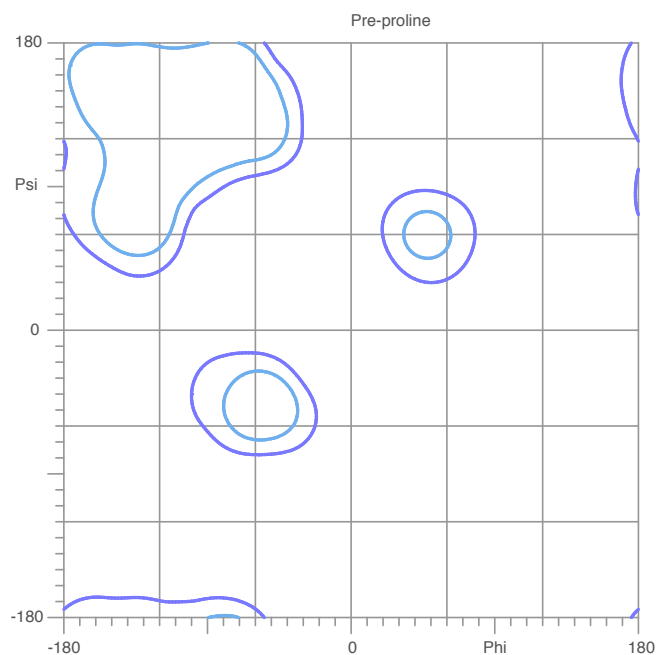
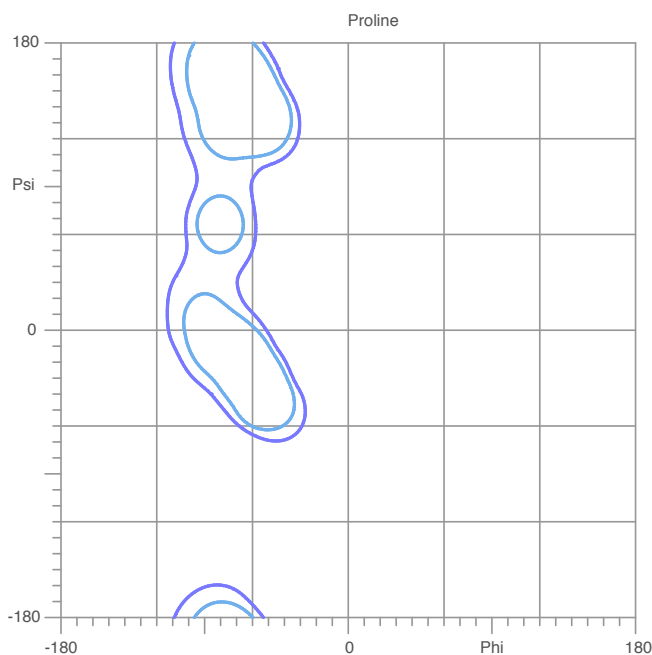
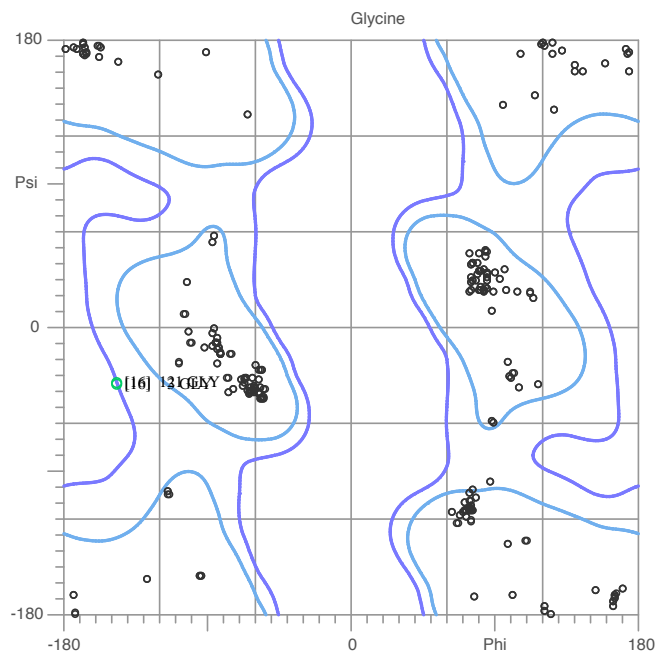
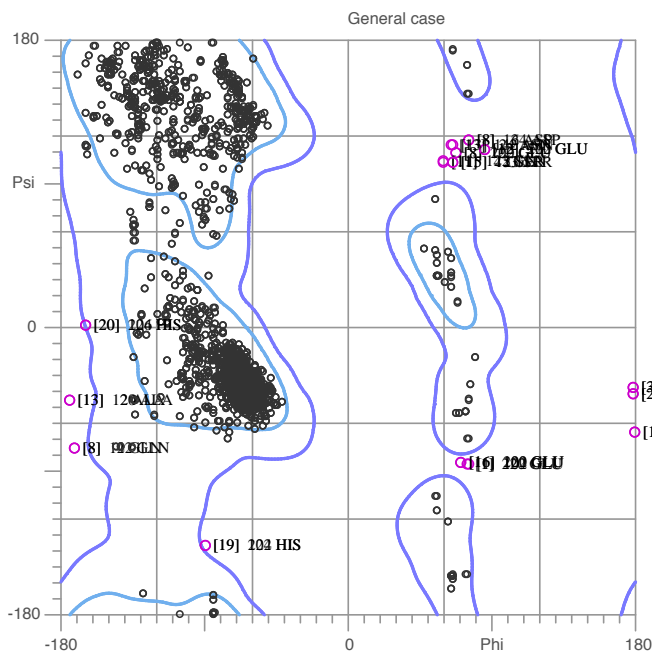


MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, all models



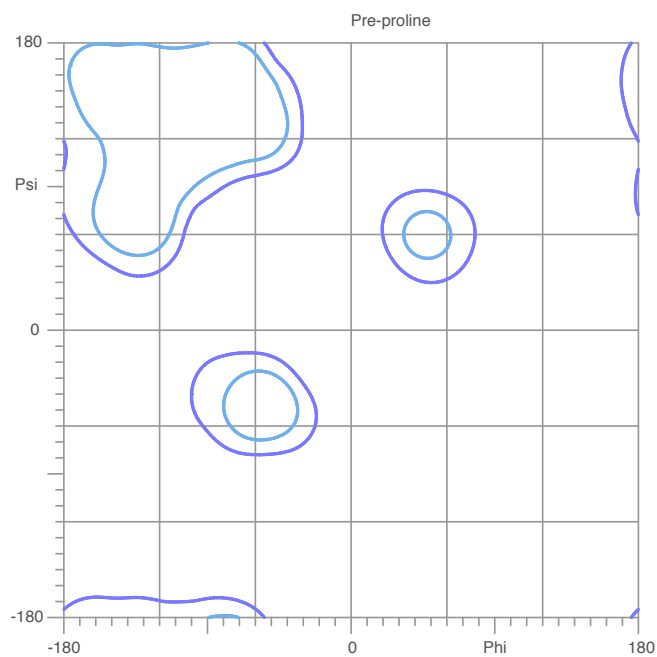
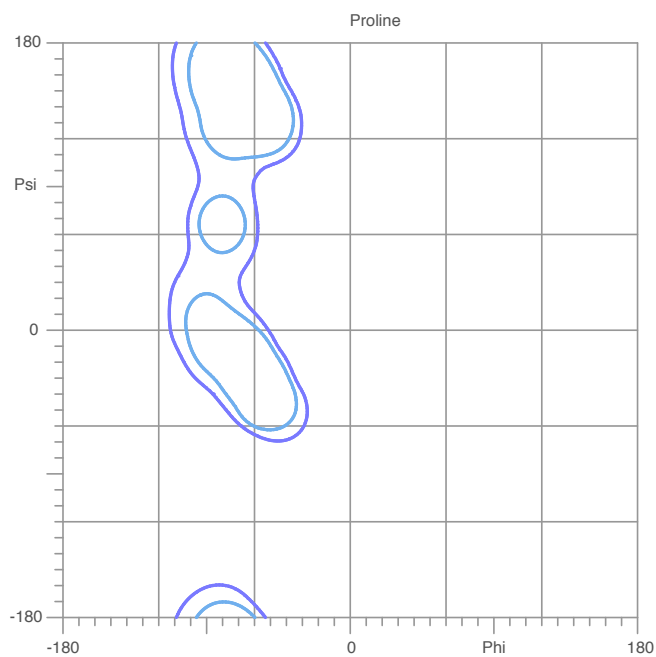
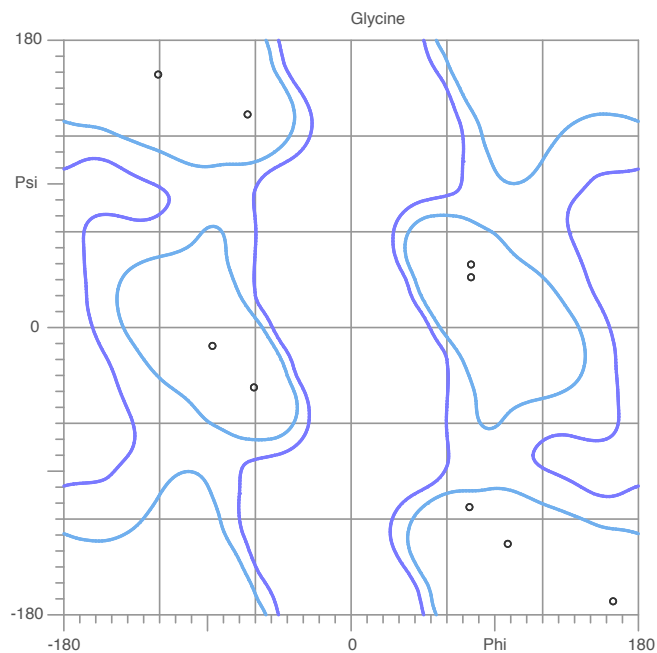
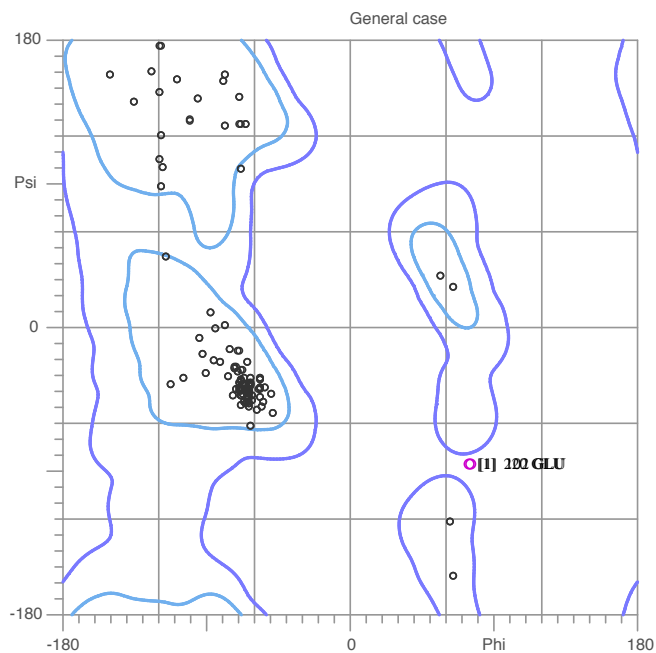
96.6% (4094/4240) of all residues were in favored (98%) regions.
99.2% (4208/4240) of all residues were in allowed (>99.8%) regions.

There were 32 outliers (phi, psi):

- | | |
|-----------------------------|------------------------------|
| [1] 102 GLU (75.0, -85.0) | [12] 102 GLU (85.3, 112.5) |
| [1] 220 GLU (75.0, -85.1) | [12] 220 GLU (85.3, 112.5) |
| [2] 24 ASN (178.4, -41.6) | [13] 2 ALA (-175.0, -45.2) |
| [2] 142 ASN (178.4, -41.7) | [13] 24 ASN (65.1, 115.0) |
| [3] 24 ASN (178.0, -37.5) | [13] 120 ALA (-175.0, -45.2) |
| [3] 142 ASN (178.1, -37.6) | [13] 142 ASN (65.0, 115.0) |
| [8] 4 GLN (-172.9, -75.1) | [15] 5 SER (65.2, 104.9) |
| [8] 6 ASP (75.0, 118.5) | [15] 123 SER (65.1, 105.0) |
| [8] 102 GLU (67.7, 110.1) | [16] 3 GLY (-147.5, -35.1) |
| [8] 122 GLN (-173.0, -75.2) | [16] 102 GLU (70.4, -84.1) |
| [8] 124 ASP (75.0, 118.5) | [16] 121 GLY (-147.6, -35.0) |
| [8] 220 GLU (67.7, 110.1) | [16] 220 GLU (70.4, -84.2) |
| [11] 4 GLN (59.2, 104.9) | [17] 24 ASN (179.4, -65.1) |
| [11] 122 GLN (59.0, 105.0) | [17] 142 ASN (179.4, -65.0) |
| | [19] 104 HIS (-90.9, -136.2) |
| | [19] 222 HIS (-90.8, -136.1) |
| | [20] 106 HIS (-165.4, 2.3) |
| | [20] 224 HIS (-165.4, 2.2) |

