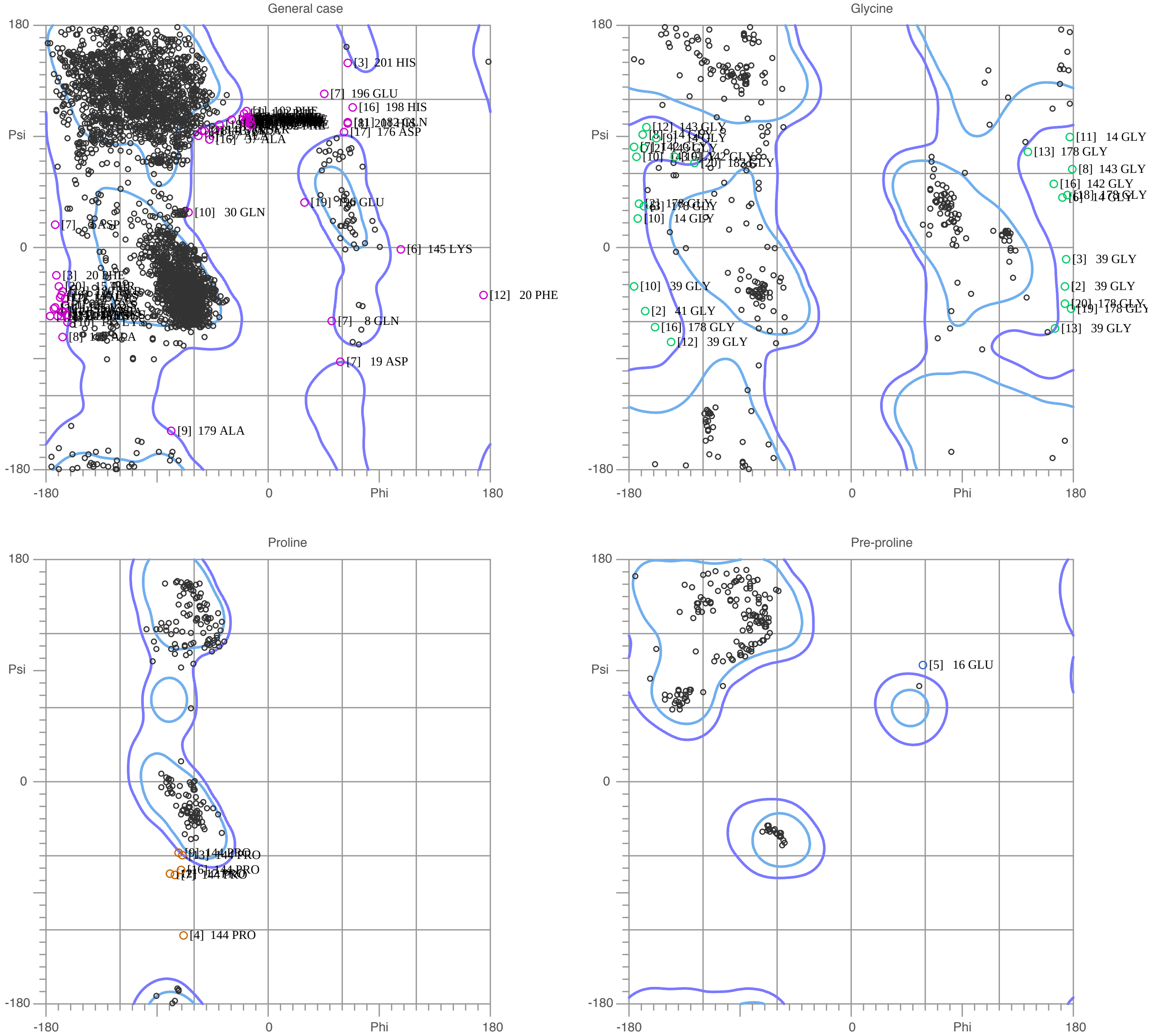
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, all models



88.4% (3536/4000) of all residues were in favored (98%) regions.
97.7% (3909/4000) of all residues were in allowed (>99.8%) regions.

There were 91 outliers (phi, psi):
- [1] 102 PHE (-18.8, 111.1)
- [1] 145 LYS (-165.2, -46.8)
- [2] 12 VAL (-165.6, -41.4)
- [2] 39 GLY (173.5, -31.2)
- [2] 41 GLY (-167.1, -51.7)
- [2] 102 PHE (-15.6, 106.7)
- [2] 143 GLY (-168.7, 81.7)
- [2] 145 LYS (-174.2, -50.0)
- [2] 178 GLY (-172.6, 36.7)
- [3] 20 PHE (-172.4, -22.8)
- [3] 39 GLY (174.6, -9.2)
- [3] 102 PHE (-20.3, 109.4)
- [3] 178 GLY (-168.6, 34.9)
- [3] 201 HIS (64.2, 150.9)
- [4] 9 SER (-54.6, 95.8)
- [4] 102 PHE (-18.2, 106.1)
- [4] 144 PRO (-69.5, -124.3)
- [5] 16 GLU (58.8, 95.5)
- [5] 102 PHE (-16.1, 106.9)
- [5] 145 LYS (-171.4, -55.2)
- [6] 14 GLY (171.2, 41.7)
- [6] 102 PHE (-17.7, 103.6)
- [6] 145 LYS (108.0, -1.7)
- [7] 3 ASP (-173.3, 19.1)
- [7] 8 GLN (51.0, -59.2)
- [7] 19 ASP (58.6, -92.8)
- [7] 102 PHE (-18.5, 104.4)
- [7] 142 GLY (-176.9, 82.4)
- [7] 144 PRO (-76.4, -76.0)
- [7] 196 GLU (45.6, 125.3)
- [8] 14 GLY (-169.0, 92.9)
- [8] 37 ALA (-57.6, 91.9)
- [8] 102 PHE (-17.7, 102.5)
- [8] 143 GLY (179.6, 64.3)
- [8] 179 ALA (-167.2, -72.9)
- [8] 201 HIS (64.9, 101.3)
- [9] 14 GLY (-158.8, 89.1)
- [9] 102 PHE (-14.0, 101.8)
- [9] 144 PRO (-74.0, -57.5)
- [9] 179 ALA (-79.4, -148.4)
- [10] 14 GLY (-173.0, 24.2)
- [10] 30 GLN (-65.5, 29.8)
- [10] 39 GLY (-176.4, -31.9)
- [10] 102 PHE (-20.9, 102.8)
- [10] 143 GLY (-174.3, 74.8)
- [10] 145 LYS (-163.1, -60.3)
- [11] 14 GLY (177.6, 90.7)
- [11] 20 PHE (-177.4, -55.2)
- [11] 102 PHE (-17.5, 99.4)
- [11] 145 LYS (-169.9, -40.9)
- [11] 182 GLN (64.1, 102.8)
- [12] 17 PRO (-80.4, -74.4)
- [12] 19 ASP (-167.8, -51.9)
- [12] 20 PHE (174.2, -38.3)
- [12] 39 GLY (-146.2, -76.3)
- [12] 102 PHE (-21.6, 104.9)
- [12] 143 GLY (-166.7, 98.8)
- [12] 145 LYS (-168.1, -55.0)
- [12] 180 TYR (-167.1, -35.7)
- [13] 39 GLY (165.5, -65.7)
- [13] 102 PHE (-16.0, 103.9)
- [13] 144 PRO (-70.2, -59.7)
- [13] 178 GLY (143.2, 78.5)
- [14] 83 SER (-43.6, 96.0)
- [14] 102 PHE (-16.2, 102.8)
- [14] 145 LYS (-173.1, -48.4)
- [14] 177 GLU (-164.2, -55.0)
- [15] 37 ALA (-30.8, 104.5)
- [15] 102 PHE (-18.4, 104.9)
- [15] 145 LYS (-163.5, -54.5)
- [16] 37 ALA (-48.8, 88.7)
- [16] 142 GLY (164.9, 52.7)
- [16] 144 PRO (-71.8, -71.1)
- [16] 178 GLY (-159.5, -64.4)
- [16] 198 HIS (68.4, 114.7)
- [17] 102 PHE (-17.9, 105.1)
- [17] 176 ASP (61.3, 94.6)
- [17] 179 ALA (-167.5, -52.5)
- [18] 37 ALA (-52.5, 95.5)
- [18] 102 PHE (-19.3, 103.4)
- [18] 178 GLY (175.2, 43.2)
- [19] 102 PHE (-15.3, 104.7)
- [19] 142 GLY (-143.9, 74.5)
- [19] 145 LYS (-168.2, -38.8)
- [19] 178 GLY (178.6, -49.8)
- [19] 196 GLU (29.3, 37.7)
- [19] 198 HIS (-40.0, 100.0)
- [20] 15 THR (-170.0, -31.9)
- [20] 102 PHE (-14.0, 100.5)
- [20] 178 GLY (173.7, -45.4)
- [20] 183 GLY (-127.4, 69.3)

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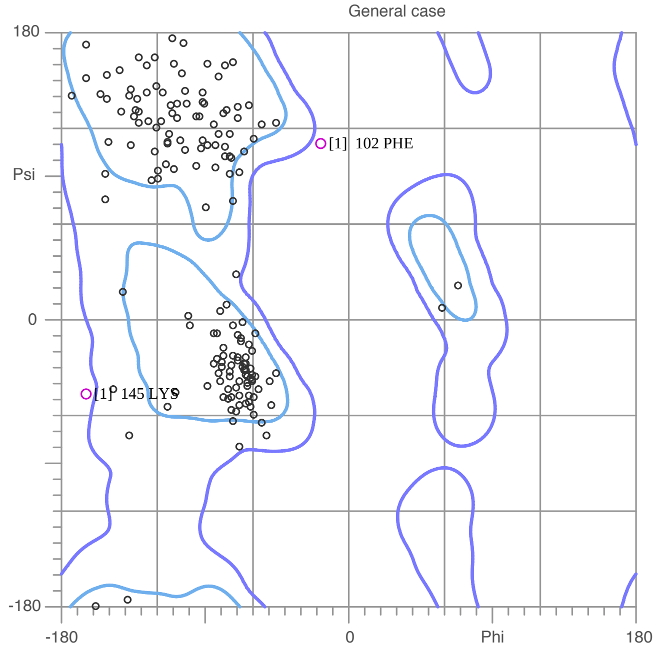
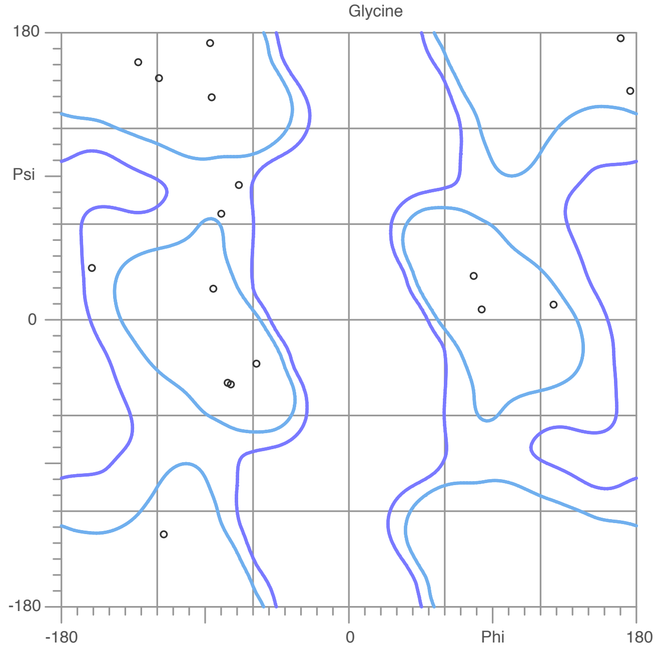
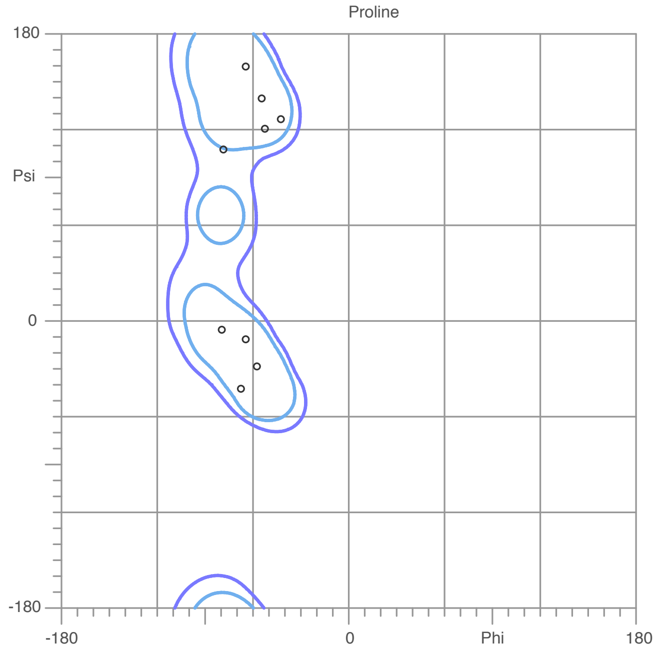
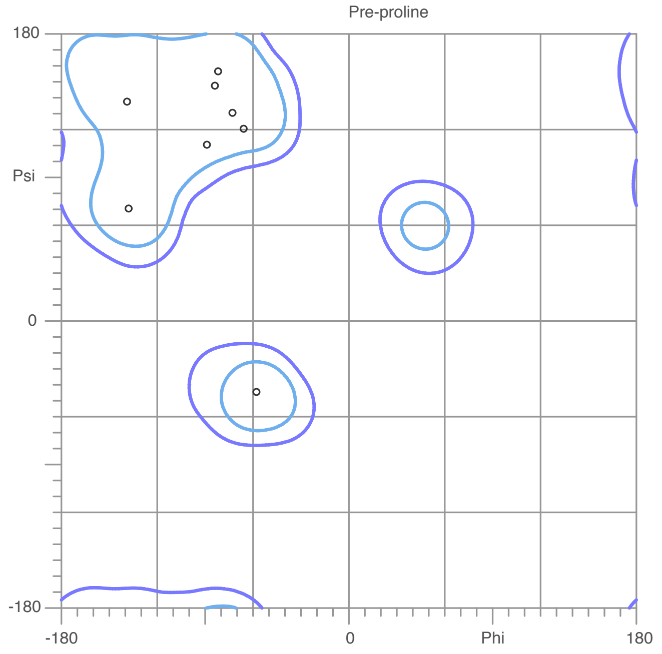
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 1









