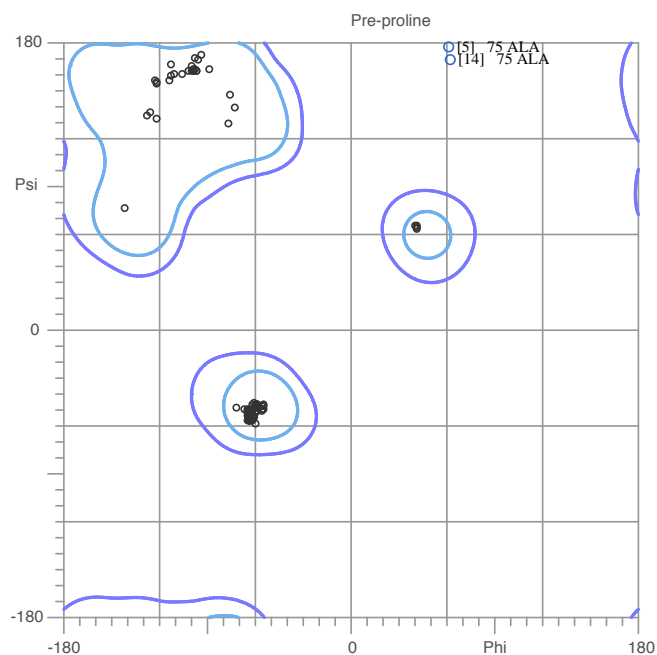
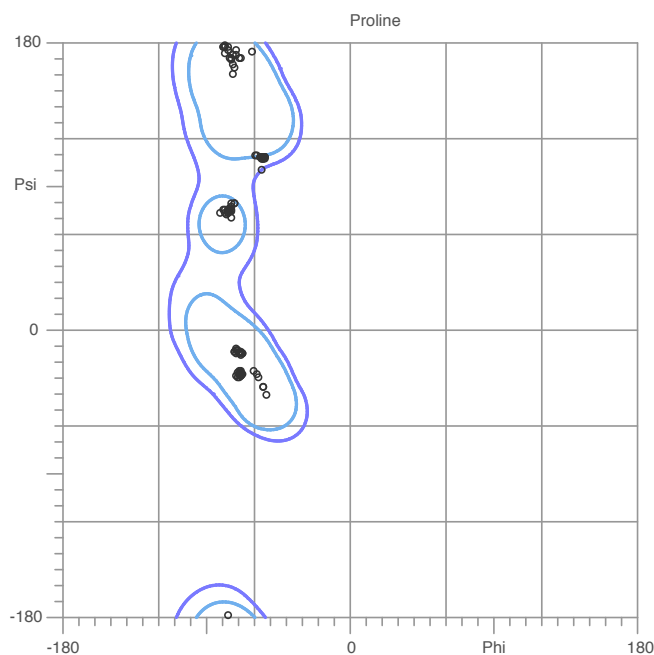
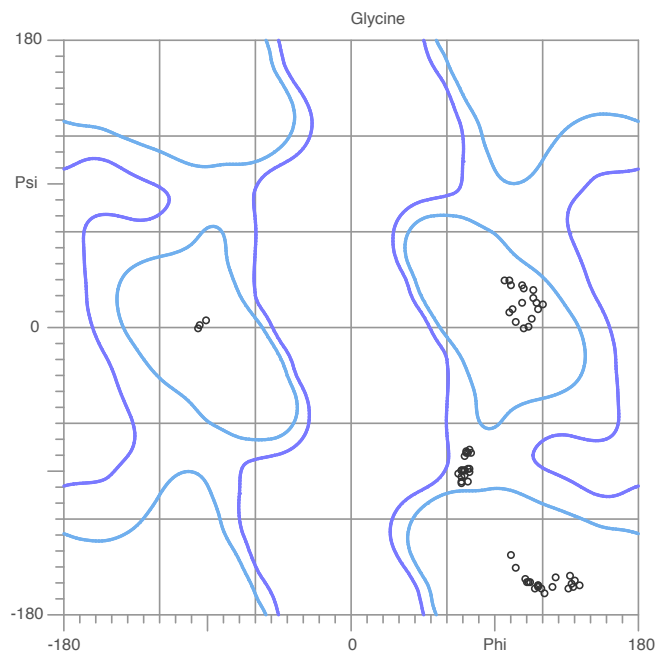
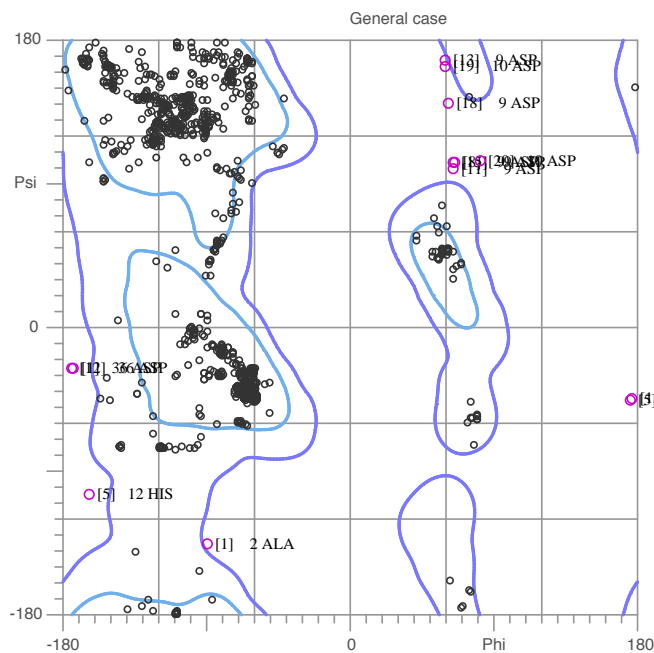


MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, all models



90.8% (1380/1520) of all residues were in favored (98%) regions.
 99.0% (1505/1520) of all residues were in allowed (>99.8%) regions.

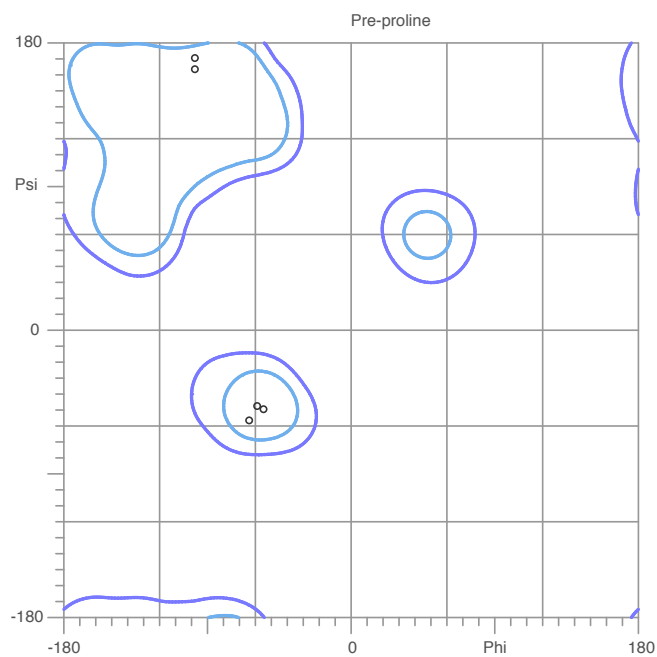
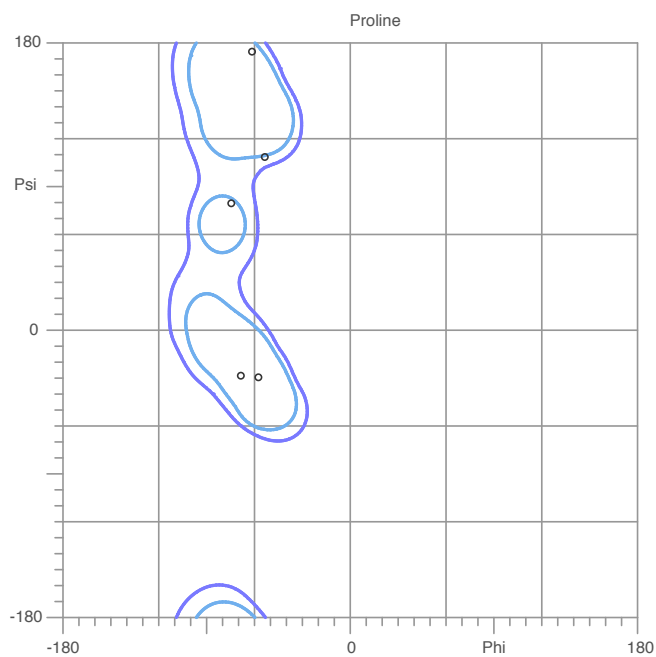
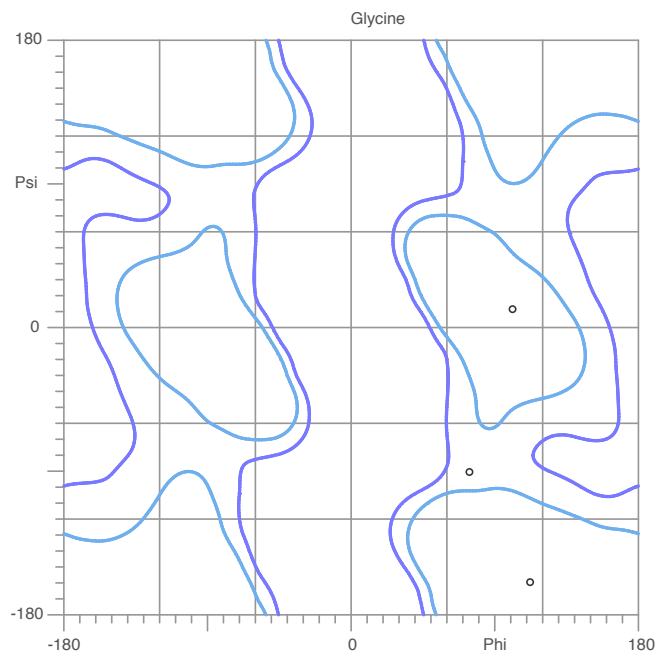
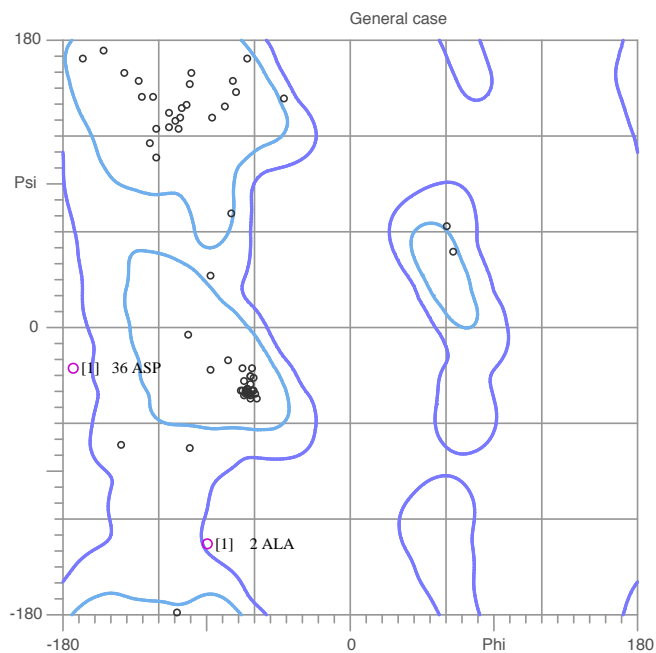
There were 15 outliers (phi, psi):

- [1] 2 ALA (-90.1, -135.0)
- [1] 36 ASP (-175.0, -25.4)
- [5] 12 HIS (-165.0, -105.0)
- [5] 36 ASP (175.1, -45.0)
- [5] 75 ALA (61.8, 178.7)

- [8] 9 ASP (65.1, 105.0)
- [11] 9 ASP (65.0, 100.3)
- [12] 36 ASP (-175.0, -25.0)
- [13] 9 ASP (60.0, 168.8)
- [14] 75 ALA (62.4, 170.3)
- [15] 9 ASP (64.8, 104.9)
- [15] 36 ASP (177.0, -44.9)
- [18] 9 ASP (62.0, 141.8)
- [19] 10 ASP (59.7, 164.8)
- [20] 10 ASP (81.3, 105.0)

