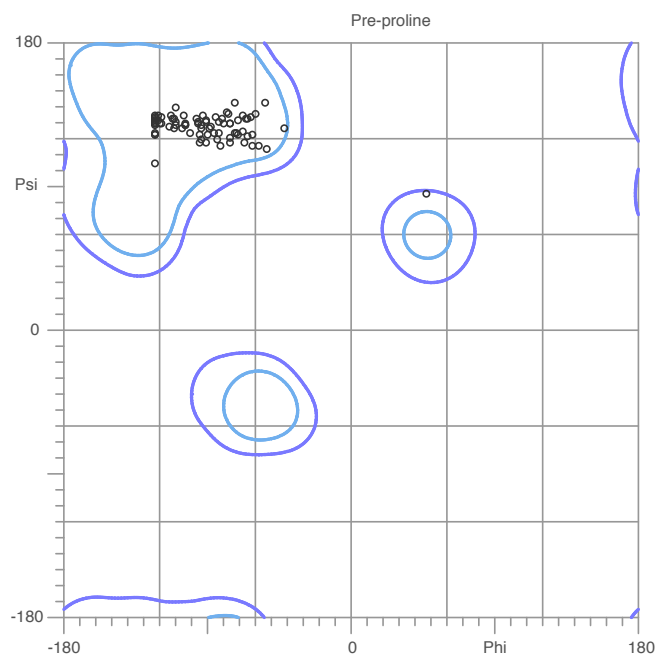
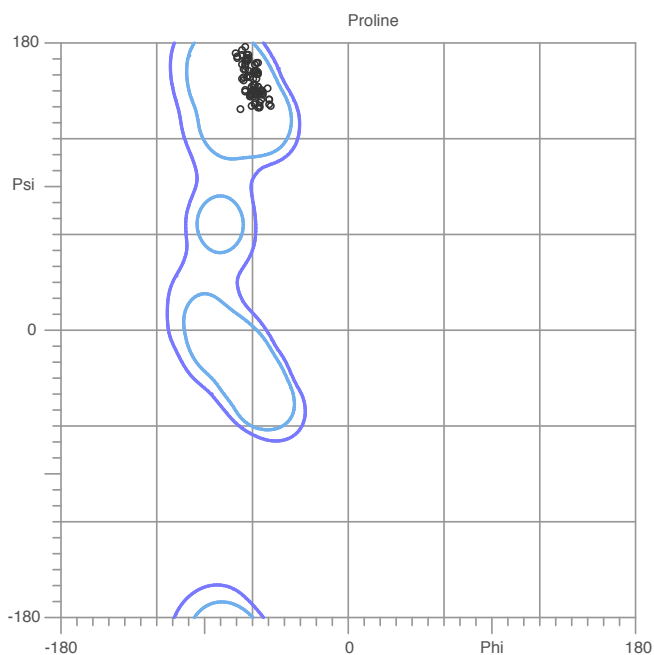
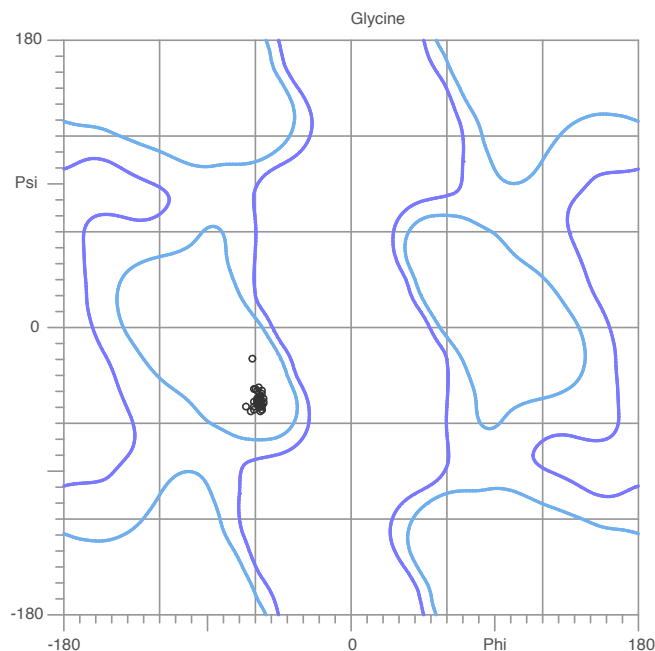
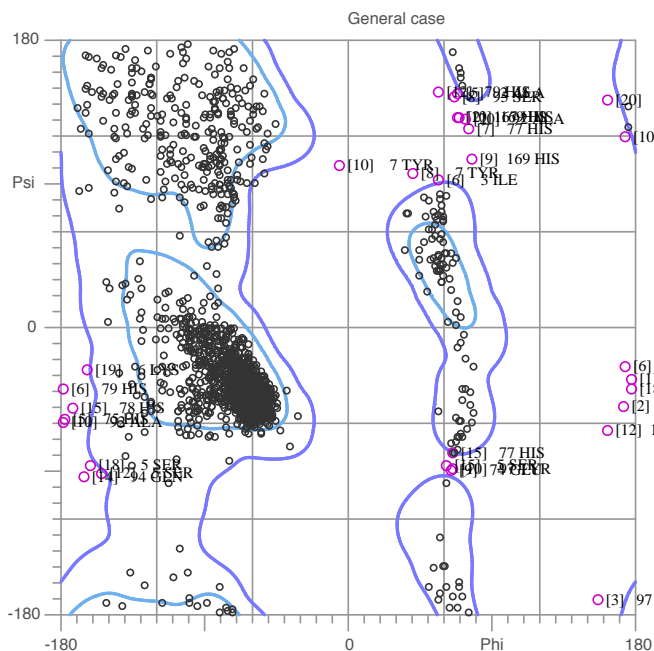


MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, all models



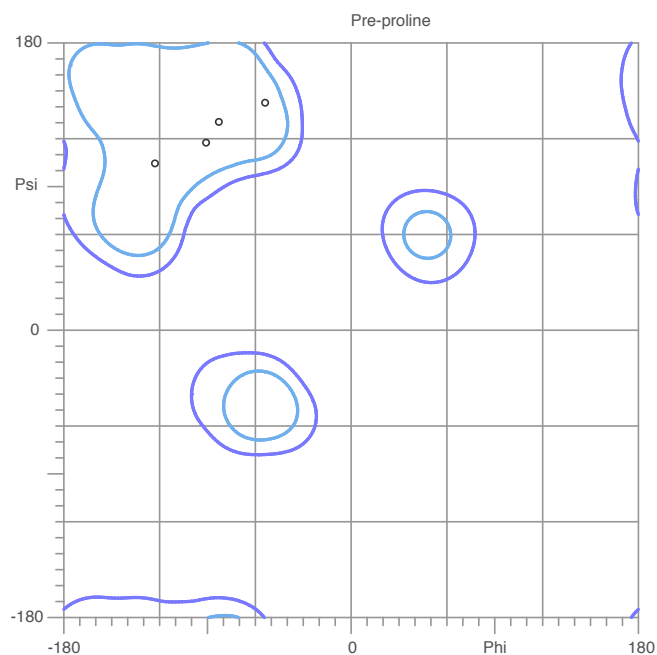
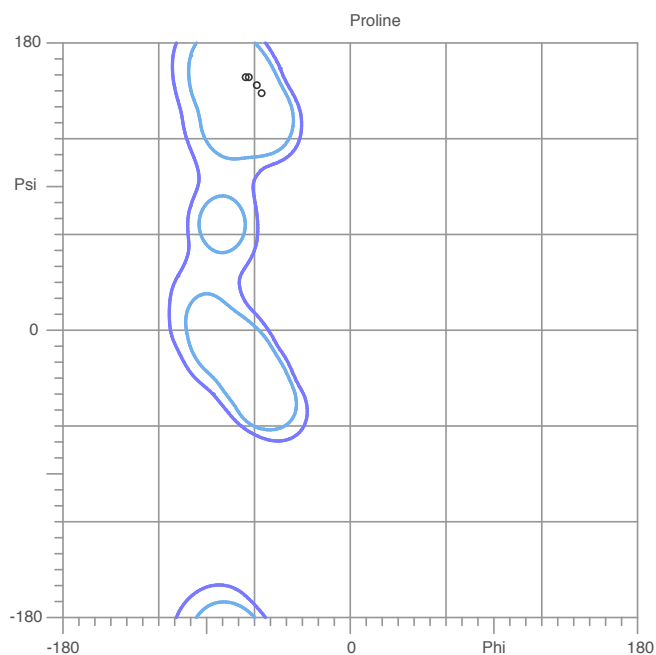
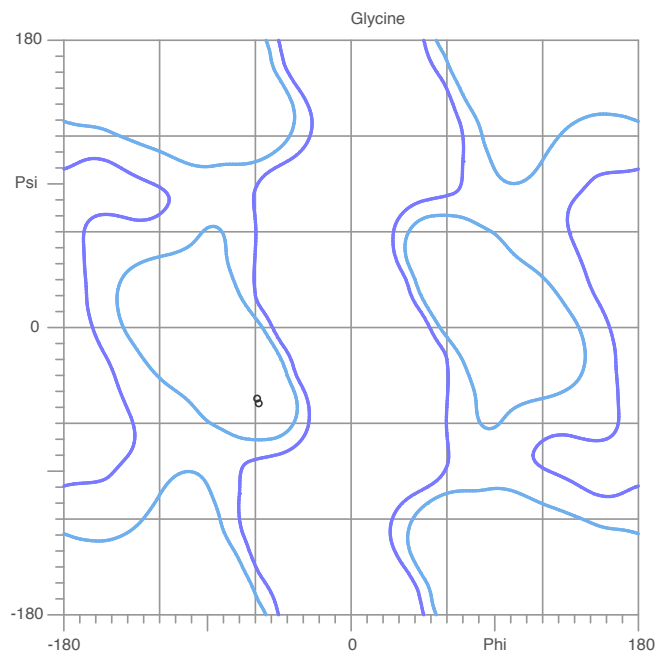
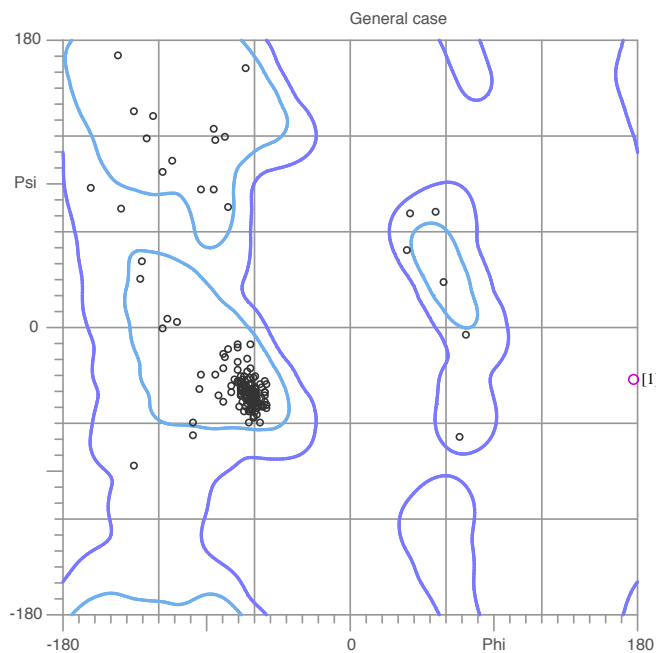
94.2% (2939/3120) of all residues were in favored (98%) regions.
99.0% (3089/3120) of all residues were in allowed (>99.8%) regions.

There were 31 outliers (phi, psi):

- | | |
|----------------------------|-----------------------------|
| [1] 79 HIS (177.0, -32.5) | [9] 169 HIS (77.8, 106.3) |
| [2] 79 HIS (172.0, -49.3) | [10] 7 TYR (-6.6, 102.5) |
| [2] 167 HIS (69.5, 132.7) | [10] 92 ALA (-179.9, -59.9) |
| [3] 97 TYR (156.1, -170.9) | [10] 97 TYR (65.1, -88.5) |
| [5] 2 ALA (68.6, 147.9) | [10] 98 SER (173.1, 120.5) |
| [5] 75 HIS (-178.0, -57.6) | [10] 169 HIS (68.3, 132.8) |
| [6] 3 ILE (56.3, 93.1) | [12] 5 SER (-155.1, -91.4) |
| [6] 79 HIS (-179.4, -38.4) | [12] 79 HIS (56.7, 148.8) |
| [6] 166 HIS (173.3, -24.5) | [12] 168 HIS (162.4, -64.5) |
| [7] 77 HIS (75.1, 125.6) | [14] 94 GLN (-166.5, -93.7) |
| [8] 7 TYR (40.0, 97.3) | [15] 5 SER (61.2, -86.3) |
| [8] 95 SER (66.4, 145.9) | [15] 77 HIS (65.6, -78.8) |
| [9] 74 GLU (64.4, -89.4) | [15] 78 HIS (-173.6, -50.6) |
| | [18] 5 SER (-162.4, -86.1) |
| | [18] 6 LYS (177.2, -38.5) |
| | [19] 6 LYS (-164.3, -26.6) |
| | [20] 8 SER (162.6, 143.2) |
| | [20] 92 ALA (73.3, 131.9) |