90.5% (181/200) 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):
[1] 102 PHE (-18.8, 111.1)
[1] 145 LYS (-165.2, -46.8)

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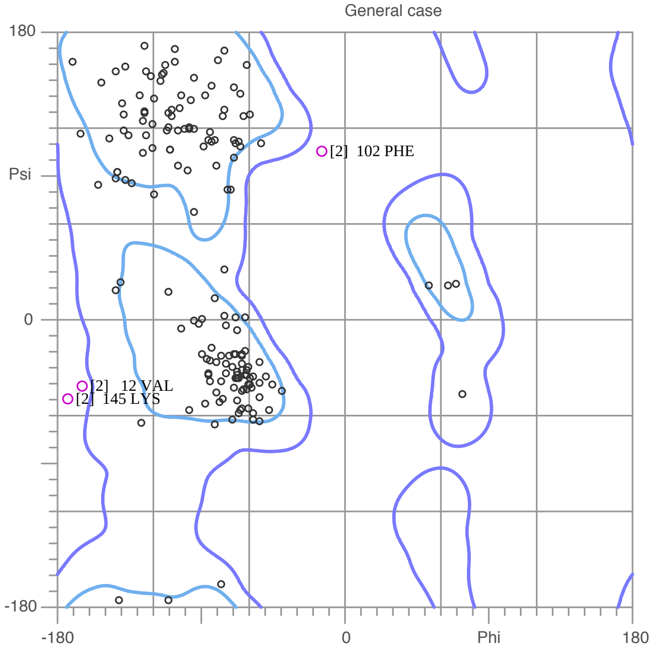
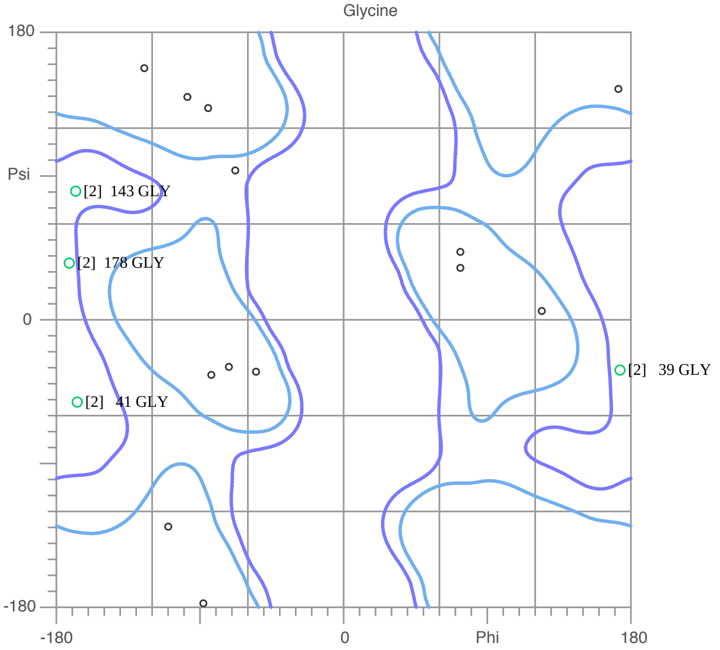
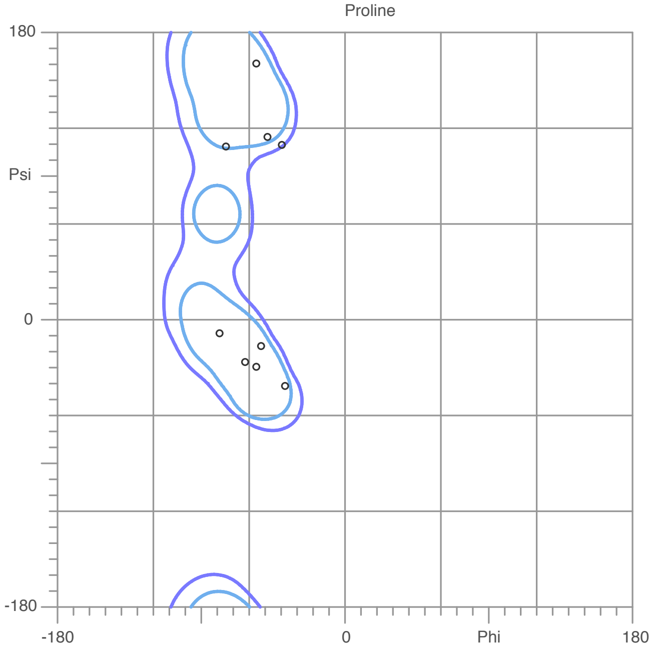
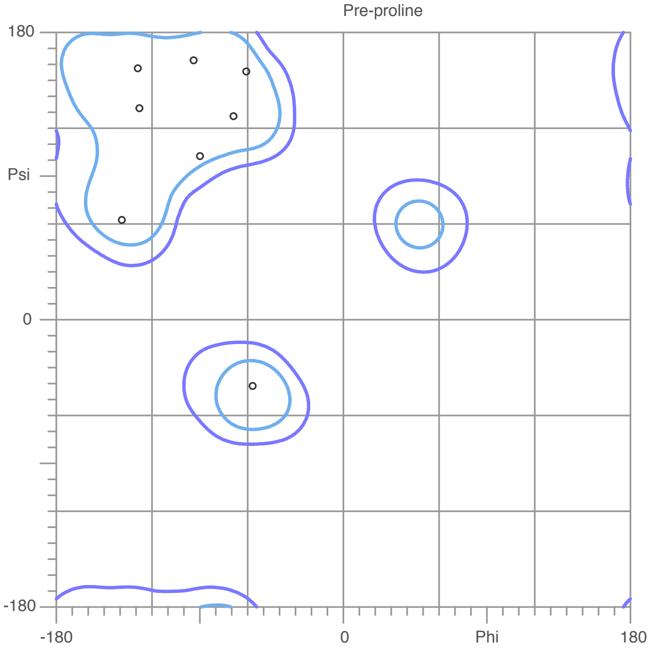
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 2









88.5% (177/200) 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):

[2] 12 VAL (-165.6, -41.4)
[2] 39 GLY (173.5, -31.2)
[2] 41 GLY (-167.1, -51.7)
[2] 102 PHE (-15.6, 106.7)
[2] 143 GLY (-168.7, 81.7)
[2] 145 LYS (-174.2, -50.0)
[2] 178 GLY (-172.6, 36.7)

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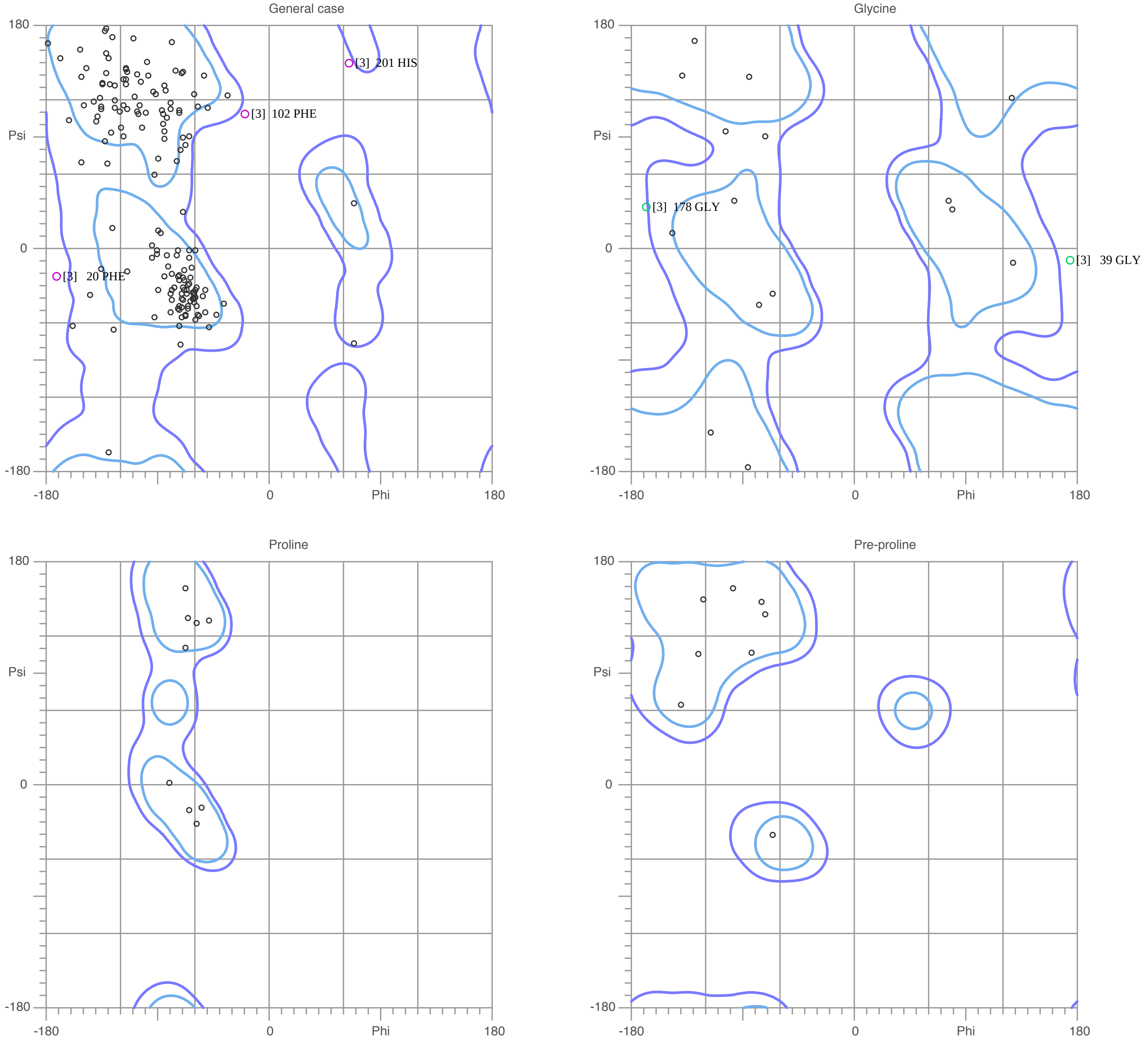
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 3



85.5% (171/200) 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):

[3] 20 PHE (-172.4, -22.8)
[3] 39 GLY (174.6, -9.2)
[3] 102 PHE (-20.3, 109.4)
[3] 178 GLY (-168.6, 34.9)
[3] 201 HIS (64.2, 150.9)

