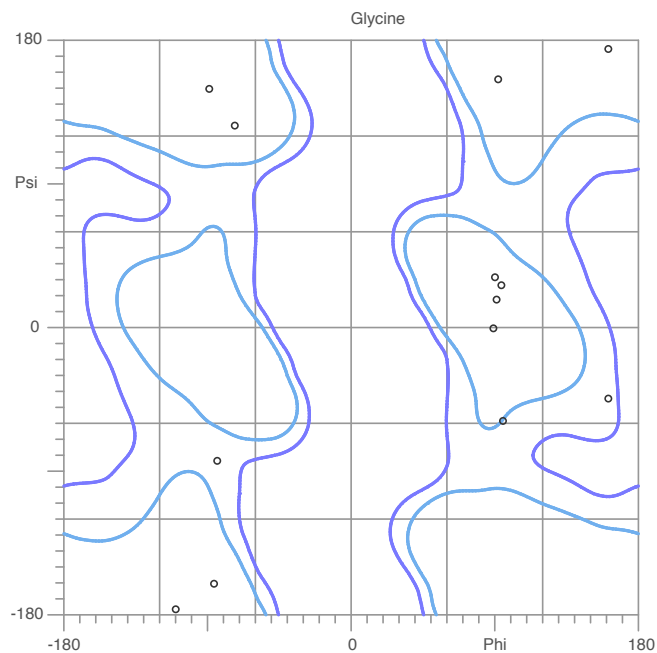
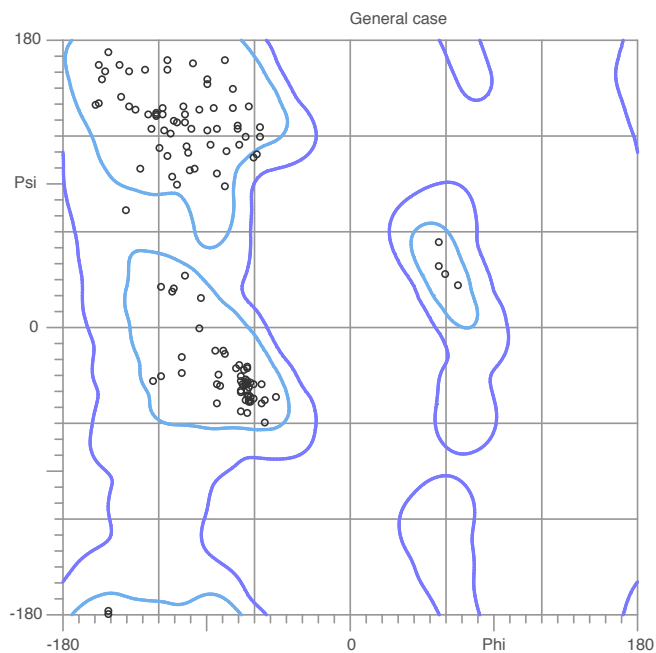


92.9% (145/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[17] 18 GLY (-155.0, -95.0)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 18



