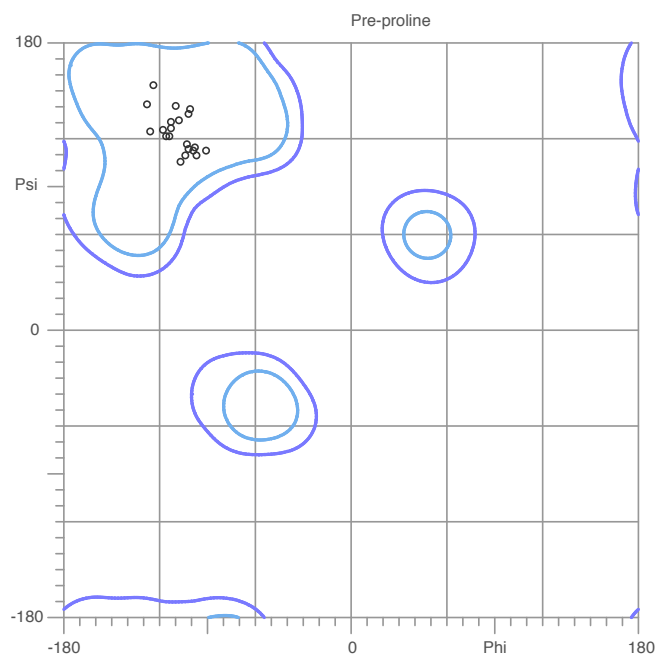
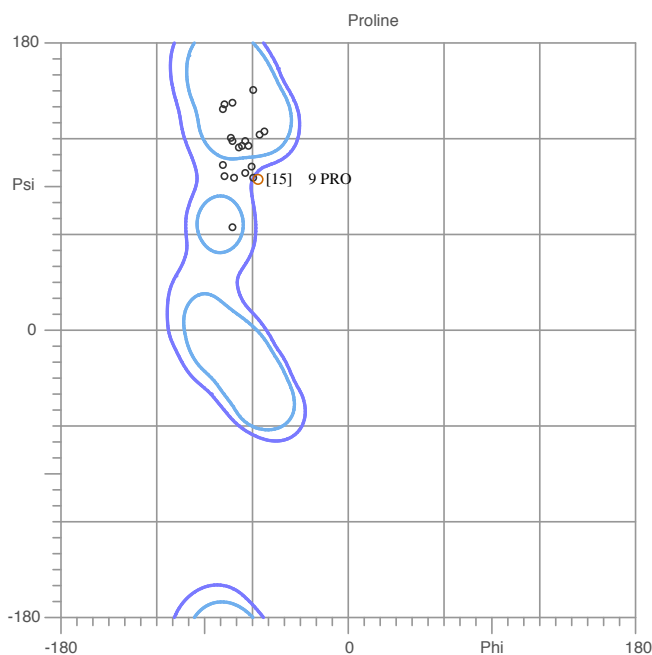
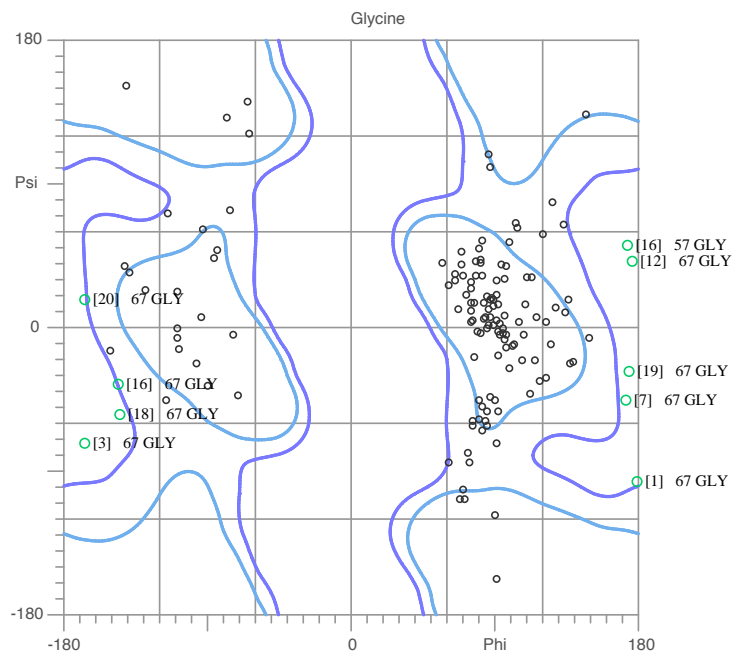
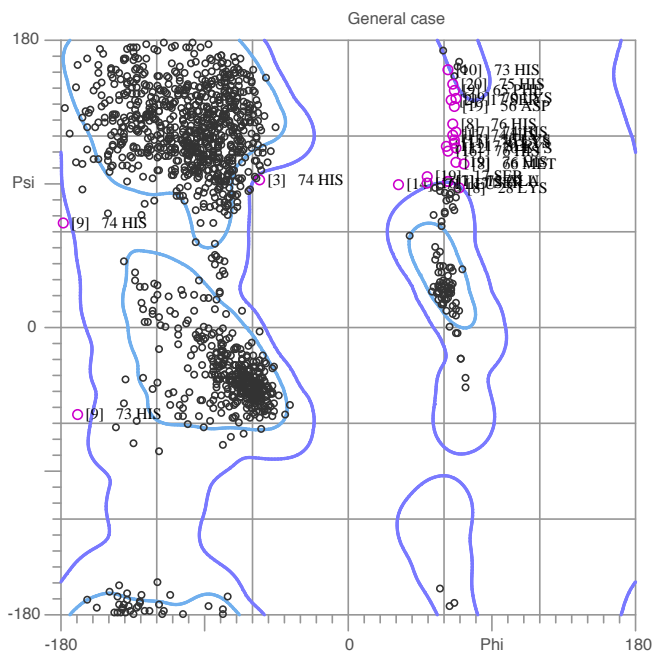


MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, all models



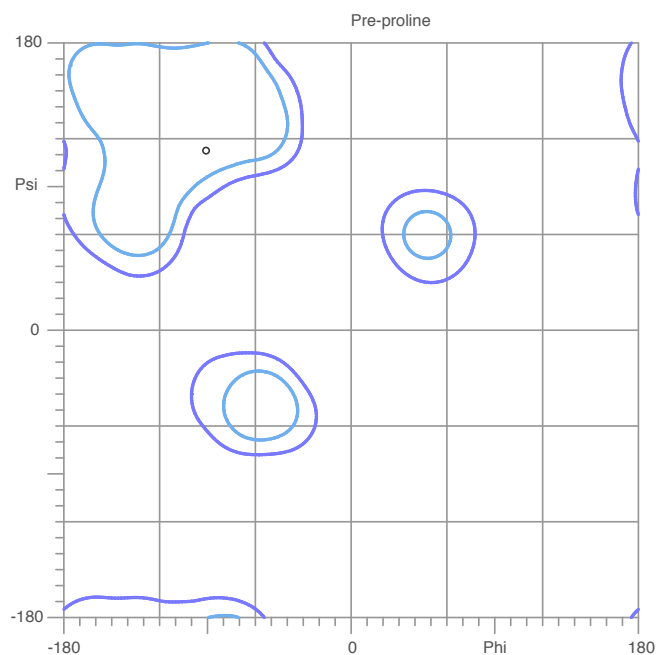
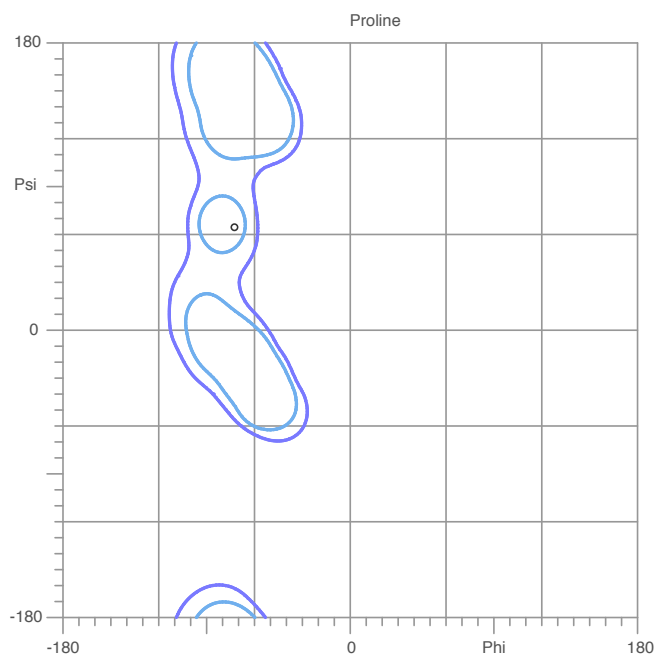
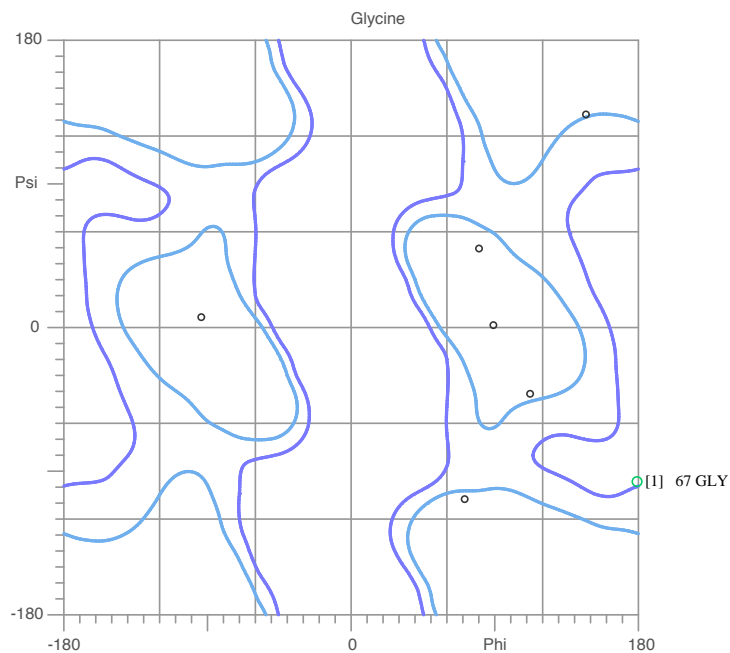
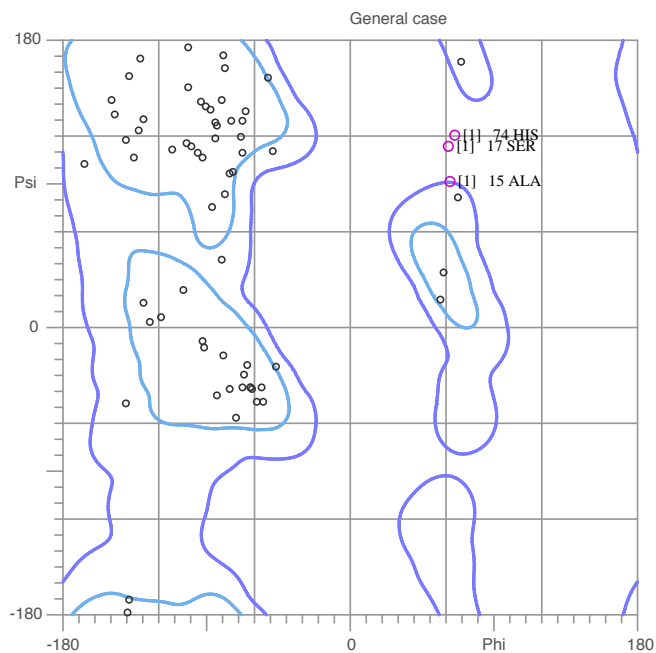
88.8% (1350/1520) of all residues were in favored (98%) regions.
97.7% (1485/1520) of all residues were in allowed (>99.8%) regions.

There were 35 outliers (phi, psi):

- | | |
|----------------------------|-----------------------------|
| [1] 15 ALA (62.8, 92.5) | [10] 73 HIS (62.8, 162.7) |
| [1] 17 SER (61.6, 114.1) | [11] 70 LYS (66.6, 116.4) |
| [1] 67 GLY (179.4, -96.7) | [12] 67 GLY (176.2, 43.0) |
| [1] 74 HIS (65.6, 121.3) | [12] 70 LYS (68.0, 113.1) |
| [2] 17 SER (64.5, 143.6) | [13] 70 LYS (66.9, 118.6) |
| [3] 67 GLY (-168.0, -72.2) | [14] 71 LEU (31.1, 90.7) |
| [3] 74 HIS (-56.2, 93.7) | [15] 9 PRO (-57.7, 95.7) |
| [7] 67 GLY (172.9, -45.2) | [16] 17 SER (49.3, 92.0) |
| [7] 72 GLU (62.9, 92.2) | [16] 57 GLY (173.6, 52.9) |
| [8] 28 LYS (69.2, 89.0) | [16] 67 GLY (-146.7, -35.7) |
| [8] 66 MET (72.6, 103.8) | [16] 76 HIS (62.8, 111.4) |
| [8] 76 HIS (65.6, 128.2) | [17] 74 HIS (67.6, 123.7) |
| [9] 65 PHE (66.4, 149.5) | [18] 67 GLY (-145.0, -54.3) |
| [9] 73 HIS (-171.0, -54.3) | [19] 17 SER (49.4, 96.0) |
| [9] 74 HIS (-180.0, 66.6) | [19] 56 ASP (66.0, 139.6) |
| | [19] 67 GLY (175.0, -27.2) |
| | [19] 70 LYS (67.8, 144.7) |
| | [19] 76 HIS (67.1, 104.4) |
| | [20] 67 GLY (-167.2, 18.0) |
| | [20] 75 HIS (65.2, 153.8) |

