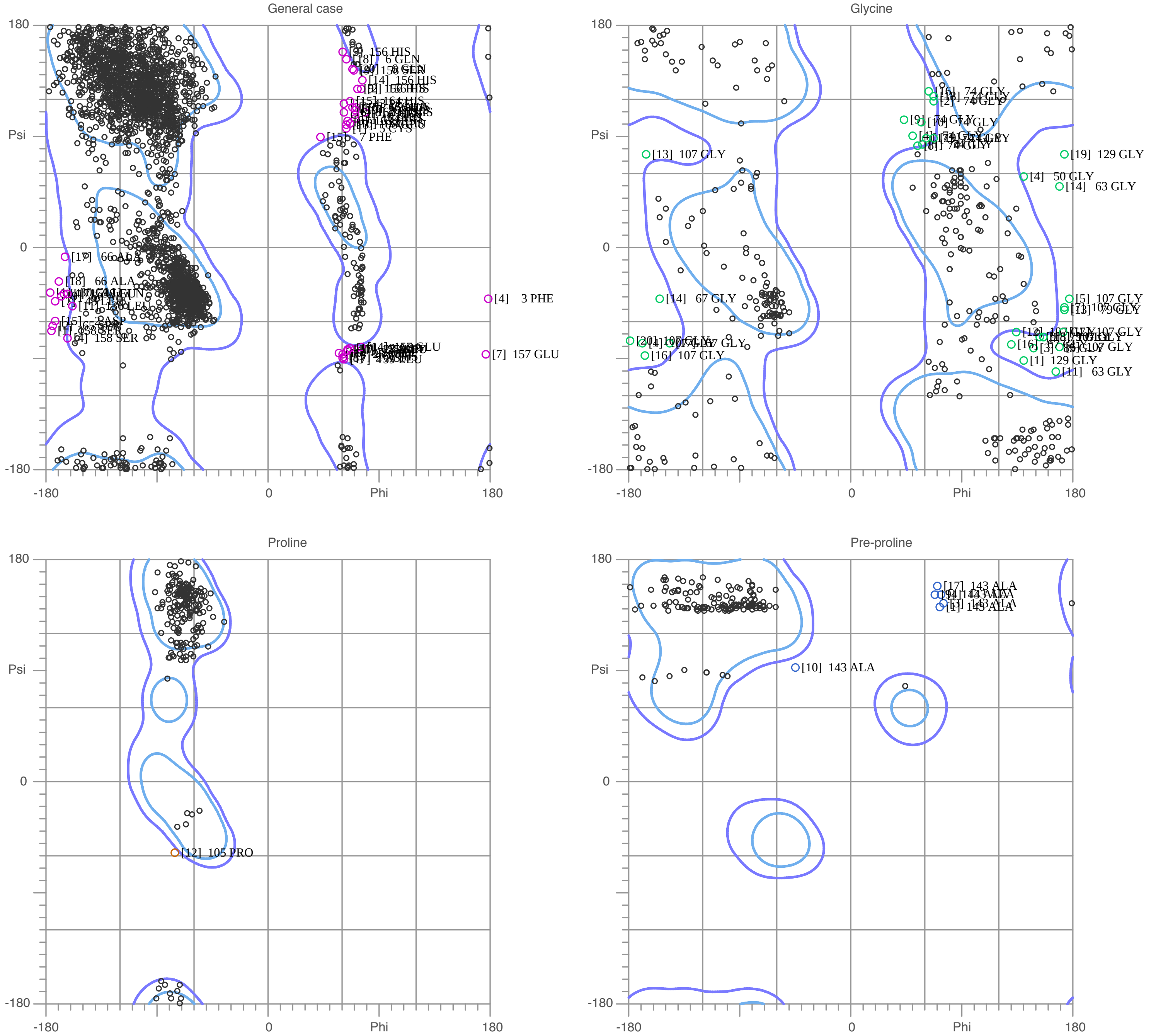
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, all models

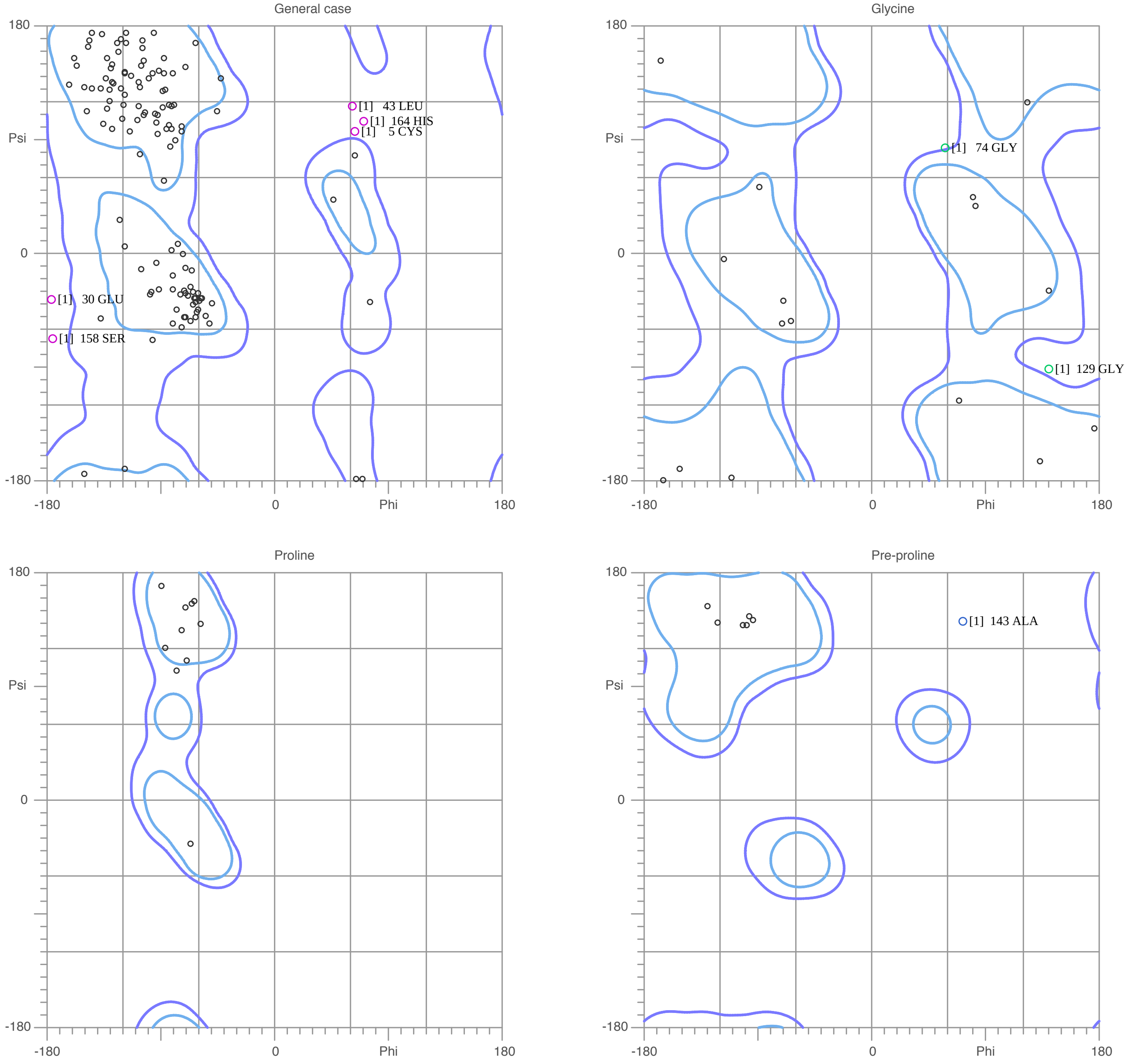


88.1% (2890/3280) of all residues were in favored (98%) regions.
97.4% (3196/3280) of all residues were in allowed (>99.8%) regions.

There were 84 outliers (phi, psi):
[1] 5 CYS (63.2, 97.5)
[1] 30 GLU (-177.6, -36.5)
[1] 43 LEU (61.8, 117.5)
[1] 74 GLY (58.3, 84.5)
[1] 129 GLY (140.4, -91.5)
[1] 143 ALA (72.8, 142.6)
[1] 158 SER (-176.2, -67.5)
[1] 164 HIS (70.1, 105.7)
[2] 6 GLN (70.3, 108.4)
[2] 65 SER (-175.5, -63.5)
[2] 74 GLY (67.3, 119.2)
[2] 156 HIS (76.0, 129.1)
[3] 85 GLY (148.4, -82.0)
[3] 143 ALA (75.1, 145.2)
[3] 156 HIS (60.7, 159.5)
[4] 3 PHE (178.8, -41.7)
[4] 50 GLY (140.8, 58.6)
[4] 74 GLY (50.2, 91.2)
[4] 107 GLY (-169.2, -77.2)
[4] 143 ALA (73.7, 152.3)
[4] 158 SER (-163.8, -73.2)
[4] 159 LEU (-166.5, -37.1)
[5] 28 MET (60.2, -86.4)
[5] 107 GLY (177.4, -41.4)
[6] 107 GLY (169.0, -80.4)
[7] 43 LEU (-173.7, -43.8)
[7] 107 GLY (173.6, -48.7)
[7] 155 LEU (70.7, -82.4)
[7] 157 GLU (176.4, -86.4)
[8] 2 ASP (61.0, -89.4)
[8] 74 GLY (54.7, 83.9)
[8] 161 HIS (78.7, 110.1)
[8] 163 HIS (64.6, 104.0)
[9] 66 ALA (-168.0, -39.9)
[9] 74 GLY (43.3, 104.2)
[9] 79 GLY (153.9, -72.5)
[9] 143 ALA (68.5, 152.0)
[9] 156 HIS (72.2, 129.6)
[9] 158 SER (69.6, 144.2)
[10] 28 MET (64.9, -82.2)
[10] 74 GLY (57.1, 102.3)
[10] 143 ALA (-45.2, 93.2)
[11] 2 ASP (64.7, -83.4)
[11] 63 GLY (166.8, -100.9)
[11] 136 LEU (-159.0, -47.2)
[12] 105 PRO (-76.9, -57.4)
[12] 107 GLY (134.0, -68.4)
[13] 79 GLY (173.8, -50.8)
[13] 107 GLY (-166.1, 76.2)
[13] 108 GLU (63.7, 100.9)
[14] 63 GLY (169.8, 50.8)
[14] 67 GLY (-155.2, -41.7)
[14] 156 HIS (76.8, 136.9)
[14] 157 GLU (75.1, -80.4)
[15] 2 ASP (-173.4, -59.5)
[15] 7 PHE (42.8, 90.5)
[15] 28 MET (57.0, -85.6)
[15] 107 GLY (156.9, -72.6)
[15] 156 HIS (71.2, 114.7)
[15] 164 HIS (66.1, 119.6)
[16] 67 GLY (130.1, -78.8)
[16] 74 GLY (63.9, 127.2)
[16] 107 GLY (-167.0, -87.2)
[16] 162 HIS (61.9, 110.6)
[17] 49 GLN (-163.6, -37.8)
[17] 66 ALA (-165.8, -7.9)
[17] 67 GLY (-147.5, -77.9)
[17] 74 GLY (61.4, 89.9)
[17] 107 GLY (172.9, -69.0)
[17] 143 ALA (70.5, 159.8)
[17] 159 LEU (61.3, -90.8)
[17] 161 HIS (61.1, -88.6)
[18] 6 GLN (63.5, 153.8)
[18] 66 ALA (-170.4, -27.7)
[18] 74 GLY (67.4, 123.7)
[18] 107 GLY (157.0, -72.6)
[18] 162 HIS (66.1, 101.5)
[19] 2 ASP (66.6, -81.1)
[19] 66 ALA (68.8, 114.1)
[19] 74 GLY (67.0, 89.4)
[19] 129 GLY (173.0, 76.3)
[19] 163 HIS (70.9, 112.0)
[20] 6 GLN (69.0, 145.5)
[20] 107 GLY (-179.9, -75.4)

# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 1



89.0% (146/164) of all residues were in favored (98%) regions.
95.1% (156/164) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):
[1] 5 CYS (63.2, 97.5)
[1] 30 GLU (-177.6, -36.5)
[1] 43 LEU (61.8, 117.5)
[1] 74 GLY (58.3, 84.5)
[1] 129 GLY (140.4, -91.5)
[1] 143 ALA (72.8, 142.6)
[1] 158 SER (-176.2, -67.5)
[1] 164 HIS (70.1, 105.7)

