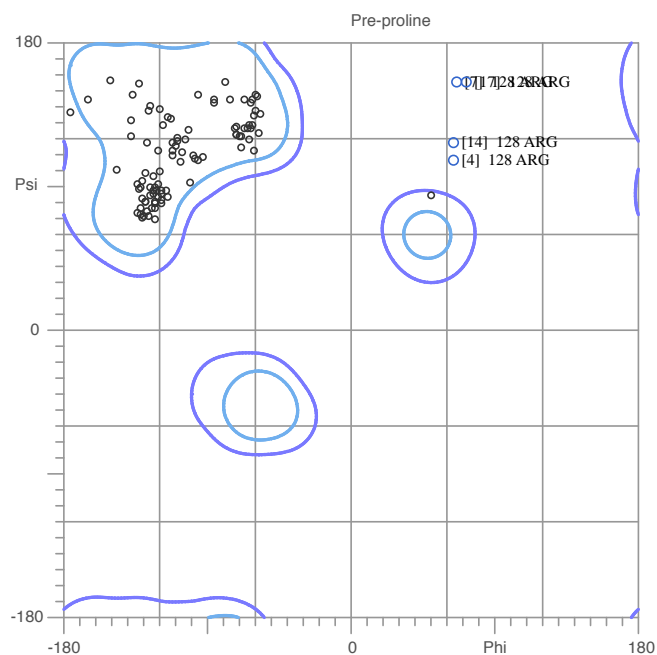
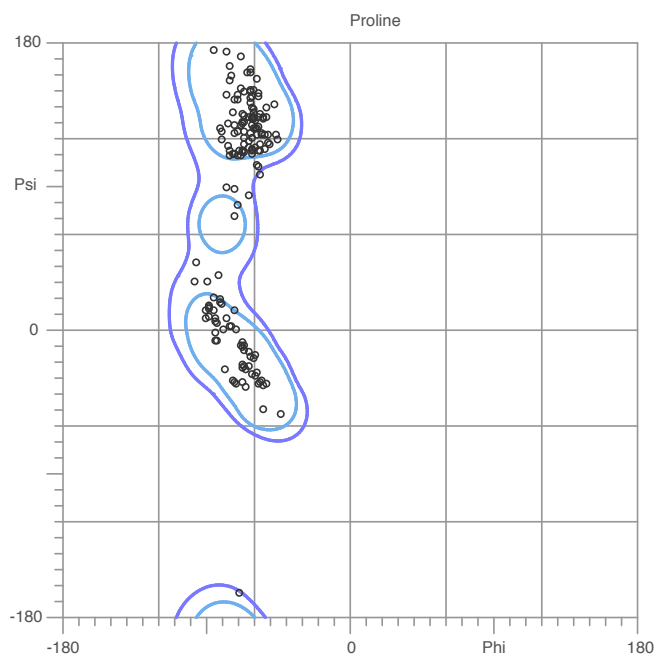
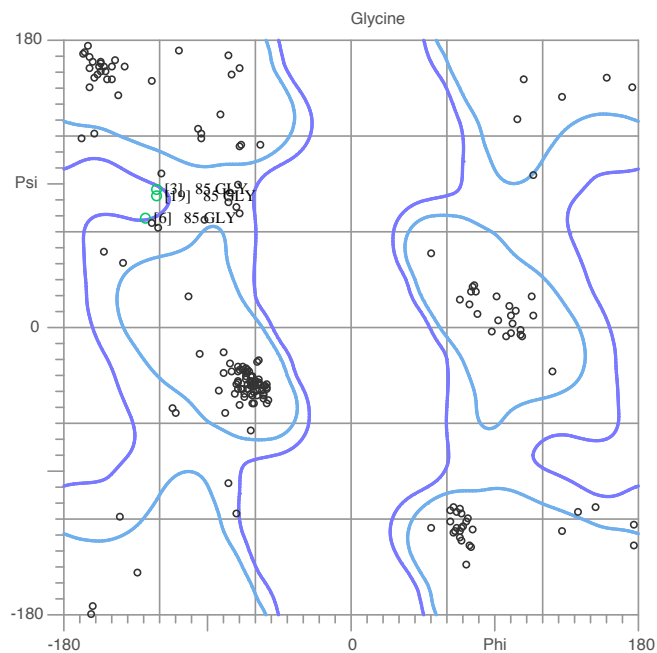
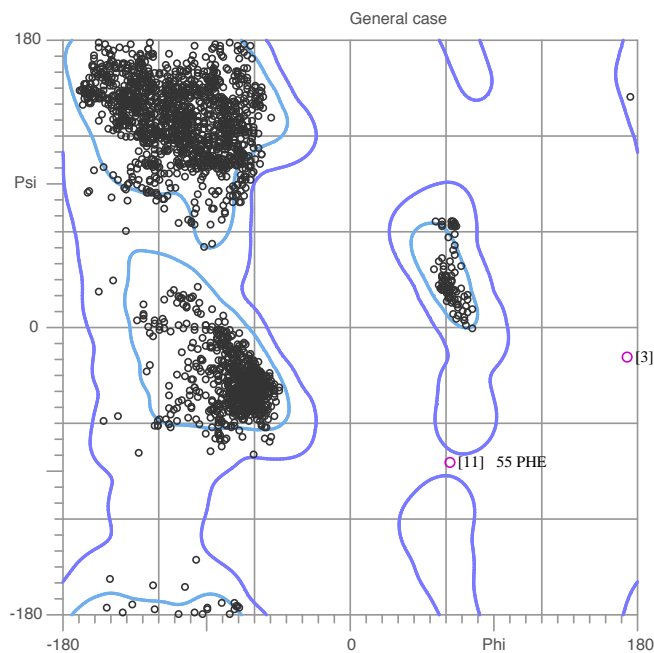


MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, all models



94.3% (2489/2640) of all residues were in favored (98%) regions.
99.7% (2631/2640) of all residues were in allowed (>99.8%) regions.

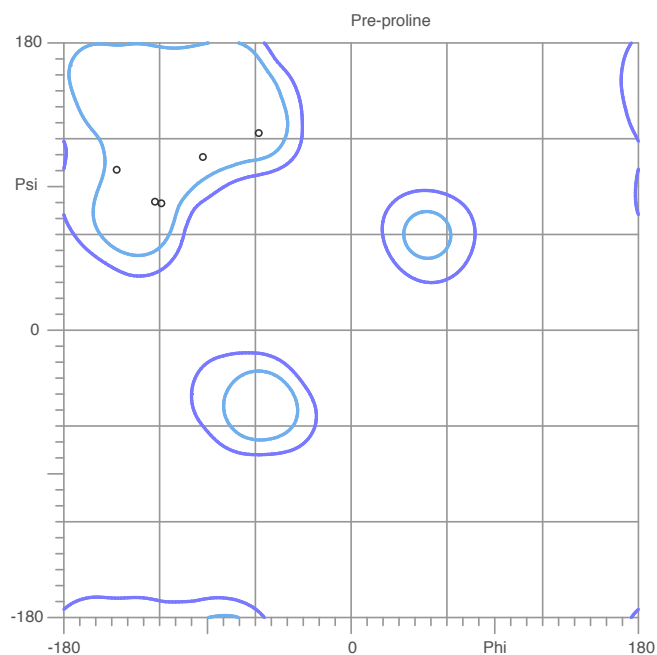
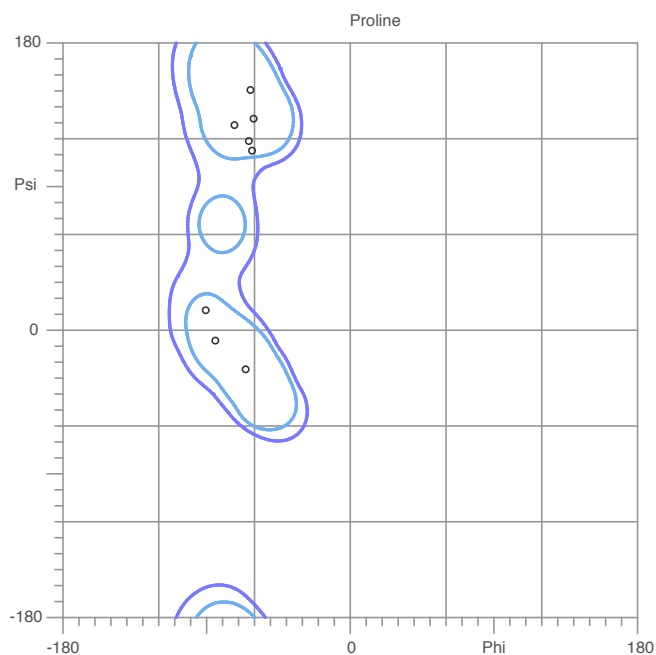
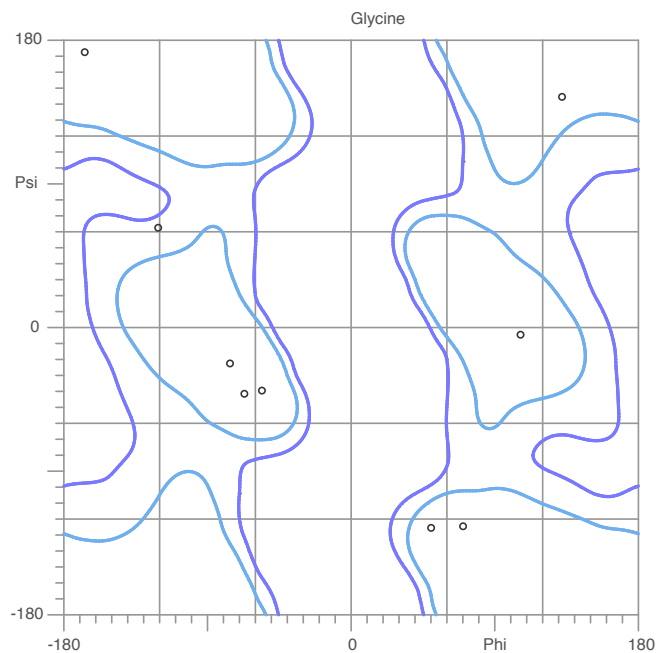
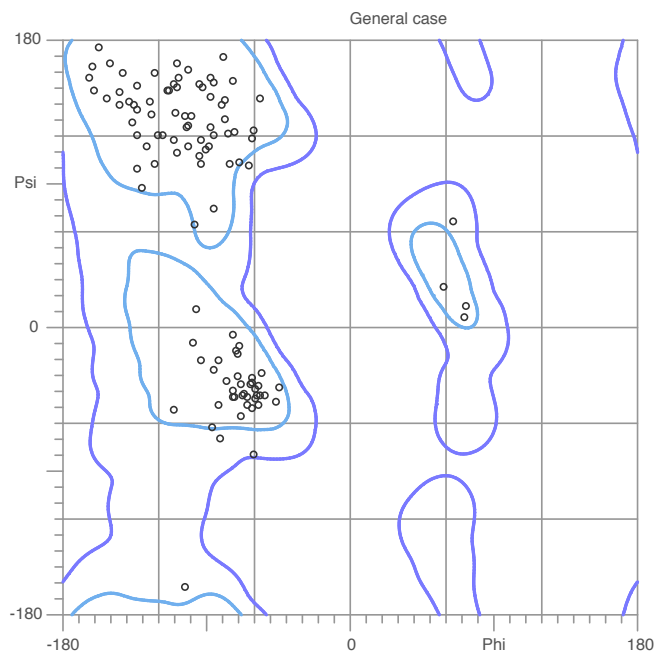
There were 9 outliers (phi, psi):

[3] 82 SER (173.3, -18.6)
[3] 85 GLY (-122.4, 87.6)

[4] 128 ARG (64.9, 107.5)
[6] 85 GLY (-129.5, 69.2)
[7] 128 ARG (66.1, 156.4)
[11] 55 PHE (62.4, -84.6)
[14] 128 ARG (64.9, 118.3)
[17] 128 ARG (72.7, 156.6)
[19] 85 GLY (-122.5, 83.0)

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 1



94.7% (125/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

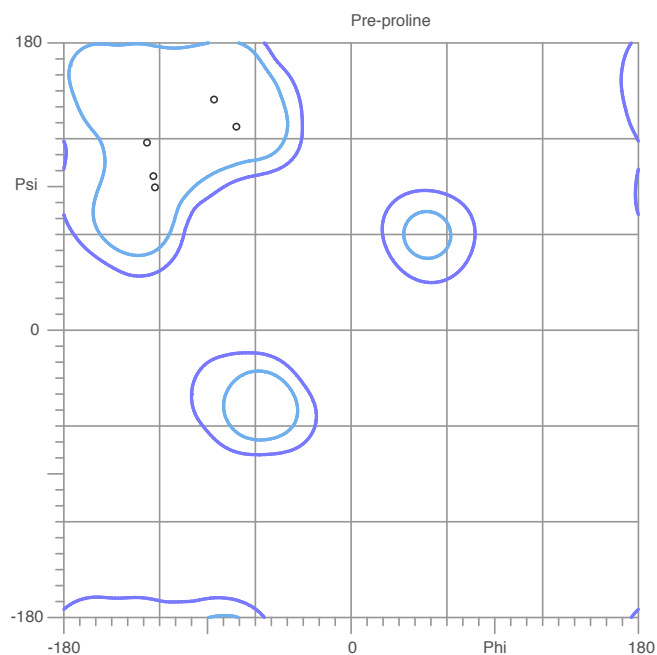
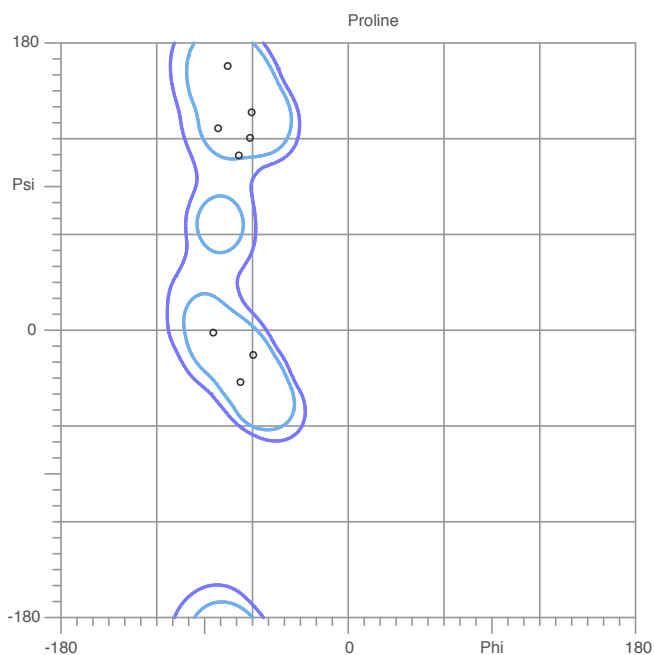
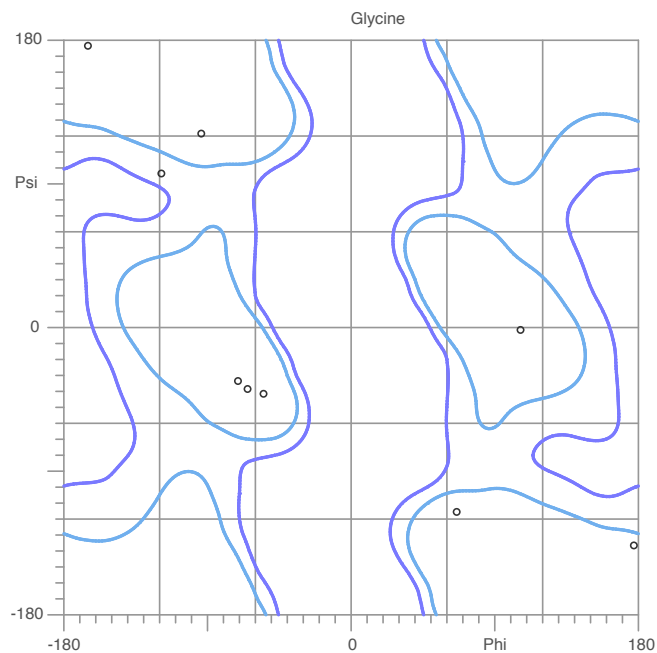
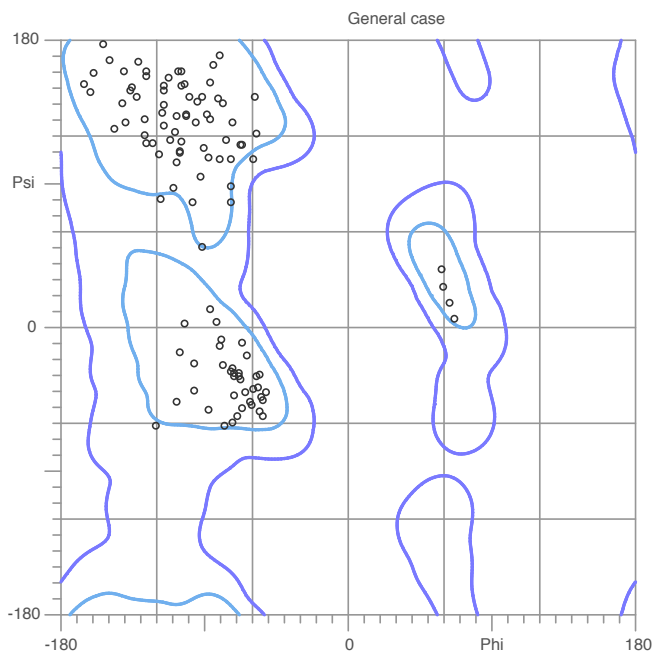
There were no outliers.