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 1



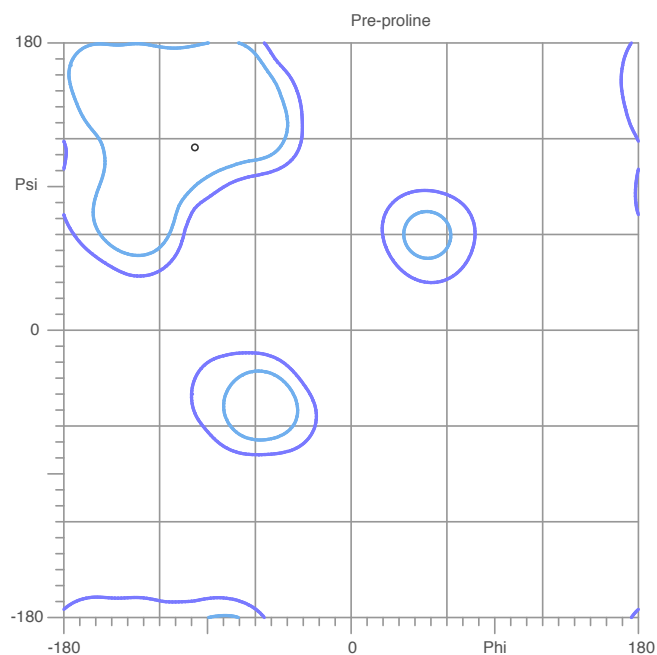
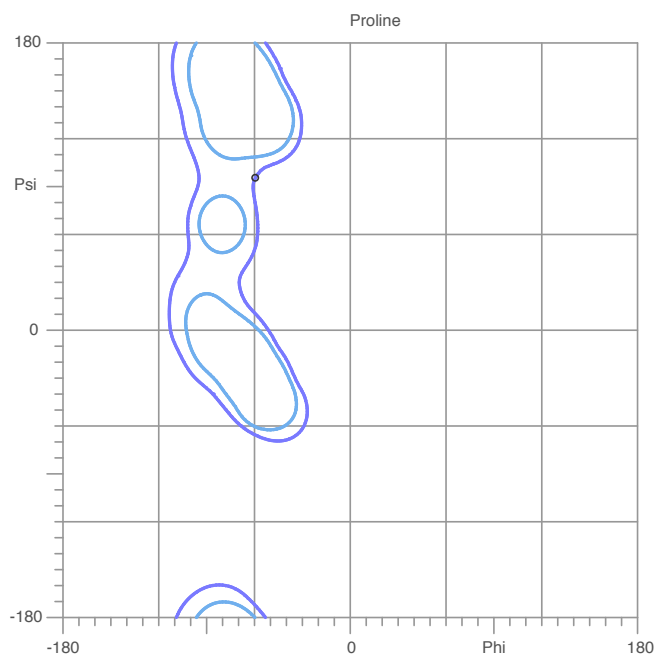
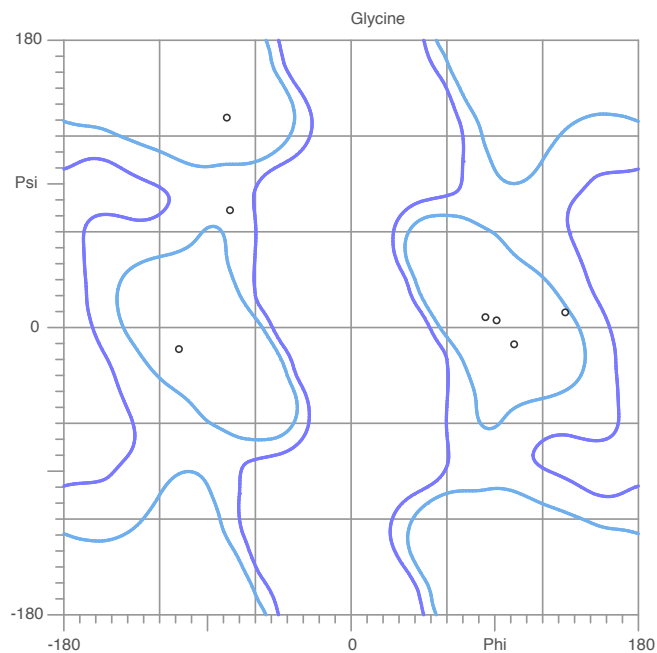
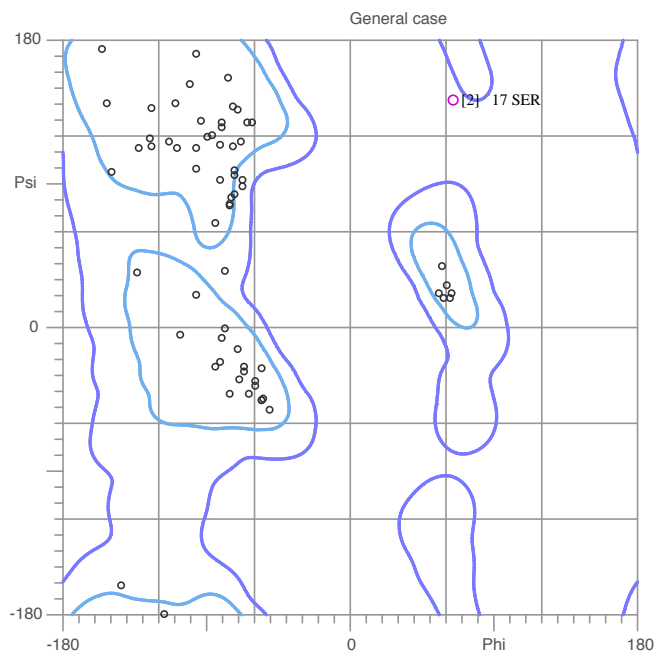
84.2% (64/76) of all residues were in favored (98%) regions.
94.7% (72/76) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [1] 15 ALA (62.8, 92.5)
- [1] 17 SER (61.6, 114.1)
- [1] 67 GLY (179.4, -96.7)
- [1] 74 HIS (65.6, 121.3)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 2

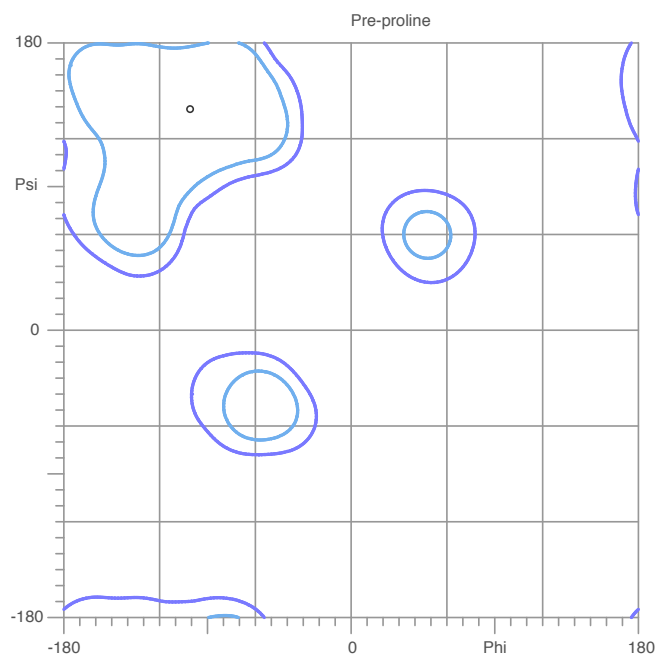
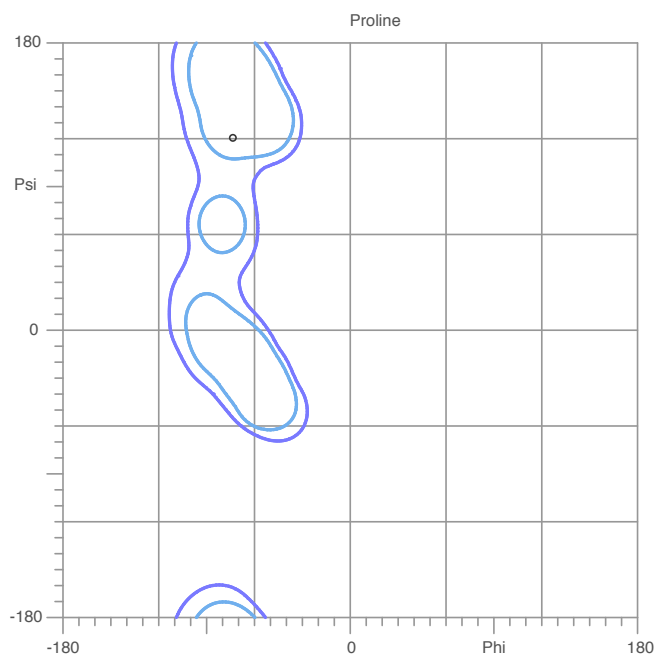
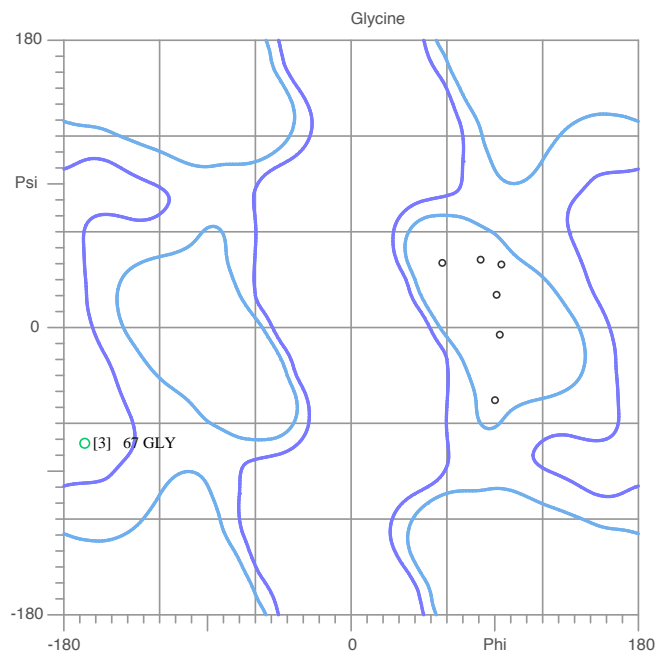
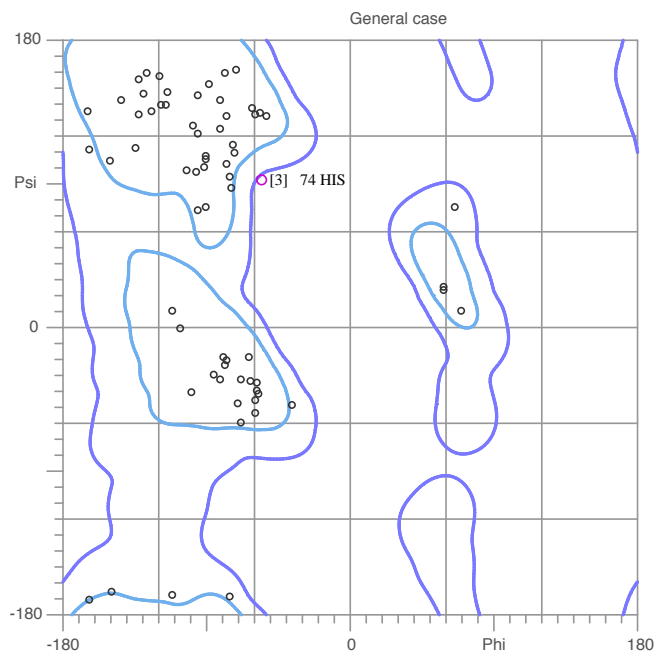


90.8% (69/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[2] 17 SER (64.5, 143.6)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 3



88.2% (67/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

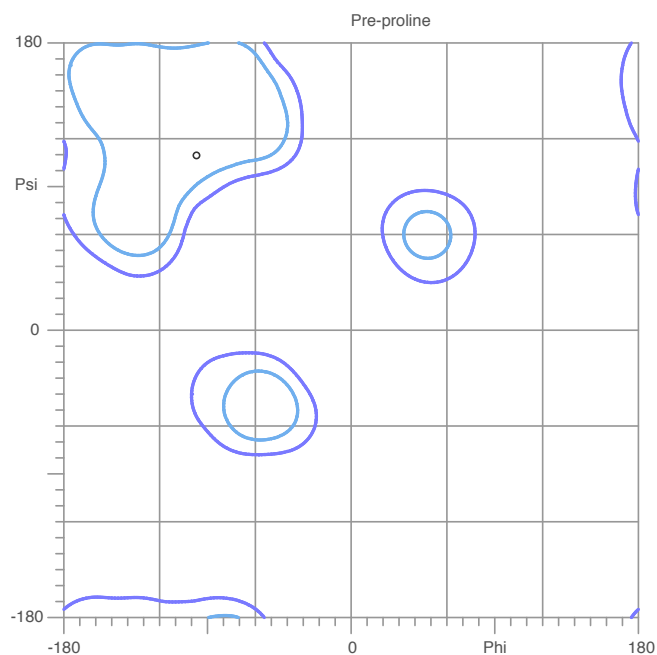
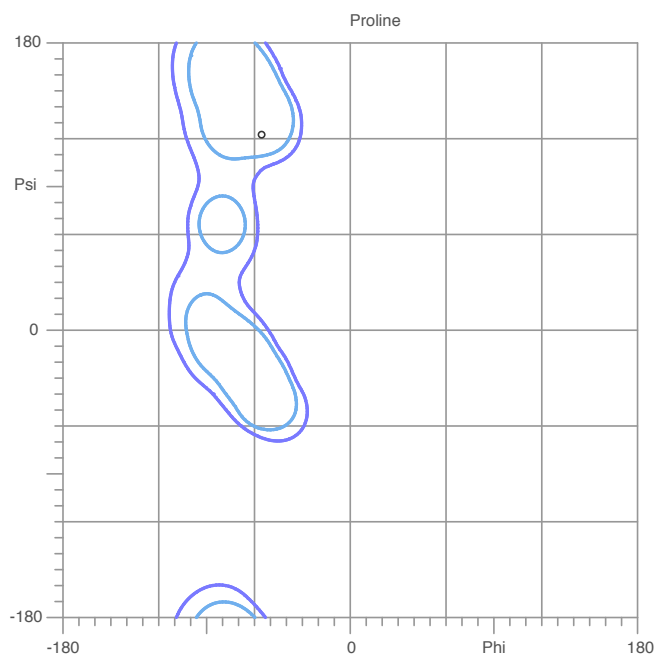
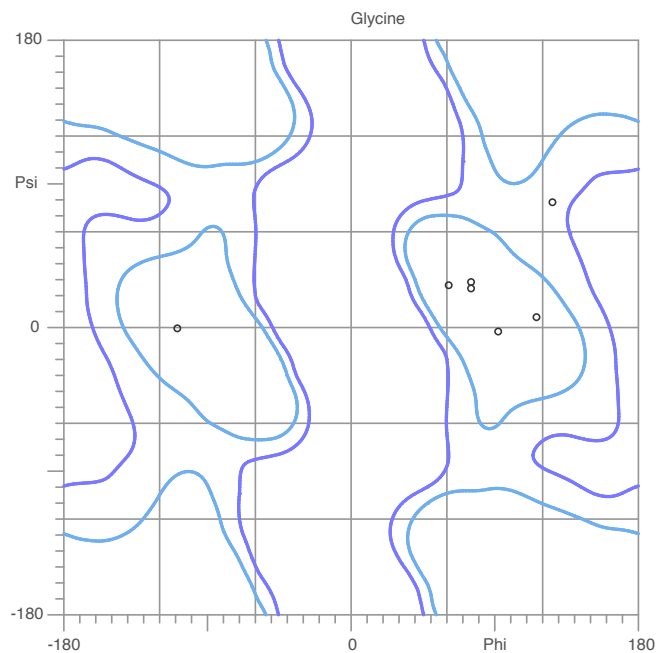
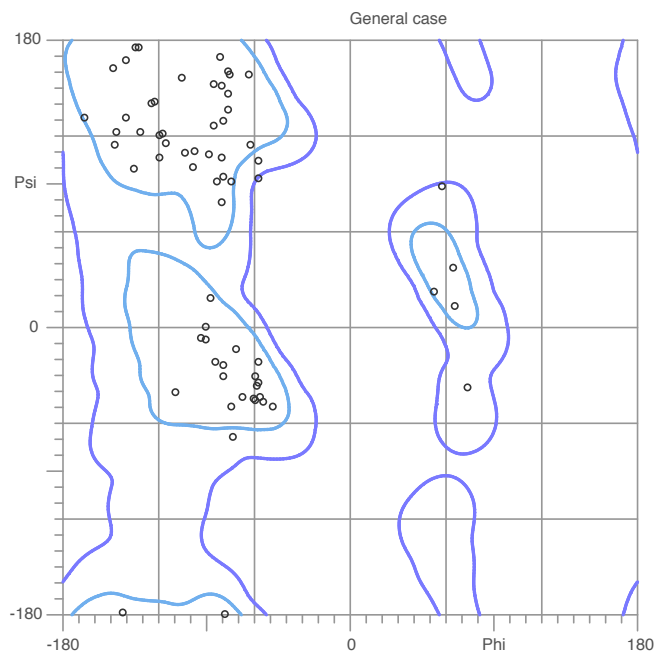
There were 2 outliers (phi, psi):

[3] 67 GLY (-168.0, -72.2)

