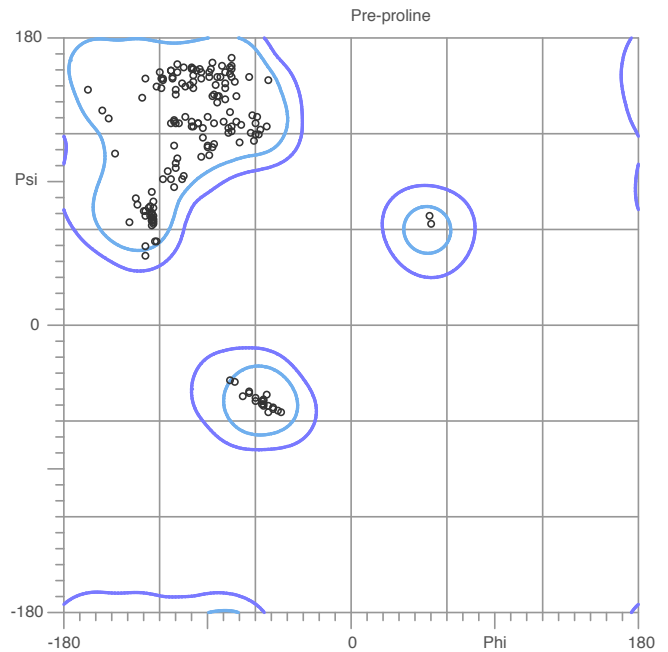
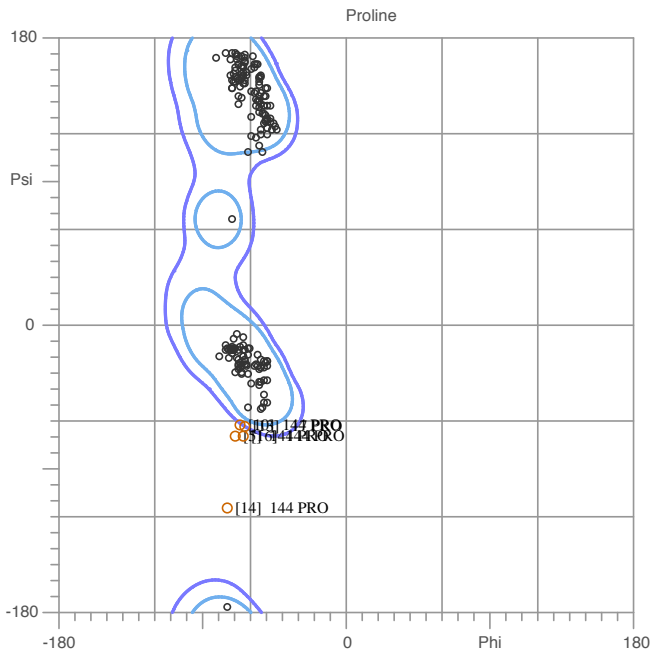
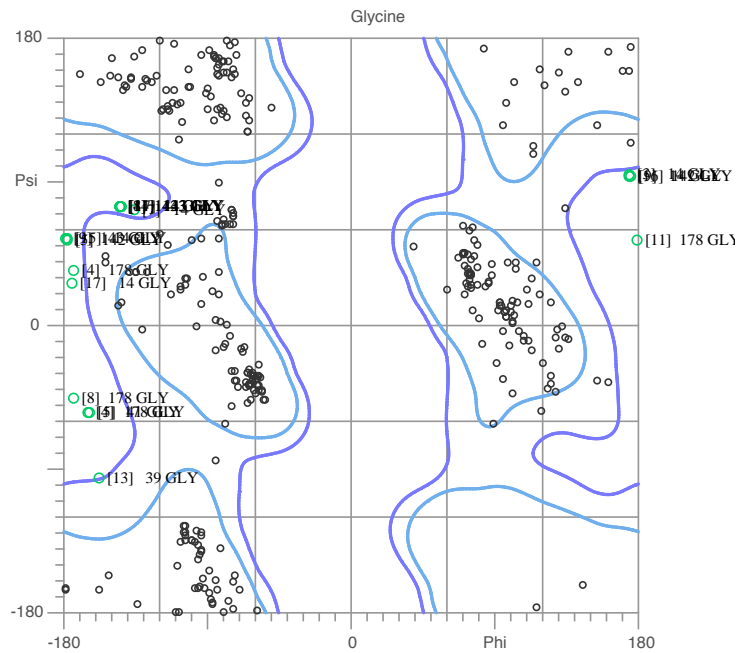
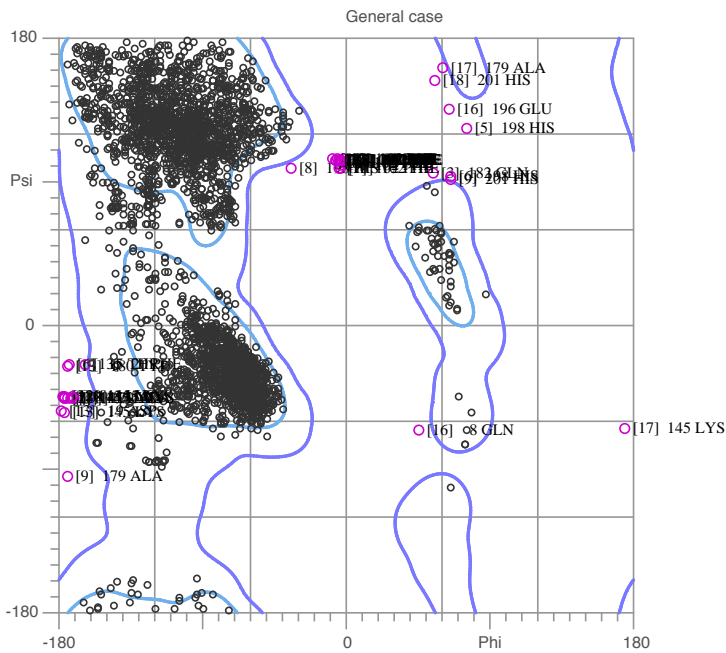


MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, all models



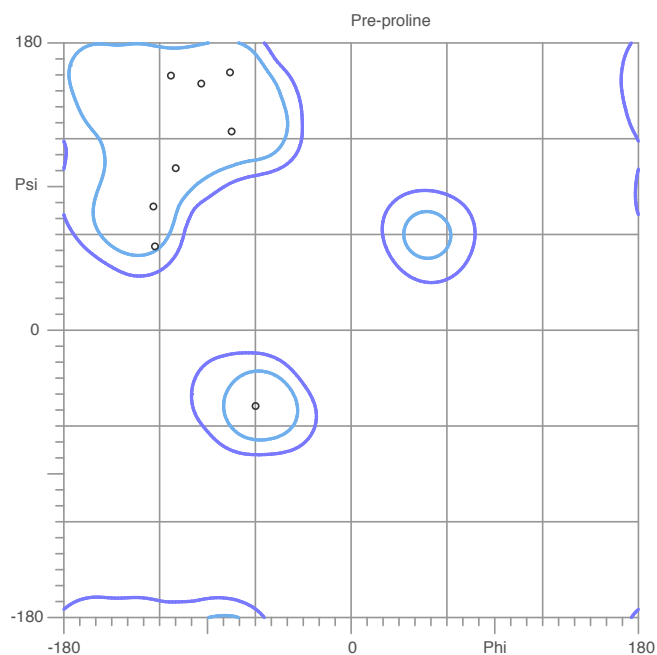
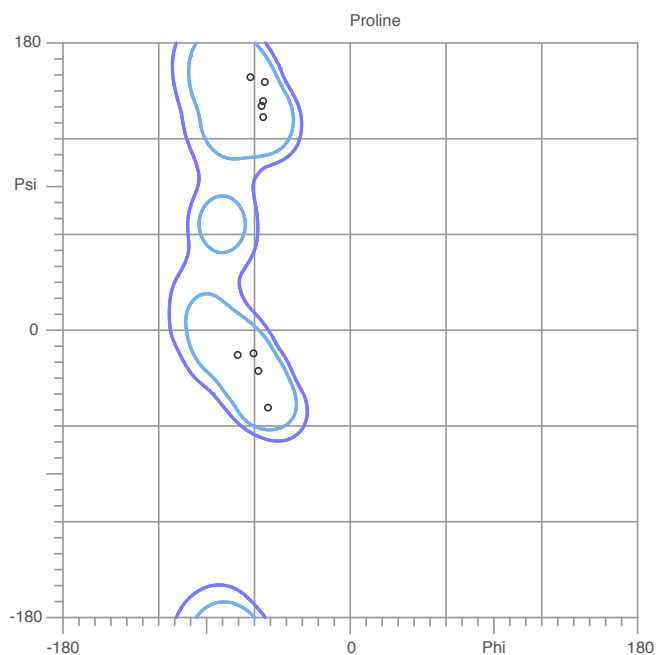
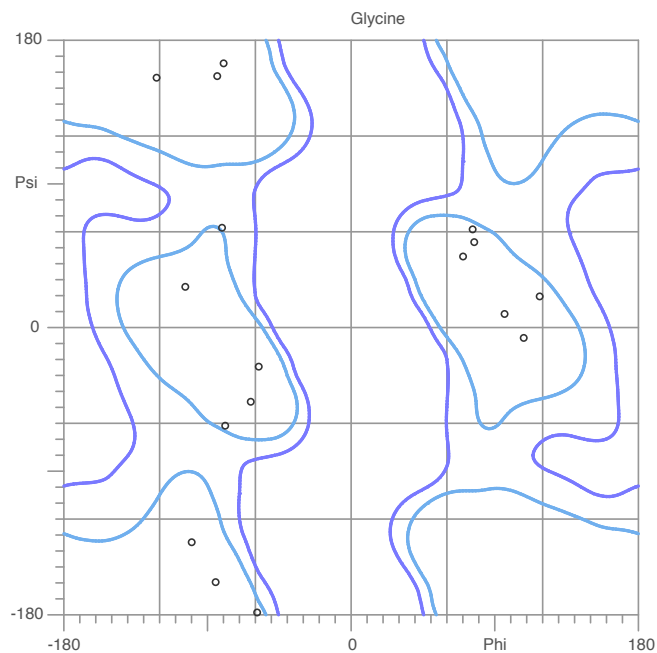
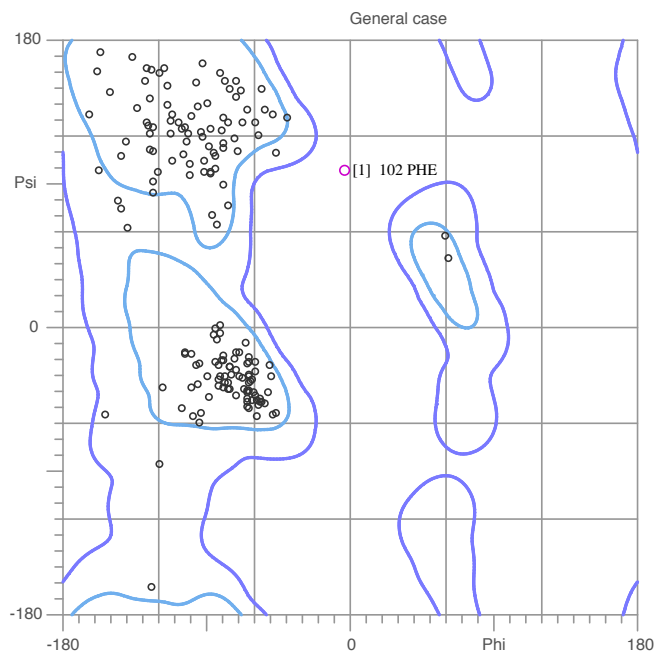
92.6% (1702/1800) of all residues were in favored (98%) regions.
98.4% (1936/1960) of all residues were in allowed (>99.8%) regions.

There were 64 outliers (phi, psi):

- (1) 102 PHE (-4.9, 96.3)
- (2) 102 PHE (-2.1, 105.1)
- (3) 145 LYS (-177.8, -45.1)
- (4) 14 GLY (175.0, 95.1)
- (5) 145 LYS (-178.9, -44.9)
- (6) 102 GLN (-55.0, 97.0)
- (7) 41 GLY (-165.0, -55.0)
- (8) 102 PHE (2.1, 105.0)
- (9) 143 GLY (-145.1, 75.0)
- (10) 145 LYS (-173.1, -45.0)
- (11) 178 GLY (-175.0, 35.0)
- (12) 145 GLY (-178.7, -54.9)
- (13) 144 PRO (-70.5, -69.7)
- (14) 178 GLY (-108.0, -55.0)
- (15) 198 HIS (75.1, 125.0)
- (16) 15 THR (-175.0, -25.0)
- (17) 102 PHE (-4.9, 103.8)
- (18) 198 HIS (65.0, 94.9)
- (19) 14 GLY (-138.6, 73.9)
- (20) 102 PHE (-1.2, 106.9)
- (21) 145 LYS (-177.7, -45.1)
- (22) 102 PHE (-5.1, 102.6)
- (23) 145 GLY (-145.0, 75.0)
- (24) 178 GLY (-175.0, -45.1)
- (25) 198 HIS (-55.1, 99.4)
- (26) 14 GLY (175.0, 95.0)
- (27) 102 PHE (-4.2, 101.7)
- (28) 143 GLY (-179.7, 55.2)
- (29) 179 ALA (-175.0, -94.9)
- (30) 201 HIS (65.0, 92.0)
- (31) 102 PHE (-5.2, 99.5)
- (32) 144 PRO (-67.6, -62.2)
- (33) 143 GLY (-145.0, 75.1)
- (34) 178 GLY (-179.9, 55.0)
- (35) 102 PHE (-9.4, 105.9)
- (36) 145 LYS (-177.2, -45.0)
- (37) 17 PRO (-65.0, -65.4)
- (38) 19 ASP (-179.9, -53.0)
- (39) 20 PHE (-164.6, -24.9)
- (40) 39 GLY (-128.4, 95.5)
- (41) 102 PHE (-4.9, 105.0)
- (42) 145 LYS (-177.0, -55.0)
- (43) 180 TYR (-175.0, -25.0)
- (44) 102 PHE (-4.9, 104.9)
- (45) 143 GLY (-145.0, 75.1)
- (46) 144 PRO (-75.1, -114.9)
- (47) 14 GLY (-178.1, 55.0)
- (48) 102 PHE (-4.9, 104.0)
- (49) 8 GLN (-45.0, -65.1)
- (50) 102 PHE (-5.8, 105.0)
- (51) 142 GLY (-174.8, 95.0)
- (52) 144 PRO (-65.3, -69.7)
- (53) 196 GLU (-64.6, 136.0)
- (54) 14 GLY (-175.0, 27.9)
- (55) 102 PHE (-5.0, 104.0)
- (56) 143 GLY (-145.0, 75.1)
- (57) 145 LYS (-174.7, -65.0)
- (58) 179 ALA (0.0, 163.0)
- (59) 102 PHE (-4.9, 104.2)
- (60) 145 LYS (-171.4, -45.2)
- (61) 201 HIS (-55.1, 154.9)
- (62) 102 PHE (-1.2, 105.0)
- (63) 179 ALA (-175.1, -45.1)
- (64) 145 LYS (-172.1, -45.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 1

