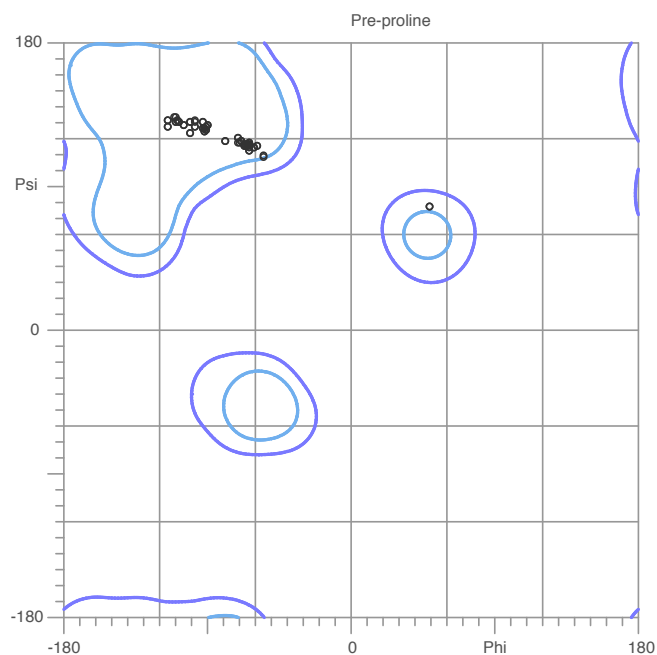
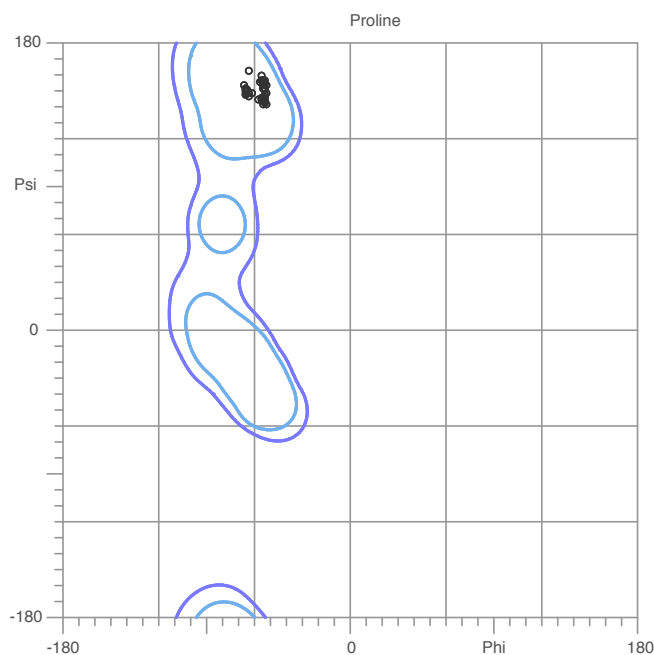
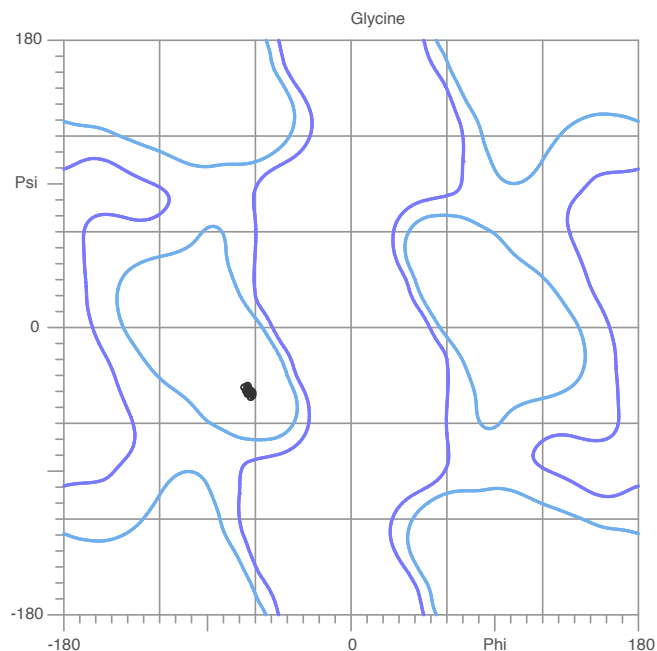
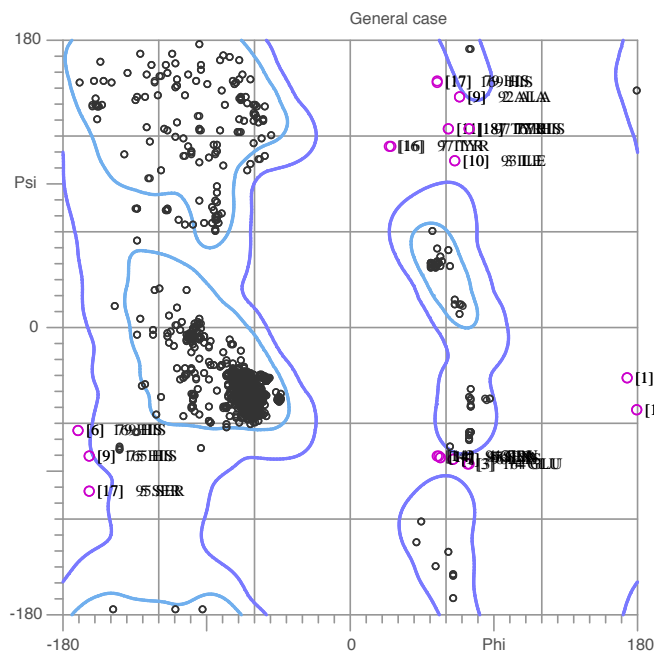


MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, all models



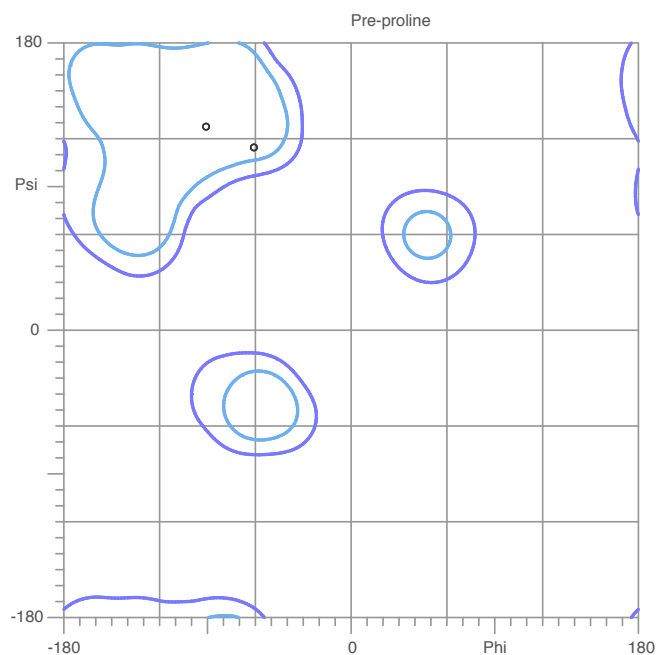
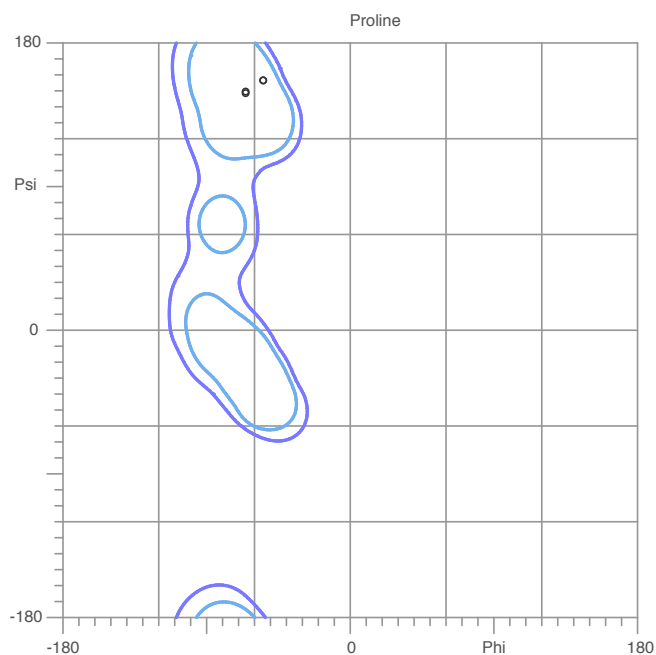
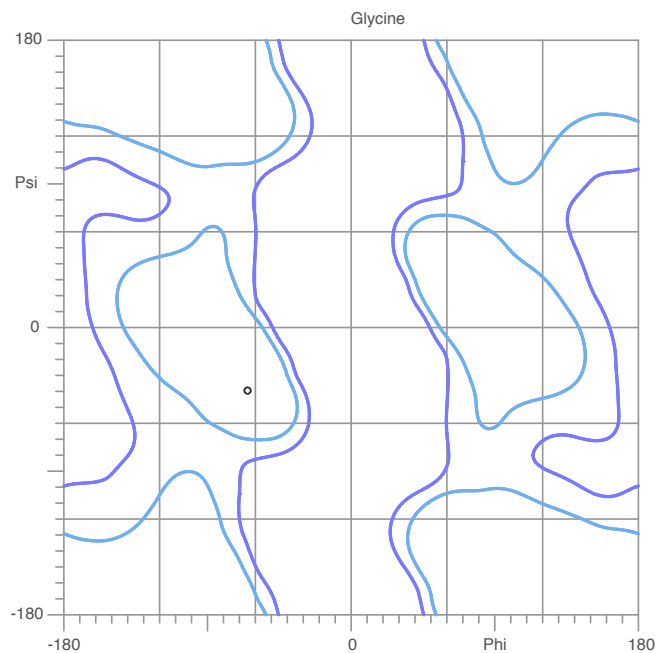
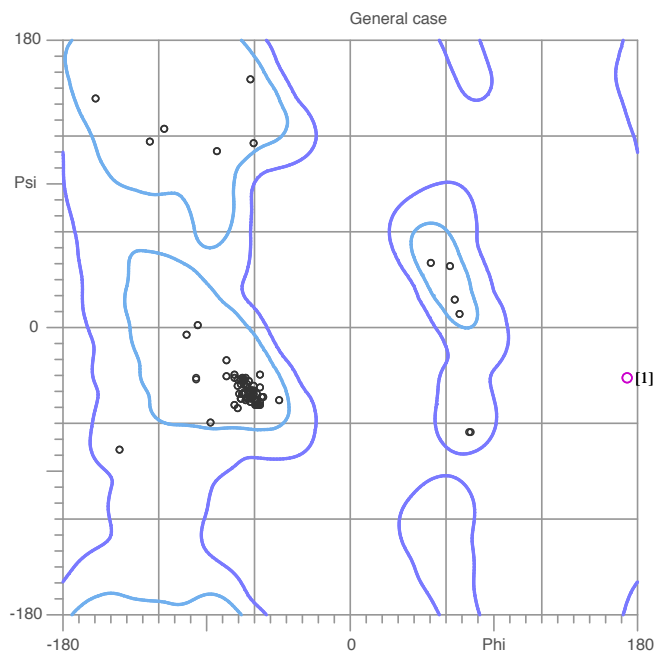
95.9% (2692/2808) of all residues were in favored (98%) regions.
98.9% (2778/2808) of all residues were in allowed (>99.8%) regions.

There were 30 outliers (phi, psi):

- | | |
|-----------------------------|------------------------------|
| [1] 79 HIS (173.3, -31.7) | [10] 79 HIS (179.1, -51.3) |
| [1] 169 HIS (173.3, -31.8) | [10] 93 ILE (65.2, 105.1) |
| [3] 74 GLU (74.0, -85.2) | [10] 169 HIS (179.2, -51.3) |
| [3] 164 GLU (73.9, -85.2) | [11] 7 TYR (61.4, 125.0) |
| [6] 79 HIS (-171.9, -64.5) | [11] 97 TYR (61.4, 125.0) |
| [6] 169 HIS (-171.9, -64.4) | [14] 4 GLN (55.0, -80.1) |
| [7] 6 LYS (64.6, -82.1) | [14] 5 SER (56.8, -81.9) |
| [7] 96 LYS (64.6, -82.0) | [14] 94 GLN (55.0, -80.1) |
| [9] 2 ALA (68.6, 145.6) | [14] 95 SER (56.8, -81.9) |
| [9] 75 HIS (-164.5, -80.3) | [16] 7 TYR (24.9, 115.0) |
| [9] 92 ALA (68.6, 145.6) | [16] 97 TYR (25.0, 115.0) |
| [9] 165 HIS (-164.4, -80.3) | [17] 5 SER (-165.0, -102.4) |
| [10] 3 ILE (65.2, 105.1) | [17] 79 HIS (55.0, 155.0) |
| | [17] 95 SER (-164.9, -102.4) |
| | [17] 169 HIS (55.0, 155.0) |
| | [18] 77 HIS (74.9, 125.0) |
| | [18] 167 HIS (74.9, 125.0) |

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 1



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.