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 1



96.2% (204/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

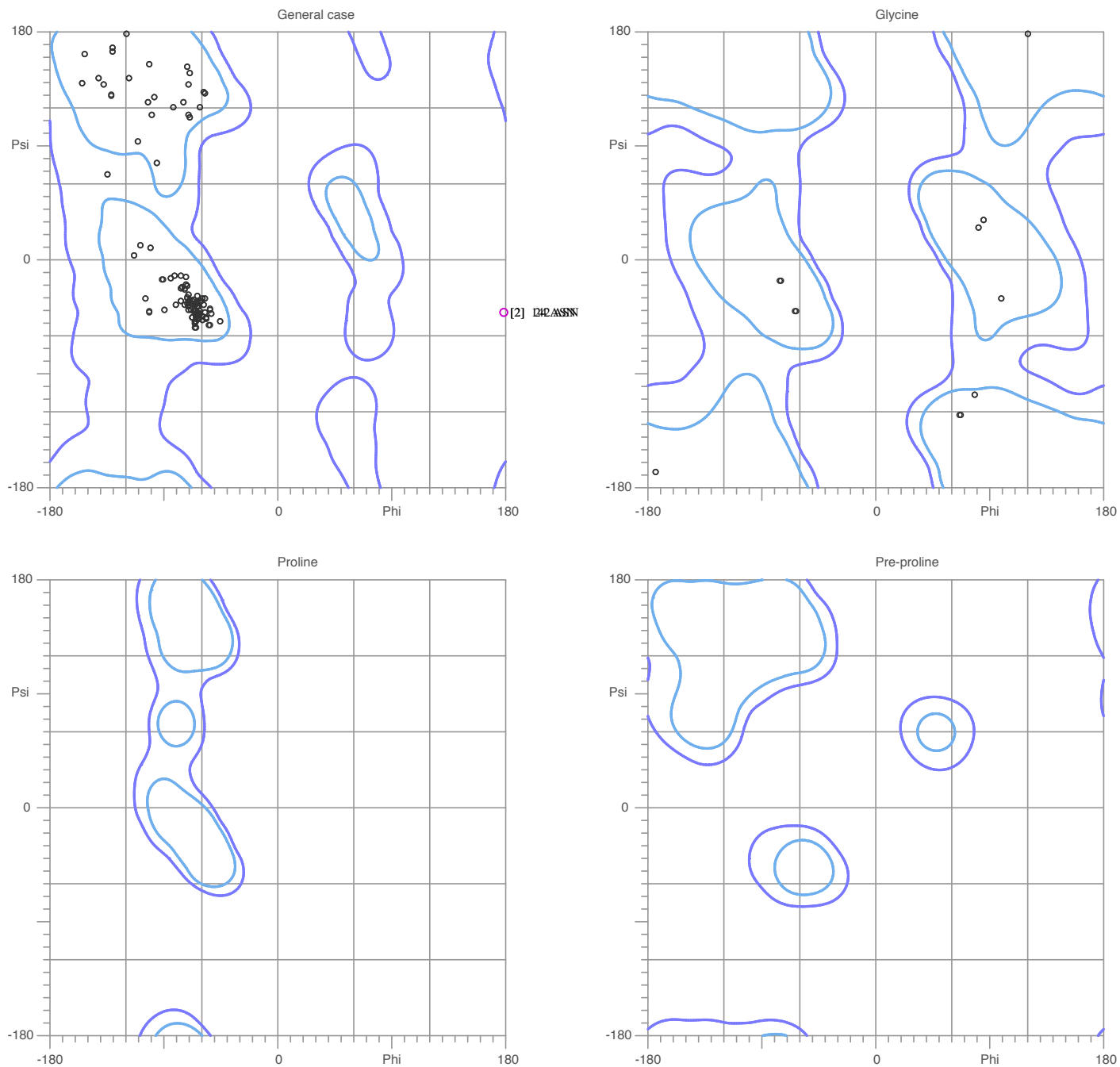
There were 2 outliers (phi, psi):

[1] 102 GLU (75.0, -85.0)

[1] 220 GLU (75.0, -85.1)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 2



98.1% (208/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

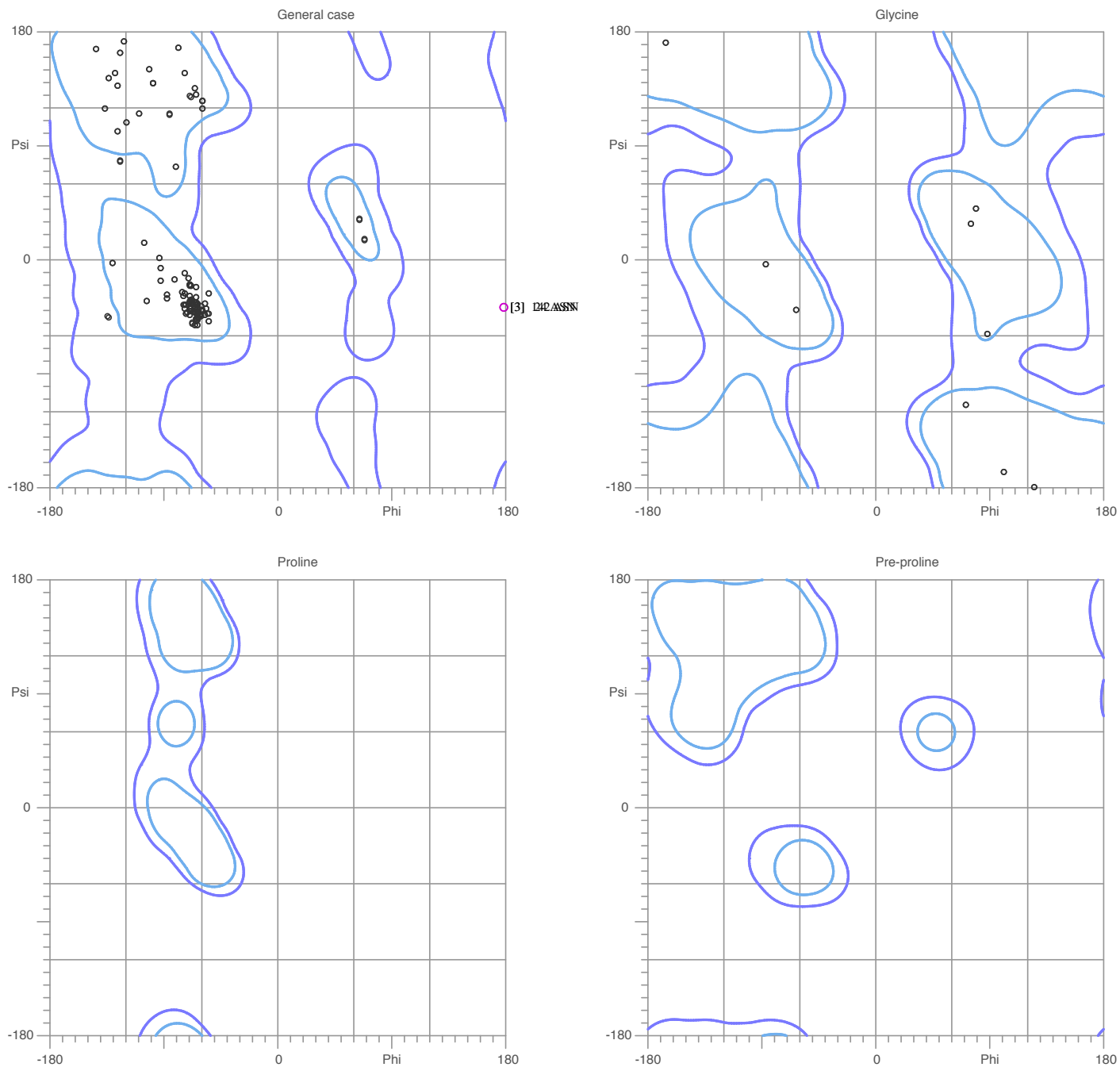
There were 2 outliers (phi, psi):

[2] 24 ASN (178.4, -41.6)

[2] 142 ASN (178.4, -41.7)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 3



97.2% (206/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

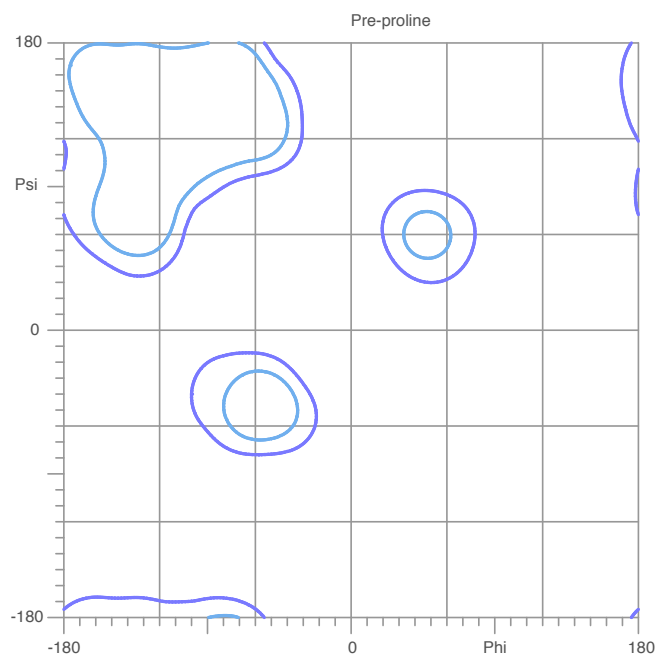
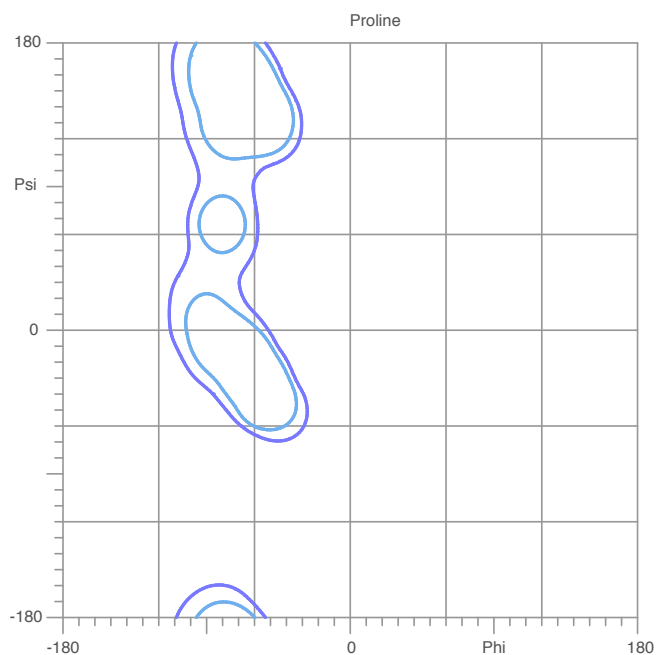
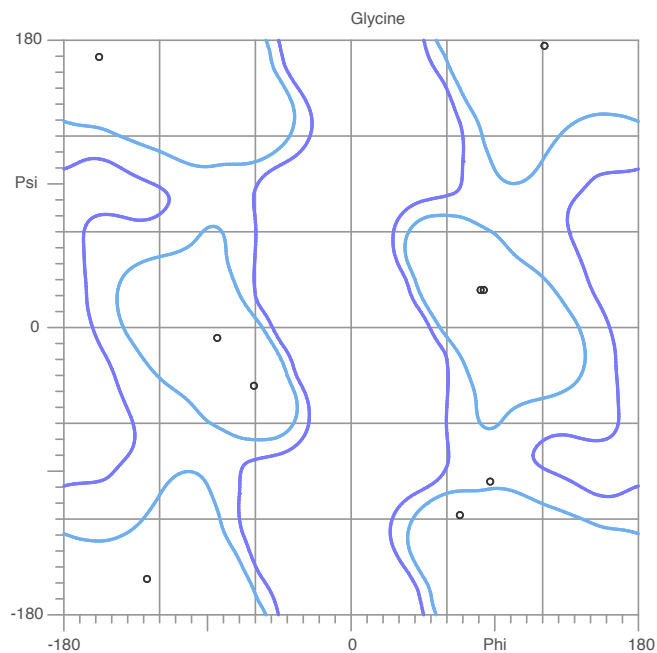
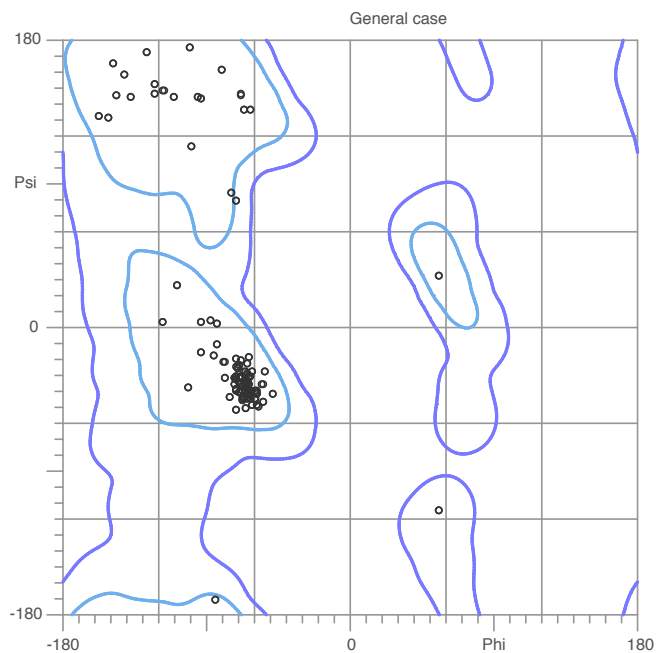
There were 2 outliers (phi, psi):

[3] 24 ASN (178.0, -37.5)

[3] 142 ASN (178.1, -37.6)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 4



97.2% (206/212) of all residues were in favored (98%) regions.
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

