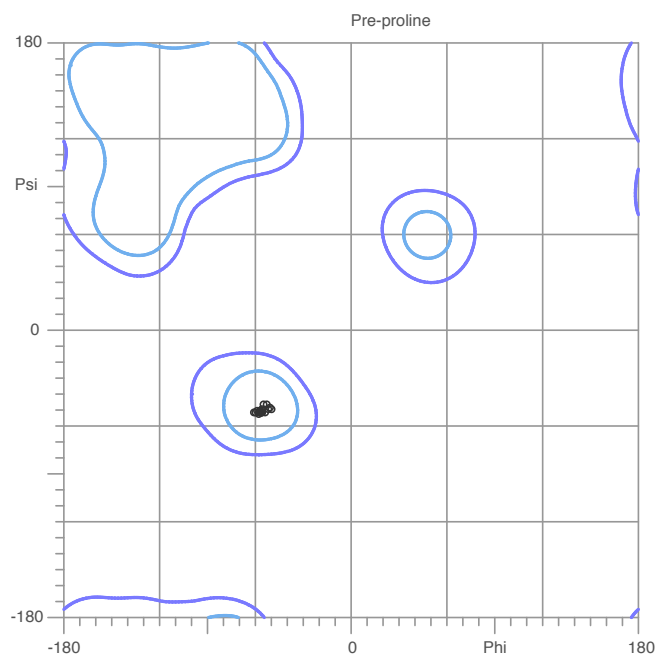
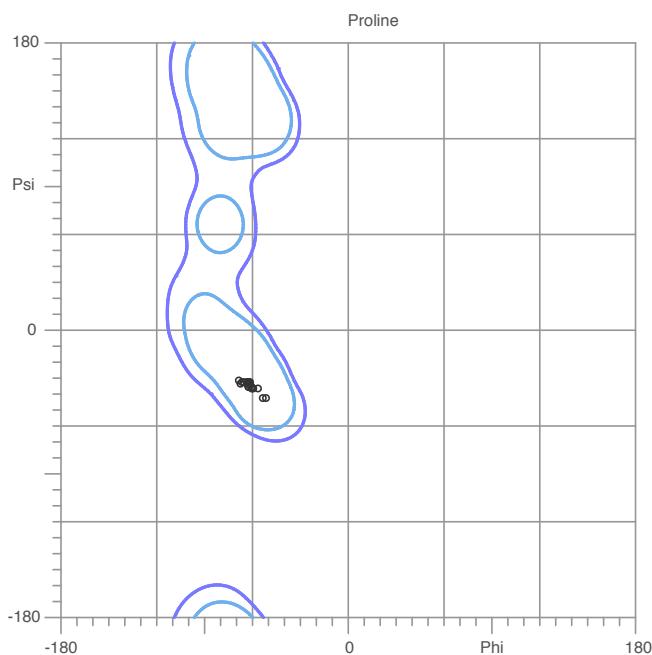
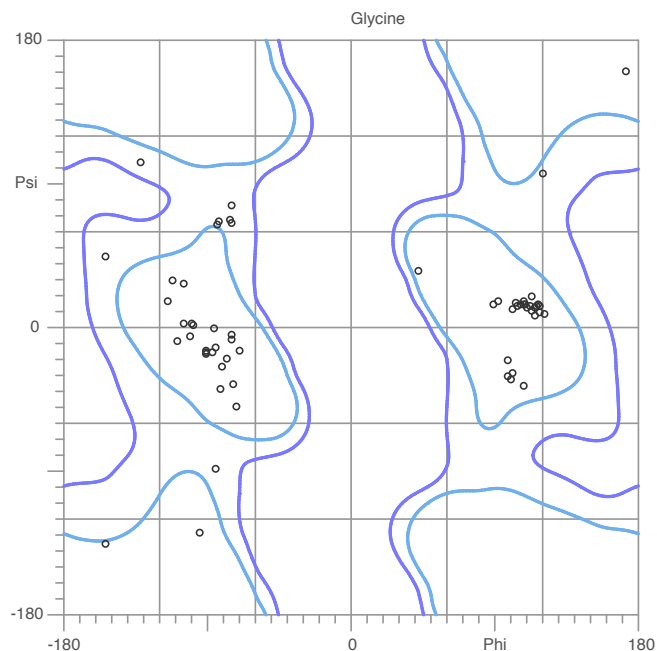
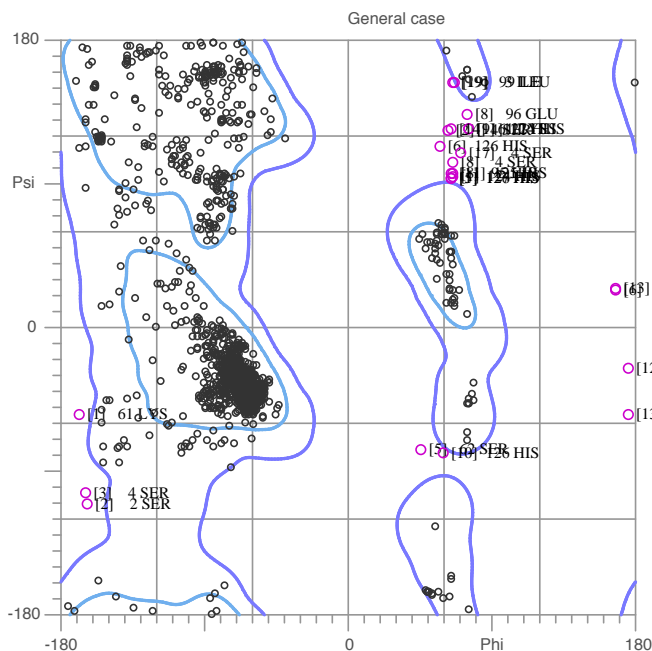


# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, all models



94.5% (2401/2540) of all residues were in favored (98%) regions.  
99.1% (2516/2540) of all residues were in allowed (>99.8%) regions.

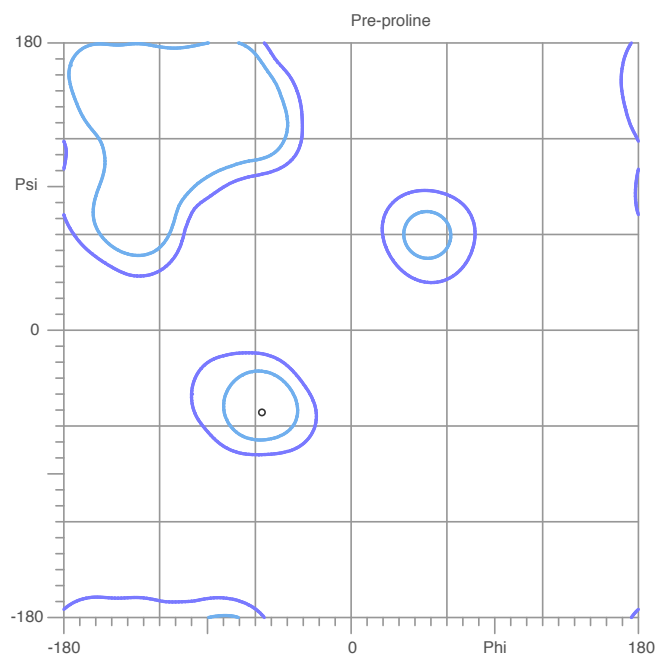
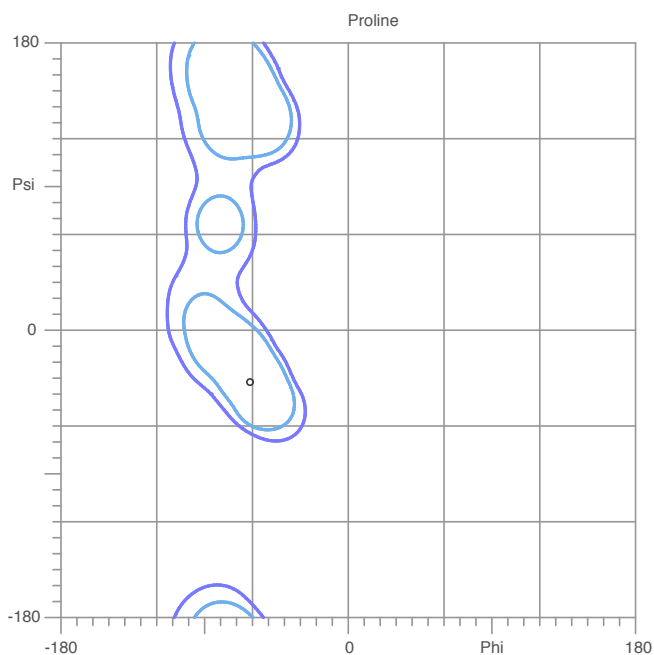
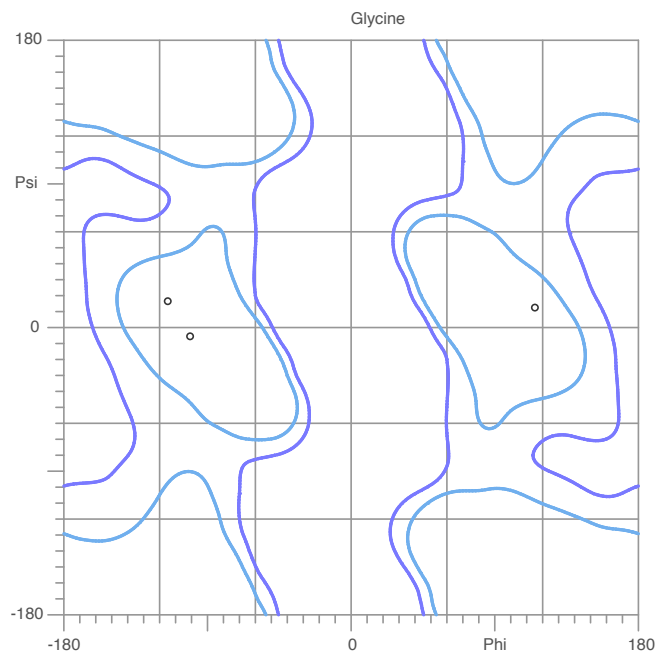
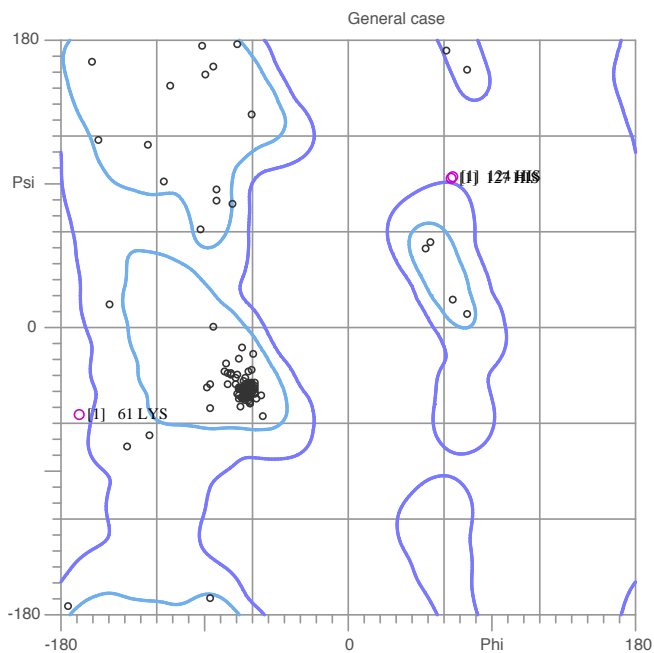
There were 24 outliers (phi, psi):

- [1] 61 LYS (-169.0, -54.9)
- [1] 124 HIS (65.6, 95.5)
- [1] 127 HIS (64.9, 95.0)
- [2] 2 SER (-164.8, -110.7)
- [2] 4 SER (62.4, 124.8)
- [3] 4 SER (-165.0, -103.4)
- [5] 62 SER (45.0, -76.2)
- [5] 126 HIS (64.9, 95.0)
- [6] 46 ASN (167.6, 25.0)
- [6] 126 HIS (57.7, 114.3)

- [8] 4 SER (65.0, 105.0)
- [8] 95 HIS (65.0, 97.2)
- [8] 96 GLU (74.5, 135.0)
- [9] 127 HIS (75.0, 125.1)
- [10] 126 HIS (59.3, -78.8)
- [11] 124 HIS (75.2, 125.1)
- [11] 125 HIS (64.8, 97.9)
- [12] 128 HIS (175.0, -25.1)
- [13] 46 ASN (167.3, 25.1)
- [13] 62 SER (175.1, -54.5)
- [14] 61 LYS (64.9, 125.8)
- [17] 4 SER (71.0, 110.1)
- [19] 3 ILE (66.7, 154.2)
- [19] 99 LEU (65.8, 155.0)

