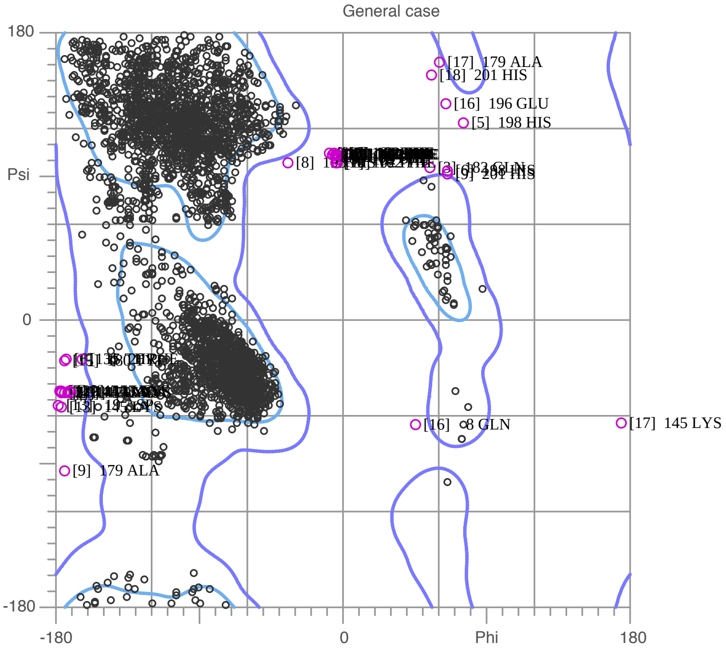
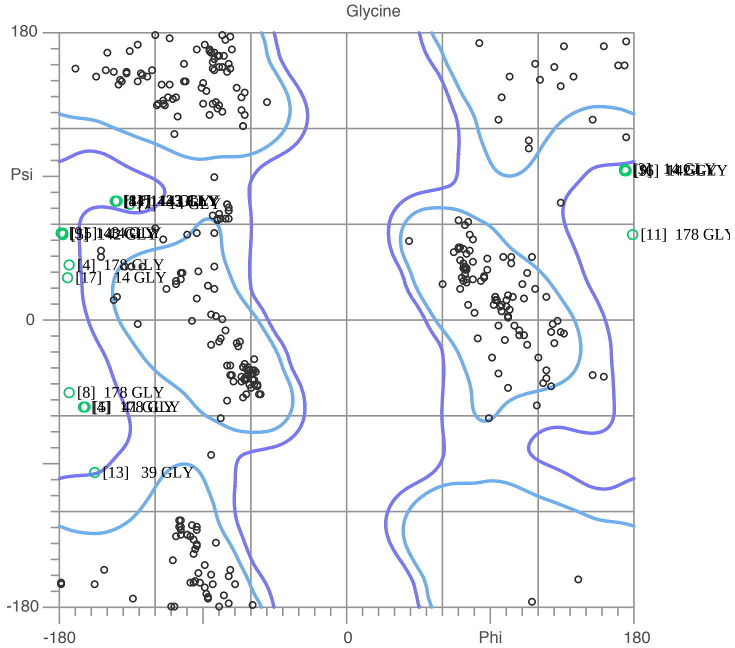
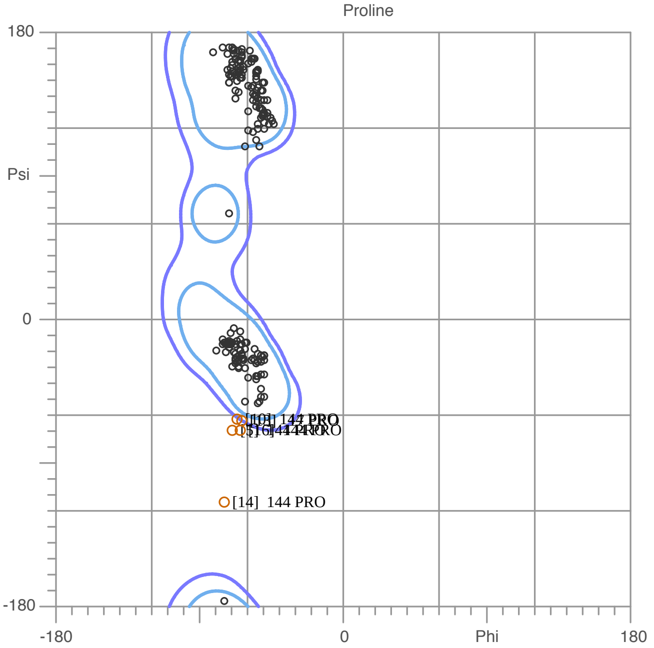
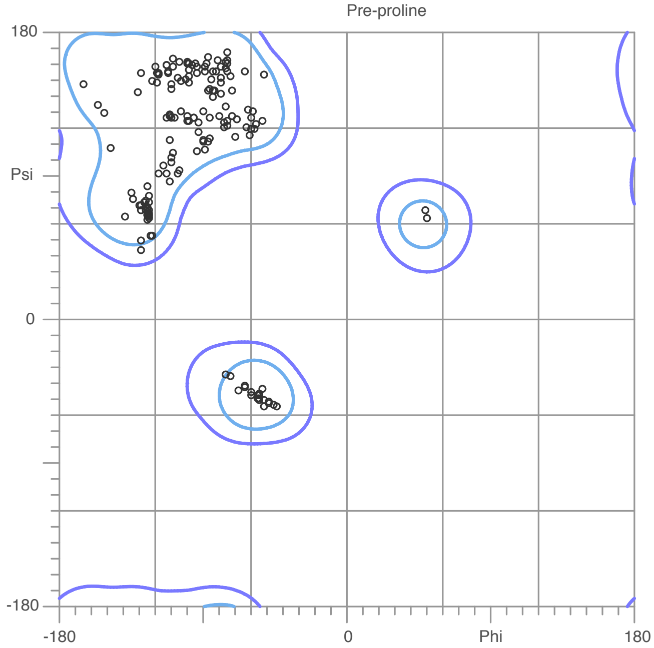
MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, all models


General case


Glycine


Proline


Pre-proline

92.6% (3702/4000) of all residues were in favored (98%) regions.
98.4% (3936/4000) of all residues were in allowed (>99.8%) regions.

There were 64 outliers (phi, psi):
[1] 102 PHE (-4.9, 99.3)
[2] 102 PHE (-2.1, 105.1)
[2] 145 LYS (-177.6, -45.1)
[3] 14 GLY (175.0, 95.1)
[3] 145 LYS (-178.9, -44.9)
[3] 182 GLN (55.0, 97.0)
[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)
[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)
[6] 15 THR (-175.0, -25.0)
[6] 102 PHE (-4.9, 103.8)
[6] 198 HIS (65.0, 94.9)
[7] 14 GLY (-136.9, 73.9)
[7] 102 PHE (-7.2, 104.9)
[7] 145 LYS (-177.7, -45.1)
[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)
[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)
[10] 102 PHE (-5.2, 99.5)
[10] 144 PRO (-67.6, -62.5)
[11] 143 GLY (-145.0, 75.1)
[11] 178 GLY (179.9, 55.0)
[12] 102 PHE (-9.4, 105.9)
[12] 145 LYS (-177.2, -45.0)
[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)
[14] 102 PHE (-4.9, 104.9)
[14] 143 GLY (-145.0, 75.1)
[14] 144 PRO (-75.1, -114.9)
[15] 14 GLY (-178.1, 55.0)
[15] 102 PHE (-4.9, 104.0)
[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)
[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)
[18] 102 PHE (-4.9, 104.2)
[18] 145 LYS (-171.4, -45.2)
[18] 201 HIS (55.0, 154.9)
[19] 102 PHE (-7.3, 105.0)
[19] 179 ALA (-175.1, -45.1)
[20] 145 LYS (-172.1, -45.0)

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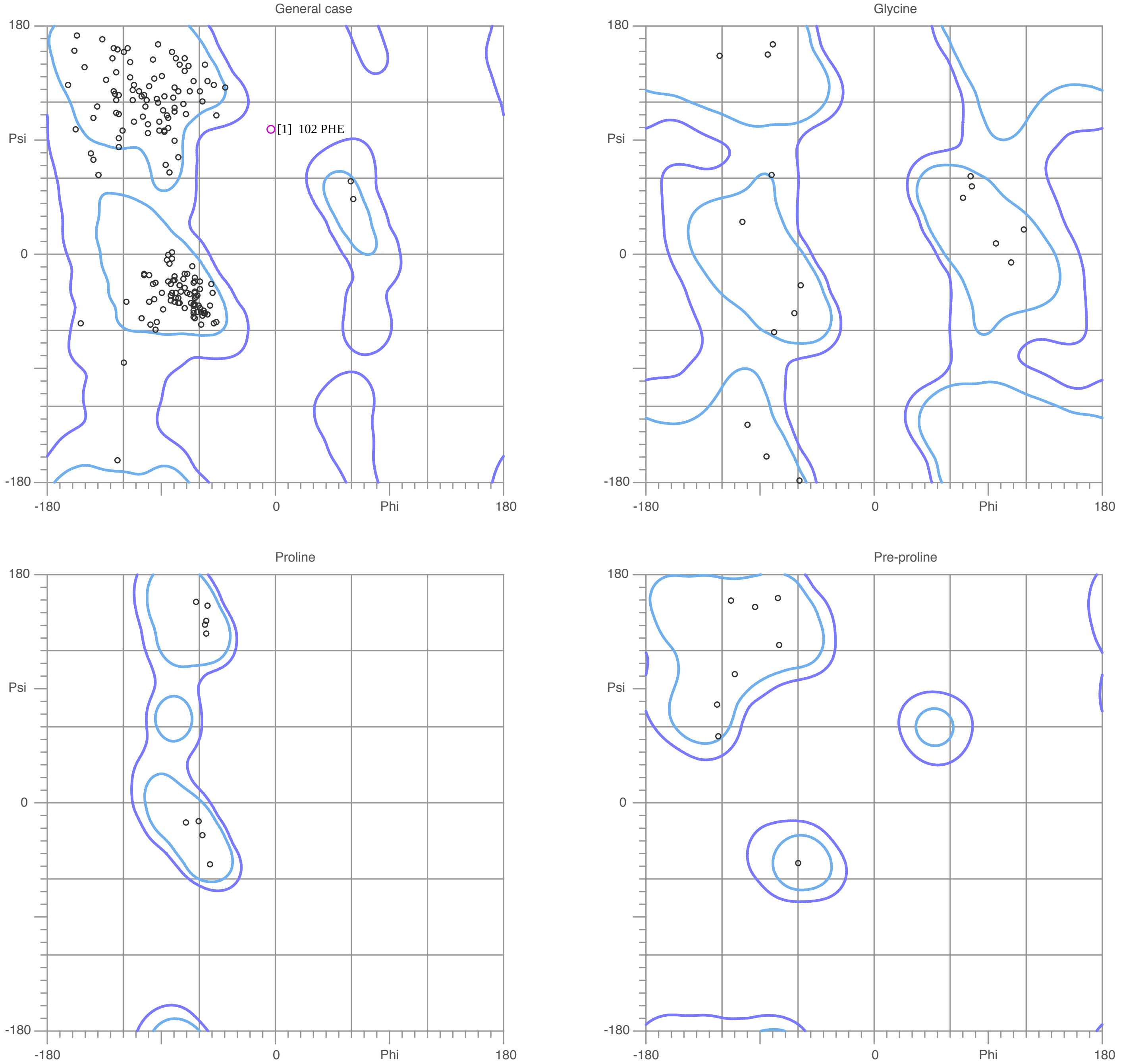
MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 1

