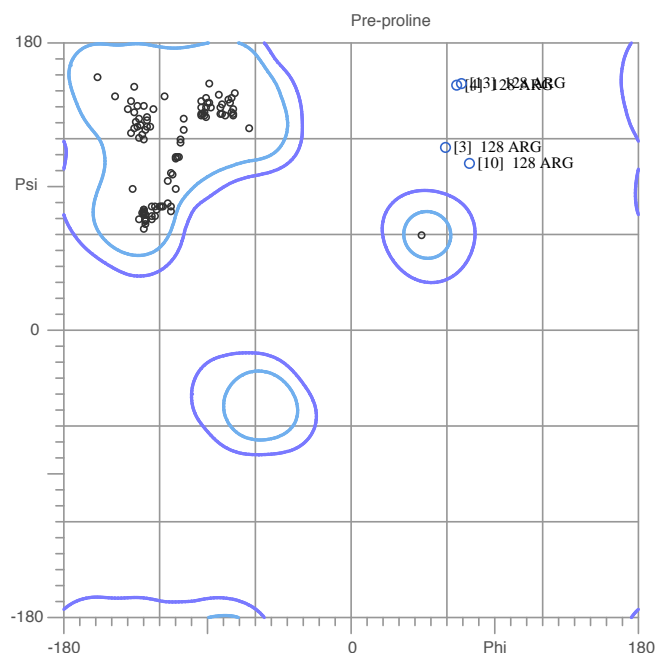
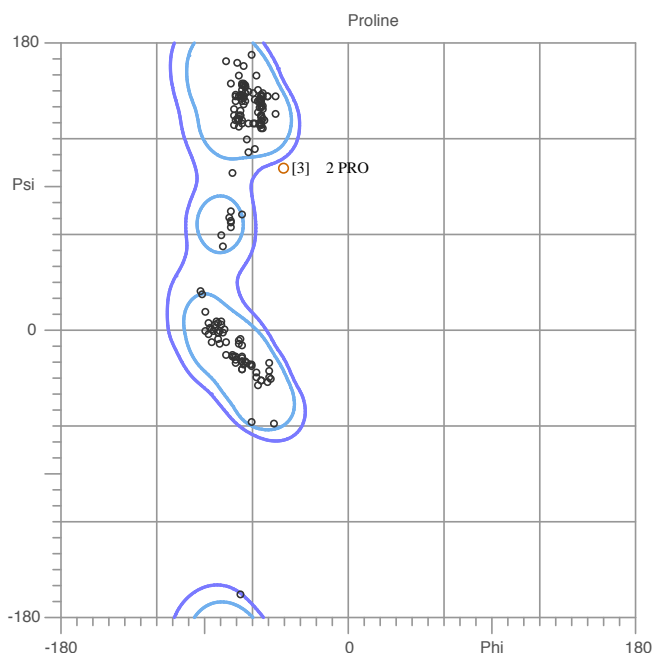
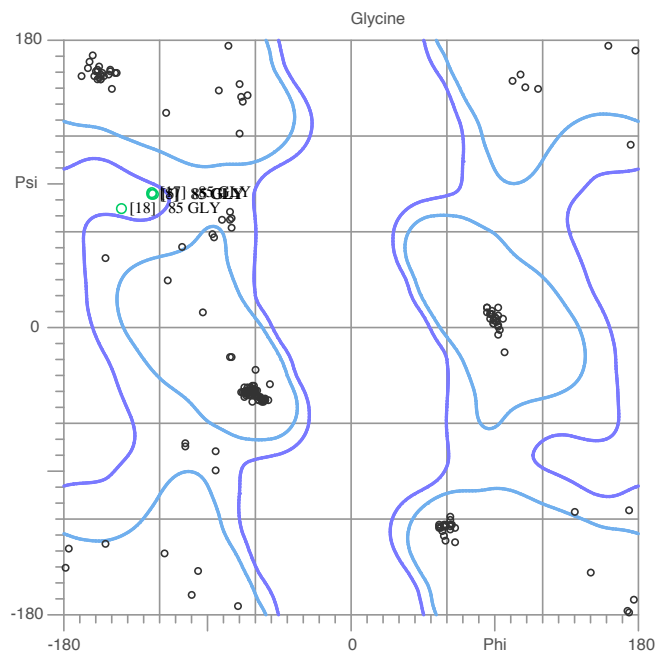
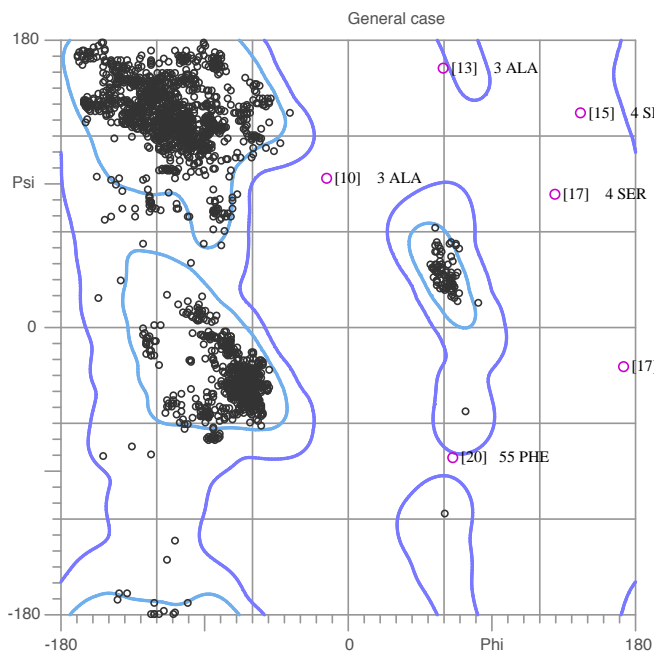


MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, all models



95.9% (2532/2640) of all residues were in favored (98%) regions.
 99.4% (2625/2640) of all residues were in allowed (>99.8%) regions.

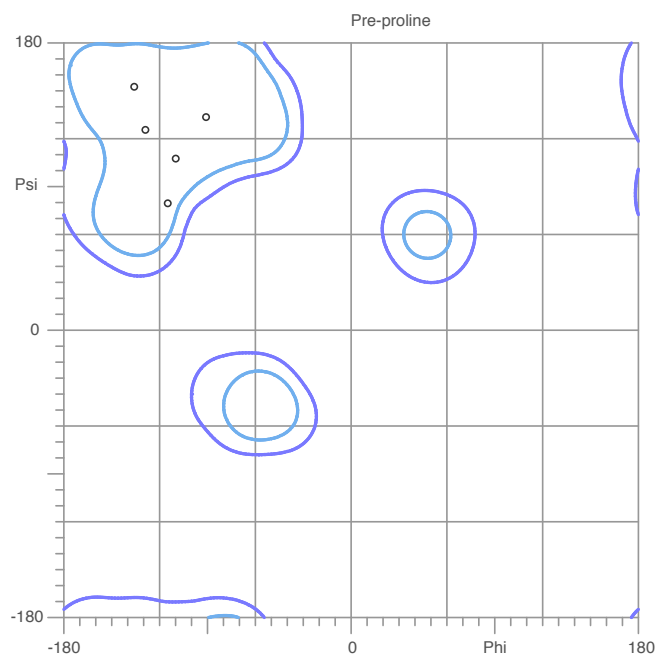
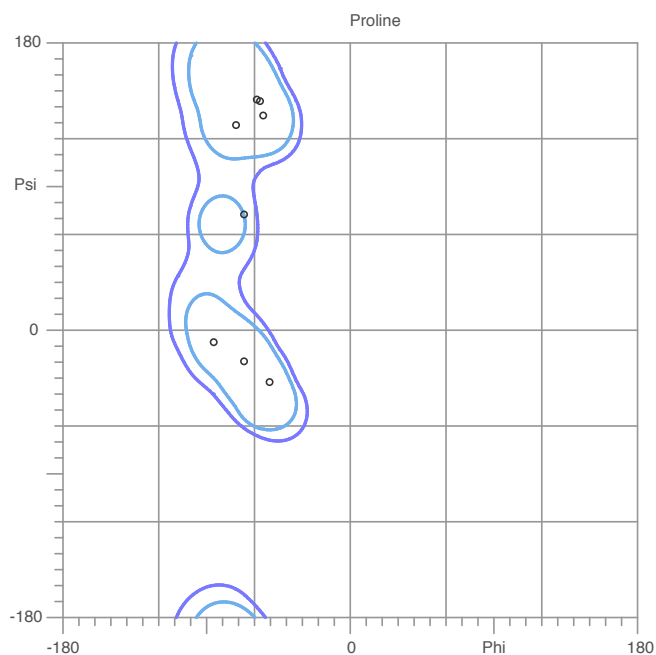
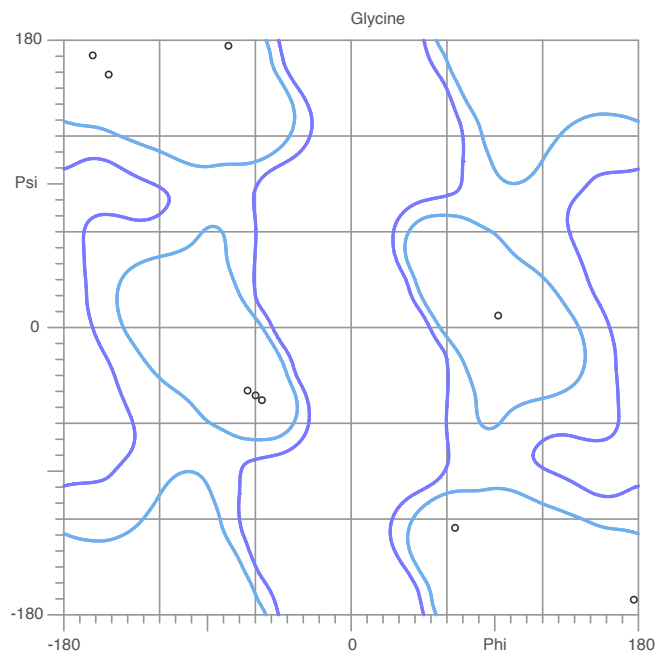
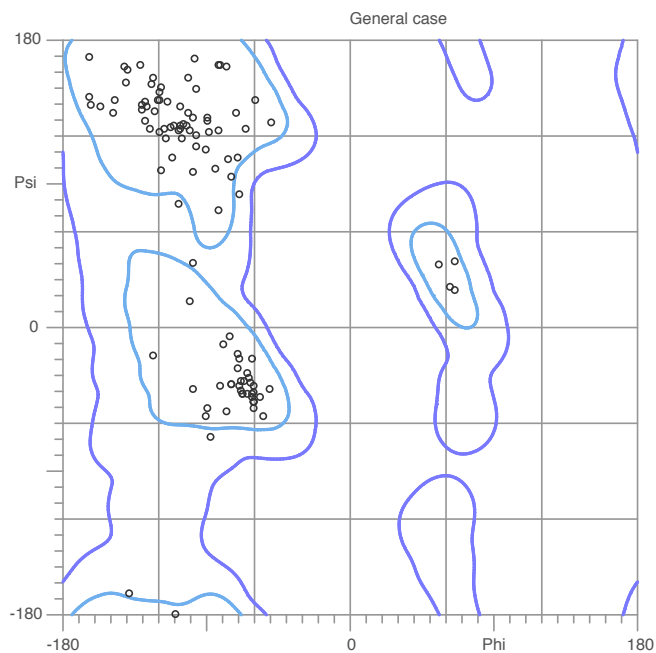
There were 15 outliers (phi, psi):

- [3] 2 PRO (-42.0, 102.8)
- [3] 128 ARG (59.2, 115.0)
- [4] 128 ARG (66.2, 155.0)
- [5] 85 GLY (-124.6, 85.0)
- [8] 85 GLY (-125.1, 85.0)

- [10] 3 ALA (-15.0, 94.8)
- [10] 128 ARG (75.0, 105.0)
- [13] 3 ALA (60.0, 163.1)
- [13] 128 ARG (69.3, 155.0)
- [15] 4 SER (145.1, 135.0)
- [17] 4 SER (129.0, 84.9)
- [17] 82 SER (172.1, -24.8)
- [17] 85 GLY (-125.0, 85.1)
- [18] 85 GLY (-144.6, 75.0)
- [20] 55 PHE (65.5, -81.5)

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 1



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.