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 1



93.6% (146/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

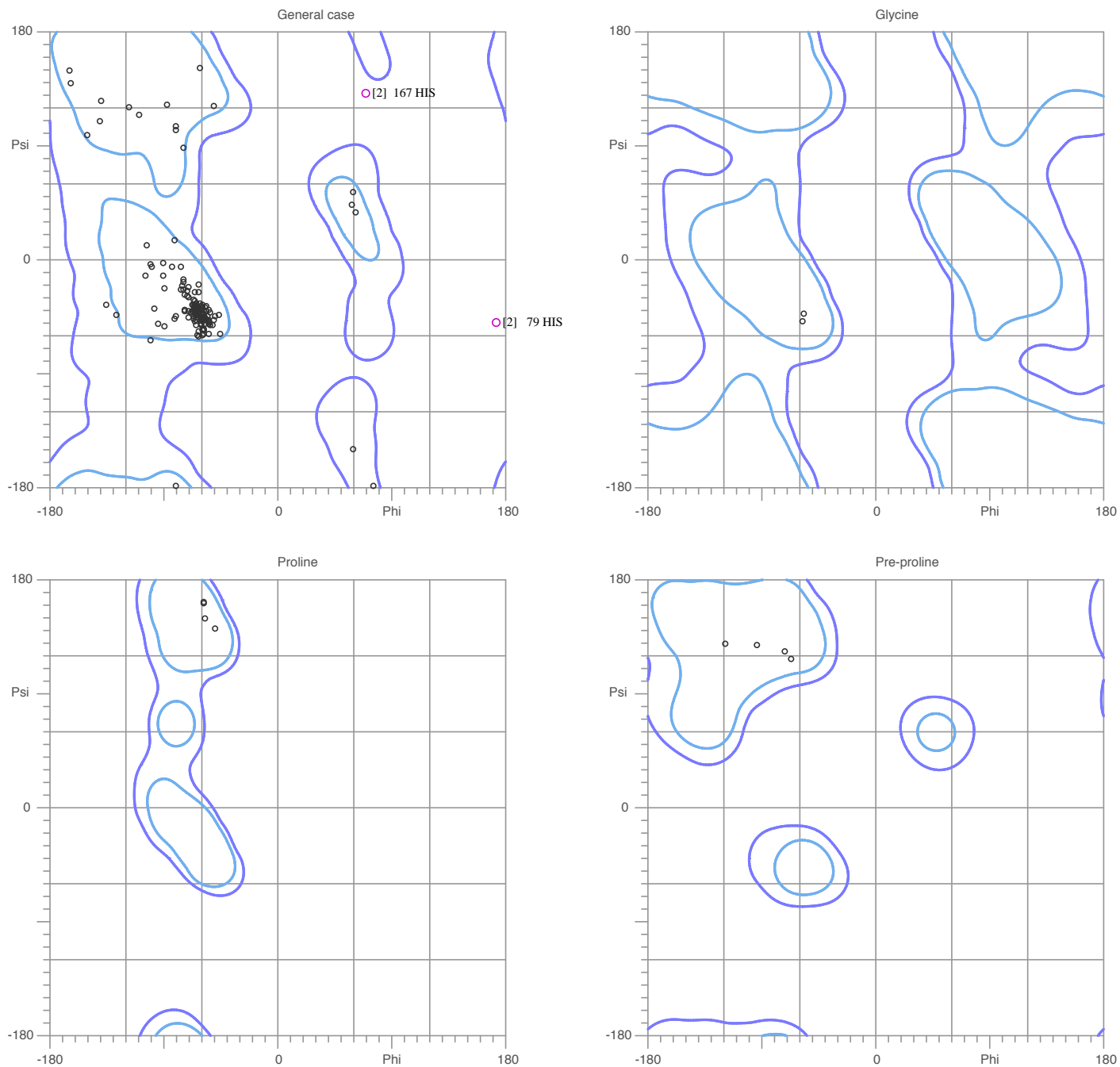
There were 1 outliers (phi, psi):
[1] 79 HIS (177.0, -32.5)

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MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 2



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.

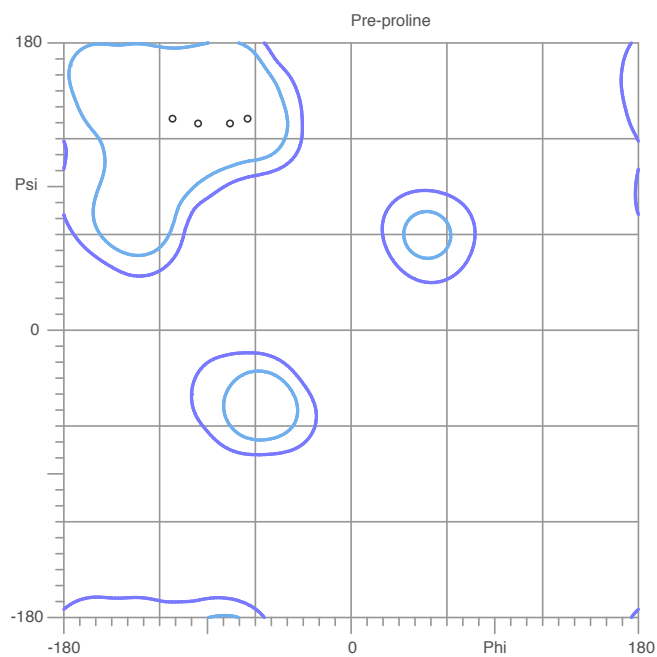
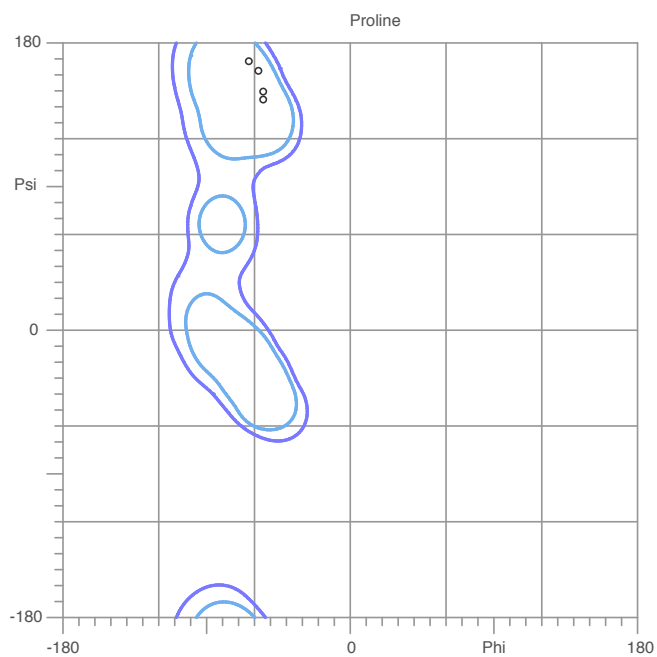
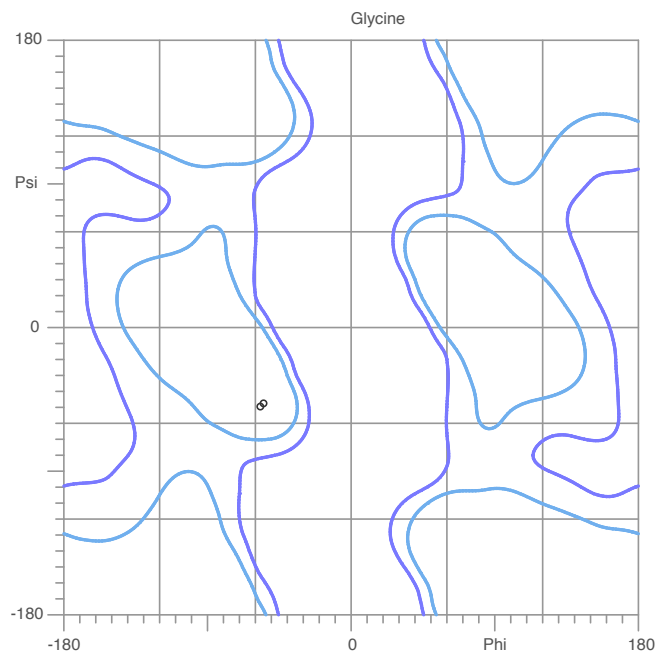
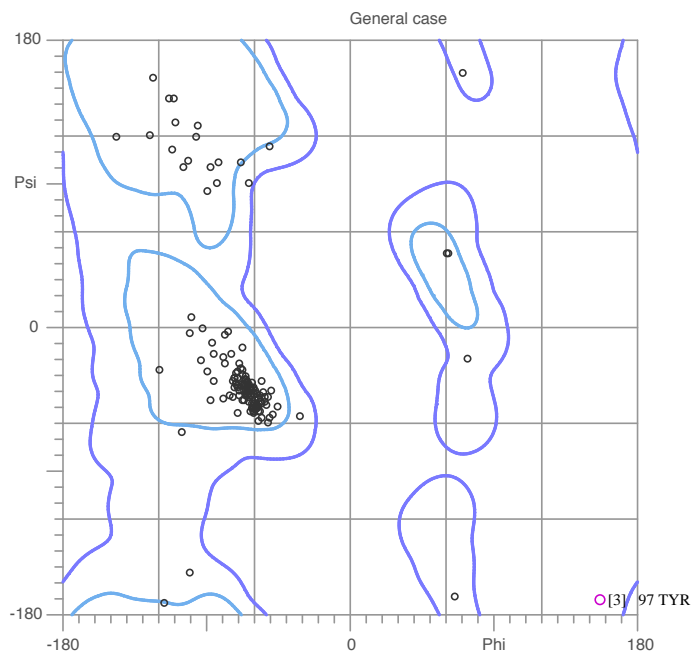
There were 2 outliers (phi, psi):

[2] 79 HIS (172.0, -49.3)

[2] 167 HIS (69.5, 132.7)

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 3



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.

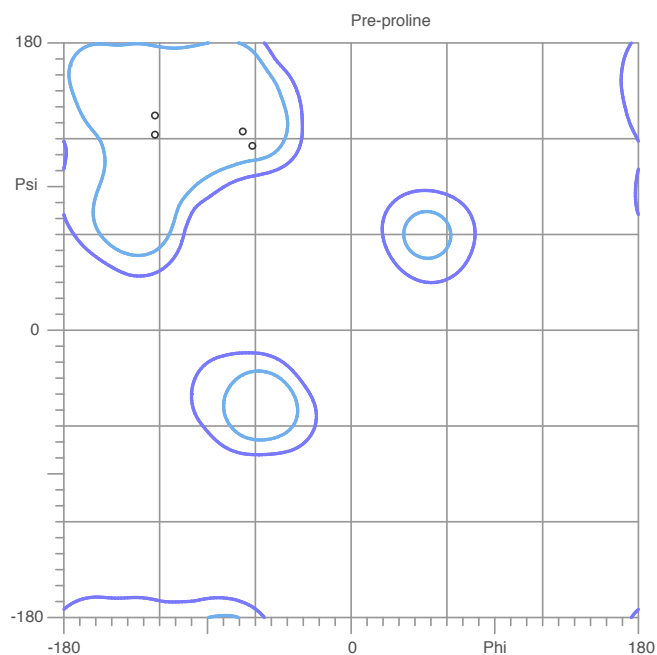
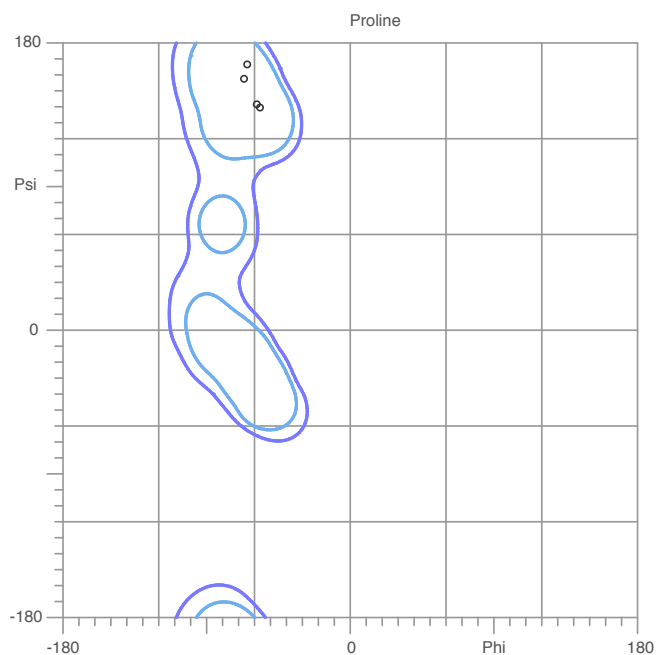
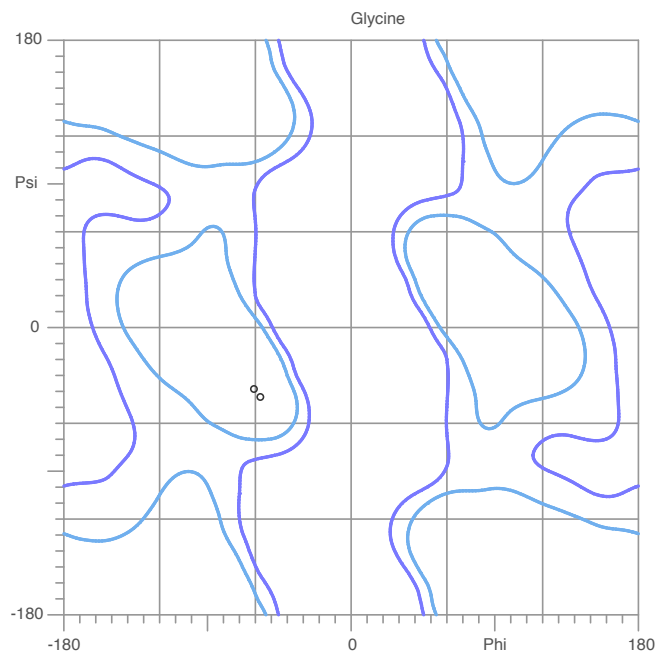
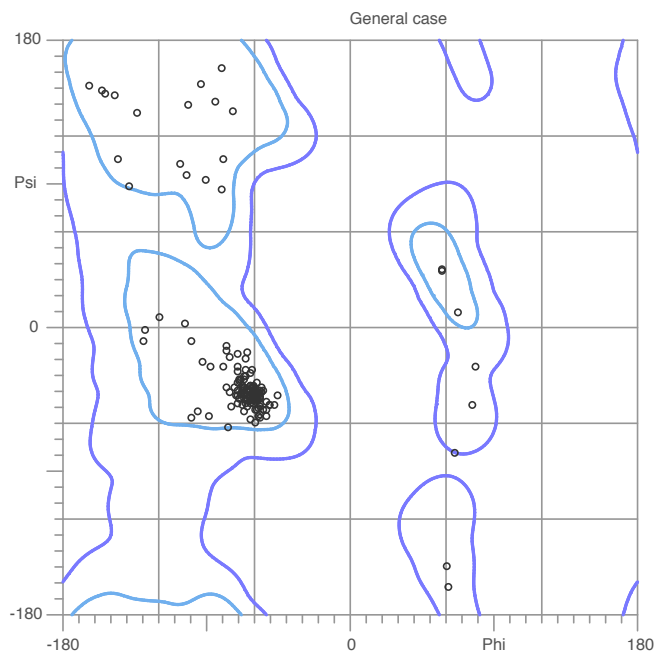
There were 1 outliers (phi, psi):
[3] 97 TYR (156.1, -170.9)

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MolProbity Ramachandran analysis

SOR77_NMR_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.