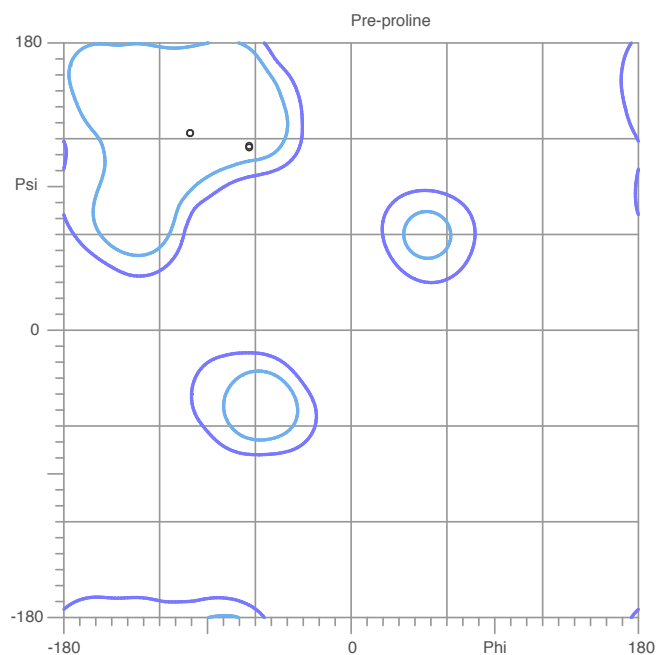
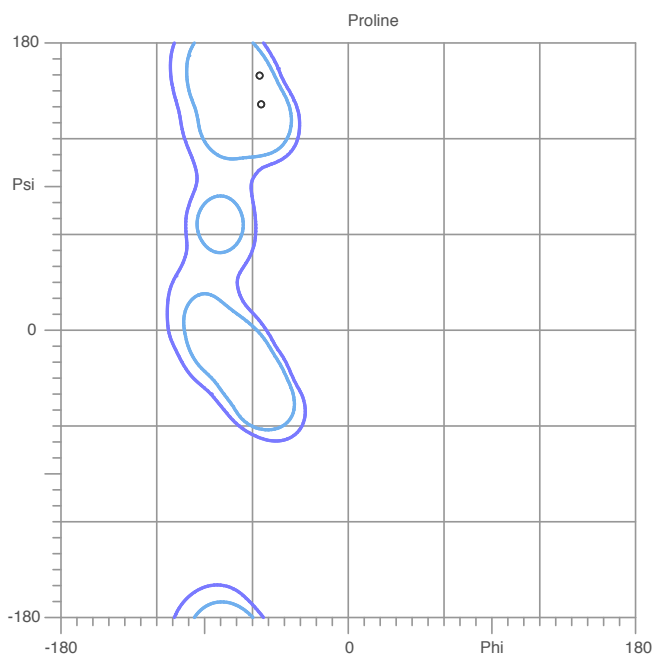
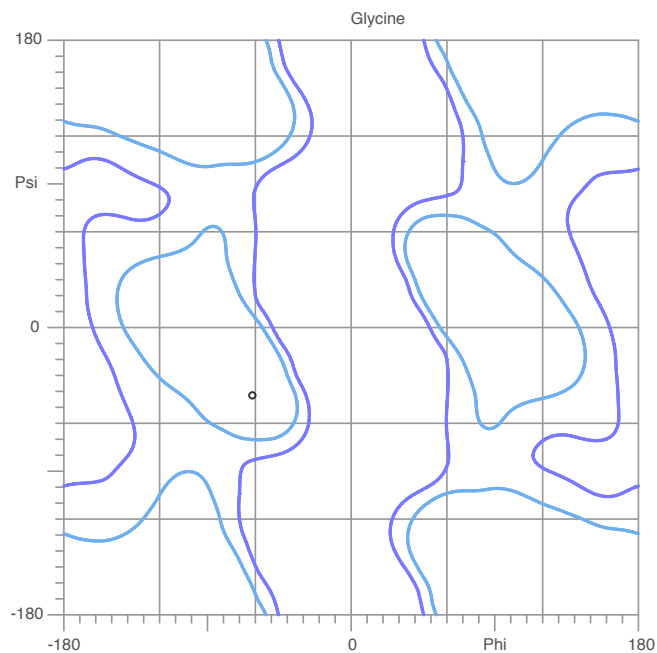
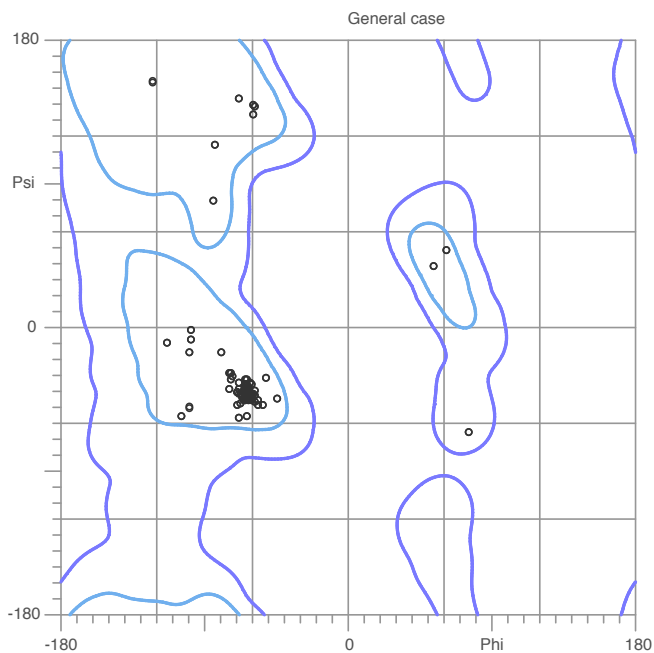
There were 2 outliers (phi, psi):

[1] 79 HIS (173.3, -31.7)

[1] 169 HIS (173.3, -31.8)

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 2



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.

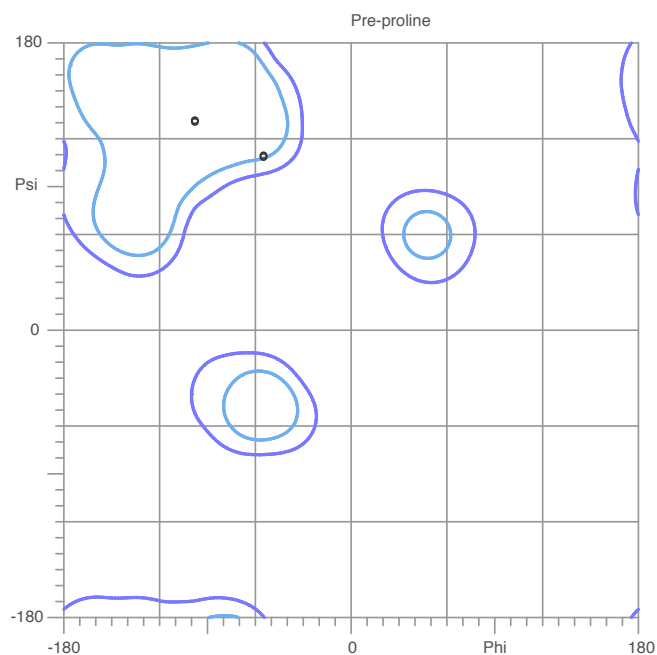
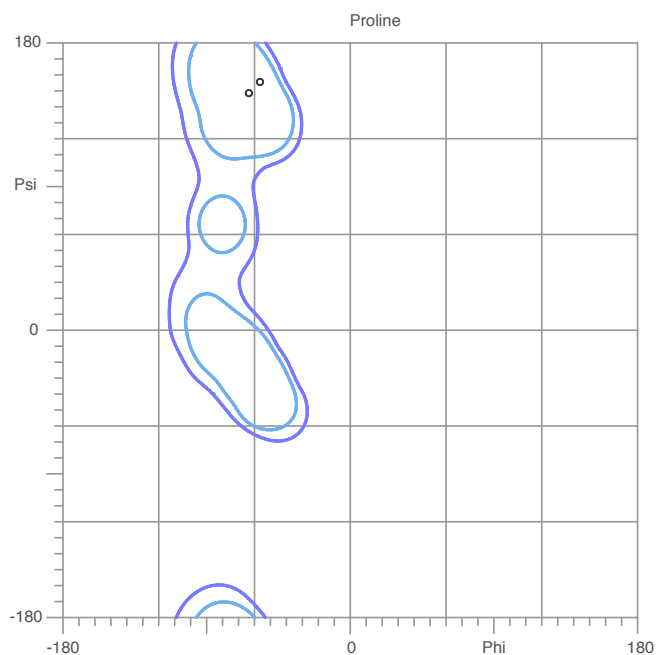
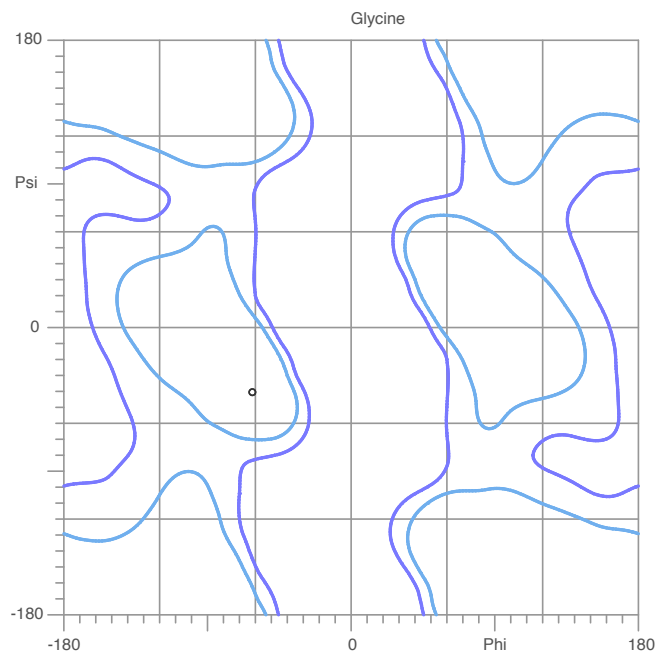
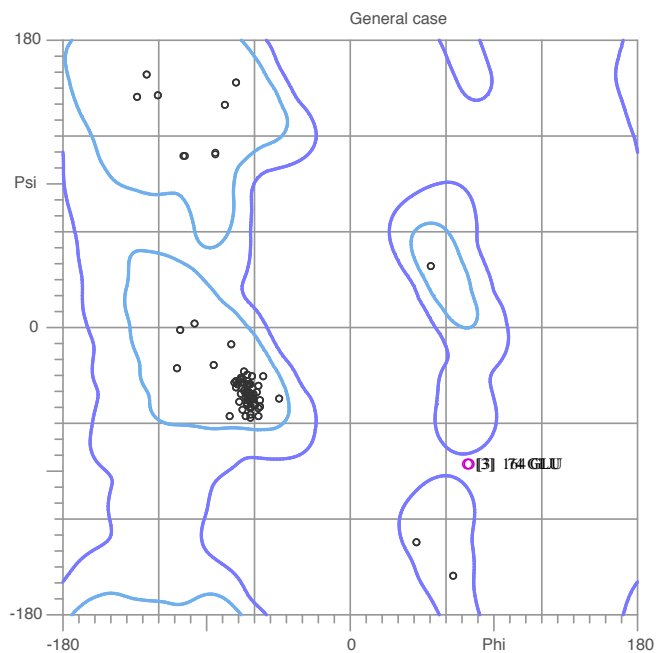
There were no outliers.

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

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MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 3



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.