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 1



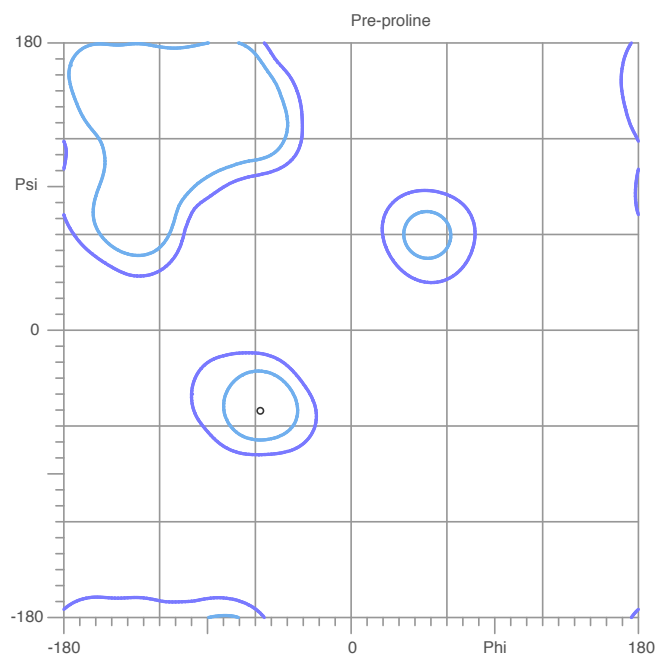
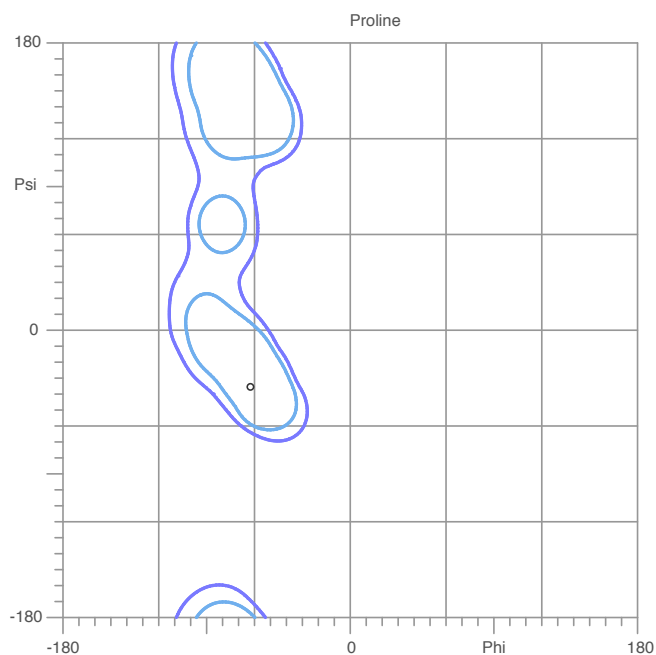
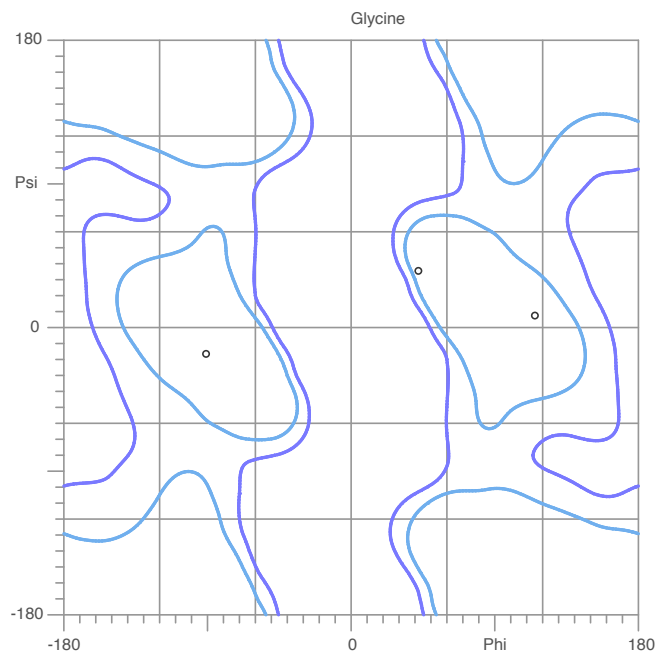
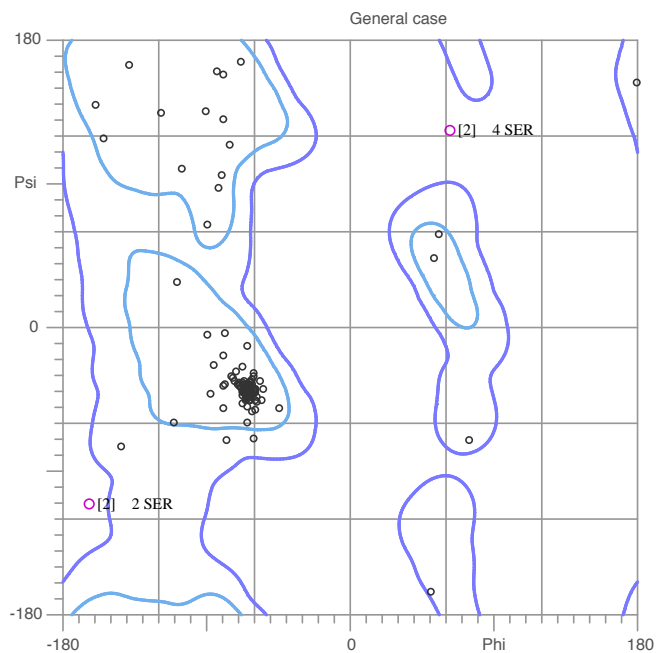
92.9% (118/127) of all residues were in favored (98%) regions.  
97.6% (124/127) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 61 LYS (-169.0, -54.9)
- [1] 124 HIS (65.6, 95.5)
- [1] 127 HIS (64.9, 95.0)

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 2



93.7% (119/127) of all residues were in favored (98%) regions.  
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

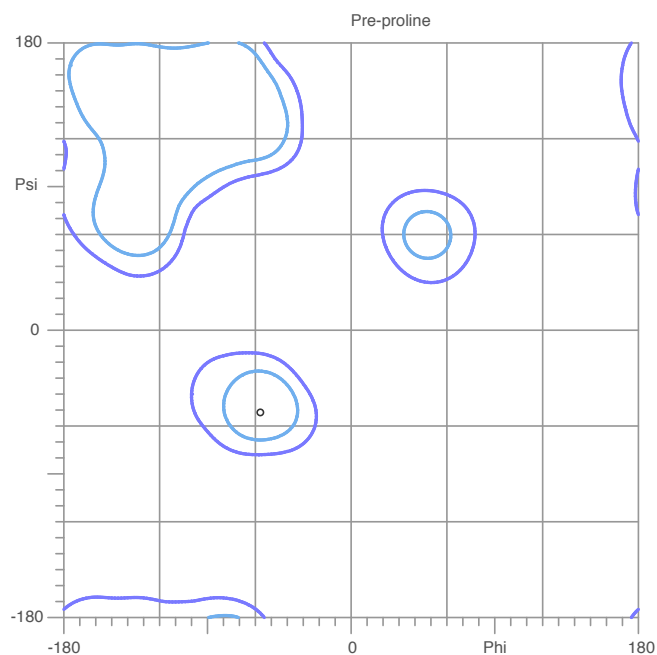
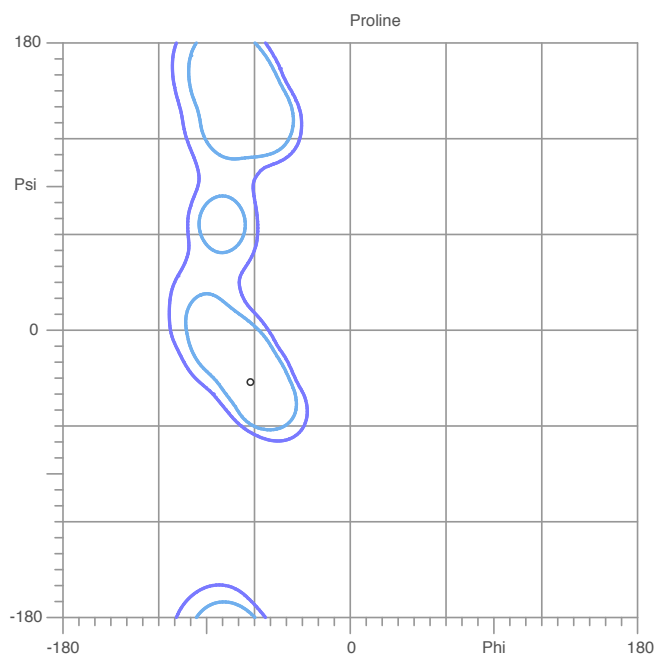
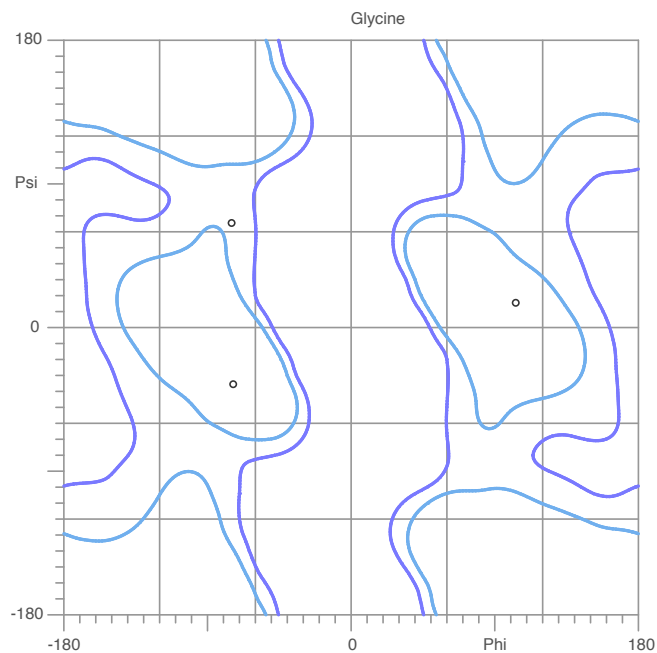
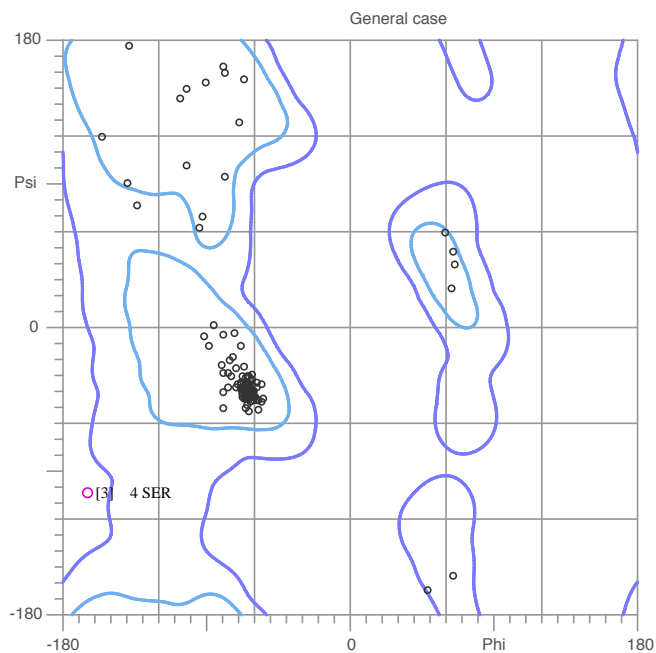
There were 2 outliers (phi, psi):

[2] 2 SER (-164.8, -110.7)

[2] 4 SER (62.4, 124.8)

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 3



96.1% (122/127) of all residues were in favored (98%) regions.  
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

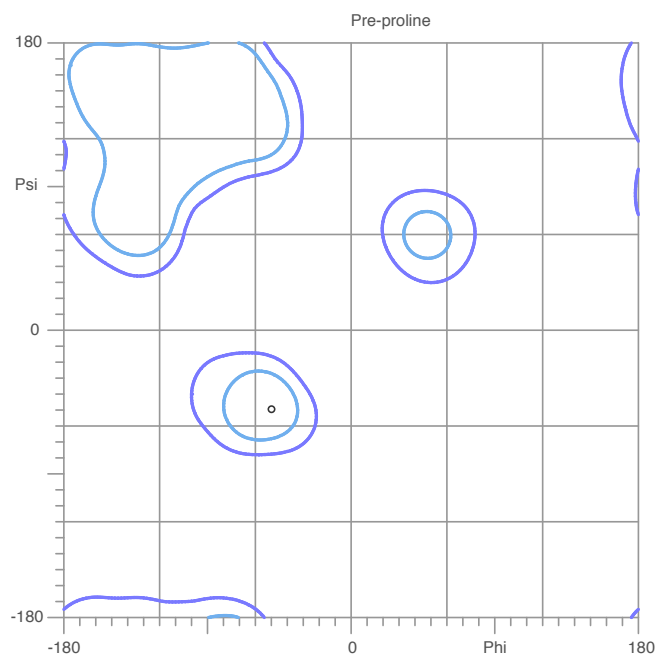
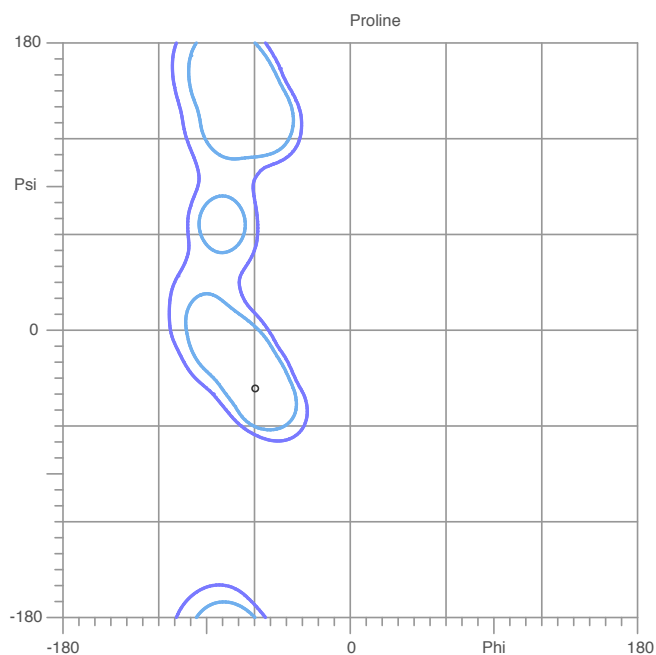
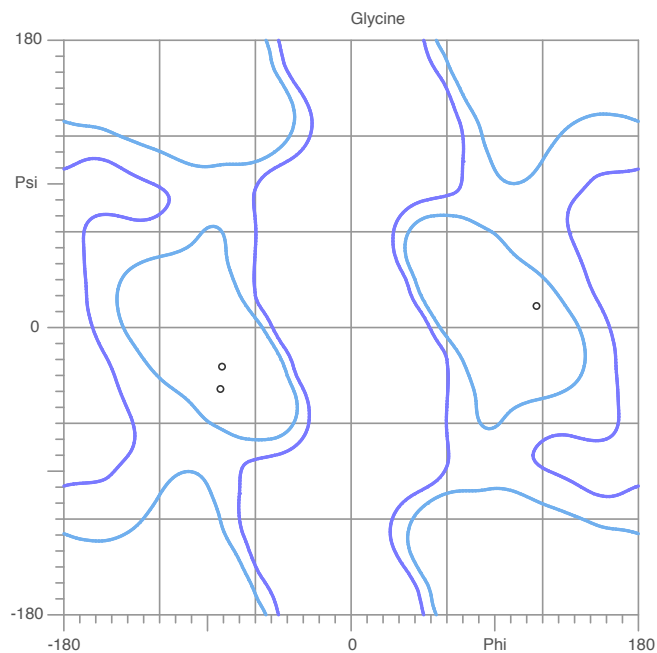
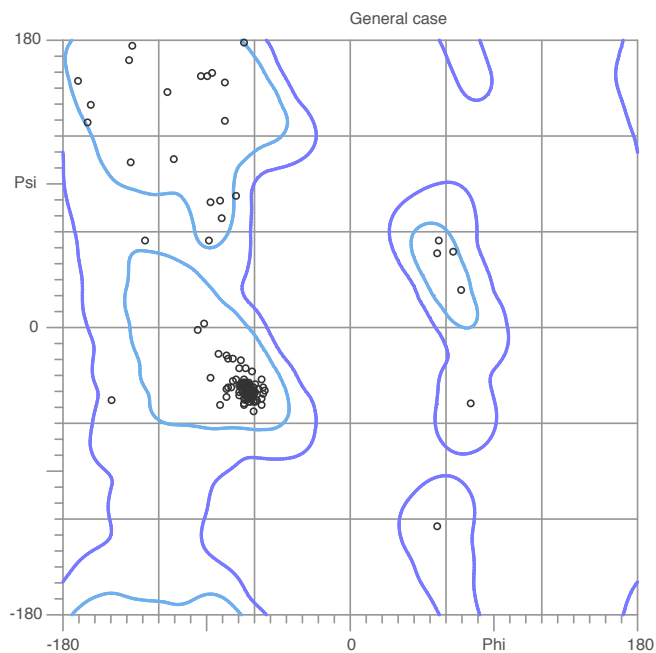
There were 1 outliers (phi, psi):  
[3] 4 SER (-165.0, -103.4)