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 1



89.5% (68/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

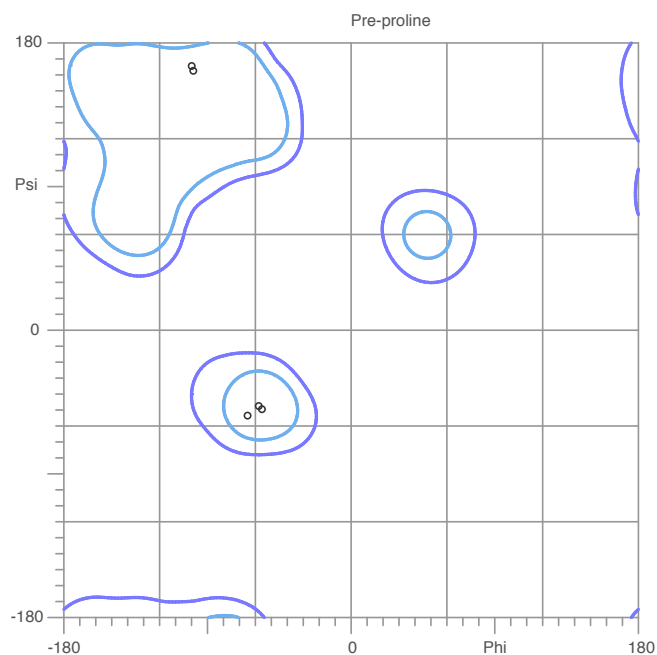
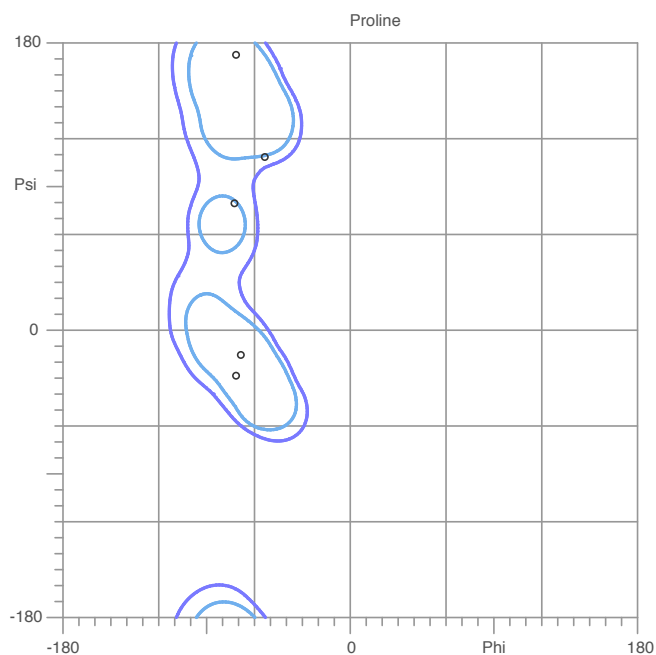
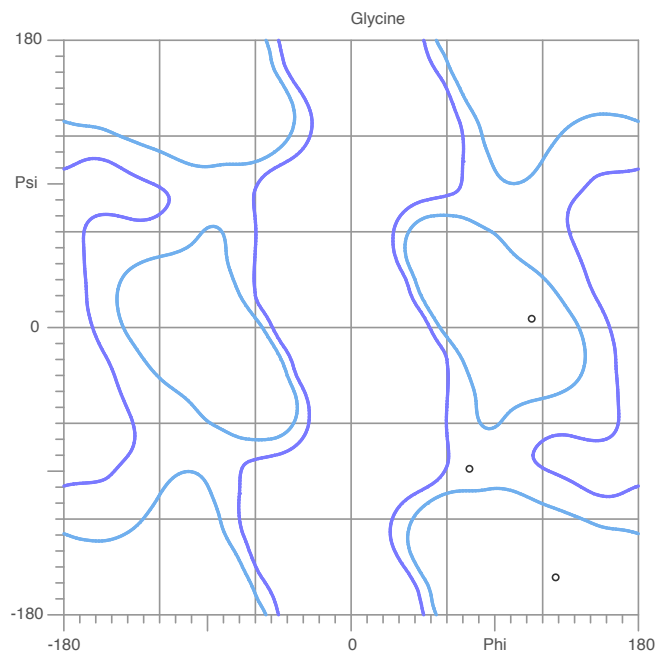
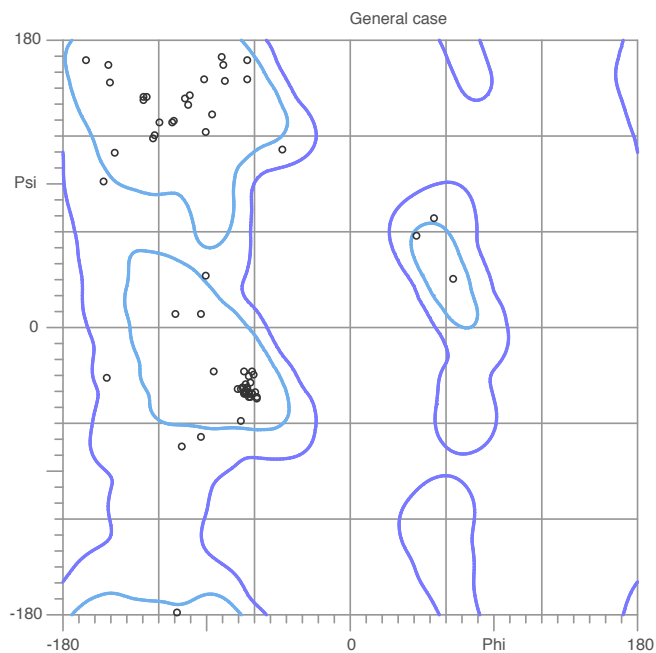
There were 2 outliers (phi, psi):

[1] 2 ALA (-90.1, -135.0)

[1] 36 ASP (-175.0, -25.4)

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 2



88.2% (67/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

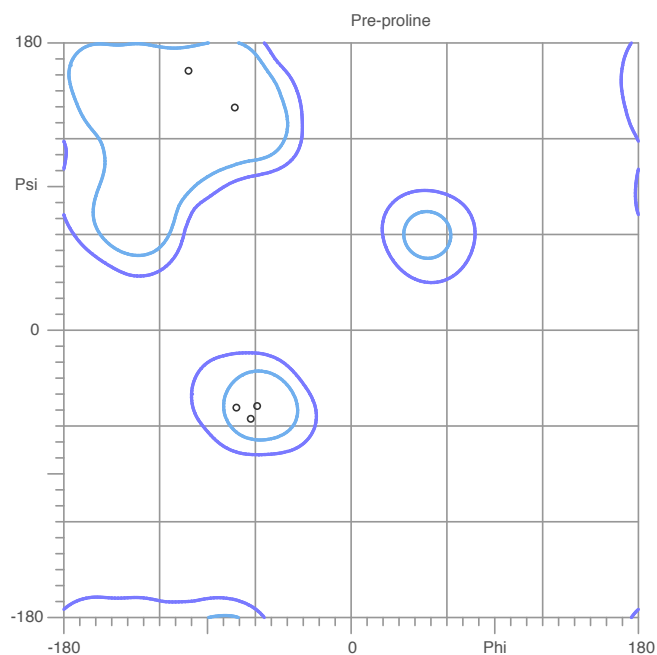
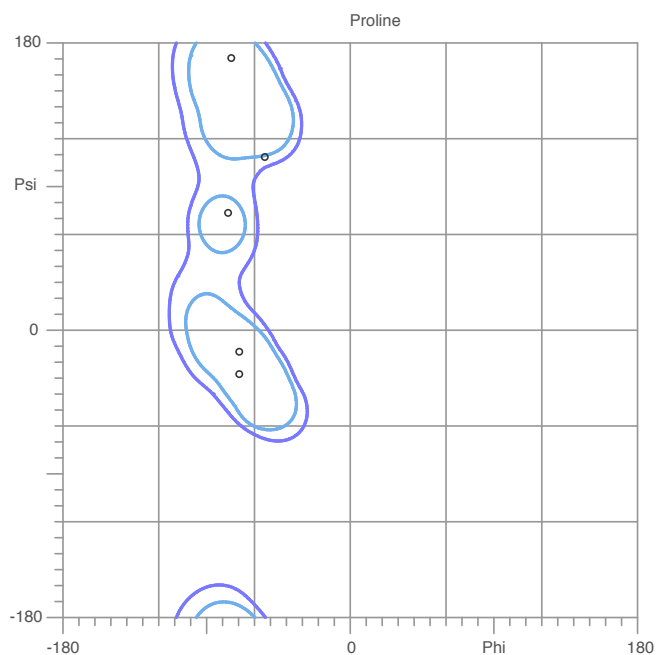
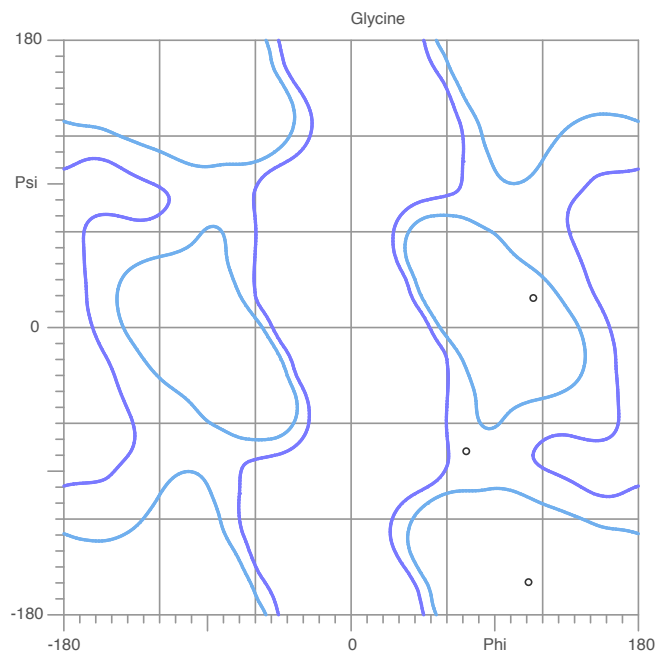
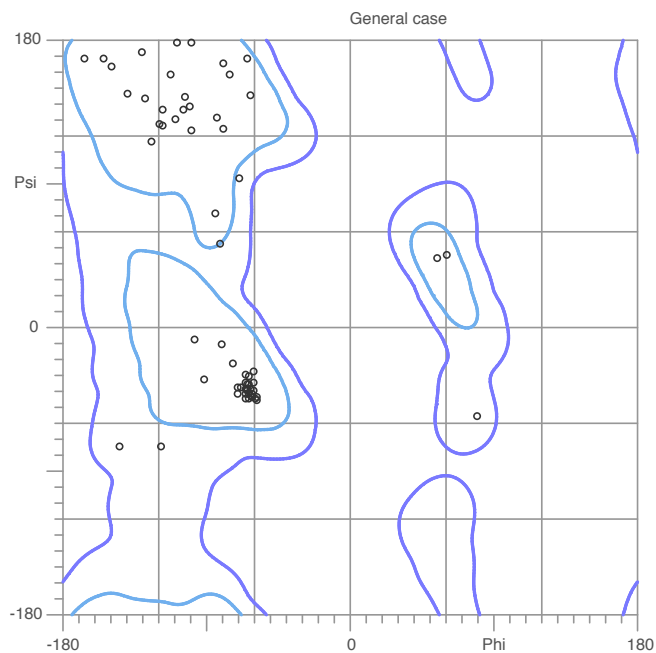
There were no outliers.

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

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

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 3



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.

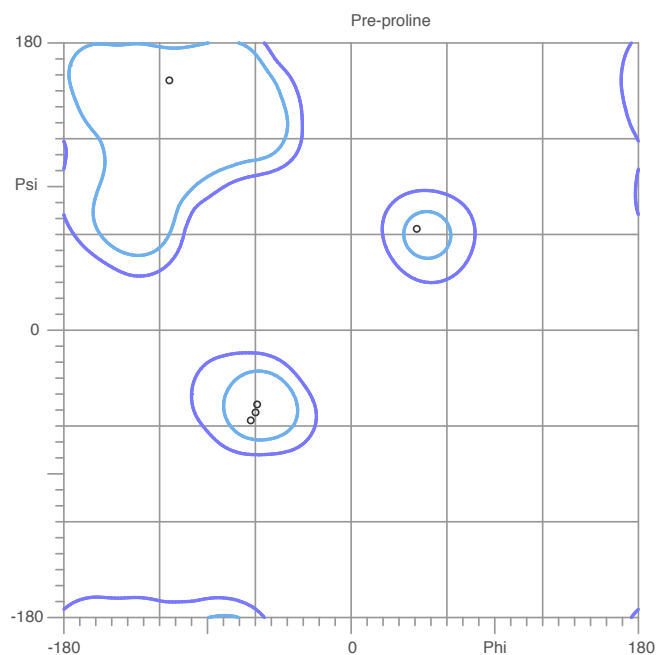
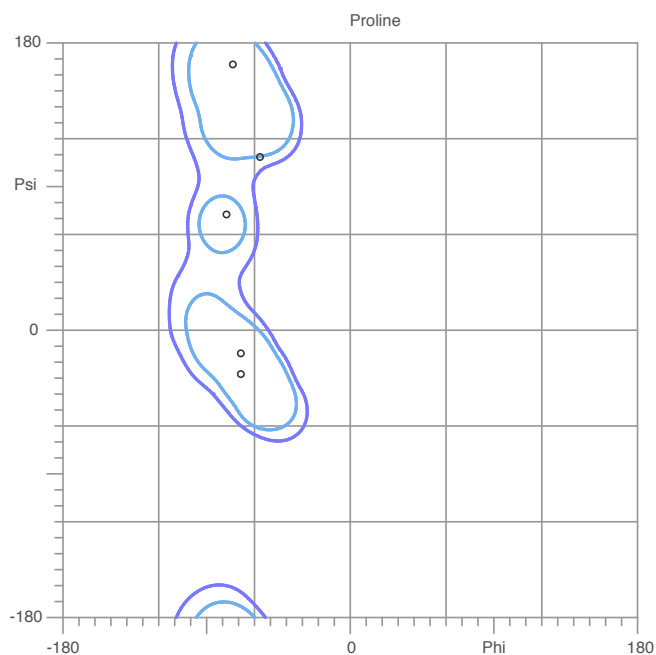
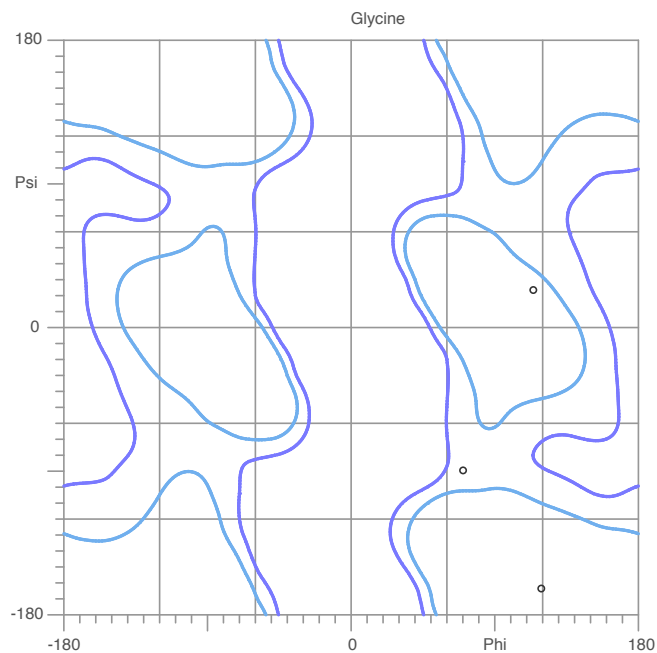
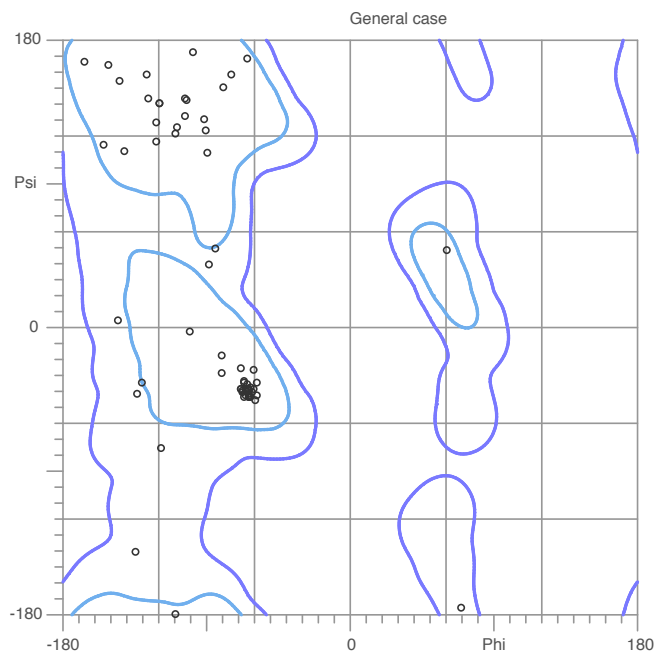
There were no outliers.