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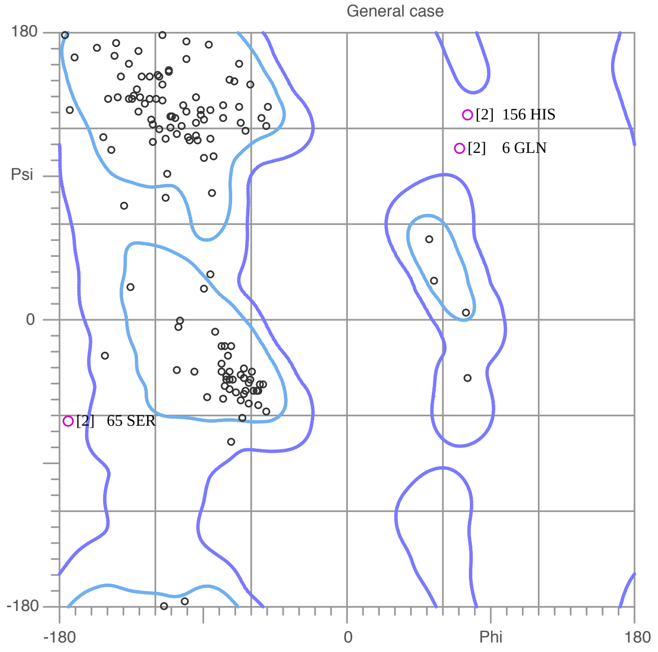
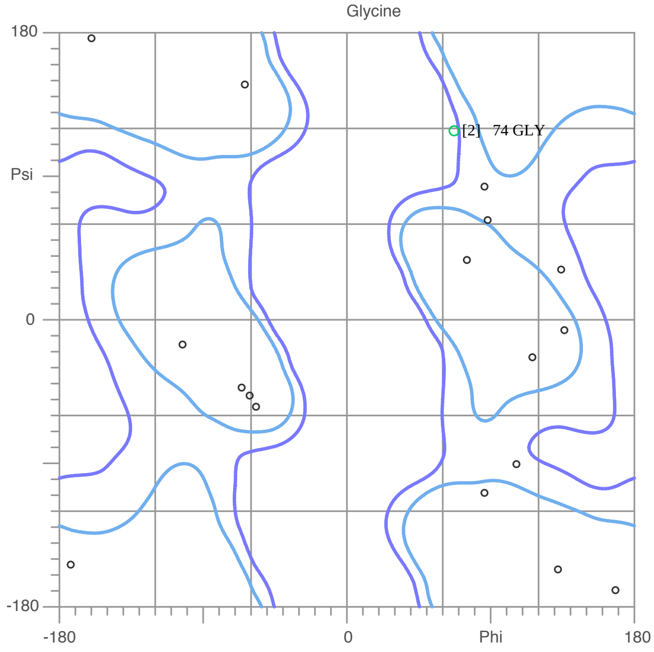
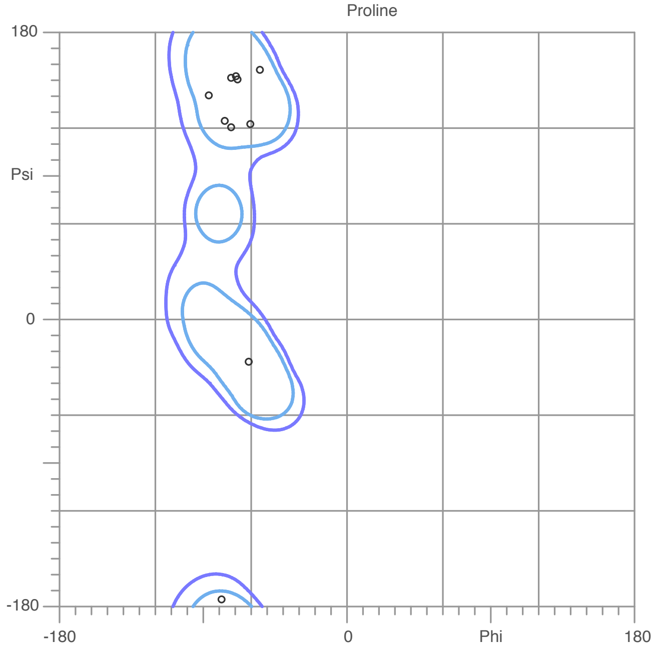
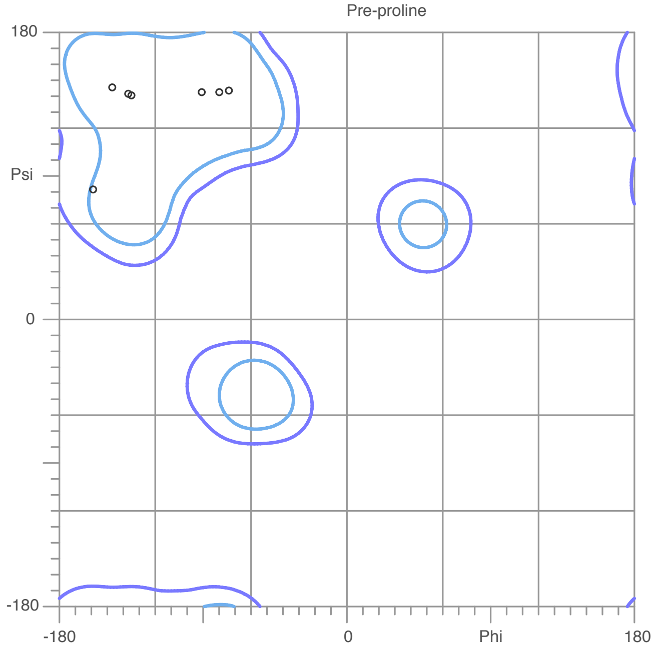
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 2


General case


Glycine


Proline


Pre-proline

90.2% (148/164) of all residues were in favored (98%) regions.
97.6% (160/164) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[2] 6 GLN (70.3, 108.4)
[2] 65 SER (-175.5, -63.5)
[2] 74 GLY (67.3, 119.2)
[2] 156 HIS (76.0, 129.1)

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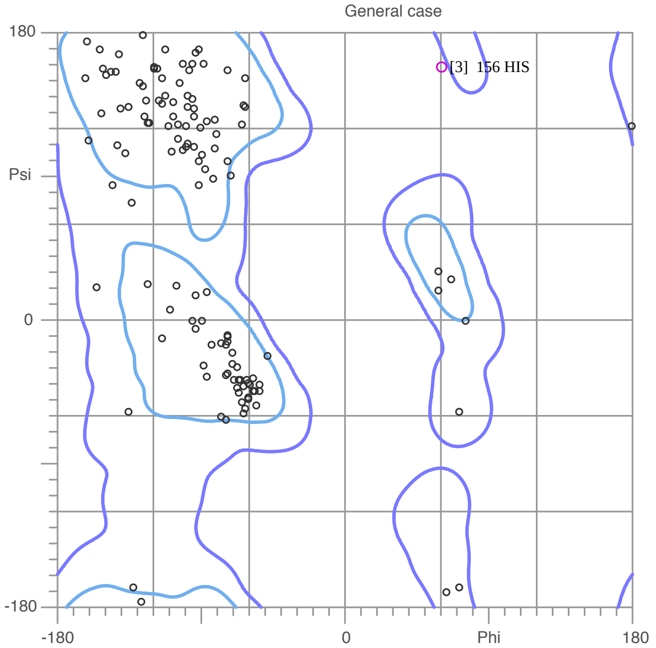
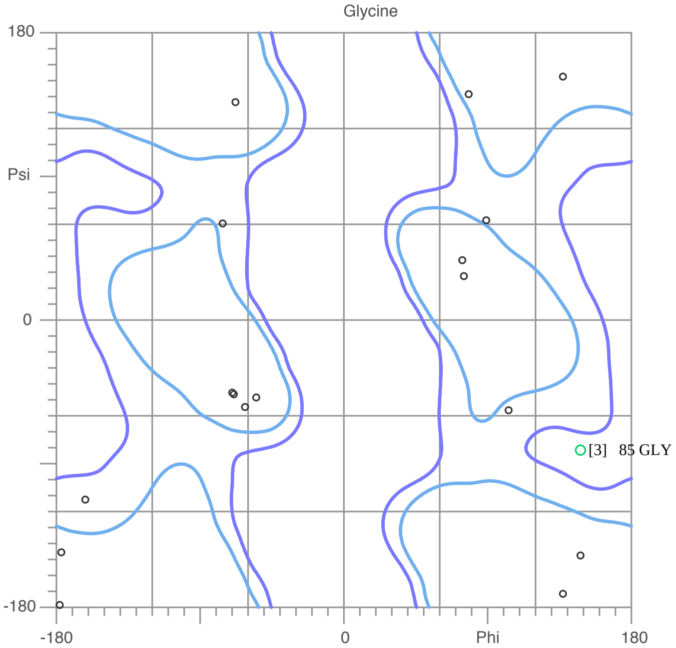
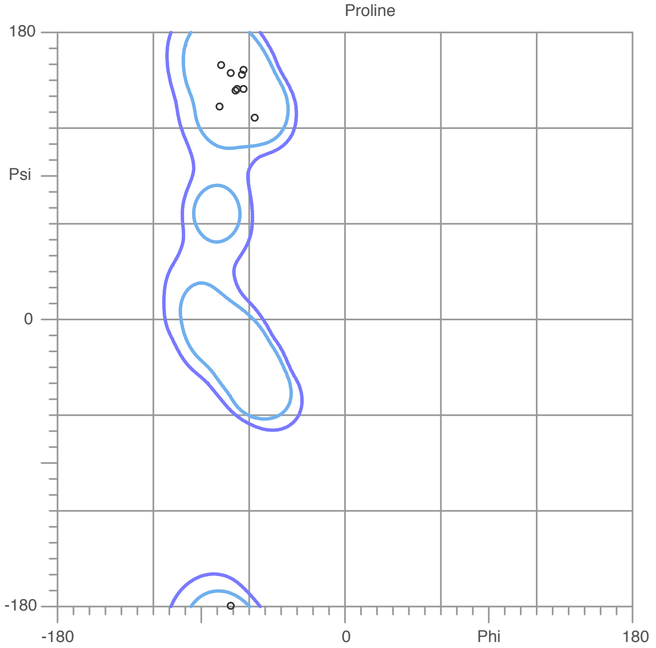
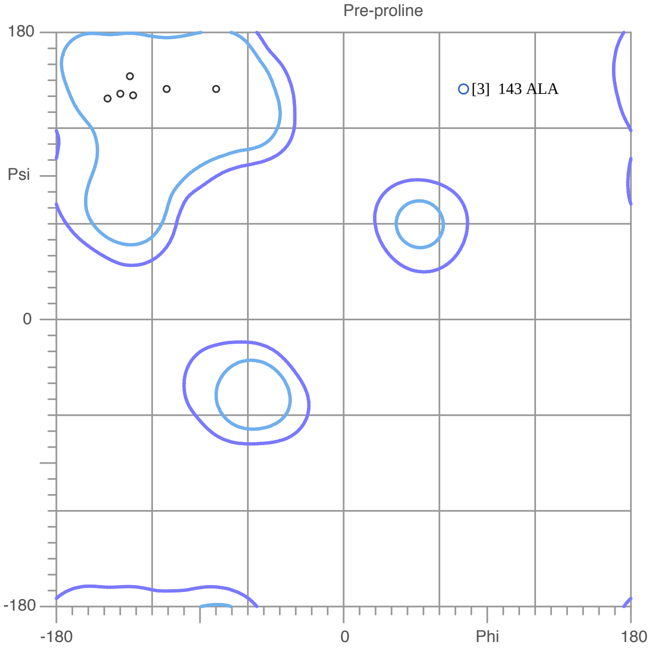
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 3









89.0% (146/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
- [3] 85 GLY (148.4, -82.0)
- [3] 143 ALA (75.1, 145.2)
- [3] 156 HIS (60.7, 159.5)

