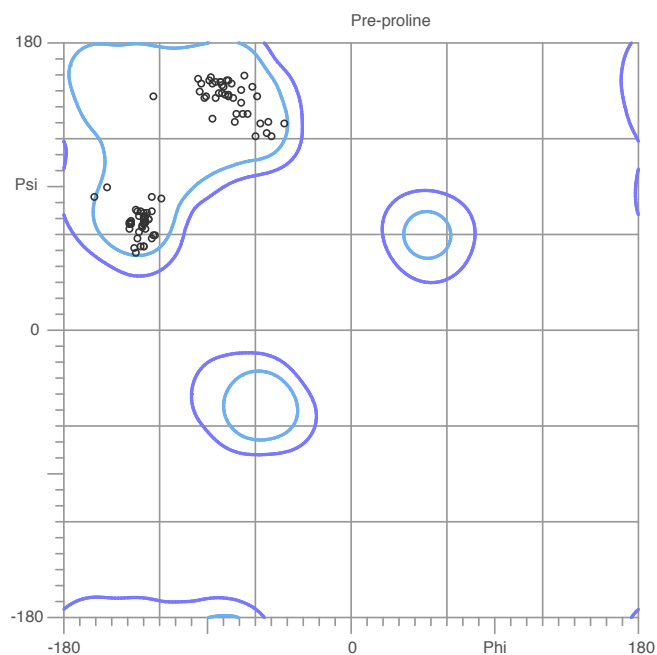
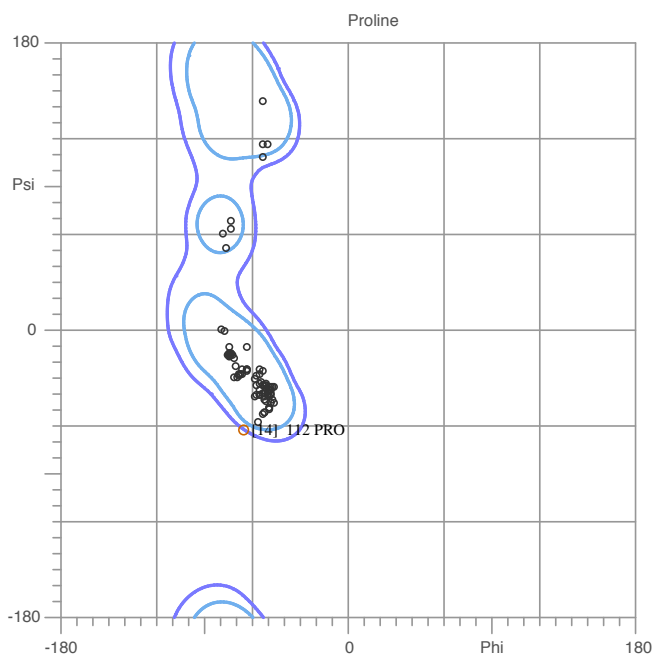
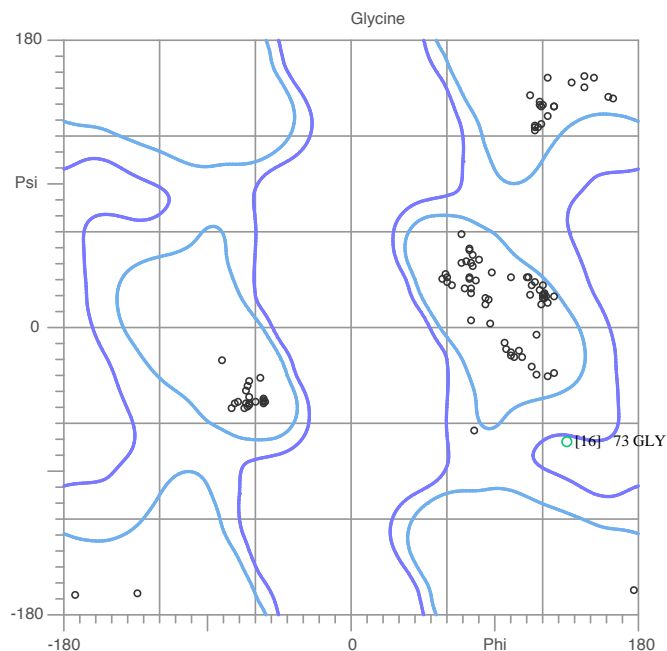
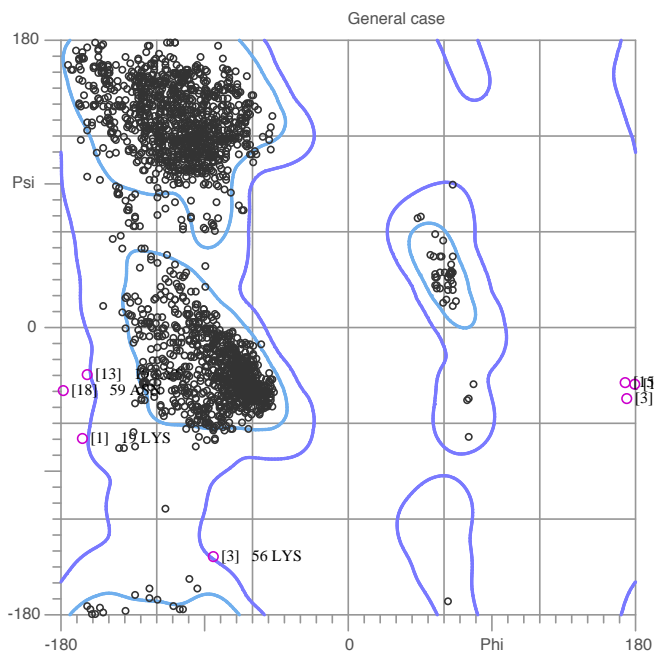


# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, all models



96.0% (2284/2380) of all residues were in favored (98%) regions.  
99.6% (2371/2380) of all residues were in allowed (>99.8%) regions.

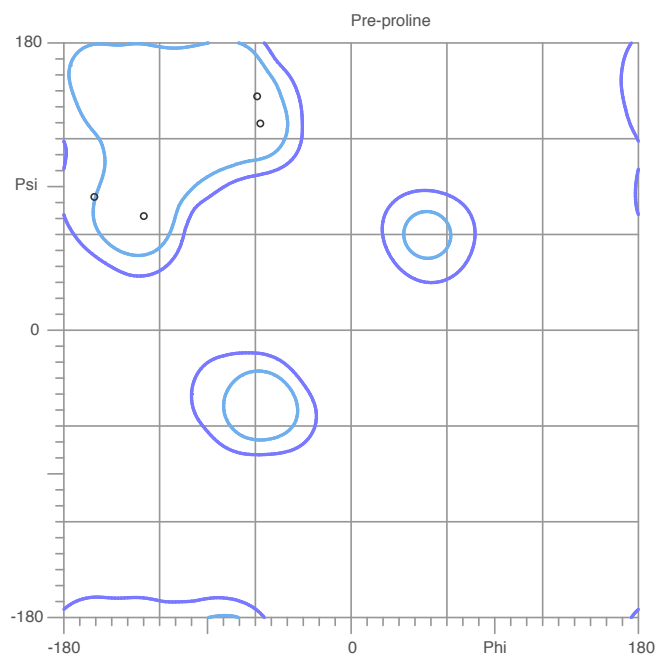
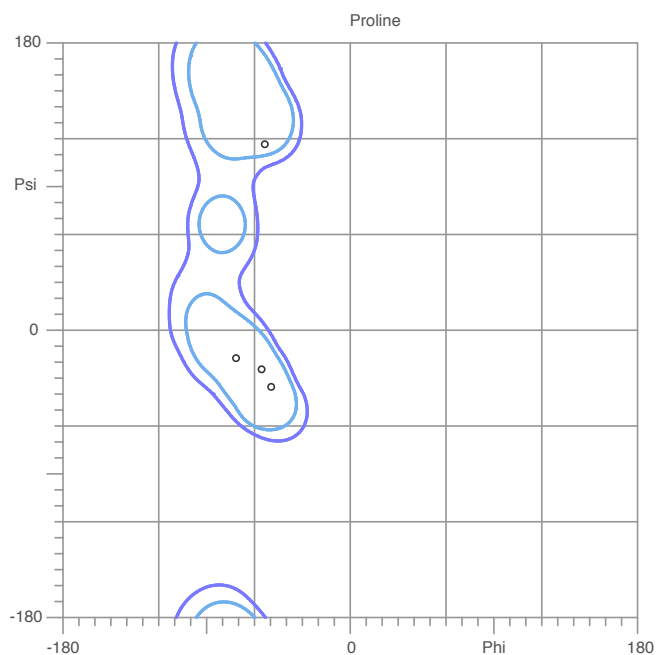
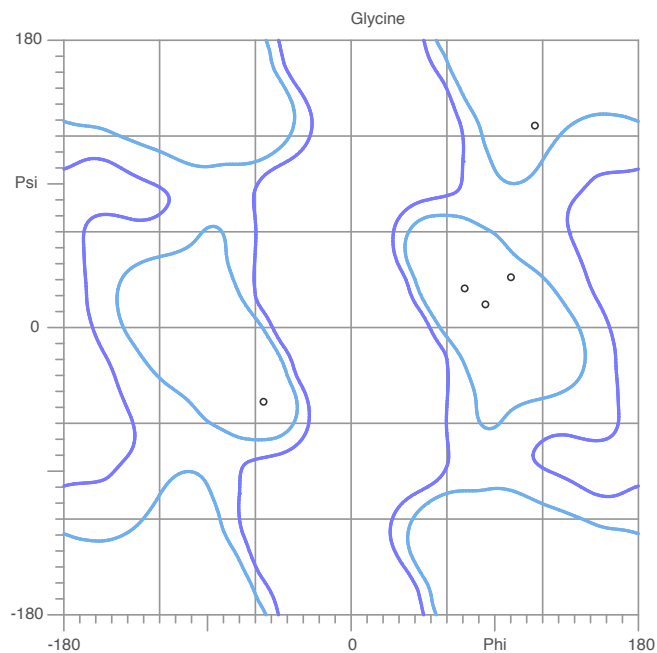
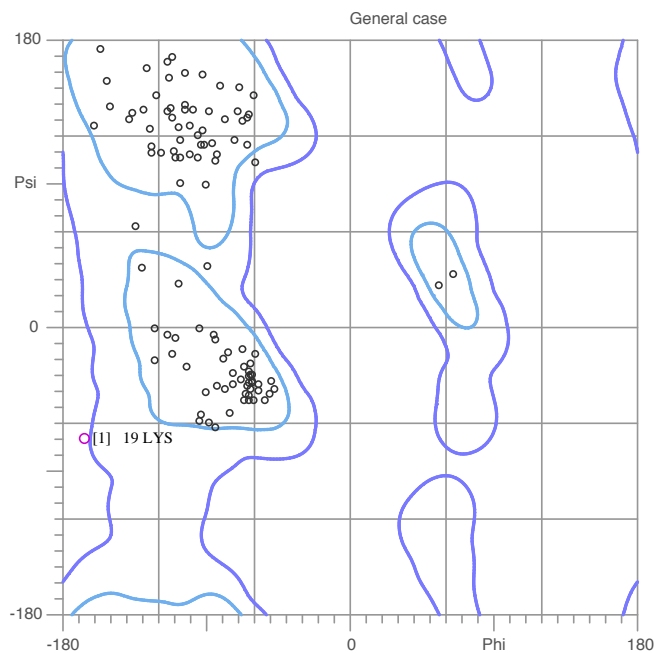
There were 9 outliers (phi, psi):

- [1] 19 LYS (-167.2, -69.7)
- [3] 56 LYS (-85.0, -143.8)

- [3] 72 ASP (174.9, -45.0)
- [12] 59 ASN (179.3, -35.8)
- [13] 19 LYS (-165.0, -29.5)
- [14] 112 PRO (-66.6, -62.8)
- [15] 59 ASN (173.9, -35.0)
- [16] 73 GLY (135.0, -71.8)
- [18] 59 ASN (-179.8, -39.7)

# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 1

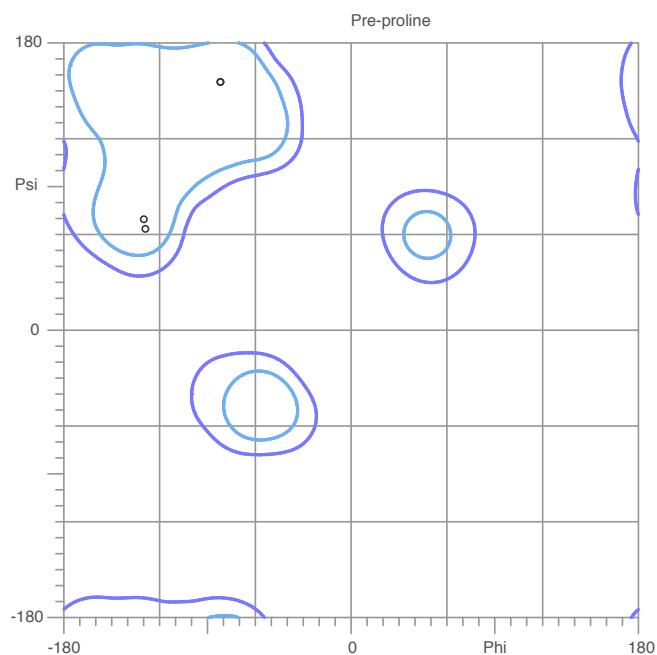
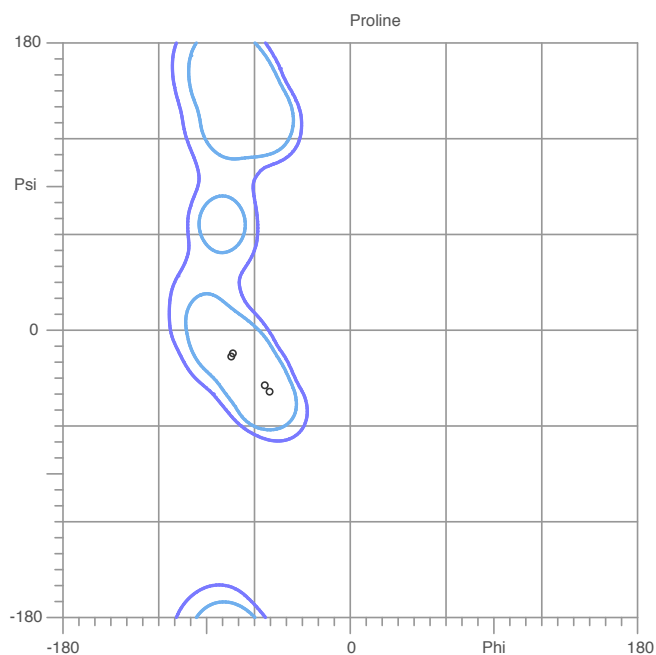
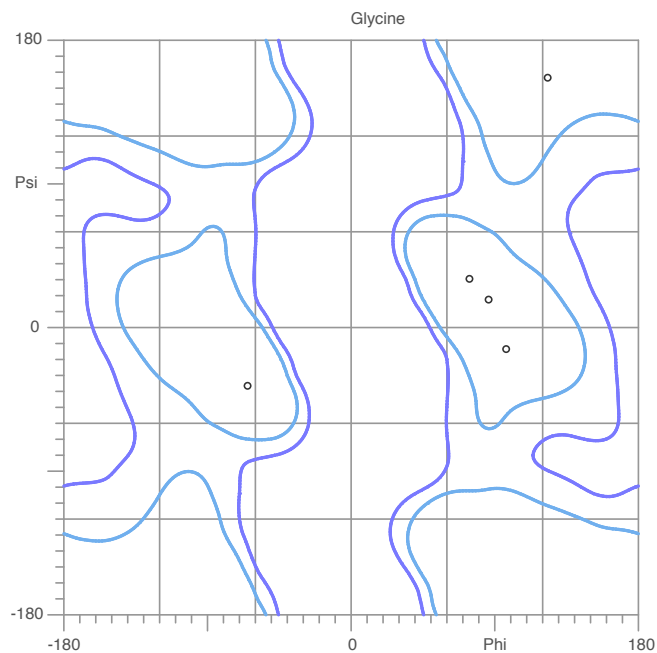
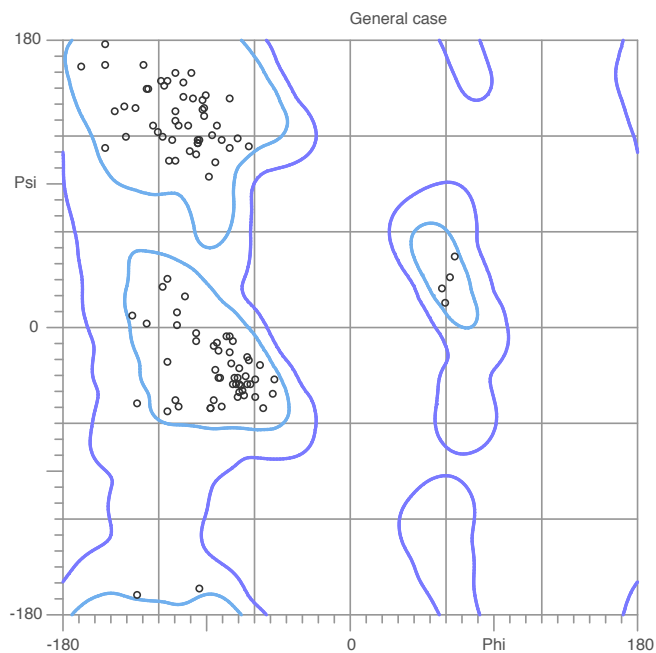


95.8% (114/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[1] 19 LYS (-167.2, -69.7)

# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 2



97.5% (116/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

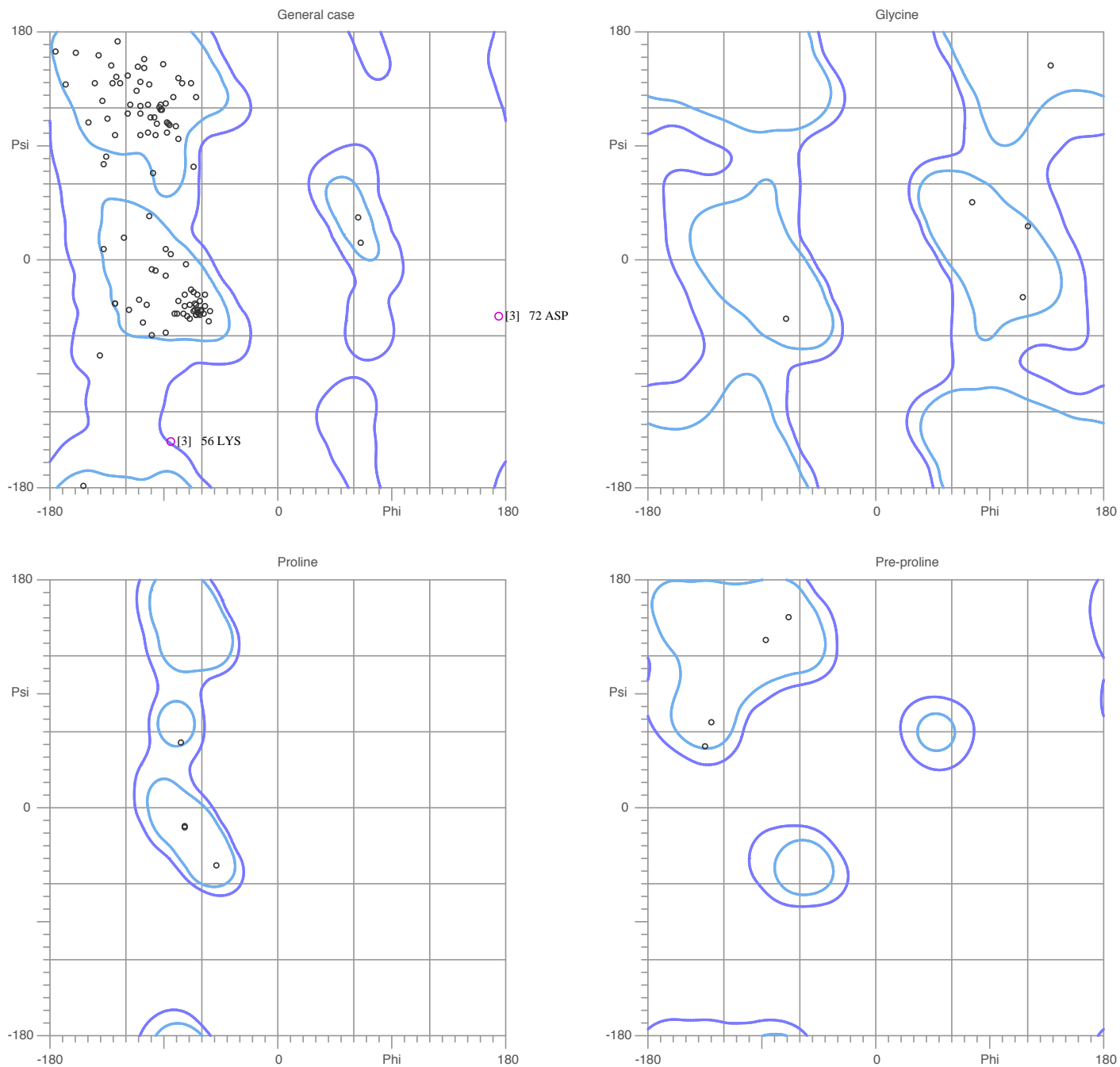
There were no outliers.

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 3



94.1% (112/119) of all residues were in favored (98%) regions.  
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

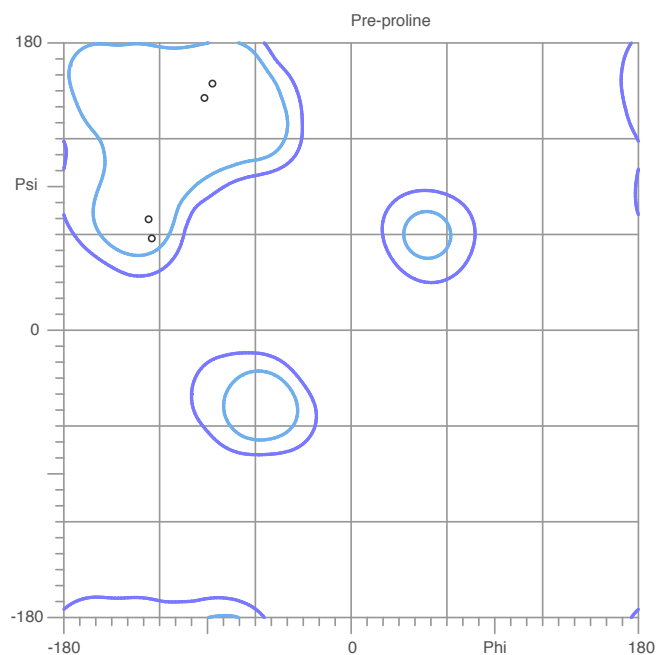
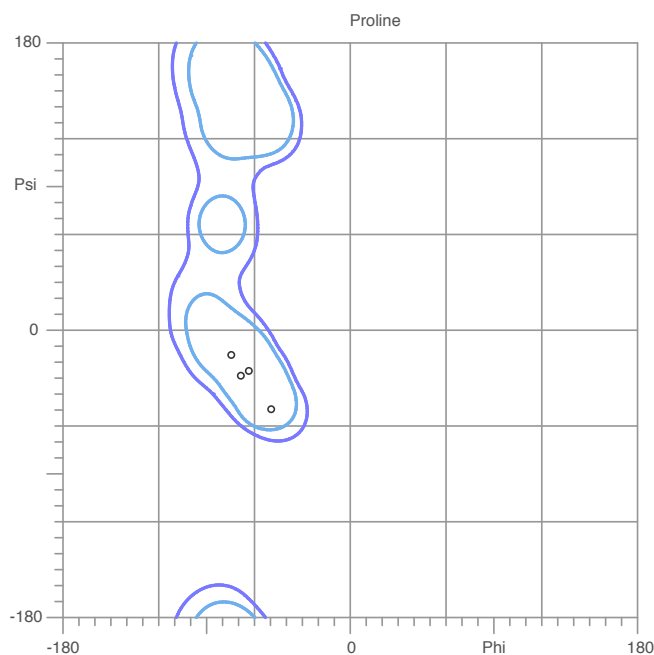
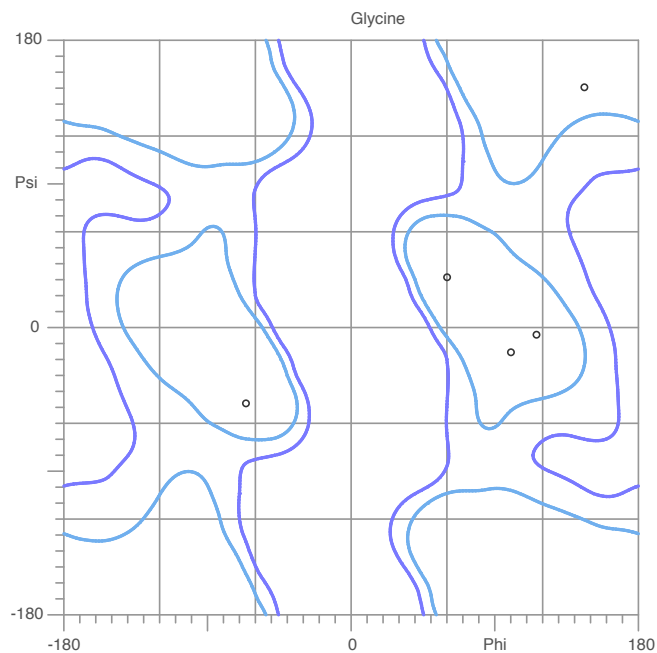
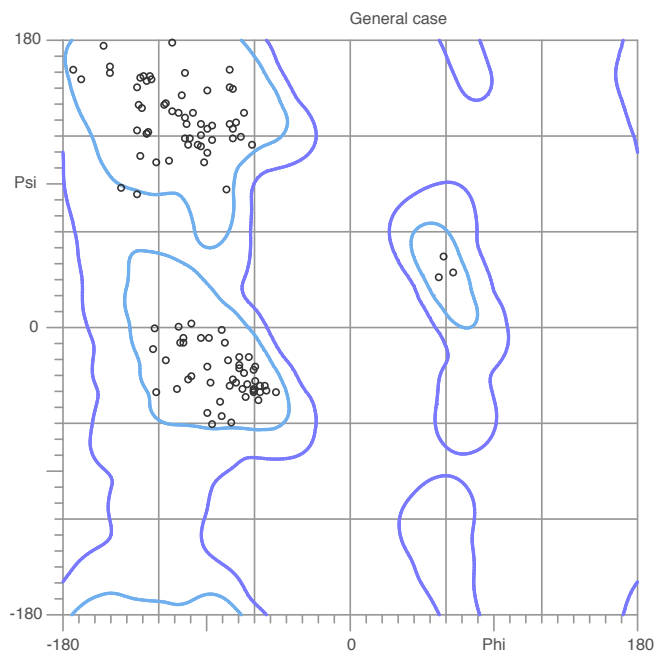
There were 2 outliers (phi, psi):

[3] 56 LYS (-85.0, -143.8)

[3] 72 ASP (174.9, -45.0)

# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 4



98.3% (117/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

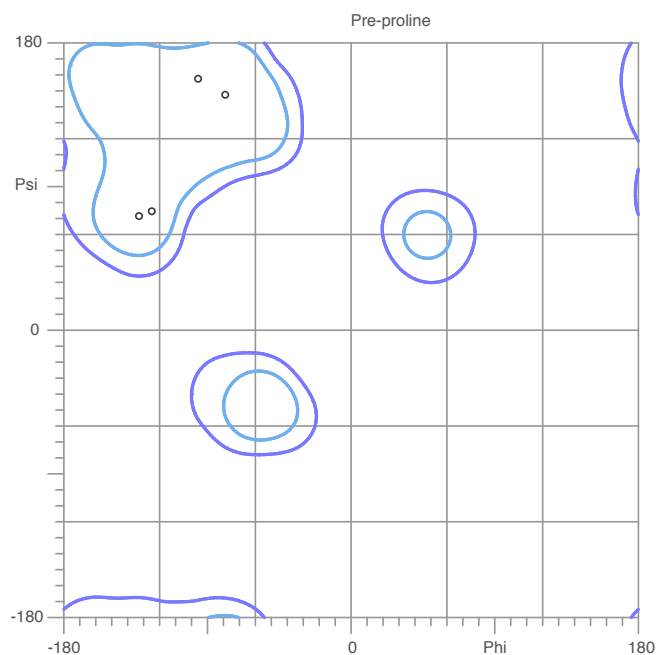
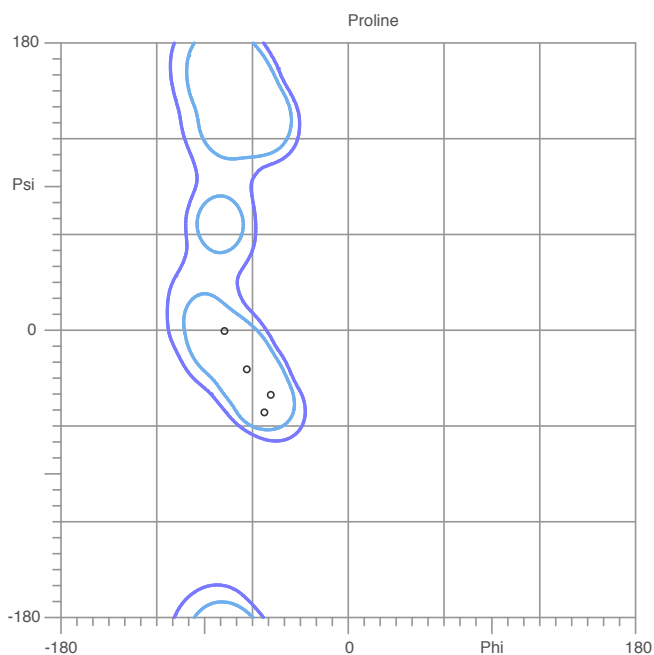
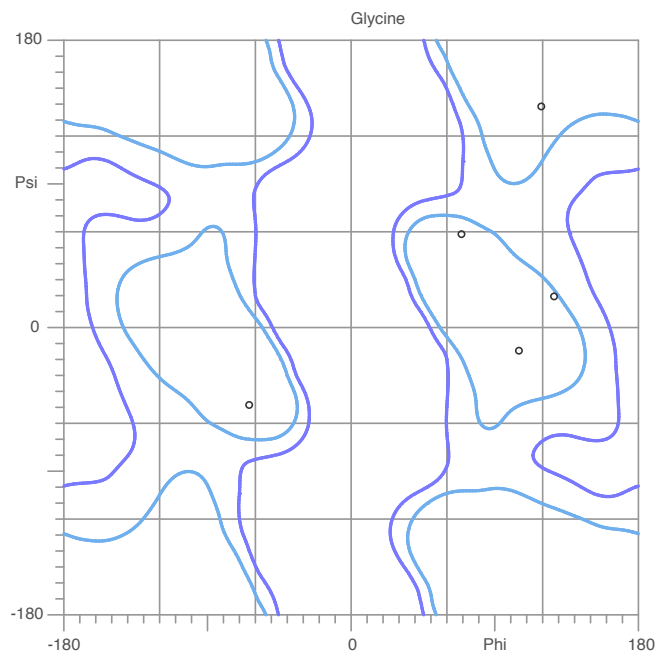
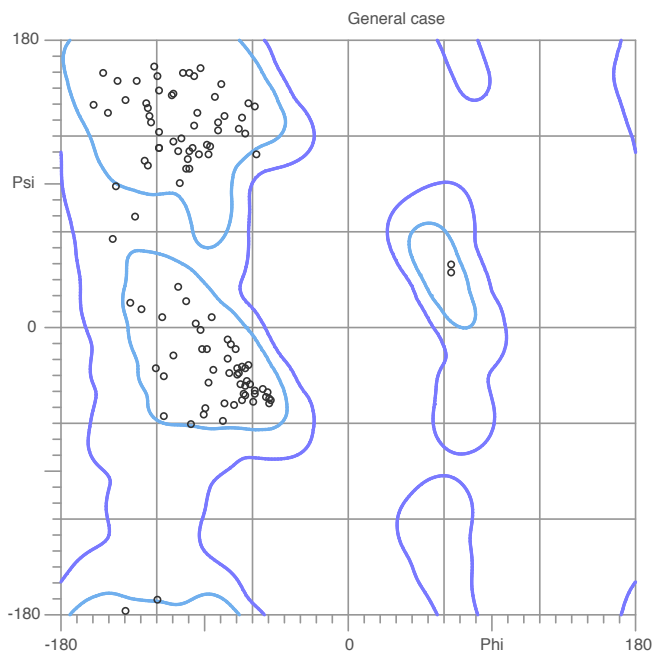
There were no outliers.

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 5



95.8% (114/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

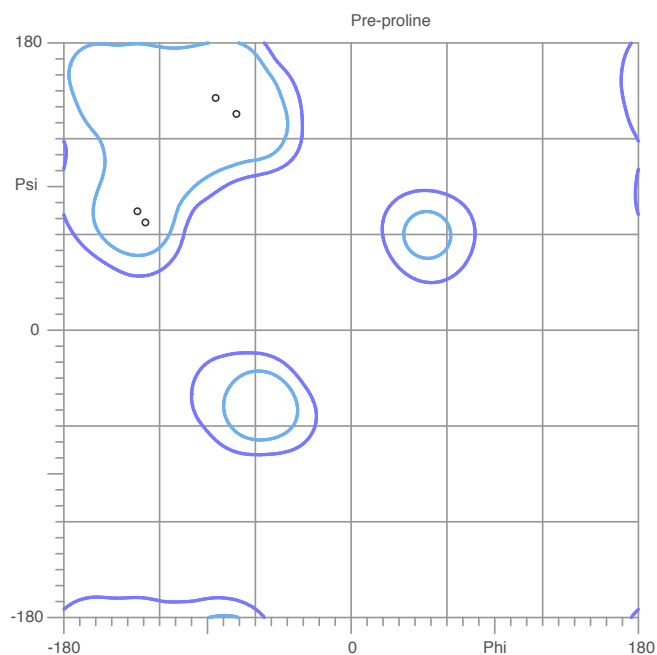
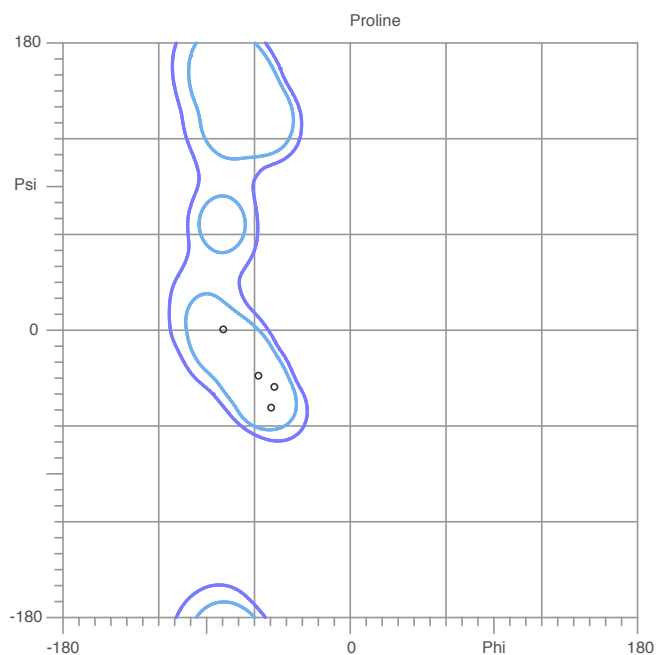
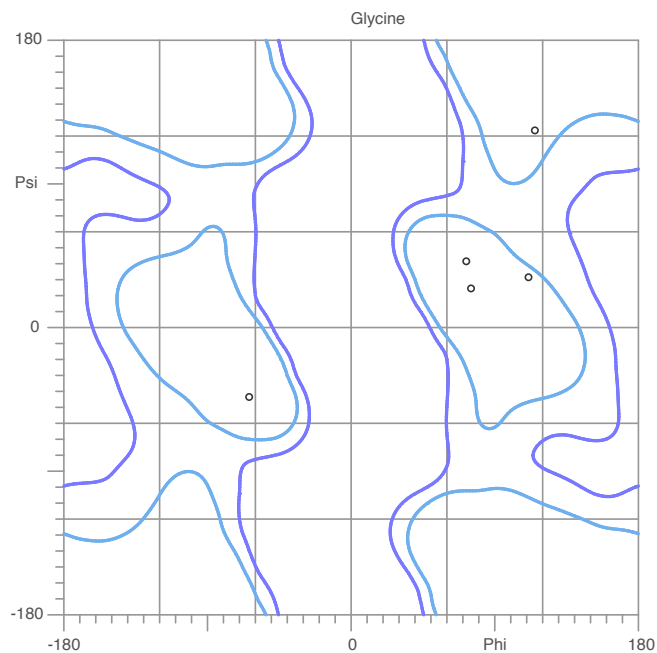
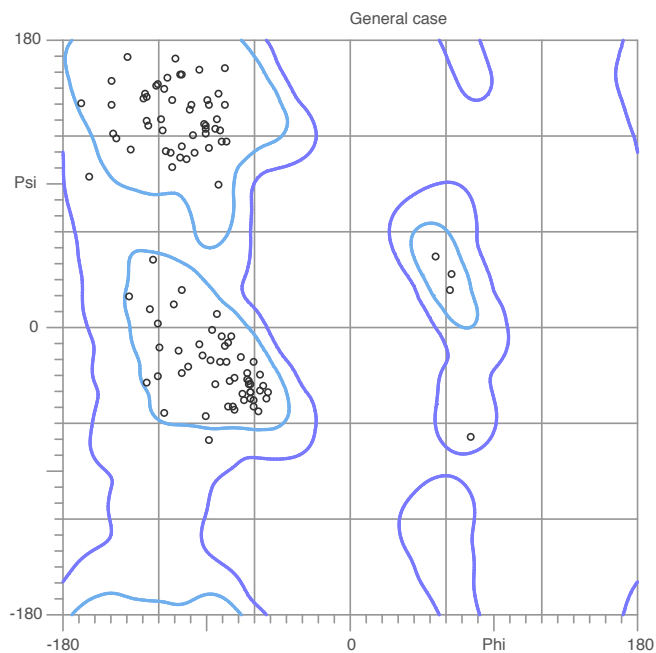
There were no outliers.

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 6



97.5% (116/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

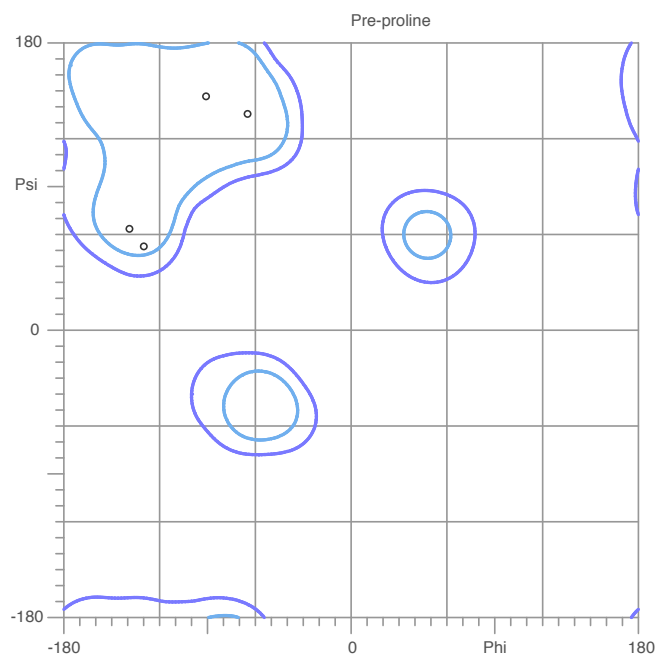
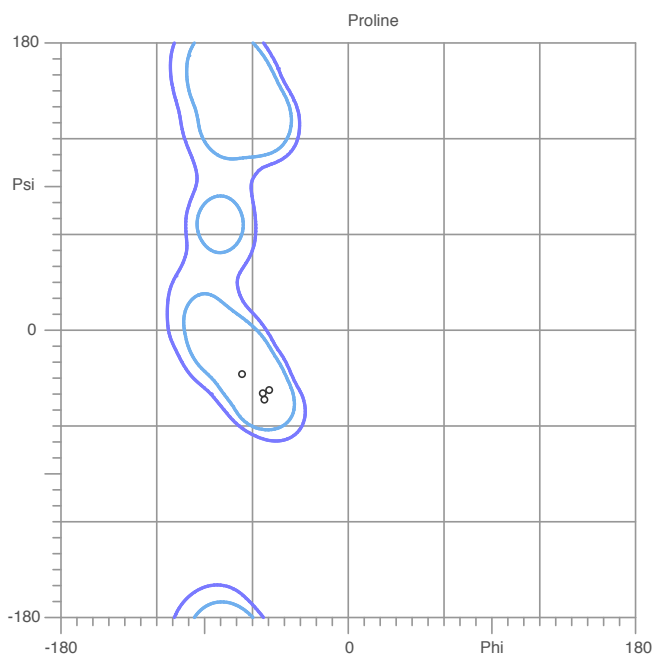
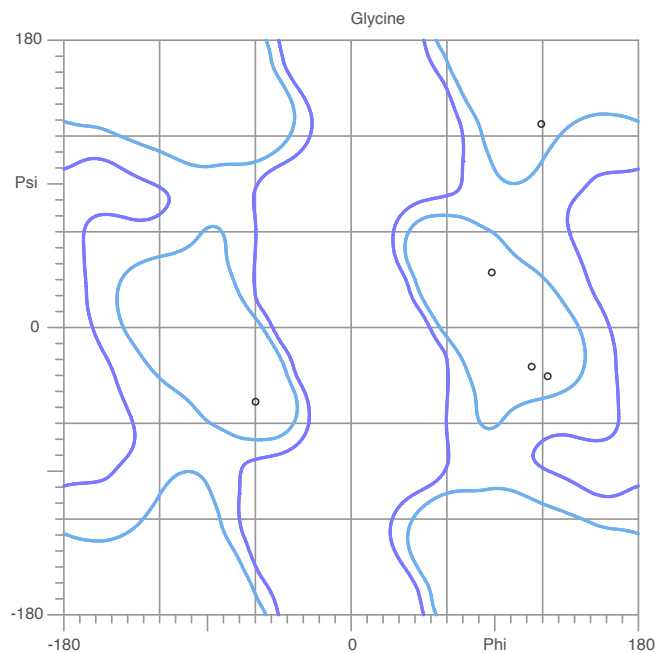
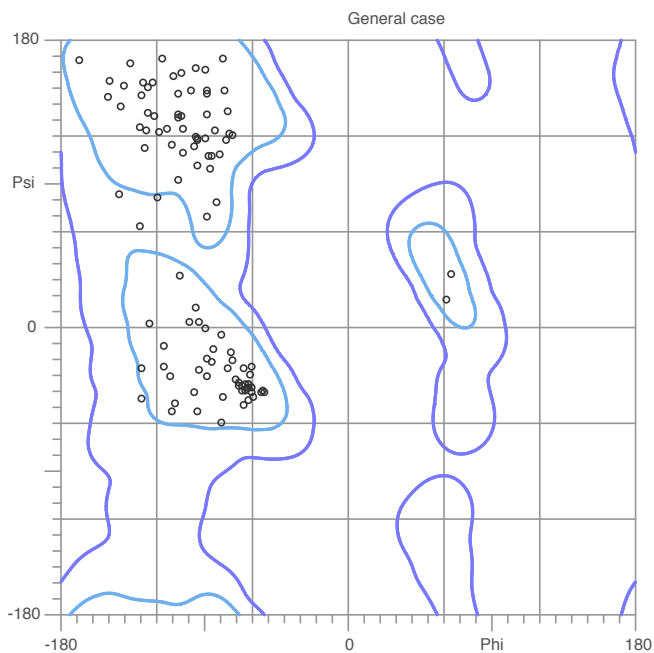
There were no outliers.

