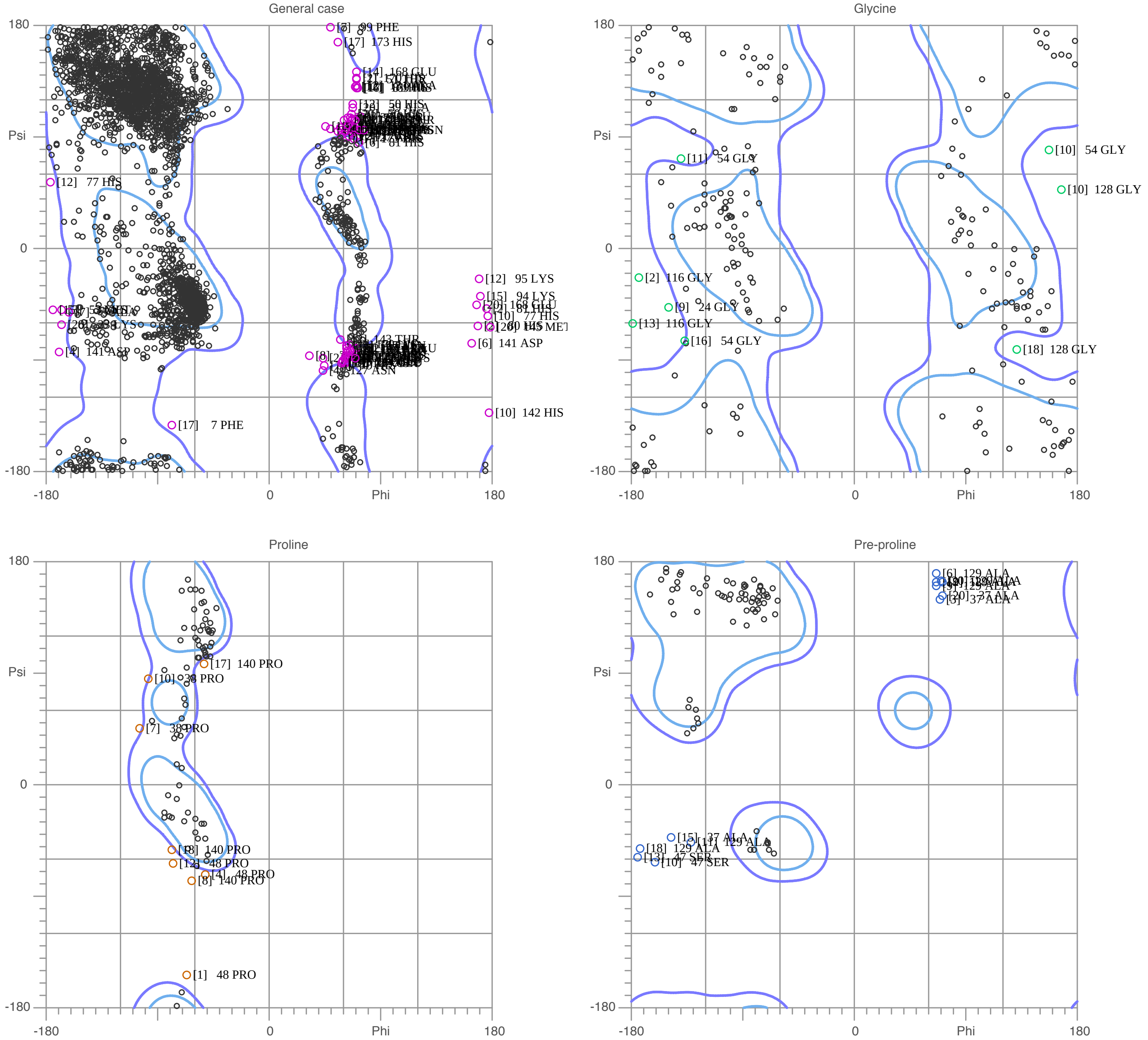
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, all models



83.7% (2679/3200) of all residues were in favored (98%) regions.
96.6% (3090/3200) of all residues were in allowed (>99.8%) regions.

