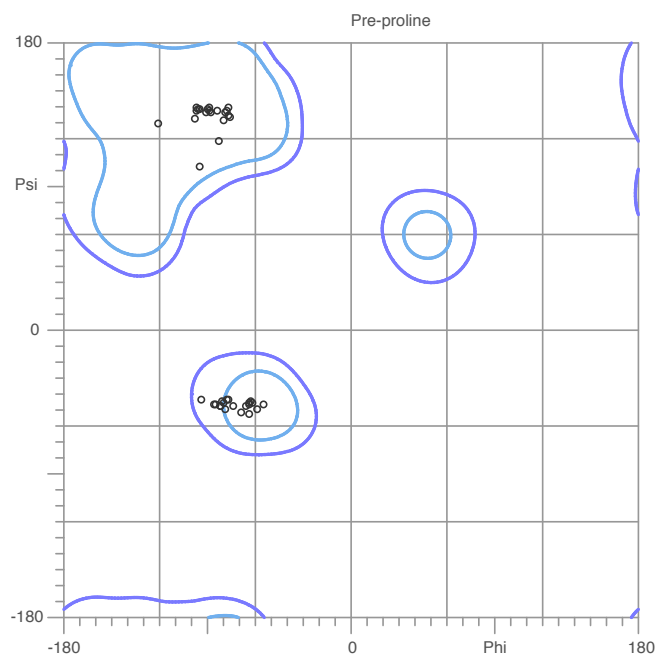
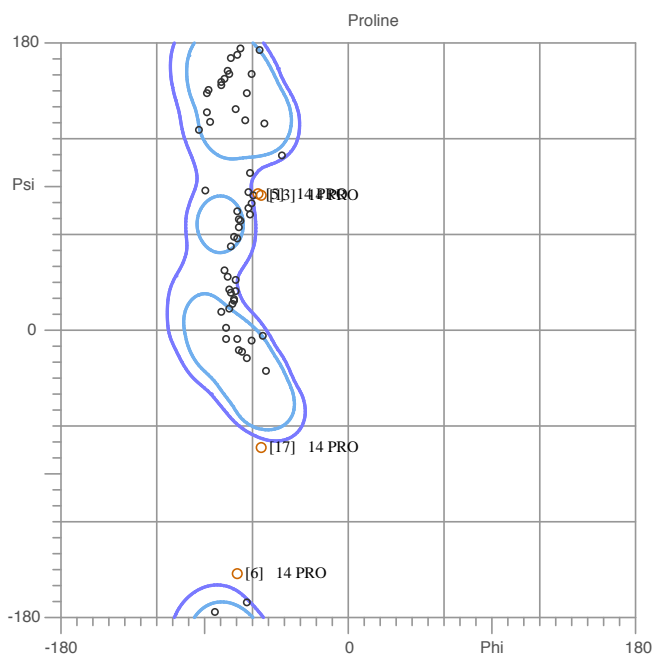
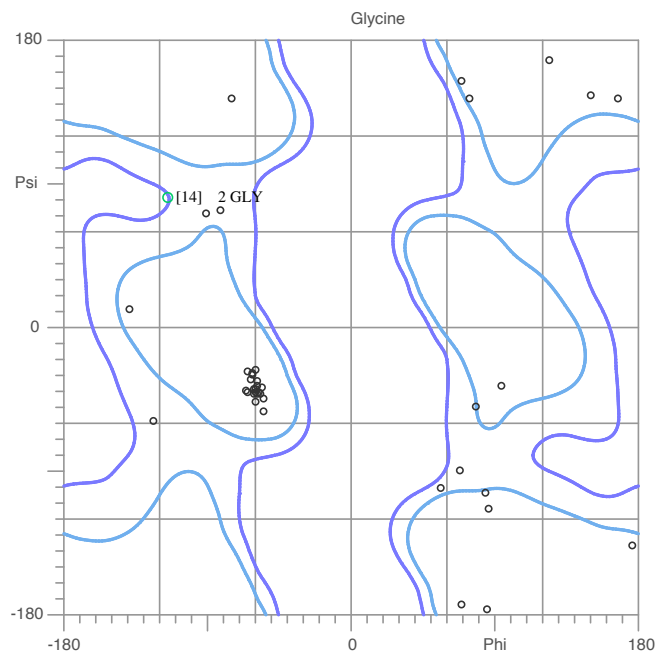
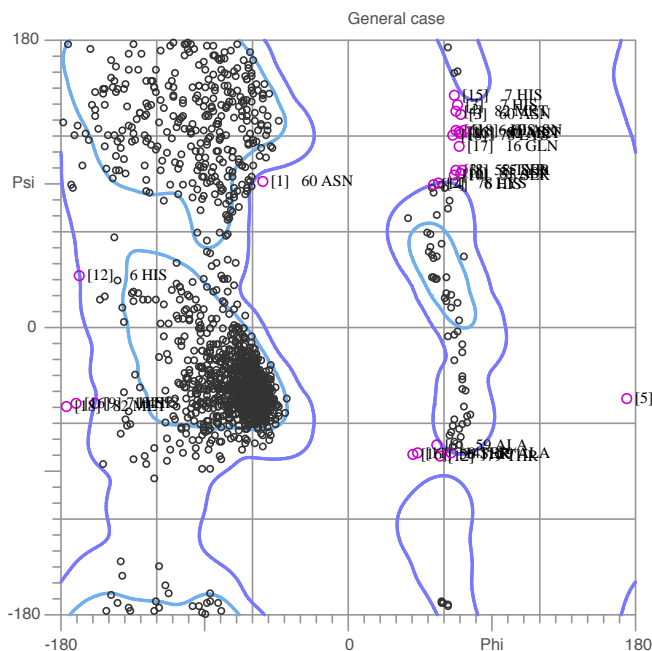


# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, all models



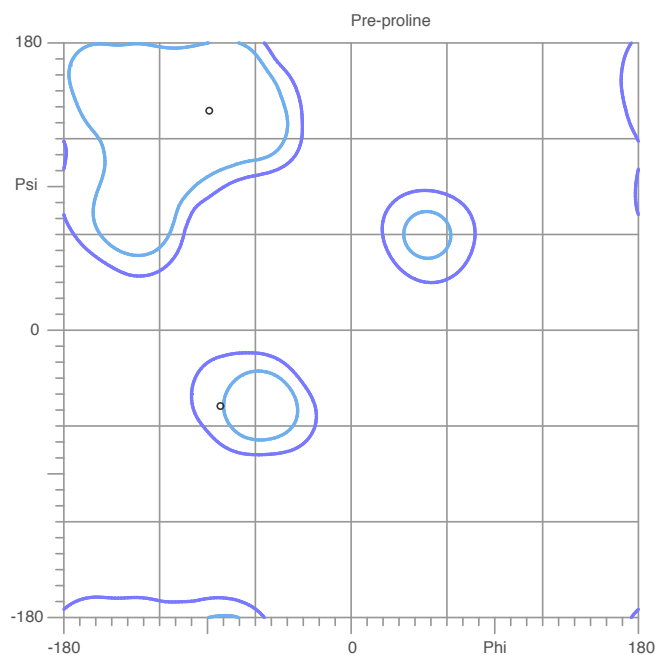
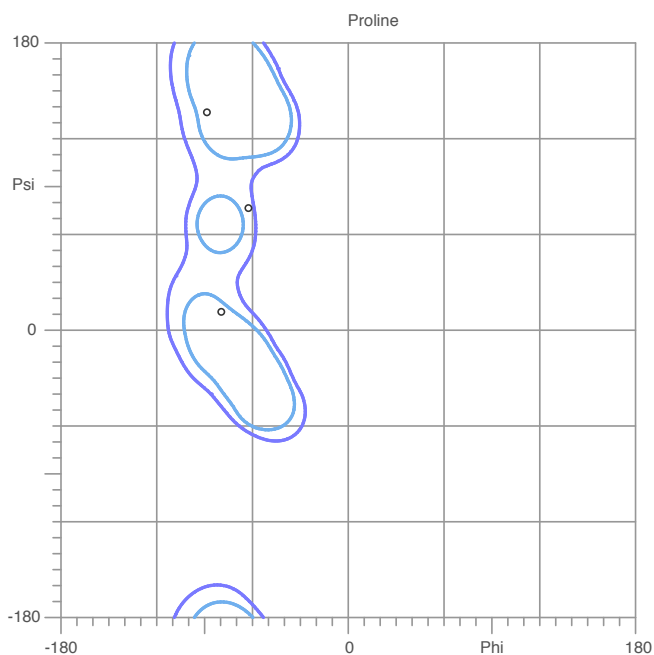
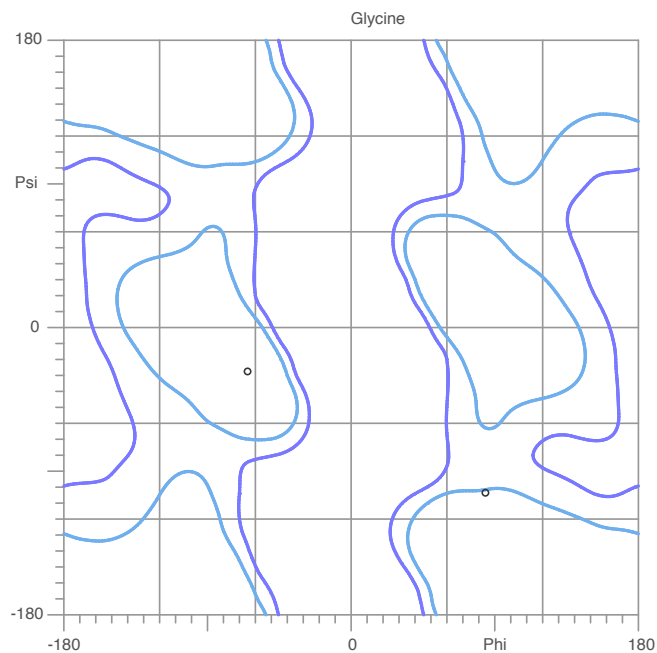
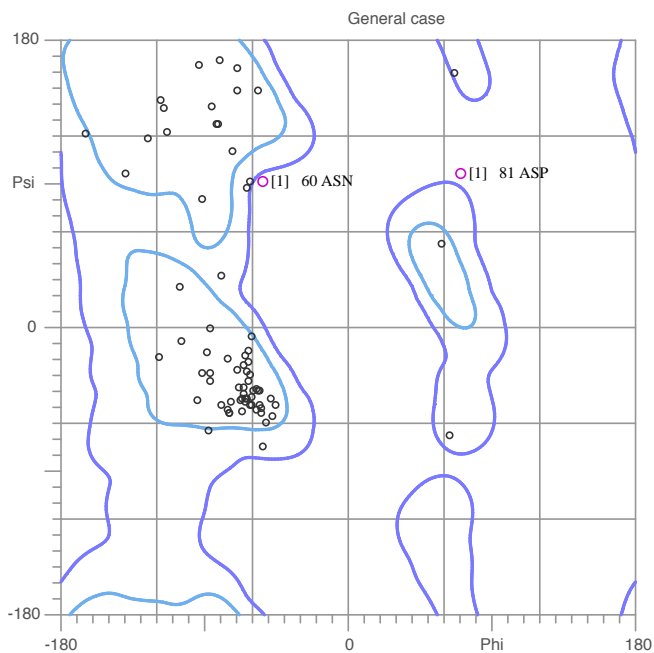
85.9% (1391/1620) of all residues were in favored (98%) regions.  
98.0% (1588/1620) of all residues were in allowed (>99.8%) regions.

There were 32 outliers (phi, psi):

- |                            |                             |
|----------------------------|-----------------------------|
| [1] 60 ASN (-54.5, 92.0)   | [10] 55 SER (66.2, 96.5)    |
| [1] 81 ASP (70.1, 97.5)    | [11] 9 SER (43.8, -78.2)    |
| [2] 78 LYS (56.3, 91.9)    | [12] 6 HIS (-169.9, 33.0)   |
| [3] 7 HIS (68.5, 140.4)    | [12] 79 THR (57.8, -80.1)   |
| [3] 58 TYR (67.4, 99.1)    | [13] 14 PRO (-55.1, 85.6)   |
| [3] 60 ASN (70.5, 134.1)   | [13] 82 MET (70.1, 122.6)   |
| [4] 82 MET (67.2, 136.7)   | [14] 2 GLY (-115.1, 82.5)   |
| [5] 14 PRO (-57.3, 86.9)   | [14] 6 HIS (53.1, 90.2)     |
| [5] 79 THR (174.3, -44.6)  | [14] 59 ALA (64.4, -78.1)   |
| [6] 6 HIS (68.0, 124.3)    | [15] 7 HIS (66.4, 146.9)    |
| [6] 14 PRO (-70.9, -152.7) | [16] 7 HIS (-171.7, -47.7)  |
| [6] 59 ALA (55.8, -73.4)   | [16] 56 THR (40.3, -79.4)   |
| [8] 55 SER (71.9, 99.5)    | [16] 60 ASN (69.3, 123.1)   |
| [9] 10 HIS (-159.3, -47.8) | [17] 14 PRO (-55.4, -73.9)  |
|                            | [17] 16 GLN (69.5, 114.5)   |
|                            | [18] 60 ASN (72.6, 124.3)   |
|                            | [18] 78 LYS (65.9, 121.8)   |
|                            | [18] 82 MET (-177.6, -49.1) |

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 1



85.2% (69/81) of all residues were in favored (98%) regions.  
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