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

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

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 2



96.2% (127/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

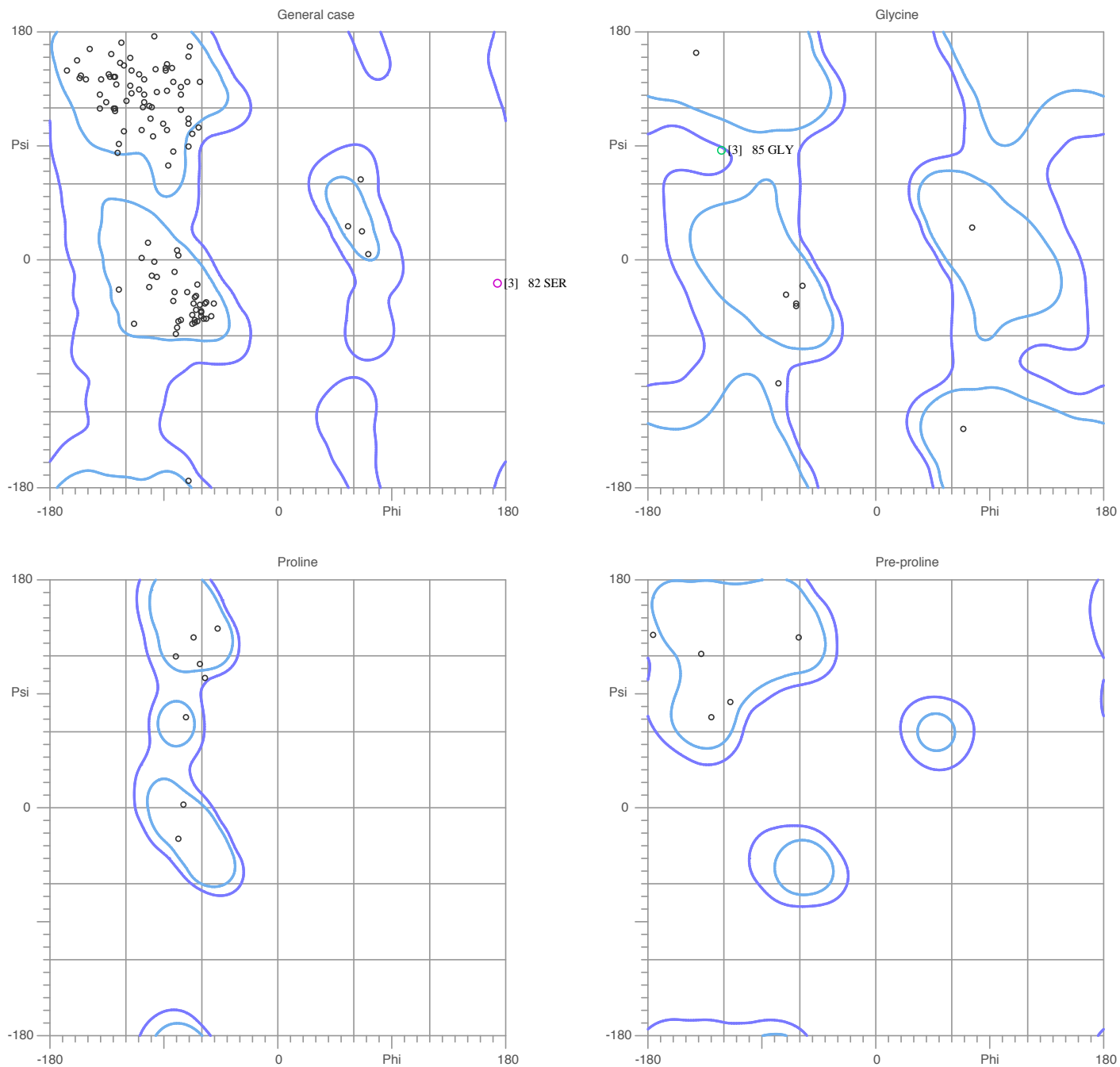
There were no outliers.

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

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

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 3



92.4% (122/132) of all residues were in favored (98%) regions.
98.5% (130/132) of all residues were in allowed (>99.8%) regions.

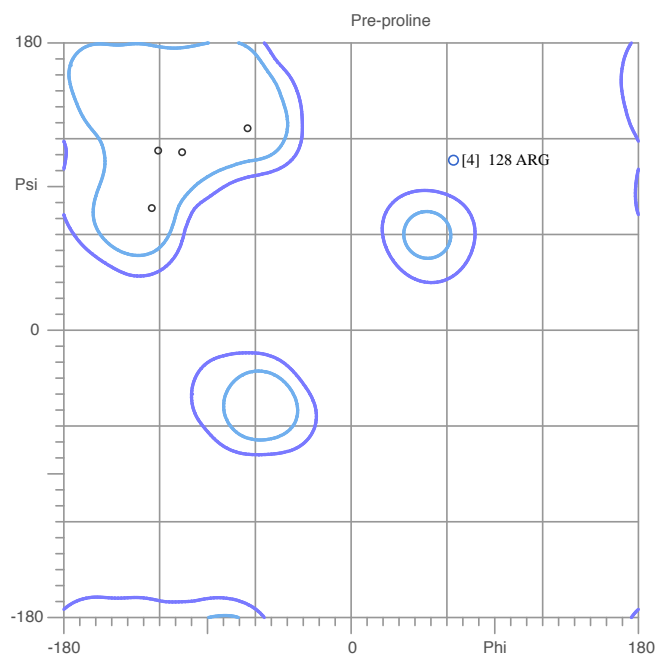
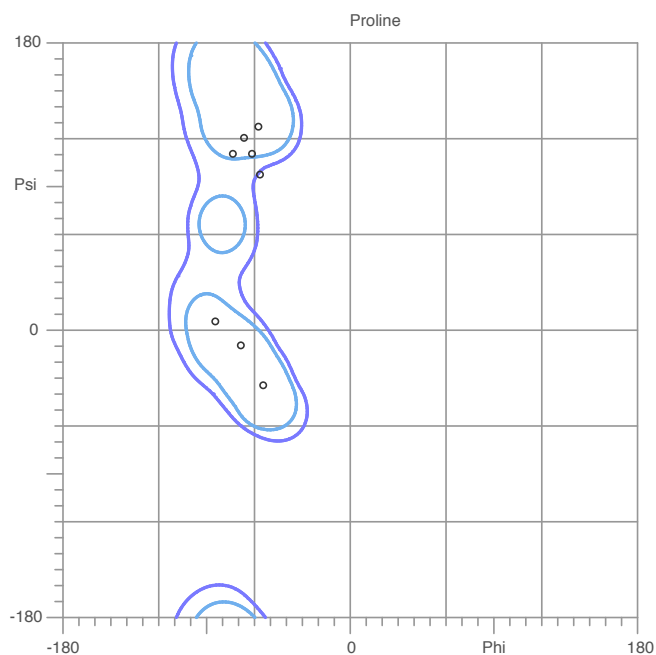
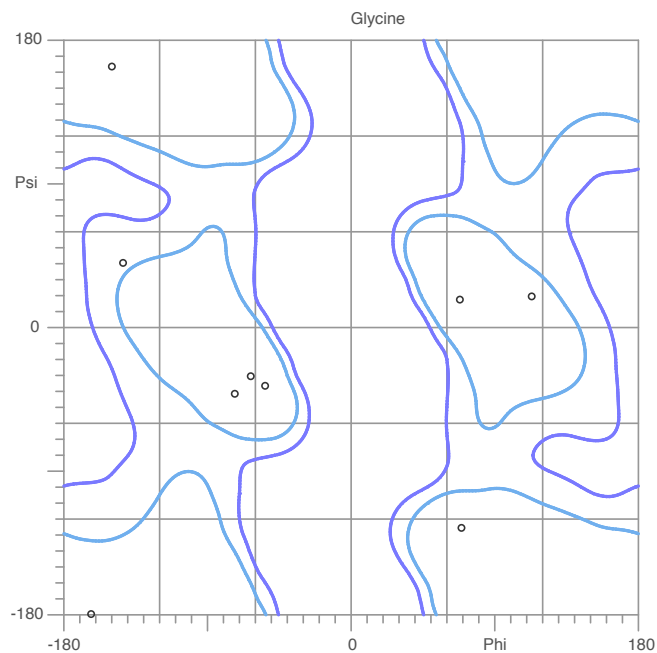
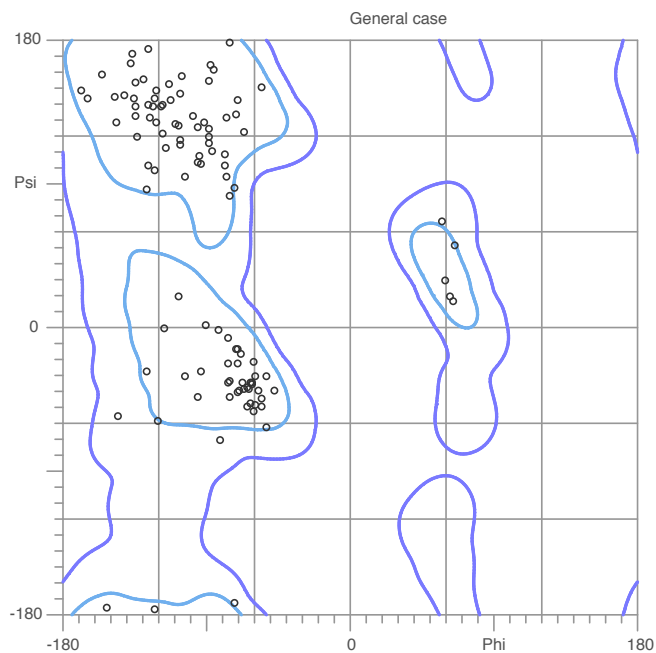
There were 2 outliers (phi, psi):

[3] 82 SER (173.3, -18.6)

[3] 85 GLY (-122.4, 87.6)

