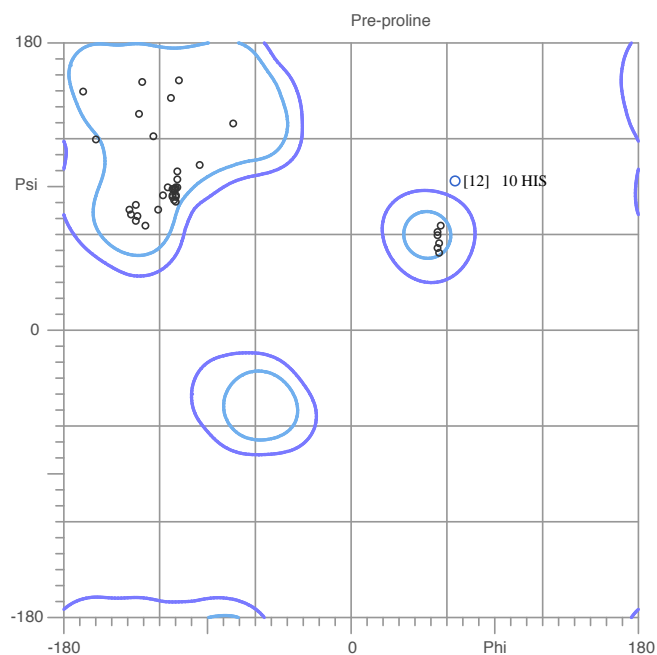
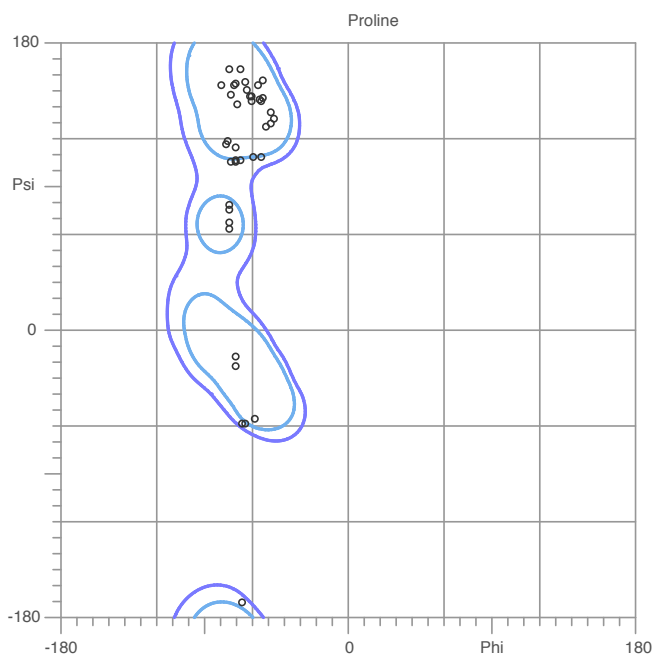
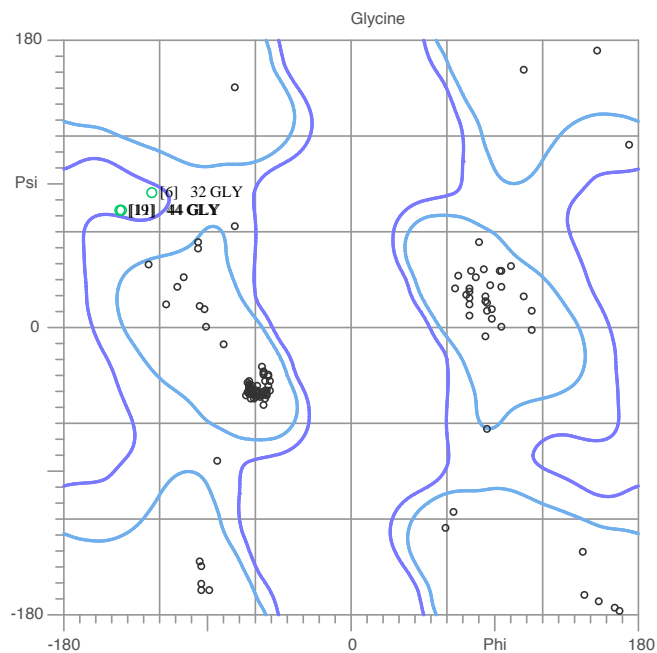
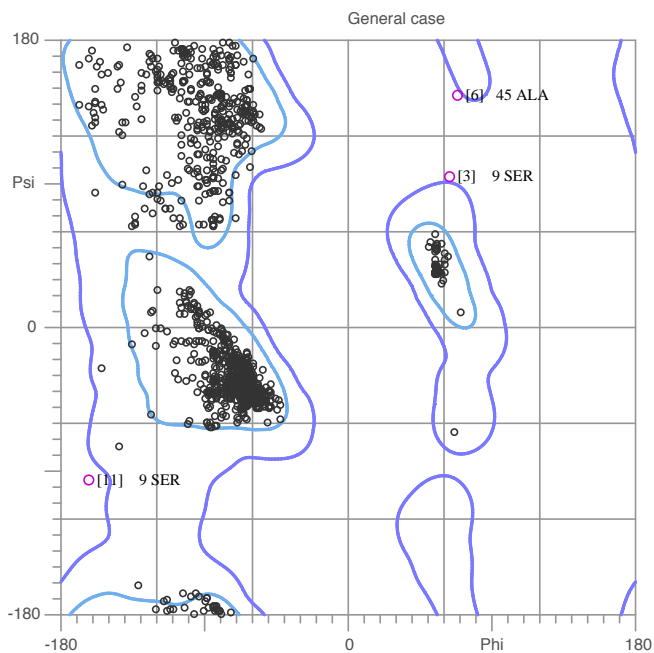


# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, all models



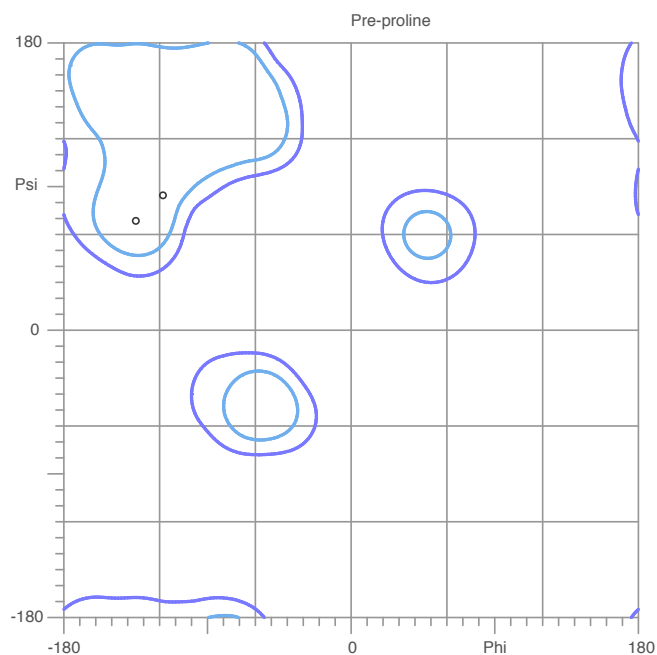
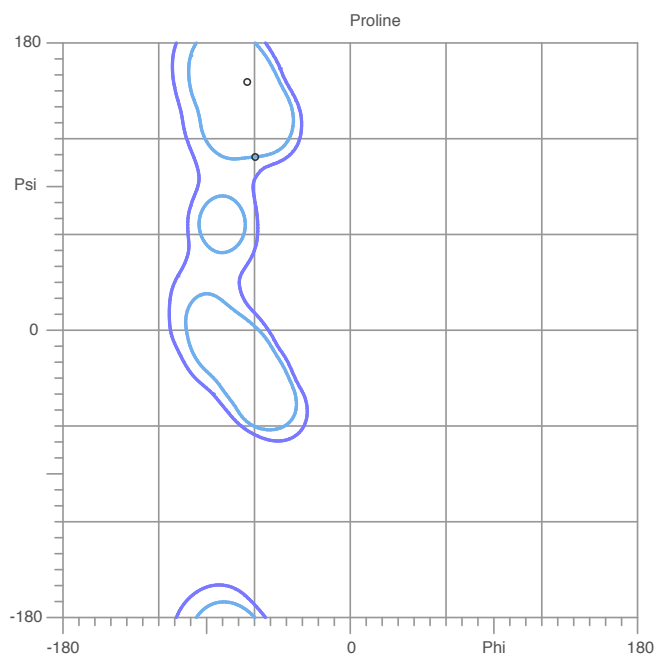
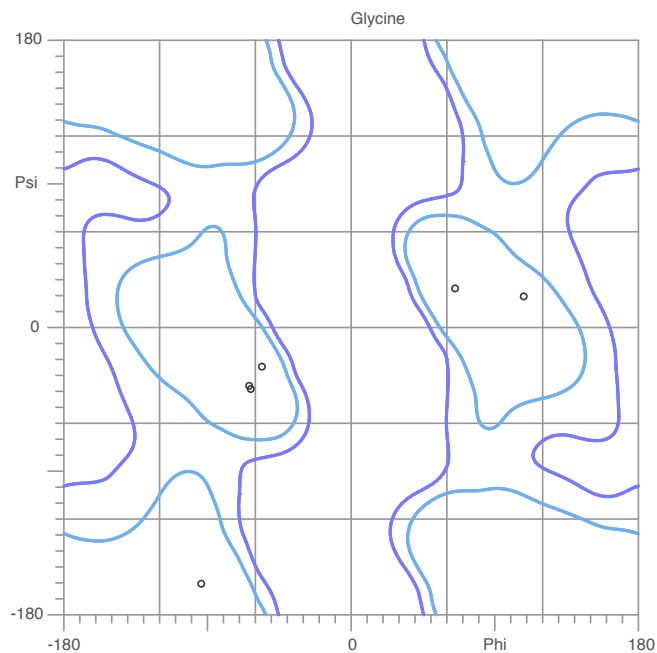
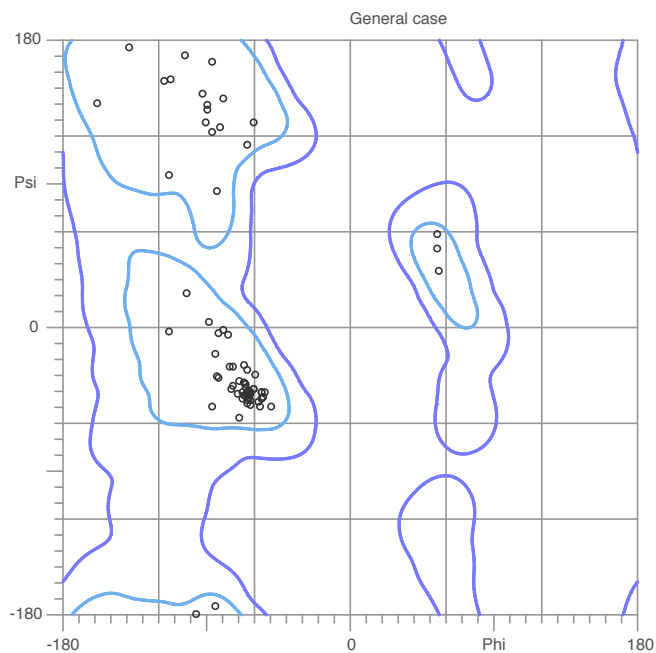
97.0% (1630/1680) of all residues were in favored (98%) regions.  
99.6% (1673/1680) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):  
[3] 9 SER (63.9, 95.2)

[6] 32 GLY (-125.1, 85.1)  
[6] 45 ALA (68.7, 146.7)  
[11] 9 SER (-163.2, -95.7)  
[11] 44 GLY (-145.0, 75.0)  
[12] 10 HIS (65.0, 94.6)  
[19] 44 GLY (-145.1, 74.9)

# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 1



100.0% (84/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

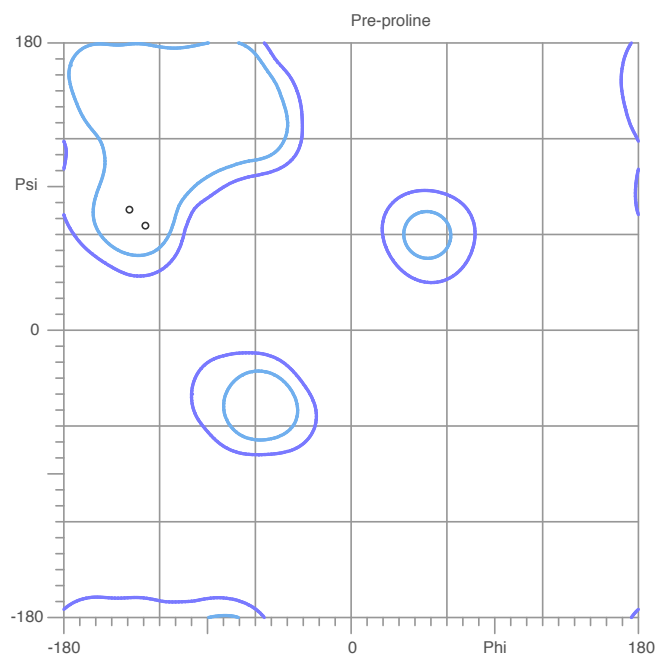
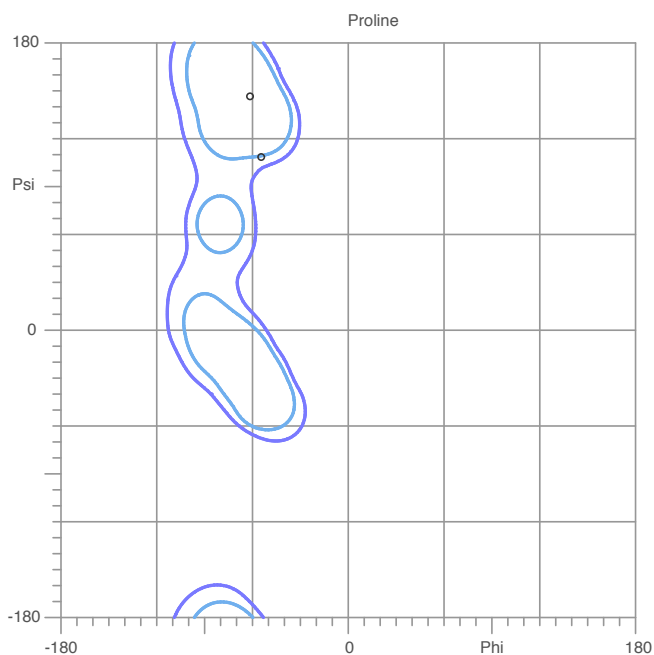
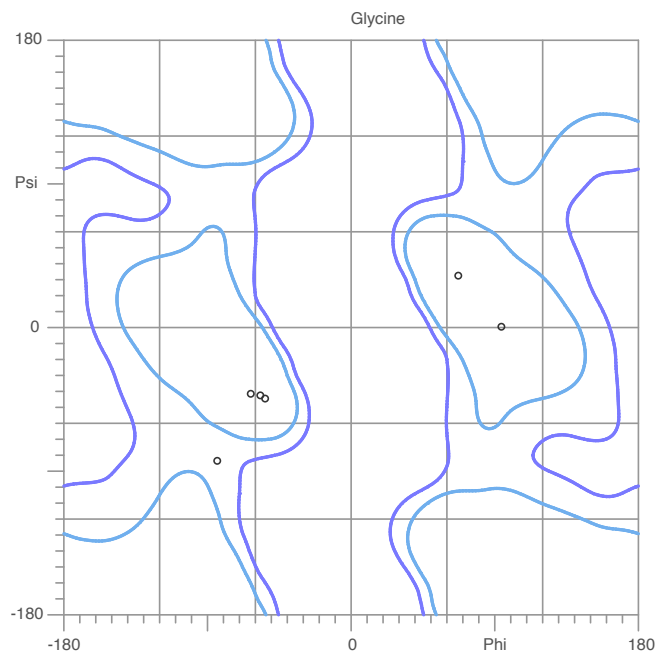
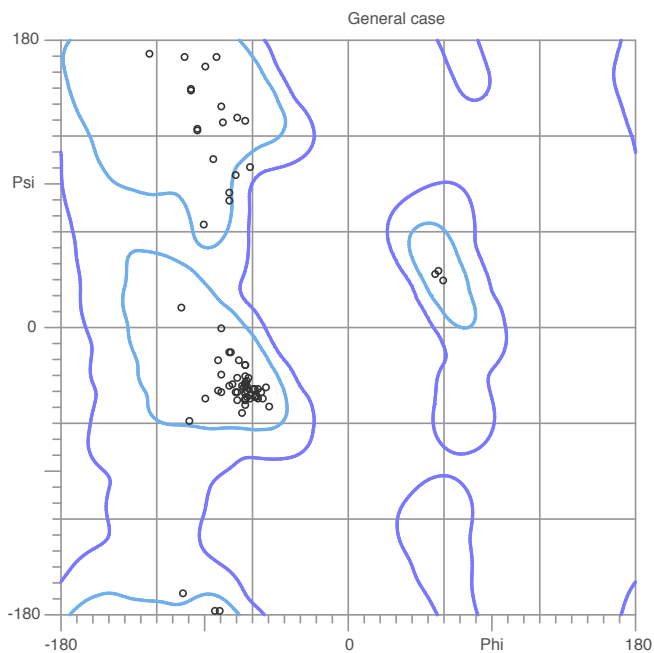
There were no outliers.