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

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

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 4



89.5% (68/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

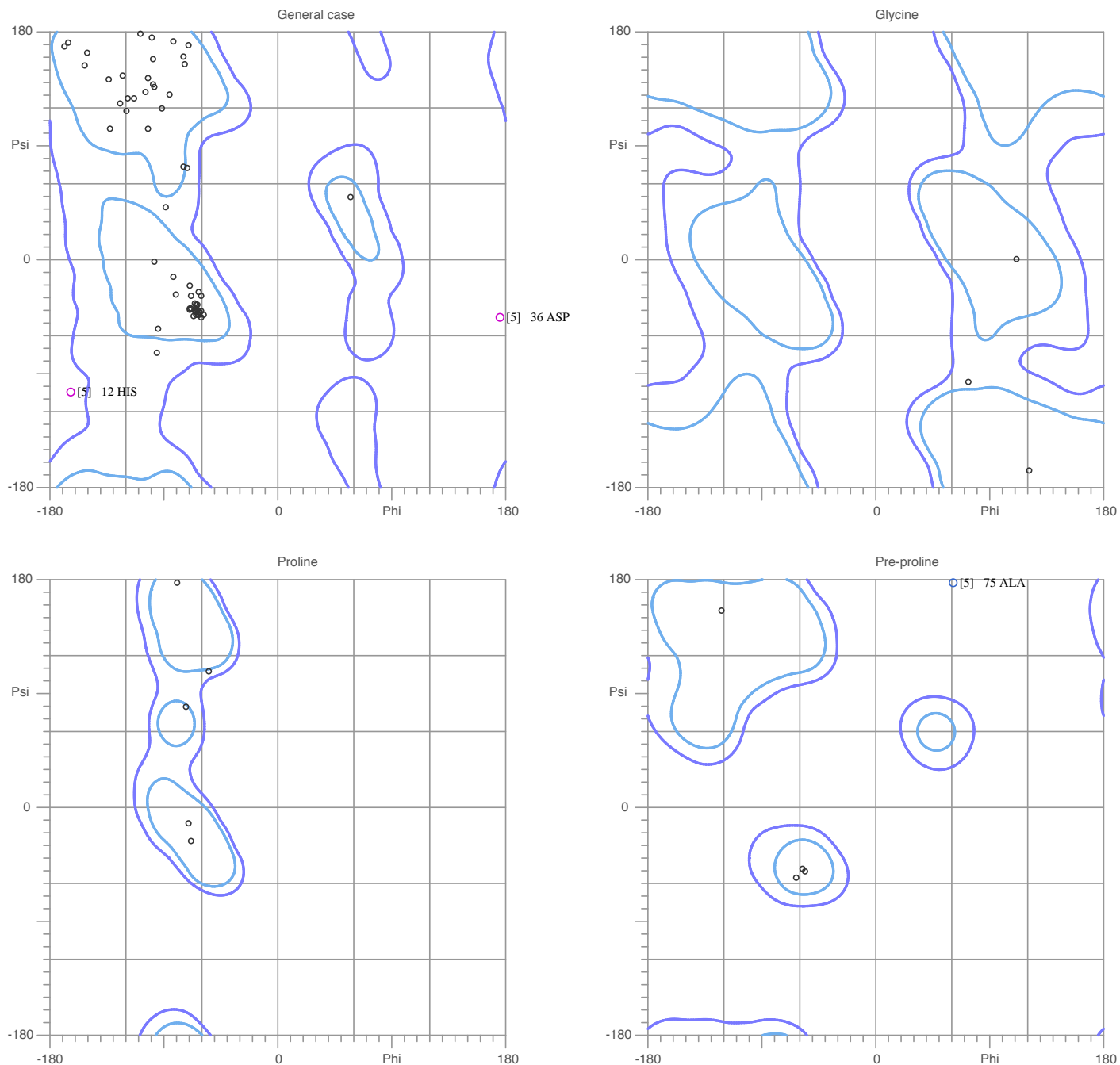
There were no outliers.

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

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

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 5



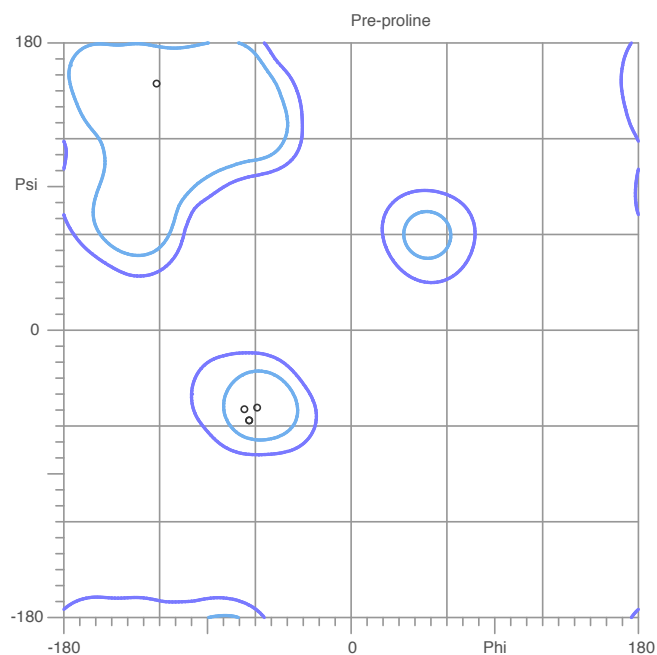
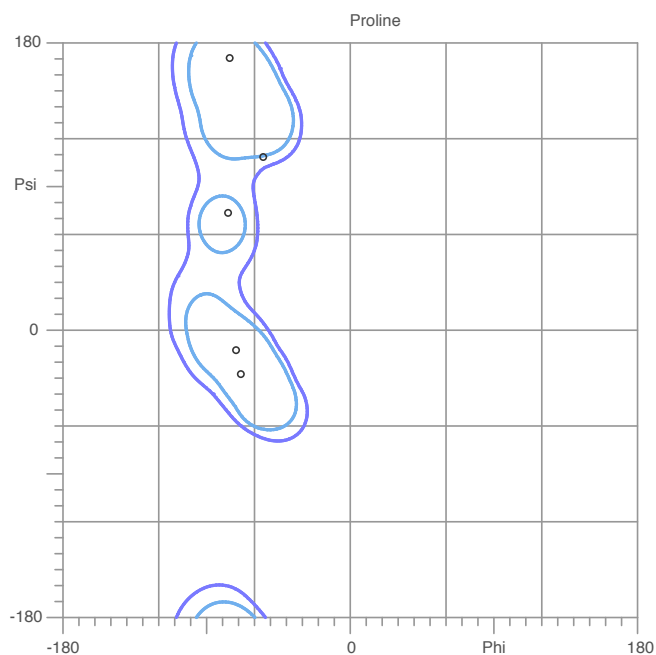
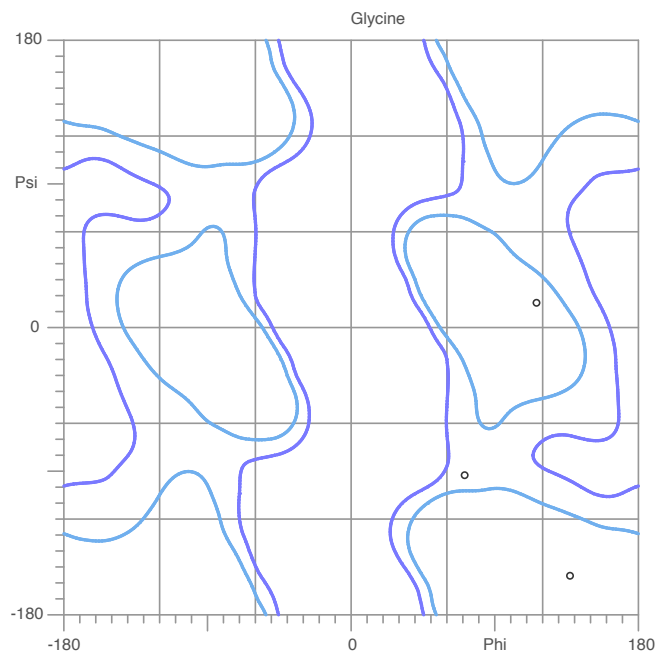
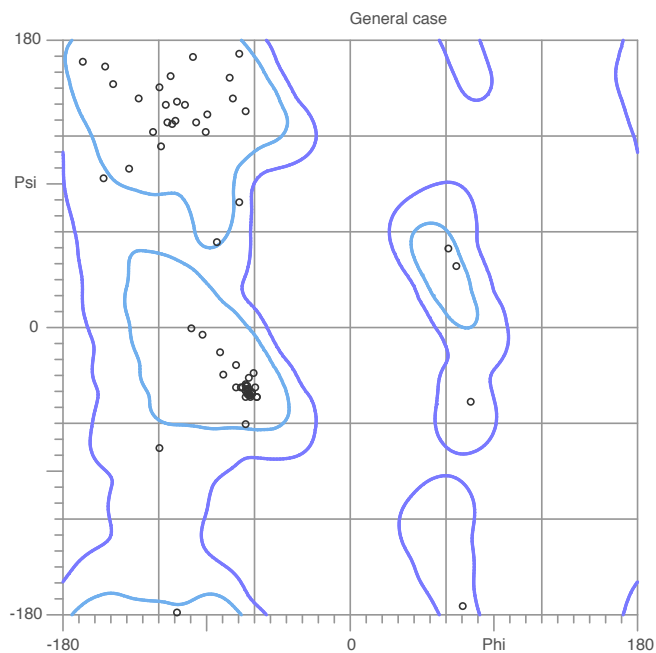
89.5% (68/76) of all residues were in favored (98%) regions.
96.1% (73/76) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [5] 12 HIS (-165.0, -105.0)
- [5] 36 ASP (175.1, -45.0)
- [5] 75 ALA (61.8, 178.7)

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 6



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.

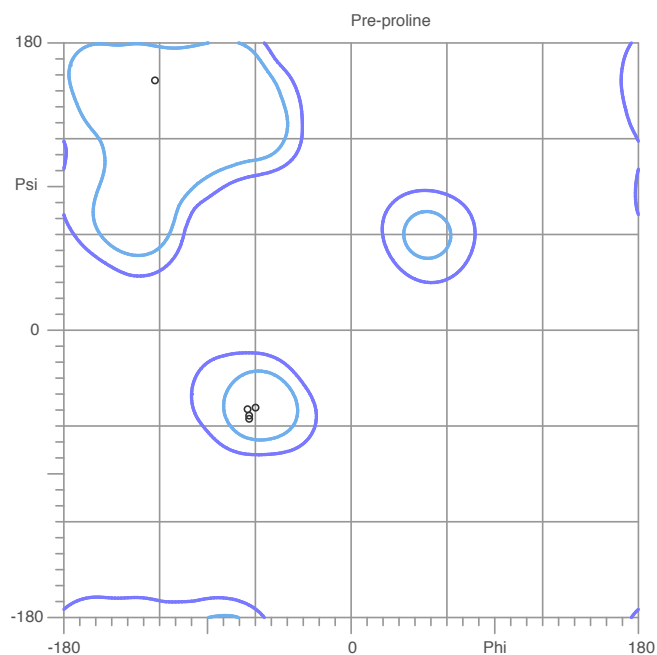
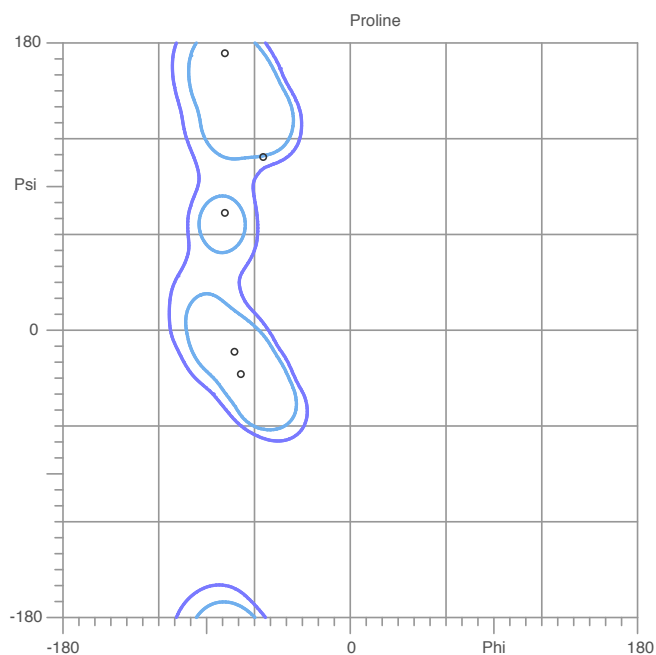
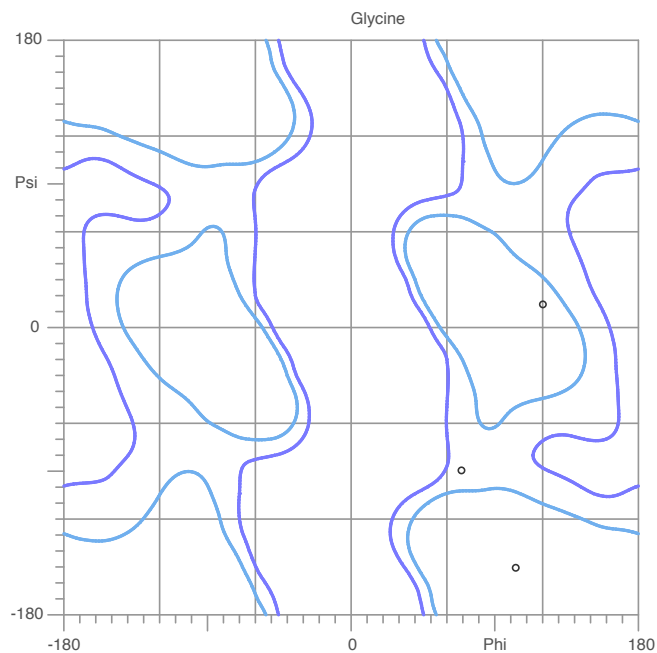
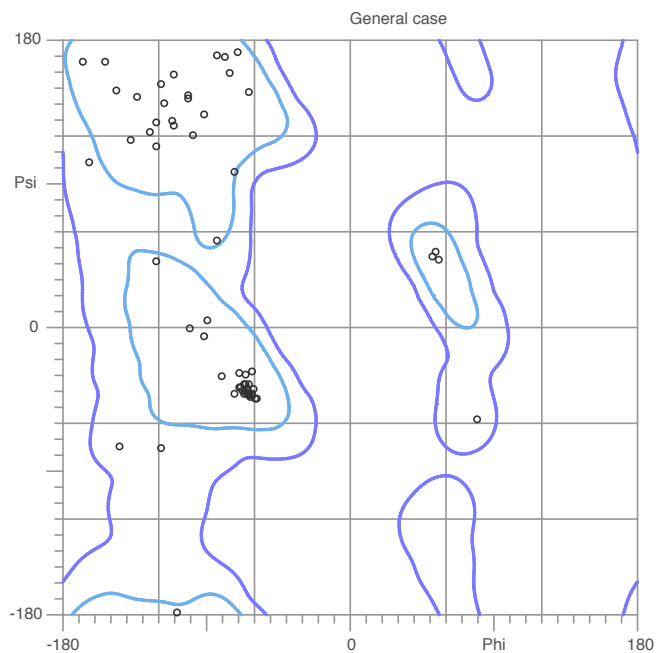
There were no outliers.