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# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 4

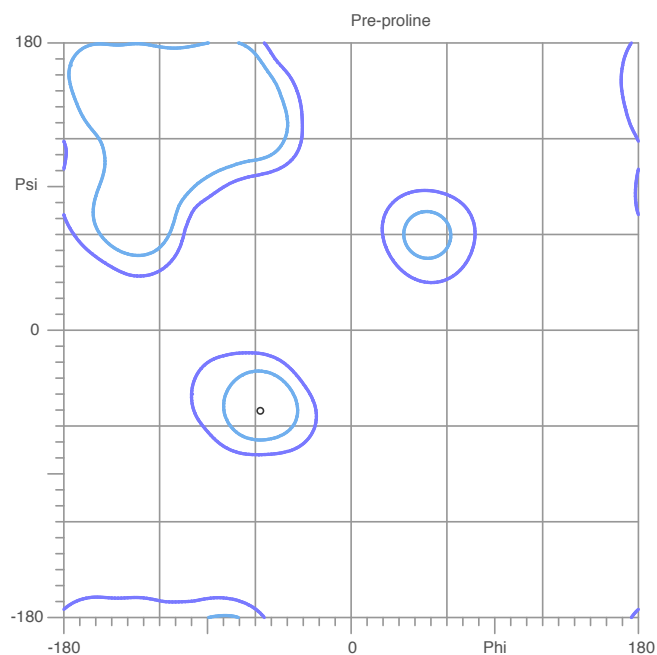
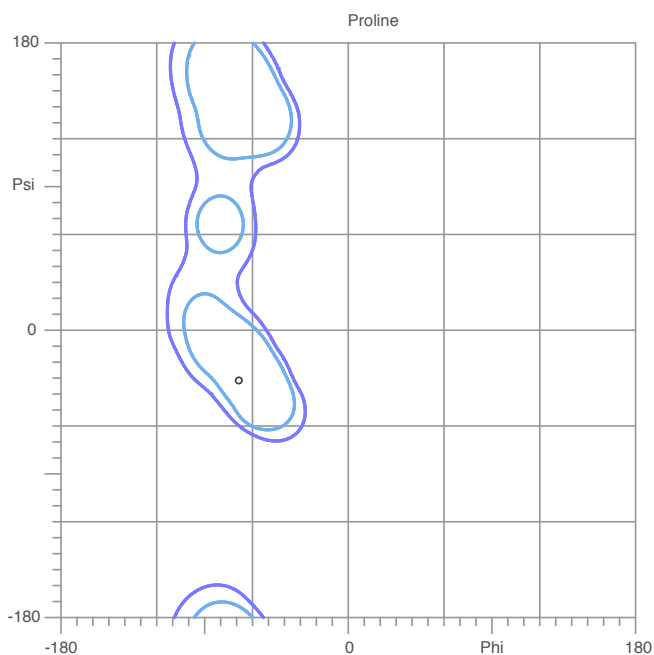
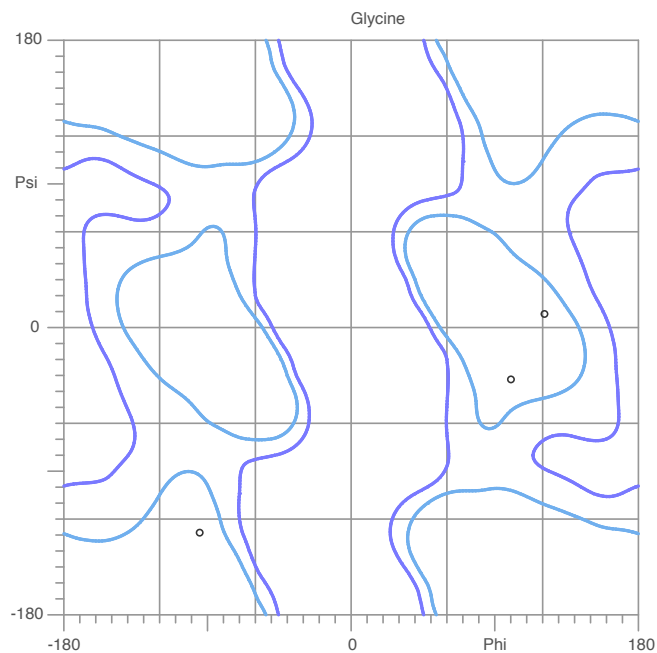
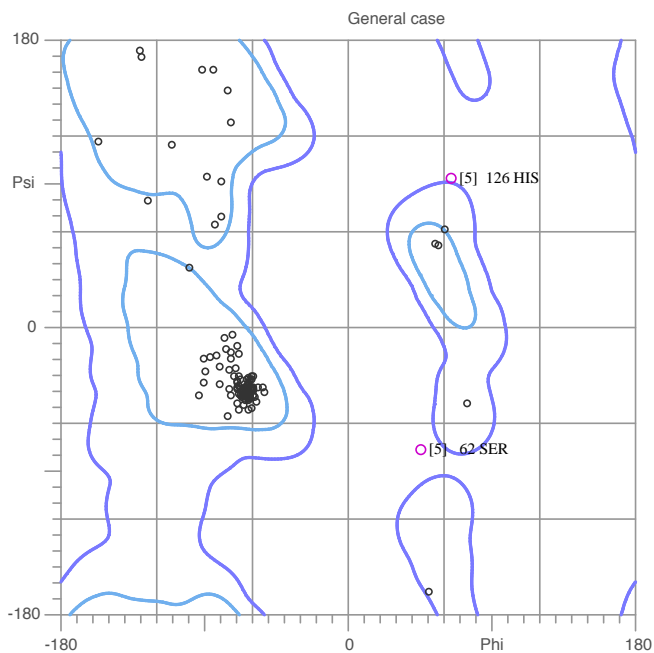


95.3% (121/127) of all residues were in favored (98%) regions.  
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 5



94.5% (120/127) of all residues were in favored (98%) regions.  
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

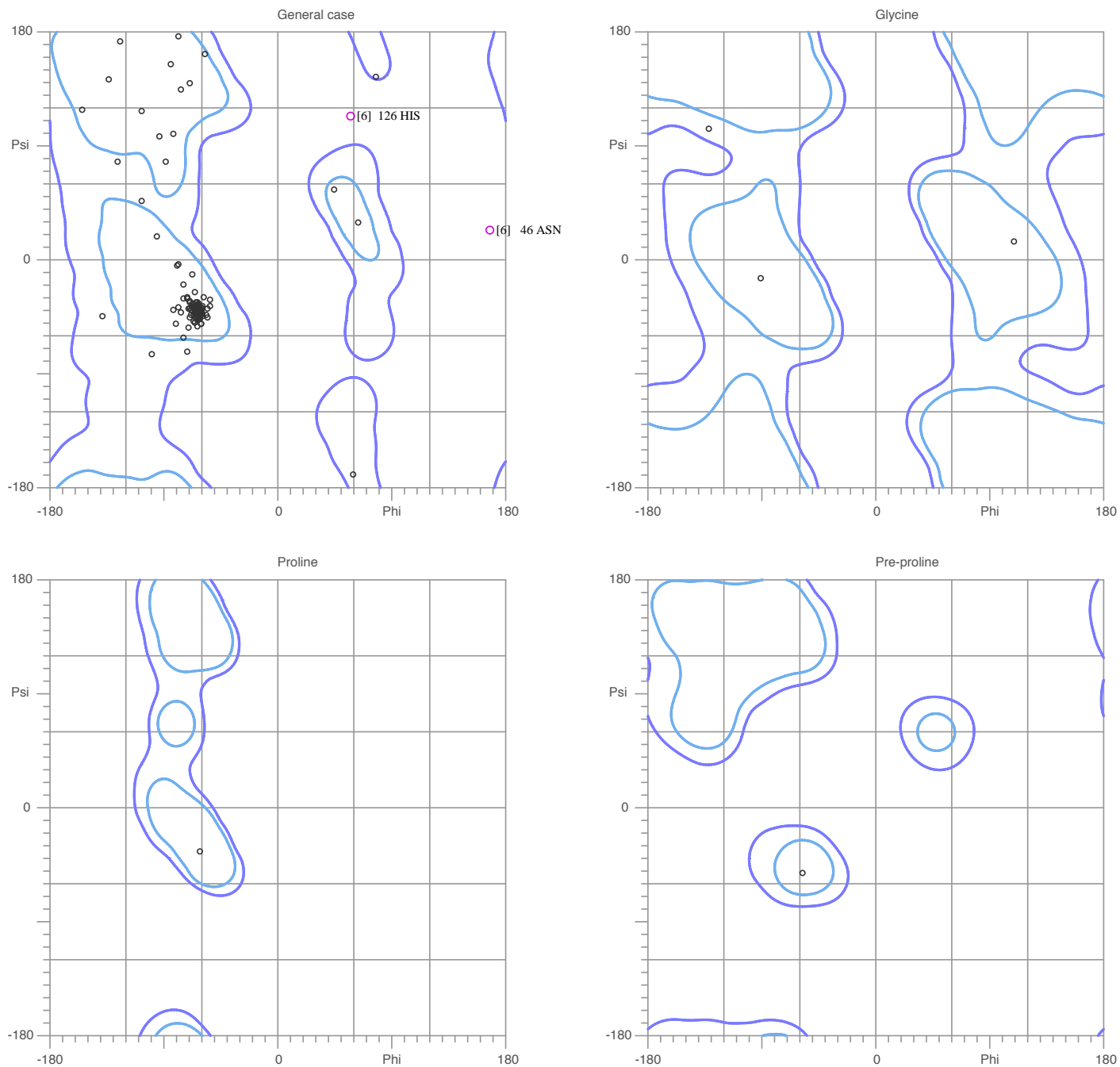
There were 2 outliers (phi, psi):

[5] 62 SER (45.0, -76.2)

[5] 126 HIS (64.9, 95.0)

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 6



92.1% (117/127) of all residues were in favored (98%) regions.  
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

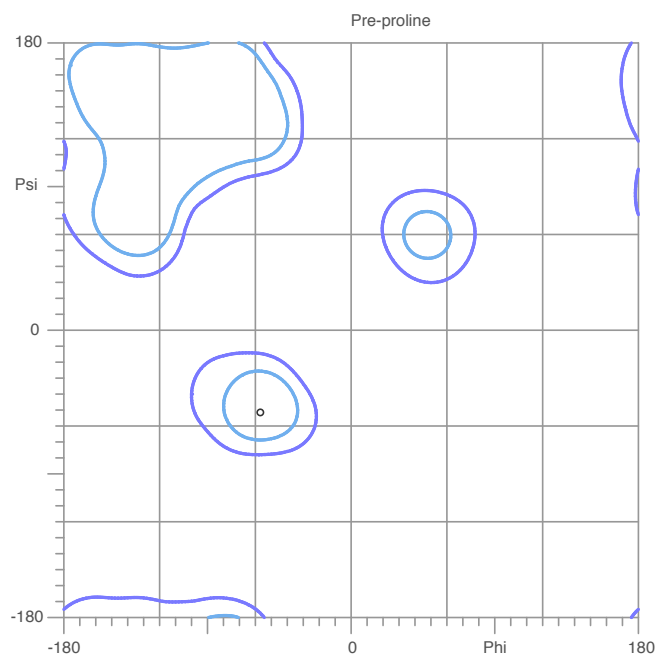
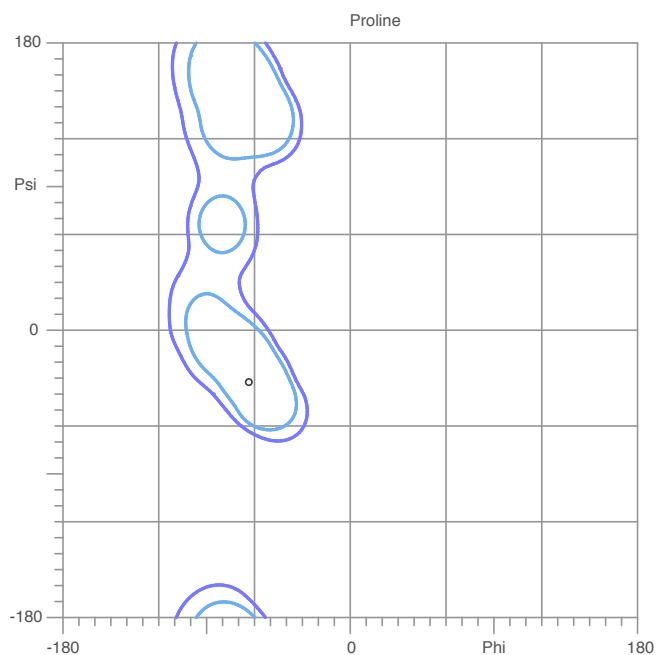
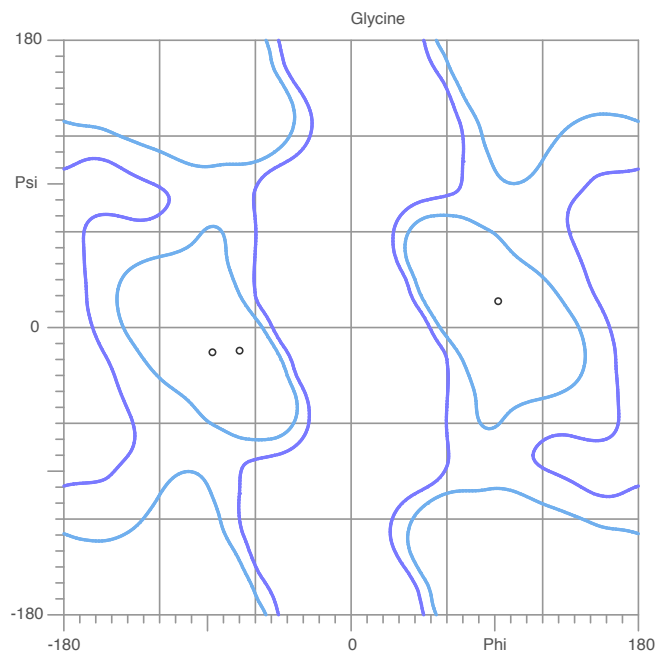
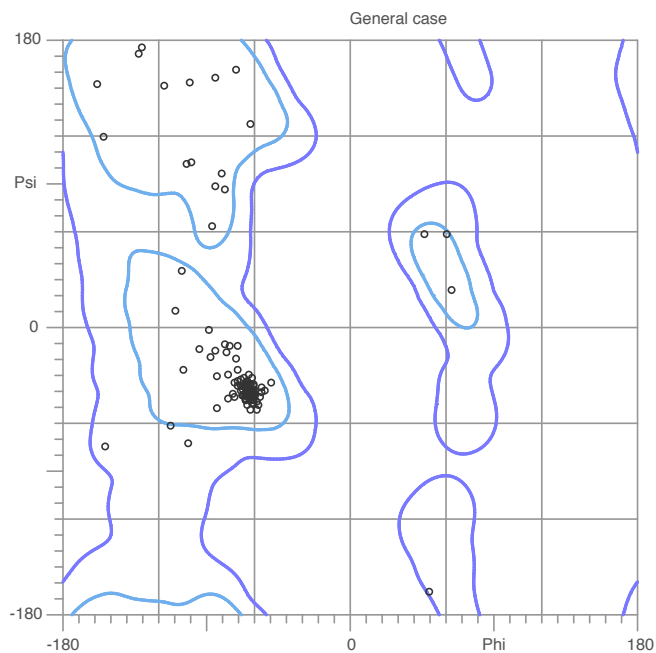
There were 2 outliers (phi, psi):

