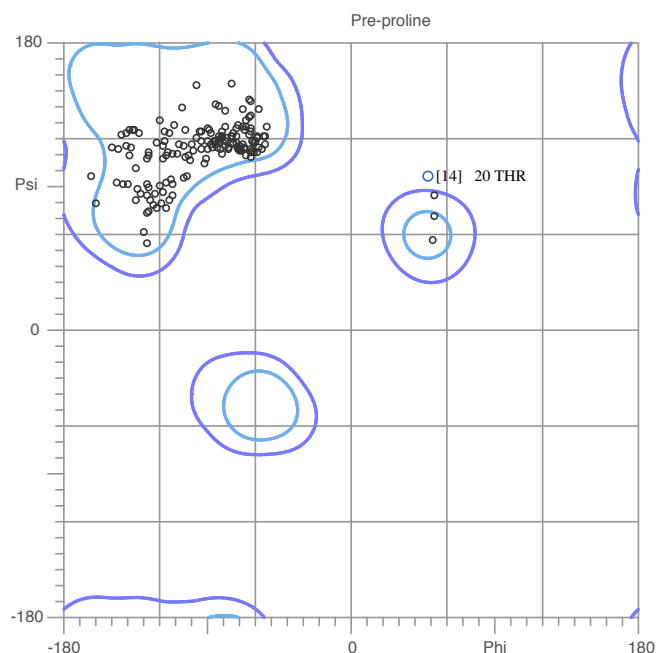
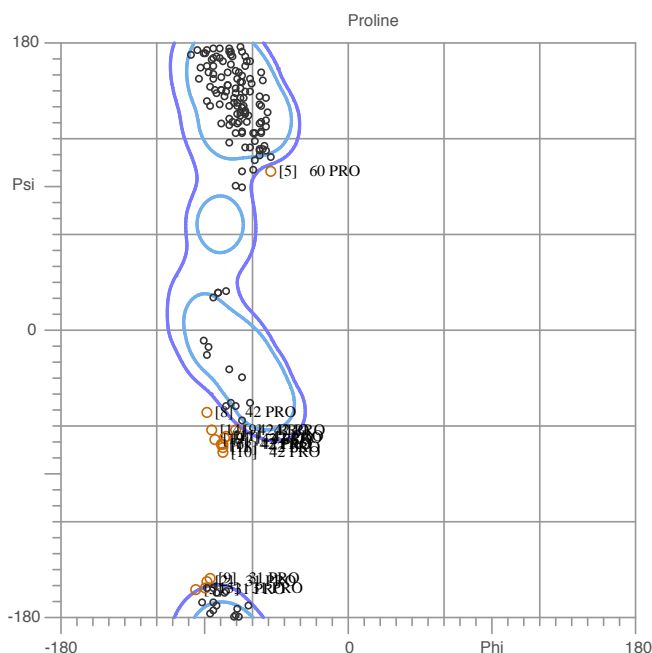
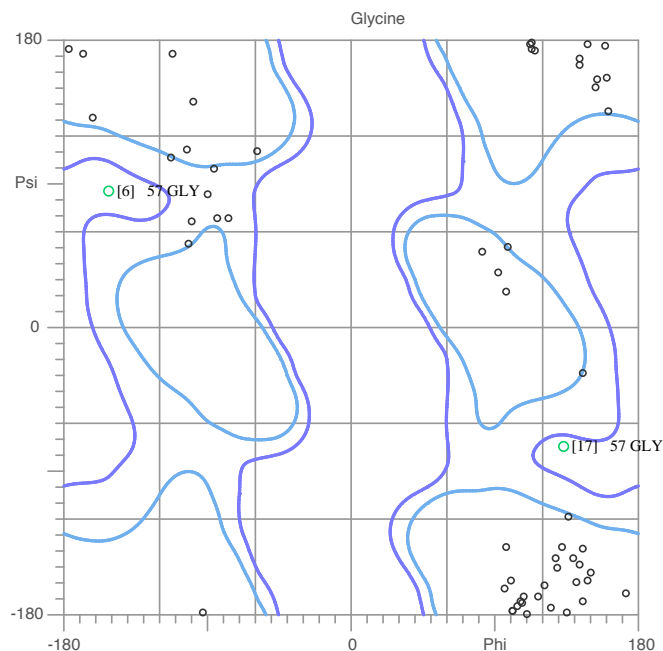
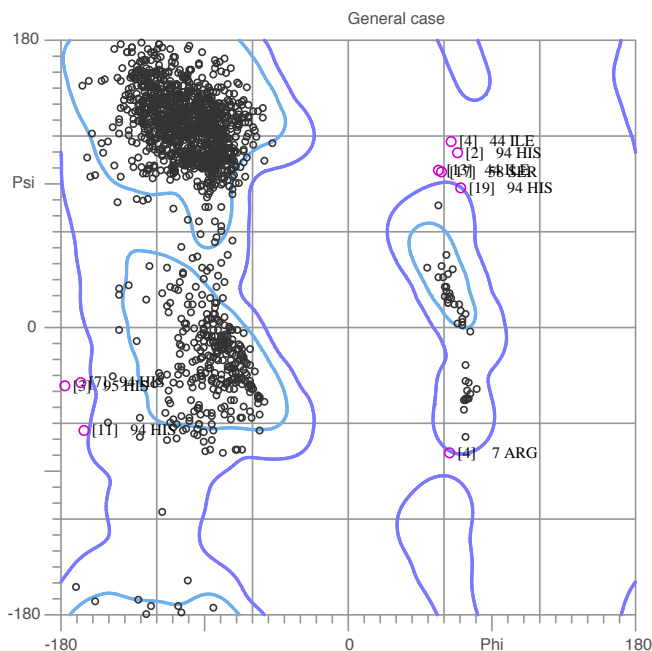


# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, all models



93.1% (1750/1880) of all residues were in favored (98%) regions.  
98.6% (1853/1880) of all residues were in allowed (>99.8%) regions.

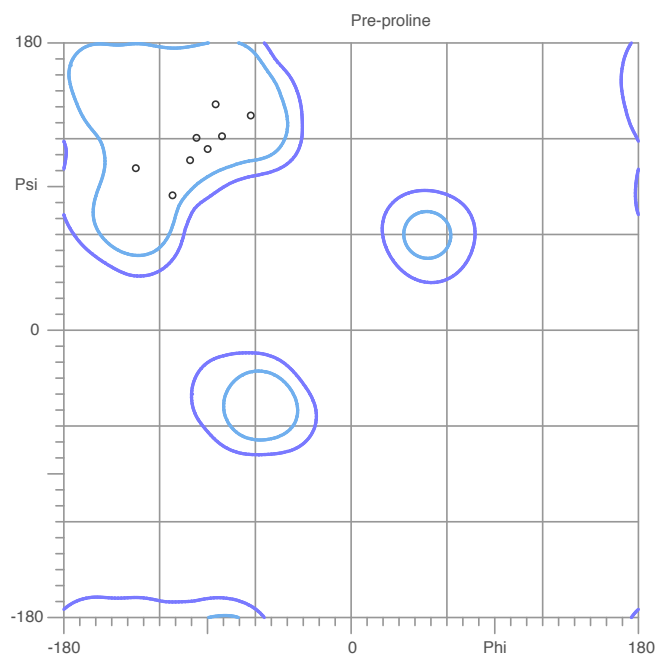
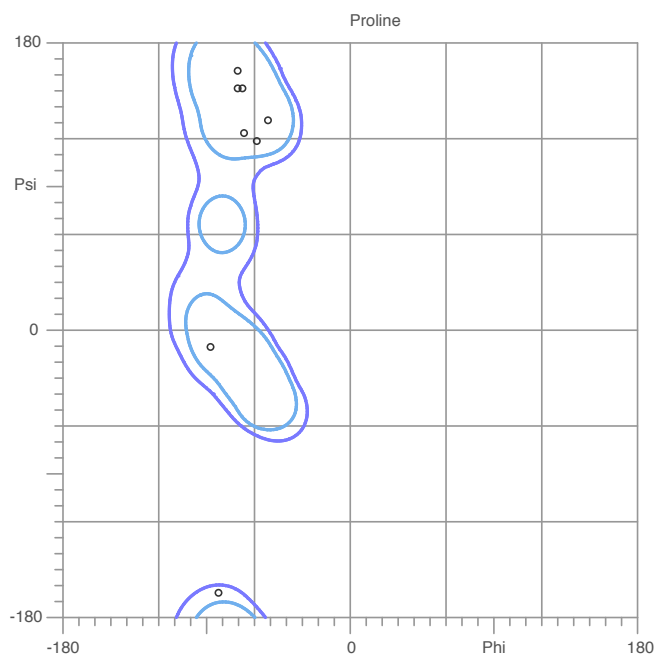
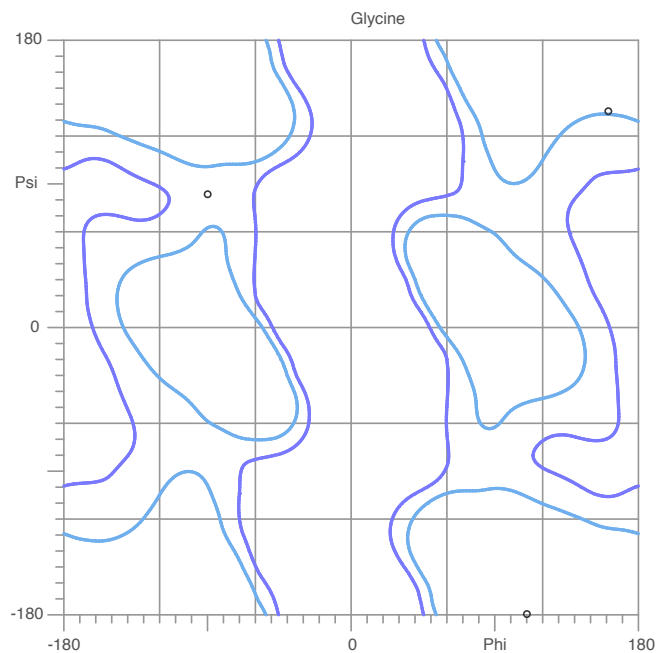
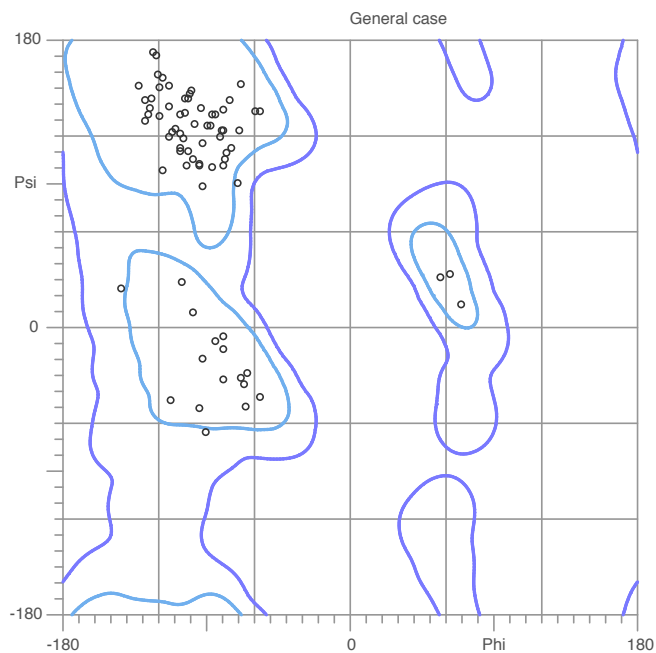
There were 27 outliers (phi, psi):

- [2] 31 PRO (-89.5, -157.7)
- [2] 94 HIS (68.3, 110.1)
- [3] 95 HIS (-178.3, -36.8)
- [4] 7 ARG (63.7, -79.0)
- [4] 44 ILE (64.9, 117.6)
- [5] 31 PRO (-96.5, -162.5)
- [5] 60 PRO (-49.8, 100.3)
- [6] 42 PRO (-79.6, -71.9)
- [6] 57 GLY (-152.9, 86.6)
- [7] 42 PRO (-80.1, -71.8)
- [7] 94 HIS (-168.5, -34.8)

- [8] 42 PRO (-89.5, -51.7)
- [9] 31 PRO (-87.1, -155.8)
- [9] 42 PRO (-71.1, -62.0)
- [10] 42 PRO (-79.8, -76.7)
- [11] 42 PRO (-77.9, -66.2)
- [11] 94 HIS (-166.9, -64.8)
- [13] 44 ILE (56.5, 100.0)
- [14] 20 THR (48.1, 97.8)
- [14] 42 PRO (-86.6, -62.9)
- [15] 31 PRO (-91.0, -161.2)
- [17] 42 PRO (-78.6, -67.6)
- [17] 57 GLY (133.8, -74.1)
- [17] 58 SER (58.4, 98.4)
- [18] 42 PRO (-79.9, -73.6)
- [19] 42 PRO (-84.8, -68.5)
- [19] 94 HIS (70.6, 89.0)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 1



94.7% (89/94) of all residues were in favored (98%) regions.  
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