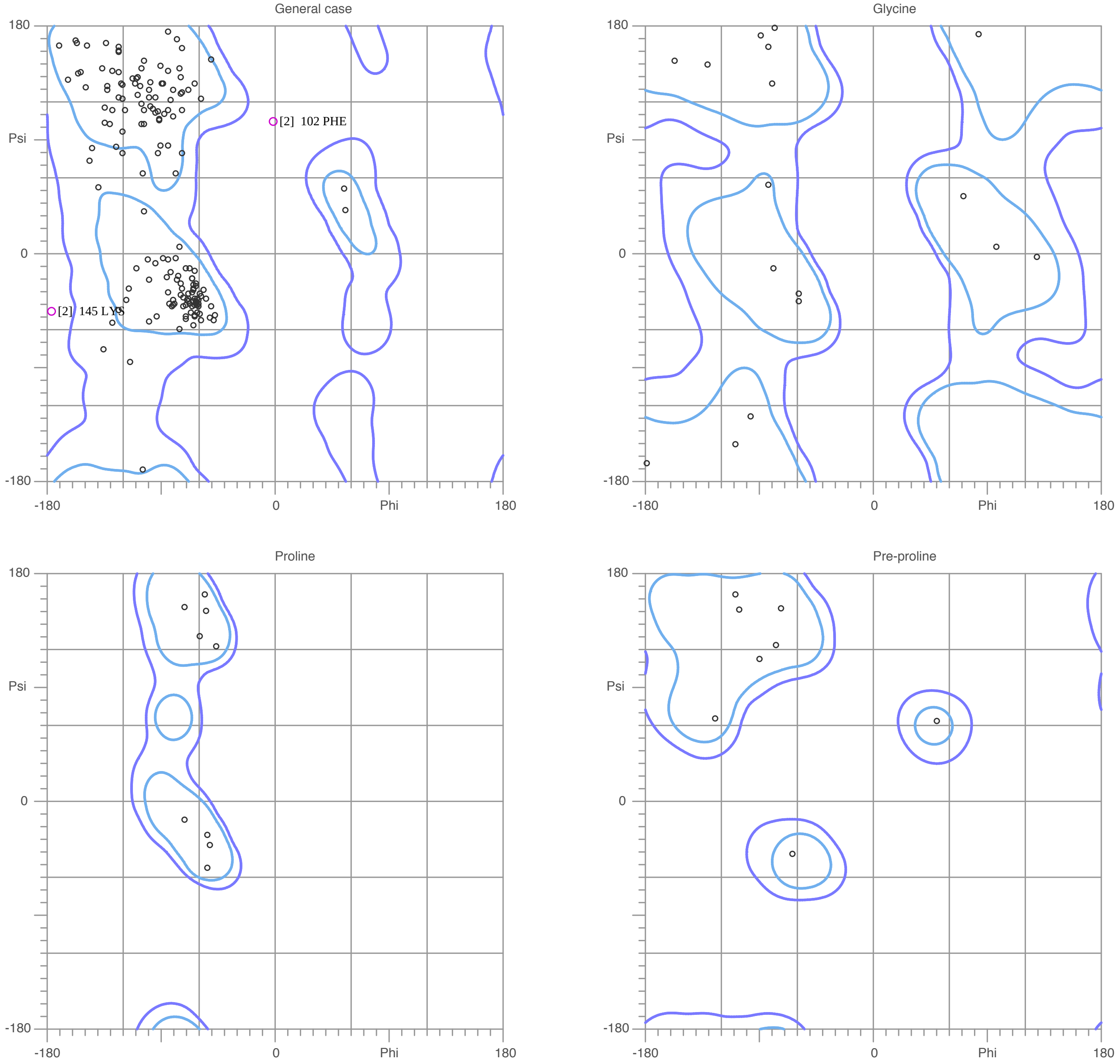


95.0% (190/200) of all residues were in favored (98%) regions.
99.5% (199/200) of all residues were in allowed (>99.8%) regions.

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

MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 2

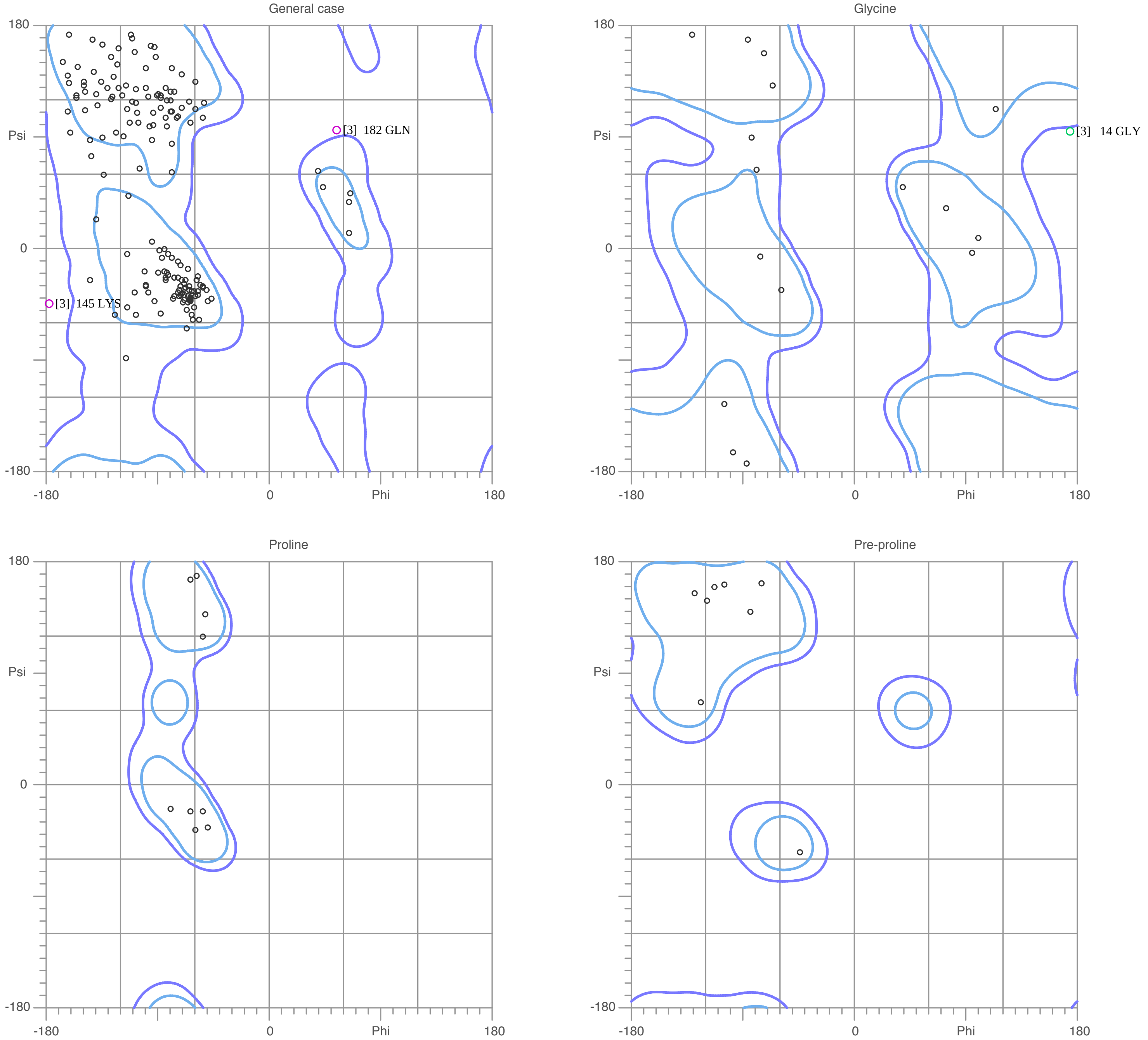


94.5% (189/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

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)

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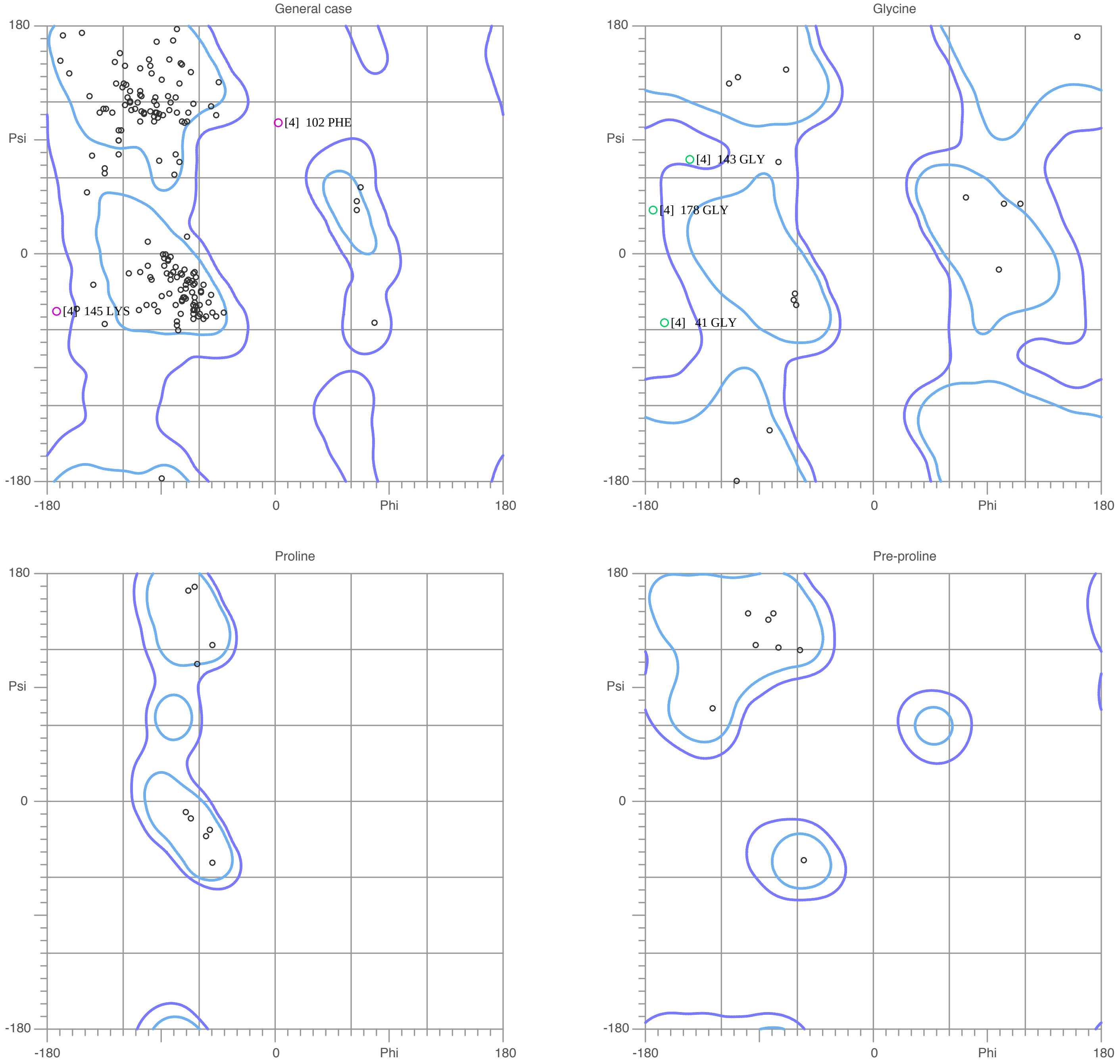
MolProbity Ramachandran analysis

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)