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 4



93.9% (124/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

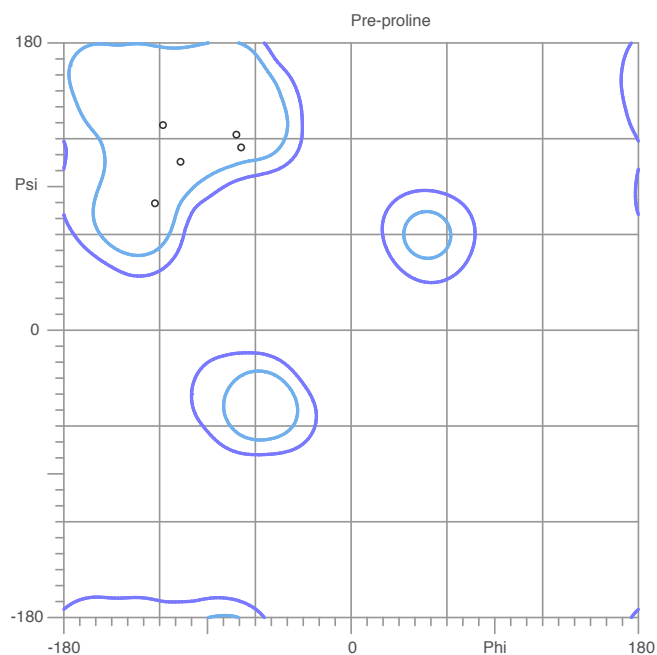
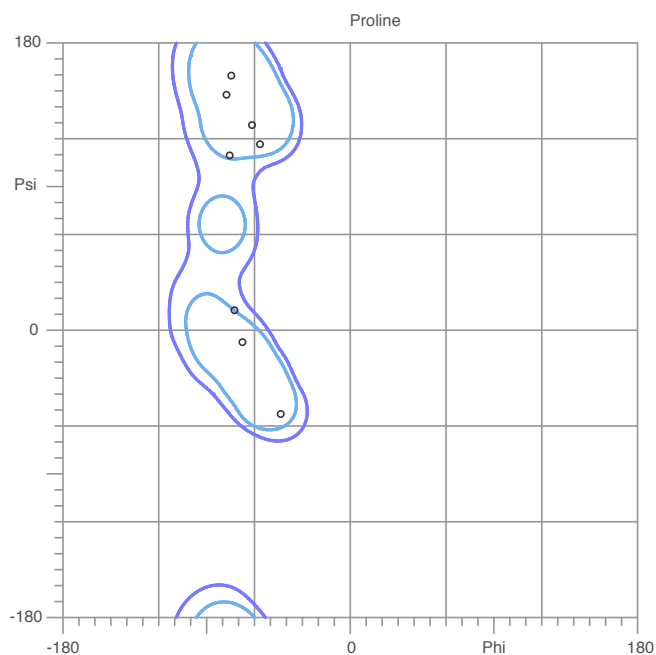
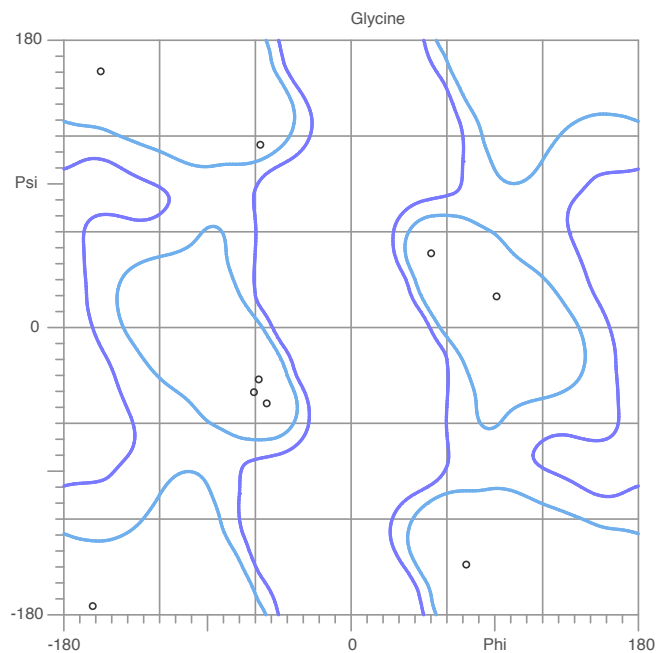
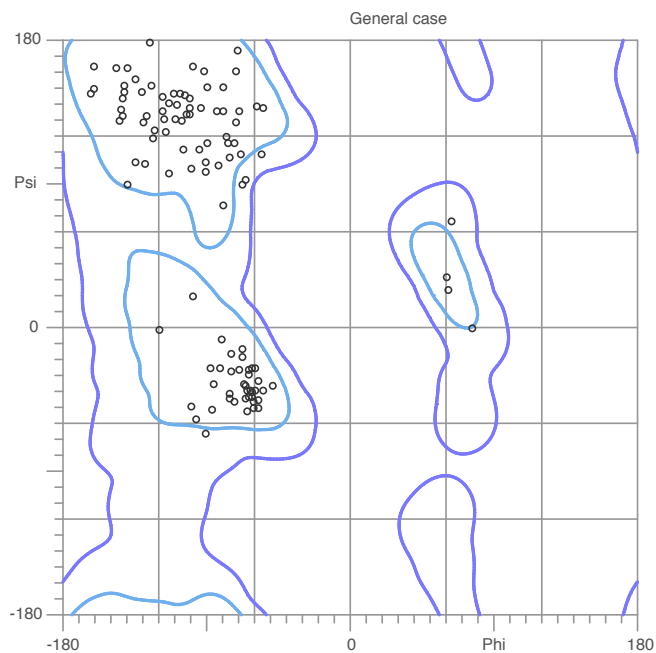
There were 1 outliers (phi, psi):
[4] 128 ARG (64.9, 107.5)

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

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 5



95.5% (126/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

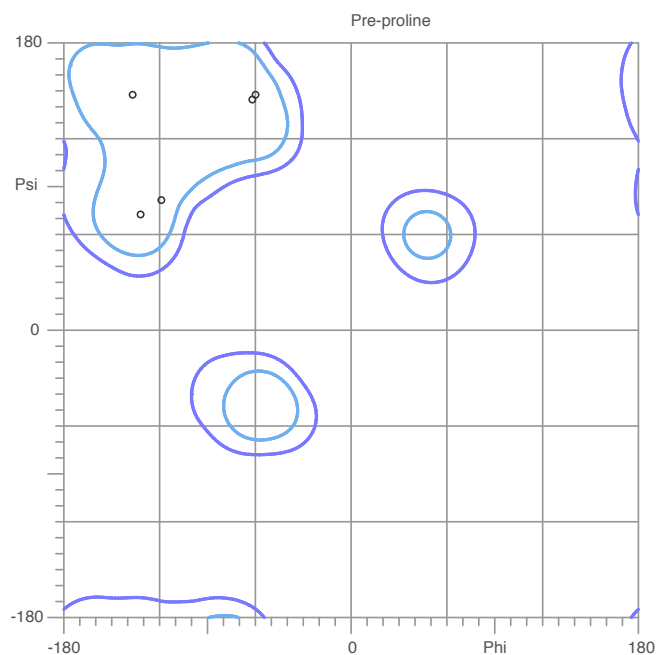
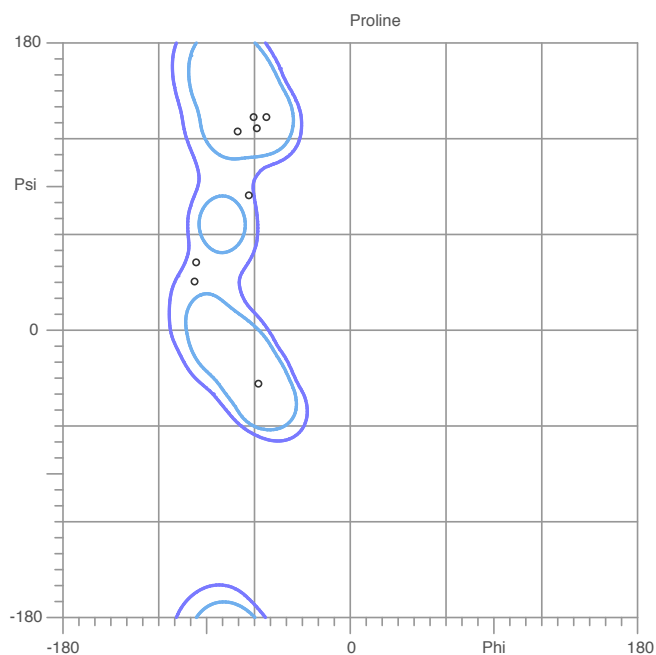
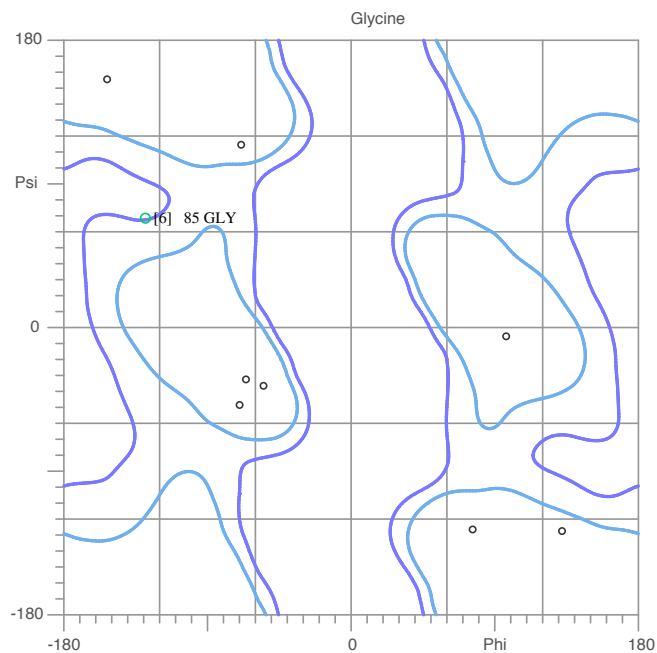
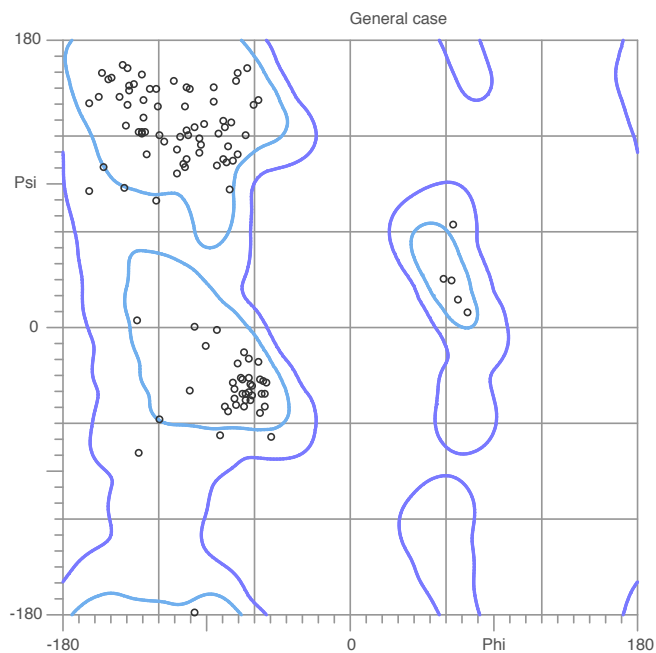
There were no outliers.

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

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 6

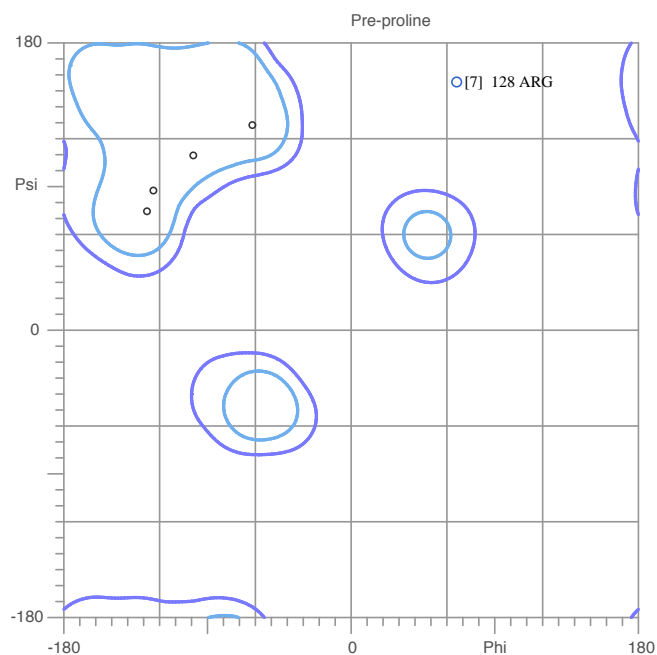
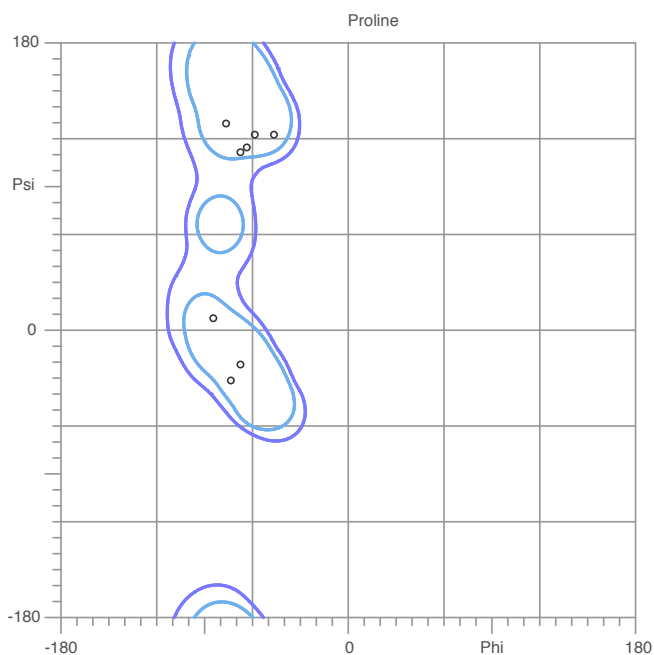
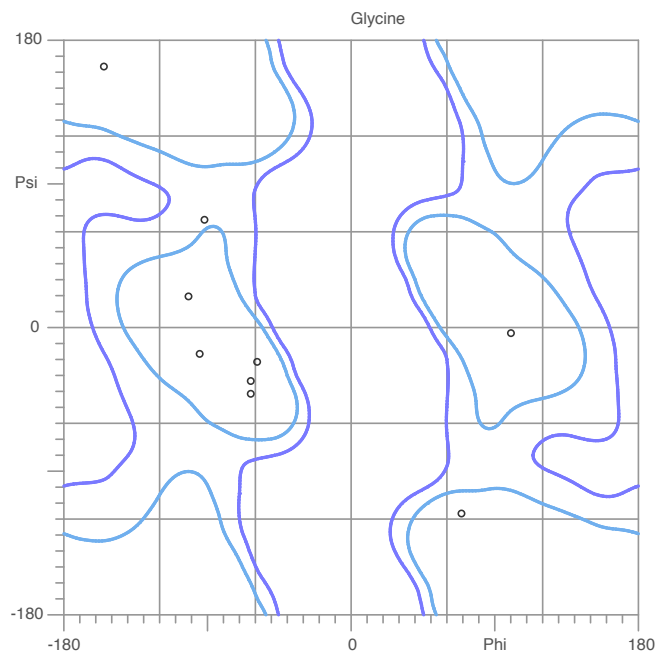
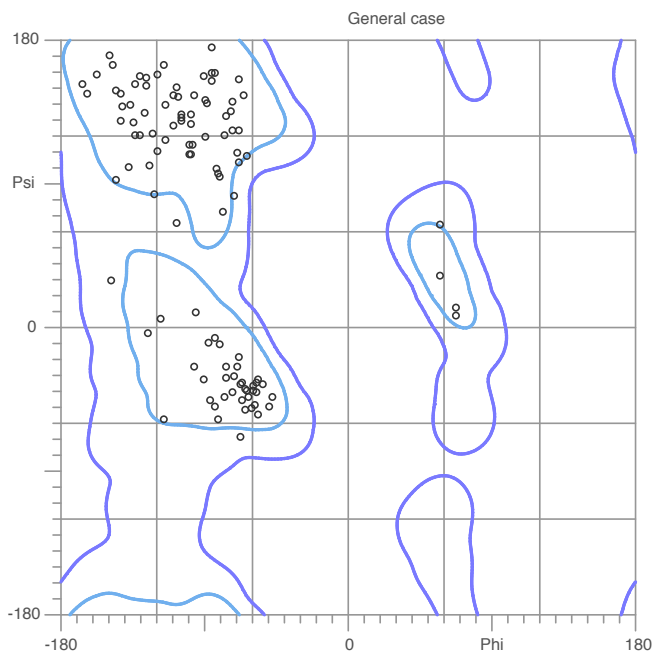


90.2% (119/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[6] 85 GLY (-129.5, 69.2)