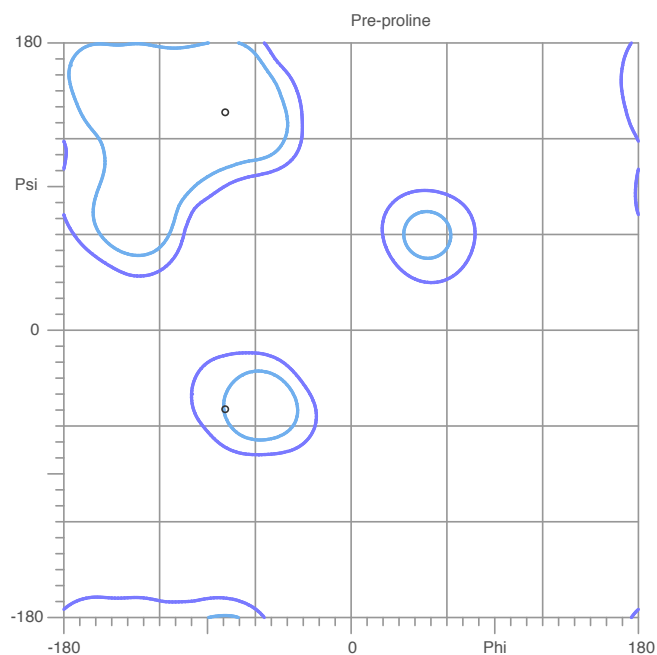
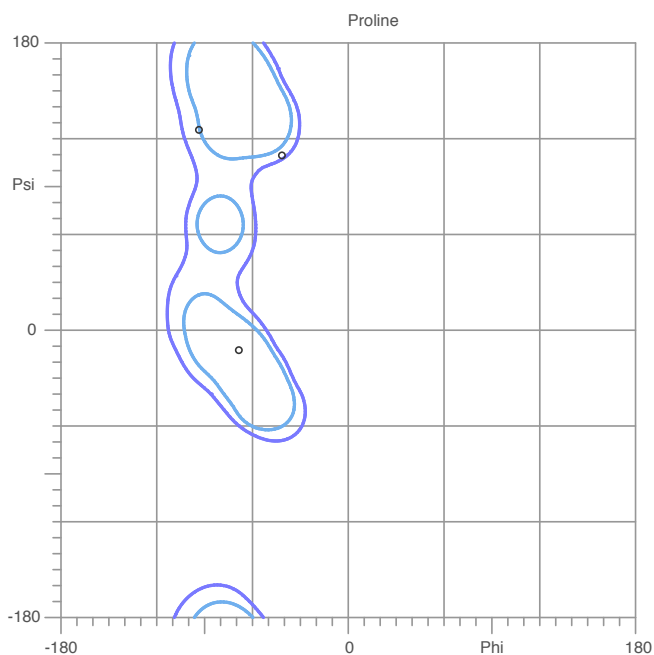
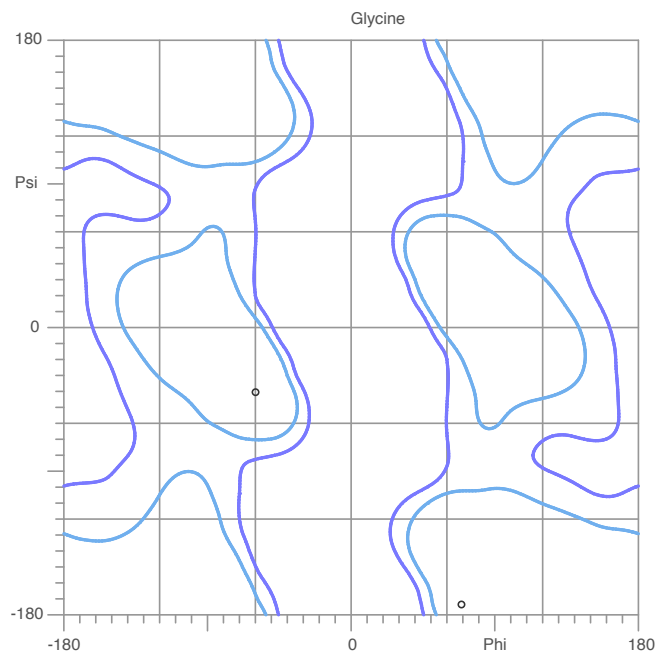
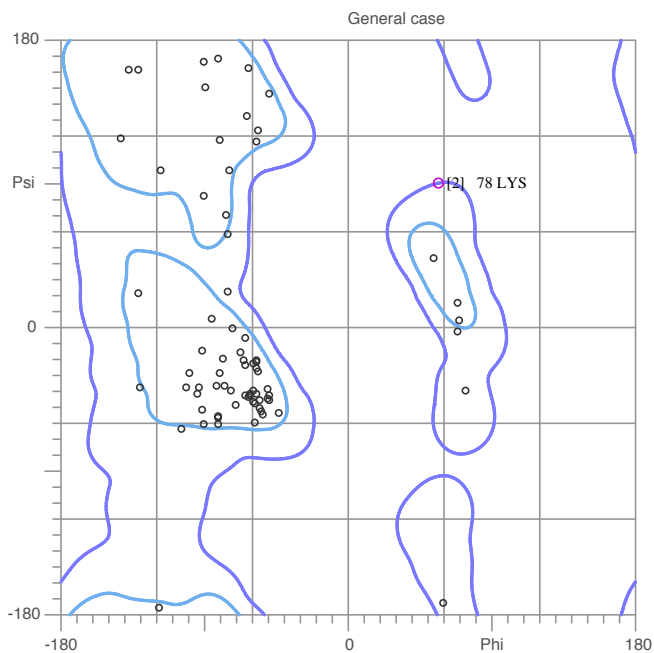
There were 2 outliers (phi, psi):

[1] 60 ASN (-54.5, 92.0)

[1] 81 ASP (70.1, 97.5)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 2



88.9% (72/81) of all residues were in favored (98%) regions.  
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

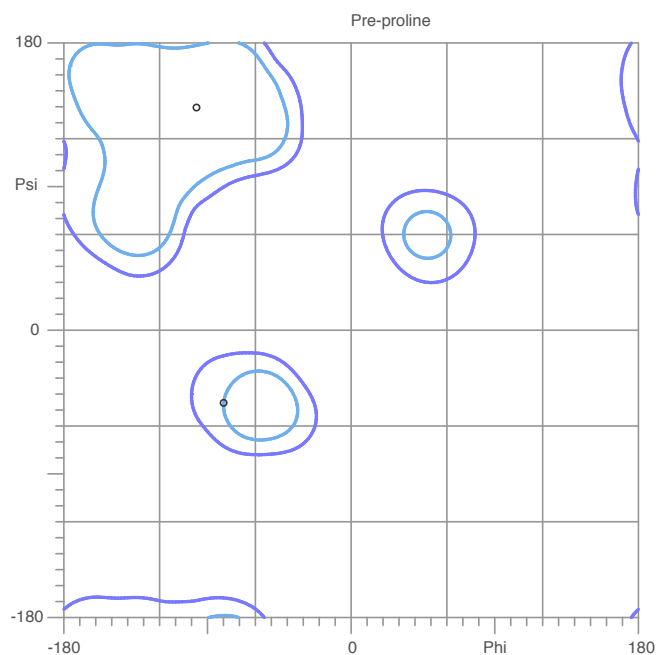
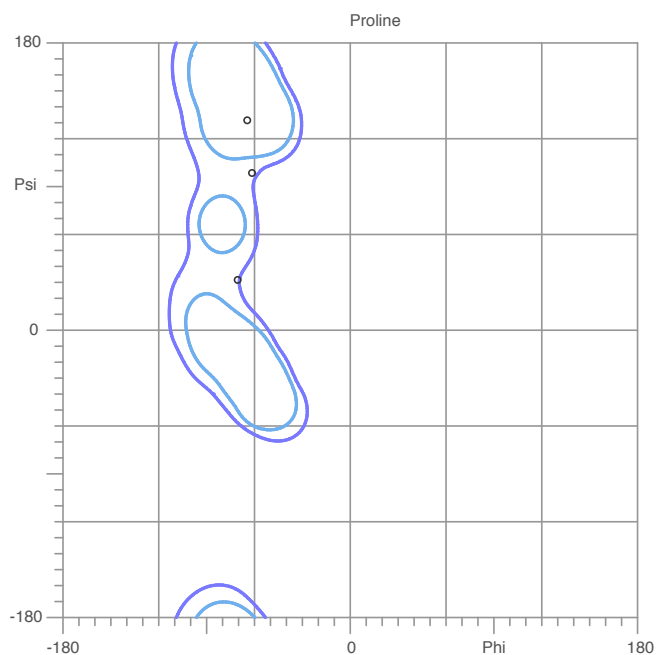
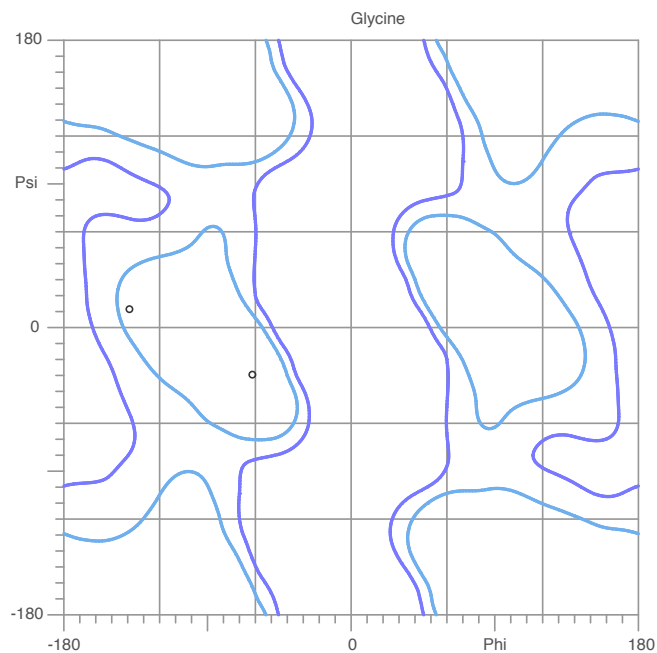
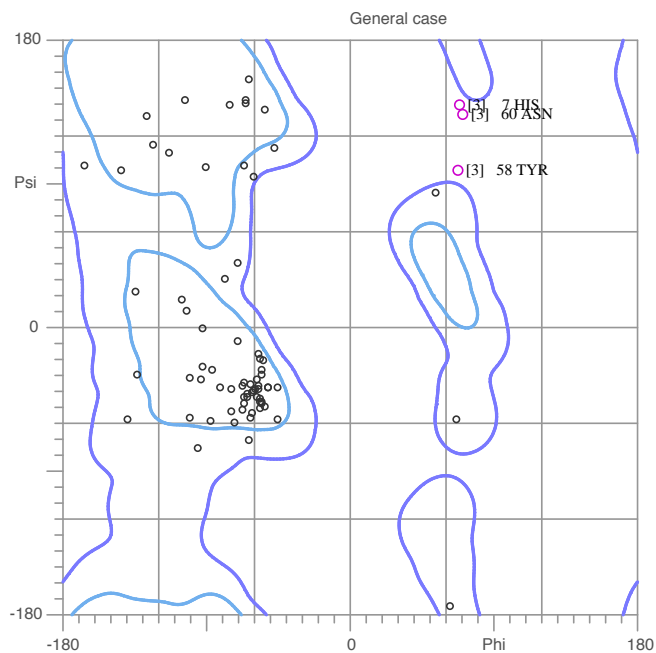
There were 1 outliers (phi, psi):  
[2] 78 LYS (56.3, 91.9)

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# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 3



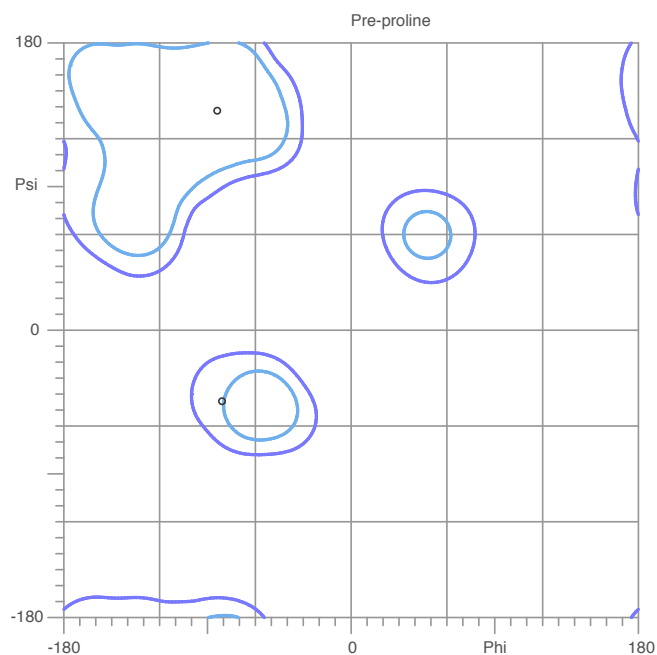
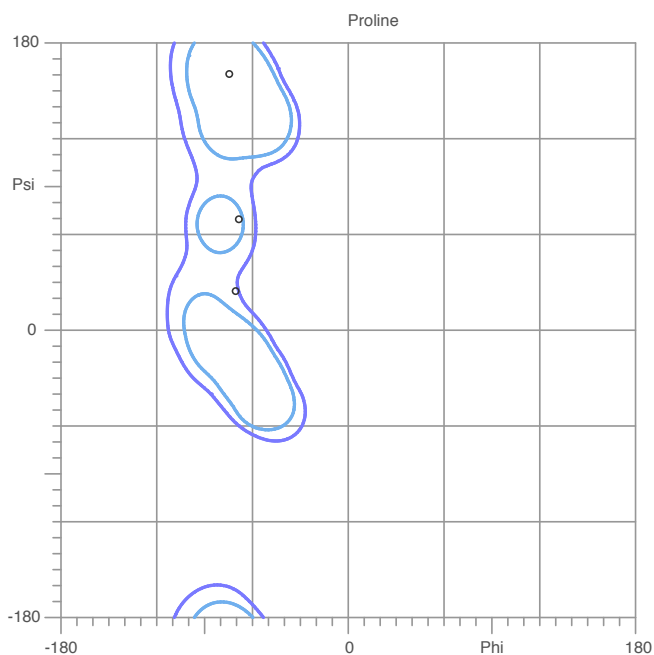
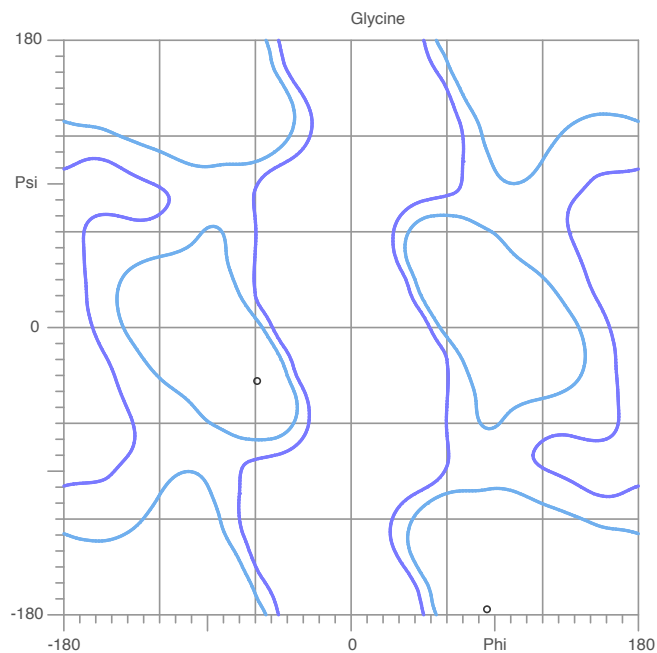
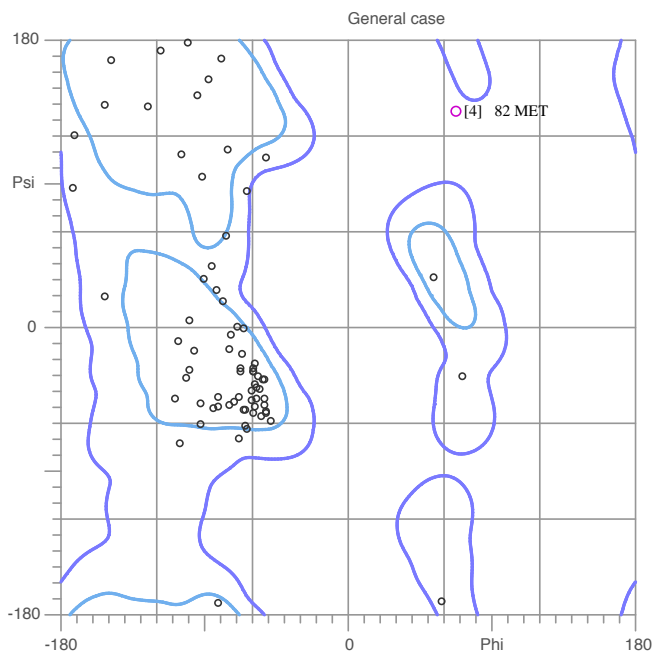
76.5% (62/81) of all residues were in favored (98%) regions.  
96.3% (78/81) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 7 HIS (68.5, 140.4)
- [3] 58 TYR (67.4, 99.1)
- [3] 60 ASN (70.5, 134.1)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 4