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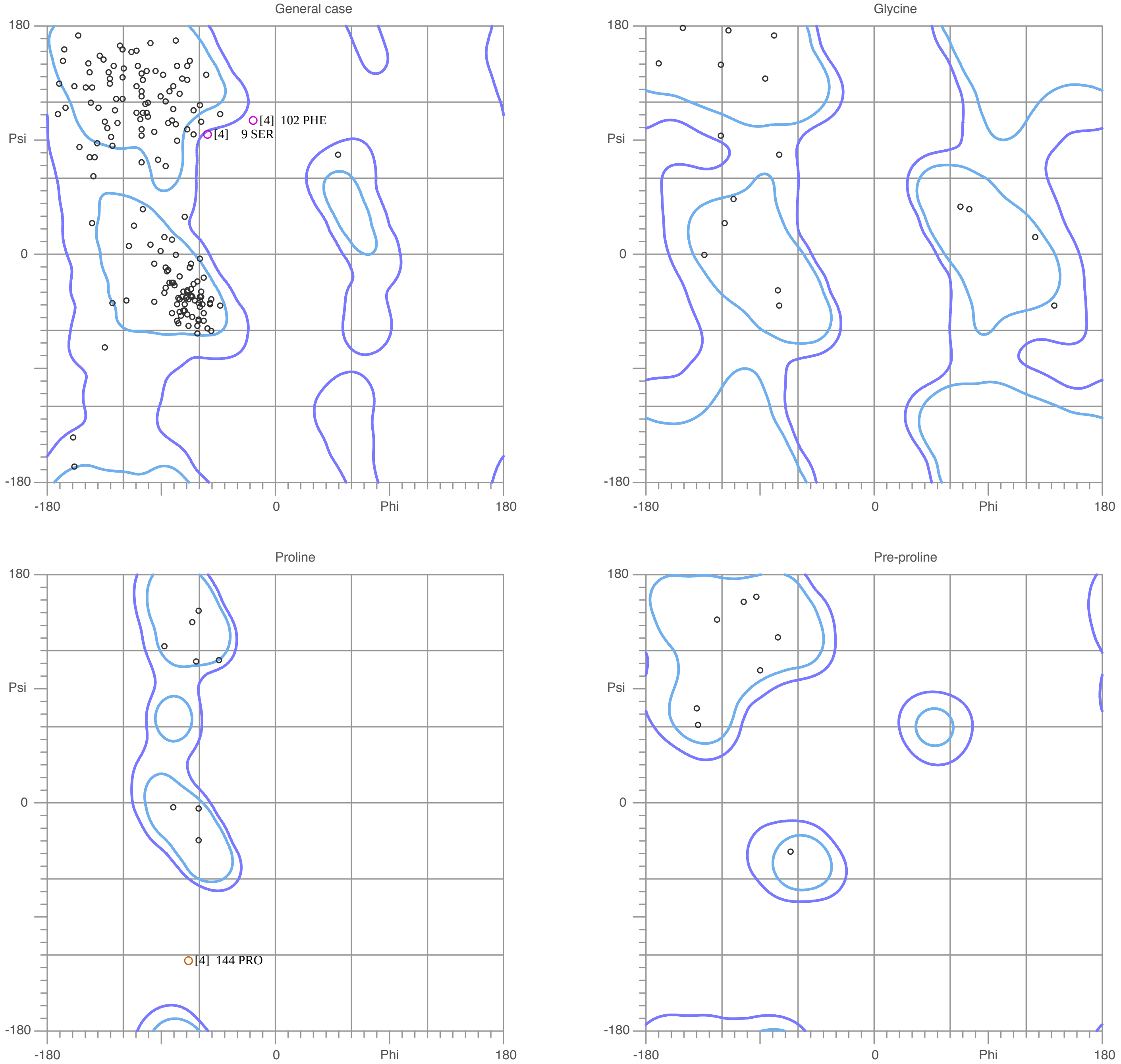
SGR145_NMR_em_bcr3.pdb, model 4



87.0% (174/200) 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):

[4] 9 SER (-54.6, 95.8)
[4] 102 PHE (-18.2, 106.1)
[4] 144 PRO (-69.5, -124.3)

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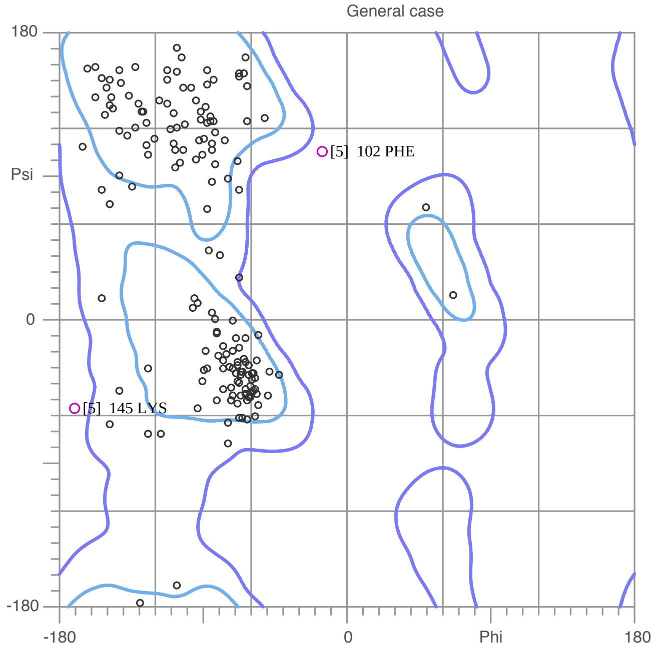
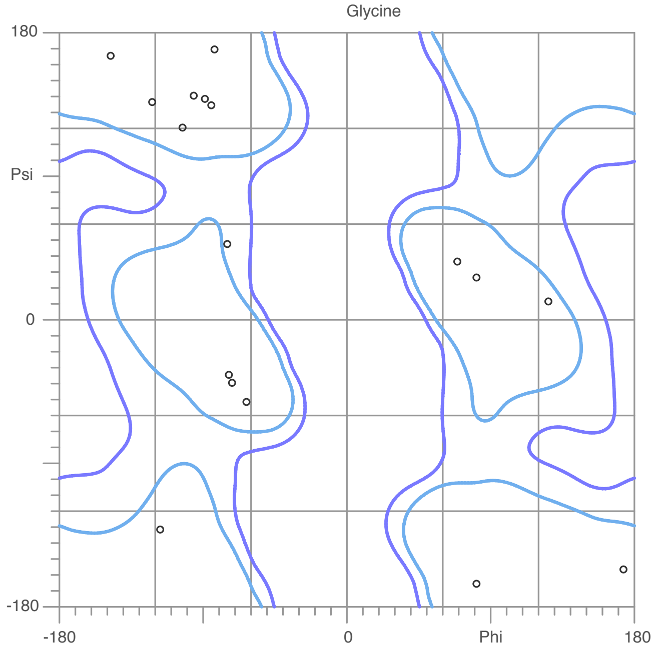
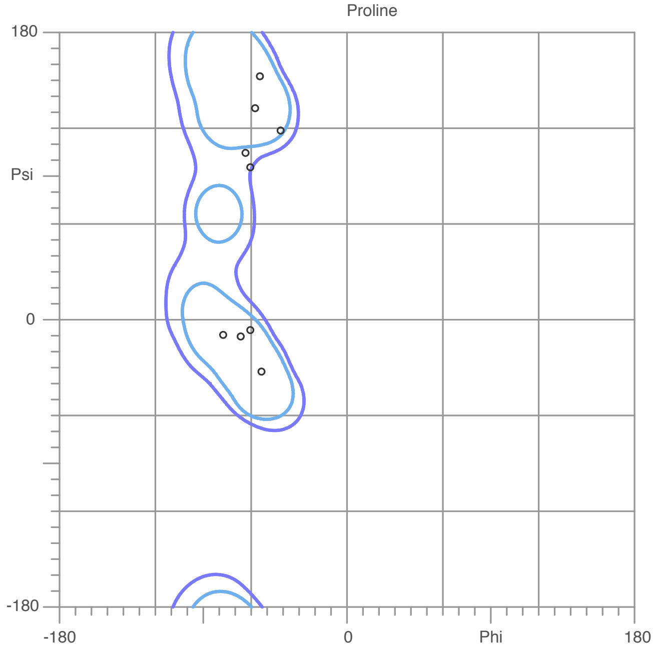
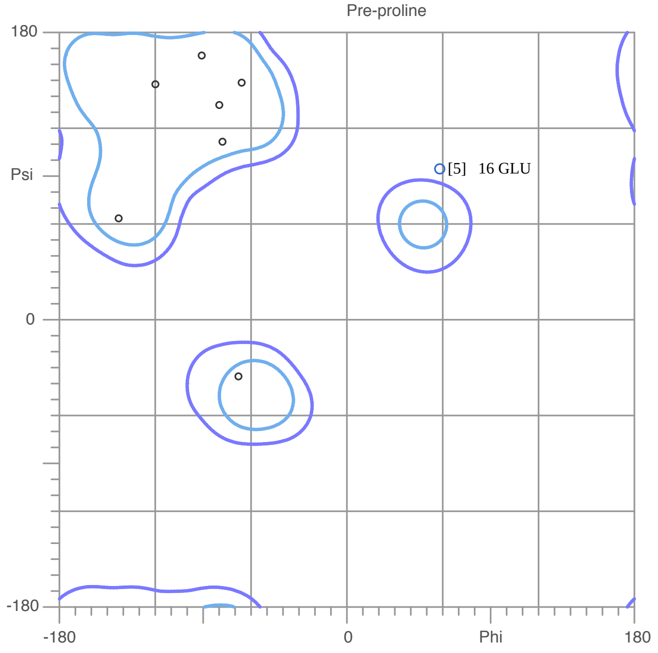
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 5







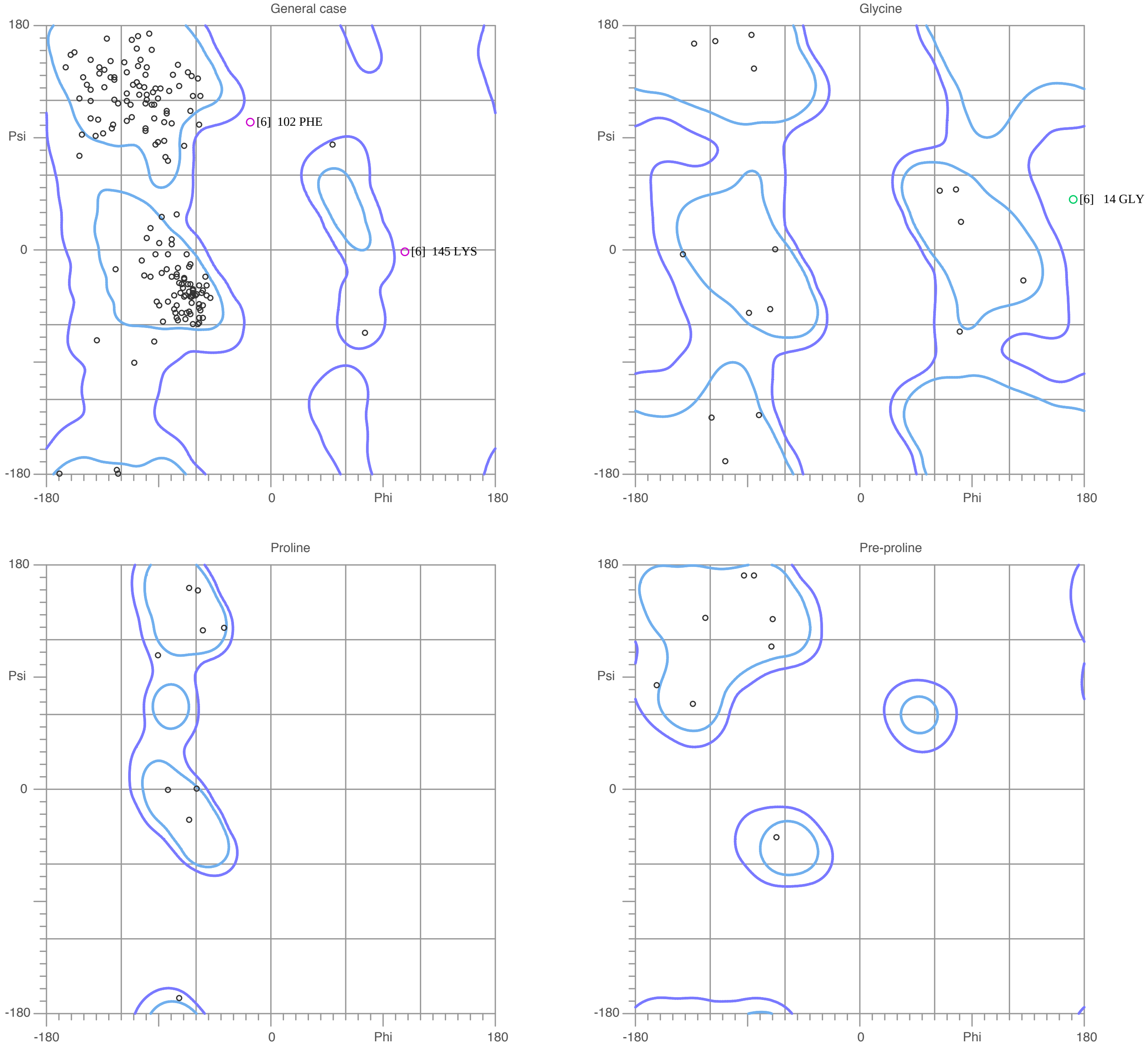


87.5% (175/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[5] 16 GLU (58.8, 95.5)
[5] 102 PHE (-16.1, 106.9)
[5] 145 LYS (-171.4, -55.2)

MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 6



90.5% (181/200) 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] 14 GLY (171.2, 41.7)
[6] 102 PHE (-17.7, 103.6)
[6] 145 LYS (108.0, -1.7)

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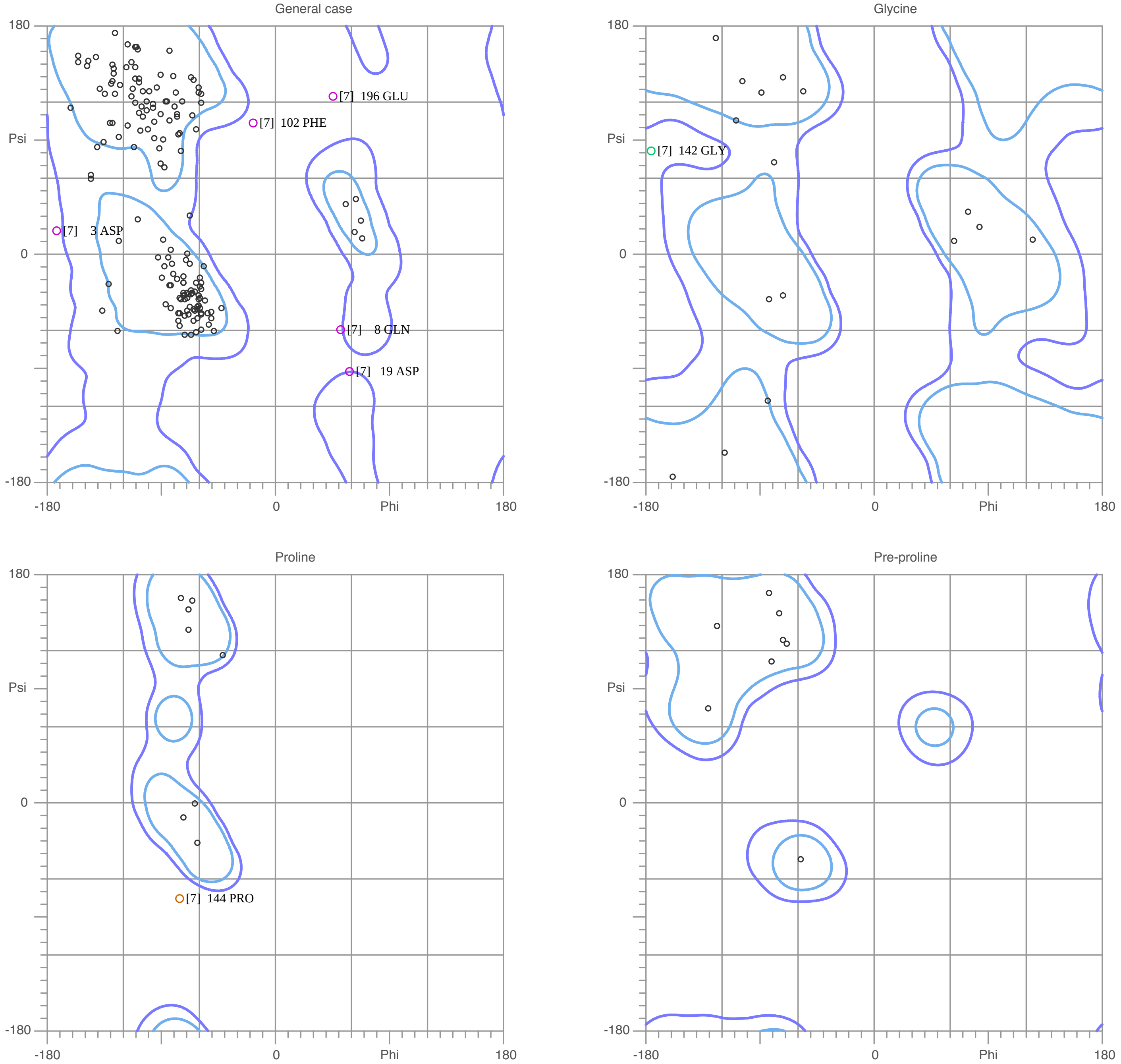
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 7



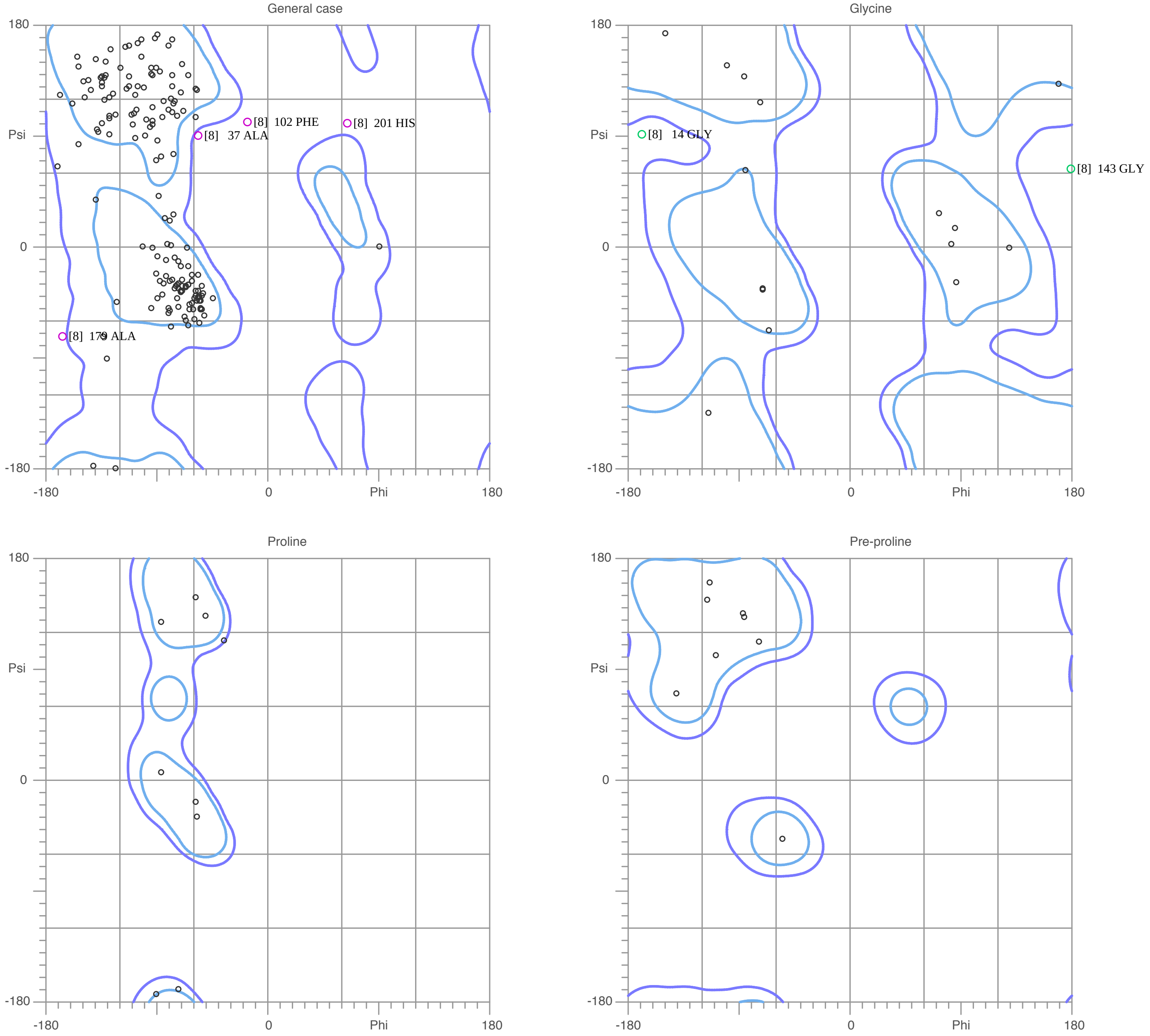
90.5% (181/200) of all residues were in favored (98%) regions.
96.5% (193/200) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):

[7]	3 ASP (-173.3, 19.1)
[7]	8 GLN (51.0, -59.2)
[7]	19 ASP (58.6, -92.8)
[7]	102 PHE (-18.5, 104.4)
[7]	142 GLY (-176.9, 82.4)
[7]	144 PRO (-76.4, -76.0)
[7]	196 GLU (45.6, 125.3)

MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 8



88.5% (177/200) of all residues were in favored (98%) regions.
97.0% (194/200) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[8] 14 GLY (-169.0, 92.9)
[8] 37 ALA (-57.6, 91.9)
[8] 102 PHE (-17.7, 102.5)
[8] 143 GLY (179.6, 64.3)
[8] 179 ALA (-167.2, -72.9)
[8] 201 HIS (64.9, 101.3)

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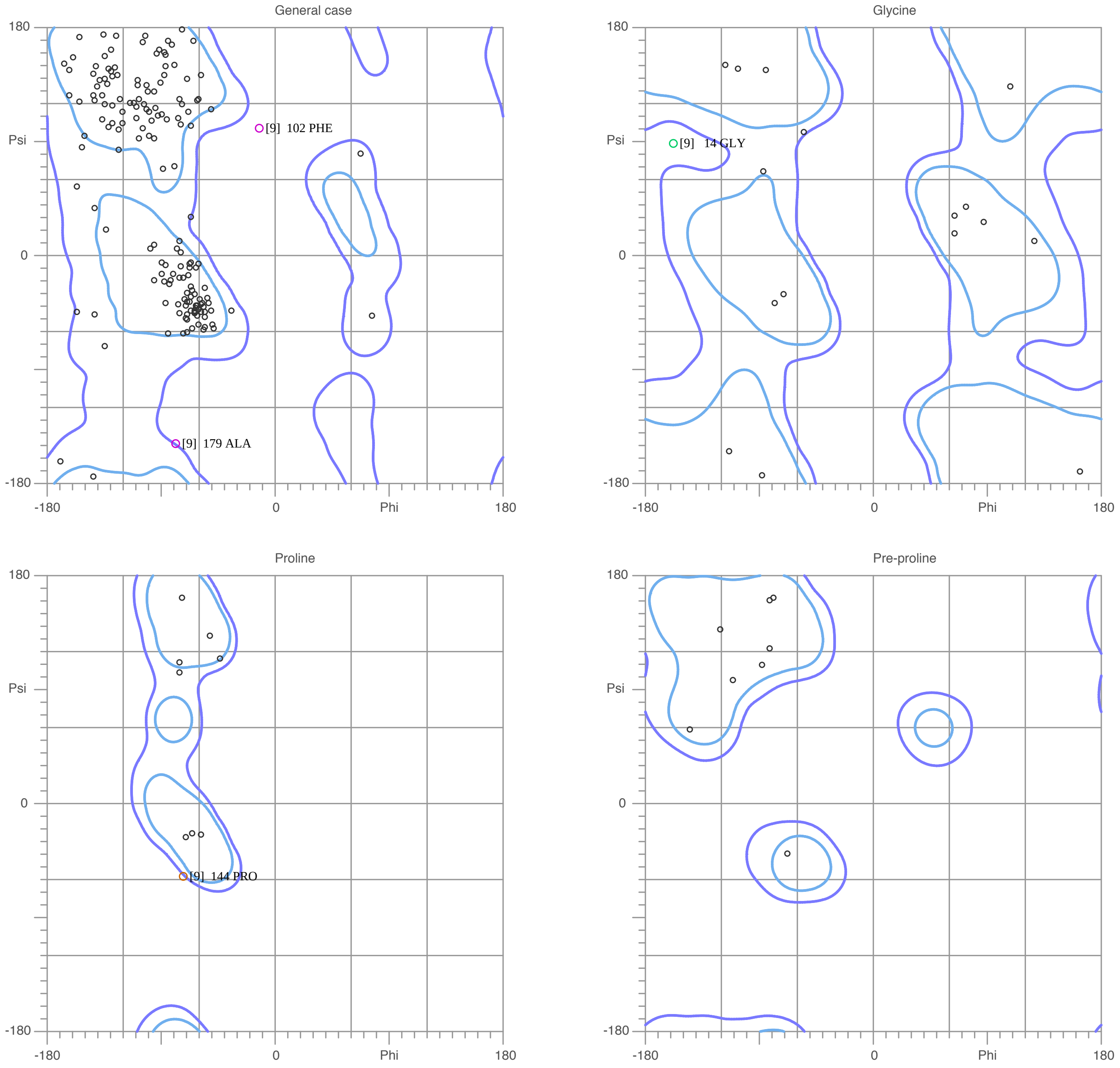
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 9

