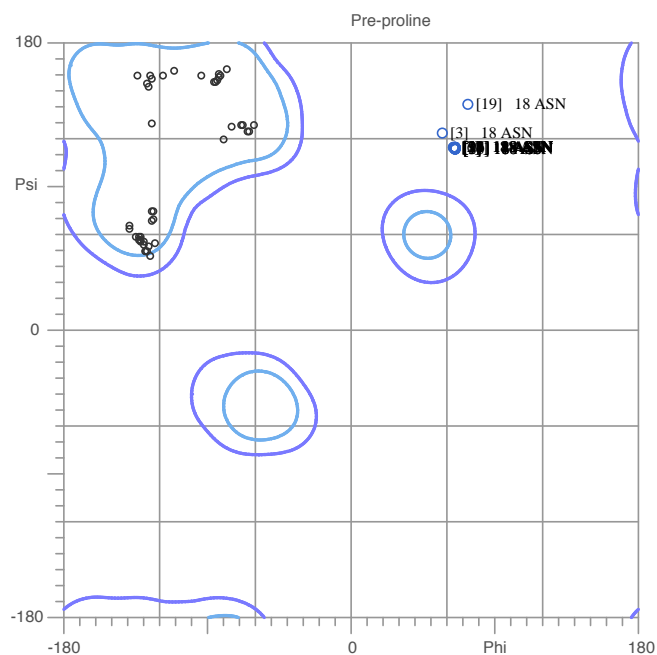
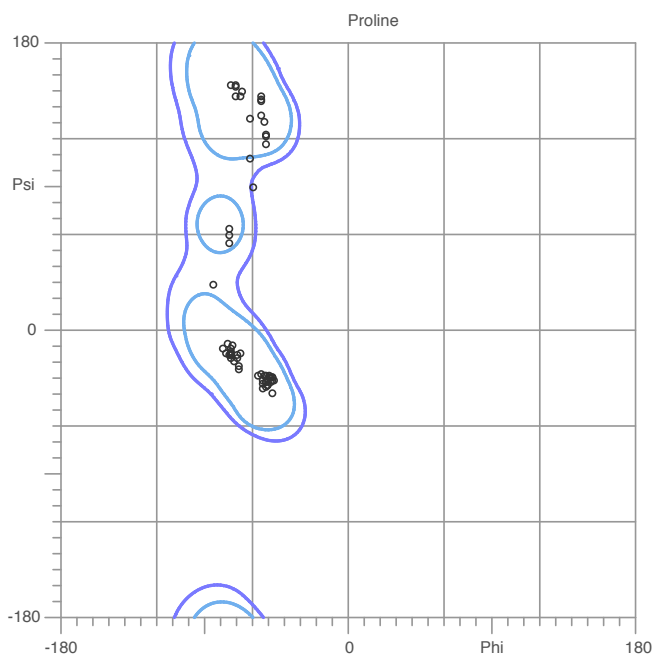
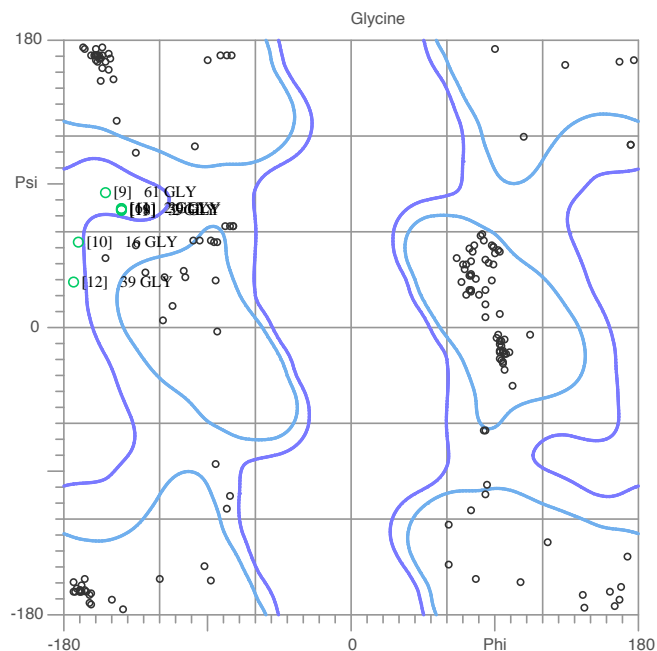
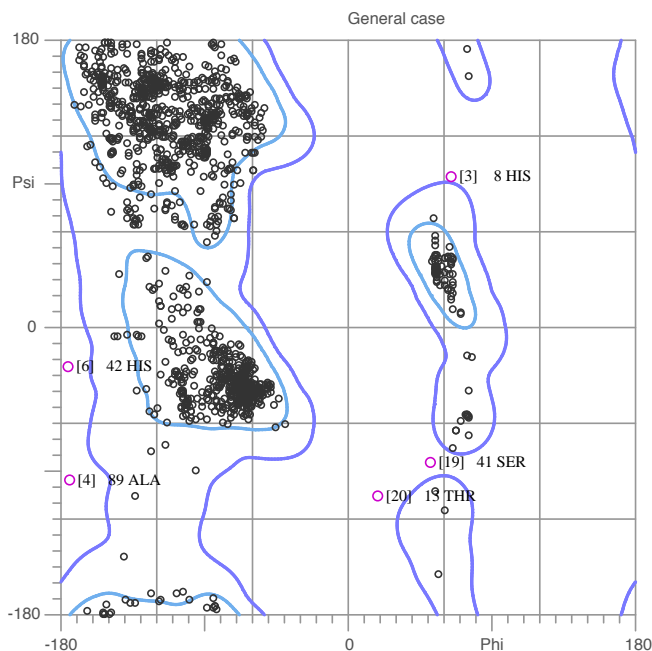


# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, all models



92.7% (1650/1780) of all residues were in favored (98%) regions.  
98.4% (1751/1780) of all residues were in allowed (>99.8%) regions.

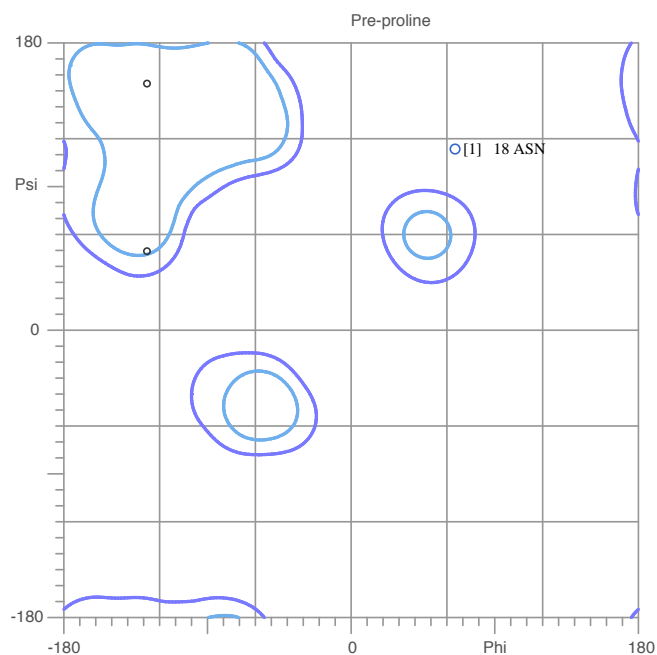
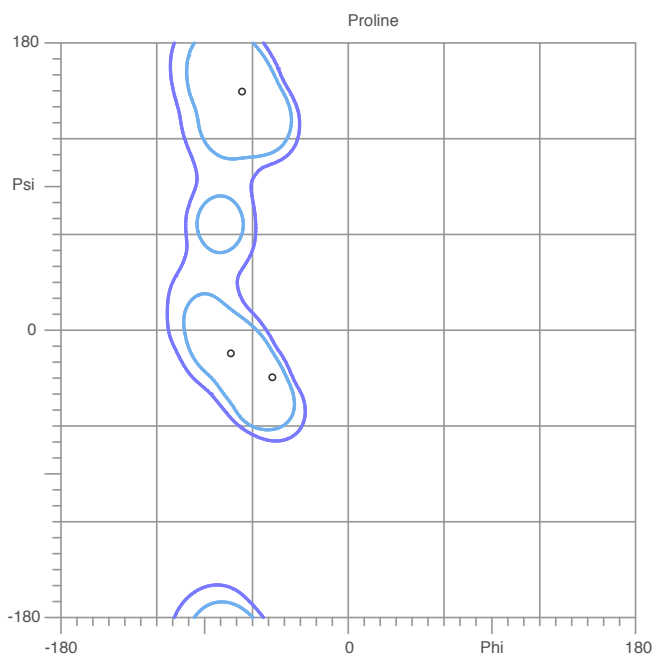
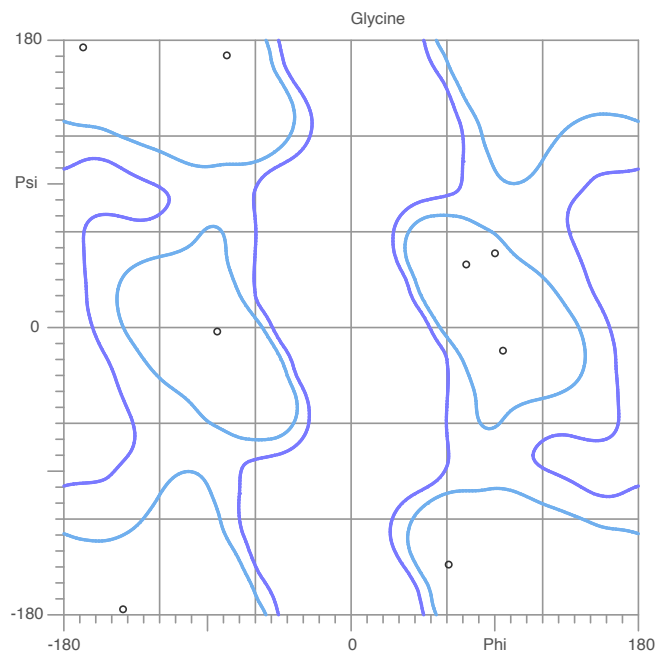
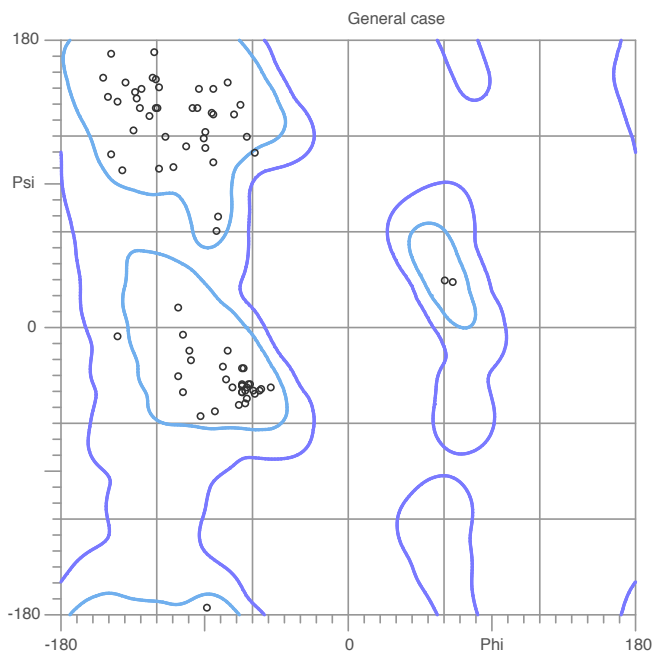
There were 29 outliers (phi, psi):

- [1] 18 ASN (65.0, 115.0)
- [2] 18 ASN (65.1, 115.0)
- [3] 8 HIS (65.0, 95.1)
- [3] 18 ASN (57.3, 124.8)
- [4] 89 ALA (-175.1, -95.0)
- [5] 18 ASN (65.0, 115.0)
- [6] 2 GLY (-144.9, 75.0)
- [6] 18 ASN (65.0, 115.0)
- [6] 42 HIS (-176.9, -25.0)
- [7] 18 ASN (64.9, 115.0)
- [8] 18 ASN (65.0, 114.9)
- [9] 18 ASN (65.0, 115.0)

- [9] 61 GLY (-155.0, 85.1)
- [10] 16 GLY (-171.9, 55.0)
- [10] 18 ASN (65.1, 115.0)
- [11] 18 ASN (65.0, 115.1)
- [11] 39 GLY (-145.0, 75.1)
- [12] 39 GLY (-175.0, 29.9)
- [13] 18 ASN (65.1, 115.0)
- [14] 18 ASN (65.0, 115.0)
- [15] 18 ASN (65.1, 115.0)
- [16] 18 ASN (65.0, 115.1)
- [17] 18 ASN (65.0, 115.0)
- [18] 2 GLY (-145.0, 74.9)
- [19] 18 ASN (73.8, 142.2)
- [19] 39 GLY (-144.9, 74.9)
- [19] 41 SER (52.0, -85.0)
- [20] 13 THR (18.3, -105.0)
- [20] 18 ASN (65.0, 115.1)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 1



