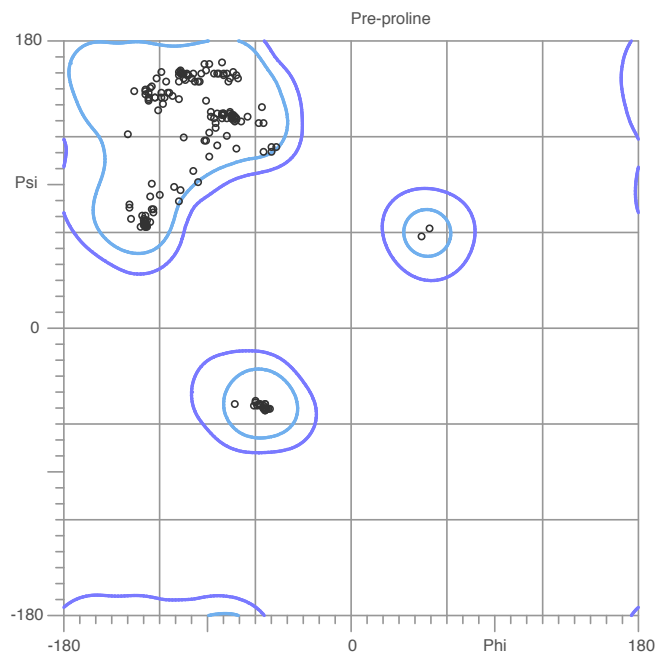
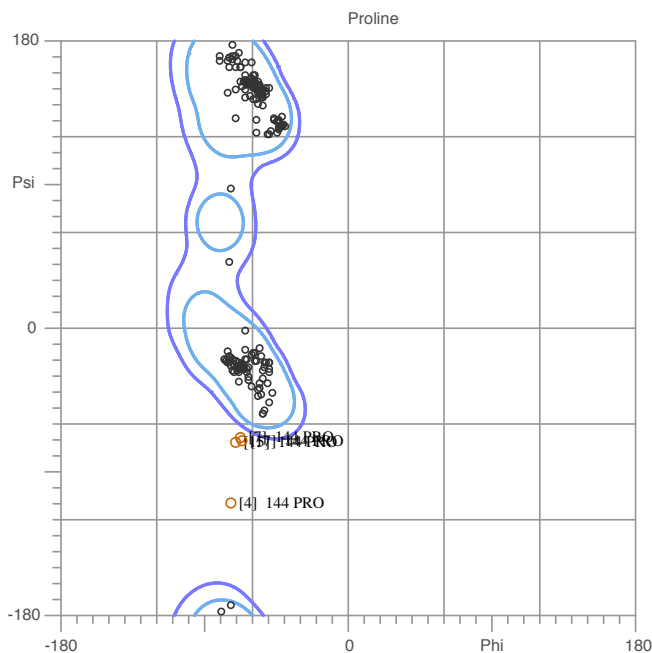
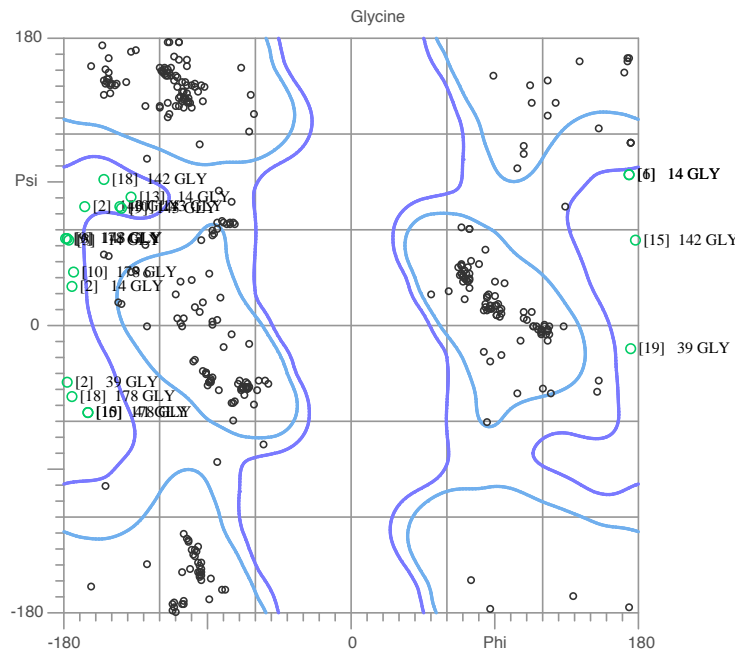
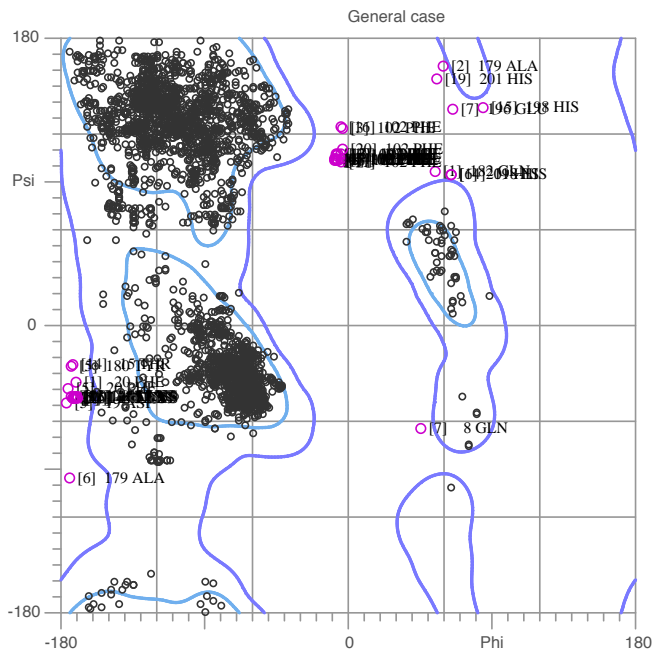


MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, all models



93.1% (3725400) of all residues were in favored (98%) regions.
98.4% (3938400) of all residues were in allowed (>99.8%) regions.

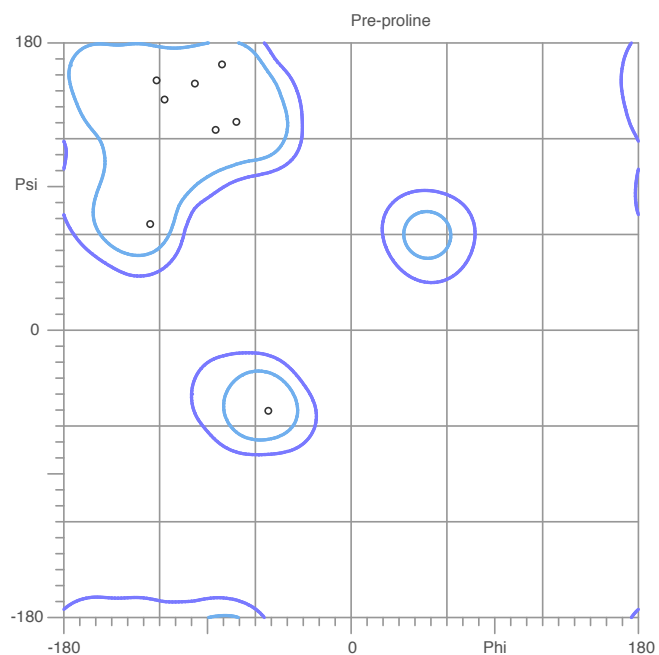
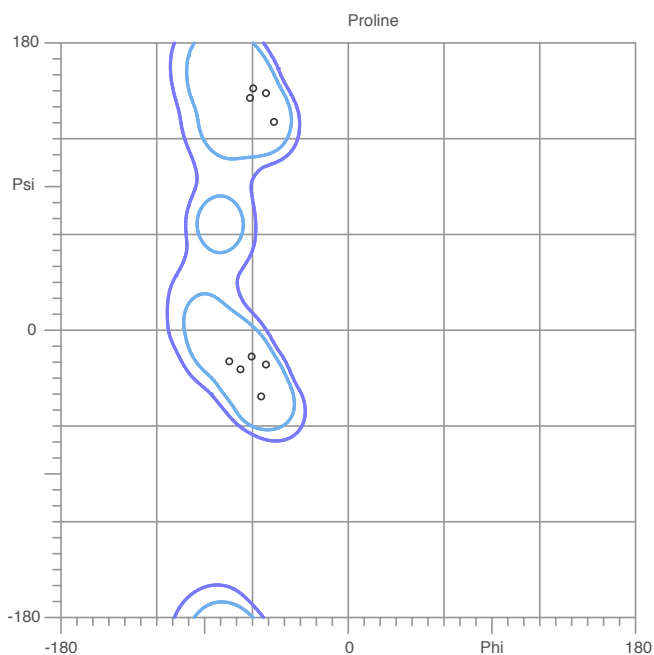
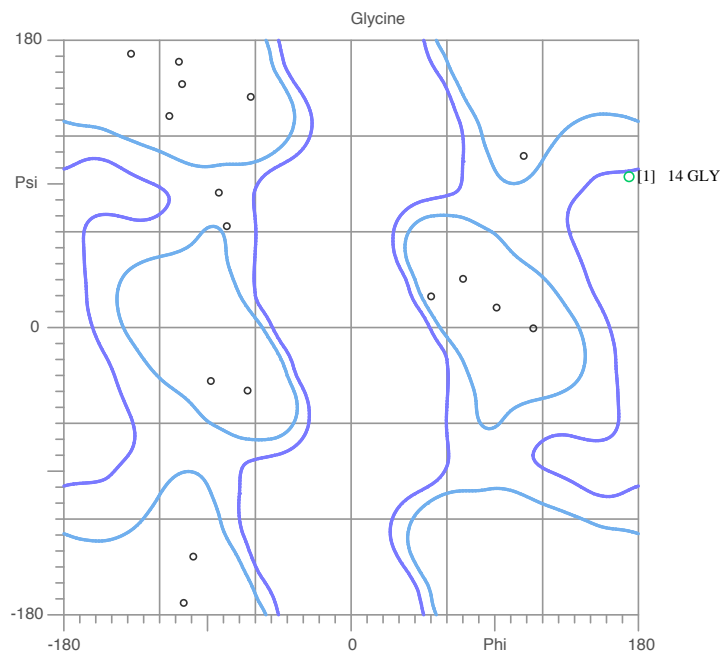
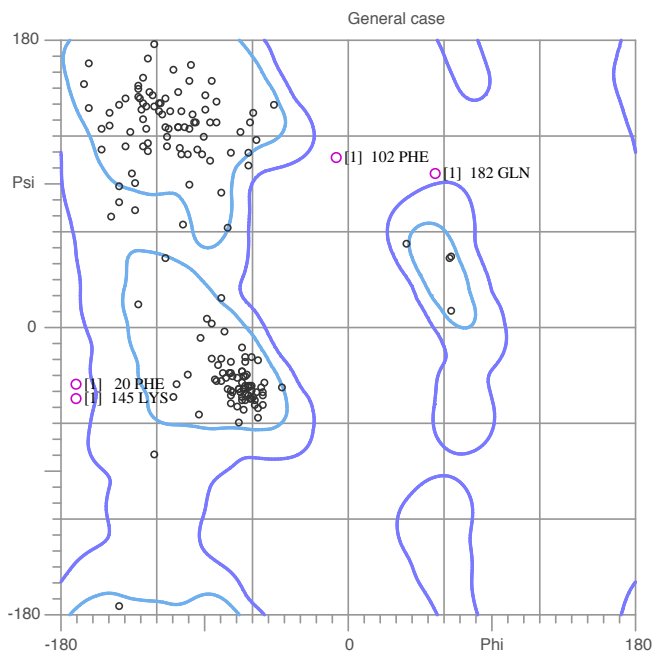
There were 62 outliers (phi, psi):

- [1] 14 GLY (-175.0, 95.0)
- [1] 20 PHE (-171.1, -36.0)
- [1] 102 PHE (-8.1, 108.0)
- [1] 145 LYS (-171.9, -45.0)
- [1] 182 GLN (85.0, 97.2)
- [2] 14 GLY (-175.1, 25.1)
- [2] 39 GLY (-178.4, -35.0)
- [2] 143 GLY (-167.5, 75.0)
- [2] 145 LYS (-175.9, -45.2)
- [2] 179 ALA (-59.4, 103.2)
- [3] 14 GLY (-177.6, 54.9)
- [3] 102 PHE (-5.0, 125.0)
- [3] 102 PHE (-6.4, 105.5)
- [4] 144 PRO (-74.8, -109.1)
- [5] 19 ASP (-177.4, -48.3)
- [5] 20 PHE (-176.8, -39.8)
- [5] 102 PHE (-4.9, 105.4)
- [5] 145 LYS (-172.5, -45.0)
- [5] 180 TYR (-175.0, 25.0)
- [6] 14 GLY (-175.0, 95.1)
- [6] 102 PHE (-9.3, 106.1)
- [6] 143 GLY (-178.3, 55.0)
- [6] 179 ALA (-175.0, 95.0)
- [6] 201 HIS (65.0, 95.0)
- [7] 8 GLN (43.0, -65.0)
- [7] 144 PRO (-68.2, -68.7)
- [7] 196 GLY (65.1, 136.7)
- [8] 102 PHE (-7.5, 104.9)
- [8] 179 ALA (-174.9, -45.0)

- [9] 102 PHE (-9.1, 104.9)
- [9] 143 GLY (-144.9, 74.9)
- [9] 178 GLY (-179.5, 55.1)
- [10] 41 GLY (-165.0, -54.9)
- [10] 102 PHE (-5.1, 108.8)
- [10] 143 GLY (-145.0, 75.1)
- [10] 145 LYS (-170.4, -45.0)
- [10] 178 GLY (-175.0, 34.9)
- [11] 102 PHE (-5.0, 103.4)
- [11] 145 LYS (-175.6, -45.1)
- [12] 102 PHE (-8.4, 108.3)
- [12] 145 LYS (-172.8, -45.0)
- [13] 14 GLY (-138.4, 81.2)
- [13] 102 PHE (-7.2, 108.1)
- [13] 145 LYS (-171.0, -44.9)
- [14] 15 THR (-173.3, -25.0)
- [14] 102 PHE (-5.1, 105.1)
- [14] 198 HIS (65.0, 95.1)
- [15] 142 GLY (-179.0, 55.0)
- [15] 178 GLY (-168.0, -45.0)
- [15] 198 HIS (65.0, 137.1)
- [16] 102 PHE (-5.1, 125.0)
- [16] 145 LYS (-171.2, -45.0)
- [17] 102 PHE (-7.4, 105.0)
- [17] 144 PRO (-67.4, -70.2)
- [18] 102 PHE (-8.4, 105.0)
- [18] 142 GLY (-155.0, 92.5)
- [18] 178 GLY (-175.0, -45.0)
- [19] 39 GLY (-175.4, -15.0)
- [19] 201 HIS (65.1, 155.0)
- [20] 102 PHE (-5.0, 111.8)
- [20] 145 LYS (-170.4, -45.0)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 1