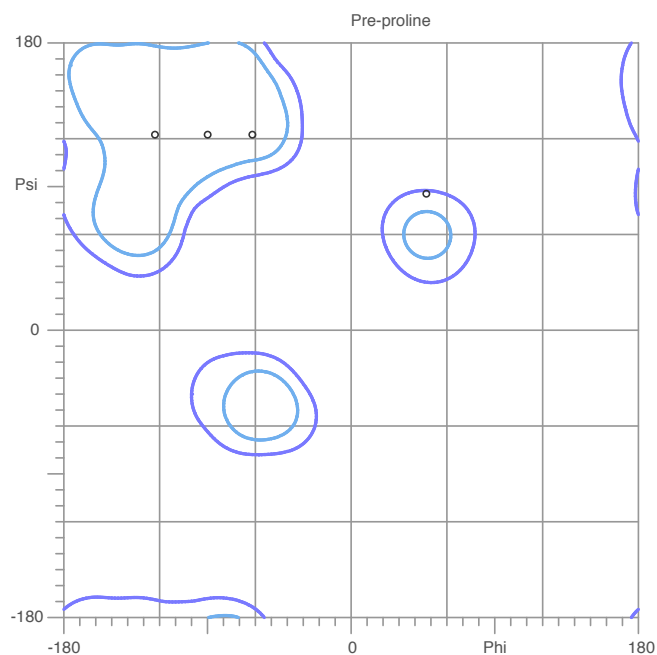
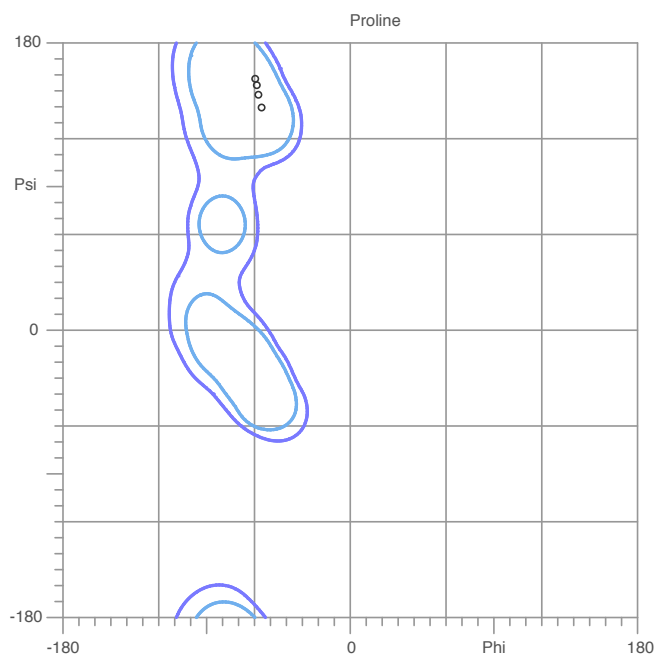
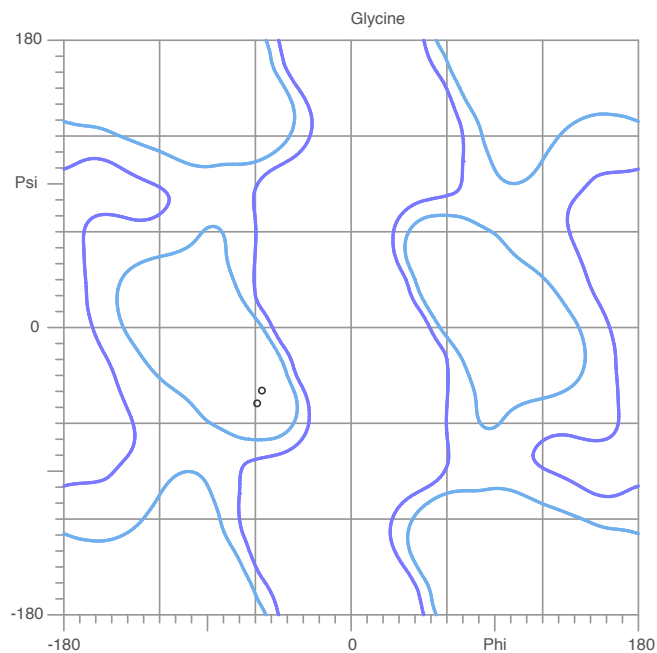
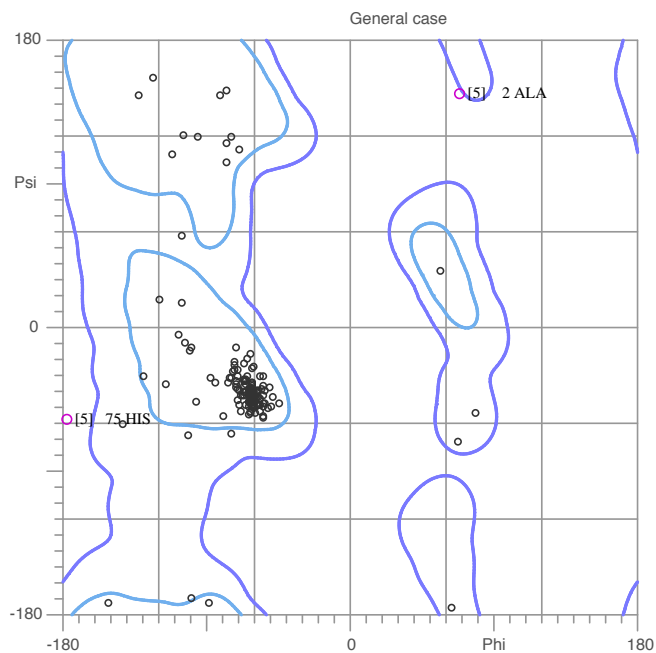
There were no outliers.

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

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MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 5



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.

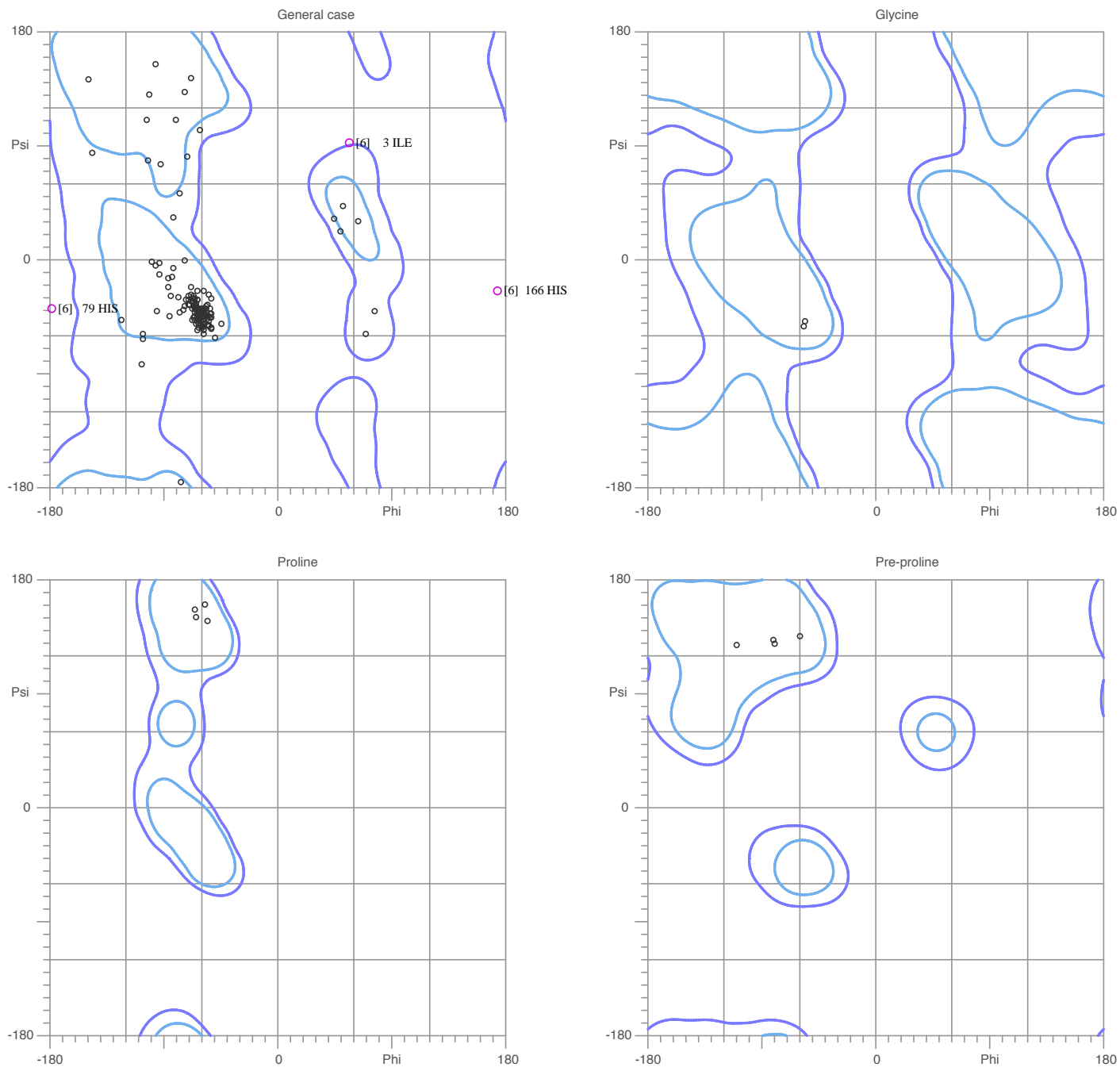
There were 2 outliers (phi, psi):

[5] 2 ALA (68.6, 147.9)

[5] 75 HIS (-178.0, -57.6)

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 6



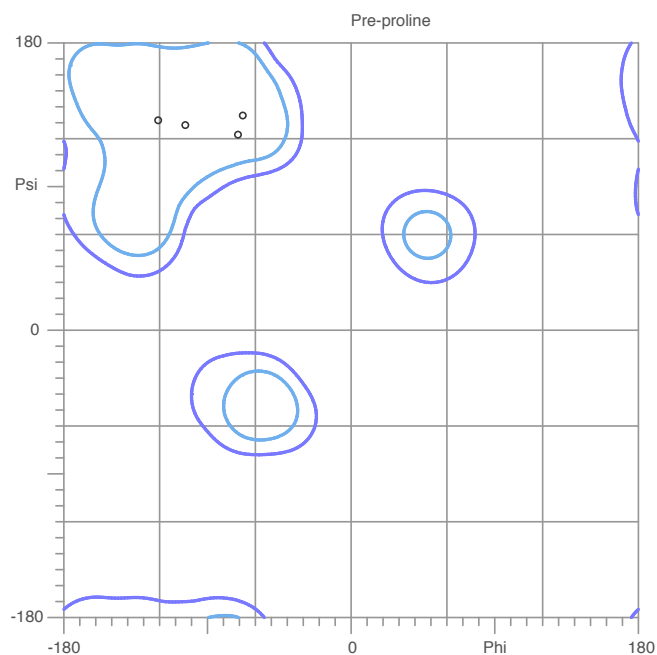
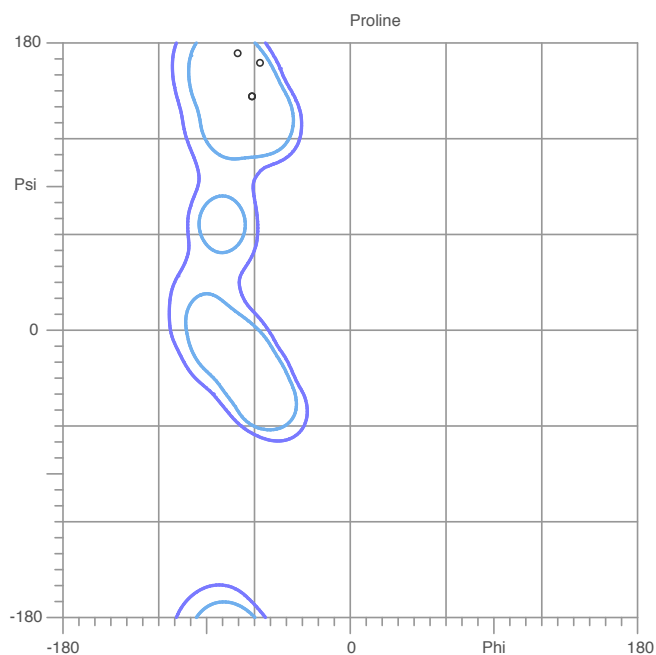
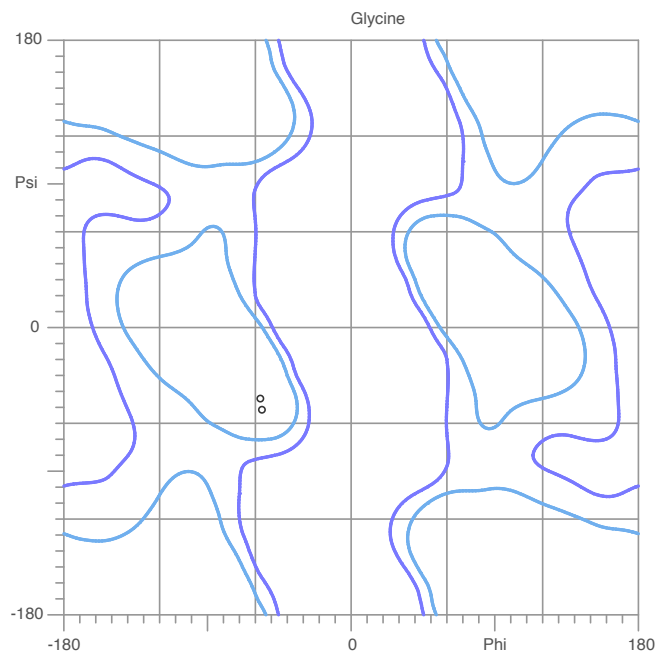
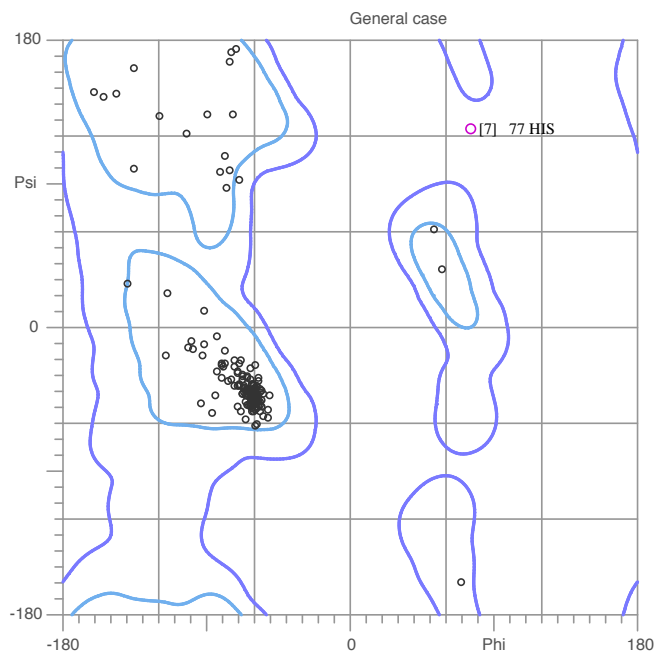
91.0% (142/156) of all residues were in favored (98%) regions.
98.1% (153/156) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 3 ILE (56.3, 93.1)
- [6] 79 HIS (-179.4, -38.4)
- [6] 166 HIS (173.3, -24.5)