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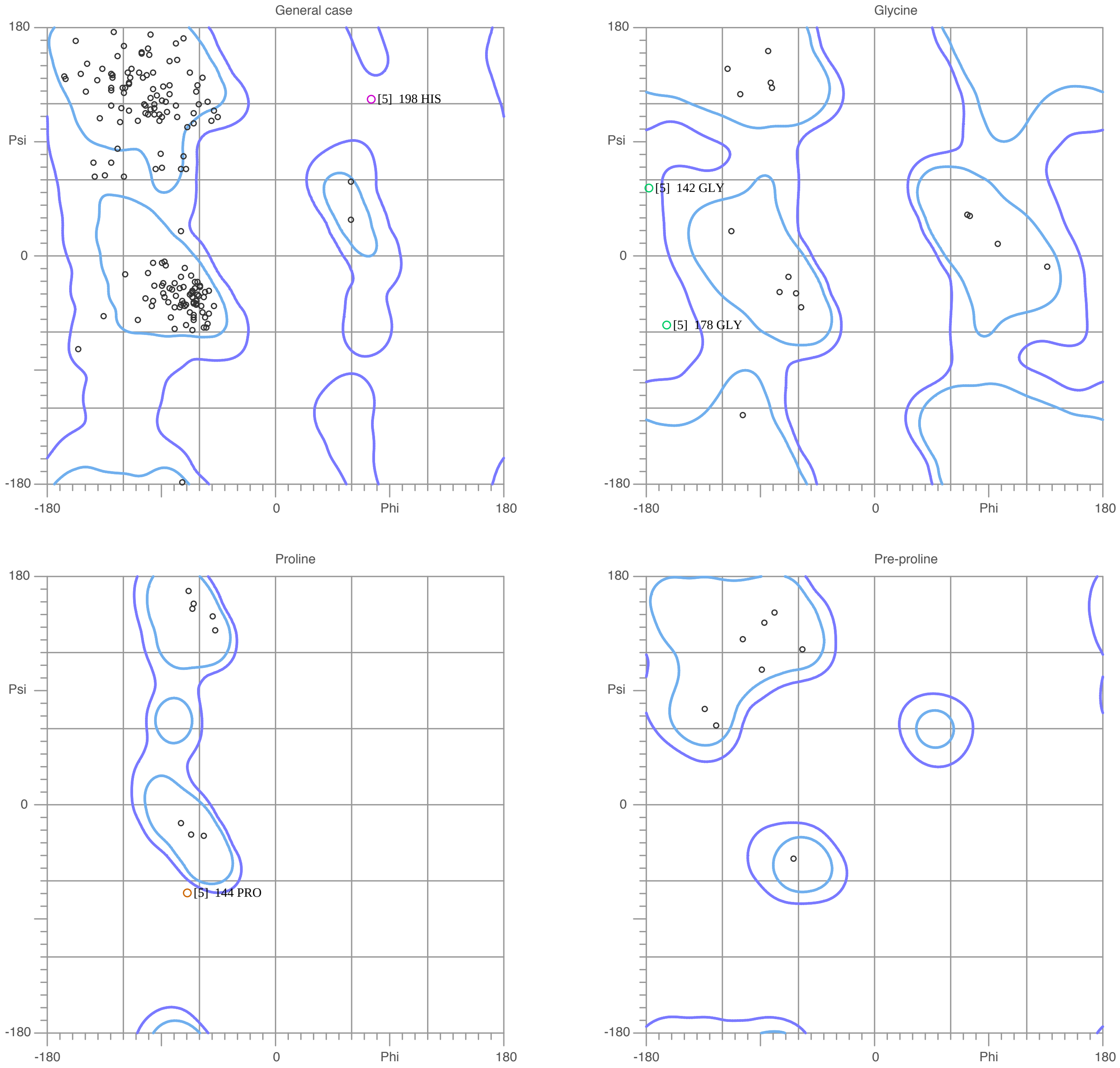
MolProbity Ramachandran analysis

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)

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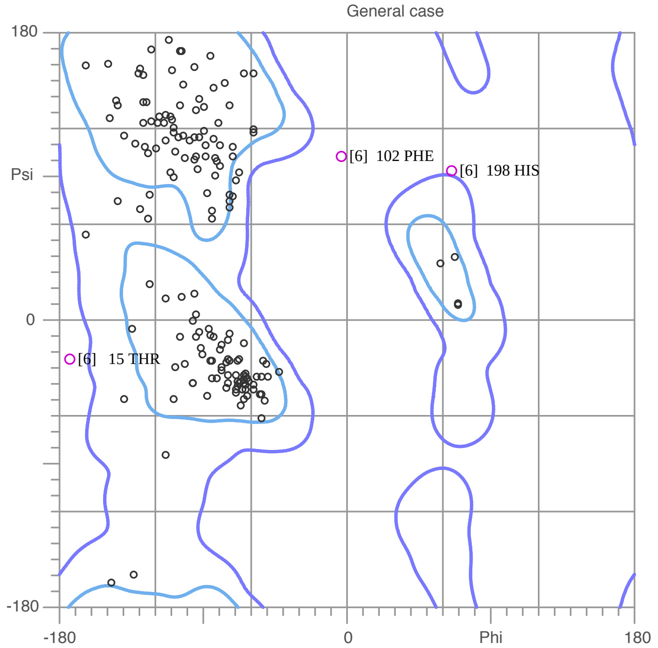
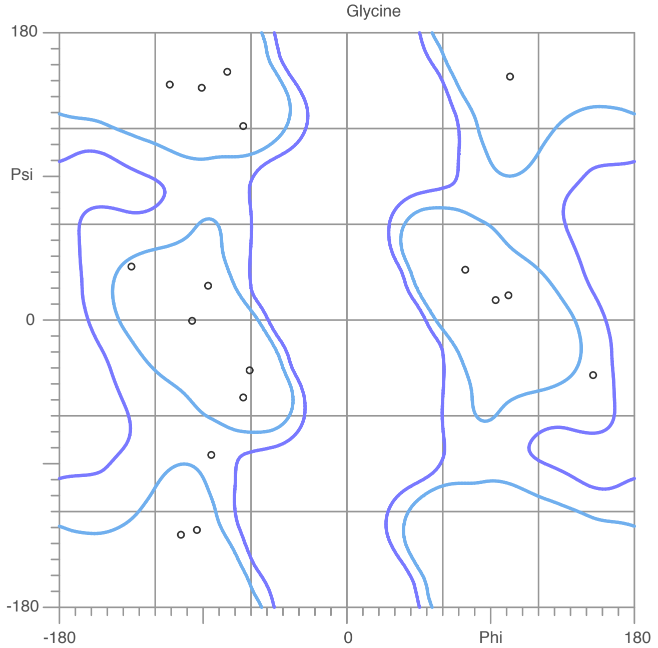
MolProbity Ramachandran analysis

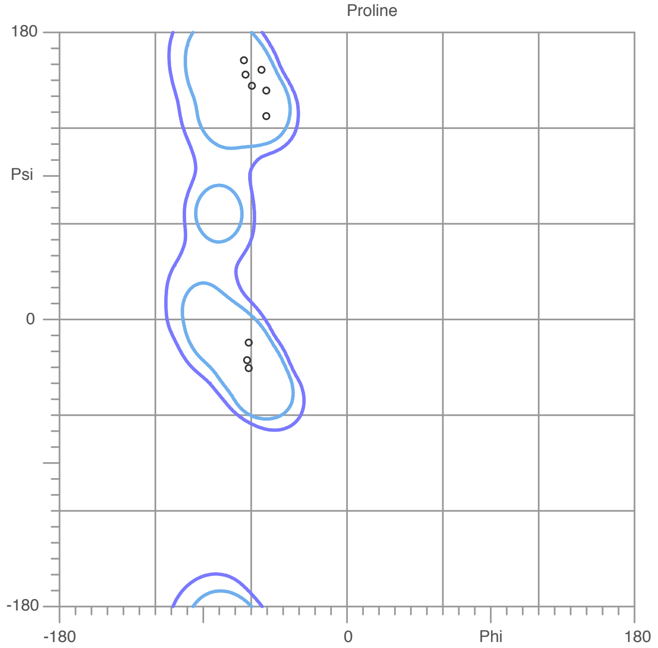
SGR145_R3_em_bcr3.pdb, model 6



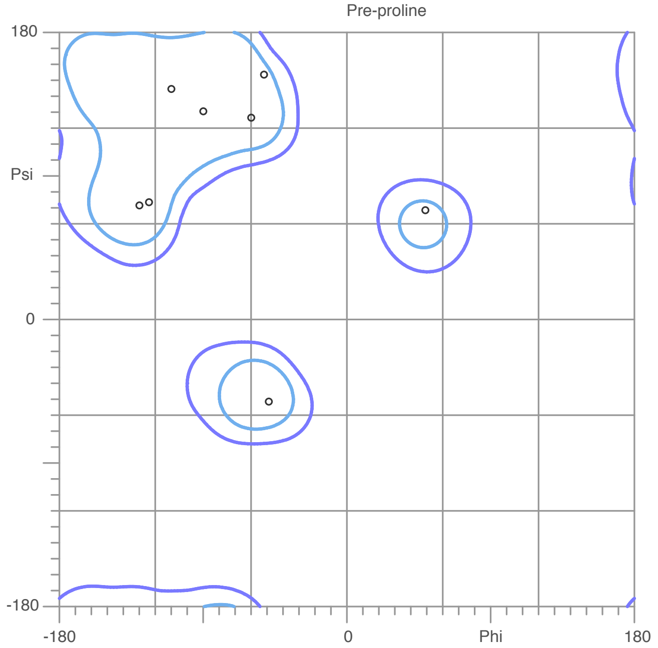
General case



Glycine



Proline



Pre-proline

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)