There were 110 outliers (phi, psi):
[1] 22 GLU (61.5, -91.5)
[1] 48 PRO (-67.7, -153.6)
[1] 51 THR (70.9, 137.7)
[1] 127 ASN (62.1, 90.9)
[2] 6 GLU (66.7, 100.4)
[2] 22 GLU (43.0, -88.1)
[2] 80 HIS (168.9, -62.9)
[2] 81 HIS (175.7, -48.7)
[2] 116 GLY (-174.5, -23.0)
[2] 129 ALA (71.4, 164.5)
[2] 170 HIS (70.8, 138.0)
[3] 3 LYS (-168.5, -49.0)
[3] 37 ALA (69.4, 150.2)
[3] 39 ALA (65.3, 106.1)
[3] 76 GLU (73.1, 107.9)
[3] 97 ALA (70.5, -80.5)
[3] 127 ASN (61.0, -92.2)
[3] 171 HIS (60.9, 105.0)
[3] 173 HIS (66.0, -87.6)
[4] 48 PRO (-52.7, -72.1)
[4] 127 ASN (43.9, -98.3)
[4] 141 ASP (-170.4, -83.4)
[5] 23 LYS (58.6, 96.7)
[6] 22 GLU (63.1, -87.0)
[6] 39 ALA (67.1, 105.2)
[6] 81 HIS (73.0, 86.6)
[6] 129 ALA (66.6, 171.6)
[6] 141 ASP (163.3, -76.5)
[6] 144 LYS (68.4, -80.8)
[7] 5 ALA (-162.7, -51.7)
[7] 38 PRO (-105.0, 46.6)
[7] 99 PHE (49.2, 179.5)
[7] 141 ASP (58.9, 92.1)
[7] 142 HIS (66.3, 104.6)
[7] 173 HIS (68.9, 89.5)
[8] 35 ASN (32.0, -86.5)
[8] 140 PRO (-63.5, -77.6)
[8] 170 HIS (64.4, -77.9)
[9] 5 ALA (65.2, -82.2)
[9] 24 GLY (-150.8, -47.5)
[9] 129 ALA (66.8, 161.9)
[10] 38 PRO (-98.9, 86.8)
[10] 47 SER (-161.6, -62.2)
[10] 51 THR (49.3, 97.5)
[10] 54 GLY (157.7, 80.6)
[10] 55 LYS (69.8, 96.8)
[10] 76 GLU (61.6, -87.3)
[10] 77 HIS (176.0, -54.1)
[10] 79 HIS (44.2, -94.9)
[10] 115 LYS (55.4, 95.8)
[10] 128 GLY (167.1, 48.3)
[10] 141 ASP (62.9, -88.1)
[10] 142 HIS (177.3, -132.3)
[10] 170 HIS (62.2, -84.1)
[11] 6 GLU (62.8, -78.5)
[11] 22 GLU (61.4, -89.3)
[11] 54 GLY (-140.3, 73.2)
[11] 96 MET (57.9, 98.1)
[11] 99 PHE (67.1, 97.9)
[11] 115 LYS (62.2, 98.8)
[11] 129 ALA (-132.4, -46.5)
[12] 7 PHE (69.9, 131.9)
[12] 23 LYS (61.4, 95.6)
[12] 48 PRO (-78.5, -63.5)
[12] 50 HIS (67.8, 117.3)
[12] 77 HIS (-177.1, 55.0)
[12] 94 LYS (66.1, -86.5)
[12] 95 LYS (169.3, -24.5)
[12] 114 GLU (70.7, -80.2)
[12] 127 ASN (62.9, -80.6)
[12] 131 ALA (70.3, 133.0)
[12] 143 THR (57.8, -73.2)
[12] 170 HIS (64.9, 91.3)
[12] 171 HIS (72.0, 96.2)
[13] 47 SER (-175.9, -58.9)
[13] 116 GLY (-179.6, -60.5)
[13] 127 ASN (62.1, -78.8)
[13] 166 ASN (76.9, 97.0)
[14] 35 ASN (65.5, -82.4)
[14] 114 GLU (59.3, -91.3)
[14] 168 GLU (70.3, 143.1)
[14] 171 HIS (68.1, 98.0)
[15] 37 ALA (-148.6, -42.5)
[15] 53 MET (-175.9, -49.2)
[15] 94 LYS (170.5, -38.3)
[15] 114 GLU (58.2, -92.3)
[15] 127 ASN (63.3, -82.0)
[15] 141 ASP (59.7, -90.0)
[16] 23 LYS (63.0, 106.0)
[16] 52 LYS (69.6, -88.4)
[16] 54 GLY (-137.7, -74.8)
[16] 81 HIS (70.8, 130.4)
[17] 7 PHE (-79.7, -142.3)
[17] 140 PRO (-53.0, 98.4)
[17] 169 HIS (71.2, 130.6)
[17] 173 HIS (55.0, 167.6)
[18] 128 GLY (131.3, -81.5)
[18] 129 ALA (-174.0, -51.8)
[18] 140 PRO (-79.5, -52.2)
[18] 143 THR (45.4, 99.3)
[19] 79 HIS (63.5, 100.2)
[19] 129 ALA (66.8, 165.0)
[20] 23 LYS (-169.0, -61.3)
[20] 37 ALA (71.0, 153.1)
[20] 39 ALA (67.8, 114.4)
[20] 50 HIS (66.4, 110.0)
[20] 129 ALA (70.7, 166.0)
[20] 143 THR (69.6, 104.8)
[20] 145 MET (178.4, -63.1)
[20] 168 GLU (167.6, -45.4)

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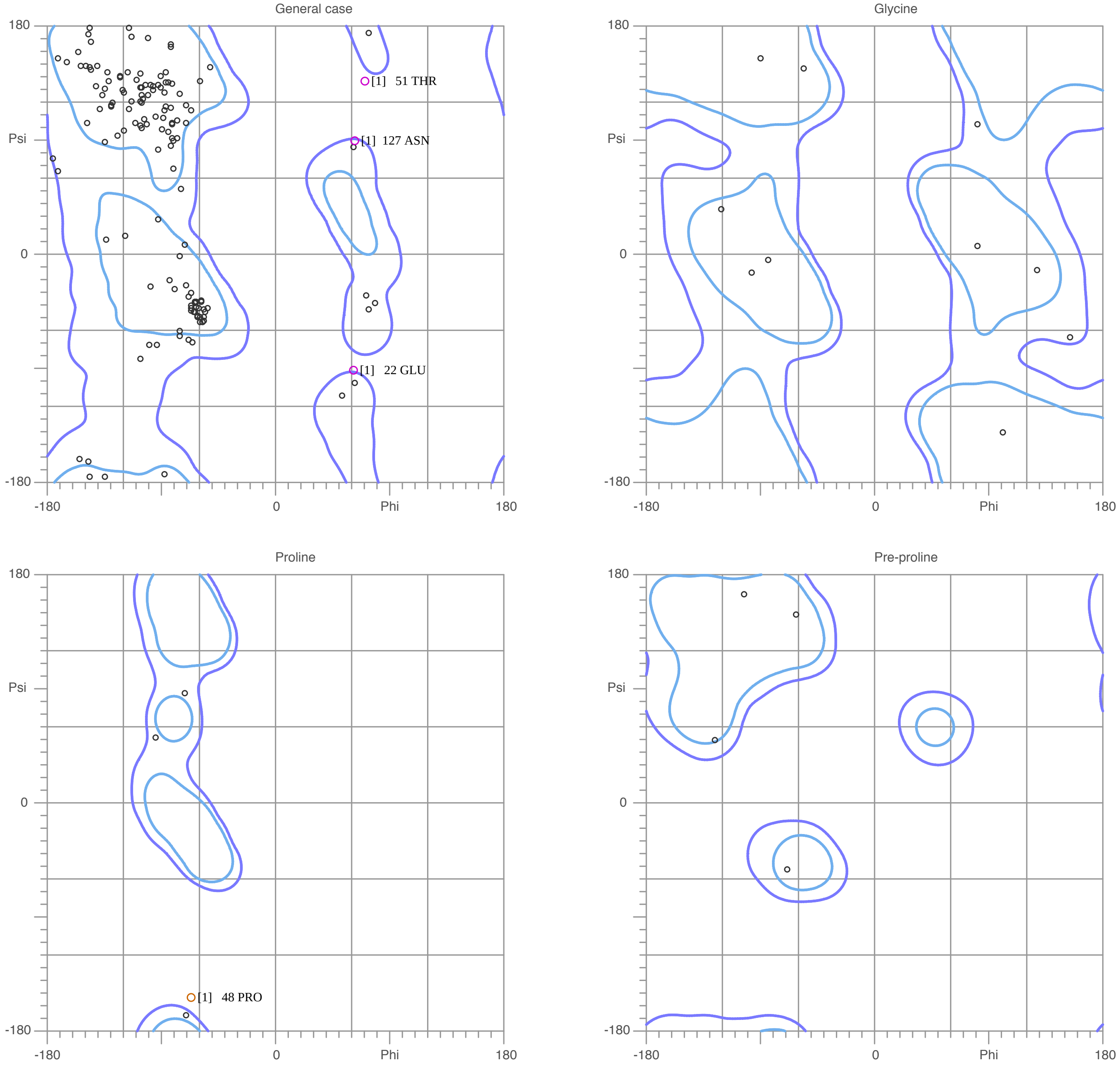
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 1