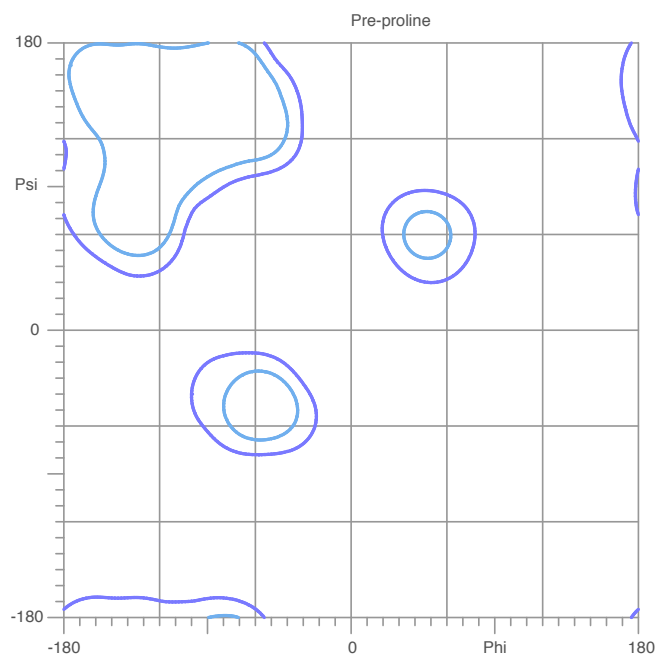
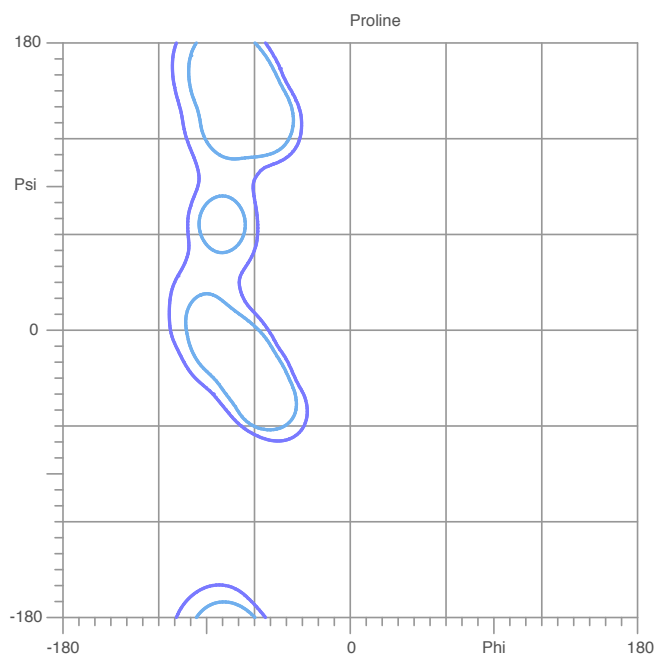
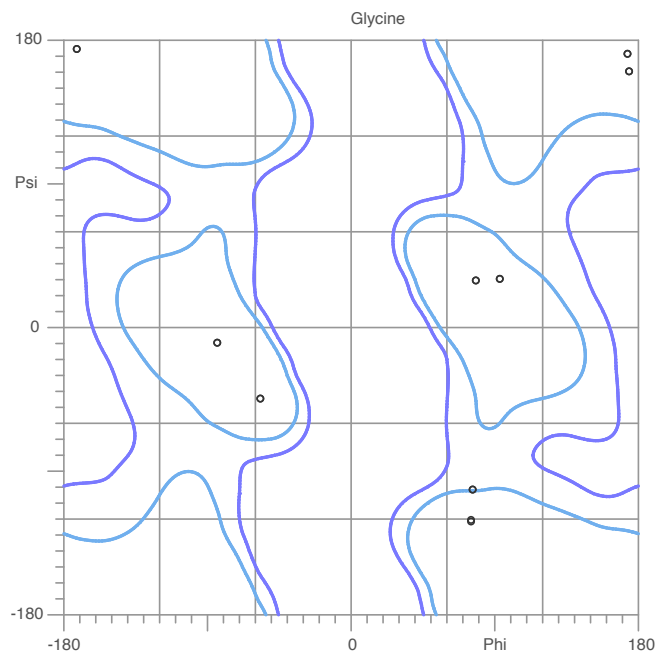
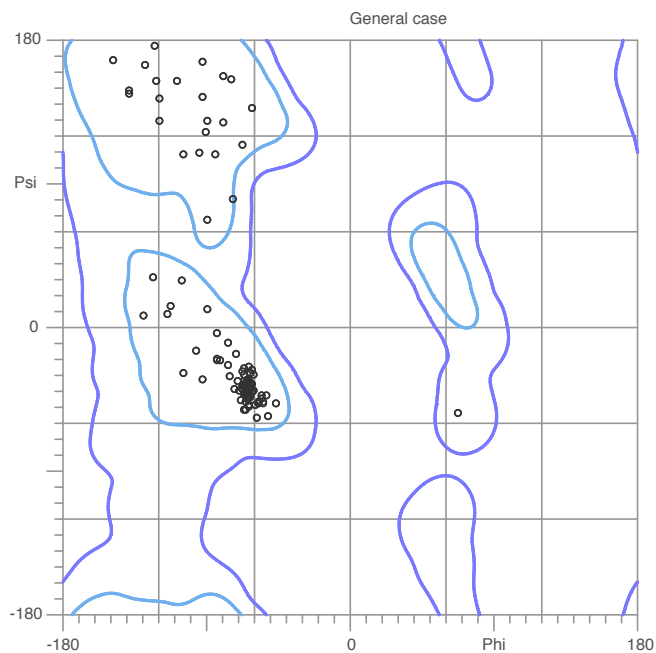
There were no outliers.

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

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MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 5



98.1% (208/212) of all residues were in favored (98%) regions.
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

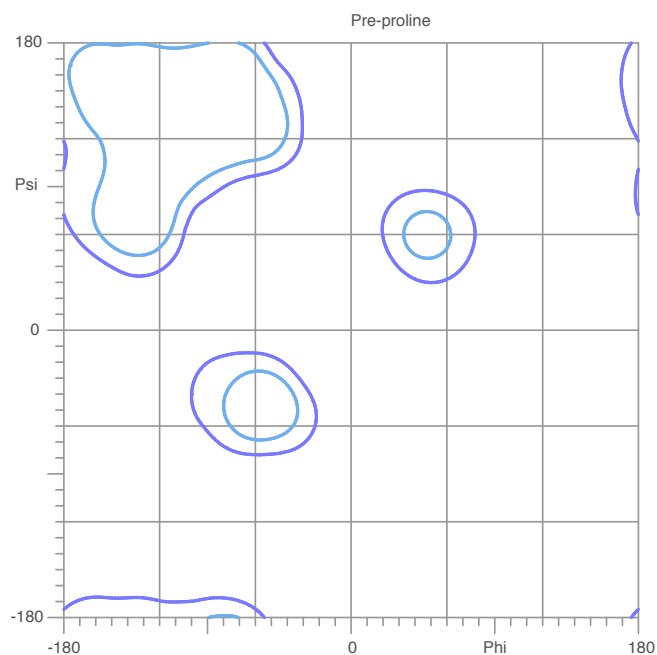
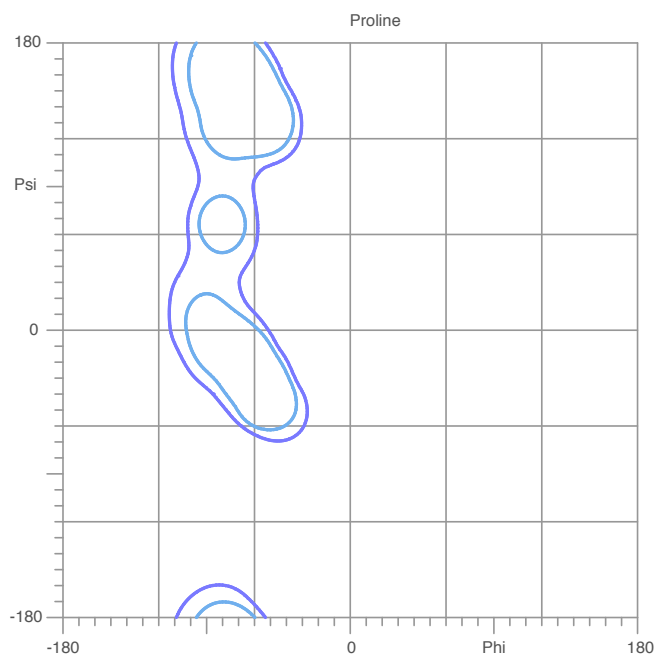
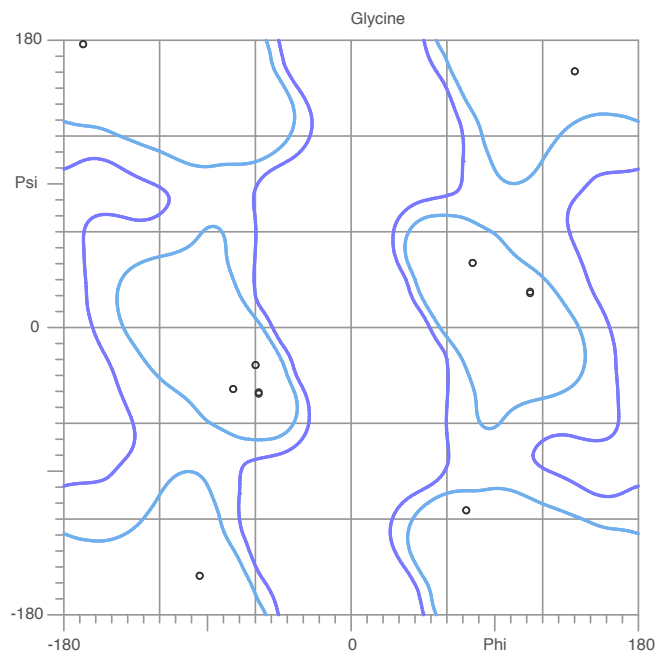
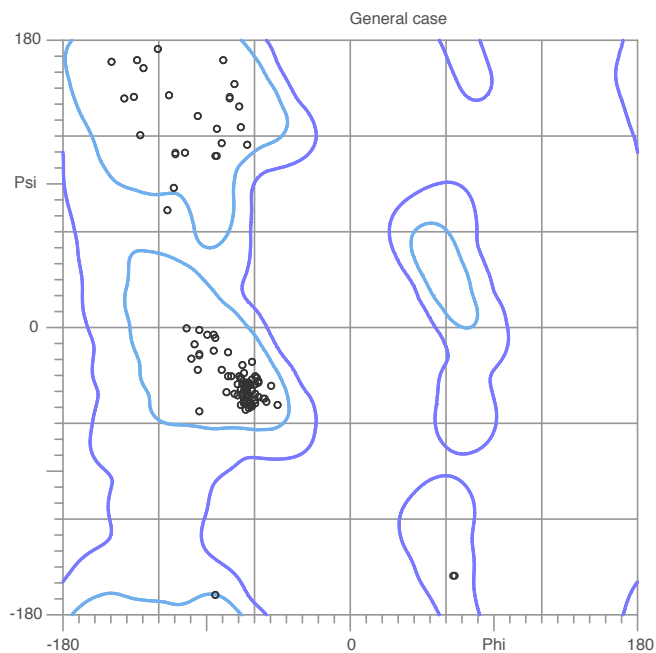
There were no outliers.

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

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

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 6



97.2% (206/212) of all residues were in favored (98%) regions.
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

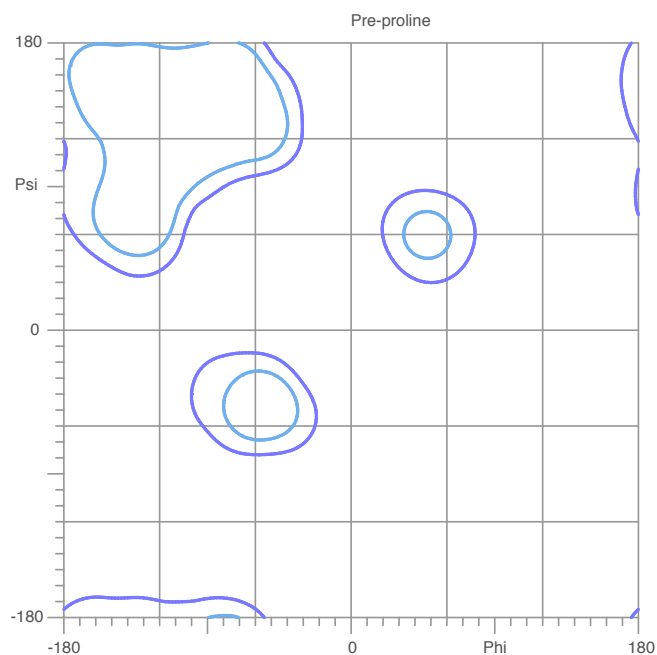
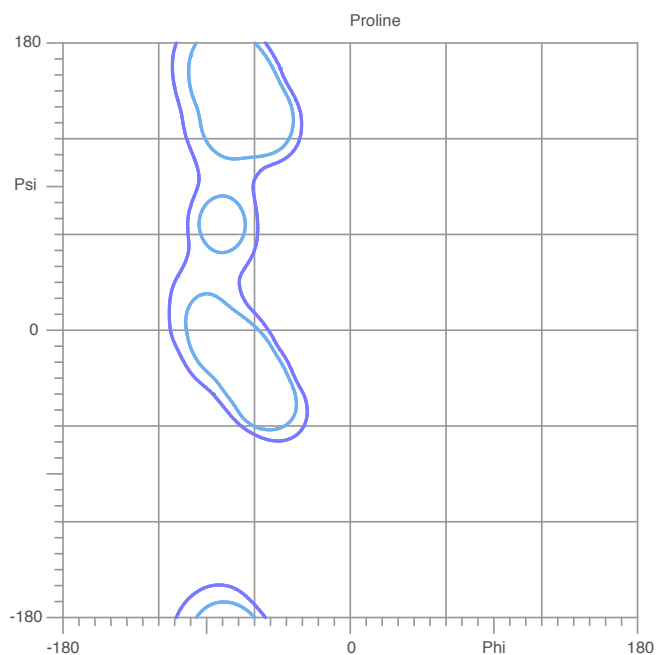
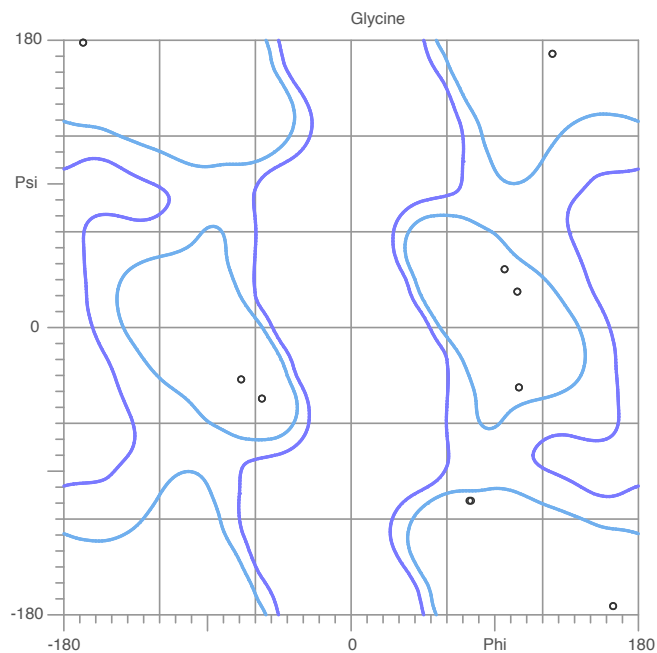
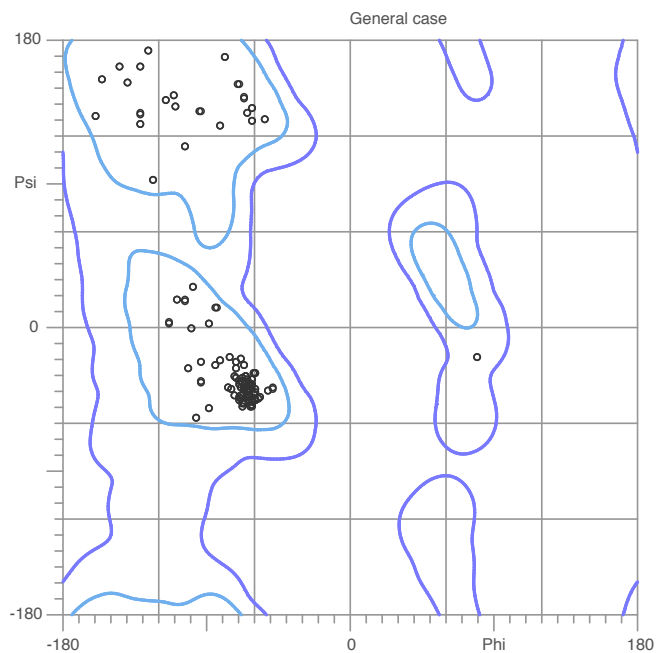
There were no outliers.