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 7



97.4% (152/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

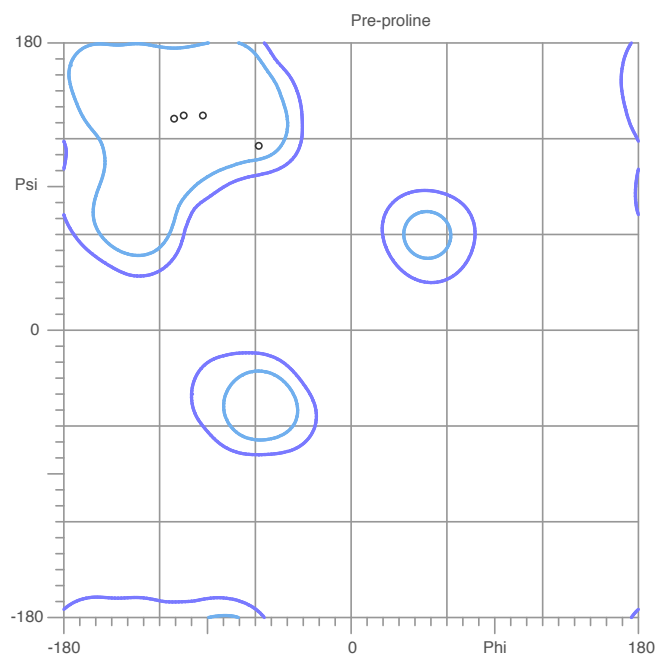
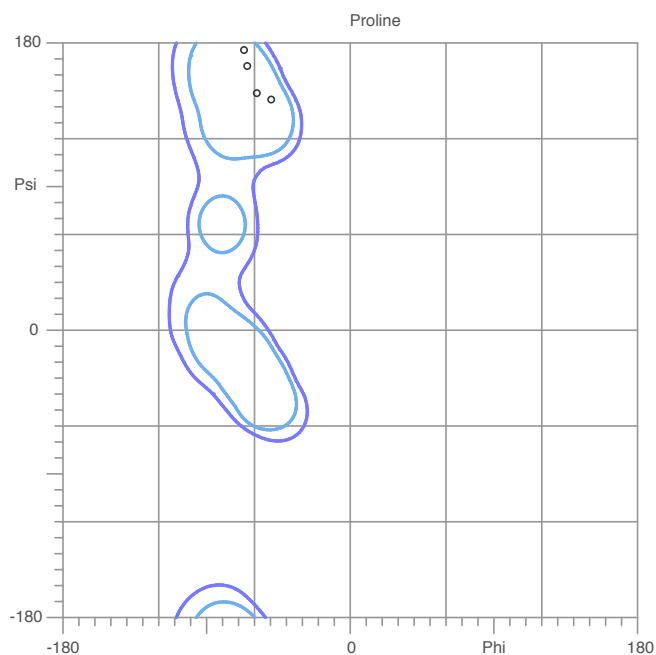
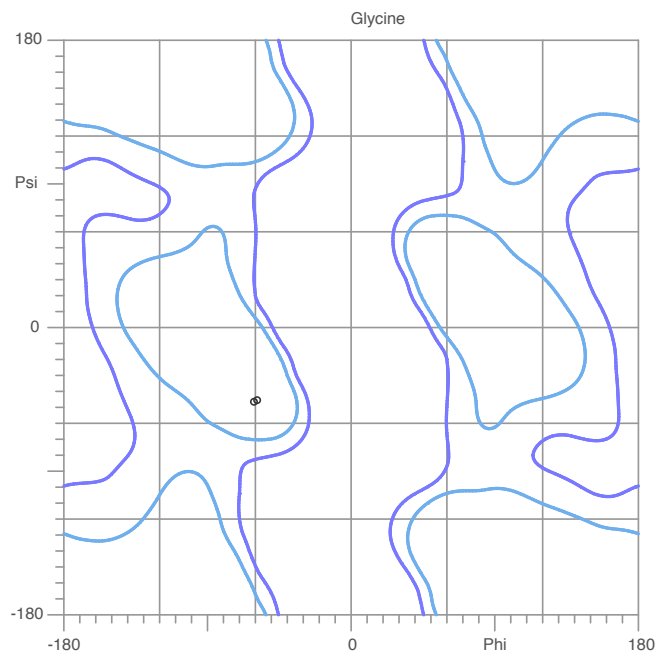
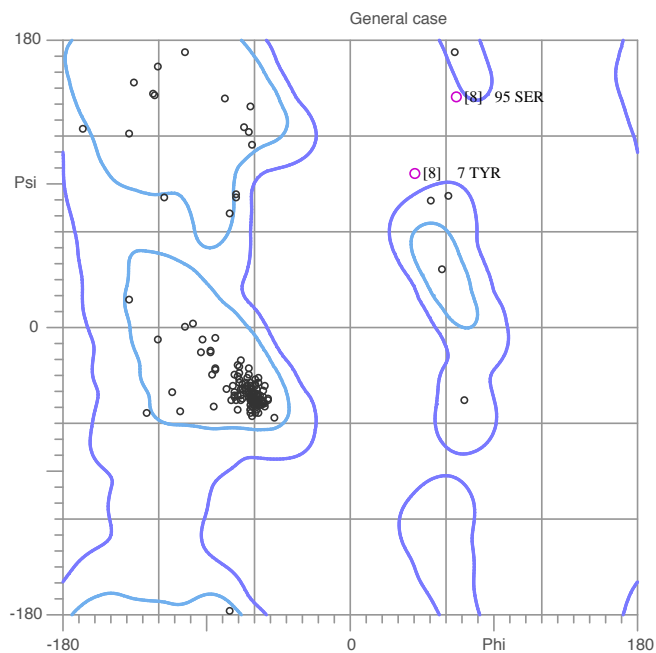
There were 1 outliers (phi, psi):
[7] 77 HIS (75.1, 125.6)

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MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 8



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.

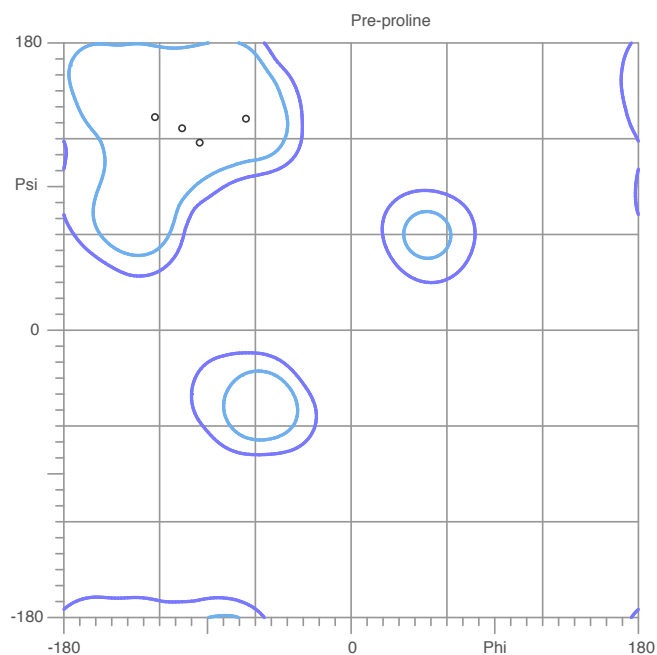
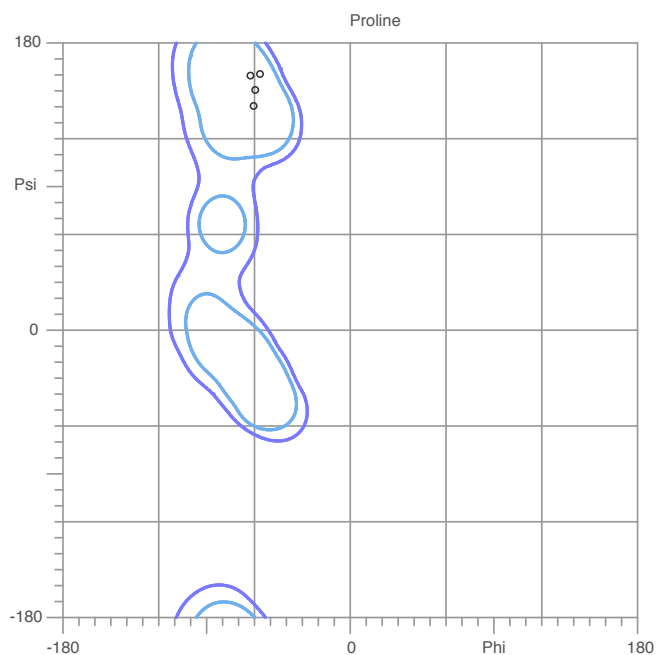
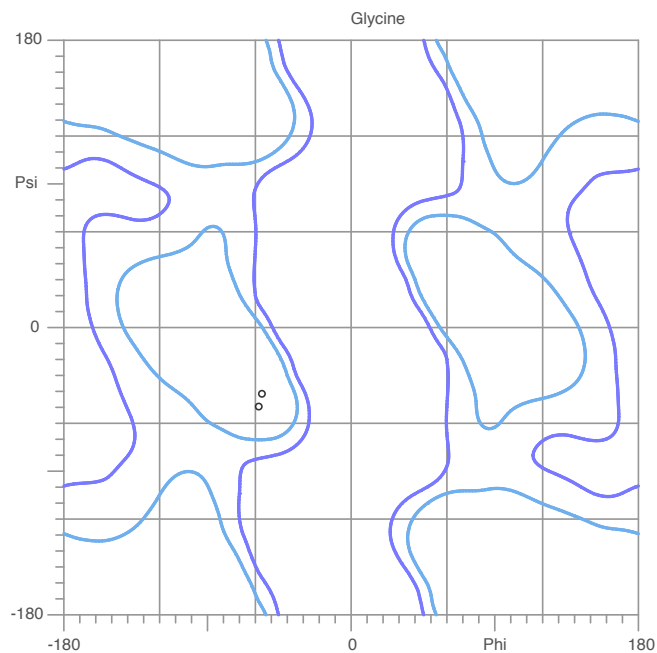
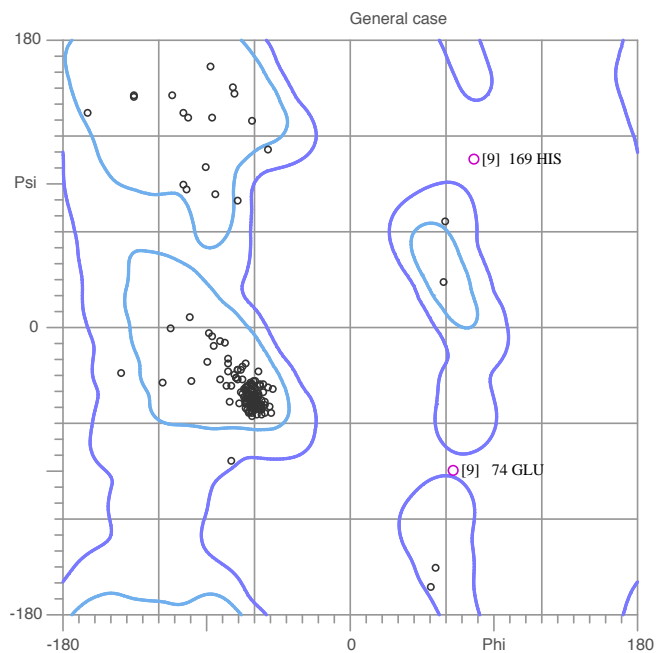
There were 2 outliers (phi, psi):

[8] 7 TYR (40.0, 97.3)

[8] 95 SER (66.4, 145.9)