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 7



94.7% (125/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

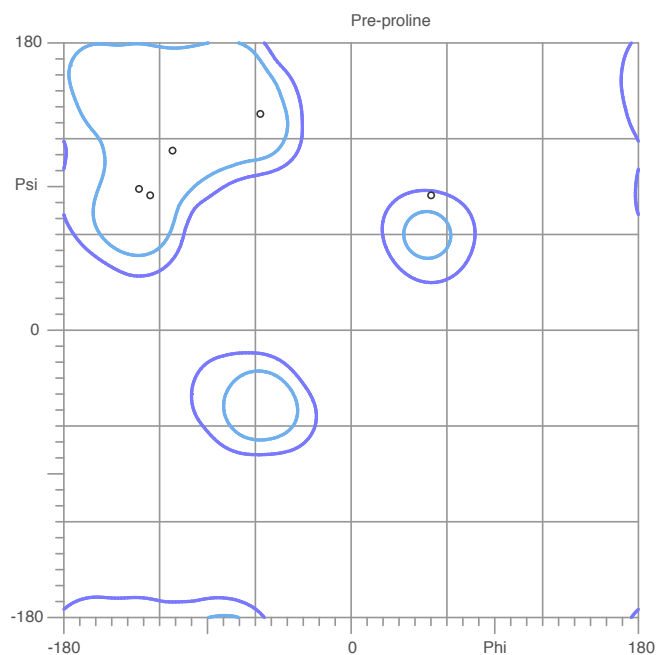
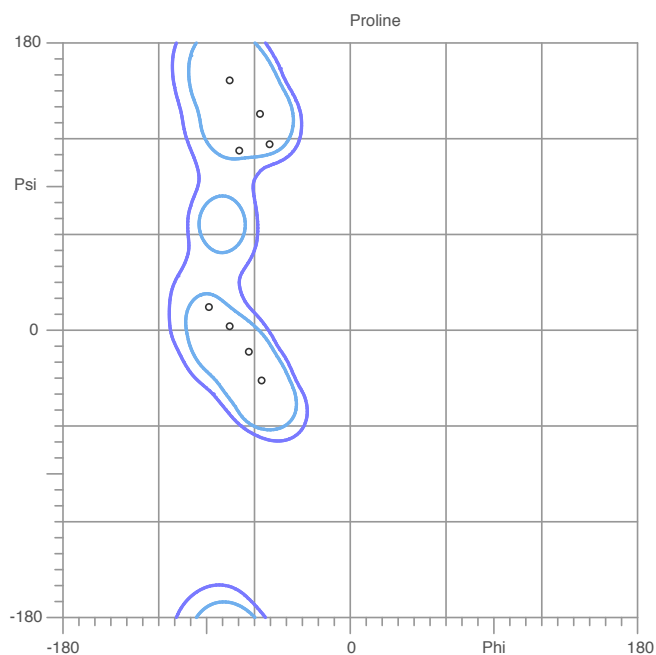
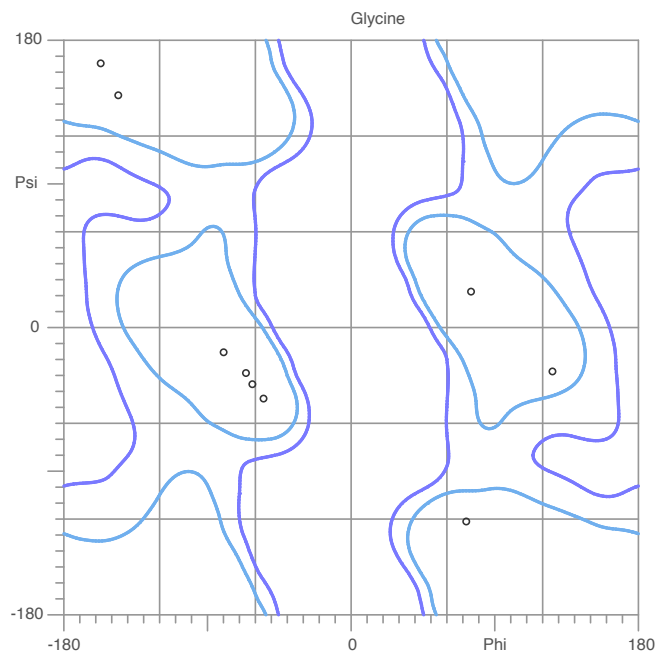
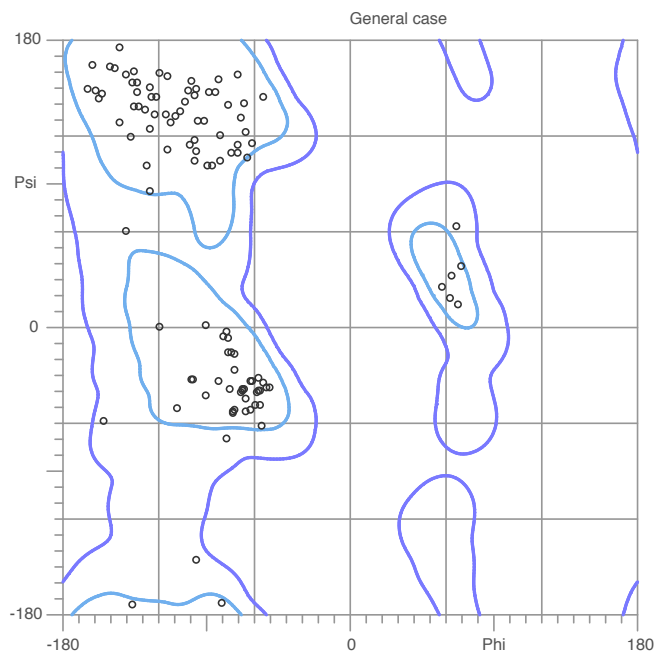
There were 1 outliers (phi, psi):
[7] 128 ARG (66.1, 156.4)

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 8



95.5% (126/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

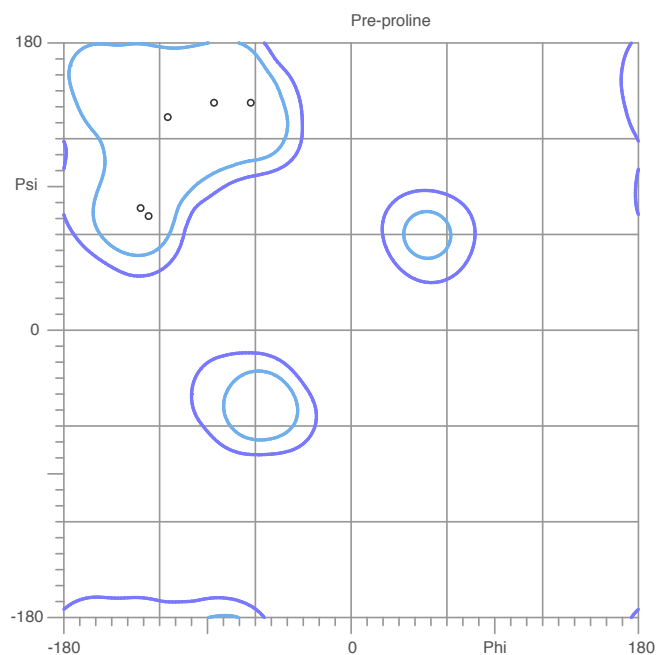
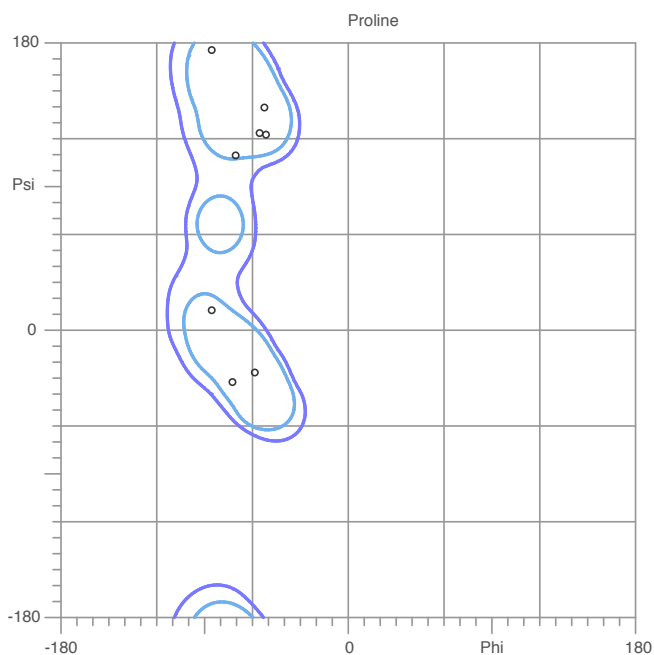
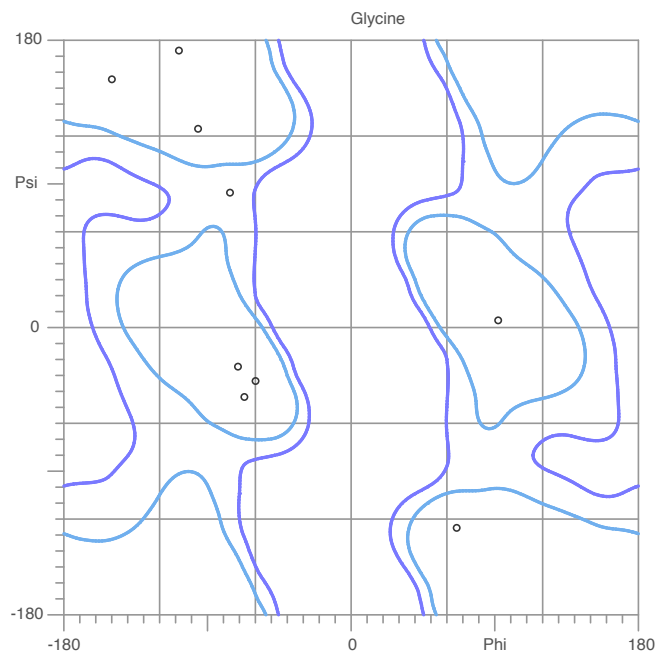
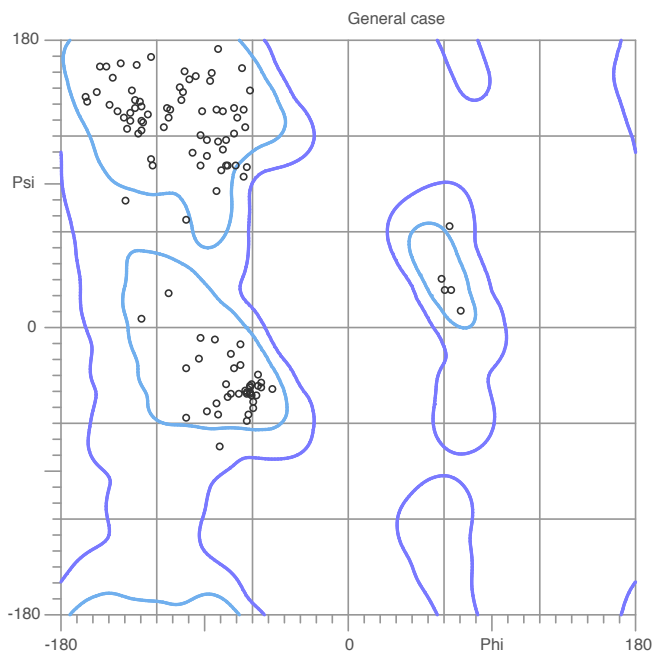
There were no outliers.

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 9

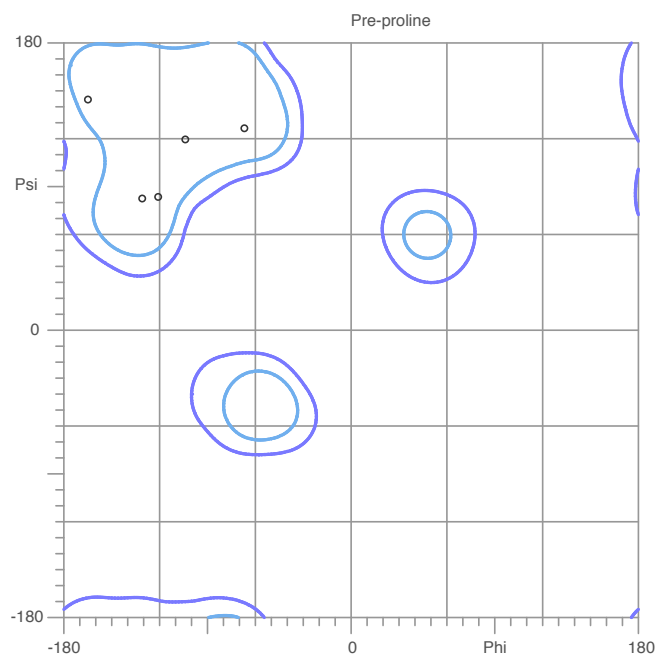
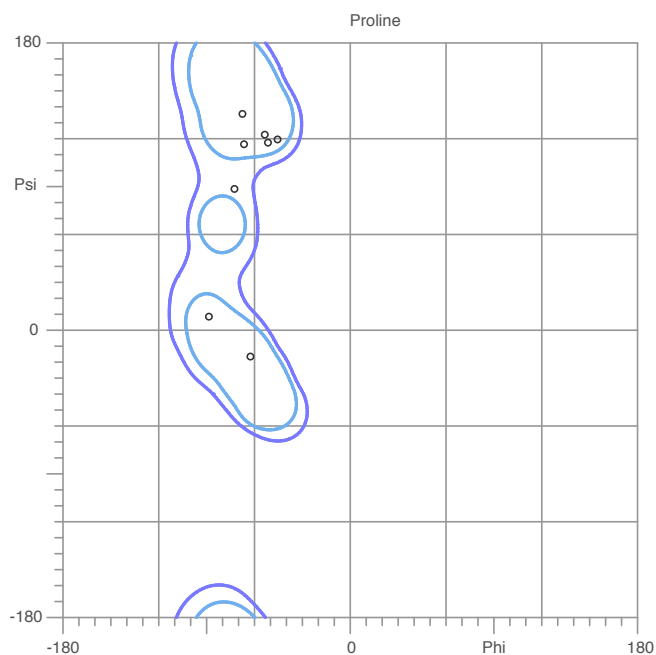
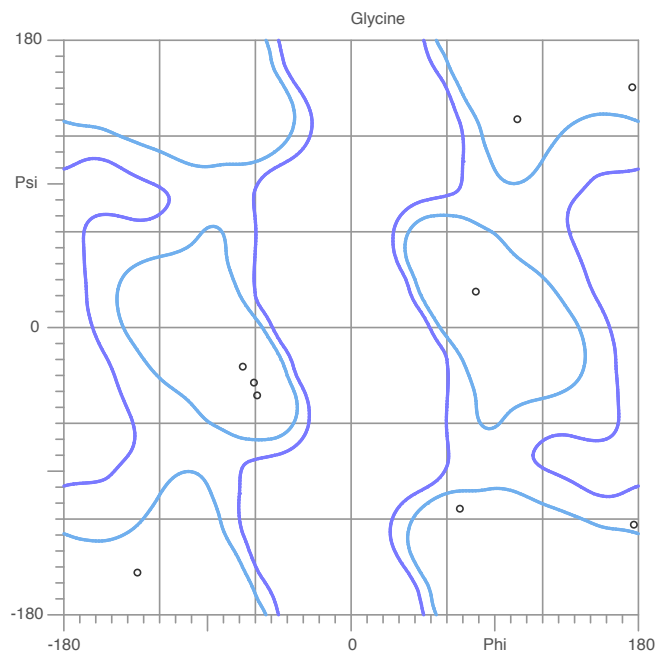
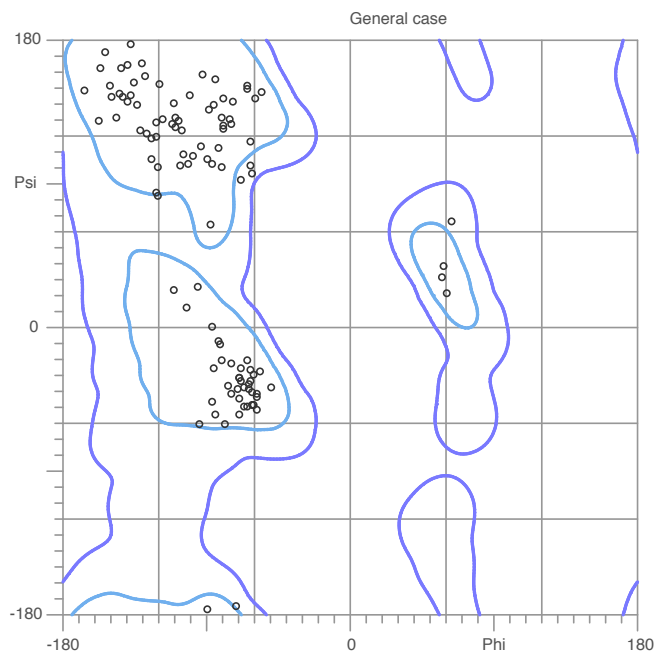


