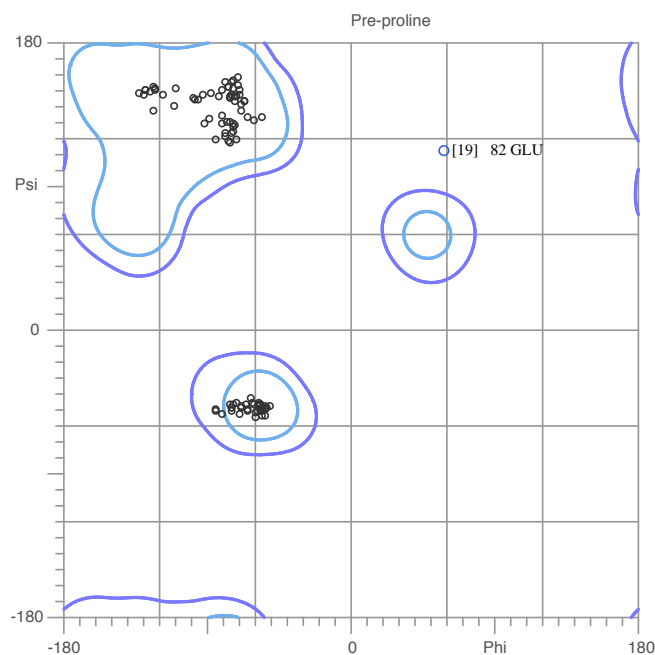
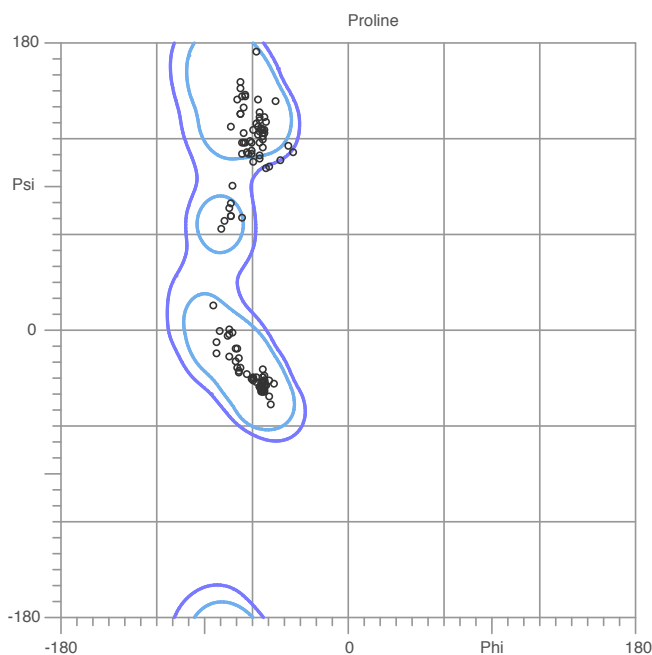
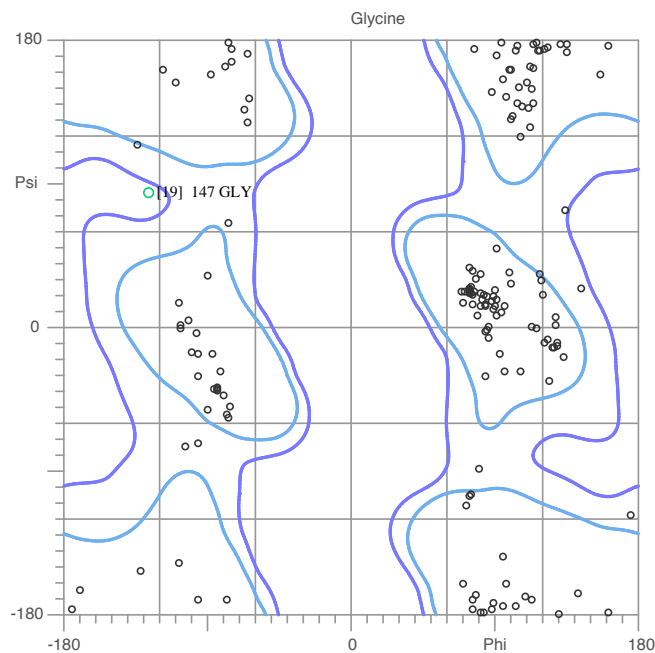
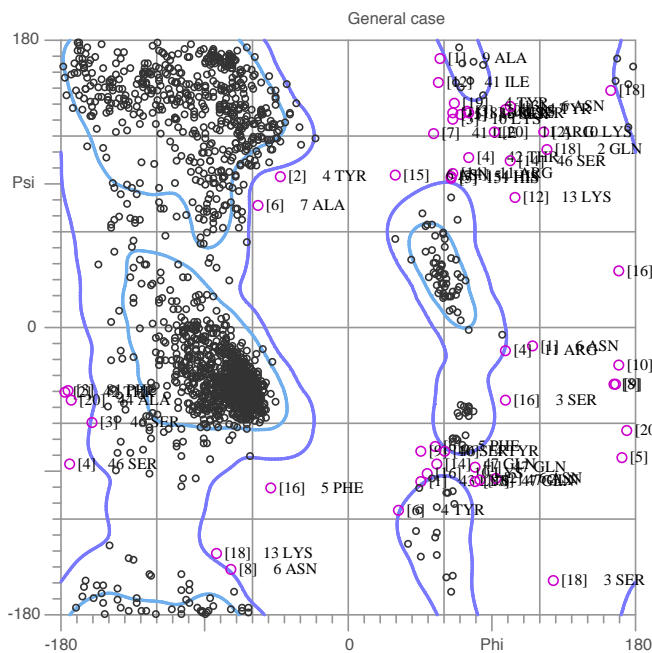


MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, all models



91.3% (2793/3060) of all residues were in favored (98%) regions.
98.2% (3008/3060) of all residues were in allowed (>99.8%) regions.

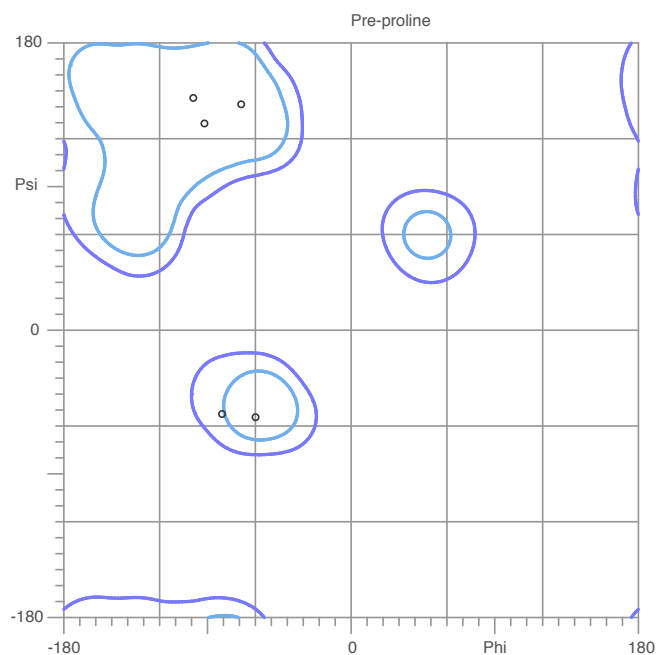
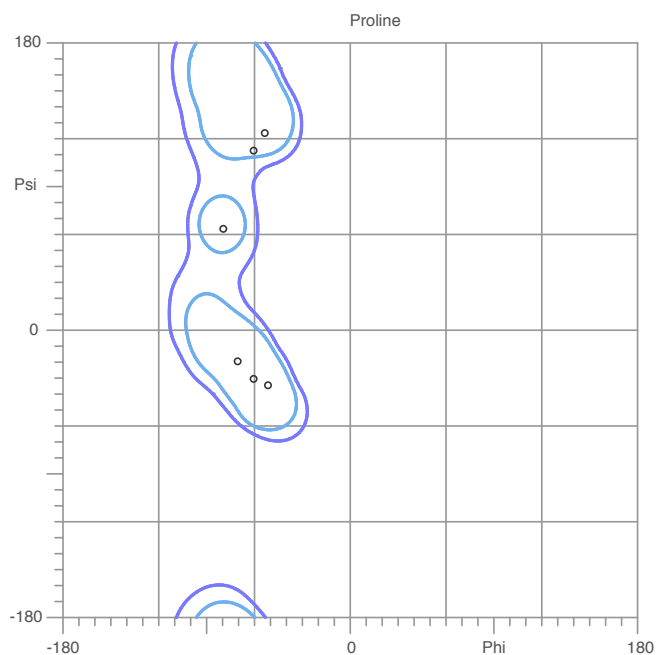
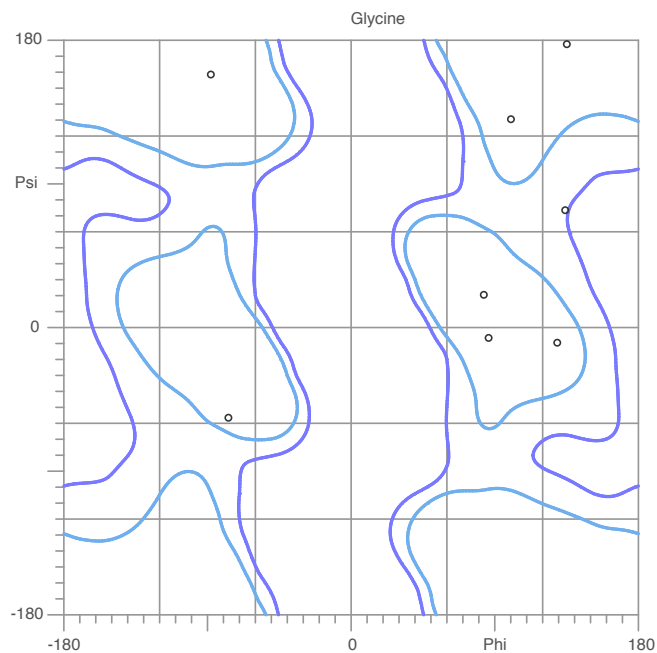
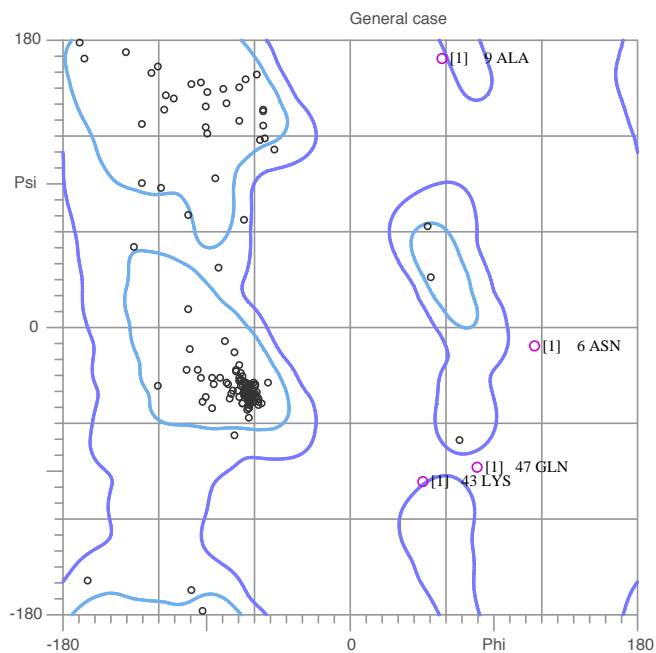
There were 55 outliers (phi, psi):

- [1] 6 ASN (115.6, -11.6)
- [11] 9 ALA (57.1, 169.7)
- [11] 43 LYS (45.2, -96.5)
- [11] 47 GLN (79.0, 87.3)
- [12] 4 TYR (-44.0, 95.7)
- [12] 6 ASN (92.7, -95.0)
- [12] 10 LYS (122.4, 124.0)
- [12] 42 THR (-178.9, -40.2)
- [13] 10 LYS (74.5, 137.0)
- [13] 46 SER (-161.7, -59.6)
- [13] 81 PHE (-176.4, -39.9)
- [14] 4 TYR (98.5, 137.3)
- [14] 11 ARG (98.7, -14.8)
- [14] 42 THR (75.0, 107.0)
- [14] 46 SER (-175.5, -85.1)
- [15] 10 LYS (66.0, 131.1)
- [15] 11 ARG (171.2, -81.3)
- [15] 46 SER (70.9, 134.8)
- [15] 151 HIS (65.0, 94.9)
- [16] 4 TYR (31.4, -114.3)
- [16] 5 PHE (54.2, -75.0)
- [16] 7 ALA (-57.5, 77.7)
- [17] 41 ILE (53.7, 122.0)
- [17] 54 HIS (65.0, 95.0)
- [18] 6 ASN (-74.8, -151.5)

- [8] 44 ALA (166.4, -35.1)
- [9] 41 ALA (167.5, -36.0)
- [9] 46 SER (45.4, -77.8)
- [10] 4 TYR (60.3, 77.2)
- [10] 44 ALA (169.8, -23.3)
- [11] 12 GLN (65.0, 135.0)
- [12] 13 LYS (104.3, 82.2)
- [12] 41 ILE (56.0, 154.2)
- [13] 6 ASN (101.9, 139.1)
- [14] 11 ARG (65.0, 97.7)
- [14] 46 SER (101.2, 105.3)
- [14] 47 GLN (55.2, -85.4)
- [15] 6 ASN (29.6, 96.1)
- [16] 2 GLN (169.5, 36.1)
- [16] 3 SER (98.6, -45.7)
- [16] 5 PHE (-49.0, -100.4)
- [16] 10 LYS (49.1, 91.7)
- [16] 47 GLN (82.9, -95.2)
- [17] 47 GLN (79.7, -96.0)
- [18] 2 GLN (124.6, 112.9)
- [18] 3 SER (128.1, -158.6)
- [18] 13 LYS (-83.0, -141.6)
- [18] 40 ASP (164.1, 149.1)
- [18] 46 SER (75.4, 135.0)
- [19] 4 TYR (66.7, 141.8)
- [19] 82 GLU (58.6, 113.3)
- [19] 147 GLY (-128.0, 85.0)
- [20] 11 ARG (91.7, 123.8)
- [20] 44 ALA (-174.9, -45.8)
- [20] 81 PHE (174.9, -64.6)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 1