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 7



96.6% (115/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

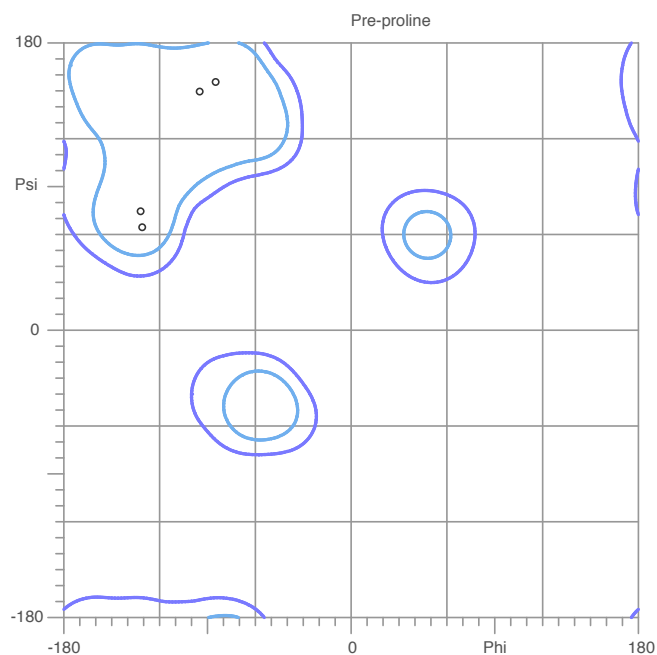
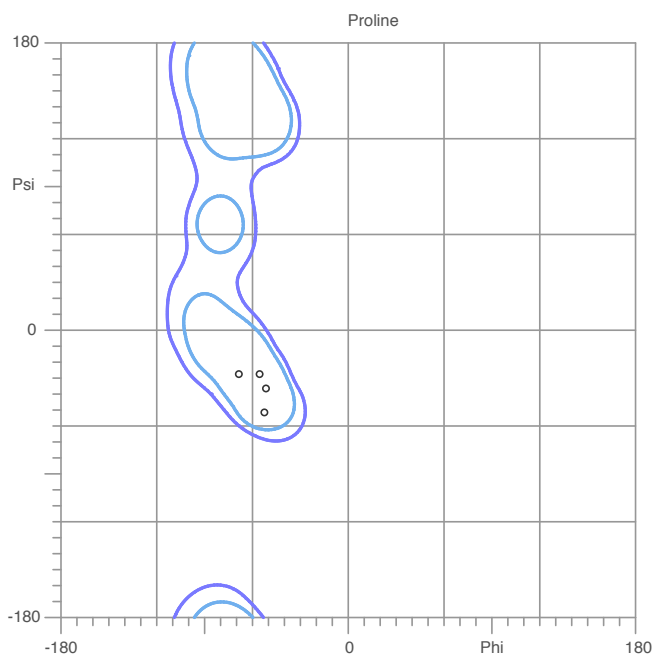
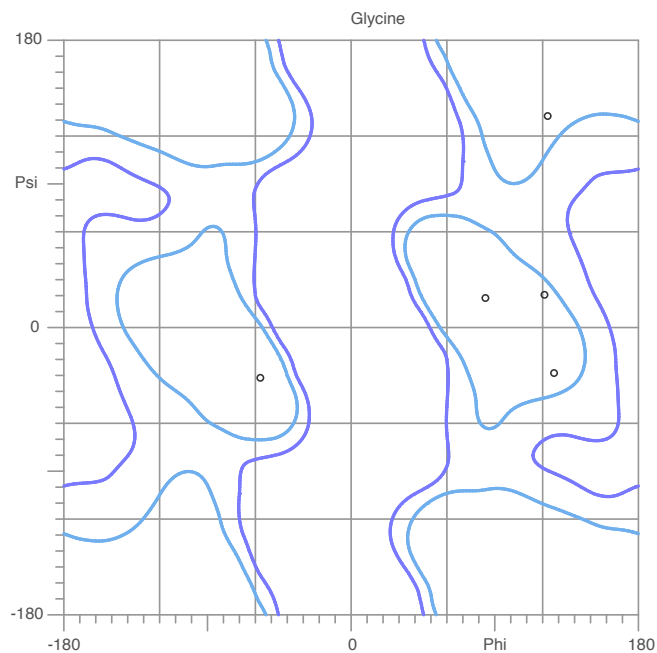
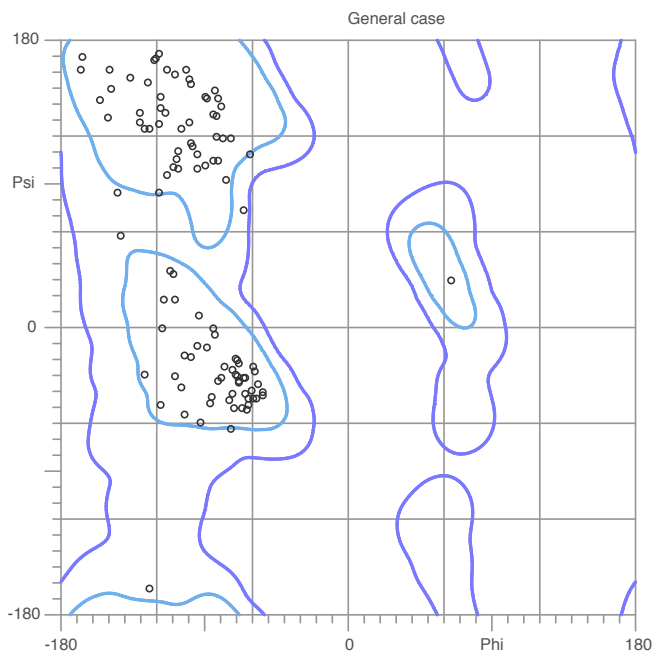
There were no outliers.

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 8



95.8% (114/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

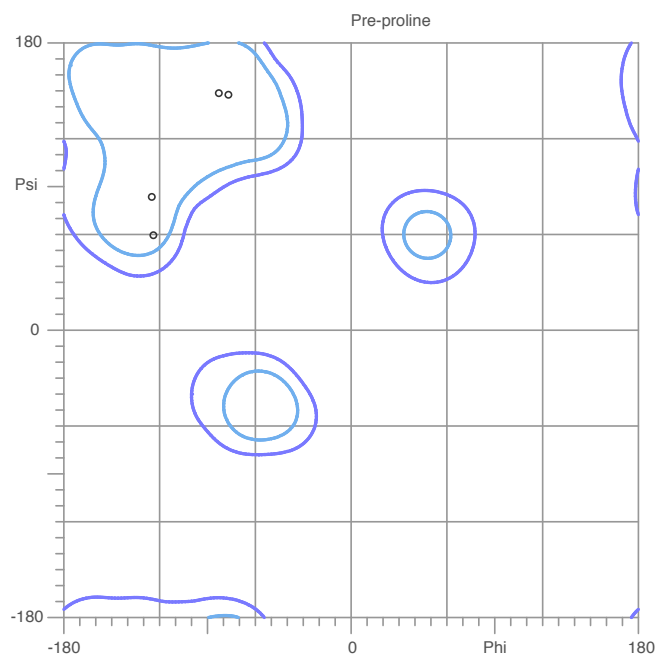
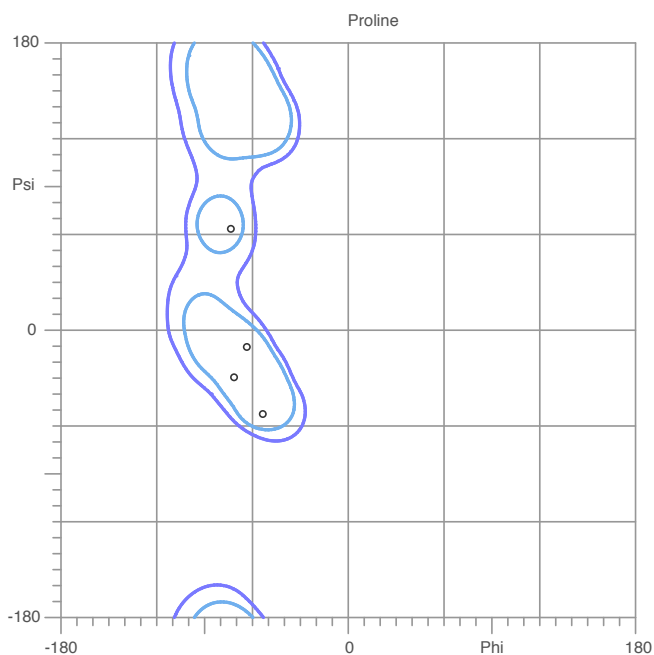
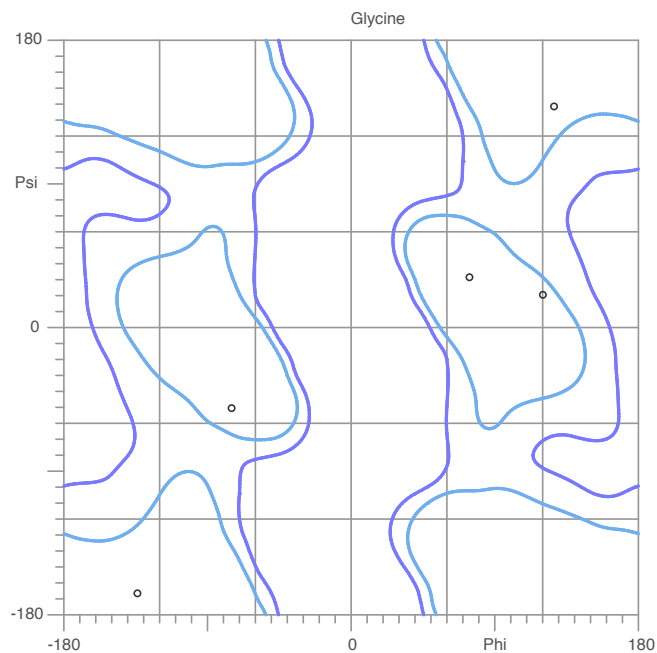
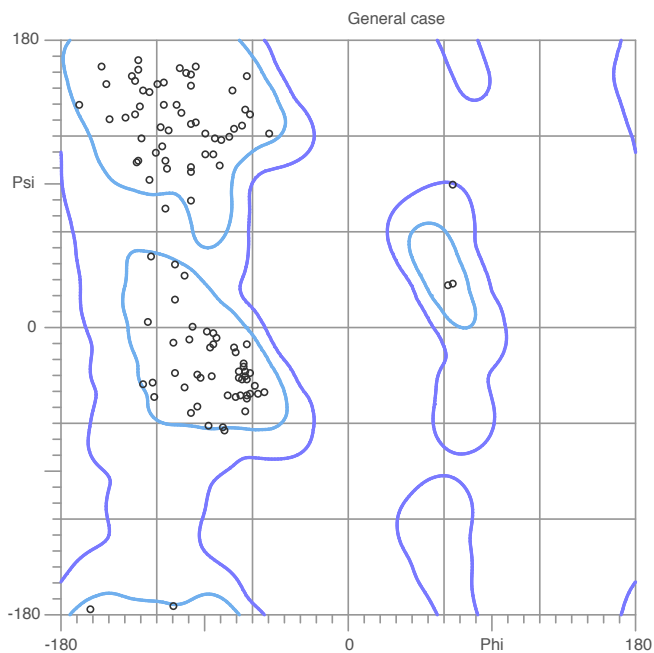
There were no outliers.

