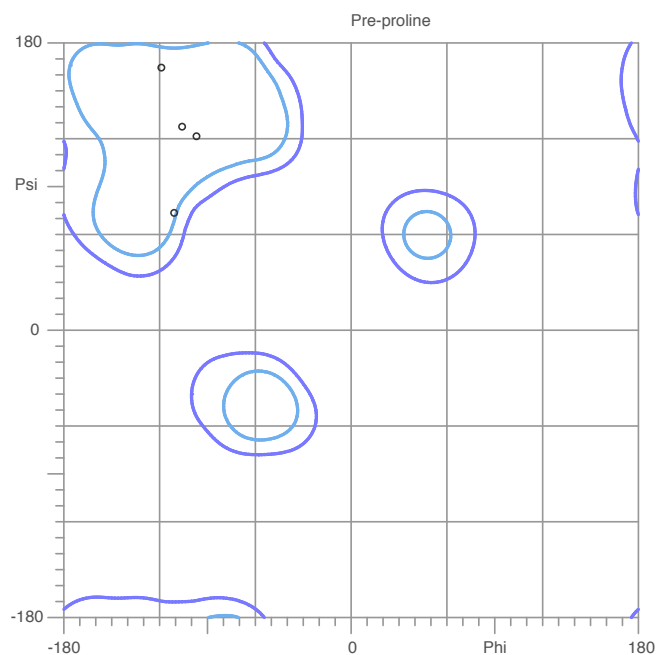
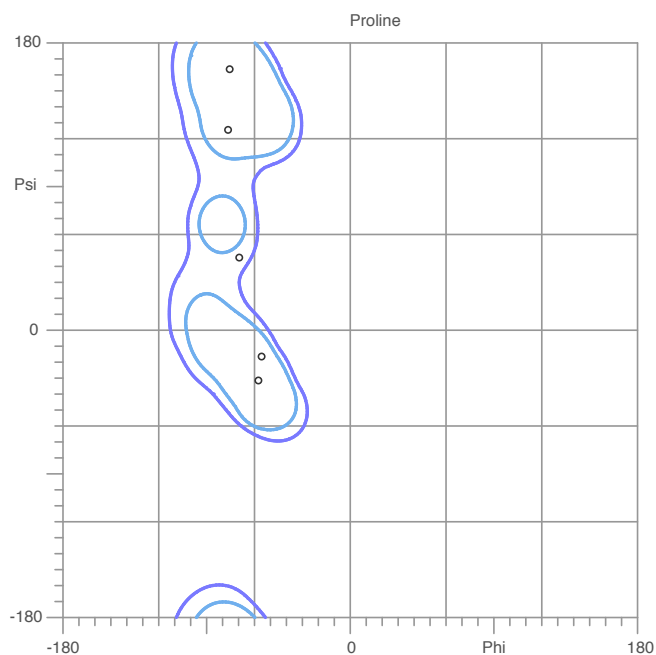
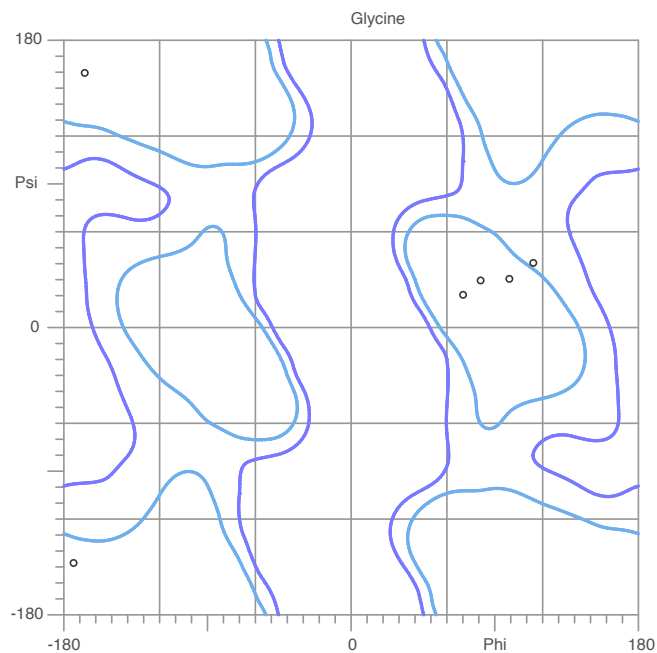
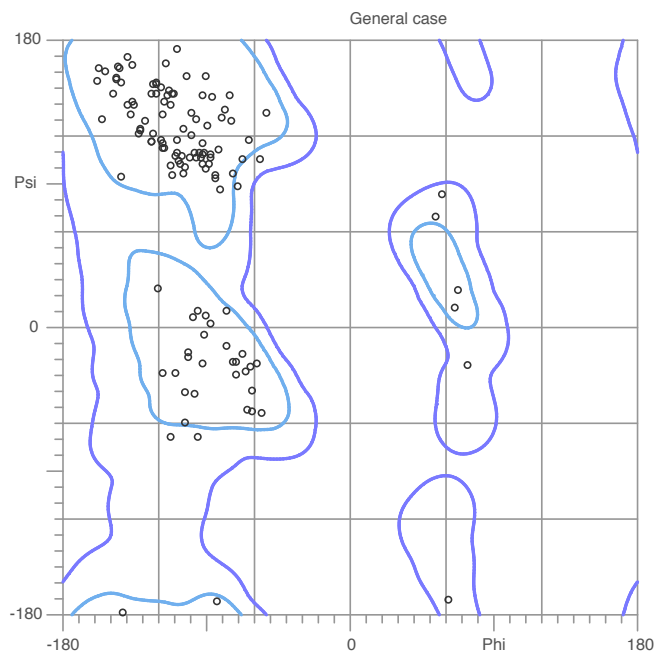




# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 1



92.9% (131/141) of all residues were in favored (98%) regions.  
100.0% (141/141) of all residues were in allowed (>99.8%) regions.

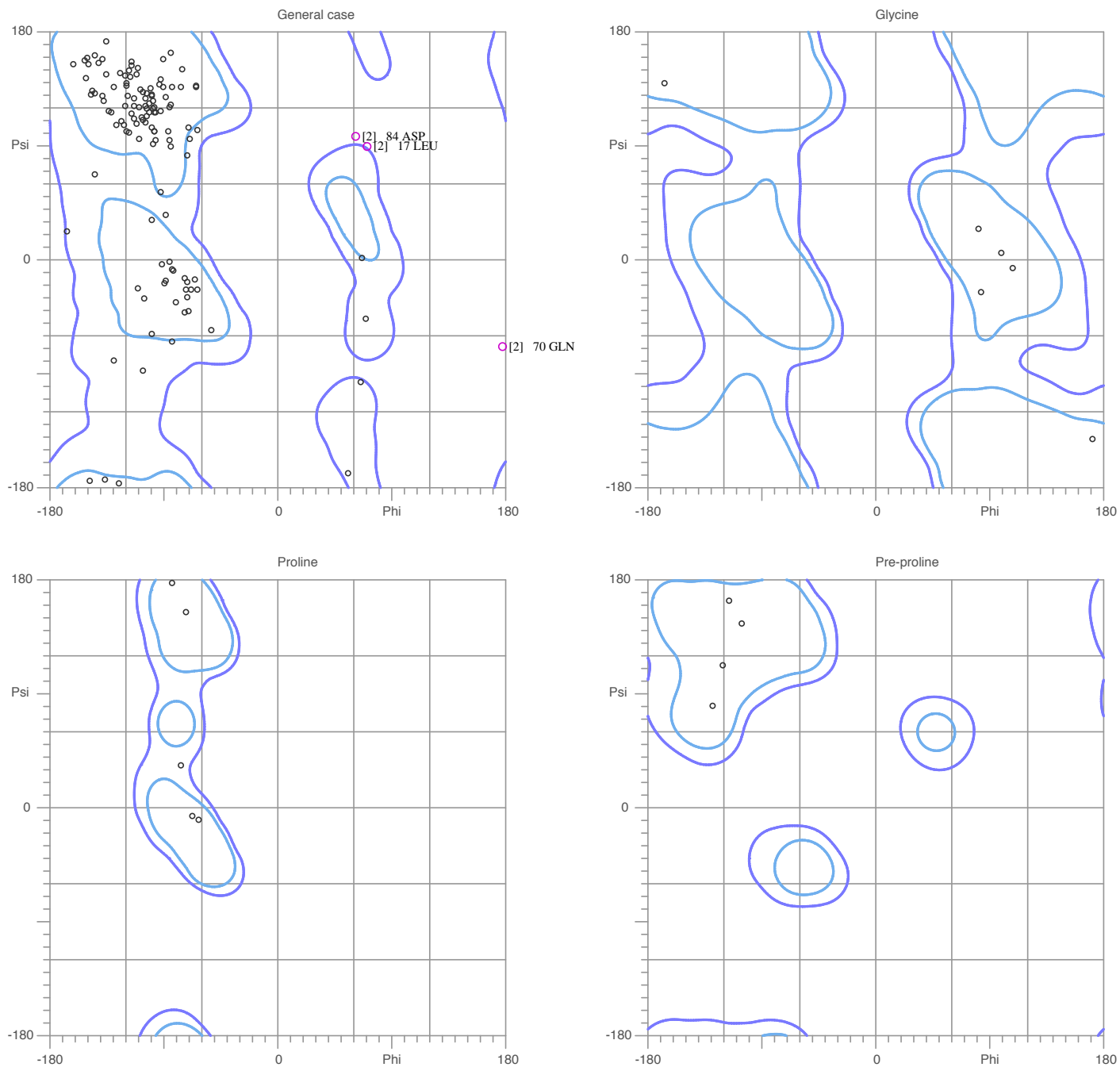
There were no outliers.

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

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

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 2



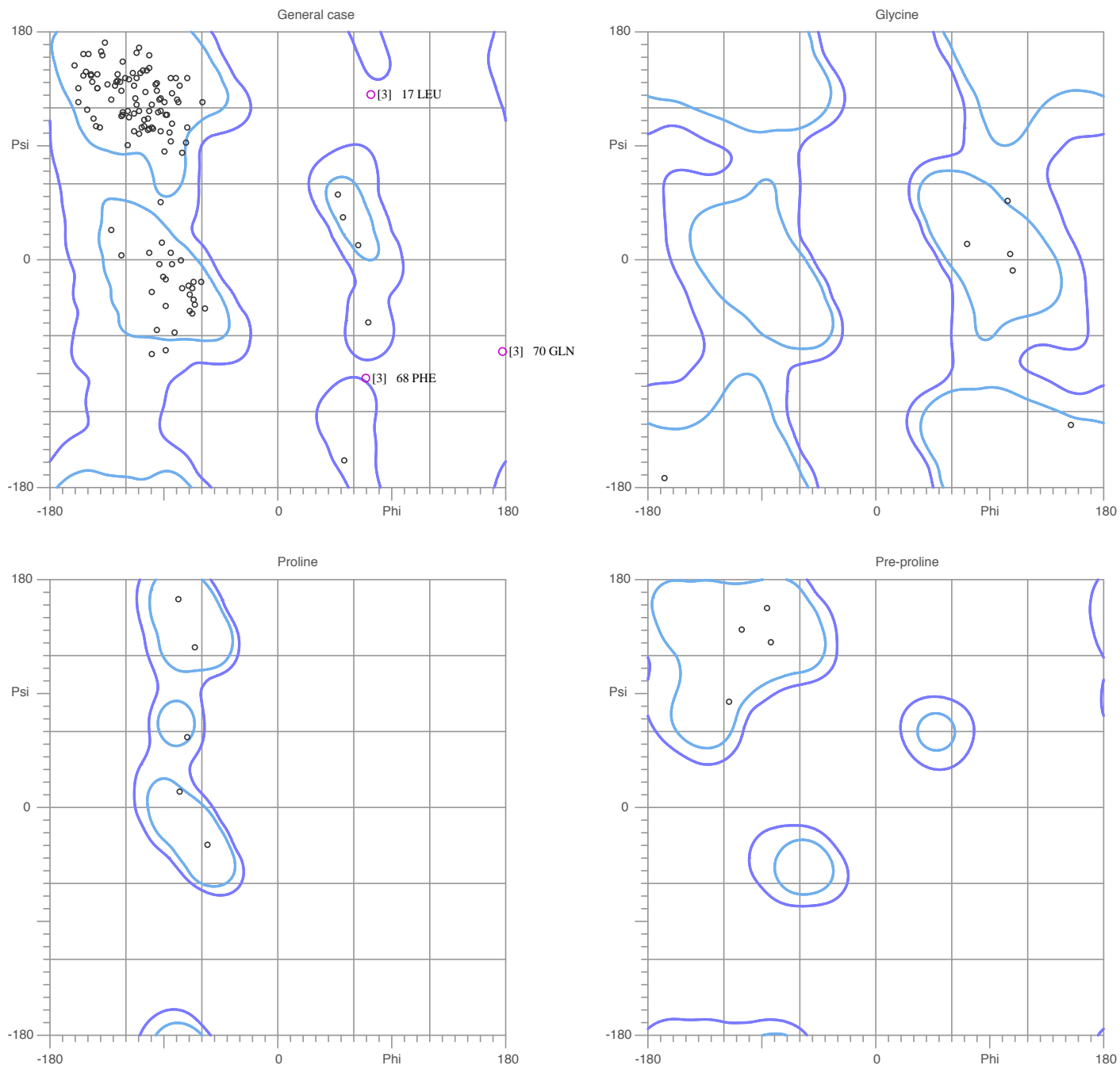
88.7% (125/141) of all residues were in favored (98%) regions.  
97.9% (138/141) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 17 LEU (70.3, 90.3)
- [2] 70 GLN (177.4, -68.3)
- [2] 84 ASP (61.6, 98.1)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 3



93.6% (132/141) of all residues were in favored (98%) regions.  
97.9% (138/141) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

