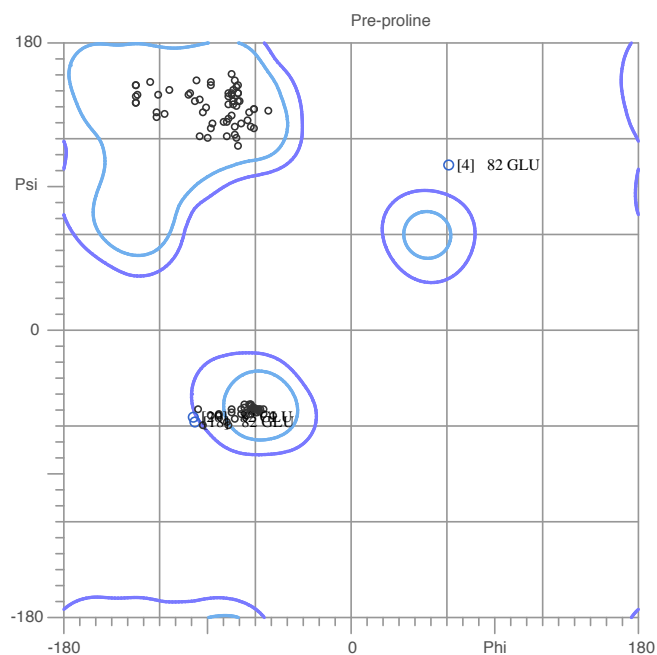
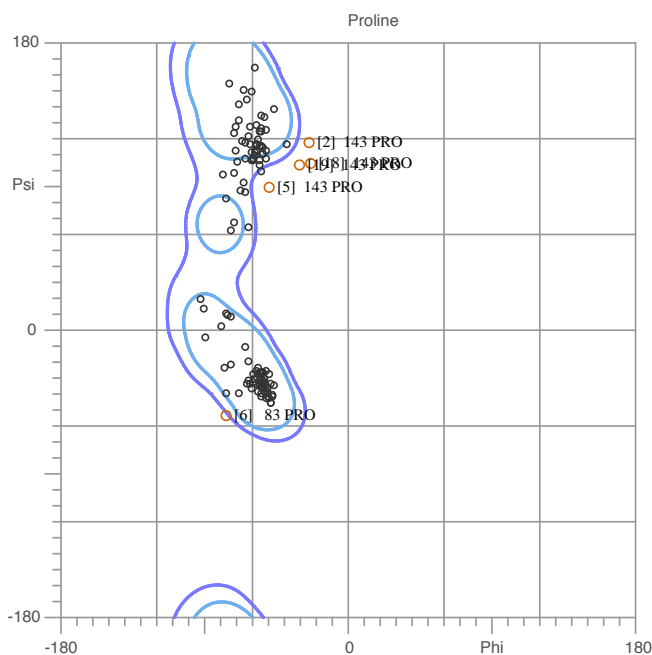
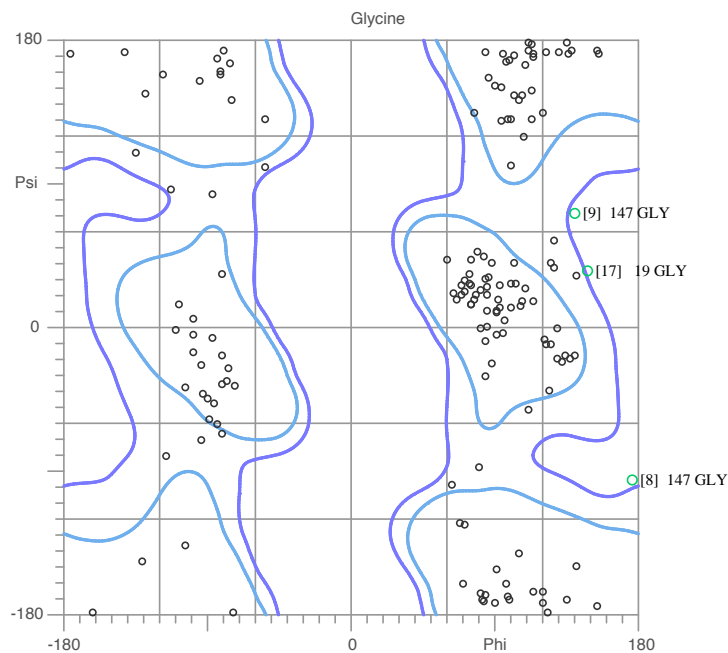
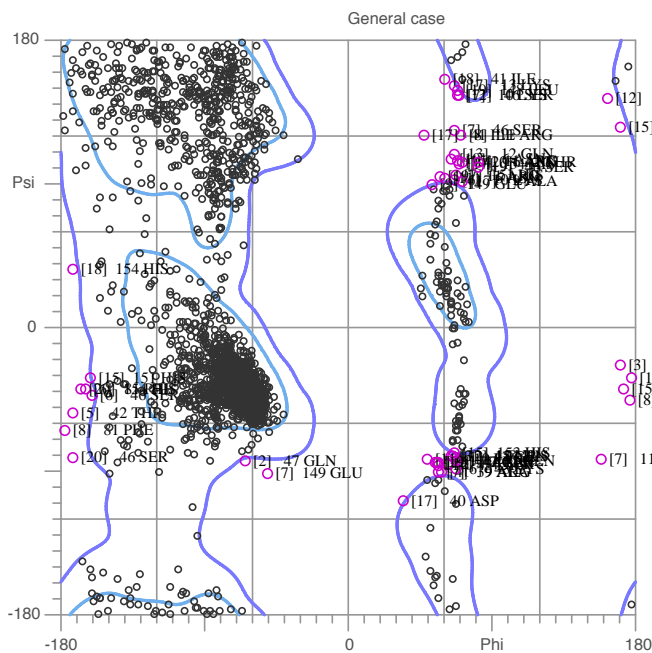


MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, all models



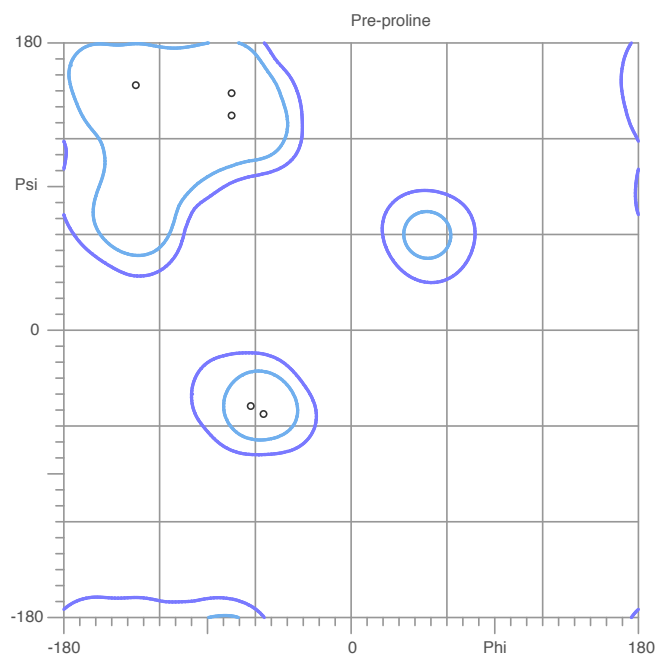
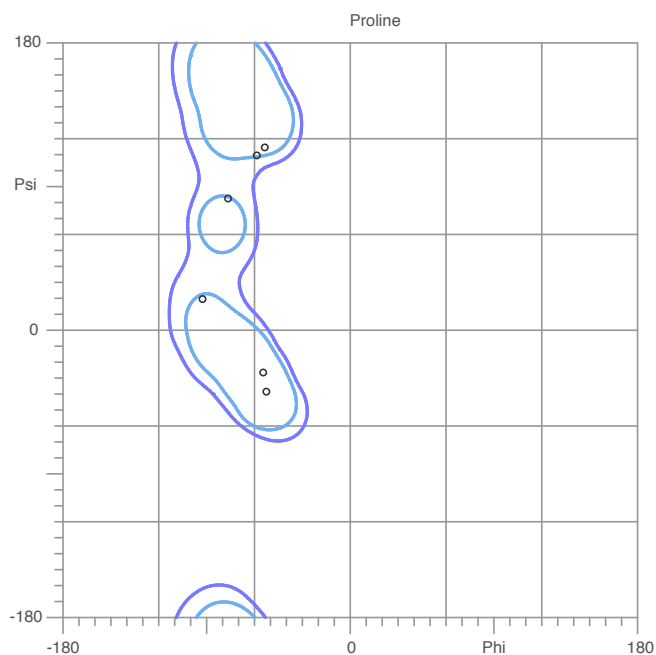
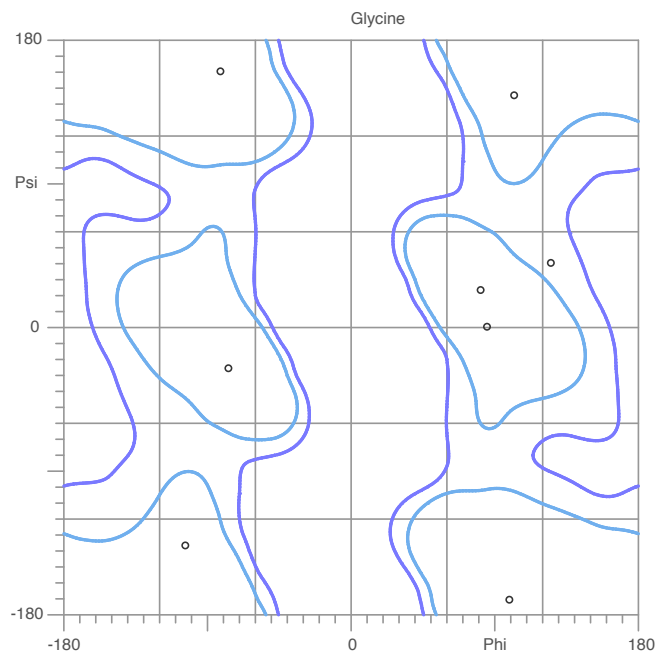
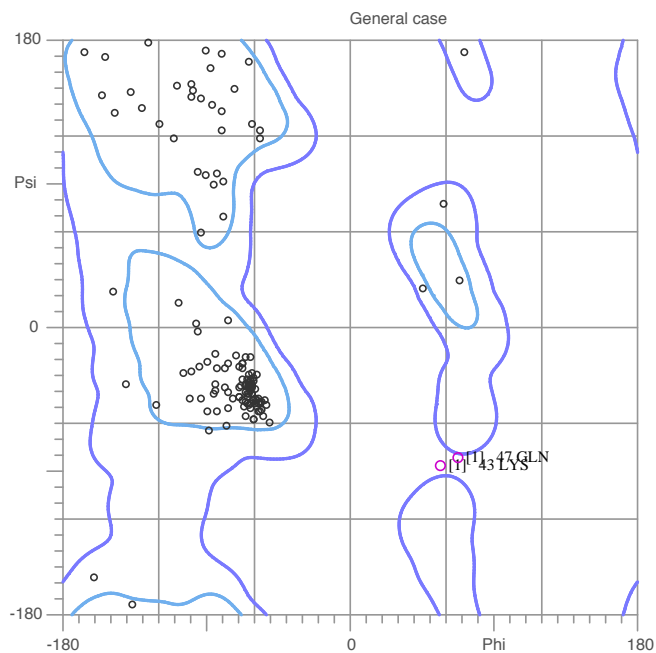
90.4% (2767/3060) of all residues were in favored (98%) regions.
97.9% (2996/3060) of all residues were in allowed (>90.8%) regions.

There were 64 outliers (phi, psi):

- | | |
|----------------------------|-------------------------------|
| (1) 41 LYS (56.0, 37.0) | (111) 6 ASN (80.1, 94.1) |
| (1) 47 GLN (67.7, 41.1) | (112) 10 LYS (49.9, 82.1) |
| (2) 4 TYR (82.3, 35.8) | (113) 47 GLN (67.5, 84.0) |
| (2) 47 GLN (45.0, 83.5) | (122) 40 ASP (163.0, 144.0) |
| (2) 143 PRO (25.4, 118.9) | (122) 46 SER (86.6, 146.5) |
| (3) 4 TYR (64.8, 36.7) | (131) 12 GLN (66.5, 109.7) |
| (3) 44 ALA (70.3, 23.7) | (141) 6 ASN (71.5, 104.2) |
| (4) 9 ALA (58.7, 30.2) | (151) 11 ARG (88.9, 106.0) |
| (5) 82 GLU (61.2, 104.0) | (151) 44 ALA (172.7, 38.2) |
| (5) 7 ALA (55.1, 84.6) | (151) 46 SER (56.8, 84.5) |
| (5) 42 THR (-173.8, -53.0) | (151) 151 HIS (162.3, 31.6) |
| (5) 143 PRO (-51.0, 95.3) | (155) 155 HIS (66.1, 79.0) |
| (6) 10 LYS (66.9, 93.8) | (155) 154 HIS (170.0, 126.9) |
| (6) 44 LYS (67.9, 38.3) | (161) 44 ALA (177.7, -31.6) |
| (6) 46 SER (-161.3, -42.2) | (171) 9 ALA (71.2, 92.1) |
| (6) 81 PHE (-165.7, -38.1) | (171) 13 LYS (66.8, 152.1) |
| (6) 81 PRO (-173.8, -53.8) | (171) 19 GLY (148.5, 38.5) |
| (7) 10 LYS (69.2, 146.7) | (171) 40 ASP (34.5, -109.0) |
| (7) 11 ARG (188.8, 82.3) | (171) 41 ILE (47.9, 121.6) |
| (7) 39 ARG (58.9, 40.4) | (171) 154 HIS (69.1, 103.1) |
| (7) 46 SER (66.4, 124.5) | (181) 41 ILE (60.3, 156.2) |
| (7) 149 GLU (-51.3, -91.9) | (181) 82 GLU (190.0, -37.4) |
| (7) 151 HIS (67.1, 96.2) | (181) 143 PRO (-21.9, 105.9) |
| (8) 11 ARG (70.3, 121.2) | (181) 154 HIS (-173.6, 37.8) |
| (8) 44 ALA (176.6, -45.8) | (191) 11 ARG (87.4, 95.1) |
| (8) 81 PHE (-178.5, -64.6) | (191) 46 SER (81.4, 101.7) |
| (8) 147 GLY (176.3, -95.8) | (191) 47 GLN (54.2, -84.4) |
| (9) 147 GLY (140.0, 72.6) | (191) 143 PRO (-31.3, 104.8) |
| (9) 149 GLU (52.1, 90.3) | (191) 148 LEU (86.6, 149.1) |
| (10) 6 ASN (65.0, 106.7) | (201) 42 THR (81.4, 104.0) |
| | (201) 46 SER (-171.6, -82.0) |
| | (201) 82 GLU (-99.3, -54.4) |
| | (201) 154 HIS (-168.6, -38.4) |

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 1



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.

