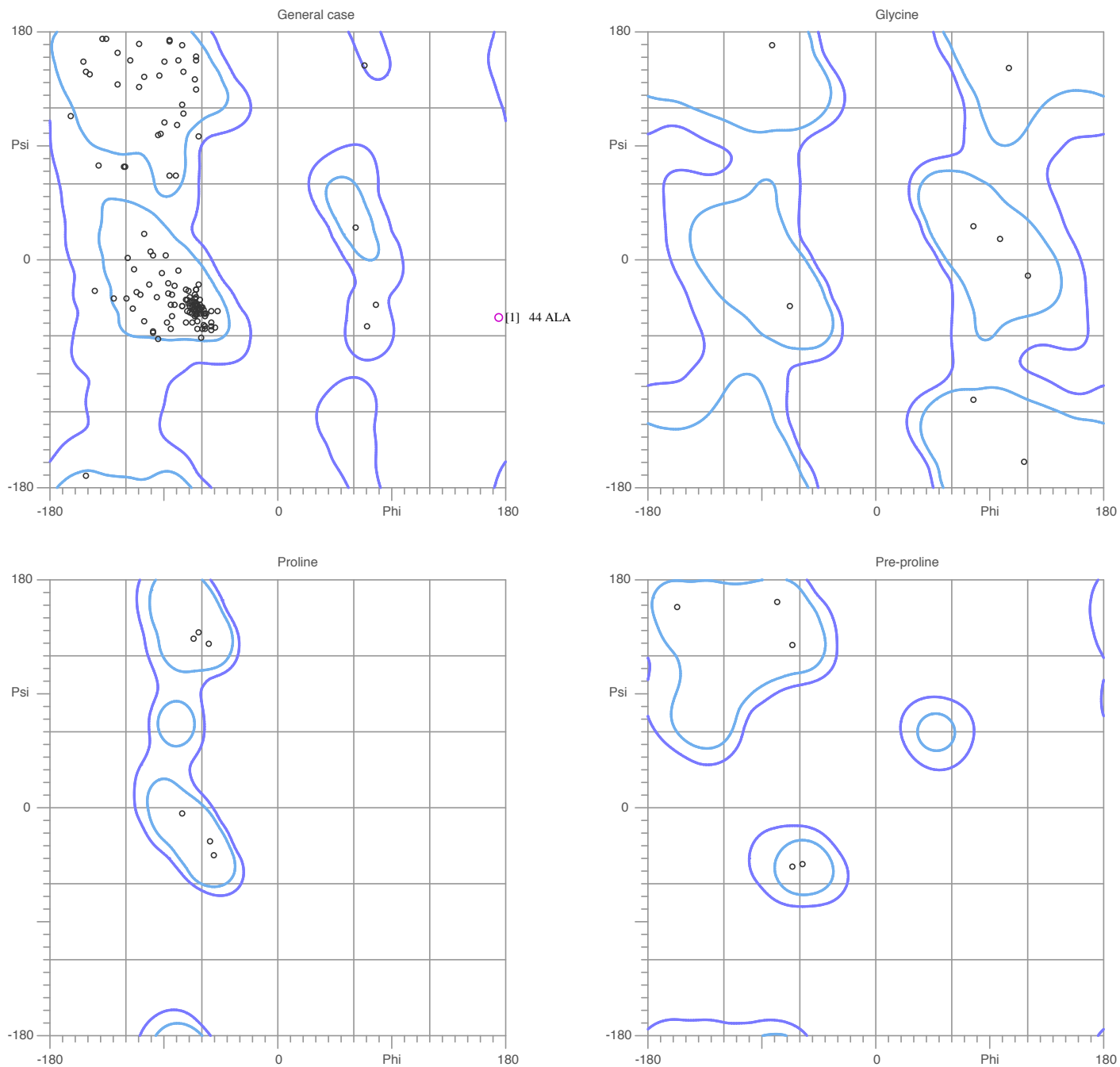




# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 1



92.8% (142/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

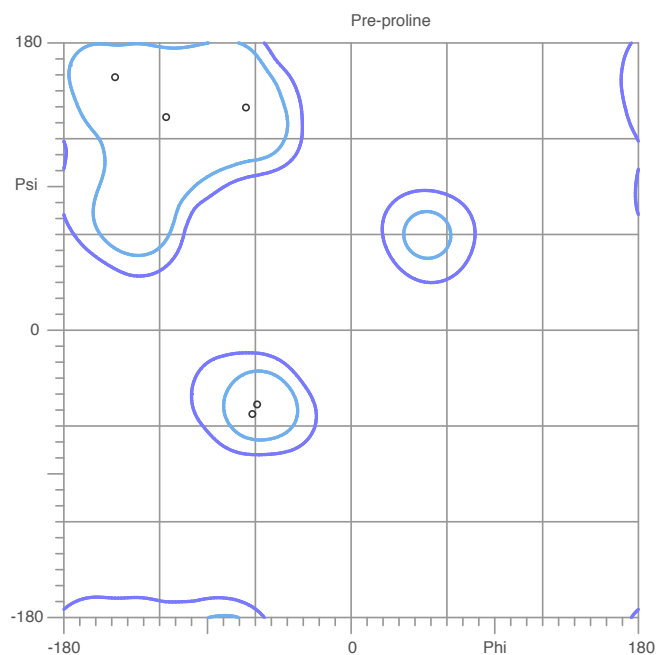
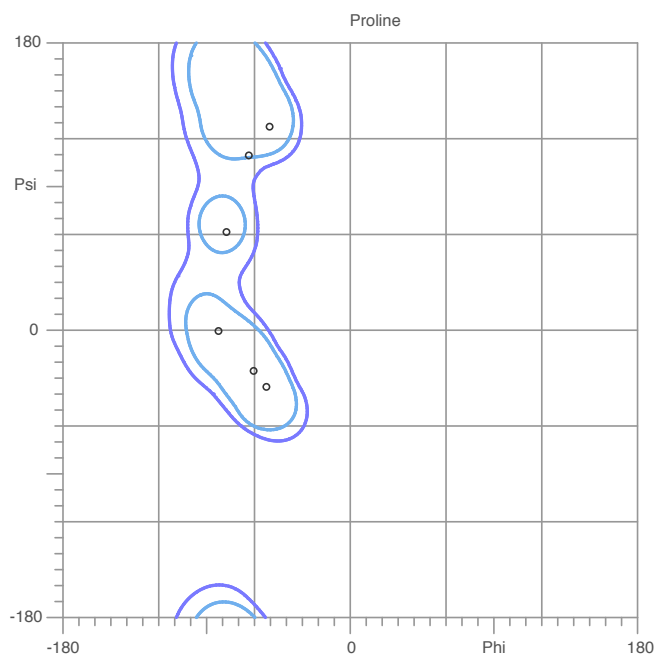
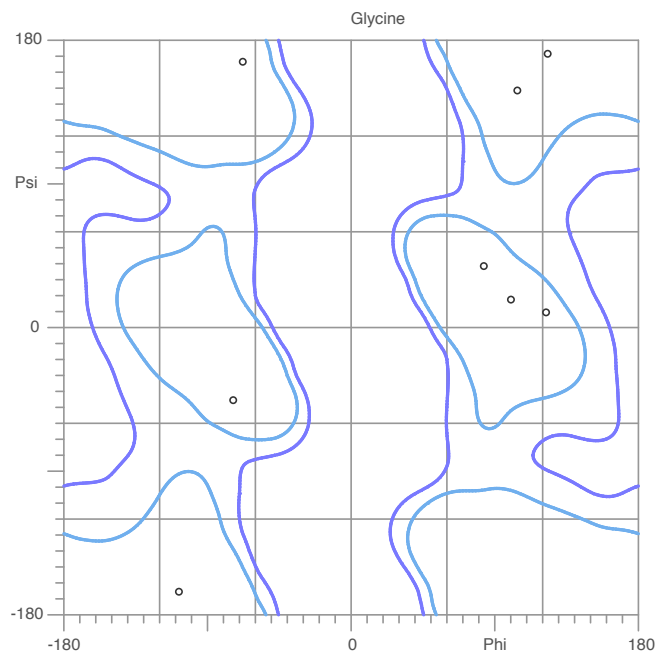
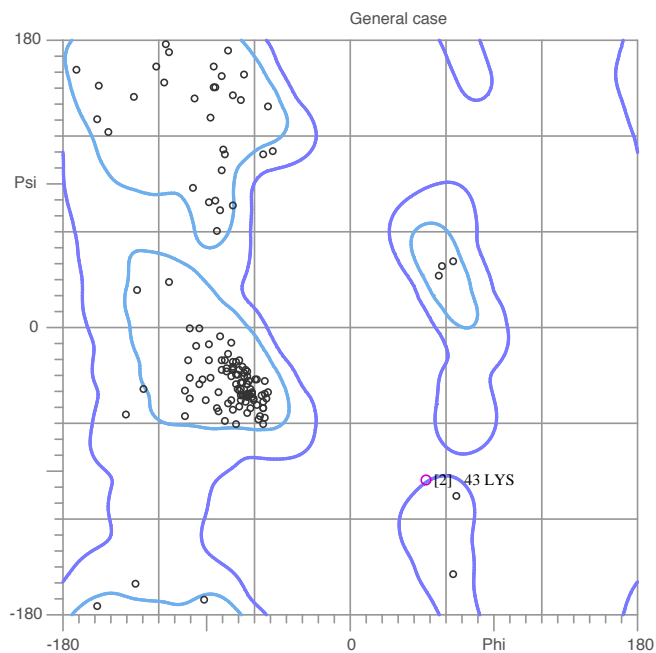
There were 1 outliers (phi, psi):  
[1] 44 ALA (174.6, -45.5)

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# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 2



94.8% (145/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

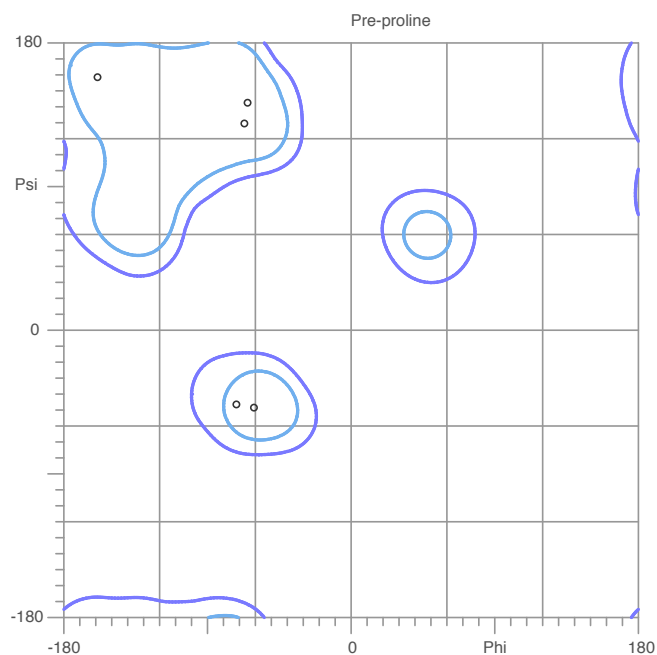
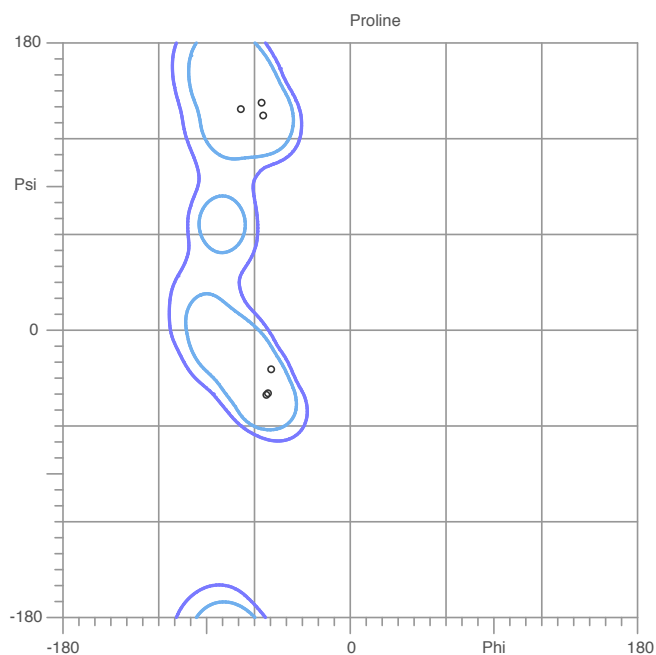
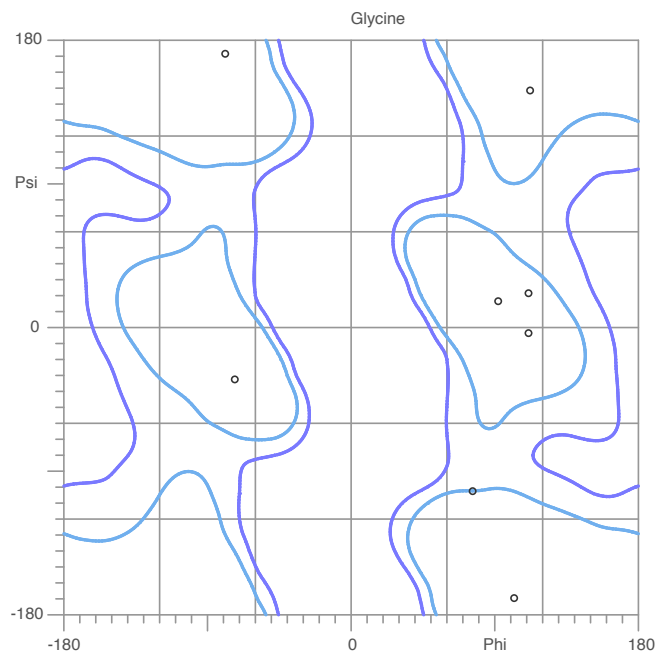
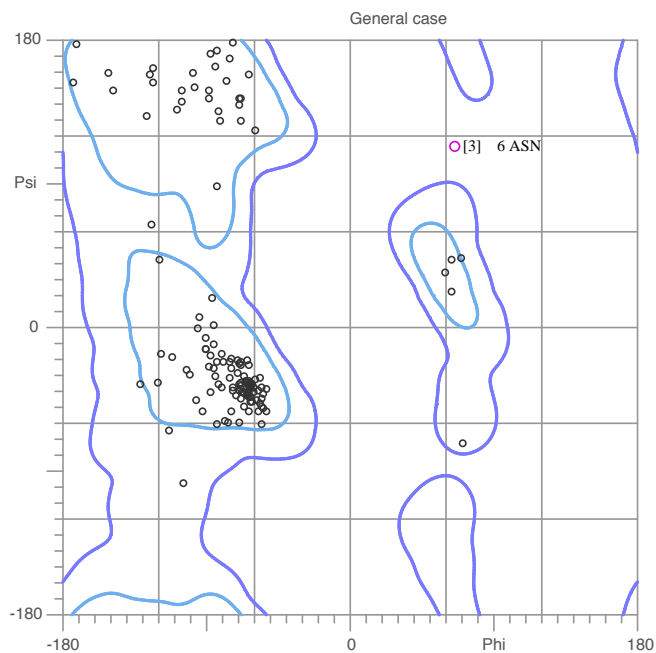
There were 1 outliers (phi, psi):  
[2] 43 LYS (47.4, -95.0)

