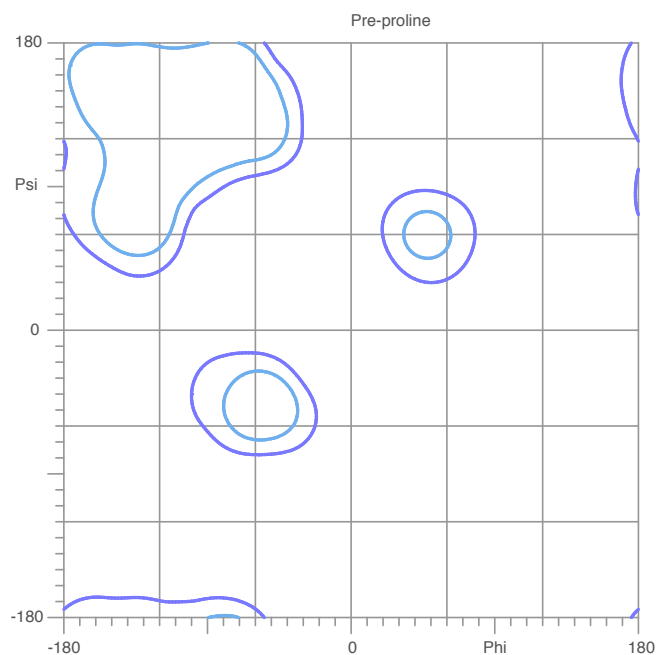
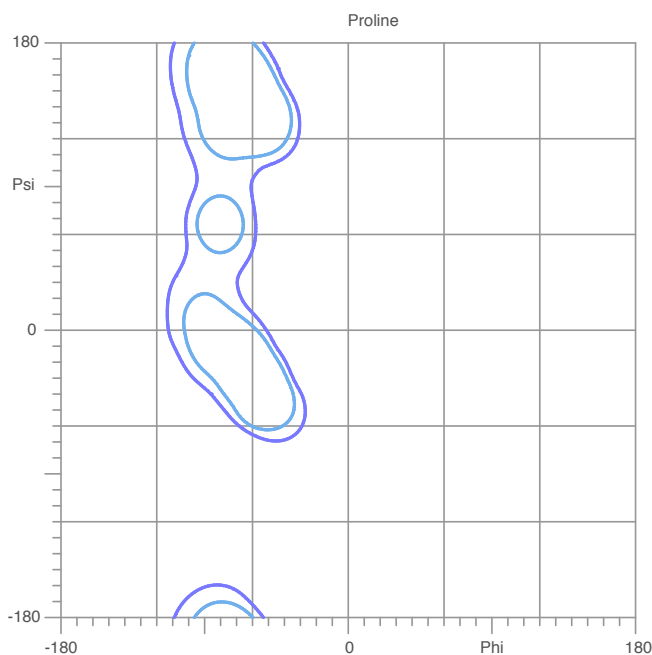
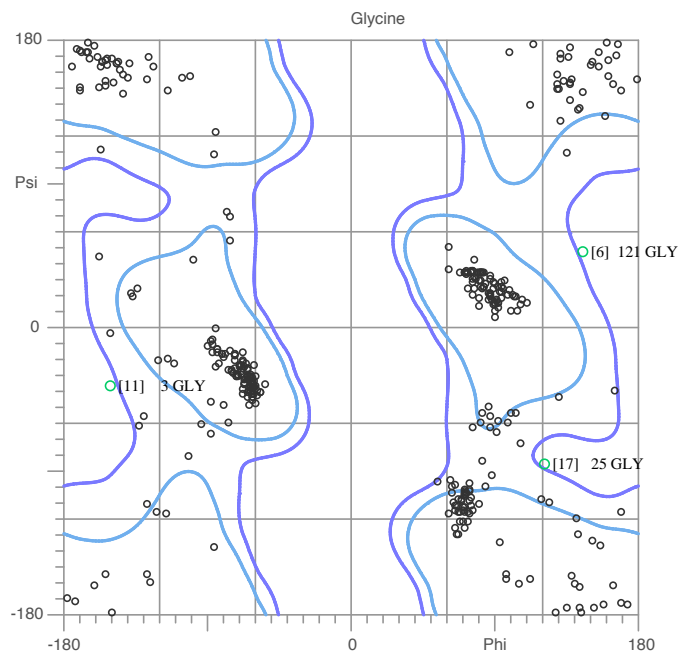
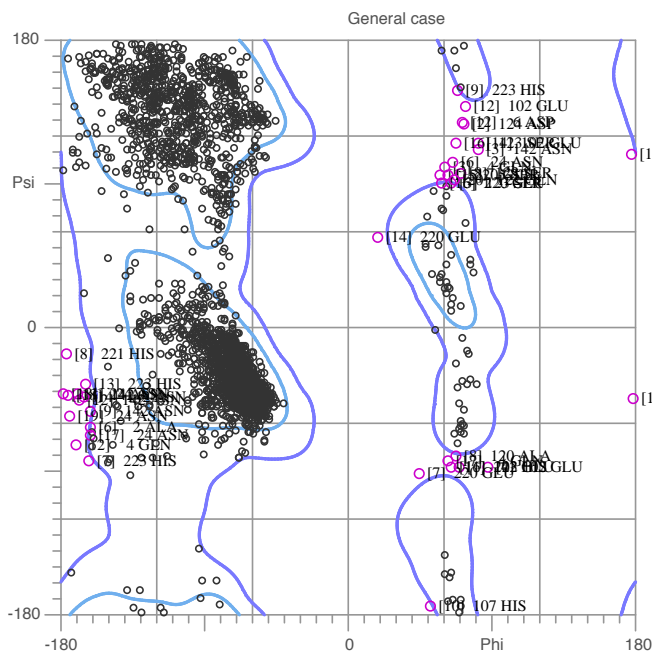


MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, all models



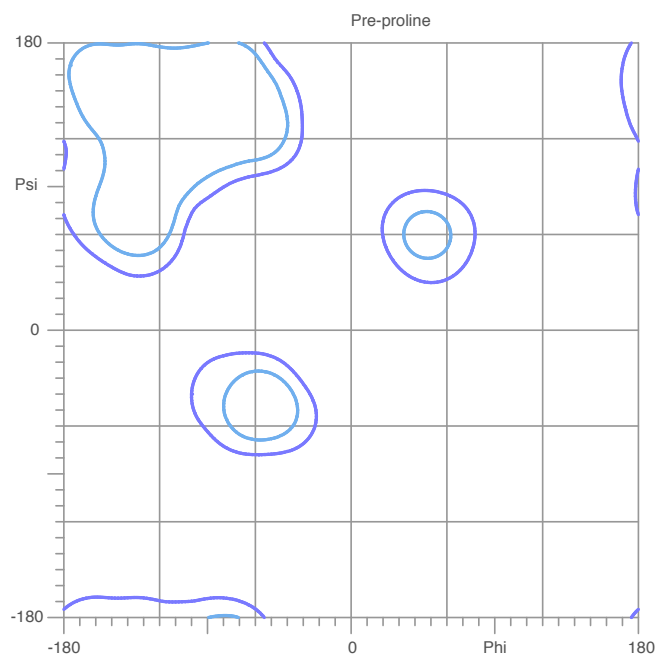
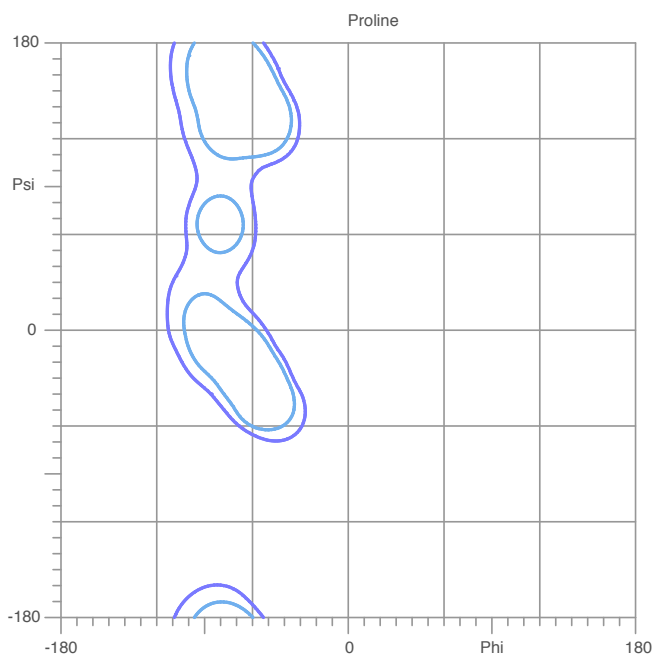
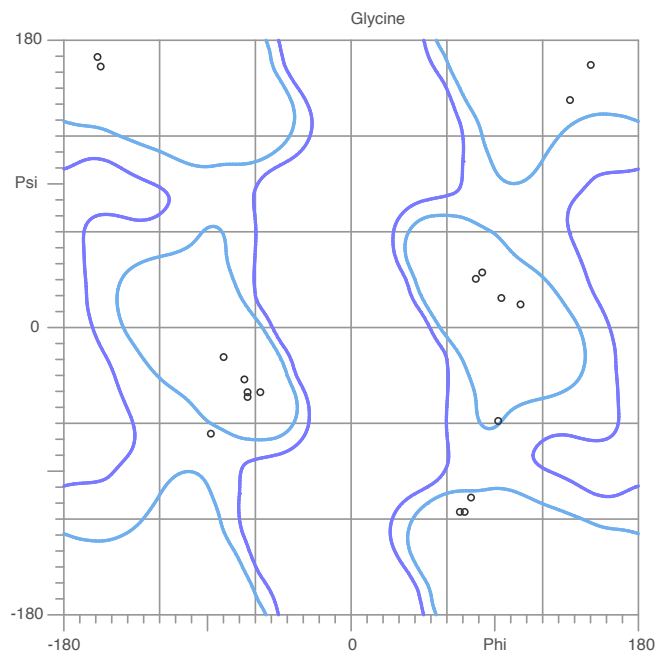
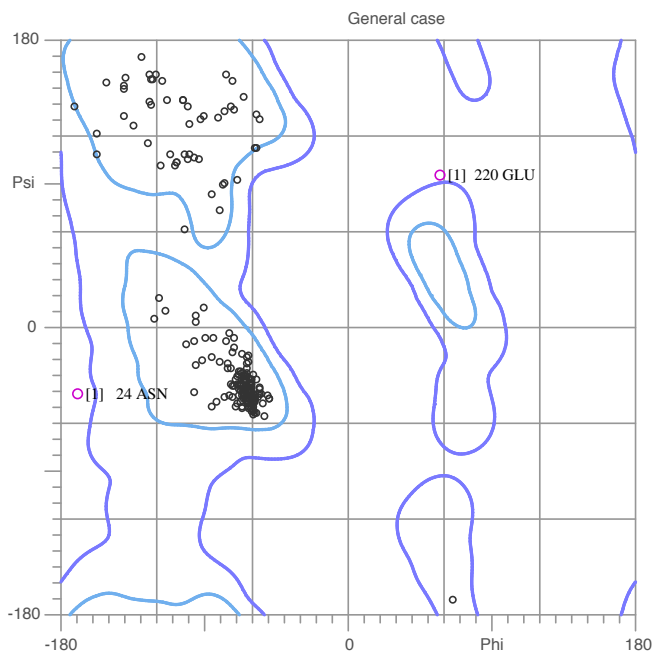
94.9% (4022/4240) of all residues were in favored (98%) regions.
99.0% (4199/4240) of all residues were in allowed (>99.8%) regions.

There were 41 outliers (phi, psi):

- | | |
|-----------------------------|------------------------------|
| [1] 24 ASN (-170.5, -41.1) | [10] 107 HIS (51.5, -174.4) |
| [1] 220 GLU (57.1, 96.2) | [11] 3 GLY (-151.7, -36.6) |
| [2] 124 ASP (72.3, 128.9) | [11] 102 GLU (64.6, -87.4) |
| [3] 4 GLN (60.3, 101.1) | [12] 4 GLN (-171.2, -73.2) |
| [3] 123 SER (64.8, 91.7) | [12] 6 ASP (71.2, 129.0) |
| [3] 142 ASN (81.5, 112.3) | [12] 102 GLU (73.1, 139.5) |
| [4] 102 GLU (87.1, -87.3) | [12] 142 ASN (-170.0, -45.8) |
| [6] 2 ALA (-162.3, -62.3) | [13] 223 HIS (-165.7, -35.8) |
| [6] 24 ASN (66.0, 104.8) | [13] 225 HIS (178.4, -44.3) |
| [6] 121 GLY (145.8, 48.8) | [14] 102 GLU (81.5, 117.0) |
| [6] 223 HIS (69.8, -87.0) | [14] 142 ASN (-166.3, -44.0) |
| [7] 220 GLU (44.8, -91.9) | [14] 220 GLU (18.5, 58.0) |
| [7] 223 HIS (-163.7, -84.0) | [15] 5 SER (62.9, 96.3) |
| [8] 120 ALA (67.2, -80.1) | [15] 223 HIS (177.9, 110.0) |
| [8] 123 SER (70.7, 97.4) | [16] 123 SER (67.3, 116.8) |
| [8] 221 HIS (-177.4, -16.1) | [16] 220 GLU (58.4, 91.4) |
| [9] 142 ASN (-162.3, -52.2) | [17] 4 GLN (62.0, -83.2) |
| [9] 223 HIS (68.4, 149.1) | [17] 24 ASN (-162.9, -67.1) |
| | [17] 25 GLY (121.9, -85.2) |
| | [18] 24 ASN (-179.3, -41.2) |
| | [18] 142 ASN (-176.0, -42.9) |
| | [19] 24 ASN (-175.8, -55.2) |
| | [20] 122 GLN (66.9, 93.4) |

MolProbity Ramachandran analysis

MBR242E_NMR_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.