80.2% (65/81) of all residues were in favored (98%) regions.  
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

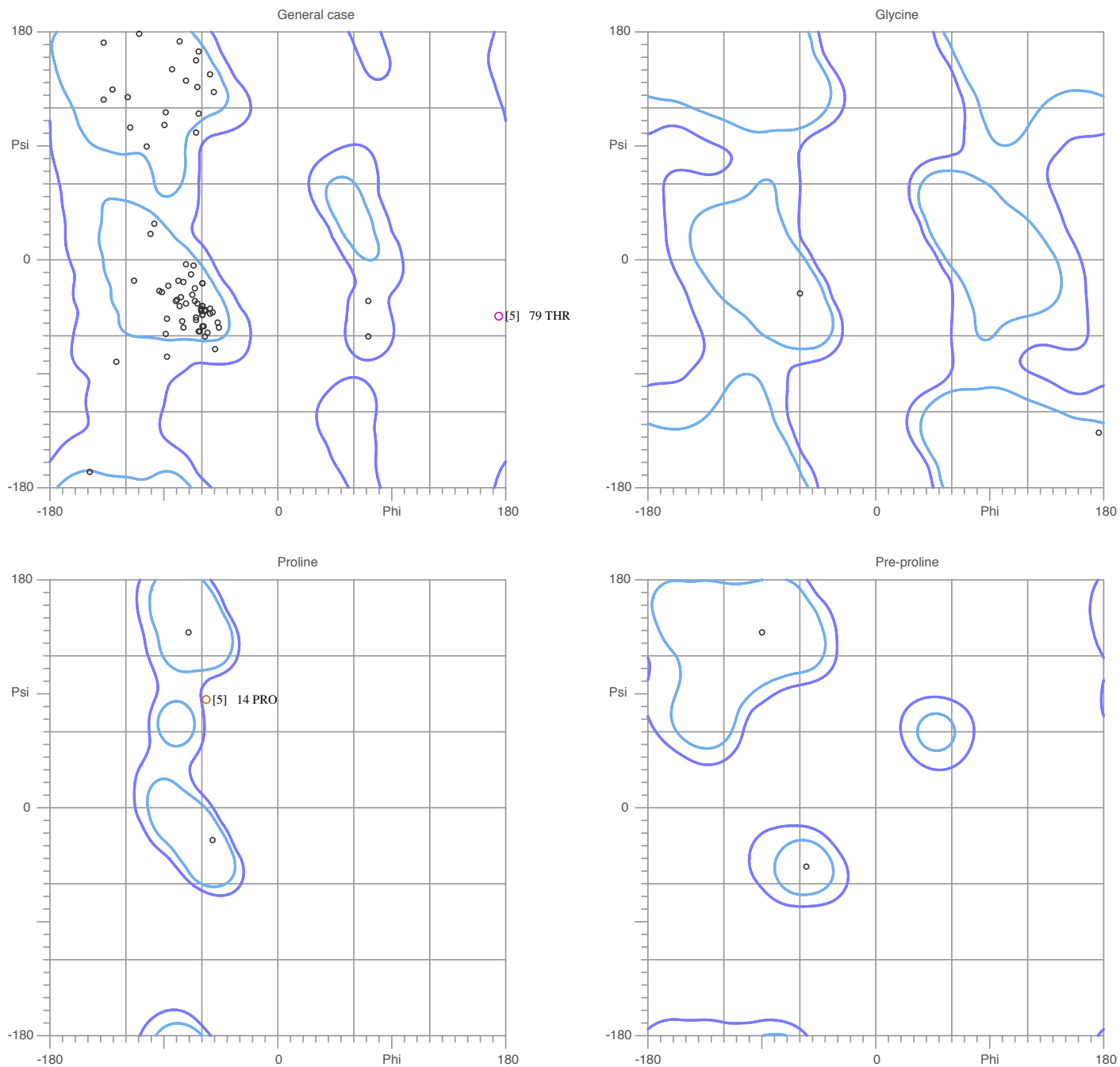
There were 1 outliers (phi, psi):  
[4] 82 MET (67.2, 136.7)

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# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 5



90.1% (73/81) of all residues were in favored (98%) regions.  
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

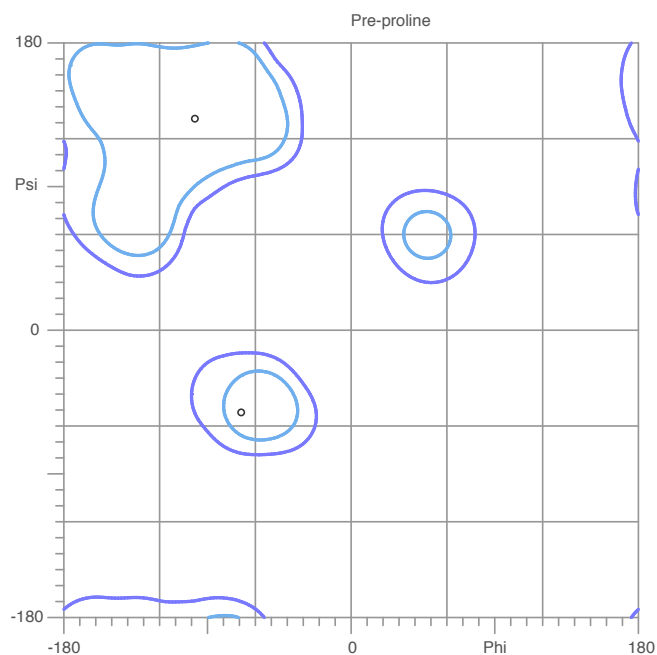
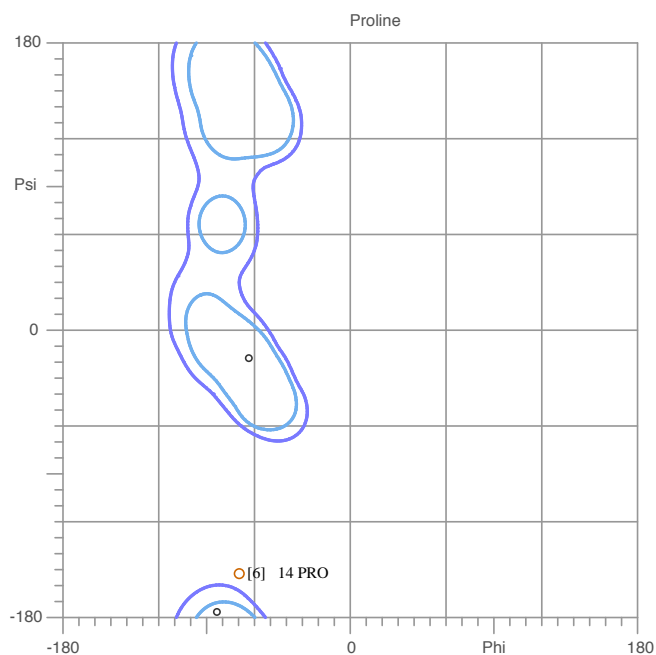
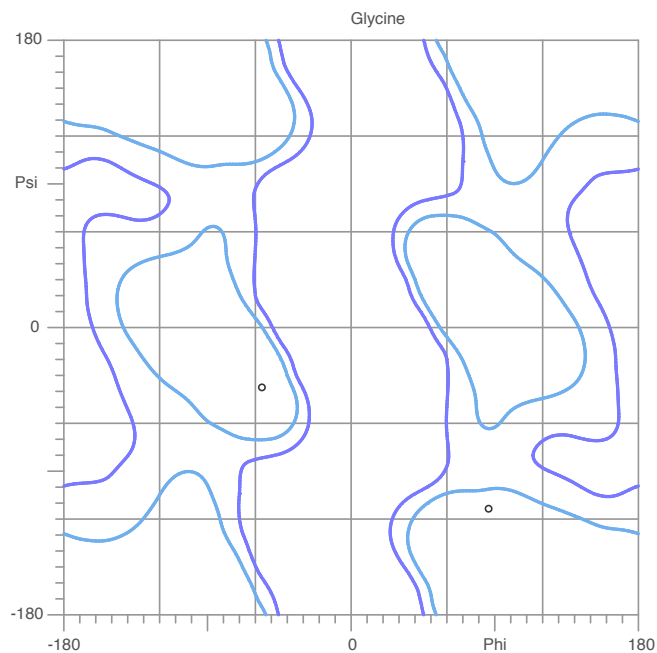
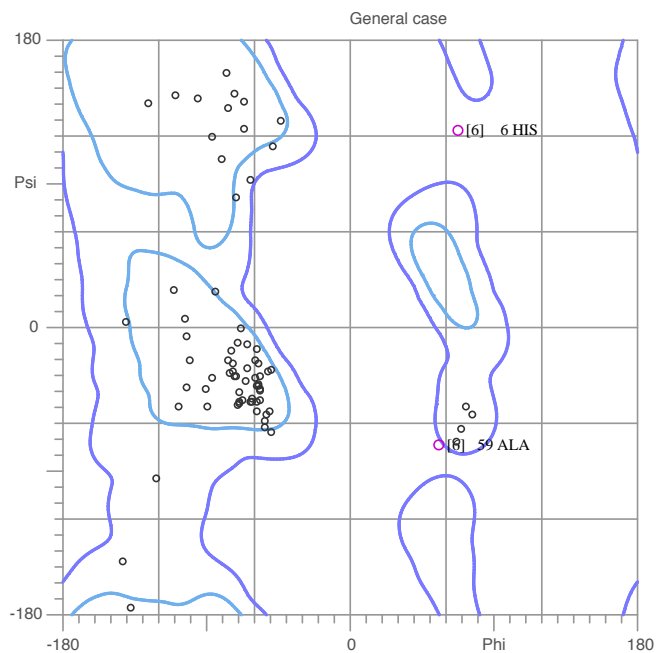
There were 2 outliers (phi, psi):

[5] 14 PRO (-57.3, 86.9)

[5] 79 THR (174.3, -44.6)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 6



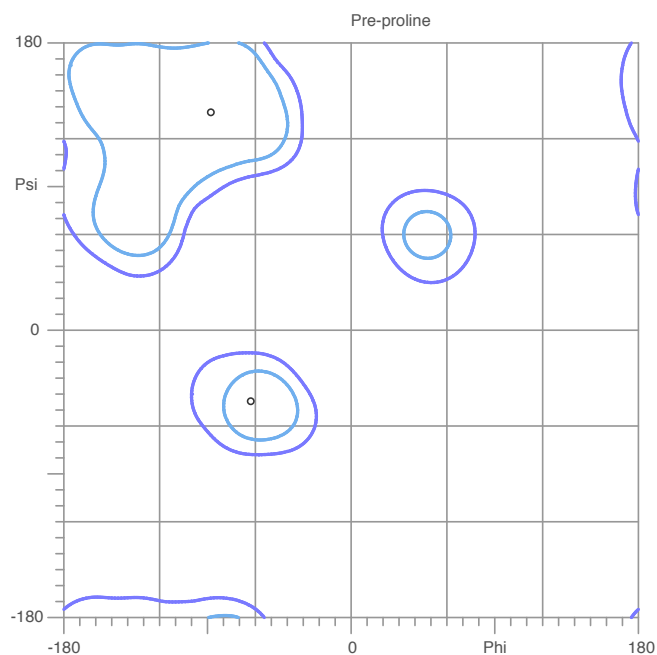
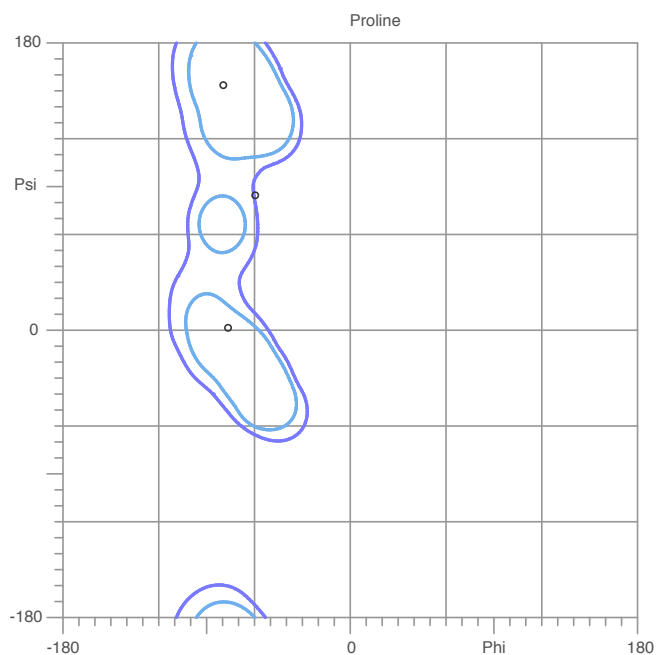
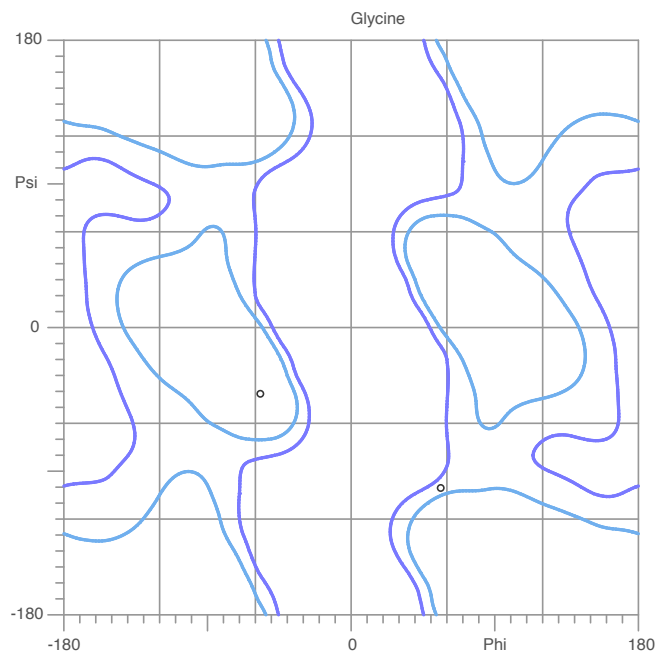
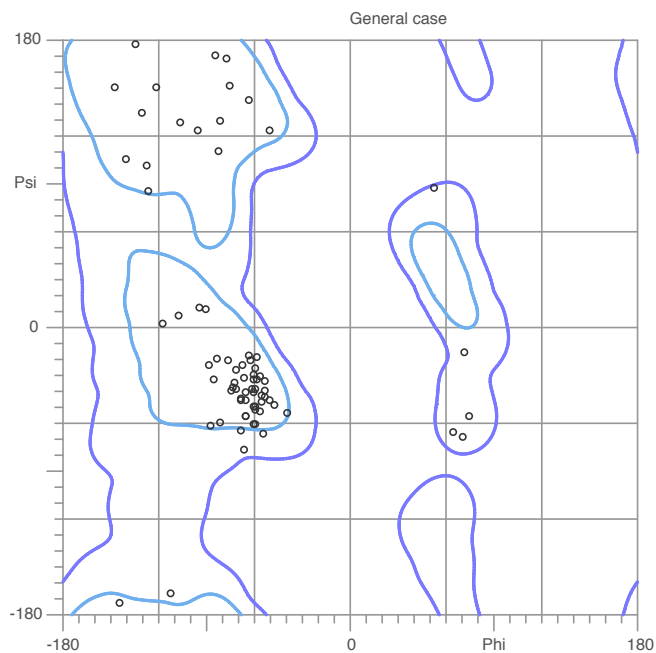
81.5% (66/81) of all residues were in favored (98%) regions.  
96.3% (78/81) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 6 HIS (68.0, 124.3)
- [6] 14 PRO (-70.9, -152.7)
- [6] 59 ALA (55.8, -73.4)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 7



