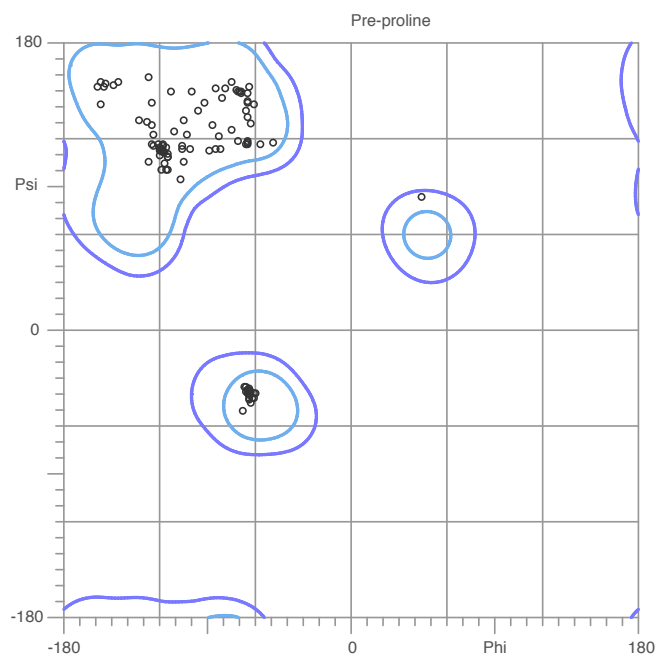
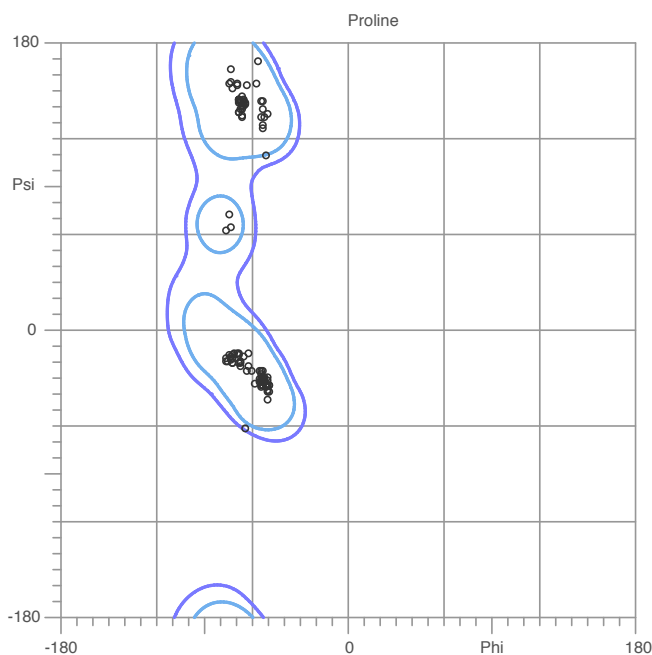
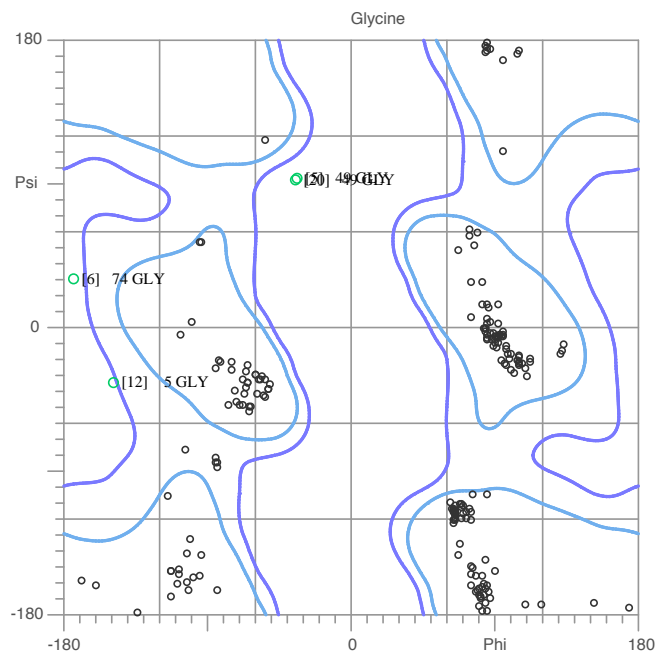
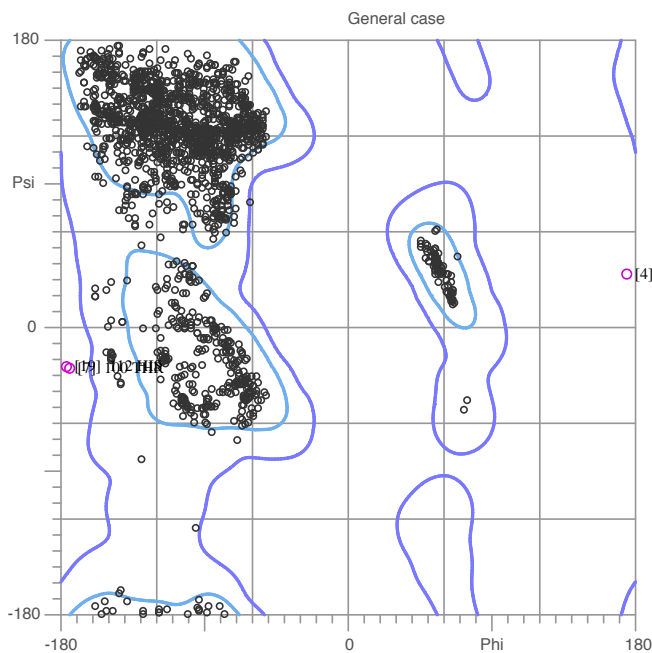


# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, all models



95.9% (2149/2240) of all residues were in favored (98%) regions.  
99.7% (2233/2240) of all residues were in allowed (>99.8%) regions.

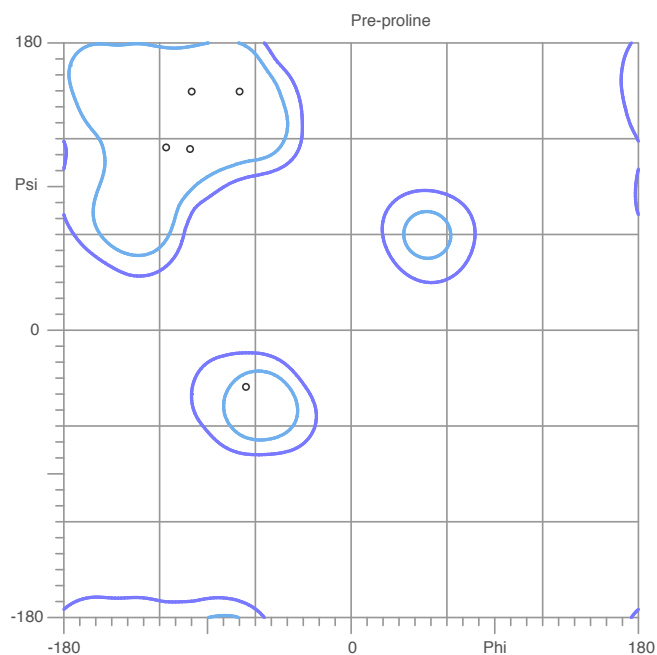
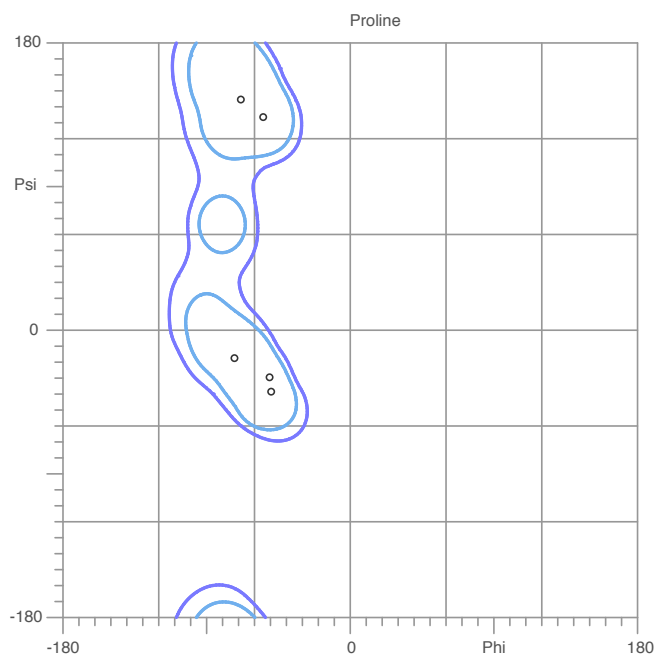
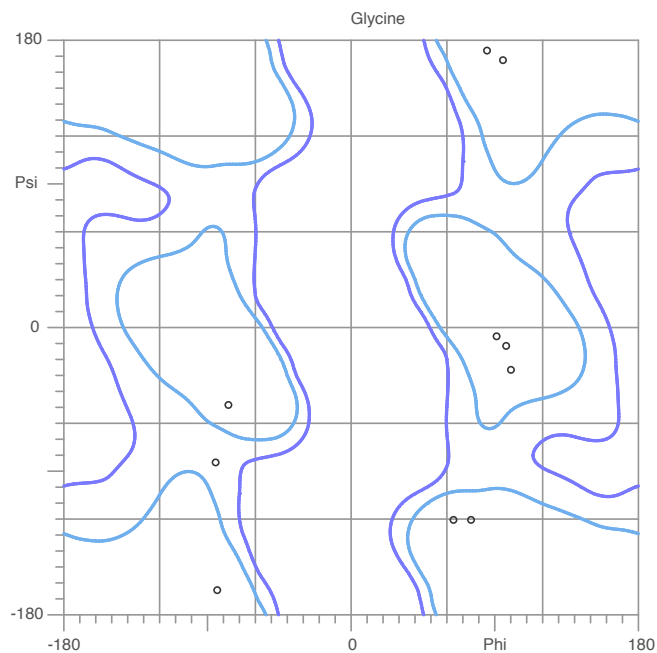
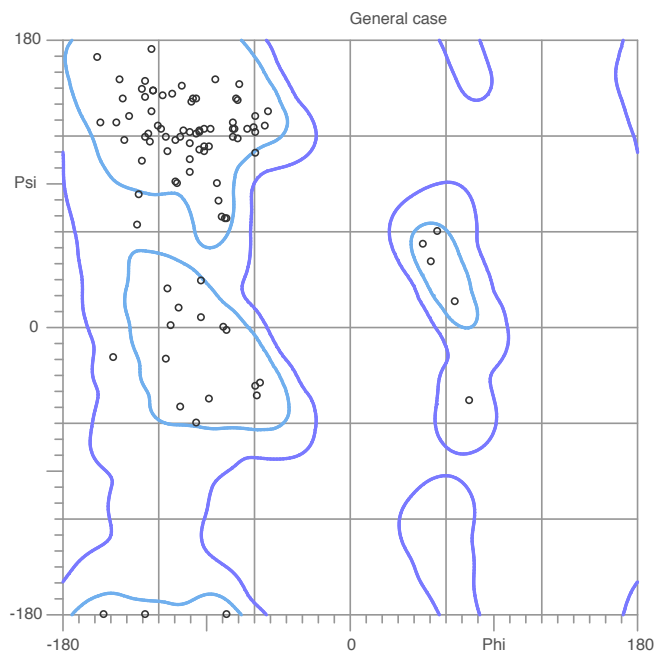
There were 7 outliers (phi, psi):

[4] 71 SER (175.0, 35.0)

[5] 49 GLY (-35.0, 94.0)  
[6] 74 GLY (-174.9, 31.8)  
[7] 100 THR (-175.0, -25.1)  
[12] 5 GLY (-149.2, -34.9)  
[19] 112 HIS (-177.0, -25.0)  
[20] 49 GLY (-35.0, 93.3)

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 1

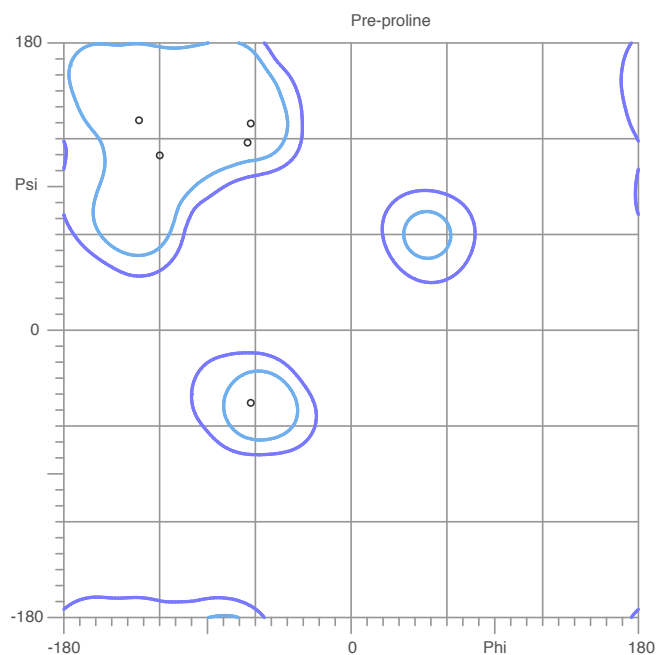
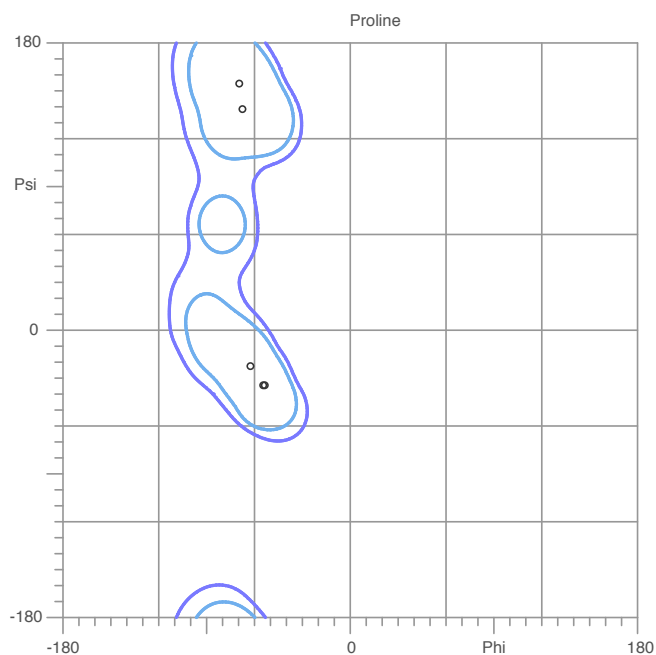
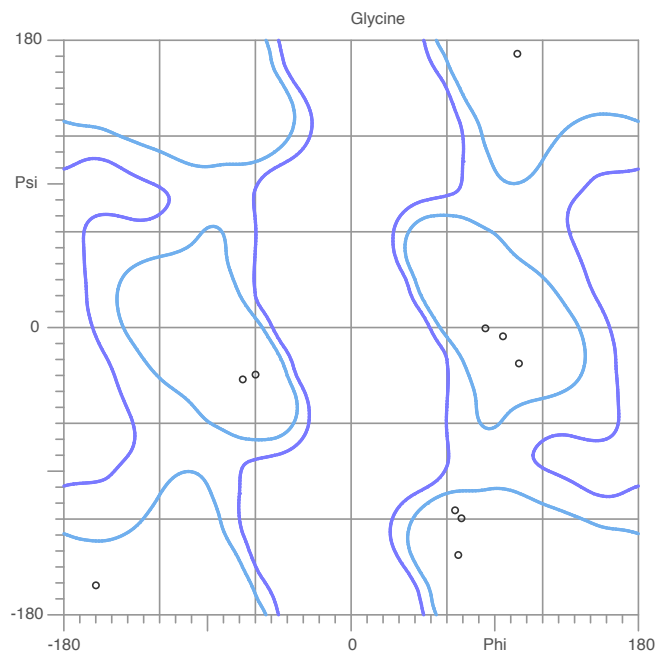
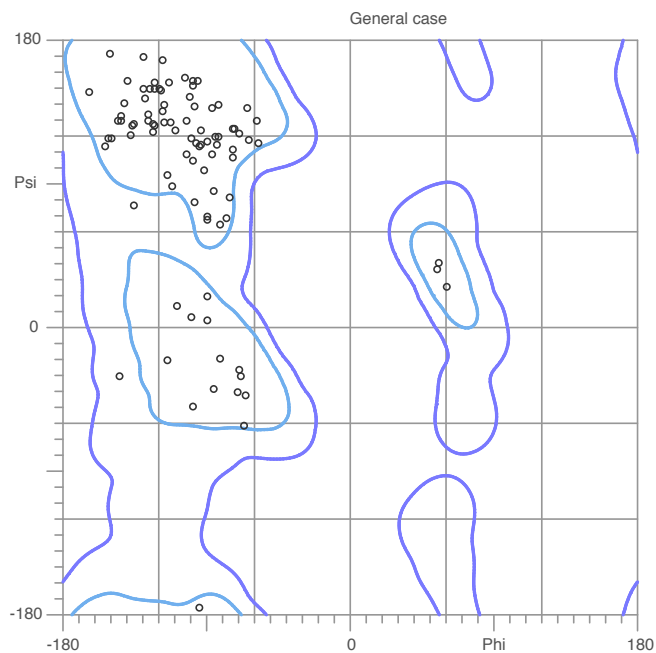


