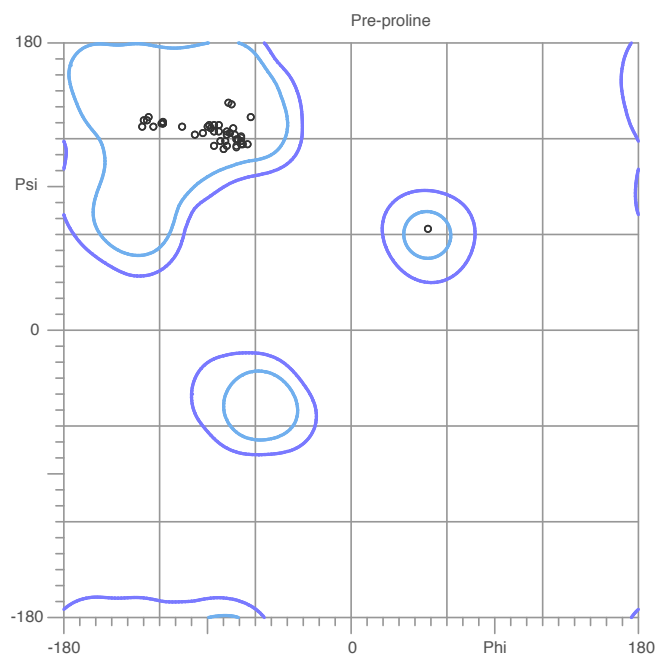
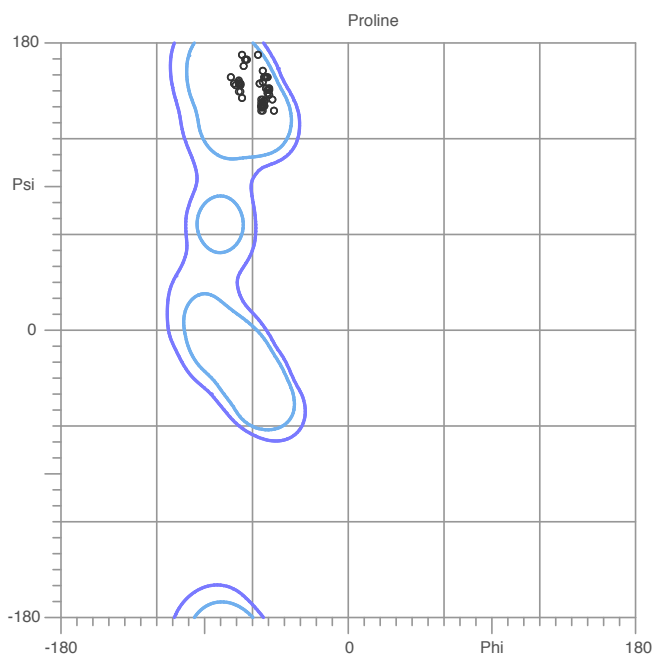
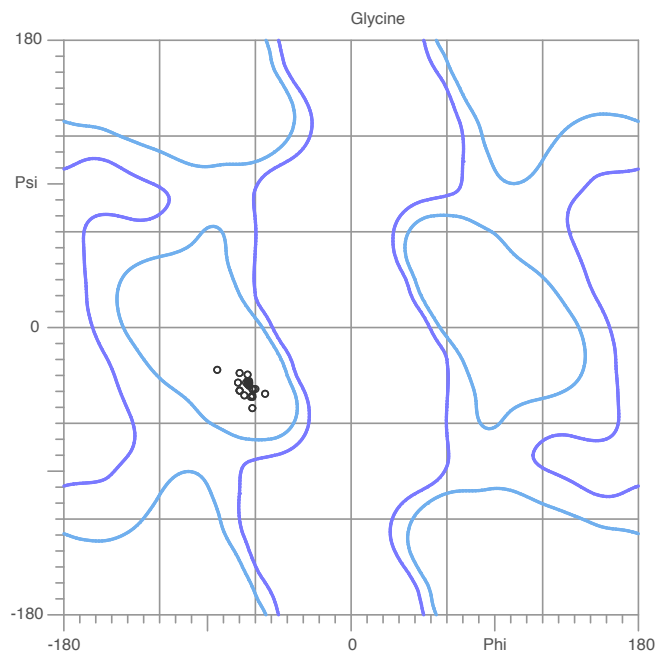
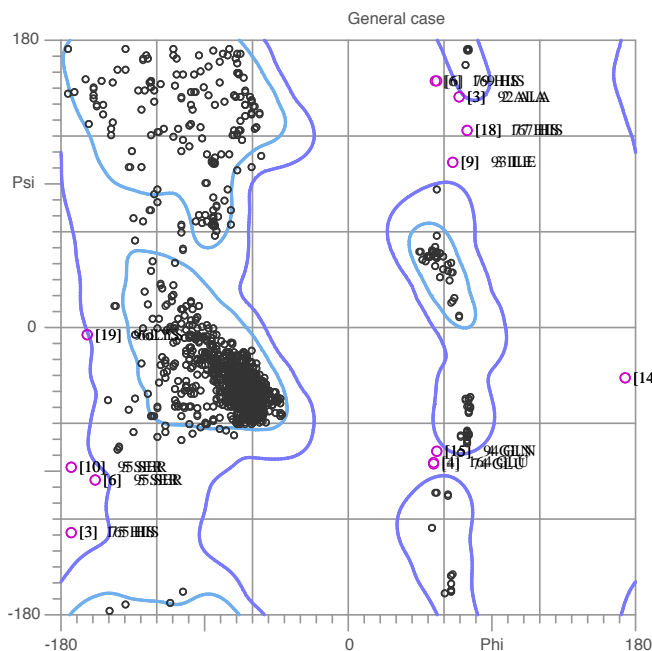


MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, all models



95.4% (2976/3120) of all residues were in favored (98%) regions.
99.3% (3098/3120) of all residues were in allowed (>99.8%) regions.

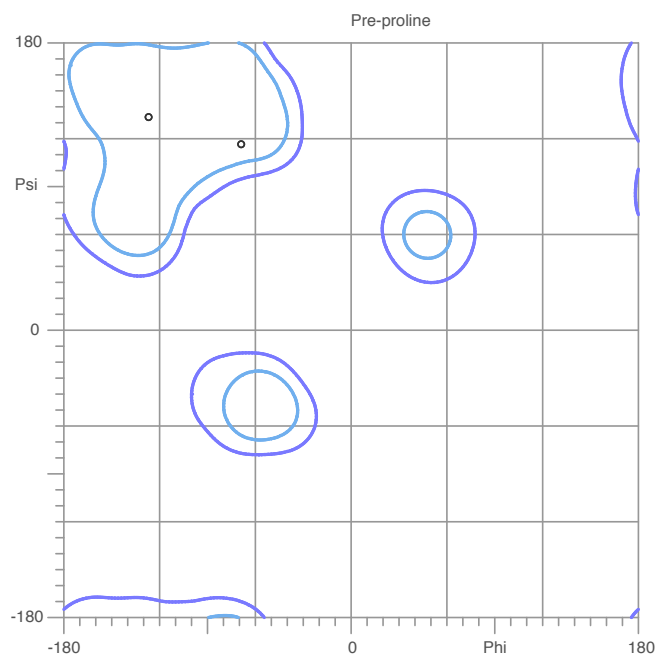
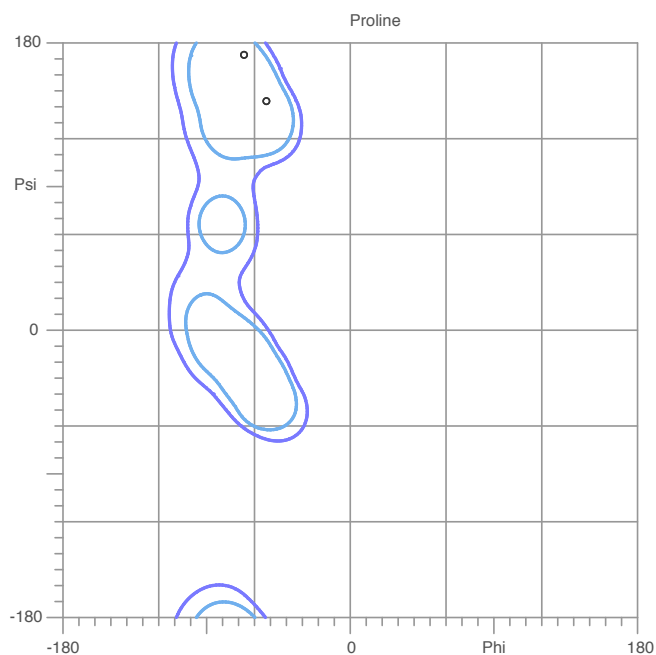
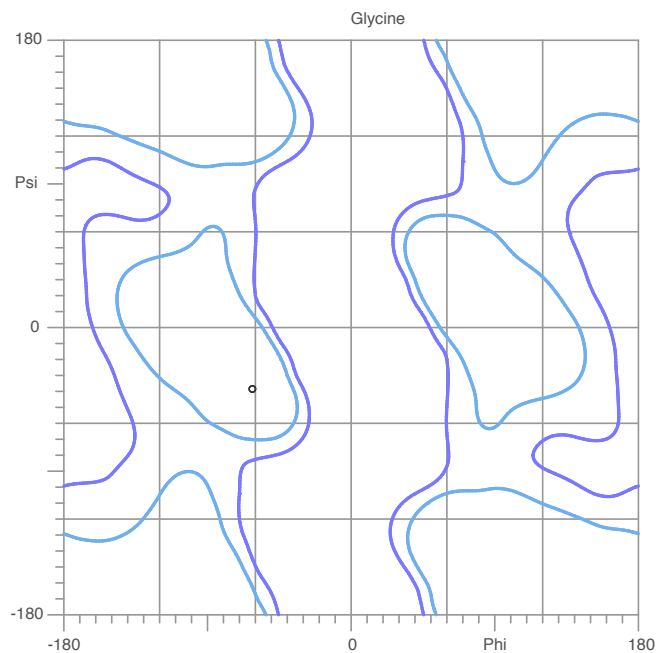
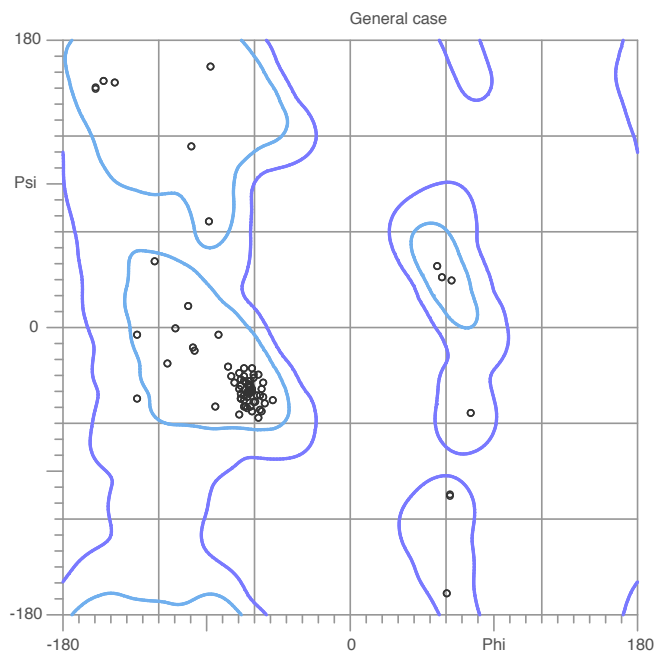
There were 22 outliers (phi, psi):

- [3] 2 ALA (69.3, 145.1)
- [3] 75 HIS (-174.8, -128.6)
- [3] 92 ALA (69.4, 145.0)
- [3] 165 HIS (-174.8, -128.7)
- [4] 74 GLU (53.3, -85.1)
- [4] 164 GLU (53.1, -85.0)
- [6] 5 SER (-160.0, -95.1)
- [6] 79 HIS (54.9, 155.2)
- [6] 95 SER (-159.9, -95.1)

- [6] 169 HIS (55.0, 155.1)
- [9] 3 ILE (65.1, 104.9)
- [9] 93 ILE (65.1, 104.8)
- [10] 5 SER (-174.1, -87.7)
- [10] 95 SER (-174.2, -87.8)
- [14] 79 HIS (173.6, -31.7)
- [14] 169 HIS (173.7, -31.8)
- [15] 4 GLN (55.0, -77.8)
- [15] 94 GLN (55.1, -77.8)
- [18] 77 HIS (75.0, 125.0)
- [18] 167 HIS (75.0, 124.9)
- [19] 6 LYS (-164.3, -4.7)
- [19] 96 LYS (-164.3, -4.7)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 1



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.