86.4% (70/81) of all residues were in favored (98%) regions.  
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

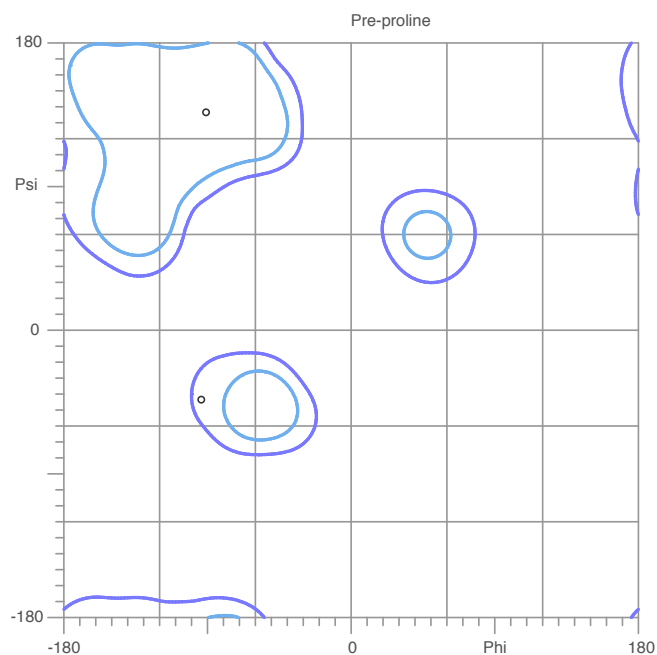
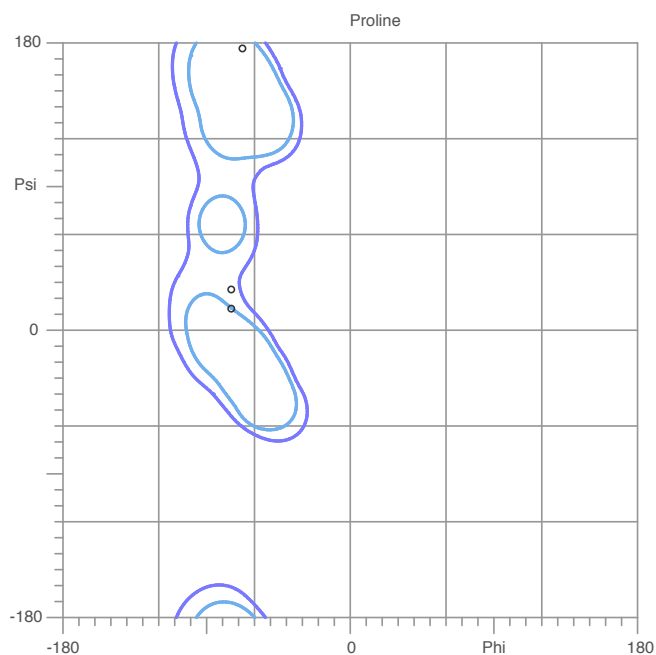
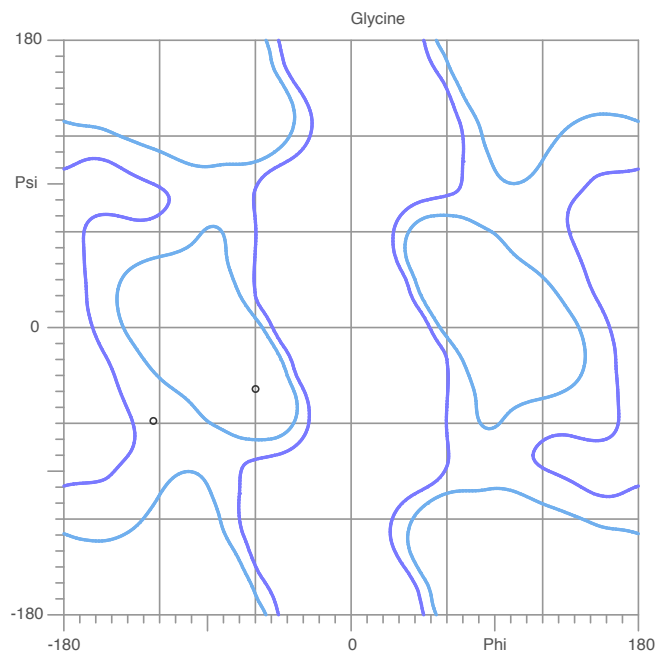
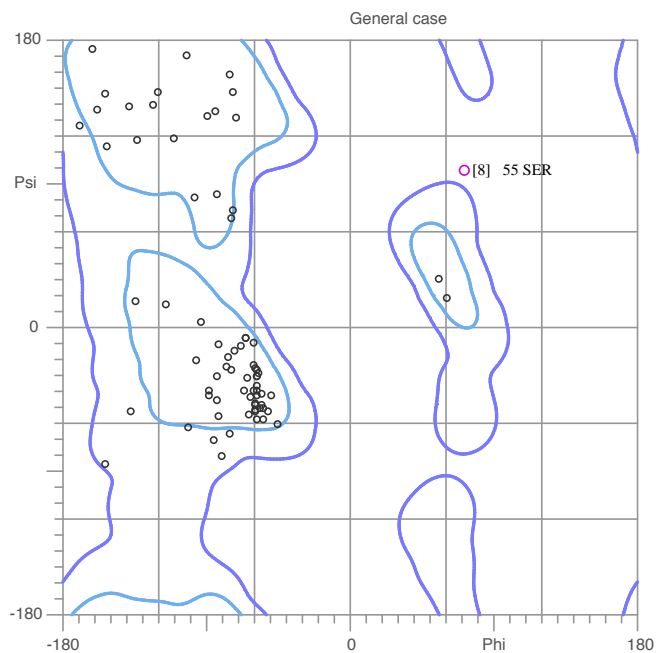
There were no outliers.

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# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 8

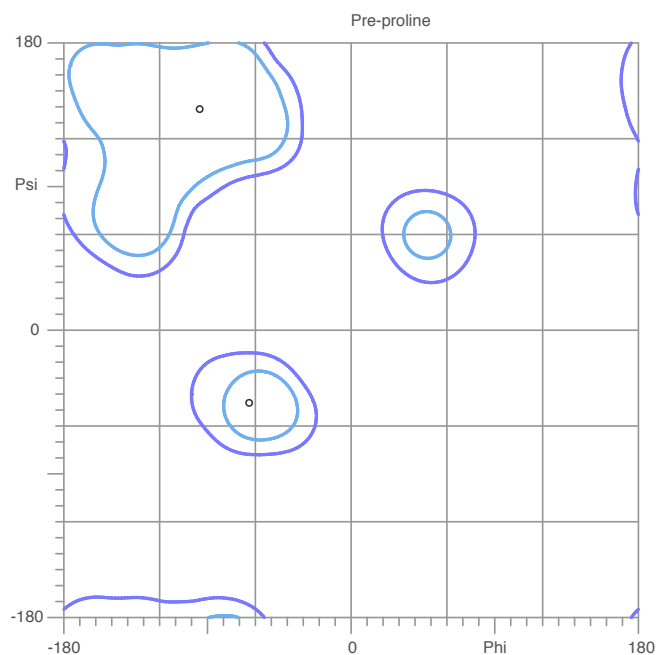
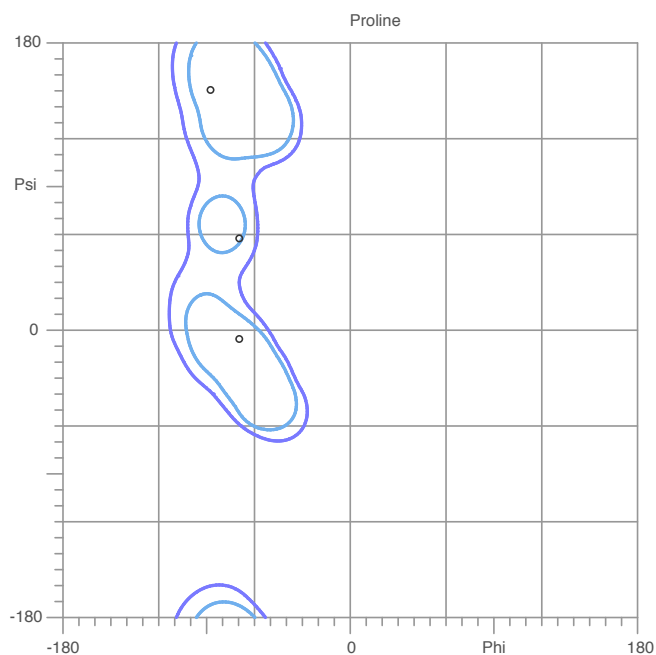
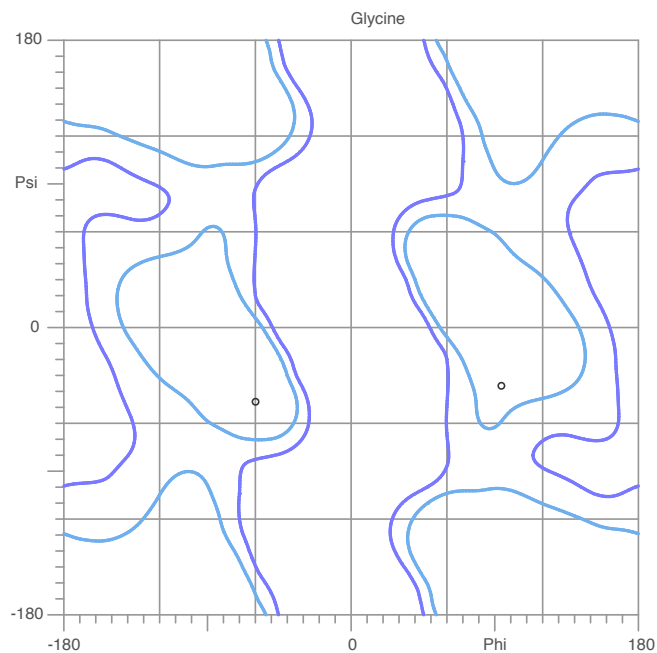
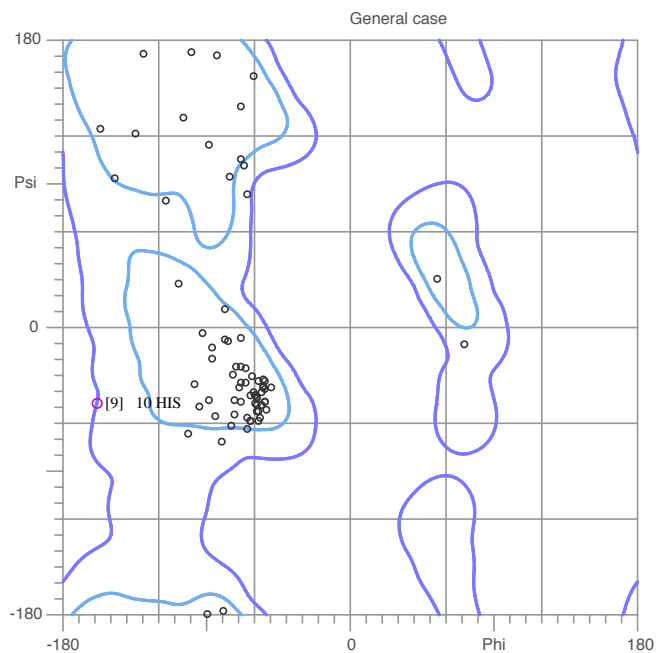


86.4% (70/81) of all residues were in favored (98%) regions.  
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[8] 55 SER (71.9, 99.5)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 9



90.1% (73/81) of all residues were in favored (98%) regions.  
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

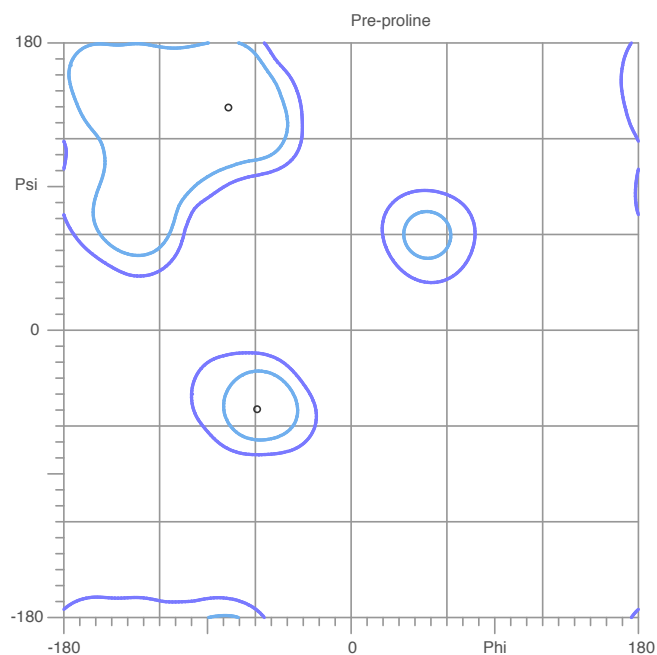
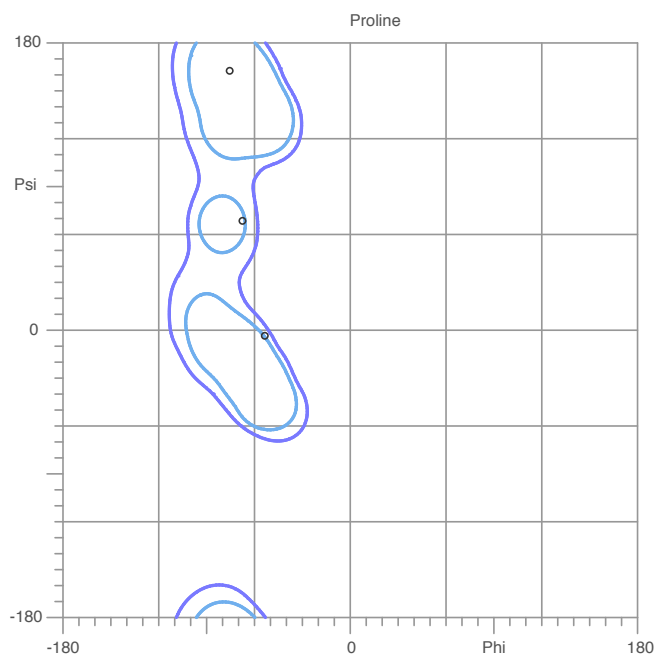
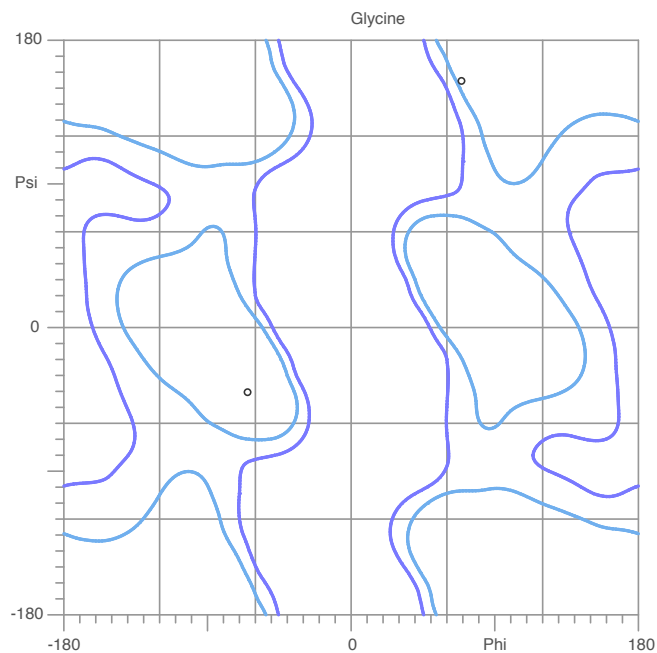
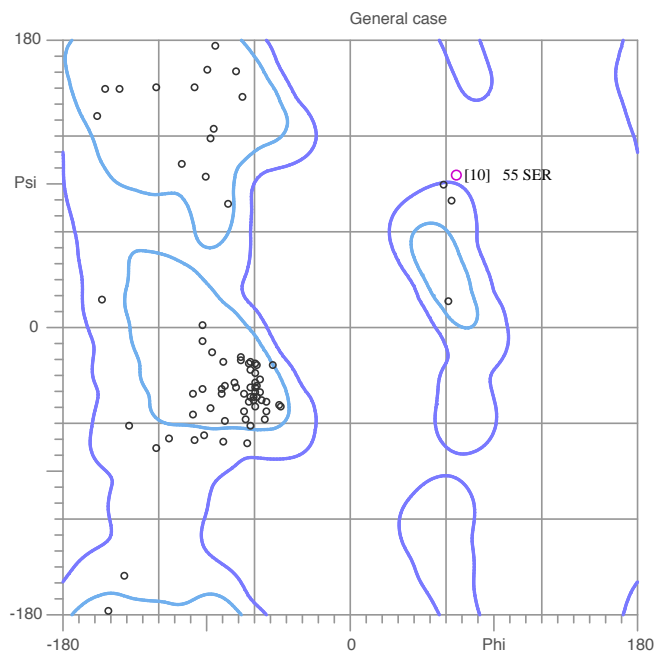
There were 1 outliers (phi, psi):  
[9] 10 HIS (-159.3, -47.8)