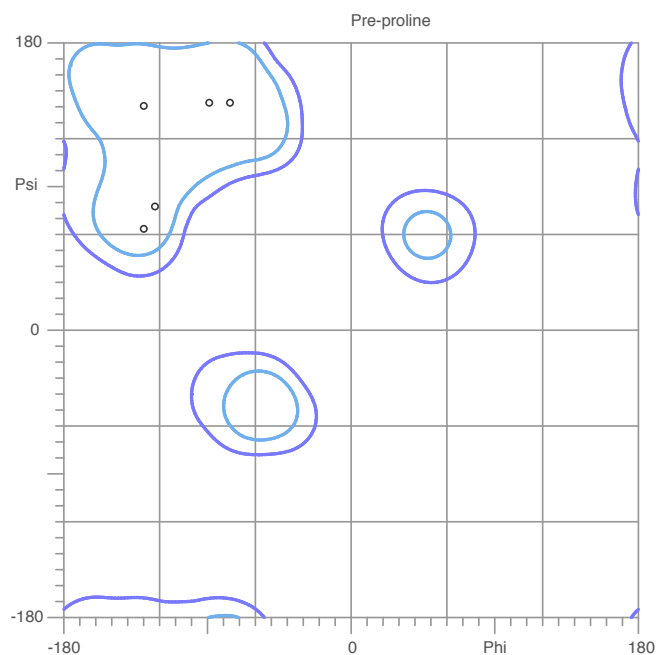
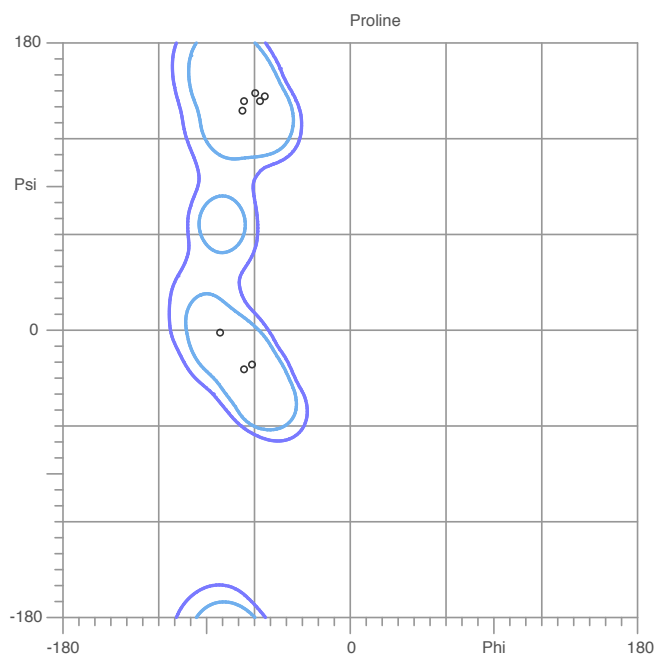
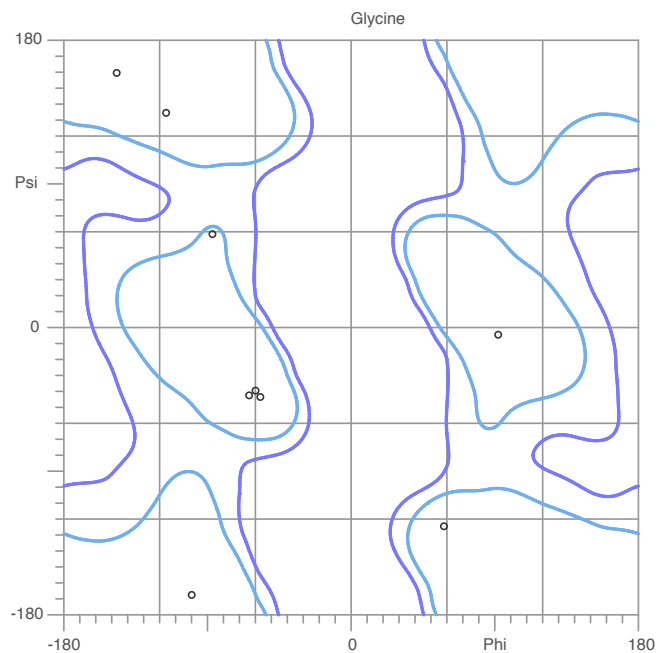
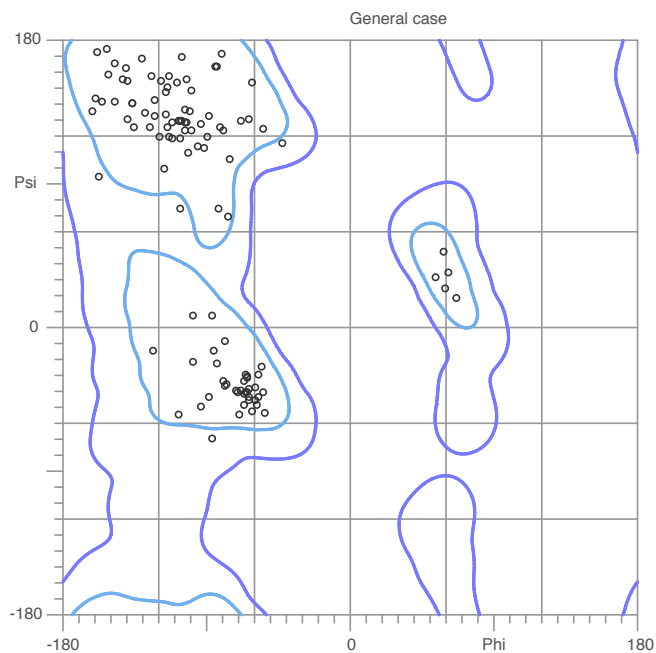
There were no outliers.

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

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MolProbity Ramachandran analysis

OR8C_R3Cons_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.

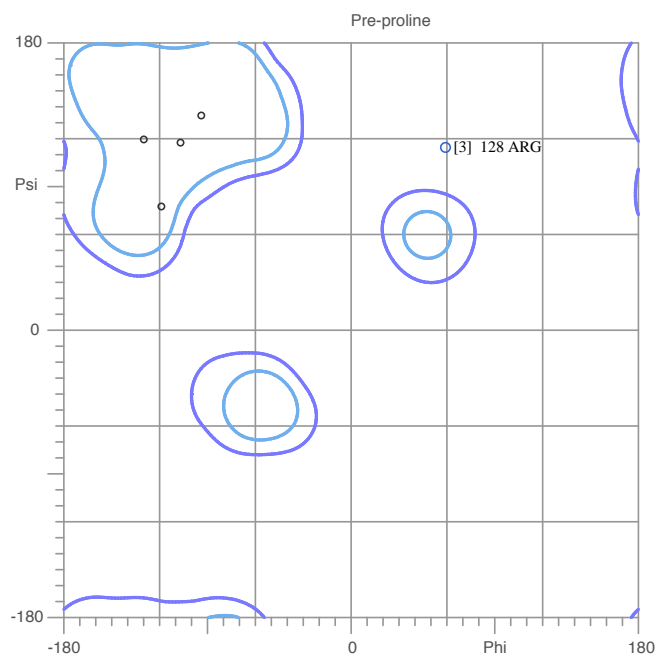
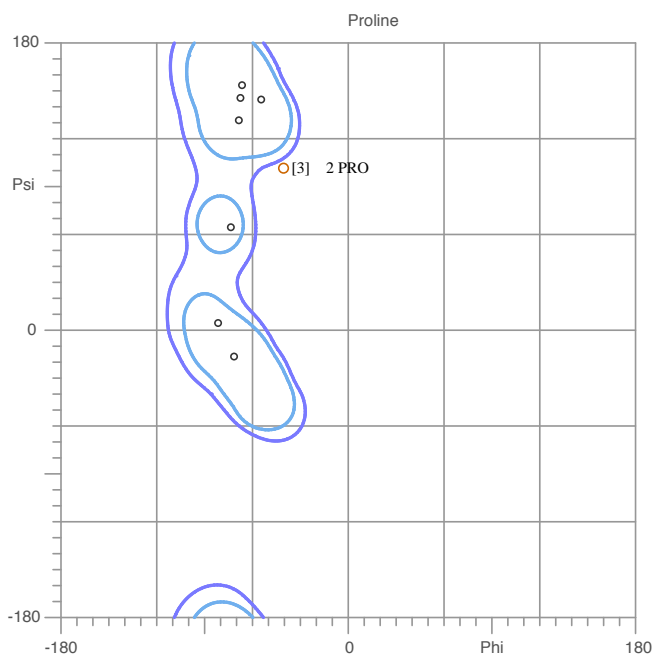
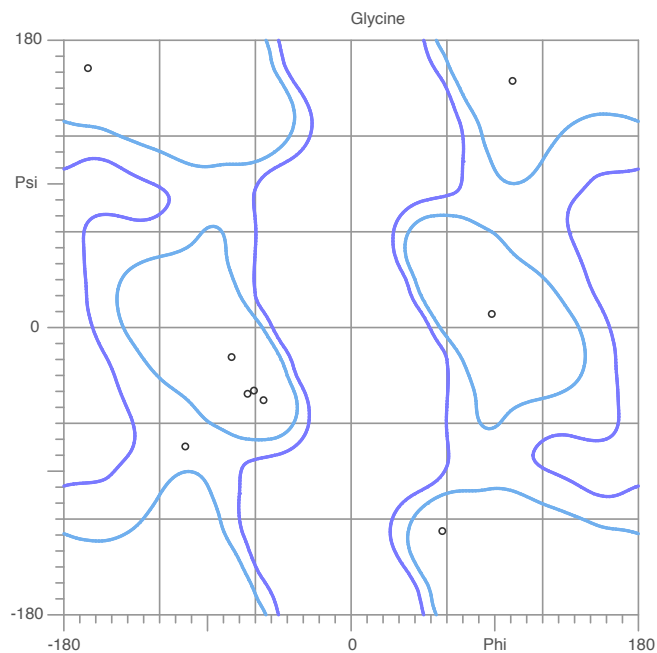
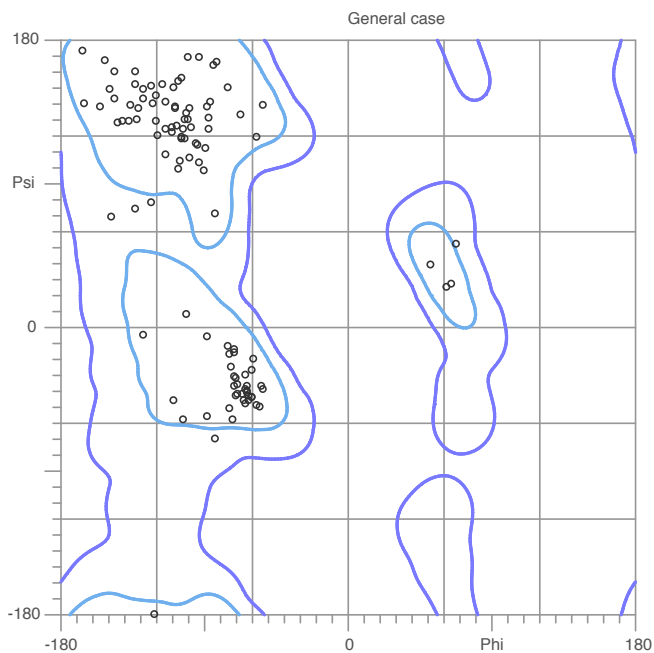
There were no outliers.

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

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MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 3



93.9% (124/132) of all residues were in favored (98%) regions.
98.5% (130/132) of all residues were in allowed (>99.8%) regions.

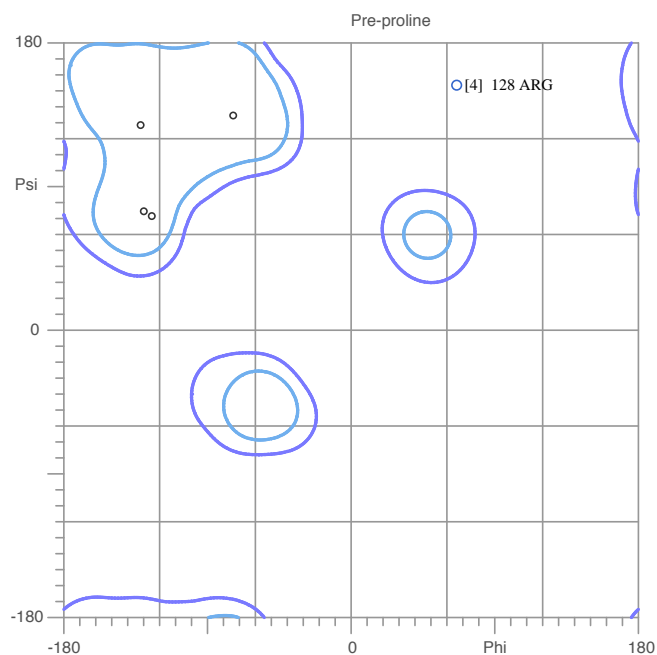
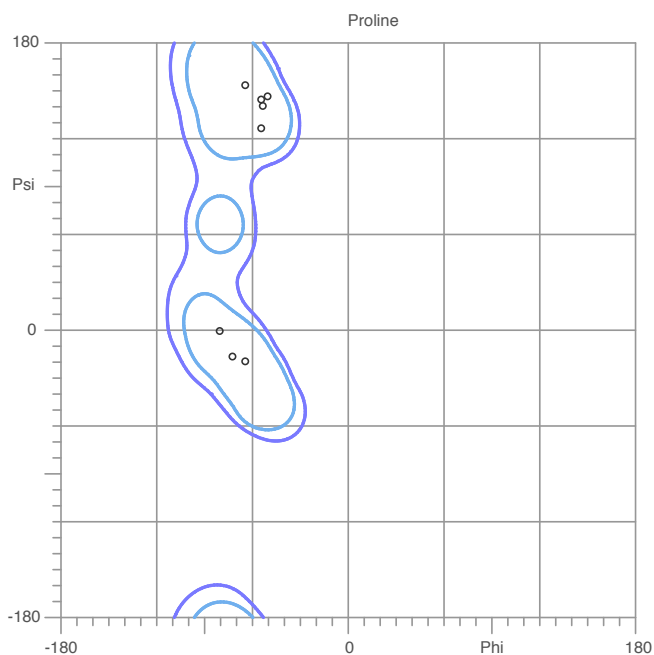
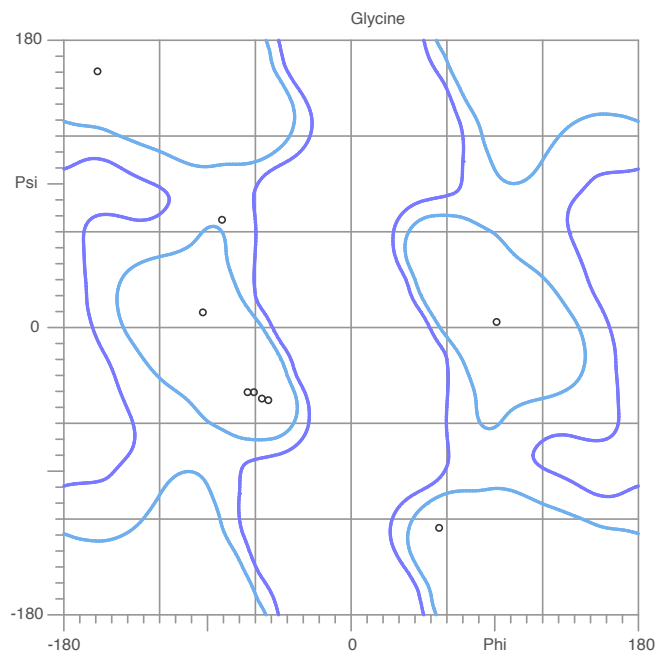
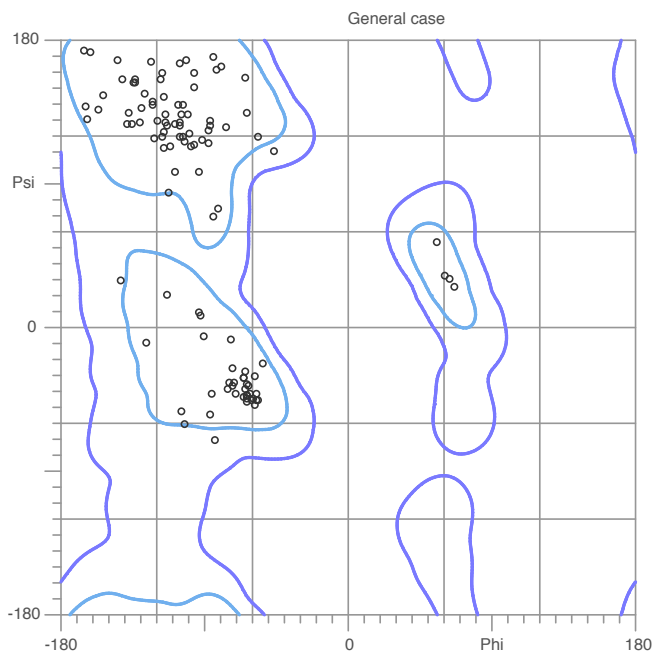
There were 2 outliers (phi, psi):

[3] 2 PRO (-42.0, 102.8)

[3] 128 ARG (59.2, 115.0)

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 4



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.

