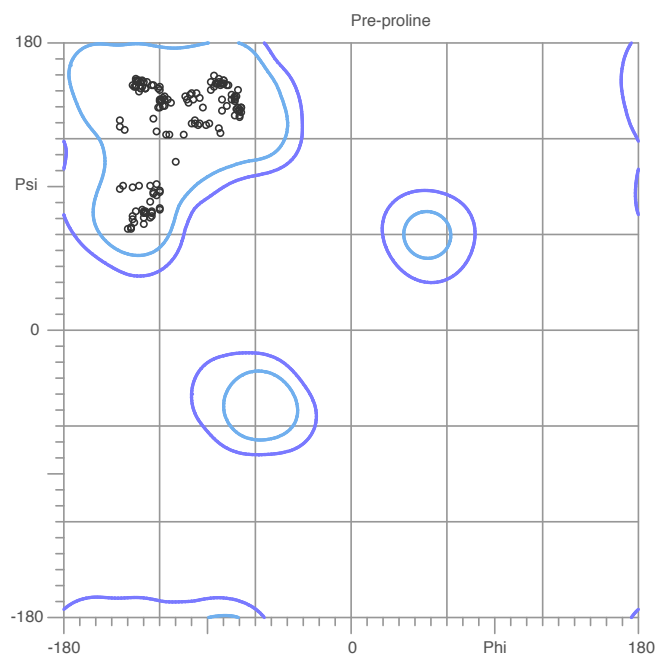
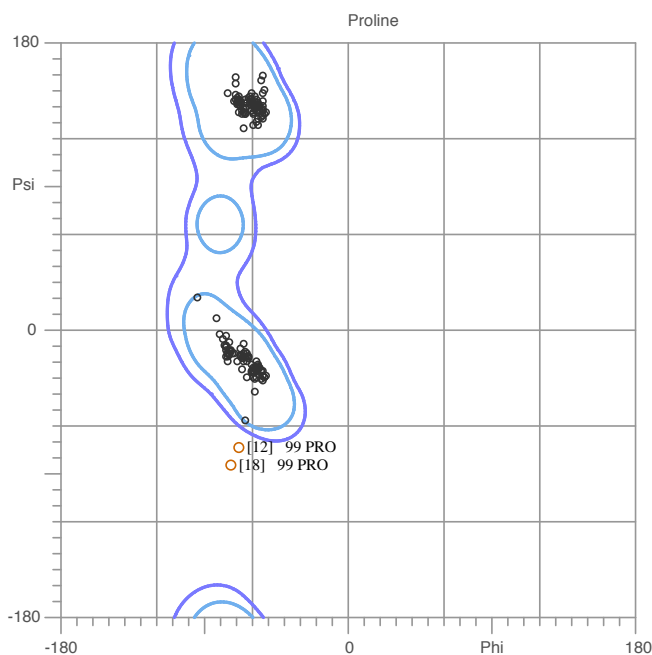
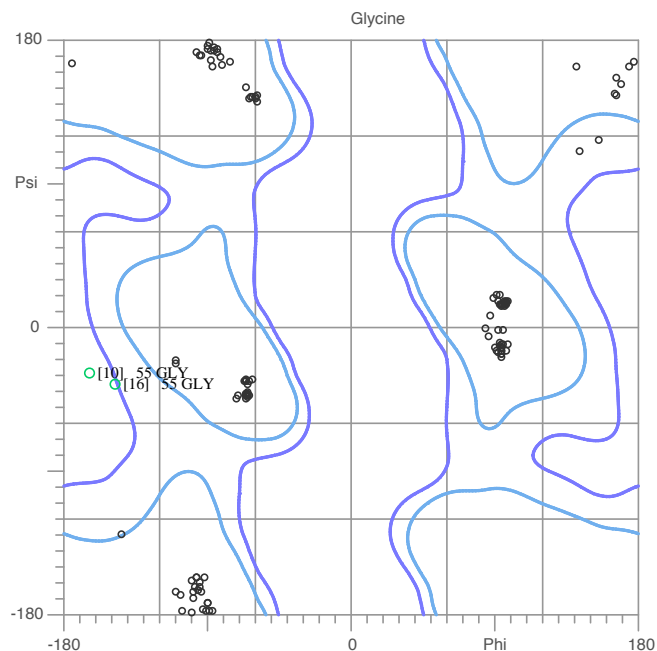
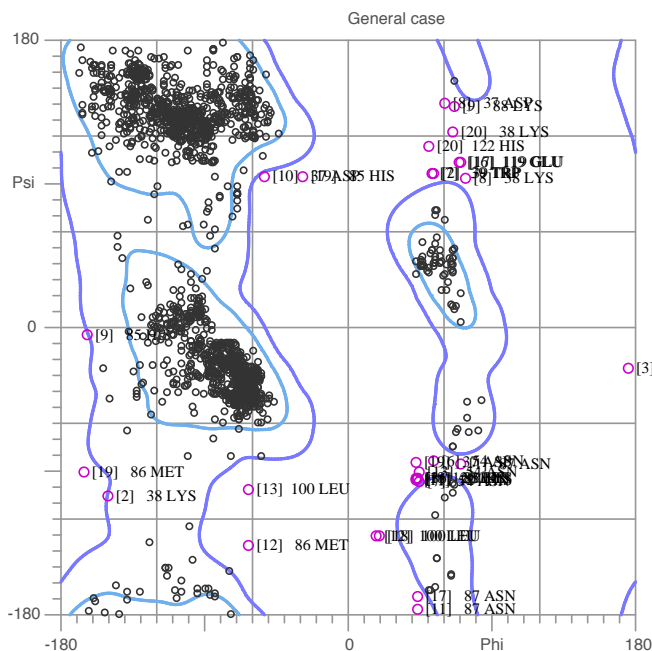


# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, all models



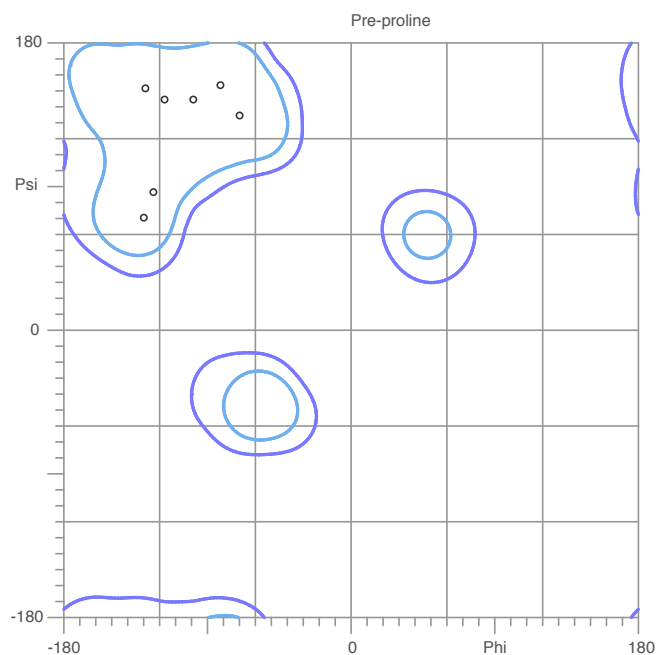
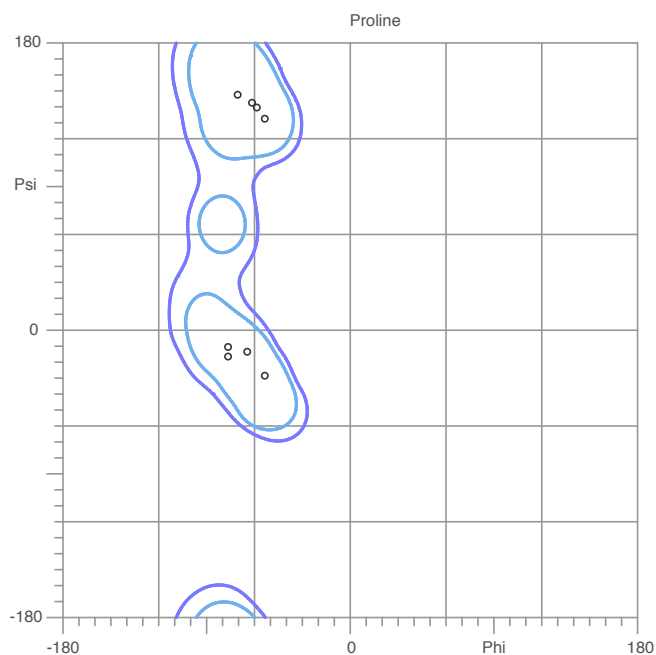
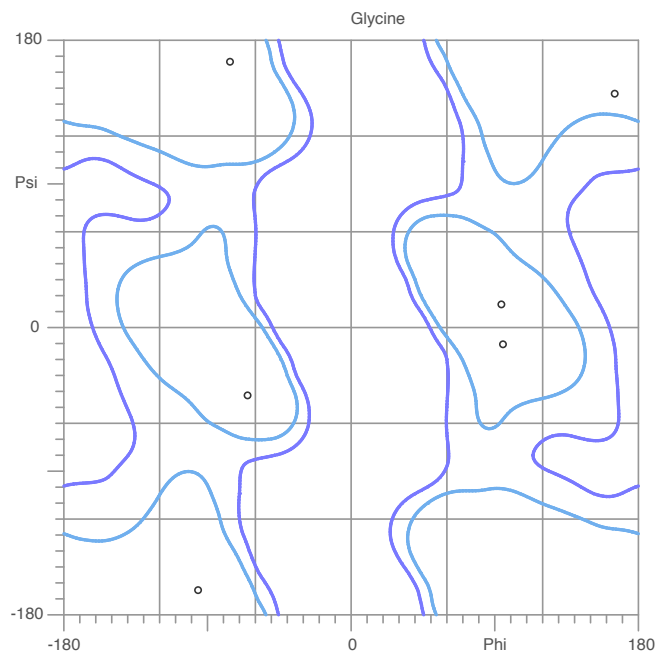
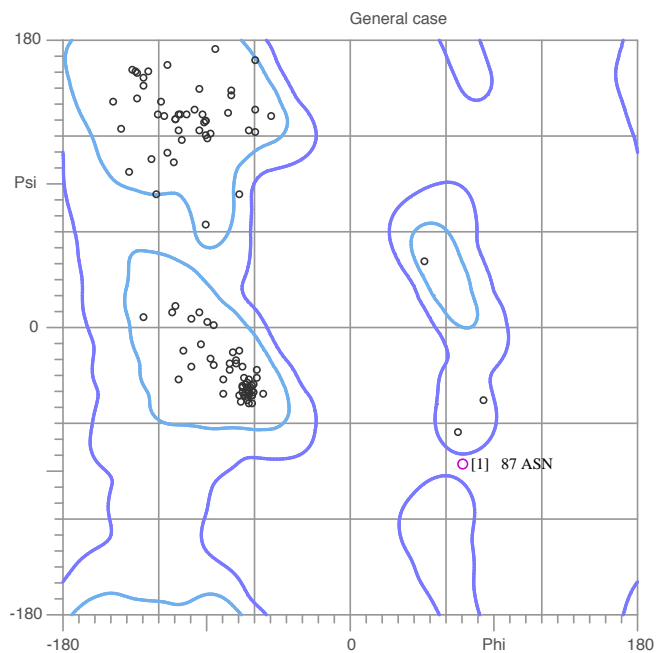
95.0% (2338/2460) of all residues were in favored (98%) regions.  
98.6% (2426/2460) of all residues were in allowed (>99.8%) regions.

There were 34 outliers (phi, psi):

- |                             |                              |
|-----------------------------|------------------------------|
| [1] 87 ASN (70.2, -85.7)    | [11] 124 HIS (42.9, -95.1)   |
| [2] 38 LYS (-151.6, -105.0) | [12] 86 MET (-63.5, -136.9)  |
| [3] 89 GLU (175.0, -25.3)   | [12] 99 PRO (-69.3, -73.6)   |
| [6] 54 ASN (53.3, -83.6)    | [12] 100 LEU (17.6, -130.7)  |
| [7] 54 ASN (44.1, -96.8)    | [13] 54 ASN (45.0, -90.7)    |
| [8] 37 ASP (60.8, 141.1)    | [13] 100 LEU (-63.5, -101.2) |
| [8] 38 LYS (73.7, 95.0)     | [16] 55 GLY (-148.5, -35.0)  |
| [9] 85 HIS (-164.9, -5.0)   | [16] 85 HIS (43.4, -95.0)    |
| [9] 88 LYS (66.6, 139.0)    | [16] 119 GLU (69.3, 104.9)   |
| [10] 37 ASP (-53.7, 95.3)   | [17] 87 ASN (43.8, -168.3)   |
| [10] 55 GLY (-164.7, -29.0) | [17] 119 GLU (70.0, 105.0)   |
| [11] 87 ASN (43.9, -176.4)  | [18] 88 LYS (42.8, -95.0)    |
|                             | [18] 99 PRO (-74.2, -85.0)   |
|                             | [18] 100 LEU (19.9, -130.7)  |
|                             | [19] 37 ASP (42.4, -84.9)    |
|                             | [19] 85 HIS (-29.7, 95.0)    |
|                             | [19] 86 MET (-166.8, -90.5)  |
|                             | [20] 38 LYS (65.0, 123.3)    |
|                             | [20] 122 HIS (51.0, 114.8)   |