[3] 74 HIS (-56.2, 93.7)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 4



92.1% (70/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

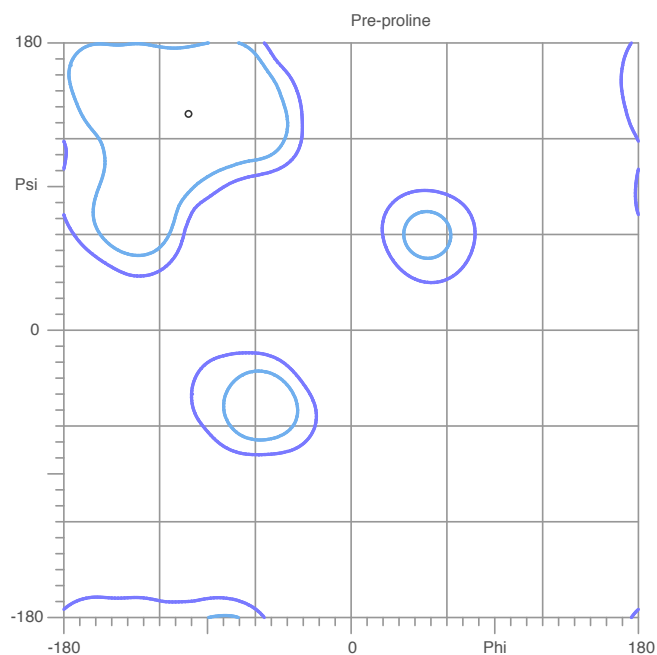
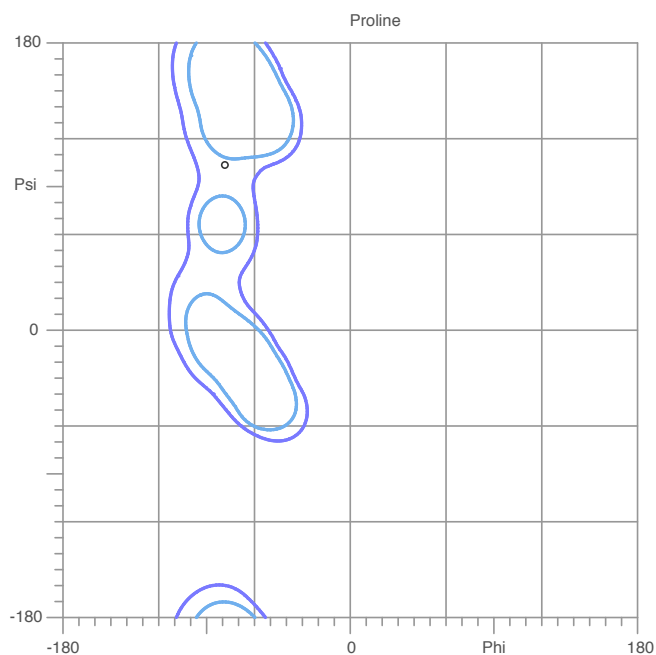
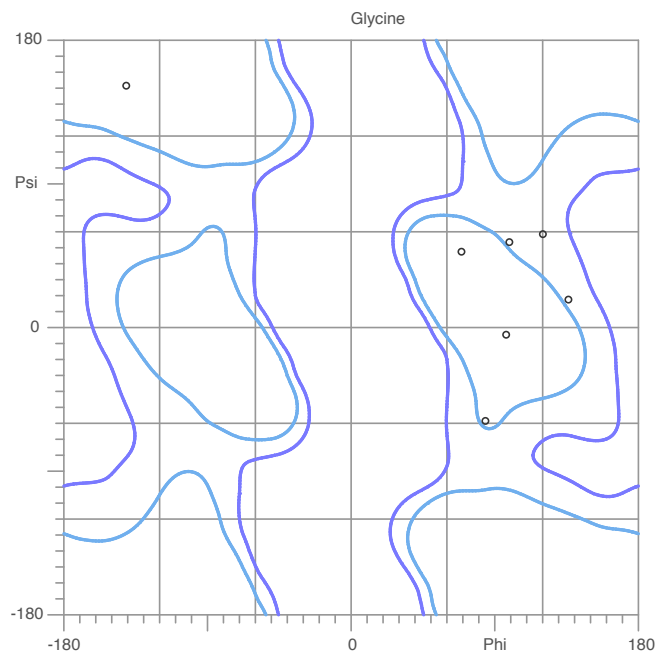
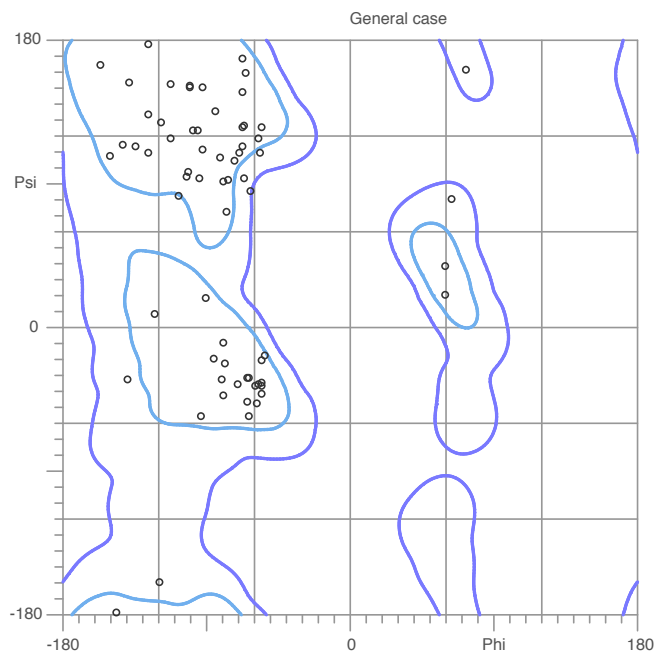
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 5



85.5% (65/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

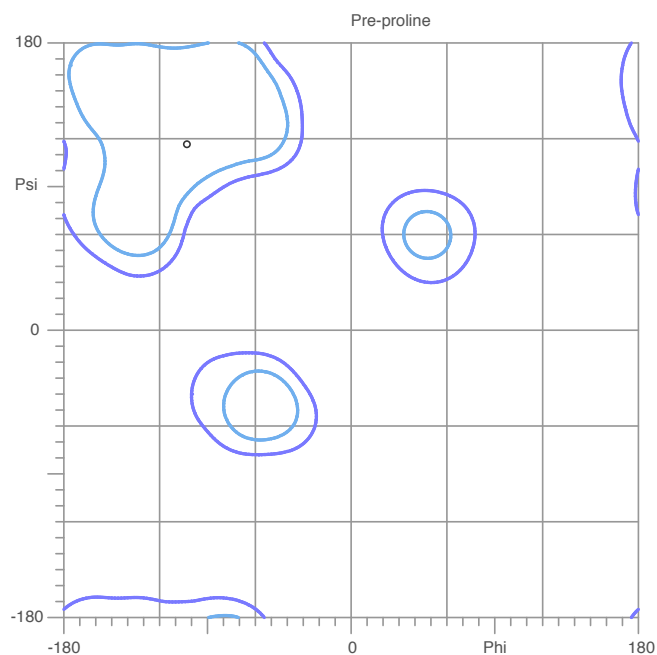
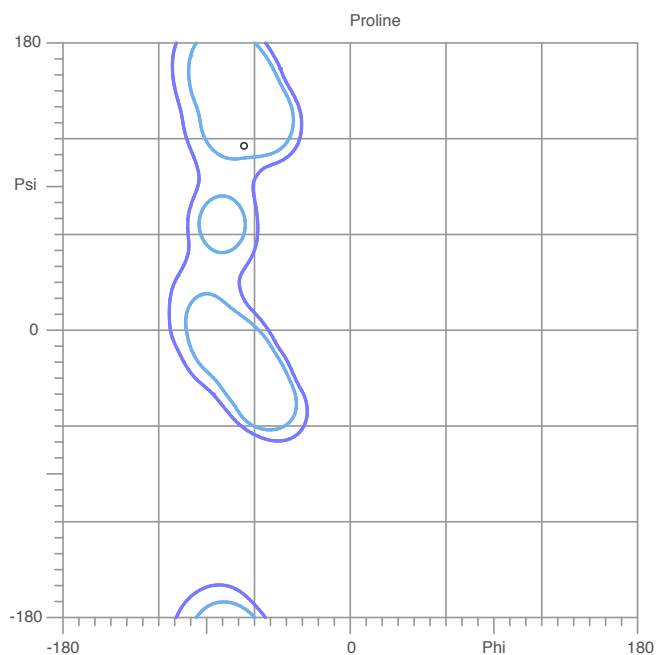
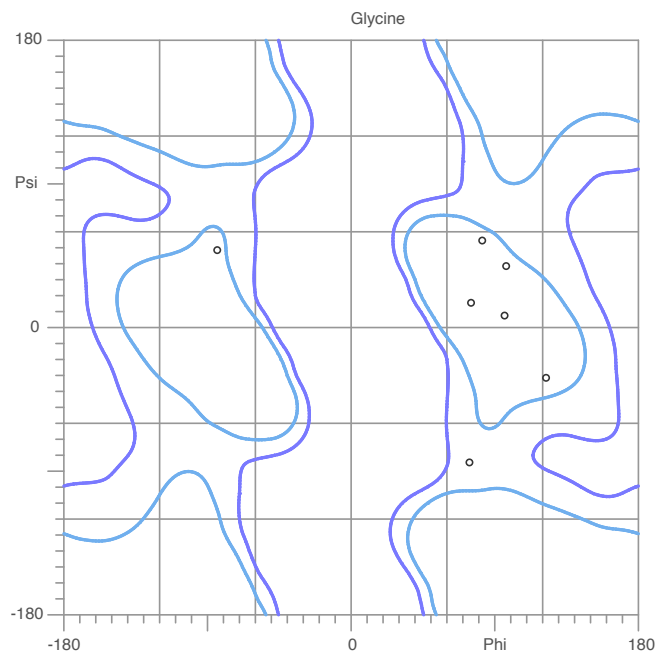
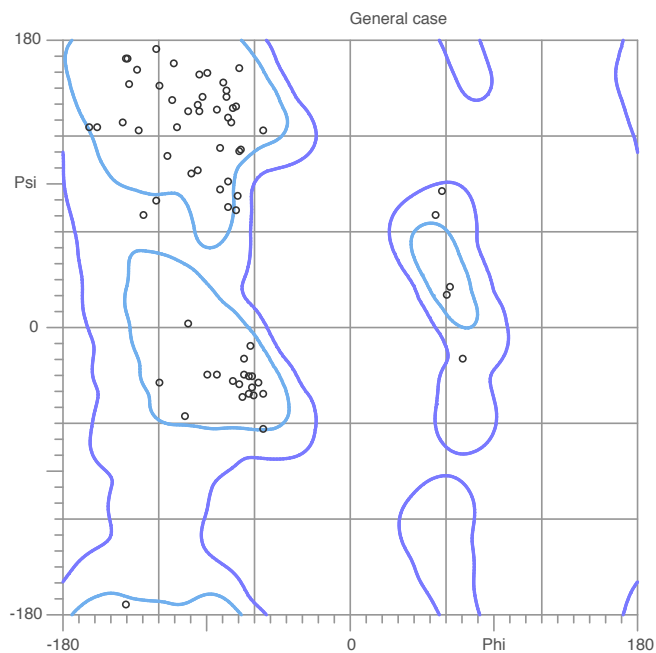
There were no outliers.

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

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MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 6



89.5% (68/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

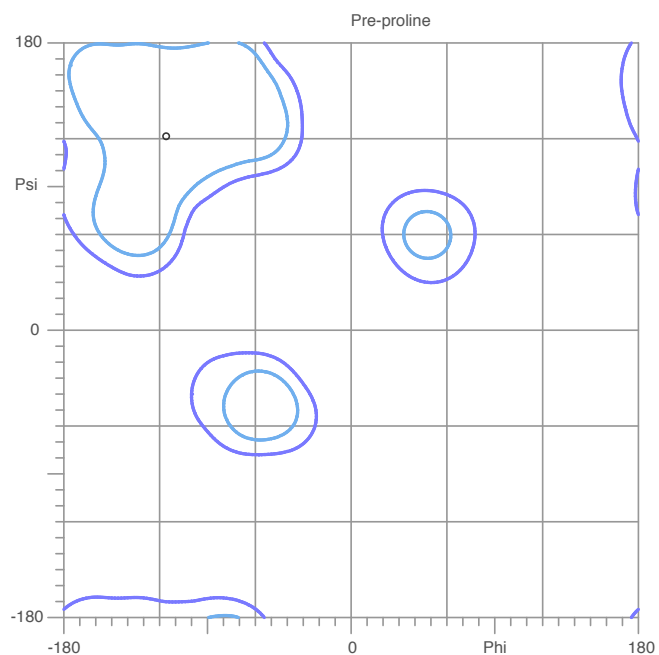
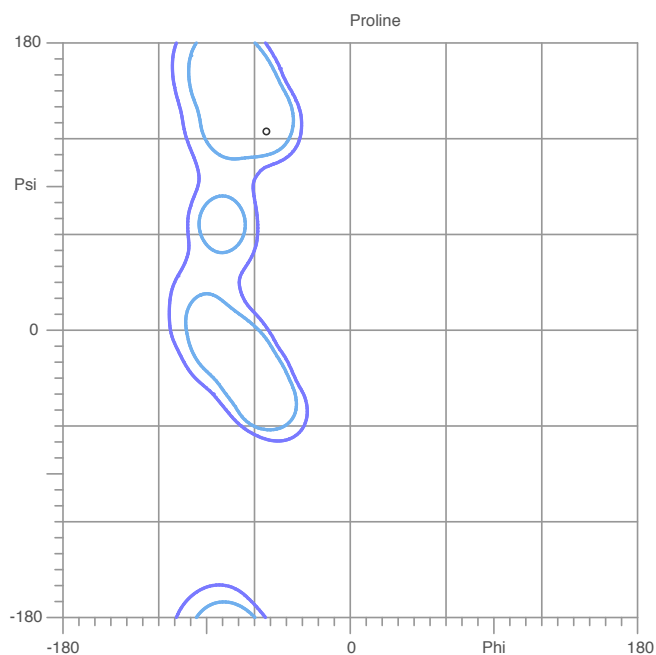
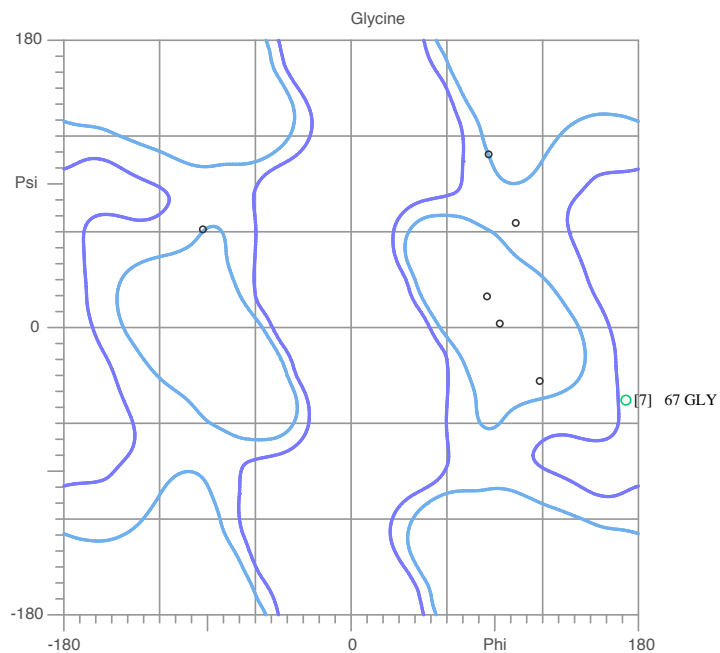
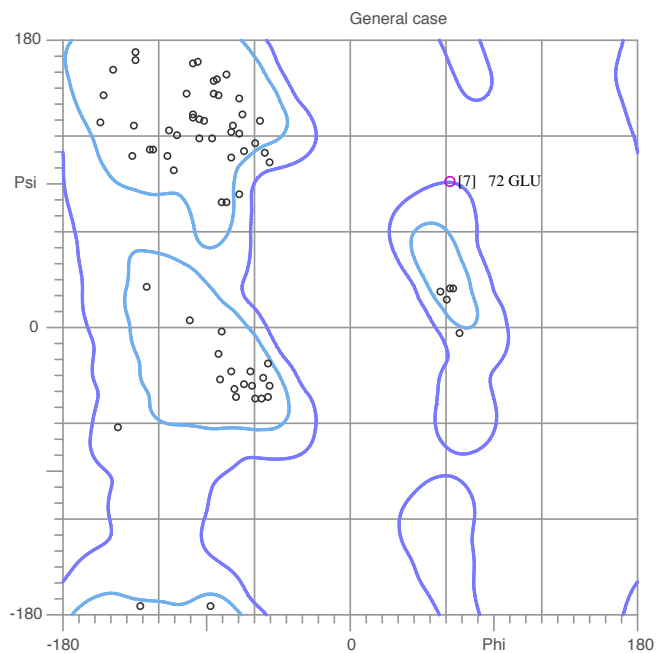
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 7