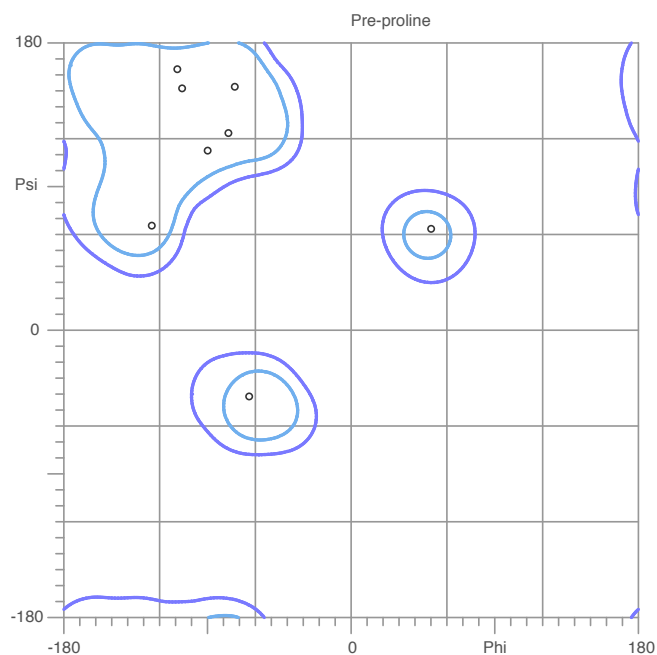
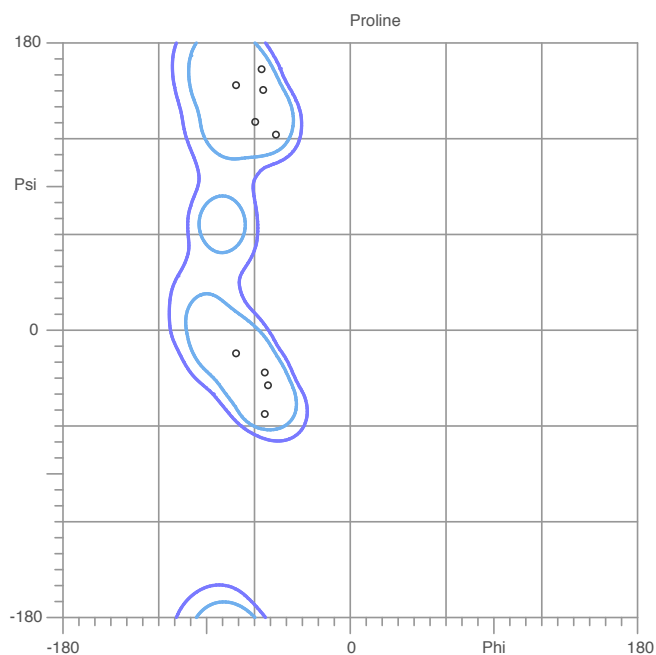
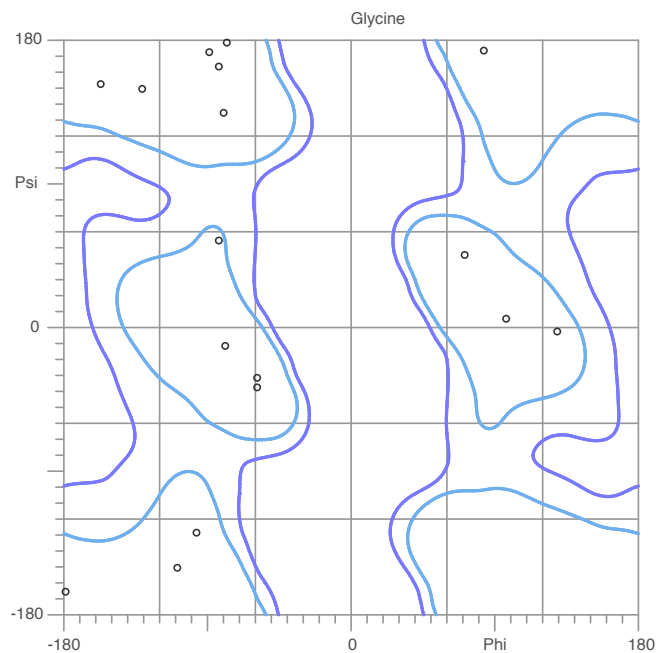
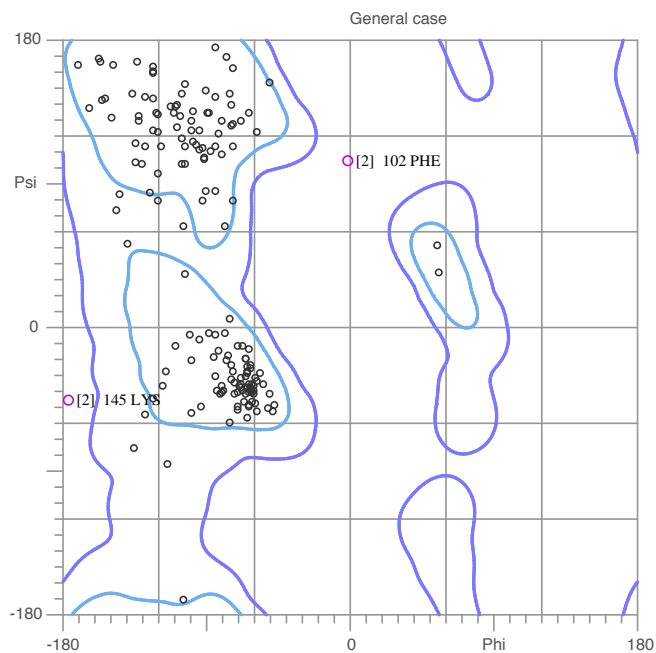


95.0% (190/200) of all residues were in favored (98%) regions.
99.5% (199/200) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[1] 102 PHE (-4.9, 99.3)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 2



94.5% (189/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

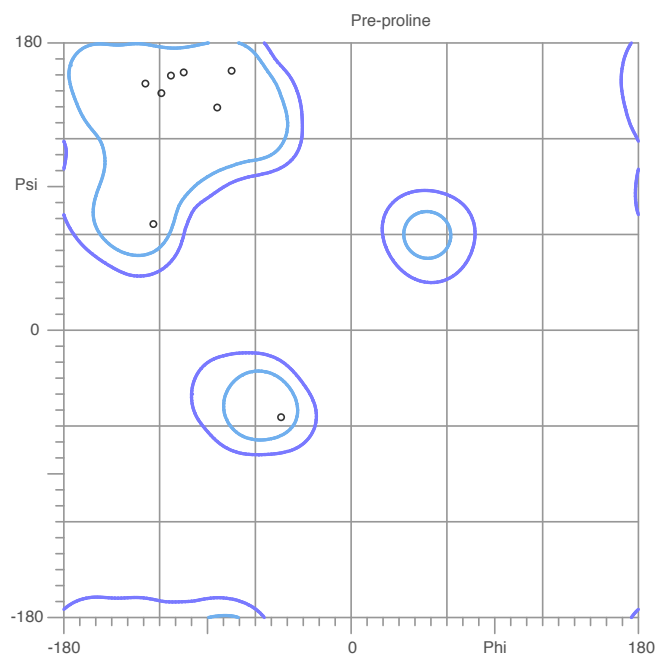
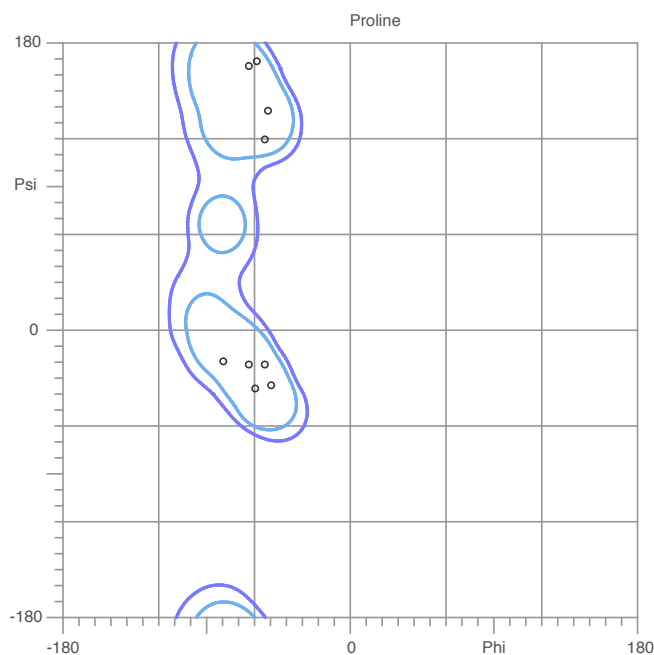
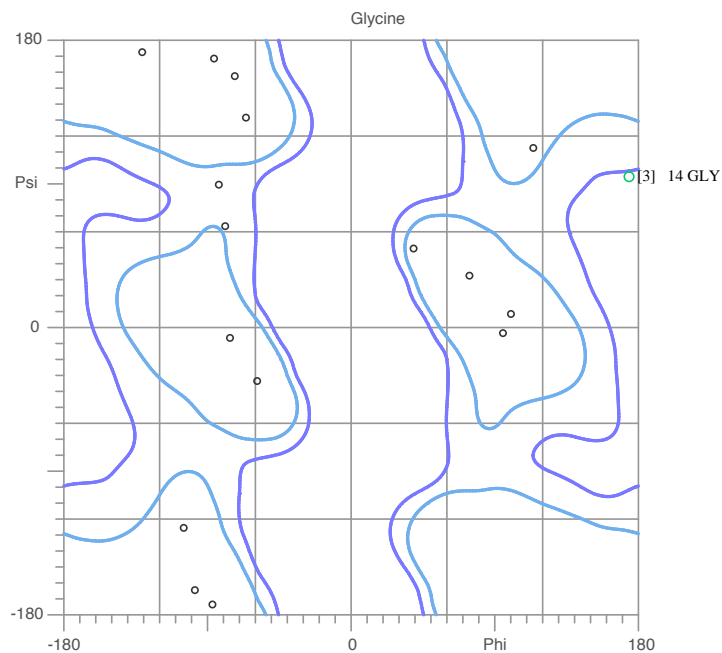
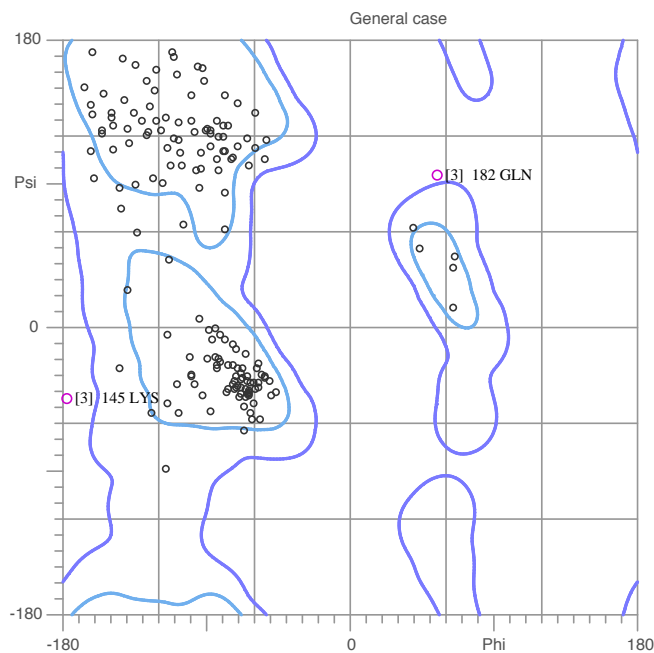
There were 2 outliers (phi, psi):

[2] 102 PHE (-2.1, 105.1)

[2] 145 LYS (-177.6, -45.1)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 3



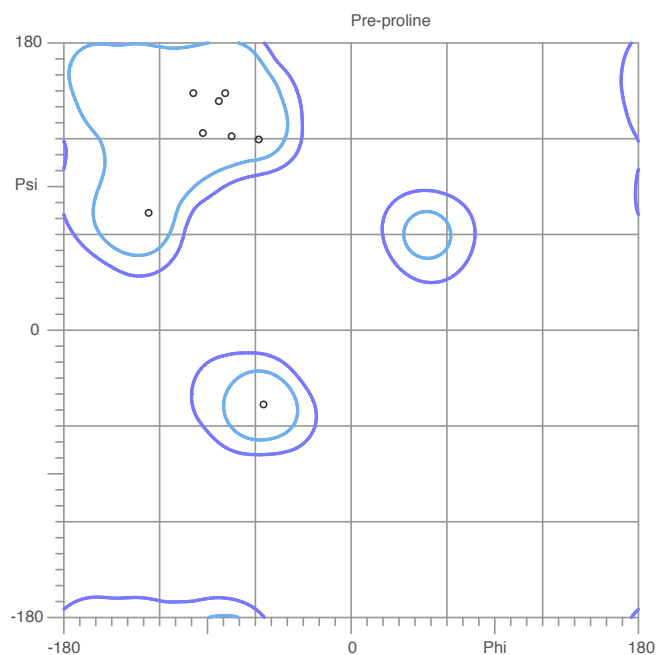
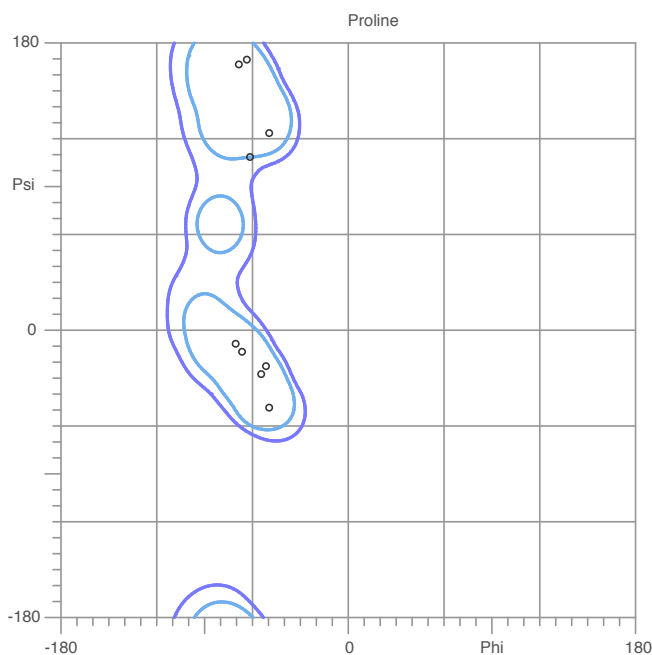
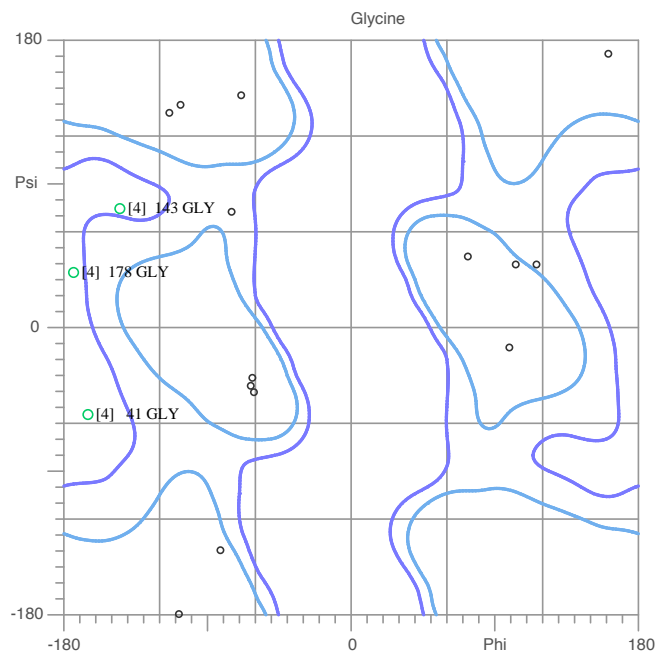
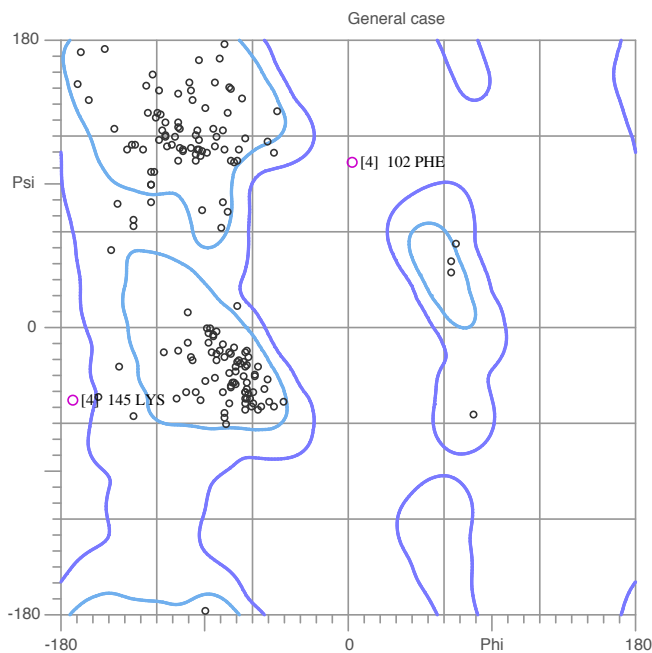
91.0% (182/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 14 GLY (175.0, 95.1)
- [3] 145 LYS (-178.9, -44.9)
- [3] 182 GLN (55.0, 97.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 4