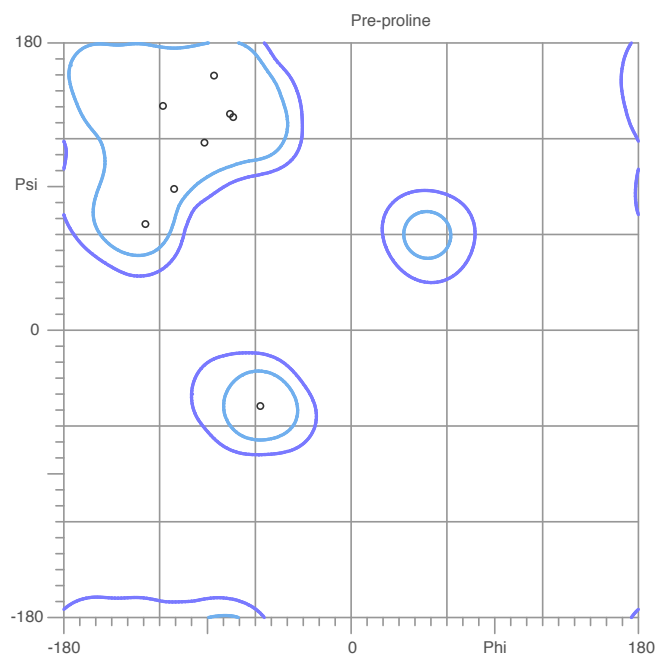
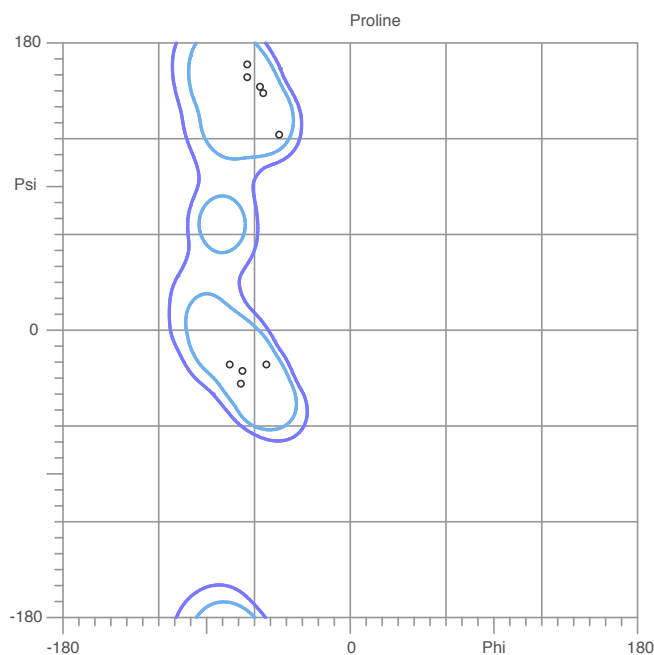
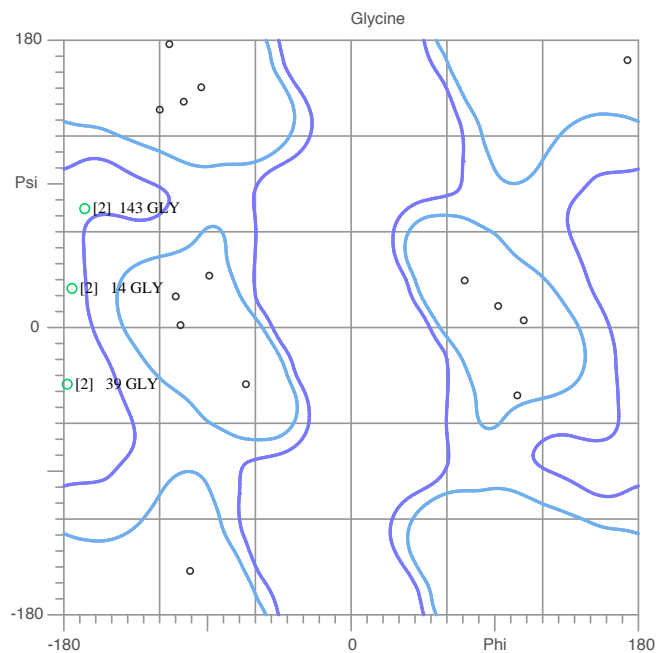
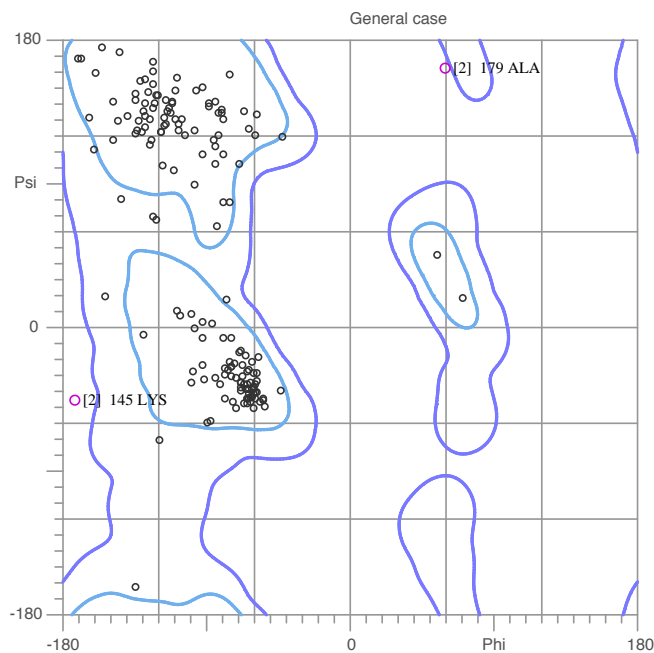
92.0% (184/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[1] 14 GLY (175.0, 95.0)
[1] 20 PHE (-171.1, -36.0)
[1] 102 PHE (-8.1, 108.0)
[1] 145 LYS (-171.9, -45.0)
[1] 182 GLN (55.0, 97.2)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 2



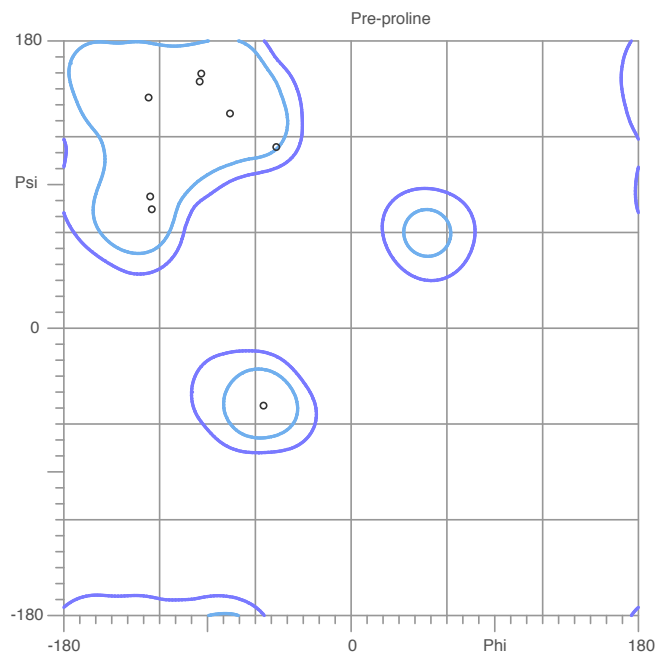
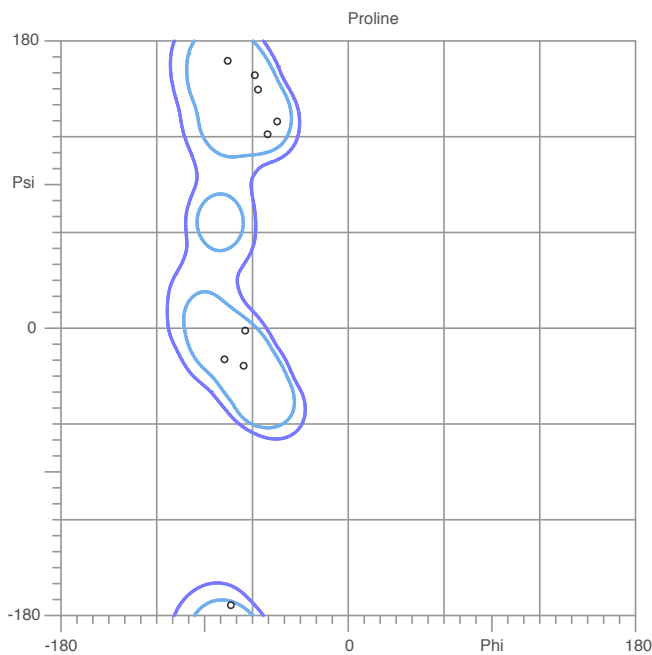
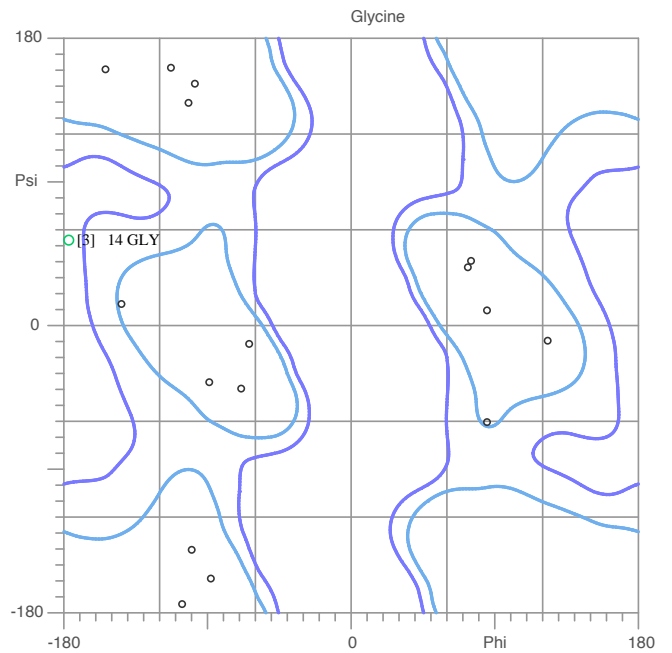
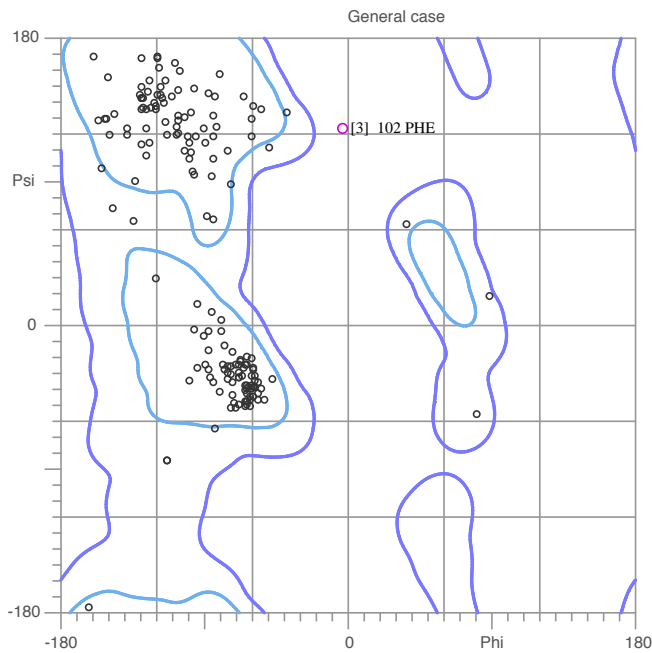
93.5% (187/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[2] 14 GLY (-175.1, 25.1)
[2] 39 GLY (-178.4, -35.0)
[2] 143 GLY (-167.5, 75.0)
[2] 145 LYS (-173.9, -45.2)
[2] 179 ALA (59.4, 163.2)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 3



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.

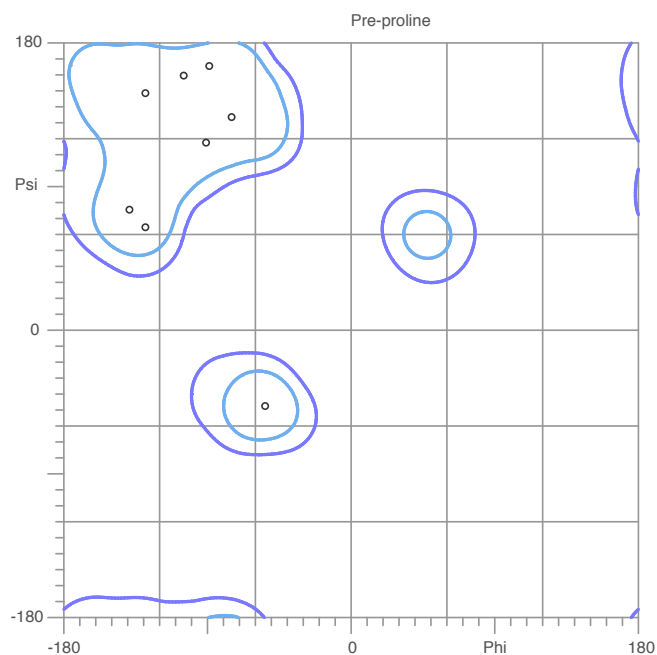
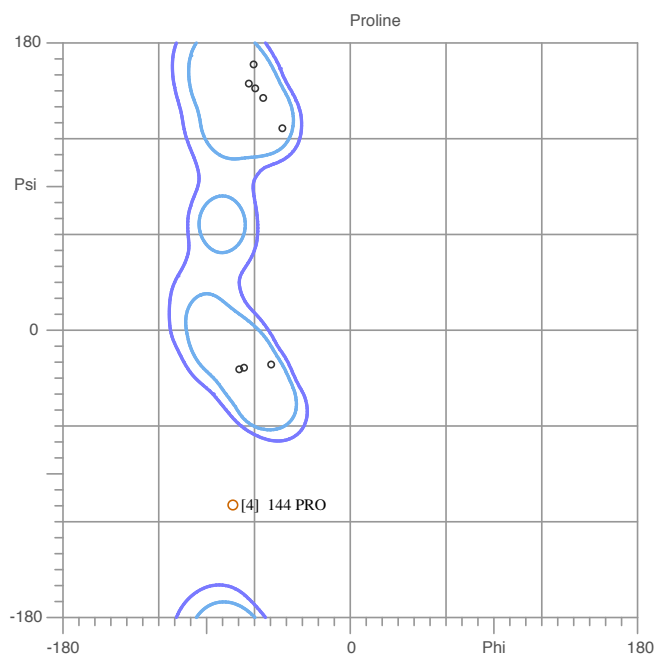
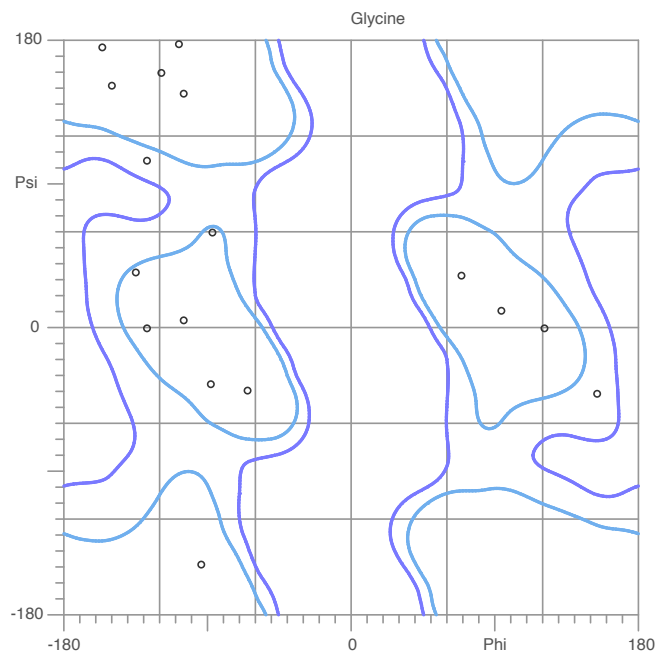
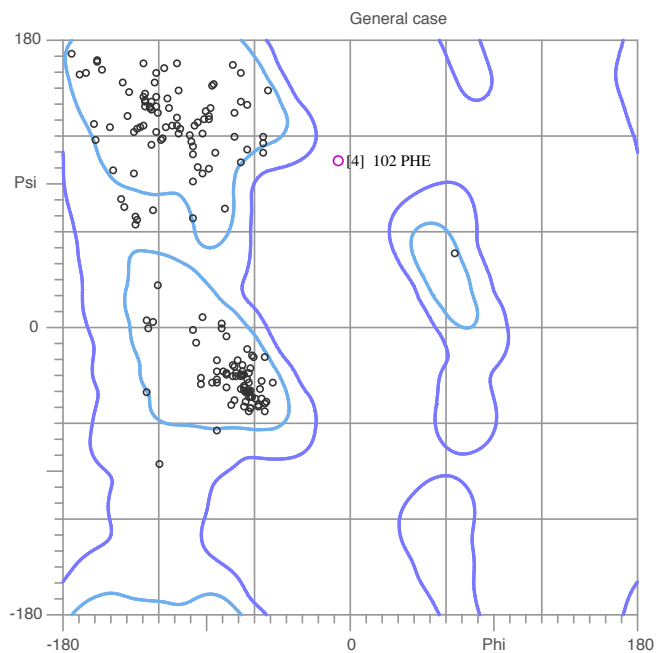
There were 2 outliers (phi, psi):