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

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 3

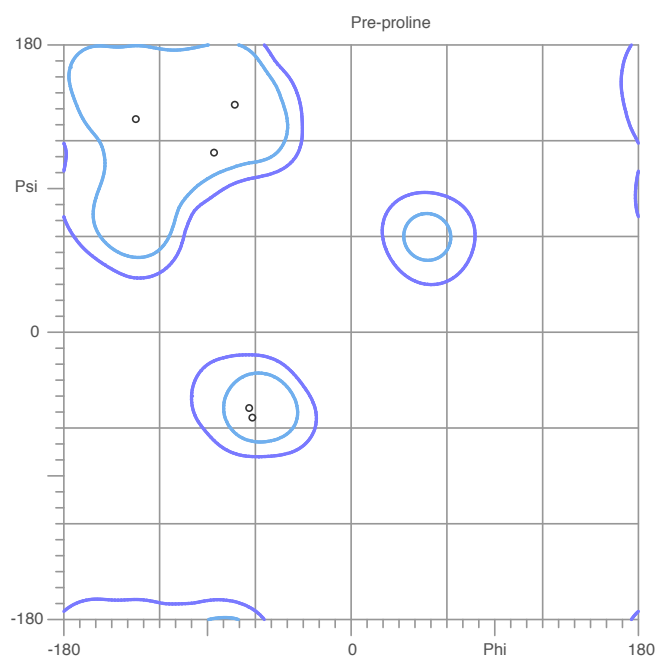
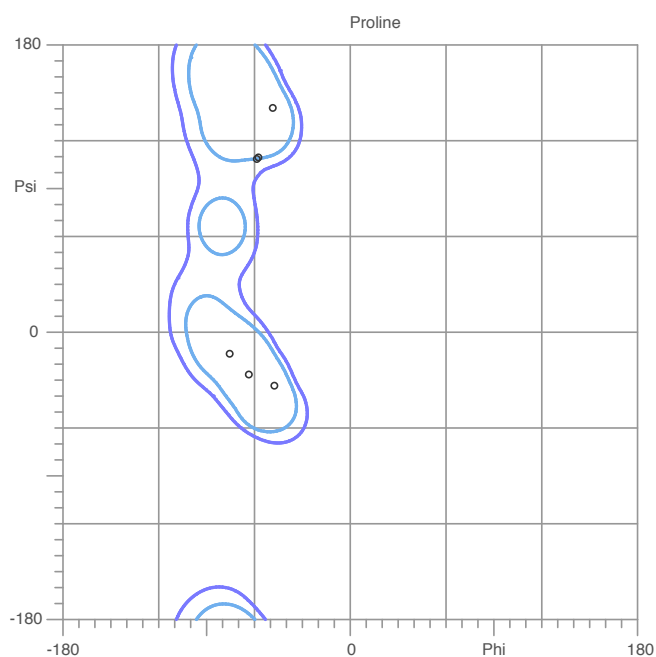
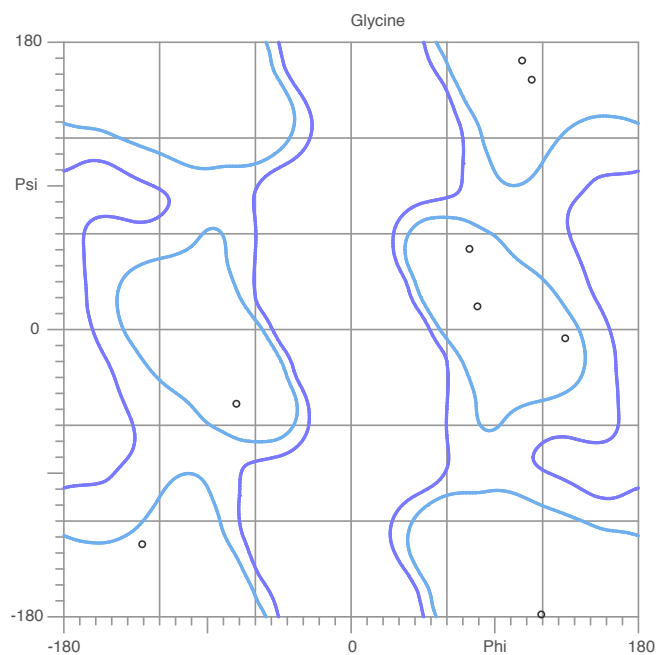
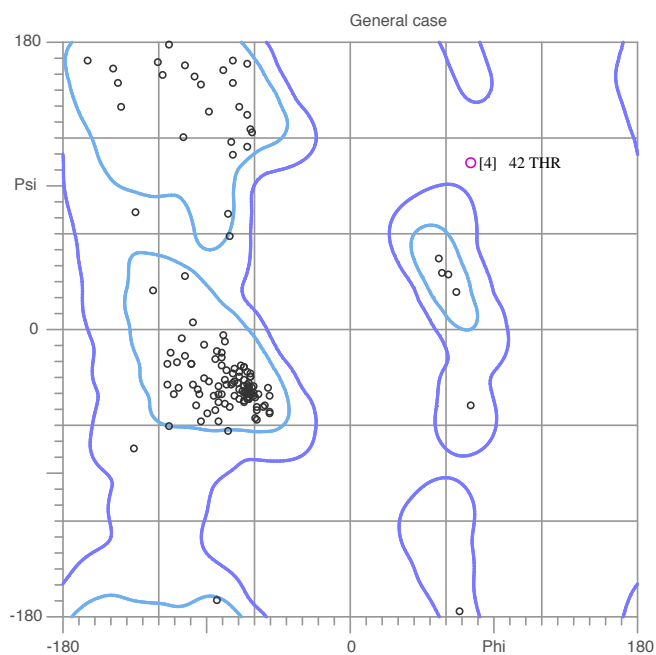


95.4% (146/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[3] 6 ASN (65.1, 114.9)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 4



95.4% (146/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

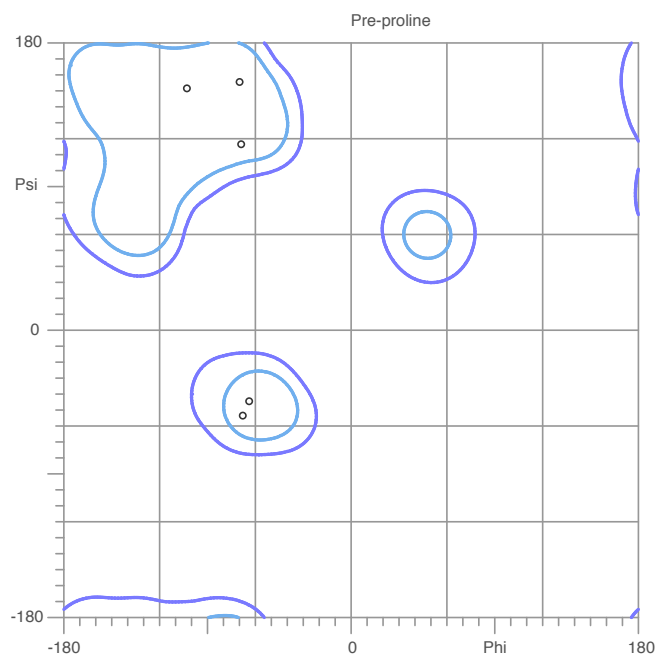
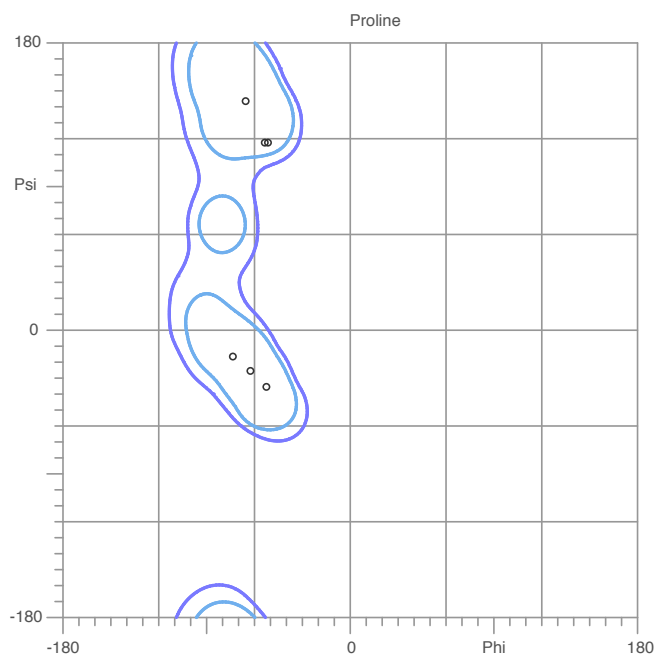
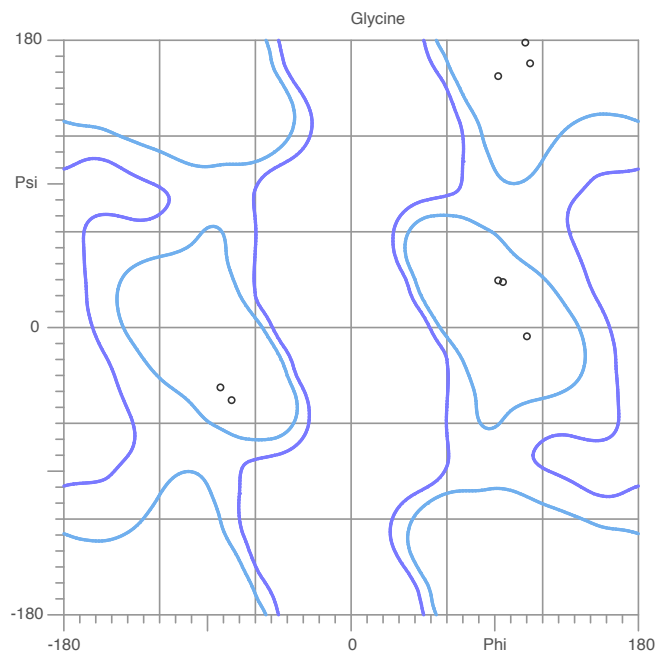
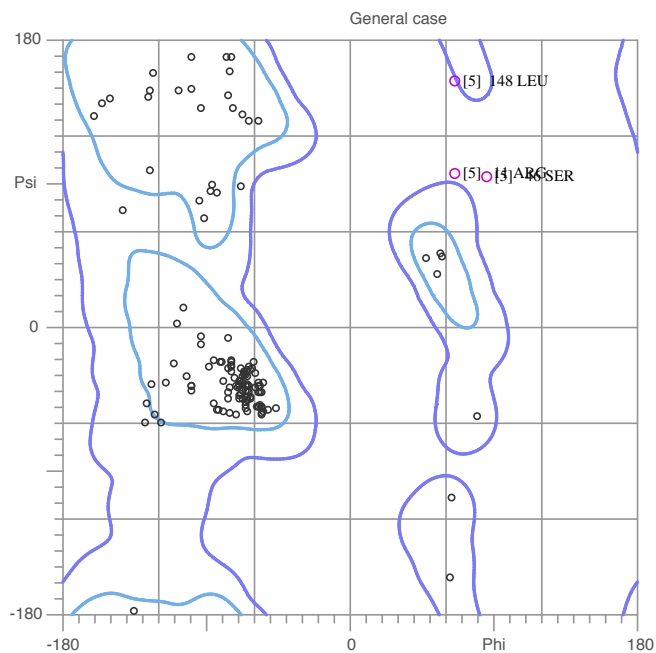
There were 1 outliers (phi, psi):  
[4] 42 THR (75.0, 105.0)

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# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 5



