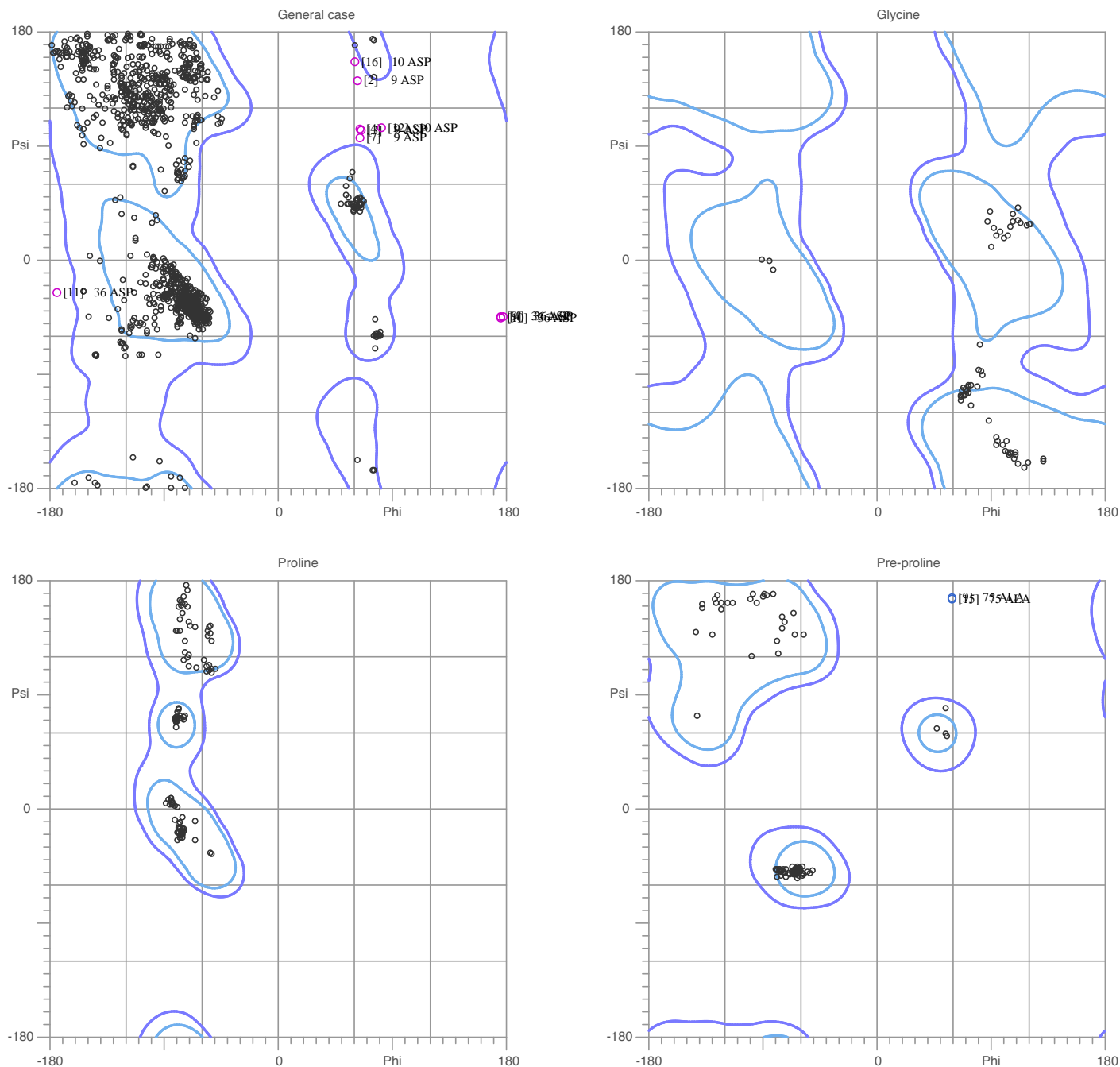


MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, all models



93.8% (1425/1520) of all residues were in favored (98%) regions.
 99.2% (1508/1520) of all residues were in allowed (>99.8%) regions.

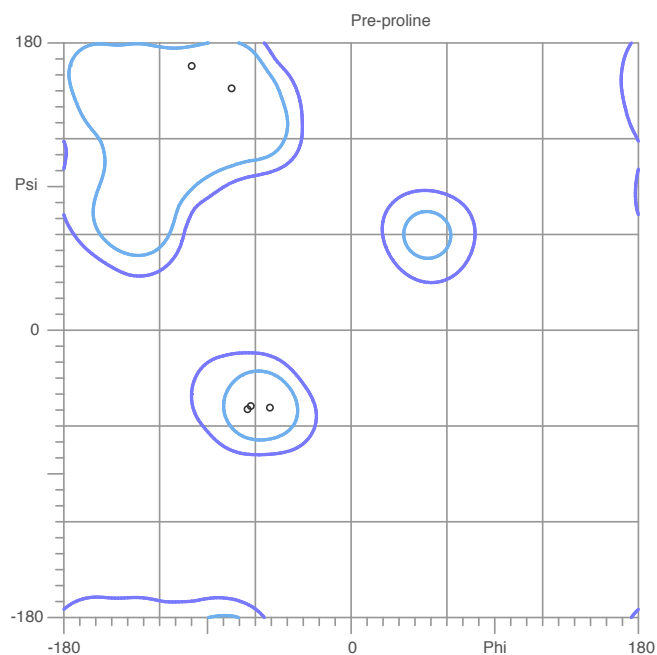
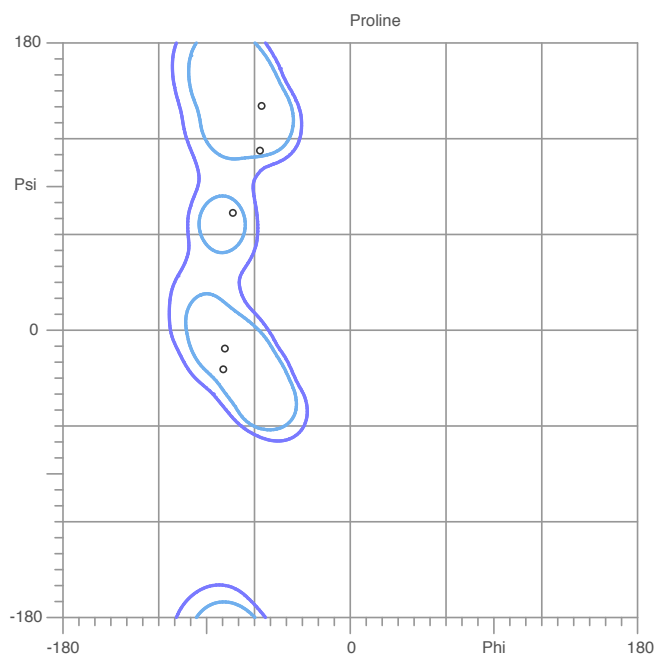
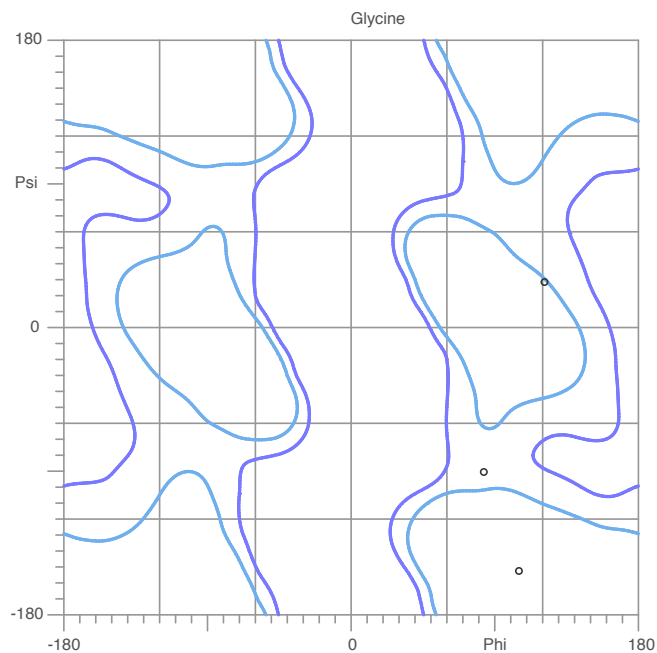
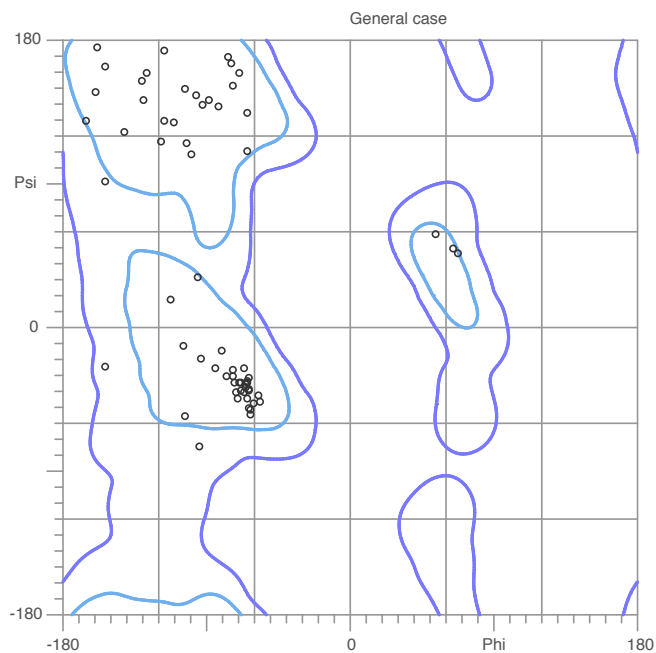
There were 12 outliers (phi, psi):

- [2] 9 ASP (62.7, 142.3)
- [3] 9 ASP (65.0, 103.6)
- [4] 9 ASP (64.4, 104.3)
- [4] 36 ASP (177.9, -44.9)

- [7] 9 ASP (65.0, 97.7)
- [9] 36 ASP (175.1, -44.9)
- [9] 75 ALA (59.9, 167.7)
- [10] 36 ASP (175.5, -45.1)
- [11] 36 ASP (-175.1, -25.5)
- [12] 10 ASP (81.8, 105.0)
- [15] 75 ALA (59.9, 166.5)
- [16] 10 ASP (60.6, 157.5)

MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 1



93.4% (71/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

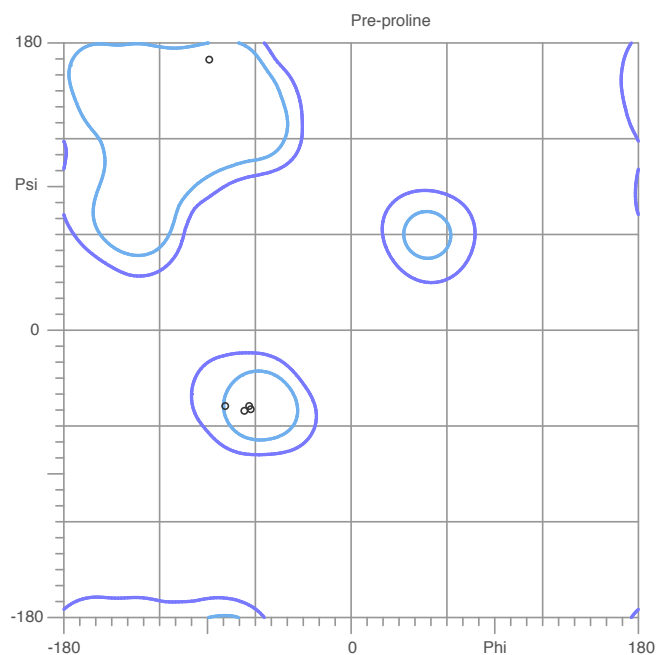
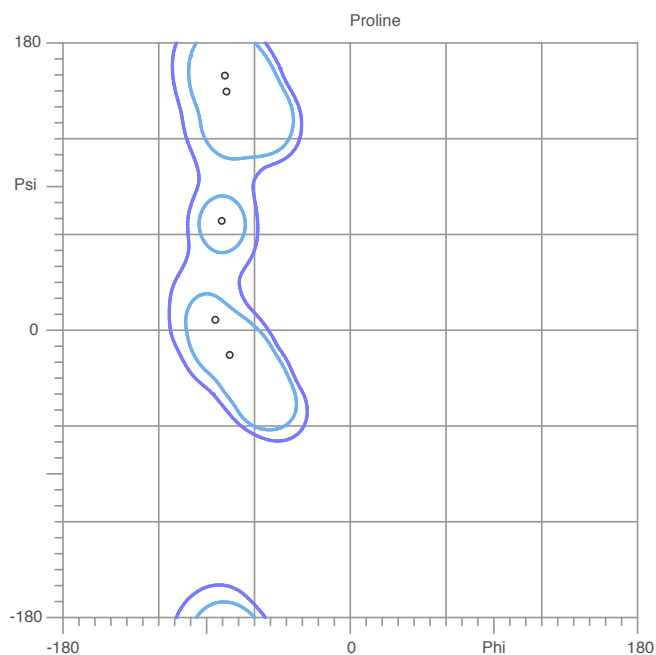
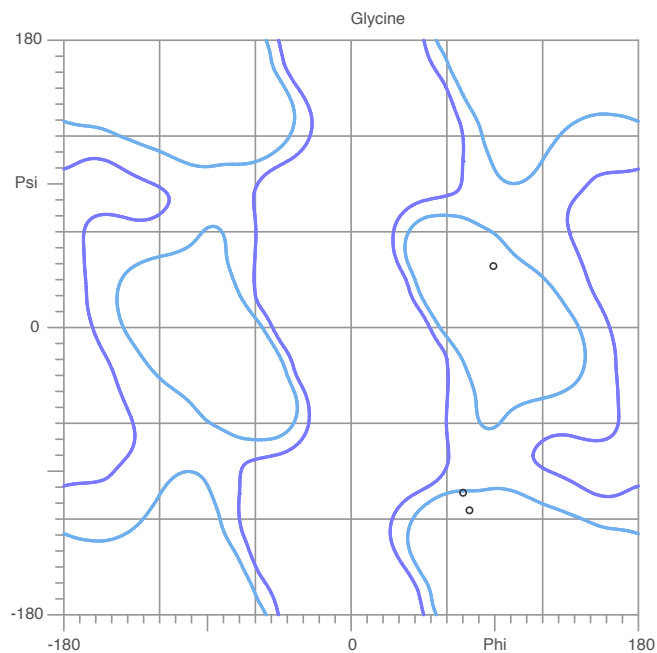
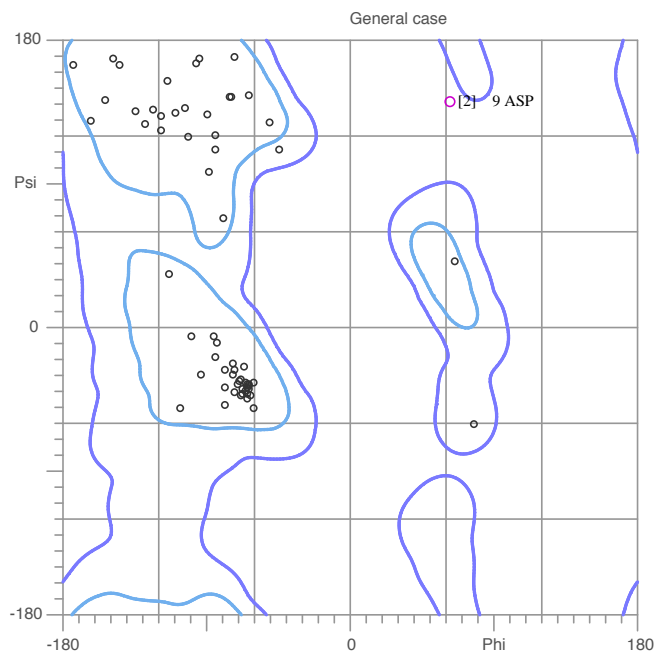
There were no outliers.

