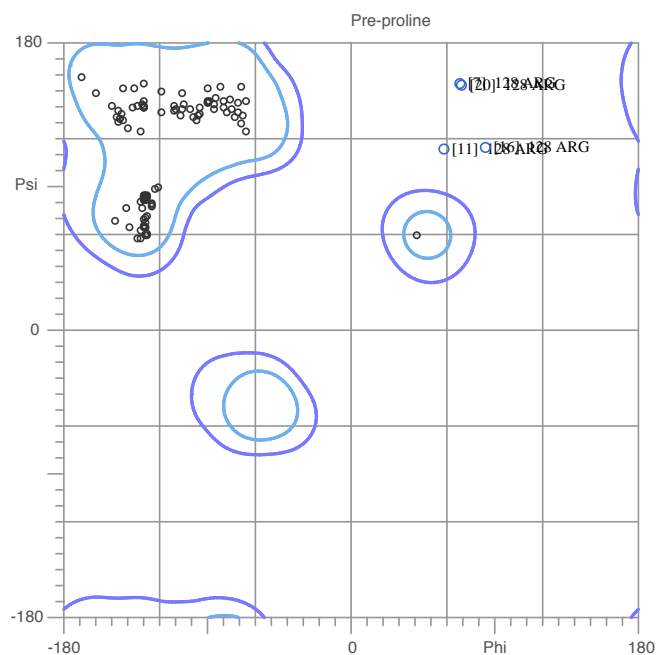
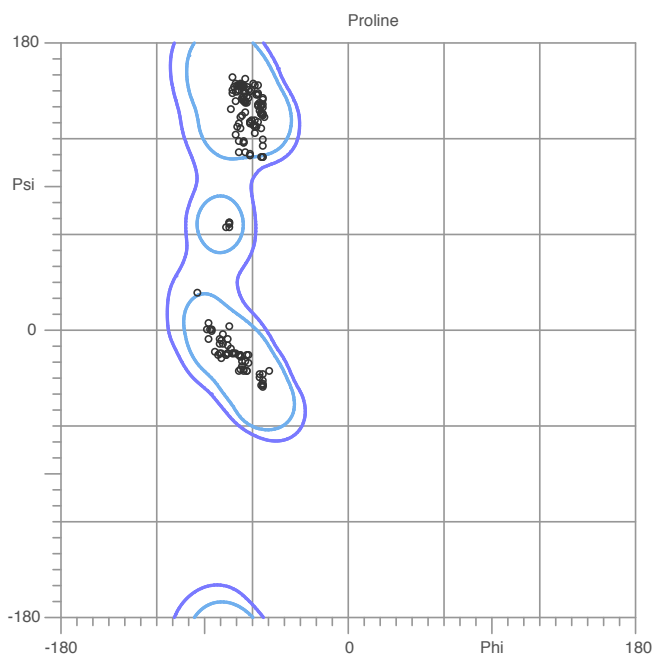
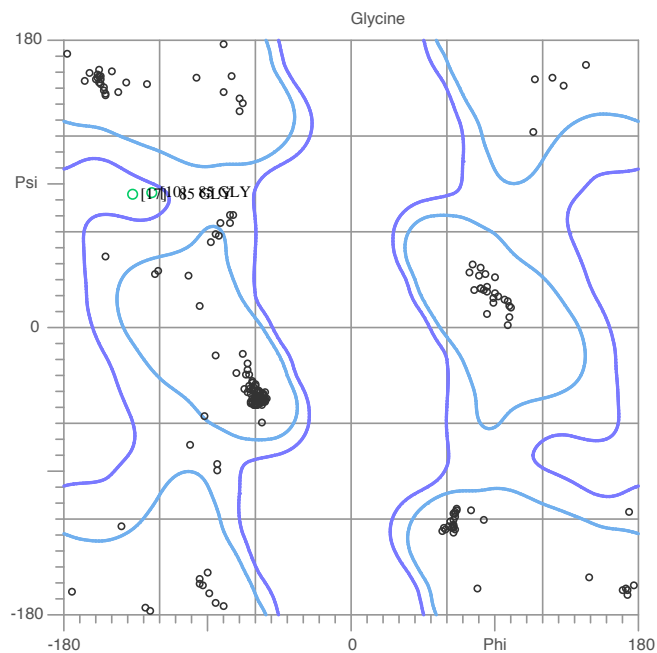
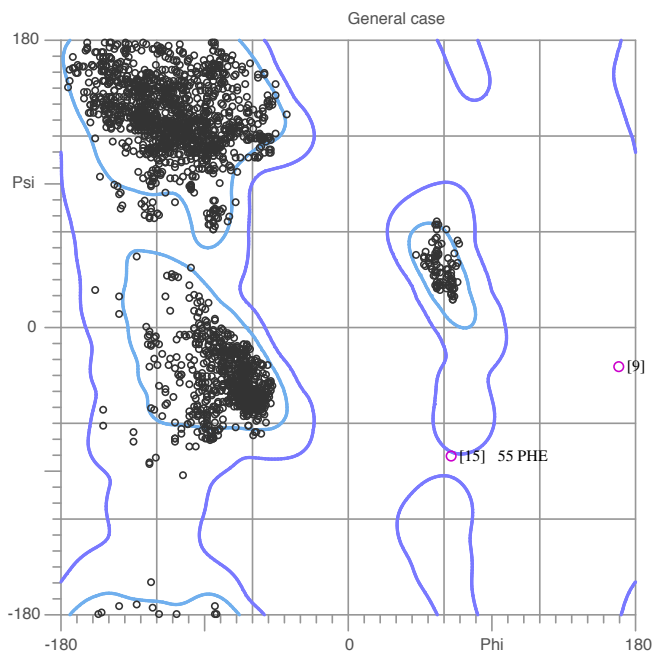


MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, all models



95.8% (2528/2640) of all residues were in favored (98%) regions.
99.7% (2632/2640) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[7] 128 ARG (68.6, 155.0)

[9] 82 SER (169.9, -24.9)

[10] 85 GLY (-125.1, 85.1)

[11] 128 ARG (59.0, 114.9)

[15] 55 PHE (64.9, -80.3)

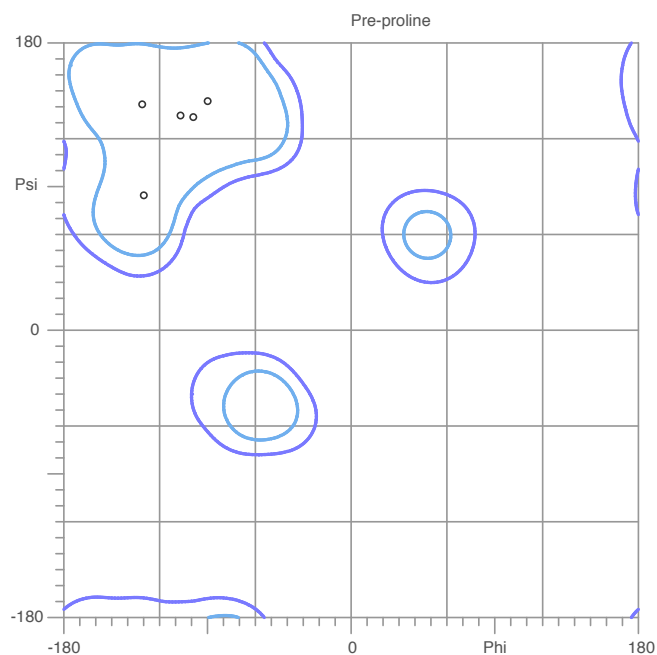
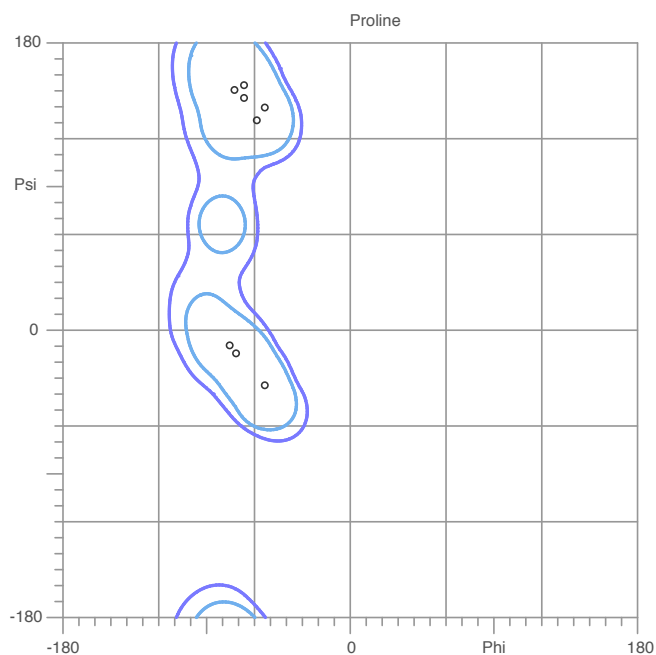
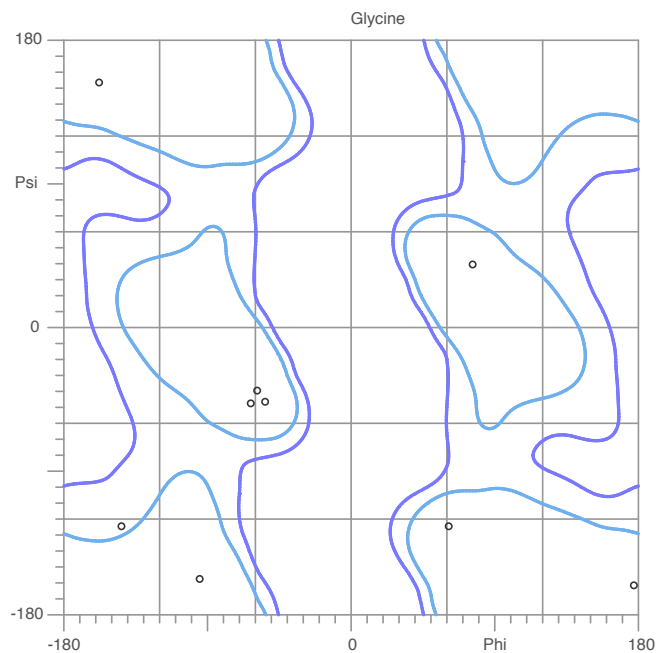
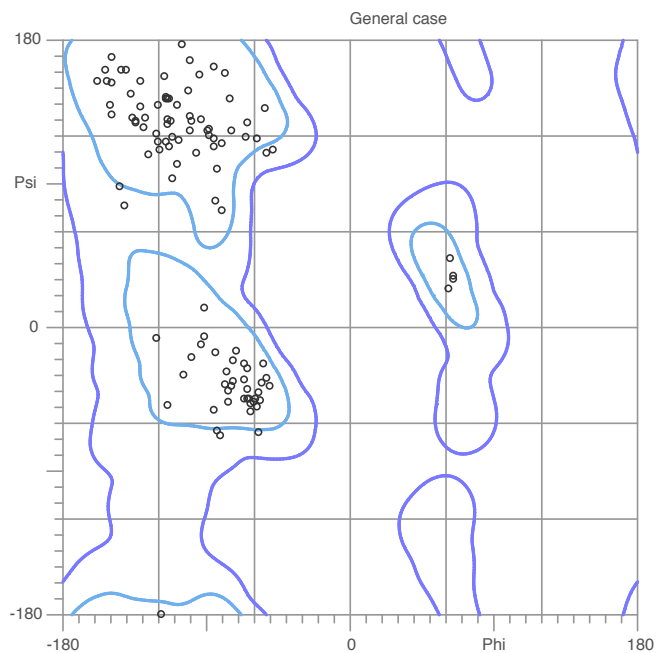
[16] 128 ARG (85.0, 115.1)

[17] 85 GLY (-137.4, 85.0)

[20] 128 ARG (69.3, 155.0)

MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 1

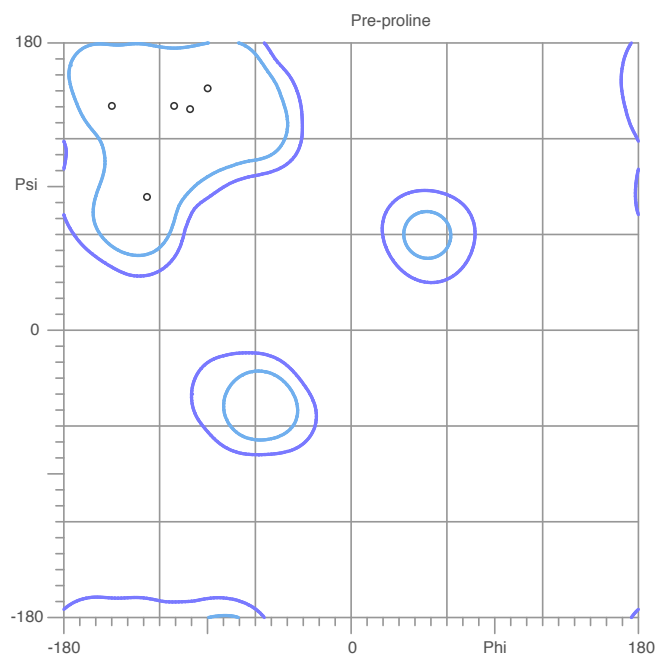
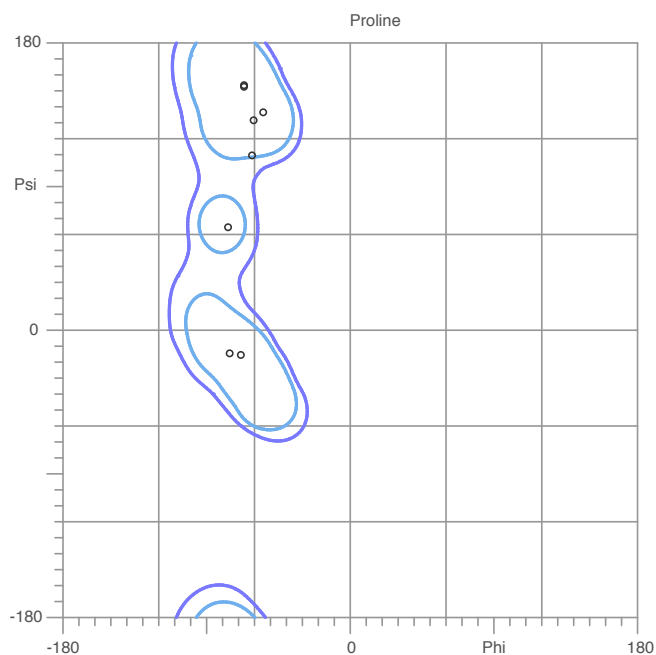
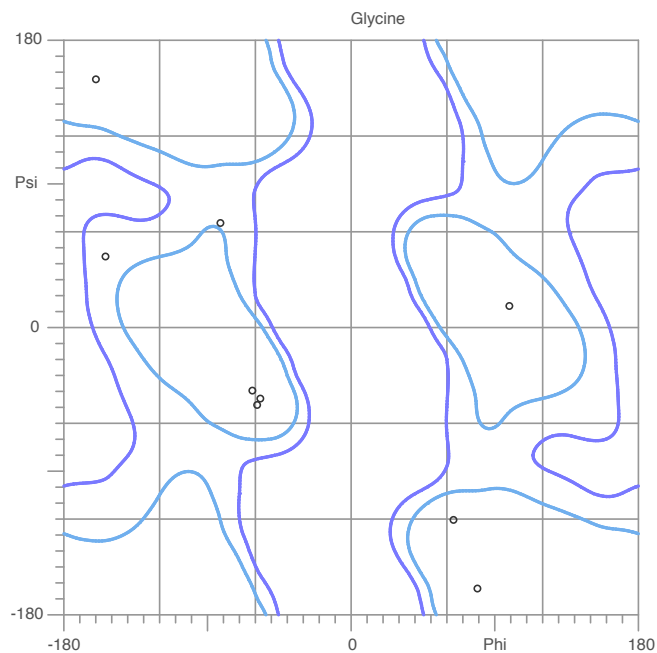
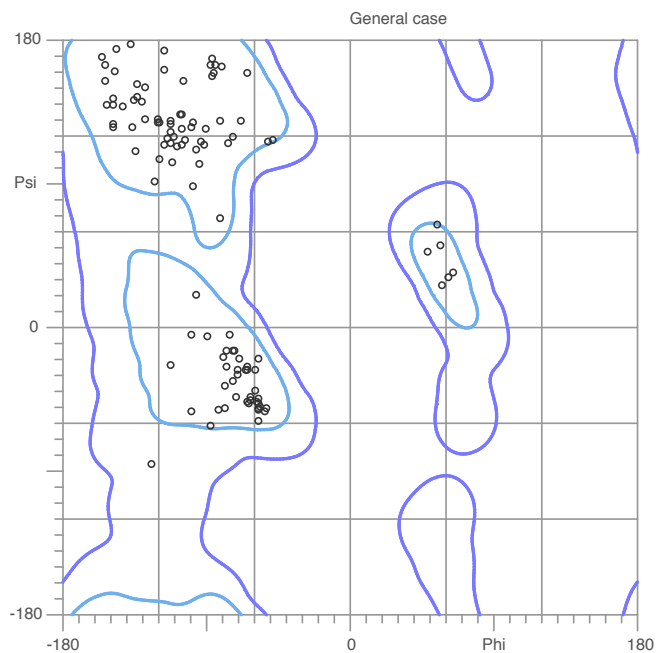