[3] 14 GLY (-177.6, 54.9)

[3] 102 PHE (-5.0, 125.0)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 4

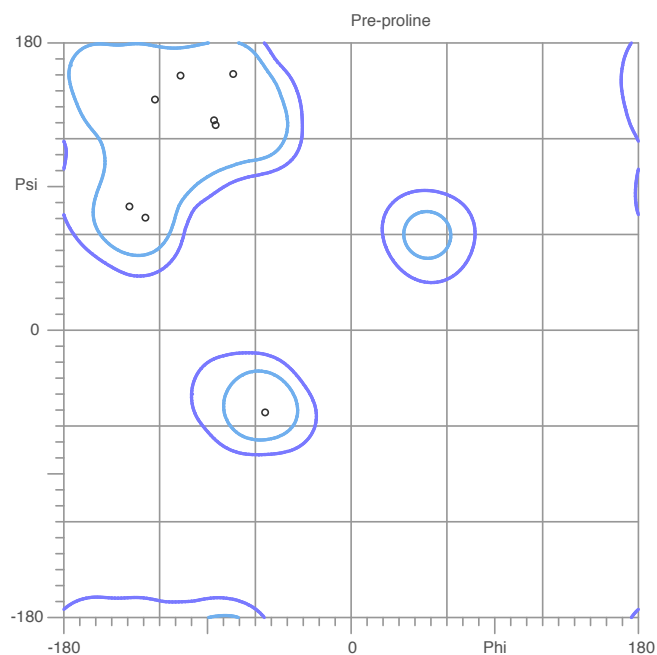
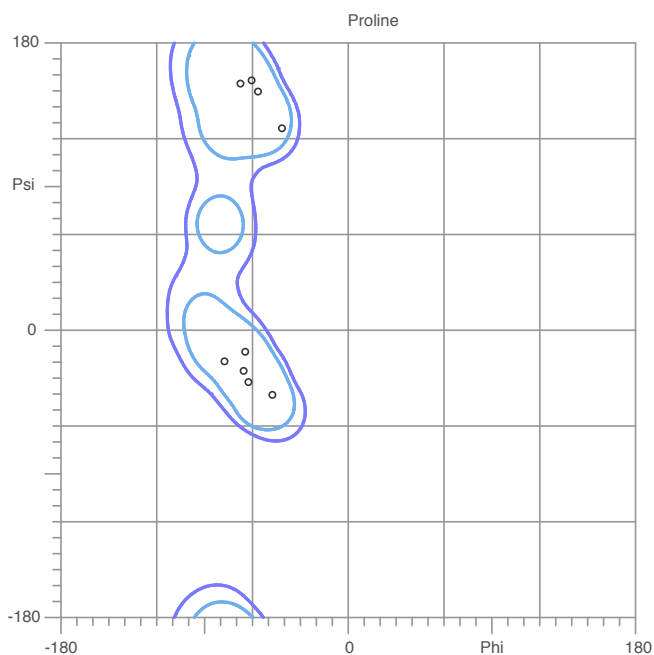
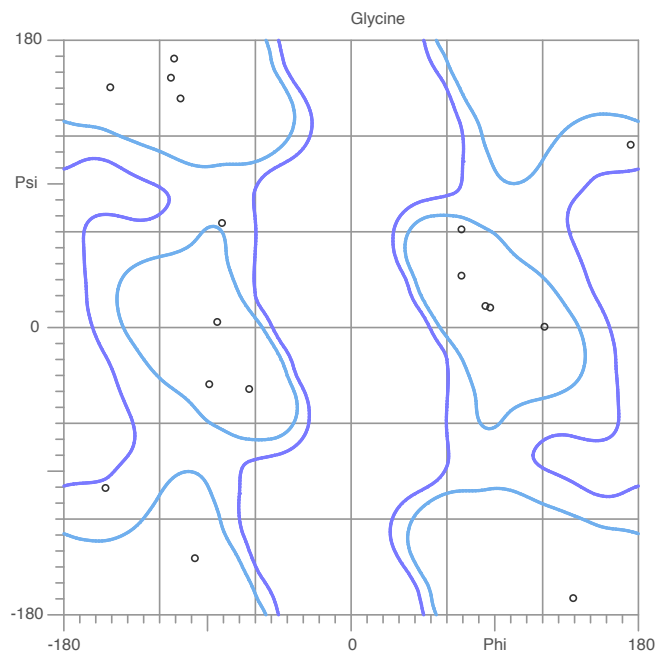
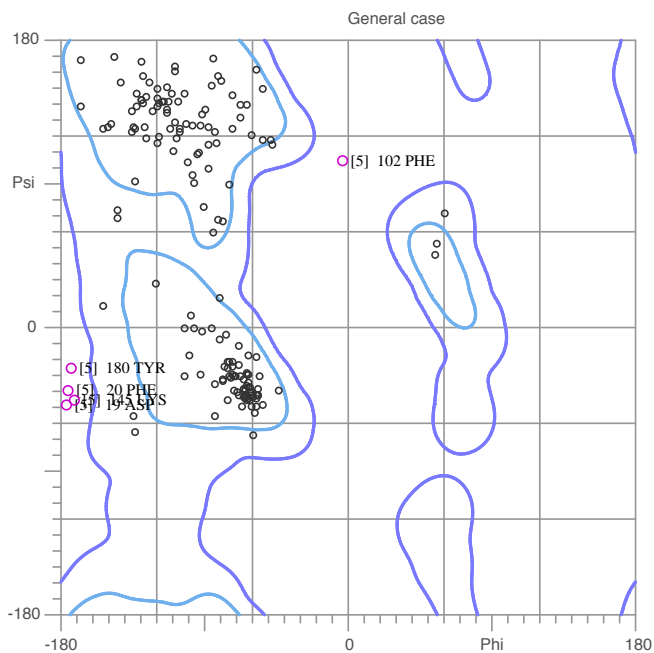


93.0% (186/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[4] 102 PHE (-8.4, 105.5)
[4] 144 PRO (-74.8, -109.1)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 5



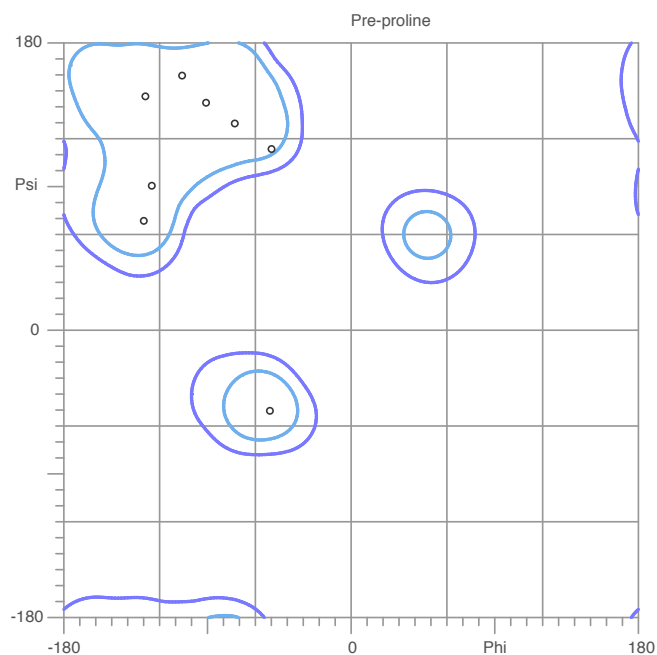
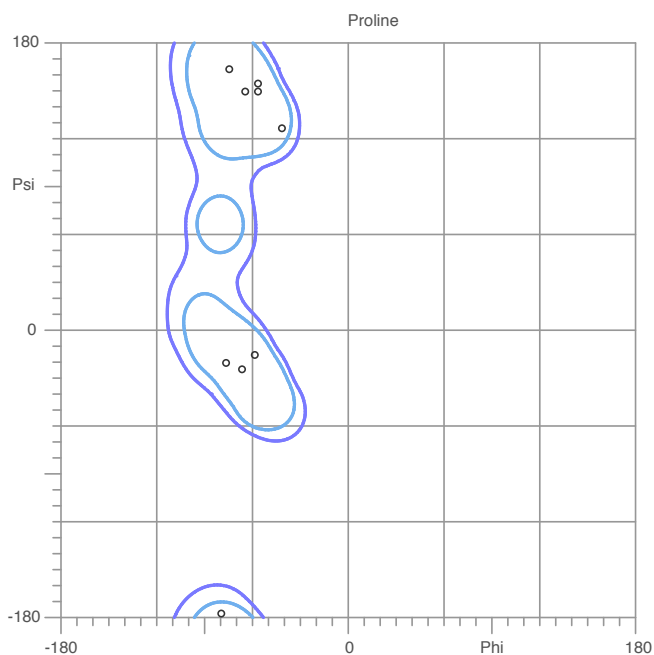
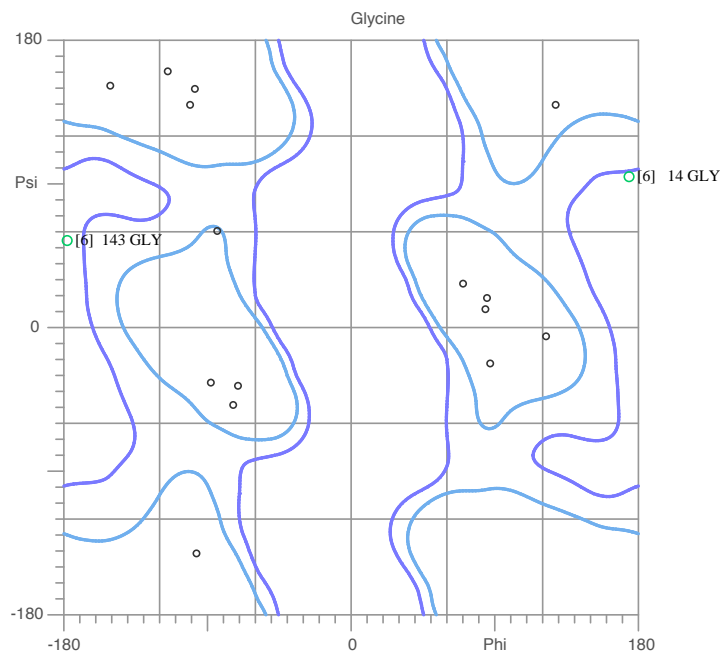
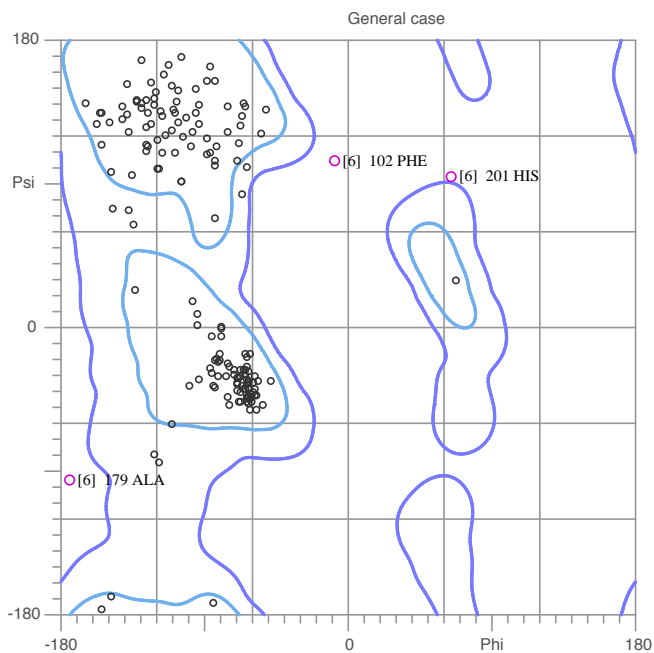
91.5% (183/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [5] 19 ASP (-177.4, -48.3)
- [5] 20 PHE (-176.8, -39.8)
- [5] 102 PHE (-4.9, 105.4)
- [5] 145 LYS (-172.5, -45.0)
- [5] 180 TYR (-175.0, -25.0)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 6



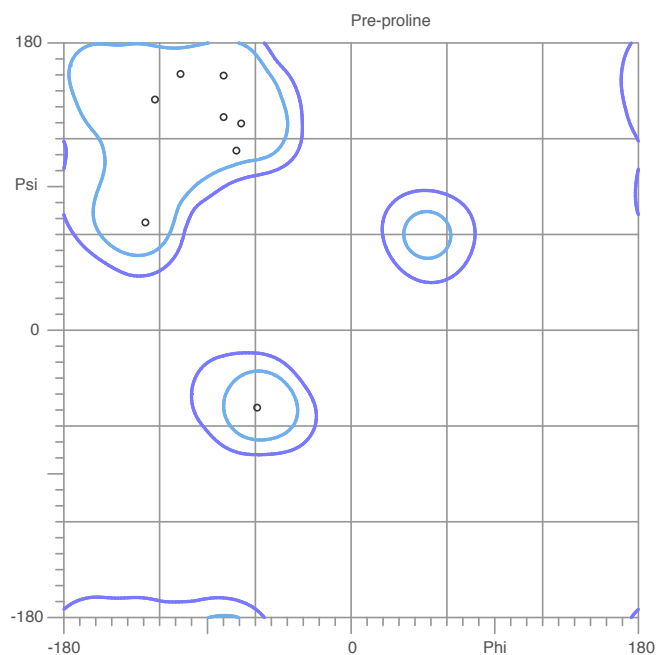
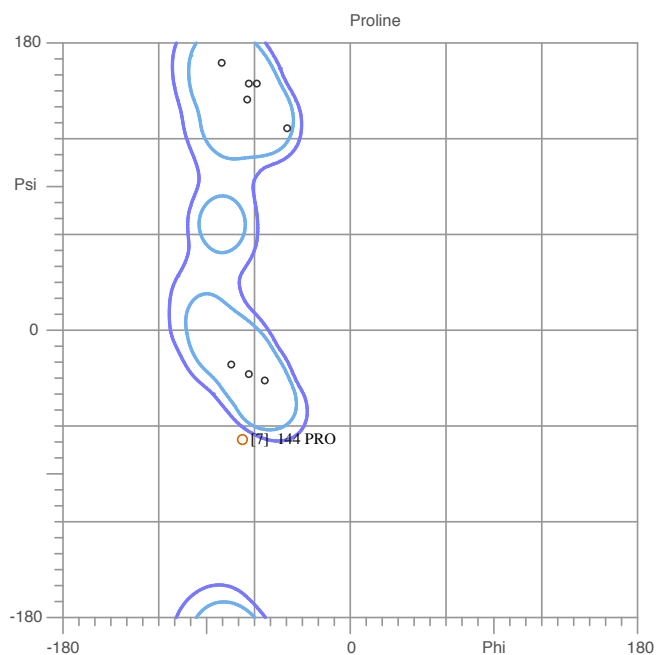
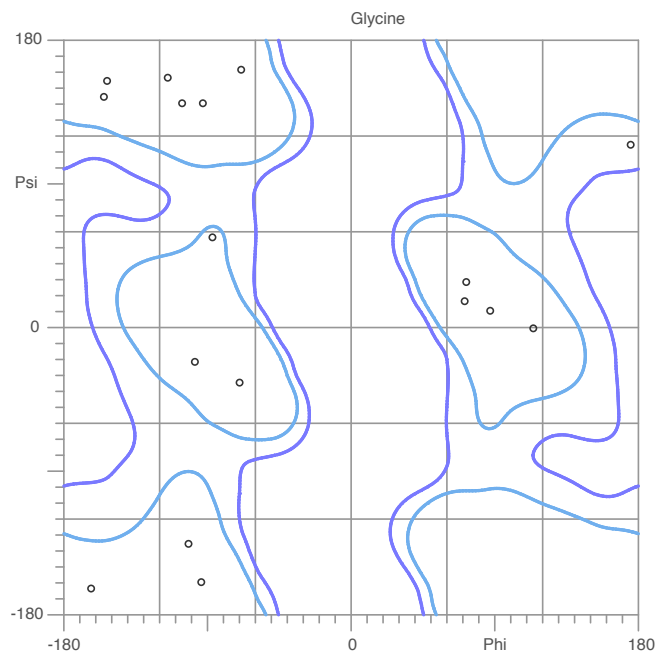
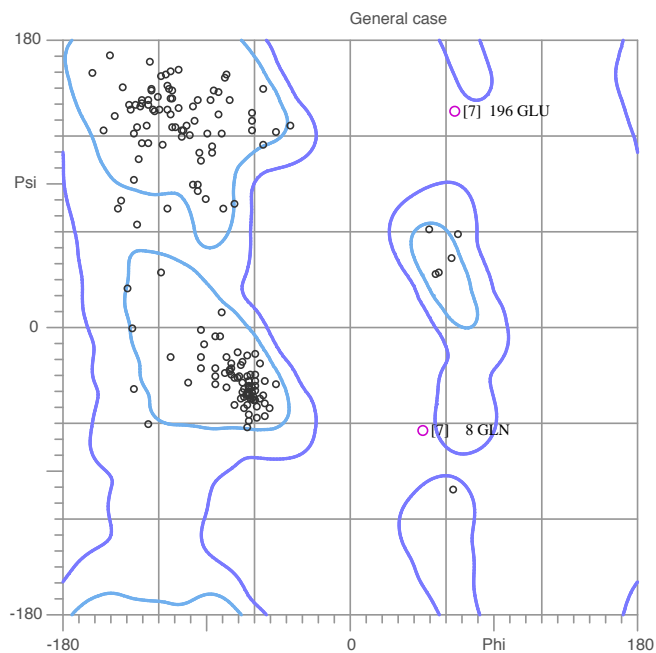
94.0% (188/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[6] 14 GLY (175.0, 95.1)
[6] 102 PHE (-9.3, 105.1)
[6] 143 GLY (-178.3, 55.0)
[6] 179 ALA (-175.0, -95.0)
[6] 201 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 7