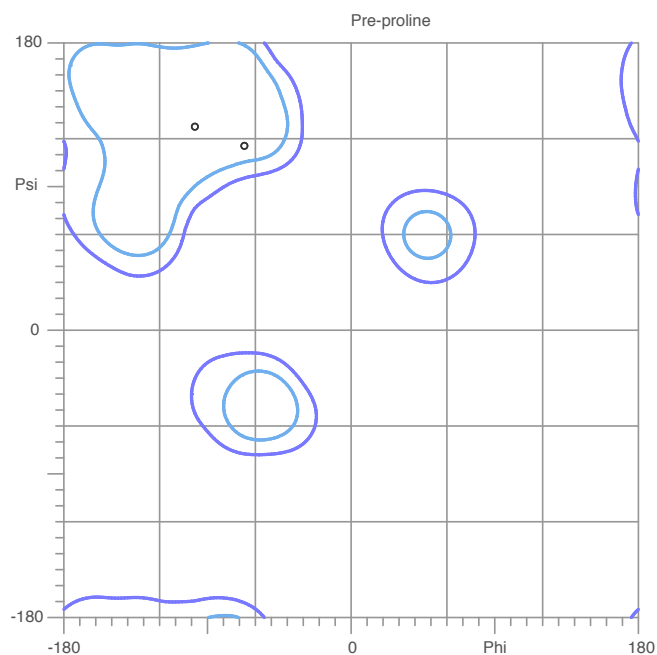
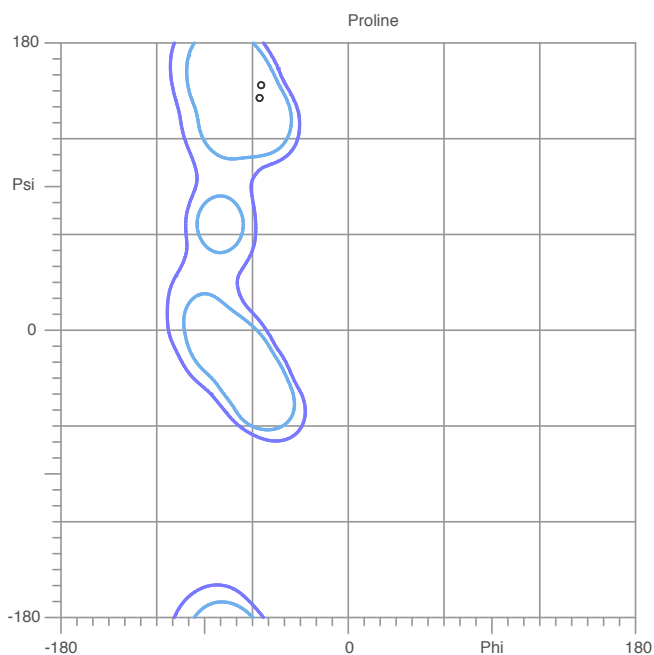
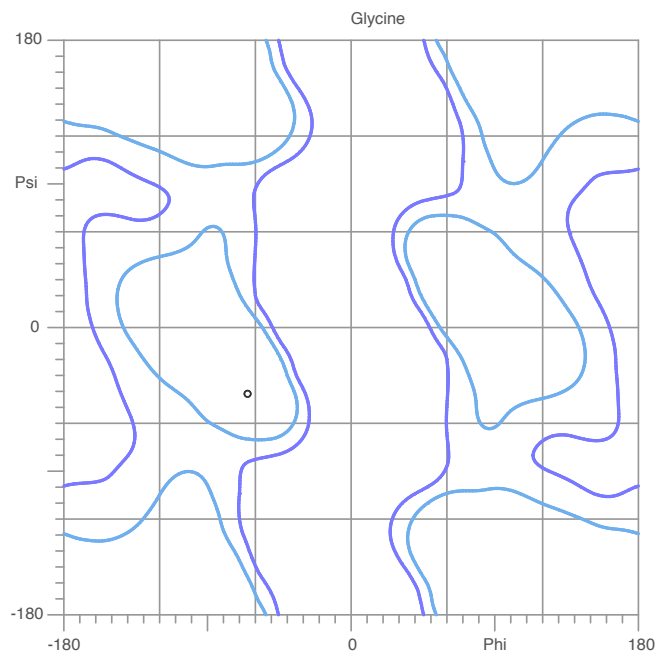
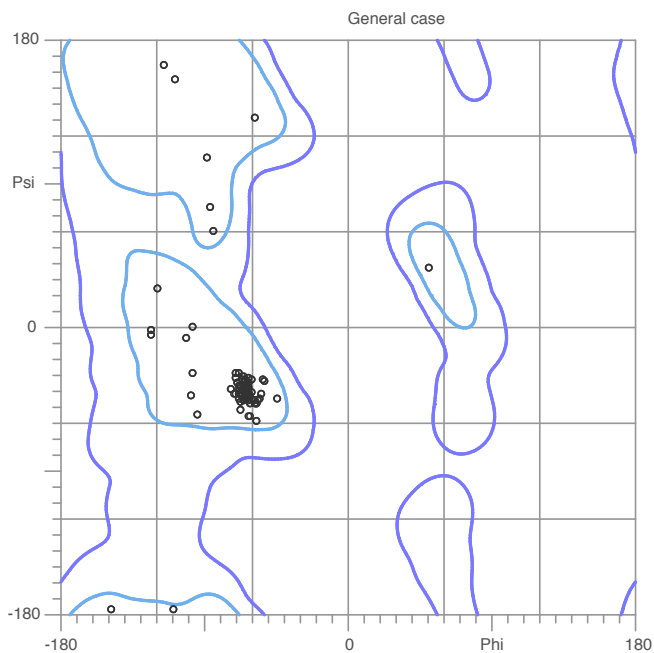
There were 2 outliers (phi, psi):

[3] 74 GLU (74.0, -85.2)

[3] 164 GLU (73.9, -85.2)

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 4



100.0% (156/156) of all residues were in favored (98%) regions.

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

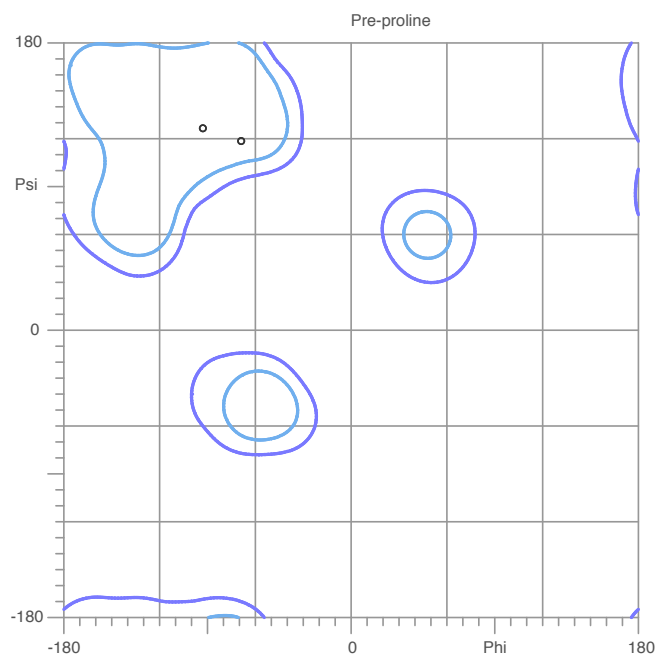
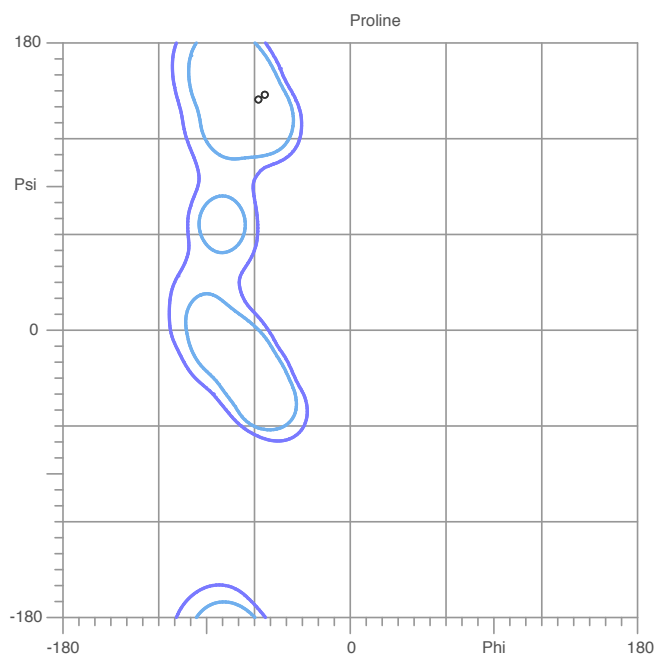
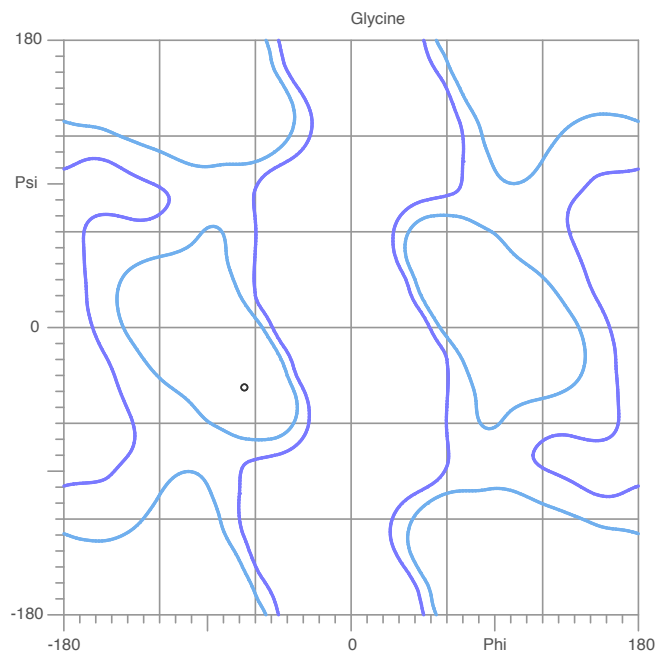
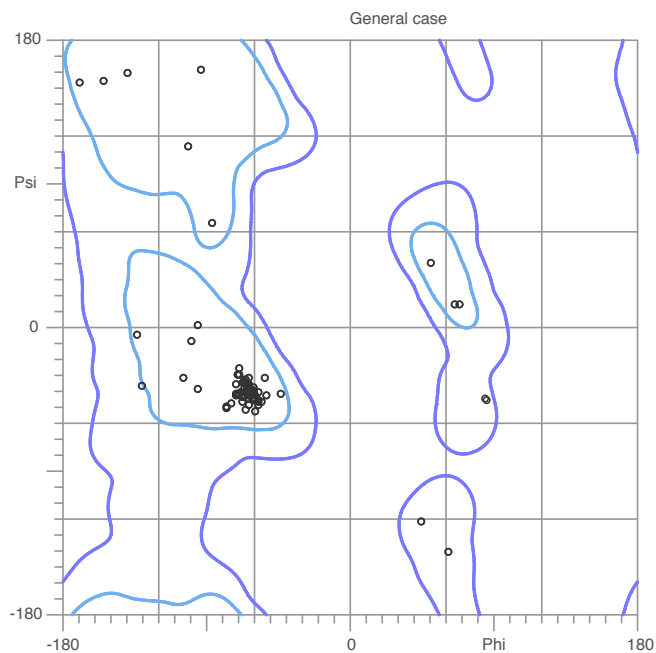
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 5



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.

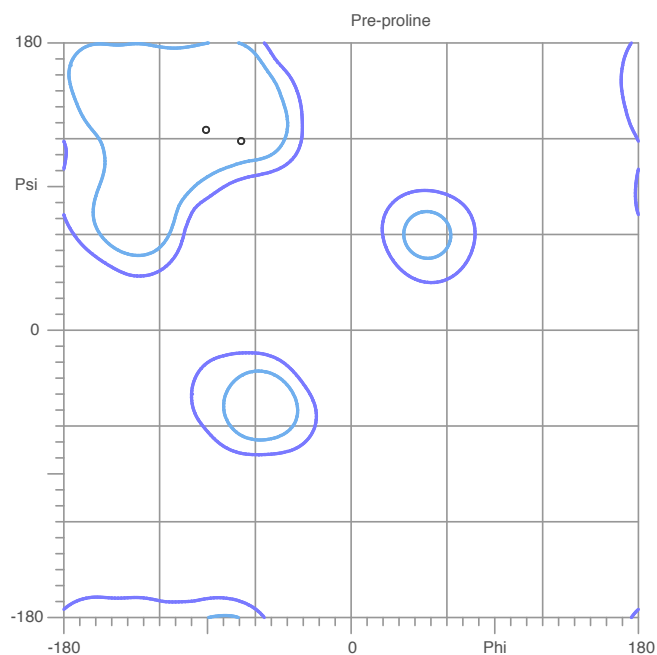
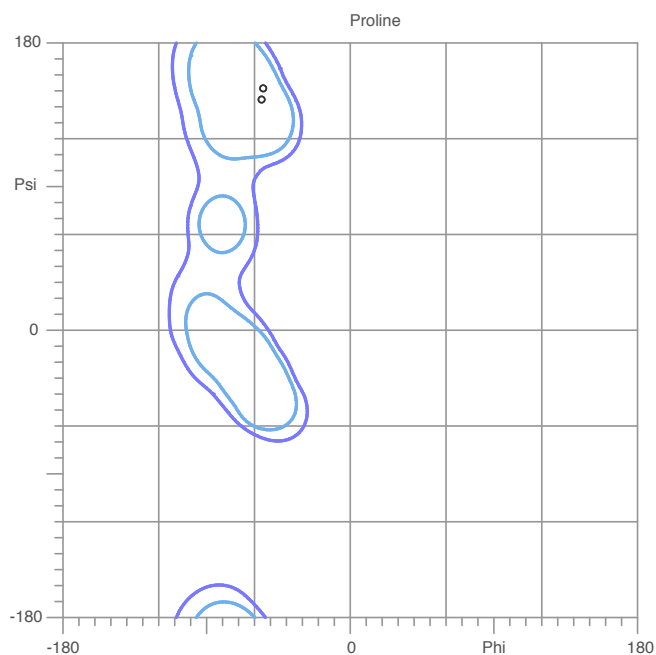
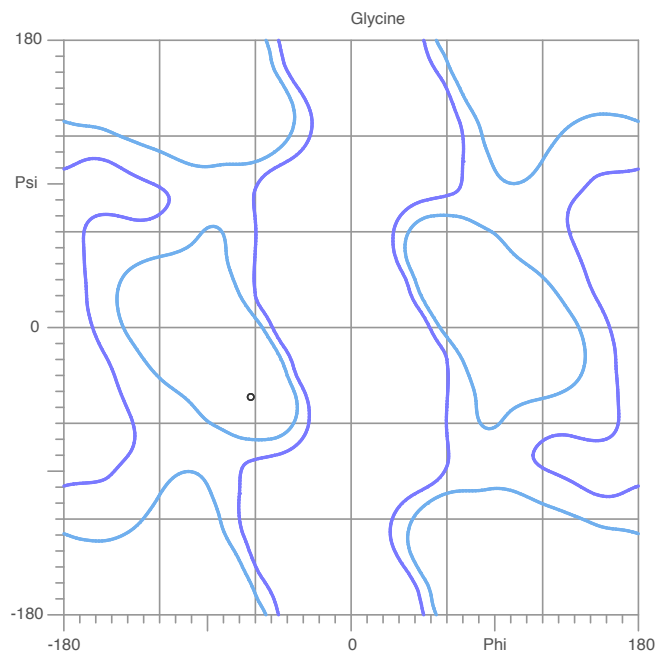
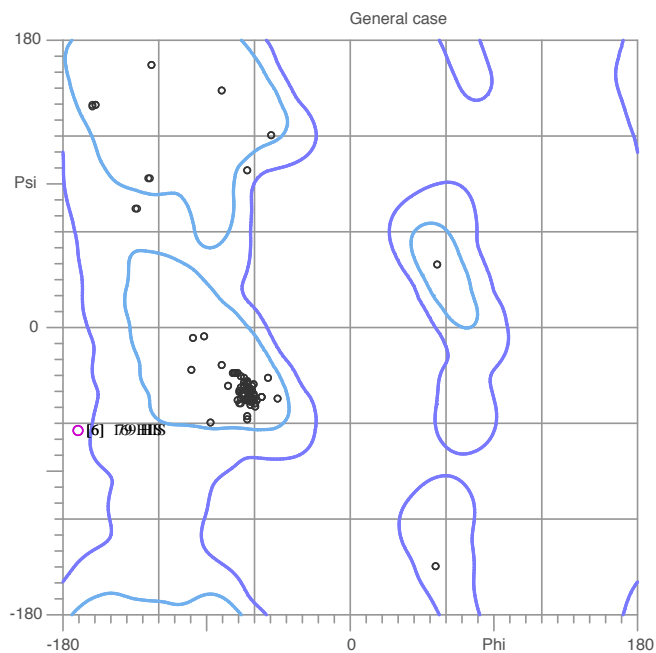
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 6



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.