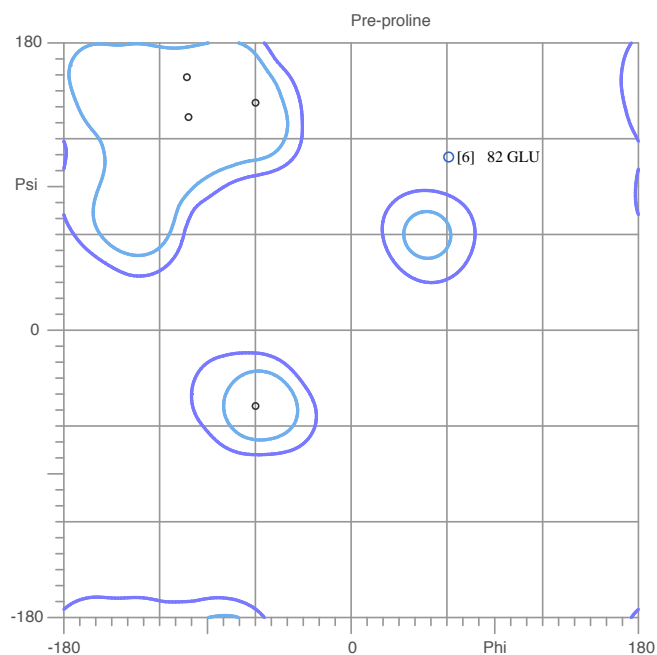
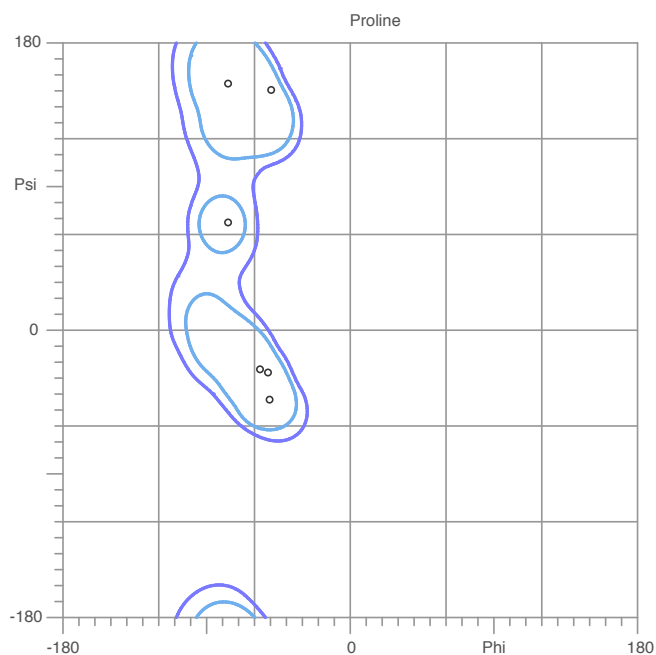
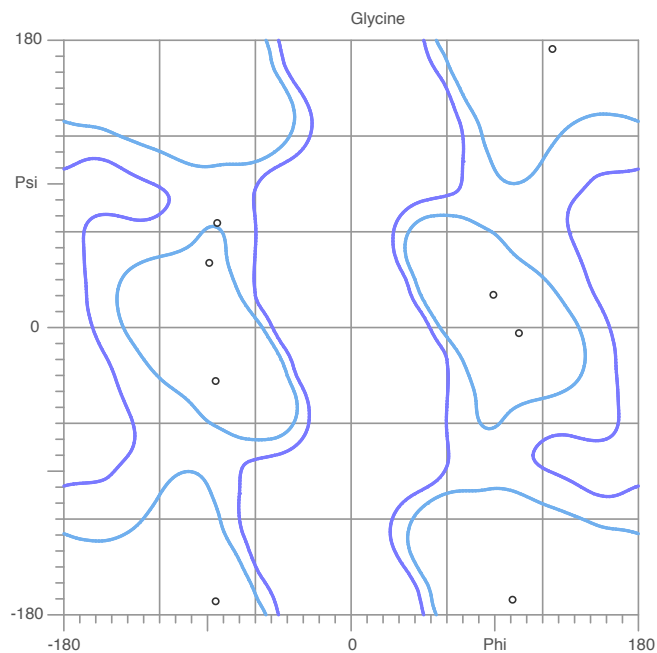
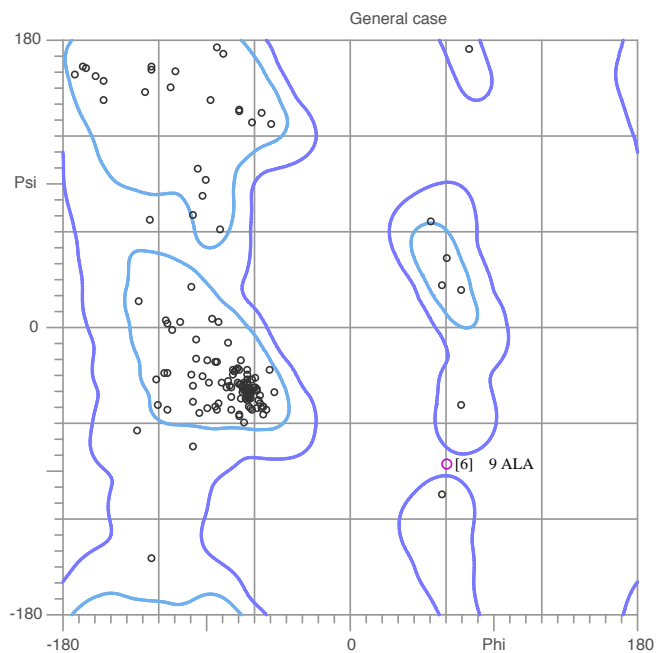
92.2% (141/153) of all residues were in favored (98%) regions.  
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [5] 11 ARG (65.1, 97.6)
- [5] 46 SER (85.5, 95.0)
- [5] 148 LEU (65.4, 155.0)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 6



92.8% (142/153) of all residues were in favored (98%) regions.  
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

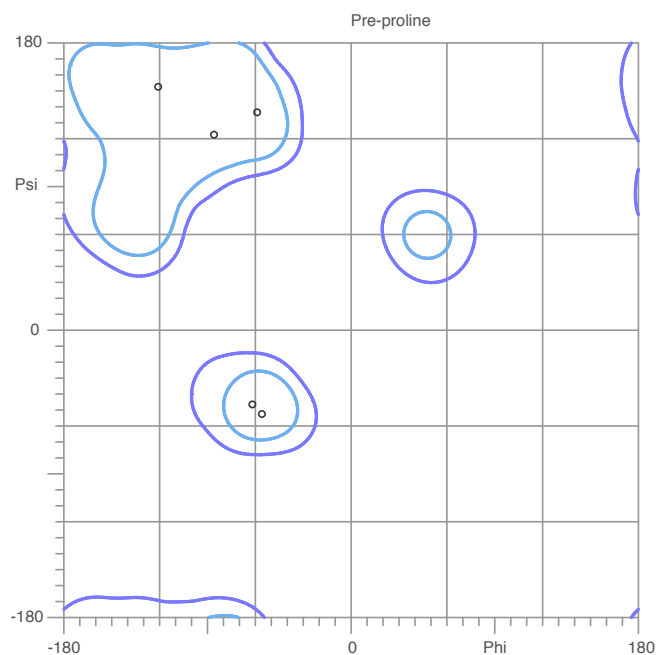
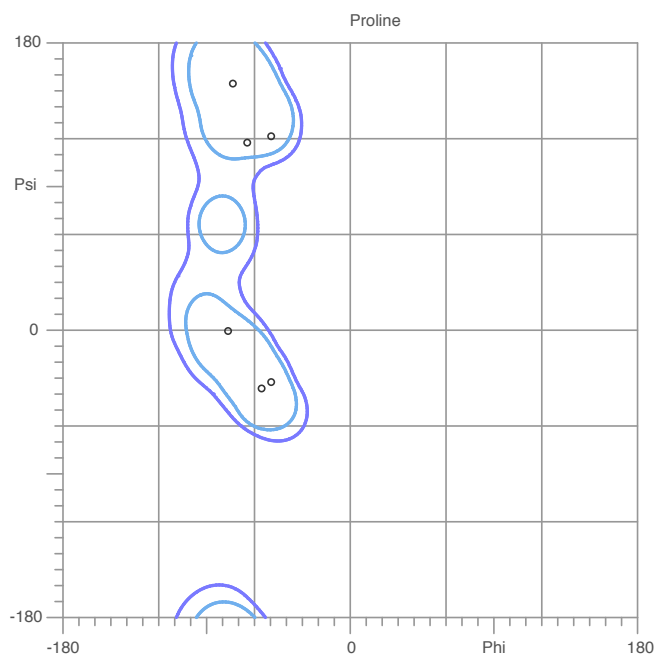
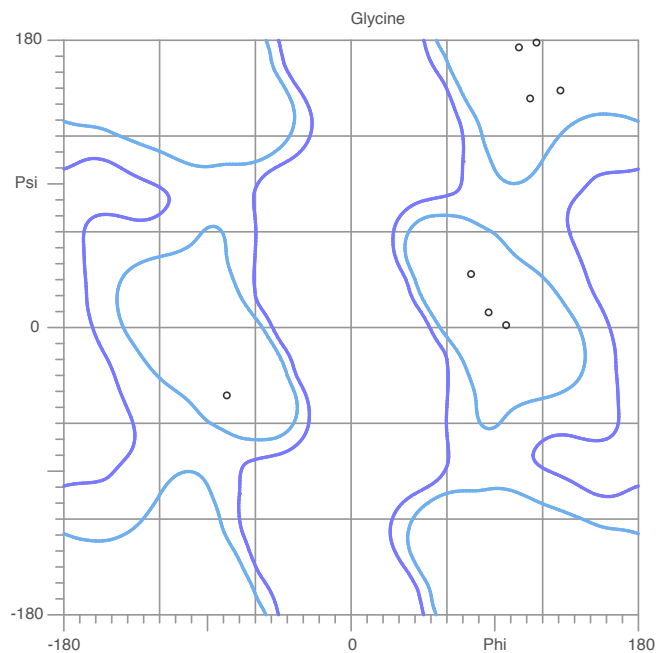
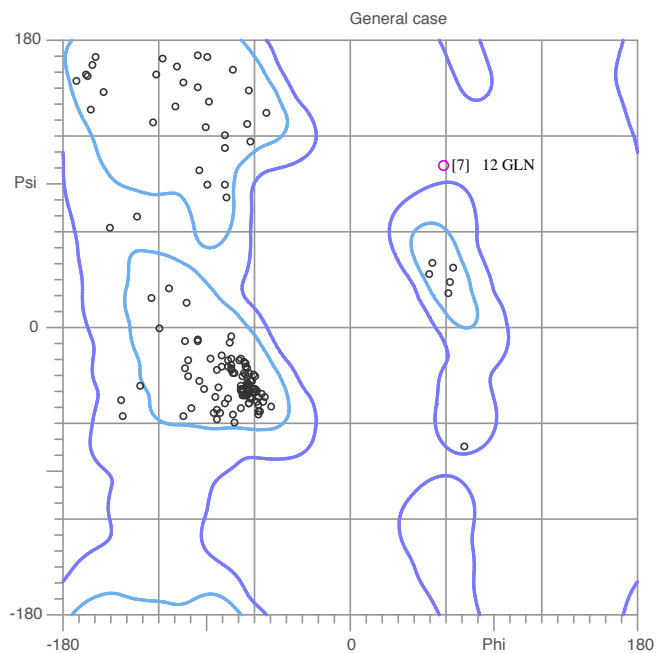
There were 2 outliers (phi, psi):

[6] 9 ALA (60.1, -85.0)

[6] 82 GLU (61.7, 110.0)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 7



95.4% (146/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

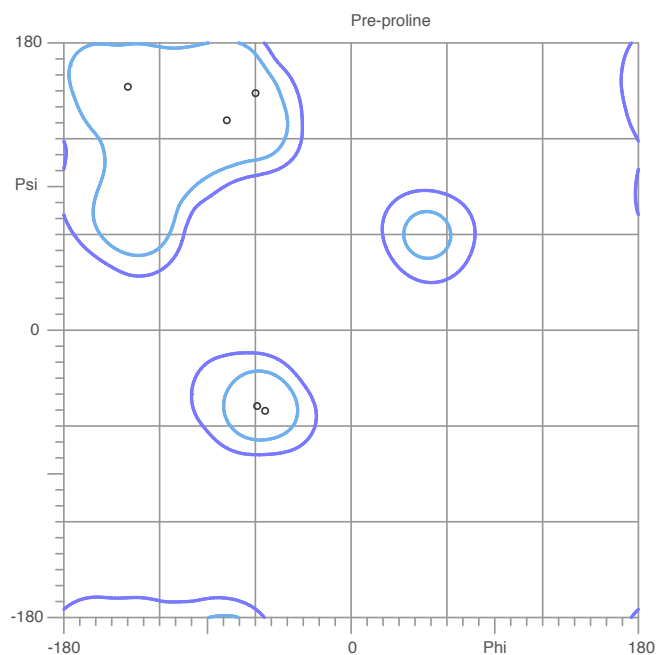
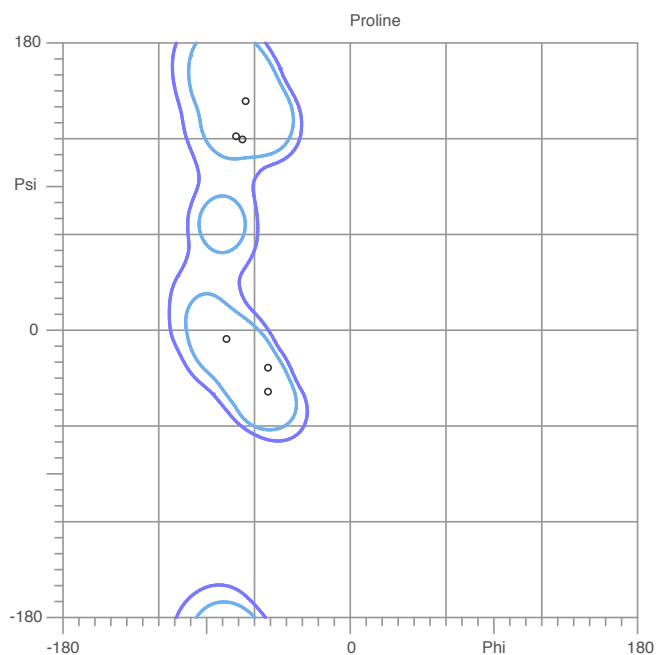
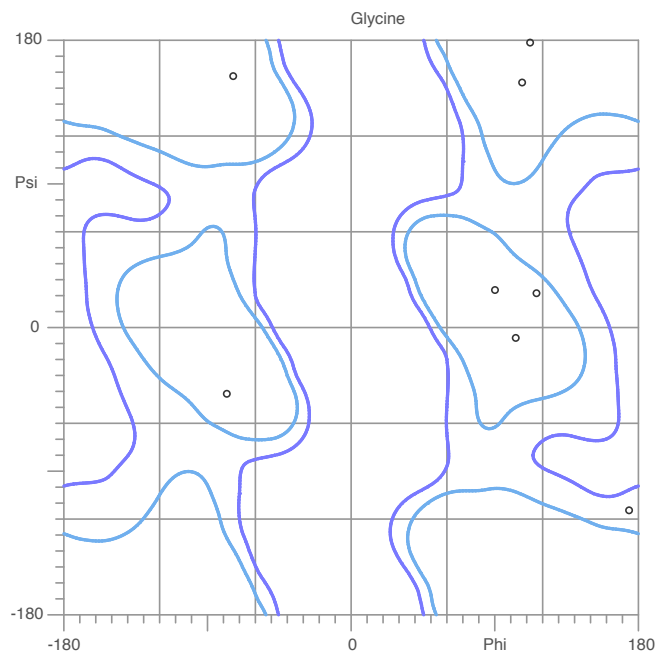
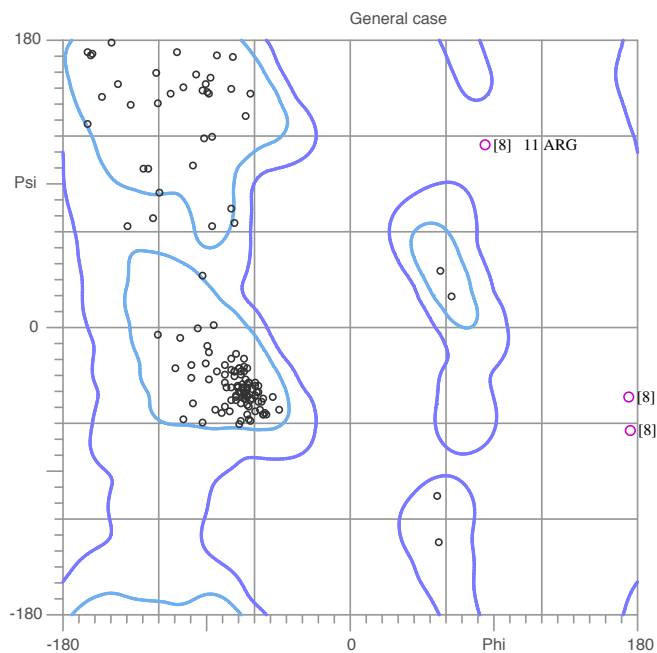
There were 1 outliers (phi, psi):  
[7] 12 GLN (58.4, 102.9)