88.2% (67/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

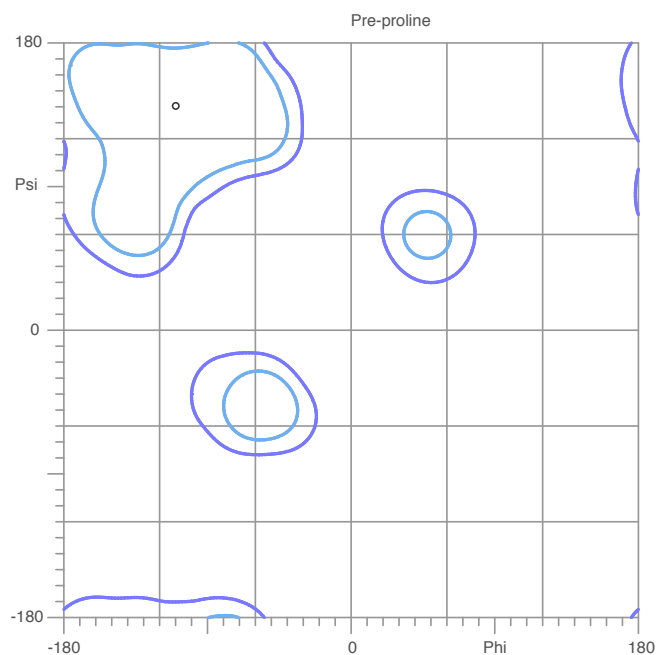
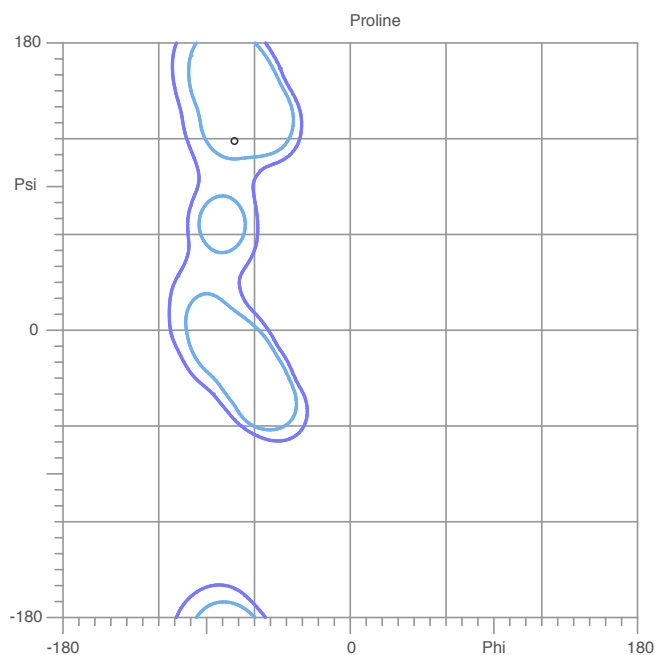
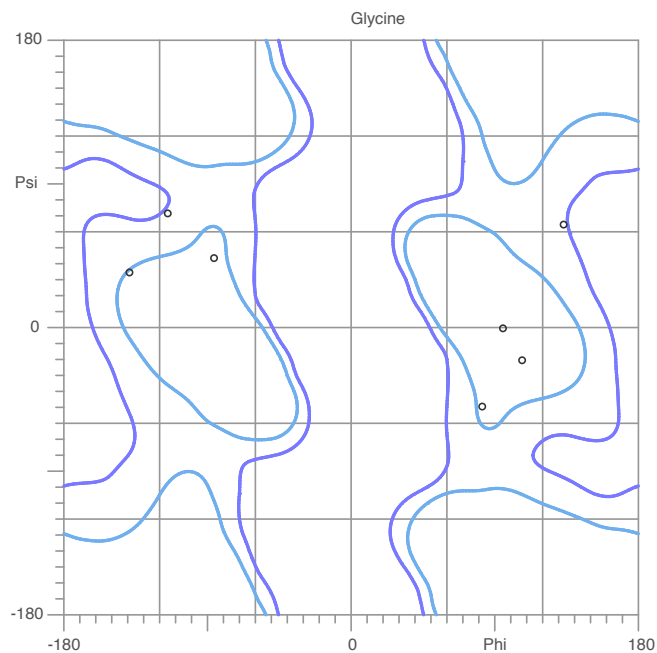
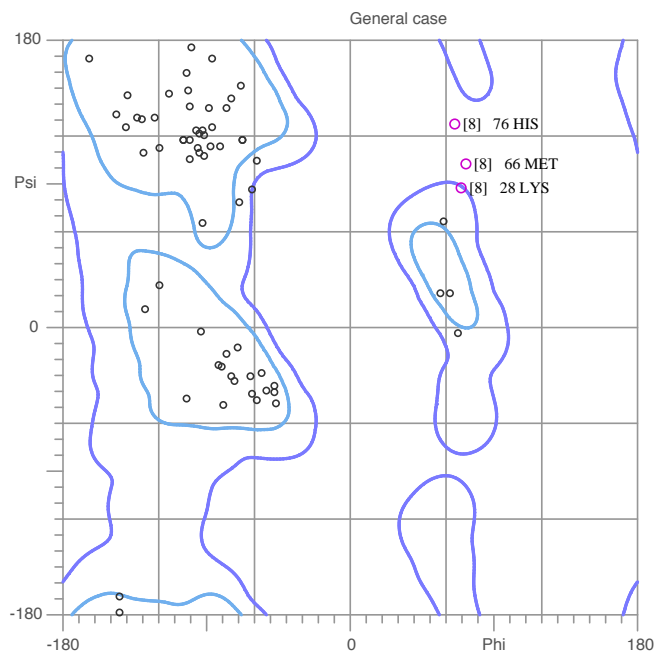
There were 2 outliers (phi, psi):

[7] 67 GLY (172.9, -45.2)

[7] 72 GLU (62.9, 92.2)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 8



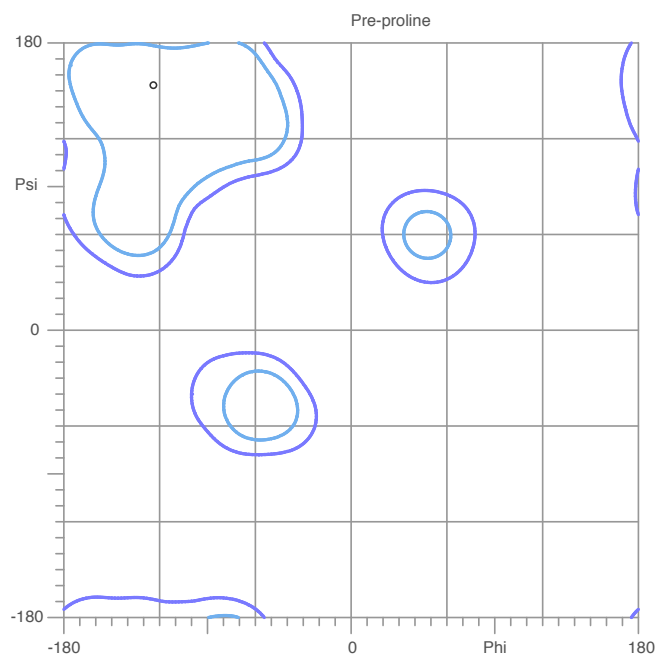
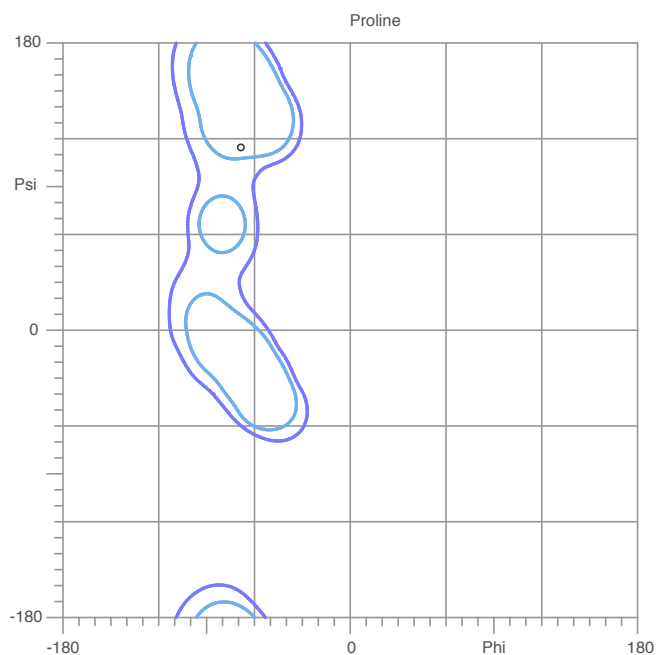
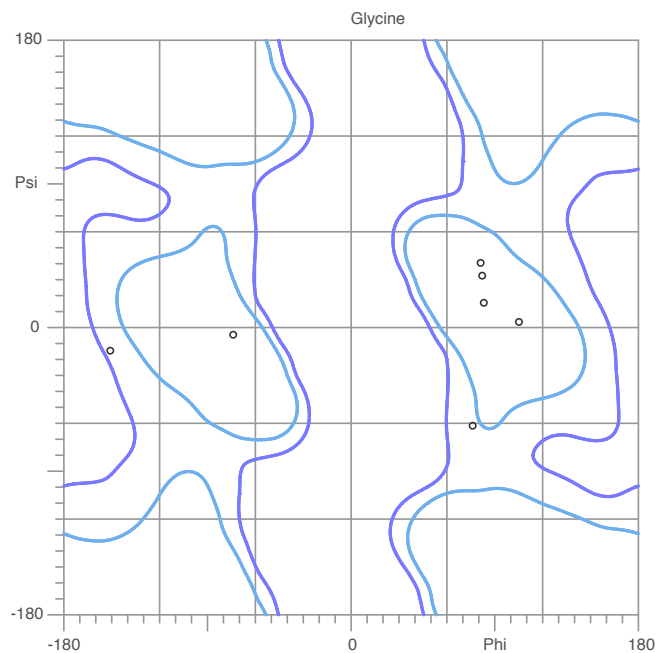
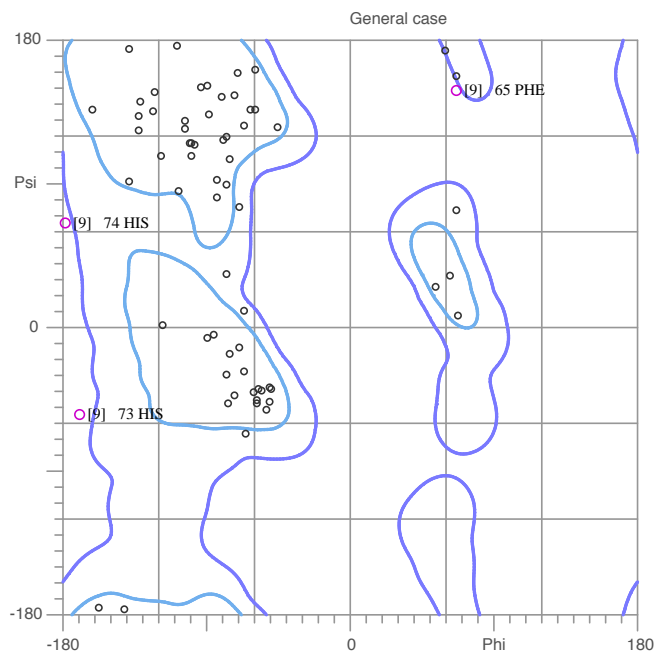
85.5% (65/76) of all residues were in favored (98%) regions.
96.1% (73/76) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 28 LYS (69.2, 89.0)
- [8] 66 MET (72.6, 103.8)
- [8] 76 HIS (65.6, 128.2)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 9