[6] 46 ASN (167.6, 25.0)

[6] 126 HIS (57.7, 114.3)

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 7

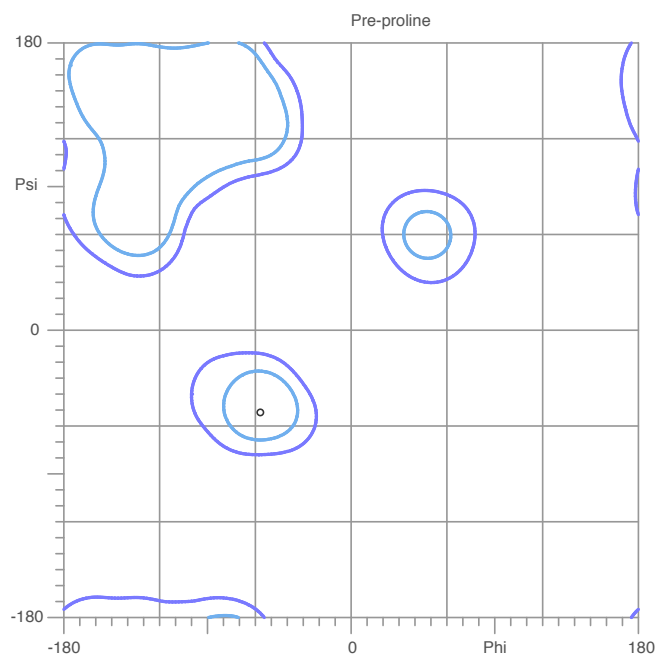
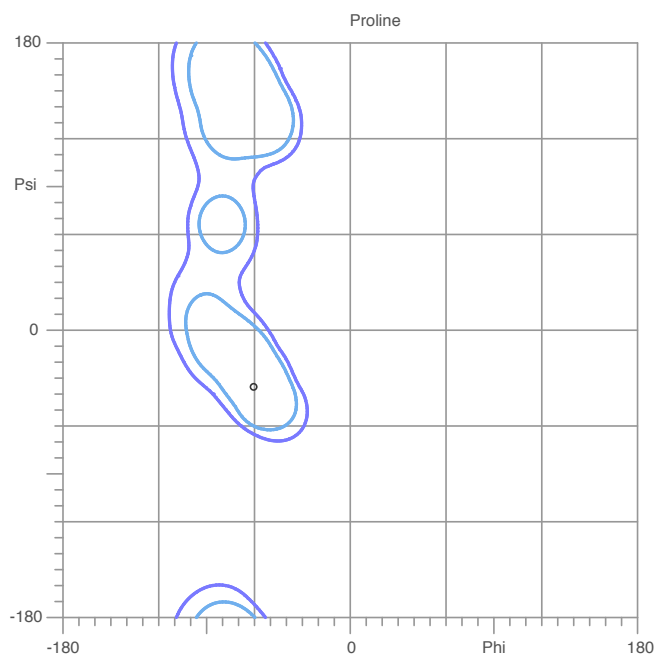
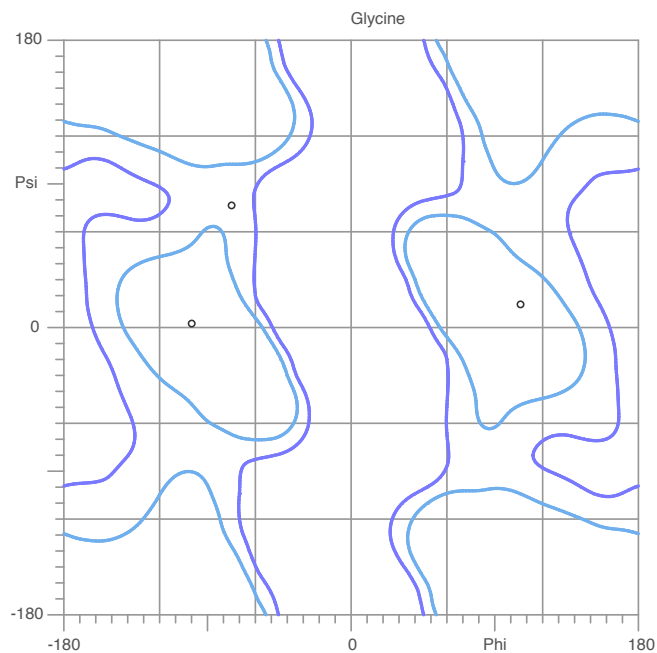
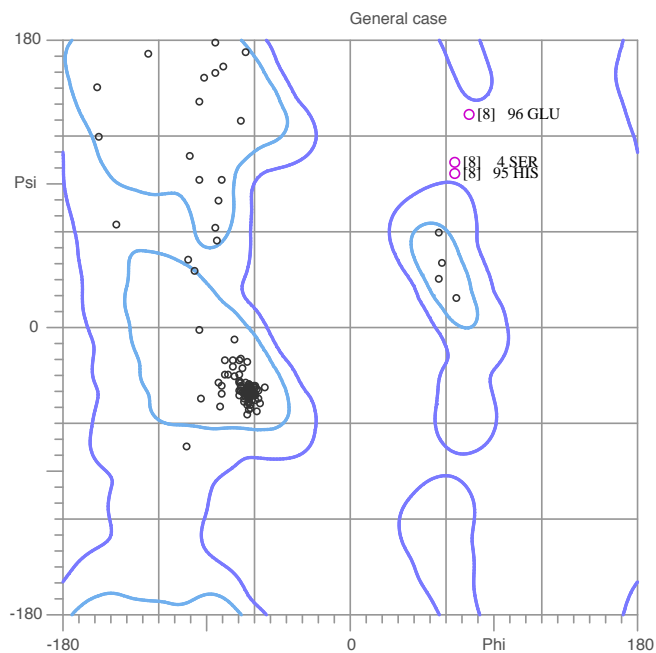


96.9% (123/127) of all residues were in favored (98%) regions.  
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 8



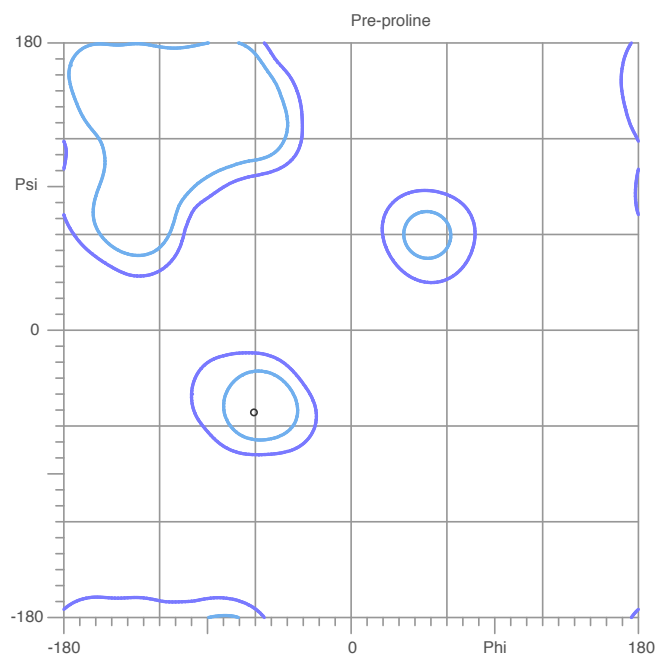
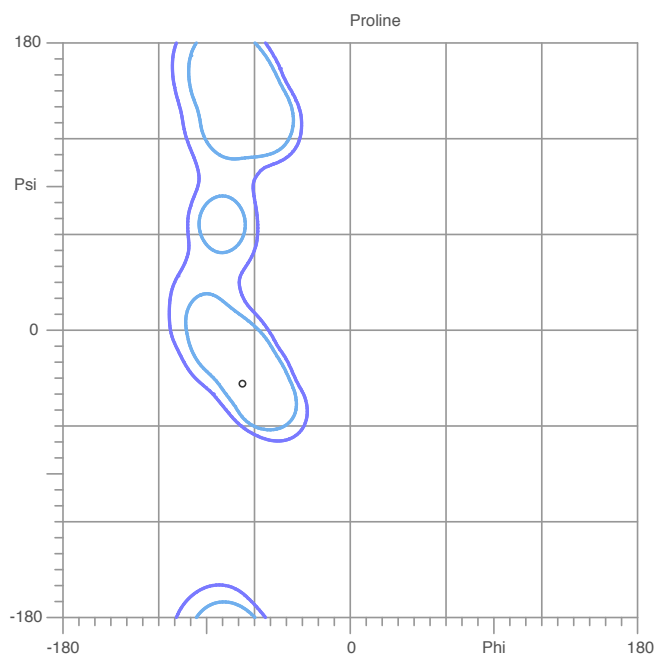
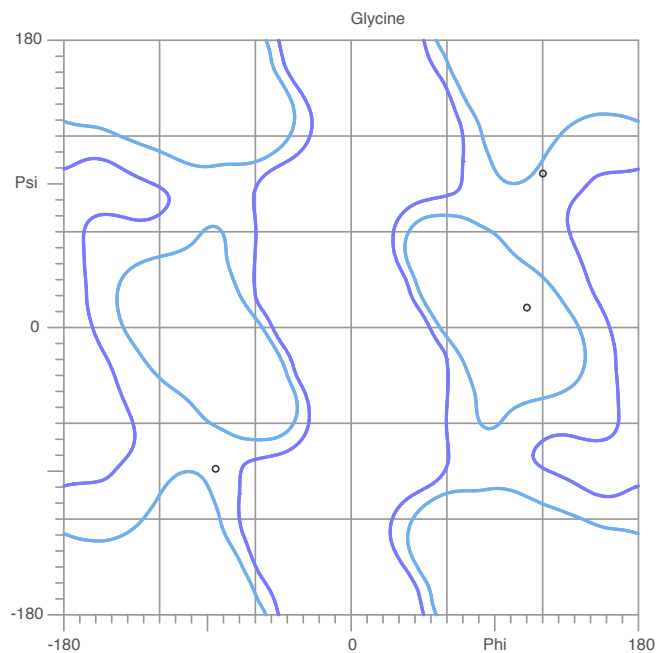
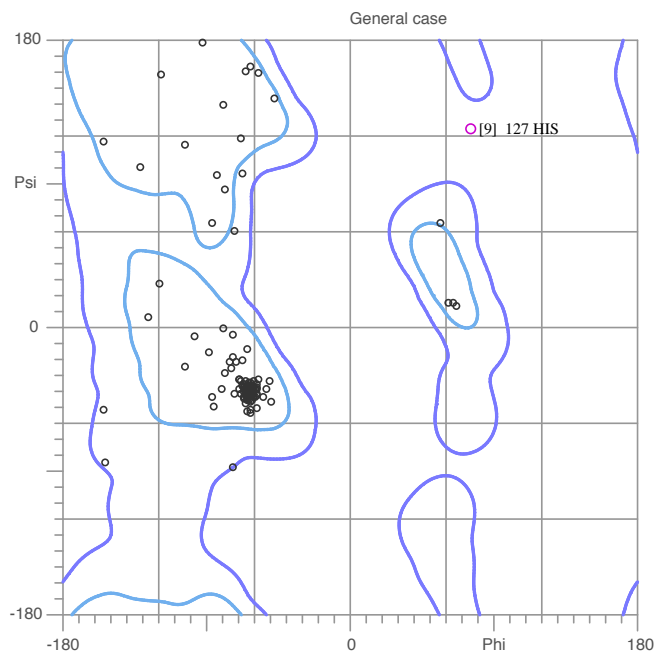
93.7% (119/127) of all residues were in favored (98%) regions.  
97.6% (124/127) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 4 SER (65.0, 105.0)
- [8] 95 HIS (65.0, 97.2)
- [8] 96 GLU (74.5, 135.0)

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 9



92.9% (118/127) of all residues were in favored (98%) regions.  
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