96.6% (86/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

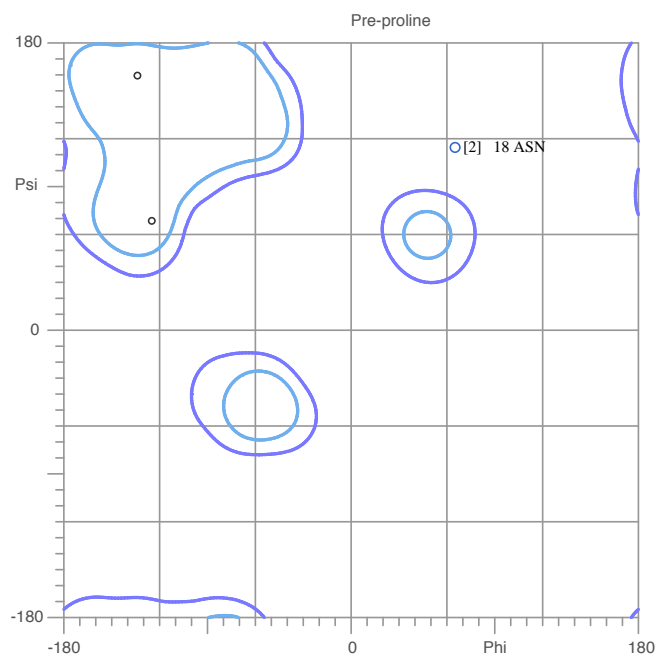
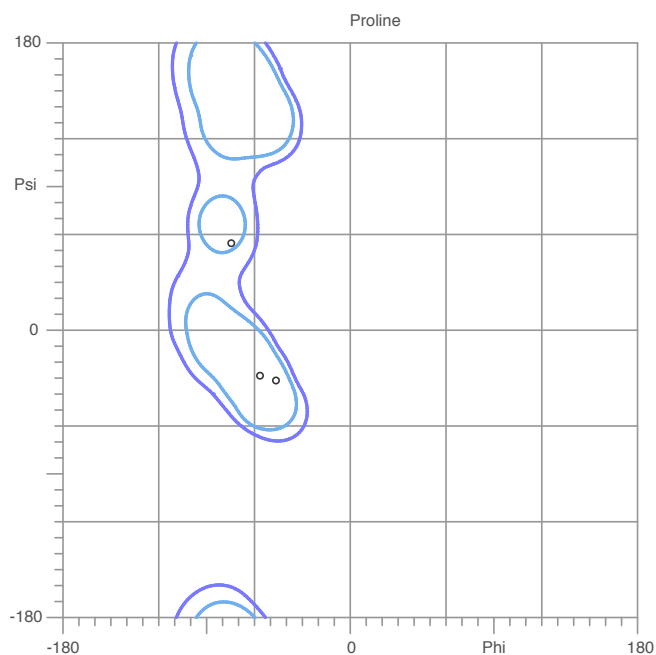
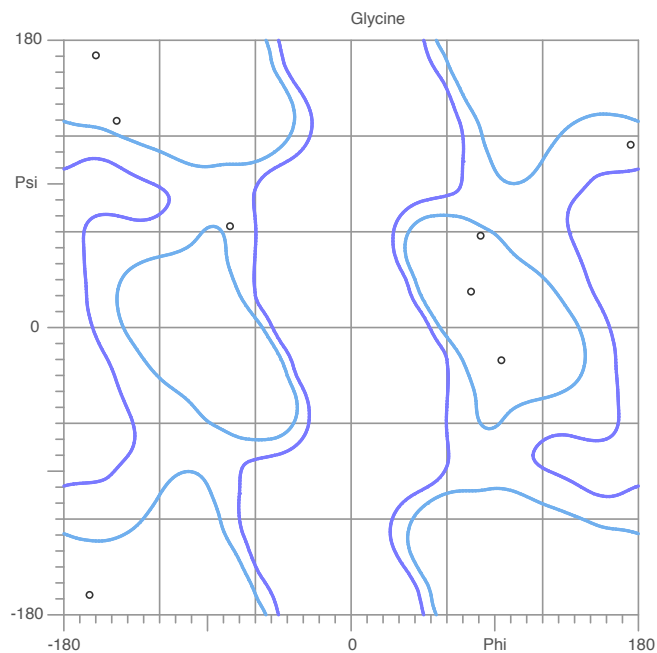
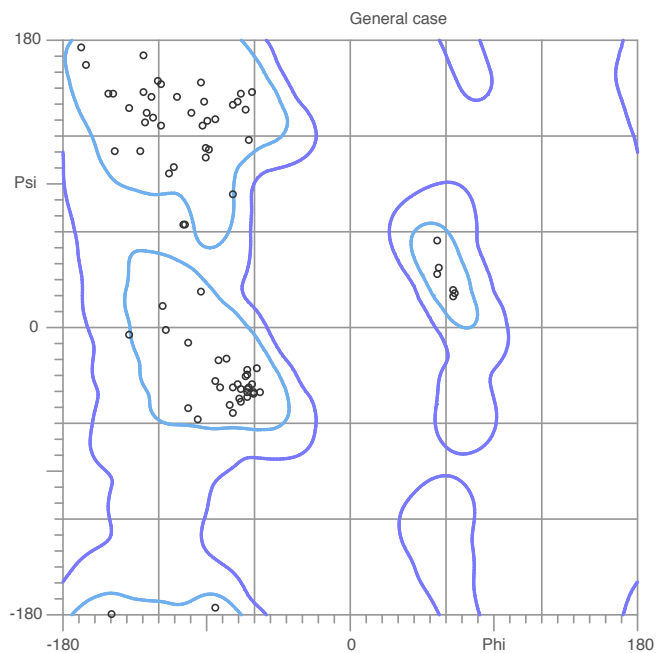
There were 1 outliers (phi, psi):  
[1] 18 ASN (65.0, 115.0)

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# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 2



93.3% (83/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

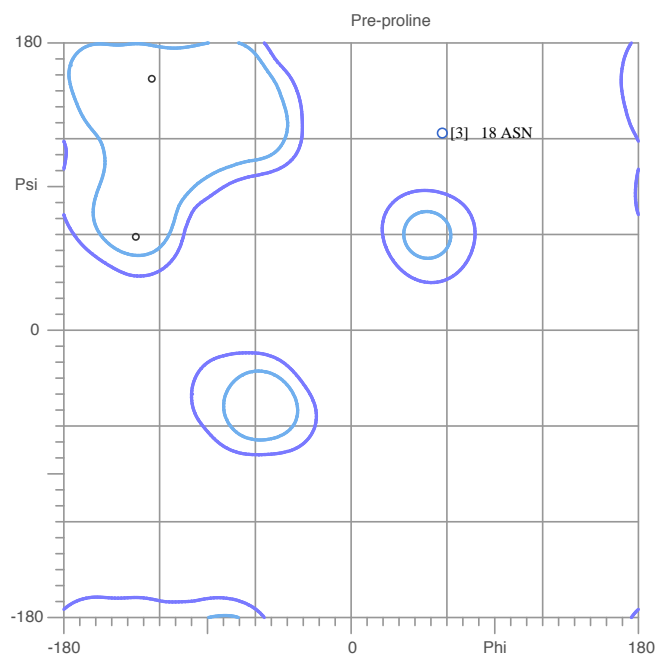
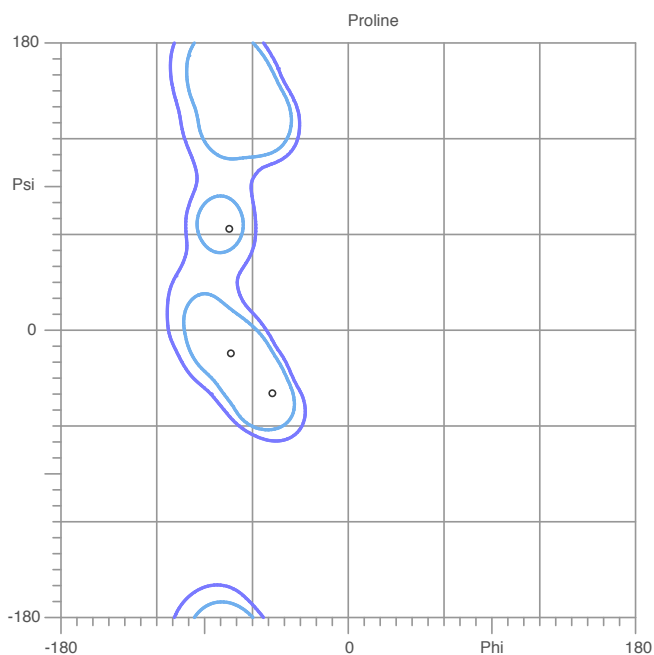
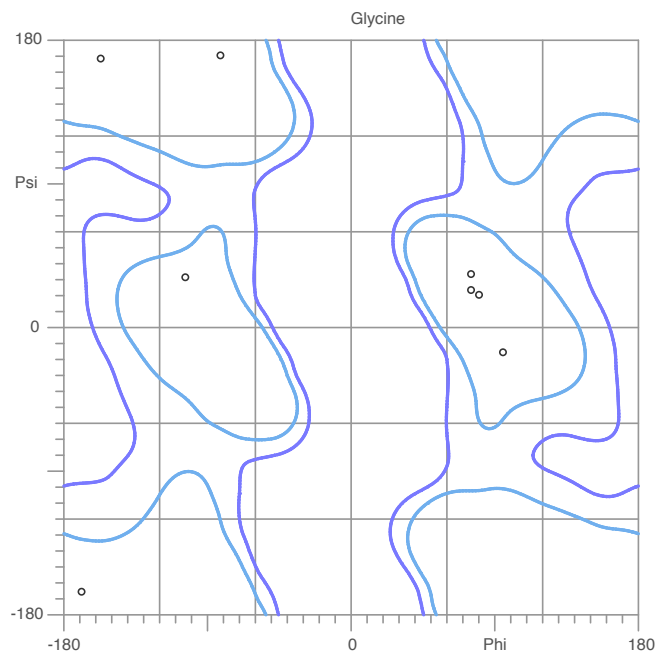
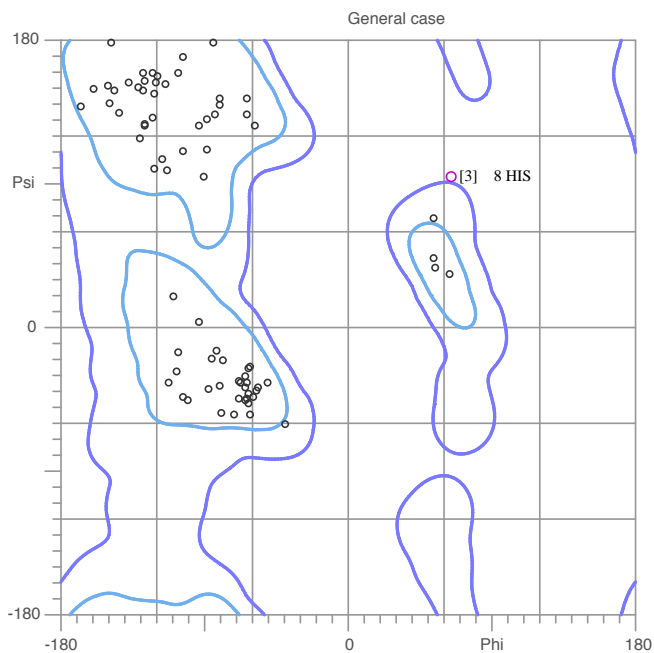
There were 1 outliers (phi, psi):  
[2] 18 ASN (65.1, 115.0)

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# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 3



95.5% (85/89) of all residues were in favored (98%) regions.  
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

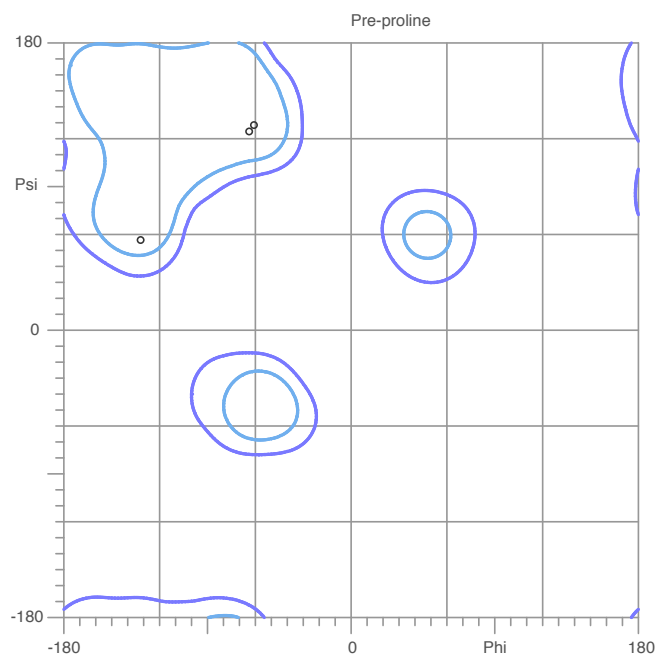
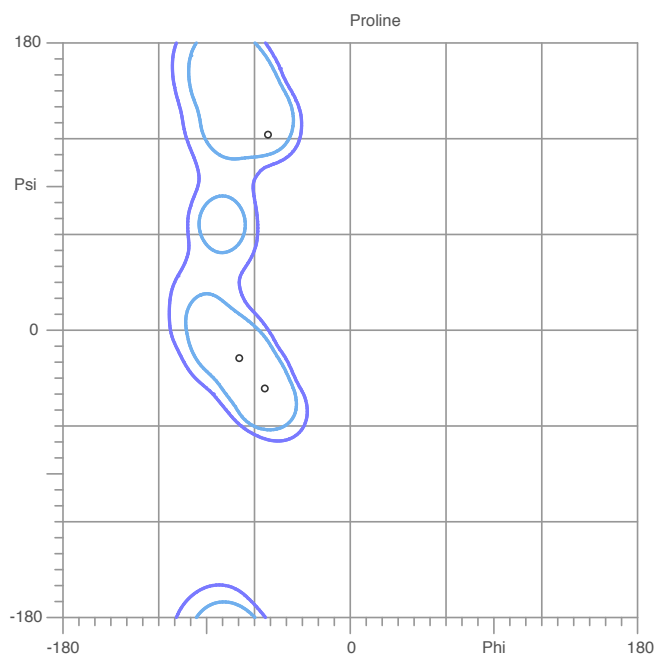
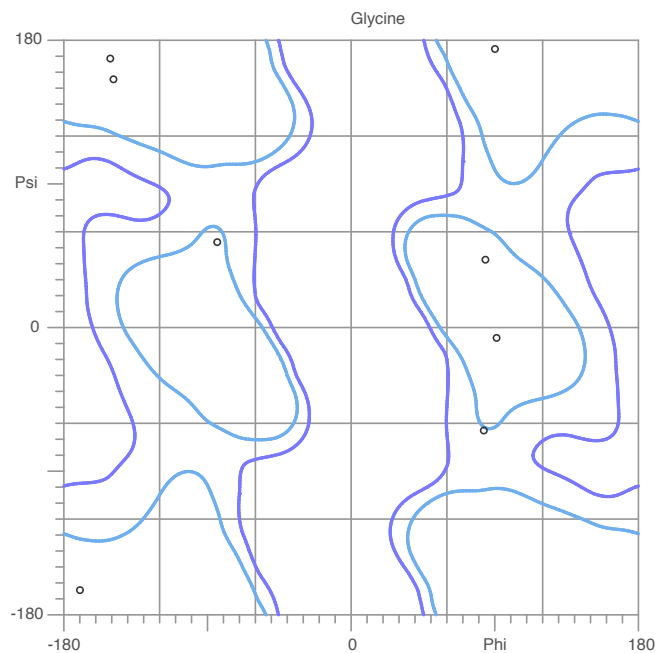
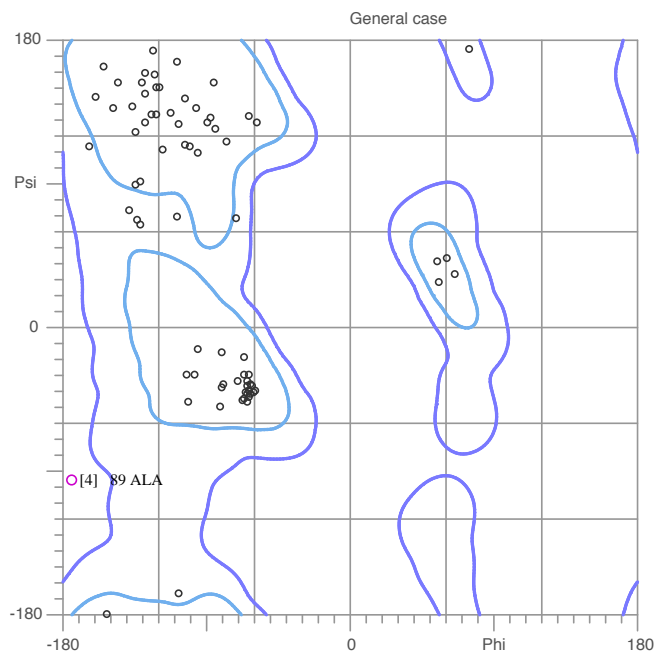
There were 2 outliers (phi, psi):

[3] 8 HIS (65.0, 95.1)