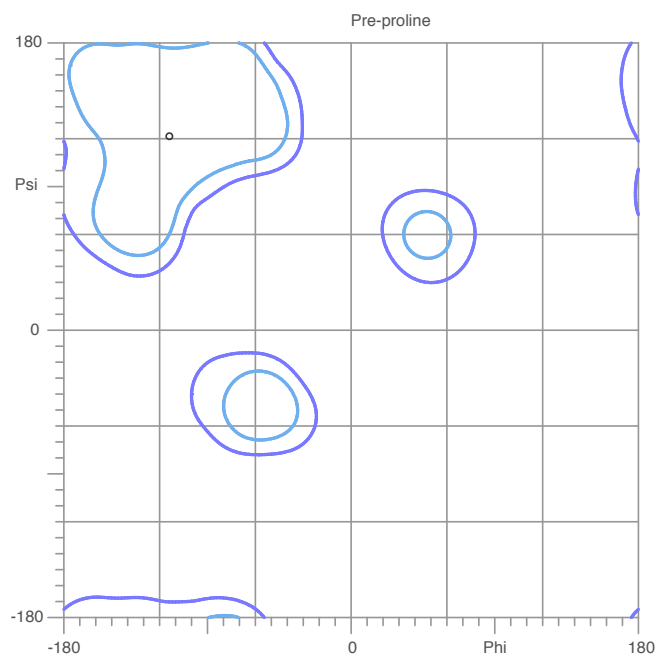
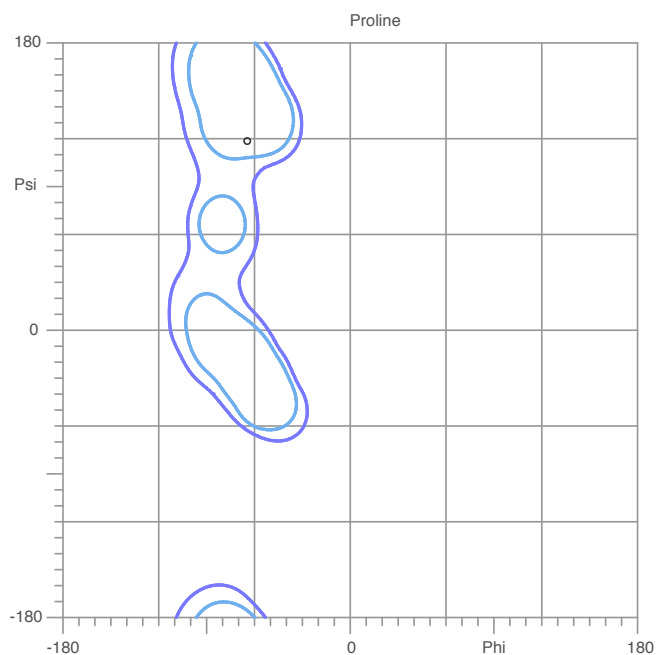
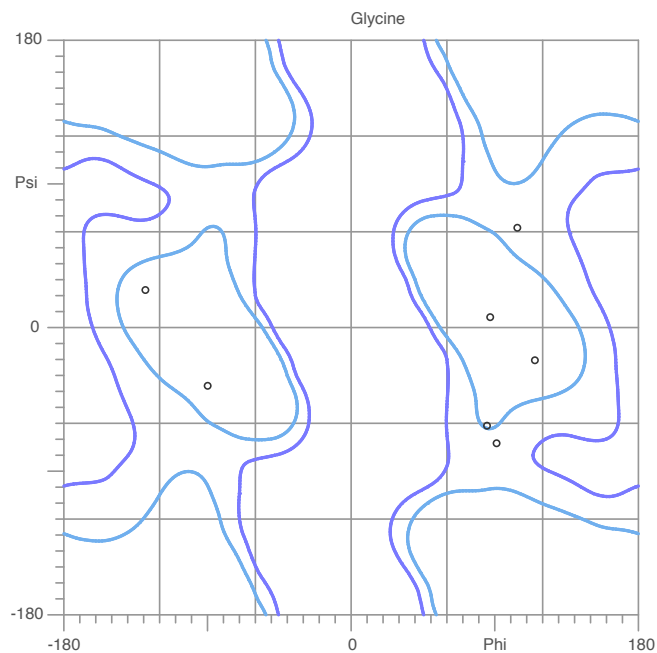
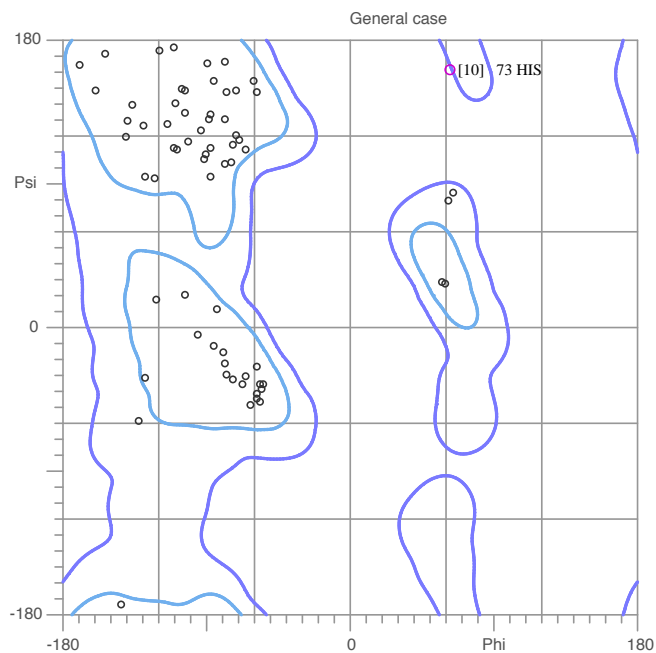
84.2% (64/76) of all residues were in favored (98%) regions.
96.1% (73/76) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [9] 65 PHE (66.4, 149.5)
- [9] 73 HIS (-171.0, -54.3)
- [9] 74 HIS (-180.0, 66.6)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 10



92.1% (70/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

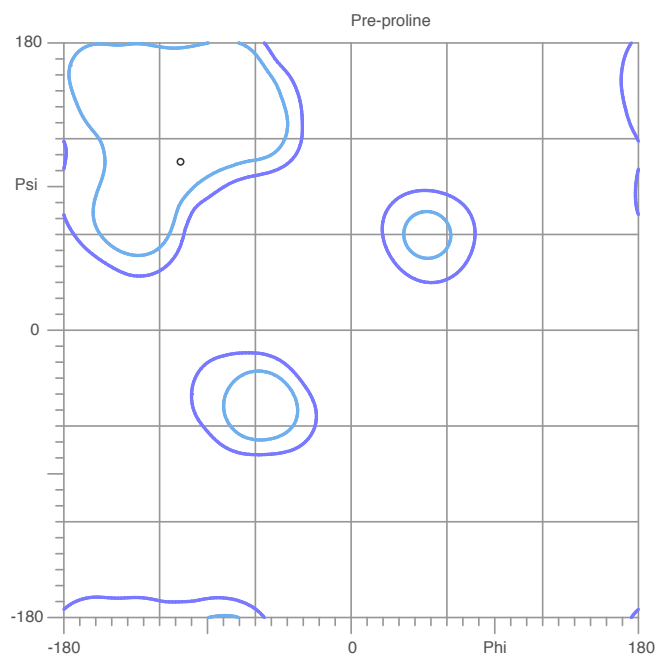
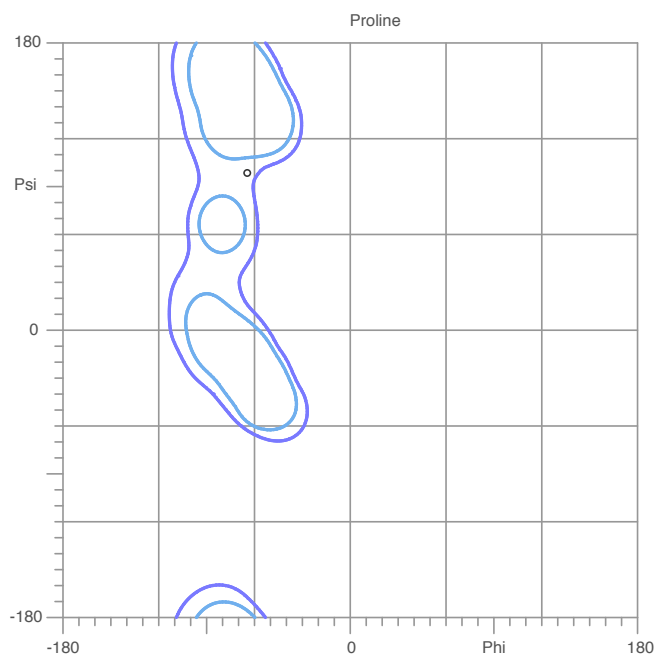
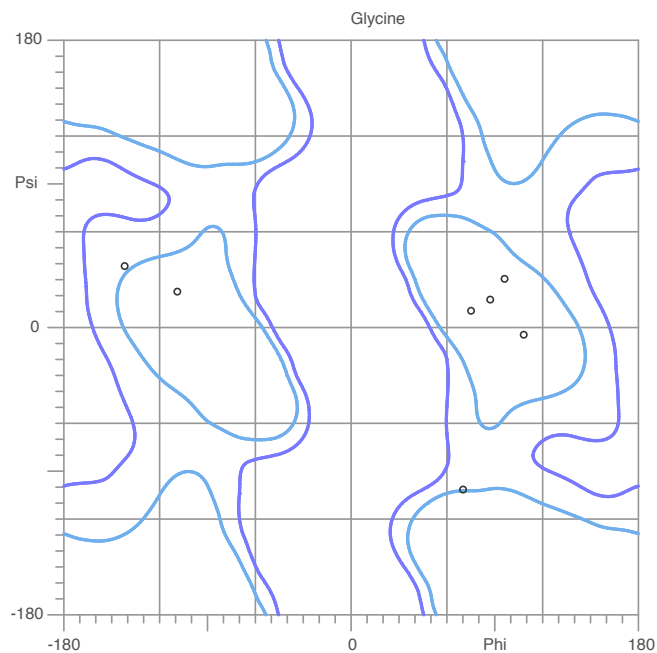
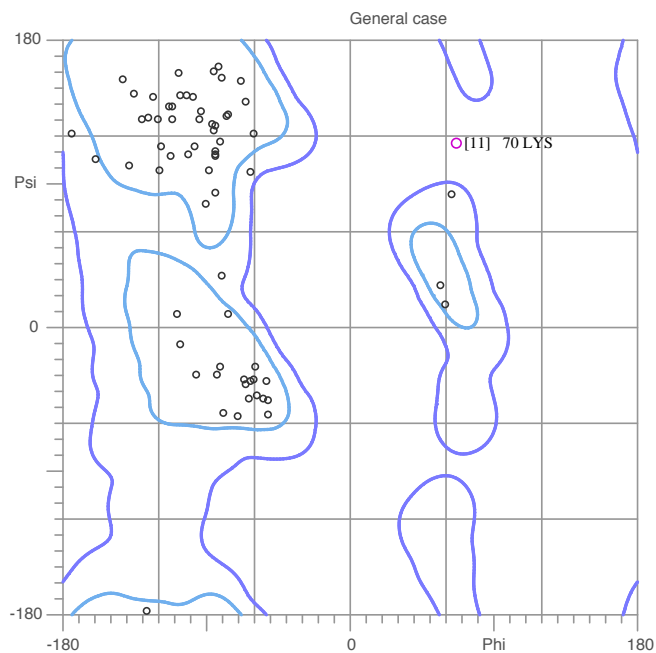
There were 1 outliers (phi, psi):
[10] 73 HIS (62.8, 162.7)

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MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 11



88.2% (67/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

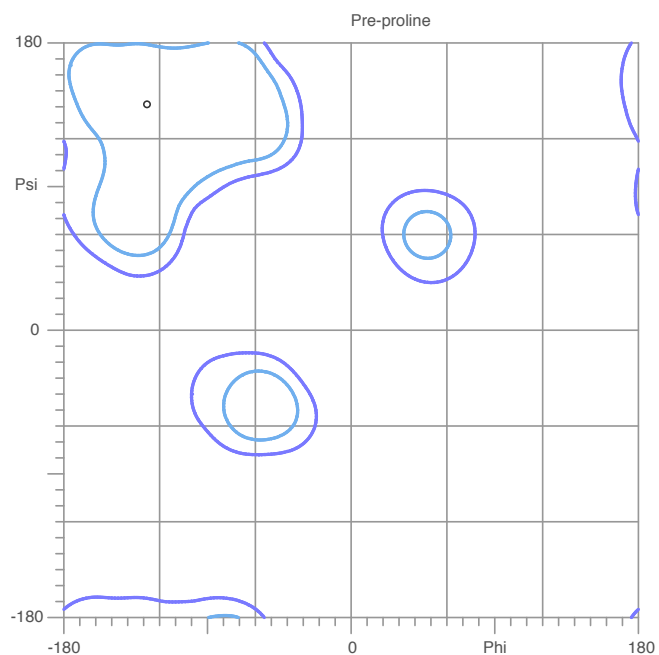
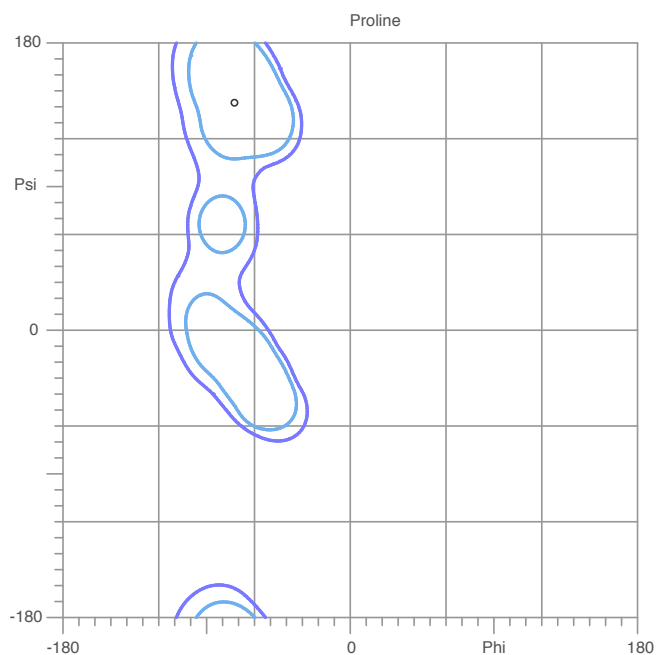
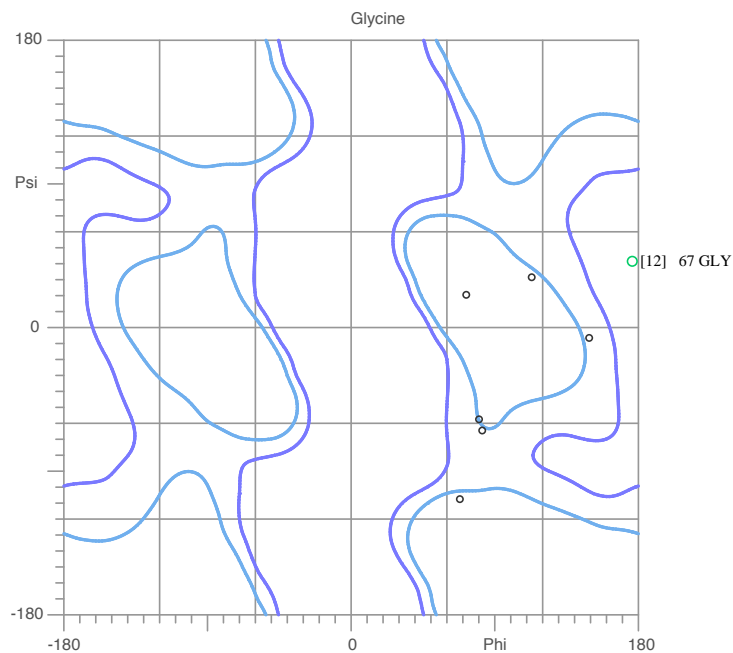
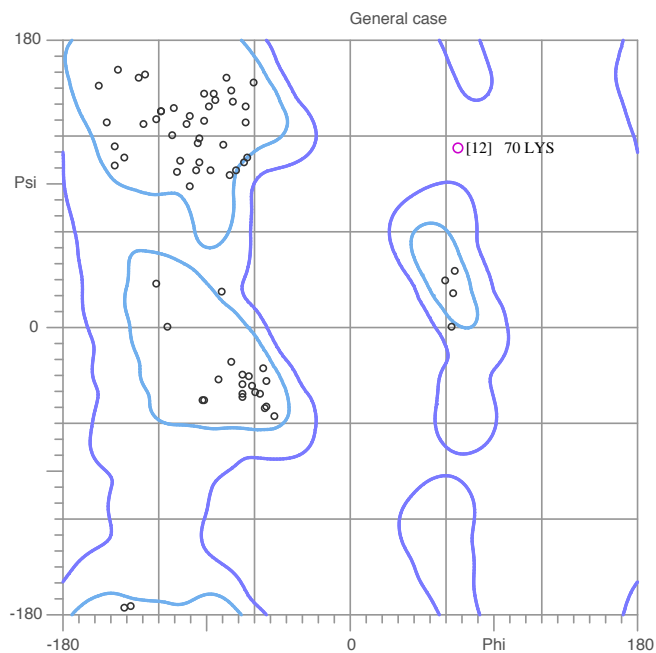
There were 1 outliers (phi, psi):
[11] 70 LYS (66.6, 116.4)

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MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 12