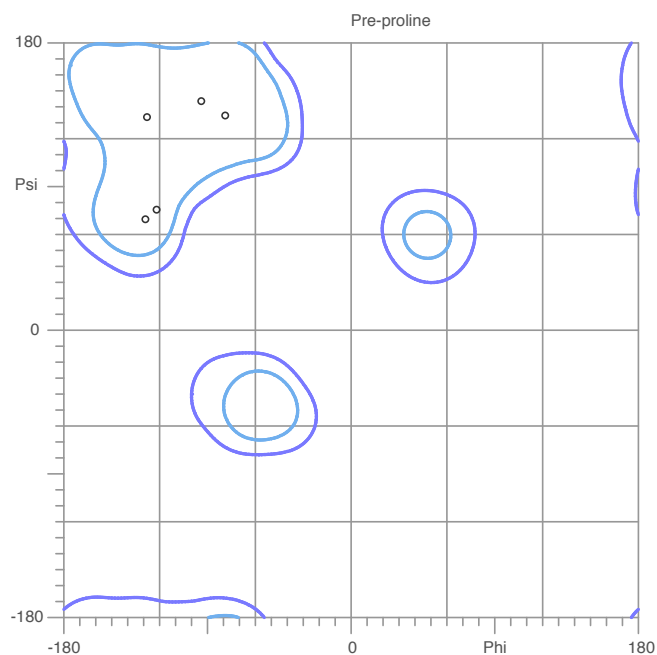
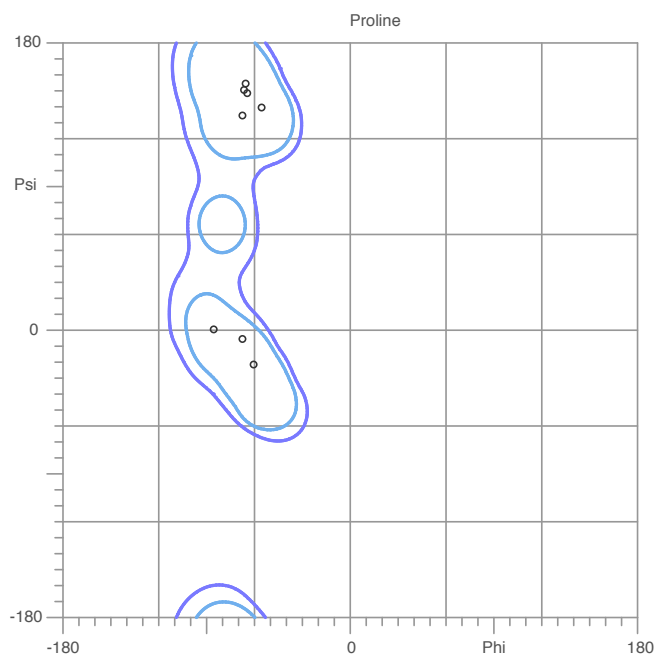
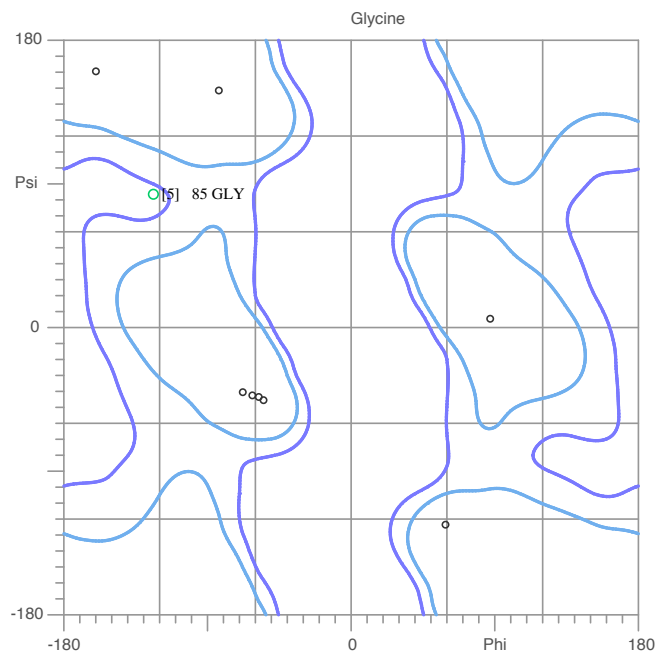
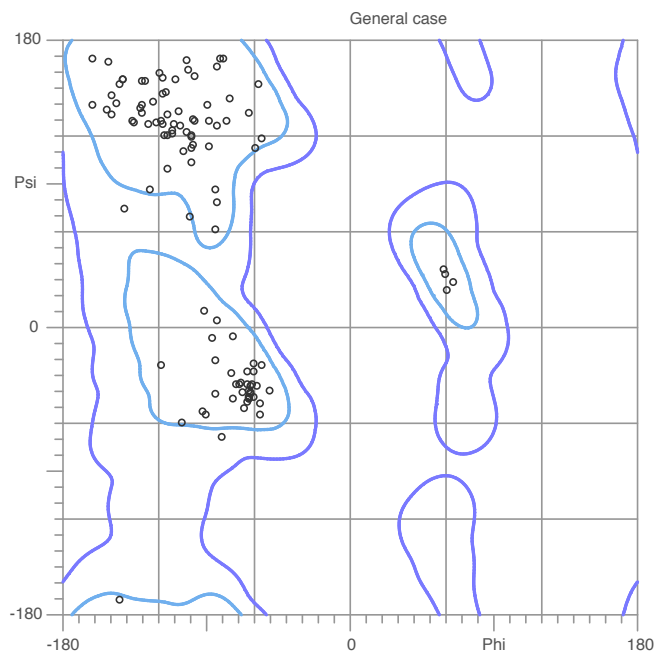
There were 1 outliers (phi, psi):
[4] 128 ARG (66.2, 155.0)

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MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 5

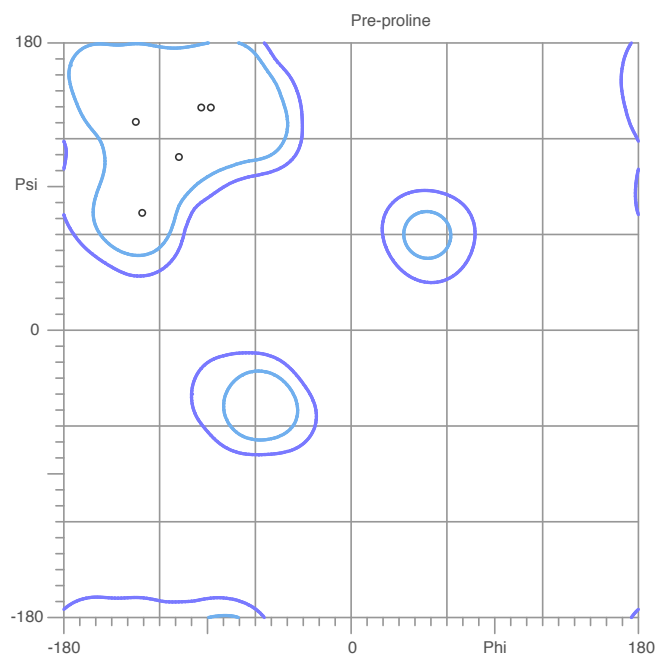
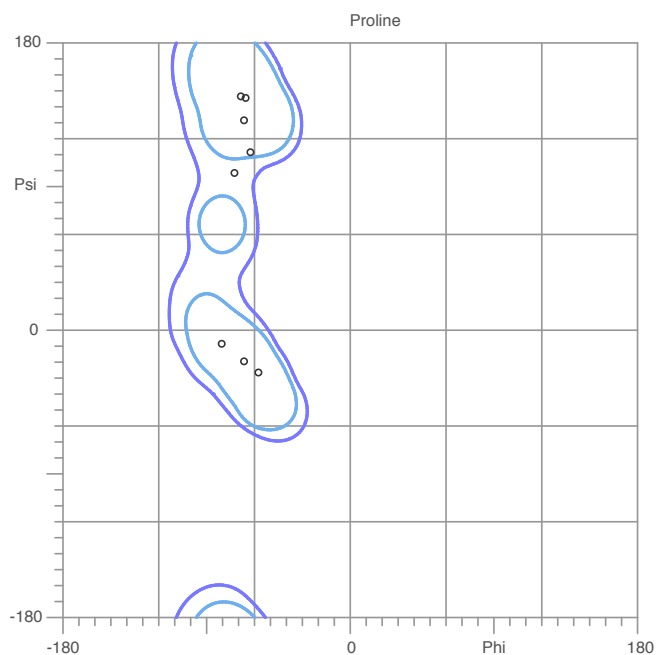
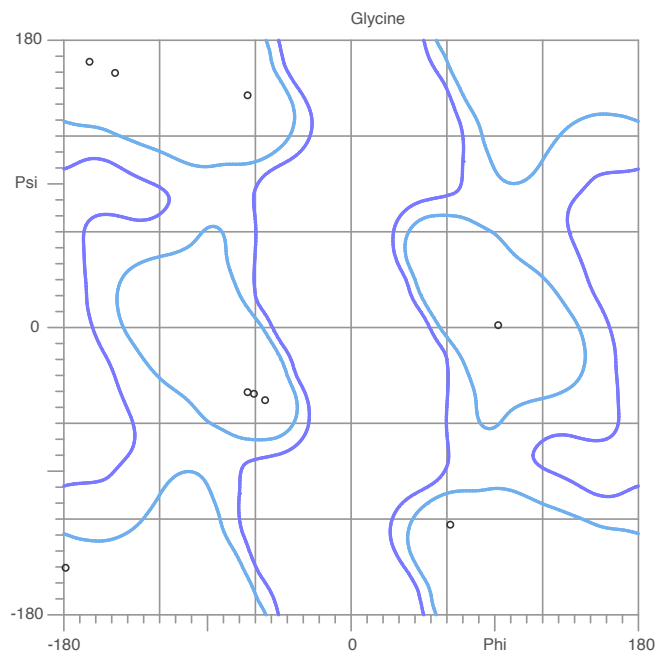
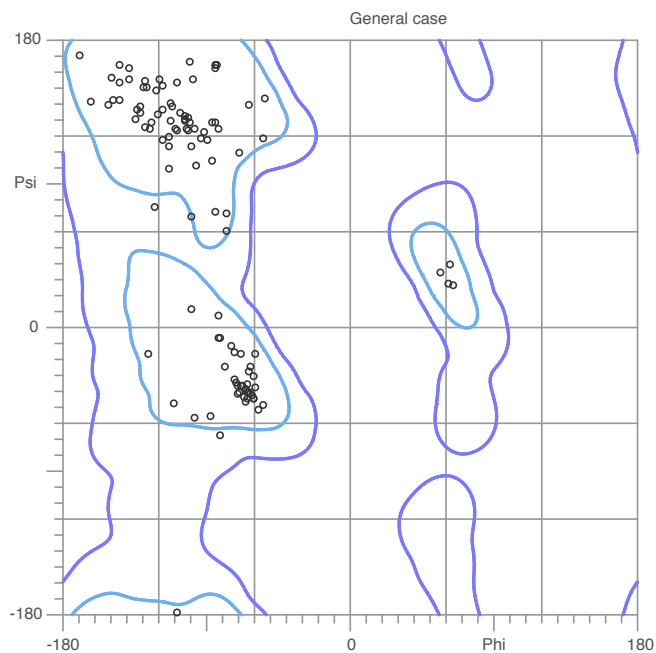


97.0% (128/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 85 GLY (-124.6, 85.0)

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 6



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.

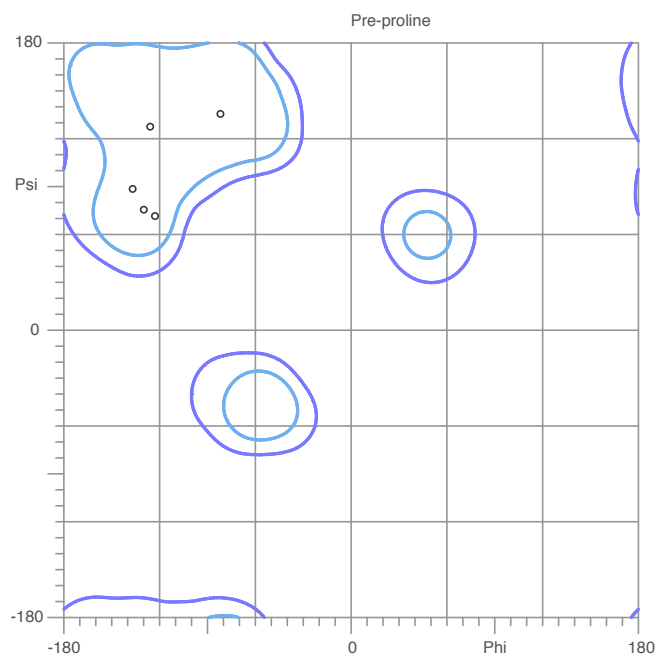
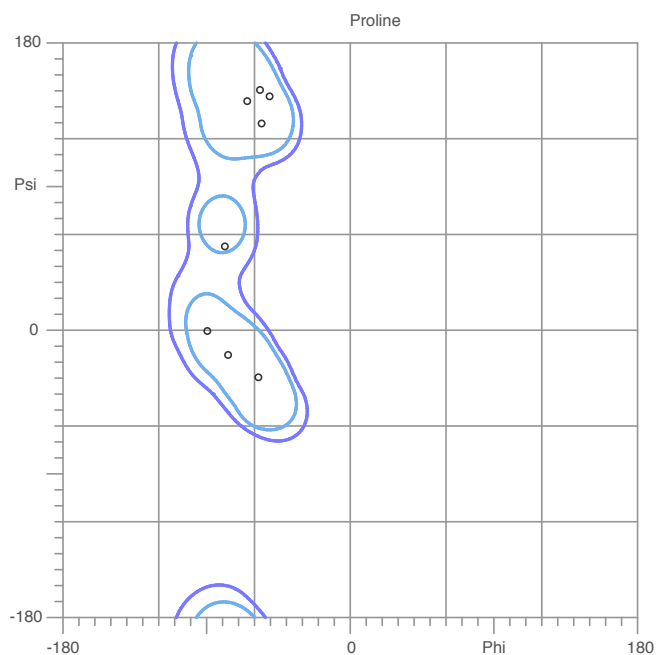
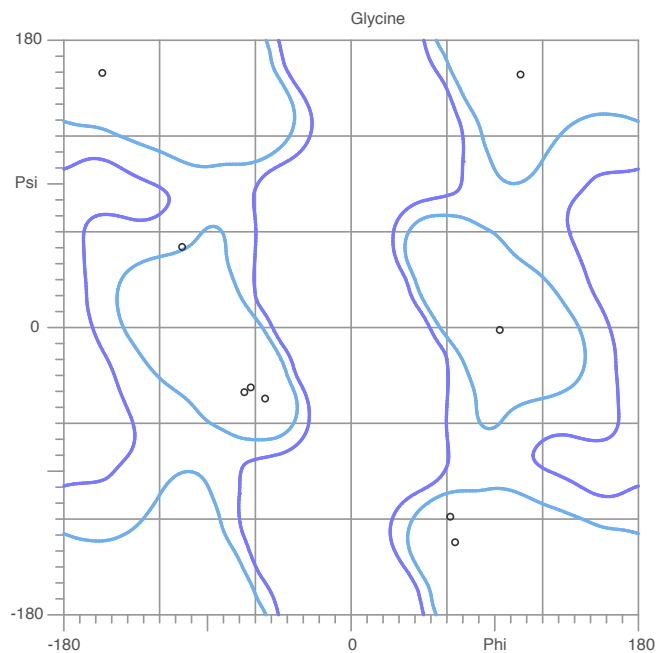
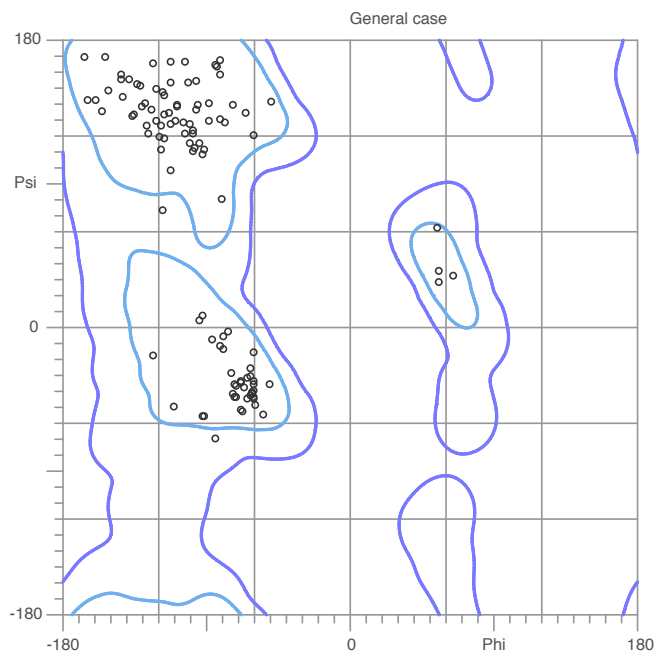
There were no outliers.