[3] 18 ASN (57.3, 124.8)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 4

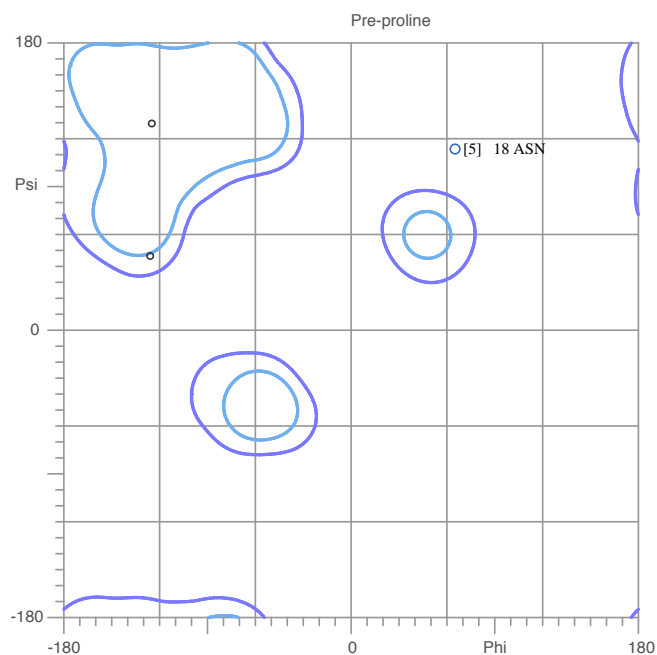
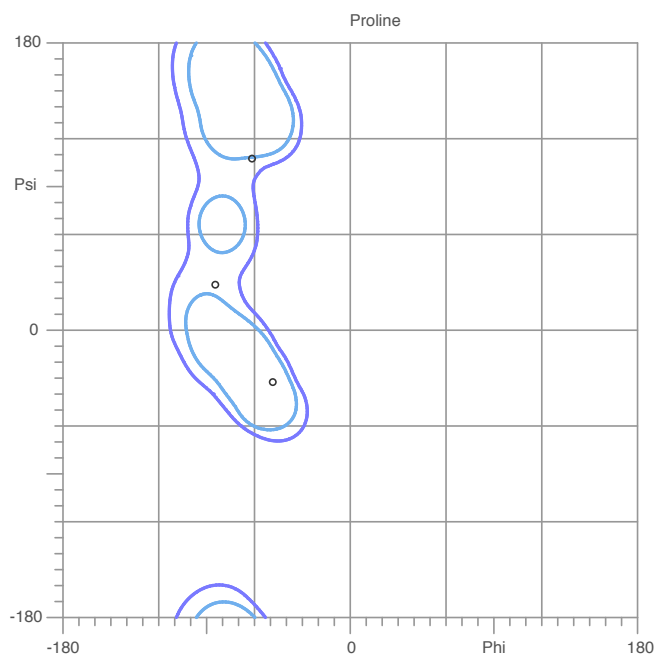
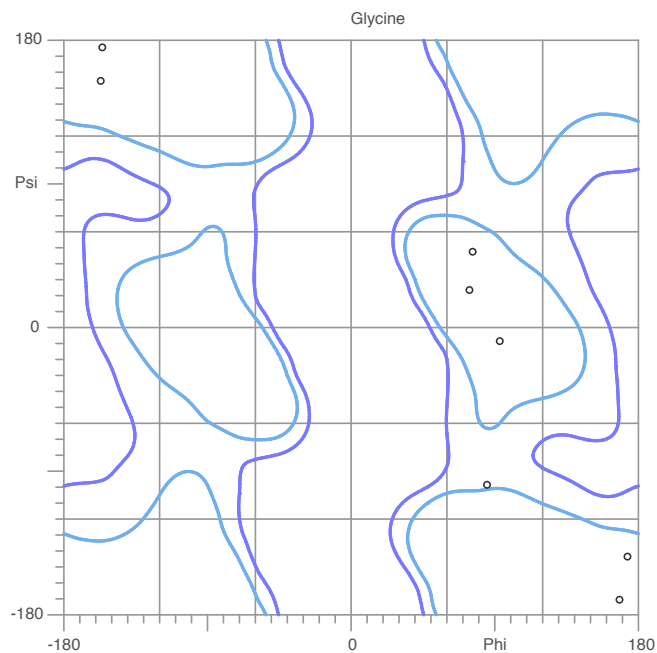
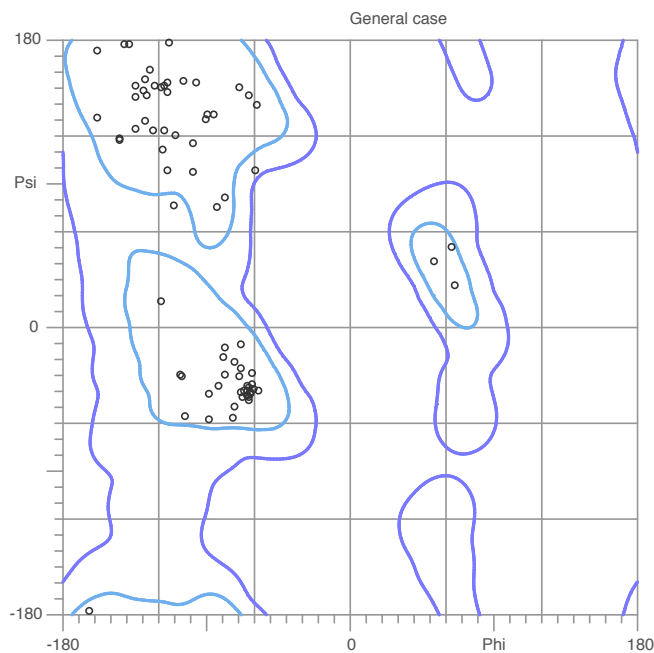


88.8% (79/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[4] 89 ALA (-175.1, -95.0)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 5



93.3% (83/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

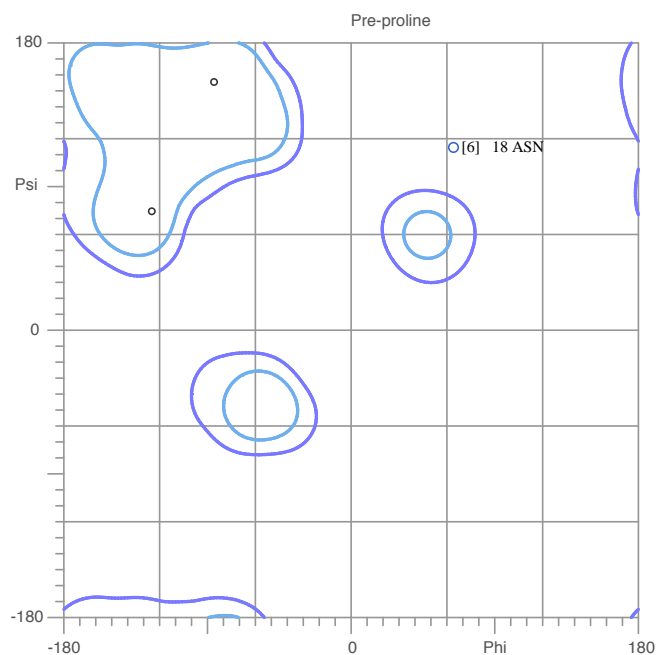
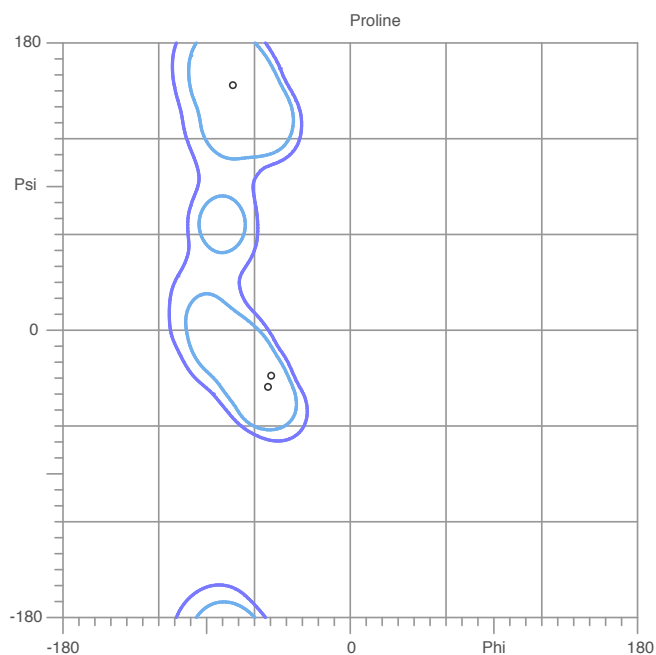
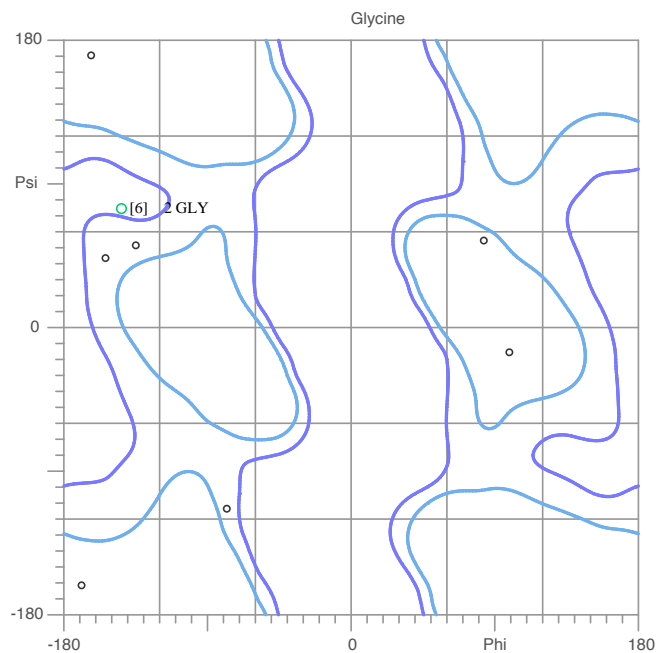
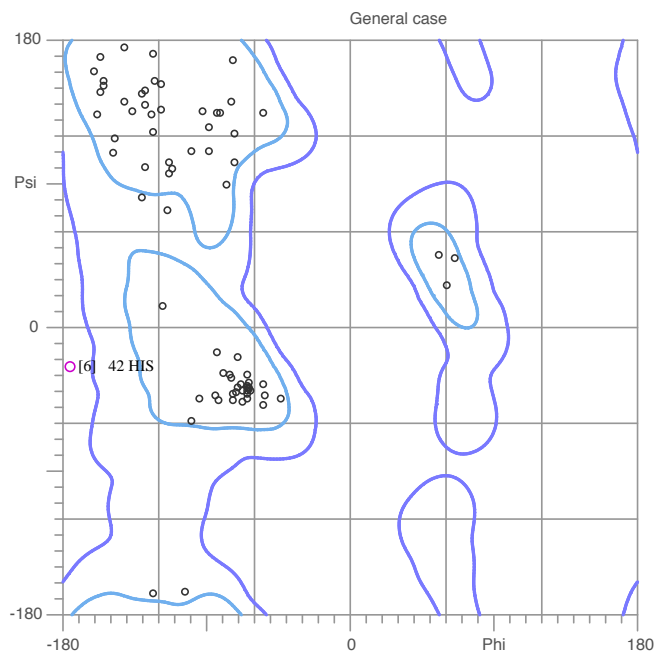
There were 1 outliers (phi, psi):  
[5] 18 ASN (65.0, 115.0)

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# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 6



88.8% (79/89) of all residues were in favored (98%) regions.  
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

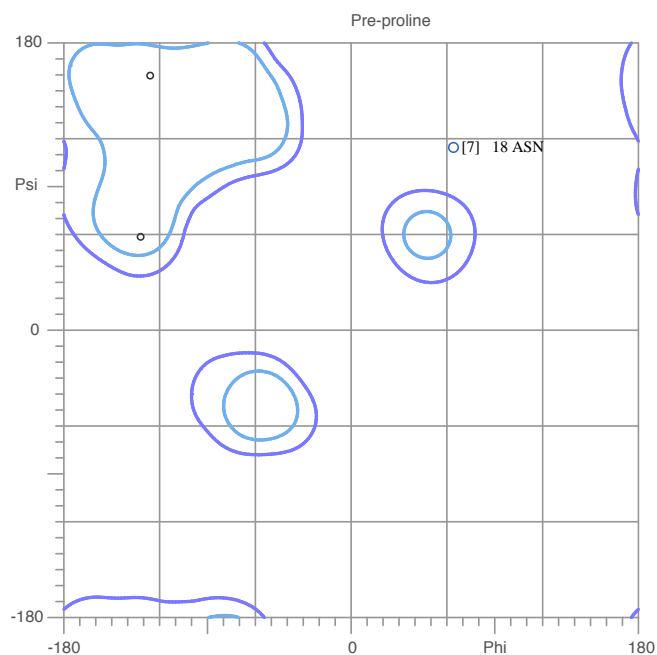
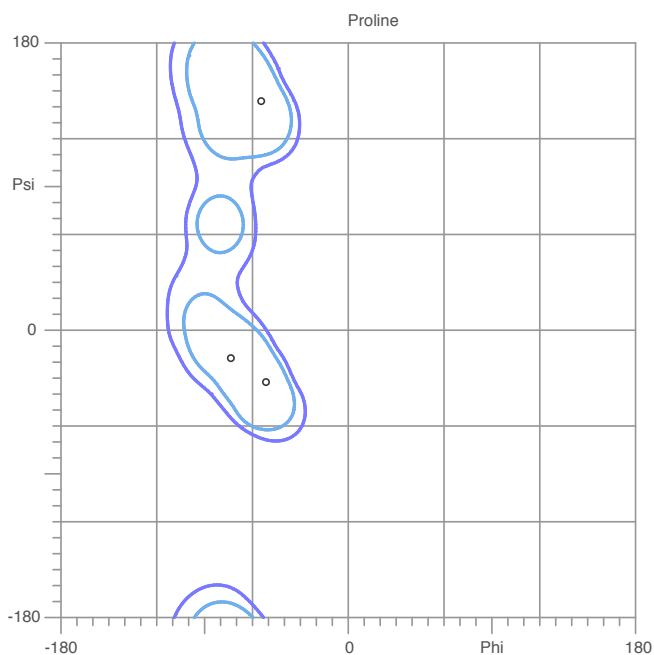
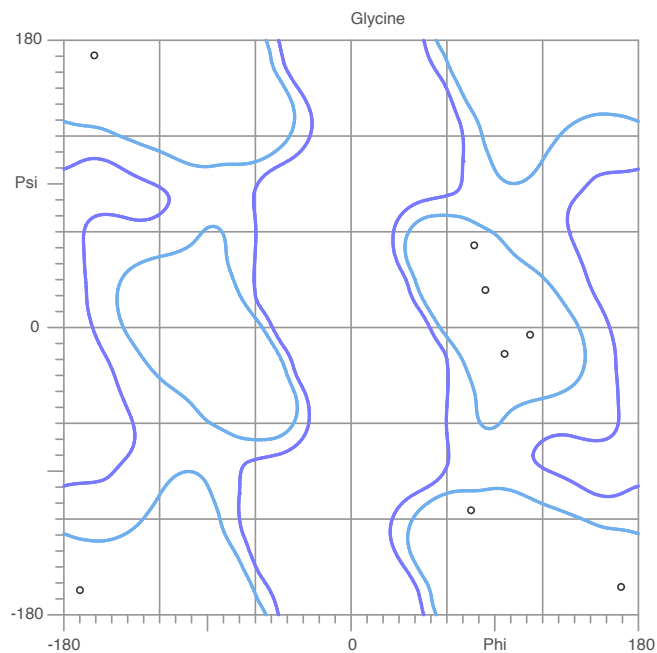
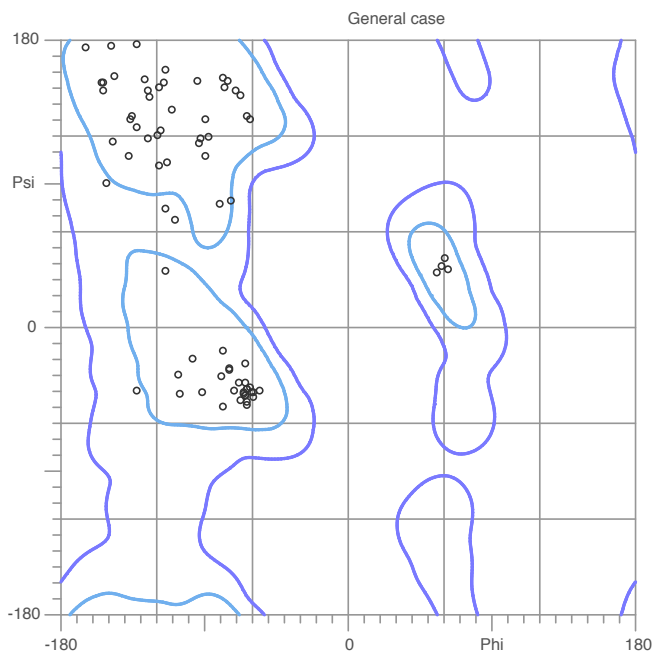
[6] 2 GLY (-144.9, 75.0)