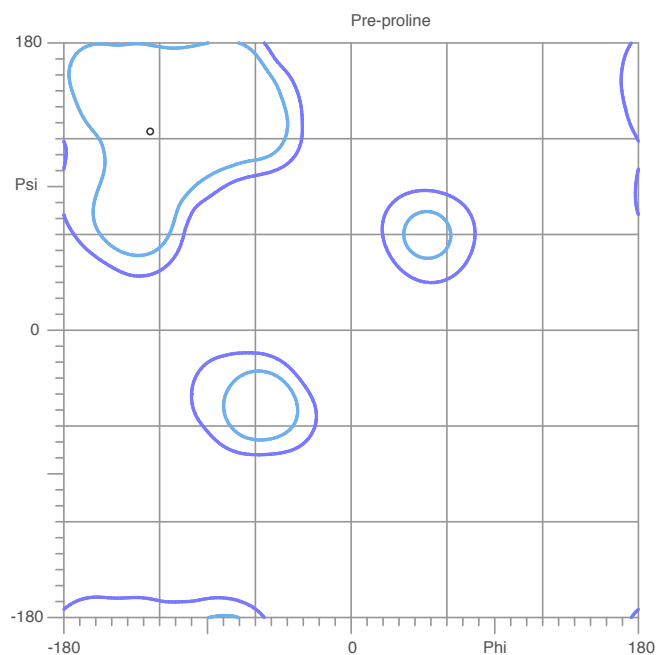
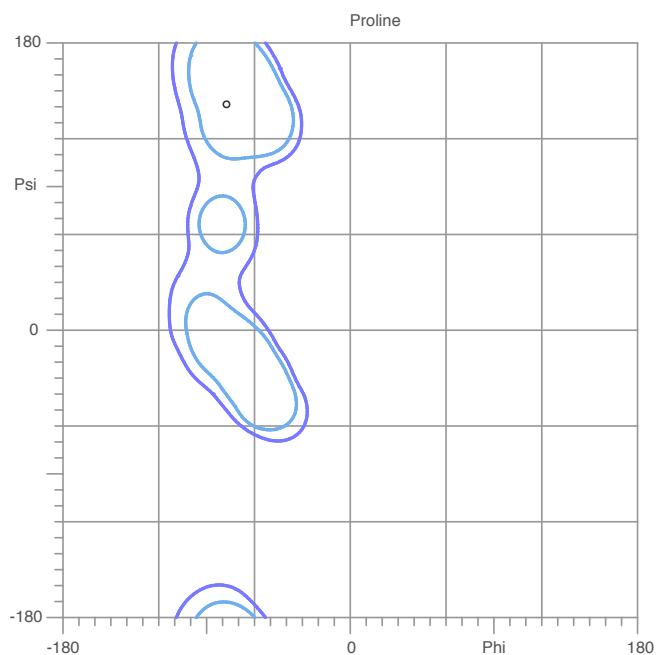
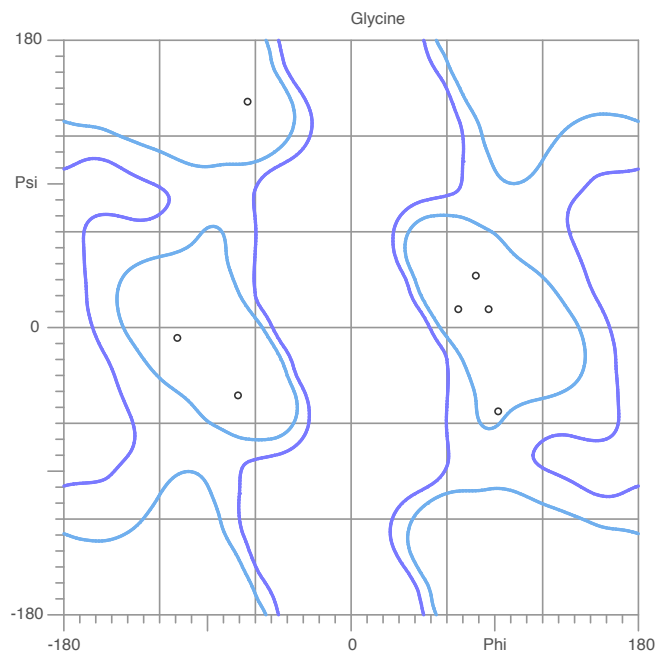
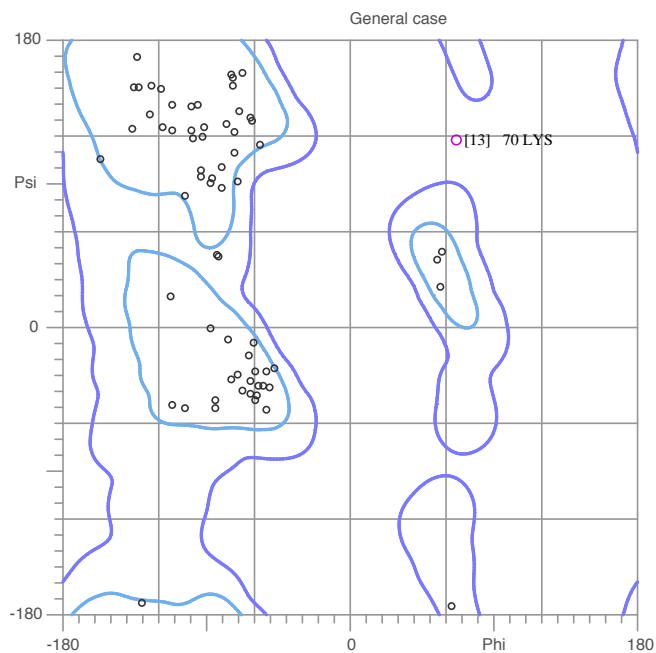


92.1% (70/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 67 GLY (176.2, 43.0)
[12] 70 LYS (68.0, 113.1)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 13



92.1% (70/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

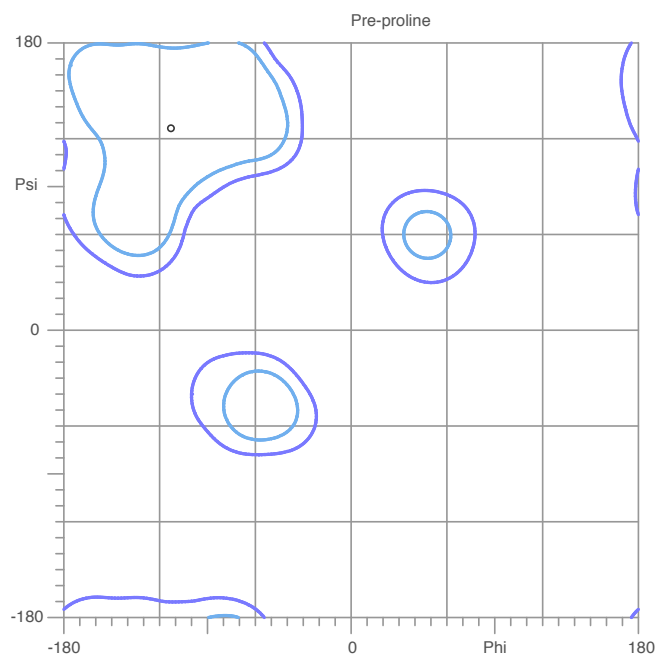
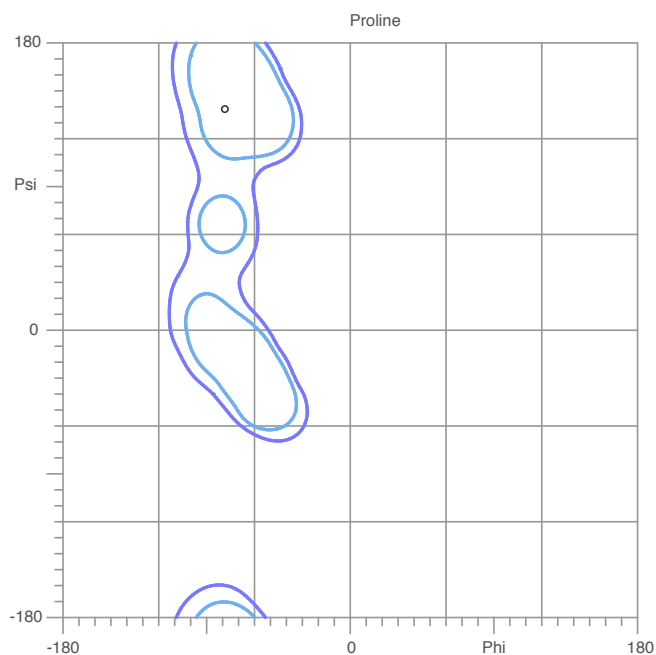
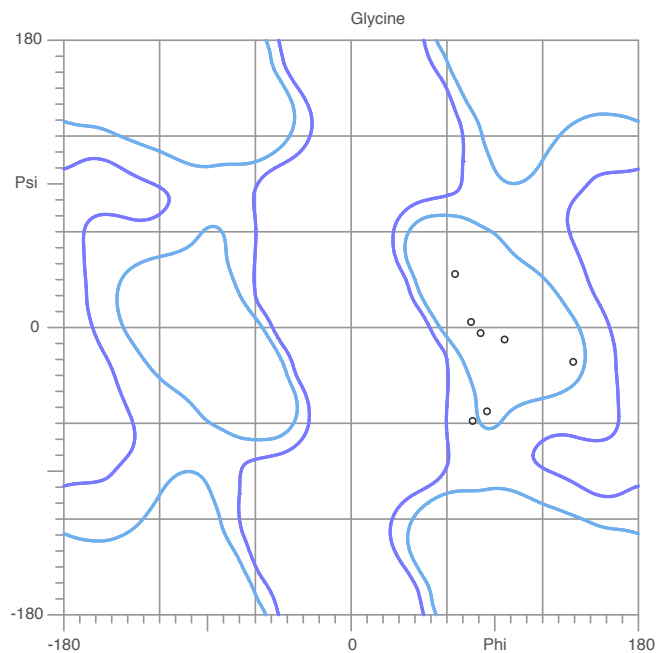
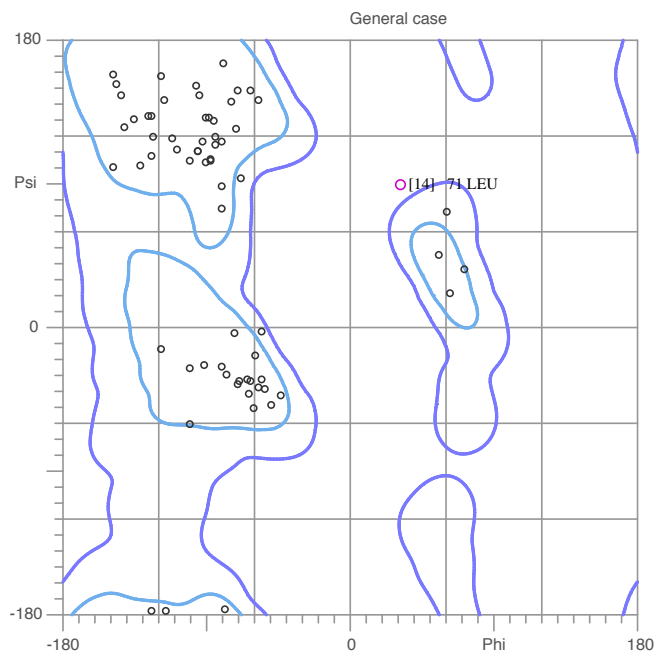
There were 1 outliers (phi, psi):
[13] 70 LYS (66.9, 118.6)

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MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 14



93.4% (71/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

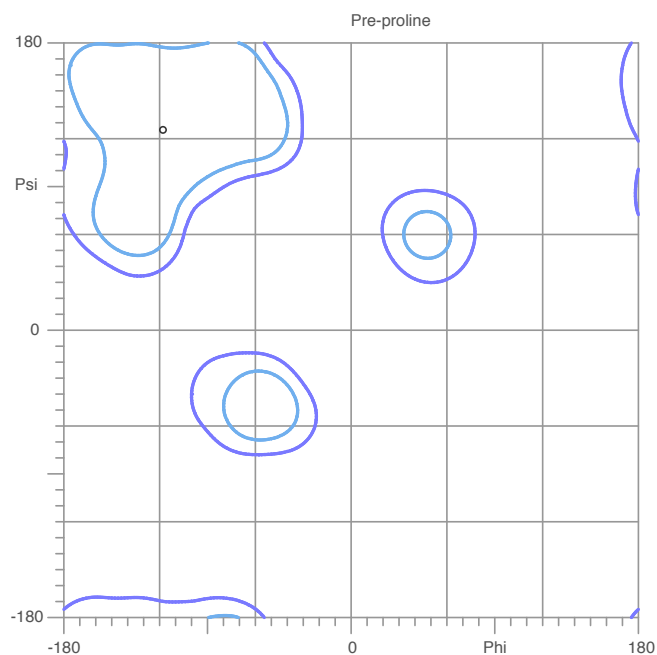
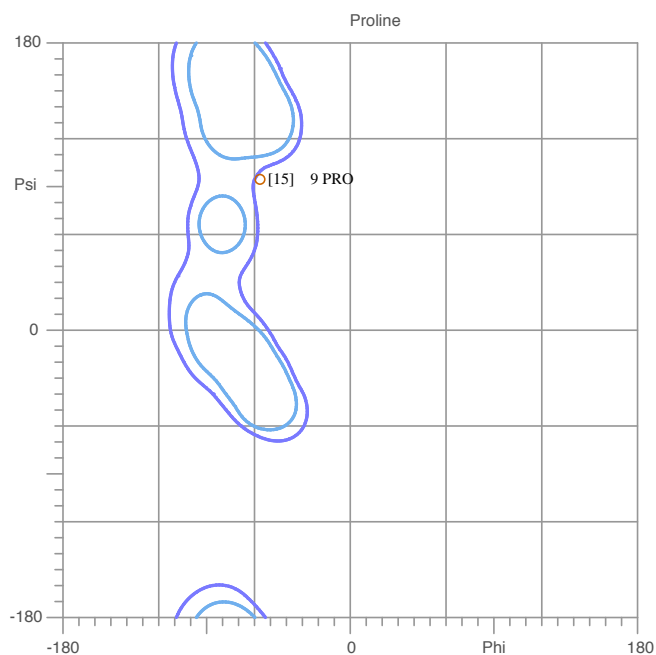
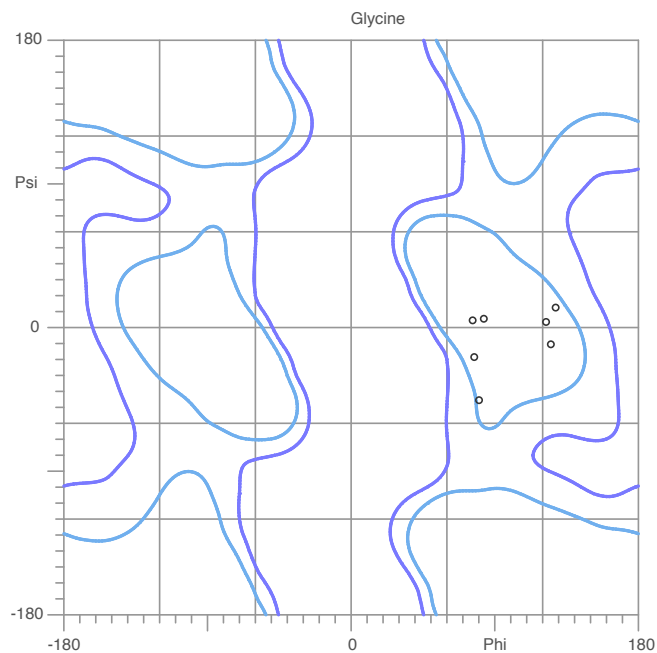
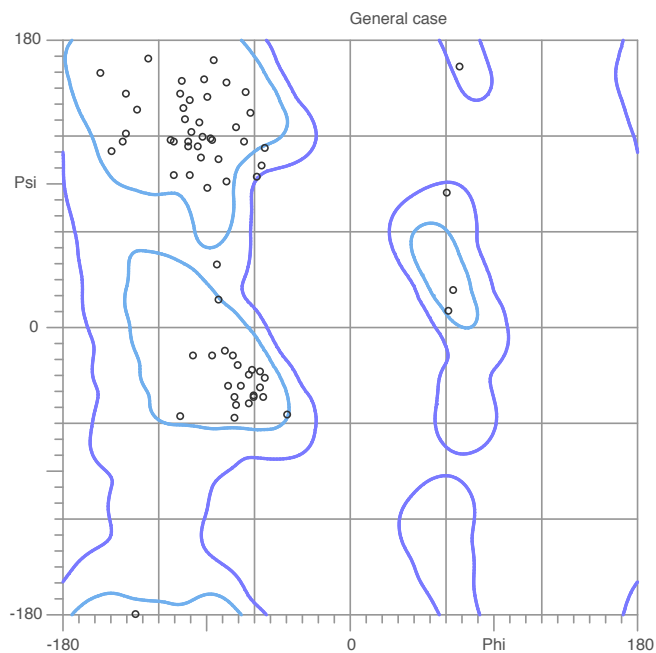
There were 1 outliers (phi, psi):
[14] 71 LEU (31.1, 90.7)

