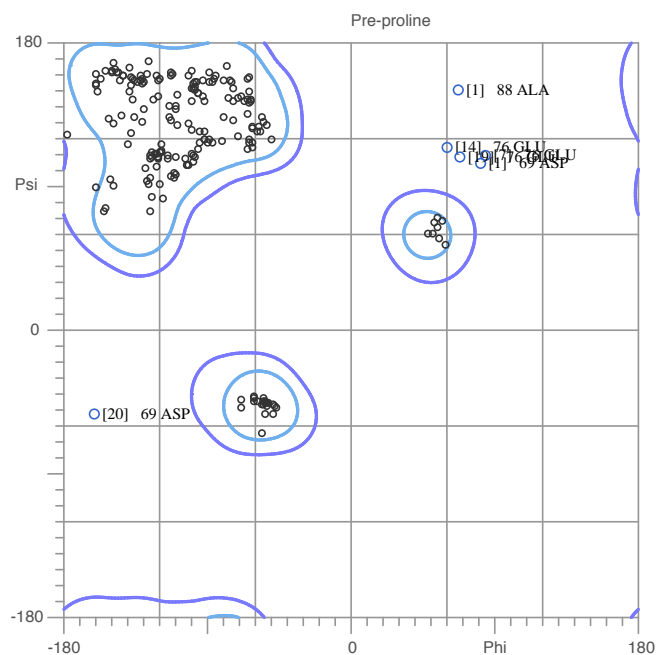
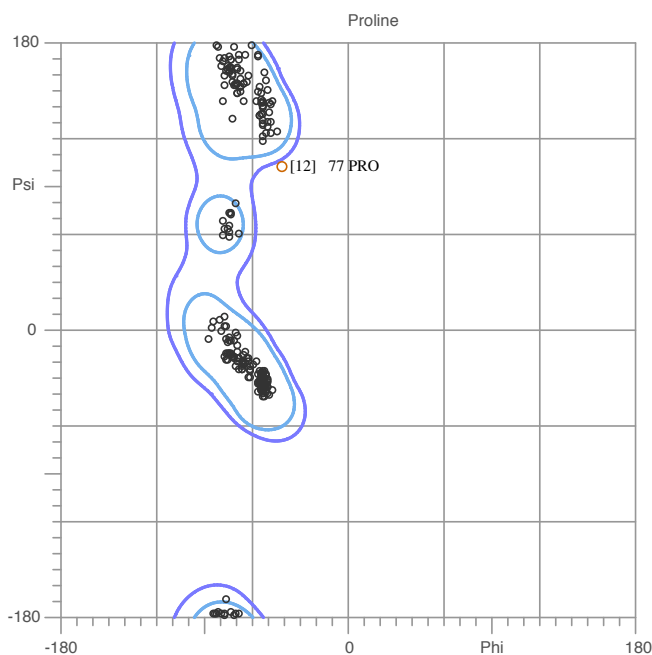
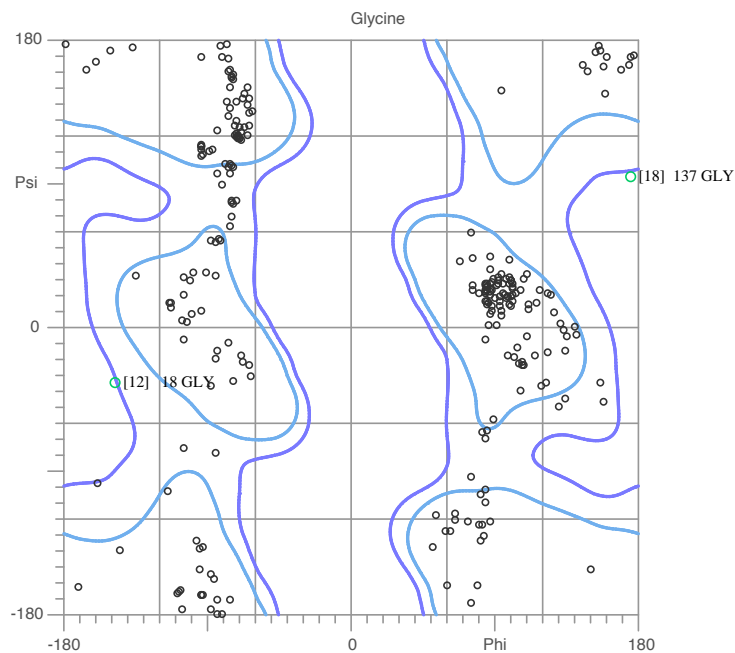
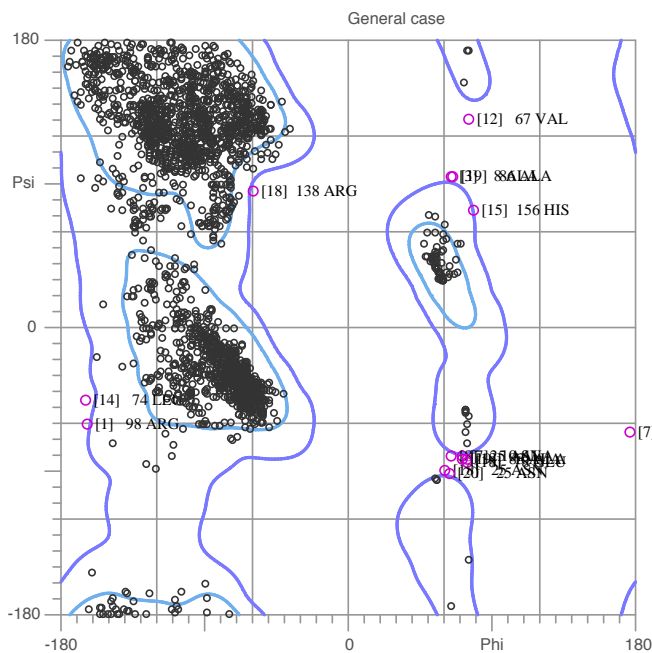


MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, all models



94.8% (2957/3120) of all residues were in favored (98%) regions.
99.2% (3096/3120) of all residues were in allowed (>99.8%) regions.

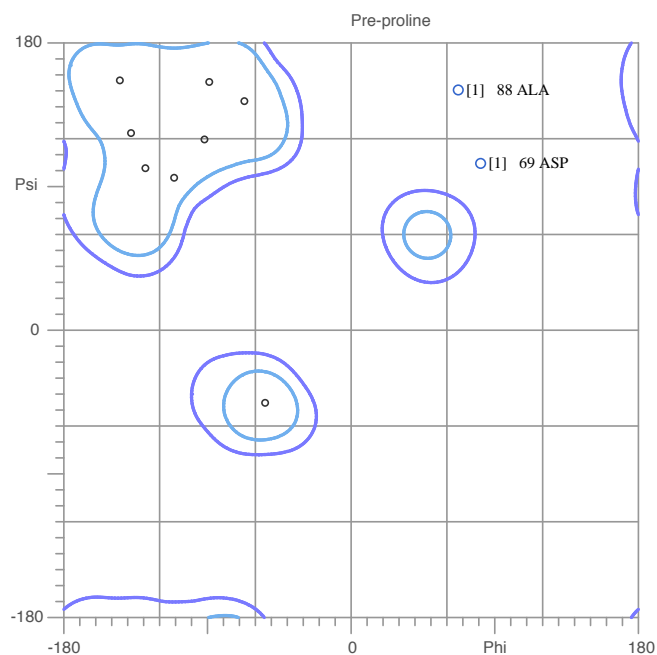
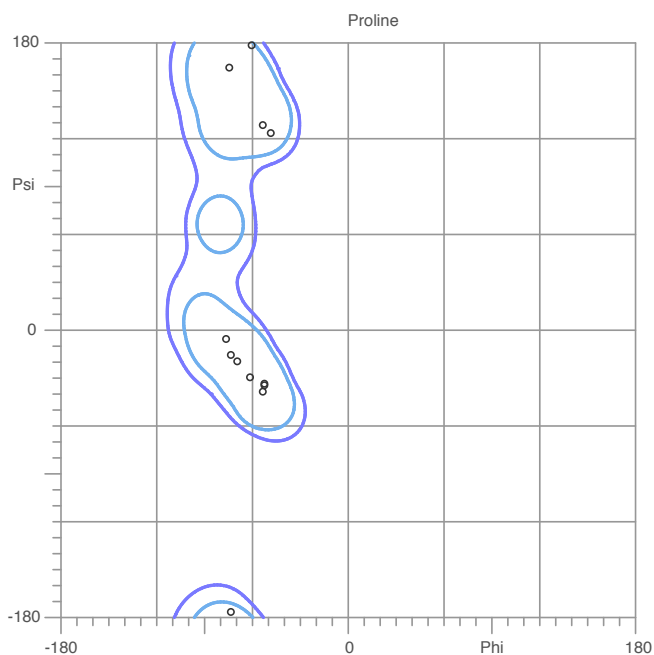
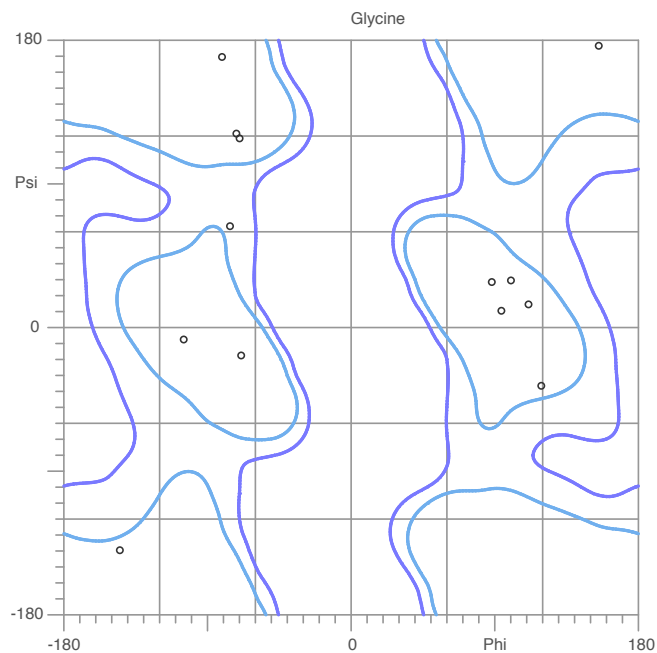
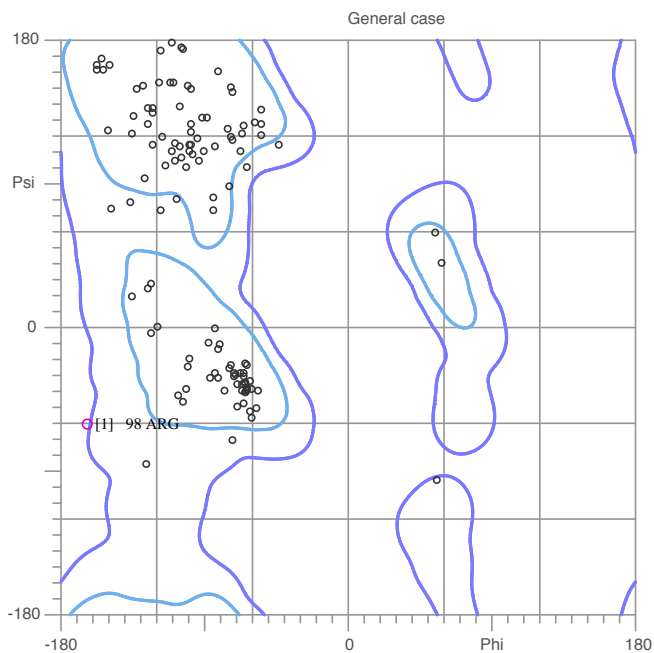
There were 24 outliers (phi, psi):

- [1] 69 ASP (81.2, 105.0)
- [1] 88 ALA (67.9, 151.4)
- [1] 98 ARG (-164.9, -60.5)
- [3] 8 ALA (64.9, 95.0)
- [7] 10 ALA (71.3, -80.6)
- [7] 76 GLU (84.9, 110.1)
- [7] 86 ALA (176.0, -65.1)
- [8] 25 ASN (65.0, -80.2)
- [12] 18 GLY (-148.0, -34.9)
- [12] 67 VAL (75.1, 131.1)

- [12] 77 PRO (-42.8, 103.0)
- [14] 74 LEU (-165.1, -45.0)
- [14] 76 GLU (60.7, 116.0)
- [15] 156 HIS (78.5, 75.0)
- [18] 10 ALA (75.0, -82.9)
- [18] 25 ASN (60.4, -89.0)
- [18] 78 GLU (75.0, -84.9)
- [18] 137 GLY (175.1, 95.1)
- [18] 138 ARG (-60.6, 86.9)
- [19] 76 GLU (68.3, 109.0)
- [19] 83 ALA (72.0, -82.1)
- [19] 86 ALA (65.0, 95.0)
- [19] 86 ALA (65.0, 95.0)
- [20] 25 ASN (63.1, -91.6)
- [20] 69 ASP (-161.6, -52.8)