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 9



97.5% (116/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

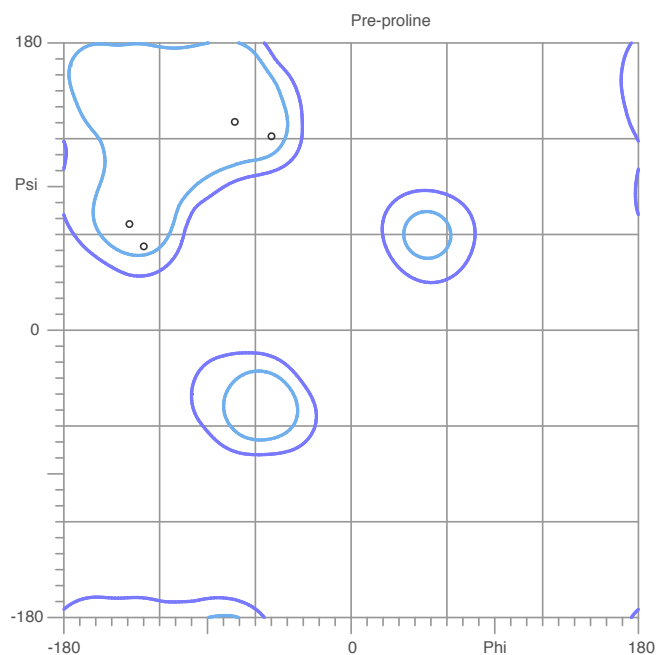
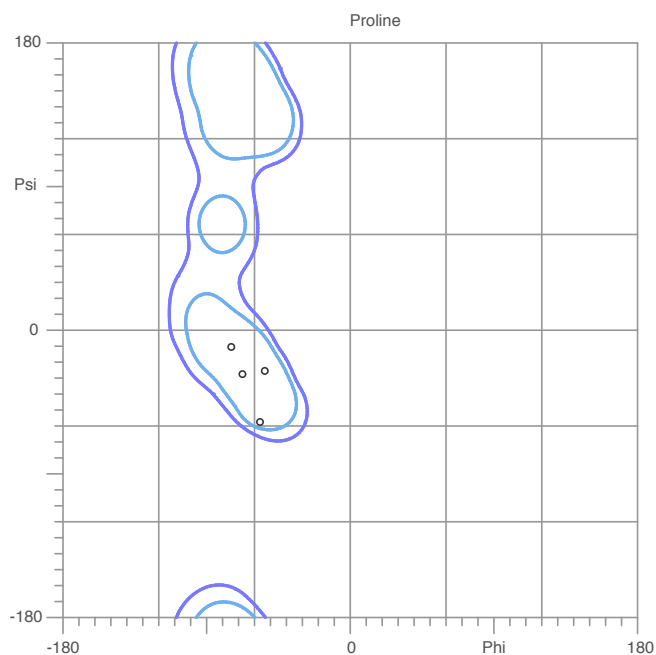
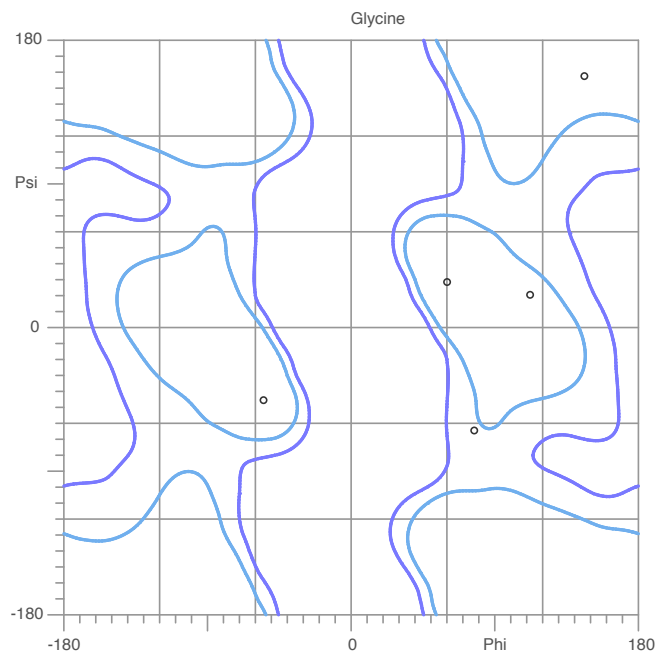
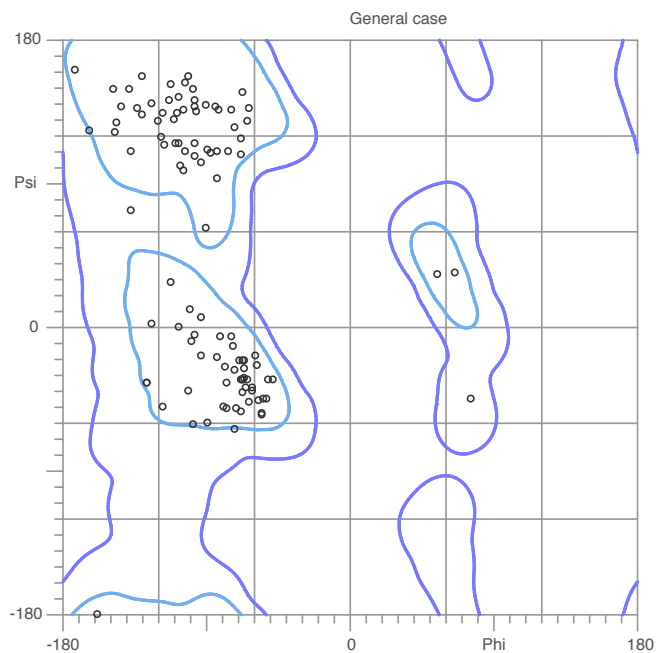
There were no outliers.

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 10

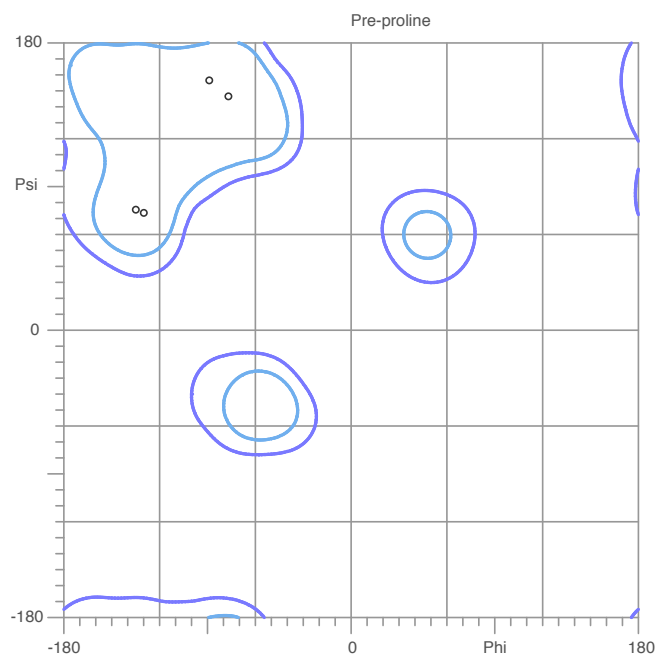
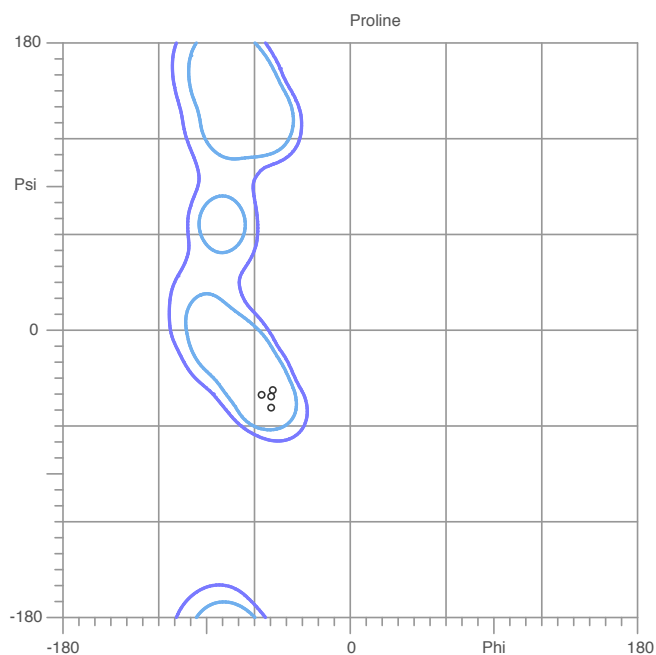
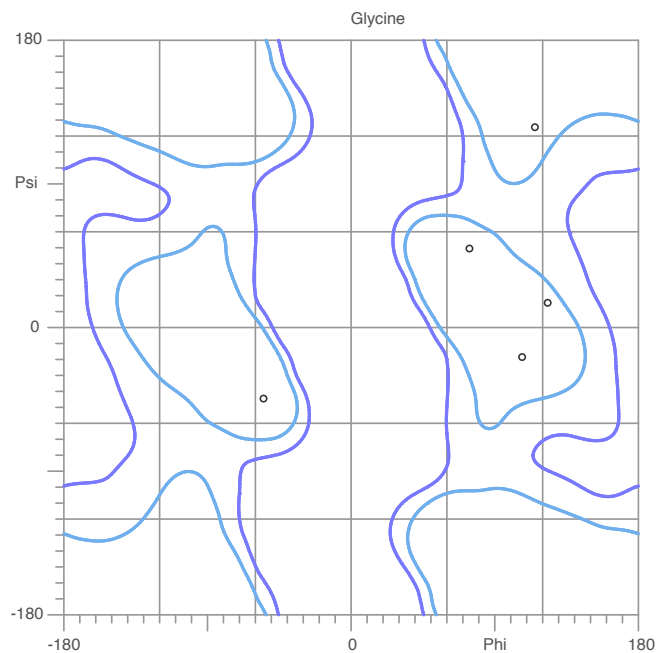
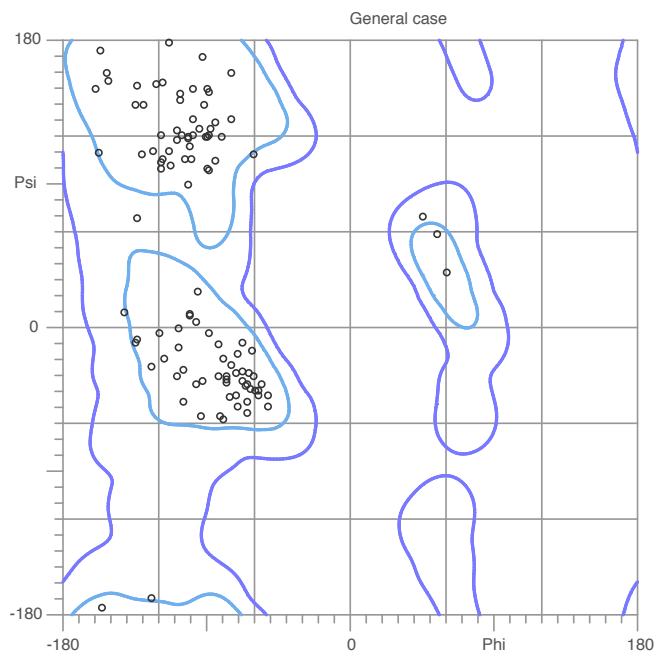


95.8% (114/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 11



95.8% (114/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

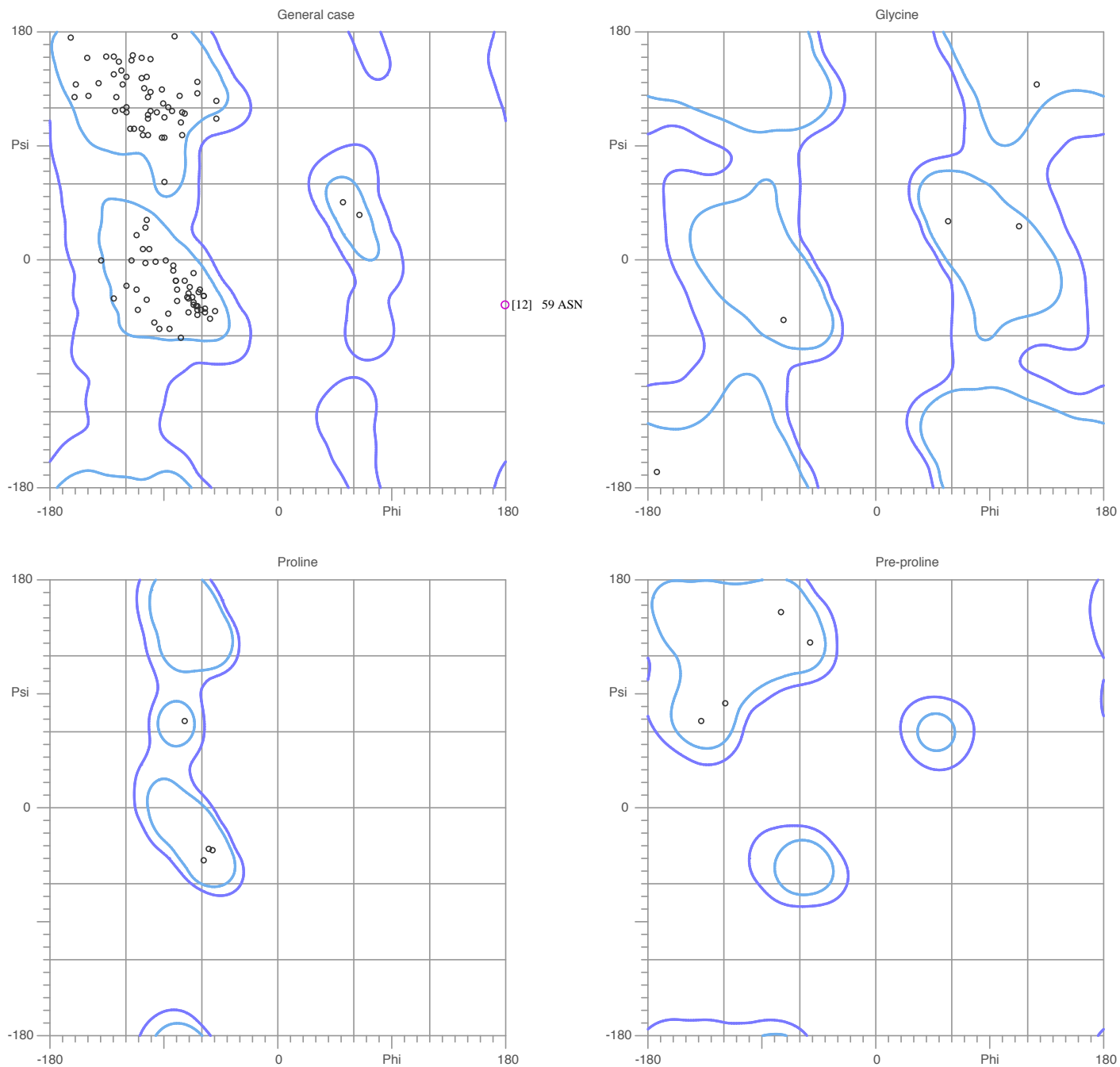
There were no outliers.