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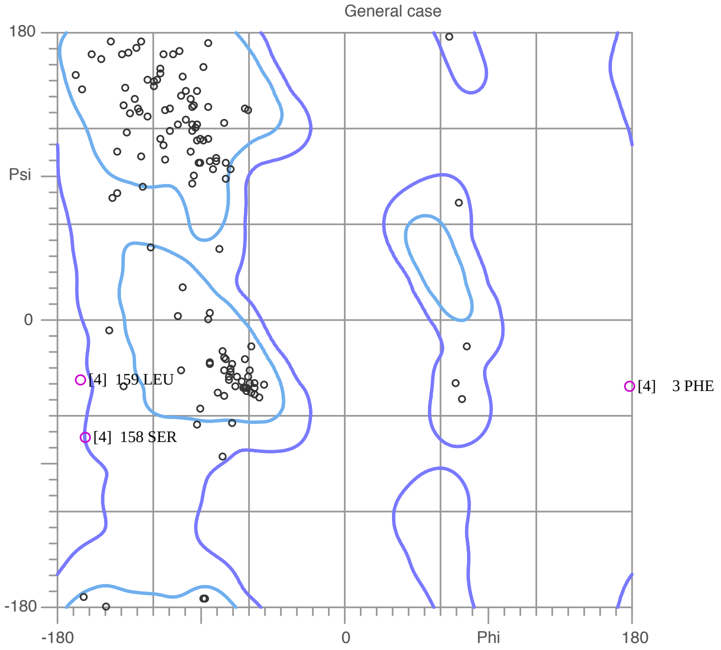
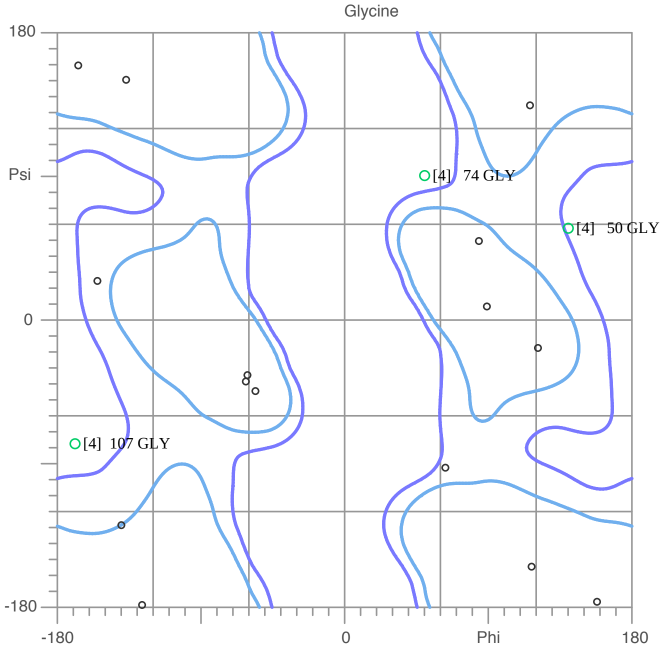
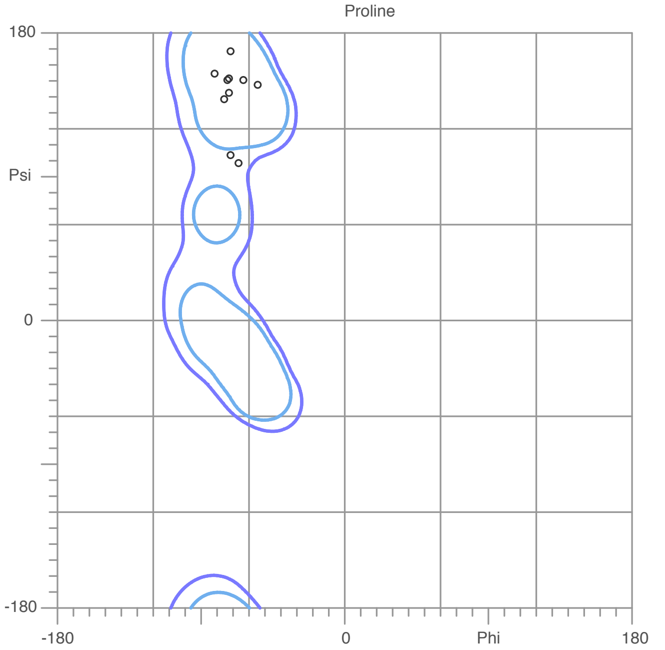
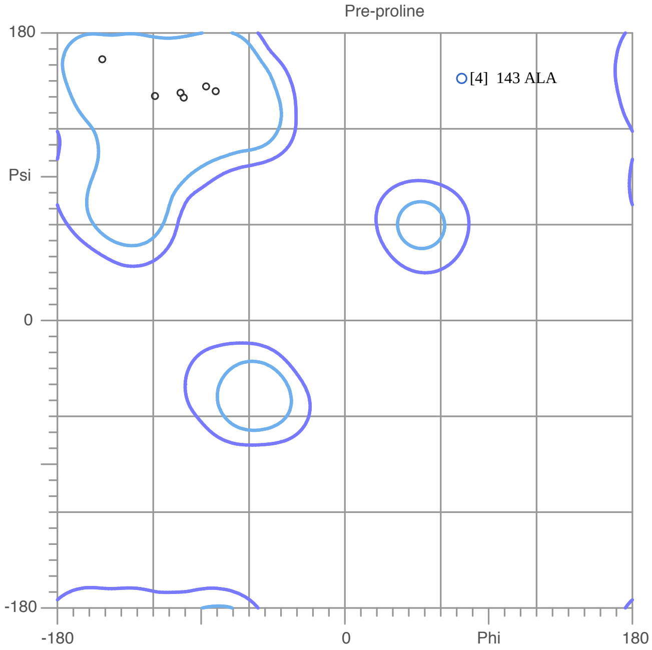
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 4









84.8% (139/164) of all residues were in favored (98%) regions.
95.7% (157/164) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):

[4] 3 PHE (178.8, -41.7)
[4] 50 GLY (140.8, 58.6)
[4] 74 GLY (50.2, 91.2)
[4] 107 GLY (-169.2, -77.2)
[4] 143 ALA (73.7, 152.3)
[4] 158 SER (-163.8, -73.2)
[4] 159 LEU (-166.5, -37.1)

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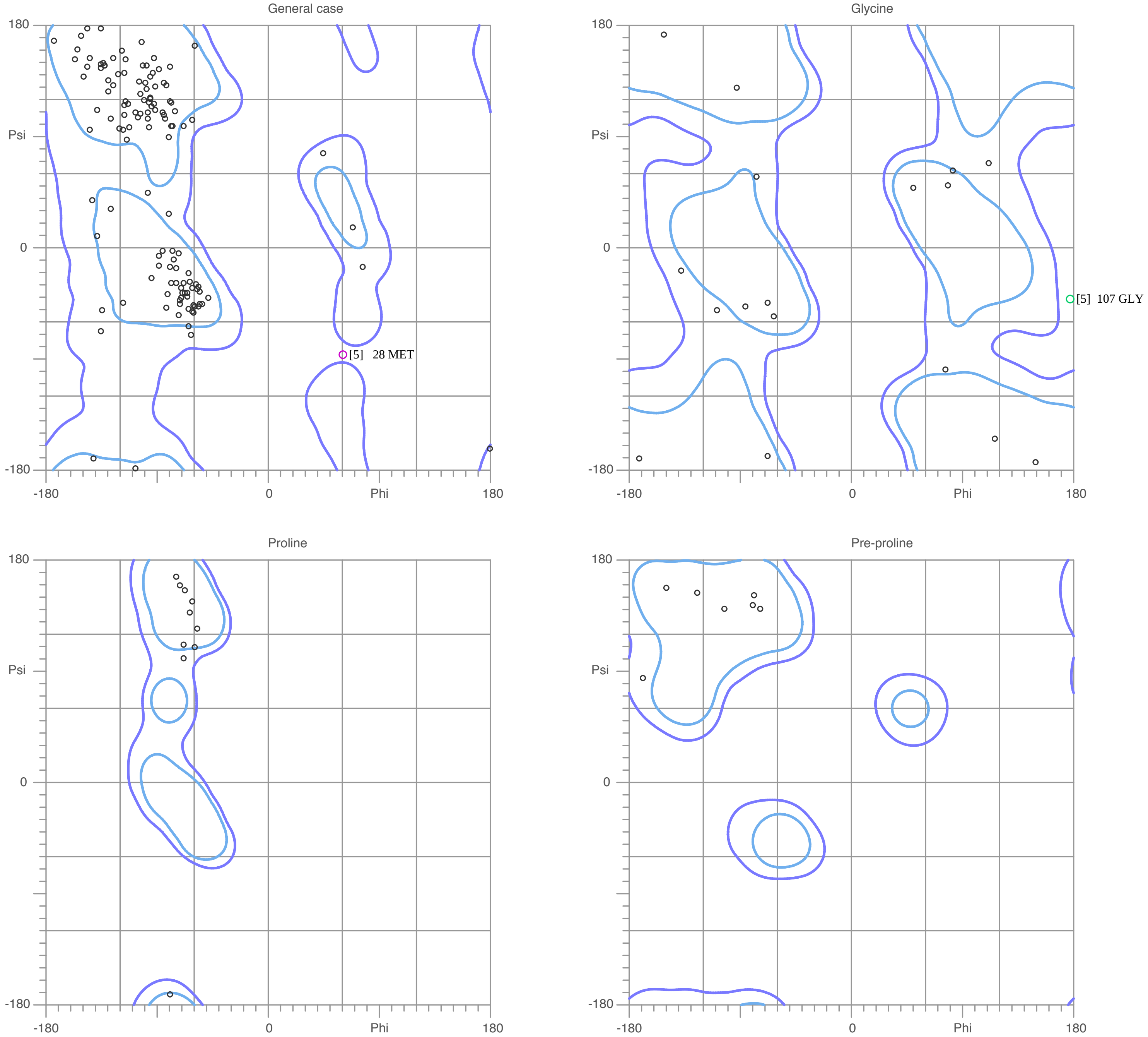
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 5



87.2% (143/164) of all residues were in favored (98%) regions.
98.8% (162/164) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[5] 28 MET (60.2, -86.4)
[5] 107 GLY (177.4, -41.4)

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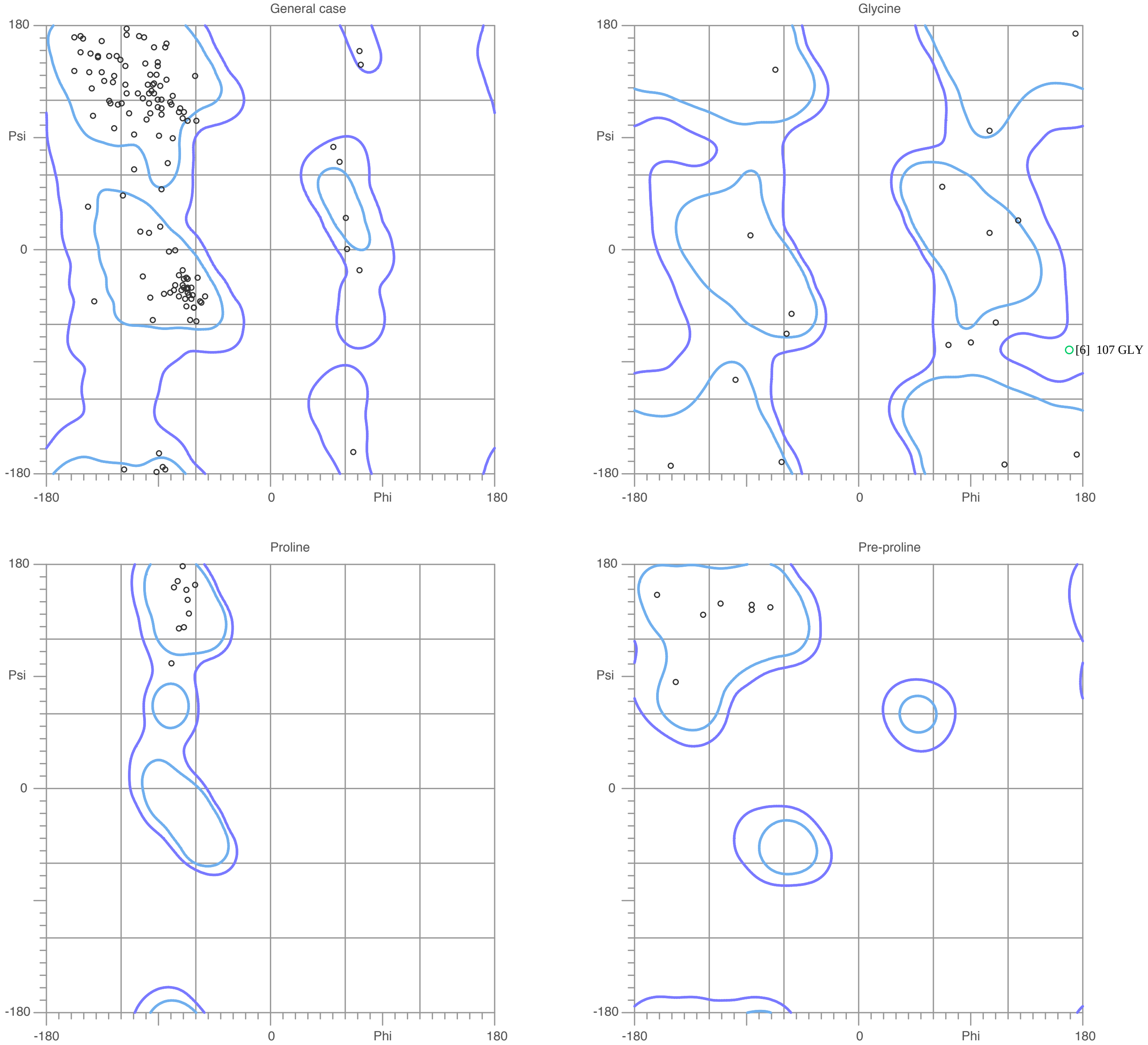
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 6