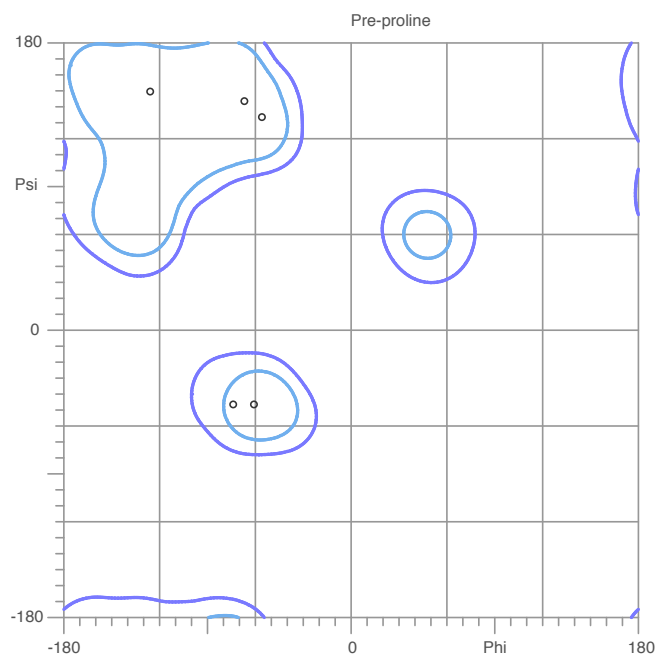
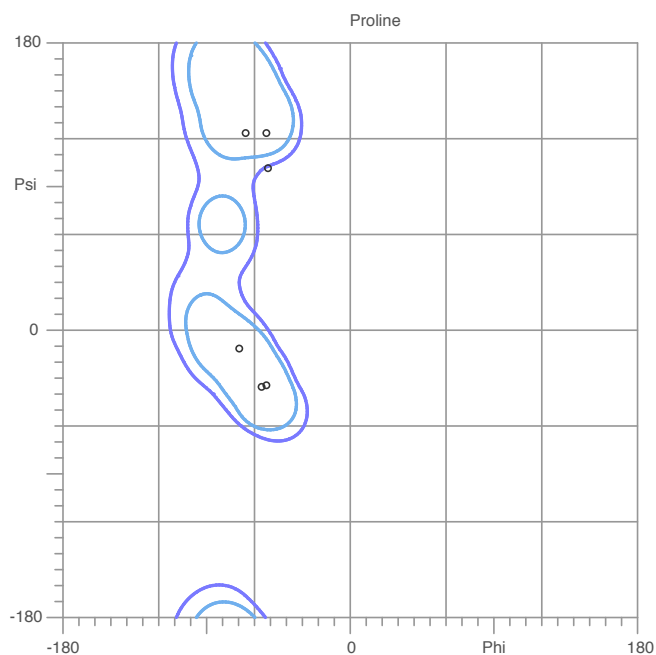
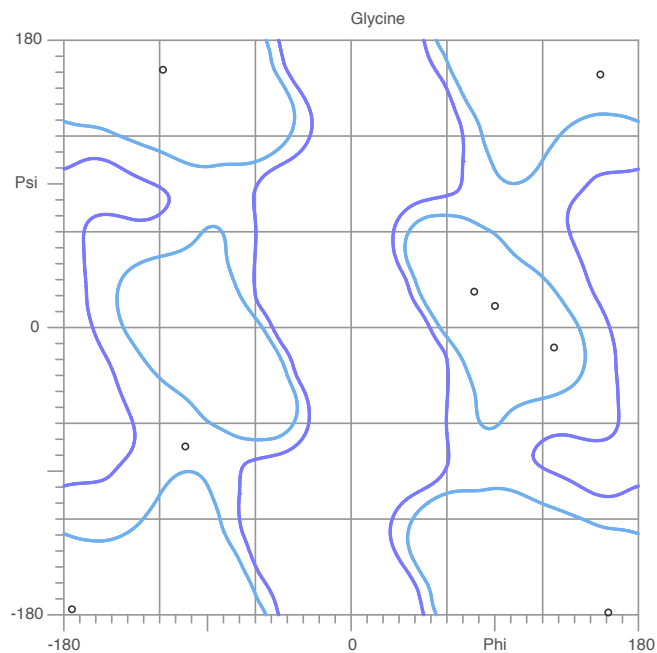
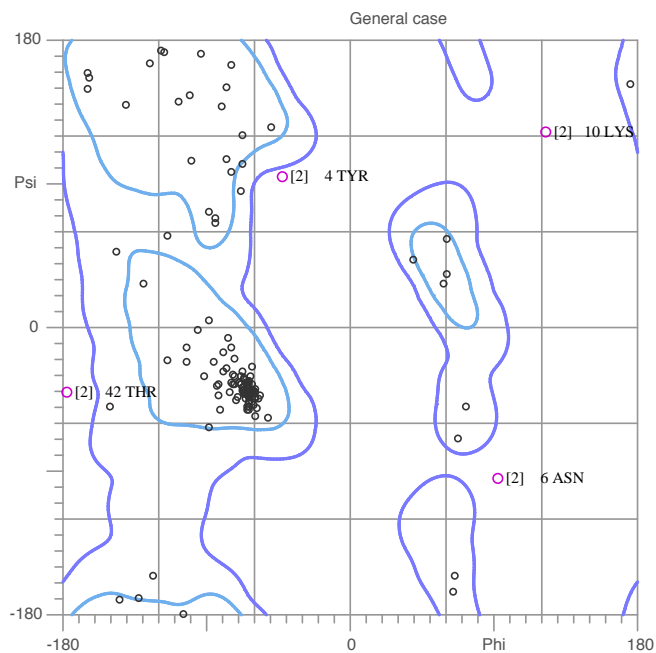
90.2% (138/153) of all residues were in favored (98%) regions.
97.4% (149/153) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [1] 6 ASN (115.6, -11.6)
- [1] 9 ALA (57.1, 169.7)
- [1] 43 LYS (45.2, -96.5)
- [1] 47 GLN (79.0, -87.3)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 2



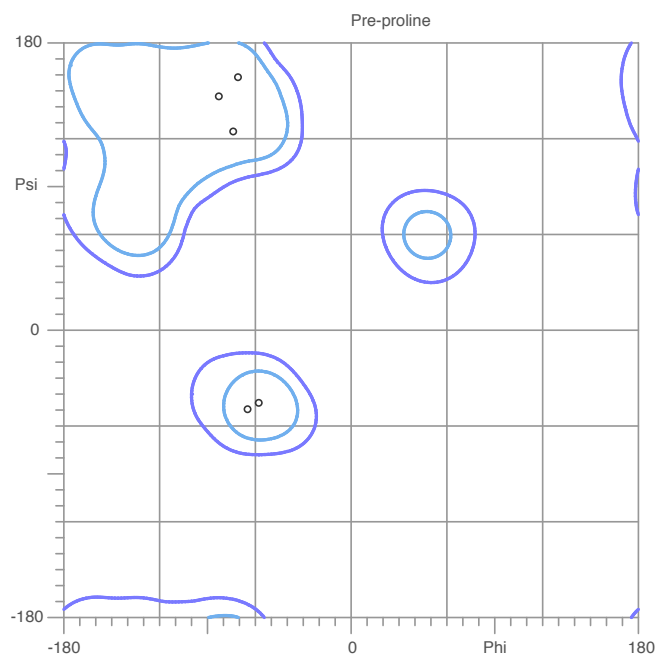
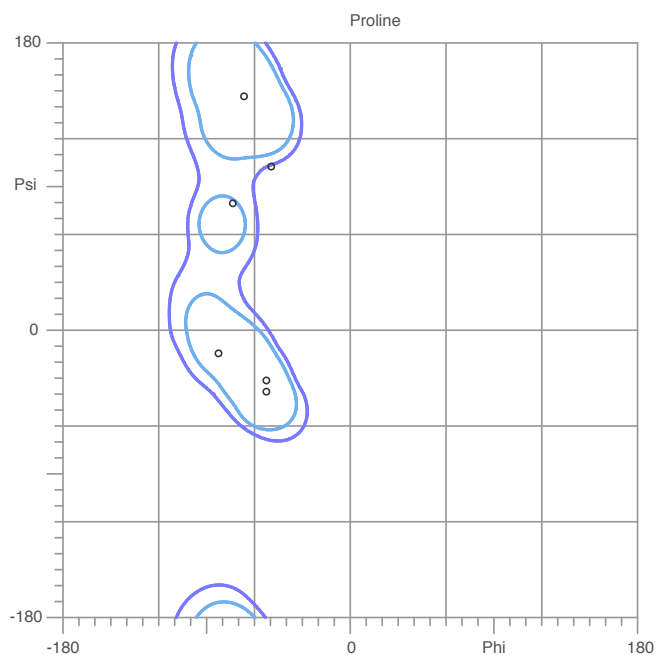
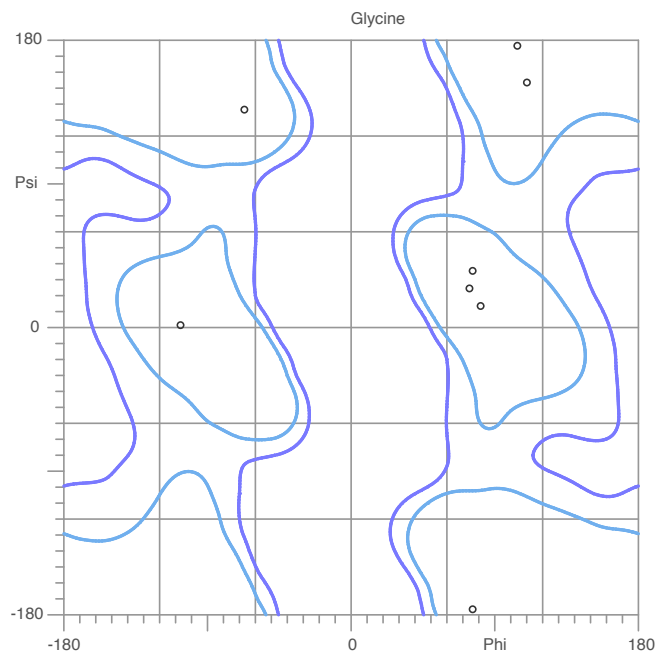
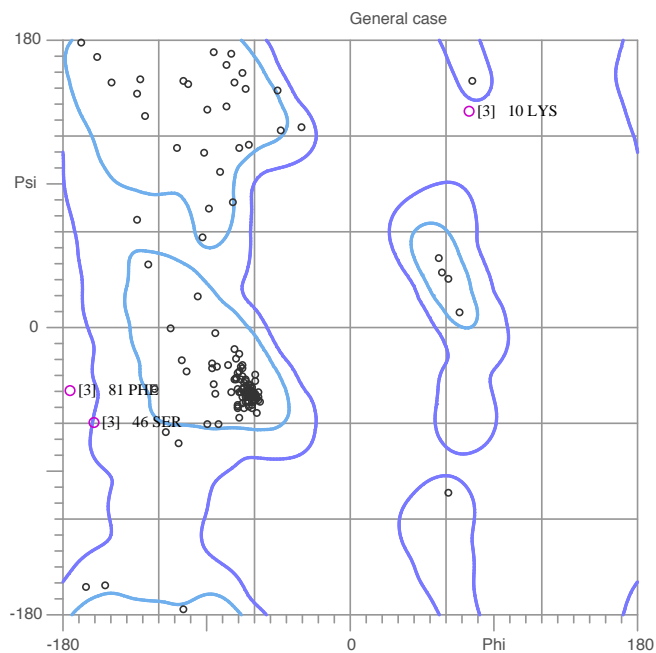
88.2% (135/153) of all residues were in favored (98%) regions.
97.4% (149/153) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [2] 4 TYR (-44.0, 95.7)
- [2] 6 ASN (92.7, -95.0)
- [2] 10 LYS (122.4, 124.0)
- [2] 42 THR (-178.9, -40.2)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 3



91.5% (140/153) 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):

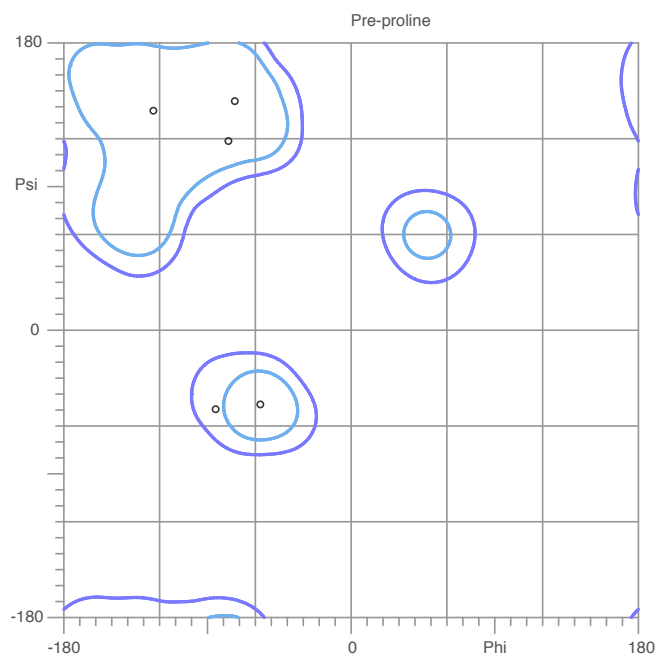
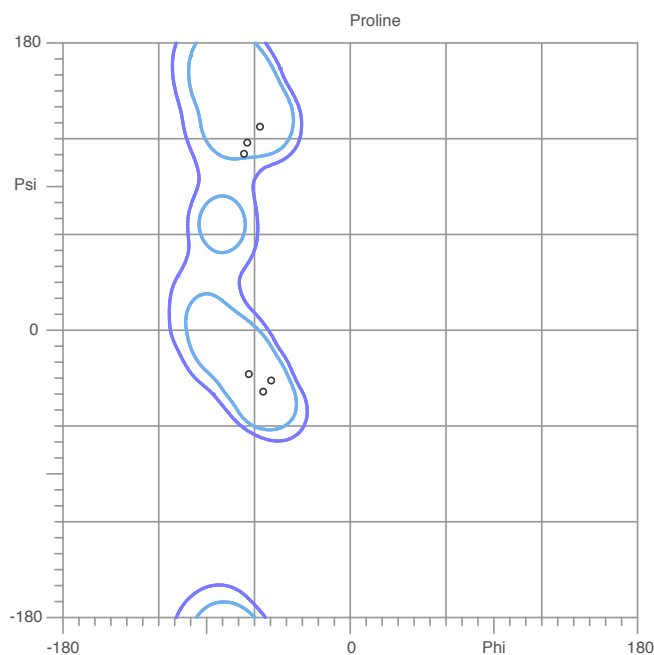
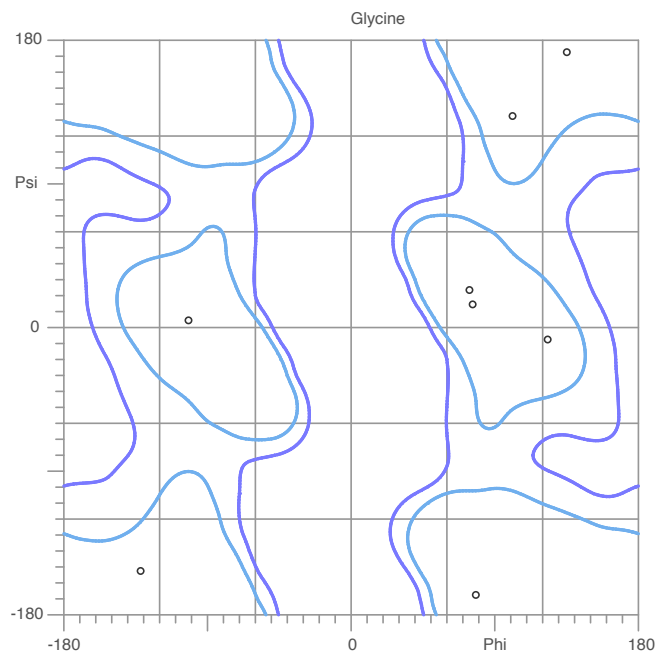
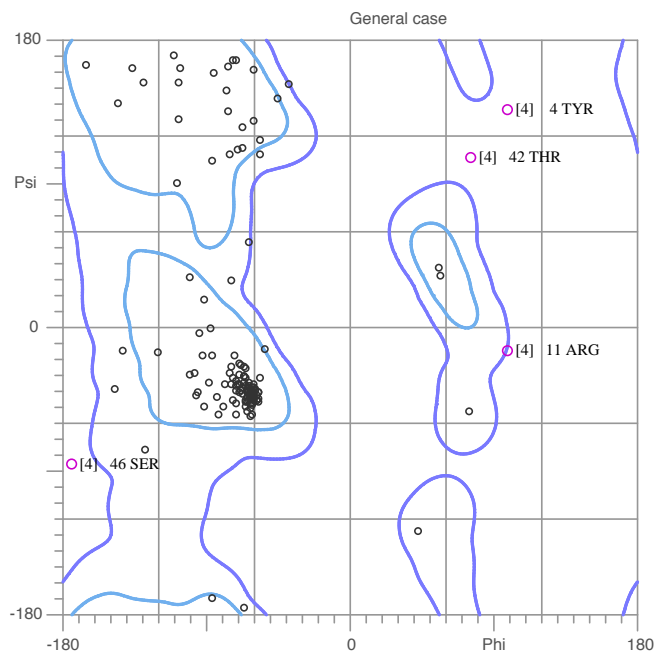
[3] 10 LYS (74.5, 137.0)