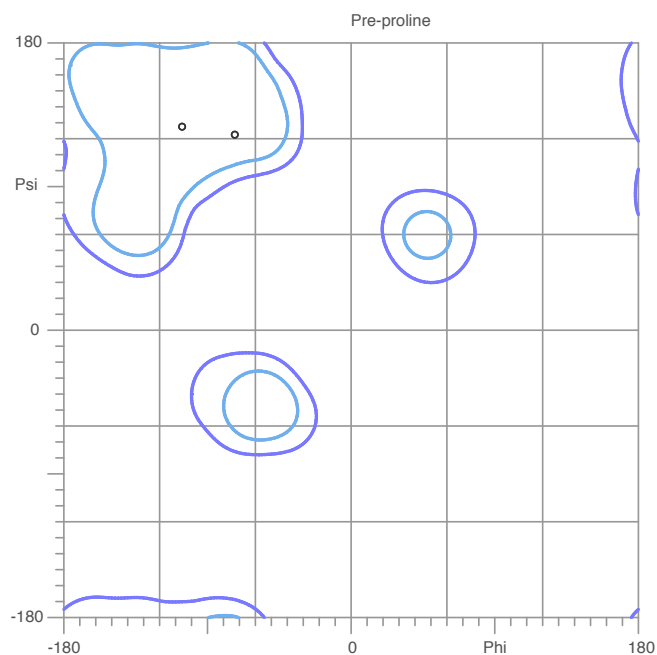
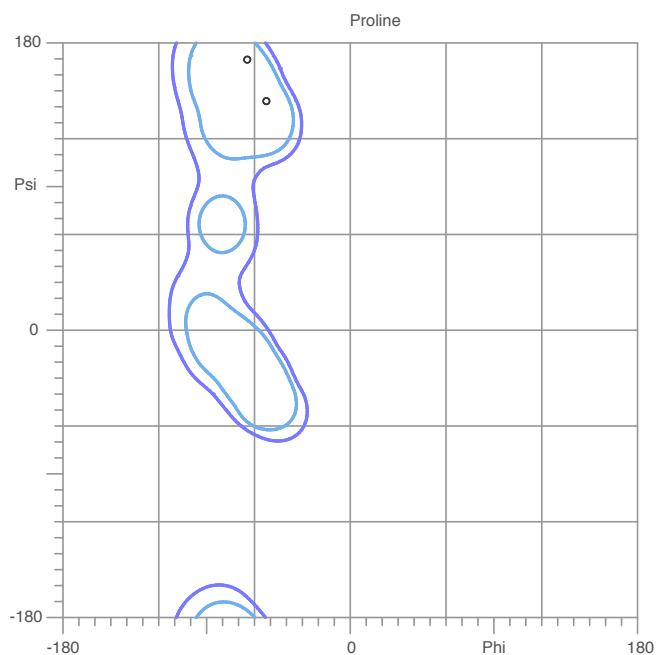
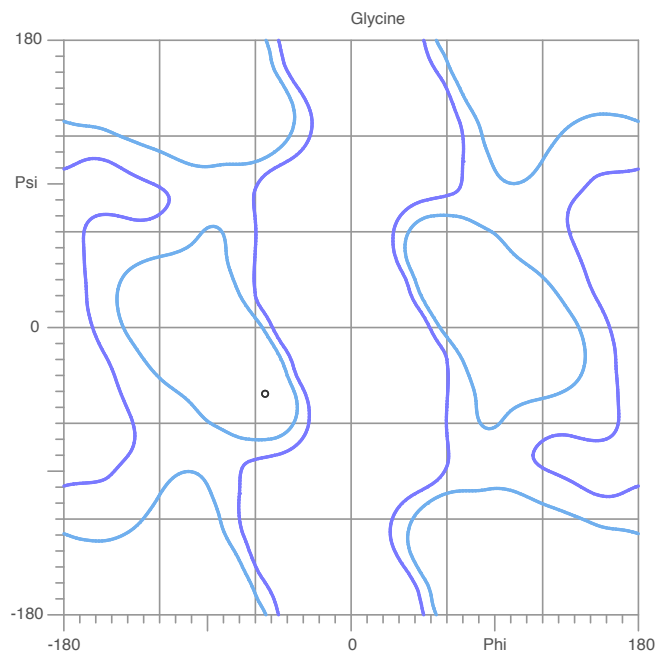
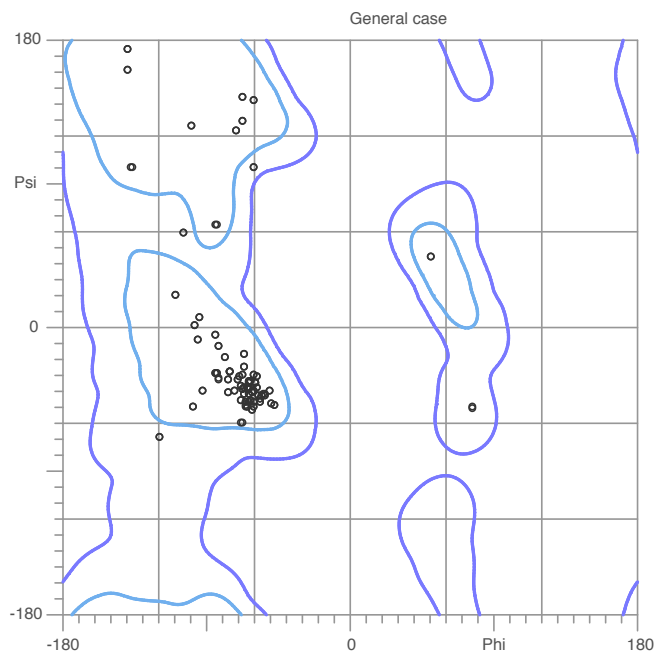
There were no outliers.

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

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MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 2



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.

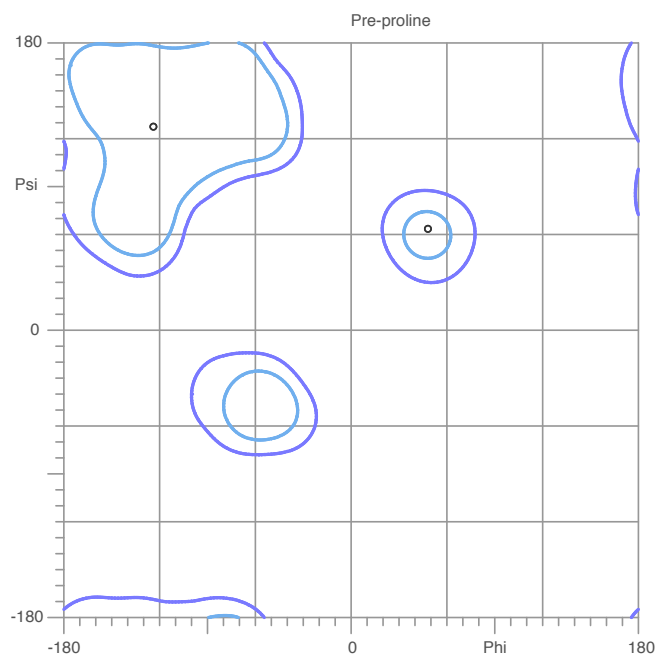
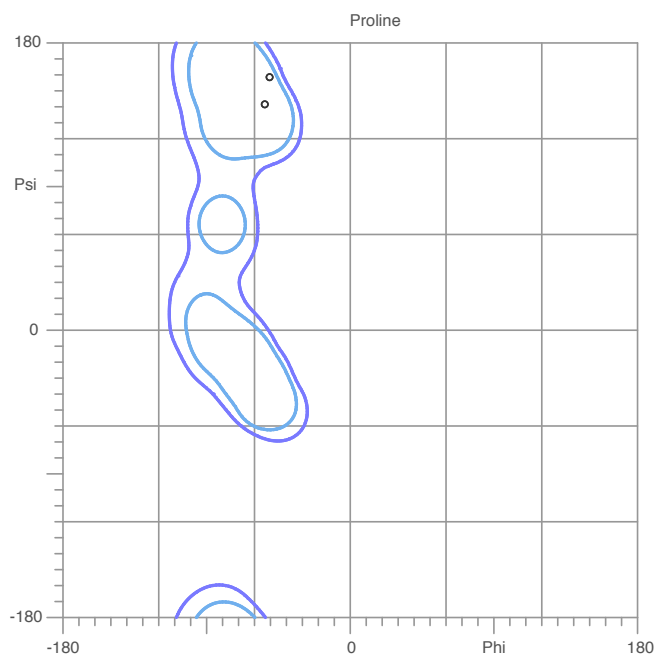
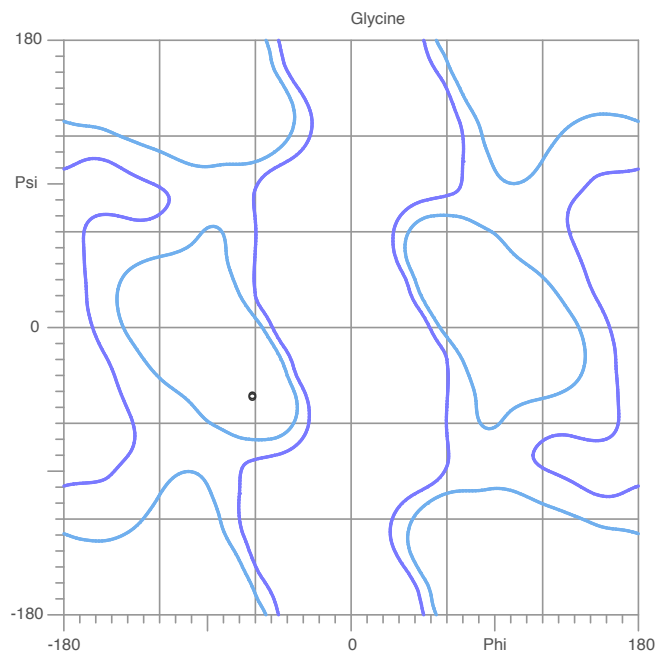
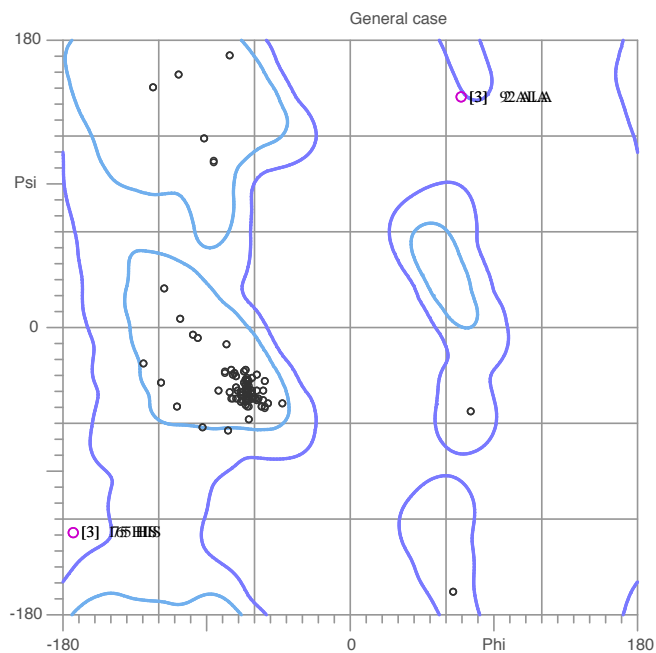
There were no outliers.

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

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MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 3



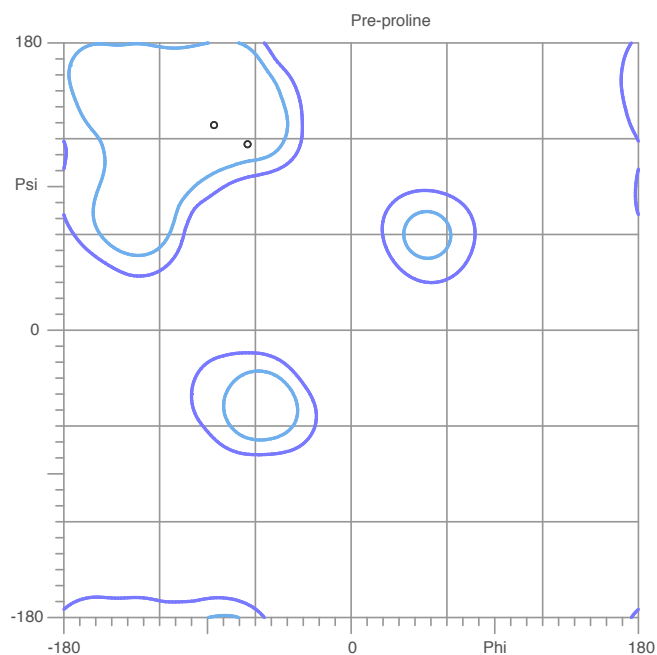
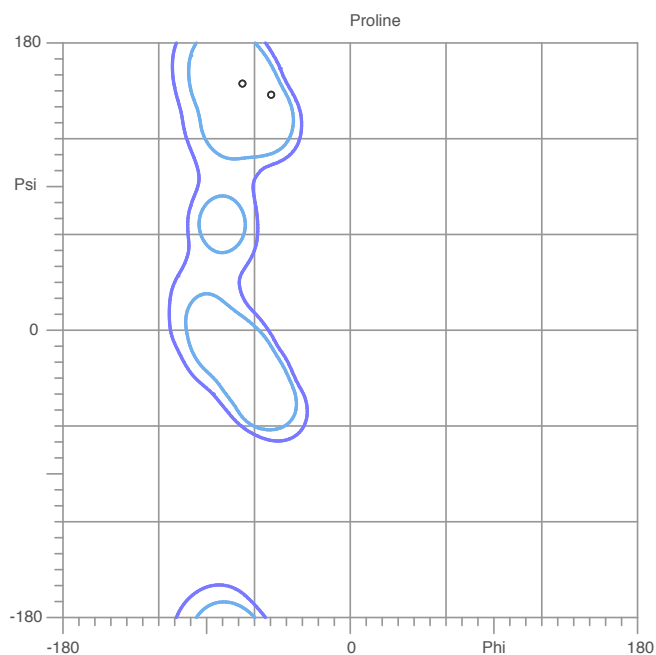
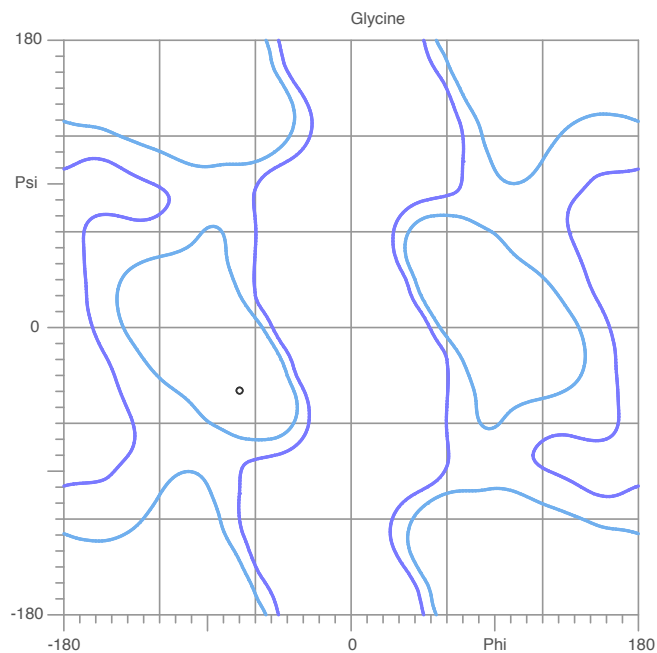
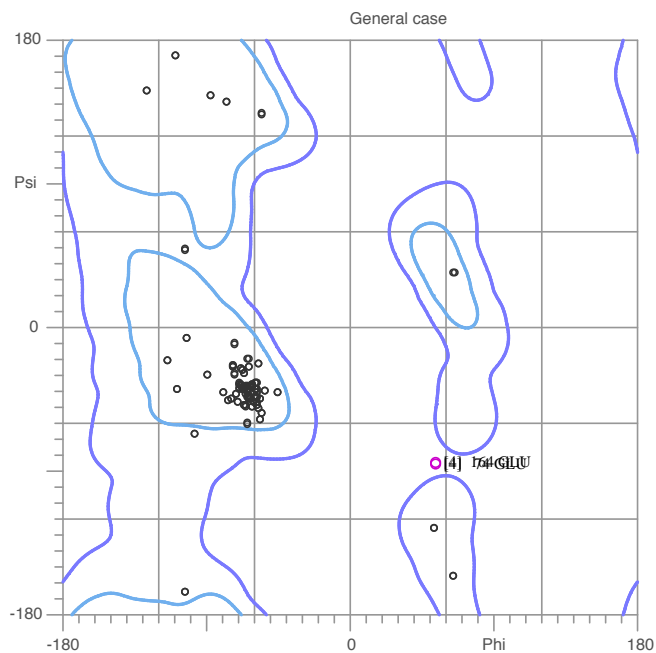
93.6% (146/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [3] 2 ALA (69.3, 145.1)
- [3] 75 HIS (-174.8, -128.6)
- [3] 92 ALA (69.4, 145.0)
- [3] 165 HIS (-174.8, -128.7)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 4