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 12



97.5% (116/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

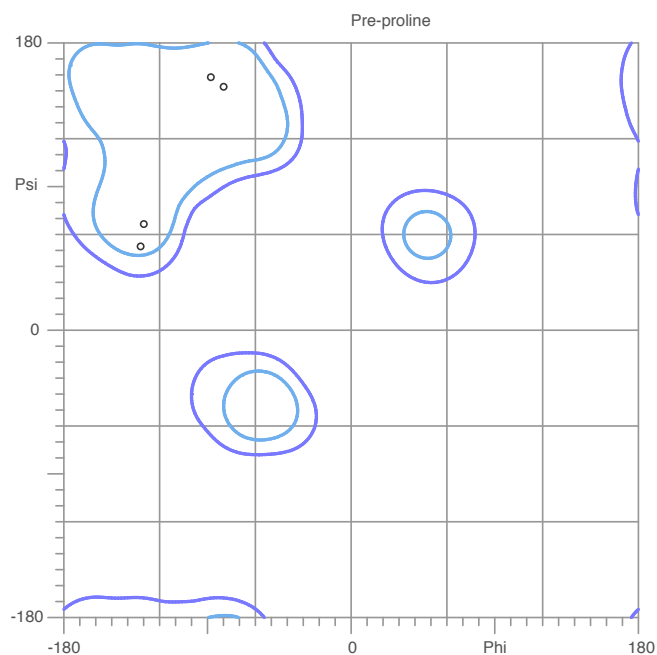
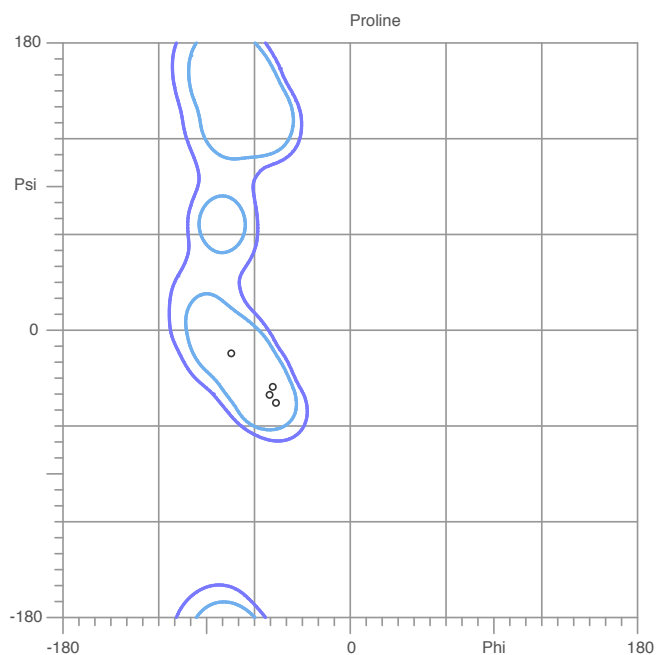
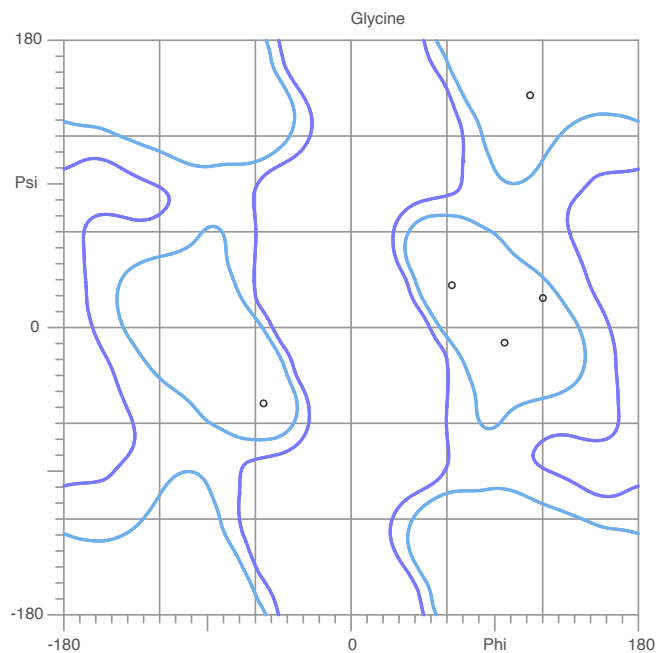
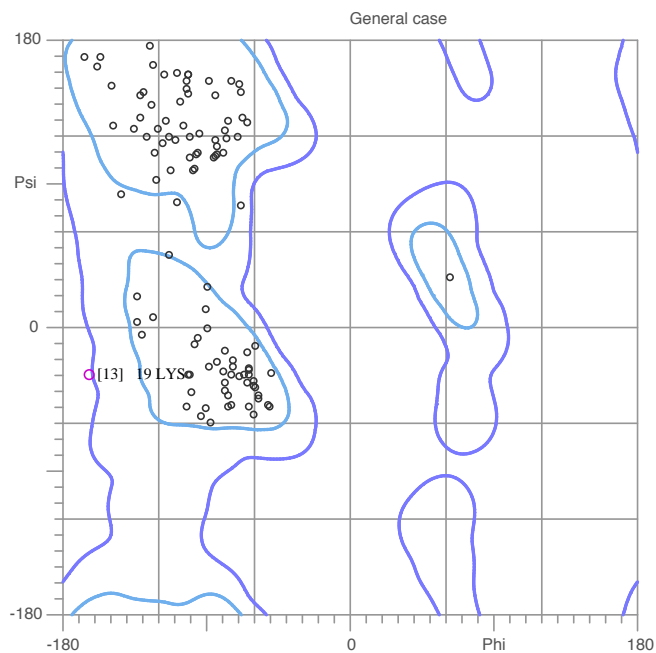
There were 1 outliers (phi, psi):  
[12] 59 ASN (179.3, -35.8)

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 13



95.8% (114/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

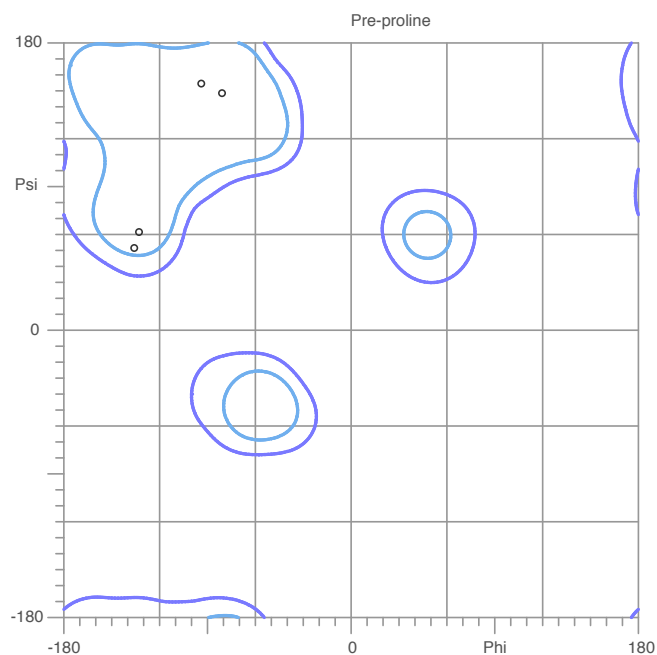
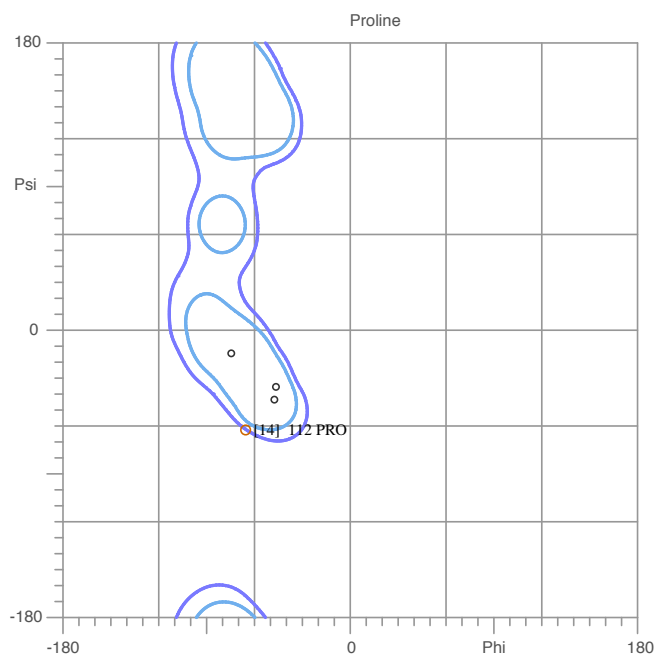
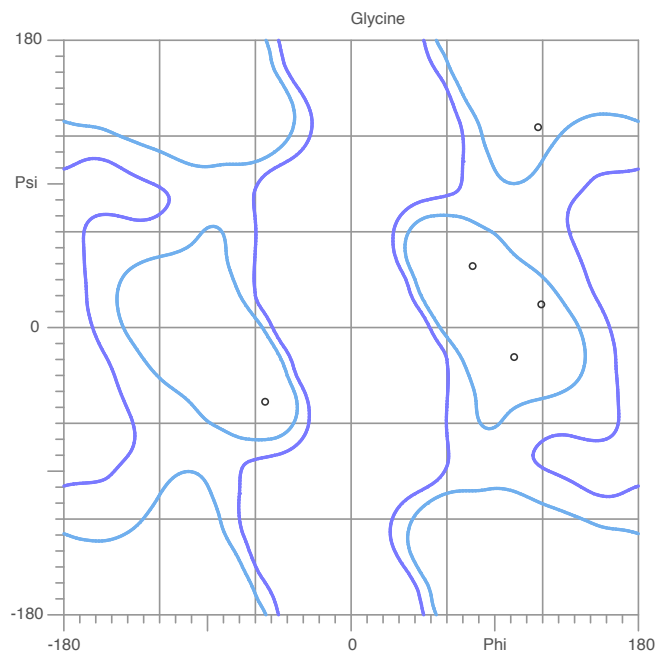
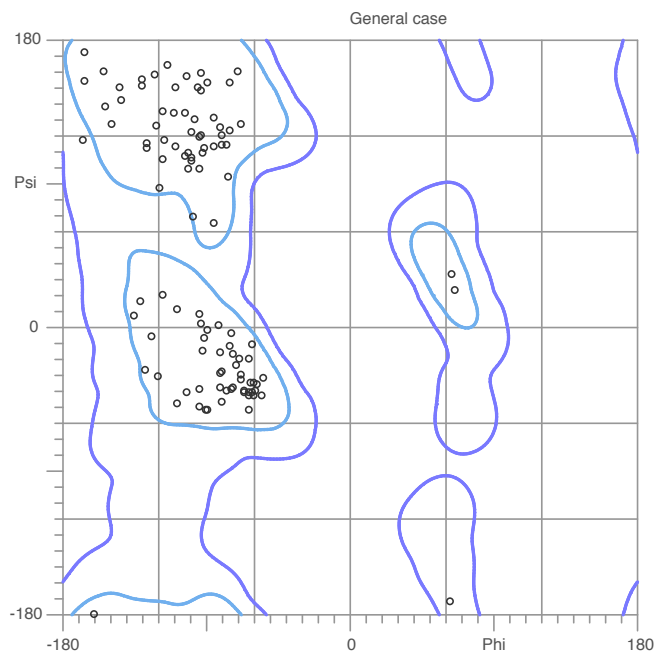
There were 1 outliers (phi, psi):  
[13] 19 LYS (-165.0, -29.5)

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 14



97.5% (116/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

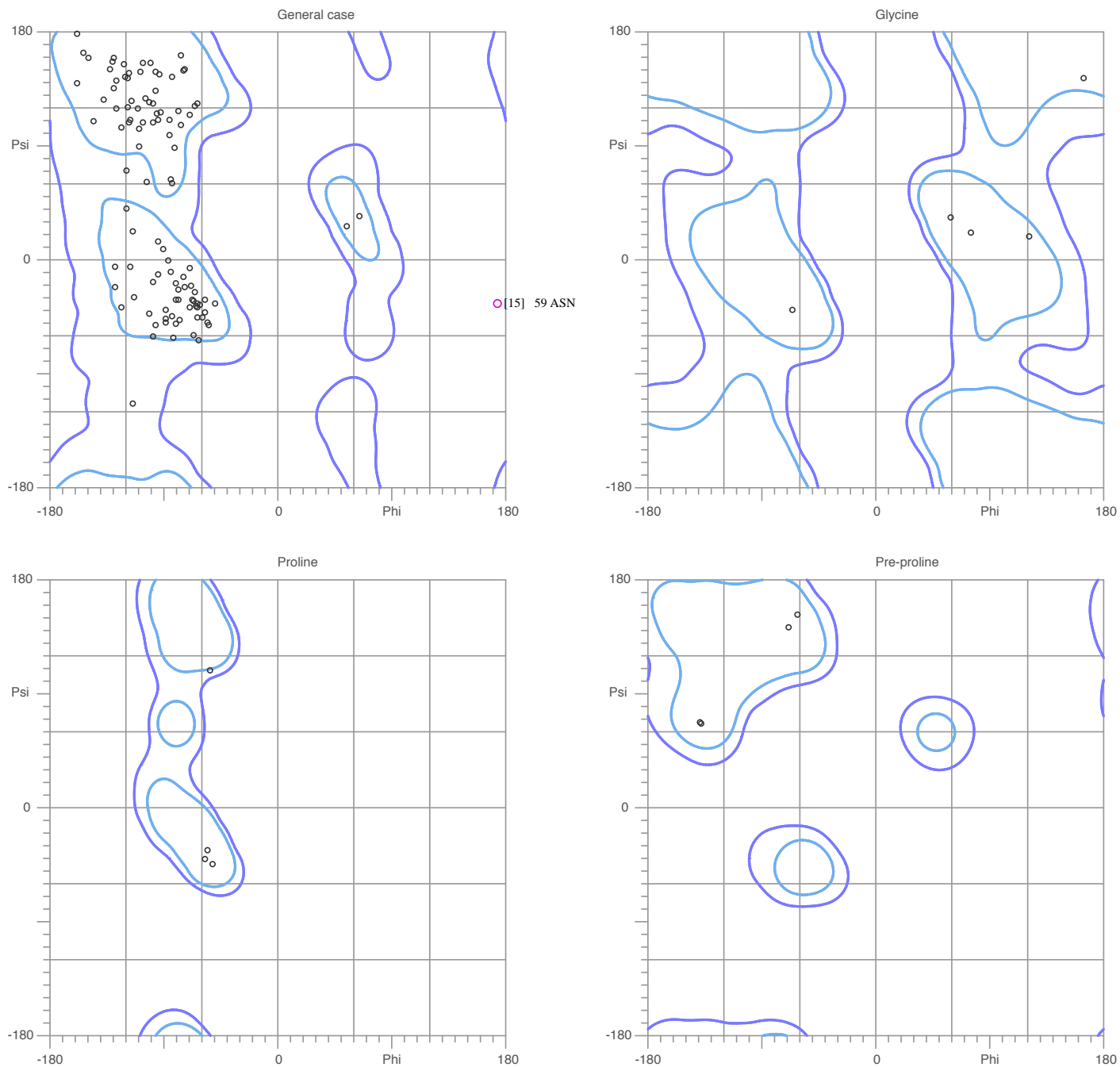
There were 1 outliers (phi, psi):  
[14] 112 PRO (-66.6, -62.8)