83.1% (133/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[1] 22 GLU (61.5, -91.5)
[1] 48 PRO (-67.7, -153.6)
[1] 51 THR (70.9, 137.7)
[1] 127 ASN (62.1, 90.9)

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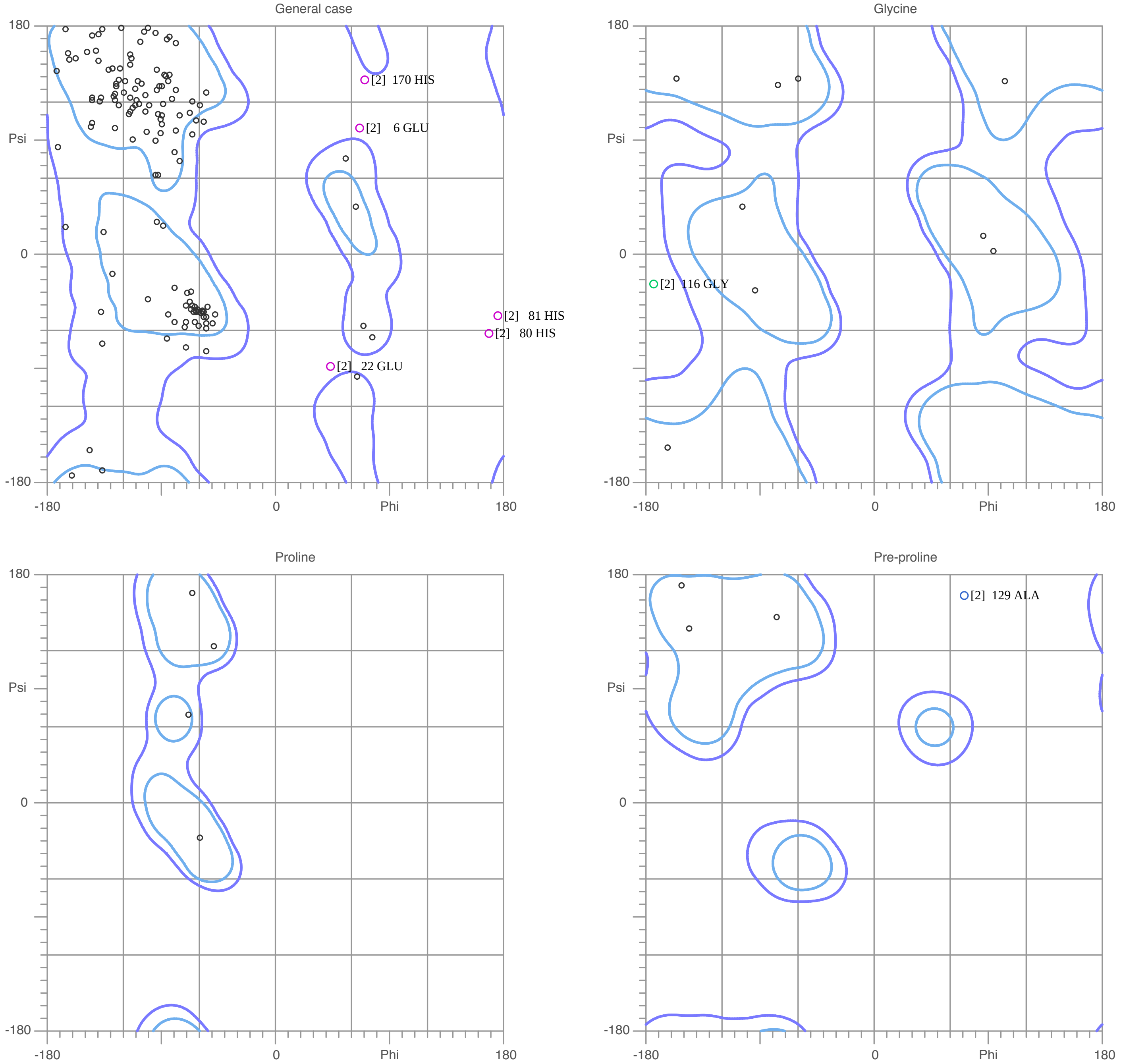
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 2



85.6% (137/160) of all residues were in favored (98%) regions.
95.6% (153/160) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[2] 6 GLU (66.7, 100.4)
[2] 22 GLU (43.0, -88.1)
[2] 80 HIS (168.9, -62.9)
[2] 81 HIS (175.7, -48.7)
[2] 116 GLY (-174.5, -23.0)
[2] 129 ALA (71.4, 164.5)
[2] 170 HIS (70.8, 138.0)