95.5% (107/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 2



98.2% (110/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

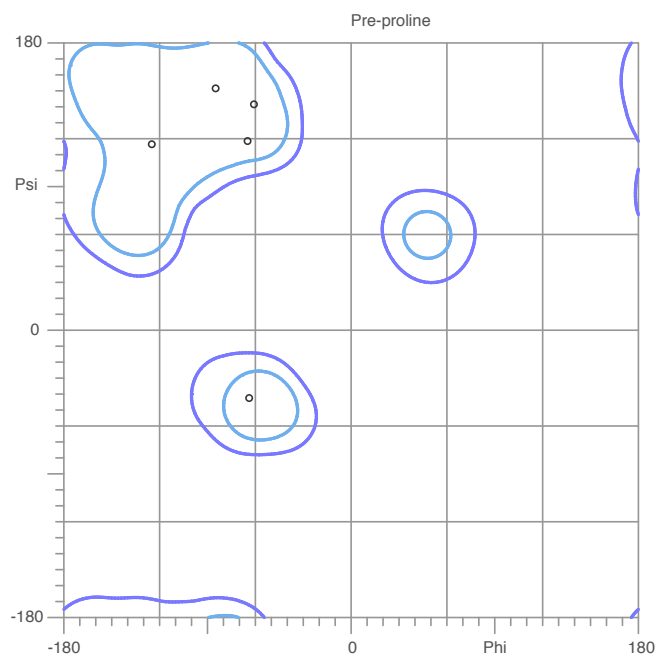
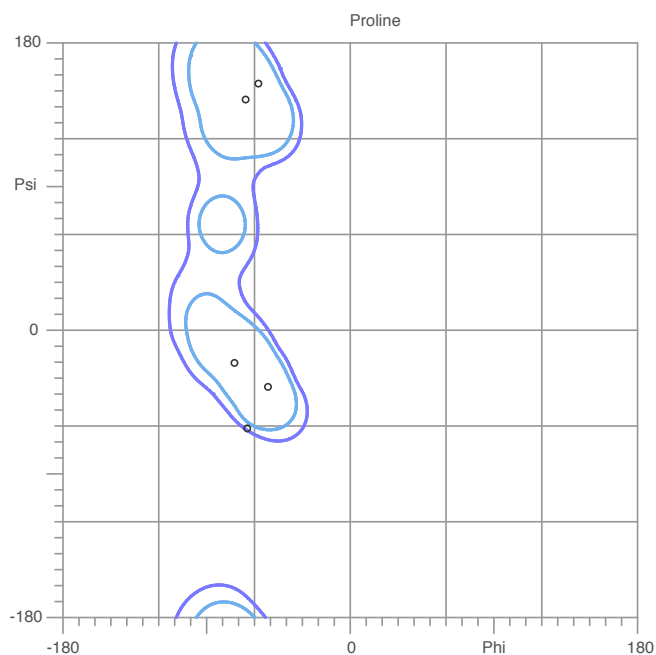
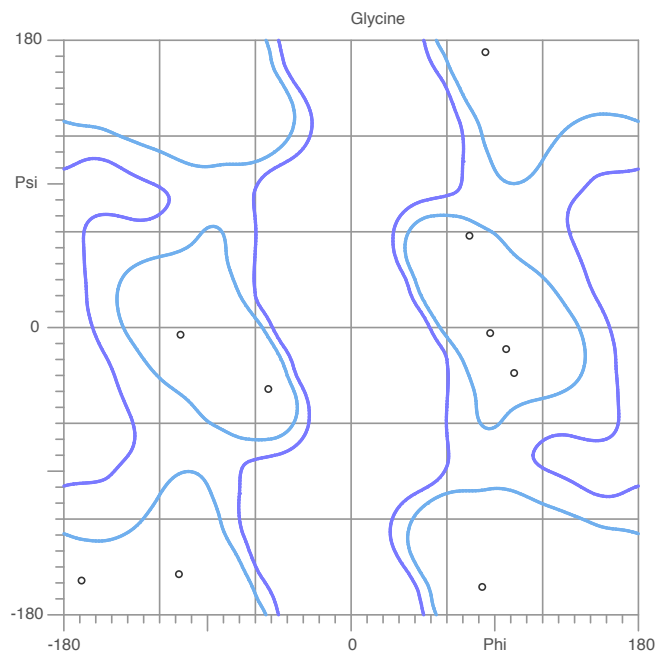
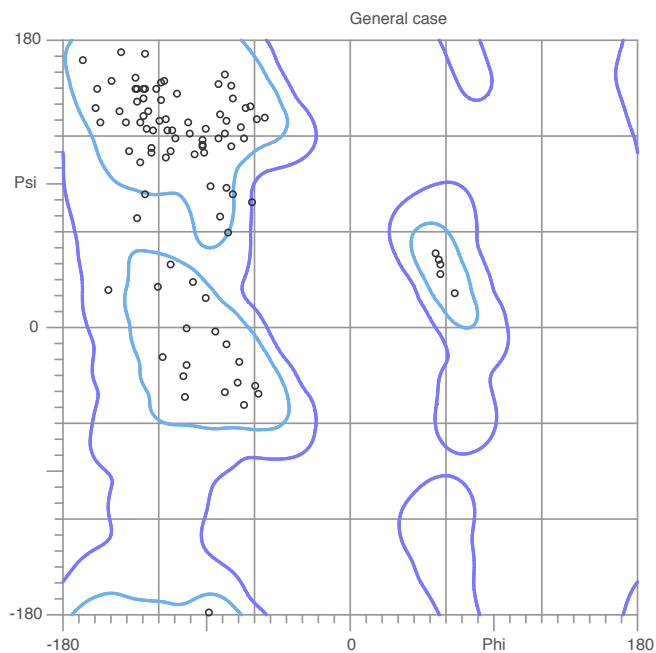
There were no outliers.

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

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

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 3



96.4% (108/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

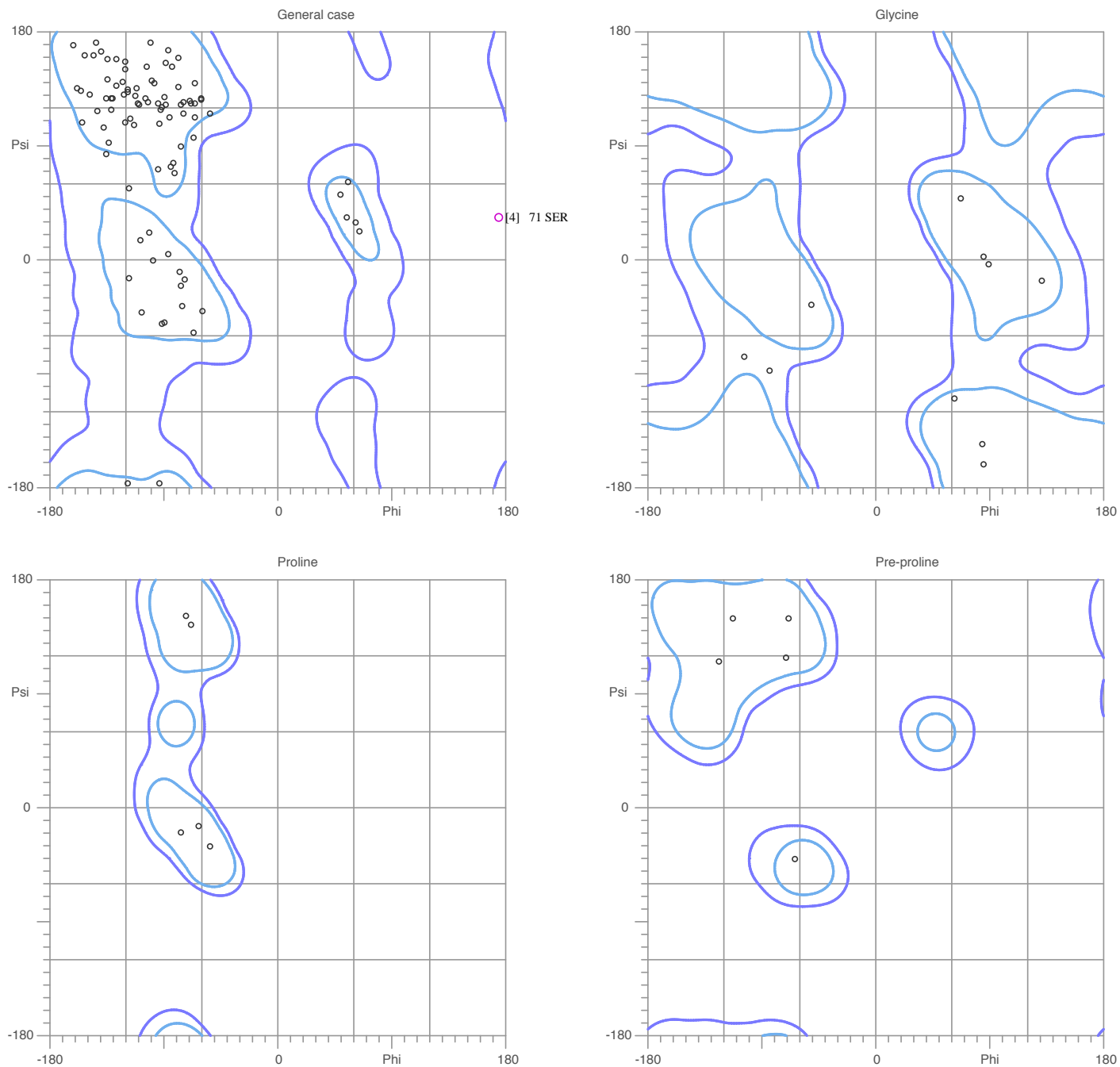
There were no outliers.

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

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

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 4



94.6% (106/112) of all residues were in favored (98%) regions.  
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