92.3% (144/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

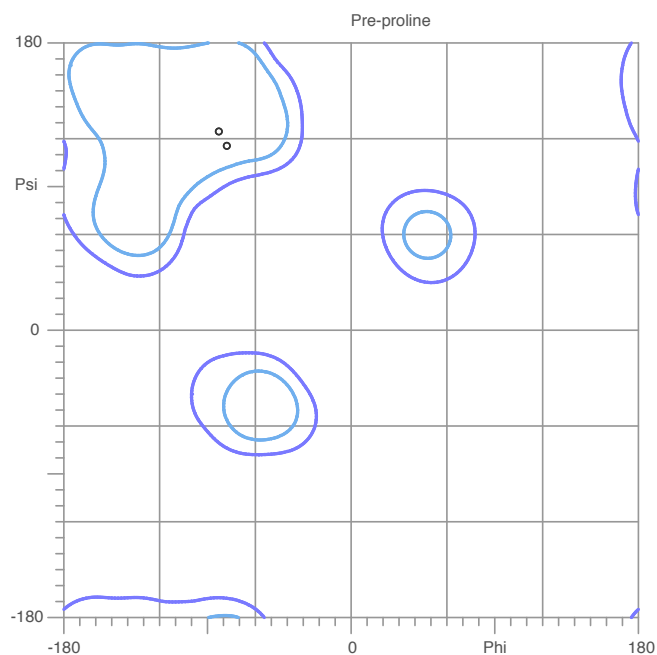
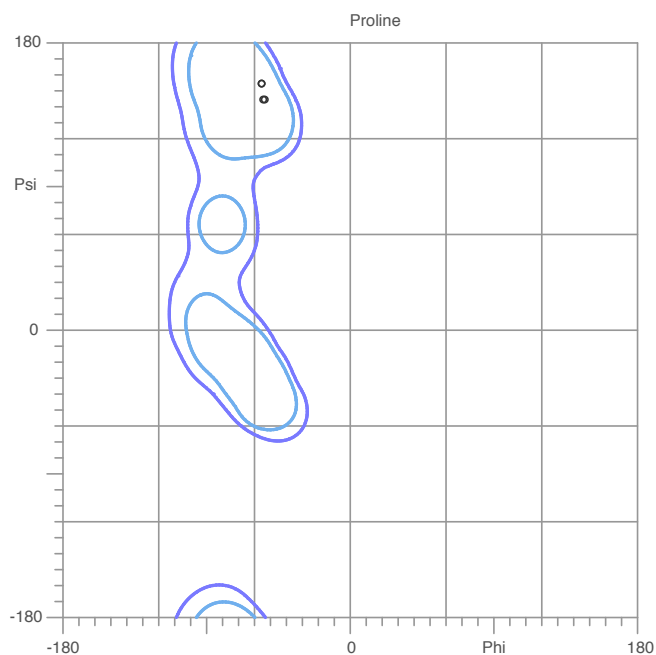
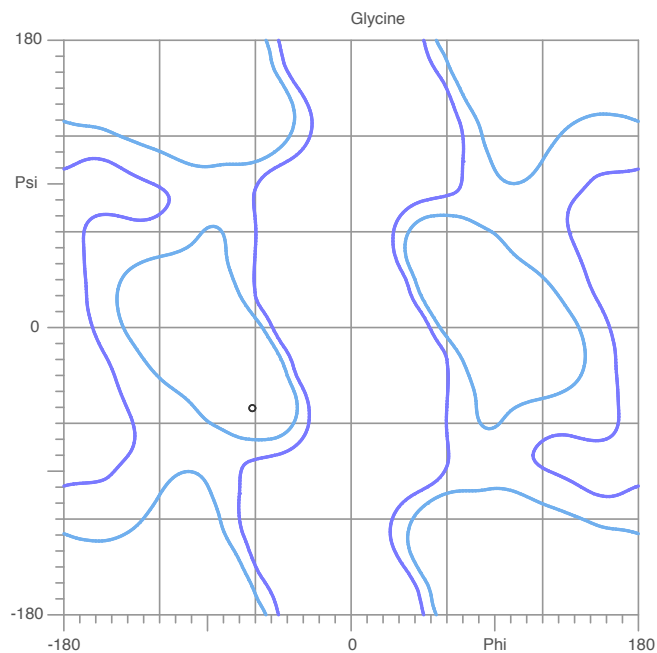
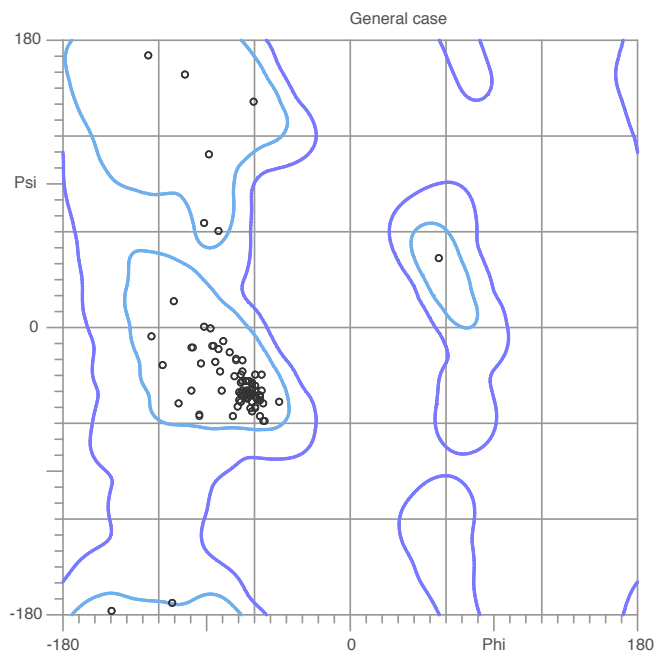
There were 2 outliers (phi, psi):

[4] 74 GLU (53.3, -85.1)

[4] 164 GLU (53.1, -85.0)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 5



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.

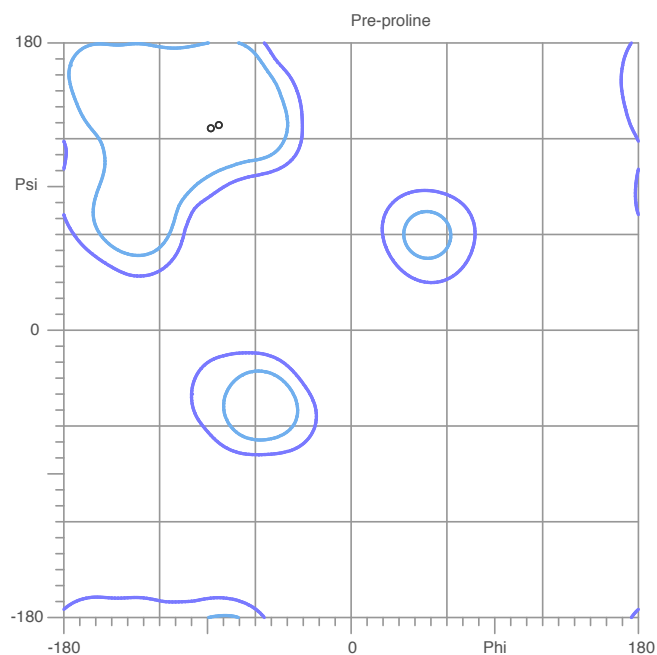
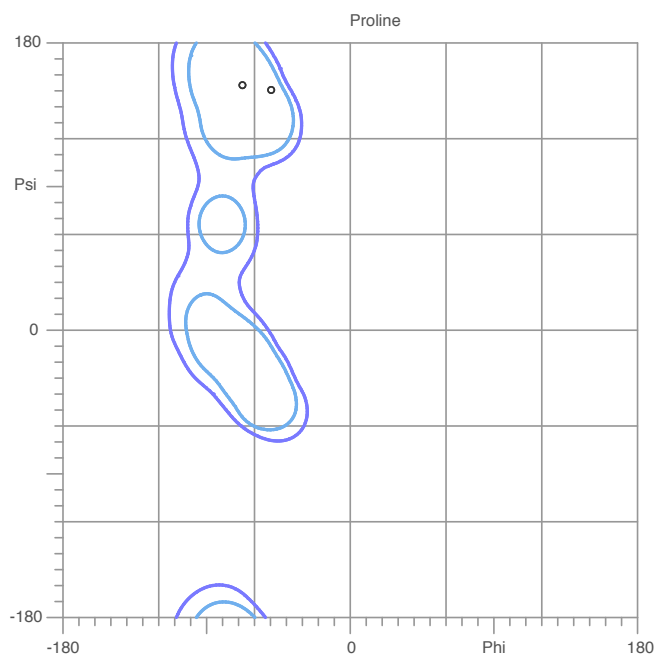
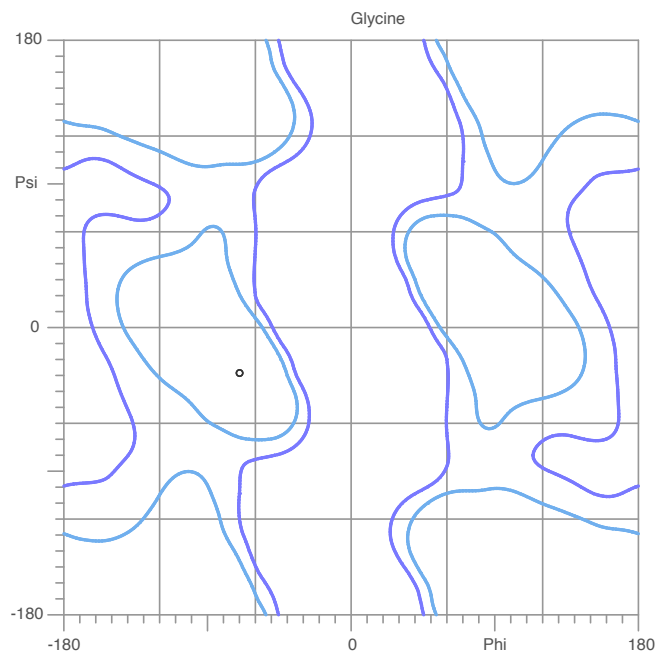
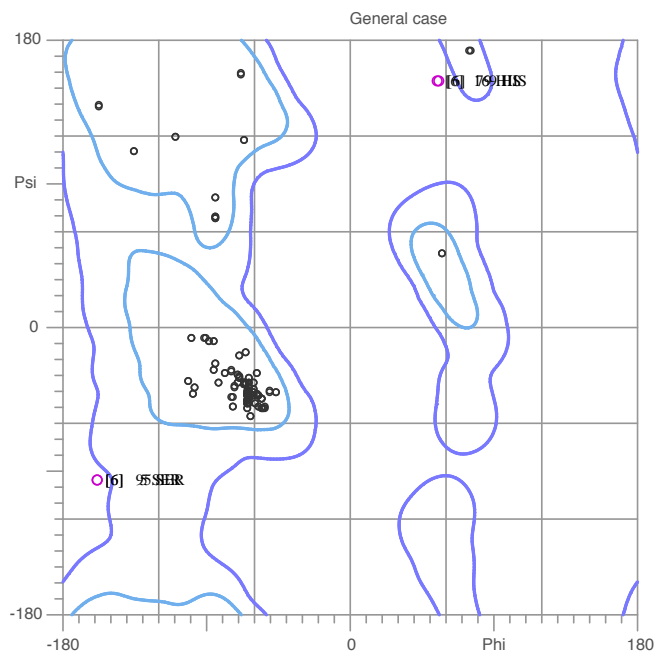
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 6



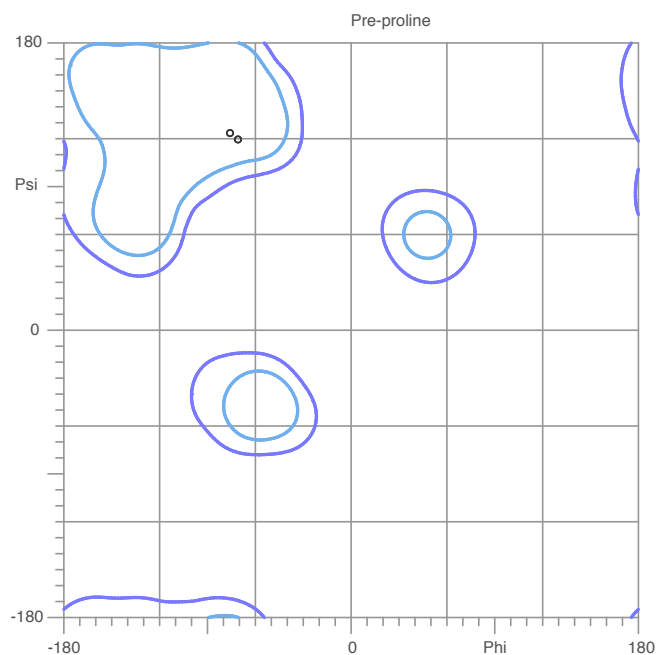
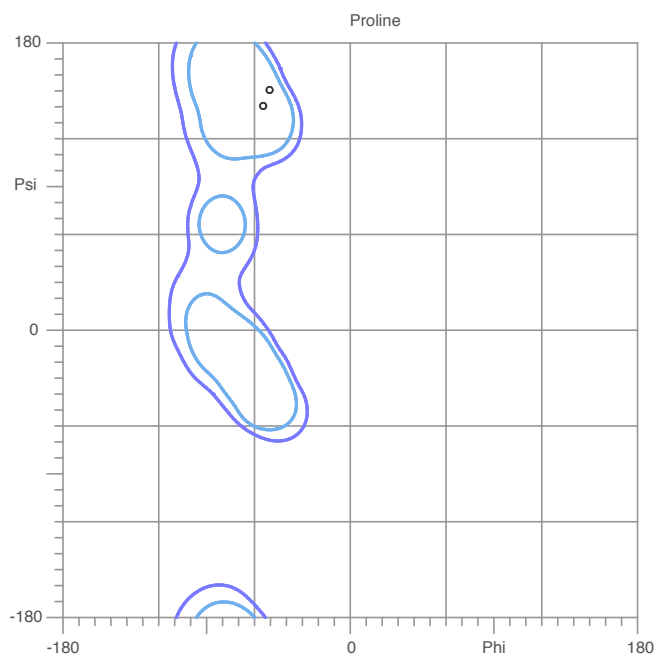
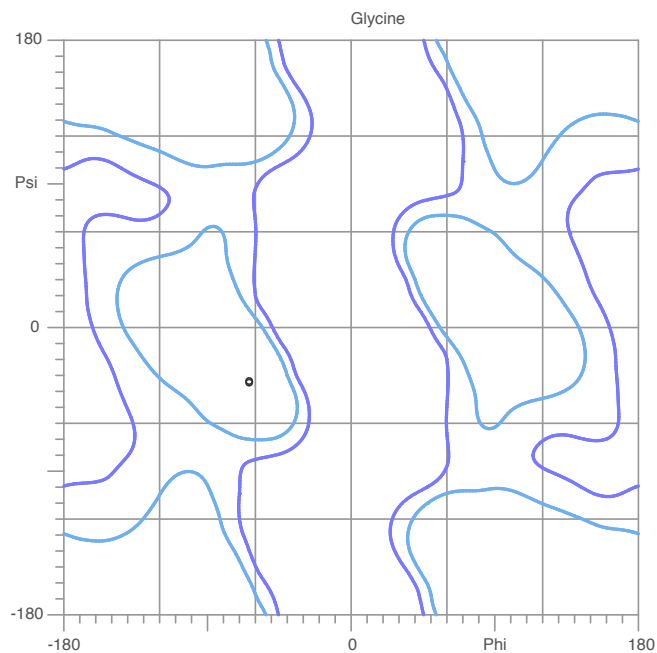
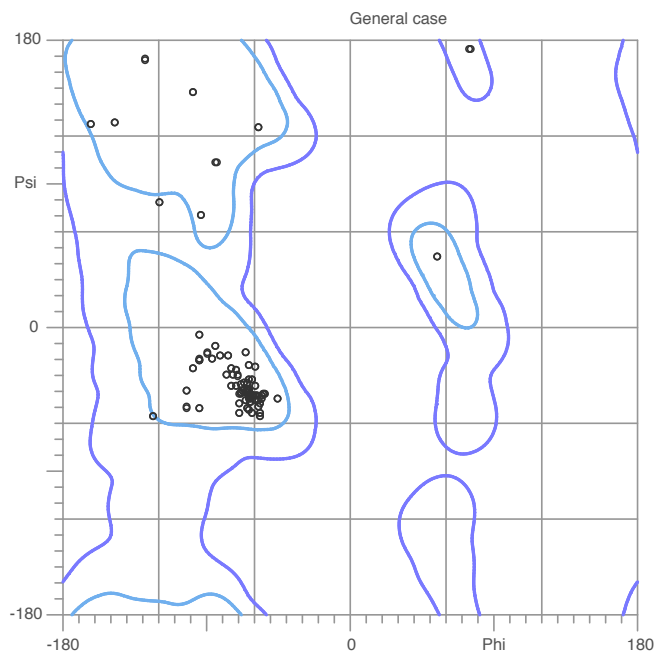
96.2% (150/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [6] 5 SER (-160.0, -95.1)
- [6] 79 HIS (54.9, 155.2)
- [6] 95 SER (-159.9, -95.1)
- [6] 169 HIS (55.0, 155.1)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 7



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.