[3] 46 SER (-161.7, -59.6)

[3] 81 PHE (-176.4, -39.9)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 4



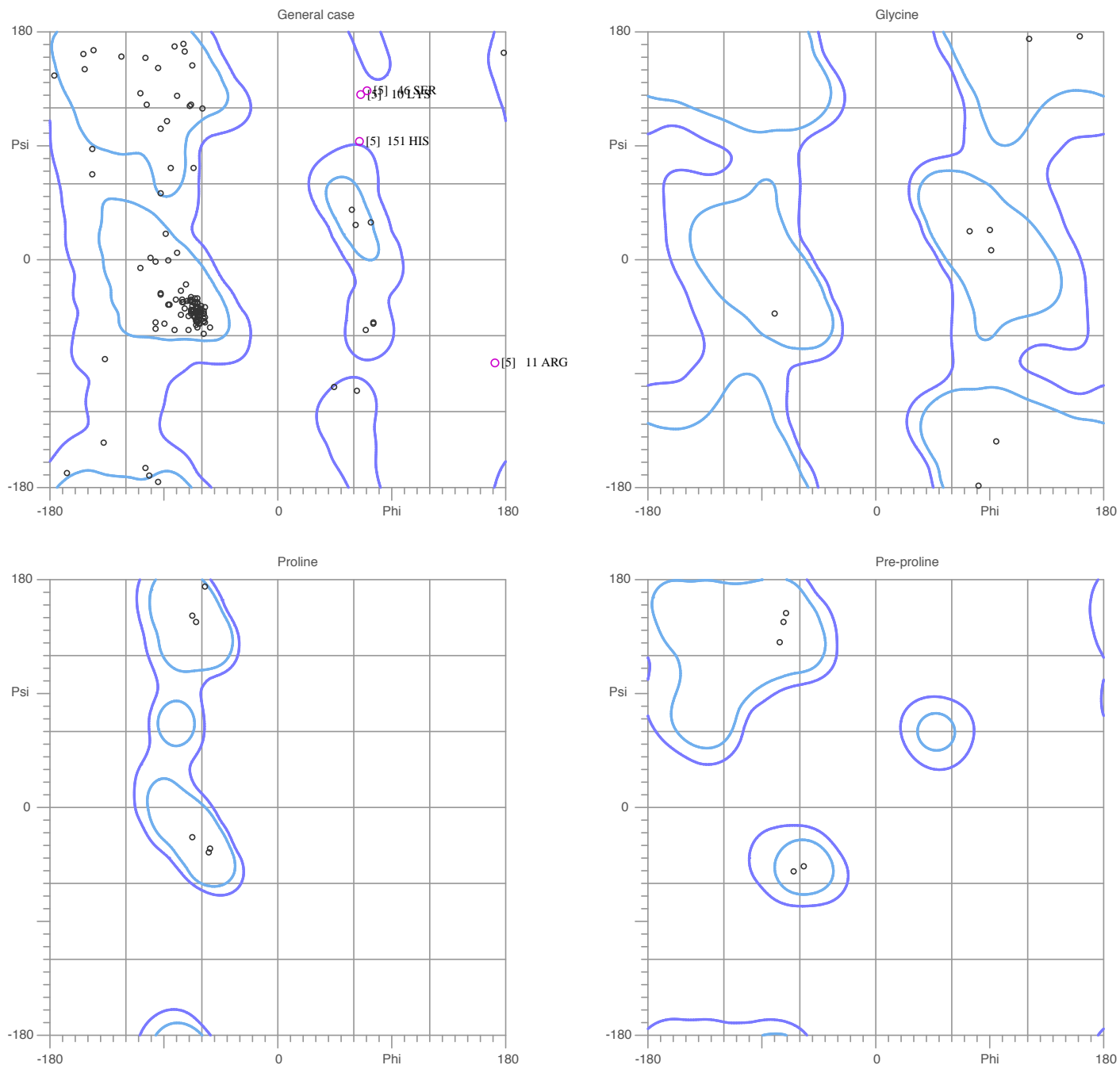
90.2% (138/153) of all residues were in favored (98%) regions.
97.4% (149/153) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [4] 4 TYR (98.5, 137.3)
- [4] 11 ARG (98.7, -14.8)
- [4] 42 THR (75.0, 107.0)
- [4] 46 SER (-175.5, -85.1)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 5



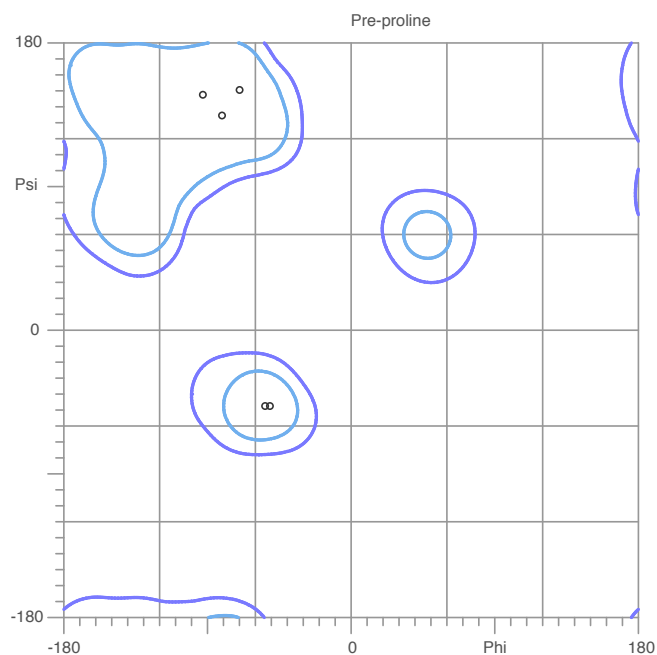
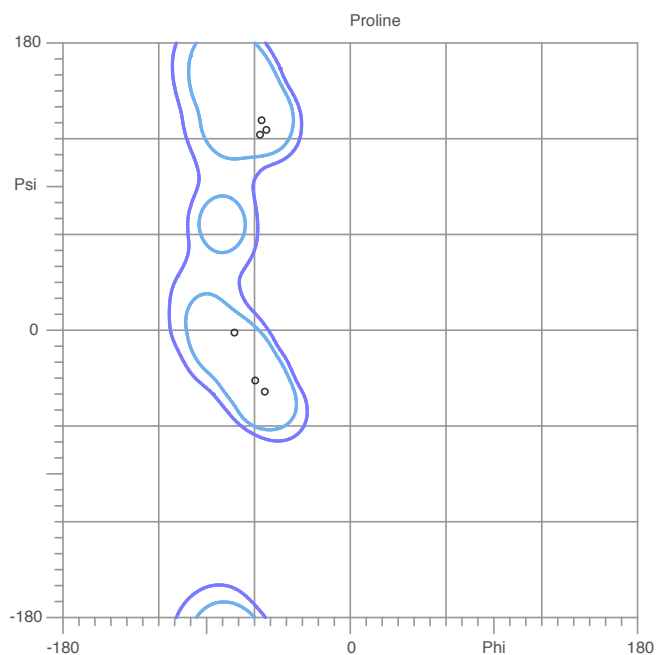
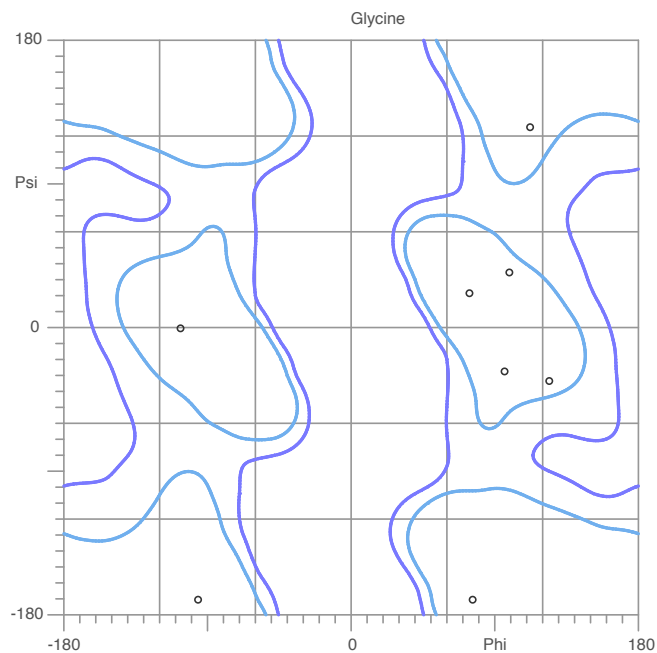
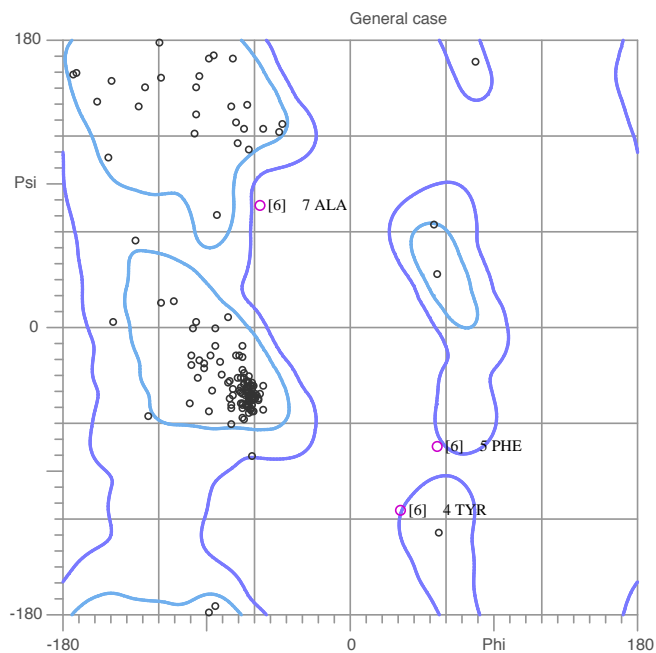
87.6% (134/153) of all residues were in favored (98%) regions.
97.4% (149/153) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [5] 10 LYS (66.0, 131.1)
- [5] 11 ARG (171.2, -81.3)
- [5] 46 SER (70.9, 134.8)
- [5] 151 HIS (65.0, 94.9)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 6