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

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

# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 2



95.2% (80/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

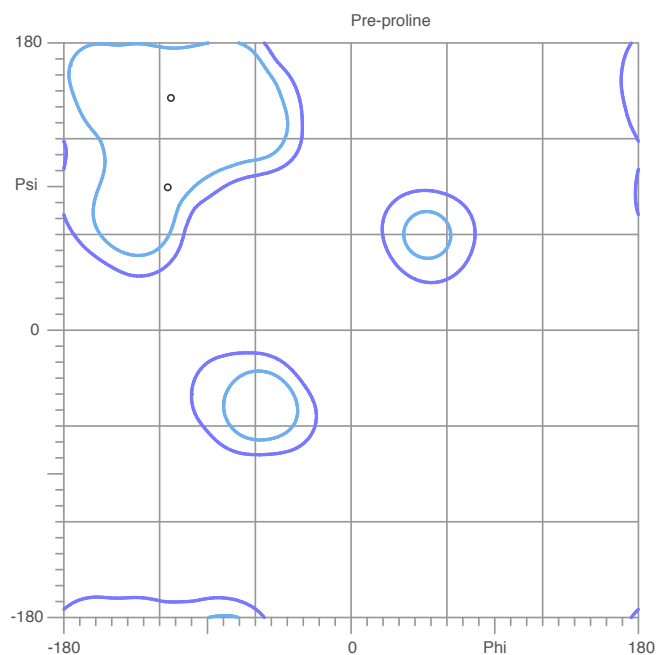
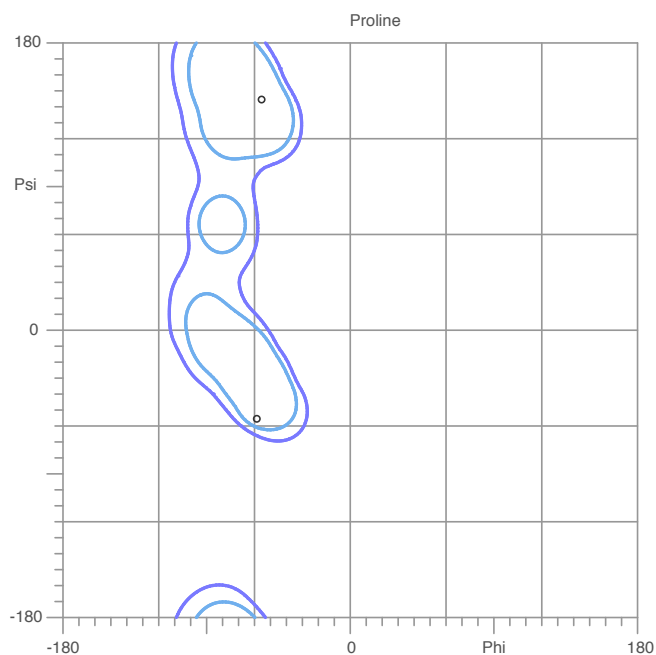
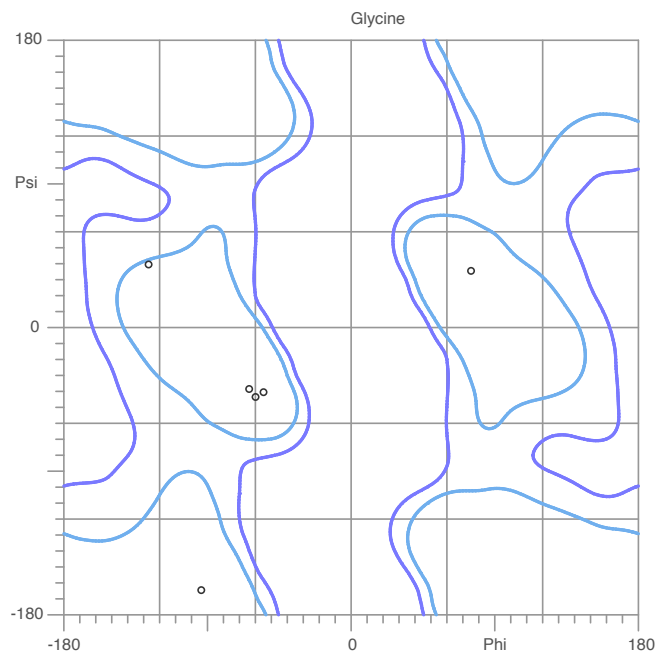
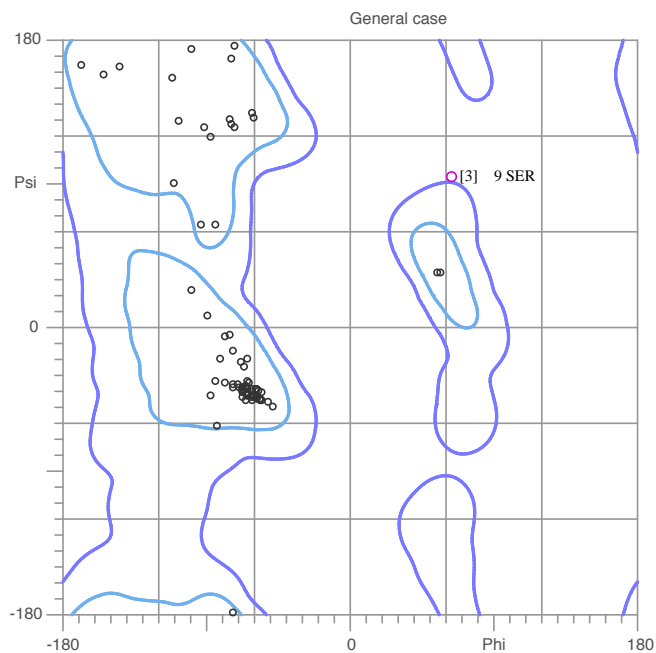
There were no outliers.

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

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

# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 3

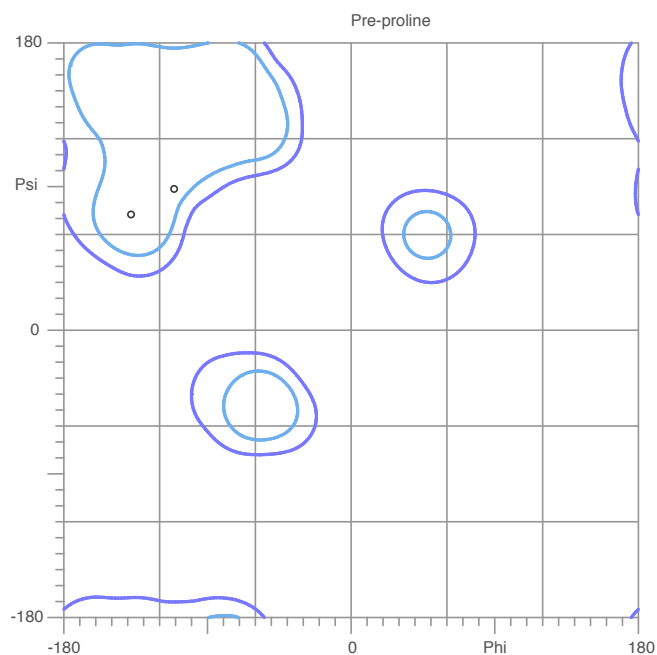
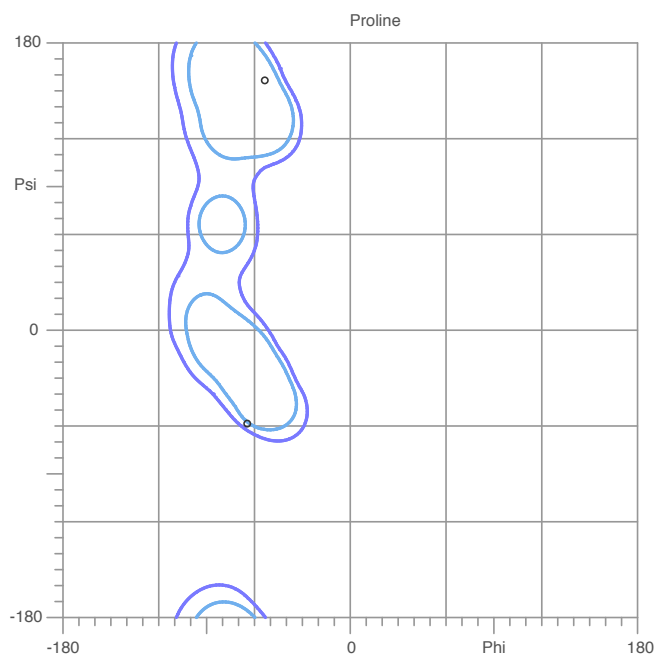
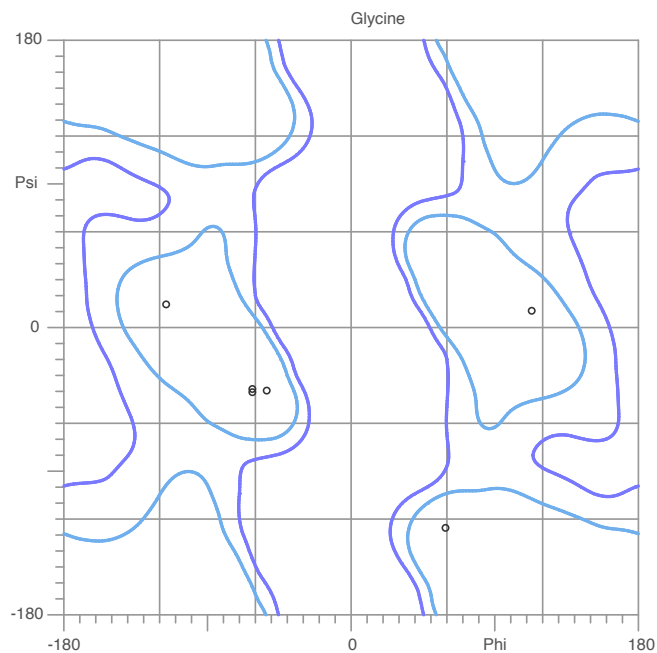
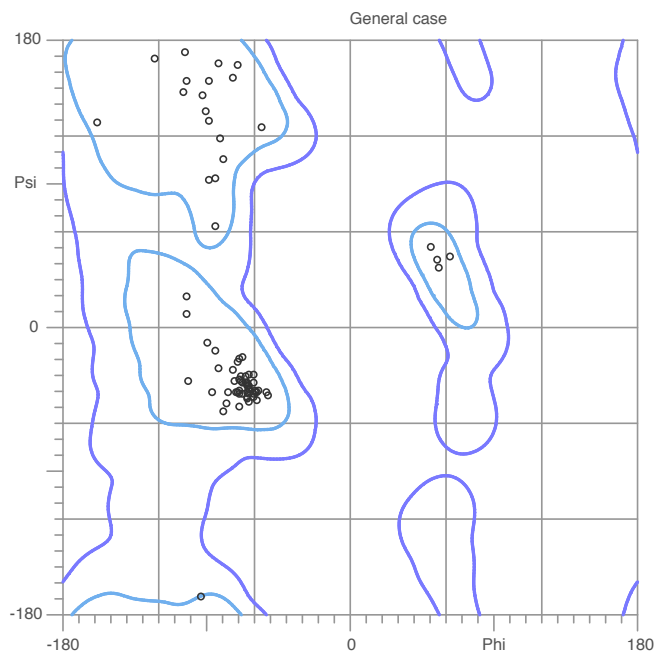


98.8% (83/84) of all residues were in favored (98%) regions.  
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[3] 9 SER (63.9, 95.2)

# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 4



98.8% (83/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

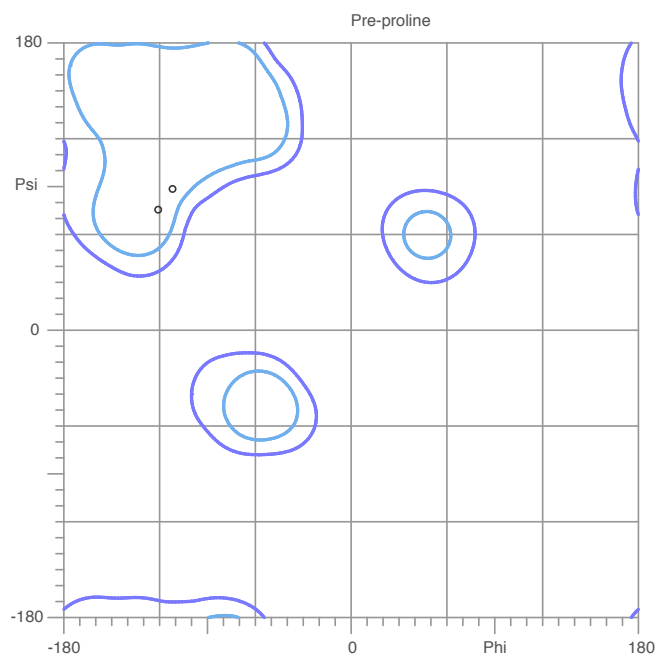
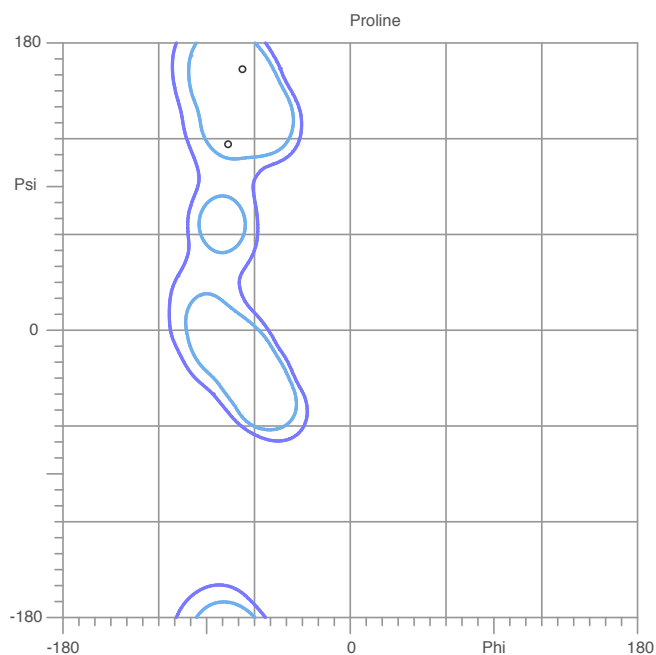
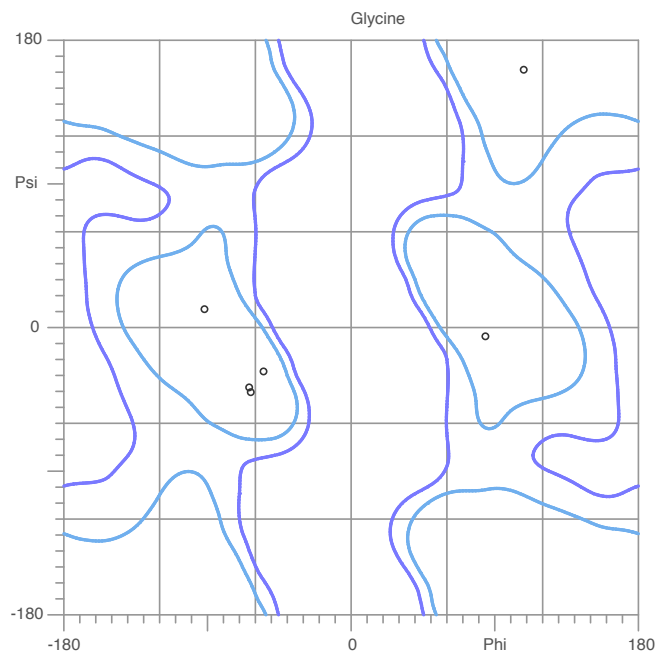
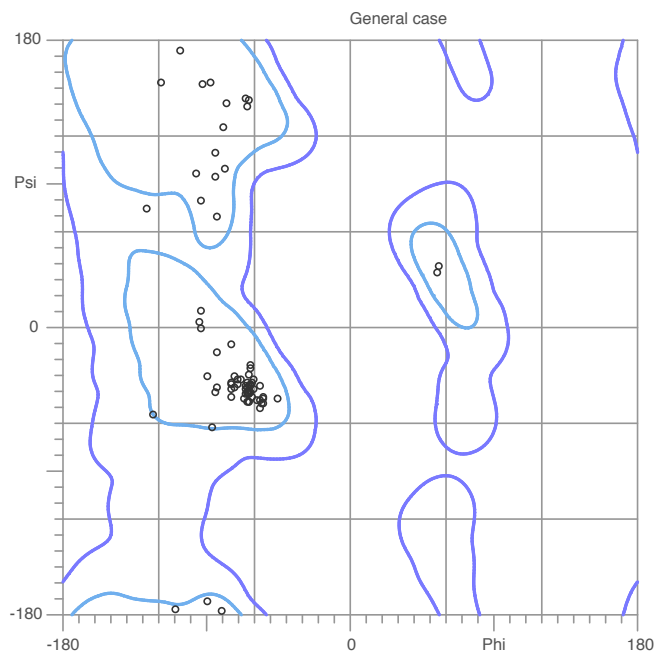
There were no outliers.

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

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 5



97.6% (82/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

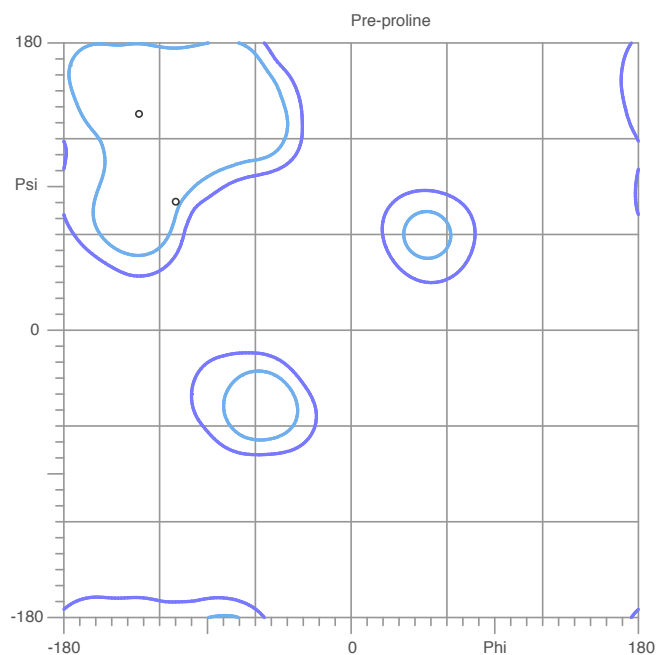
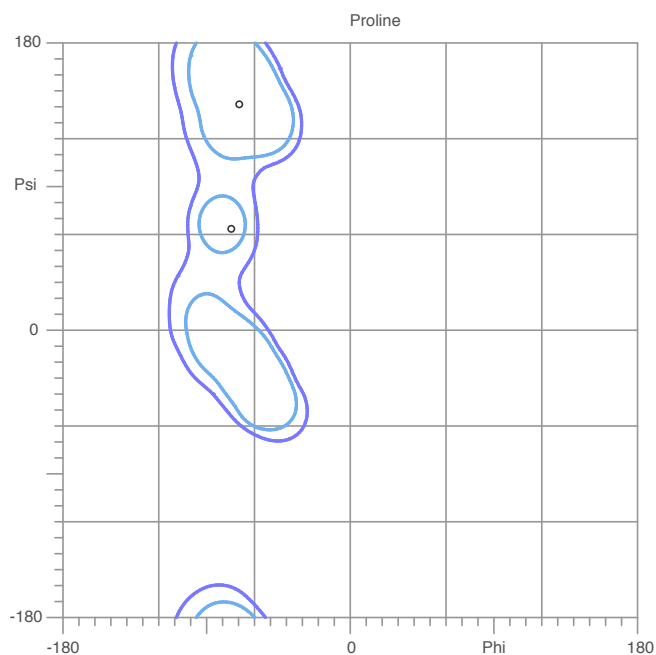
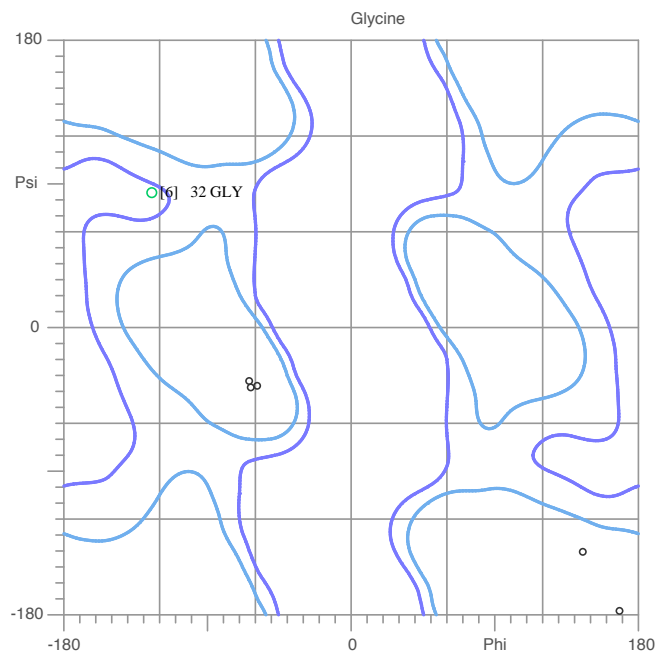
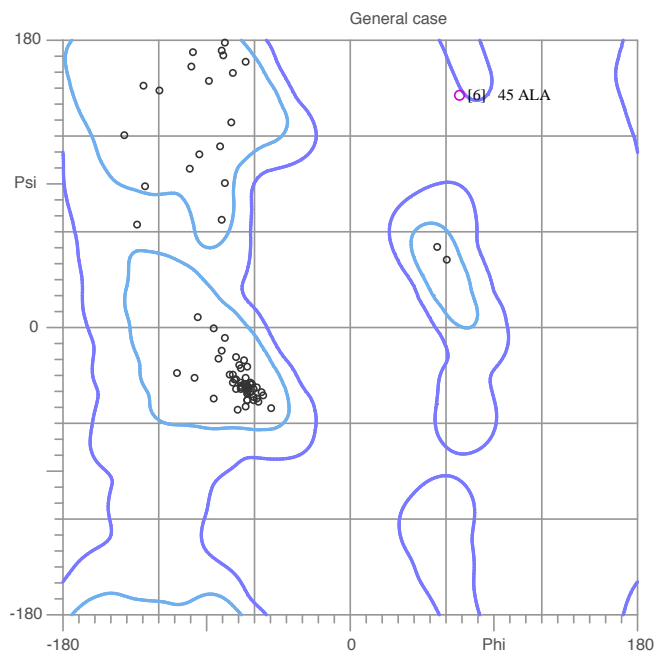
There were no outliers.

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

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 6



96.4% (81/84) of all residues were in favored (98%) regions.  
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

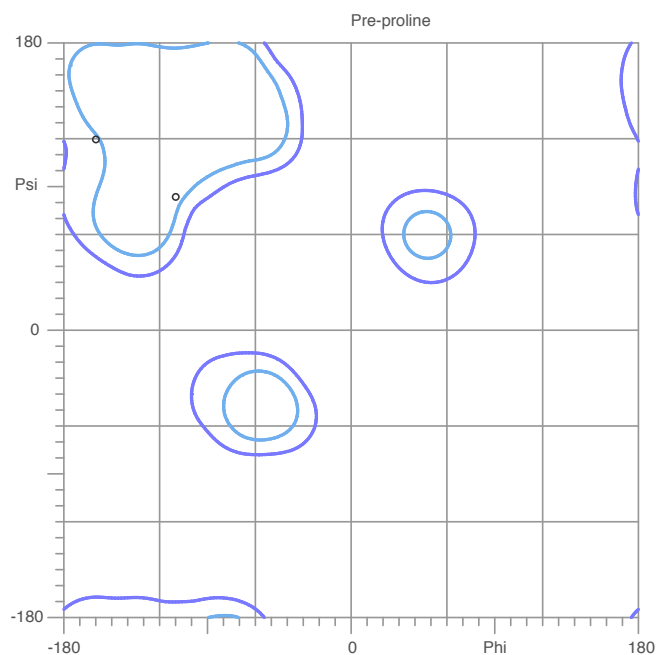
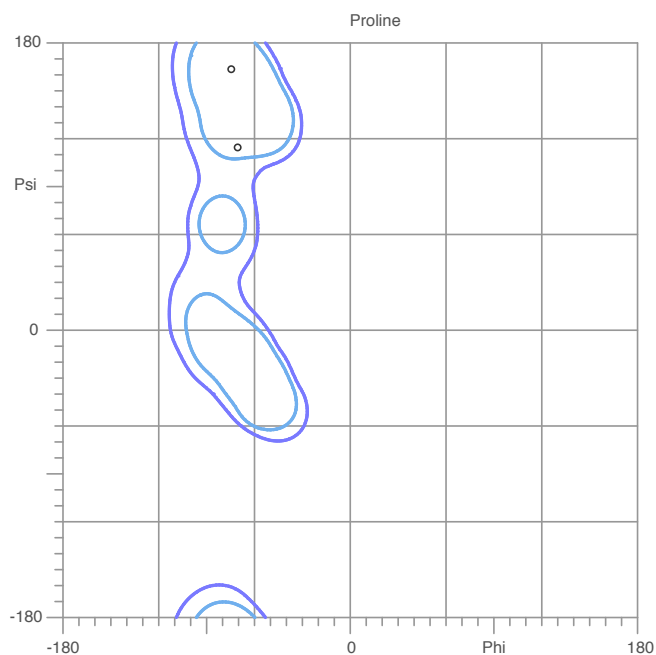
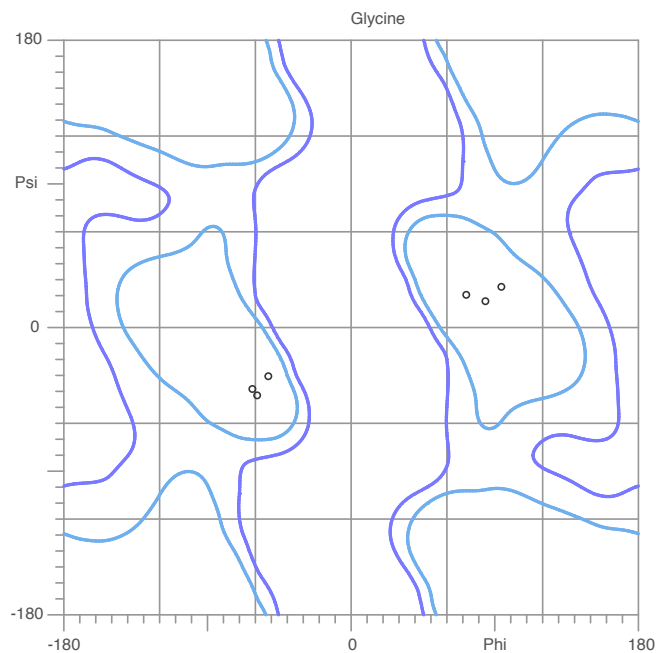
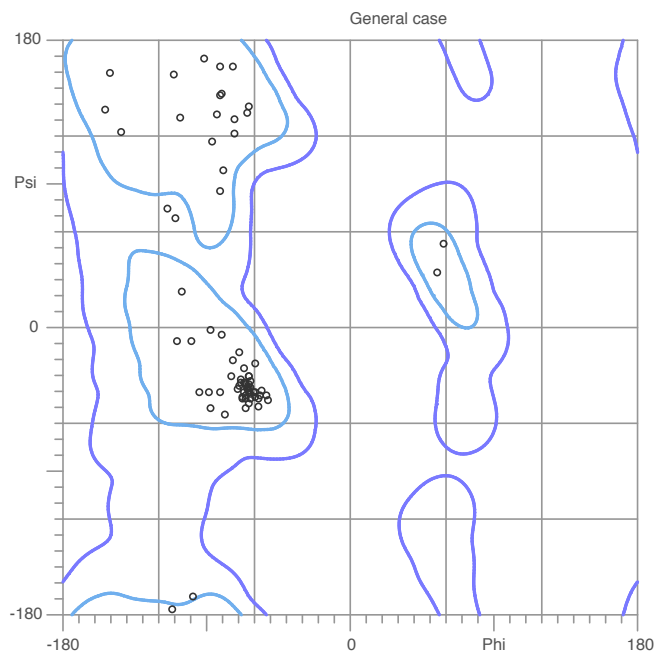
There were 2 outliers (phi, psi):