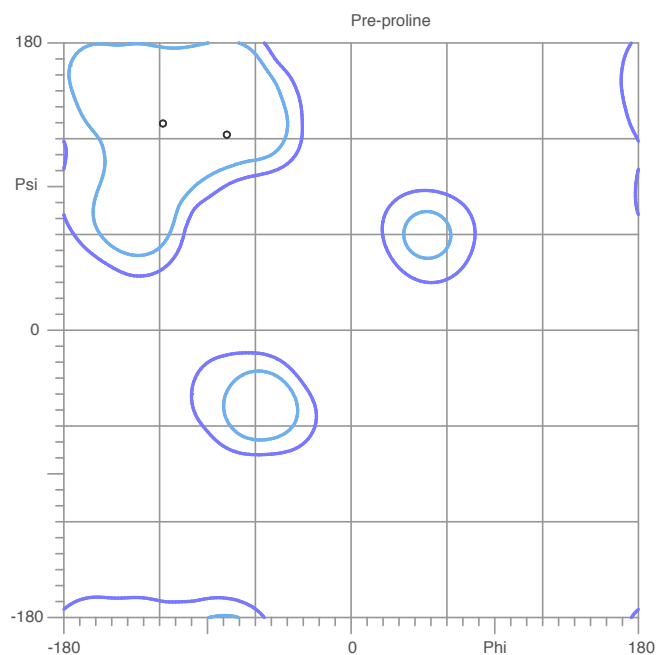
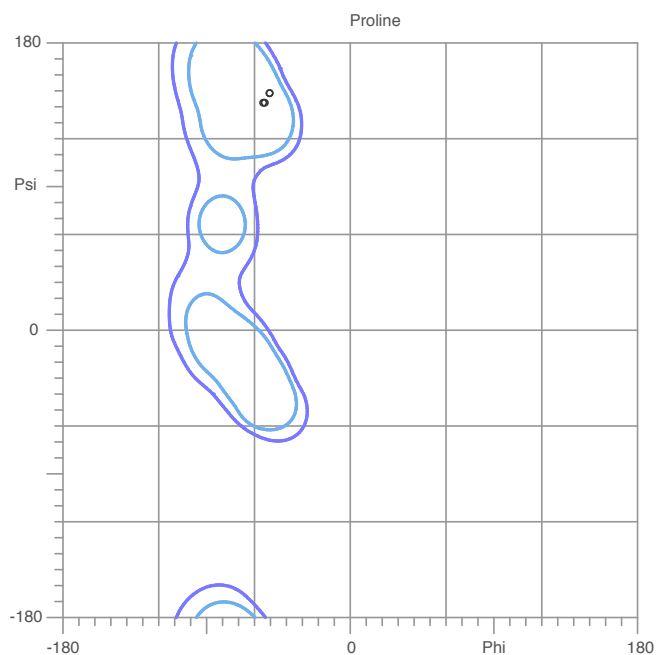
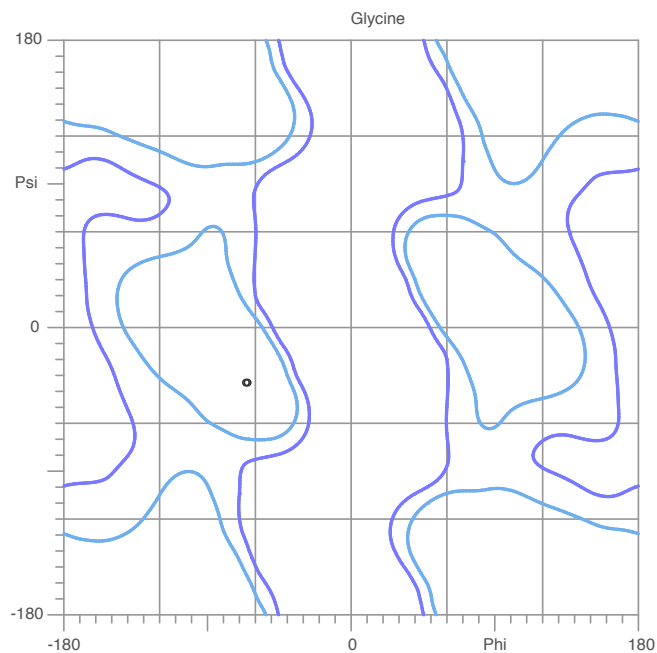
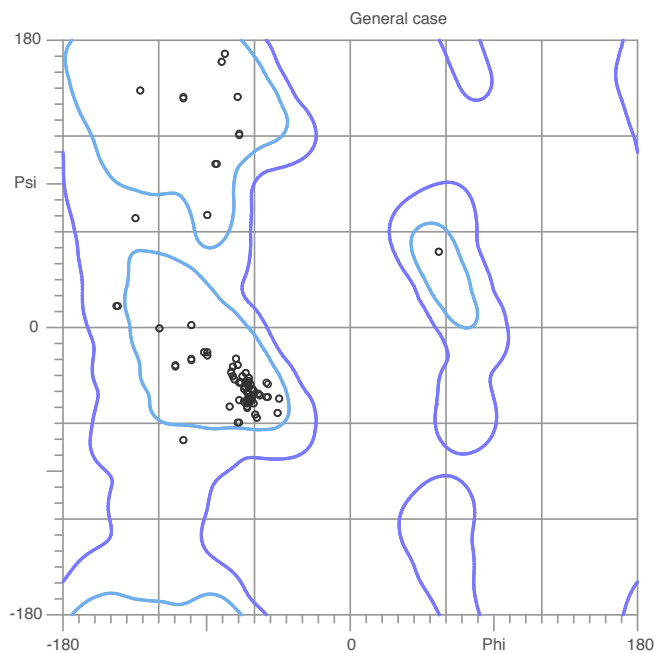
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 8



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.

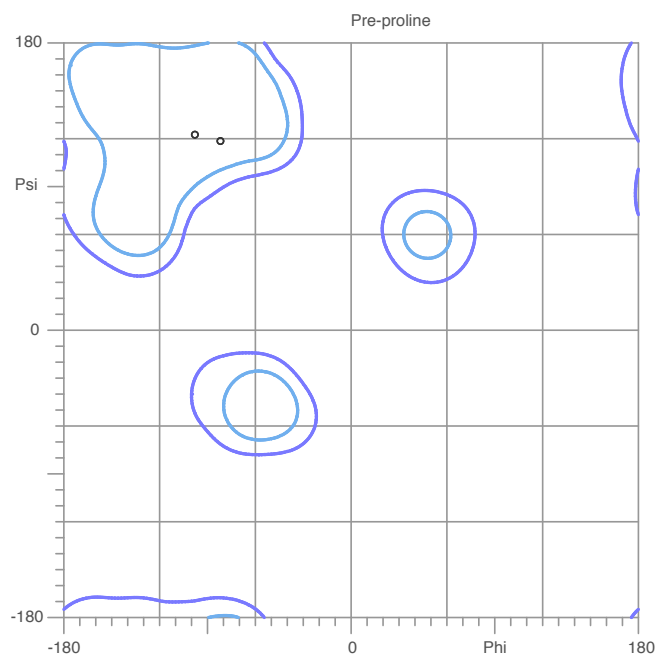
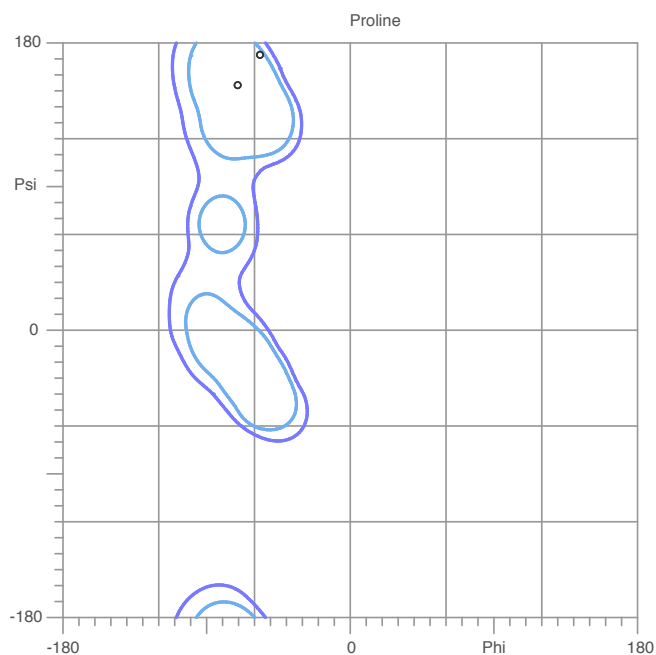
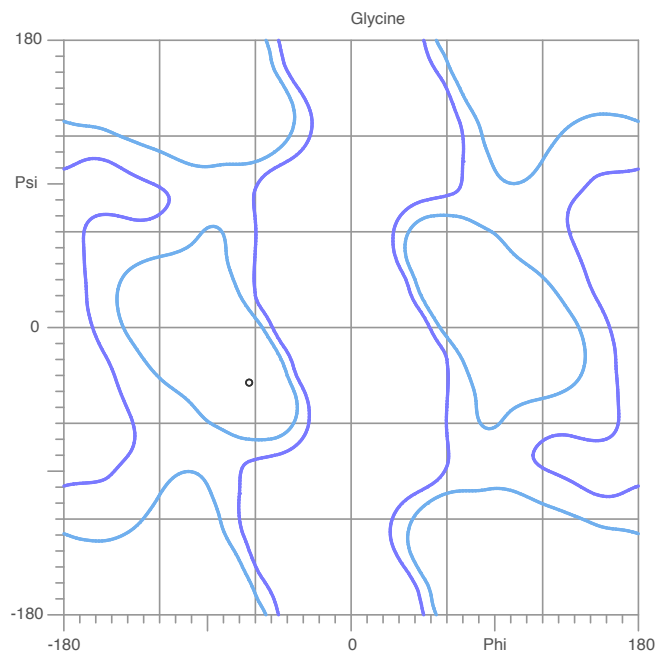
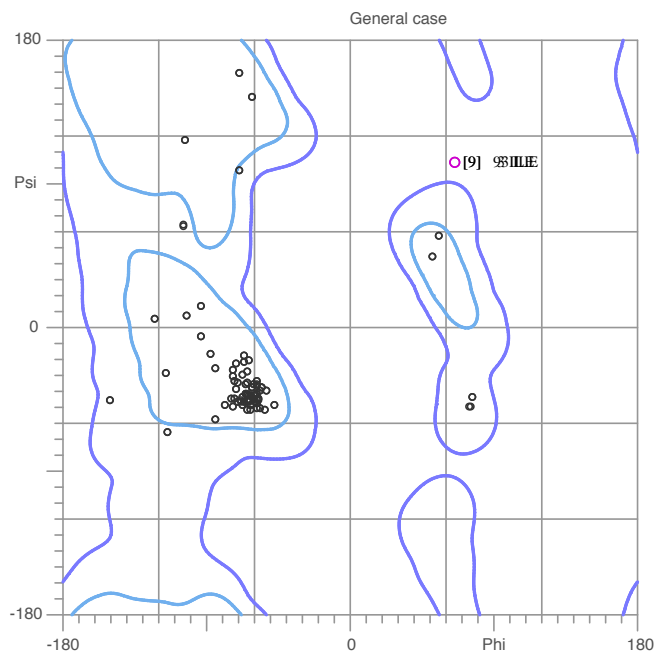
There were no outliers.