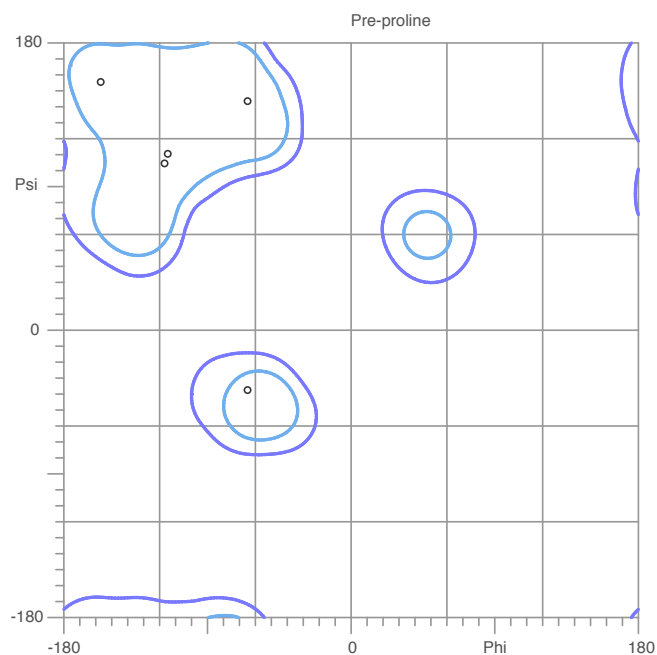
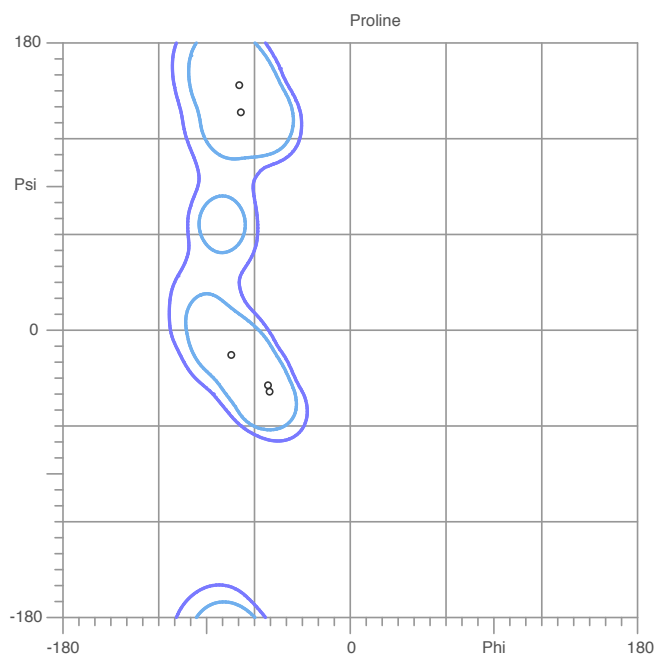
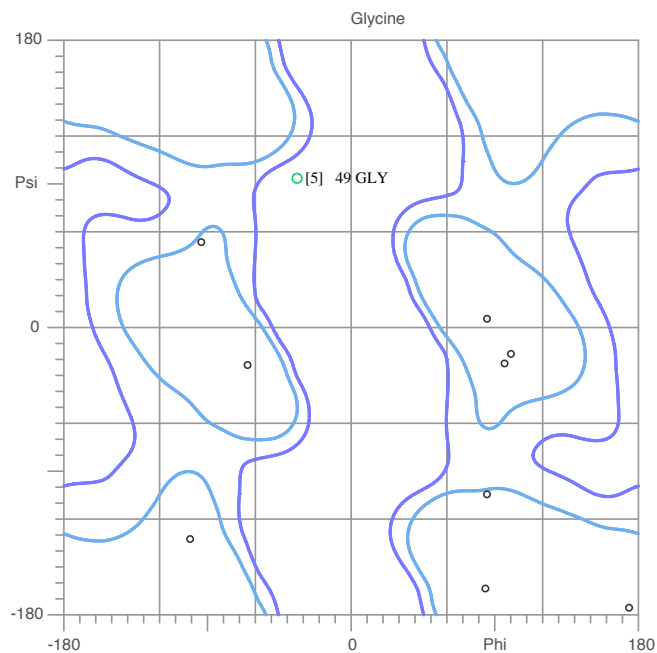
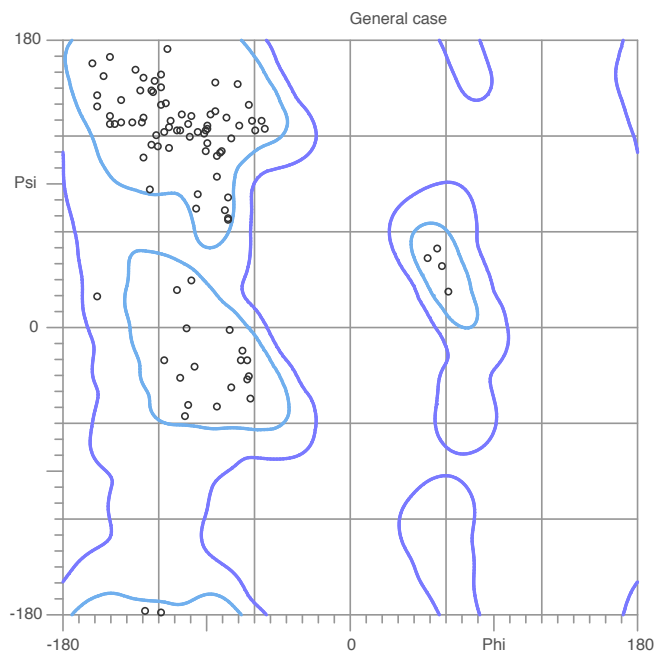
There were 1 outliers (phi, psi):  
[4] 71 SER (175.0, 35.0)

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

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

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 5

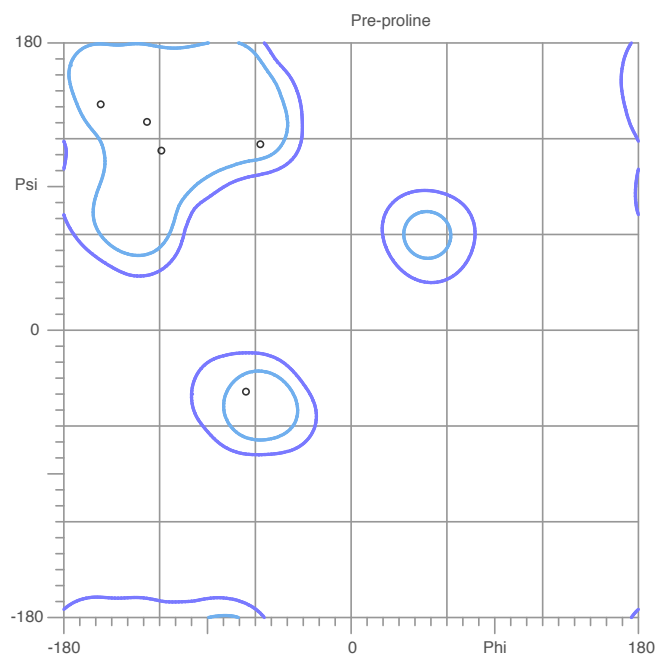
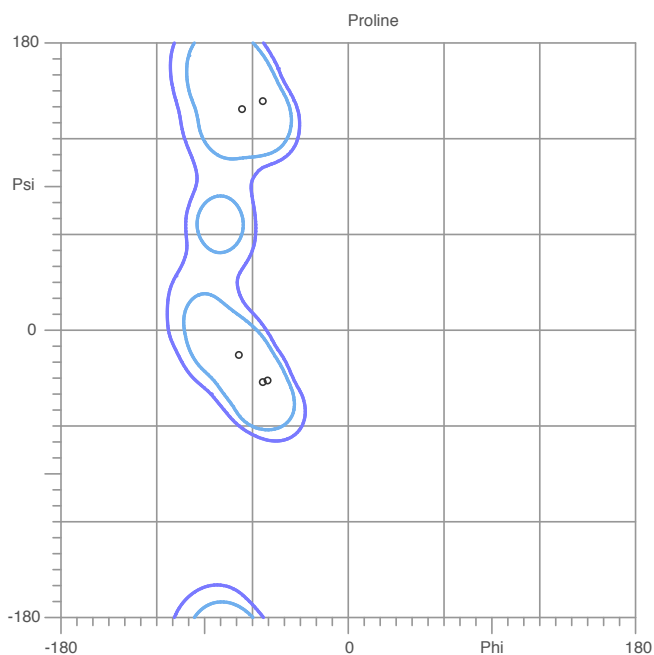
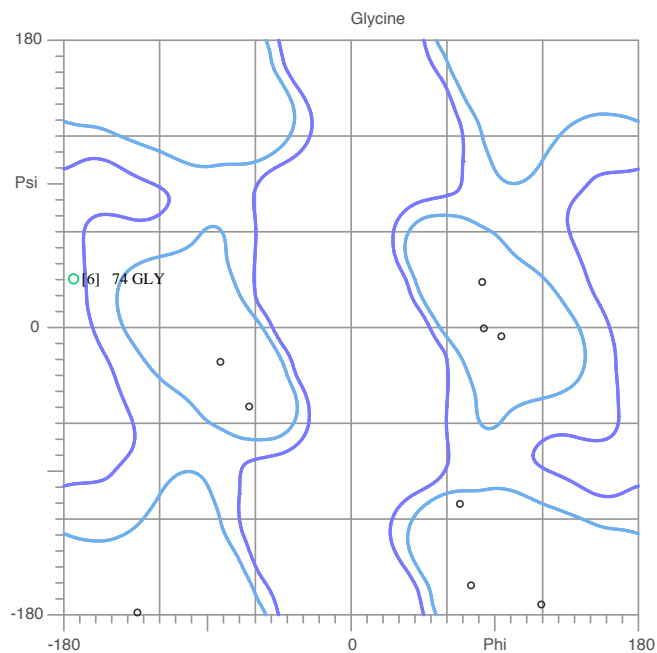
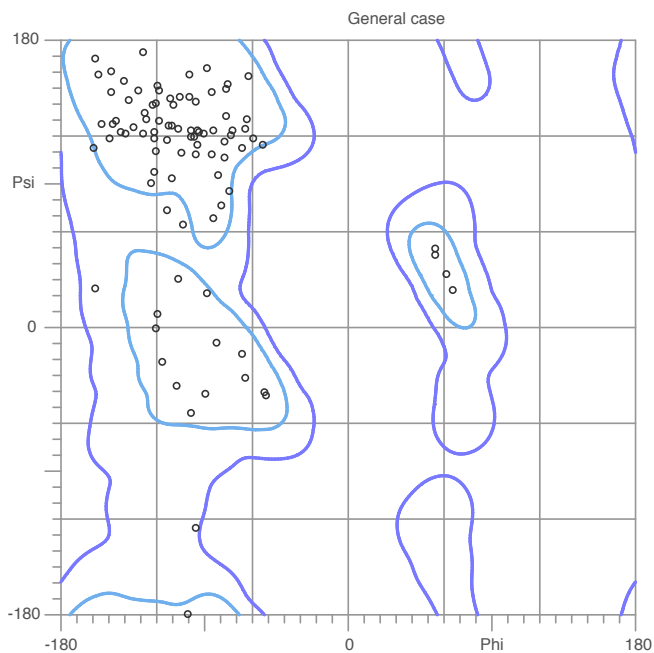


98.2% (110/112) of all residues were in favored (98%) regions.  
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[5] 49 GLY (-35.0, 94.0)

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 6

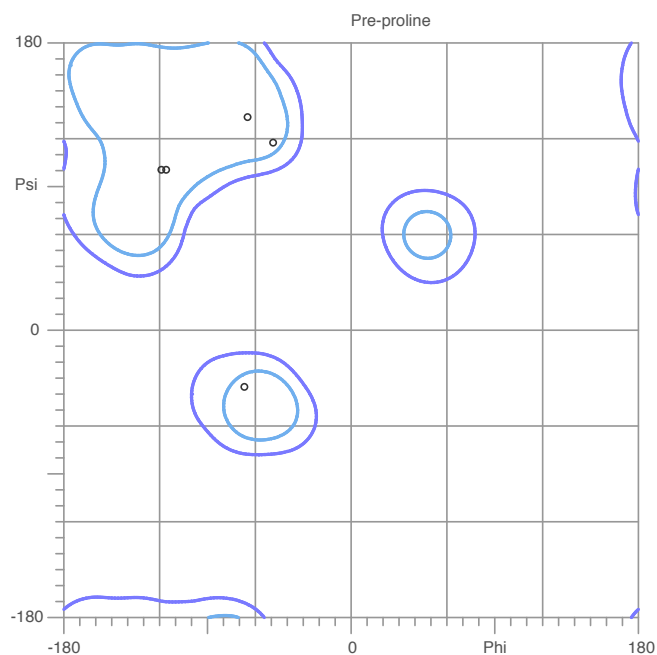
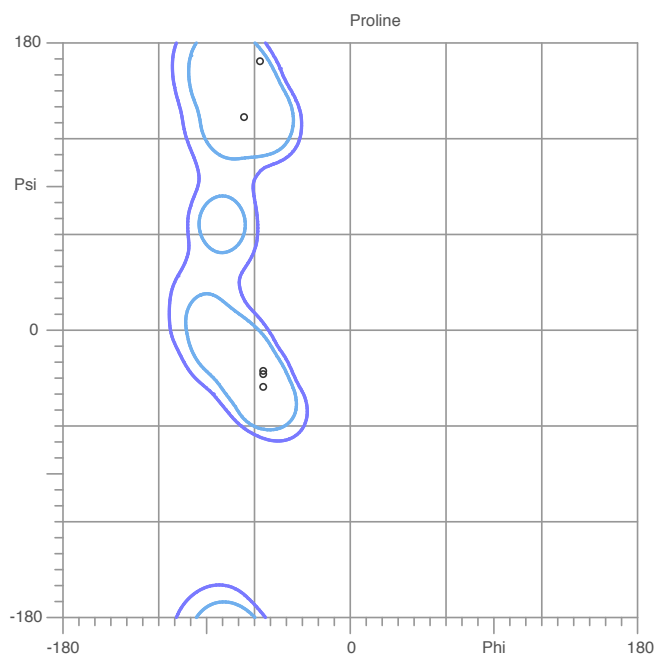
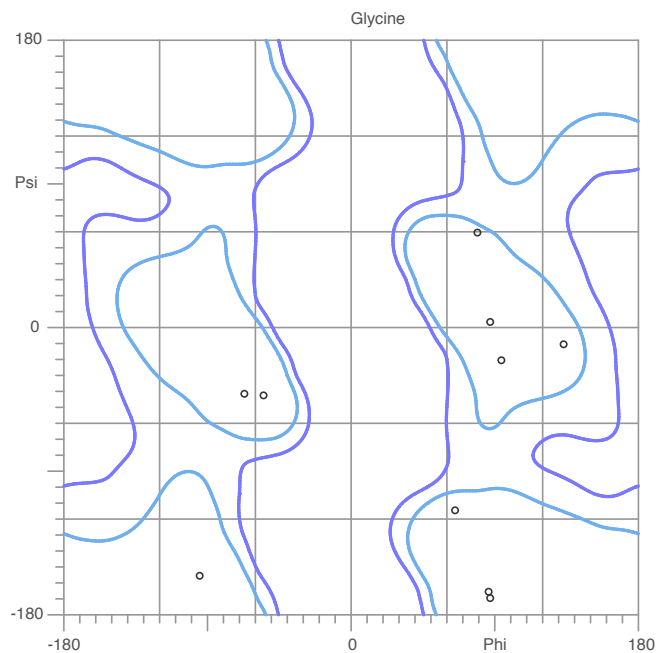
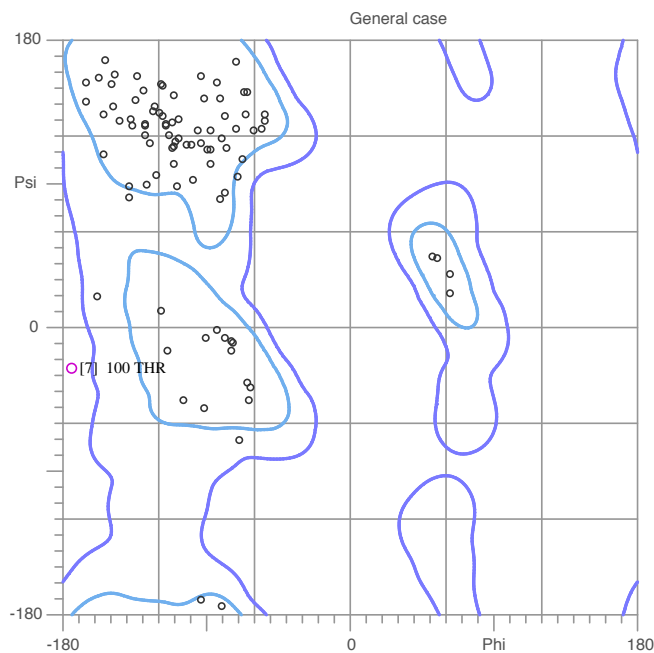


94.6% (106/112) of all residues were in favored (98%) regions.  
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[6] 74 GLY (-174.9, 31.8)