[6] 18 ASN (65.0, 115.0)

[6] 42 HIS (-176.9, -25.0)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 7



94.4% (84/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

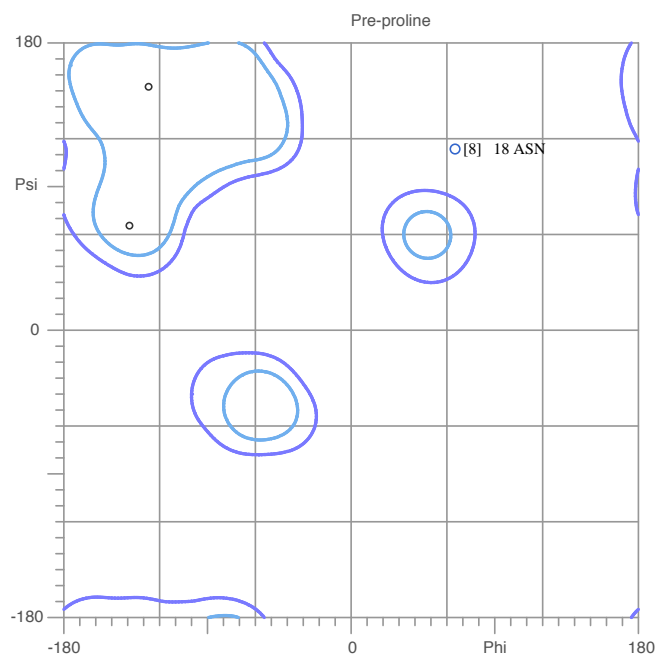
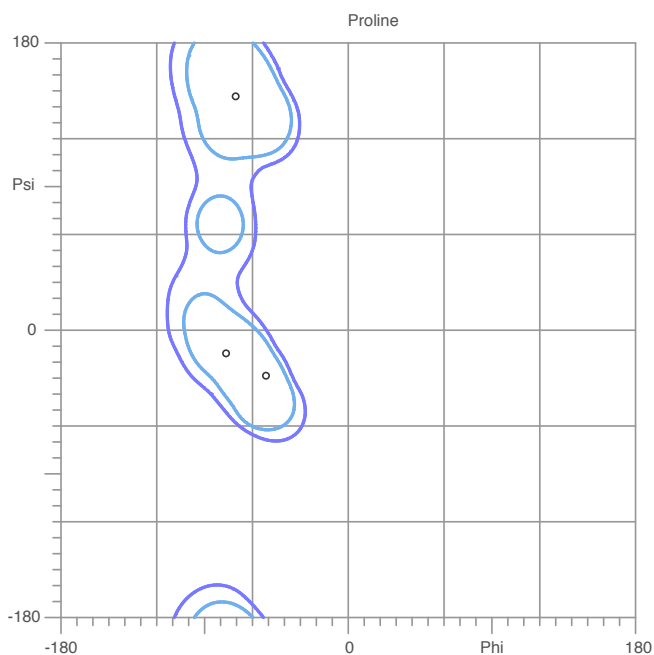
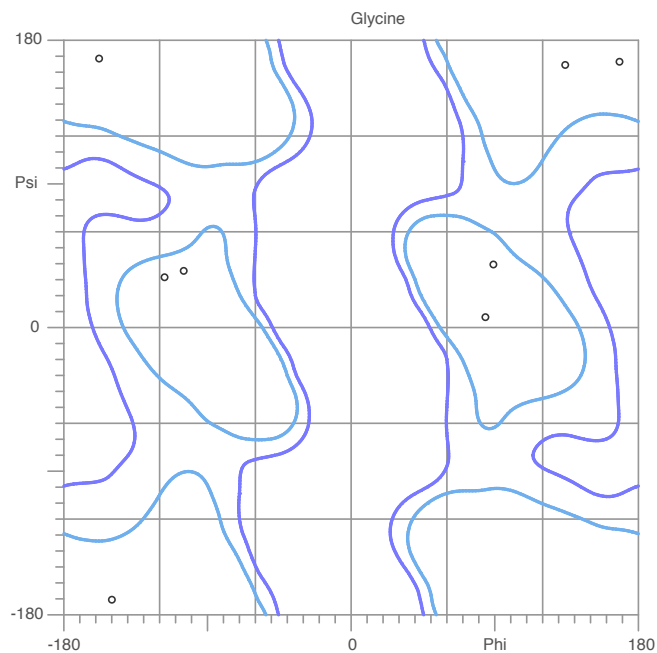
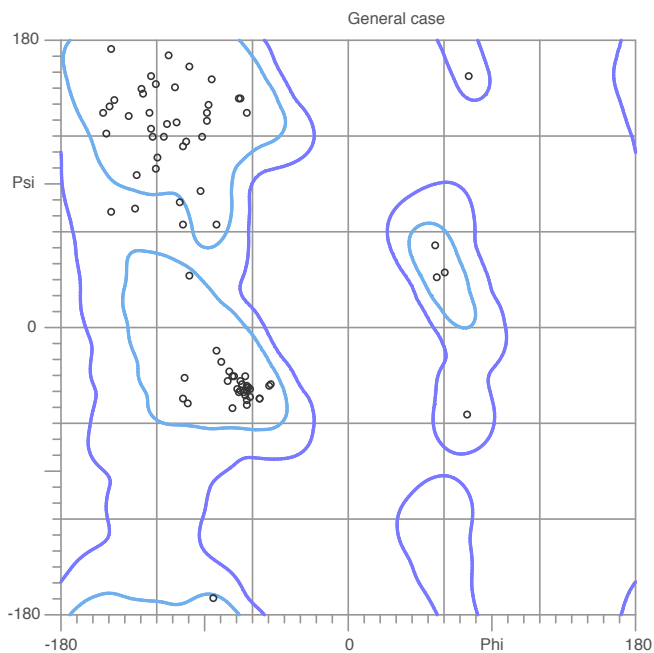
There were 1 outliers (phi, psi):  
[7] 18 ASN (64.9, 115.0)

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# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 8



92.1% (82/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

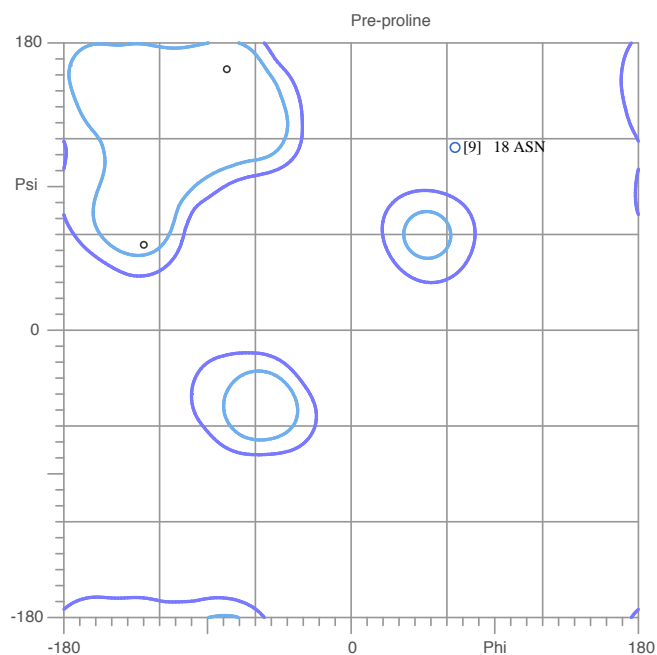
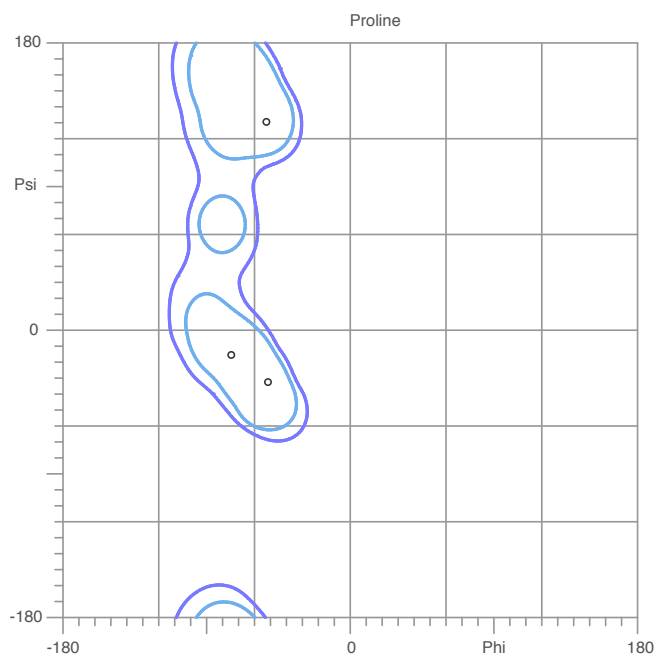
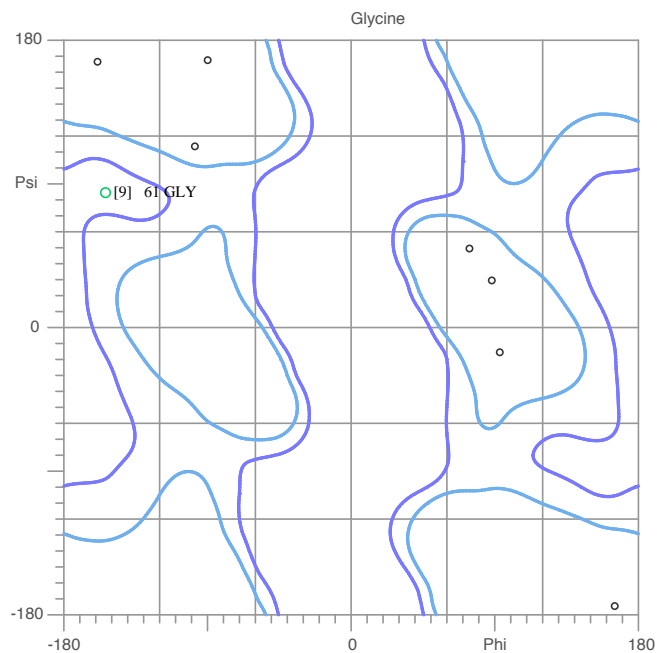
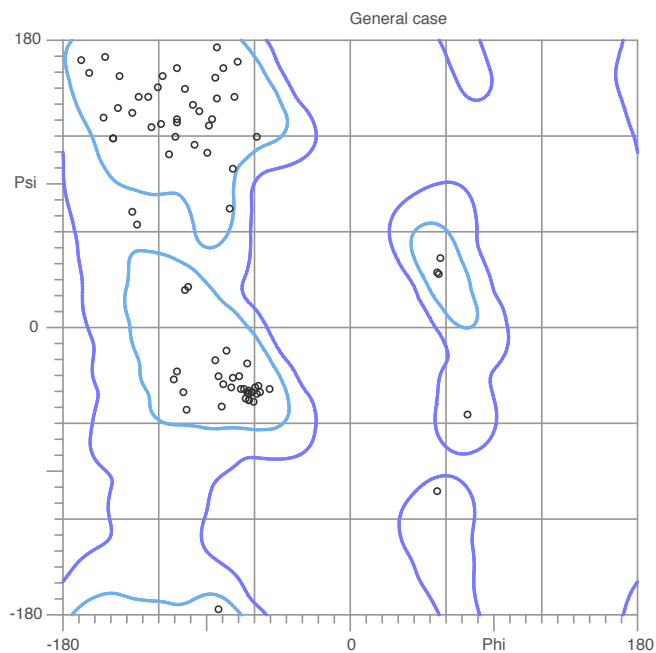
There were 1 outliers (phi, psi):  
[8] 18 ASN (65.0, 114.9)

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# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 9



93.3% (83/89) of all residues were in favored (98%) regions.  
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