[6] 32 GLY (-125.1, 85.1)

[6] 45 ALA (68.7, 146.7)

# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 7



95.2% (80/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

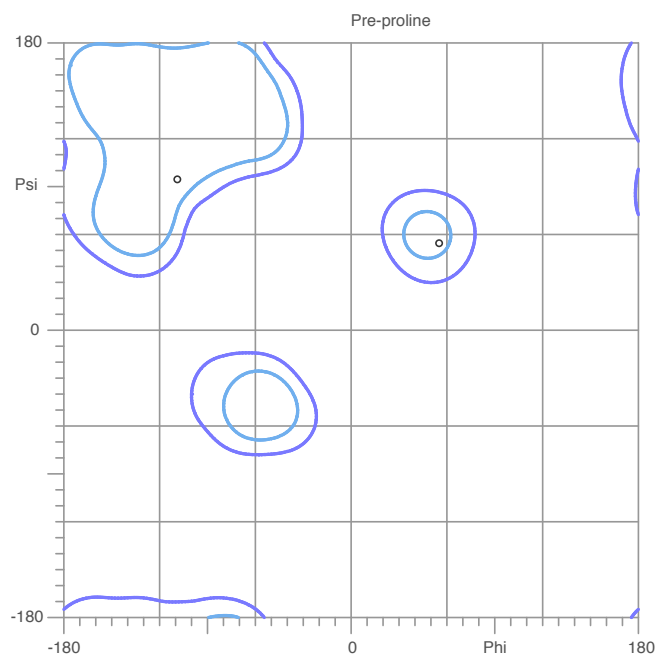
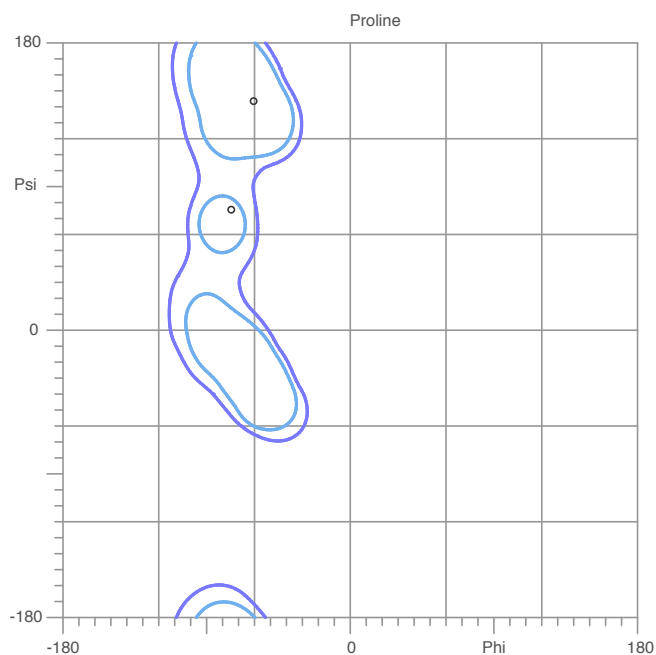
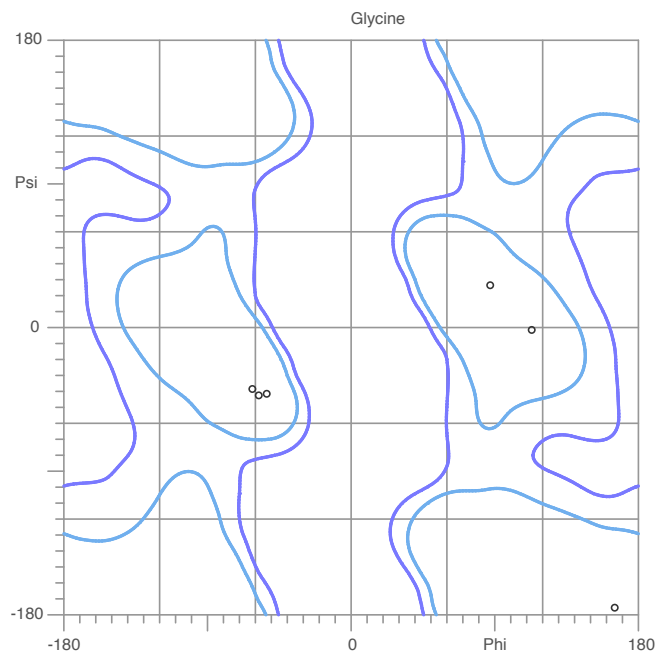
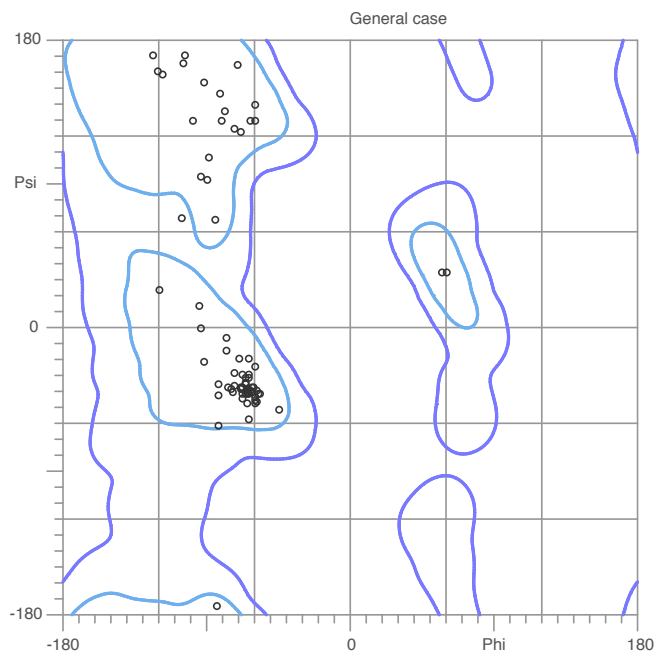
There were no outliers.

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 8



98.8% (83/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

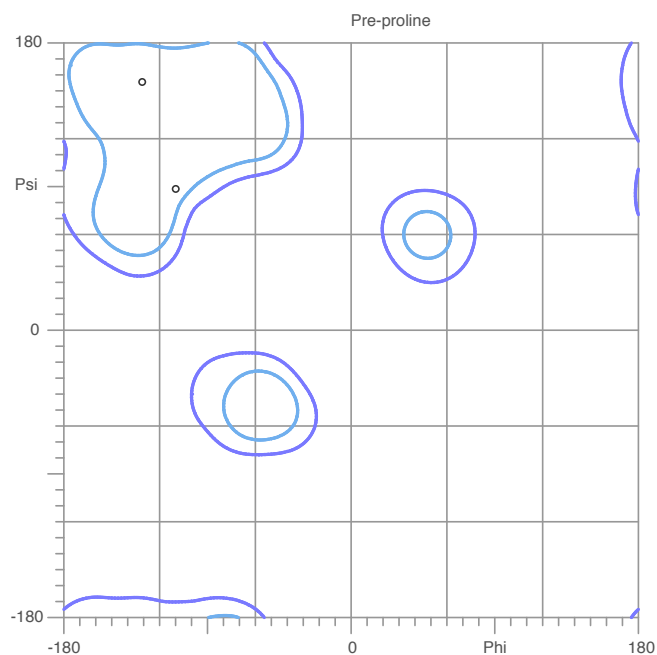
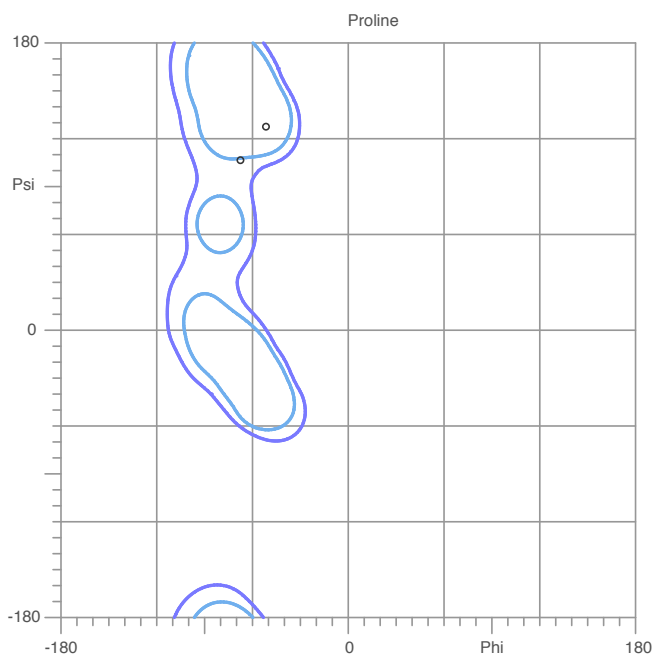
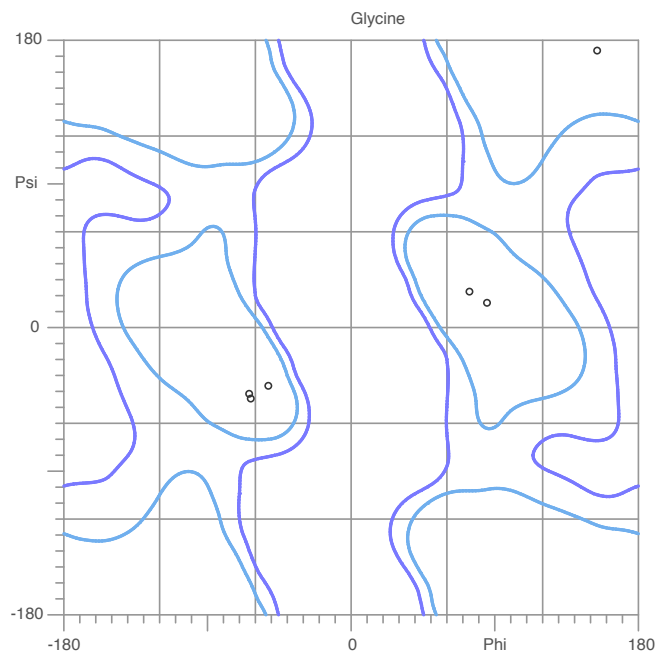
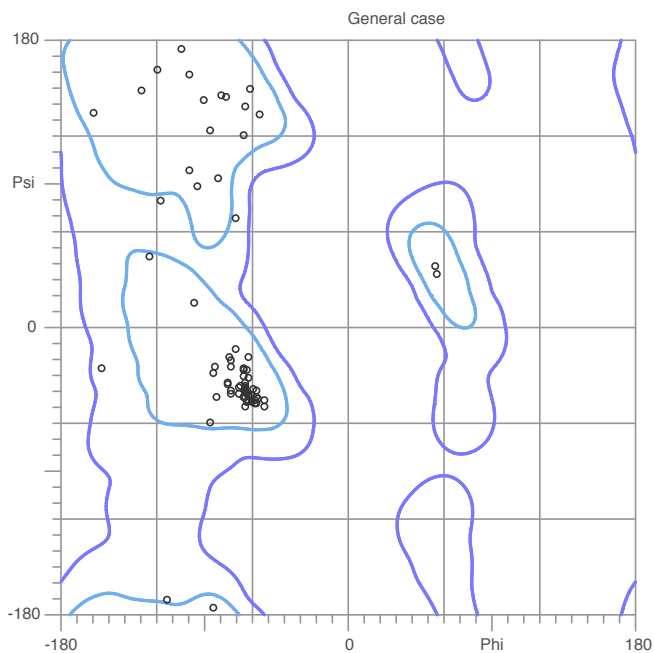
There were no outliers.