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 7

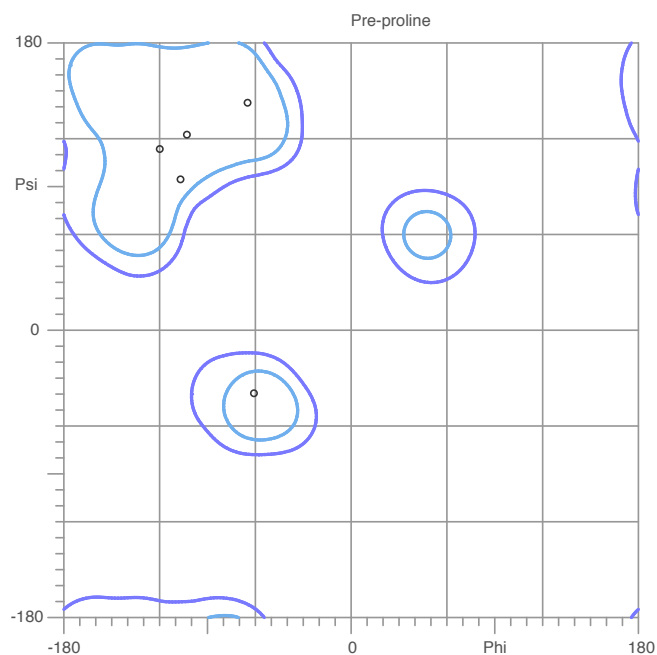
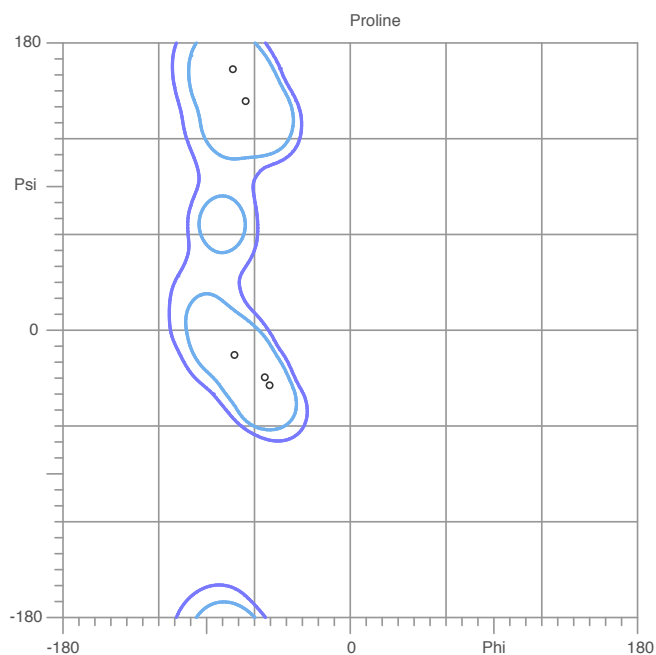
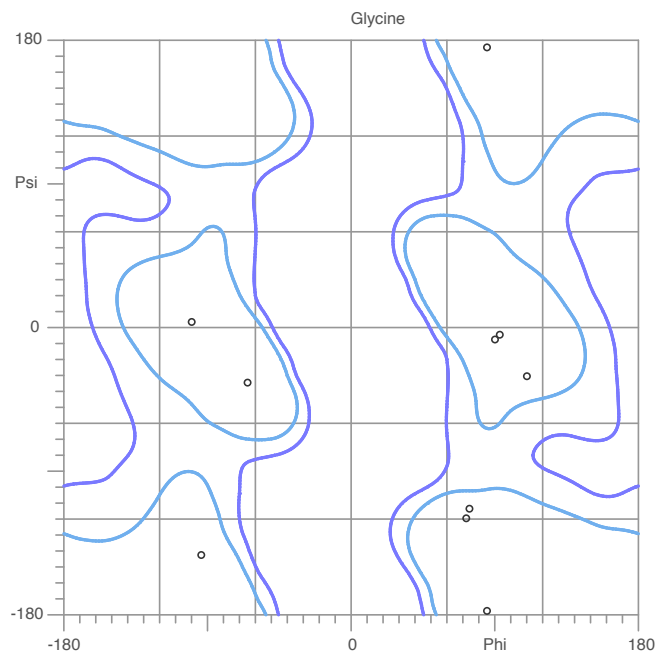
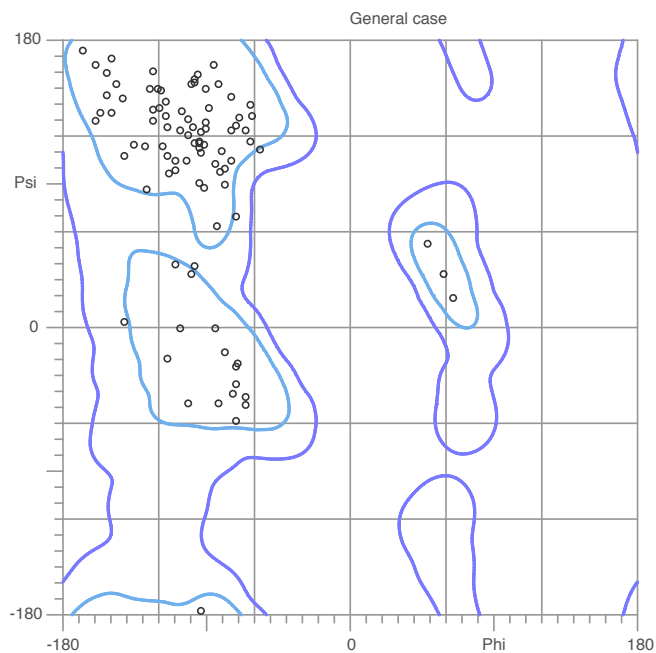


95.5% (107/112) of all residues were in favored (98%) regions.  
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[7] 100 THR (-175.0, -25.1)

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 8



96.4% (108/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

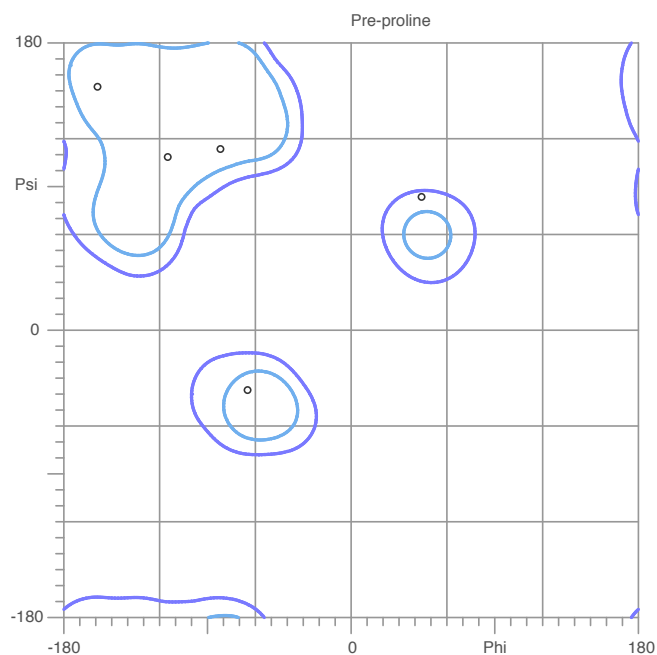
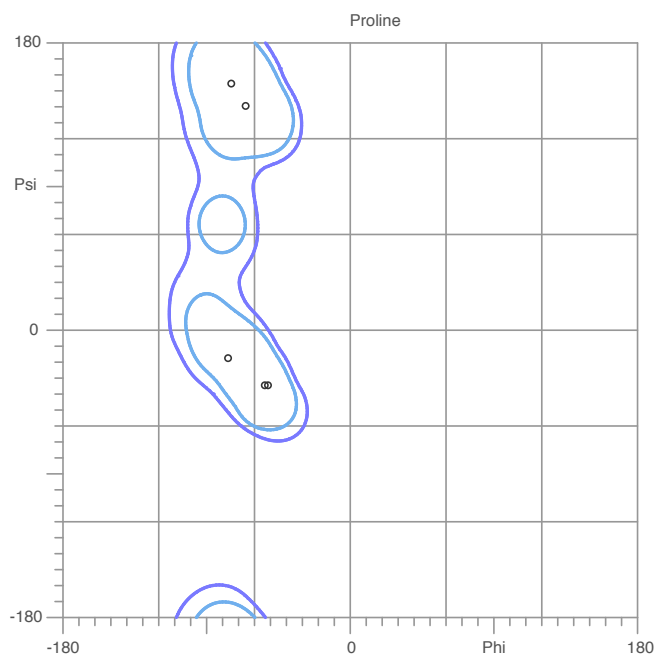
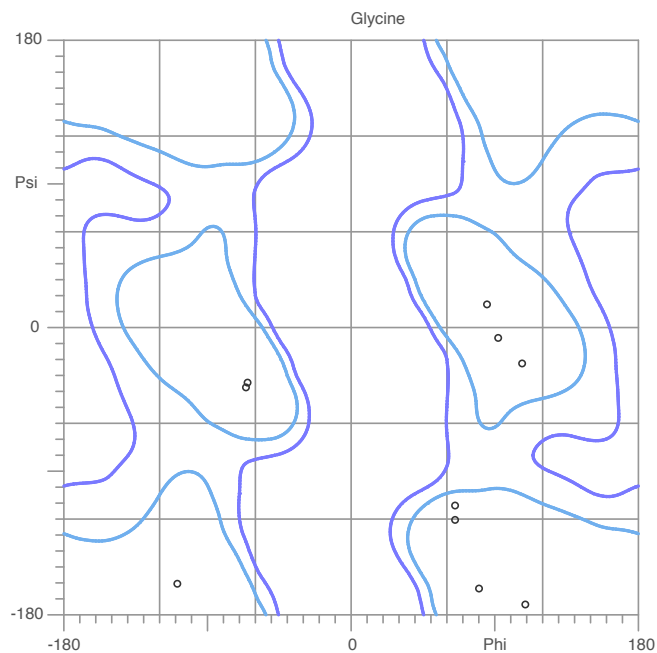
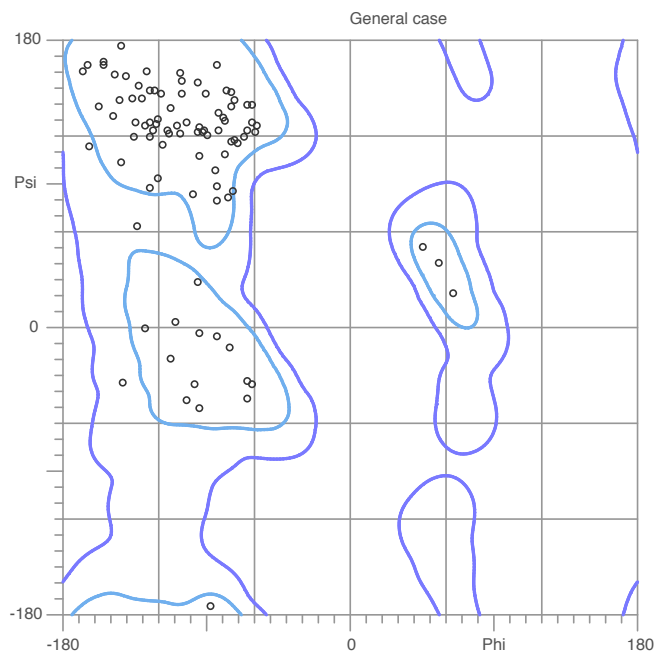
There were no outliers.

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# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 9

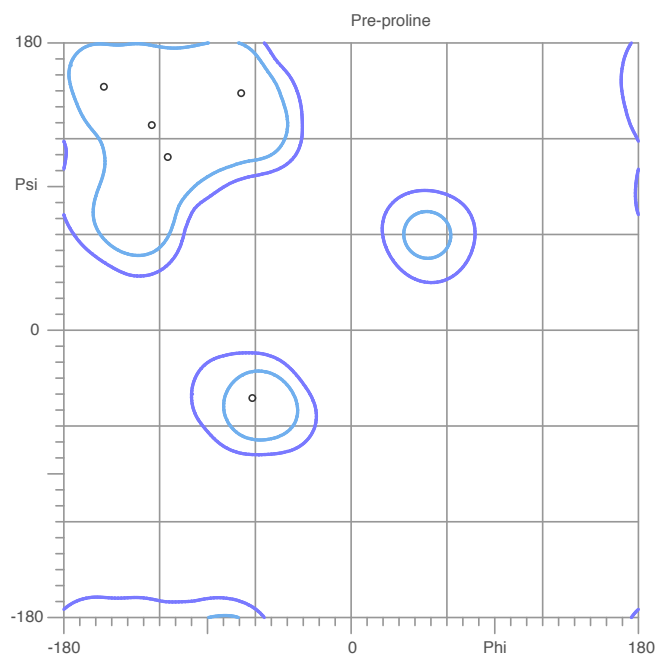
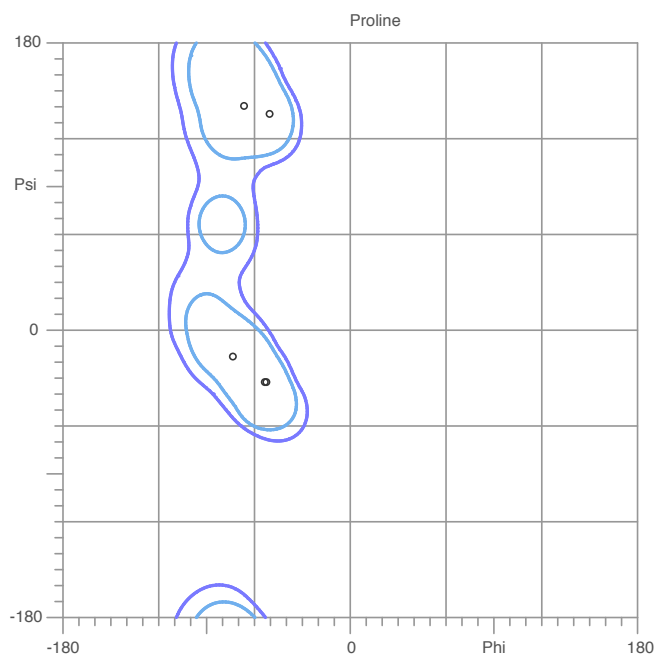
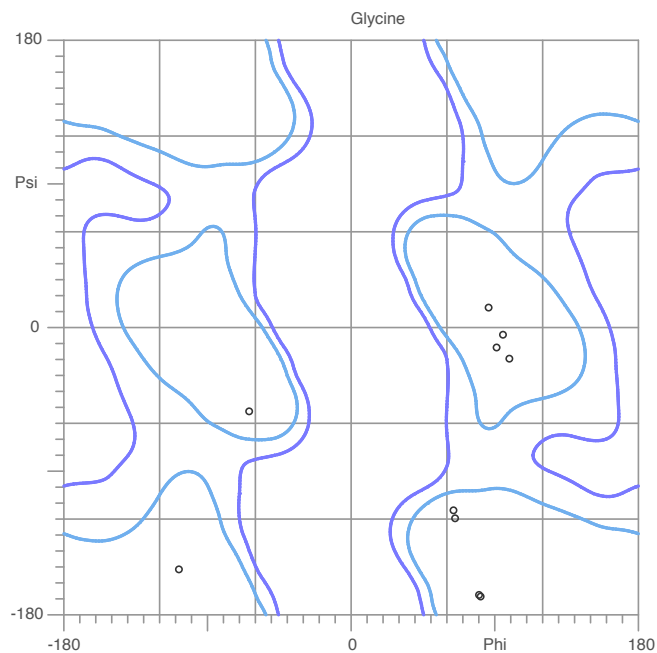
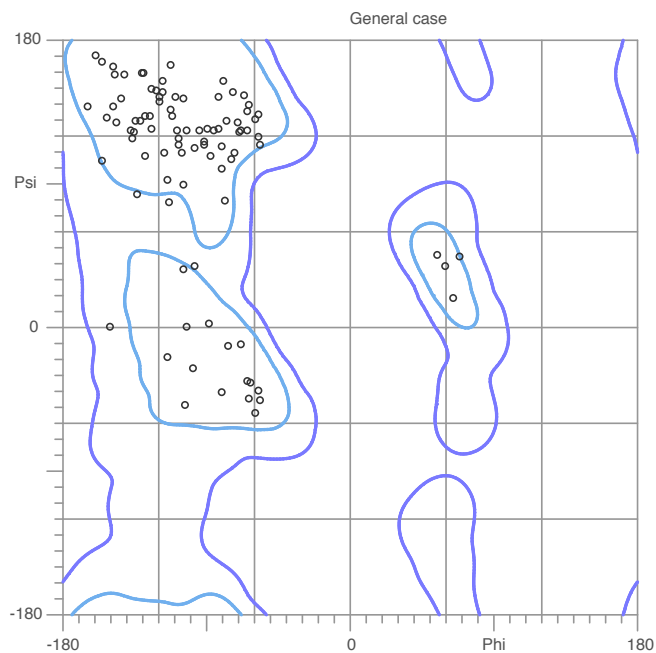