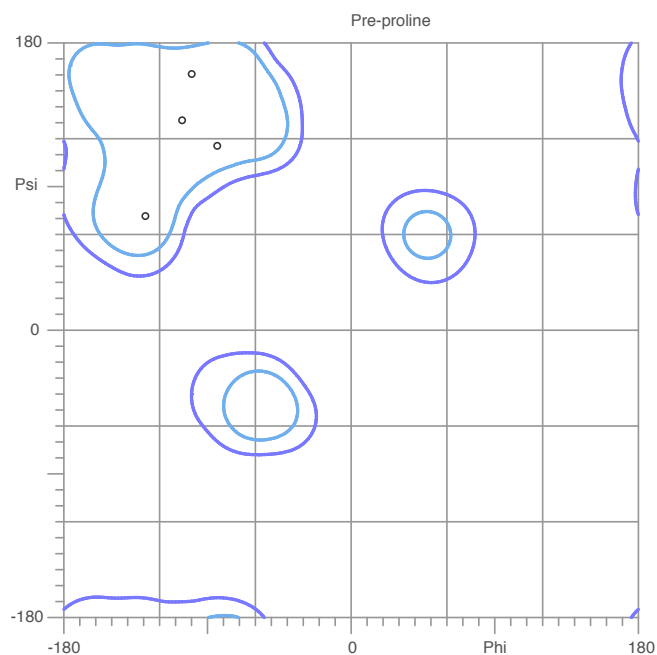
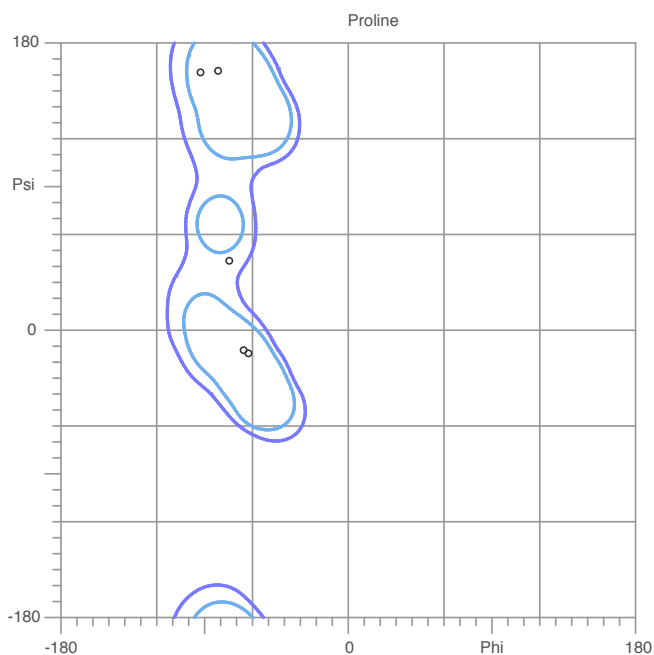
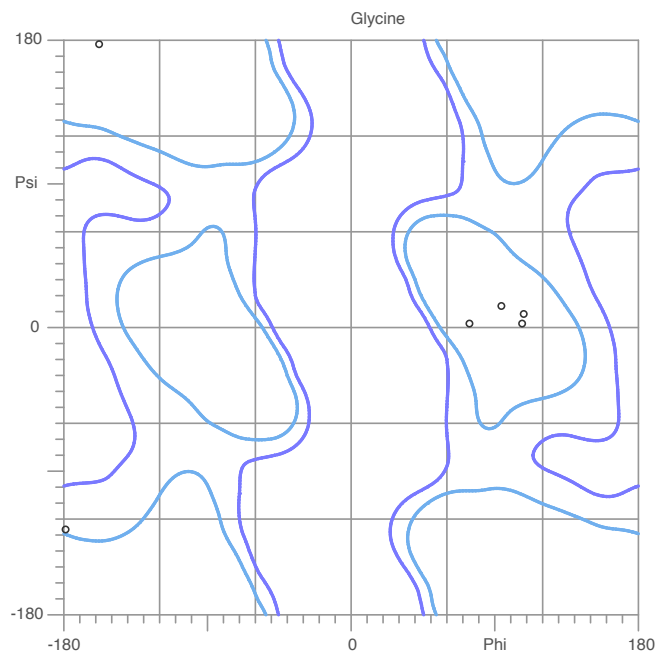
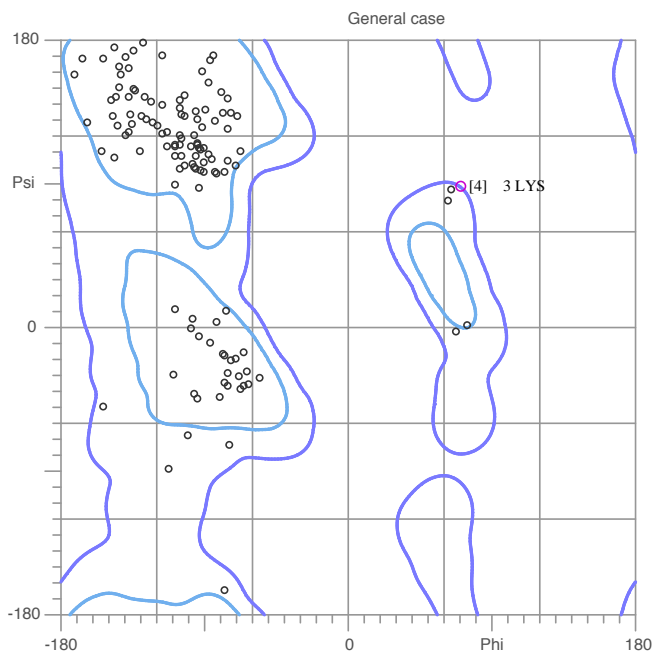
[3] 17 LEU (74.0, 131.8)

[3] 68 PHE (69.3, -93.2)

[3] 70 GLN (177.5, -72.8)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 4

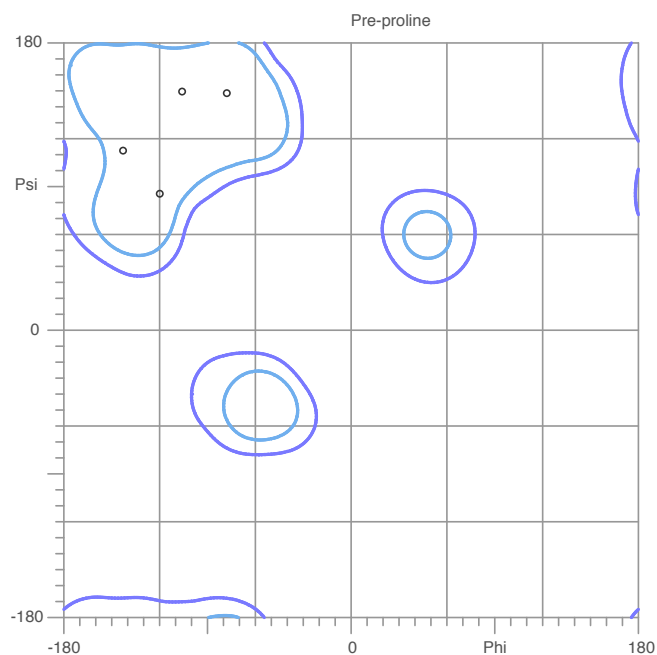
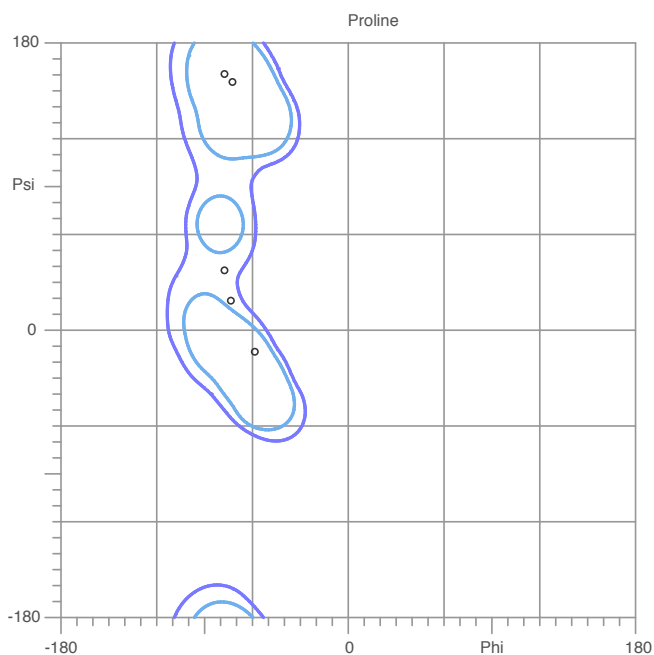
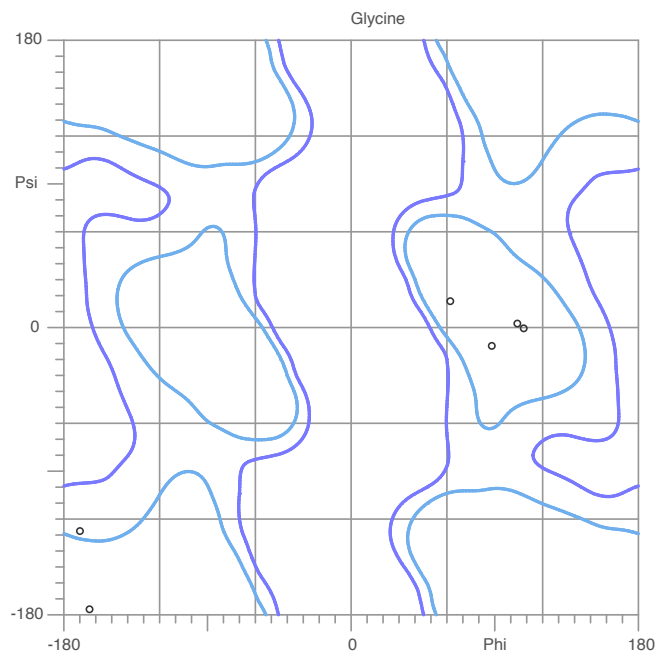
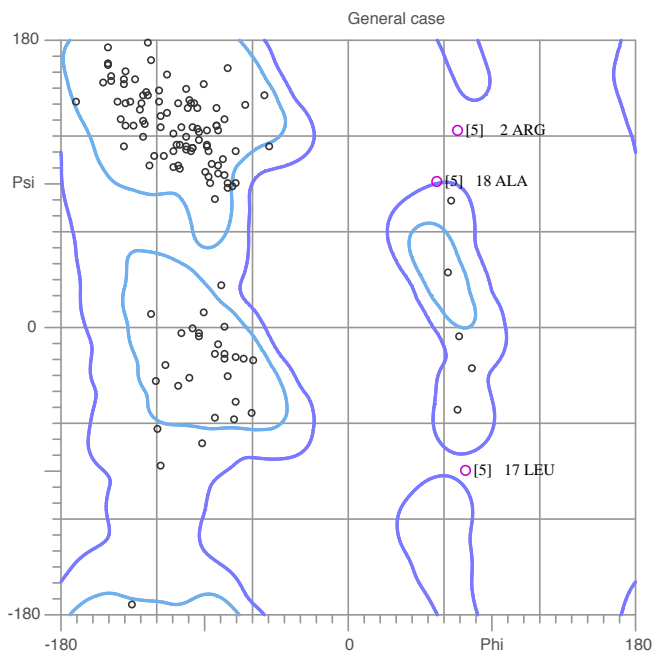


92.2% (130/141) of all residues were in favored (98%) regions.  
99.3% (140/141) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[4] 3 LYS (70.5, 89.4)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 5



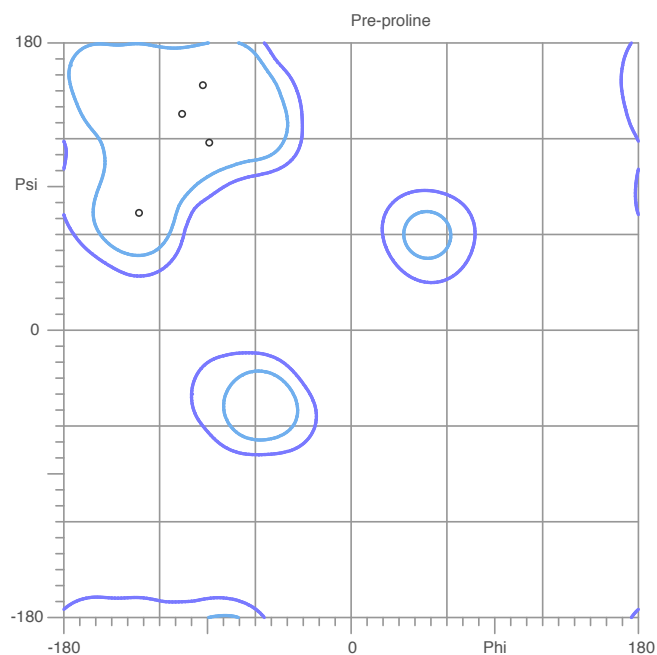
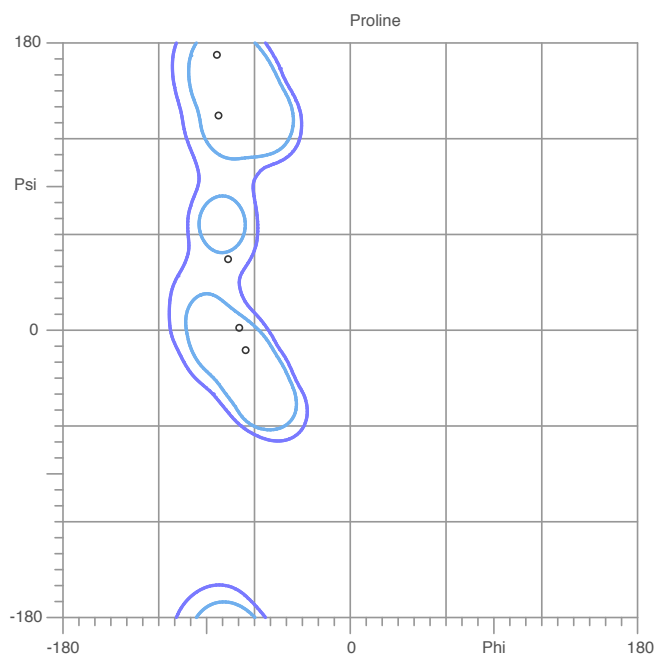
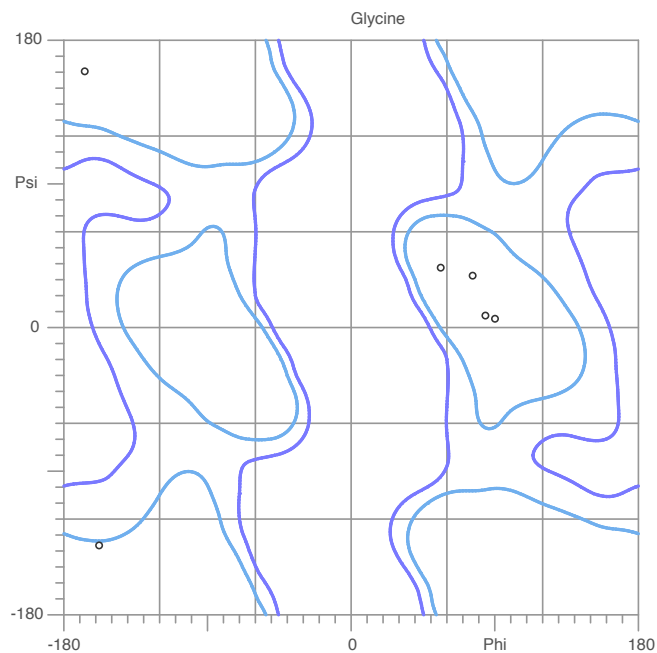
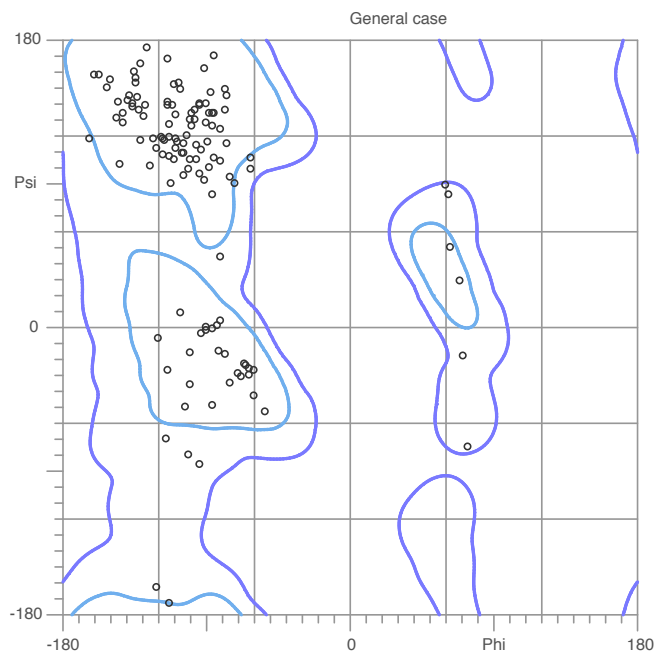
88.7% (125/141) of all residues were in favored (98%) regions.  
97.9% (138/141) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [5] 2 ARG (68.8, 124.6)
- [5] 17 LEU (73.2, -90.0)
- [5] 18 ALA (55.5, 93.0)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 6