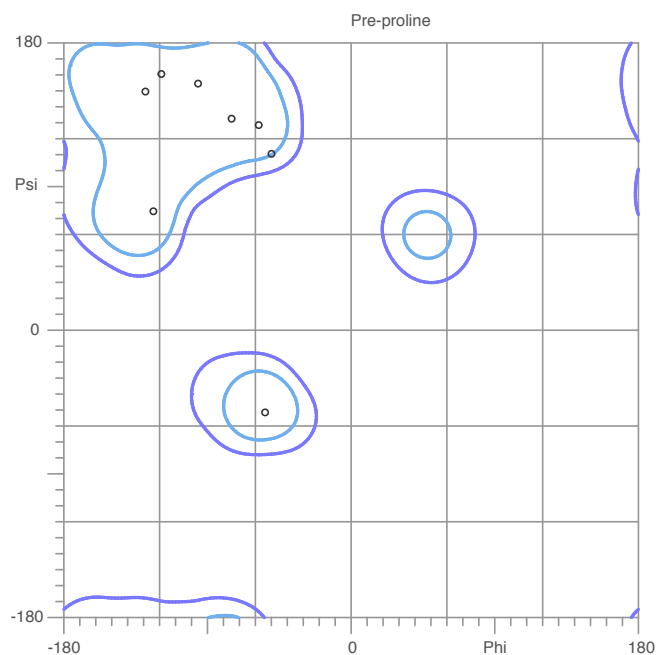
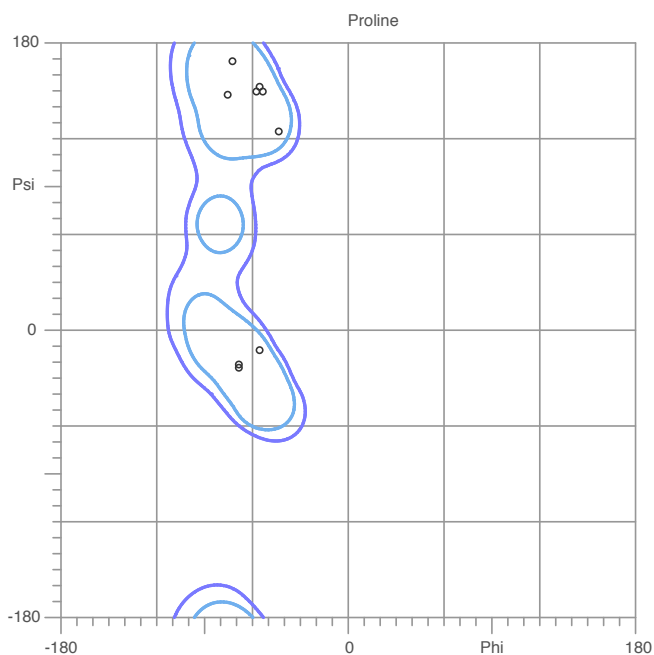
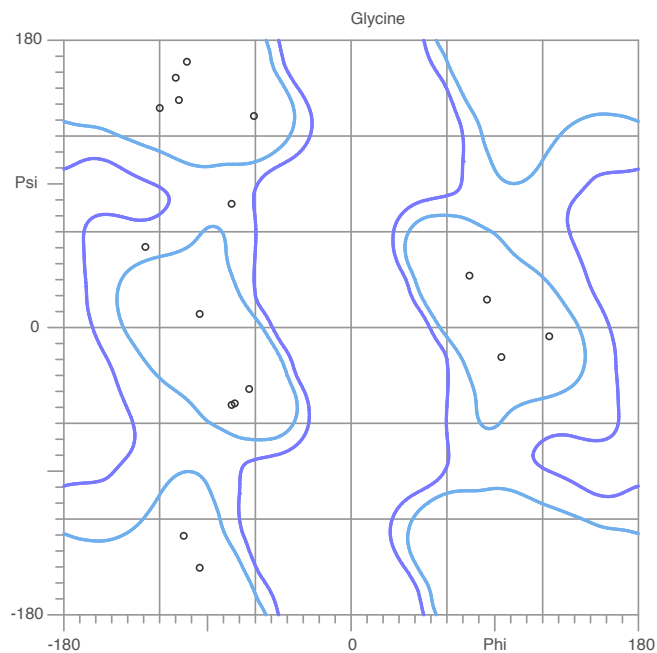
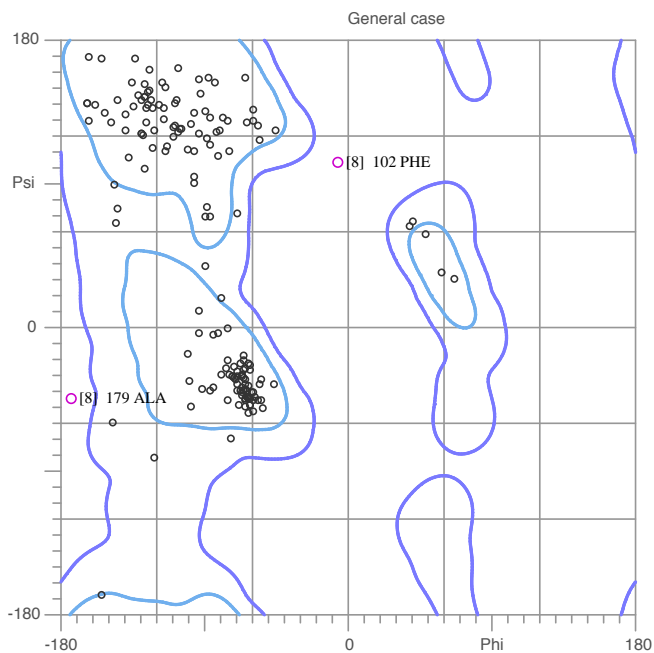
93.0% (186/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [7] 8 GLN (45.0, -65.0)
- [7] 144 PRO (-68.2, -68.7)
- [7] 196 GLU (65.1, 136.7)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 8

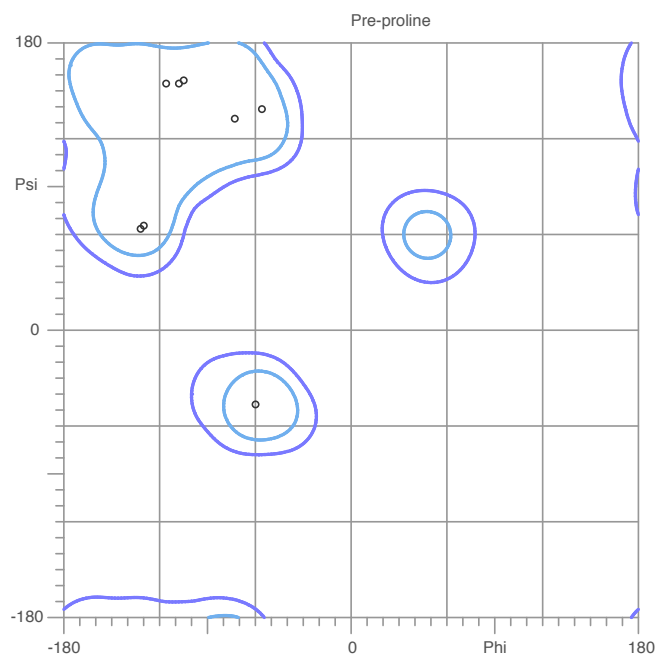
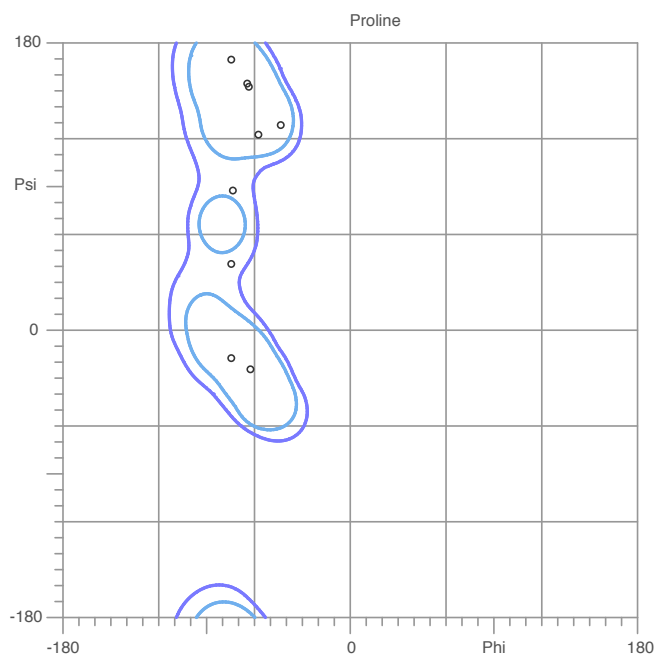
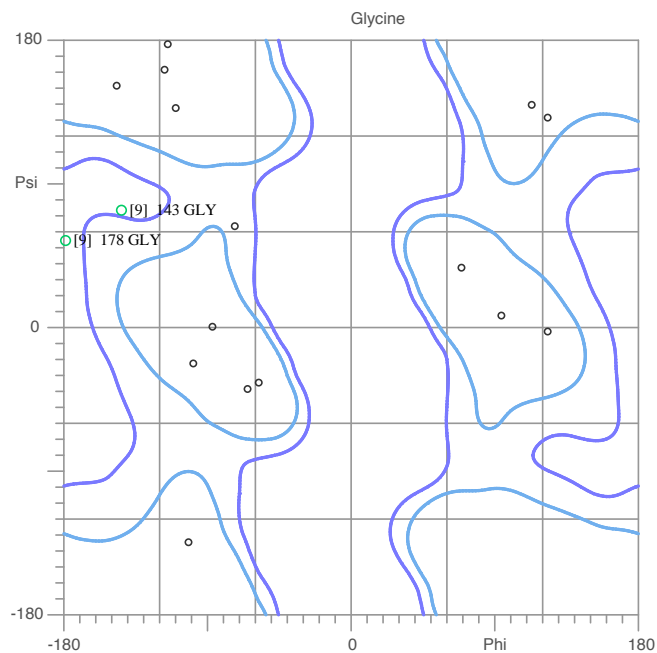
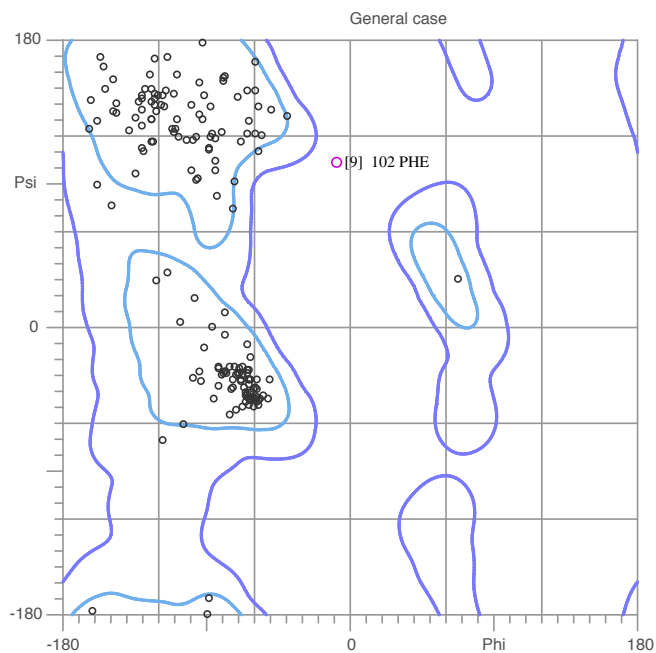


92.0% (184/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[8] 102 PHE (-7.5, 104.9)
[8] 179 ALA (-174.9, -45.0)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 9



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):