96.4% (108/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 10



95.5% (107/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

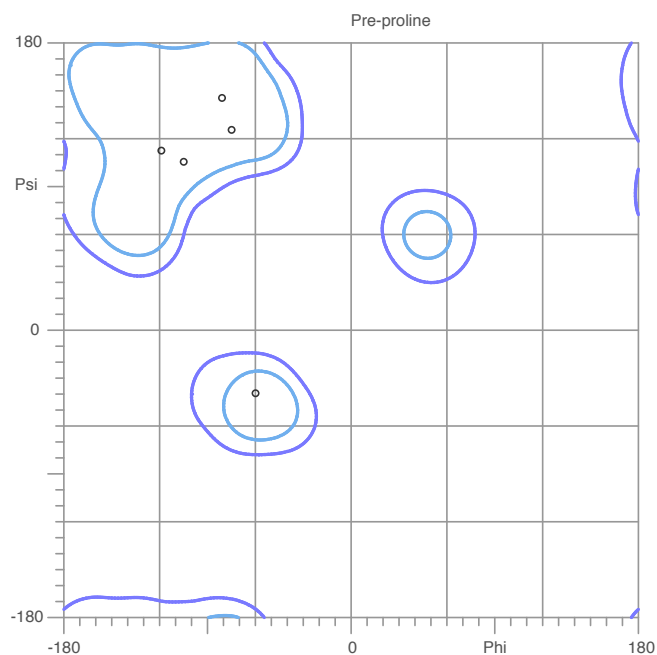
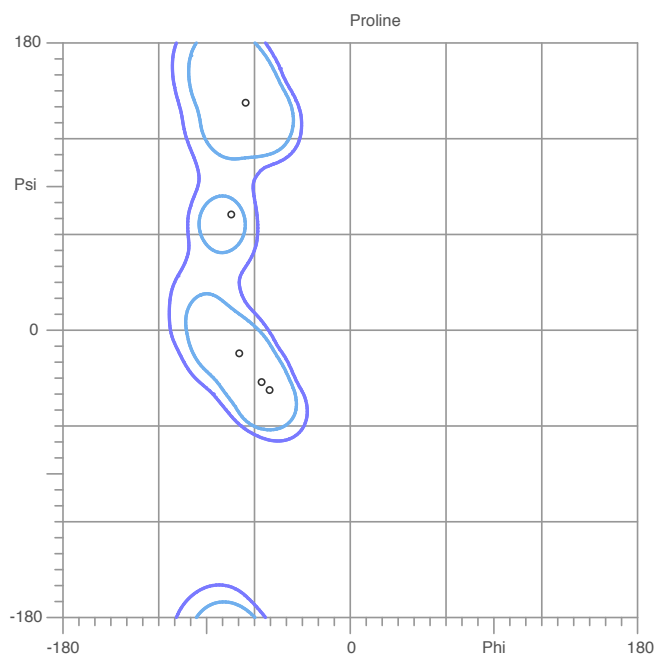
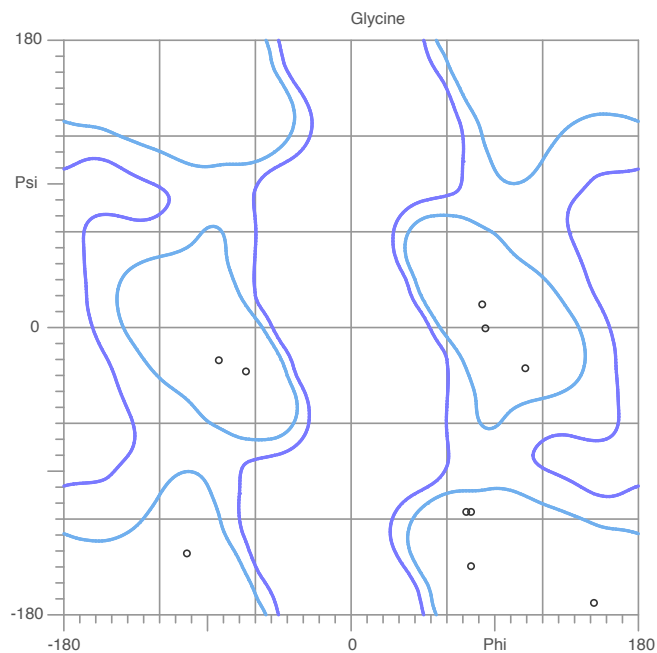
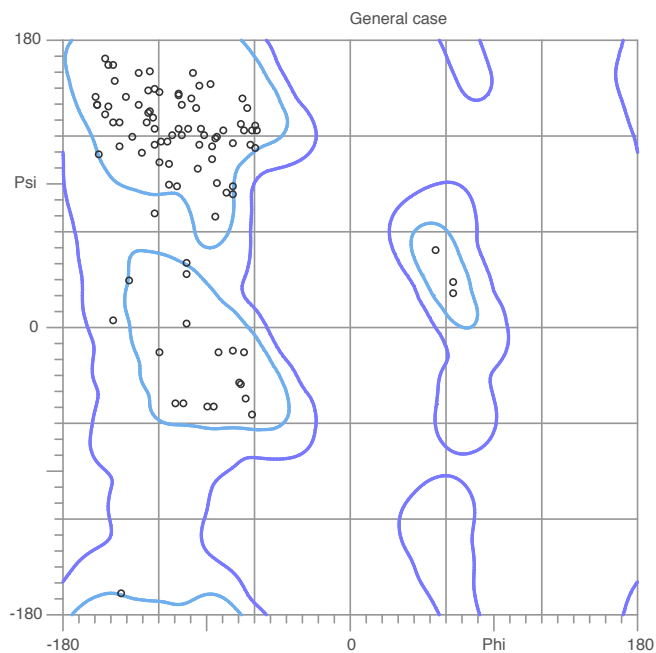
There were no outliers.

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

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# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 11

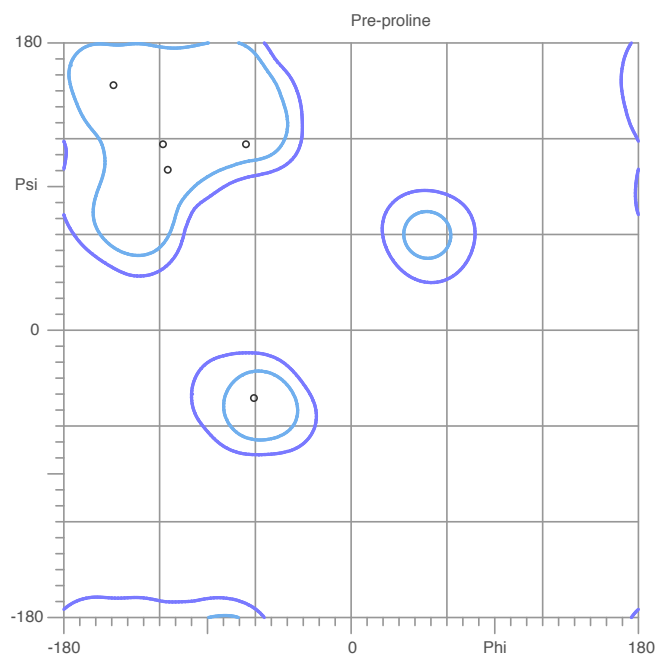
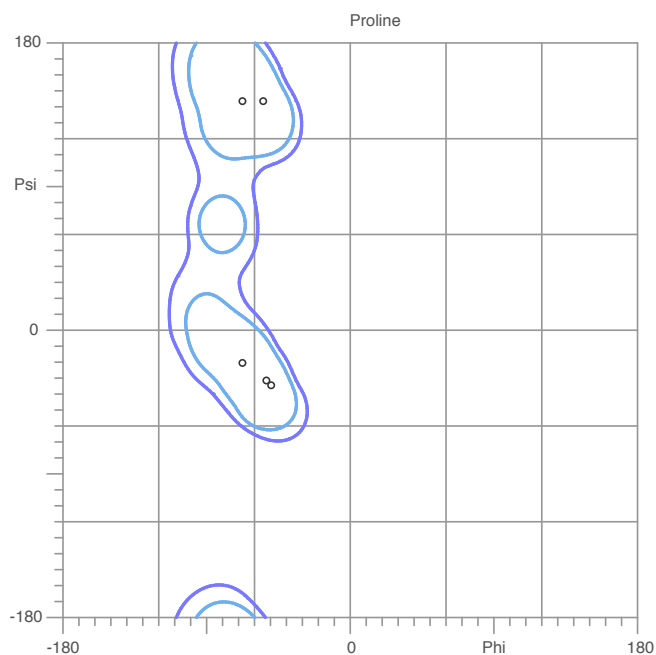
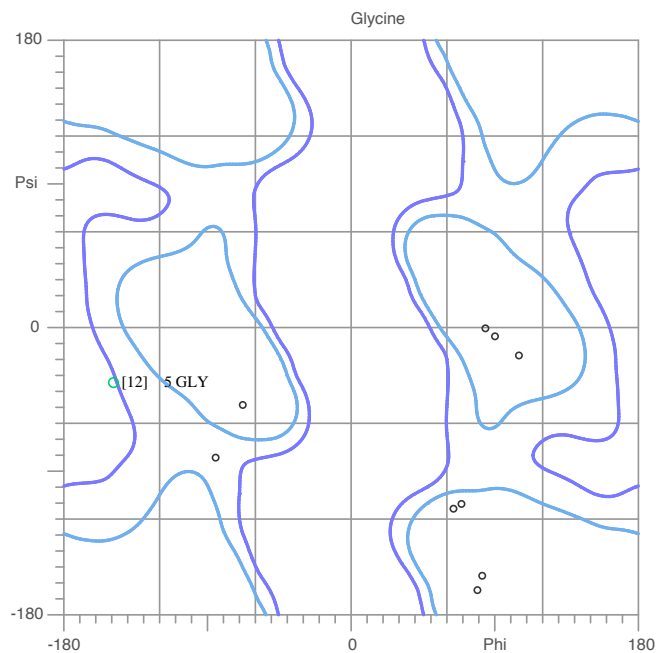
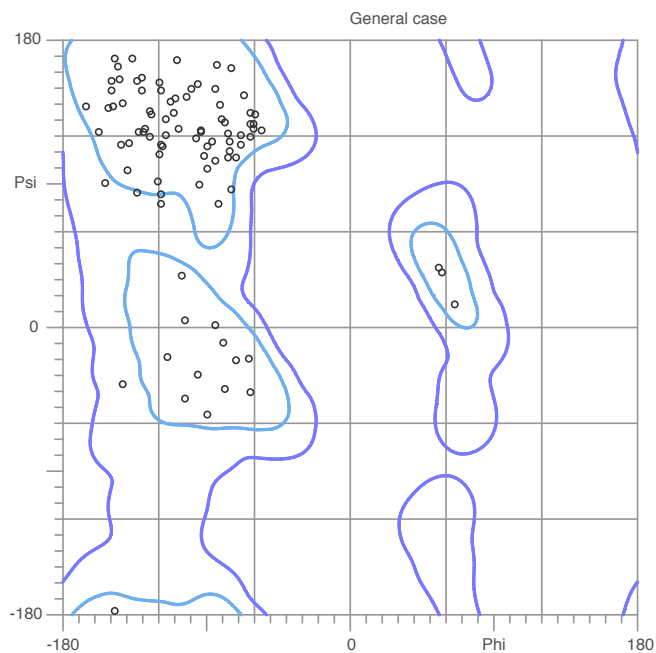