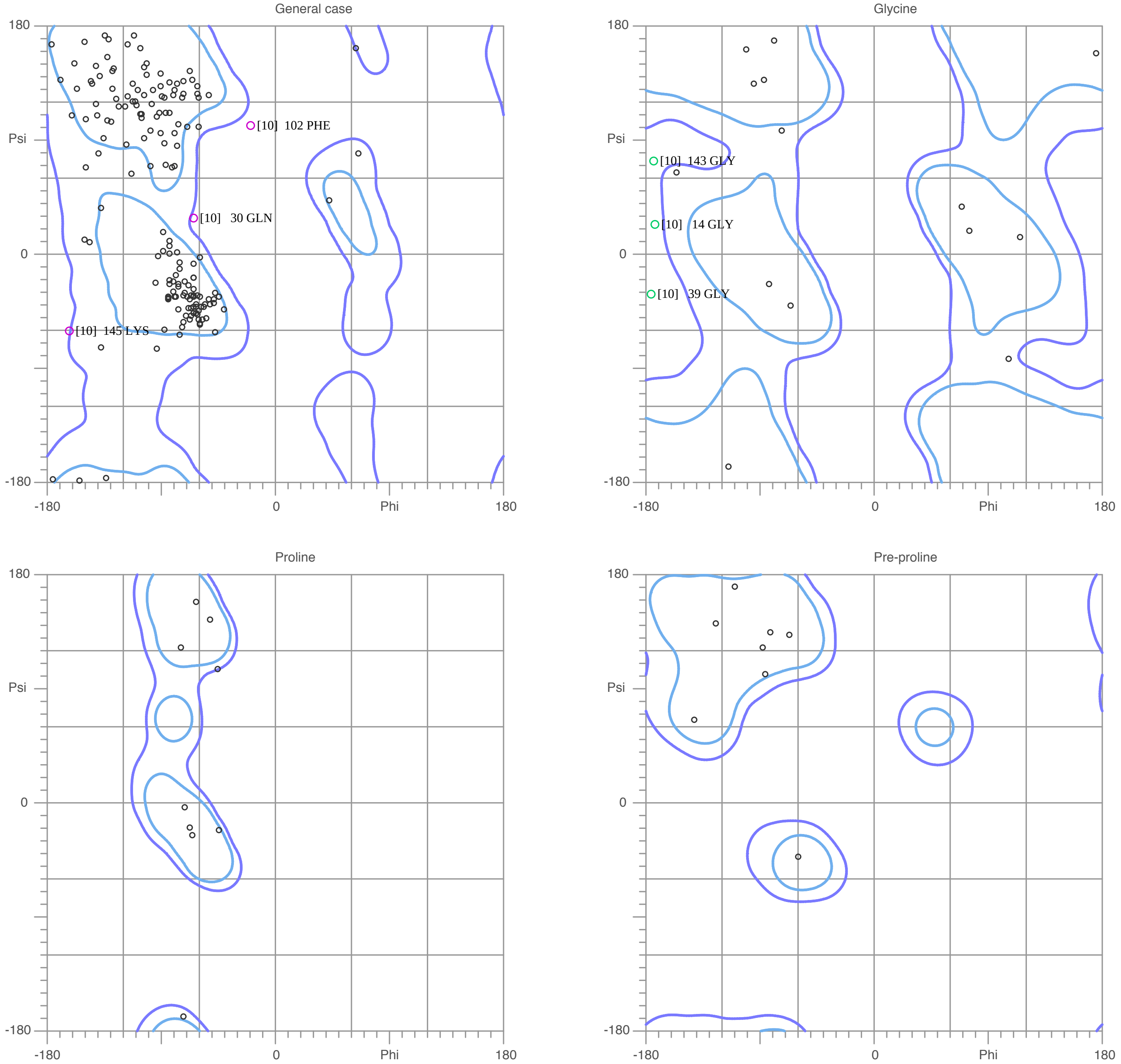


90.5% (181/200) of all residues were in favored (98%) regions.
98.0% (196/200) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[9] 14 GLY (-158.8, 89.1)
[9] 102 PHE (-14.0, 101.8)
[9] 144 PRO (-74.0, -57.5)
[9] 179 ALA (-79.4, -148.4)

MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 10



87.5% (175/200) of all residues were in favored (98%) regions.
97.0% (194/200) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[10] 14 GLY (-173.0, 24.2)
[10] 30 GLN (-65.5, 29.8)
[10] 39 GLY (-176.4, -31.9)
[10] 102 PHE (-20.9, 102.8)
[10] 143 GLY (-174.3, 74.8)
[10] 145 LYS (-163.1, -60.3)

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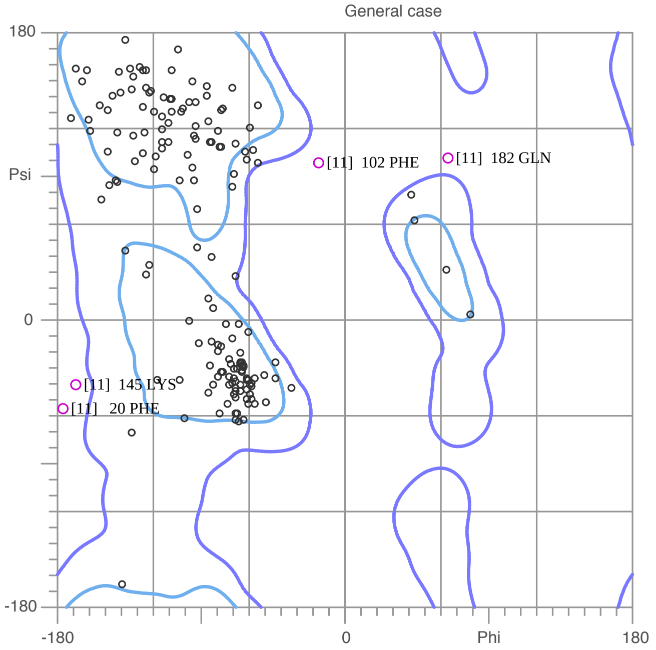
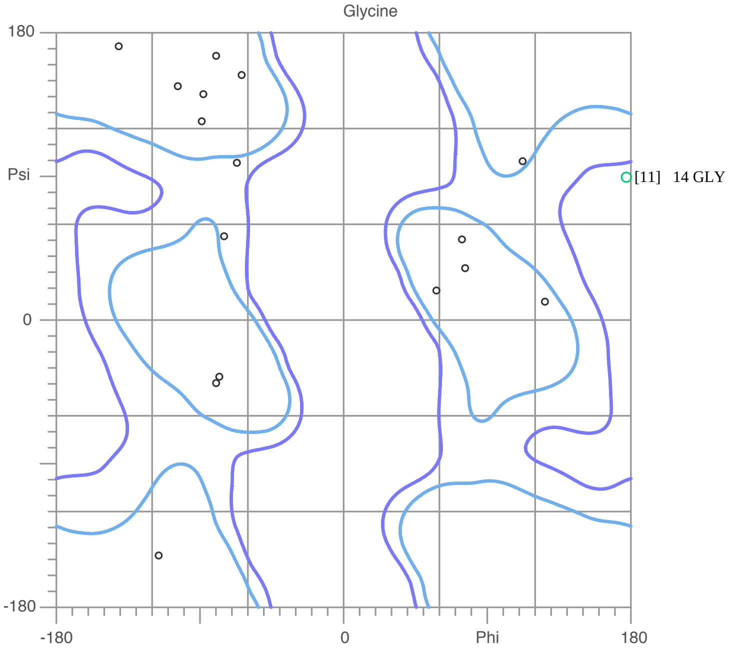
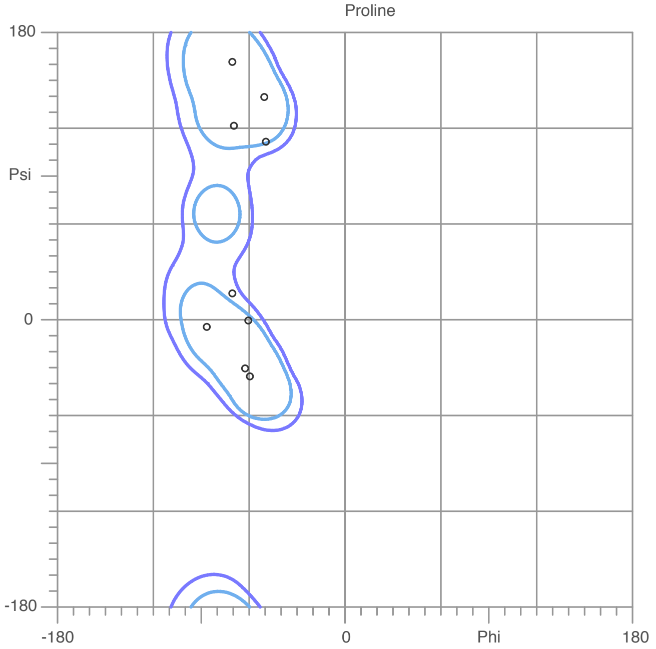
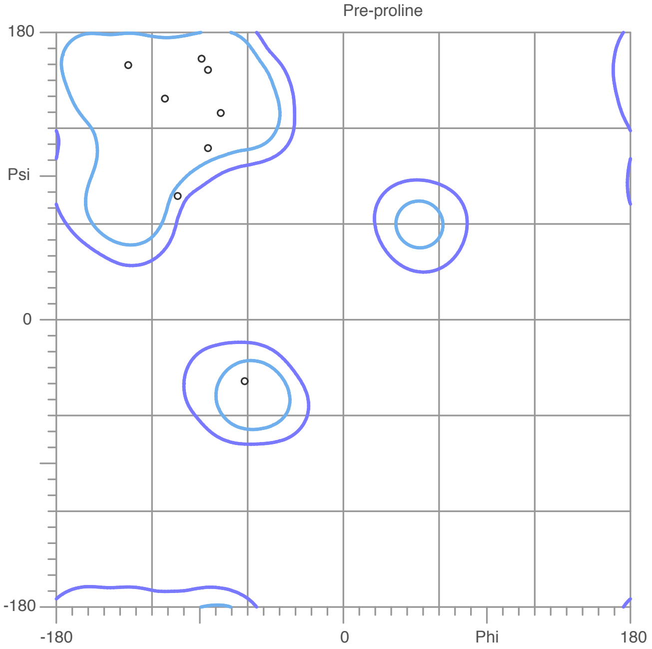
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 11


General case


Glycine


Proline


Pre-proline

84.5% (169/200) 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):

[11] 14 GLY (177.6, 90.7)
[11] 20 PHE (-177.4, -55.2)
[11] 102 PHE (-17.5, 99.4)
[11] 145 LYS (-169.9, -40.9)
[11] 182 GLN (64.1, 102.8)