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

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MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 9



91.0% (142/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

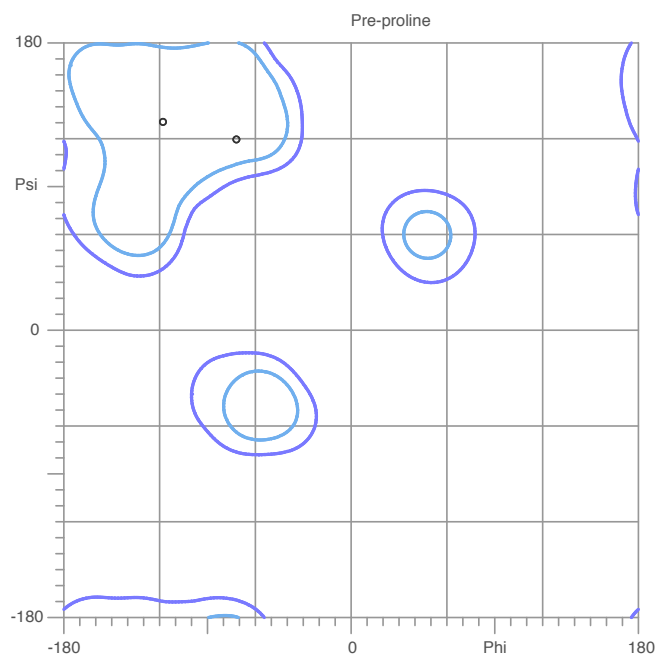
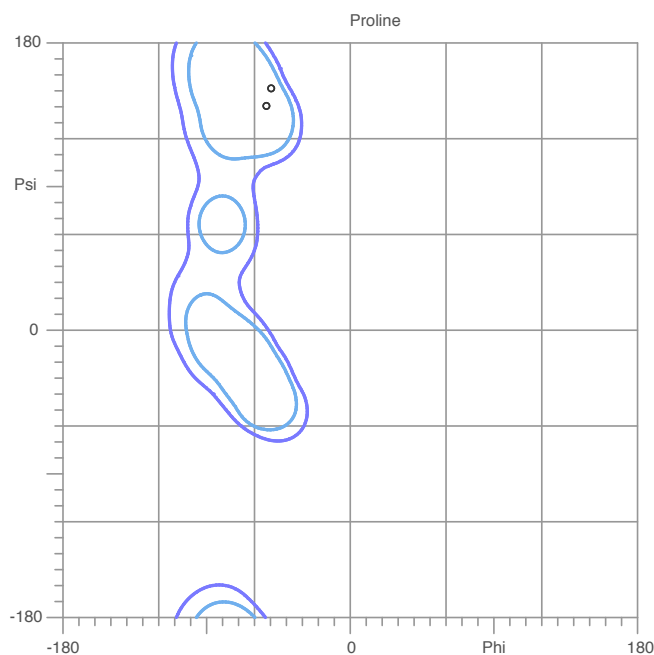
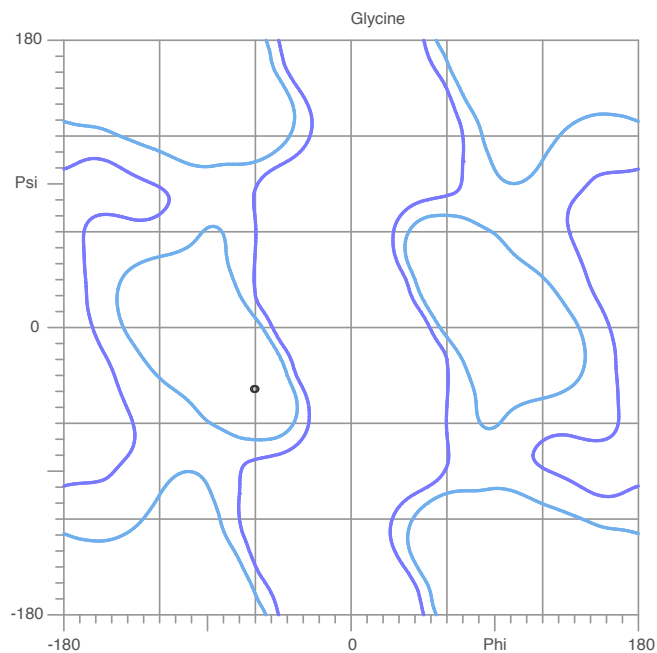
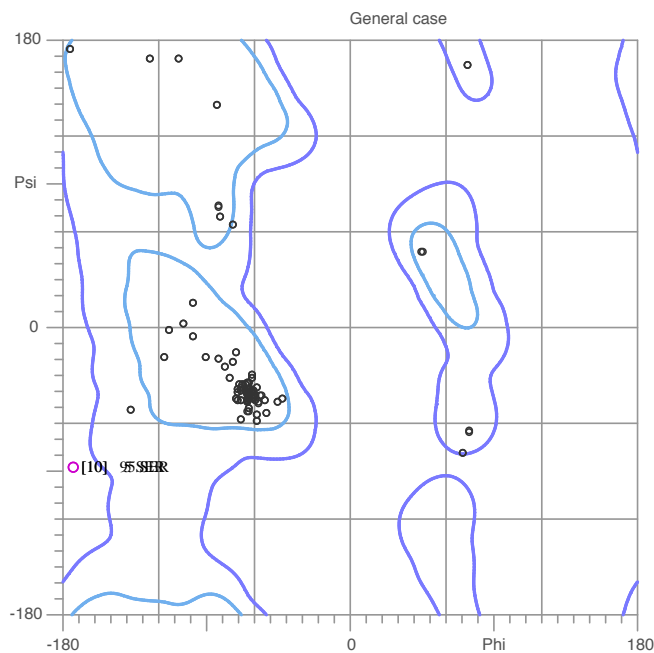
There were 2 outliers (phi, psi):

[9] 3 ILE (65.1, 104.9)

[9] 93 ILE (65.1, 104.8)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 10

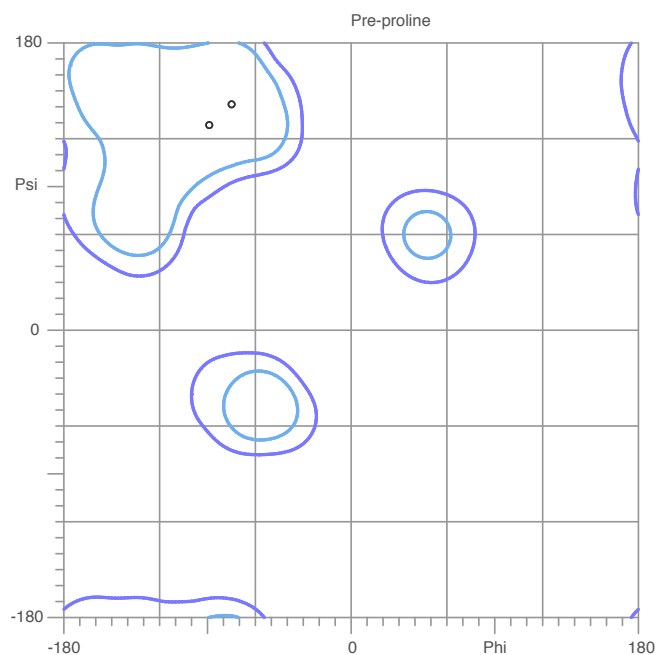
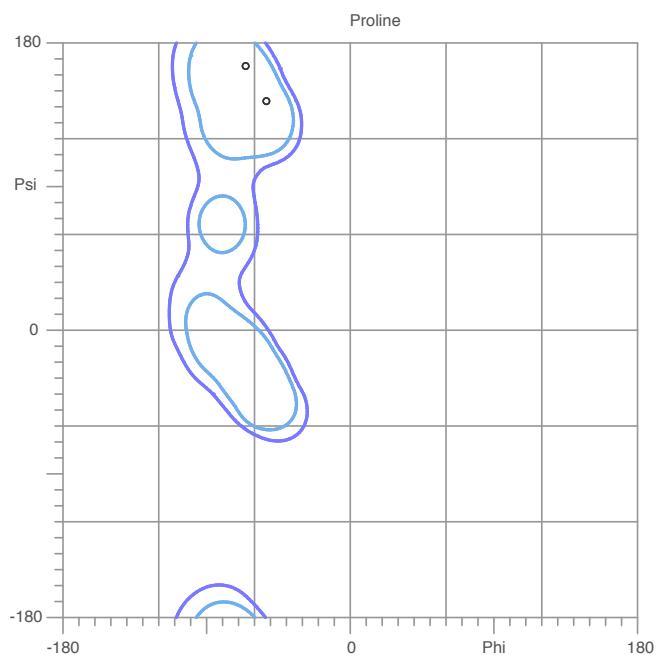
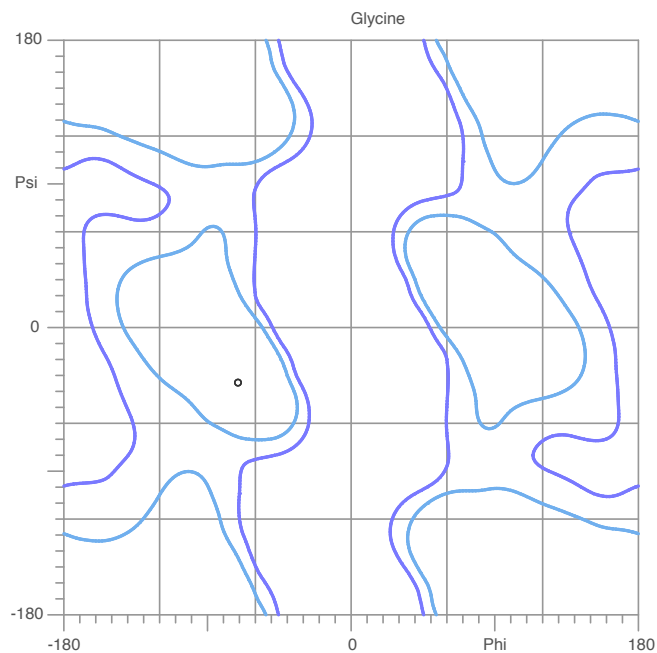
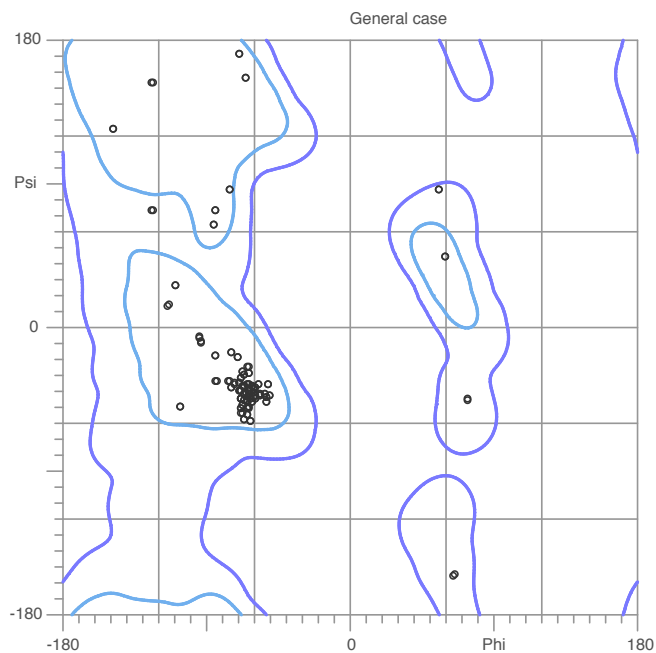


92.3% (144/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[10] 5 SER (-174.1, -87.7)
[10] 95 SER (-174.2, -87.8)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 11

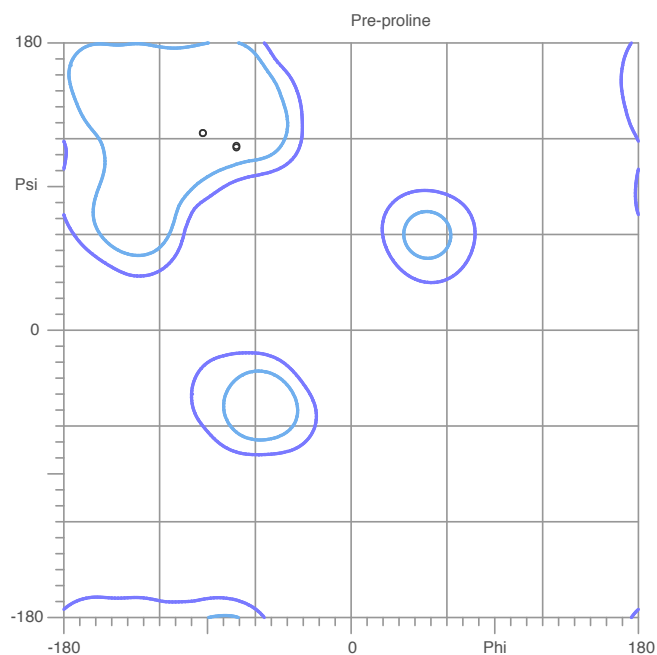
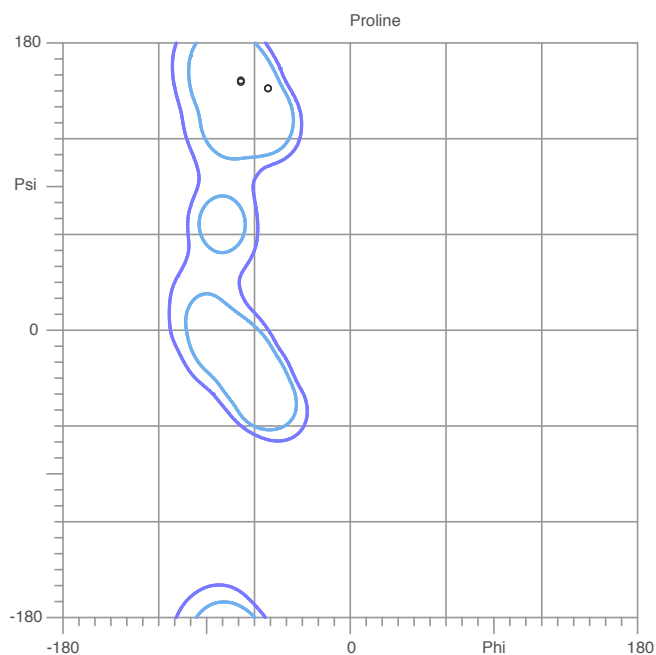
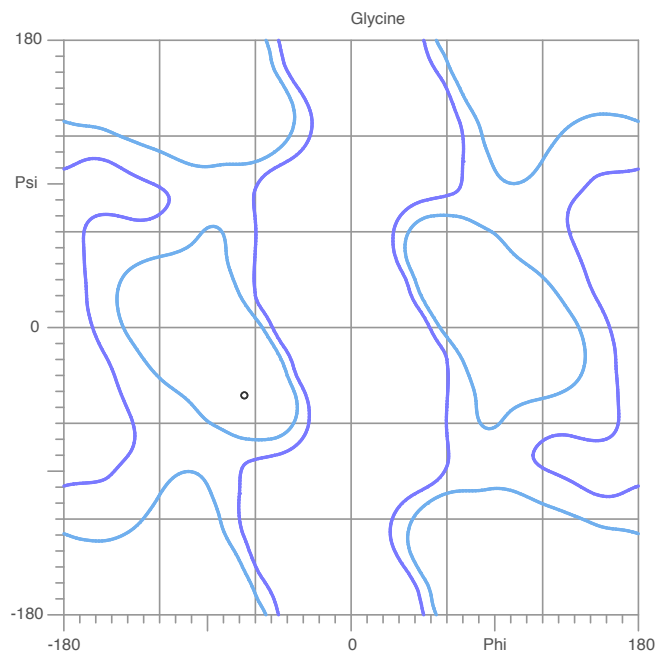
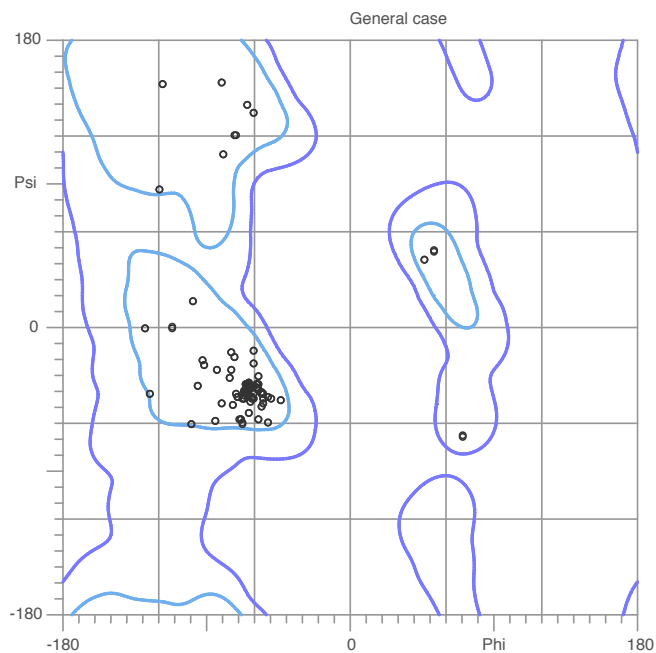