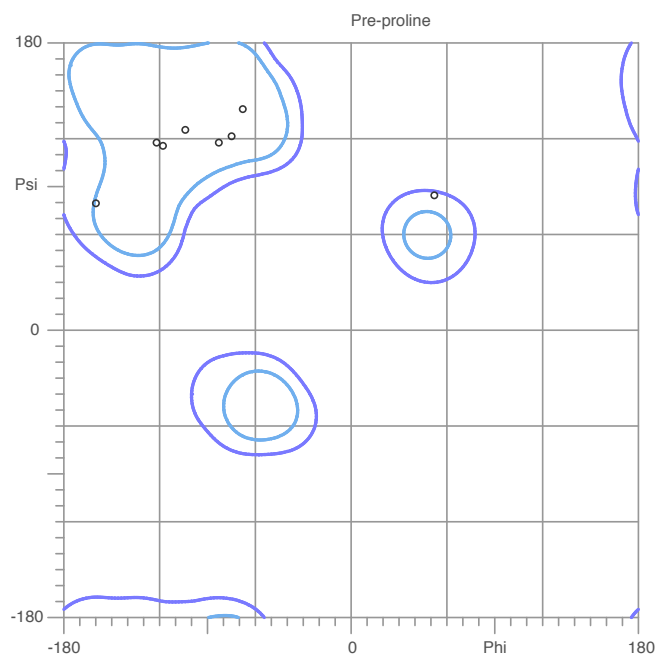
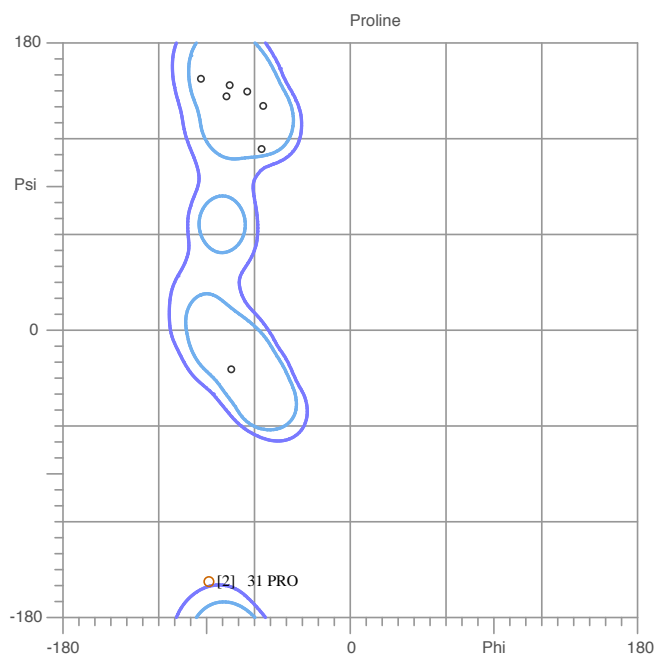
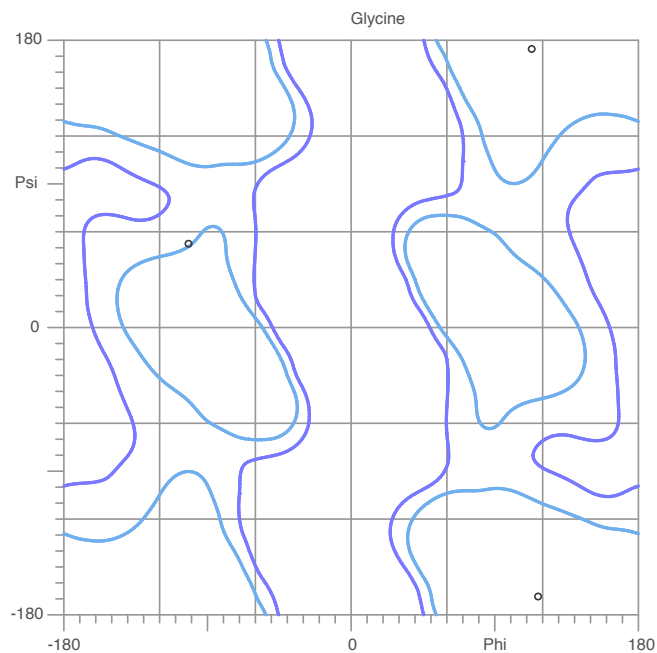
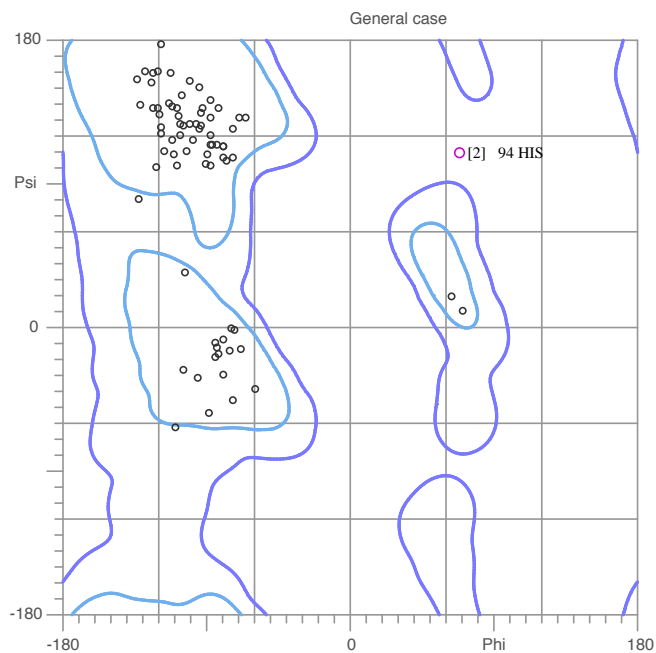
There were no outliers.

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# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 2



93.6% (88/94) of all residues were in favored (98%) regions.  
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

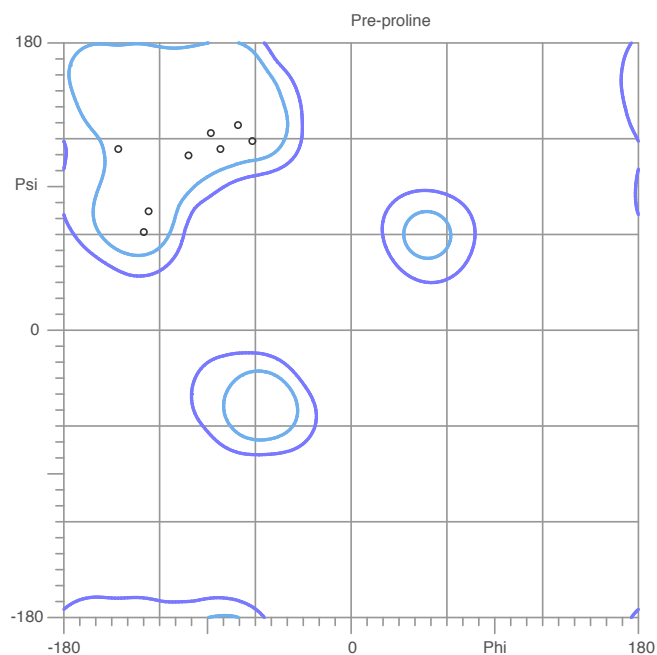
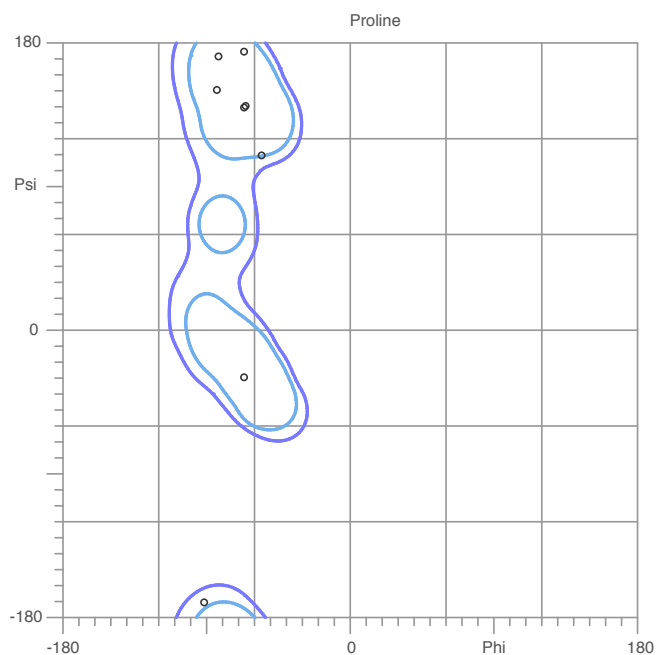
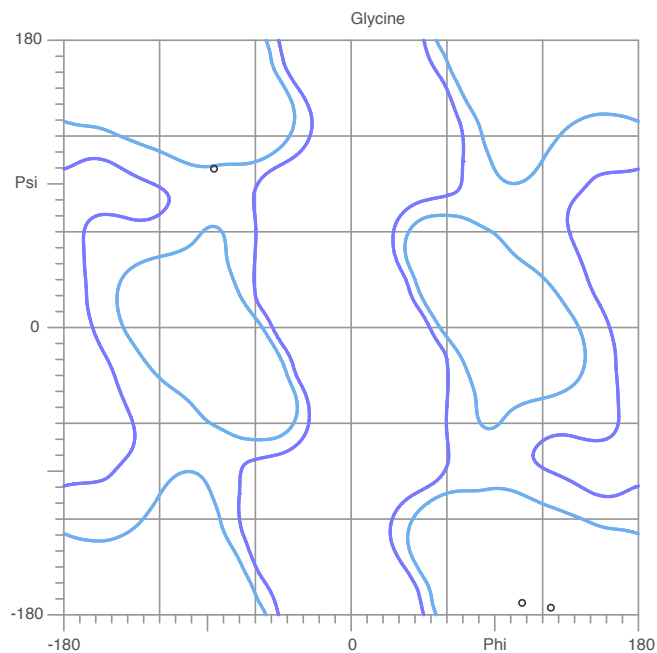
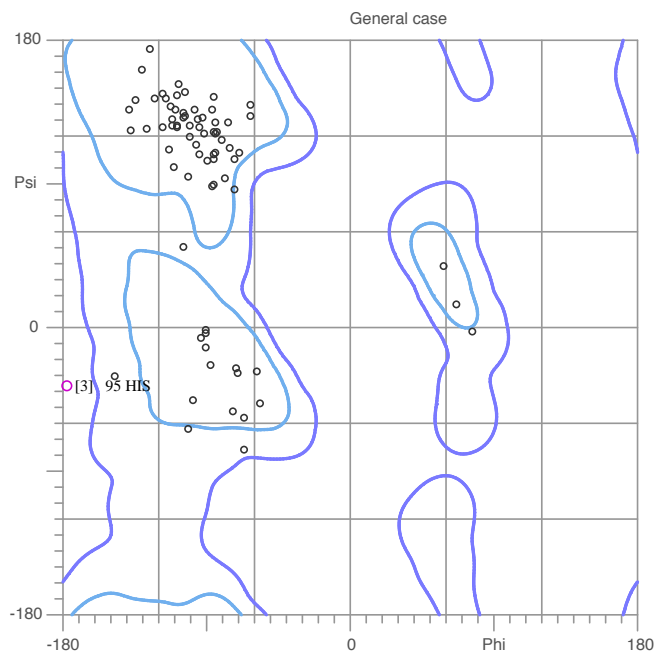
There were 2 outliers (phi, psi):

[2] 31 PRO (-89.5, -157.7)

[2] 94 HIS (68.3, 110.1)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 3



91.5% (86/94) of all residues were in favored (98%) regions.  
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

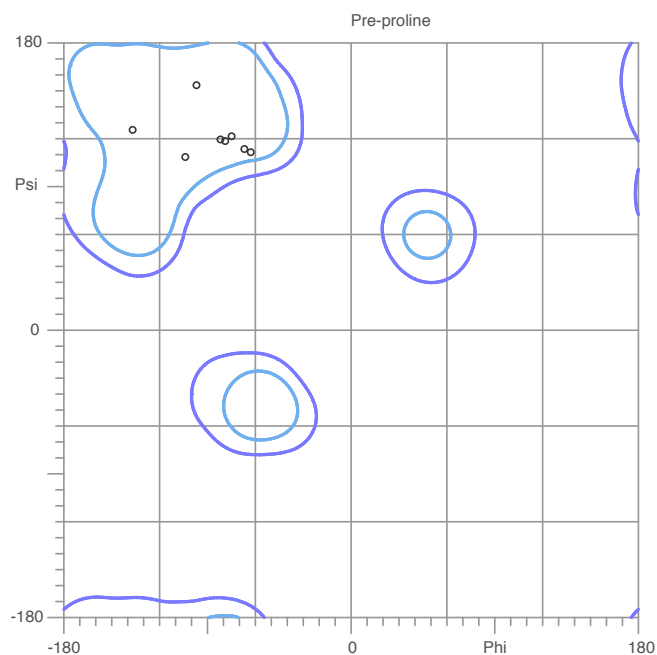
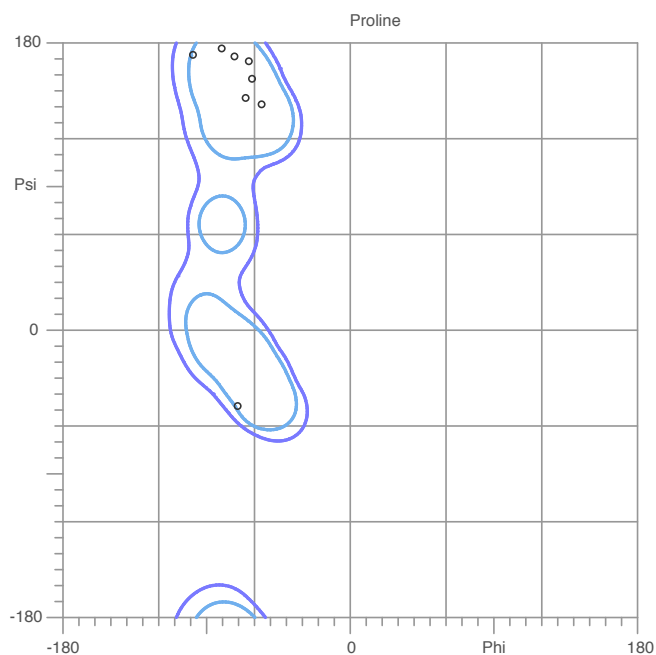
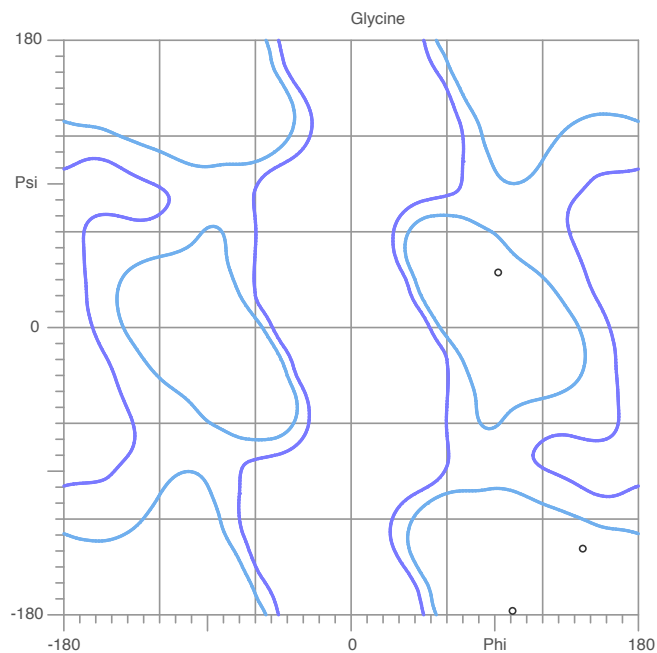
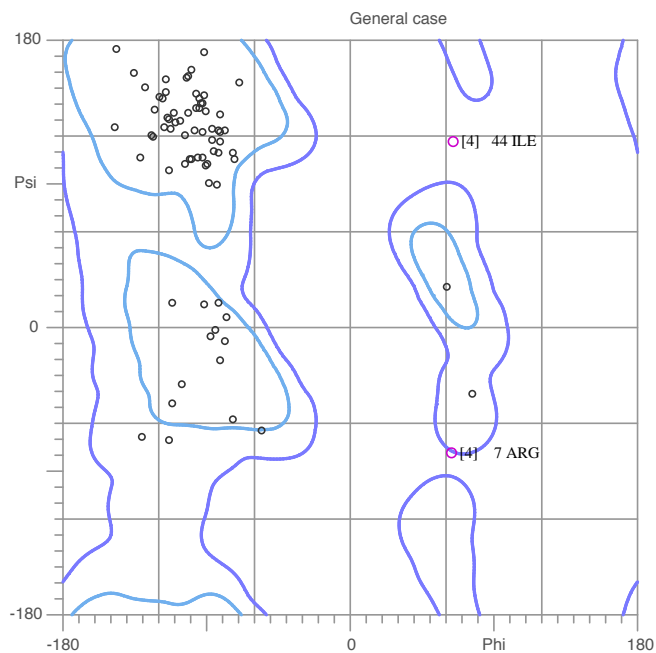
There were 1 outliers (phi, psi):  
[3] 95 HIS (-178.3, -36.8)

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# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 4



93.6% (88/94) of all residues were in favored (98%) regions.  
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