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MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 7

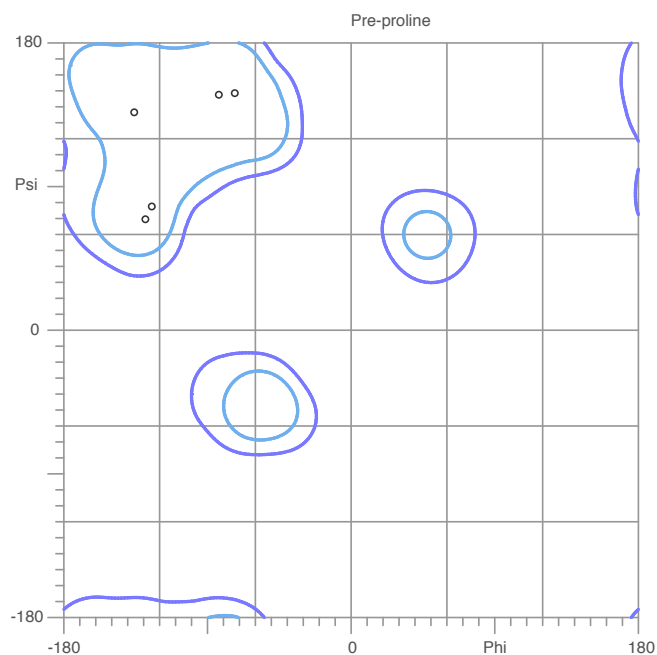
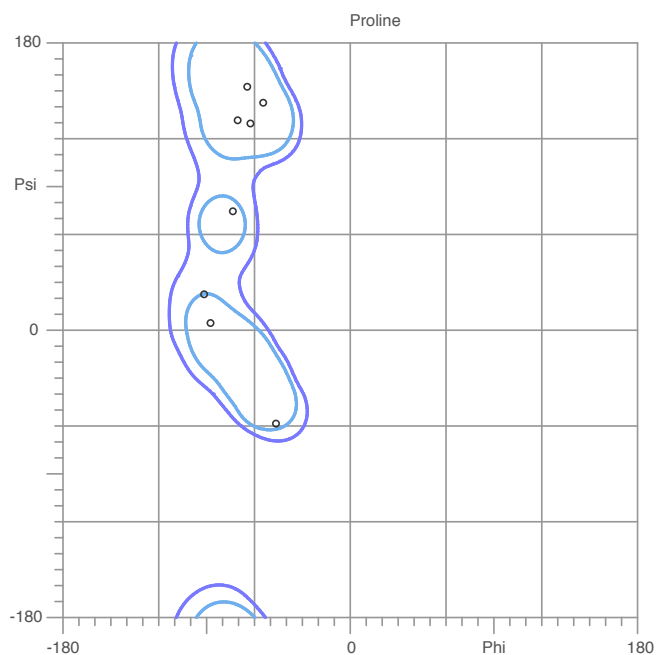
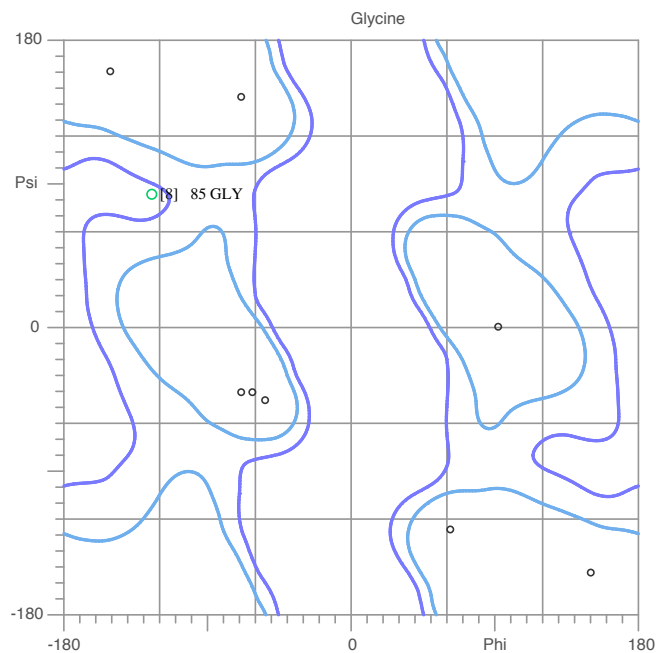
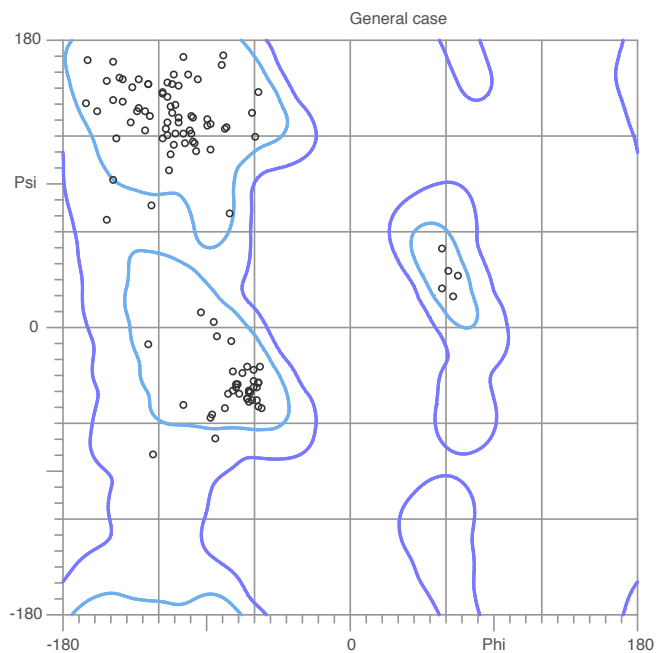


97.7% (129/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 8

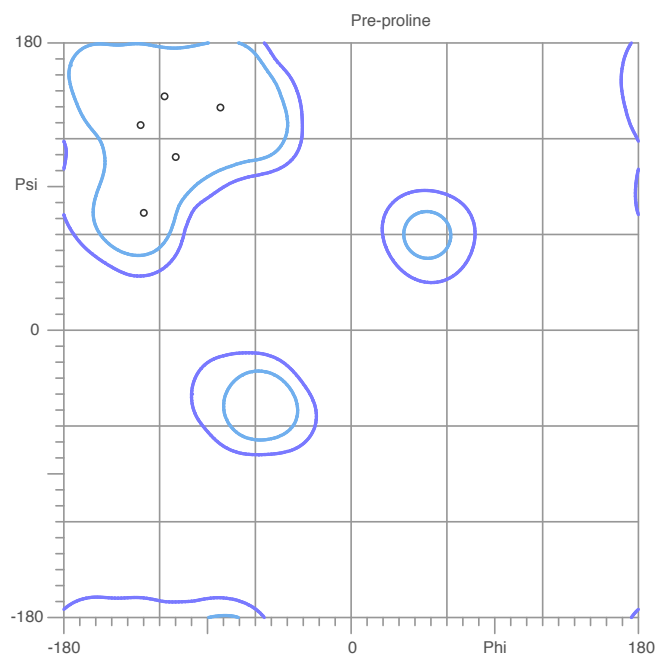
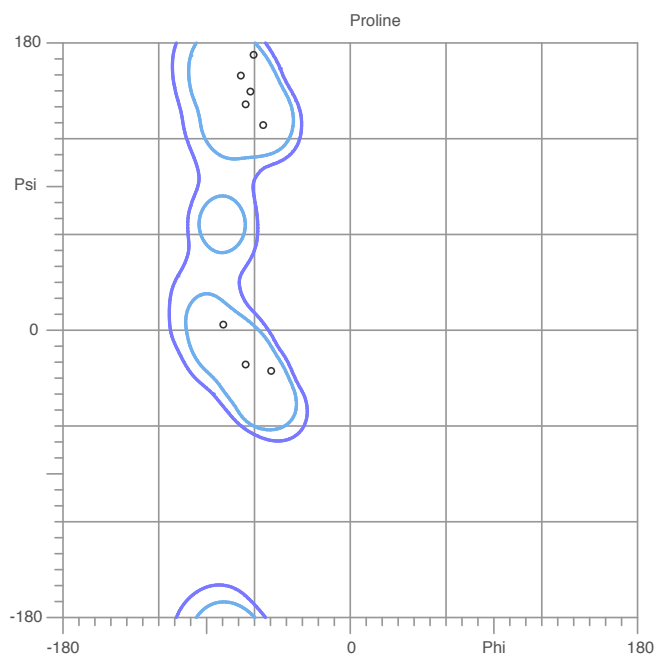
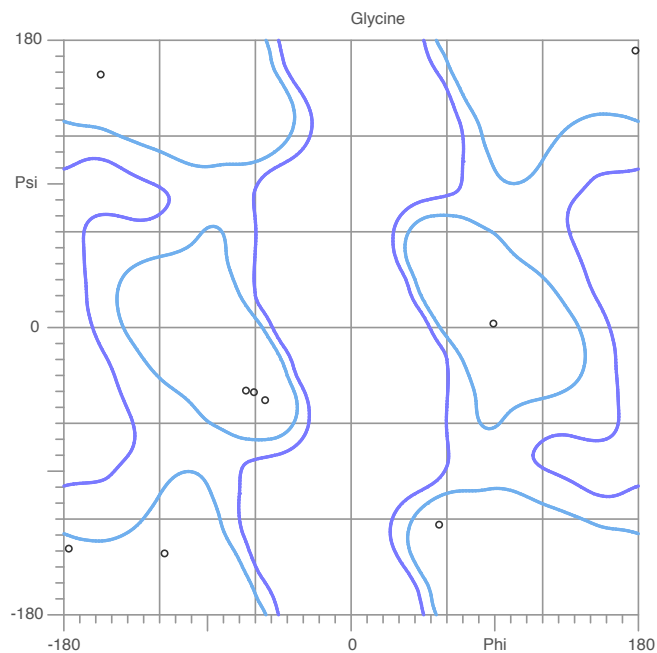
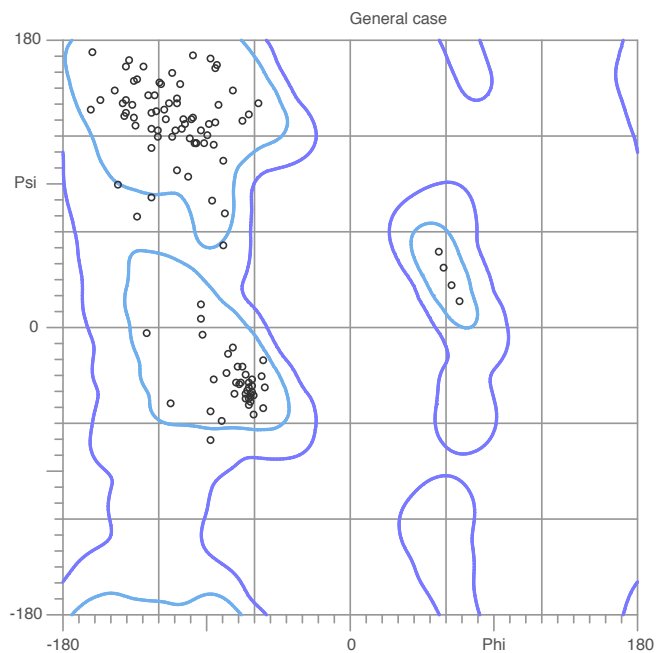


94.7% (125/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 85 GLY (-125.1, 85.0)

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 9



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.