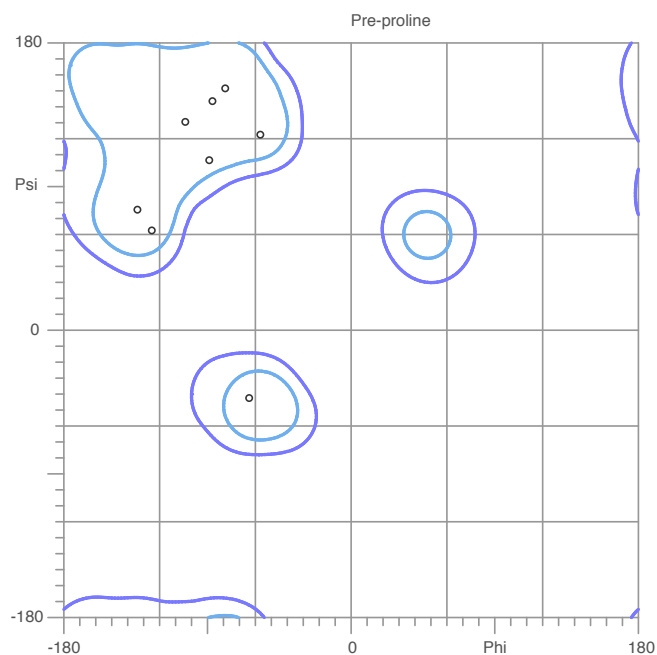
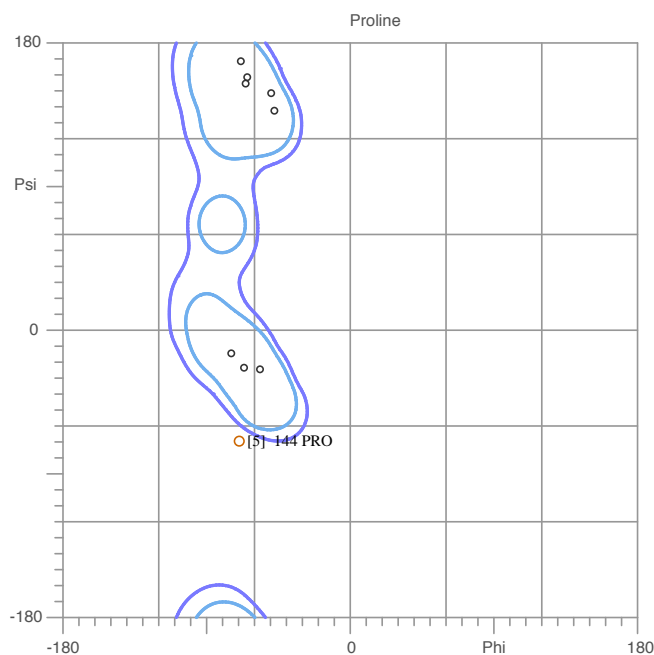
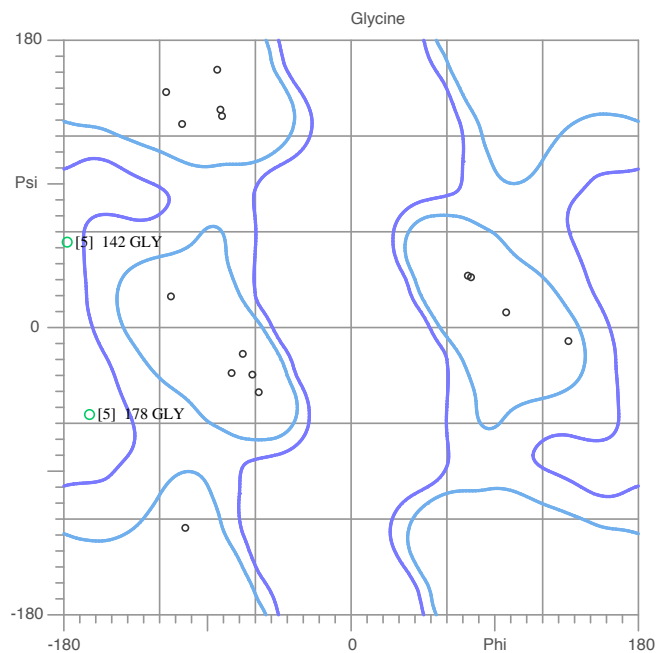
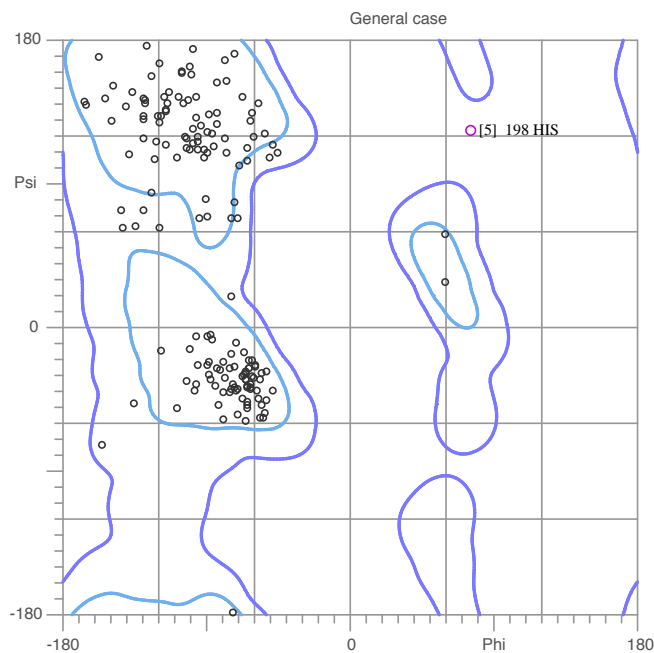
90.5% (181/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [4] 41 GLY (-165.0, -55.0)
- [4] 102 PHE (2.1, 105.0)
- [4] 143 GLY (-145.1, 75.0)
- [4] 145 LYS (-173.1, -45.0)
- [4] 178 GLY (-175.0, 35.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 5



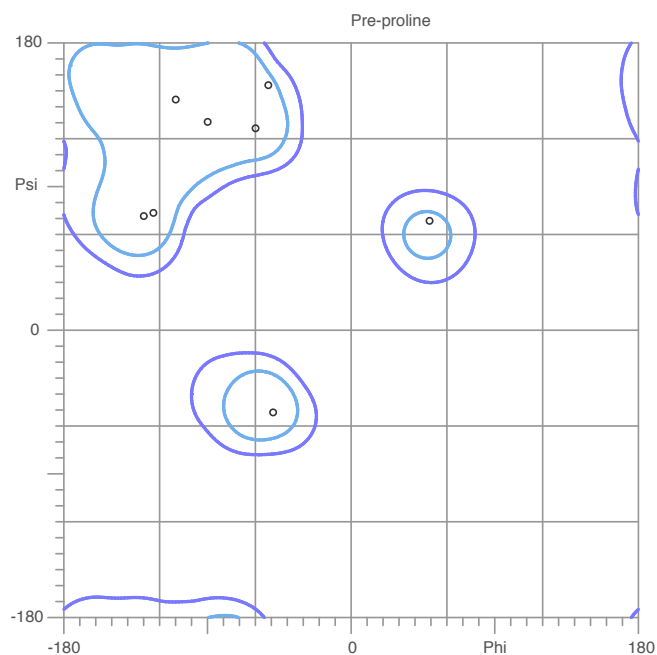
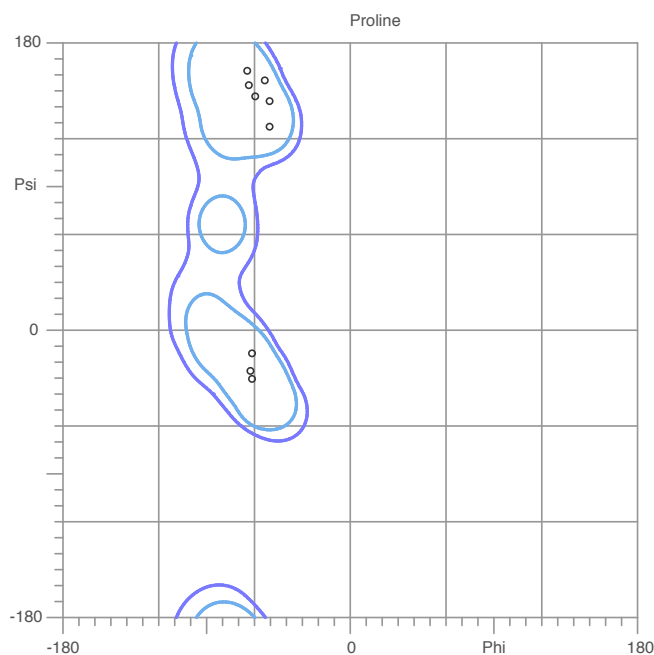
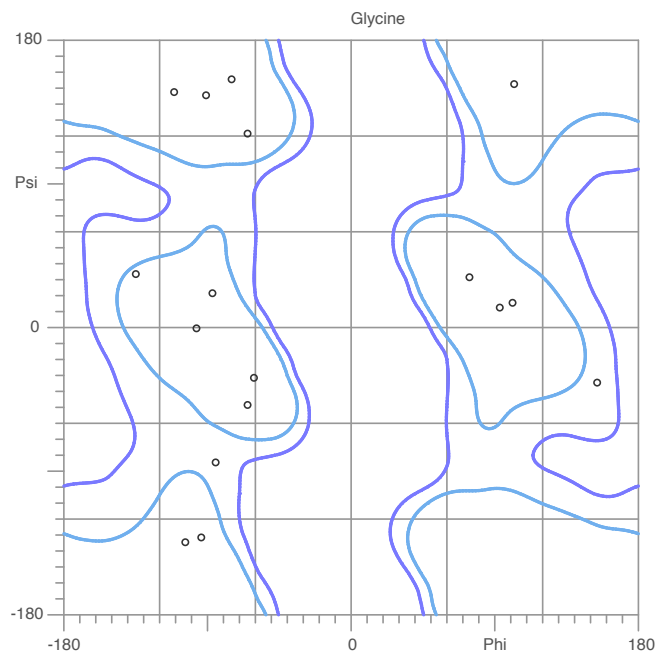
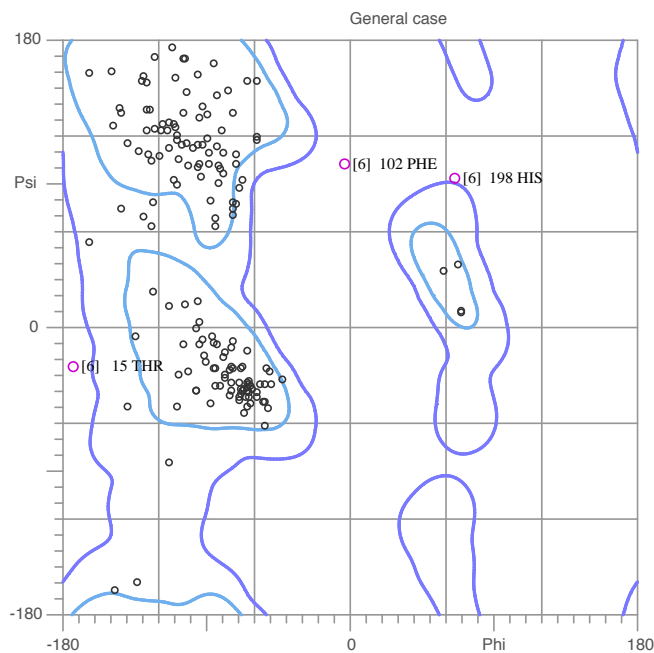
91.5% (183/200) of all residues were in favored (98%) regions.
98.0% (196/200) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [5] 142 GLY (-178.7, 54.9)
- [5] 144 PRO (-70.5, -69.7)
- [5] 178 GLY (-165.0, -55.0)
- [5] 198 HIS (75.1, 125.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 6



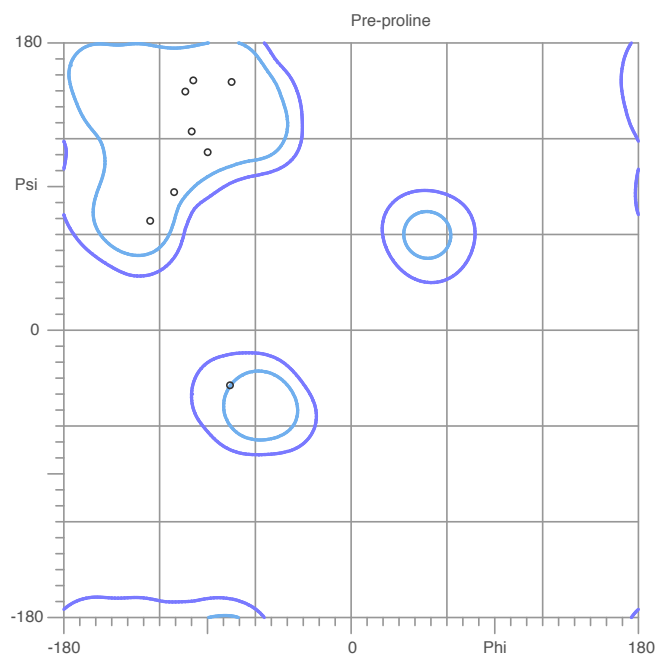
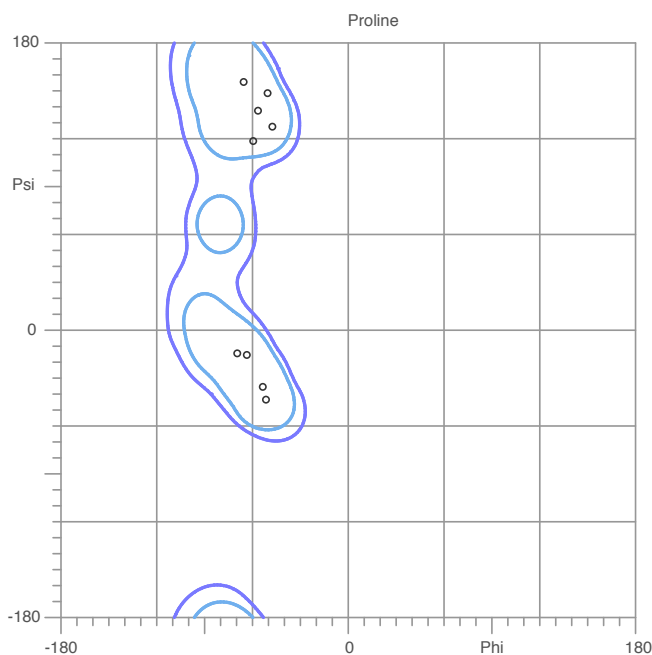
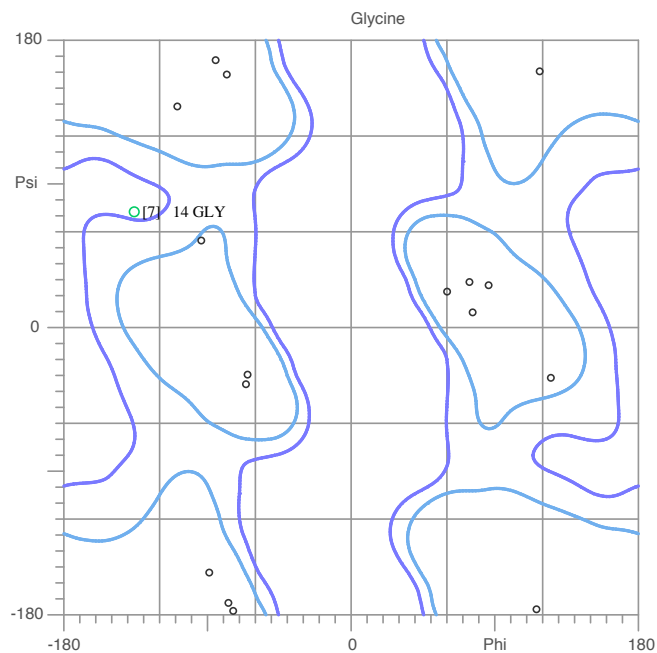
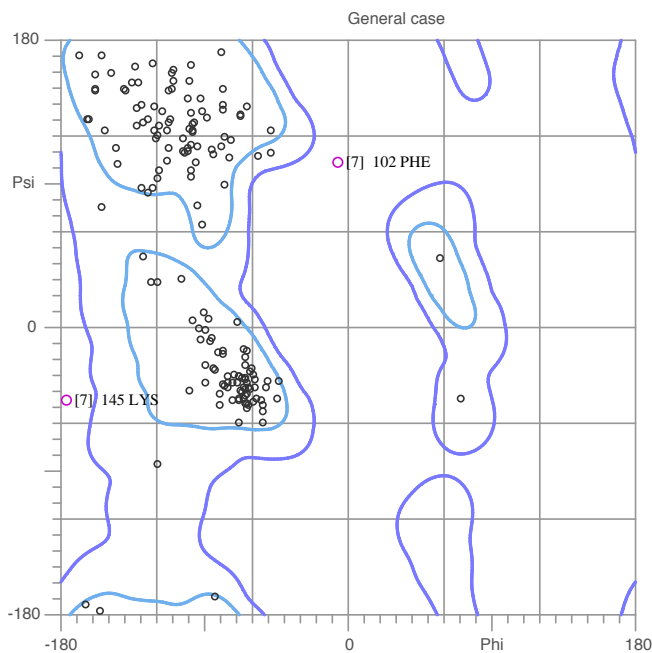
91.5% (183/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 15 THR (-175.0, -25.0)
- [6] 102 PHE (-4.9, 103.8)
- [6] 198 HIS (65.0, 94.9)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 7