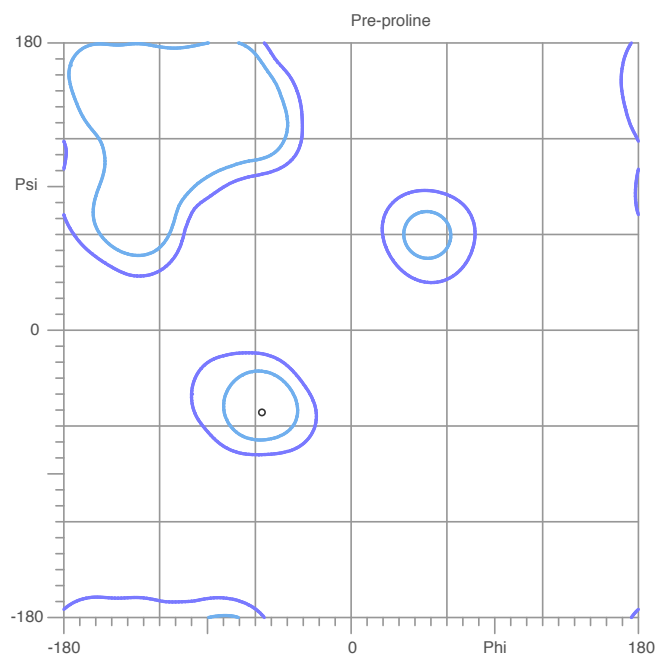
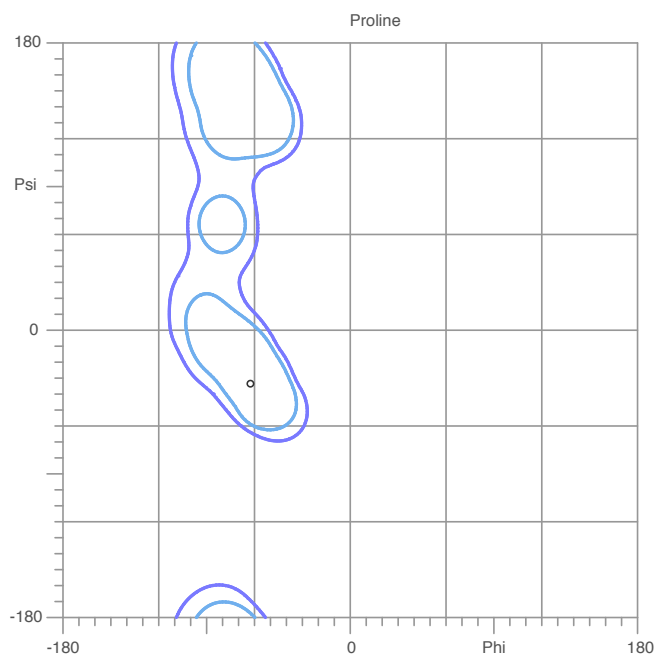
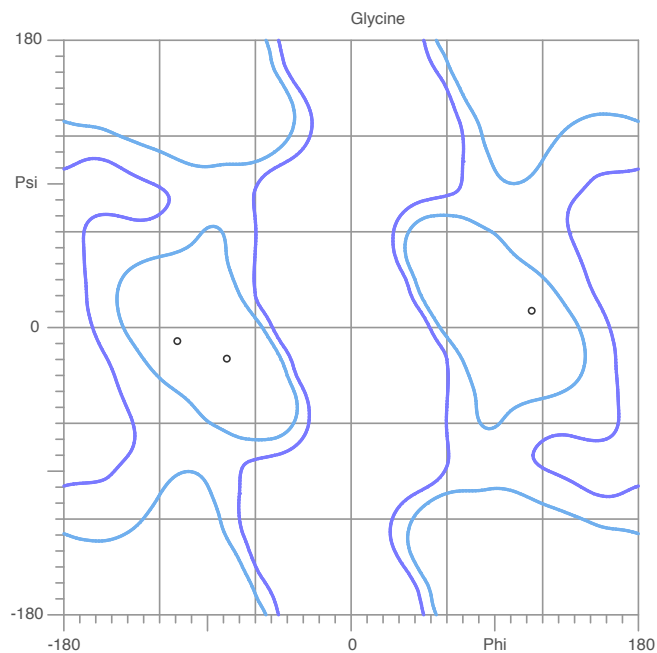
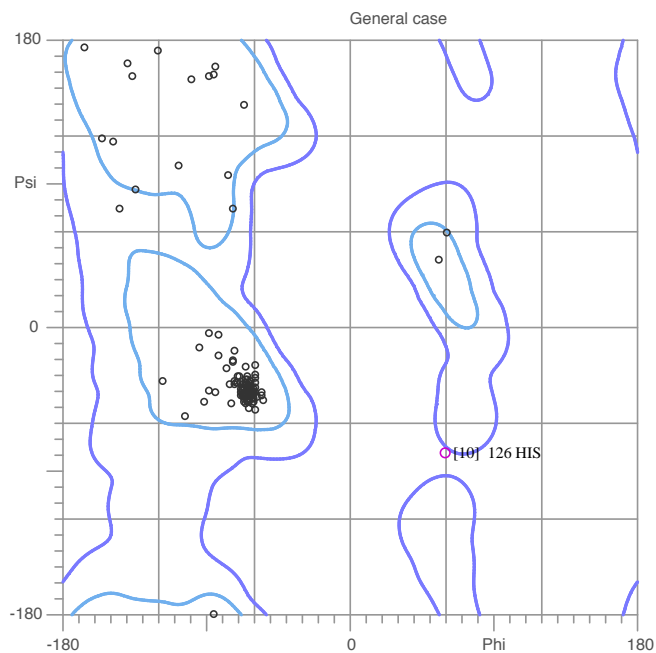
There were 1 outliers (phi, psi):  
[9] 127 HIS (75.0, 125.1)

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# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 10



98.4% (125/127) of all residues were in favored (98%) regions.  
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

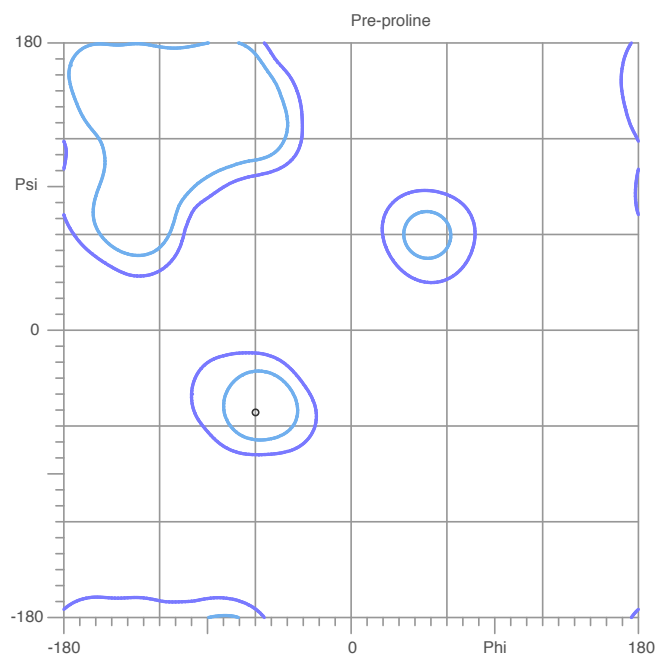
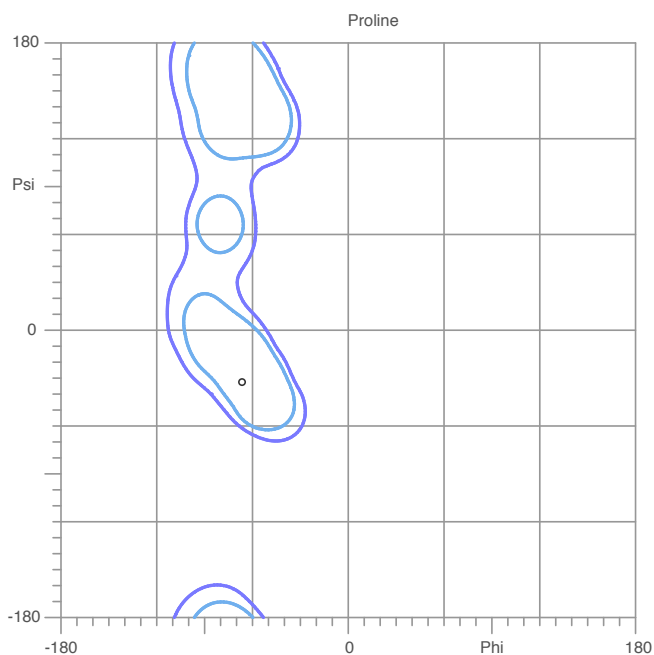
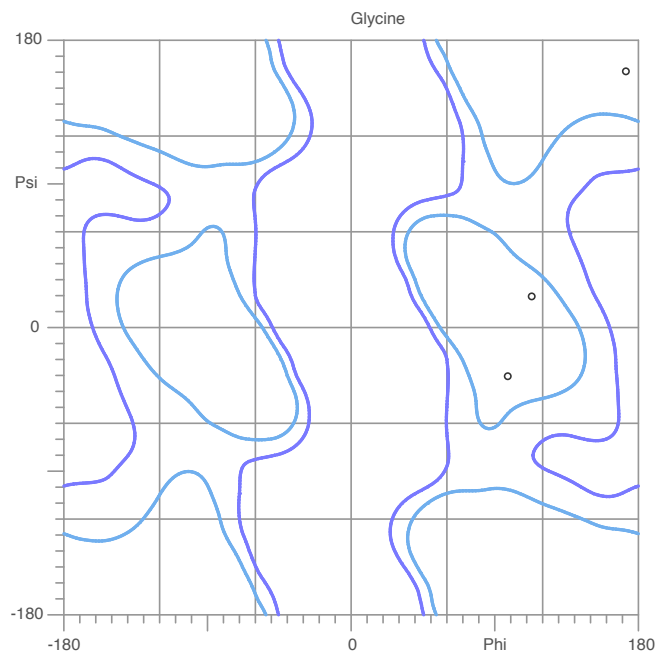
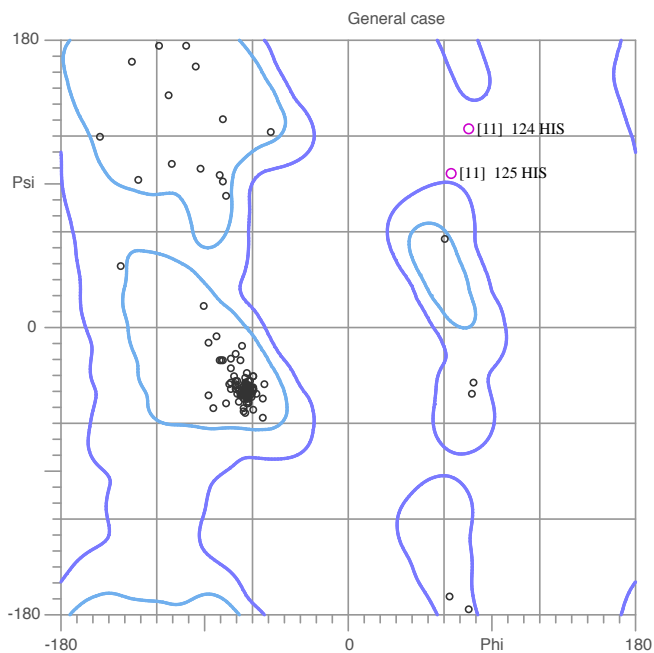
There were 1 outliers (phi, psi):  
[10] 126 HIS (59.3, -78.8)

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# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 11

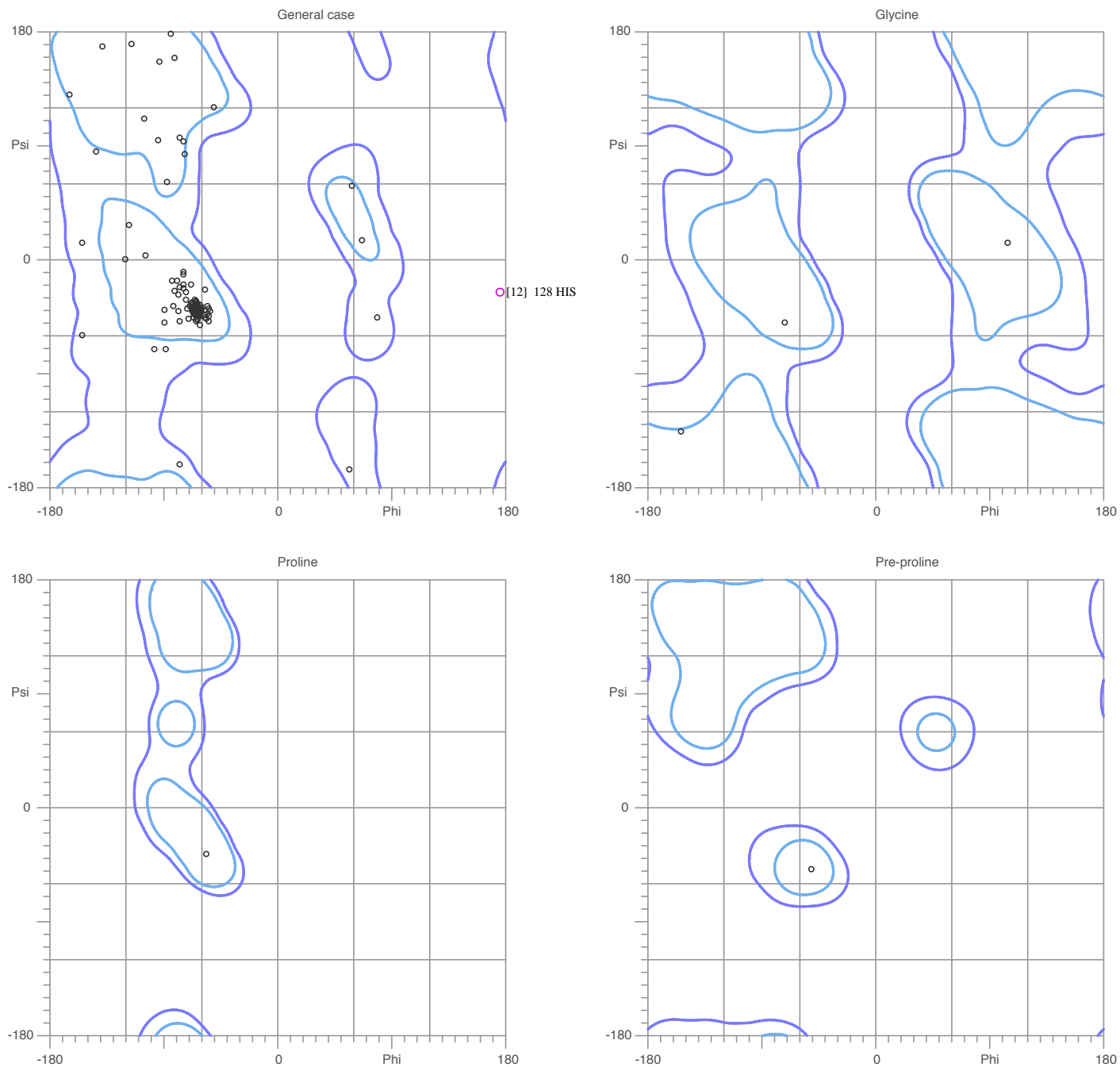


94.5% (120/127) of all residues were in favored (98%) regions.  
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[11] 124 HIS (75.2, 125.1)  
[11] 125 HIS (64.8, 97.9)

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 12



92.9% (118/127) of all residues were in favored (98%) regions.  
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