94.9% (148/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 12



97.4% (152/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

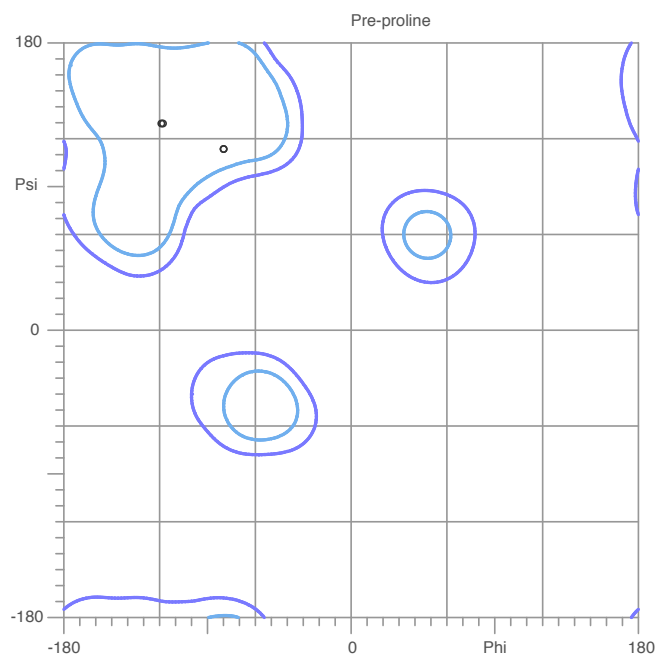
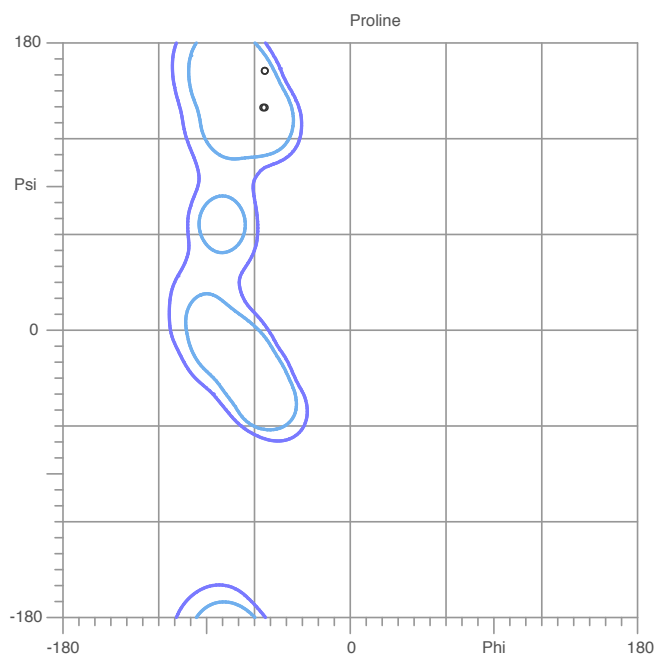
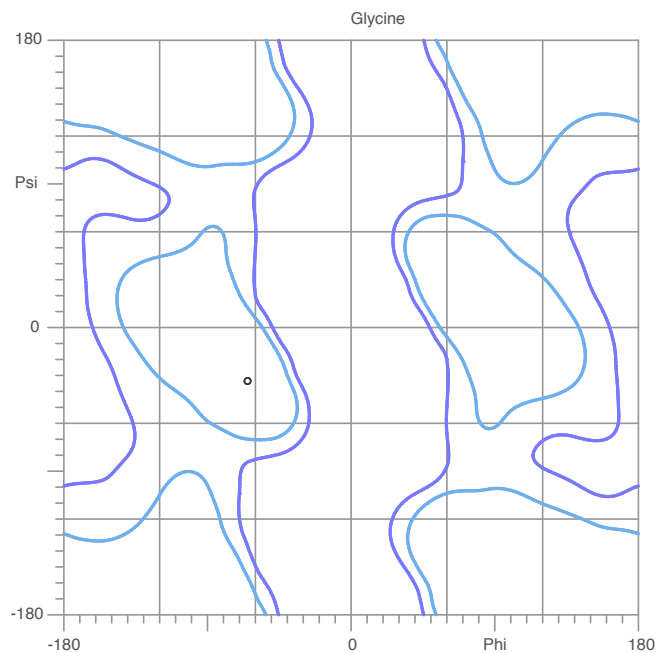
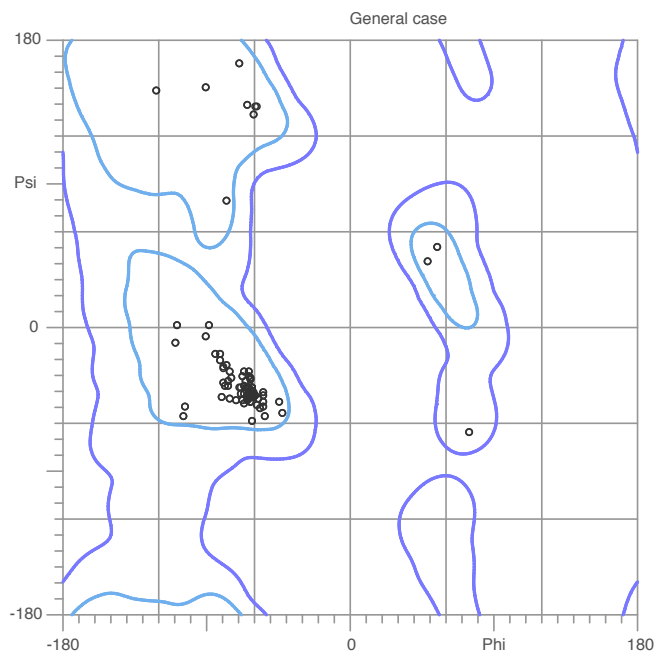
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 13



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.

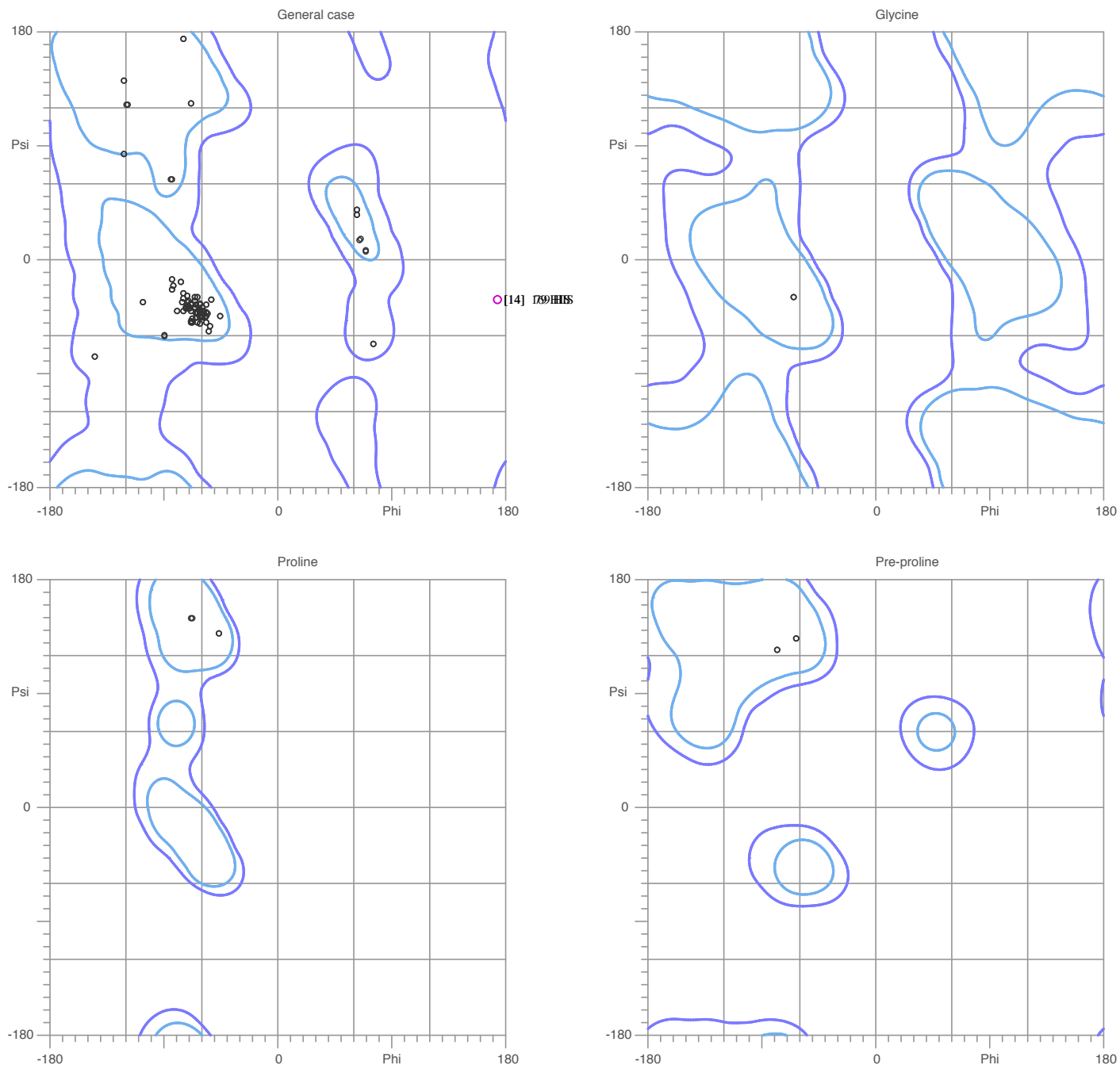
There were no outliers.

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

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MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 14



96.2% (150/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

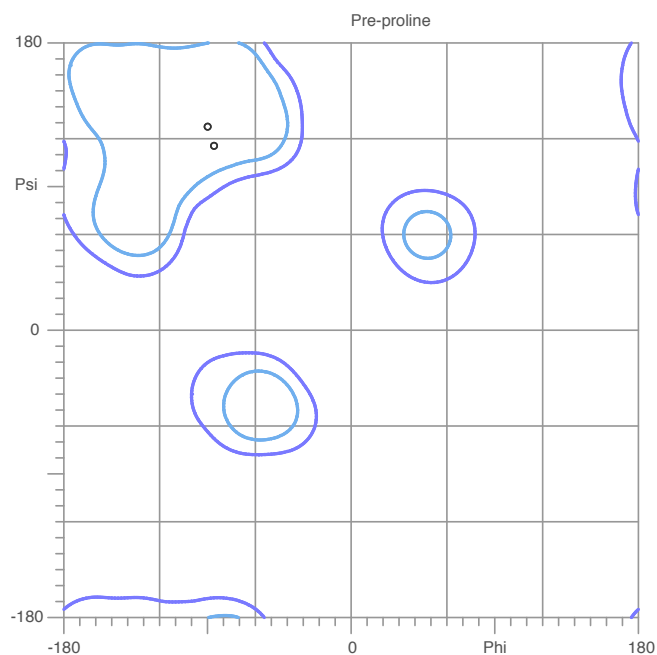
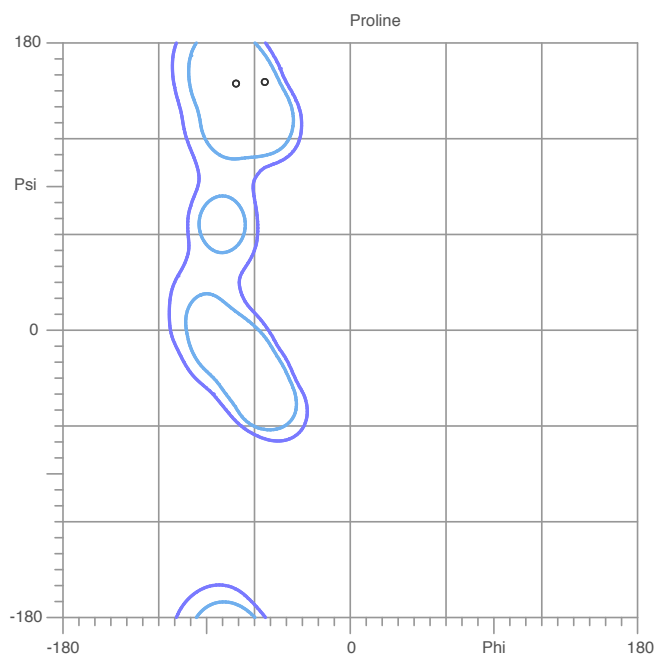
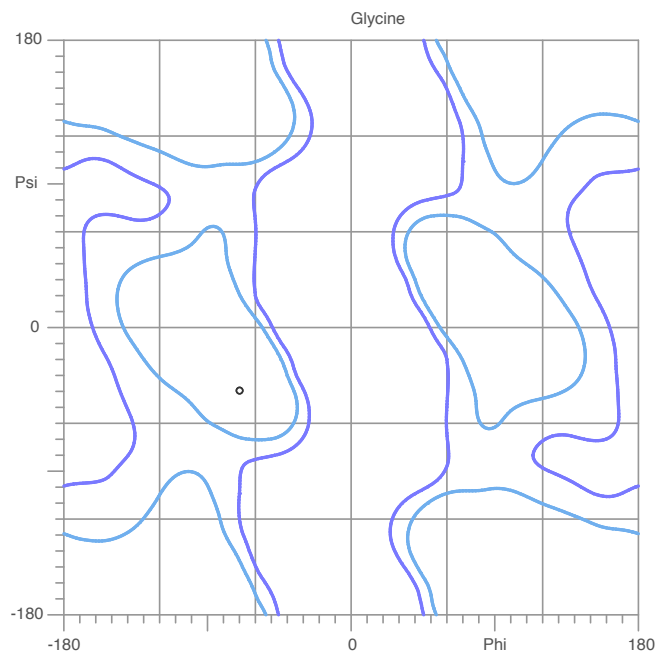
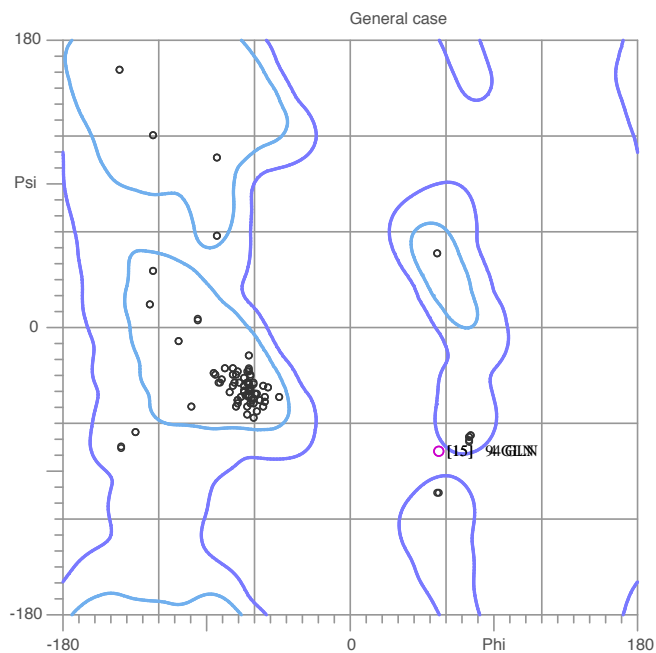
There were 2 outliers (phi, psi):