90.8% (128/141) of all residues were in favored (98%) regions.  
100.0% (141/141) of all residues were in allowed (>99.8%) regions.

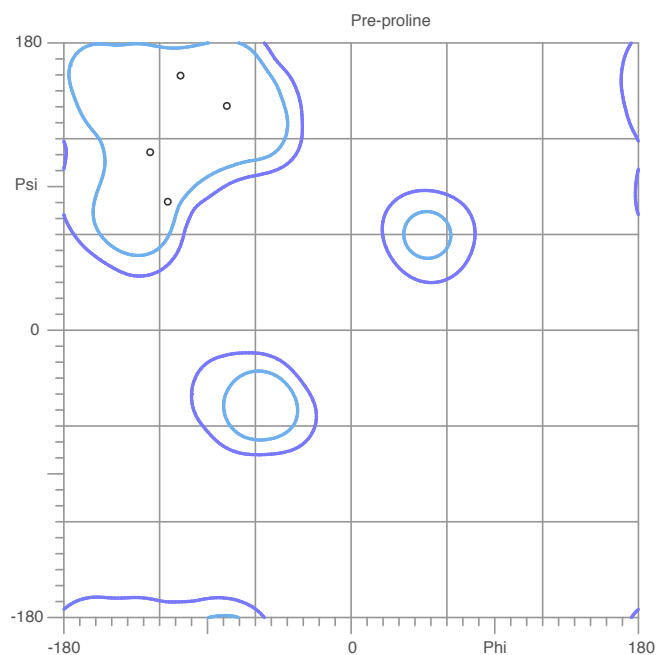
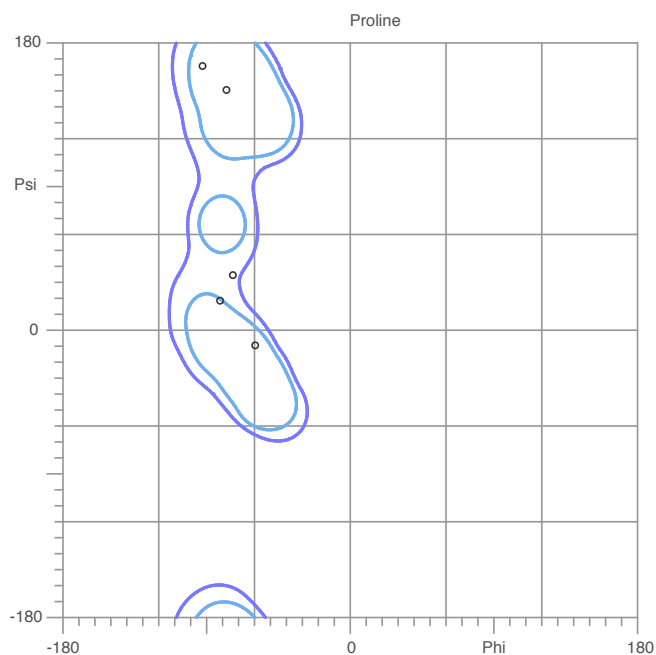
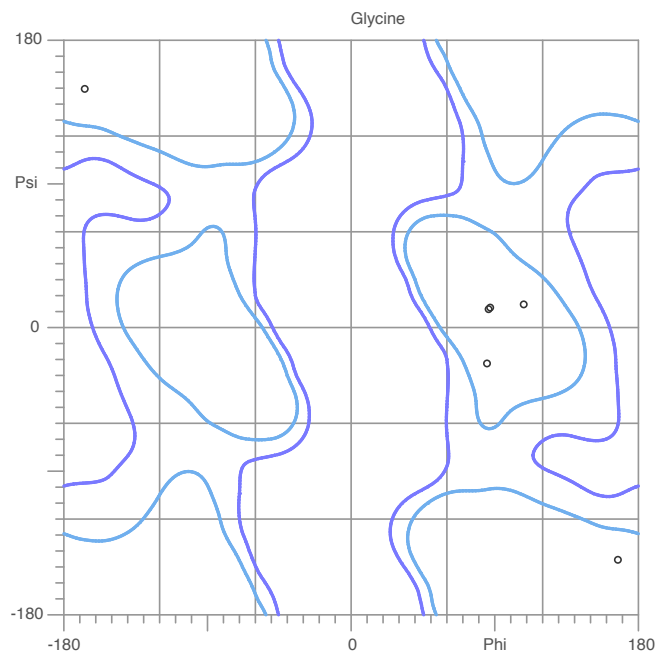
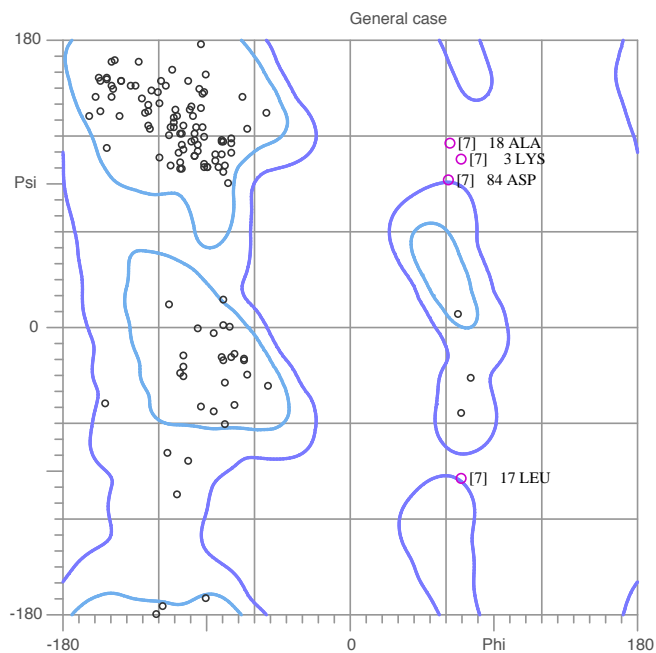
There were no outliers.

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

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

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 7



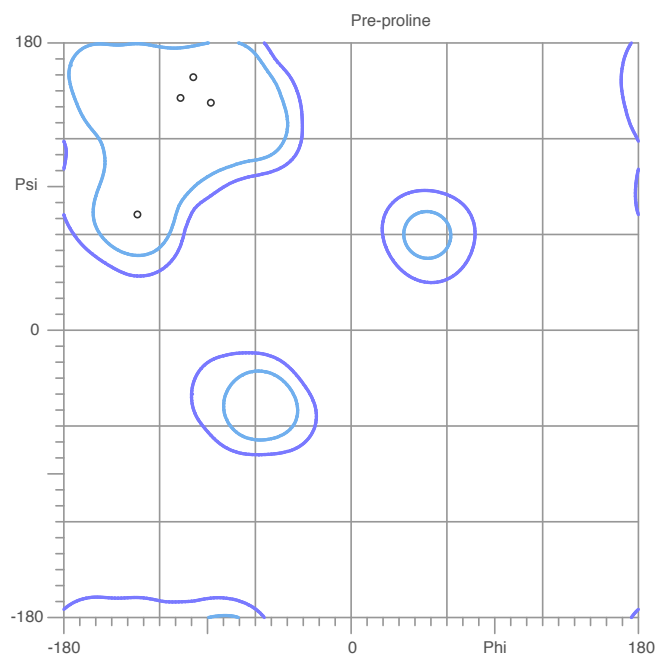
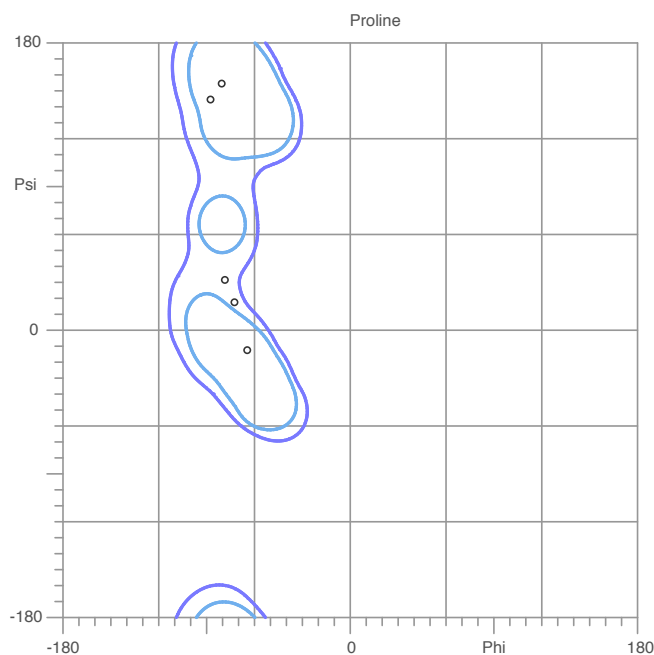
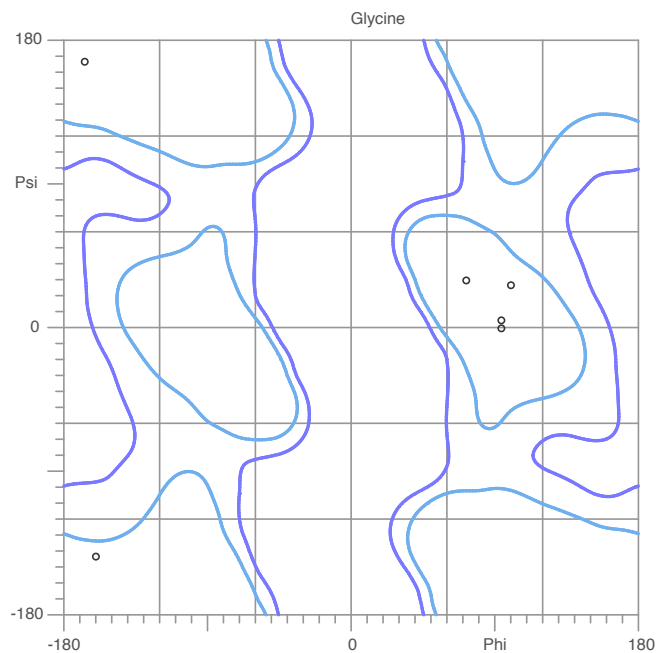
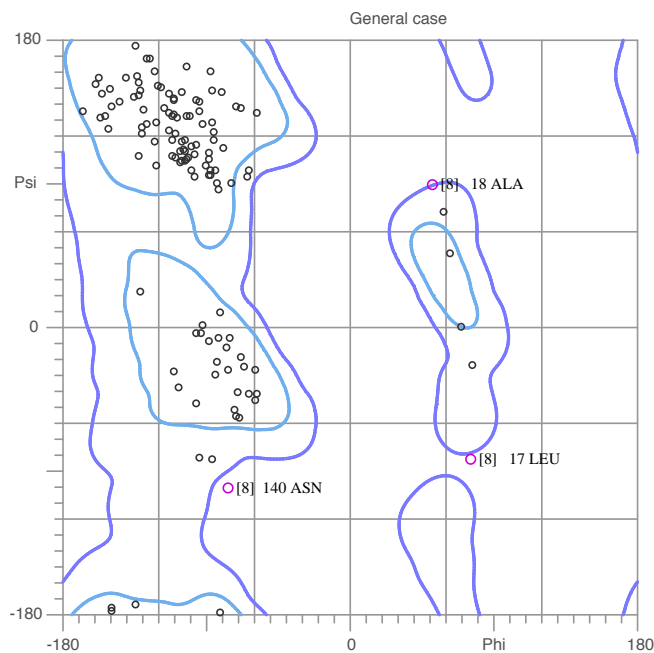
91.5% (129/141) of all residues were in favored (98%) regions.  
97.2% (137/141) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [7] 3 LYS (69.6, 106.8)
- [7] 17 LEU (69.3, -94.7)
- [7] 18 ALA (63.0, 116.7)
- [7] 84 ASP (61.1, 93.8)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 8