93.9% (124/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 2



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.

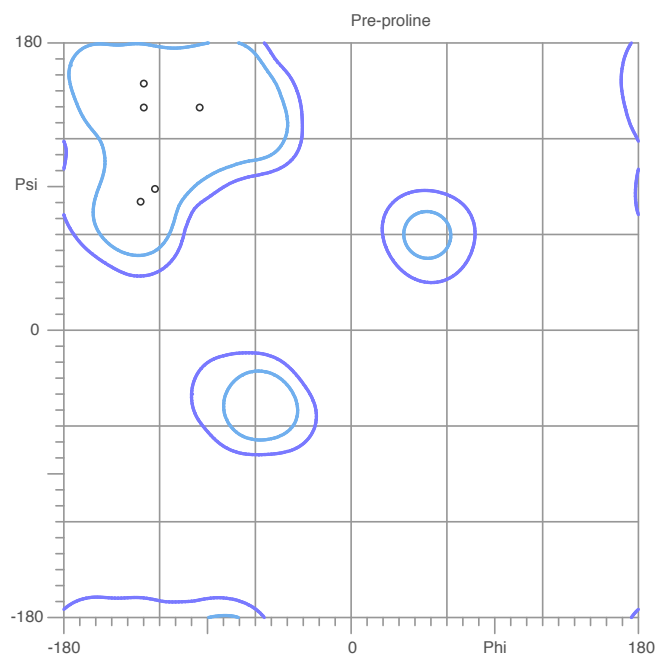
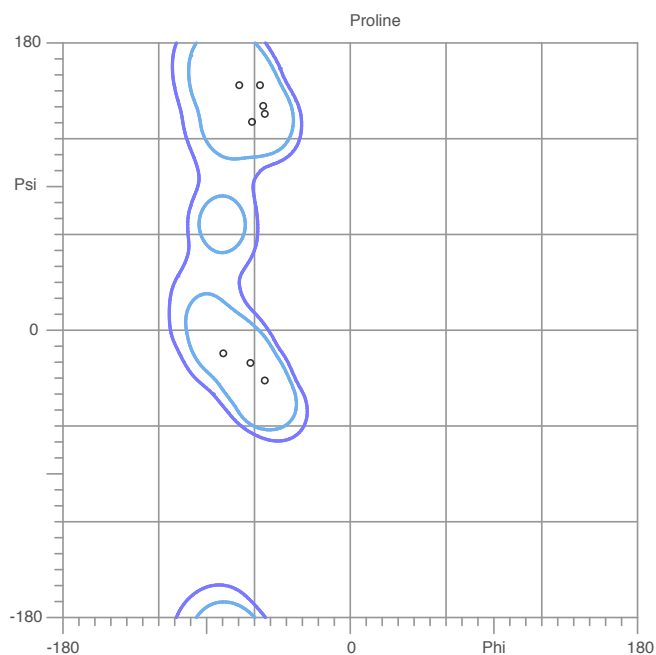
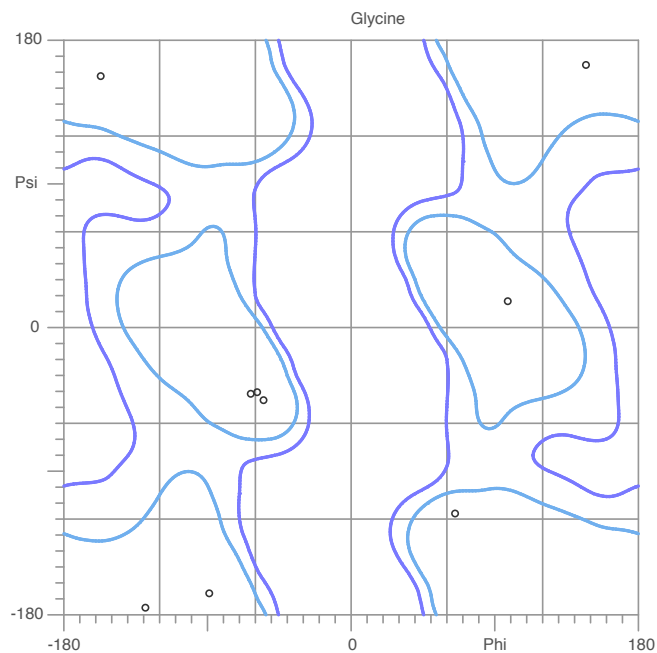
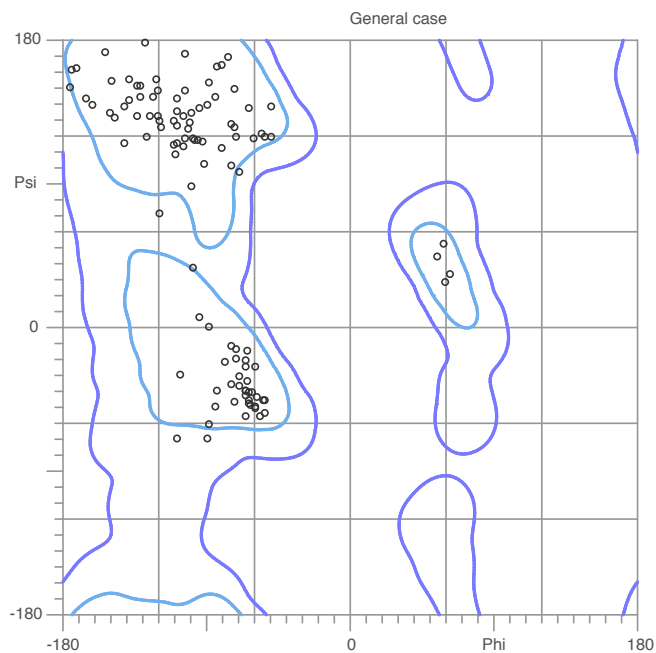
There were no outliers.

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

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 3



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.

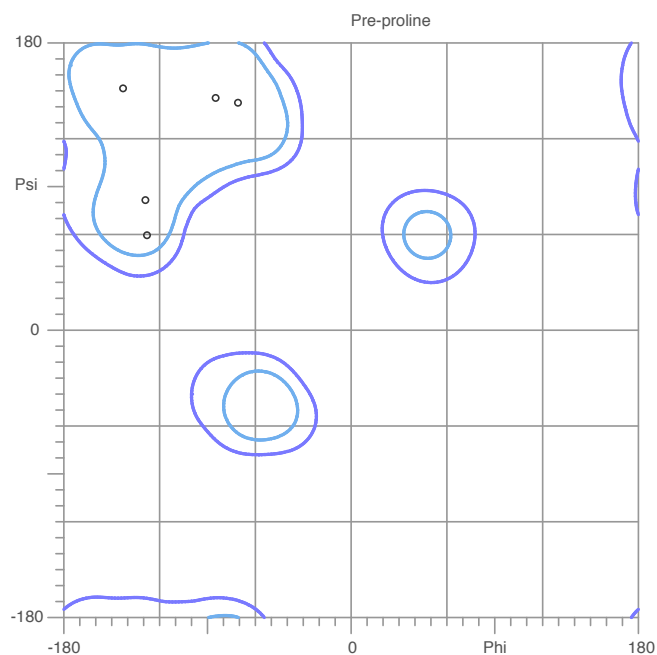
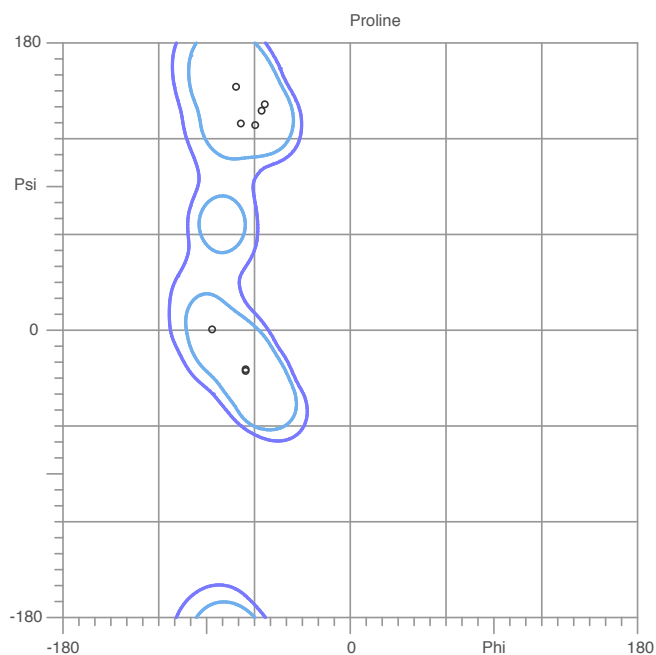
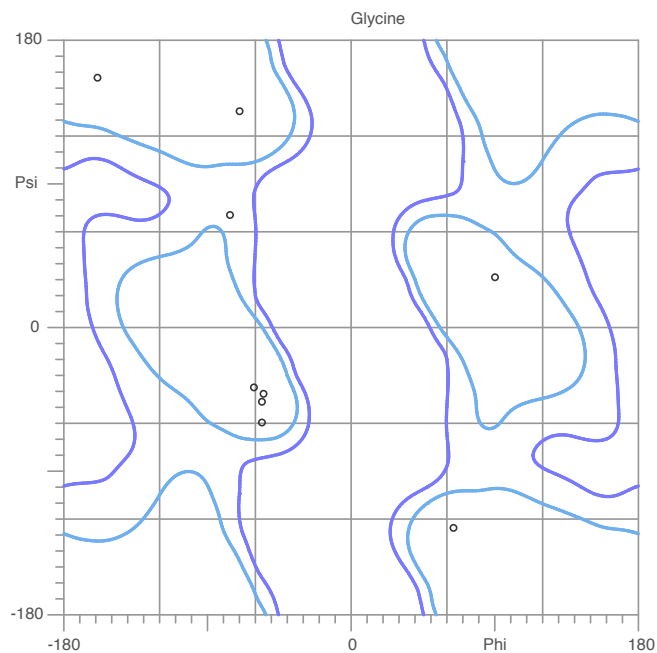
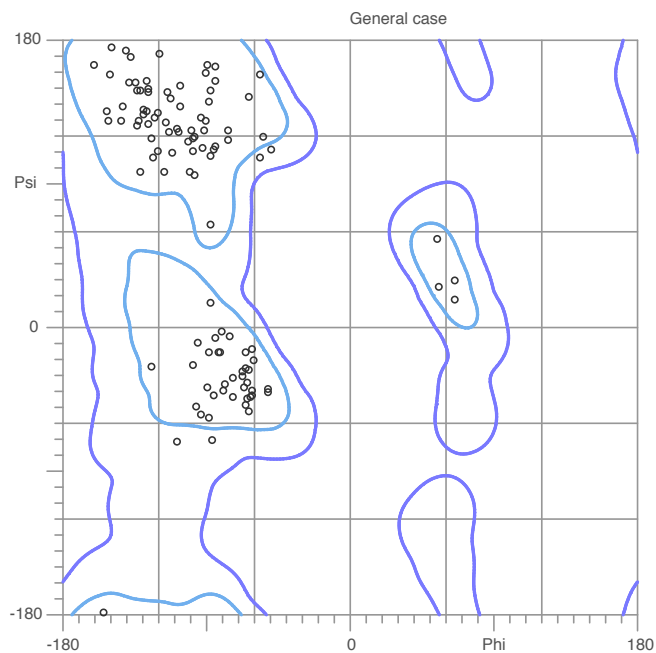
There were no outliers.