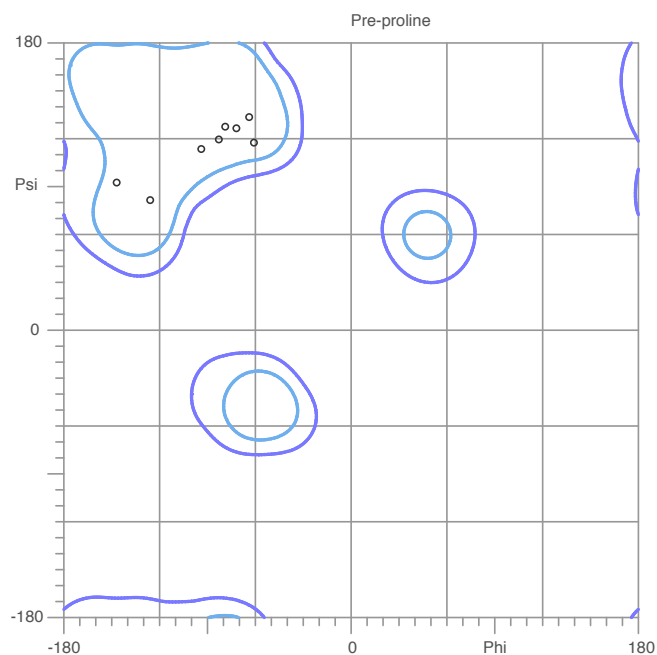
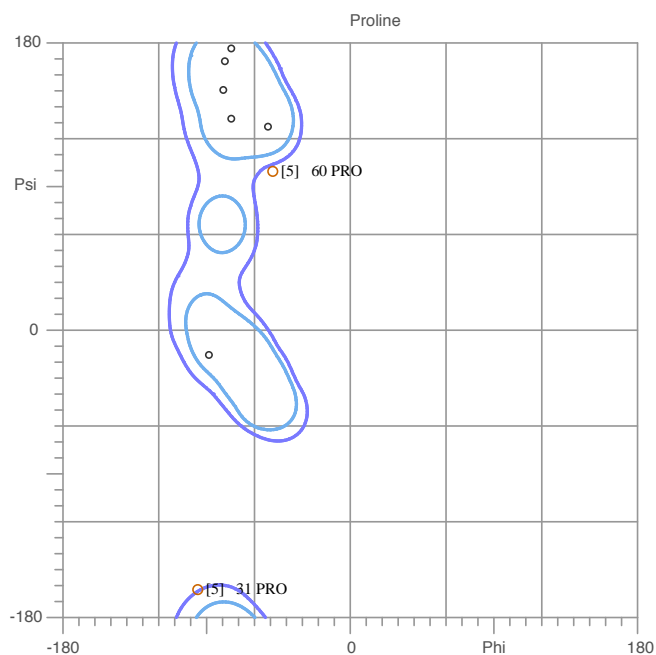
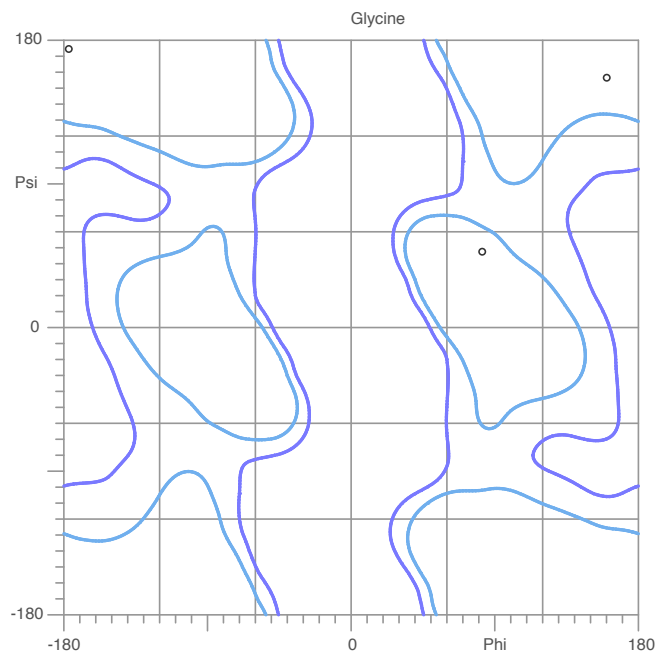
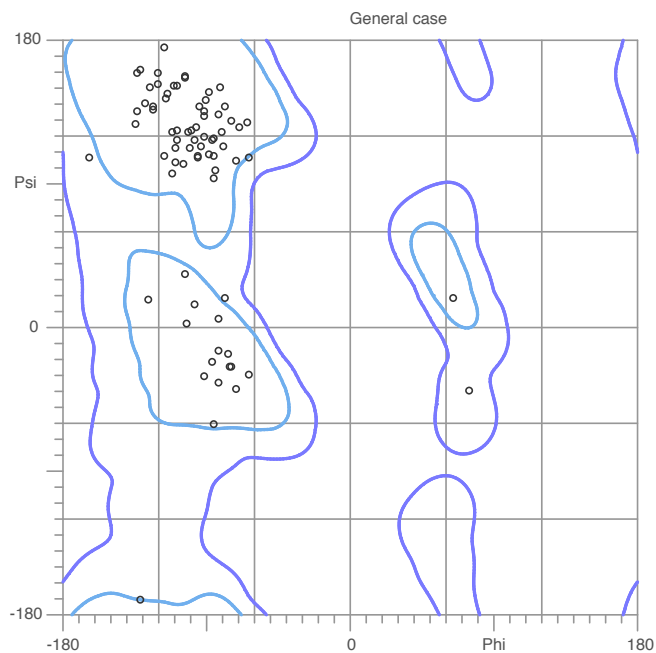
There were 2 outliers (phi, psi):

[4] 7 ARG (63.7, -79.0)

[4] 44 ILE (64.9, 117.6)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 5



94.7% (89/94) of all residues were in favored (98%) regions.  
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

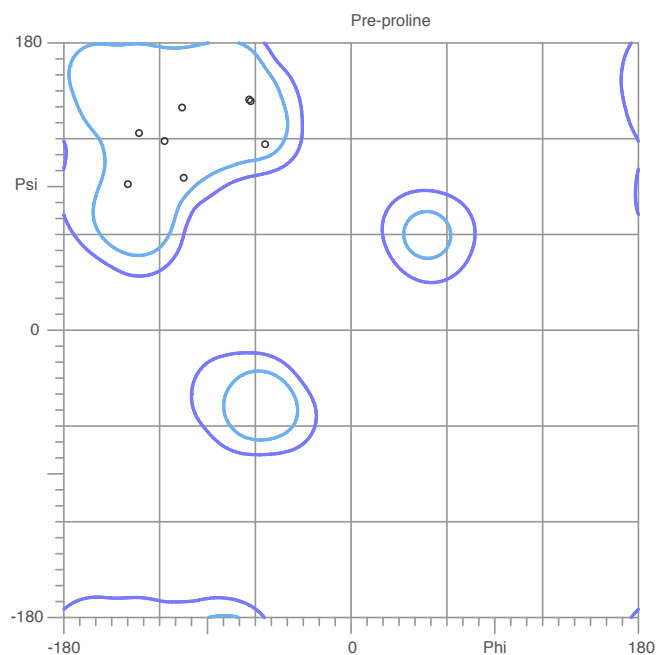
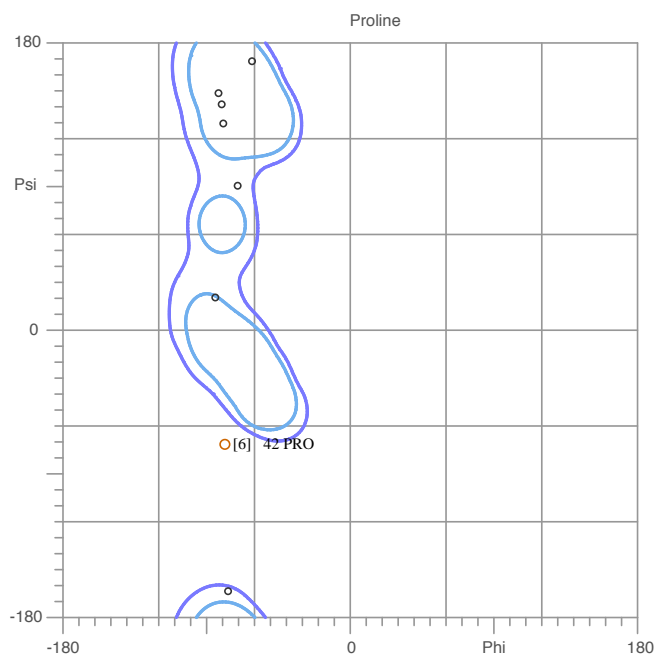
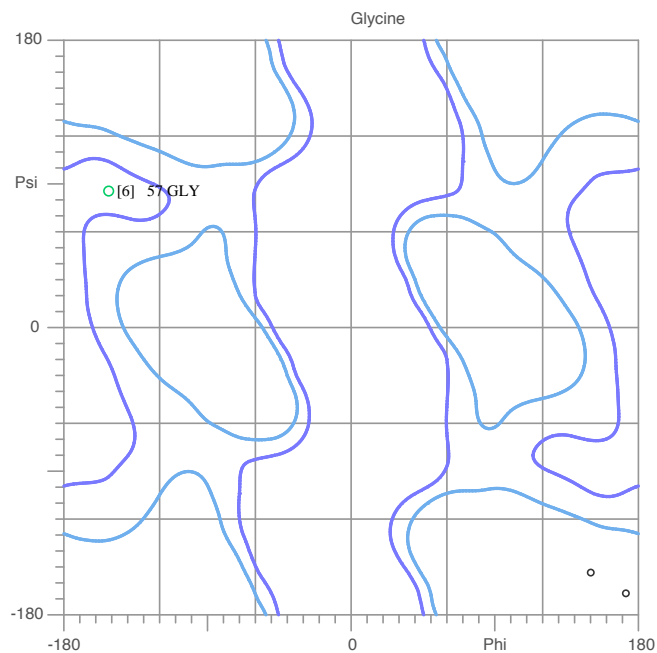
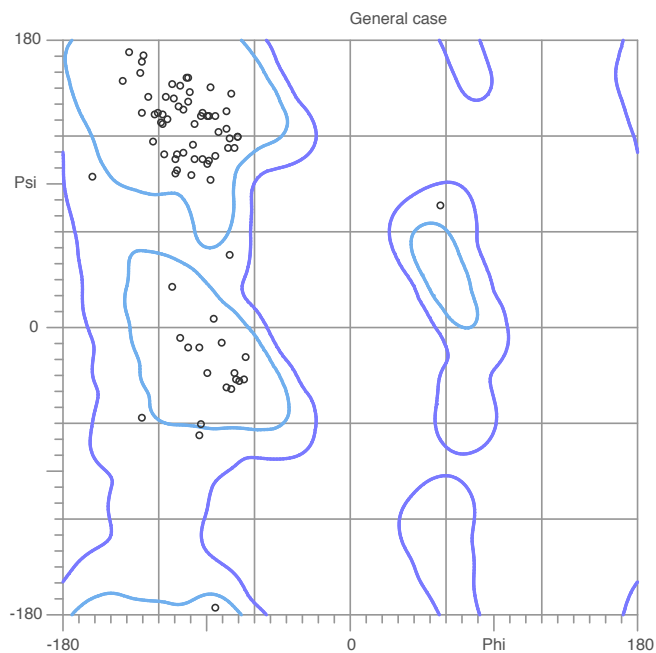
There were 2 outliers (phi, psi):

[5] 31 PRO (-96.5, -162.5)

[5] 60 PRO (-49.8, 100.3)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 6



90.4% (85/94) of all residues were in favored (98%) regions.  
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

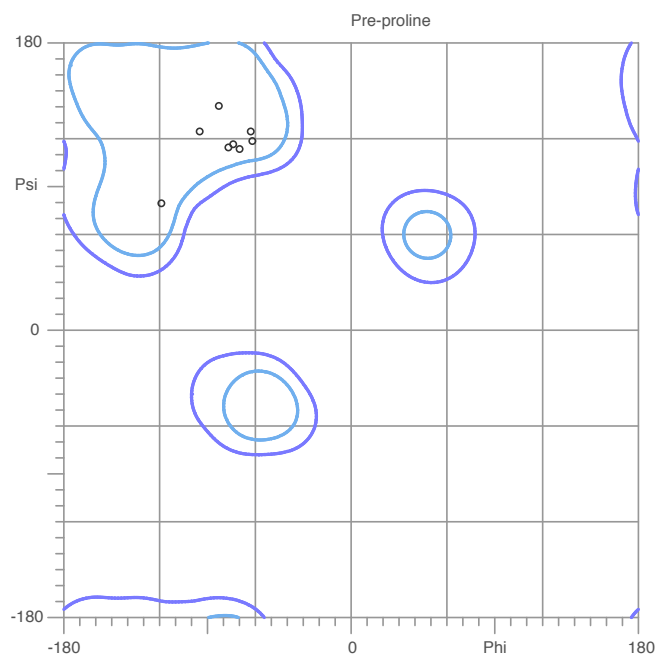
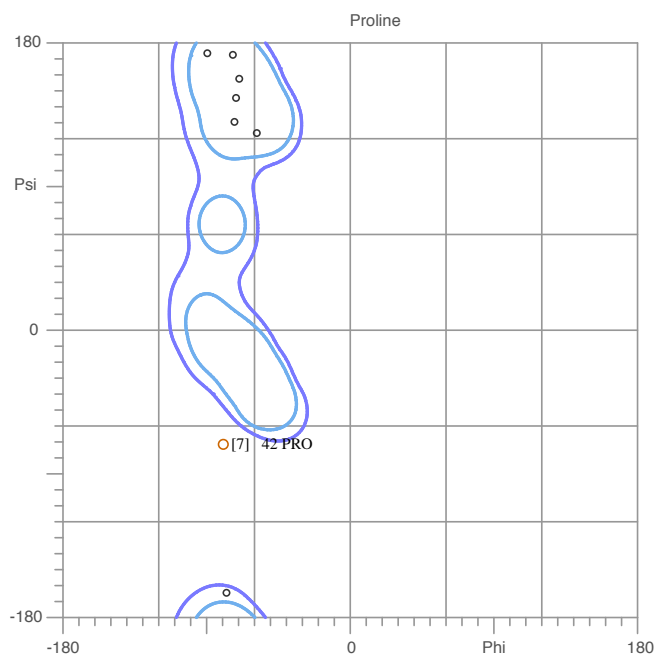
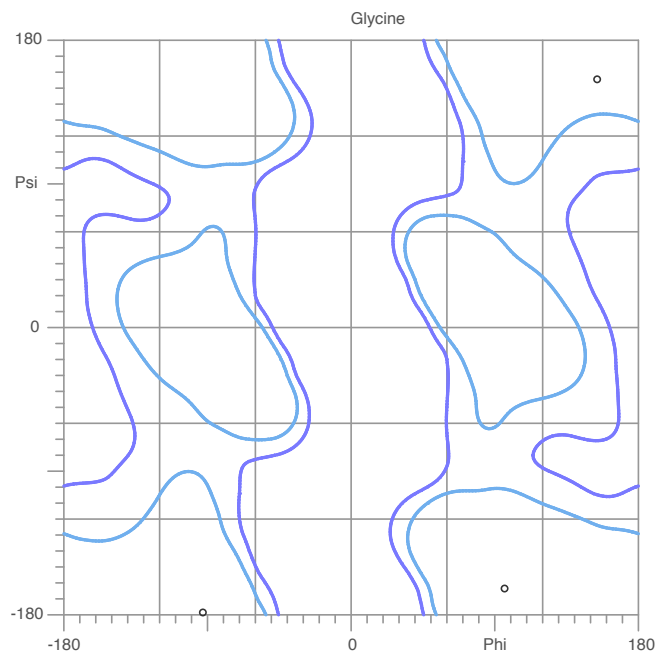
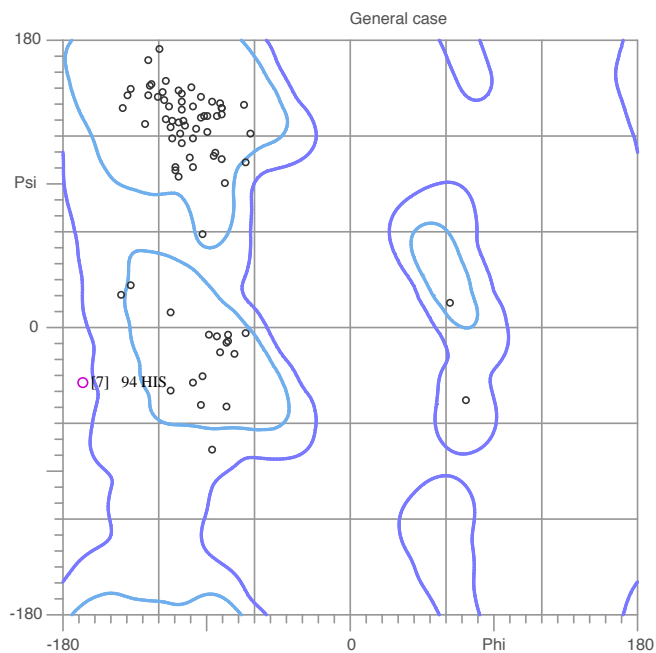
There were 2 outliers (phi, psi):