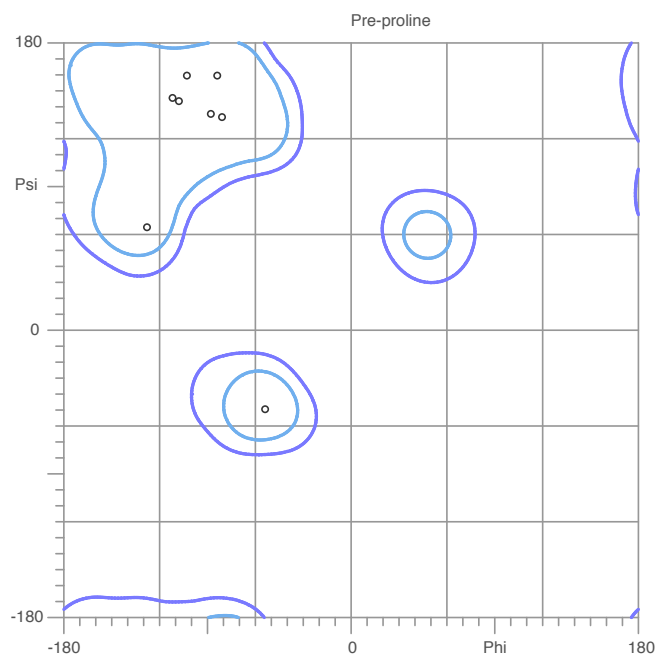
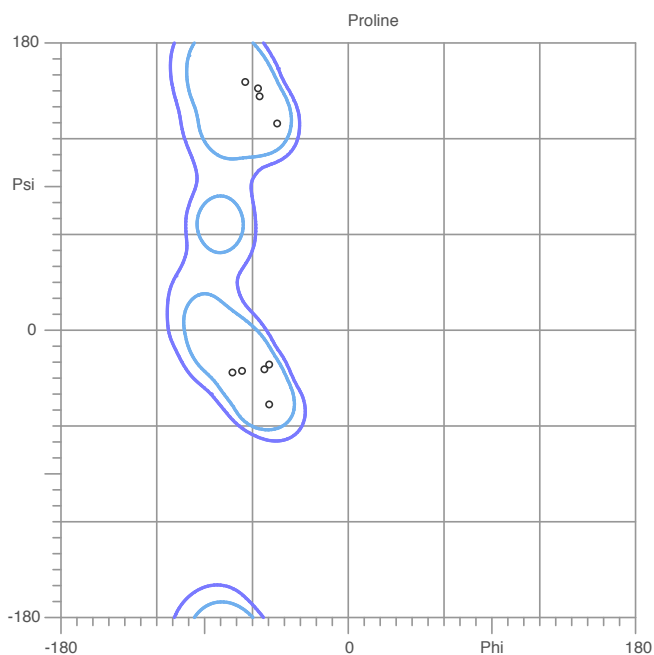
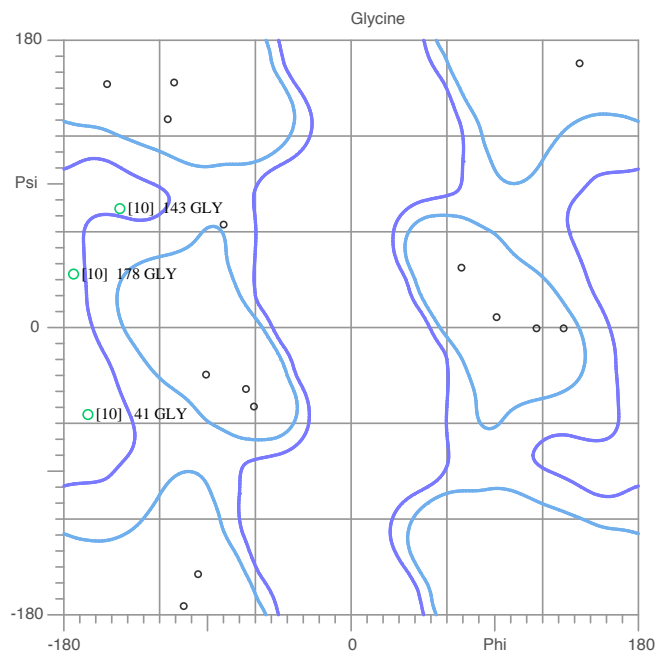
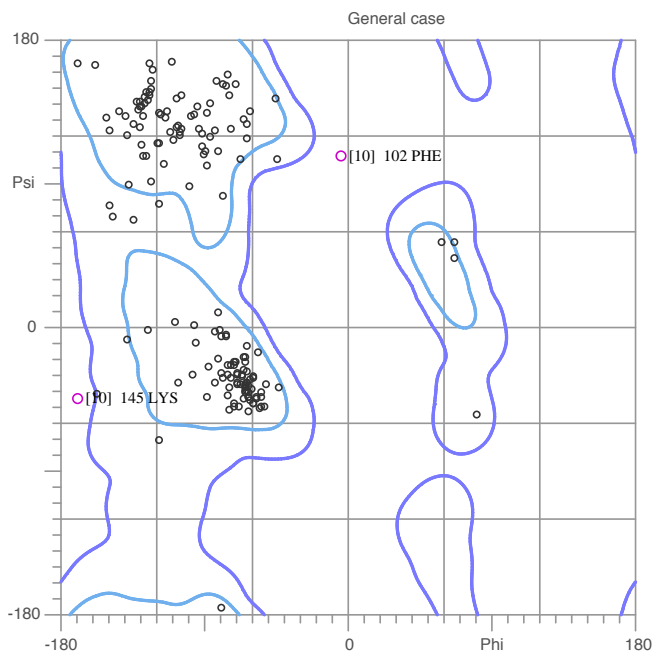
[9] 102 PHE (-9.1, 104.9)

[9] 143 GLY (-144.9, 74.9)

[9] 178 GLY (-179.5, 55.1)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 10



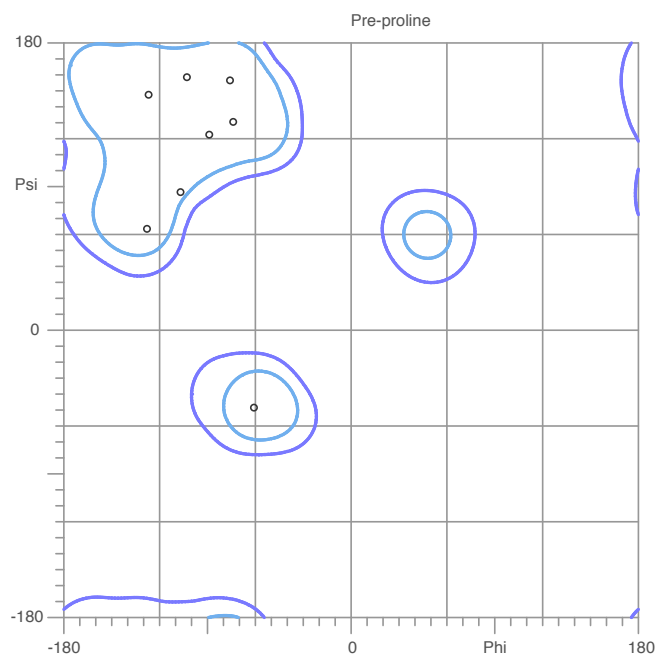
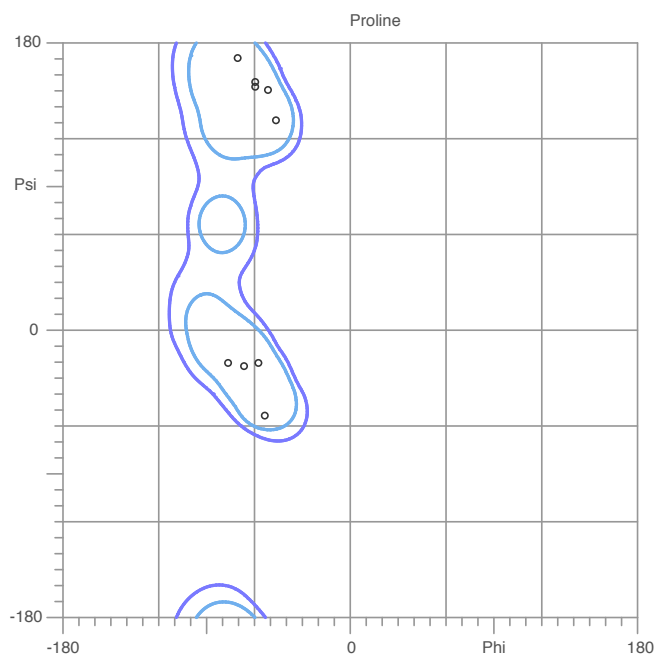
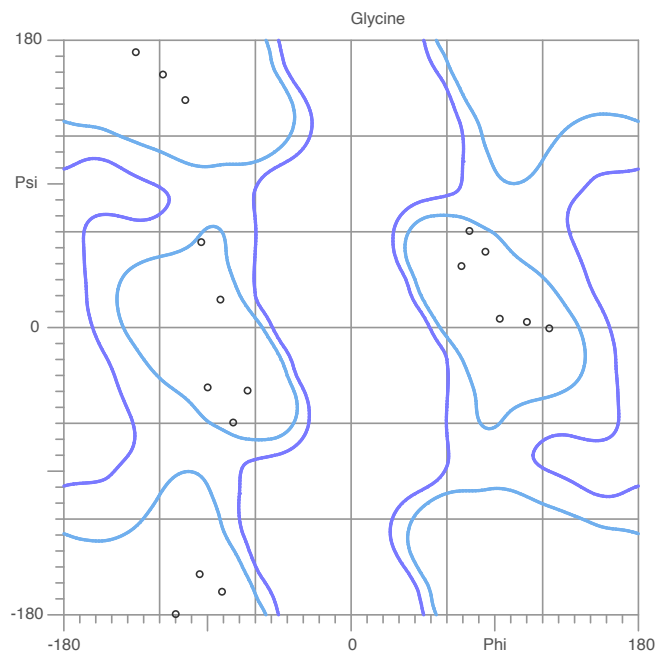
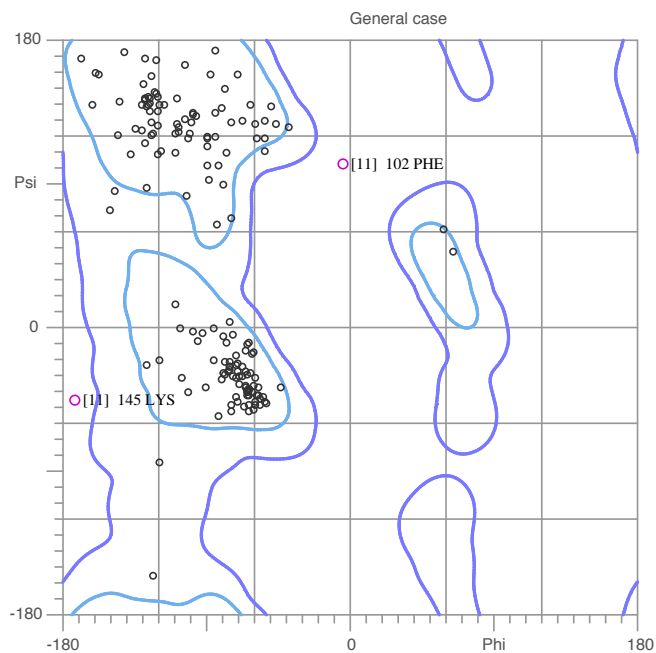
92.0% (184/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[10] 41 GLY (-165.0, -54.9)
[10] 102 PHE (-5.1, 108.8)
[10] 143 GLY (-145.0, 75.1)
[10] 145 LYS (-170.4, -45.0)
[10] 178 GLY (-175.0, 34.9)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 11

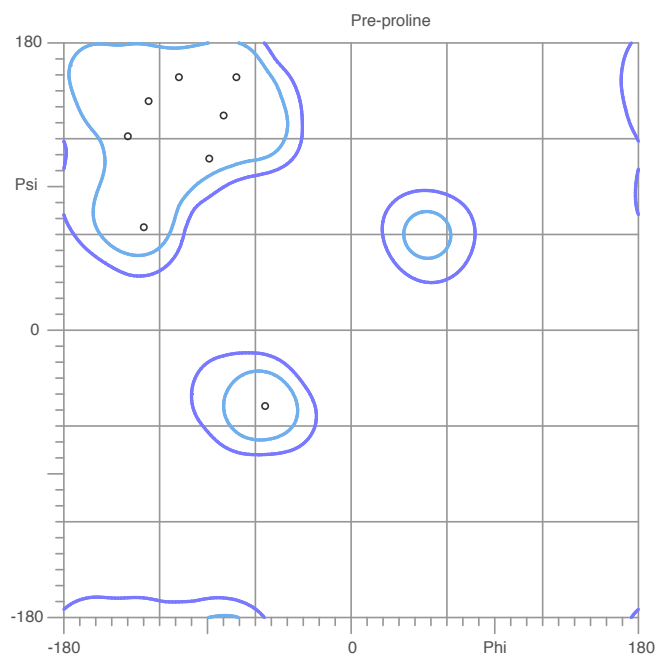
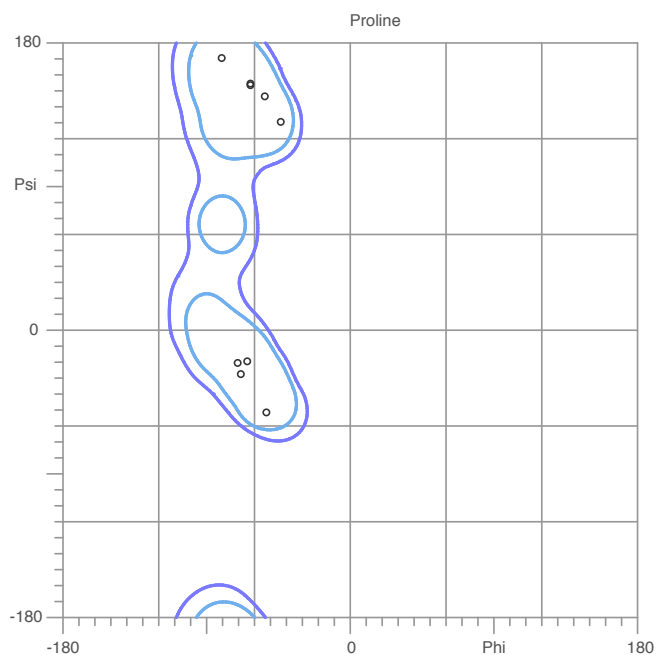
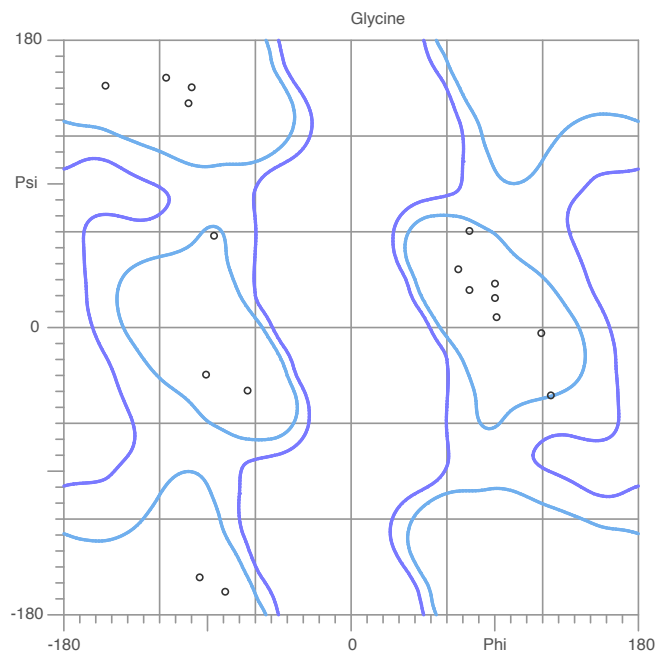
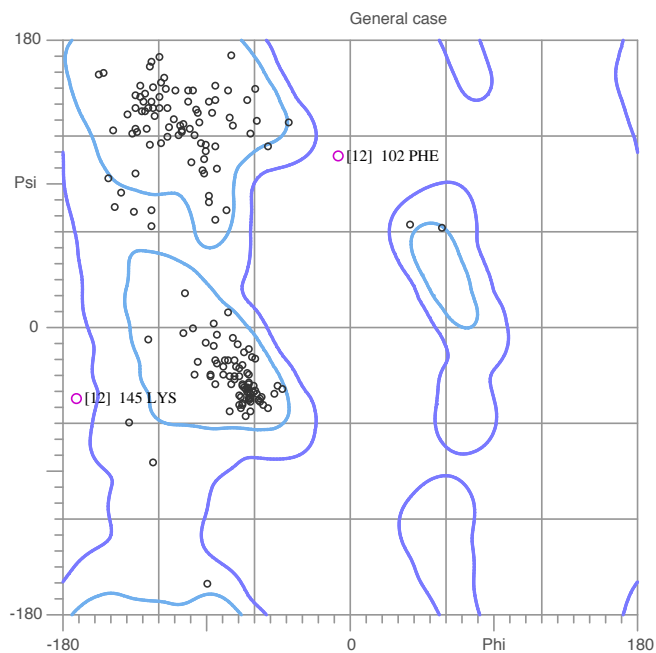


