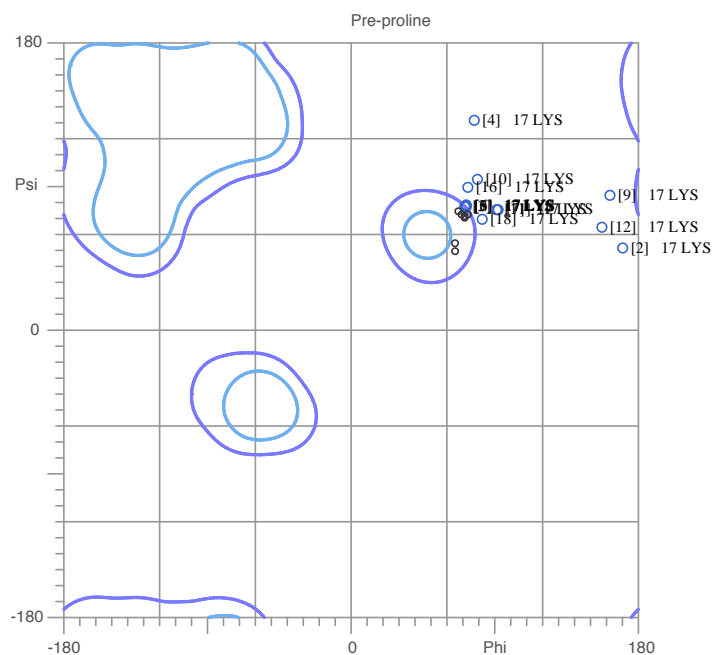
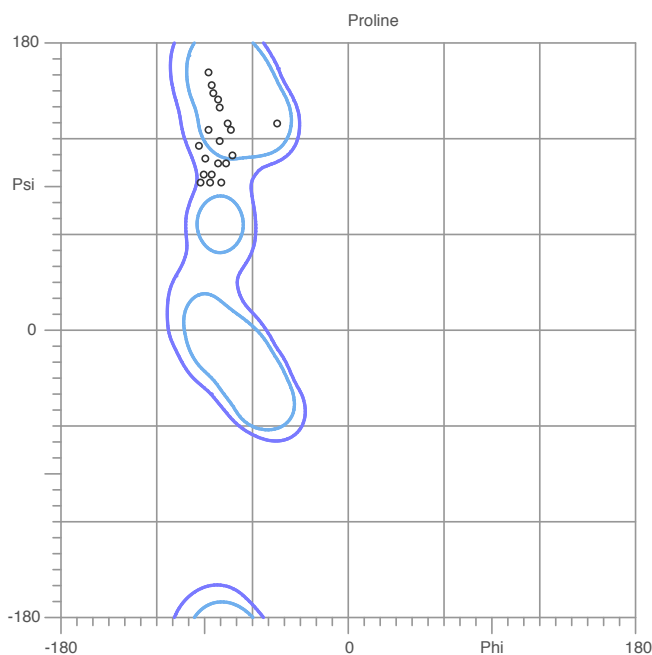
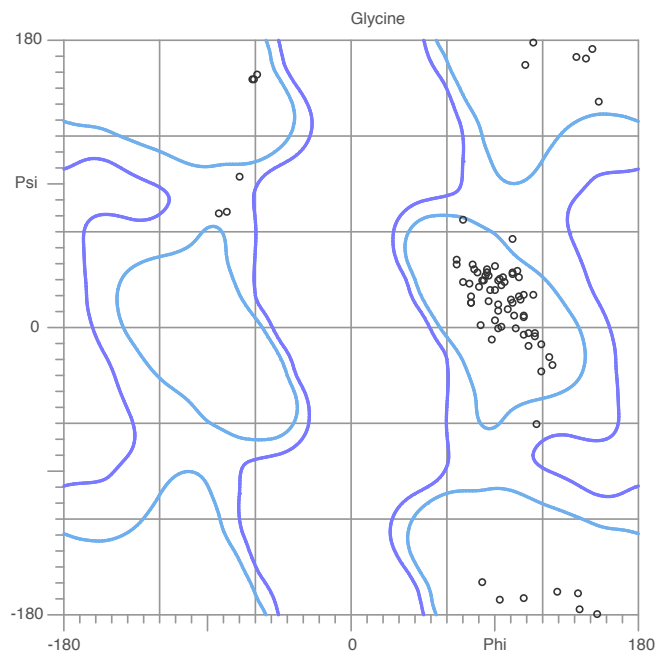
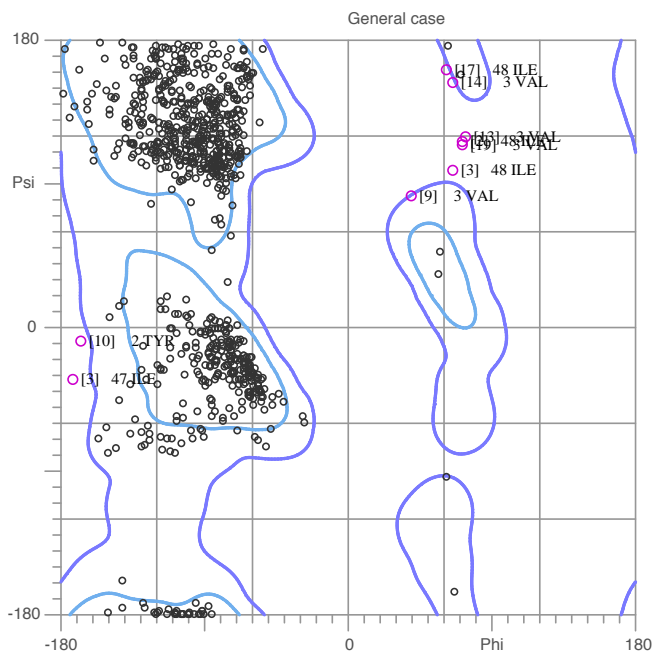


# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, all models



90.0% (864/960) of all residues were in favored (98%) regions.  
97.7% (938/960) of all residues were in allowed (>99.8%) regions.

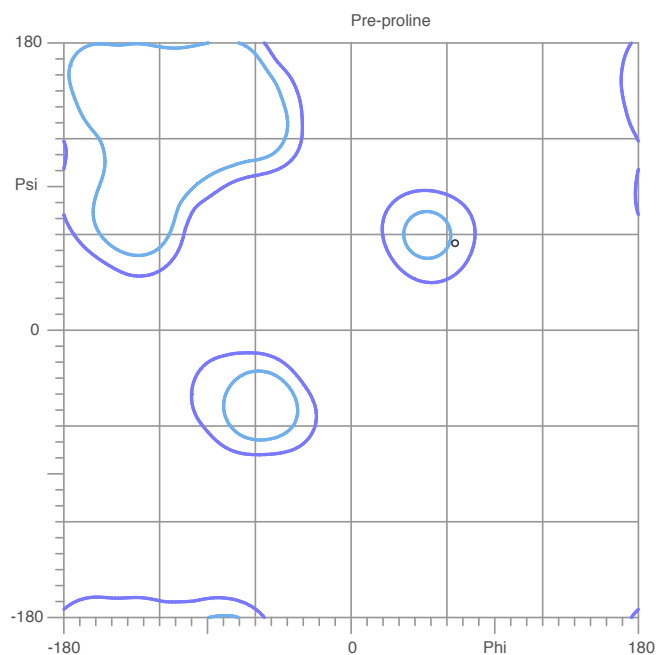
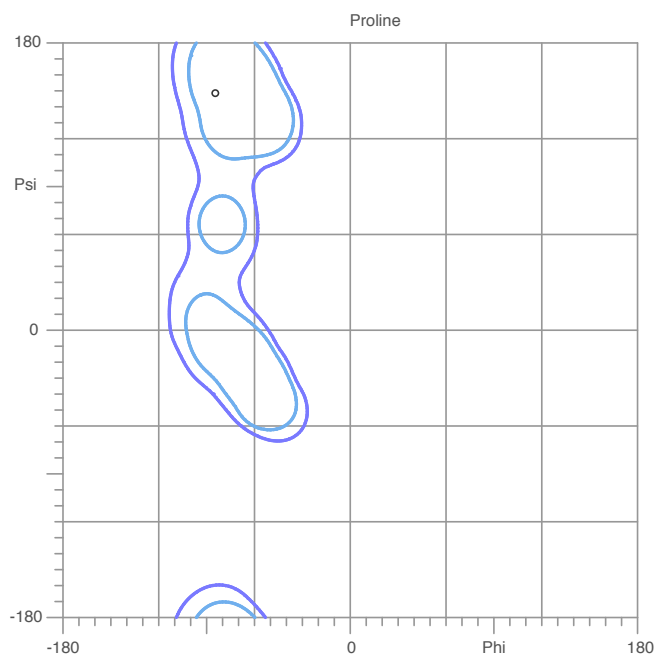
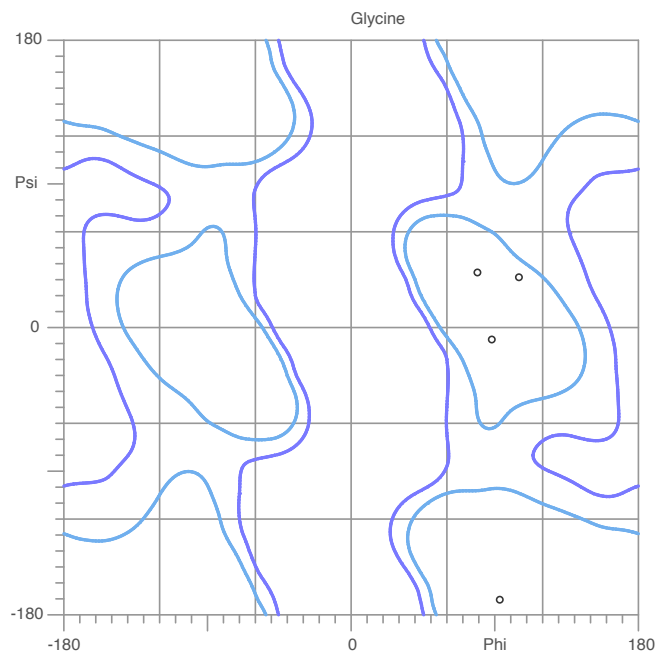
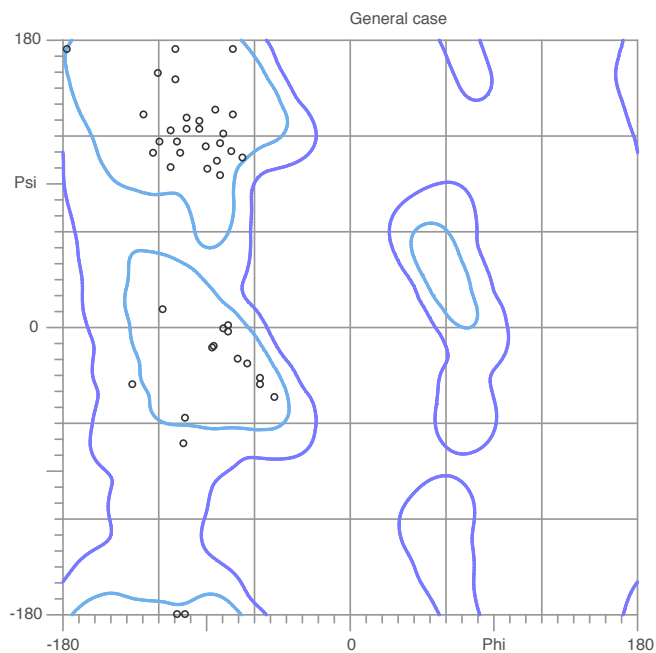
There were 22 outliers (phi, psi):

- [2] 17 LYS (170.3, 52.3)
- [2] 48 ILE (71.2, 117.6)
- [3] 17 LYS (71.6, 78.4)
- [3] 47 ILE (-173.1, -32.6)
- [3] 48 ILE (65.2, 99.8)
- [4] 17 LYS (77.1, 132.8)
- [5] 17 LYS (72.6, 78.5)
- [6] 17 LYS (73.0, 79.7)
- [7] 17 LYS (92.8, 76.7)

- [8] 17 LYS (72.7, 78.5)
- [9] 3 VAL (39.4, 83.7)
- [9] 17 LYS (162.5, 86.0)
- [10] 2 TYR (-168.8, -8.1)
- [10] 17 LYS (79.5, 95.4)
- [11] 17 LYS (91.6, 77.0)
- [12] 17 LYS (157.9, 65.6)
- [13] 3 VAL (73.1, 120.2)
- [14] 3 VAL (65.4, 154.8)
- [16] 17 LYS (73.8, 90.4)
- [17] 48 ILE (61.6, 162.3)
- [18] 17 LYS (82.6, 70.3)
- [19] 3 VAL (71.2, 115.2)

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 1



91.7% (44/48) of all residues were in favored (98%) regions.  
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