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 1

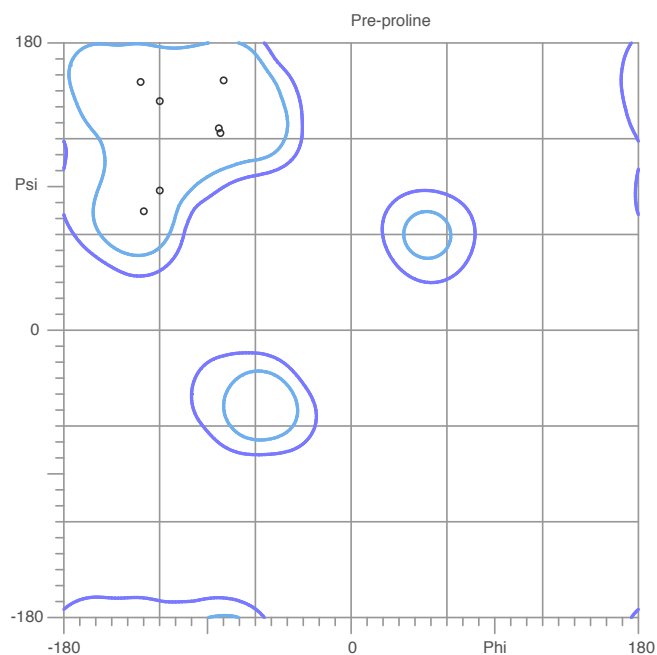
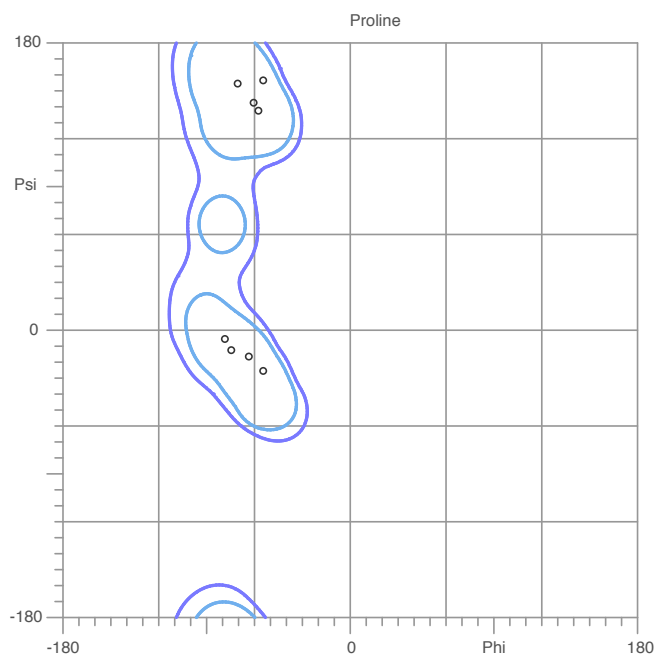
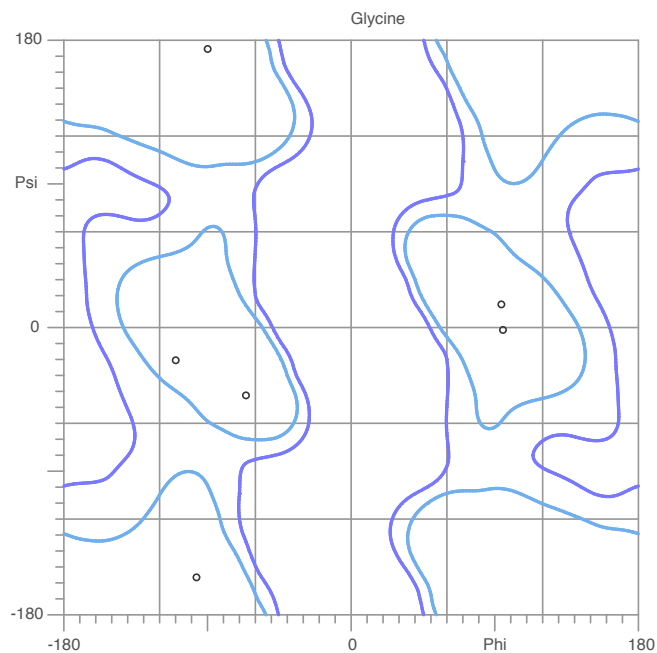
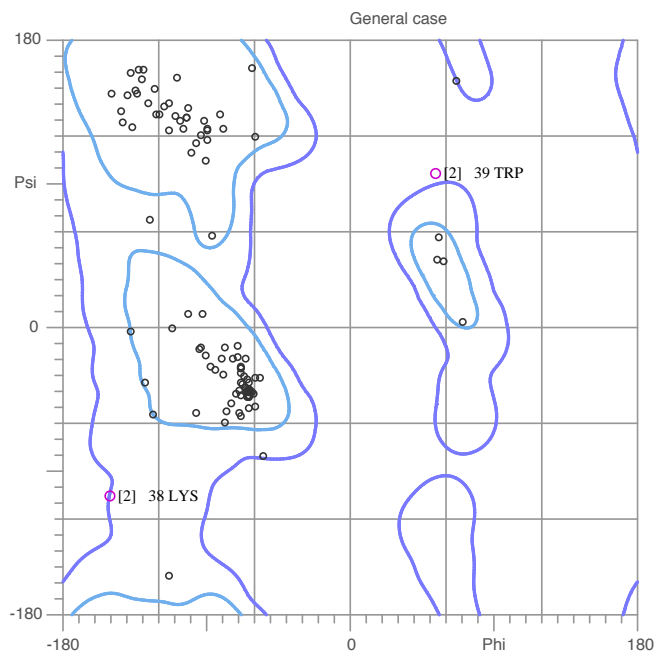


96.7% (119/123) of all residues were in favored (98%) regions.  
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[1] 87 ASN (70.2, -85.7)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 2

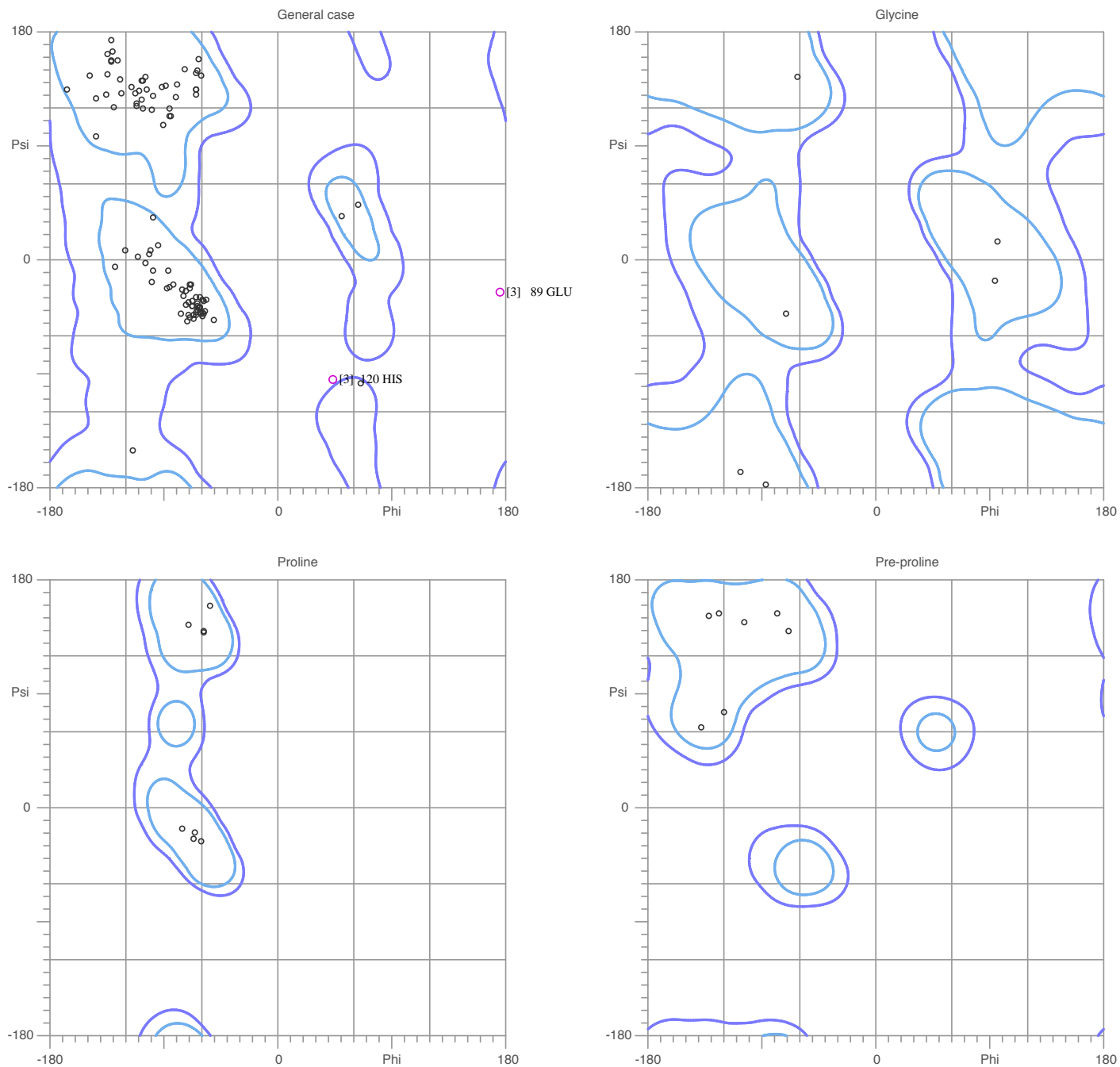


93.5% (115/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[2] 38 LYS (-151.6, -105.0)  
[2] 39 TRP (53.5, 97.5)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 3



96.7% (119/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

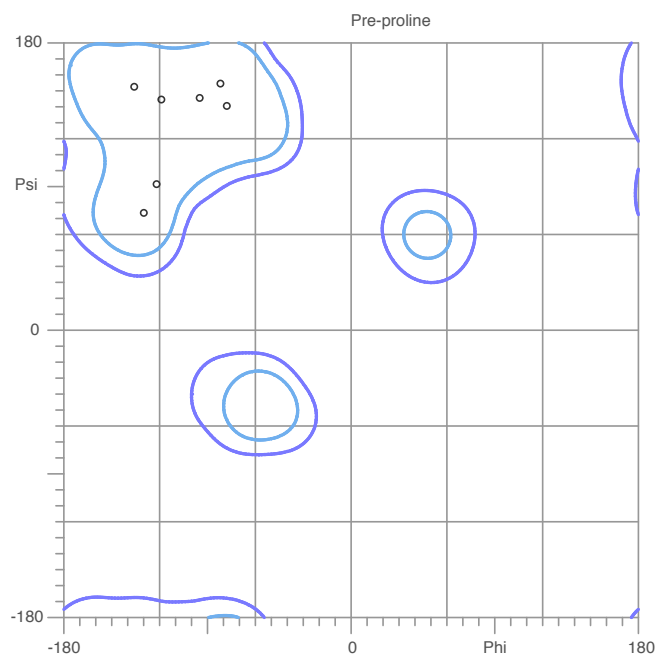
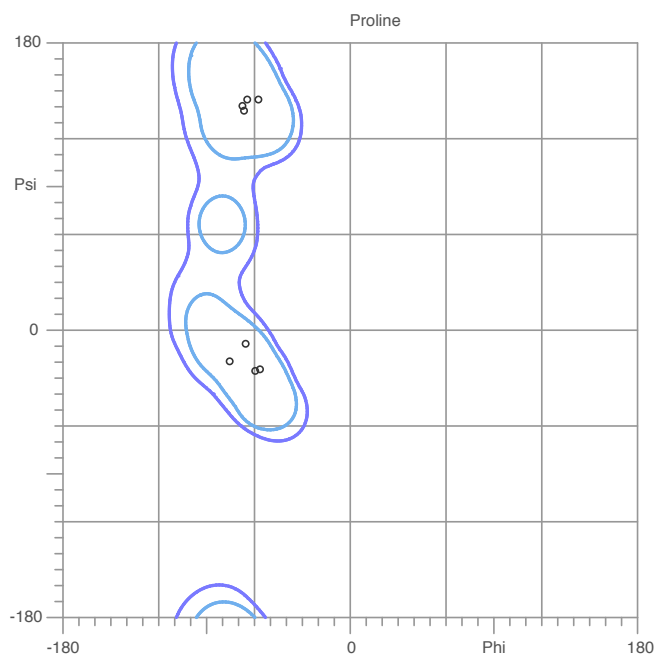
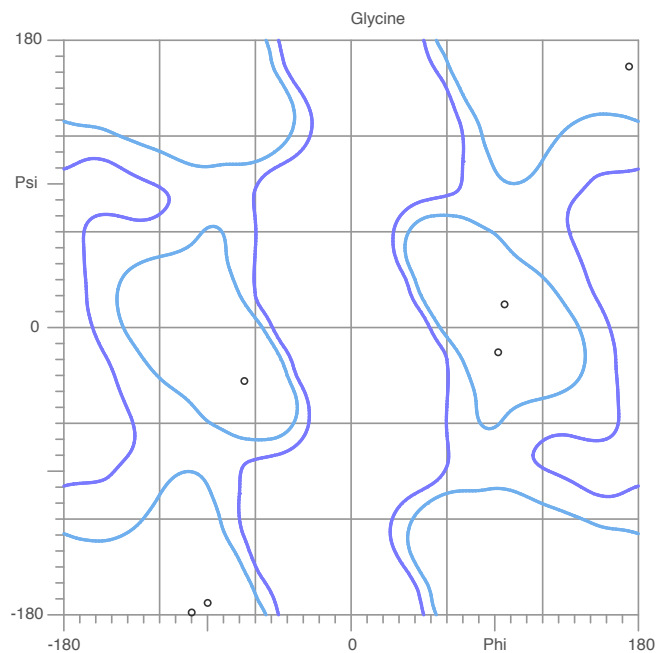
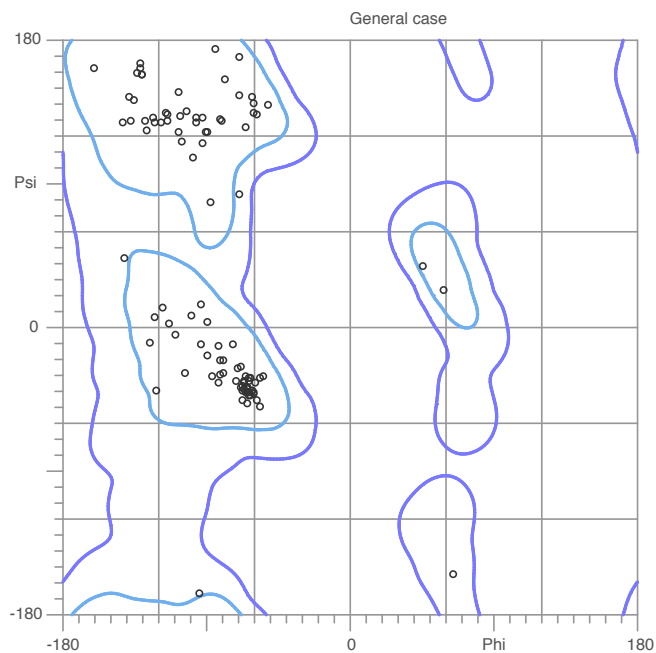
There were 2 outliers (phi, psi):

[3] 89 GLU (175.0, -25.3)

[3] 120 HIS (43.4, -95.0)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 4



96.7% (119/123) of all residues were in favored (98%) regions.  
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