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 2



96.1% (73/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

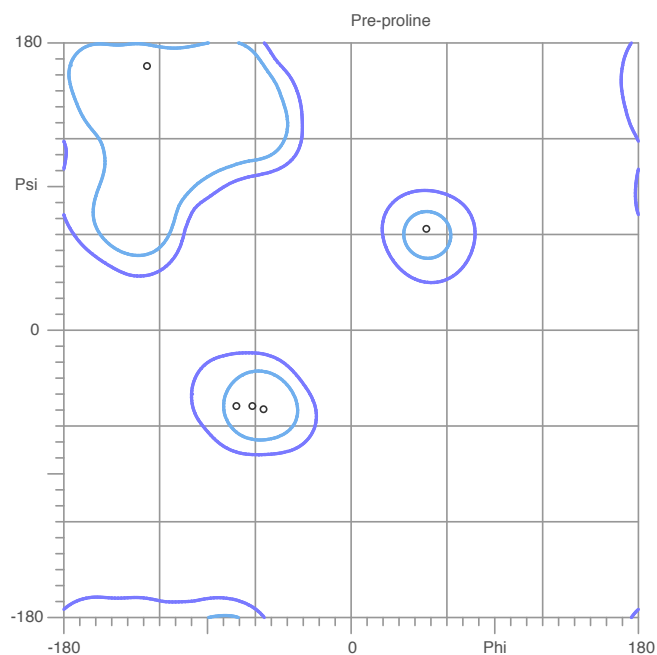
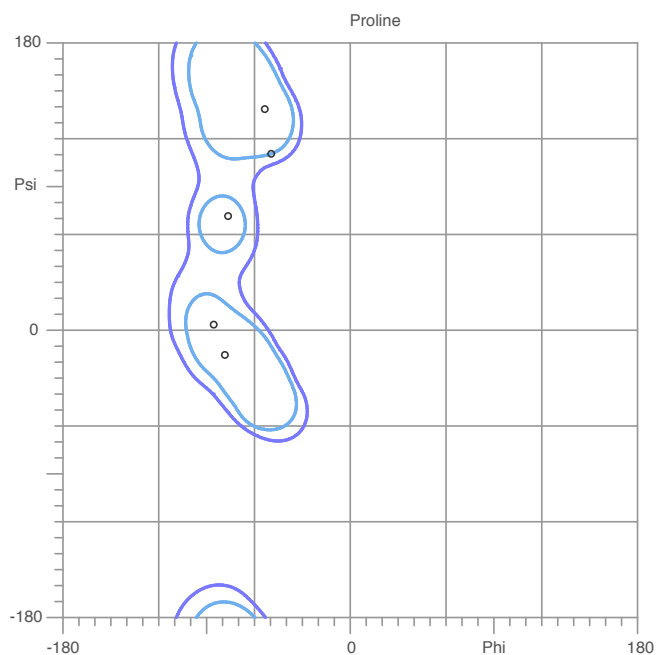
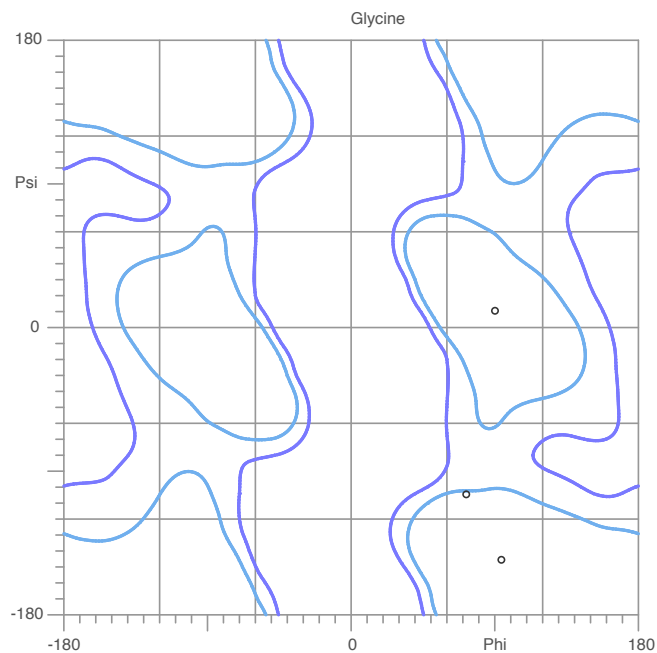
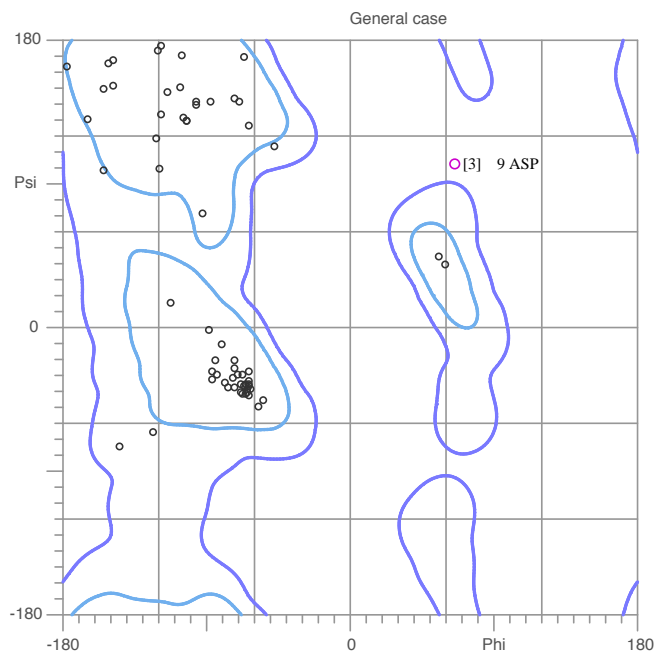
There were 1 outliers (phi, psi):
[2] 9 ASP (62.7, 142.3)

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 3

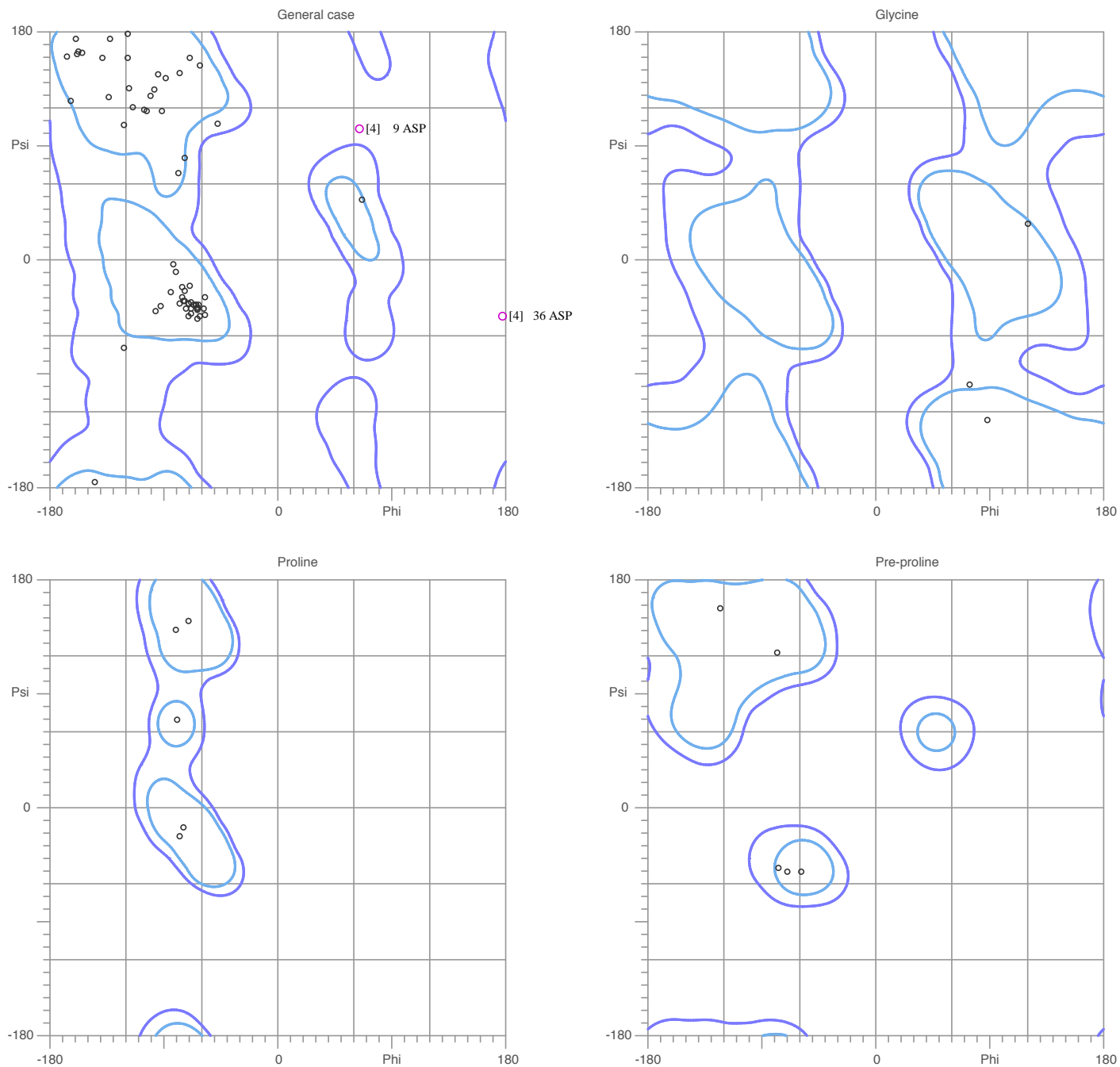


93.4% (71/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 9 ASP (65.0, 103.6)

MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 4



92.1% (70/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

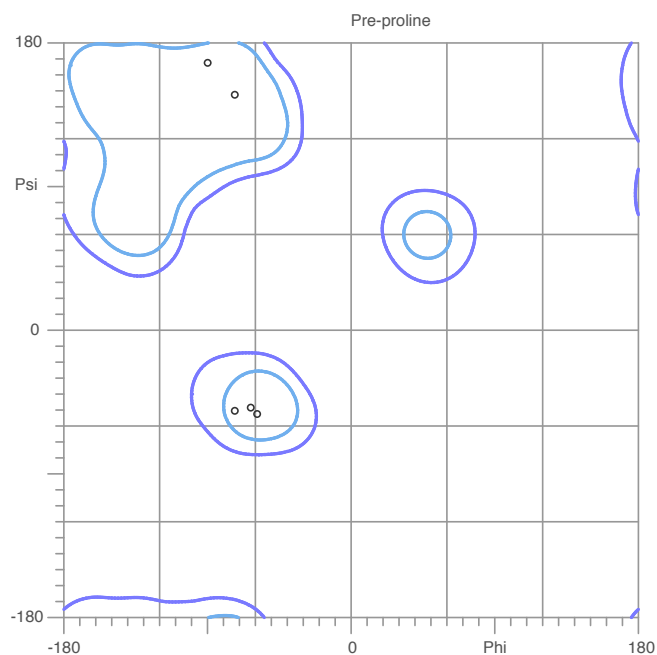
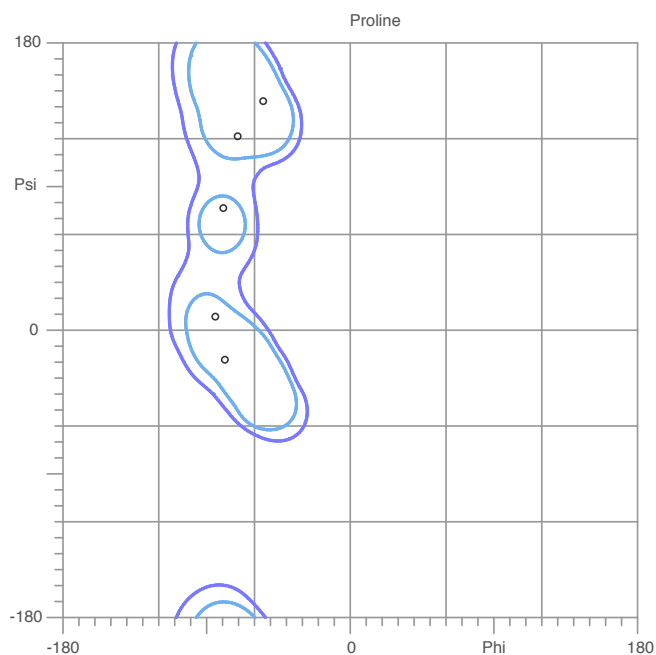
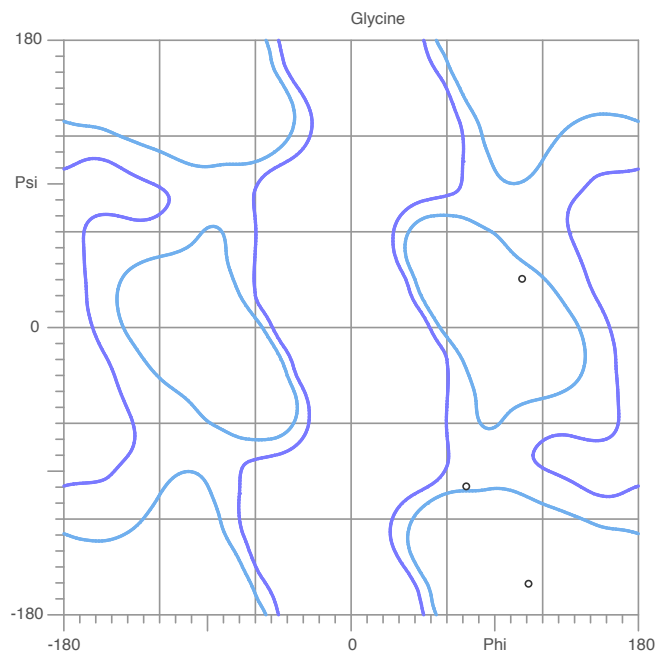
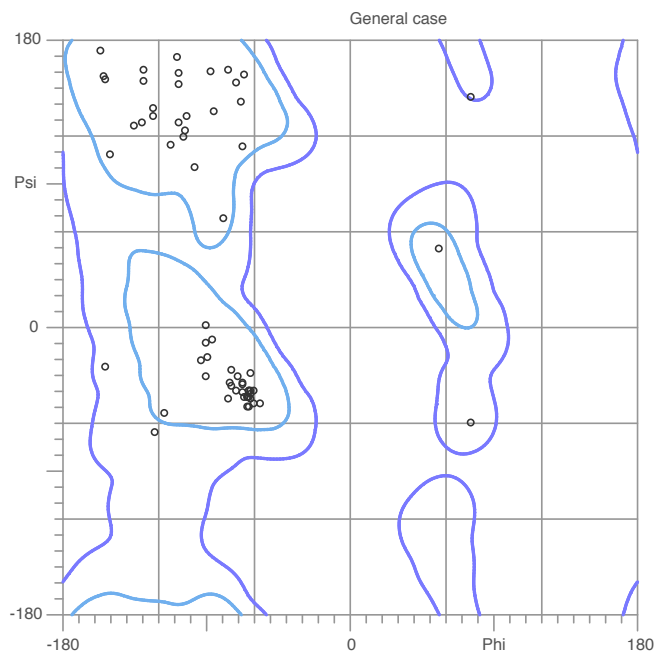
There were 2 outliers (phi, psi):

[4] 9 ASP (64.4, 104.3)

[4] 36 ASP (177.9, -44.9)

MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 5



93.4% (71/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

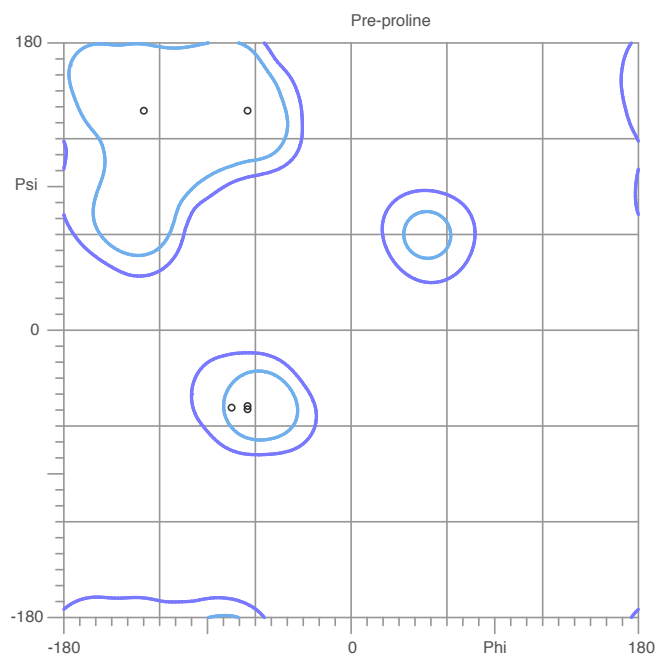
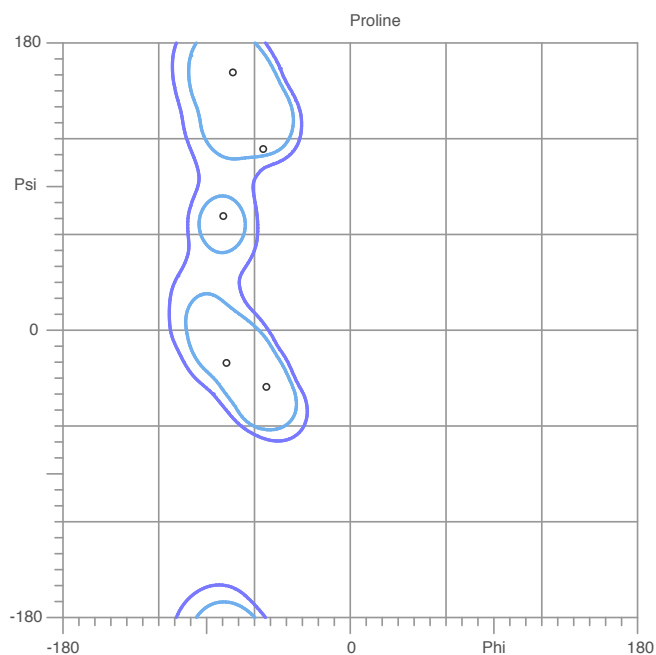
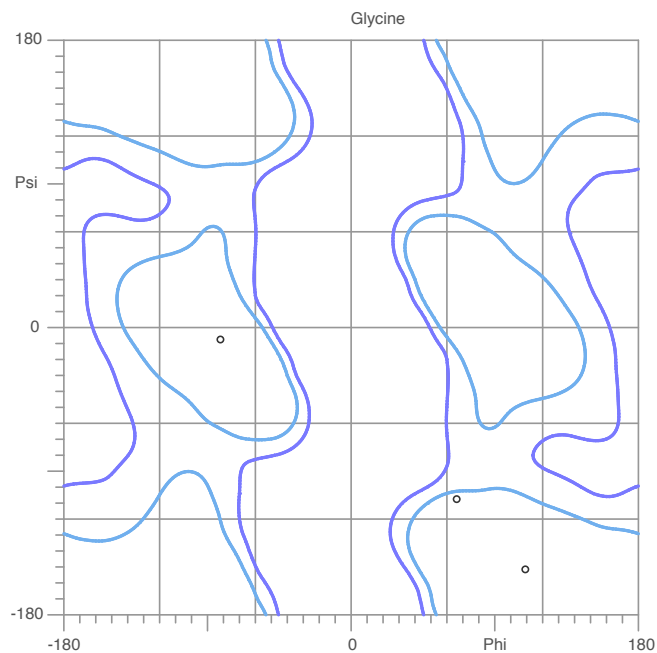
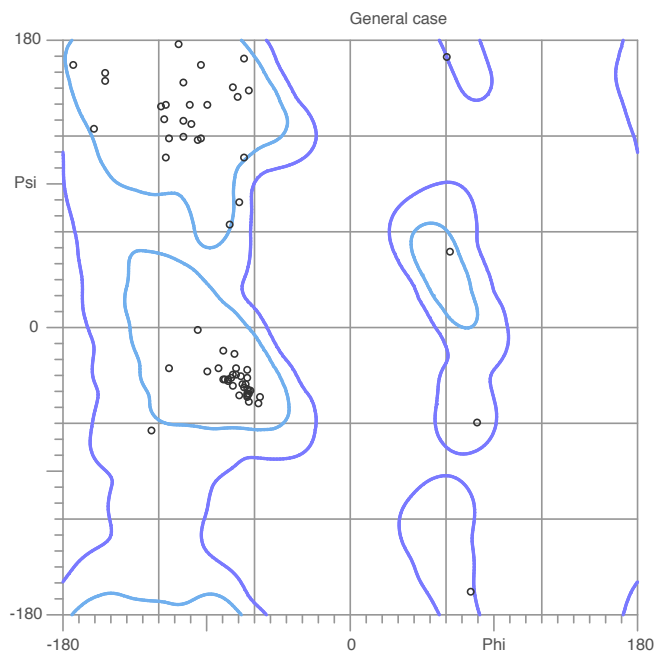
There were no outliers.

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 6



93.4% (71/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

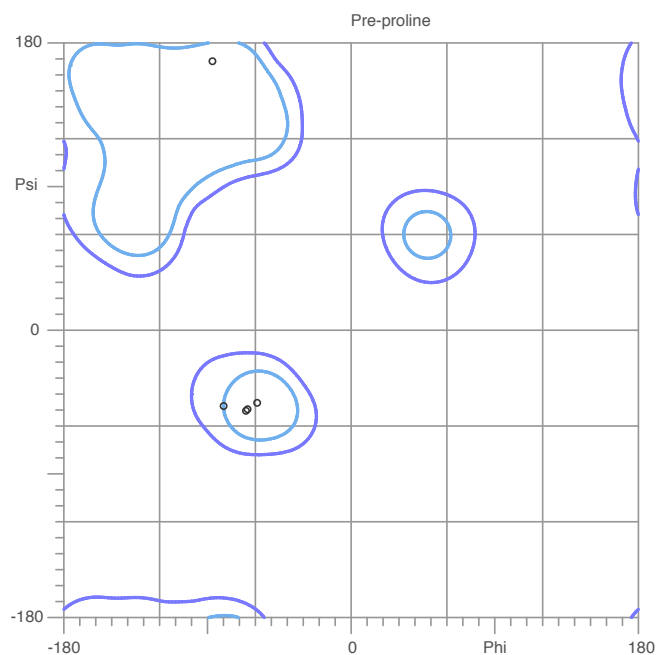
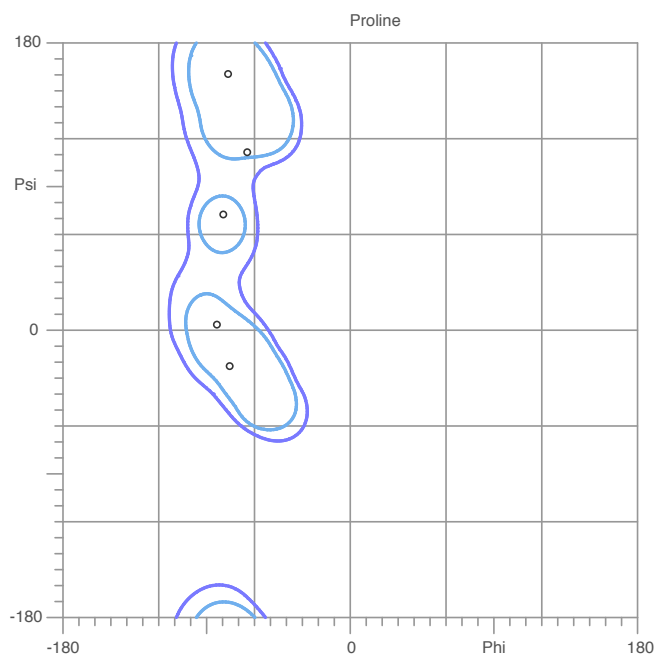
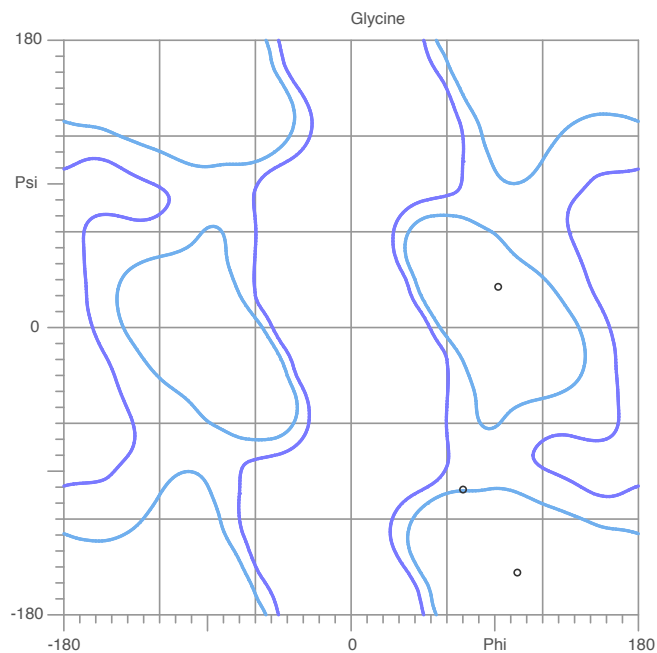
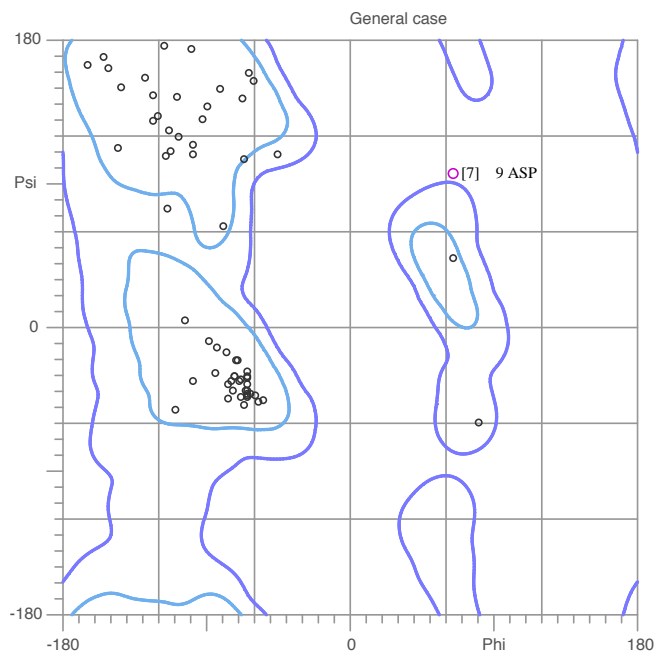
There were no outliers.