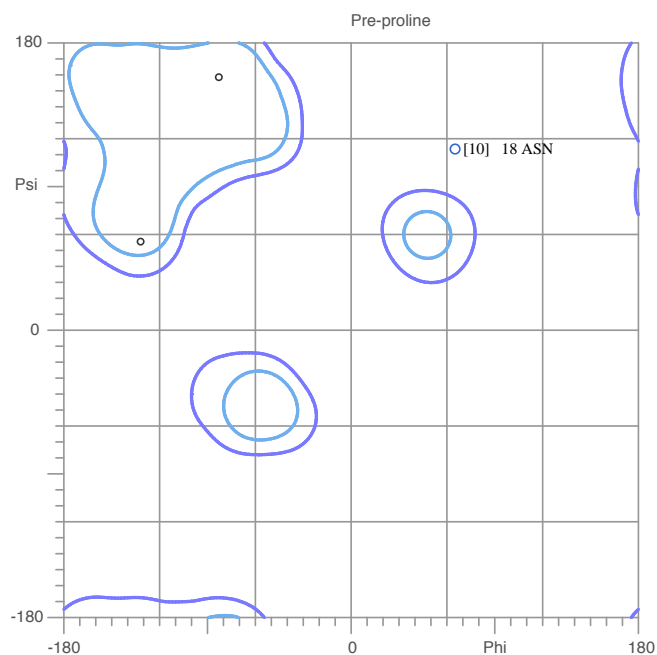
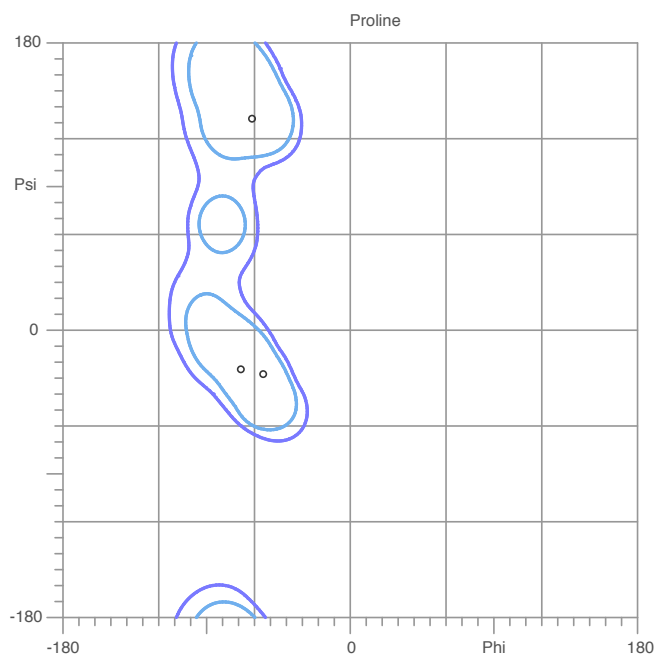
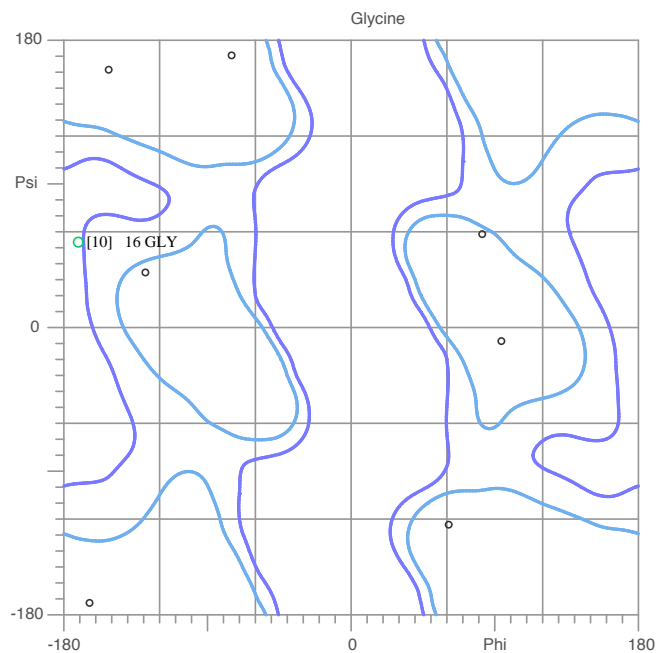
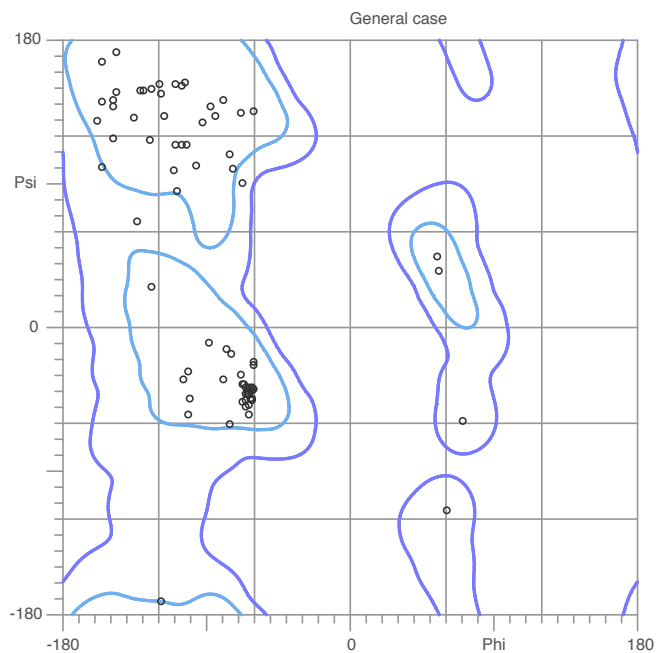
There were 2 outliers (phi, psi):

[9] 18 ASN (65.0, 115.0)

[9] 61 GLY (-155.0, 85.1)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 10



92.1% (82/89) of all residues were in favored (98%) regions.  
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

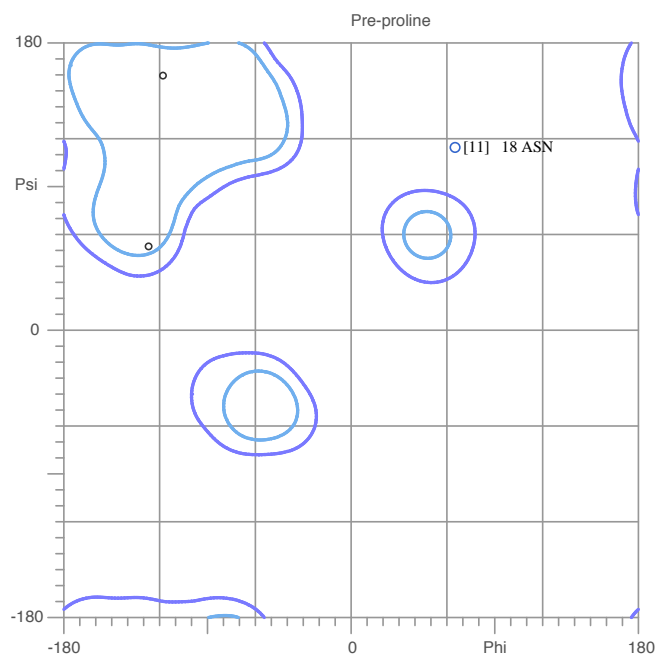
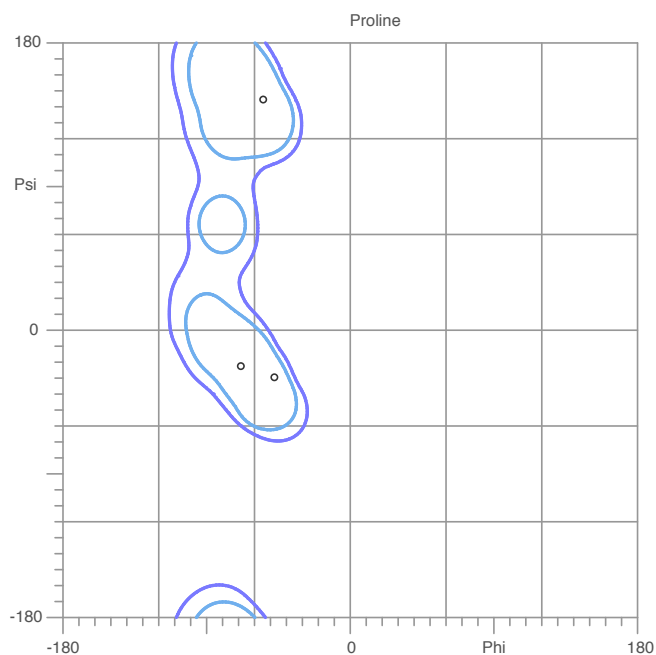
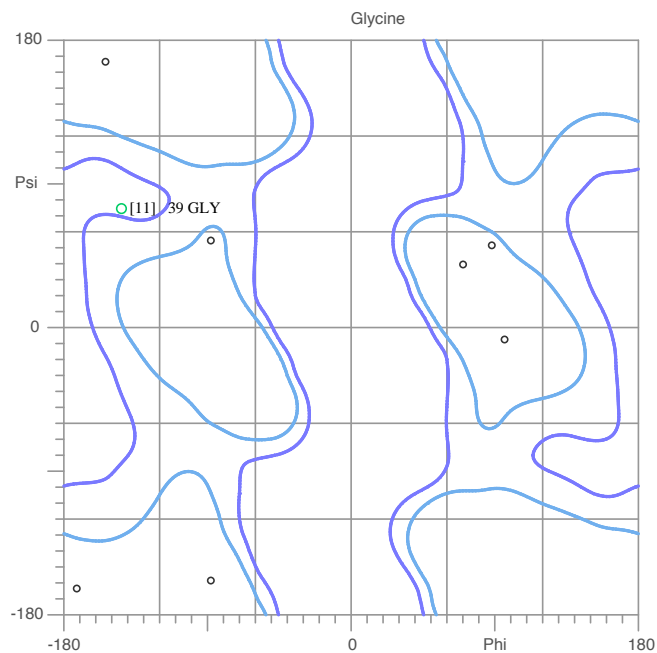
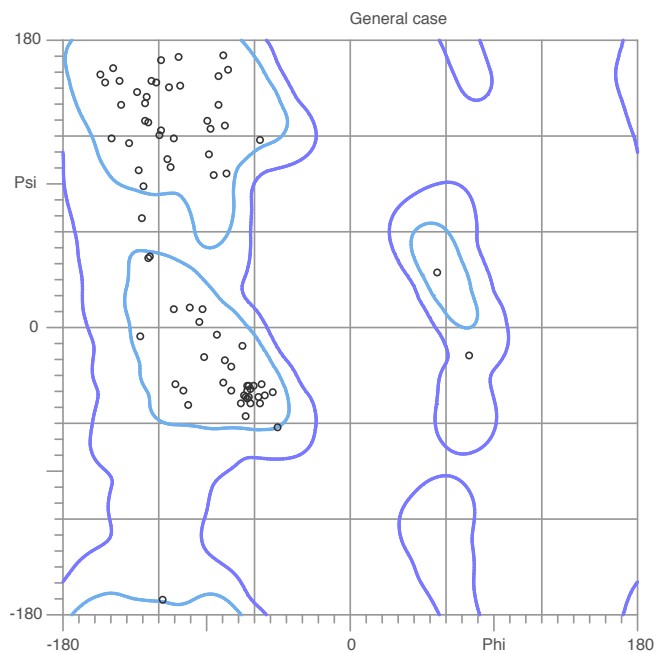
There were 2 outliers (phi, psi):

[10] 16 GLY (-171.9, 55.0)

[10] 18 ASN (65.1, 115.0)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 11

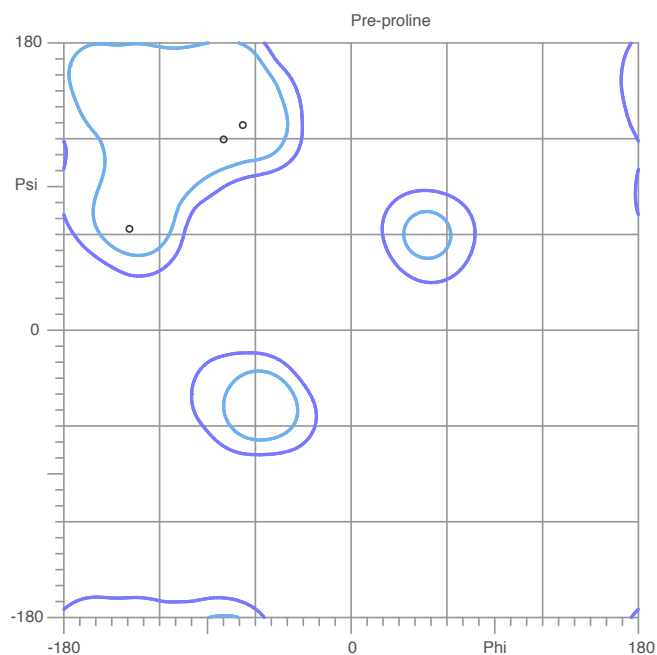
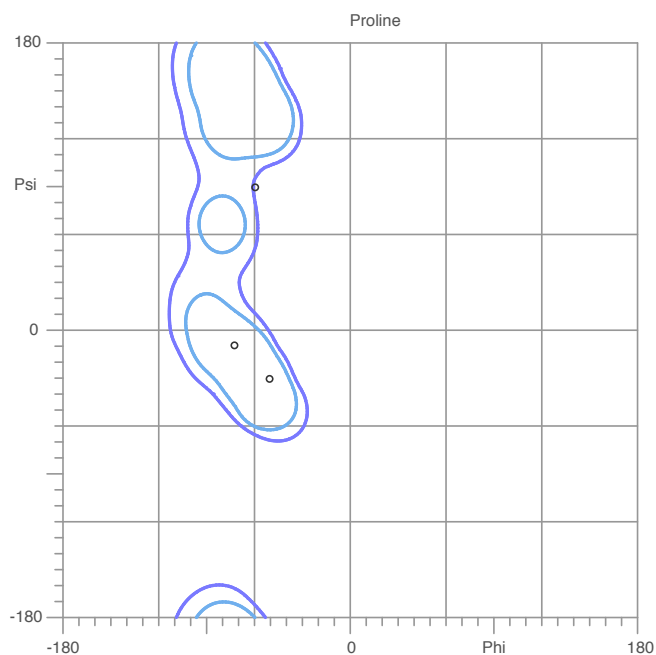
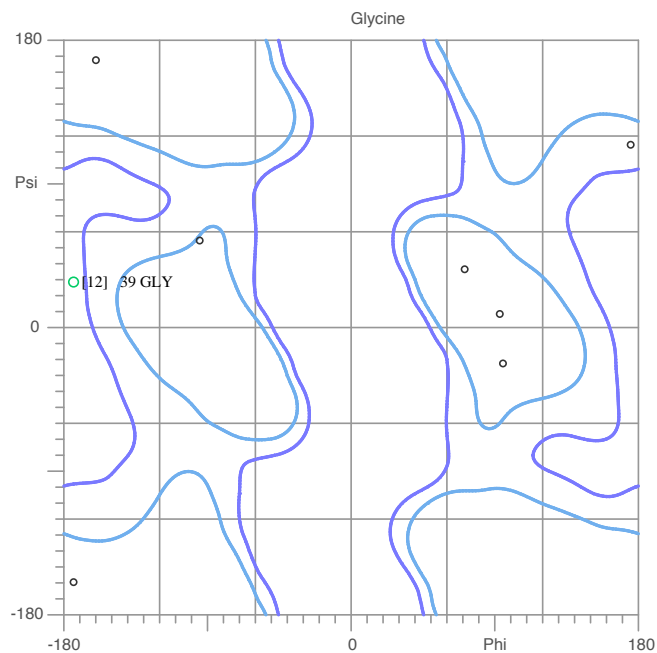
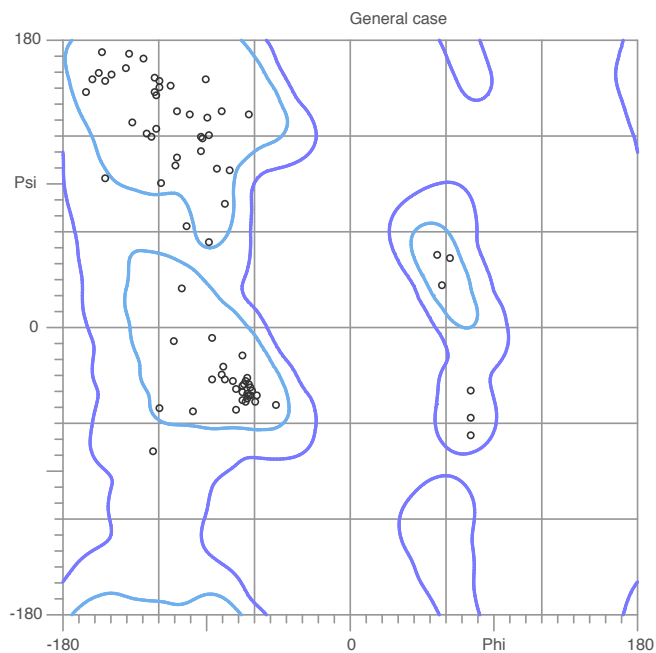


94.4% (84/89) of all residues were in favored (98%) regions.  
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[11] 18 ASN (65.0, 115.1)  
[11] 39 GLY (-145.0, 75.1)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 12