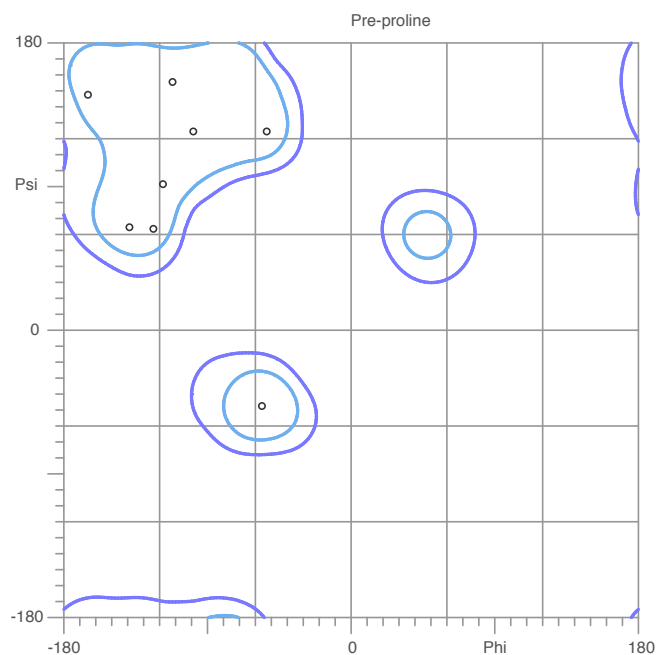
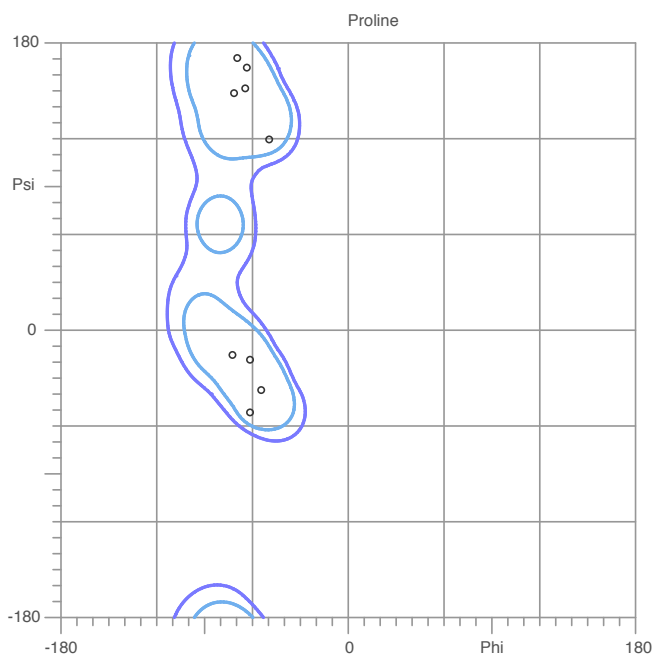
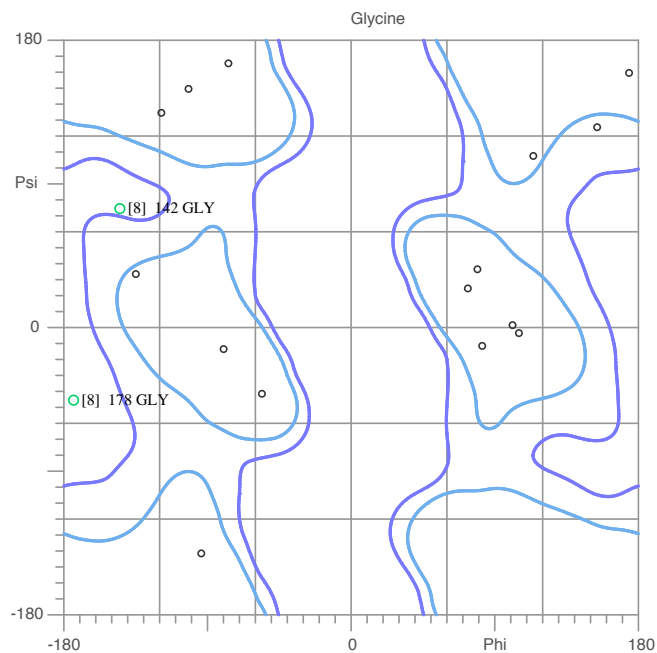
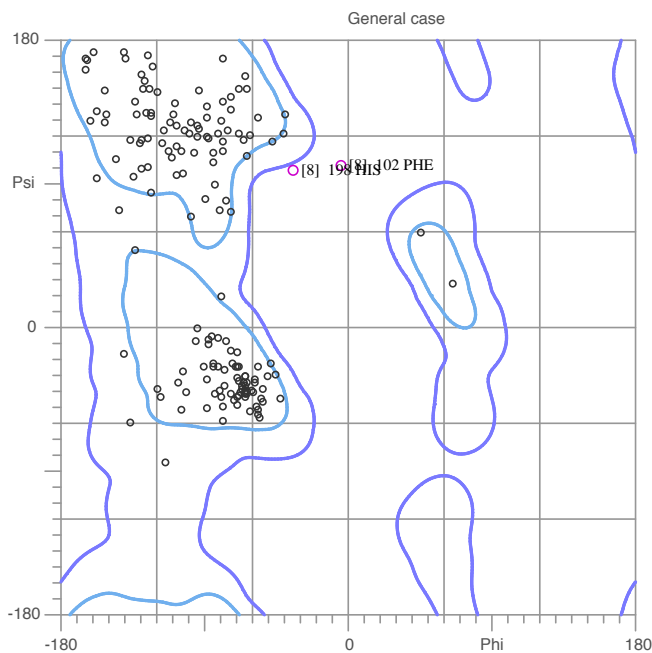
95.5% (191/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [7] 14 GLY (-136.9, 73.9)
- [7] 102 PHE (-7.2, 104.9)
- [7] 145 LYS (-177.7, -45.1)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 8



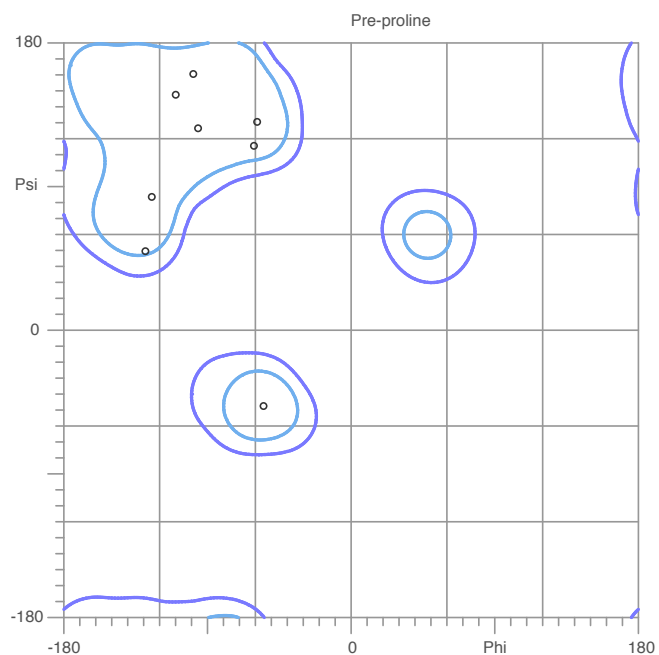
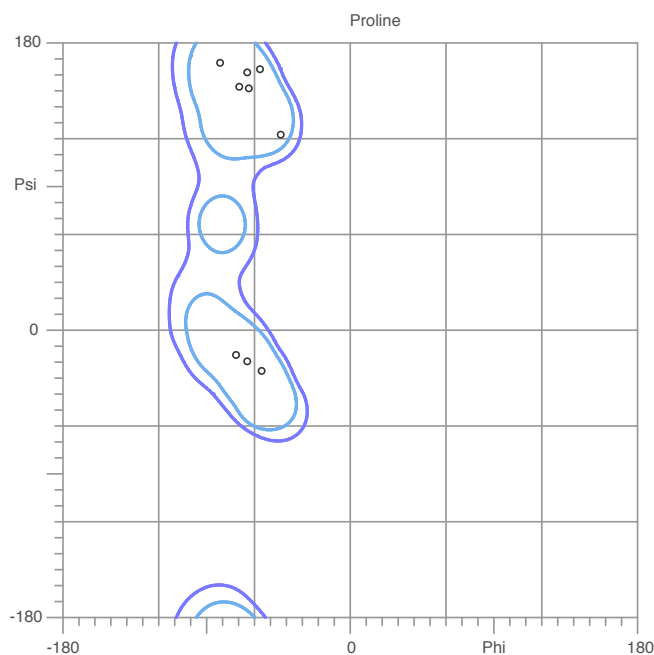
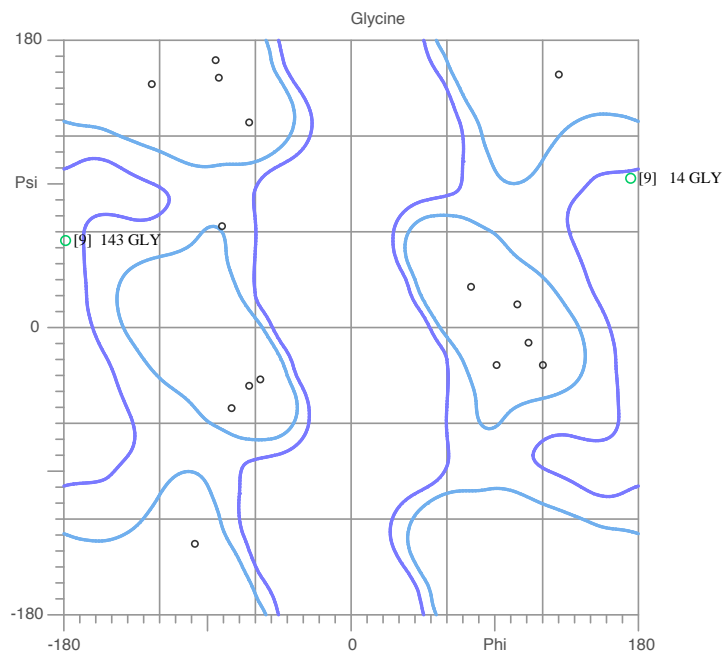
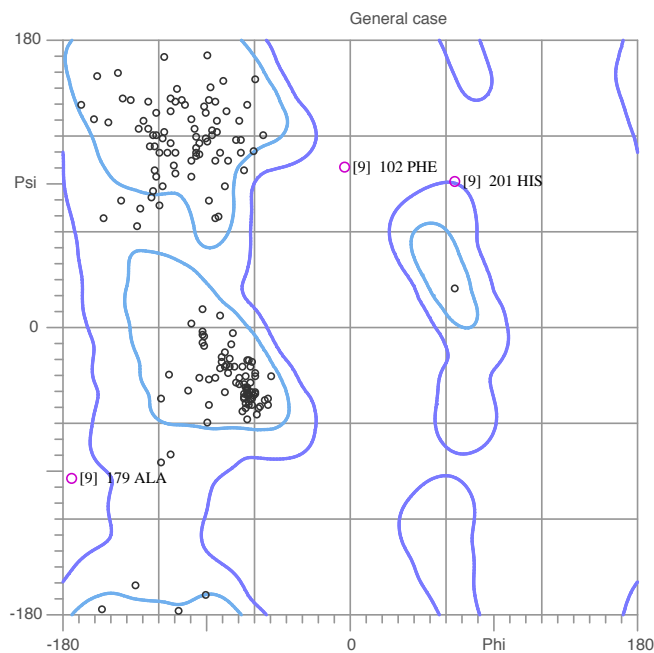
93.0% (186/200) of all residues were in favored (98%) regions.
98.0% (196/200) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [8] 102 PHE (-5.1, 102.6)
- [8] 142 GLY (-145.0, 75.0)
- [8] 178 GLY (-175.0, -45.1)
- [8] 198 HIS (-35.1, 99.4)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 9