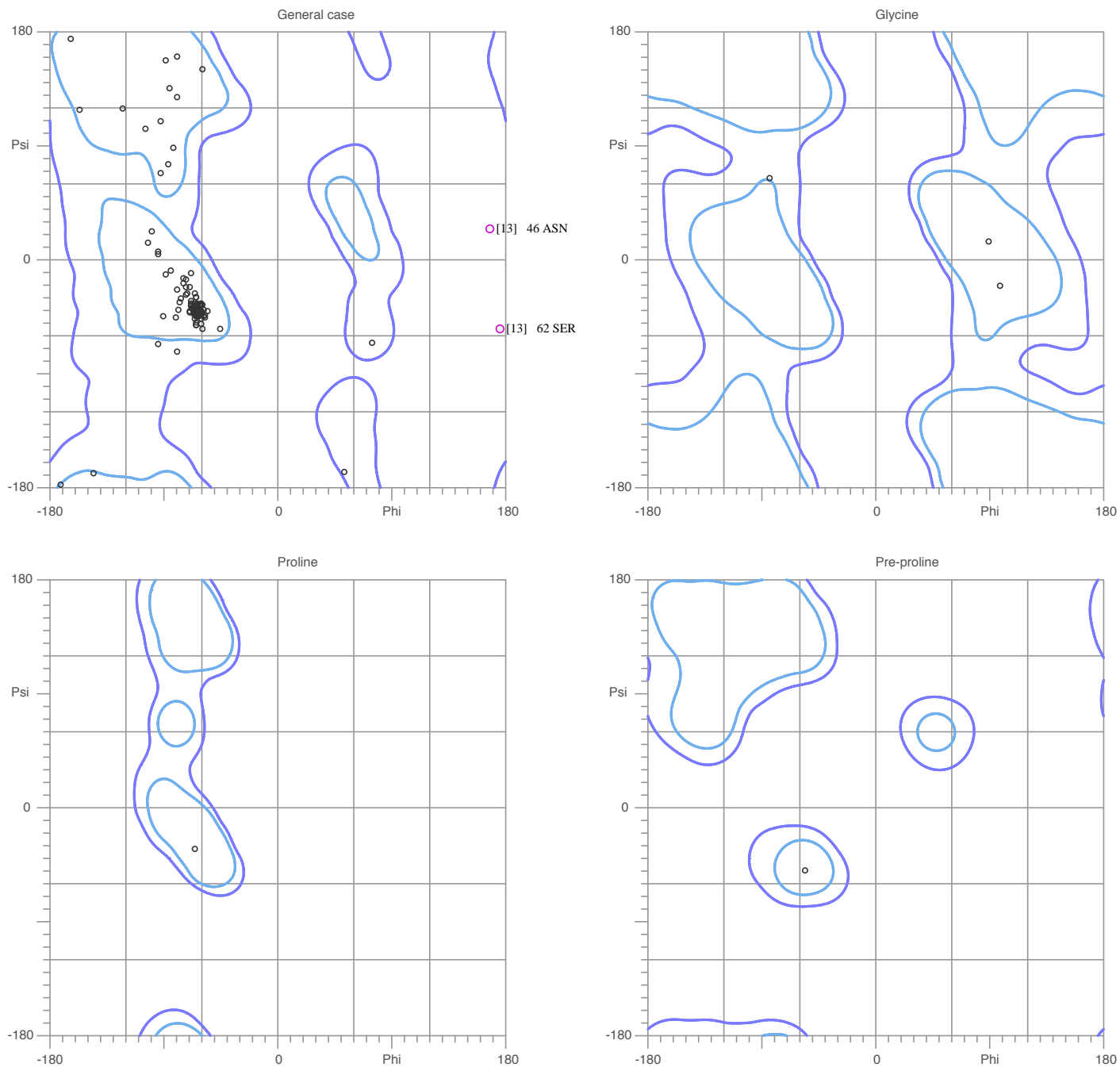
There were 1 outliers (phi, psi):  
[12] 128 HIS (175.0, -25.1)

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# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 13

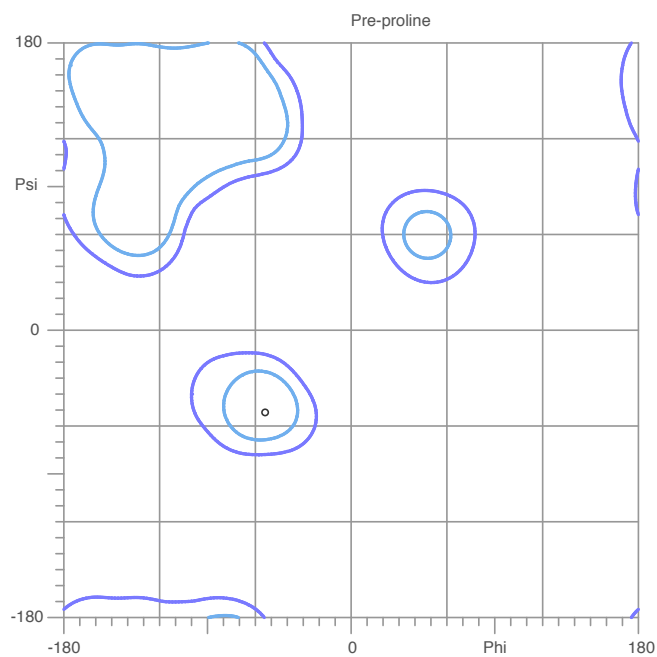
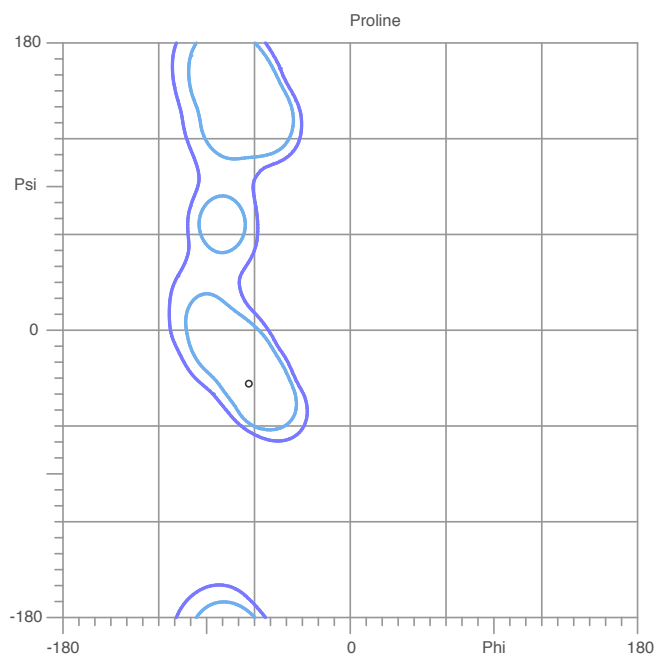
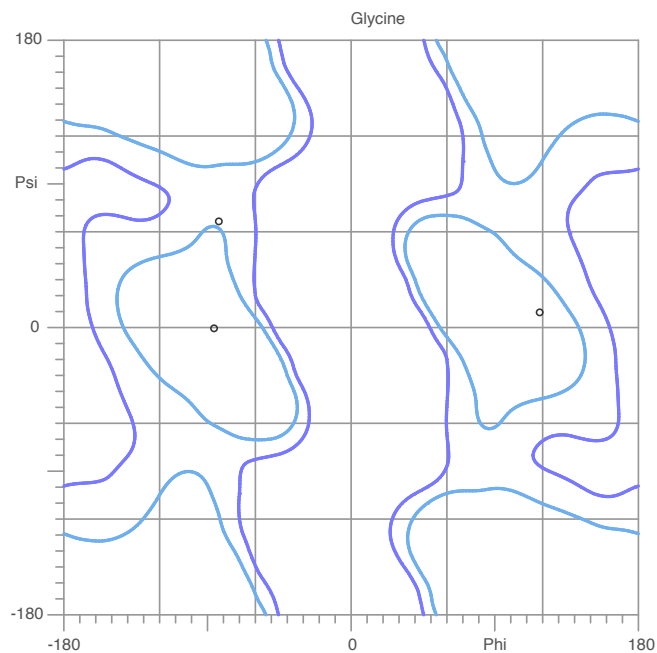
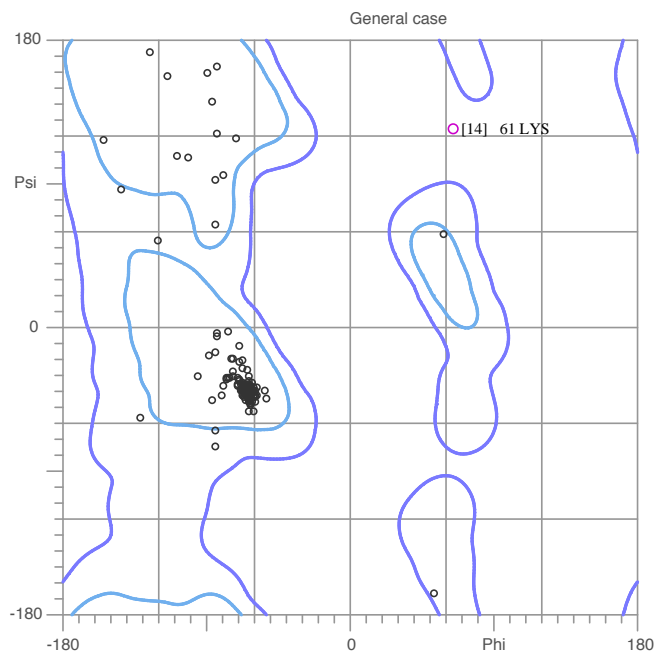


93.7% (119/127) of all residues were in favored (98%) regions.  
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[13] 46 ASN (167.3, 25.1)  
[13] 62 SER (175.1, -54.5)

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 14



93.7% (119/127) of all residues were in favored (98%) regions.  
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

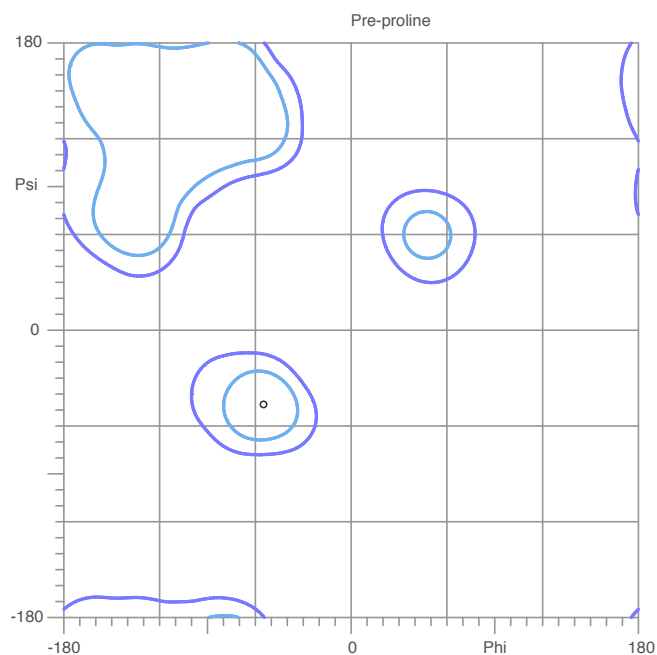
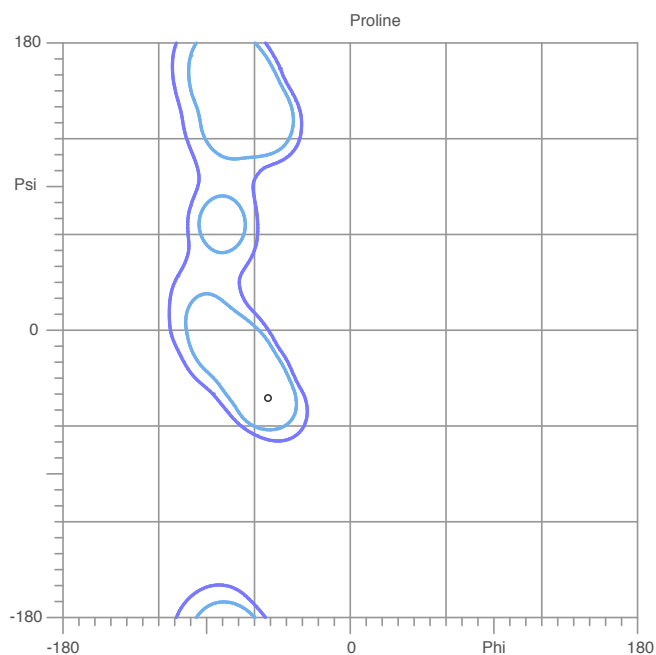
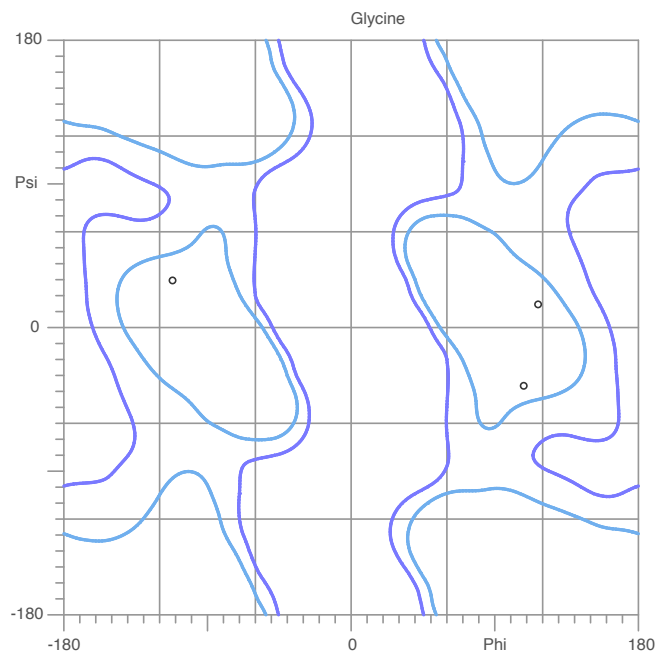
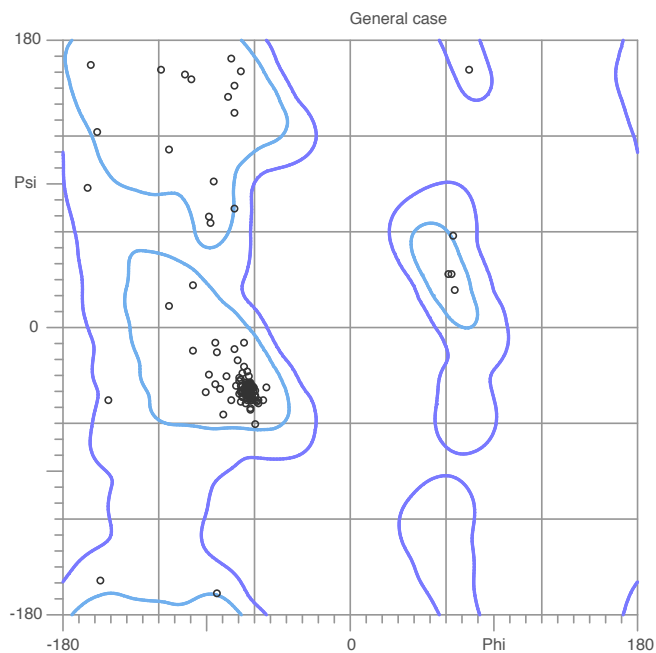
There were 1 outliers (phi, psi):  
[14] 61 LYS (64.9, 125.8)