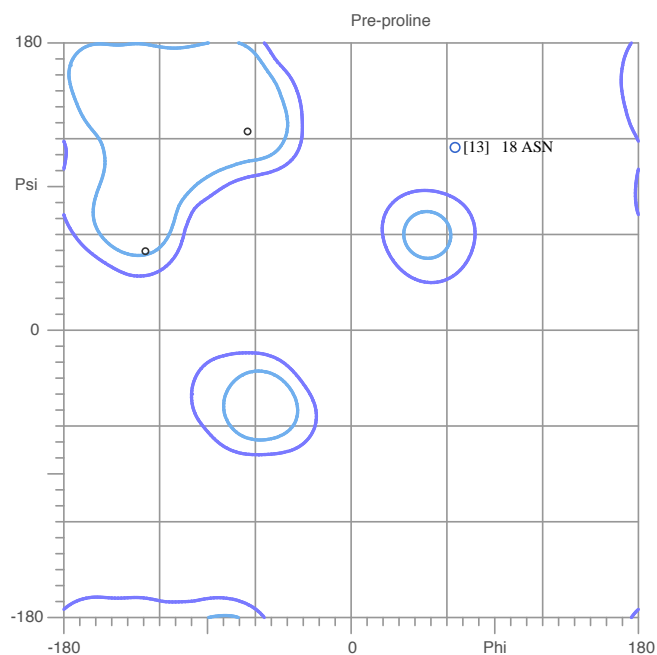
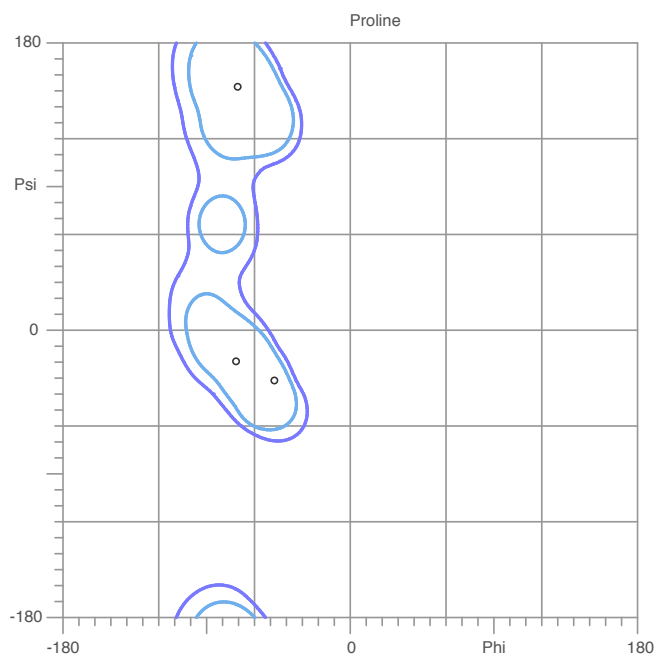
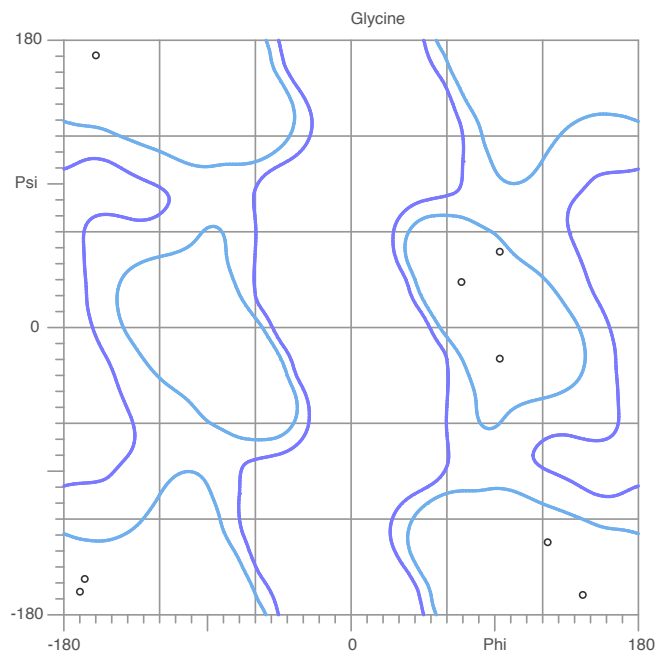
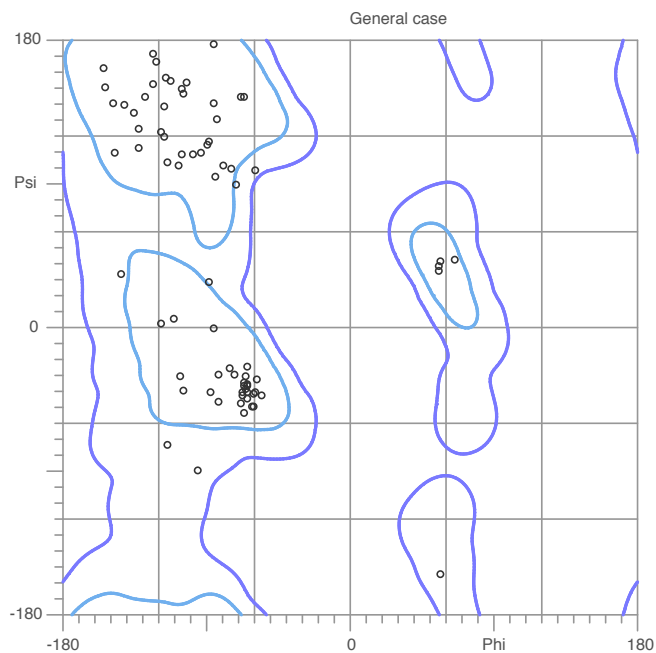


89.9% (80/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[12] 39 GLY (-175.0, 29.9)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 13



92.1% (82/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

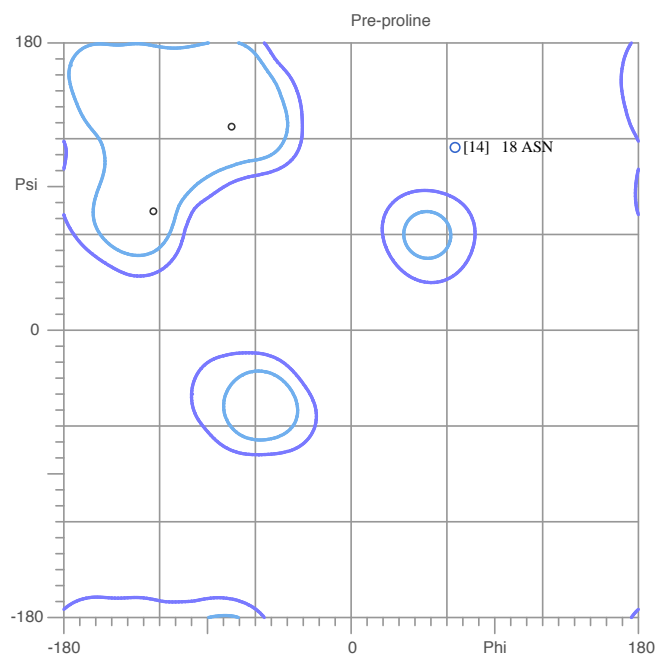
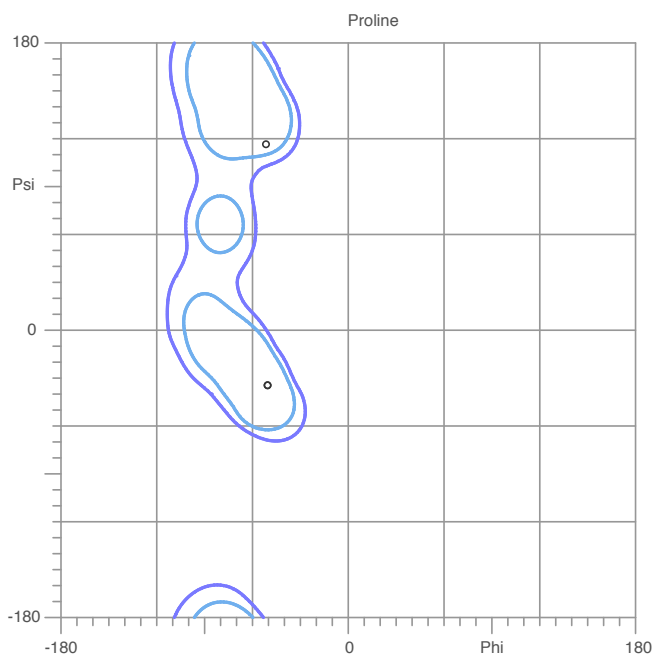
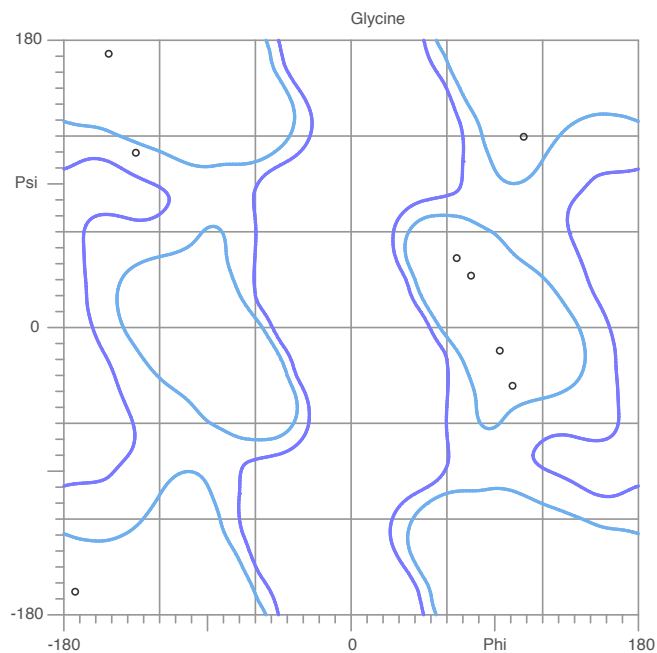
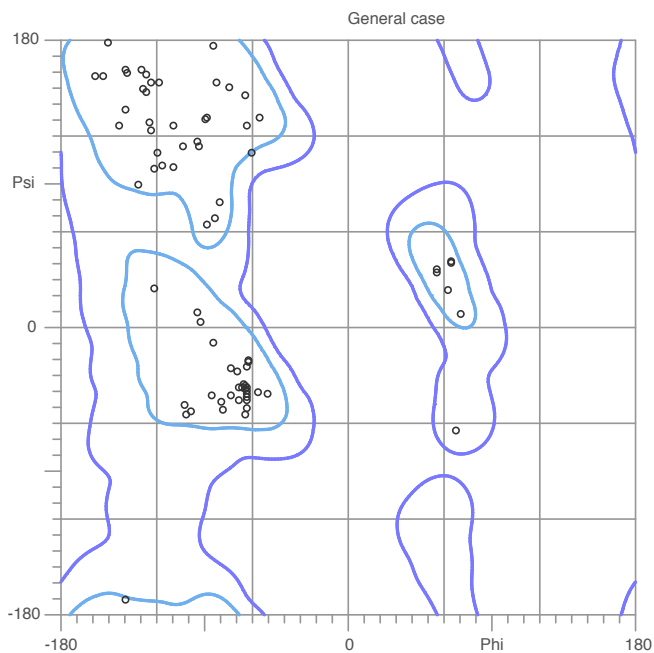
There were 1 outliers (phi, psi):  
[13] 18 ASN (65.1, 115.0)

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# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 14



96.6% (86/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

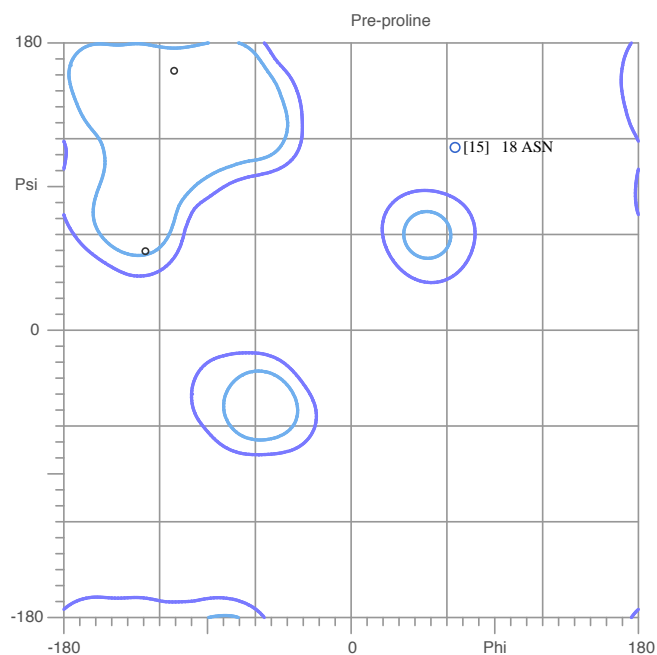
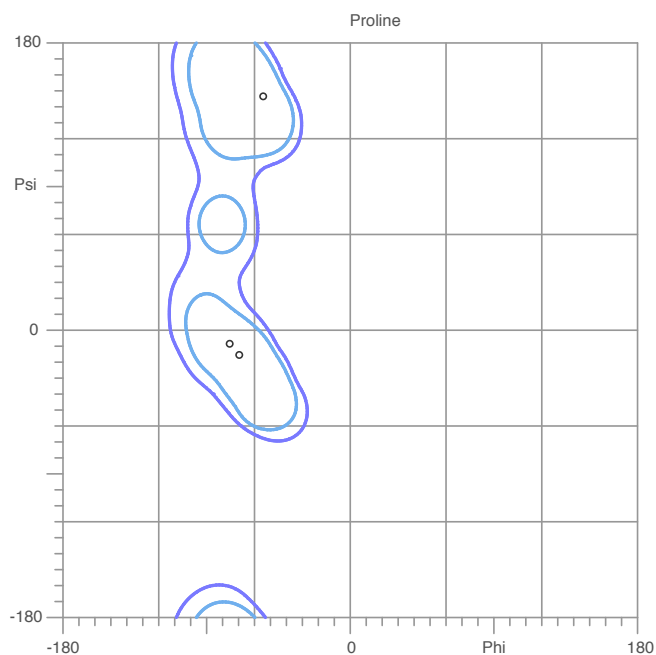
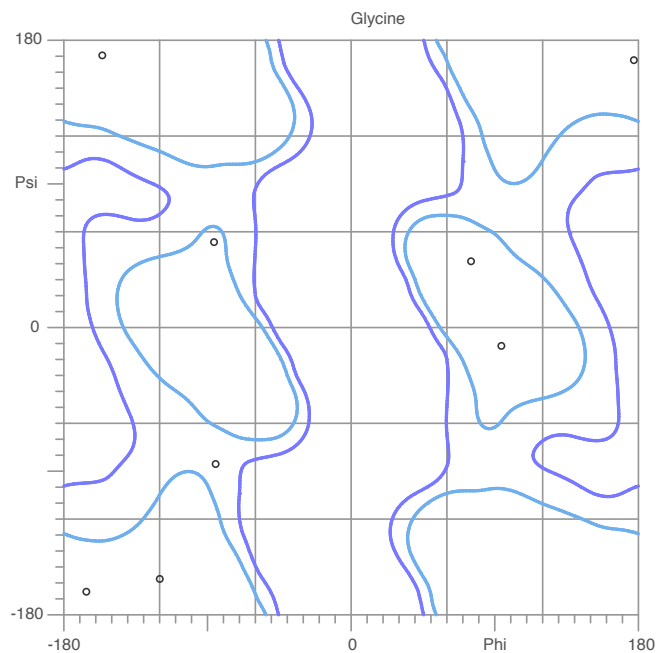
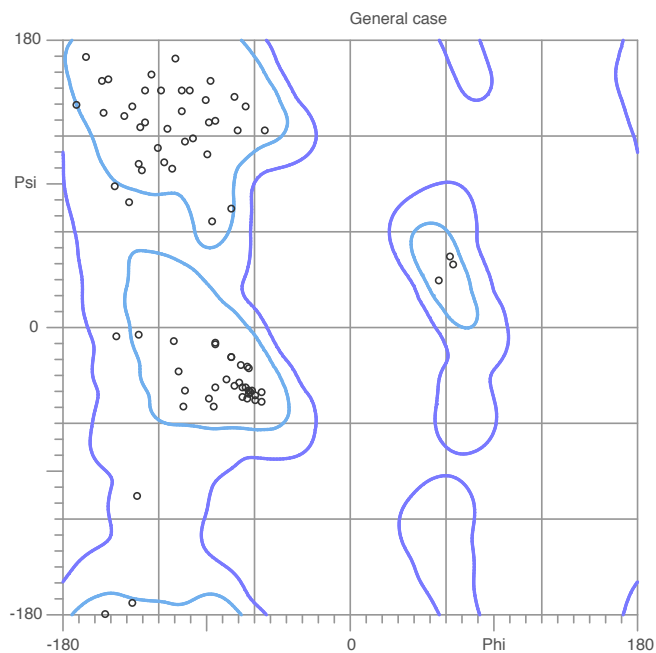
There were 1 outliers (phi, psi):  
[14] 18 ASN (65.0, 115.0)