95.5% (107/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 12

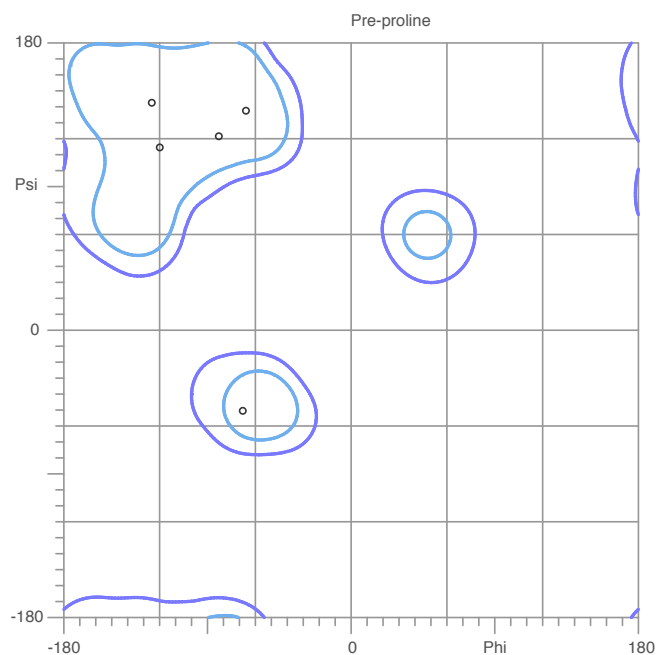
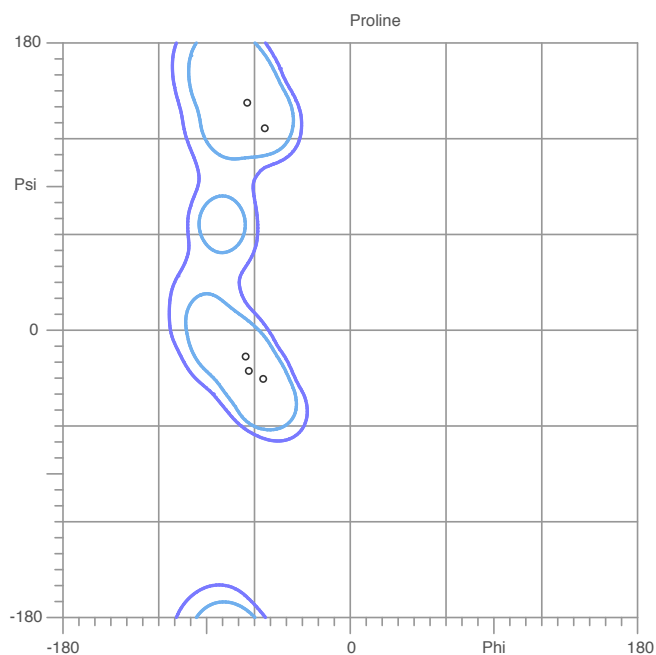
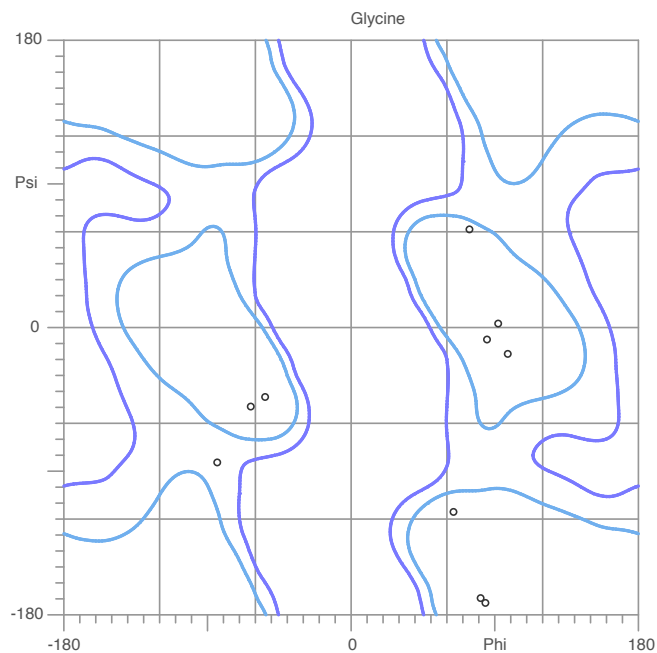
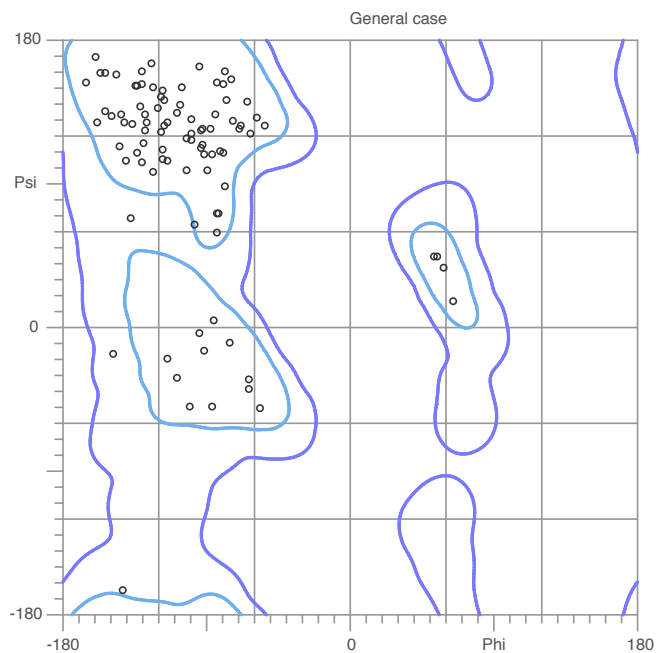


94.6% (106/112) of all residues were in favored (98%) regions.  
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[12] 5 GLY (-149.2, -34.9)

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 13



96.4% (108/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

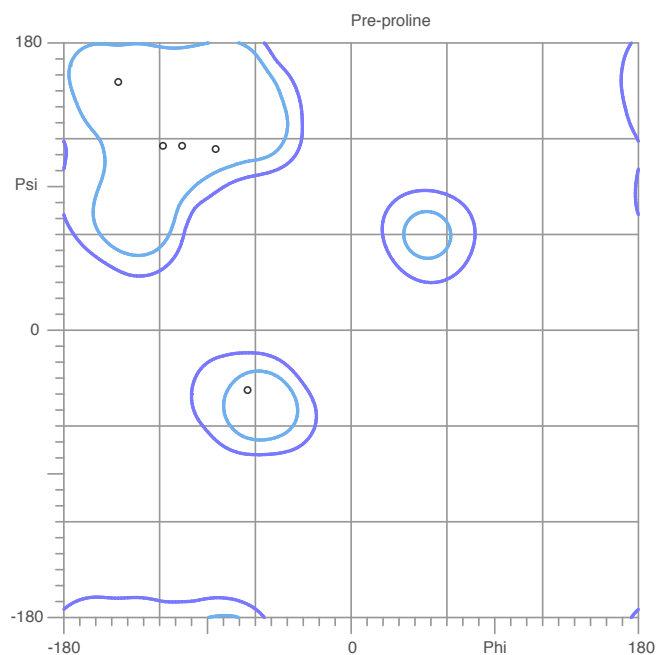
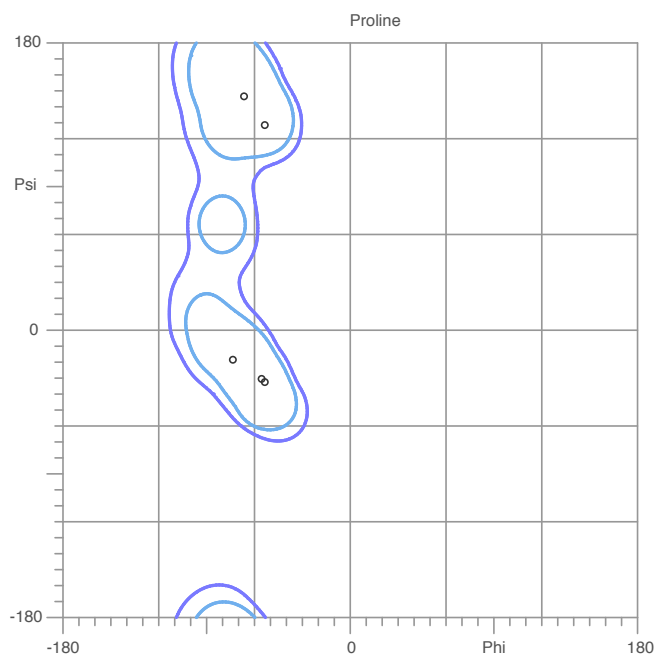
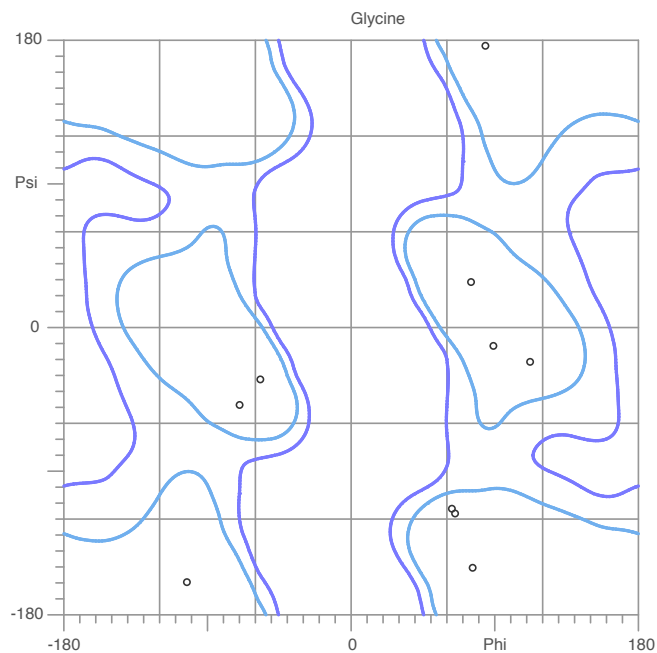
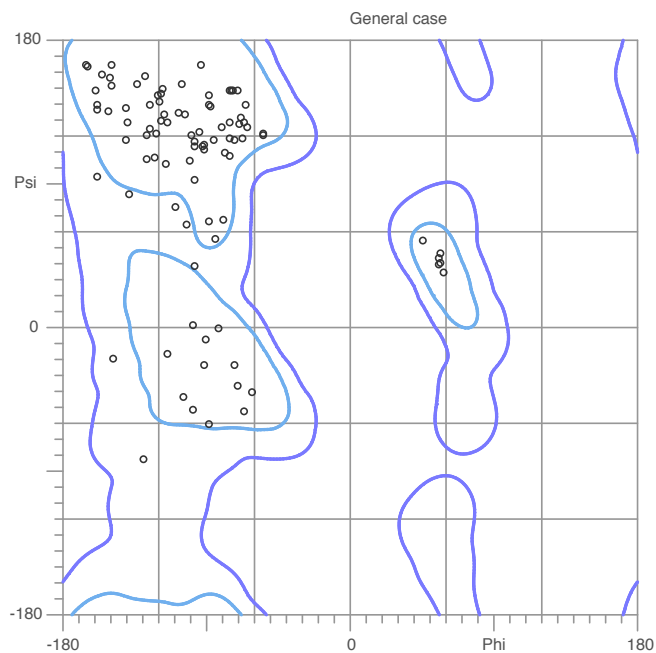
There were no outliers.

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# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 14

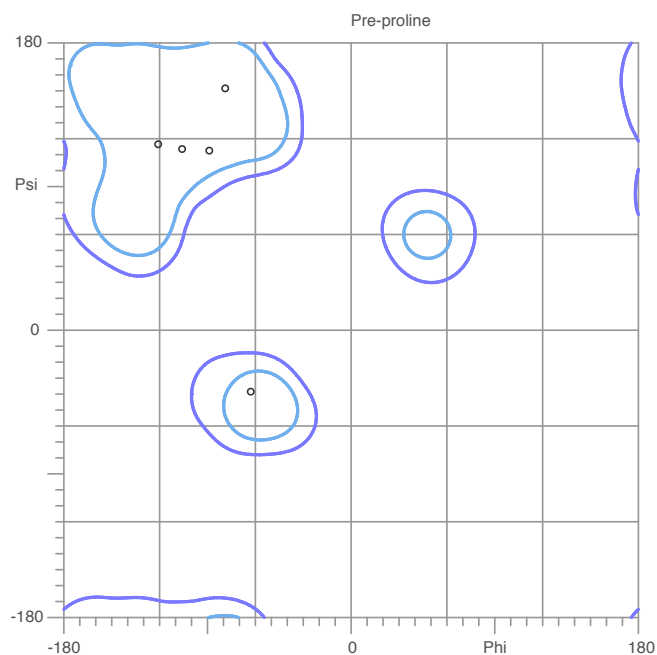
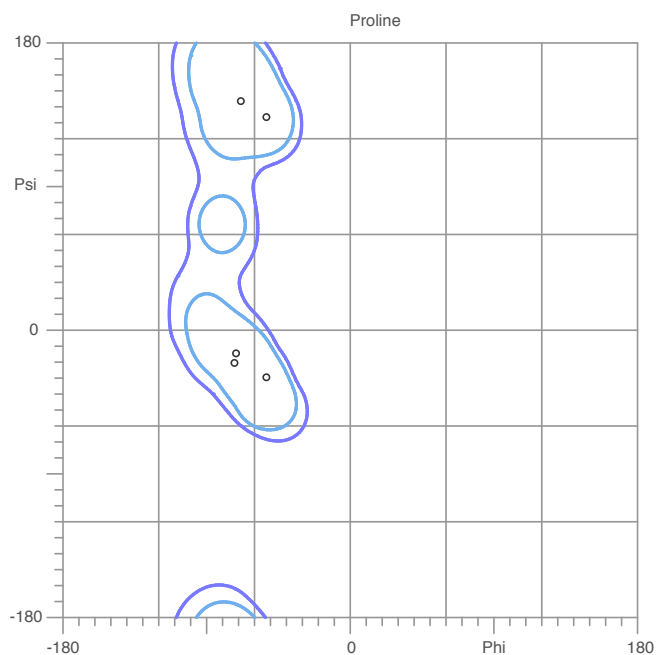
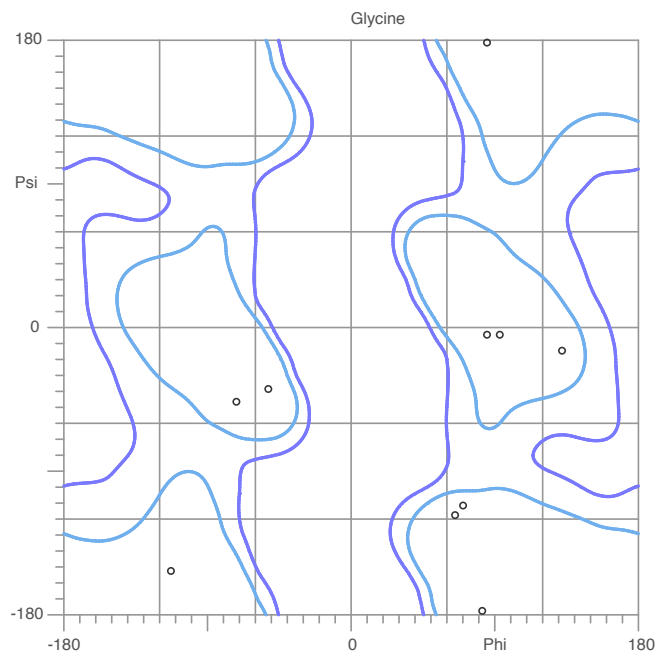
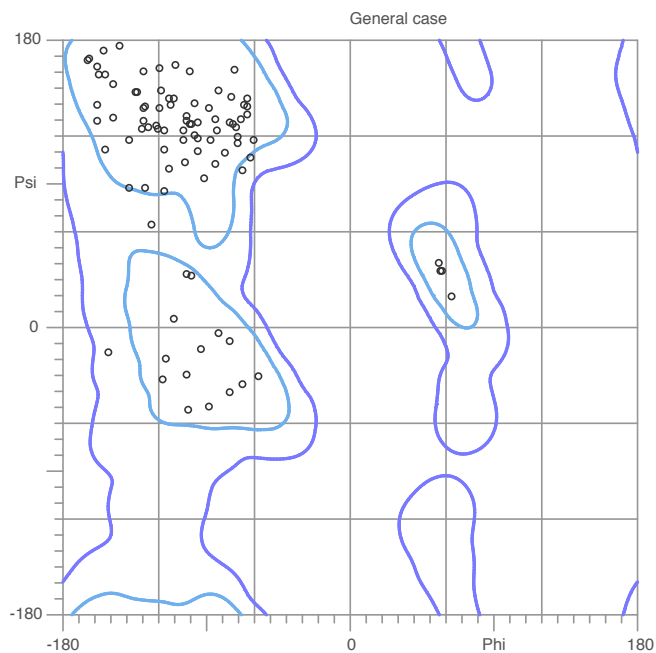


