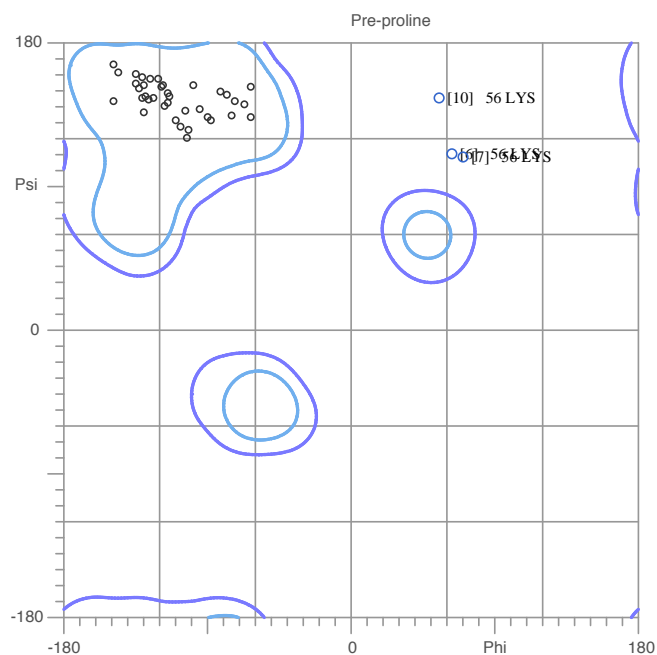
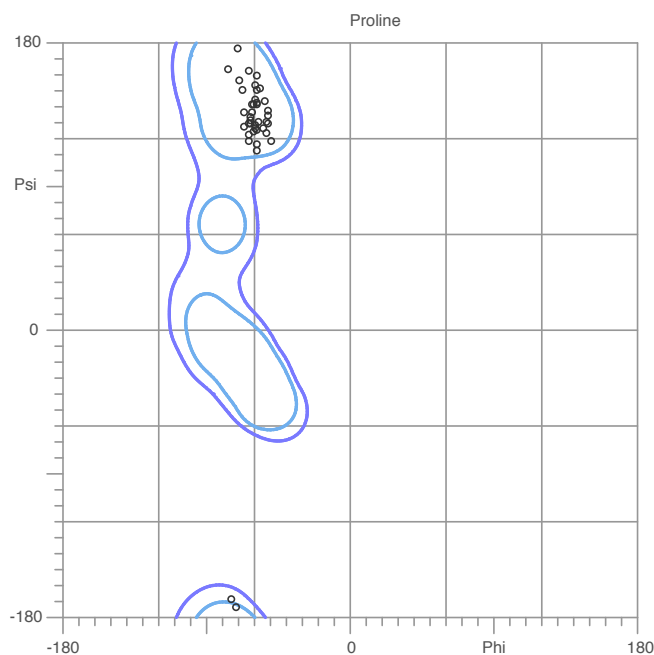
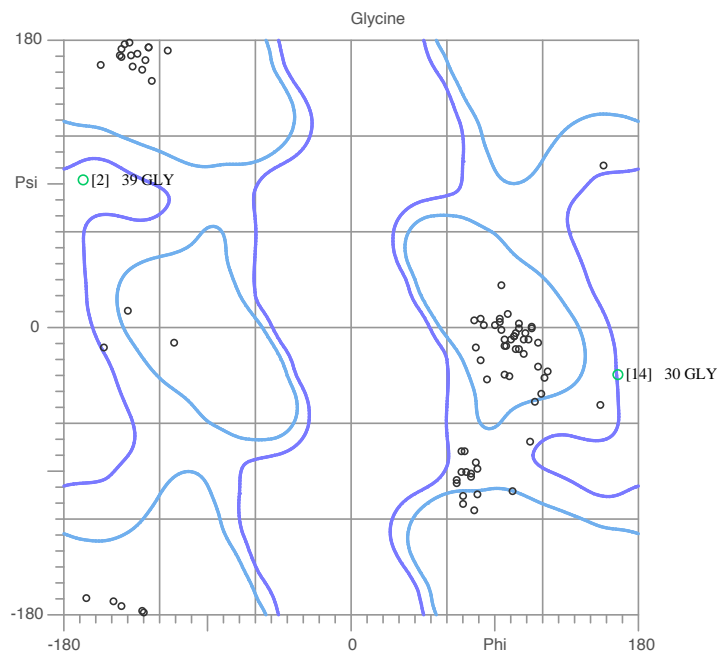
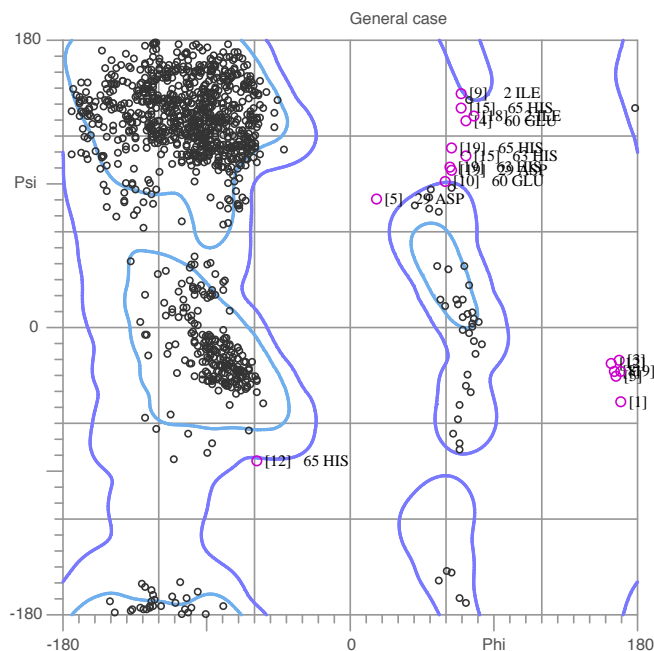


# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, all models



89.7% (1148/1280) of all residues were in favored (98%) regions.  
98.3% (1258/1280) of all residues were in allowed (>99.8%) regions.

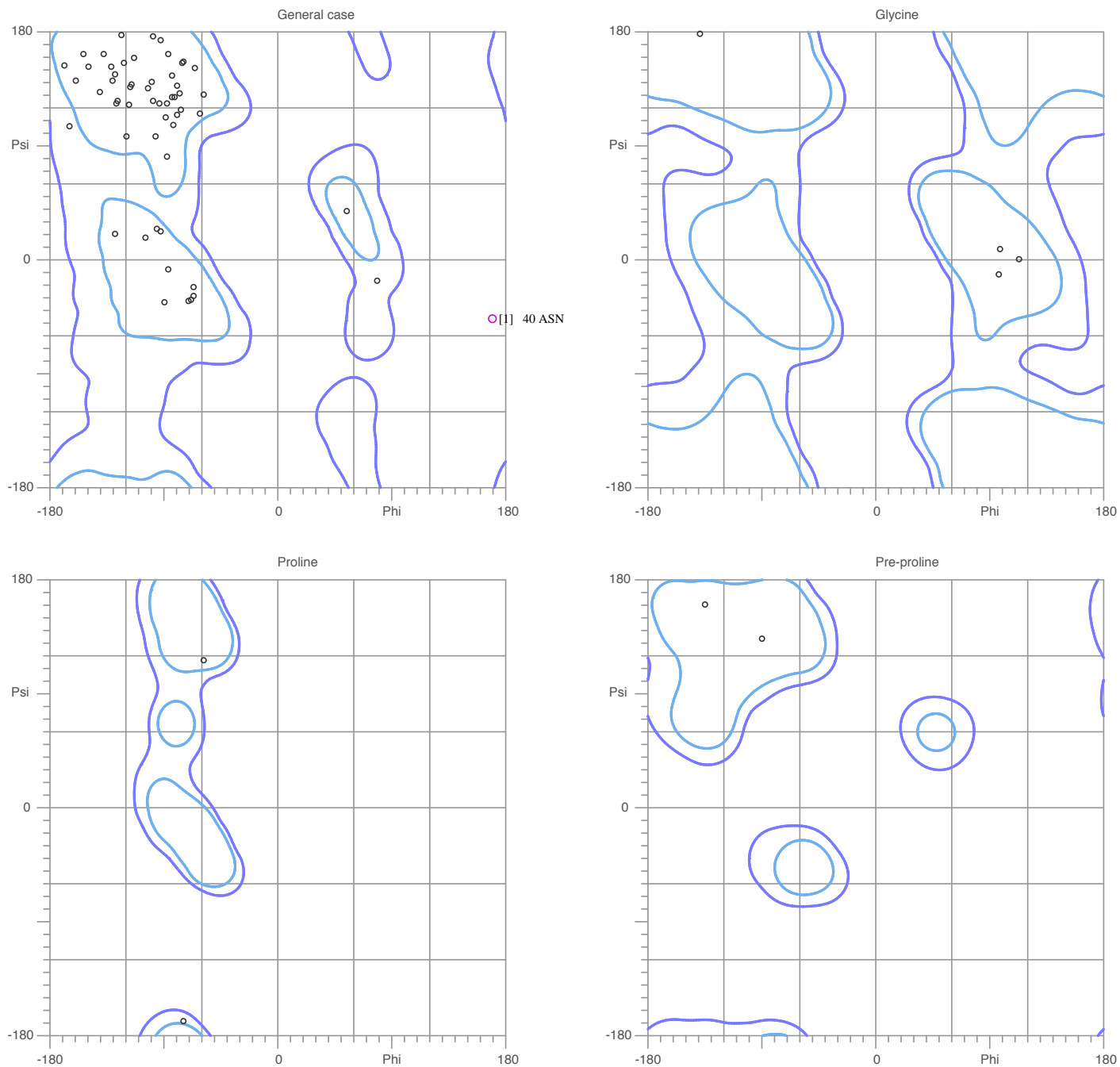
There were 22 outliers (phi, psi):

- [1] 40 ASN (169.3, -46.4)
- [2] 39 GLY (-168.7, 93.5)
- [3] 19 ARG (168.9, -20.4)
- [4] 60 GLU (72.0, 130.9)
- [5] 19 ARG (166.7, -30.8)
- [5] 29 ASP (16.2, 81.9)
- [6] 56 LYS (63.3, 111.4)
- [7] 56 LYS (70.3, 109.3)
- [8] 19 ARG (165.2, -27.8)

- [9] 2 ILE (69.9, 147.4)
- [10] 56 LYS (55.7, 146.9)
- [10] 60 GLU (59.0, 92.9)
- [12] 19 ARG (163.6, -22.4)
- [12] 65 HIS (-59.6, -83.4)
- [14] 30 GLY (168.0, -29.6)
- [15] 63 HIS (72.4, 108.2)
- [15] 65 HIS (69.6, 138.5)
- [18] 2 ILE (77.1, 133.3)
- [19] 19 ARG (169.9, -27.1)
- [19] 29 ASP (63.0, 99.8)
- [19] 63 HIS (62.9, 101.7)
- [19] 65 HIS (63.9, 113.5)

# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 1



93.8% (60/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

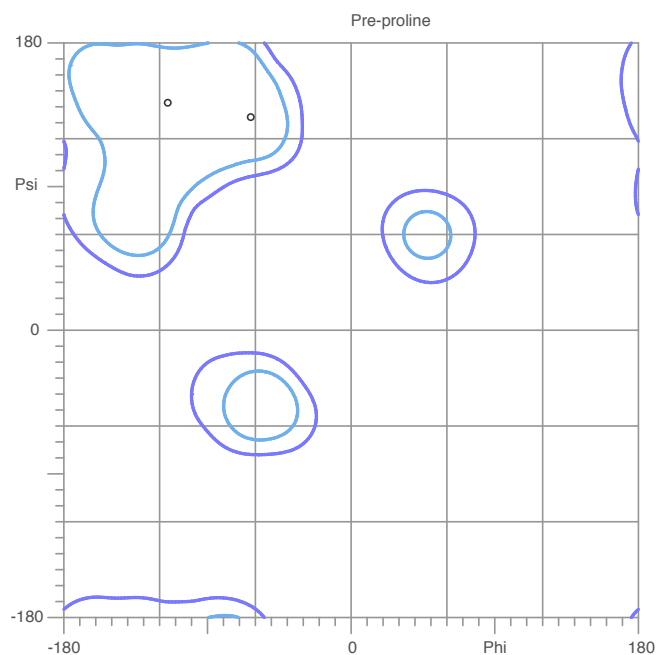
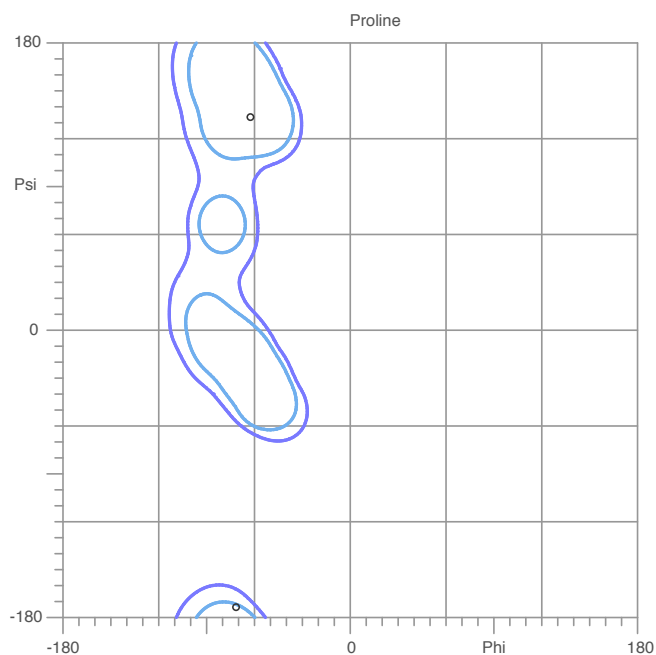
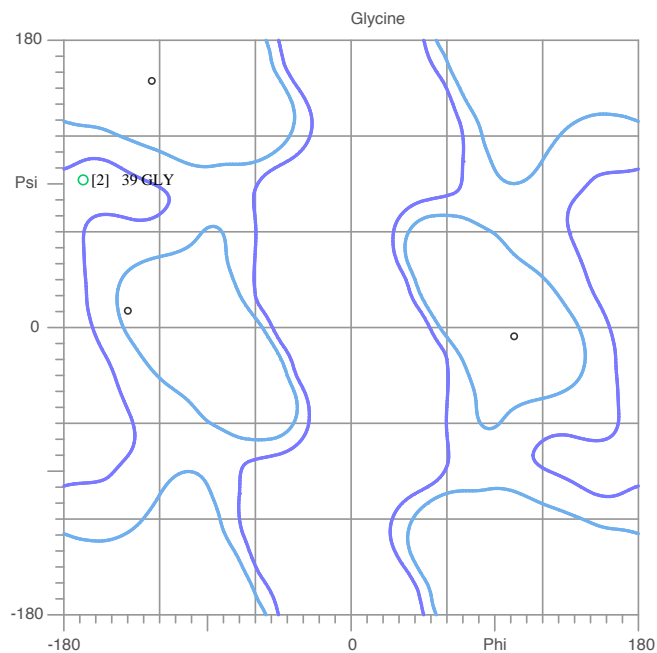
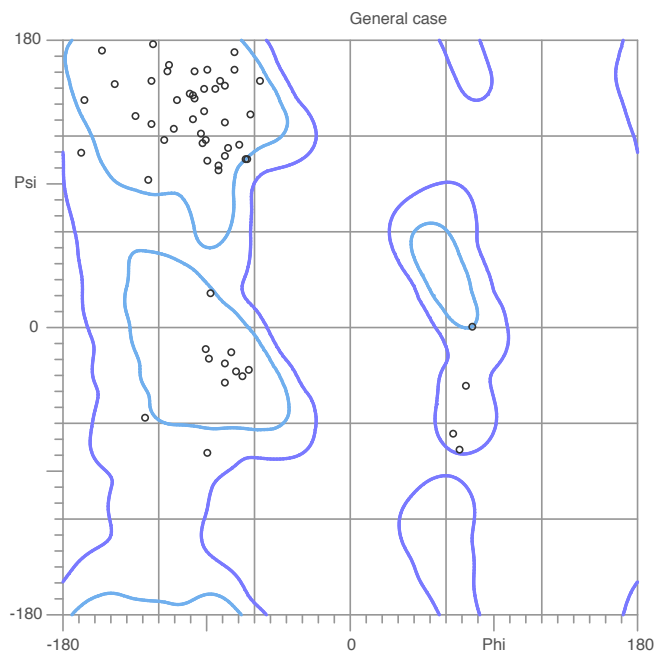
There were 1 outliers (phi, psi):  
[1] 40 ASN (169.3, -46.4)