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 9



94.2% (147/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

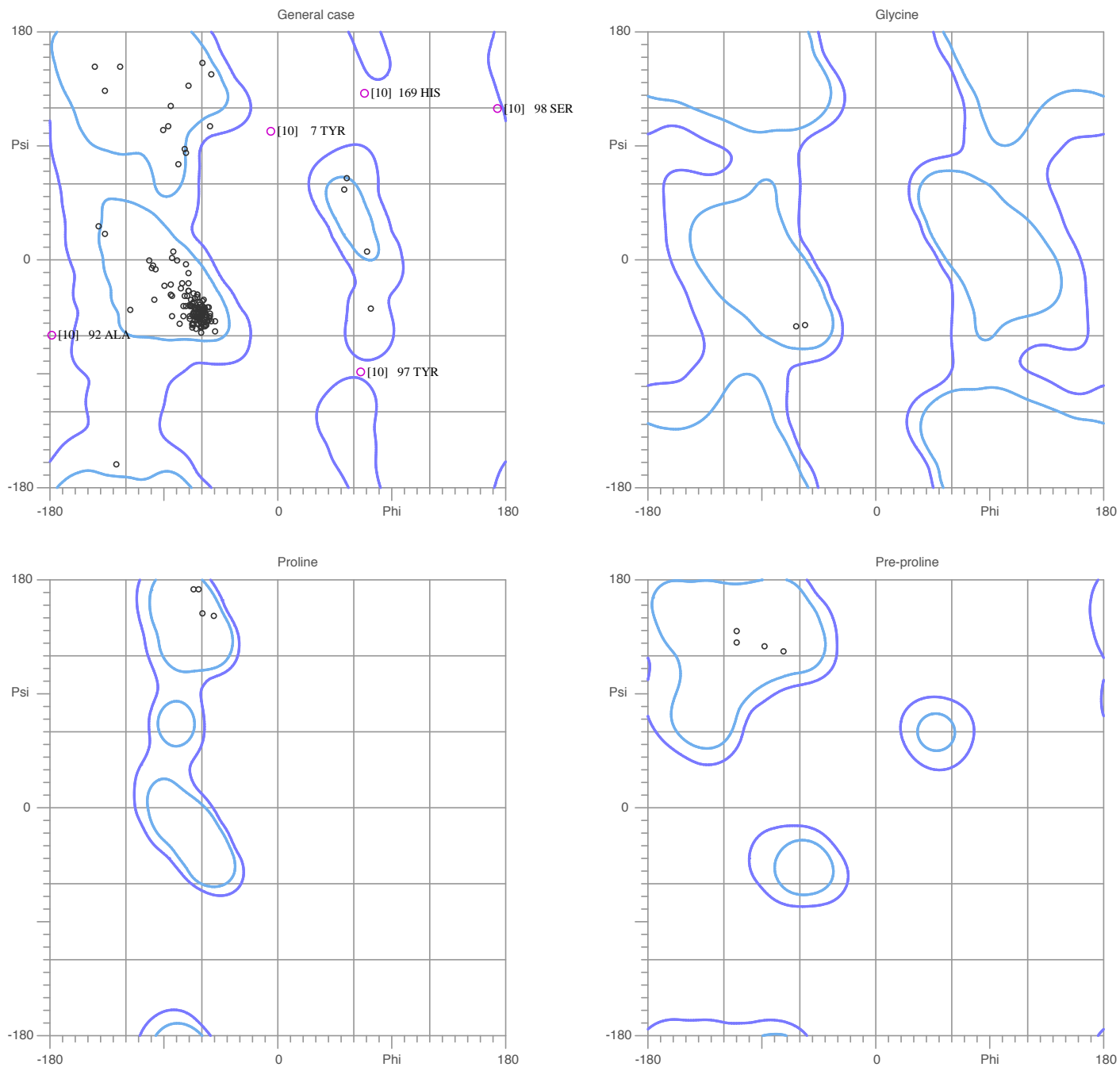
There were 2 outliers (phi, psi):

[9] 74 GLU (64.4, -89.4)

[9] 169 HIS (77.8, 106.3)

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 10



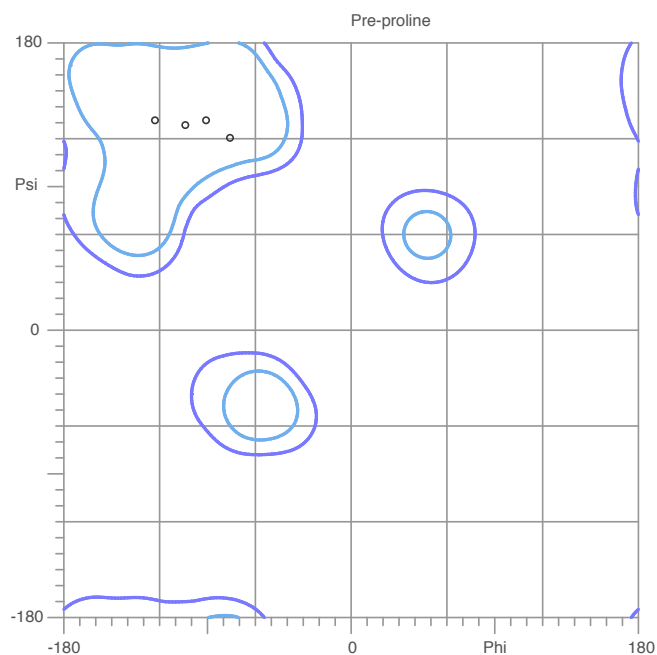
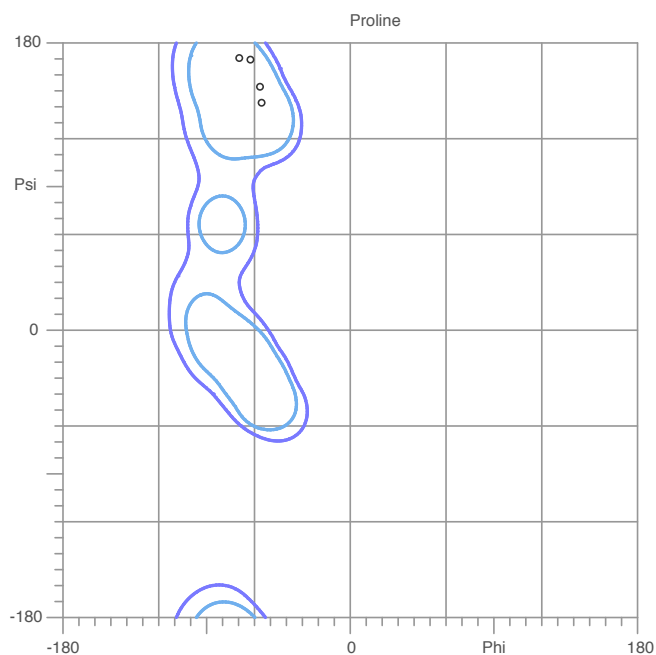
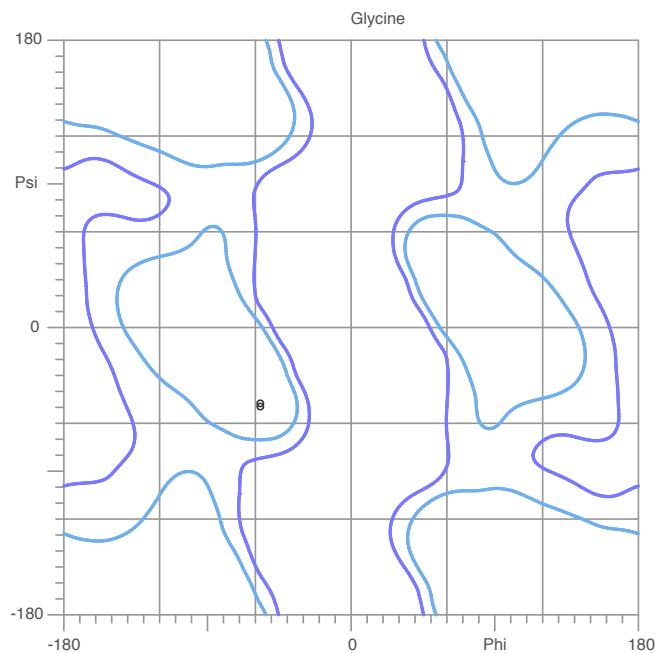
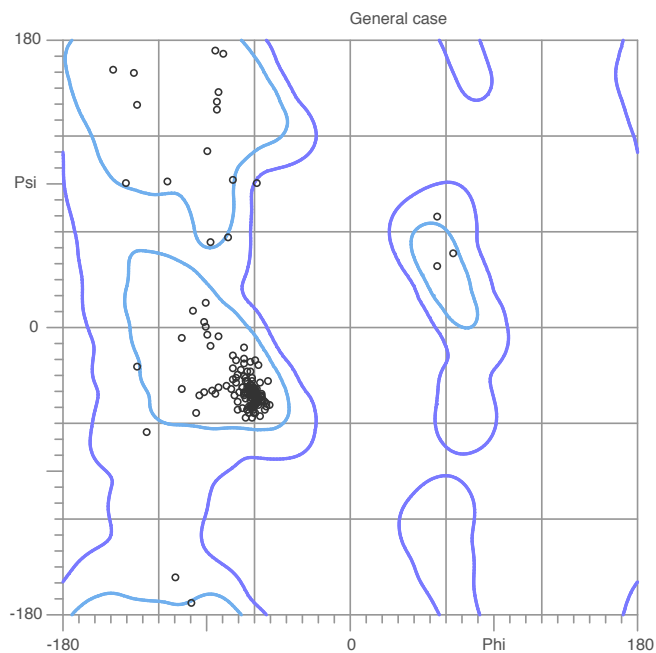
92.9% (145/156) of all residues were in favored (98%) regions.
96.8% (151/156) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[10] 7 TYR (-6.6, 102.5)
[10] 92 ALA (-179.9, -59.9)
[10] 97 TYR (65.1, -88.5)
[10] 98 SER (173.1, 120.5)
[10] 169 HIS (68.3, 132.8)

MolProbity Ramachandran analysis

SOR77_NMR_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.

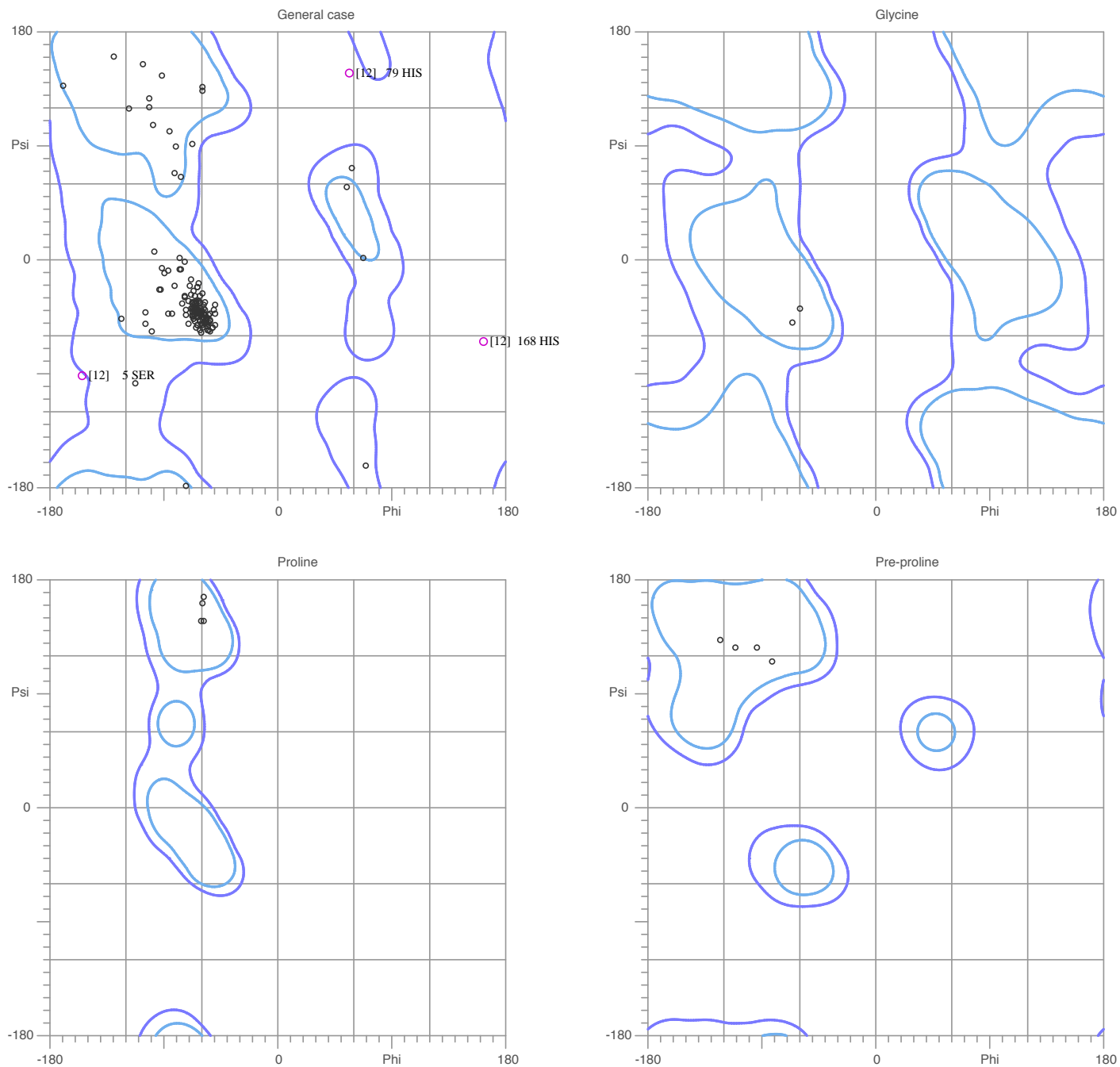
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 12