95.5% (149/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

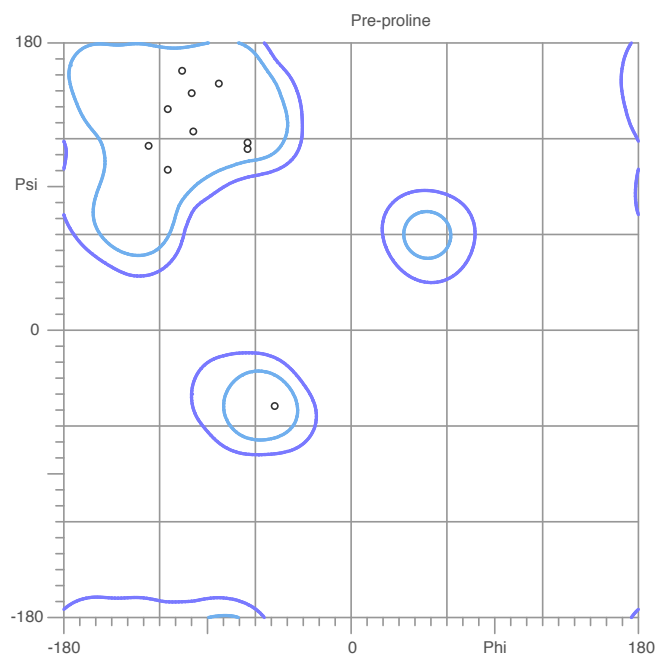
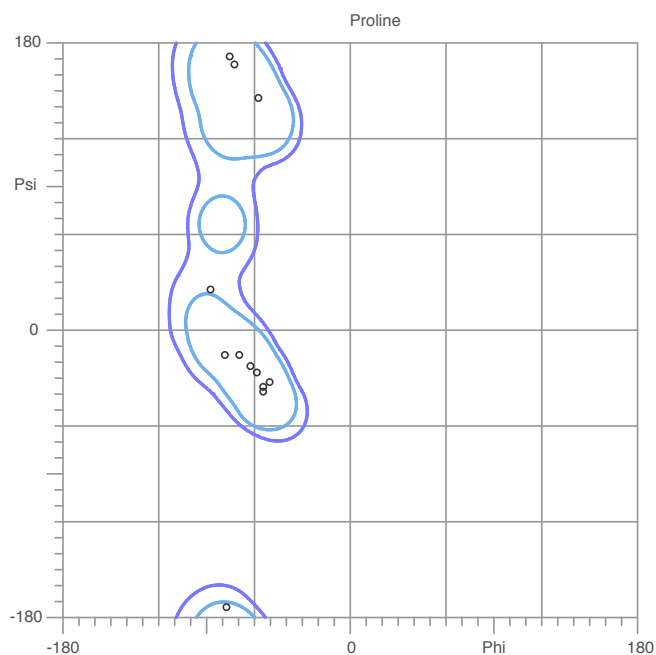
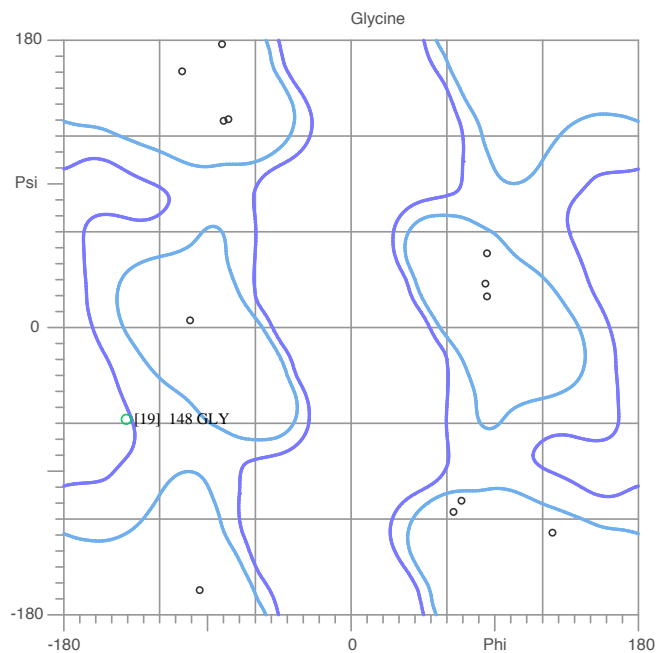
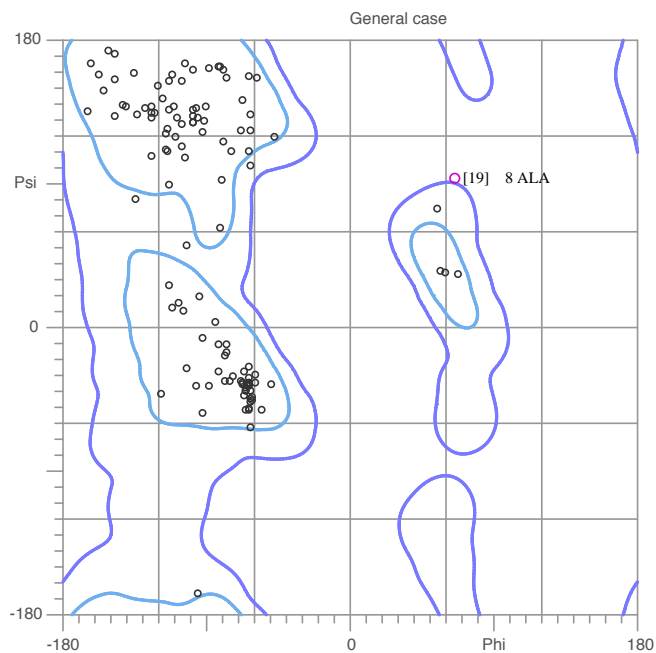
There were no outliers.

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MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 19