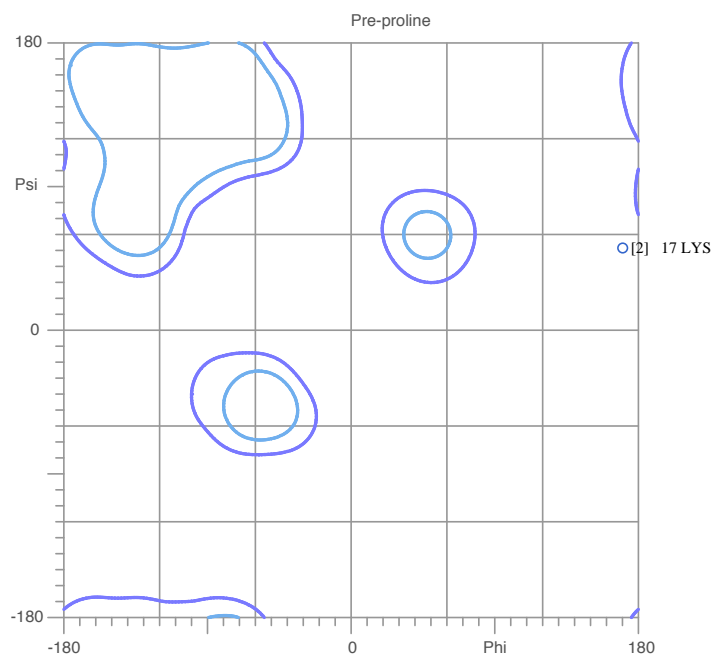
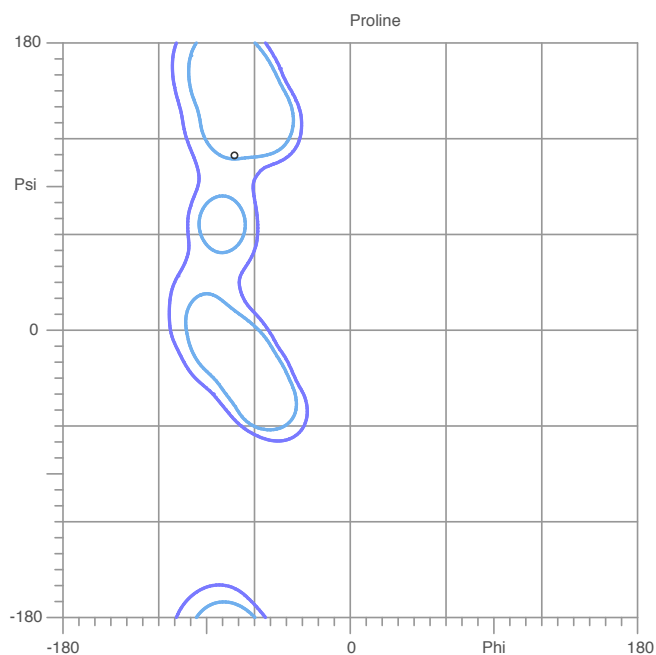
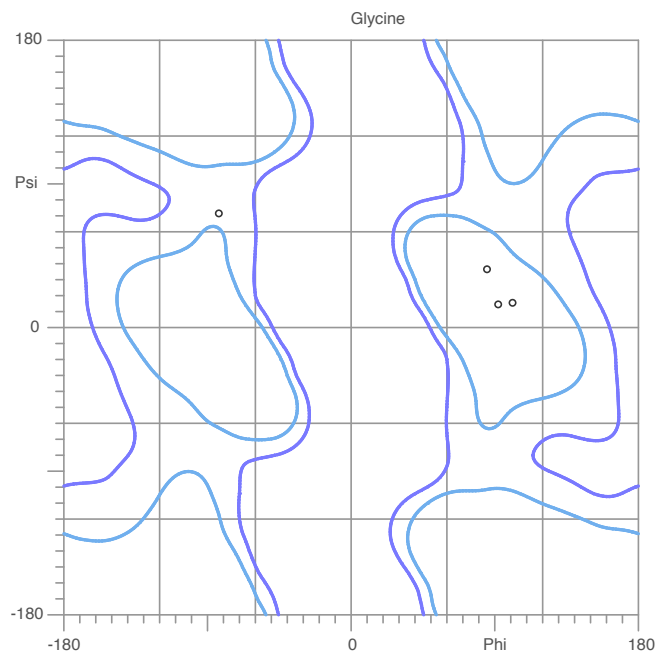
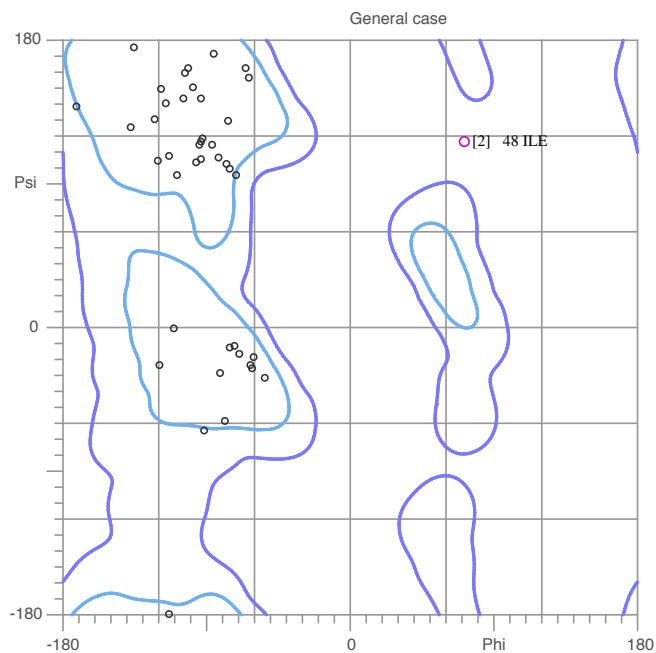
There were no outliers.

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# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 2



89.6% (43/48) of all residues were in favored (98%) regions.  
95.8% (46/48) of all residues were in allowed (>99.8%) regions.

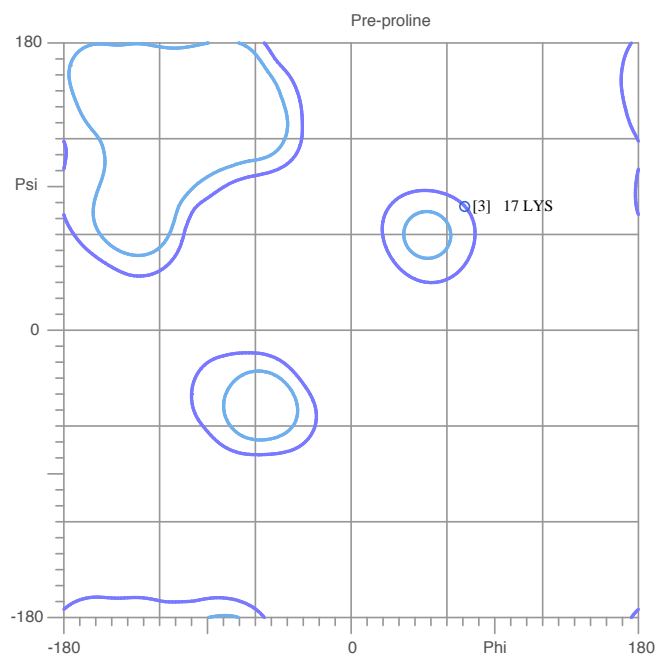
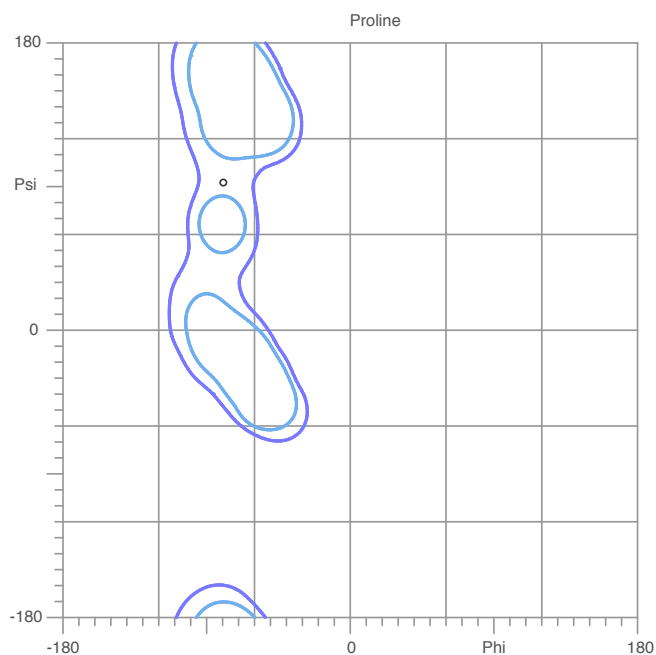
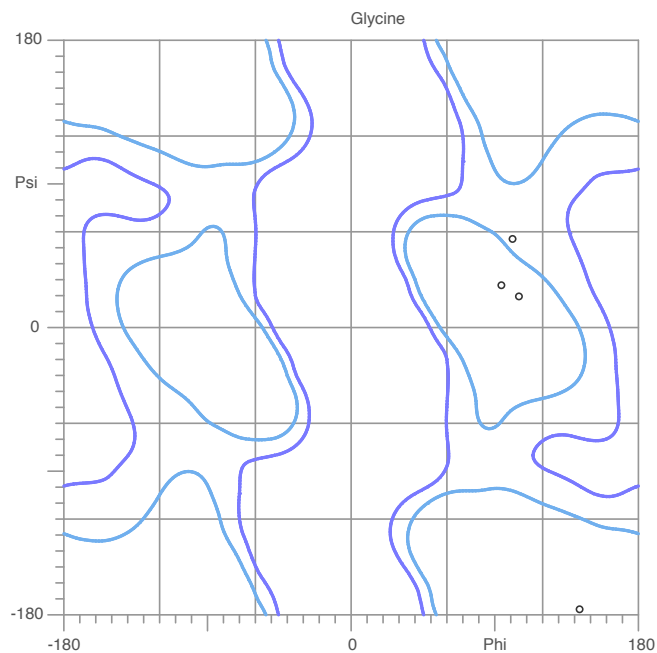
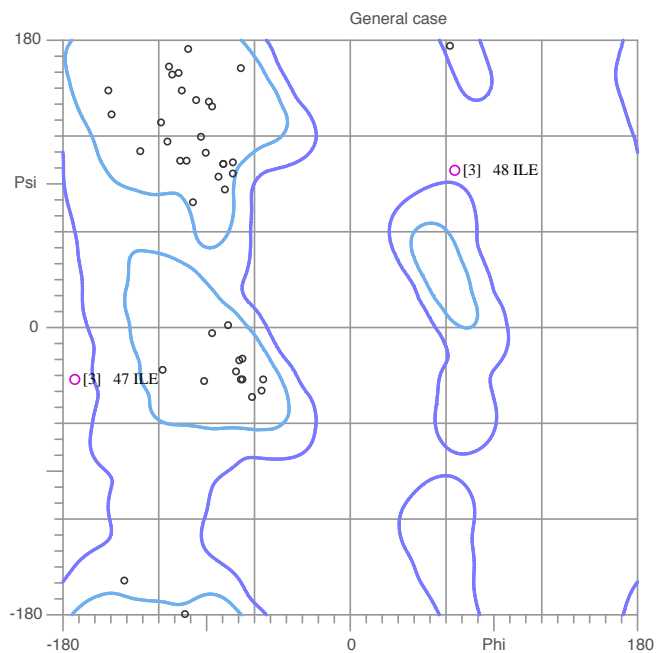
There were 2 outliers (phi, psi):

[2] 17 LYS (170.3, 52.3)

[2] 48 ILE (71.2, 117.6)

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 3



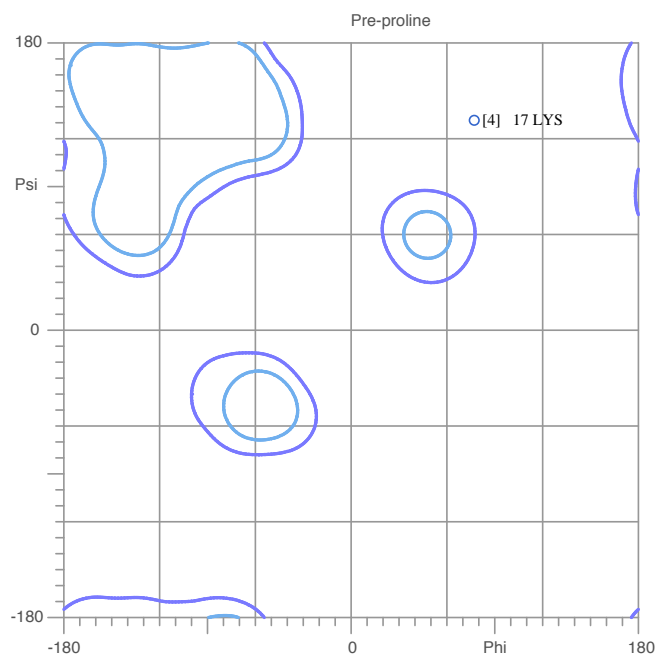
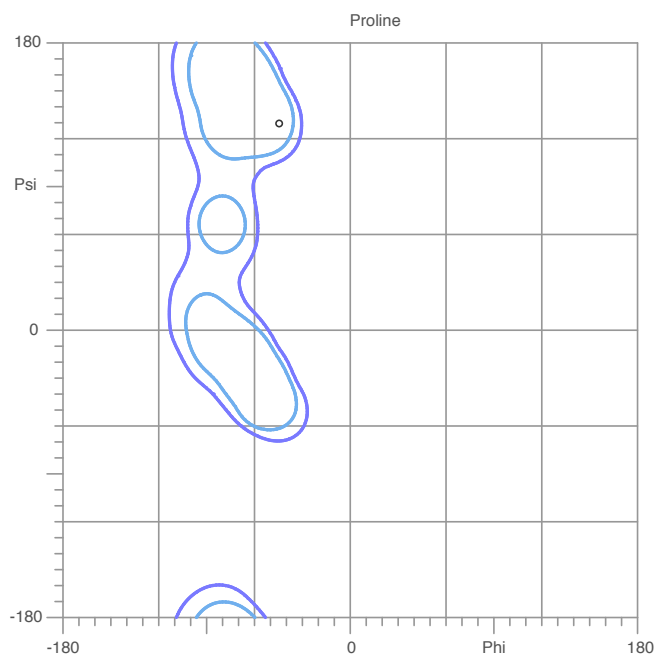
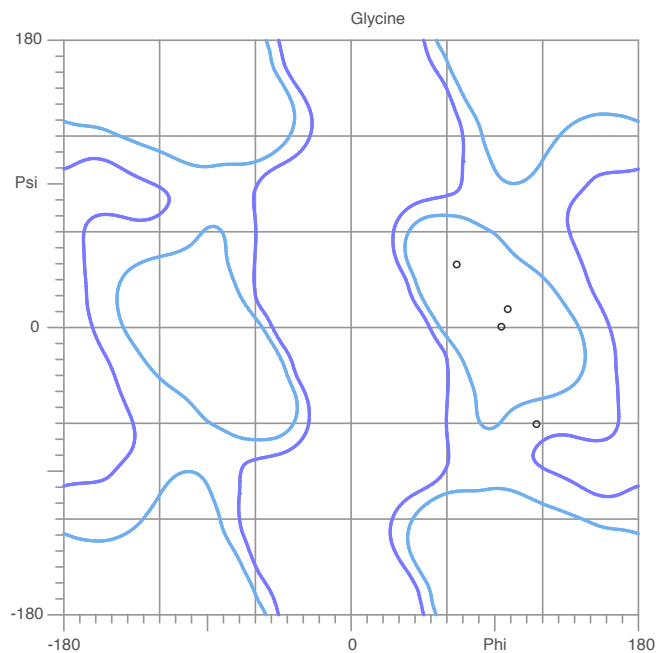
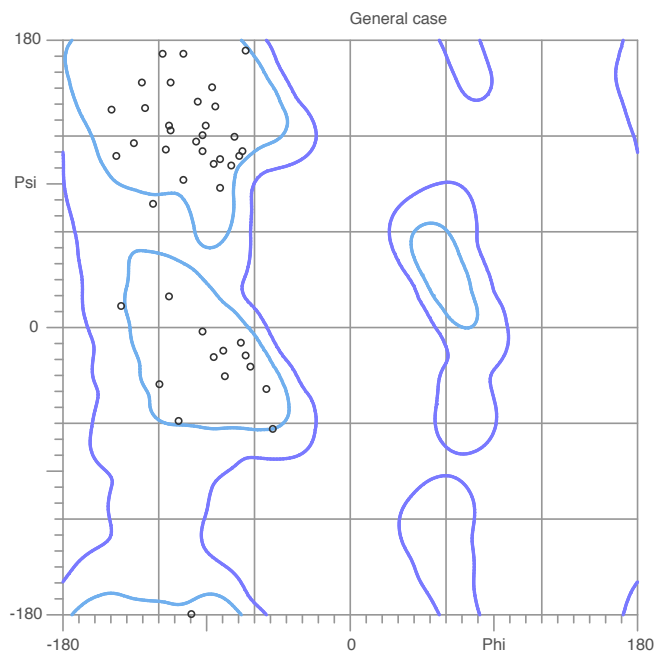
85.4% (41/48) of all residues were in favored (98%) regions.  
93.8% (45/48) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 17 LYS (71.6, 78.4)
- [3] 47 ILE (-173.1, -32.6)
- [3] 48 ILE (65.2, 99.8)