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

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MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 7



99.1% (210/212) of all residues were in favored (98%) regions.
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

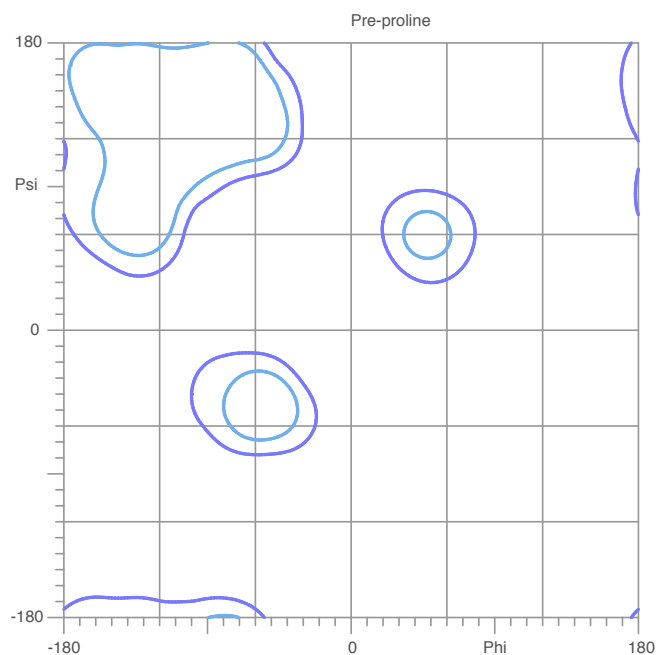
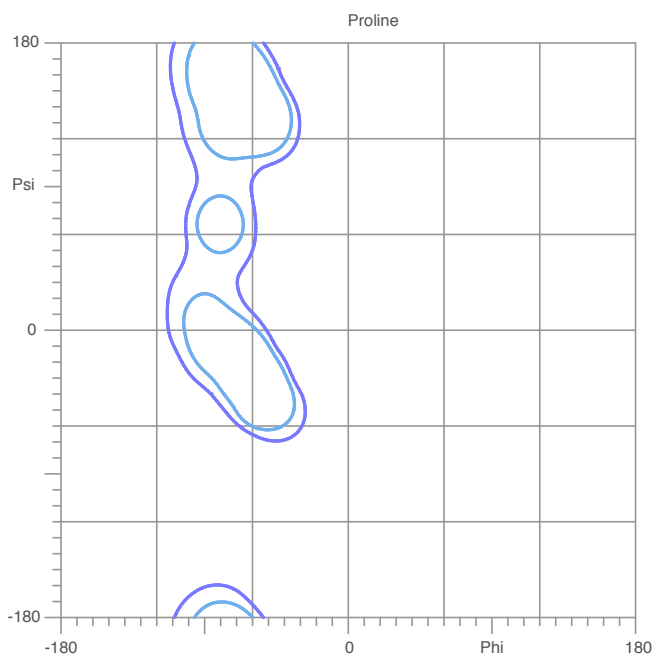
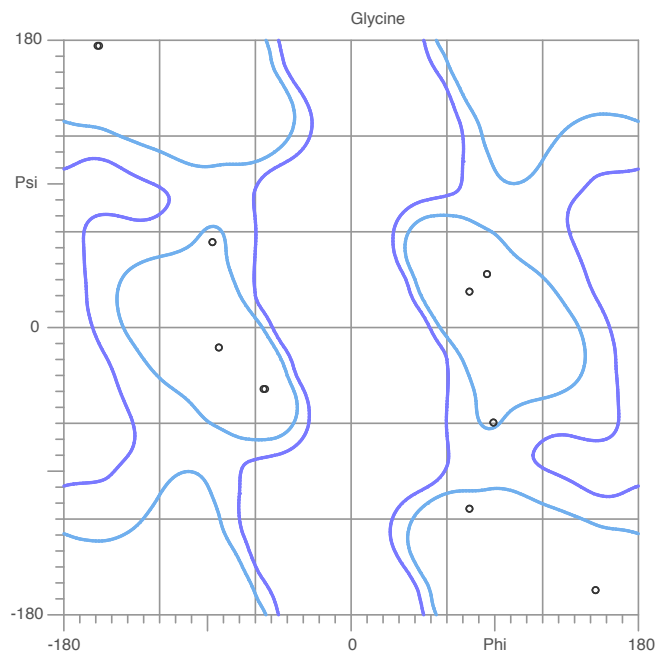
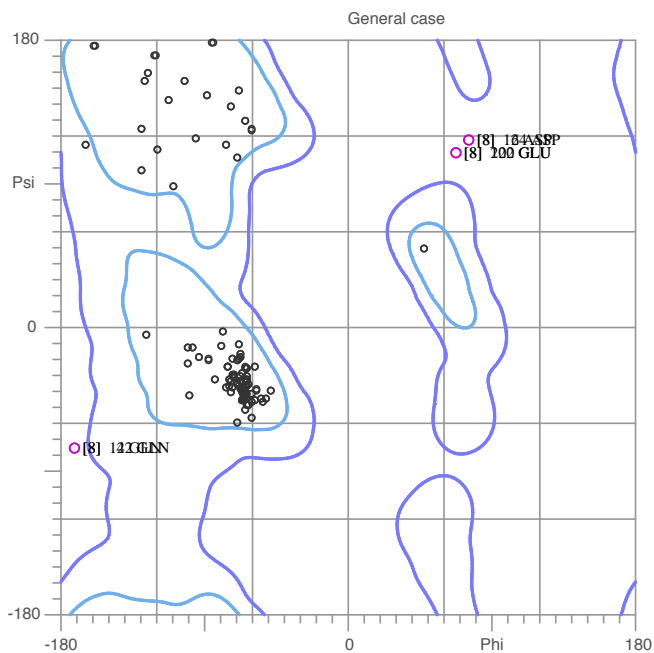
There were no outliers.

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

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MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 8



96.2% (204/212) of all residues were in favored (98%) regions.
97.2% (206/212) of all residues were in allowed (>99.8%) regions.

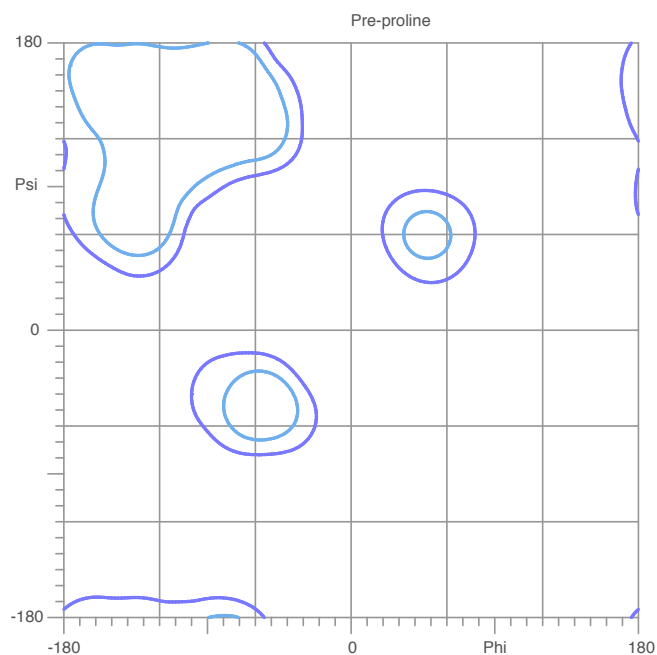
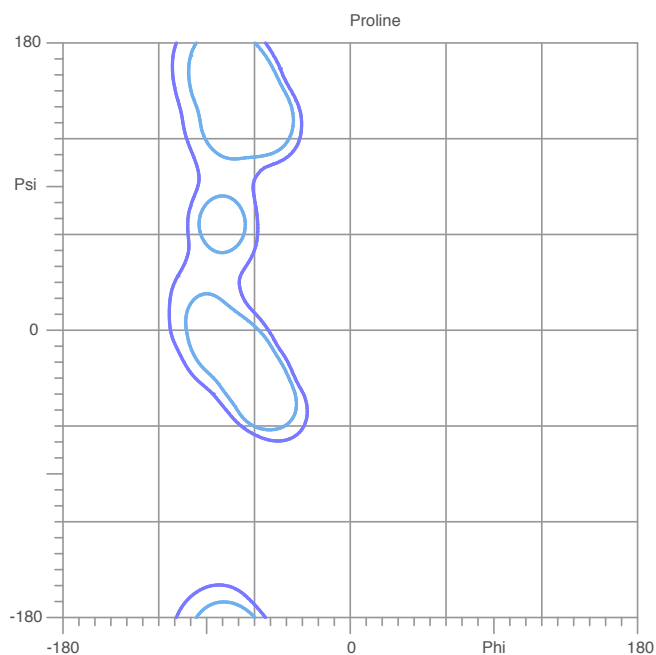
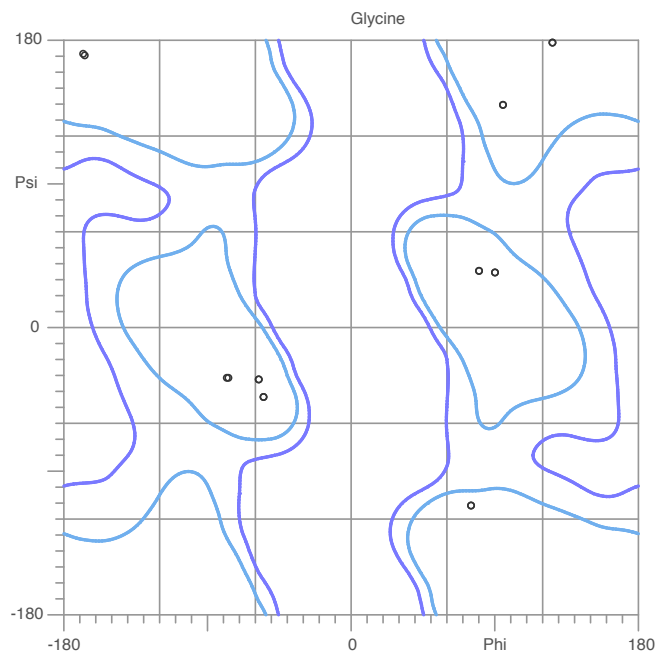
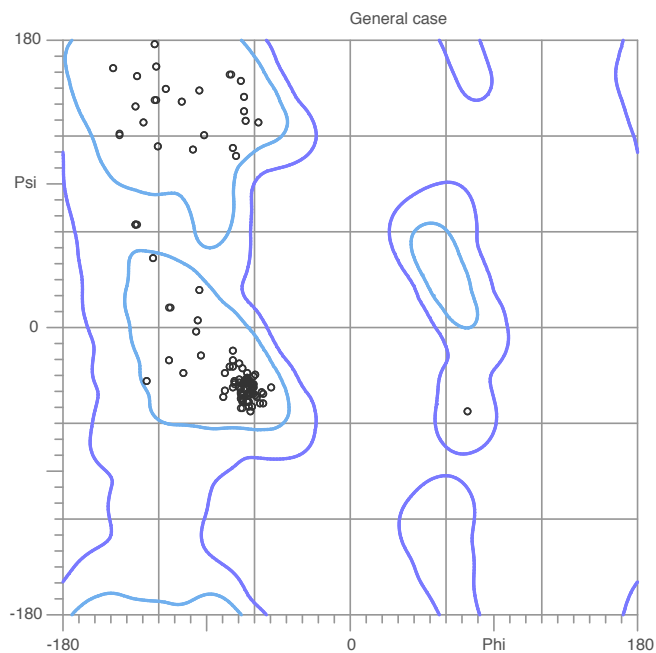
There were 6 outliers (phi, psi):

[8] 4 GLN (-172.9, -75.1)

[8] 6 ASP (75.0, 118.5)
[8] 102 GLU (67.7, 110.1)
[8] 122 GLN (-173.0, -75.2)
[8] 124 ASP (75.0, 118.5)
[8] 220 GLU (67.7, 110.1)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 9



97.2% (206/212) of all residues were in favored (98%) regions.
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

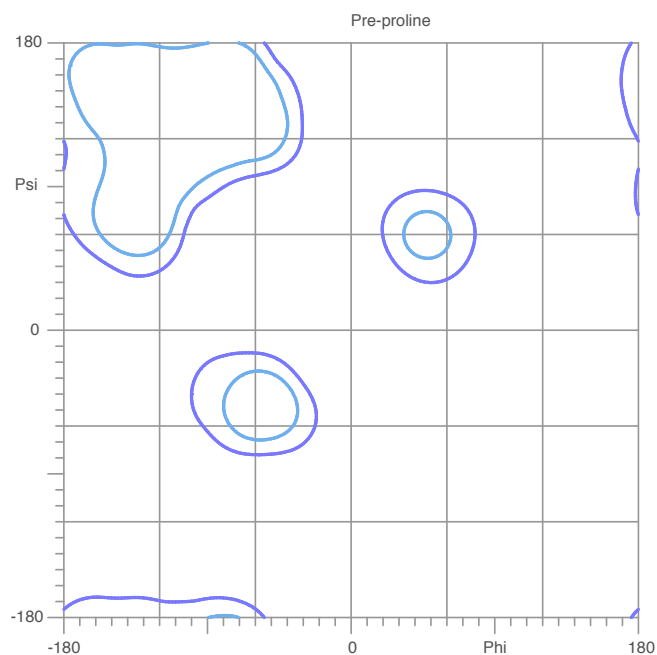
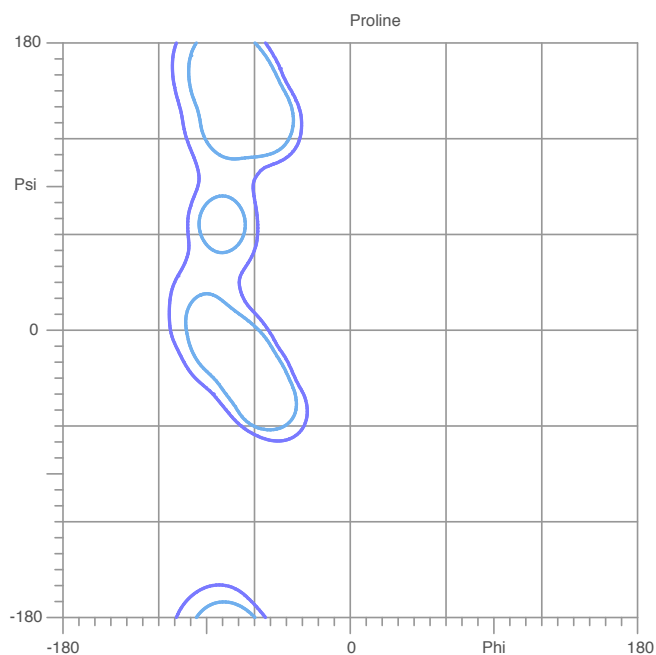
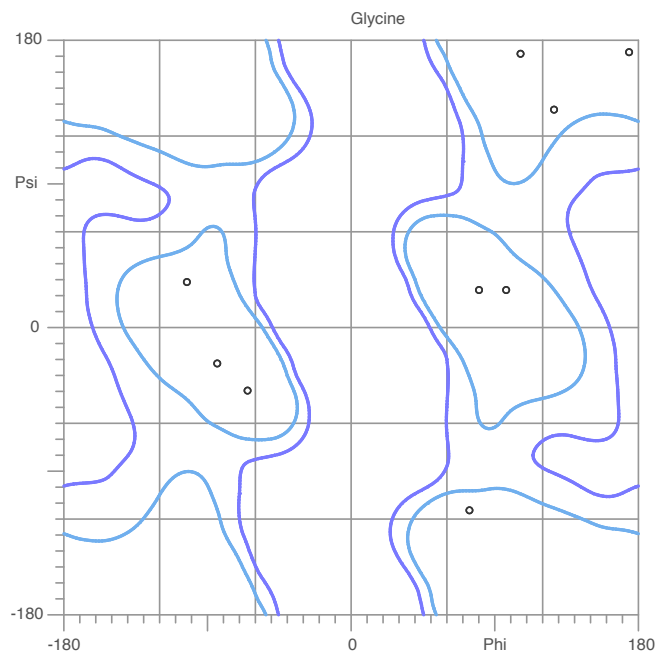
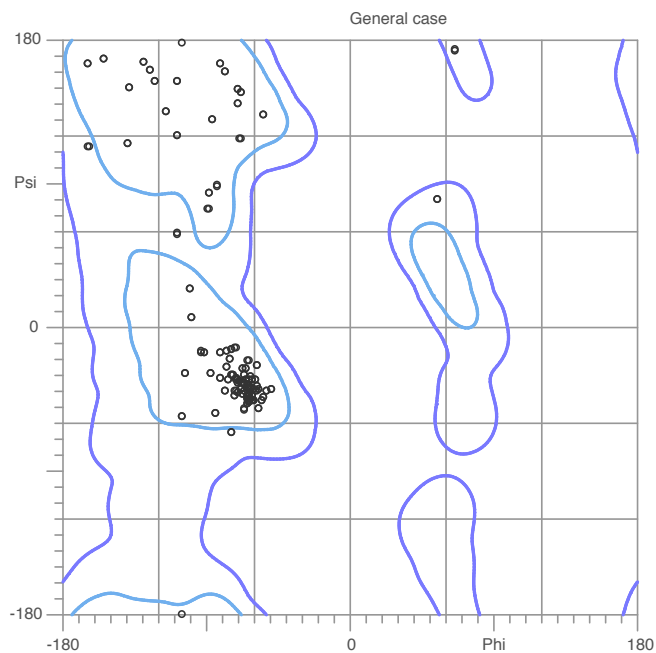
There were no outliers.