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MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 7



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.

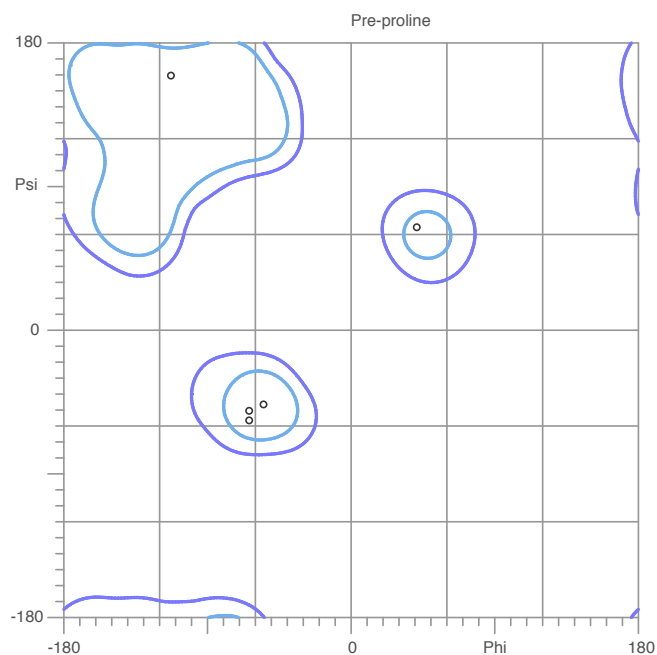
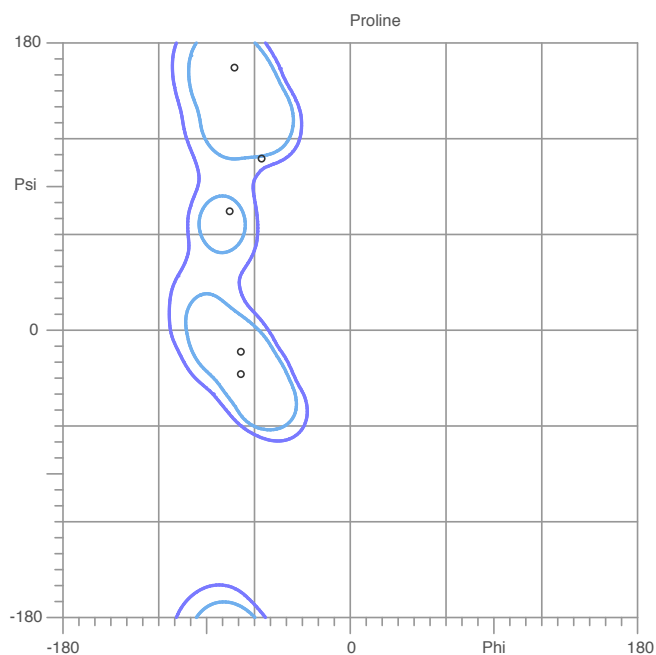
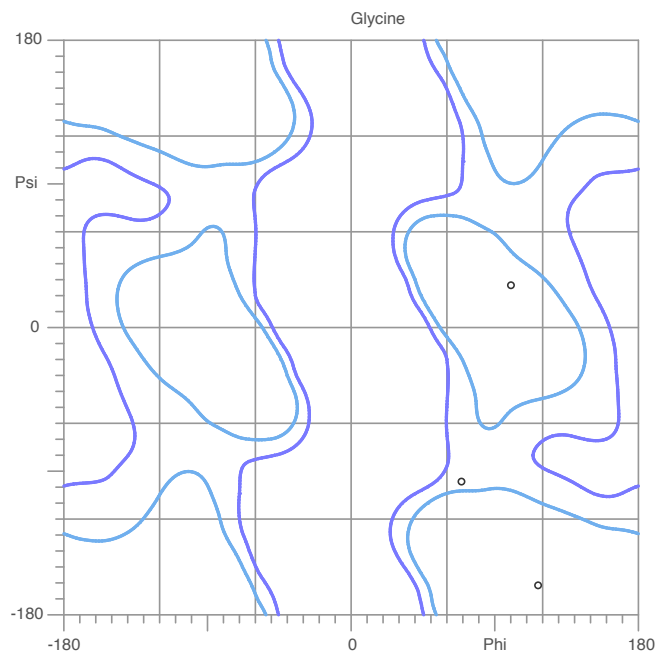
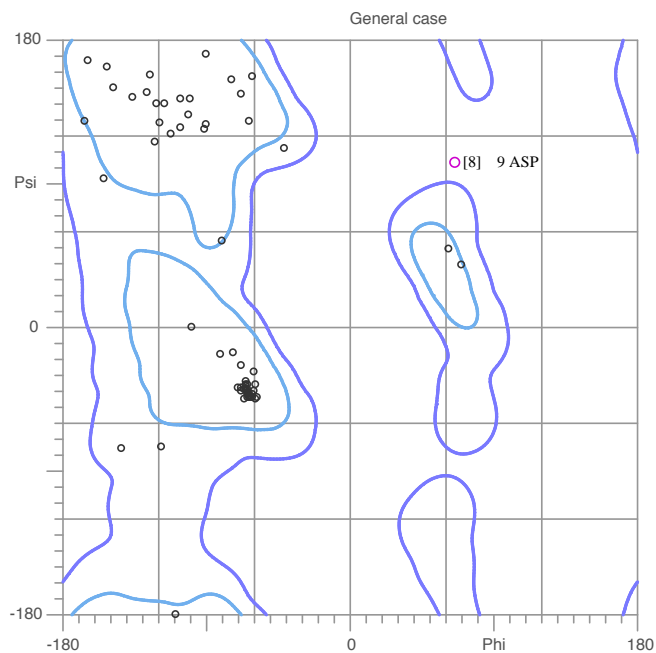
There were no outliers.

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

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MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 8

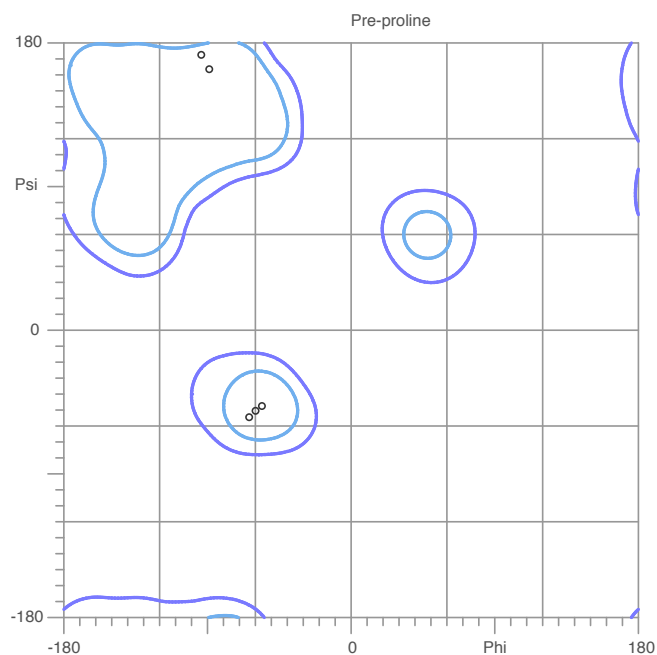
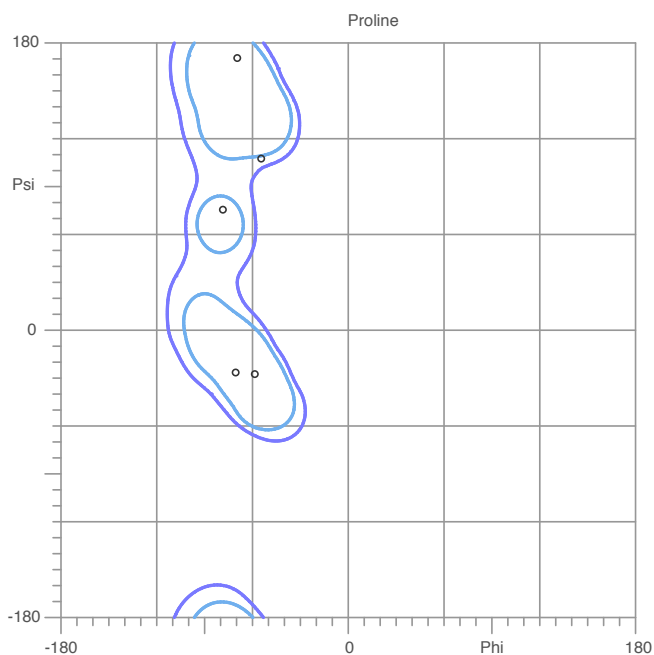
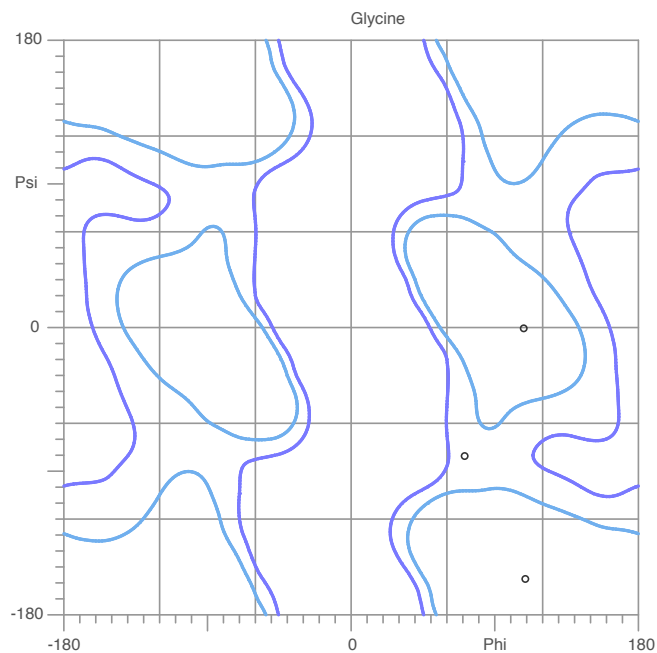
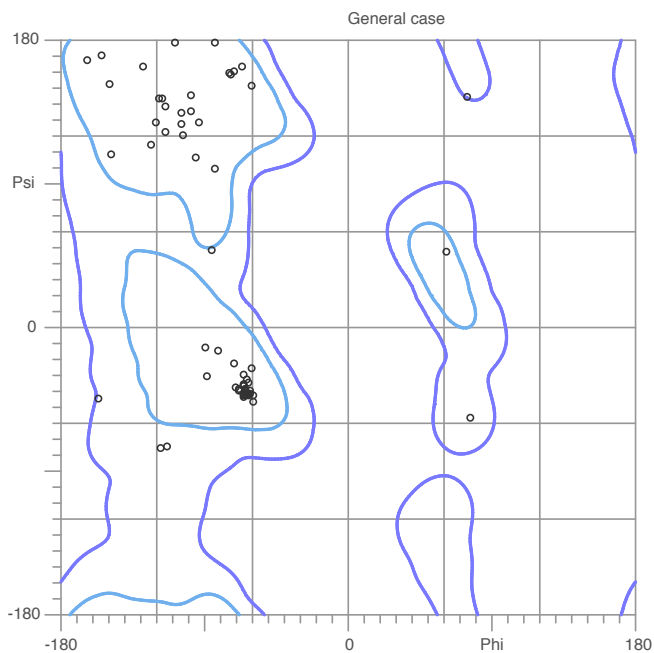


89.5% (68/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 9 ASP (65.1, 105.0)

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 9



89.5% (68/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

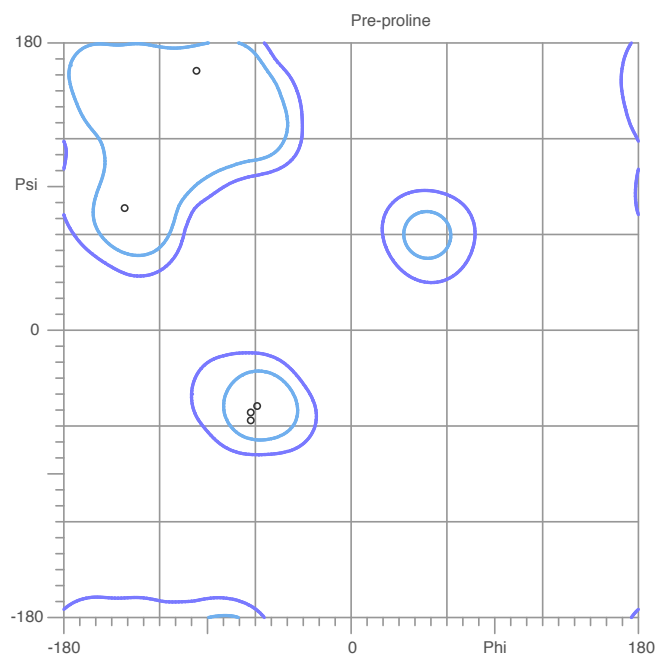
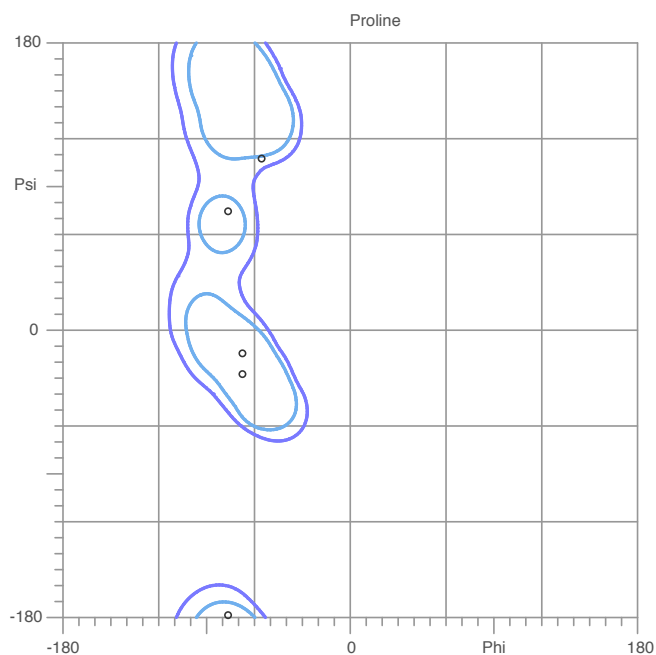
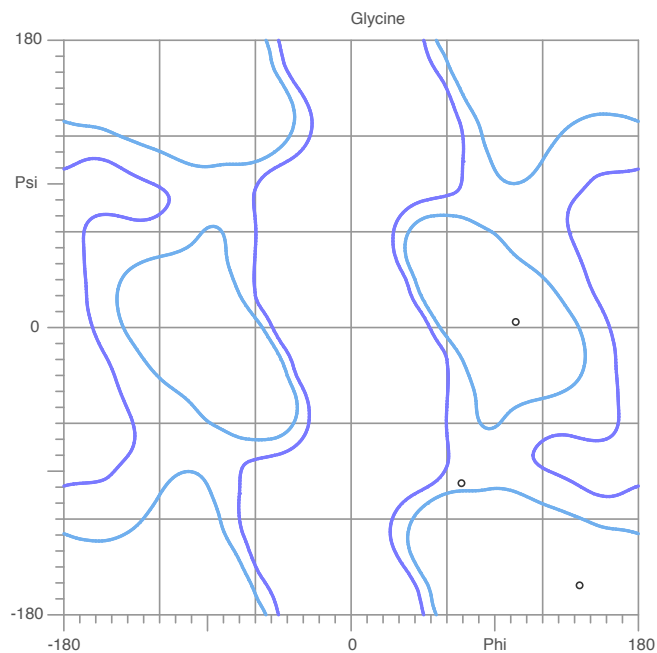
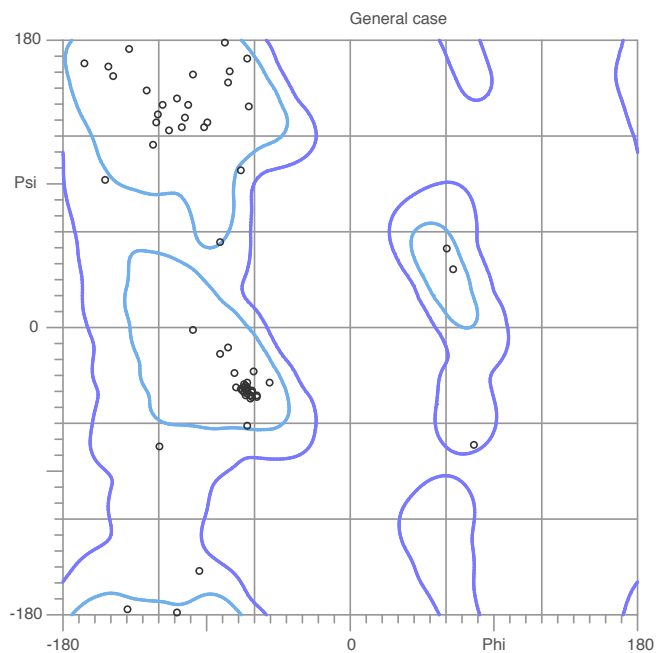
There were no outliers.