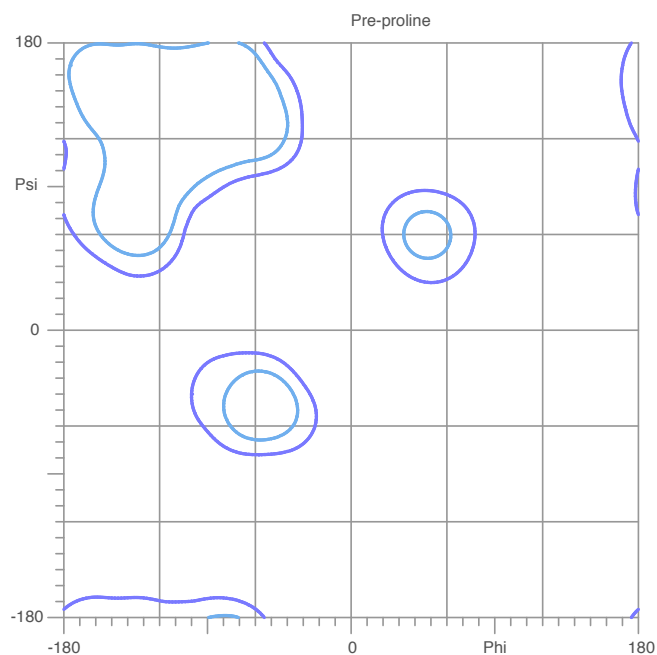
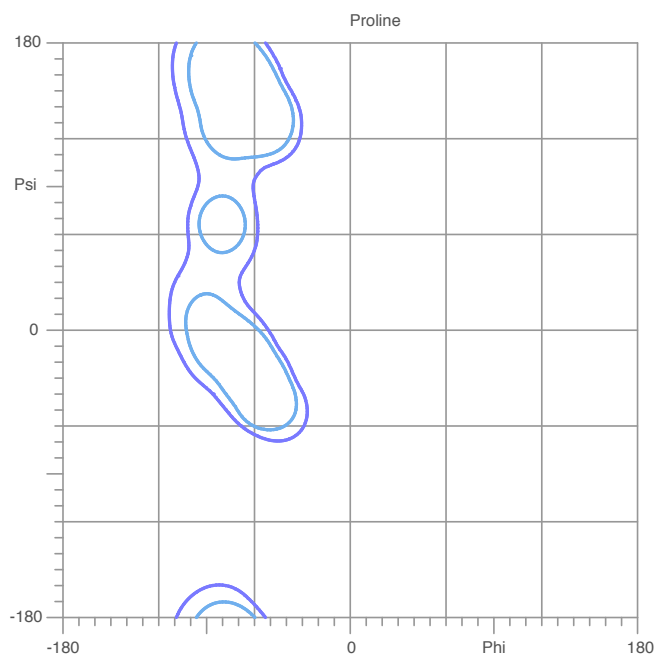
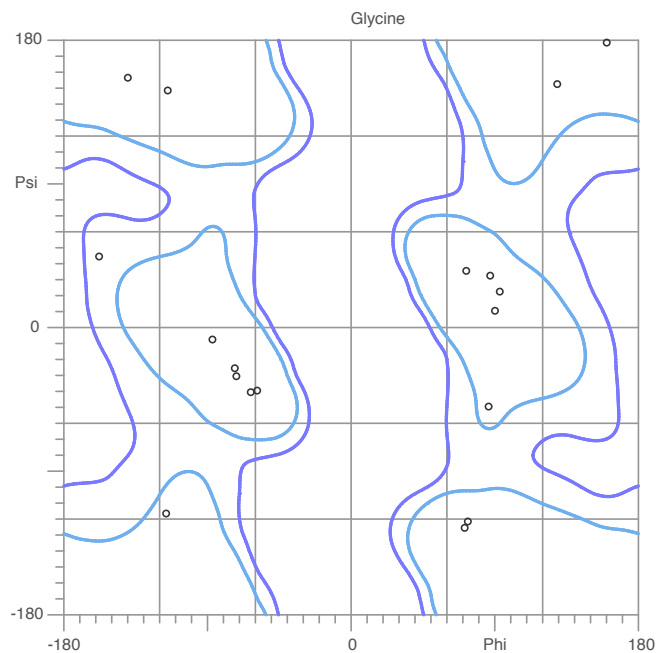
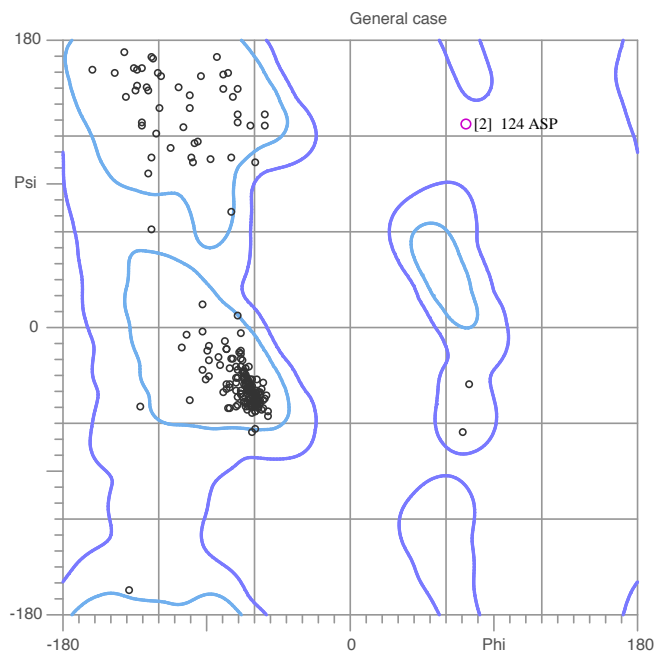
There were 2 outliers (phi, psi):

[1] 24 ASN (-170.5, -41.1)

[1] 220 GLU (57.1, 96.2)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 2



95.8% (203/212) of all residues were in favored (98%) regions.
99.5% (211/212) of all residues were in allowed (>99.8%) regions.

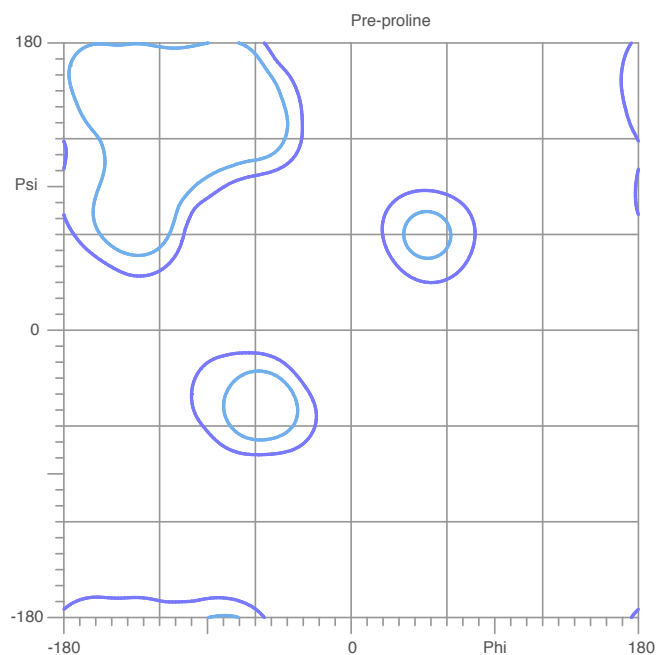
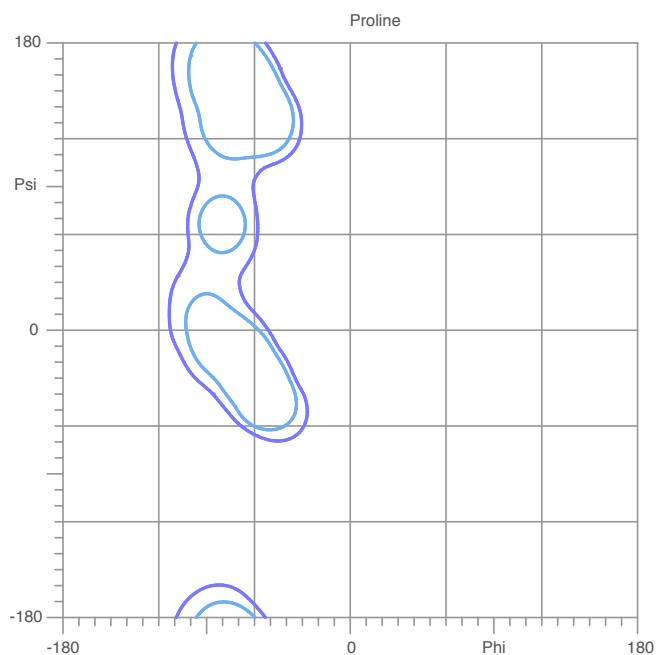
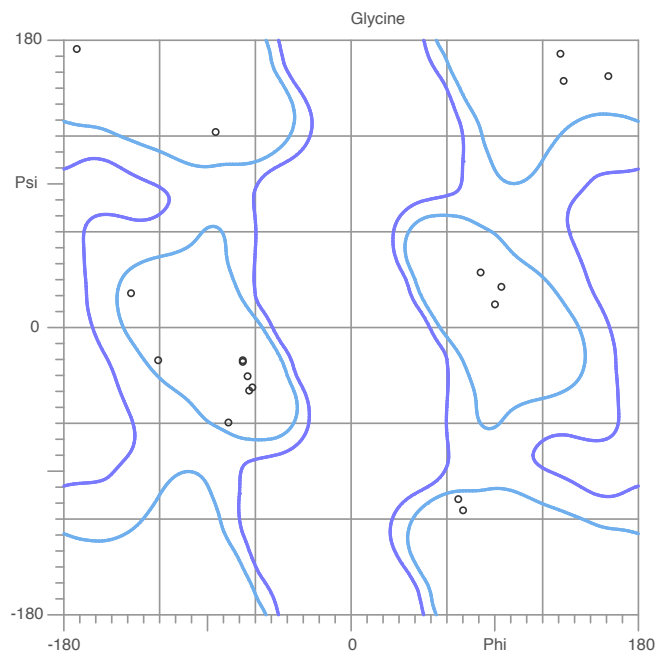
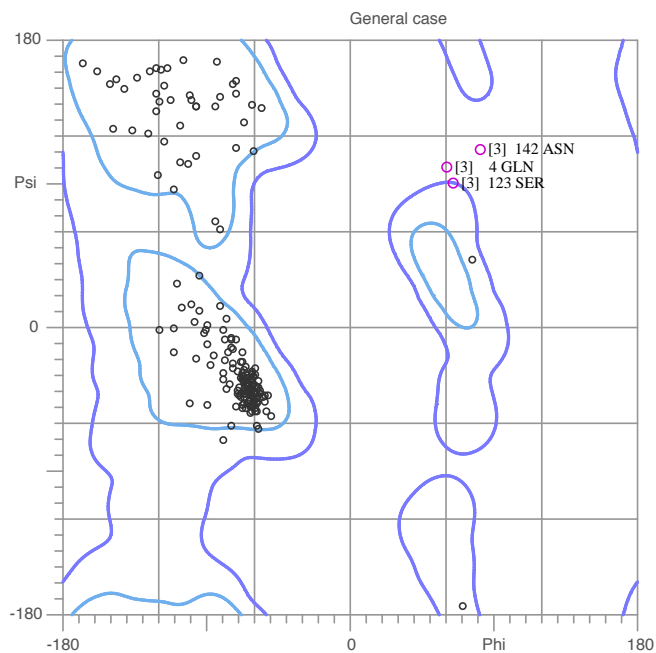
There were 1 outliers (phi, psi):
[2] 124 ASP (72.3, 128.9)

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MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 3



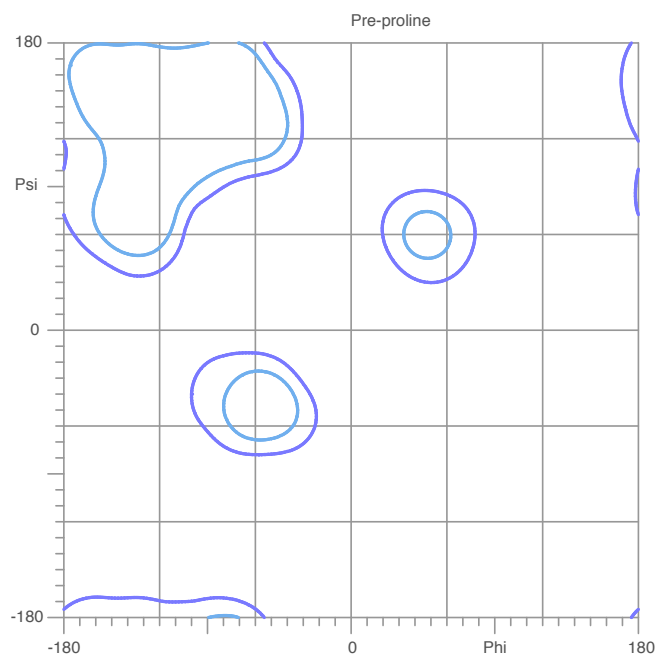
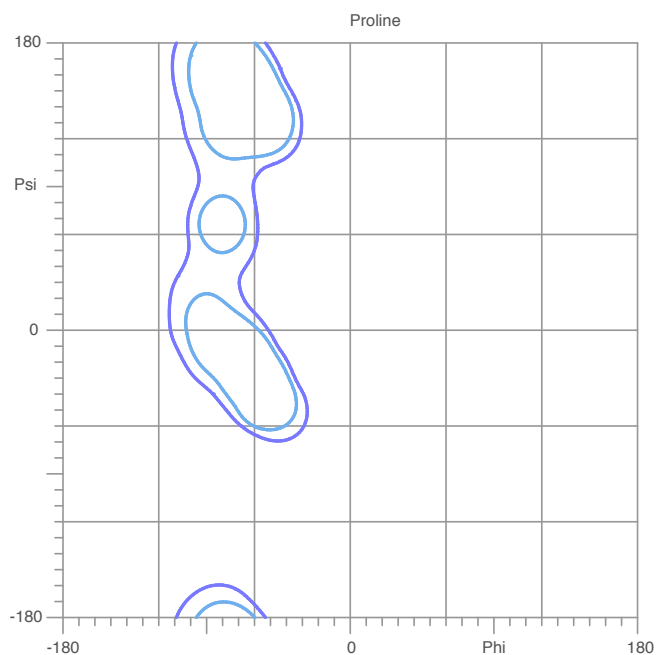
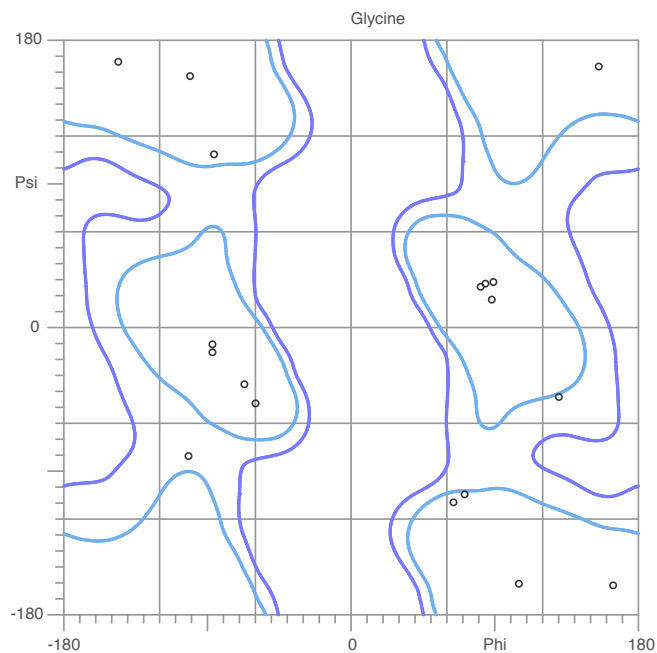
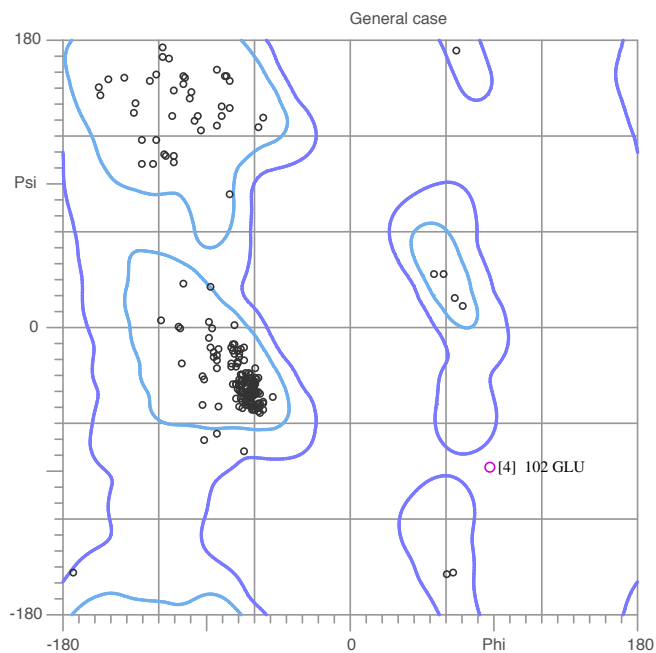
97.2% (206/212) of all residues were in favored (98%) regions.
98.6% (209/212) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 4 GLN (60.3, 101.1)
- [3] 123 SER (64.8, 91.7)
- [3] 142 ASN (81.5, 112.3)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 4



95.3% (202/212) of all residues were in favored (98%) regions.
99.5% (211/212) of all residues were in allowed (>99.8%) regions.