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 1



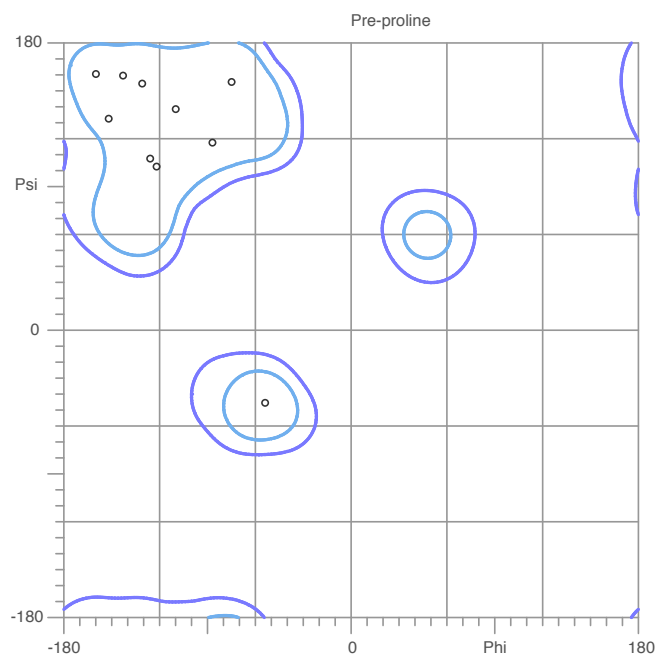
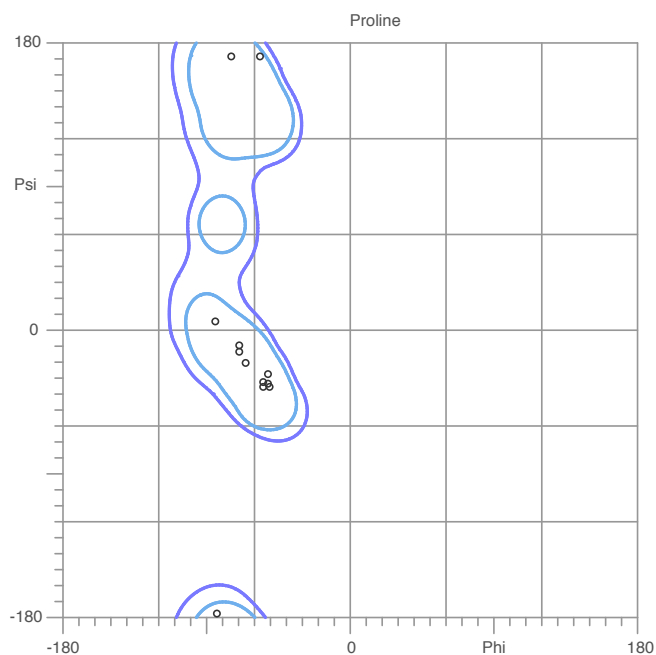
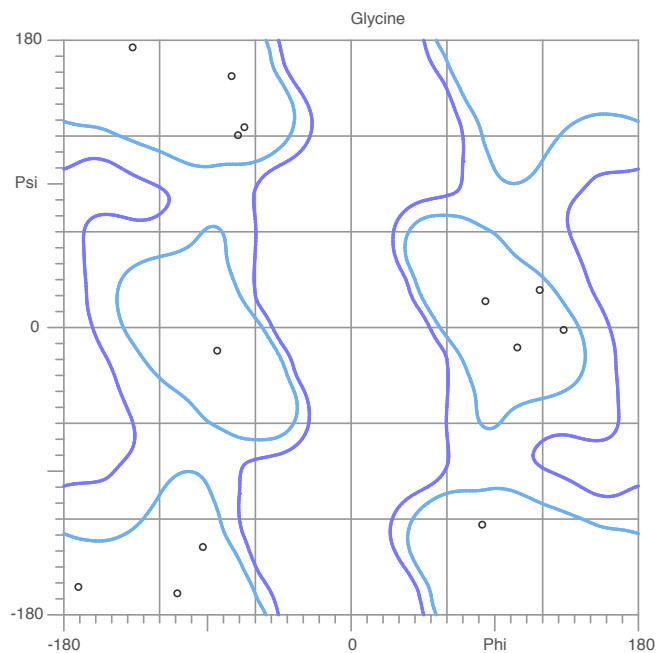
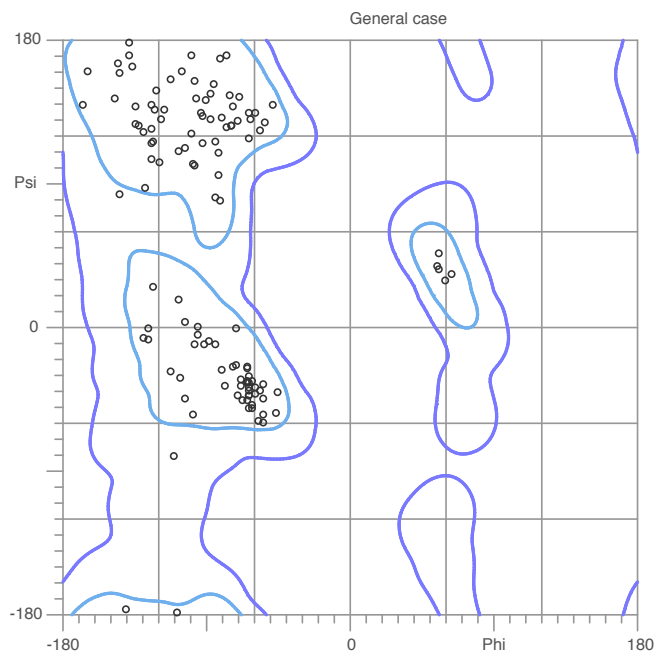
91.7% (143/156) of all residues were in favored (98%) regions.
98.1% (153/156) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 69 ASP (81.2, 105.0)
- [1] 88 ALA (67.9, 151.4)
- [1] 98 ARG (-164.9, -60.5)

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 2



98.7% (154/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

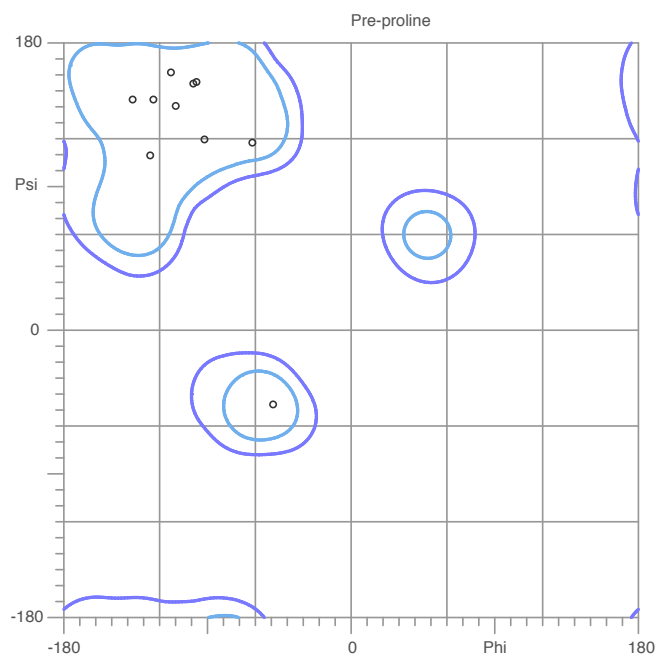
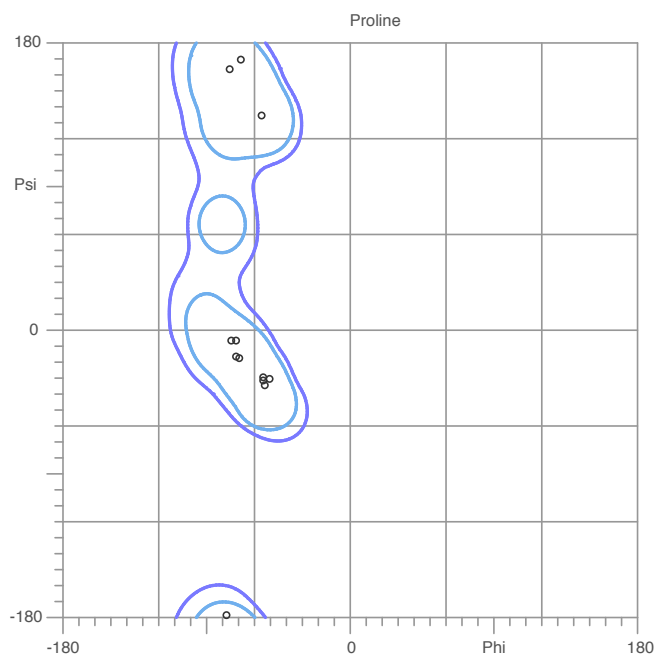
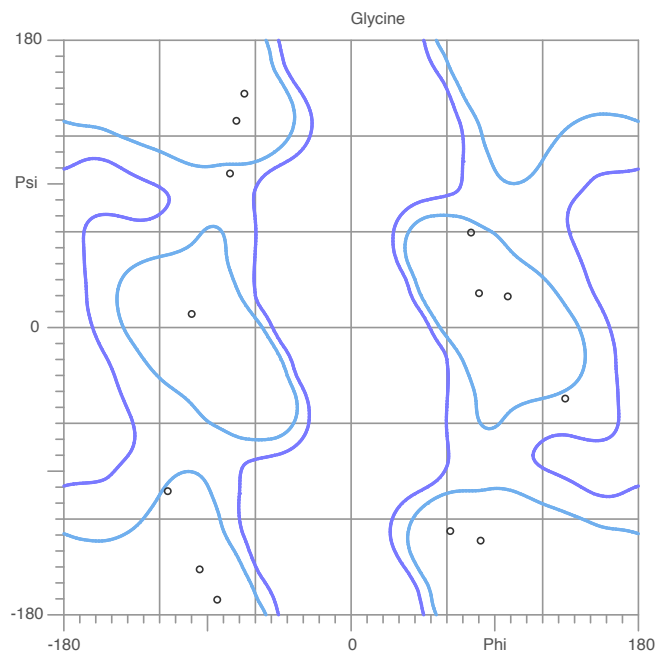
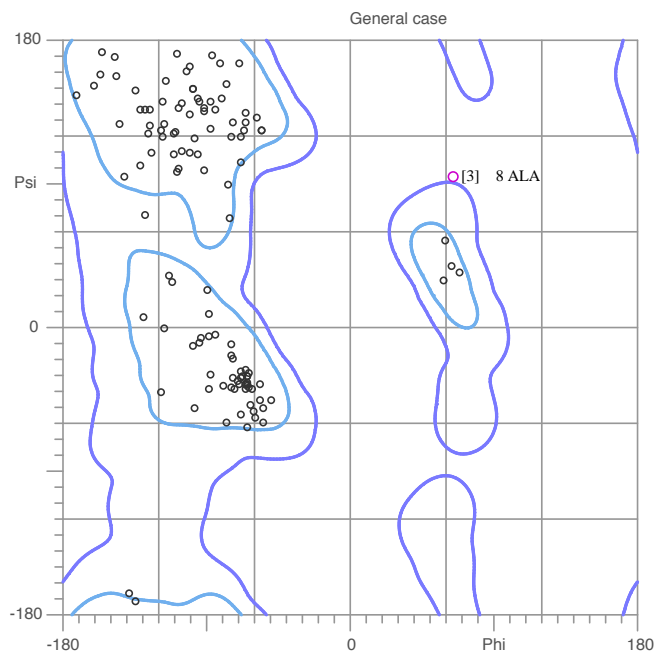
There were no outliers.

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

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MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 3

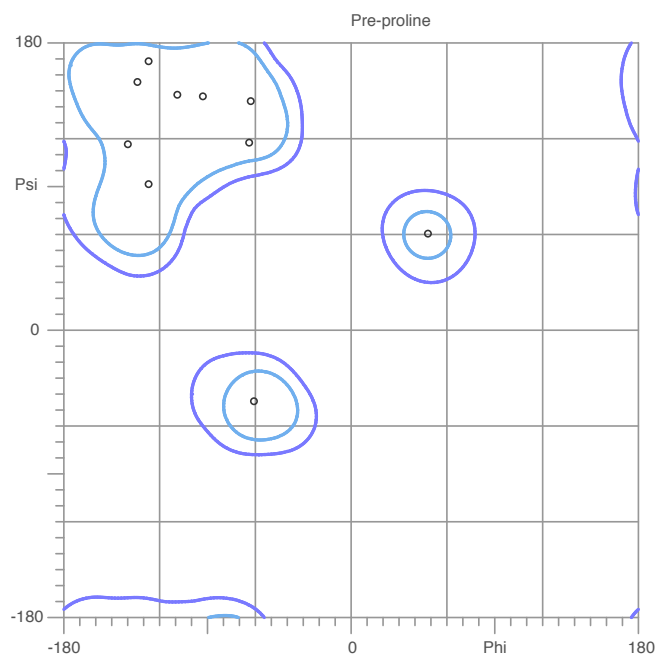
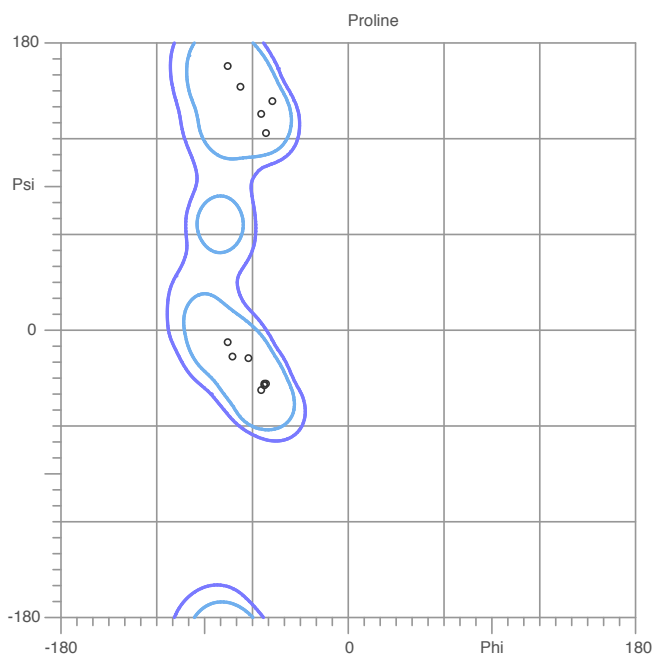
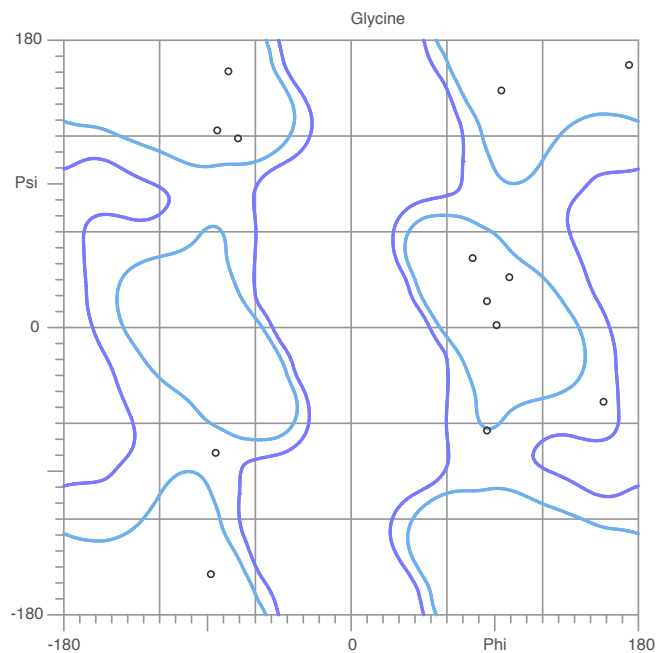
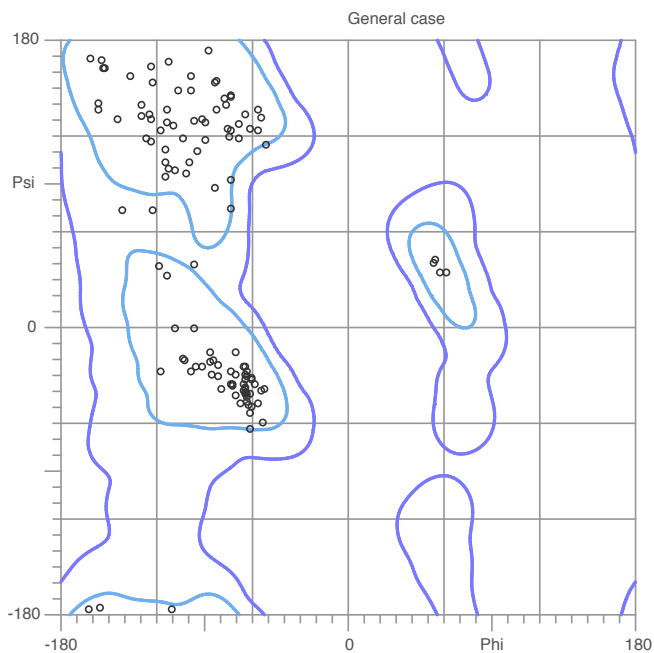


96.8% (151/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 8 ALA (64.9, 95.0)

MolProbity Ramachandran analysis

BER31_R3_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.