[14] 79 HIS (173.6, -31.7)

[14] 169 HIS (173.7, -31.8)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 15



91.0% (142/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

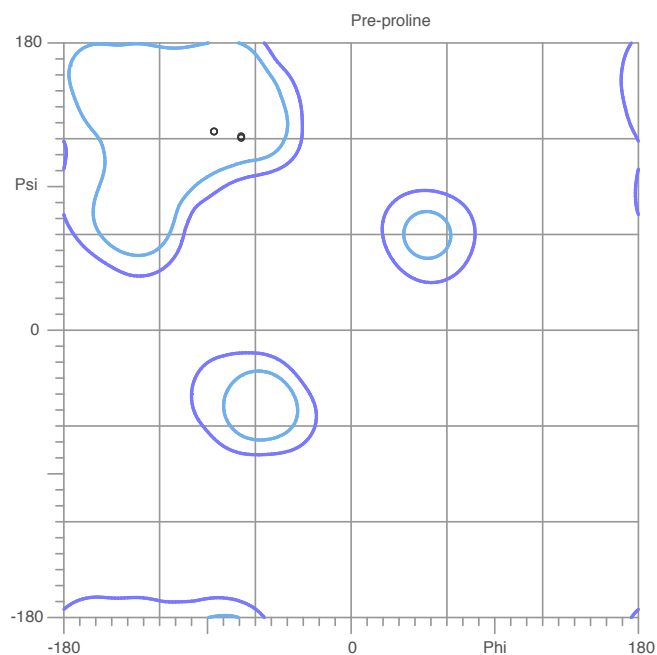
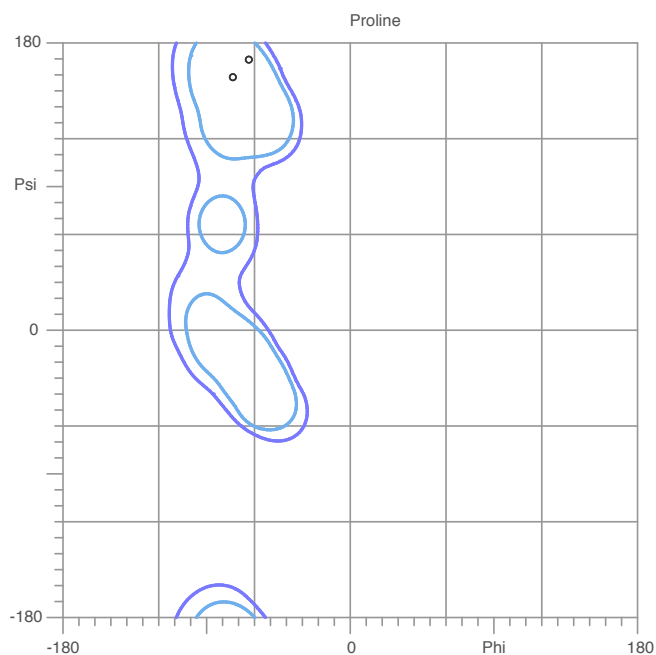
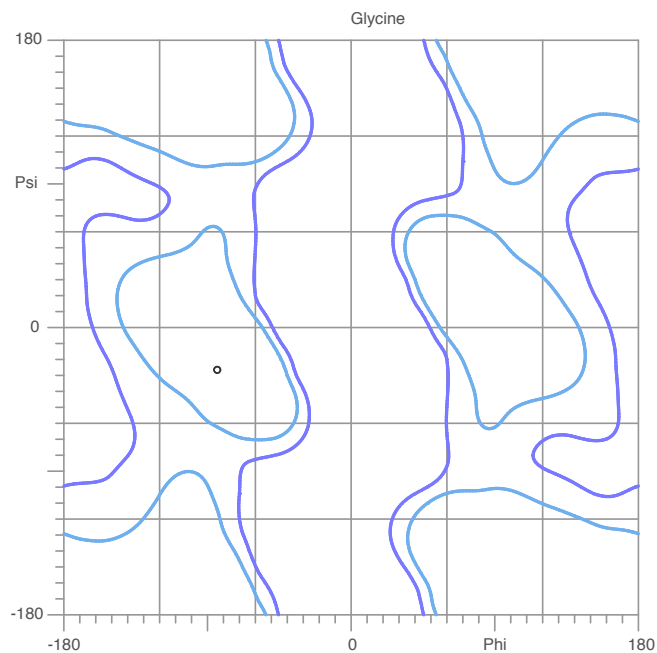
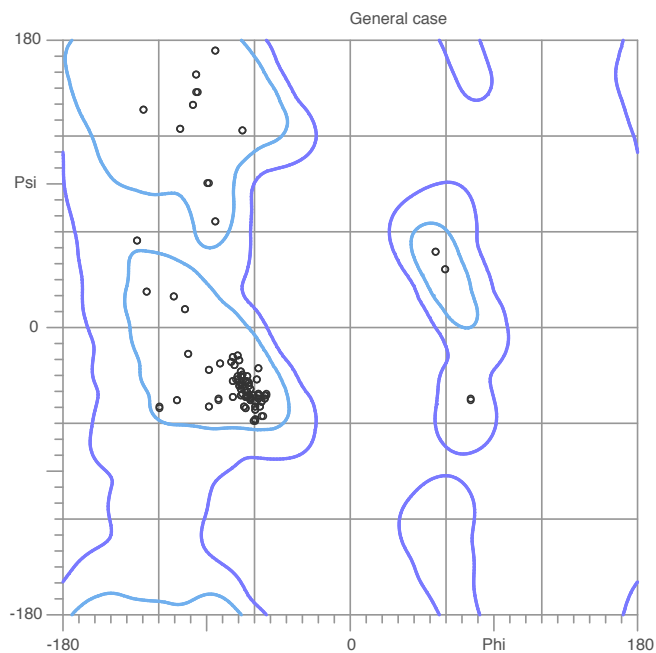
There were 2 outliers (phi, psi):

[15] 4 GLN (55.0, -77.8)

[15] 94 GLN (55.1, -77.8)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 16



97.4% (152/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

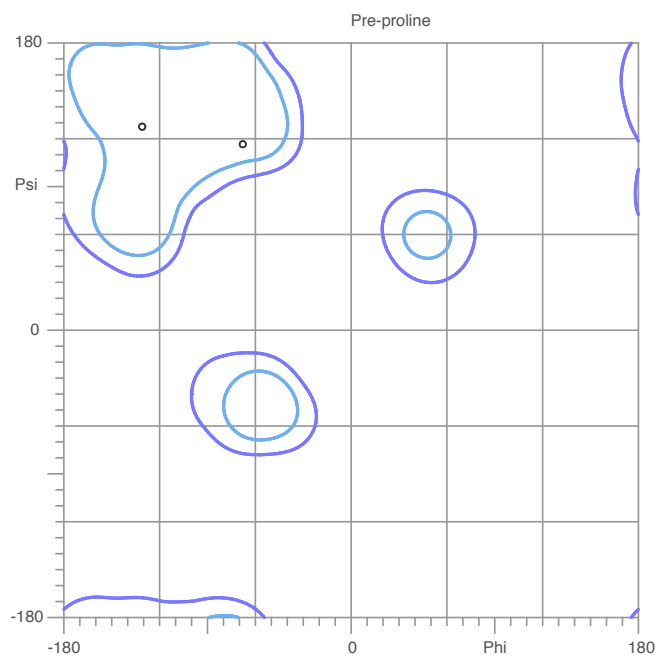
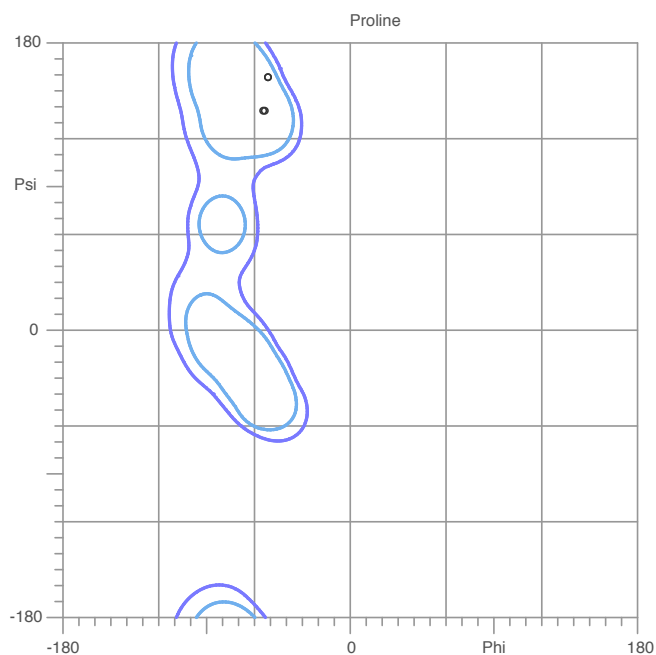
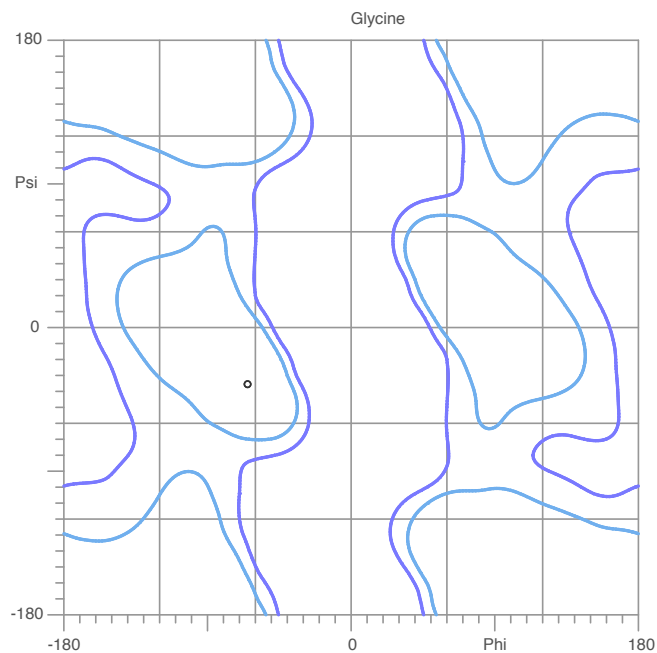
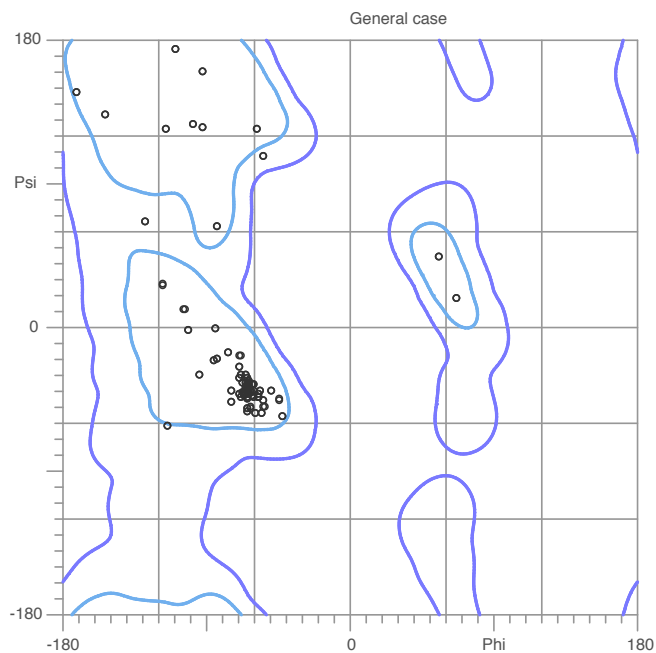
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 17



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.