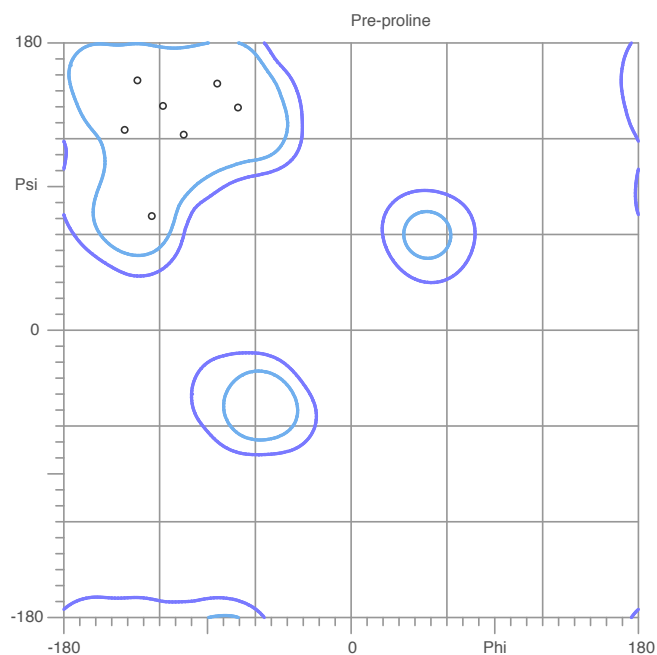
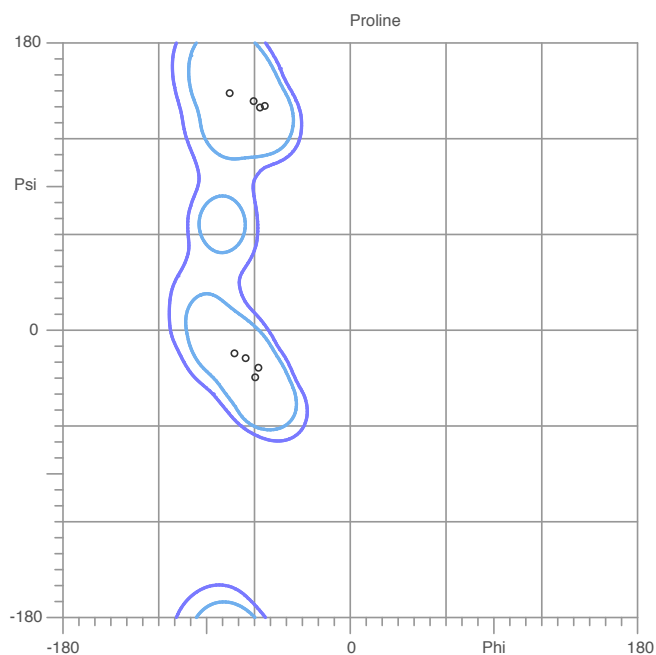
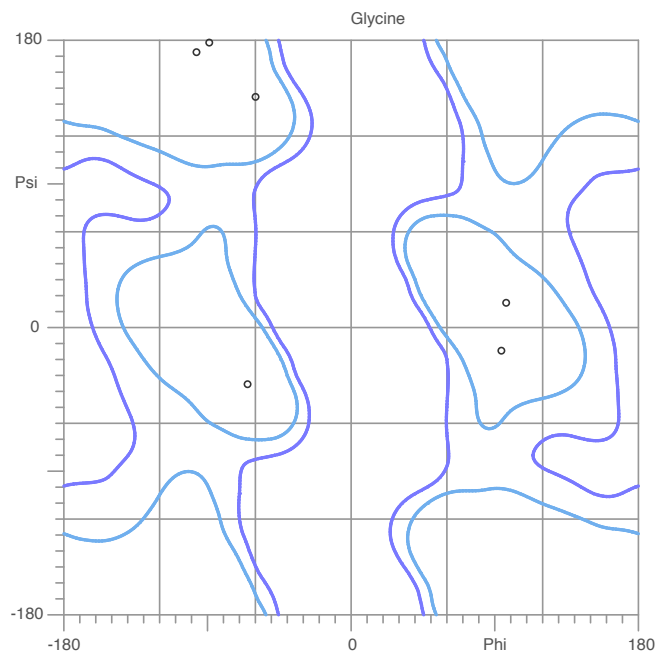
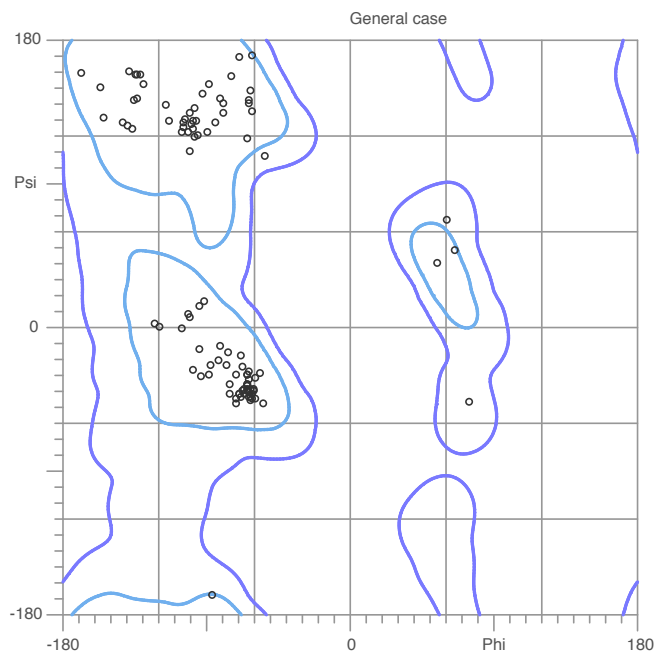
There were no outliers.

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

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

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 5



97.6% (120/123) of all residues were in favored (98%) regions.  
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

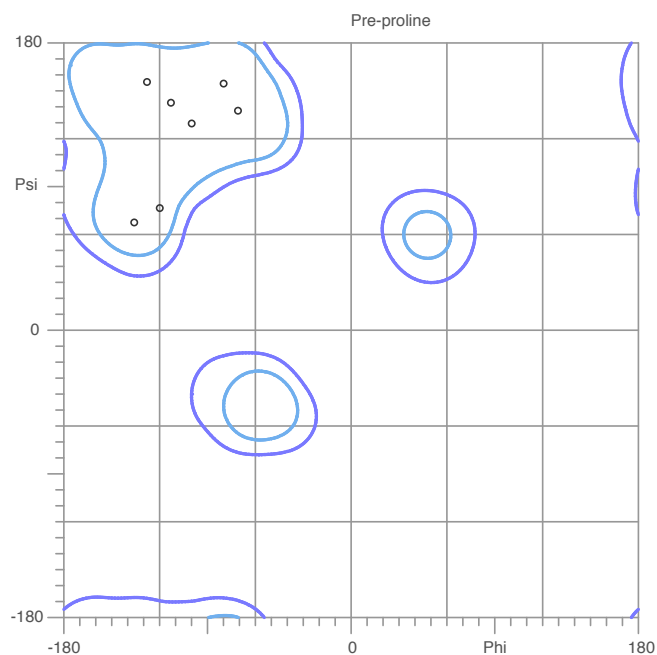
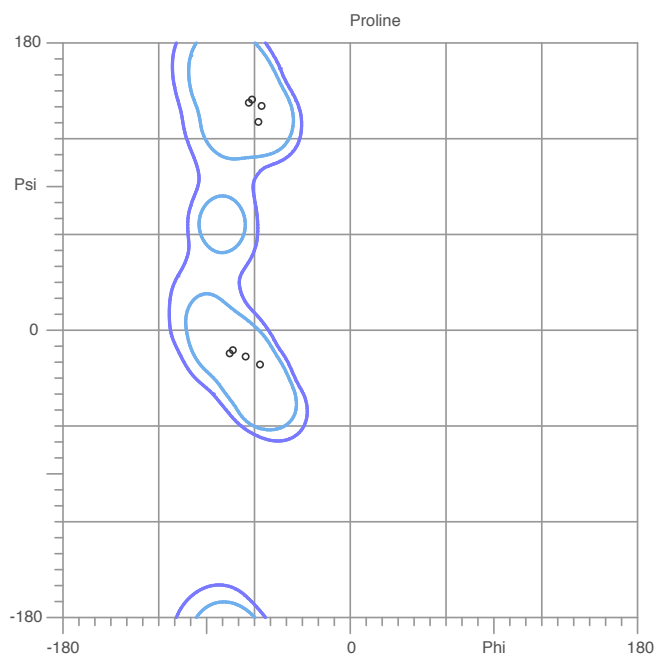
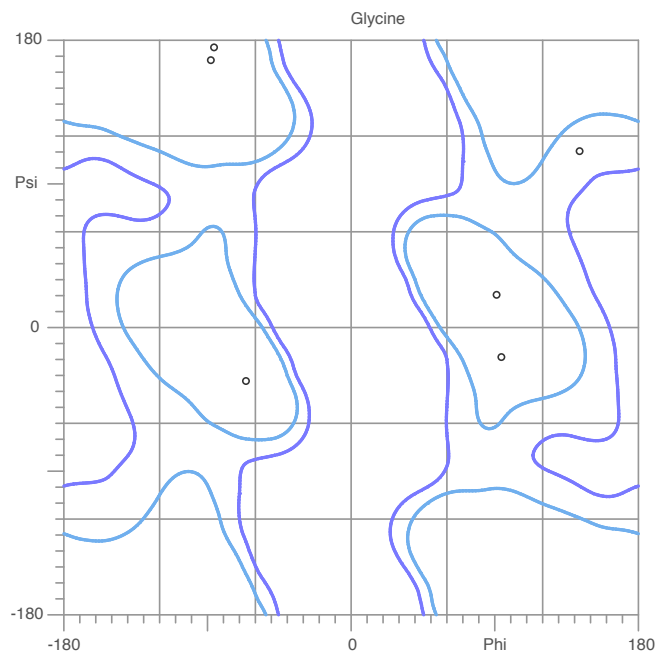
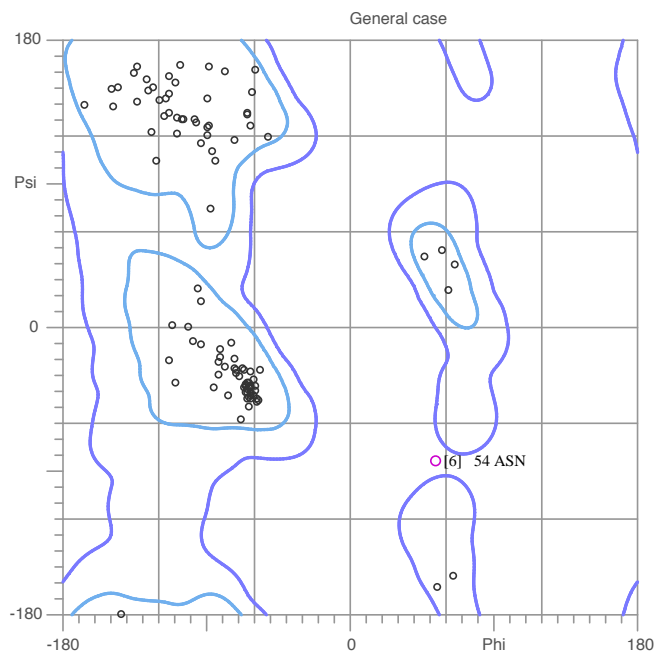
There were no outliers.

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

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

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 6



96.7% (119/123) of all residues were in favored (98%) regions.  
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

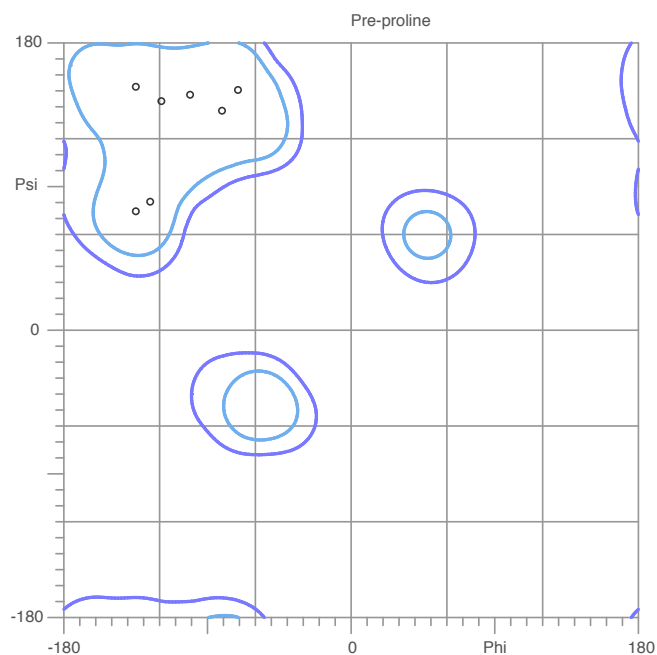
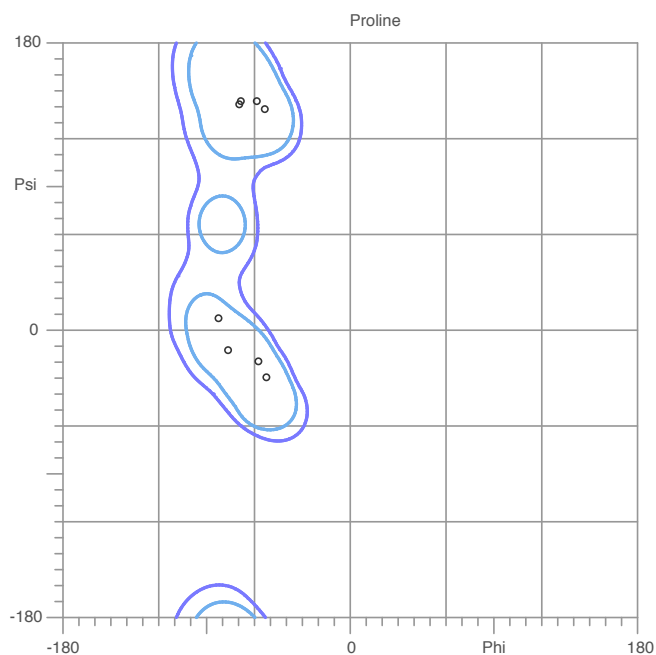
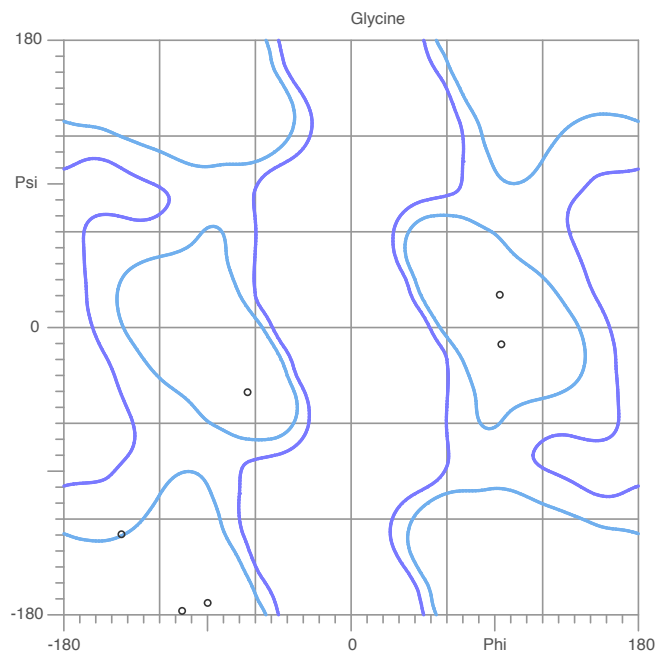
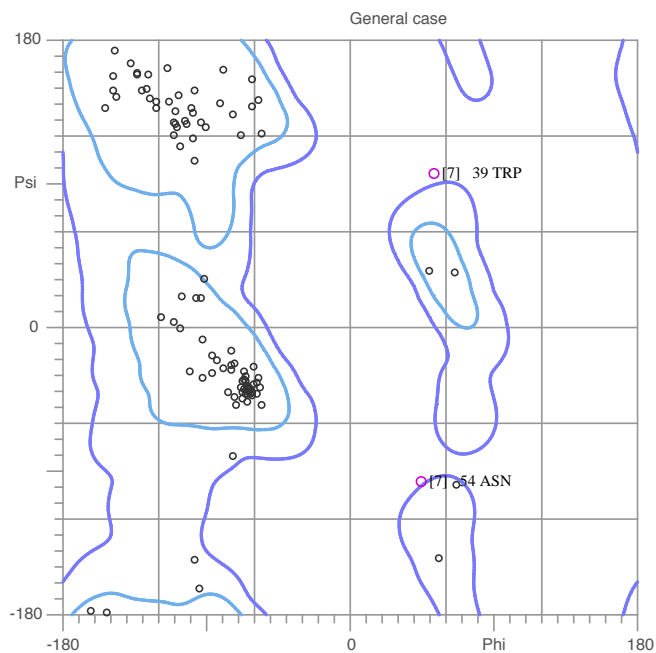
There were 1 outliers (phi, psi):  
[6] 54 ASN (53.3, -83.6)