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MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 10



90.8% (69/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

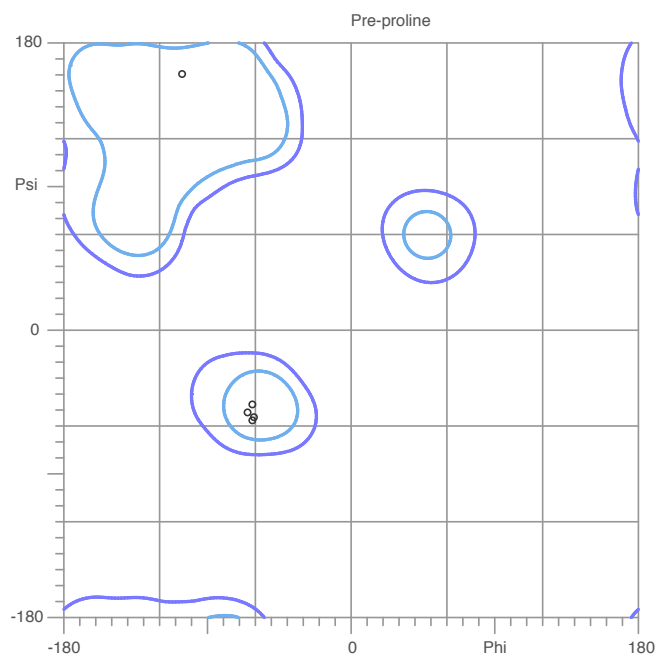
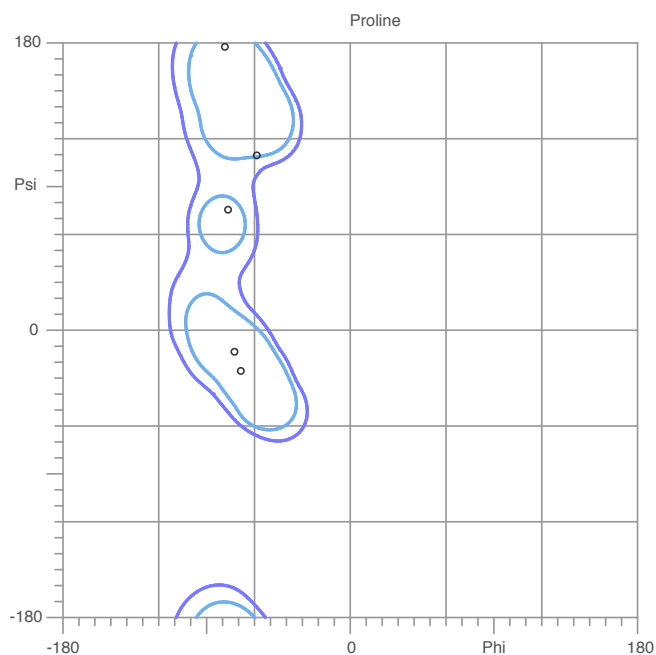
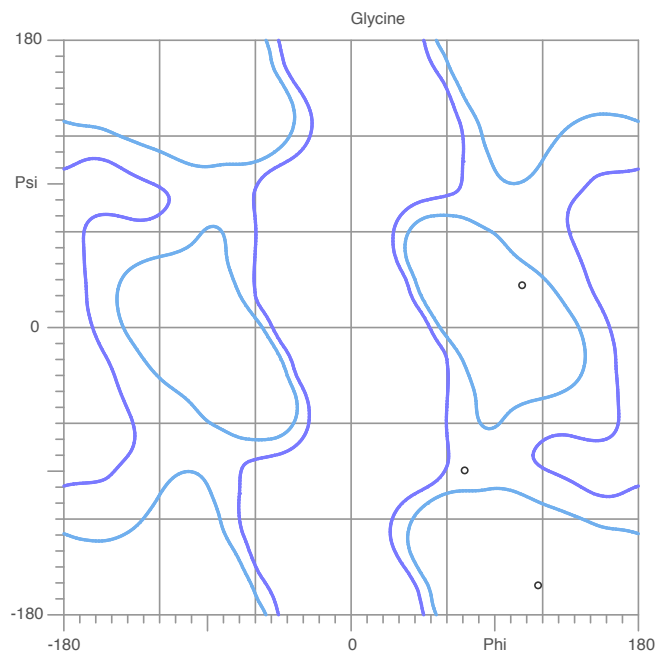
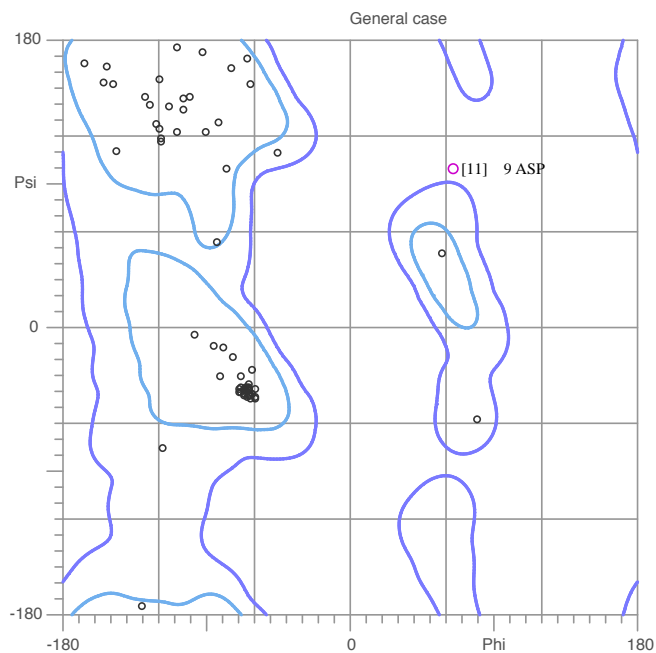
There were no outliers.

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

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

MolProbity Ramachandran analysis

XCR50_R3Cons_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.

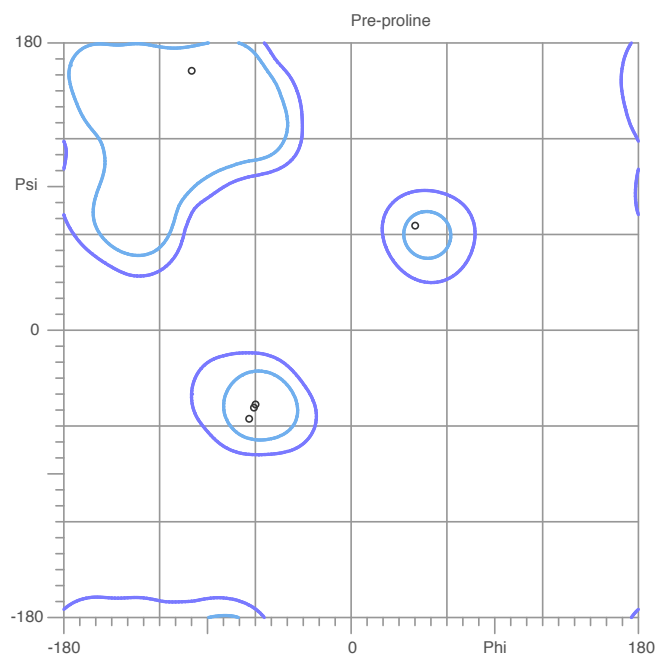
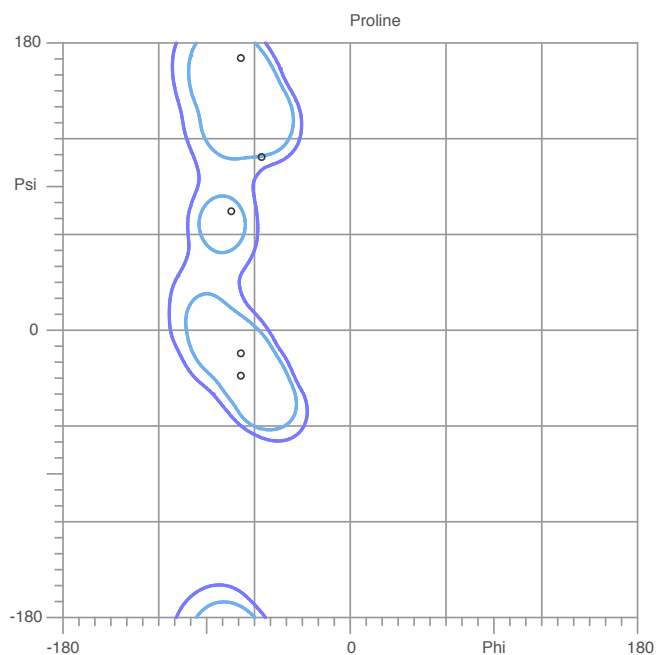
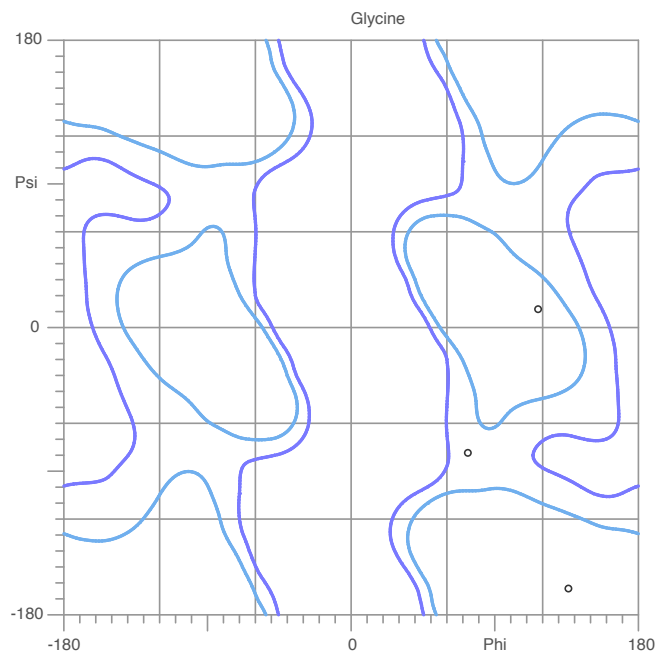
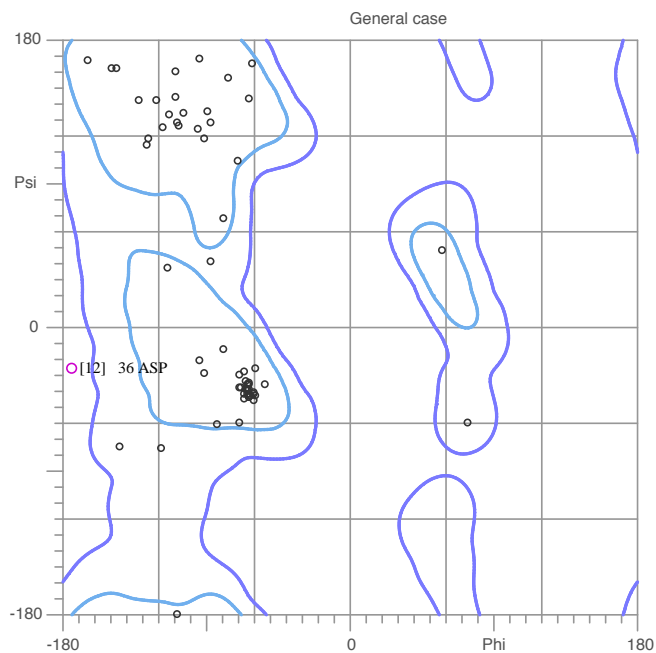
There were 1 outliers (phi, psi):
[11] 9 ASP (65.0, 100.3)

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

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

MolProbity Ramachandran analysis

XCR50_R3Cons_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.