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 2



89.1% (57/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

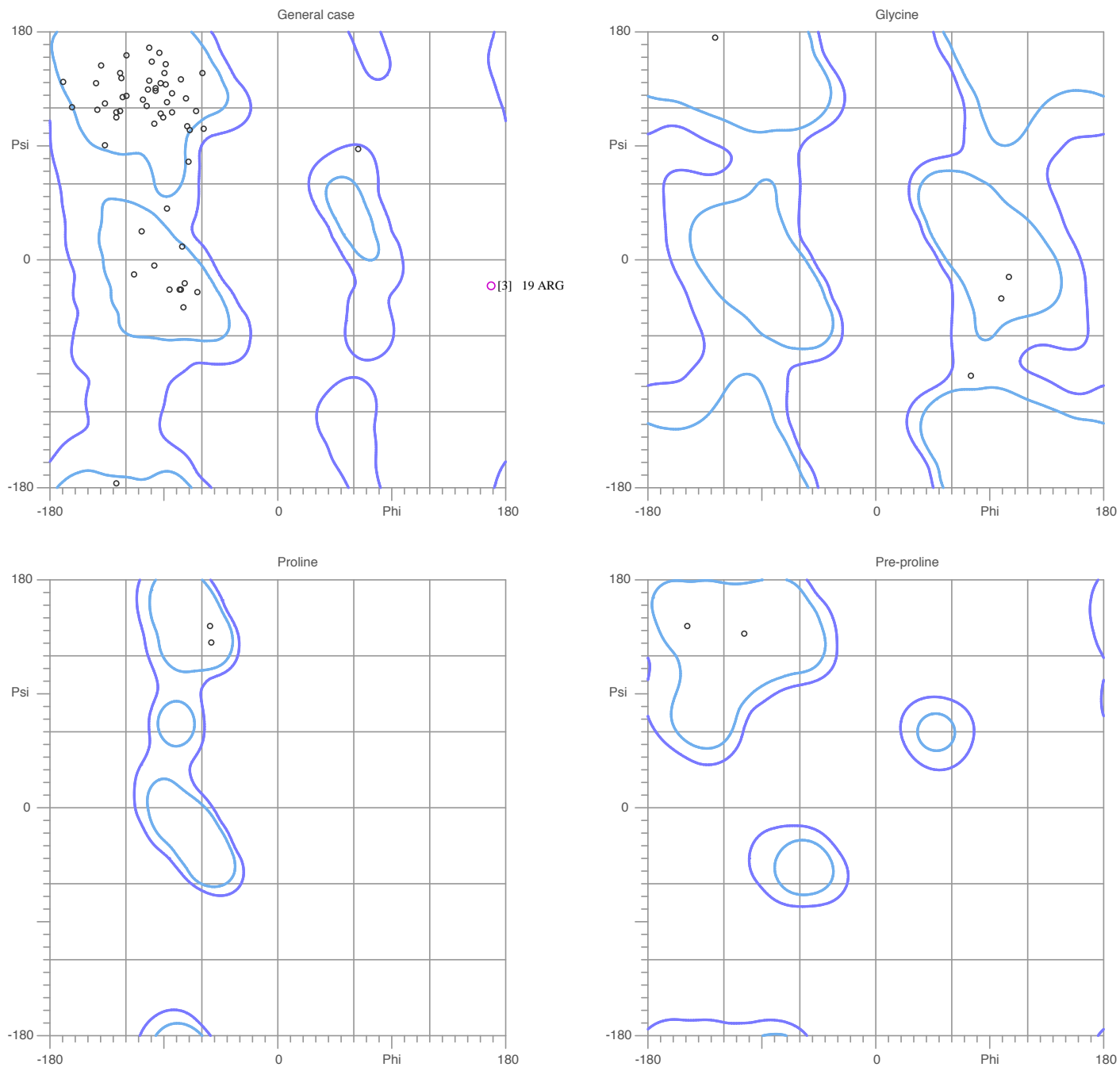
There were 1 outliers (phi, psi):  
[2] 39 GLY (-168.7, 93.5)

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

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 3



89.1% (57/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

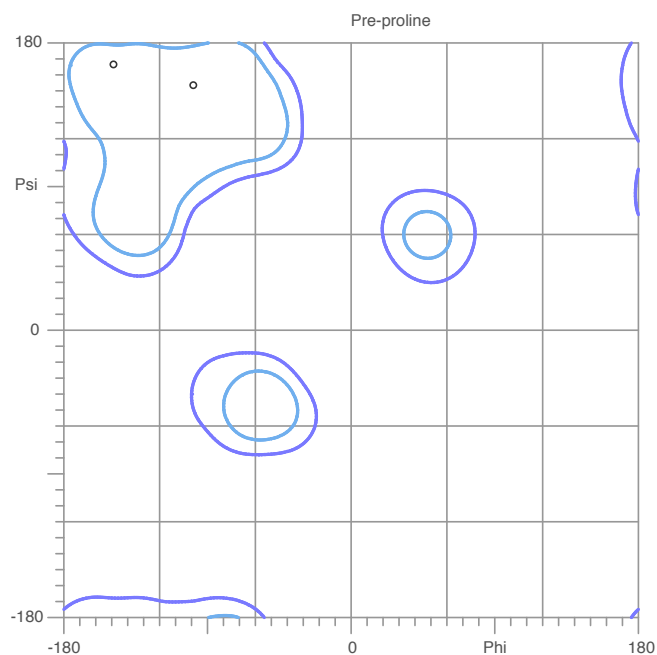
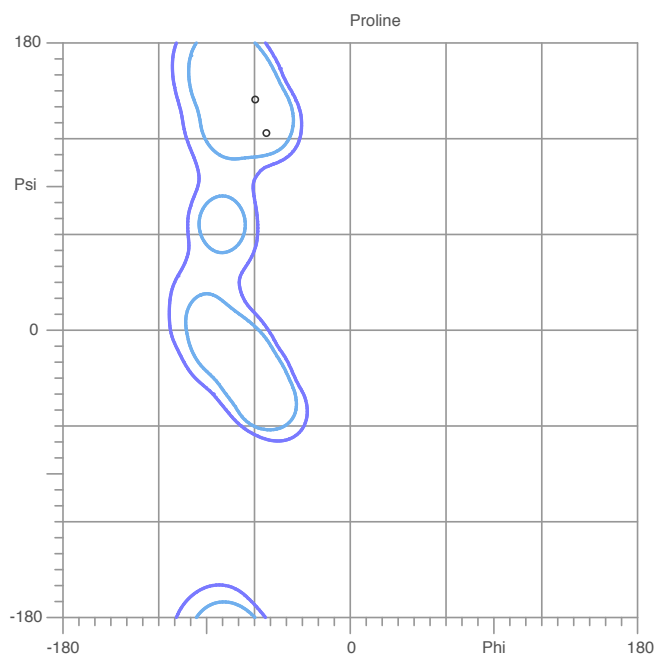
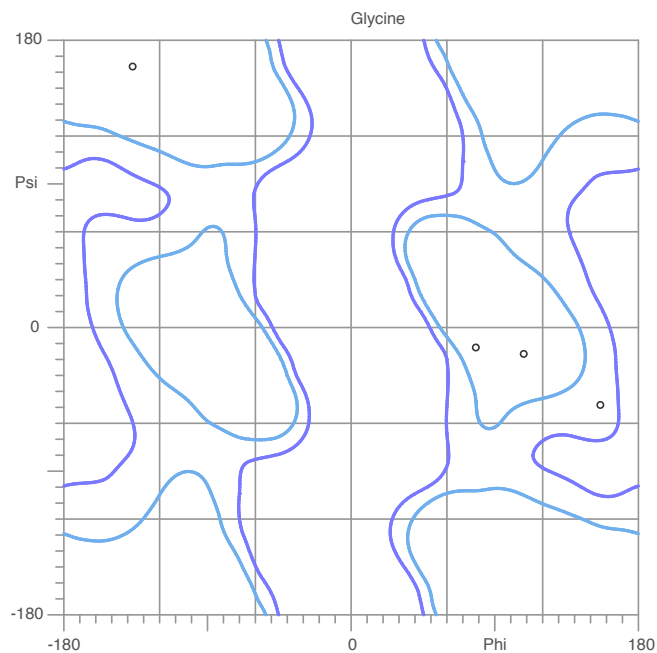
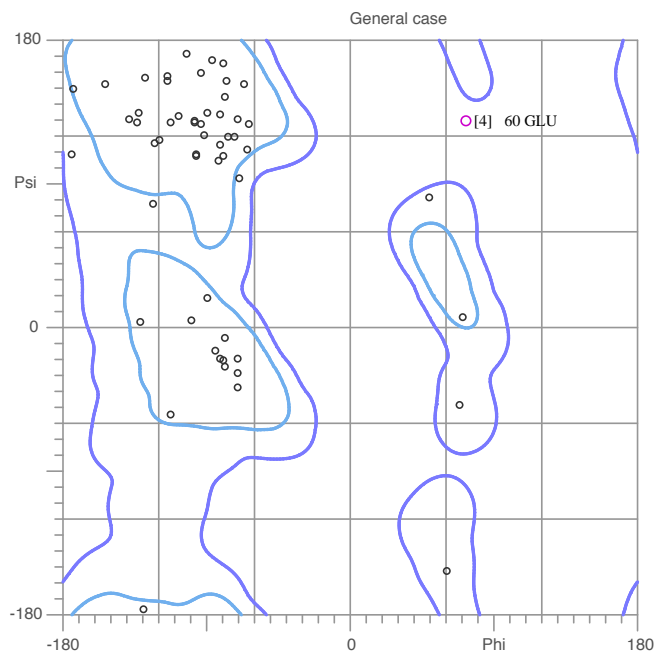
There were 1 outliers (phi, psi):  
[3] 19 ARG (168.9, -20.4)