95.5% (191/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[11] 102 PHE (-5.0, 103.4)
[11] 145 LYS (-173.6, -45.1)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 12

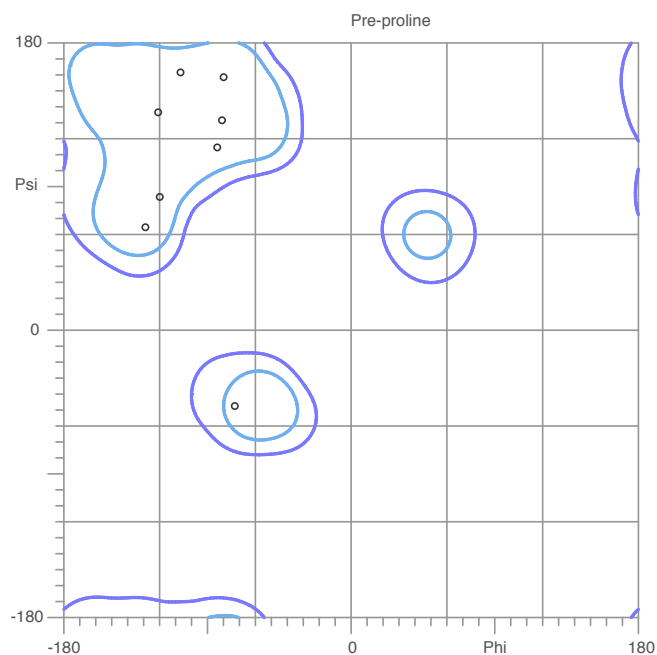
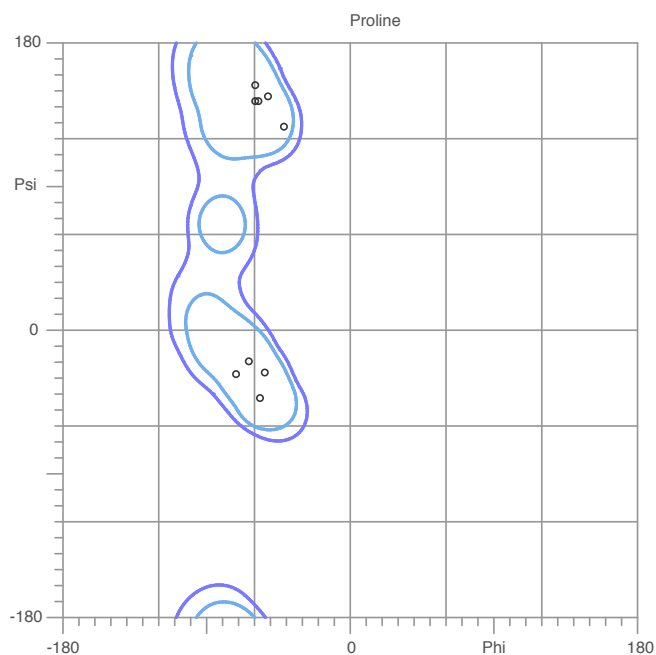
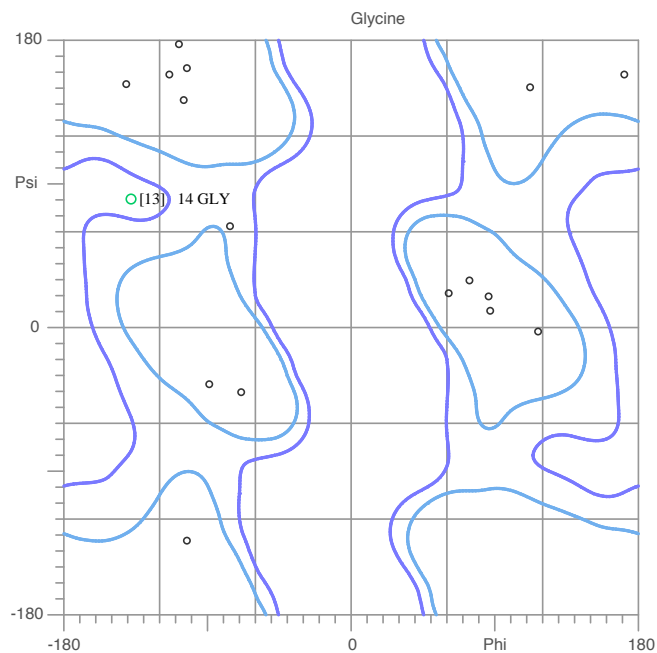
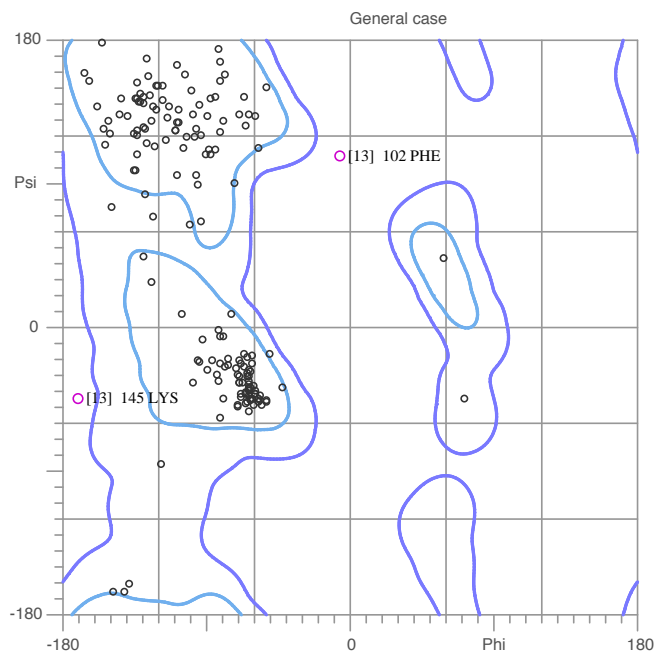


93.0% (186/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 102 PHE (-8.4, 108.3)
[12] 145 LYS (-172.8, -45.0)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 13

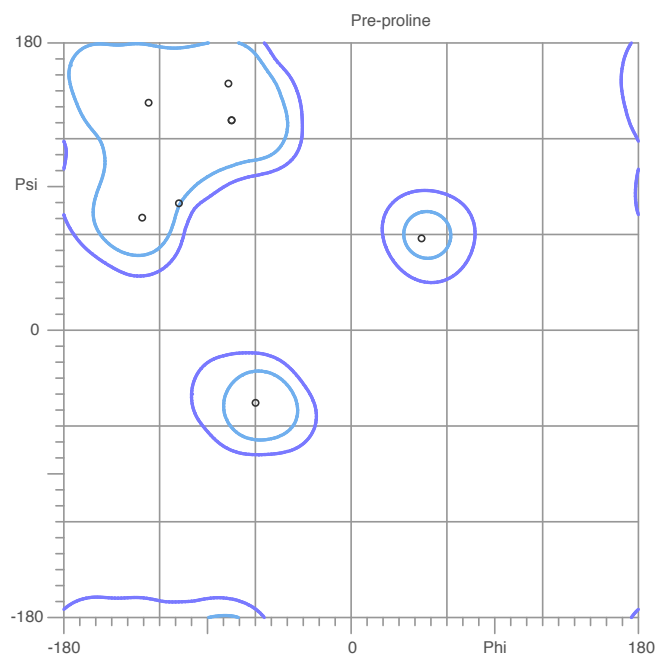
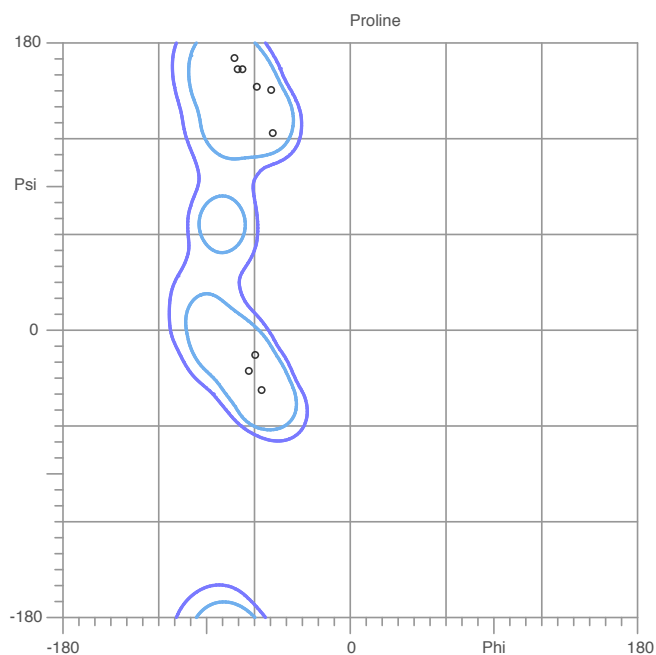
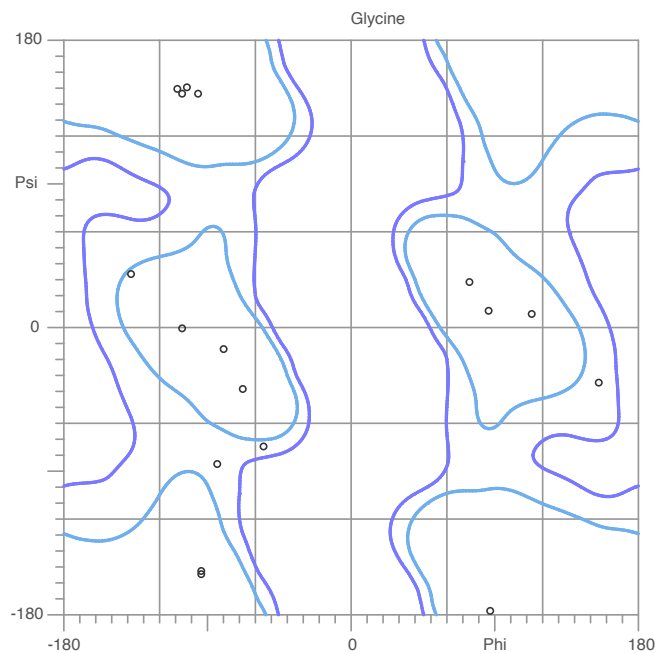
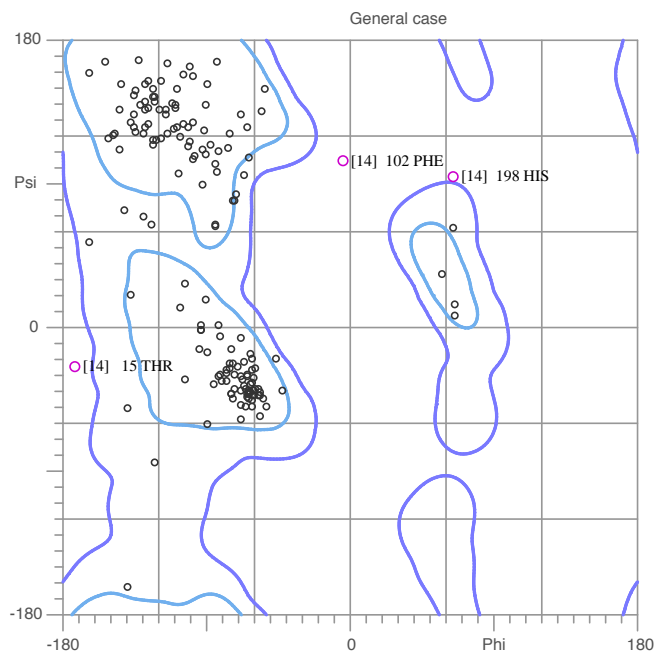


93.5% (187/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[13] 14 GLY (-138.4, 81.2)
[13] 102 PHE (-7.2, 108.1)
[13] 145 LYS (-171.0, -44.9)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 14



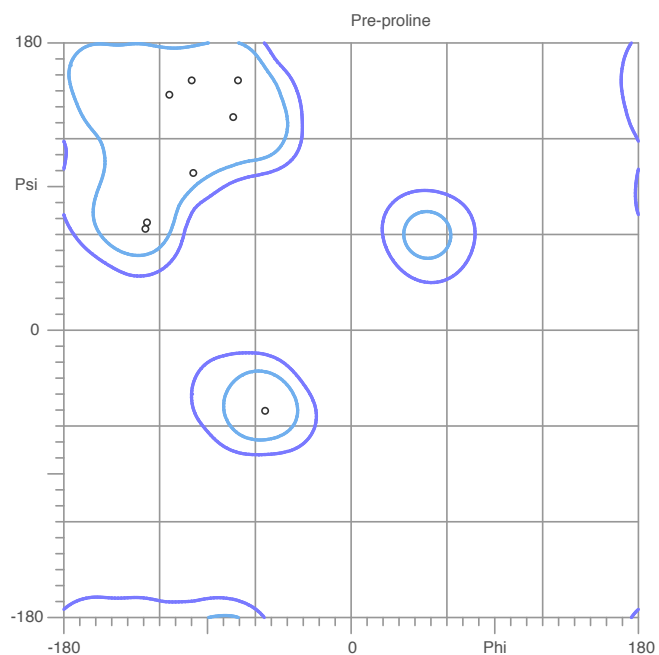
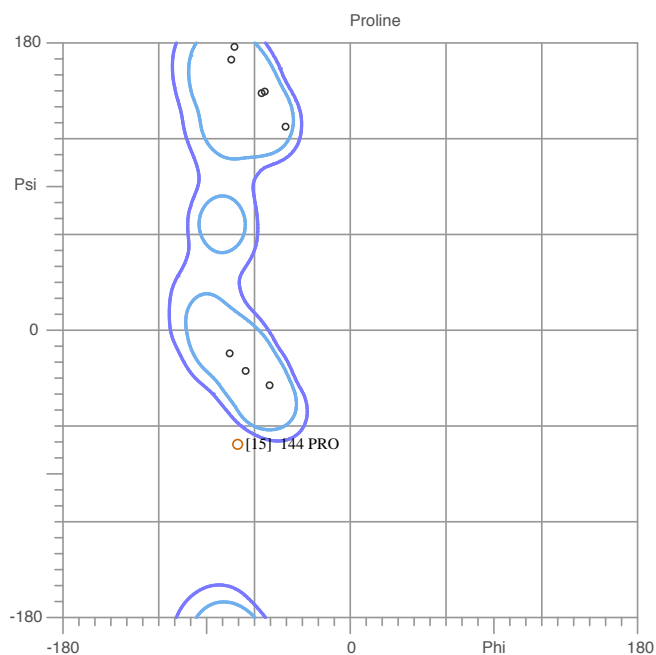
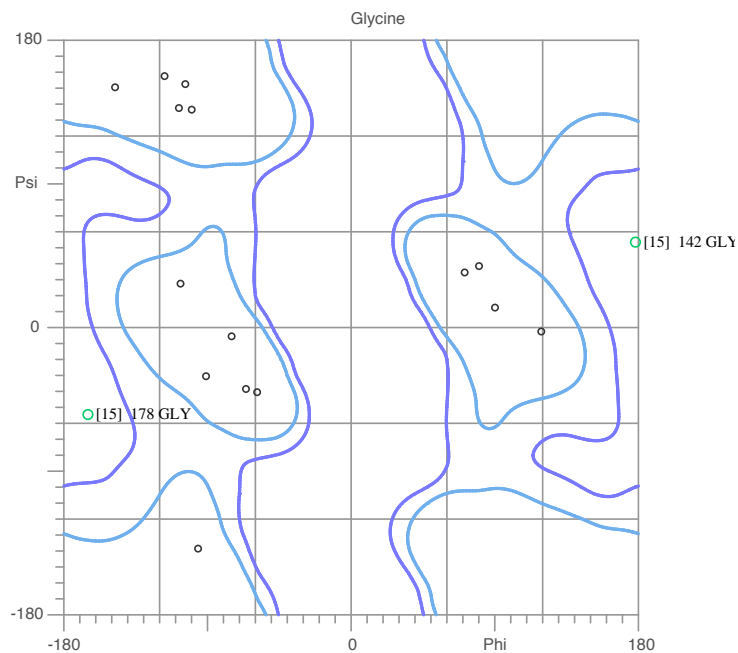
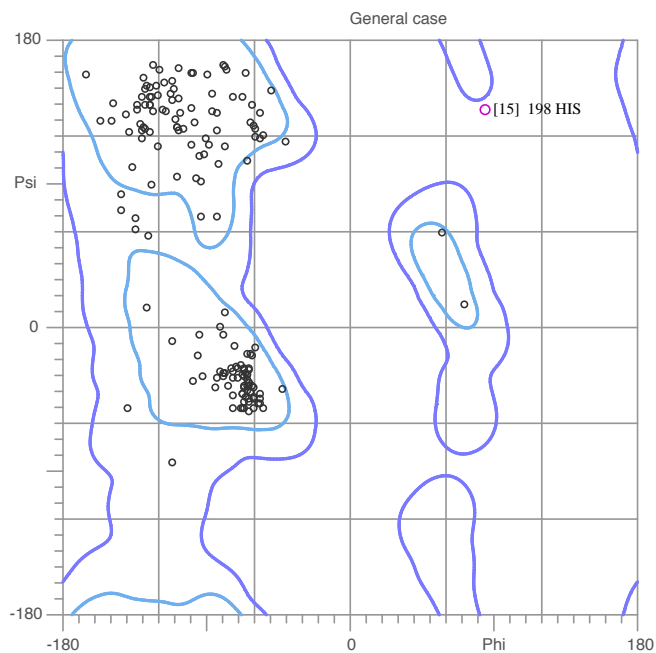
91.0% (182/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [14] 15 THR (-173.3, -25.0)
- [14] 102 PHE (-5.1, 105.1)
- [14] 198 HIS (65.0, 95.1)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 15