[6] 42 PRO (-79.6, -71.9)

[6] 57 GLY (-152.9, 86.6)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 7



93.6% (88/94) of all residues were in favored (98%) regions.  
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

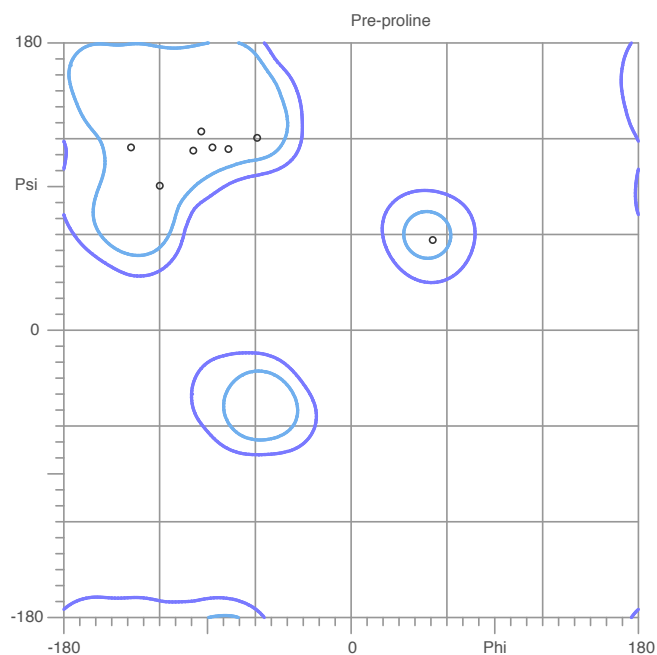
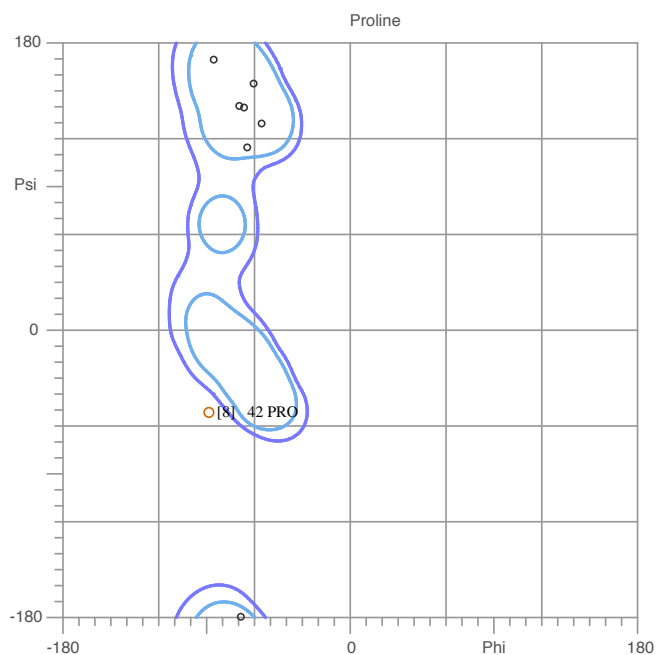
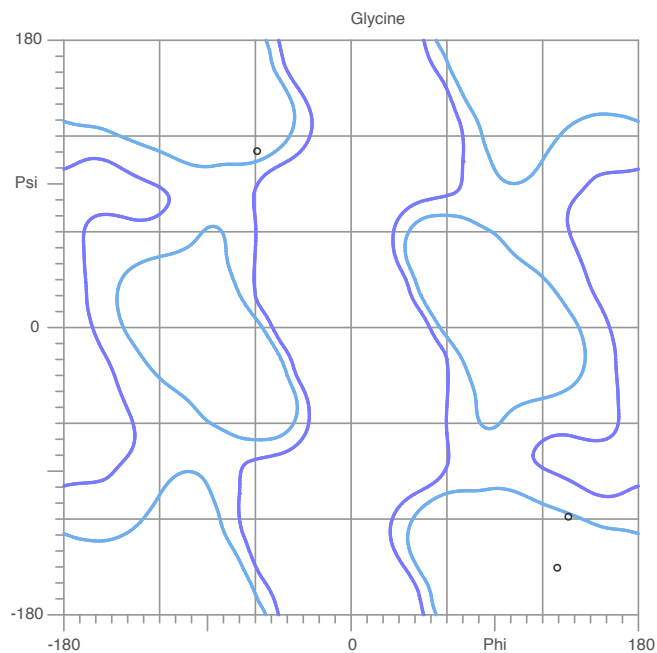
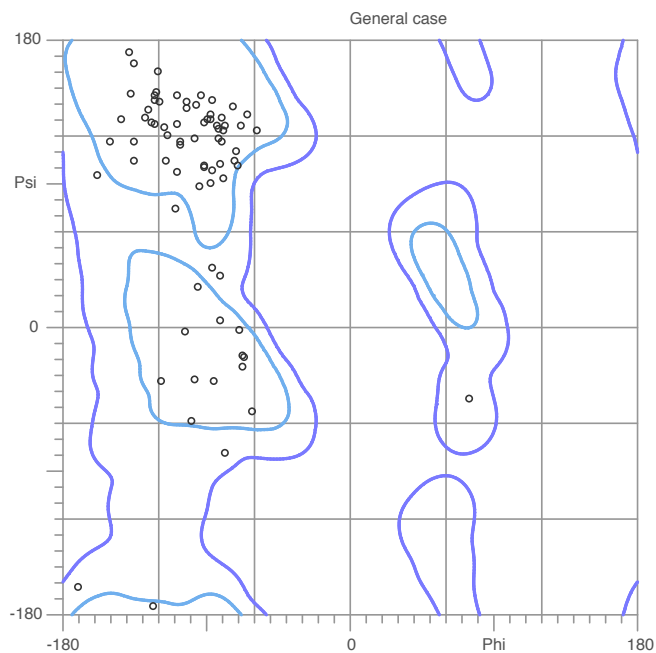
There were 2 outliers (phi, psi):

[7] 42 PRO (-80.1, -71.8)

[7] 94 HIS (-168.5, -34.8)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 8

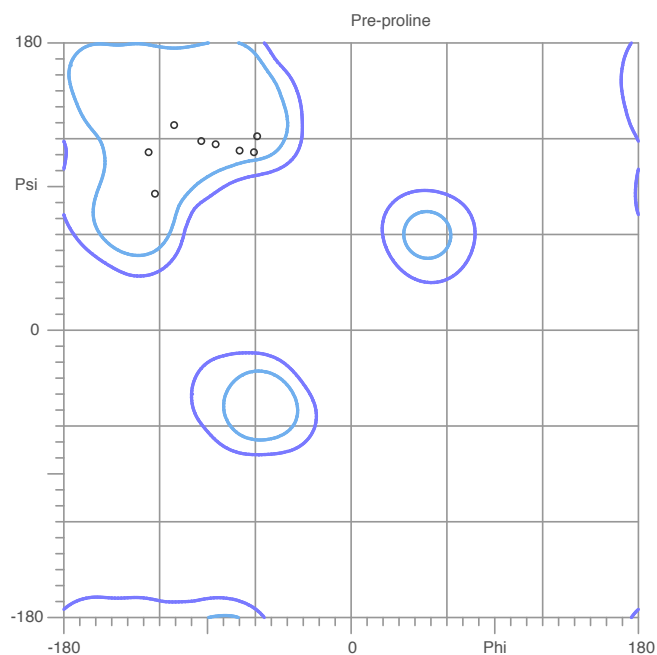
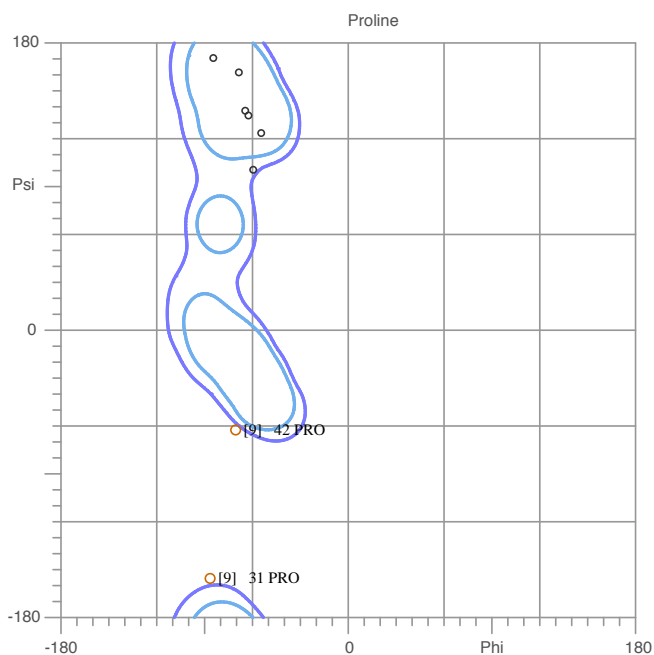
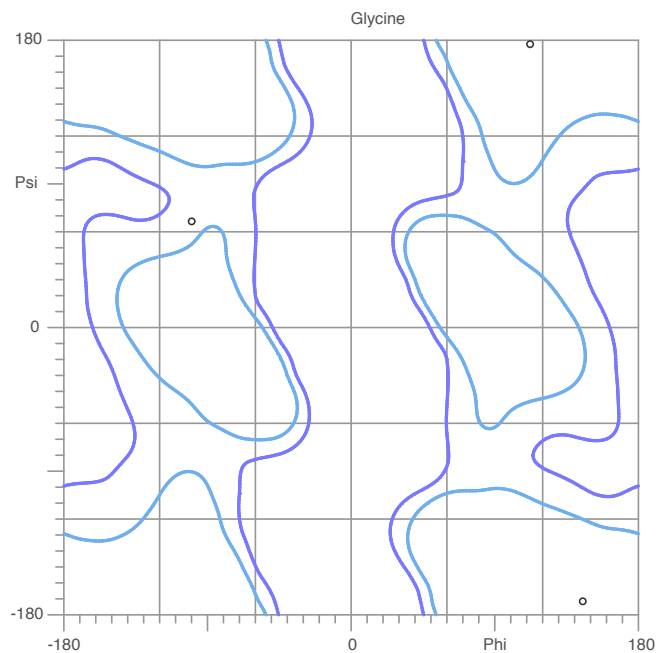
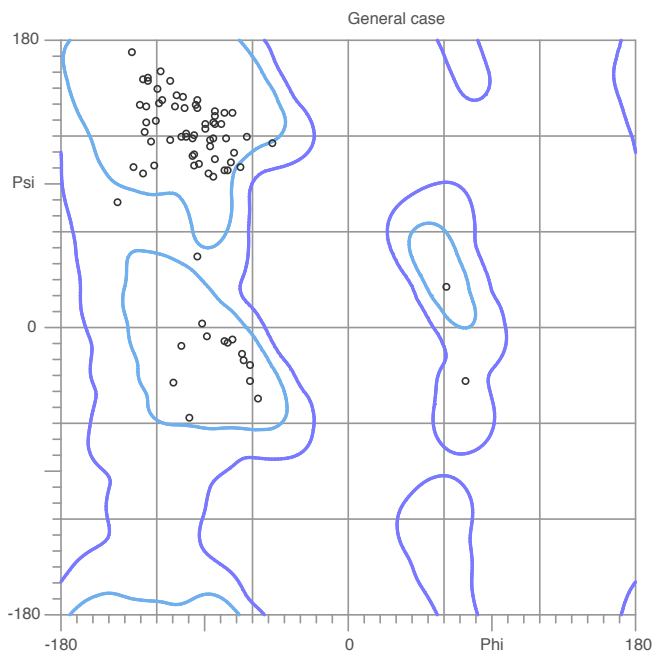


91.5% (86/94) of all residues were in favored (98%) regions.  
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[8] 42 PRO (-89.5, -51.7)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 9



91.5% (86/94) of all residues were in favored (98%) regions.  
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