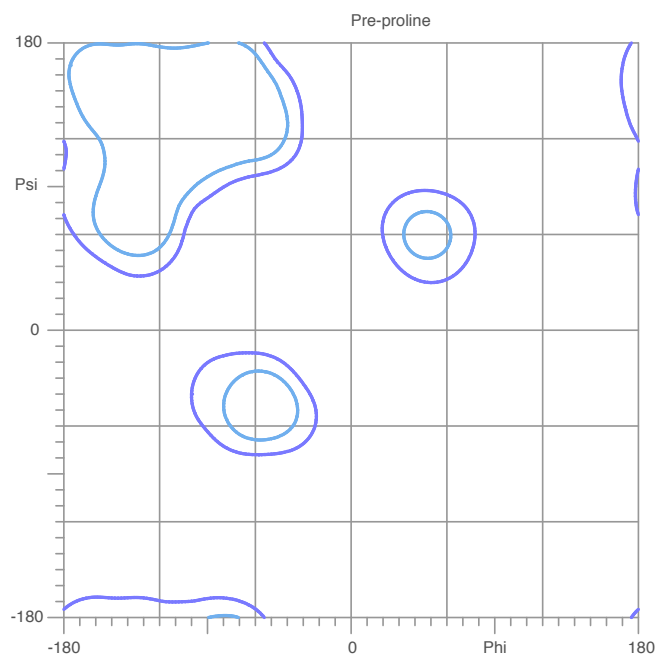
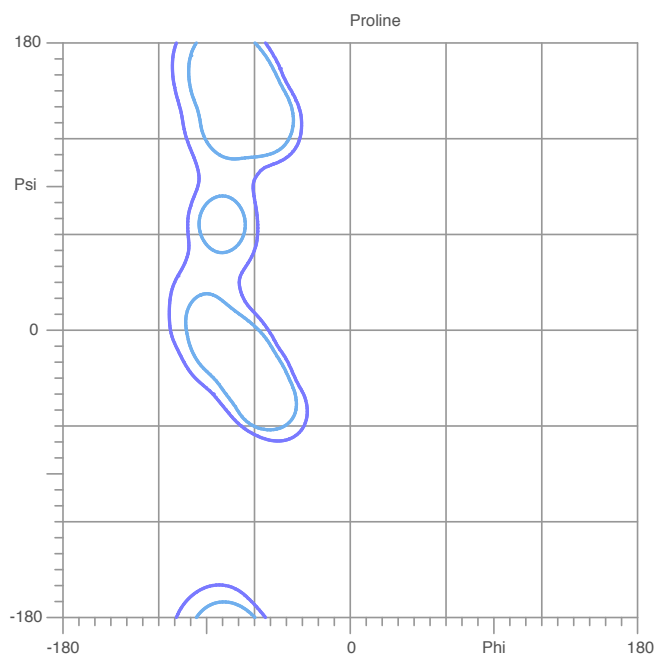
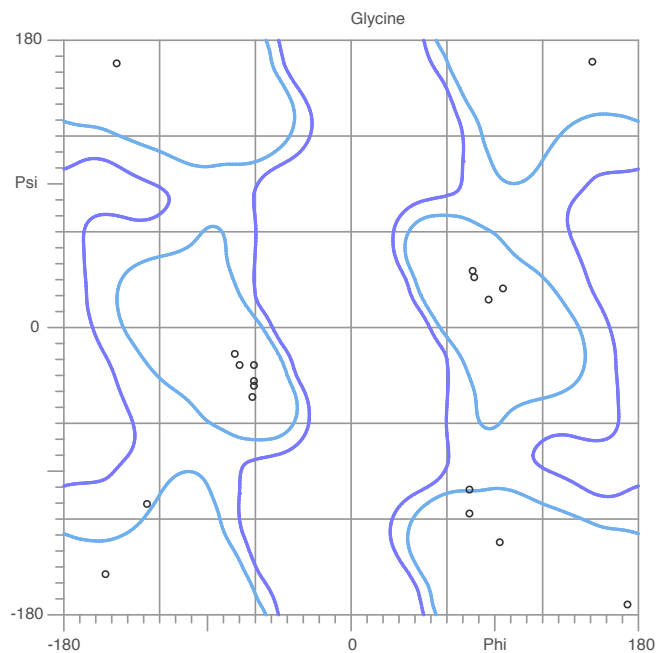
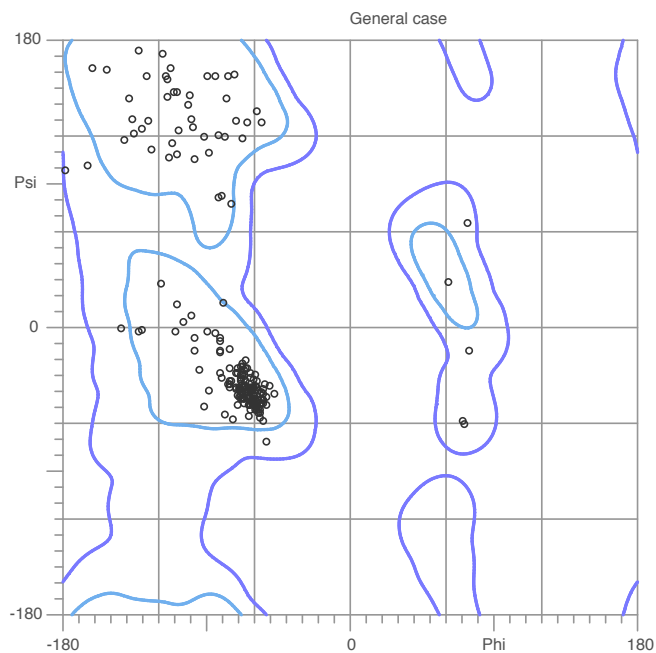
There were 1 outliers (phi, psi):
[4] 102 GLU (87.1, -87.3)

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MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 5



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.

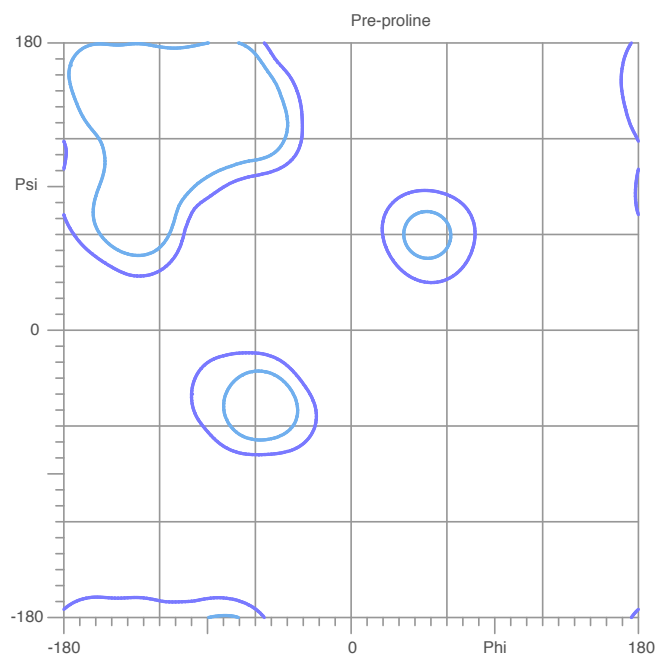
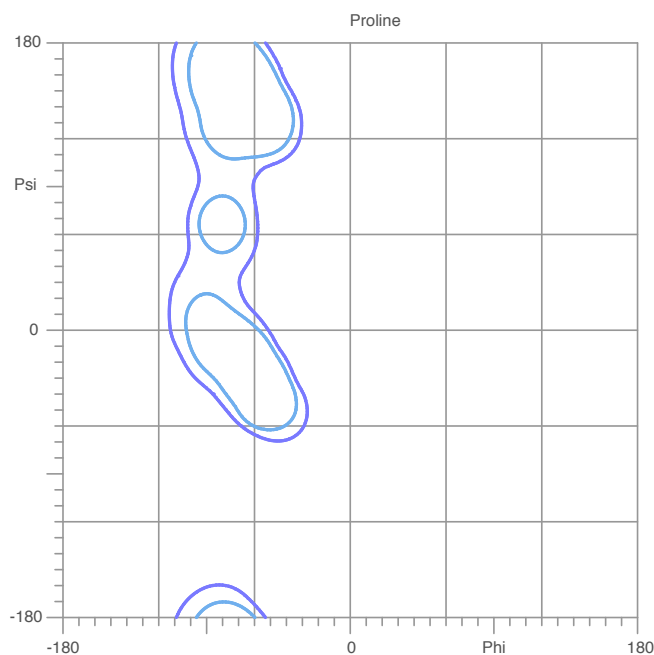
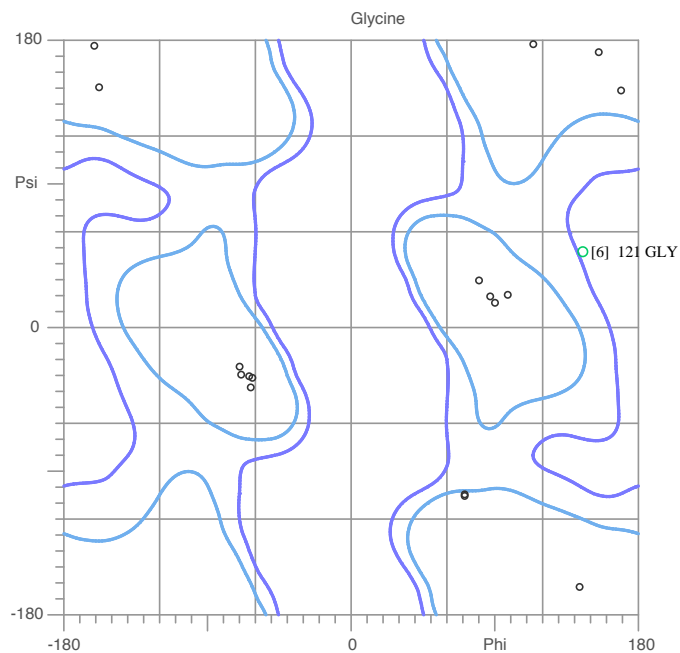
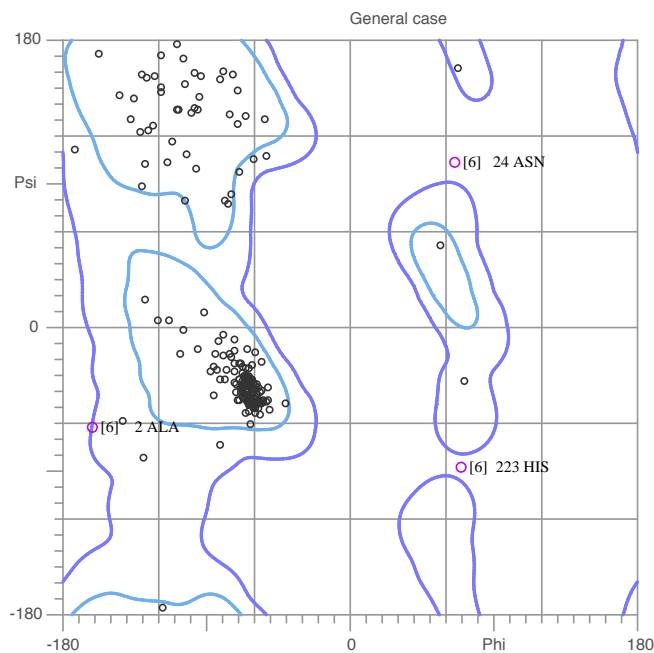
There were no outliers.

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MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 6