92.2% (130/141) of all residues were in favored (98%) regions.  
97.9% (138/141) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

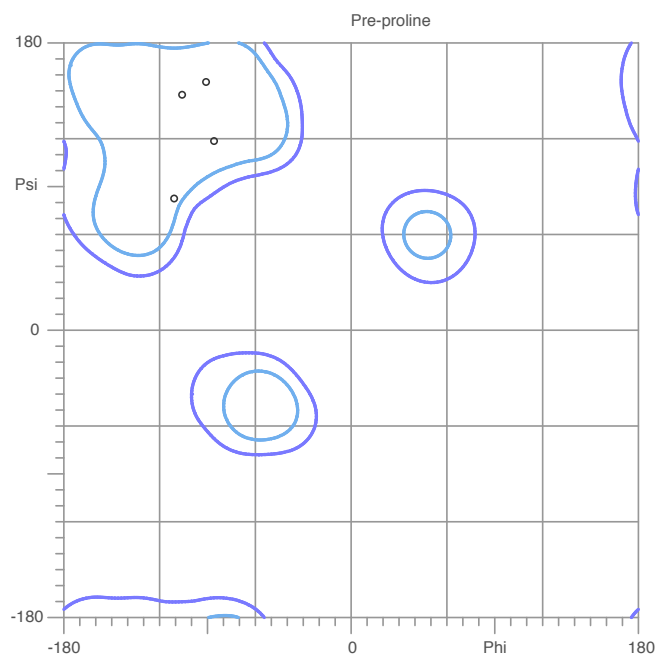
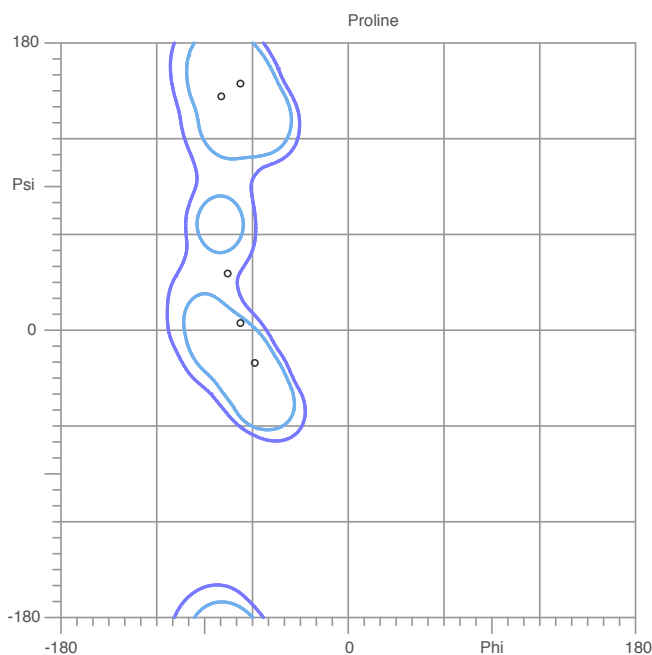
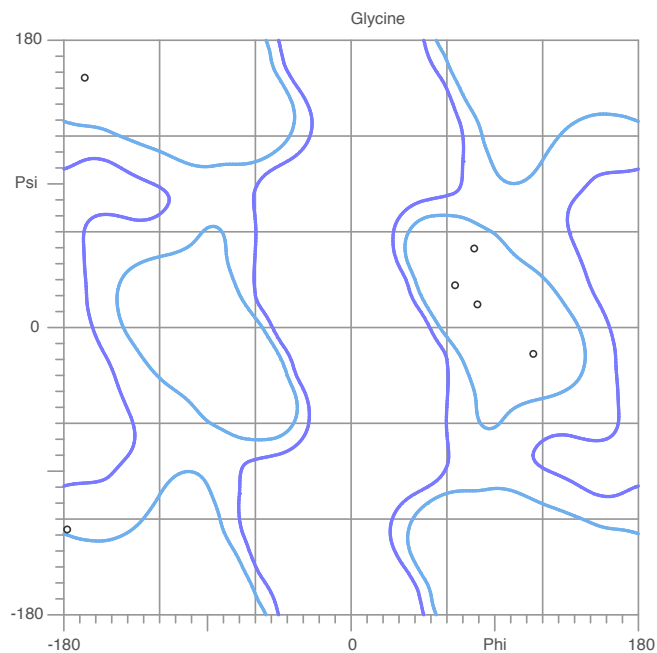
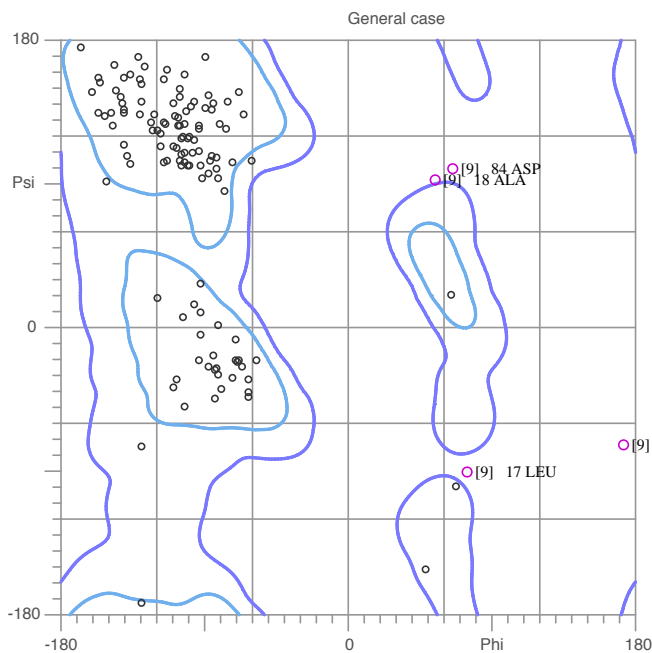
[8] 17 LEU (75.8, -82.1)

[8] 18 ALA (51.5, 90.7)

[8] 140 ASN (-77.5, -100.1)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 9



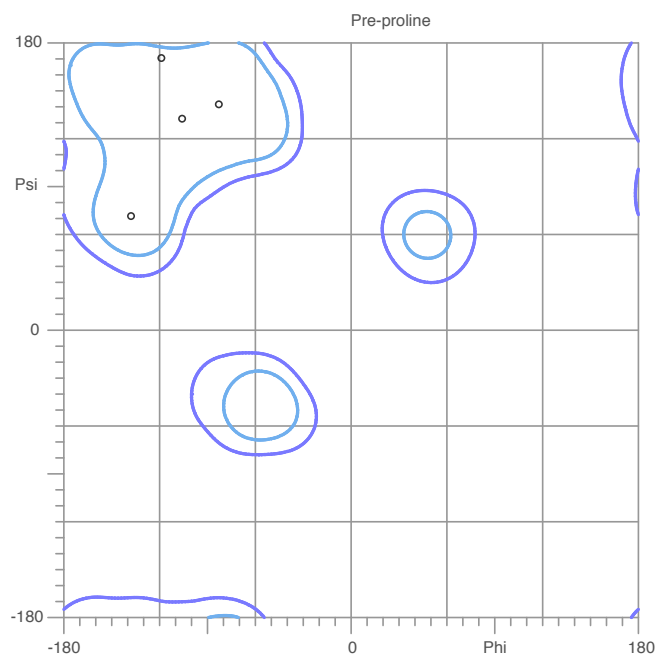
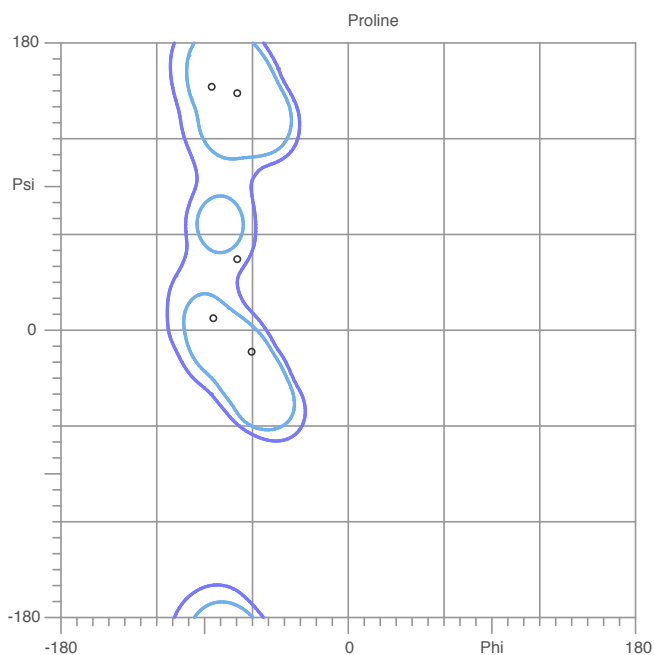
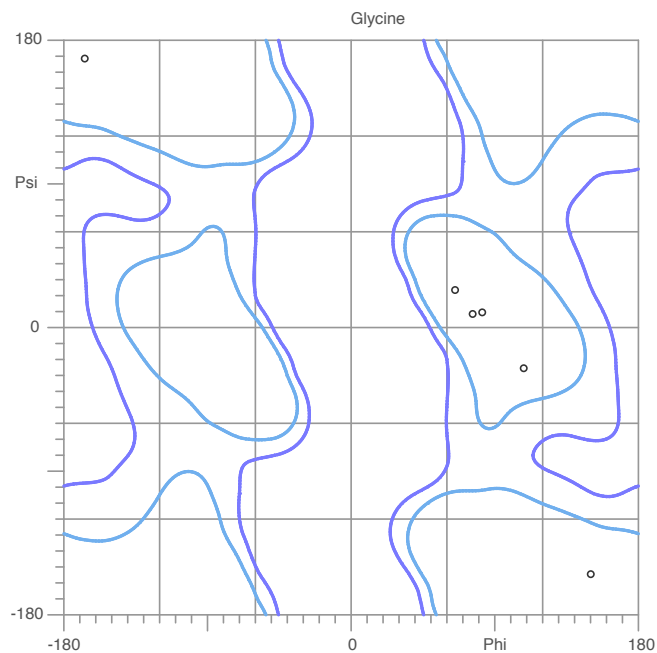
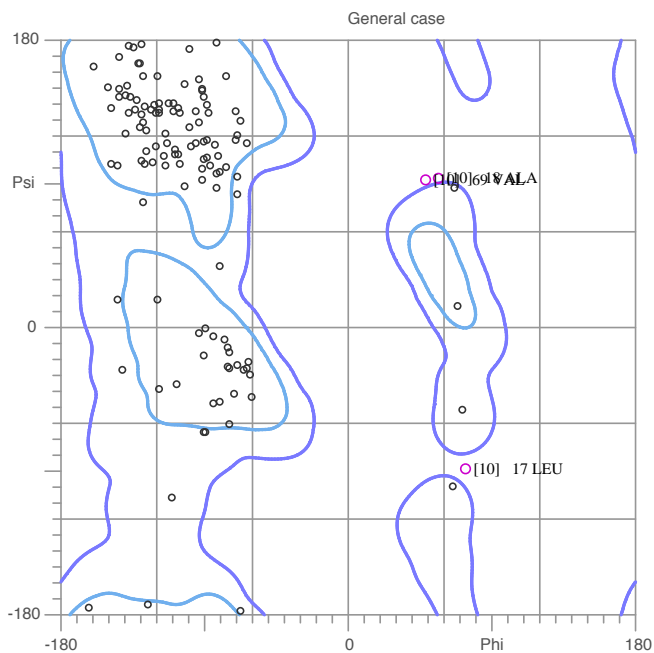
92.2% (130/141) of all residues were in favored (98%) regions.  
97.2% (137/141) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [9] 17 LEU (74.0, -90.6)
- [9] 18 ALA (54.1, 93.1)
- [9] 70 GLN (172.7, -73.4)
- [9] 84 ASP (65.3, 100.0)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 10