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 4



89.6% (43/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

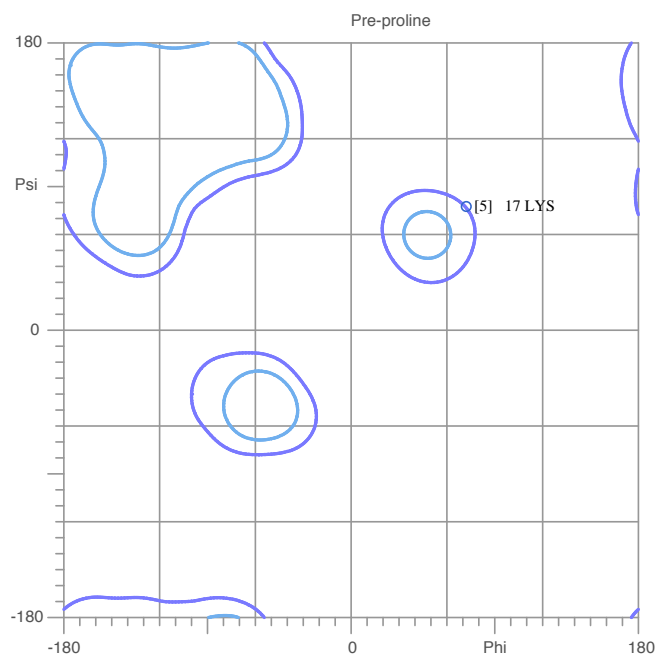
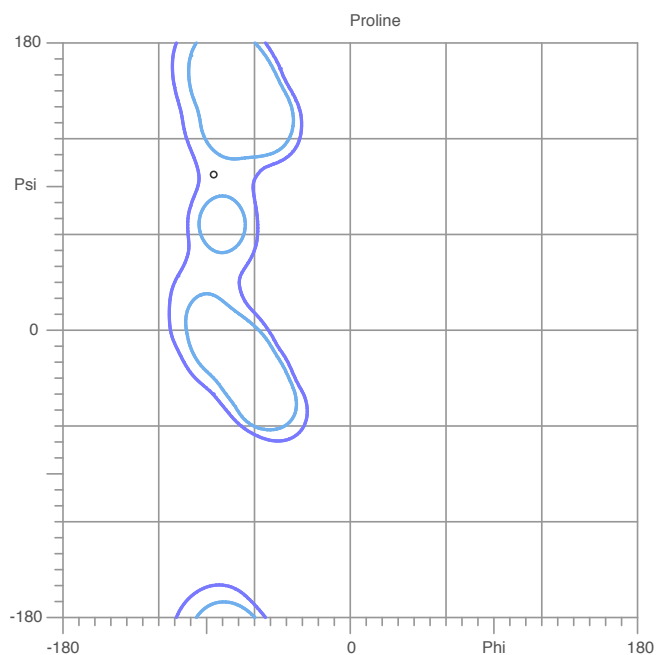
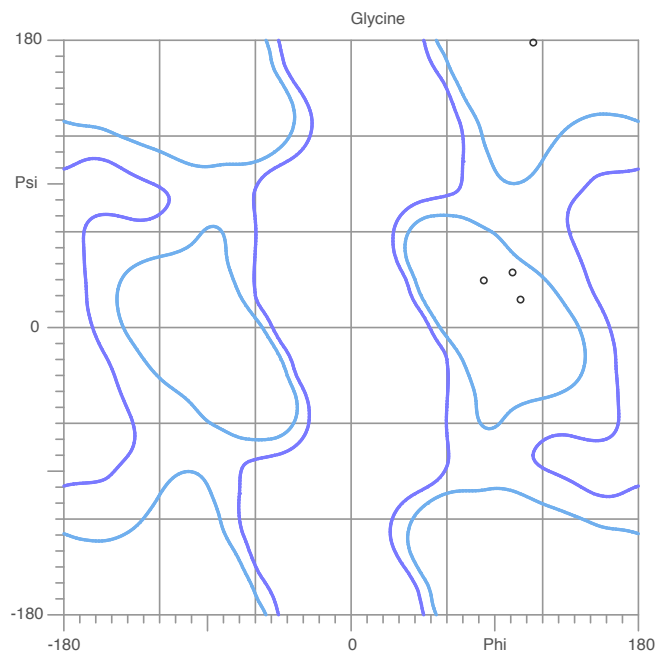
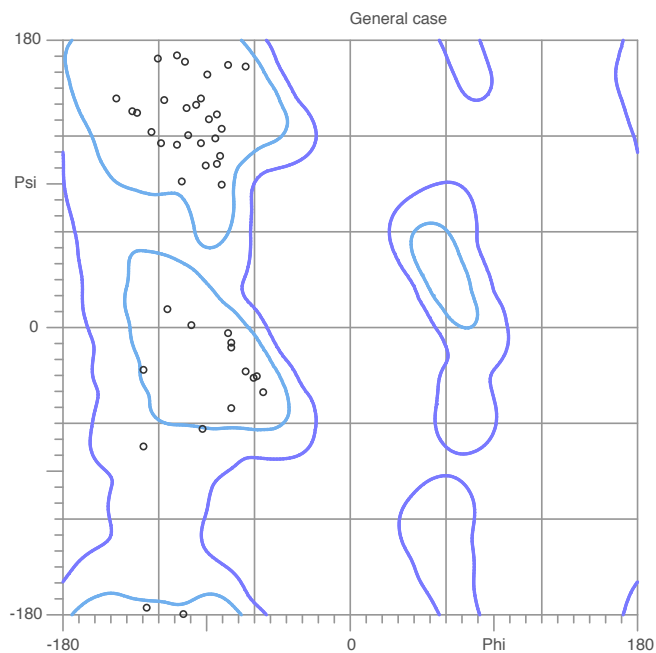
There were 1 outliers (phi, psi):  
[4] 17 LYS (77.1, 132.8)

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# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 5



91.7% (44/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

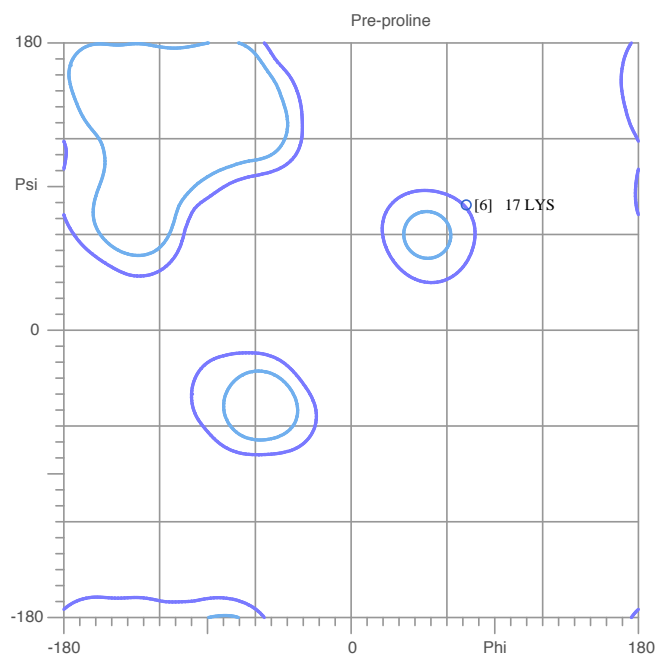
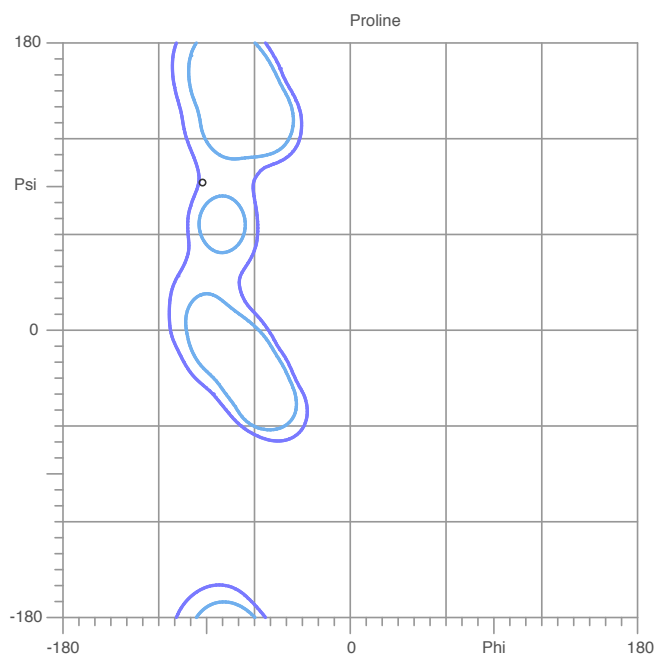
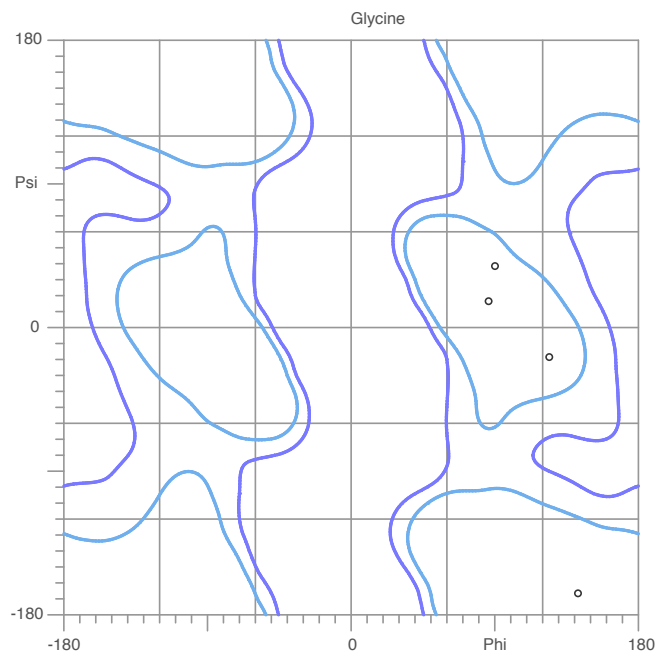
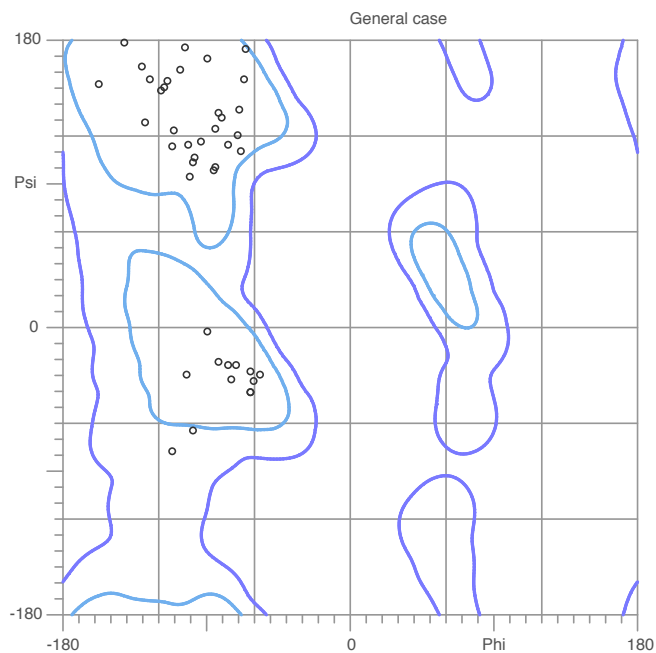
There were 1 outliers (phi, psi):  
[5] 17 LYS (72.6, 78.5)

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

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

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 6

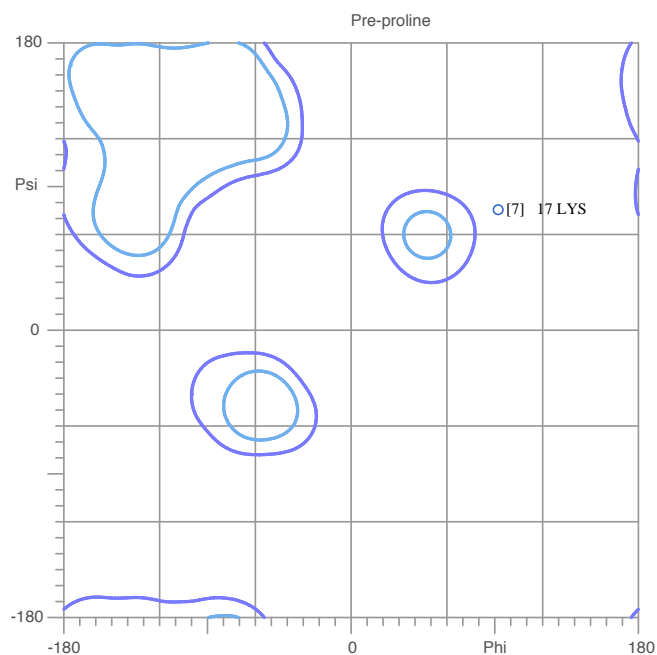
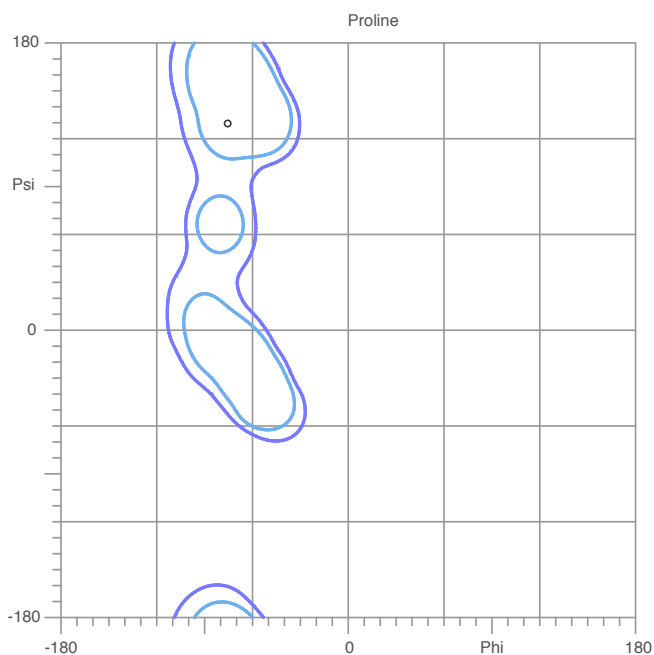
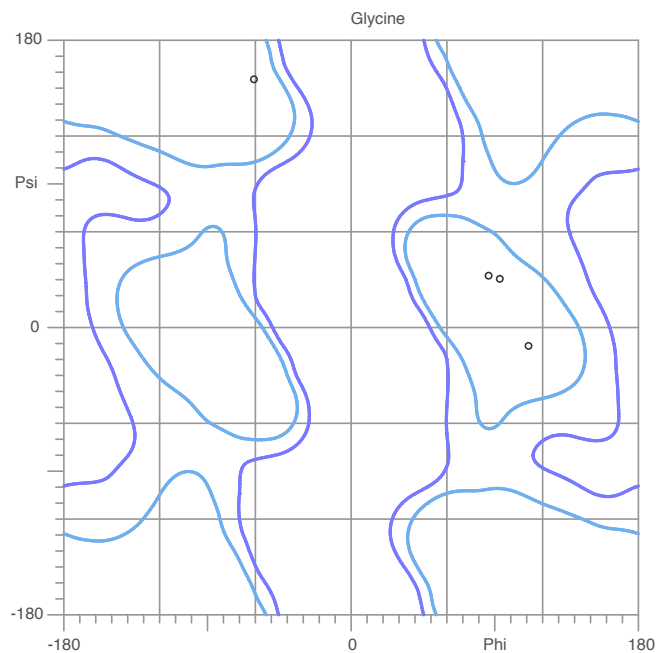
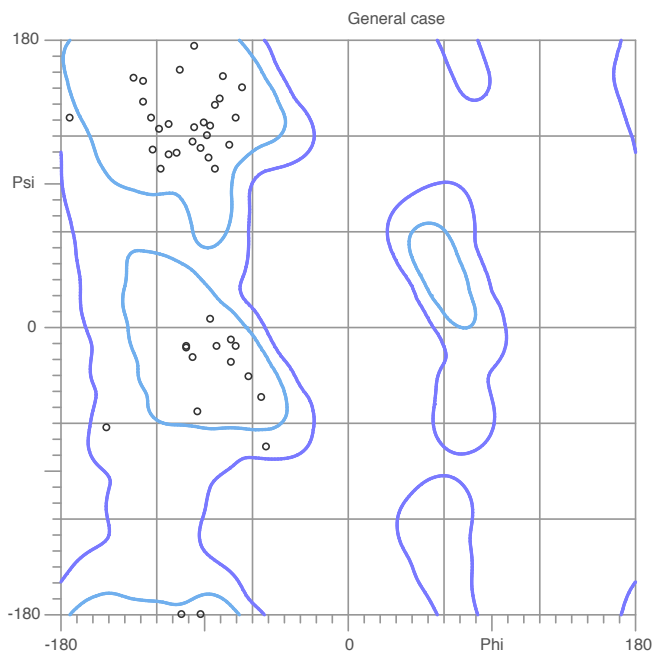