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MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 15



90.8% (69/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

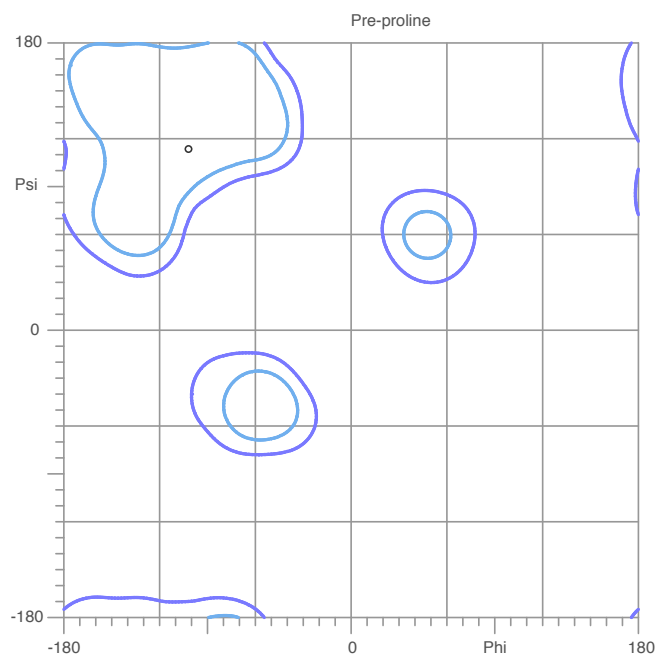
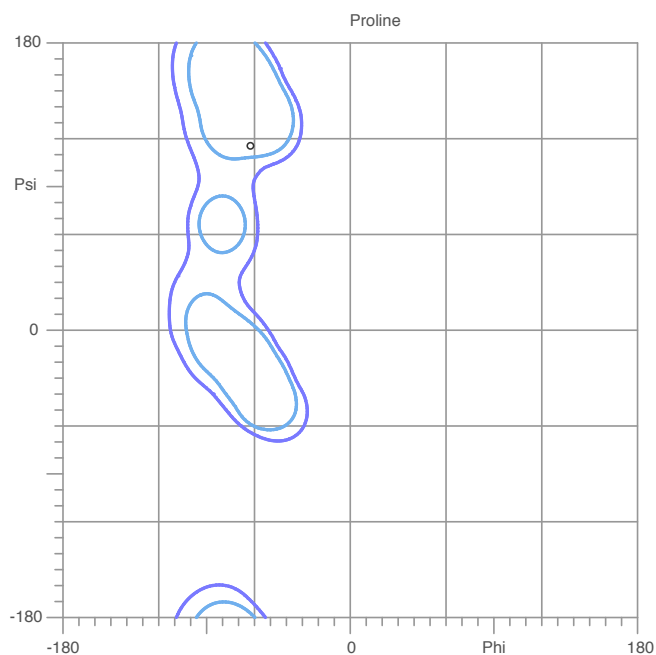
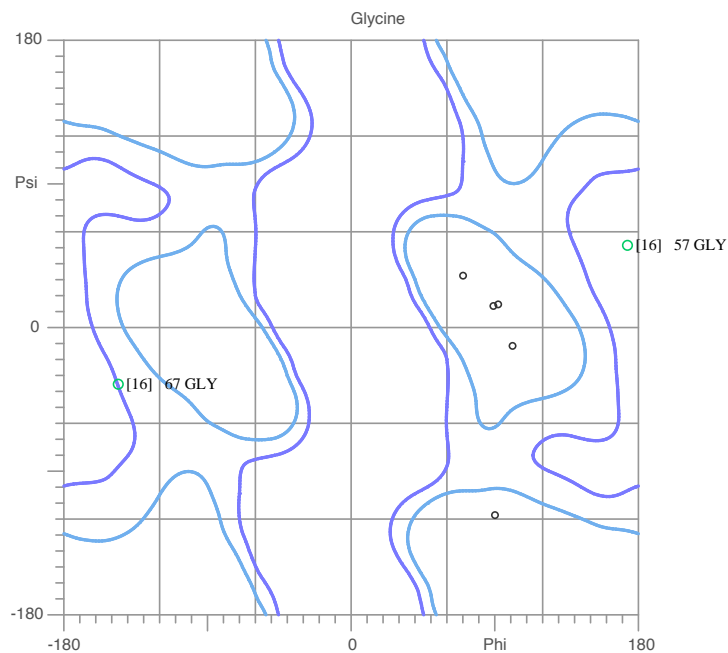
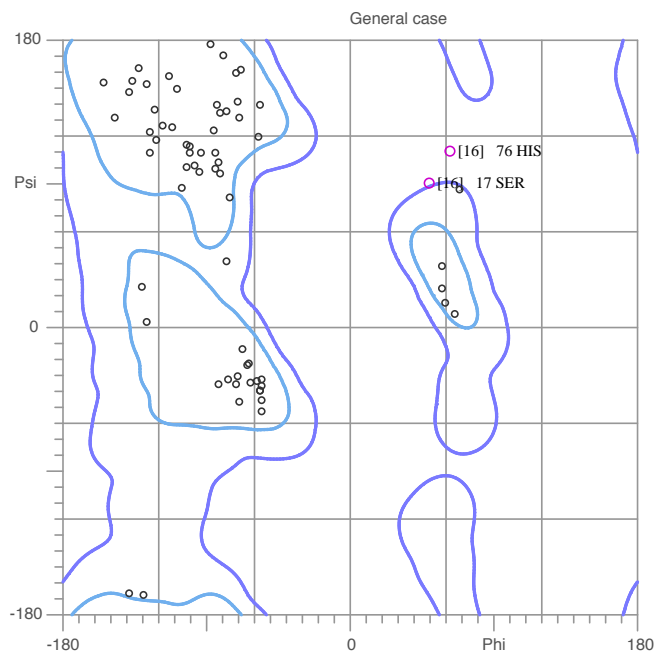
There were 1 outliers (phi, psi):
[15] 9 PRO (-57.7, 95.7)

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MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 16



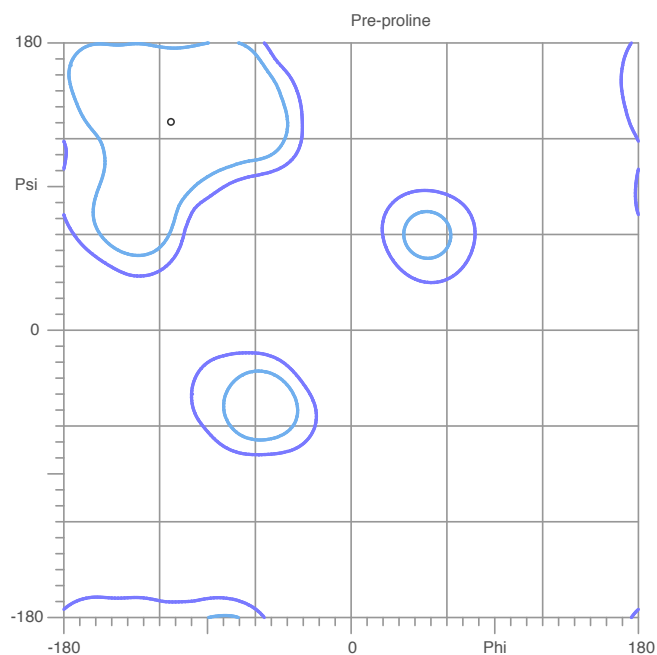
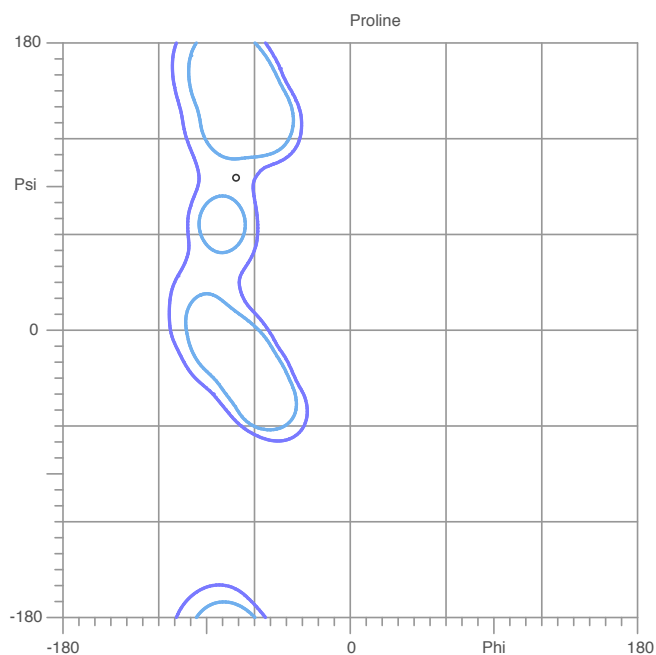
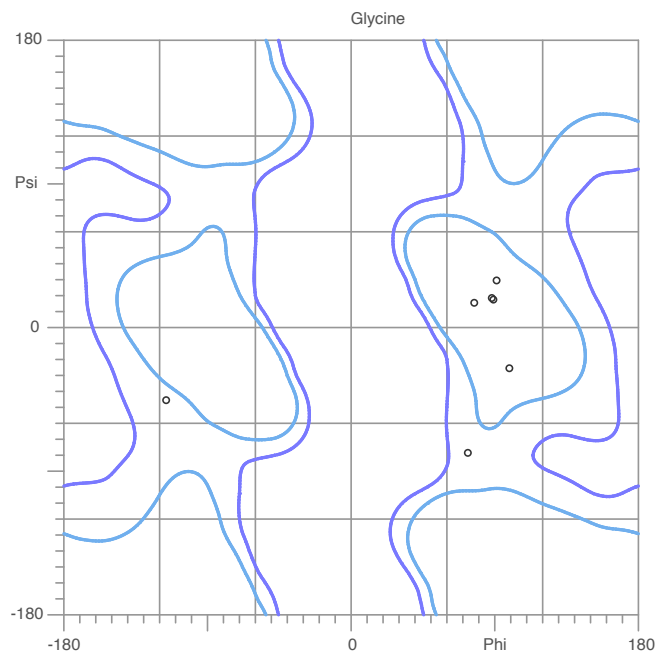
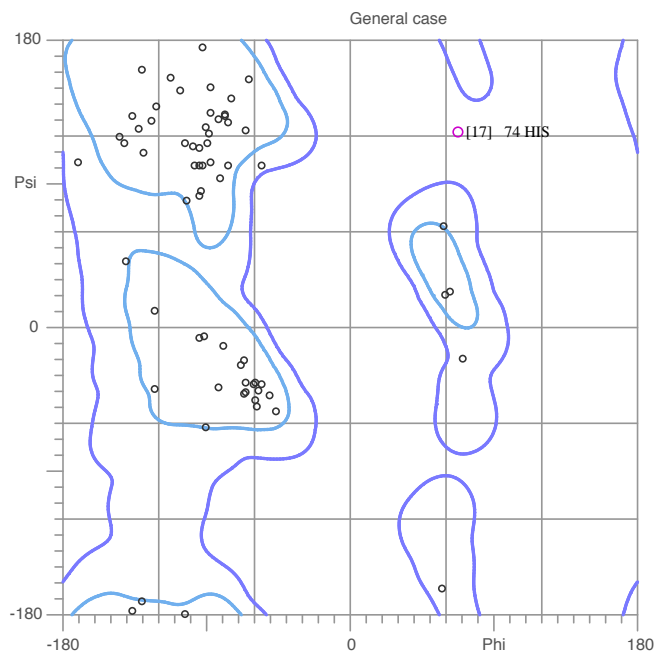
89.5% (68/76) of all residues were in favored (98%) regions.
94.7% (72/76) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [16] 17 SER (49.3, 92.0)
- [16] 57 GLY (173.6, 52.9)
- [16] 67 GLY (-146.7, -35.7)
- [16] 76 HIS (62.8, 111.4)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 17