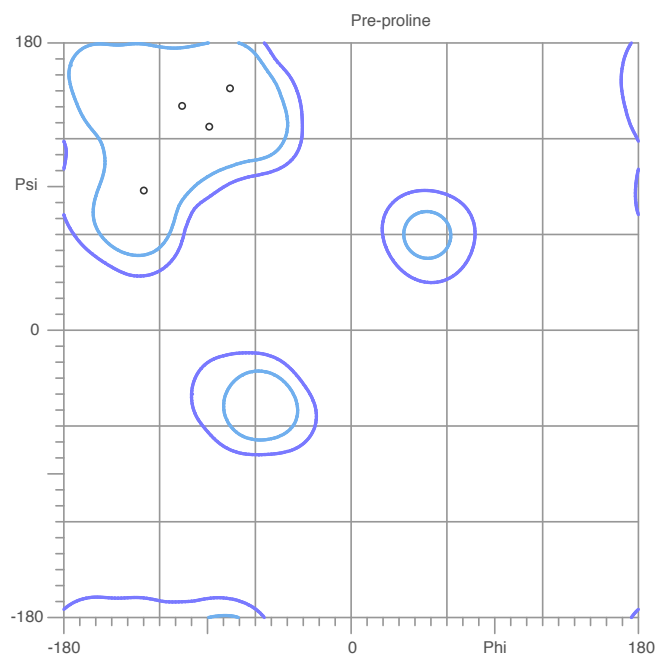
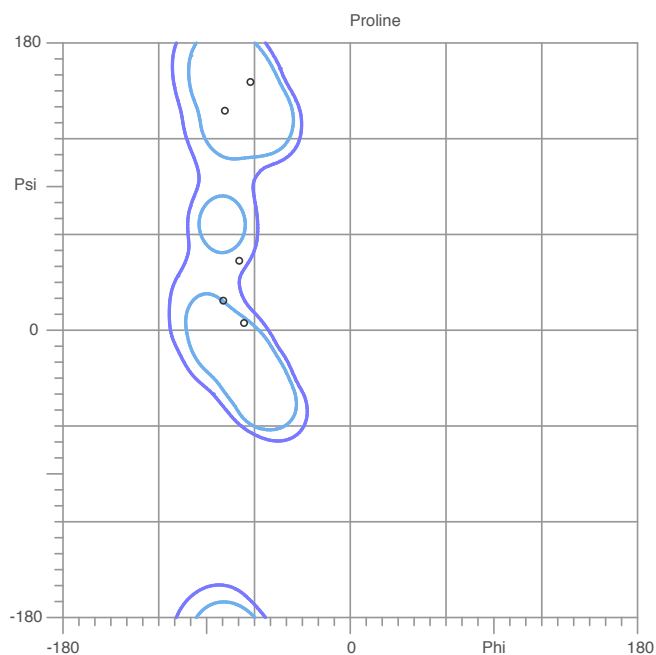
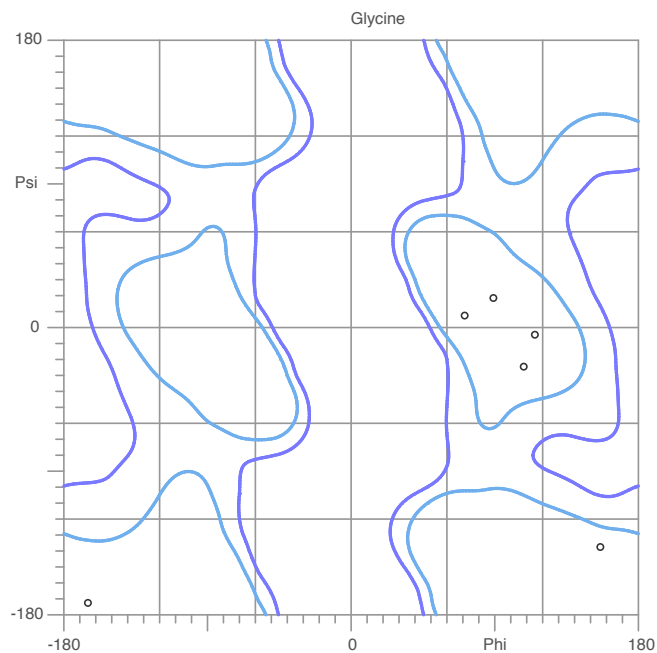
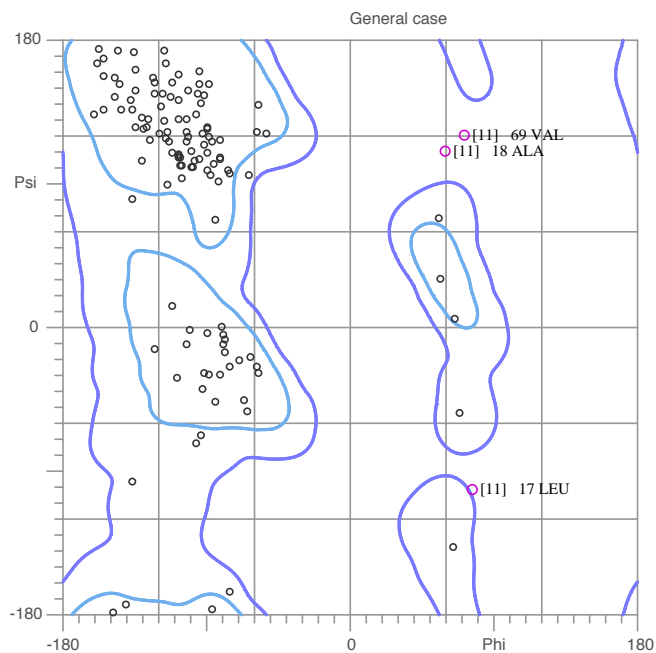
87.9% (124/141) of all residues were in favored (98%) regions.  
97.9% (138/141) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [10] 17 LEU (73.7, -88.6)
- [10] 18 ALA (56.2, 94.0)
- [10] 69 VAL (48.3, 93.5)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 11



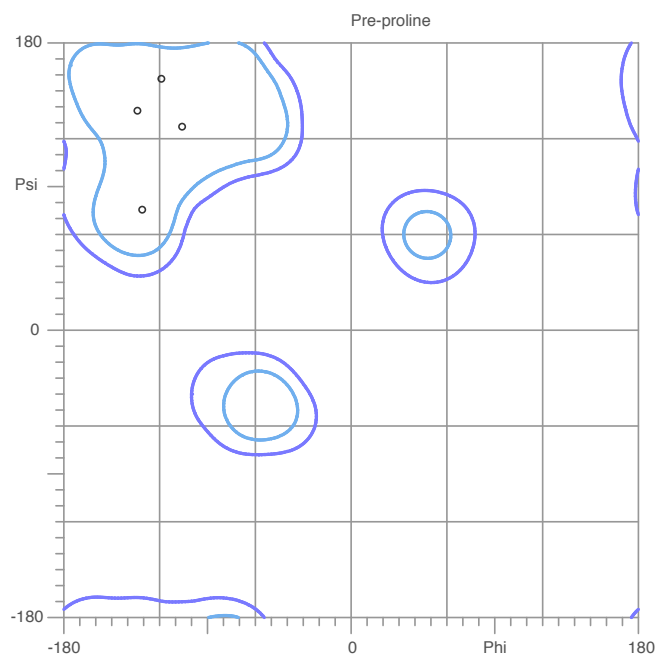
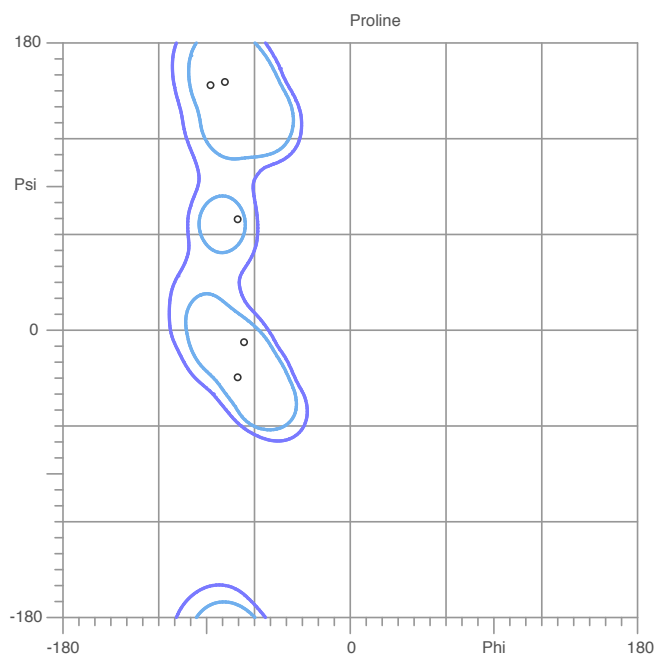
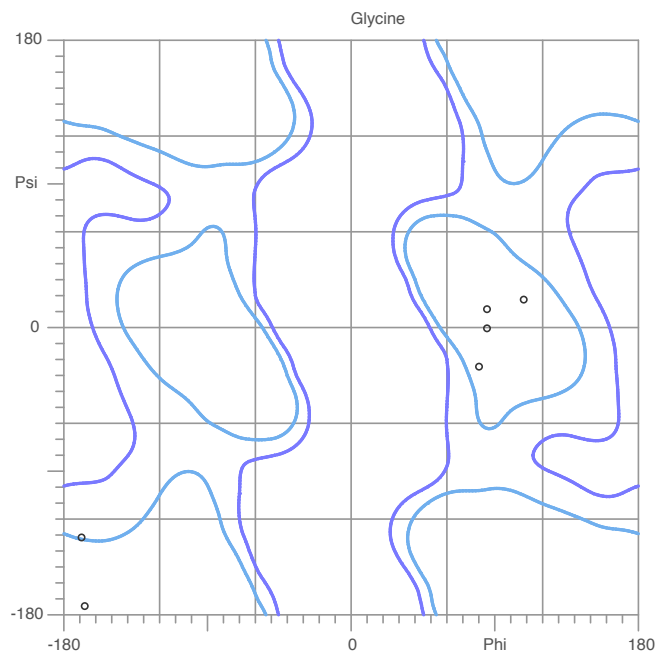
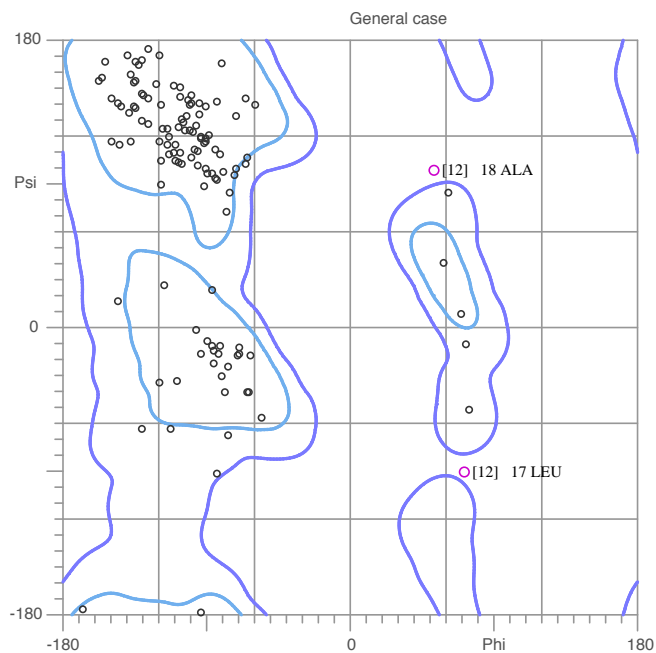
90.1% (127/141) of all residues were in favored (98%) regions.  
97.9% (138/141) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [11] 17 LEU (76.2, -101.3)
- [11] 18 ALA (59.5, 111.3)
- [11] 69 VAL (71.6, 121.8)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 12



91.5% (129/141) of all residues were in favored (98%) regions.  
98.6% (139/141) of all residues were in allowed (>99.8%) regions.

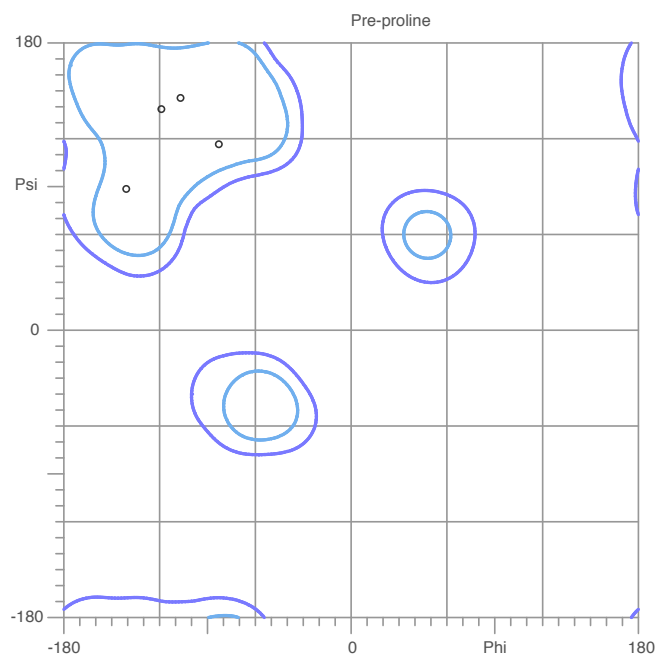
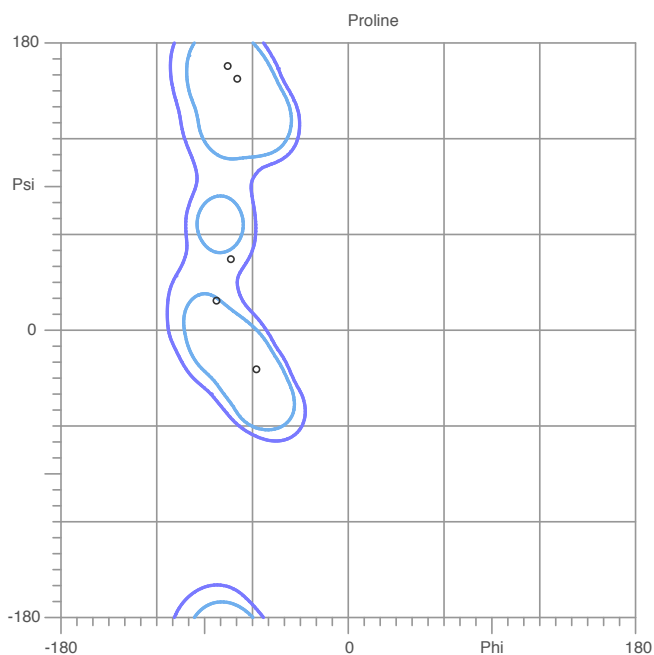
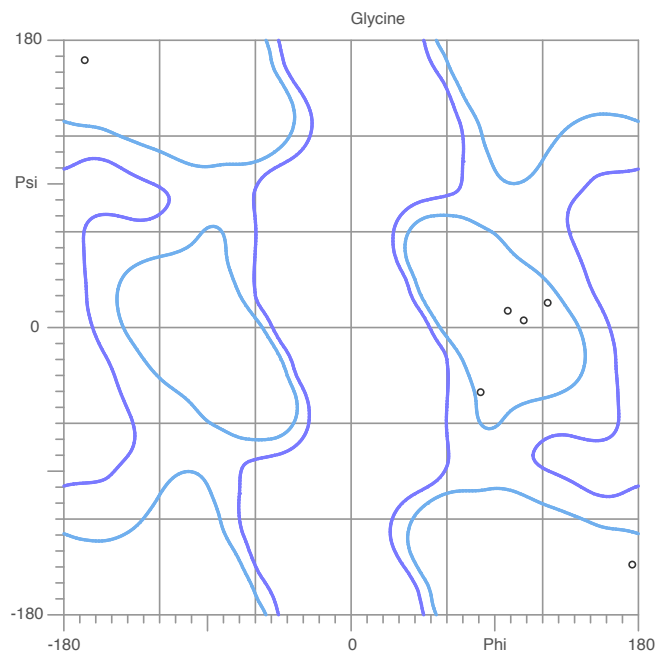
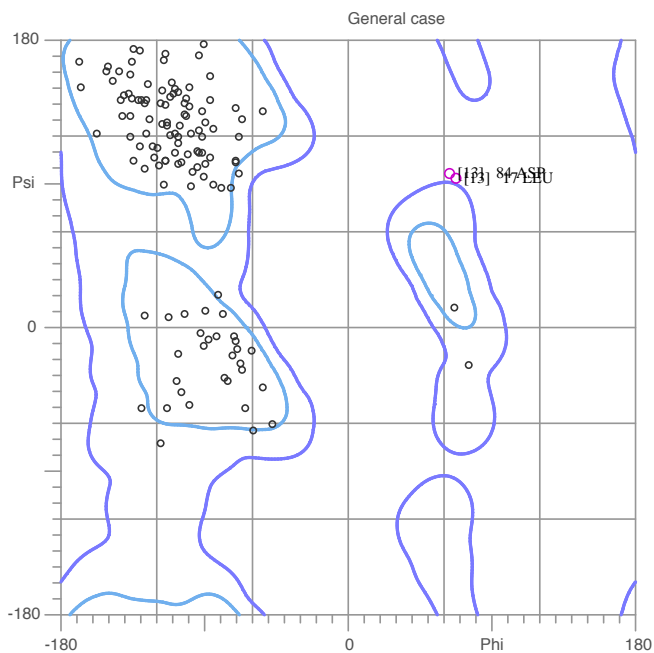
There were 2 outliers (phi, psi):

[12] 17 LEU (71.8, -90.7)

[12] 18 ALA (52.4, 99.6)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 13



93.6% (132/141) of all residues were in favored (98%) regions.  
98.6% (139/141) of all residues were in allowed (>99.8%) regions.