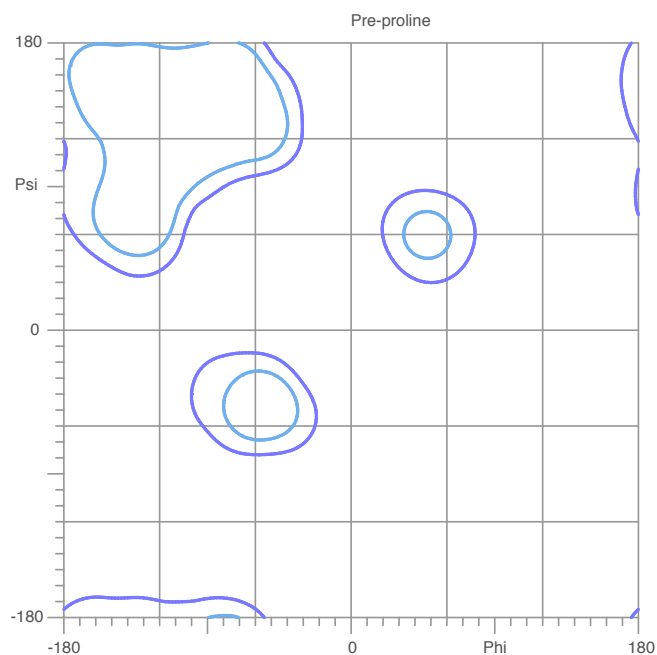
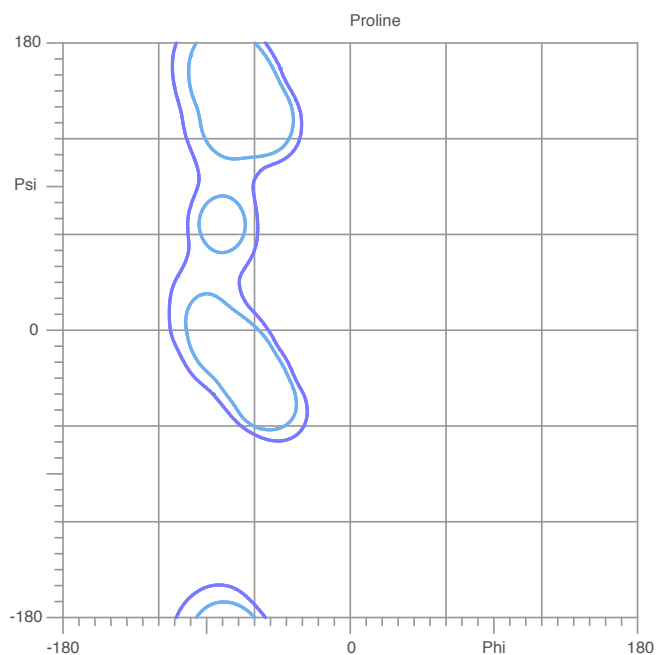
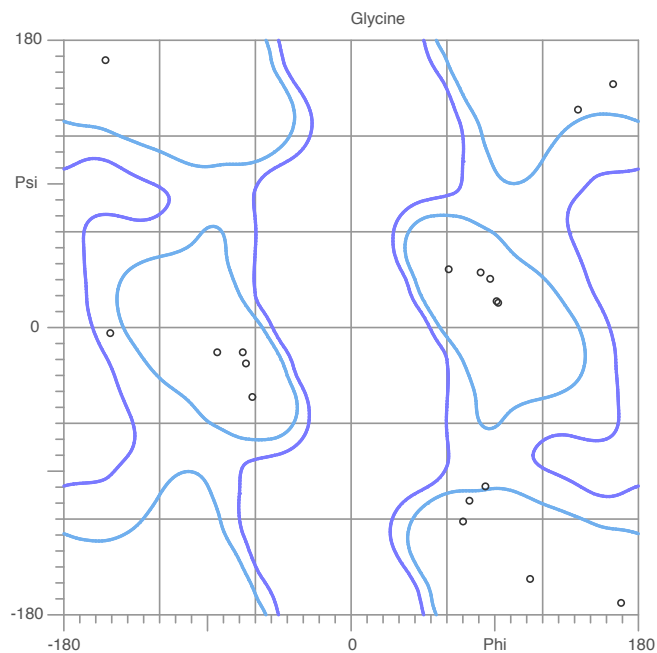
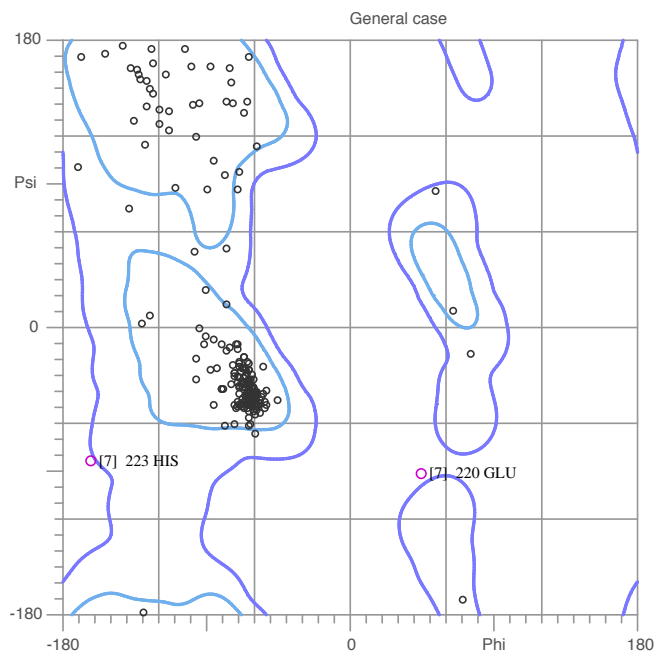
93.9% (199/212) of all residues were in favored (98%) regions.
98.1% (208/212) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [6] 2 ALA (-162.3, -62.3)
- [6] 24 ASN (66.0, 104.8)
- [6] 121 GLY (145.8, 48.8)
- [6] 223 HIS (69.8, -87.0)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 7

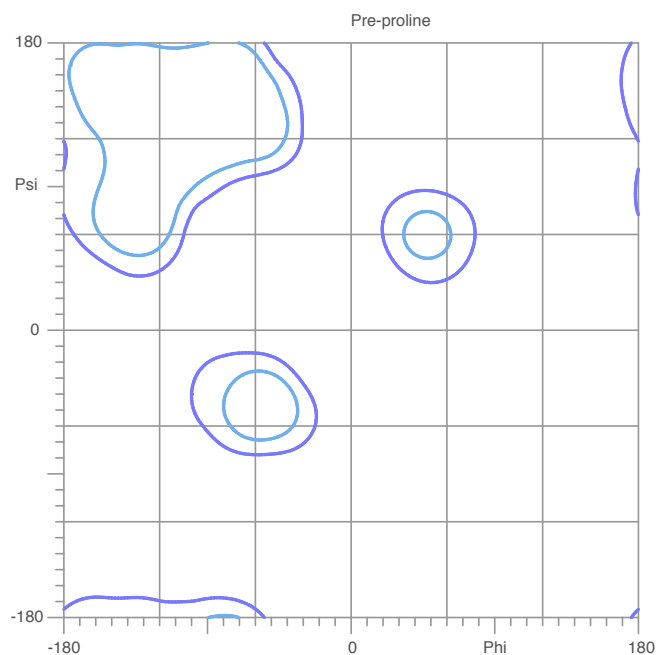
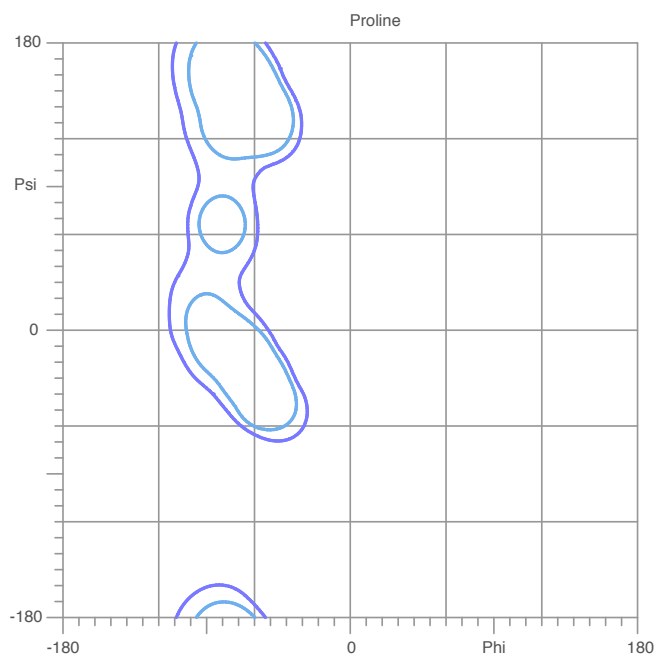
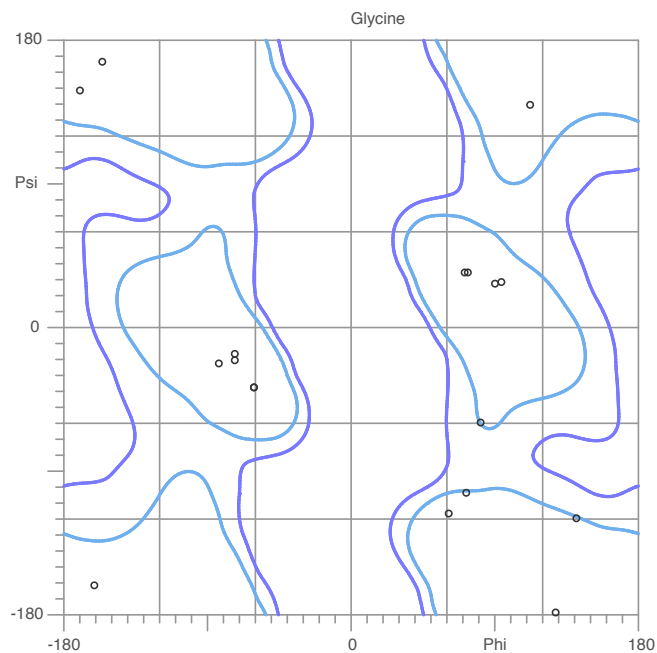
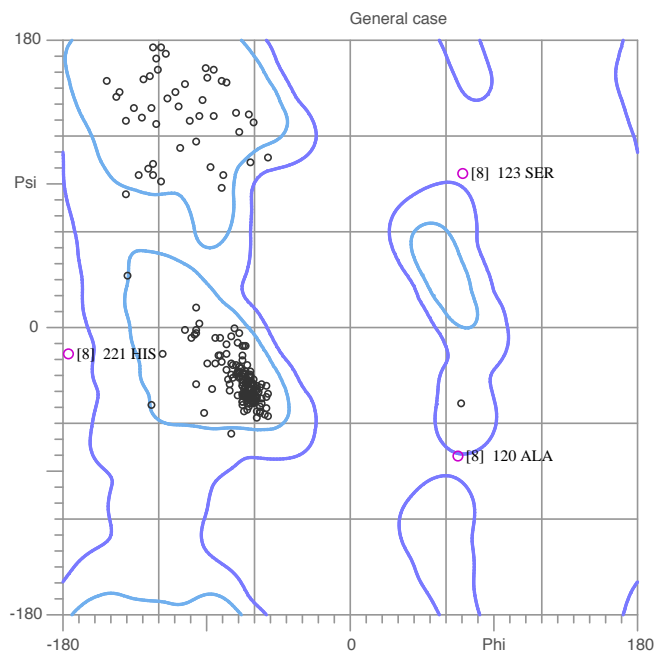


92.9% (197/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[7] 220 GLU (44.8, -91.9)
[7] 223 HIS (-163.7, -84.0)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 8



95.8% (203/212) of all residues were in favored (98%) regions.
98.6% (209/212) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

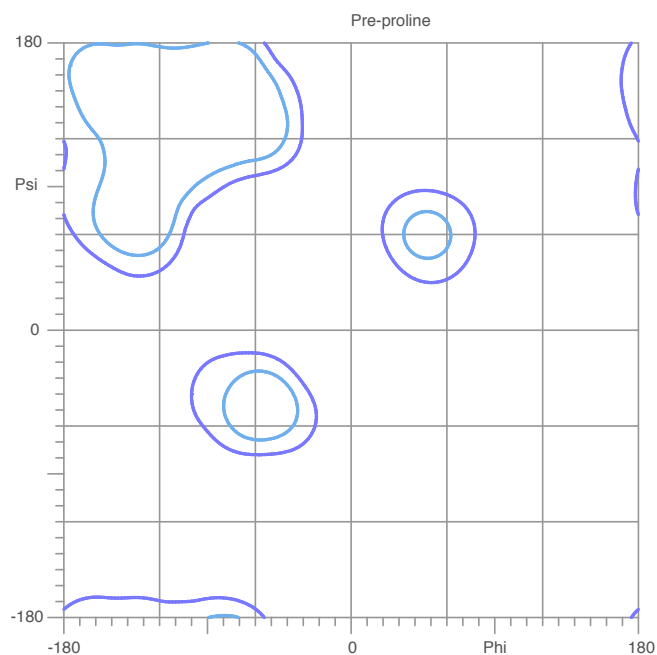
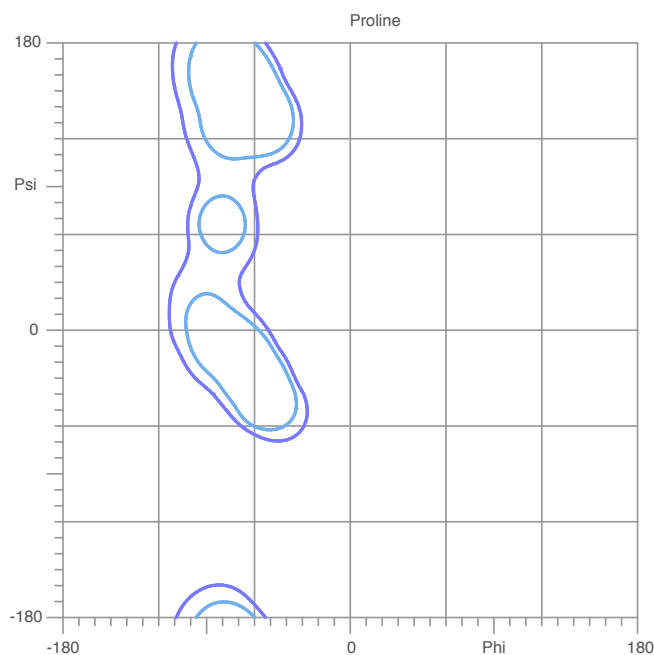
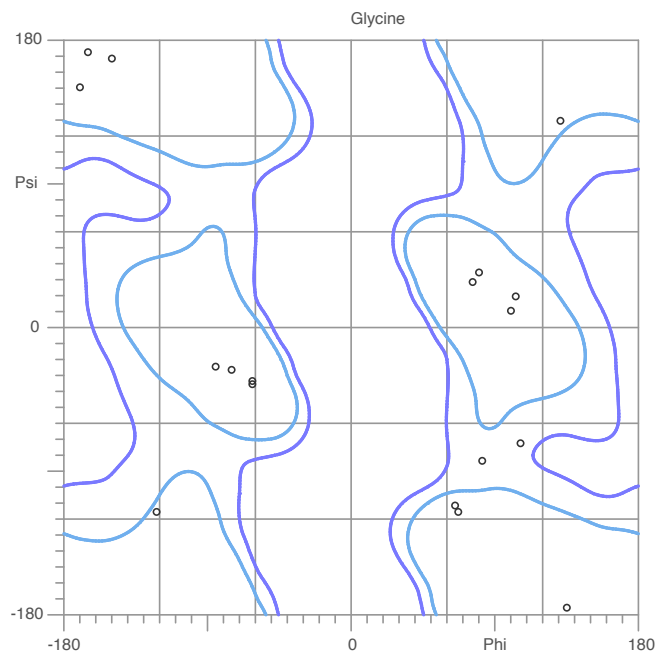
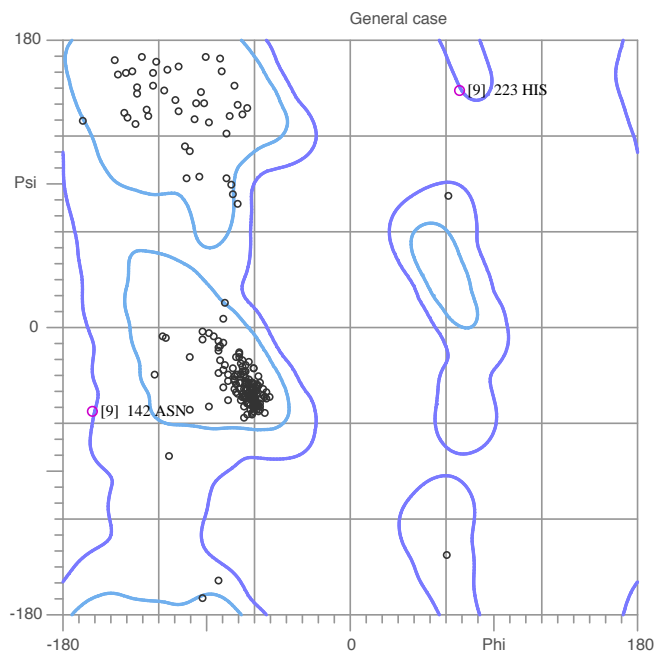
[8] 120 ALA (67.2, -80.1)

[8] 123 SER (70.7, 97.4)

[8] 221 HIS (-177.4, -16.1)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 9