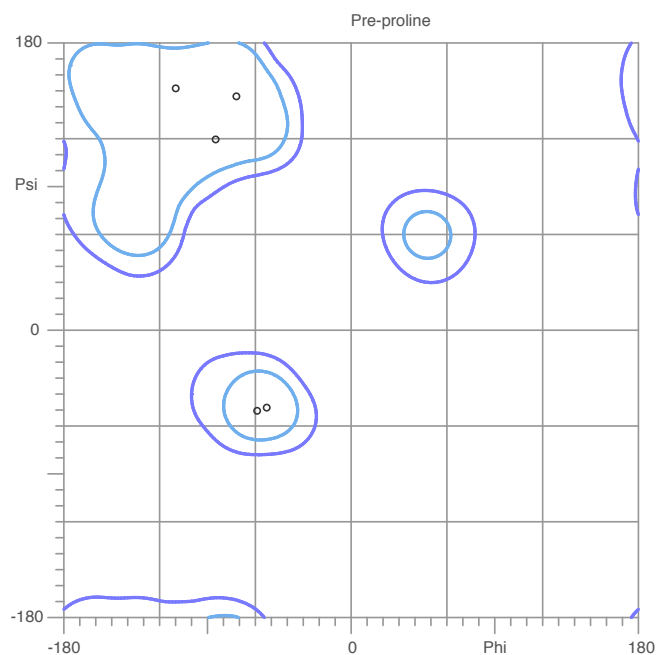
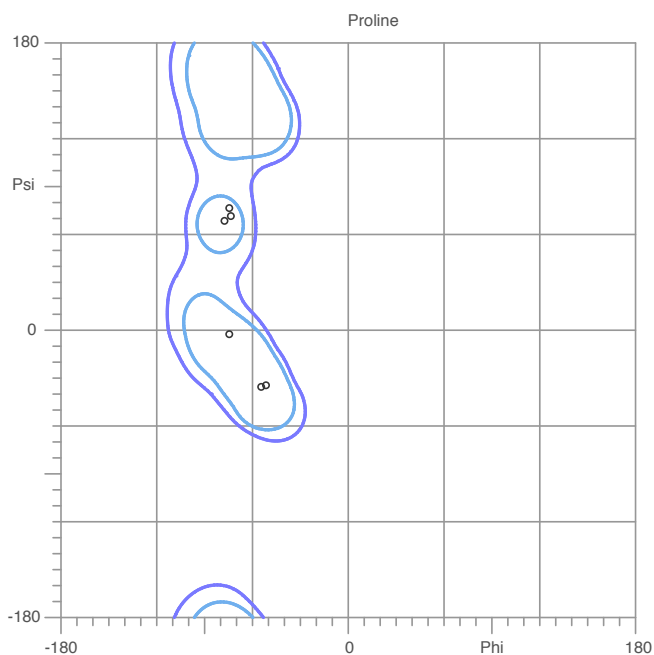
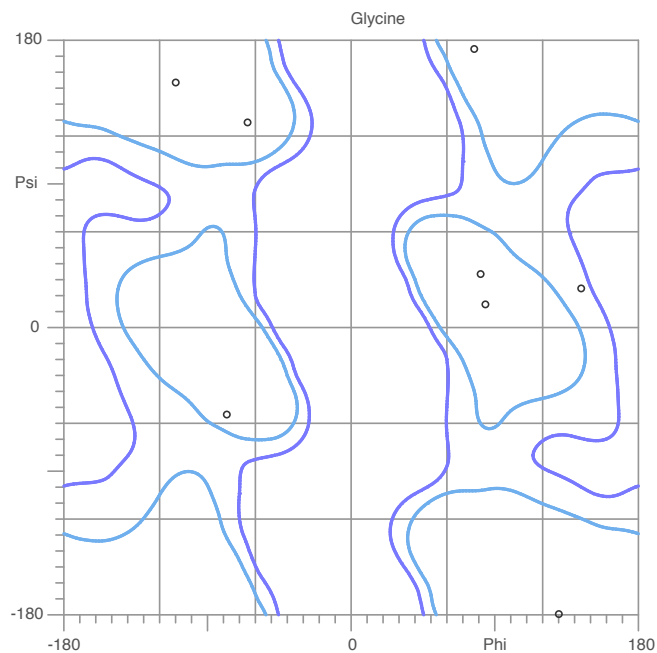
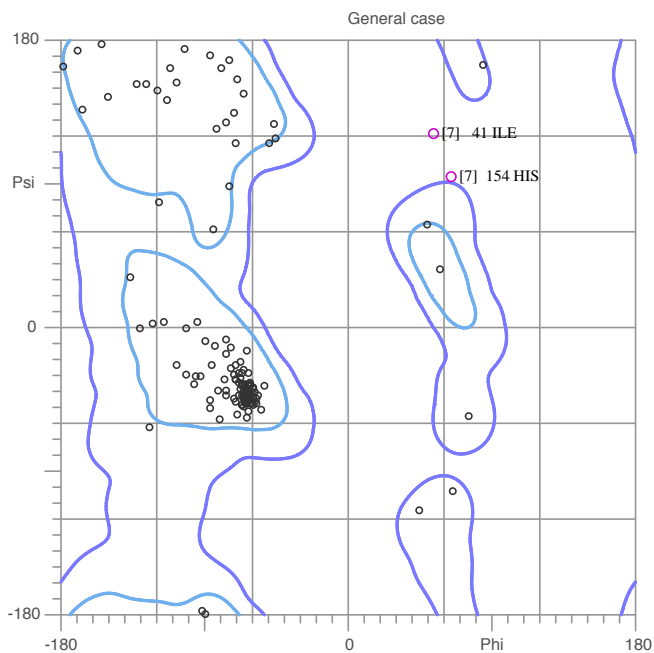
93.5% (143/153) of all residues were in favored (98%) regions.
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 4 TYR (31.4, -114.3)
- [6] 5 PHE (54.2, -75.0)
- [6] 7 ALA (-57.5, 77.7)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 7



93.5% (143/153) of all residues were in favored (98%) regions.
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

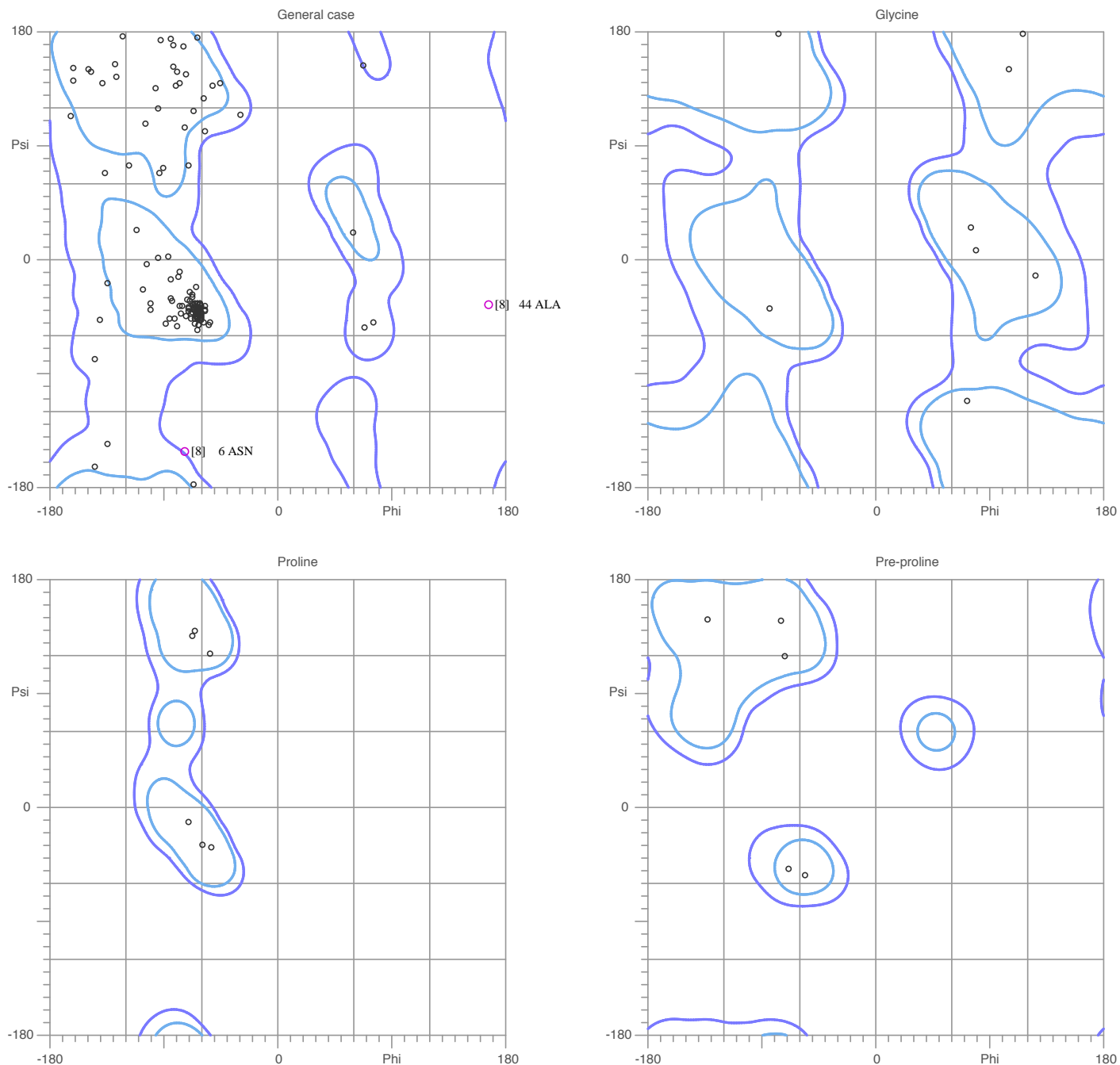
There were 2 outliers (phi, psi):

[7] 41 ILE (53.7, 122.0)

[7] 154 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 8



88.2% (135/153) of all residues were in favored (98%) regions.
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

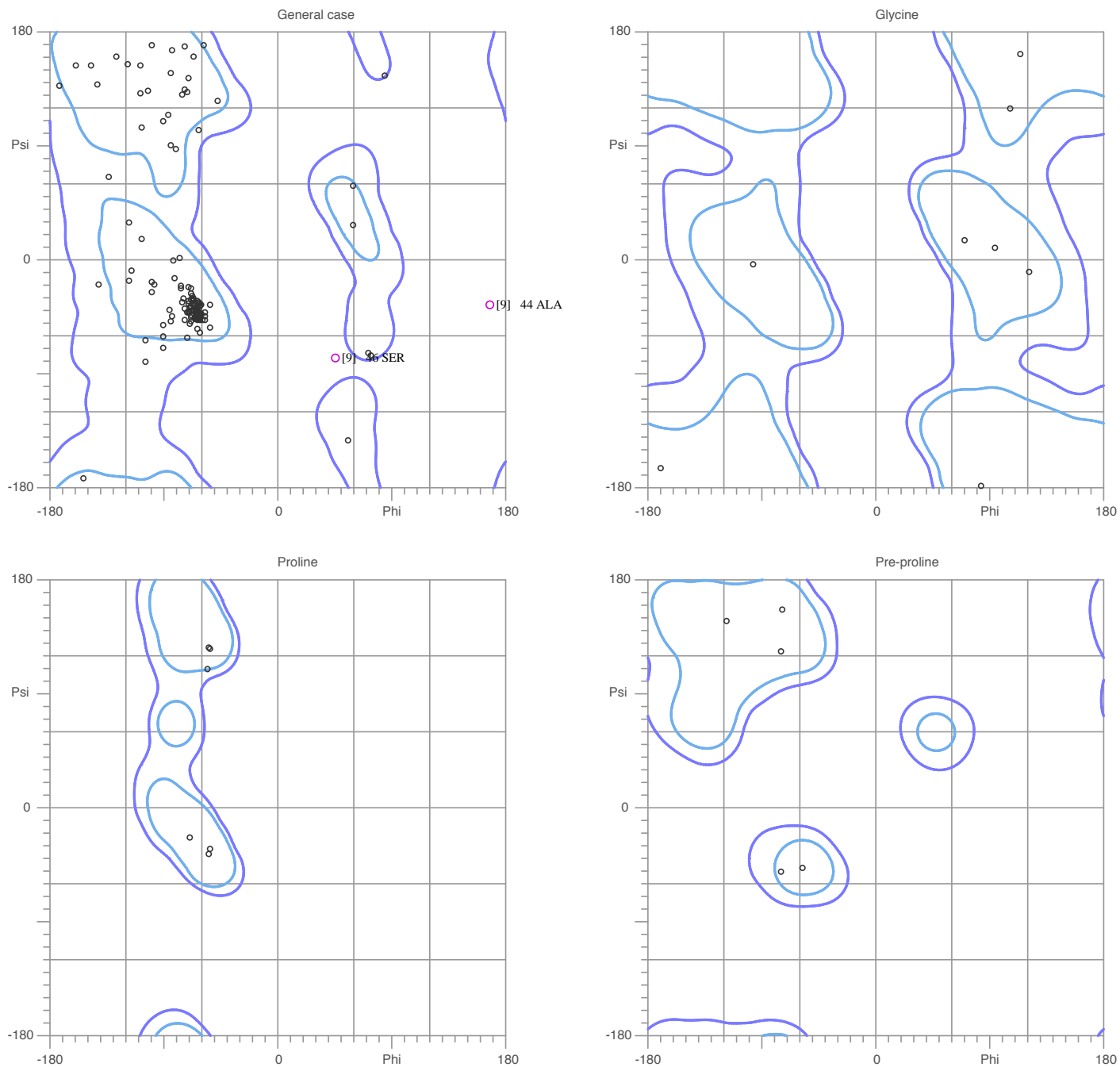
There were 2 outliers (phi, psi):

[8] 6 ASN (-74.8, -151.5)

[8] 44 ALA (166.4, -35.1)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 9



90.8% (139/153) of all residues were in favored (98%) regions.
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

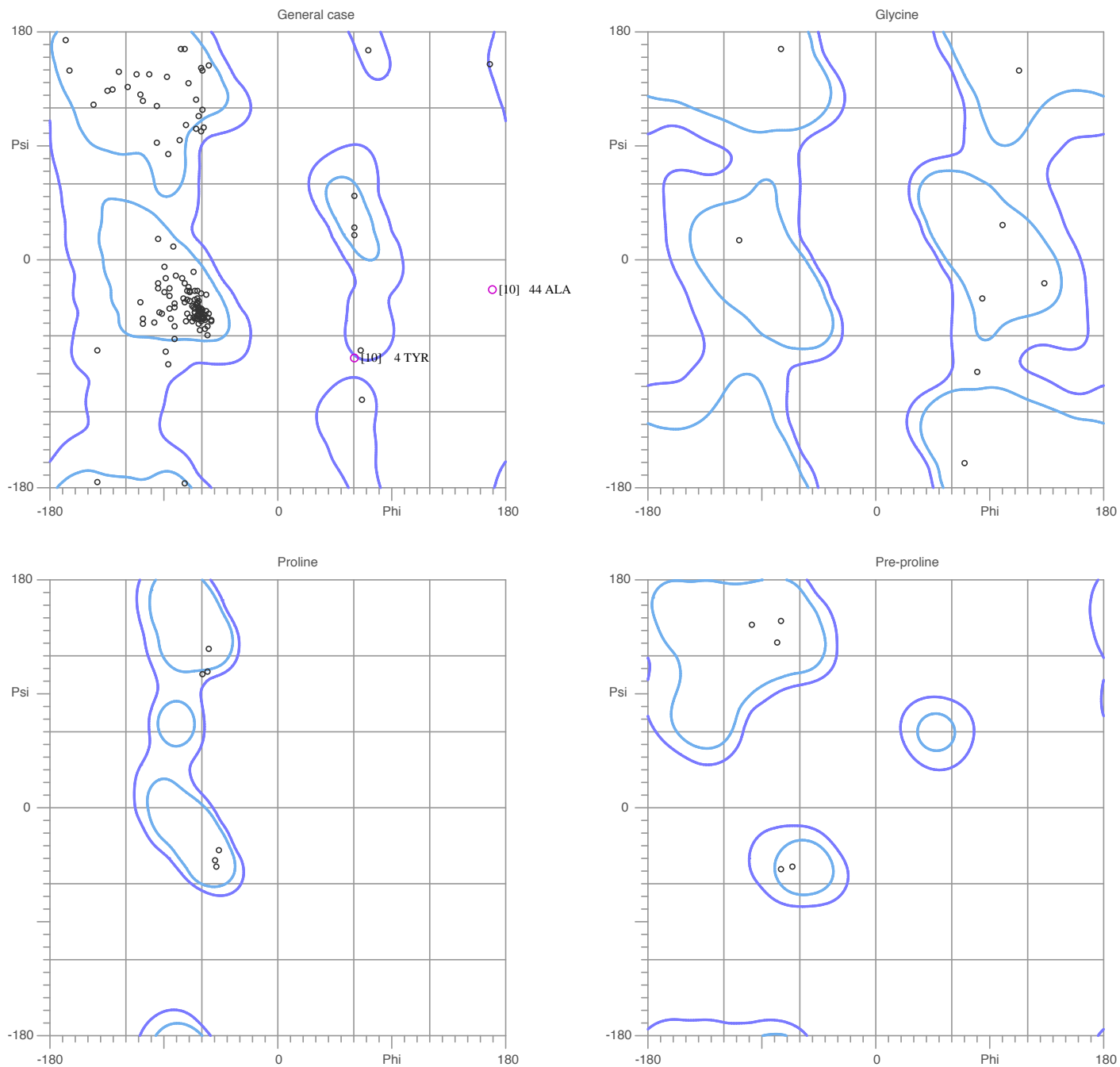
There were 2 outliers (phi, psi):

[9] 44 ALA (167.5, -36.0)

[9] 46 SER (45.4, -77.8)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 10



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.