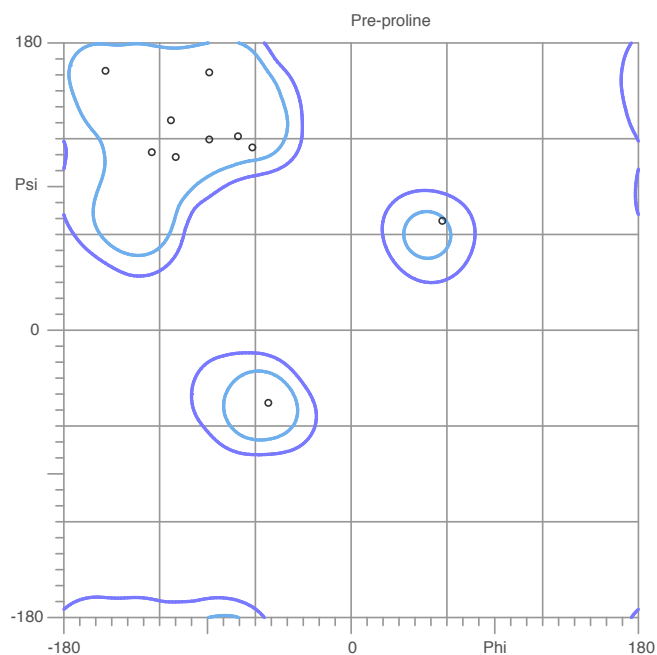
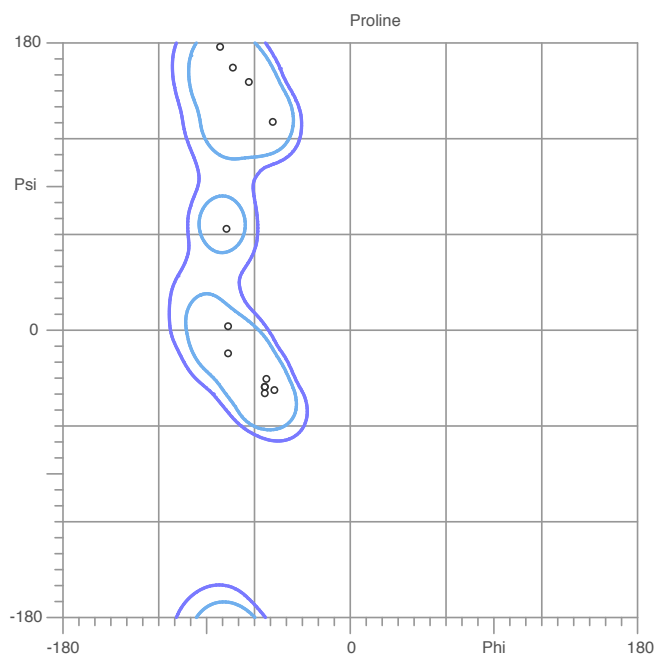
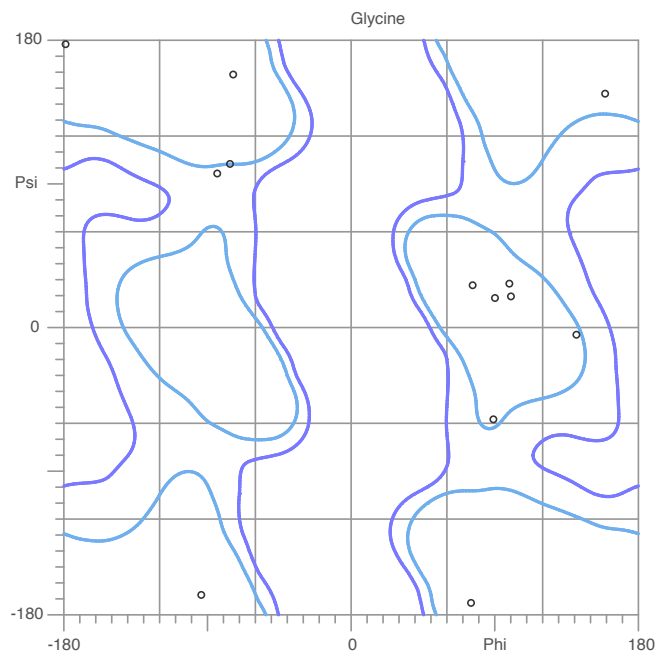
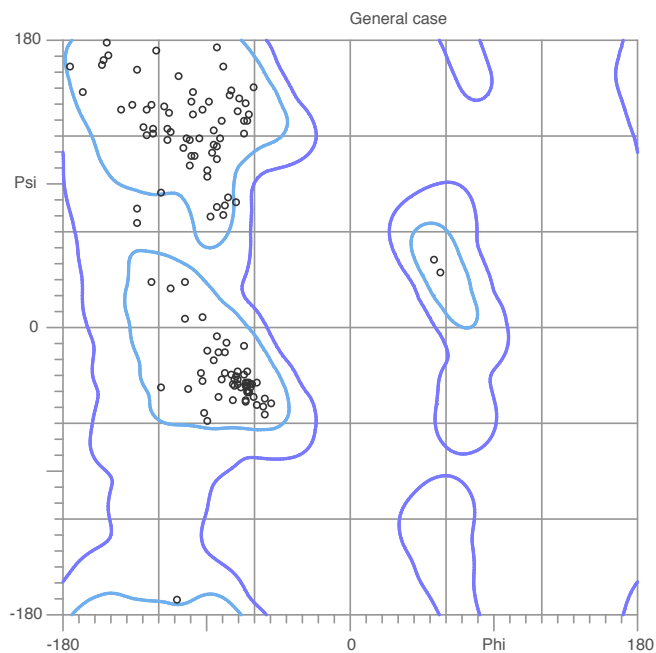
There were no outliers.

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

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MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 5

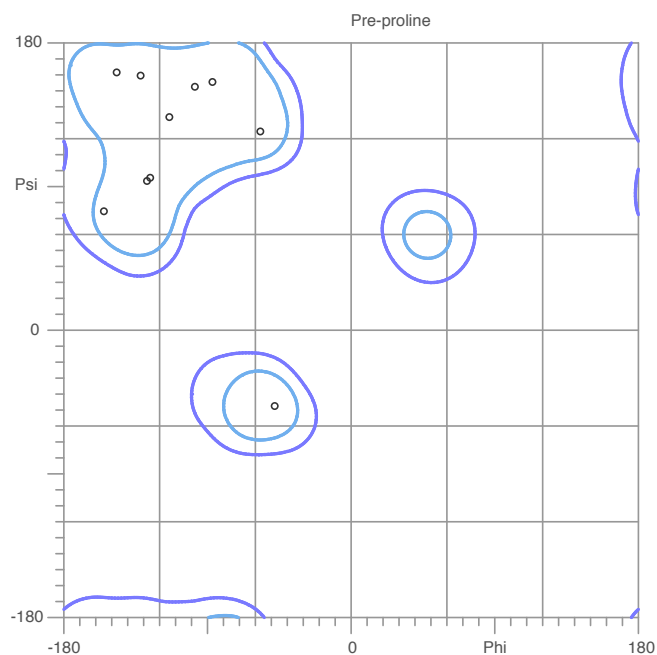
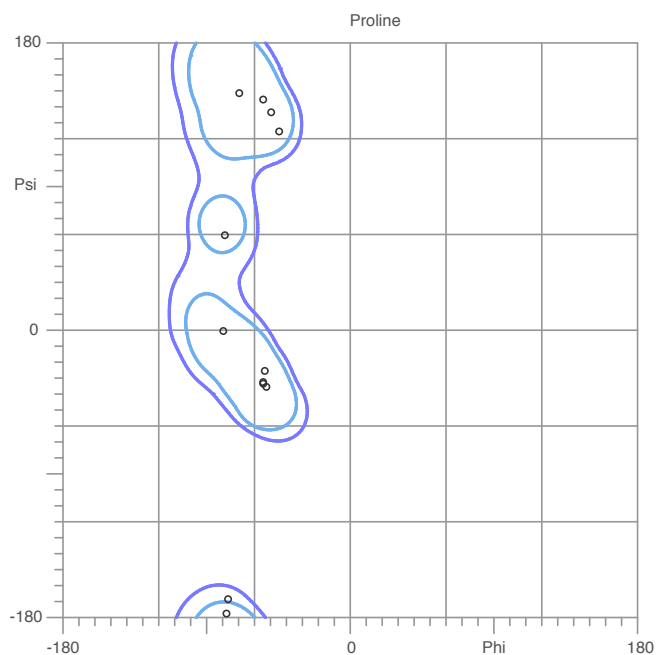
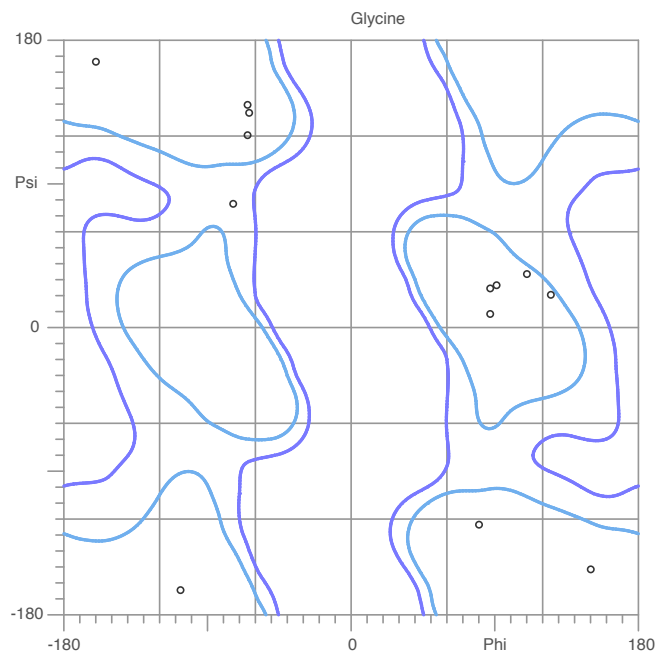
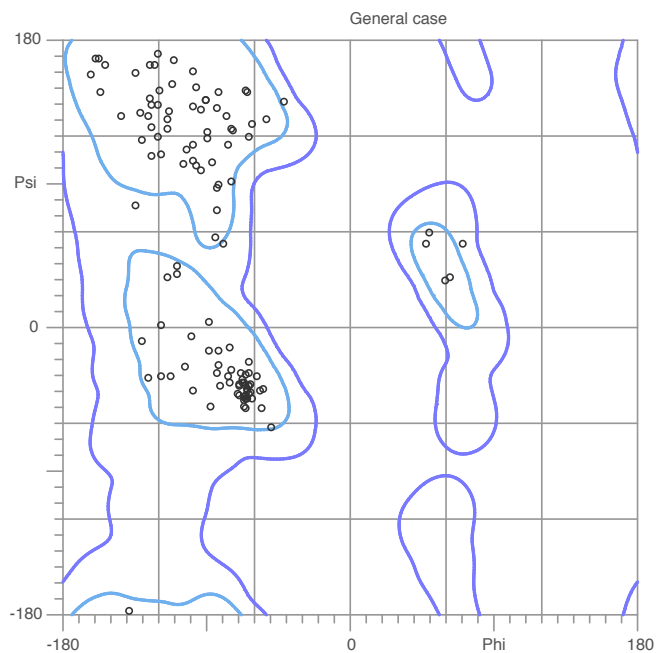


96.8% (151/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 6



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.

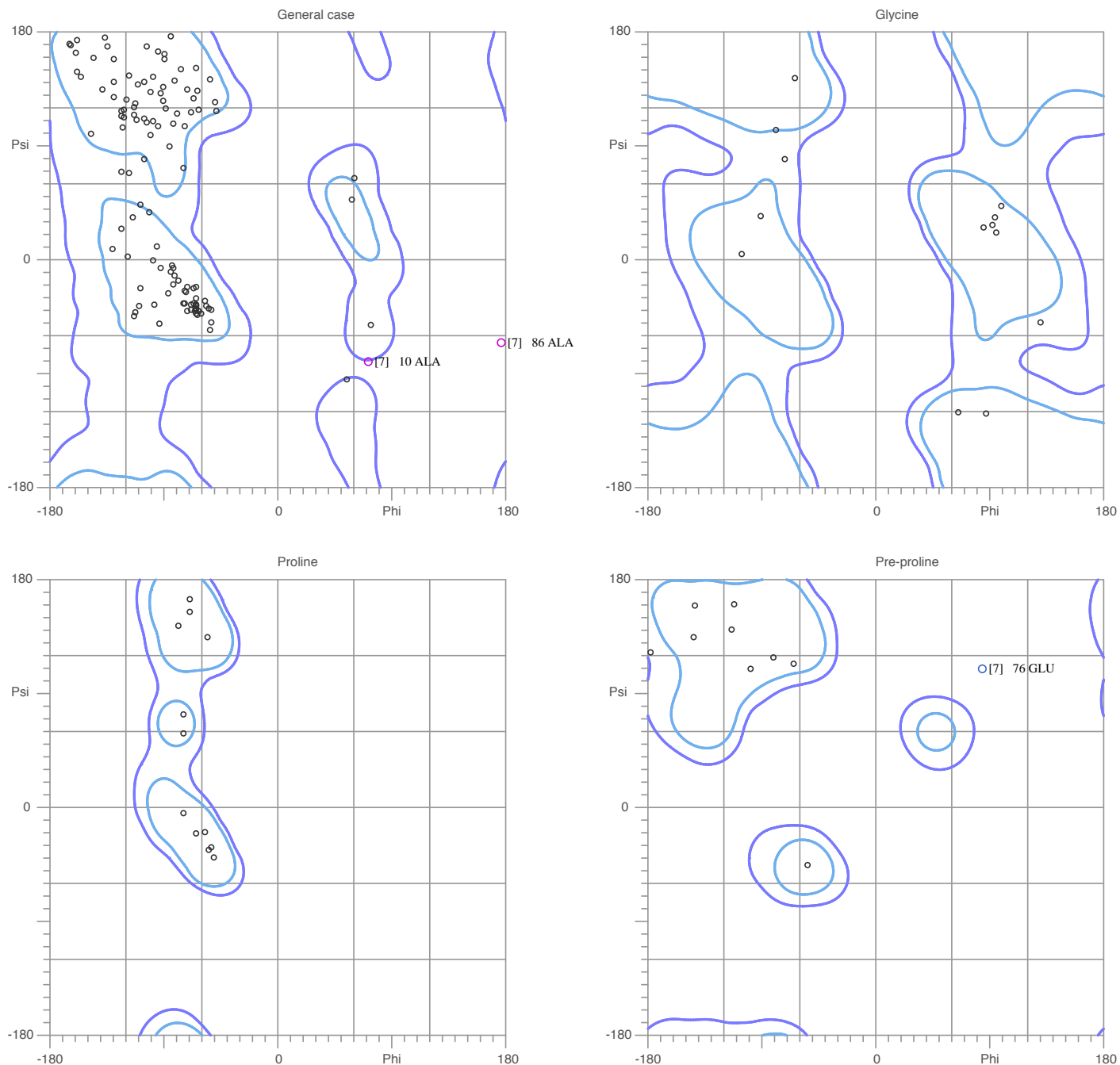
There were no outliers.