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# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 8



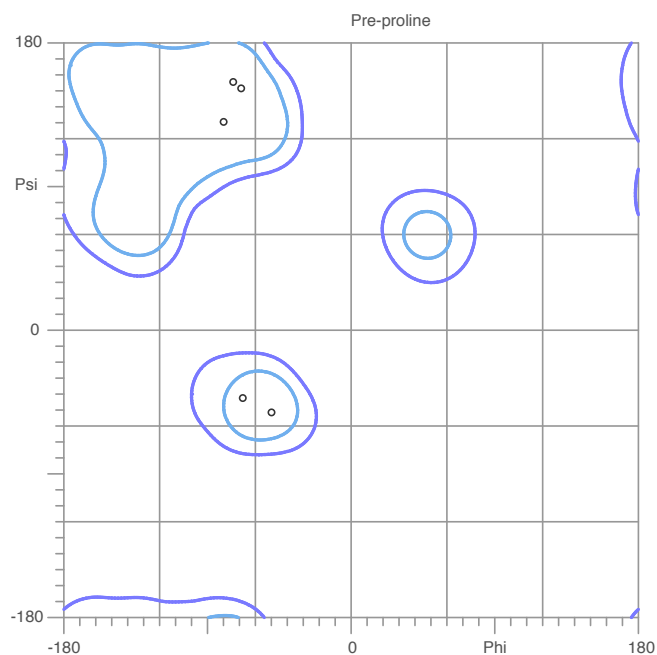
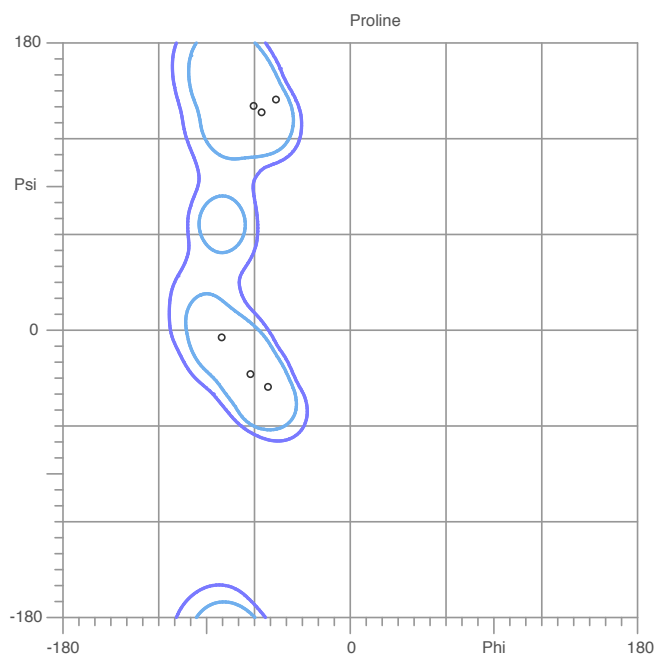
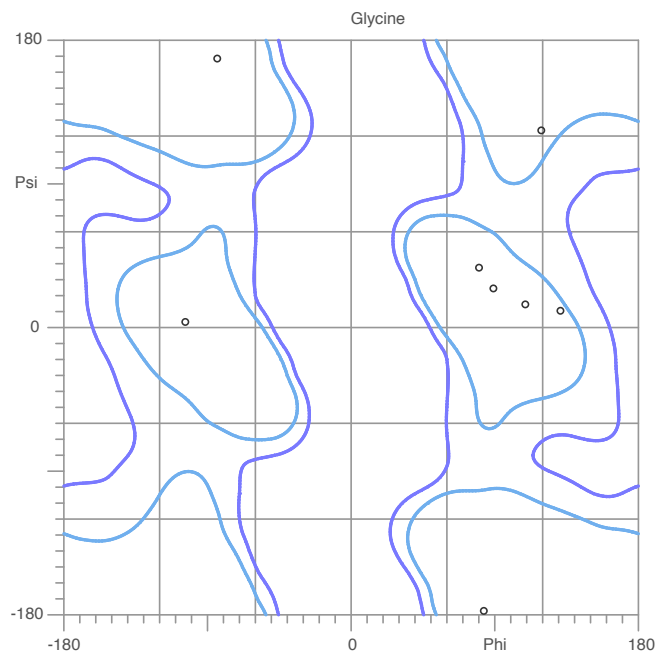
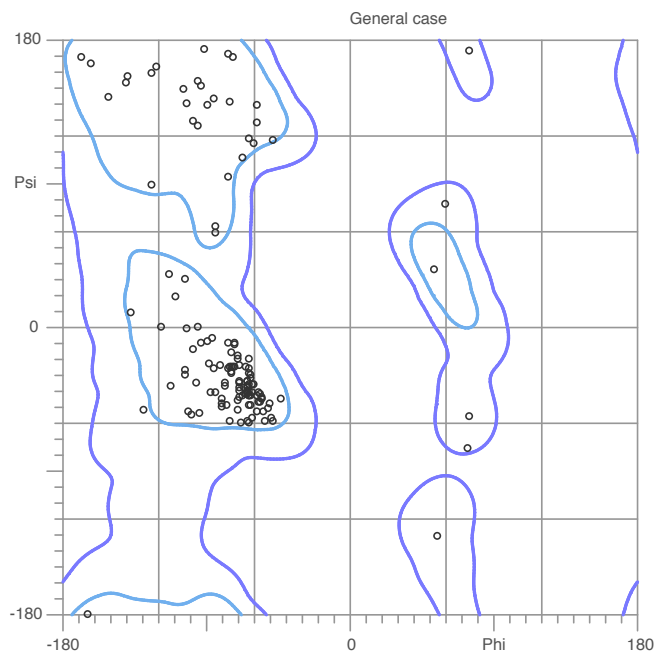
93.5% (143/153) of all residues were in favored (98%) regions.  
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 11 ARG (85.0, 115.0)
- [8] 44 ALA (174.9, -43.9)
- [8] 81 PHE (175.1, -65.0)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 9



96.1% (147/153) of all residues were in favored (98%) regions.  
100.0% (153/153) of all residues were in allowed (>99.8%) regions.

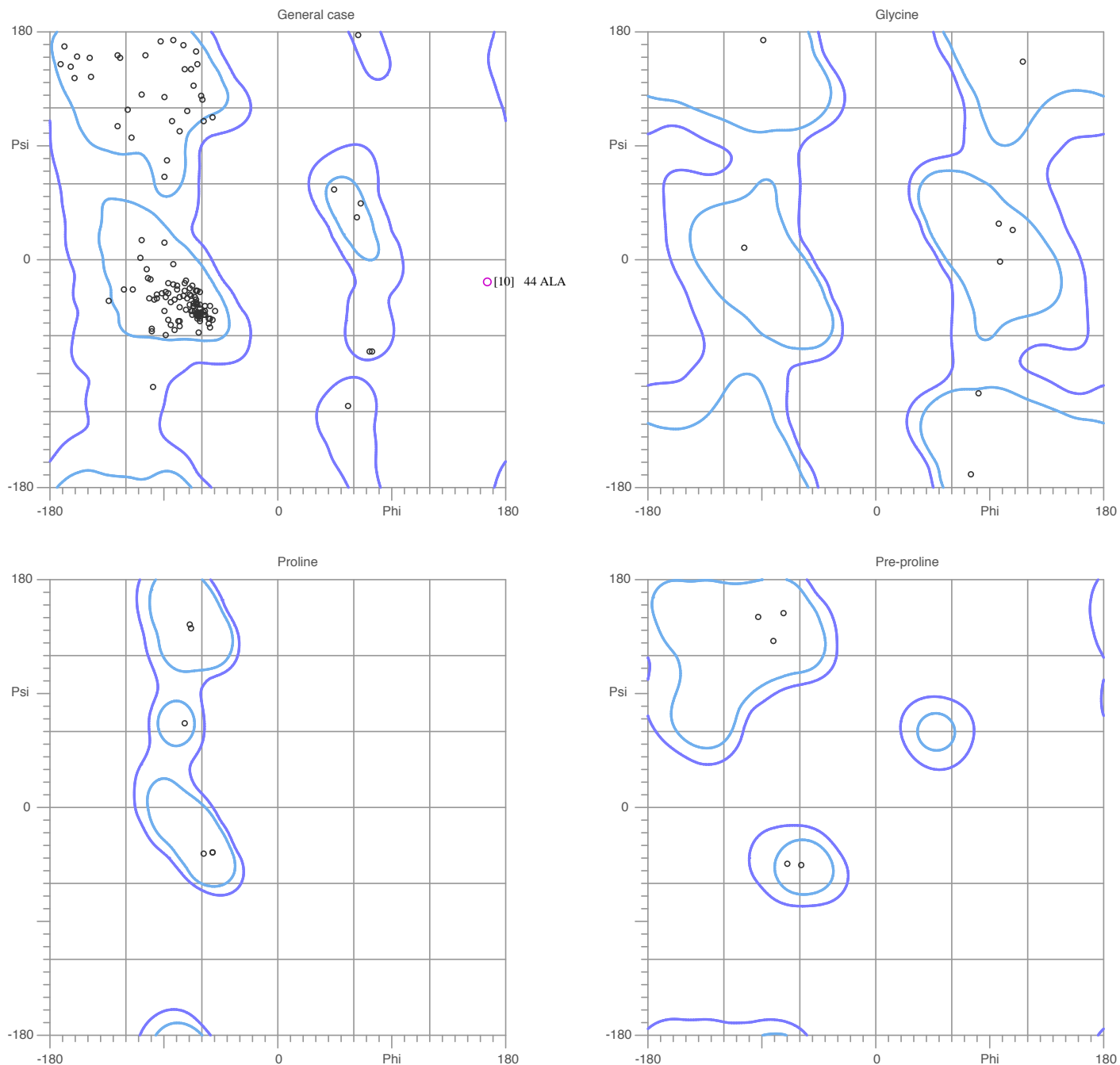
There were no outliers.