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 7

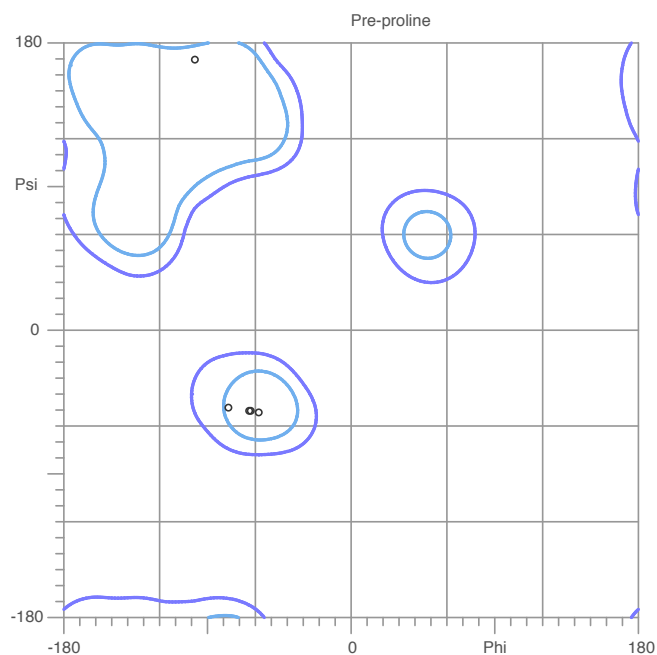
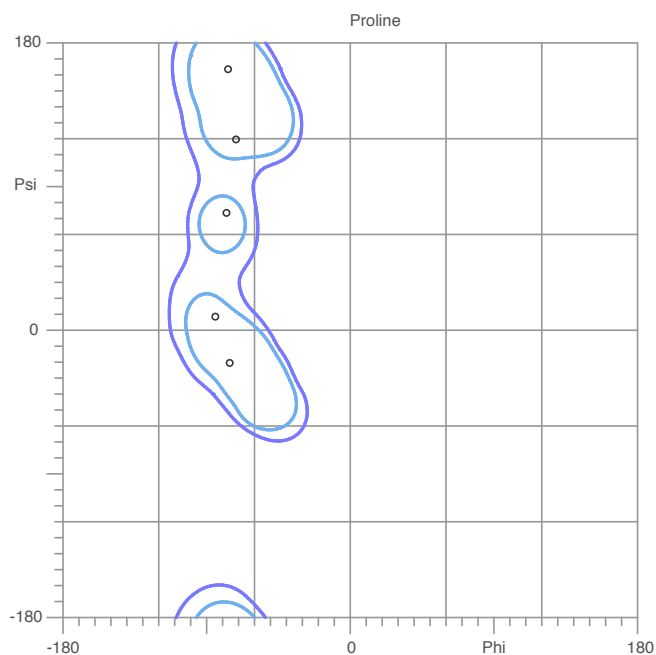
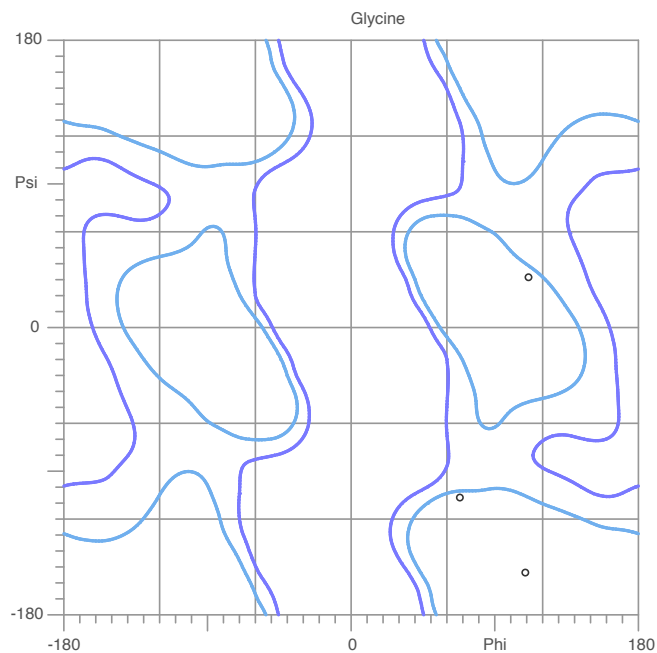
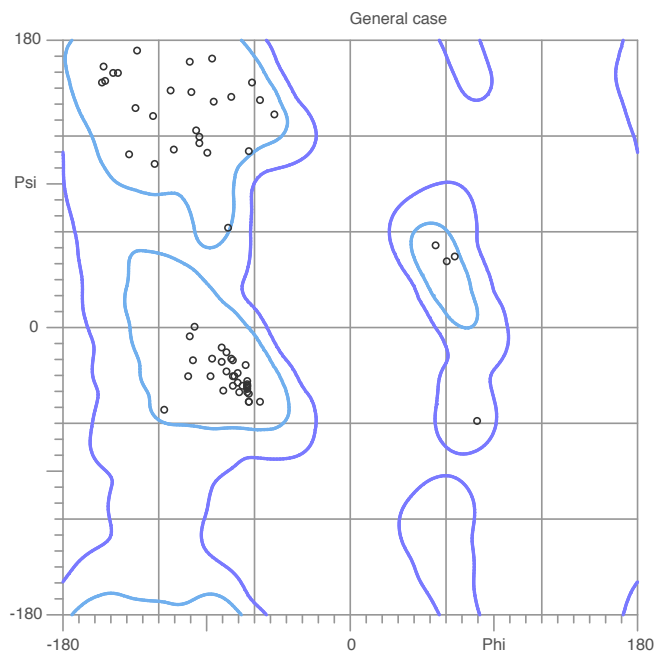


92.1% (70/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[7] 9 ASP (65.0, 97.7)

MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 8



98.7% (75/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

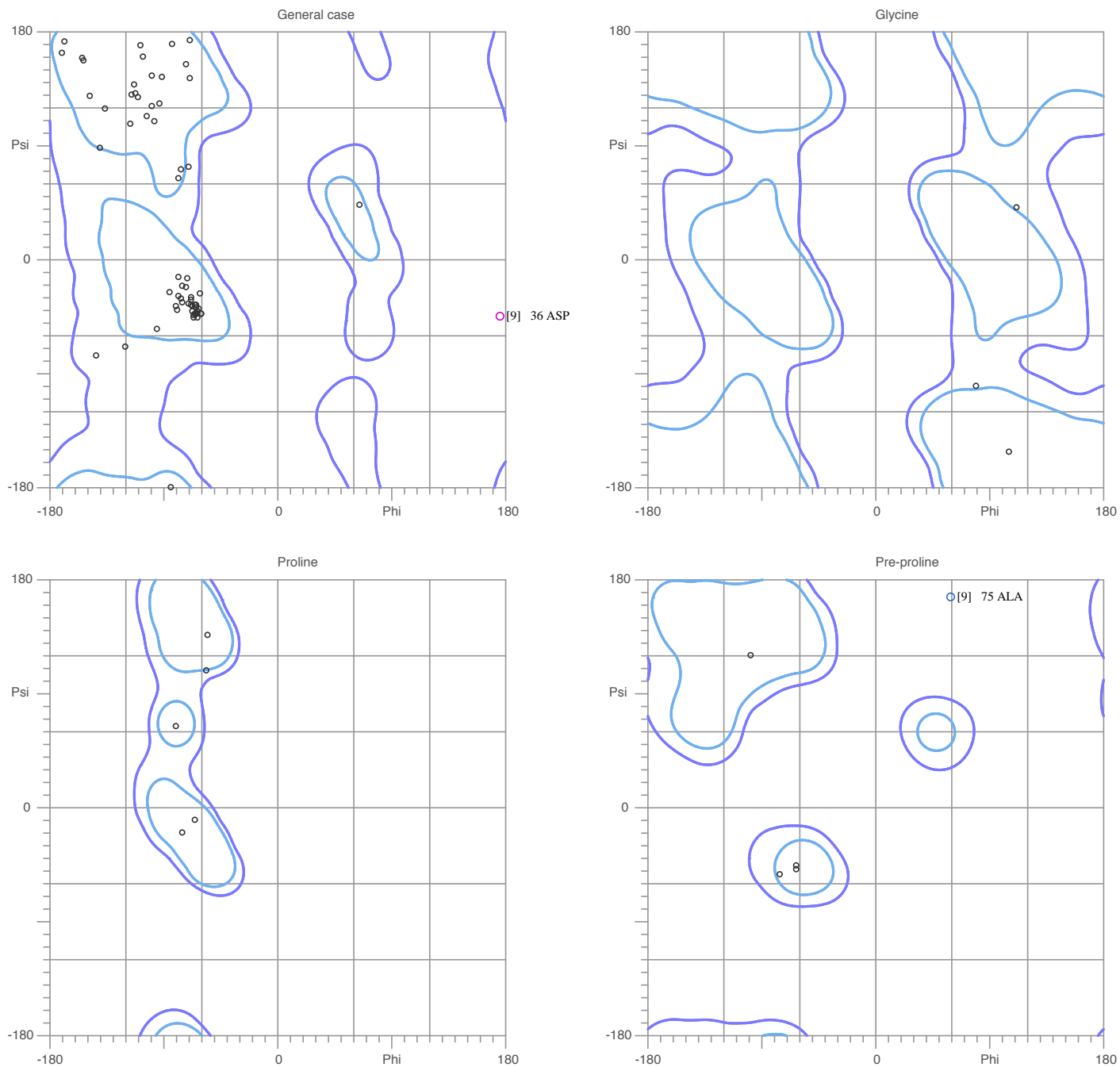
There were no outliers.

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 9



90.8% (69/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

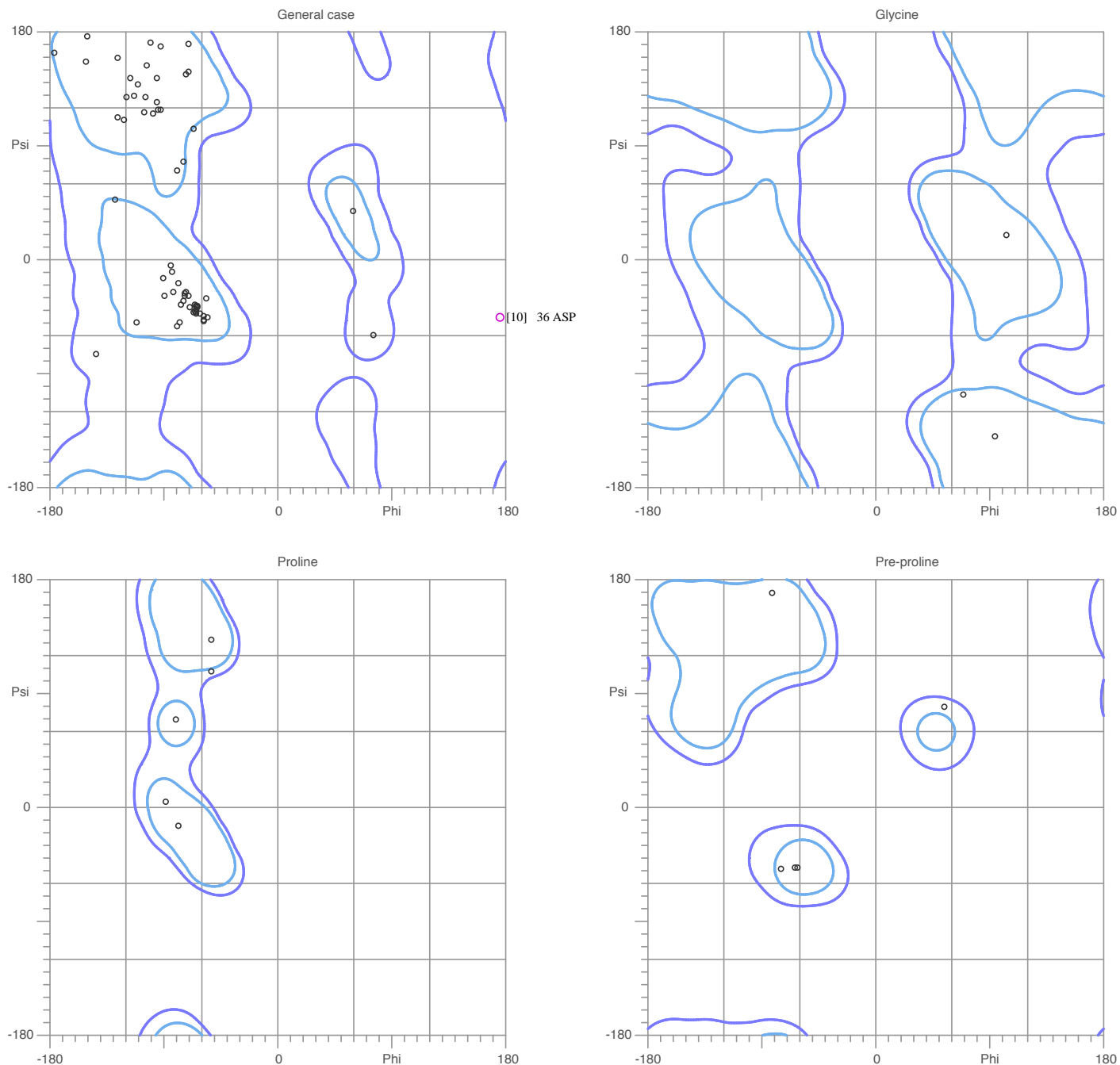
There were 2 outliers (phi, psi):

[9] 36 ASP (175.1, -44.9)

[9] 75 ALA (59.9, 167.7)

MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 10



92.1% (70/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

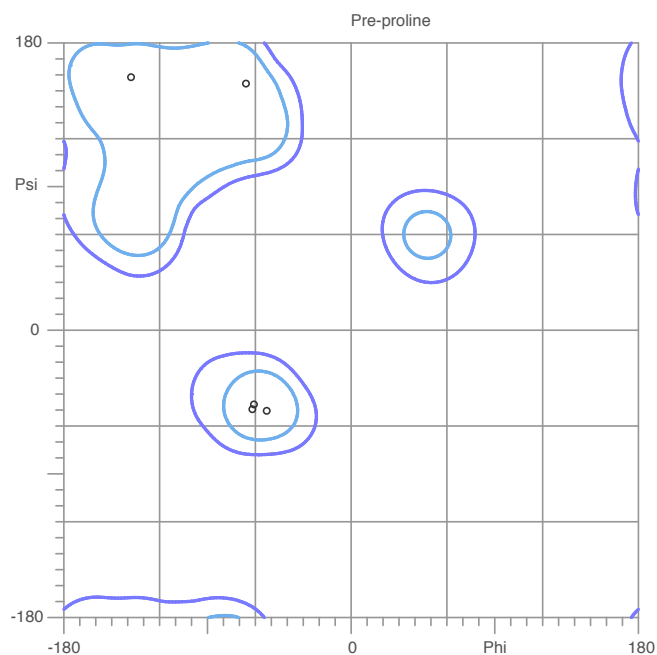
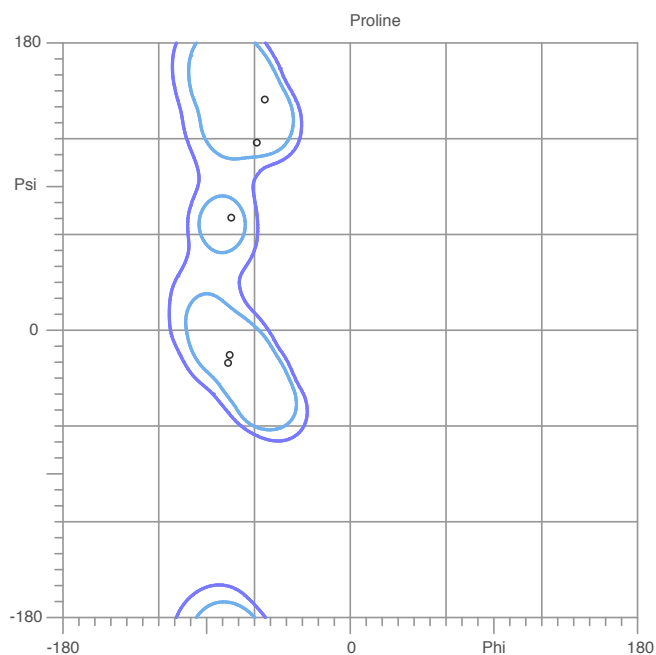
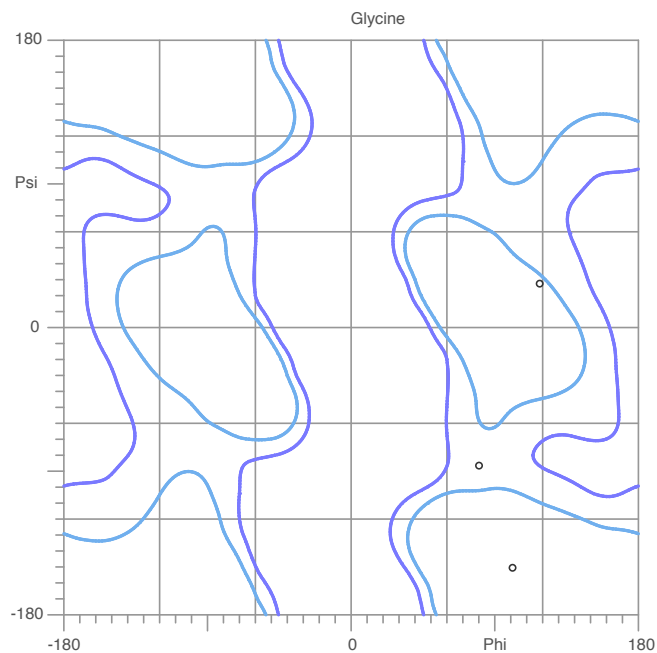
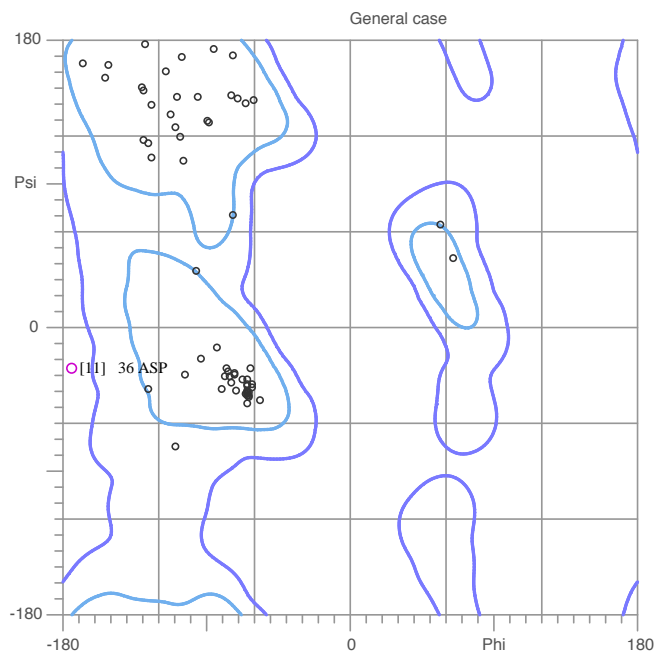
There were 1 outliers (phi, psi):
[10] 36 ASP (175.5, -45.1)

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 11



93.4% (71/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

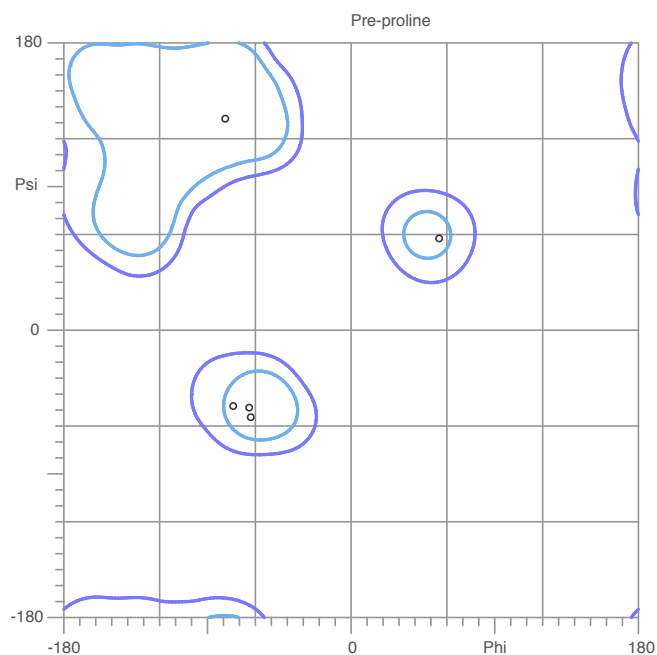
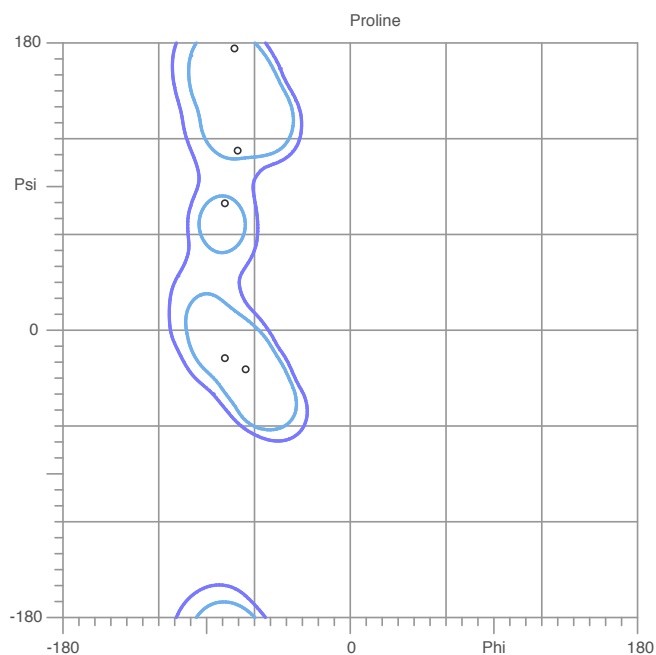
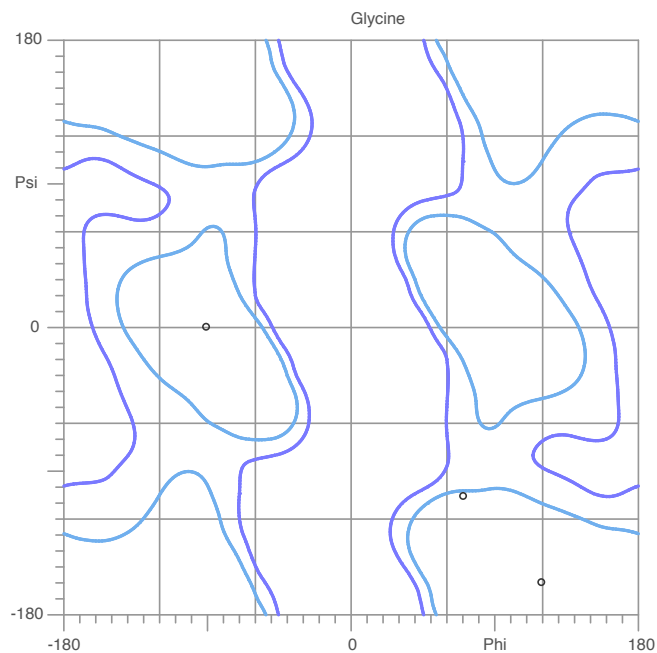
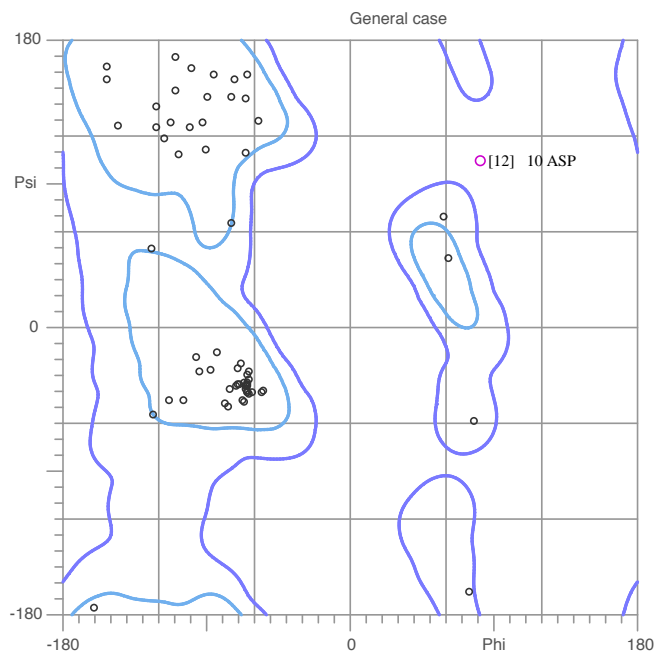
There were 1 outliers (phi, psi):
[11] 36 ASP (-175.1, -25.5)

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 12



92.1% (70/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

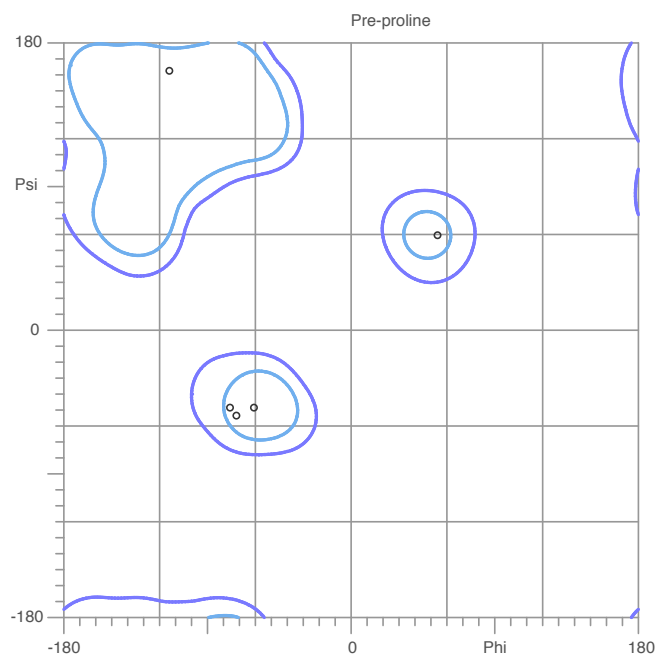
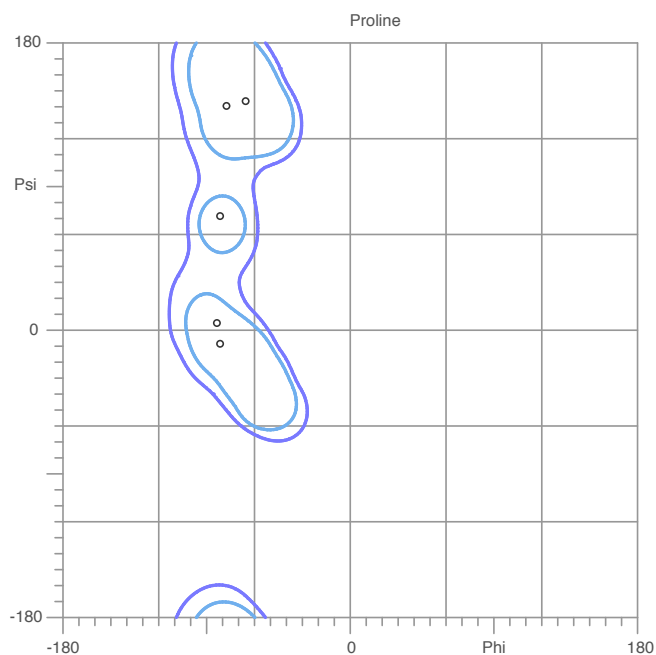
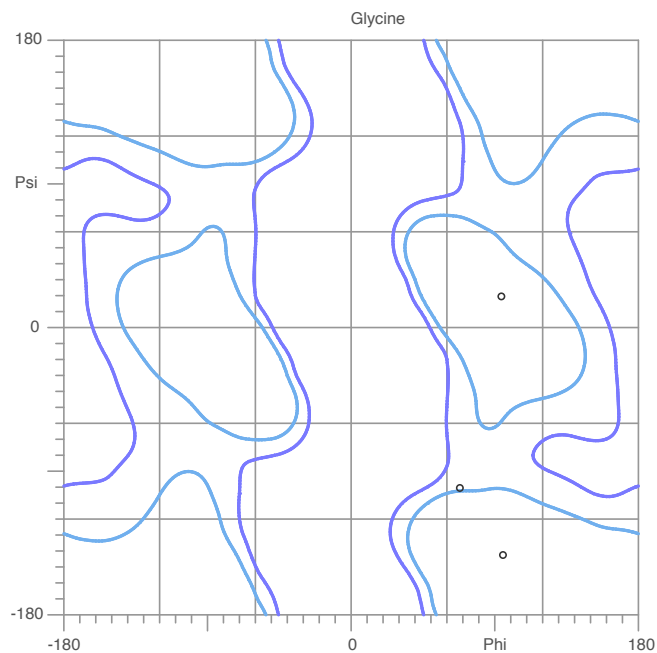
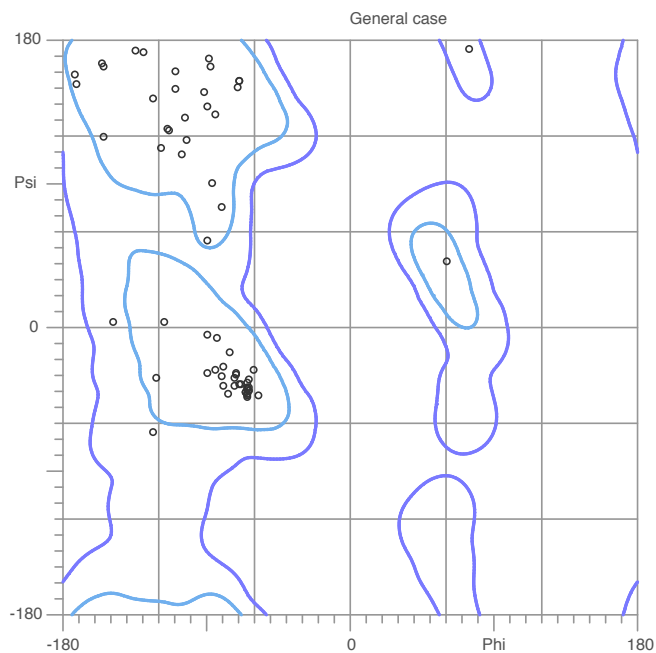
There were 1 outliers (phi, psi):
[12] 10 ASP (81.8, 105.0)