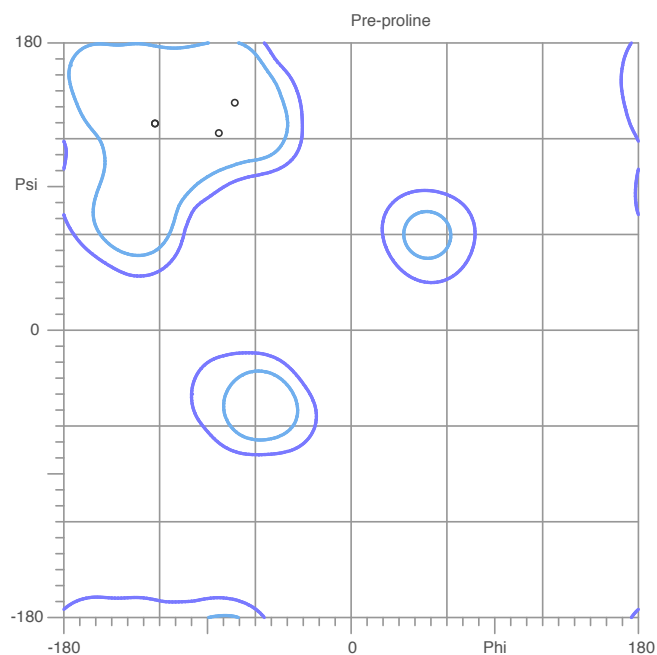
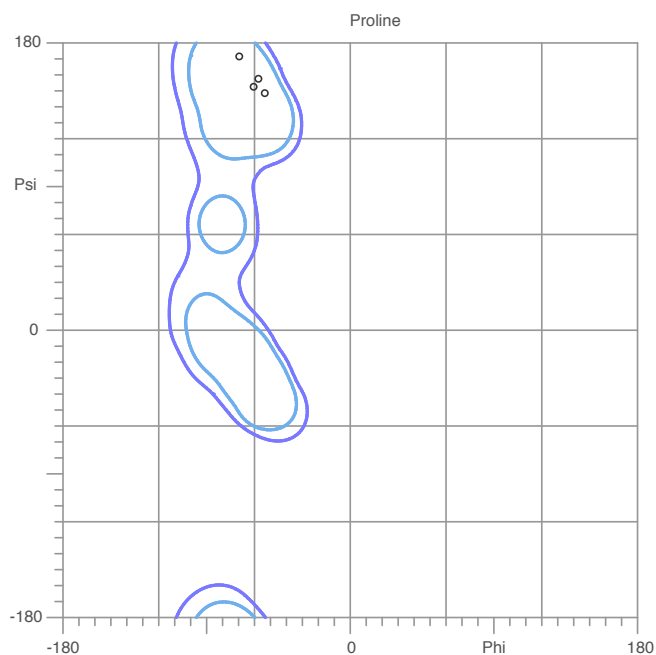
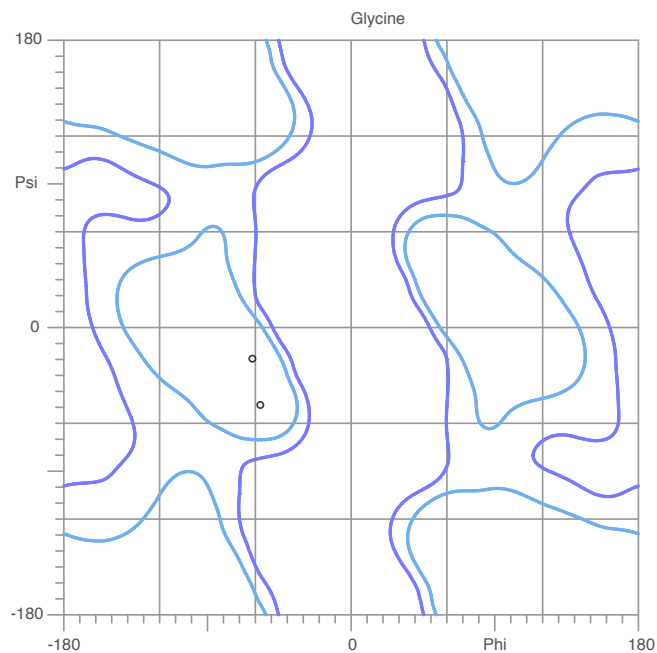
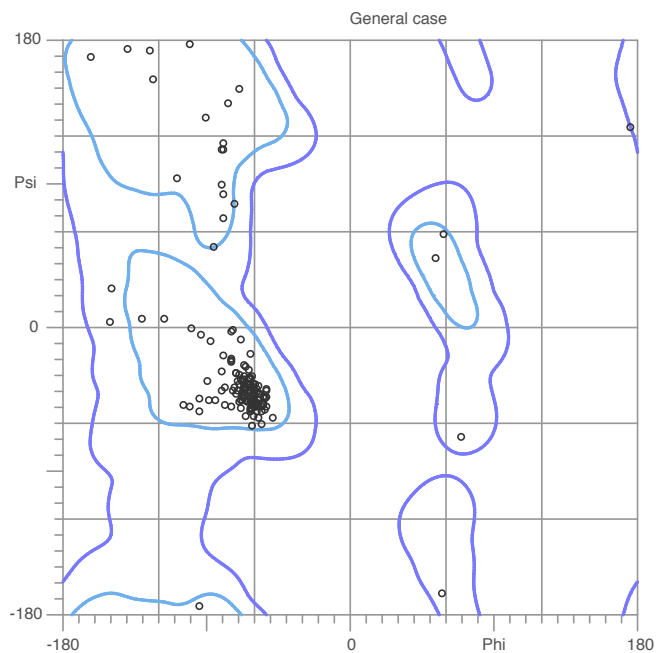
95.5% (149/156) of all residues were in favored (98%) regions.
98.1% (153/156) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [12] 5 SER (-155.1, -91.4)
- [12] 79 HIS (56.7, 148.8)
- [12] 168 HIS (162.4, -64.5)

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 13



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.

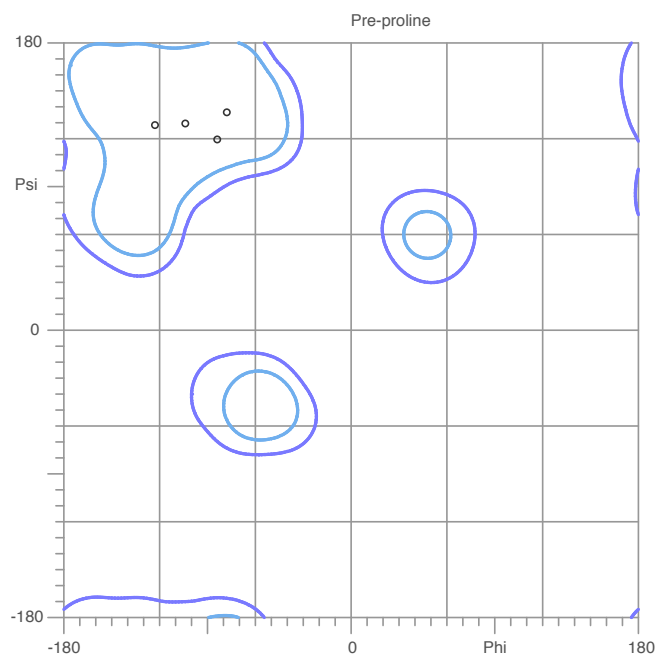
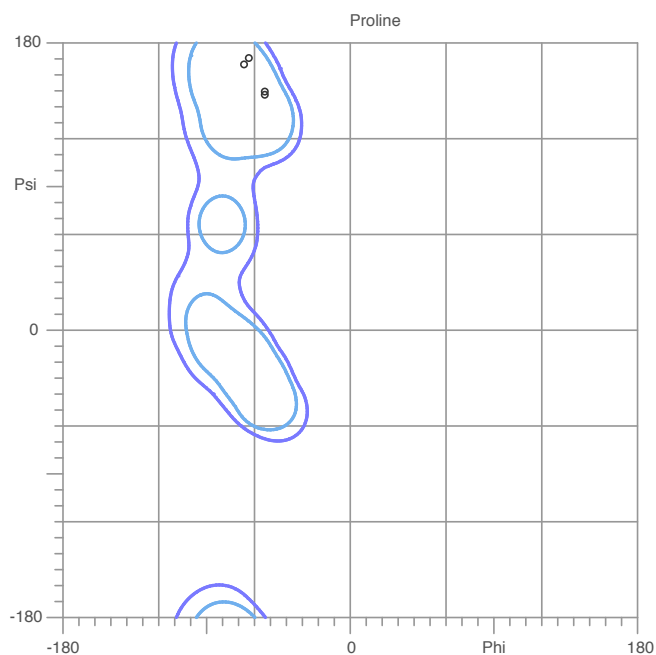
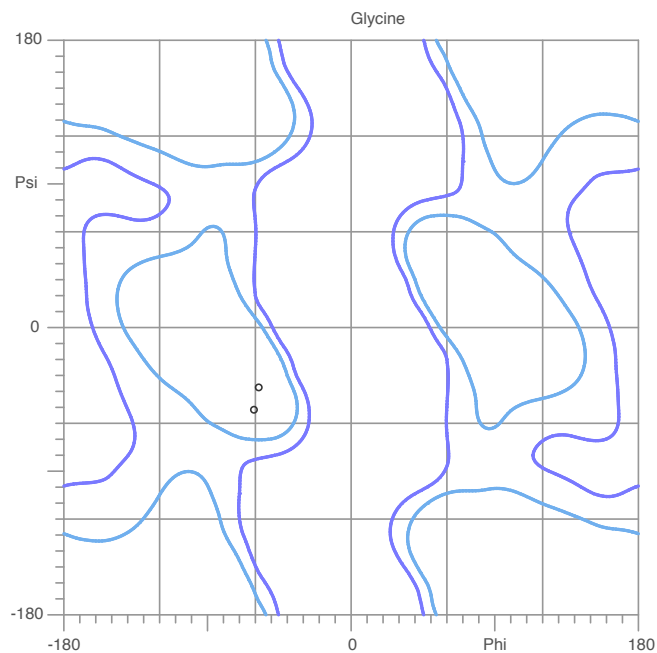
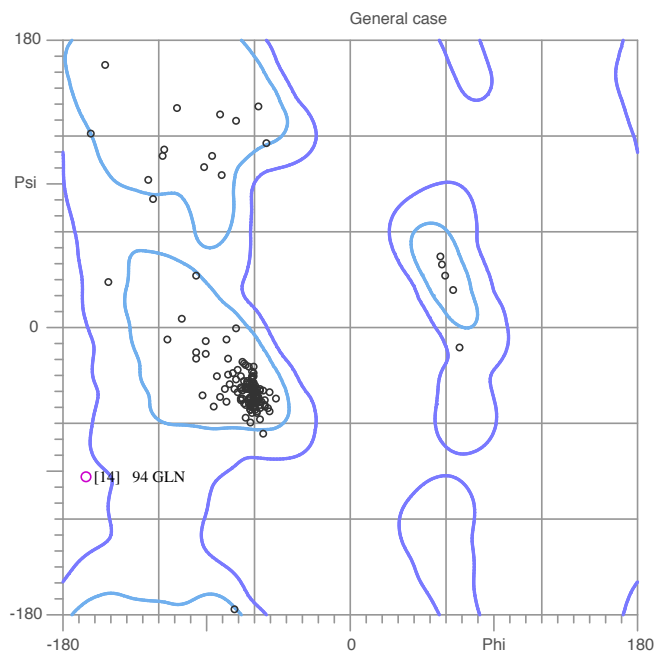
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 14



96.2% (150/156) of all residues were in favored (98%) regions.
99.4% (155/156) of all residues were in allowed (>99.8%) regions.

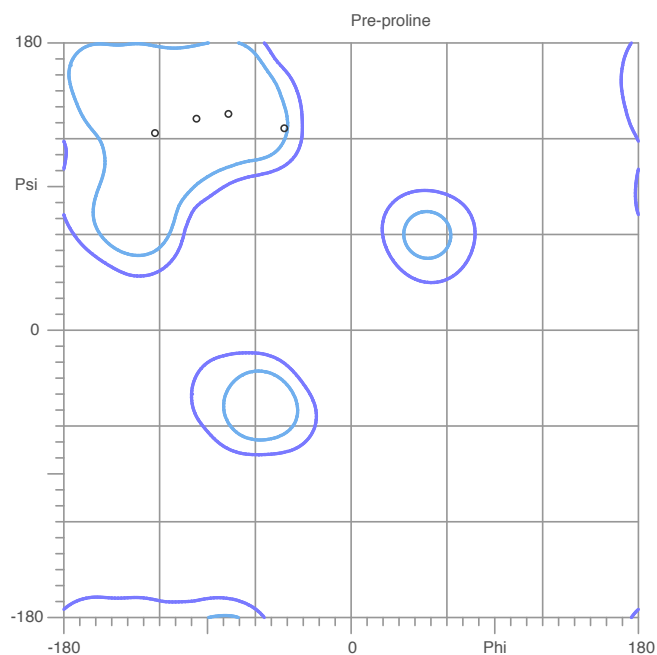
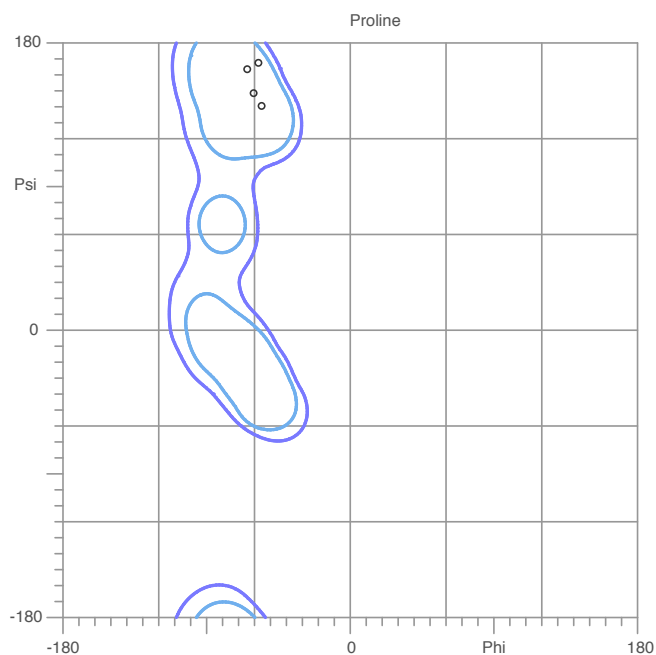
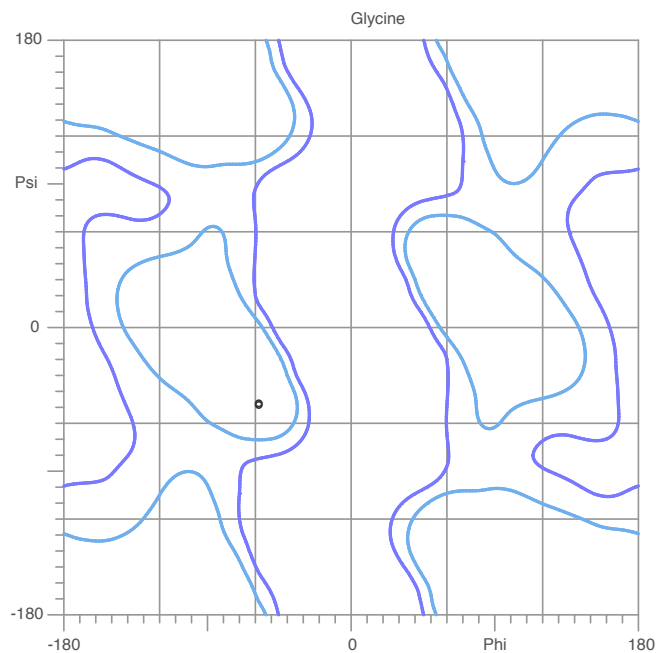
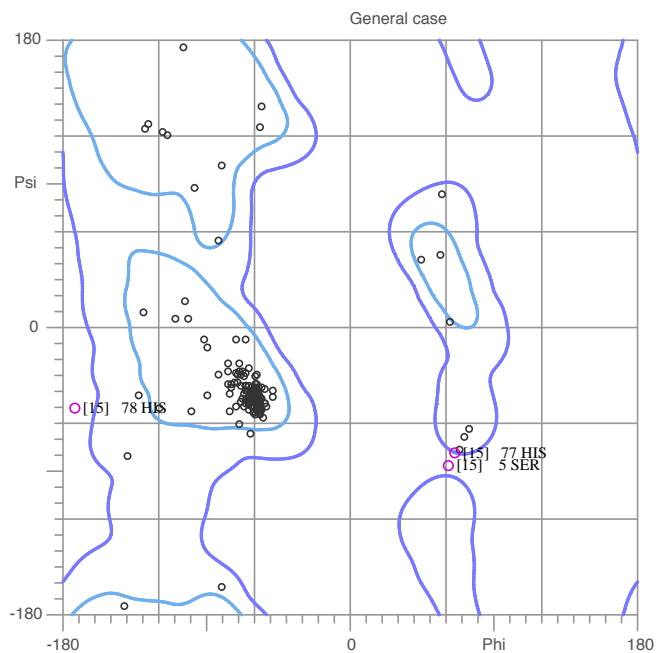
There were 1 outliers (phi, psi):
[14] 94 GLN (-166.5, -93.7)