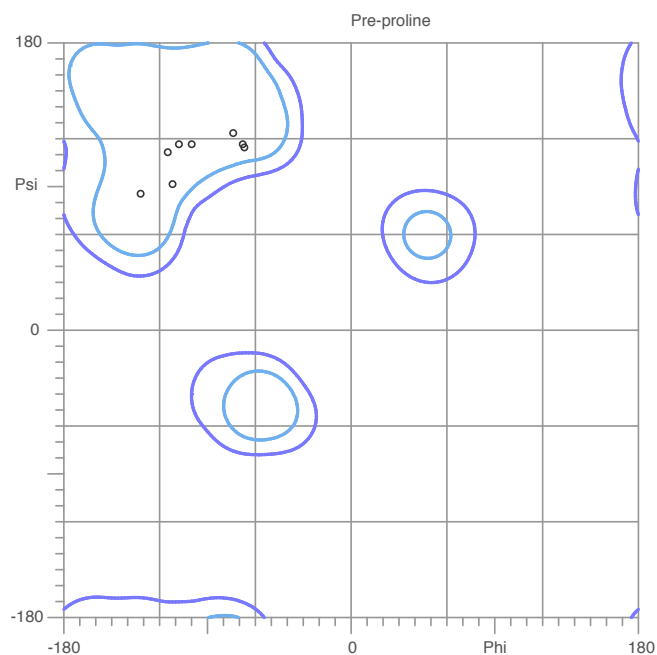
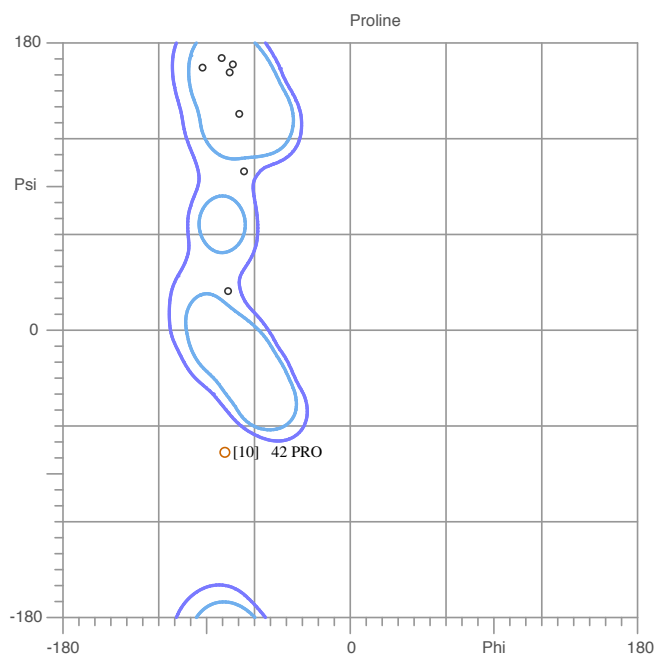
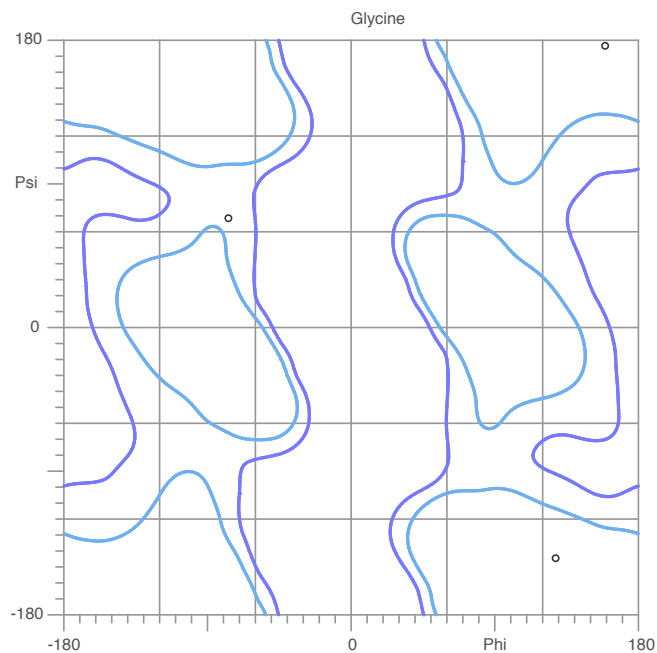
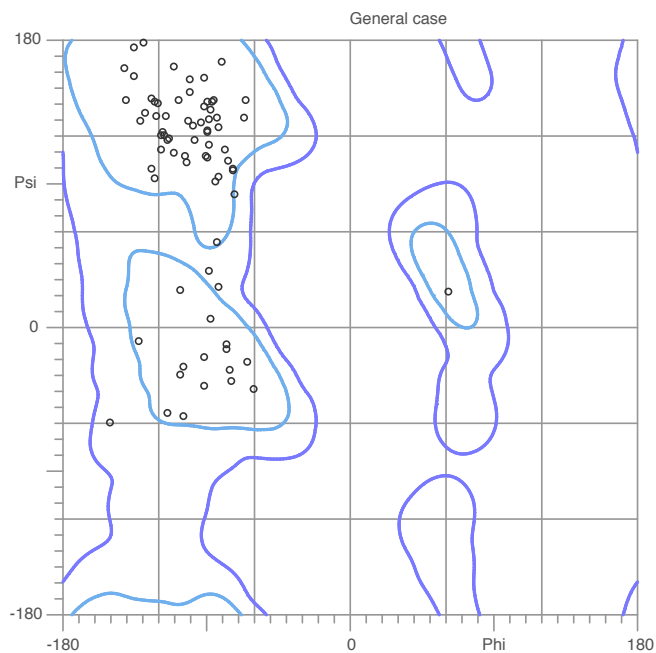
There were 2 outliers (phi, psi):

[9] 31 PRO (-87.1, -155.8)

[9] 42 PRO (-71.1, -62.0)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 10



92.6% (87/94) of all residues were in favored (98%) regions.  
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

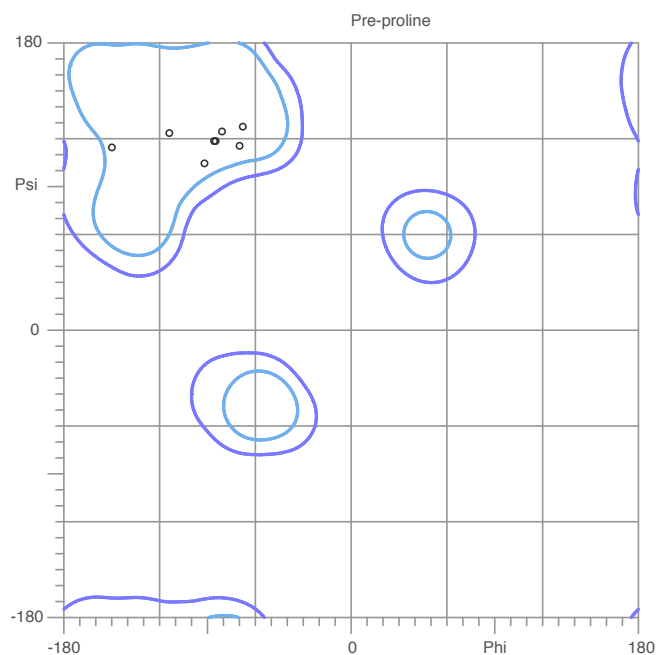
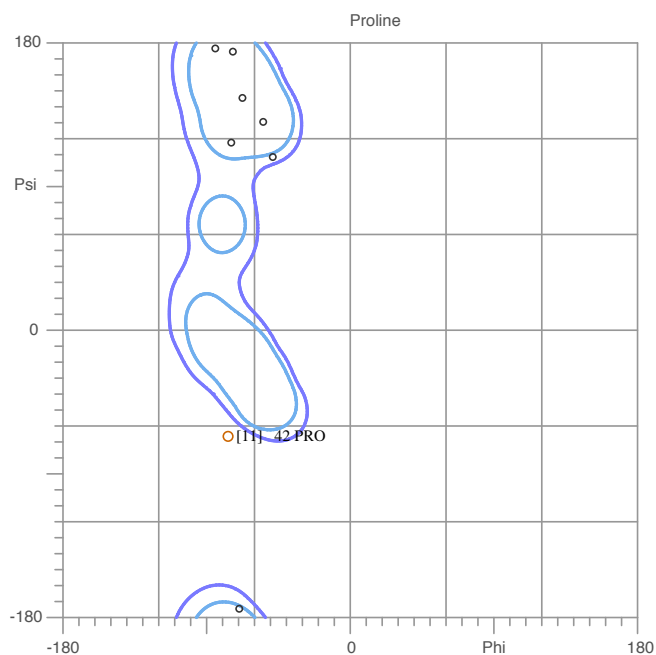
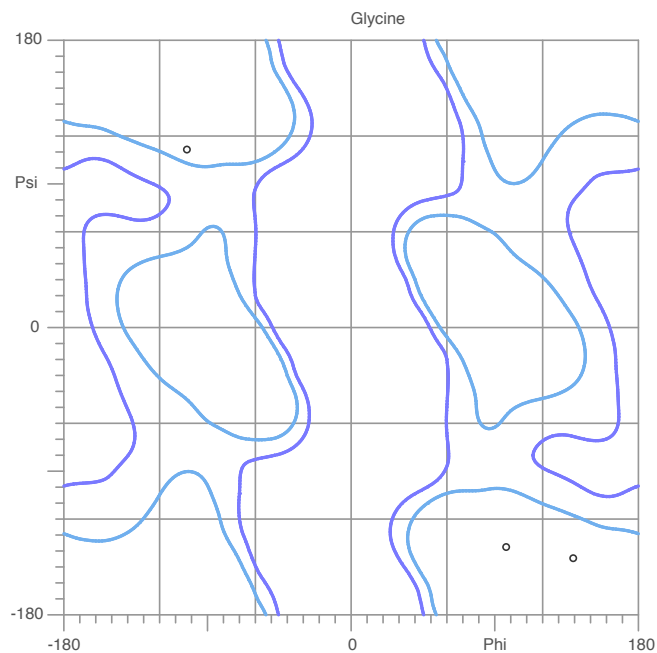
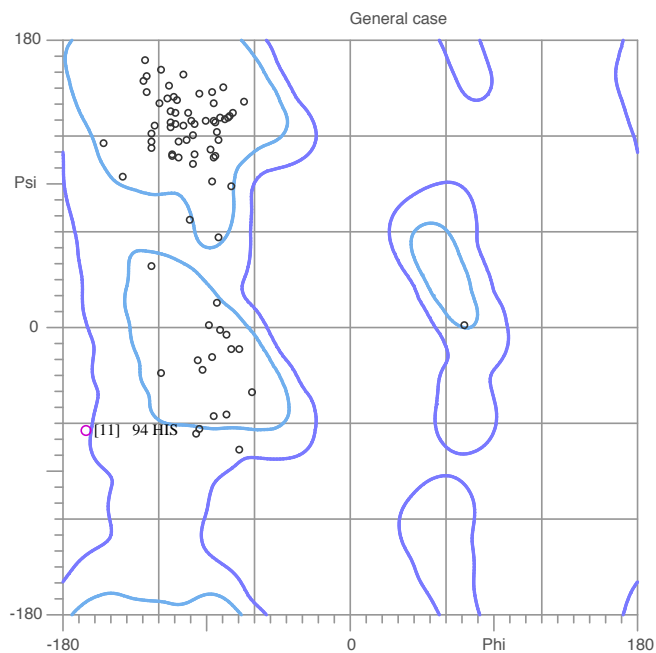
There were 1 outliers (phi, psi):  
[10] 42 PRO (-79.8, -76.7)

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# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 11



92.6% (87/94) of all residues were in favored (98%) regions.  
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

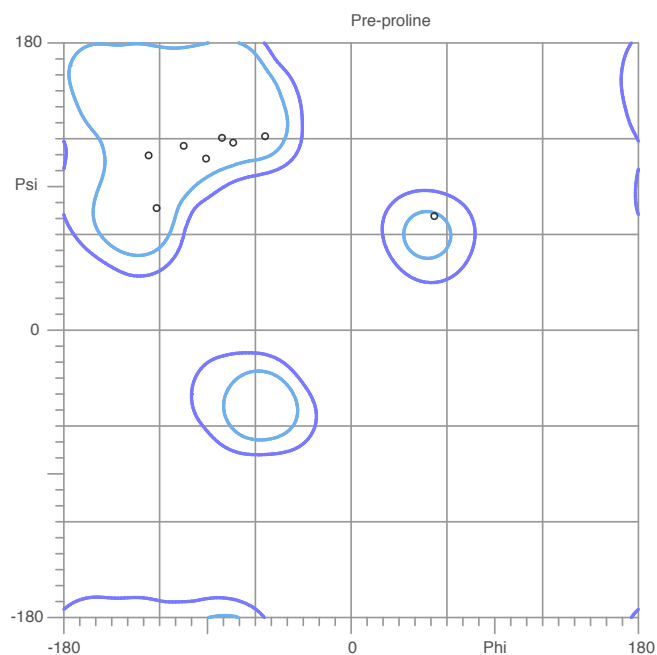
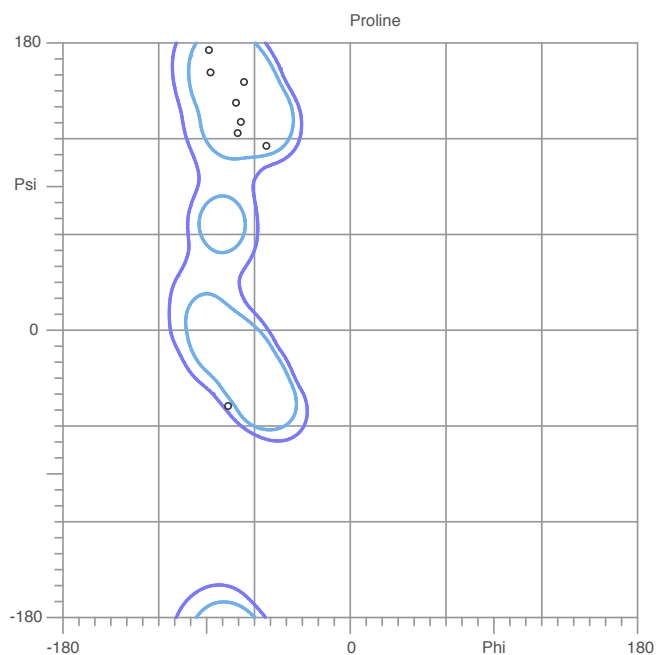
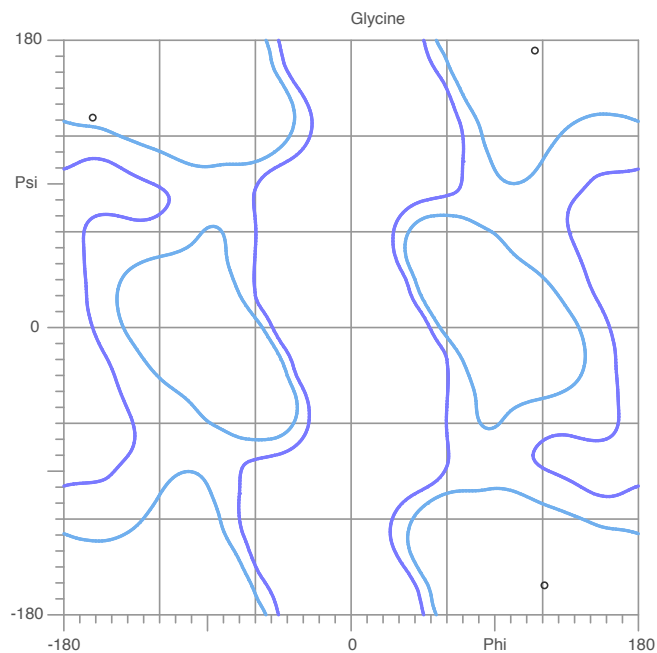
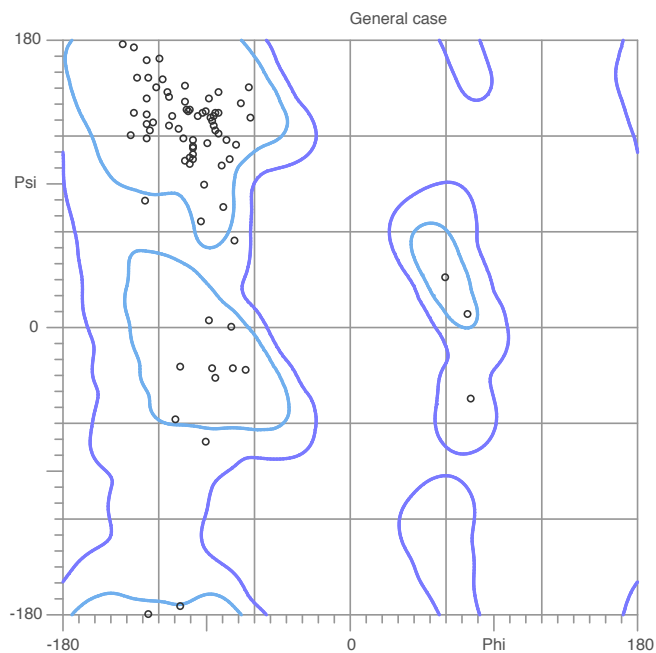
There were 2 outliers (phi, psi):

[11] 42 PRO (-77.9, -66.2)

[11] 94 HIS (-166.9, -64.8)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 12



94.7% (89/94) of all residues were in favored (98%) regions.  
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