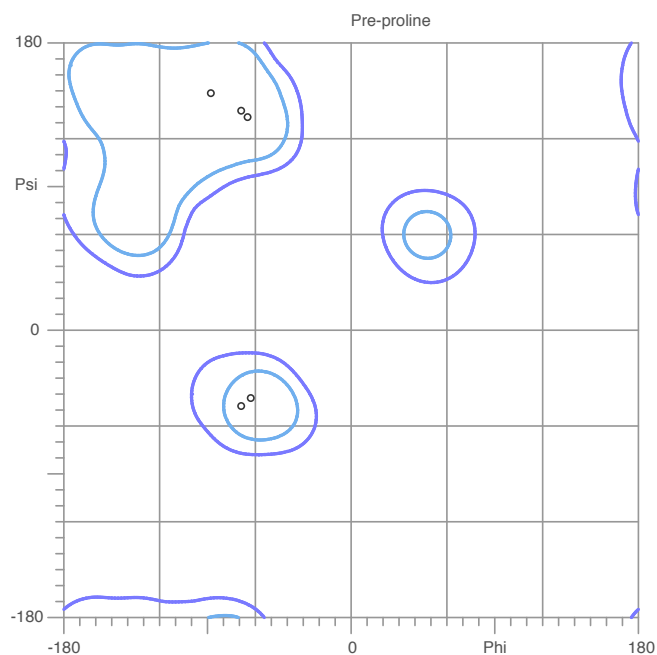
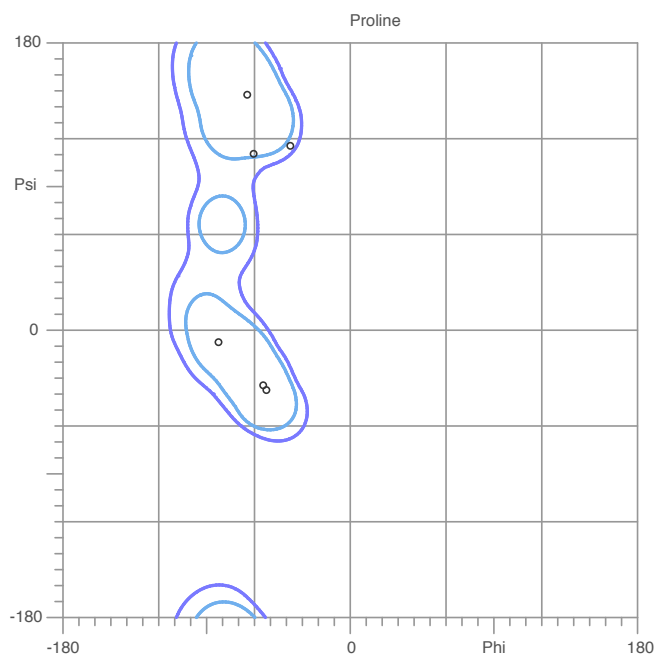
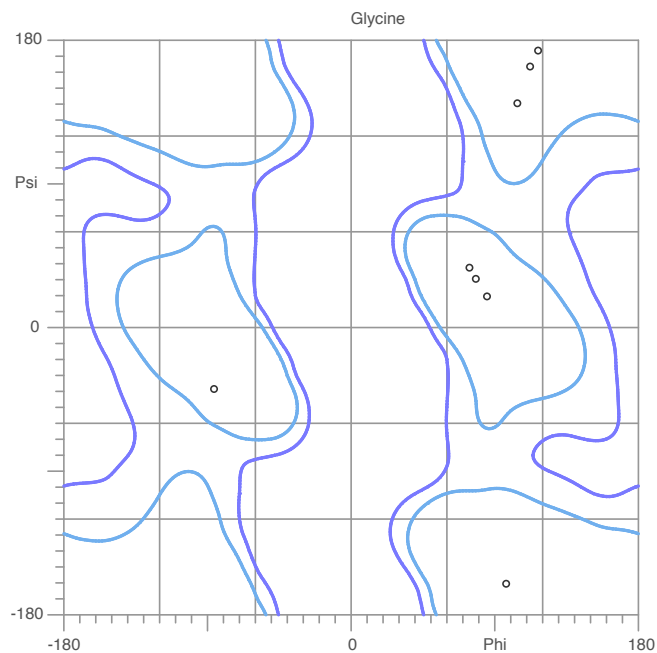
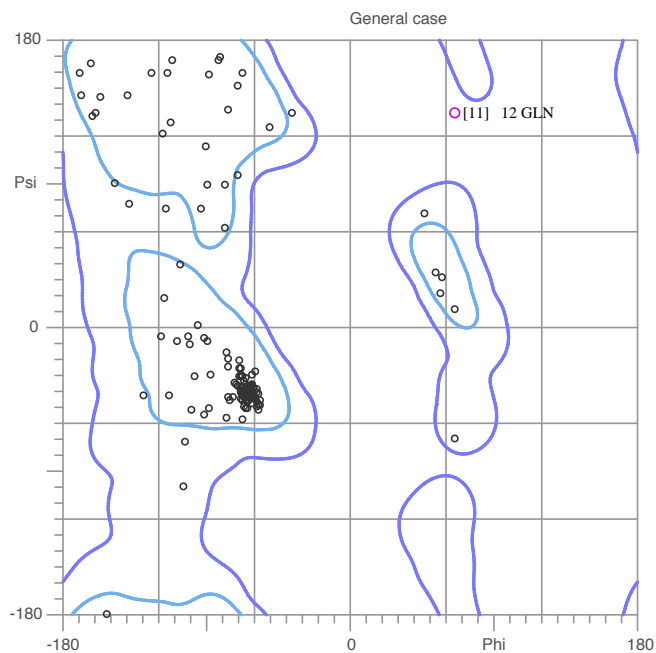
There were 2 outliers (phi, psi):

[10] 4 TYR (60.3, -77.2)

[10] 44 ALA (169.8, -23.3)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 11



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.

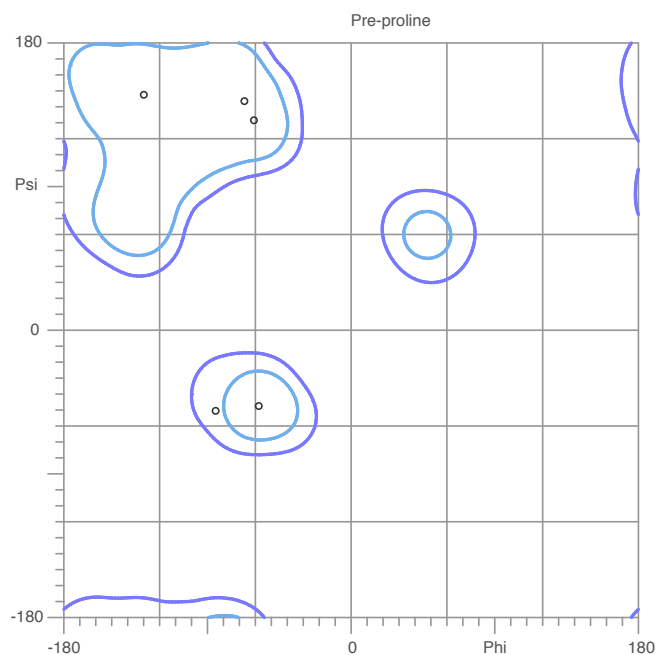
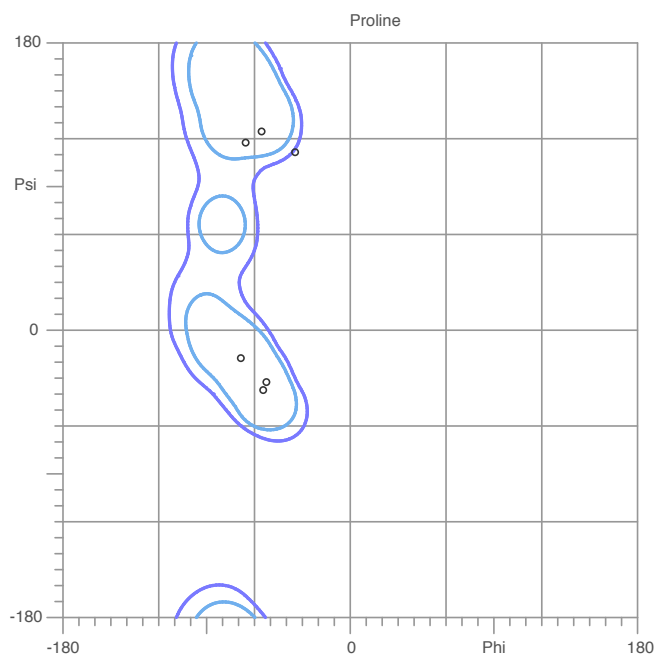
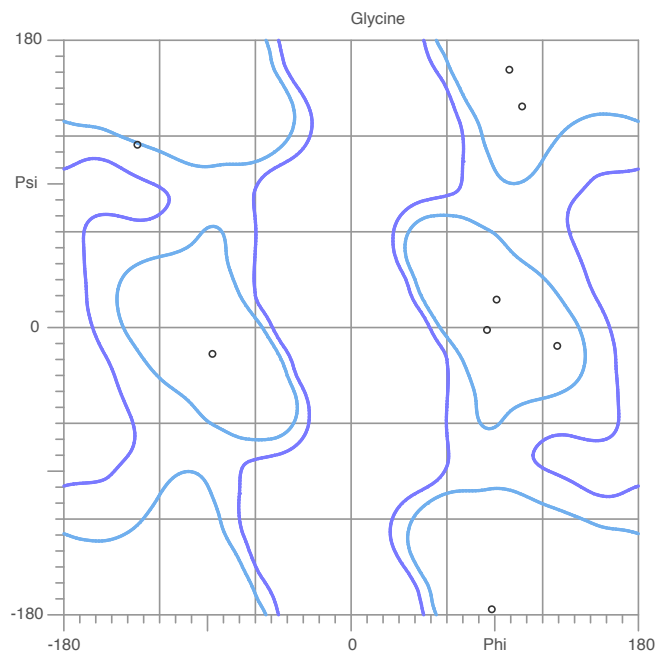
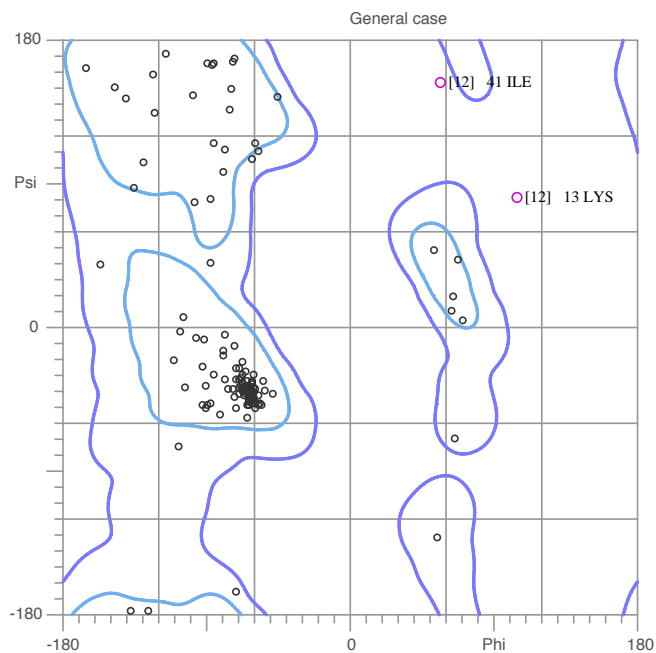
There were 1 outliers (phi, psi):
[11] 12 GLN (65.0, 135.0)