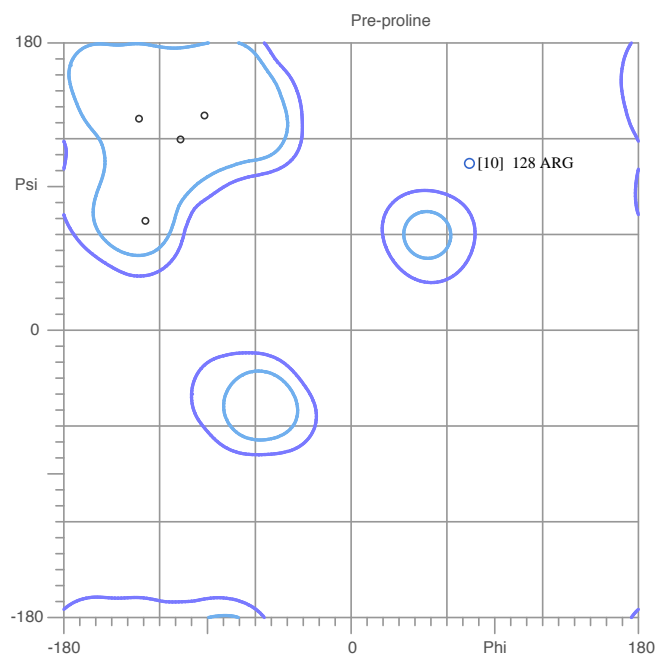
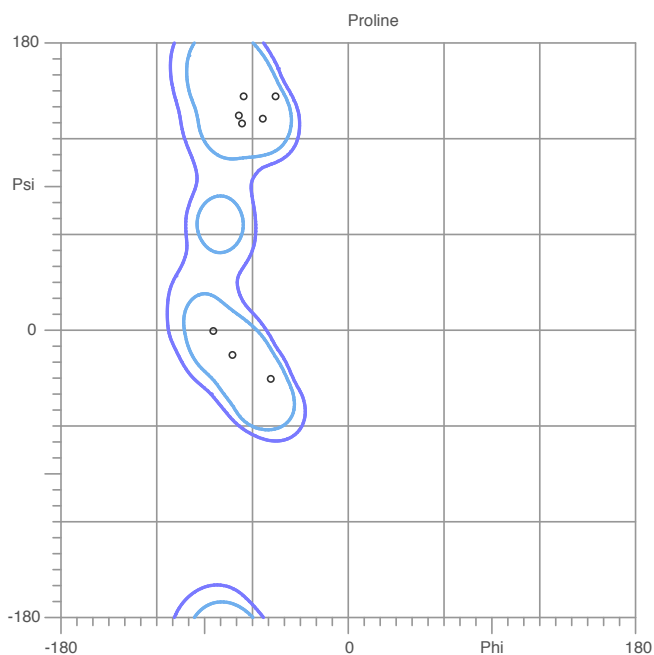
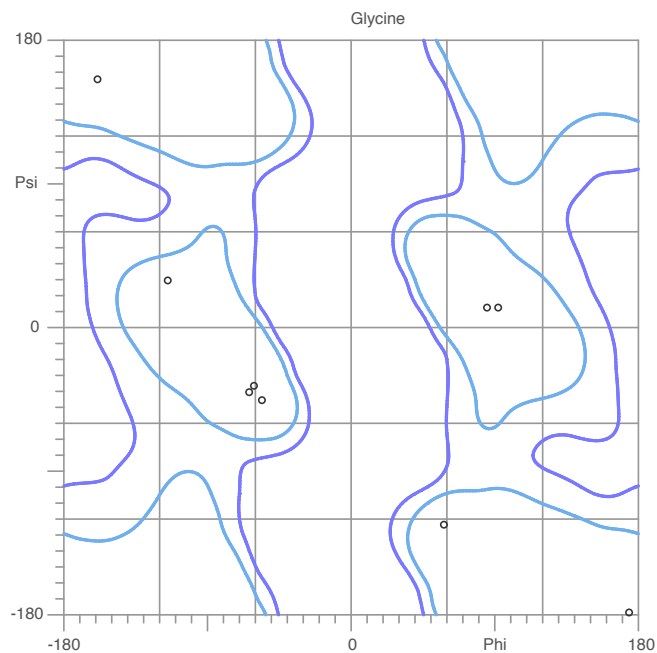
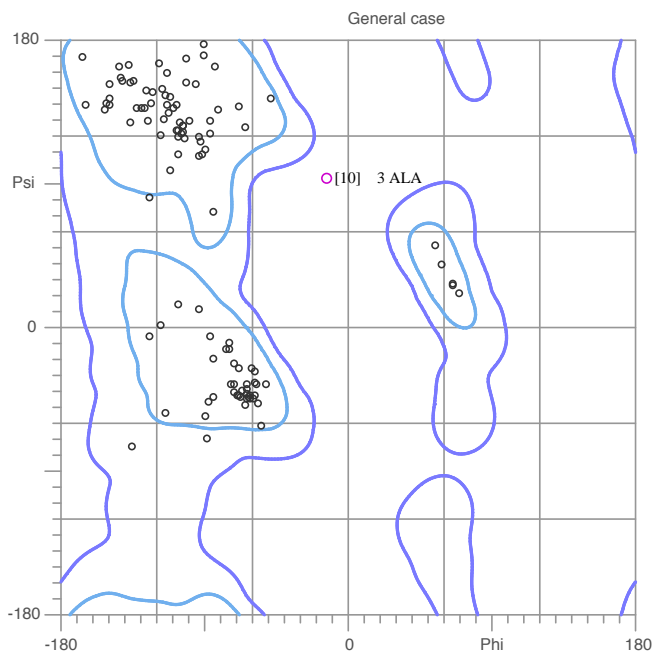
There were no outliers.

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MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 10

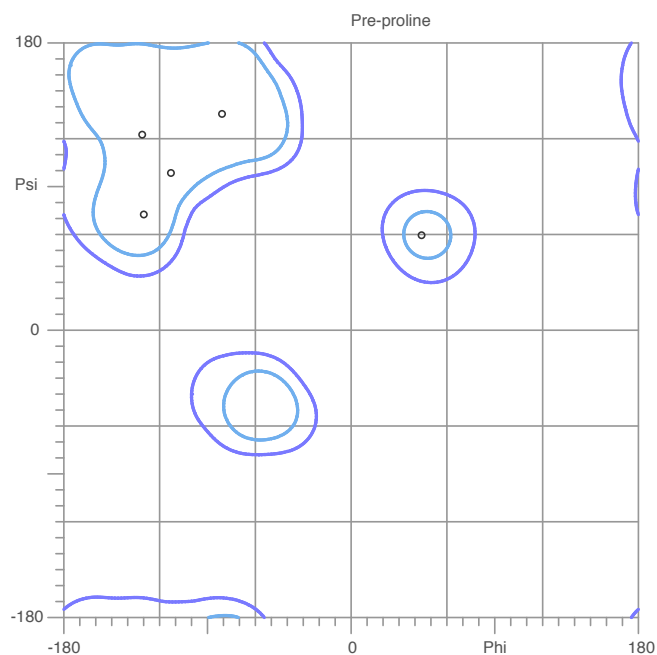
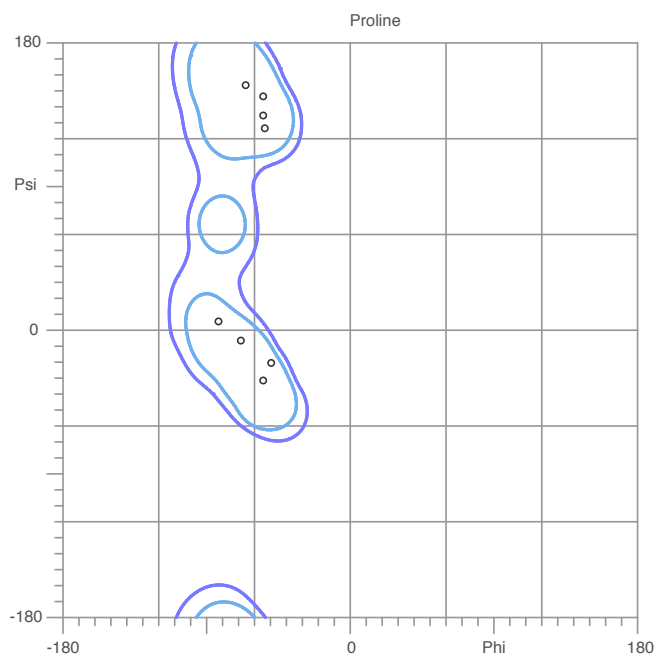
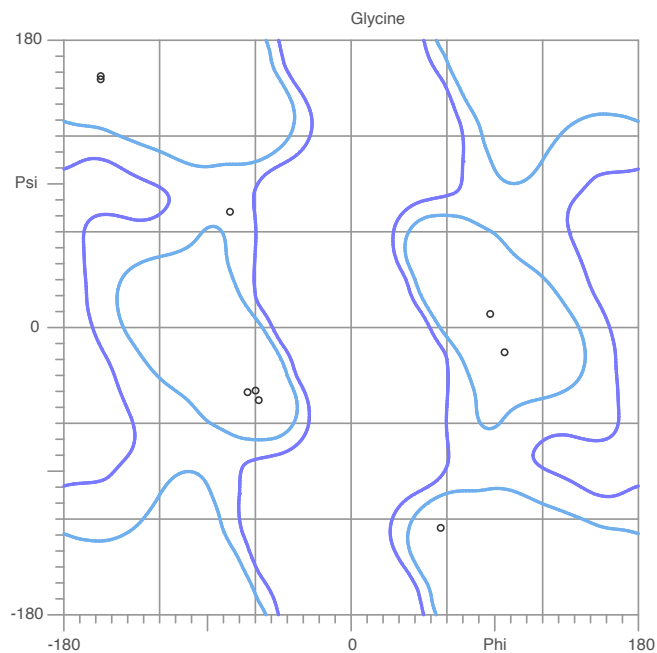
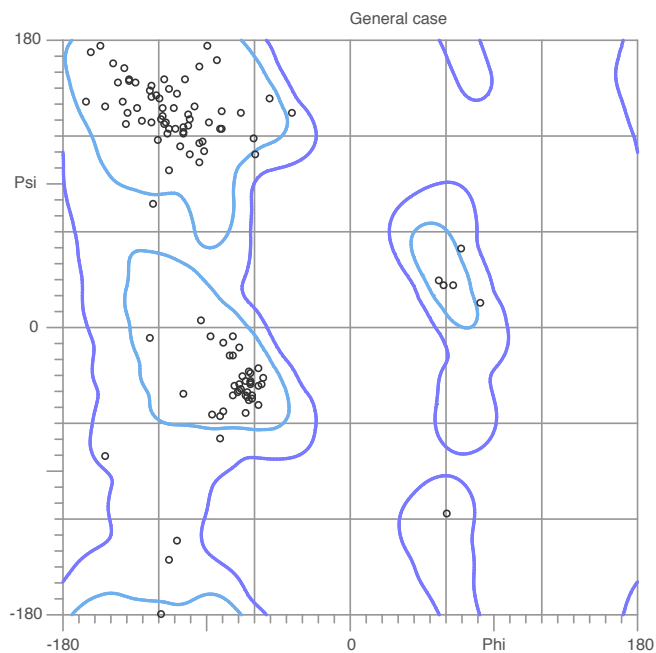


96.2% (127/132) of all residues were in favored (98%) regions.
98.5% (130/132) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[10] 3 ALA (-15.0, 94.8)
[10] 128 ARG (75.0, 105.0)

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 11

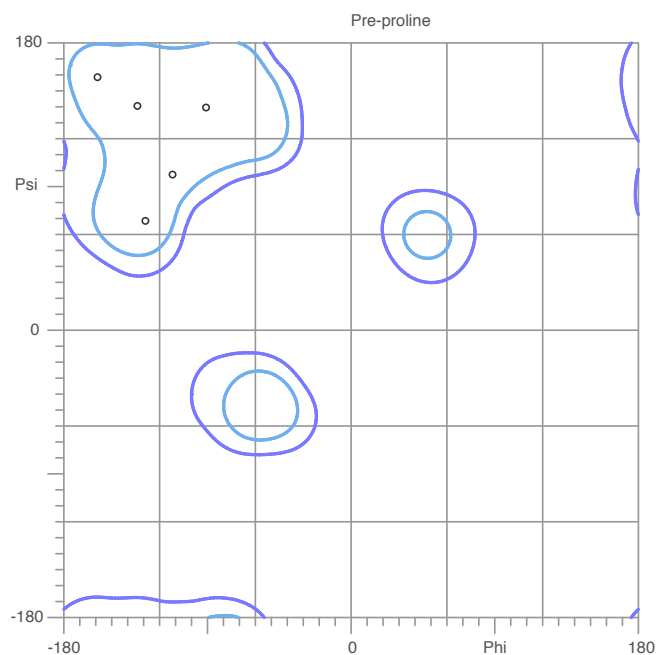
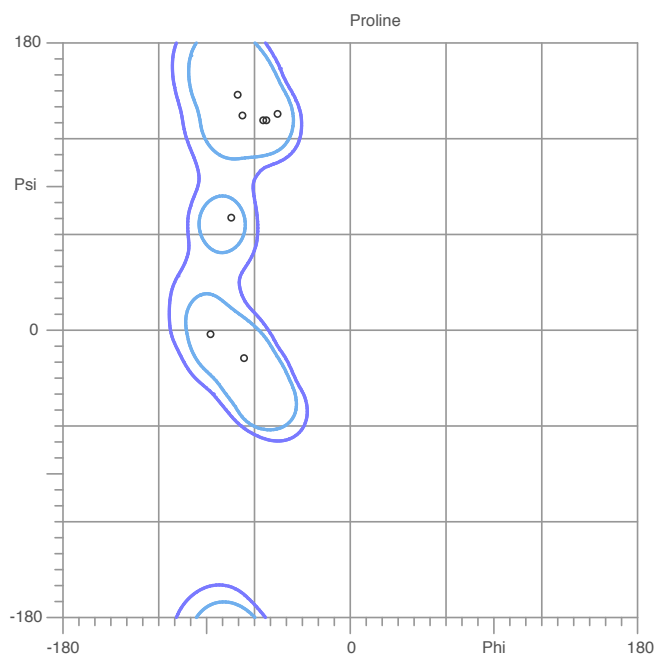
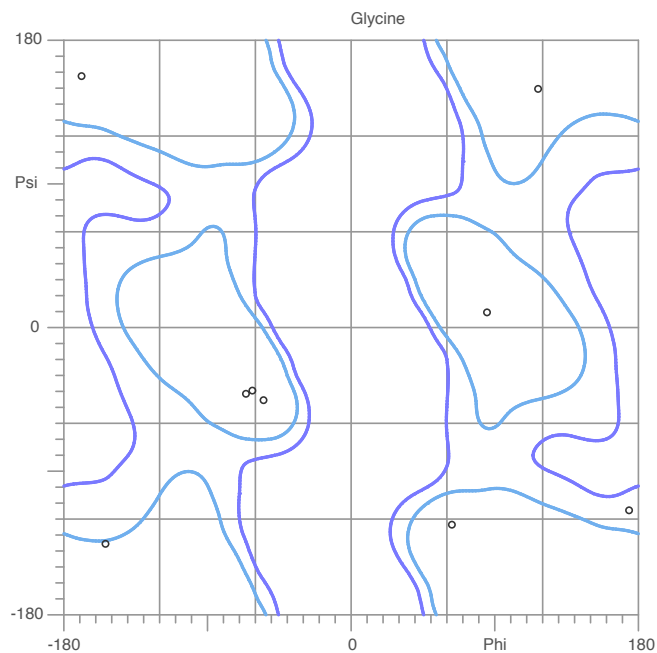
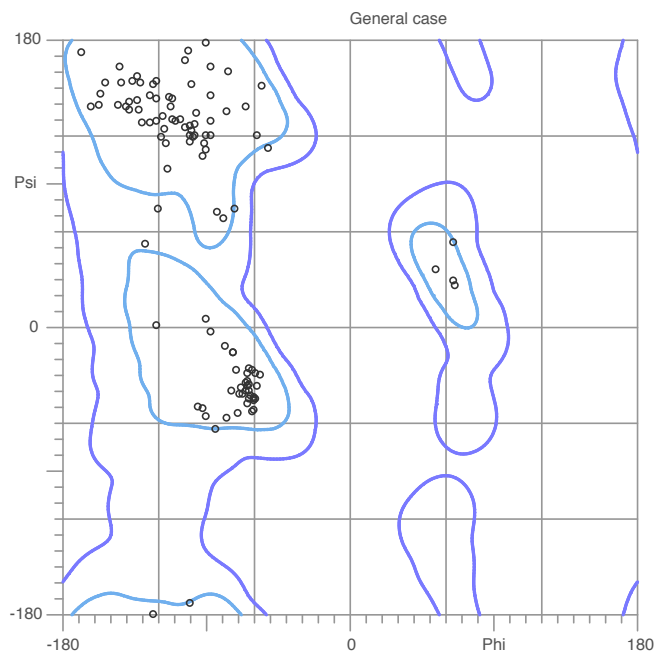


91.7% (121/132) of all residues were in favored (98%) regions.
100.0% (132/132) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 12



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.