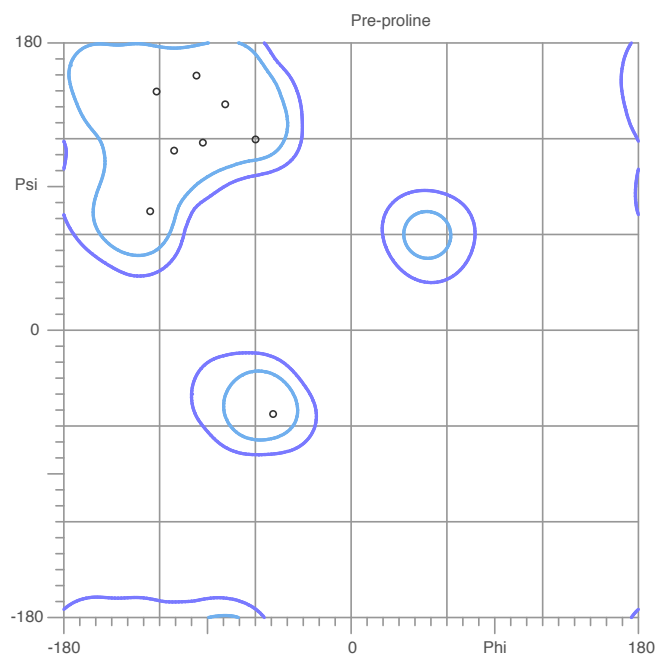
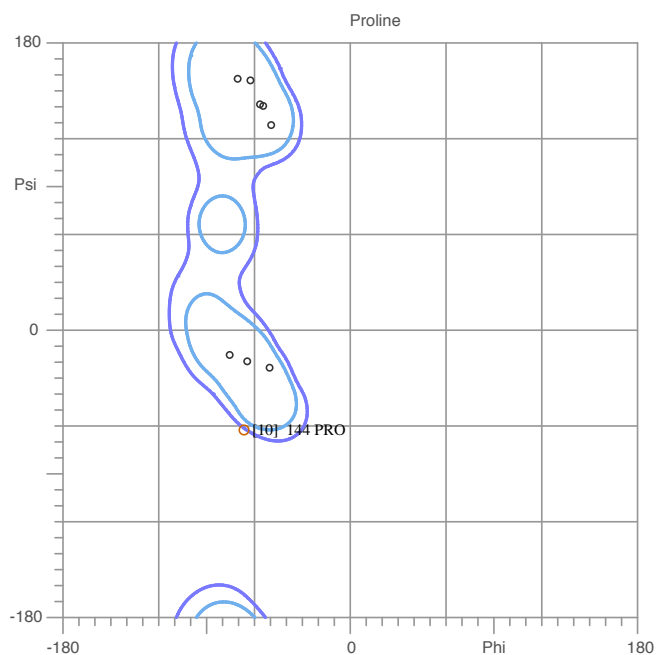
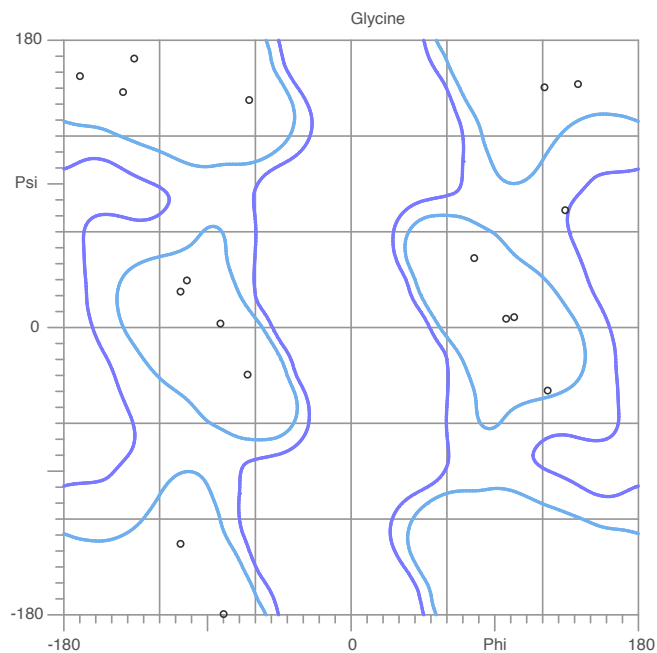
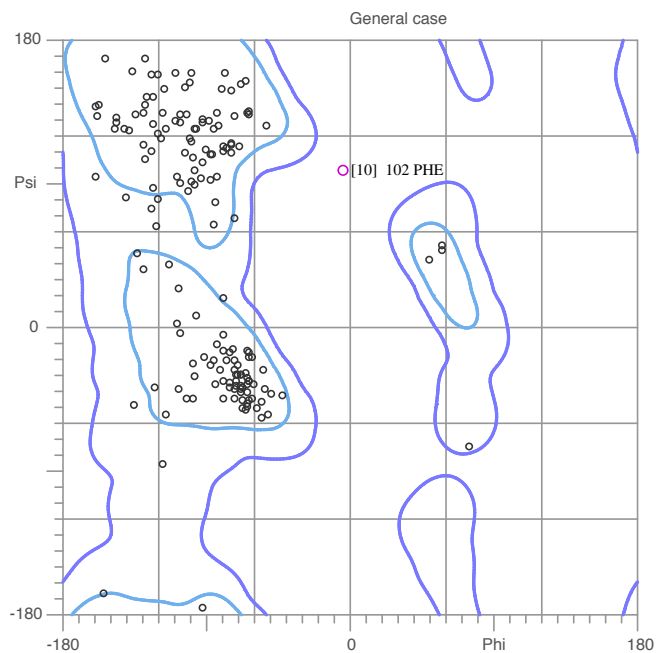
91.5% (183/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[9] 14 GLY (175.0, 95.0)
[9] 102 PHE (-4.2, 101.7)
[9] 143 GLY (-179.7, 55.3)
[9] 179 ALA (-175.0, -94.9)
[9] 201 HIS (65.0, 92.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 10

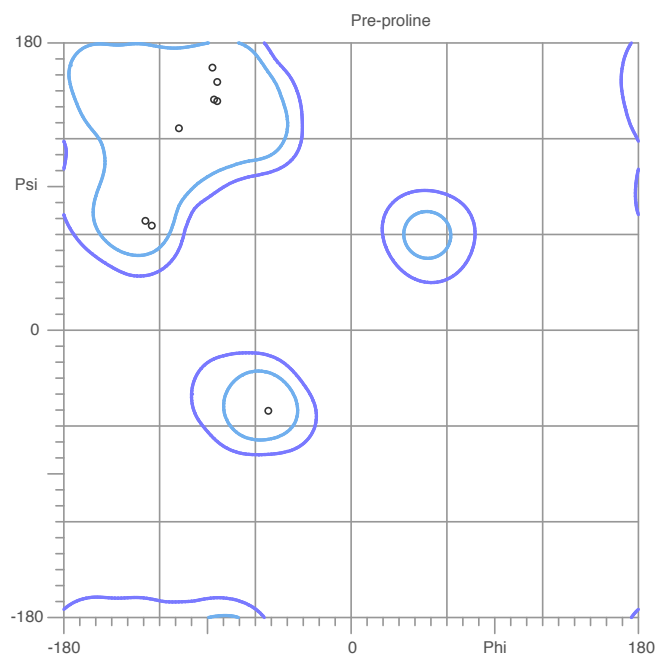
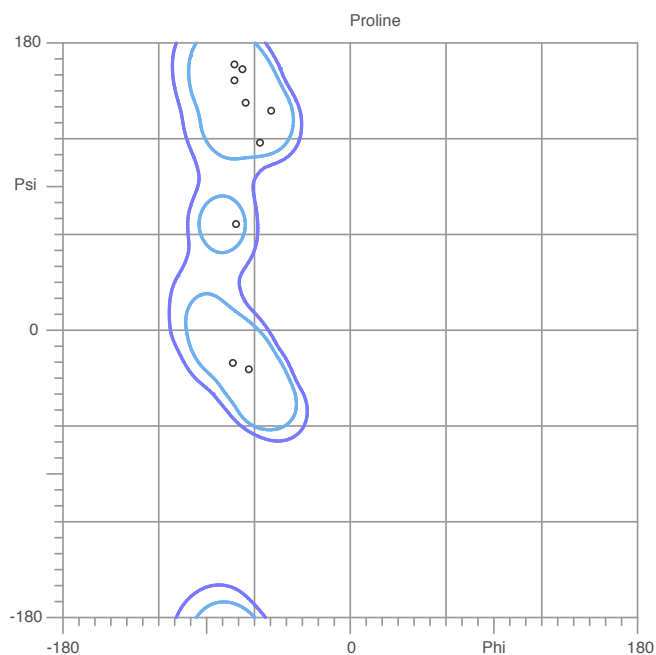
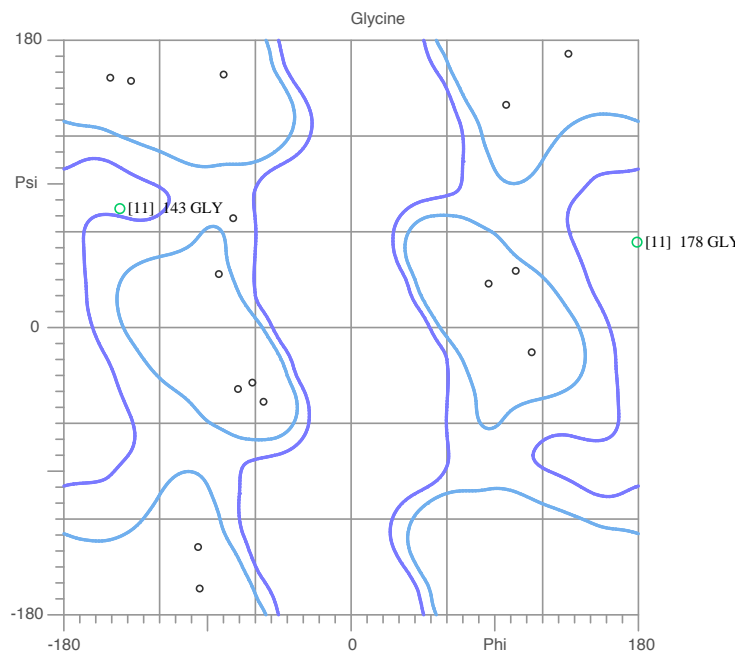
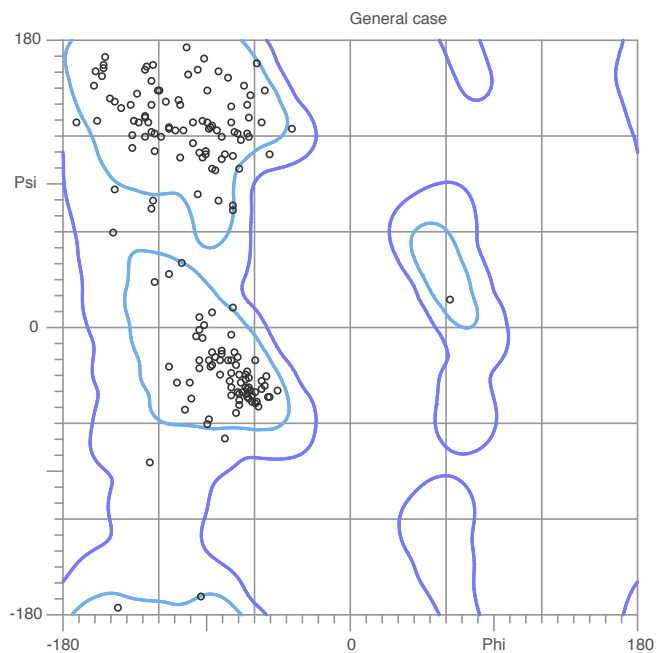


93.5% (187/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[10] 102 PHE (-5.2, 99.5)
[10] 144 PRO (-67.6, -62.5)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 11

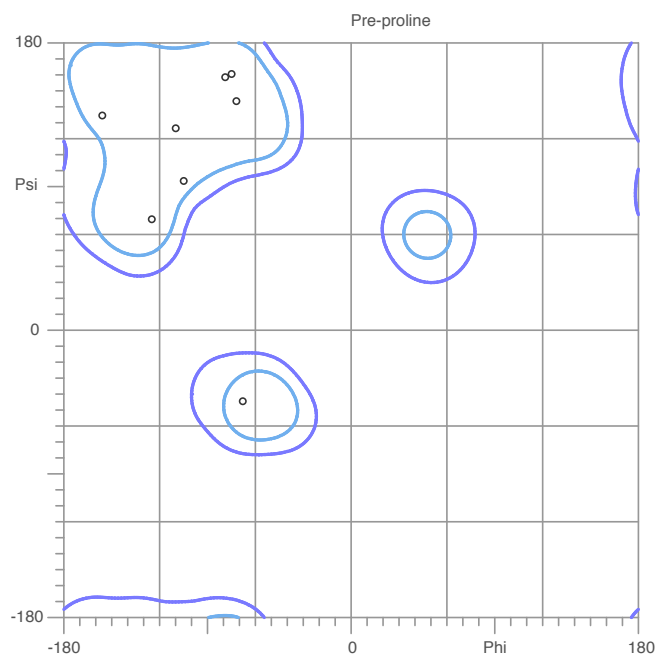
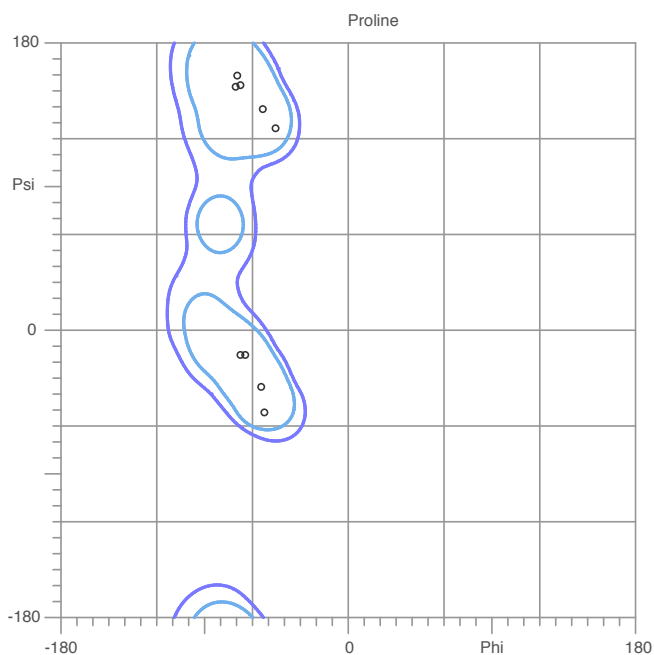
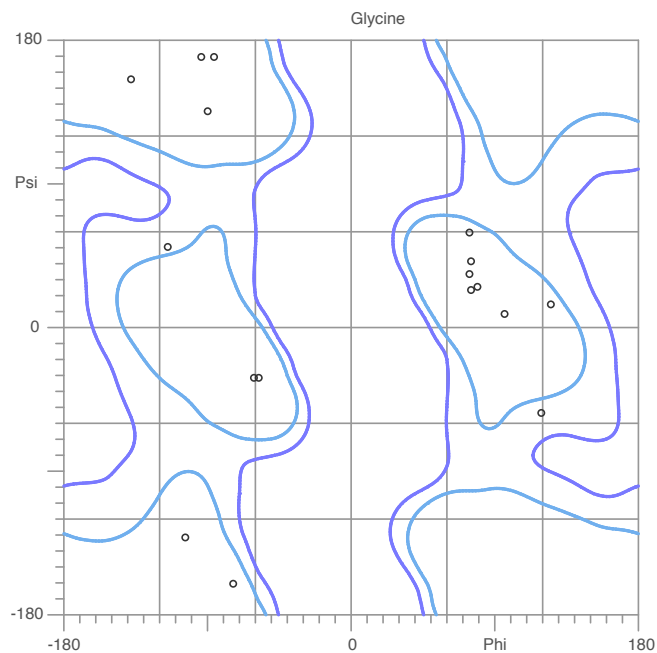
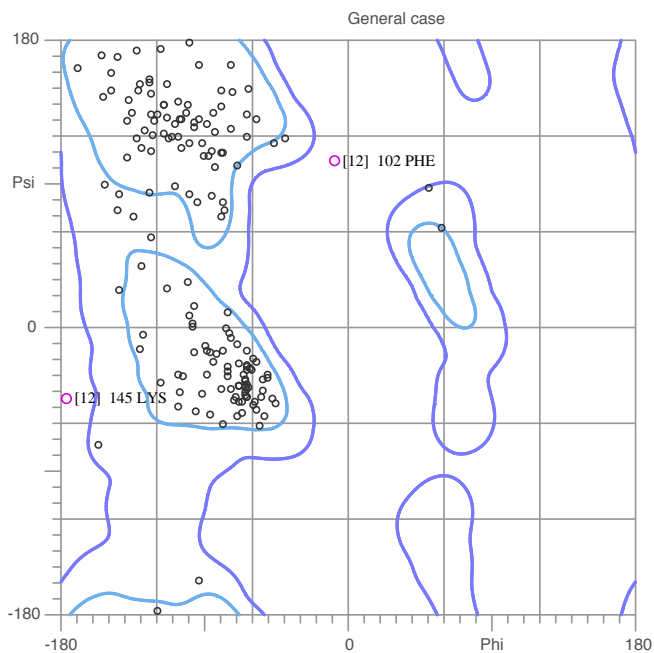