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

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

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 12

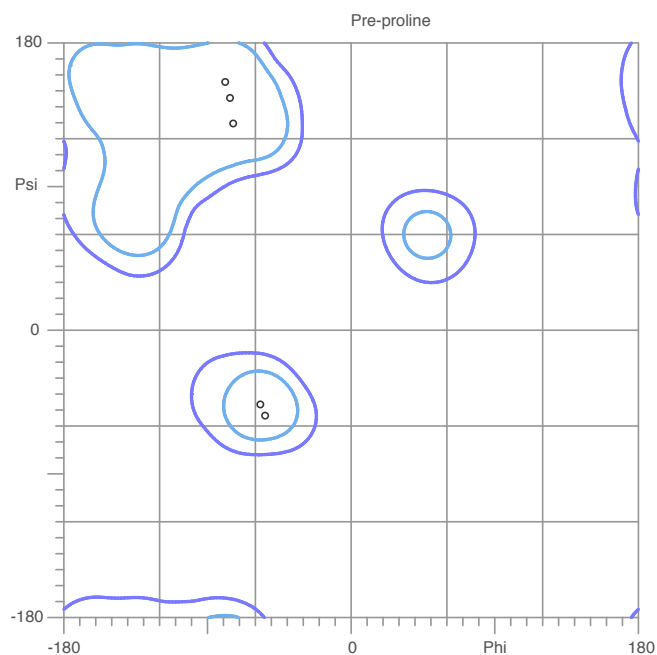
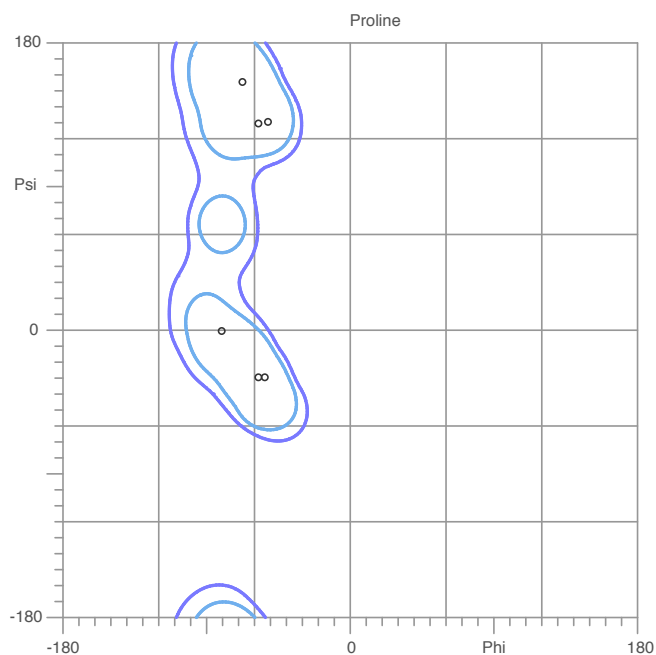
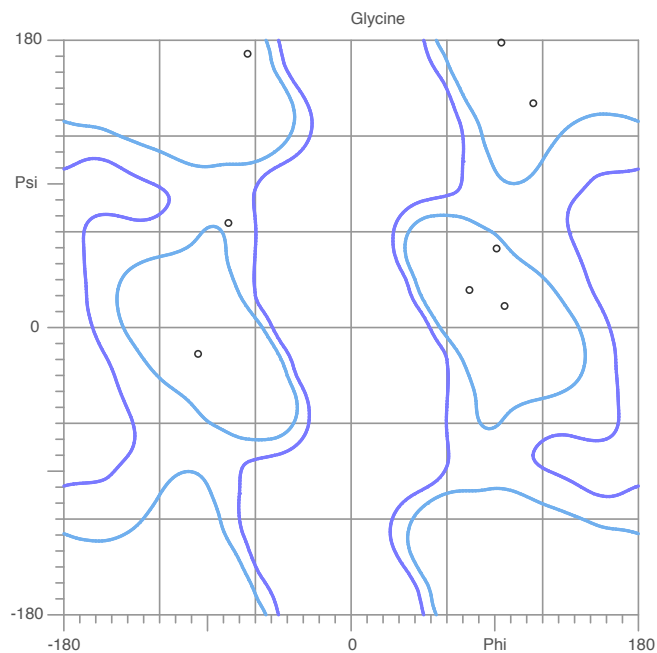
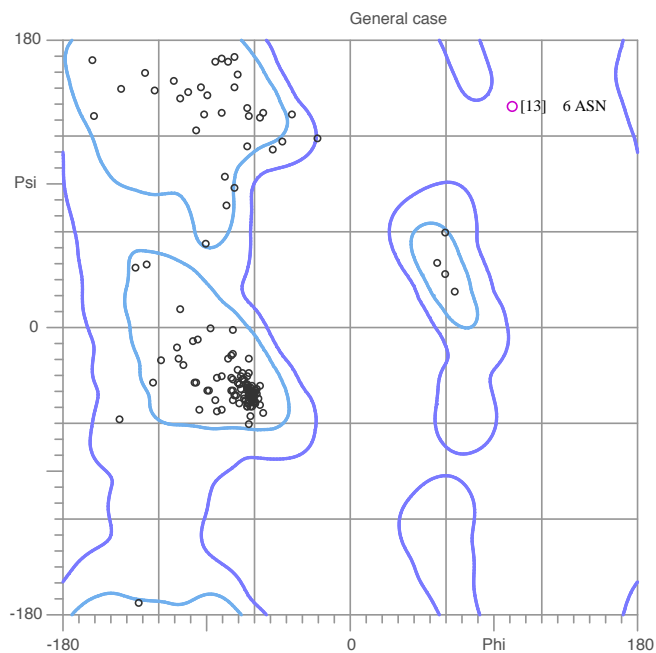


92.8% (142/153) of all residues were in favored (98%) regions.
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 13 LYS (104.3, 82.2)
[12] 41 ILE (56.0, 154.2)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 13



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.

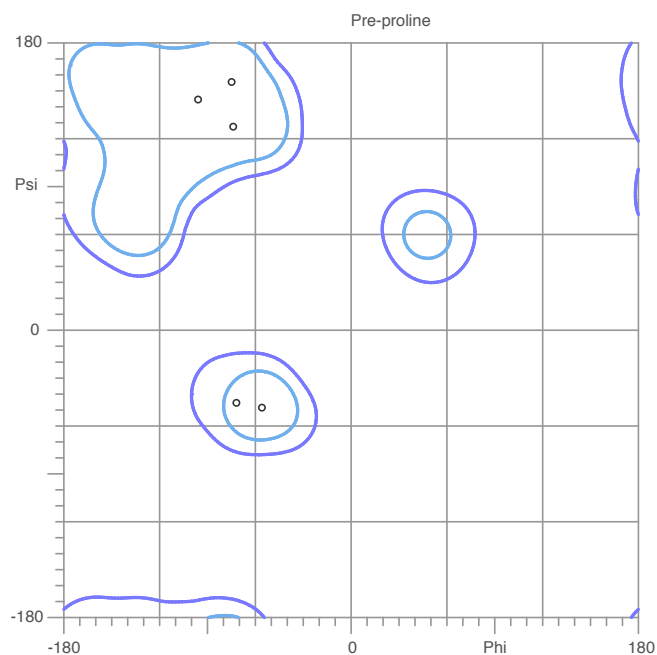
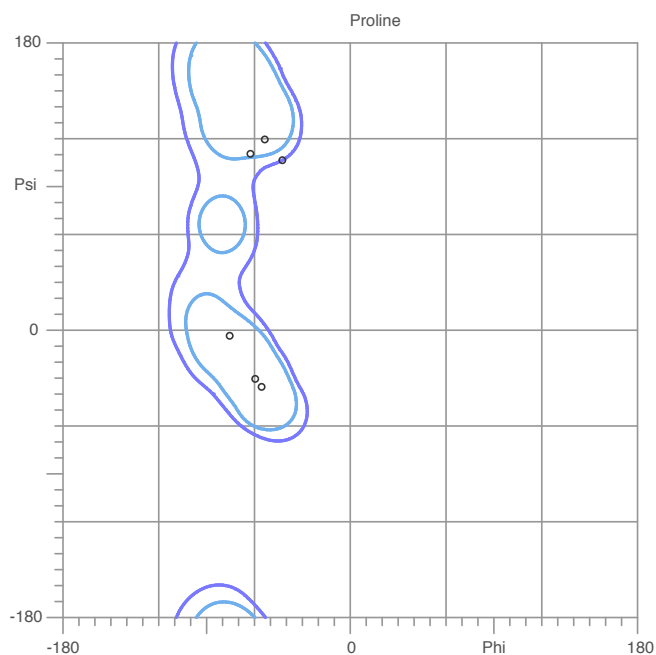
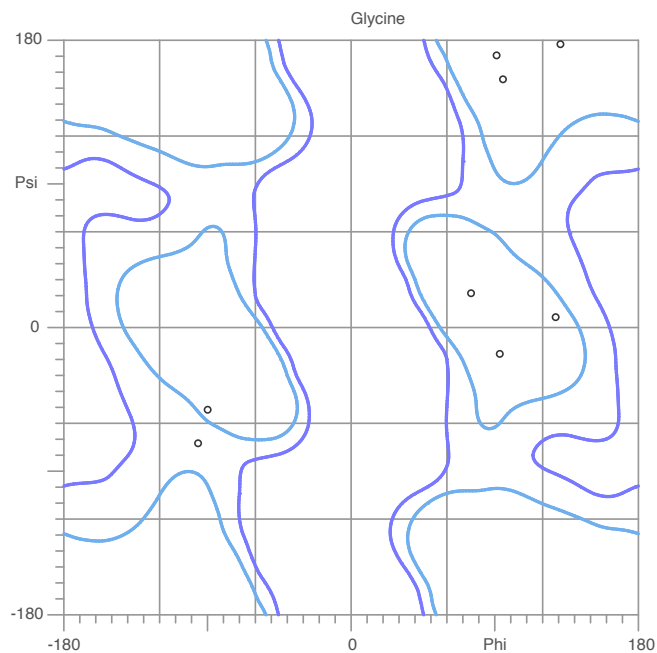
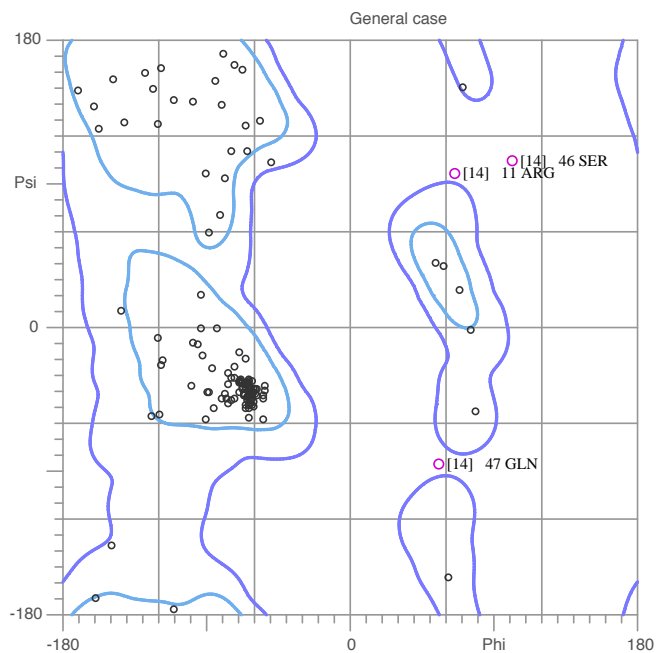
There were 1 outliers (phi, psi):
[13] 6 ASN (101.9, 139.1)

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

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

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 14



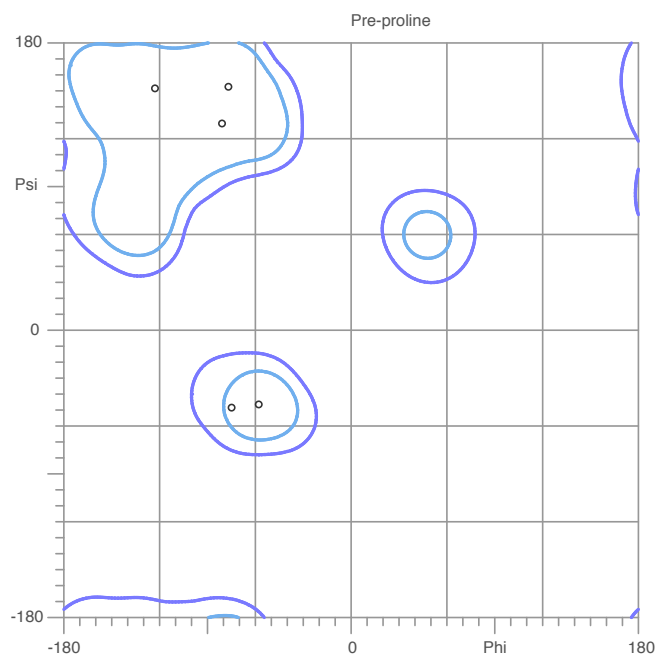
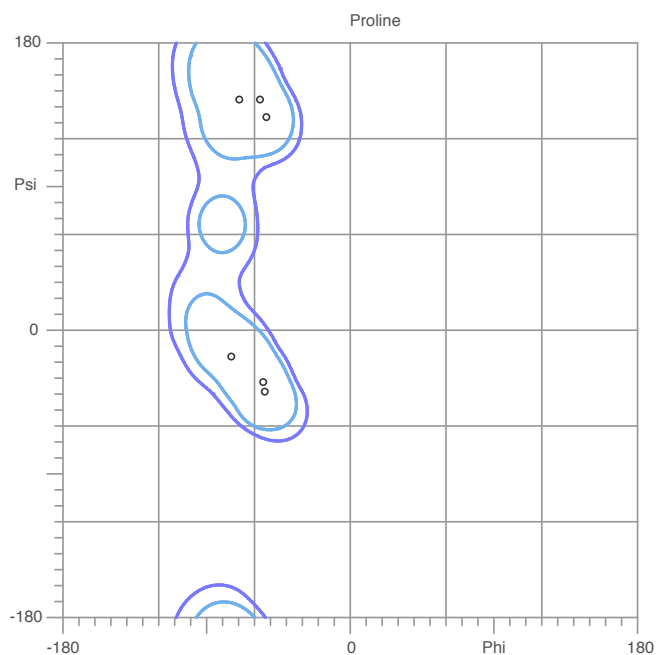
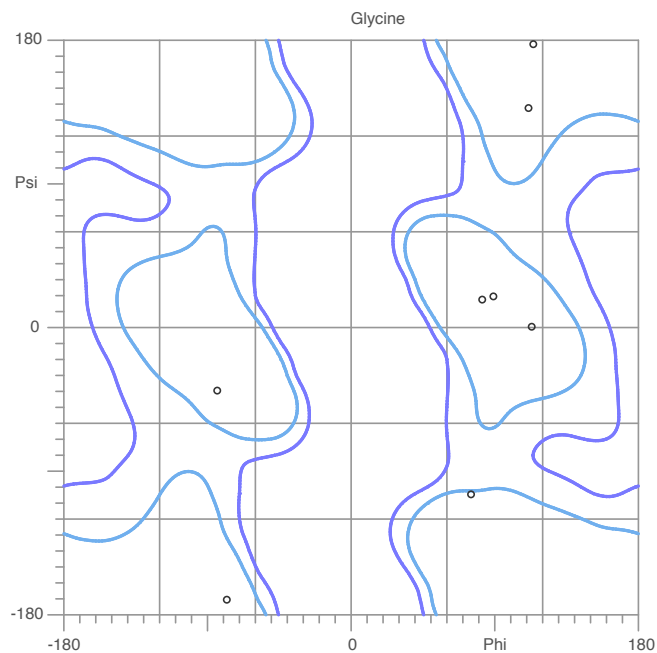
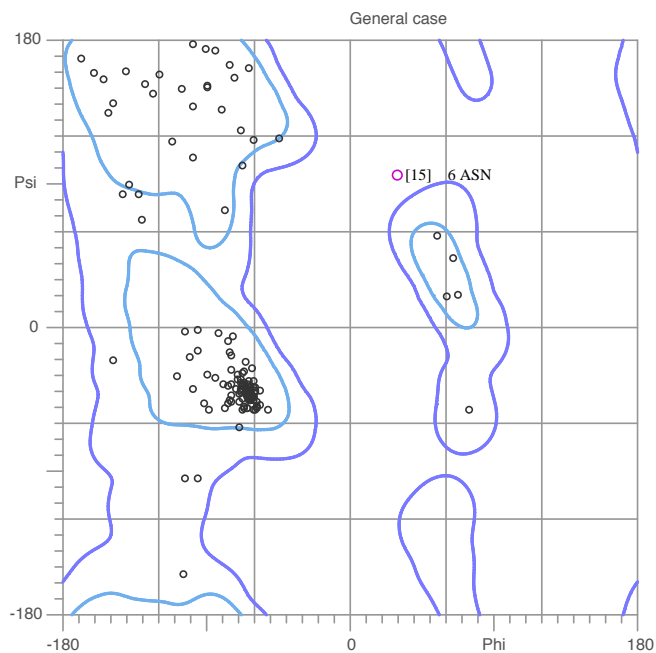
91.5% (140/153) of all residues were in favored (98%) regions.
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [14] 11 ARG (65.0, 97.7)
- [14] 46 SER (101.2, 105.3)
- [14] 47 GLN (55.2, -85.4)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 15



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.