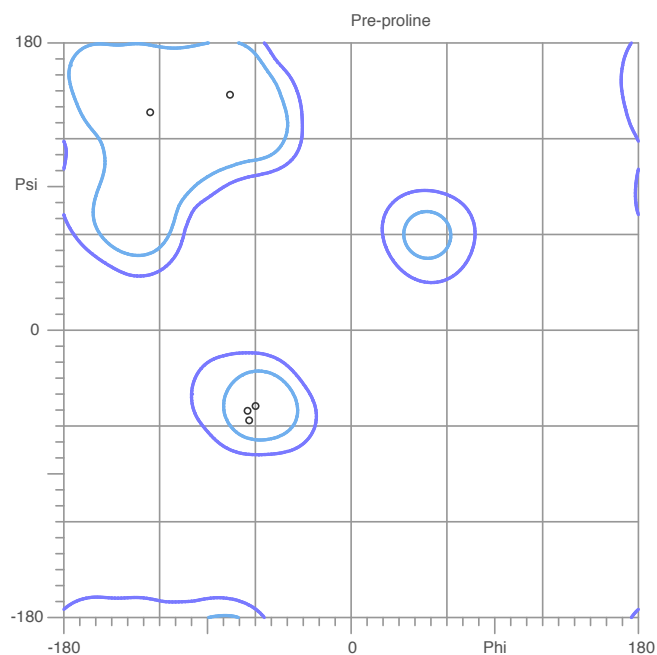
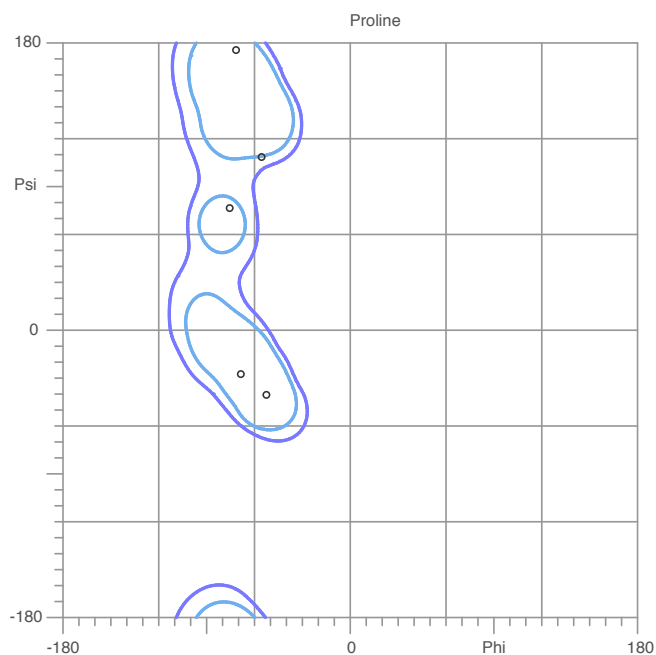
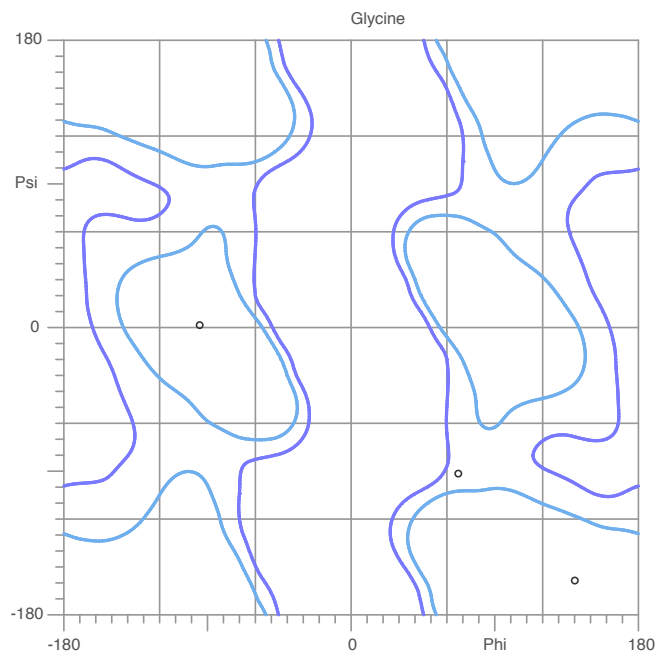
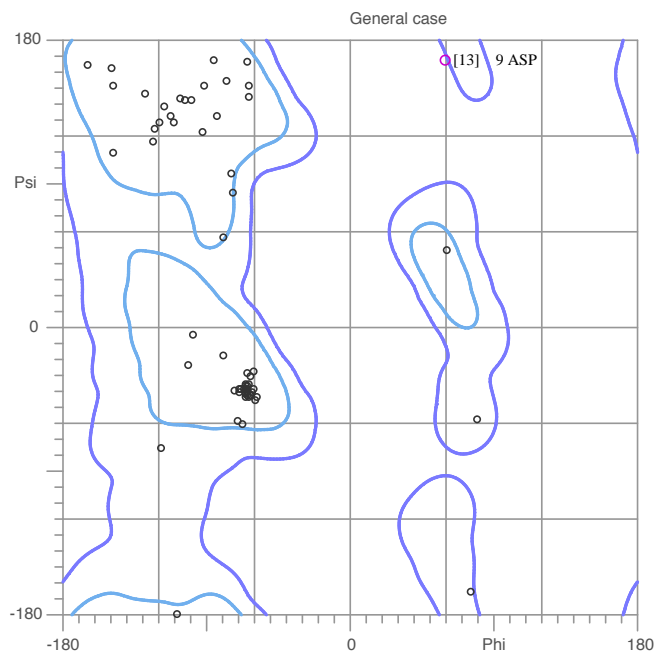
There were 1 outliers (phi, psi):
[12] 36 ASP (-175.0, -25.0)

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

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

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 13



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.

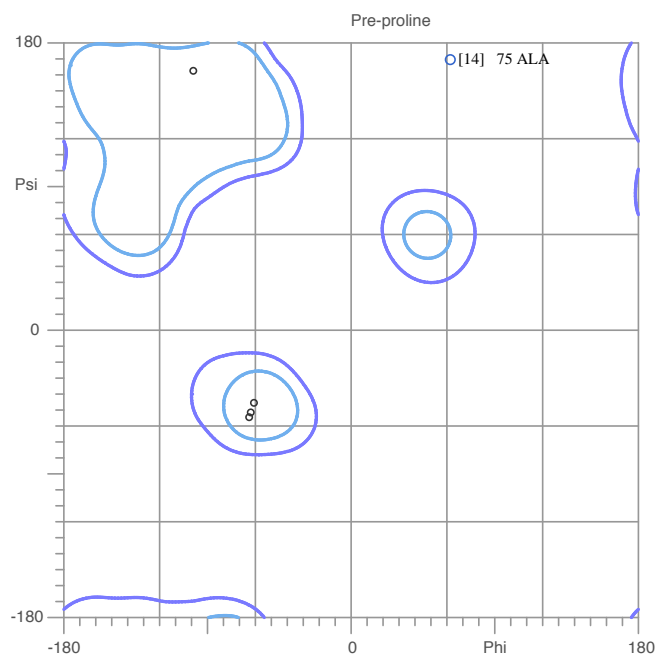
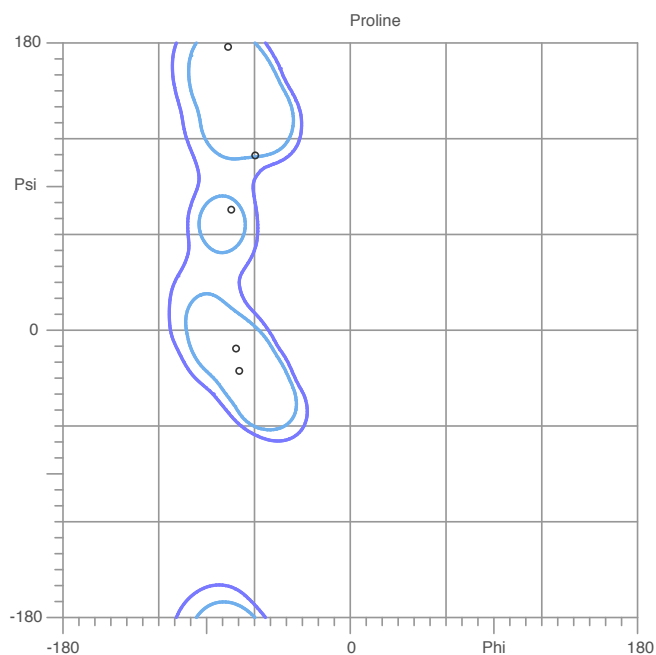
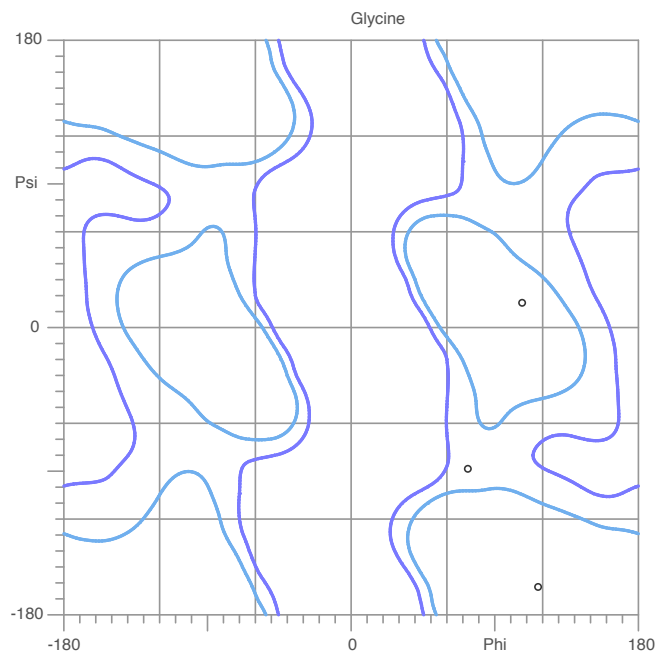
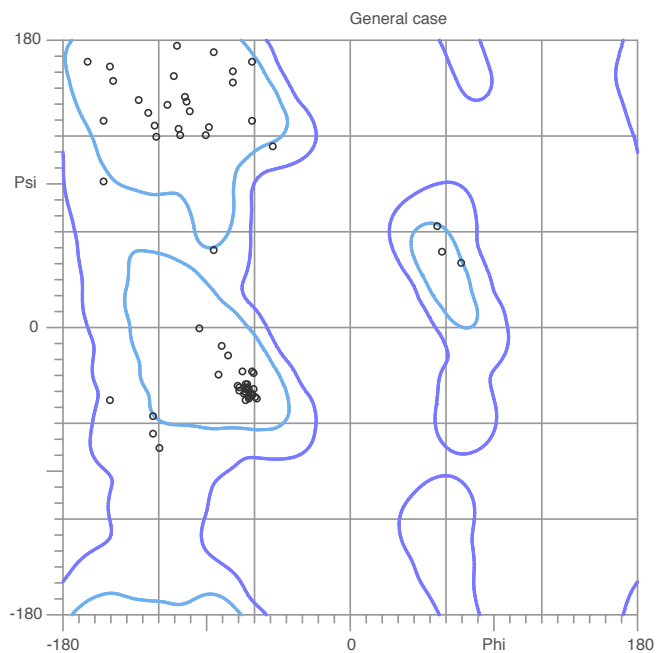
There were 1 outliers (phi, psi):
[13] 9 ASP (60.0, 168.8)

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

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

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 14



88.2% (67/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

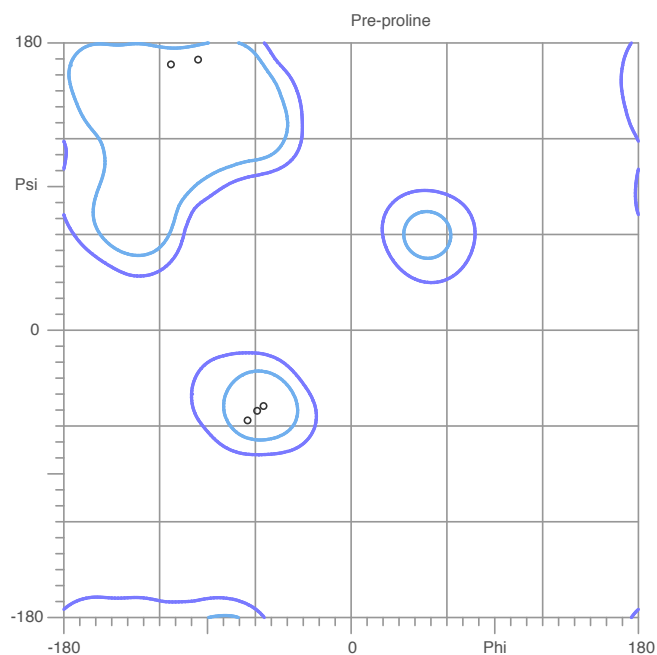
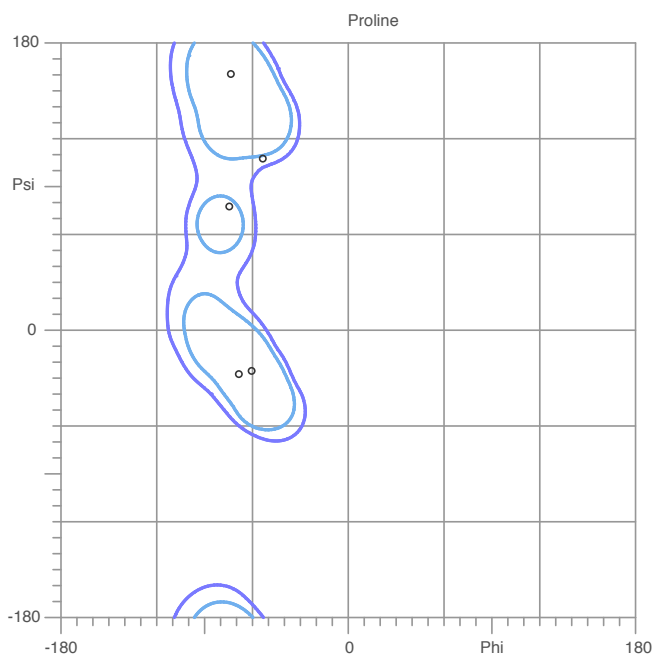
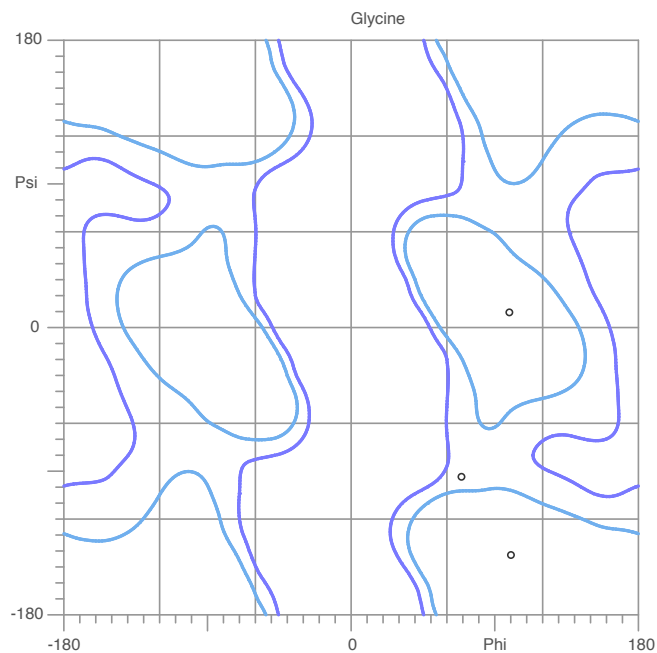
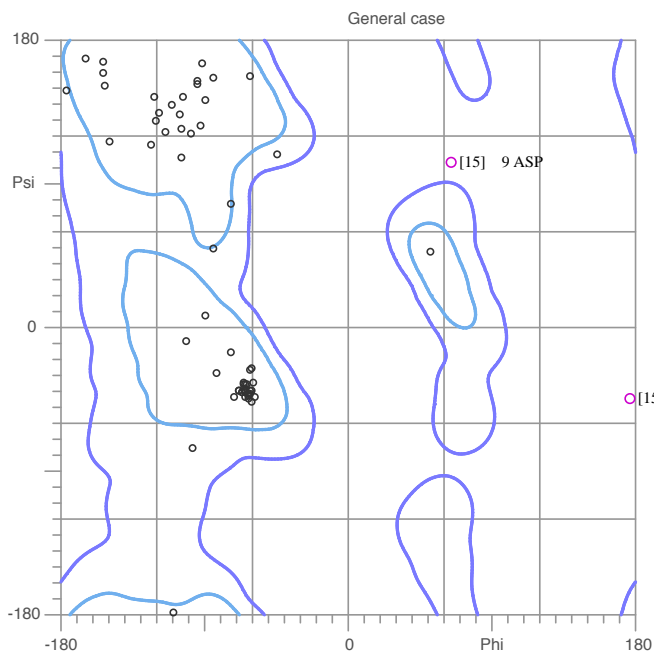
There were 1 outliers (phi, psi):
[14] 75 ALA (62.4, 170.3)

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

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

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 15



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.