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# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 10



94.1% (144/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

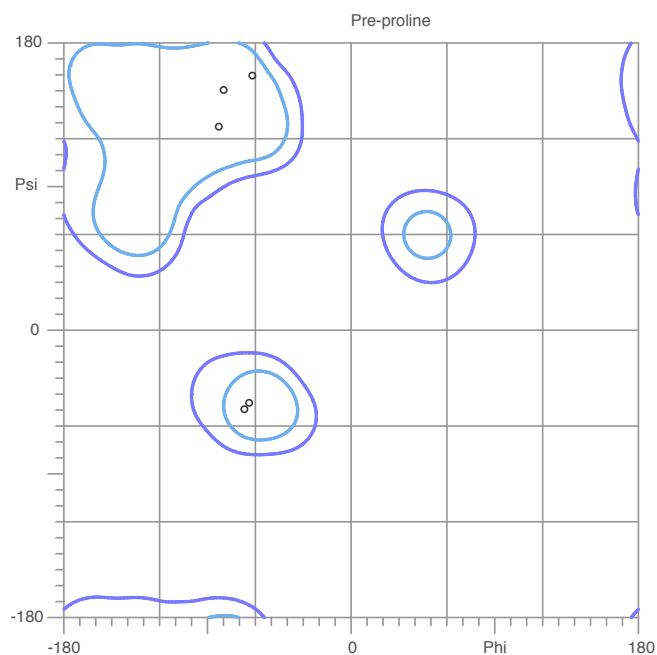
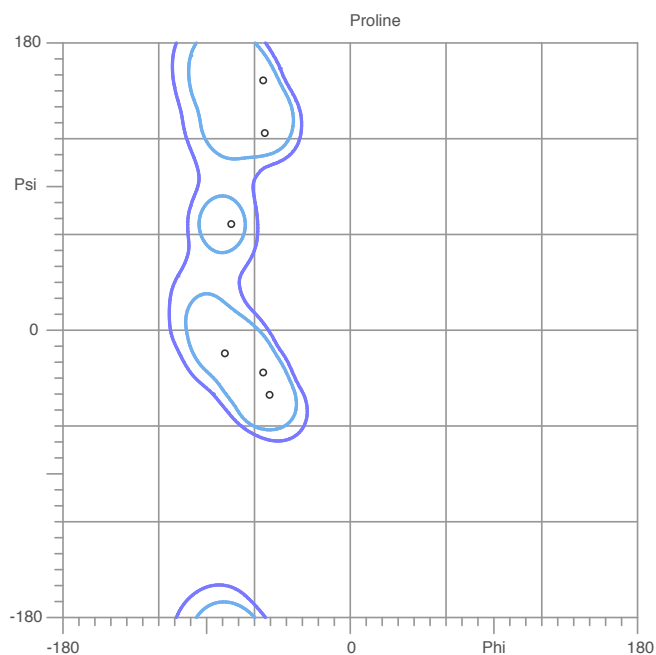
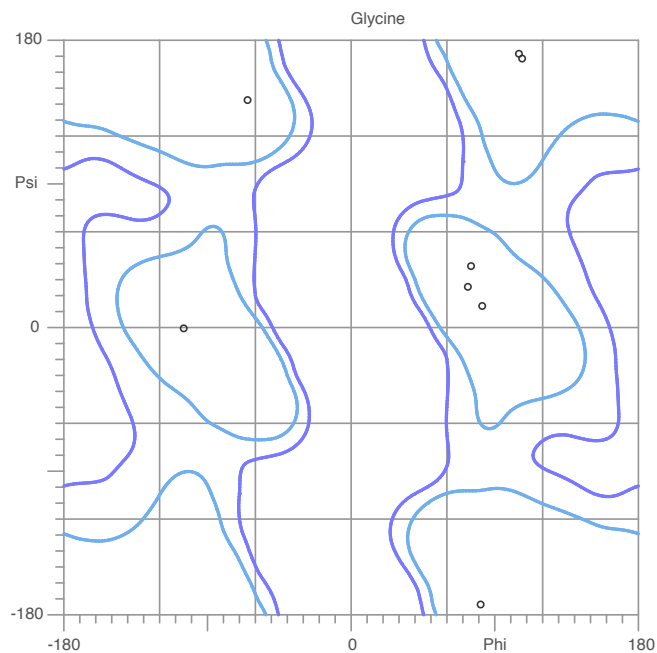
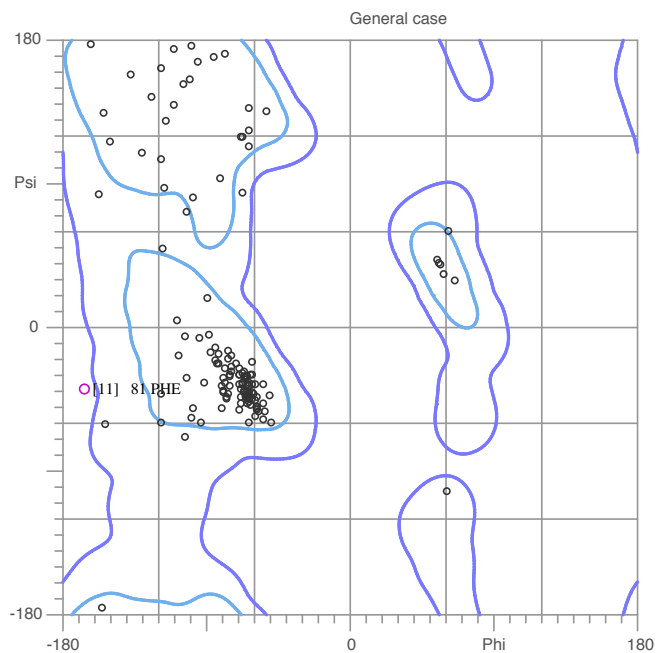
There were 1 outliers (phi, psi):  
[10] 44 ALA (165.4, -17.8)

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# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 11

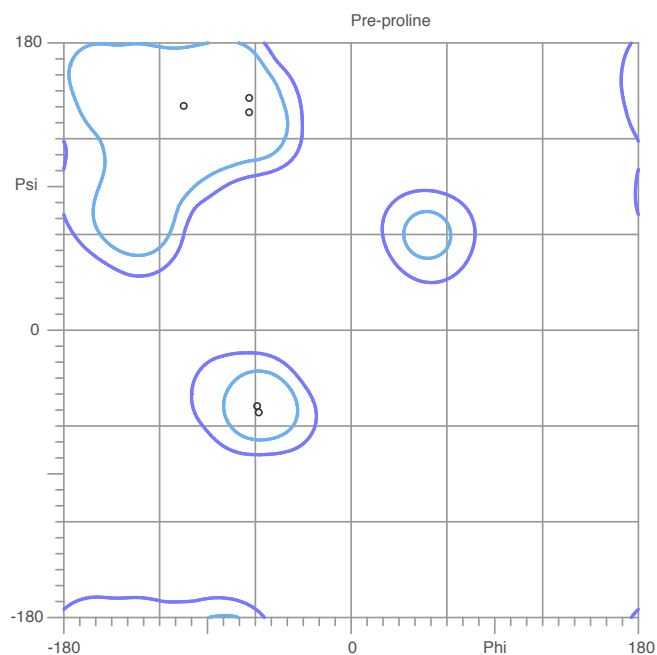
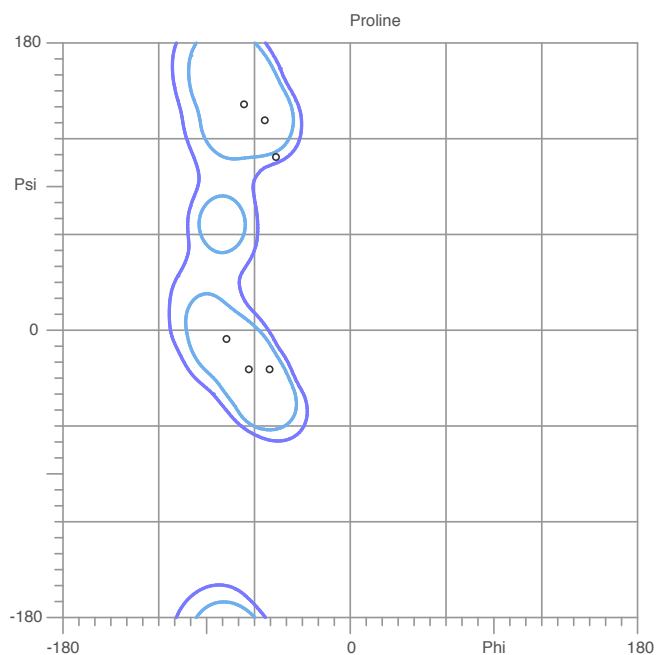
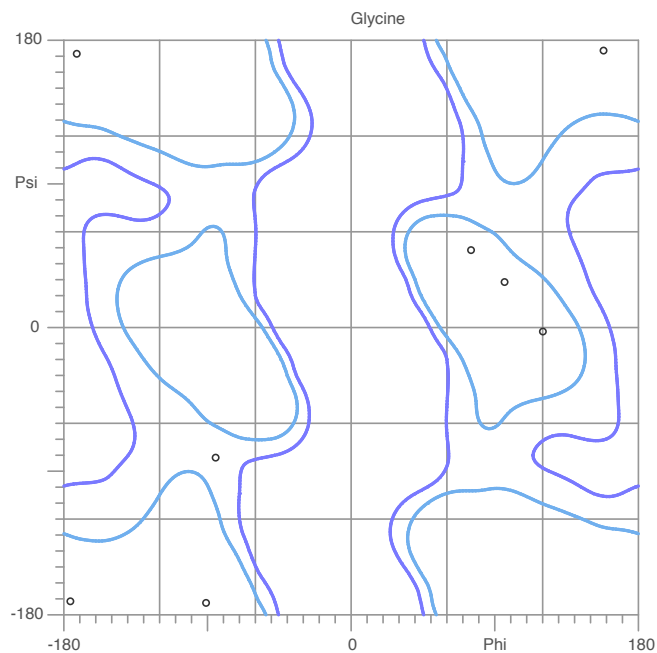
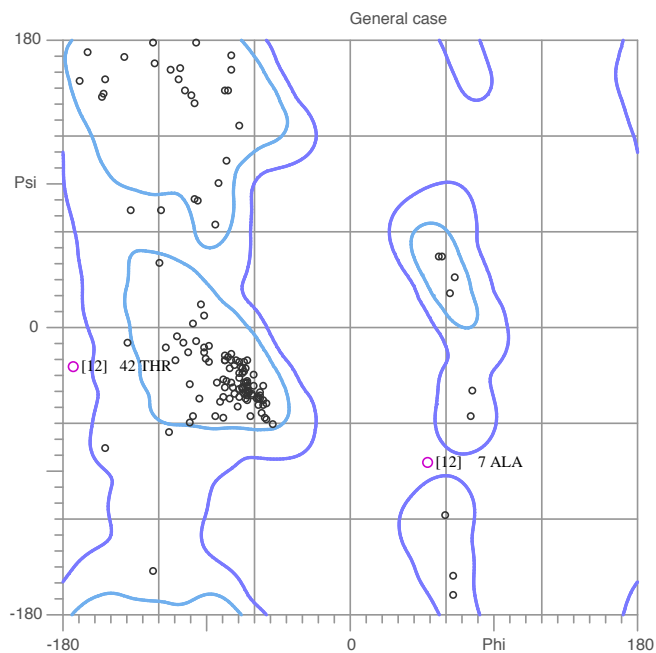


93.5% (143/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[11] 81 PHE (-167.8, -38.7)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 12

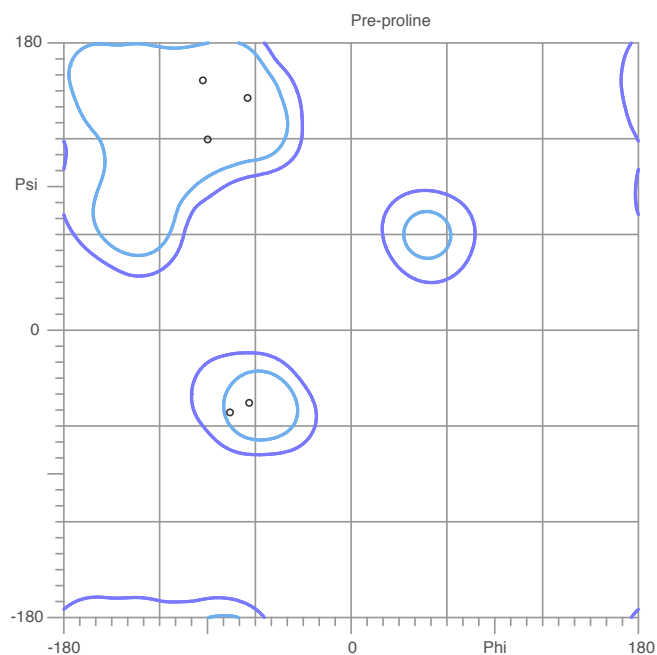
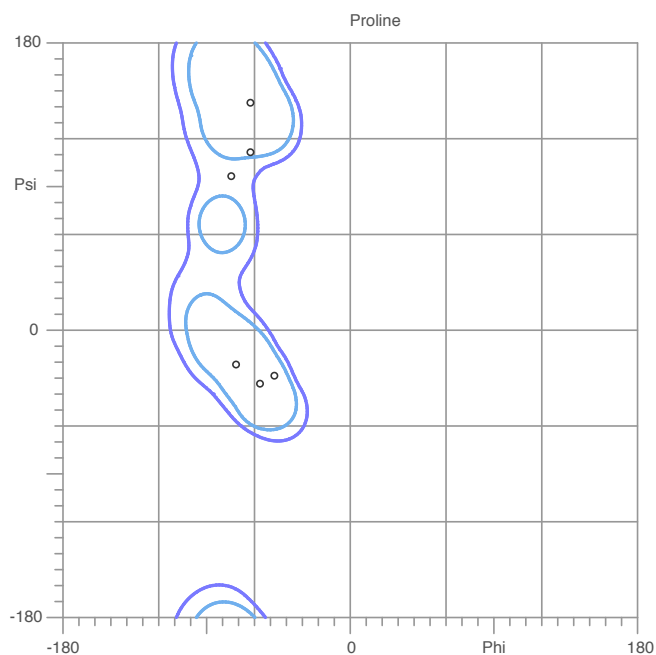
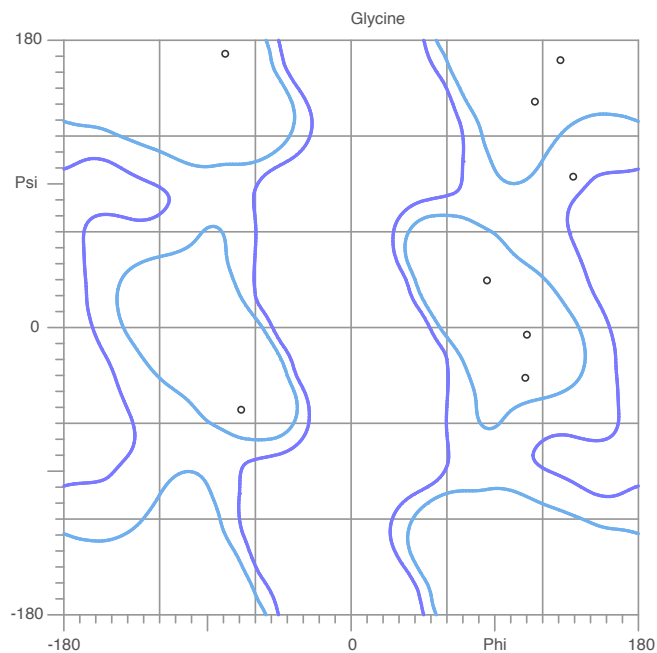
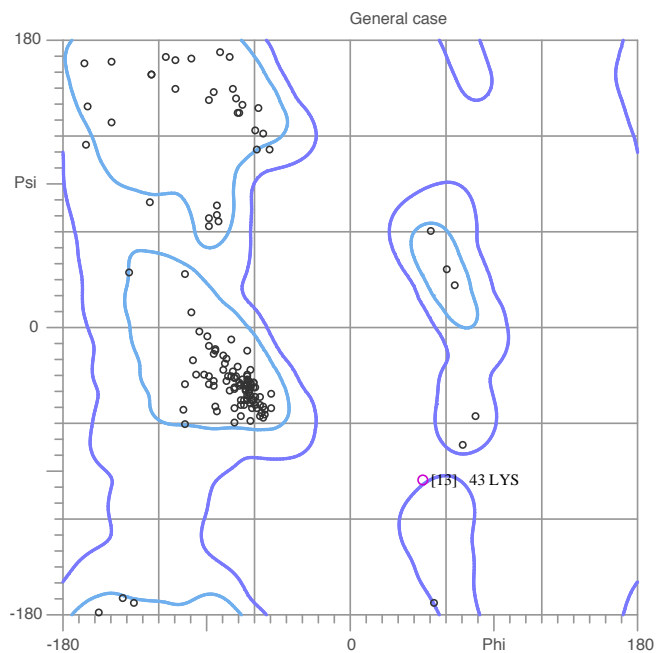