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MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 10



95.3% (202/212) of all residues were in favored (98%) regions.
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

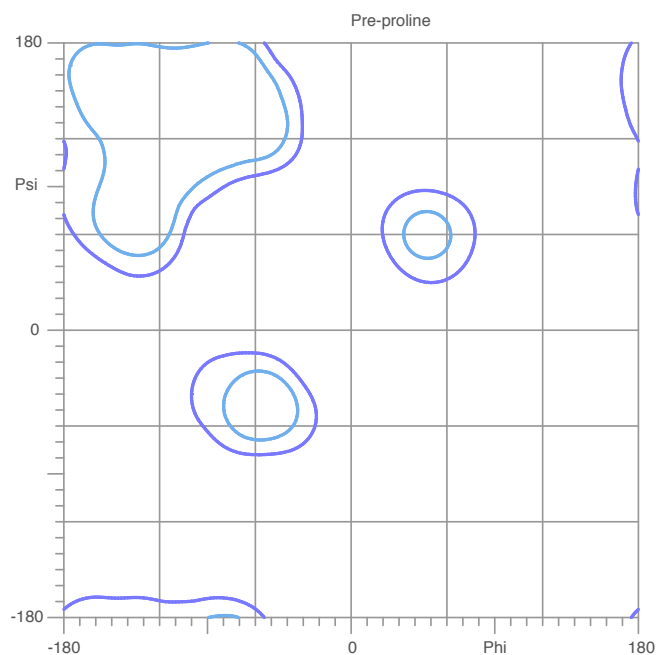
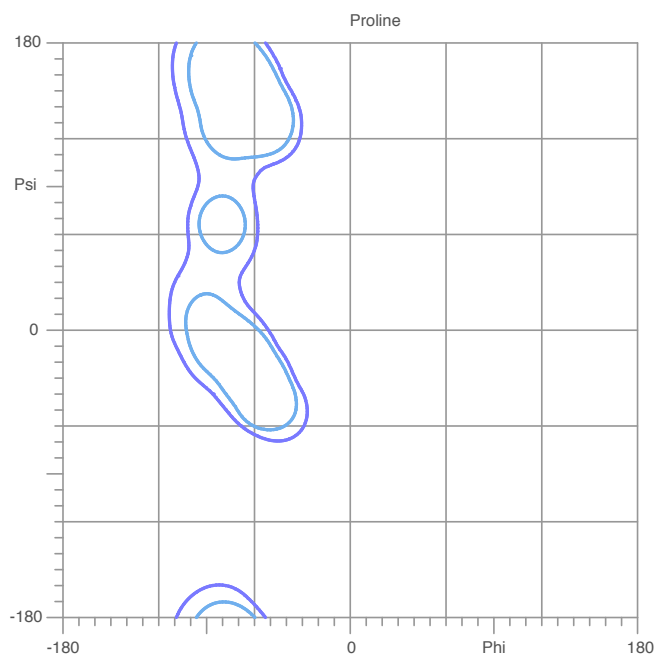
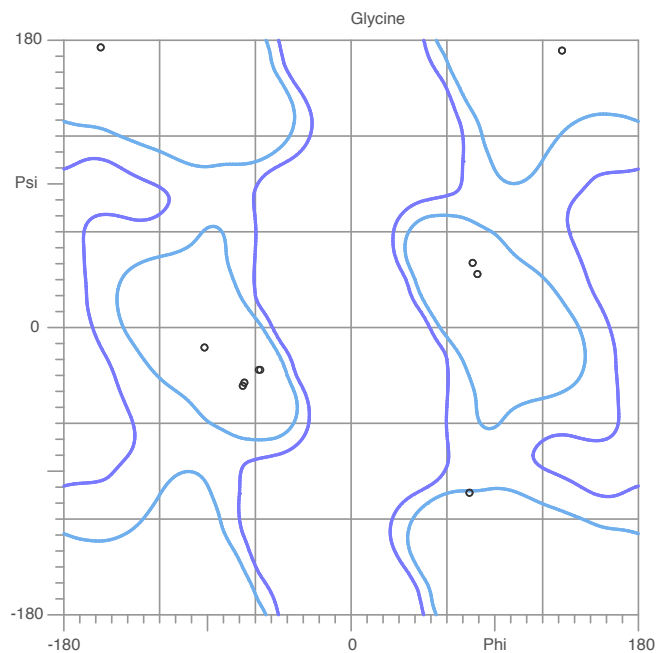
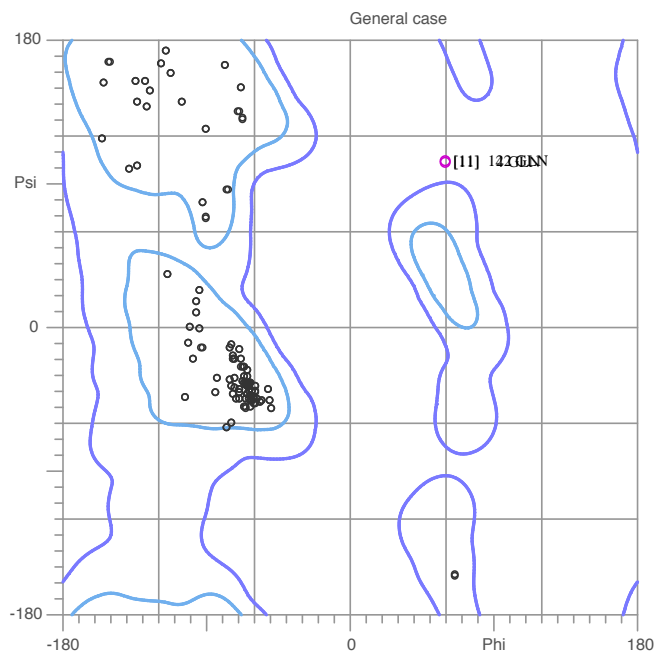
There were no outliers.

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

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MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 11

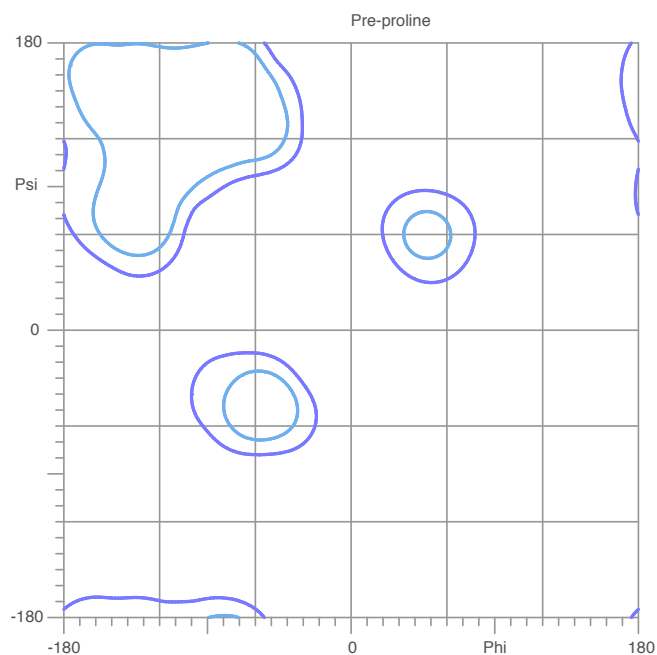
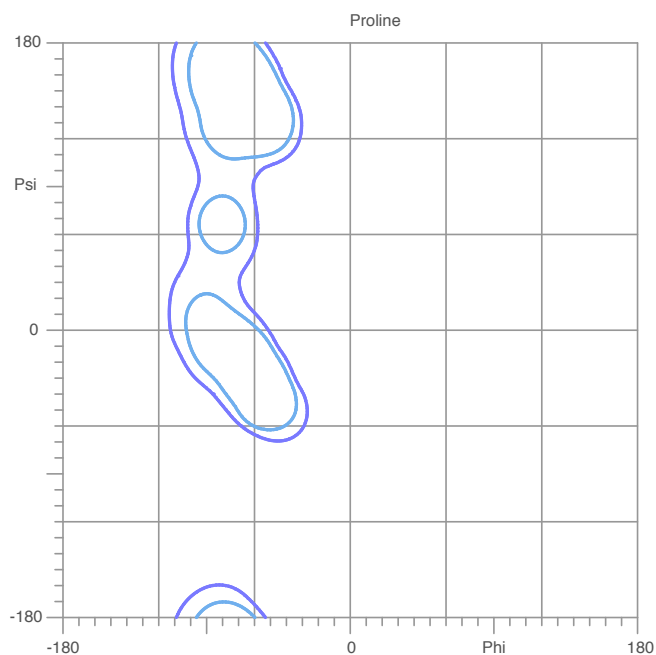
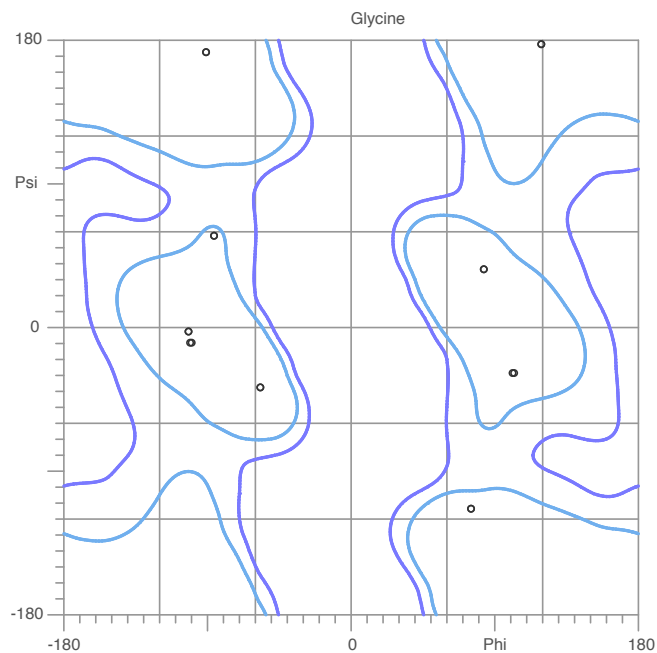
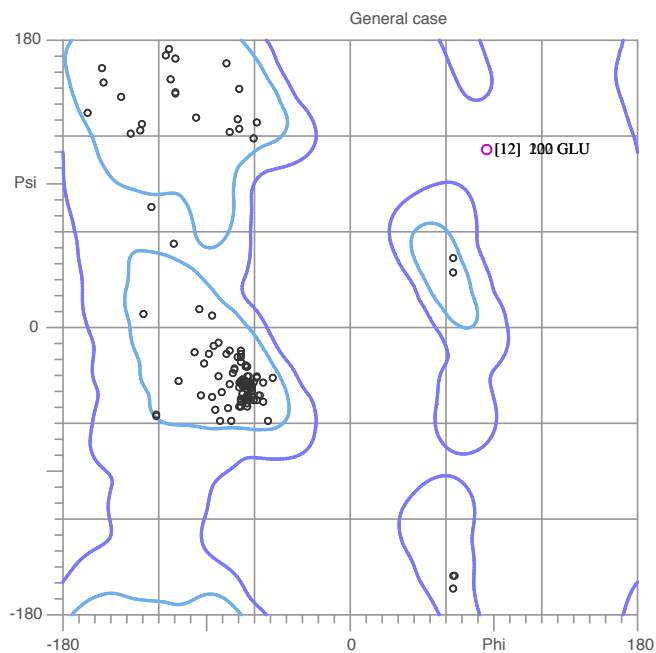


98.1% (208/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[11] 4 GLN (59.2, 104.9)
[11] 122 GLN (59.0, 105.0)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 12