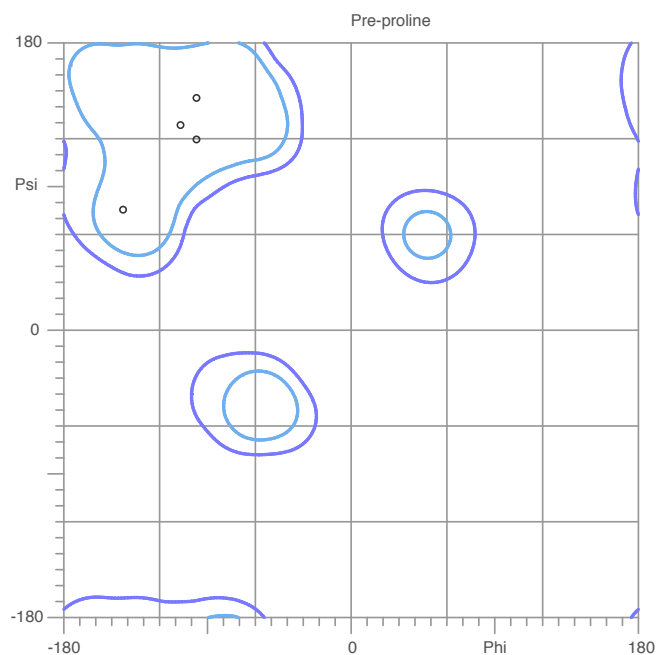
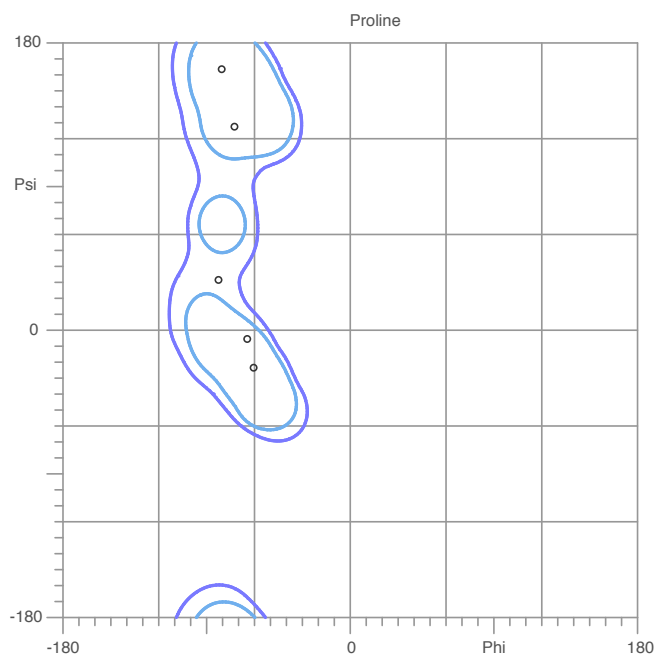
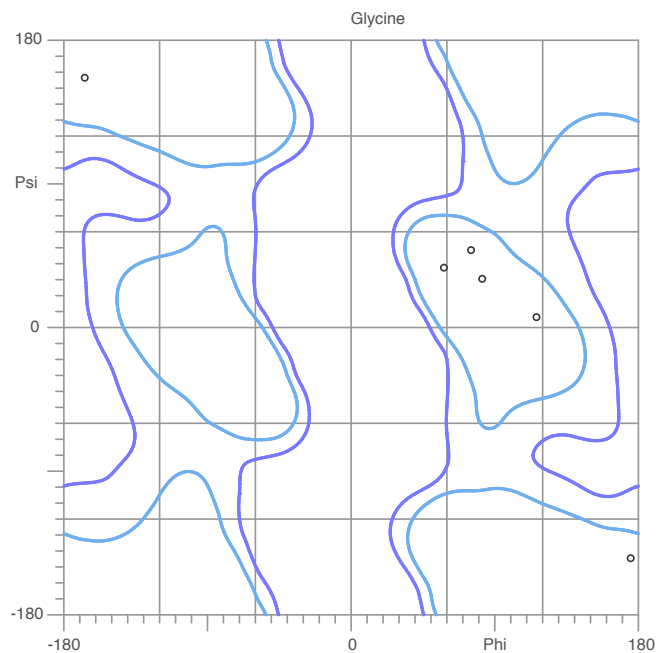
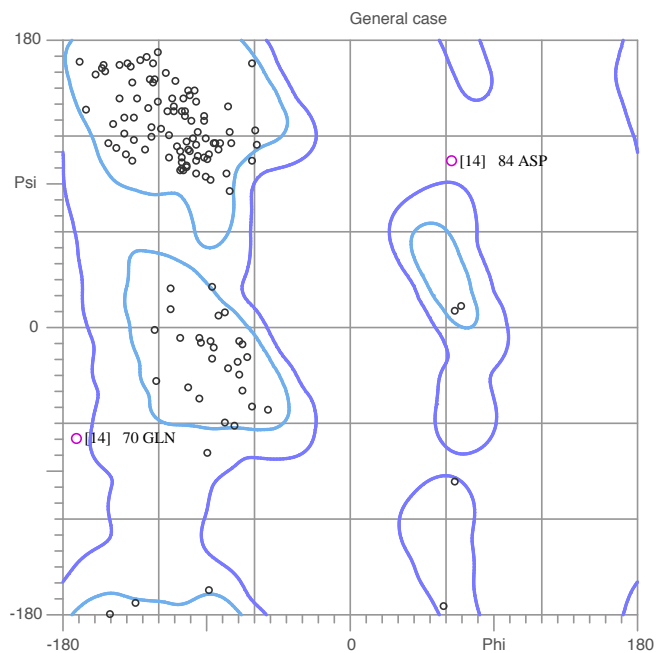
There were 2 outliers (phi, psi):

[13] 17 LEU (67.4, 94.2)

[13] 84 ASP (63.8, 97.6)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 14

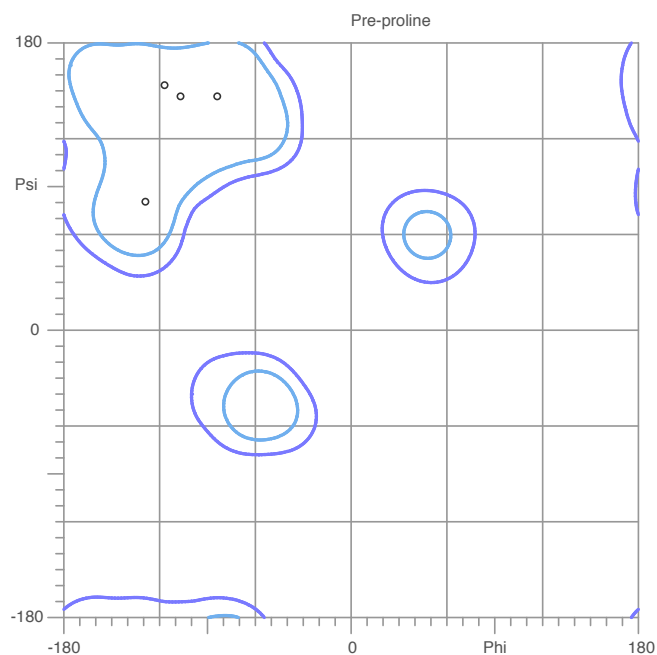
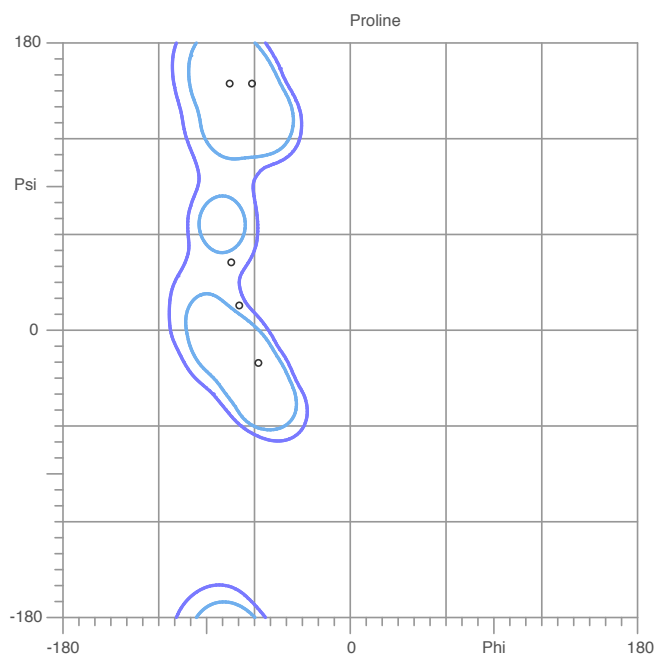
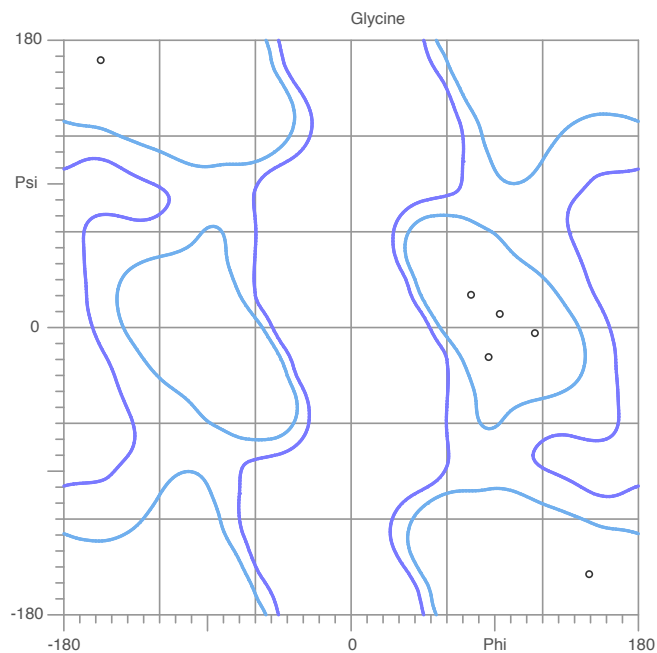
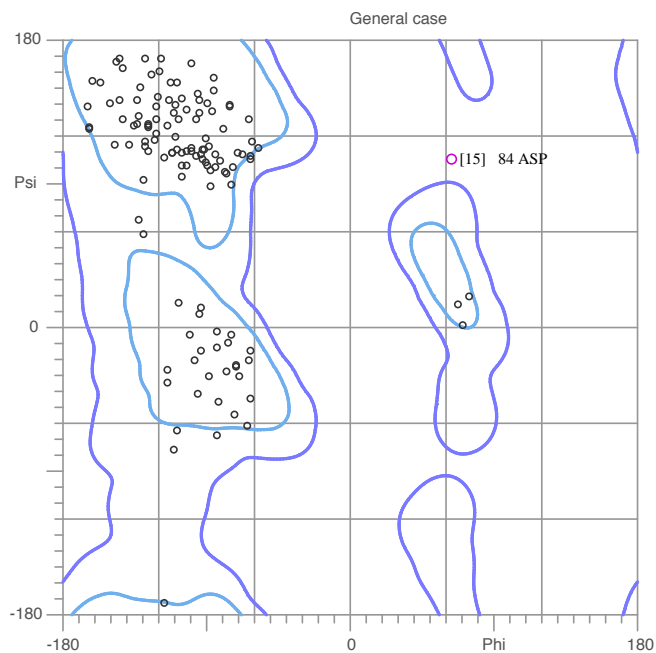


93.6% (132/141) of all residues were in favored (98%) regions.  
98.6% (139/141) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[14] 70 GLN (-172.7, -69.8)  
[14] 84 ASP (63.2, 105.9)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 15