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 9



94.0% (79/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

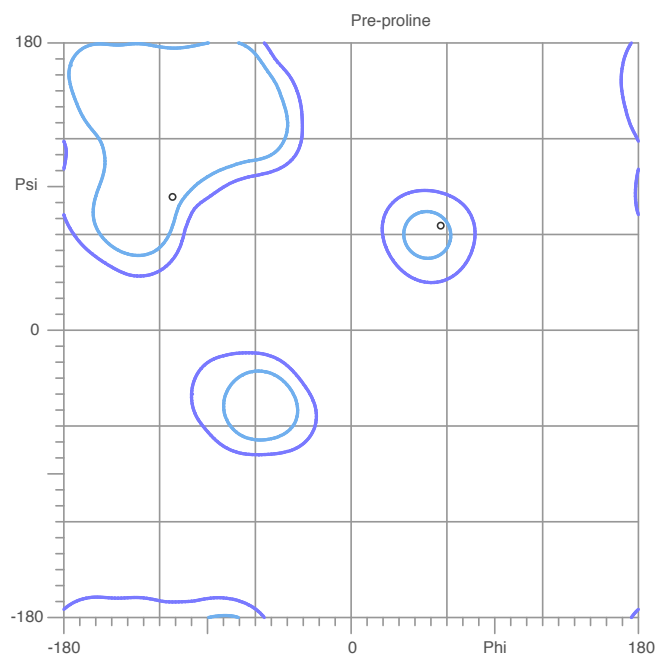
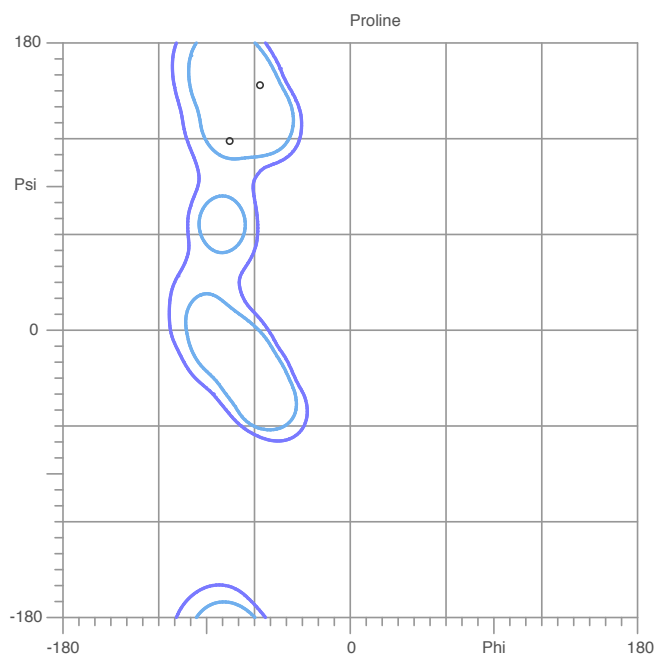
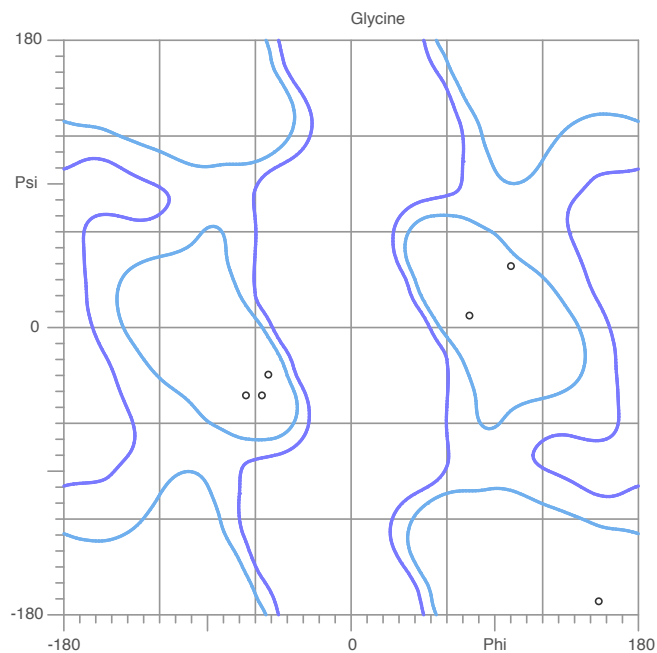
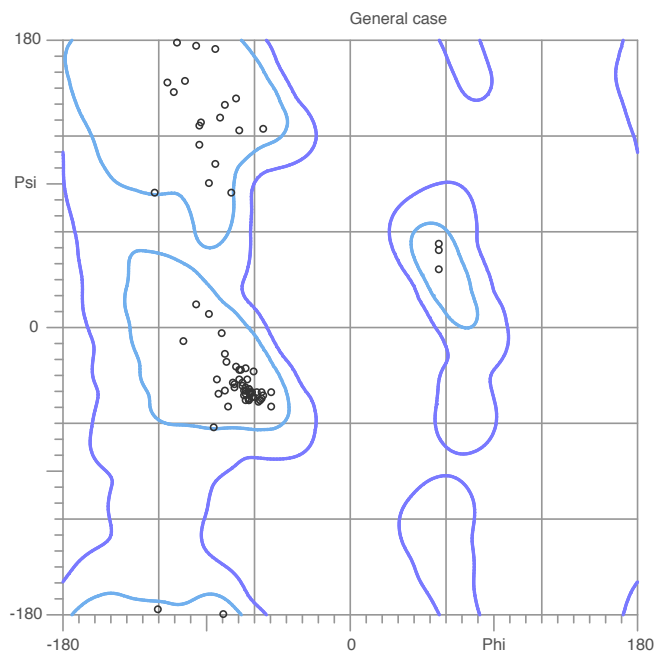
There were no outliers.

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 10



100.0% (84/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

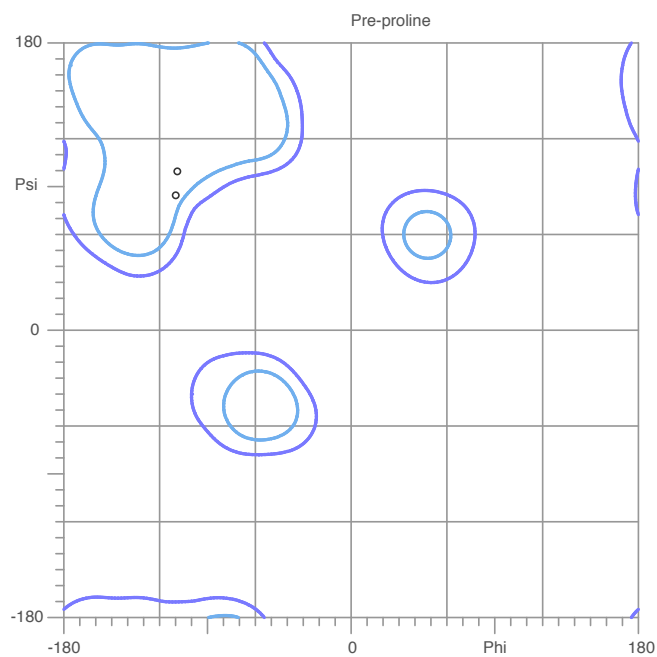
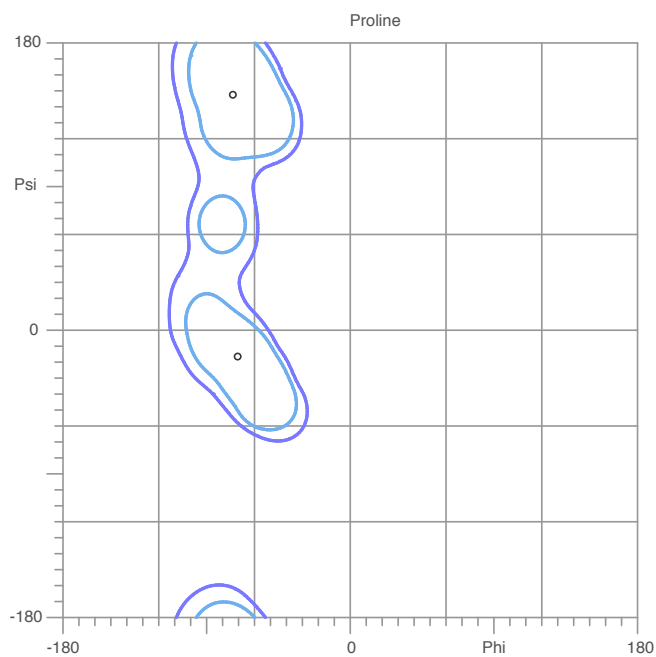
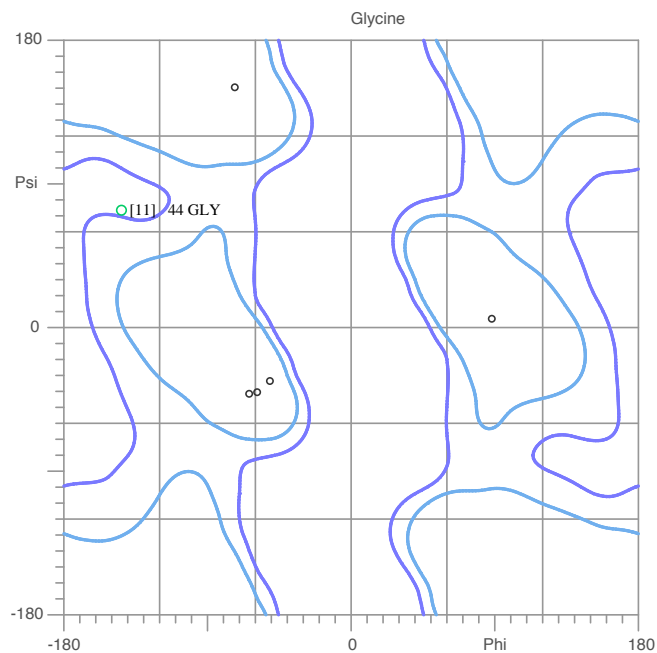
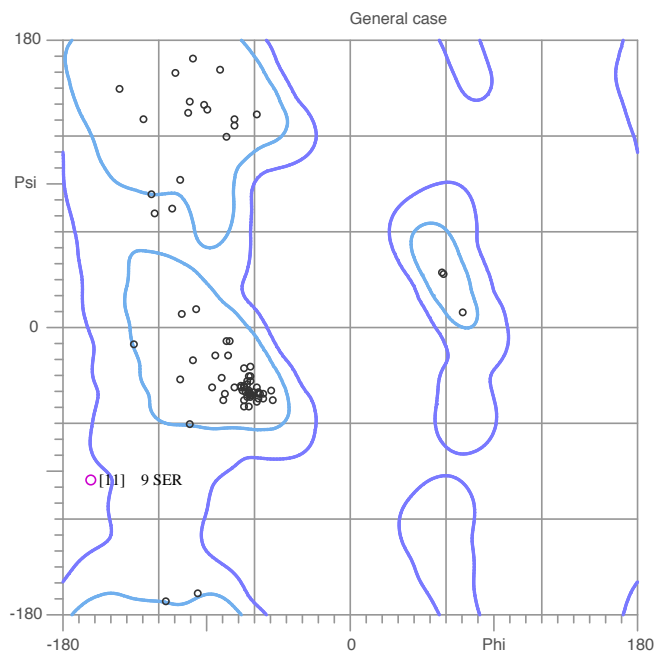
There were no outliers.

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 11



91.7% (77/84) of all residues were in favored (98%) regions.  
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

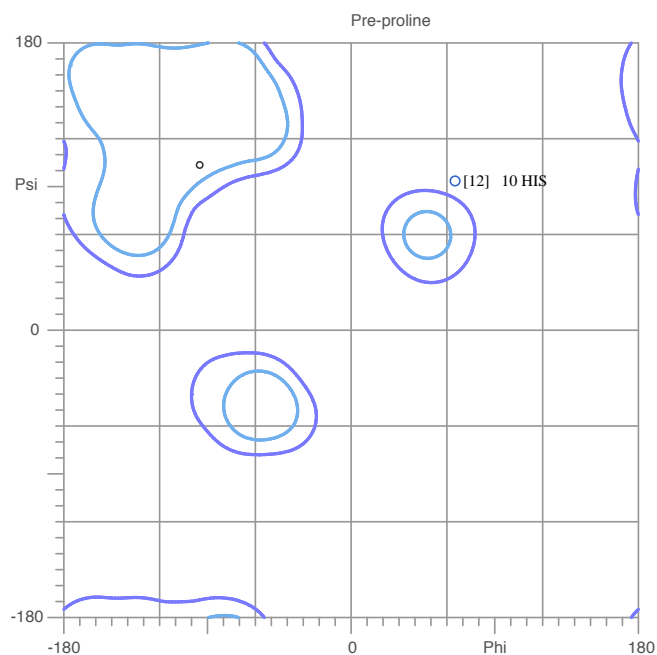
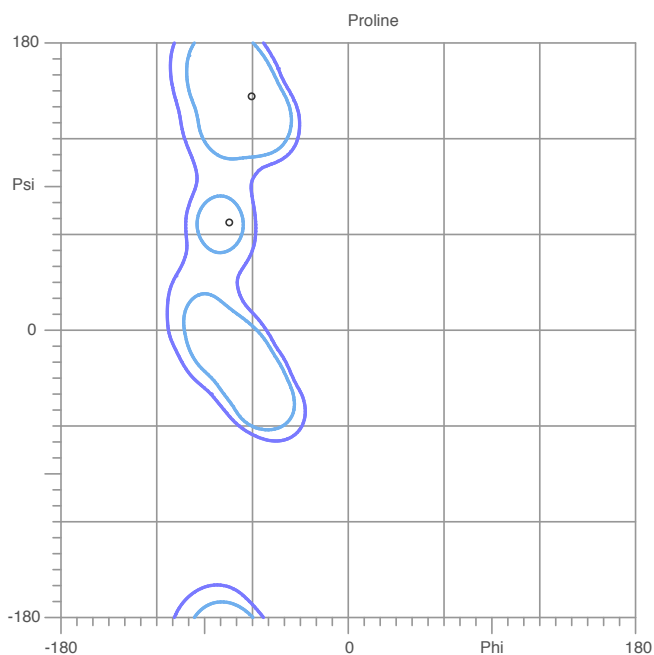
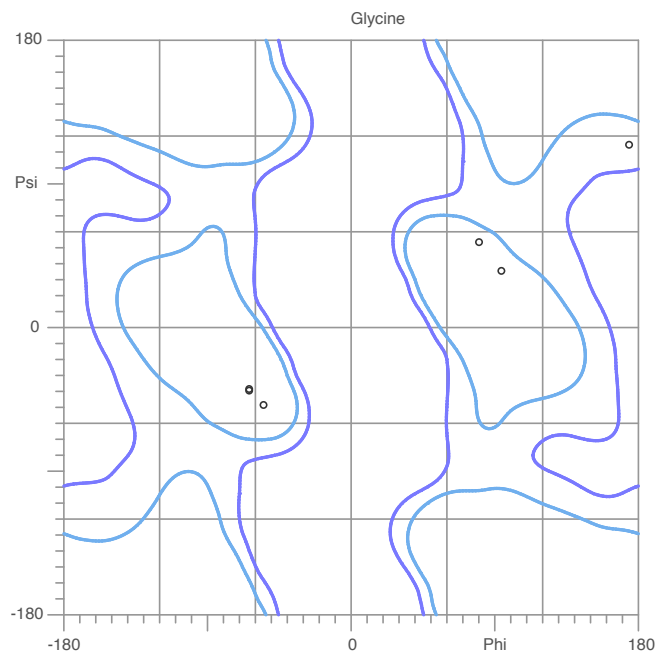
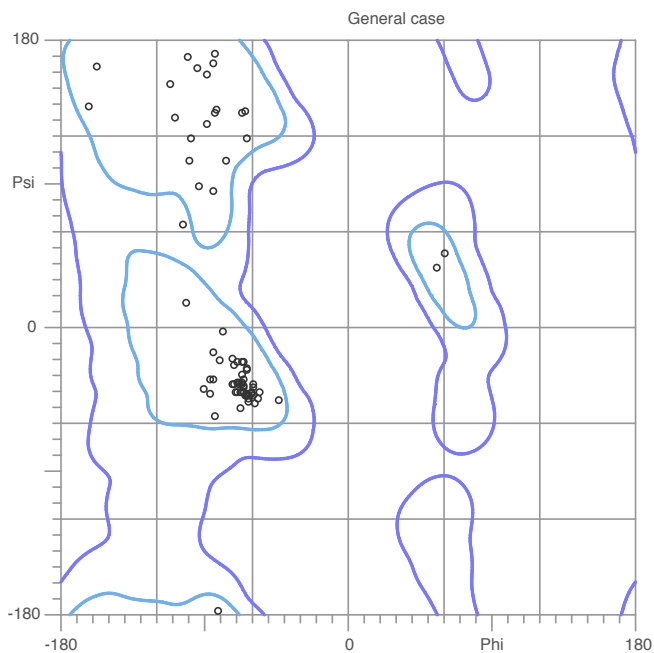
There were 2 outliers (phi, psi):

[11] 9 SER (-163.2, -95.7)

[11] 44 GLY (-145.0, 75.0)

# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 12



96.4% (81/84) of all residues were in favored (98%) regions.  
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