88.4% (145/164) of all residues were in favored (98%) regions.
99.4% (163/164) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[6] 107 GLY (169.0, -80.4)

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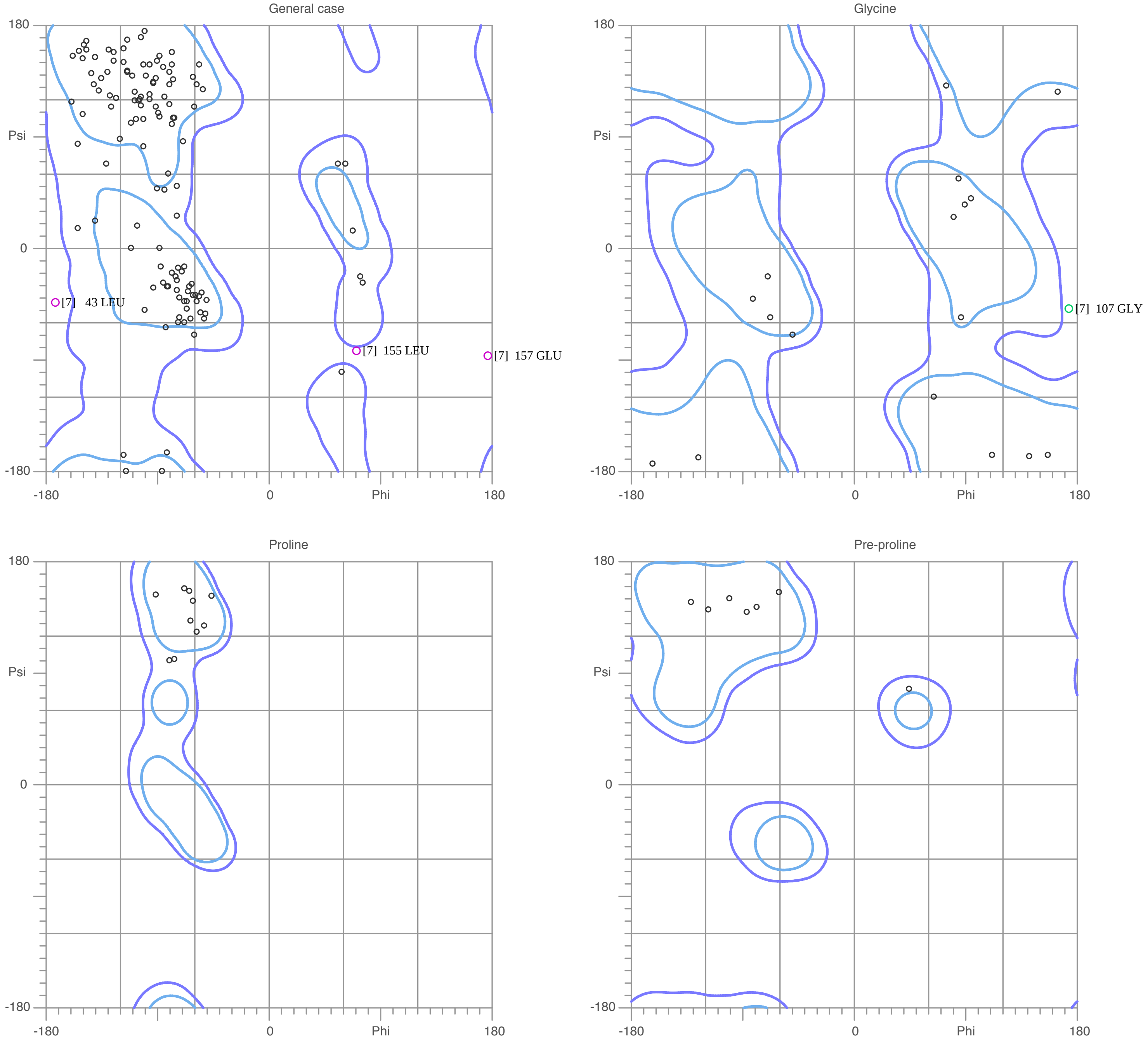
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 7



84.1% (138/164) of all residues were in favored (98%) regions.
97.6% (160/164) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[7] 43 LEU (-173.7, -43.8)
[7] 107 GLY (173.6, -48.7)
[7] 155 LEU (70.7, -82.4)
[7] 157 GLU (176.4, -86.4)

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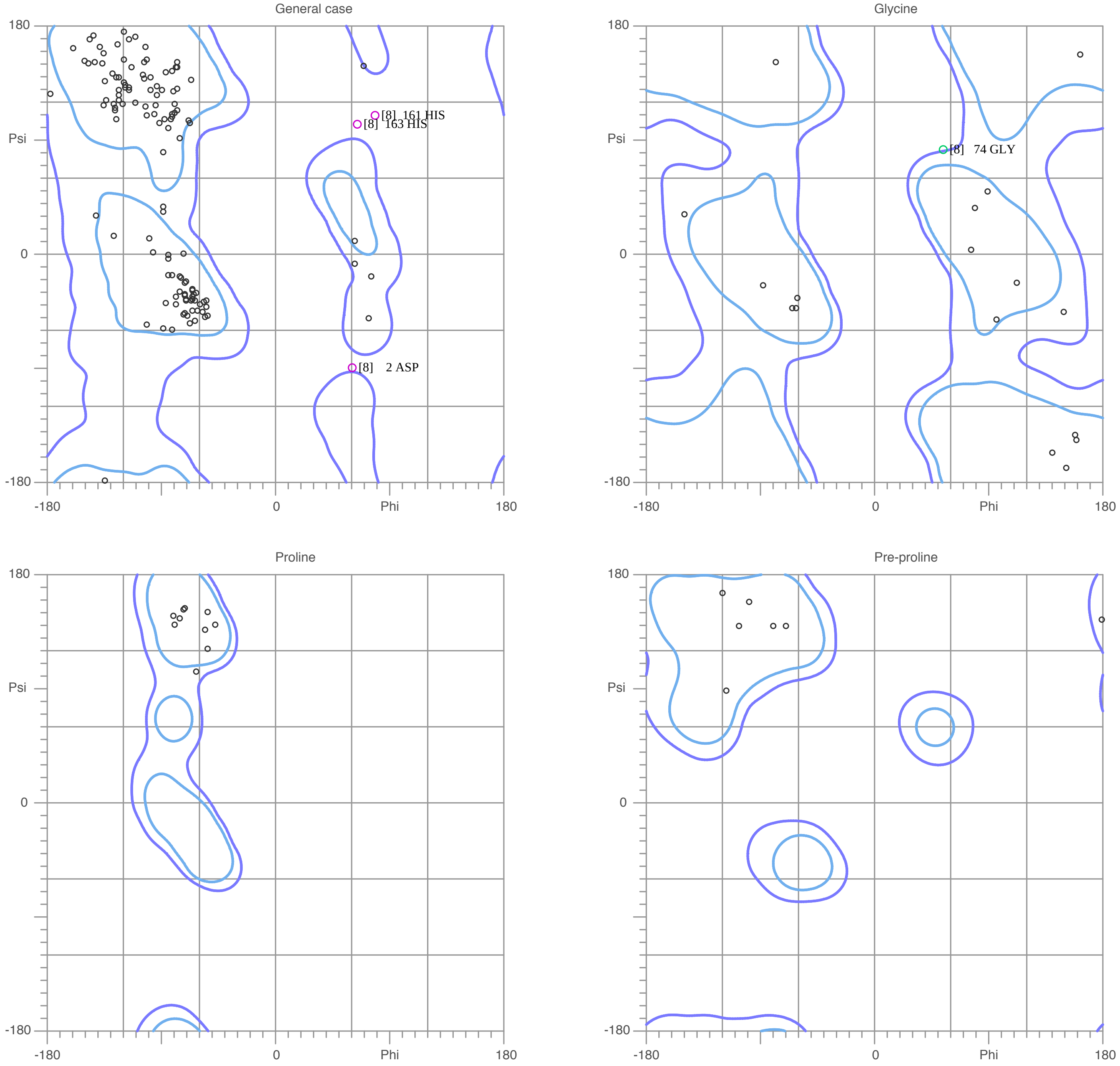
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 8



90.2% (148/164) of all residues were in favored (98%) regions.
97.6% (160/164) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[8] 2 ASP (61.0, -89.4)
[8] 74 GLY (54.7, 83.9)
[8] 161 HIS (78.7, 110.1)
[8] 163 HIS (64.6, 104.0)

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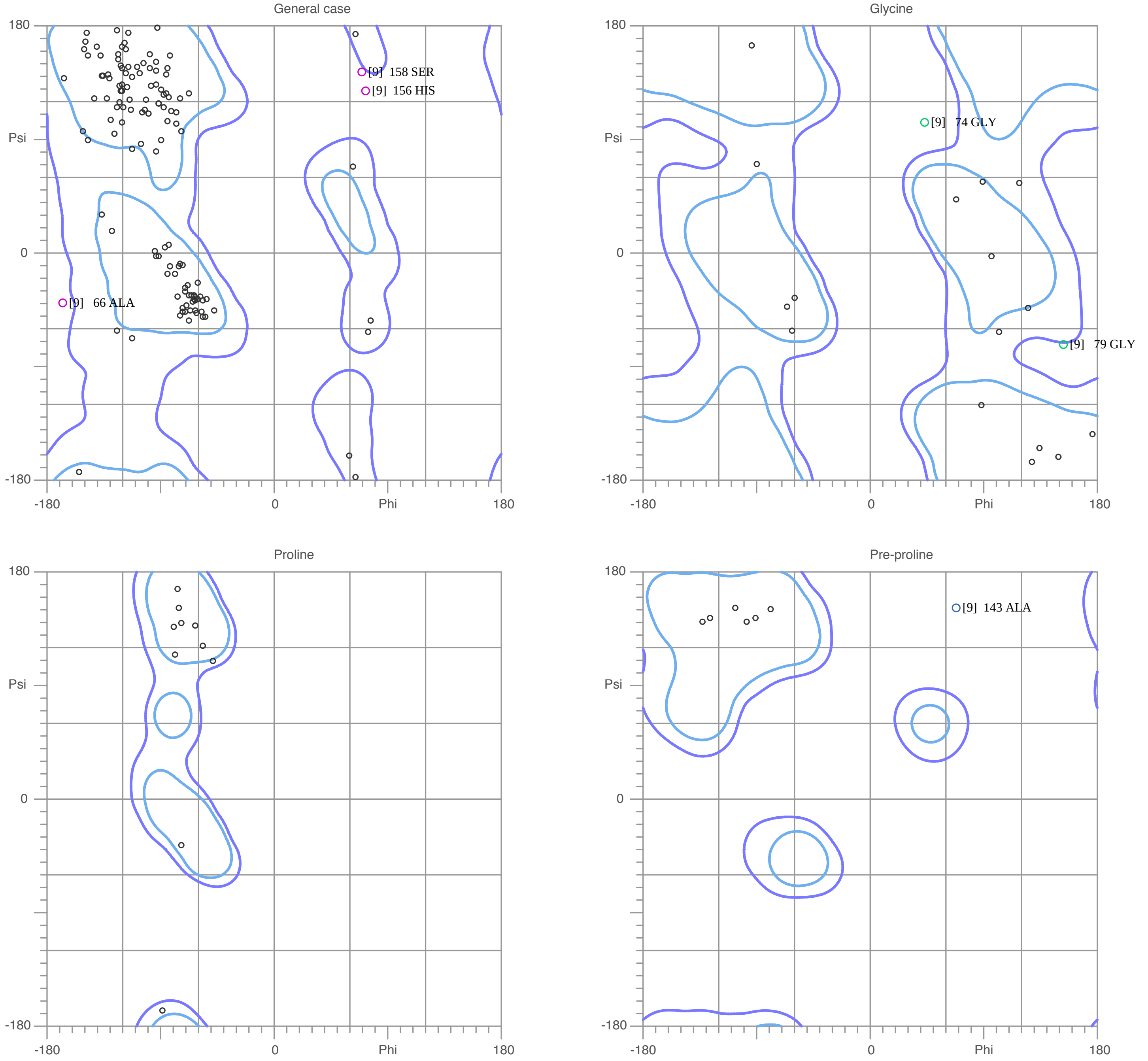
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 9