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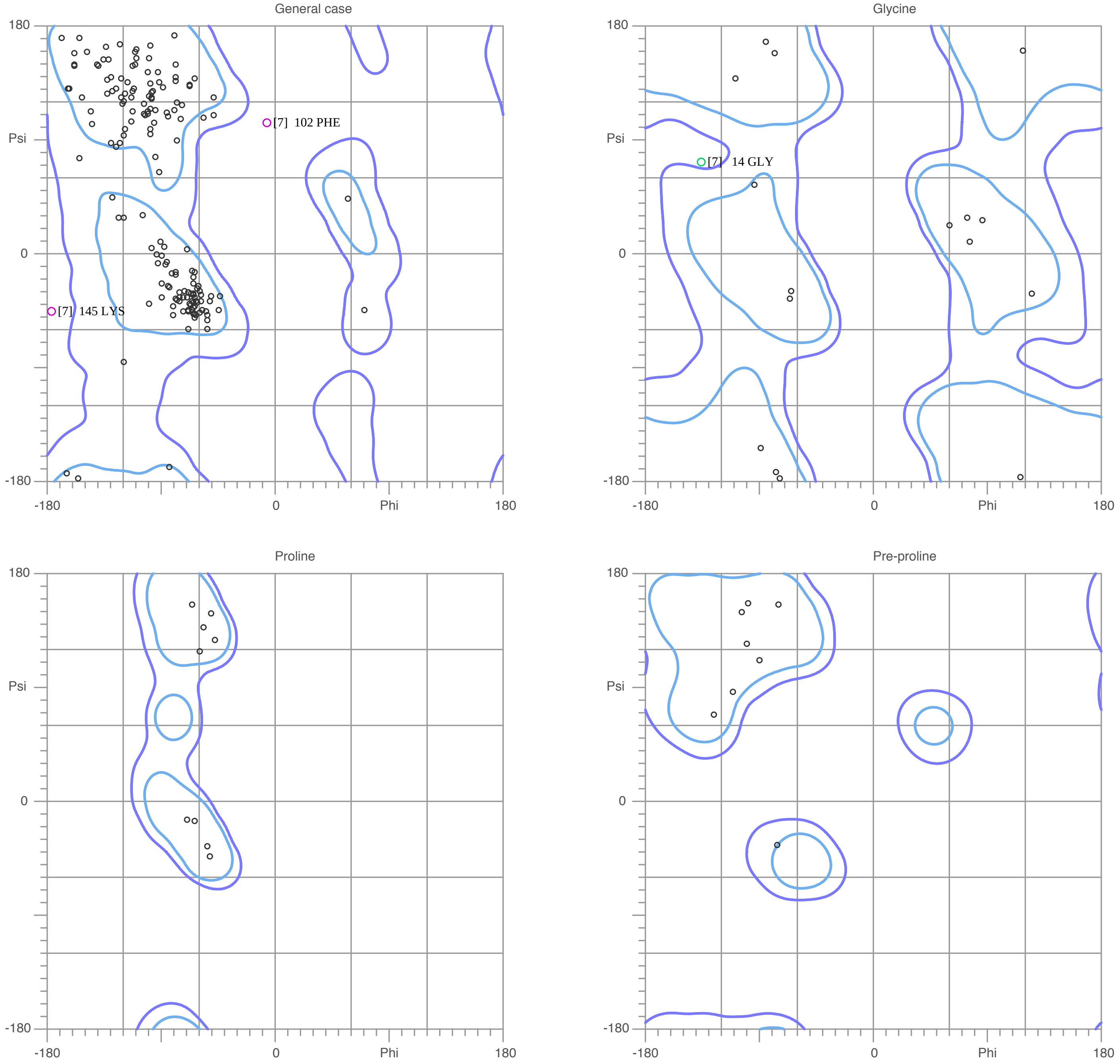
MolProbity Ramachandran analysis

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)

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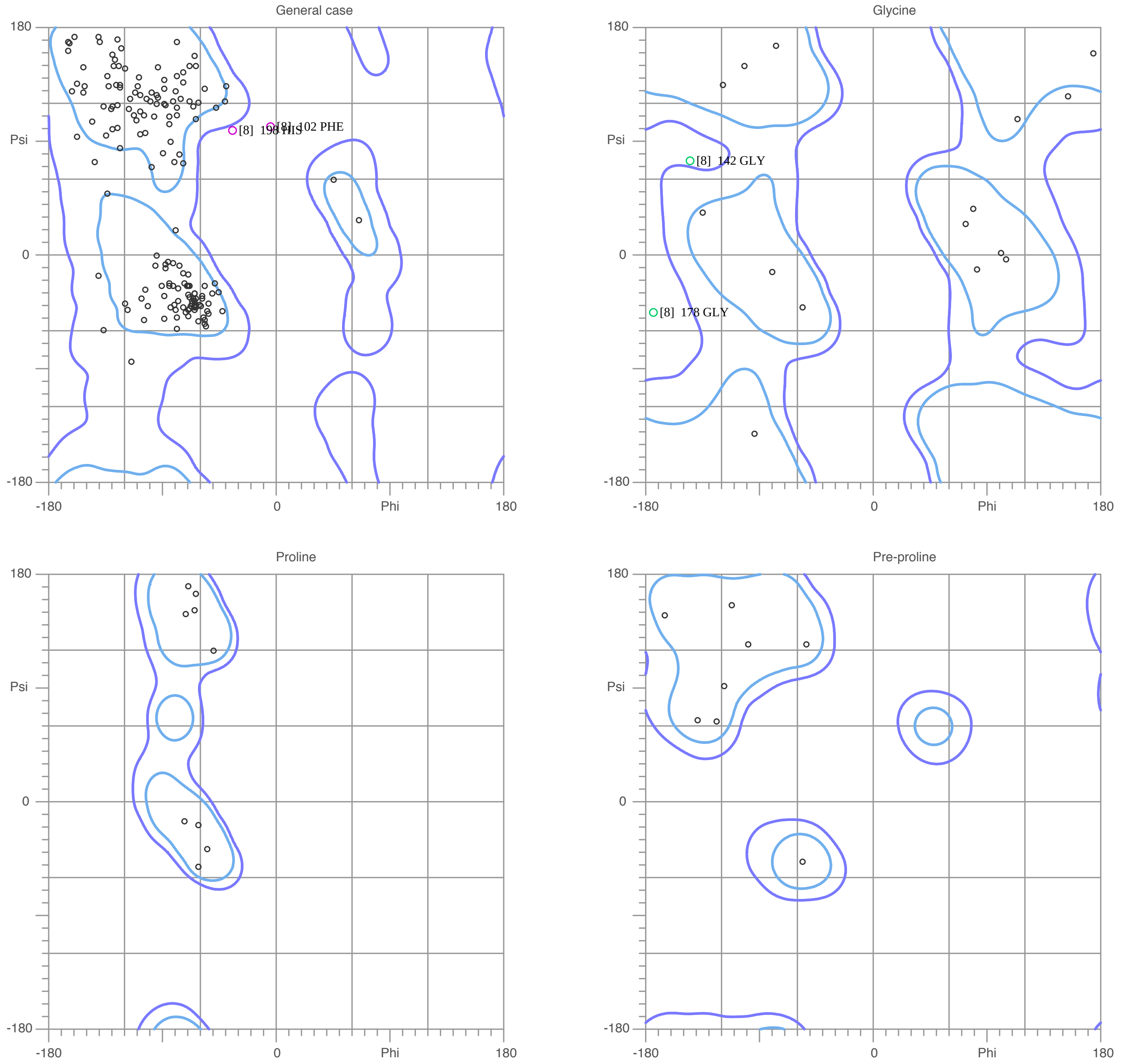
MolProbity Ramachandran analysis

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)

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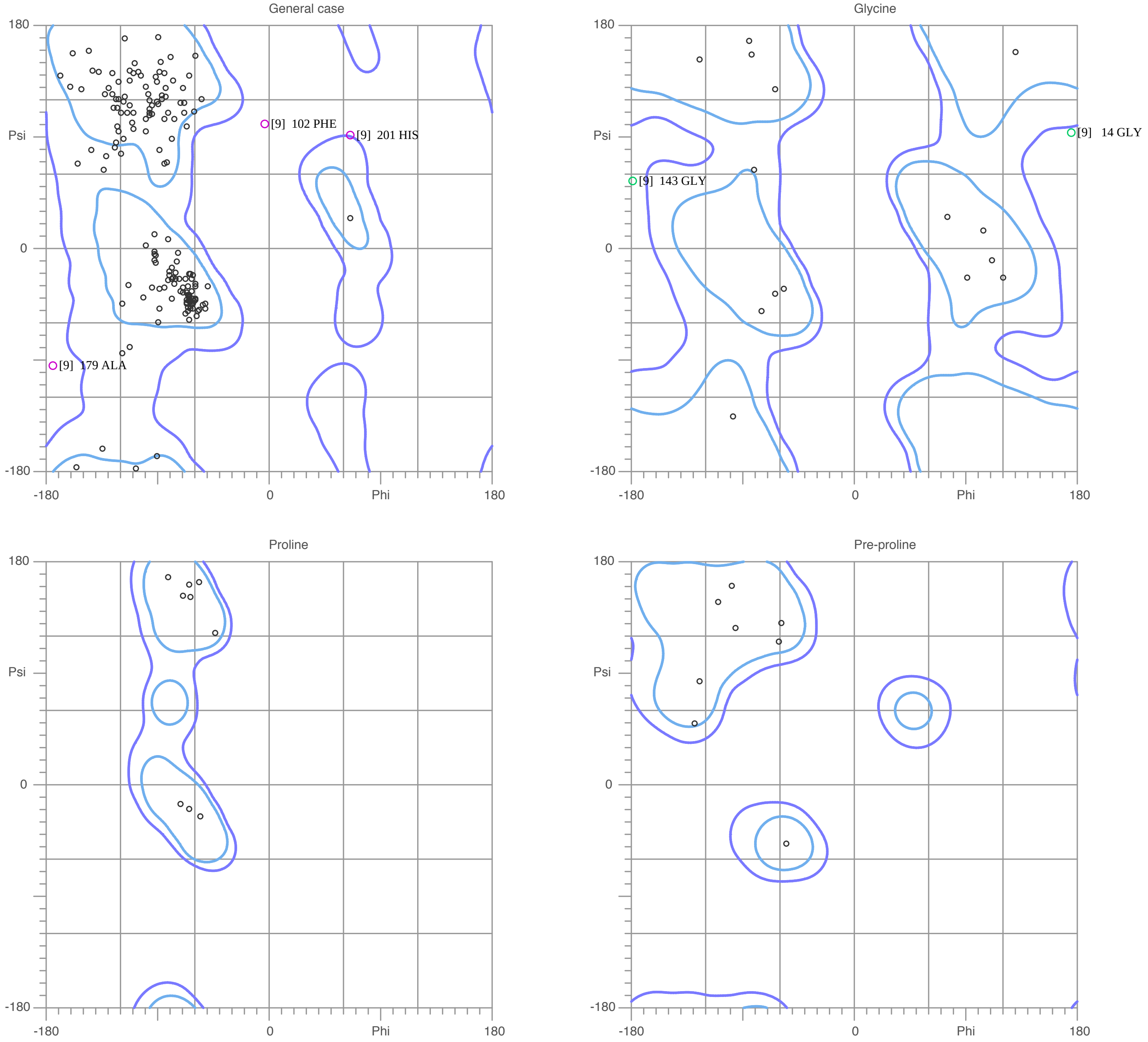
MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 9