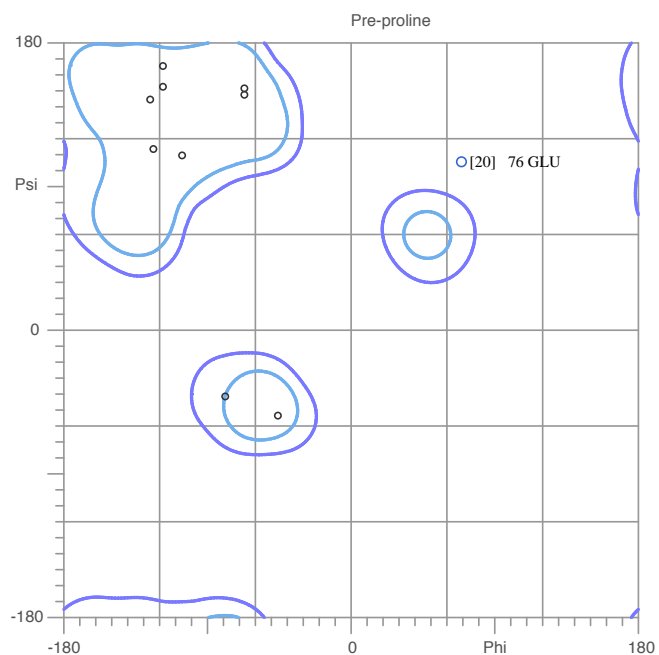
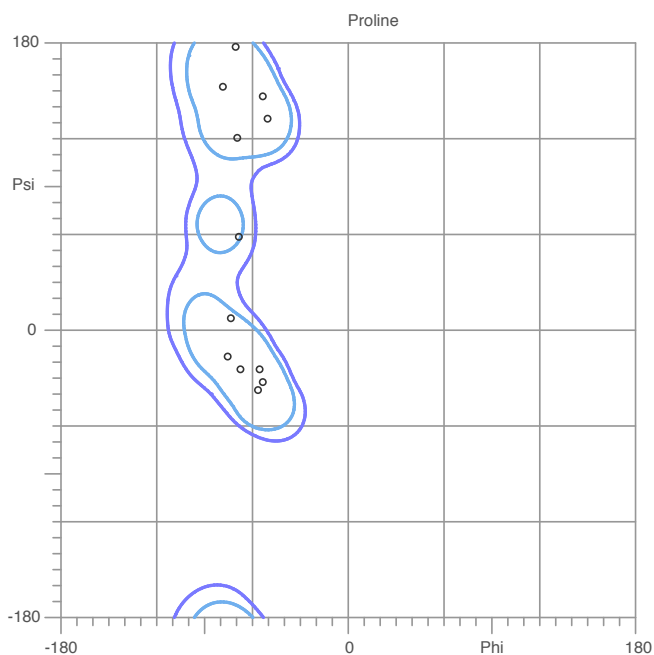
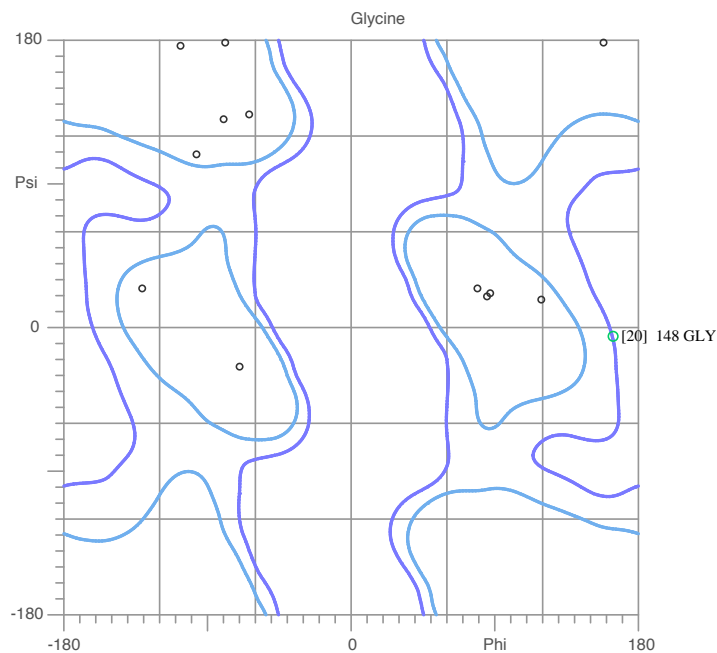
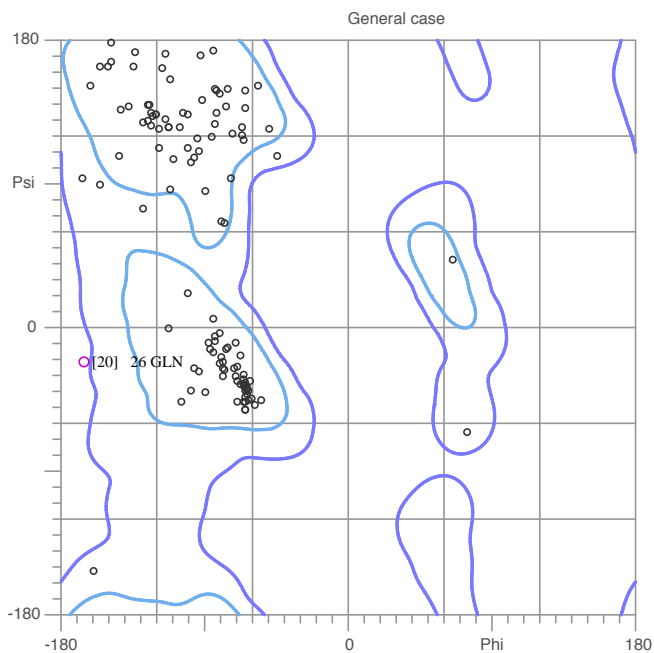


94.9% (148/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 8 ALA (65.1, 95.0)
[19] 148 GLY (-141.1, -57.7)

MolProbity Ramachandran analysis

BER31_R3Cons_em_bcr3.pdb, model 20



93.6% (146/156) 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):
[20] 26 GLN (-166.3, -21.4)
[20] 76 GLU (69.0, 106.6)
[20] 148 GLY (165.0, -5.0)