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# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 10



85.2% (69/81) of all residues were in favored (98%) regions.  
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

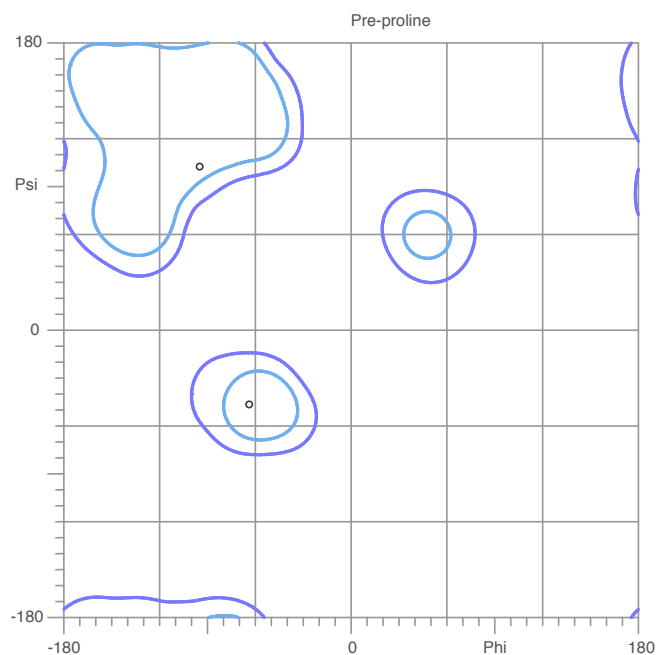
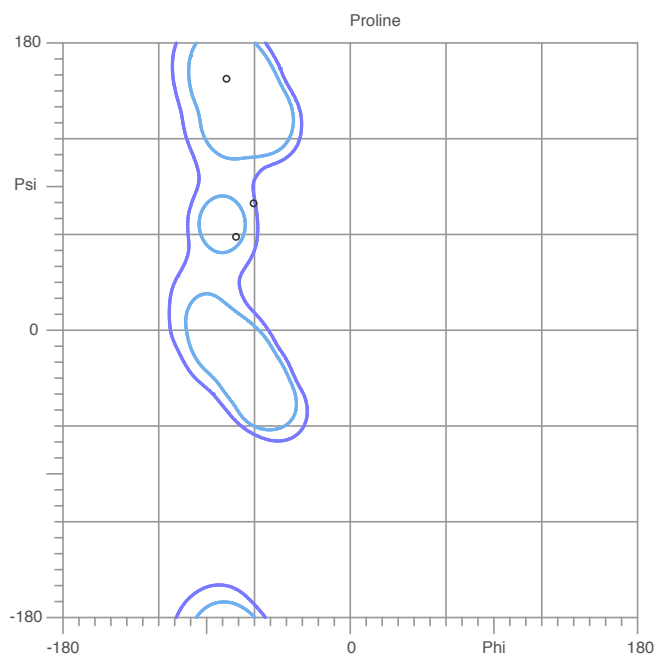
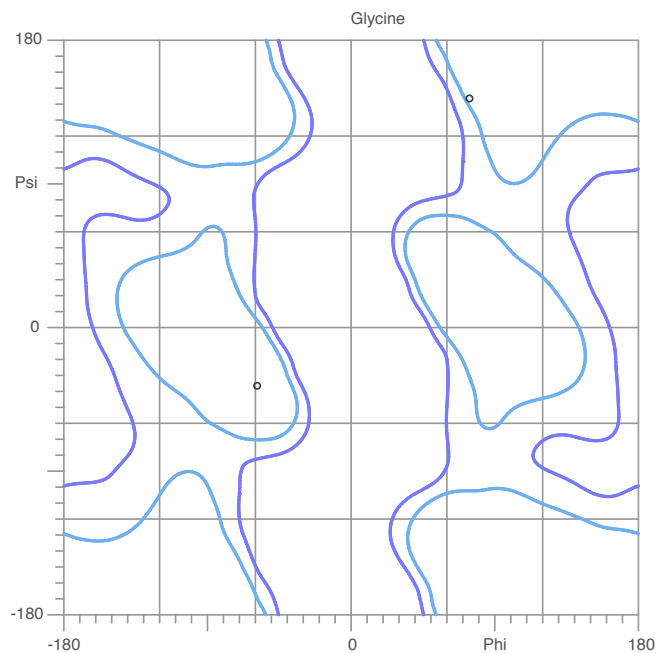
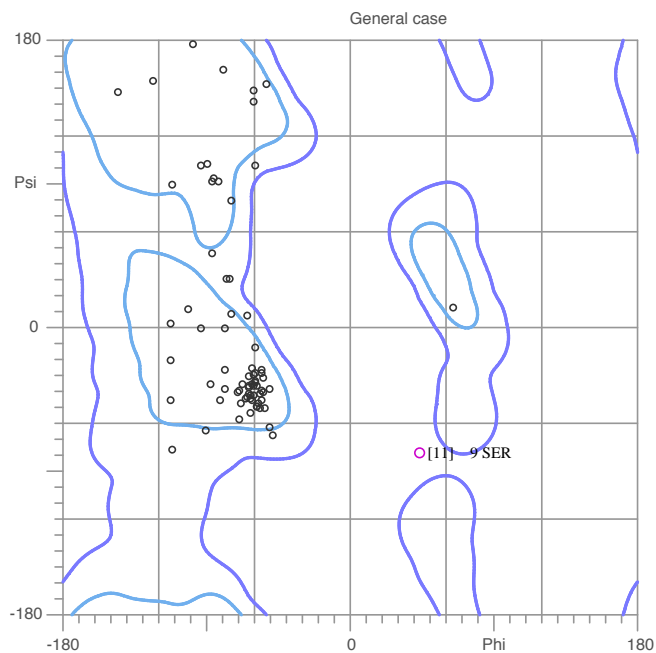
There were 1 outliers (phi, psi):  
[10] 55 SER (66.2, 96.5)

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# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 11



87.7% (71/81) of all residues were in favored (98%) regions.  
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

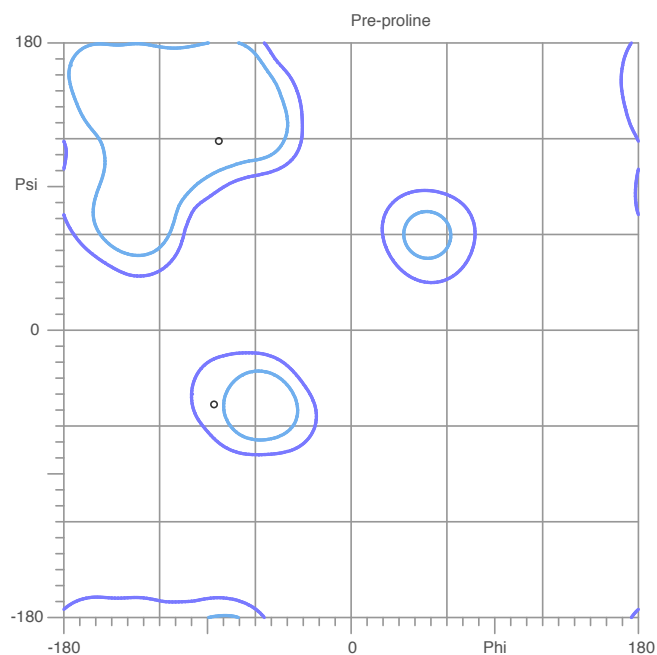
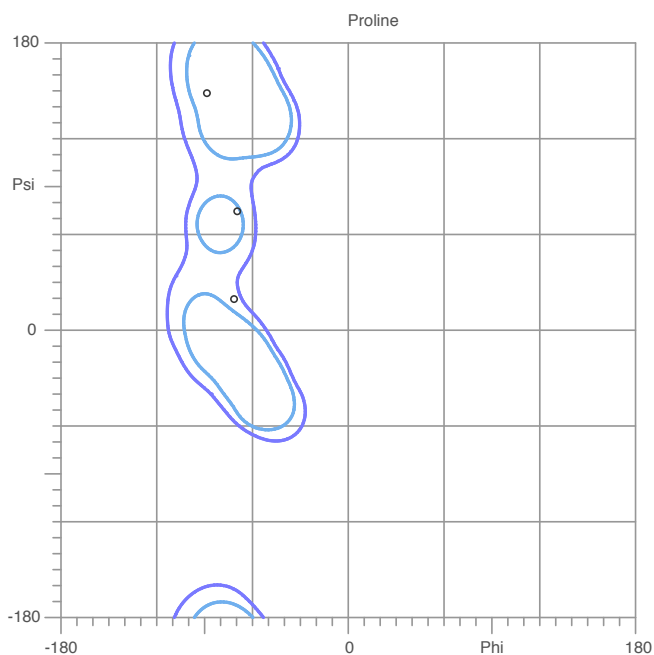
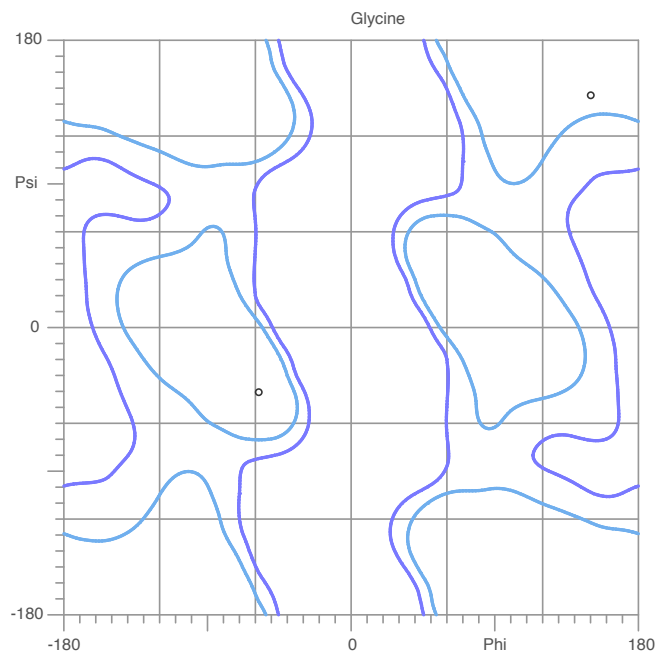
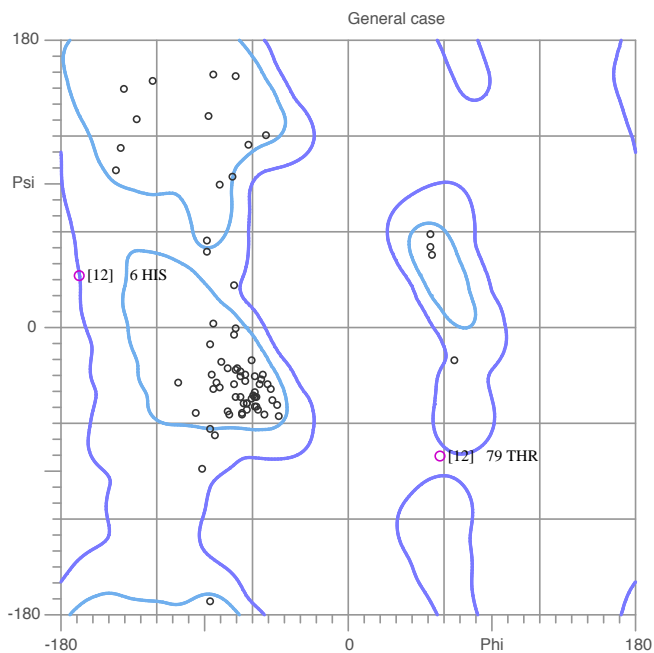
There were 1 outliers (phi, psi):  
[11] 9 SER (43.8, -78.2)

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

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# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 12



88.9% (72/81) of all residues were in favored (98%) regions.  
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