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 4



87.5% (56/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

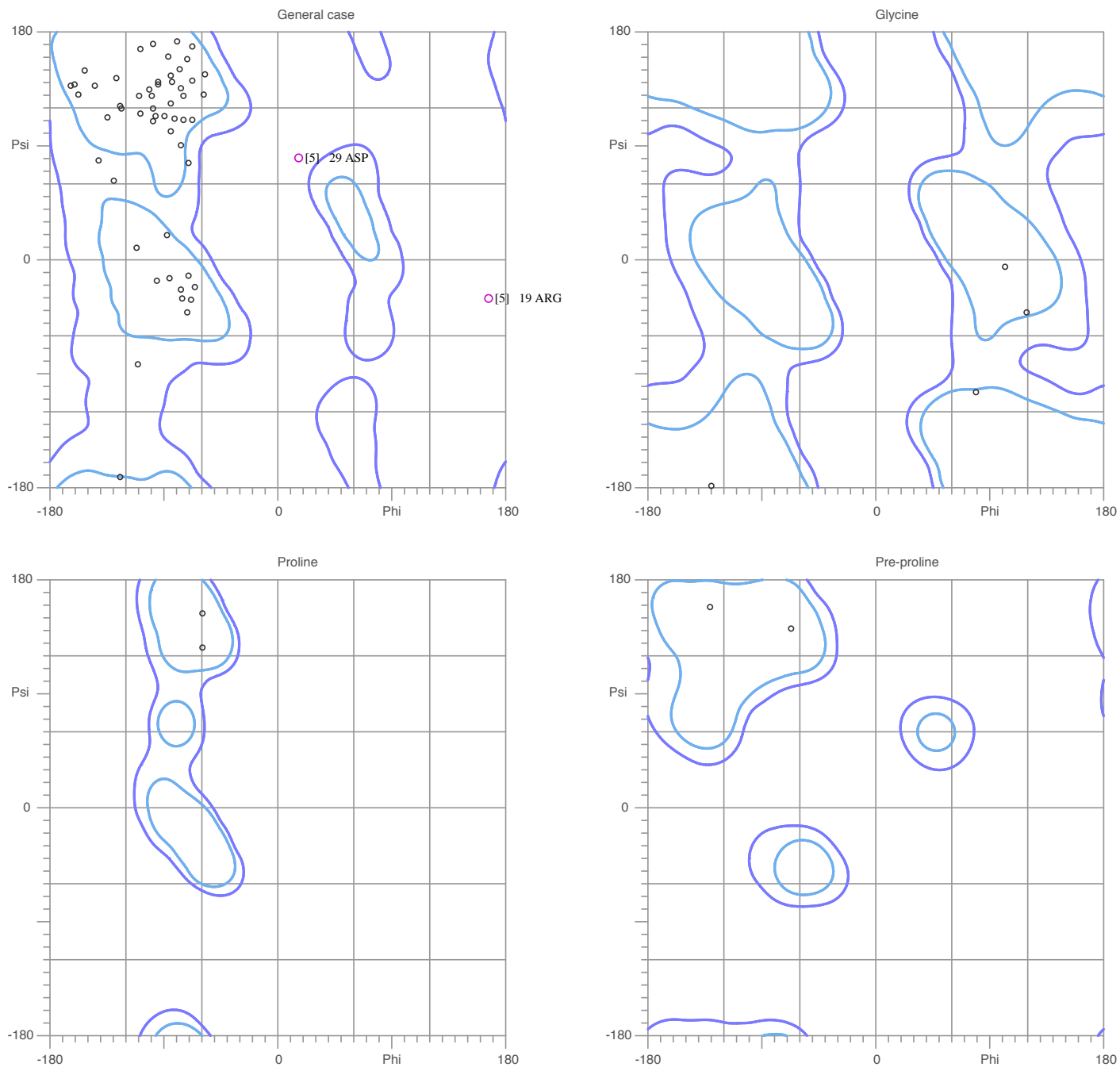
There were 1 outliers (phi, psi):  
[4] 60 GLU (72.0, 130.9)

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 5



89.1% (57/64) of all residues were in favored (98%) regions.  
96.9% (62/64) of all residues were in allowed (>99.8%) regions.

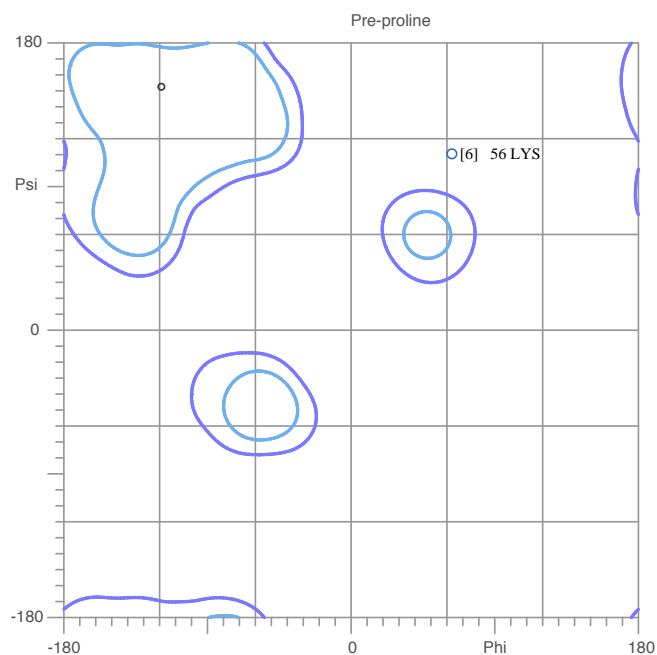
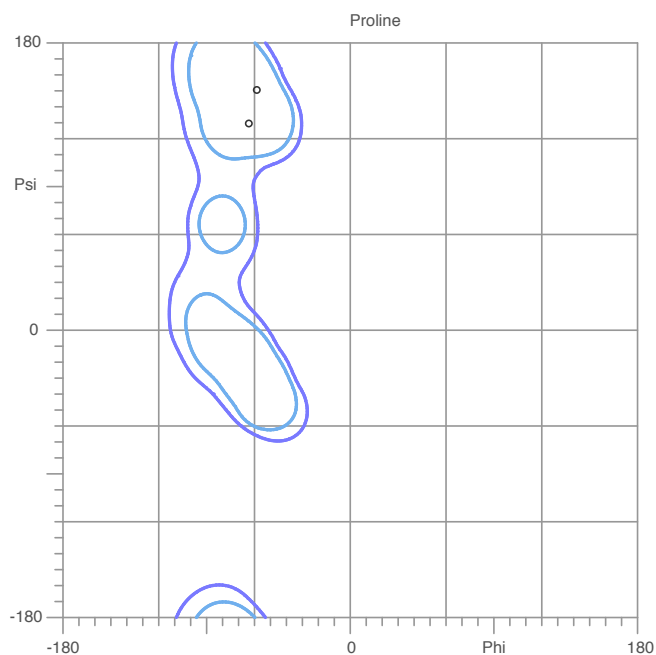
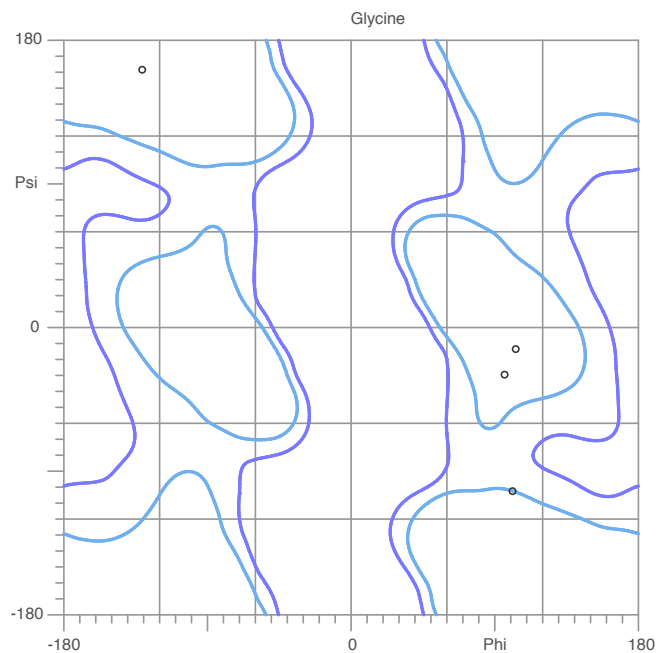
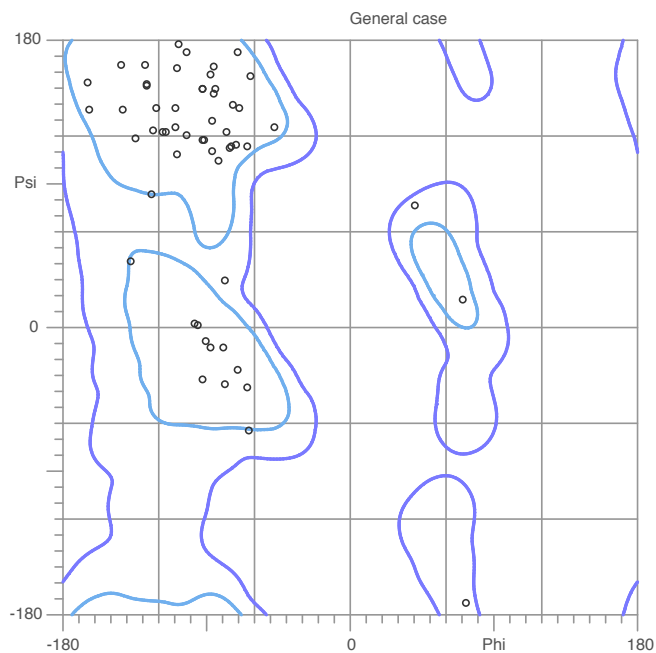
There were 2 outliers (phi, psi):

[5] 19 ARG (166.7, -30.8)

[5] 29 ASP (16.2, 81.9)

# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 6



90.6% (58/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

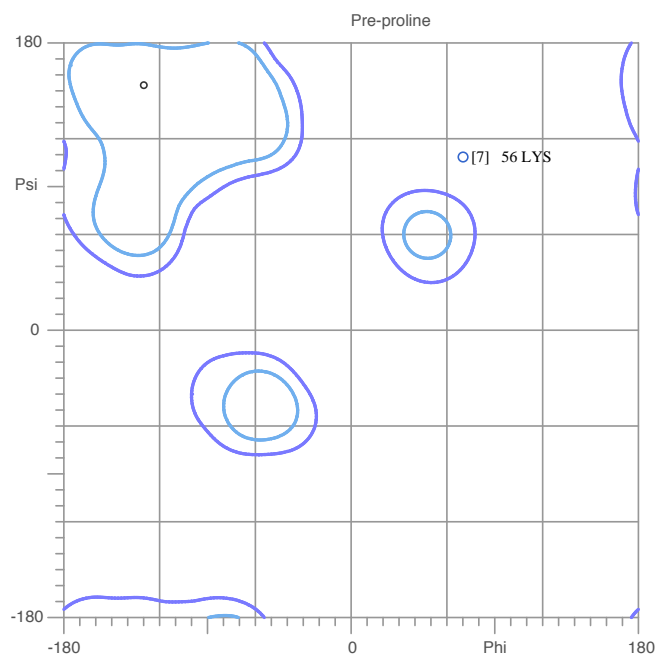
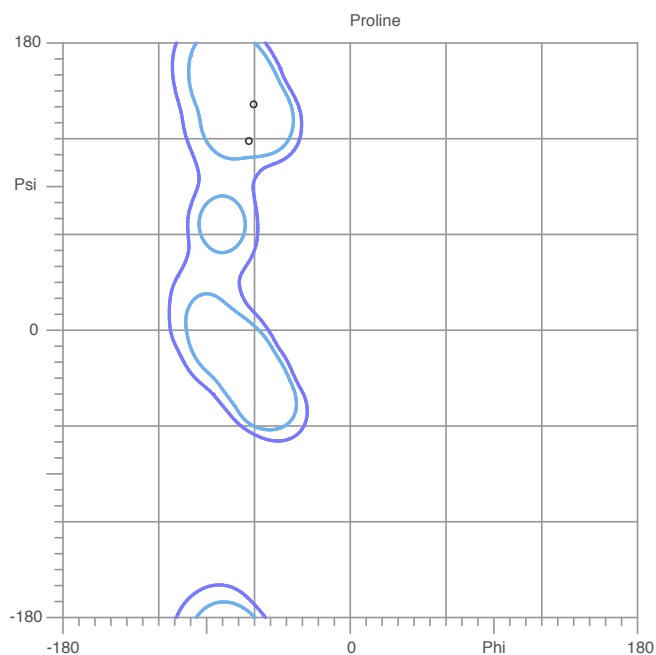
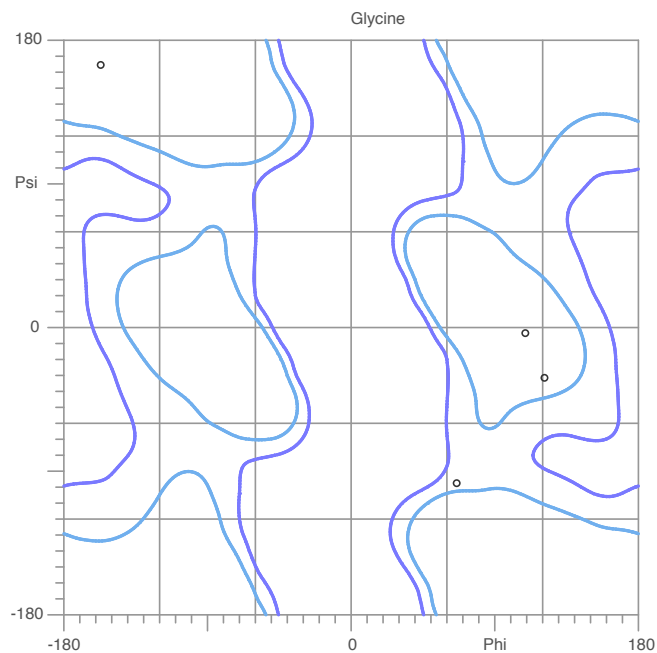
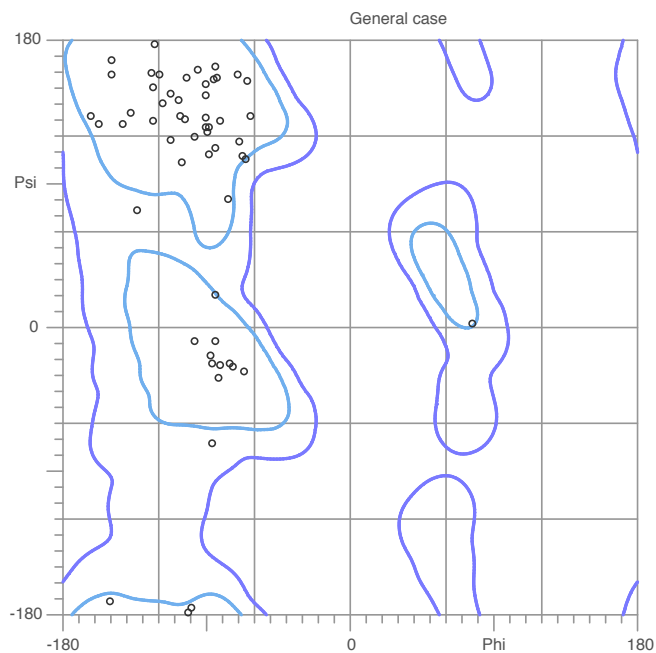
There were 1 outliers (phi, psi):  
[6] 56 LYS (63.3, 111.4)