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# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 15

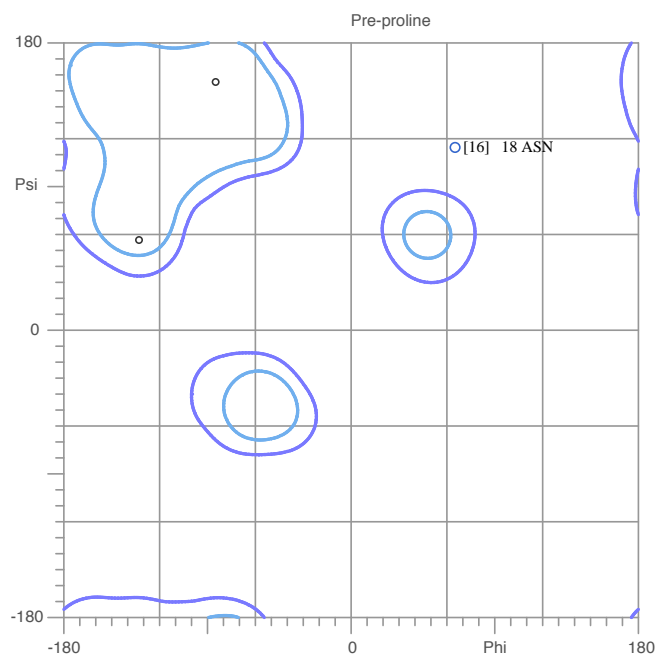
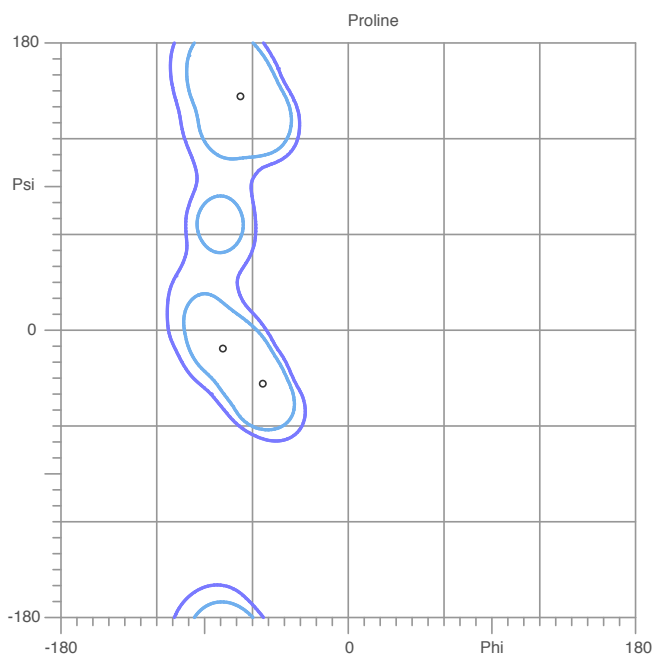
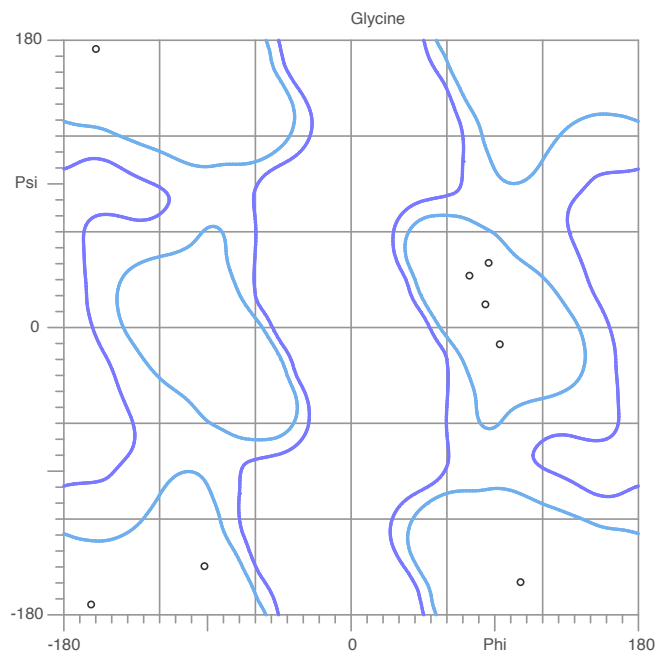
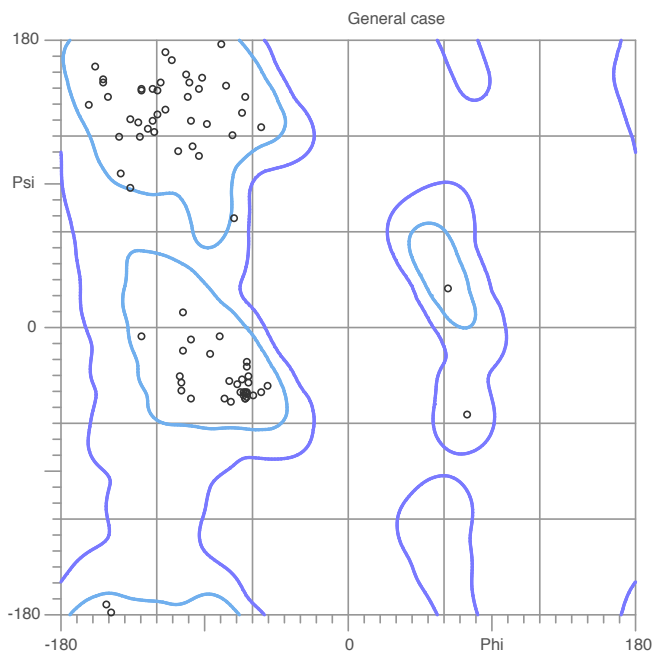


92.1% (82/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[15] 18 ASN (65.1, 115.0)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 16



96.6% (86/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

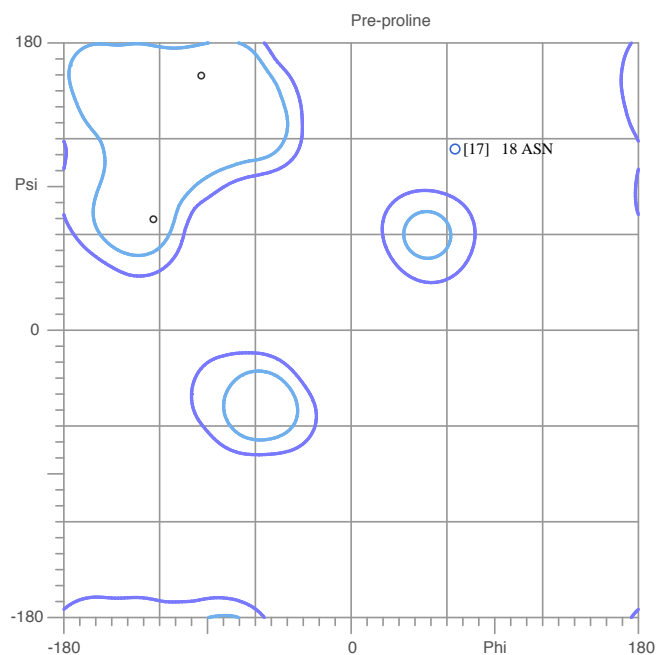
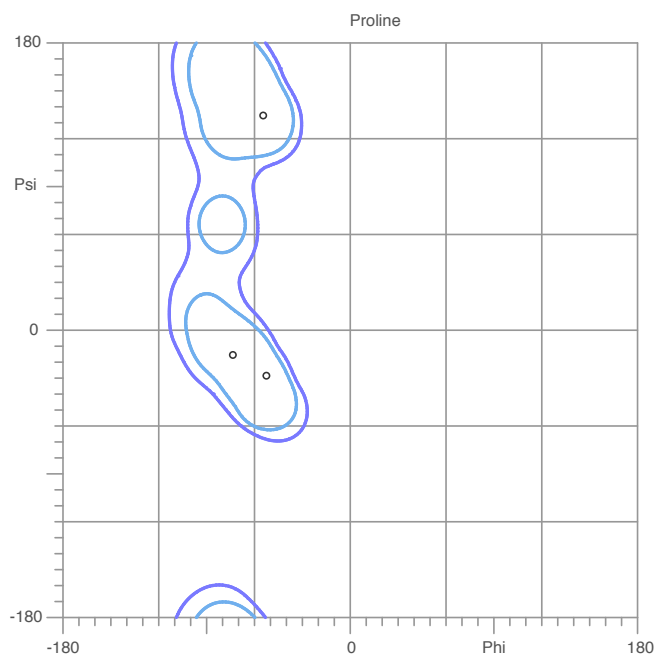
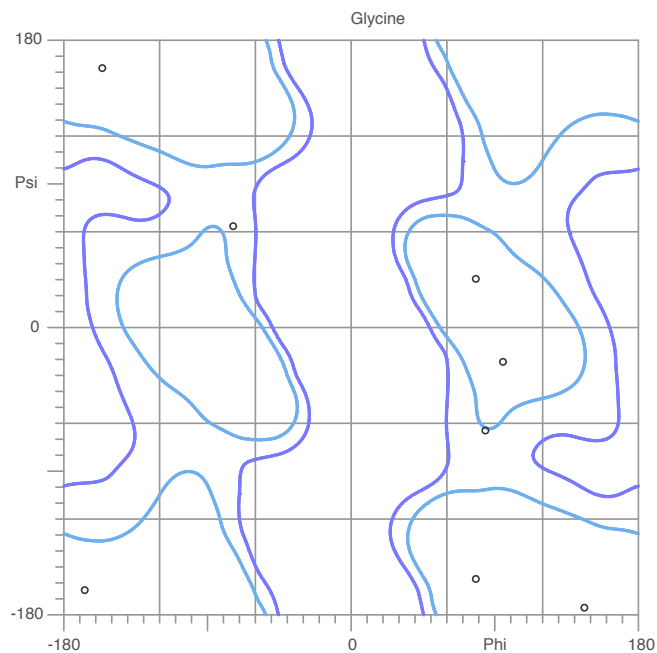
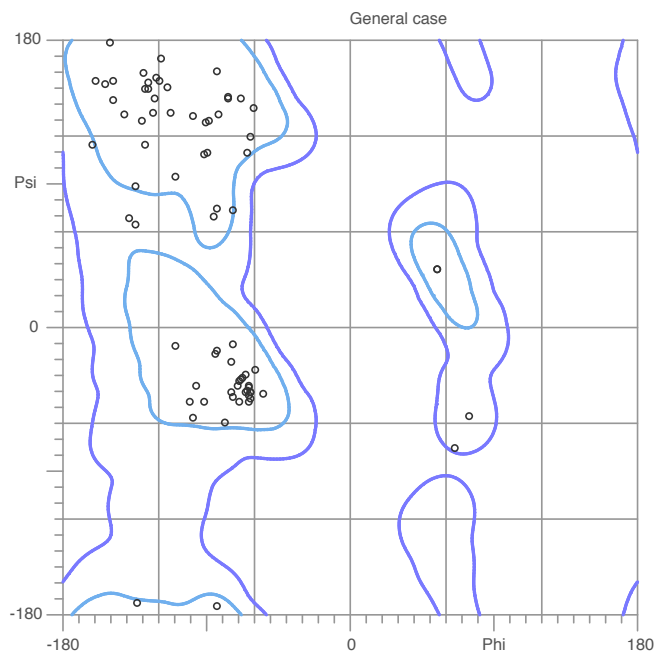
There were 1 outliers (phi, psi):  
[16] 18 ASN (65.0, 115.1)

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# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 17