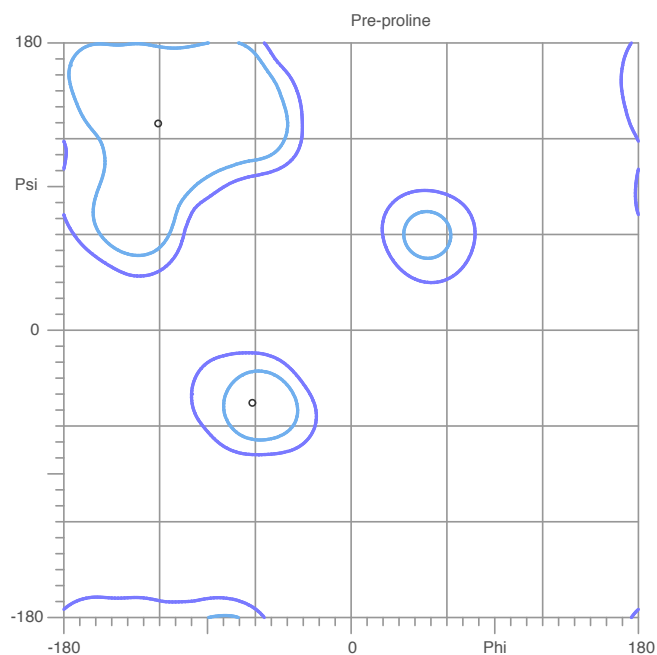
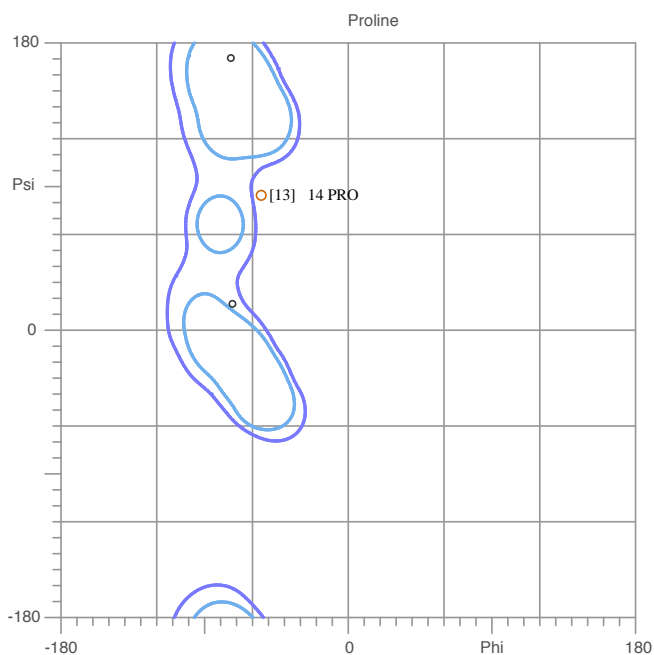
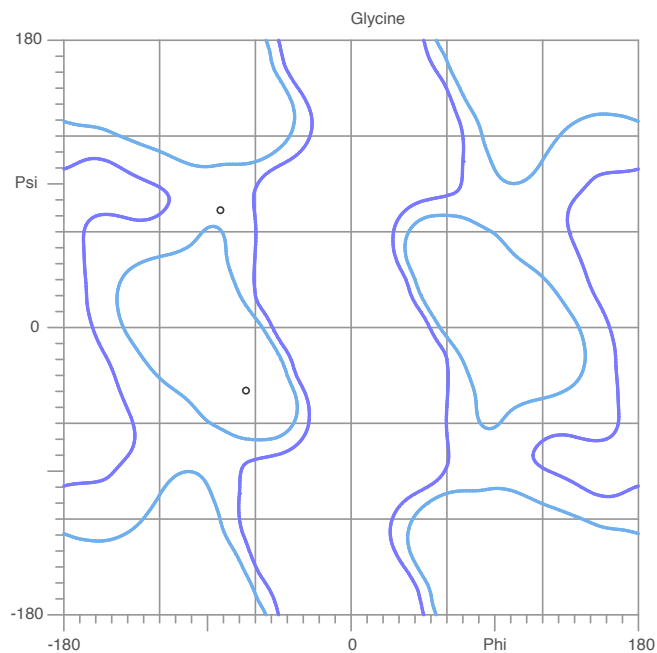
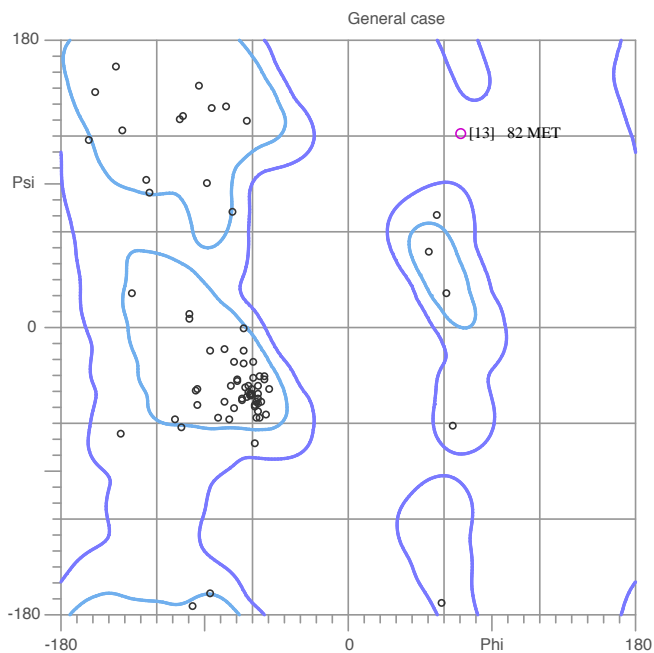
There were 2 outliers (phi, psi):

[12] 6 HIS (-169.9, 33.0)

[12] 79 THR (57.8, -80.1)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 13

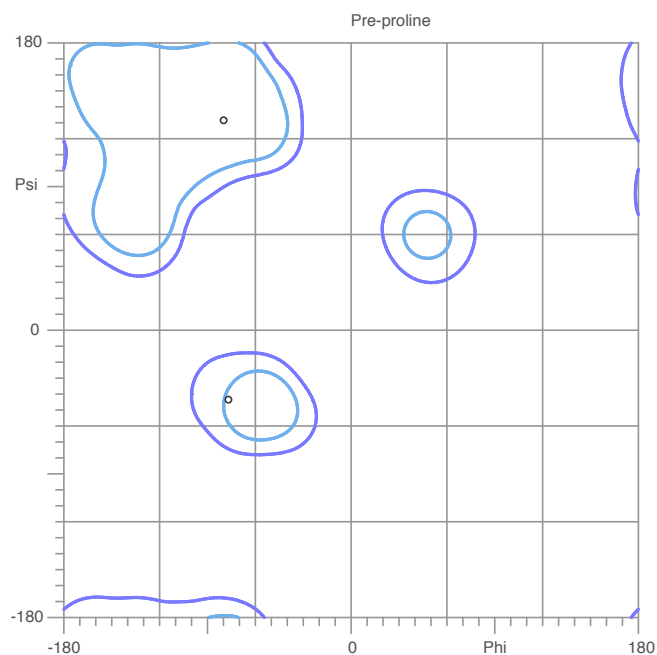
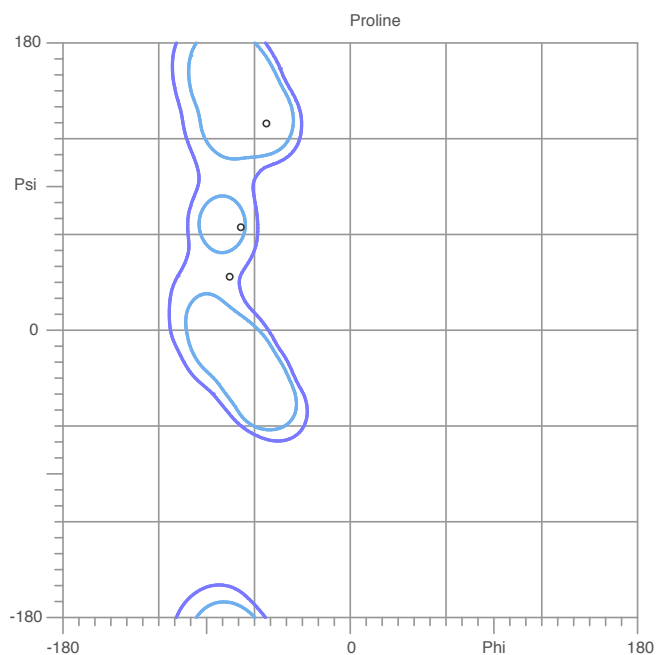
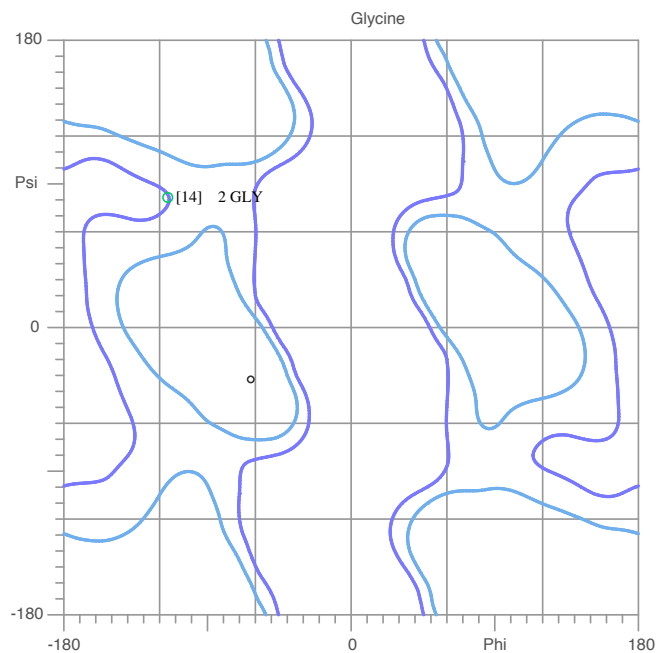
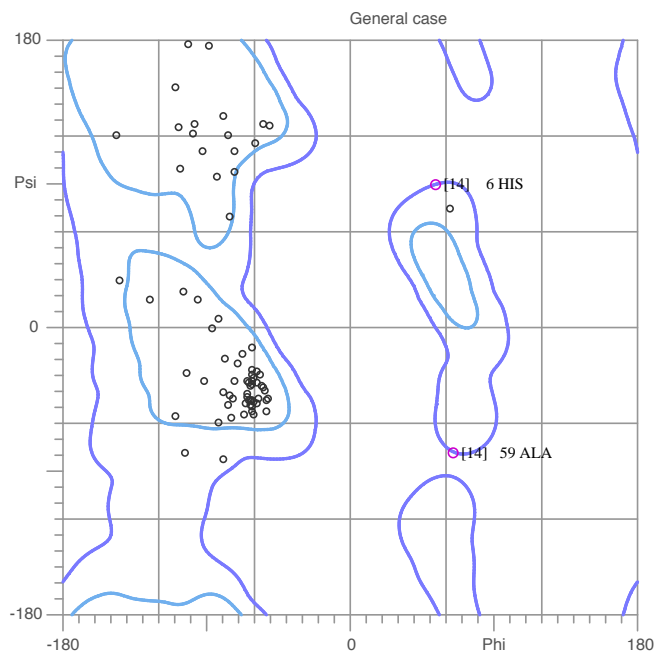


85.2% (69/81) of all residues were in favored (98%) regions.  
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[13] 14 PRO (-55.1, 85.6)  
[13] 82 MET (70.1, 122.6)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 14



90.1% (73/81) of all residues were in favored (98%) regions.  
96.3% (78/81) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

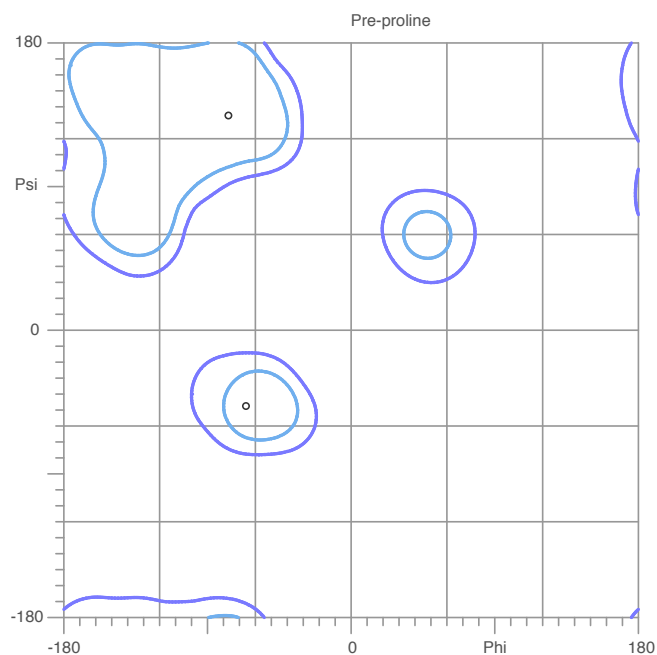
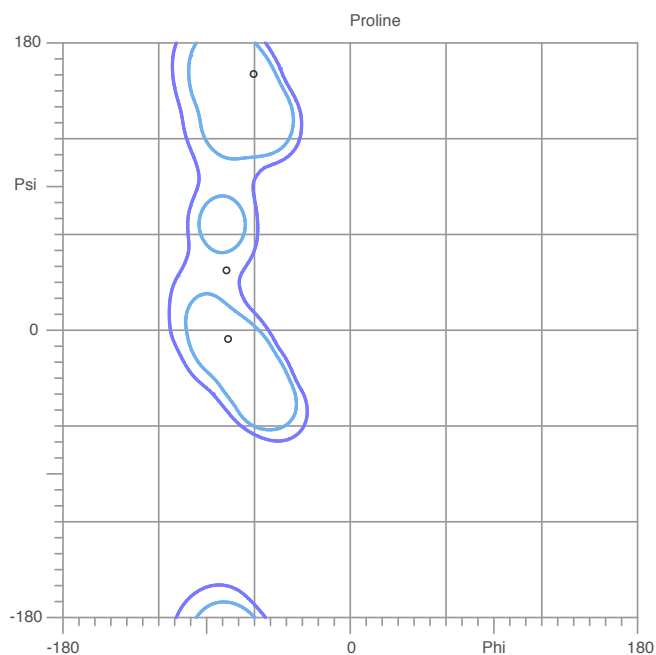
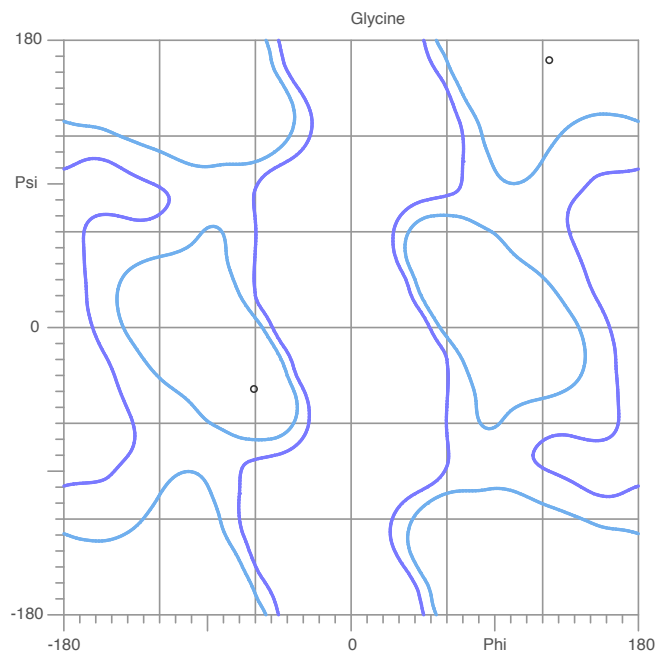
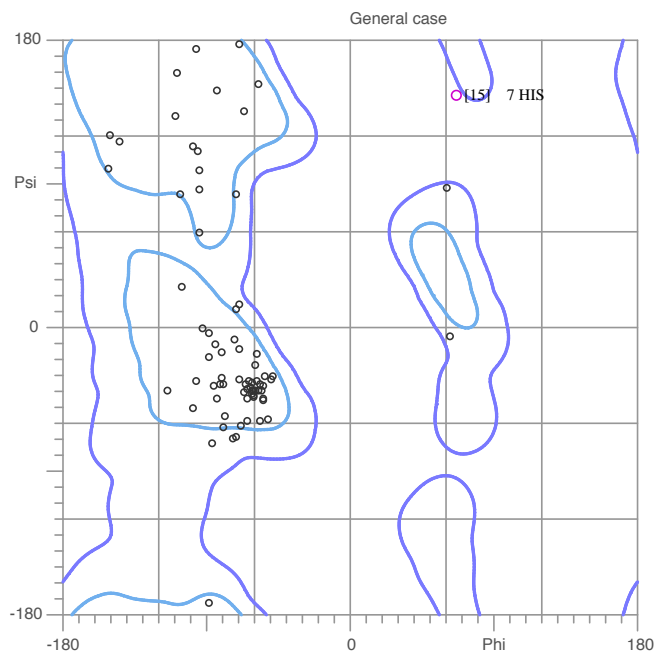
[14] 2 GLY (-115.1, 82.5)