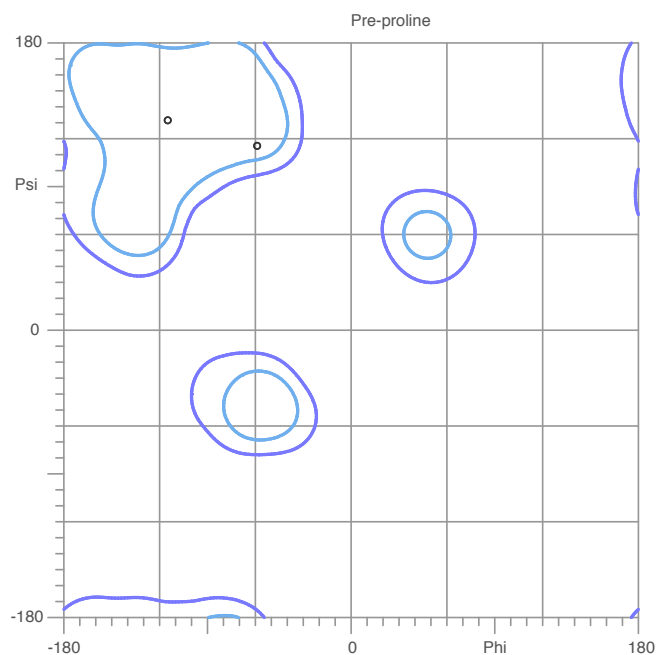
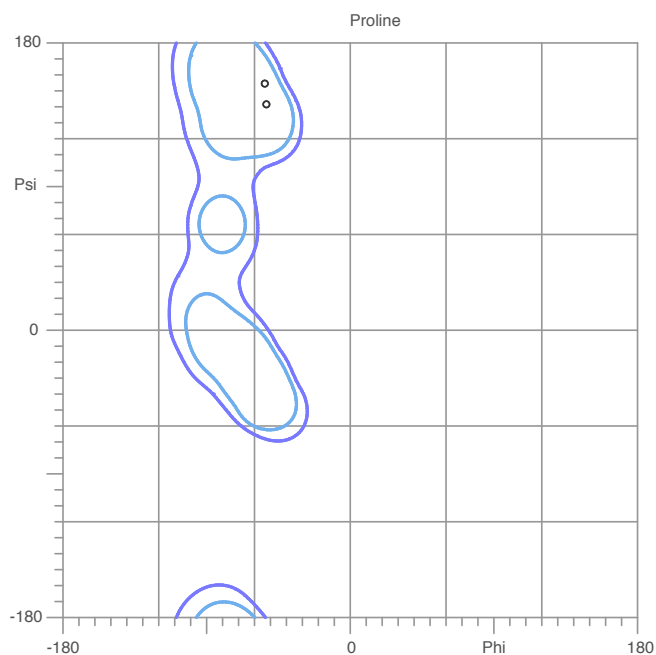
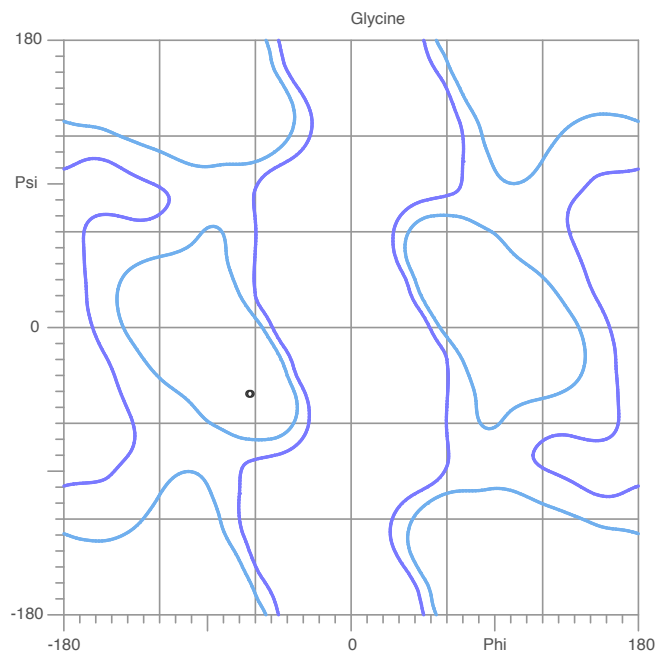
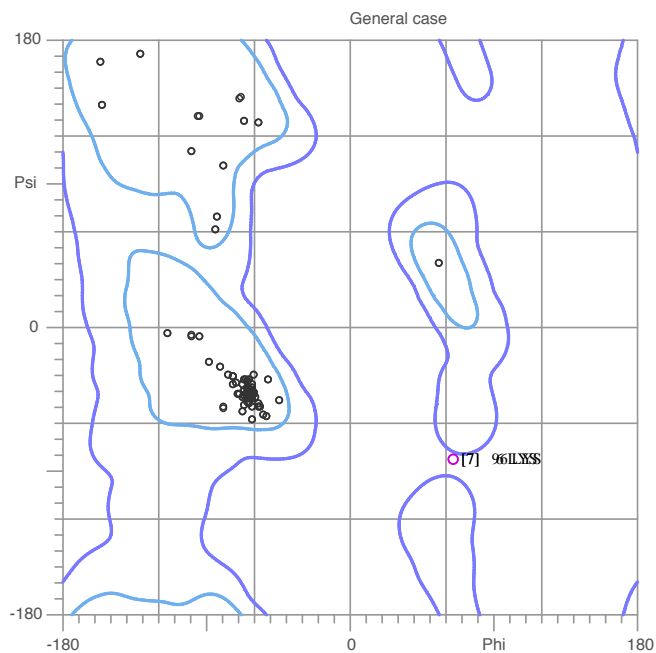
There were 2 outliers (phi, psi):

[6] 79 HIS (-171.9, -64.5)

[6] 169 HIS (-171.9, -64.4)

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 7



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

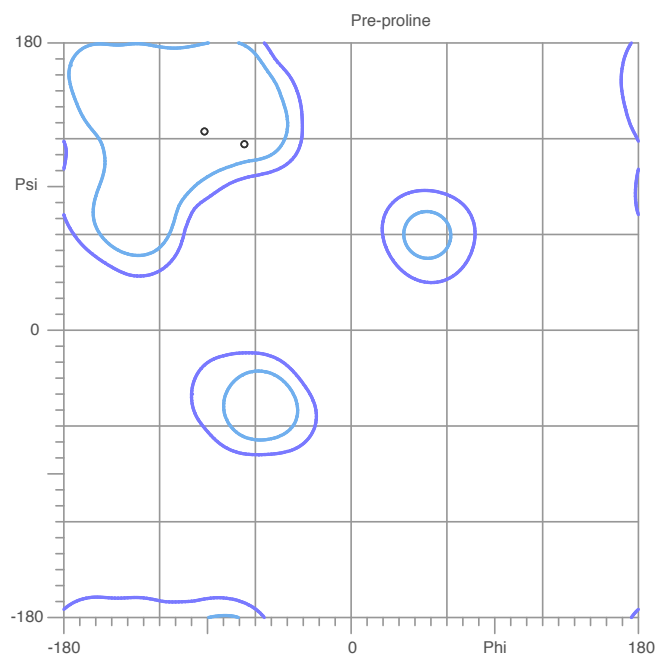
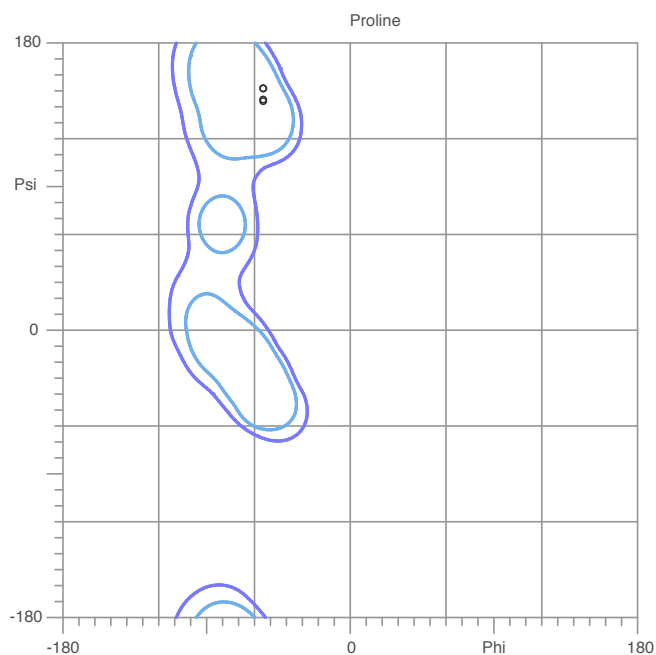
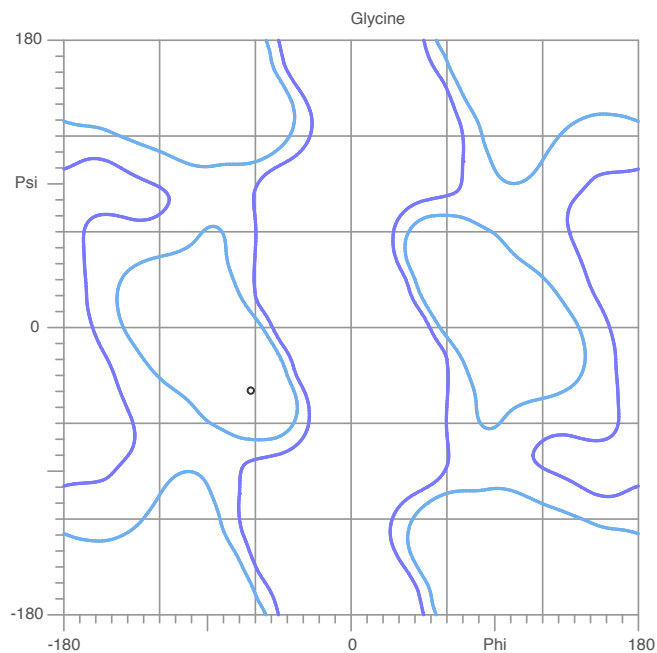
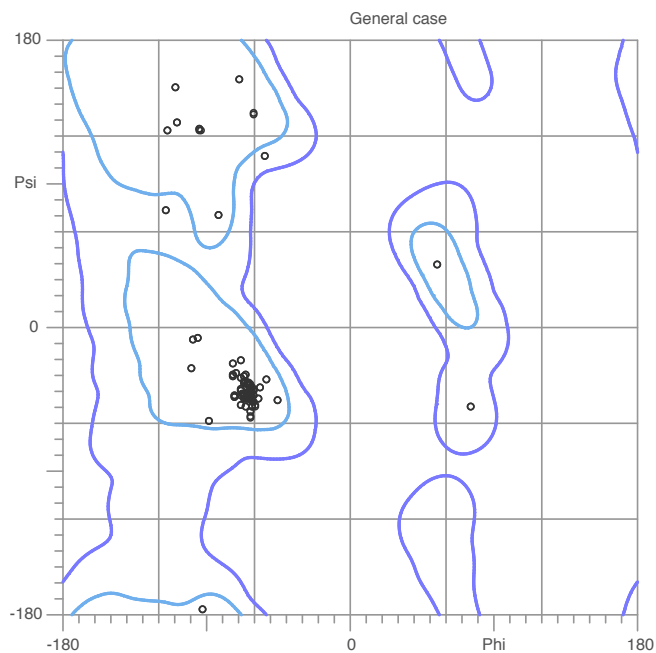
There were 2 outliers (phi, psi):

[7] 6 LYS (64.6, -82.1)

[7] 96 LYS (64.6, -82.0)

MolProbity Ramachandran analysis

SOR77_R3Cons_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.