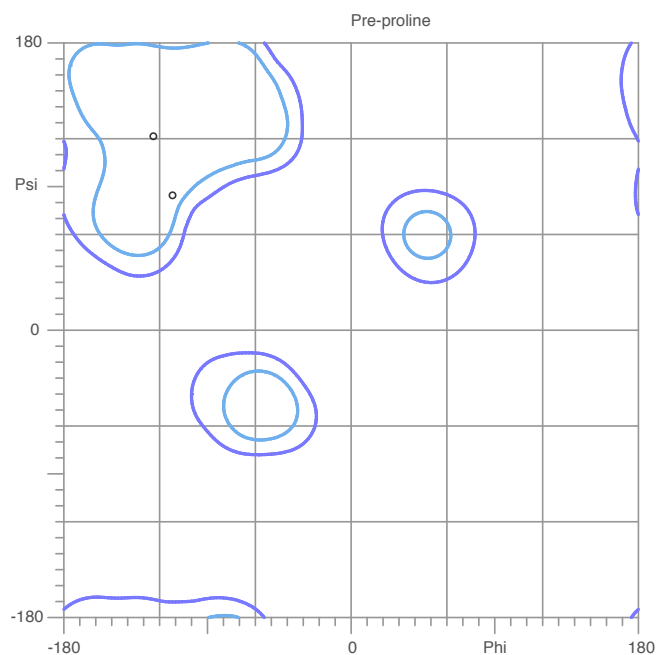
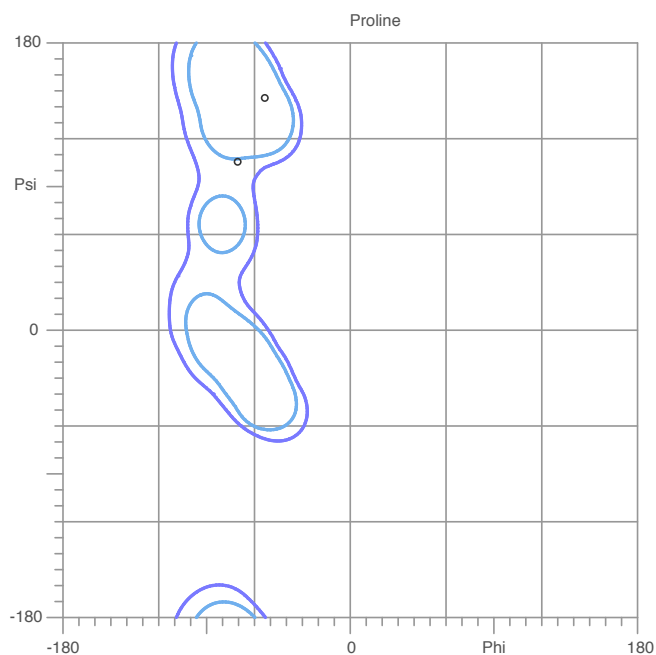
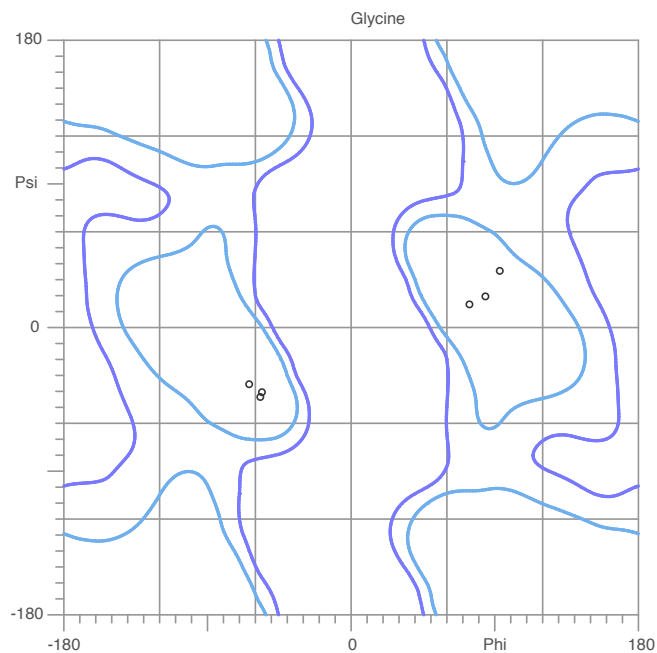
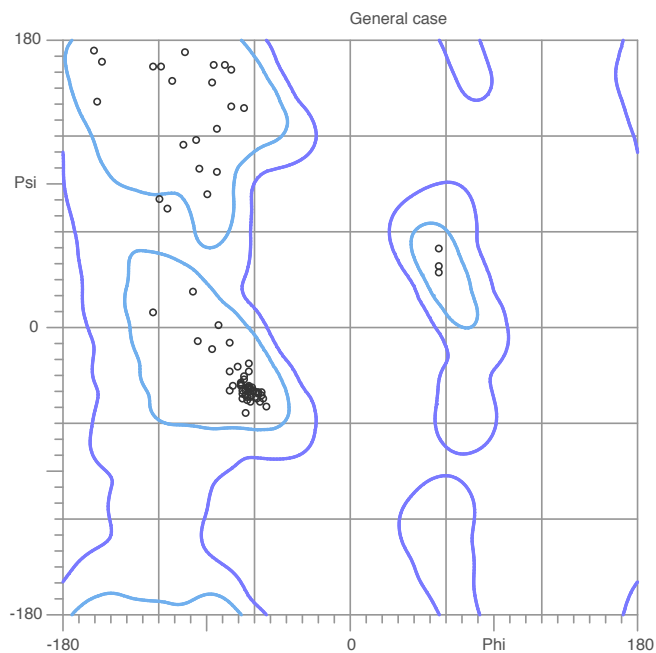
There were 1 outliers (phi, psi):  
[12] 10 HIS (65.0, 94.6)

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 13



96.4% (81/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

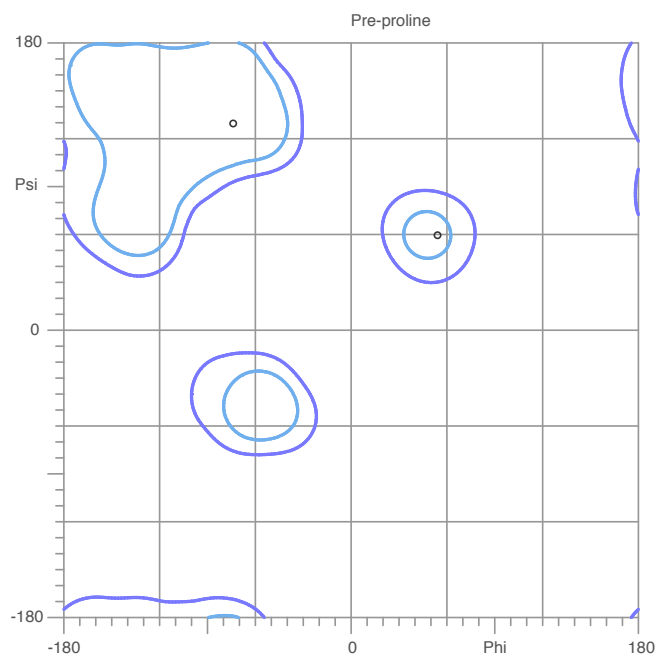
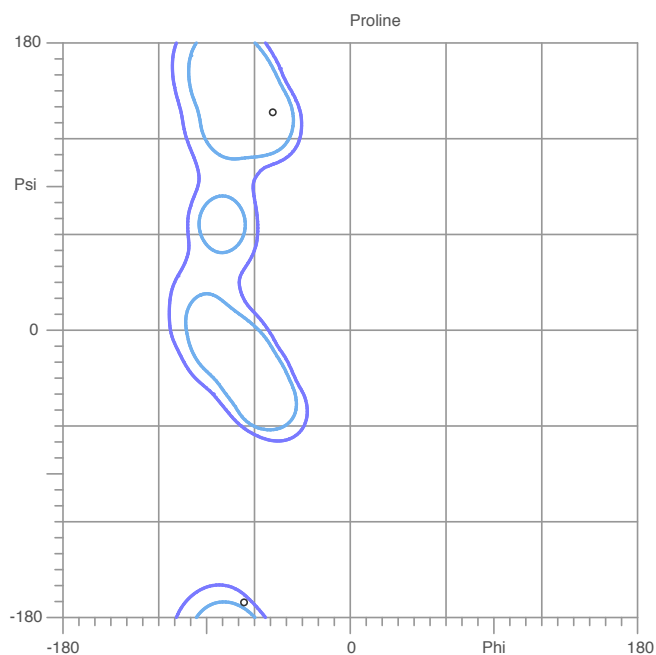
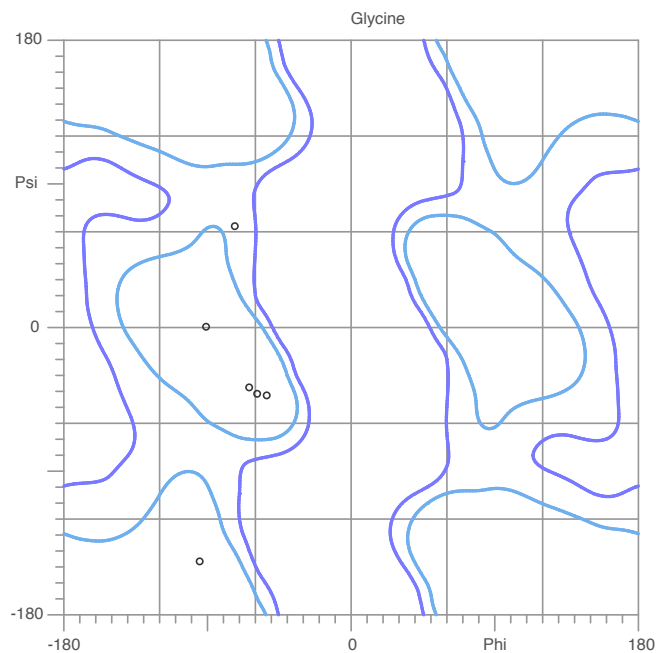
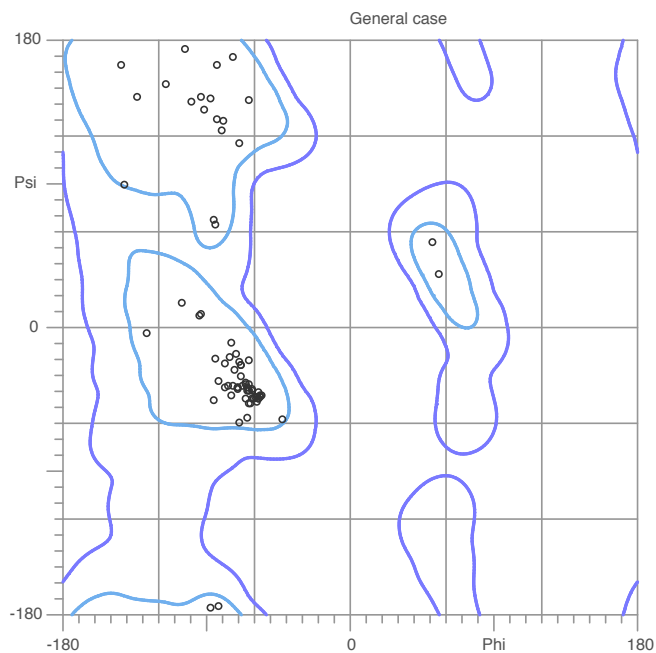
There were no outliers.

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 14



97.6% (82/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

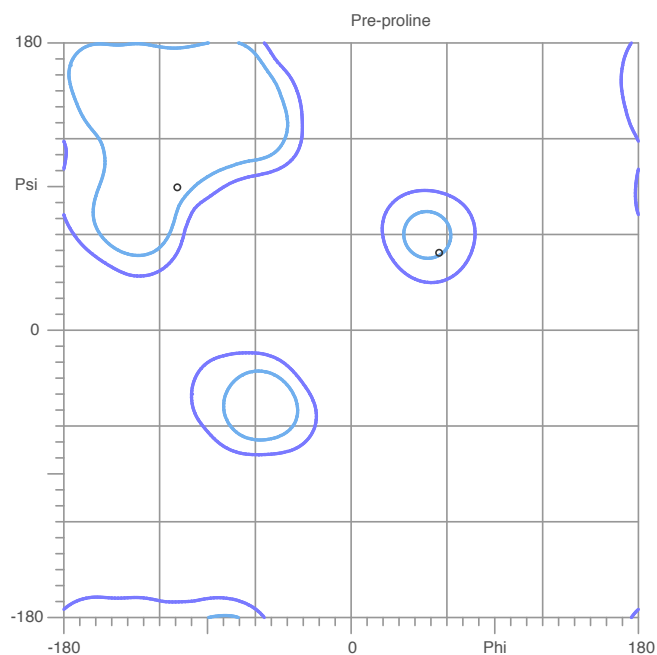
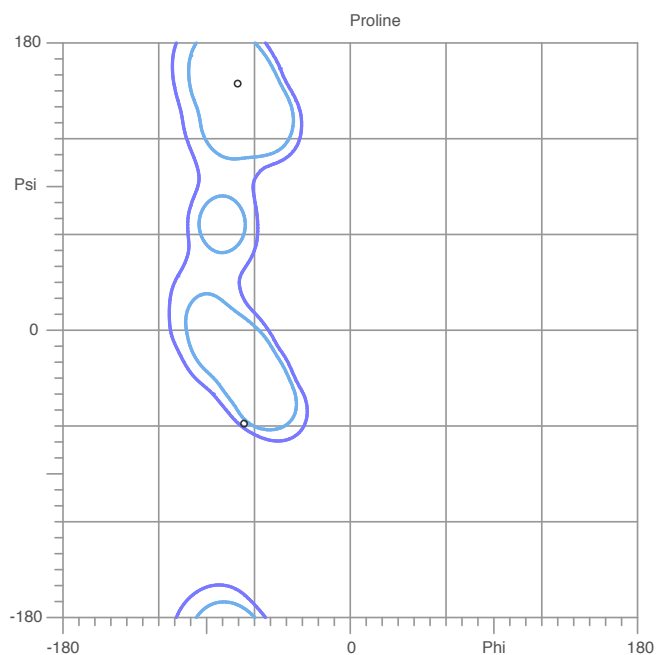
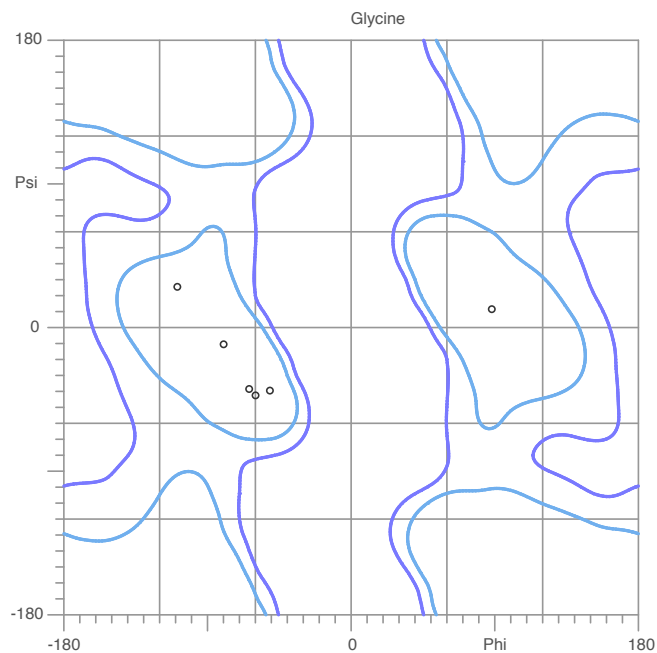
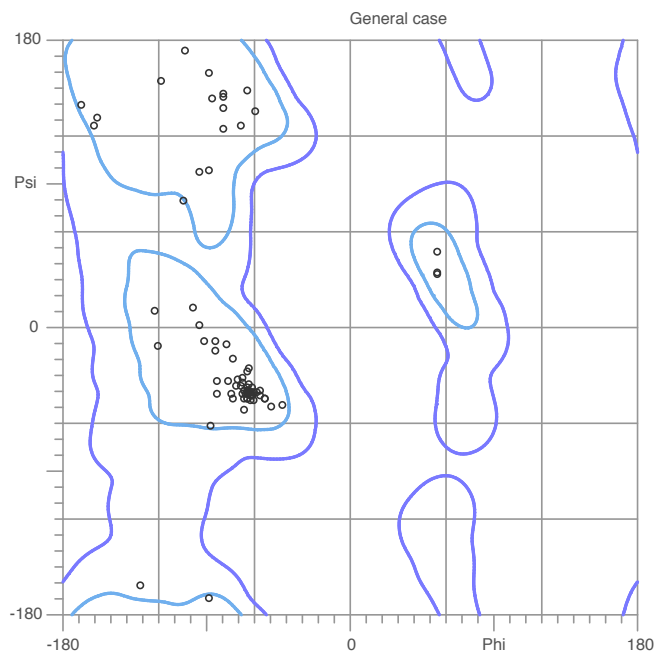
There were no outliers.