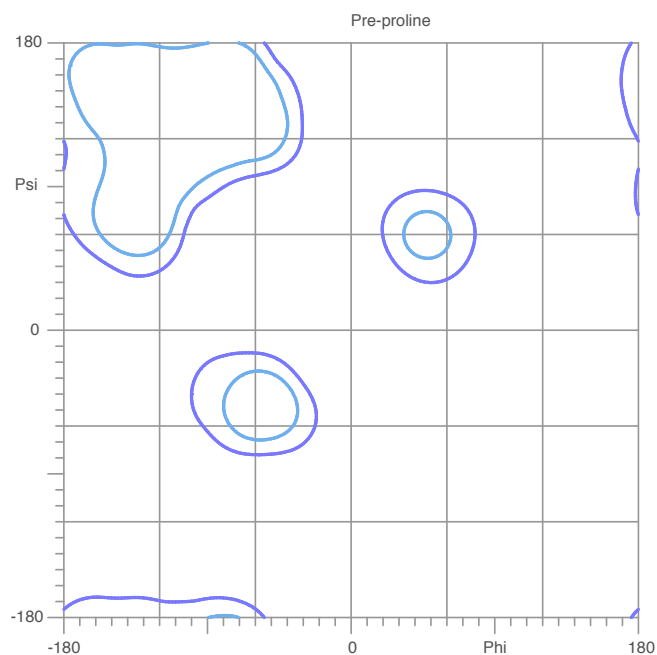
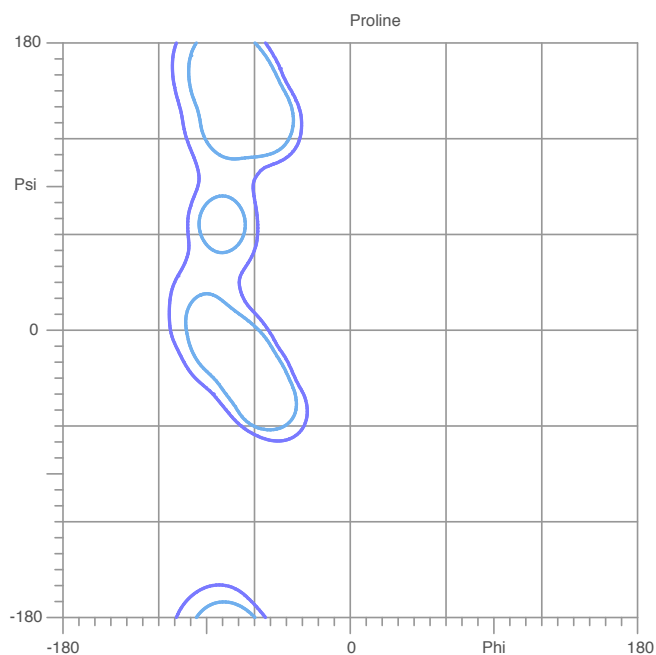
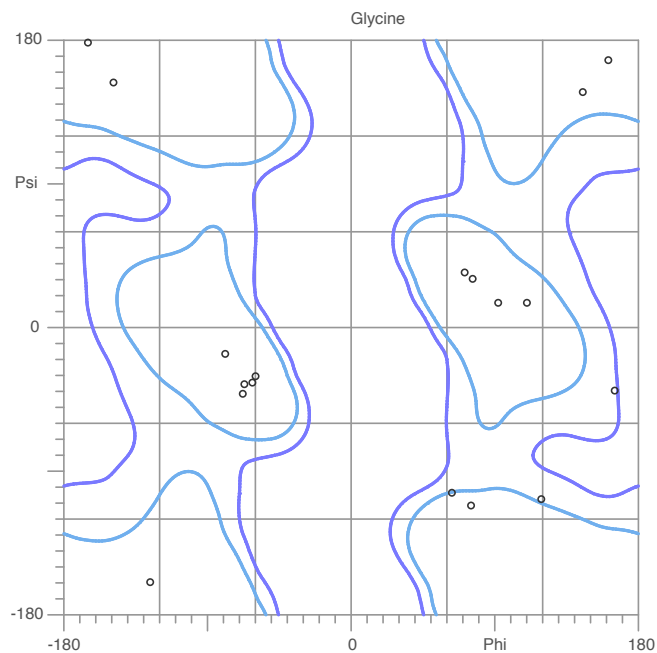
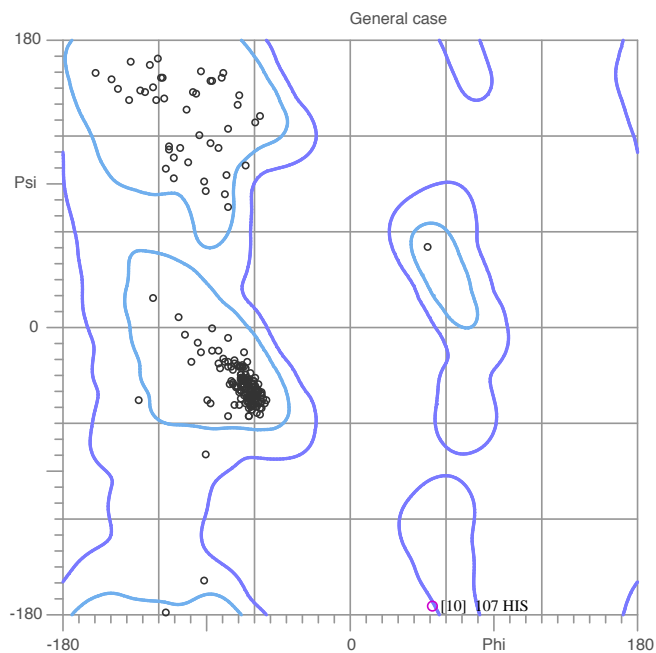


94.8% (201/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[9] 142 ASN (-162.3, -52.2)
[9] 223 HIS (68.4, 149.1)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 10



96.7% (205/212) of all residues were in favored (98%) regions.
99.5% (211/212) of all residues were in allowed (>99.8%) regions.

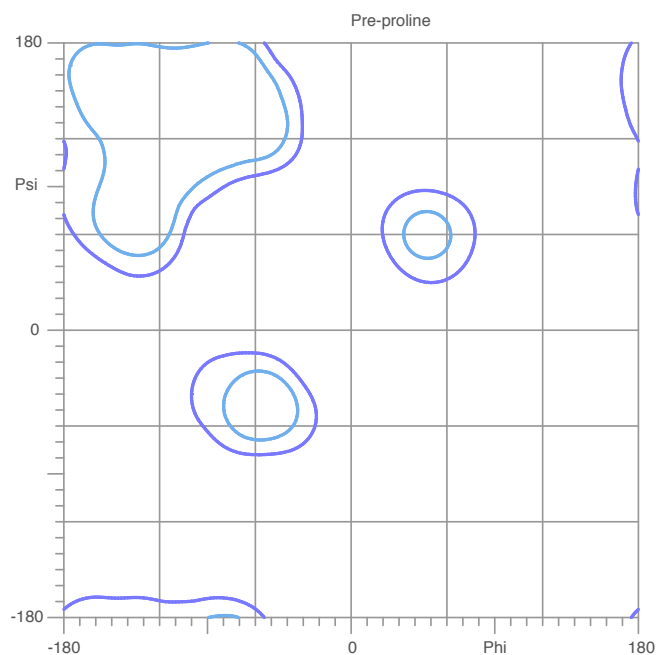
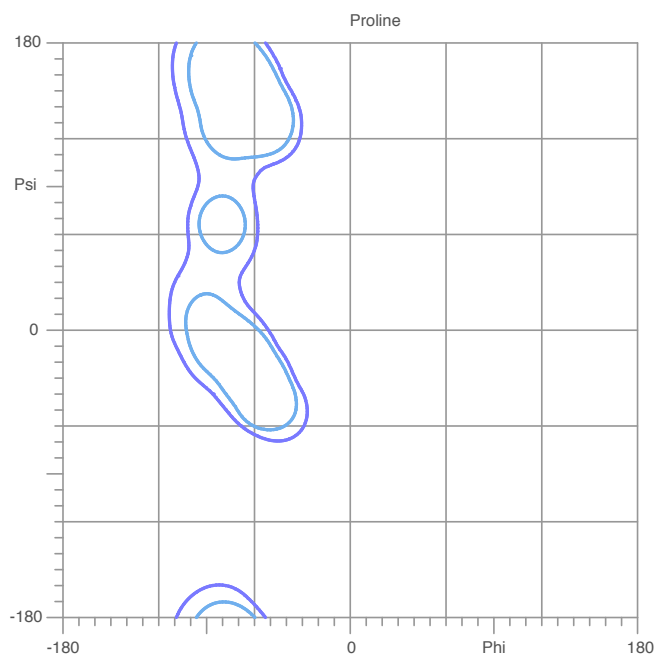
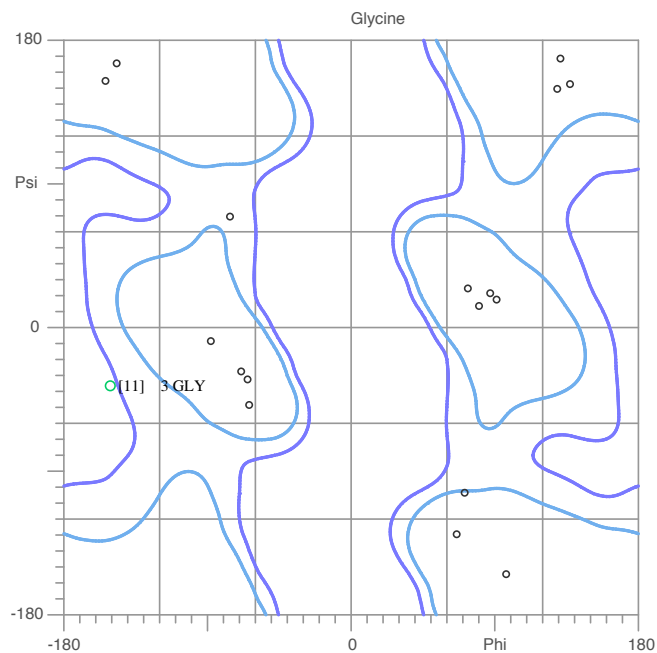
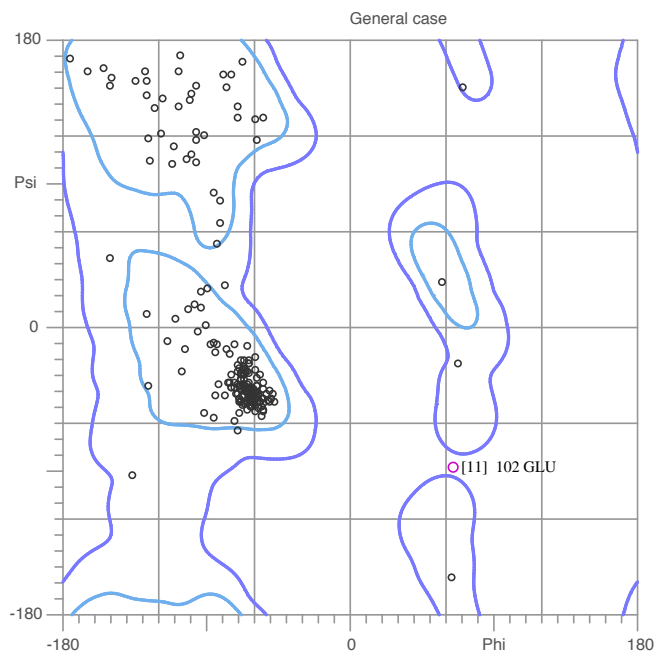
There were 1 outliers (phi, psi):
[10] 107 HIS (51.5, -174.4)

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MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 11

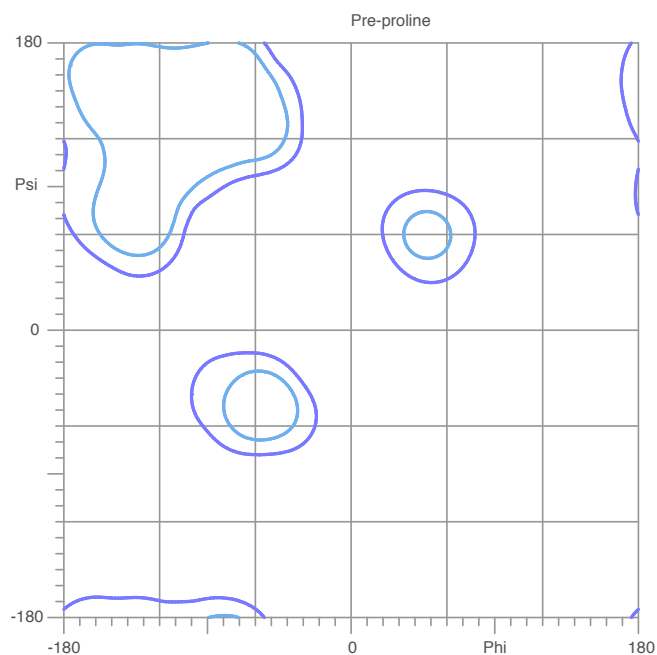
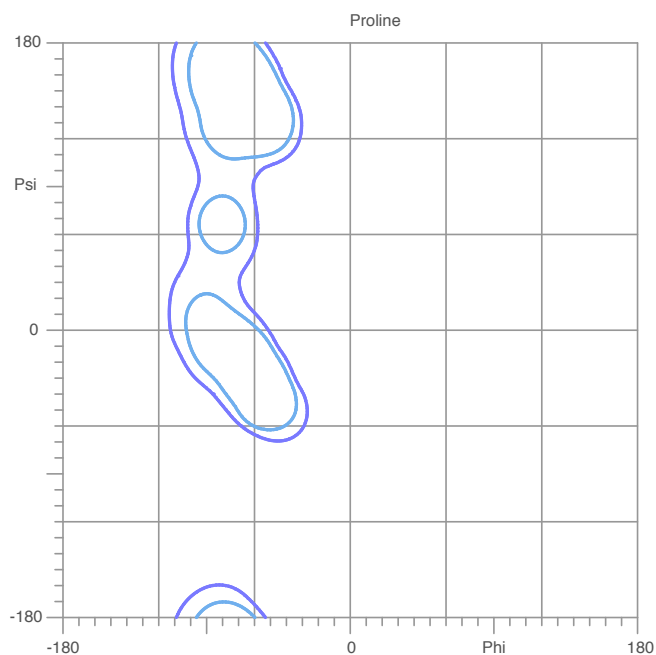
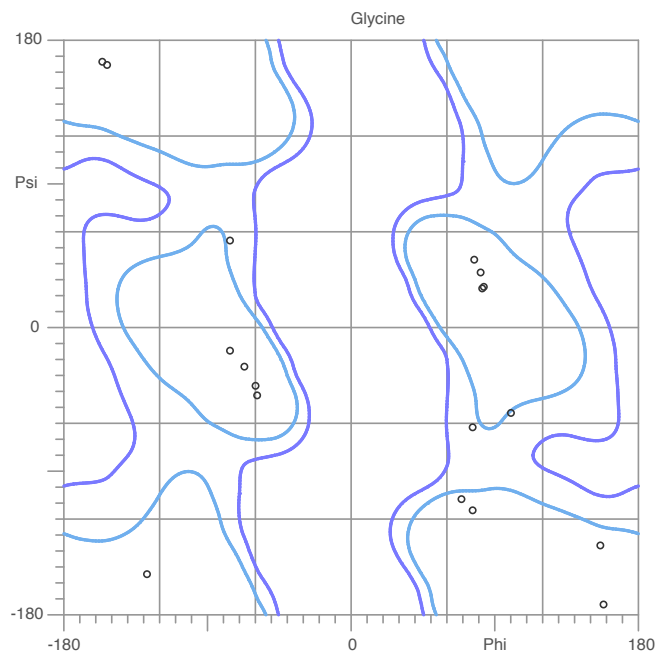
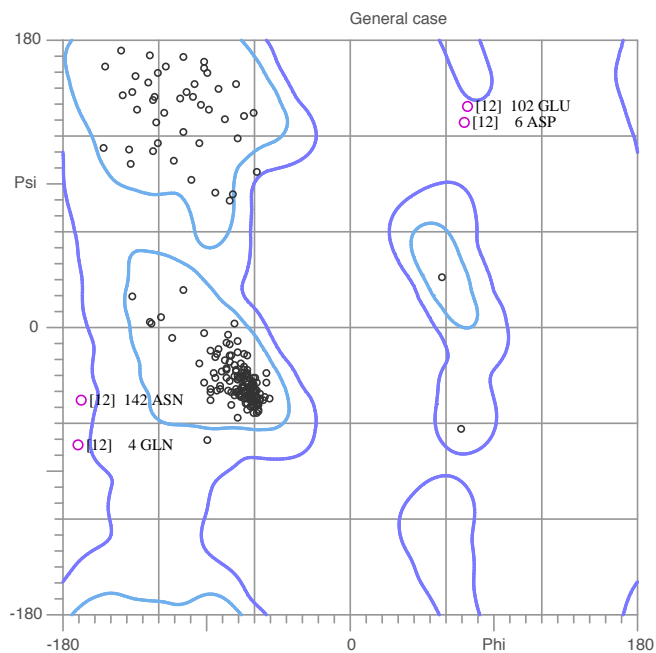