87.2% (143/164) of all residues were in favored (98%) regions.
96.3% (158/164) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[9] 66 ALA (-168.0, -39.9)
[9] 74 GLY (43.3, 104.2)
[9] 79 GLY (153.9, -72.5)
[9] 143 ALA (68.5, 152.0)
[9] 156 HIS (72.2, 129.6)
[9] 158 SER (69.6, 144.2)

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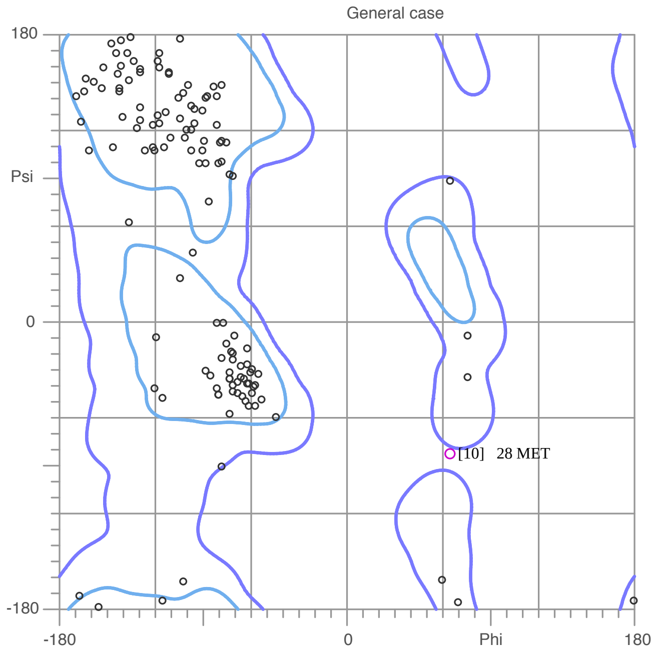
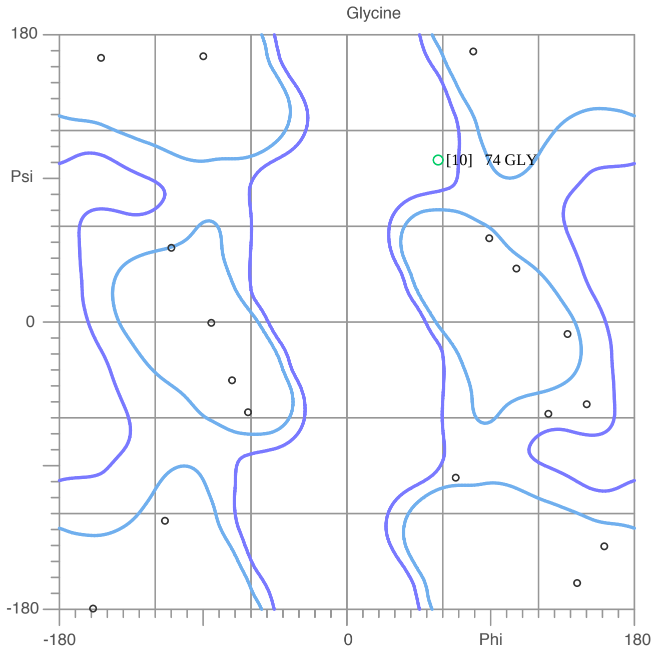
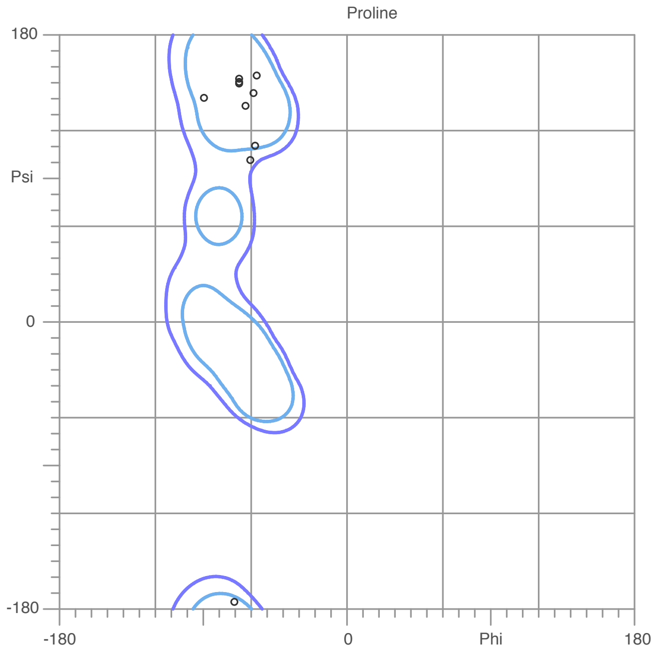
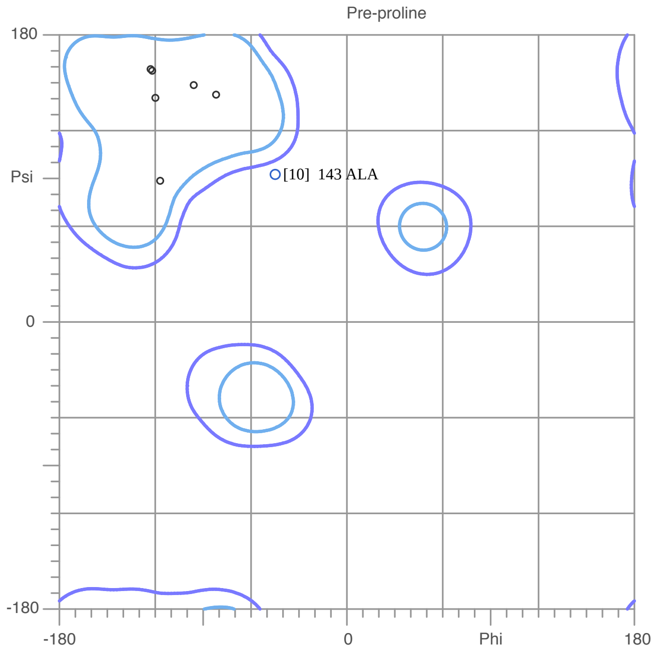
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 10


General case


Glycine


Proline

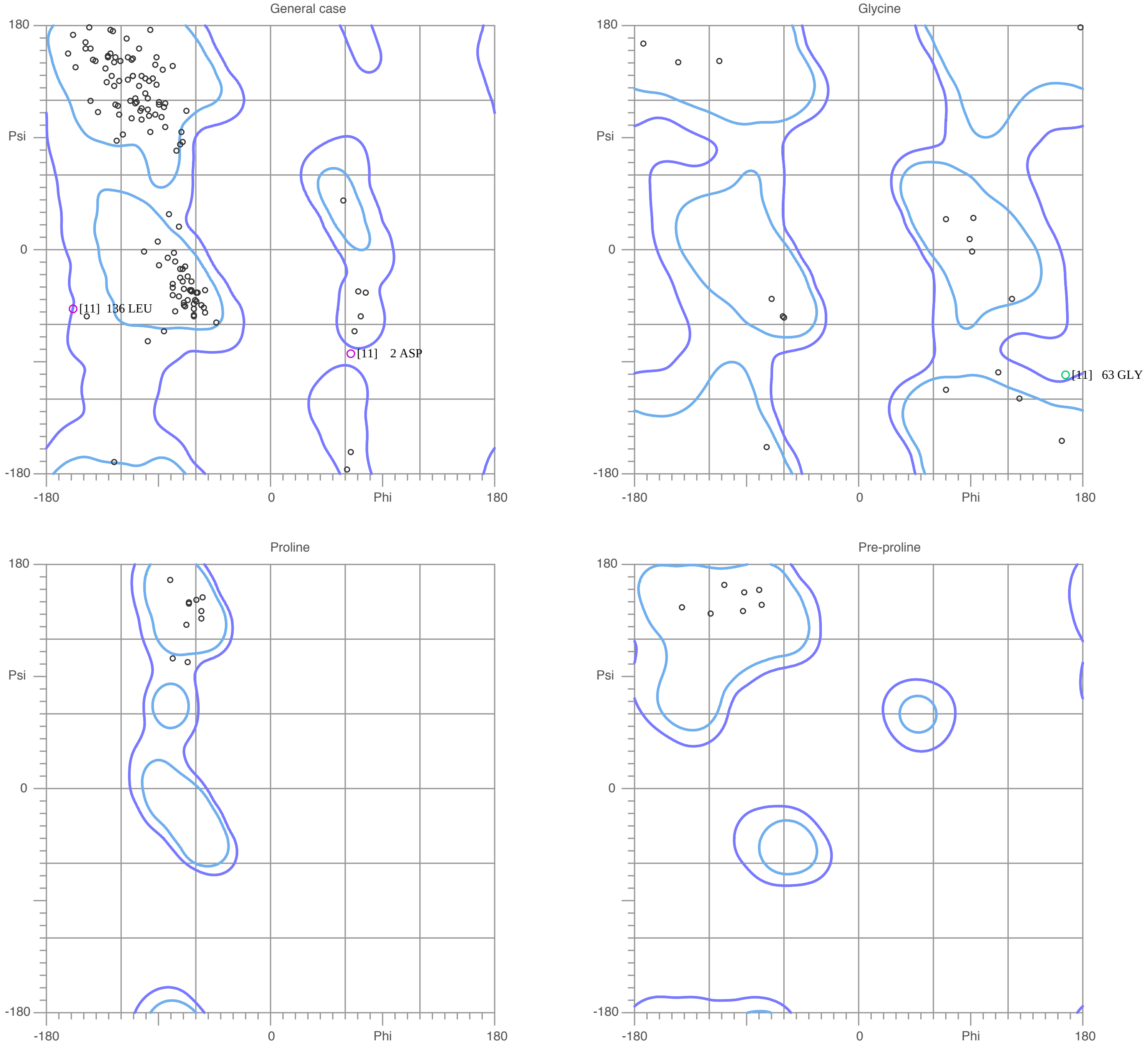

Pre-proline

86.6% (142/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[10] 28 MET (64.9, -82.2)
[10] 74 GLY (57.1, 102.3)
[10] 143 ALA (-45.2, 93.2)

# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 11

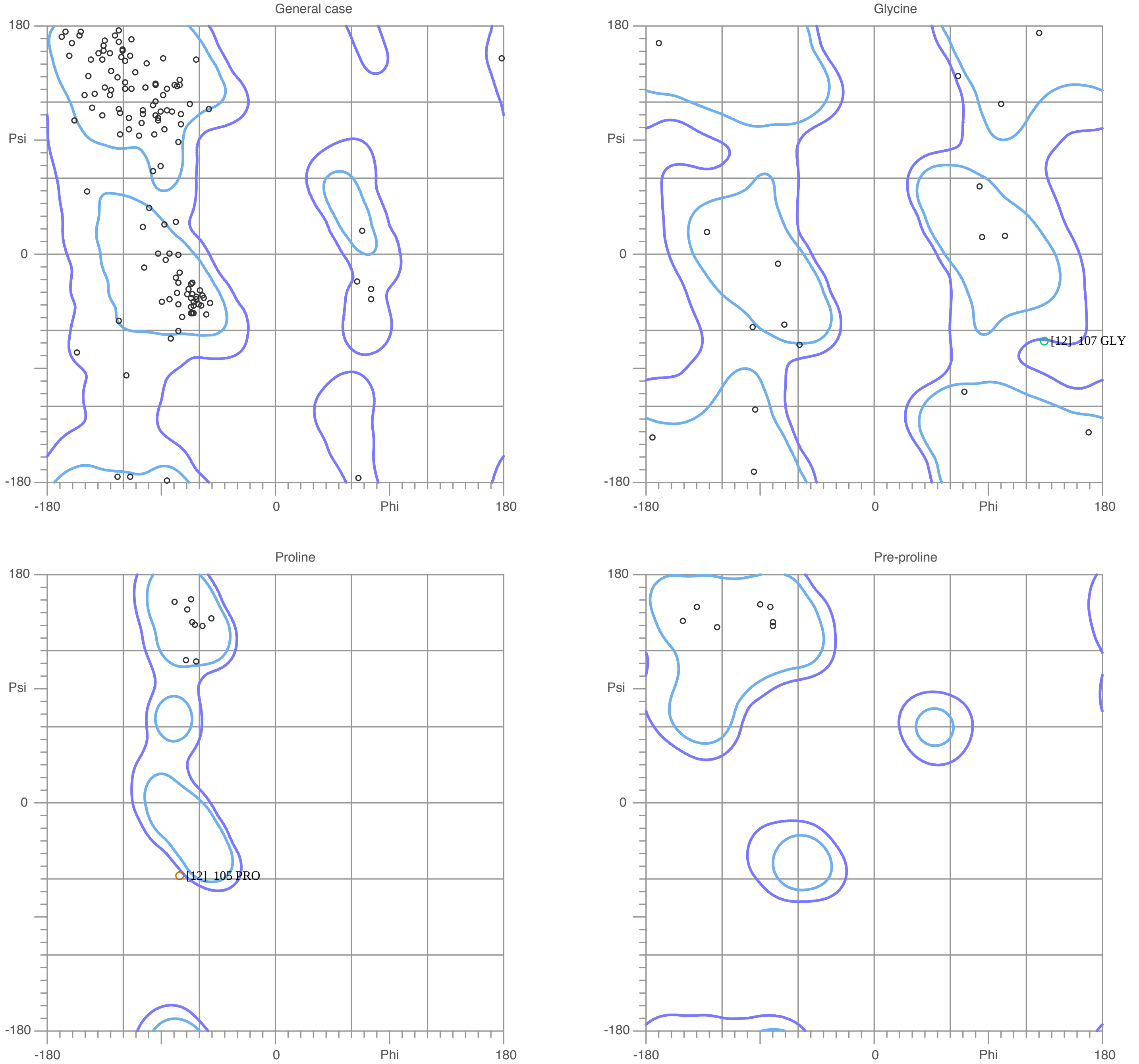


88.4% (145/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[11] 2 ASP (64.7, -83.4)
[11] 63 GLY (166.8, -100.9)
[11] 136 LEU (-159.0, -47.2)

# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 12



89.6% (147/164) of all residues were in favored (98%) regions.
98.8% (162/164) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 105 PRO (-76.9, -57.4)
[12] 107 GLY (134.0, -68.4)

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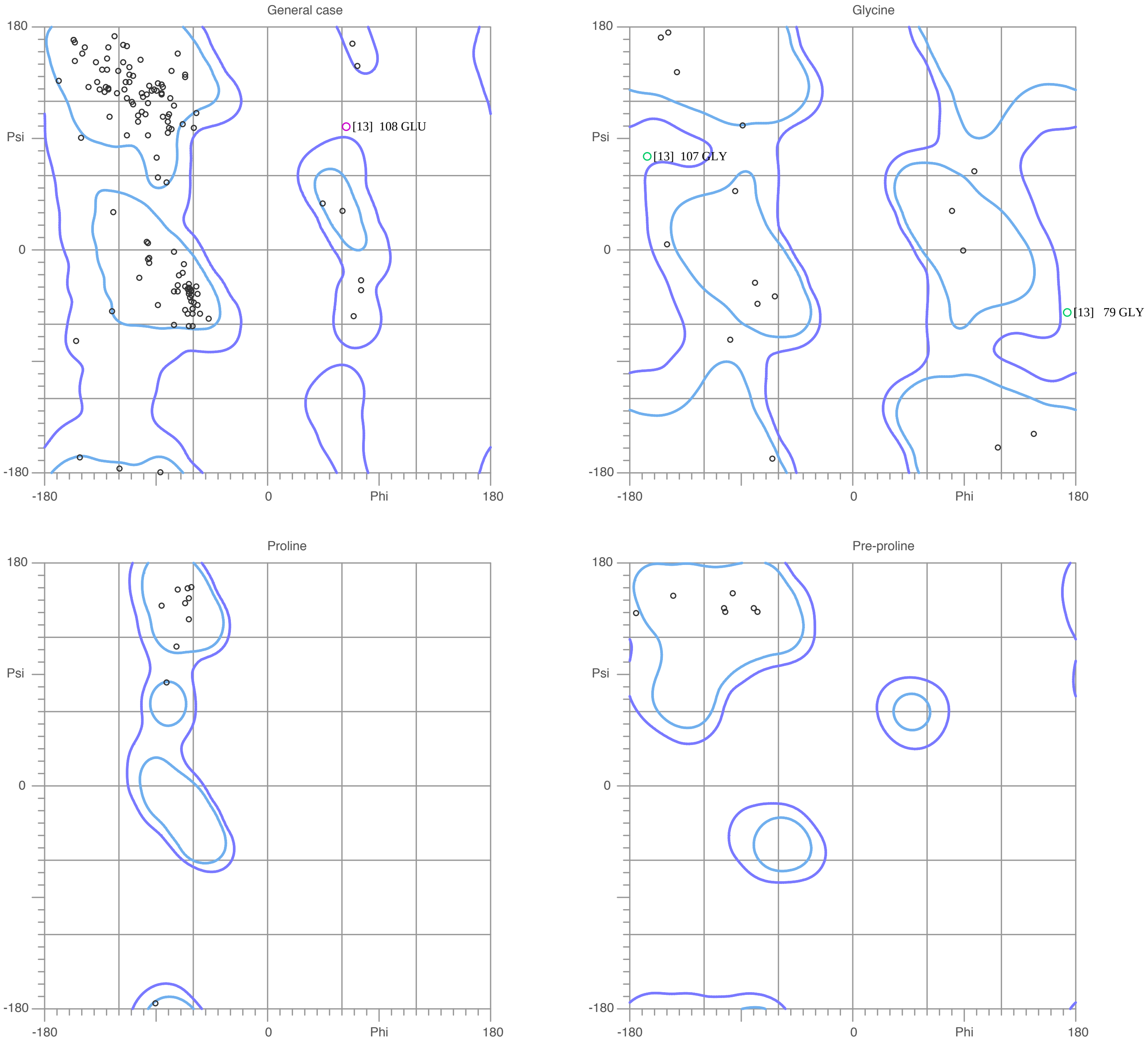
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 13

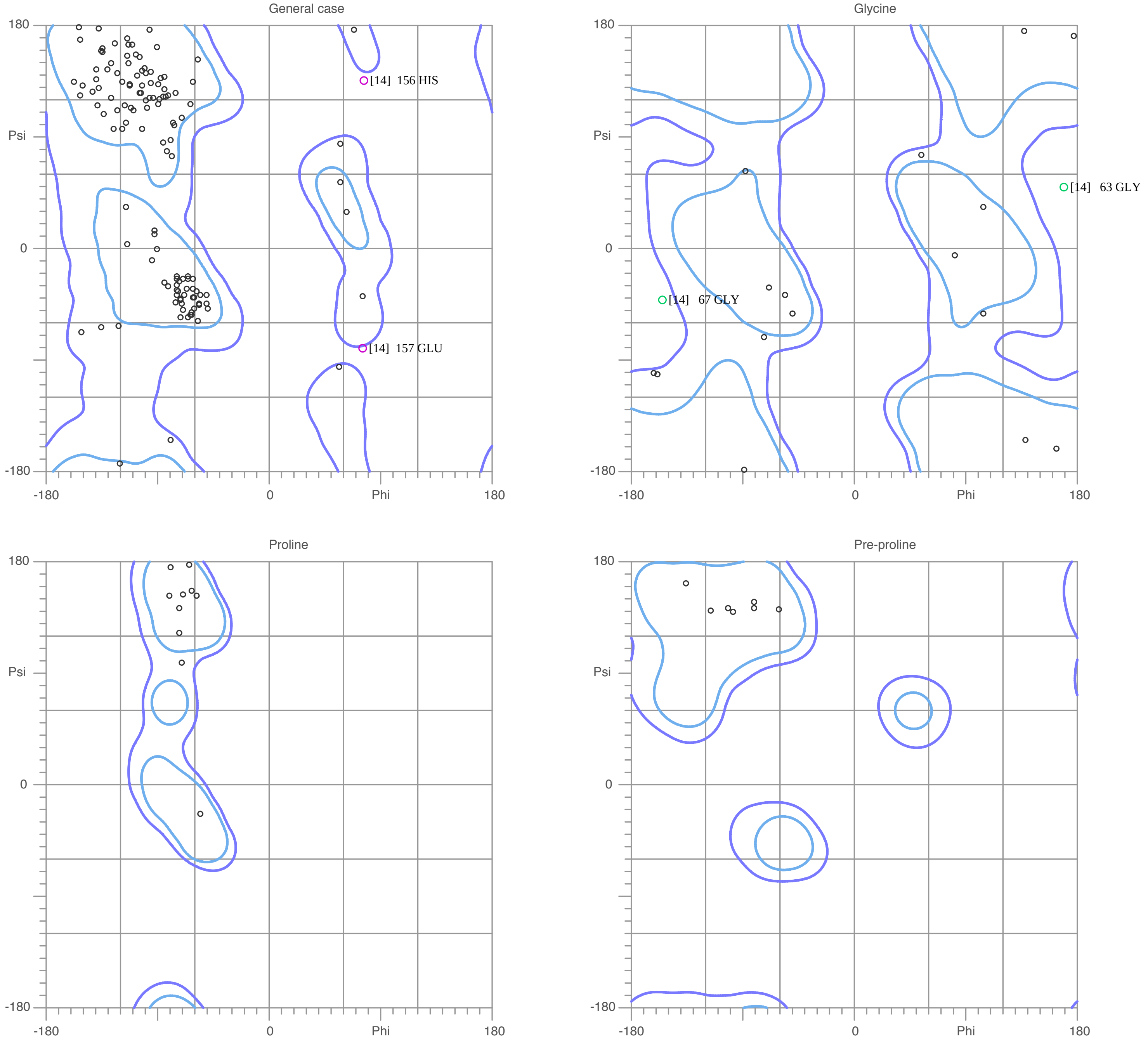


89.6% (147/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[13] 79 GLY (173.8, -50.8)
[13] 107 GLY (-166.1, 76.2)
[13] 108 GLU (63.7, 100.9)

# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 14



88.4% (145/164) of all residues were in favored (98%) regions.
97.6% (160/164) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[14] 63 GLY (169.8, 50.8)
[14] 67 GLY (-155.2, -41.7)
[14] 156 HIS (76.8, 136.9)
[14] 157 GLU (75.1, -80.4)