93.8% (105/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 15



97.3% (109/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

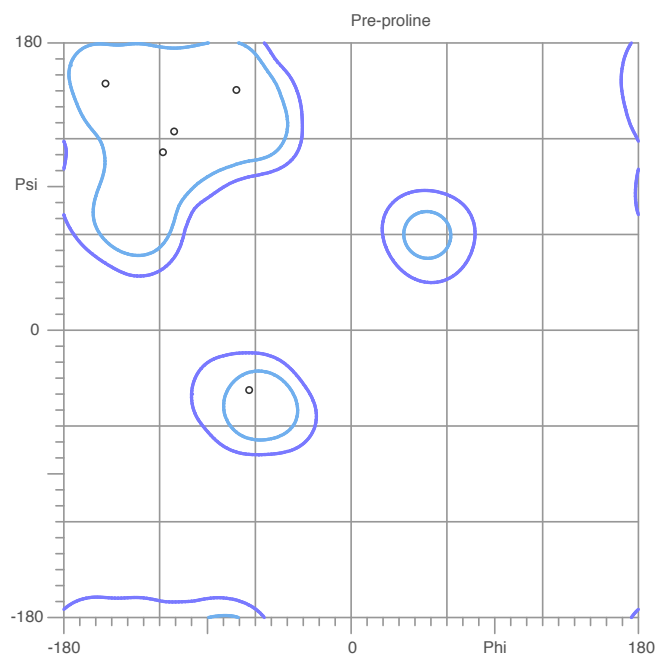
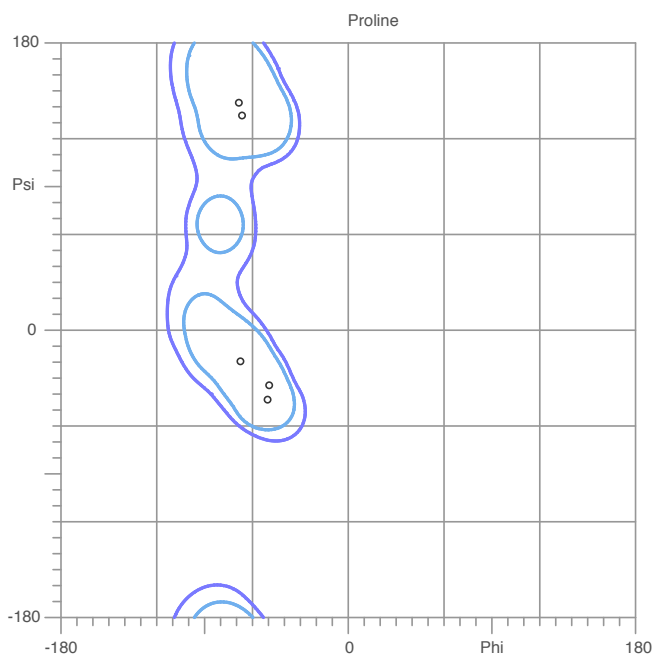
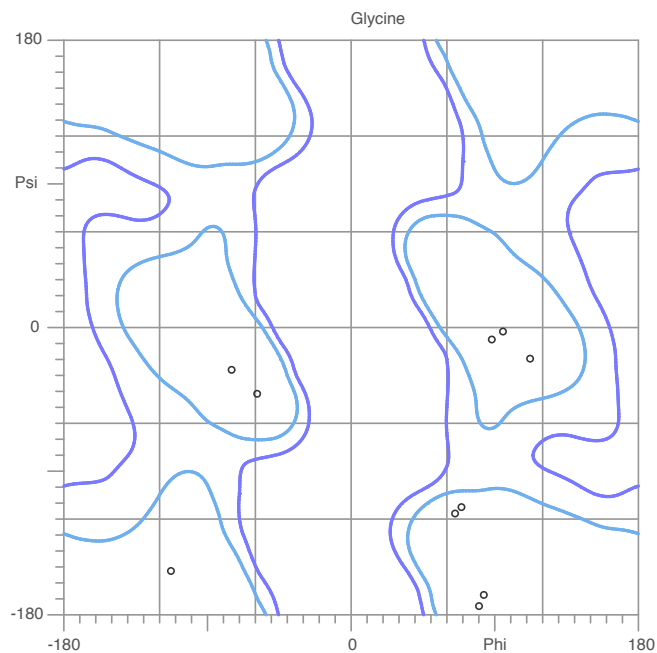
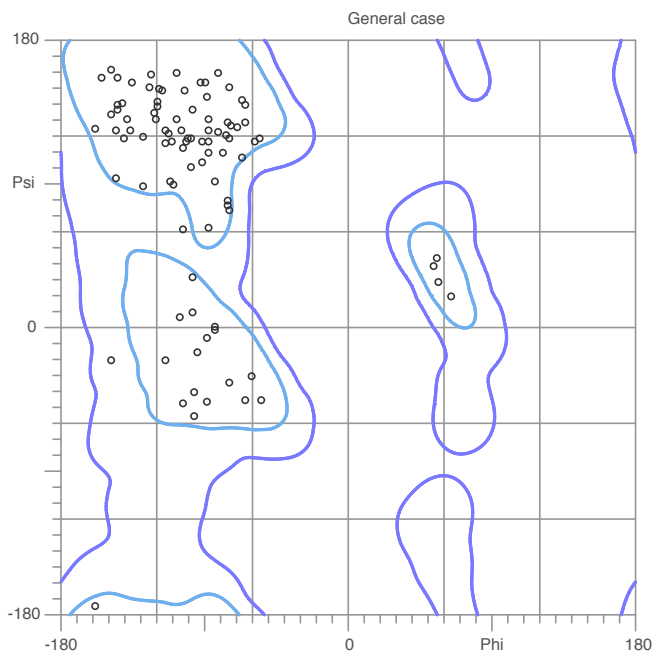
There were no outliers.

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

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# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 16



98.2% (110/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

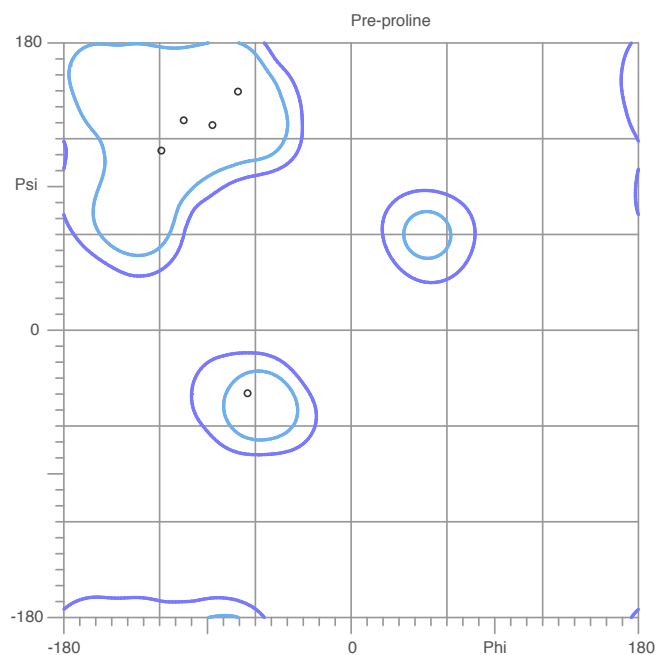
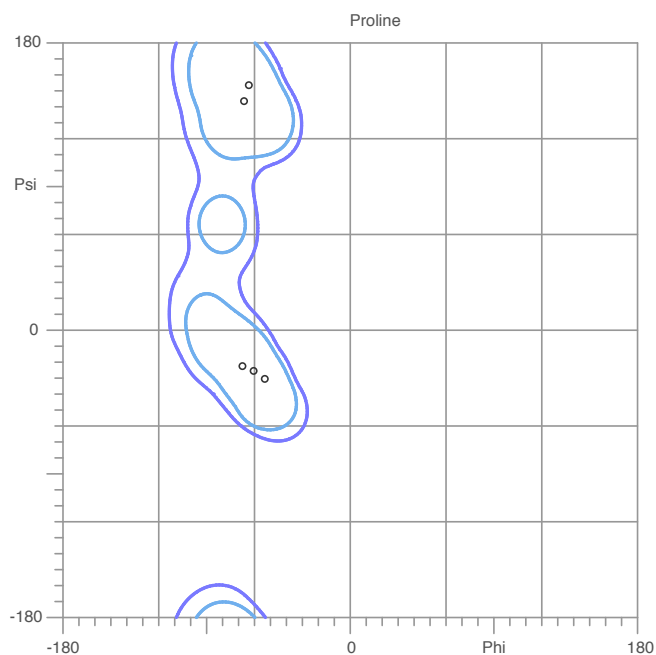
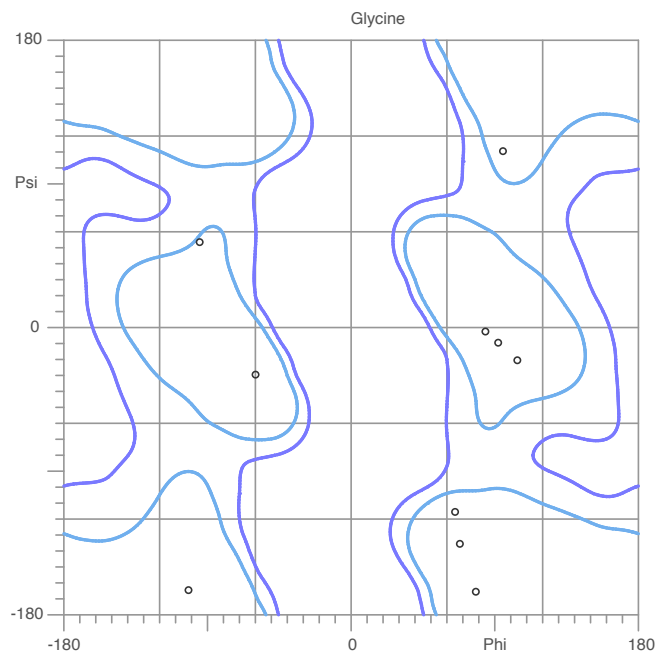
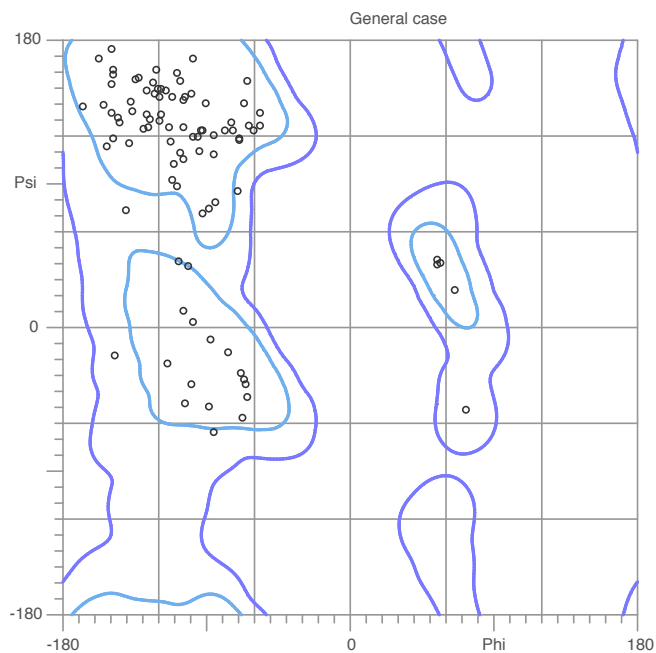
There were no outliers.

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

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# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 17