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MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 7



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):

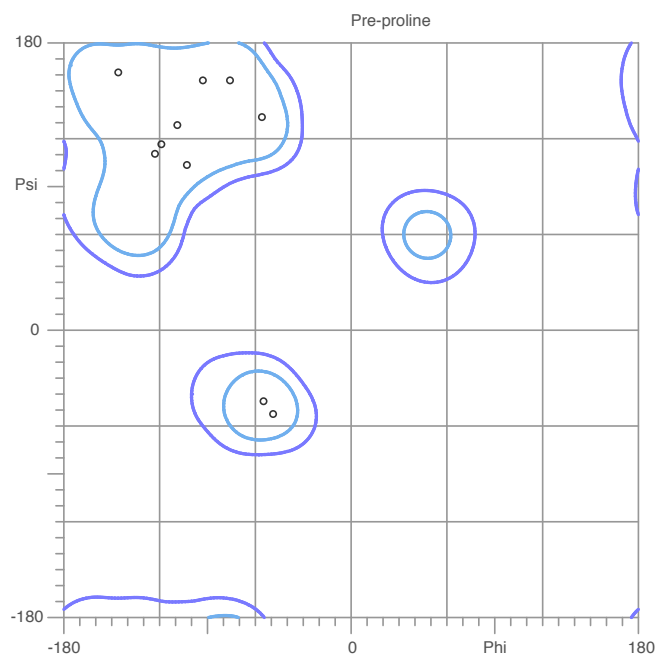
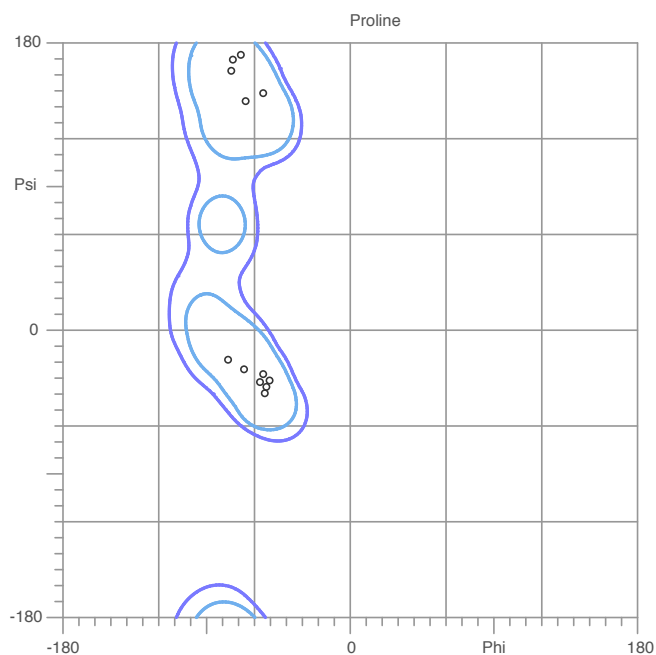
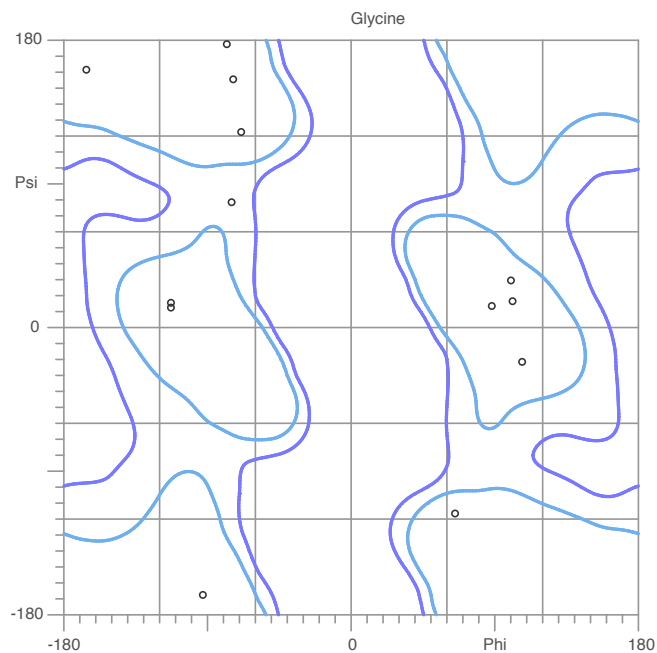
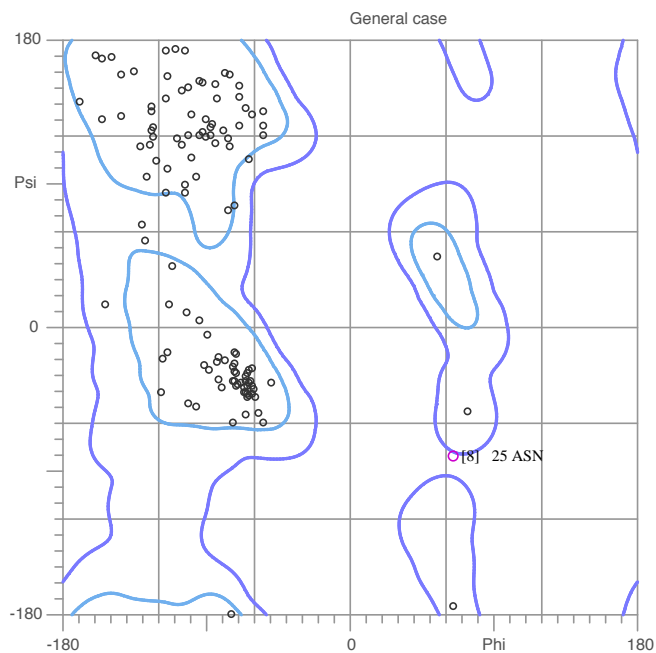
[7] 10 ALA (71.3, -80.6)

[7] 76 GLU (84.9, 110.1)

[7] 86 ALA (176.0, -65.1)

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 8



95.5% (149/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

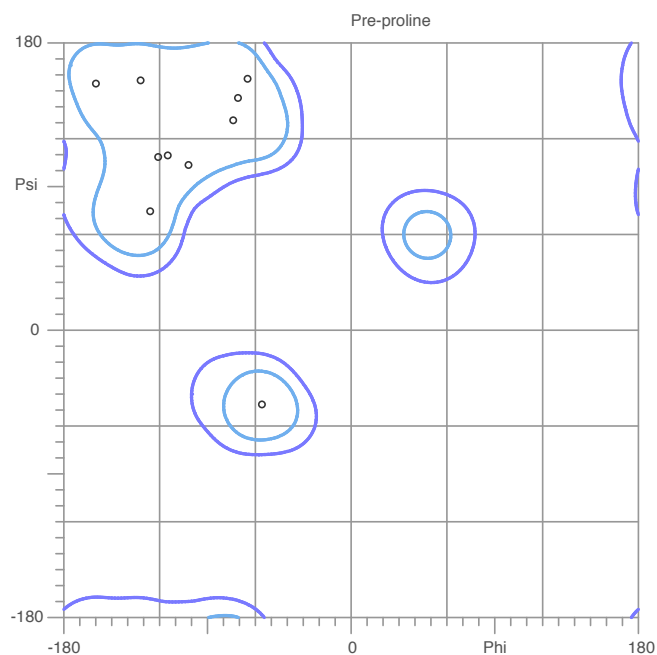
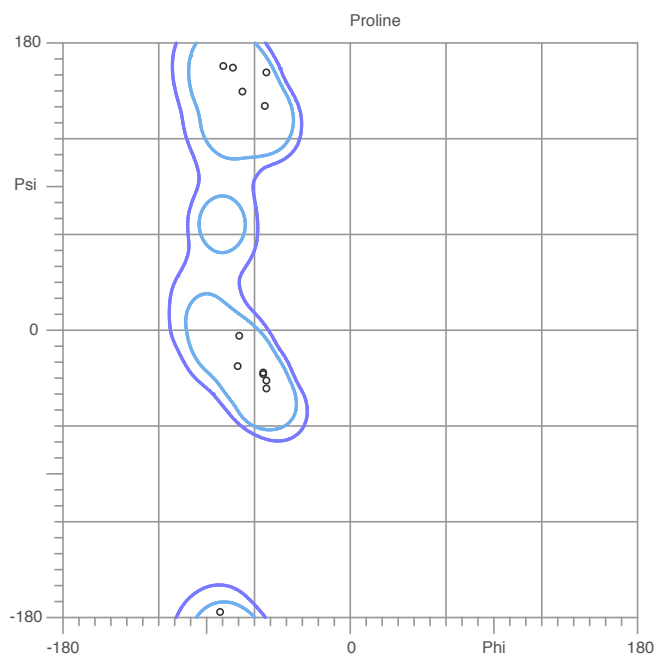
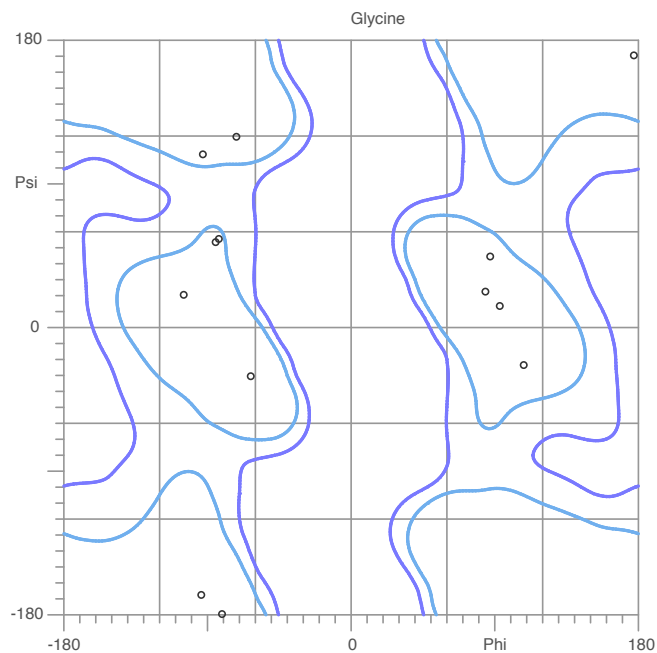
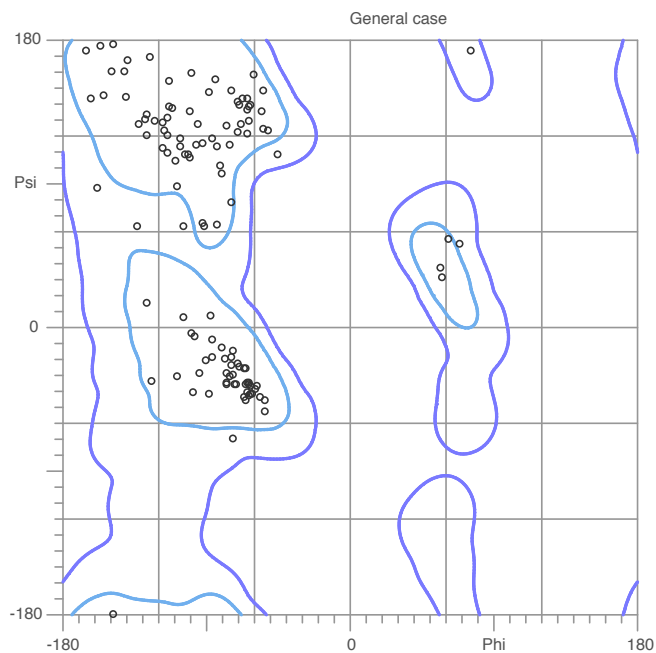
There were 1 outliers (phi, psi):
[8] 25 ASN (65.0, -80.2)

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MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 9



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.

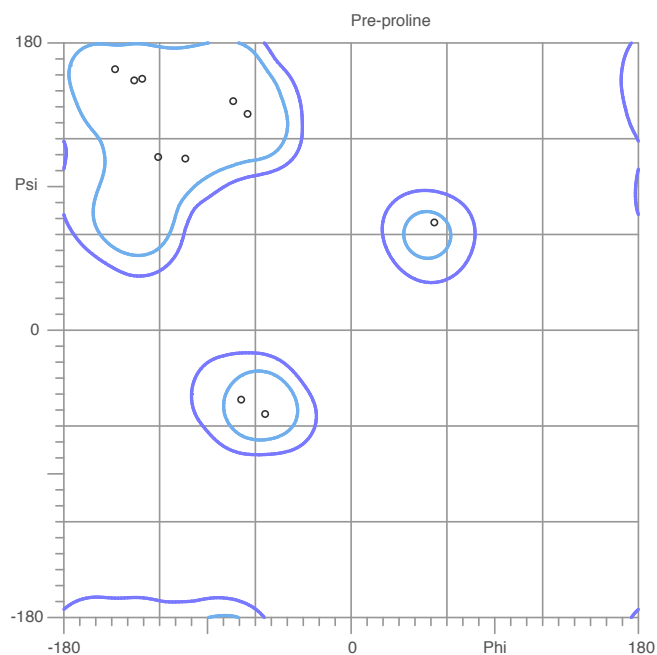
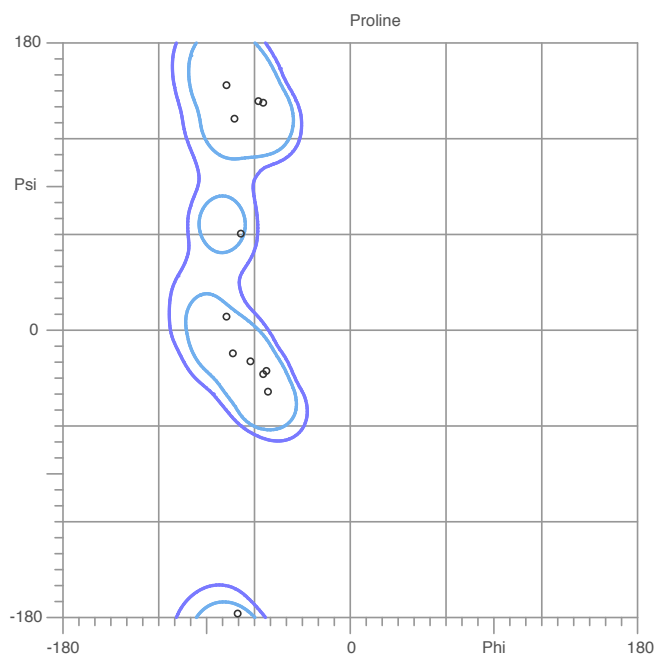
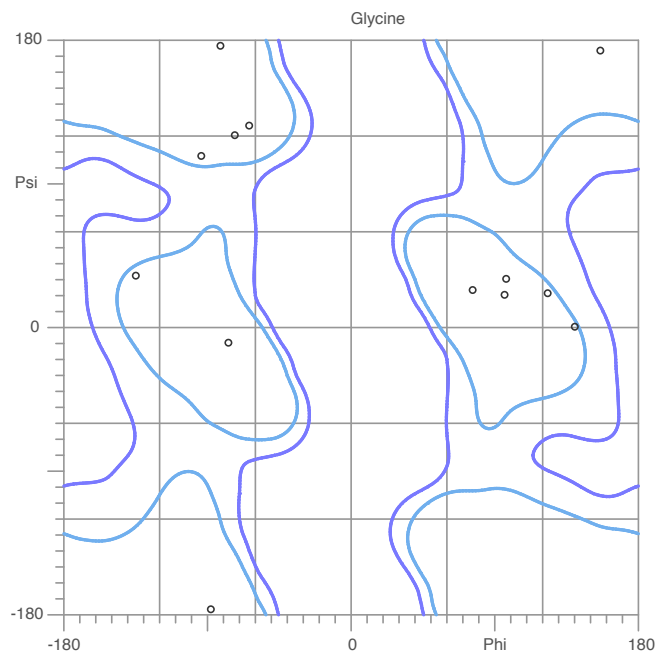
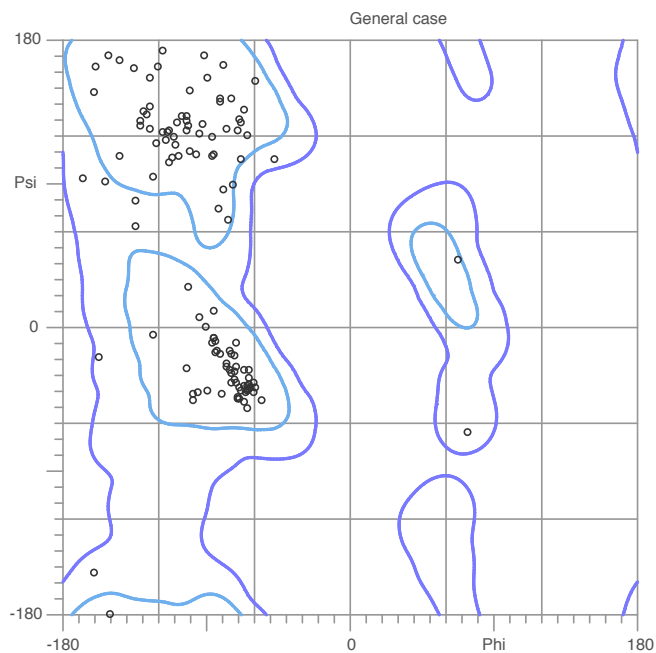
There were no outliers.