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MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 15



92.3% (144/156) 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):

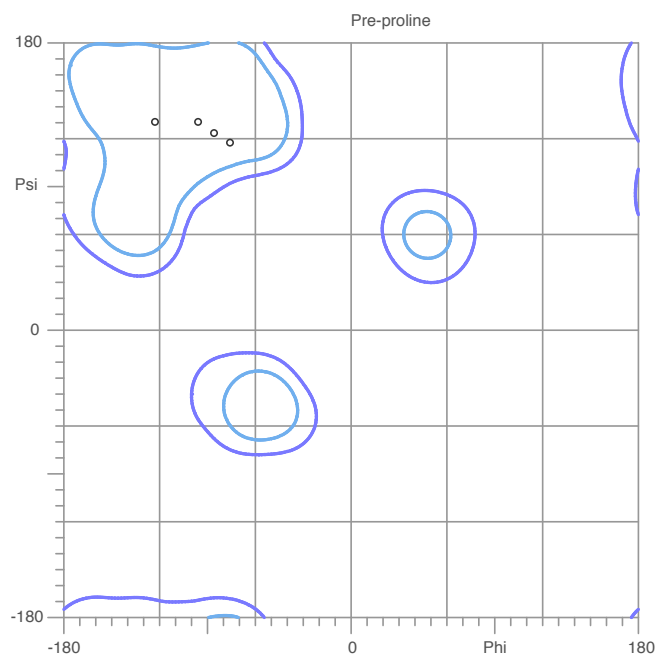
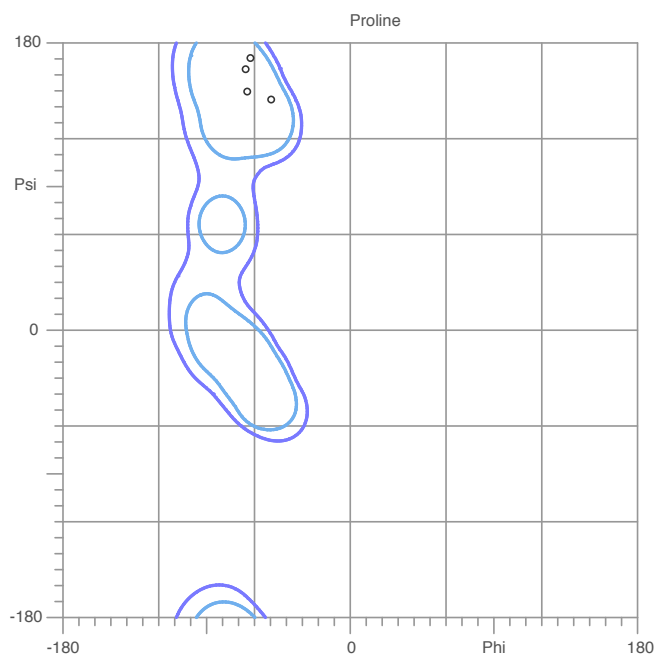
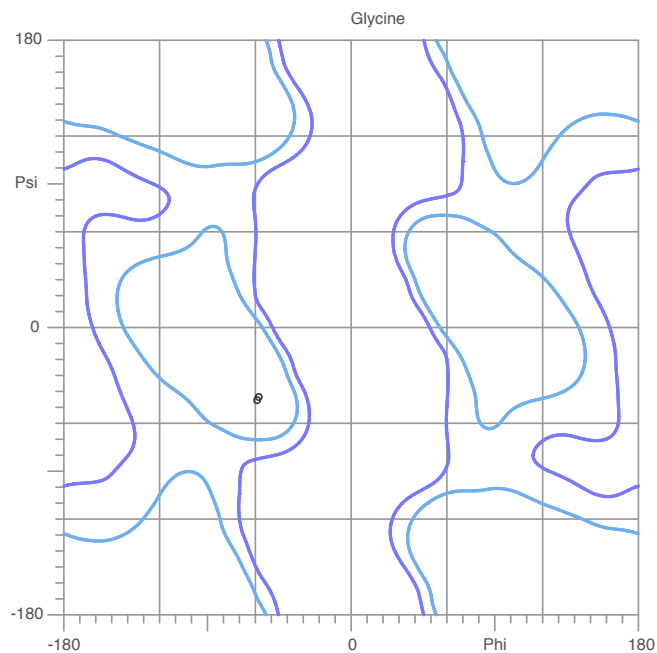
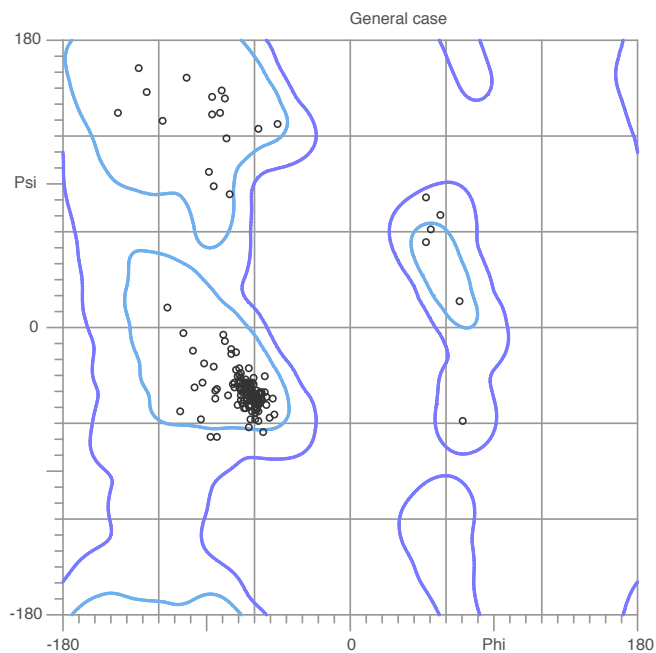
[15] 5 SER (61.2, -86.3)

[15] 77 HIS (65.6, -78.8)

[15] 78 HIS (-173.6, -50.6)

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 16



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.

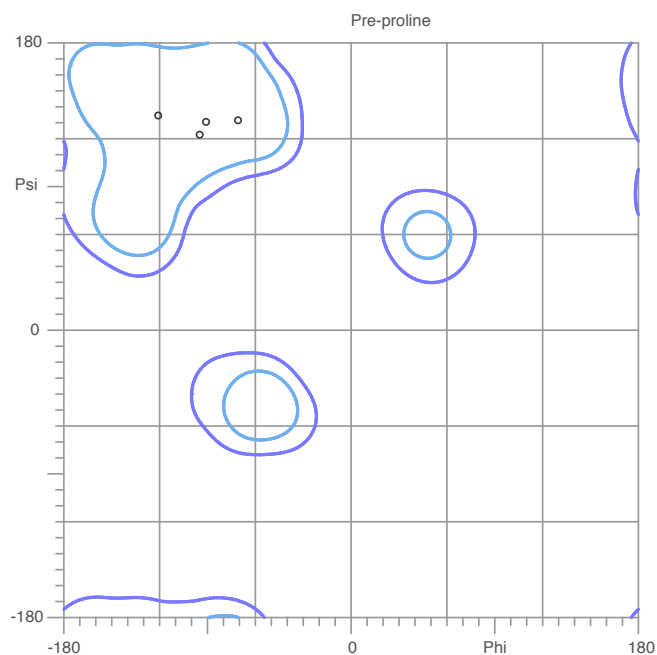
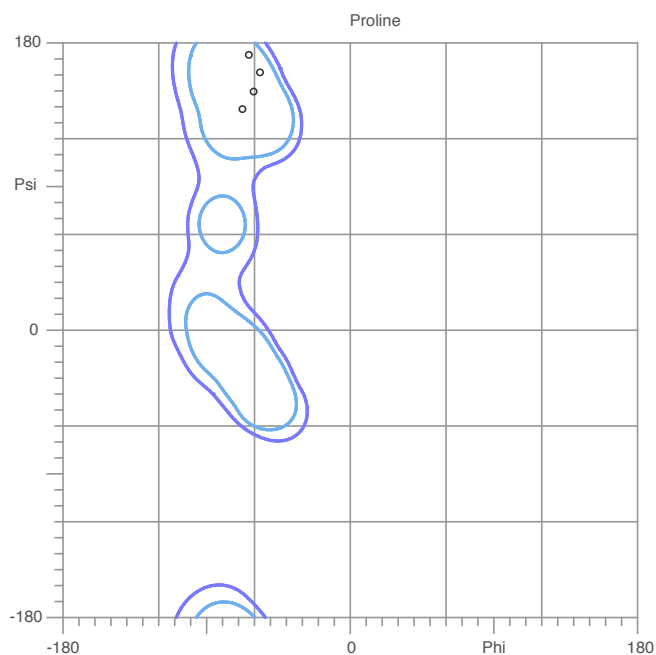
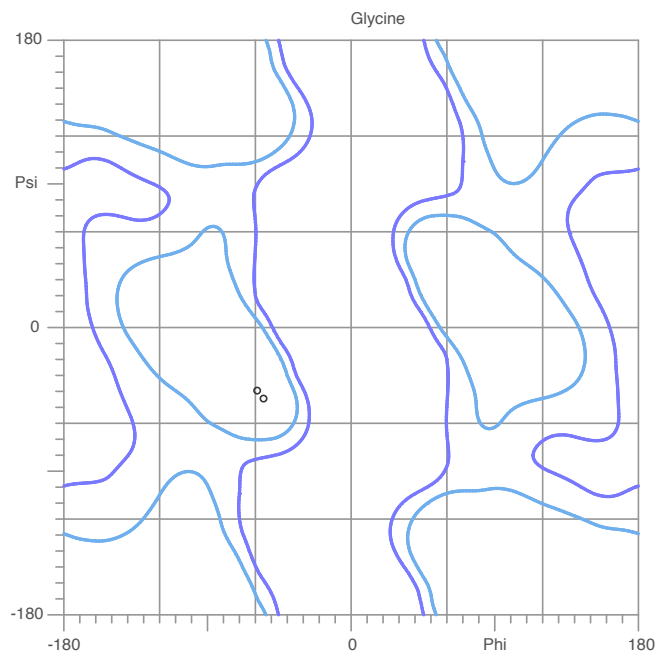
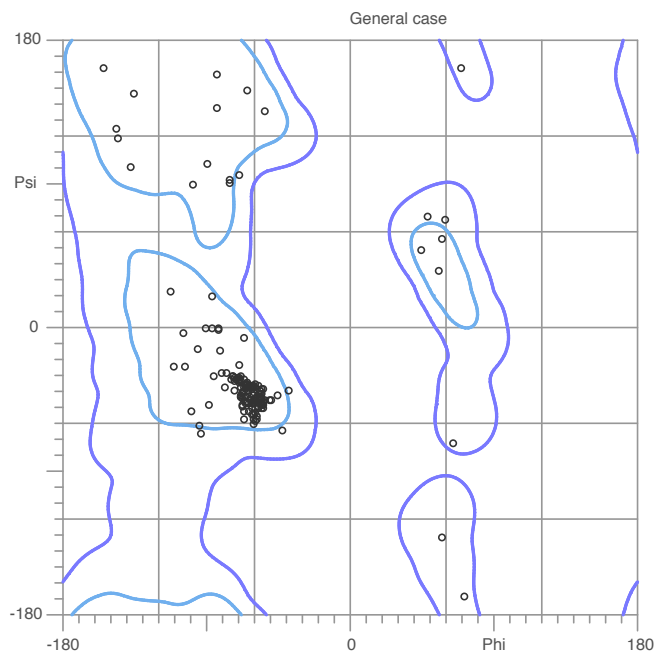
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 17