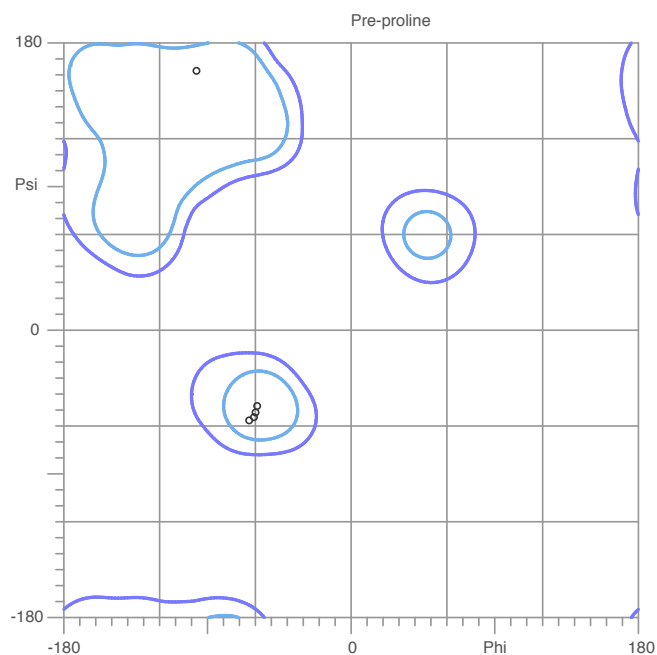
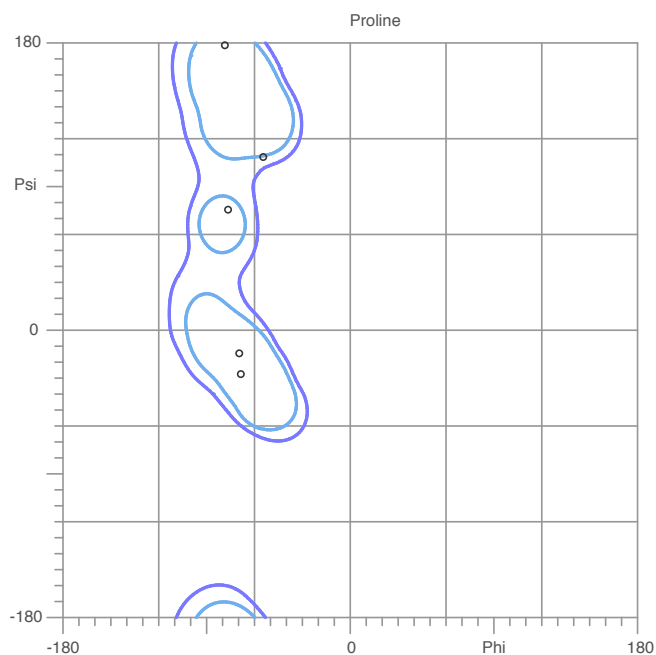
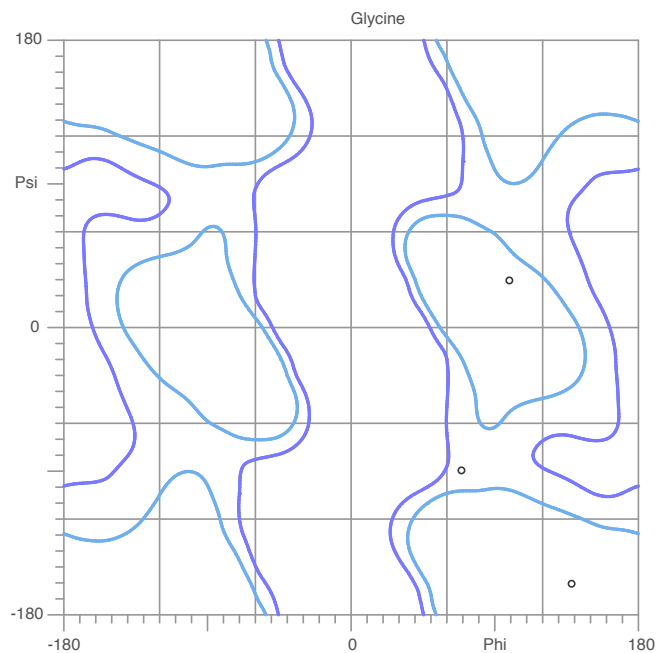
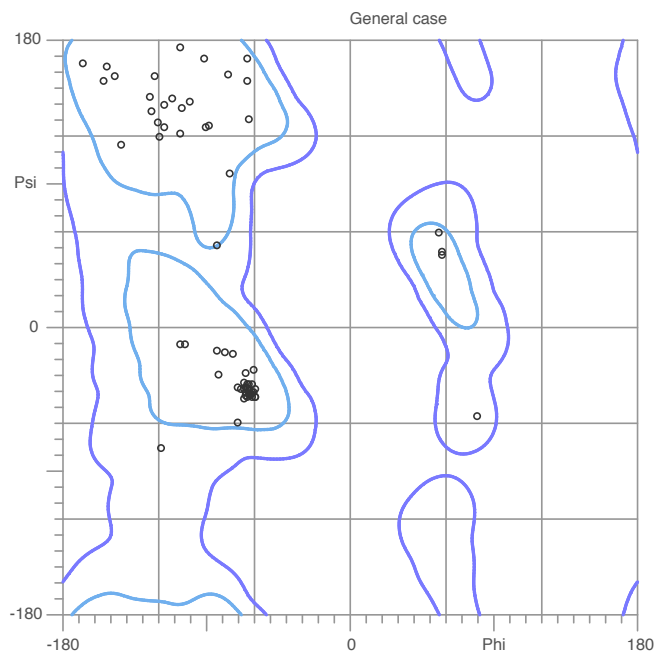
There were 2 outliers (phi, psi):

[15] 9 ASP (64.8, 104.9)

[15] 36 ASP (177.0, -44.9)

MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 16



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.

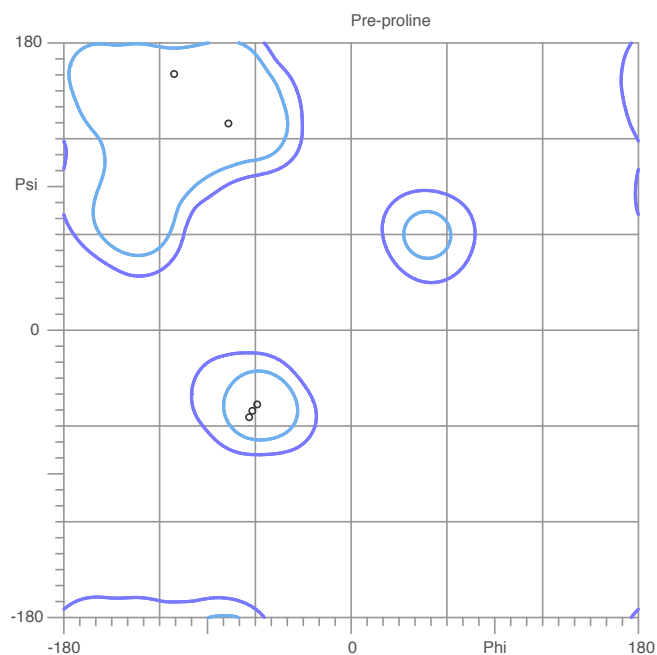
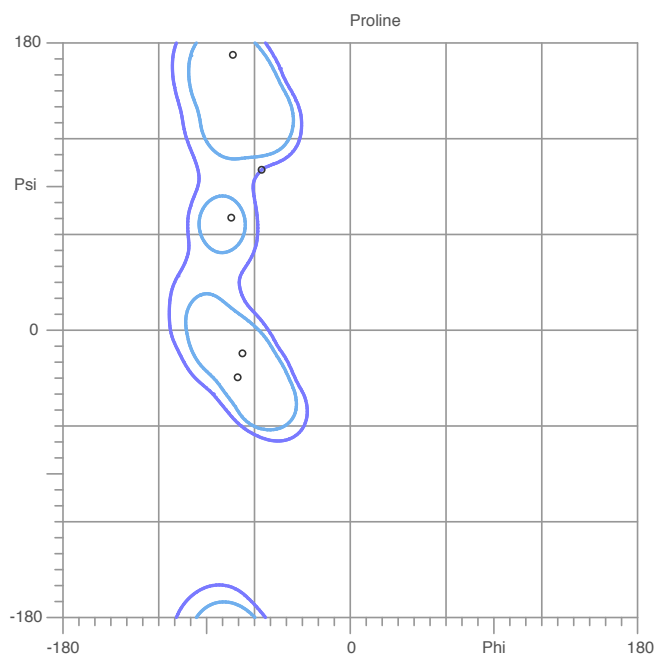
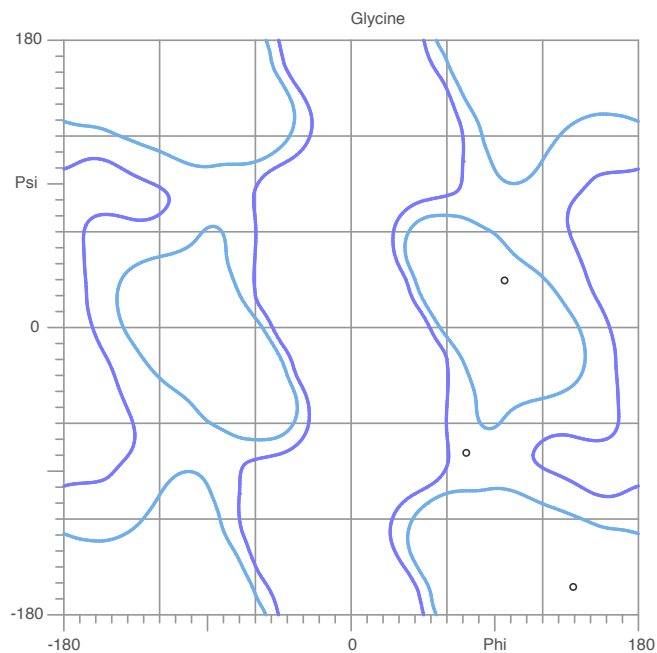
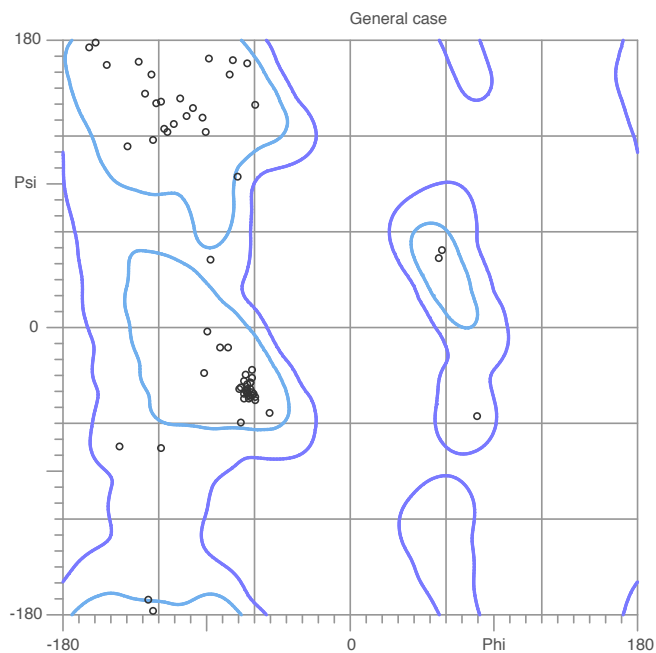
There were no outliers.

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MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 17