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

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

MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 13



94.7% (72/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

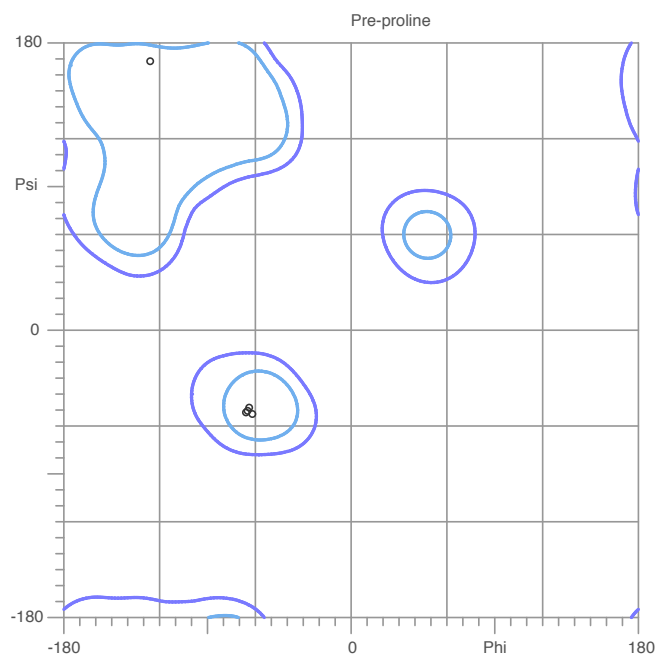
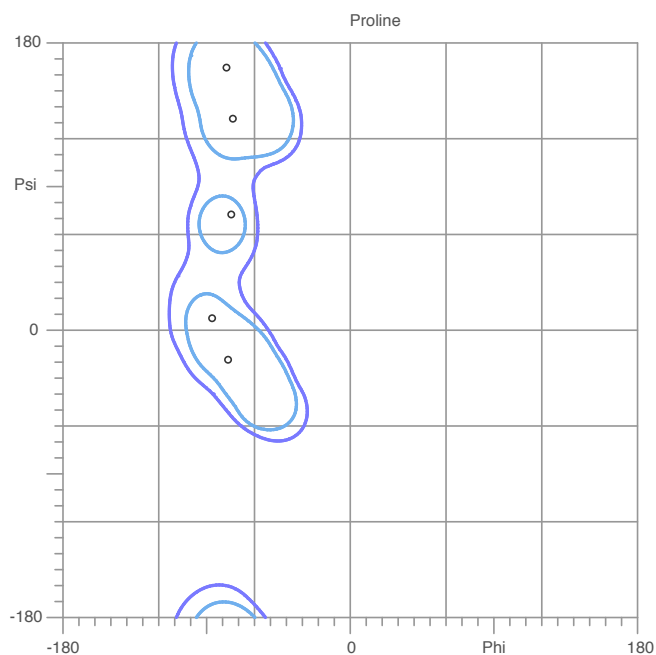
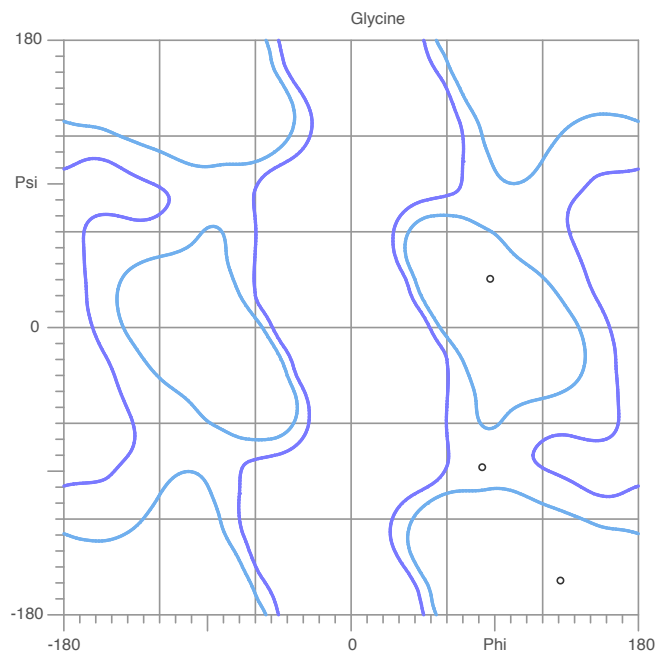
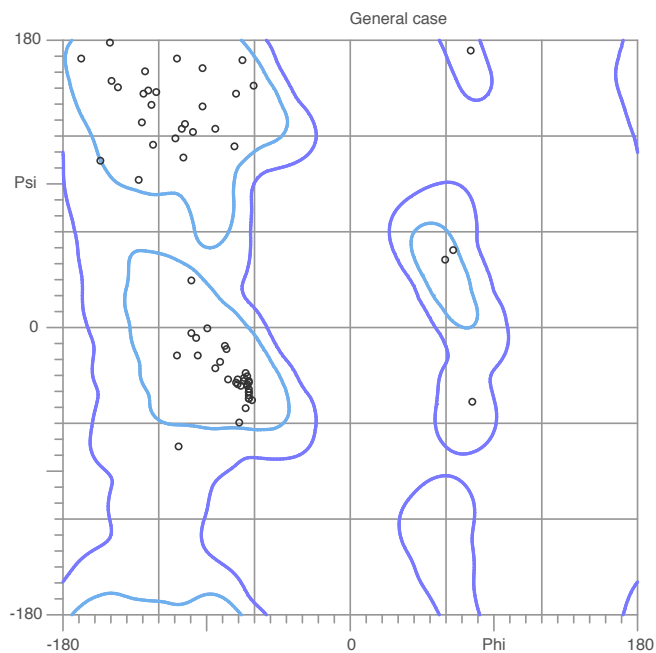
There were no outliers.

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 14

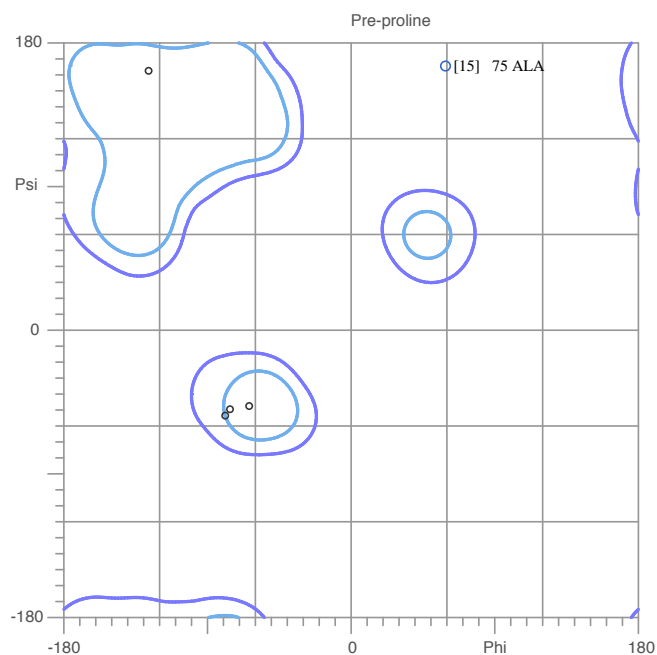
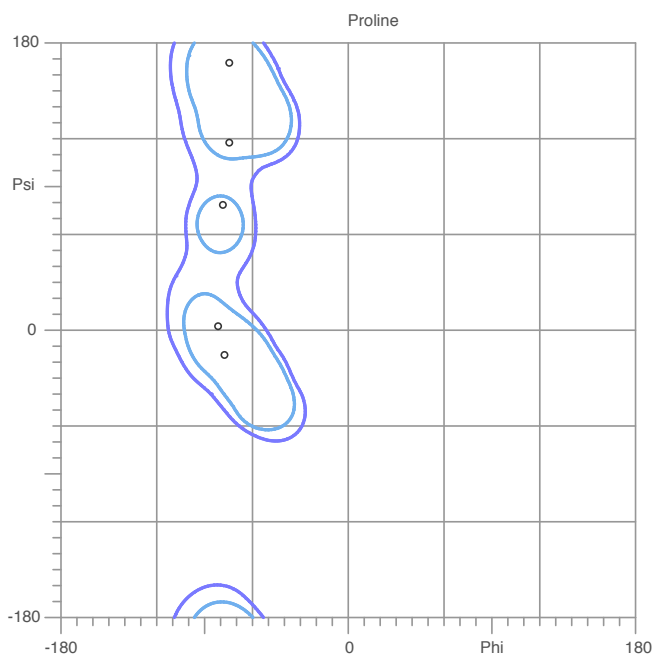
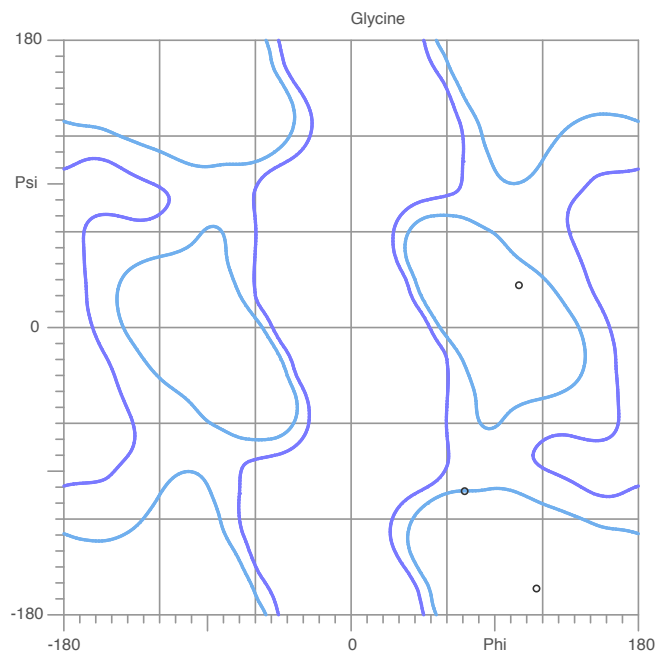
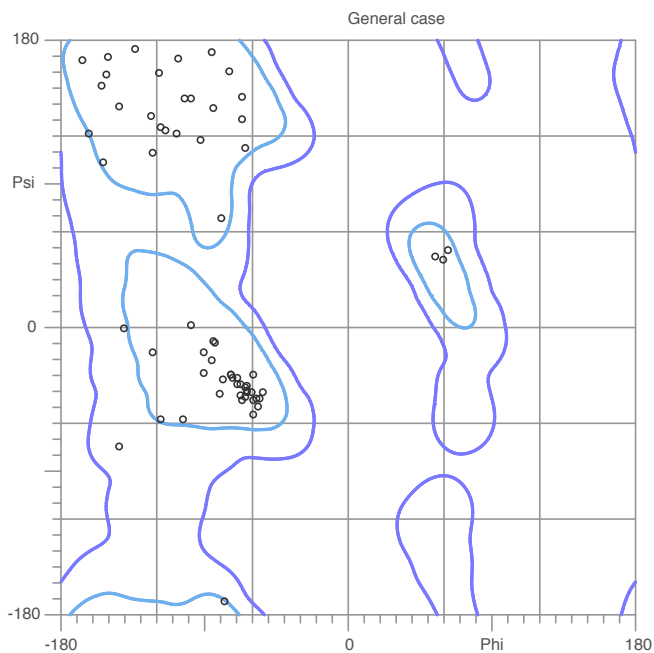