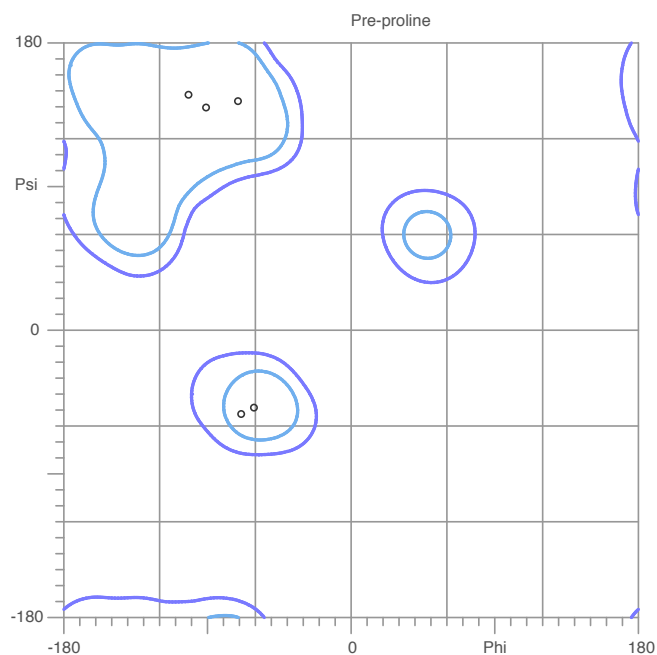
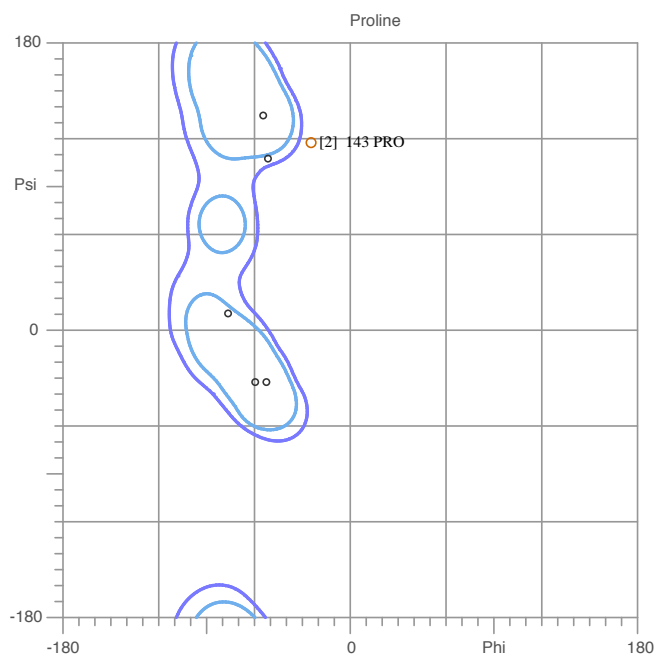
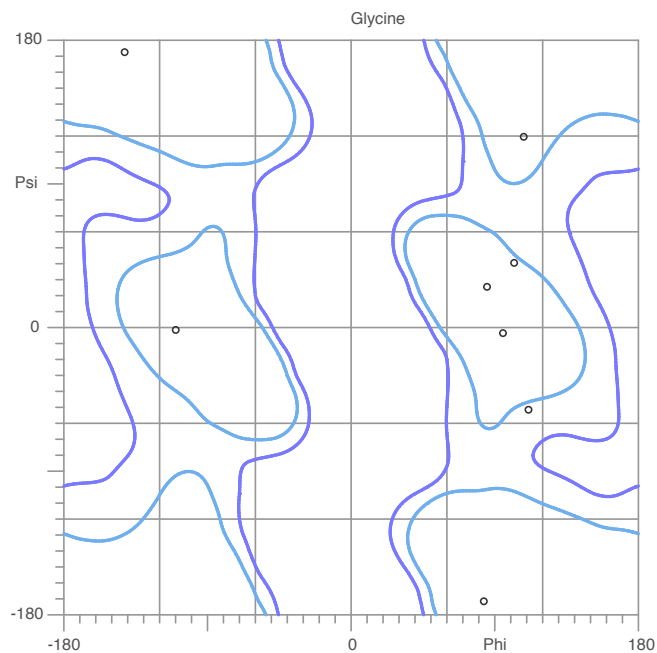
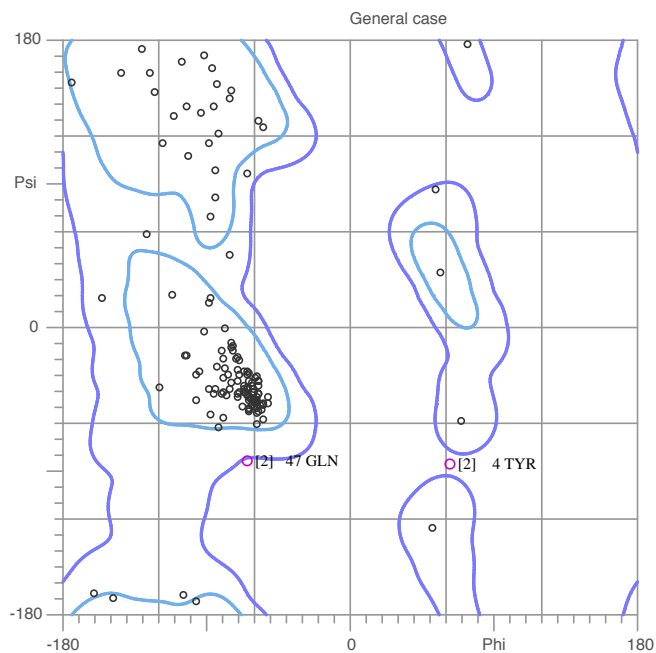
There were 2 outliers (phi, psi):

[1] 43 LYS (56.0, -87.0)

[1] 47 GLN (67.7, -81.1)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 2



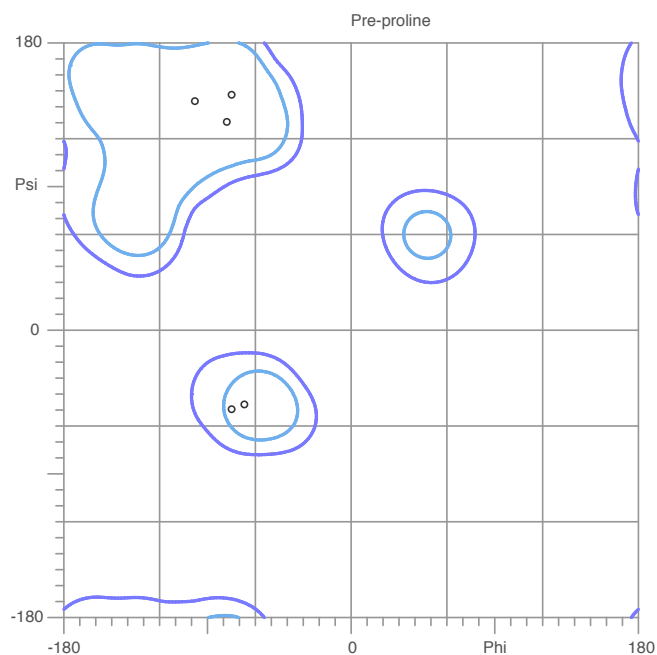
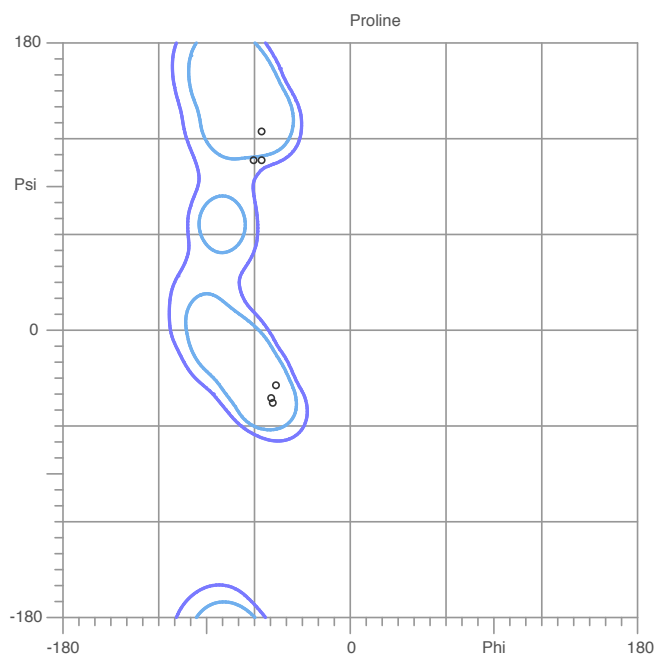
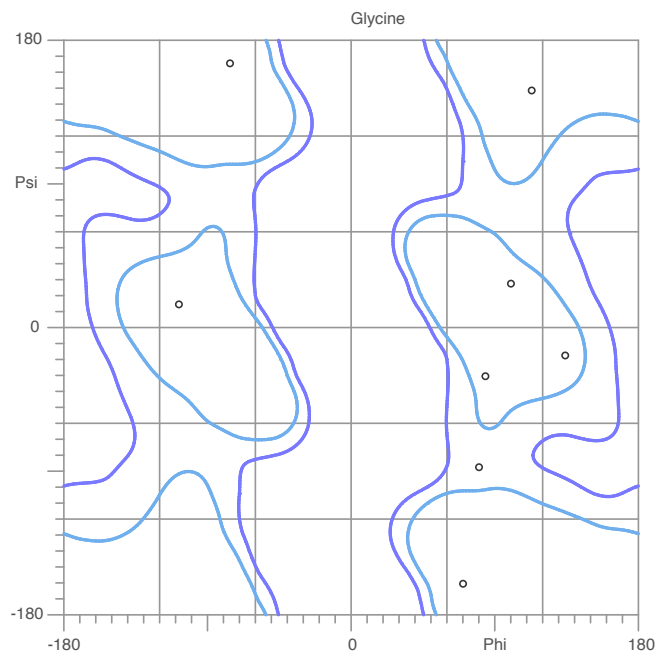
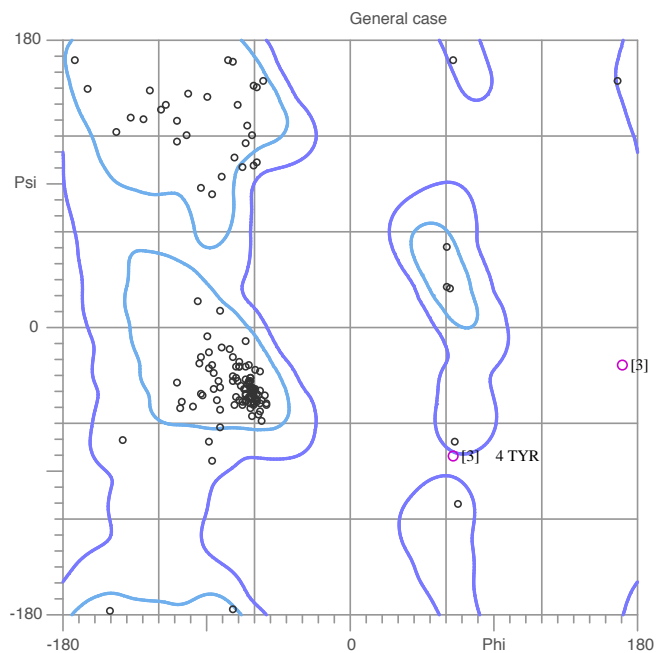
90.2% (138/153) of all residues were in favored (98%) regions.
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 4 TYR (62.3, -85.8)
- [2] 47 GLN (-65.0, -83.5)
- [2] 143 PRO (-25.4, 118.9)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 3



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.

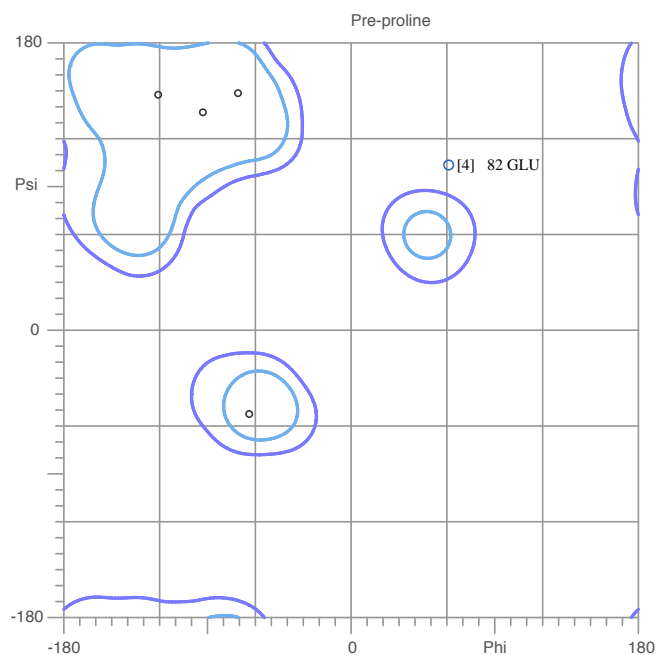
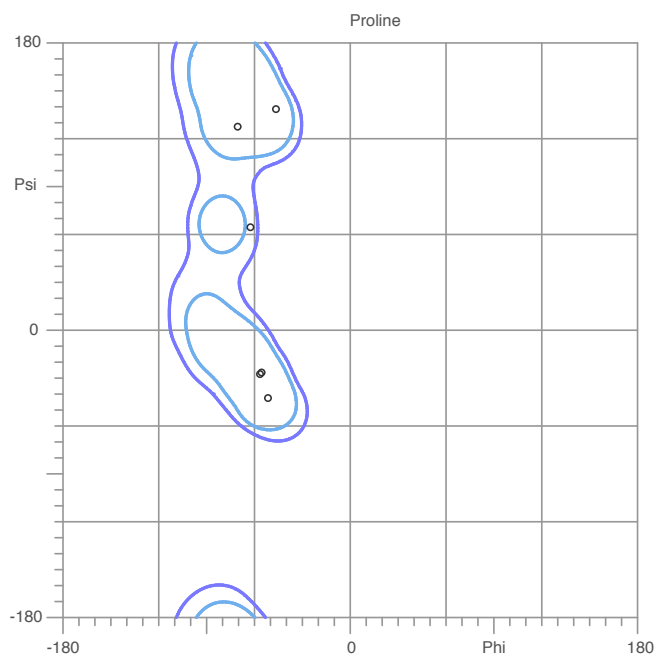
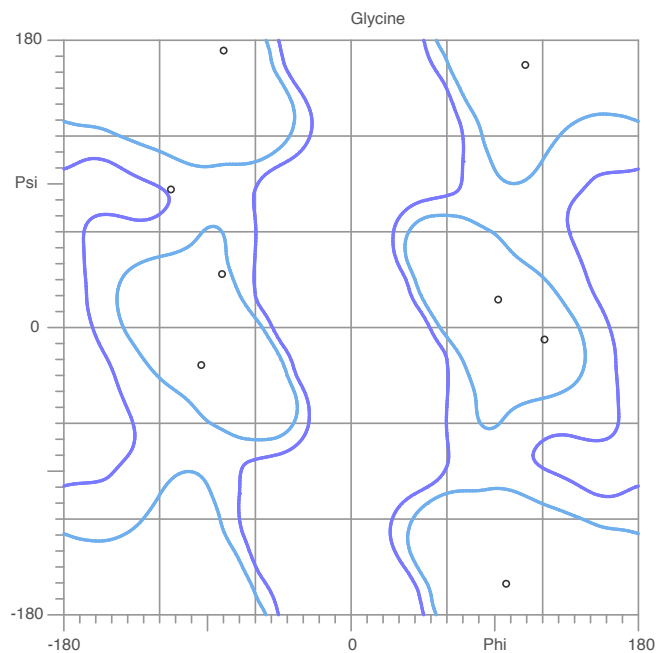
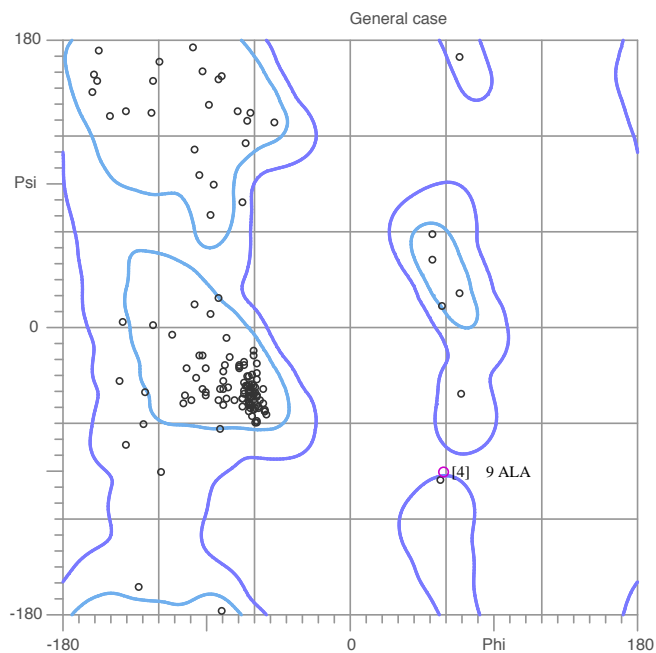
There were 2 outliers (phi, psi):