89.5% (68/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

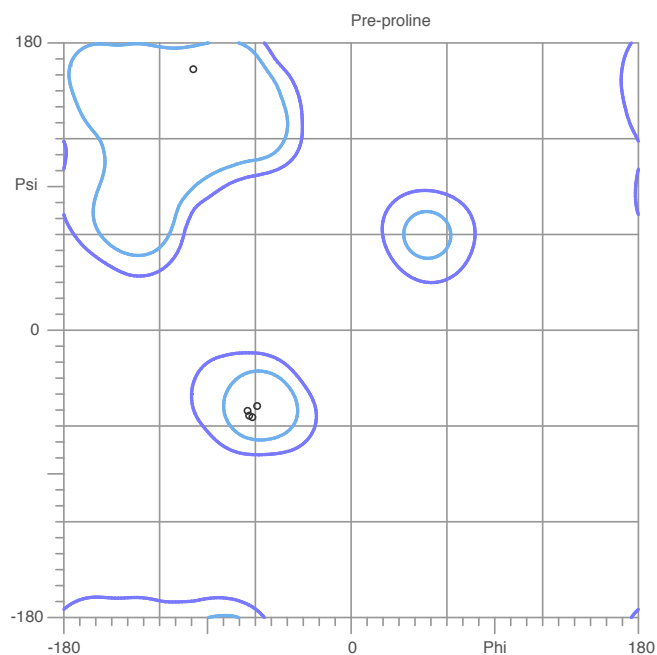
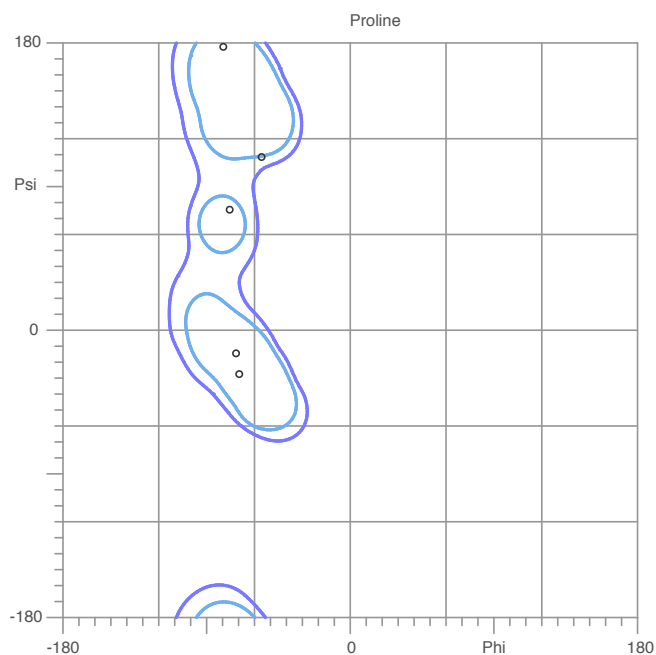
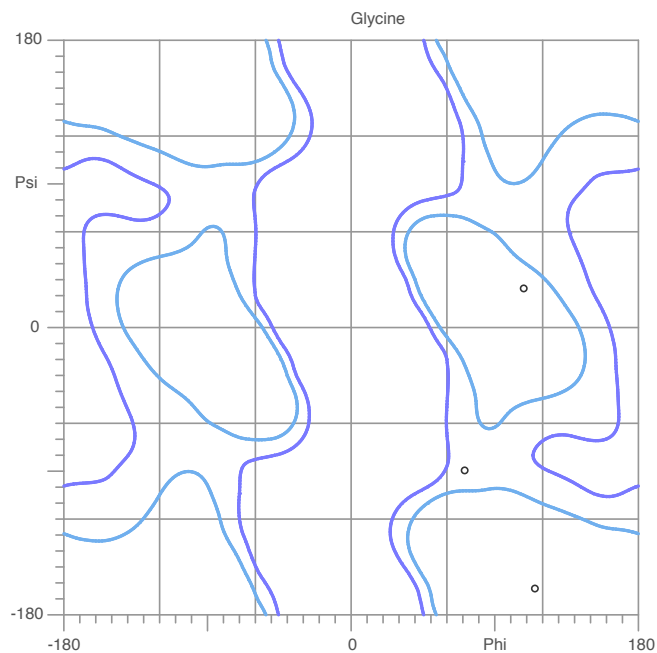
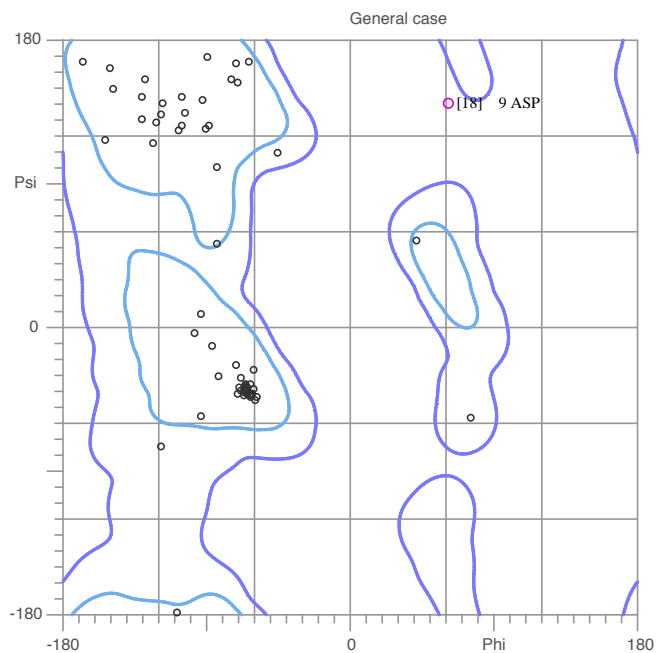
There were no outliers.

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MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 18



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.

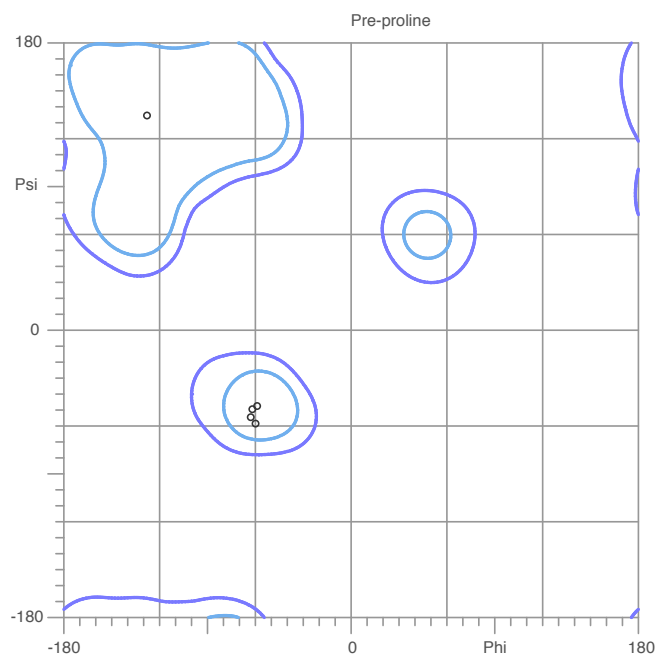
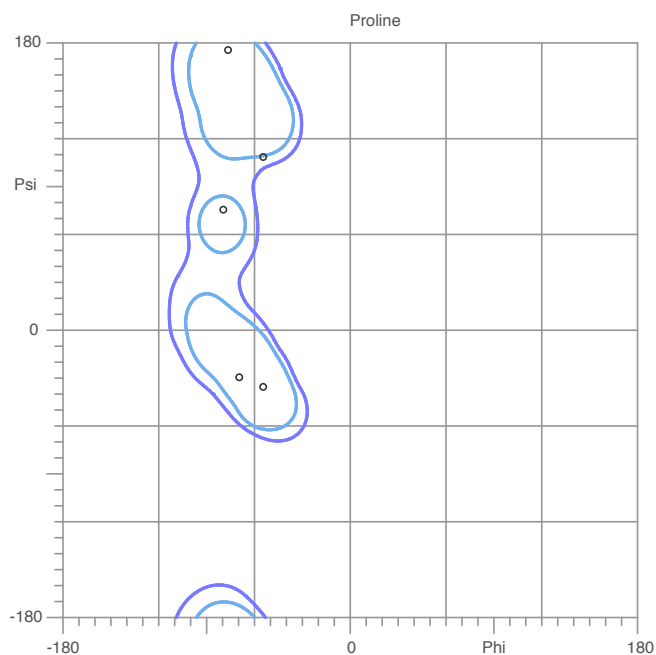
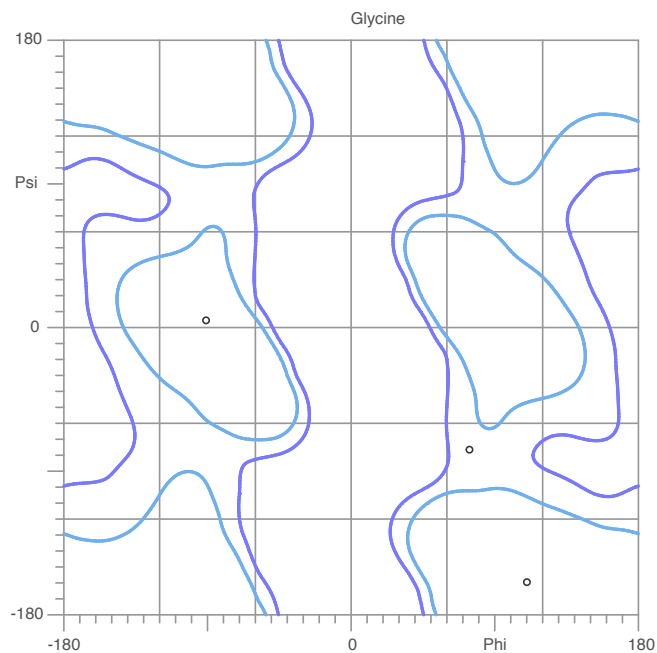
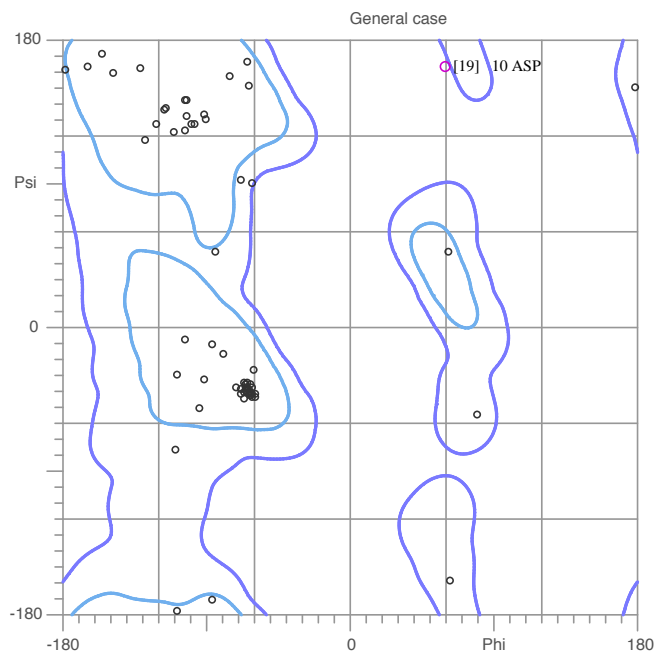
There were 1 outliers (phi, psi):
[18] 9 ASP (62.0, 141.8)

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MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 19



86.8% (66/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

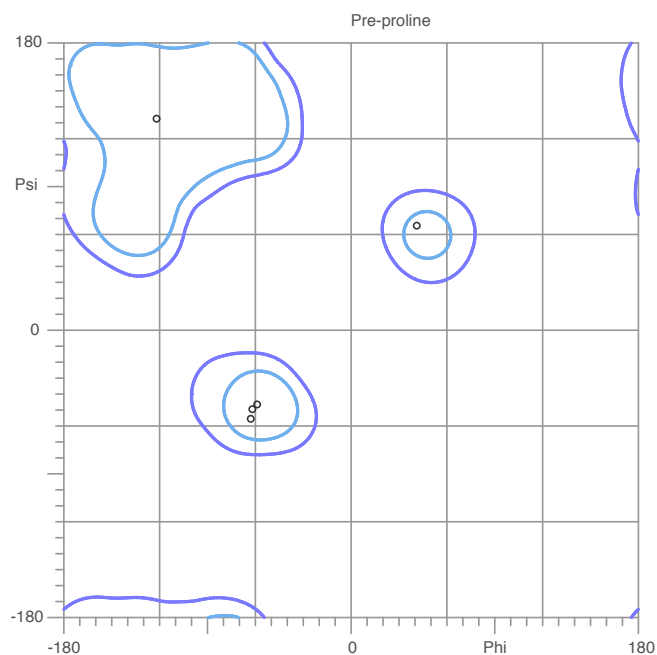
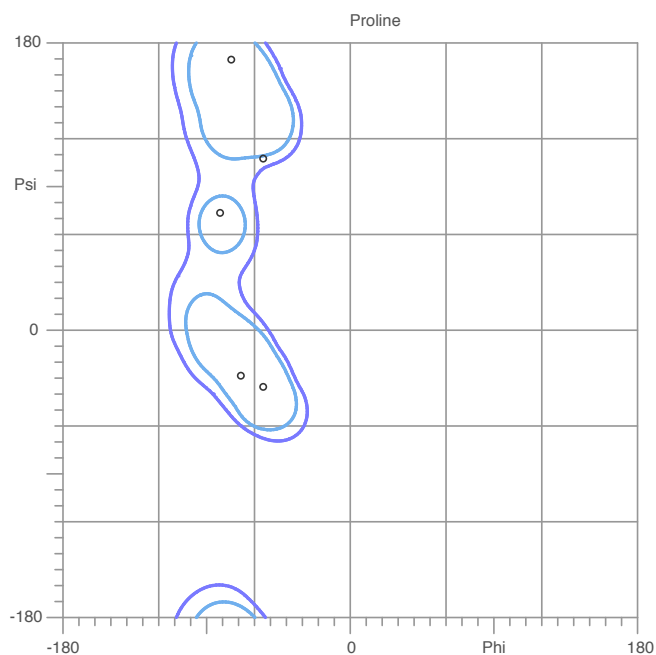
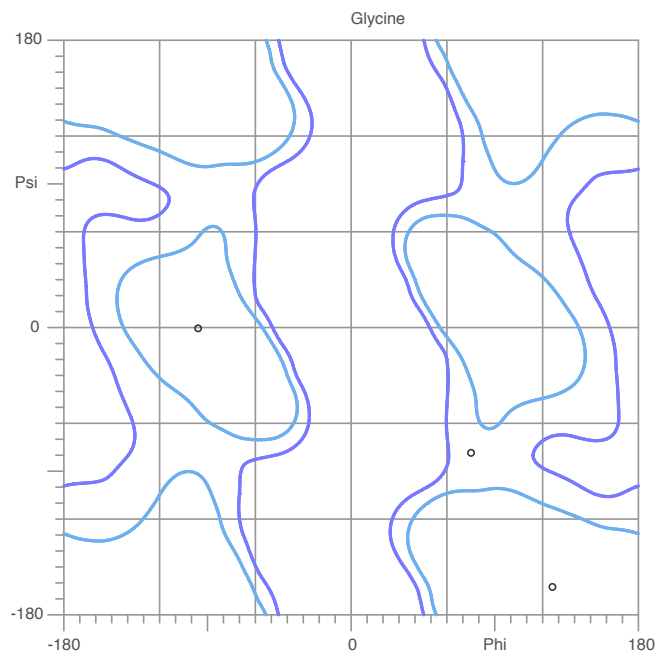
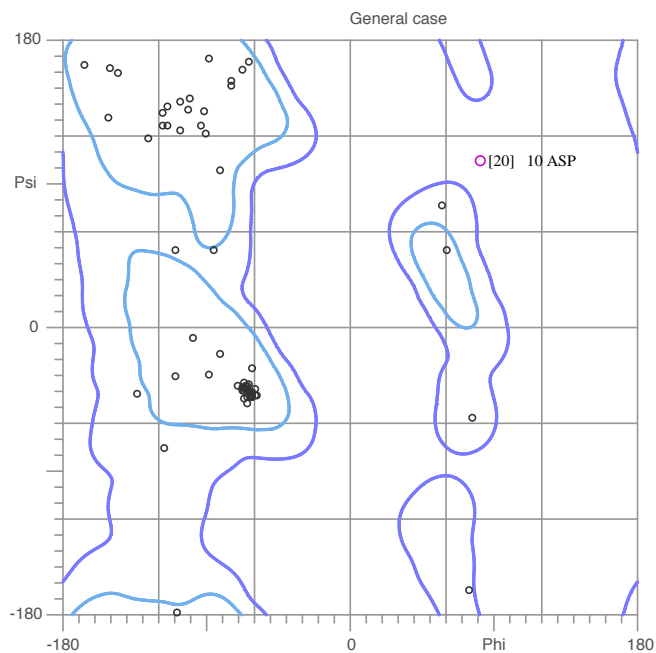
There were 1 outliers (phi, psi):
[19] 10 ASP (59.7, 164.8)

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MolProbity Ramachandran analysis

XCR50_R3Cons_em_bcr3.pdb, model 20



88.2% (67/76) 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):
[20] 10 ASP (81.3, 105.0)

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