94.7% (125/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 10



94.7% (125/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

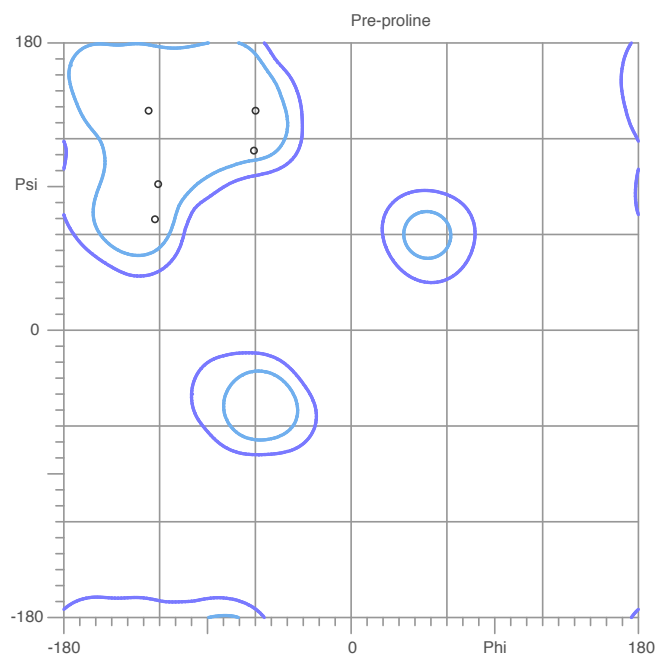
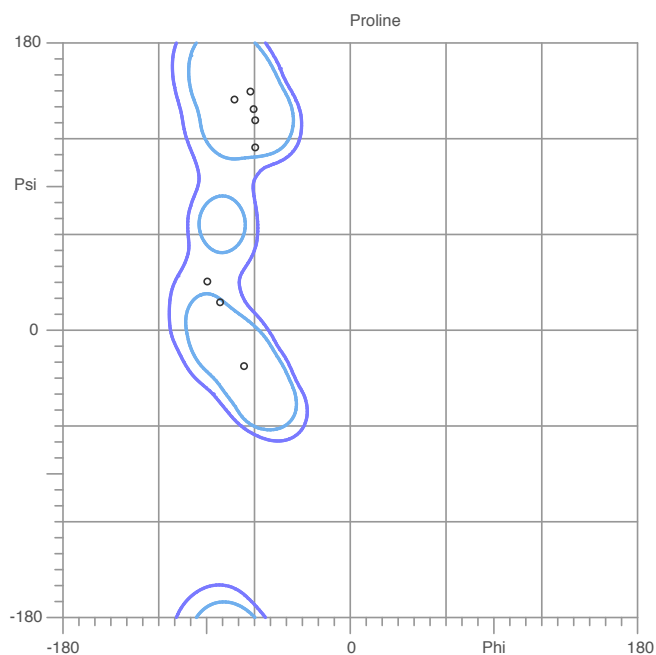
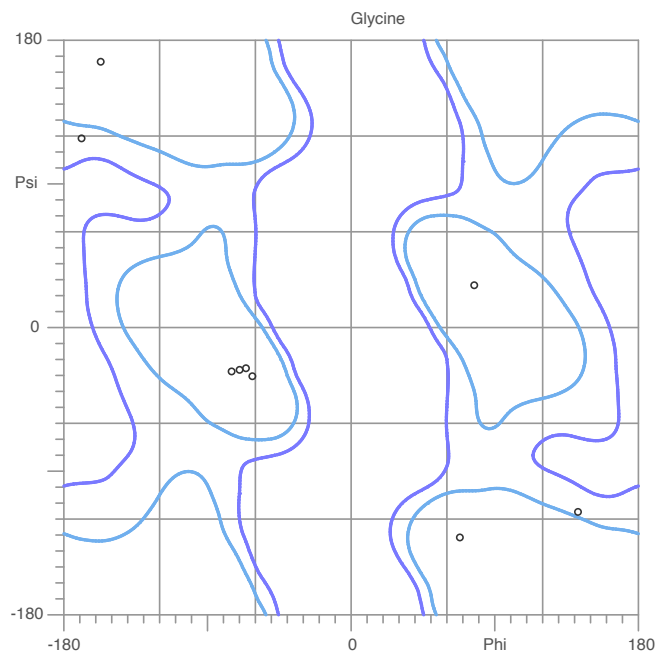
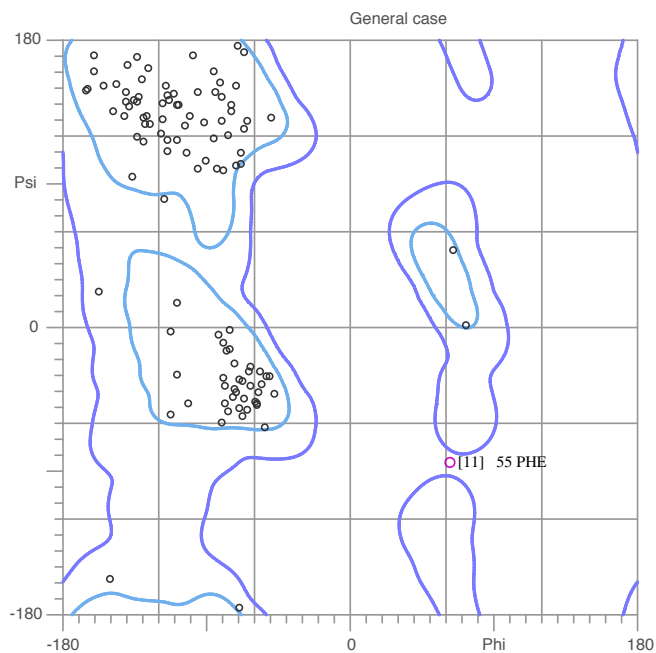
There were no outliers.

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 11



93.9% (124/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

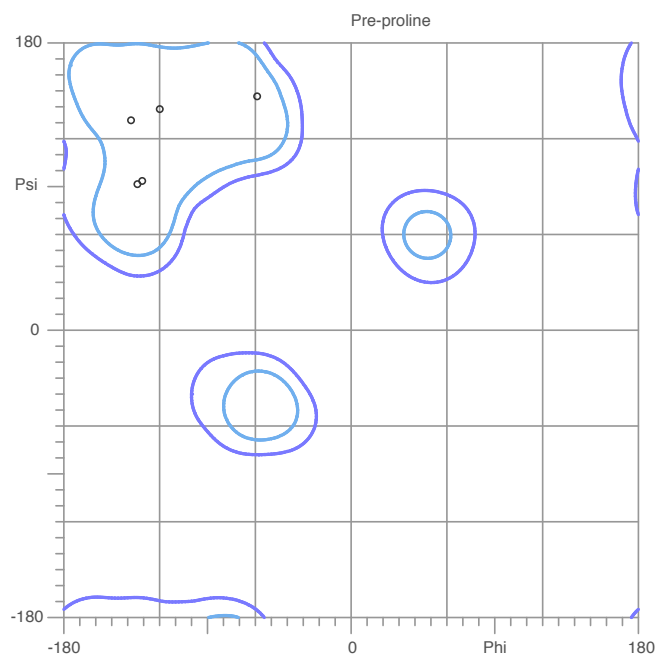
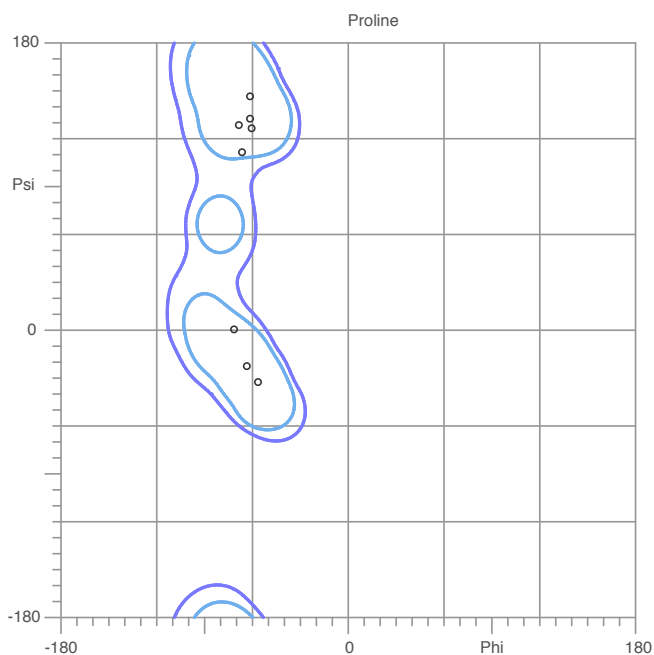
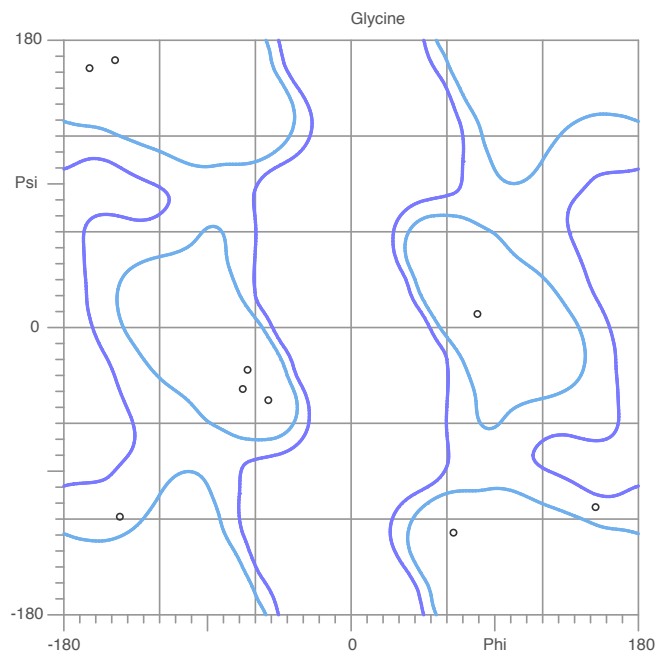
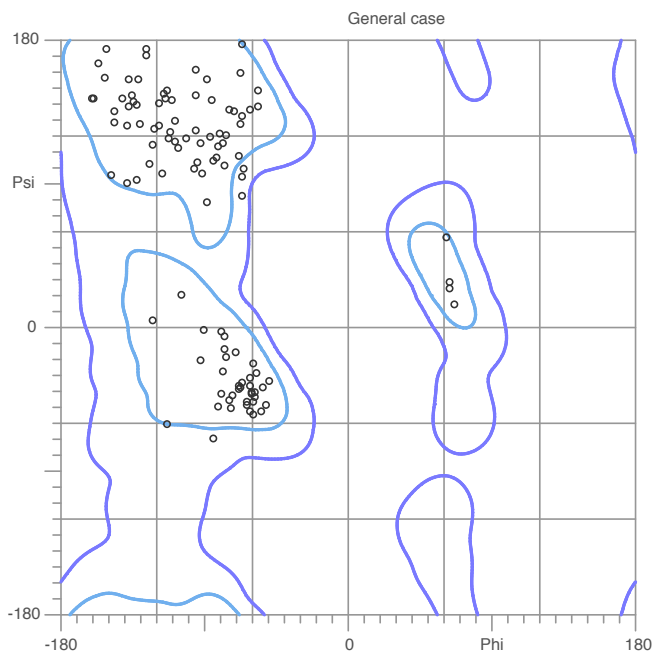
There were 1 outliers (phi, psi):
[11] 55 PHE (62.4, -84.6)