[3] 4 TYR (64.8, -80.7)

[3] 44 ALA (170.3, -23.7)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 4



89.5% (137/153) of all residues were in favored (98%) regions.
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

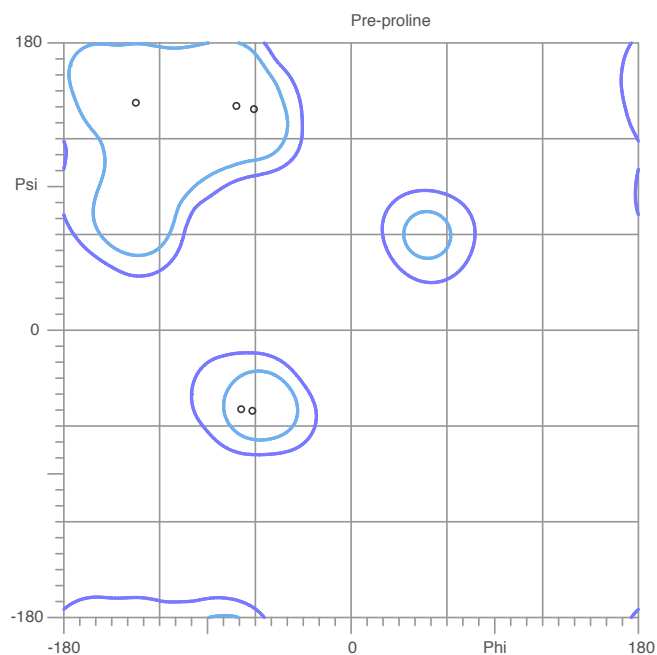
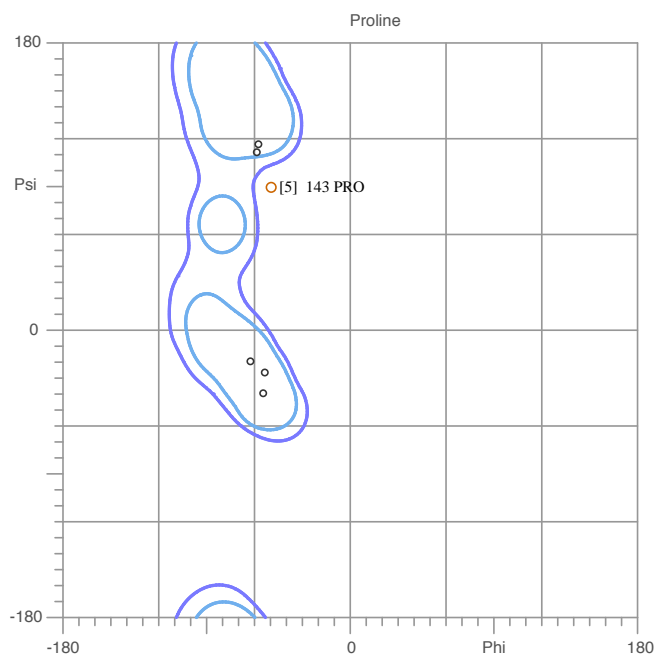
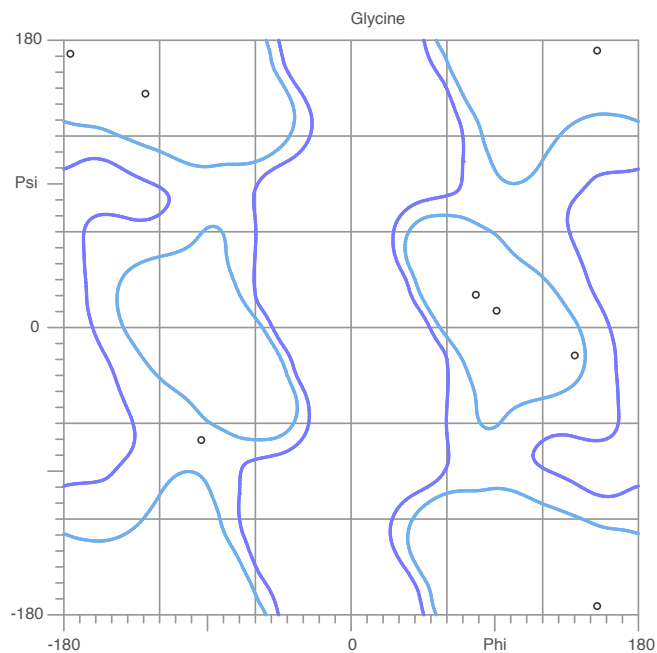
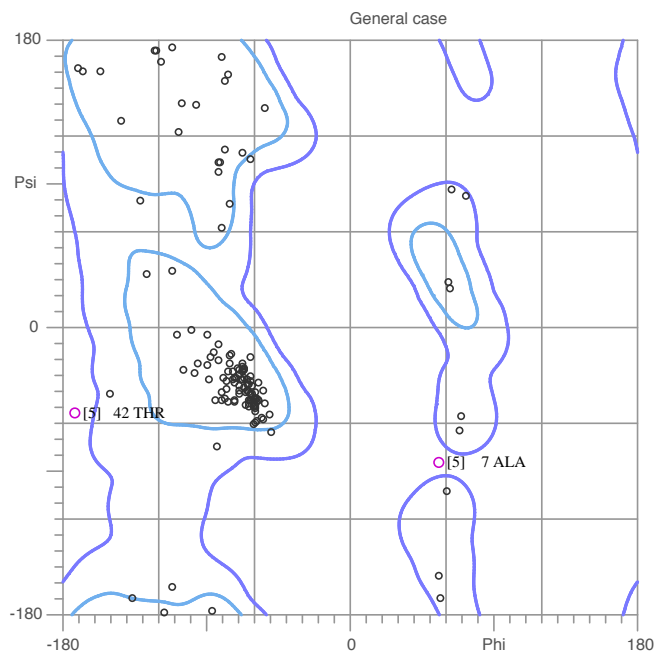
There were 2 outliers (phi, psi):

[4] 9 ALA (58.7, -90.2)

[4] 82 GLU (61.2, 104.0)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 5



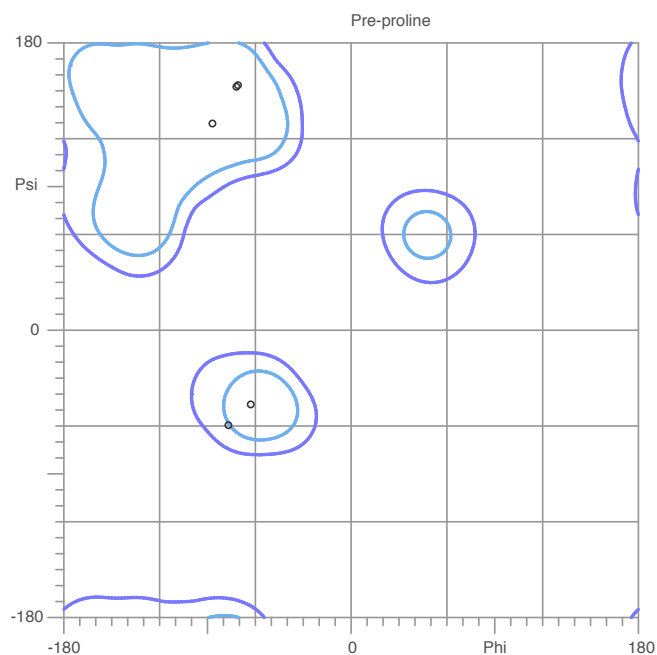
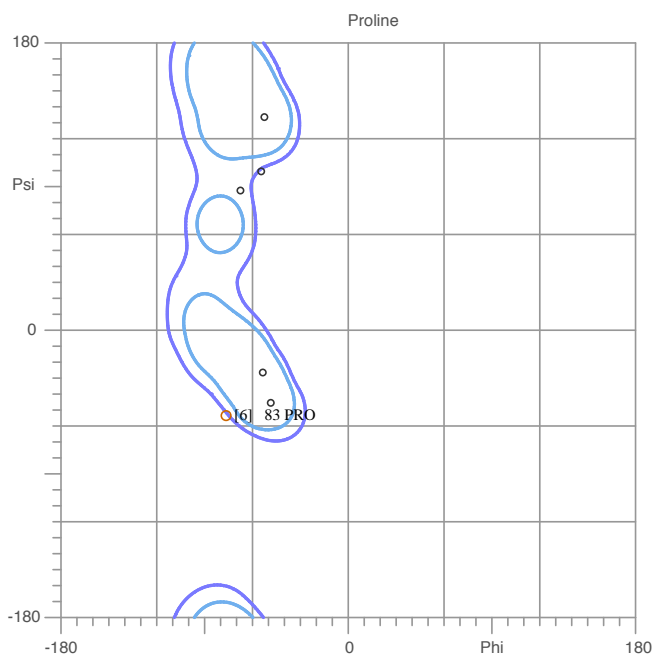
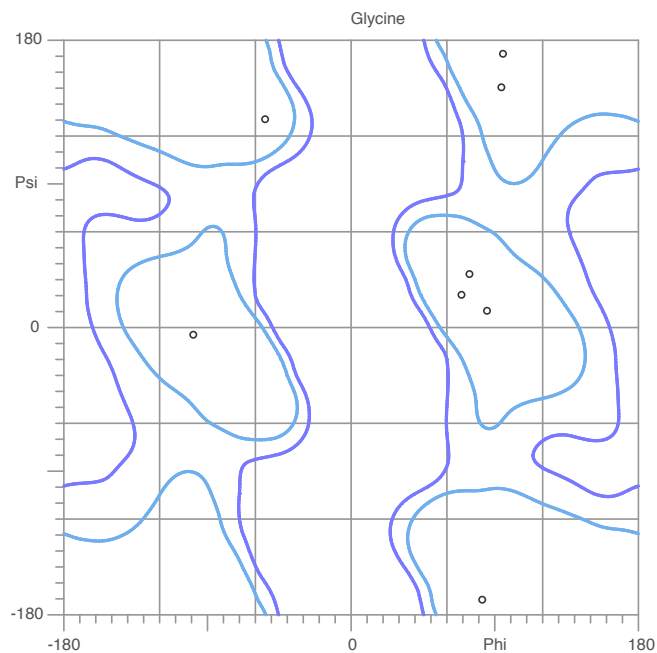
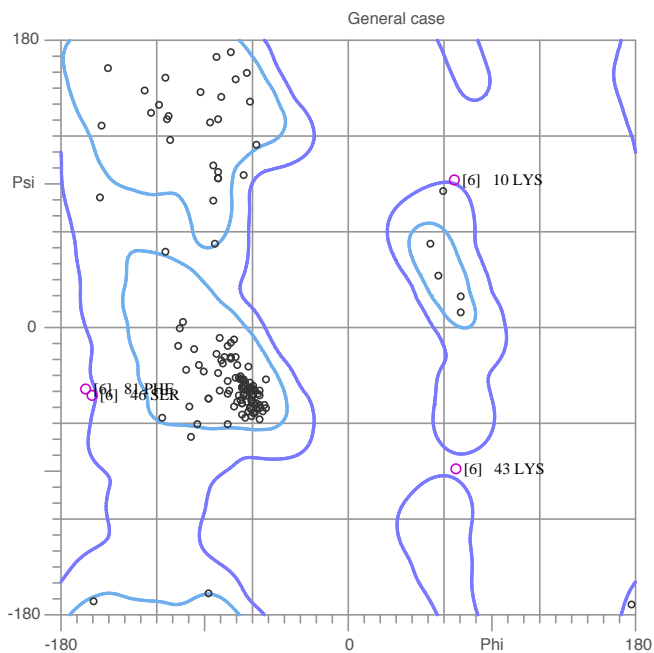
88.9% (136/153) of all residues were in favored (98%) regions.
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [5] 7 ALA (55.1, -84.6)
- [5] 42 THR (-173.8, -53.0)
- [5] 143 PRO (-51.0, 90.5)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 6