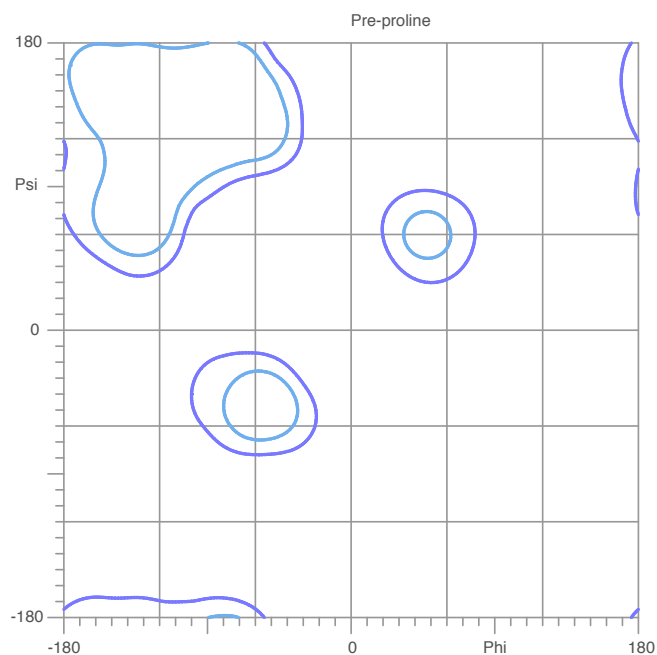
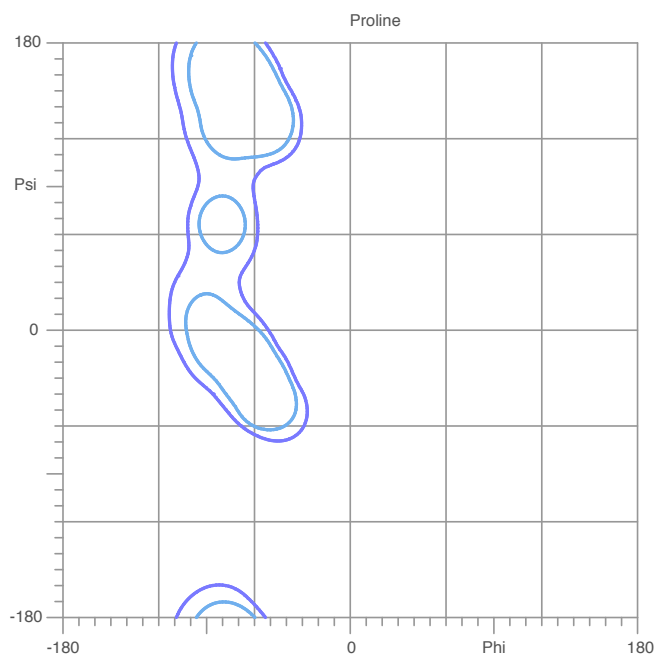
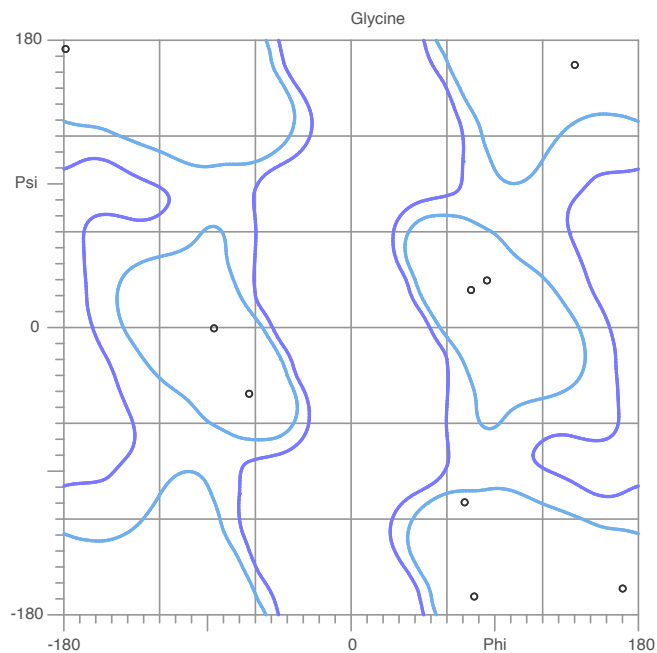
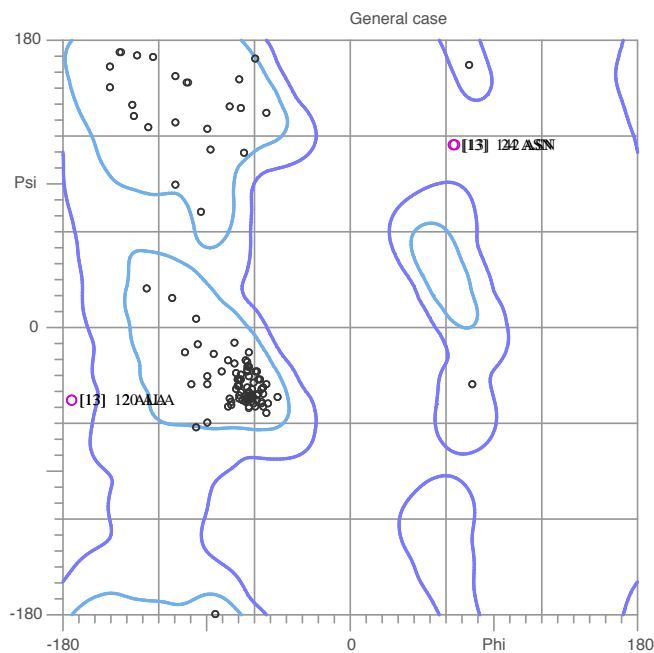


95.3% (202/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 102 GLU (85.3, 112.5)
[12] 220 GLU (85.3, 112.5)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 13



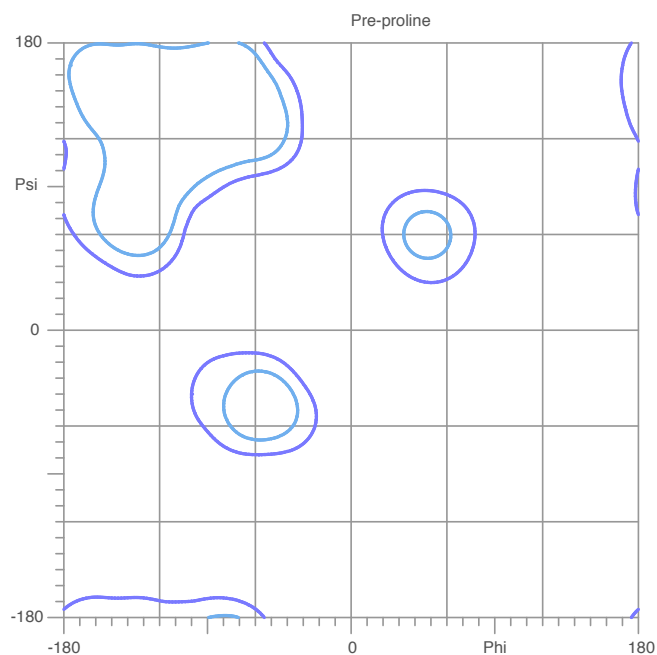
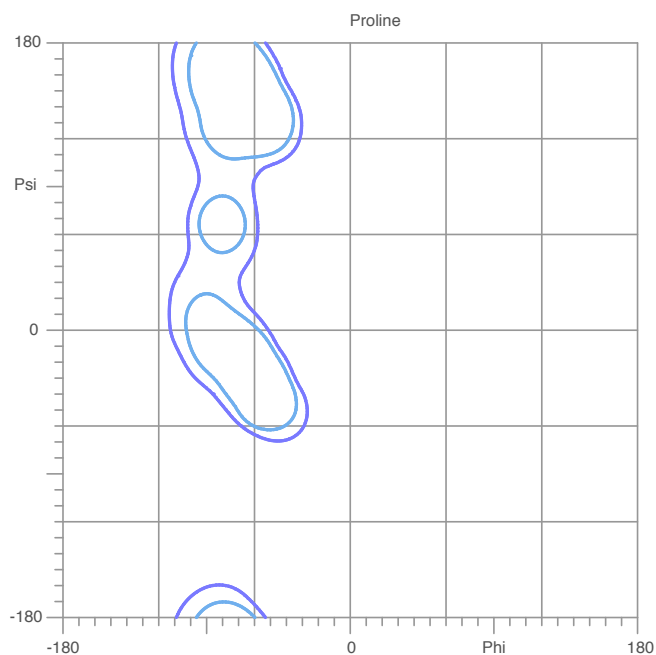
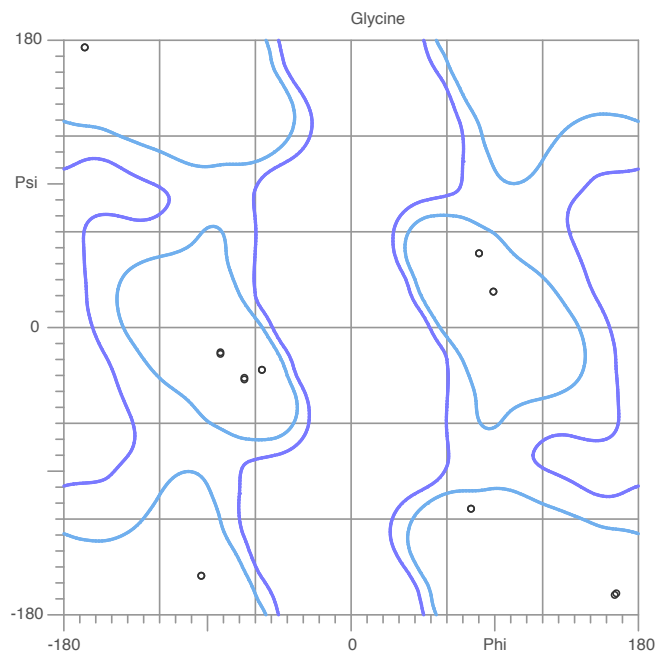
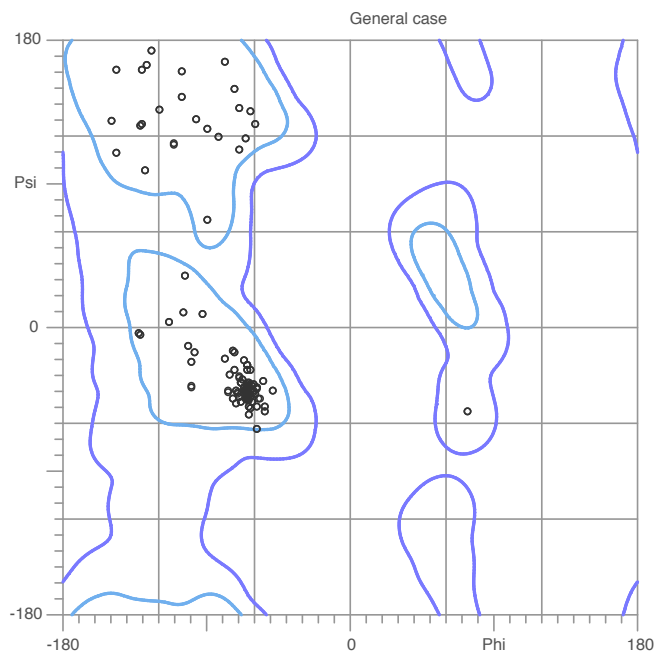
95.3% (202/212) of all residues were in favored (98%) regions.
98.1% (208/212) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [13] 2 ALA (-175.0, -45.2)
- [13] 24 ASN (65.1, 115.0)
- [13] 120 ALA (-175.0, -45.2)
- [13] 142 ASN (65.0, 115.0)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 14



99.1% (210/212) of all residues were in favored (98%) regions.
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

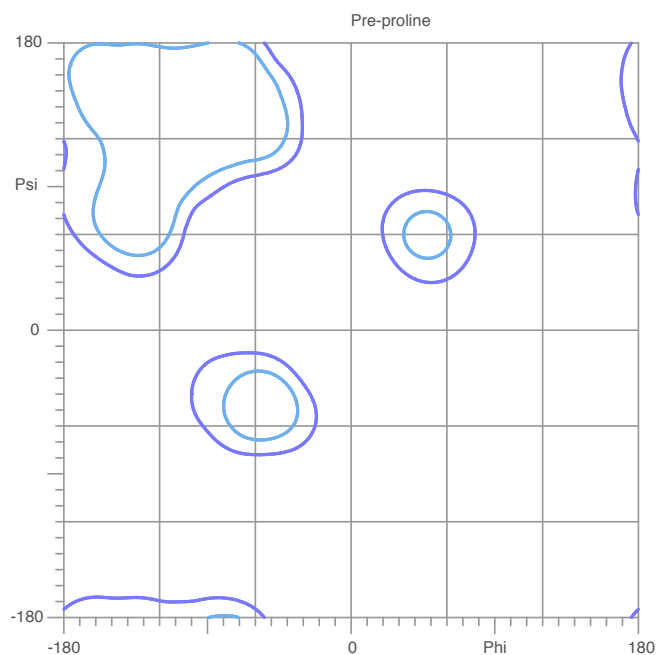
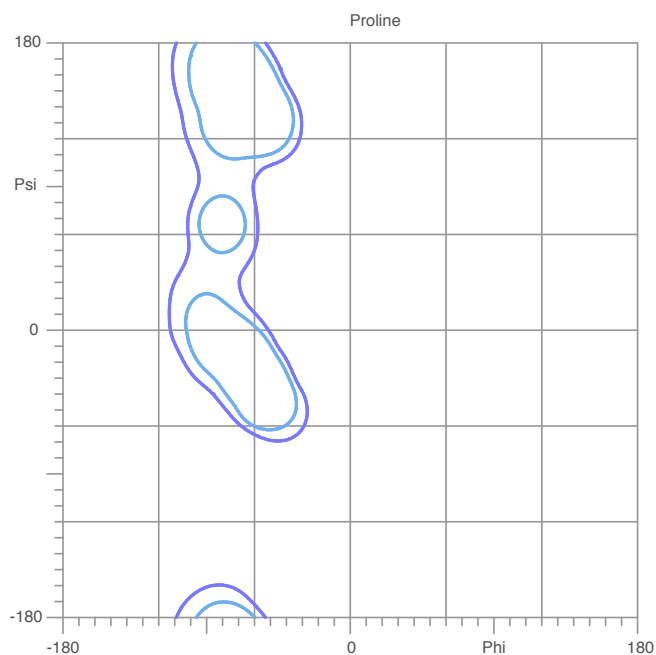
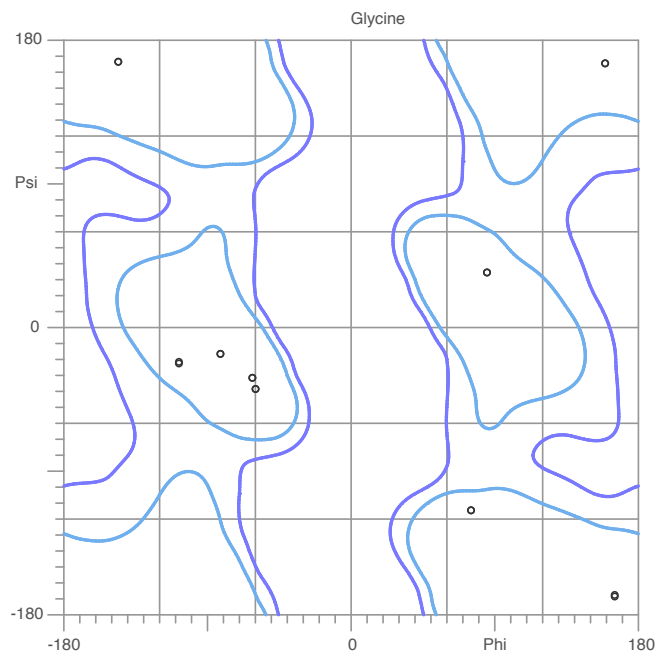
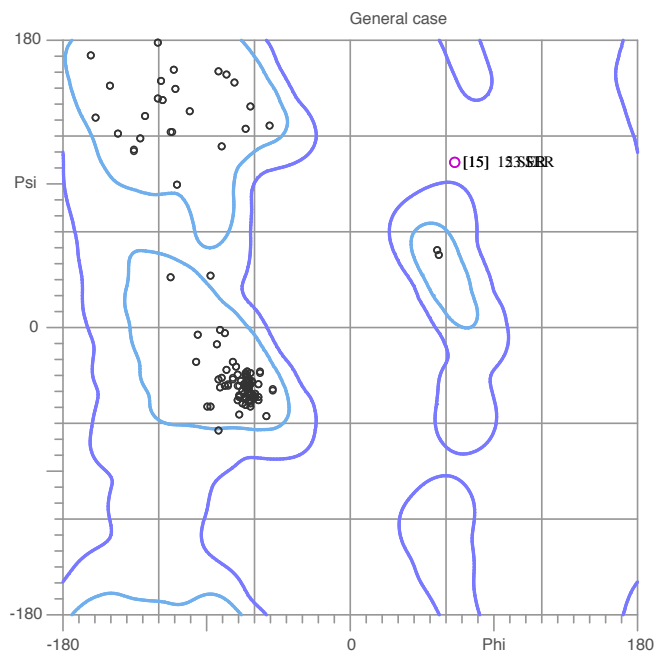
There were no outliers.