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# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 15



95.3% (121/127) of all residues were in favored (98%) regions.  
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

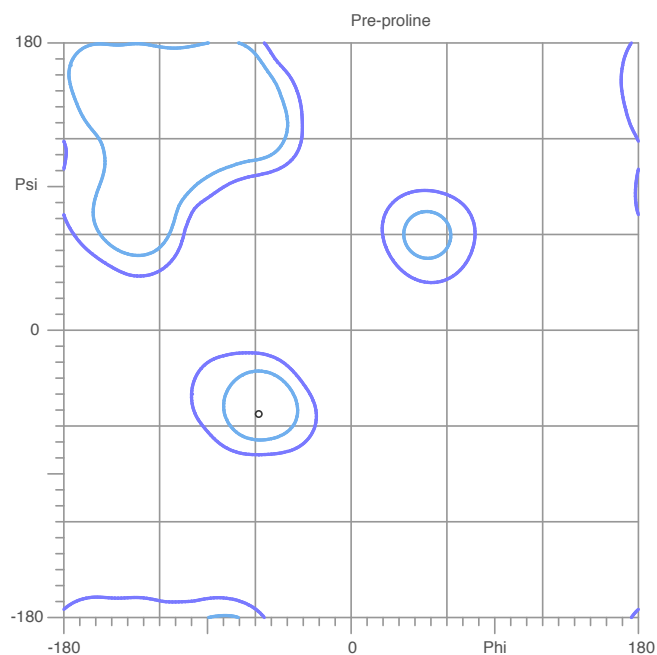
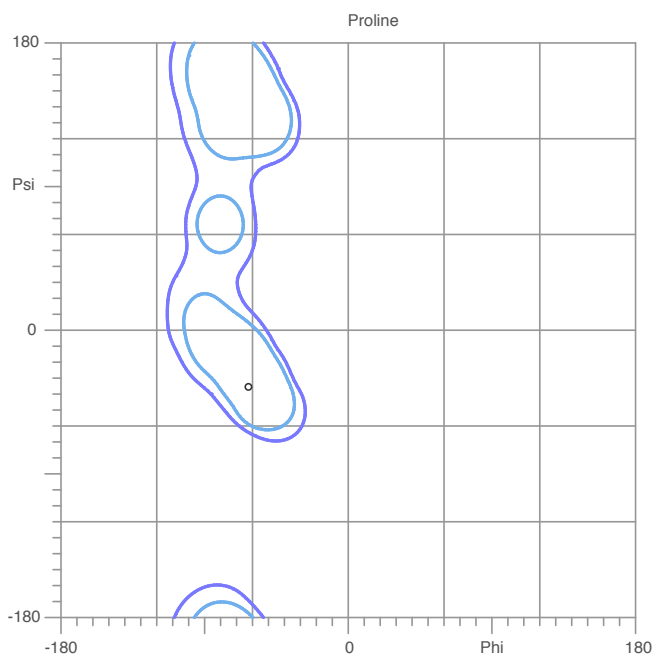
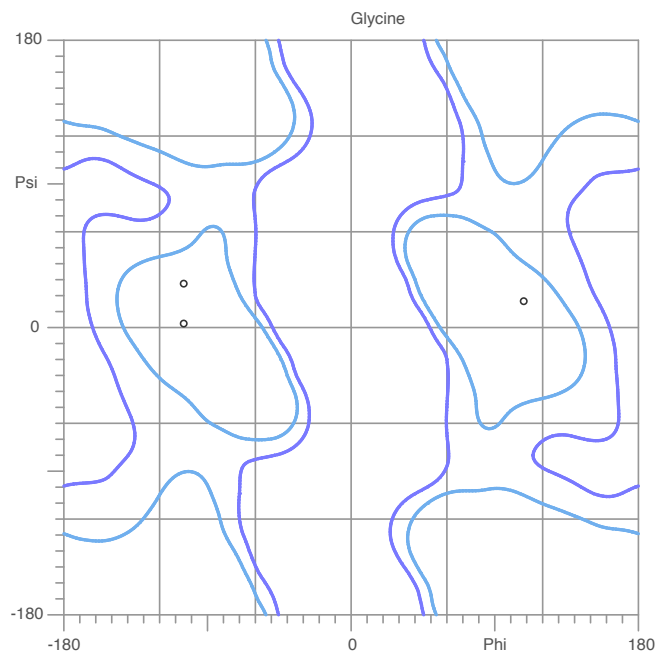
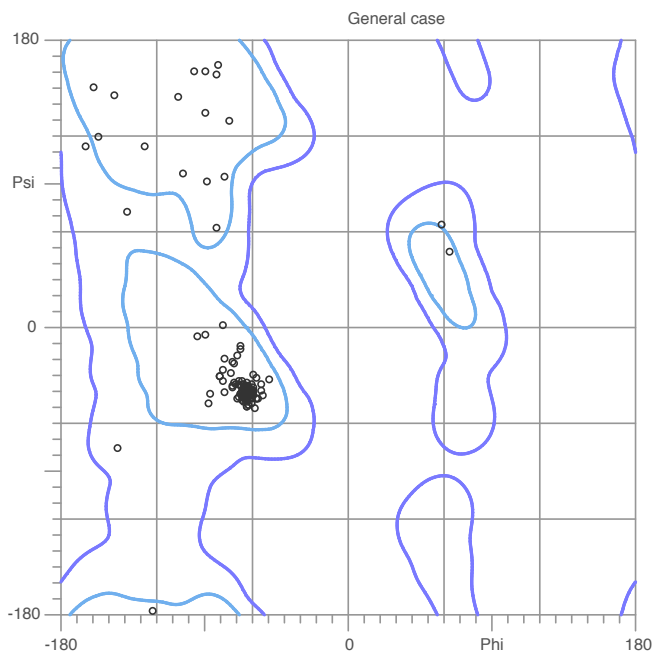
There were no outliers.

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# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 16



96.9% (123/127) of all residues were in favored (98%) regions.  
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

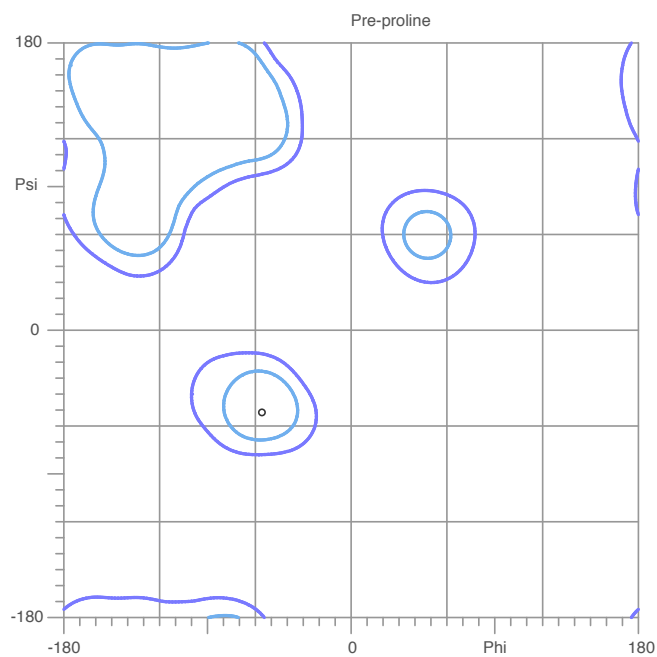
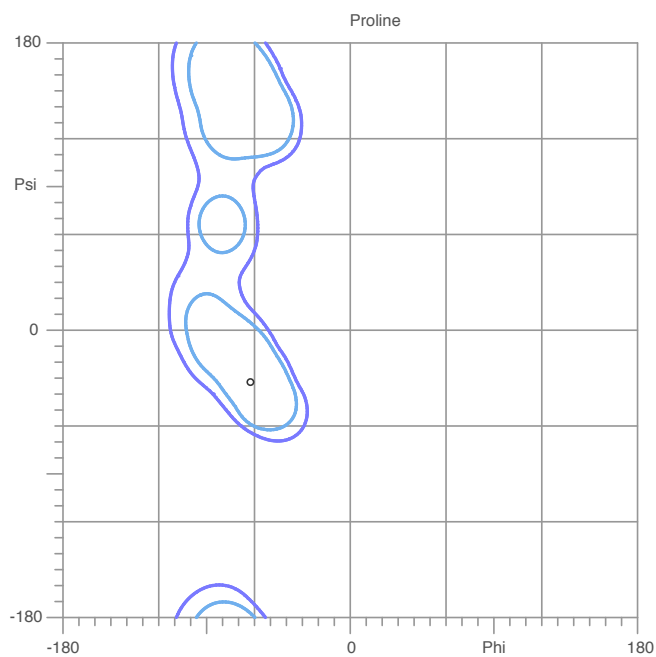
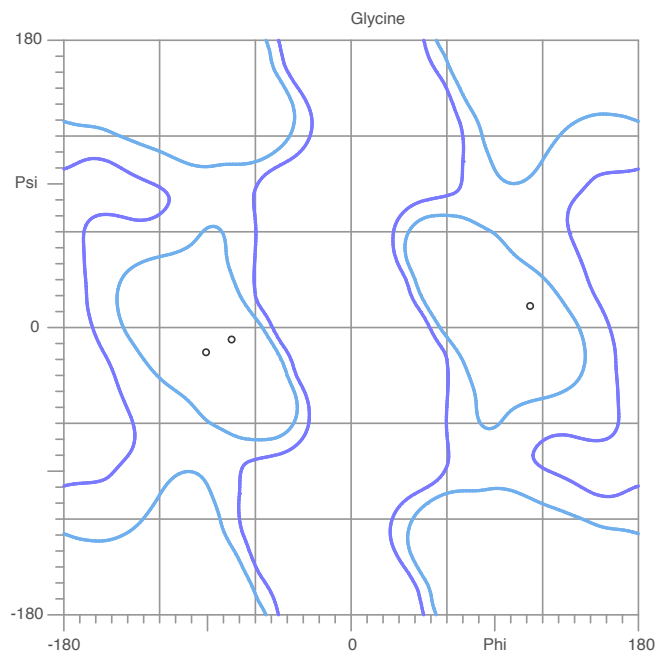
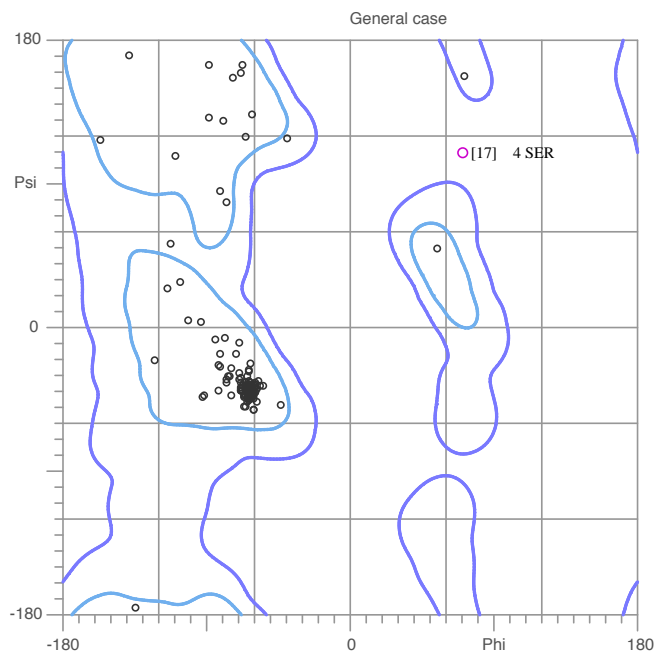
There were no outliers.

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# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 17



96.9% (123/127) of all residues were in favored (98%) regions.  
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