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

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

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 7



92.7% (114/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

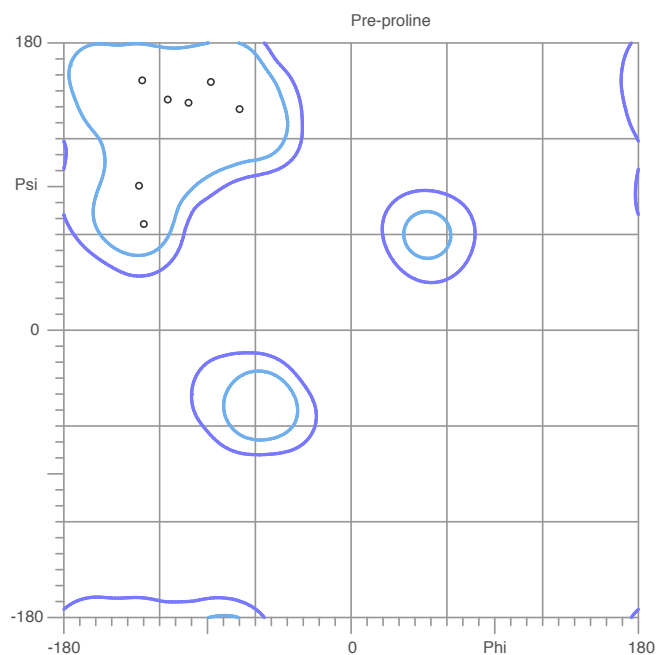
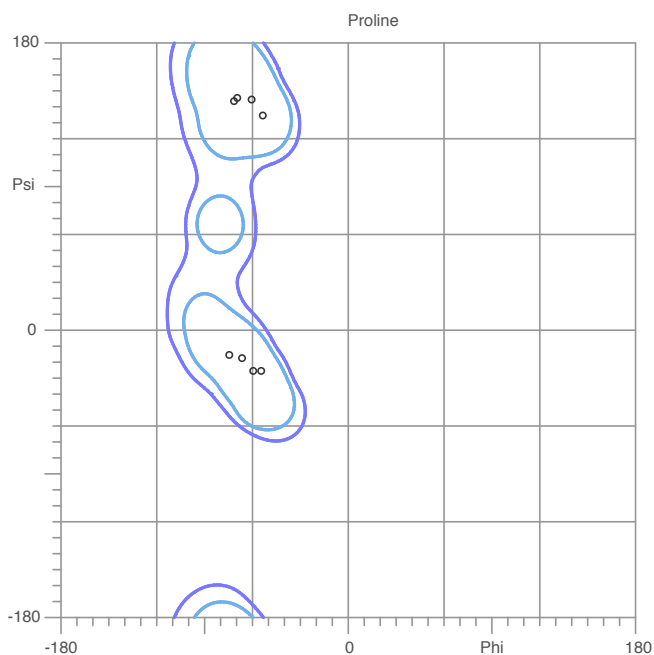
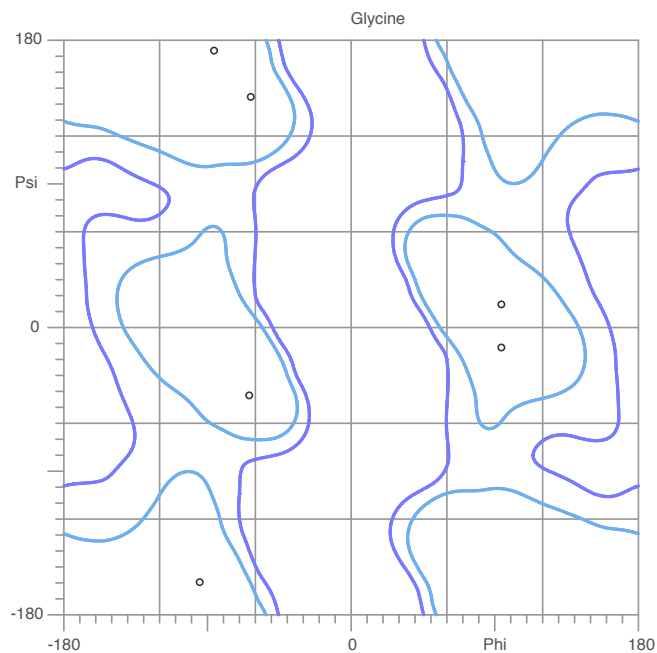
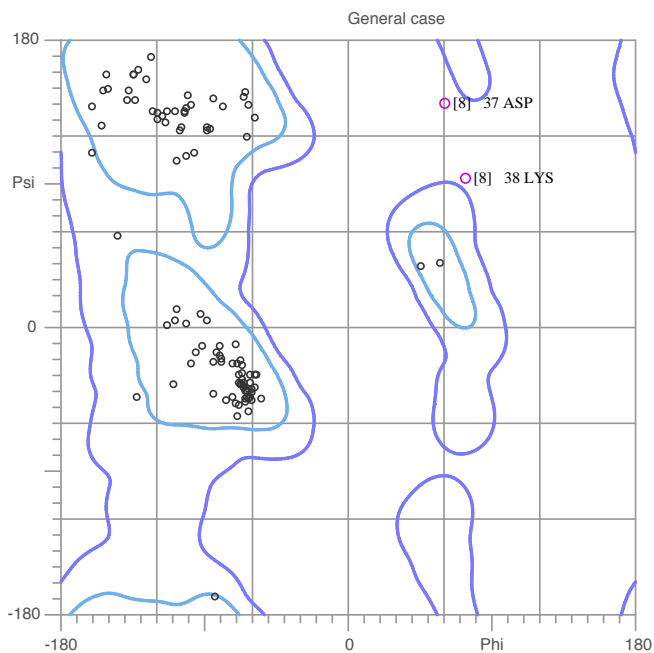
There were 2 outliers (phi, psi):

[7] 39 TRP (52.8, 97.3)

[7] 54 ASN (44.1, -96.8)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 8



95.9% (118/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

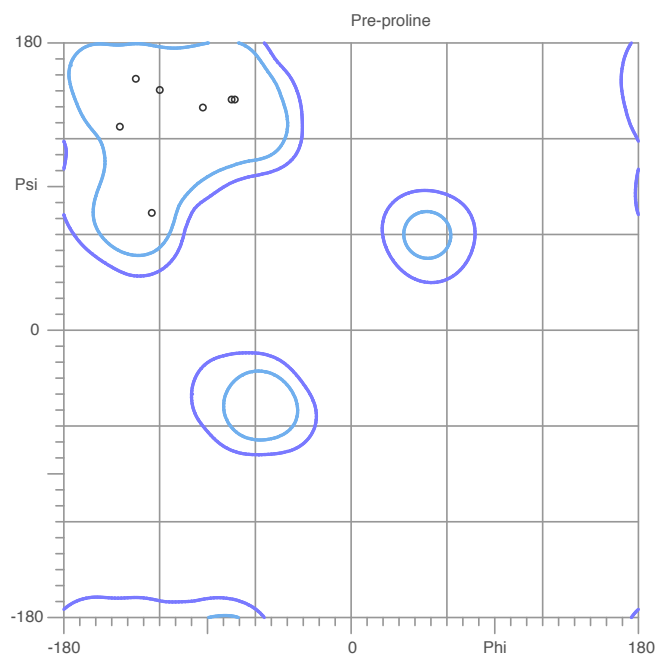
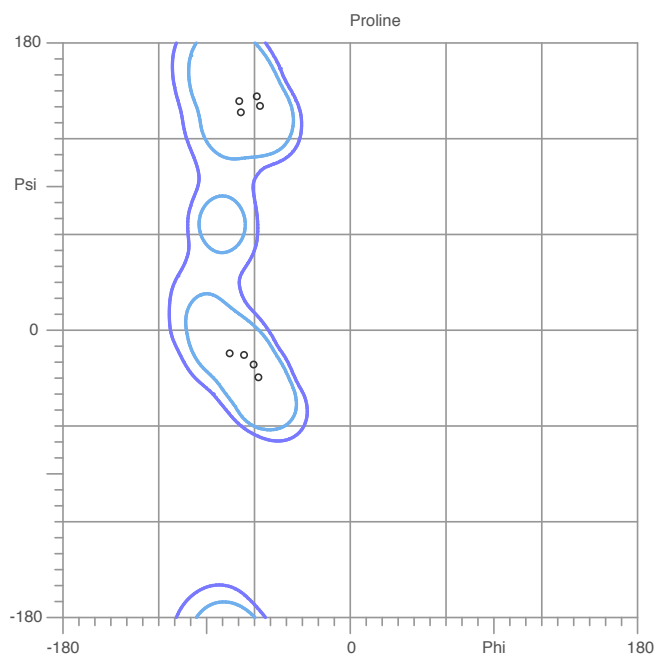
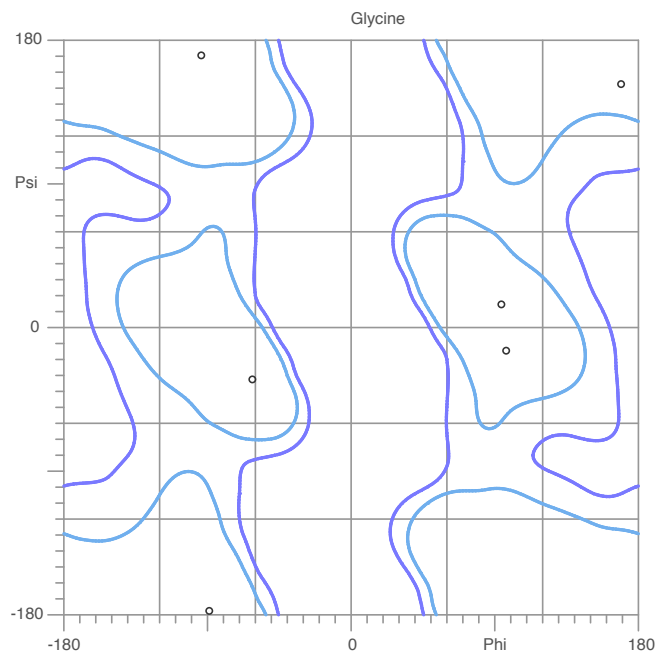
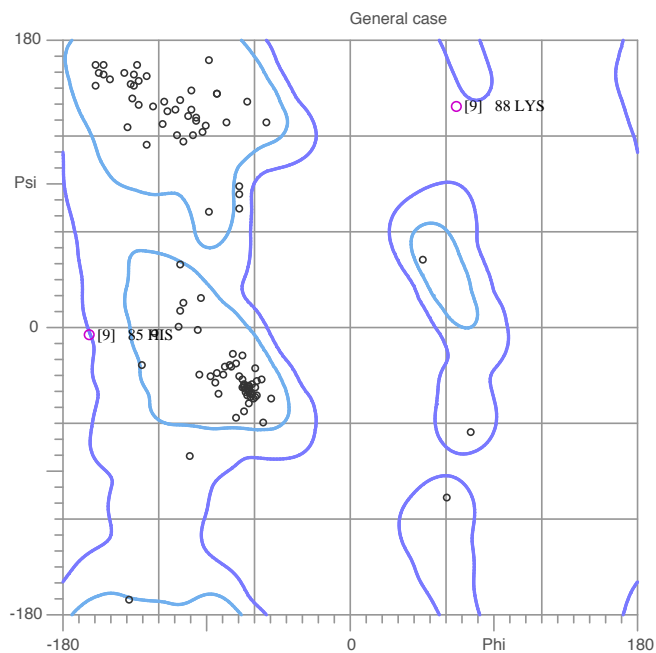
There were 2 outliers (phi, psi):

[8] 37 ASP (60.8, 141.1)

[8] 38 LYS (73.7, 95.0)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 9



93.5% (115/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

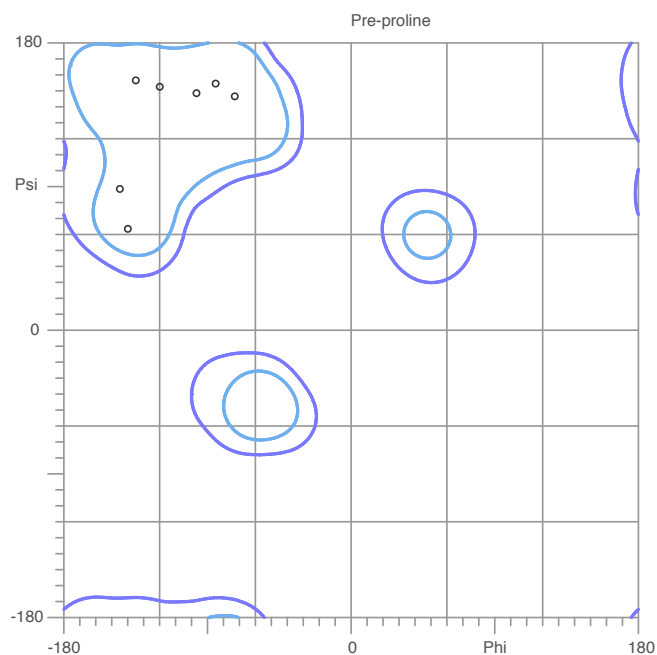
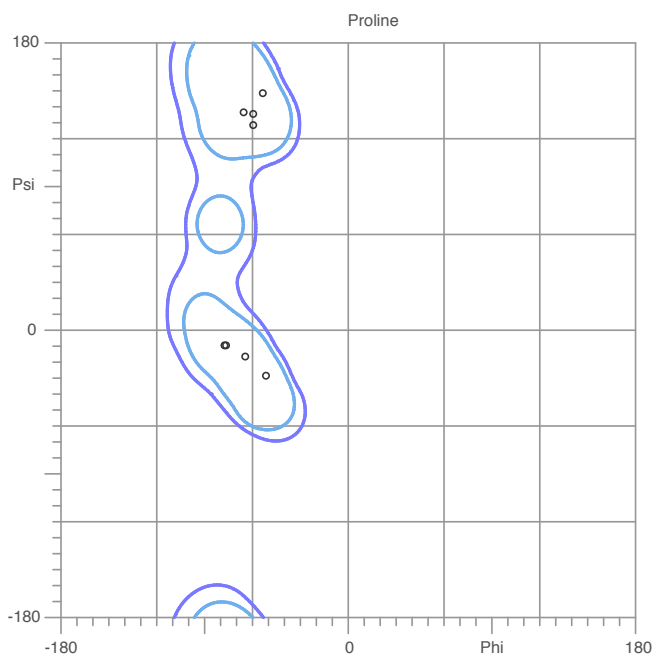
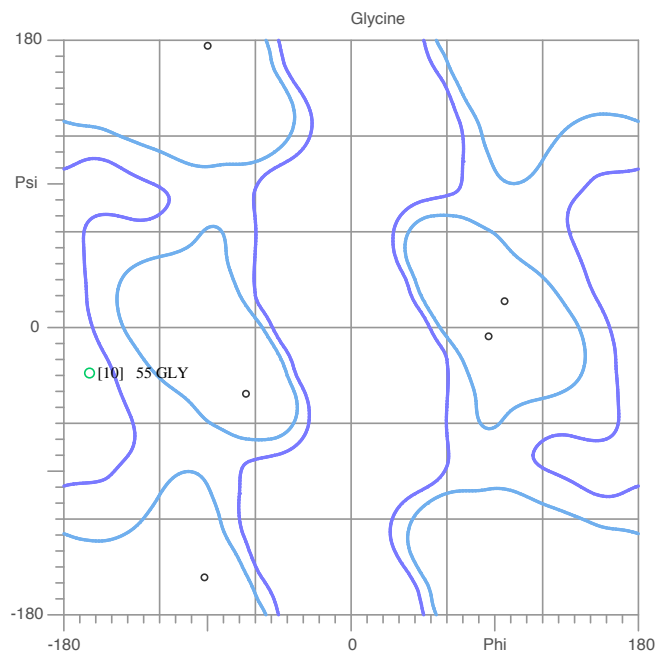
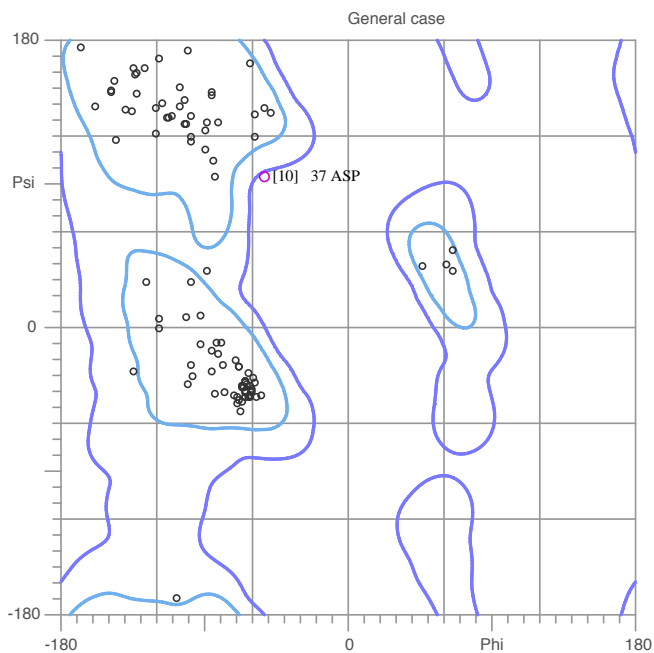
There were 2 outliers (phi, psi):