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

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 12



94.7% (125/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

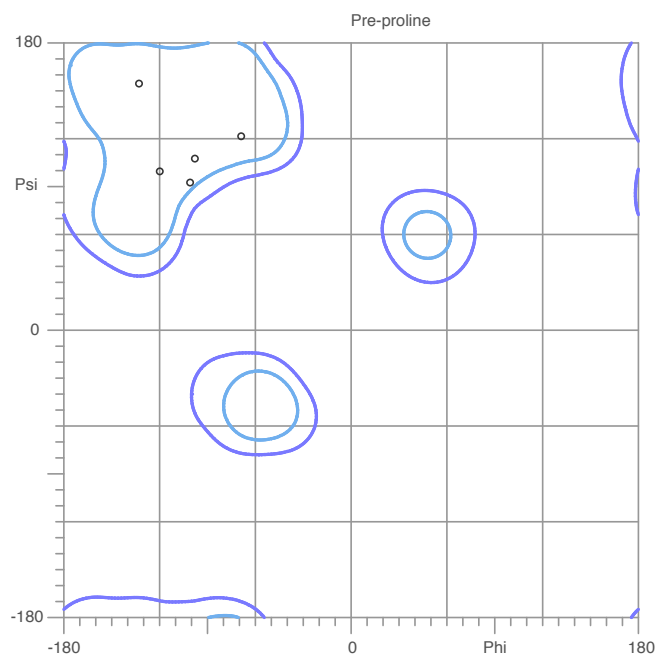
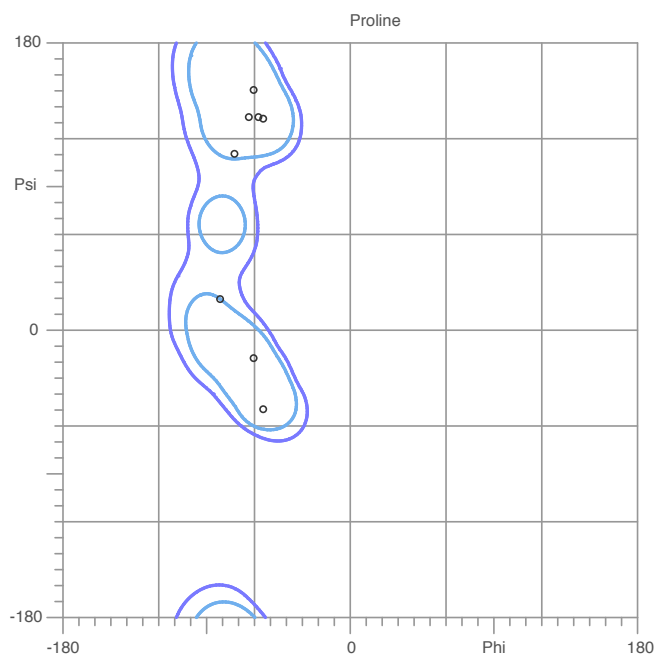
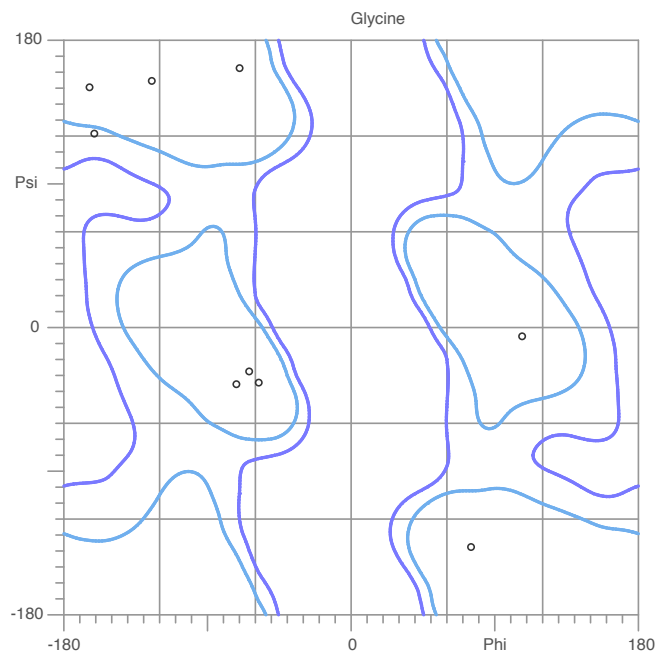
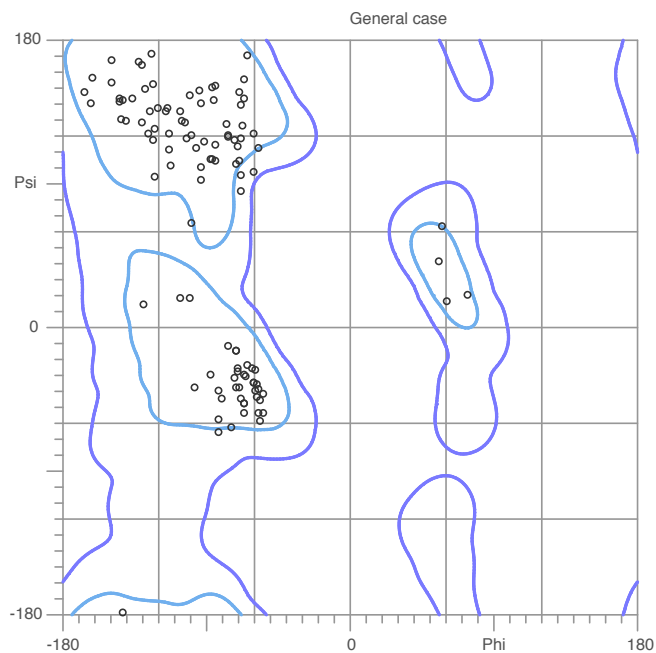
There were no outliers.

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 13

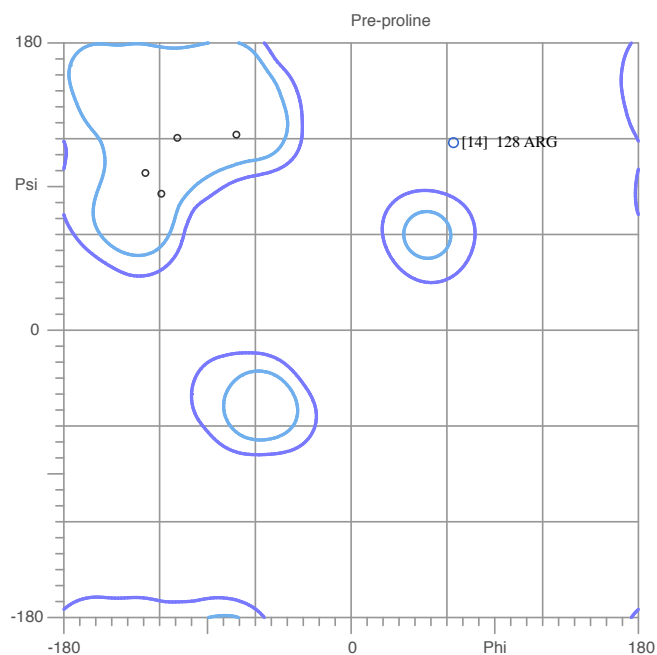
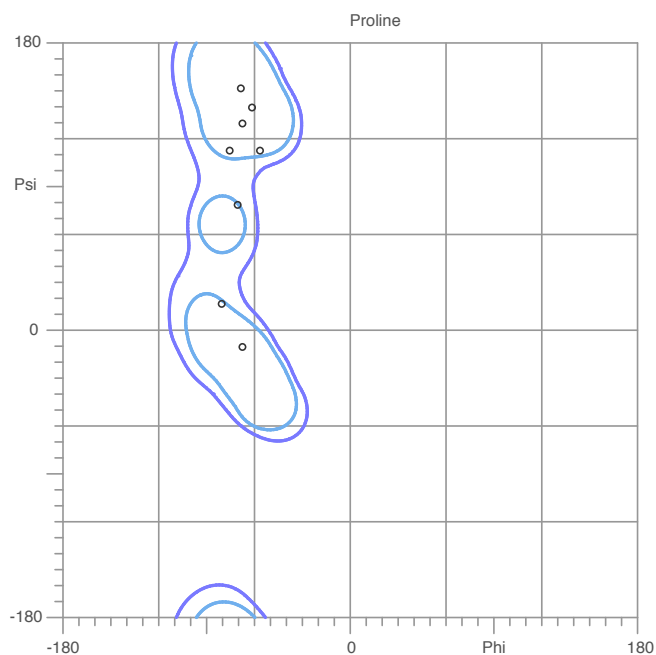
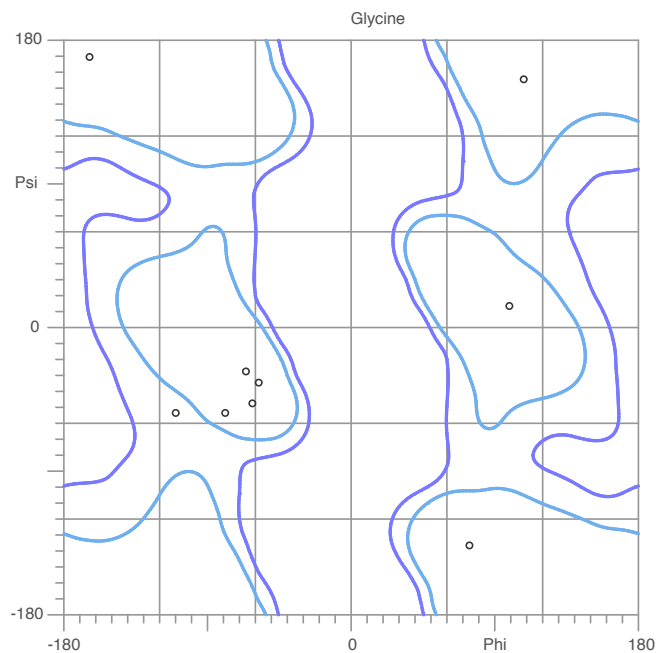
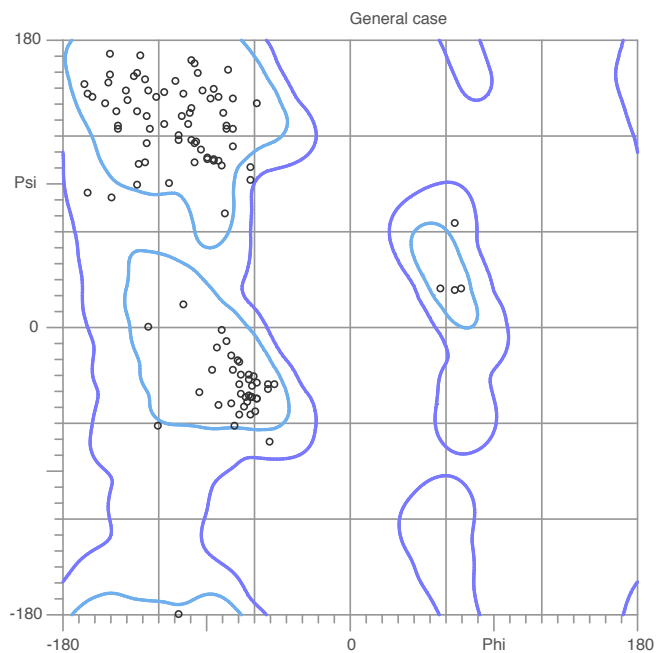


93.9% (124/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 14



93.2% (123/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

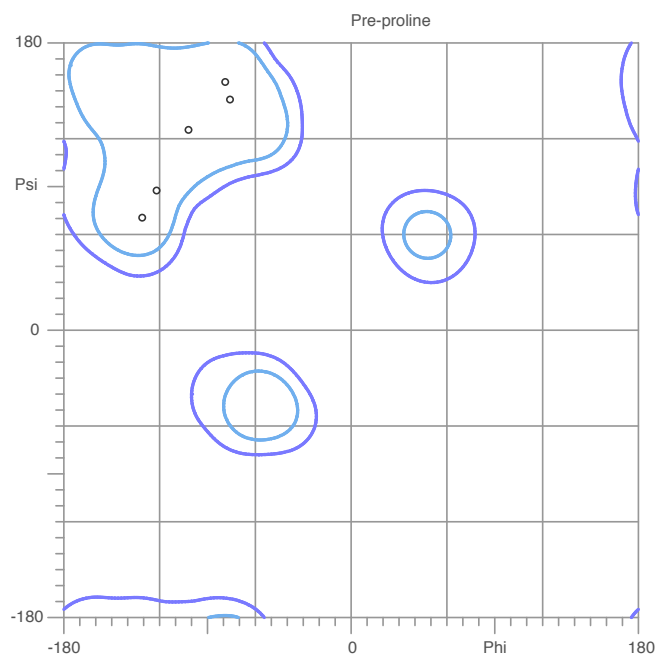
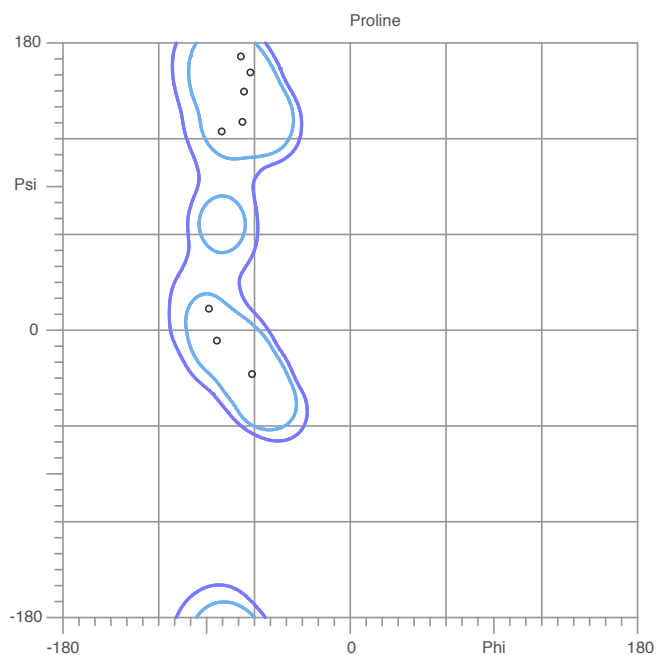
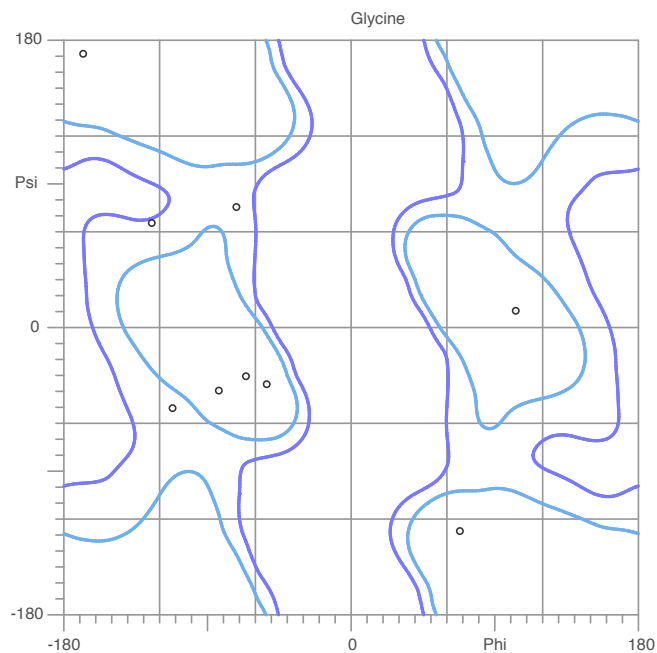
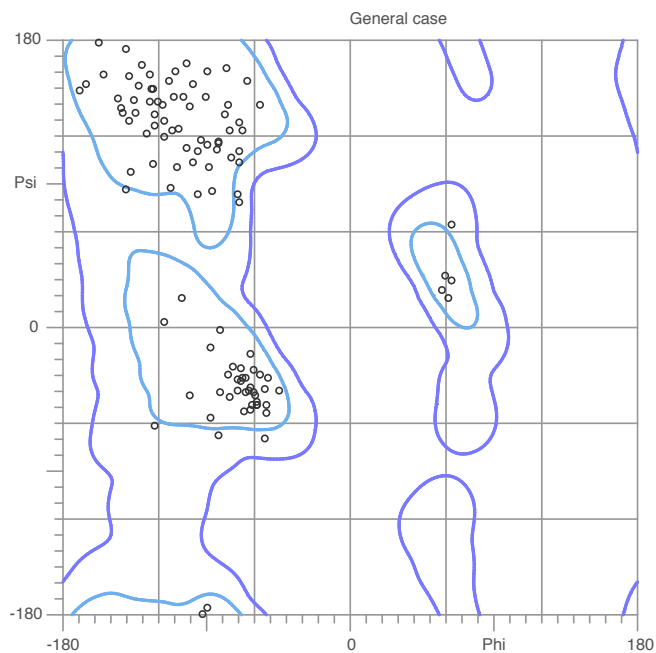
There were 1 outliers (phi, psi):
[14] 128 ARG (64.9, 118.3)