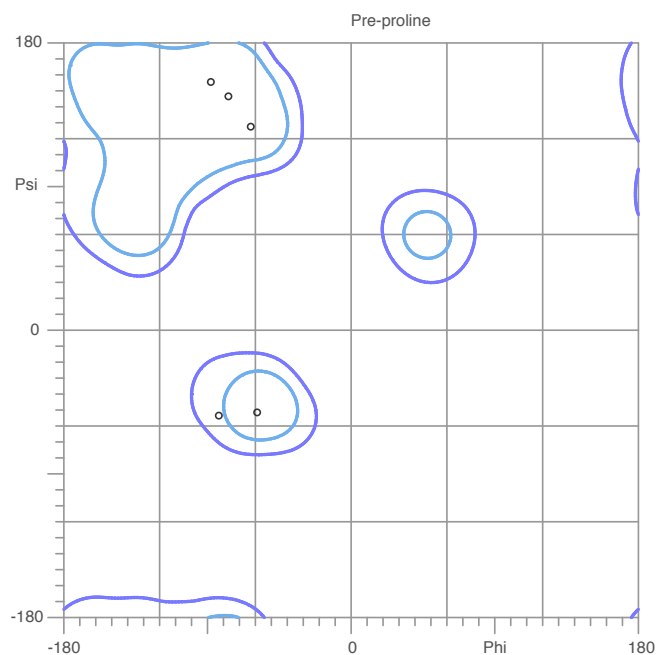
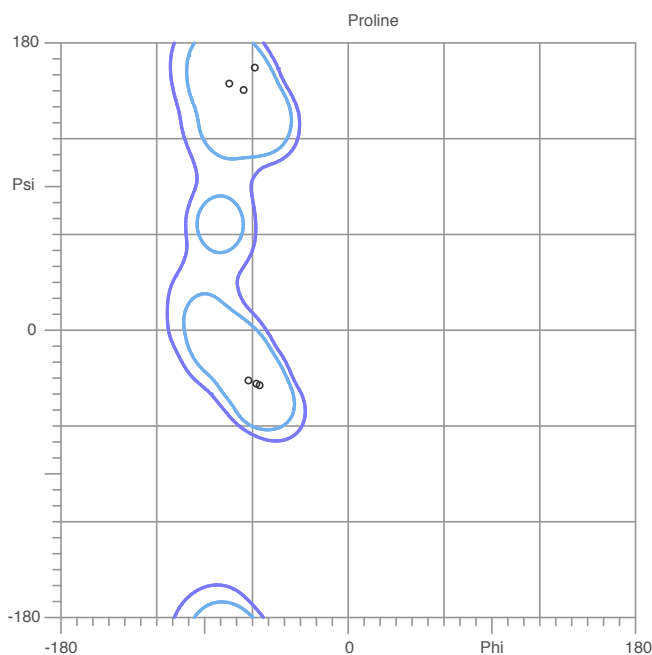
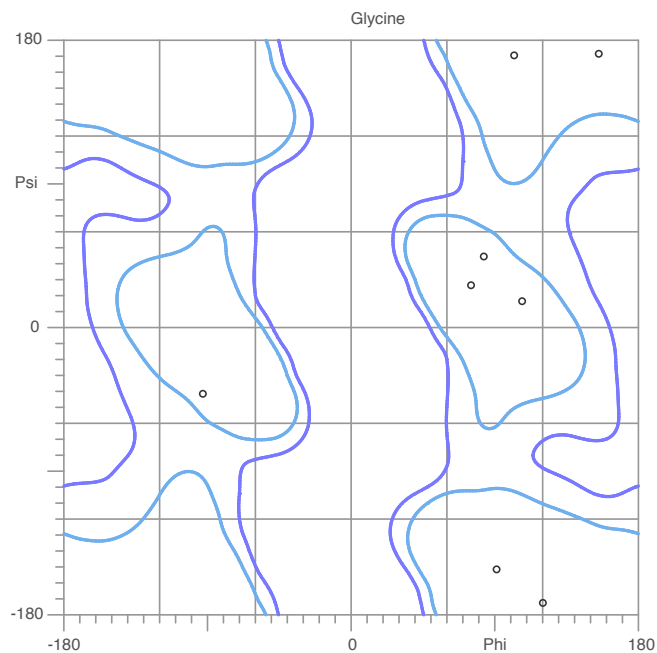
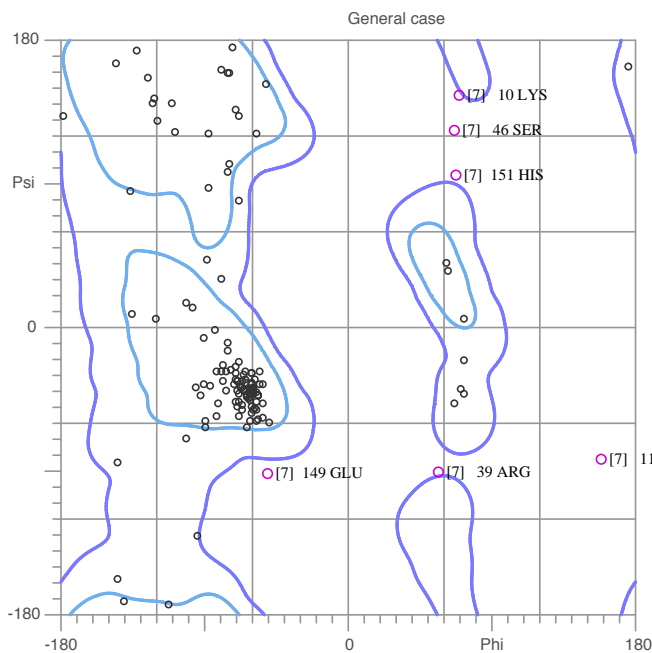
90.2% (138/153) of all residues were in favored (98%) regions.
96.7% (148/153) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[6] 10 LYS (66.9, 93.8)
[6] 43 LYS (67.9, -88.3)
[6] 46 SER (-161.3, -42.8)
[6] 81 PHE (-165.7, -38.1)
[6] 83 PRO (-77.9, -53.8)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 7



86.3% (132/153) of all residues were in favored (98%) regions.
96.1% (147/153) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[7] 10 LYS (69.2, 146.7)

[7] 11 ARG (158.8, -82.3)

[7] 39 ARG (56.9, -90.4)

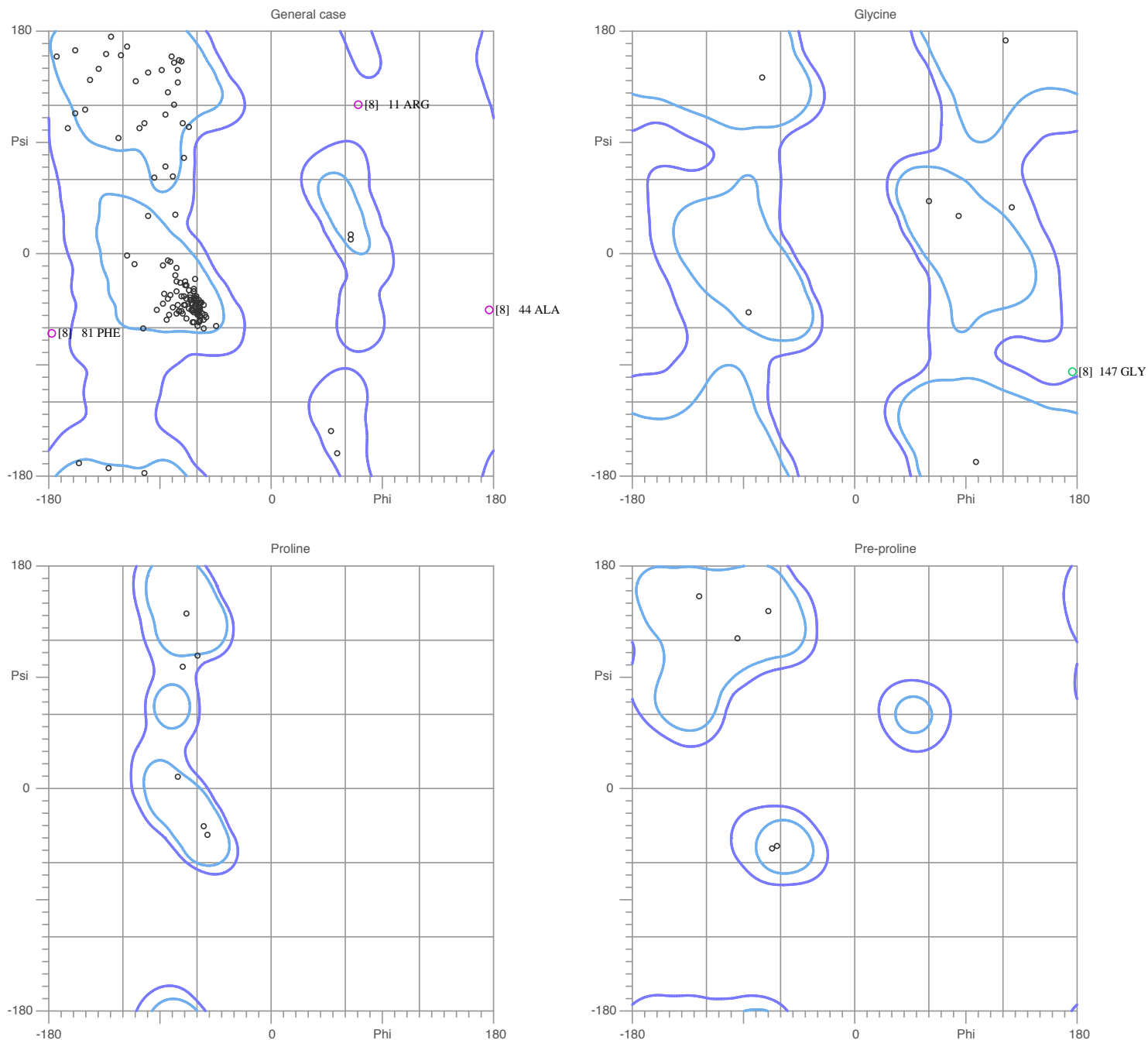
[7] 46 SER (66.4, 124.5)

[7] 149 GLU (-51.3, -91.9)

[7] 151 HIS (67.1, 96.2)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 8



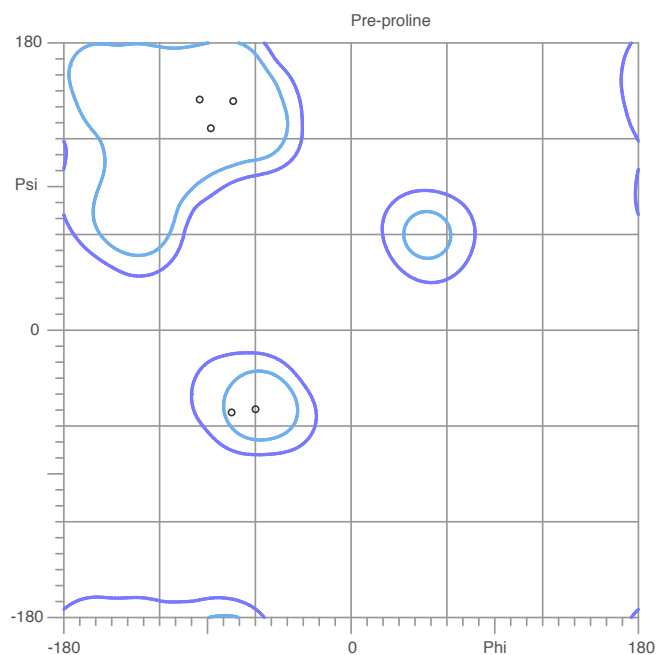
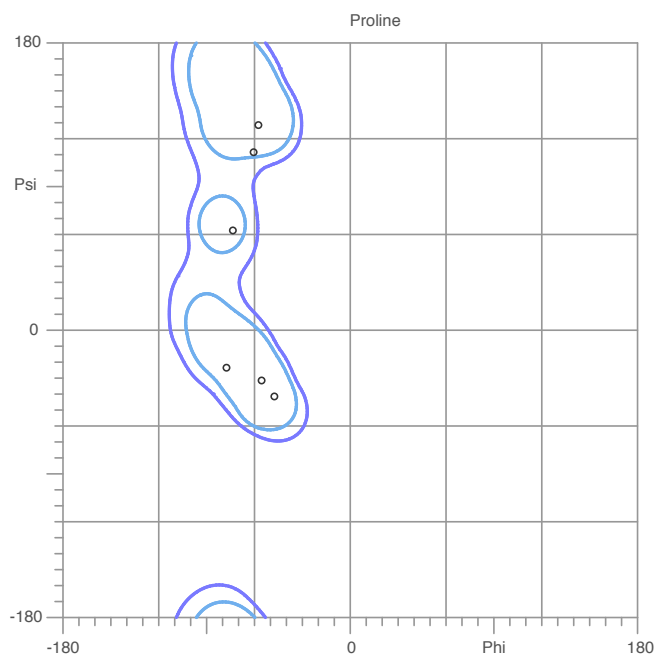
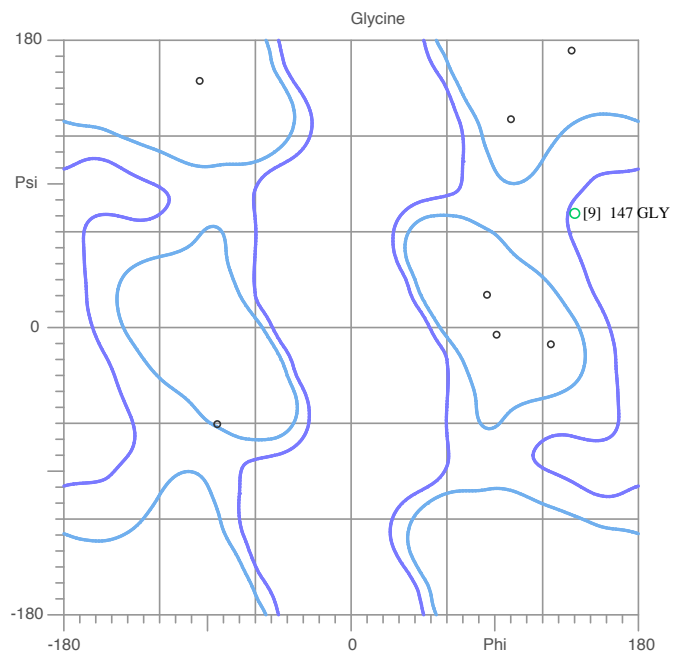
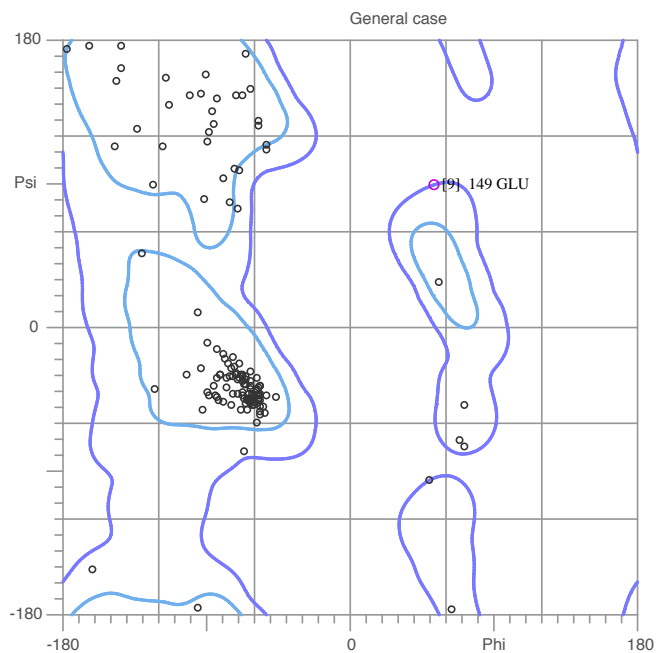
91.5% (140/153) of all residues were in favored (98%) regions.
97.4% (149/153) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [8] 11 ARG (70.3, 121.2)
- [8] 44 ALA (176.6, -45.8)
- [8] 81 PHE (-178.5, -64.6)
- [8] 147 GLY (176.3, -95.8)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 9