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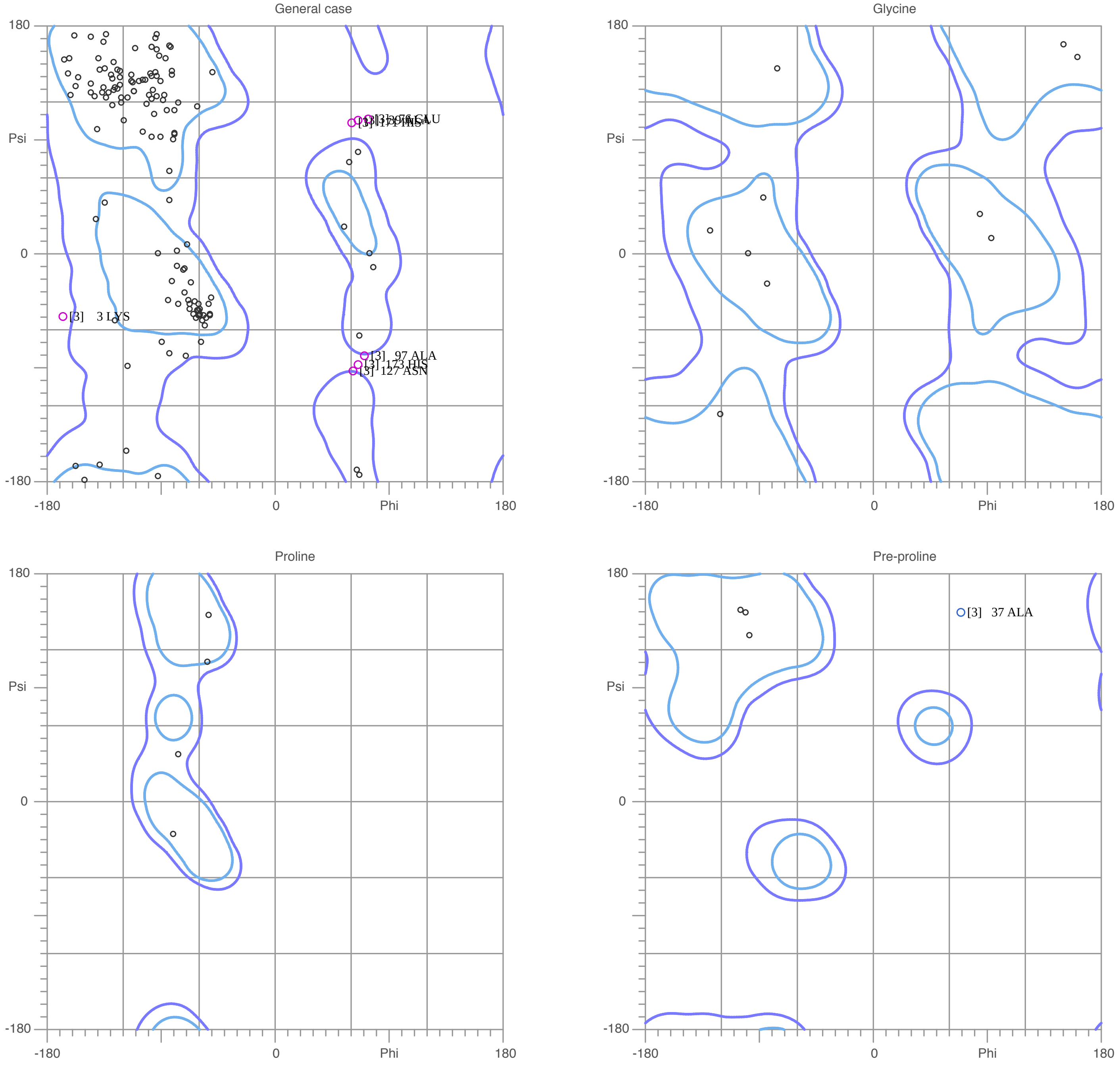
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 3



83.1% (133/160) of all residues were in favored (98%) regions.
95.0% (152/160) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[3] 3 LYS (-168.5, -49.0)
[3] 37 ALA (69.4, 150.2)
[3] 39 ALA (65.3, 106.1)
[3] 76 GLU (73.1, 107.9)
[3] 97 ALA (70.5, -80.5)
[3] 127 ASN (61.0, -92.2)
[3] 171 HIS (60.9, 105.0)
[3] 173 HIS (66.0, -87.6)

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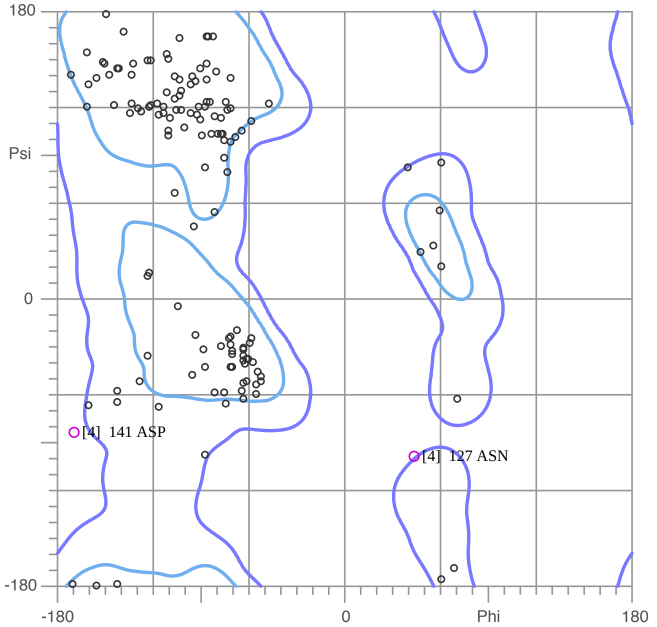
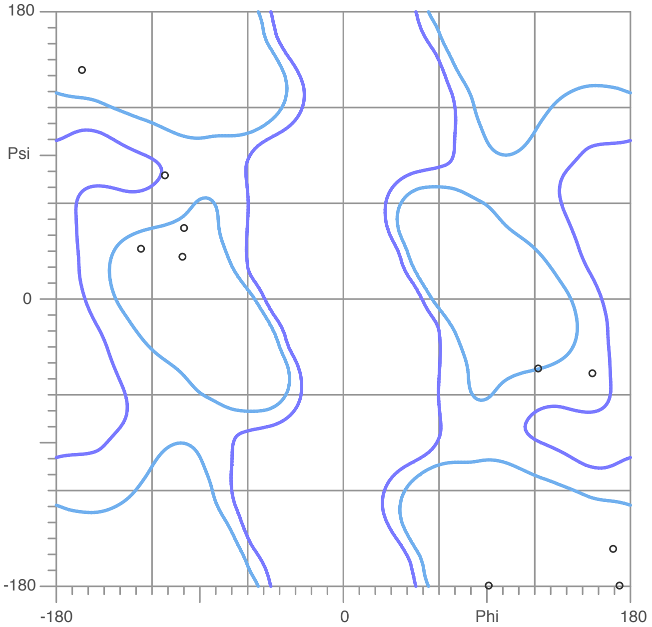
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 4