[14] 6 HIS (53.1, 90.2)

[14] 59 ALA (64.4, -78.1)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 15



87.7% (71/81) of all residues were in favored (98%) regions.  
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

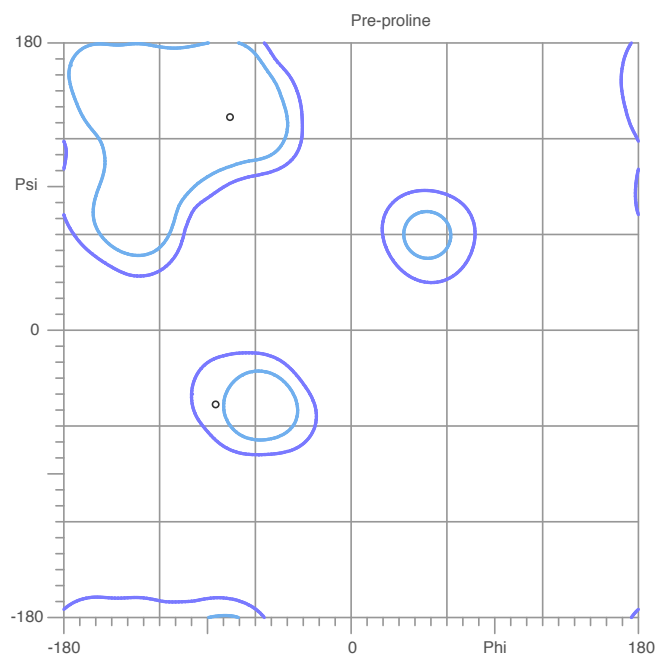
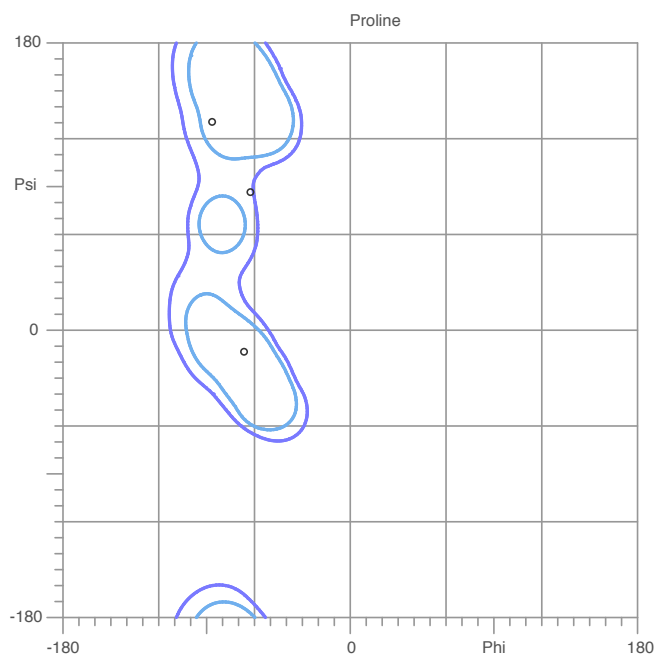
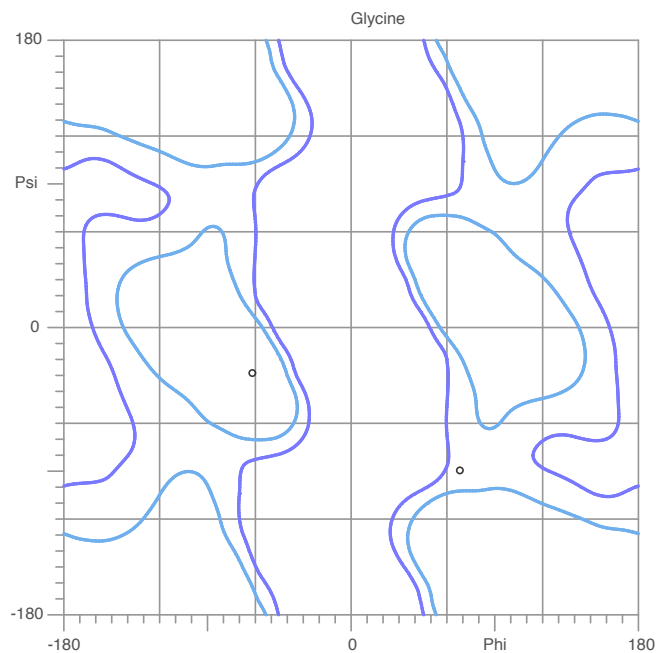
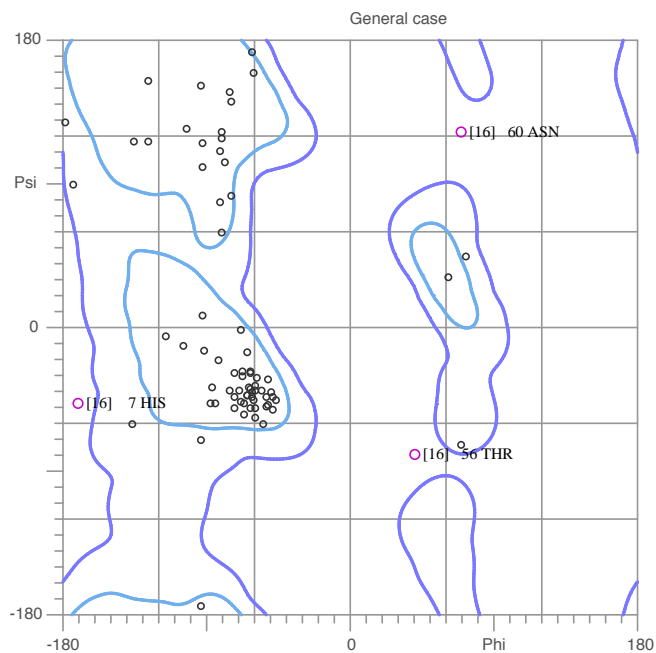
There were 1 outliers (phi, psi):  
[15] 7 HIS (66.4, 146.9)

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# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 16



84.0% (68/81) of all residues were in favored (98%) regions.  
96.3% (78/81) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

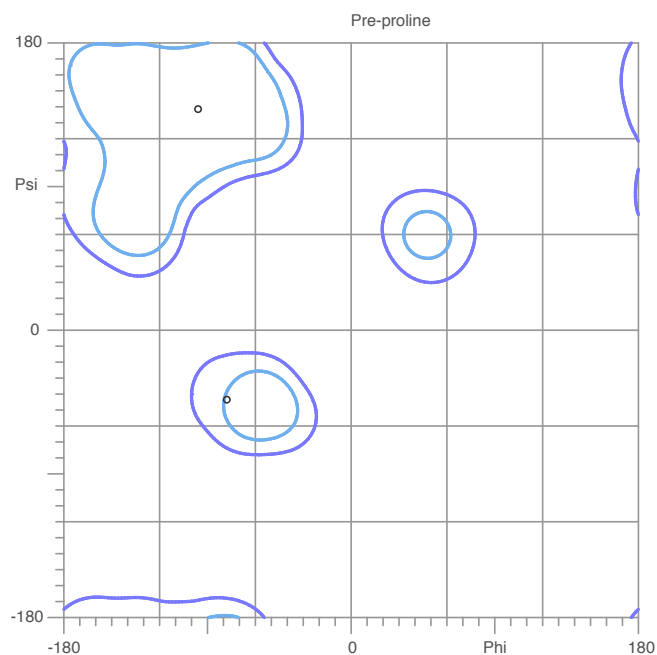
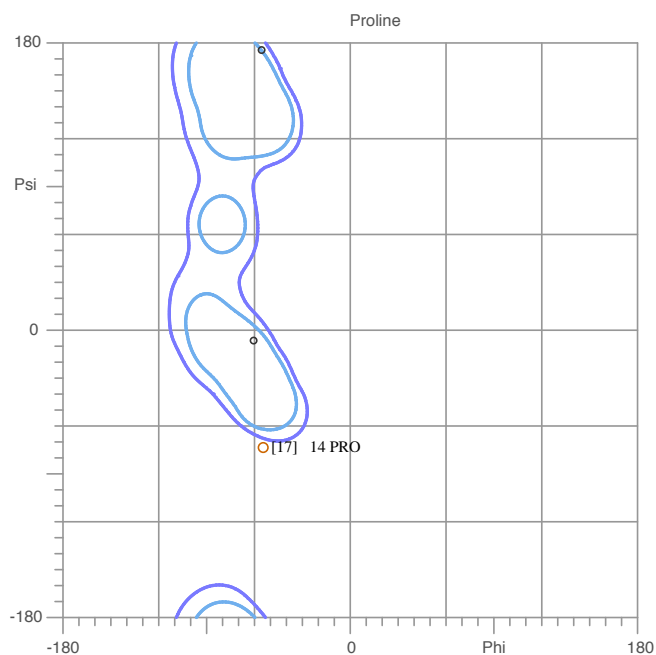
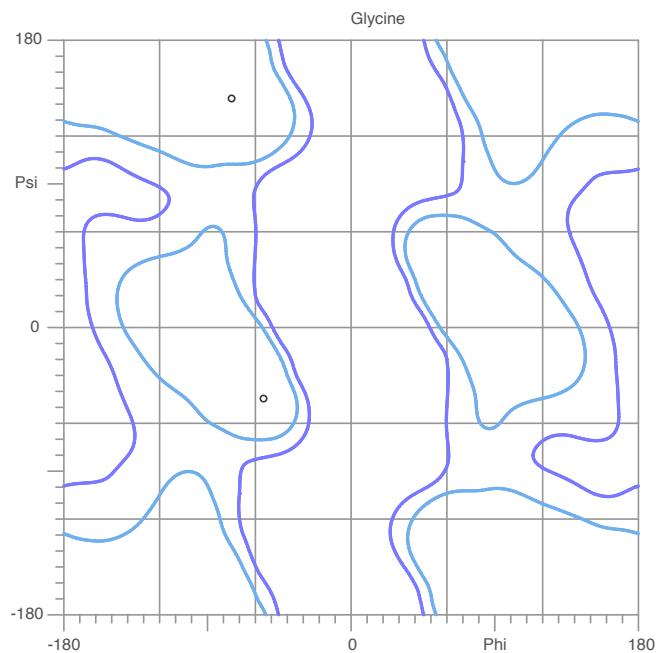
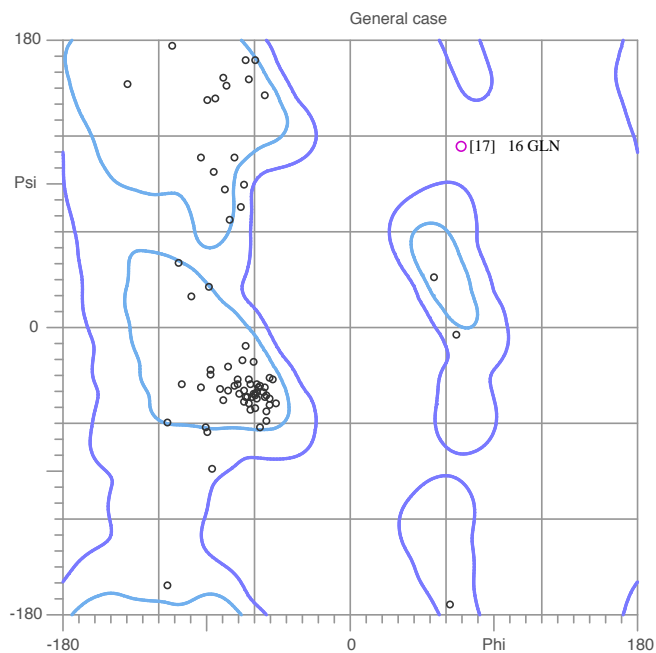
[16] 7 HIS (-171.7, -47.7)

[16] 56 THR (40.3, -79.4)

[16] 60 ASN (69.3, 123.1)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 17



87.7% (71/81) of all residues were in favored (98%) regions.  
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