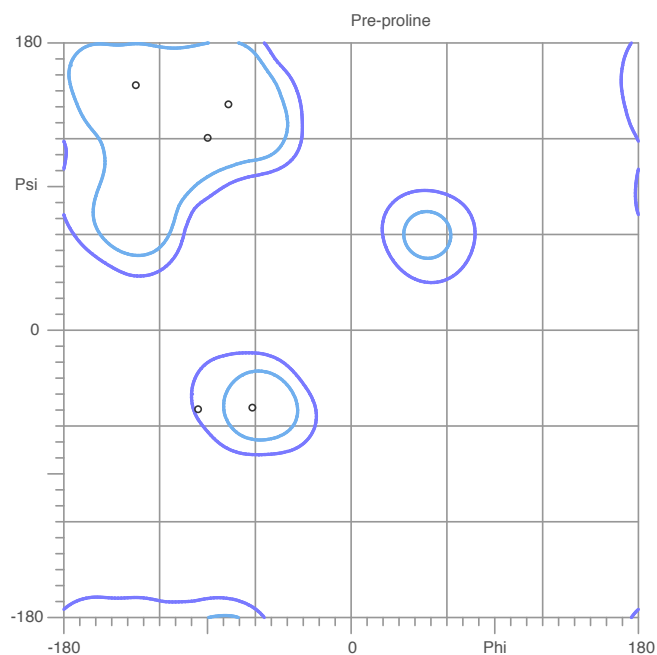
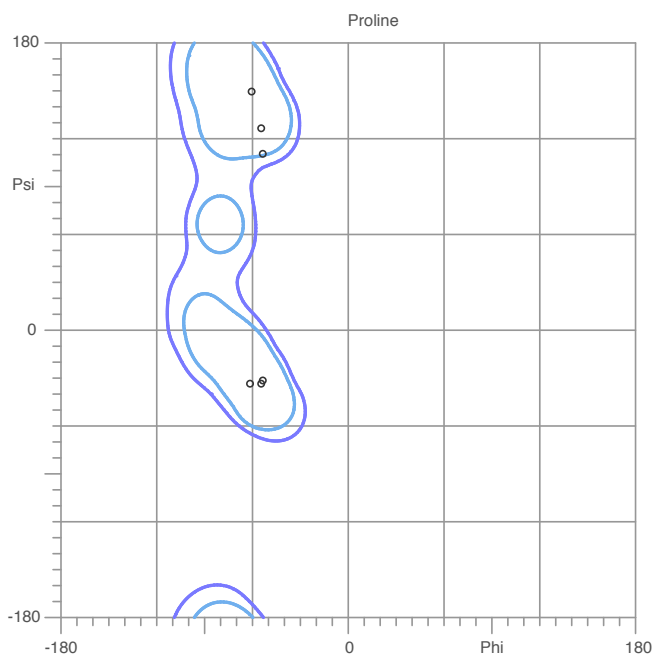
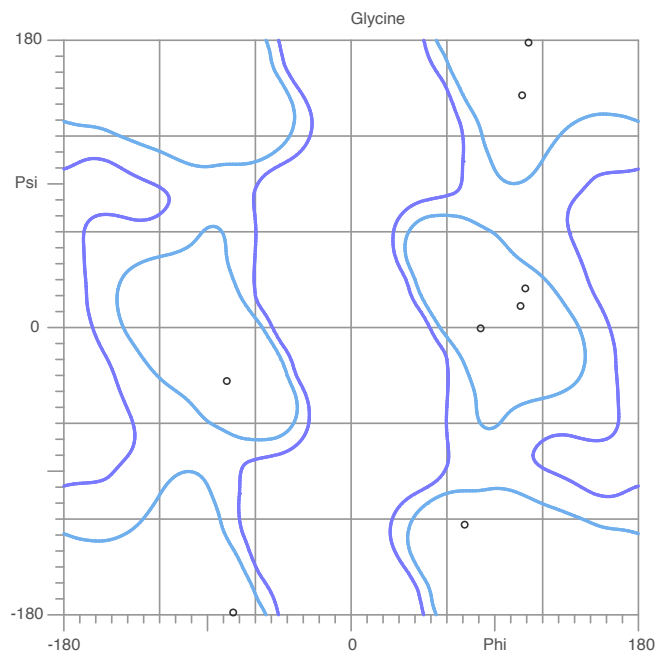
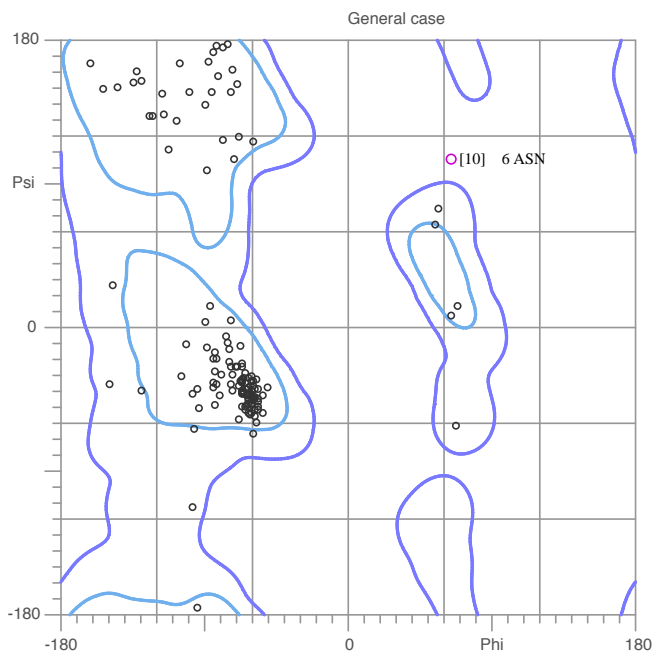


91.5% (140/153) of all residues were in favored (98%) regions.
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[9] 147 GLY (140.8, 72.6)
[9] 149 GLU (52.1, 90.3)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 10



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.

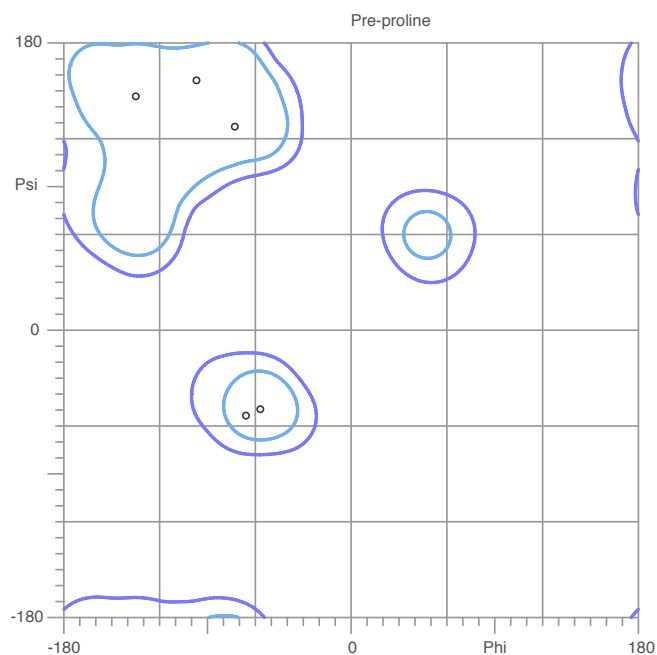
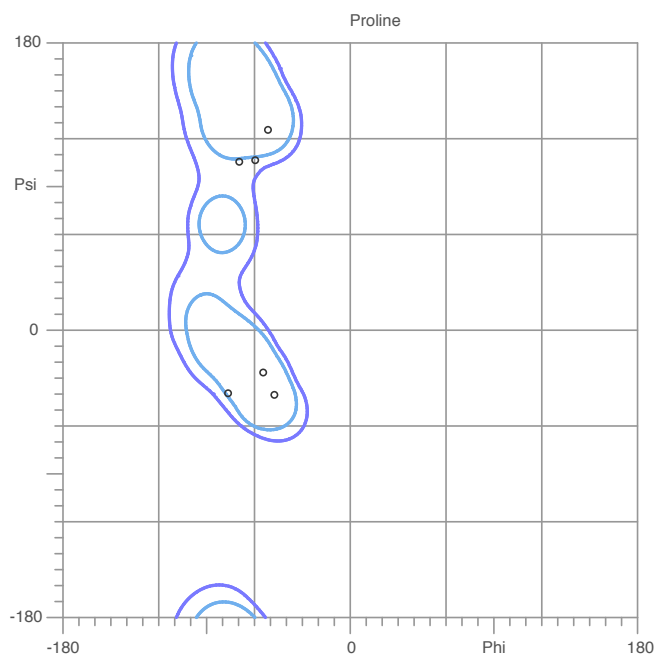
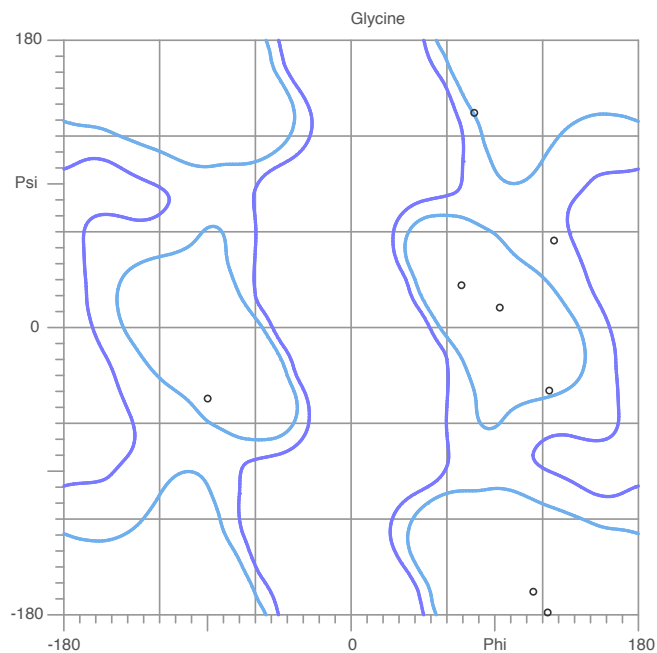
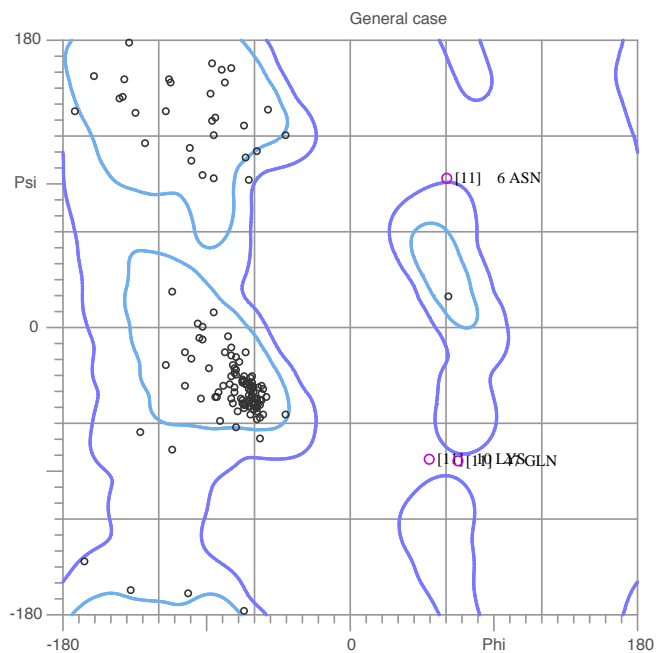
There were 1 outliers (phi, psi):
[10] 6 ASN (65.0, 106.7)

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MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 11



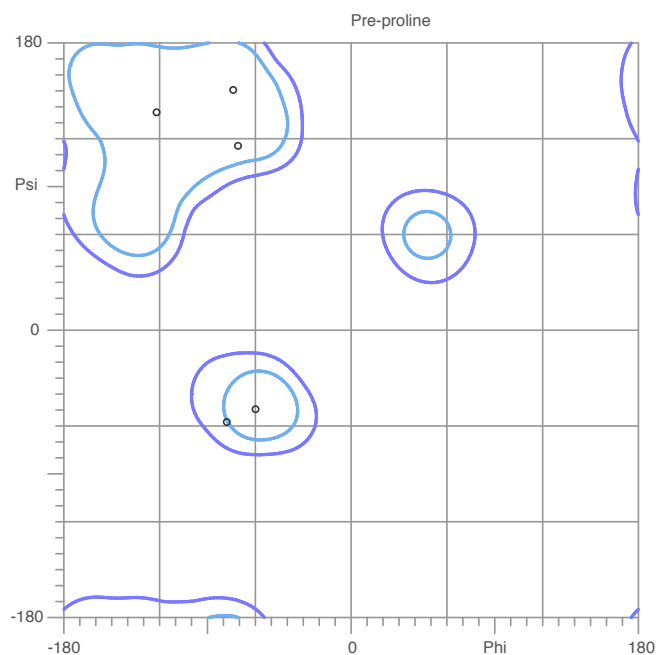
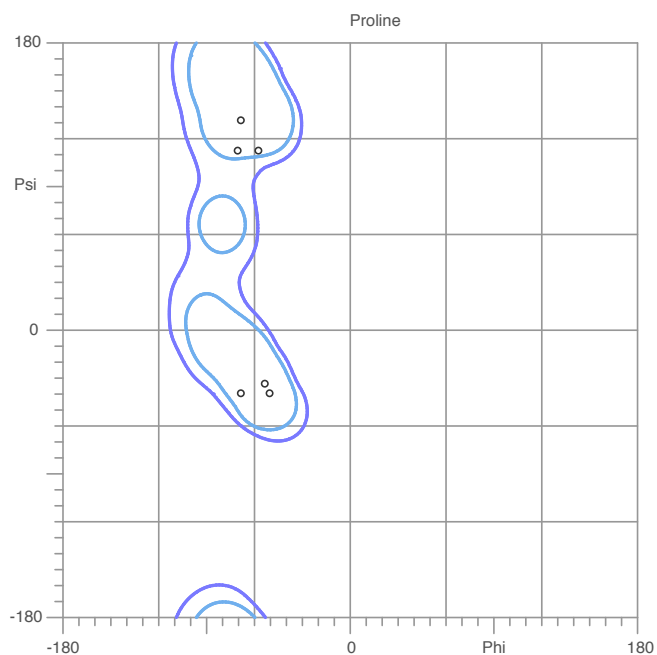
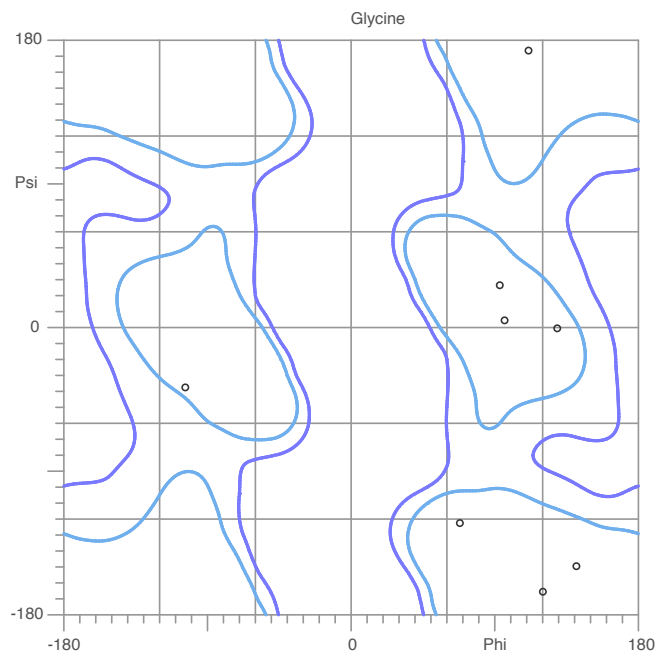
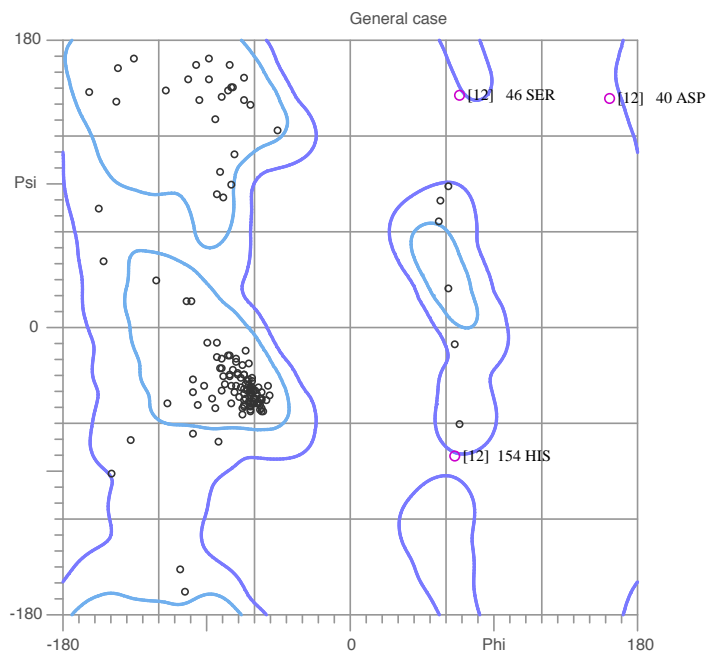
90.2% (138/153) of all residues were in favored (98%) regions.
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [11] 6 ASN (60.1, 94.1)
- [11] 10 LYS (49.9, -82.1)
- [11] 47 GLN (67.5, -84.0)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 12