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 7



93.8% (60/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

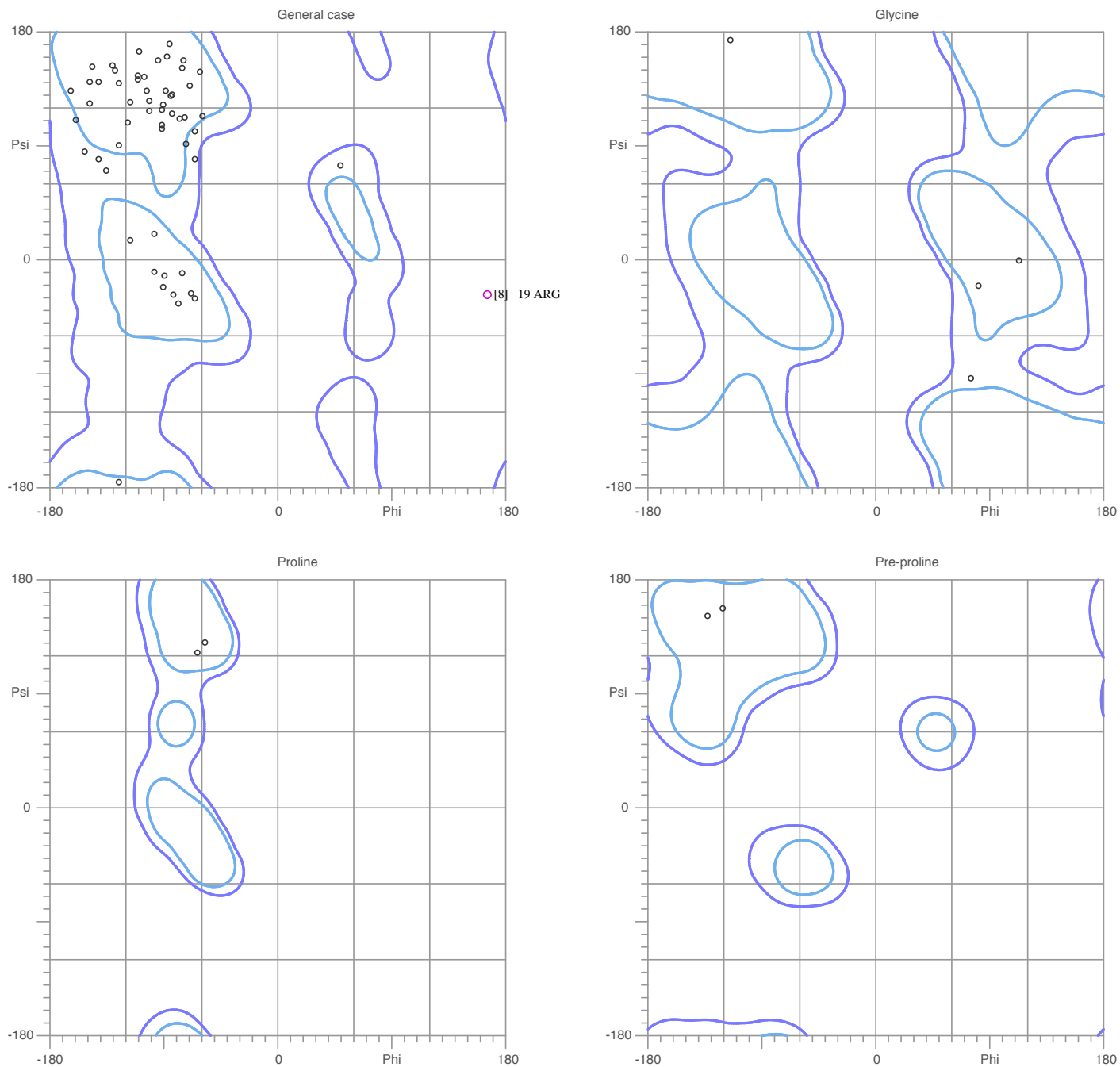
There were 1 outliers (phi, psi):  
[7] 56 LYS (70.3, 109.3)

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 8



85.9% (55/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

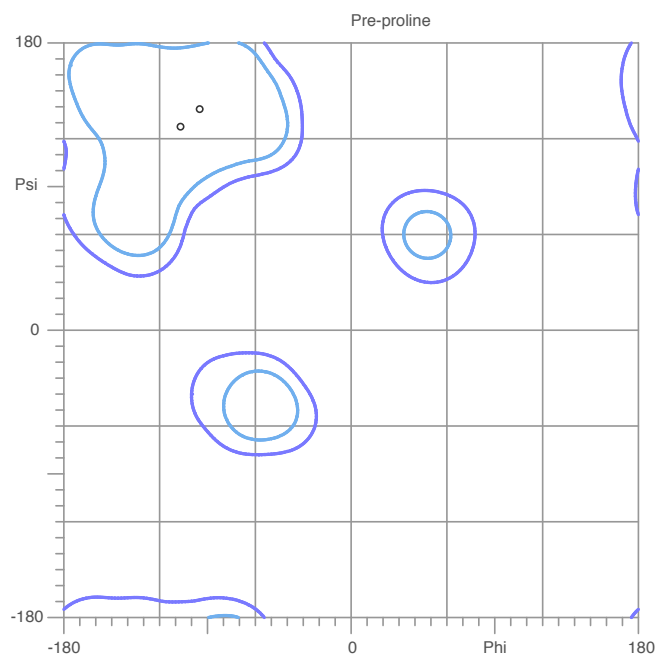
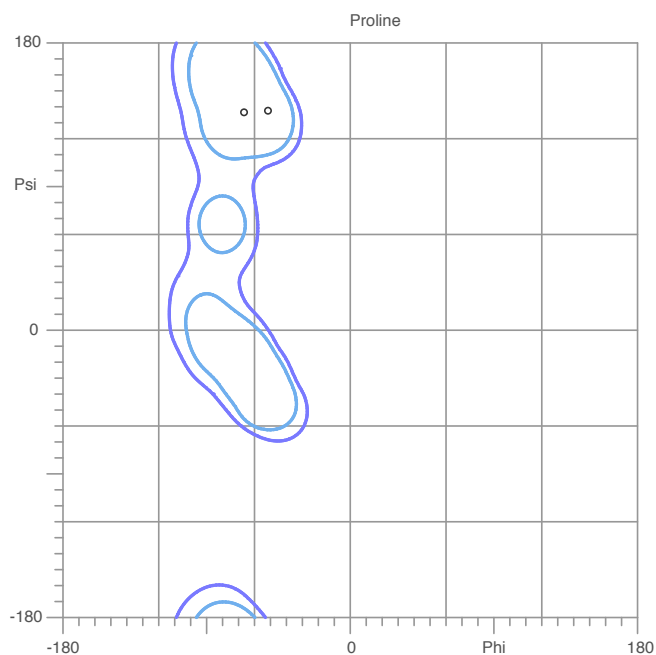
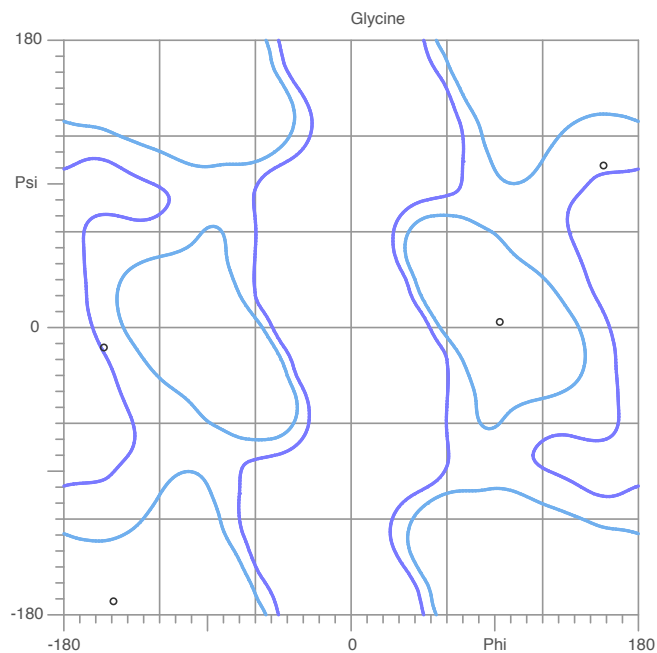
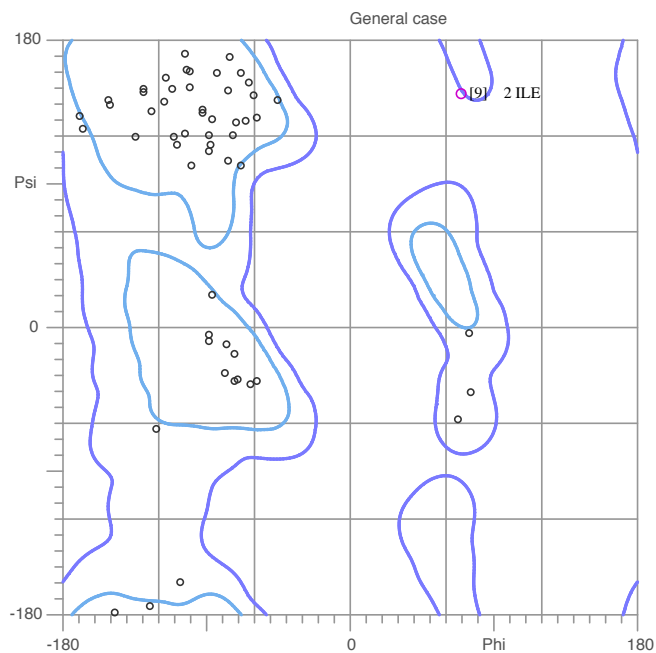
There were 1 outliers (phi, psi):  
[8] 19 ARG (165.2, -27.8)

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 9

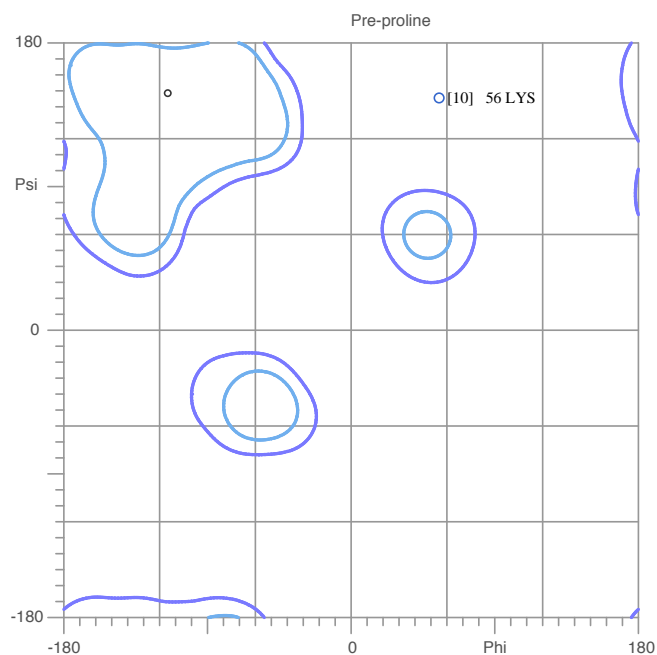
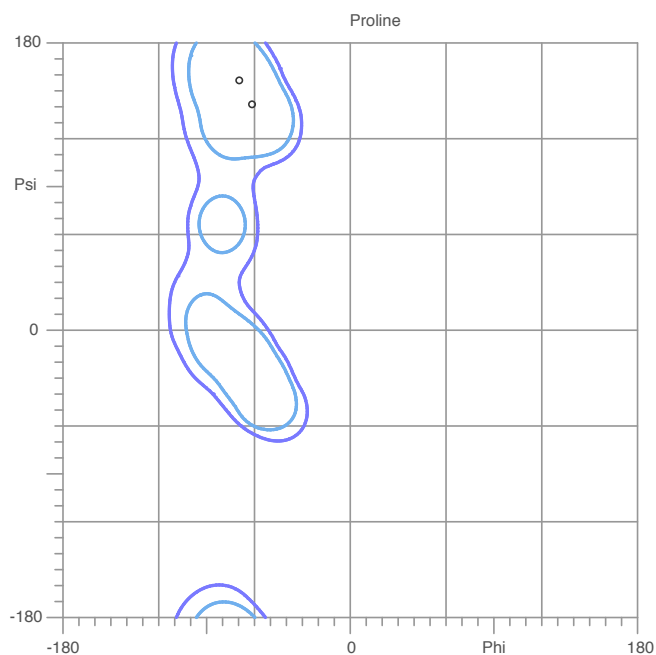
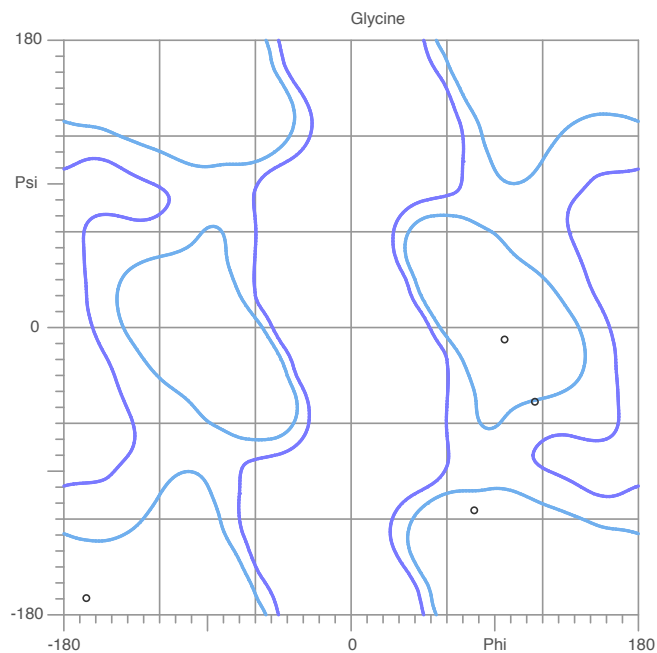
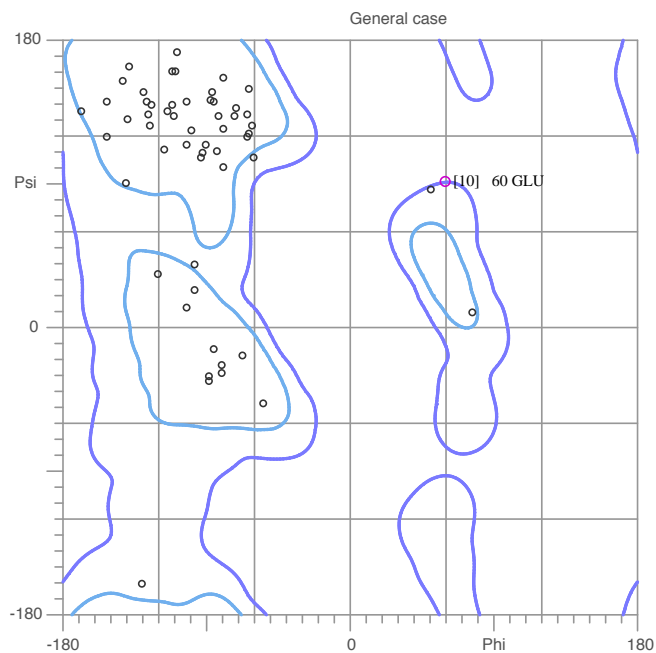