90.2% (138/153) of all residues were in favored (98%) regions.  
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[12] 7 ALA (48.4, -85.0)  
[12] 42 THR (-175.0, -25.0)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 13

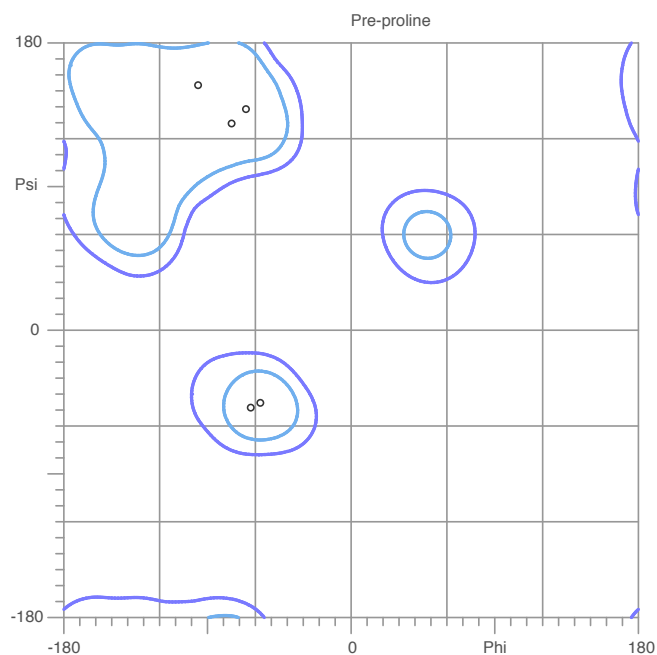
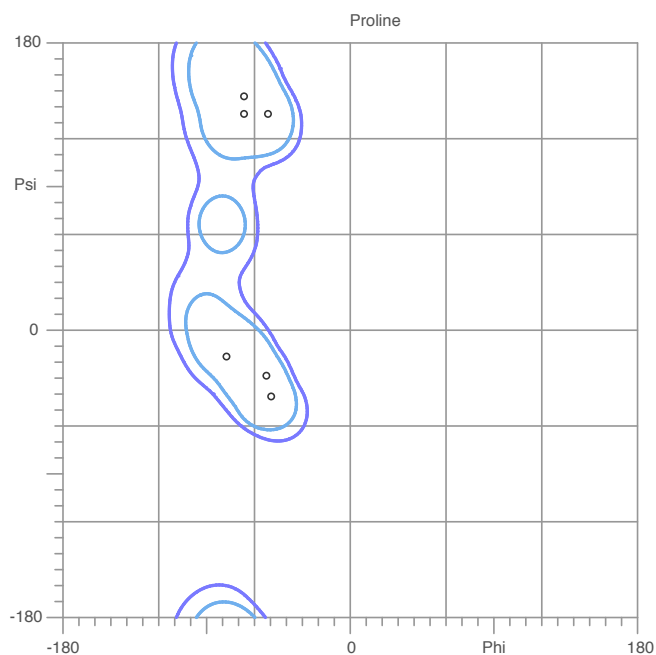
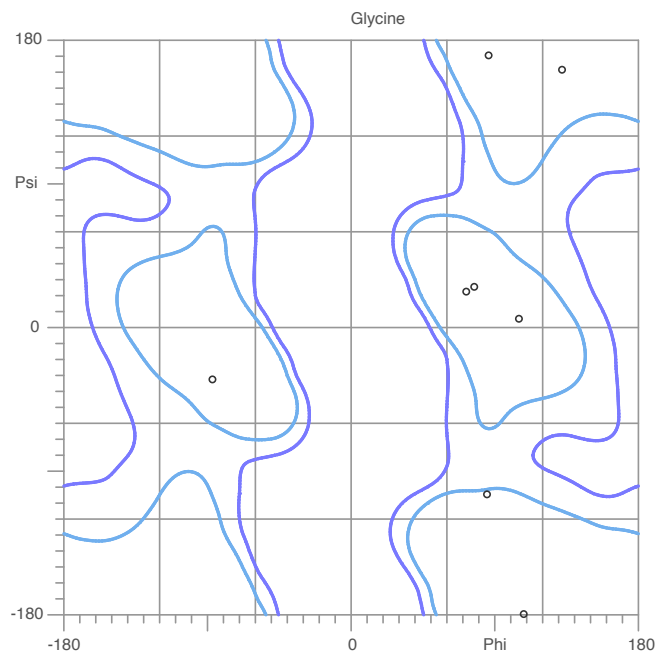
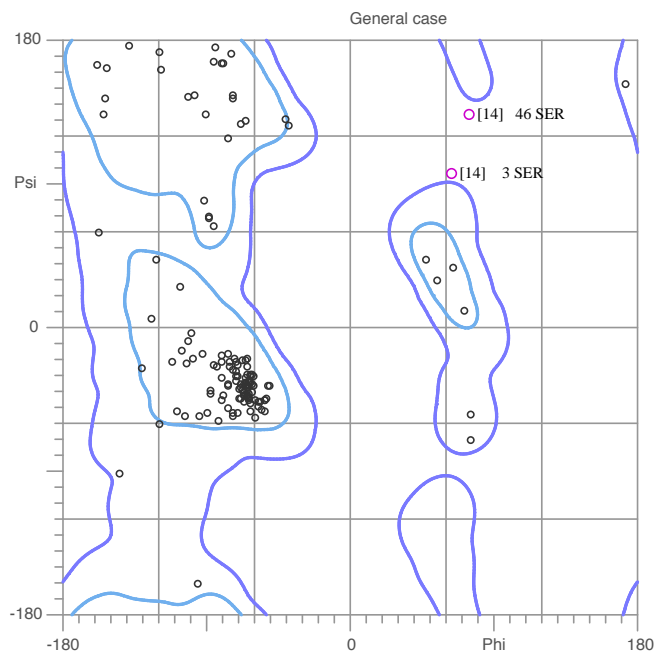


93.5% (143/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):  
[13] 43 LYS (45.0, -95.0)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 14



92.8% (142/153) of all residues were in favored (98%) regions.  
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

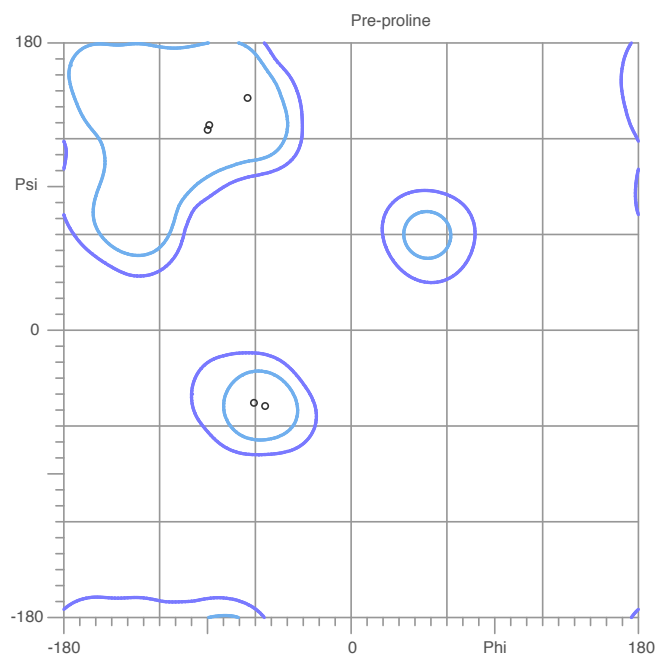
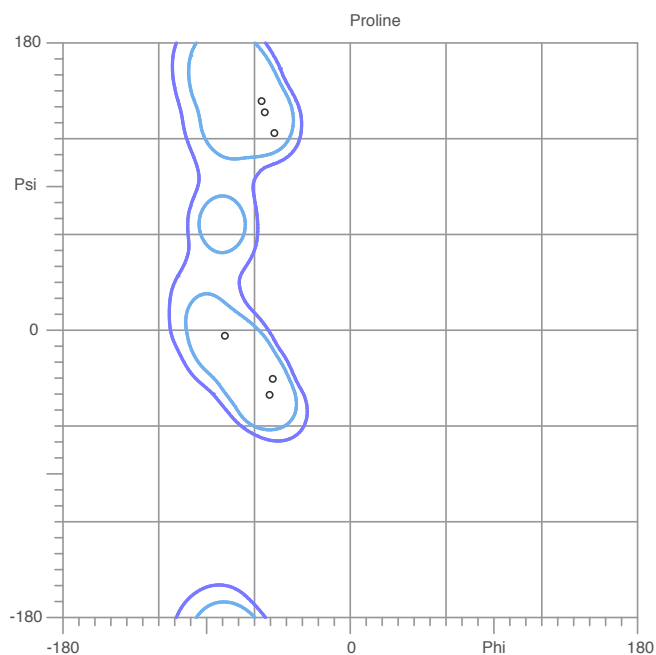
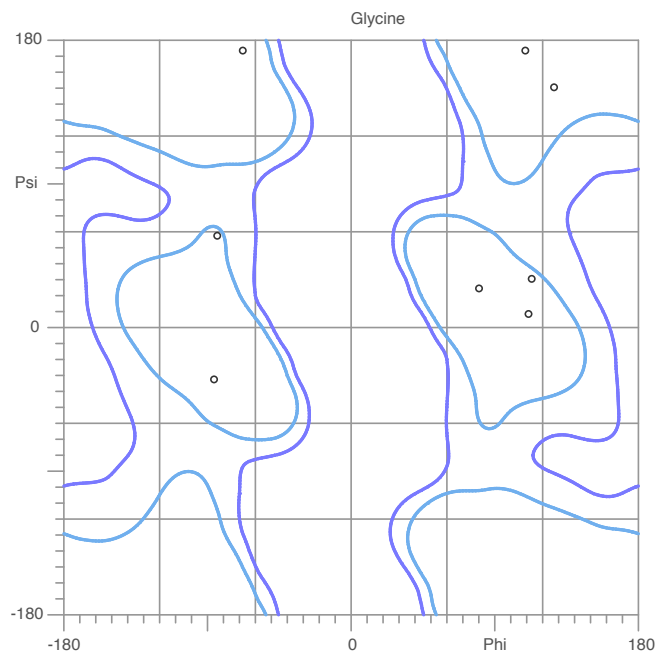
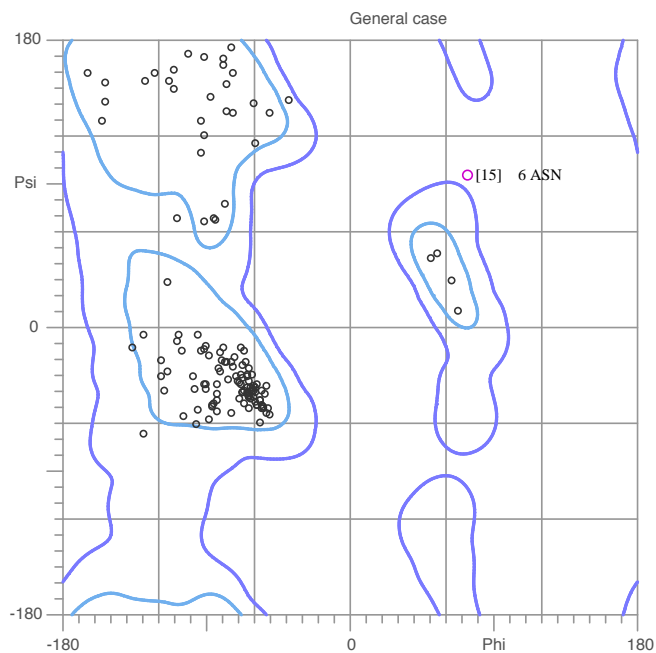
There were 2 outliers (phi, psi):

[14] 3 SER (64.0, 97.4)

[14] 46 SER (74.0, 134.9)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 15