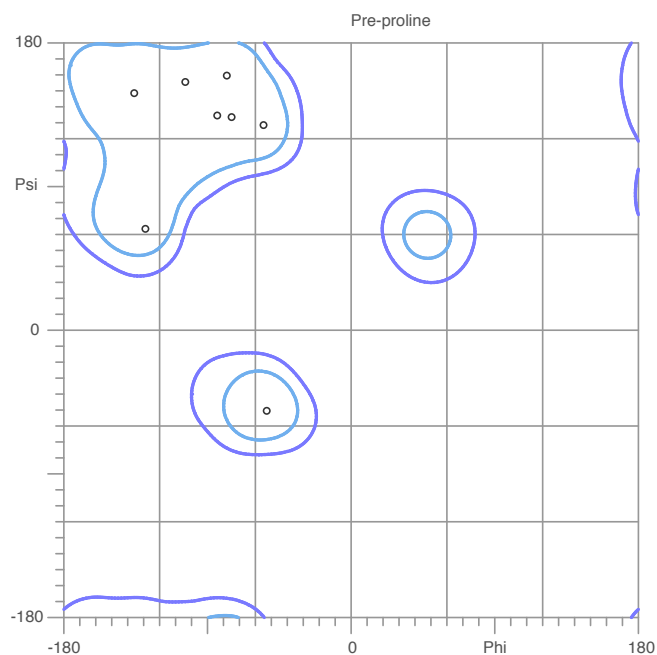
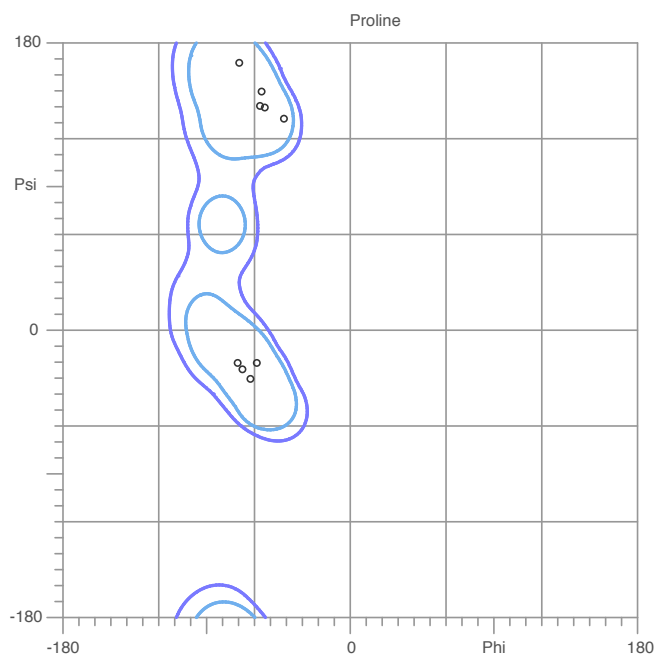
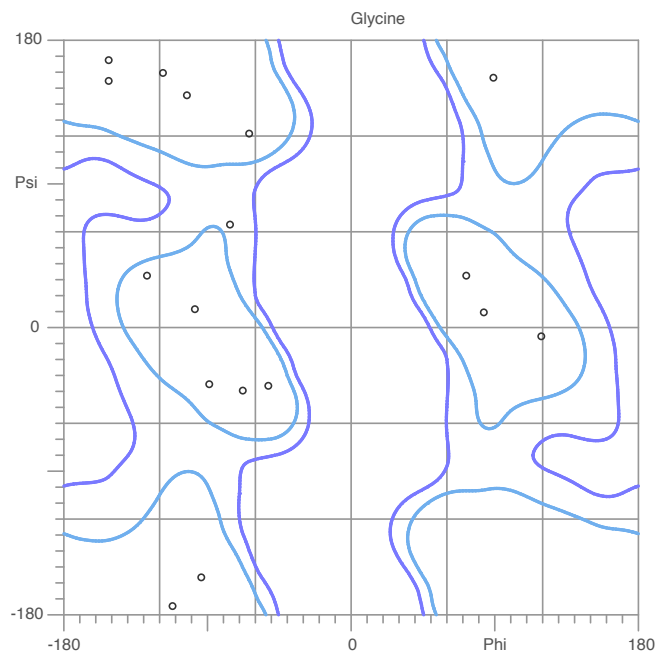
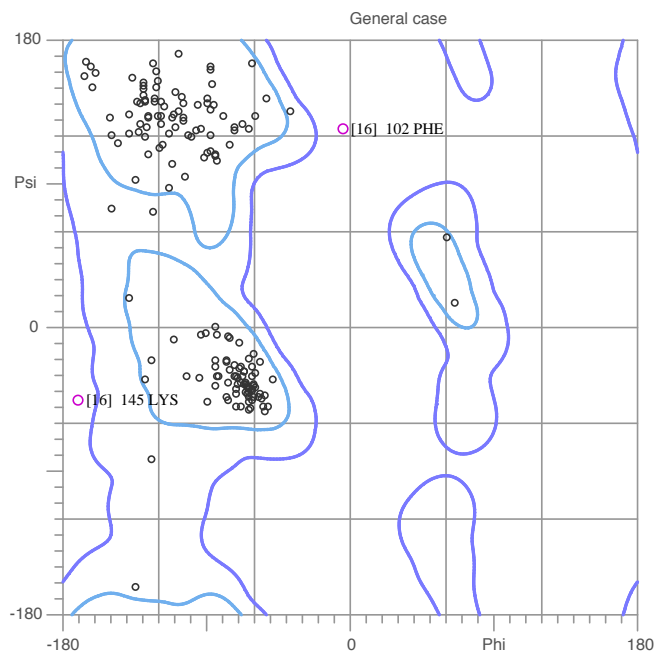
93.5% (187/200) of all residues were in favored (98%) regions.
98.0% (196/200) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [15] 142 GLY (179.0, 55.0)
- [15] 144 PRO (-71.8, -71.0)
- [15] 178 GLY (-165.0, -55.0)
- [15] 198 HIS (85.0, 137.1)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 16

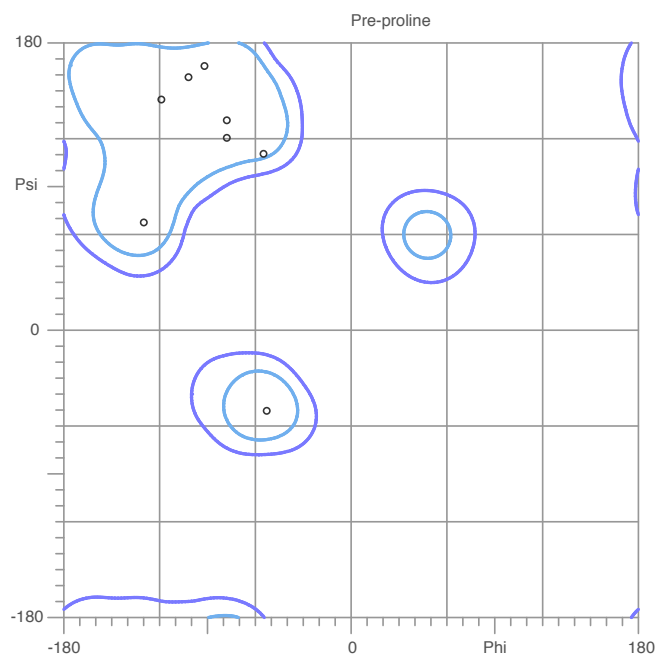
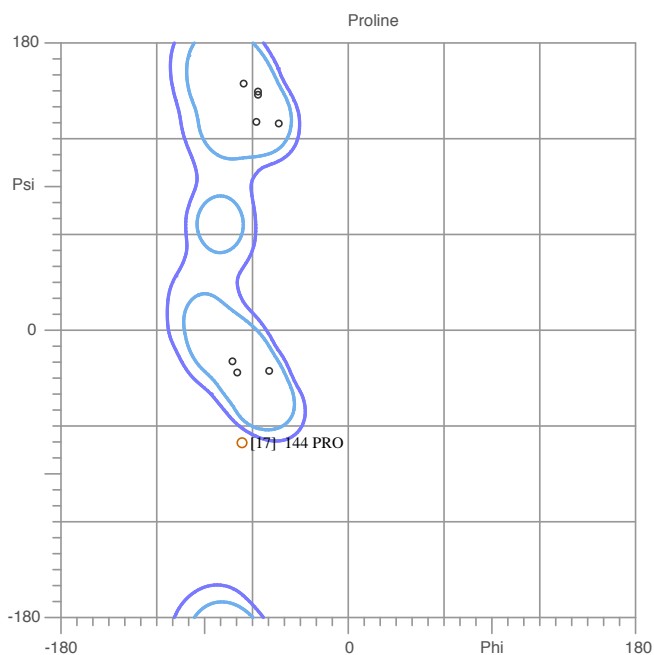
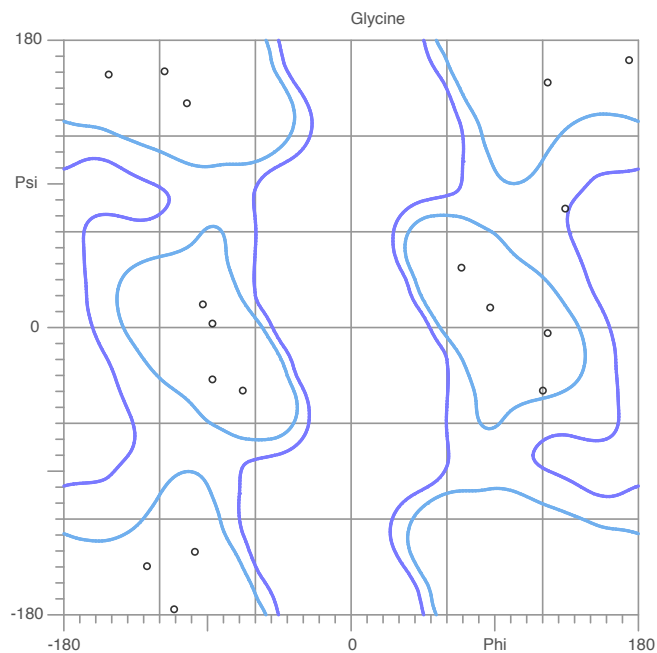
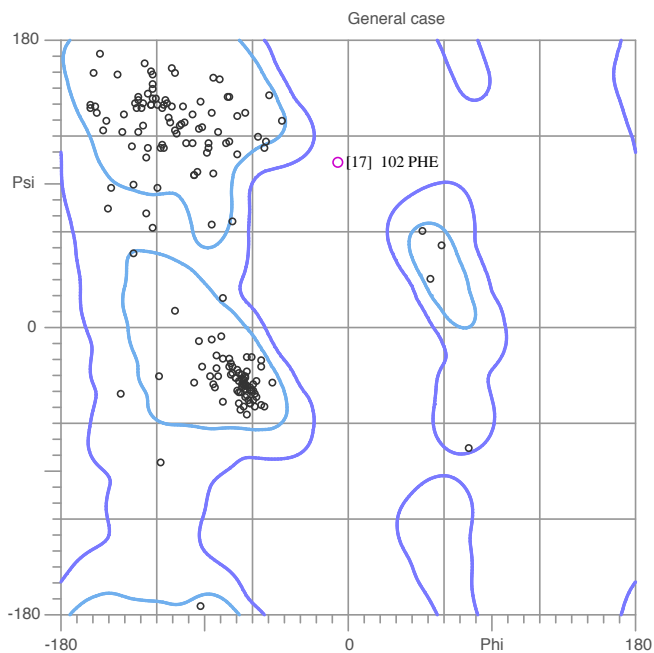


96.0% (192/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[16] 102 PHE (-5.1, 125.0)
[16] 145 LYS (-171.2, -45.0)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 17