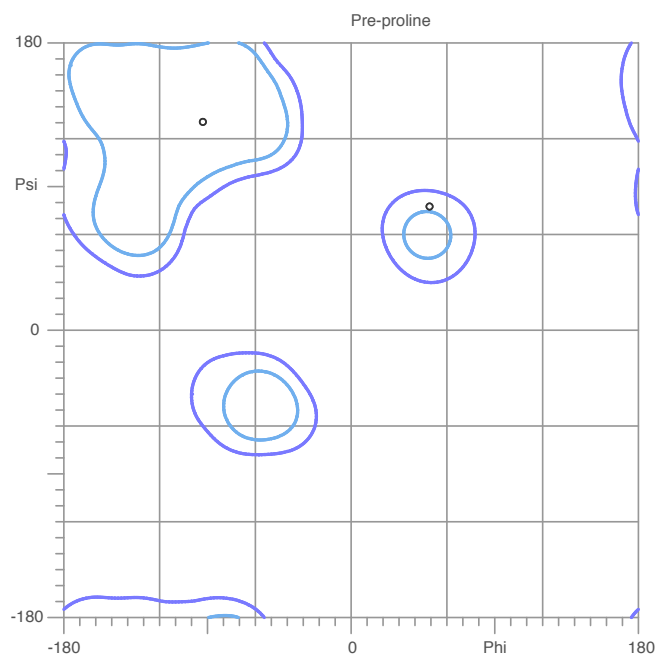
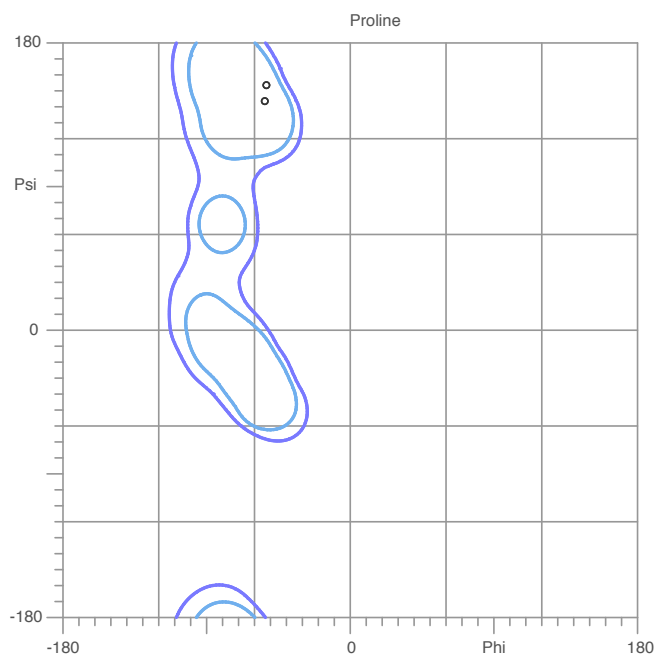
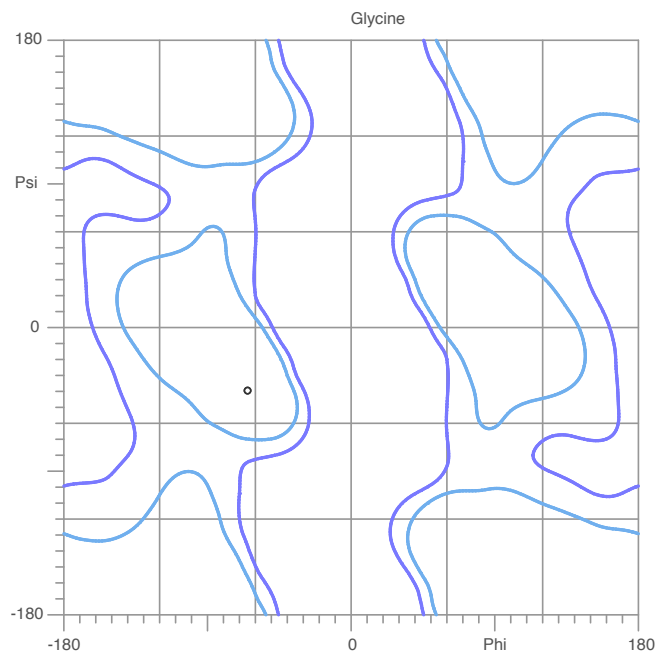
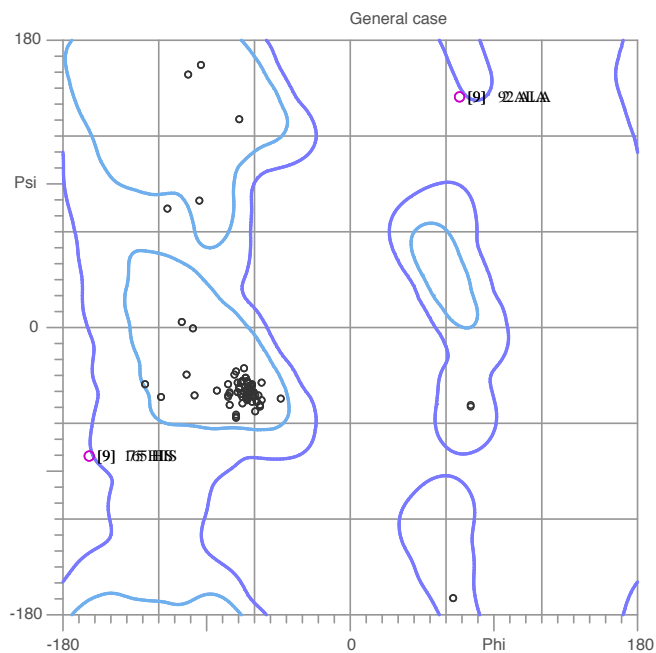
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 9



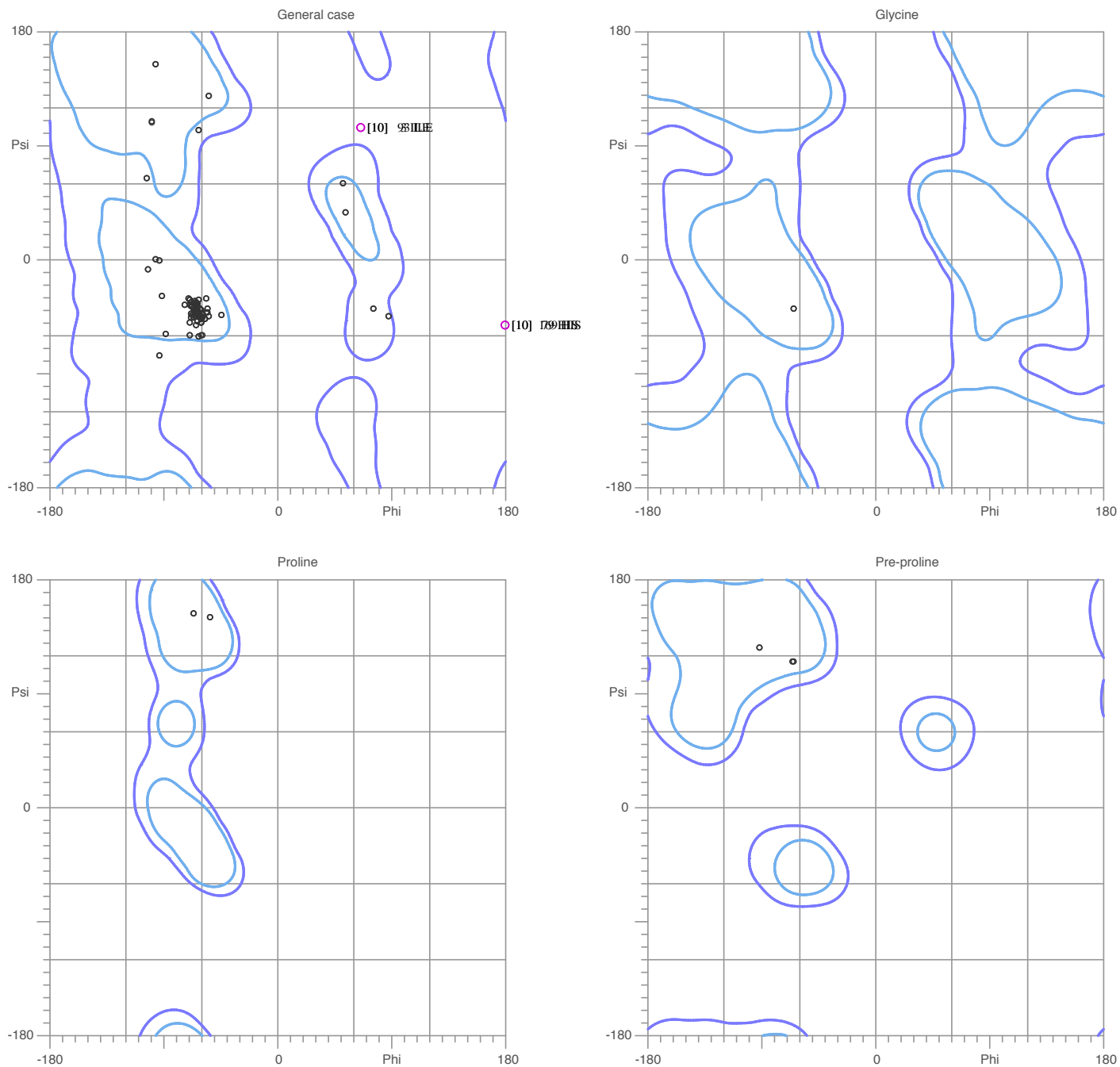
92.3% (144/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [9] 2 ALA (68.6, 145.6)
- [9] 75 HIS (-164.5, -80.3)
- [9] 92 ALA (68.6, 145.6)
- [9] 165 HIS (-164.4, -80.3)

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 10



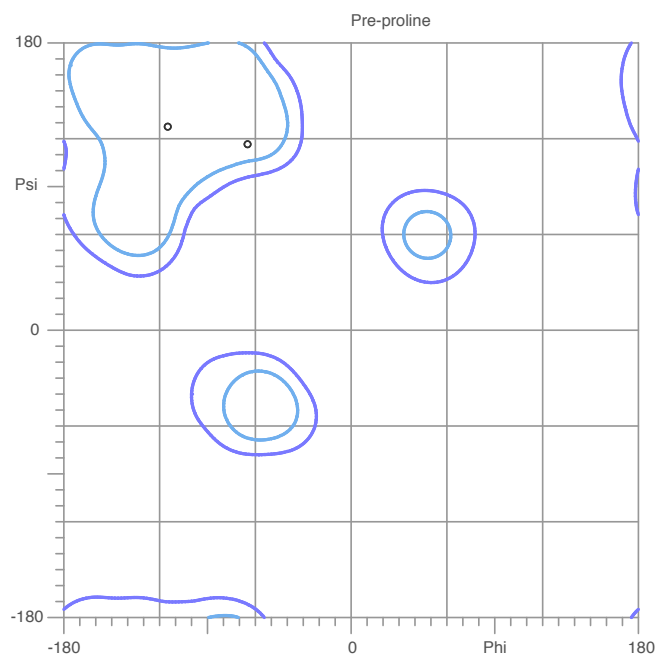
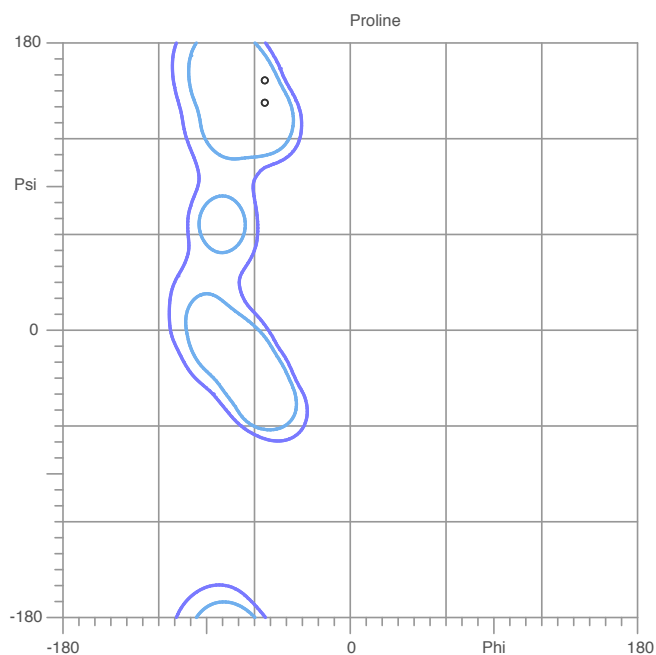
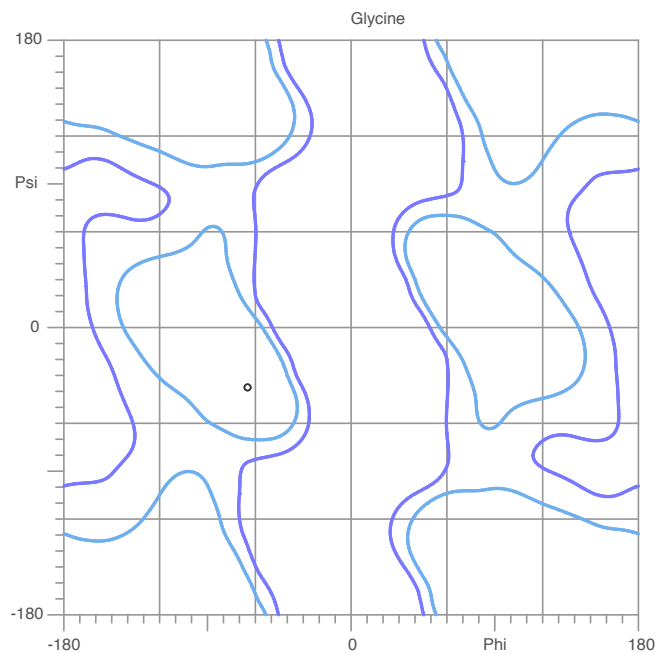
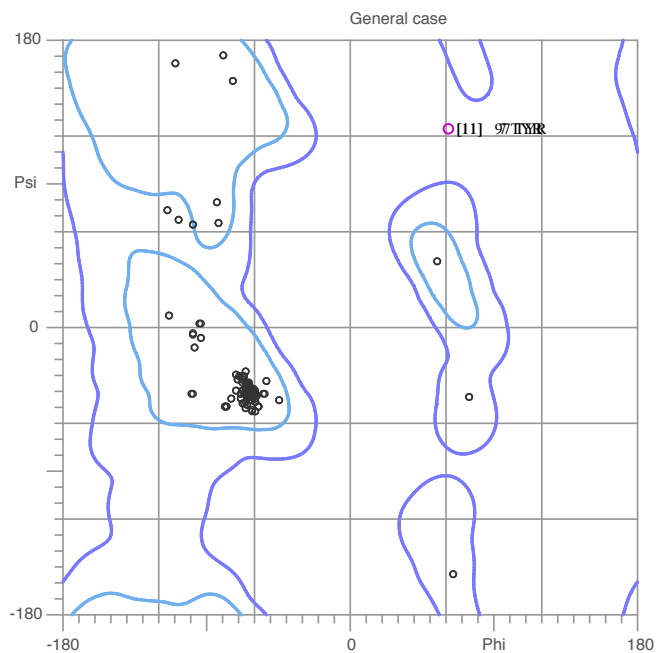
91.0% (142/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [10] 3 ILE (65.2, 105.1)
- [10] 79 HIS (179.1, -51.3)
- [10] 93 ILE (65.2, 105.1)
- [10] 169 HIS (179.2, -51.3)

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 11



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.