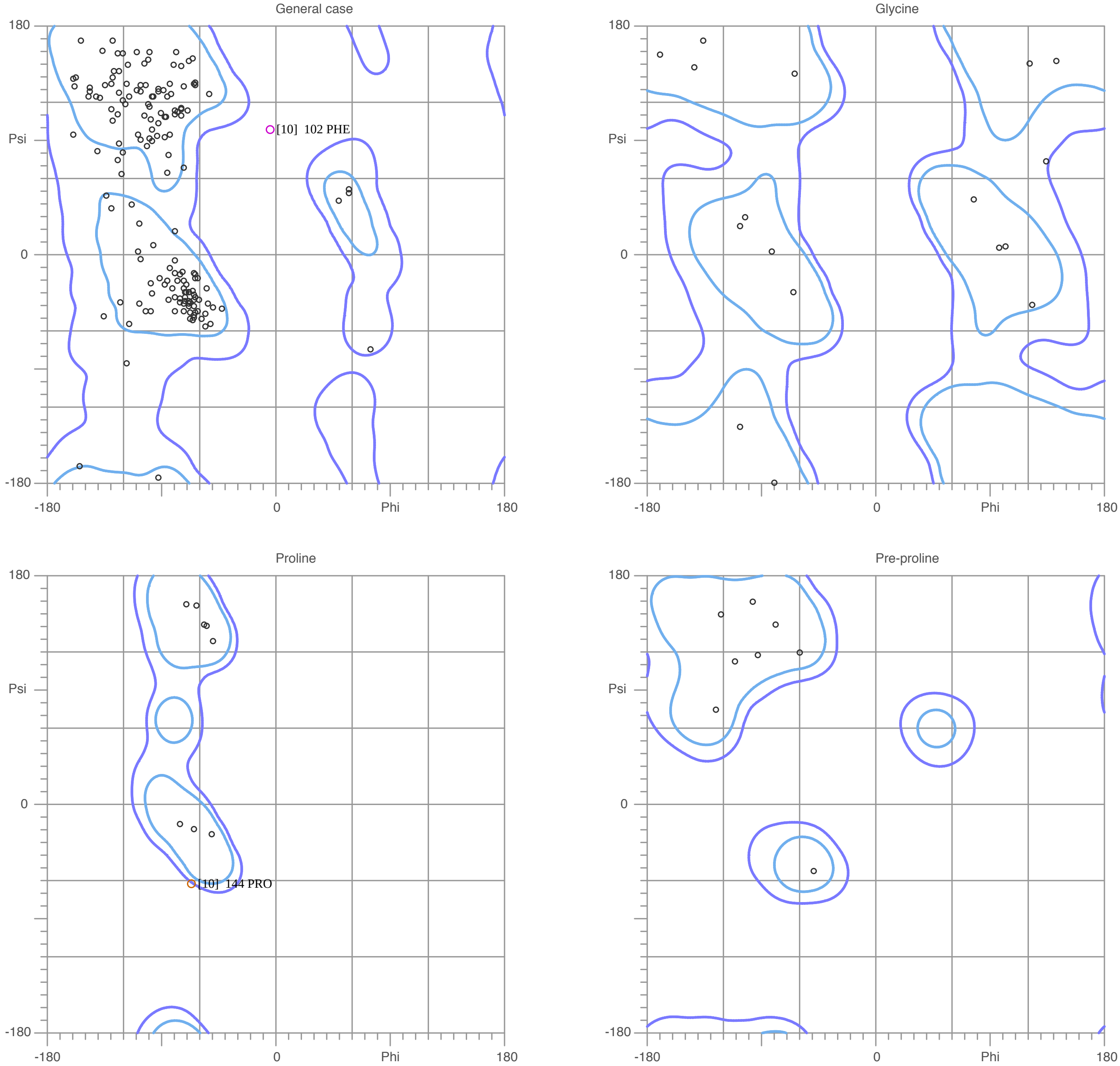
91.5% (183/200) of all residues were in favored (98%) regions.
97.5% (195/200) of all residues were in allowed (>99.8%) regions.

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)

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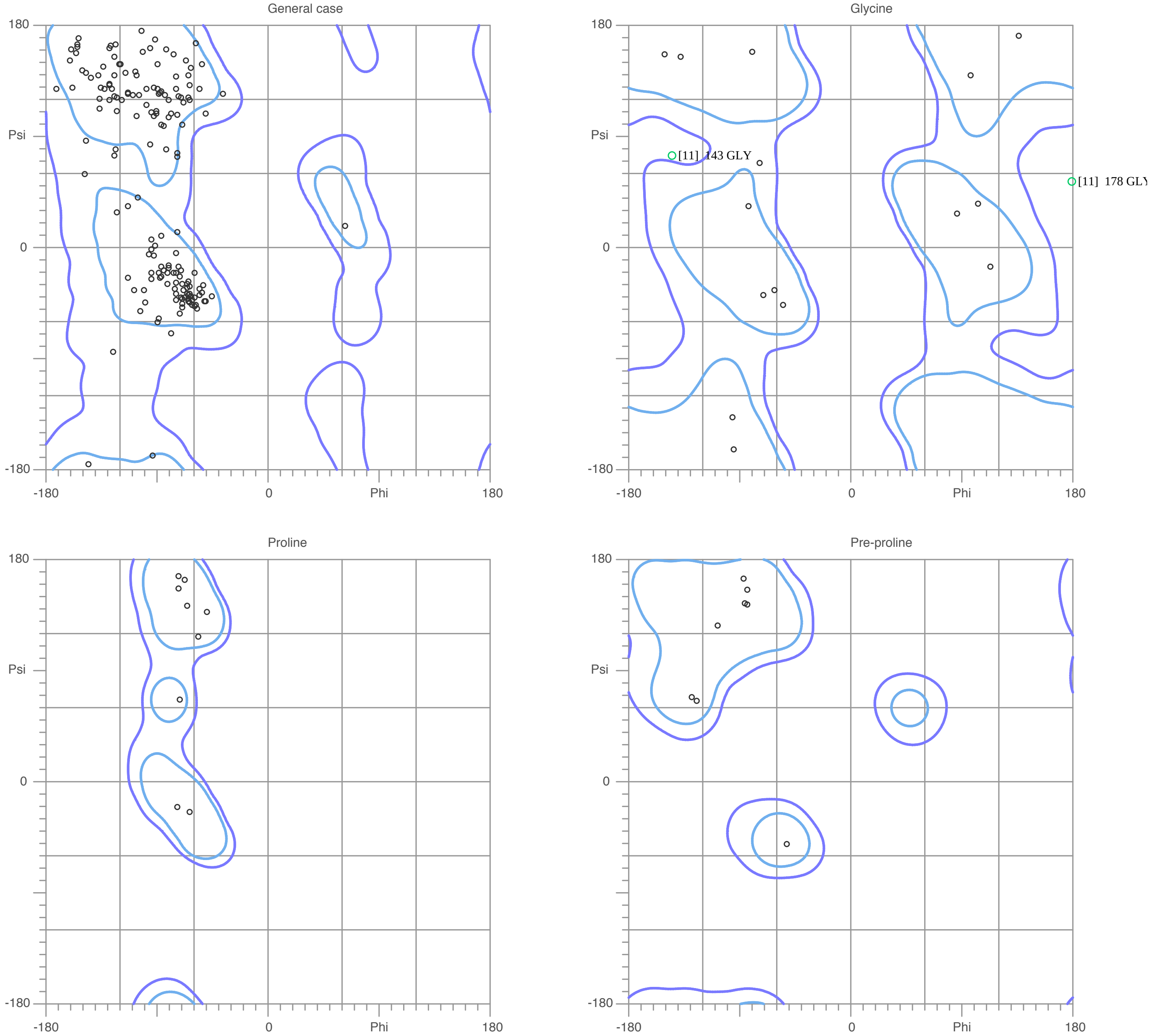
MolProbity Ramachandran analysis

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)

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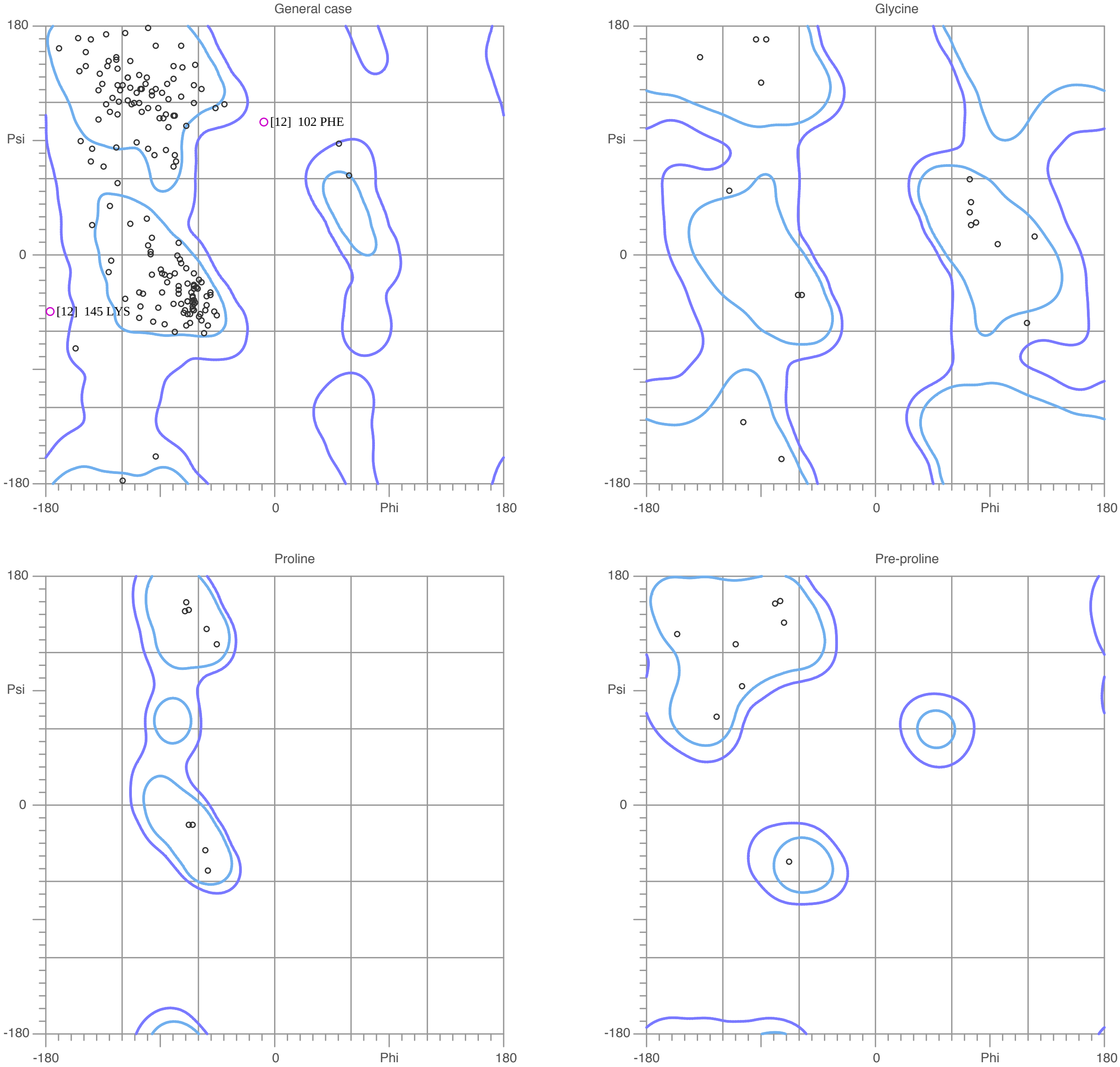
MolProbity Ramachandran analysis

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)