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

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MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 15



97.2% (206/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

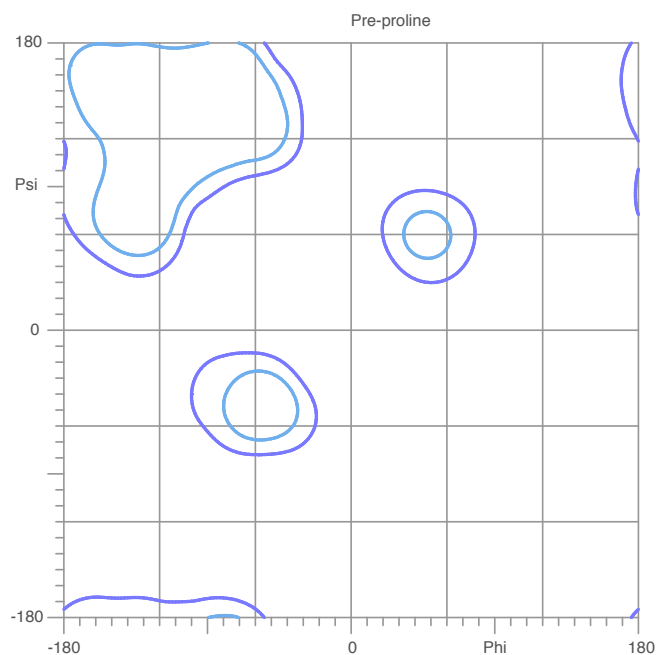
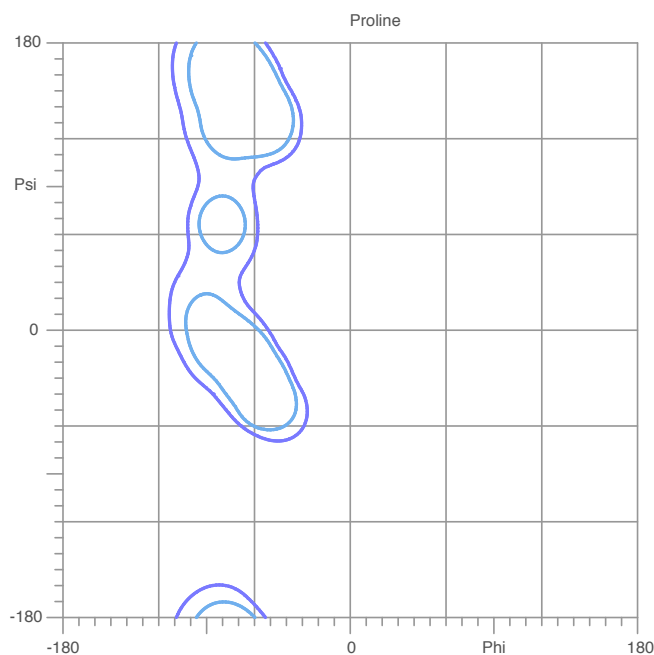
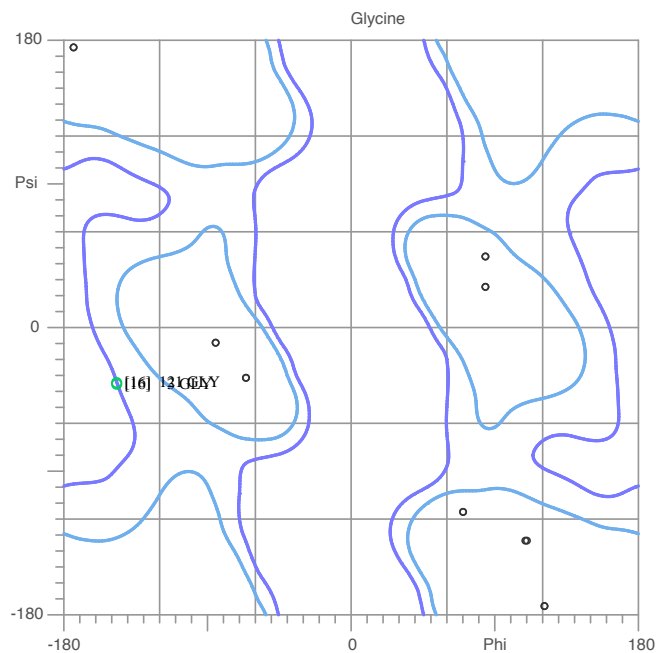
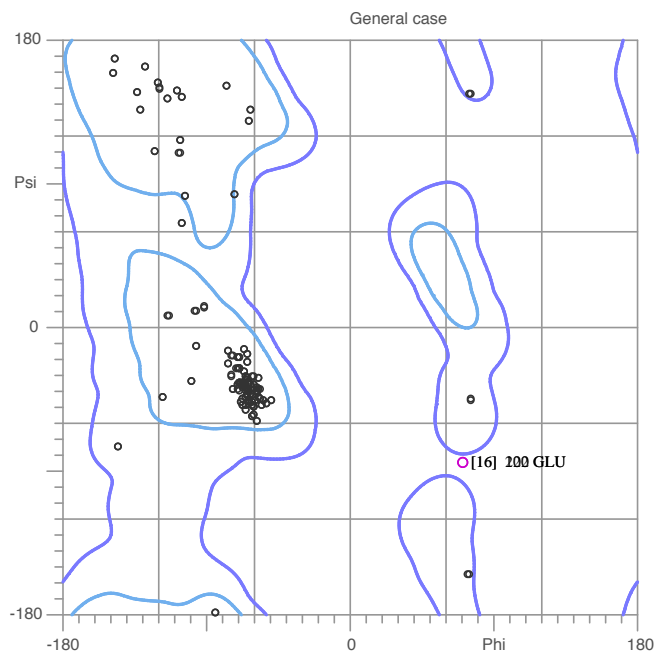
There were 2 outliers (phi, psi):

[15] 5 SER (65.2, 104.9)

[15] 123 SER (65.1, 105.0)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 16



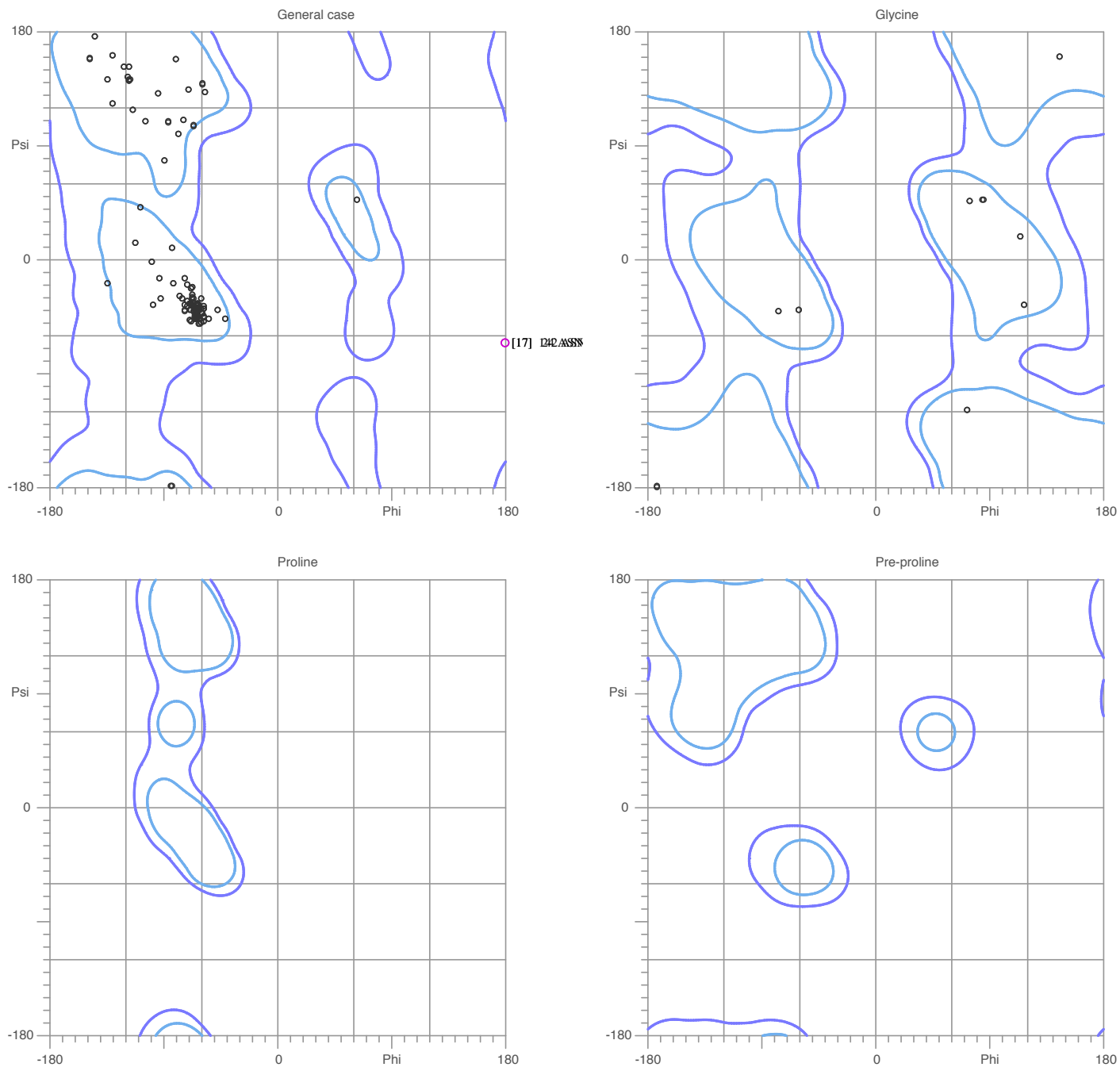
93.4% (198/212) of all residues were in favored (98%) regions.
98.1% (208/212) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [16] 3 GLY (-147.5, -35.1)
- [16] 102 GLU (70.4, -84.1)
- [16] 121 GLY (-147.6, -35.0)
- [16] 220 GLU (70.4, -84.2)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 17