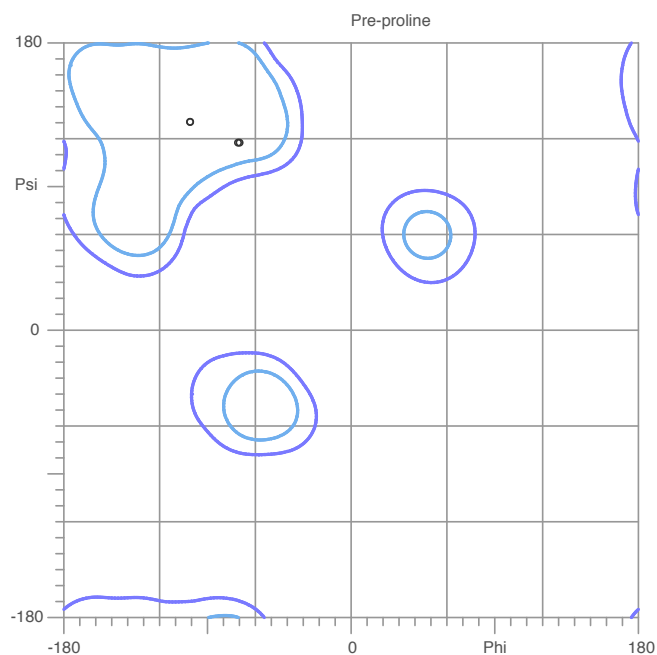
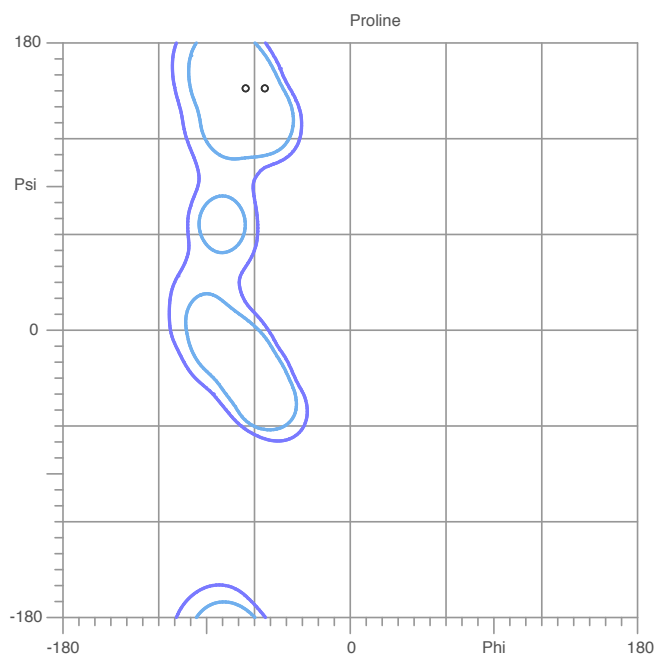
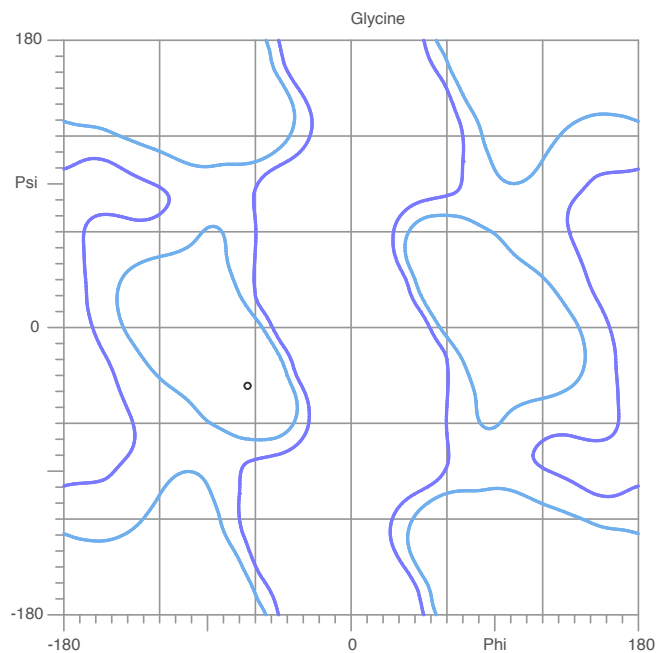
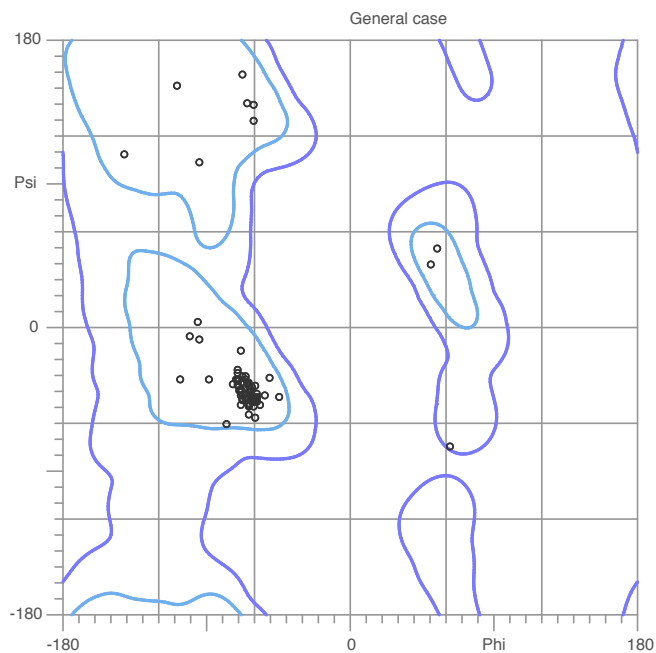
There were 2 outliers (phi, psi):

[11] 7 TYR (61.4, 125.0)

[11] 97 TYR (61.4, 125.0)

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 12



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.

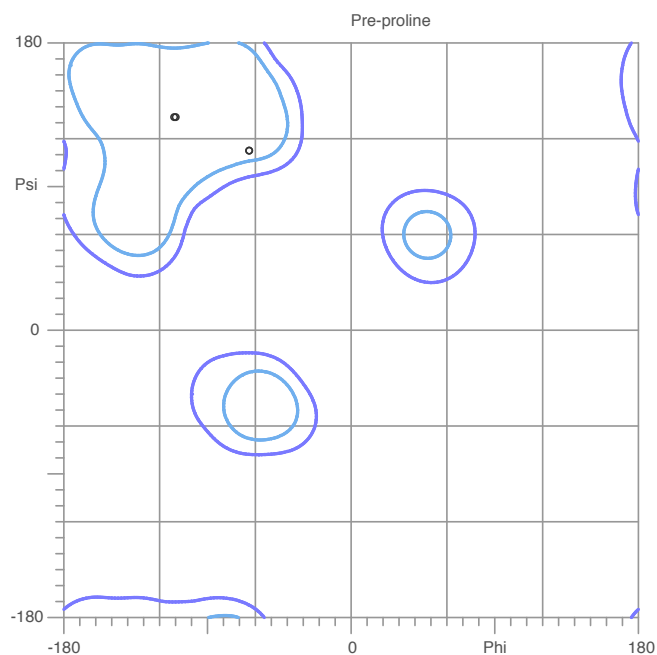
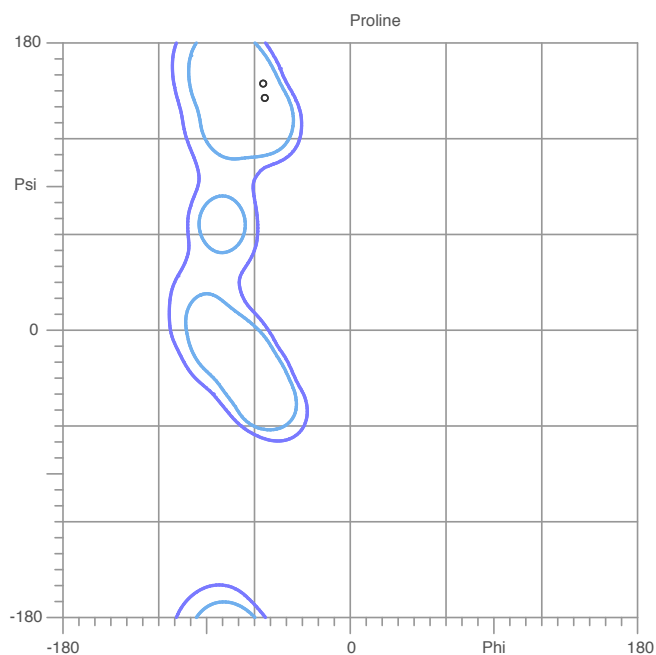
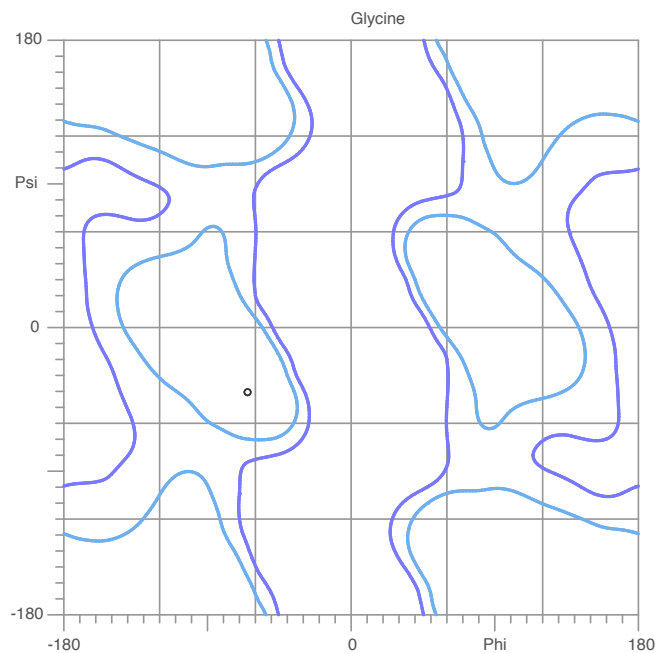
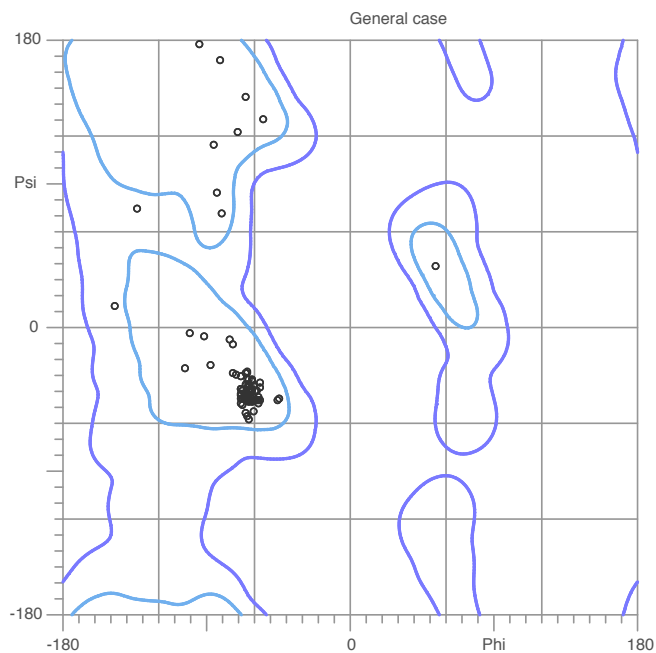
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 13



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.