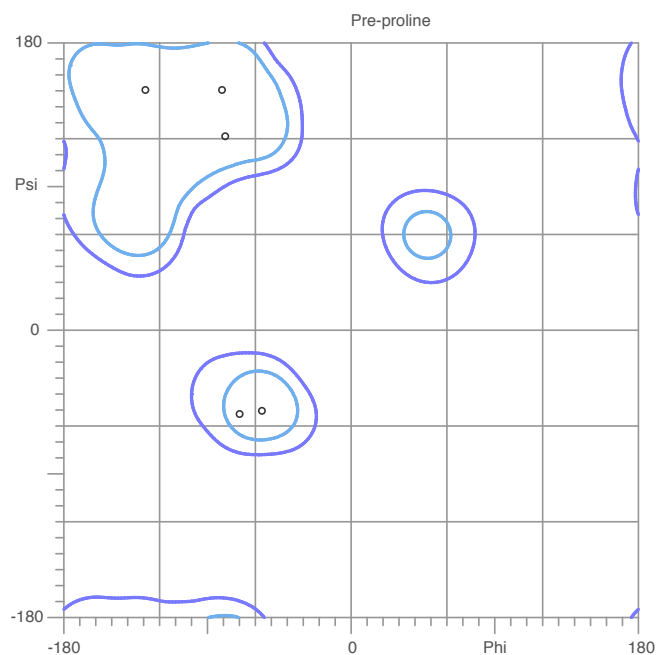
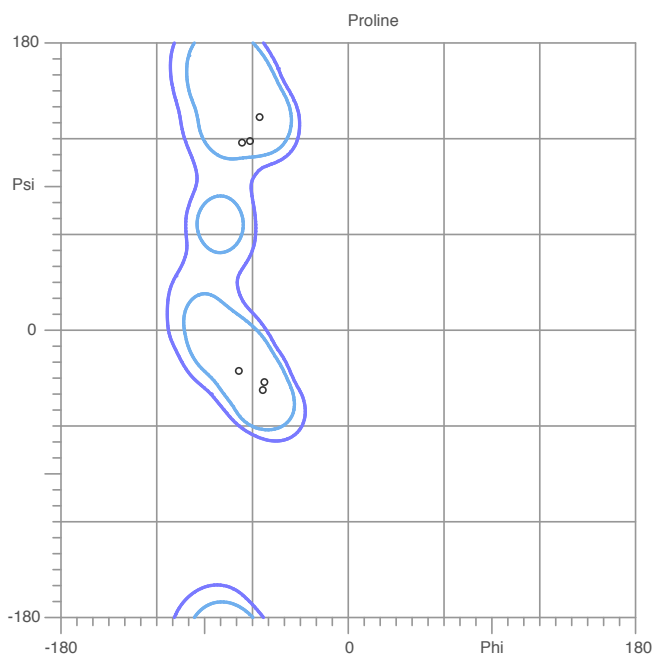
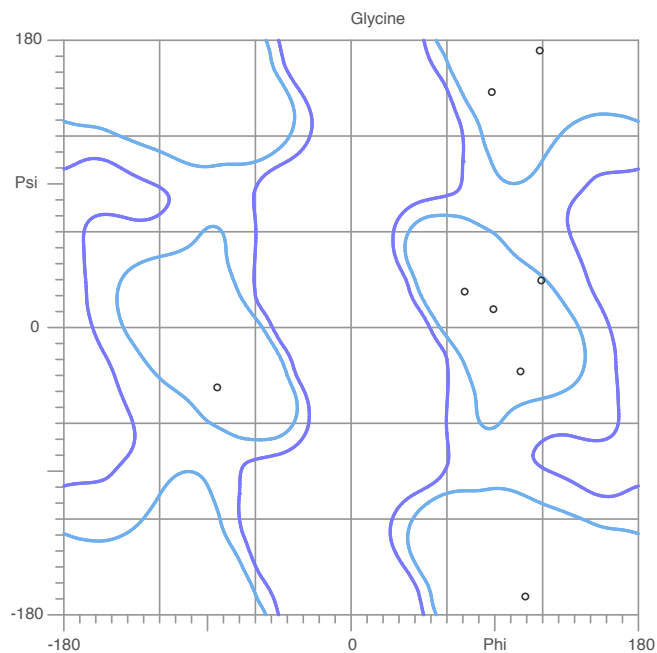
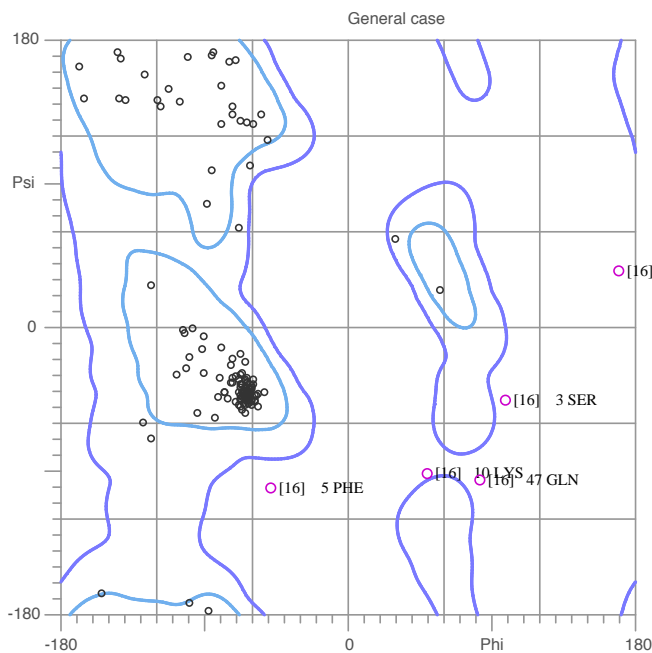
There were 1 outliers (phi, psi):
[15] 6 ASN (29.6, 96.1)

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

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

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 16



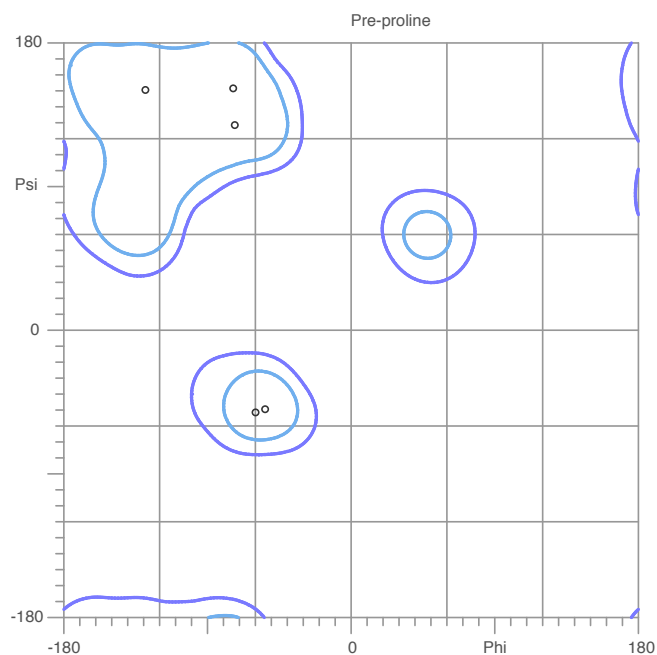
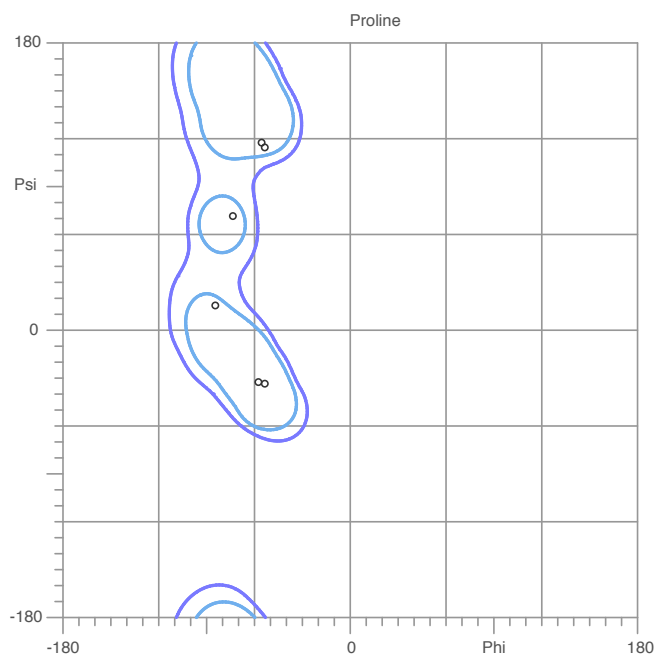
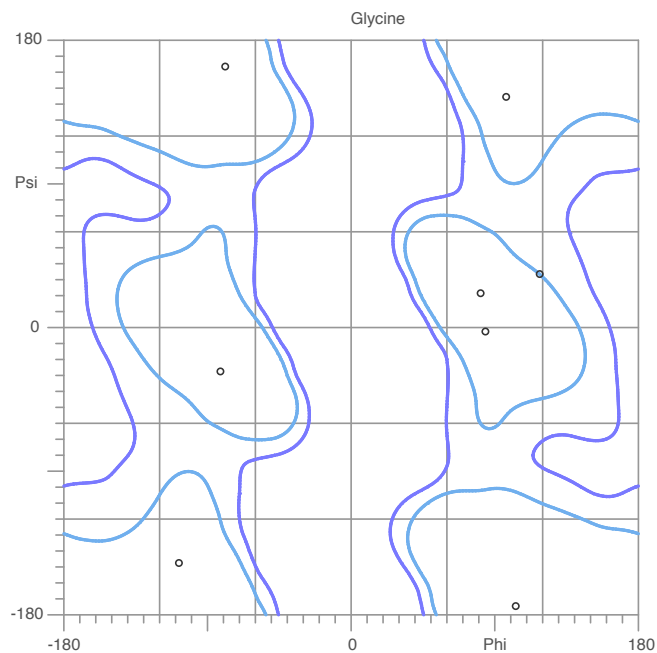
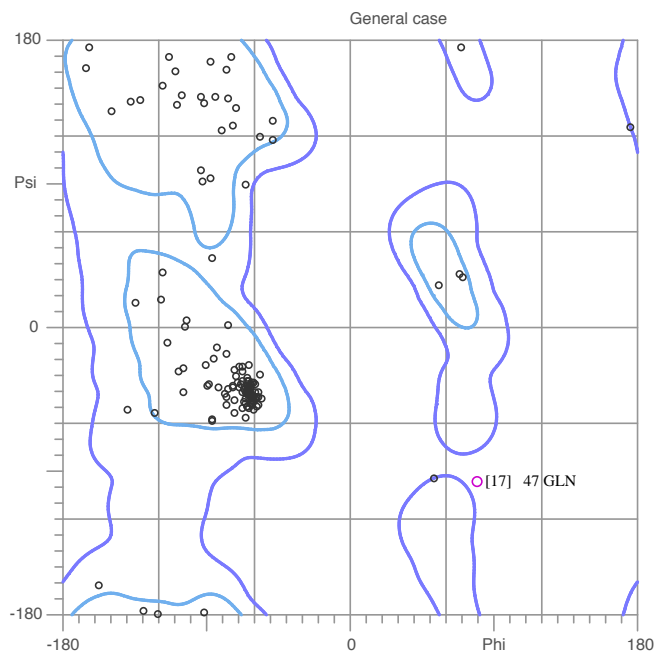
92.8% (142/153) of all residues were in favored (98%) regions.
96.7% (148/153) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[16] 2 GLN (169.5, 36.1)
[16] 3 SER (98.6, -45.7)
[16] 5 PHE (-49.0, -100.4)
[16] 10 LYS (49.1, -91.7)
[16] 47 GLN (82.9, -95.2)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 17



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.