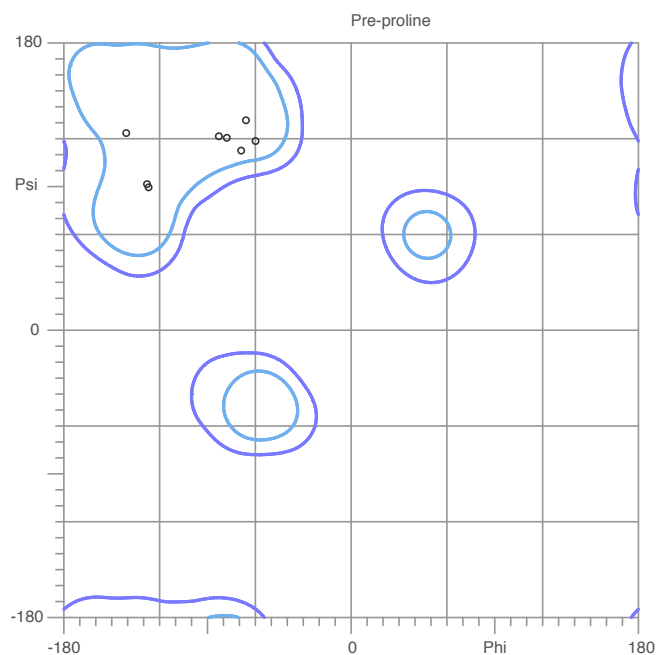
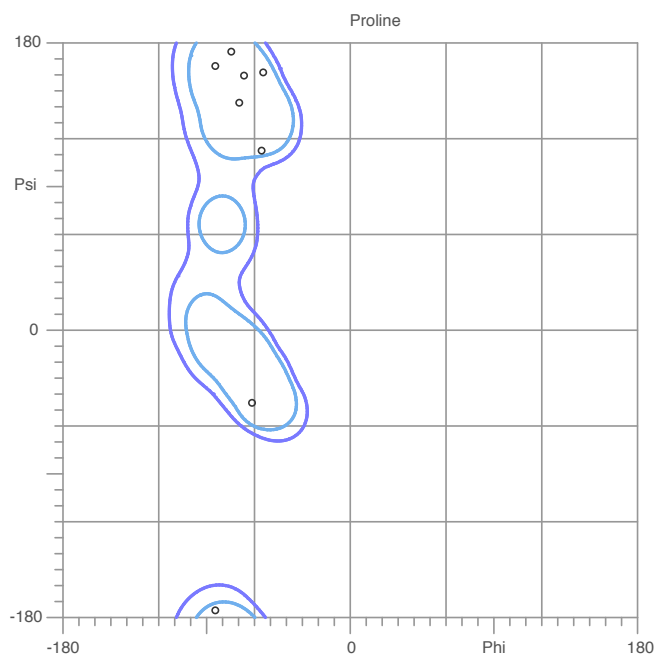
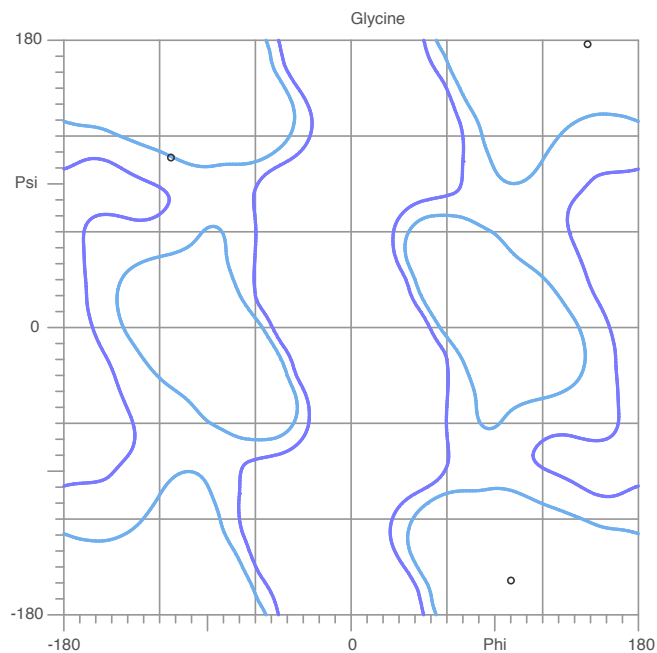
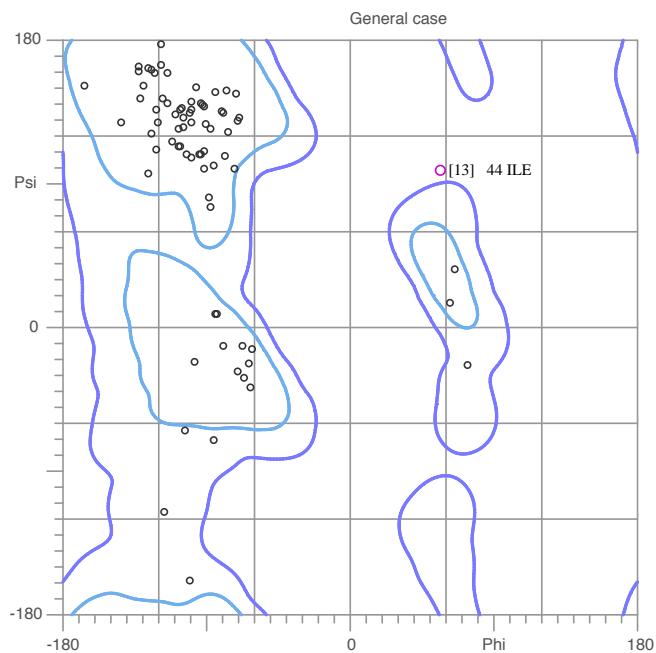
There were no outliers.

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

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# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 13



92.6% (87/94) of all residues were in favored (98%) regions.  
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

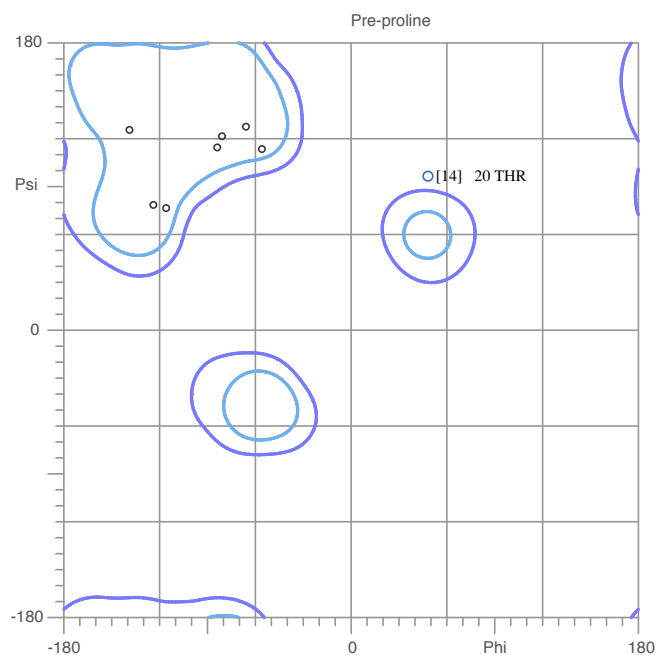
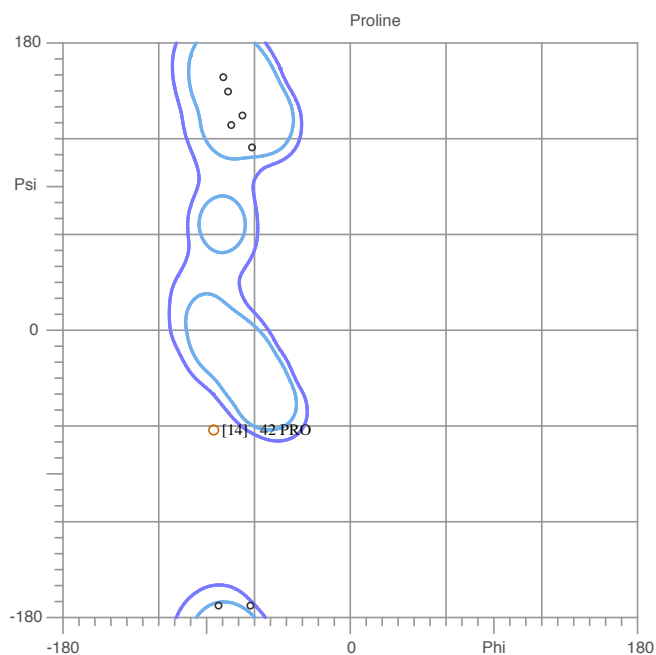
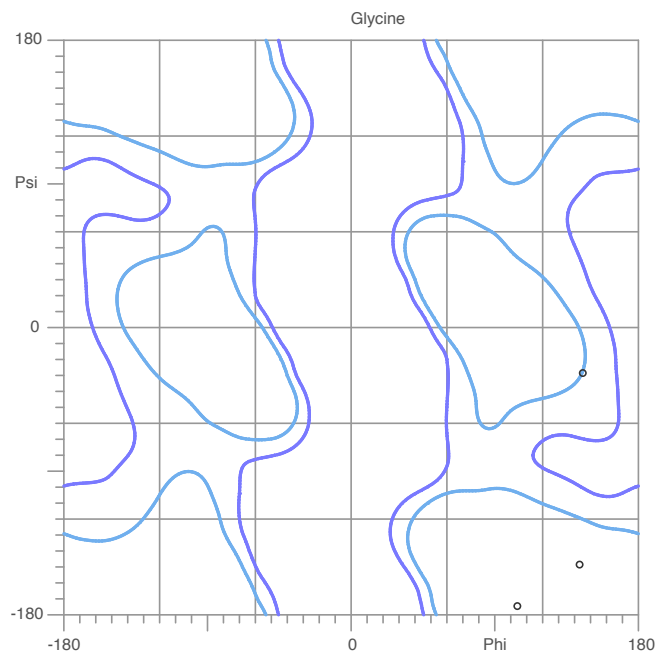
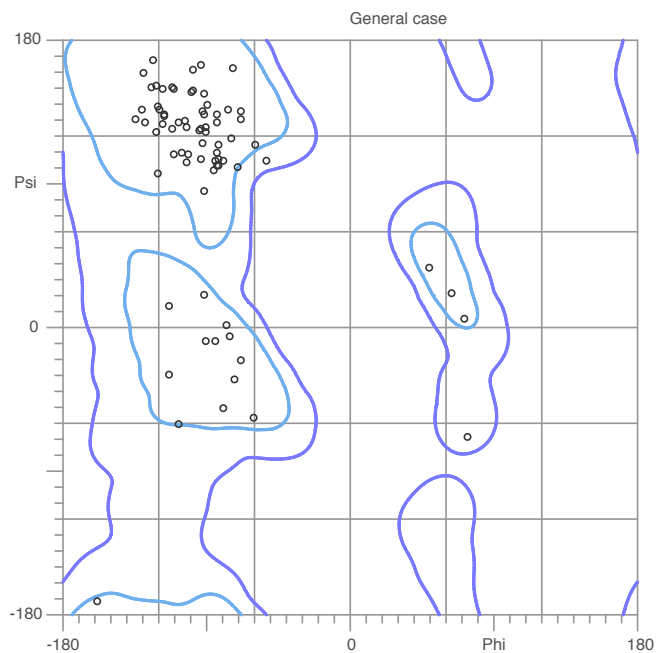
There were 1 outliers (phi, psi):  
[13] 44 ILE (56.5, 100.0)

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

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# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 14



93.6% (88/94) of all residues were in favored (98%) regions.  
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

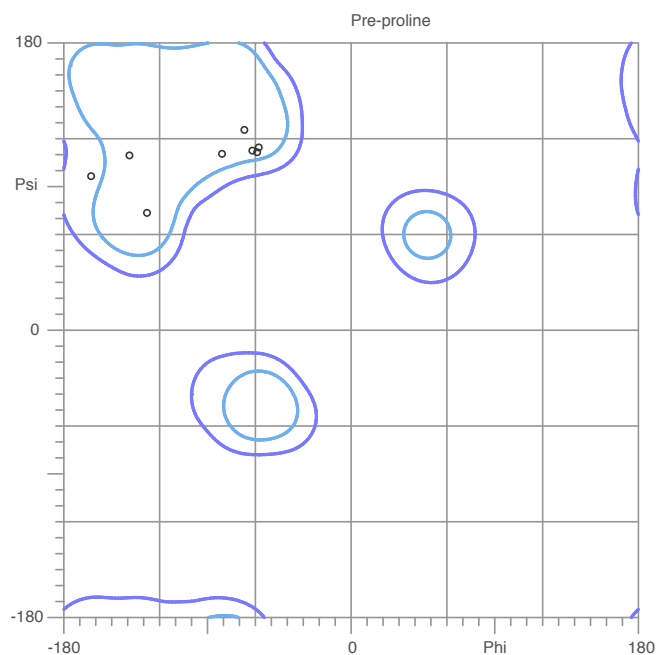
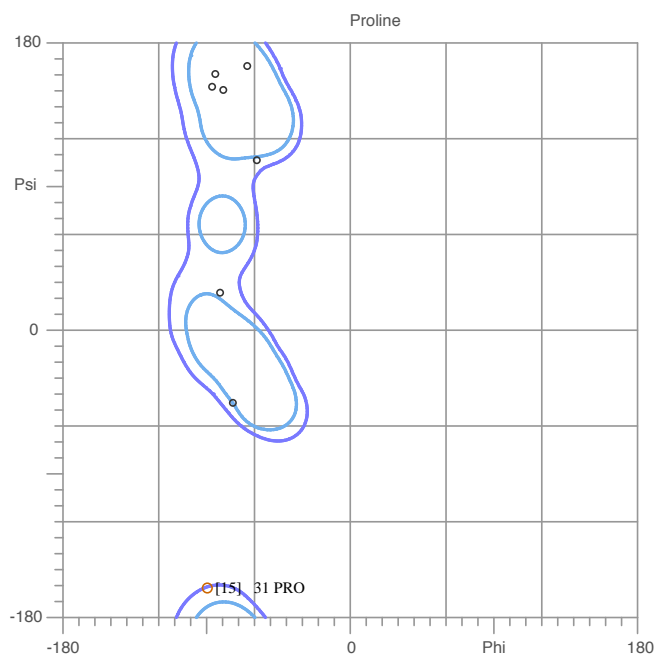
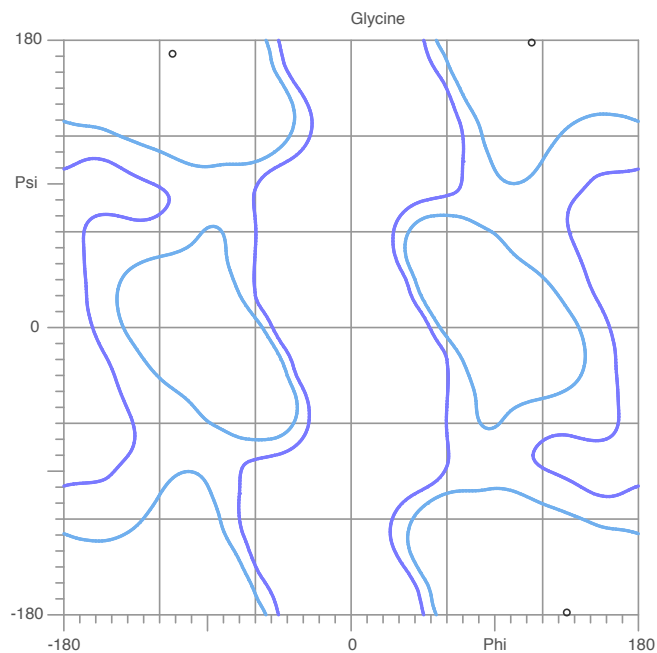
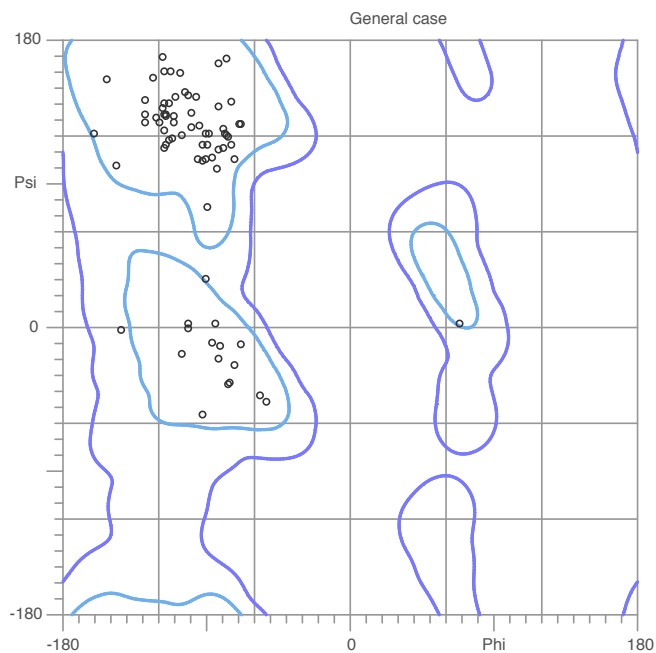
There were 2 outliers (phi, psi):