93.6% (146/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

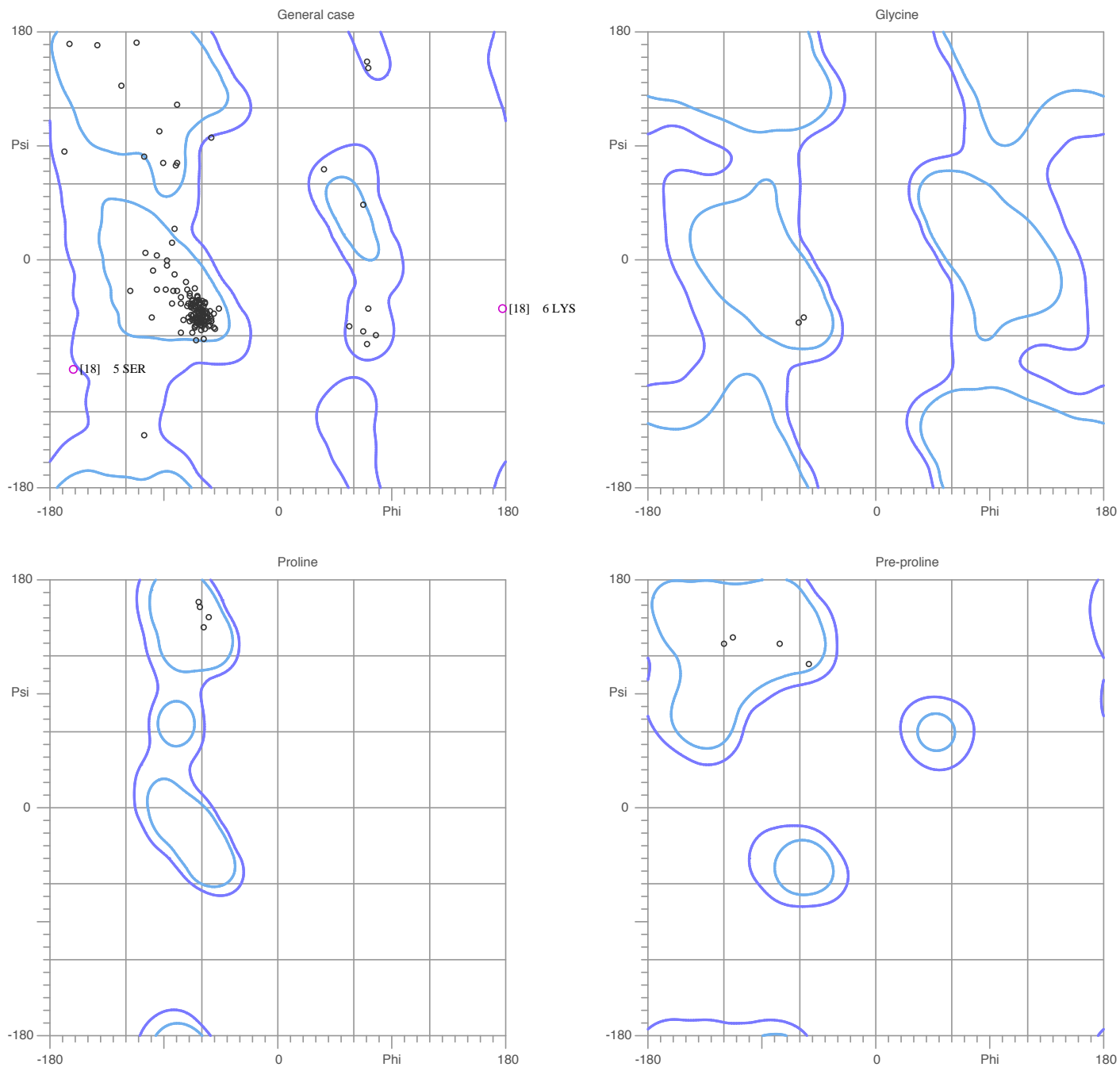
There were no outliers.

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

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MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 18



90.4% (141/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

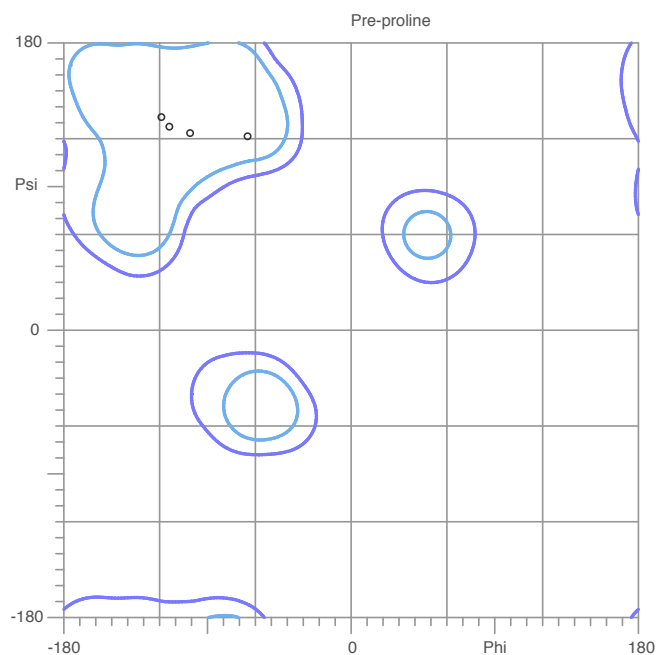
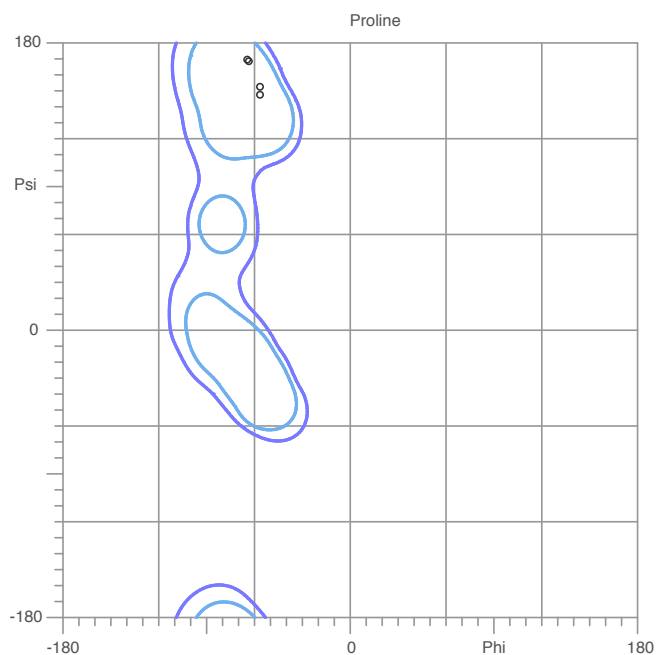
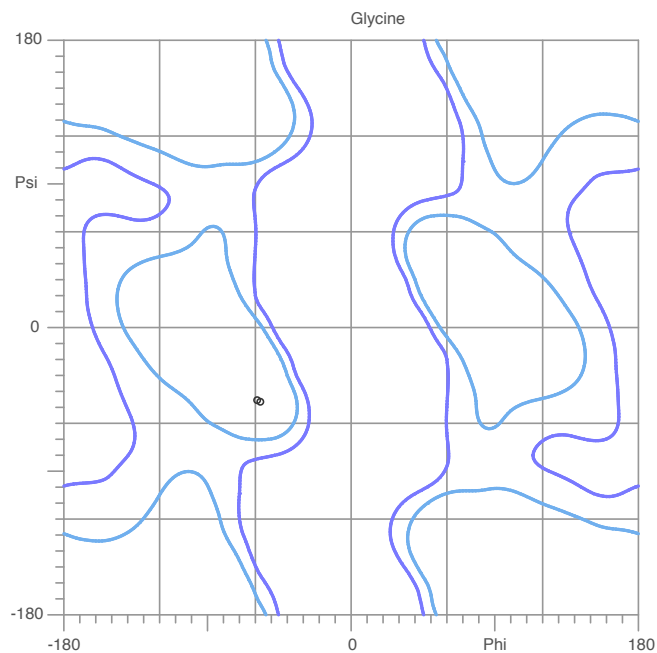
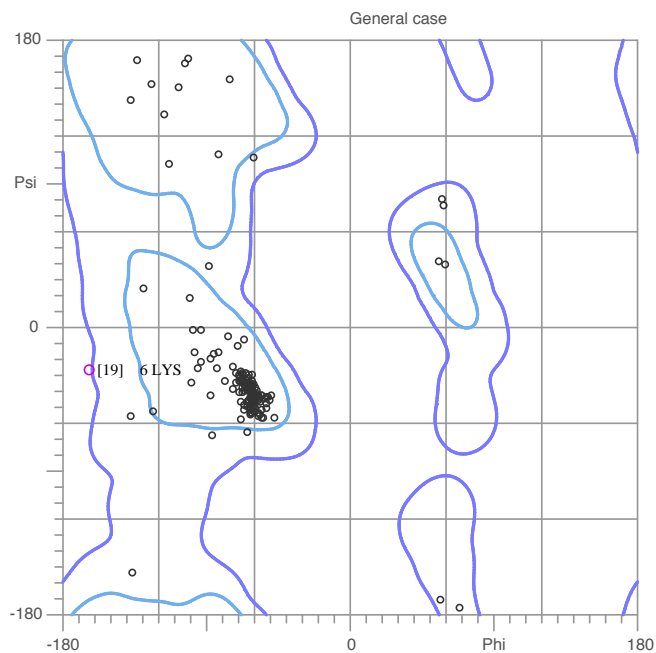
There were 2 outliers (phi, psi):

[18] 5 SER (-162.4, -86.1)

[18] 6 LYS (177.2, -38.5)

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 19



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.

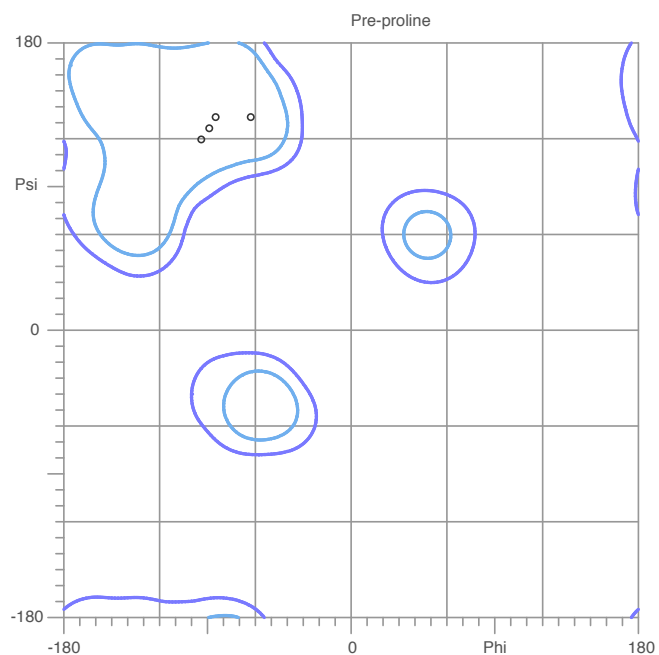
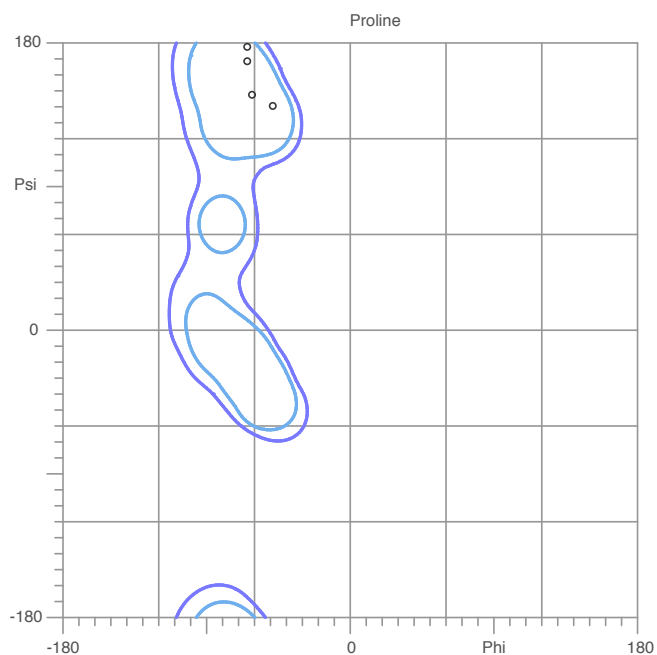
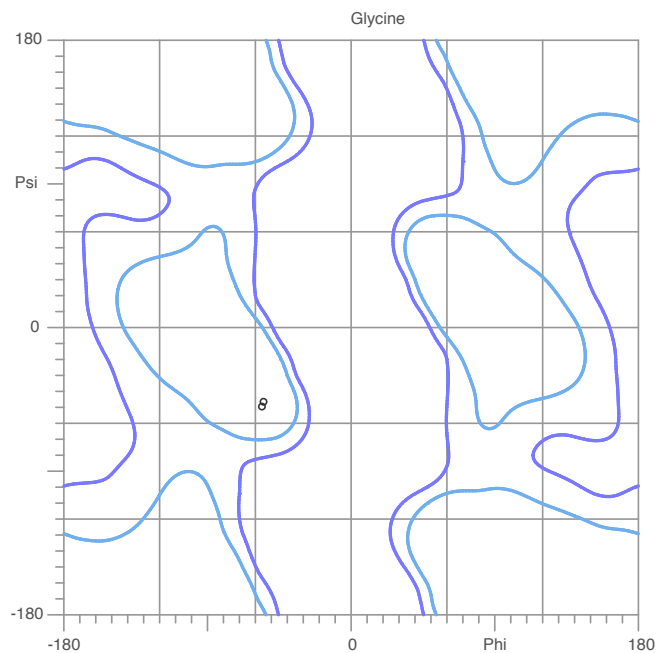
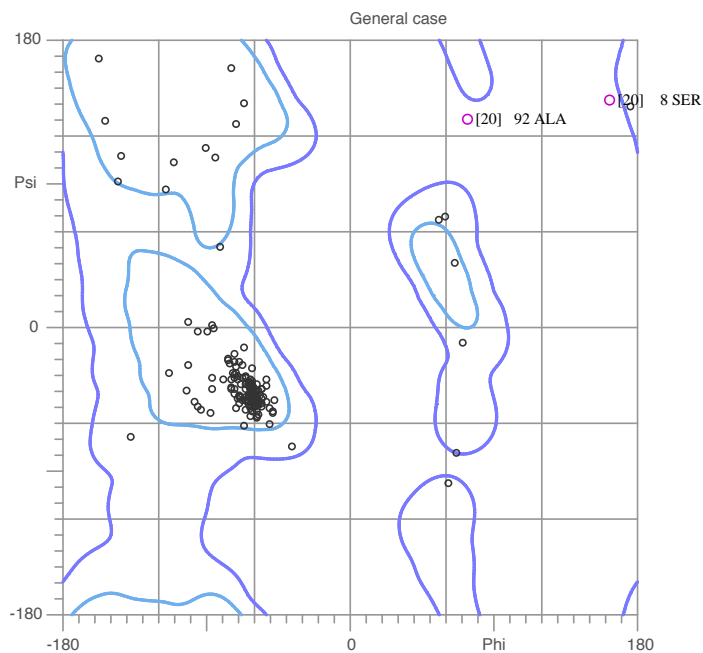
There were 1 outliers (phi, psi):
[19] 6 LYS (-164.3, -26.6)

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

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

MolProbity Ramachandran analysis

SOR77_NMR_em_bcr3.pdb, model 20



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):
[20] 8 SER (162.6, 143.2)
[20] 92 ALA (73.3, 131.9)