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

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 15



95.8% (114/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

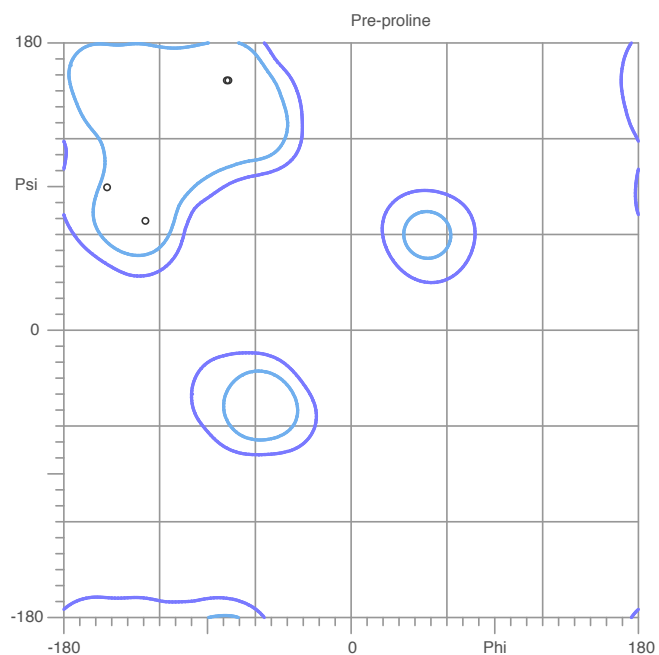
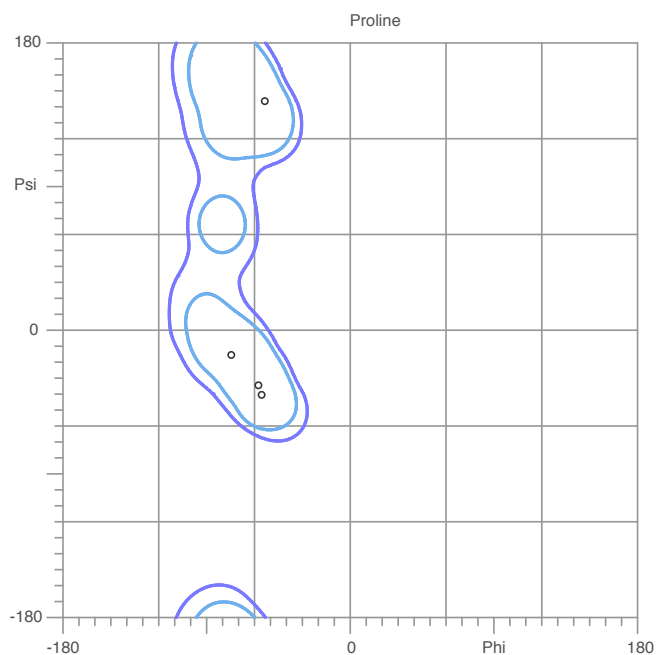
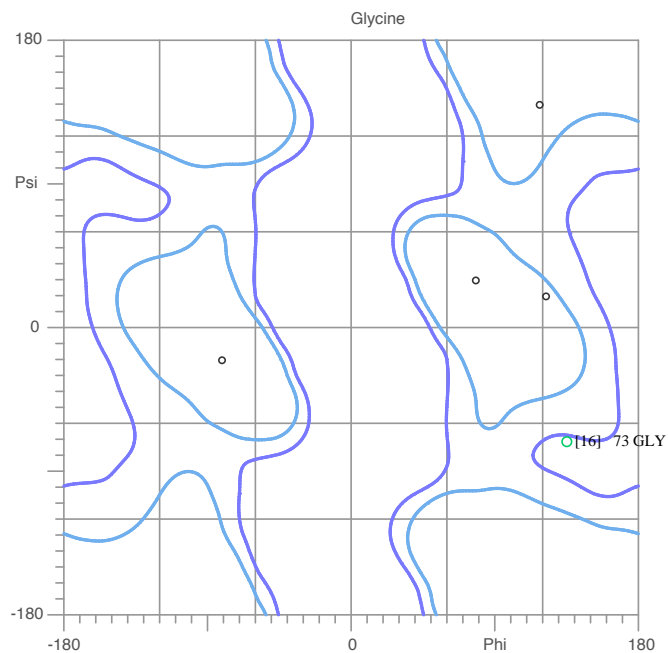
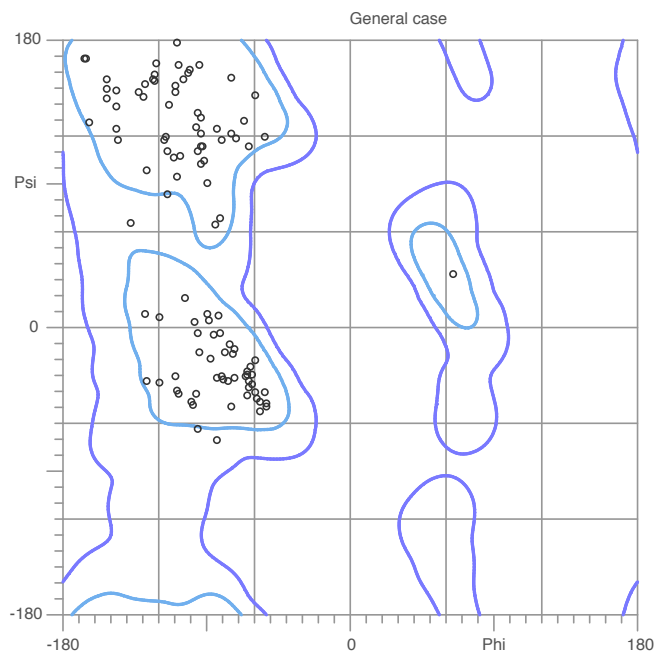
There were 1 outliers ( $\phi$ ,  $\psi$ ):  
[15] 59 ASN (173.9, -35.0)

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

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 16

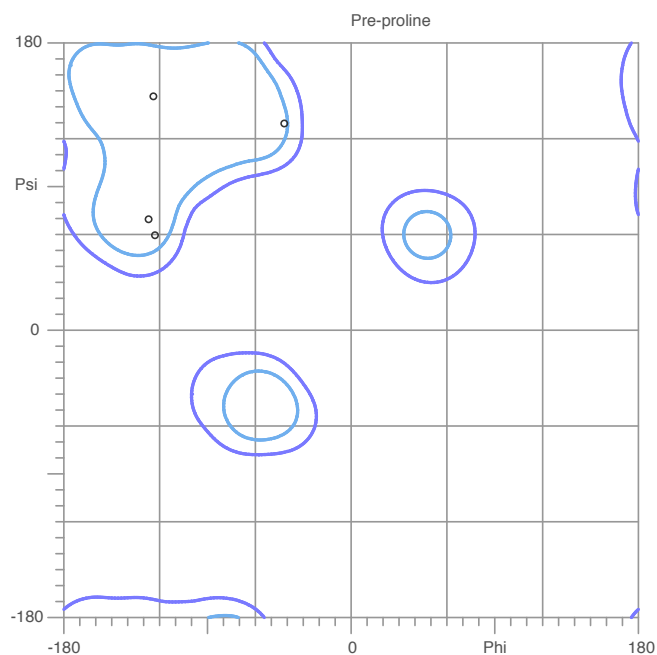
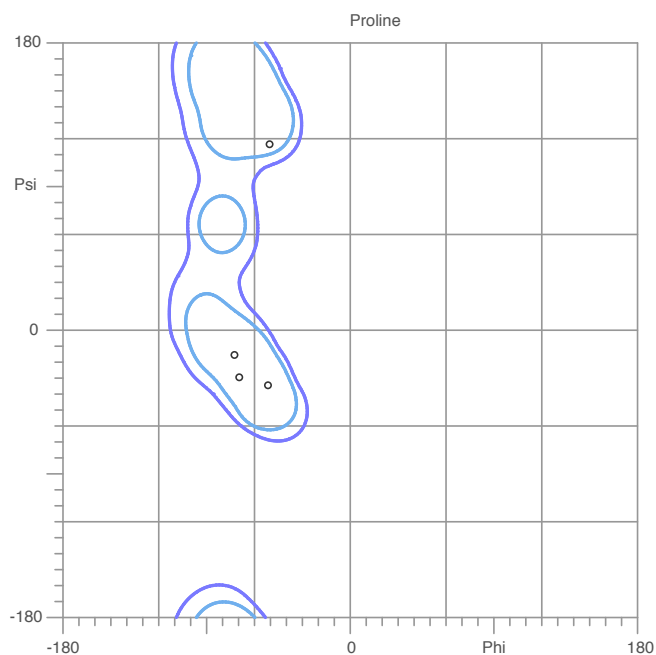
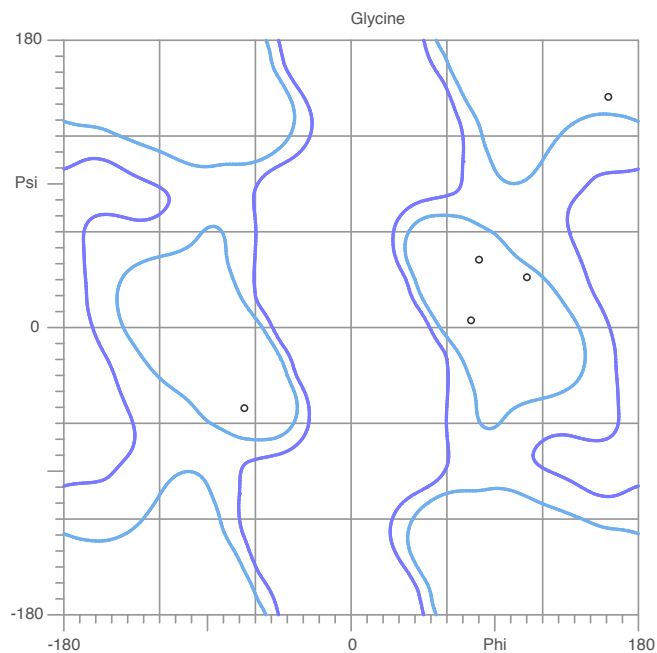
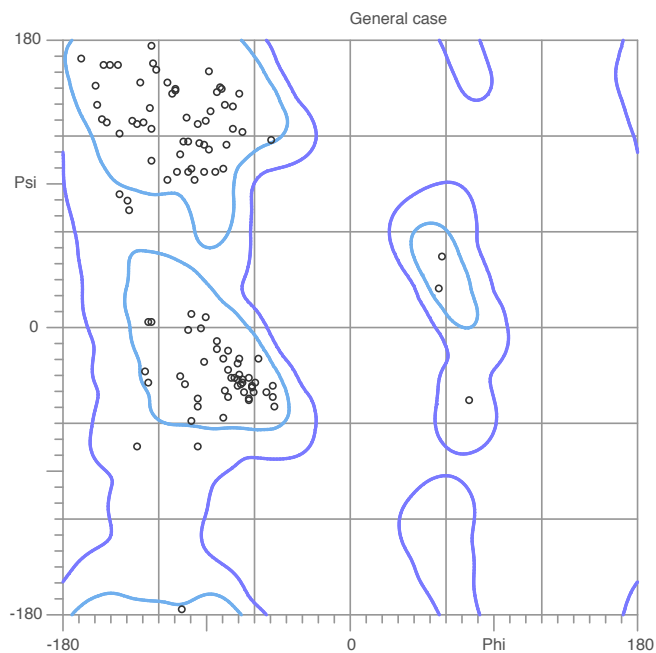


96.6% (115/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[16] 73 GLY (135.0, -71.8)

# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 17



95.0% (113/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

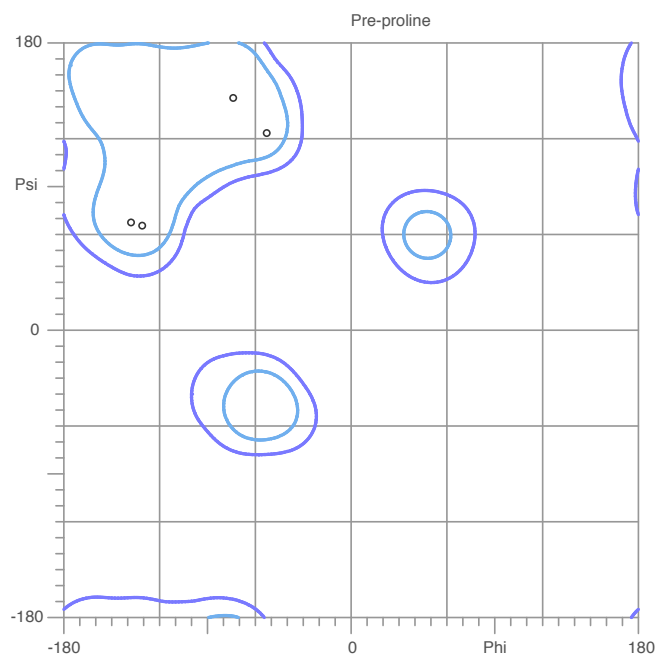
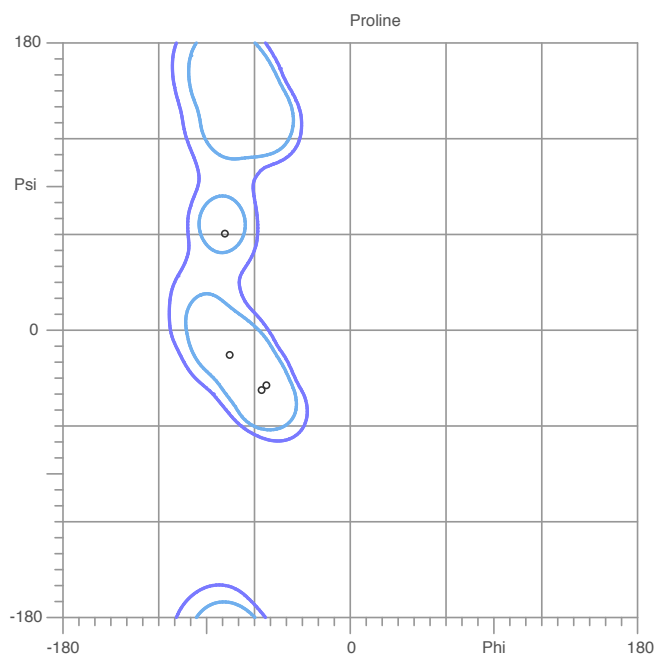
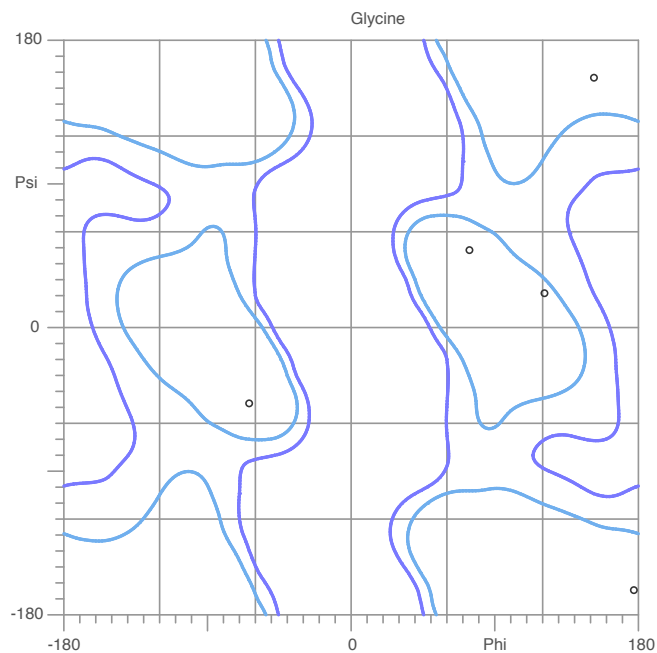
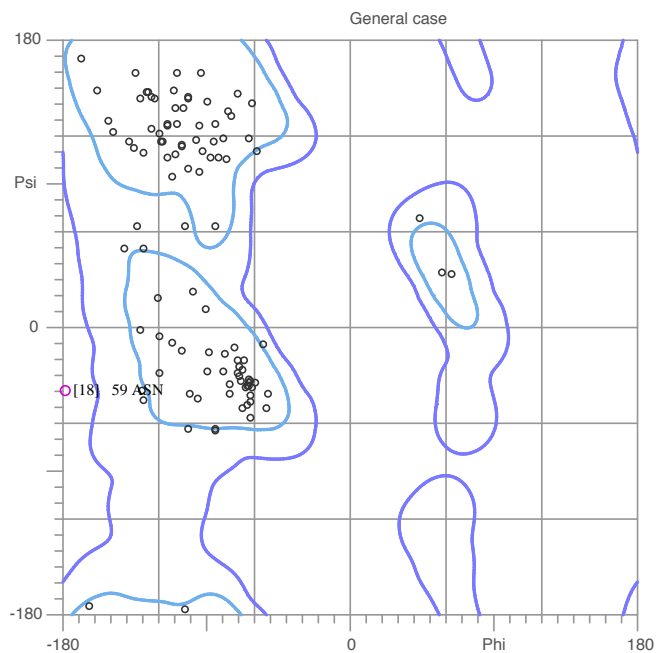
There were no outliers.