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

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 4

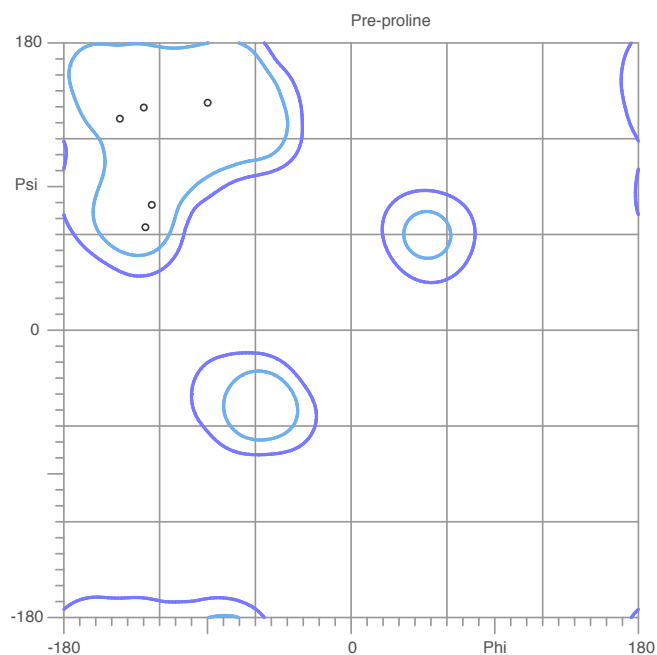
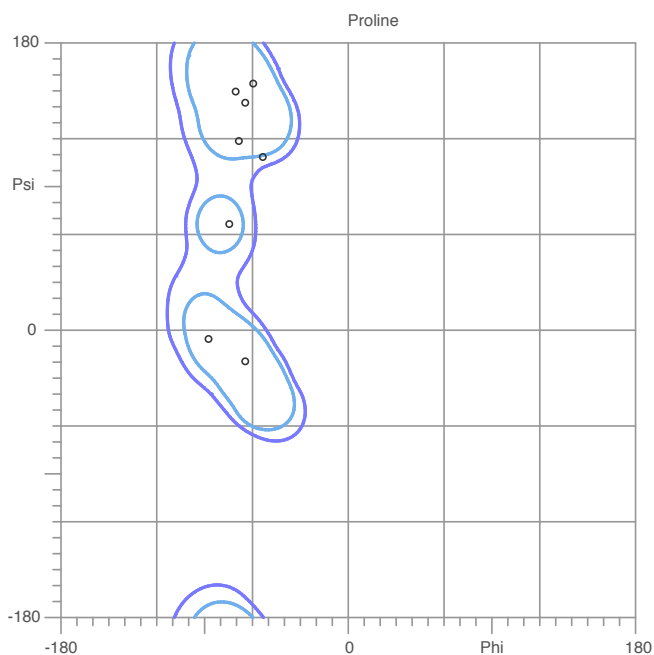
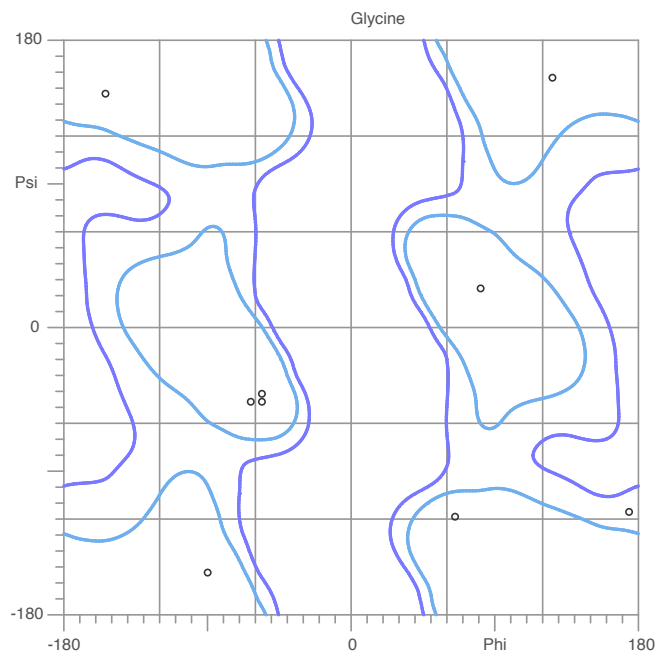
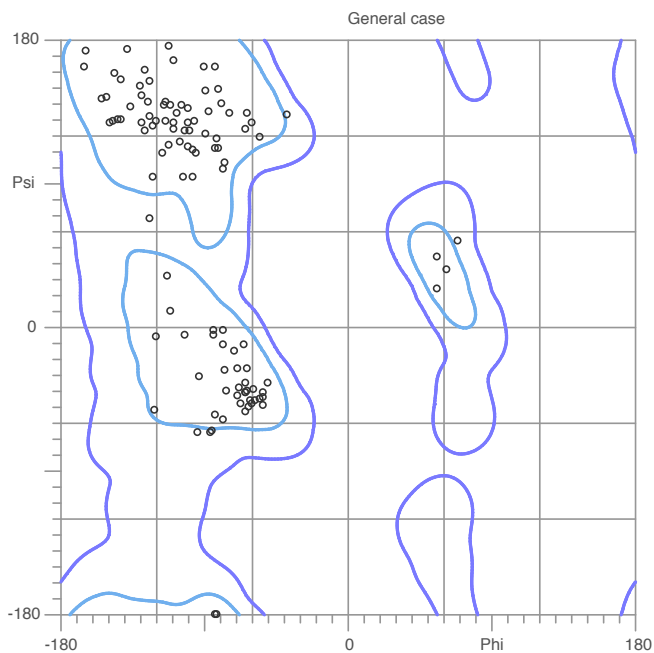


96.2% (127/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 5

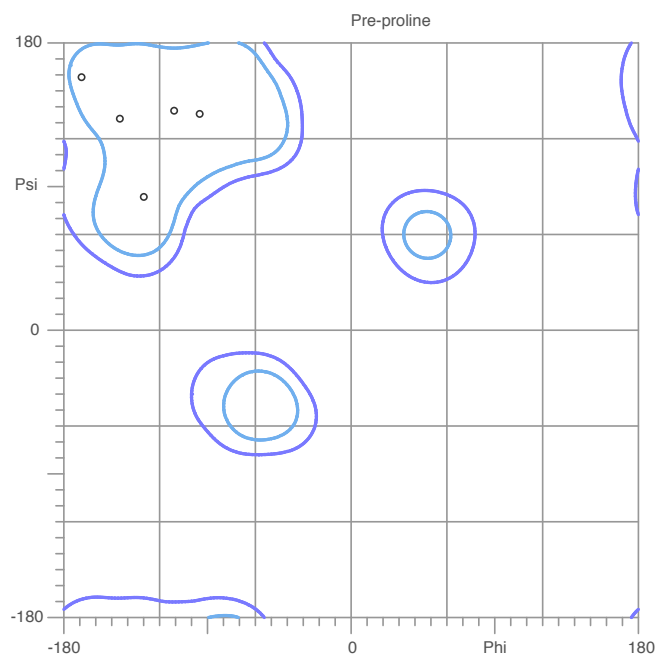
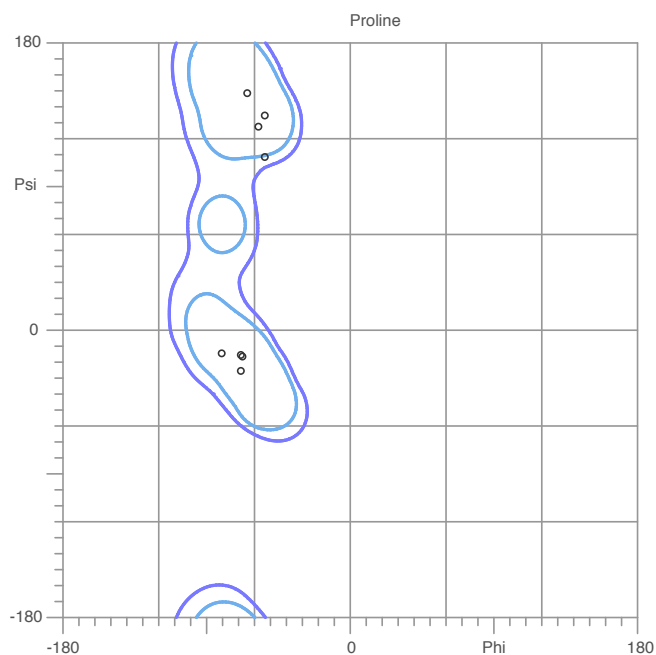
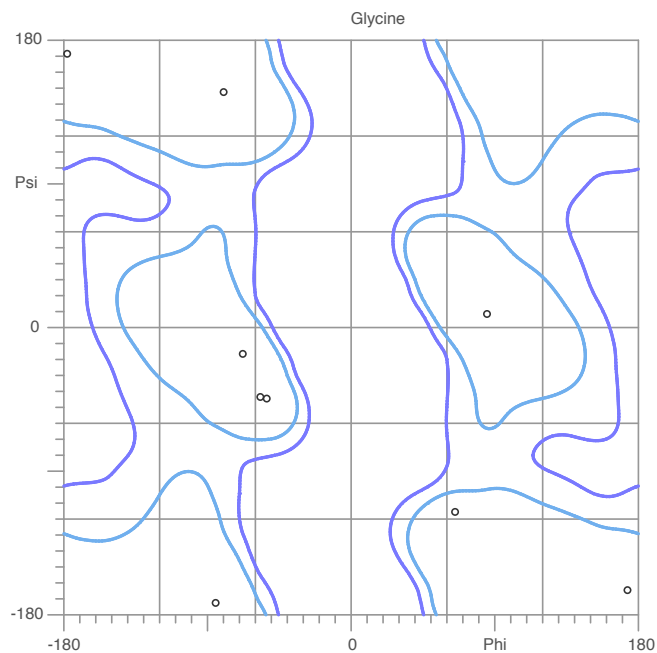
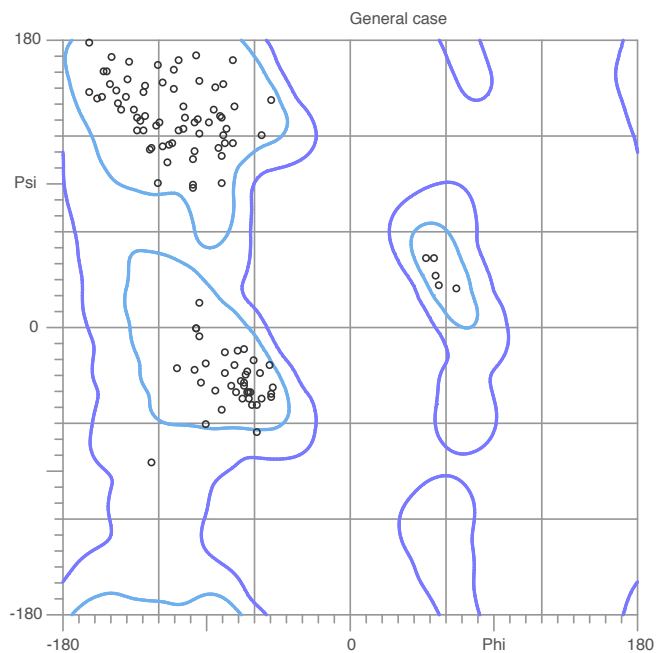


94.7% (125/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 6



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.

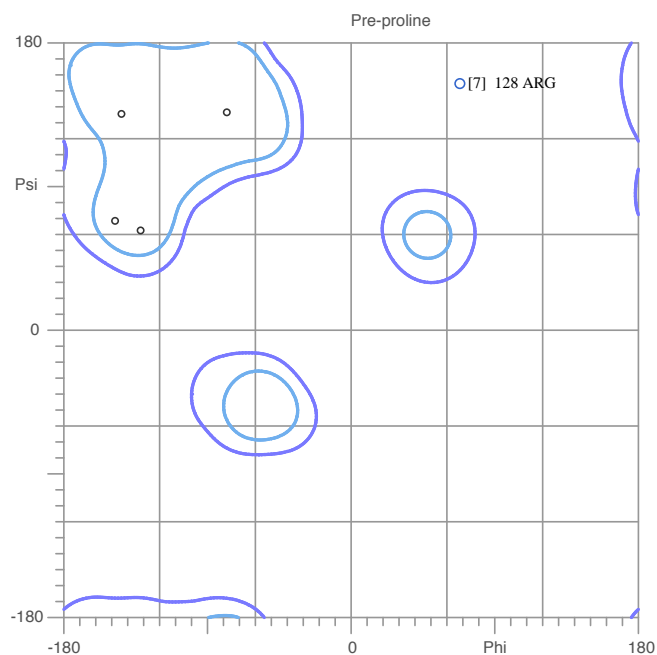
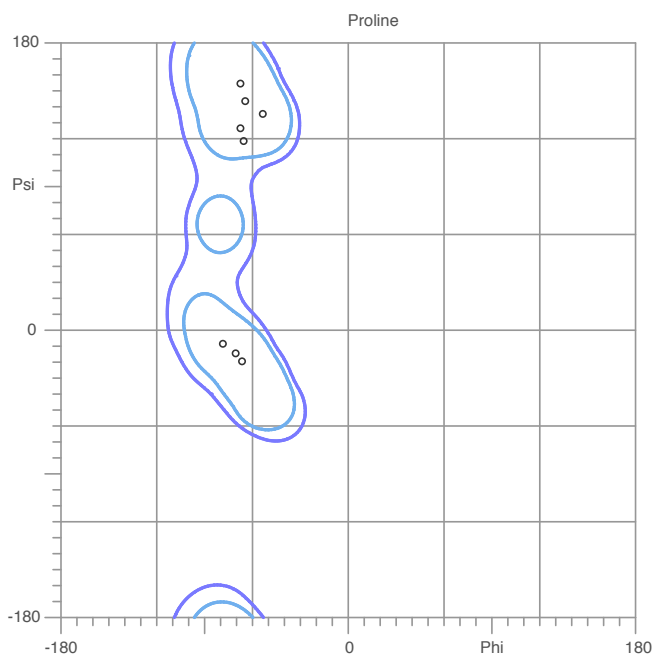
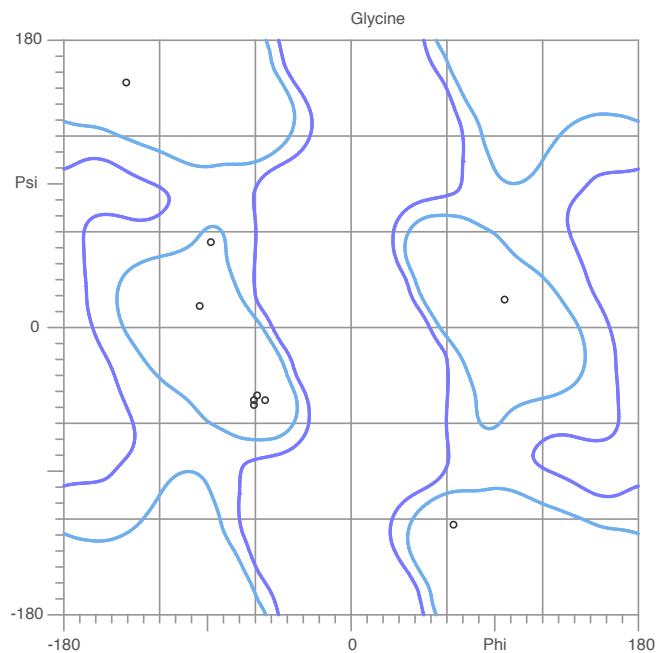
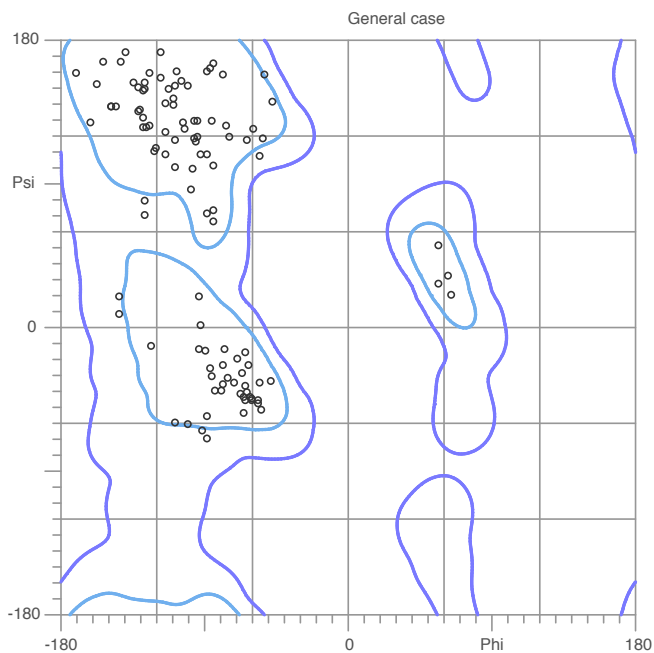
There were no outliers.