84.4% (54/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[9] 2 ILE (69.9, 147.4)

# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 10

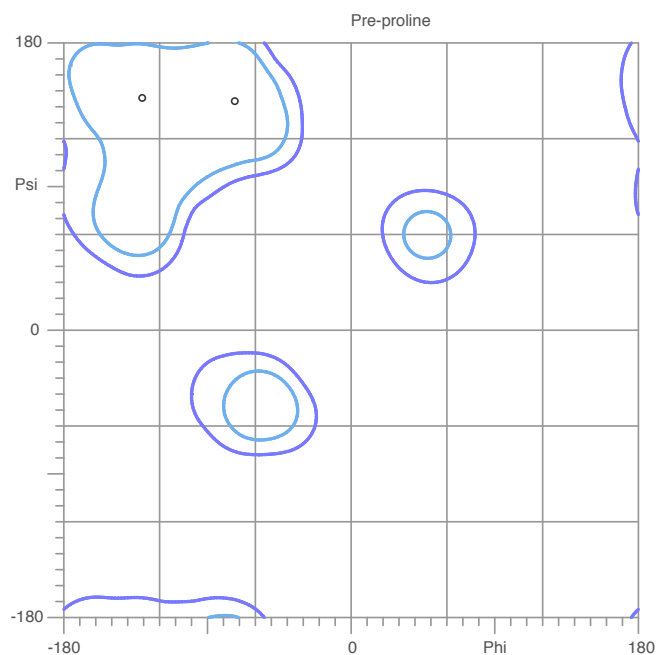
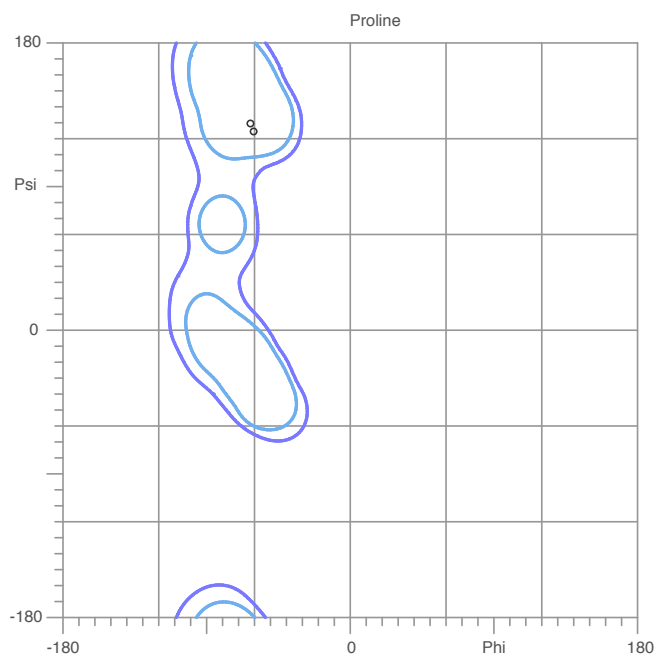
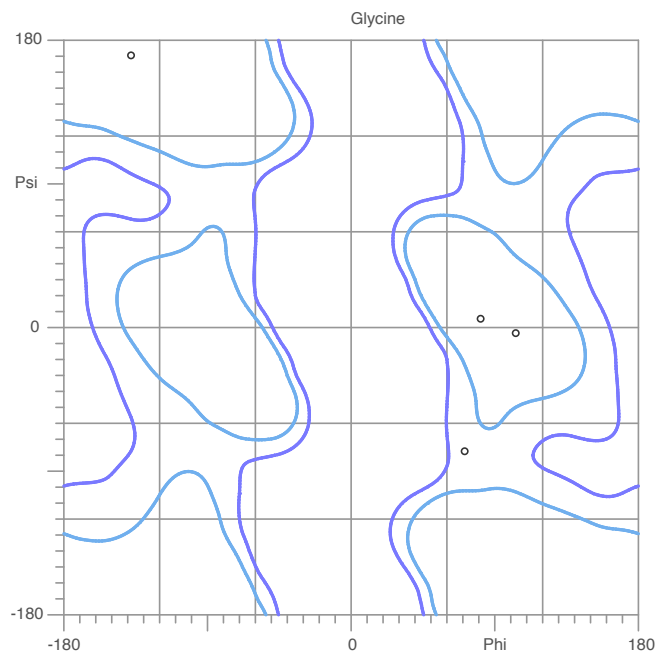
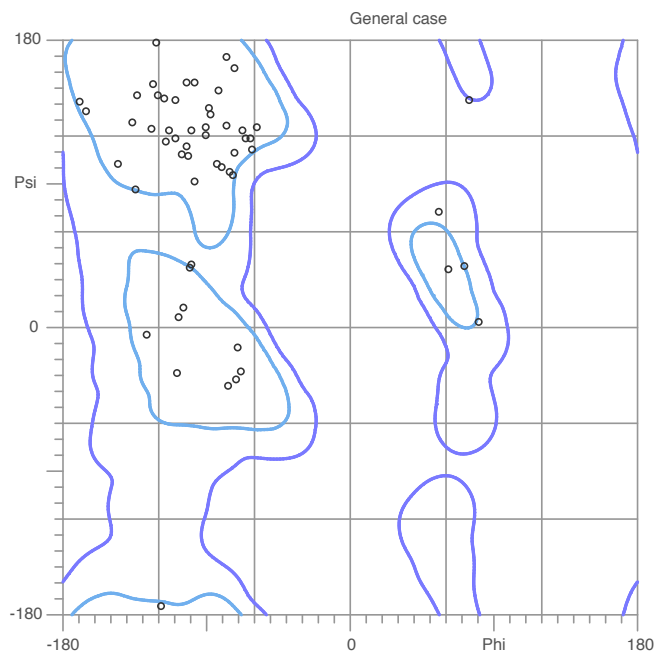


89.1% (57/64) of all residues were in favored (98%) regions.  
96.9% (62/64) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[10] 56 LYS (55.7, 146.9)  
[10] 60 GLU (59.0, 92.9)

# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 11



90.6% (58/64) of all residues were in favored (98%) regions.  
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

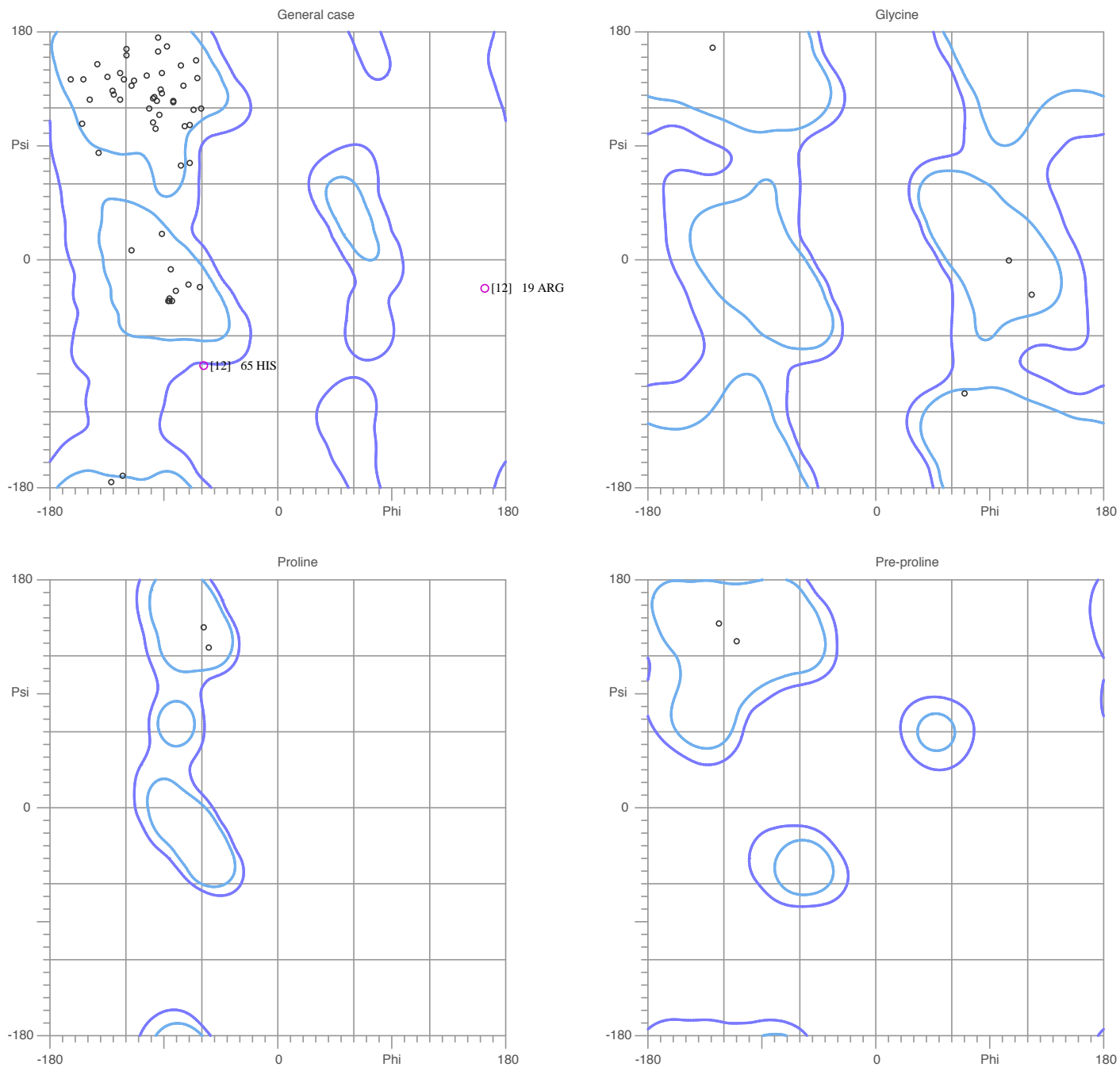
There were no outliers.

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 12

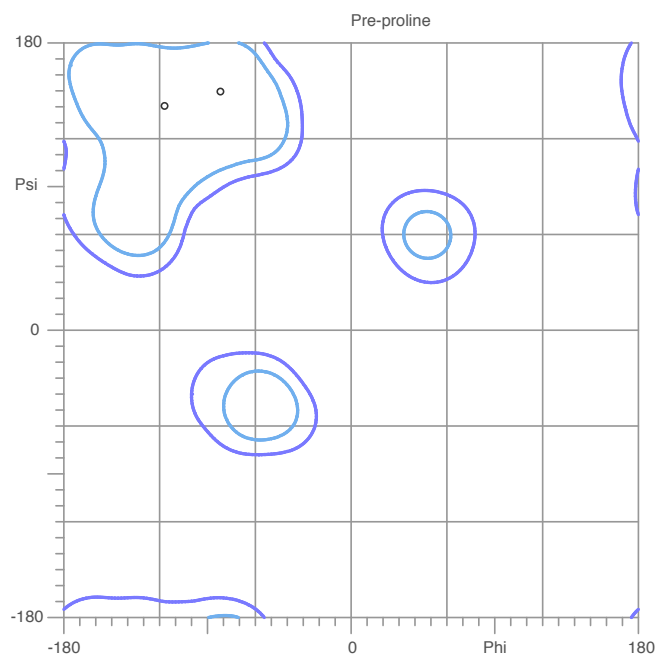
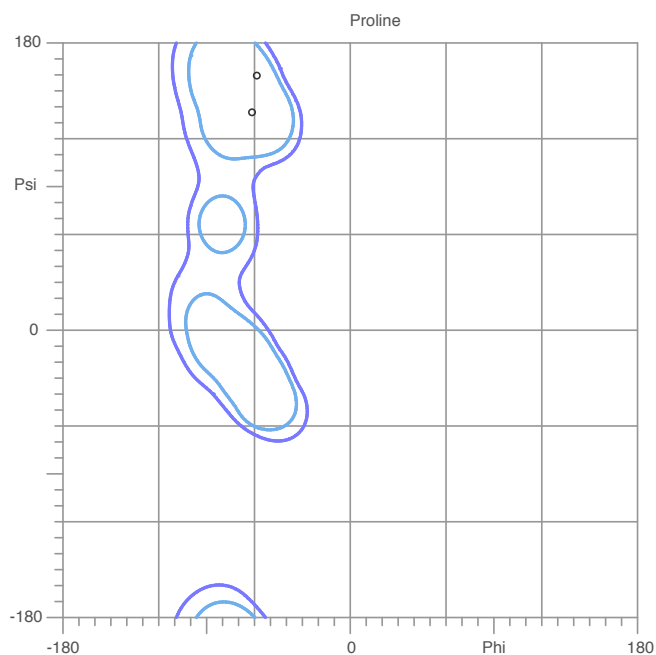
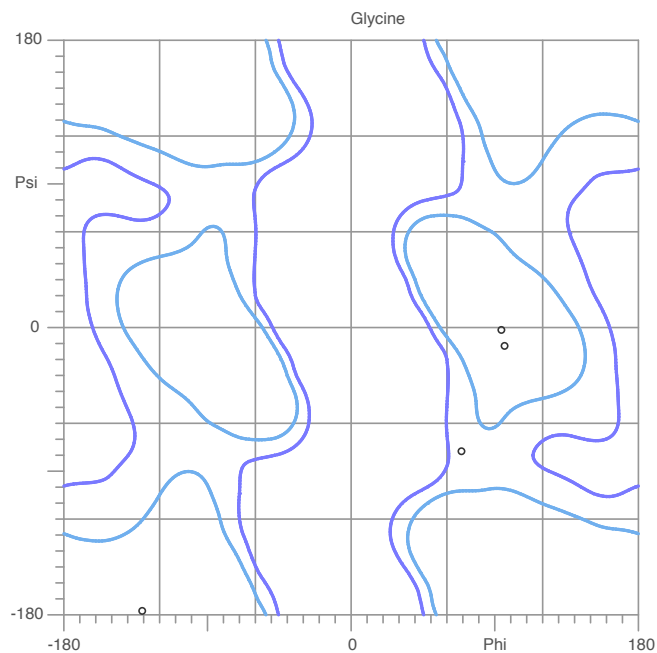
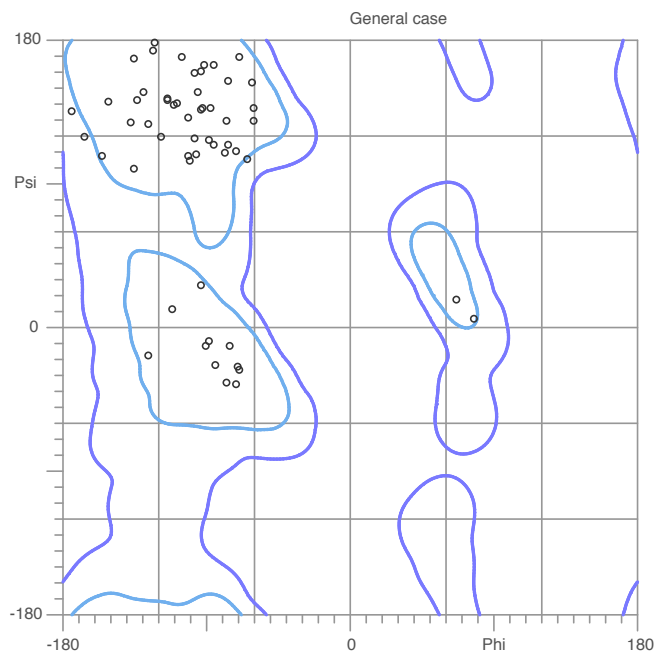