92.5% (185/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[11] 143 GLY (-145.0, 75.1)
[11] 178 GLY (179.9, 55.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 12

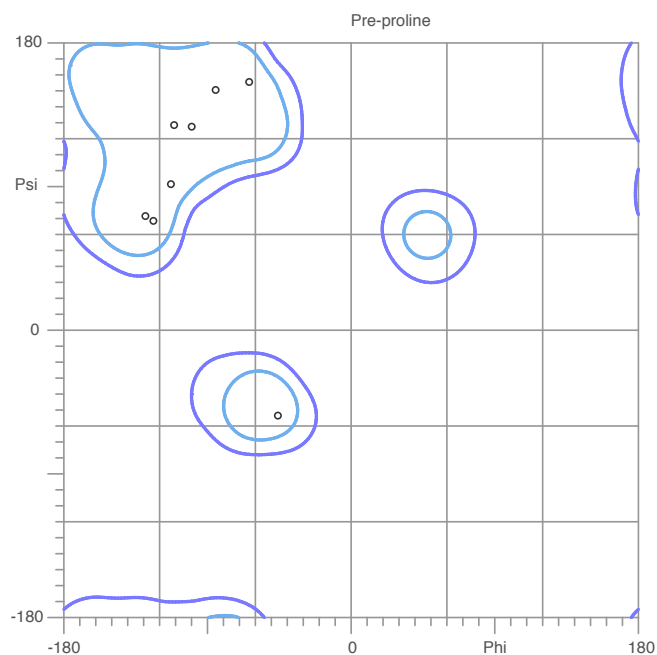
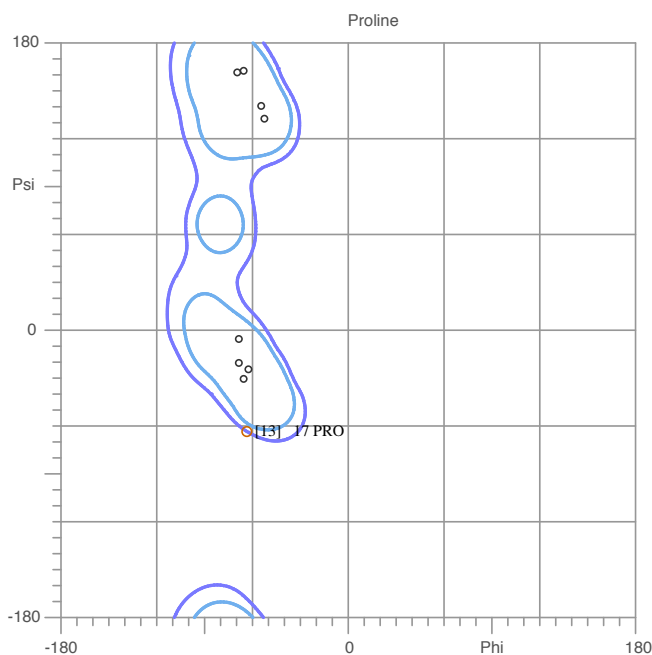
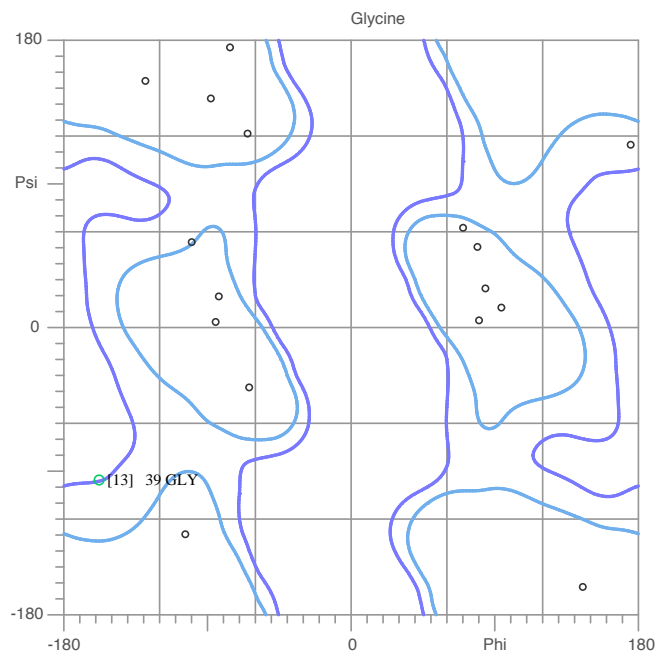
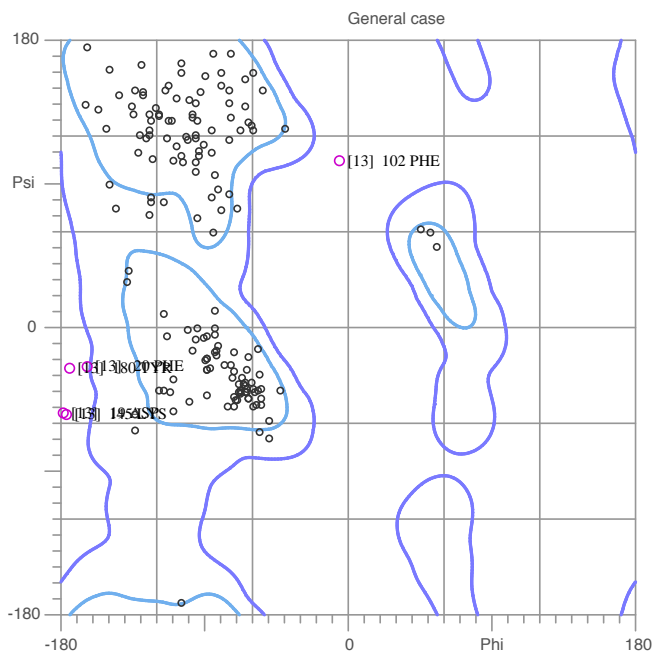


92.0% (184/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 102 PHE (-9.4, 105.9)
[12] 145 LYS (-177.2, -45.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 13



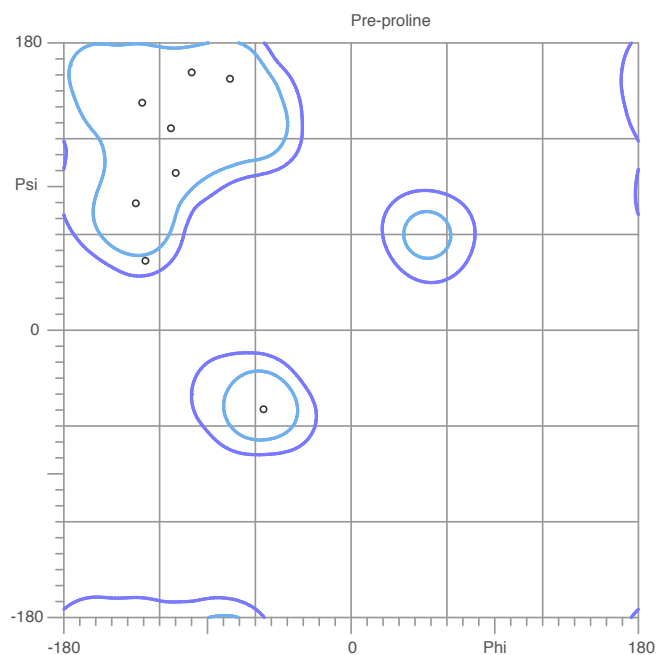
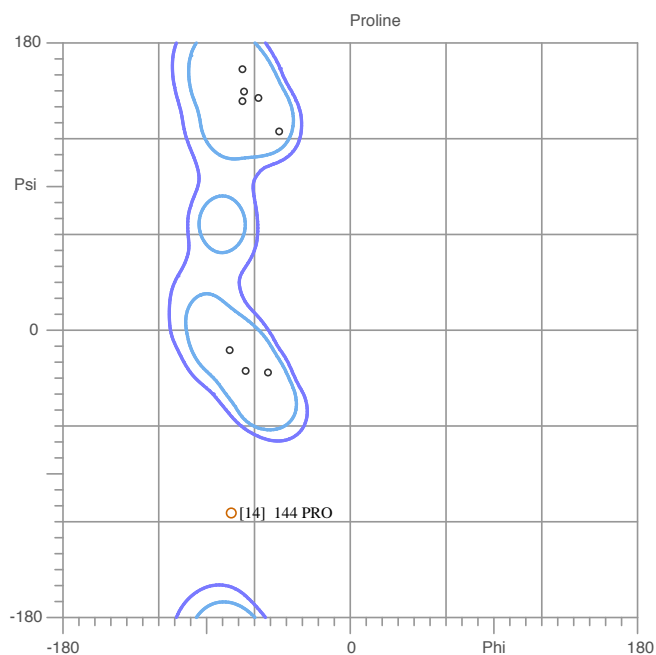
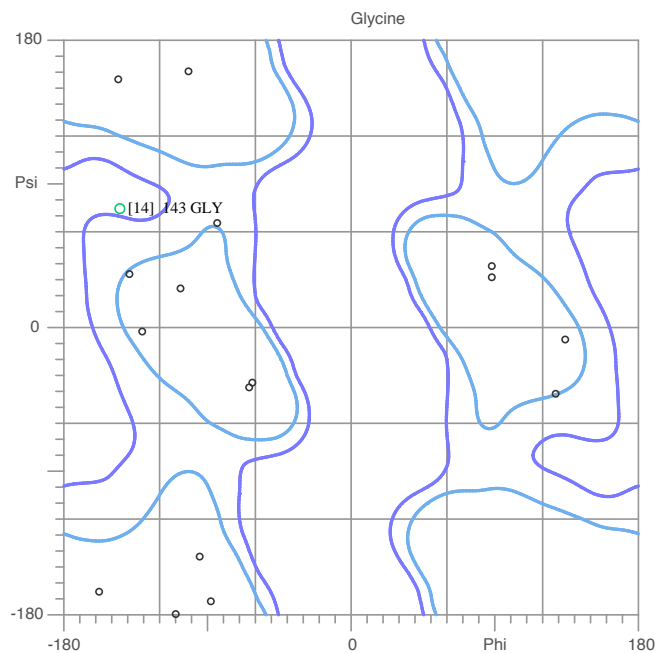
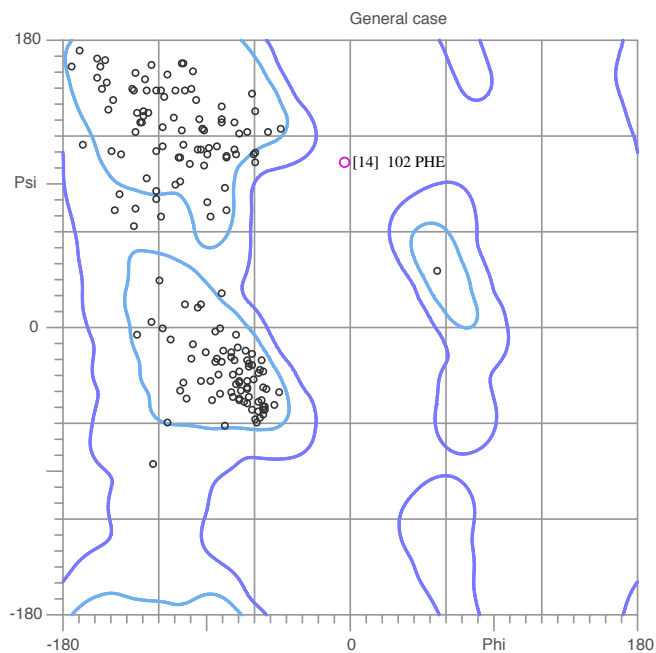
89.0% (178/200) of all residues were in favored (98%) regions.
96.5% (193/200) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[13] 17 PRO (-65.0, -63.4)

[13] 19 ASP (-179.9, -53.0)
[13] 20 PHE (-164.6, -24.9)
[13] 39 GLY (-158.4, -95.5)
[13] 102 PHE (-6.9, 105.0)
[13] 145 LYS (-177.0, -55.0)
[13] 180 TYR (-175.0, -25.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 14



92.0% (184/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

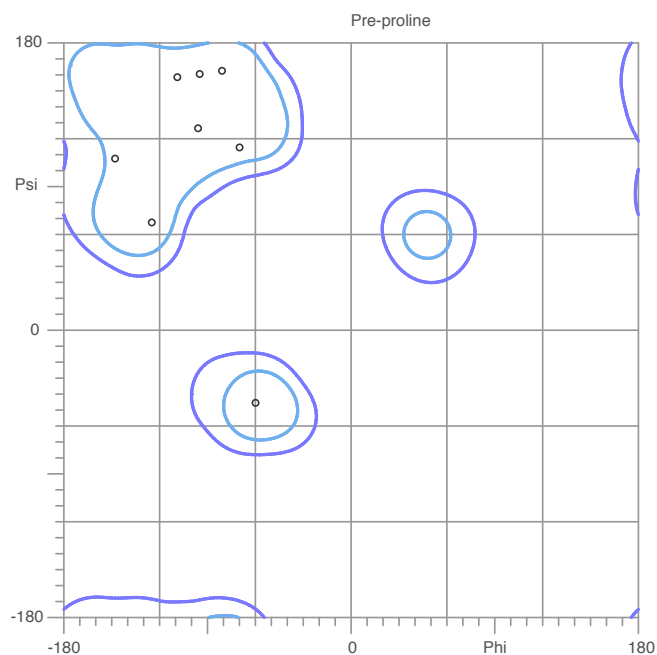
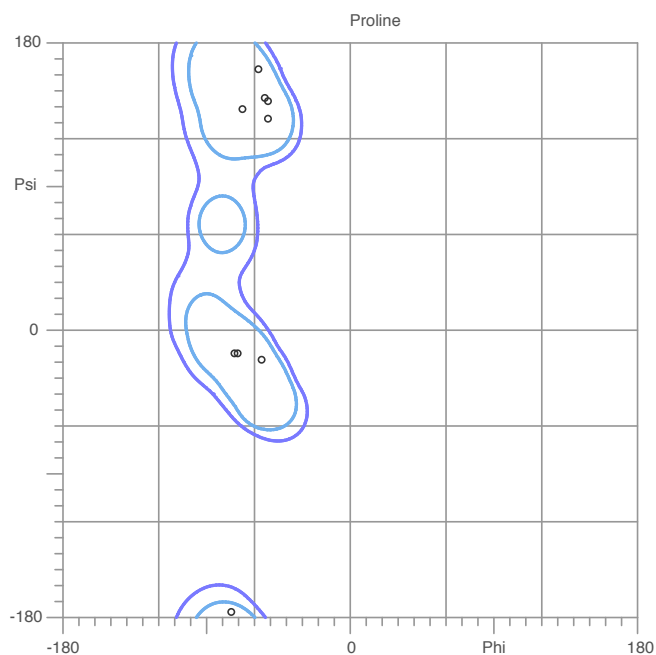
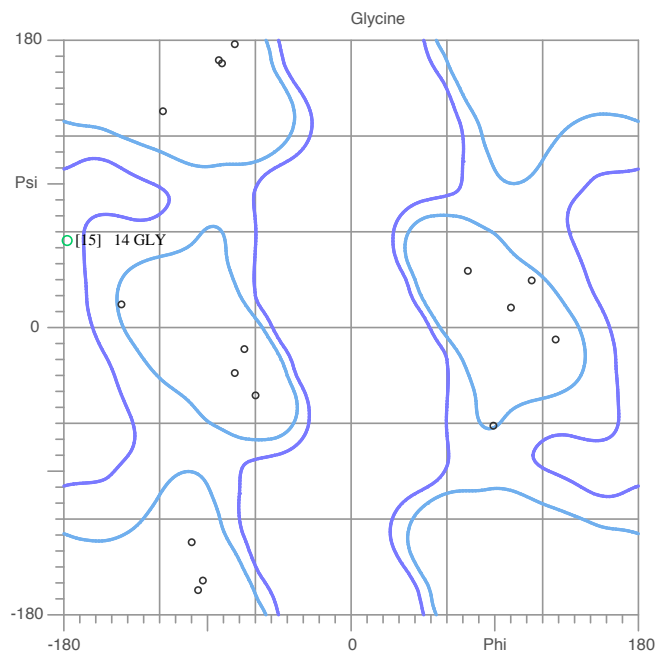
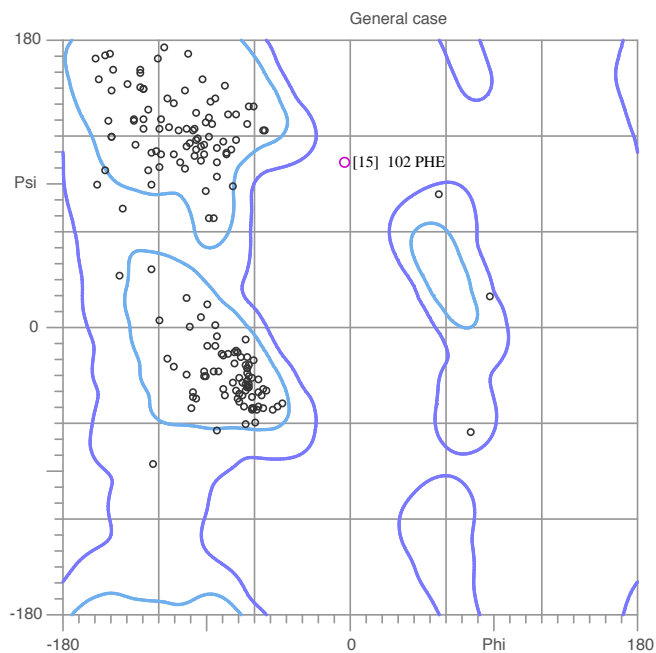
[14] 102 PHE (-4.9, 104.9)