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 7



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.

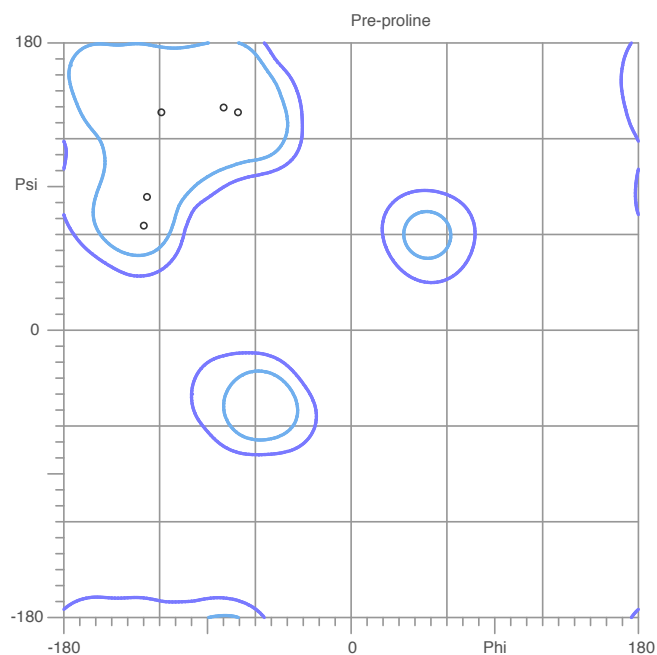
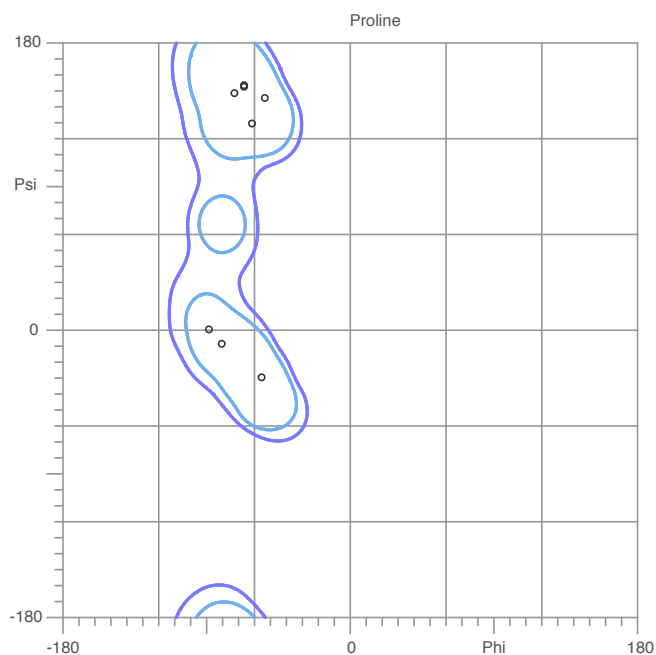
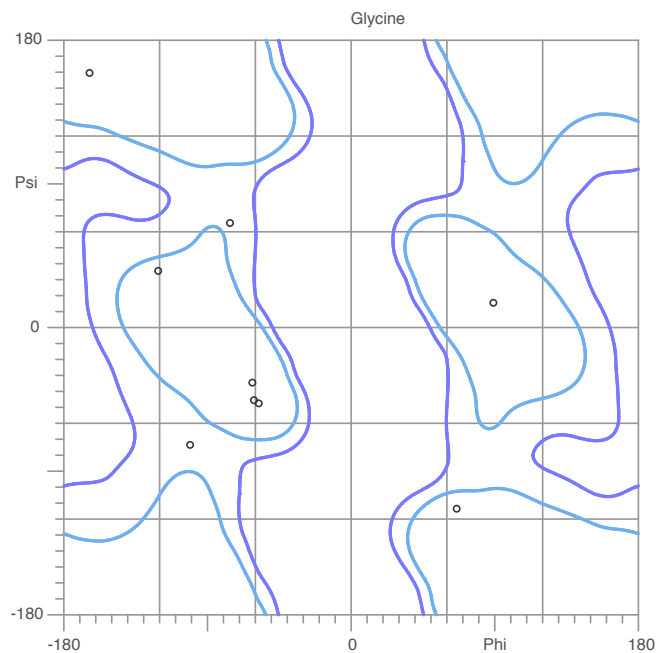
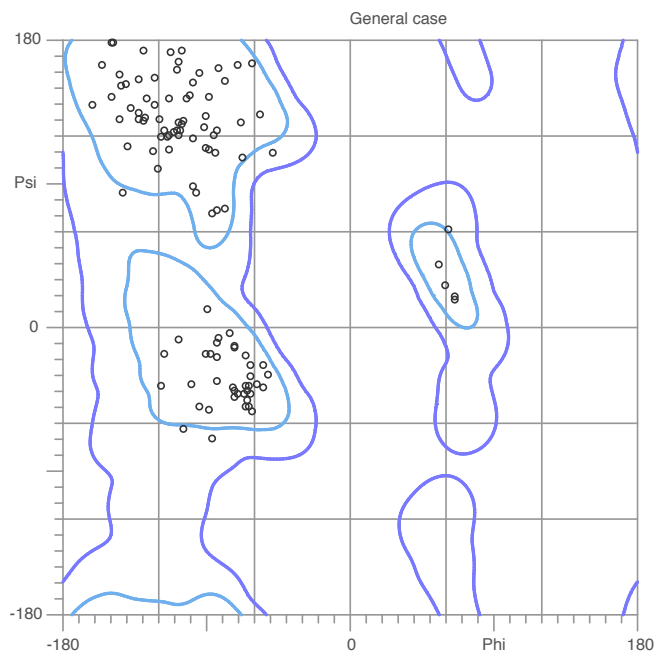
There were 1 outliers (phi, psi):
[7] 128 ARG (68.6, 155.0)

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 8



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.

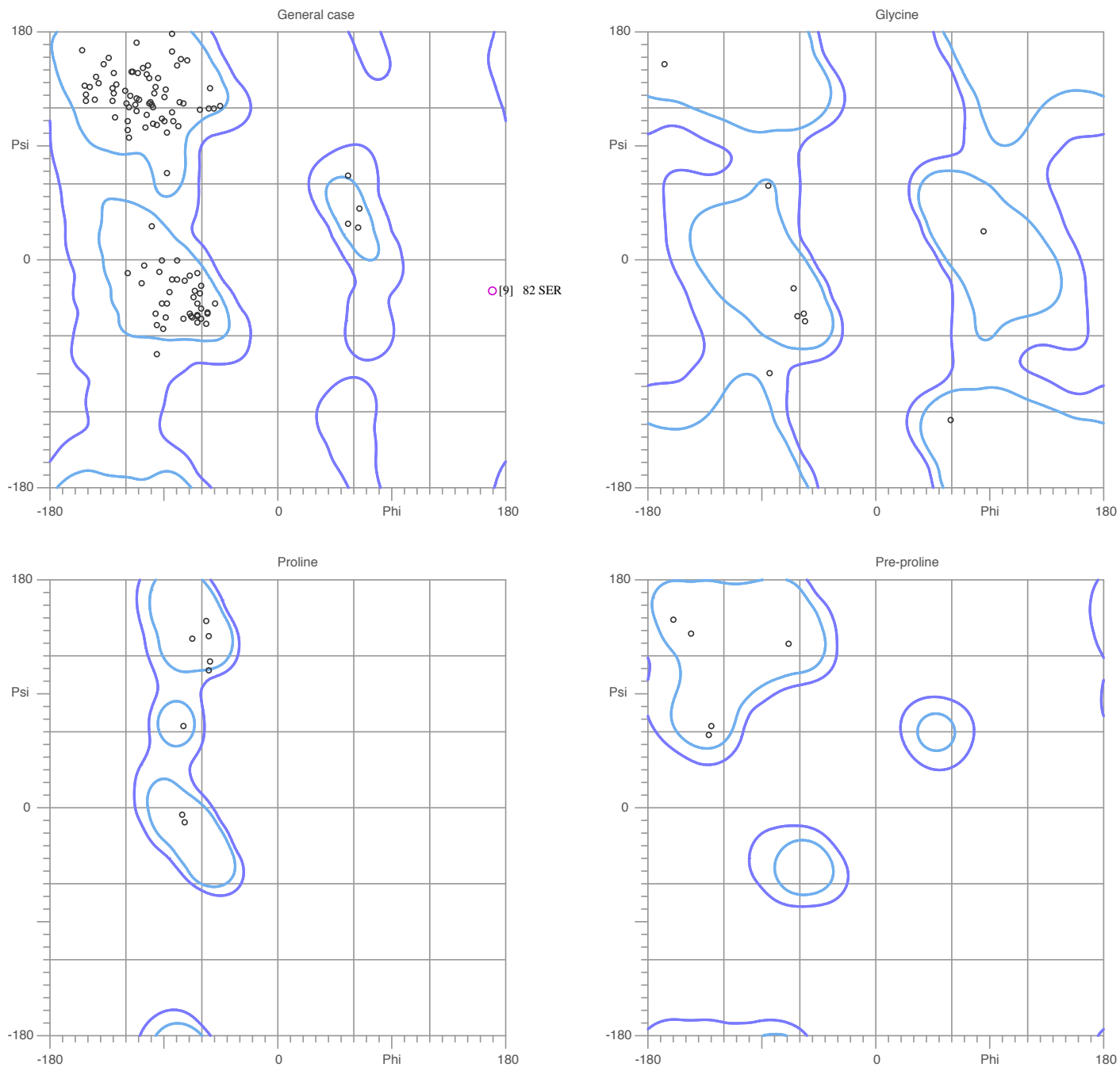
There were no outliers.

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

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 9



97.0% (128/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

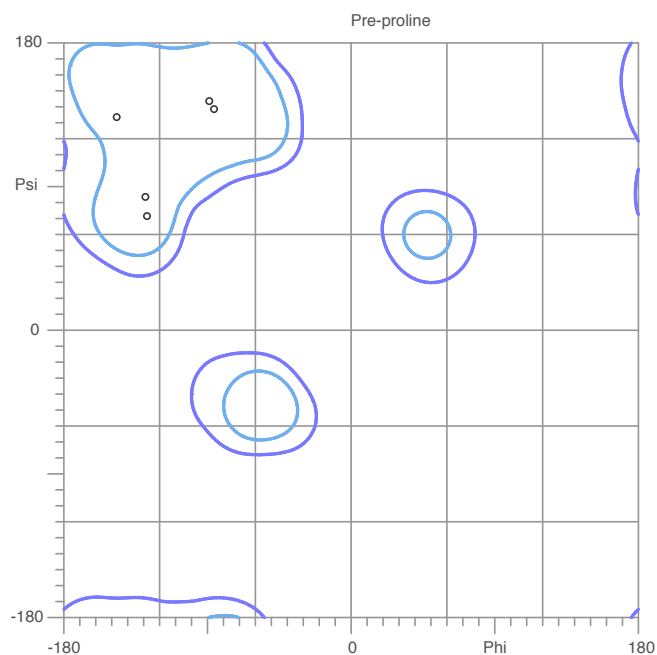
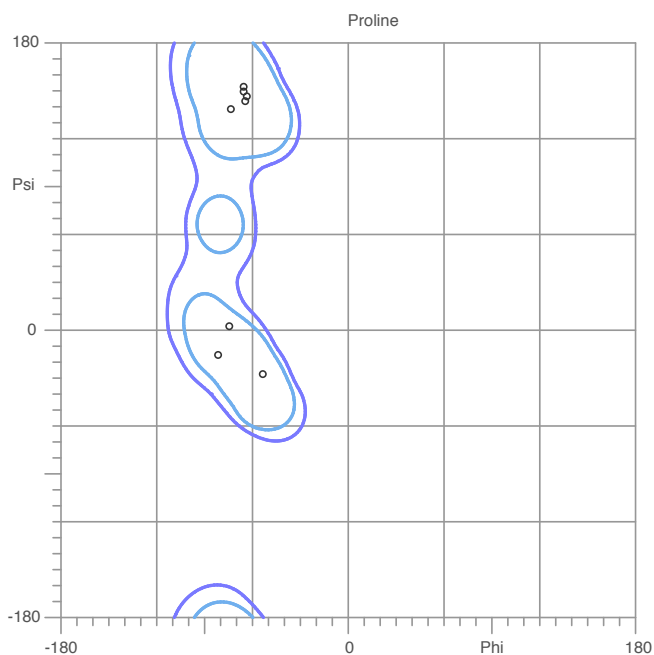
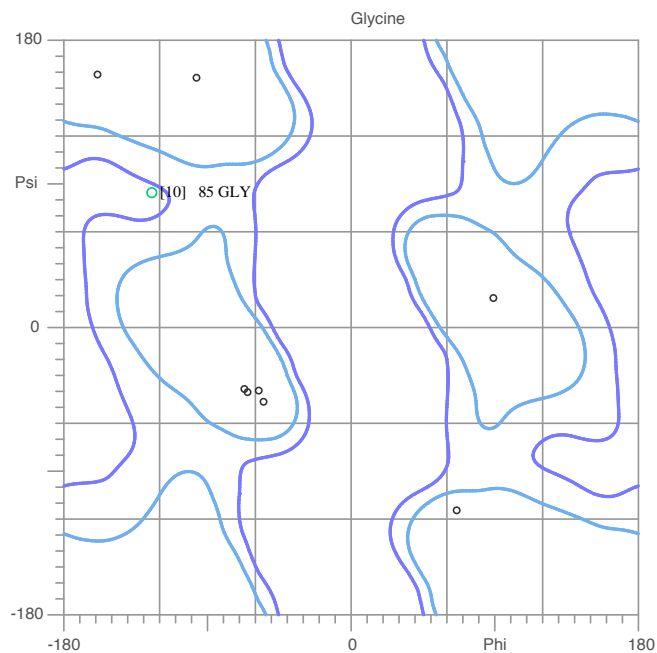
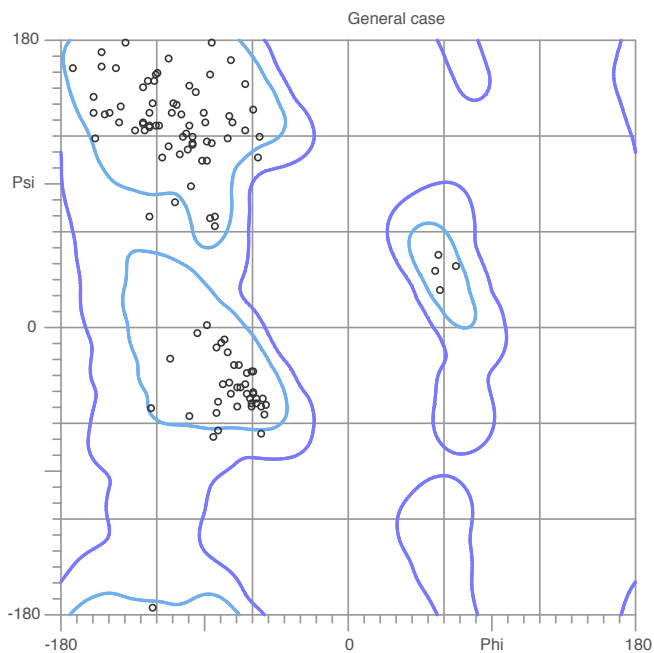
There were 1 outliers (phi, psi):
[9] 82 SER (169.9, -24.9)

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 10



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.