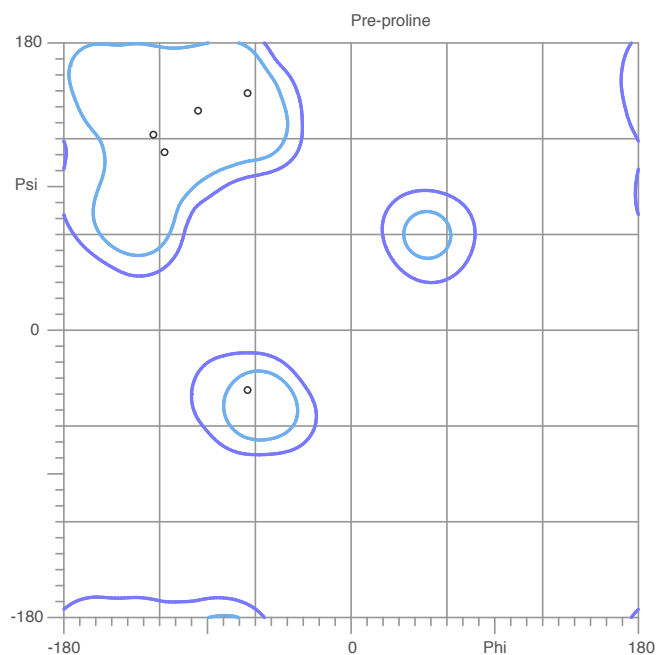
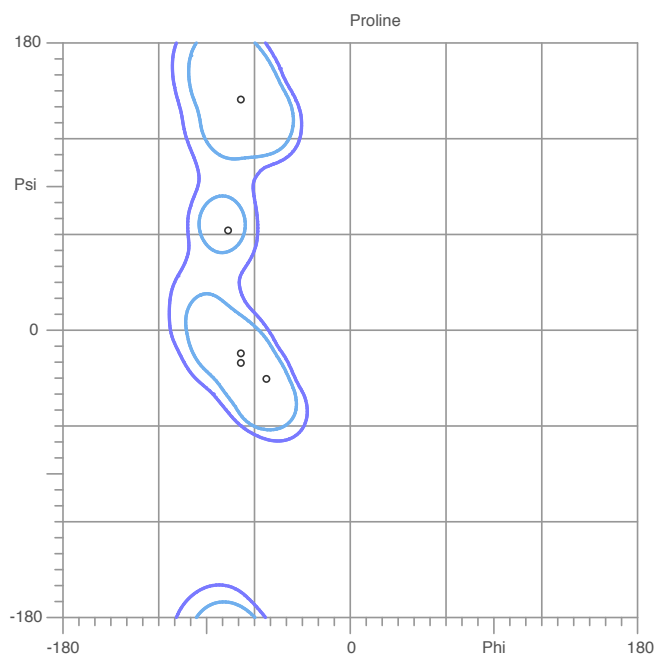
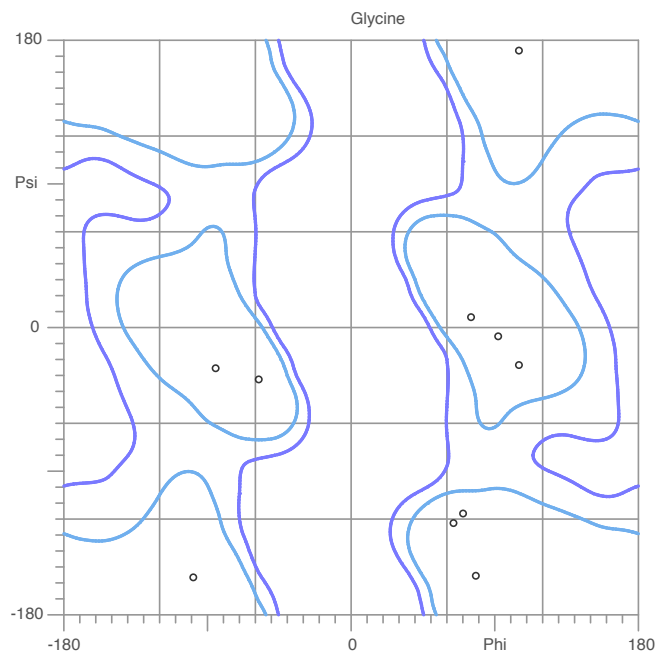
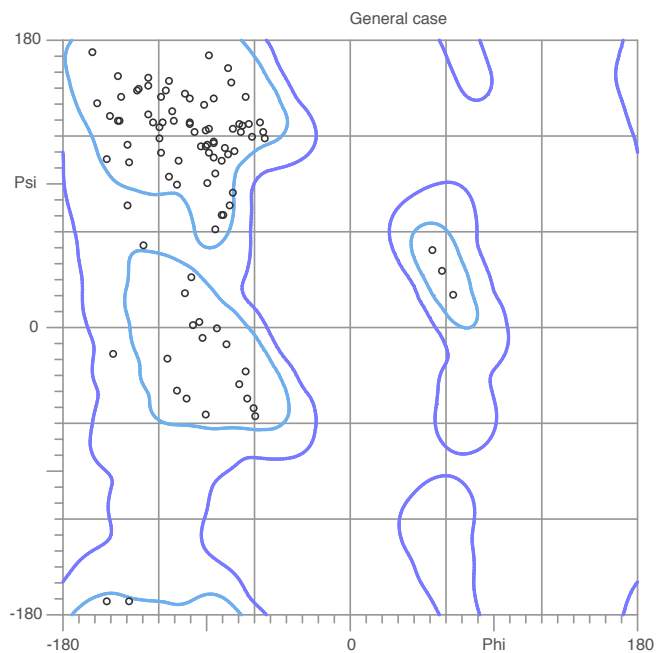


93.8% (105/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 18

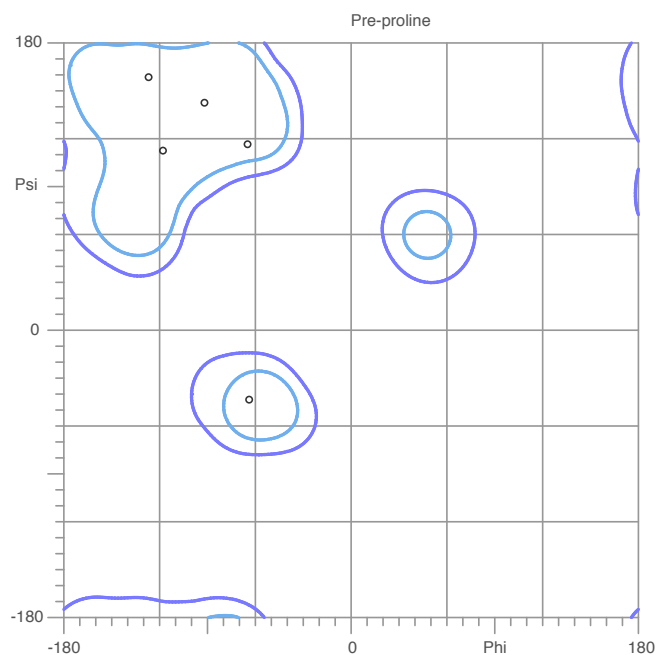
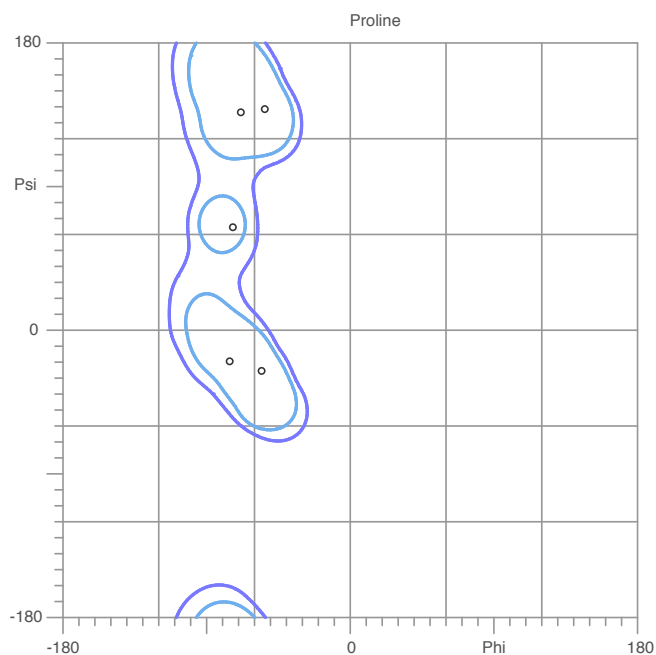
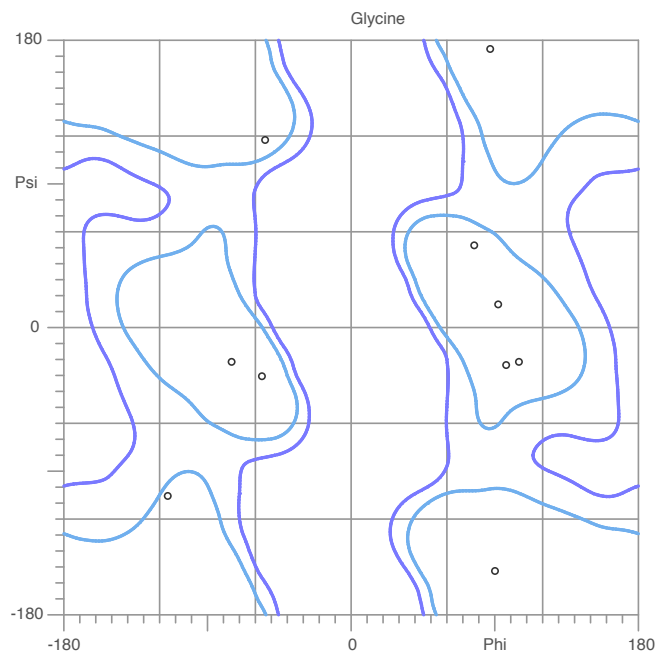
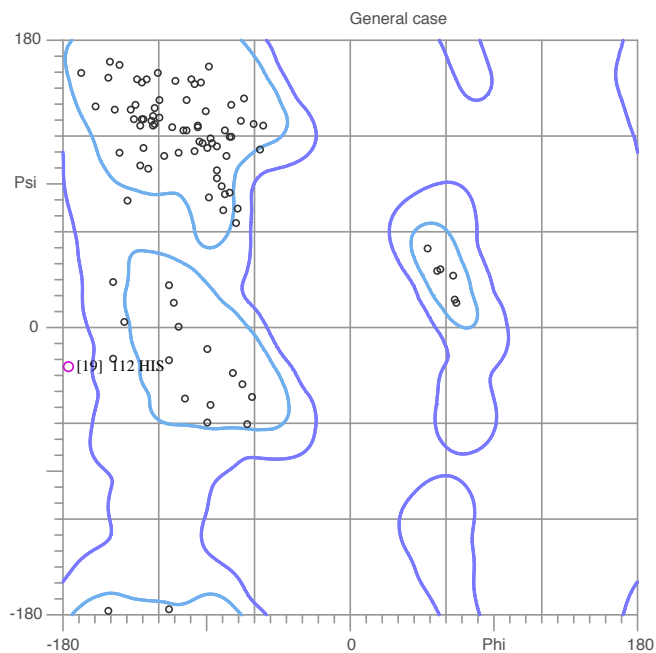


97.3% (109/112) of all residues were in favored (98%) regions.  
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 19

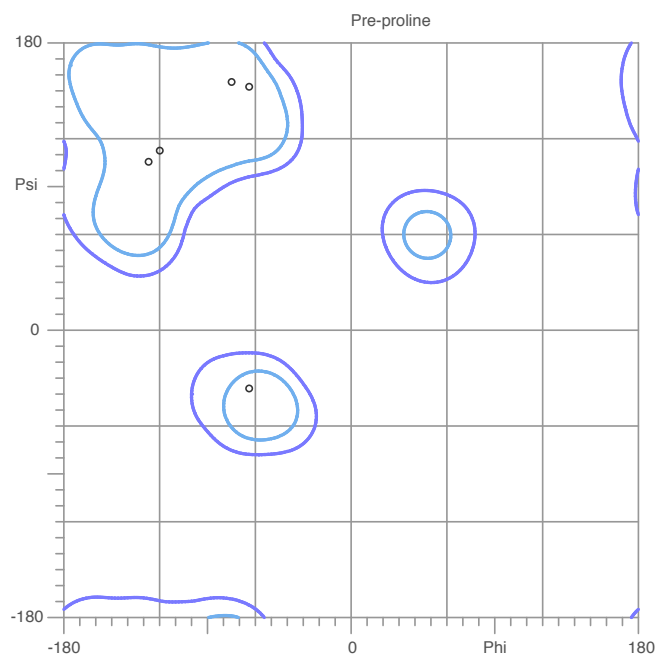
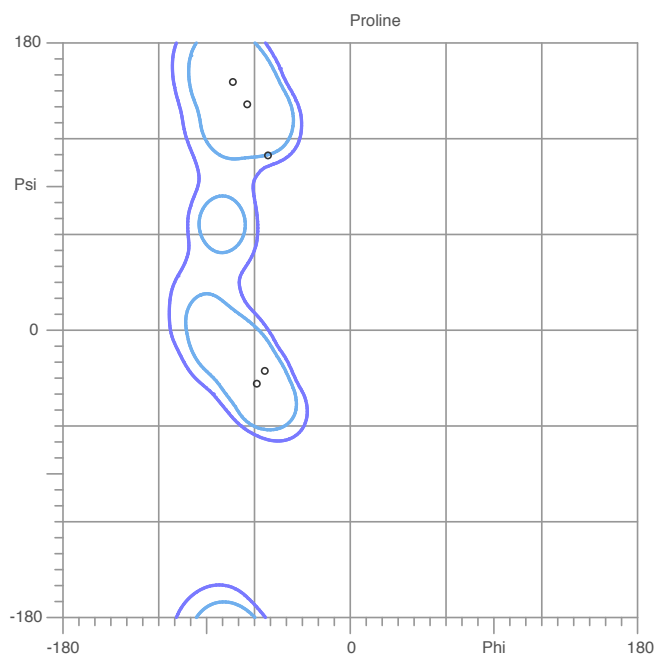
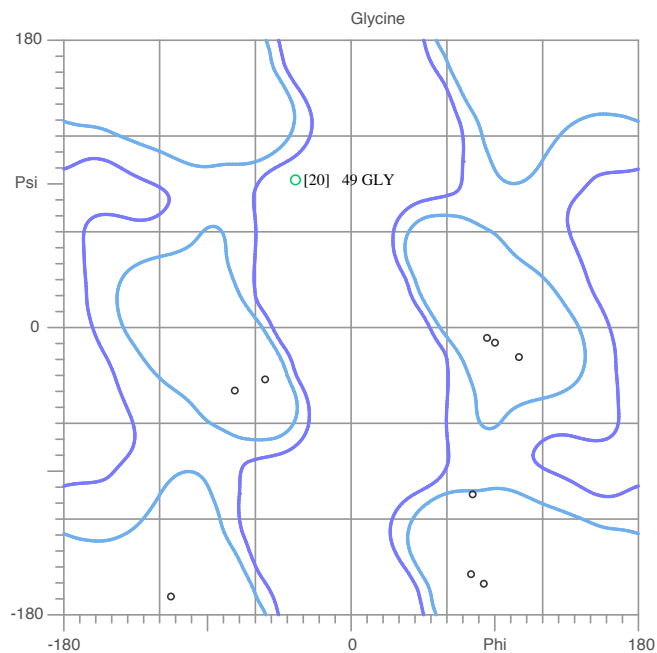
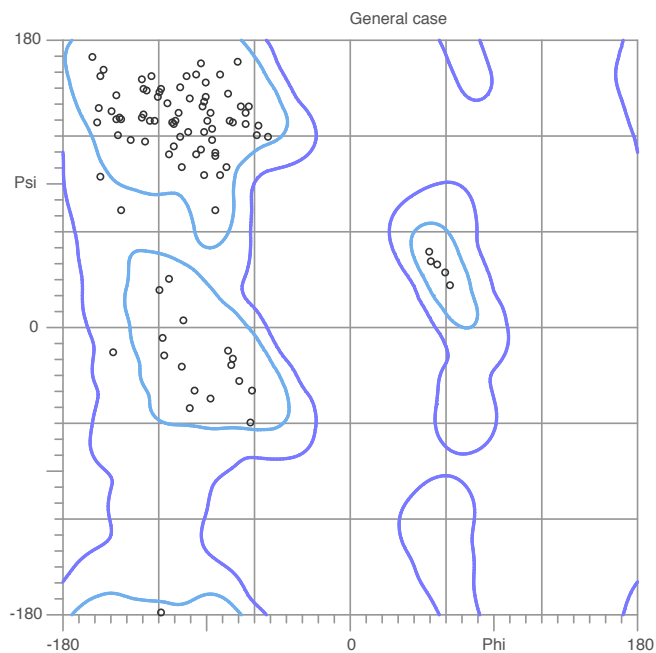


93.8% (105/112) of all residues were in favored (98%) regions.  
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[19] 112 HIS (-177.0, -25.0)

# MolProbity Ramachandran analysis

LKR112\_R3\_em\_bcr3.pdb, model 20



96.4% (108/112) of all residues were in favored (98%) regions.  
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[20] 49 GLY (-35.0, 93.3)

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

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