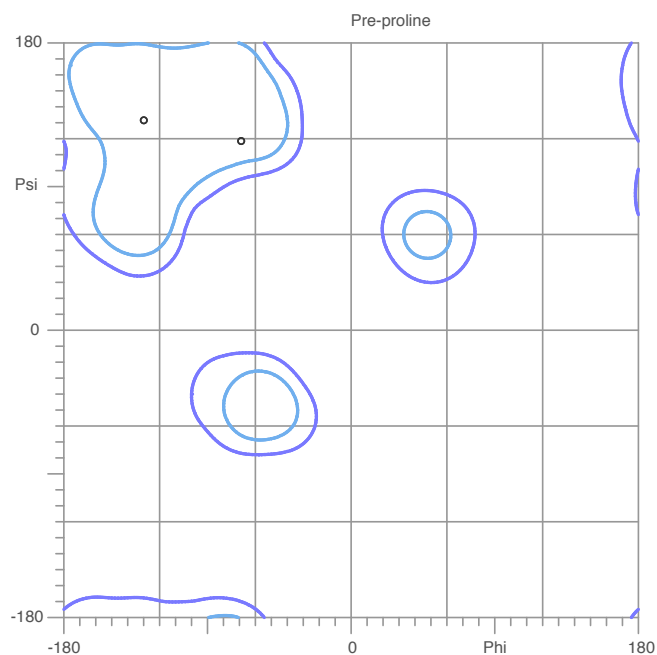
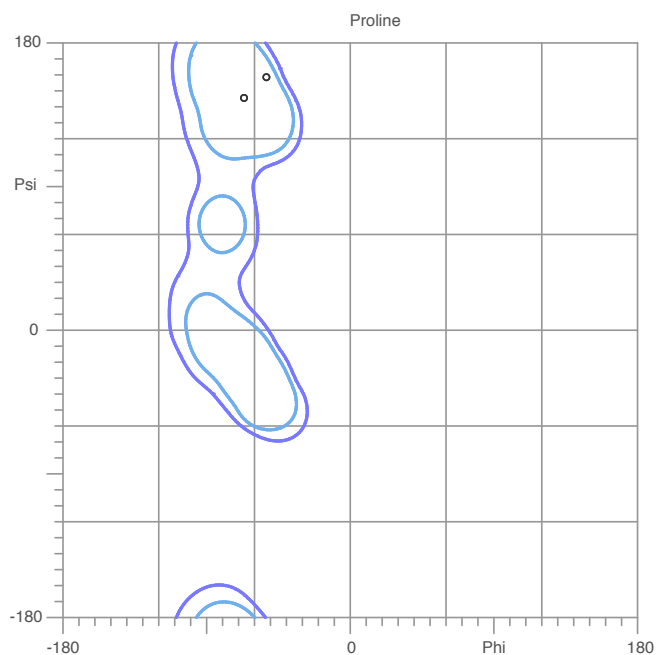
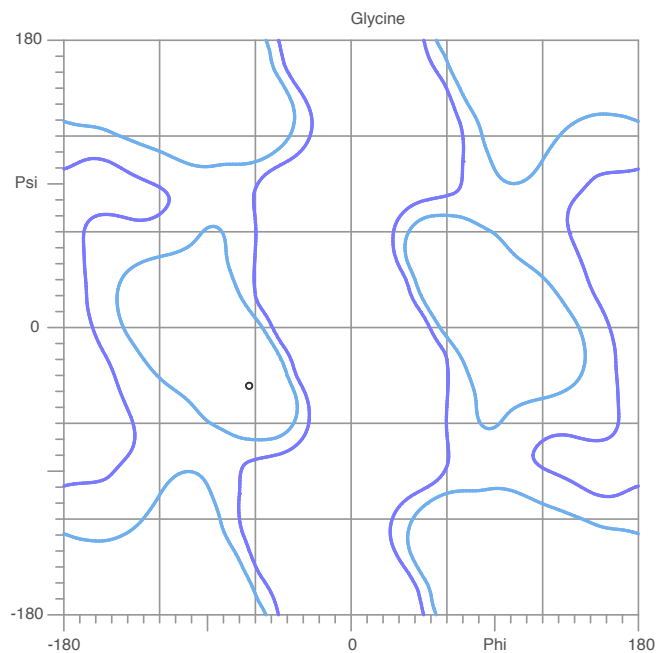
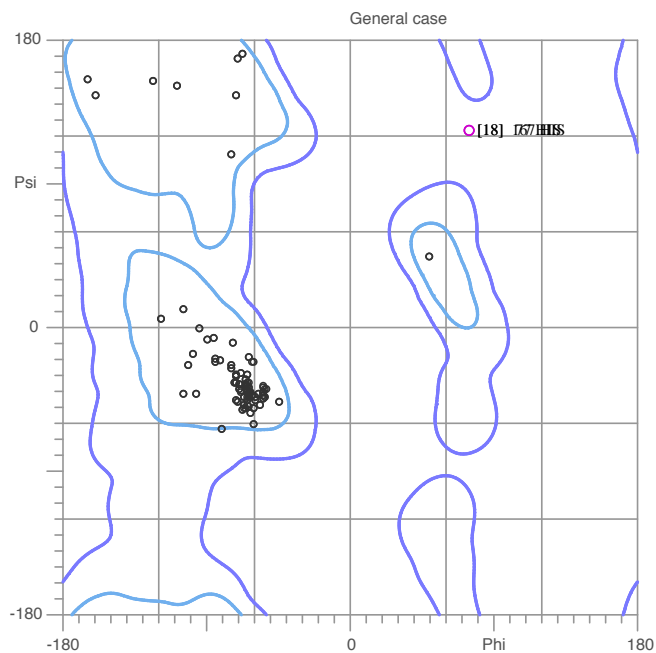
There were no outliers.

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

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MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 18



97.4% (152/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

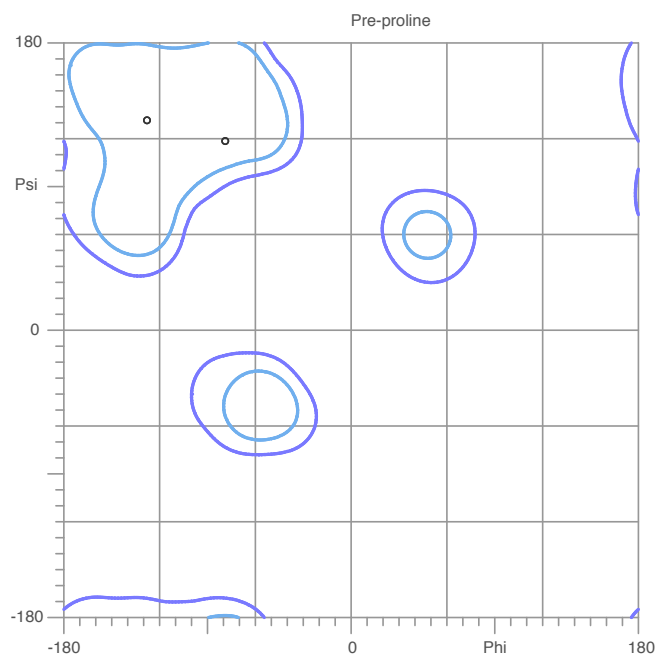
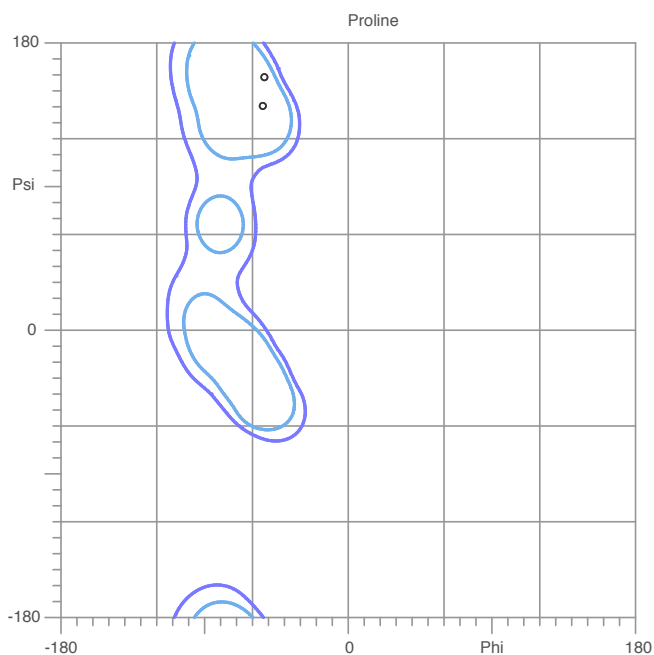
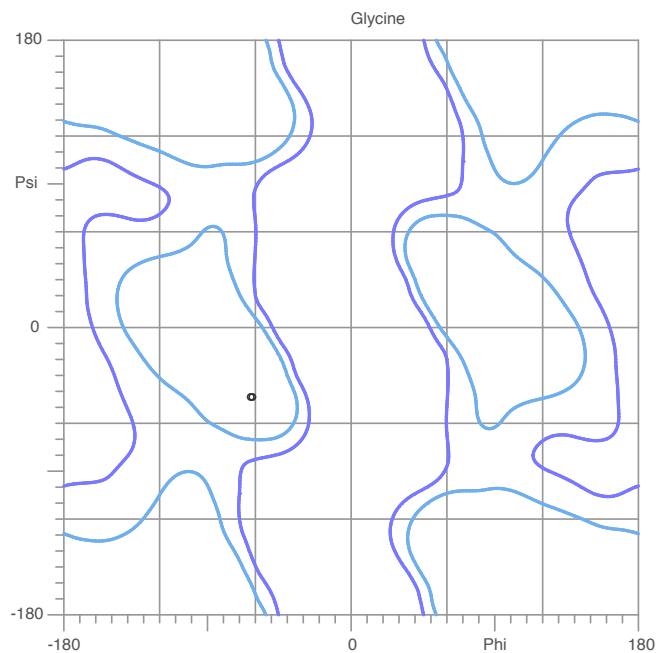
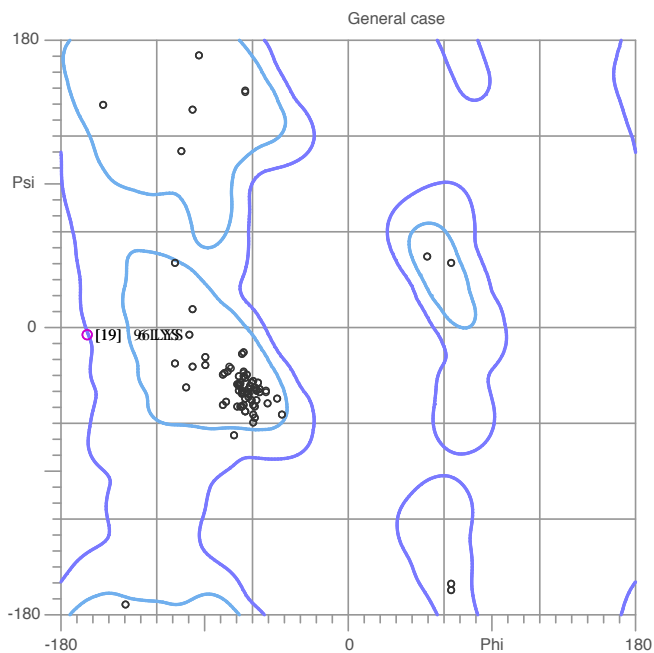
There were 2 outliers (phi, psi):

[18] 77 HIS (75.0, 125.0)

[18] 167 HIS (75.0, 124.9)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 19



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.

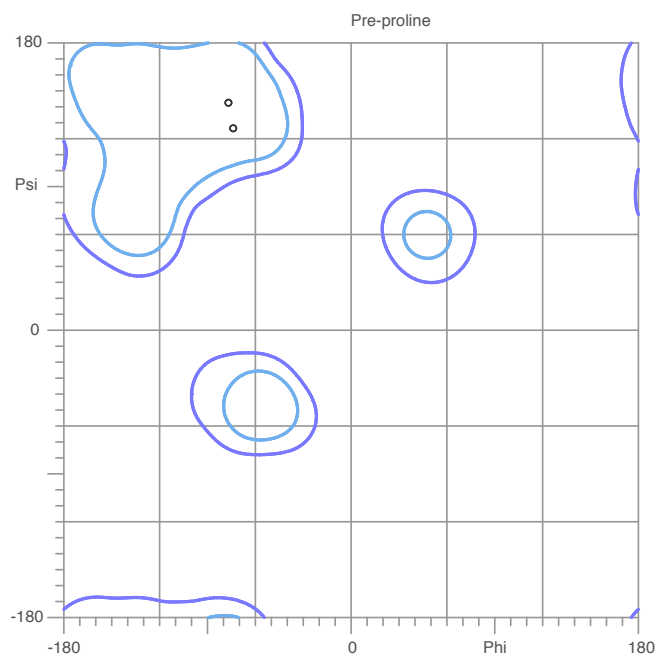
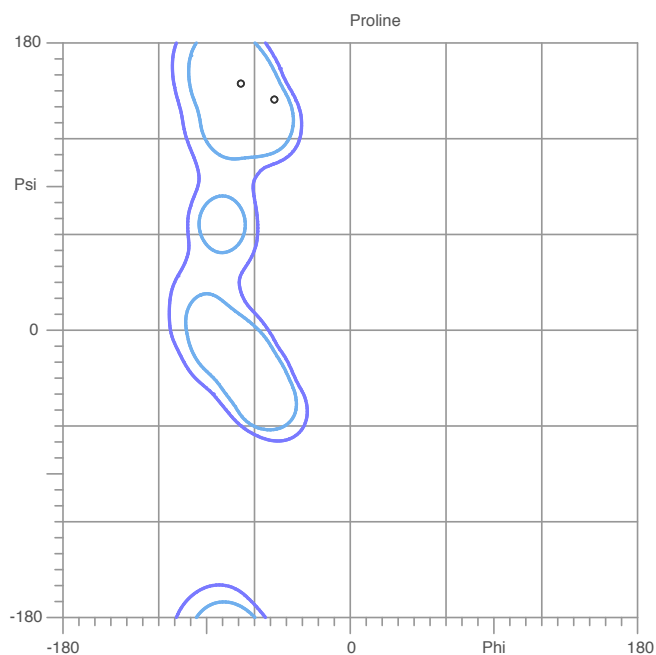
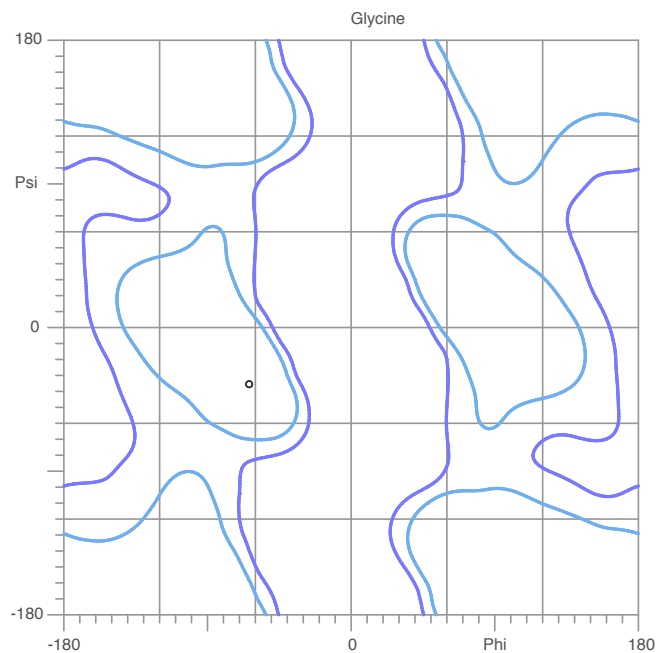
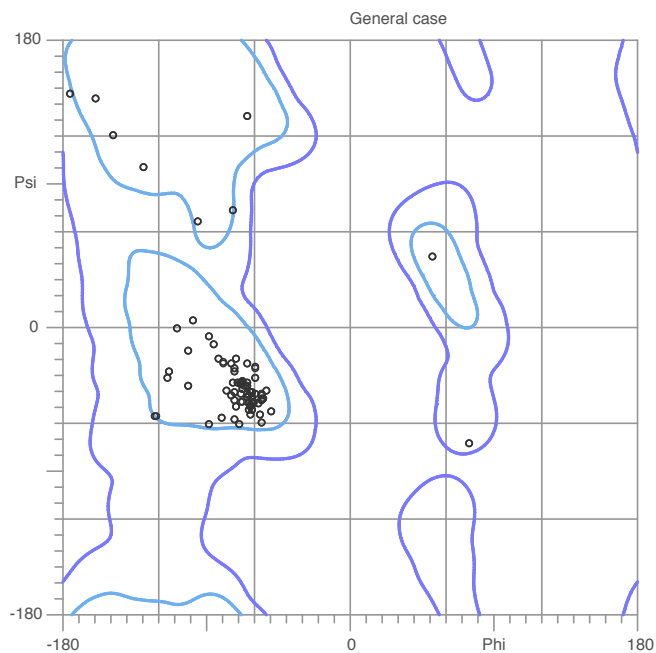
There were 2 outliers (phi, psi):

[19] 6 LYS (-164.3, -4.7)

[19] 96 LYS (-164.3, -4.7)

MolProbity Ramachandran analysis

SOR77_R3_em_bcr3.pdb, model 20



97.4% (152/156) 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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