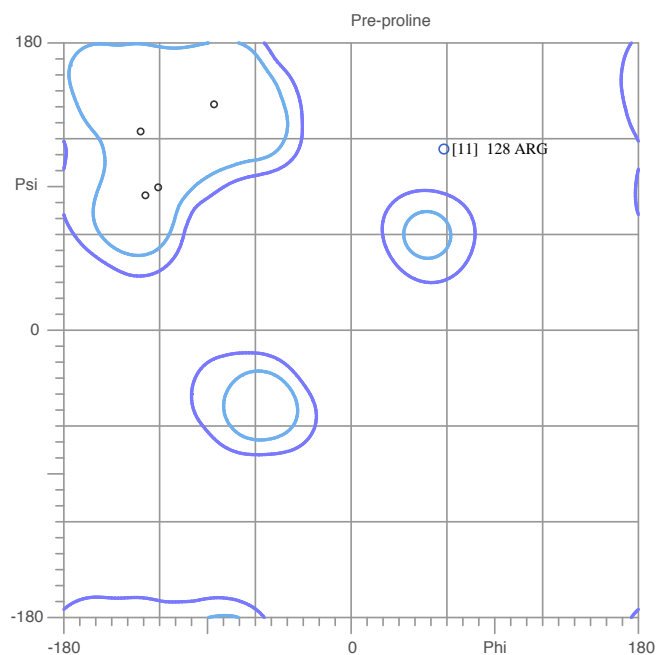
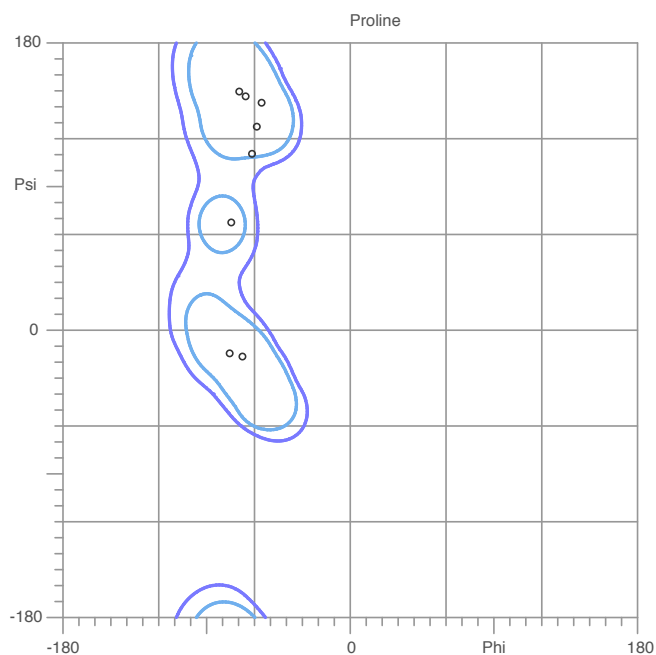
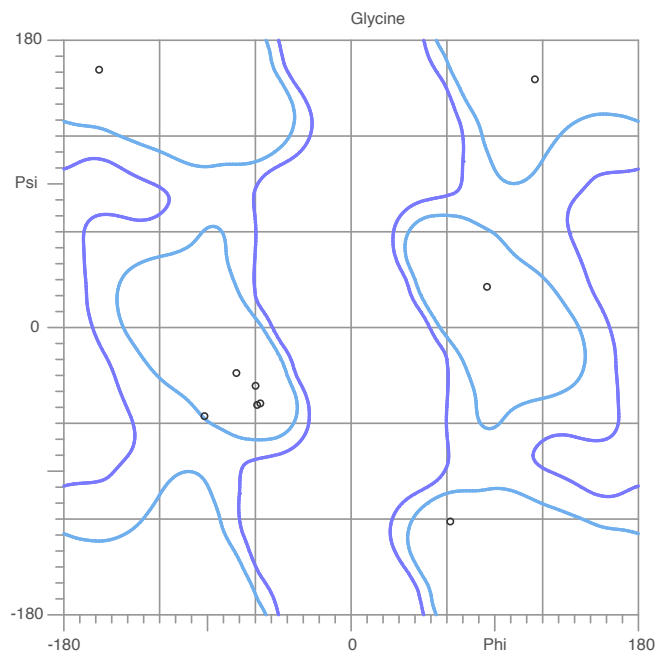
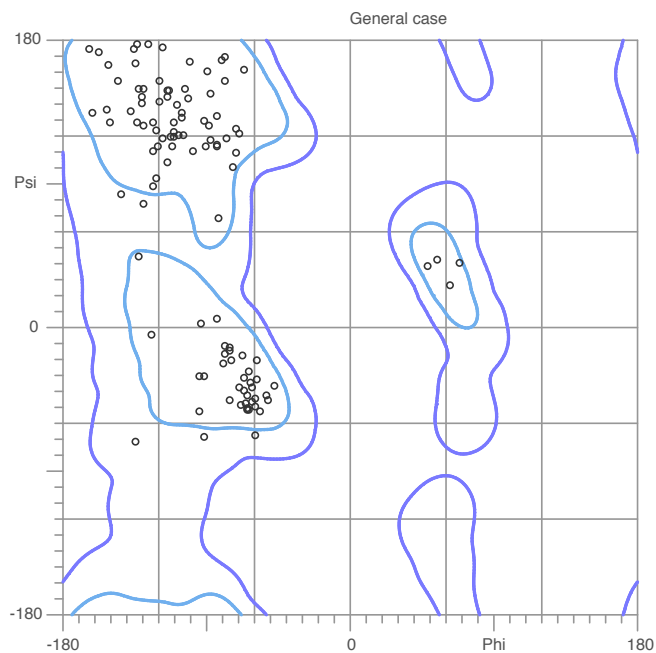
There were 1 outliers (phi, psi):
[10] 85 GLY (-125.1, 85.1)

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 11

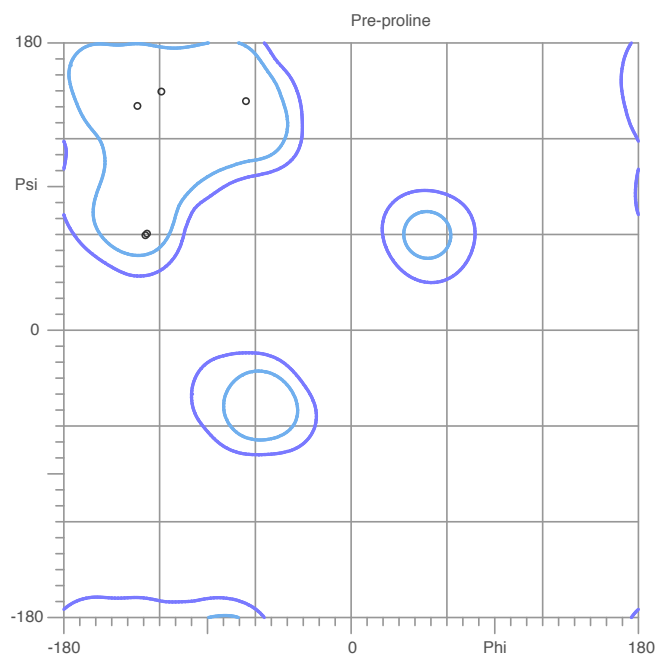
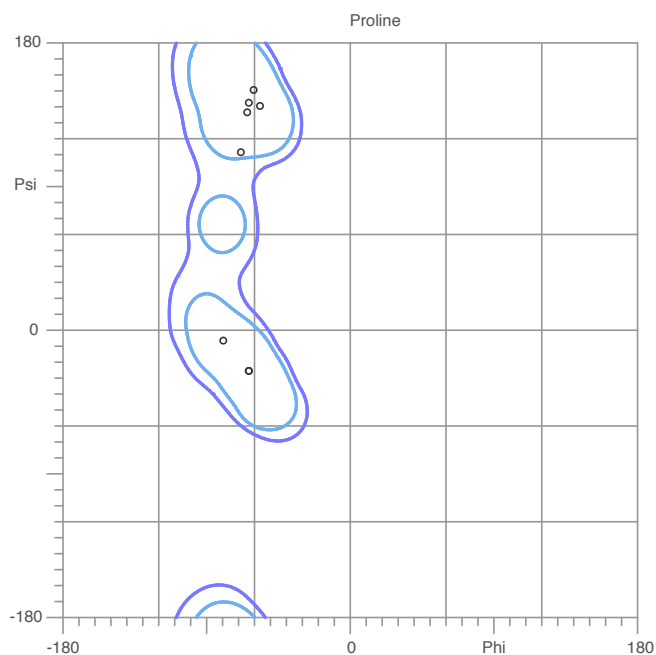
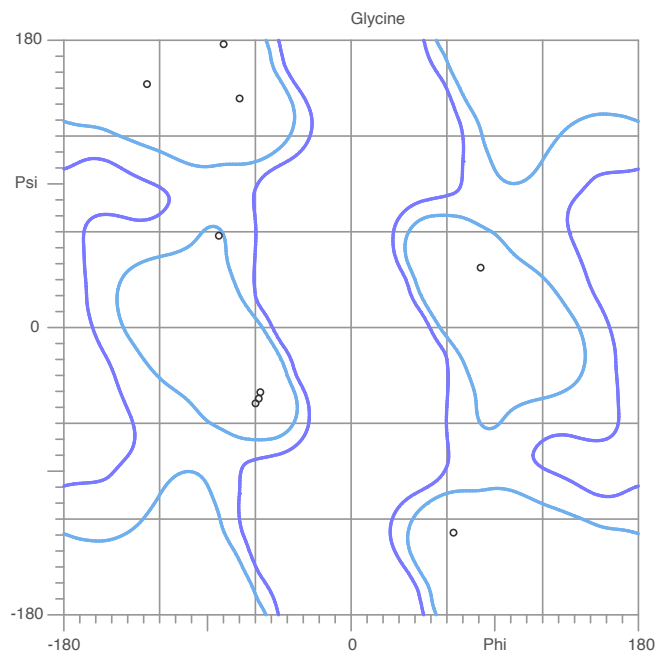
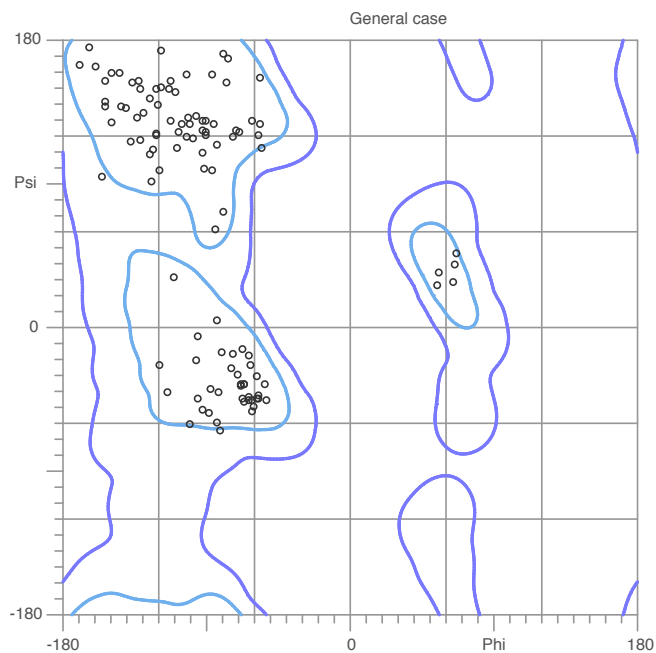


95.5% (126/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[11] 128 ARG (59.0, 114.9)

MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 12



98.5% (130/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

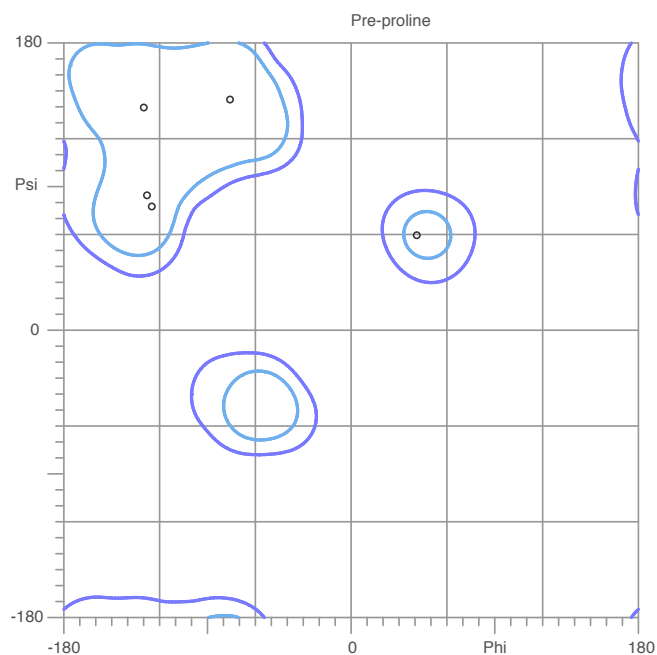
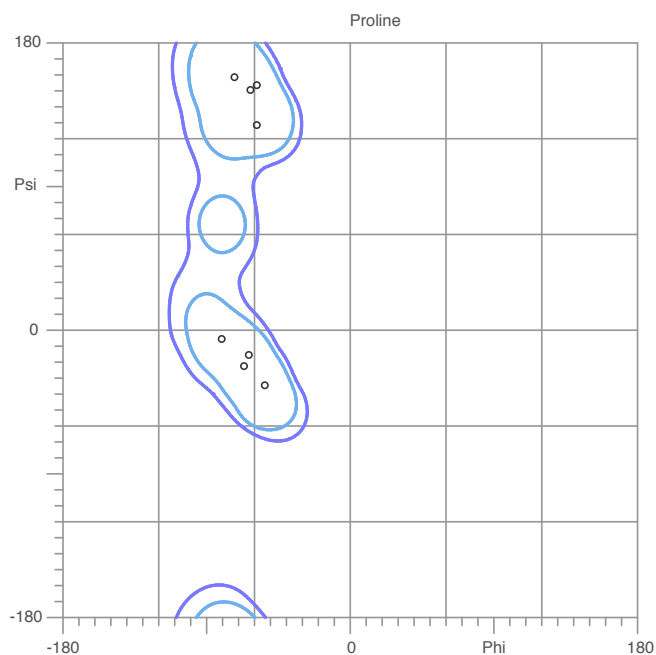
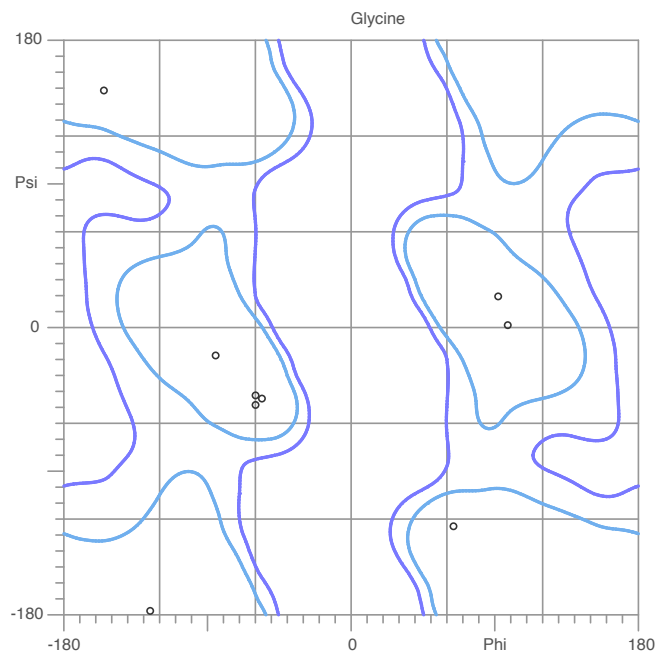
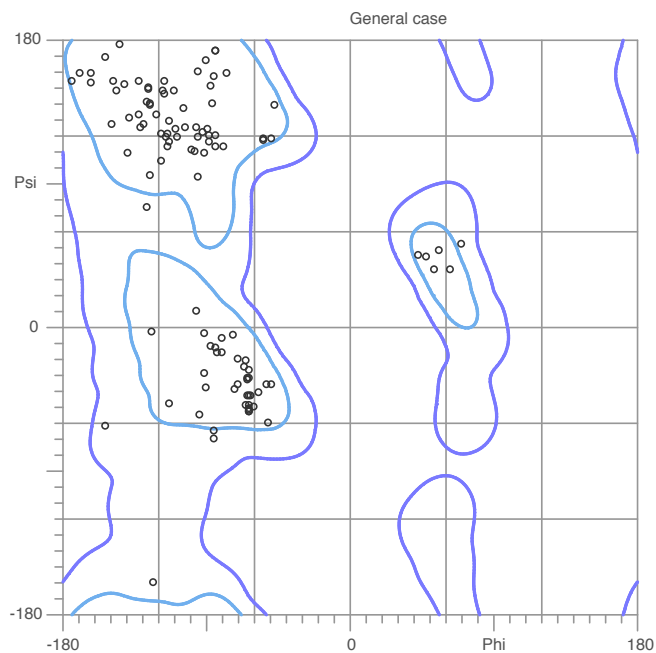
There were no outliers.

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 13

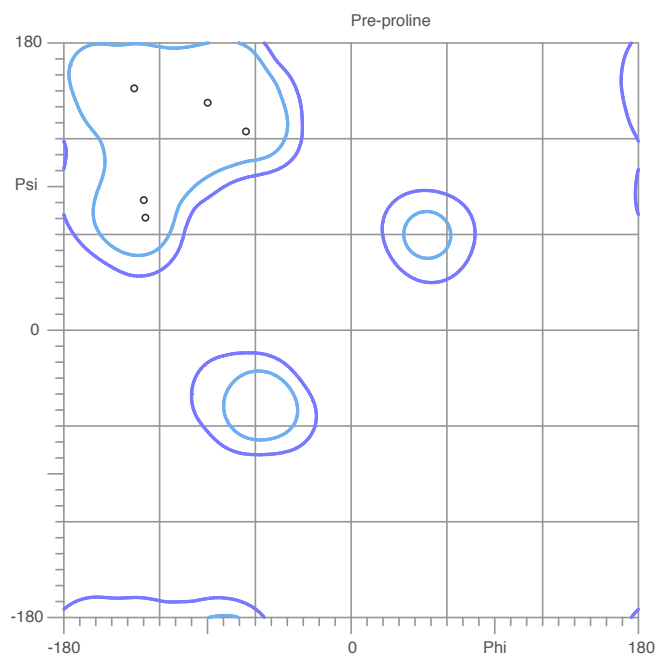
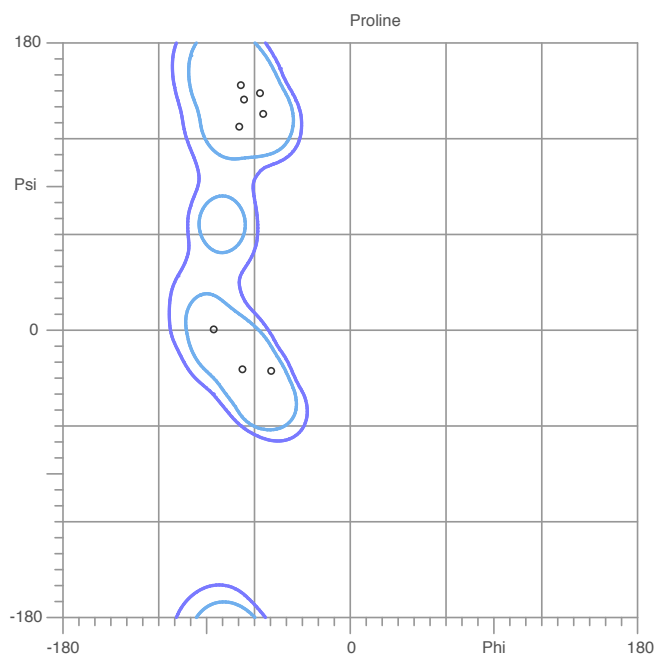
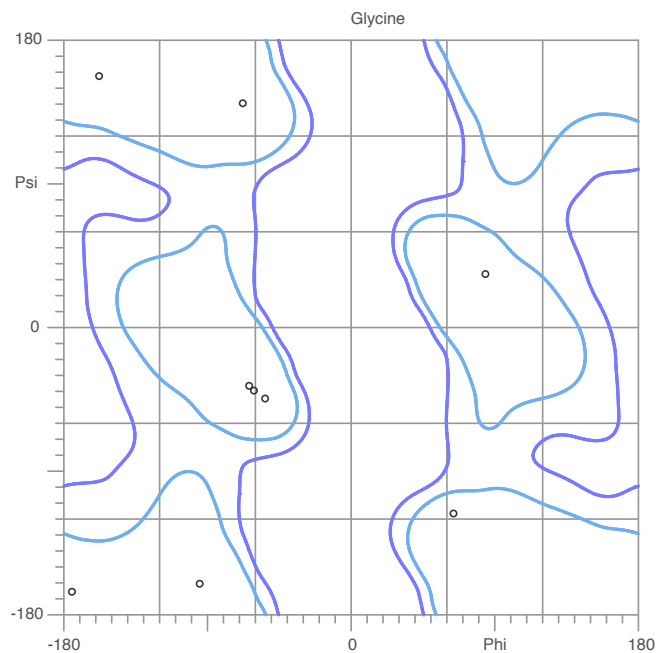
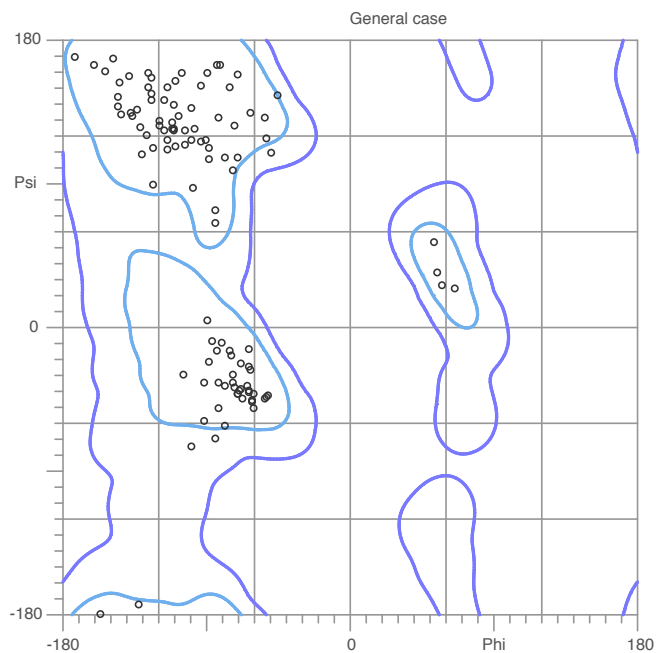


95.5% (126/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 14



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.

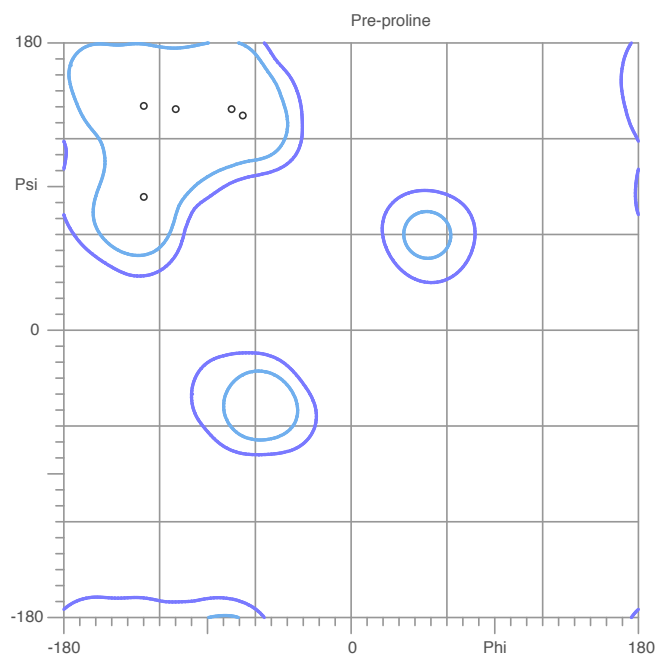
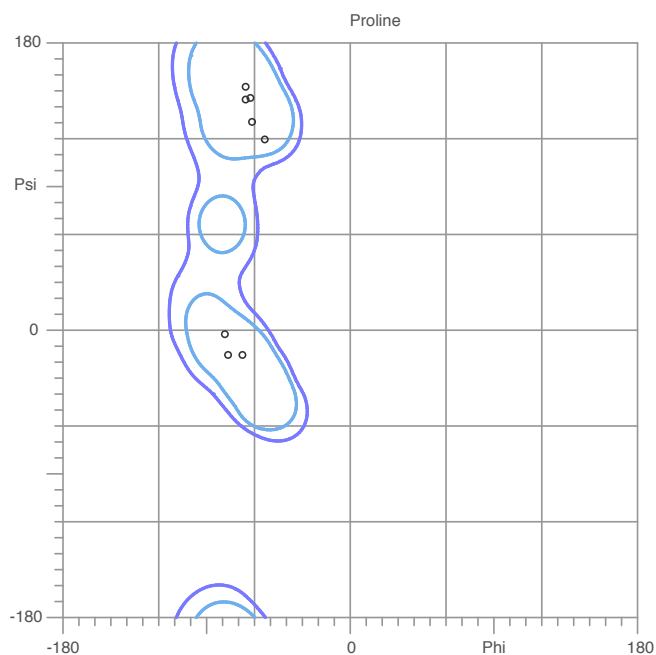
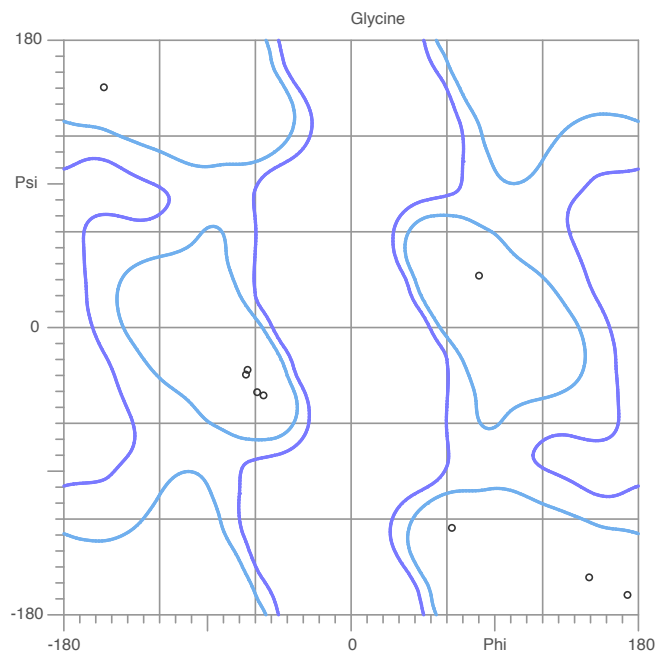
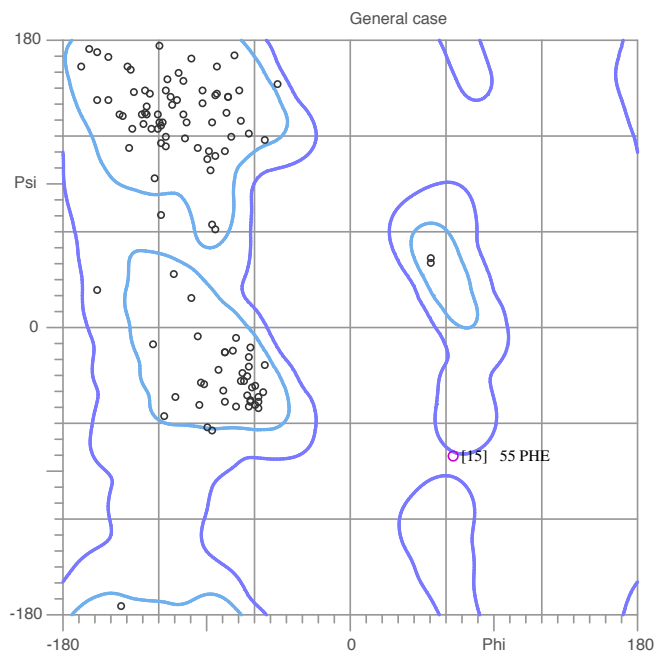
There were no outliers.