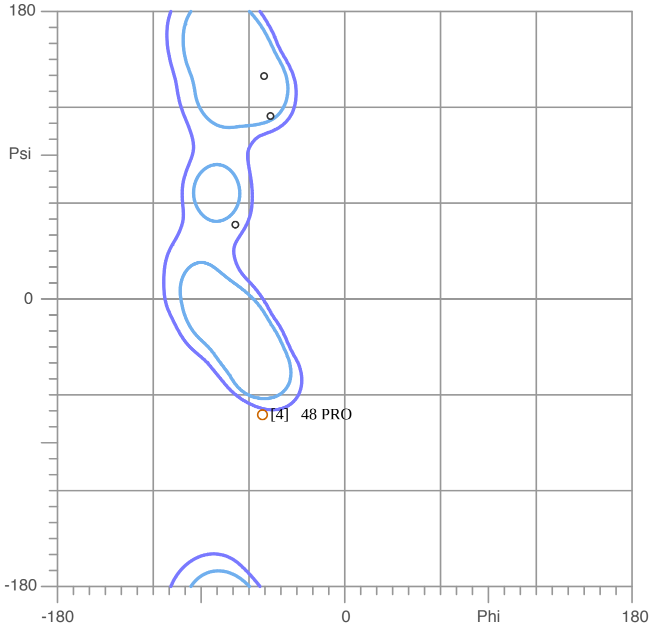
General case



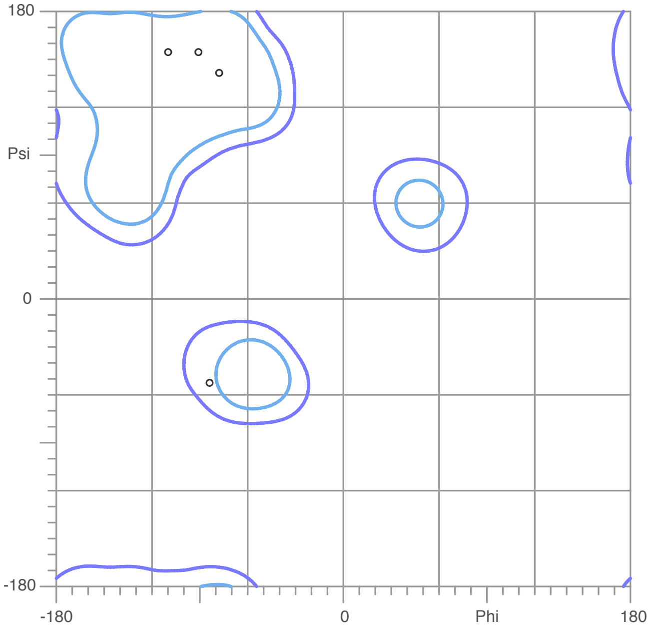
Glycine



Proline



Pre-proline



86.9% (139/160) of all residues were in favored (98%) regions.
98.1% (157/160) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[4] 48 PRO (-52.7, -72.1)
[4] 127 ASN (43.9, -98.3)
[4] 141 ASP (-170.4, -83.4)

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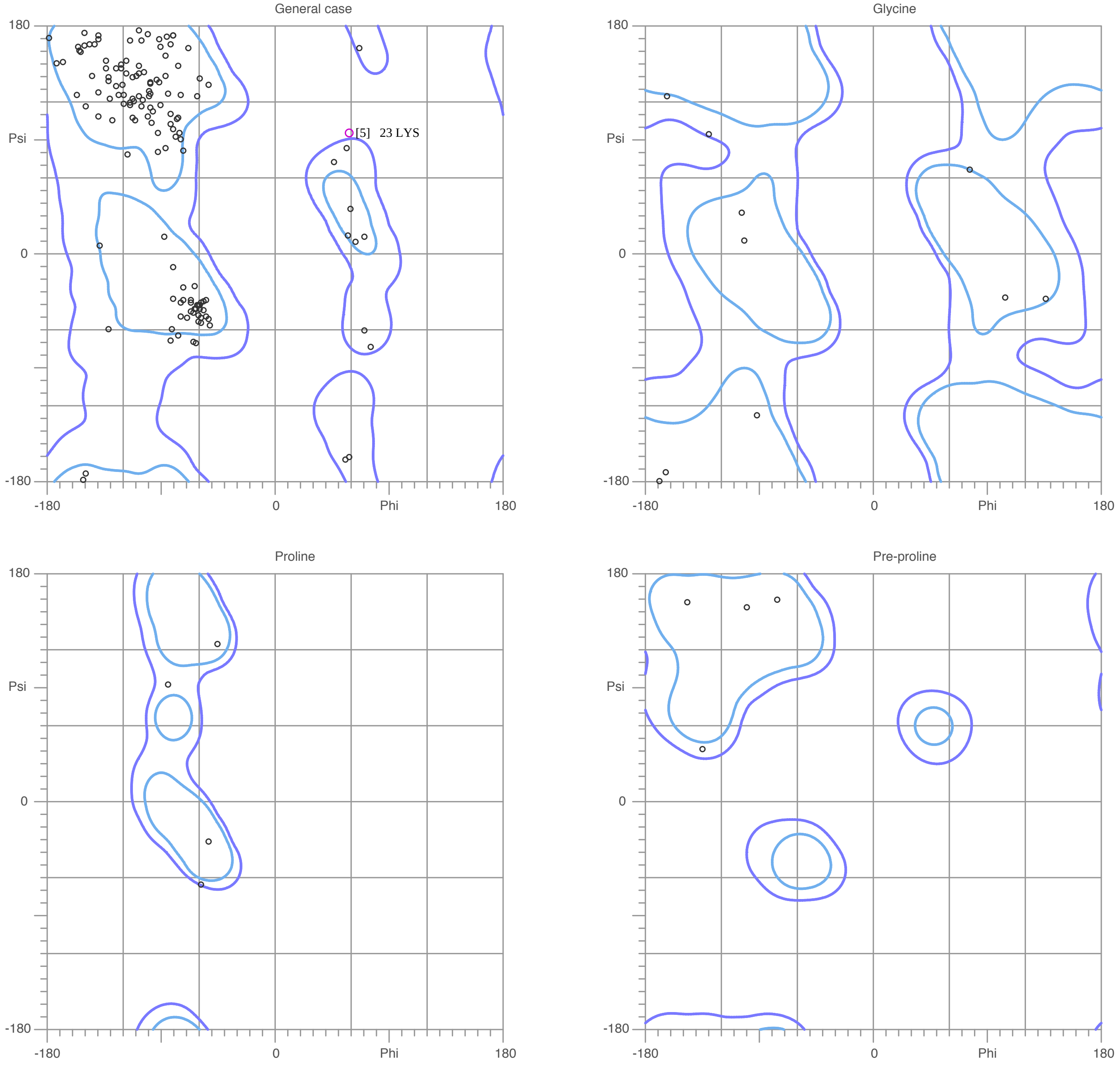
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 5