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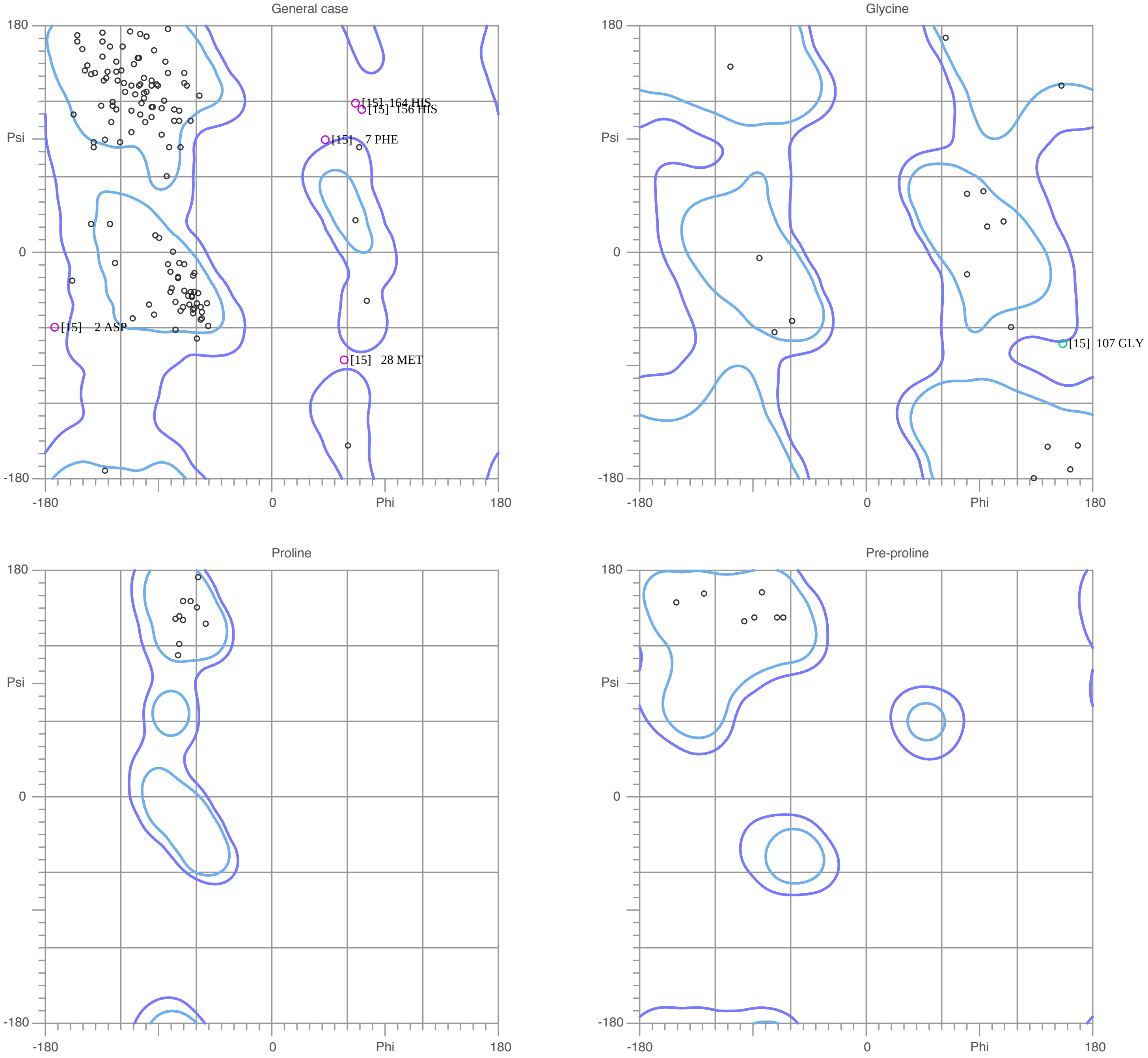
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 15



89.6% (147/164) of all residues were in favored (98%) regions.
96.3% (158/164) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[15] 2 ASP (-173.4, -59.5)
[15] 7 PHE (42.8, 90.5)
[15] 28 MET (57.0, -85.6)
[15] 107 GLY (156.9, -72.6)
[15] 156 HIS (71.2, 114.7)
[15] 164 HIS (66.1, 119.6)

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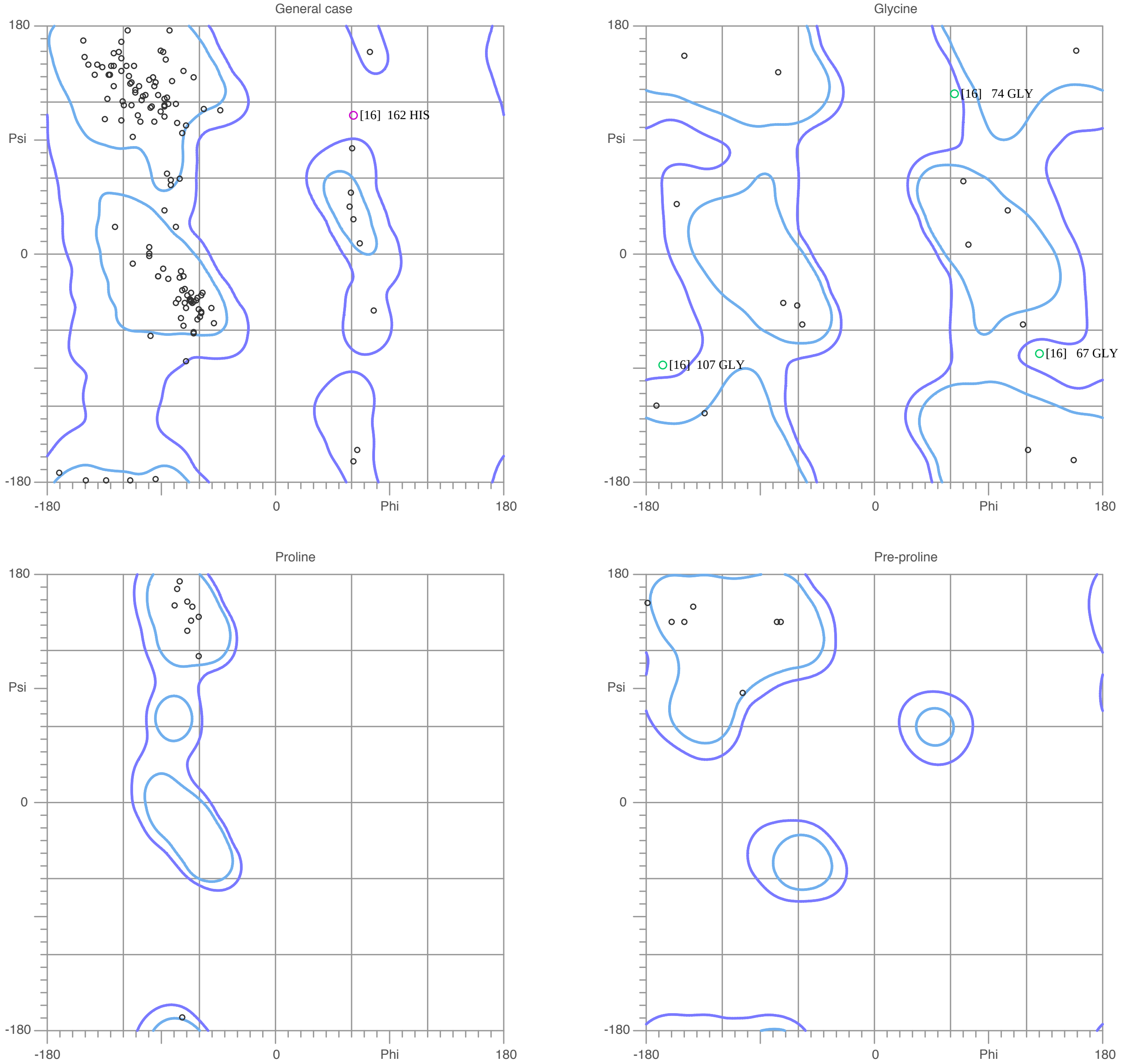
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 16



87.8% (144/164) of all residues were in favored (98%) regions.
97.6% (160/164) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[16] 67 GLY (130.1, -78.8)
[16] 74 GLY (63.9, 127.2)
[16] 107 GLY (-167.0, -87.2)
[16] 162 HIS (61.9, 110.6)

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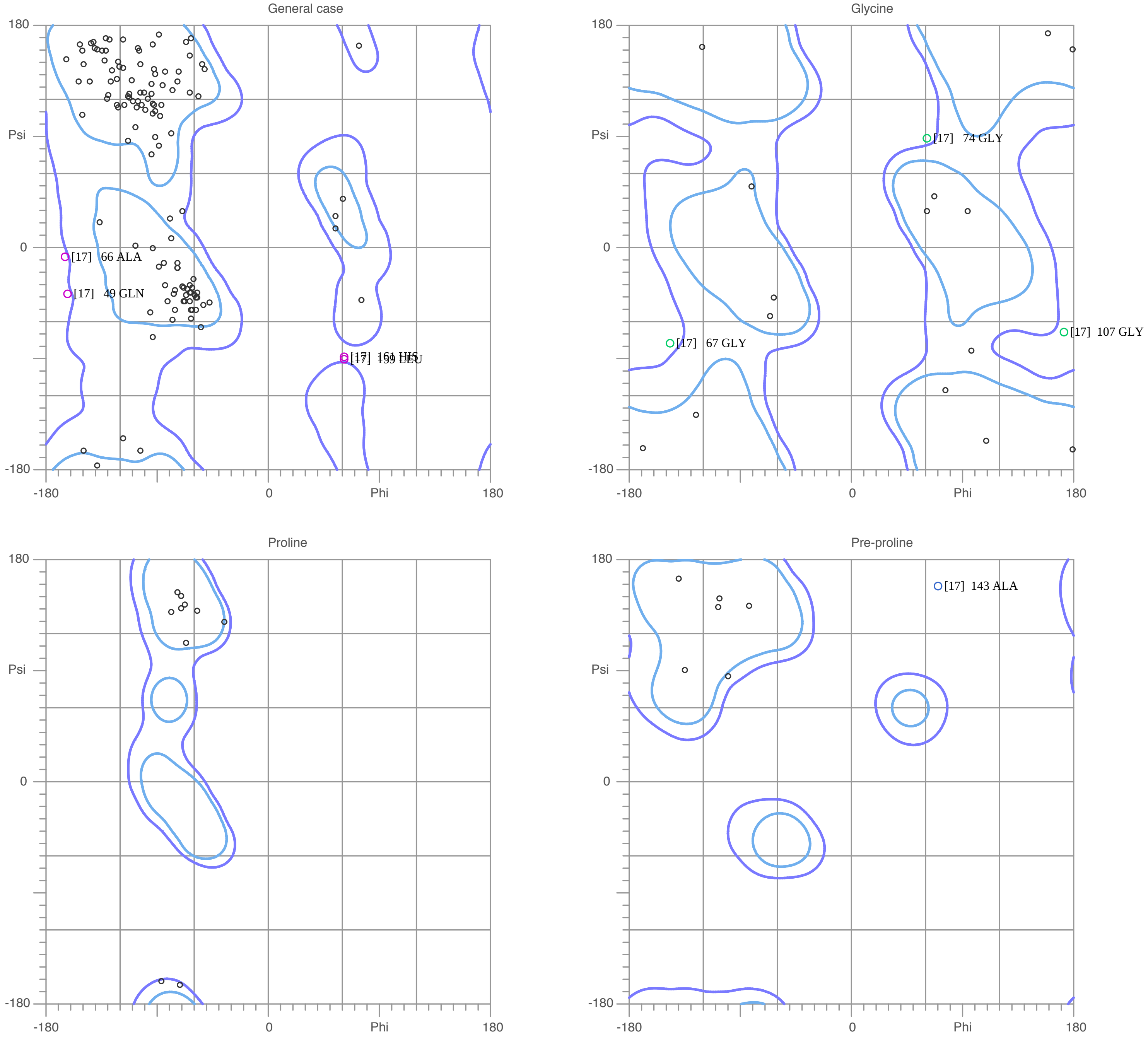
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 17



87.2% (143/164) of all residues were in favored (98%) regions.
95.1% (156/164) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):
[17] 49 GLN (-163.6, -37.8)
[17] 66 ALA (-165.8, -7.9)
[17] 67 GLY (-147.5, -77.9)
[17] 74 GLY (61.4, 89.9)
[17] 107 GLY (172.9, -69.0)
[17] 143 ALA (70.5, 159.8)
[17] 159 LEU (61.3, -90.8)
[17] 161 HIS (61.1, -88.6)