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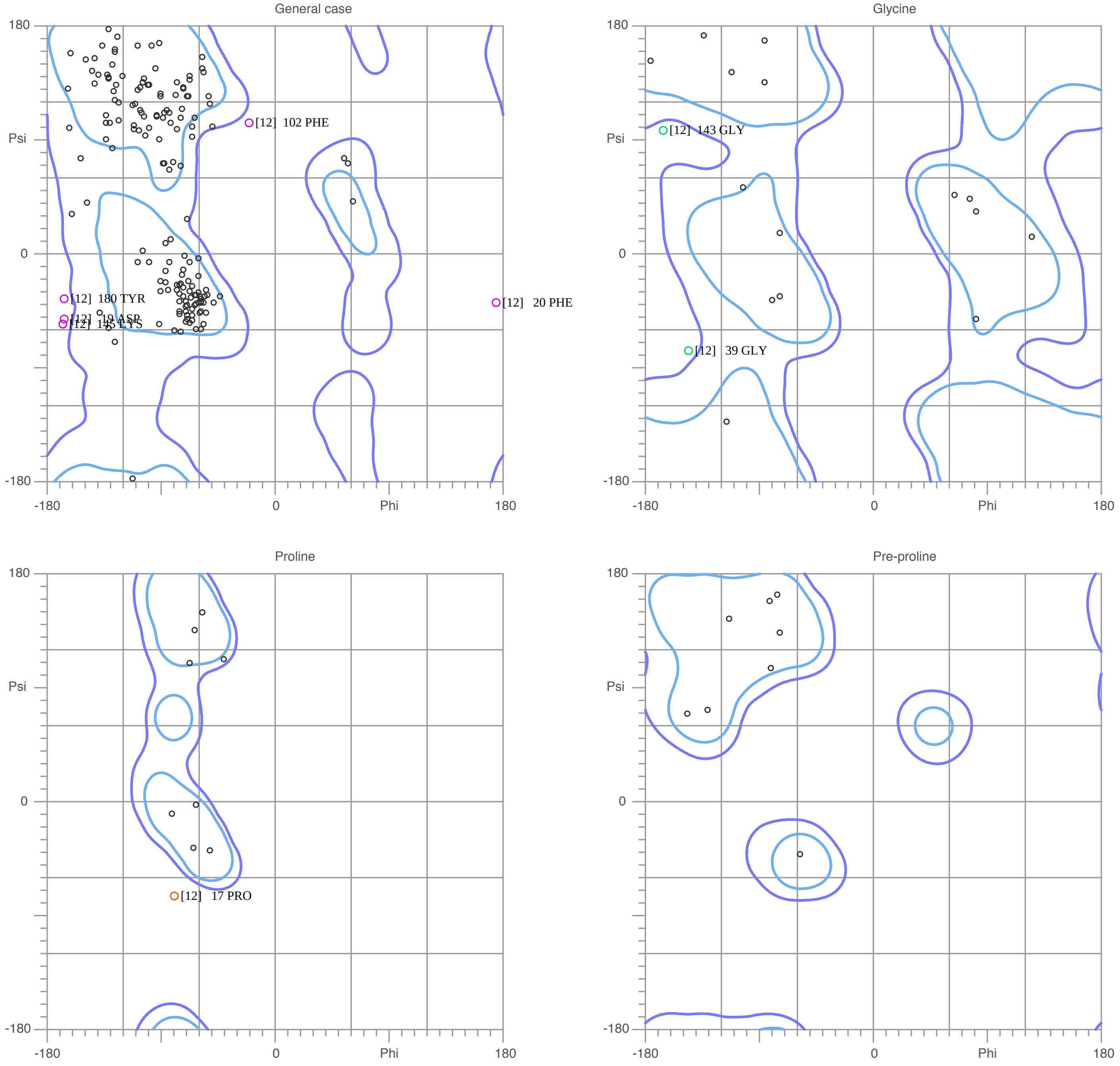
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 12



88.0% (176/200) of all residues were in favored (98%) regions.
96.0% (192/200) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):
[12] 17 PRO (-80.4, -74.4)
[12] 19 ASP (-167.8, -51.9)
[12] 20 PHE (174.2, -38.3)
[12] 39 GLY (-146.2, -76.3)
[12] 102 PHE (-21.6, 104.9)
[12] 143 GLY (-166.7, 98.8)
[12] 145 LYS (-168.1, -55.0)
[12] 180 TYR (-167.1, -35.7)

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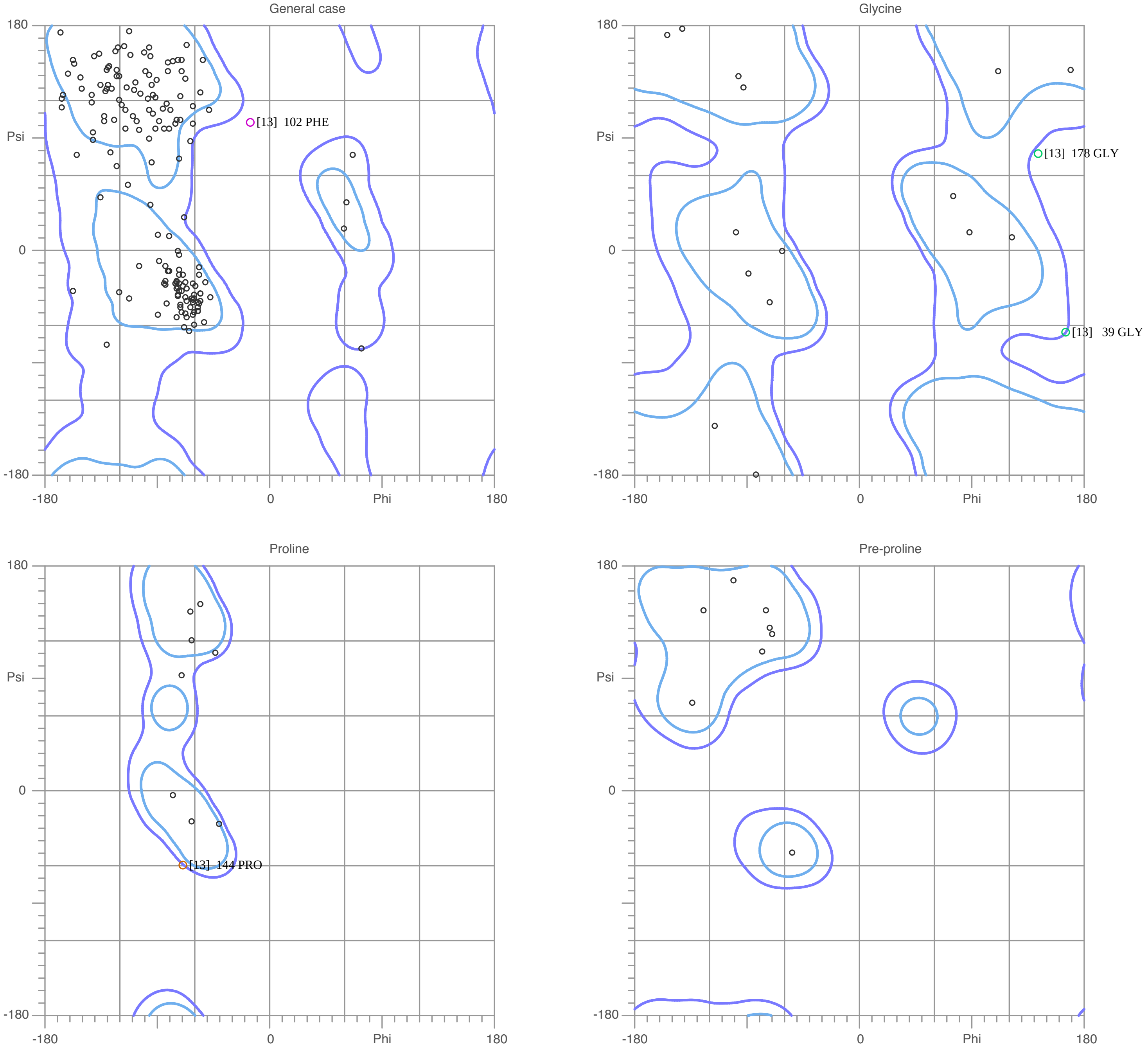
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 13



88.5% (177/200) 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):
[13] 39 GLY (165.5, -65.7)
[13] 102 PHE (-16.0, 103.9)
[13] 144 PRO (-70.2, -59.7)
[13] 178 GLY (143.2, 78.5)

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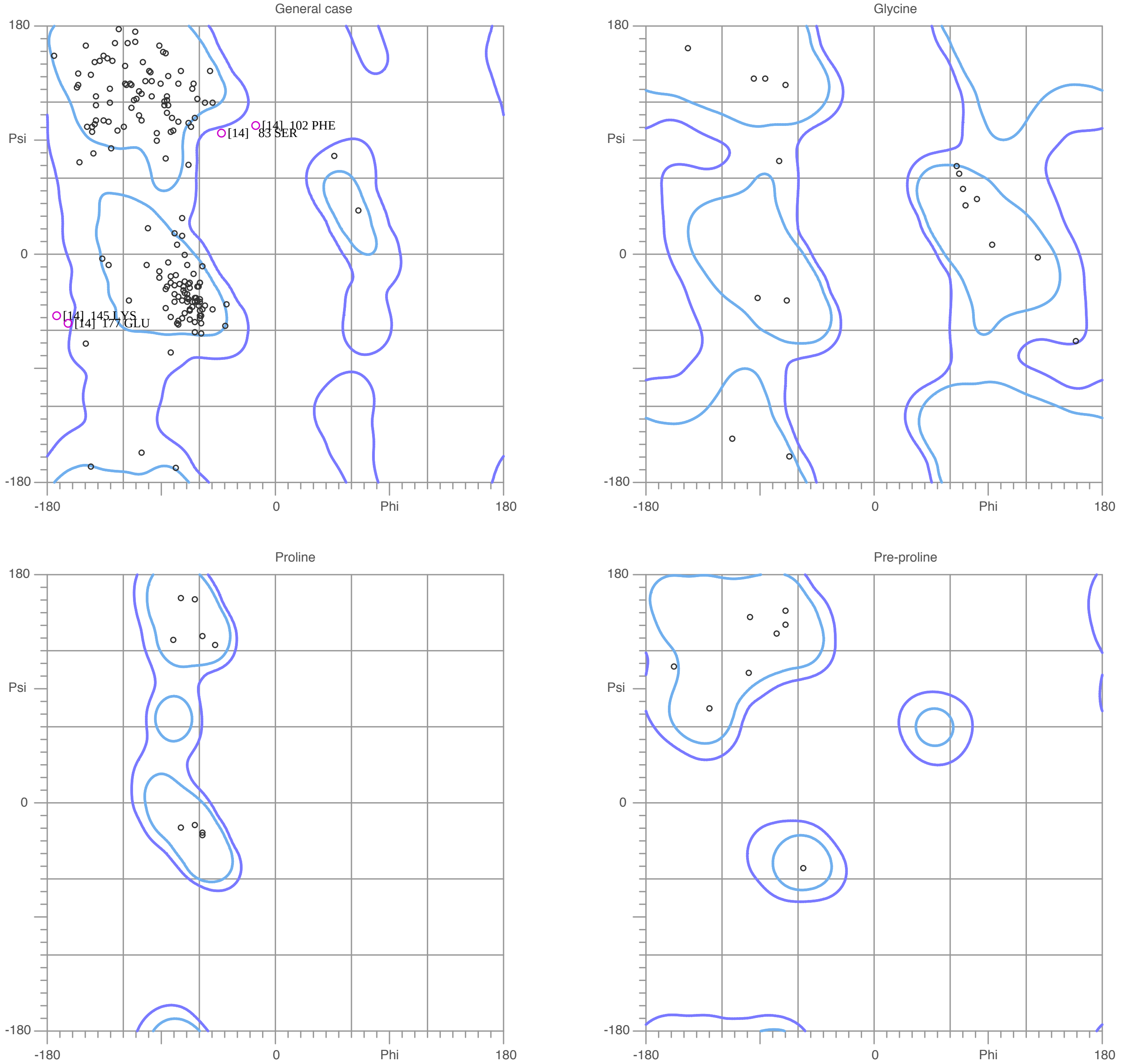
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 14



89.0% (178/200) 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):
[14] 83 SER (-43.6, 96.0)
[14] 102 PHE (-16.2, 102.8)
[14] 145 LYS (-173.1, -48.4)
[14] 177 GLU (-164.2, -55.0)