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

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# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 18



89.9% (107/119) of all residues were in favored (98%) regions.  
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

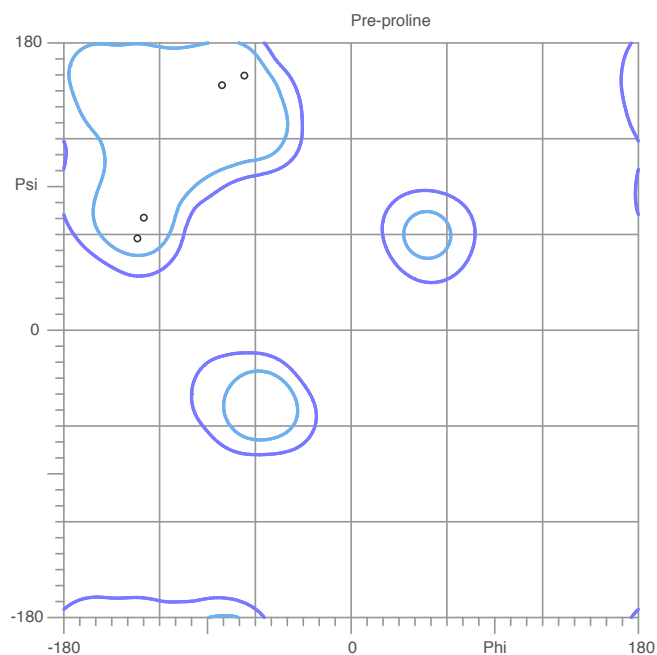
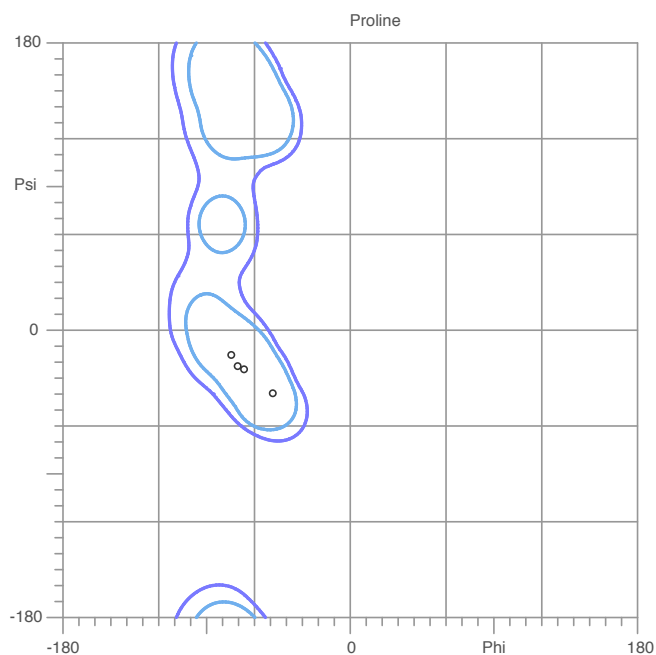
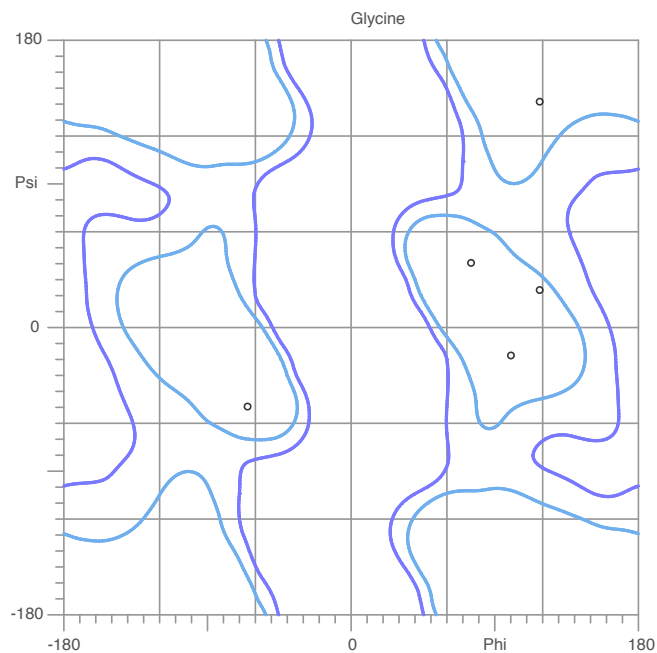
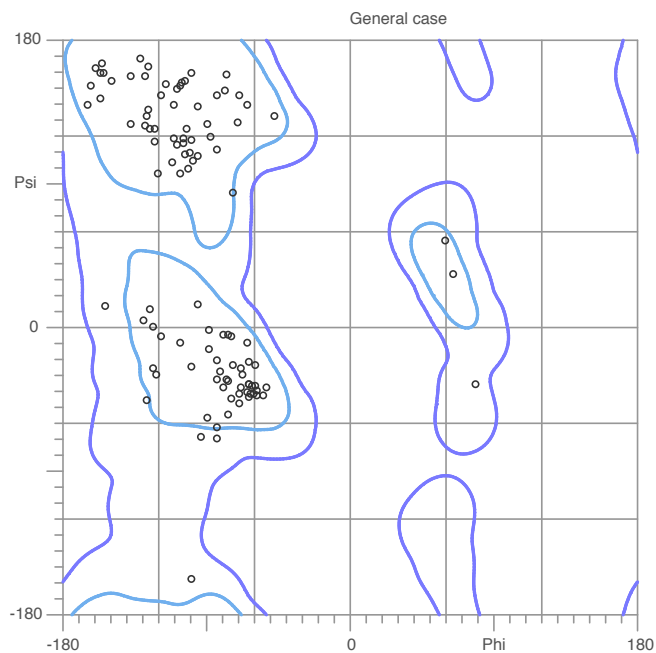
There were 1 outliers (phi, psi):  
[18] 59 ASN (-179.8, -39.7)

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

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

# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 19



95.0% (113/119) of all residues were in favored (98%) regions.  
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

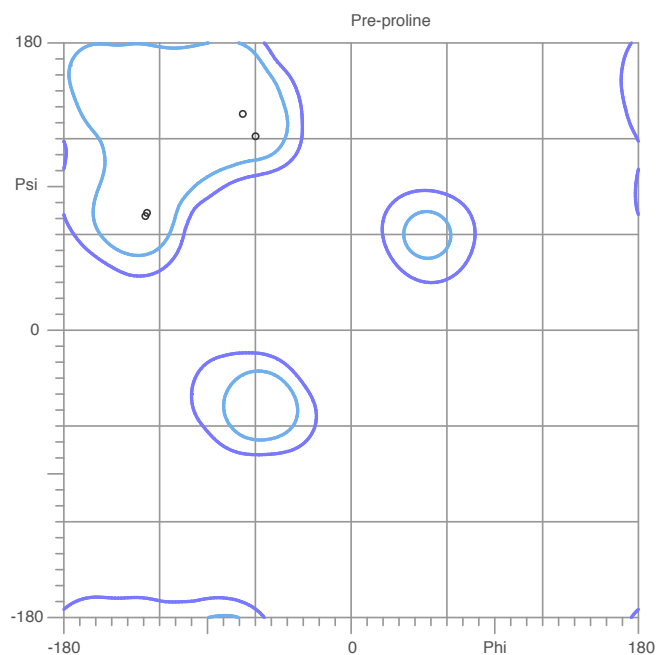
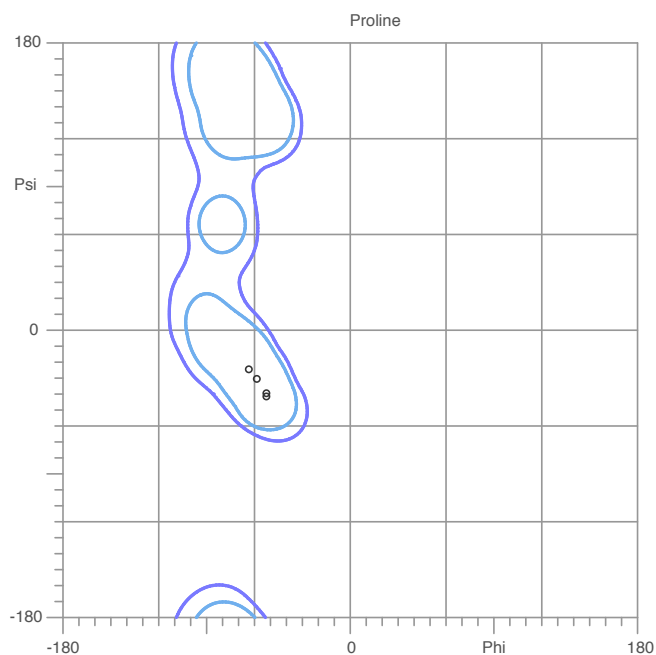
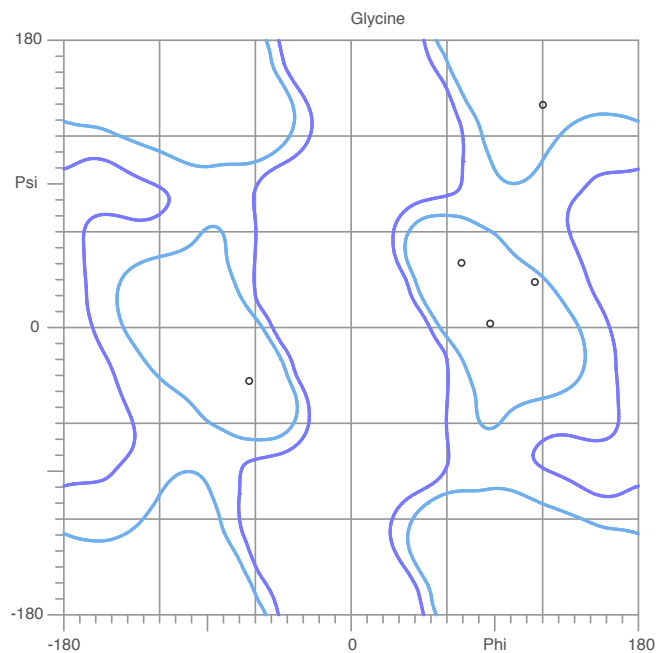
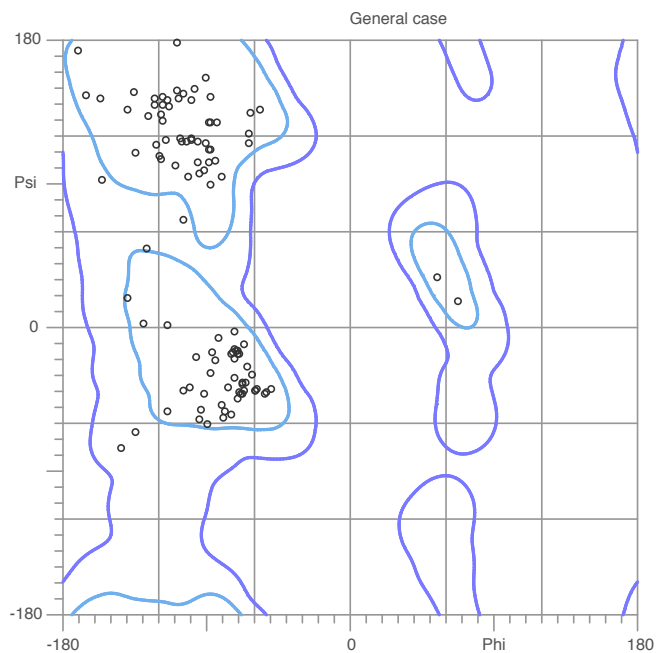
There were no outliers.

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

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

# MolProbity Ramachandran analysis

UUR17A\_R3\_em\_bcr3.pdb, model 20



95.8% (114/119) of all residues were in favored (98%) regions.  
100.0% (119/119) 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)