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

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MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 10



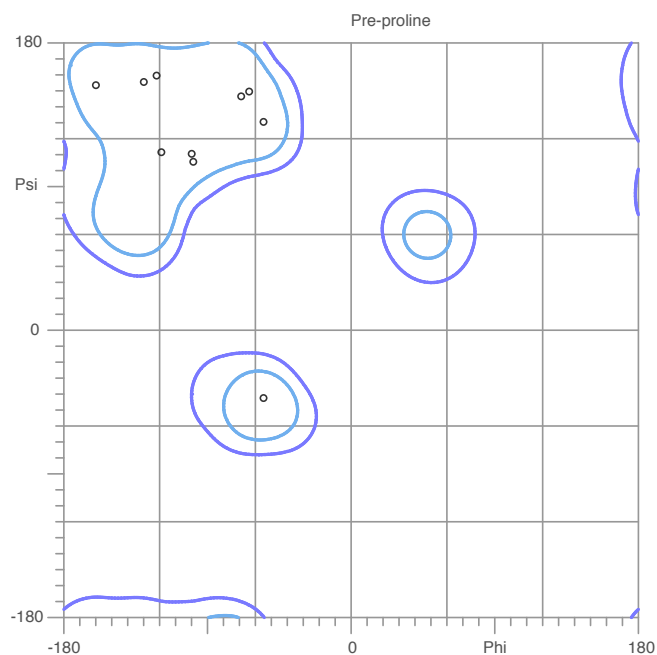
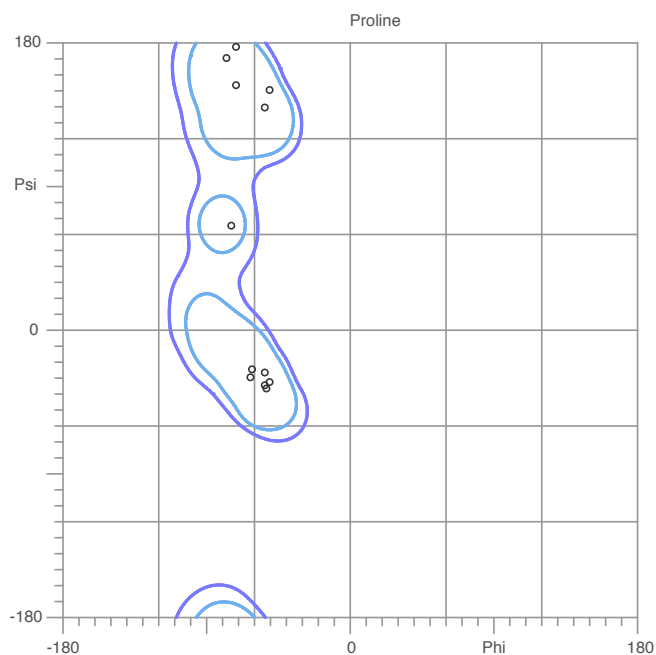
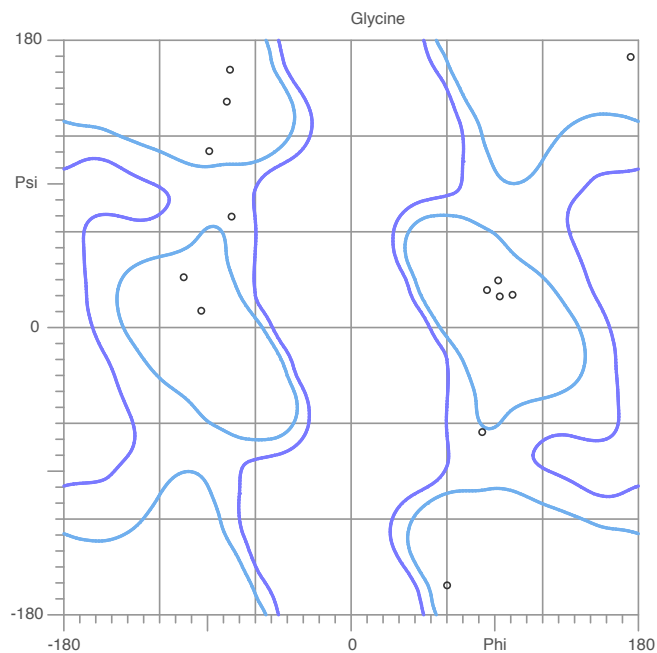
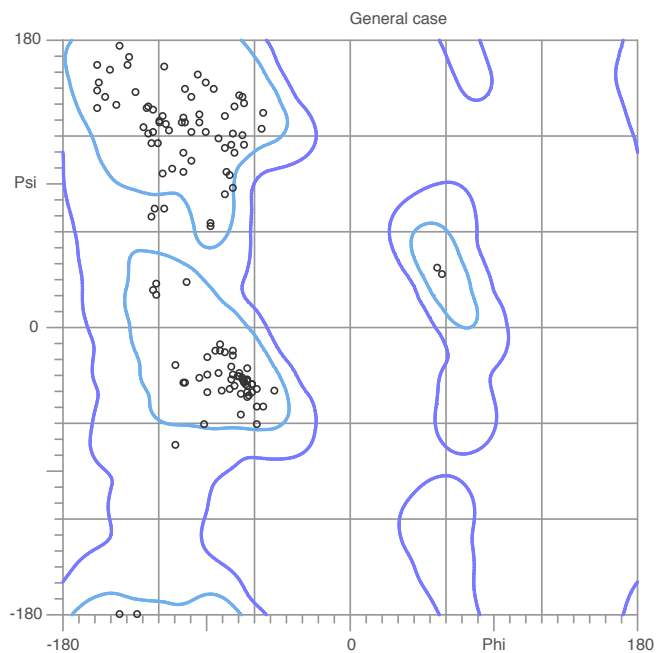
94.9% (148/156) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 11

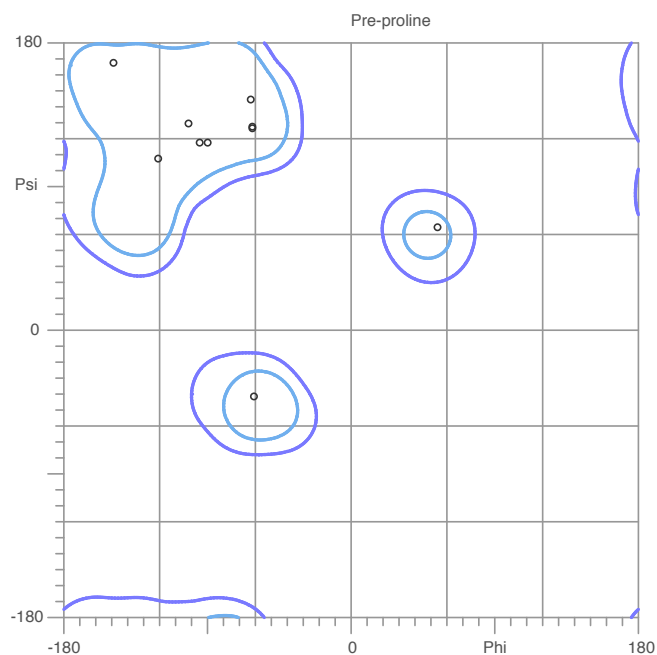
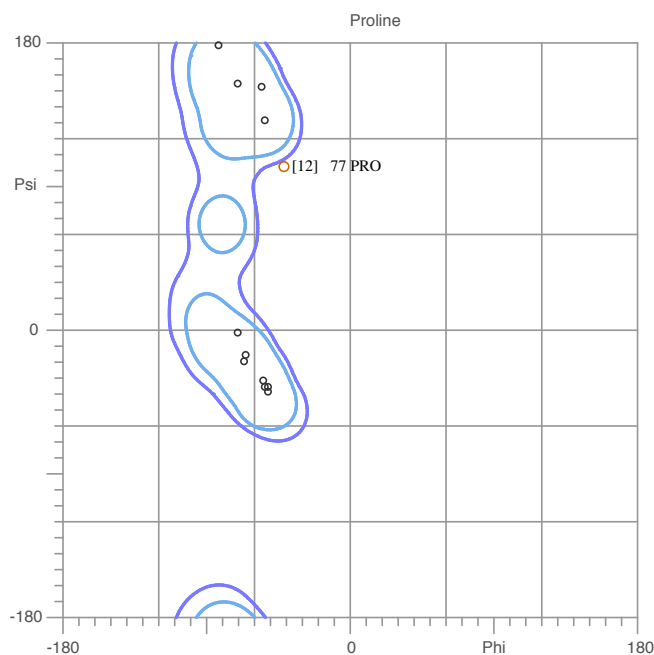
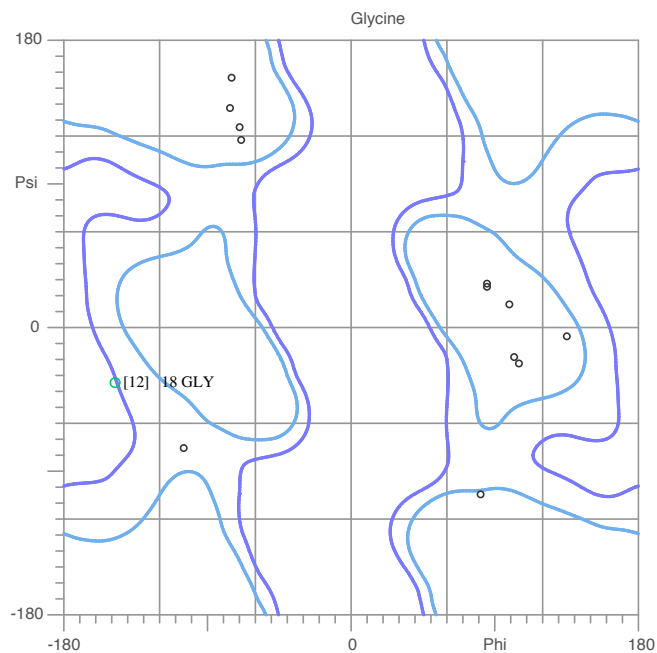
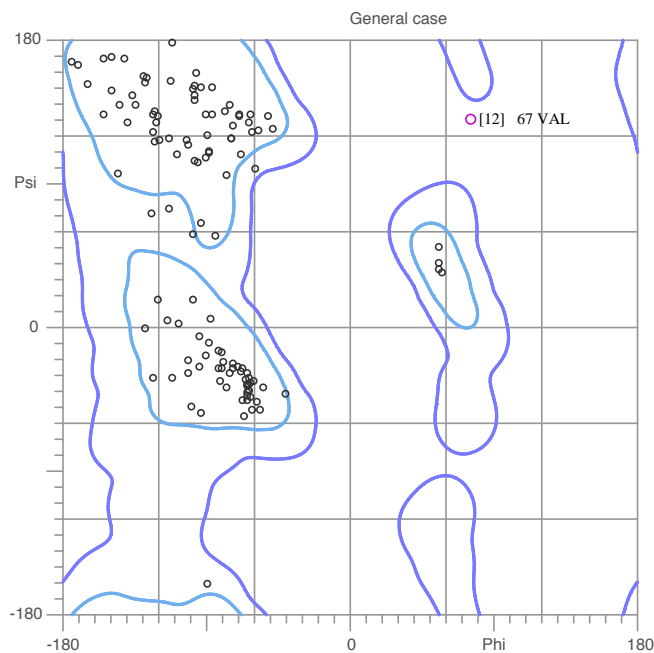


96.2% (150/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 12



94.2% (147/156) 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):