[14] 20 THR (48.1, 97.8)

[14] 42 PRO (-86.6, -62.9)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 15

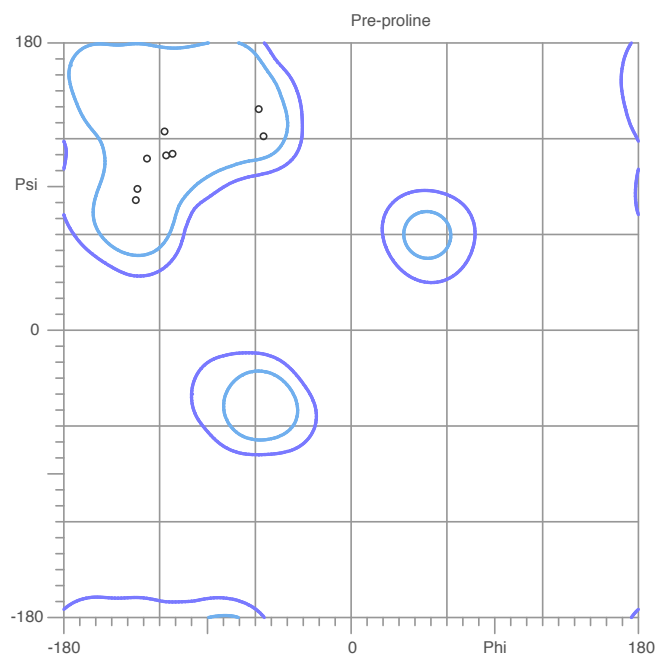
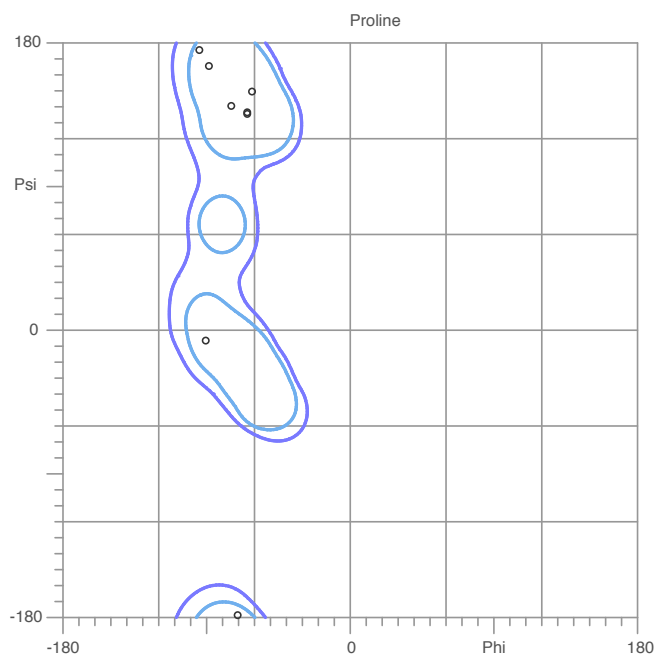
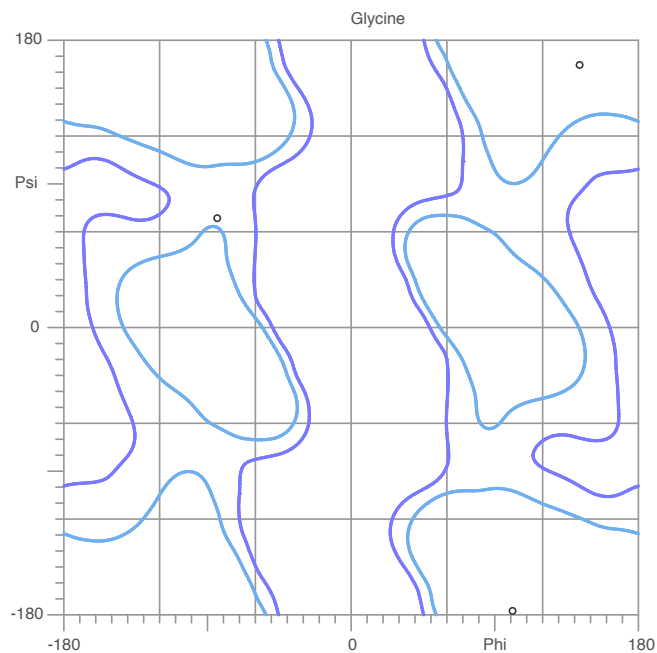
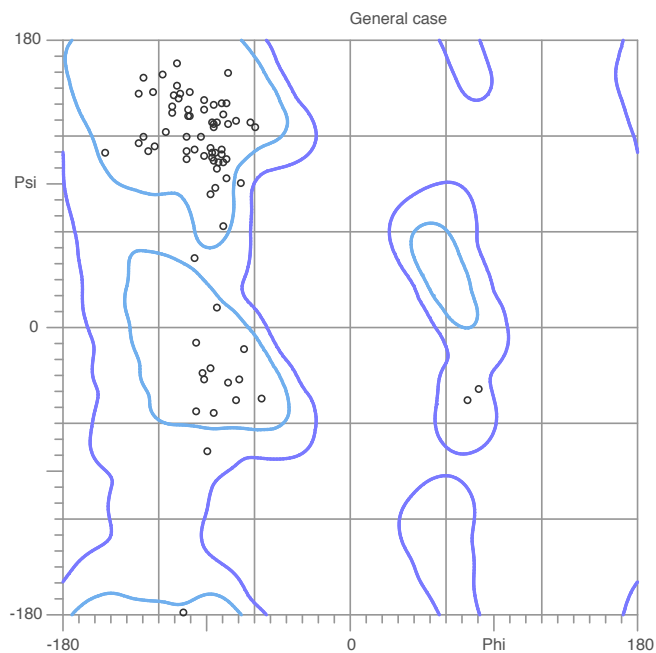


92.6% (87/94) of all residues were in favored (98%) regions.  
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[15] 31 PRO (-91.0, -161.2)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 16



93.6% (88/94) of all residues were in favored (98%) regions.  
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

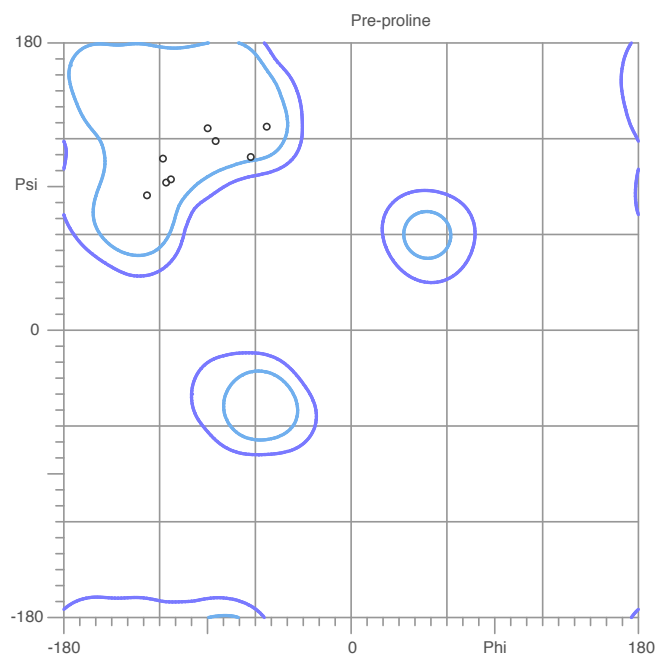
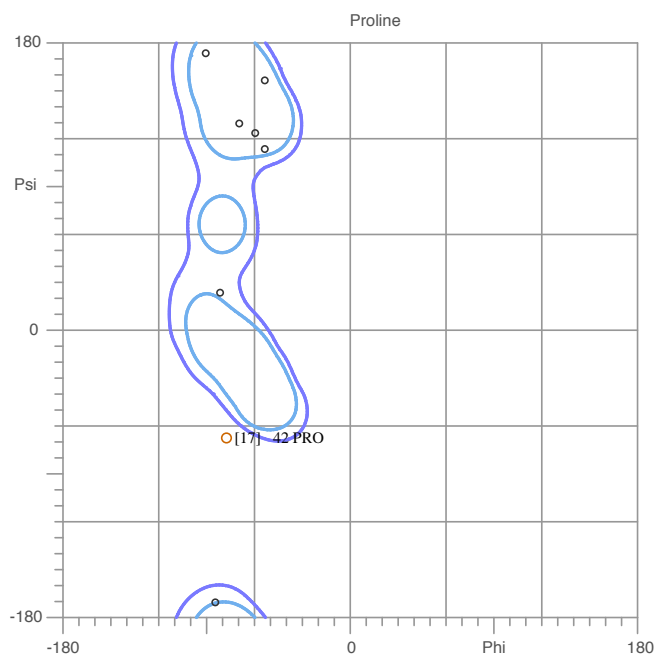
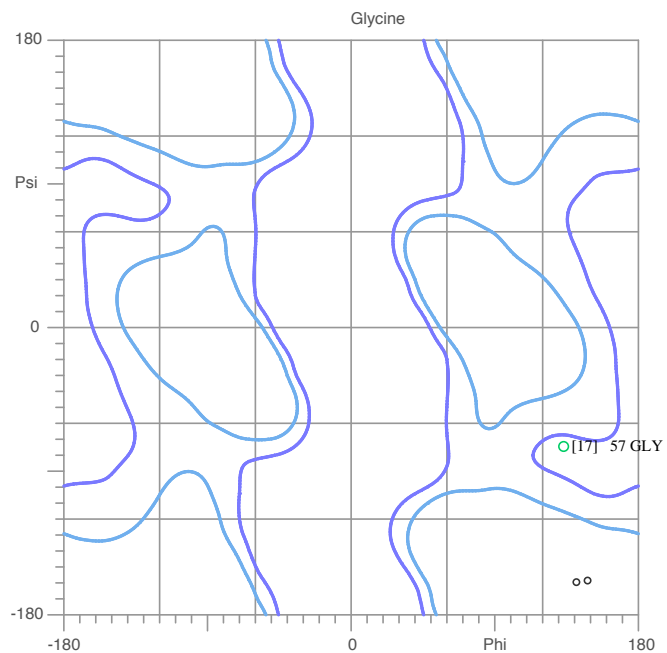
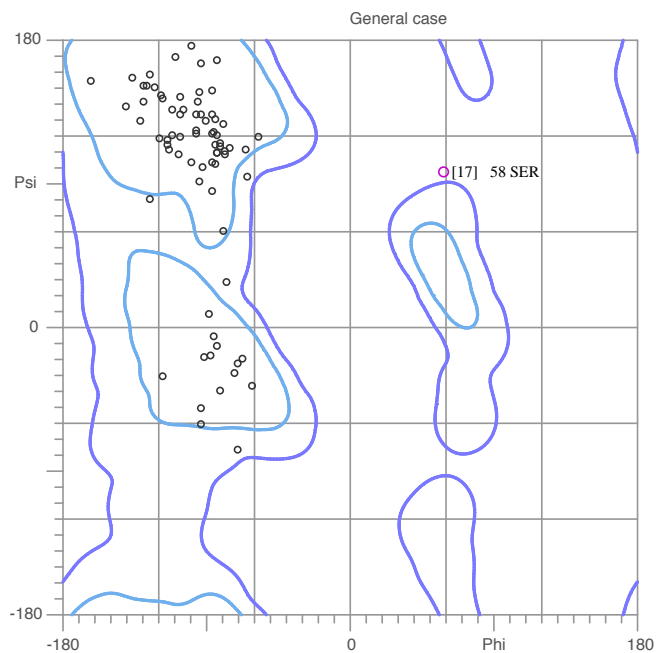
There were no outliers.