[14] 143 GLY (-145.0, 75.1)

[14] 144 PRO (-75.1, -114.9)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 15



94.5% (189/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

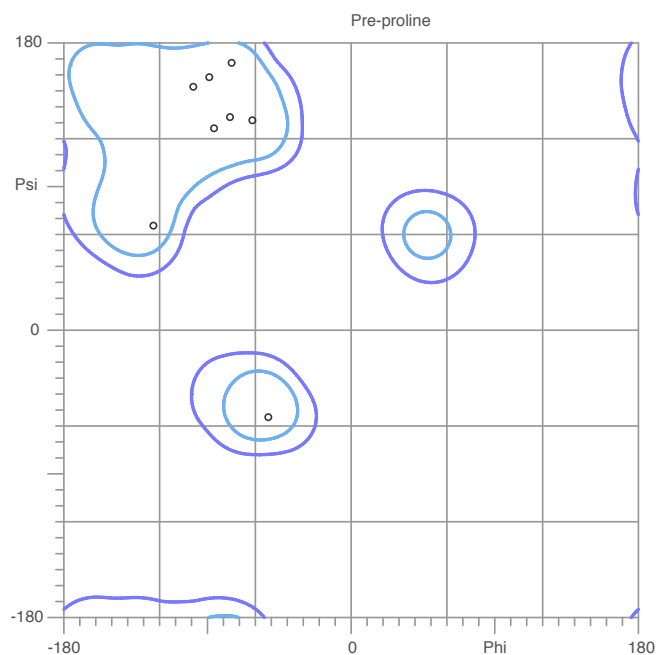
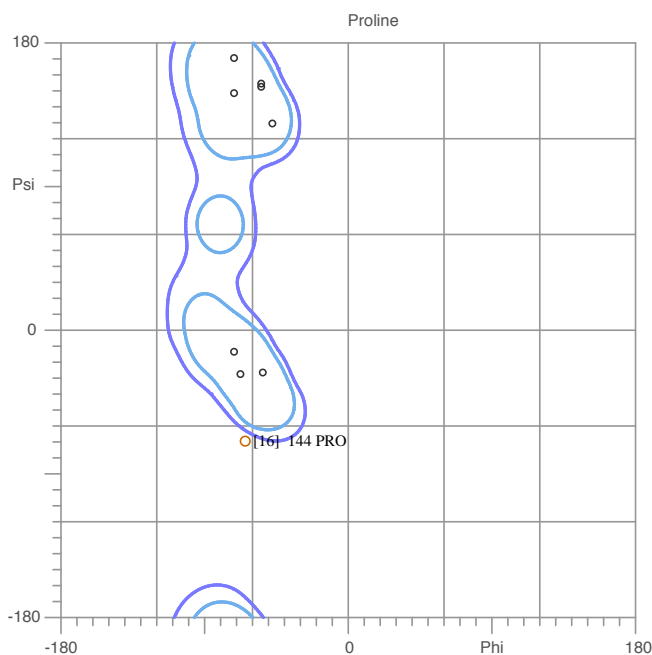
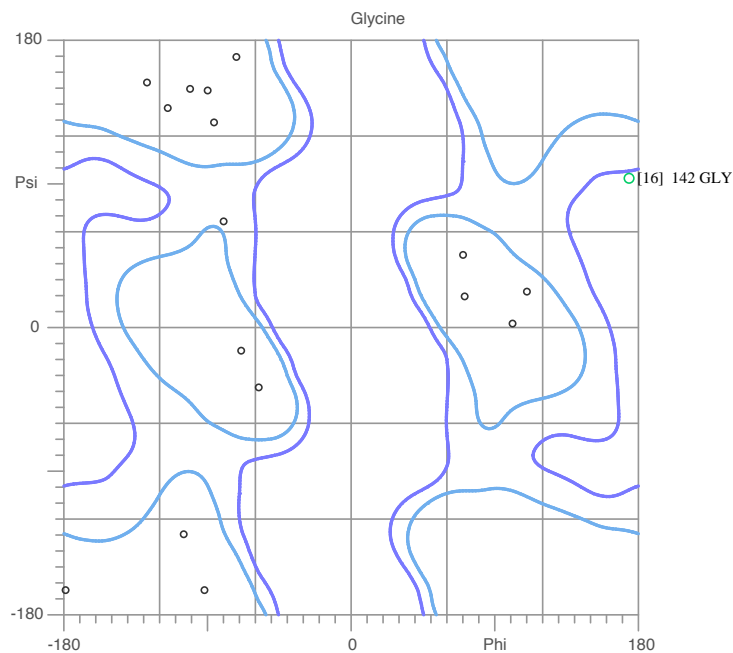
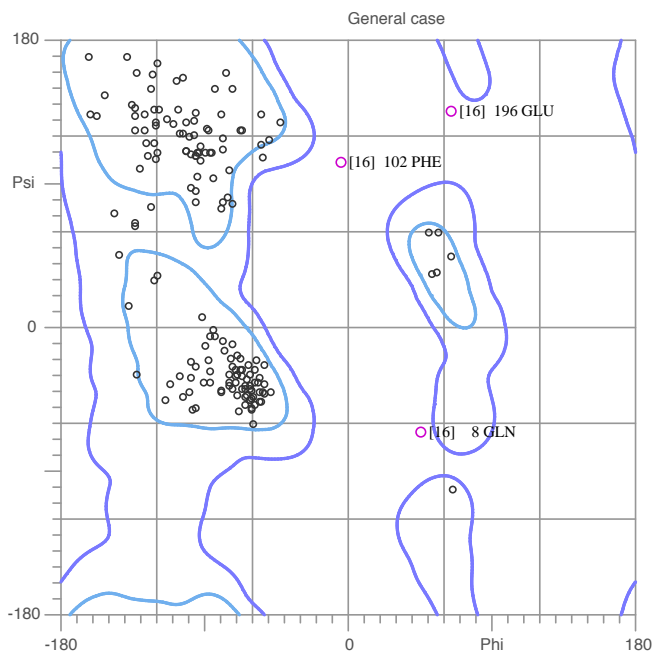
There were 2 outliers (phi, psi):

[15] 14 GLY (-178.1, 55.0)

[15] 102 PHE (-4.9, 104.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 16



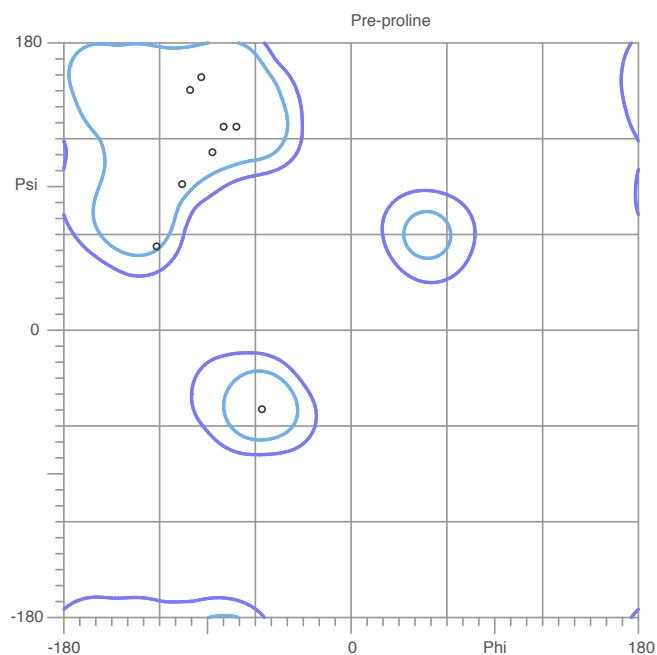
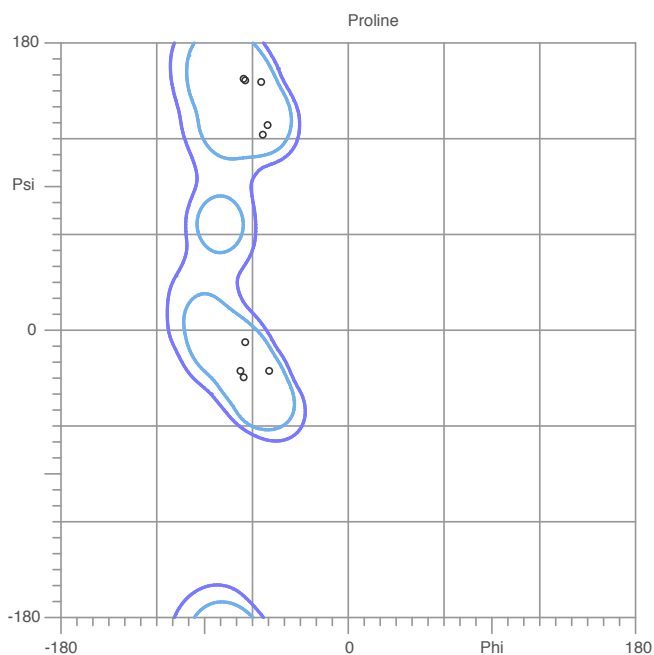
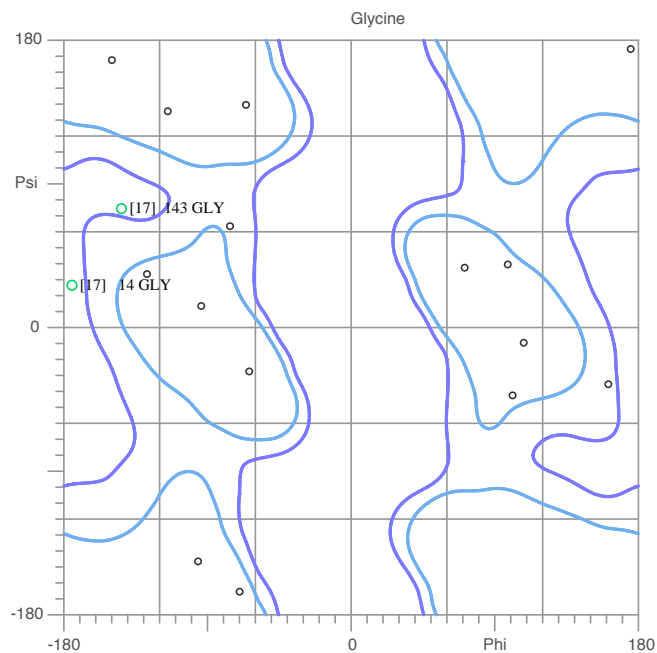
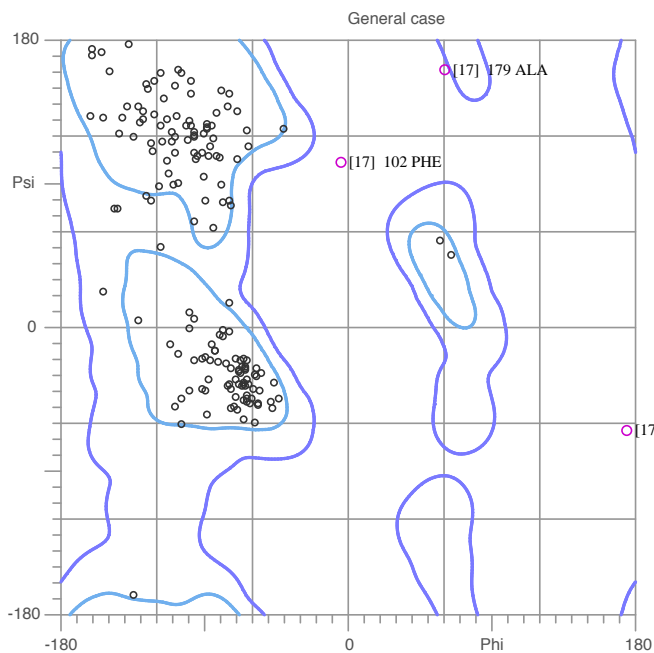
93.0% (186/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[16] 8 GLN (45.0, -65.1)
[16] 102 PHE (-5.8, 105.0)
[16] 142 GLY (174.8, 95.0)
[16] 144 PRO (-65.3, -69.7)
[16] 196 GLU (64.6, 136.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 17