93.4% (71/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 15



93.4% (71/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

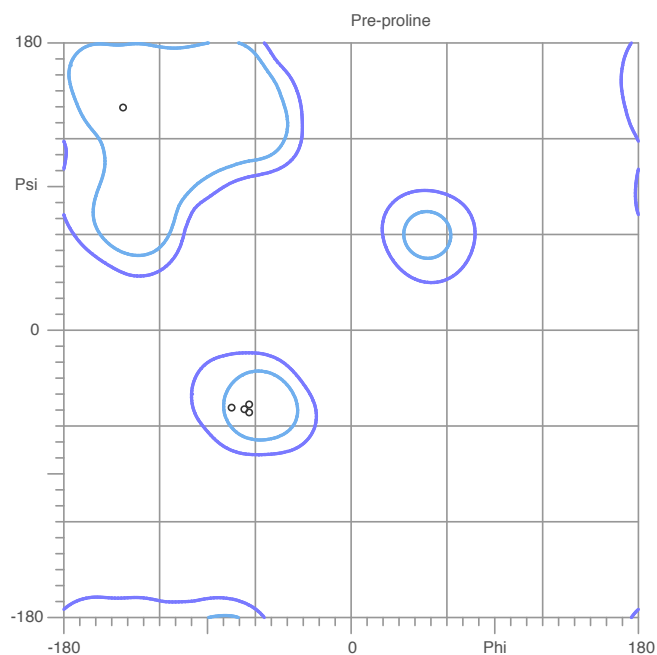
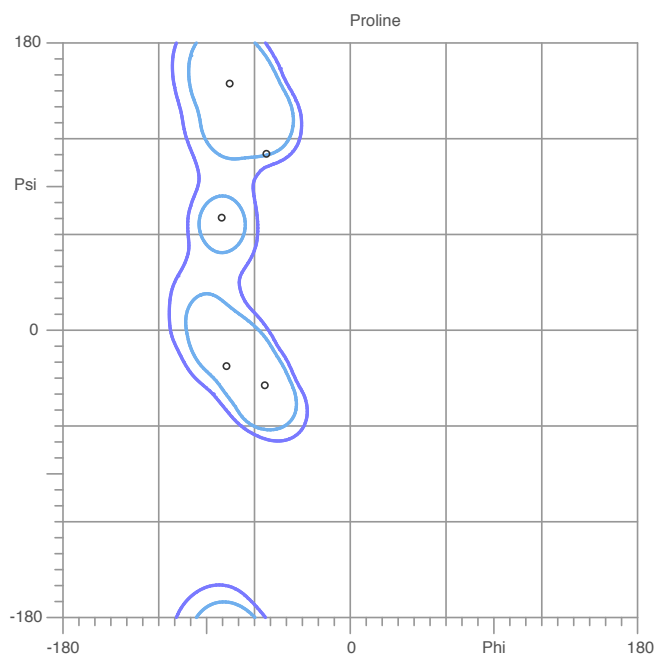
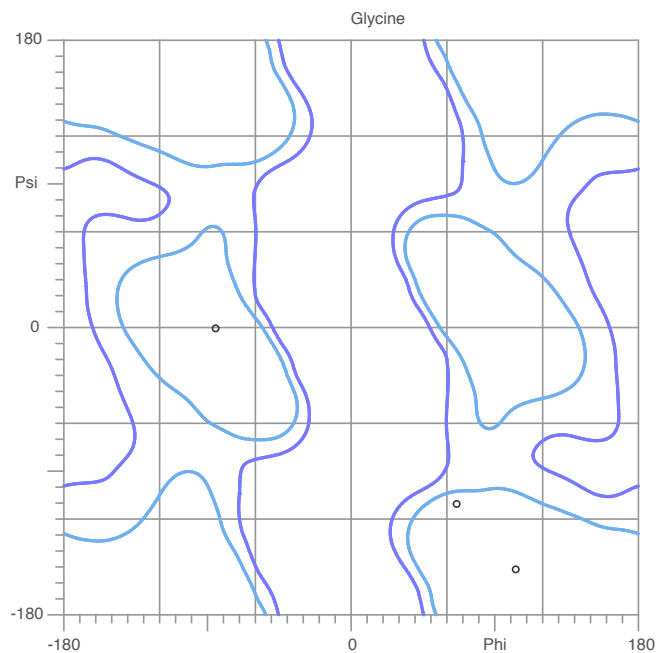
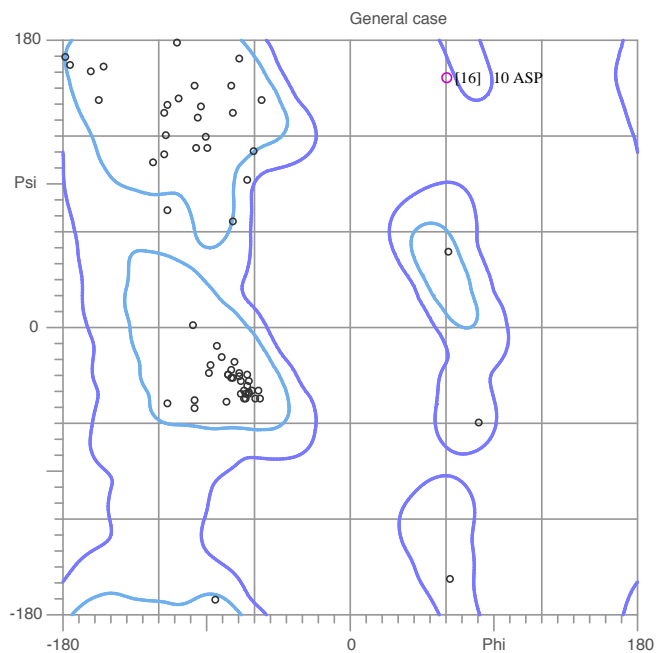
There were 1 outliers (phi, psi):
[15] 75 ALA (59.9, 166.5)

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 16



92.1% (70/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

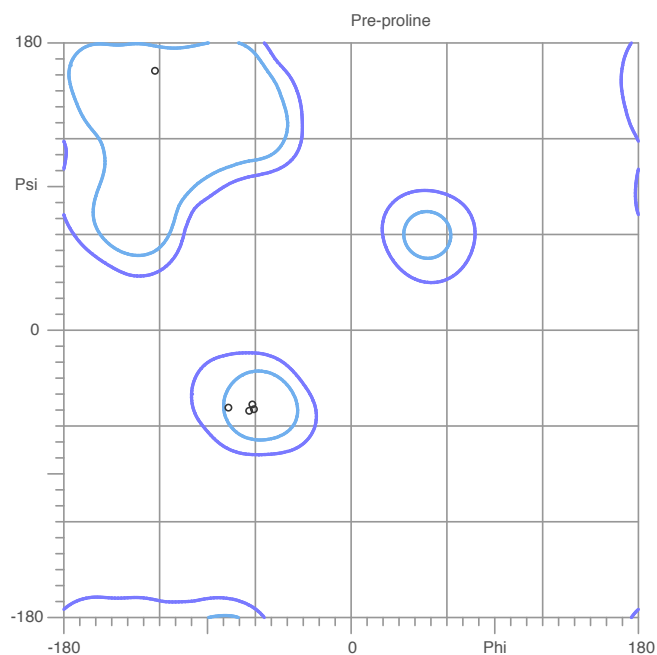
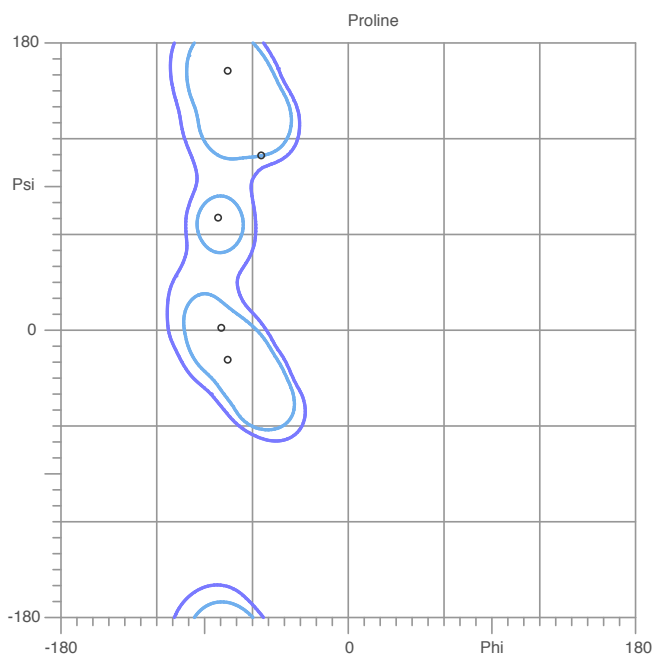
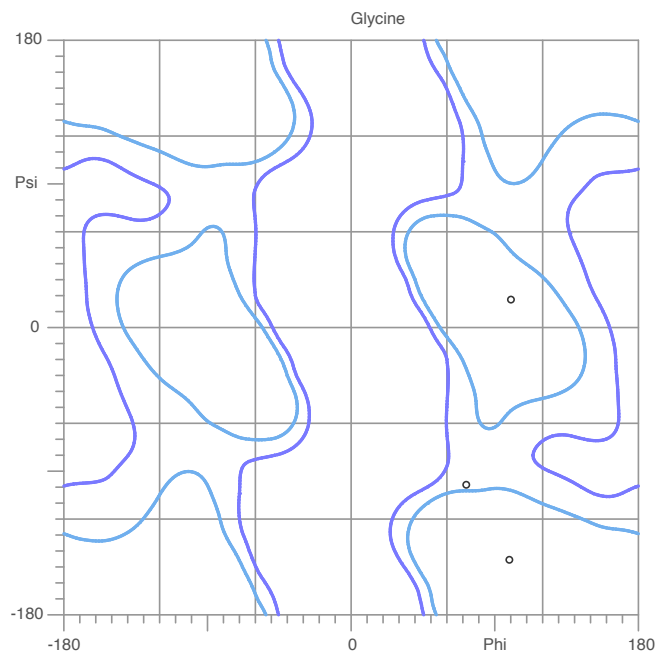
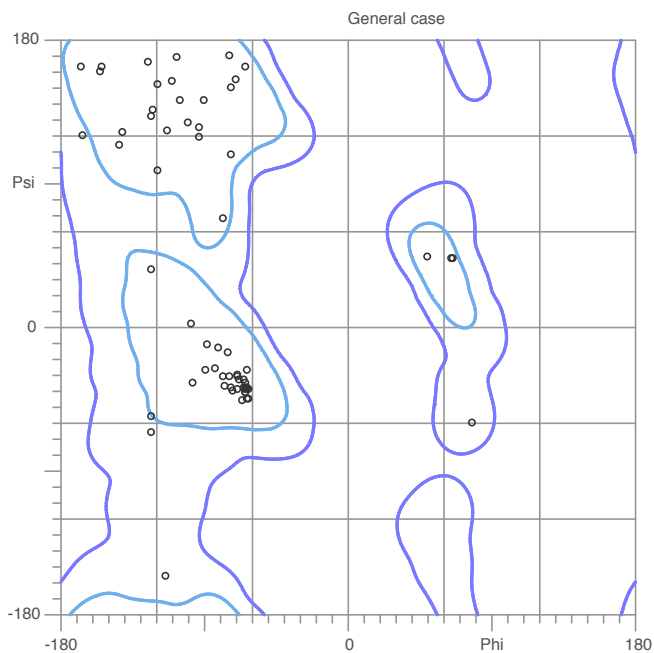
There were 1 outliers (phi, psi):
[16] 10 ASP (60.6, 157.5)

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 17



92.1% (70/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

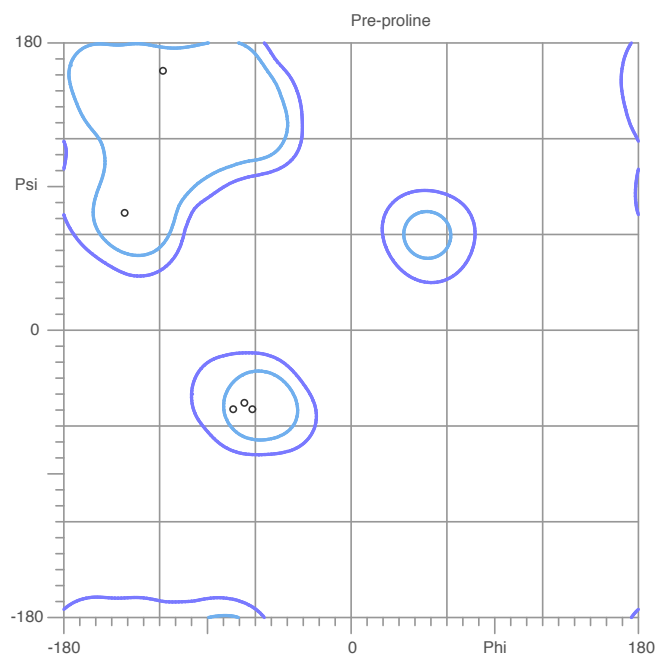
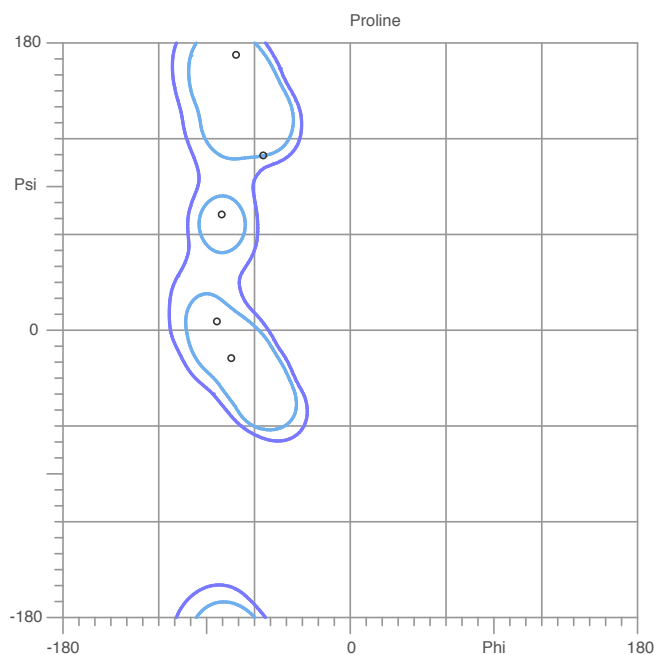
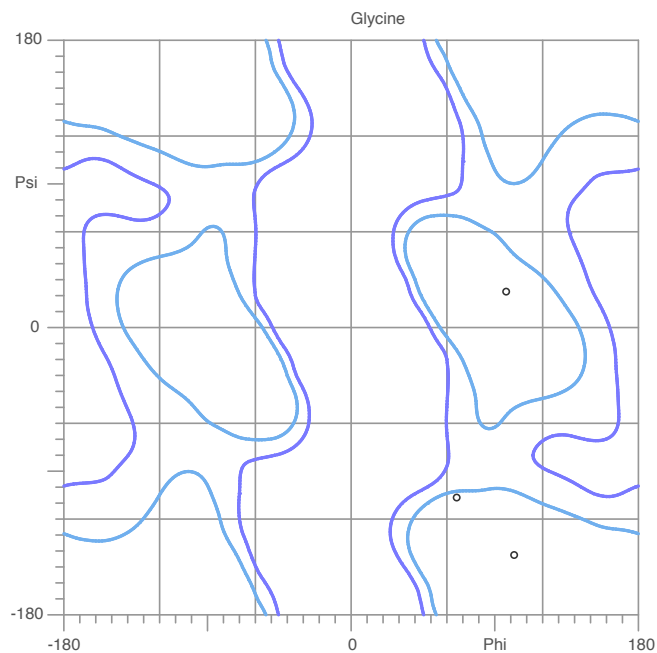
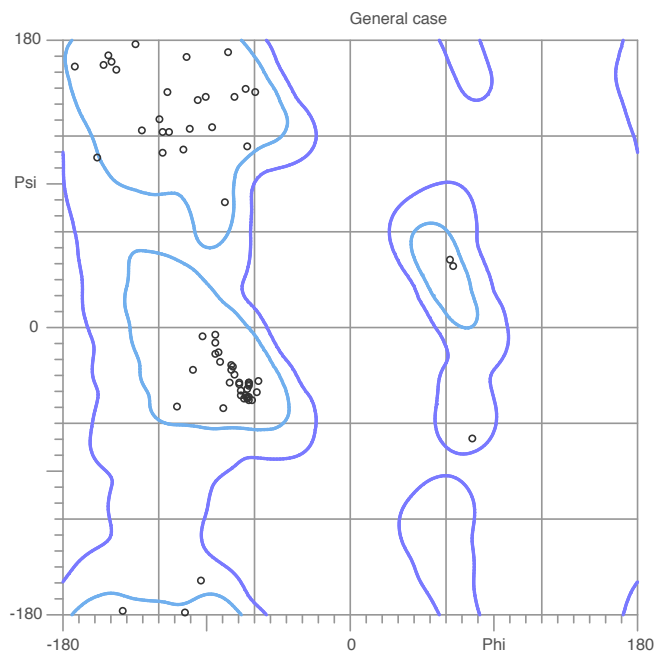
There were no outliers.