91.7% (44/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[6] 17 LYS (73.0, 79.7)

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 7



91.7% (44/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

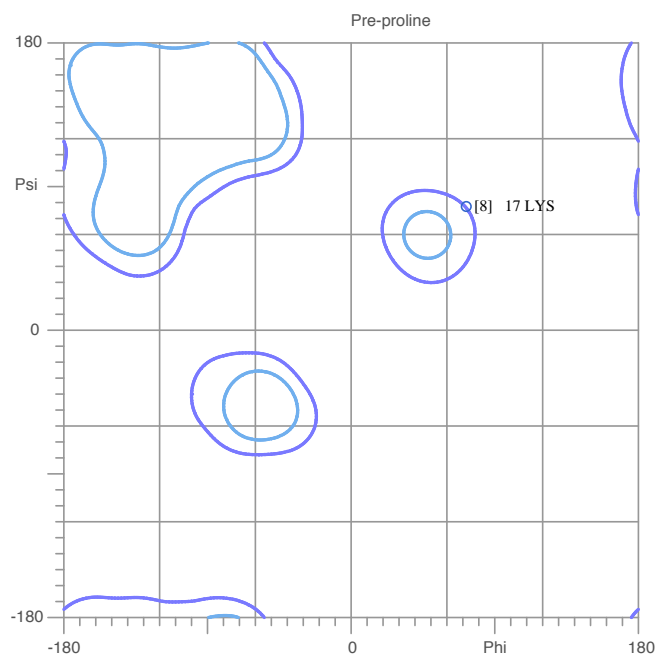
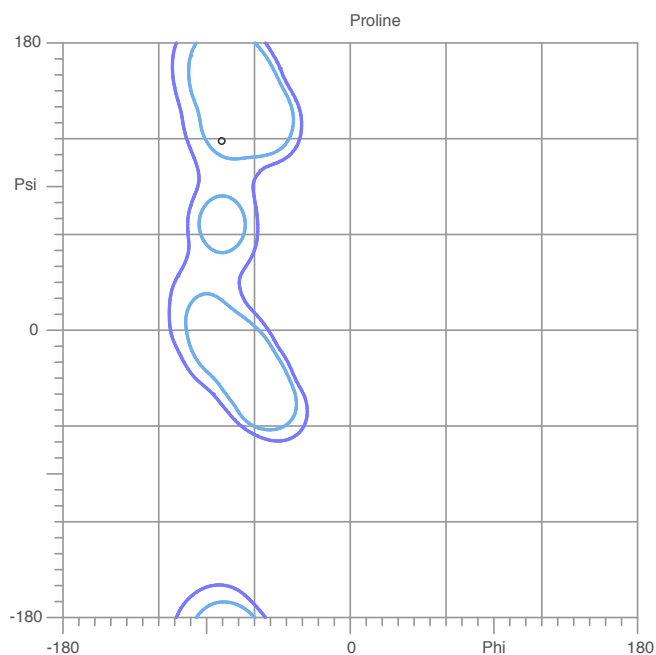
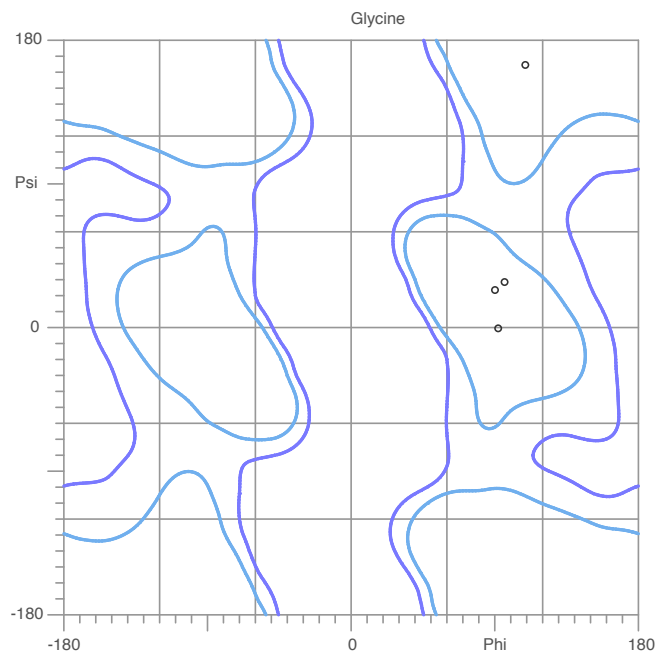
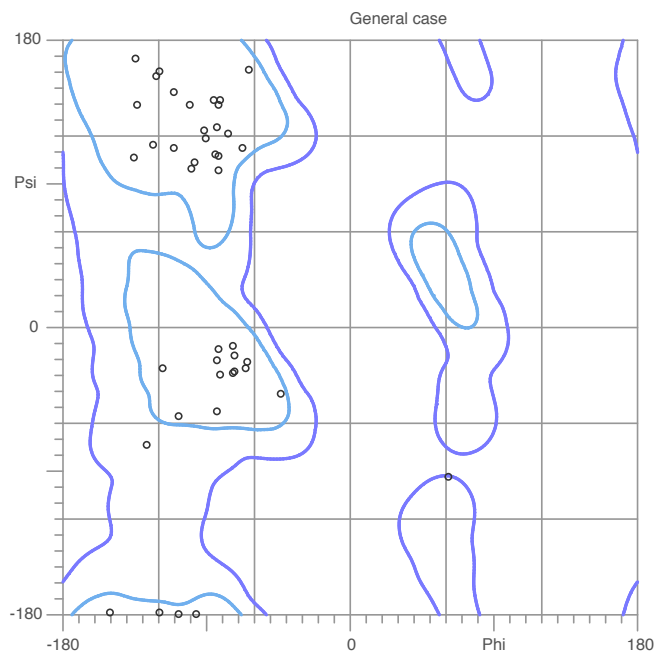
There were 1 outliers (phi, psi):  
[7] 17 LYS (92.8, 76.7)

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# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 8



93.8% (45/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

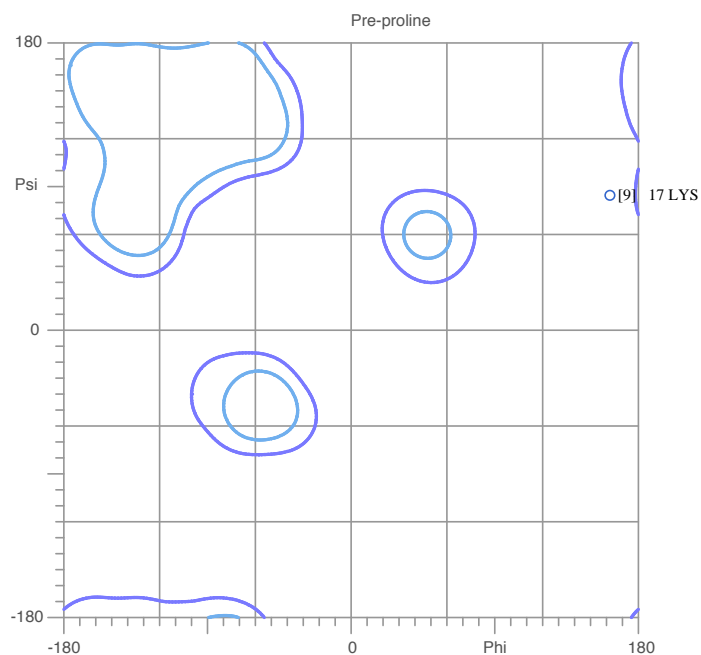
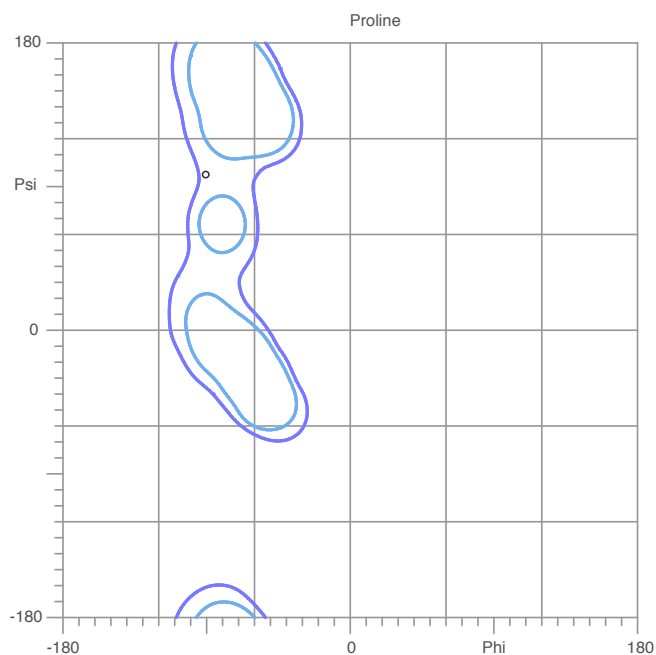
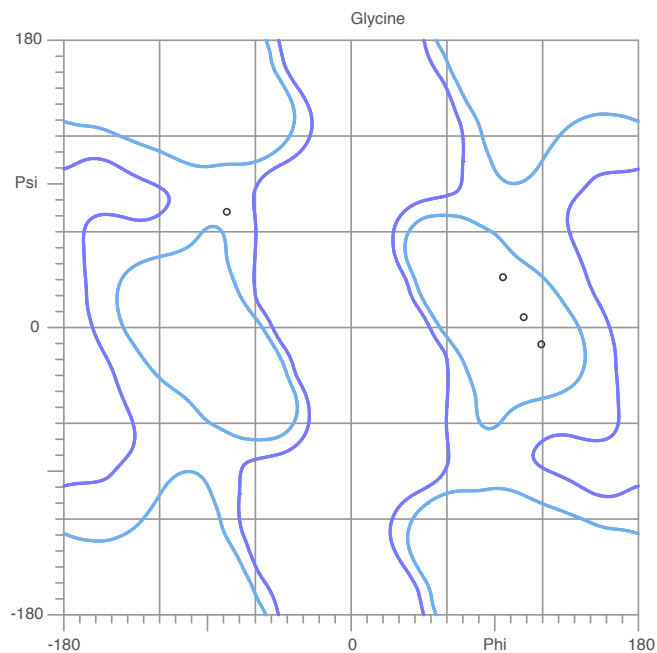
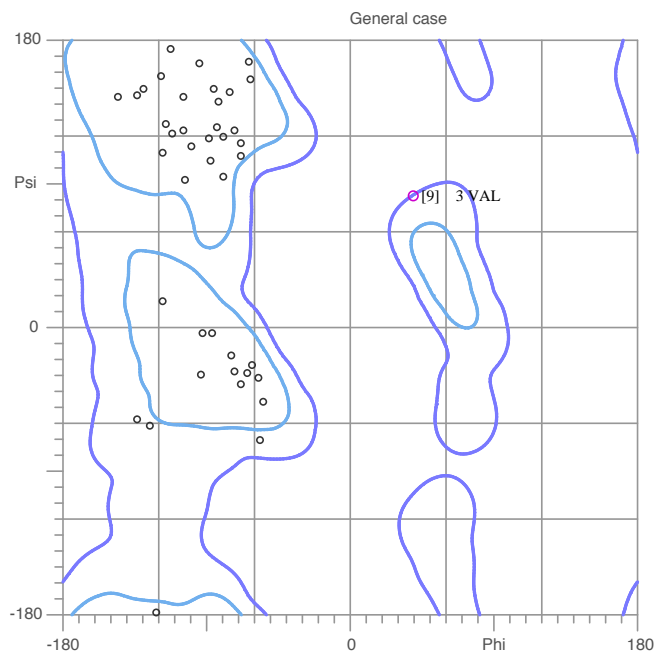
There were 1 outliers (phi, psi):  
[8] 17 LYS (72.7, 78.5)

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# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 9



85.4% (41/48) of all residues were in favored (98%) regions.  
95.8% (46/48) of all residues were in allowed (>99.8%) regions.