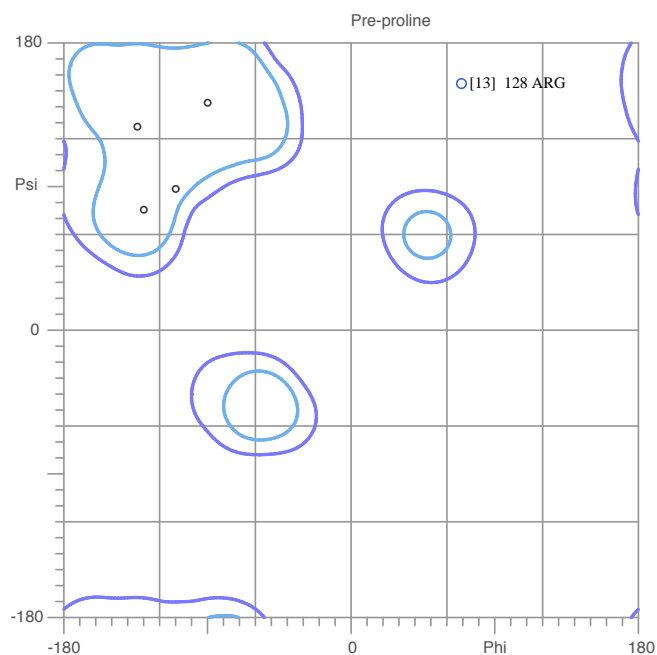
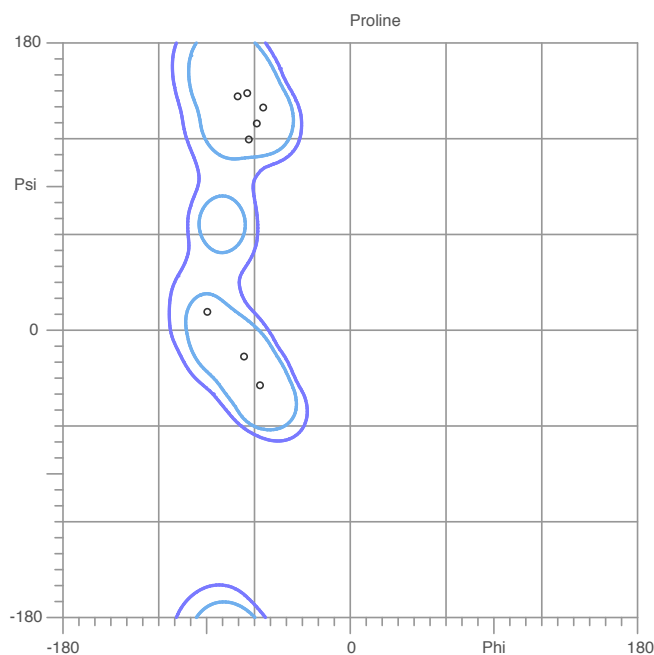
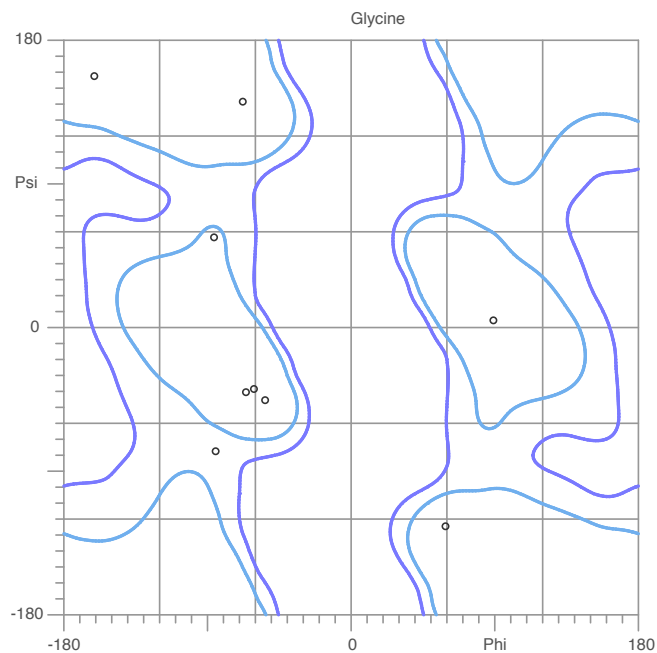
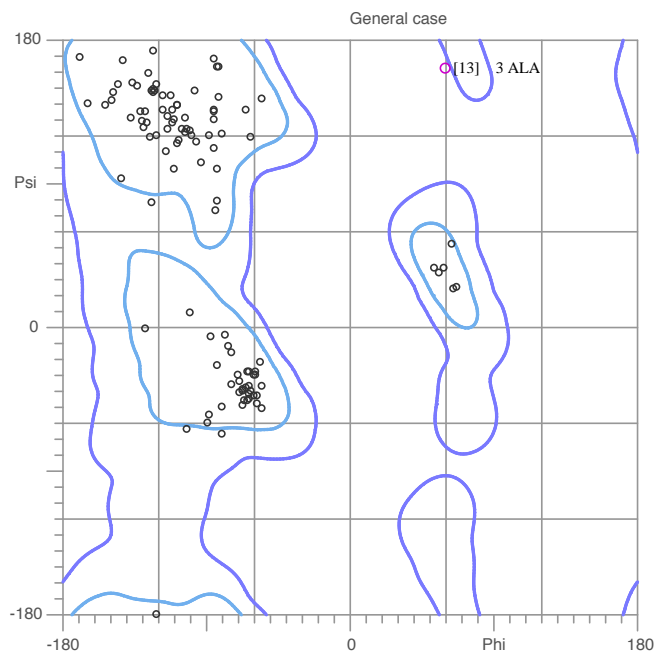
There were no outliers.

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MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 13

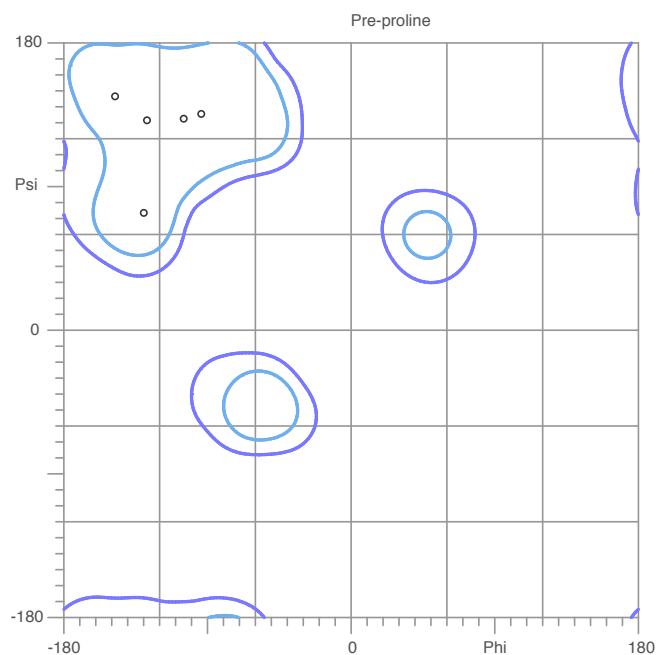
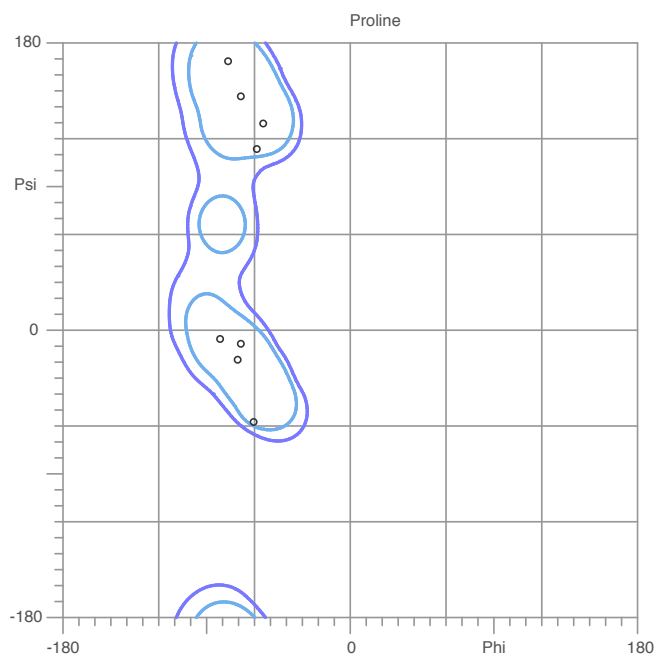
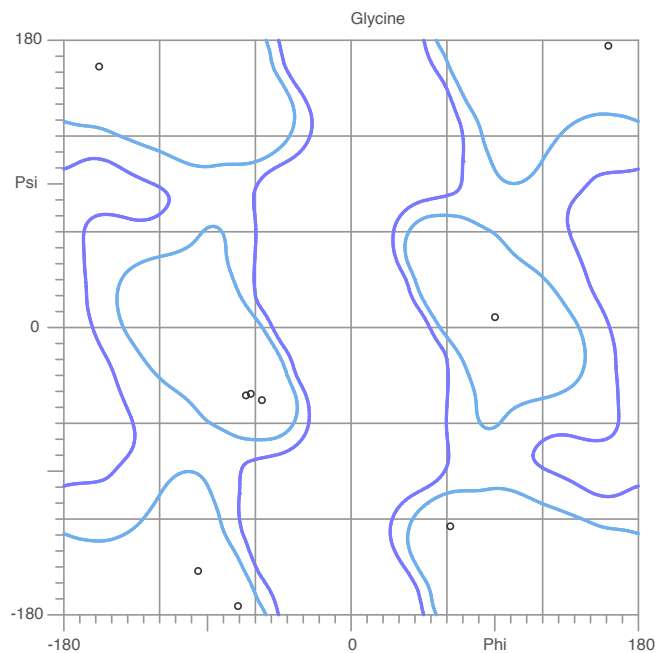
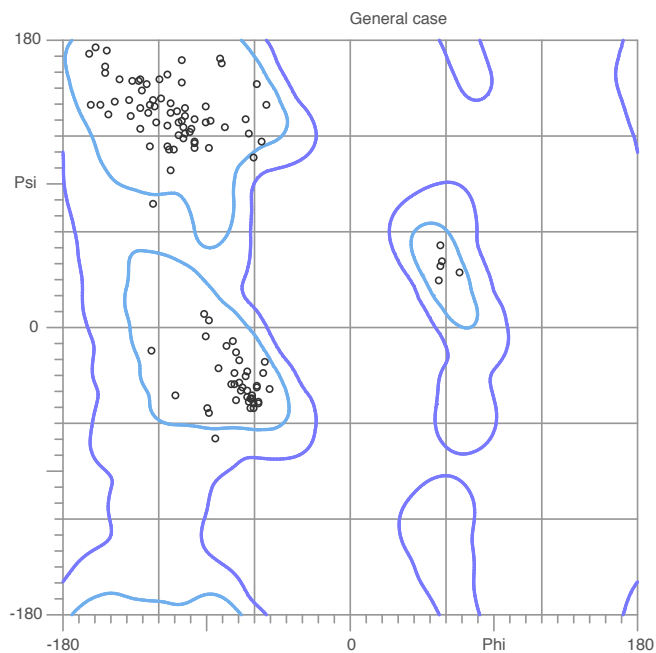


95.5% (126/132) of all residues were in favored (98%) regions.
98.5% (130/132) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[13] 3 ALA (60.0, 163.1)
[13] 128 ARG (69.3, 155.0)

MolProbity Ramachandran analysis

OR8C_R3Cons_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.