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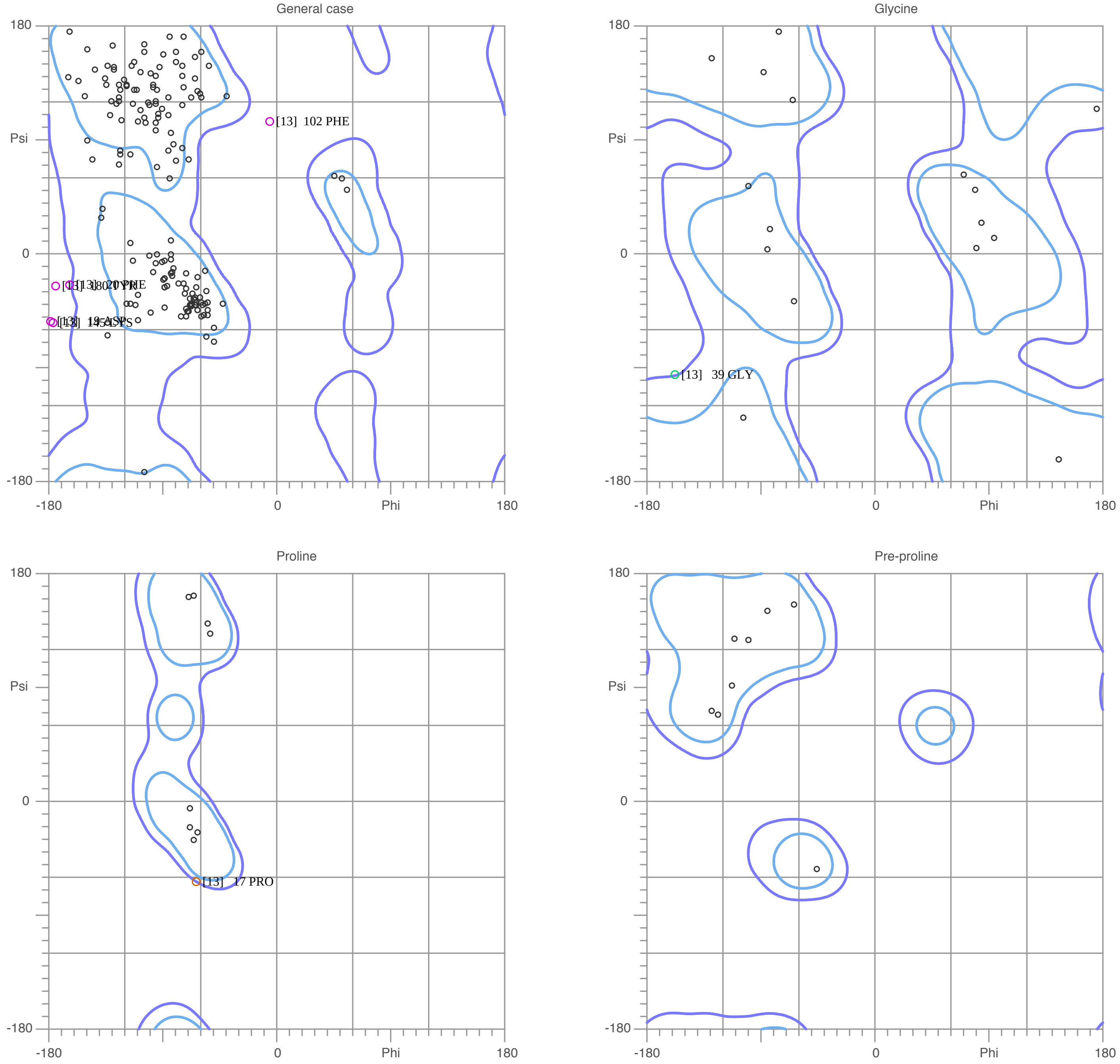
MolProbity Ramachandran analysis

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)

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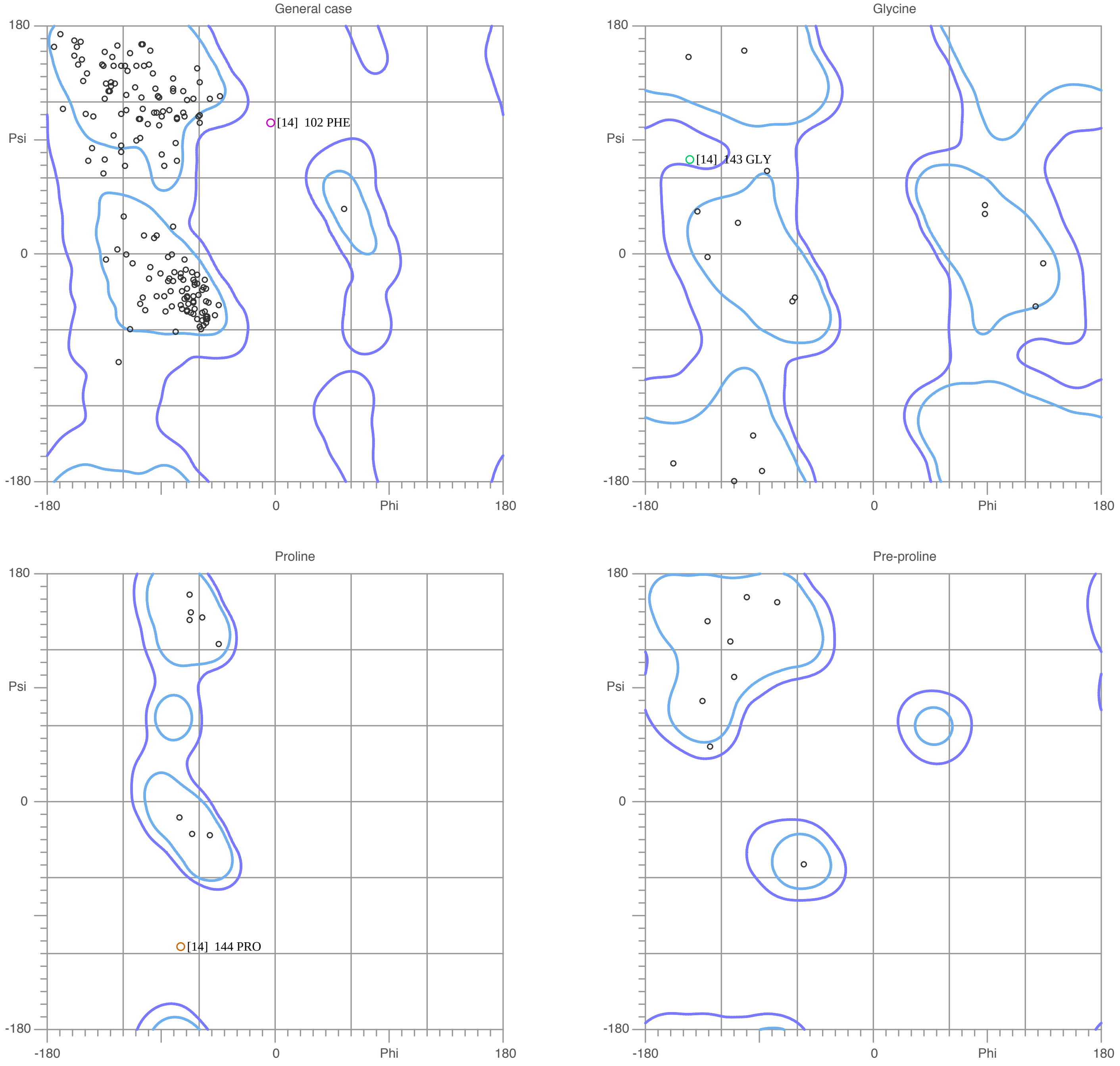
MolProbity Ramachandran analysis

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)

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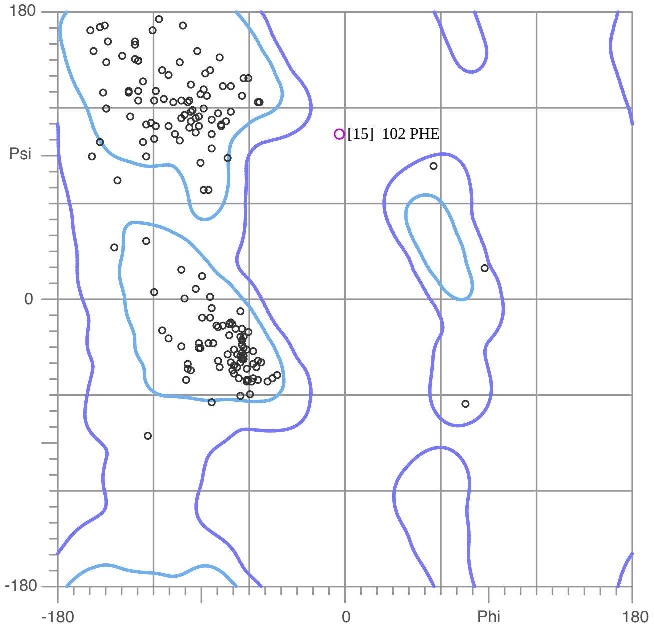
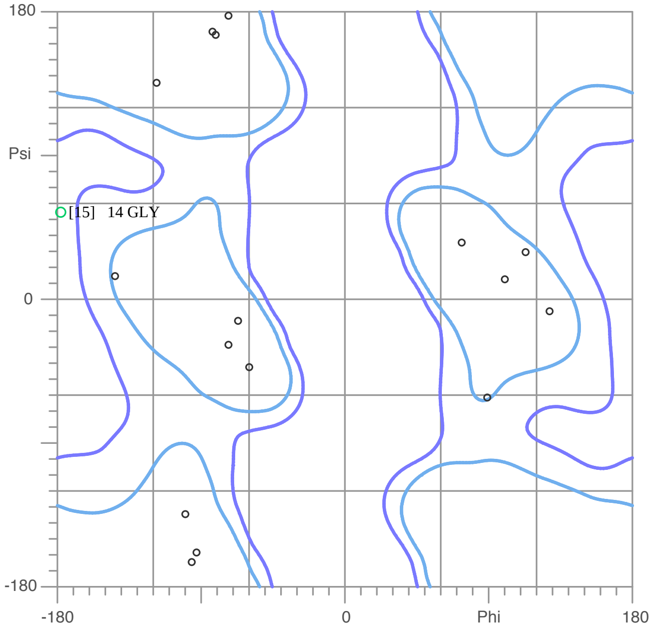
MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 15