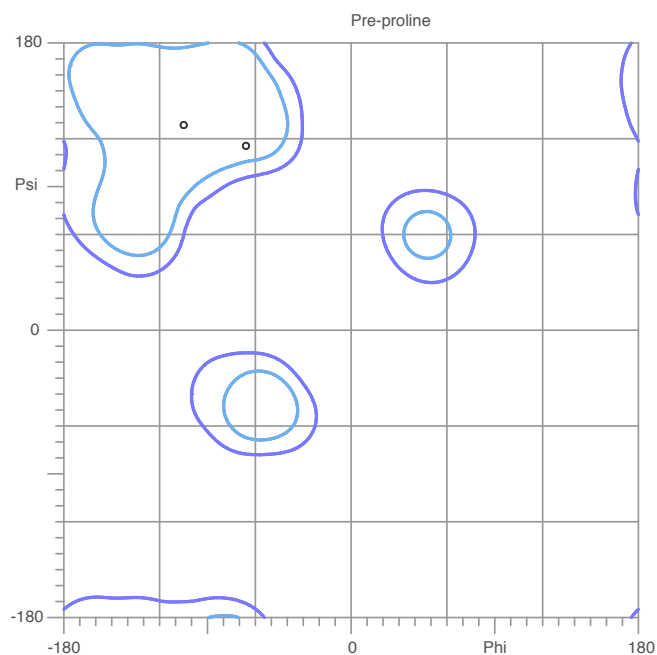
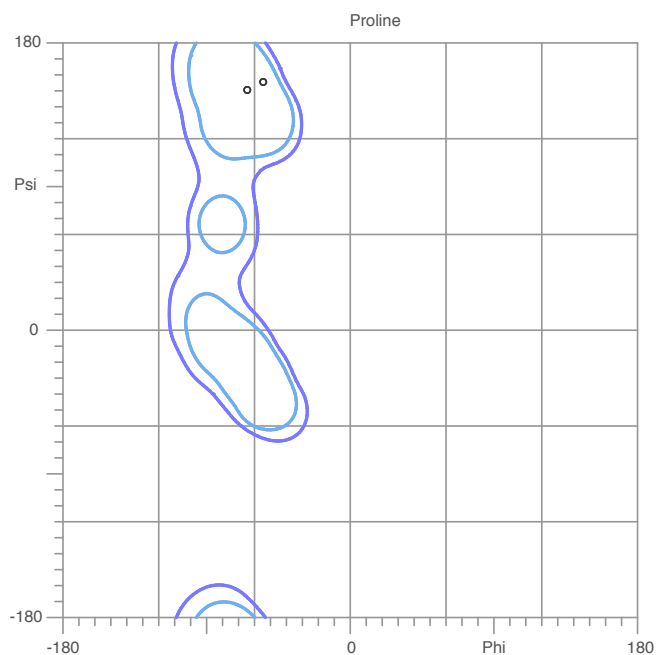
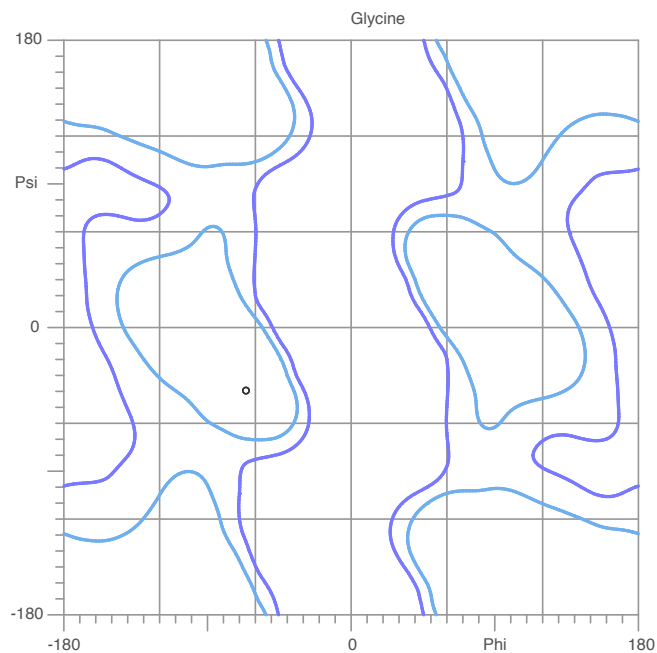
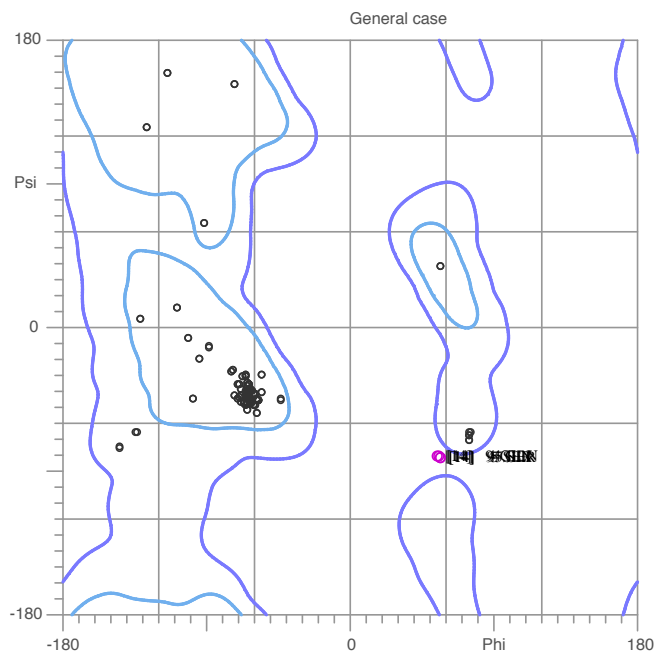
There were no outliers.

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MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 14



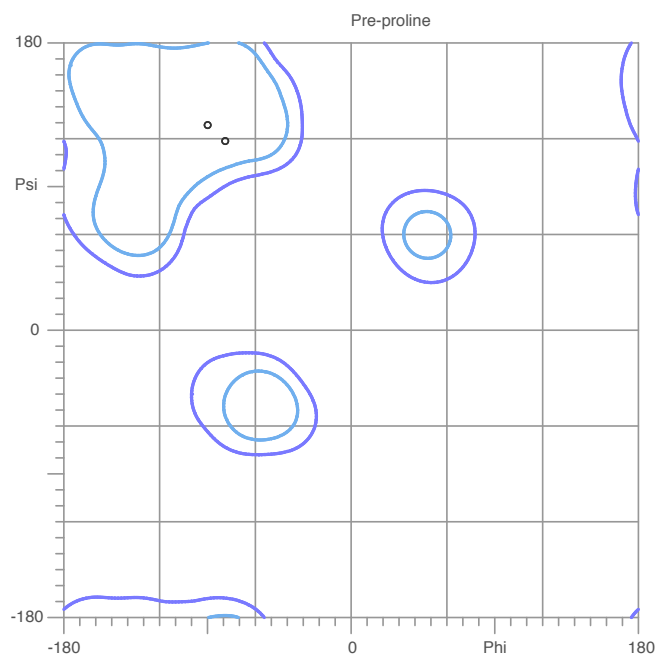
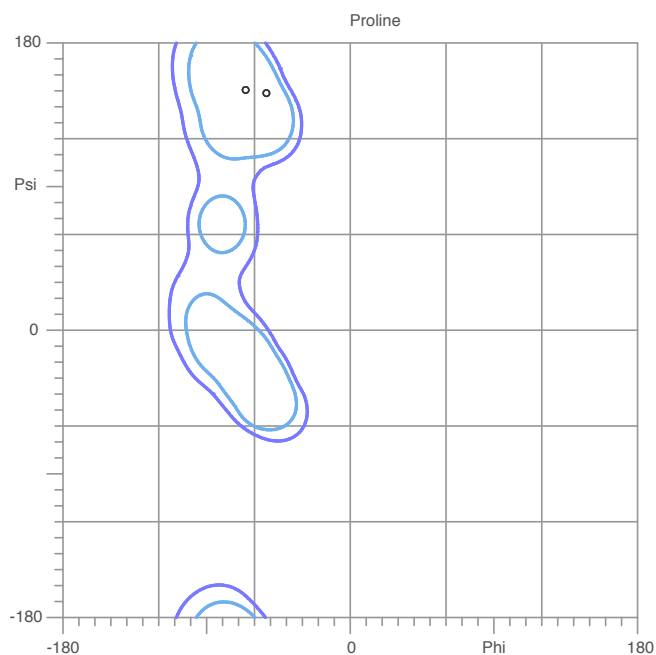
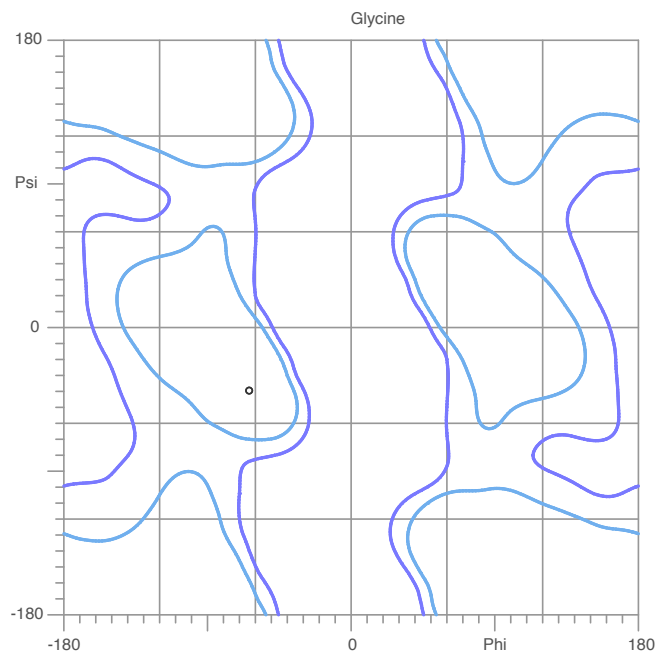
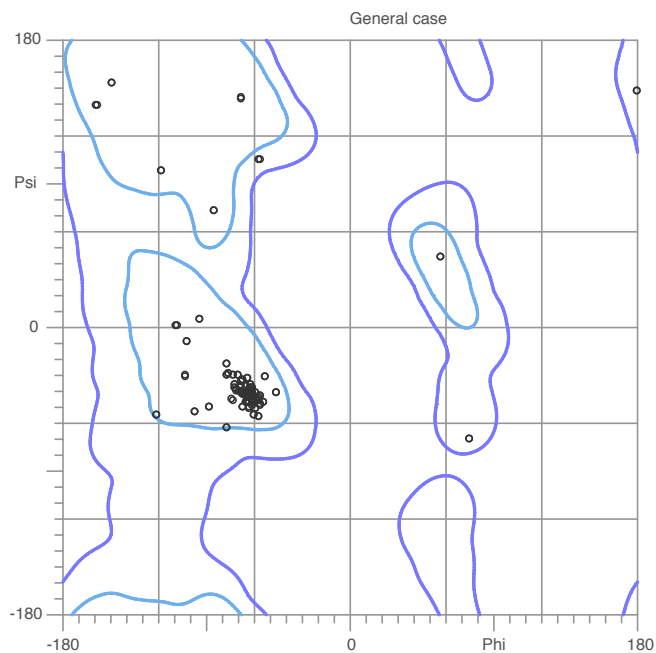
91.0% (142/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [14] 4 GLN (55.0, -80.1)
- [14] 5 SER (56.8, -81.9)
- [14] 94 GLN (55.0, -80.1)
- [14] 95 SER (56.8, -81.9)

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 15



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.

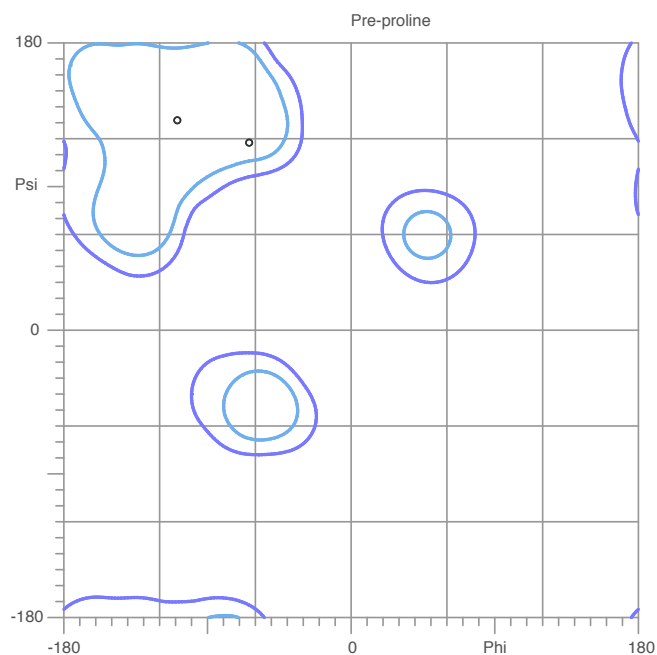
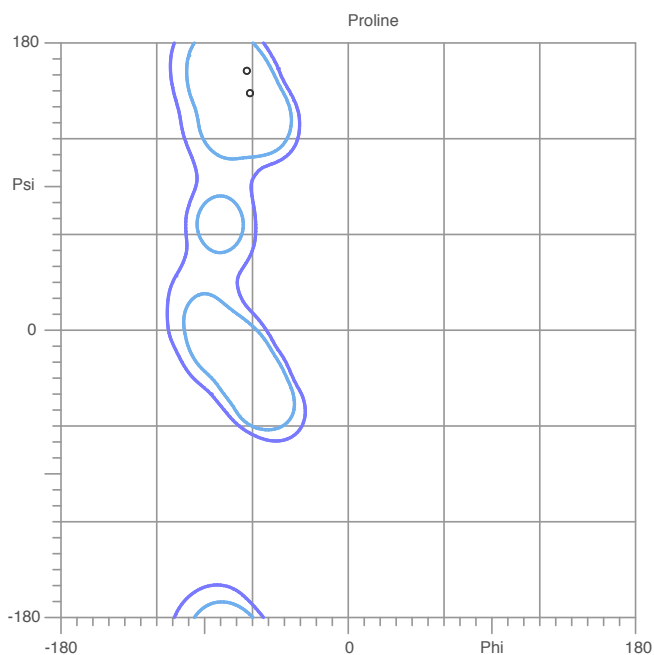
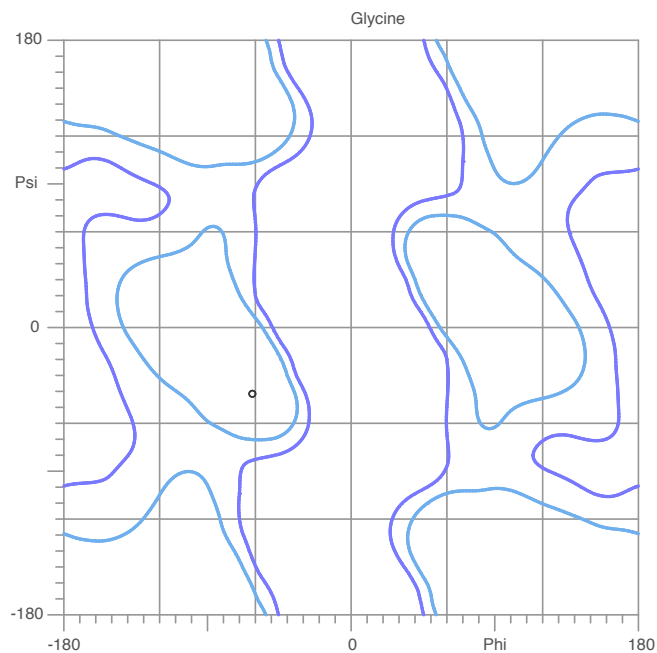
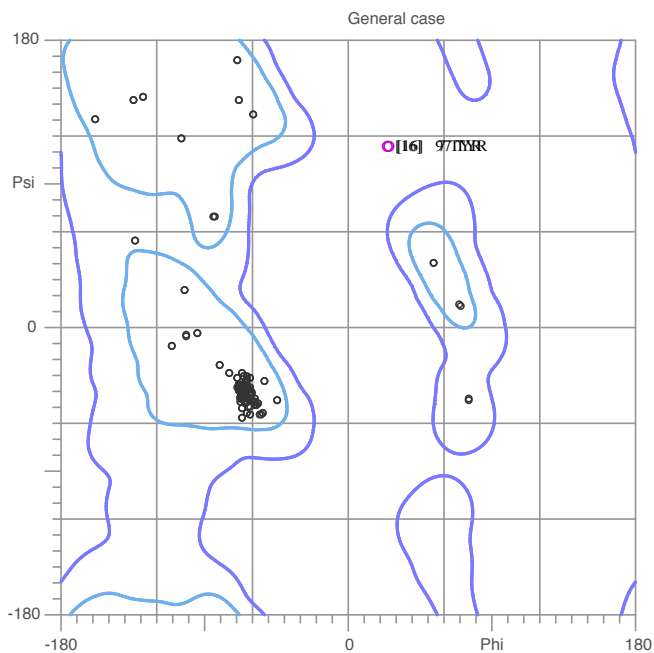
There were no outliers.