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 15

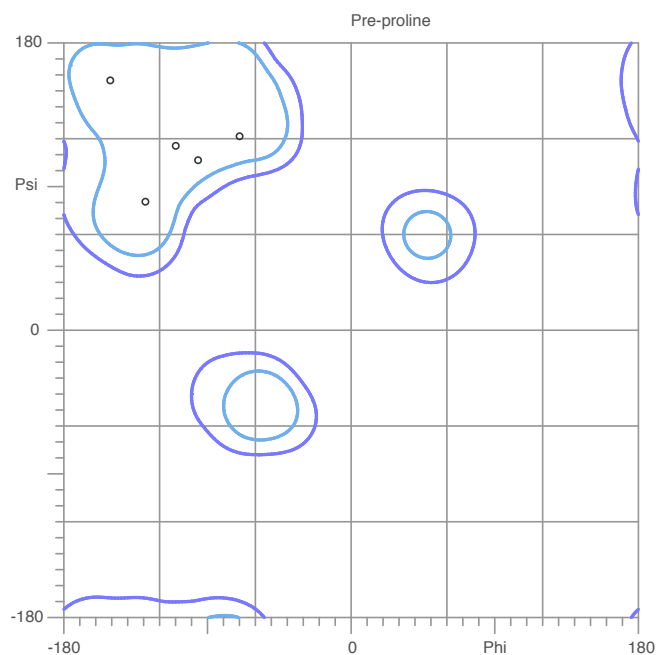
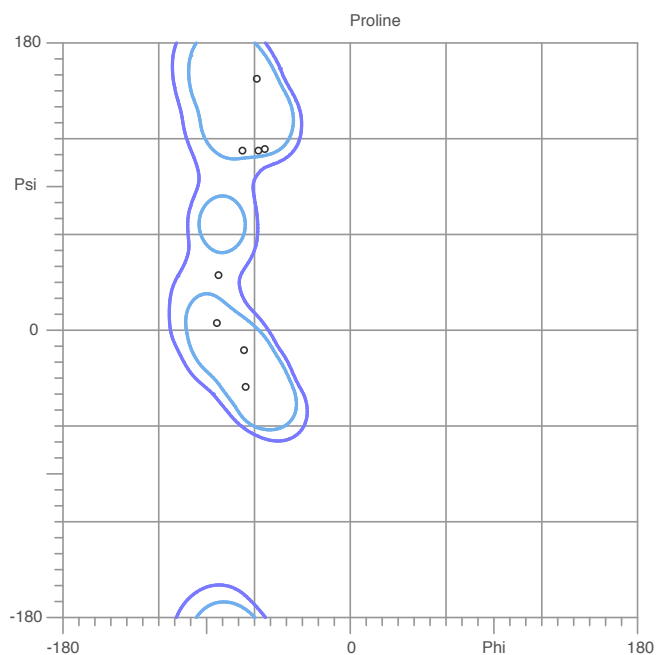
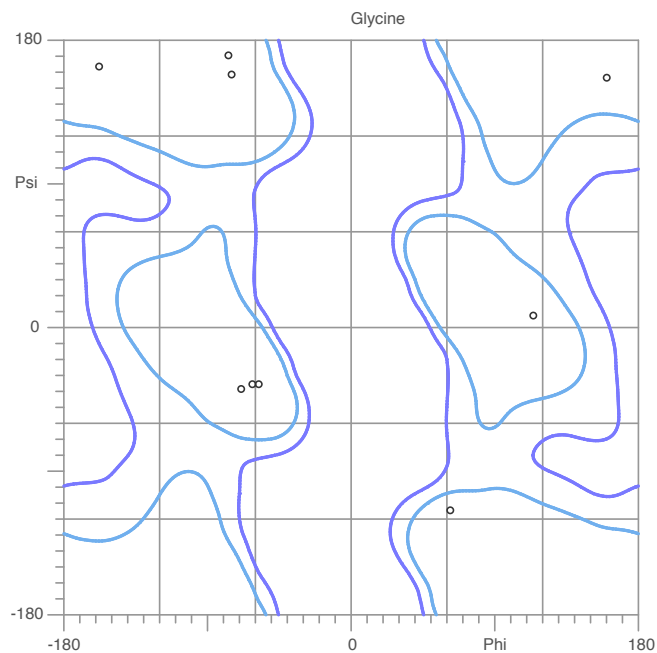
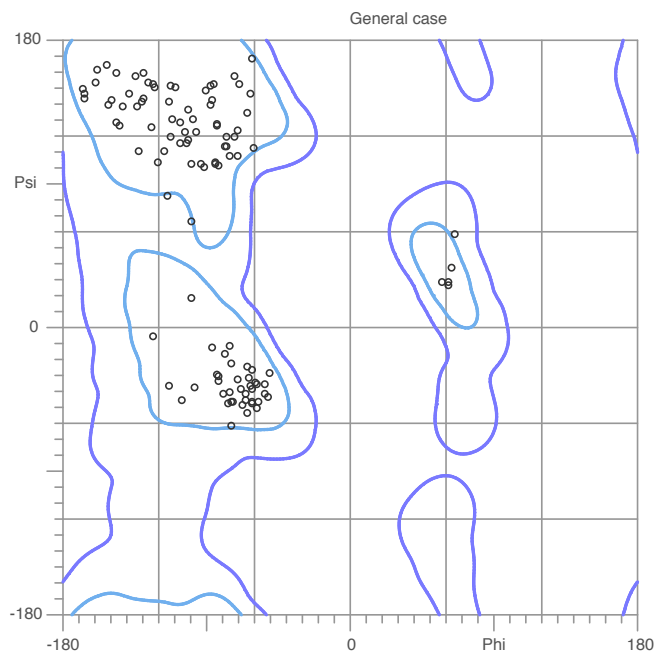


92.4% (122/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 16



97.7% (129/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

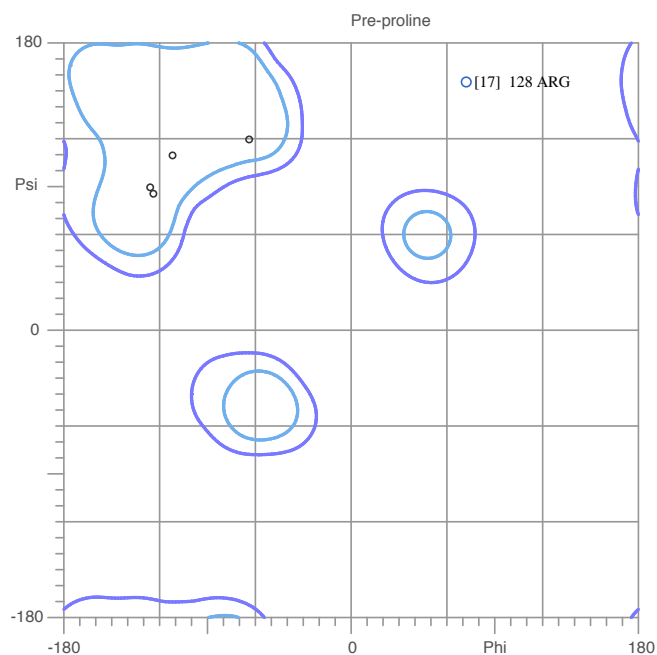
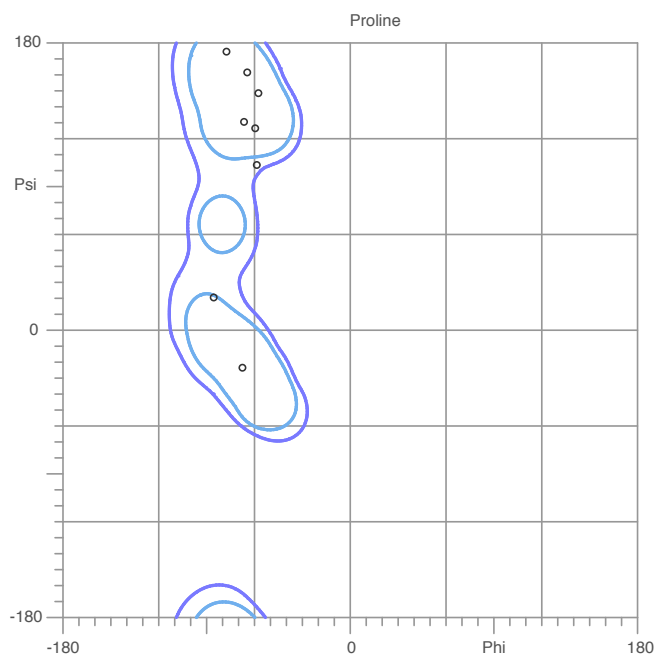
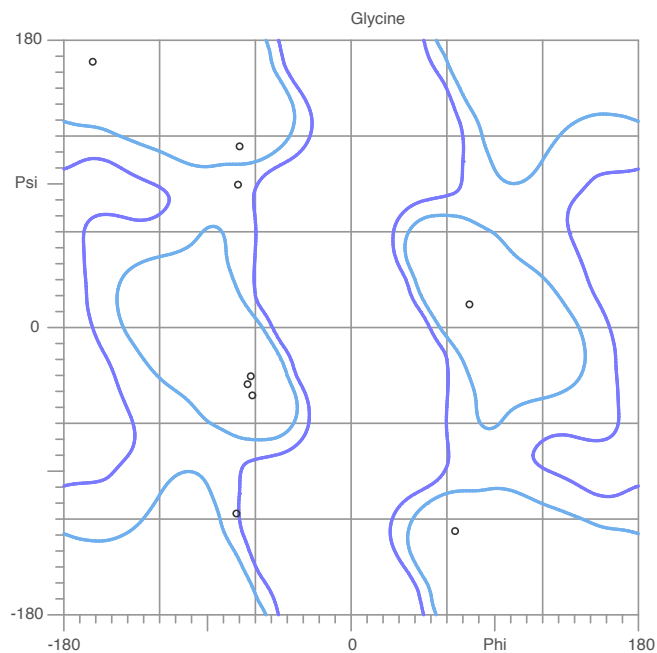
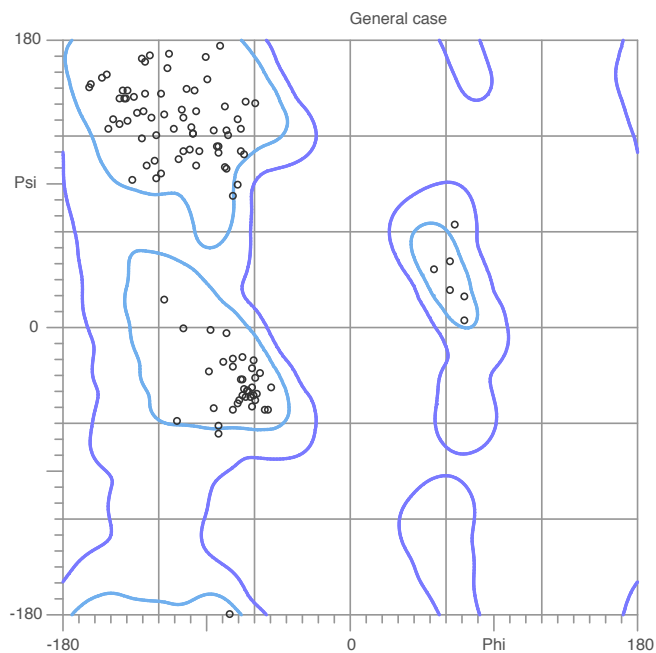
There were no outliers.