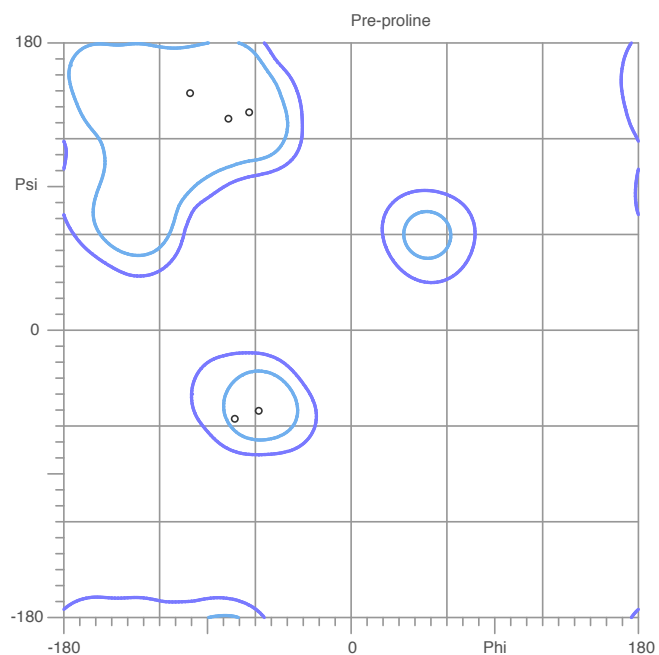
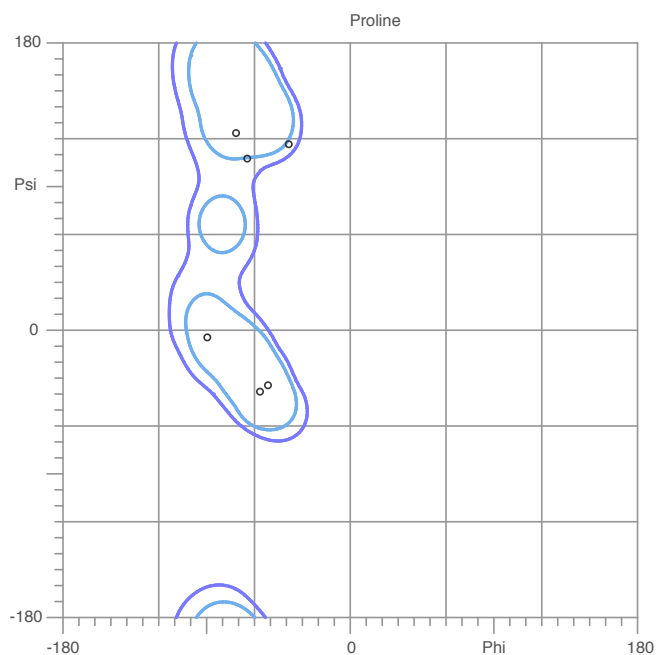
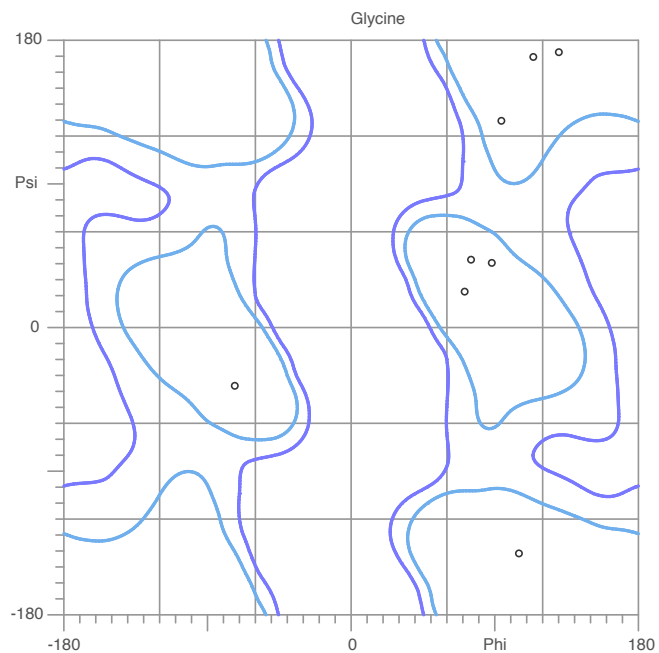
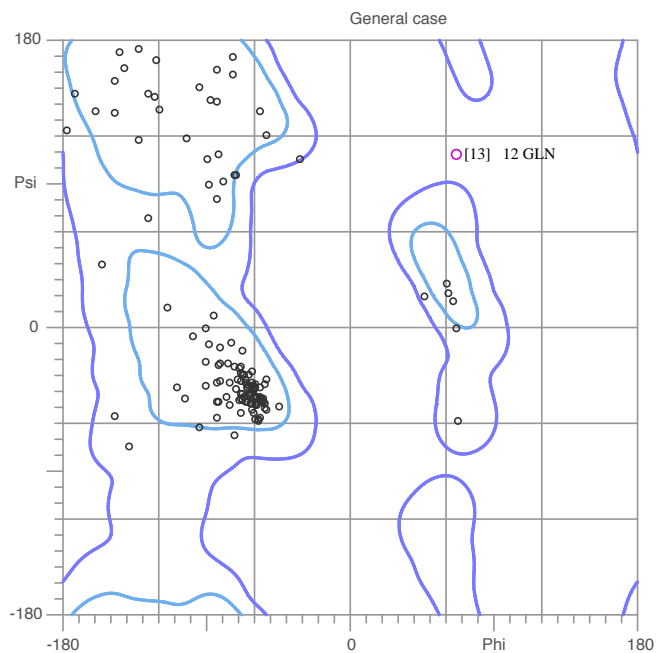
88.9% (136/153) of all residues were in favored (98%) regions.
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [12] 40 ASP (163.0, 144.3)
- [12] 46 SER (68.6, 146.5)
- [12] 154 HIS (65.9, -80.1)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 13



92.2% (141/153) of all residues were in favored (98%) regions.
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

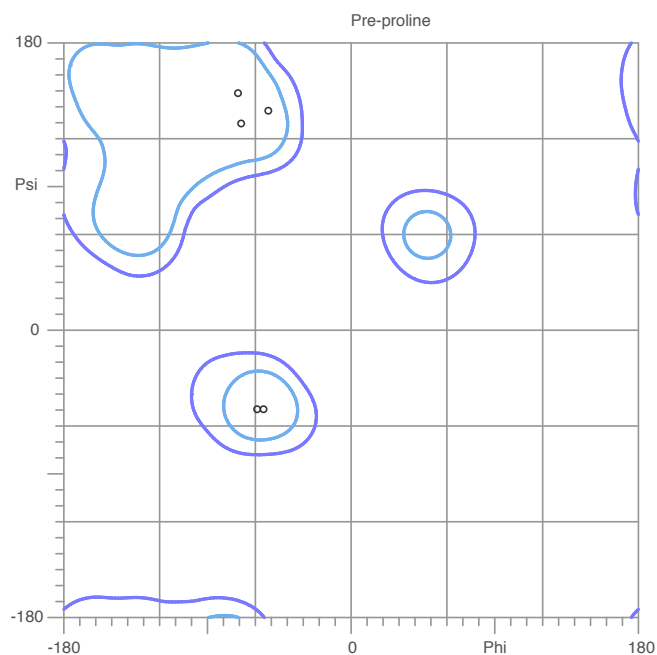
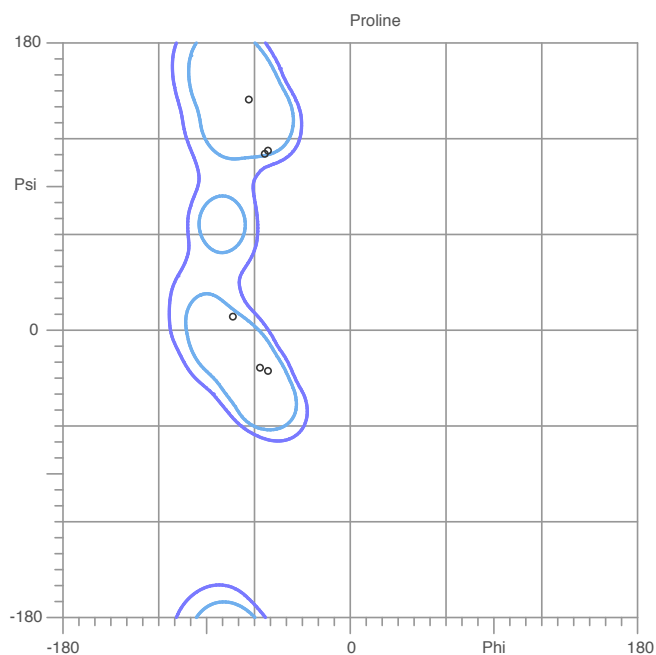
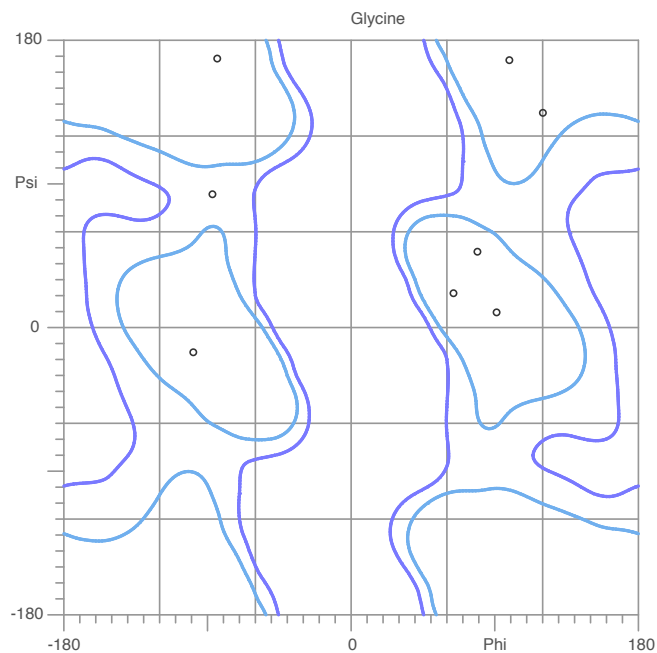
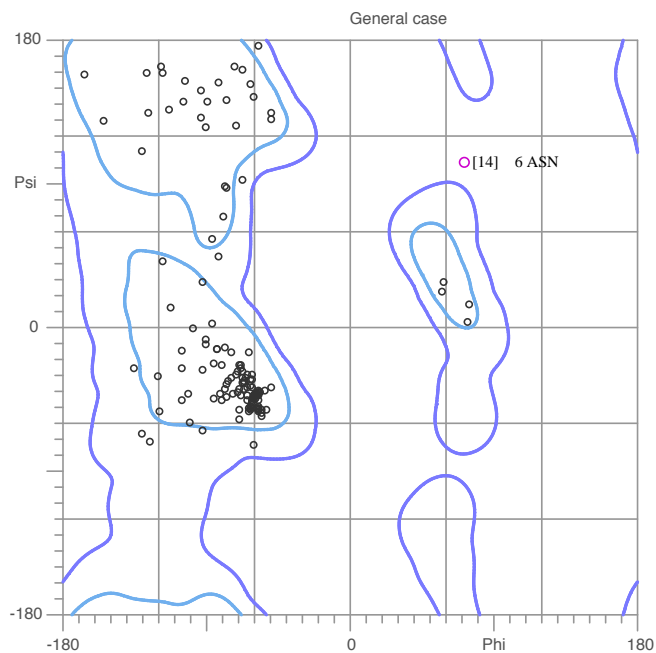
There were 1 outliers (phi, psi):
[13] 12 GLN (66.5, 109.7)

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MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 14



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.

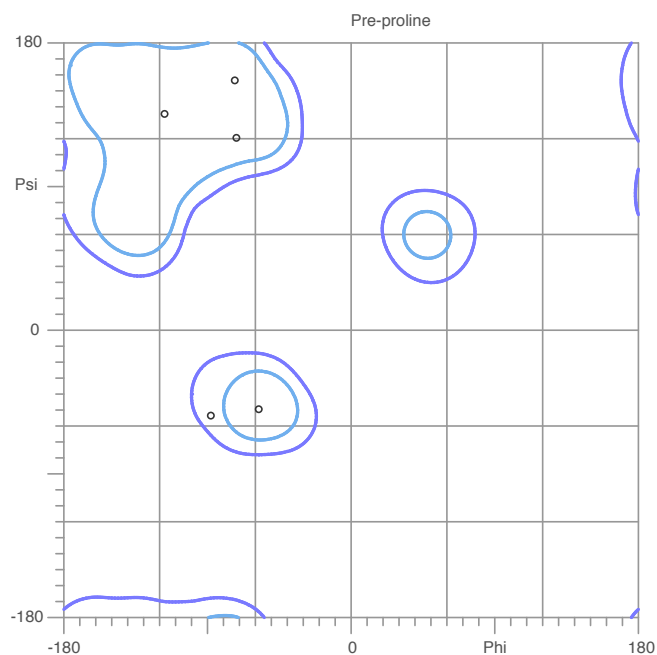
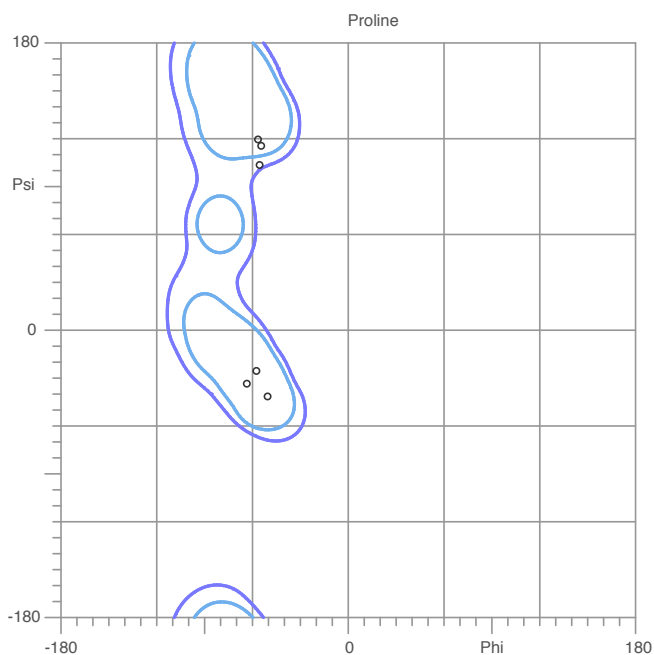
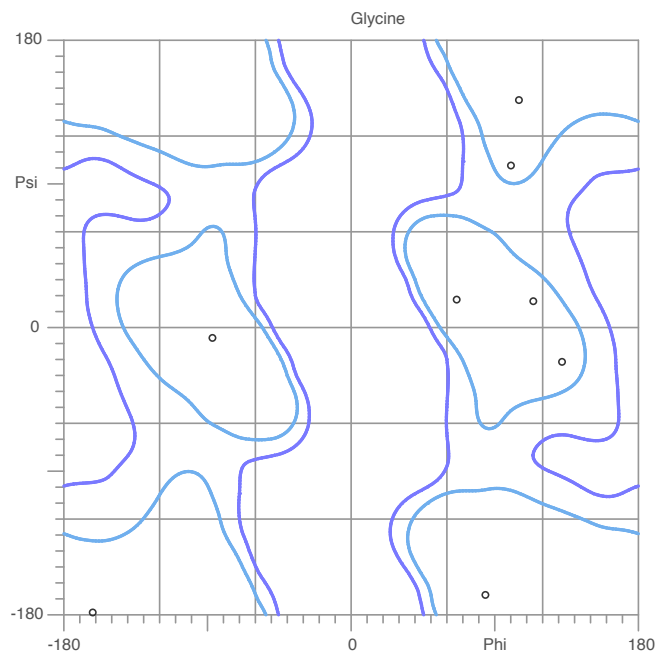
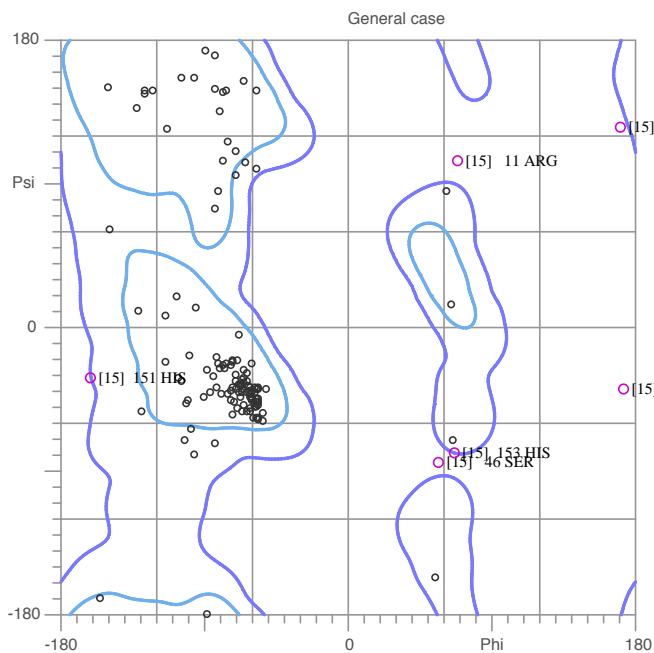
There were 1 outliers (phi, psi):
[14] 6 ASN (71.5, 104.2)