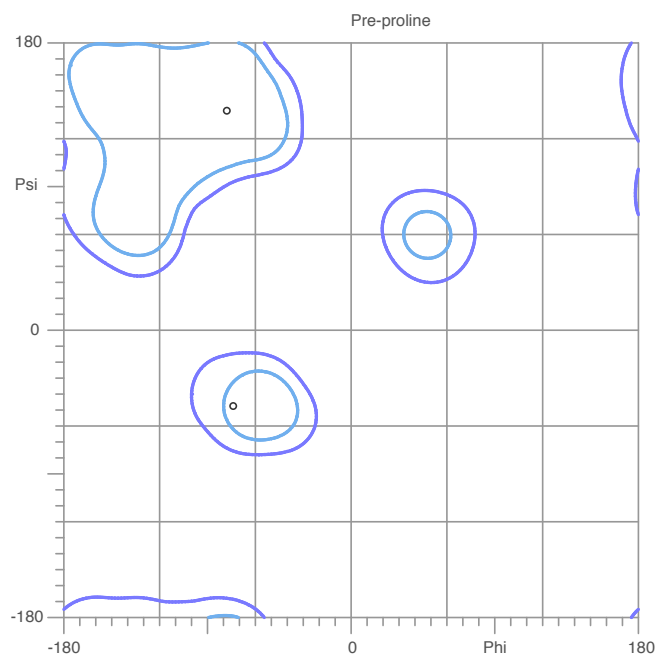
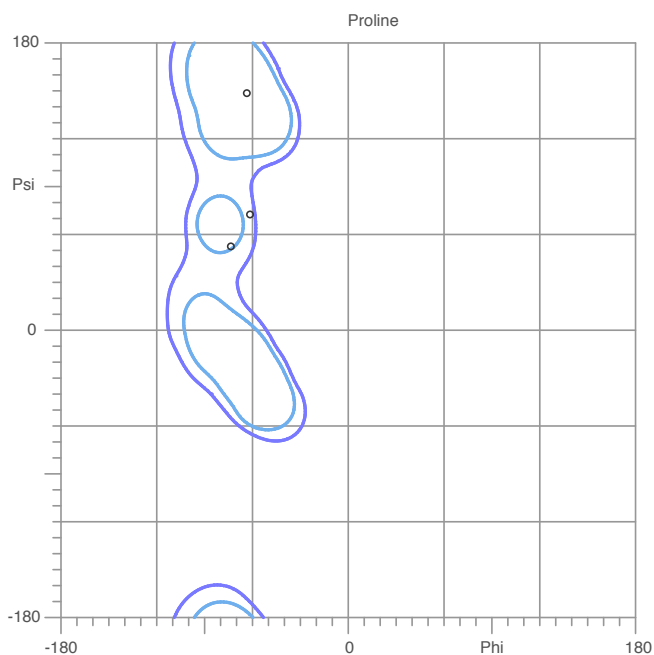
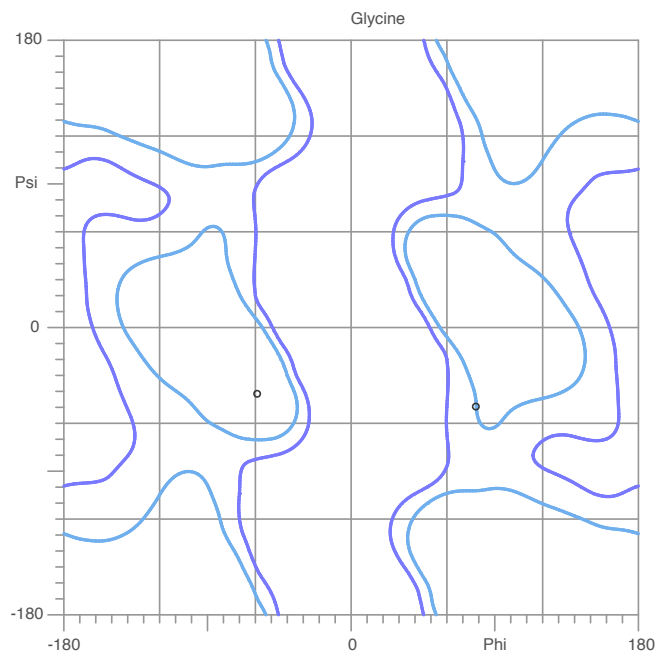
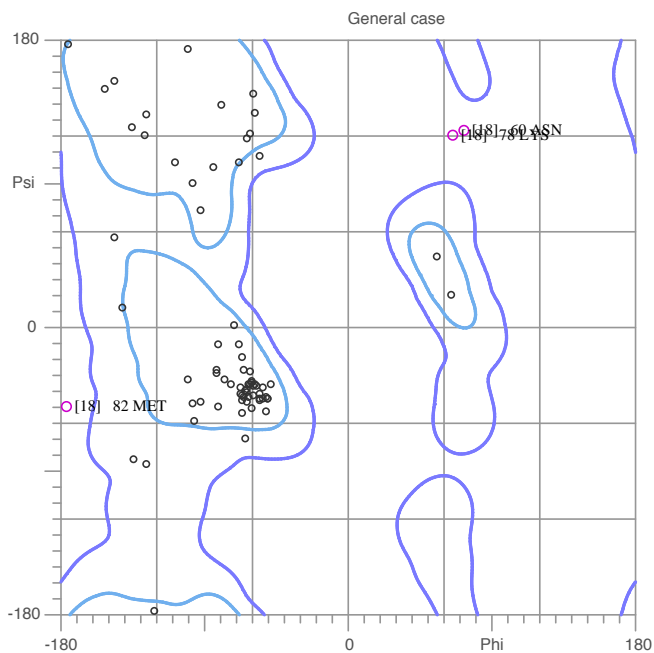
There were 2 outliers (phi, psi):

[17] 14 PRO (-55.4, -73.9)

[17] 16 GLN (69.5, 114.5)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 18



85.2% (69/81) of all residues were in favored (98%) regions.  
96.3% (78/81) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

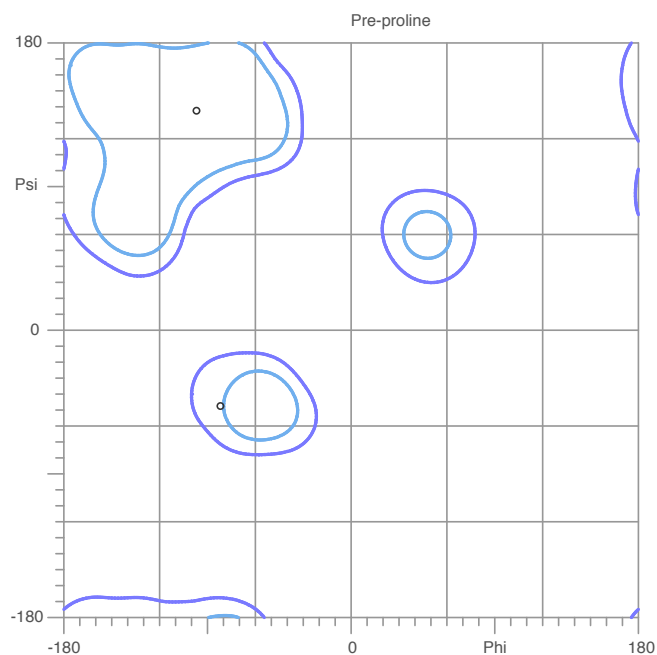
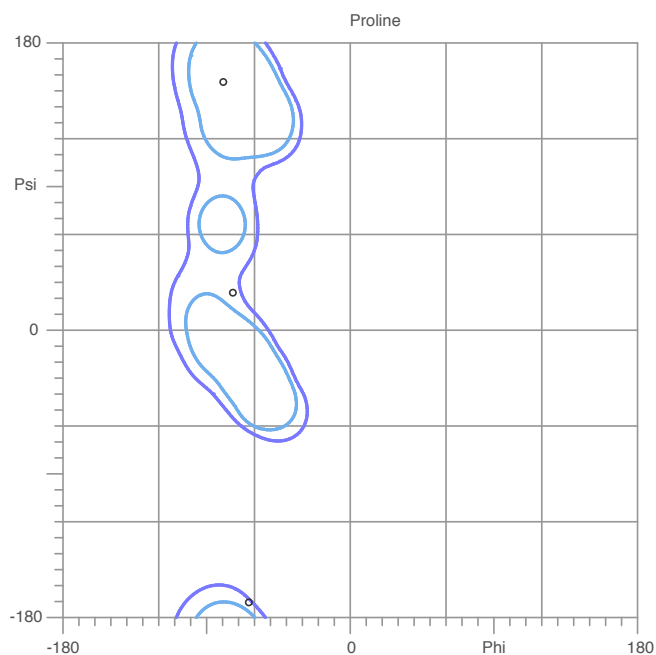
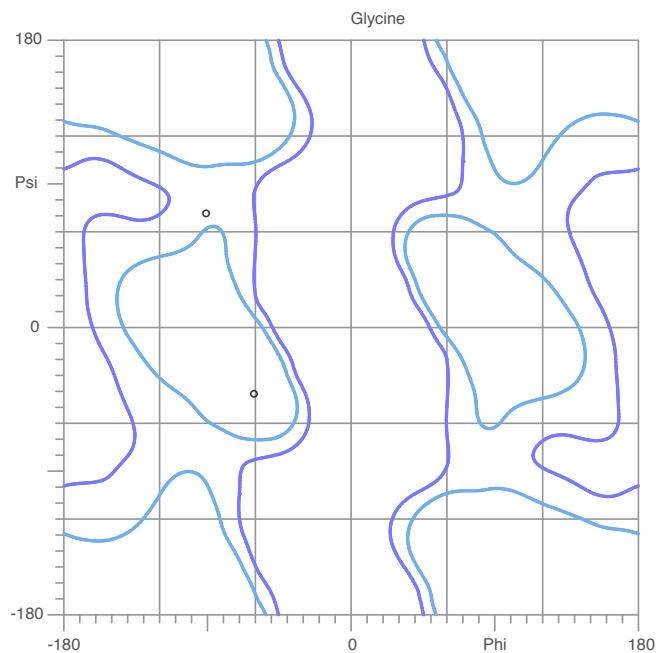
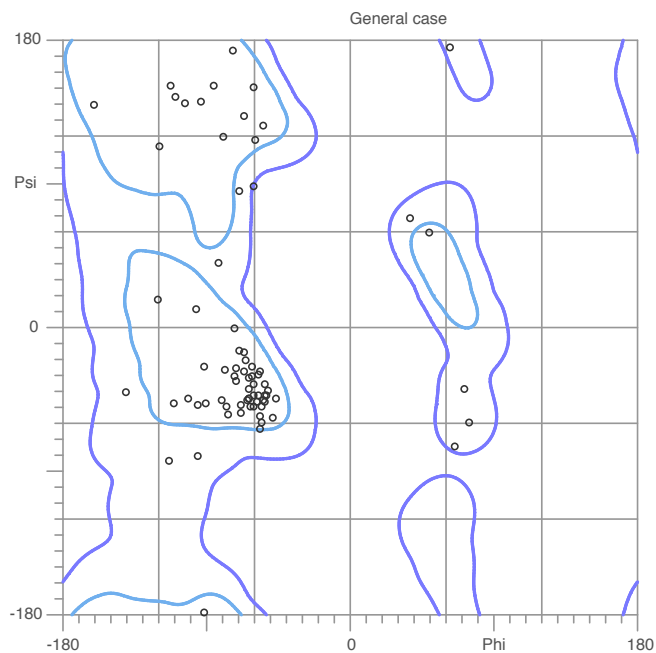
[18] 60 ASN (72.6, 124.3)

[18] 78 LYS (65.9, 121.8)

[18] 82 MET (-177.6, -49.1)

# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 19



81.5% (66/81) of all residues were in favored (98%) regions.  
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

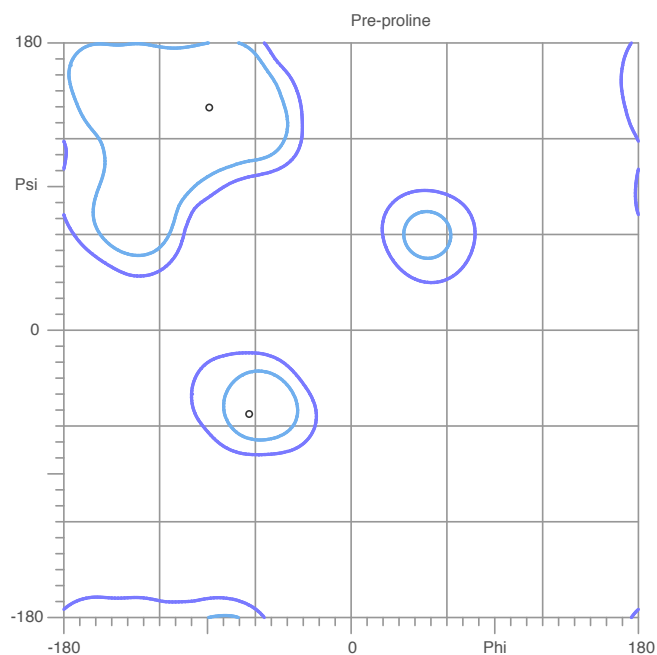
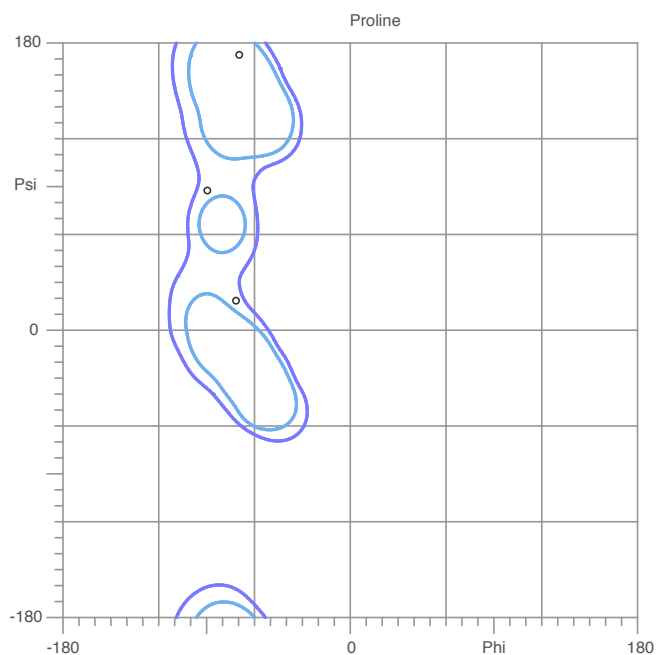
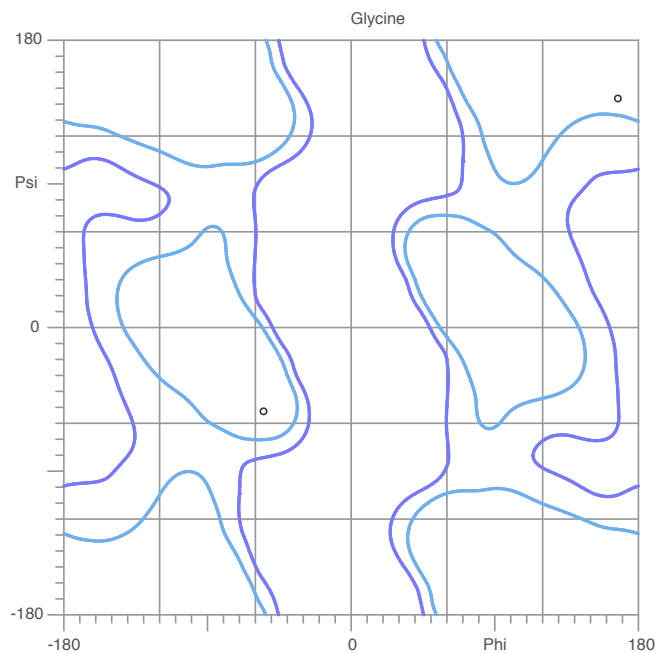
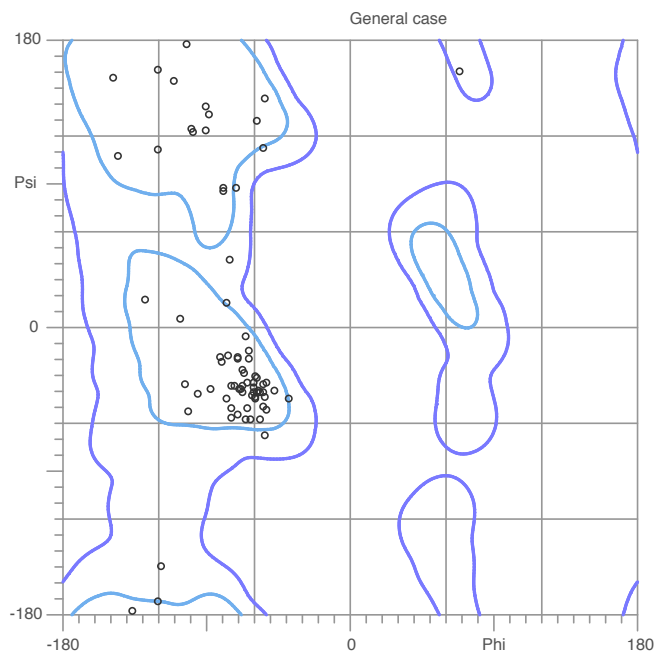
There were no outliers.

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# MolProbity Ramachandran analysis

HR4435B\_NMR\_em\_bcr3.pdb, model 20



88.9% (72/81) of all residues were in favored (98%) regions.  
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

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