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

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 17



94.7% (125/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

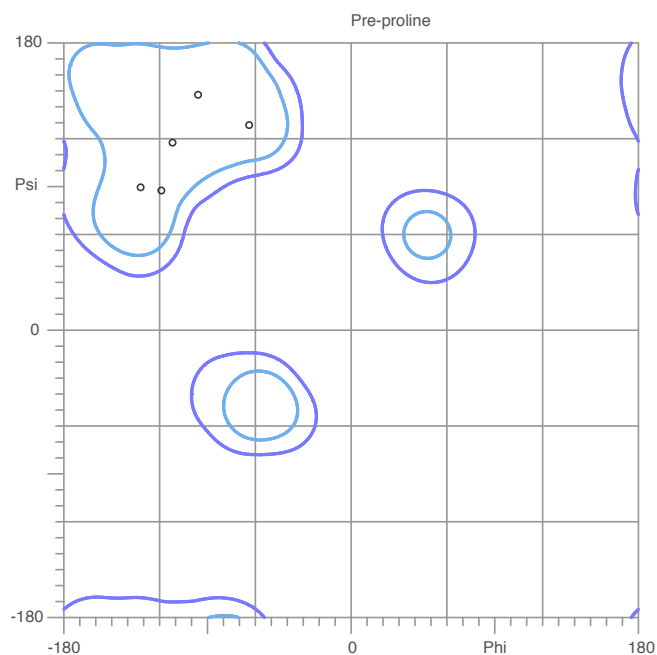
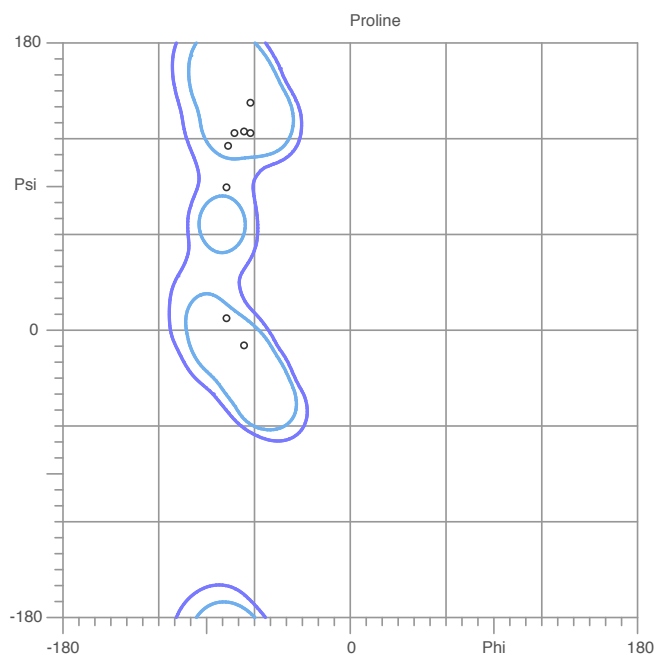
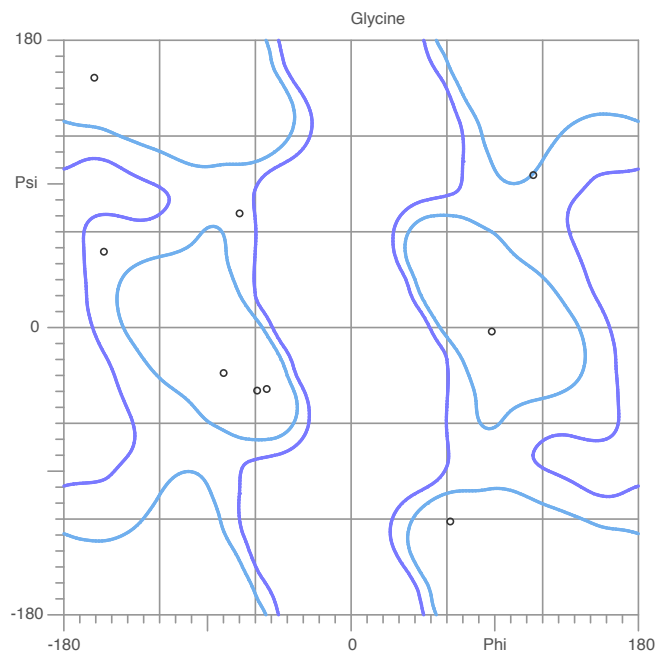
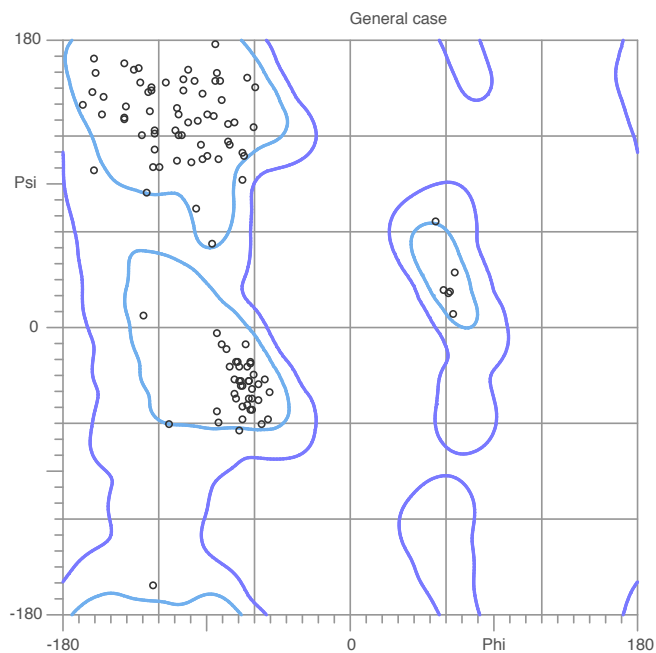
There were 1 outliers (phi, psi):
[17] 128 ARG (72.7, 156.6)

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 18

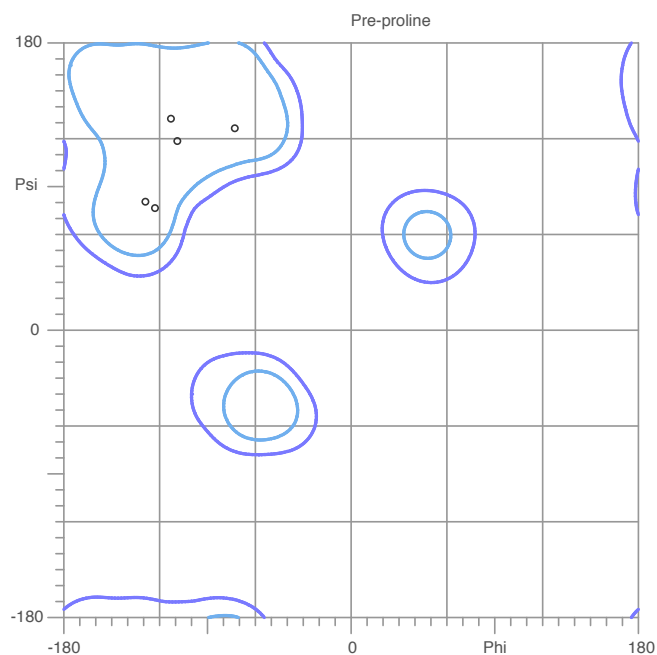
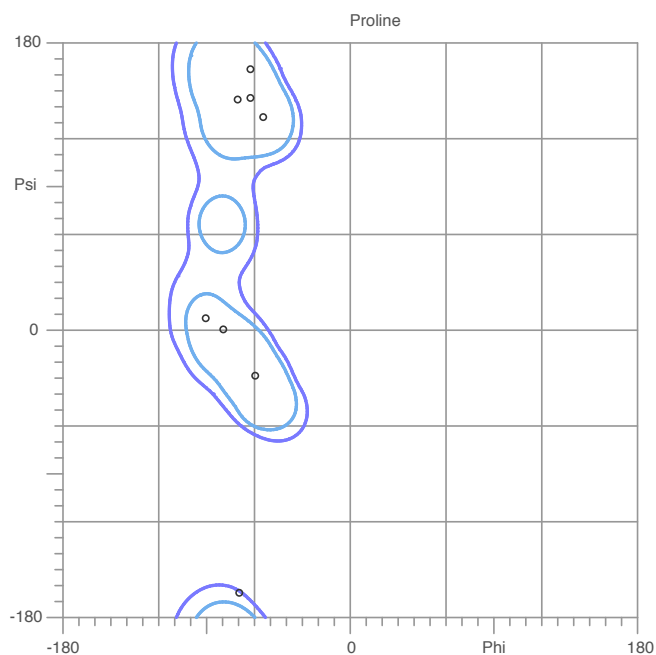
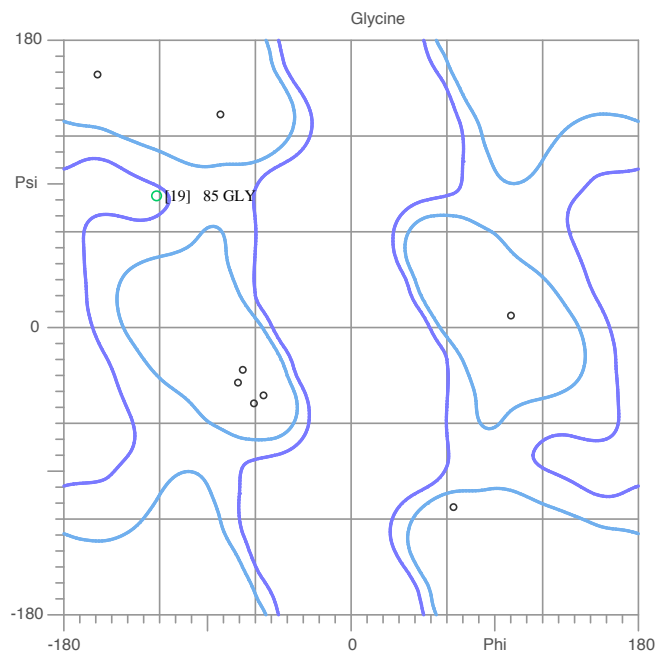
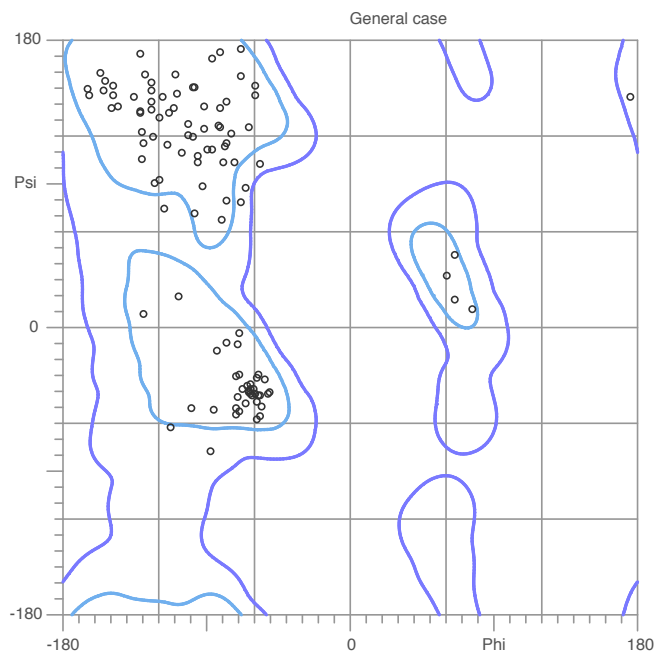


92.4% (122/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 19



93.2% (123/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

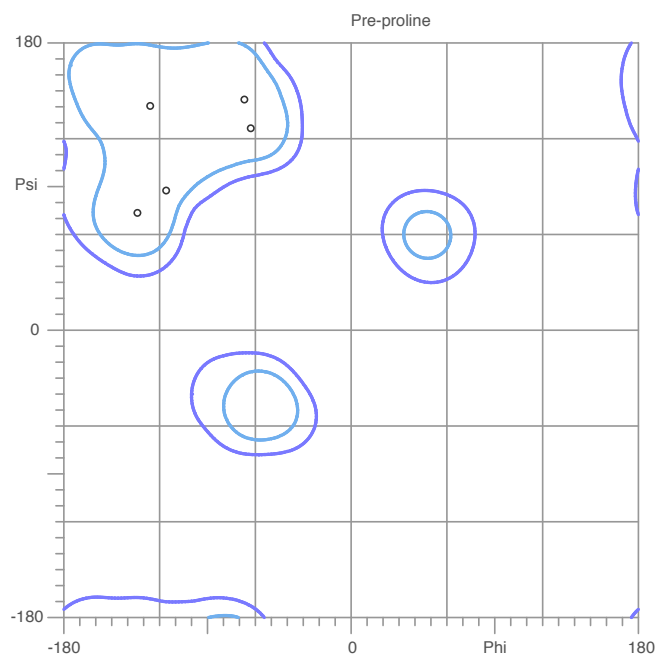
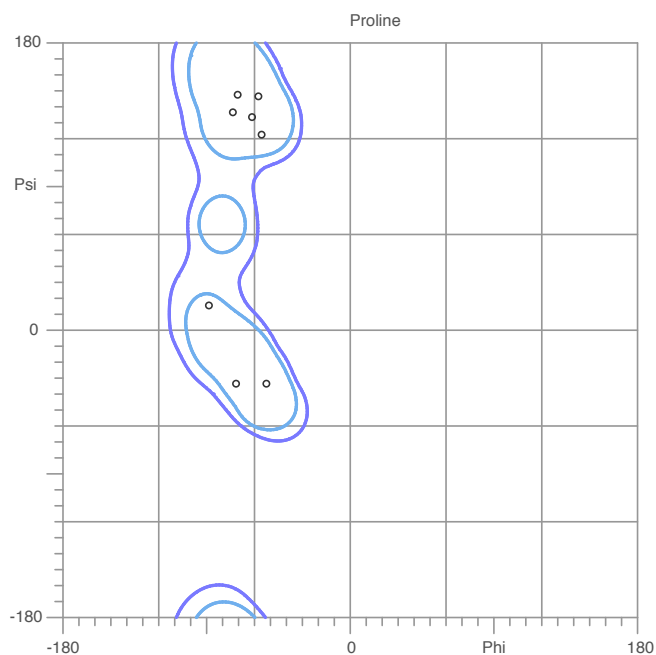
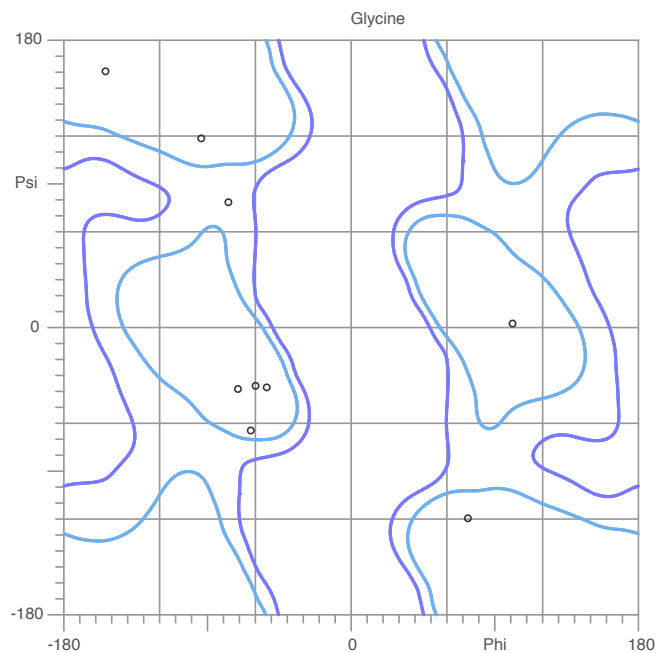
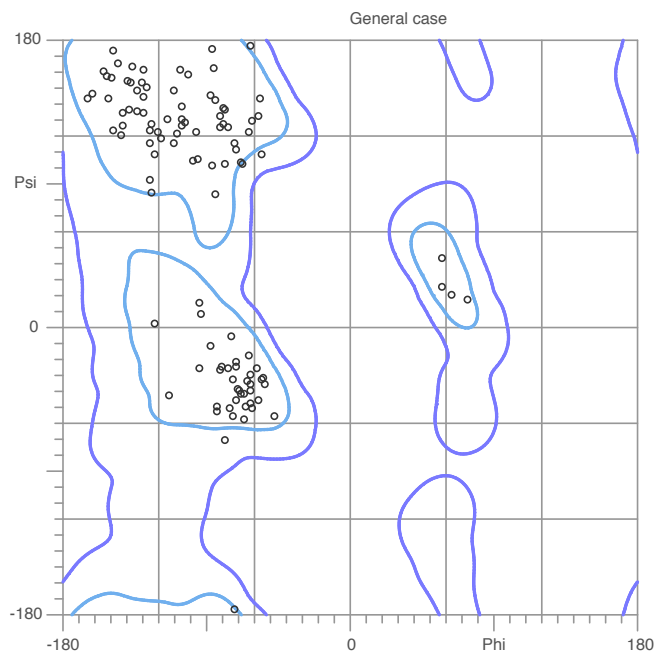
There were 1 outliers (phi, psi):
[19] 85 GLY (-122.5, 83.0)

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MolProbity Ramachandran analysis

OR8C_NMR_em_bcr3.pdb, model 20



97.0% (128/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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