[9] 85 HIS (-164.9, -5.0)

[9] 88 LYS (66.6, 139.0)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 10

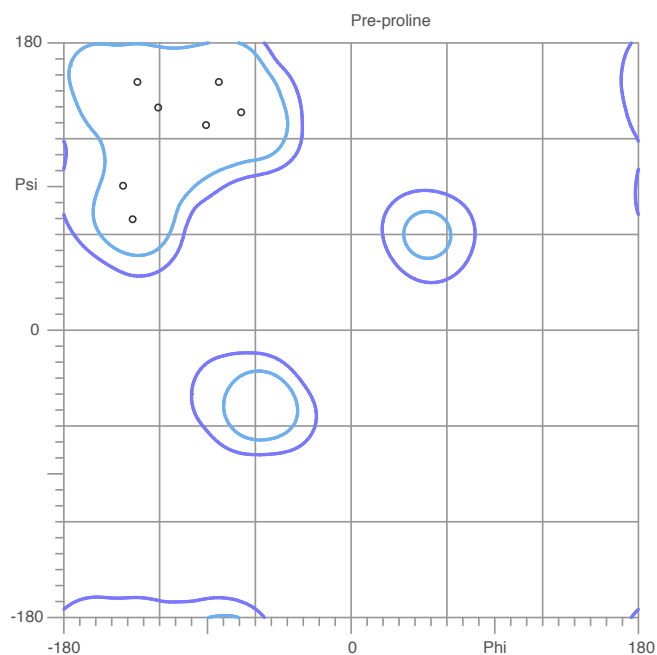
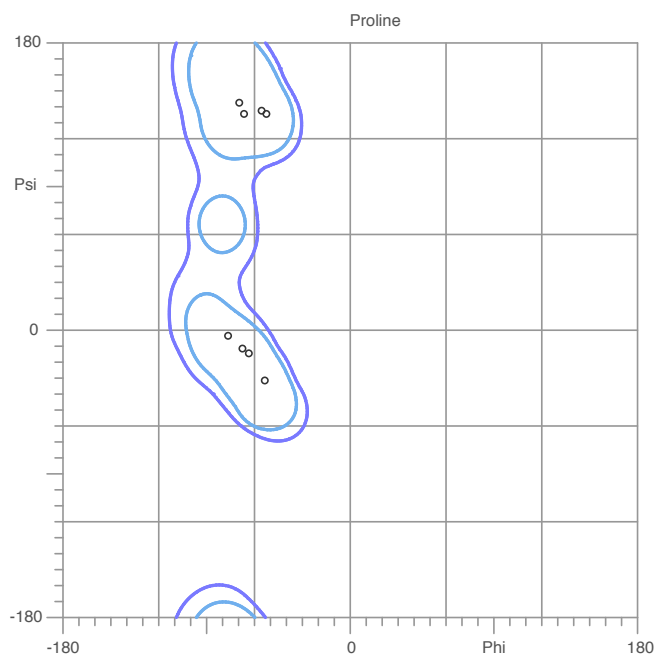
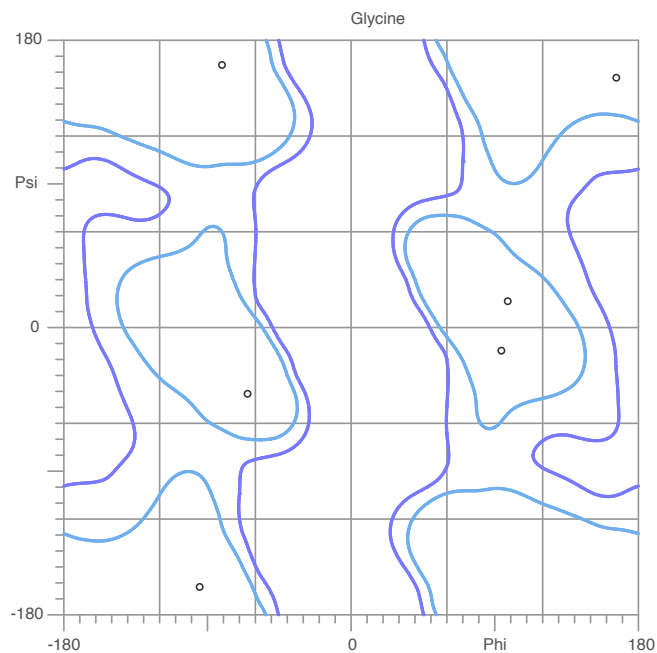
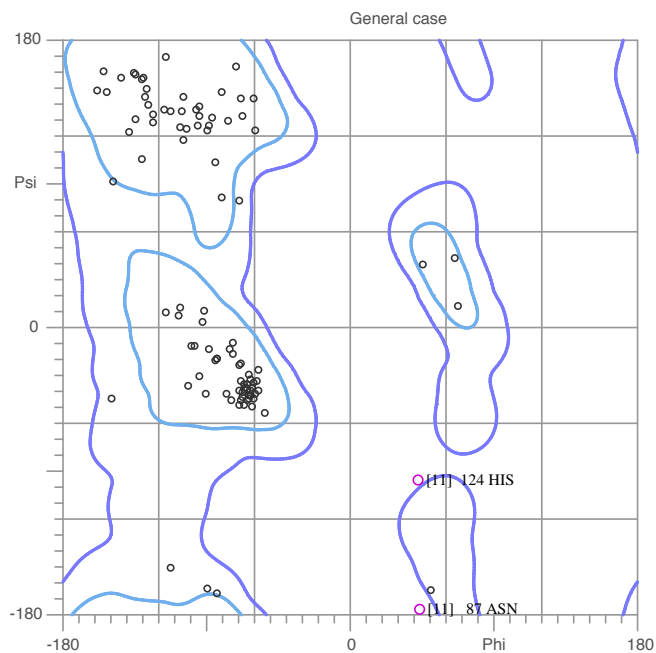


95.9% (118/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[10] 37 ASP (-53.7, 95.3)  
[10] 55 GLY (-164.7, -29.0)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 11

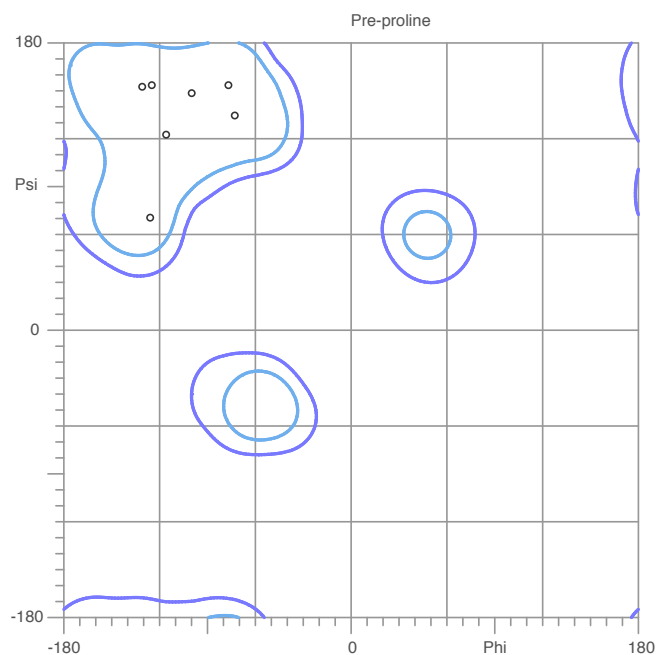
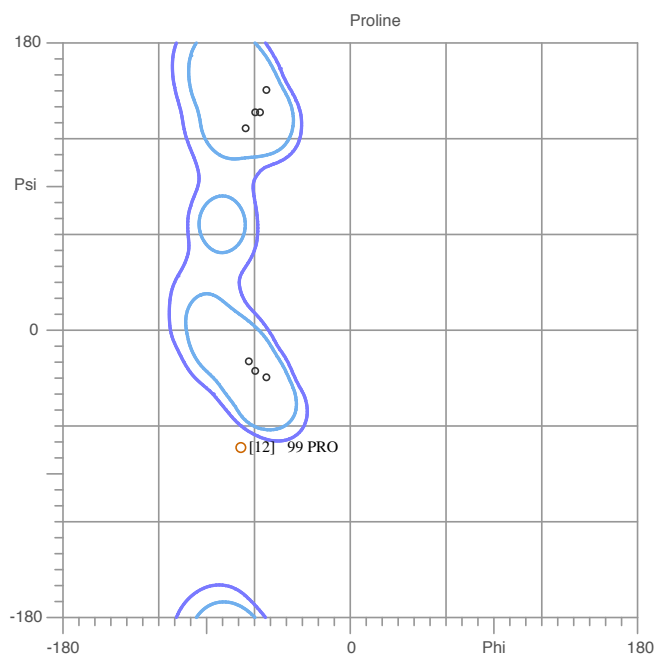
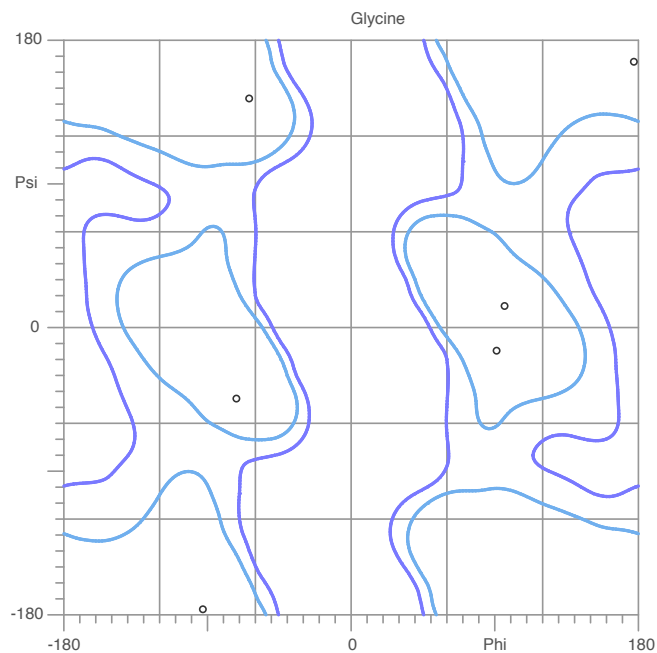
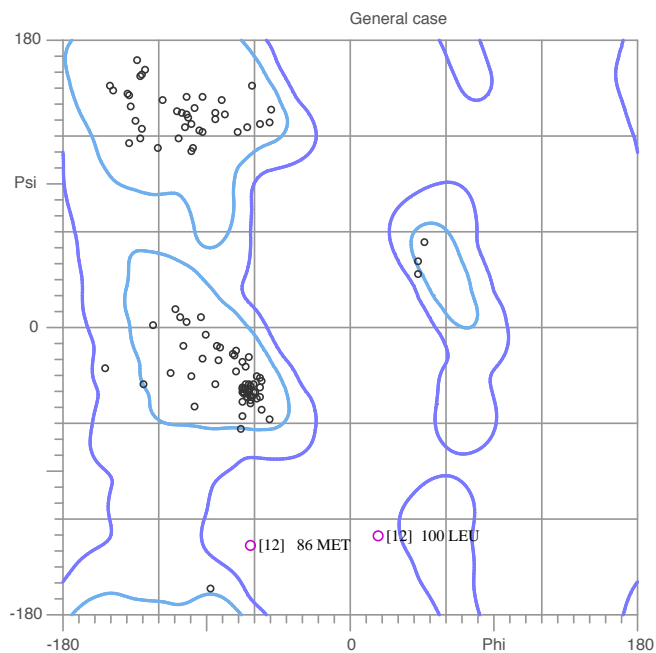


92.7% (114/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[11] 87 ASN (43.9, -176.4)  
[11] 124 HIS (42.9, -95.1)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 12



93.5% (115/123) of all residues were in favored (98%) regions.  
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