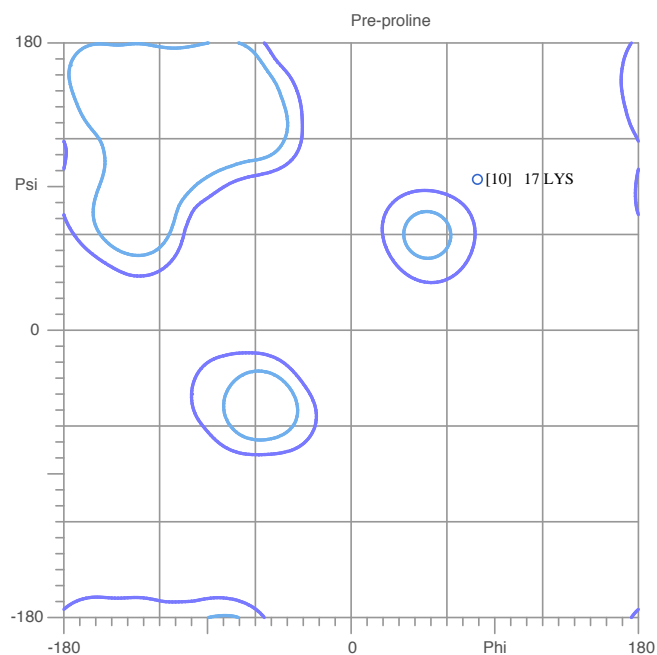
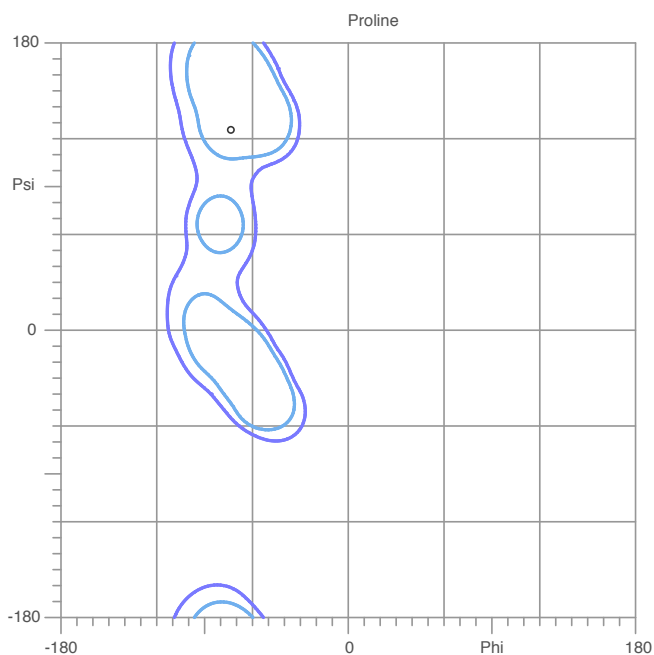
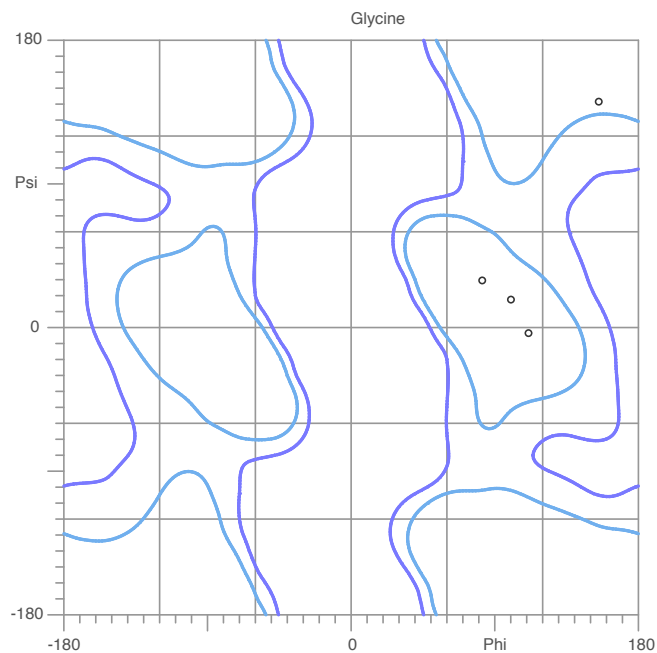
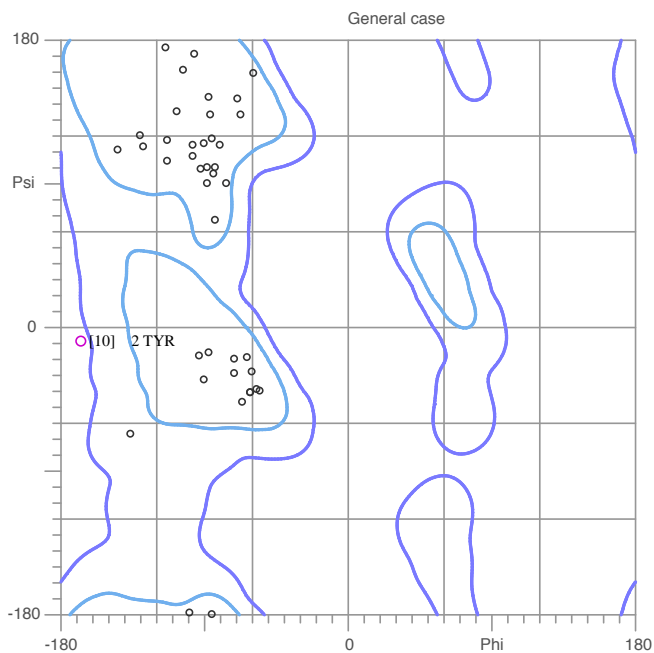
There were 2 outliers (phi, psi):

[9] 3 VAL (39.4, 83.7)

[9] 17 LYS (162.5, 86.0)

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 10

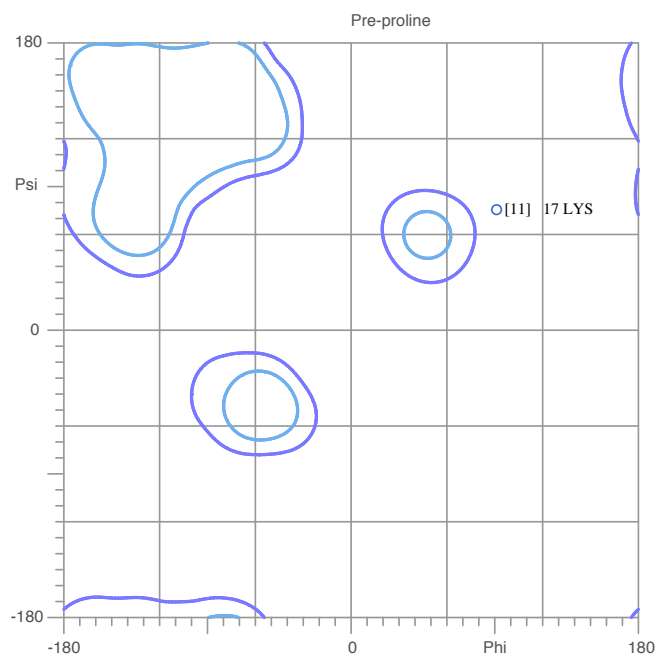
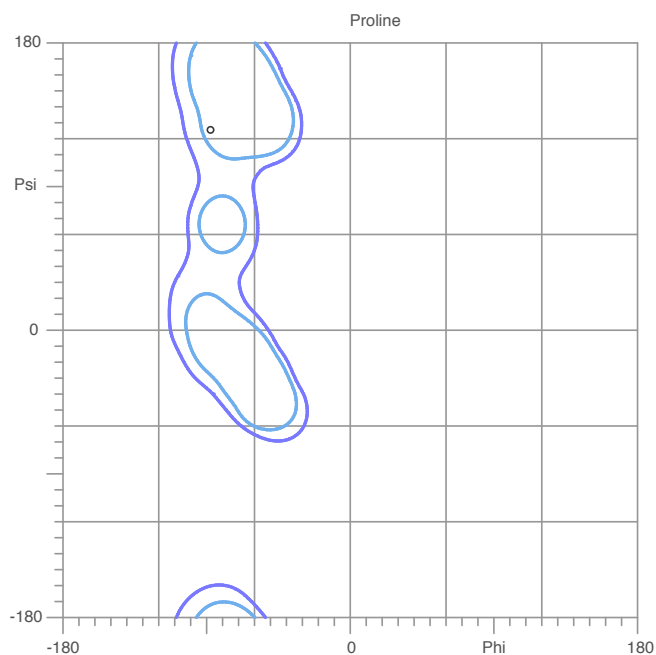
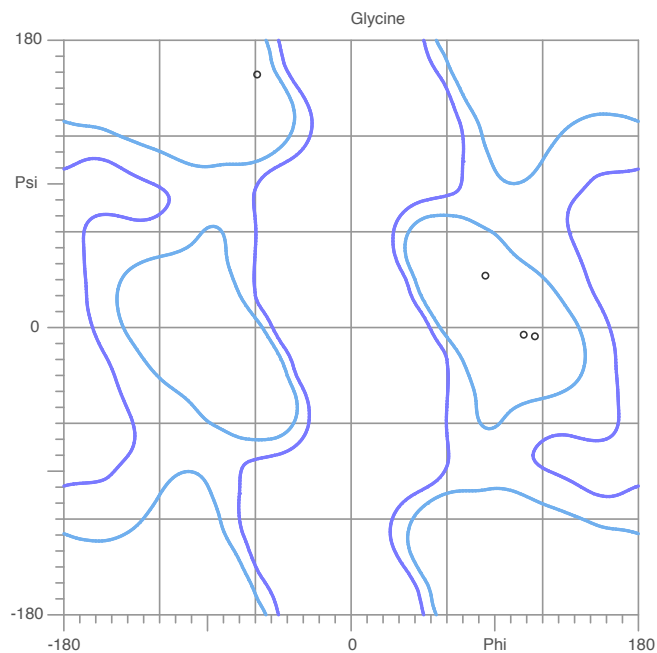
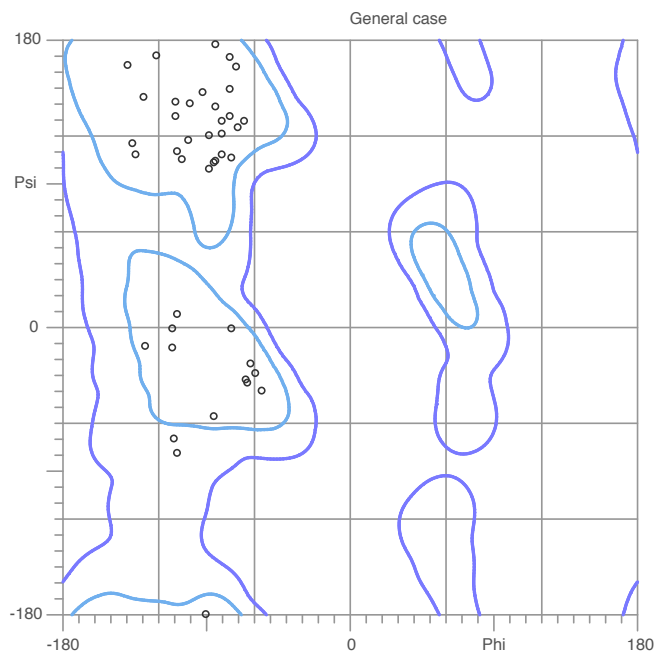


93.8% (45/48) of all residues were in favored (98%) regions.  
95.8% (46/48) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[10] 2 TYR (-168.8, -8.1)  
[10] 17 LYS (79.5, 95.4)

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 11



93.8% (45/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

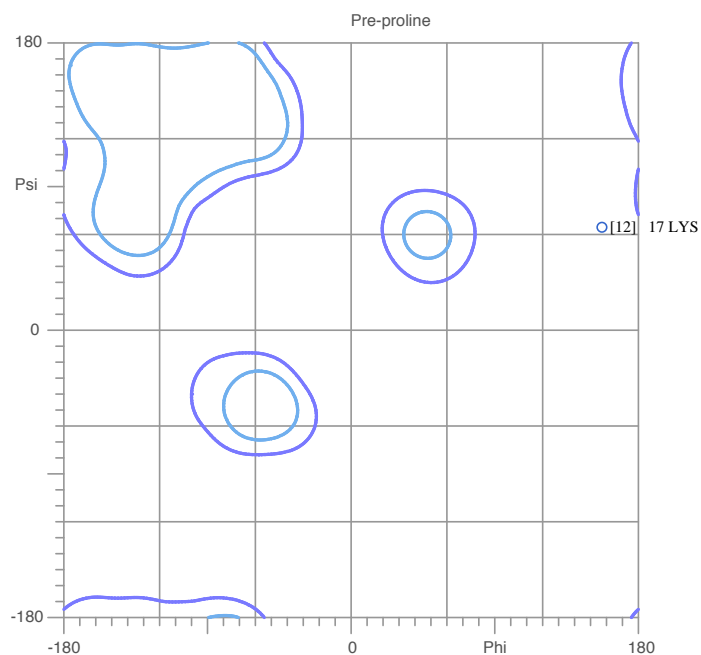
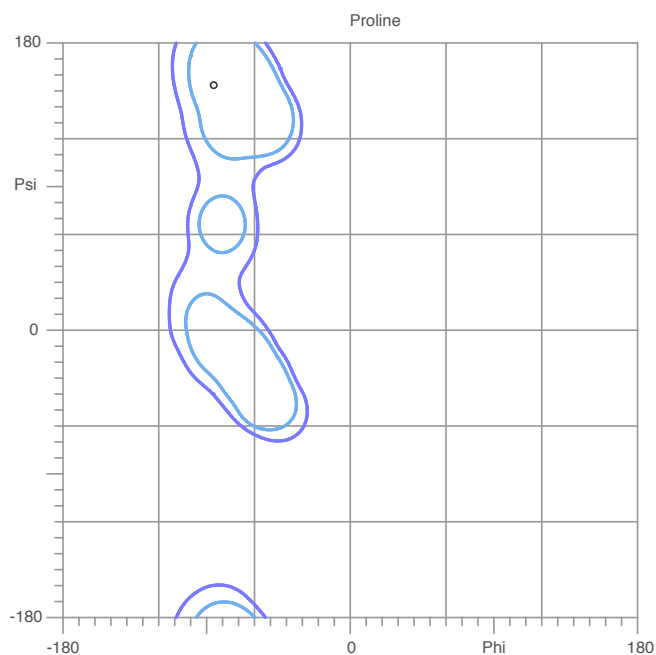
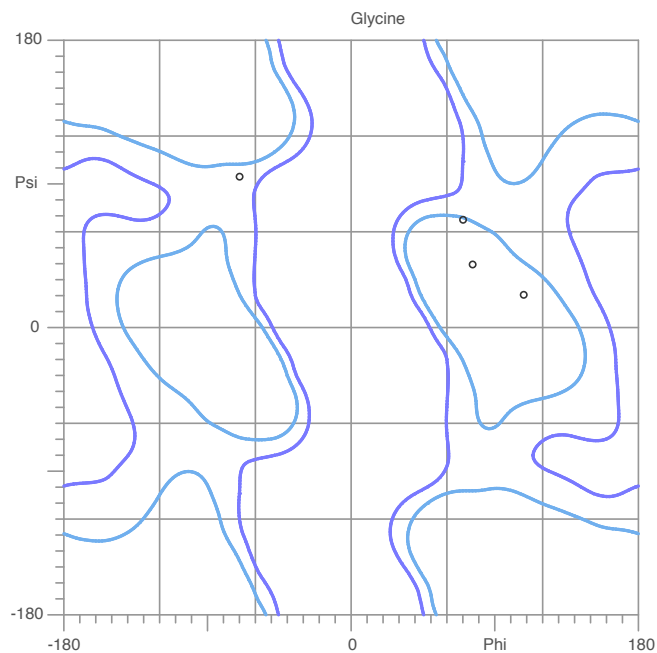
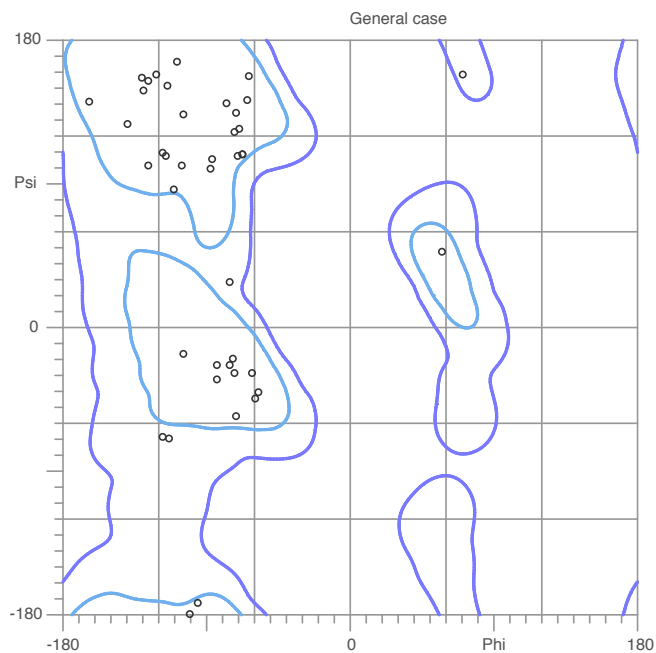
There were 1 outliers (phi, psi):  
[11] 17 LYS (91.6, 77.0)