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

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MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 18



96.1% (73/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

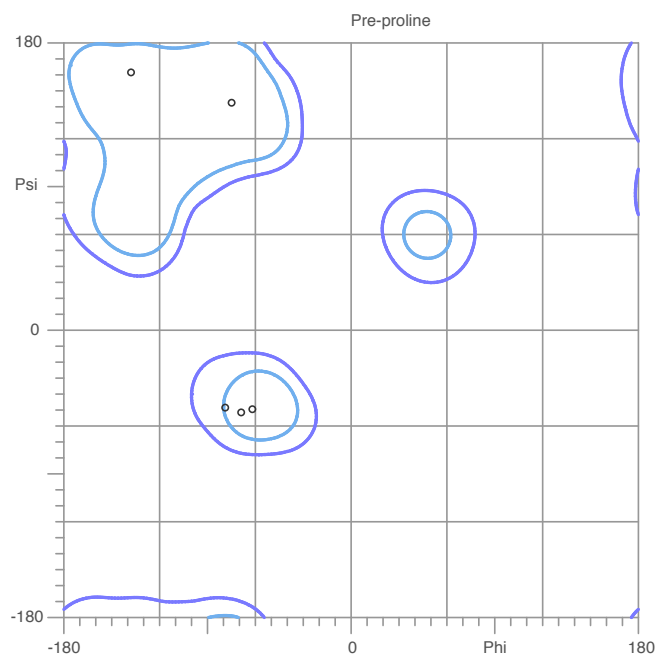
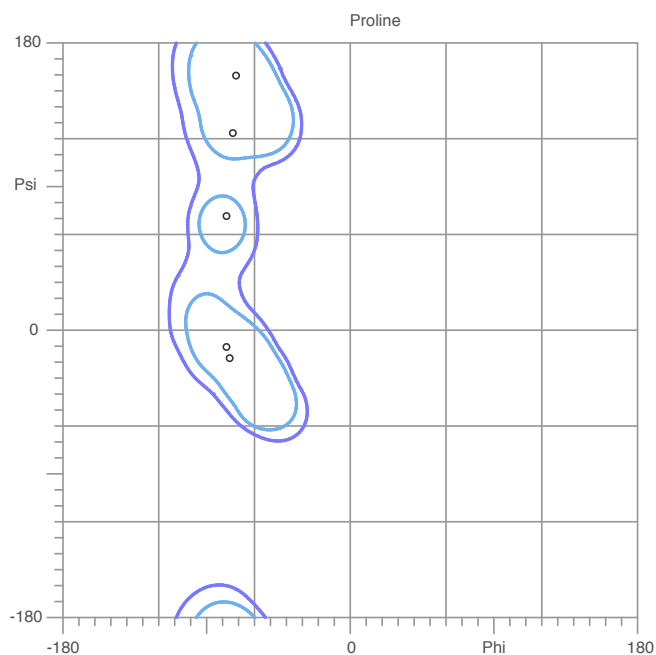
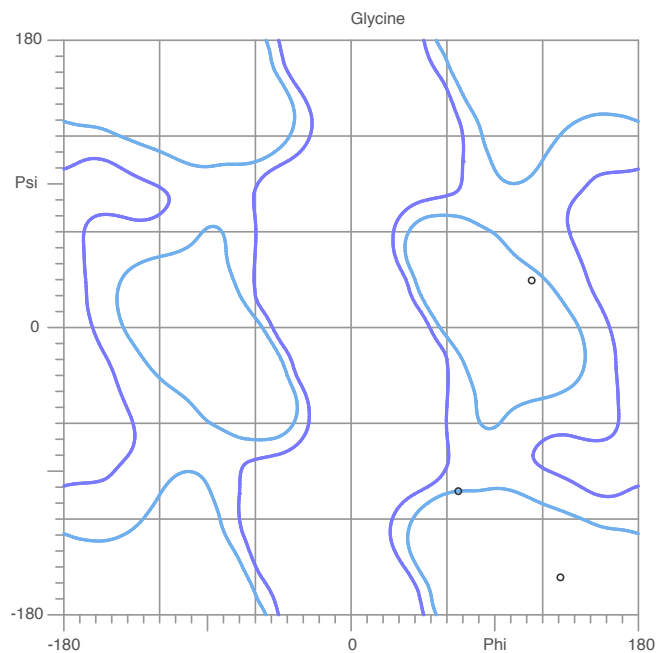
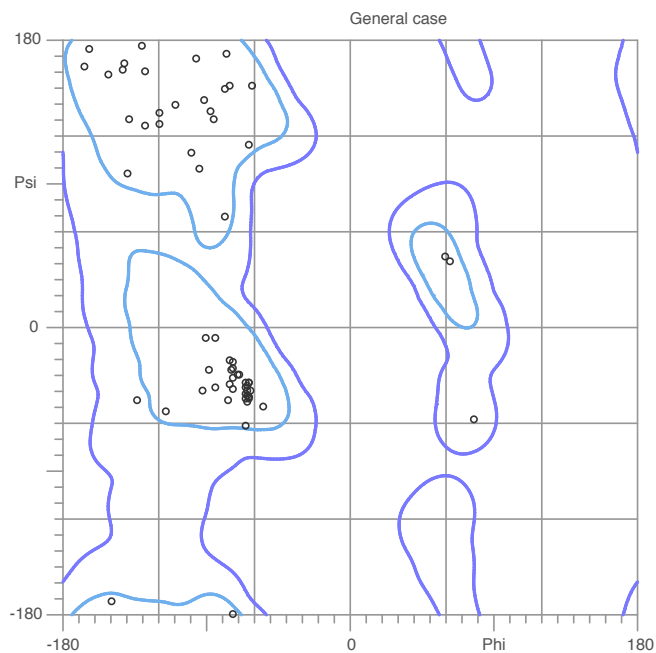
There were no outliers.

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

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

MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 19



97.4% (74/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

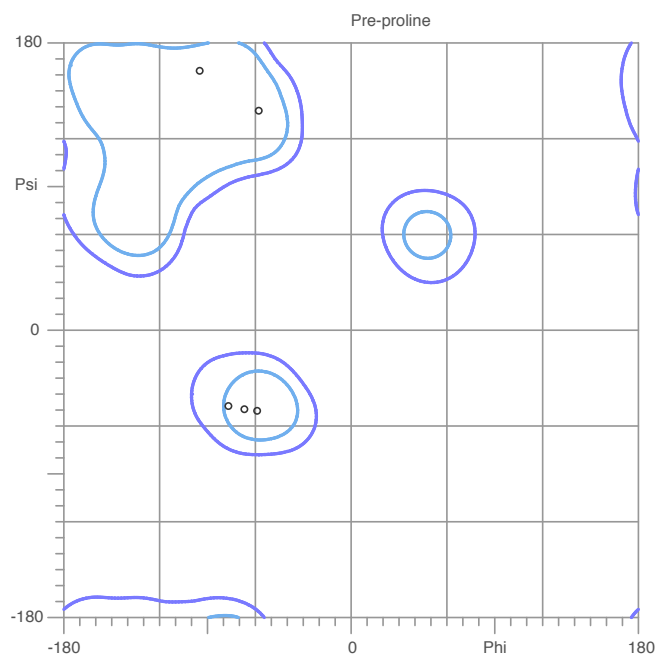
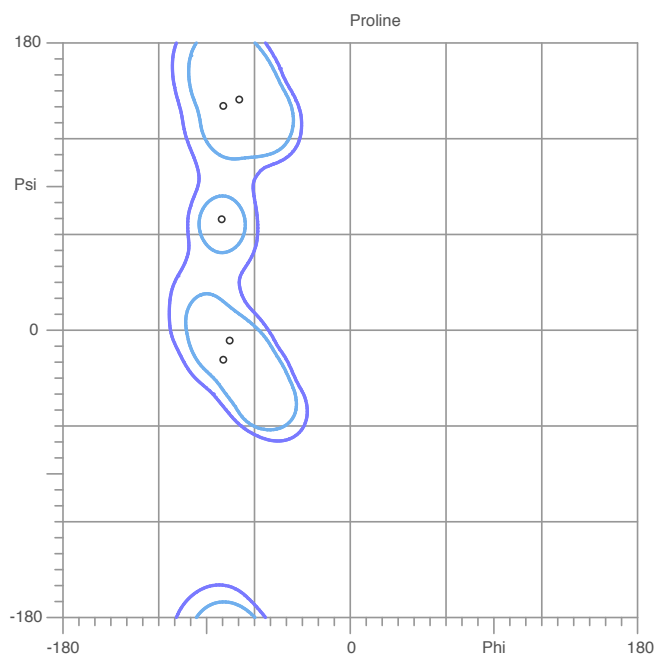
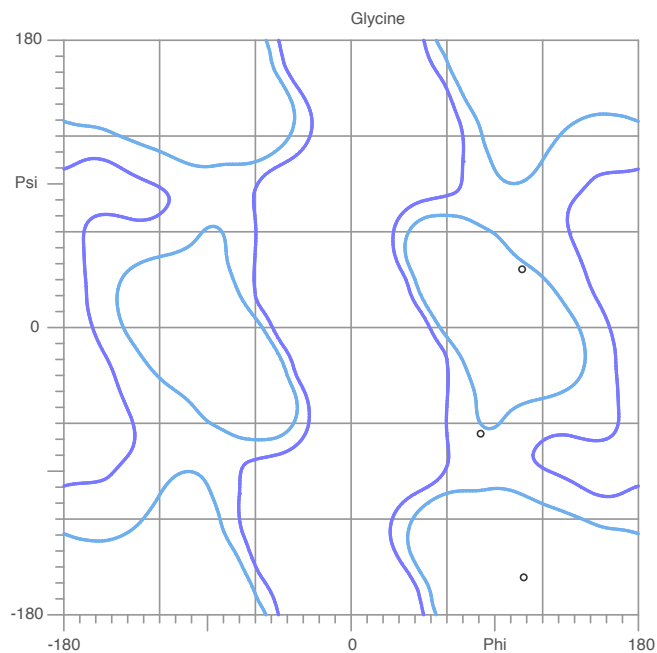
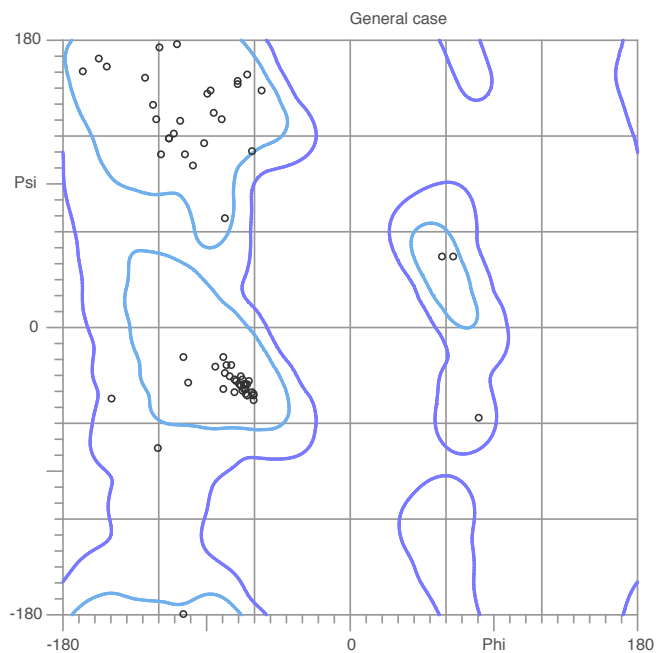
There were no outliers.

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

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

MolProbity Ramachandran analysis

XCR50_R3_em_bcr3.pdb, model 20



94.7% (72/76) of all residues were in favored (98%) regions.
100.0% (76/76) 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)