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

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 15



96.2% (127/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

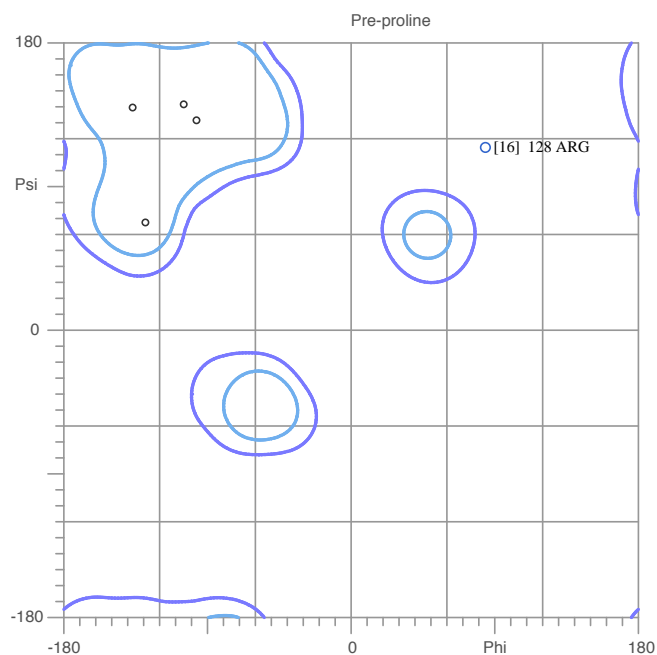
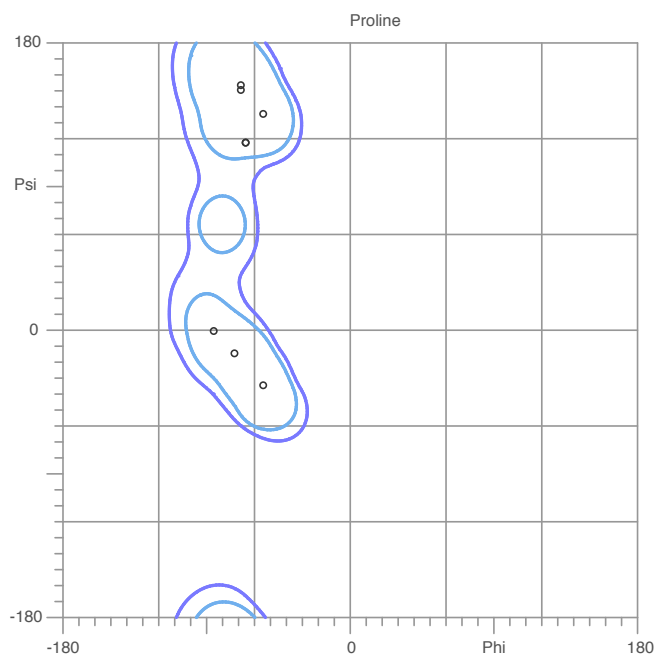
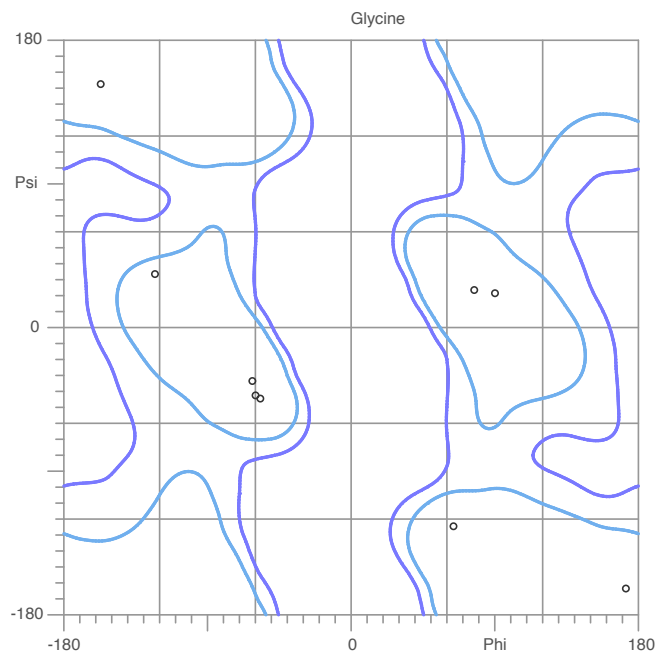
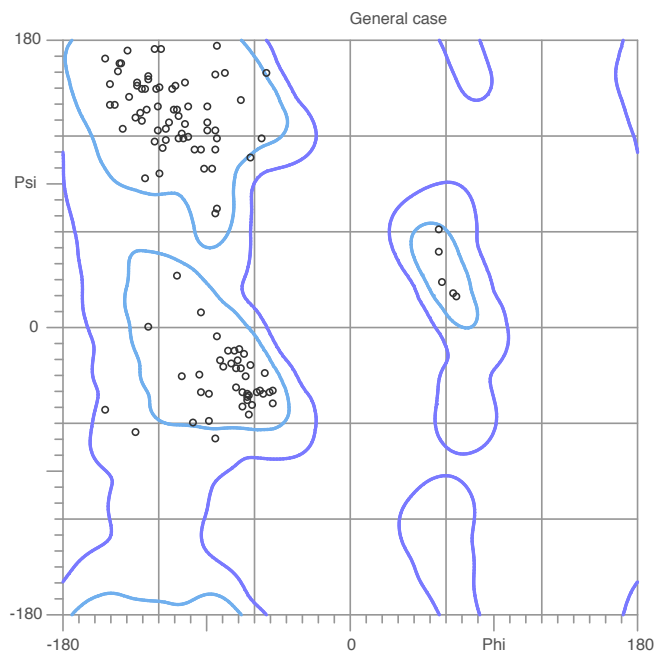
There were 1 outliers (phi, psi):
[15] 55 PHE (64.9, -80.3)

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

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 16



95.5% (126/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

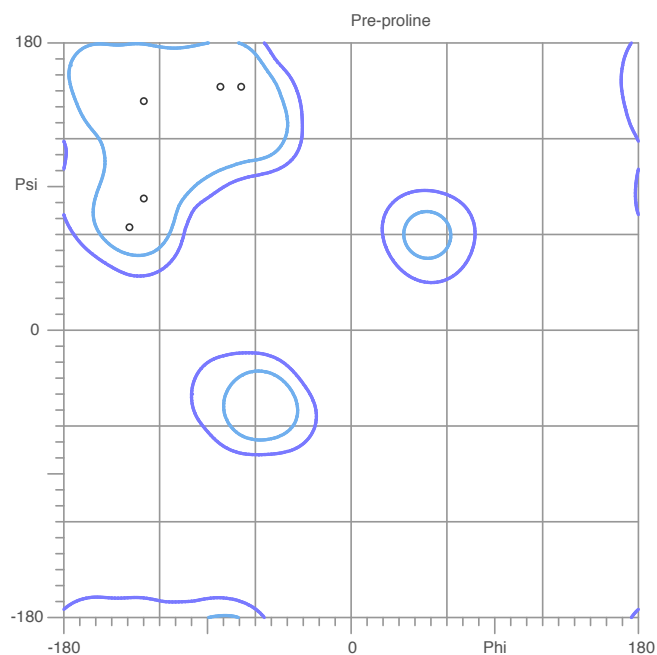
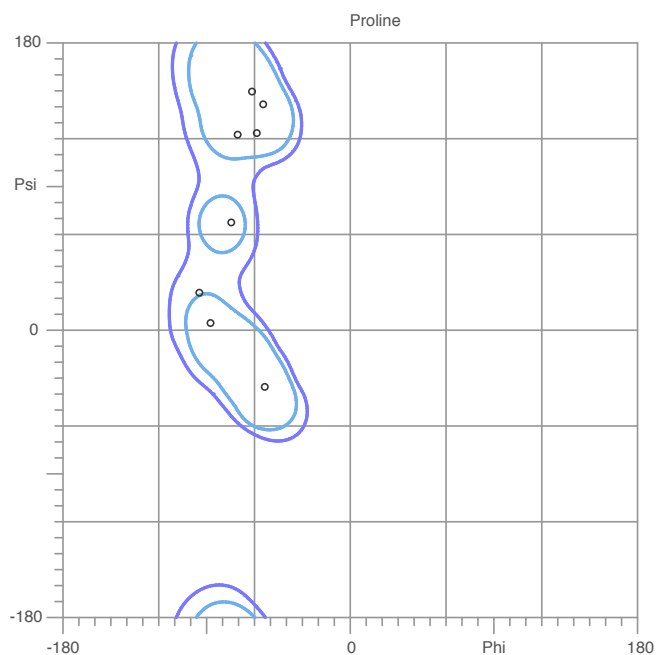
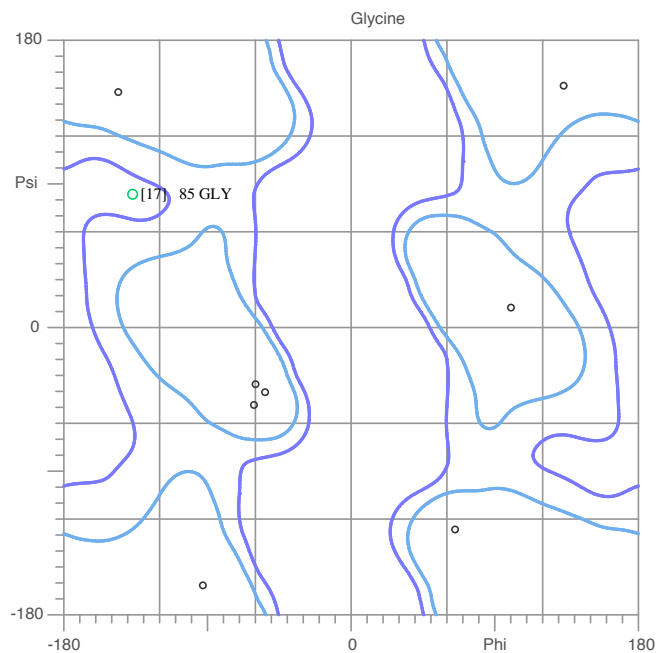
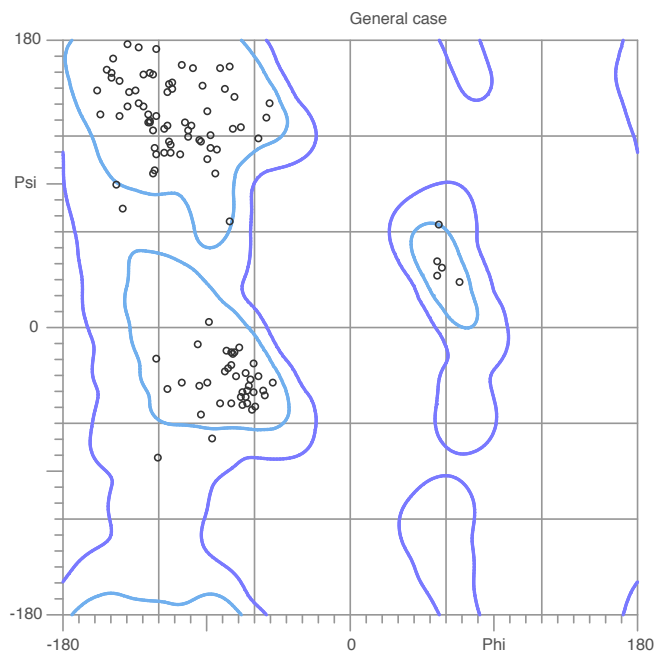
There were 1 outliers (phi, psi):
[16] 128 ARG (85.0, 115.1)

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

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MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 17