93.0% (186/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

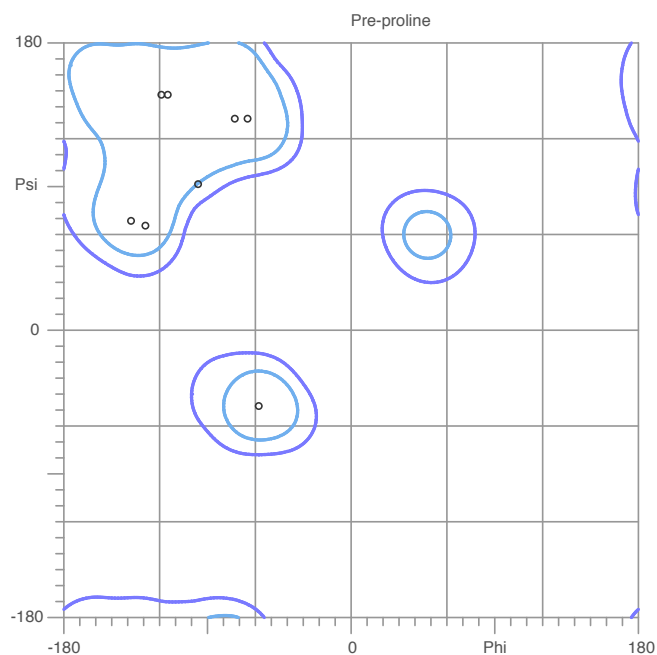
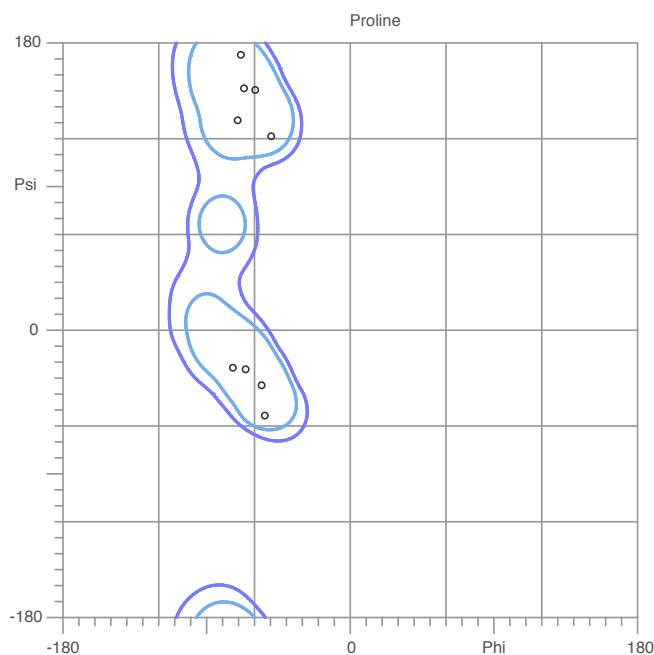
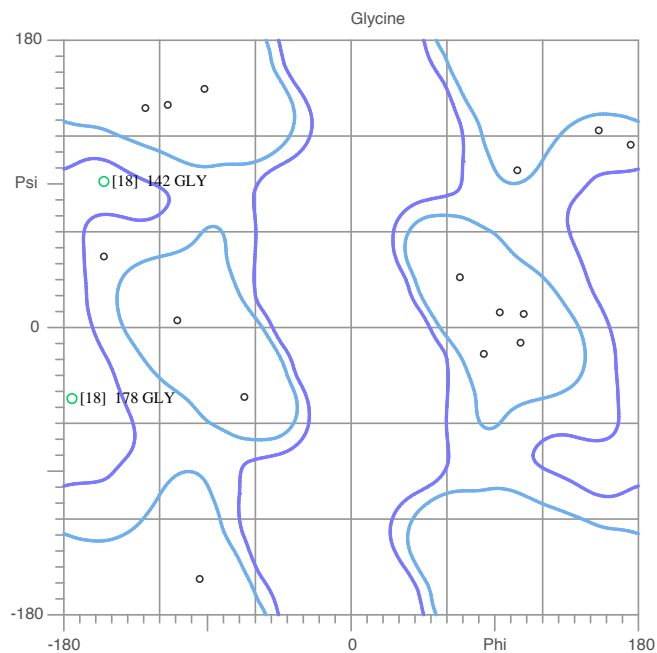
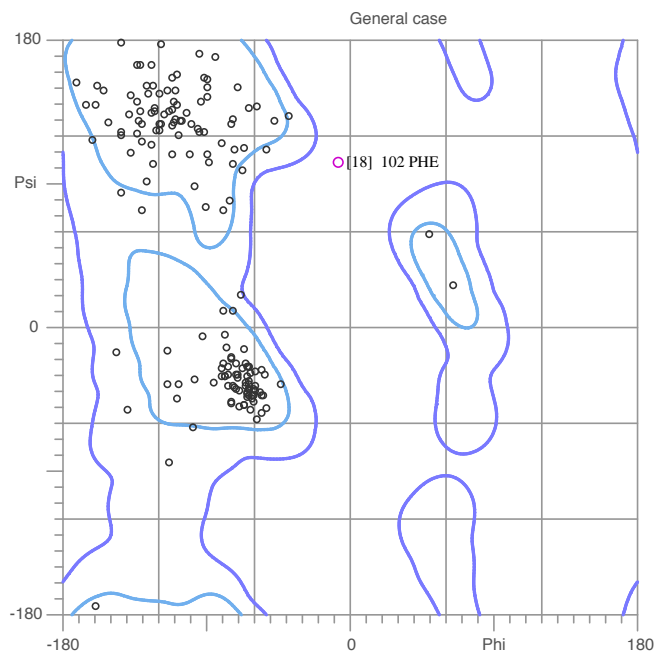
There were 2 outliers (phi, psi):

[17] 102 PHE (-7.4, 105.0)

[17] 144 PRO (-67.4, -70.2)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 18



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):

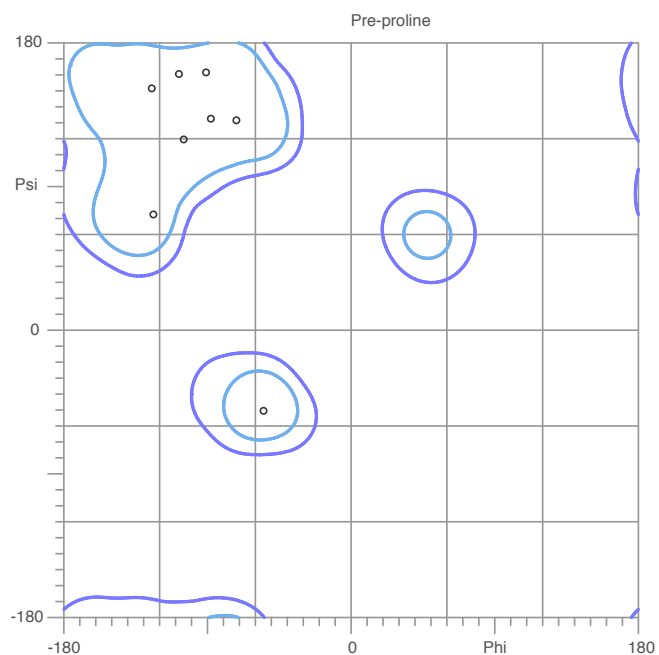
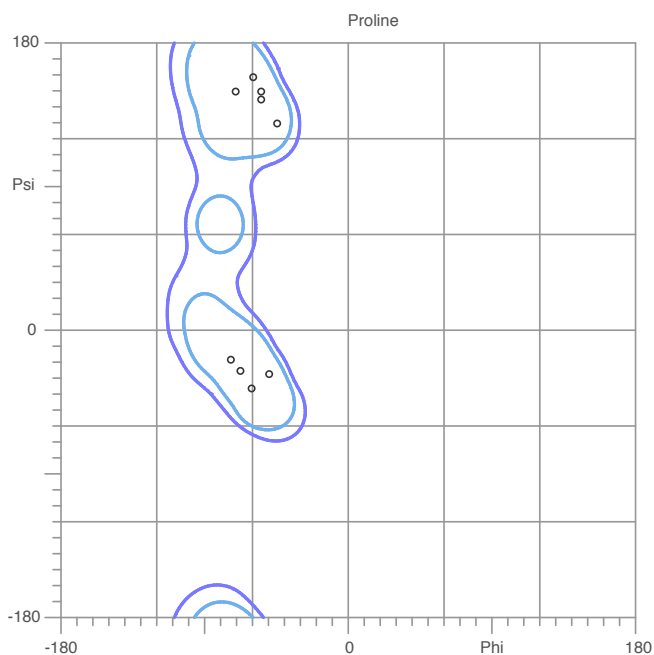
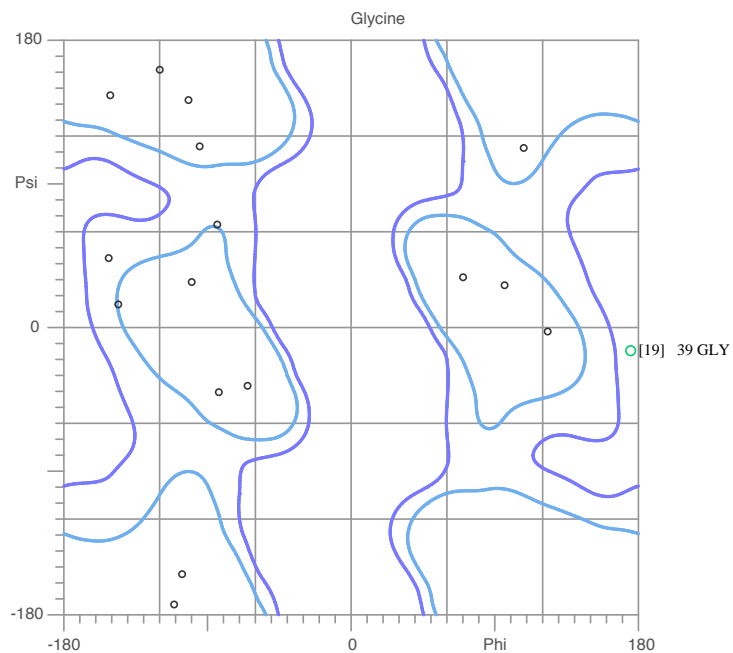
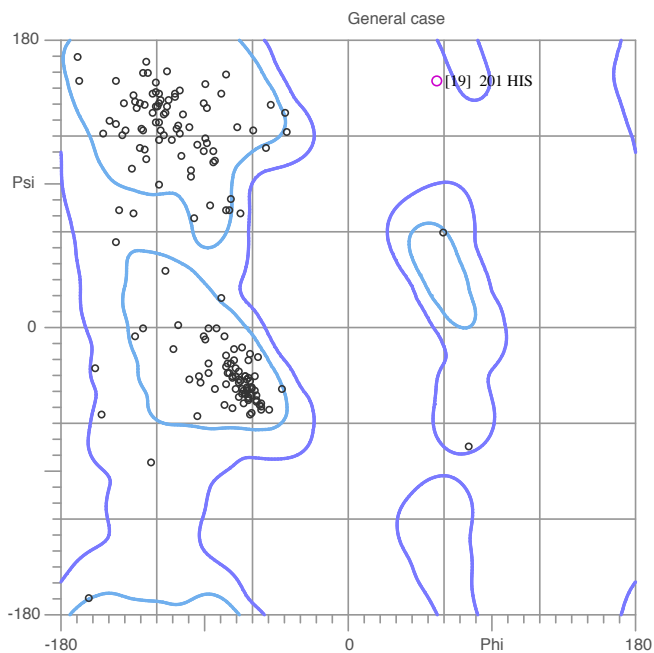
[18] 102 PHE (-8.4, 105.0)

[18] 142 GLY (-155.0, 92.5)

[18] 178 GLY (-175.0, -45.0)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 19

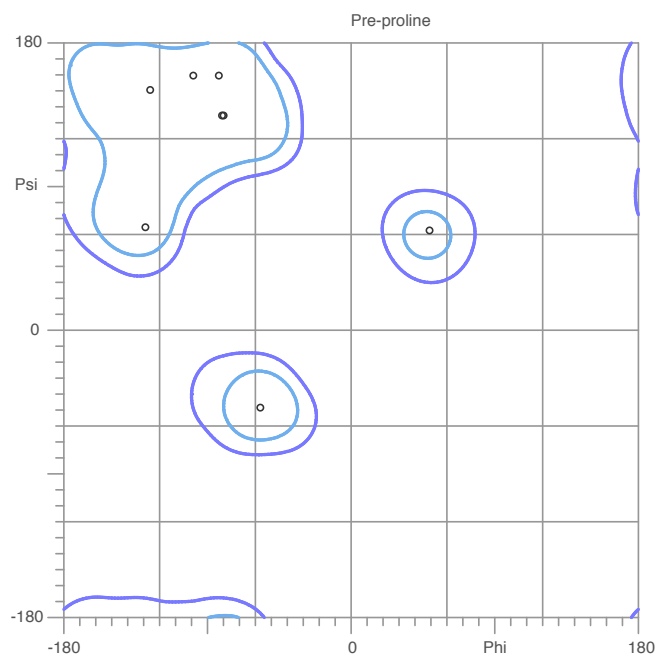
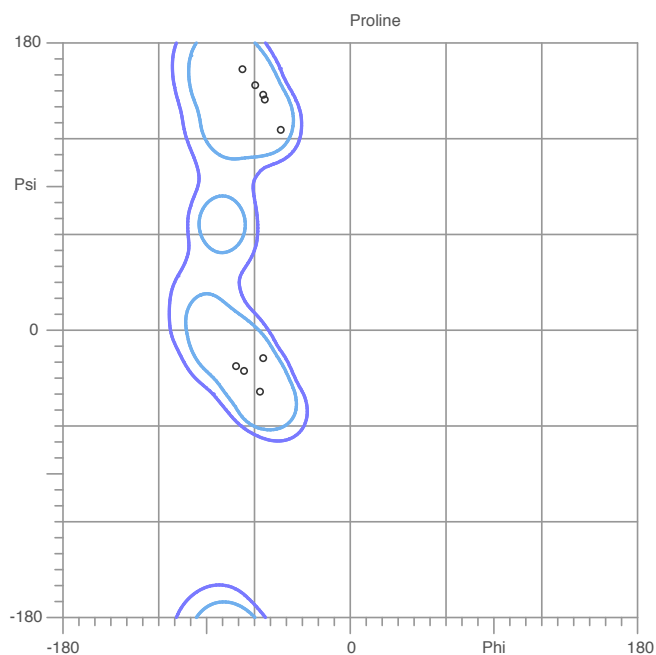
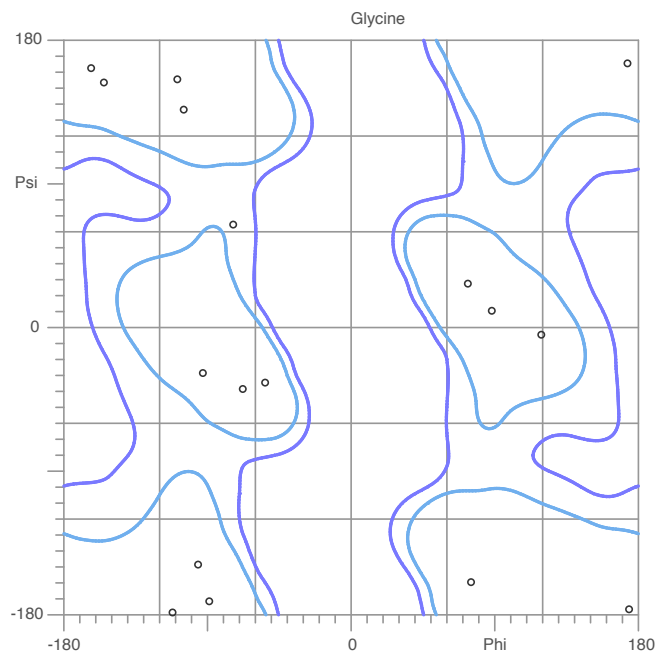
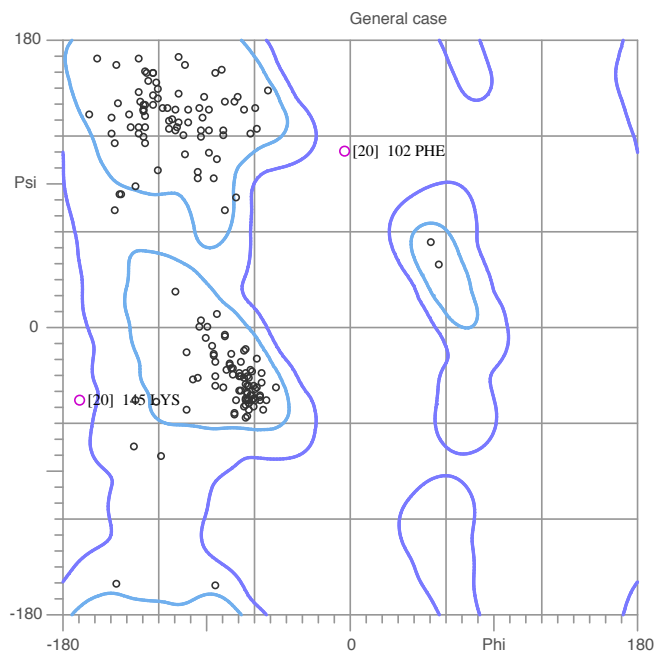


91.5% (183/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 39 GLY (175.4, -15.0)
[19] 201 HIS (55.1, 155.0)

MolProbity Ramachandran analysis

SGR145_R3Cons_em_bcr3.pdb, model 20



94.0% (188/200) 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):
[20] 102 PHE (-5.0, 111.8)
[20] 145 LYS (-170.4, -45.0)