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

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 15



86.9% (133/153) of all residues were in favored (98%) regions.
96.1% (147/153) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[15] 11 ARG (68.9, 106.0)

[15] 44 ALA (172.7, -38.2)

[15] 46 SER (56.8, -84.5)

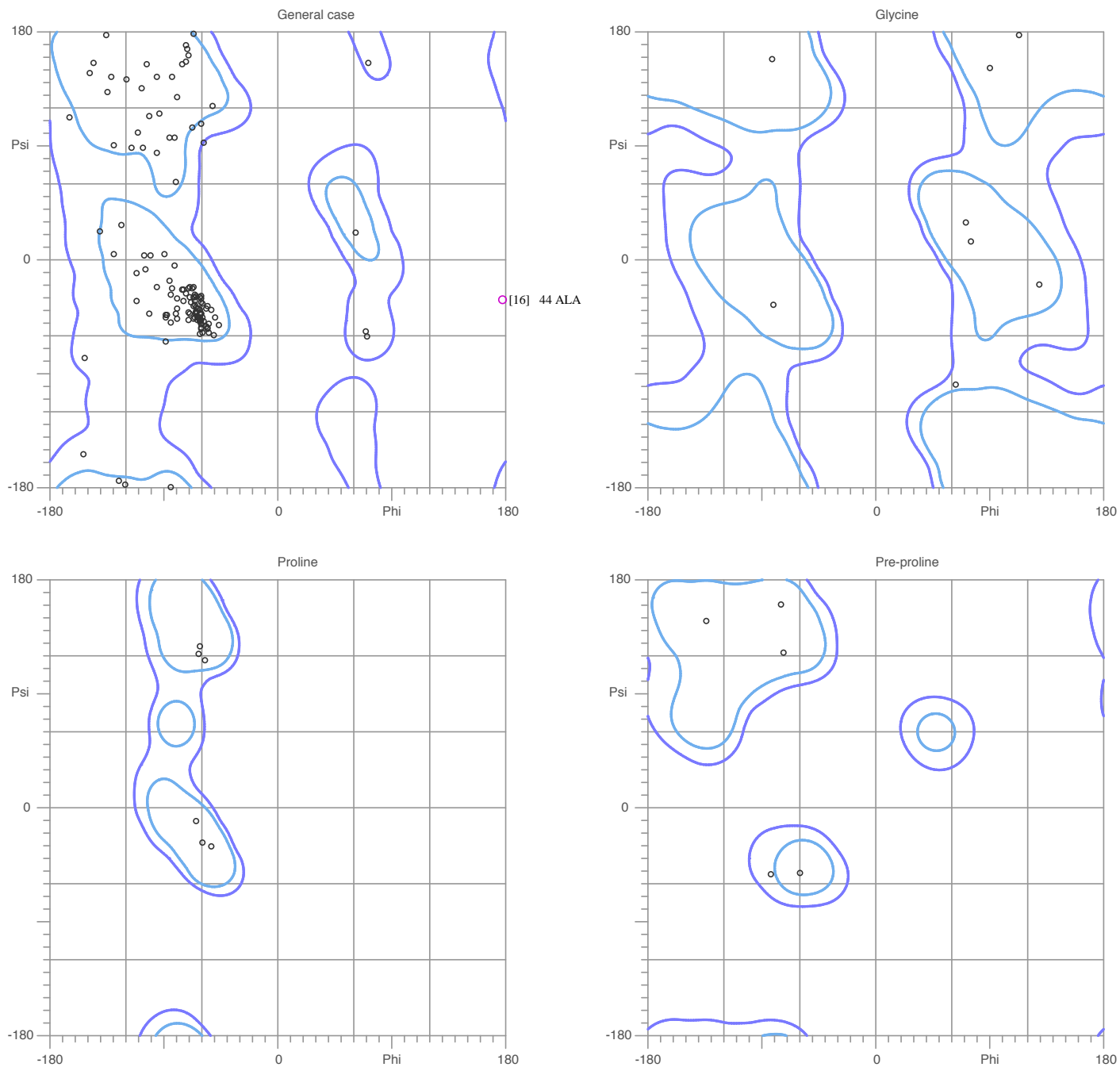
[15] 151 HIS (-162.3, -31.6)

[15] 153 HIS (66.1, -79.0)

[15] 154 HIS (170.0, 126.9)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 16



90.8% (139/153) of all residues were in favored (98%) regions.
99.3% (152/153) of all residues were in allowed (>99.8%) regions.

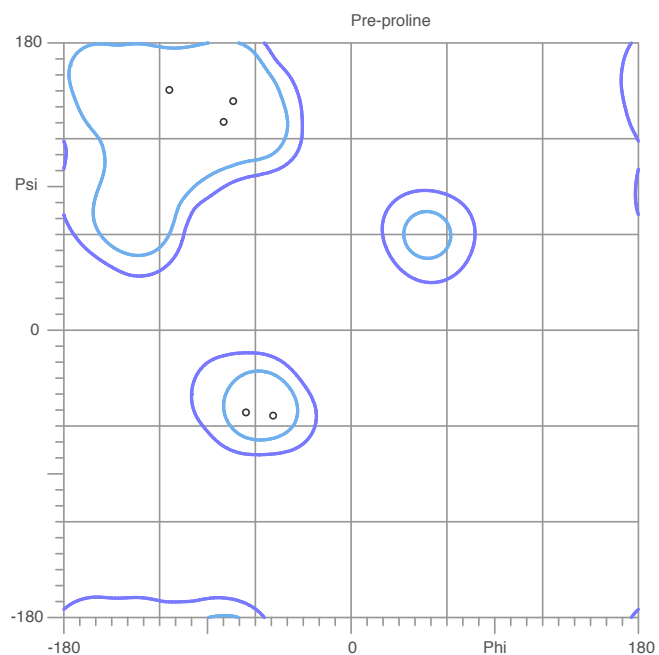
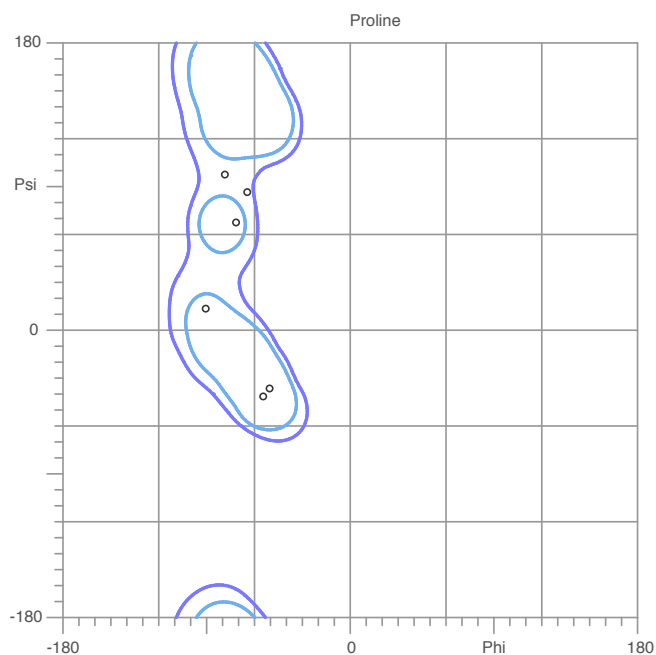
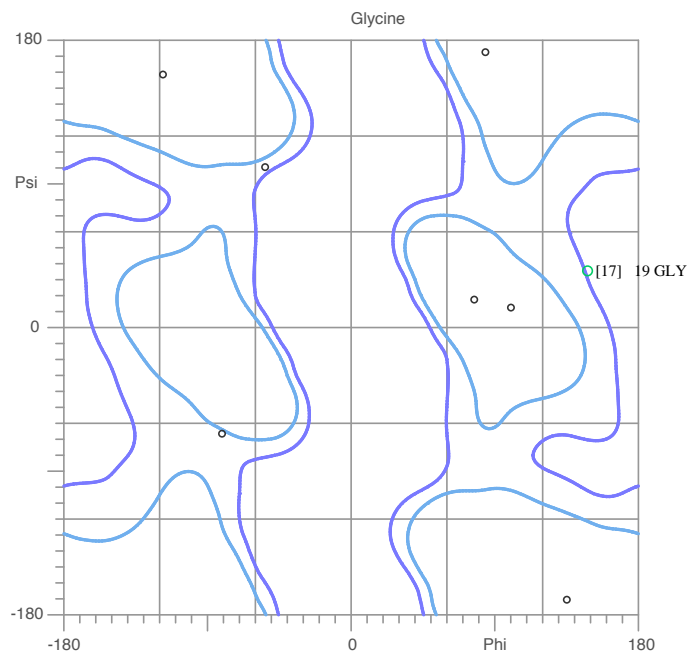
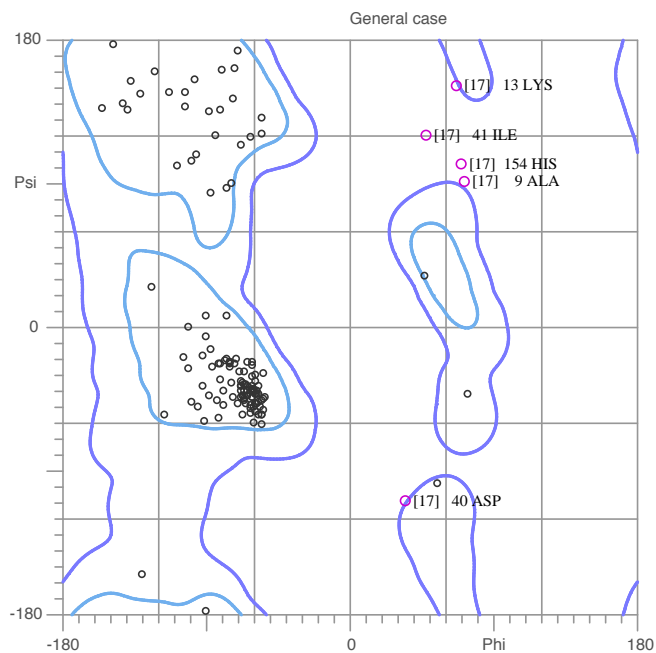
There were 1 outliers (phi, psi):
[16] 44 ALA (177.7, -31.6)