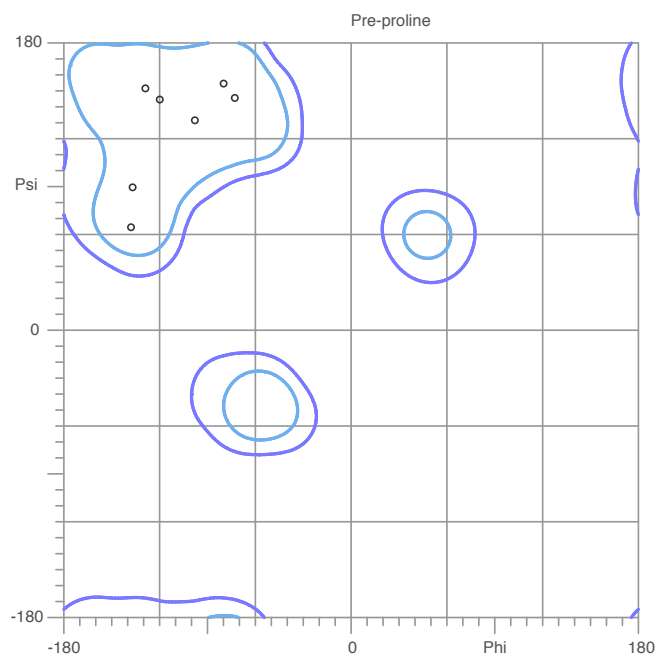
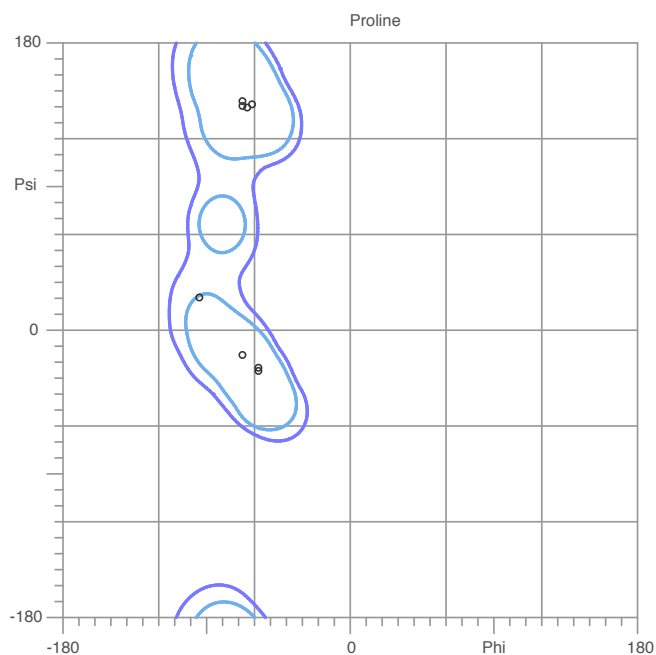
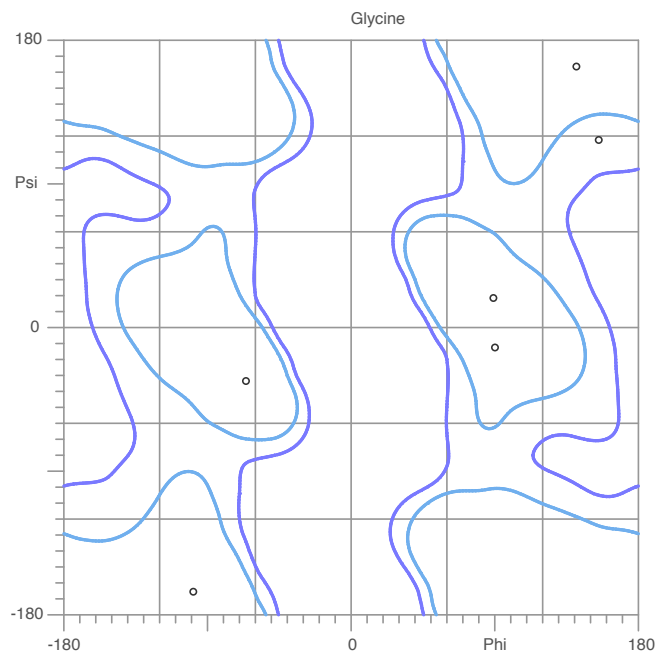
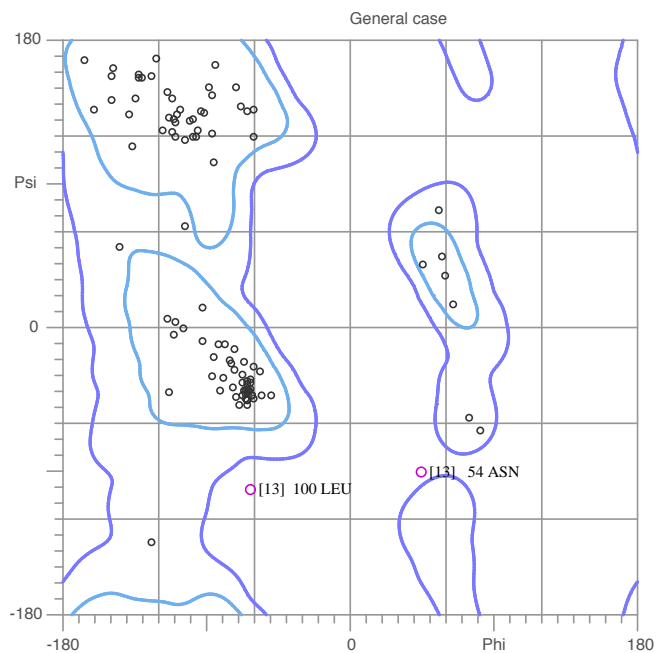
[12] 86 MET (-63.5, -136.9)

[12] 99 PRO (-69.3, -73.6)

[12] 100 LEU (17.6, -130.7)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 13

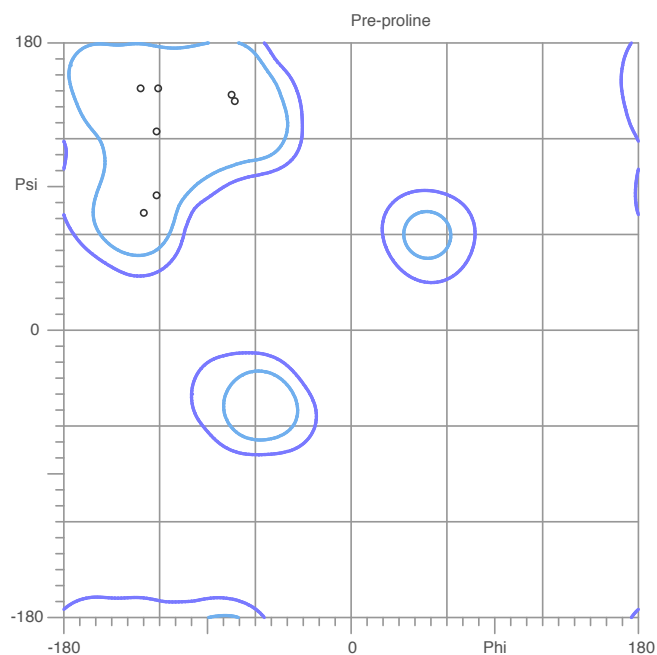
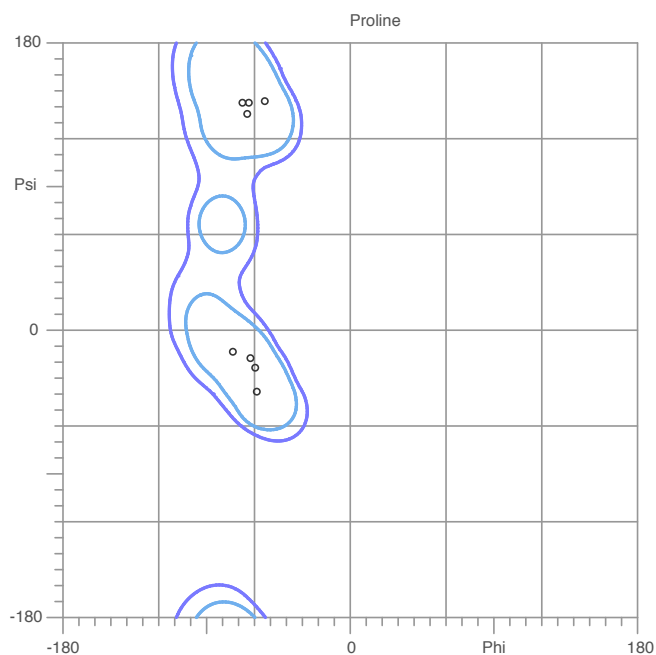
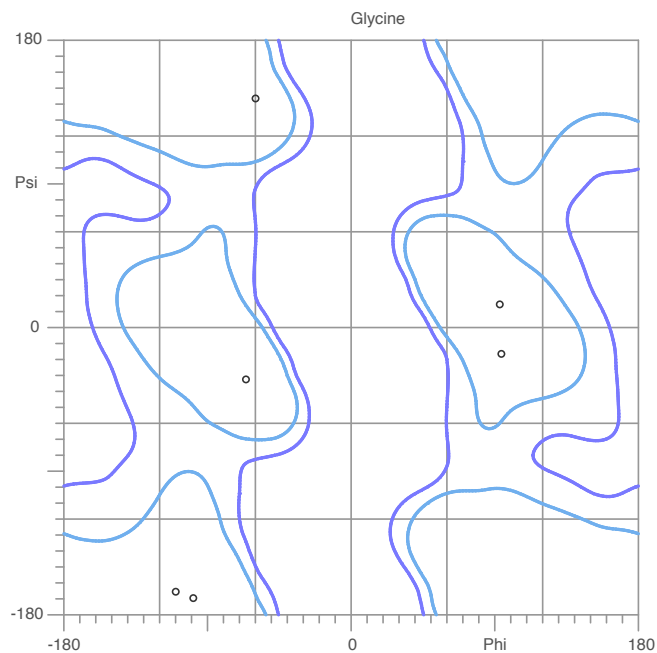
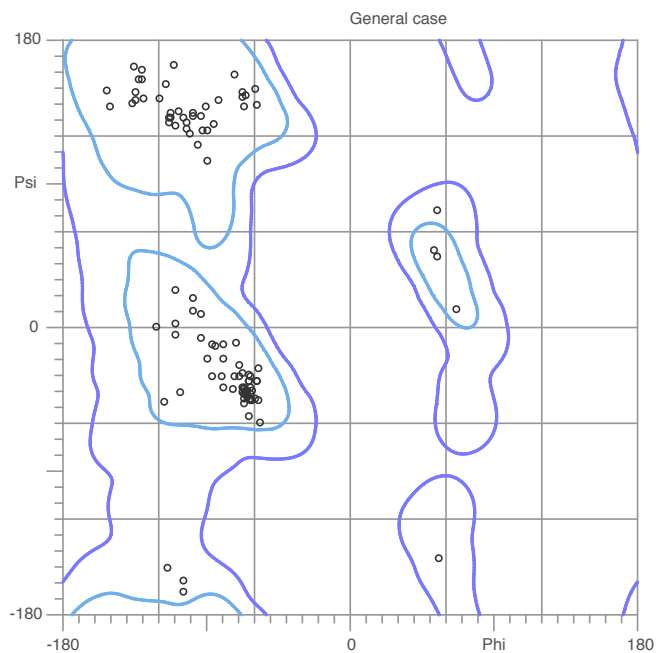


92.7% (114/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[13] 54 ASN (45.0, -90.7)  
[13] 100 LEU (-63.5, -101.2)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 14



95.9% (118/123) of all residues were in favored (98%) regions.  
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

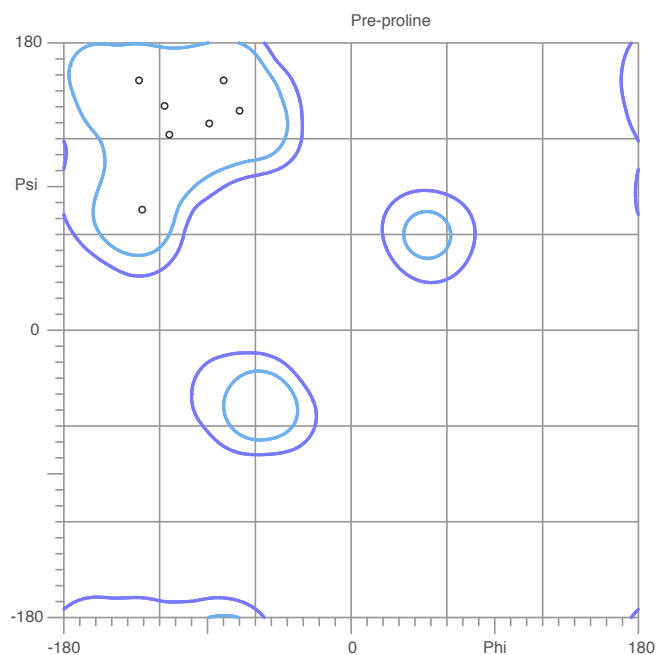
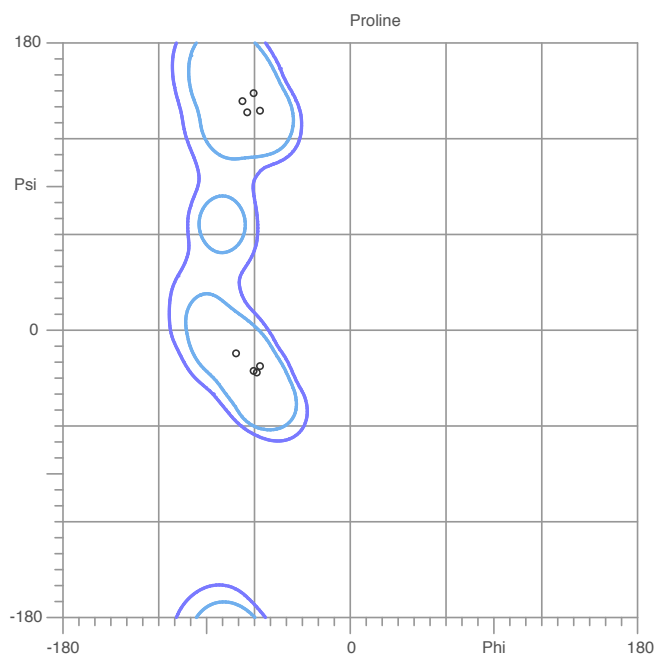
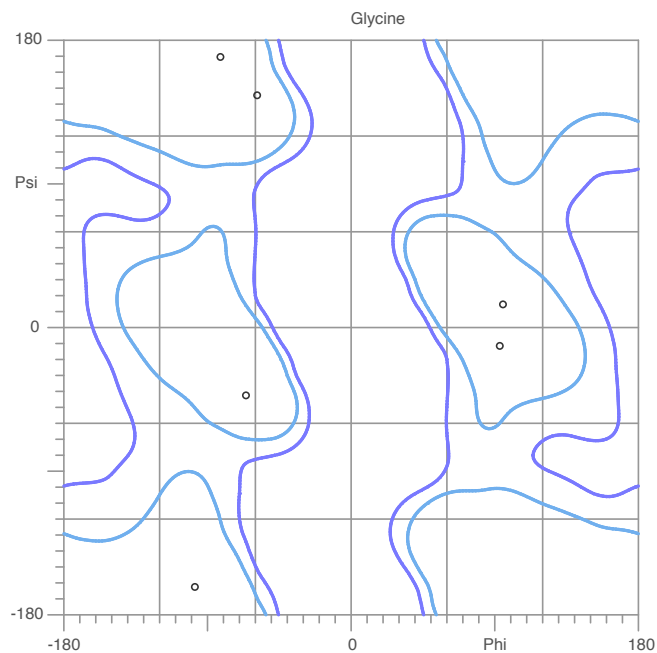
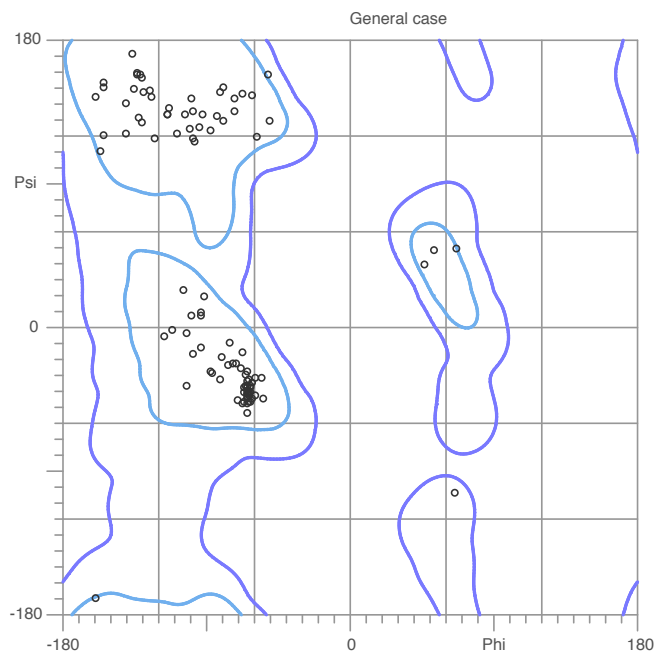
There were no outliers.