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

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 12



87.5% (42/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

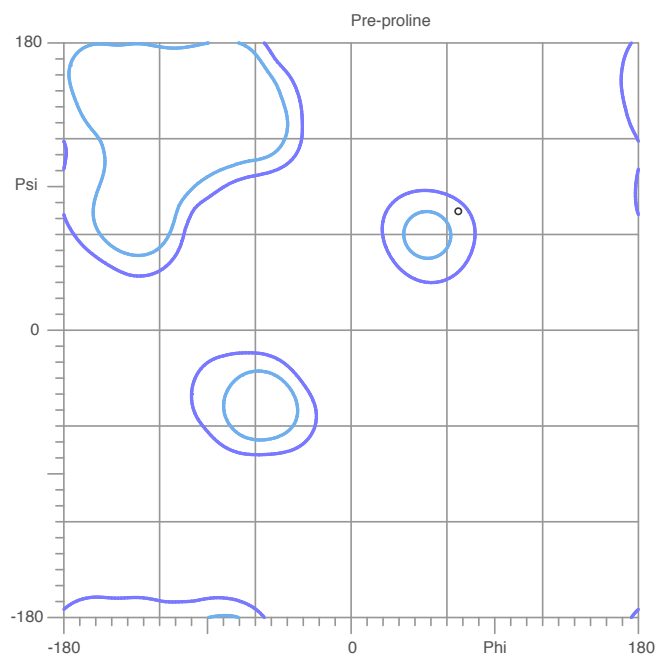
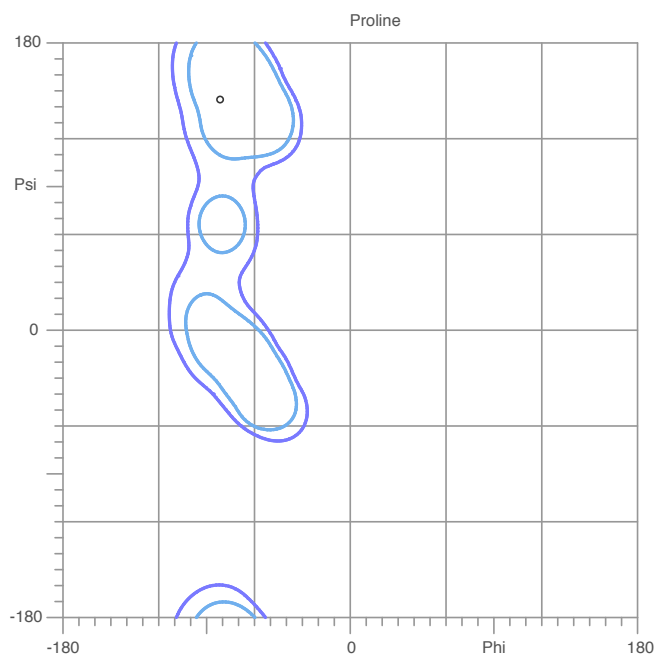
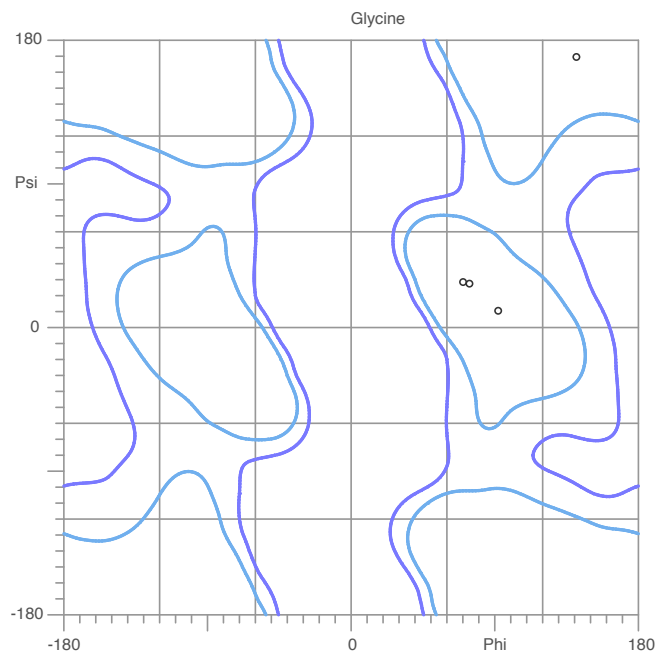
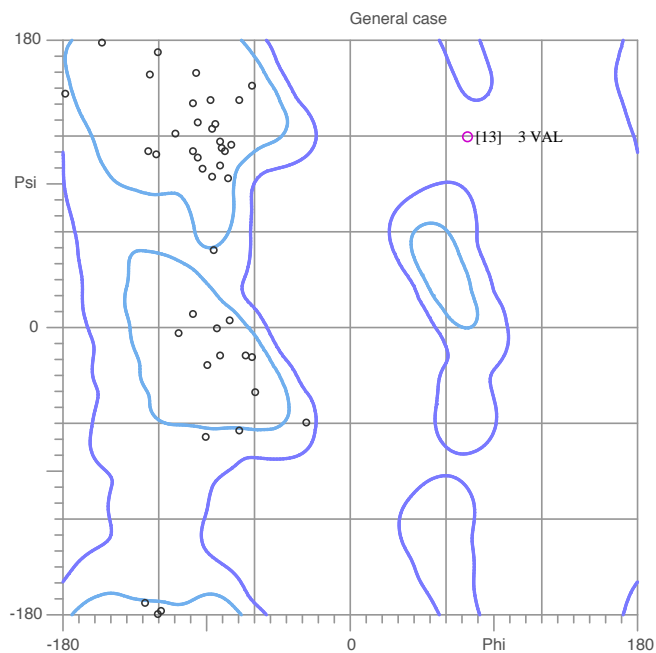
There were 1 outliers (phi, psi):  
[12] 17 LYS (157.9, 65.6)

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

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 13

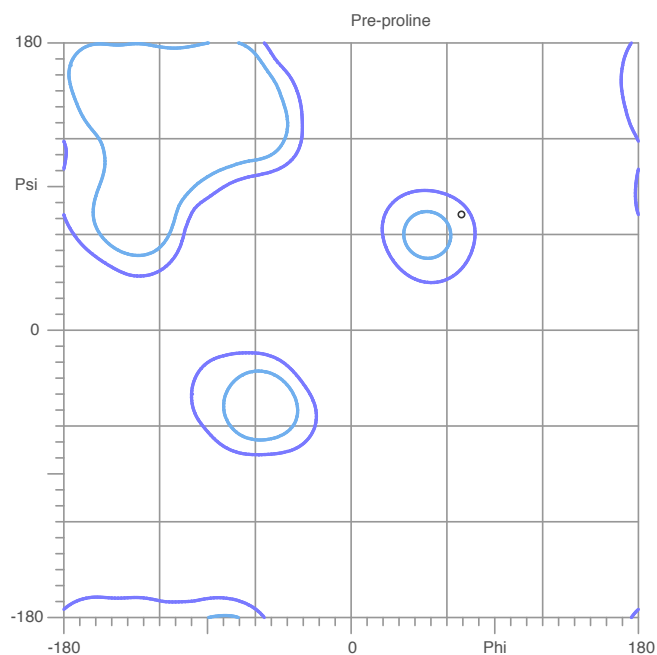
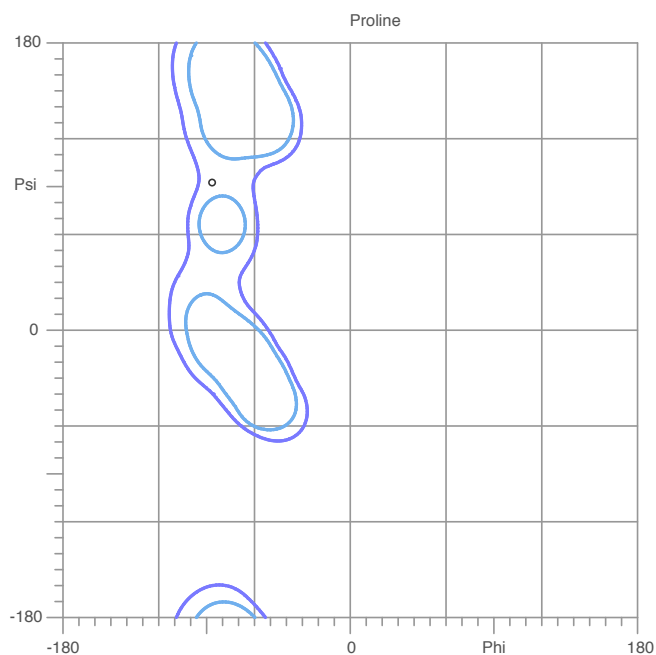
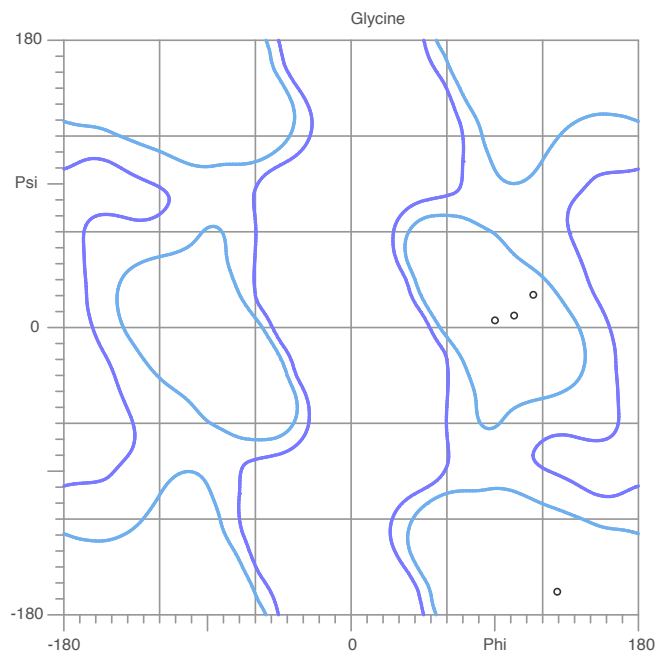
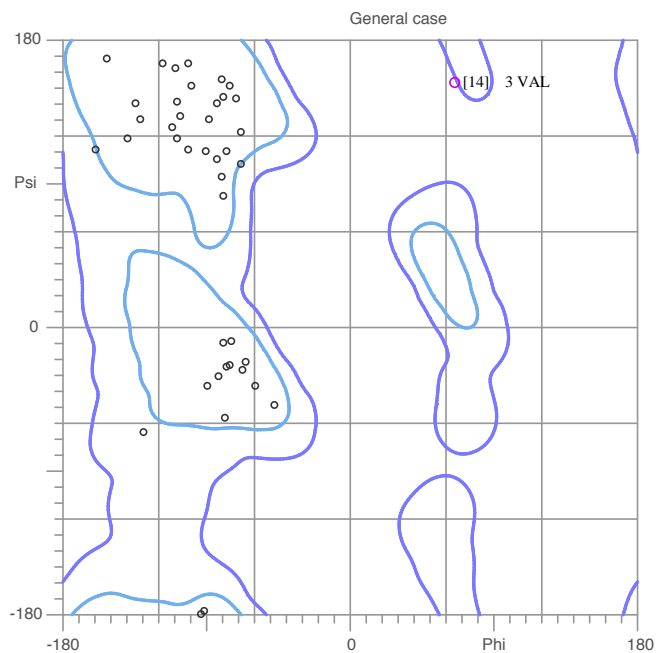


85.4% (41/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[13] 3 VAL (73.1, 120.2)

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 14



89.6% (43/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

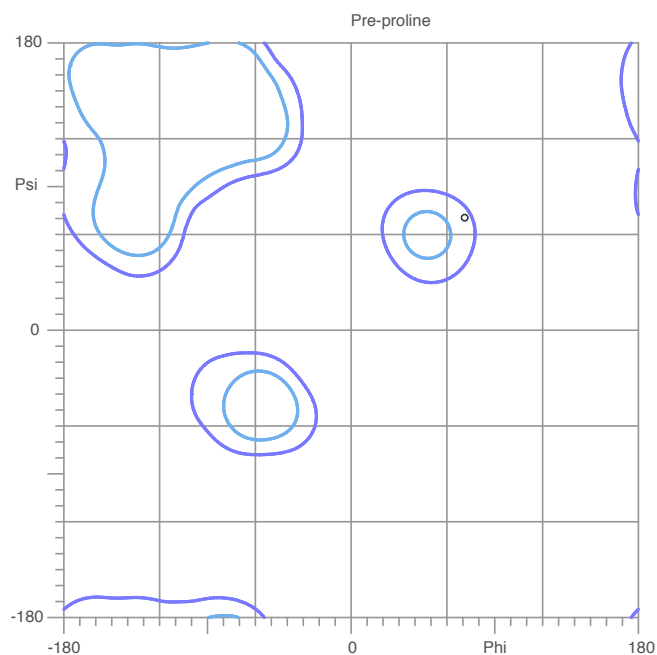
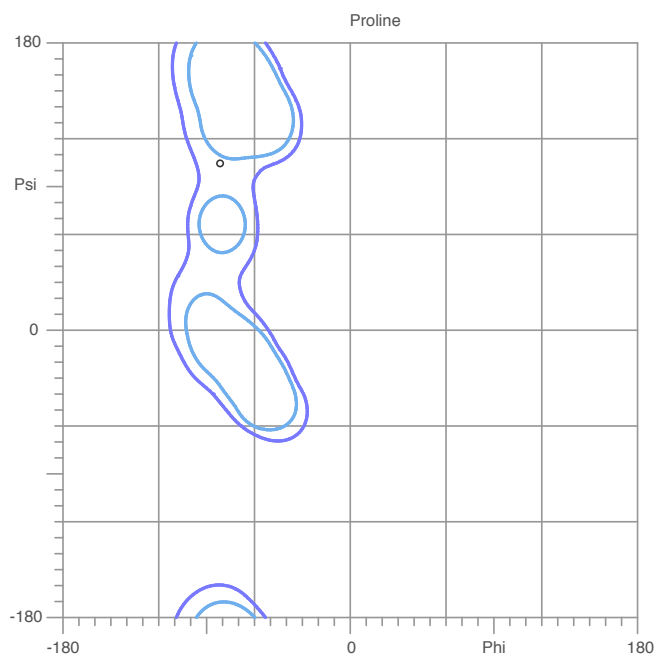
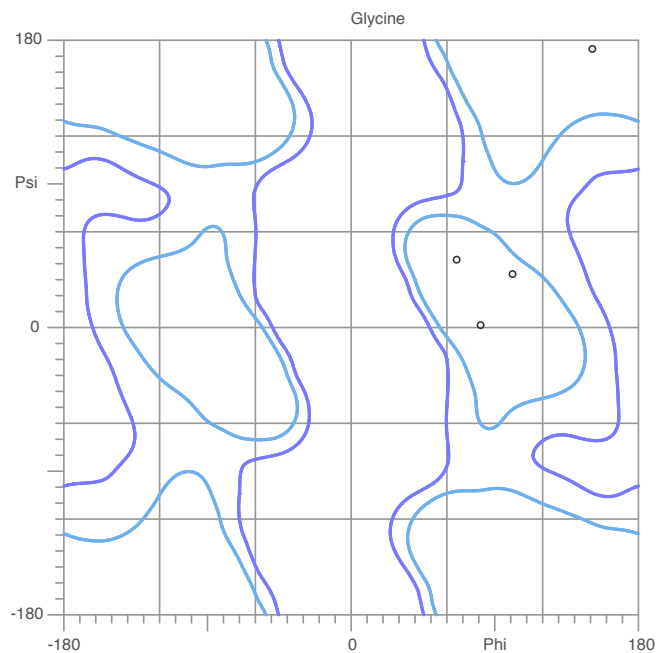
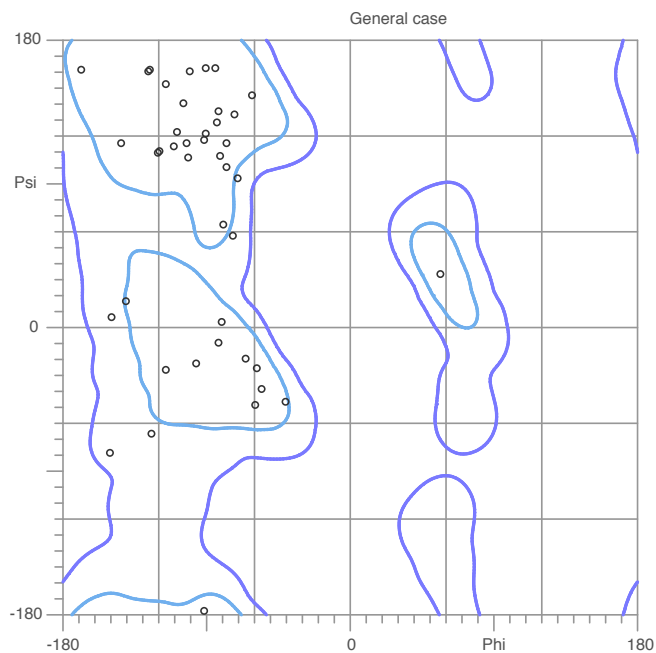
There were 1 outliers (phi, psi):  
[14] 3 VAL (65.4, 154.8)