91.0% (81/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

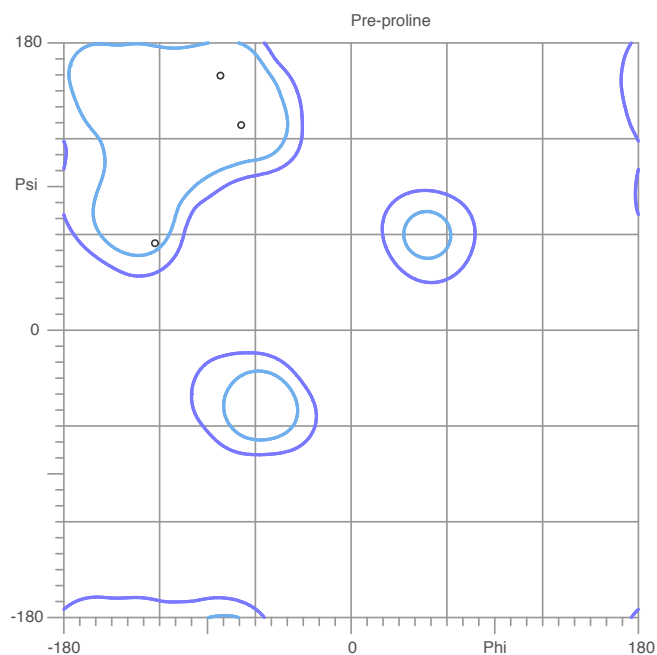
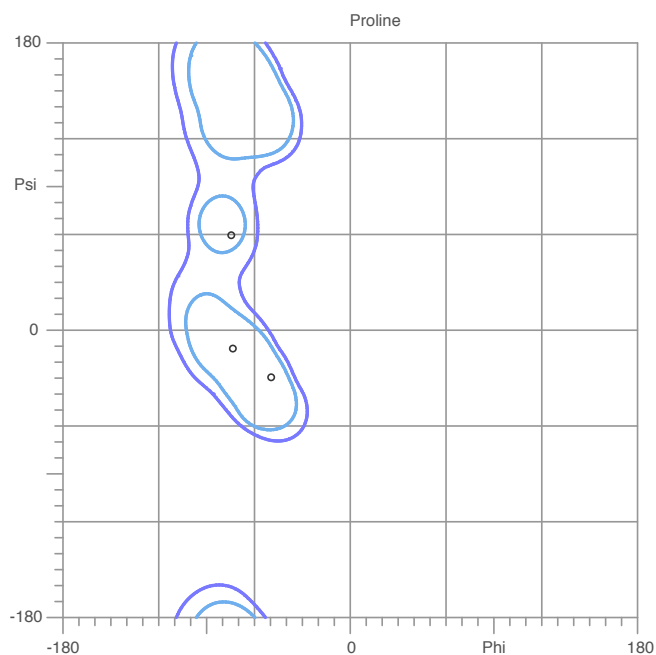
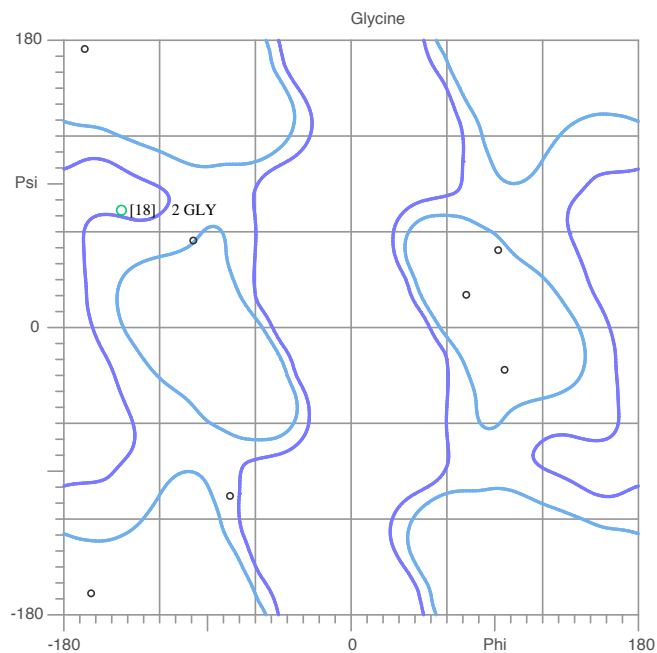
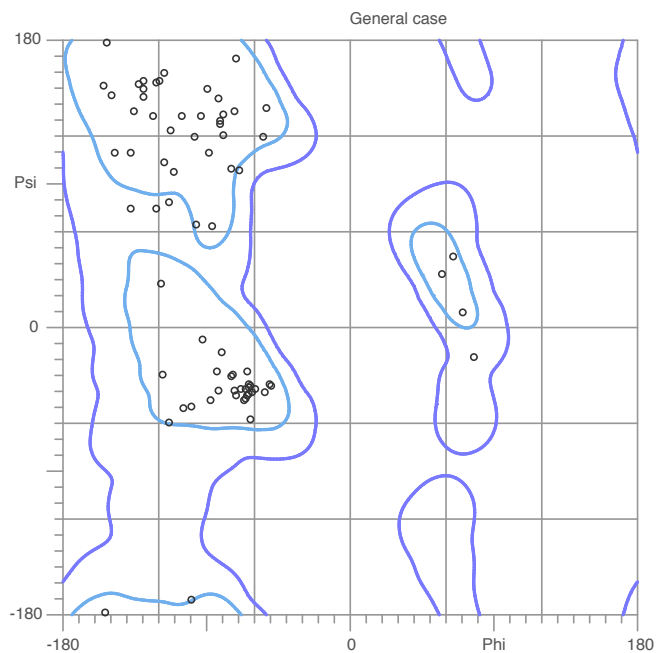
There were 1 outliers (phi, psi):  
[17] 18 ASN (65.0, 115.0)

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# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 18



89.9% (80/89) of all residues were in favored (98%) regions.  
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

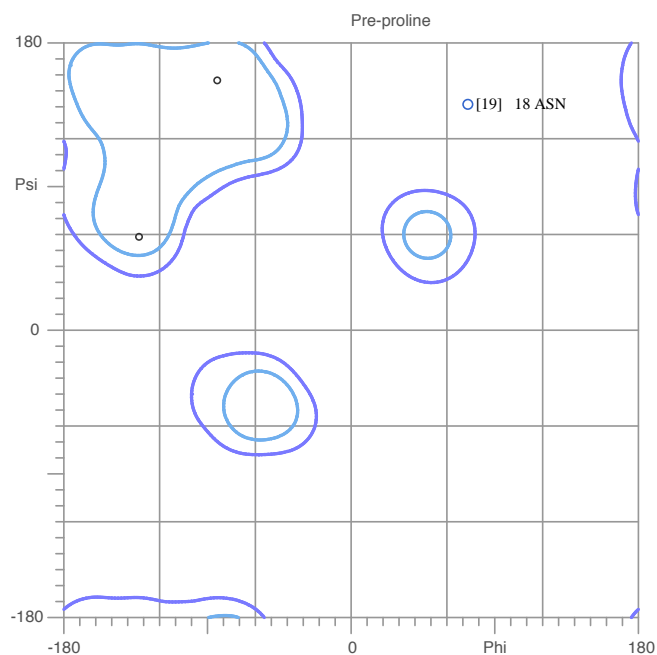
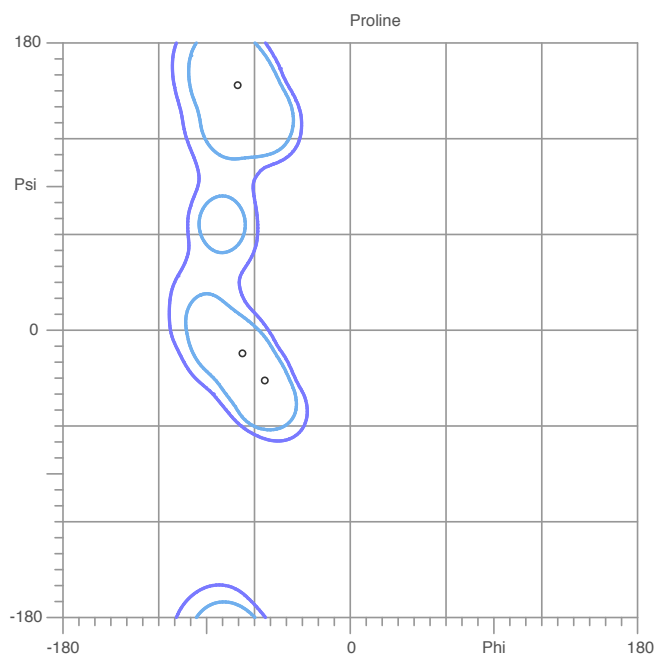
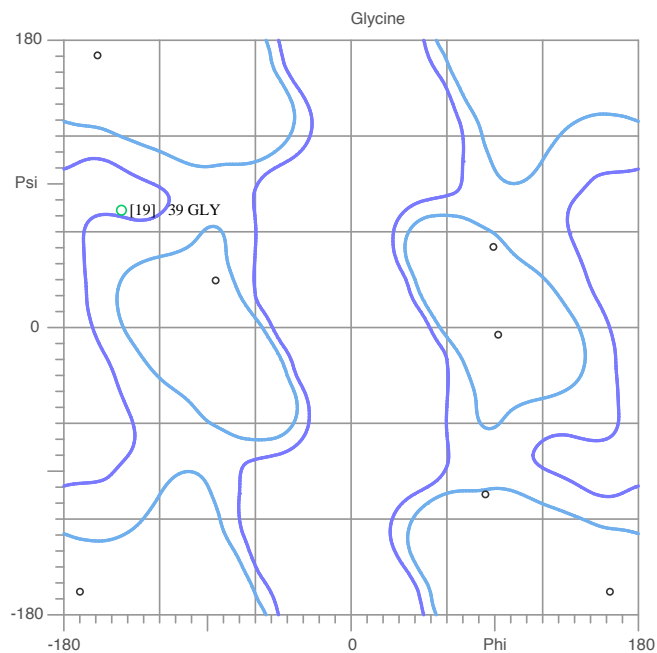
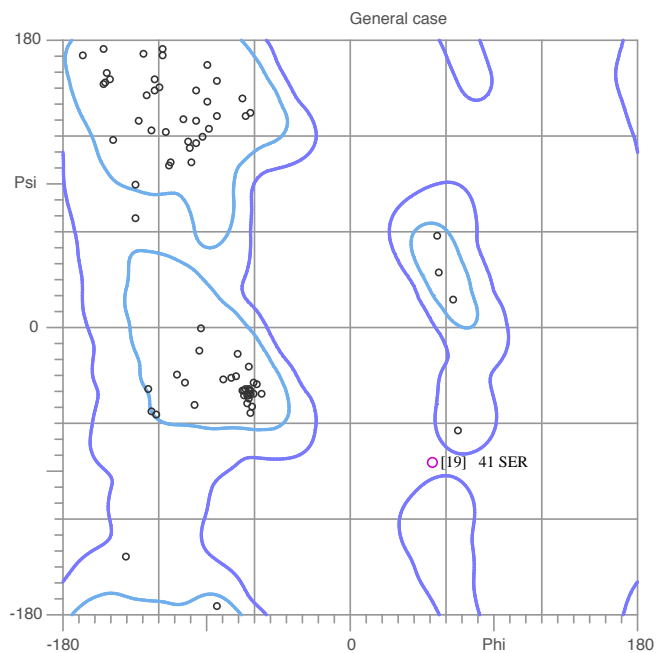
There were 1 outliers (phi, psi):  
[18] 2 GLY (-145.0, 74.9)

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

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

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 19



92.1% (82/89) of all residues were in favored (98%) regions.  
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

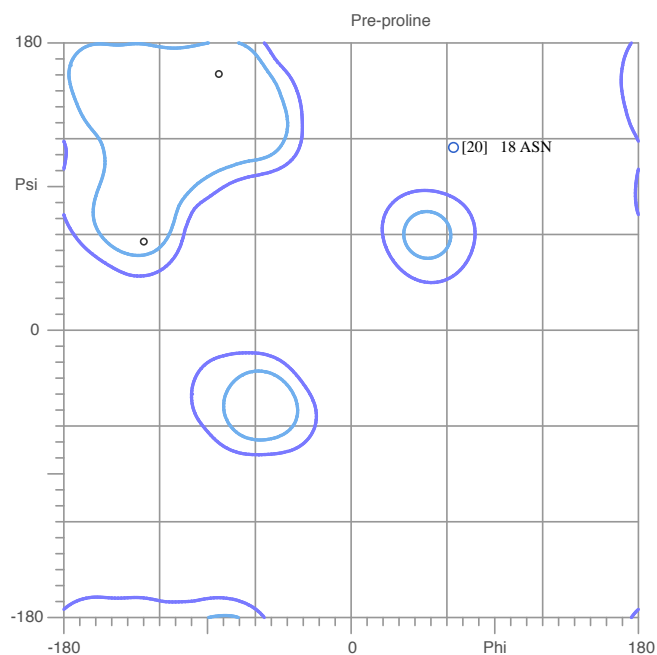
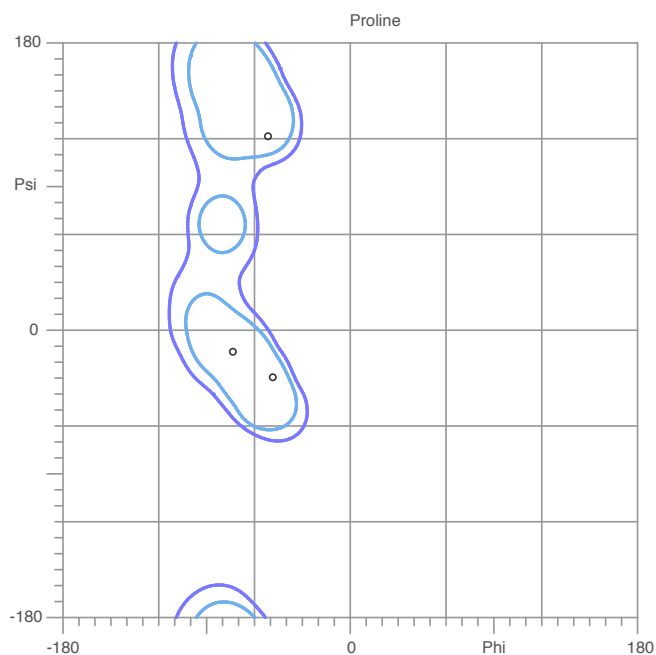
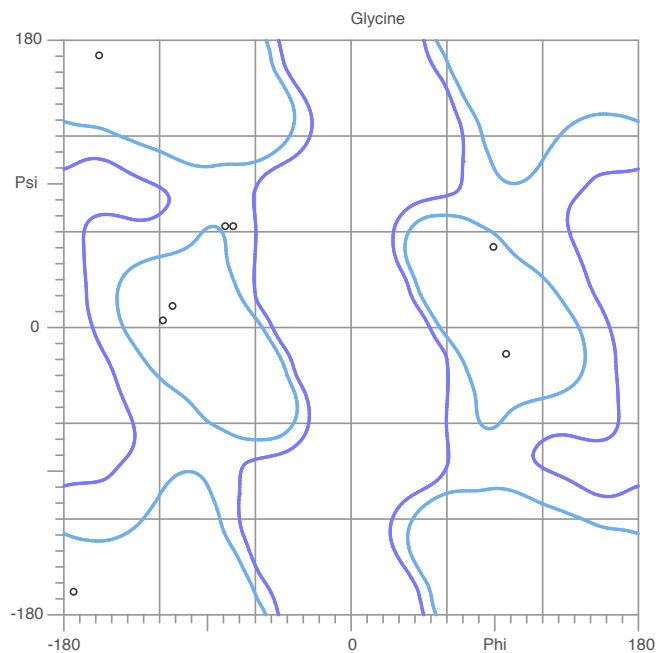
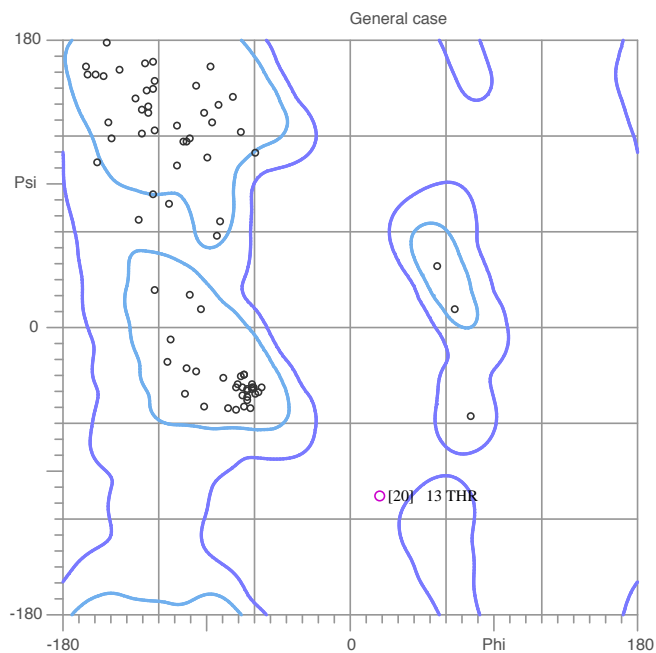
[19] 18 ASN (73.8, 142.2)

[19] 39 GLY (-144.9, 74.9)

[19] 41 SER (52.0, -85.0)

# MolProbity Ramachandran analysis

HR4527E\_R3\_em\_bcr3.pdb, model 20



91.0% (81/89) of all residues were in favored (98%) regions.  
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[20] 13 THR (18.3, -105.0)

[20] 18 ASN (65.0, 115.1)