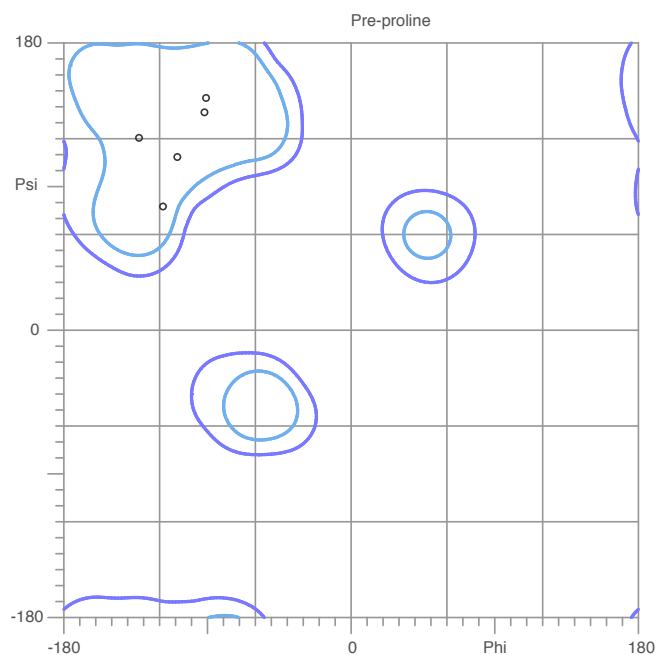
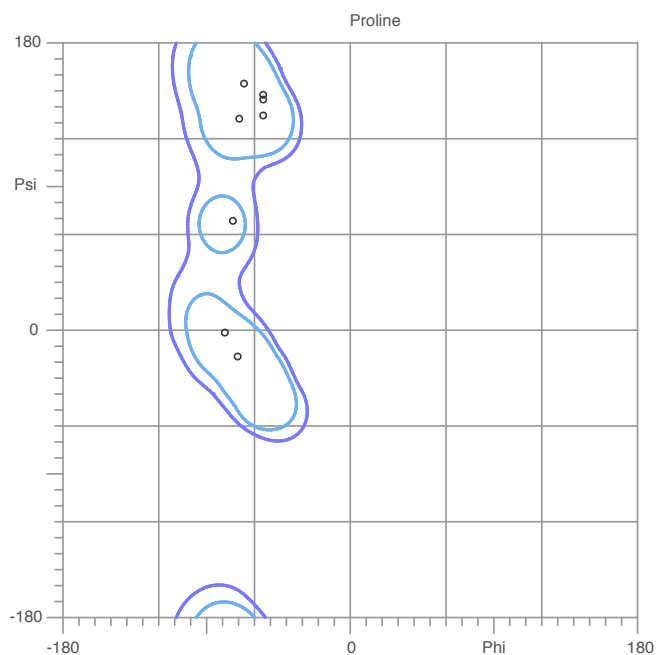
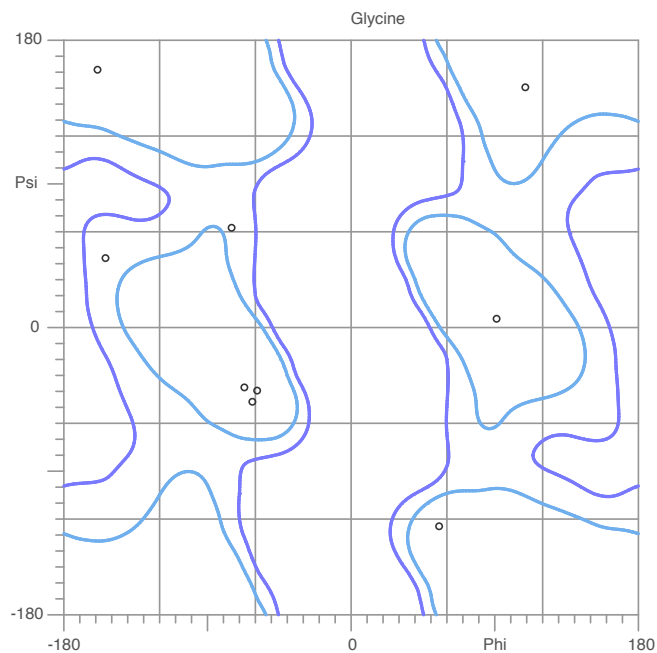
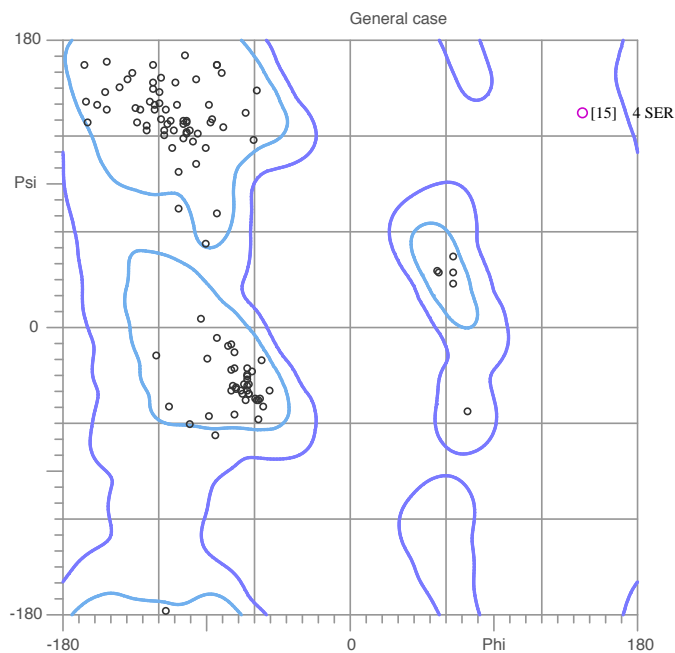
There were no outliers.

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

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MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 15



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.

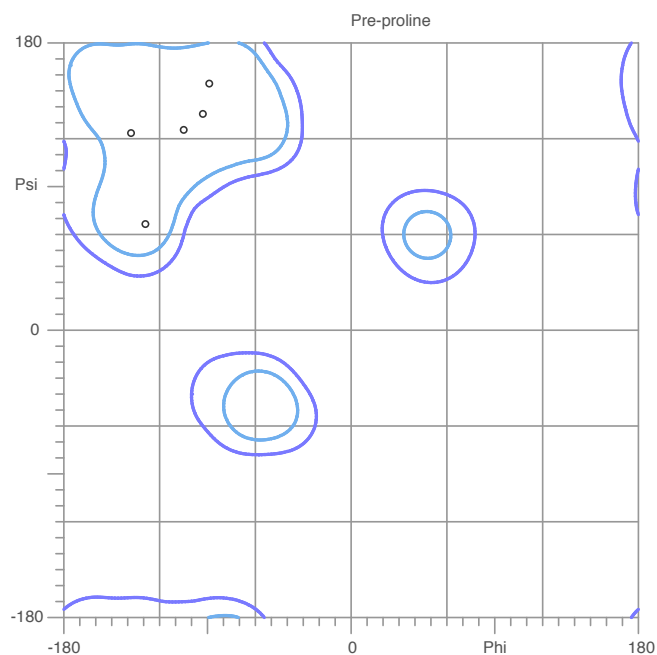
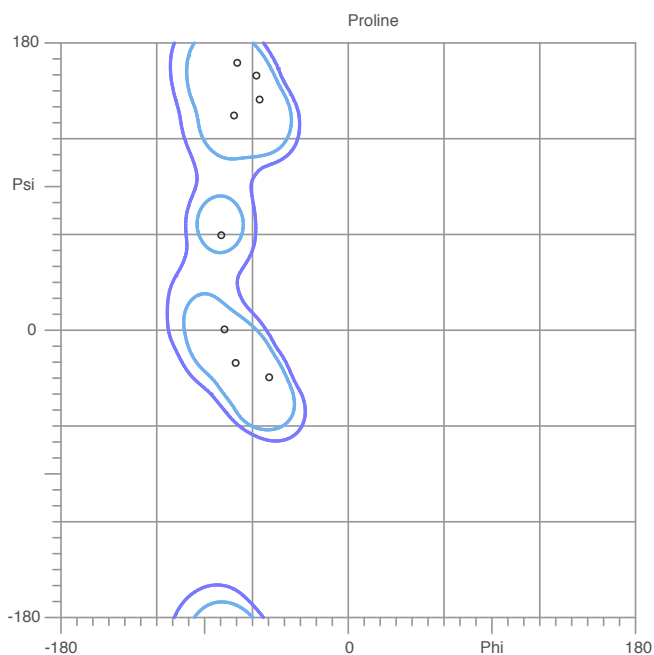
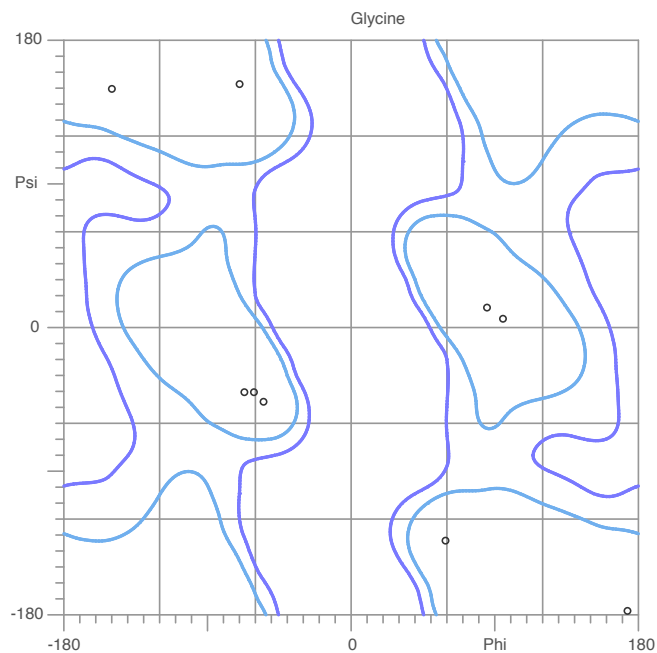
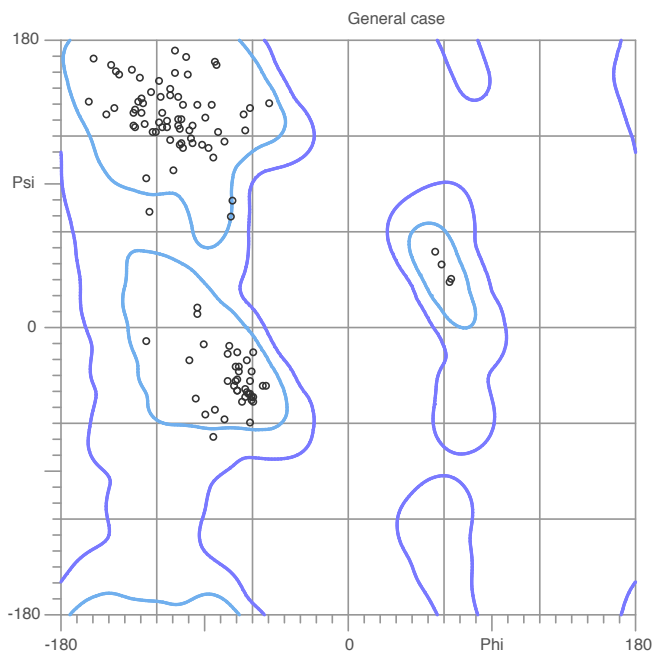
There were 1 outliers (phi, psi):
[15] 4SER (145.1, 135.0)

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MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 16



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.

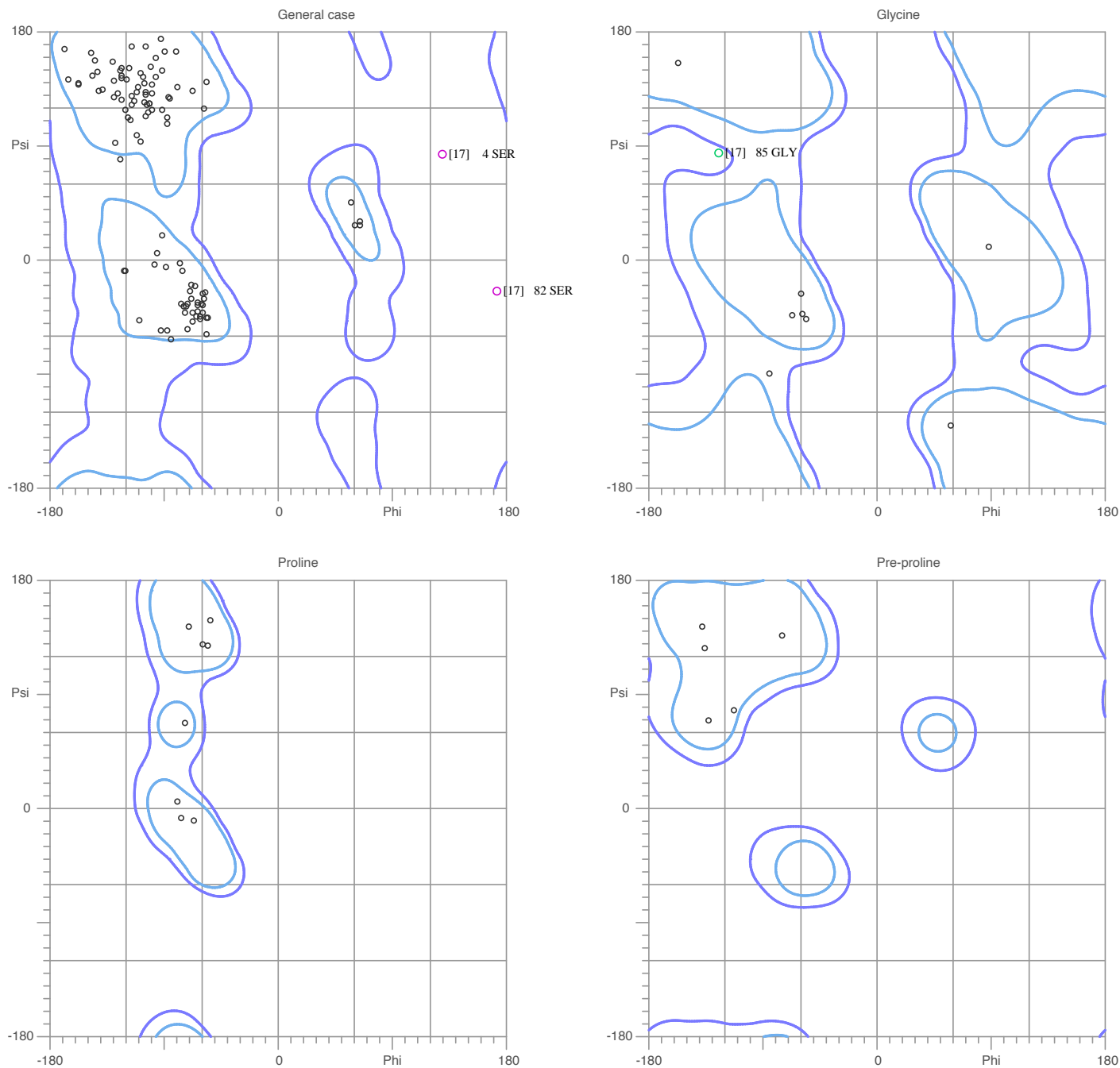
There were no outliers.

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

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

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 17



96.2% (127/132) of all residues were in favored (98%) regions.
97.7% (129/132) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