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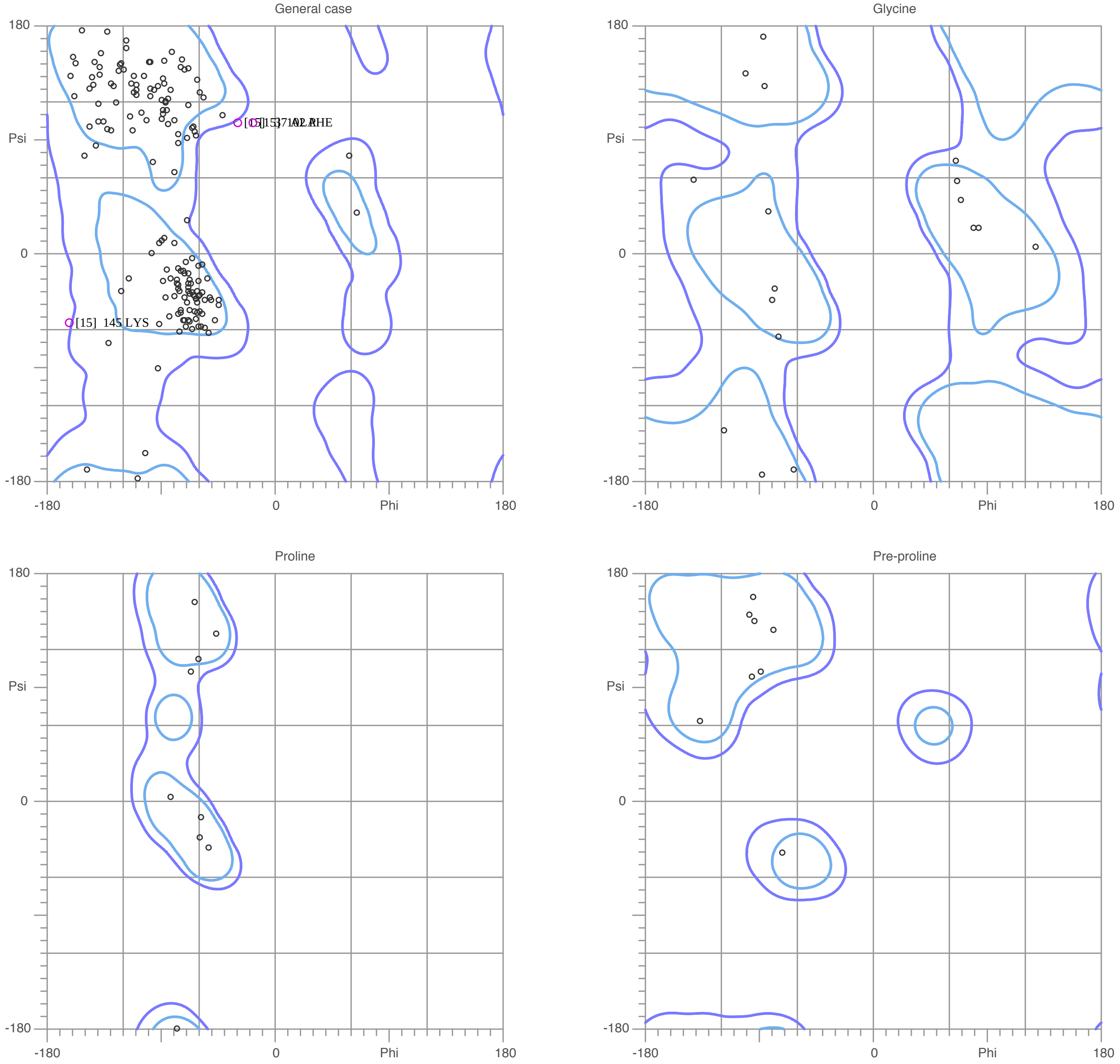
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 15



90.5% (181/200) 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):
[15] 37 ALA (-30.8, 104.5)
[15] 102 PHE (-18.4, 104.9)
[15] 145 LYS (-163.5, -54.5)

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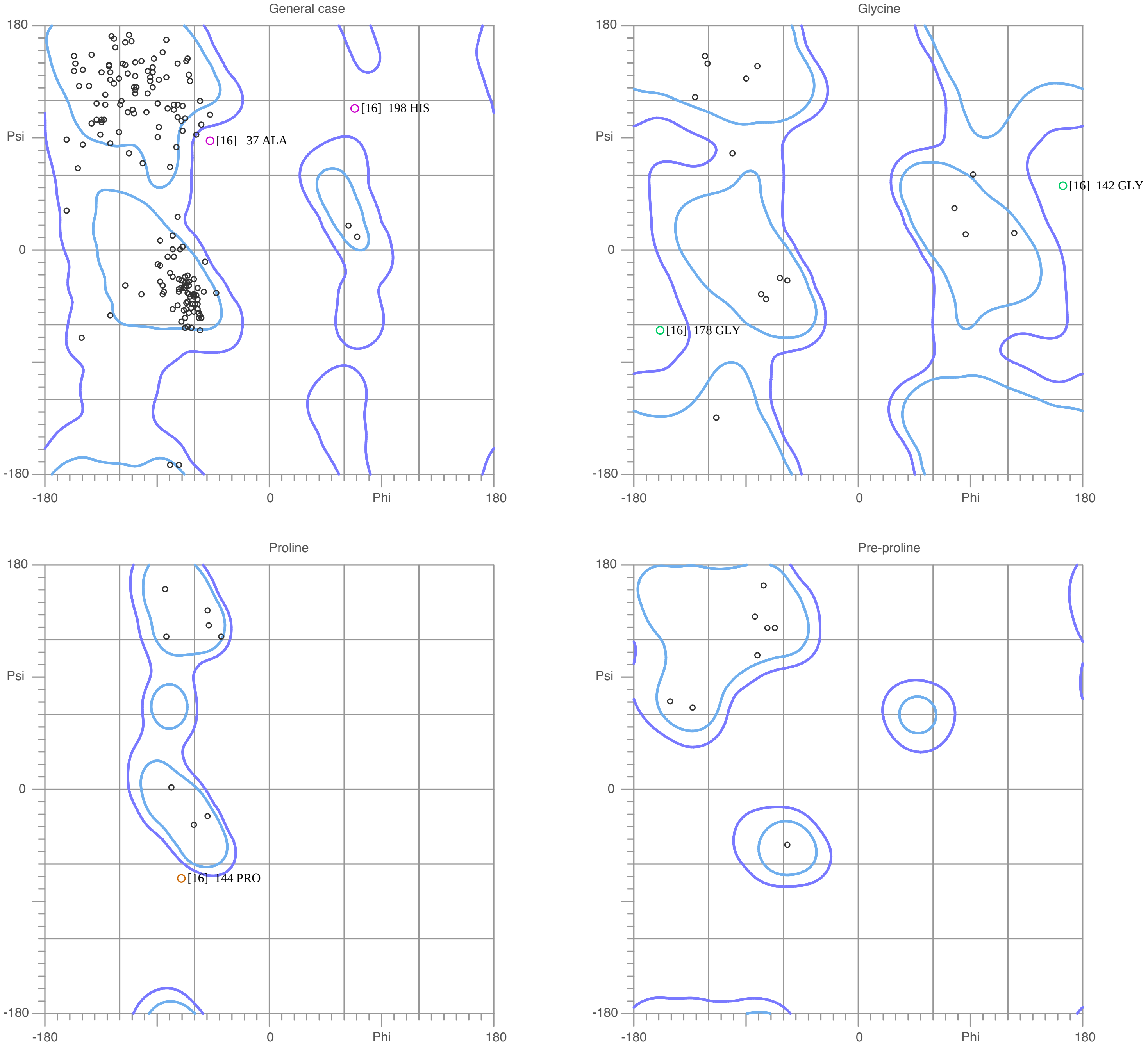
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 16



88.5% (177/200) 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] 37 ALA (-48.8, 88.7)
[16] 142 GLY (164.9, 52.7)
[16] 144 PRO (-71.8, -71.1)
[16] 178 GLY (-159.5, -64.4)
[16] 198 HIS (68.4, 114.7)

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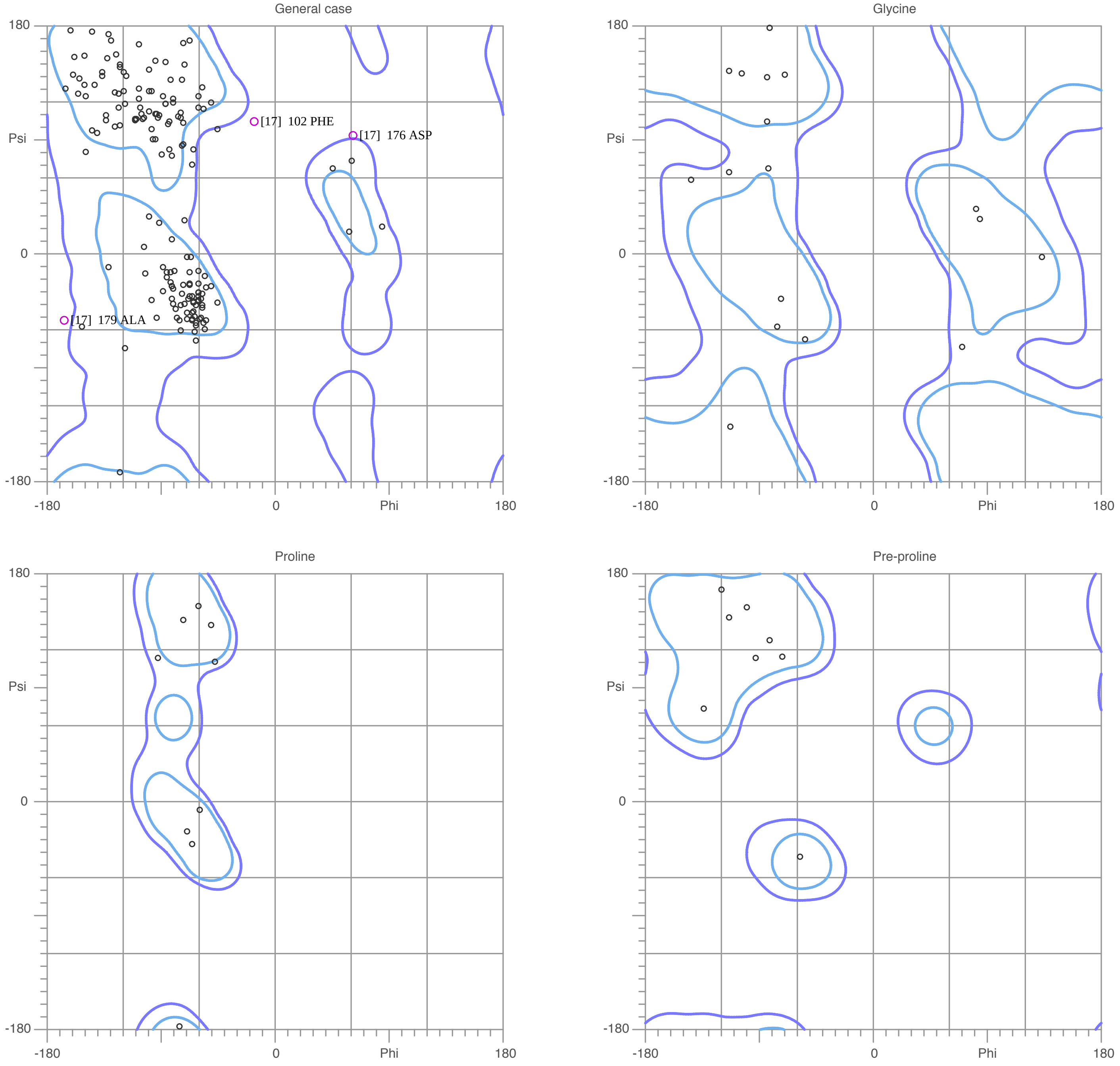
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 17

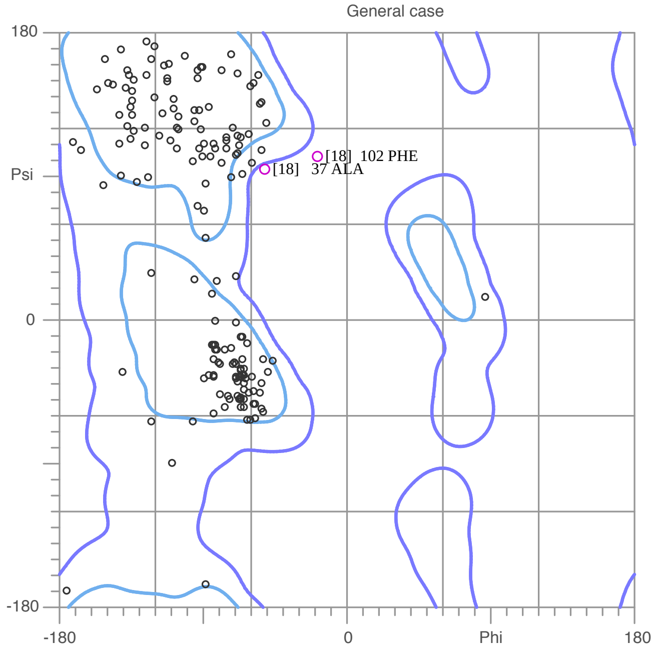


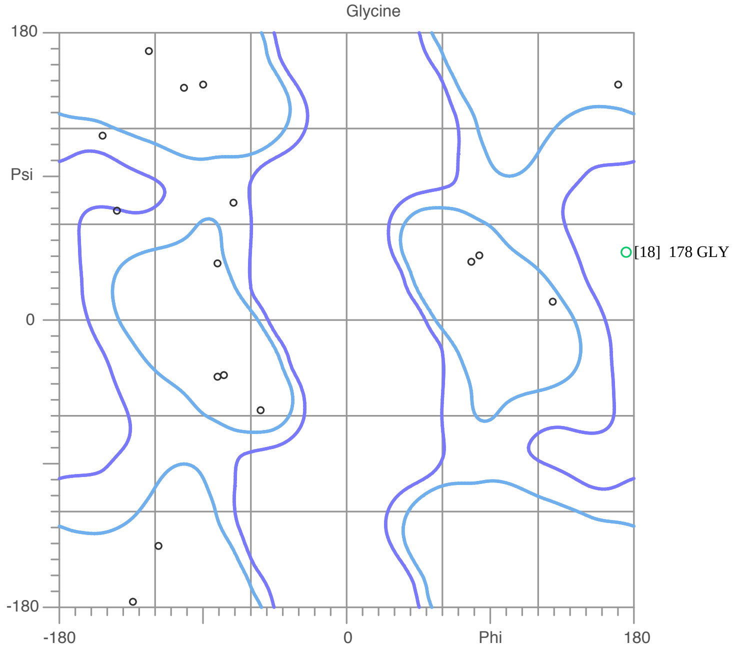
90.0% (180/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