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

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 15



96.4% (81/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

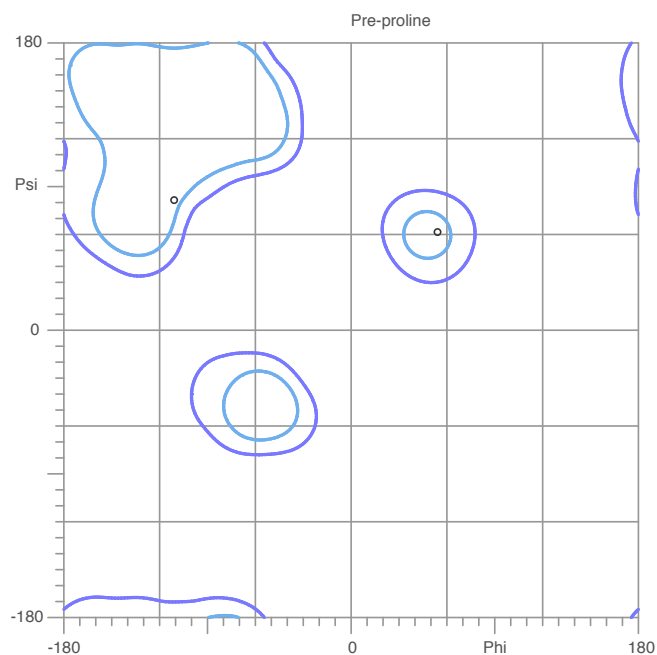
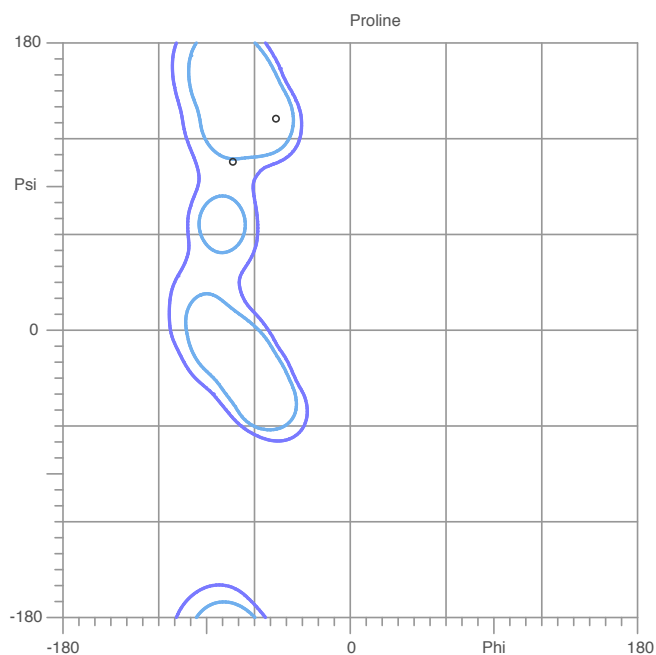
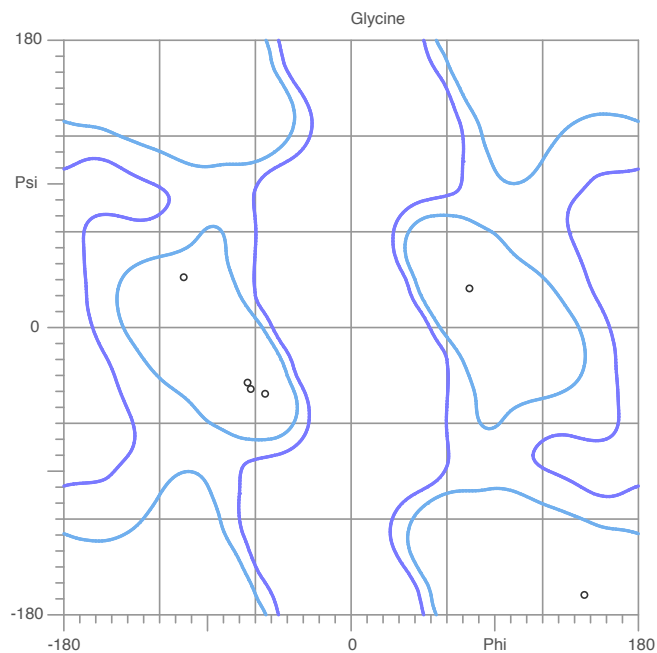
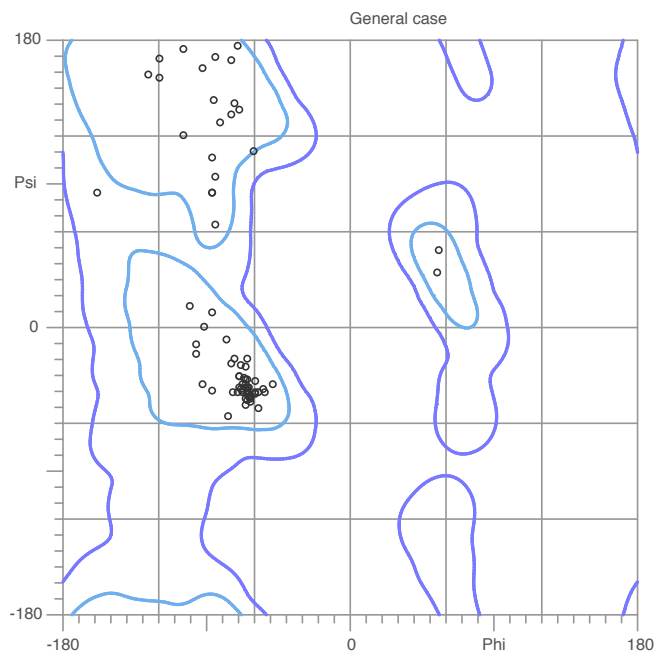
There were no outliers.

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

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 16



97.6% (82/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

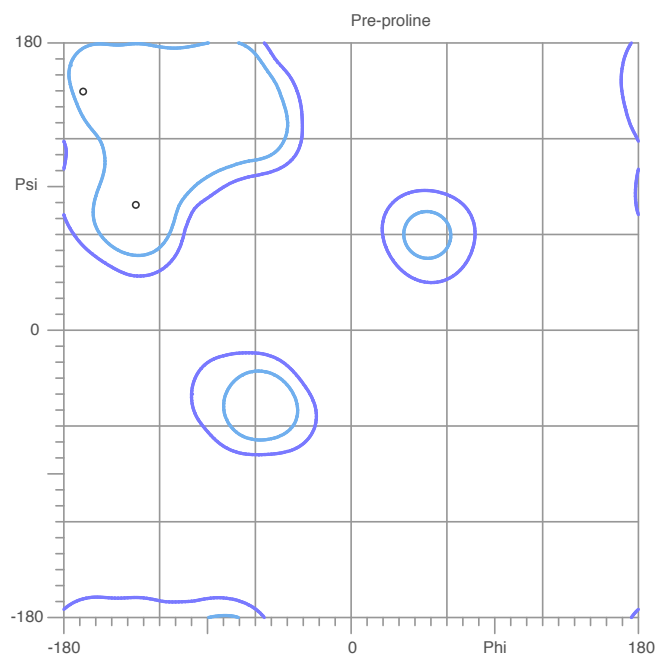
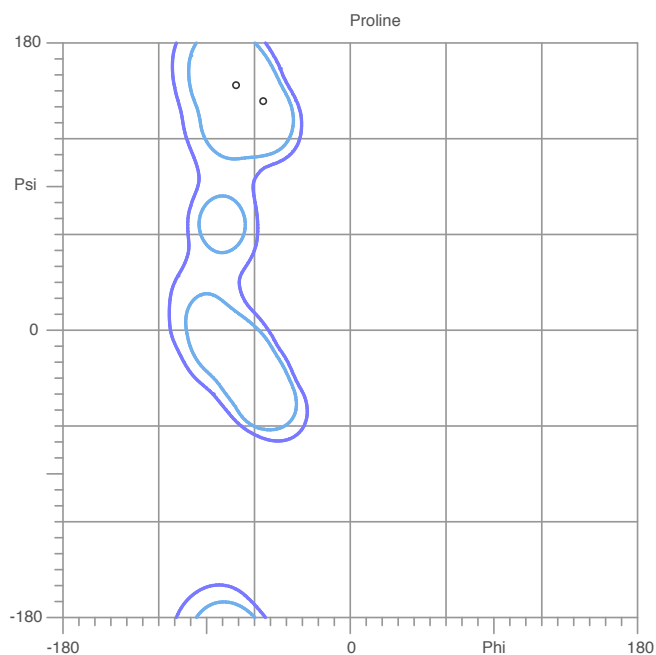
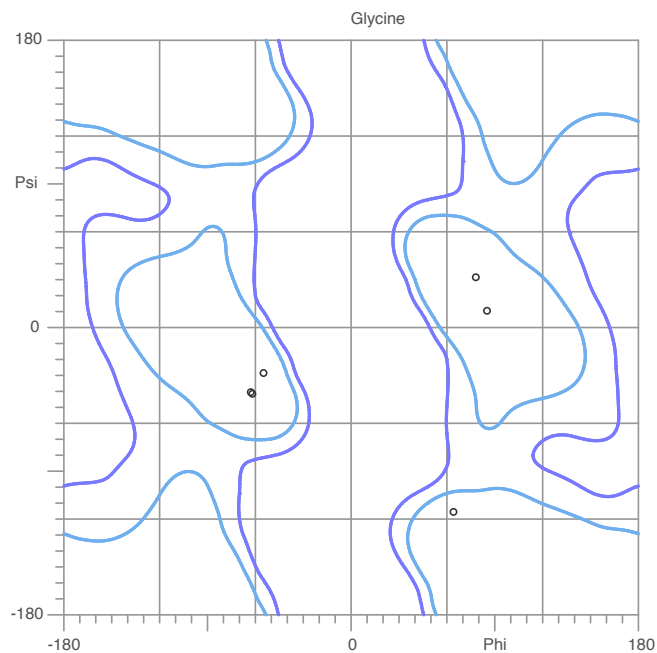
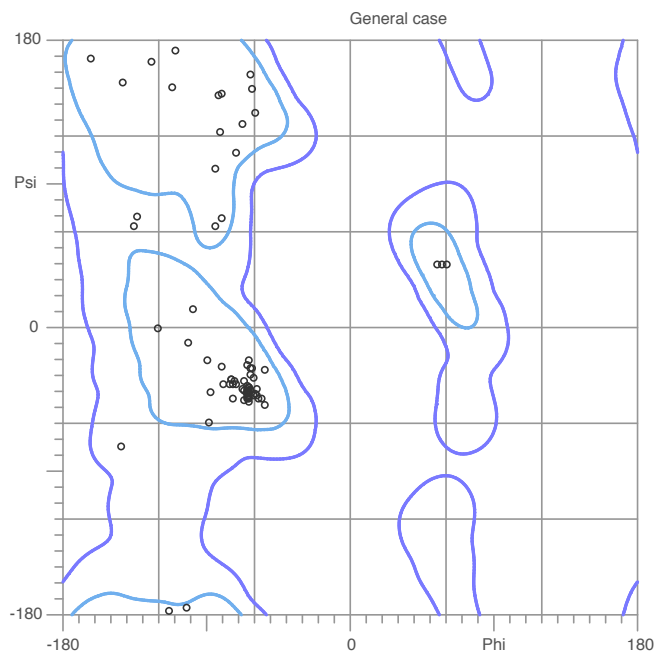
There were no outliers.