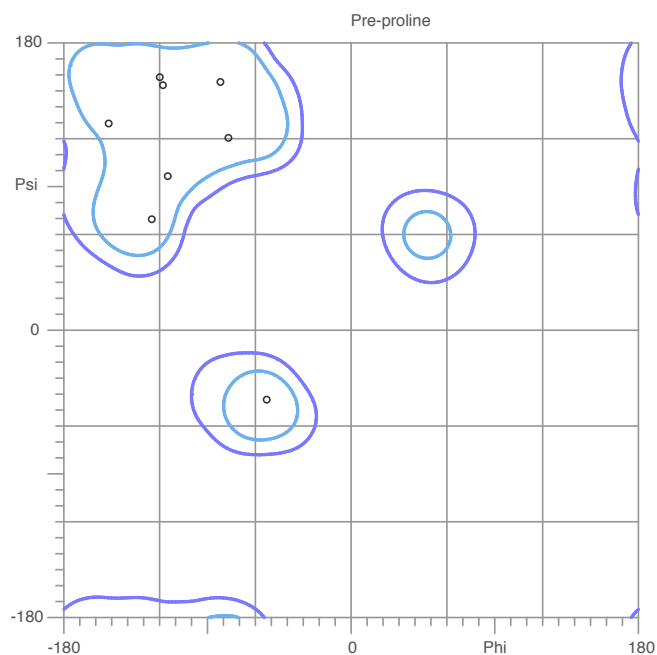
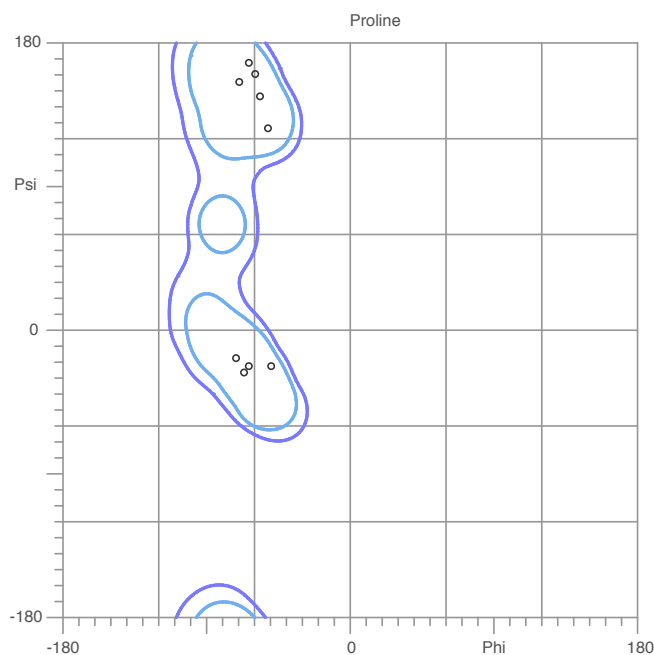
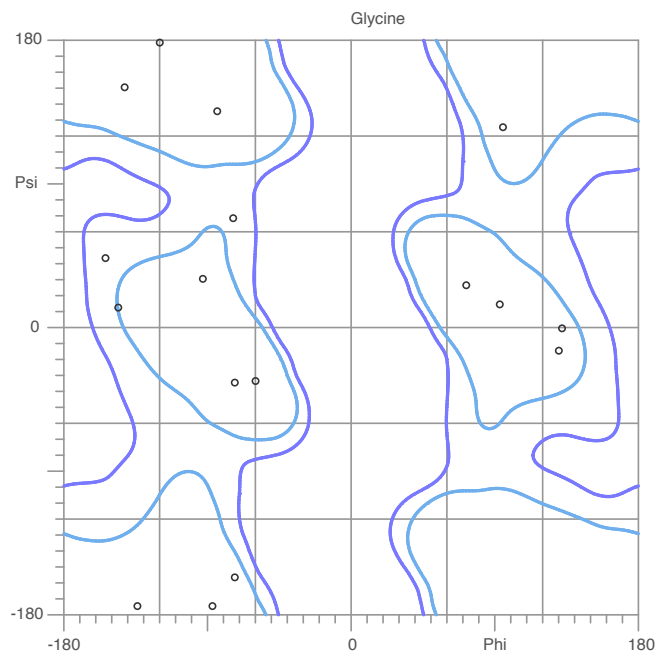
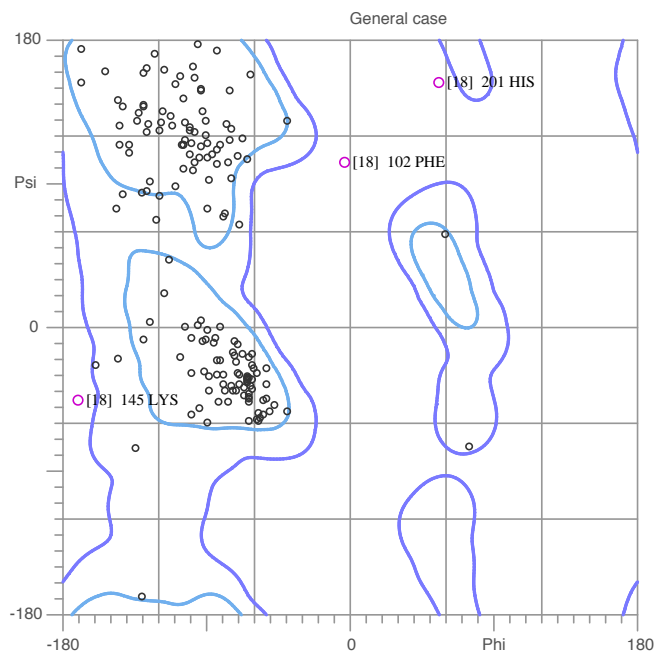
92.5% (185/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[17] 14 GLY (-175.0, 27.9)
[17] 102 PHE (-5.0, 104.0)
[17] 143 GLY (-145.0, 75.1)
[17] 145 LYS (174.7, -65.0)
[17] 179 ALA (60.6, 163.0)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 18



93.0% (186/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

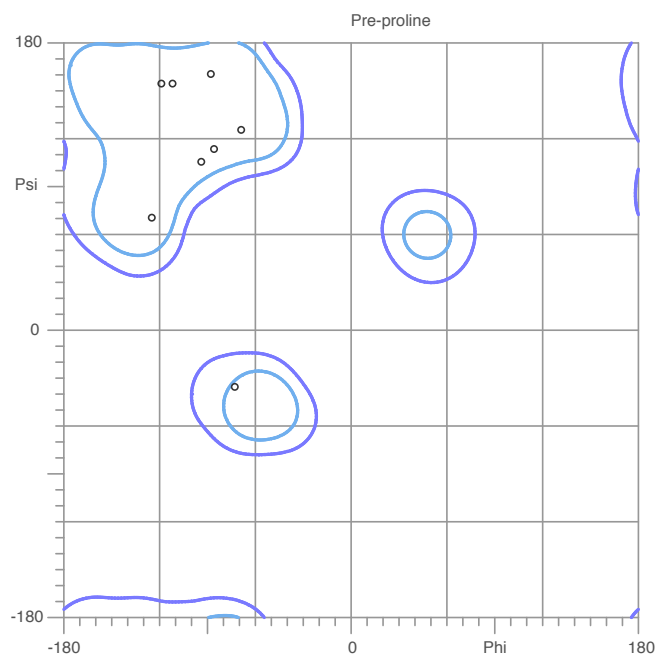
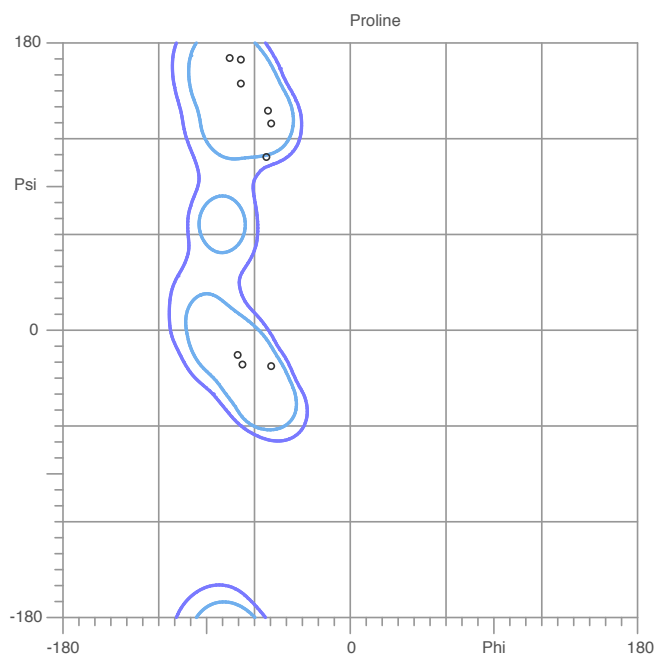
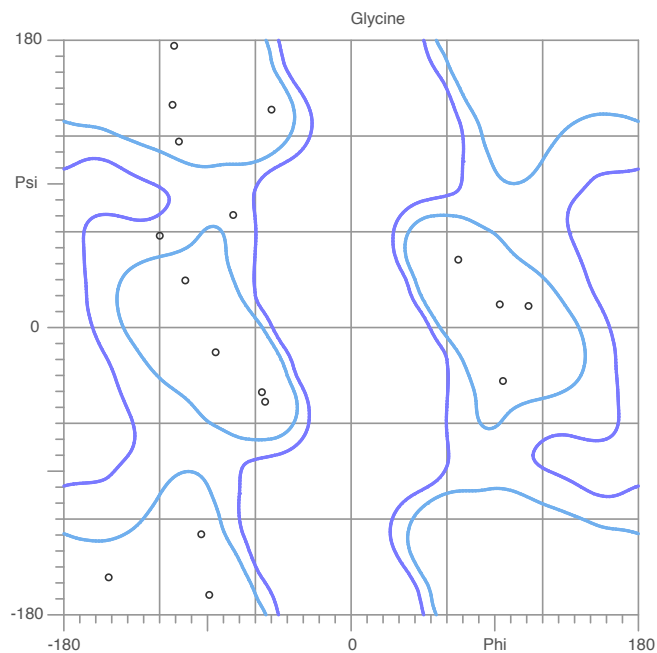
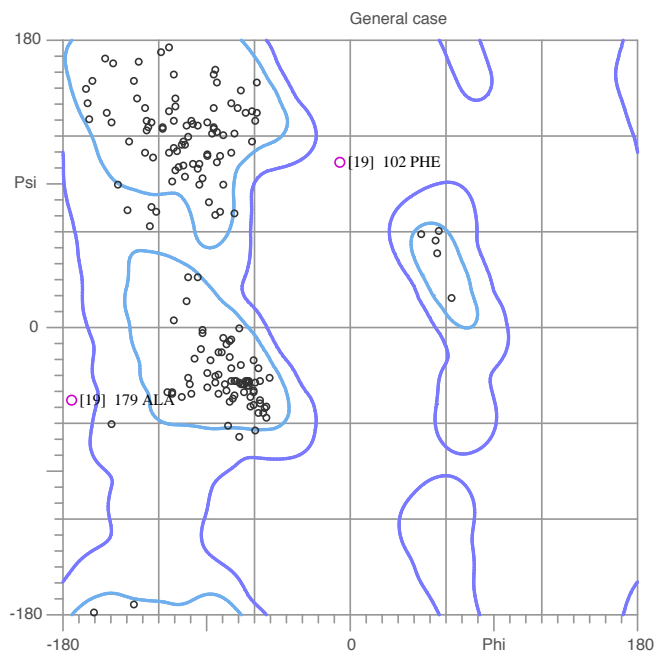
[18] 102 PHE (-4.9, 104.2)

[18] 145 LYS (-171.4, -45.2)

[18] 201 HIS (55.0, 154.9)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 19



93.5% (187/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

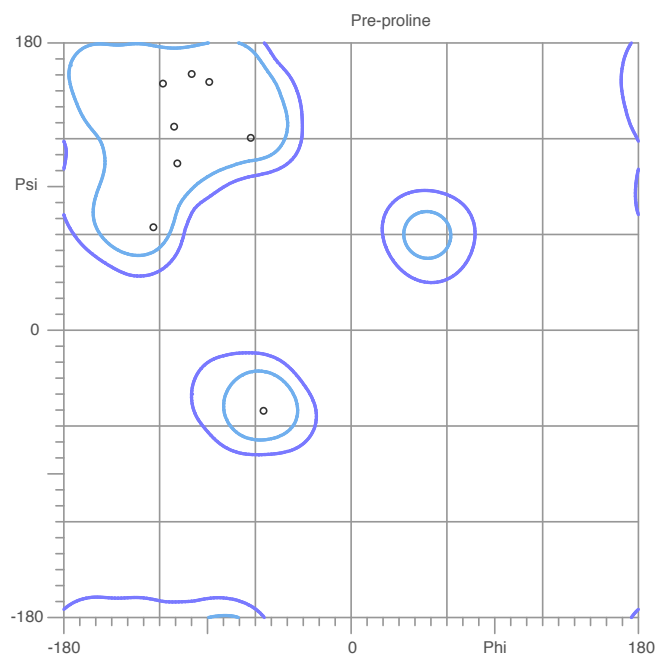
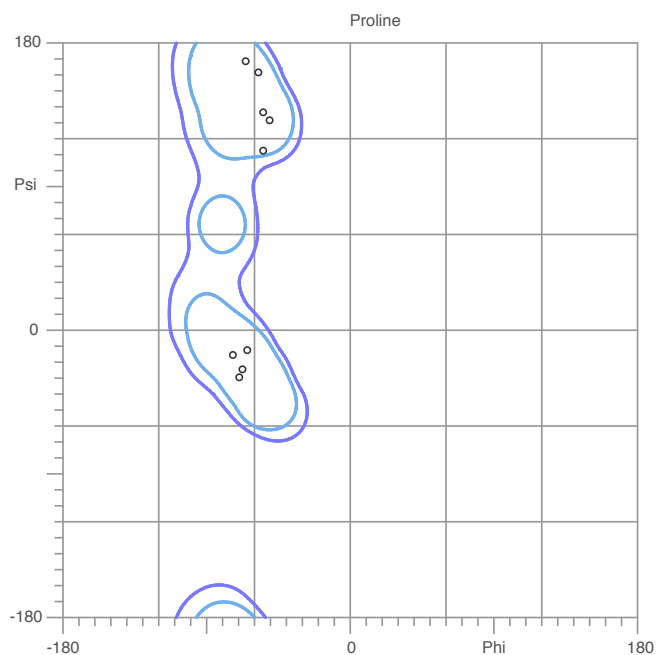
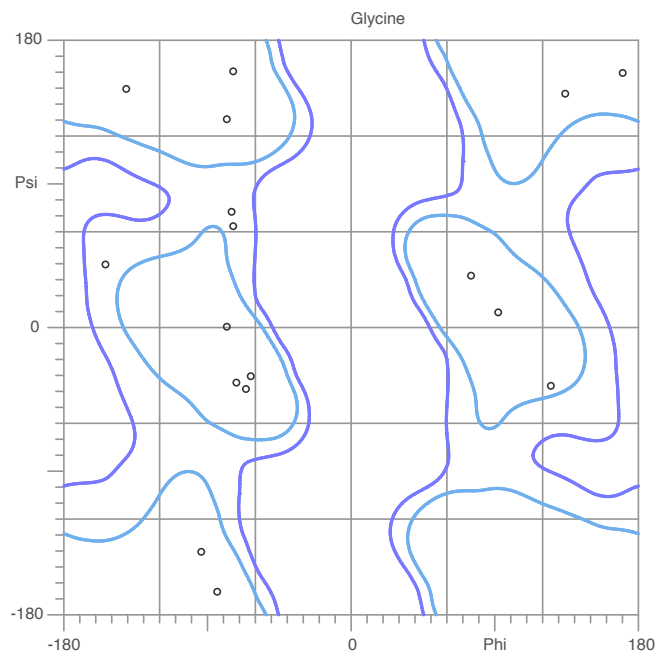
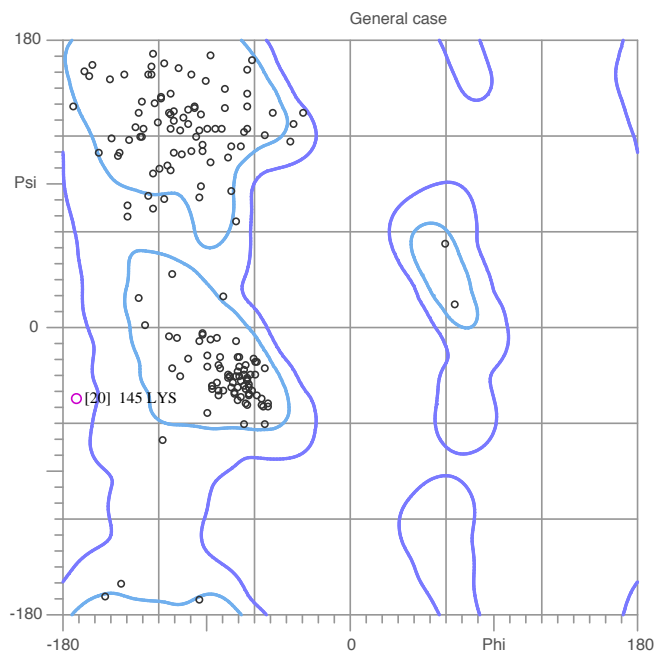
There were 2 outliers (phi, psi):

[19] 102 PHE (-7.3, 105.0)

[19] 179 ALA (-175.1, -45.1)

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 20



91.5% (183/200) of all residues were in favored (98%) regions.
99.5% (199/200) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 145 LYS (-172.1, -45.0)

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

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