95.3% (202/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[11] 3 GLY (-151.7, -36.6)
[11] 102 GLU (64.6, -87.4)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 12



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):

[12] 4 GLN (-171.2, -73.2)

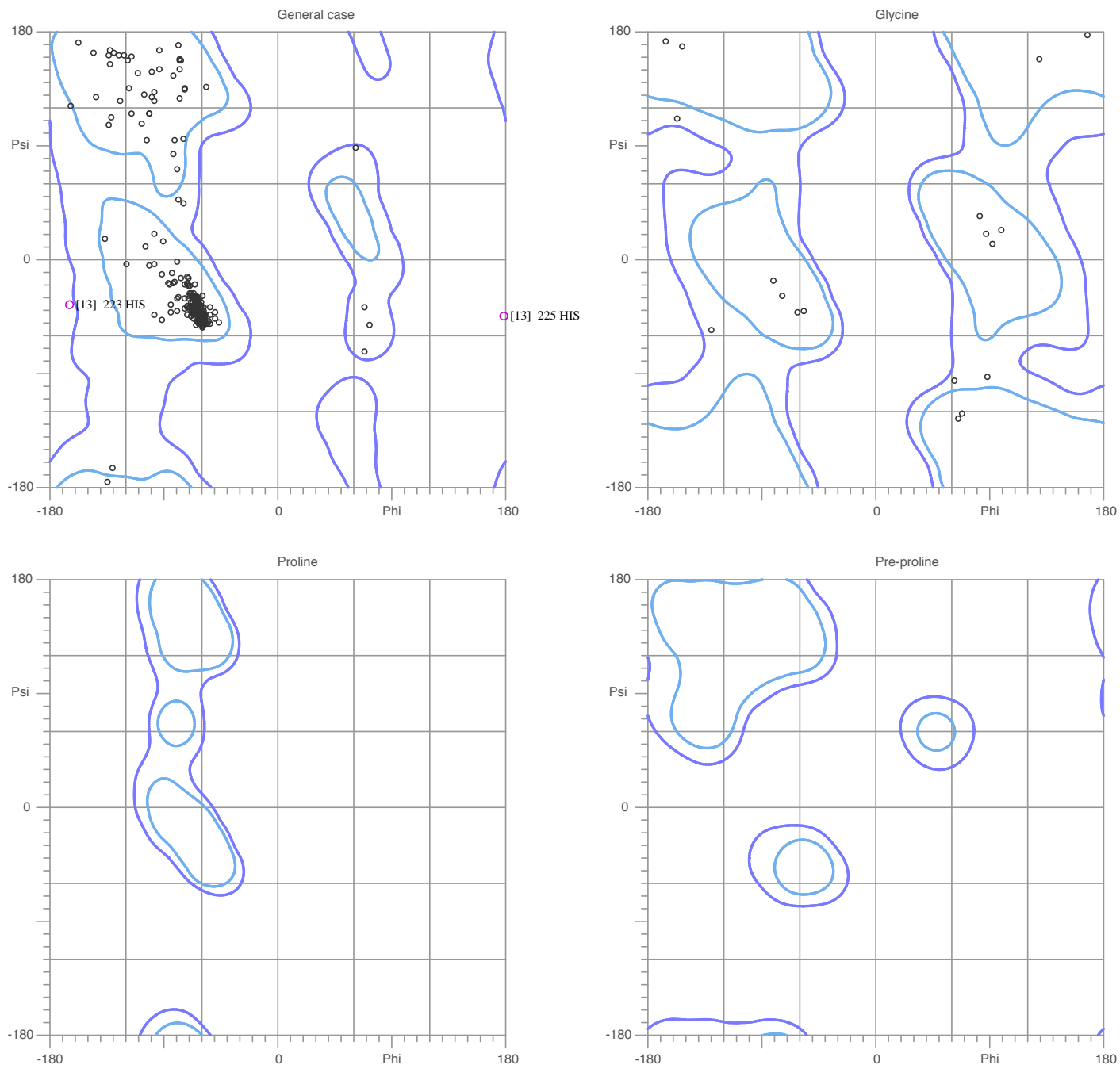
[12] 6 ASP (71.2, 129.0)

[12] 102 GLU (73.1, 139.5)

[12] 142 ASN (-170.0, -45.8)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 13

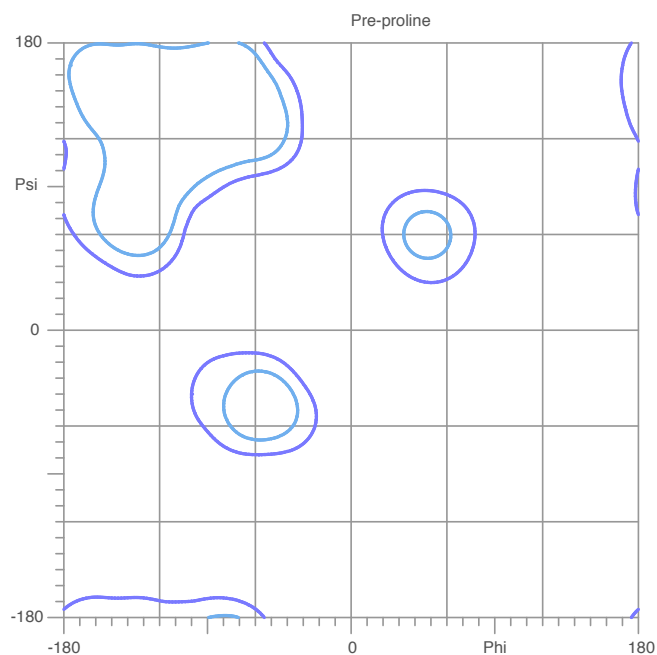
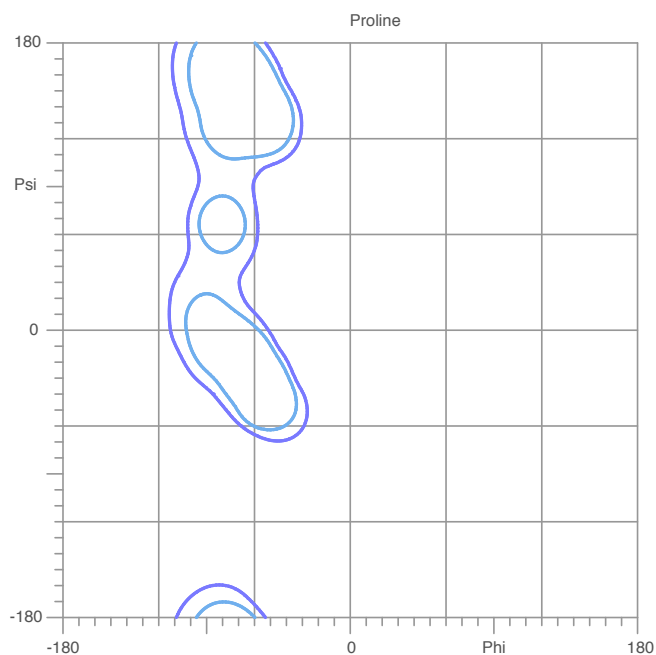
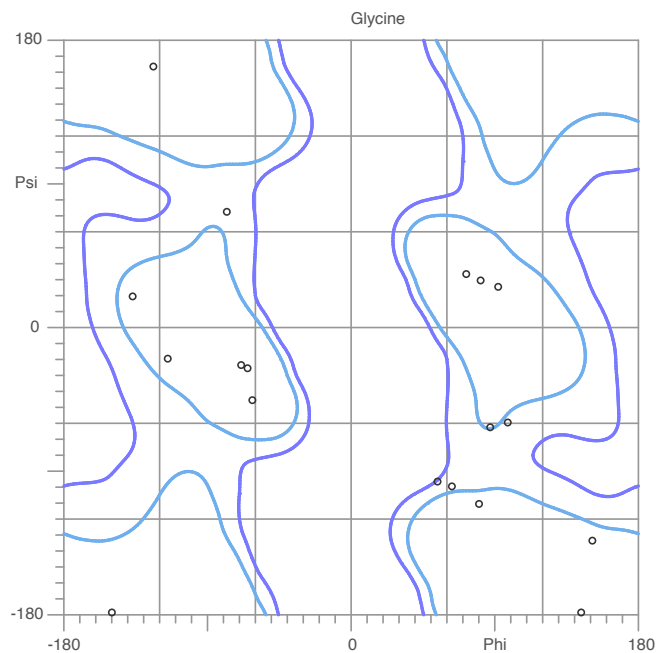
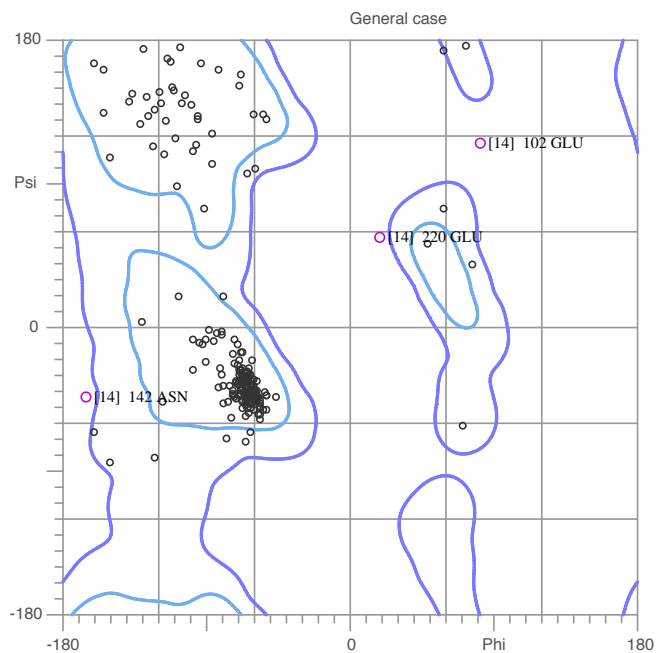


93.4% (198/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[13] 223 HIS (-165.7, -35.8)
[13] 225 HIS (178.4, -44.3)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 14



90.1% (191/212) of all residues were in favored (98%) regions.
98.6% (209/212) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

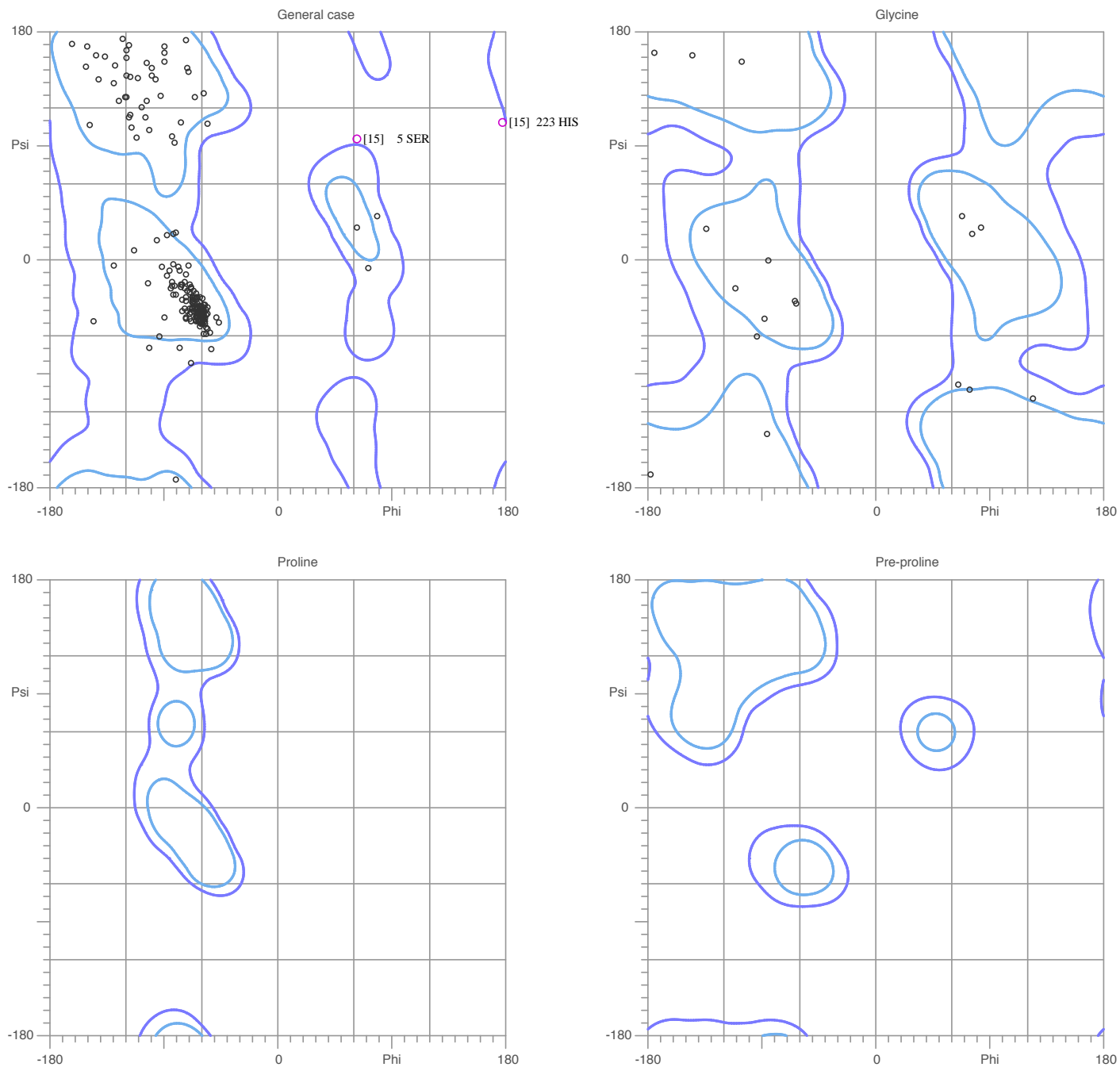
[14] 102 GLU (81.5, 117.0)