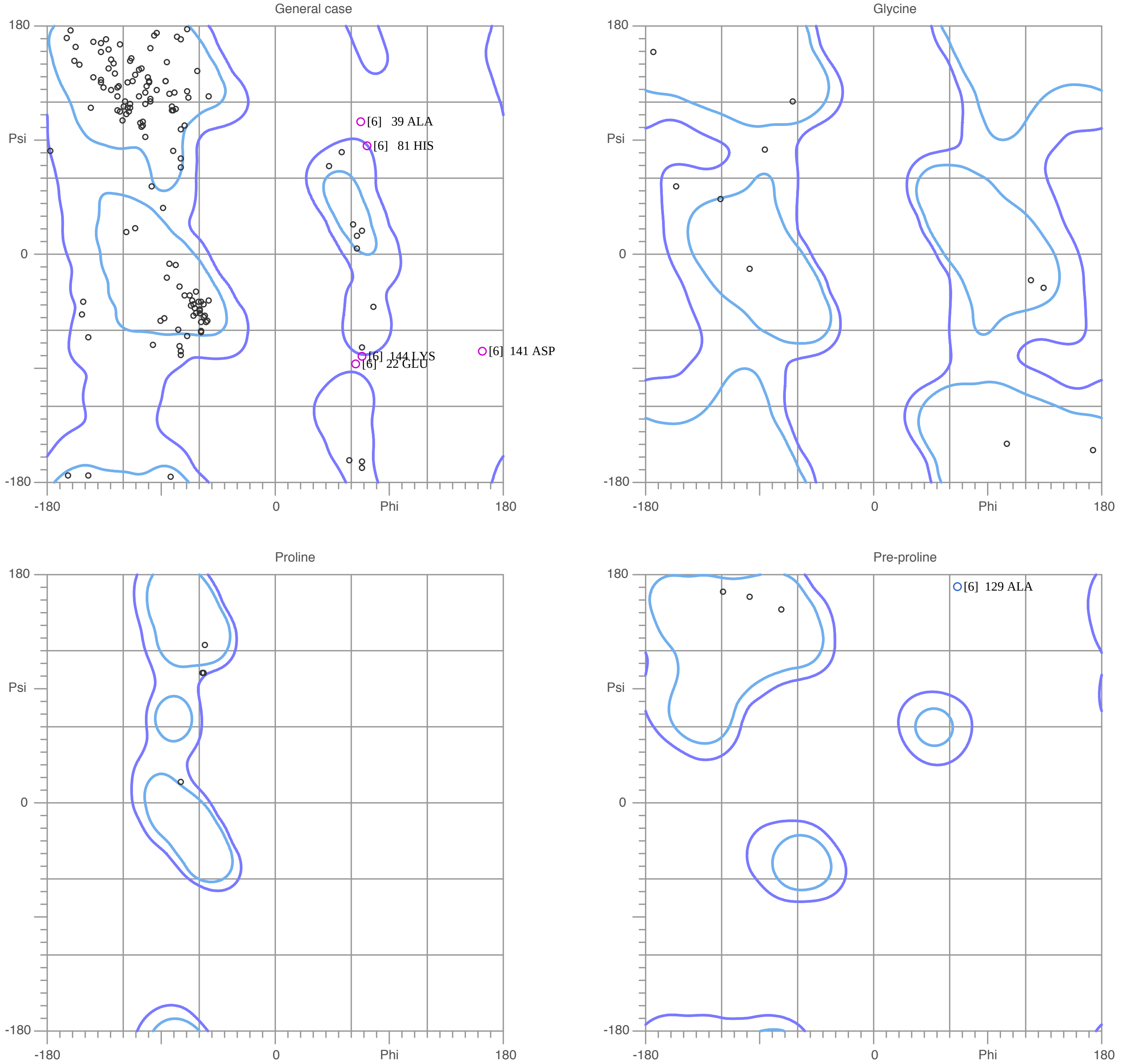


86.2% (138/160) of all residues were in favored (98%) regions.
99.4% (159/160) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 23 LYS (58.6, 96.7)

MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 6



81.2% (130/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
  [6] 22 GLU (63.1, -87.0)
  [6] 39 ALA (67.1, 105.2)
  [6] 81 HIS (73.0, 86.6)
  [6] 129 ALA (66.6, 171.6)
  [6] 141 ASP (163.3, -76.5)
  [6] 144 LYS (68.4, -80.8)