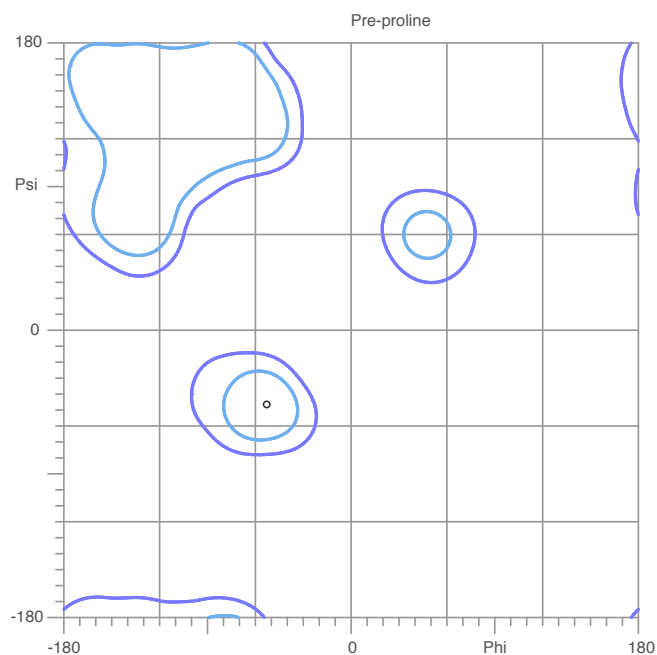
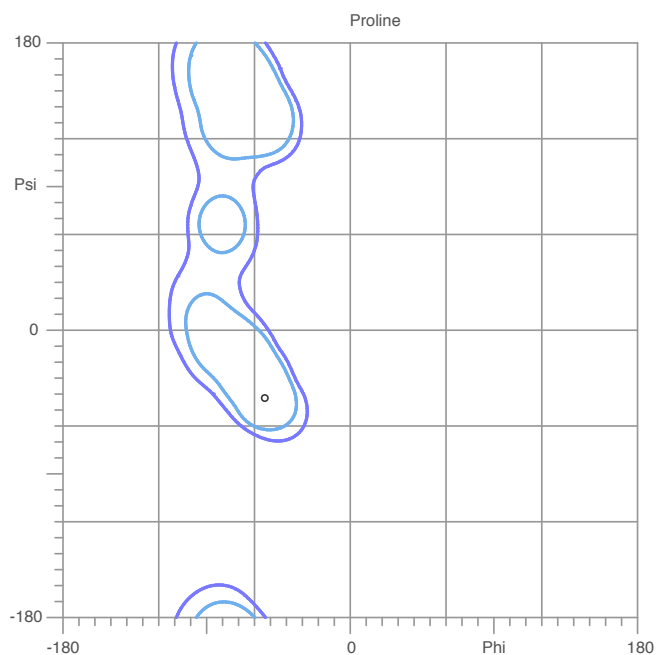
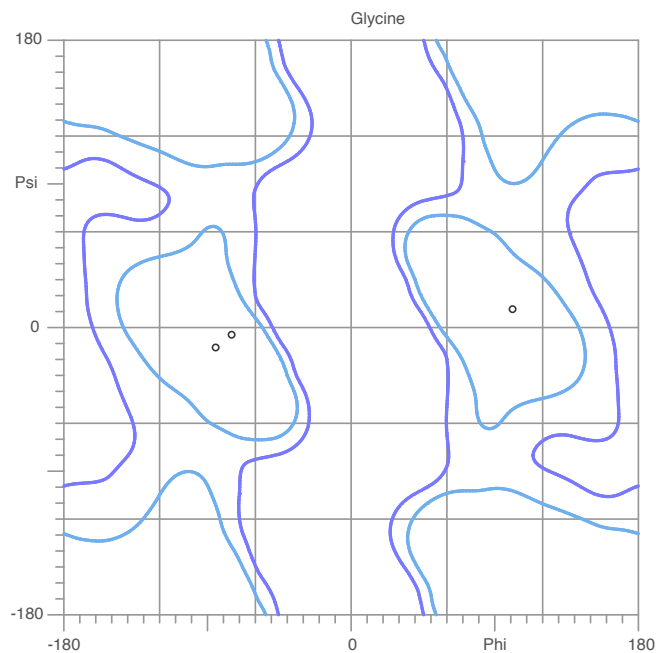
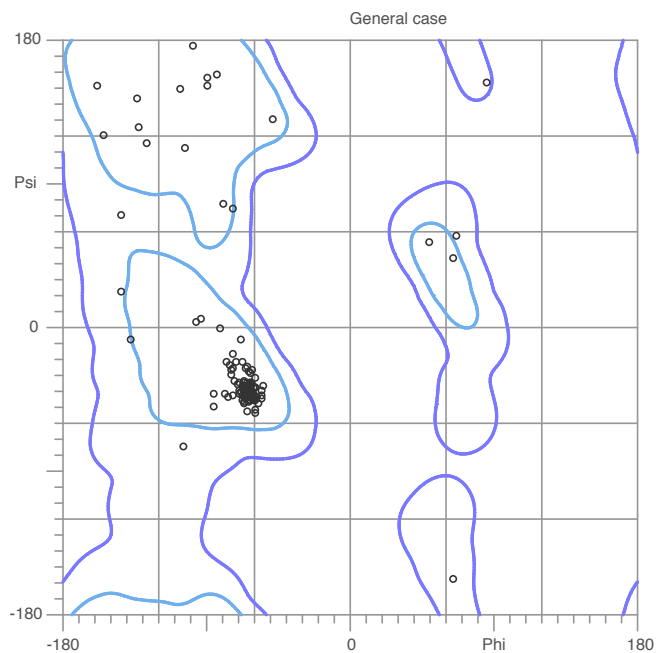
There were 1 outliers (phi, psi):  
[17] 4 SER (71.0, 110.1)

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# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 18



94.5% (120/127) of all residues were in favored (98%) regions.  
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

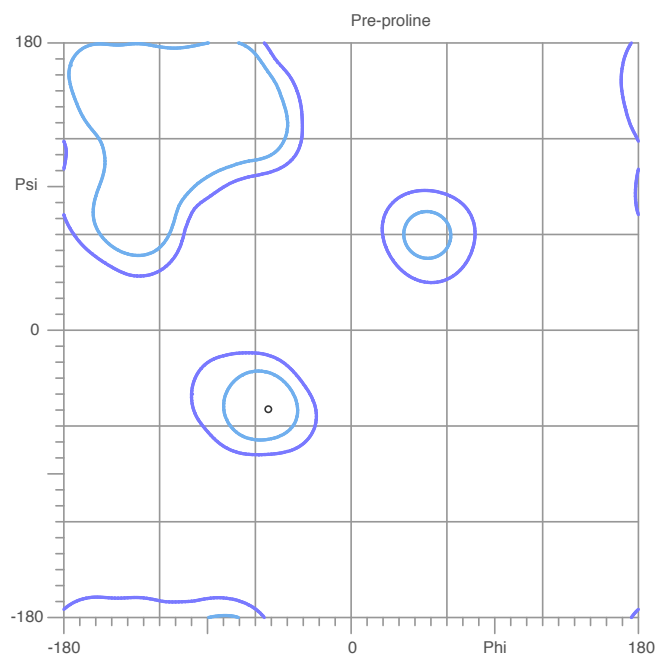
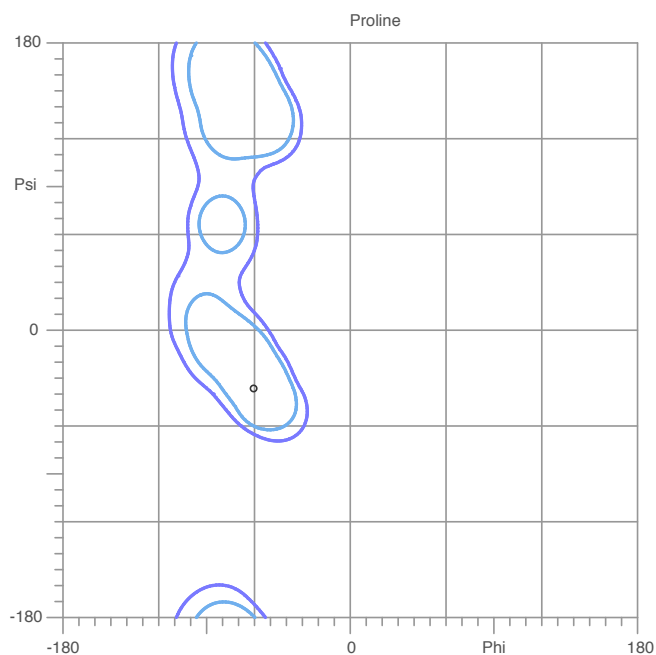
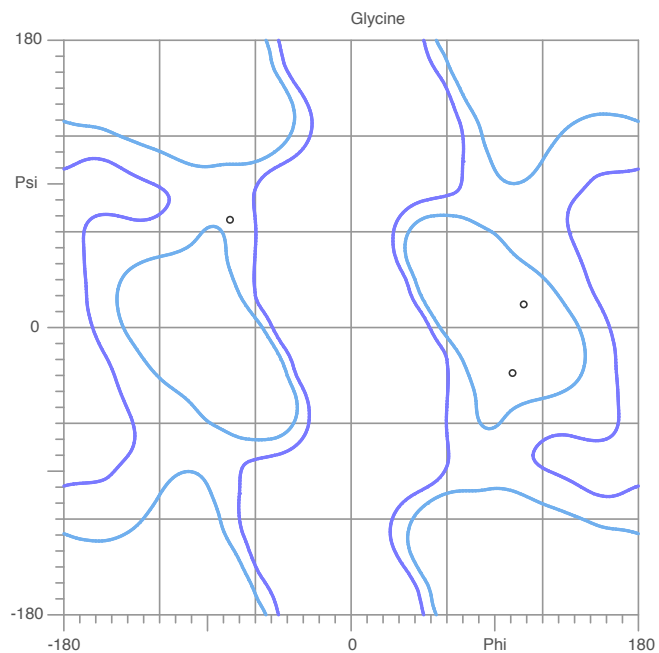
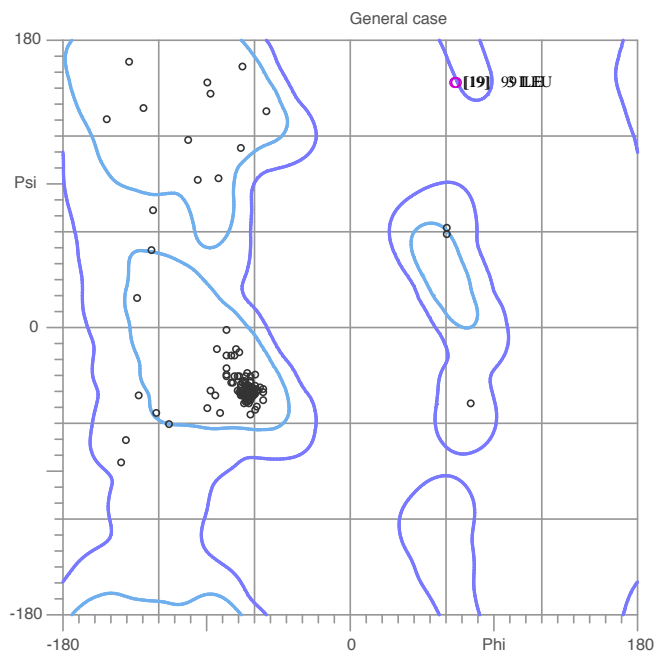
There were no outliers.

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# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 19



92.1% (117/127) of all residues were in favored (98%) regions.  
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

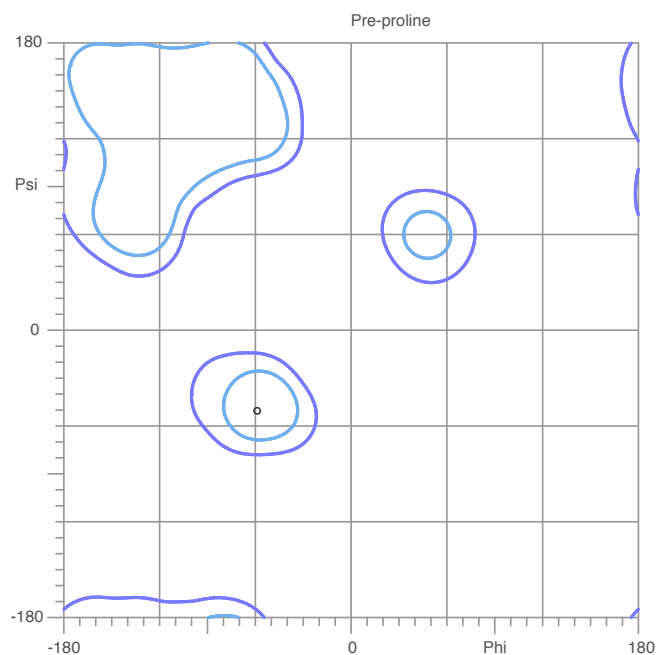
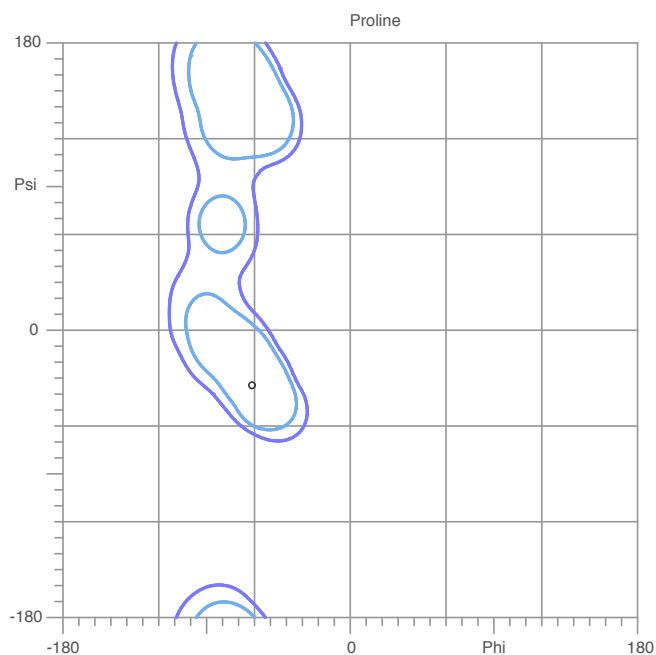
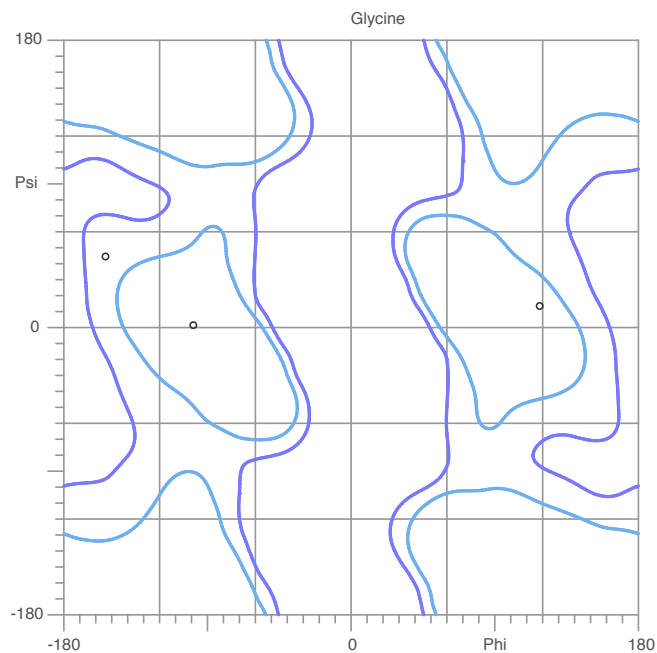
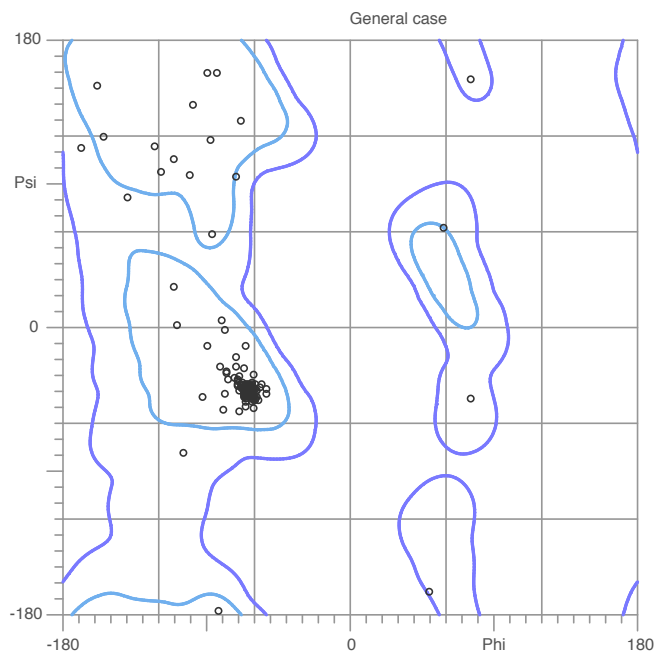
There were 2 outliers (phi, psi):

[19] 3 ILE (66.7, 154.2)

[19] 99 LEU (65.8, 155.0)

# MolProbity Ramachandran analysis

SSR10\_R3Cons\_em\_bcr3.pdb, model 20



93.7% (119/127) of all residues were in favored (98%) regions.  
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

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