96.7% (148/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

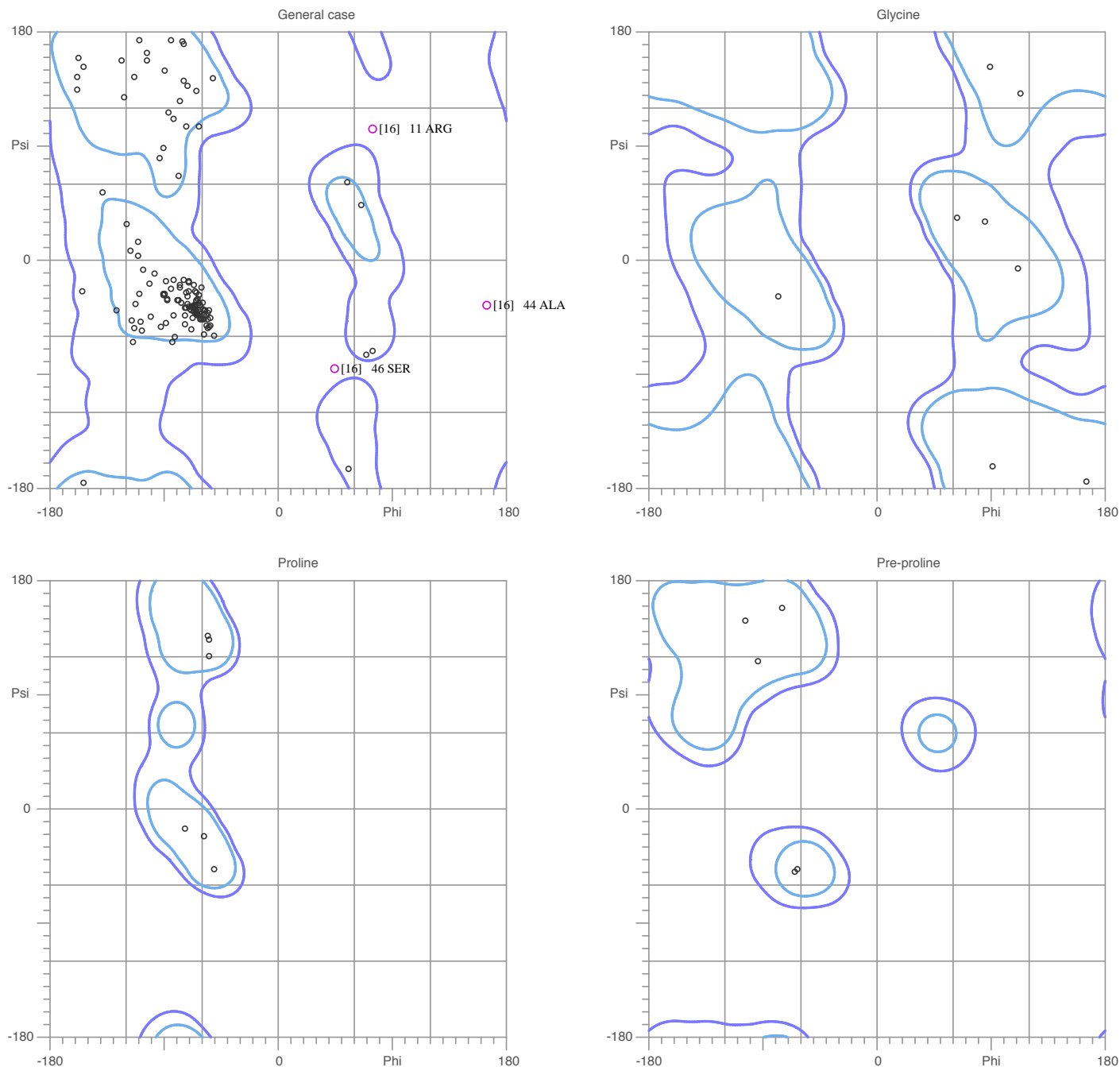
There were 1 outliers (phi, psi):  
[15] 6 ASN (73.6, 96.6)

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# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 16



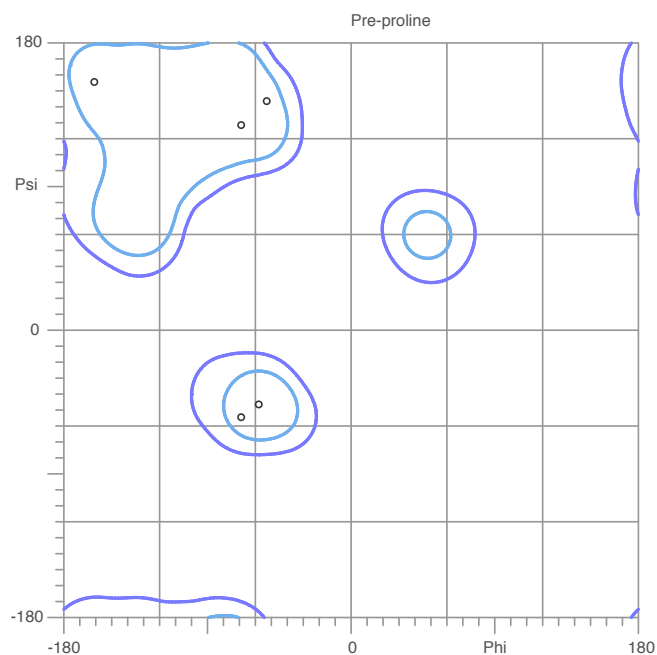
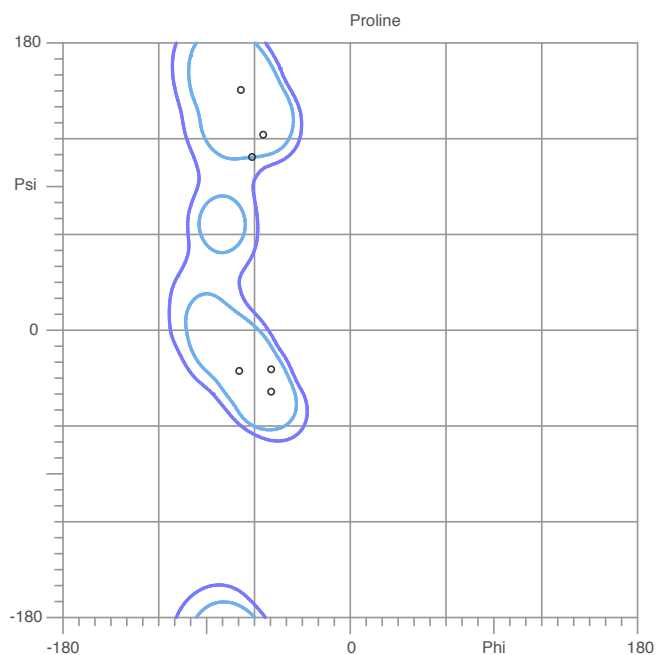
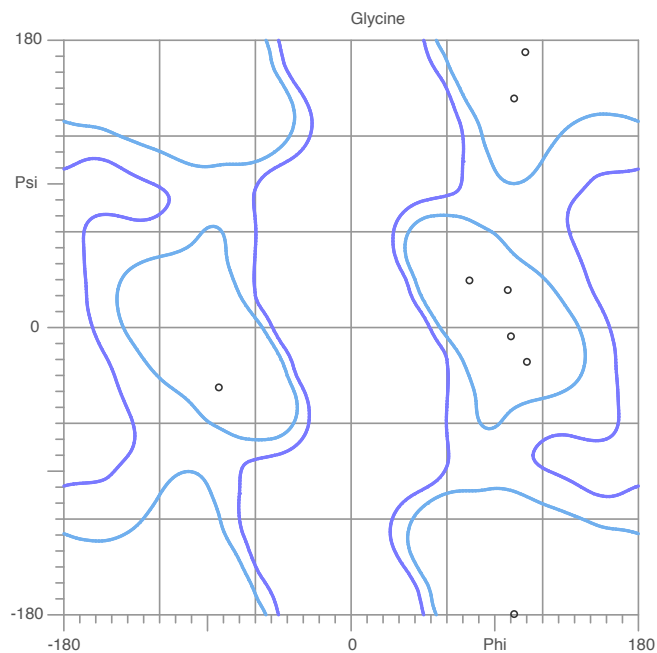
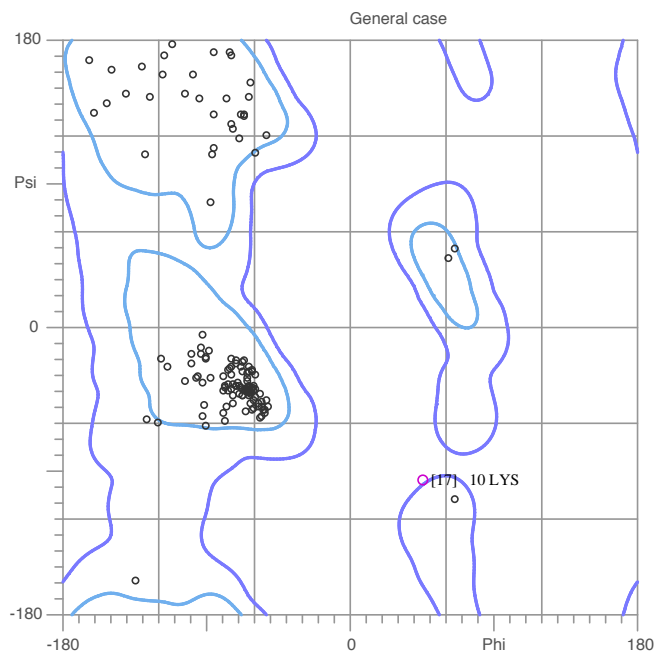
92.2% (141/153) of all residues were in favored (98%) regions.  
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [16] 11 ARG (74.9, 104.9)
- [16] 44 ALA (165.0, -35.1)
- [16] 46 SER (44.1, -85.1)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 17



96.1% (147/153) of all residues were in favored (98%) regions.  
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

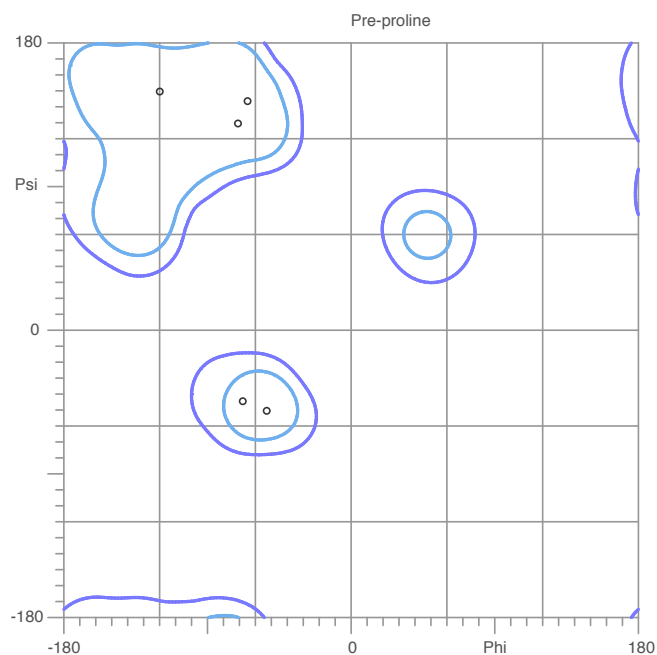
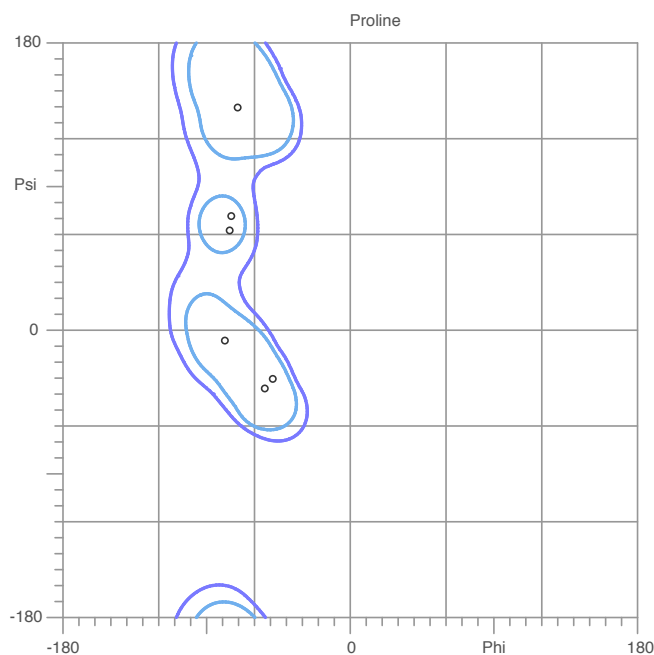
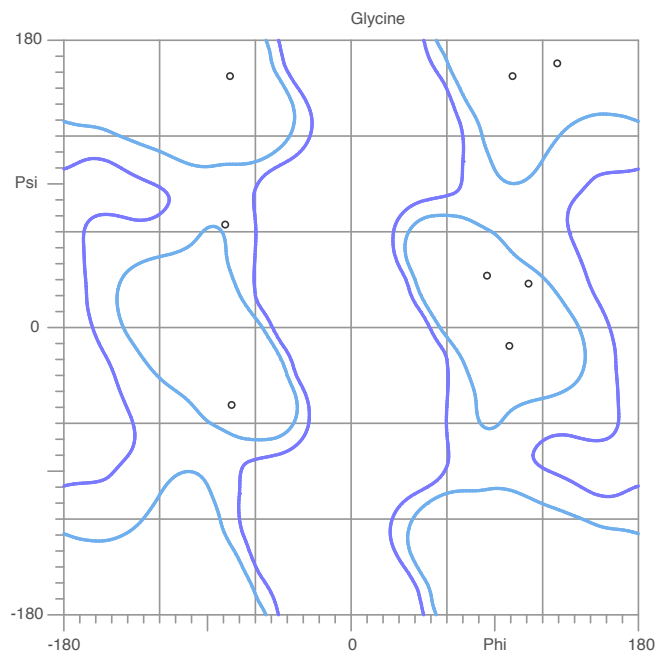
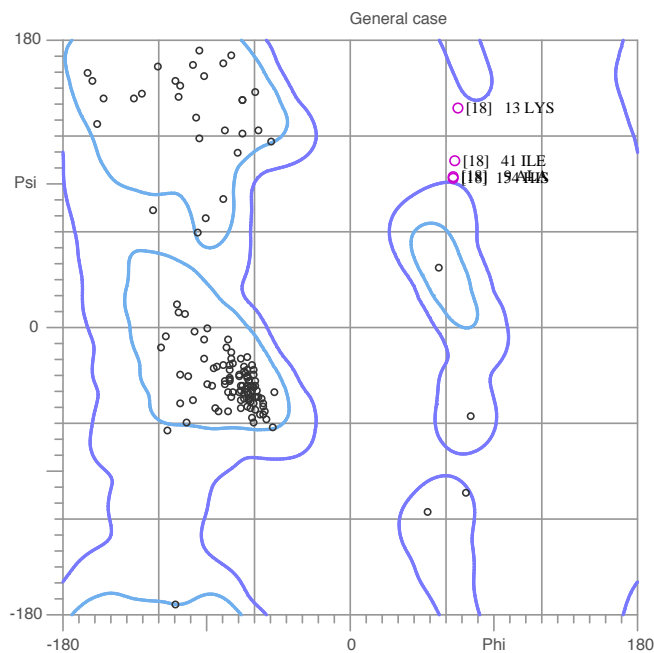
There were 1 outliers (phi, psi):  
[17] 10 LYS (45.0, -95.1)