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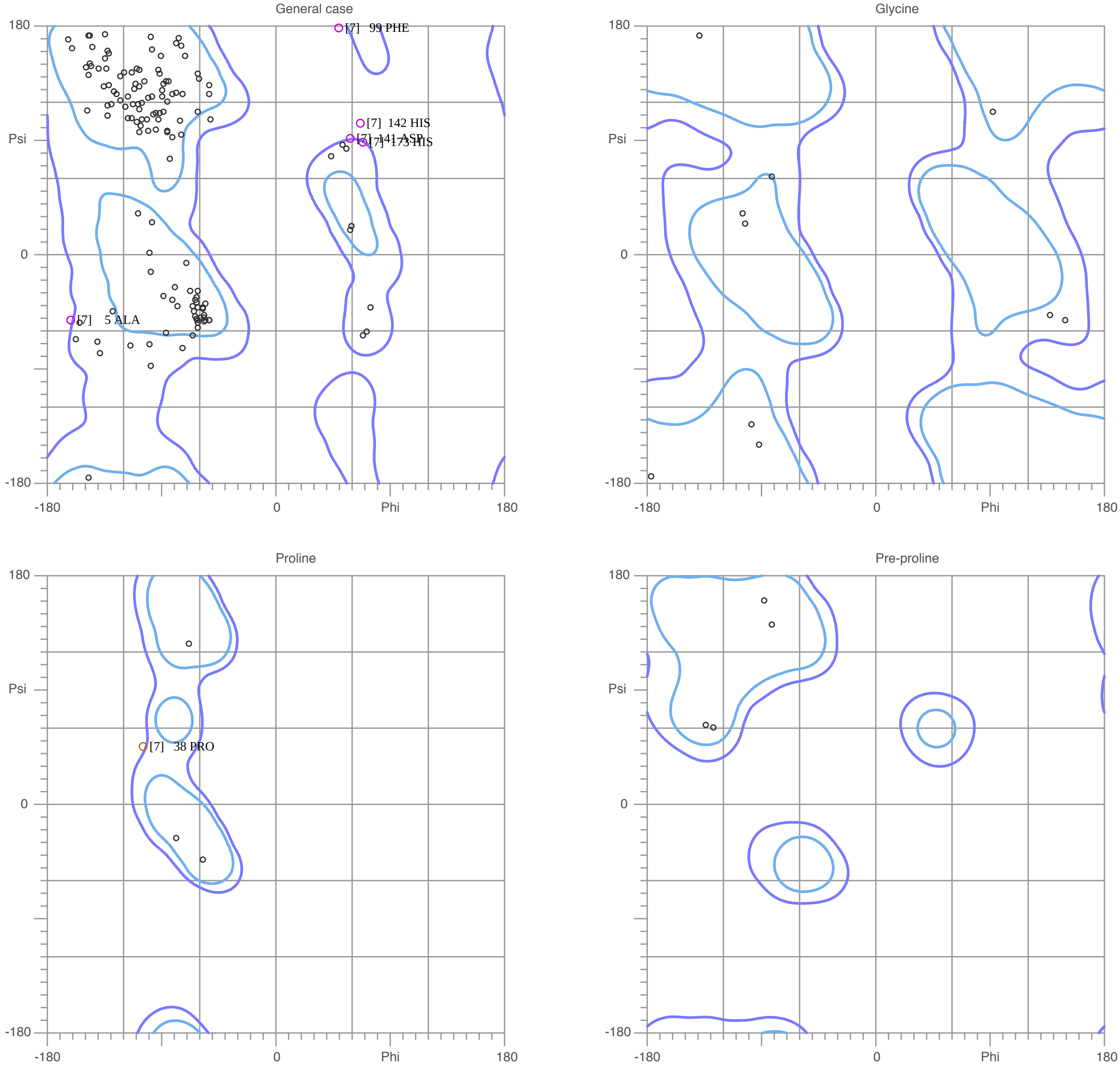
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 7



83.8% (134/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[7] 5 ALA (-162.7, -51.7)
[7] 38 PRO (-105.0, 46.6)
[7] 99 PHE (49.2, 179.5)
[7] 141 ASP (58.9, 92.1)
[7] 142 HIS (66.3, 104.6)
[7] 173 HIS (68.9, 89.5)

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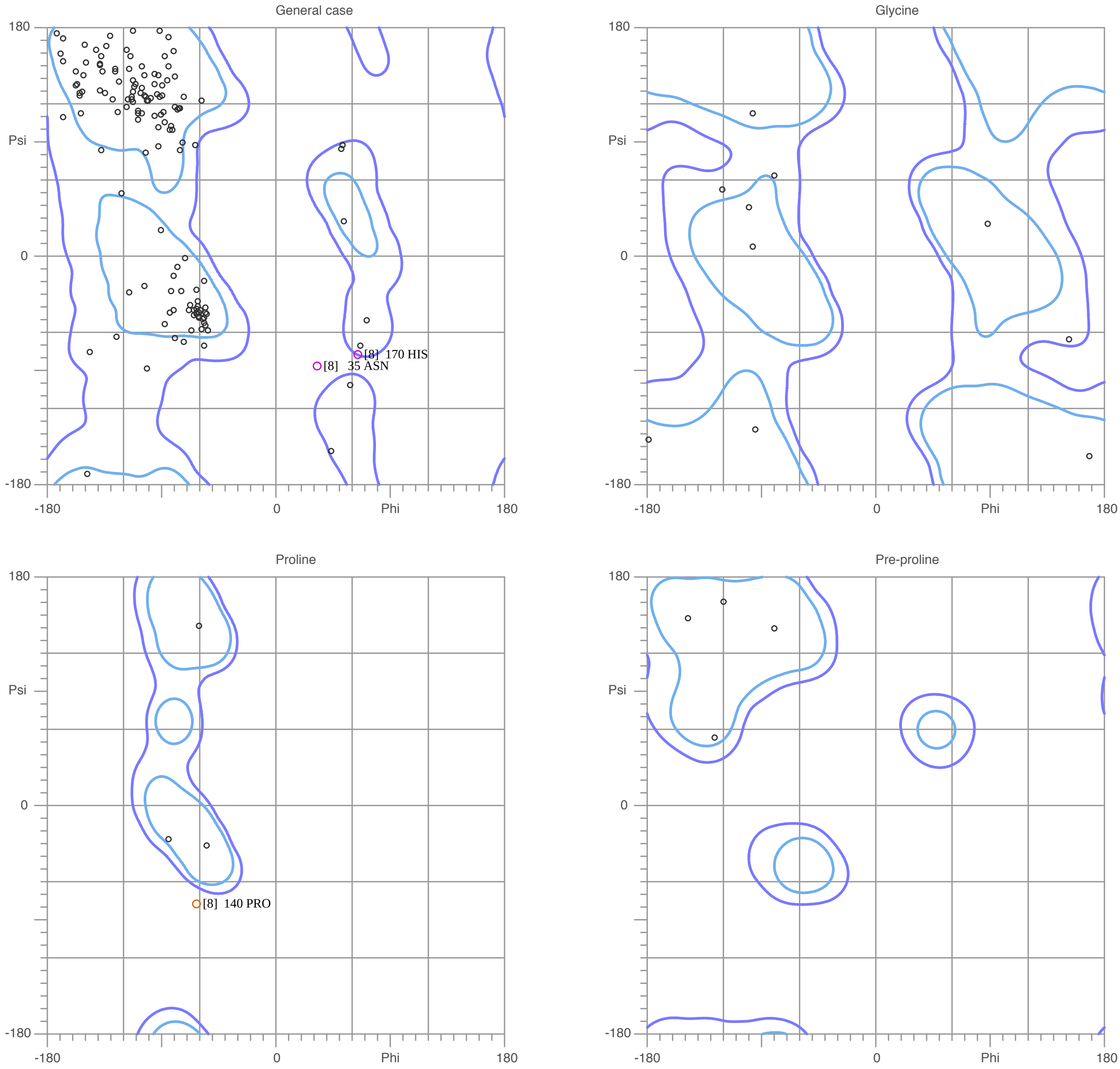
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 8