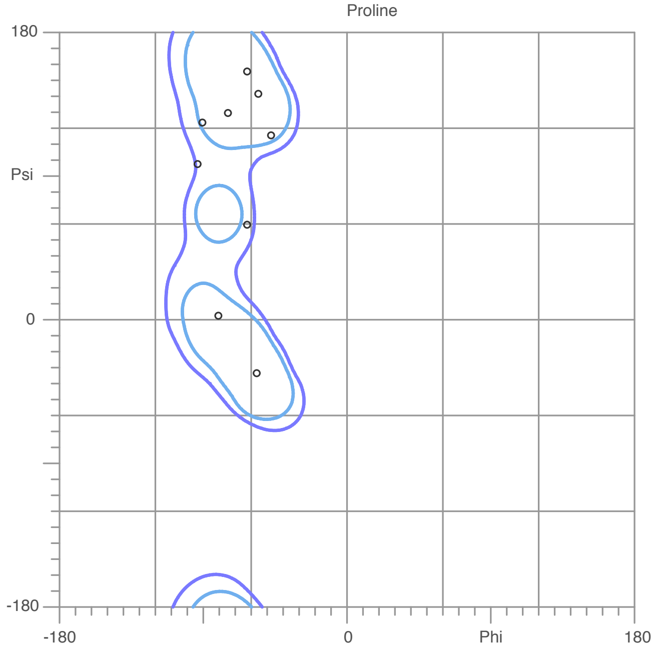
There were 3 outliers (phi, psi):
[17] 102 PHE (-17.9, 105.1)
[17] 176 ASP (61.3, 94.6)
[17] 179 ALA (-167.5, -52.5)

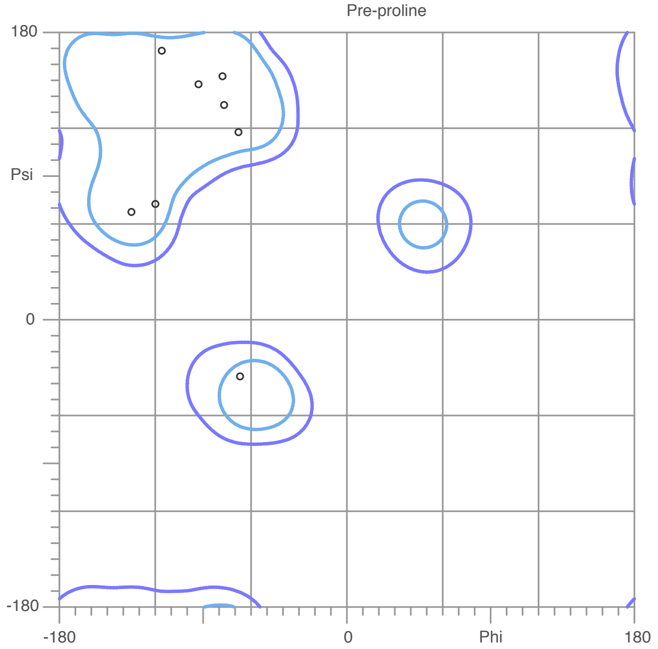
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 18







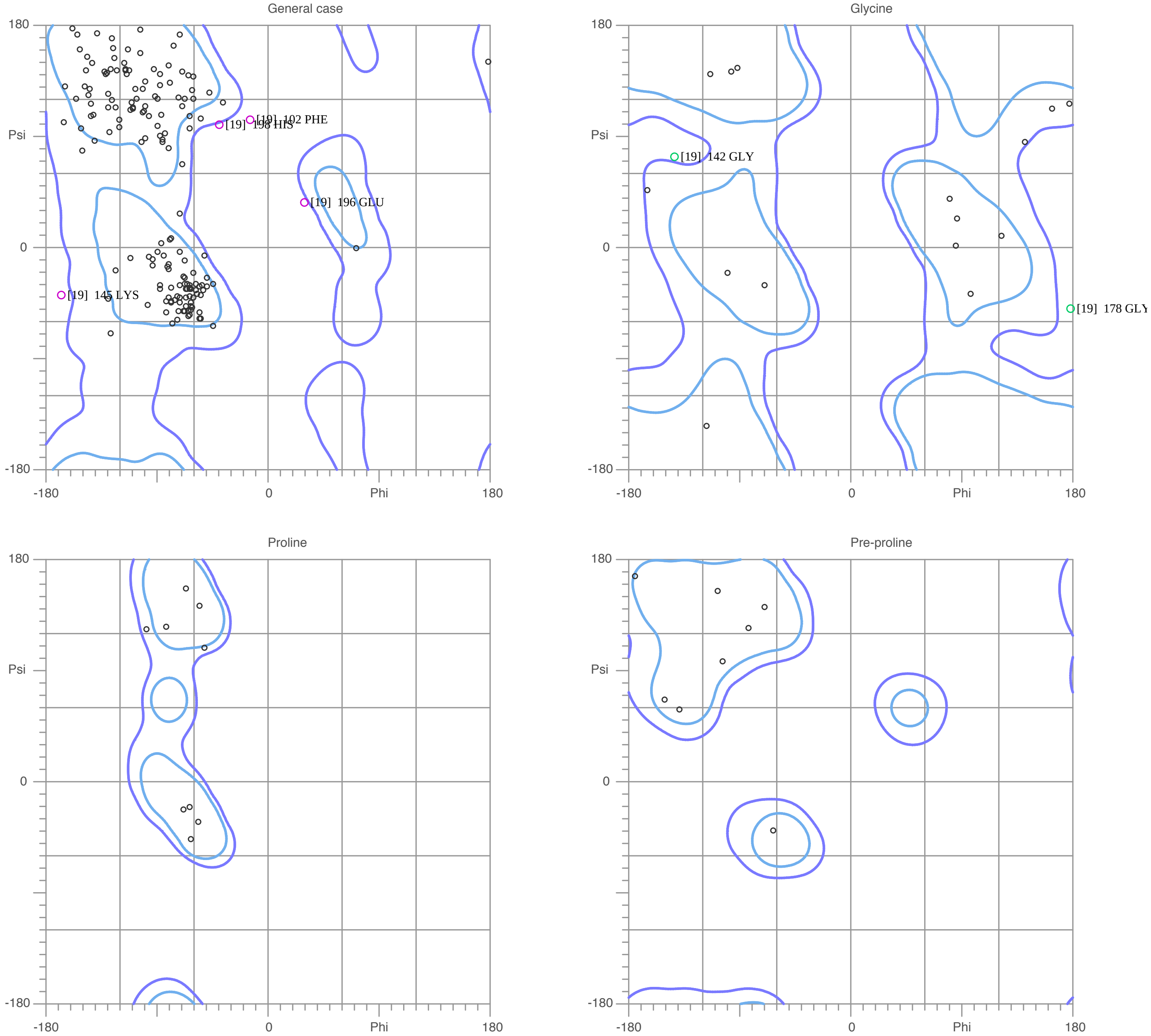


88.5% (177/200) of all residues were in favored (98%) regions.
98.5% (197/200) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[18] 37 ALA (-52.5, 95.5)
[18] 102 PHE (-19.3, 103.4)
[18] 178 GLY (175.2, 43.2)

MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 19



86.0% (172/200) of all residues were in favored (98%) regions.
97.0% (194/200) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[19] 102 PHE (-15.3, 104.7)
[19] 142 GLY (-143.9, 74.5)
[19] 145 LYS (-168.2, -38.8)
[19] 178 GLY (178.6, -49.8)
[19] 196 GLU (29.3, 37.7)
[19] 198 HIS (-40.0, 100.0)

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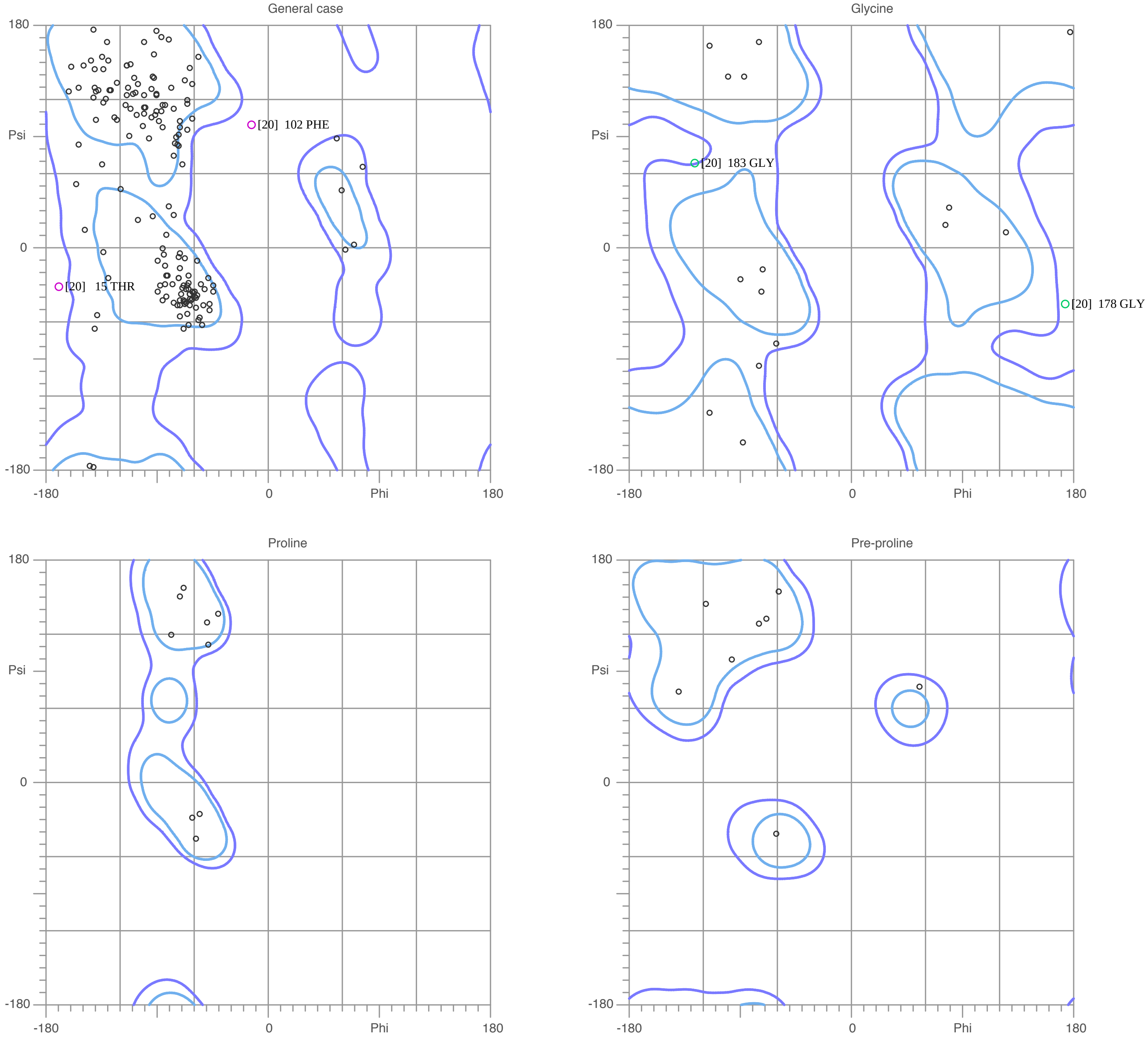
MolProbity Ramachandran analysis

SGR145_NMR_em_bcr3.pdb, model 20



88.0% (176/200) 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):
[20] 15 THR (-170.0, -31.9)
[20] 102 PHE (-14.0, 100.5)
[20] 178 GLY (173.7, -45.4)
[20] 183 GLY (-127.4, 69.3)

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