[14] 142 ASN (-166.3, -44.0)

[14] 220 GLU (18.5, 58.0)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 15



92.5% (196/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

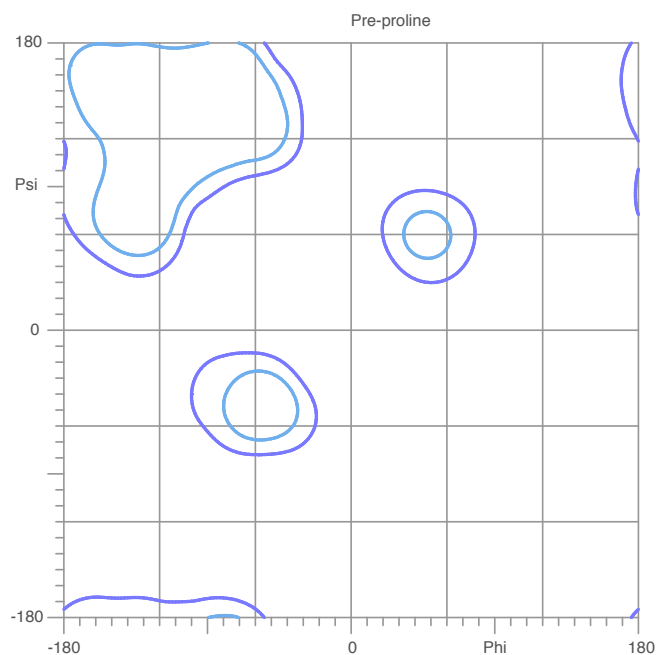
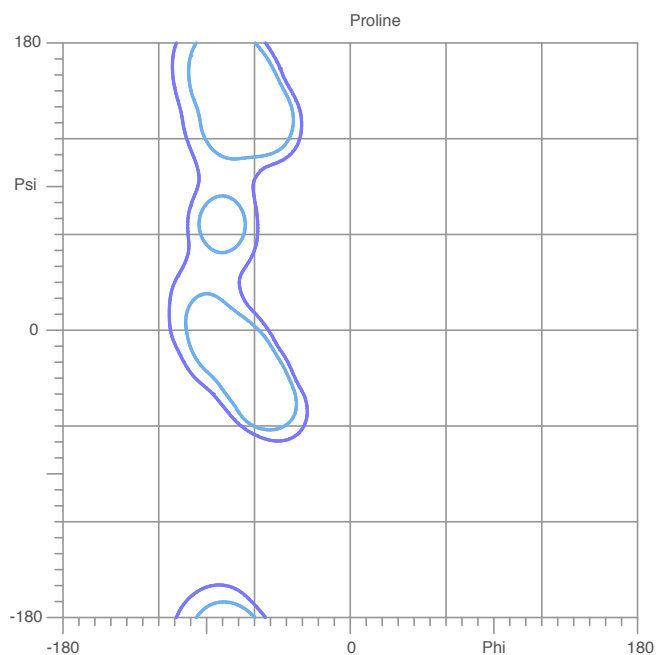
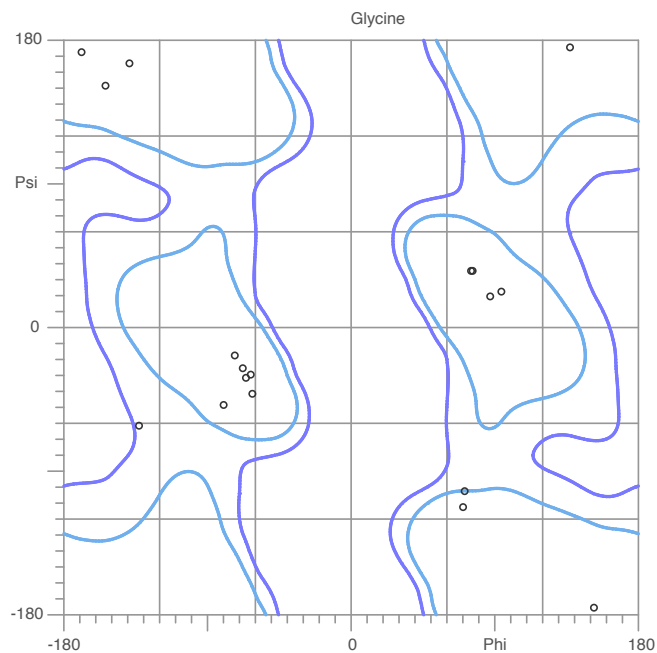
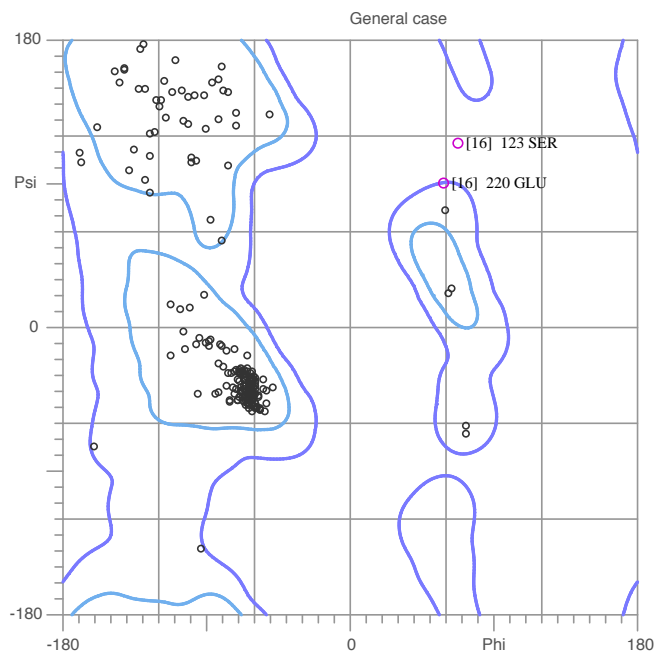
There were 2 outliers (phi, psi):
[15] 5 SER (62.9, 96.3)
[15] 223 HIS (177.9, 110.0)

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

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MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 16



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.

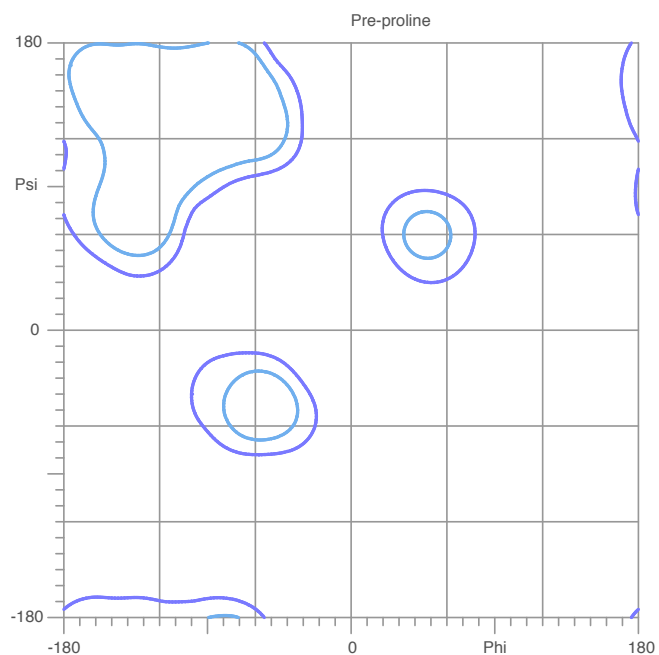
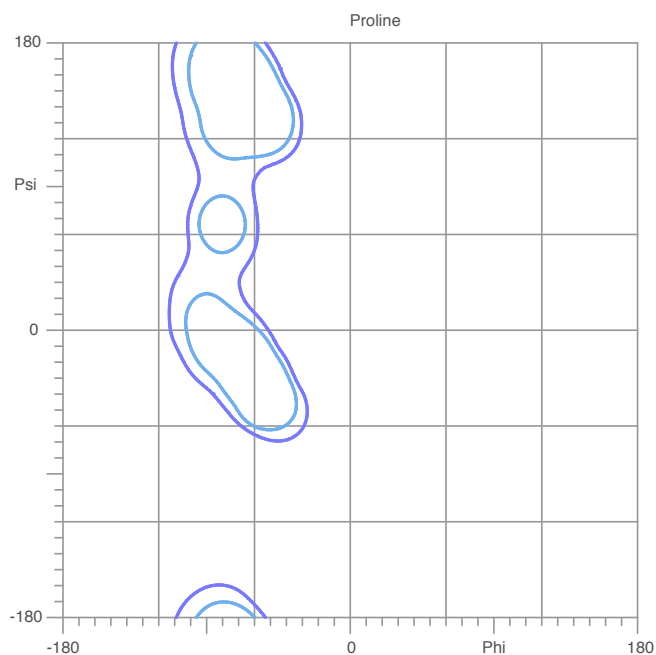
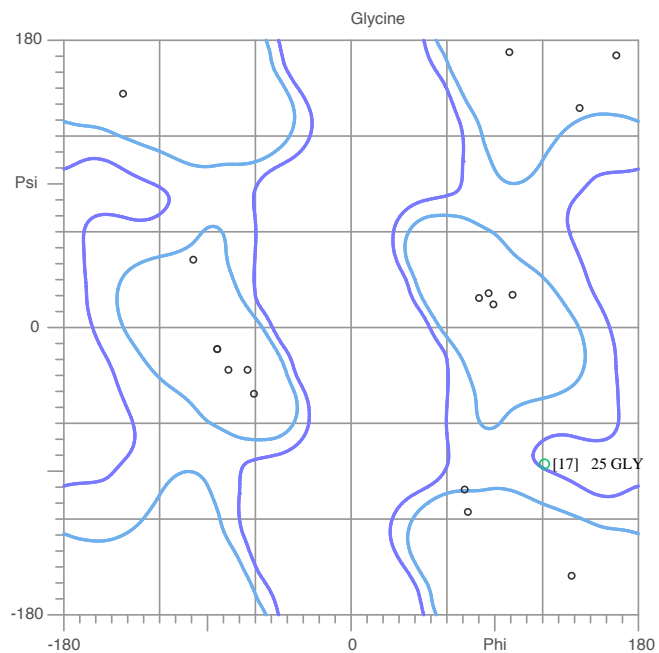
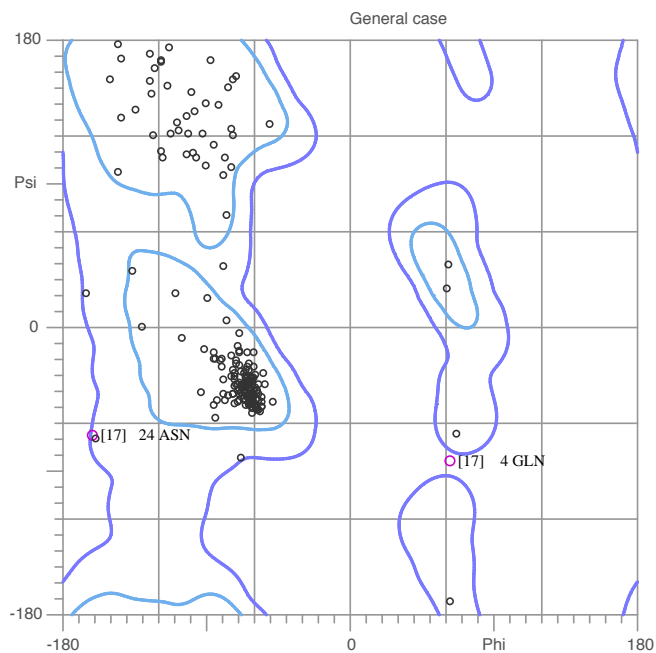
There were 2 outliers (phi, psi):
[16] 123 SER (67.3, 116.8)
[16] 220 GLU (58.4, 91.4)

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MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 17