86.8% (66/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

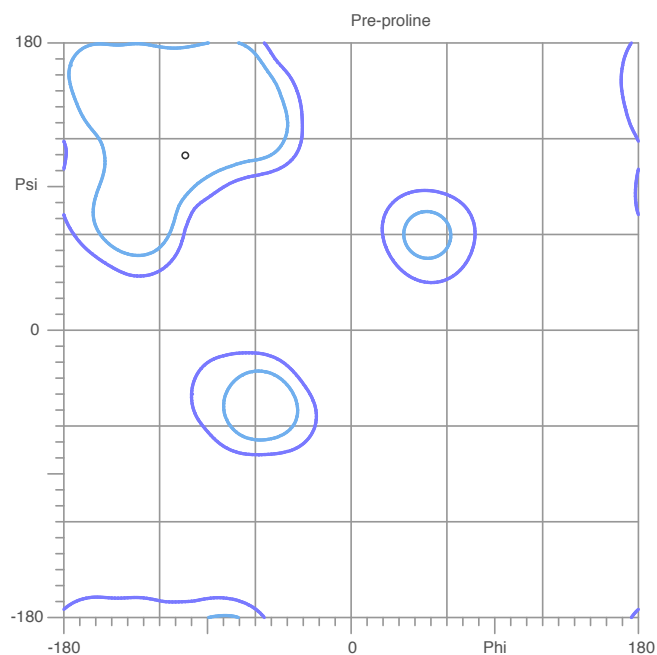
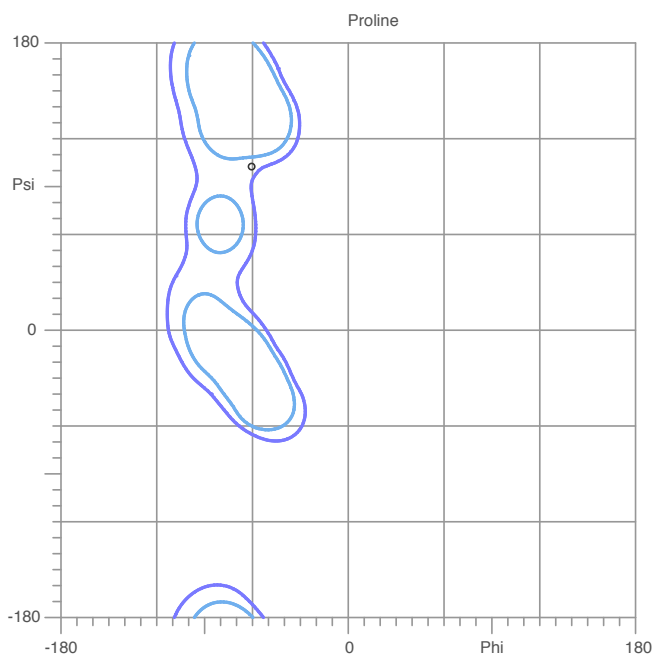
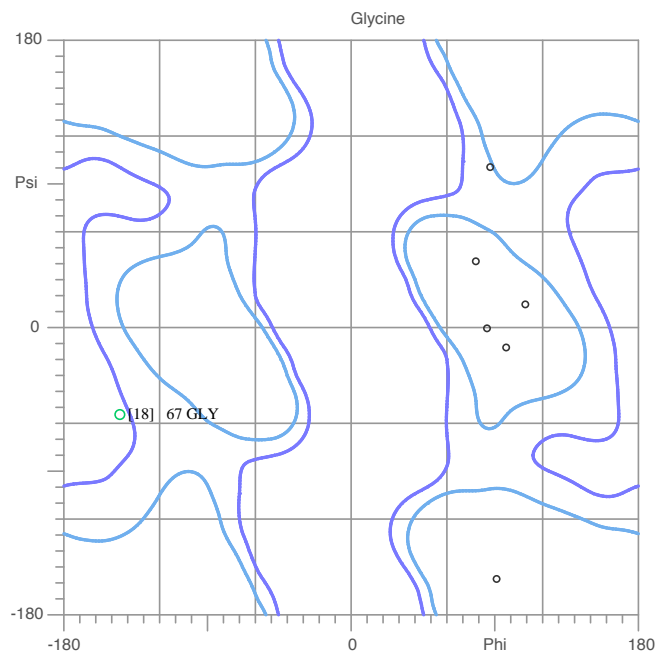
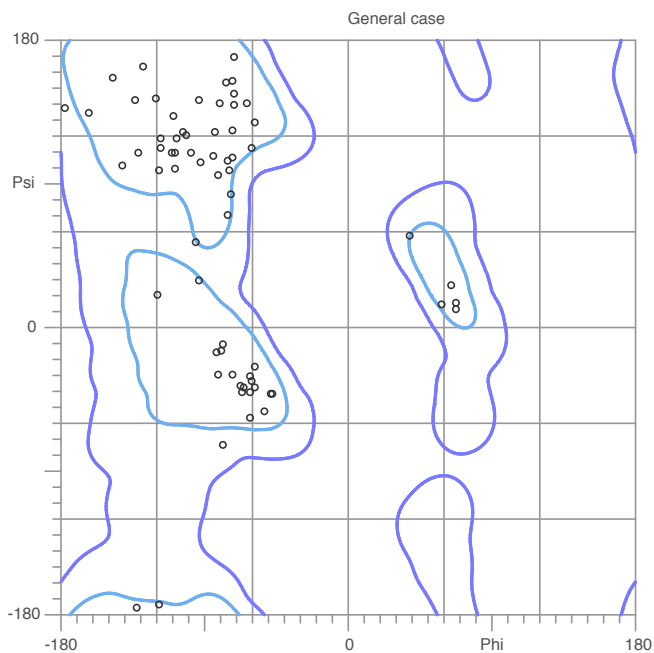
There were 1 outliers (phi, psi):
[17] 74 HIS (67.6, 123.7)

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MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 18

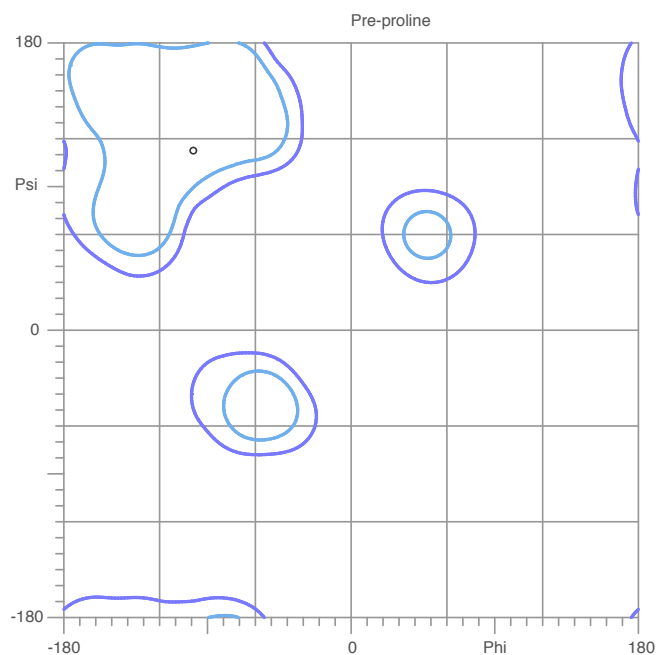
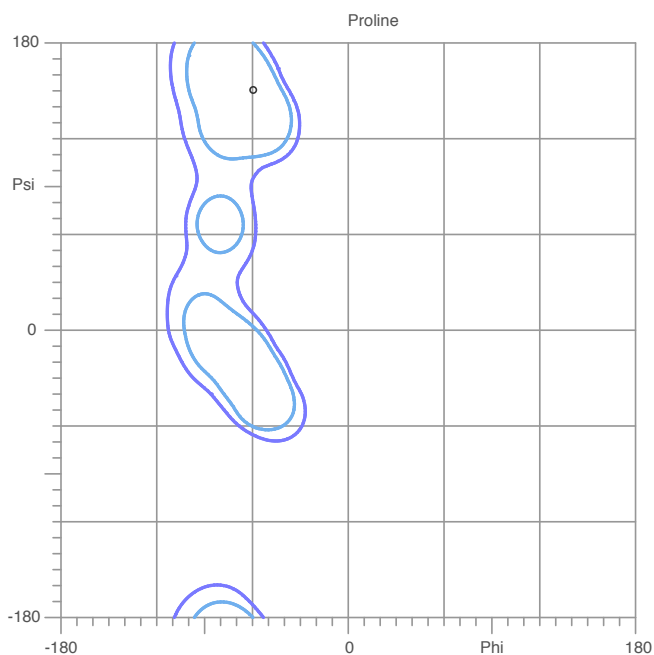
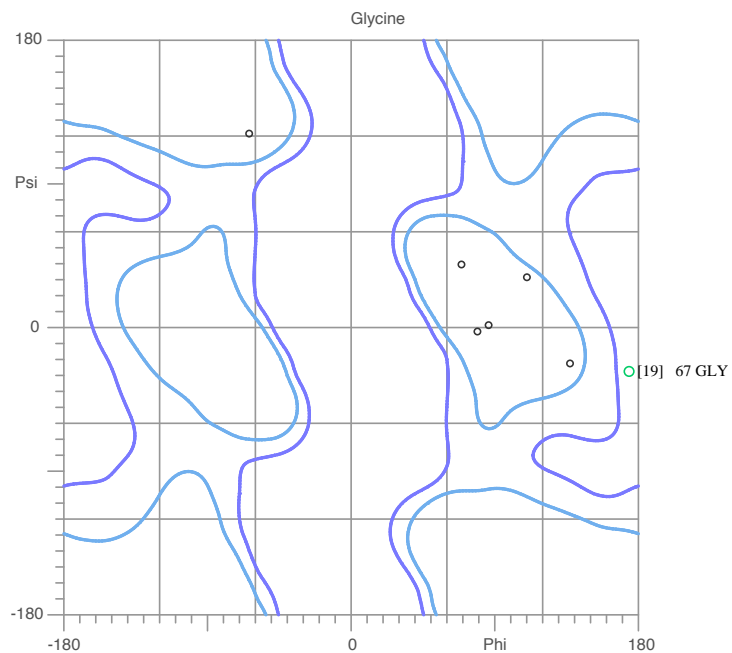
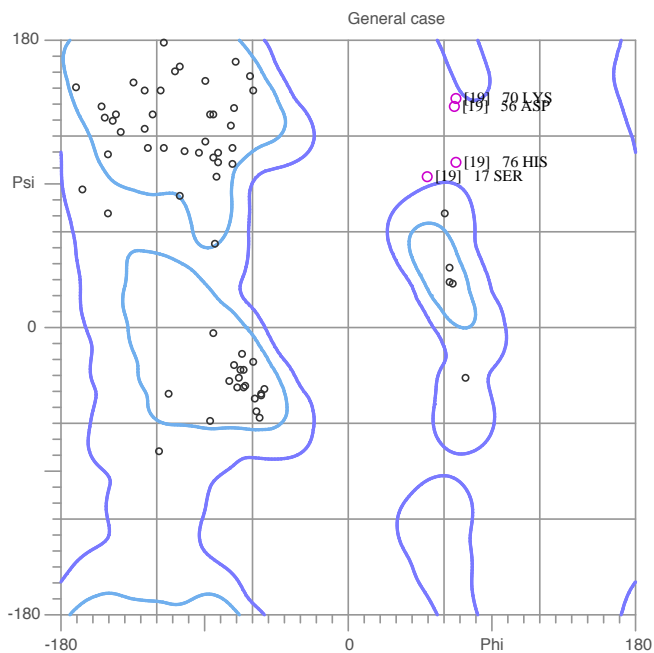


90.8% (69/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[18] 67 GLY (-145.0, -54.3)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 19



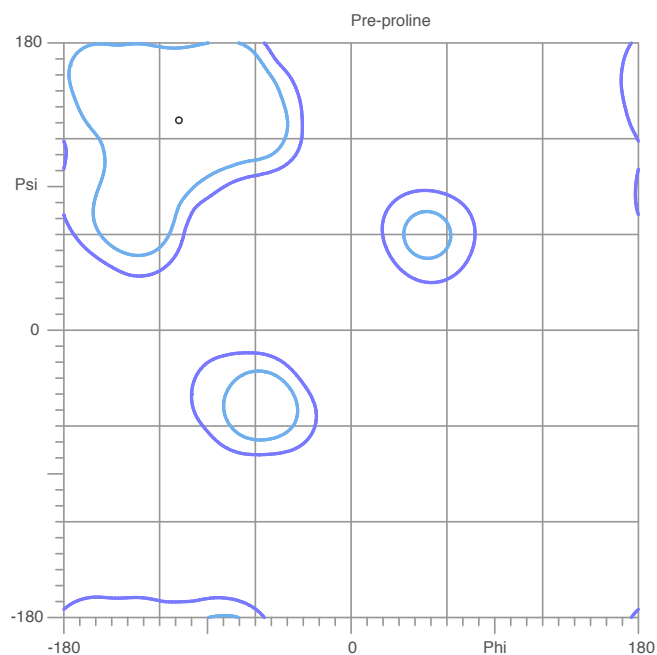
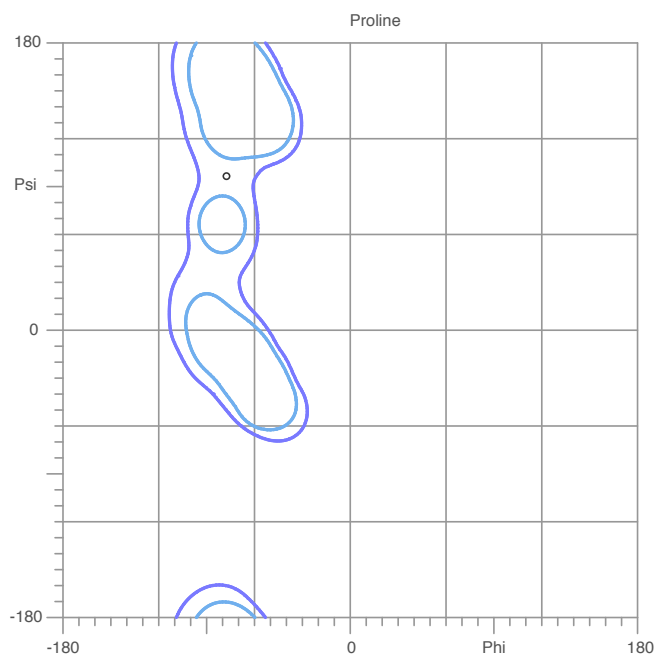
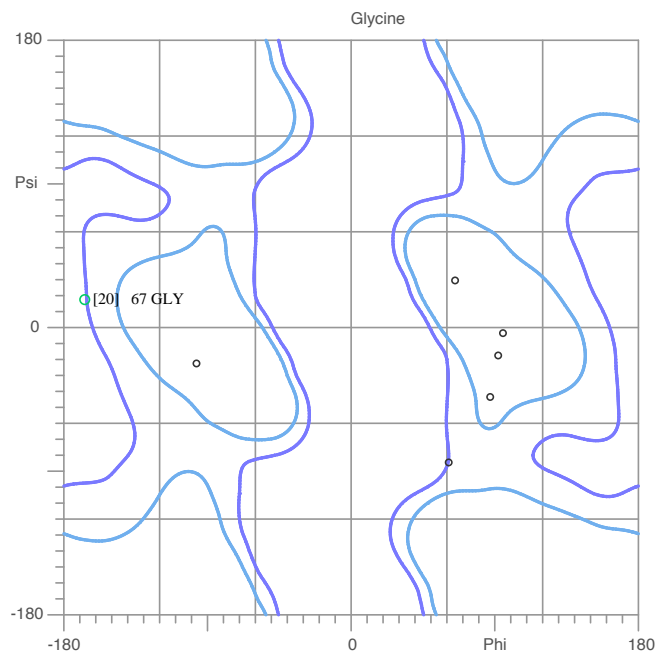
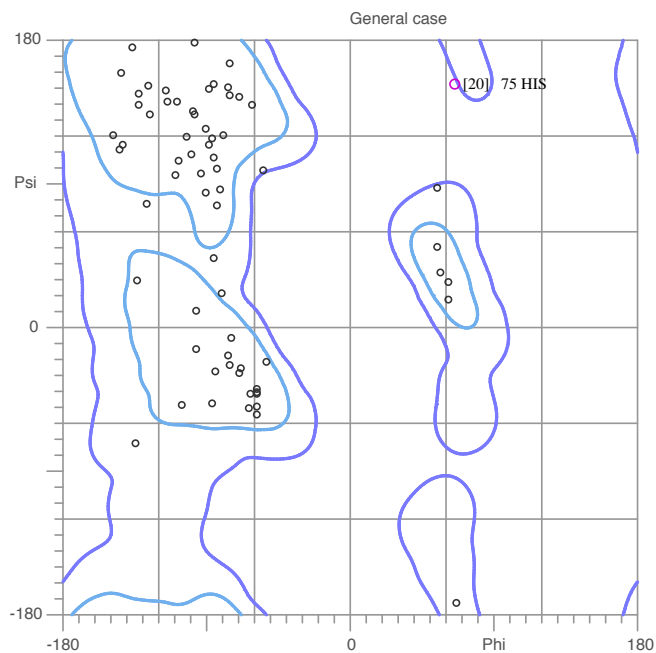
86.8% (66/76) of all residues were in favored (98%) regions.
93.4% (71/76) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[19] 17 SER (49.4, 96.0)
[19] 56 ASP (66.0, 139.6)
[19] 67 GLY (175.0, -27.2)
[19] 70 LYS (67.8, 144.7)
[19] 76 HIS (67.1, 104.4)

MolProbity Ramachandran analysis

GMR137_NMR_em_bcr3.pdb, model 20



85.5% (65/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[20] 67 GLY (-167.2, 18.0)
[20] 75 HIS (65.2, 153.8)

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