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

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 15



85.4% (41/48) of all residues were in favored (98%) regions.  
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

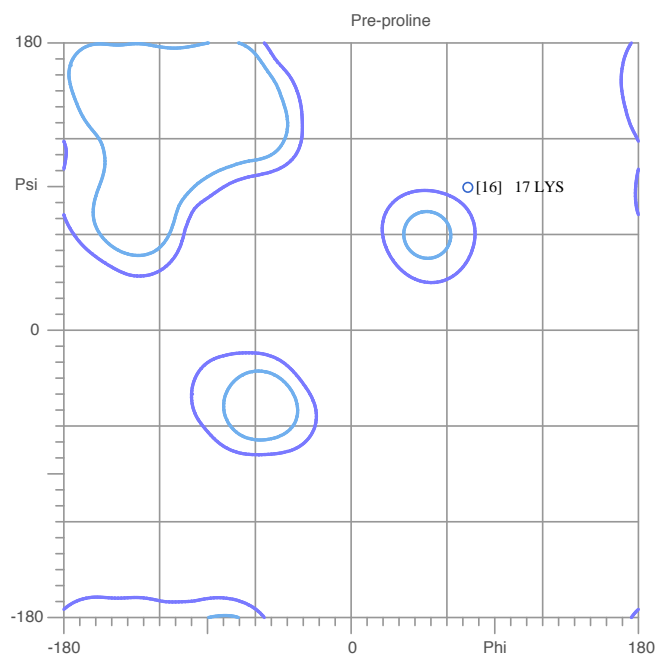
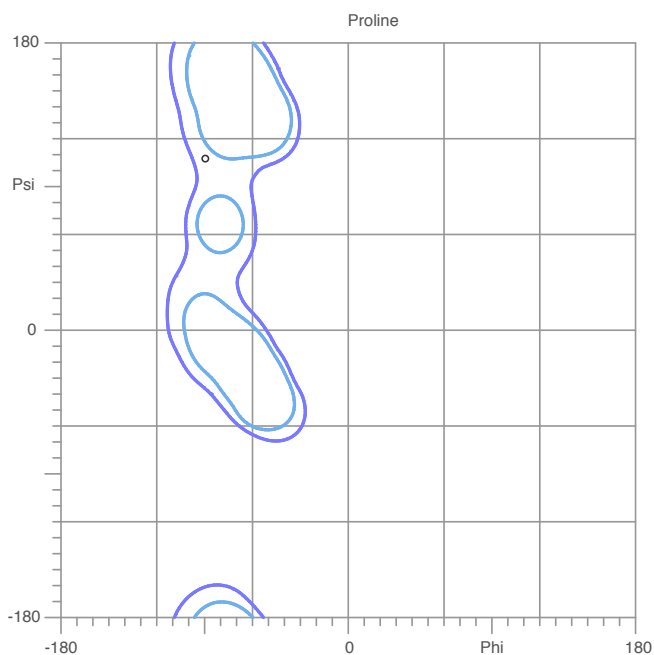
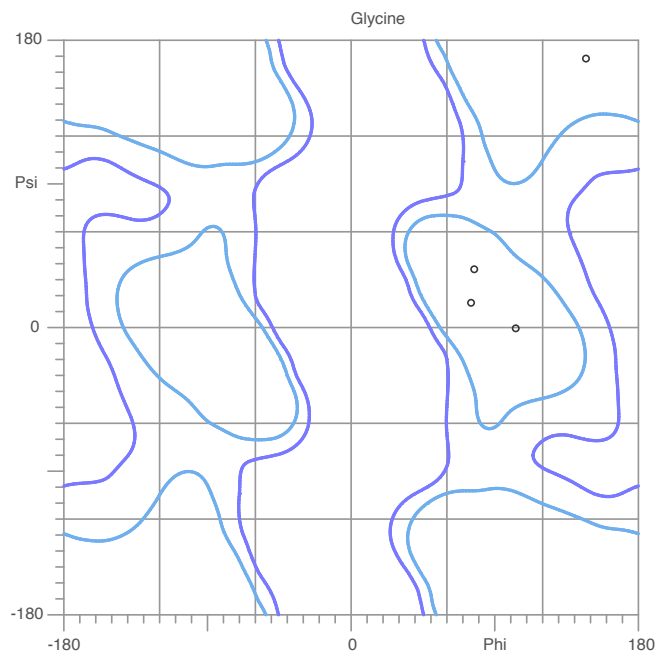
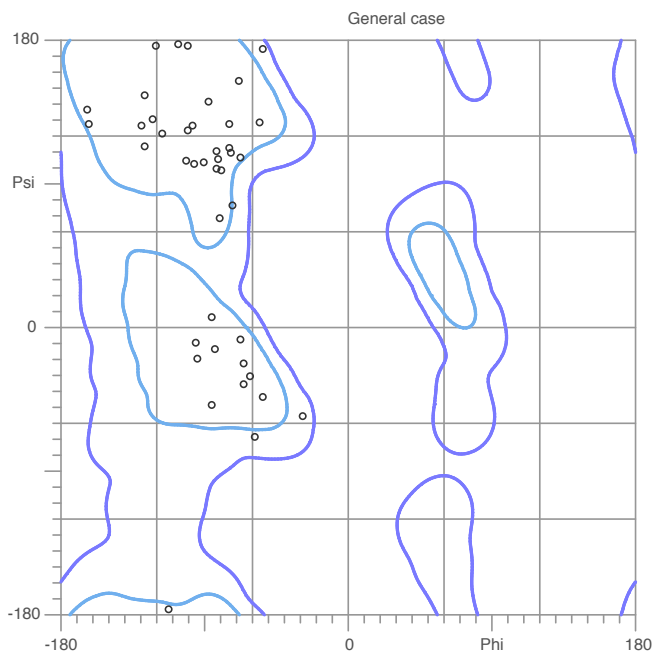
There were no outliers.

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

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 16



89.6% (43/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

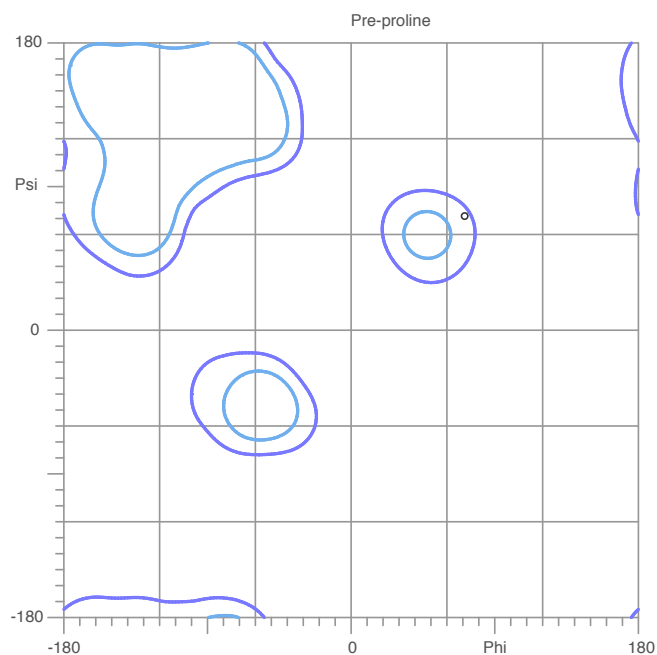
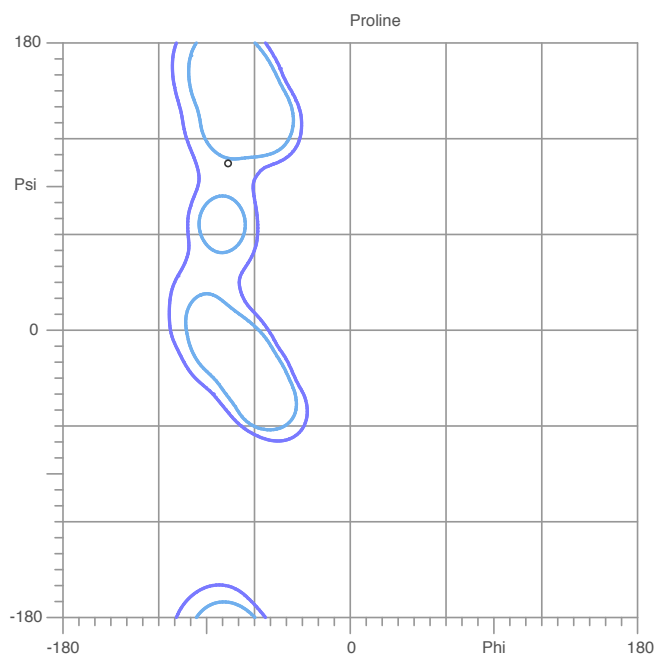
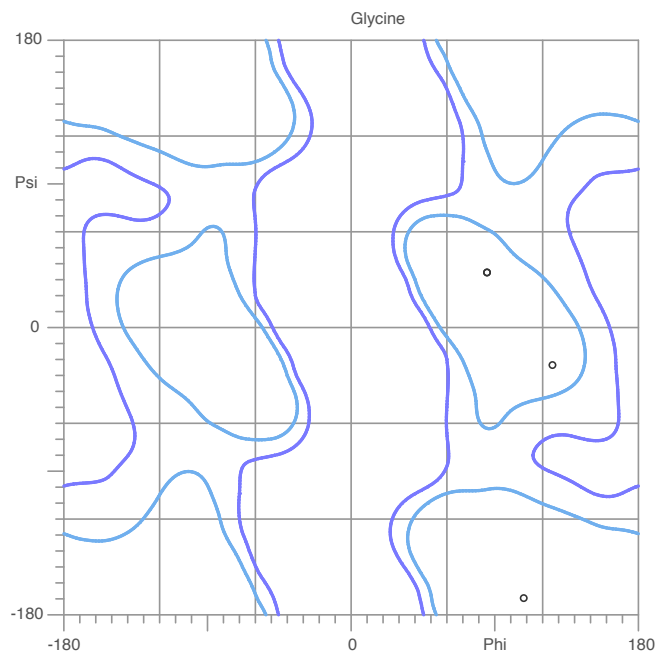
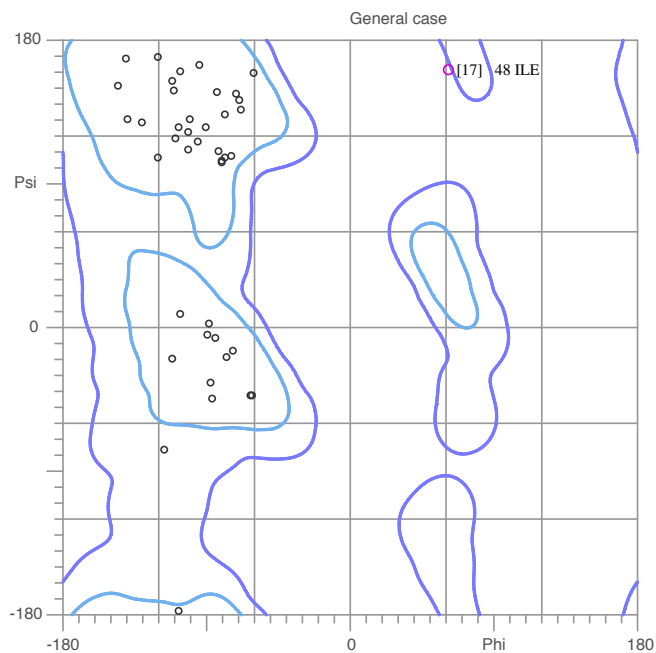
There were 1 outliers (phi, psi):  
[16] 17 LYS (73.8, 90.4)