92.2% (59/64) of all residues were in favored (98%) regions.  
96.9% (62/64) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[12] 19 ARG (163.6, -22.4)  
[12] 65 HIS (-59.6, -83.4)

# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 13



95.3% (61/64) of all residues were in favored (98%) regions.  
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

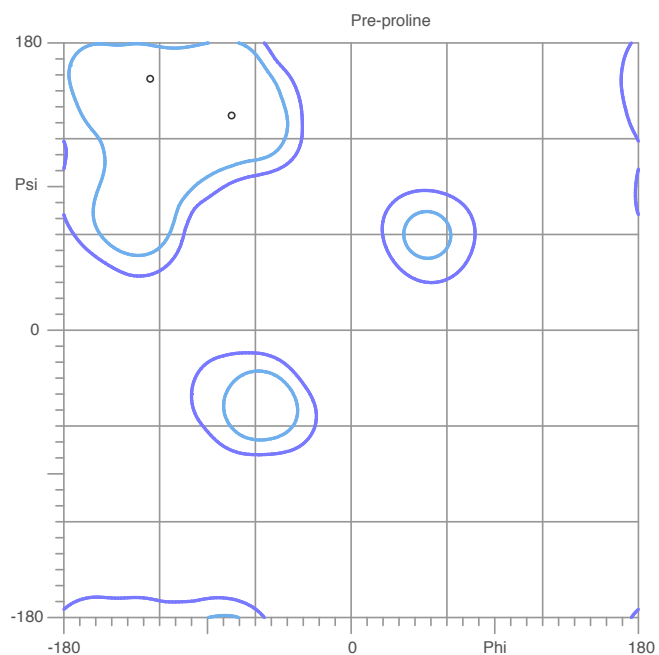
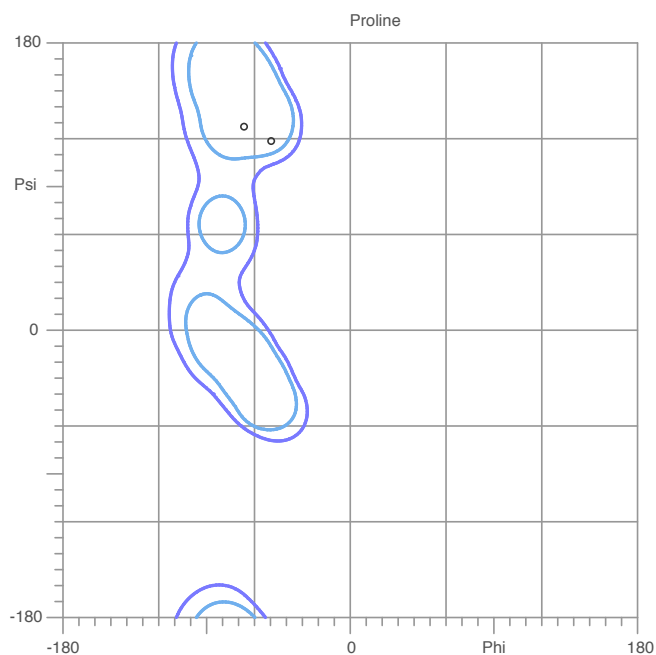
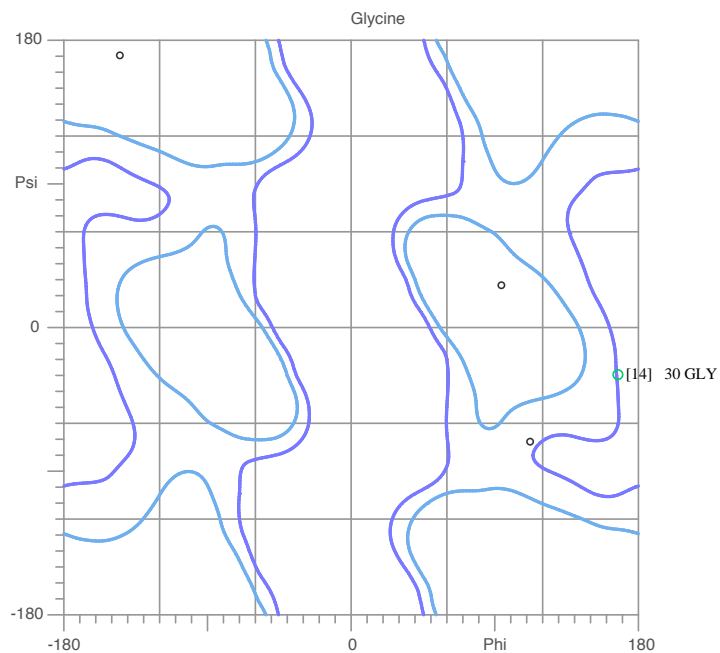
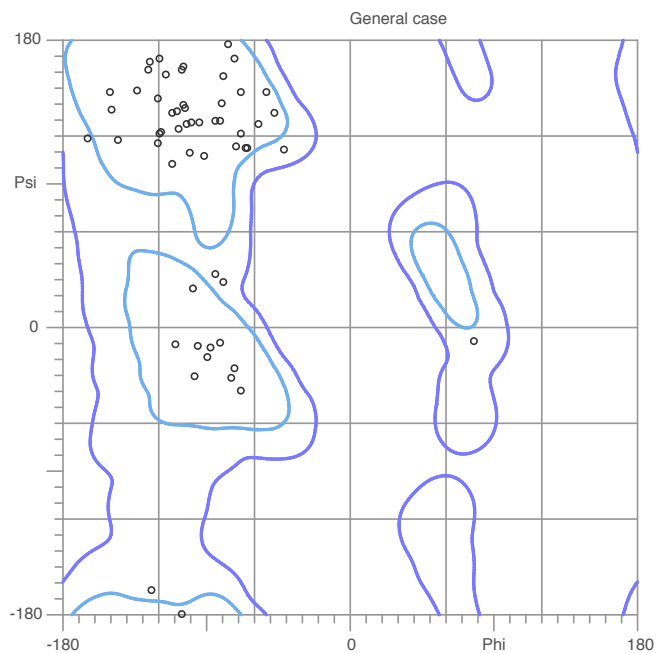
There were no outliers.

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 14



87.5% (56/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

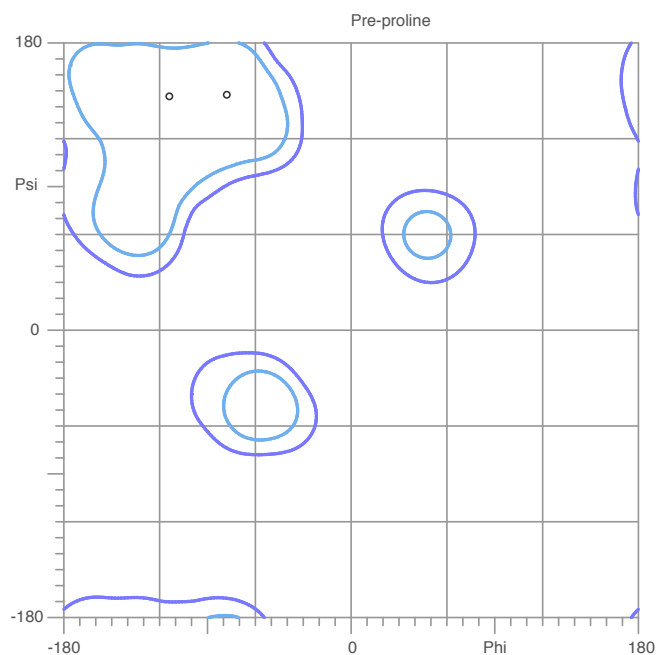
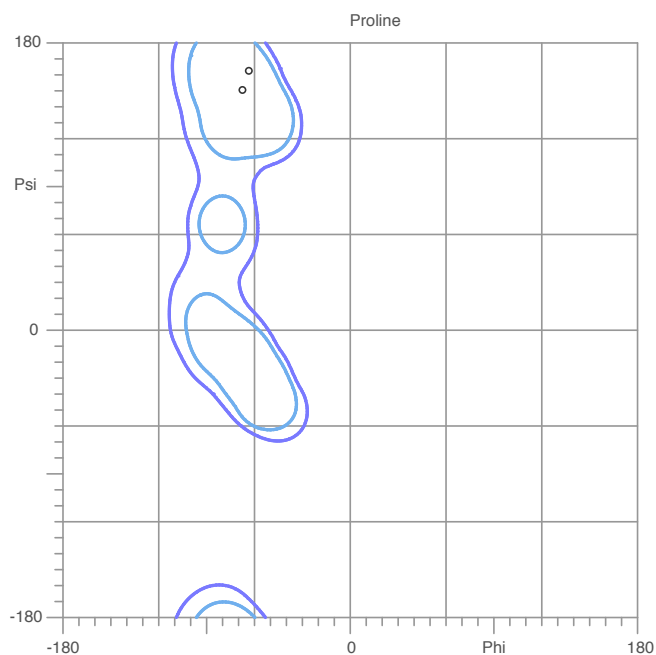
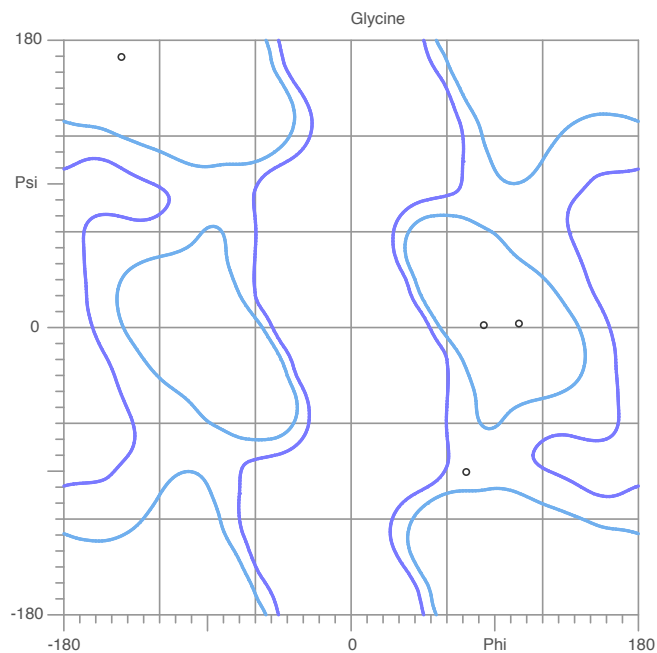
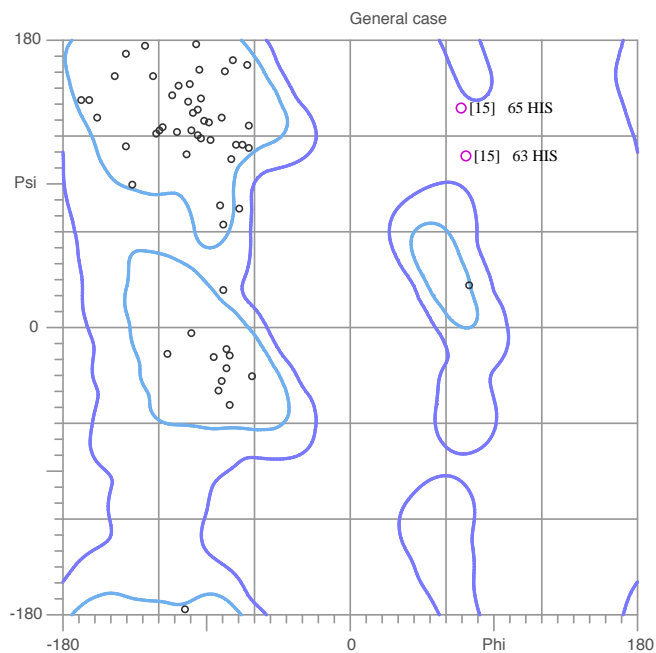
There were 1 outliers (phi, psi):  
[14] 30 GLY (168.0, -29.6)

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 15



92.2% (59/64) of all residues were in favored (98%) regions.  
96.9% (62/64) of all residues were in allowed (>99.8%) regions.