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

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# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 15



97.6% (120/123) of all residues were in favored (98%) regions.  
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

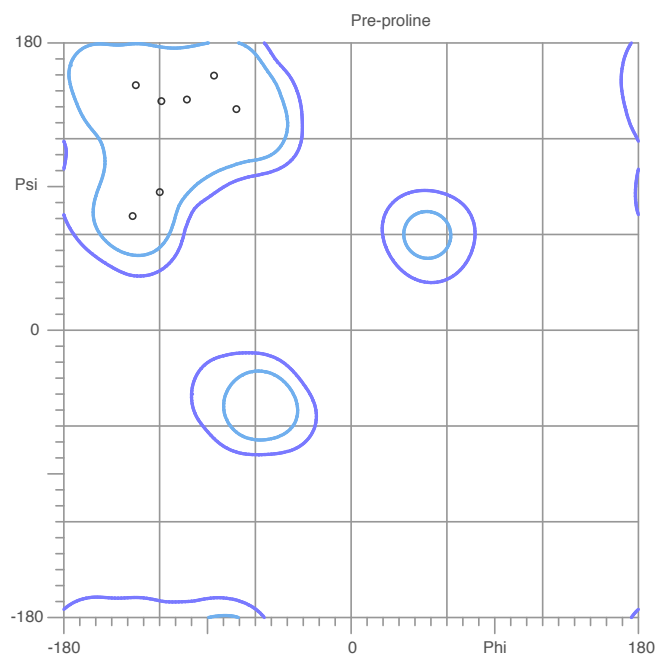
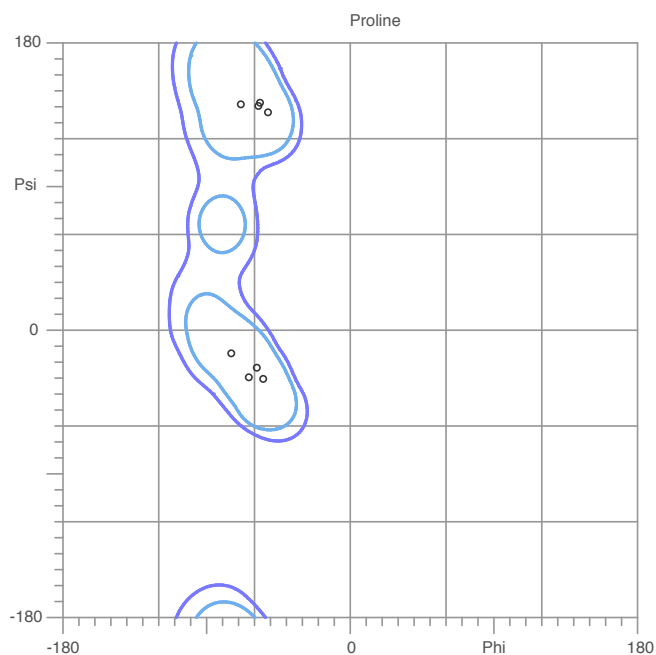
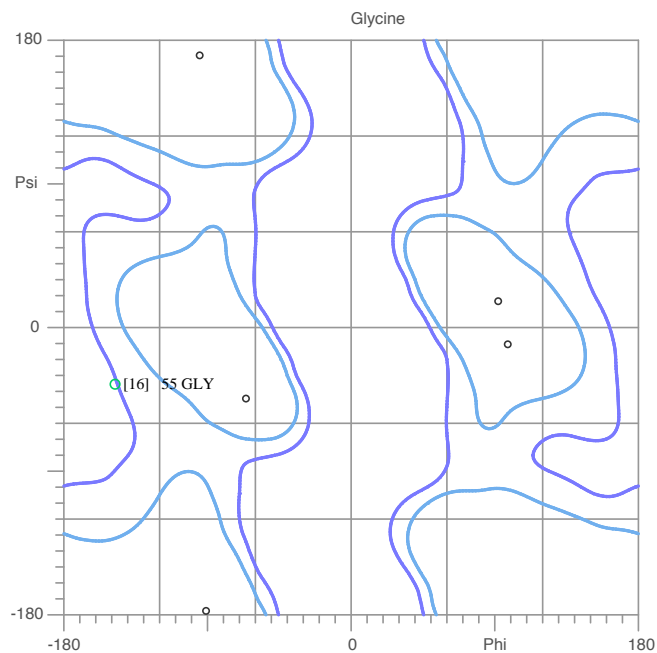
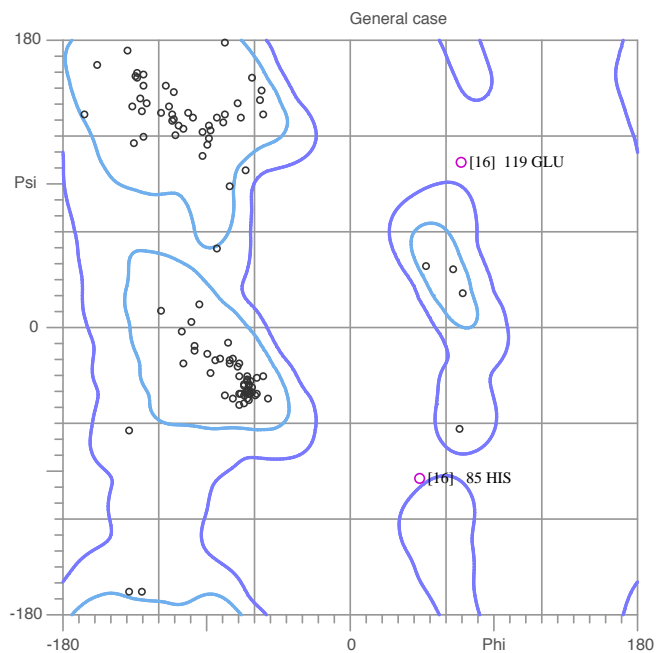
There were no outliers.

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

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

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 16



92.7% (114/123) of all residues were in favored (98%) regions.  
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

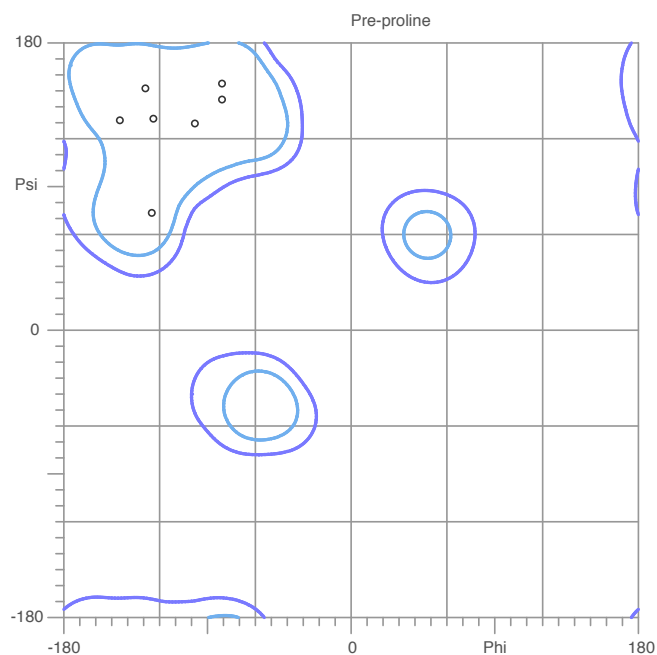
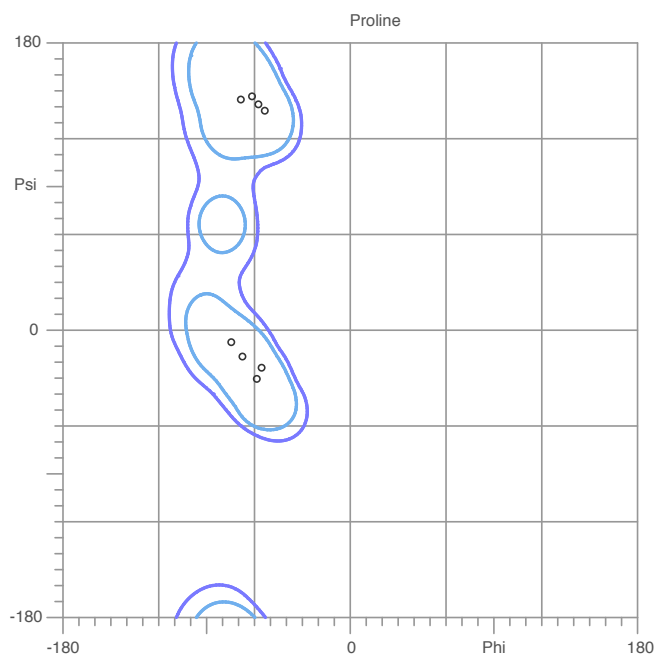
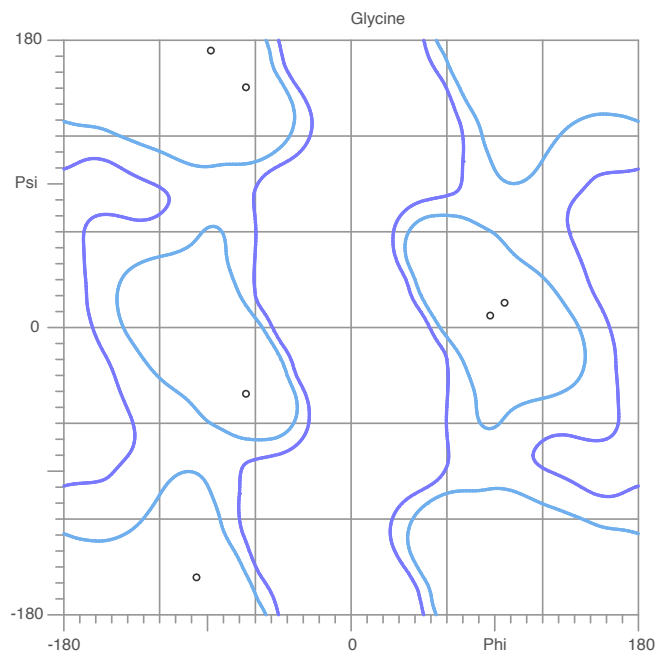
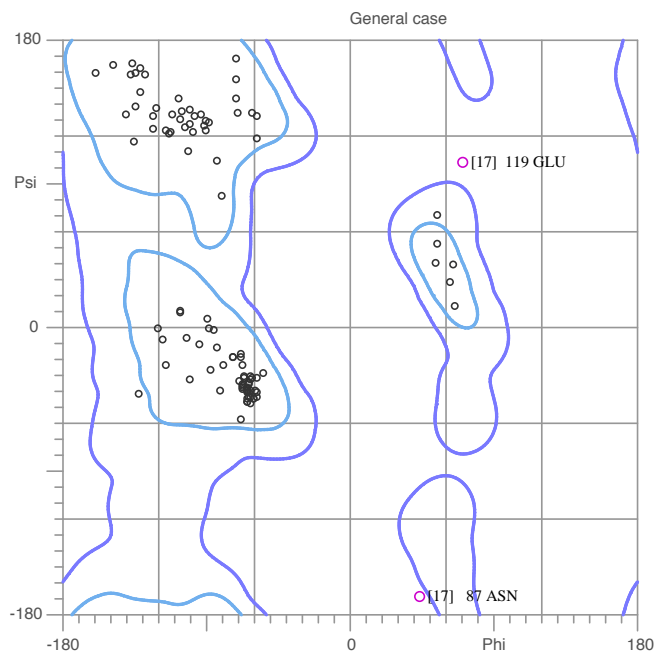
[16] 55 GLY (-148.5, -35.0)

[16] 85 HIS (43.4, -95.0)

[16] 119 GLU (69.3, 104.9)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 17