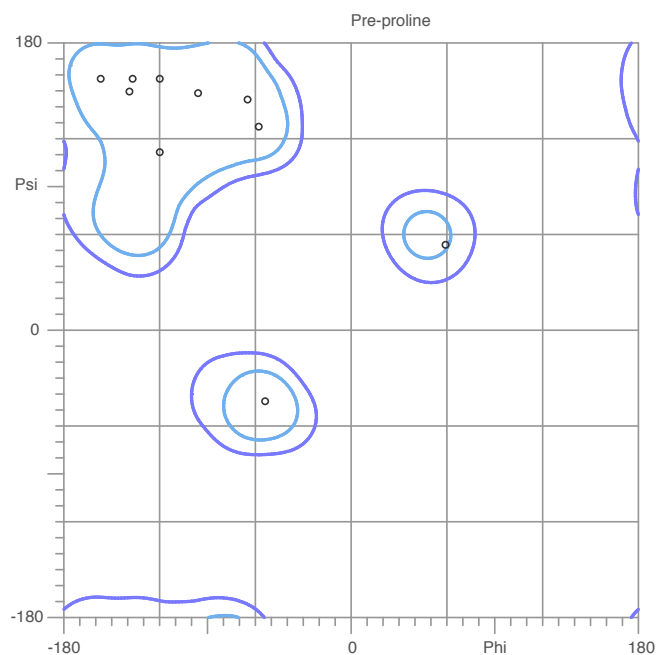
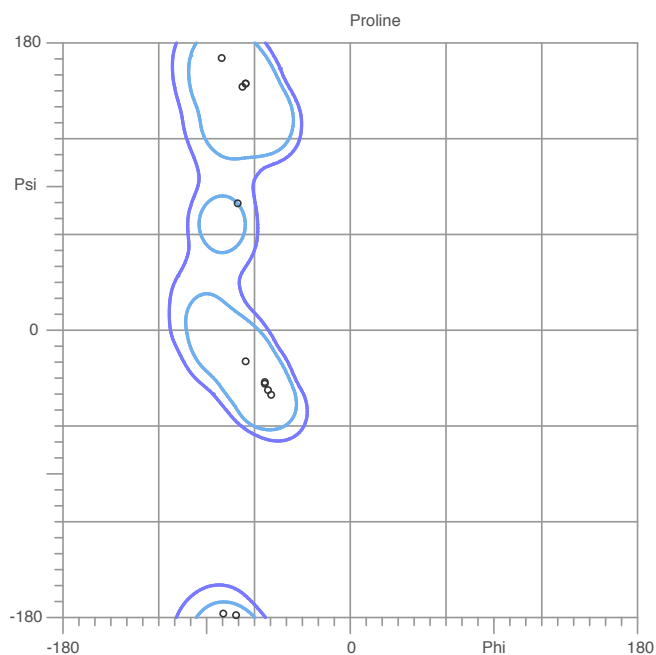
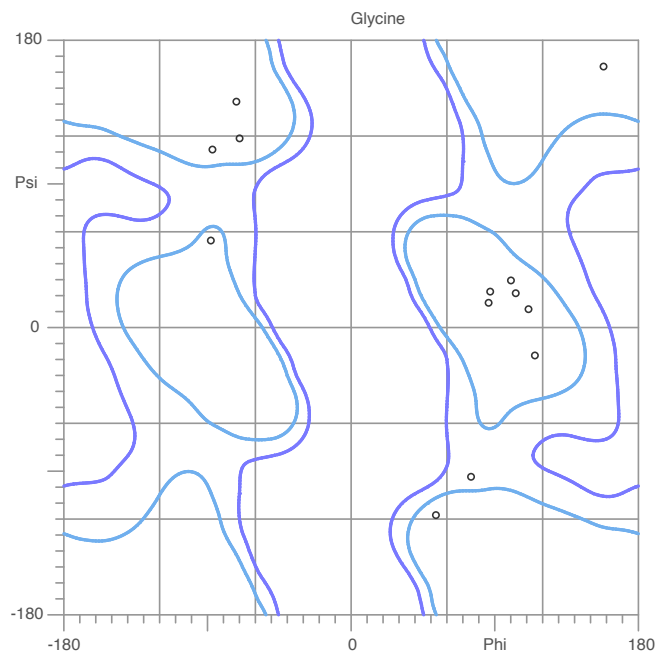
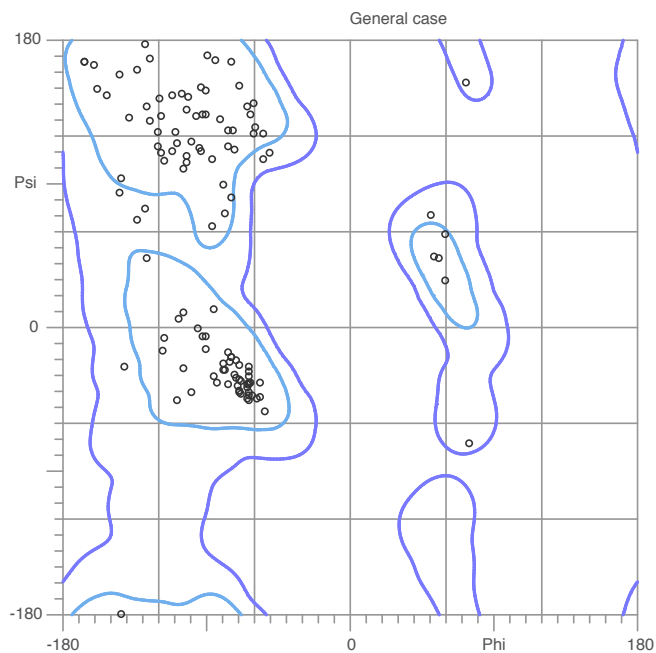
[12] 18 GLY (-148.0, -34.9)

[12] 67 VAL (75.1, 131.1)

[12] 77 PRO (-42.8, 103.0)

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 13



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.

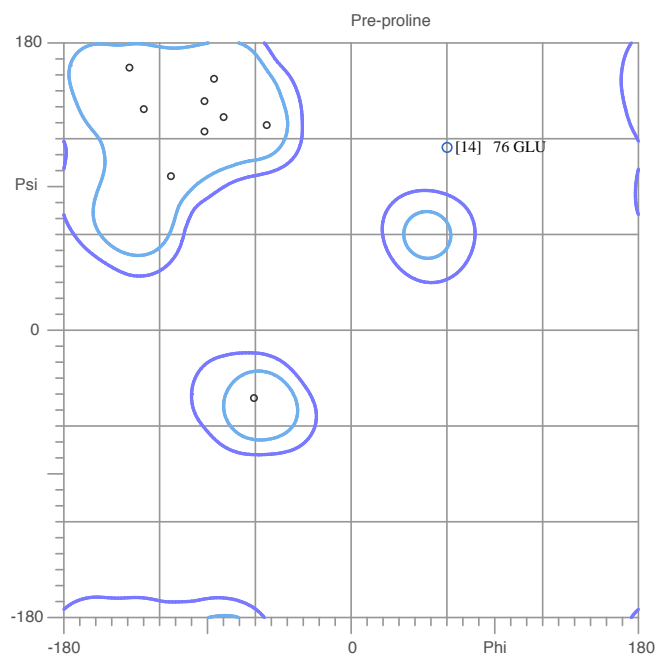
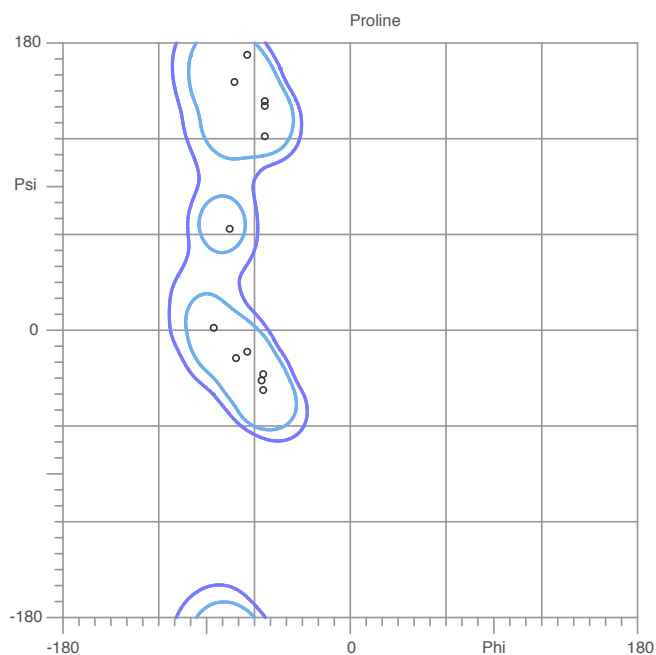
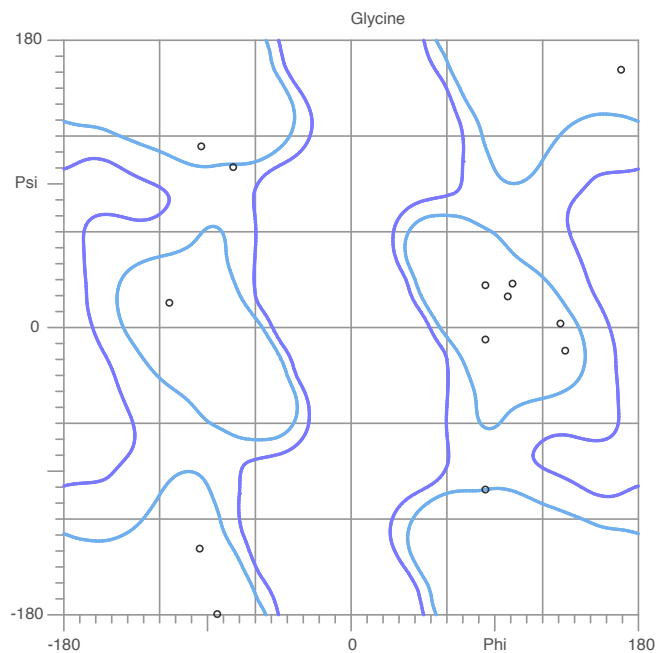
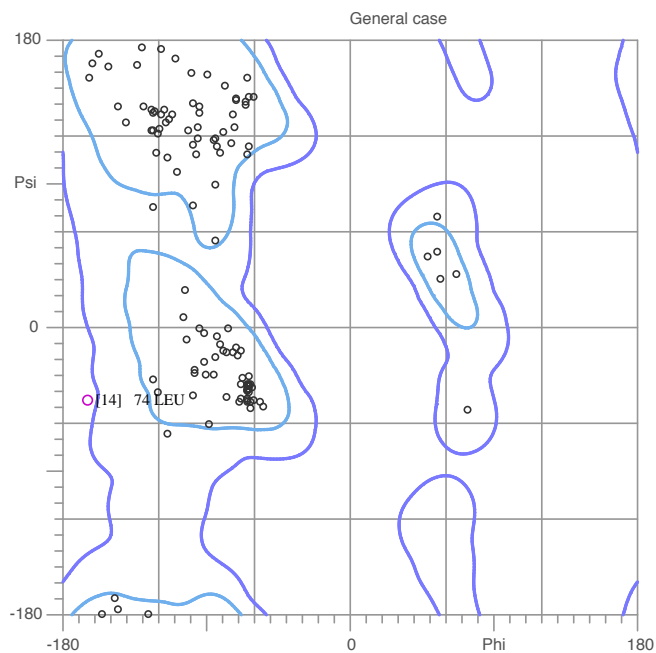
There were no outliers.

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

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MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 14

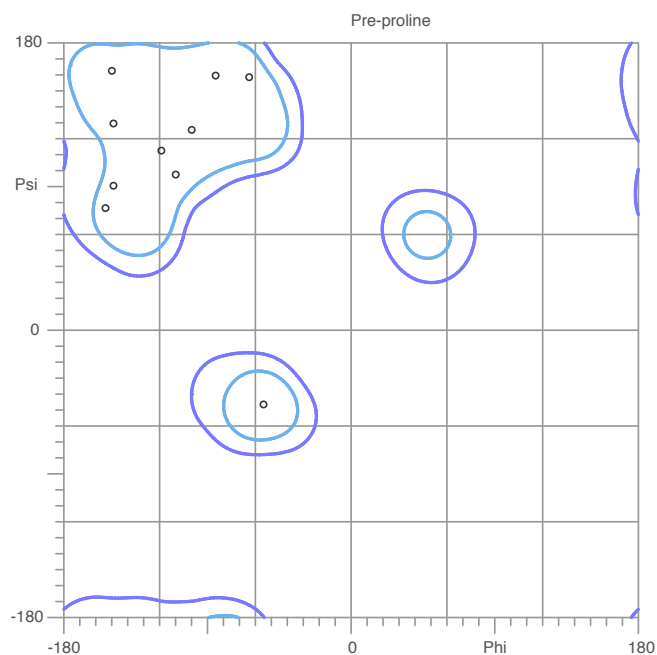
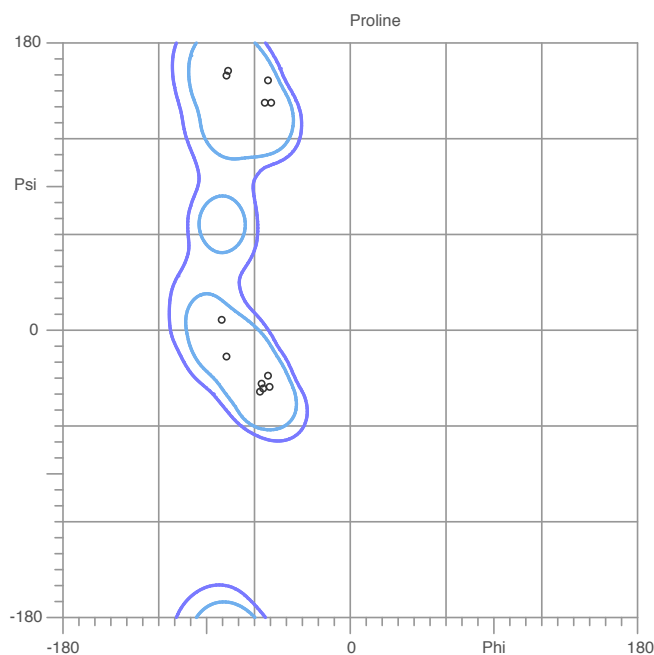
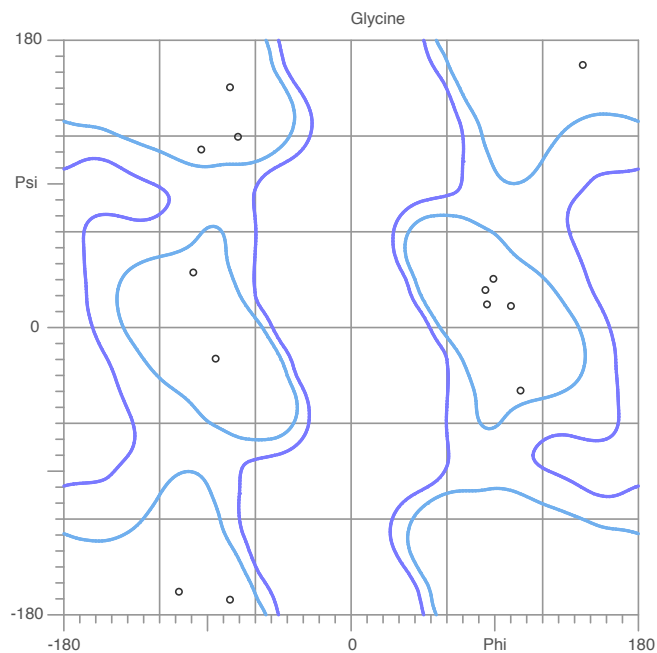
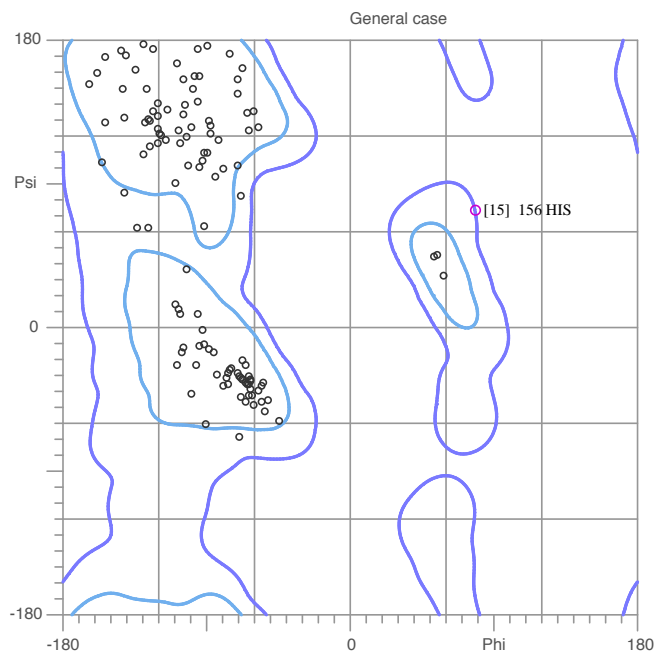