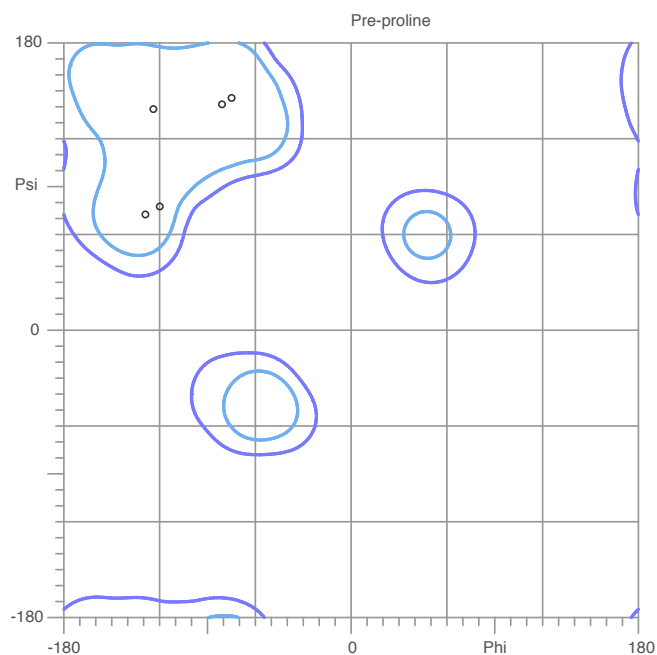
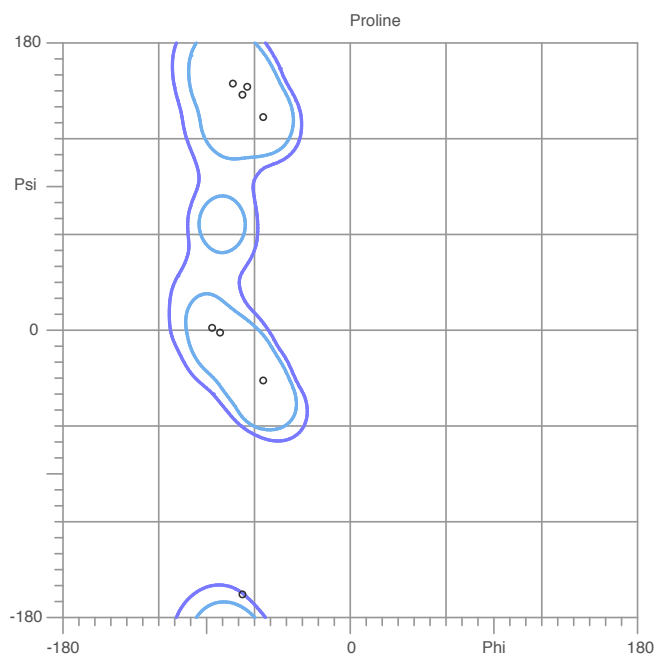
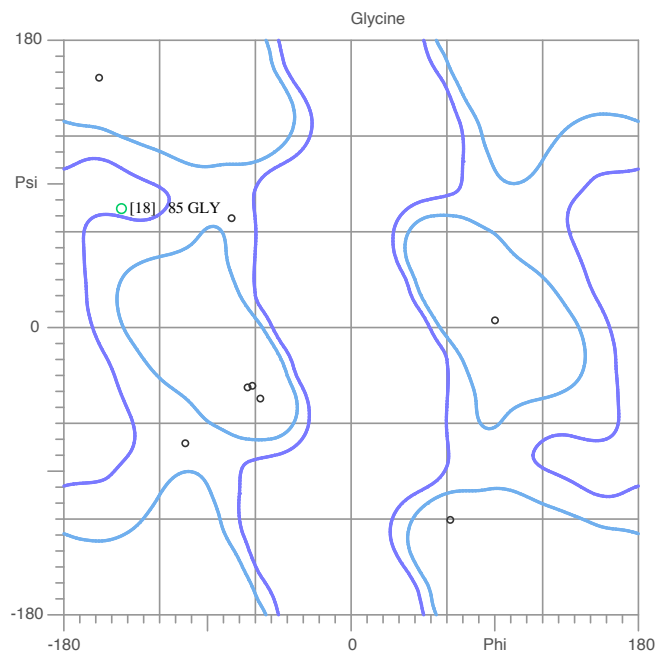
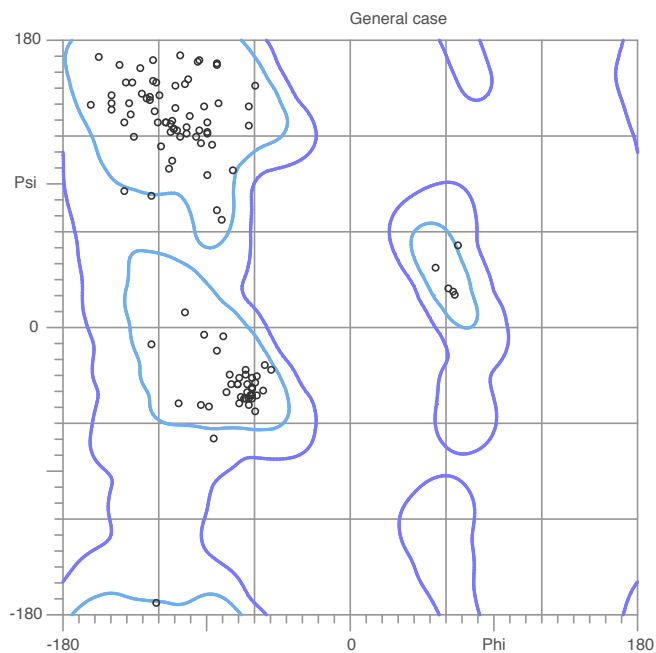
[17] 4 SER (129.0, 84.9)

[17] 82 SER (172.1, -24.8)

[17] 85 GLY (-125.0, 85.1)

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 18

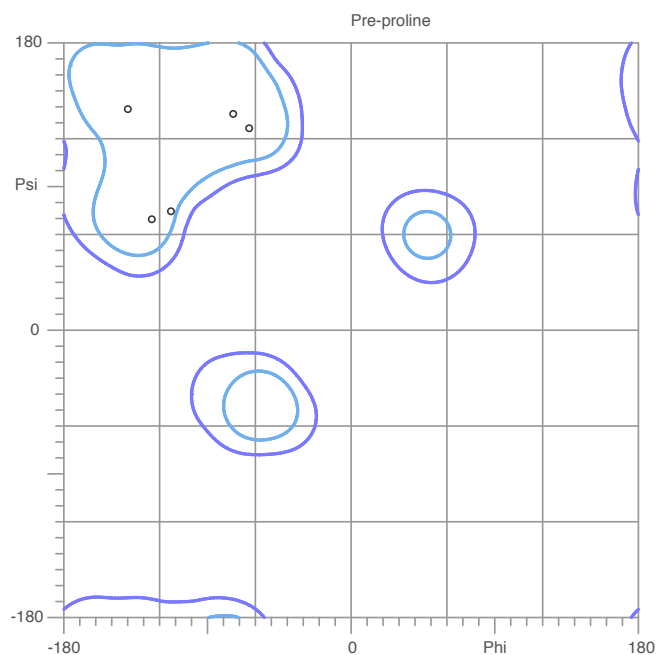
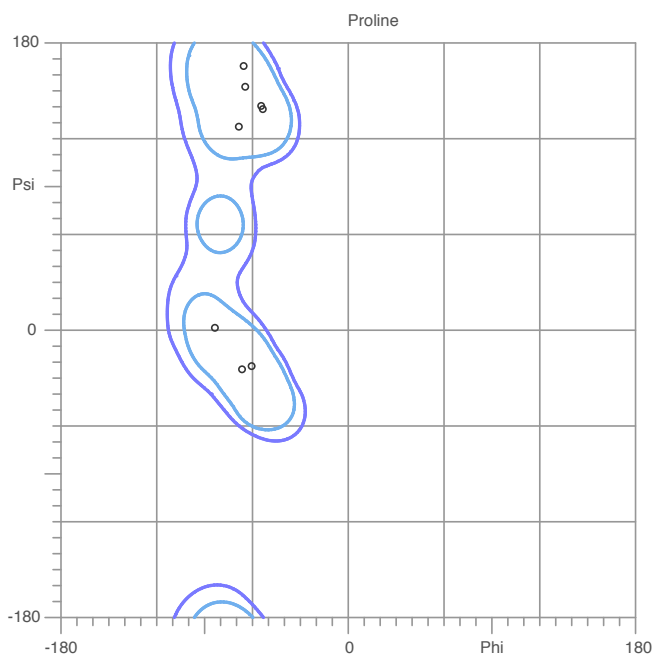
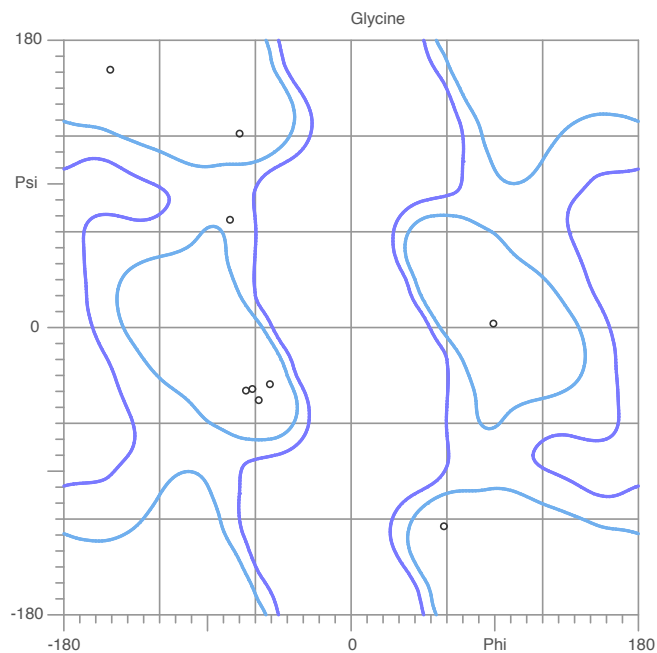
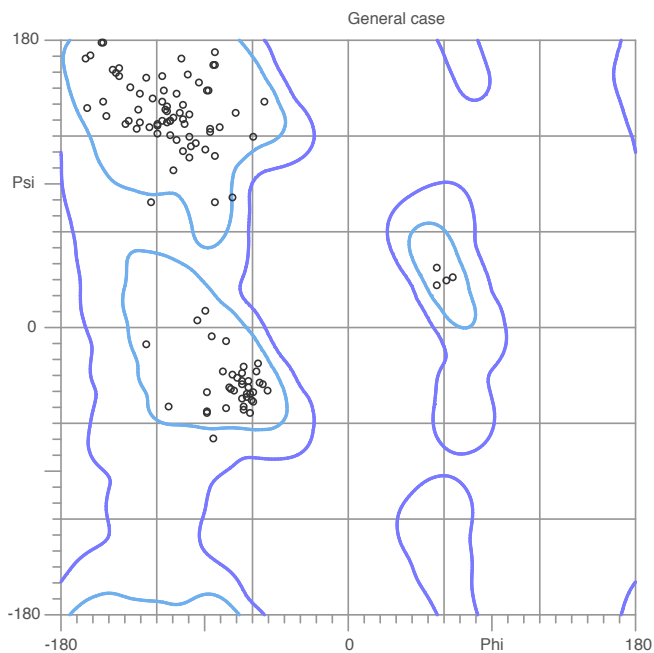


93.9% (124/132) of all residues were in favored (98%) regions.
99.2% (131/132) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[18] 85 GLY (-144.6, 75.0)

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 19



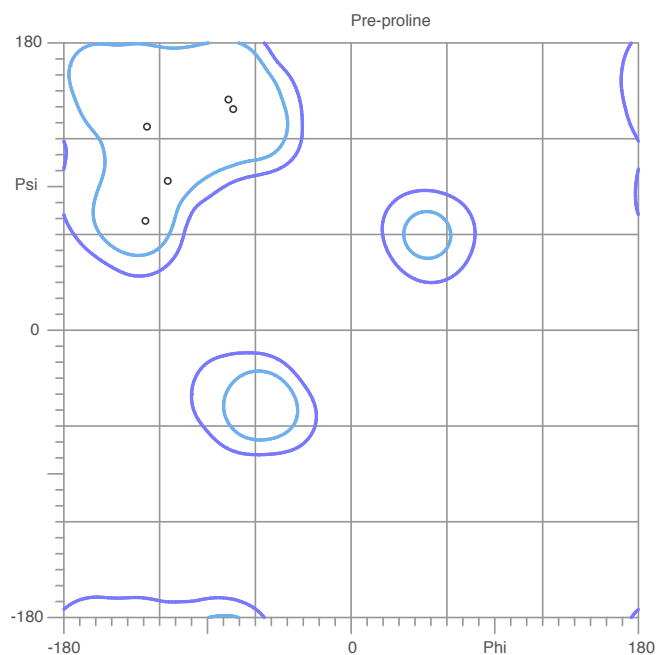
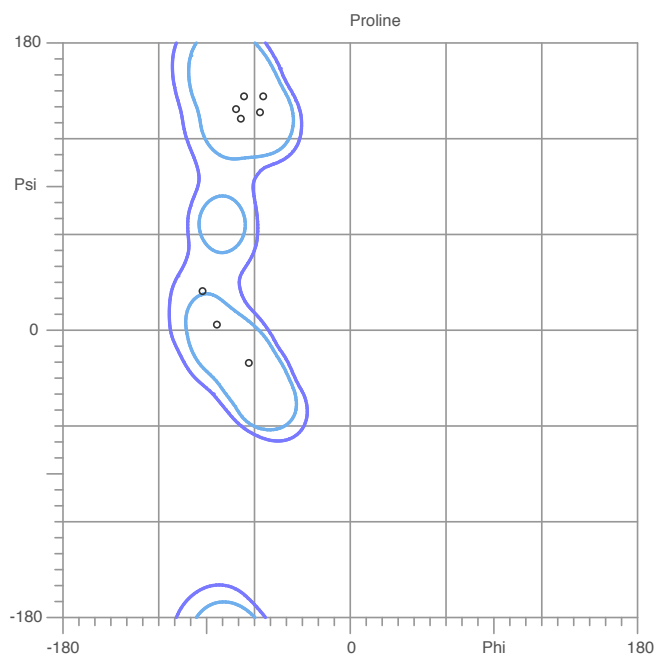
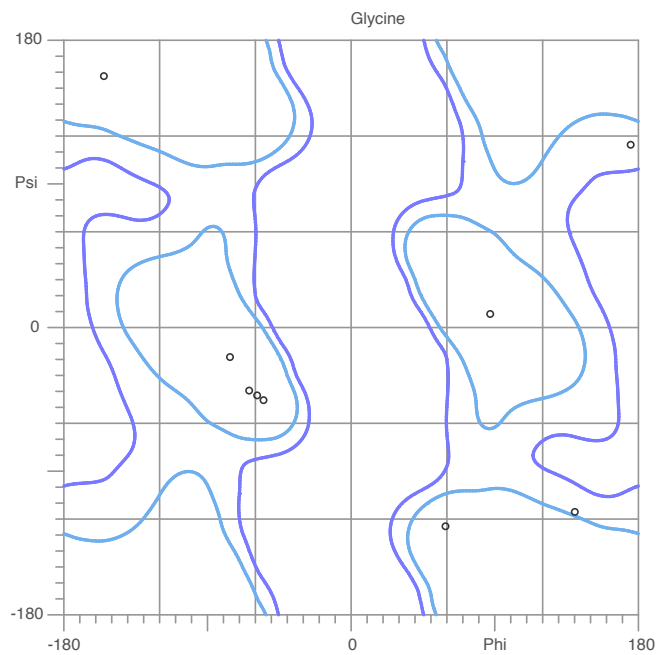
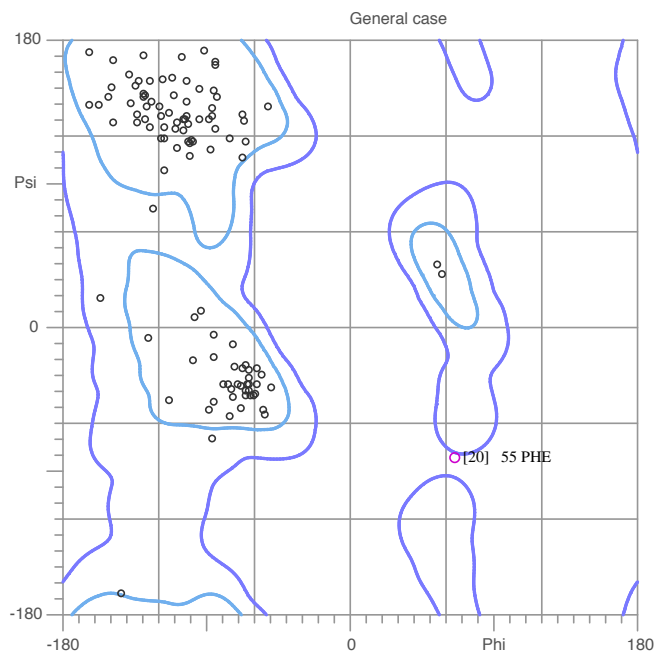
97.7% (129/132) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

OR8C_R3Cons_em_bcr3.pdb, model 20



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):
[20] 55 PHE (65.5, -81.5)