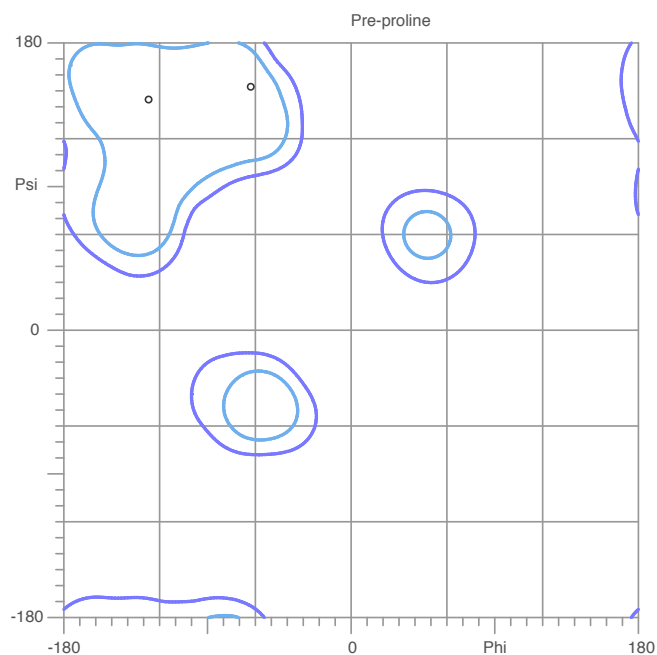
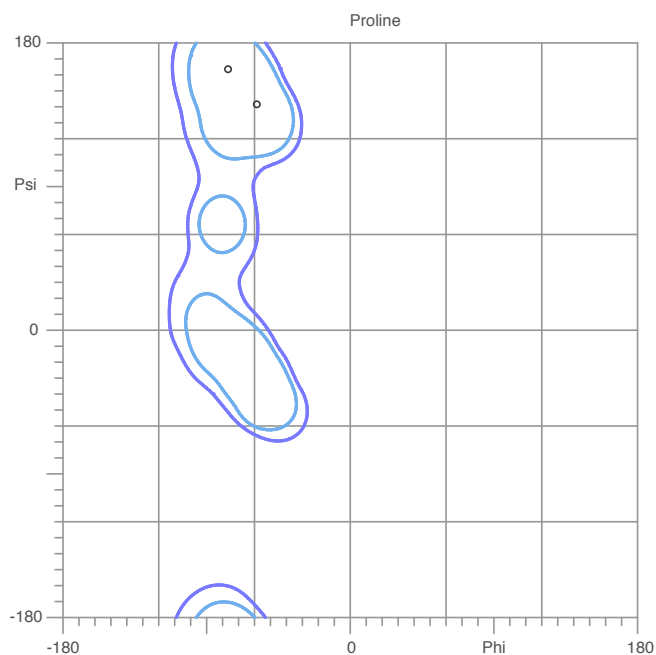
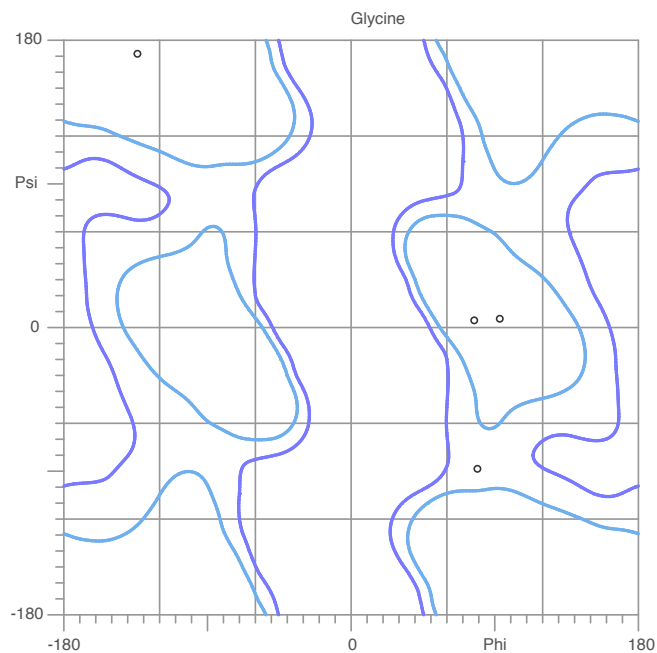
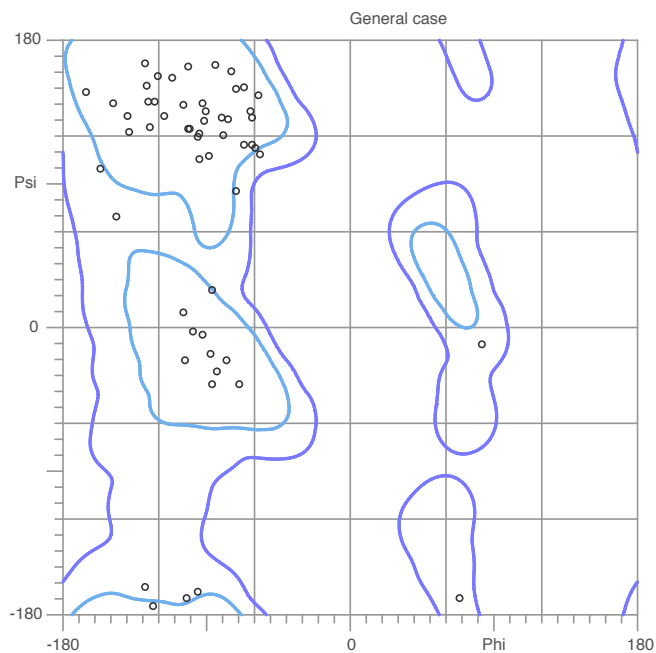
There were 2 outliers (phi, psi):

[15] 63 HIS (72.4, 108.2)

[15] 65 HIS (69.6, 138.5)

# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 16



84.4% (54/64) of all residues were in favored (98%) regions.  
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

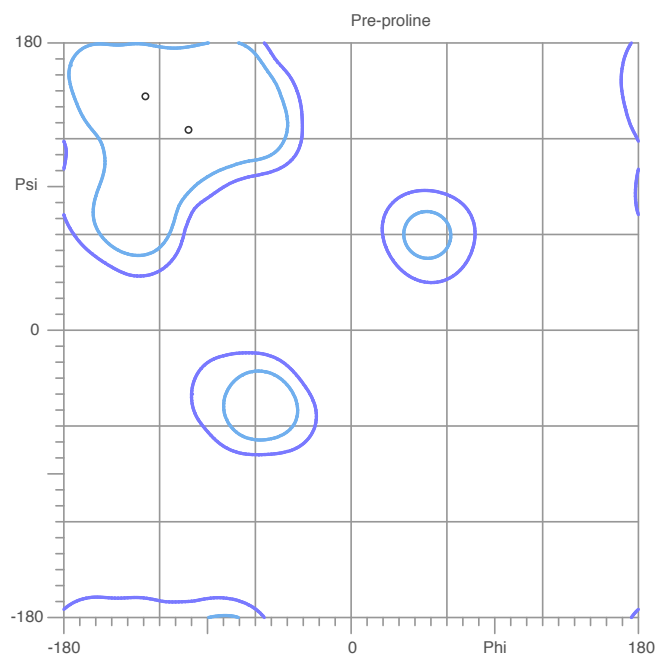
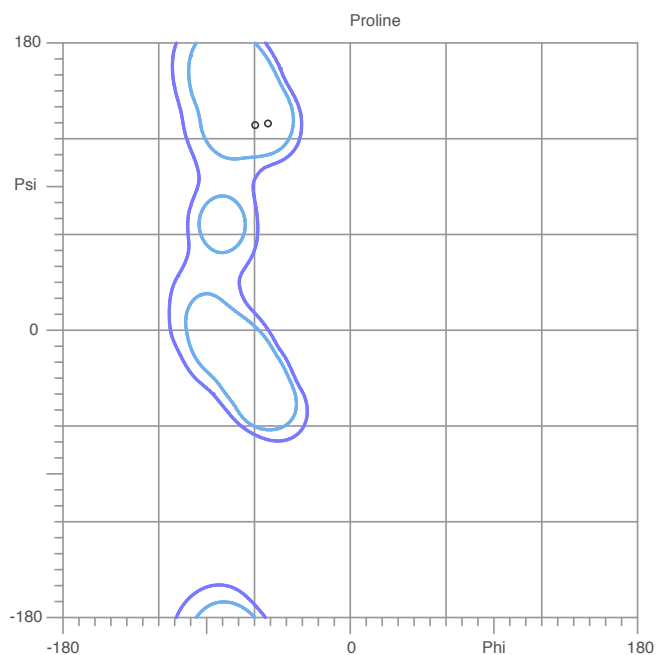
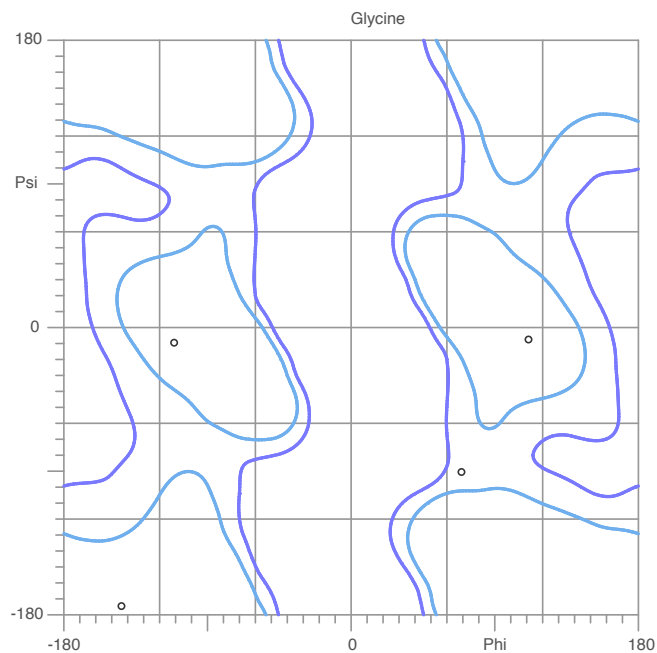
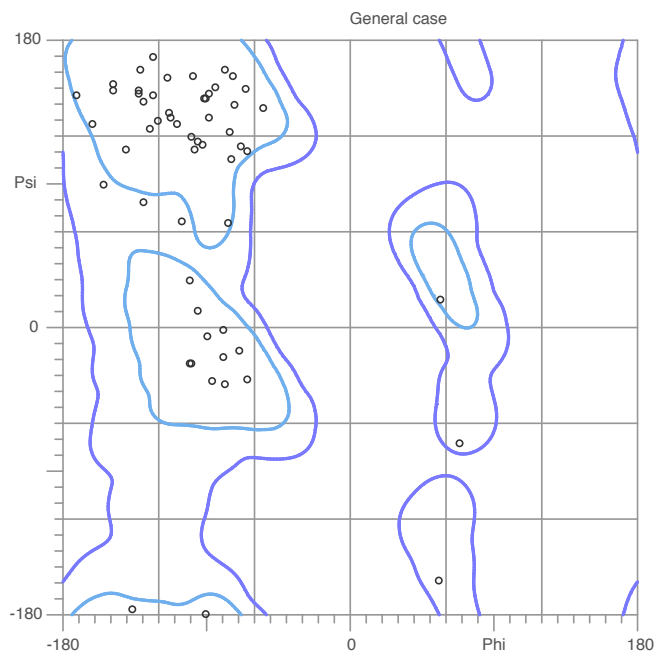
There were no outliers.