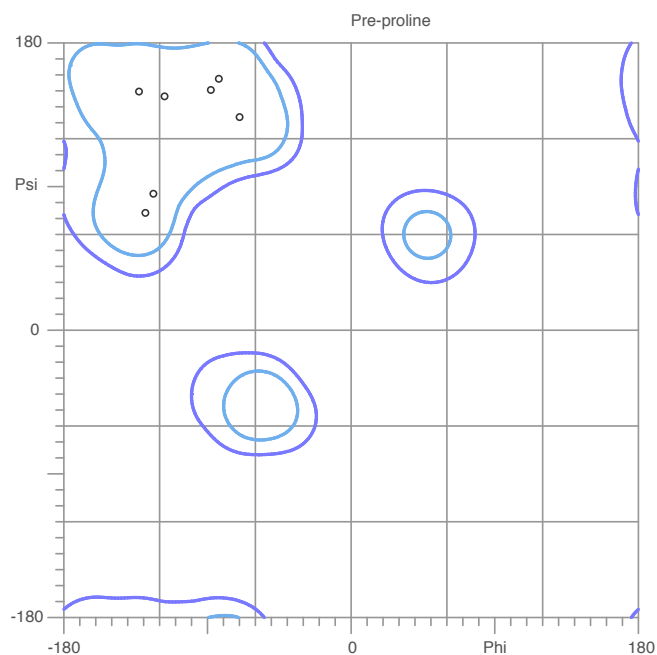
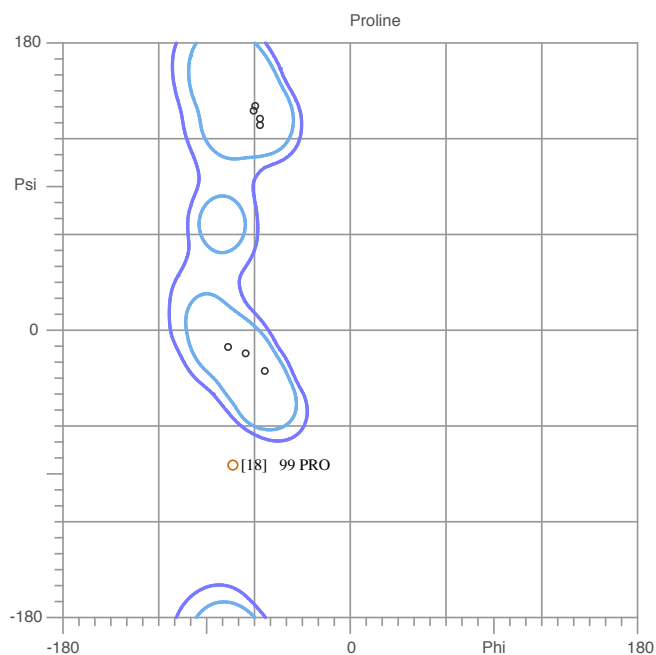
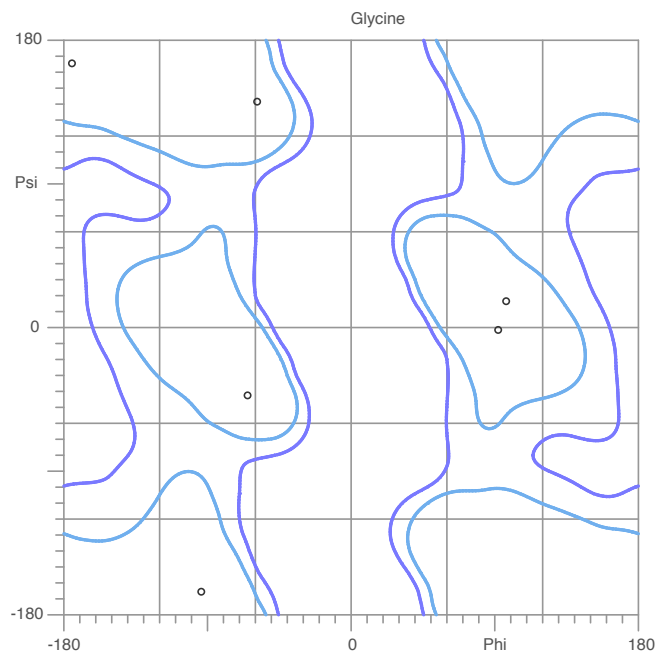
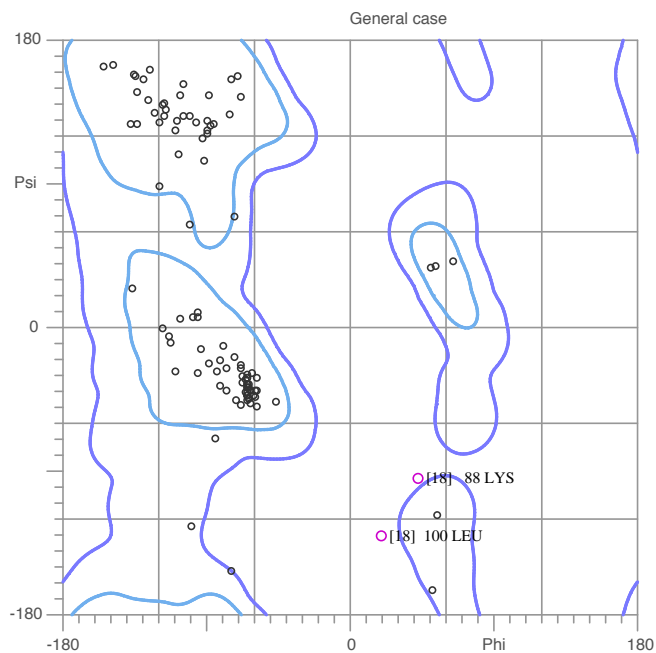


96.7% (119/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[17] 87 ASN (43.8, -168.3)  
[17] 119 GLU (70.0, 105.0)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 18



92.7% (114/123) of all residues were in favored (98%) regions.  
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

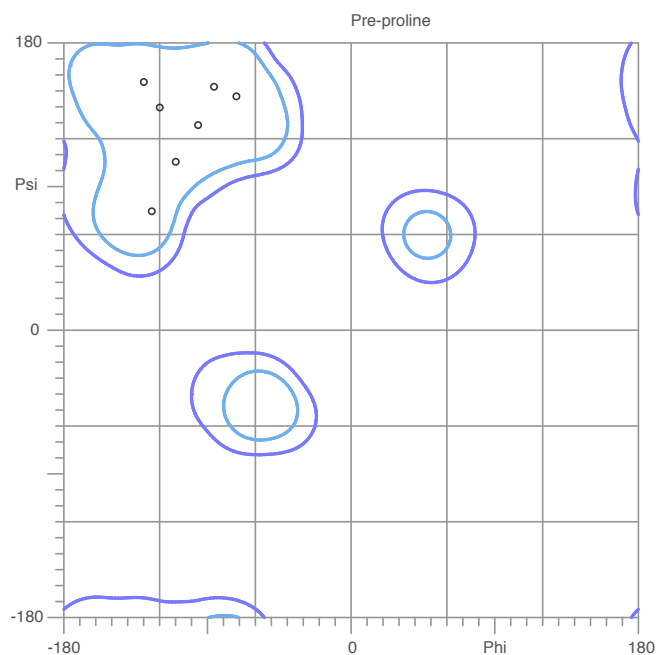
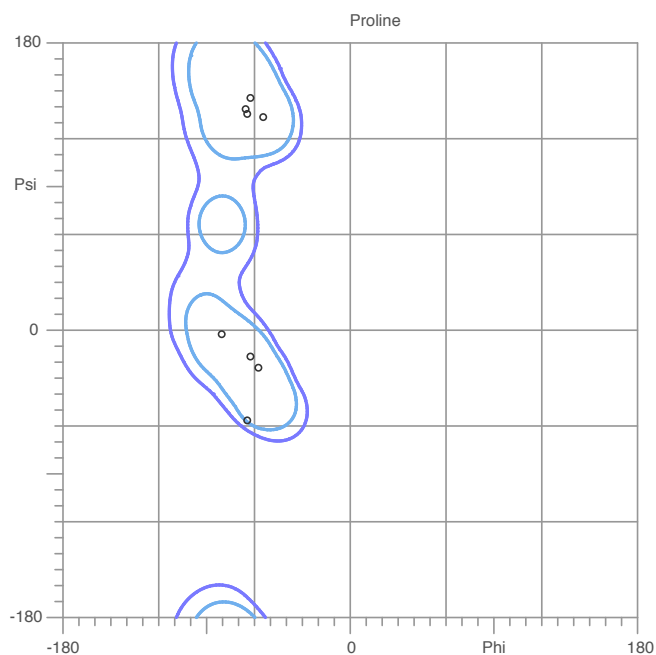
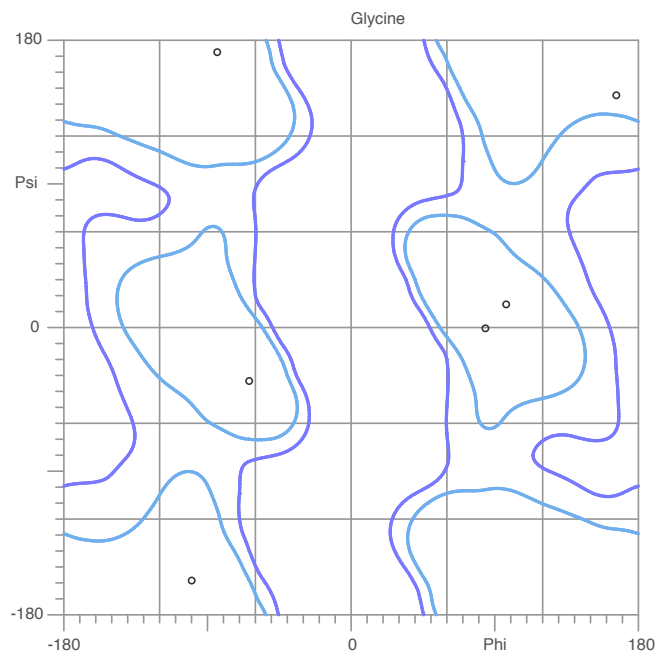
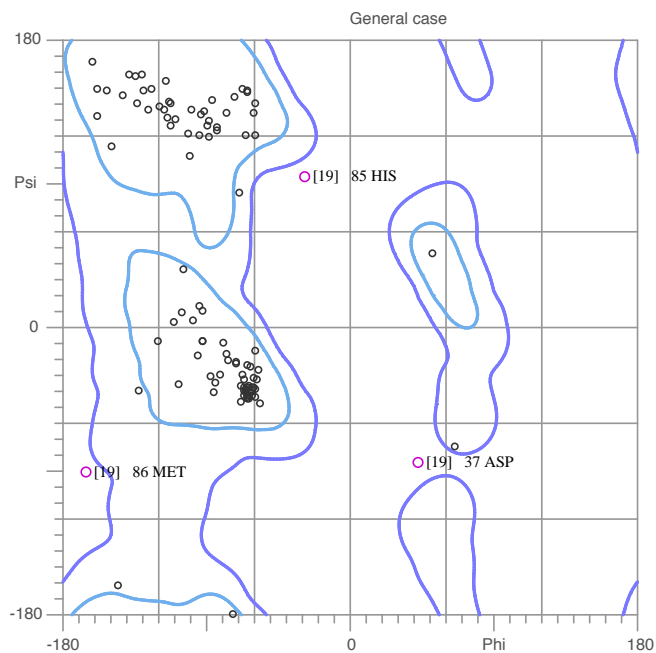
[18] 88 LYS (42.8, -95.0)

[18] 99 PRO (-74.2, -85.0)

[18] 100 LEU (19.9, -130.7)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 19



93.5% (115/123) of all residues were in favored (98%) regions.  
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

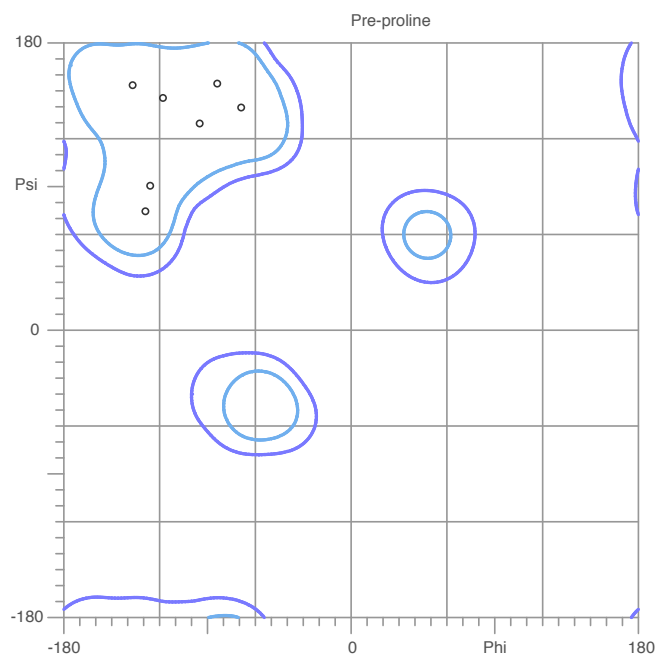
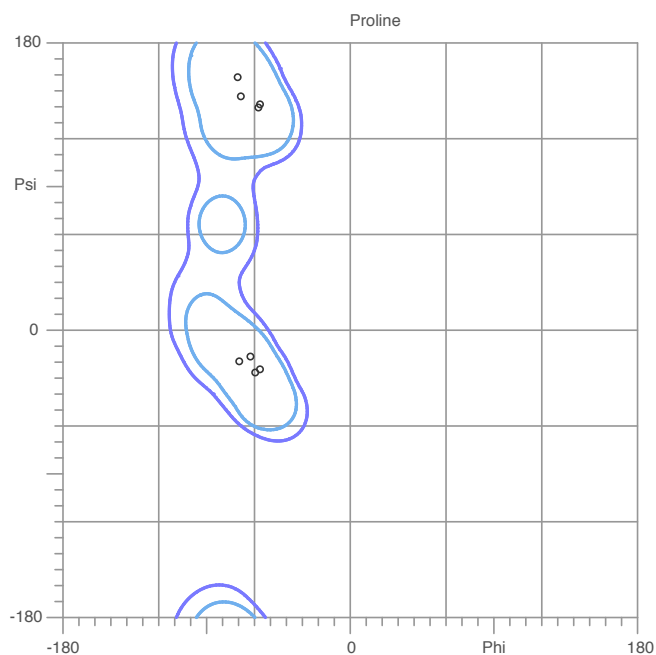
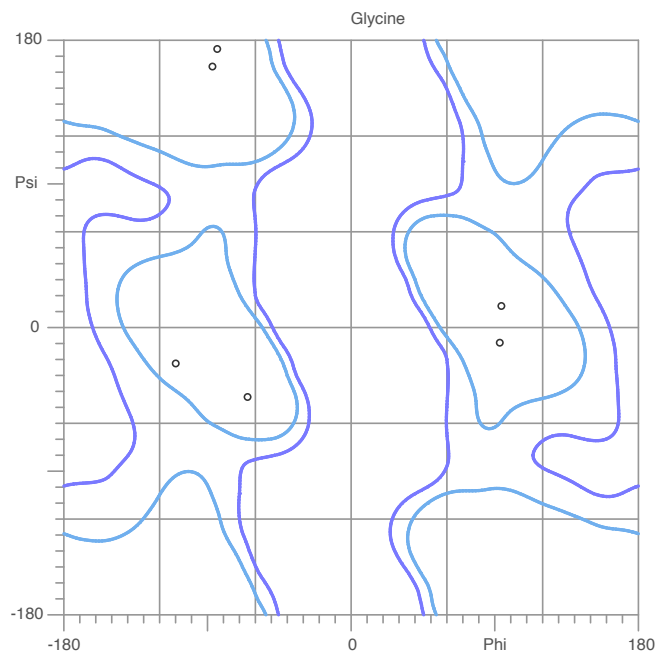
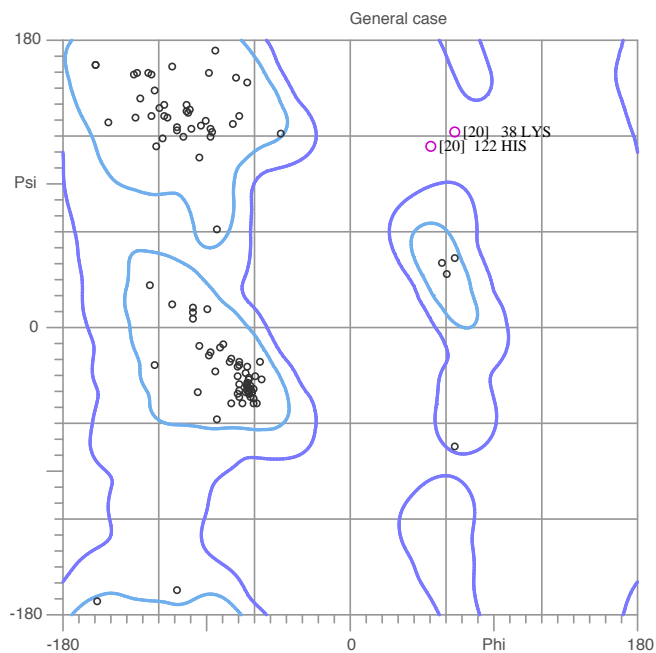
[19] 37 ASP (42.4, -84.9)

[19] 85 HIS (-29.7, 95.0)

[19] 86 MET (-166.8, -90.5)

# MolProbity Ramachandran analysis

PSR293\_R3Cons\_em\_bcr3.pdb, model 20



96.7% (119/123) of all residues were in favored (98%) regions.  
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[20] 38 LYS (65.0, 123.3)  
[20] 122 HIS (51.0, 114.8)