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# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 17



90.4% (85/94) of all residues were in favored (98%) regions.  
96.8% (91/94) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

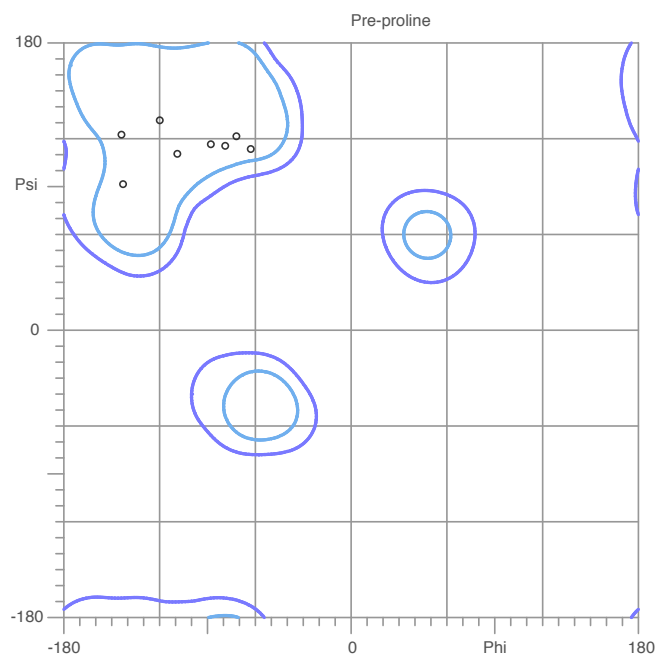
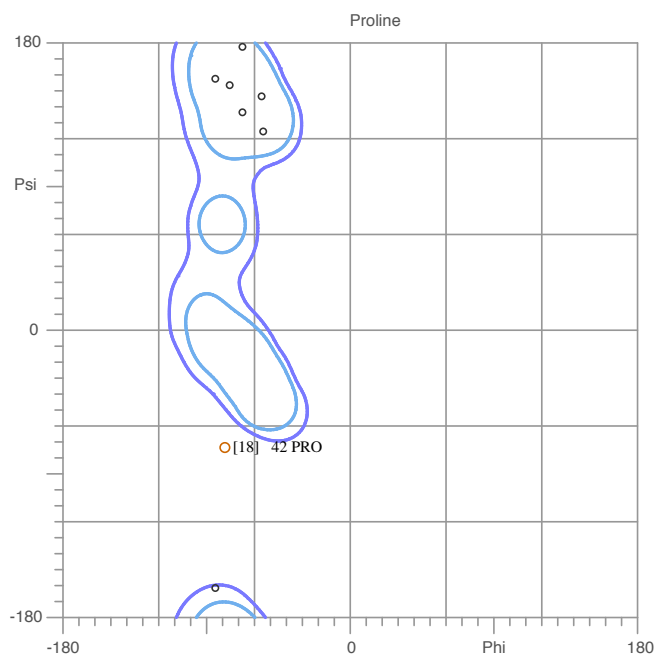
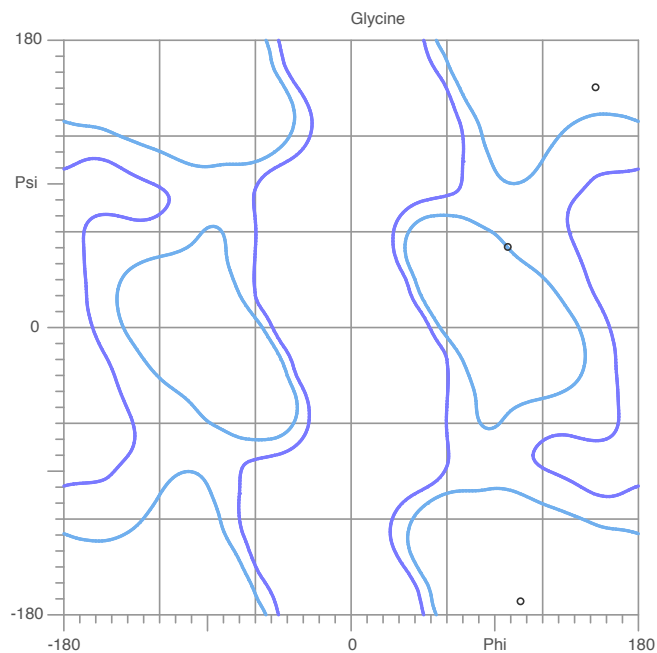
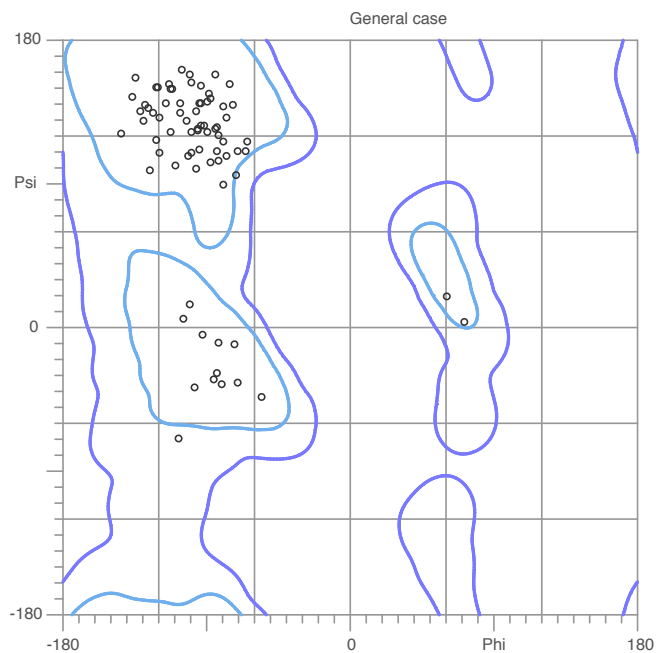
[17] 42 PRO (-78.6, -67.6)

[17] 57 GLY (133.8, -74.1)

[17] 58 SER (58.4, 98.4)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 18



95.7% (90/94) of all residues were in favored (98%) regions.  
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

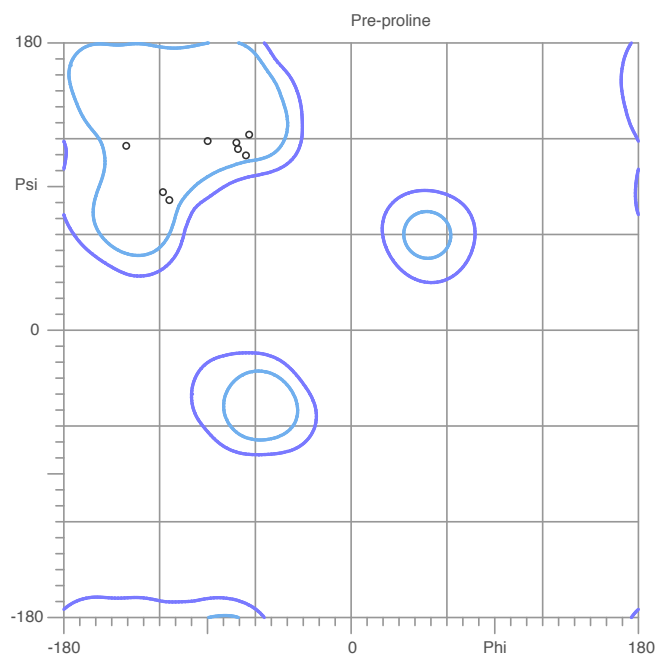
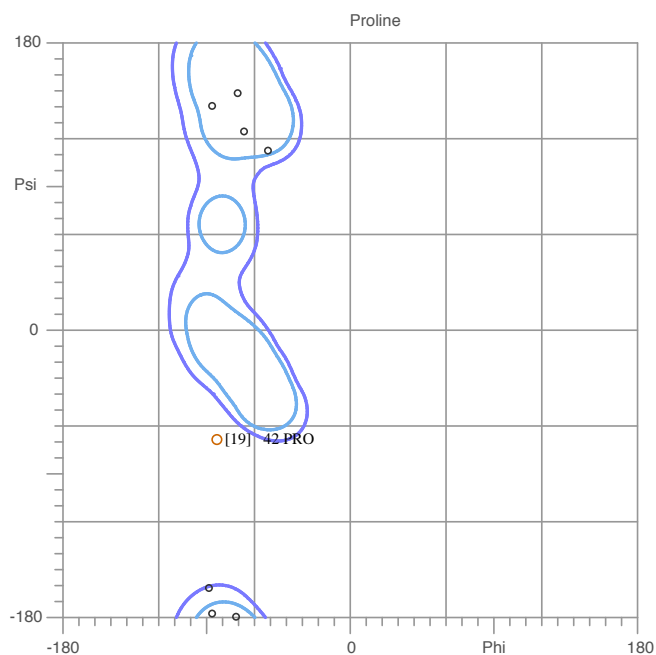
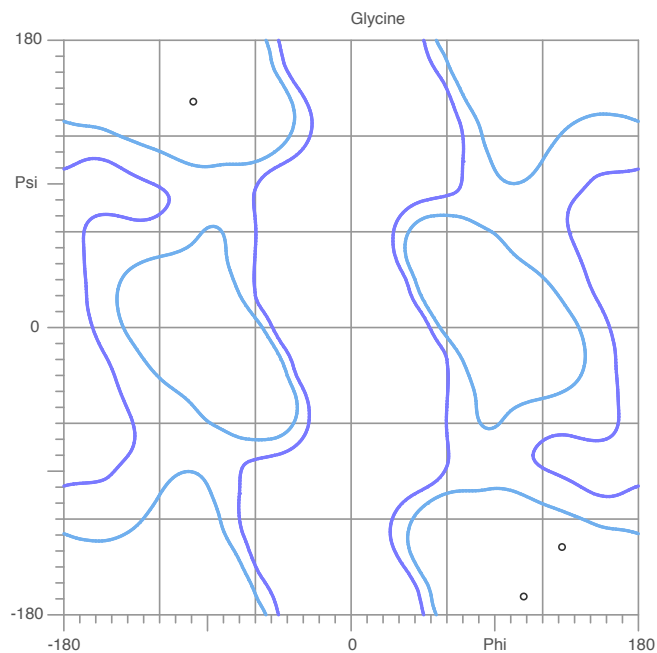
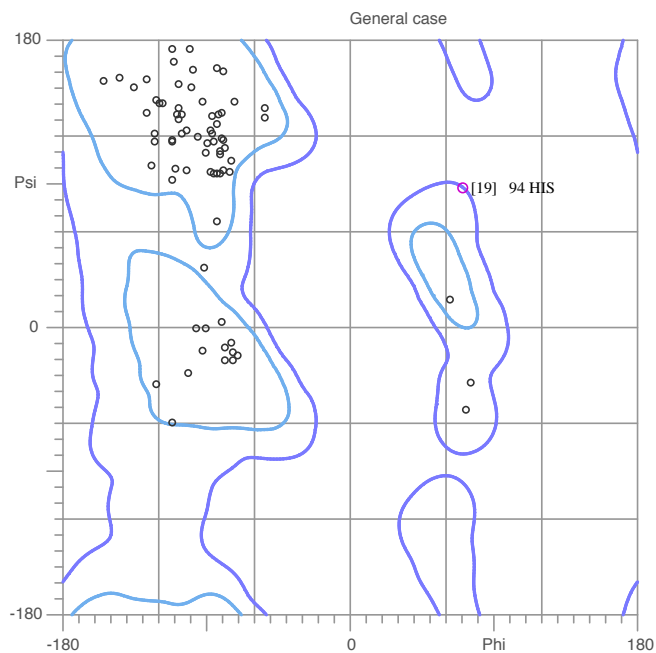
There were 1 outliers (phi, psi):  
[18] 42 PRO (-79.9, -73.6)

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# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 19

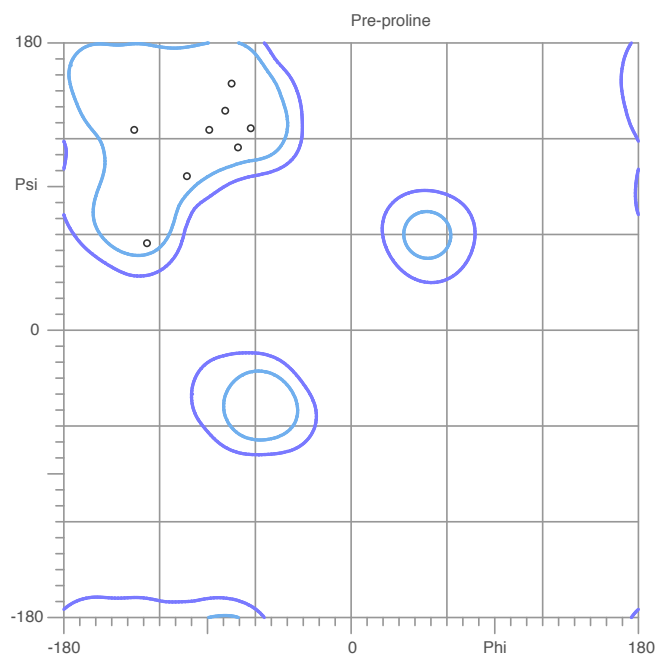
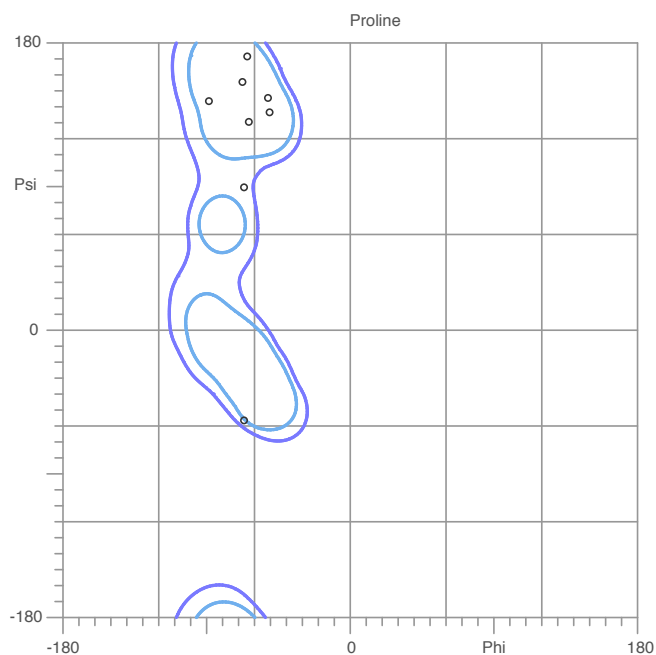
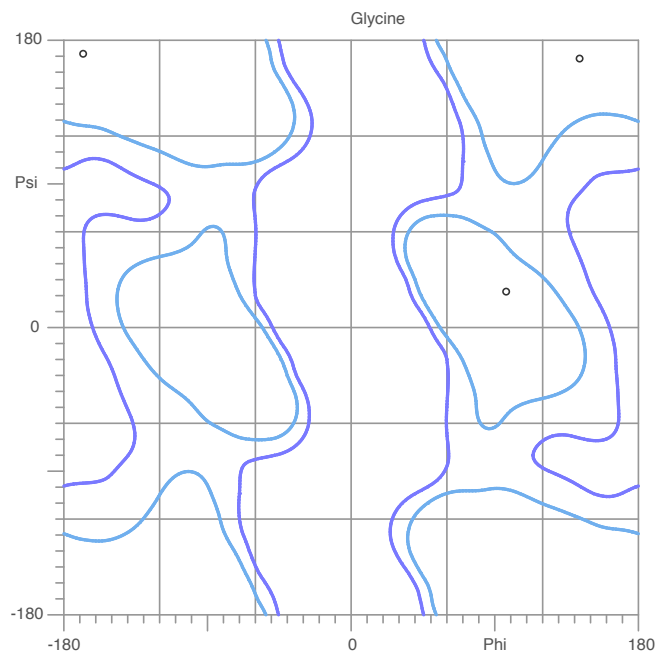
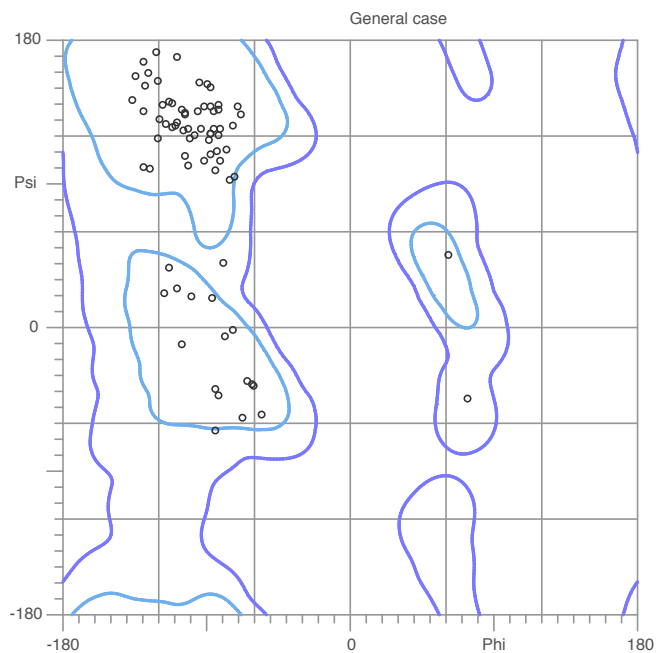


93.6% (88/94) of all residues were in favored (98%) regions.  
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[19] 42 PRO (-84.8, -68.5)  
[19] 94 HIS (70.6, 89.0)

# MolProbity Ramachandran analysis

DHR29B\_NMR\_em\_bcr3.pdb, model 20



94.7% (89/94) of all residues were in favored (98%) regions.  
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

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