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

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 17



91.7% (44/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

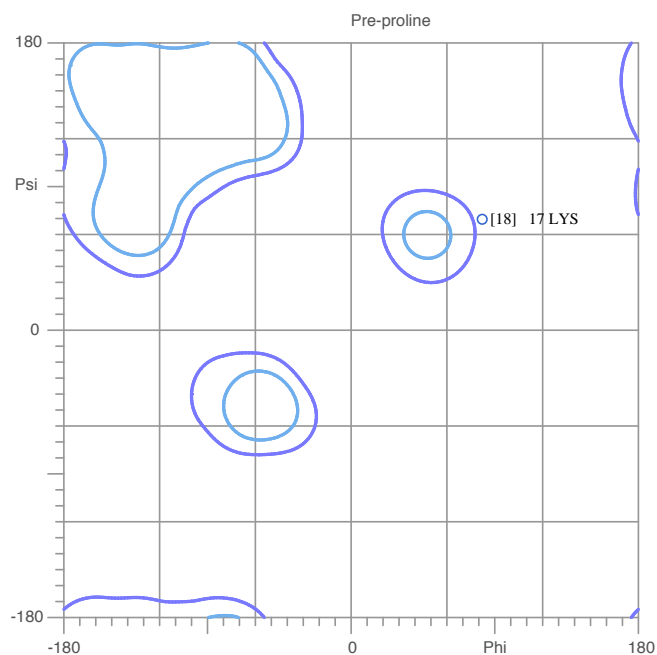
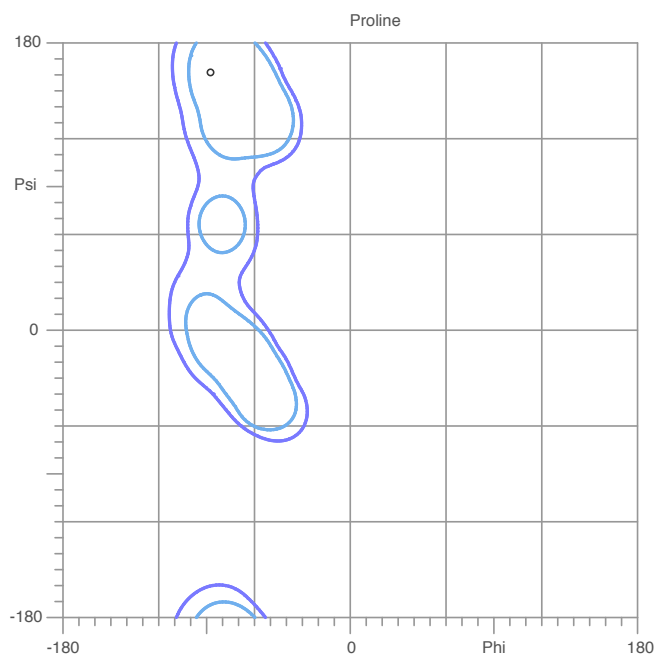
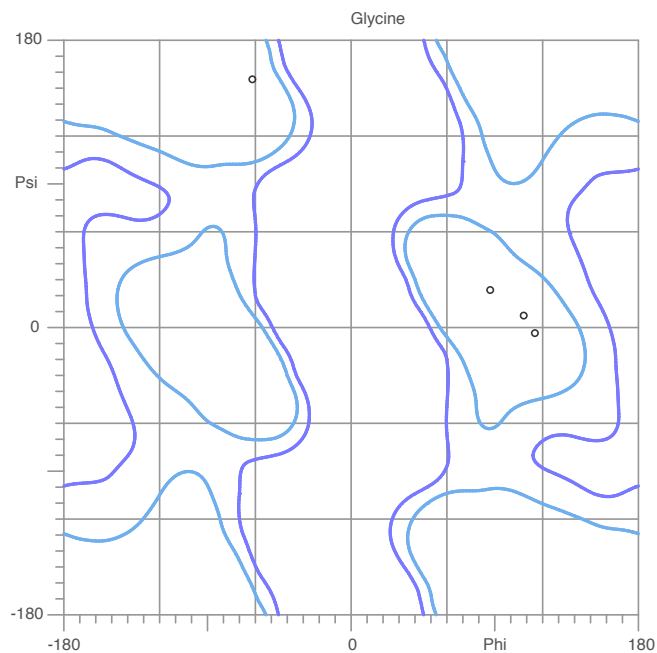
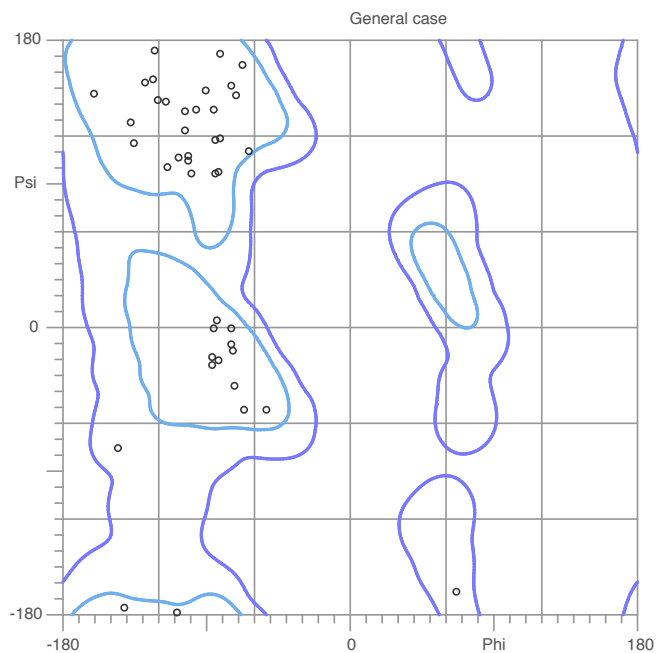
There were 1 outliers (phi, psi):  
[17] 48 ILE (61.6, 162.3)

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

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 18



93.8% (45/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

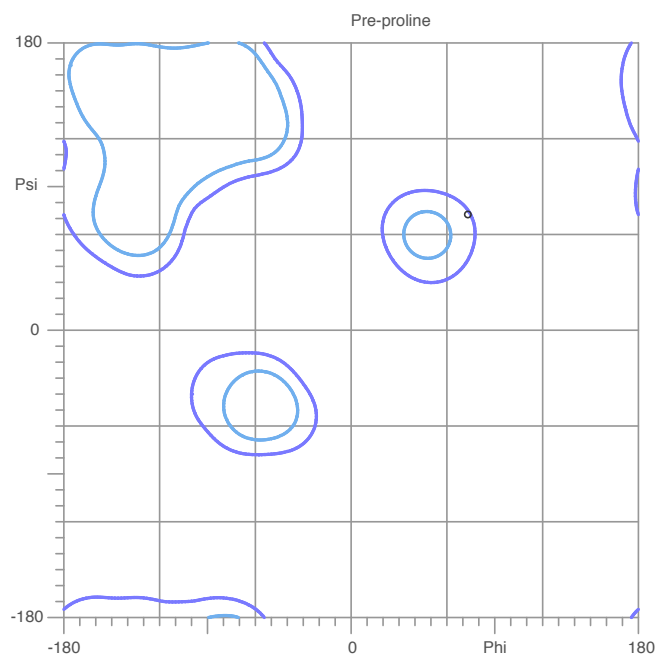
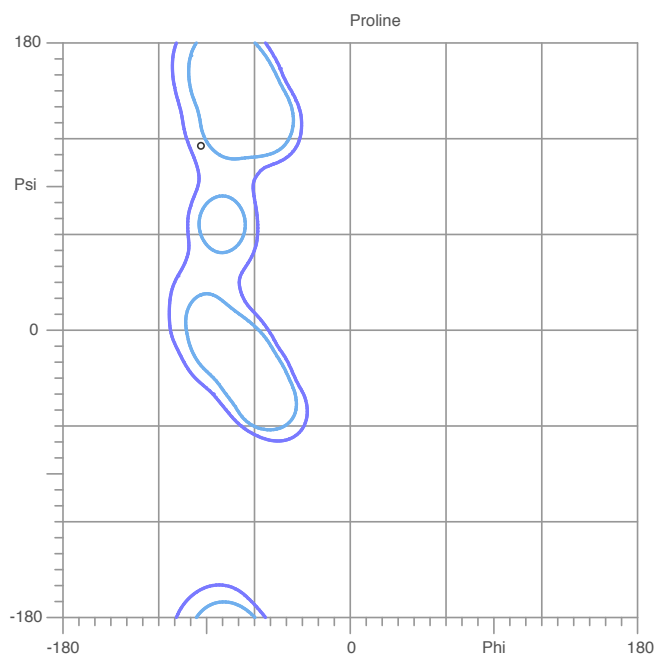
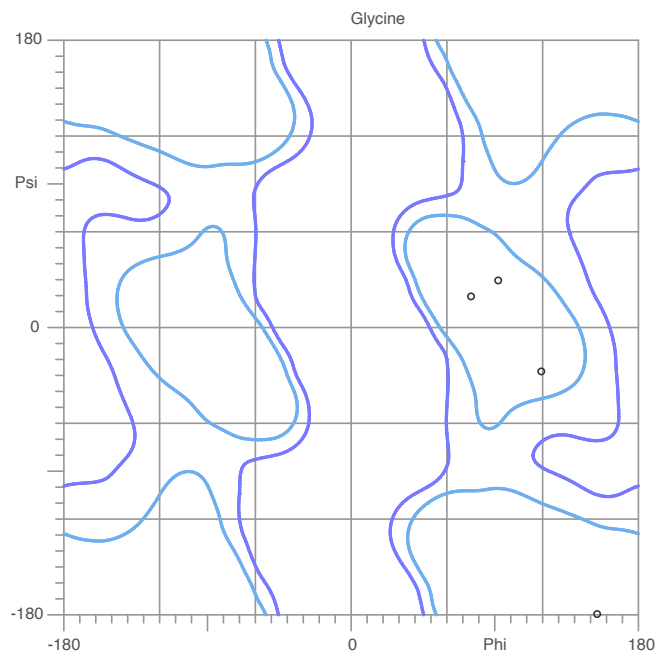
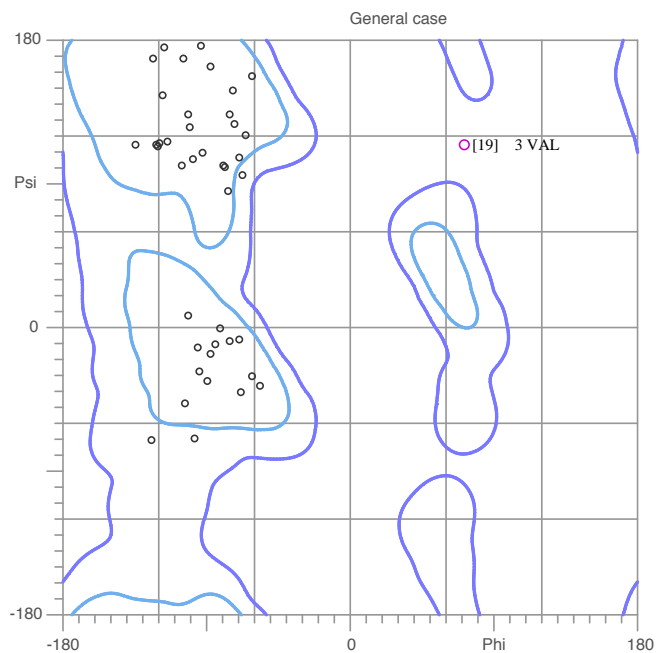
There were 1 outliers (phi, psi):  
[18] 17 LYS (82.6, 70.3)

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

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 19



87.5% (42/48) of all residues were in favored (98%) regions.  
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

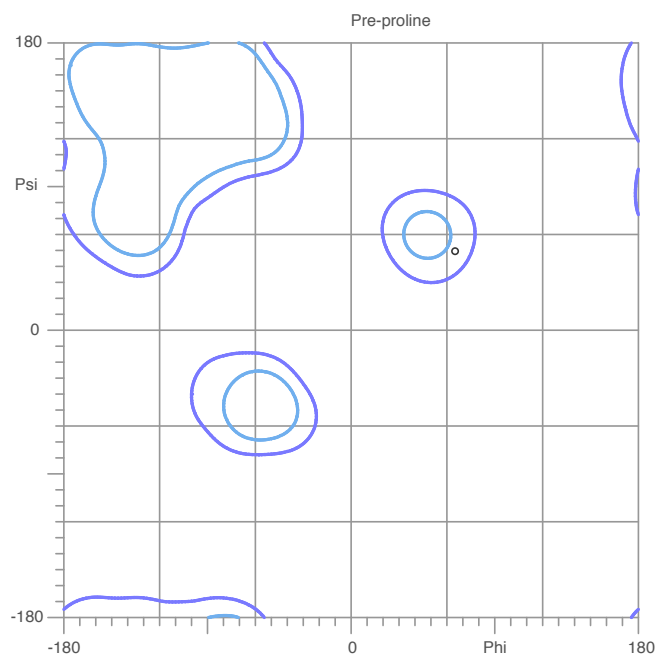
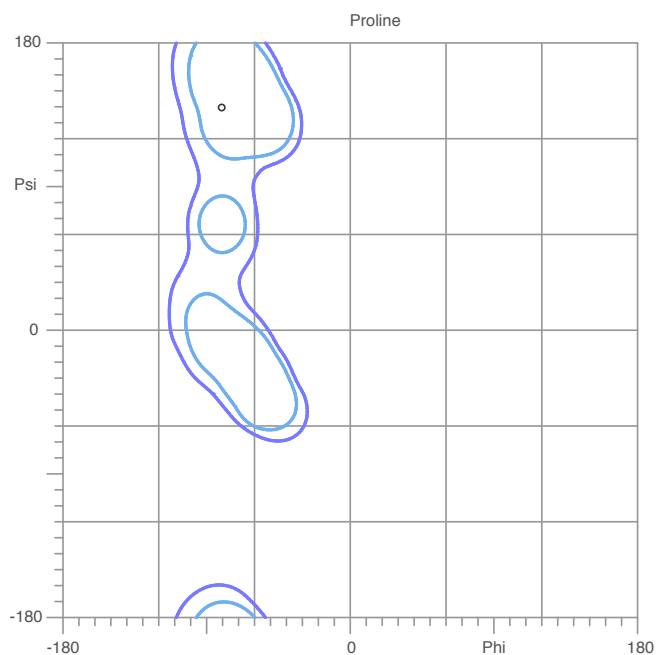
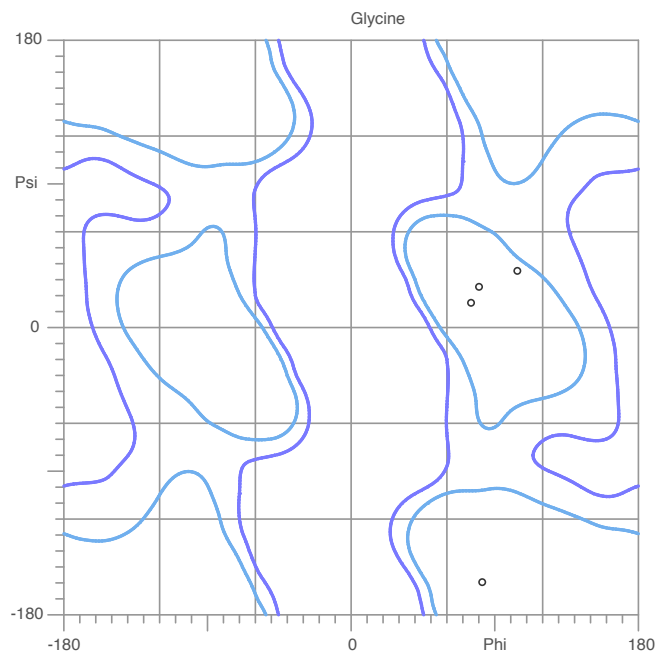
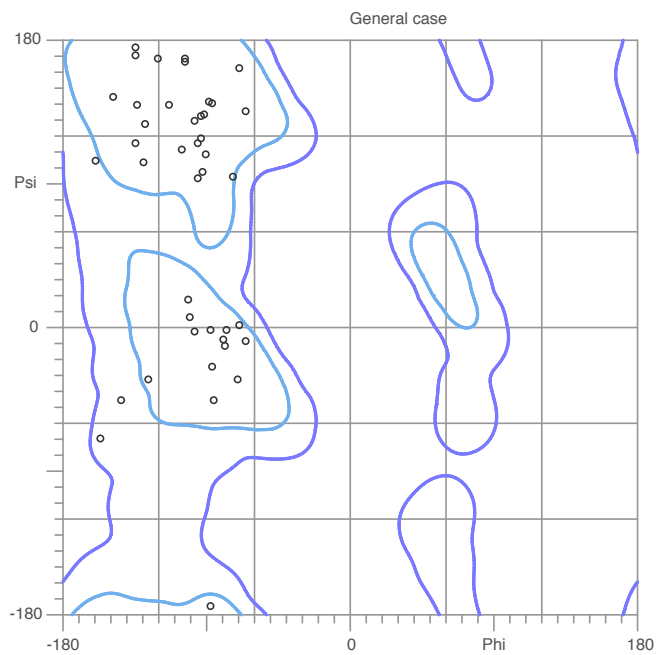
There were 1 outliers (phi, psi):  
[19] 3 VAL (71.2, 115.2)

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

# MolProbity Ramachandran analysis

ER382A\_NMR\_em\_bcr3.pdb, model 20



91.7% (44/48) of all residues were in favored (98%) regions.  
100.0% (48/48) 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)