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

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

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 17



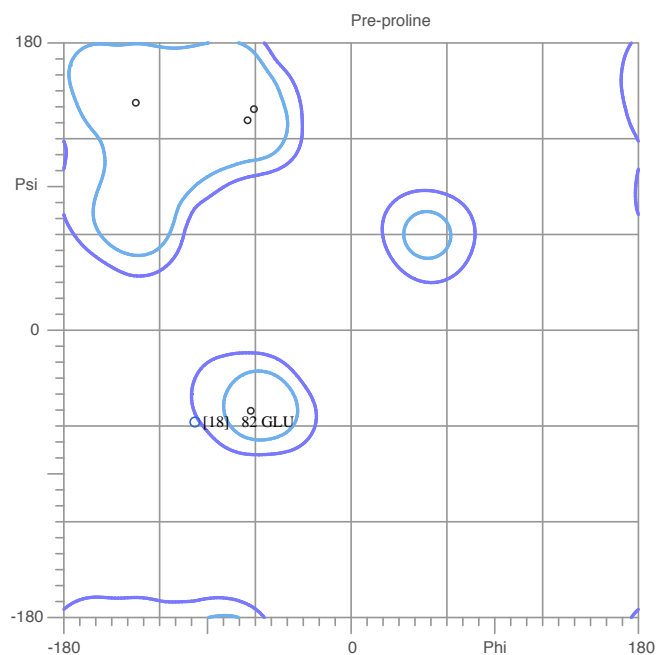
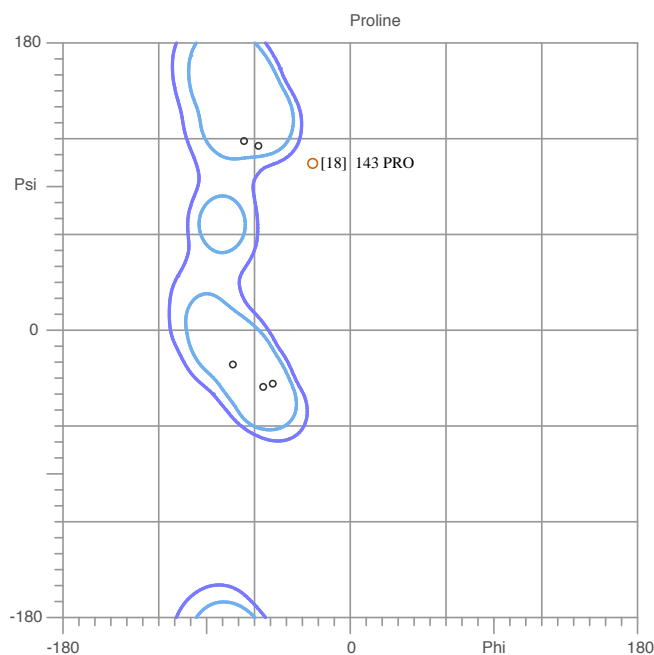
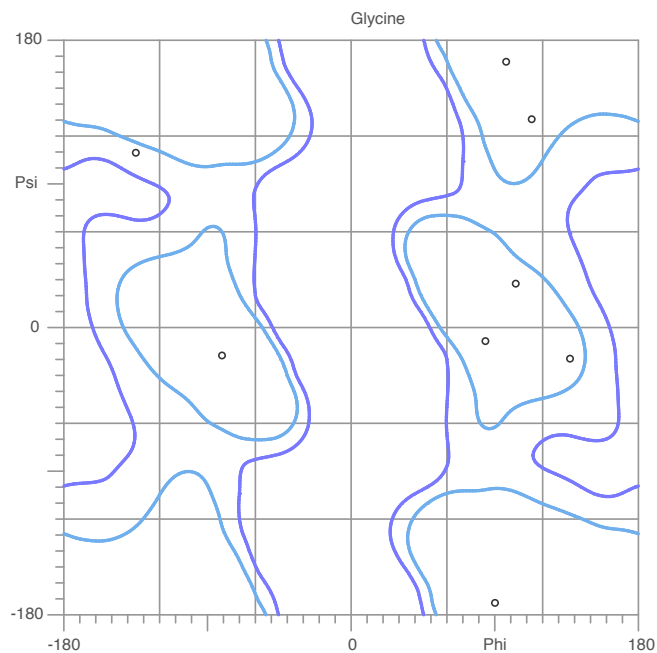
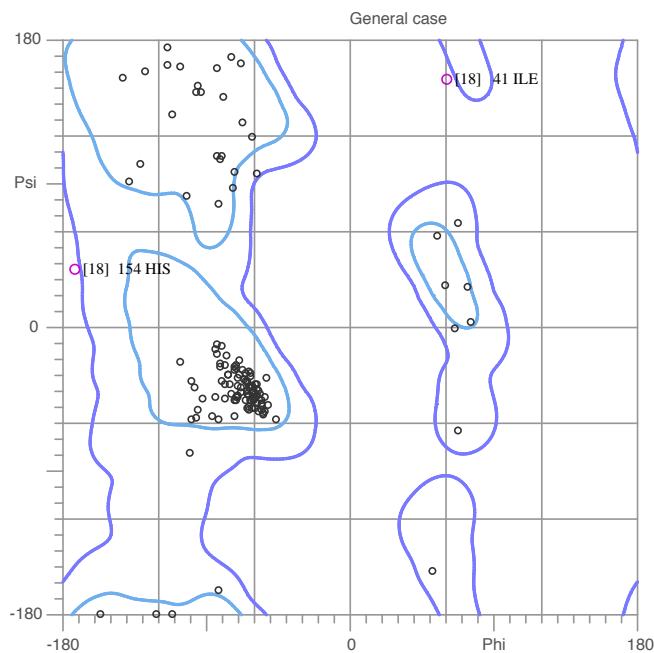
91.5% (140/153) of all residues were in favored (98%) regions.
96.1% (147/153) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[17] 9 ALA (71.2, 92.1)

[17] 13 LYS (66.8, 152.1)
[17] 19 GLY (148.5, 36.5)
[17] 40 ASP (34.5, -109.0)
[17] 41 ILE (47.9, 121.6)
[17] 154 HIS (69.1, 103.1)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 18



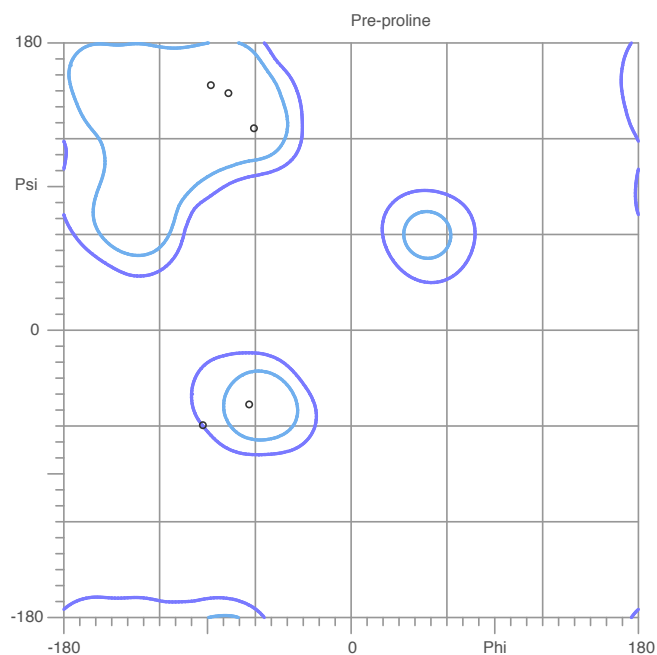
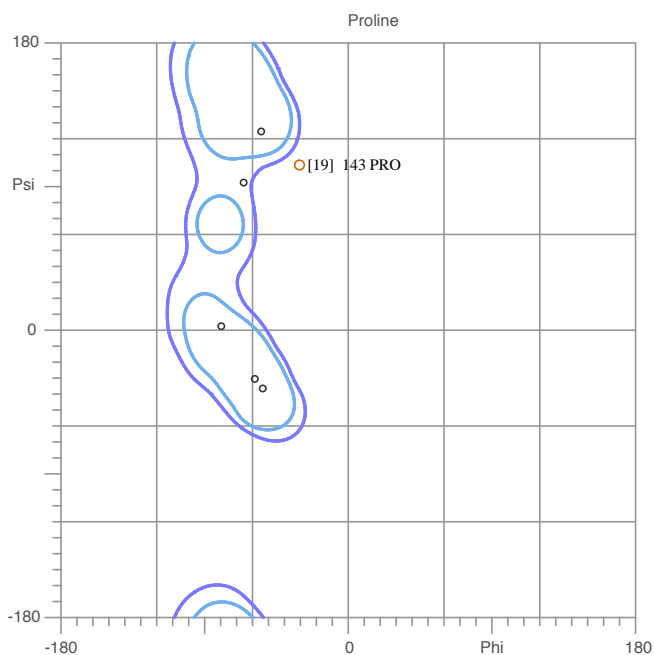
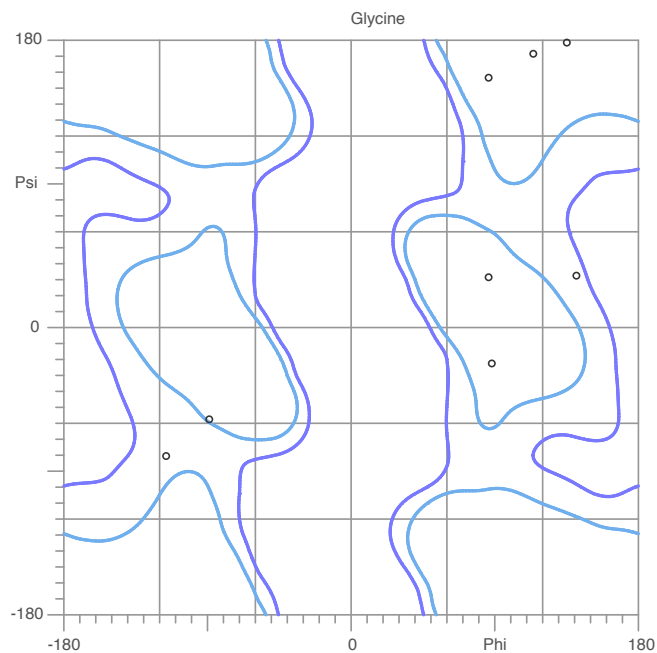
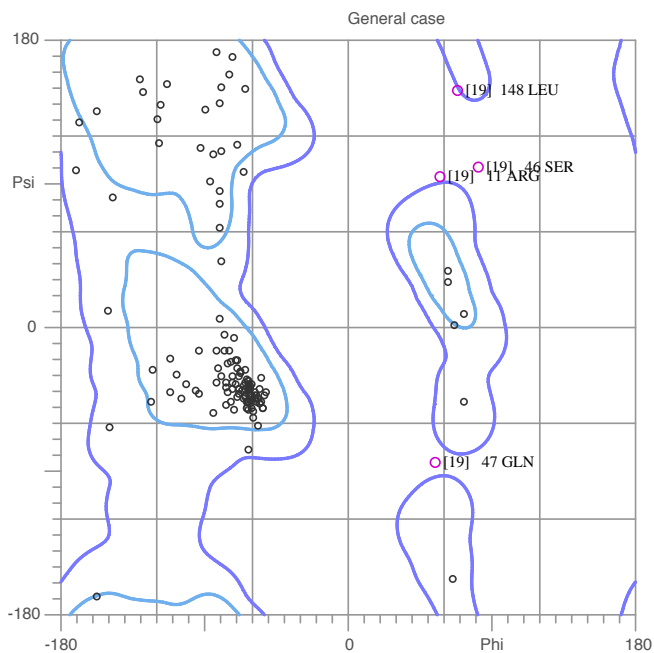
92.2% (141/153) of all residues were in favored (98%) regions.
97.4% (149/153) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [18] 41 ILE (60.3, 156.2)
- [18] 82 GLU (-98.0, -57.4)
- [18] 143 PRO (-24.9, 105.9)
- [18] 154 HIS (-173.6, 37.8)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 19



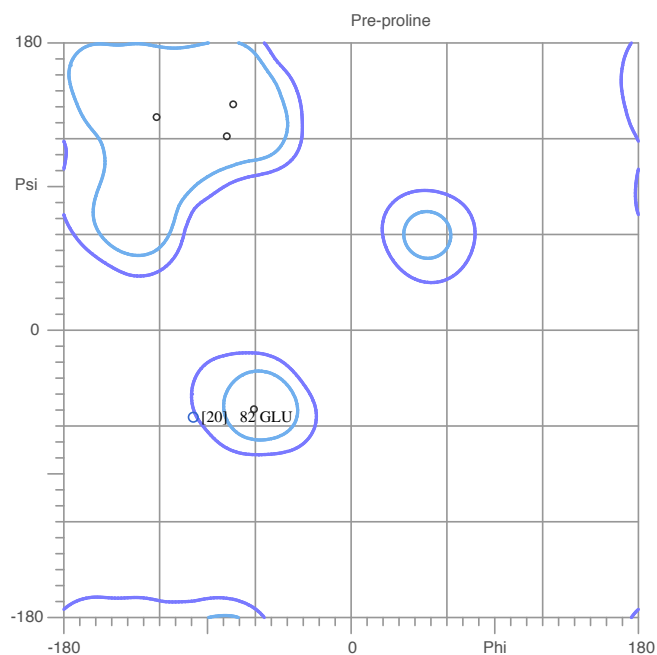
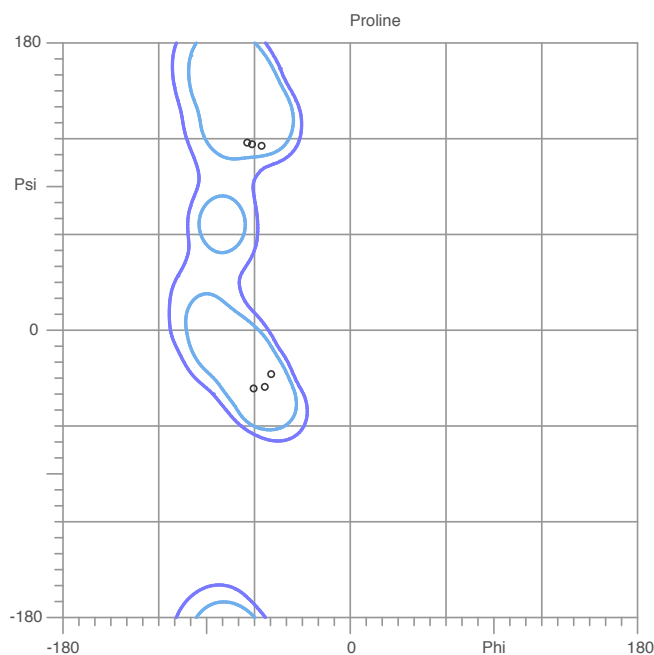
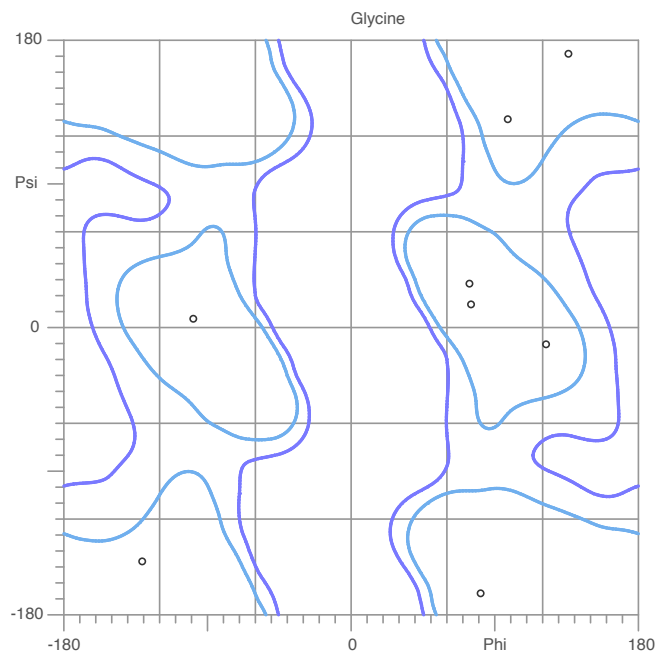
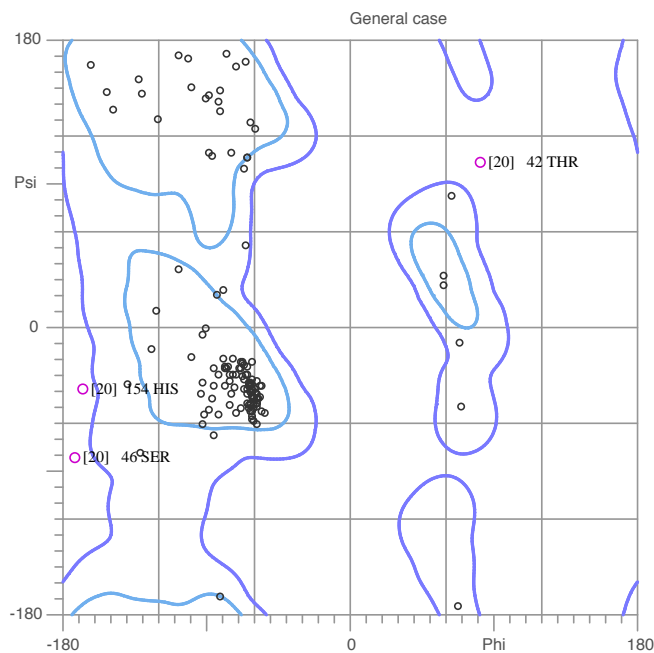
87.6% (134/153) of all residues were in favored (98%) regions.
96.7% (148/153) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[19] 11 ARG (57.4, 95.1)
[19] 46 SER (81.6, 101.7)
[19] 47 GLN (54.2, -84.4)
[19] 143 PRO (-31.3, 104.8)
[19] 148 LEU (68.6, 149.1)

MolProbity Ramachandran analysis

SGR209C_NMR_em_bcr3.pdb, model 20



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):

- [20] 42 THR (81.4, 104.0)
- [20] 46 SER (-173.6, -82.0)
- [20] 82 GLU (-99.3, -54.4)
- [20] 154 HIS (-168.6, -38.4)