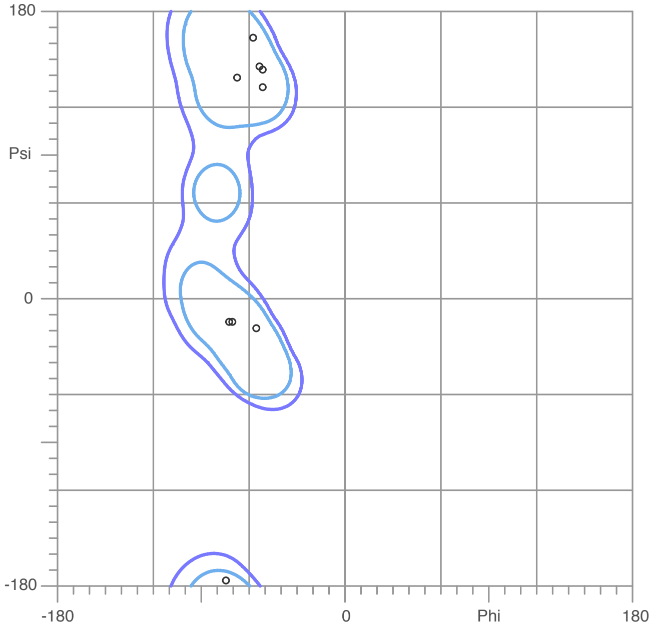
General case



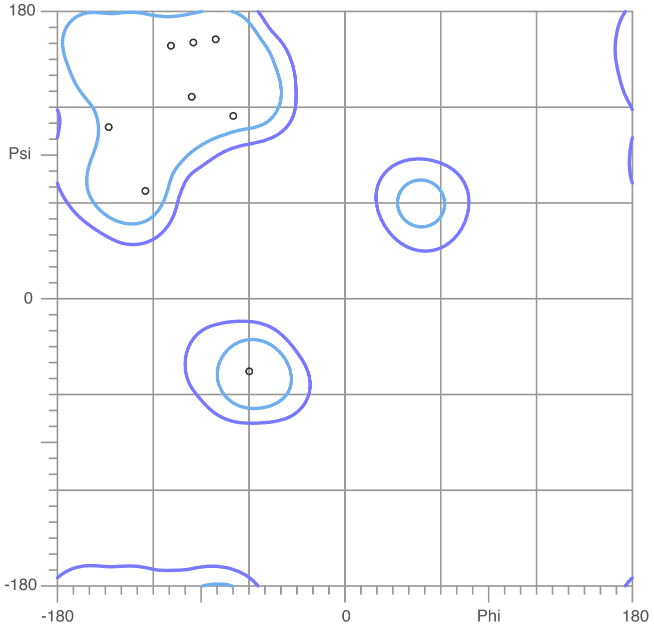
Glycine



Proline



Pre-proline

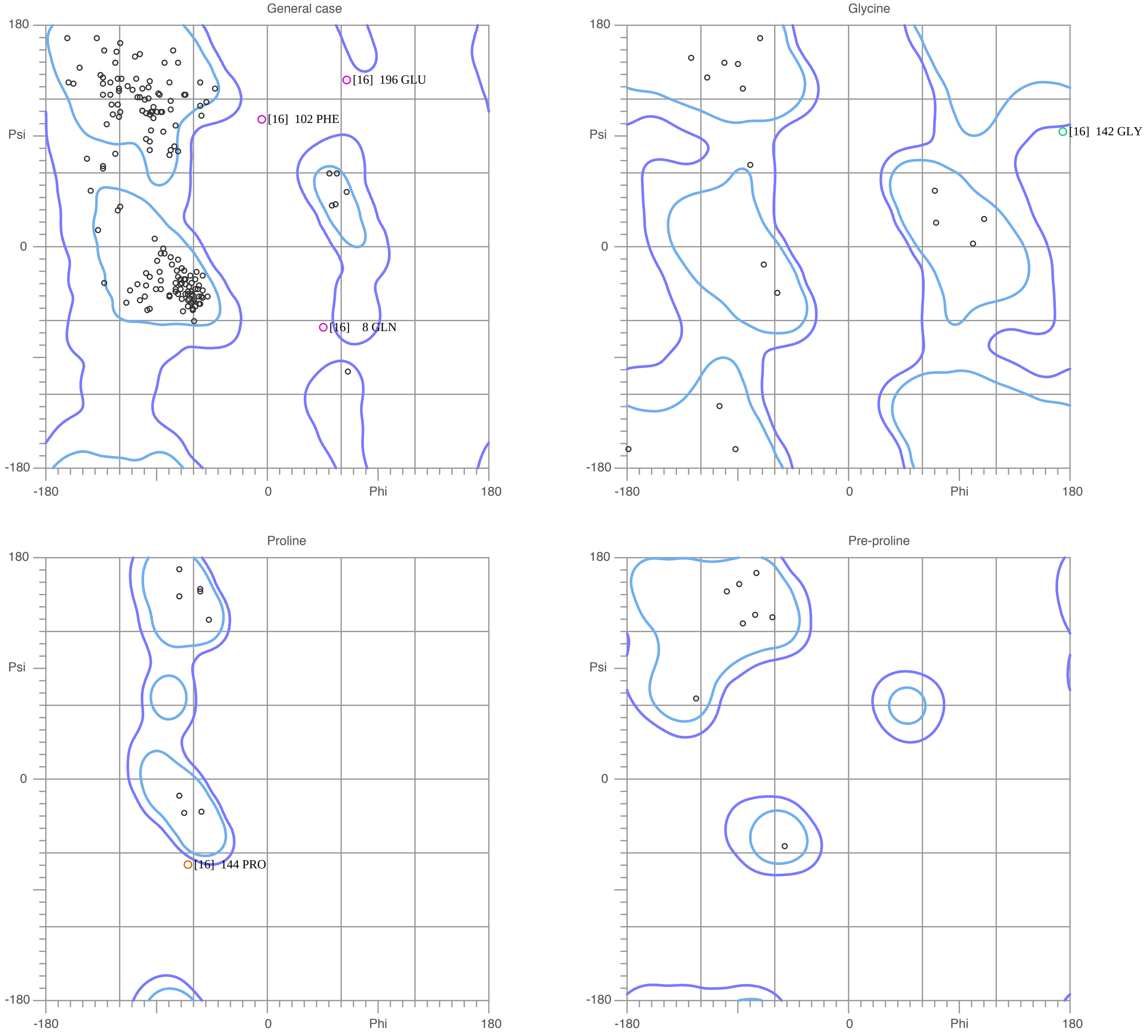


94.5% (189/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

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)

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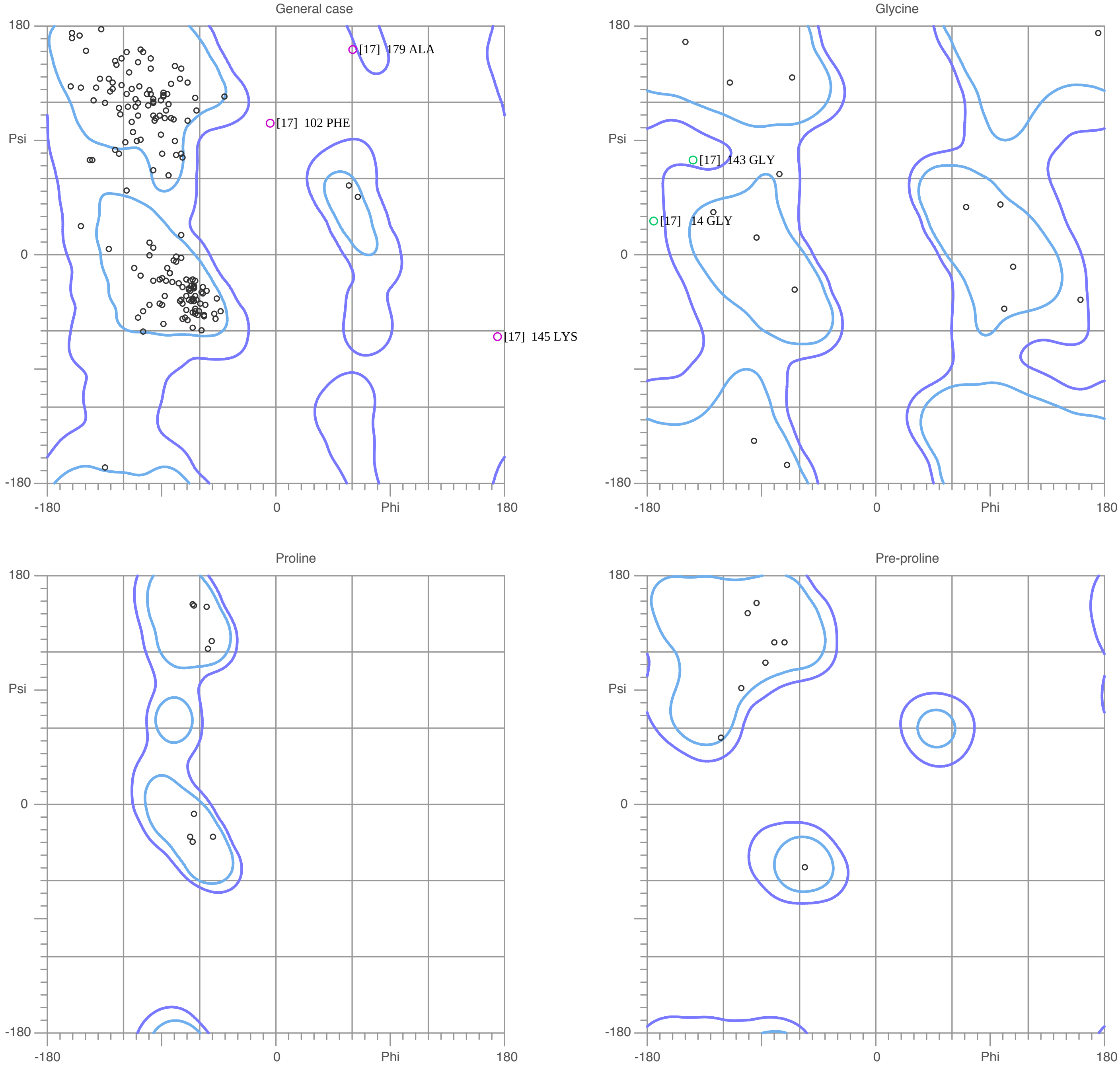
MolProbity Ramachandran analysis

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)

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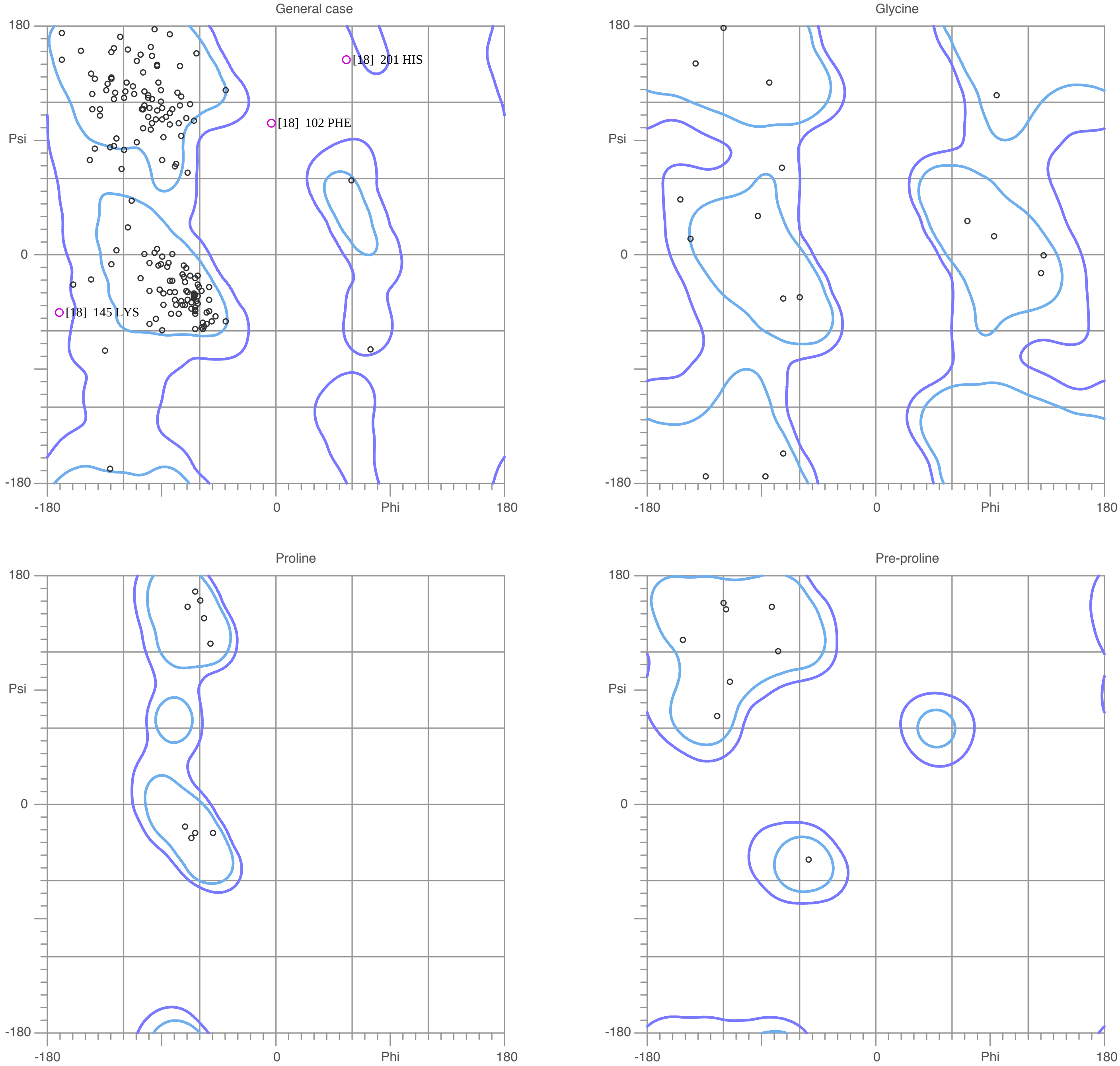
MolProbity Ramachandran analysis

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)