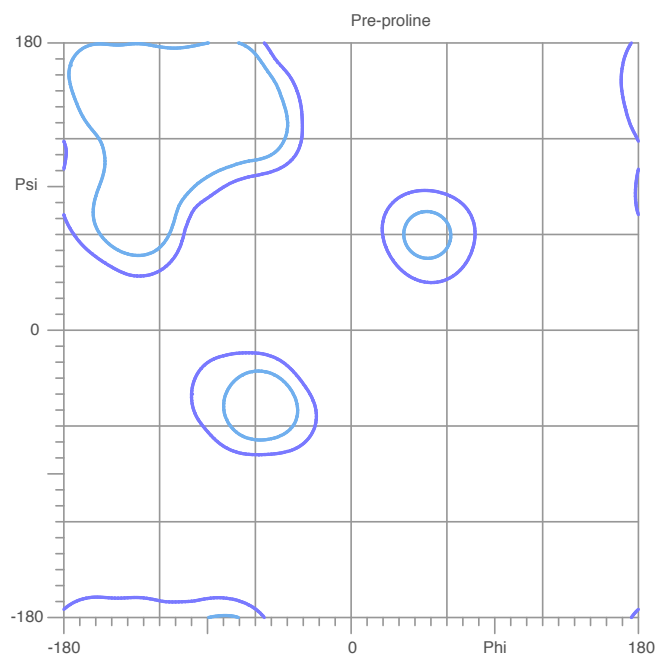
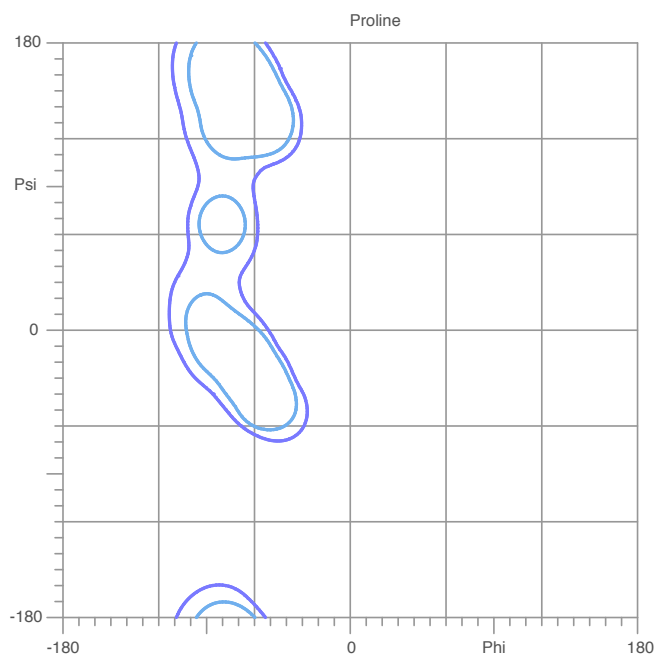
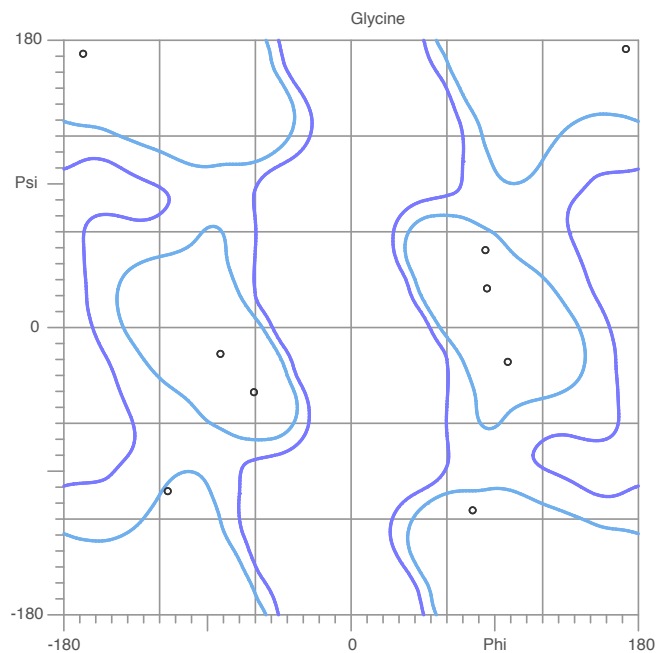
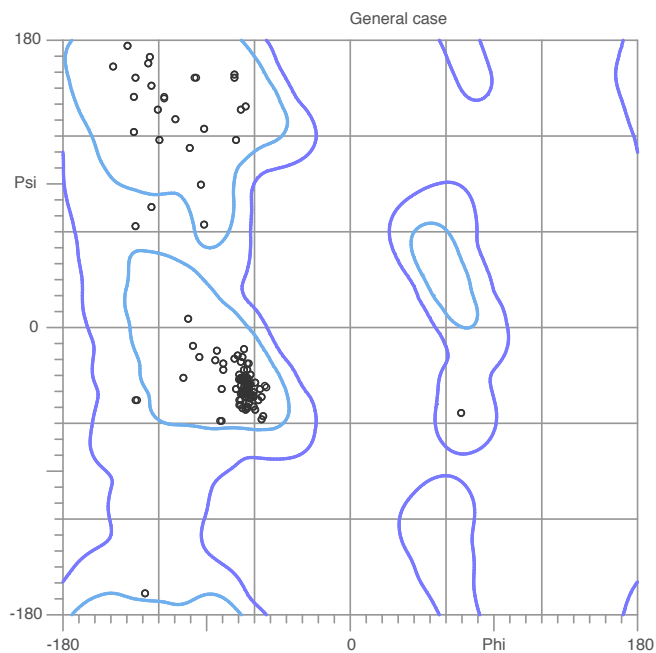


98.1% (208/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[17] 24 ASN (179.4, -65.1)
[17] 142 ASN (179.4, -65.0)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 18



95.3% (202/212) of all residues were in favored (98%) regions.
100.0% (212/212) of all residues were in allowed (>99.8%) regions.

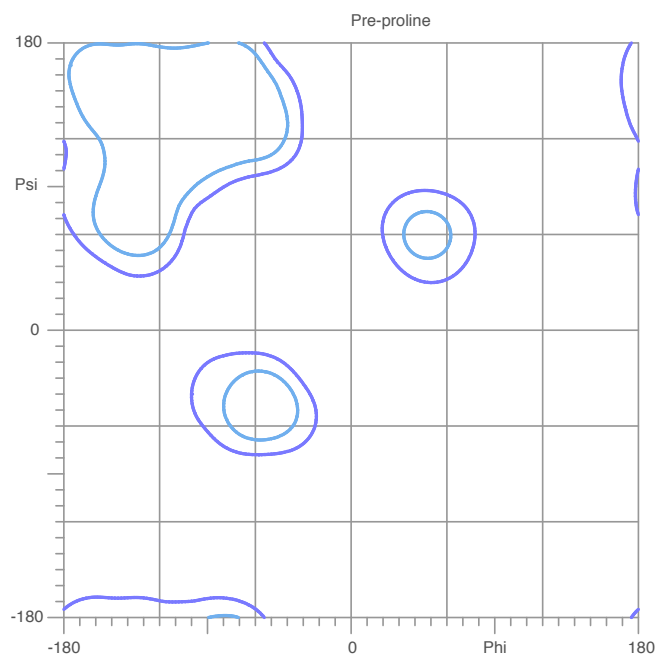
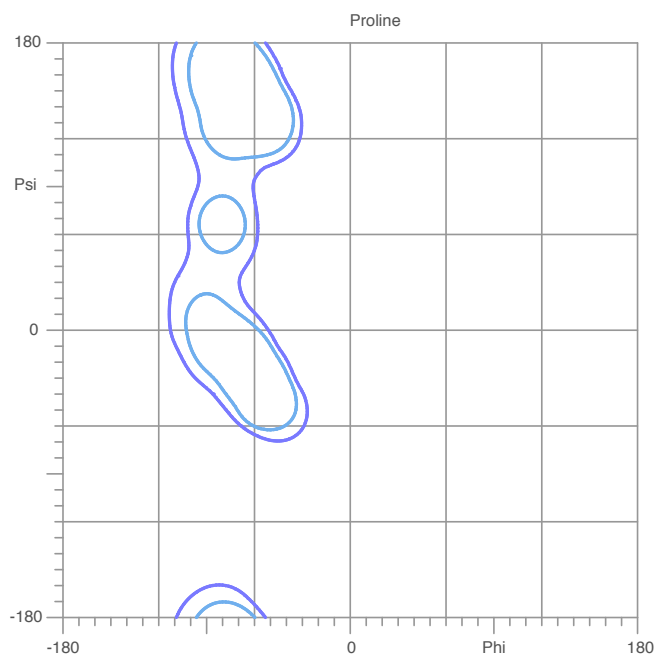
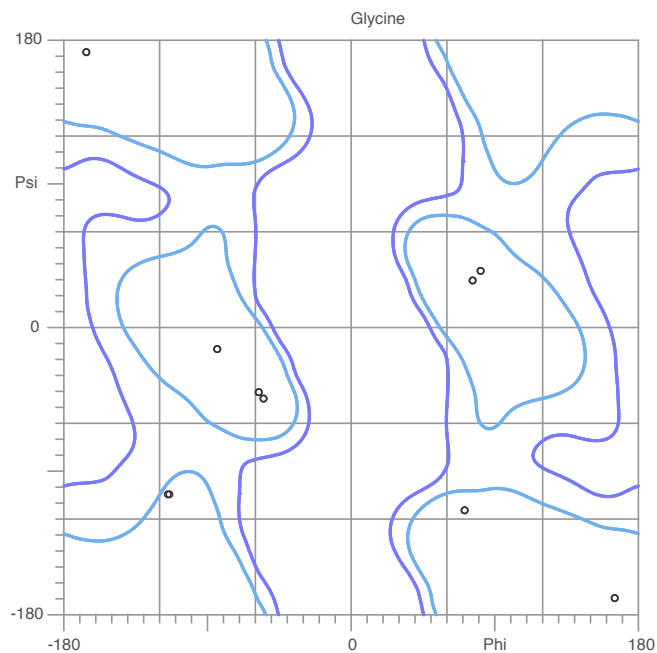
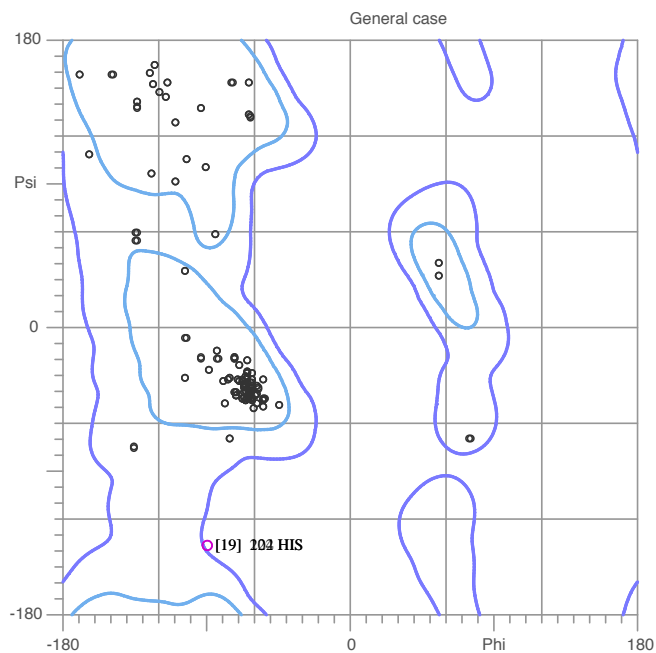
There were no outliers.

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

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

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 19

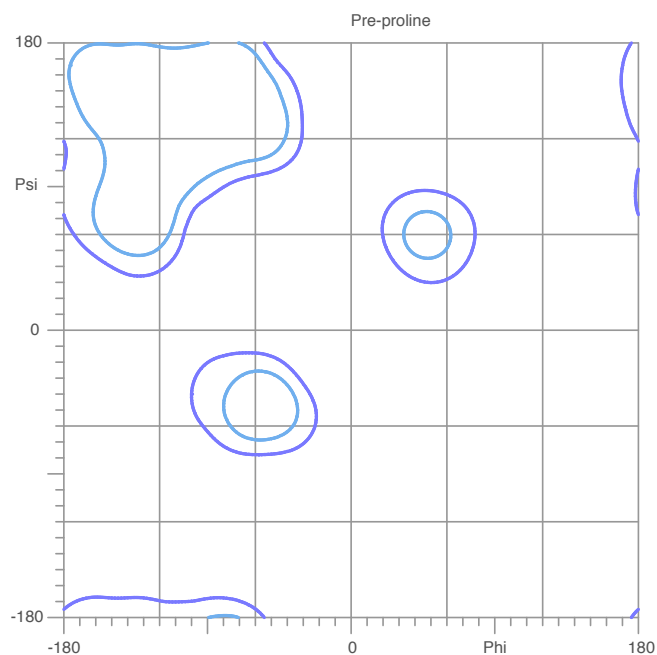
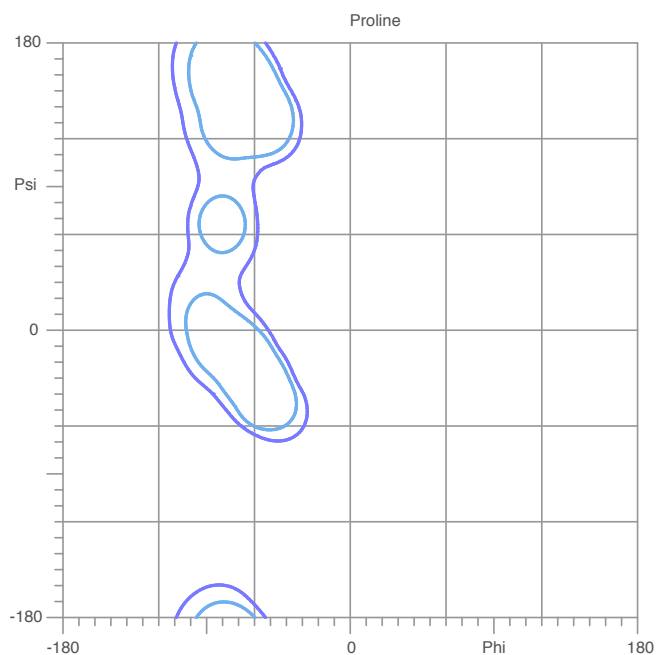
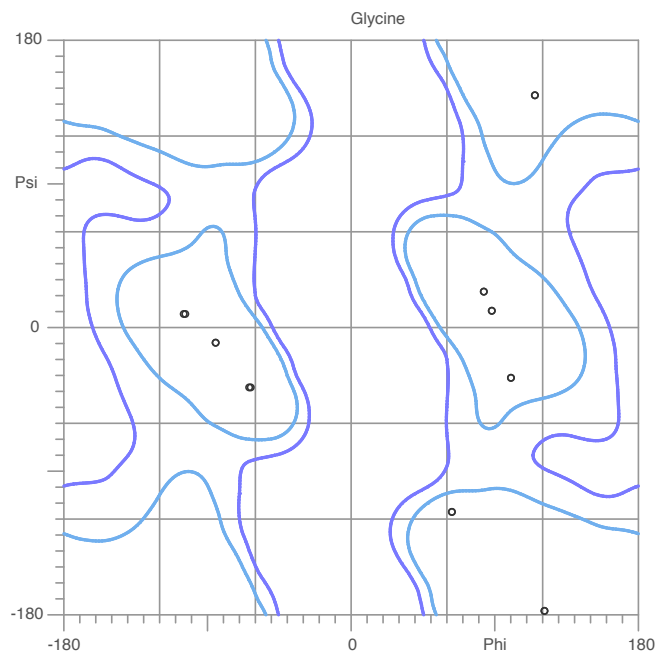
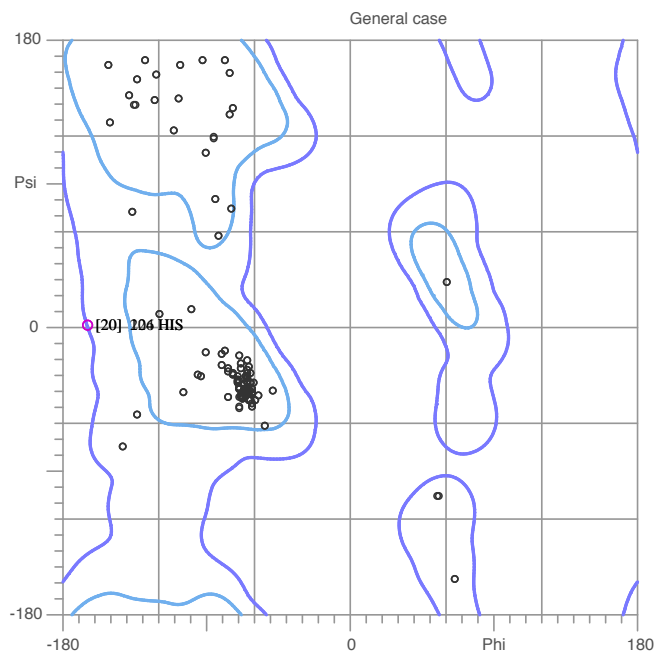


93.4% (198/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 104 HIS (-90.9, -136.2)
[19] 222 HIS (-90.8, -136.1)

MolProbity Ramachandran analysis

MBR242E_R3_em_bcr3.pdb, model 20



94.3% (200/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[20] 106 HIS (-165.4, 2.3)

[20] 224 HIS (-165.4, 2.2)