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

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 17



90.6% (58/64) of all residues were in favored (98%) regions.  
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

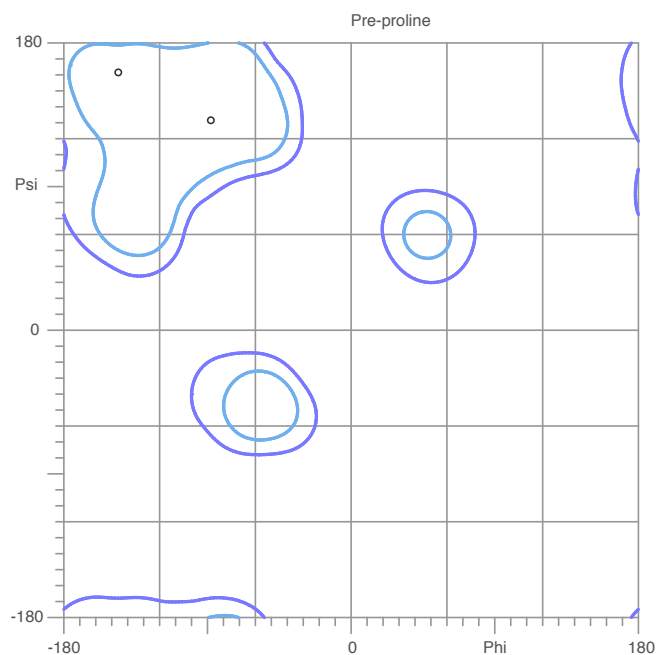
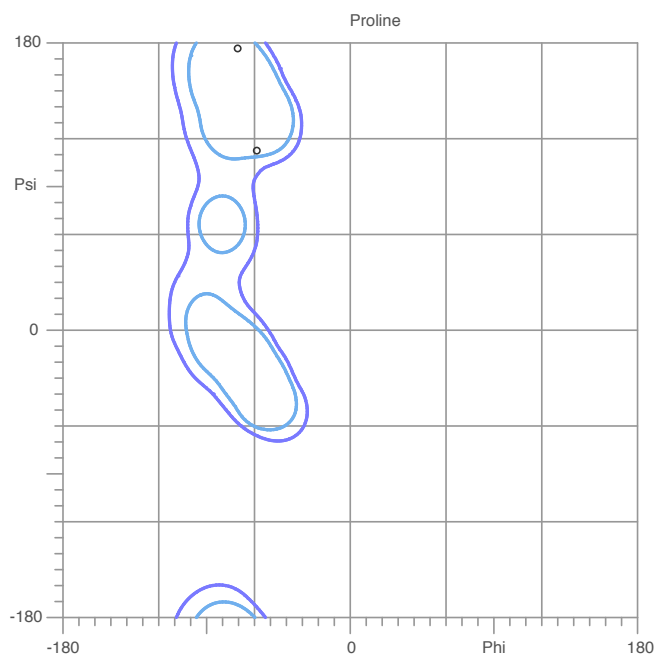
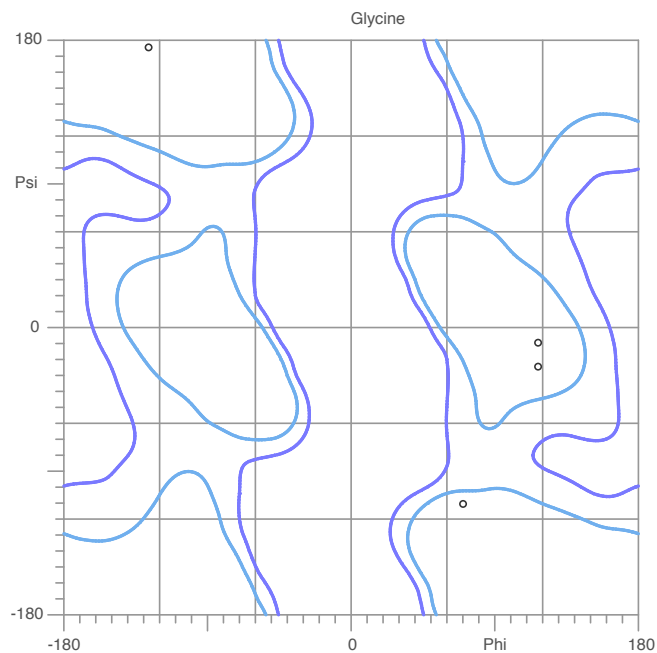
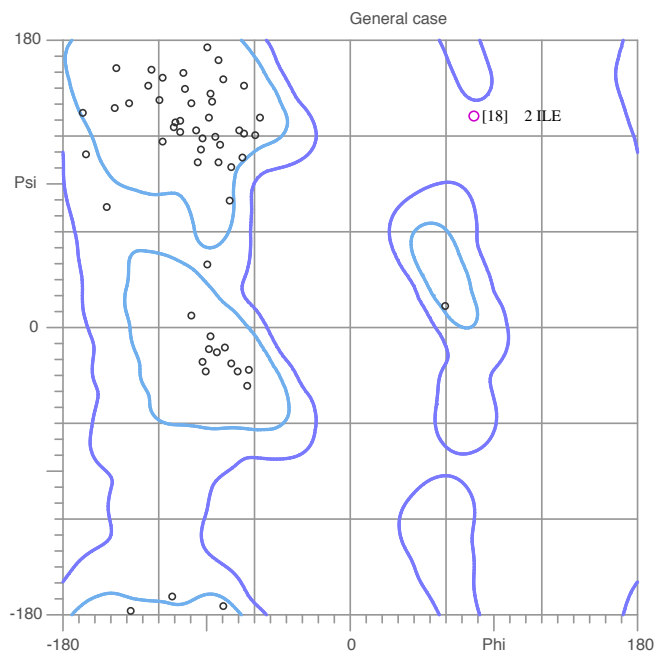
There were no outliers.

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

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# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 18



92.2% (59/64) of all residues were in favored (98%) regions.  
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

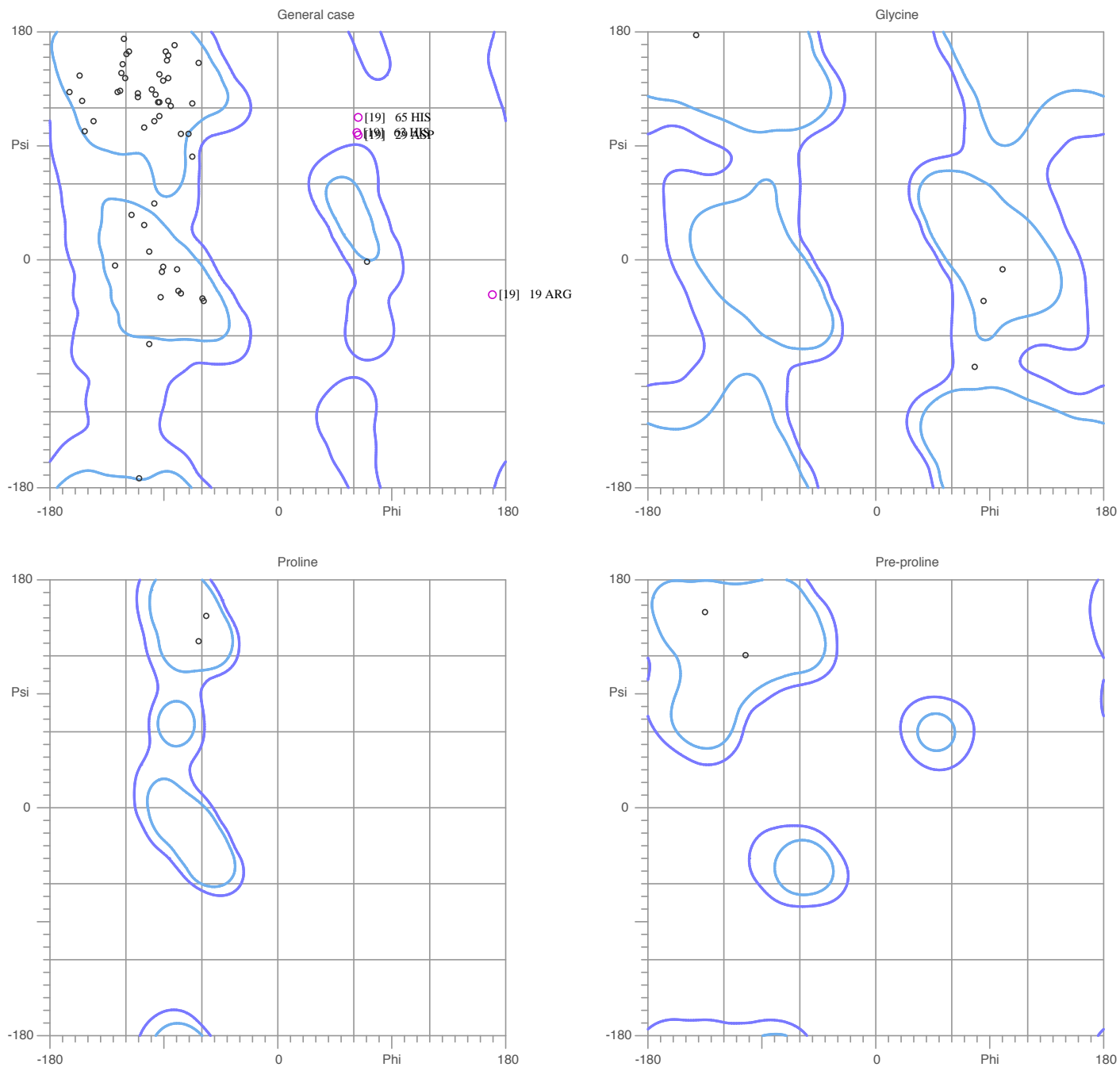
There were 1 outliers (phi, psi):  
[18] 2 ILE (77.1, 133.3)

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

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

# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 19



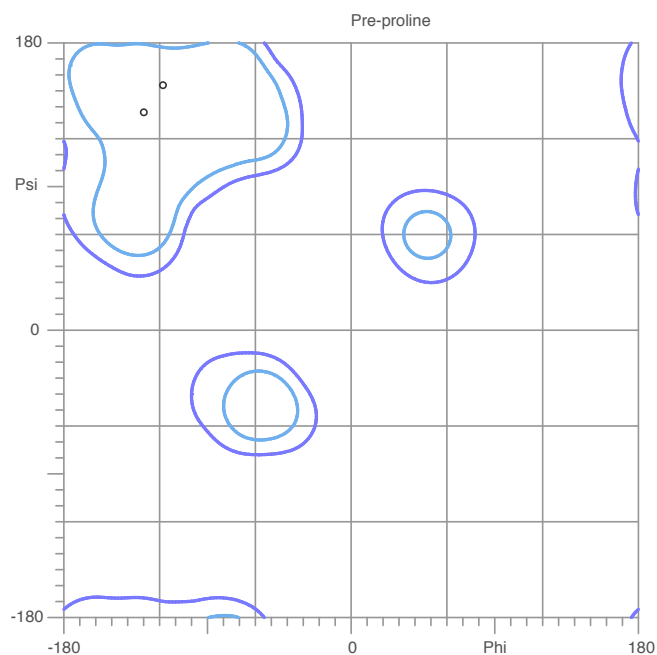
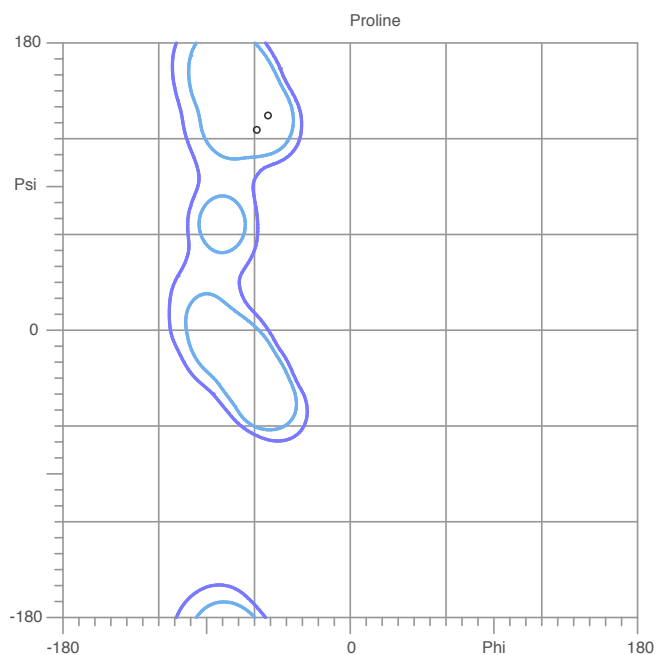
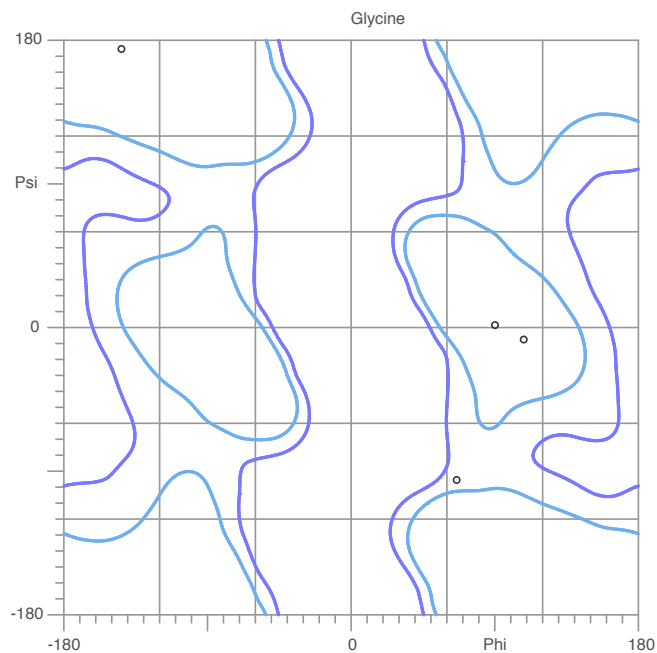
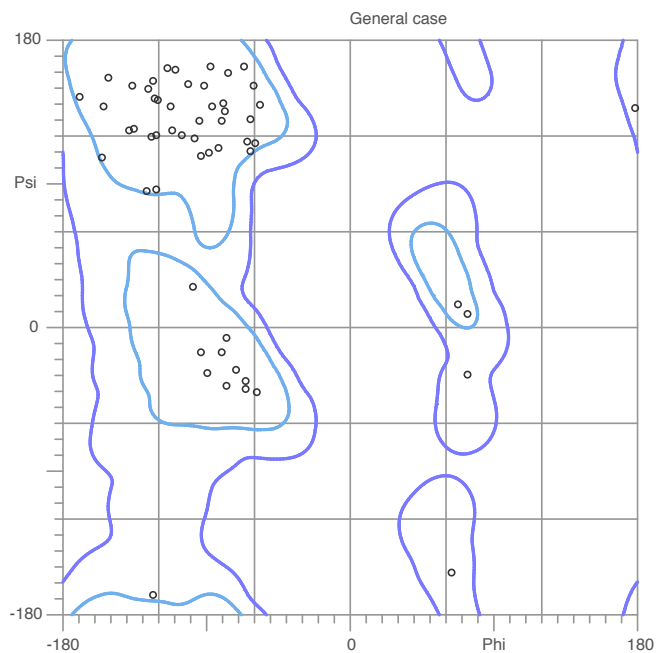
84.4% (54/64) of all residues were in favored (98%) regions.  
93.8% (60/64) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [19] 19 ARG (169.9, -27.1)
- [19] 29 ASP (63.0, 99.8)
- [19] 63 HIS (62.9, 101.7)
- [19] 65 HIS (63.9, 113.5)

# MolProbity Ramachandran analysis

SGR42\_NMR\_em\_bcr3.pdb, model 20



92.2% (59/64) of all residues were in favored (98%) regions.  
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

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