94.9% (148/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[14] 74 LEU (-165.1, -45.0)
[14] 76 GLU (60.7, 116.0)

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 15



95.5% (149/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

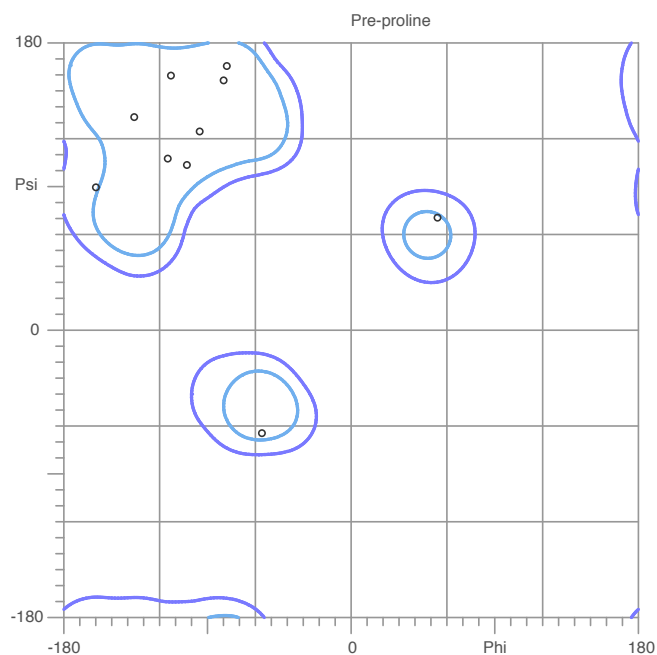
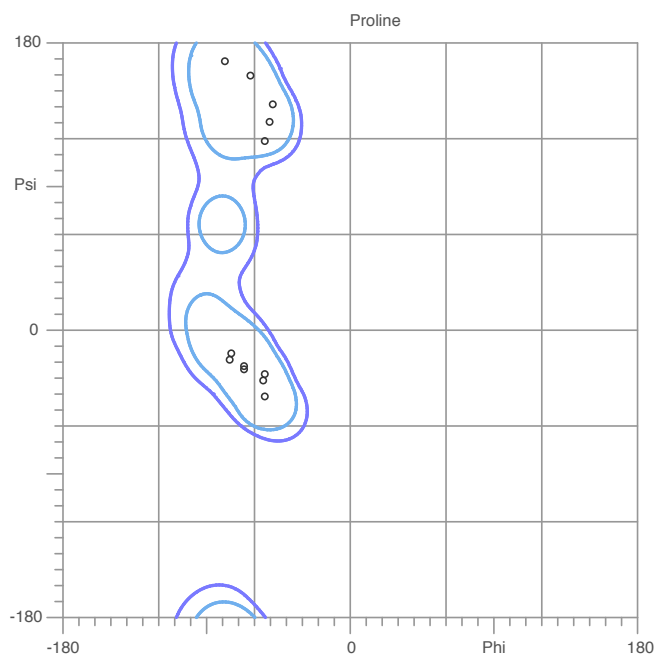
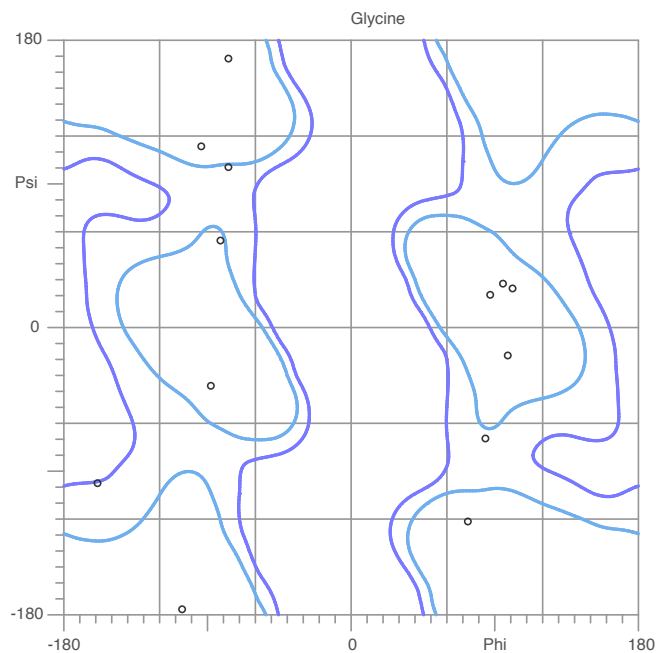
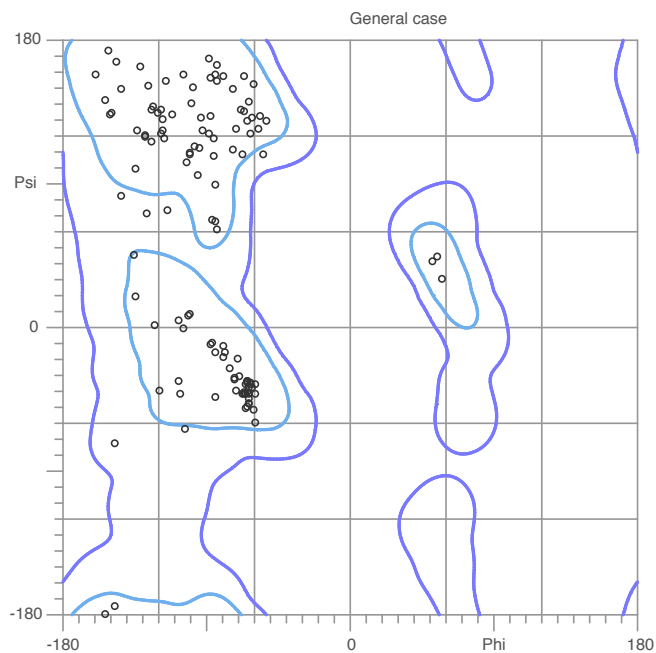
There were 1 outliers (phi, psi):
[15] 156 HIS (78.5, 75.0)

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

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MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 16



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.

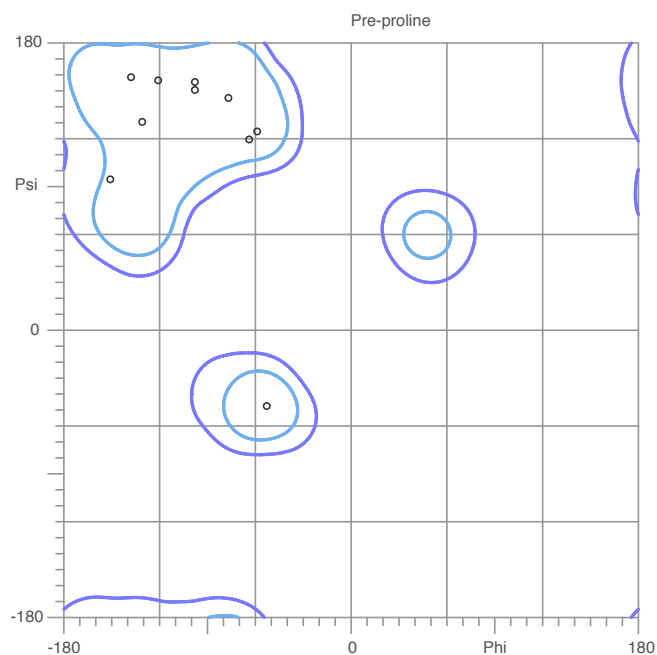
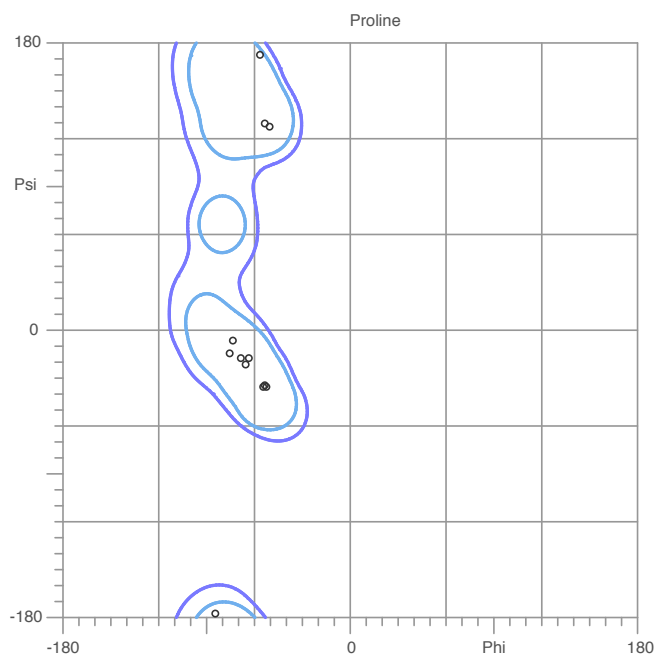
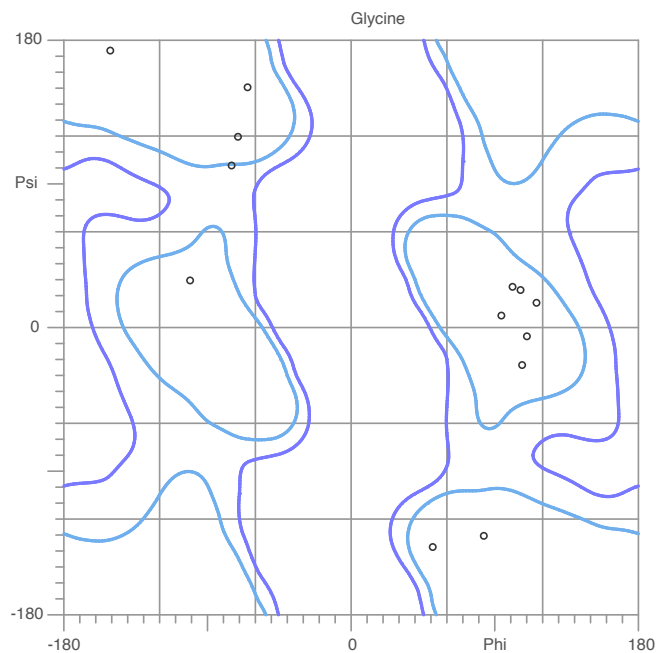
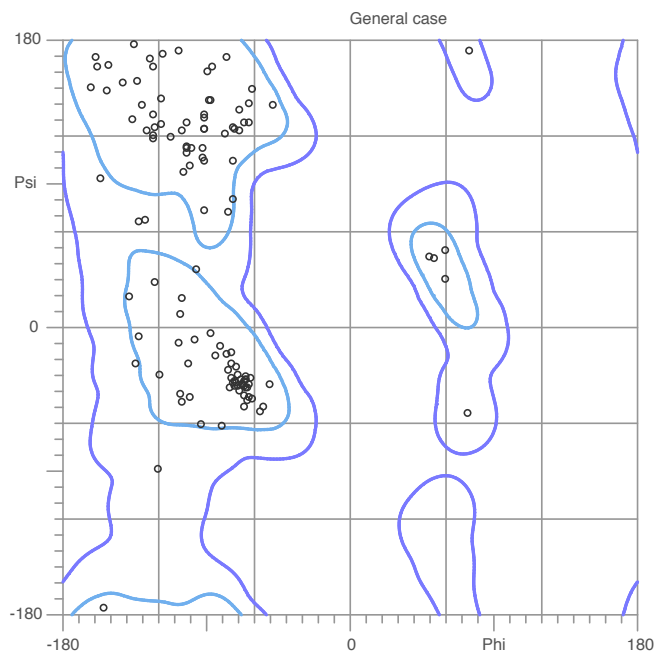
There were no outliers.

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

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

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 17



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.