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# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 18



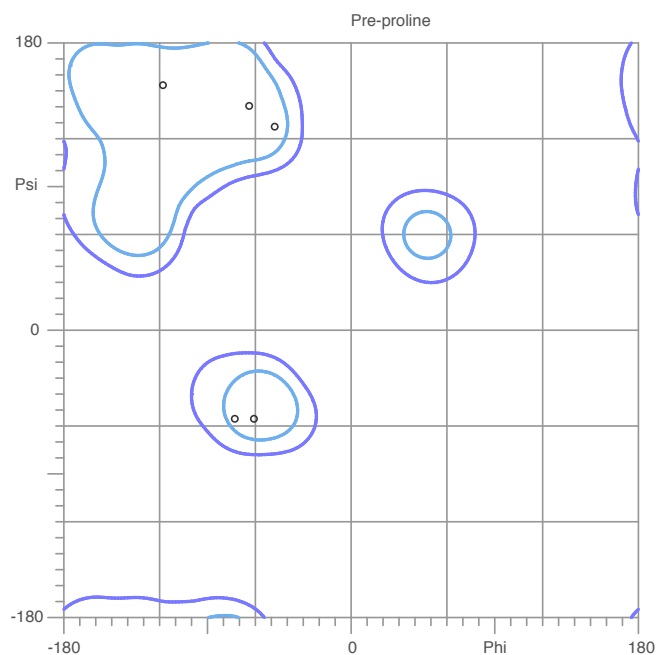
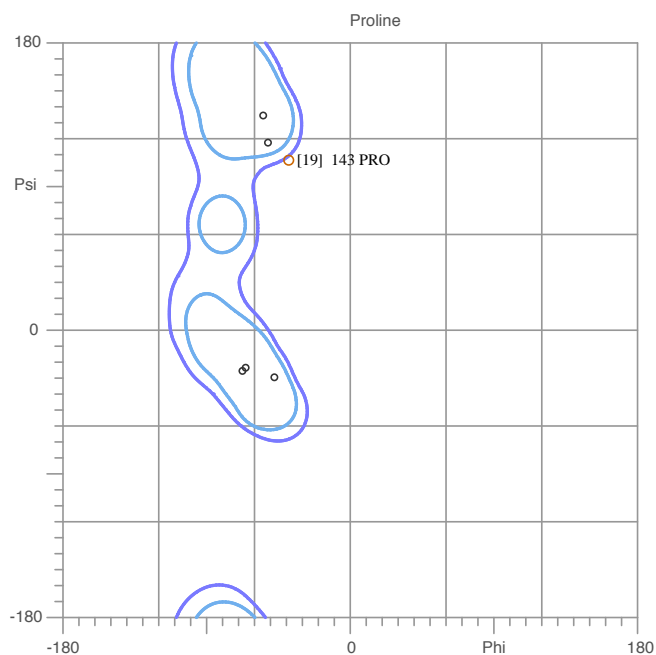
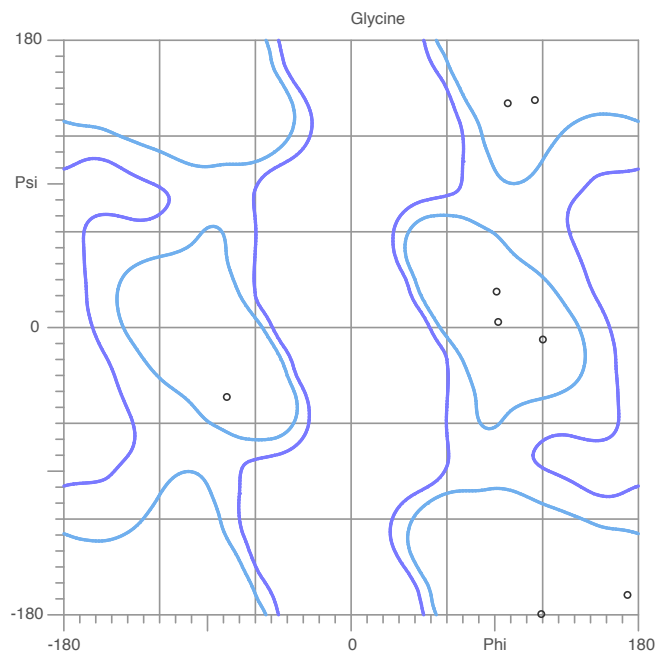
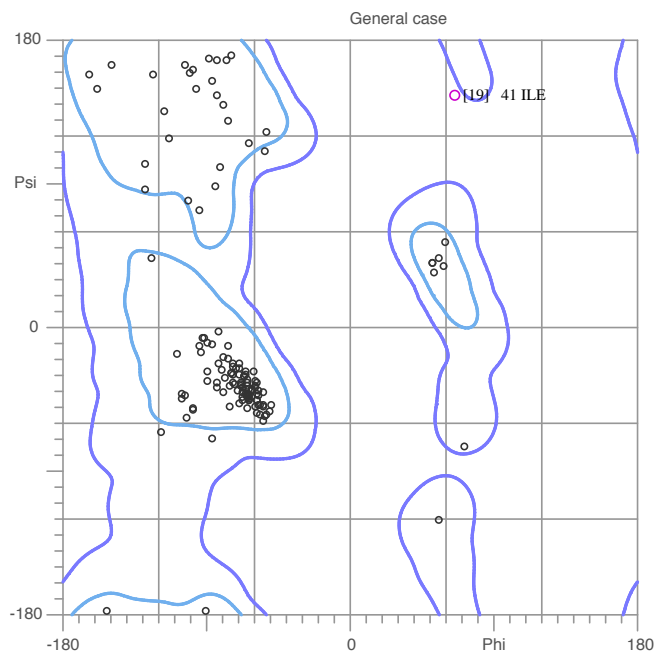
92.8% (142/153) of all residues were in favored (98%) regions.  
97.4% (149/153) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [18] 9 ALA (65.0, 95.1)
- [18] 13 LYS (67.9, 138.0)
- [18] 41 ILE (65.0, 105.0)
- [18] 154 HIS (65.0, 95.0)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 19

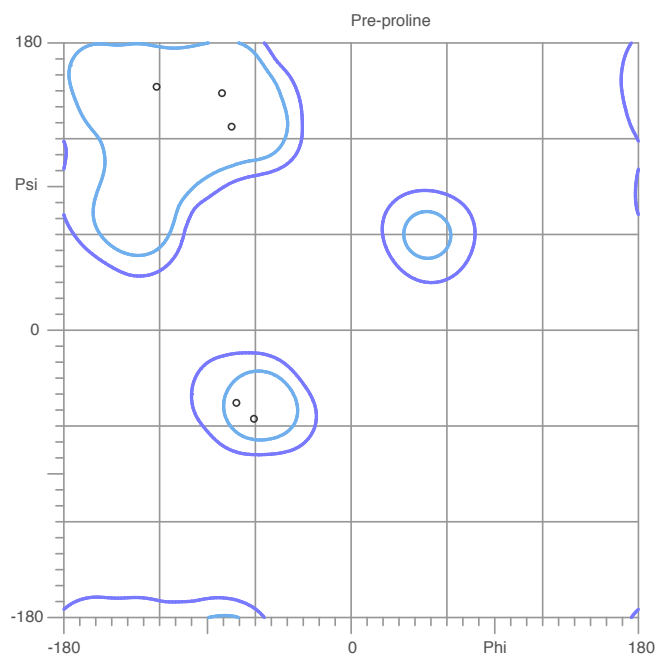
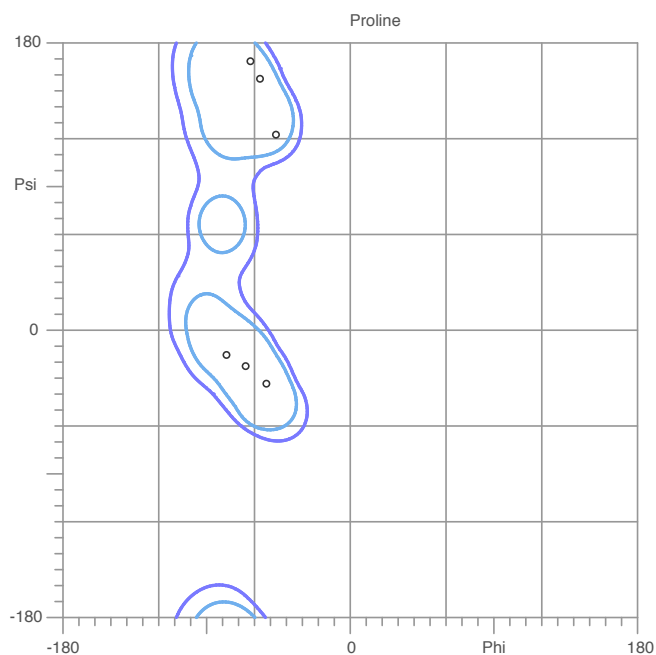
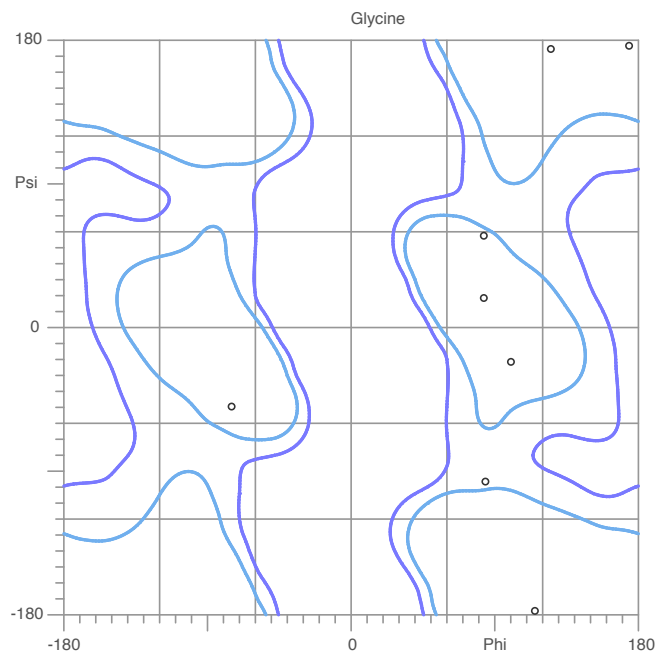
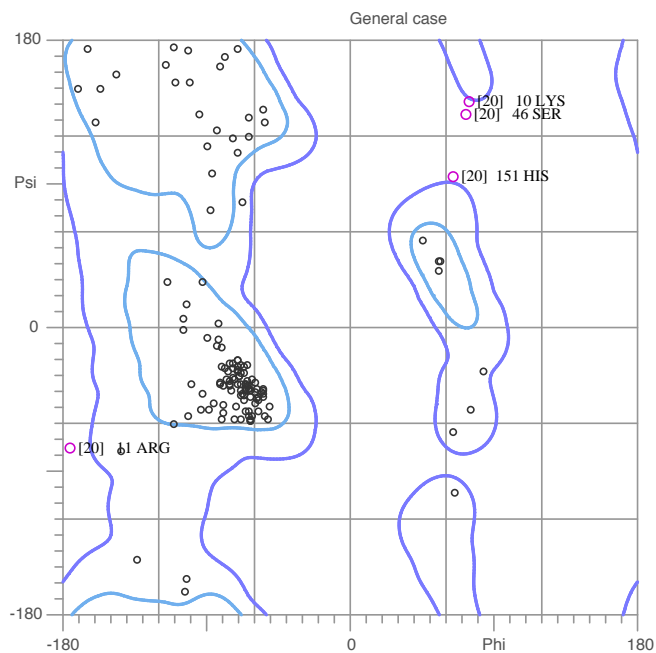


95.4% (146/153) of all residues were in favored (98%) regions.  
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):  
[19] 41 ILE (65.1, 146.8)  
[19] 143 PRO (-39.0, 107.3)

# MolProbity Ramachandran analysis

SGR209C\_R3\_em\_bcr3.pdb, model 20



90.8% (139/153) of all residues were in favored (98%) regions.  
97.4% (149/153) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [20] 10 LYS (74.9, 143.0)
- [20] 11 ARG (-176.8, -75.1)
- [20] 46 SER (72.6, 134.8)
- [20] 151 HIS (65.0, 95.0)