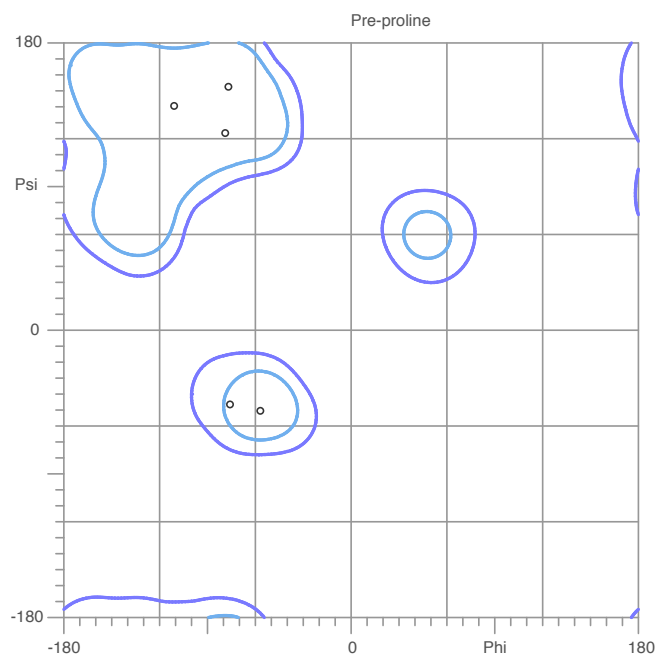
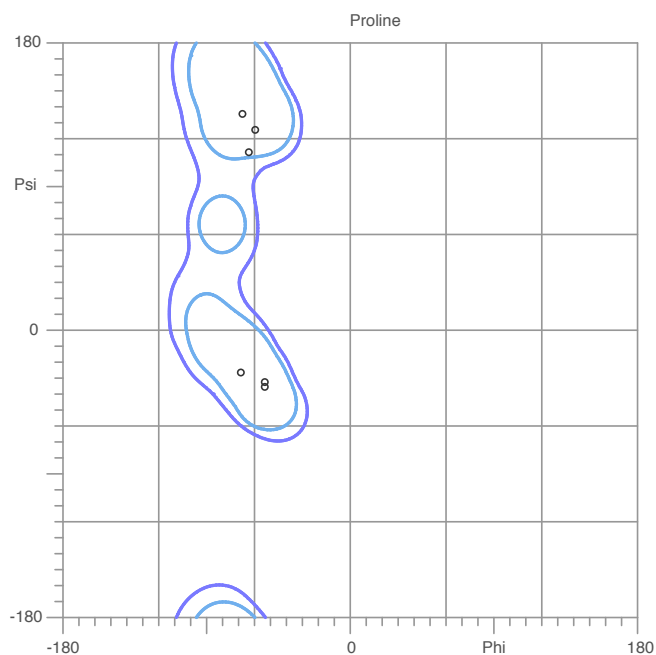
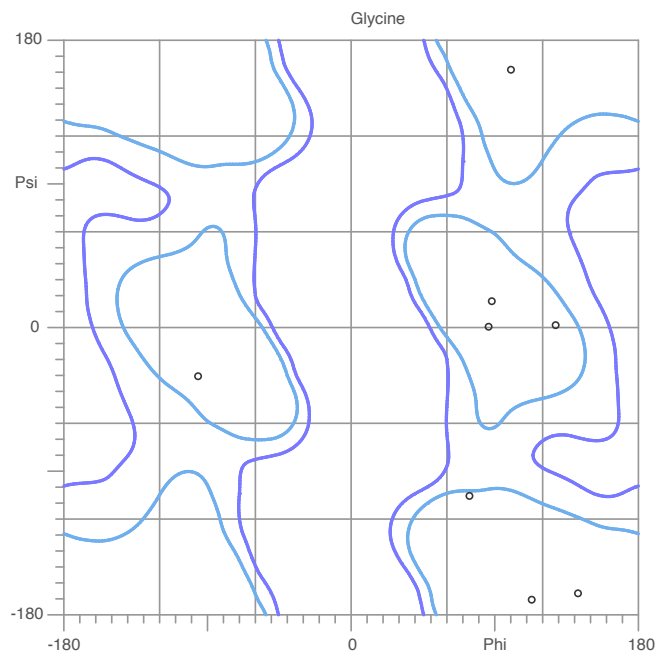
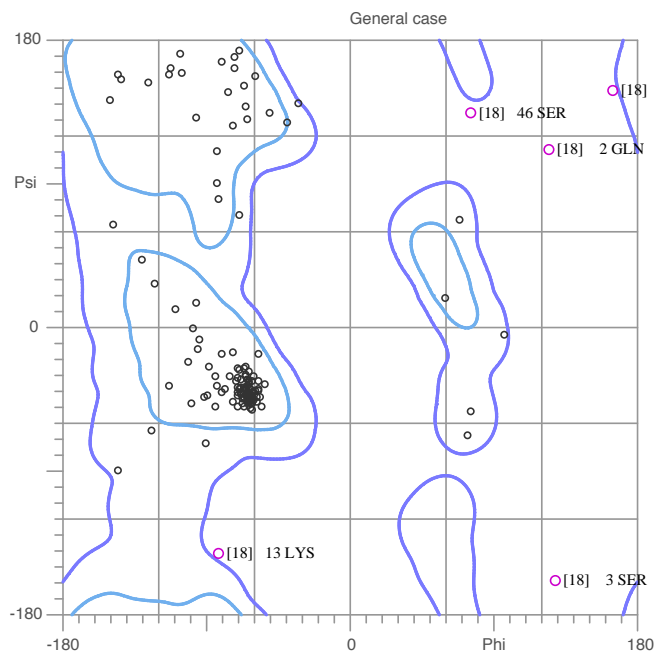
There were 1 outliers (phi, psi):
[17] 47 GLN (79.7, -96.0)

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

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

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 18



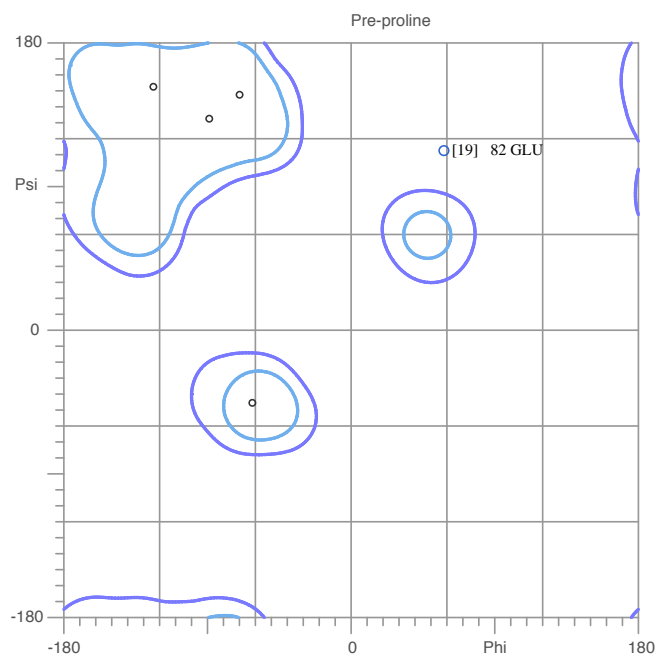
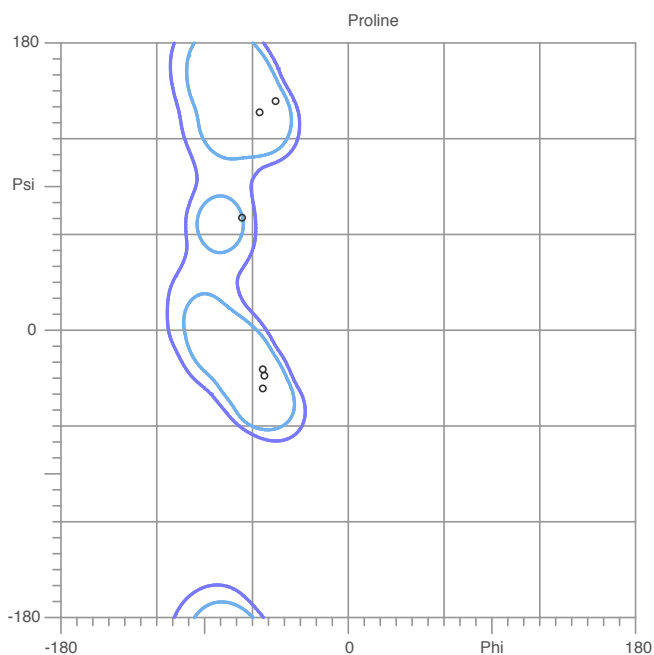
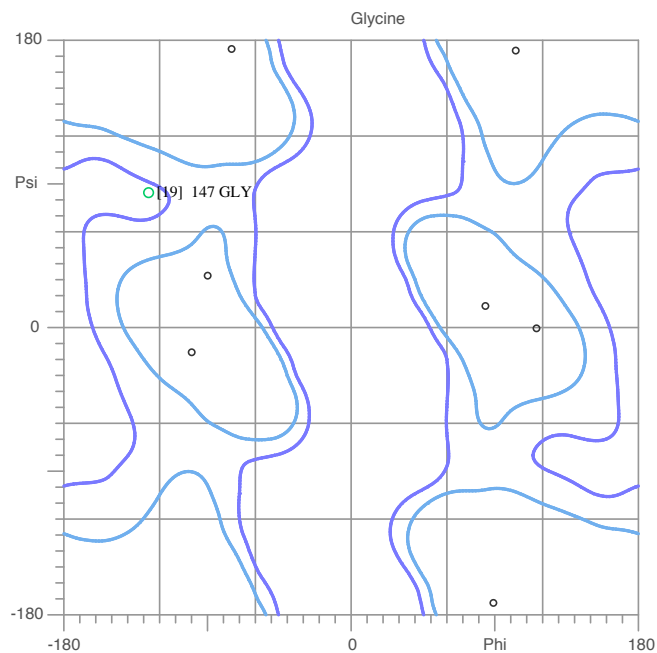
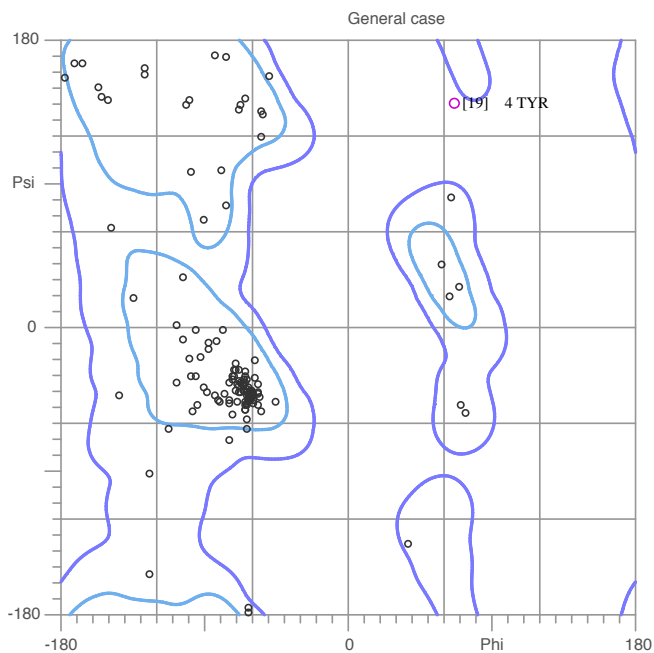
90.2% (138/153) of all residues were in favored (98%) regions.
96.7% (148/153) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[18] 2 GLN (124.6, 112.9)
[18] 3 SER (128.1, -158.6)
[18] 13 LYS (-83.0, -141.6)
[18] 40 ASP (164.1, 149.1)
[18] 46 SER (75.4, 135.0)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 19



88.9% (136/153) 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):

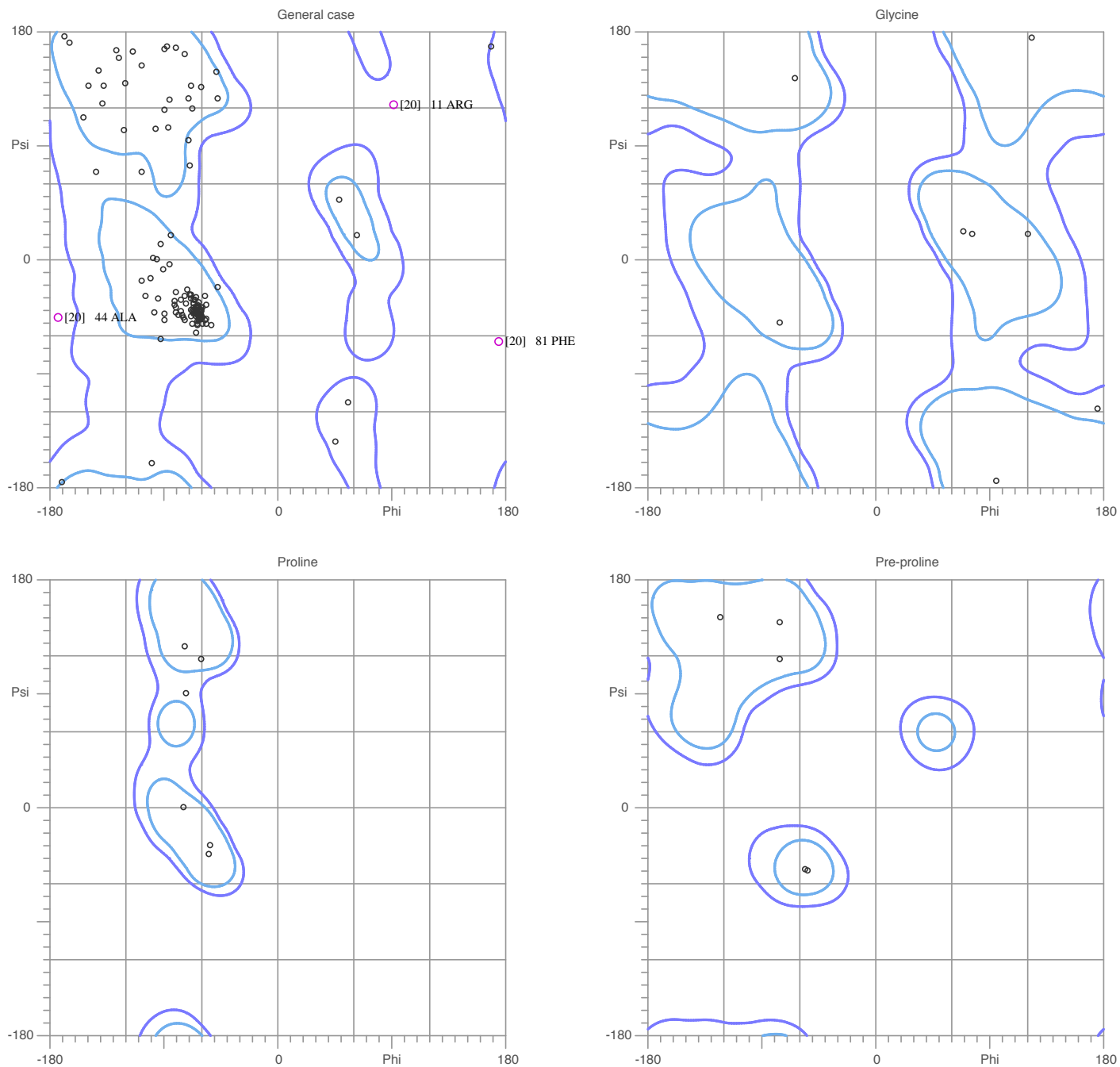
[19] 4 TYR (66.7, 141.8)

[19] 82 GLU (58.6, 113.3)

[19] 147 GLY (-128.0, 85.0)

MolProbity Ramachandran analysis

SGR209C_R3Cons_em_bcr3.pdb, model 20



89.5% (137/153) 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):

- [20] 11 ARG (91.7, 123.8)
- [20] 44 ALA (-174.9, -45.8)
- [20] 81 PHE (174.9, -64.6)