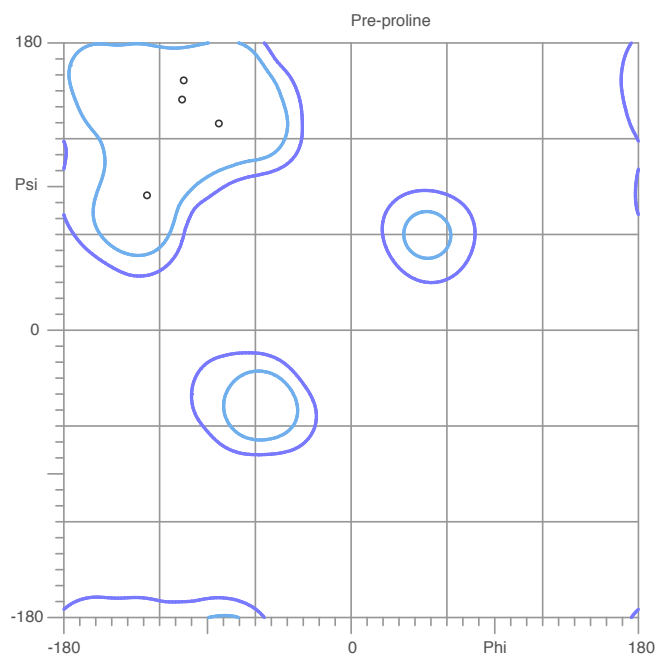
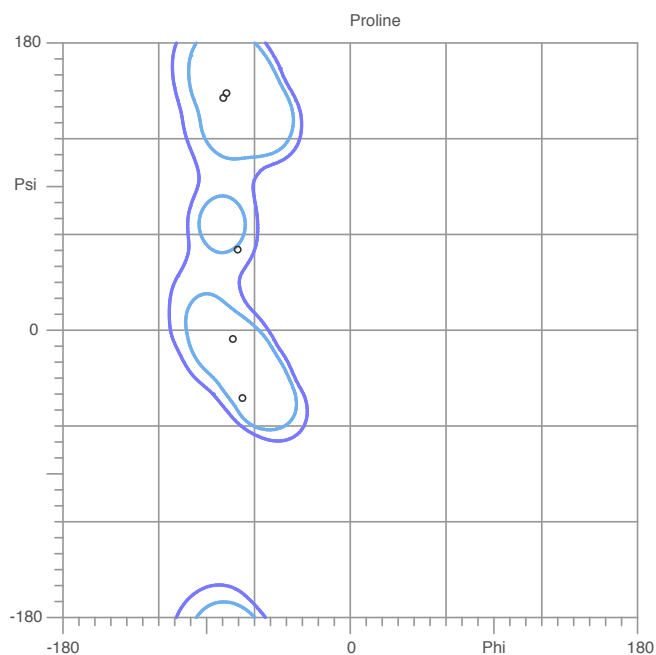
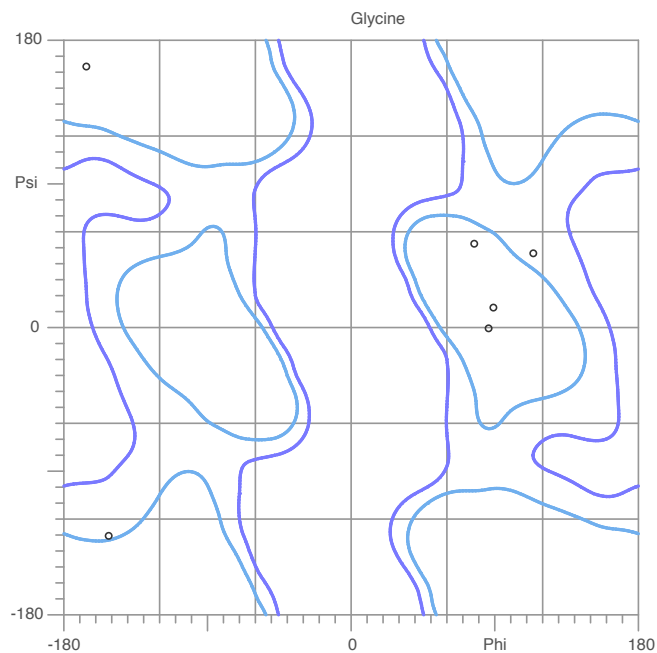
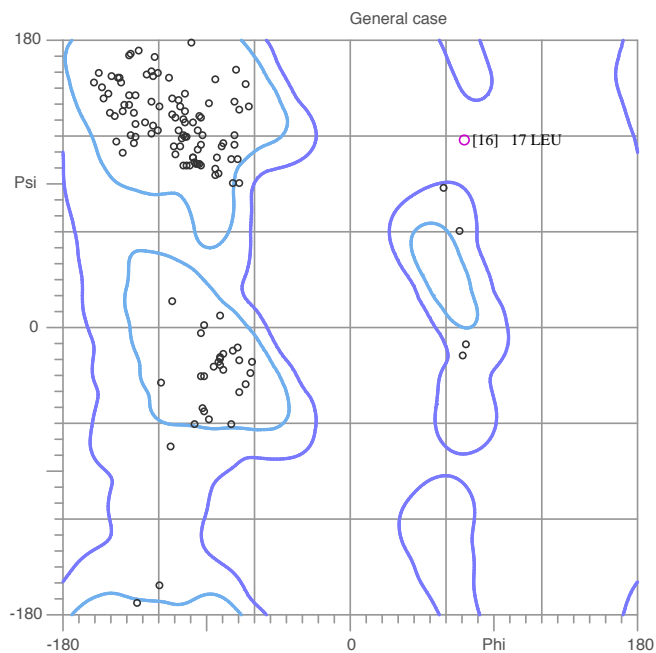


93.6% (132/141) of all residues were in favored (98%) regions.  
99.3% (140/141) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[15] 84 ASP (63.5, 106.8)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 16



92.2% (130/141) of all residues were in favored (98%) regions.  
99.3% (140/141) of all residues were in allowed (>99.8%) regions.

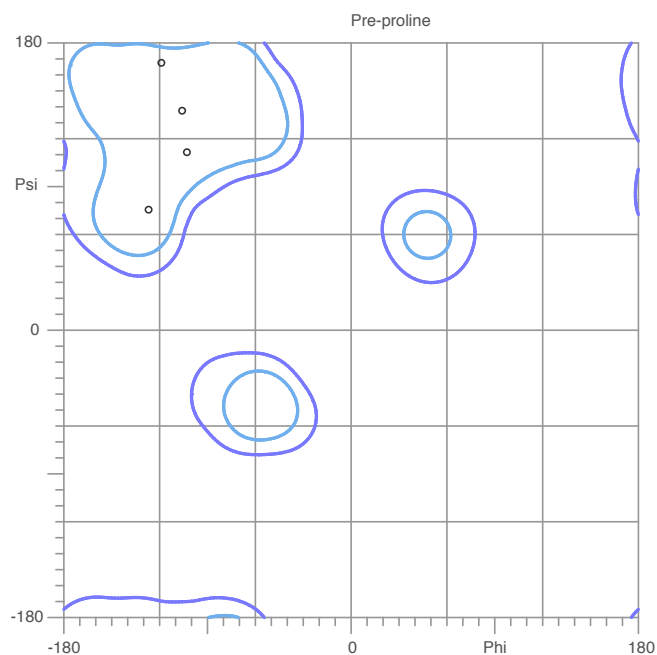
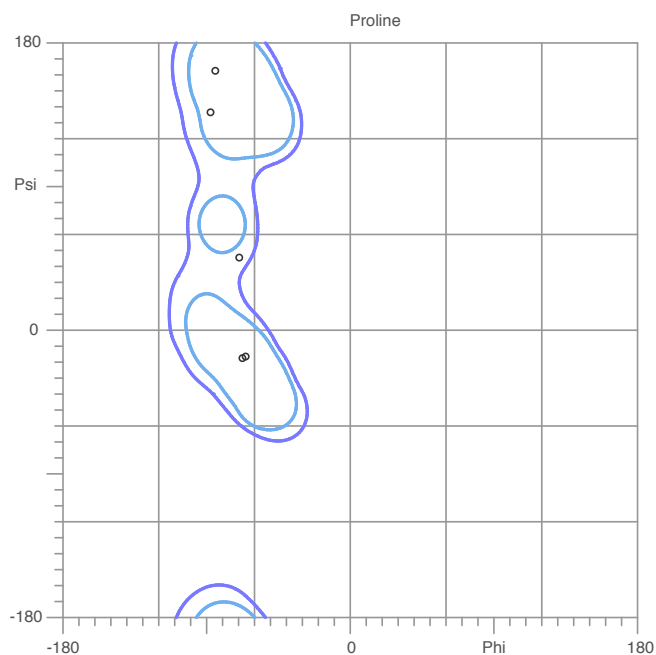
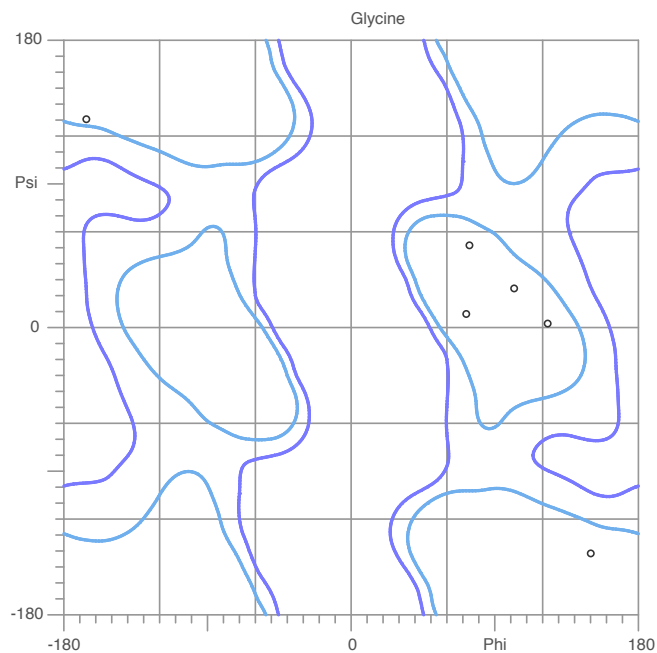
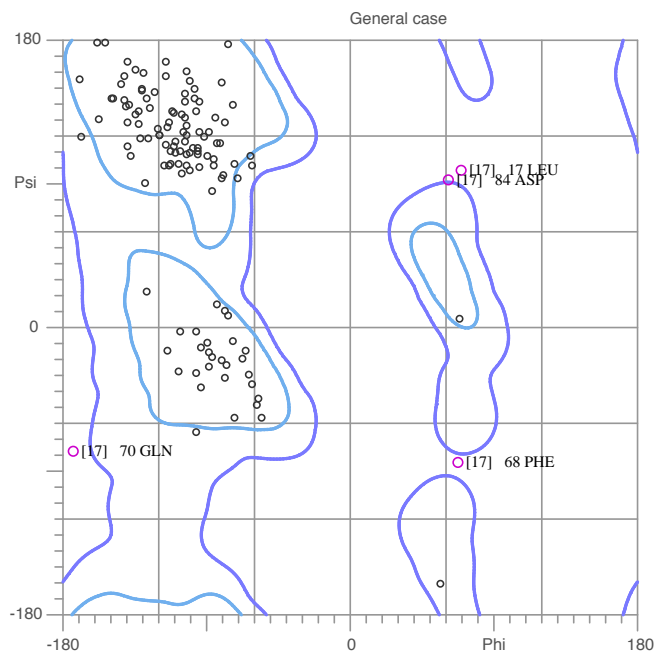
There were 1 outliers (phi, psi):  
[16] 17 LEU (71.0, 118.8)

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# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 17



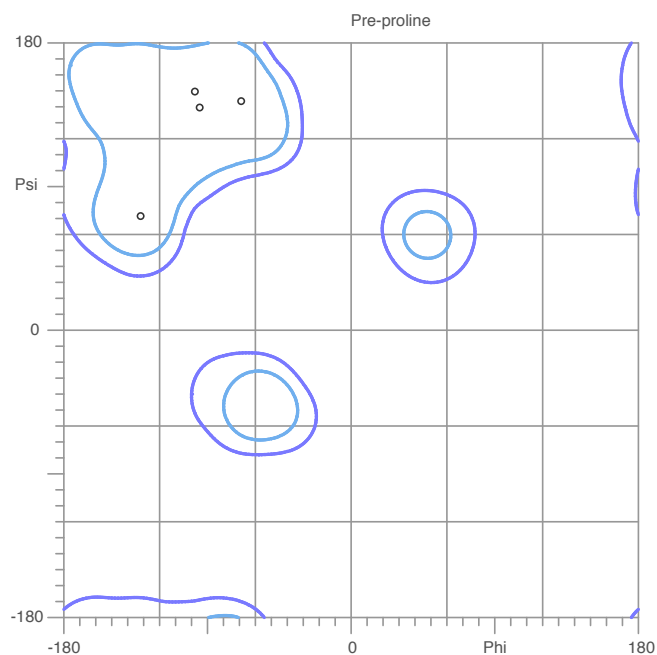
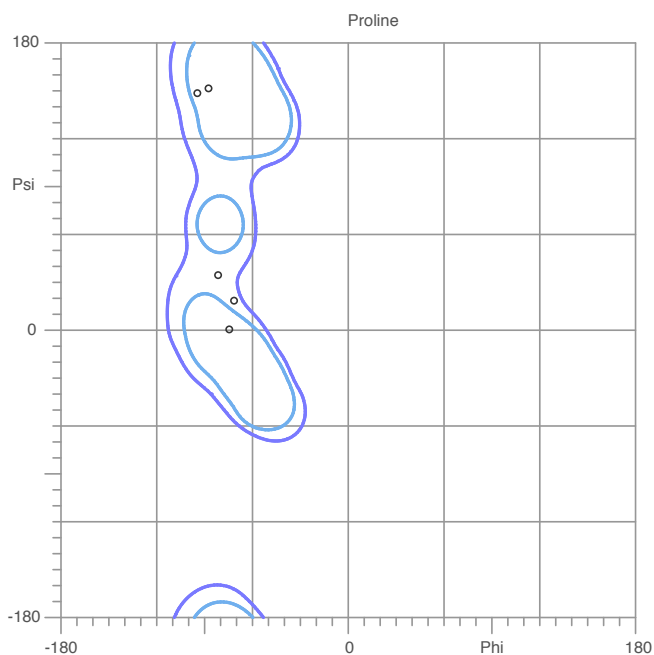
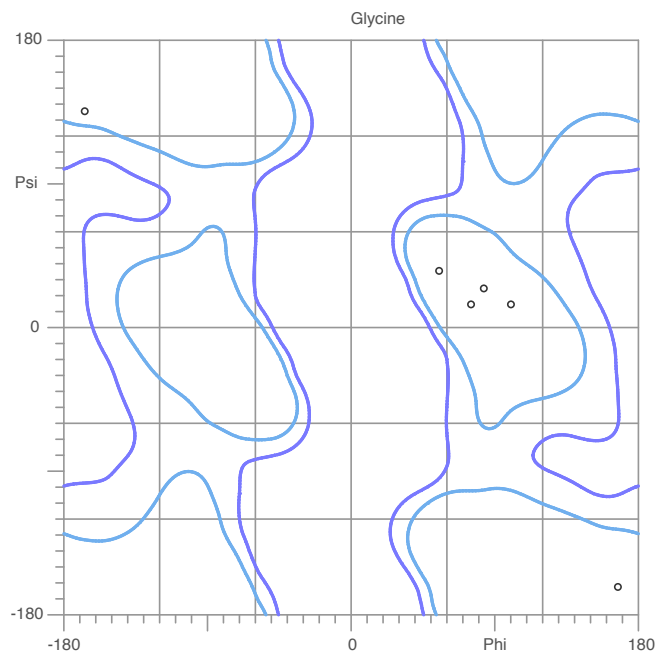
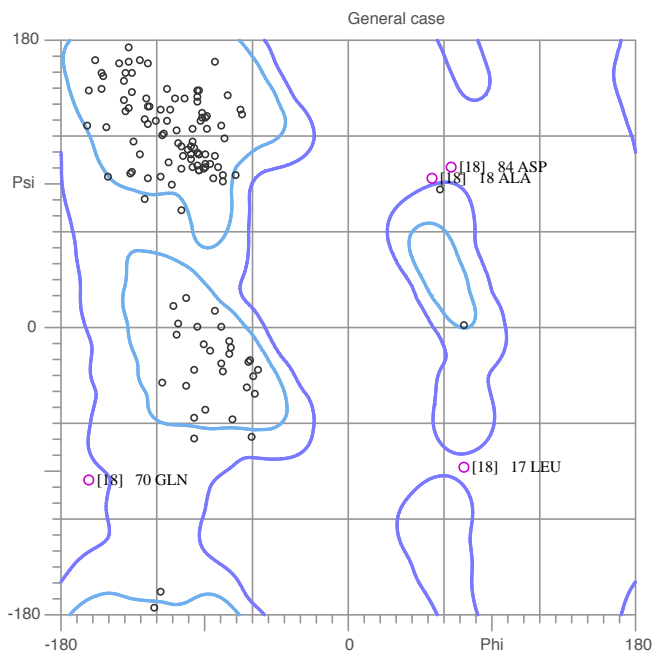
92.9% (131/141) of all residues were in favored (98%) regions.  
97.2% (137/141) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [17] 17 LEU (69.4, 99.7)
- [17] 68 PHE (67.9, -85.0)
- [17] 70 GLN (-174.2, -77.5)
- [17] 84 ASP (61.5, 93.1)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 18