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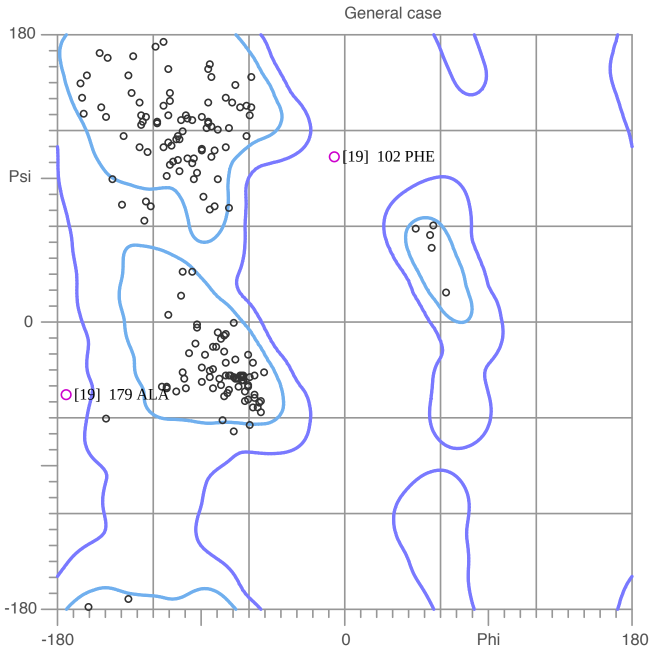
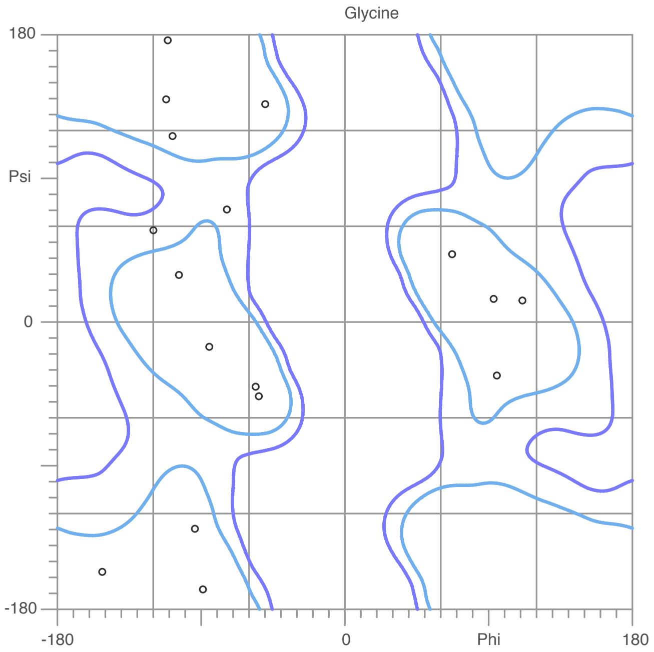
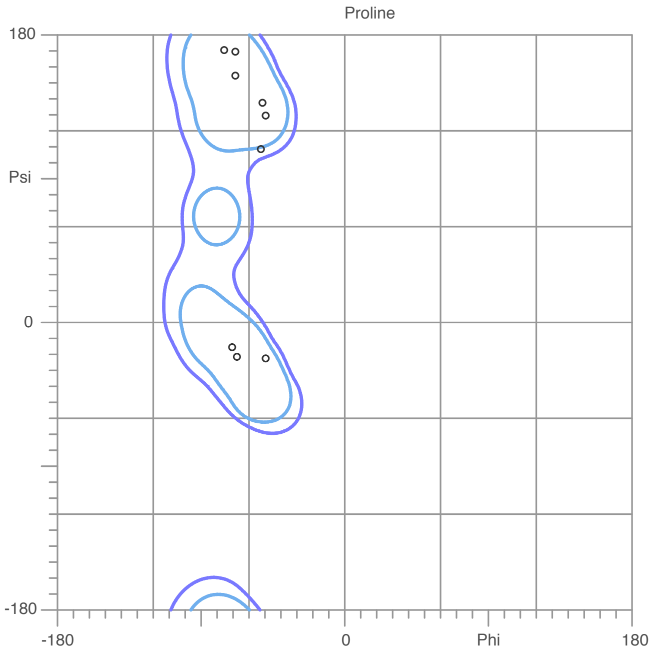
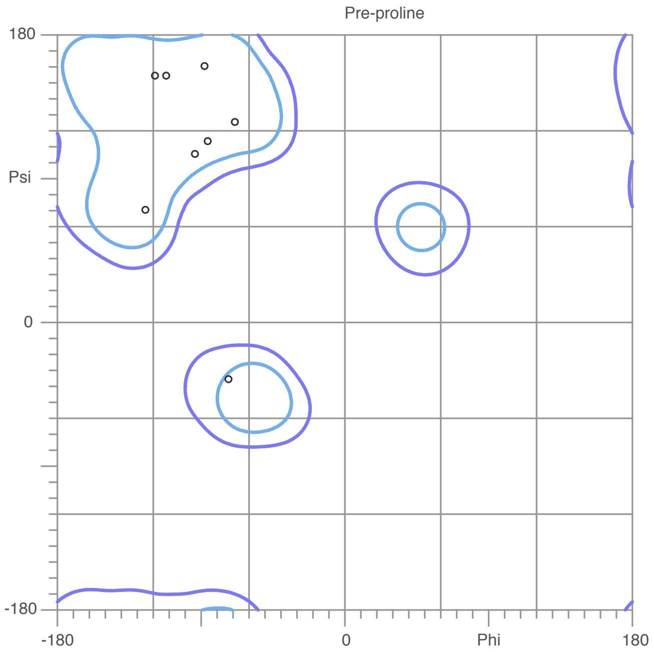
MolProbity Ramachandran analysis

SGR145_R3_em_bcr3.pdb, model 19


General case


Glycine


Proline

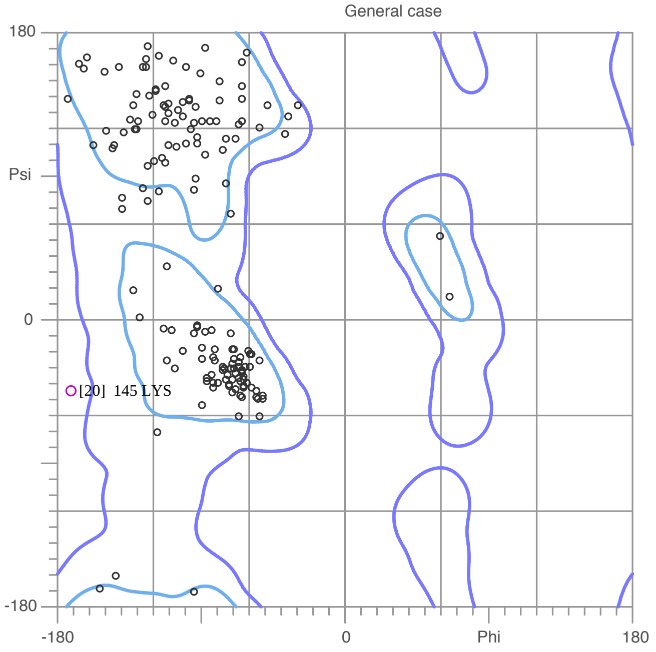

Pre-proline

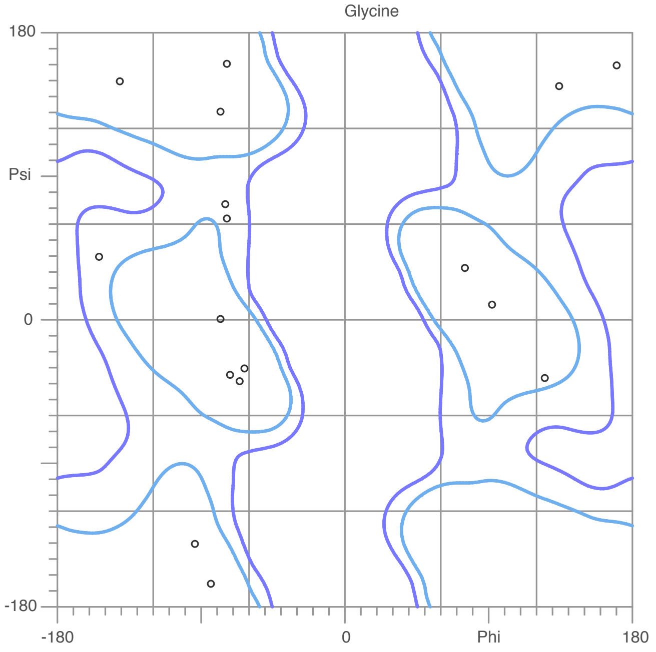
93.5% (187/200) of all residues were in favored (98%) regions.
99.0% (198/200) of all residues were in allowed (>99.8%) regions.

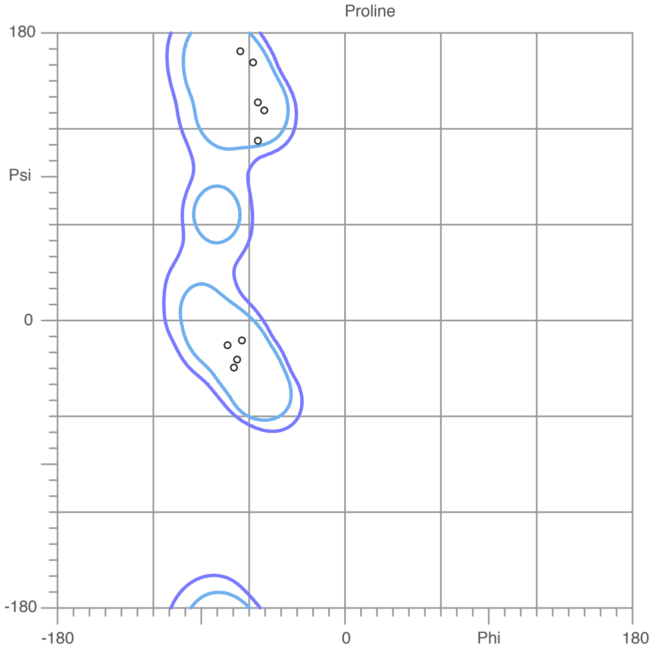
There were 2 outliers (phi, psi):
[19] 102 PHE (-7.3, 105.0)
[19] 179 ALA (-175.1, -45.1)

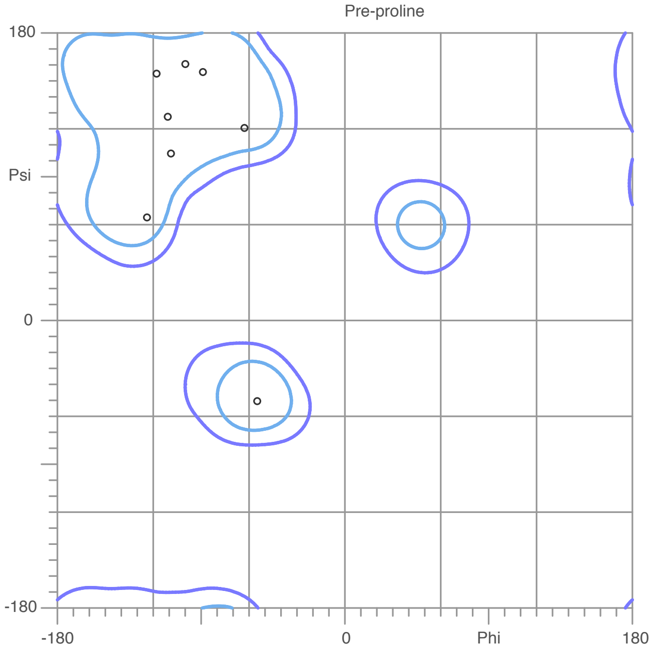
MolProbity Ramachandran analysis

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)