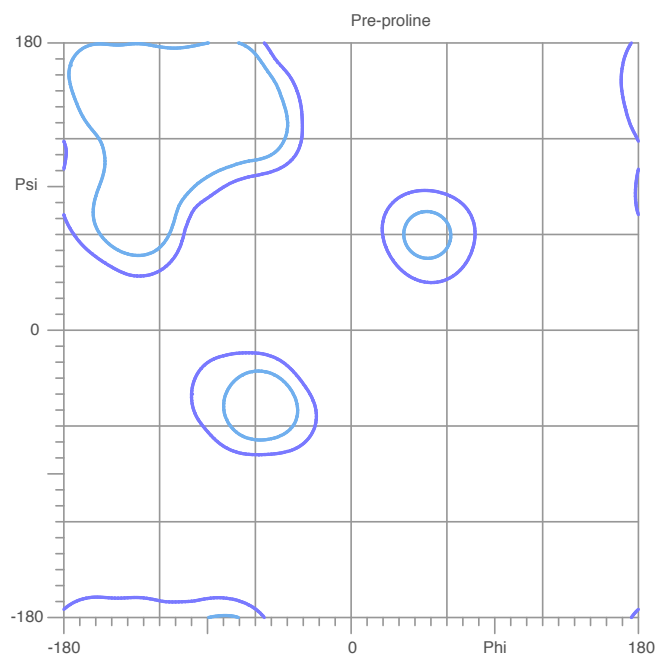
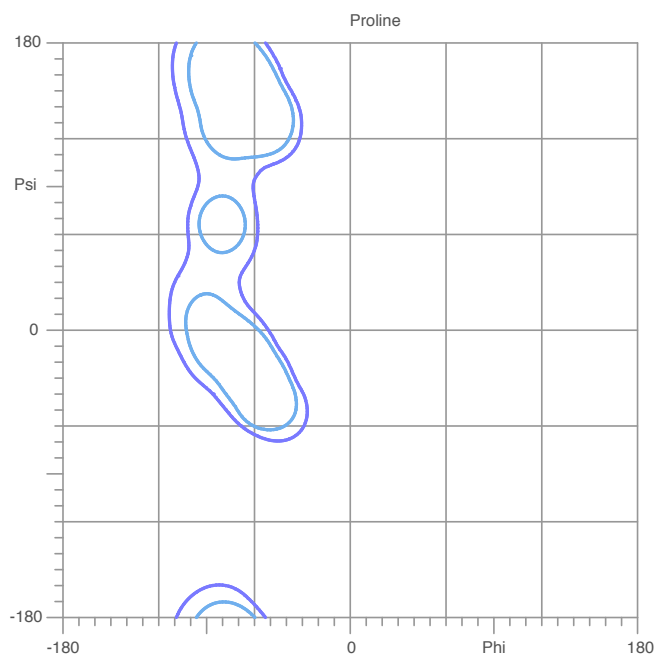
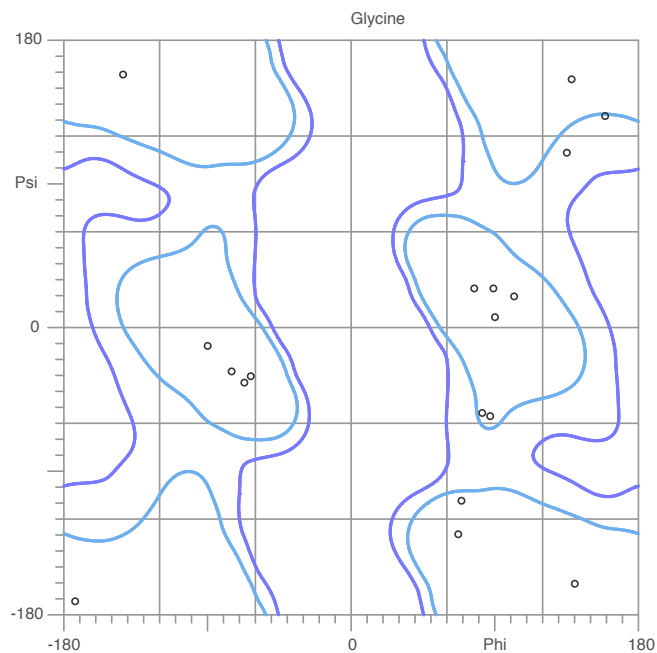
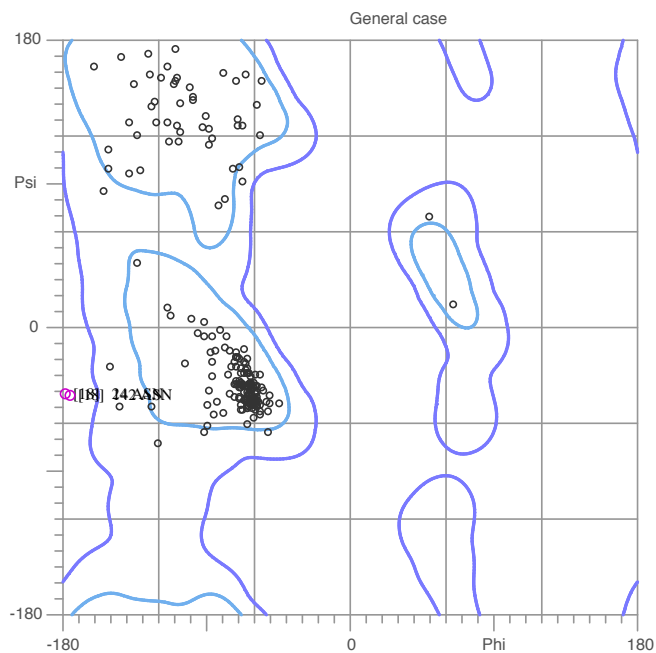
95.3% (202/212) of all residues were in favored (98%) regions.
98.6% (209/212) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [17] 4 GLN (62.0, -83.2)
- [17] 24 ASN (-162.9, -67.1)
- [17] 25 GLY (121.9, -85.2)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 18

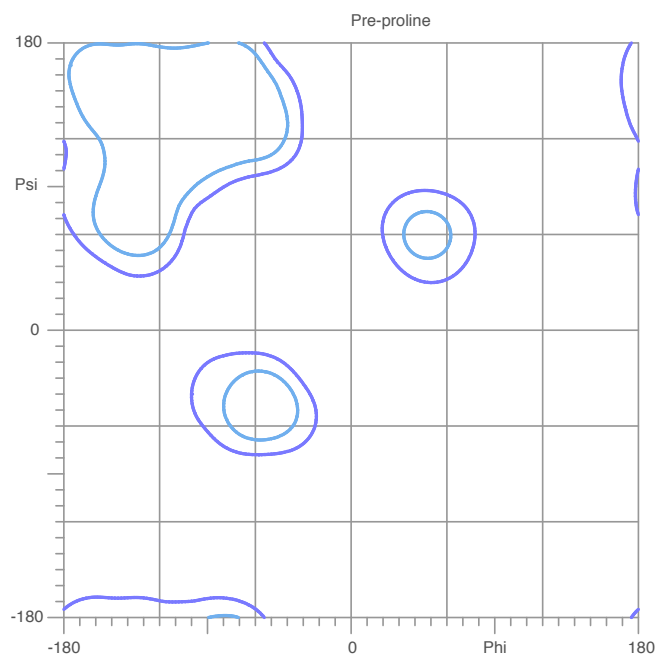
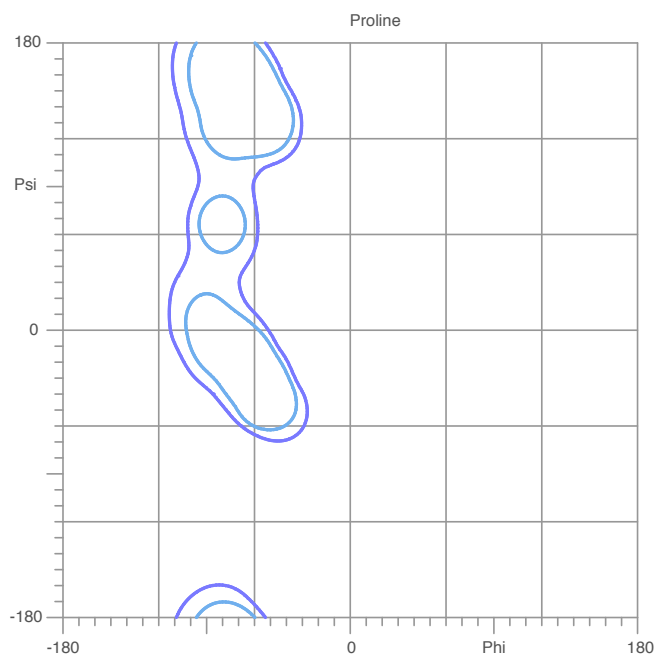
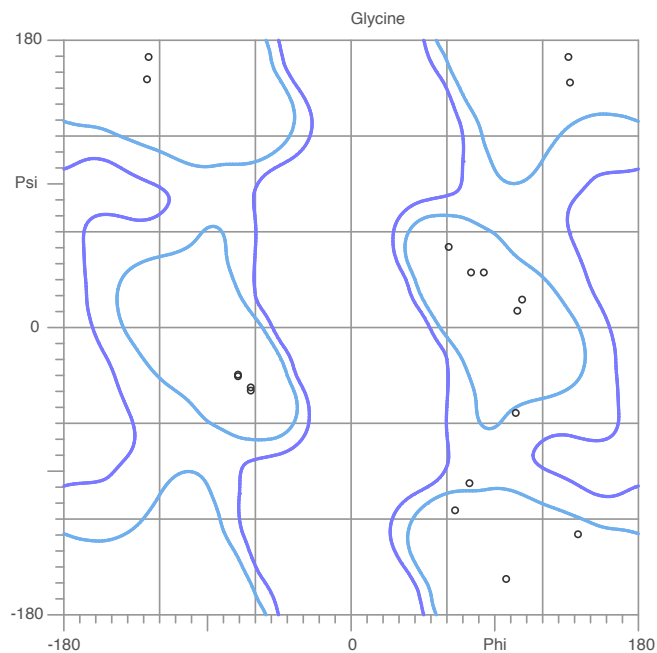
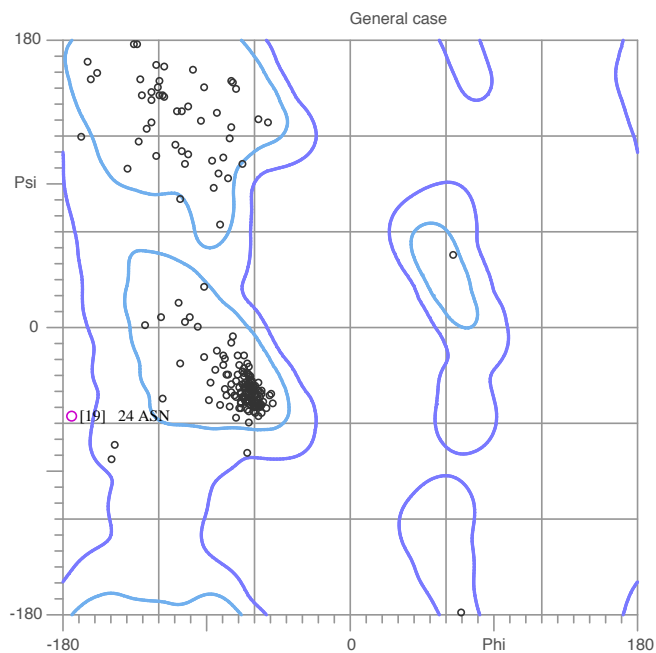


94.8% (201/212) of all residues were in favored (98%) regions.
99.1% (210/212) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 24 ASN (-179.3, -41.2)
[18] 142 ASN (-176.0, -42.9)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 19

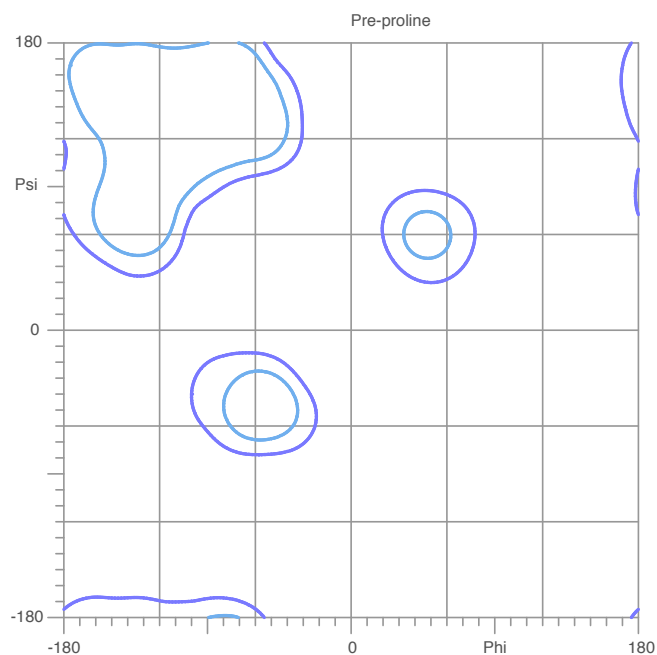
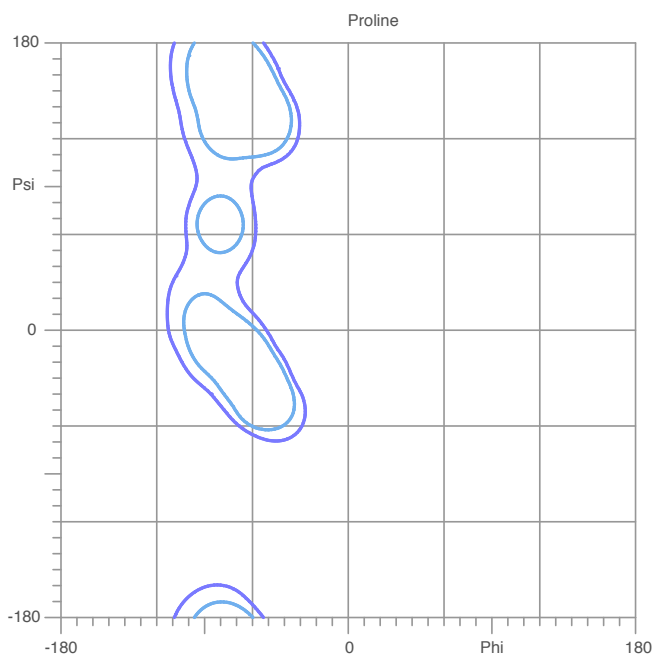
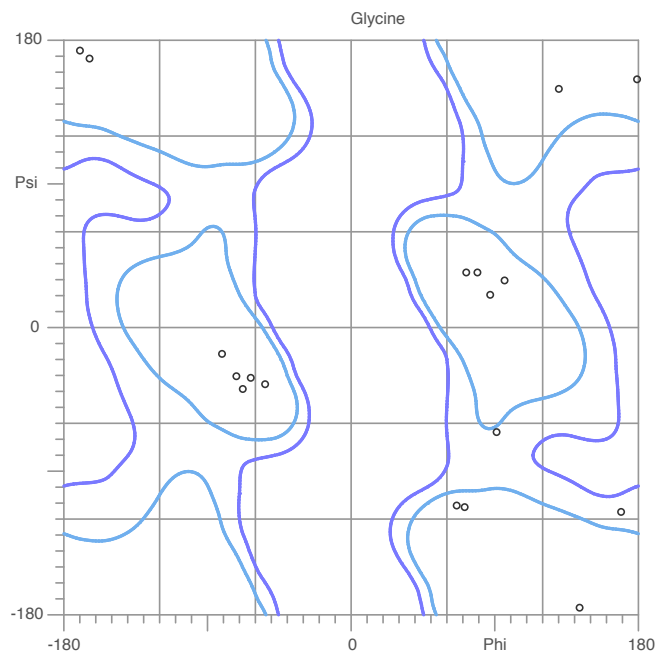
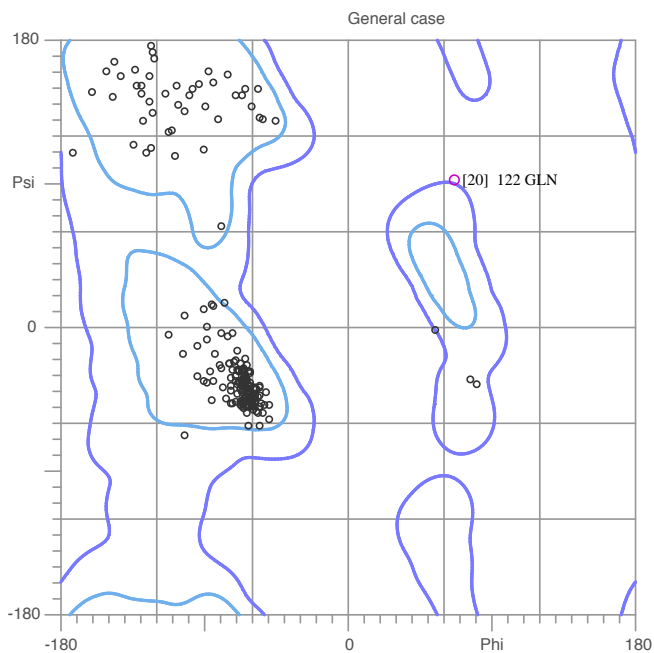


95.8% (203/212) of all residues were in favored (98%) regions.
99.5% (211/212) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[19] 24 ASN (-175.8, -55.2)

MolProbity Ramachandran analysis

MBR242E_NMR_em_bcr3.pdb, model 20



95.8% (203/212) of all residues were in favored (98%) regions.
99.5% (211/212) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 122 GLN (66.9, 93.4)

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