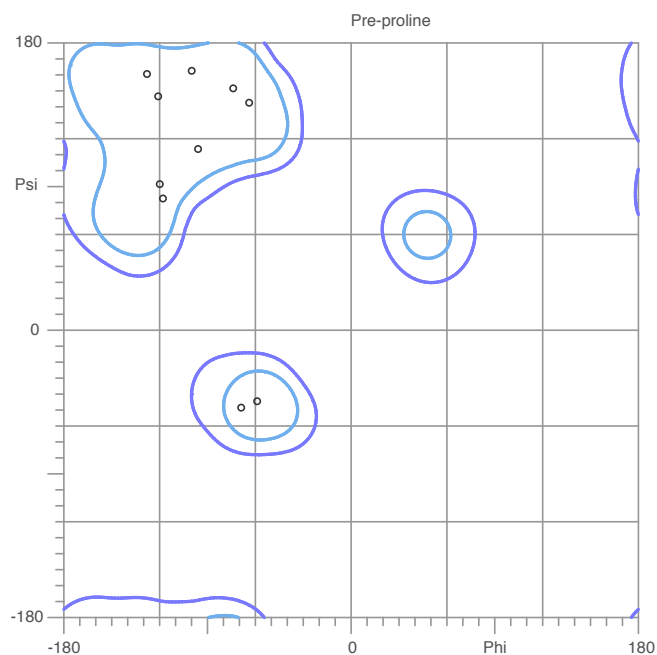
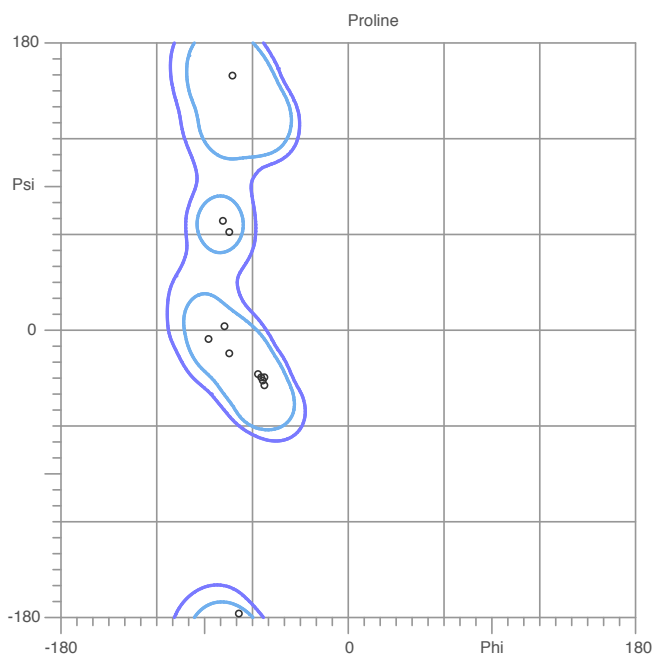
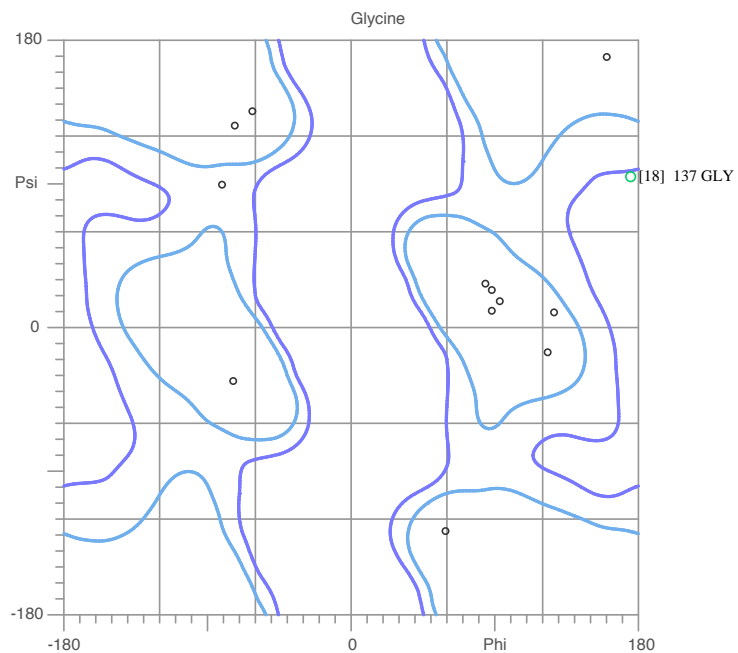
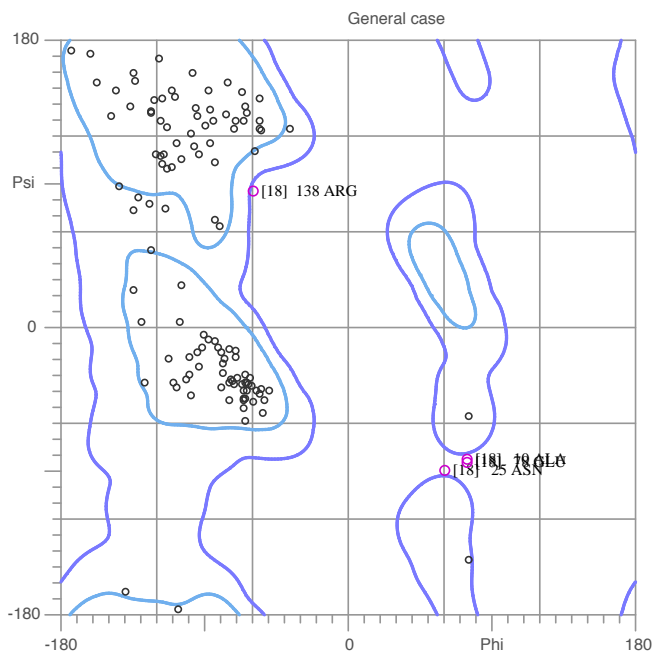
There were no outliers.

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

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

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 18



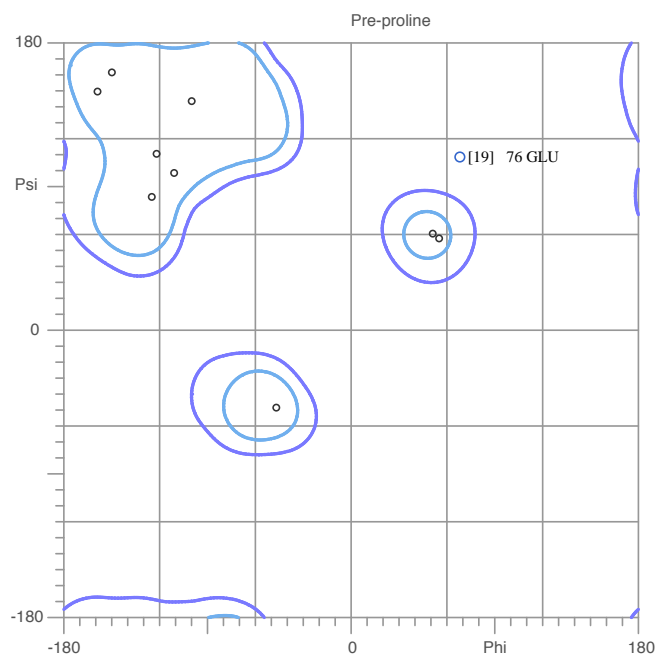
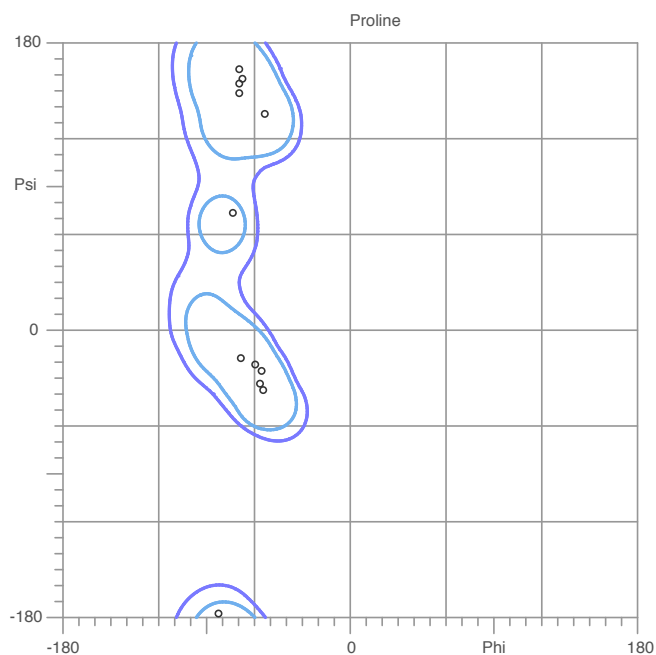
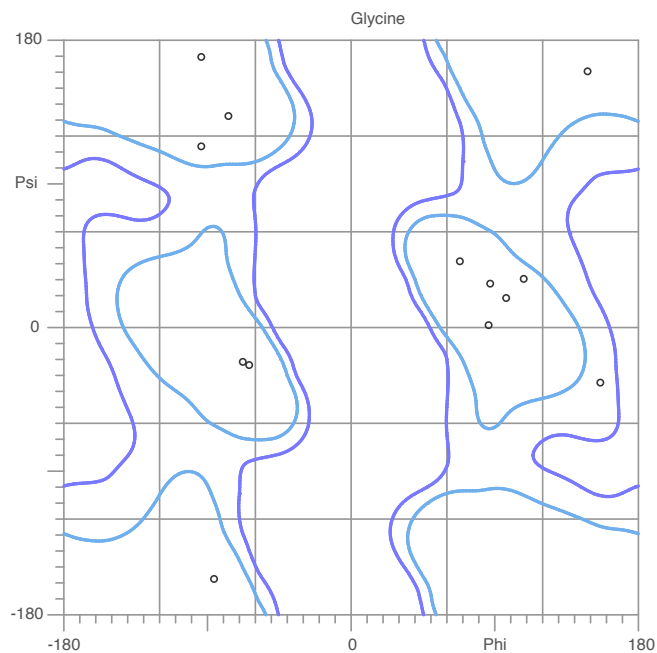
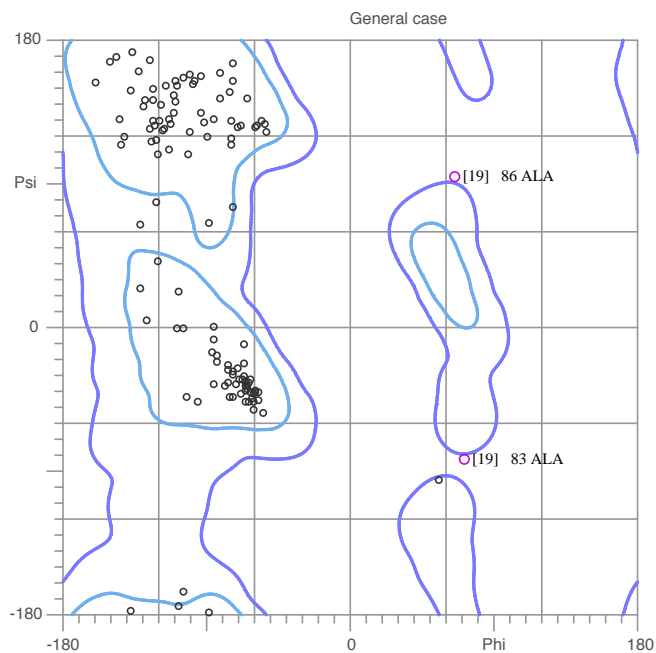
90.4% (141/156) of all residues were in favored (98%) regions.
96.8% (151/156) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[18] 10 ALA (75.0, -82.9)
[18] 25 ASN (60.4, -89.0)
[18] 78 GLU (75.0, -84.9)
[18] 137 GLY (175.1, 95.1)
[18] 138 ARG (-60.6, 86.9)

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 19



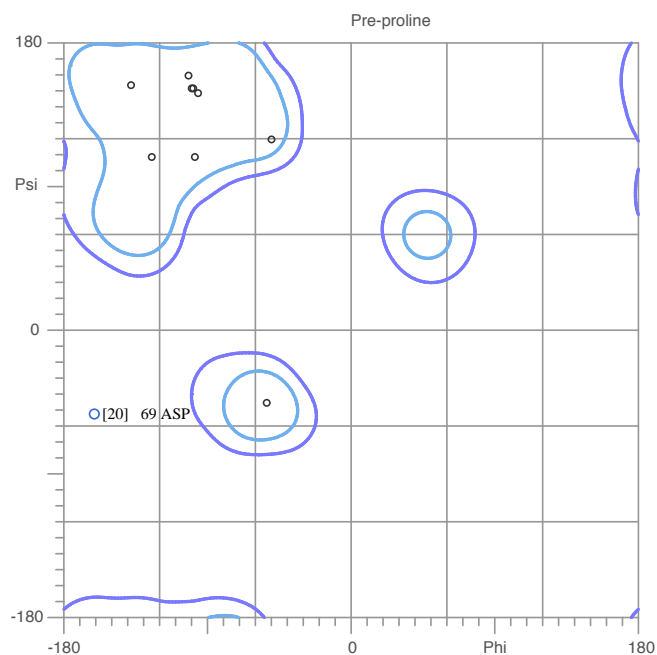
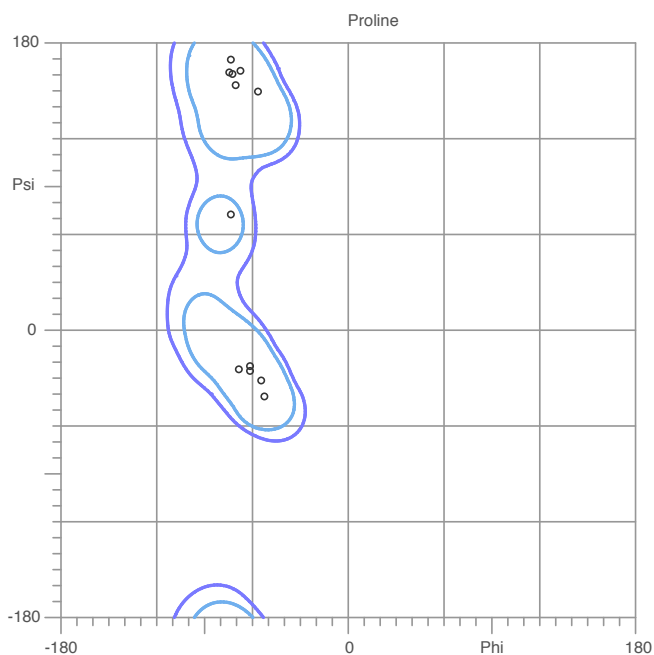
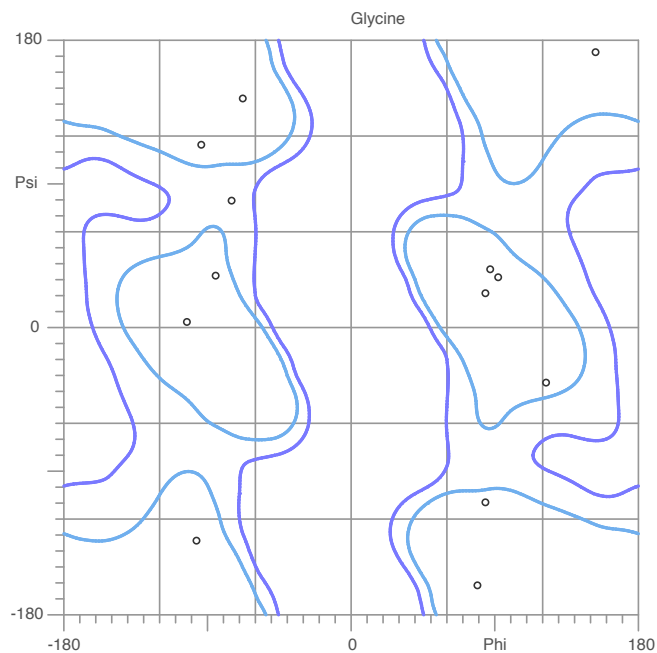
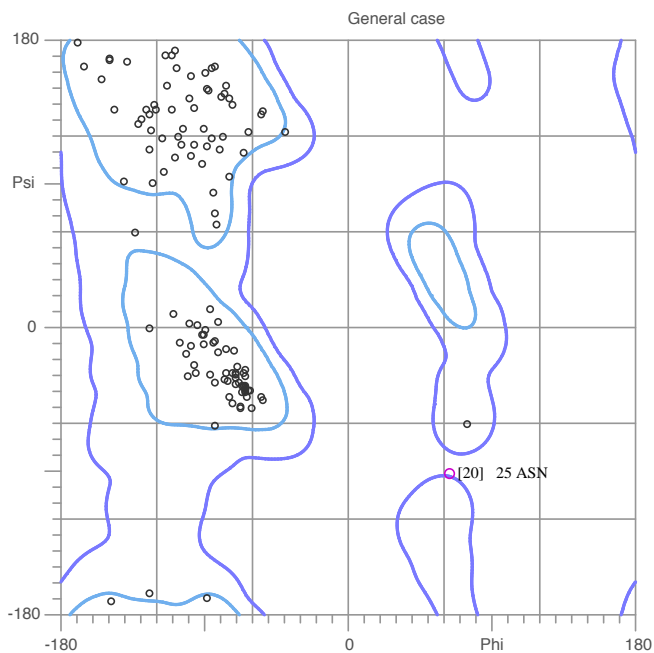
94.9% (148/156) of all residues were in favored (98%) regions.
98.1% (153/156) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [19] 76 GLU (68.3, 109.0)
- [19] 83 ALA (72.0, -82.1)
- [19] 86 ALA (65.0, 95.0)

MolProbity Ramachandran analysis

BER31_R3_em_bcr3.pdb, model 20



95.5% (149/156) 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):
[20] 25 ASN (63.1, -91.6)
[20] 69 ASP (-161.6, -52.8)