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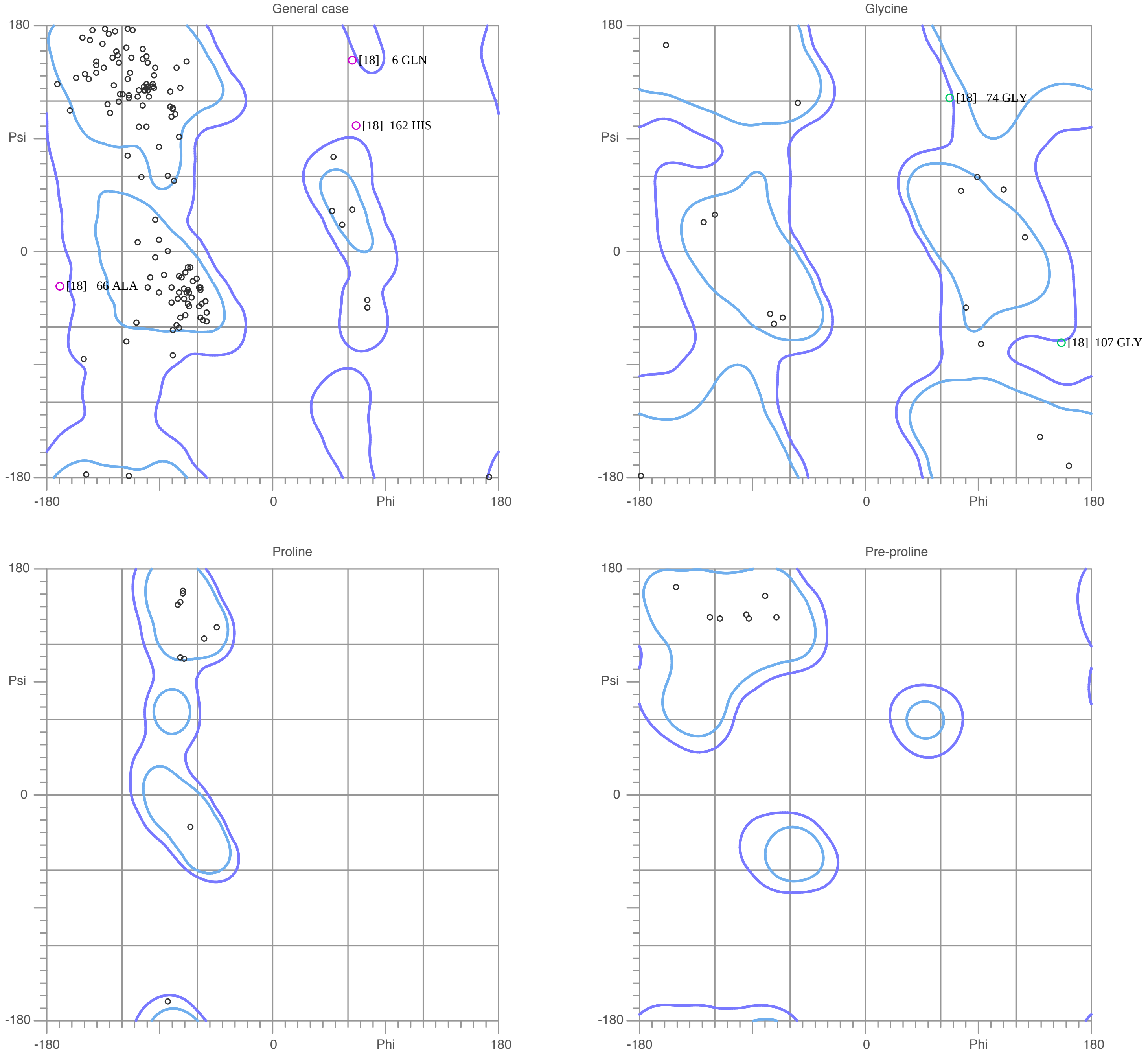
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 18



87.8% (144/164) of all residues were in favored (98%) regions.
97.0% (159/164) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[18] 6 GLN (63.5, 153.8)
[18] 66 ALA (-170.4, -27.7)
[18] 74 GLY (67.4, 123.7)
[18] 107 GLY (157.0, -72.6)
[18] 162 HIS (66.1, 101.5)

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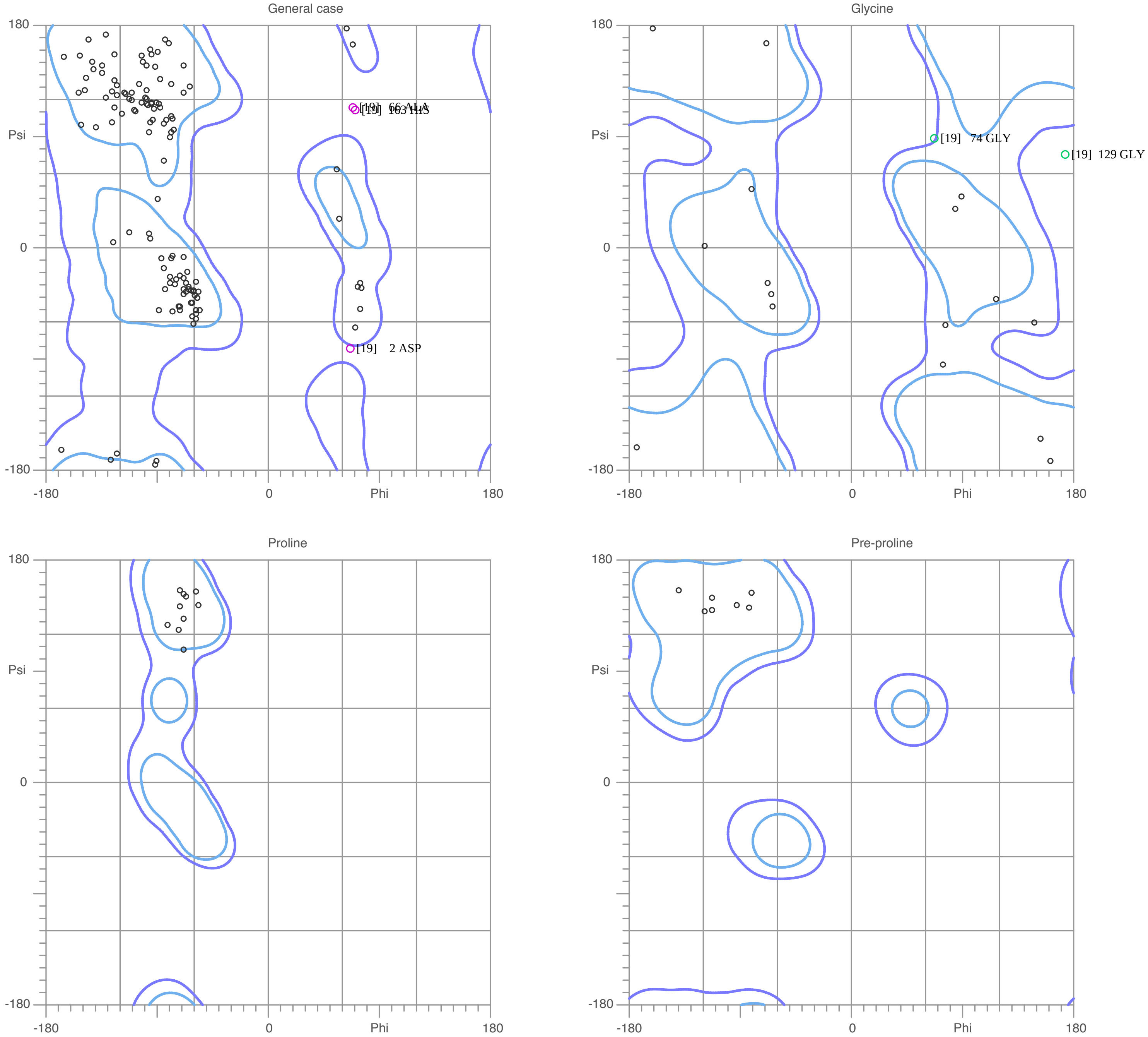
Lovell, Davis, et al. Proteins 50:437 (2003)

# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 19



88.4% (145/164) of all residues were in favored (98%) regions.
97.0% (159/164) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[19] 2 ASP (66.6, -81.1)
[19] 66 ALA (68.8, 114.1)
[19] 74 GLY (67.0, 89.4)
[19] 129 GLY (173.0, 76.3)
[19] 163 HIS (70.9, 112.0)

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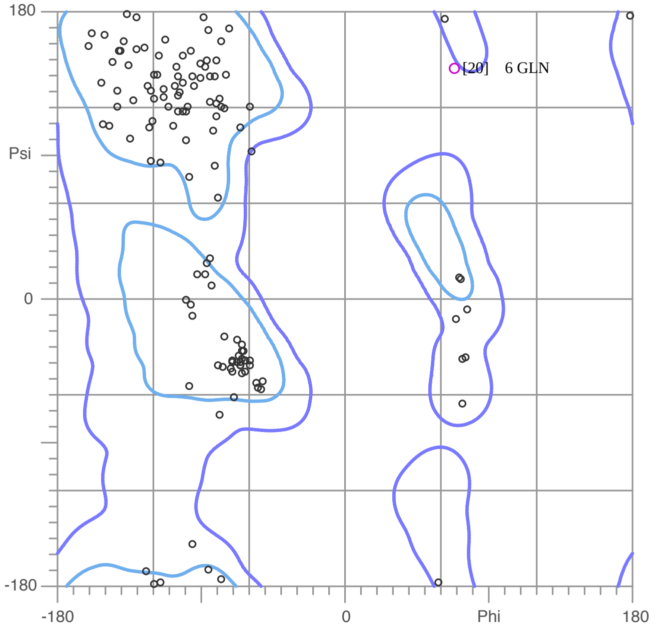
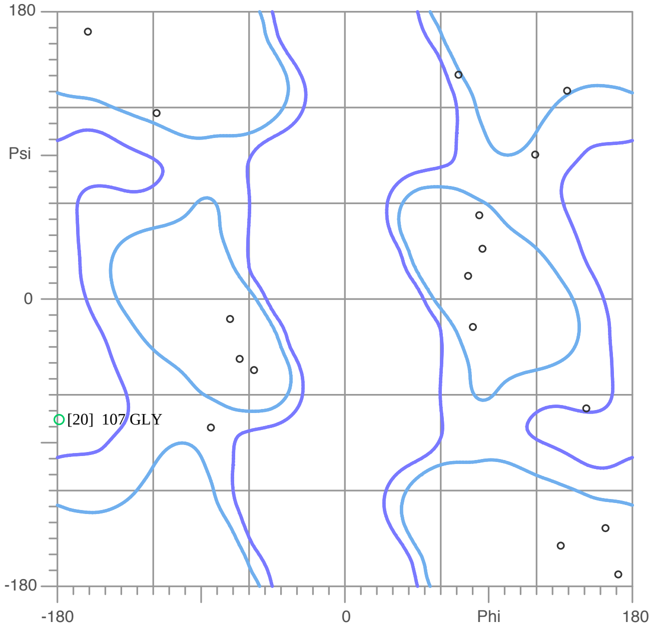
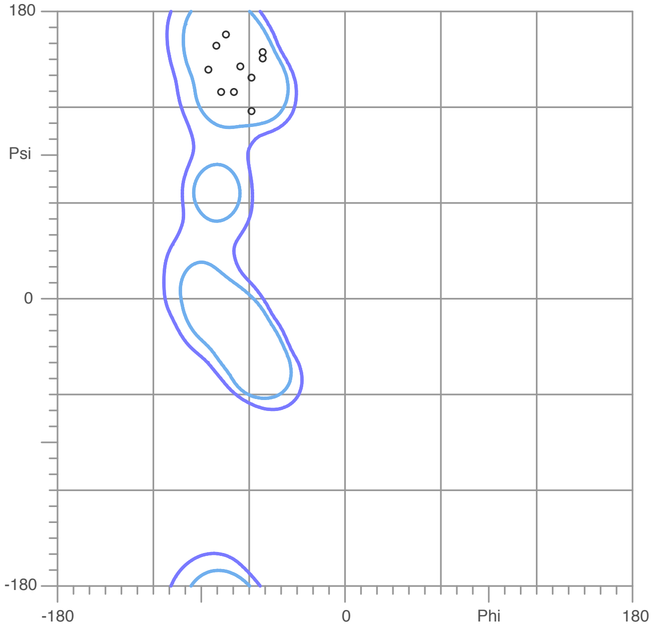
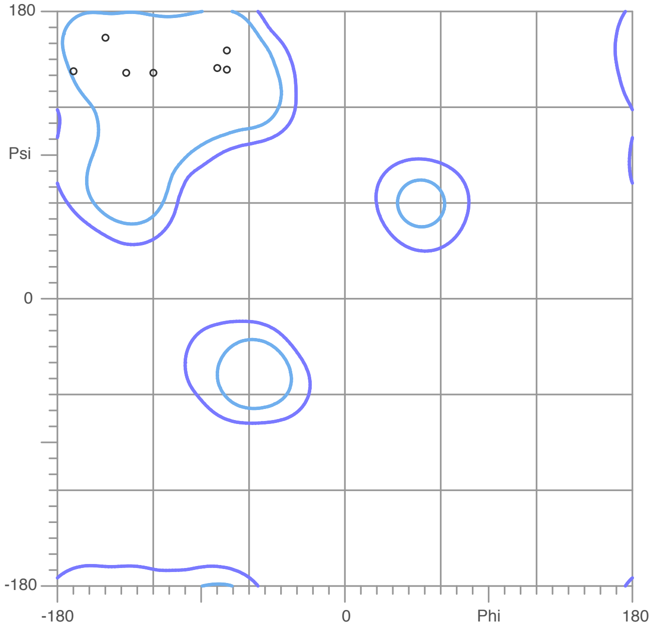
# MolProbity Ramachandran analysis

CTR107_NMR_em_bcr3.pdb, model 20


General case


Glycine


Proline


Pre-proline

88.4% (145/164) of all residues were in favored (98%) regions.
98.8% (162/164) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[20] 6 GLN (69.0, 145.5)
[20] 107 GLY (-179.9, -75.4)

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