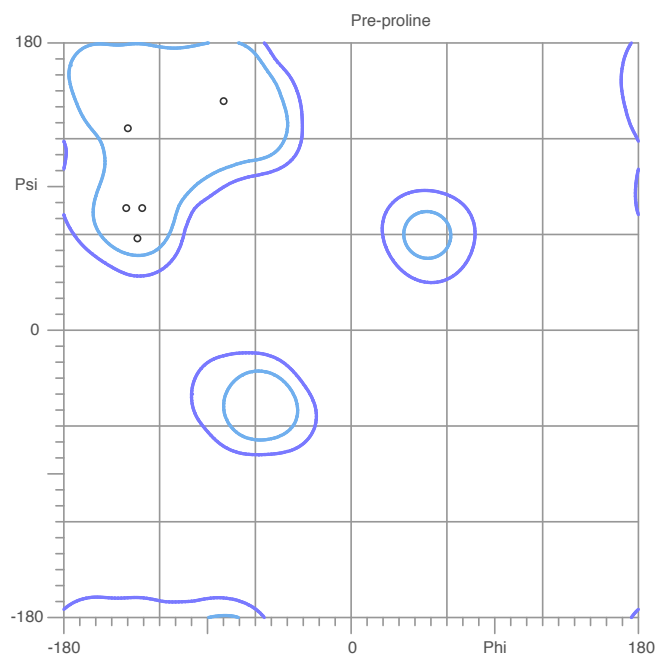
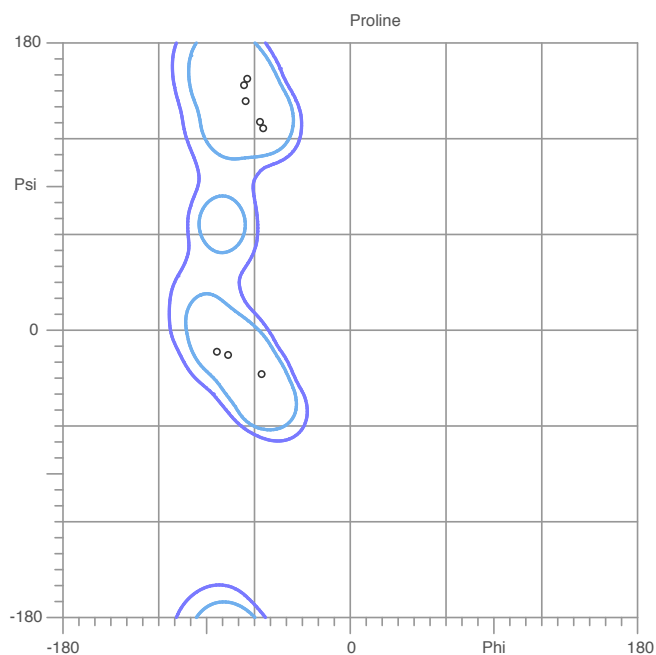
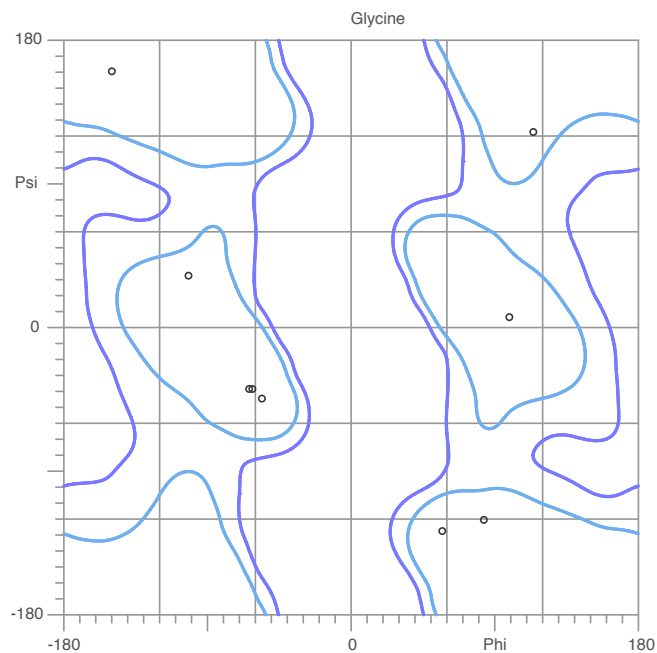
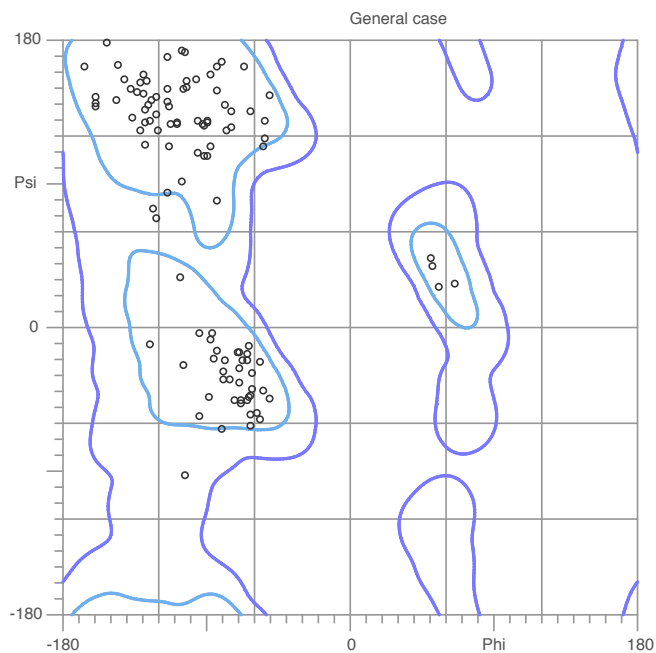


94.7% (125/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[17] 85 GLY (-137.4, 85.0)

MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 18



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.

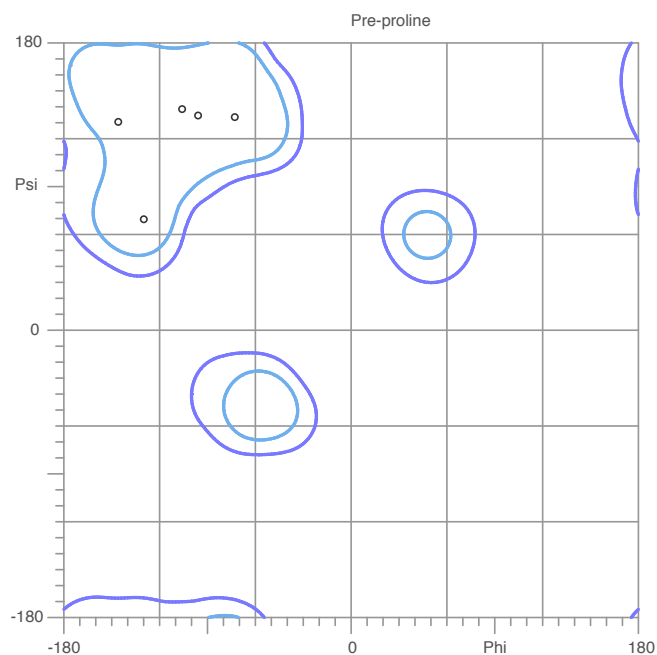
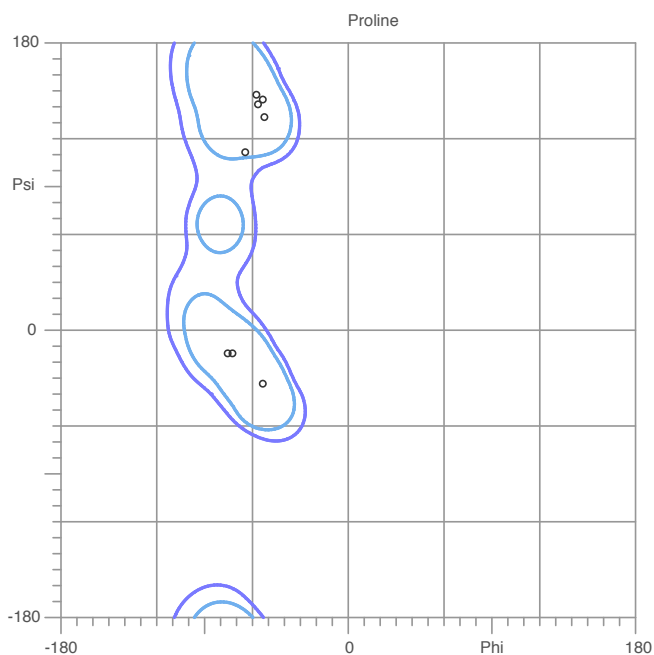
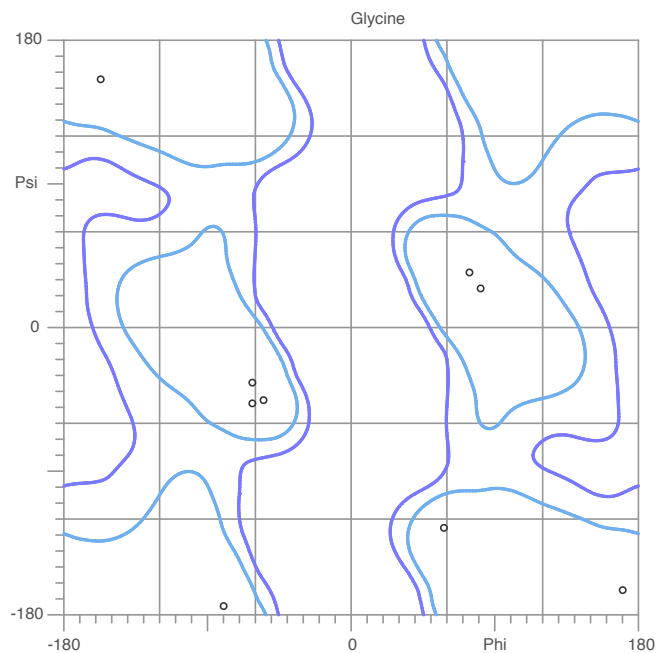
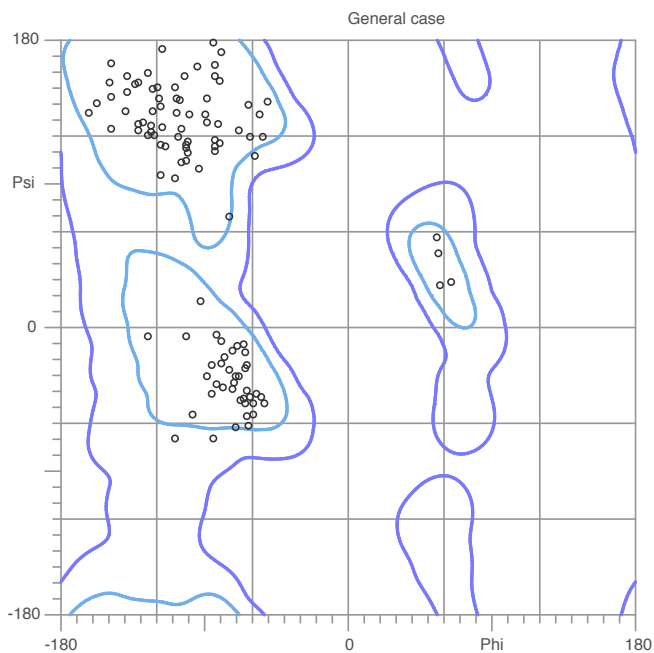
There were no outliers.

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

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

MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 19



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.

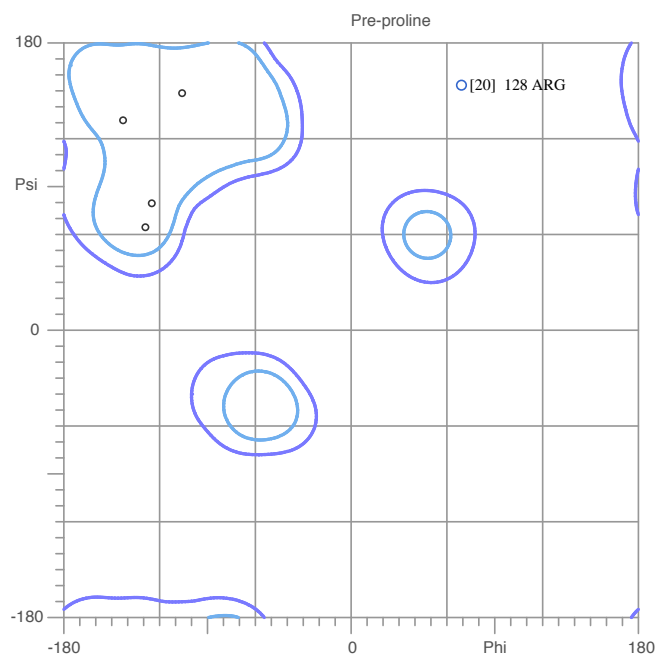
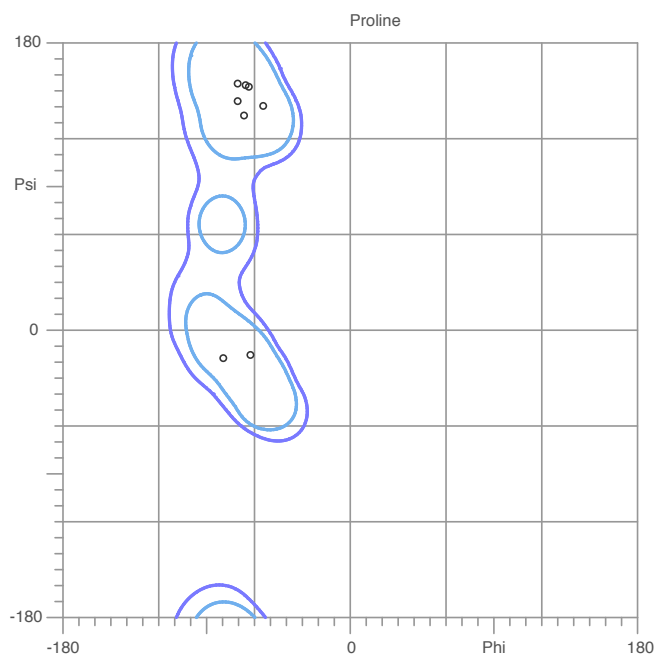
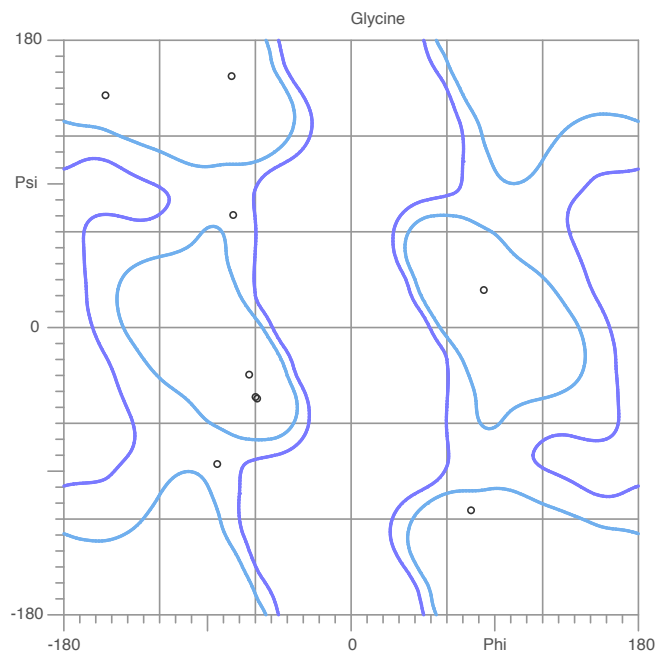
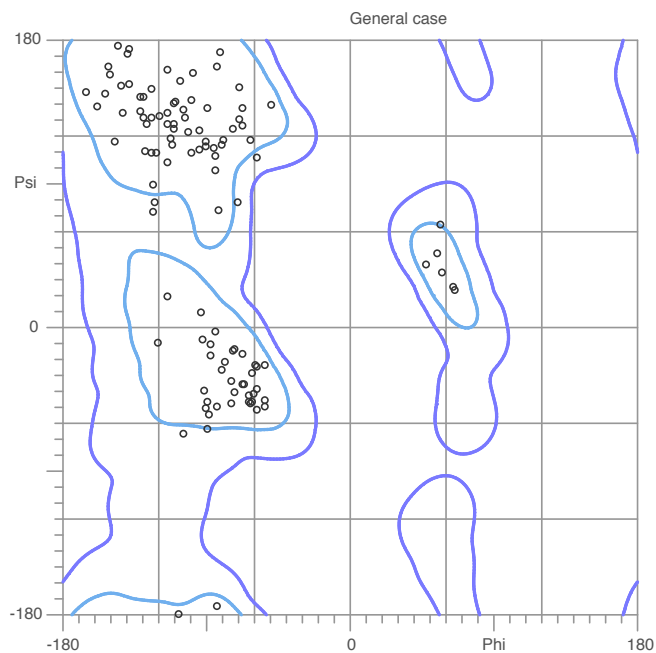
There were no outliers.

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

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

MolProbity Ramachandran analysis

OR8C_R3_em_bcr3.pdb, model 20



92.4% (122/132) 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):
[20] 128 ARG (69.3, 155.0)

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

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