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

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 17



96.4% (81/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

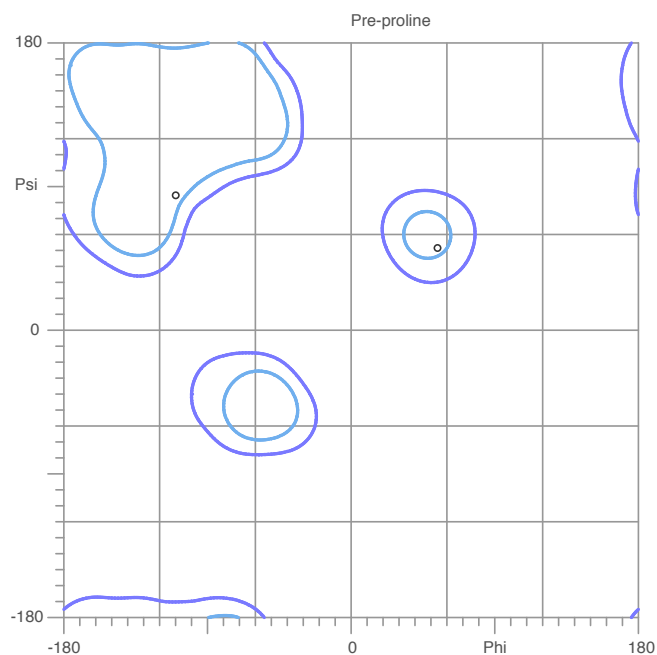
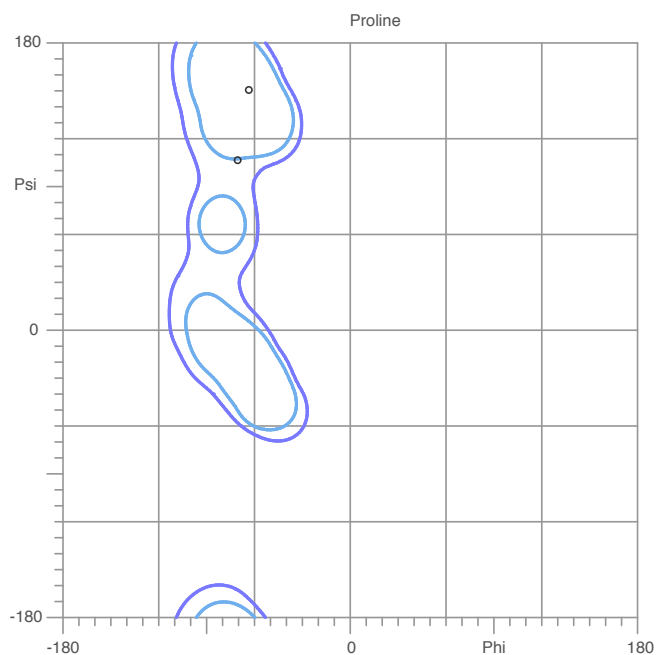
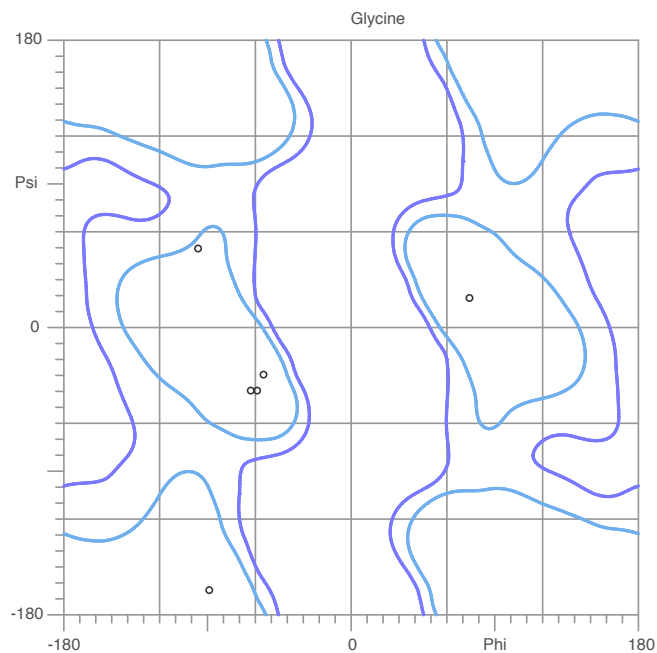
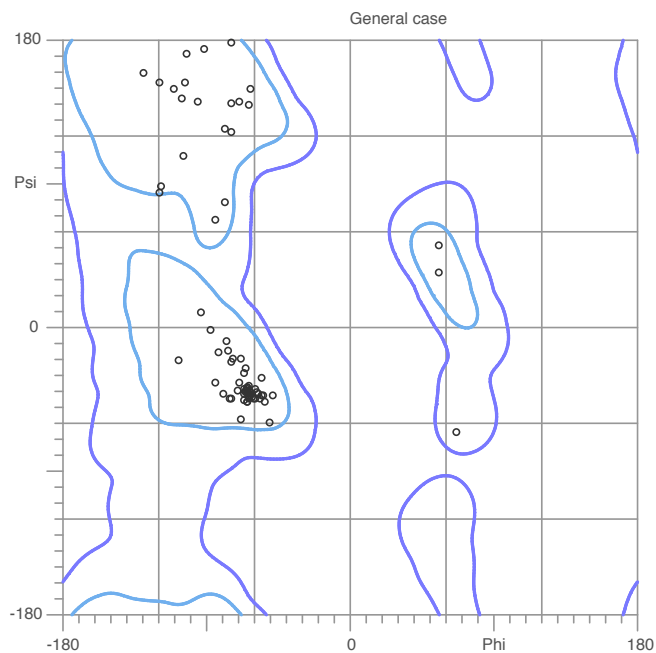
There were no outliers.

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 18



97.6% (82/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

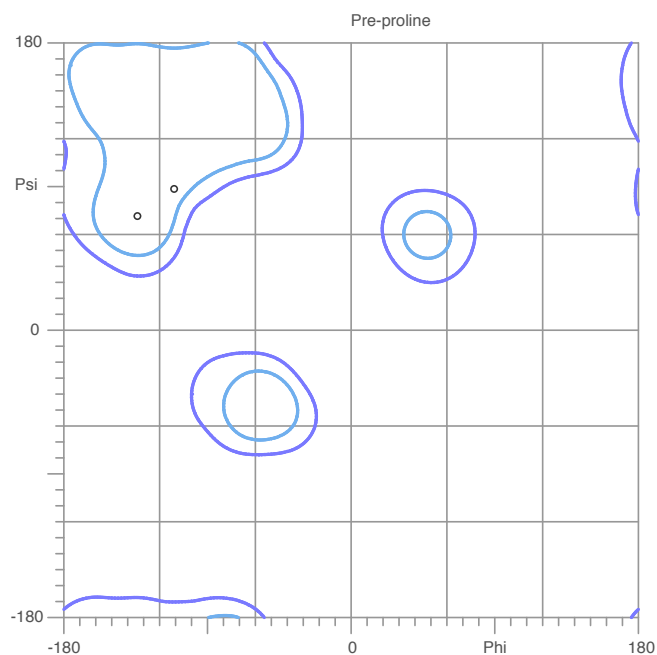
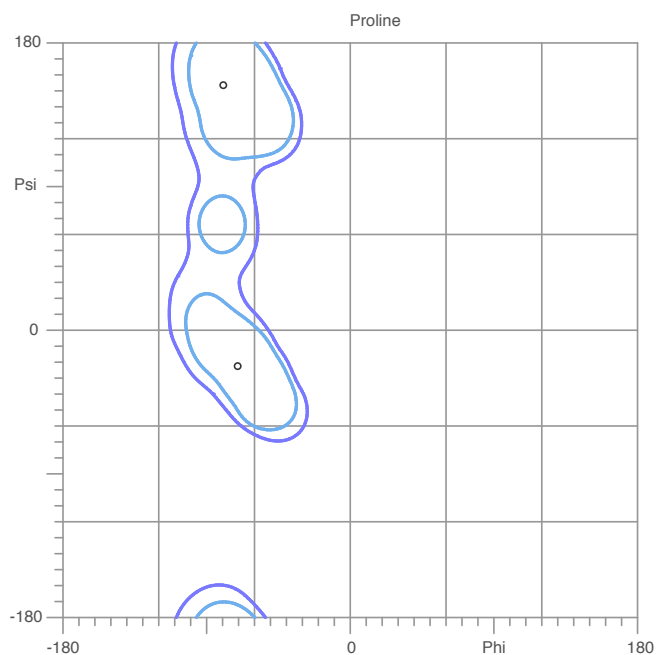
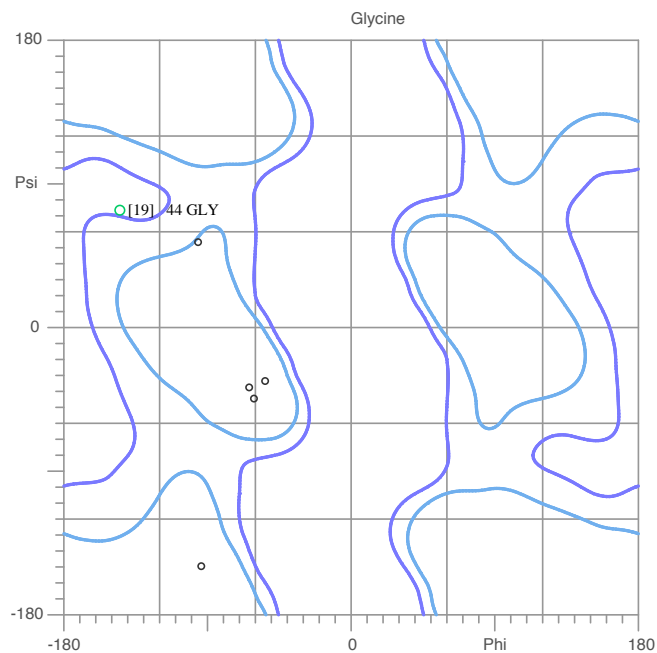
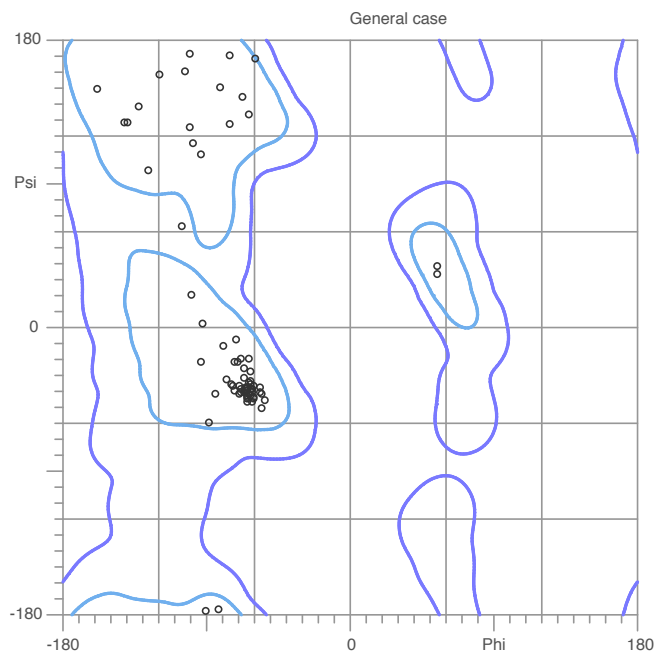
There were no outliers.

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

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 19



97.6% (82/84) of all residues were in favored (98%) regions.  
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

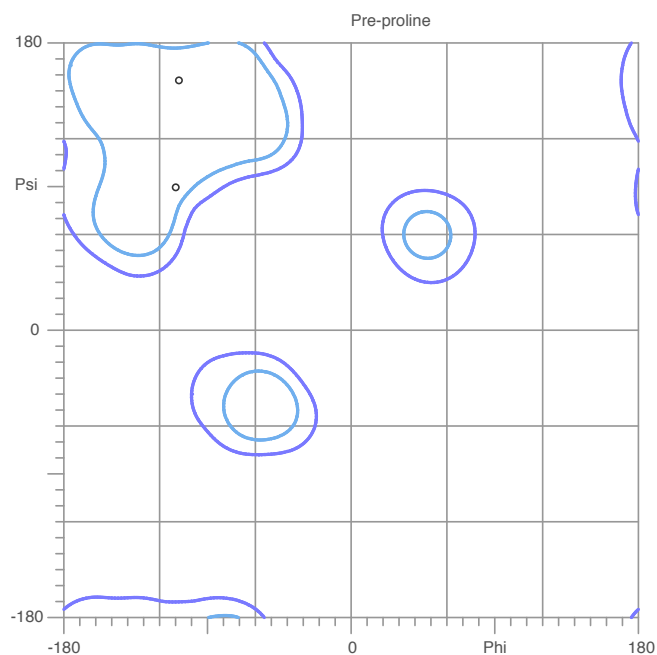
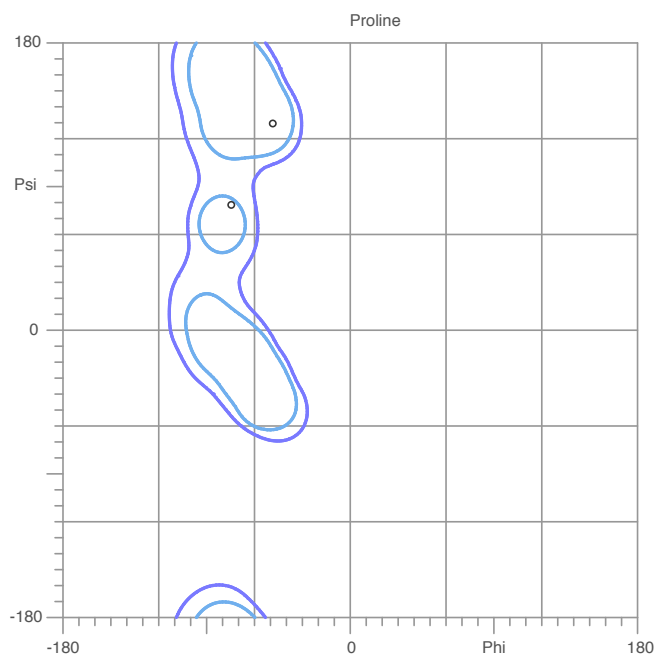
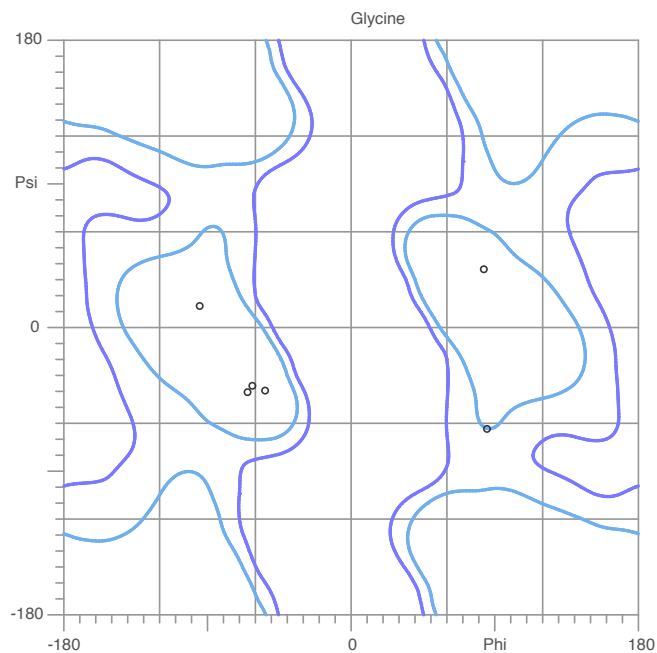
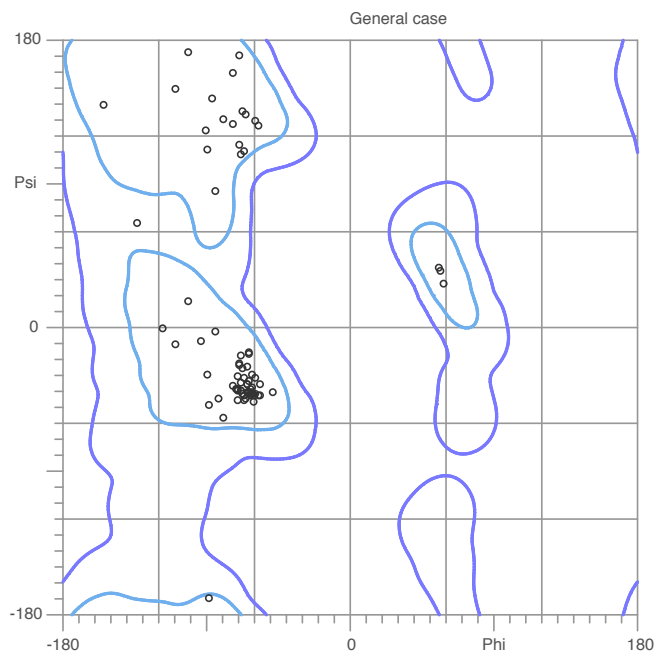
There were 1 outliers (phi, psi):  
[19] 44 GLY (-145.1, 74.9)

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

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# MolProbity Ramachandran analysis

HR3102A\_R3\_em\_bcr3.pdb, model 20



97.6% (82/84) of all residues were in favored (98%) regions.  
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

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