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

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

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 16



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.

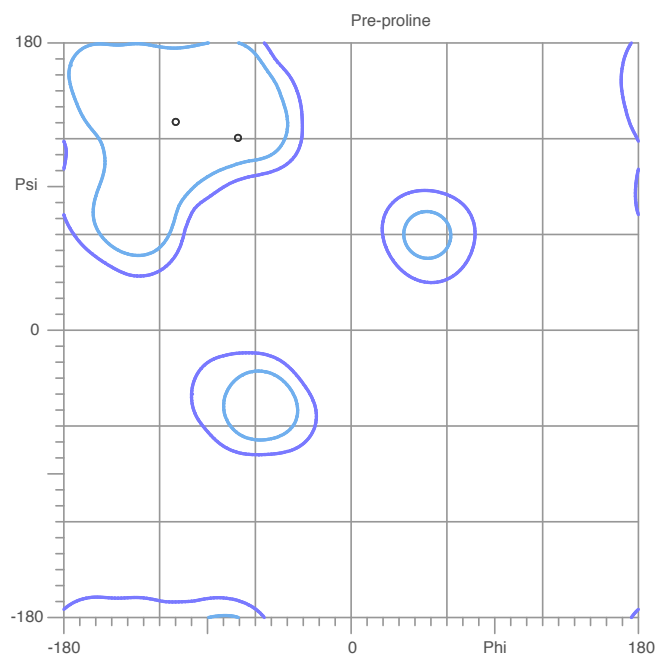
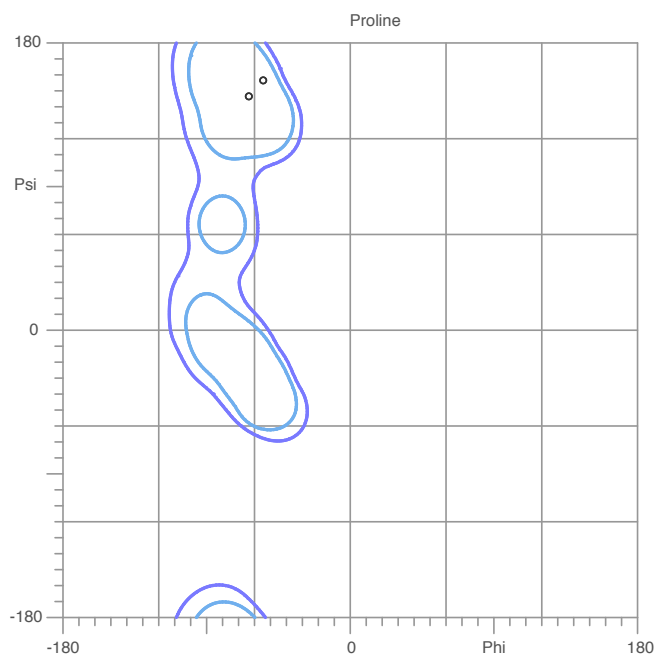
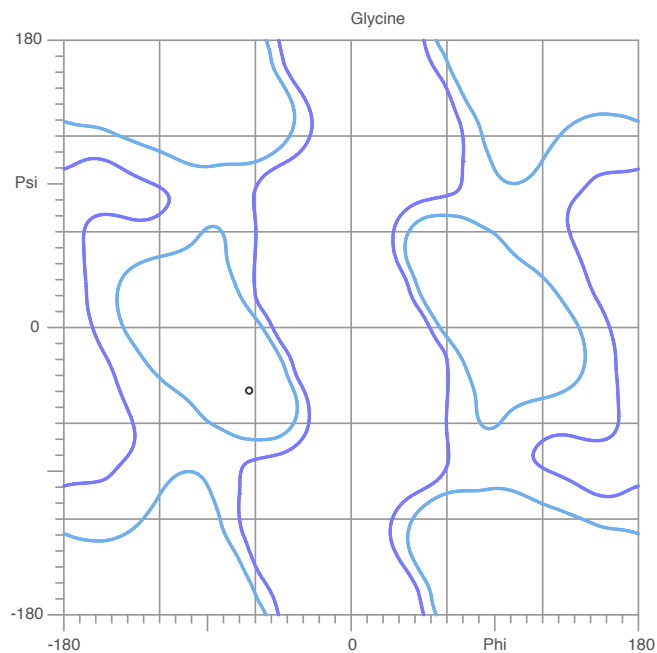
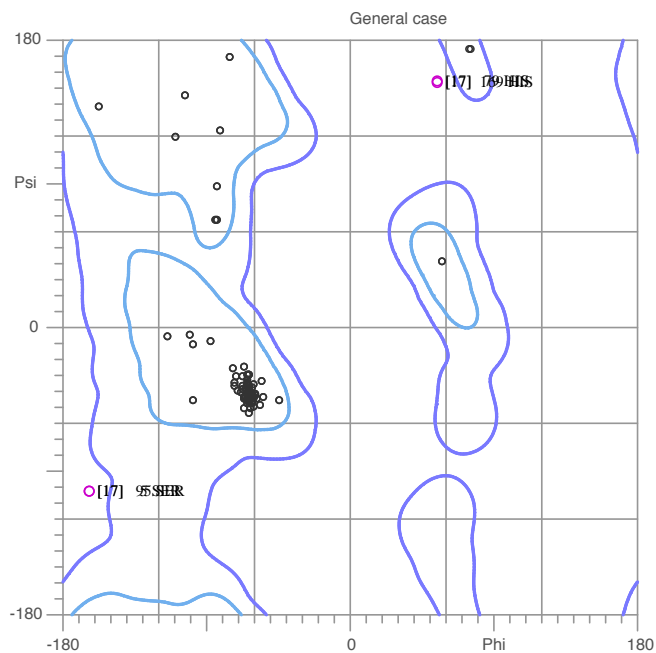
There were 2 outliers (phi, psi):

[16] 7 TYR (24.9, 115.0)

[16] 97 TYR (25.0, 115.0)

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 17



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):

[17] 5 SER (-165.0, -102.4)

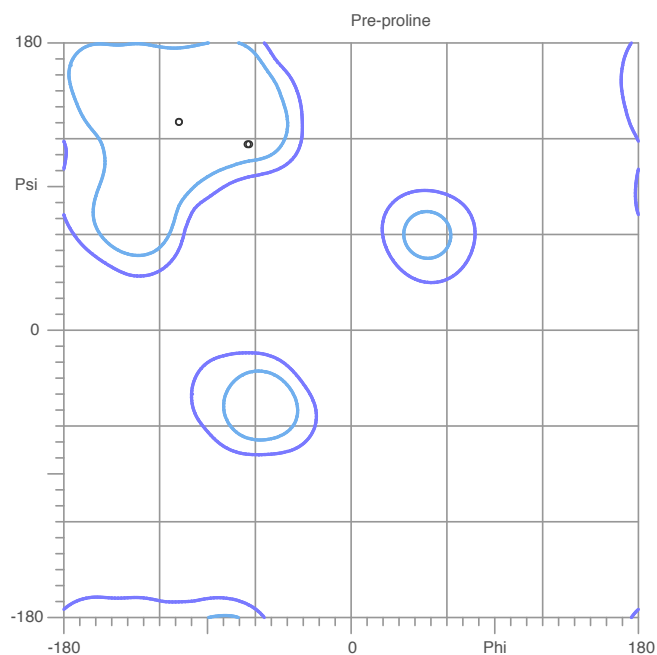
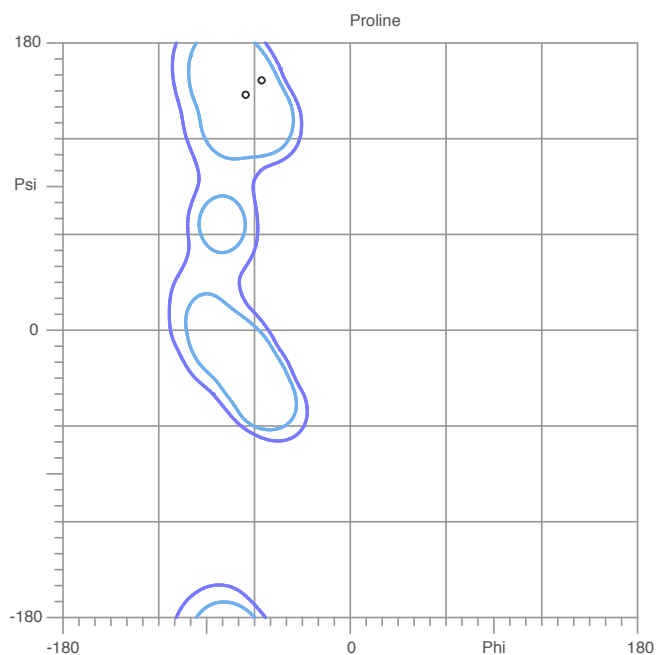
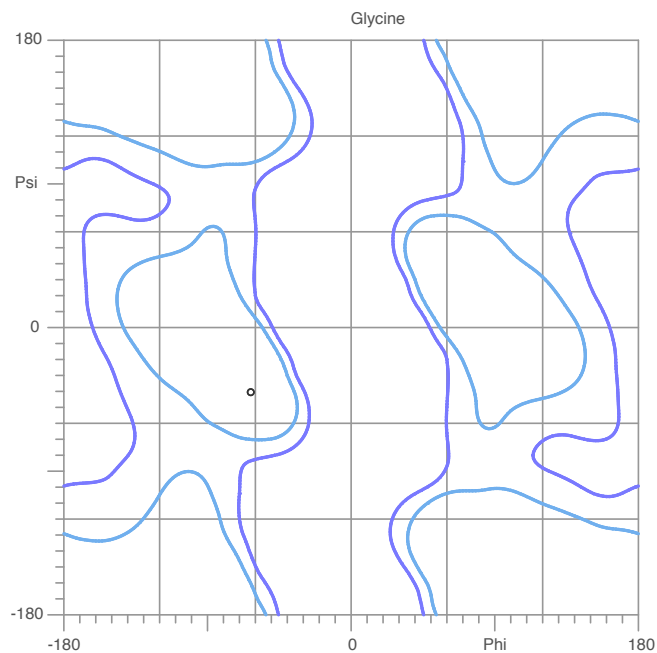
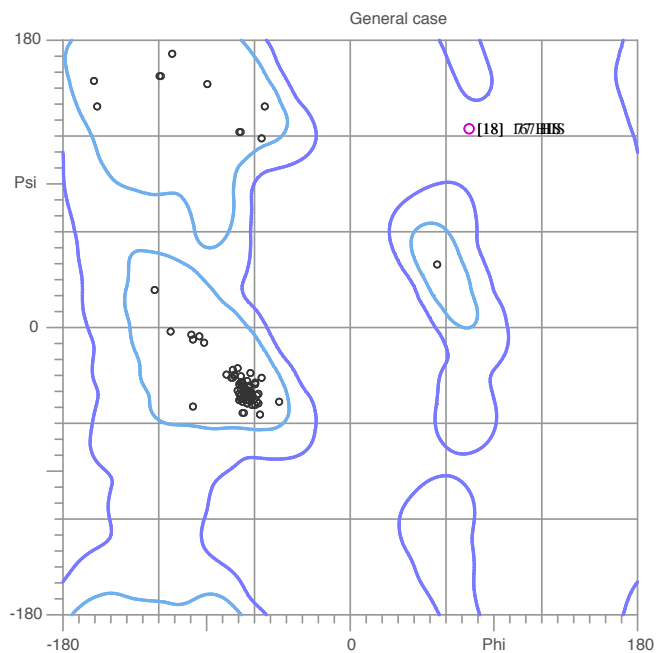
[17] 79 HIS (55.0, 155.0)

[17] 95 SER (-164.9, -102.4)

[17] 169 HIS (55.0, 155.0)

MolProbity Ramachandran analysis

SOR77_R3Cons_em_bcr3.pdb, model 18



98.7% (154/156) 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 (74.9, 125.0)

[18] 167 HIS (74.9, 125.0)