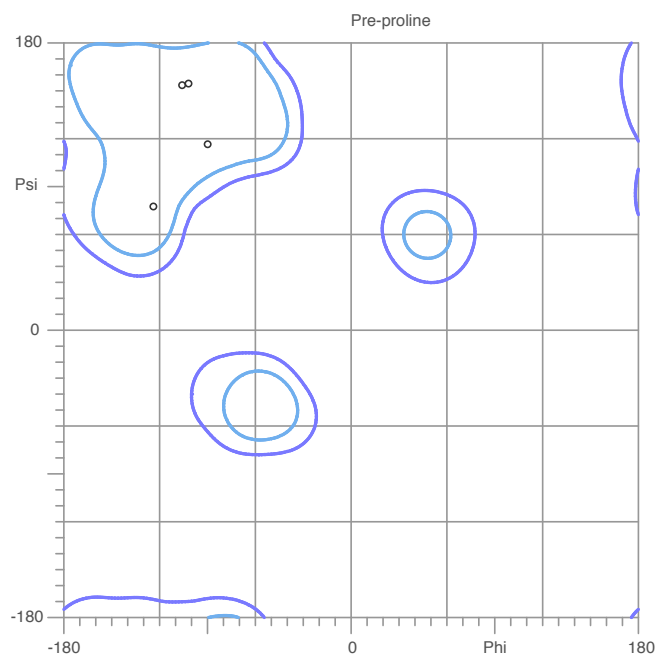
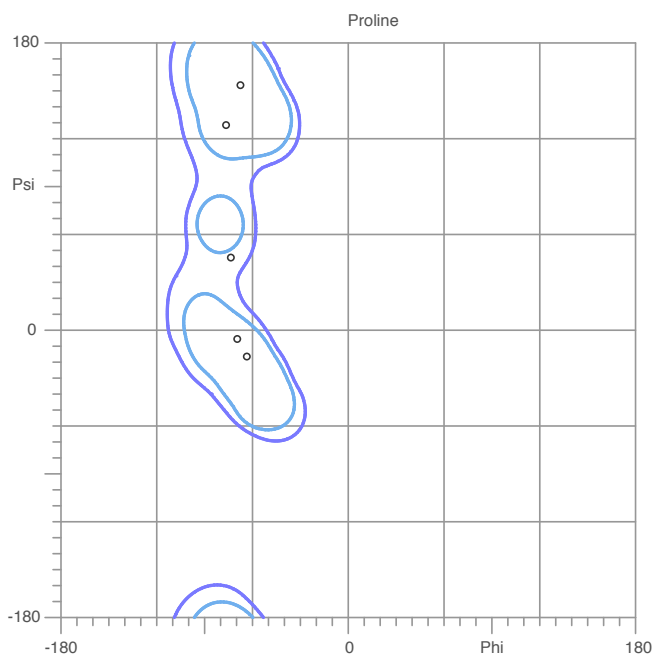
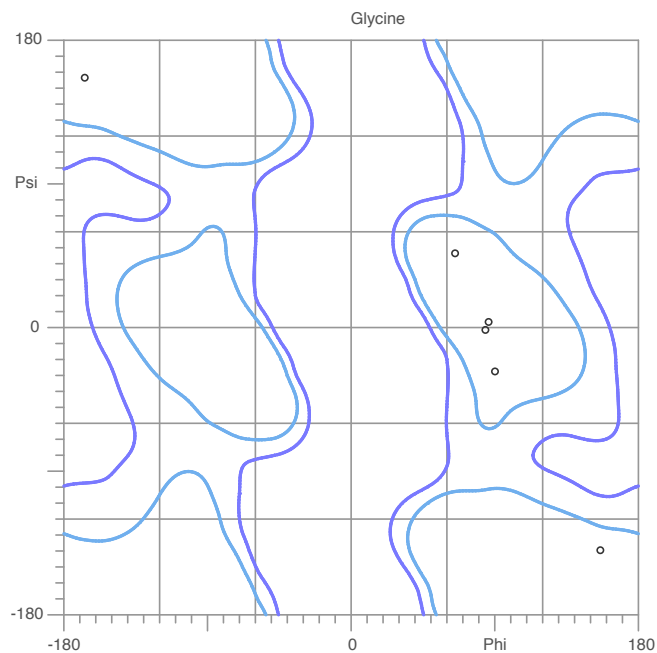
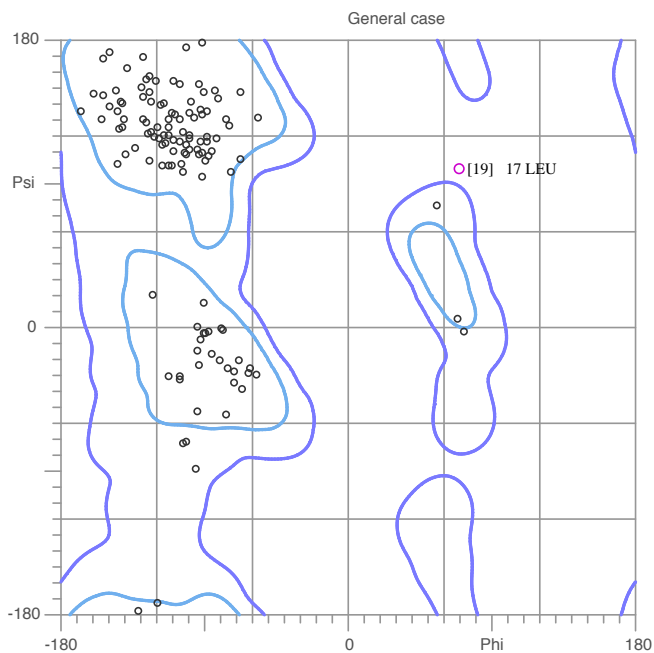
90.1% (127/141) of all residues were in favored (98%) regions.  
97.2% (137/141) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [18] 17 LEU (72.2, -87.7)
- [18] 18 ALA (52.7, 94.9)
- [18] 70 GLN (-163.4, -95.3)
- [18] 84 ASP (64.4, 101.7)

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 19



95.0% (134/141) of all residues were in favored (98%) regions.  
99.3% (140/141) of all residues were in allowed (>99.8%) regions.

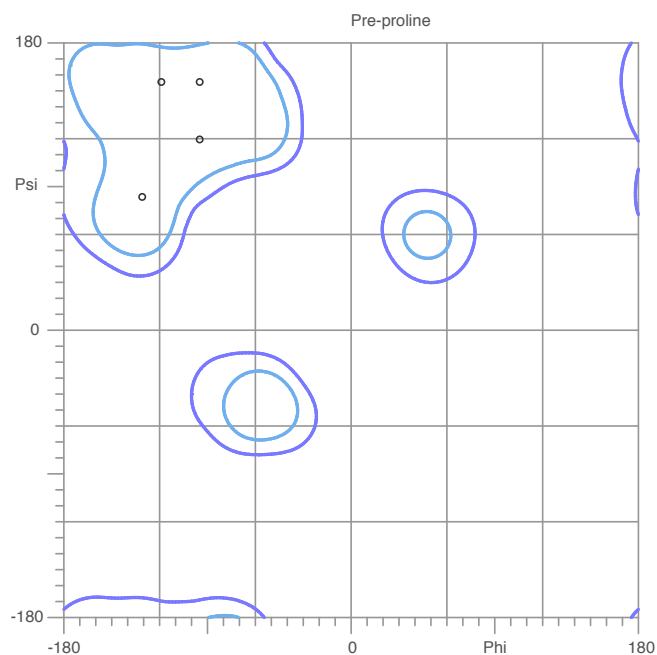
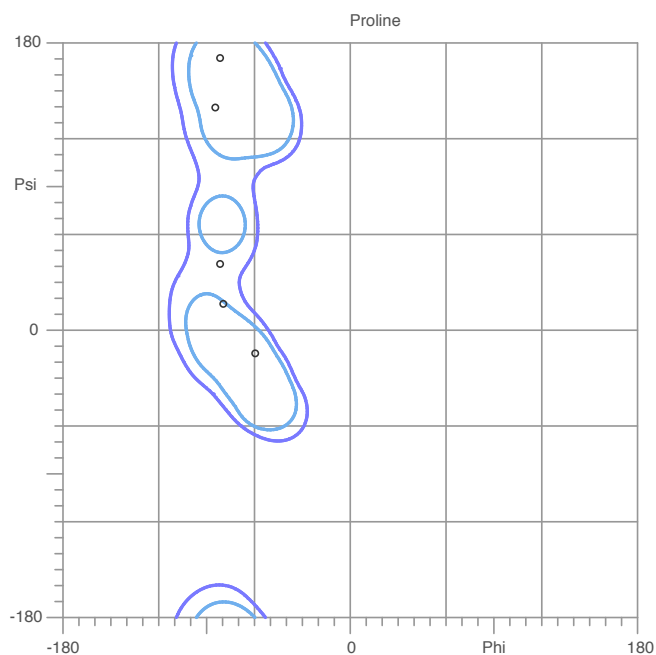
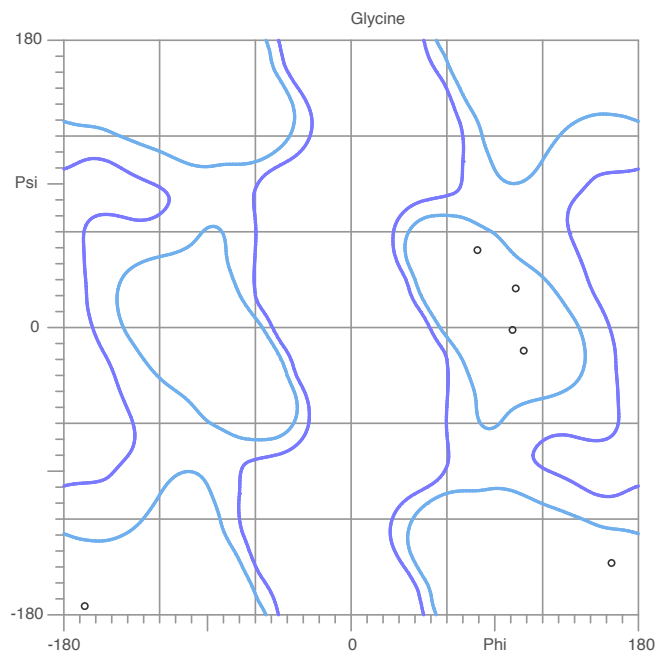
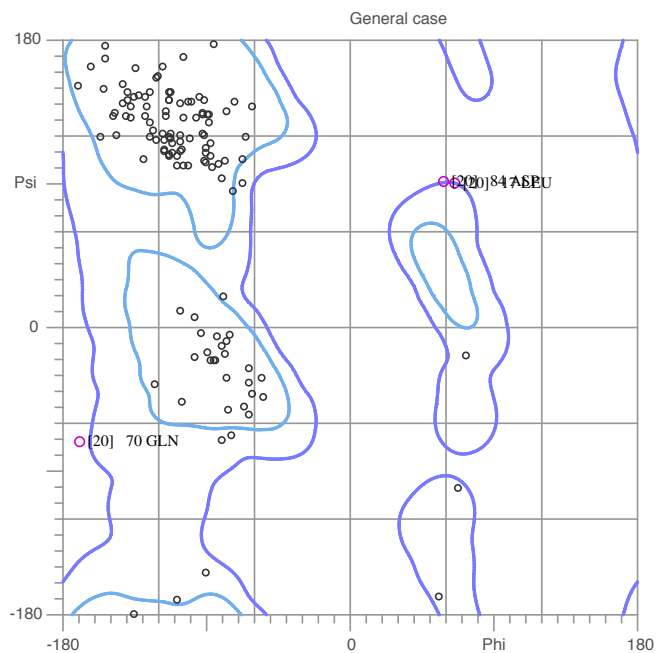
There were 1 outliers (phi, psi):  
[19] 17 LEU (69.8, 100.7)

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

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

# MolProbity Ramachandran analysis

HR1958\_NMR\_em\_bcr3.pdb, model 20



90.8% (128/141) of all residues were in favored (98%) regions.  
97.9% (138/141) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [20] 17 LEU (65.7, 91.8)
- [20] 70 GLN (-170.1, -72.0)
- [20] 84 ASP (58.4, 93.0)