86.2% (138/160) of all residues were in favored (98%) regions.
98.1% (157/160) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[8] 35 ASN (32.0, -86.5)
[8] 140 PRO (-63.5, -77.6)
[8] 170 HIS (64.4, -77.9)

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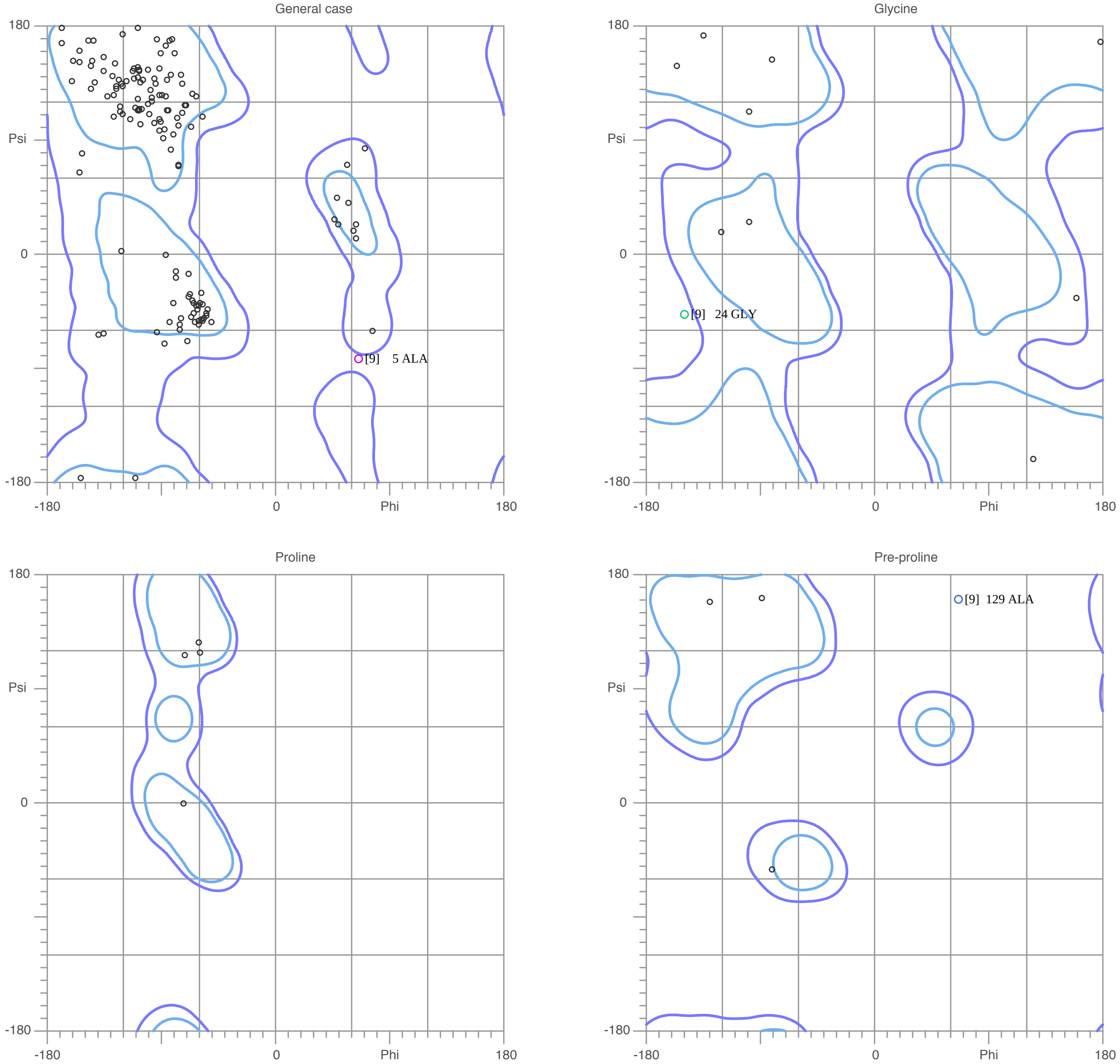
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 9



88.8% (142/160) of all residues were in favored (98%) regions.
98.1% (157/160) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[9] 5 ALA (65.2, -82.2)
[9] 24 GLY (-150.8, -47.5)
[9] 129 ALA (66.8, 161.9)

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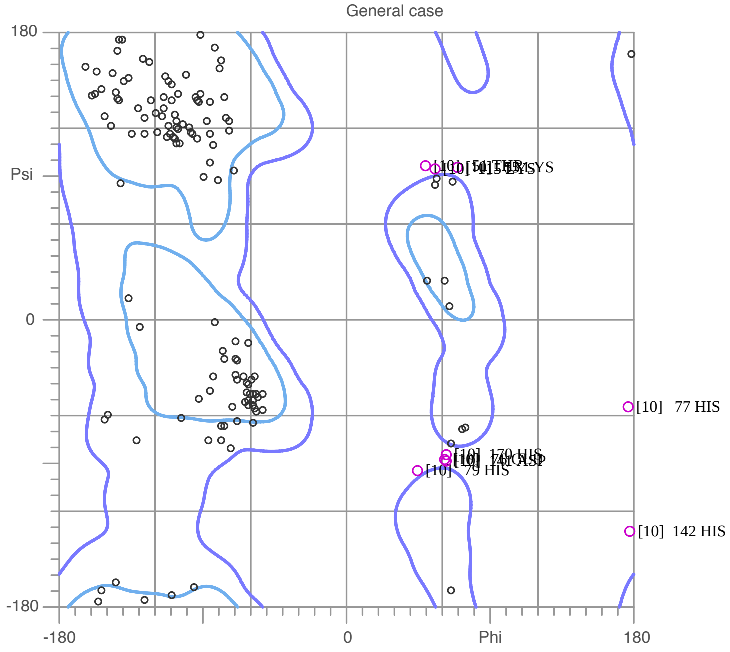
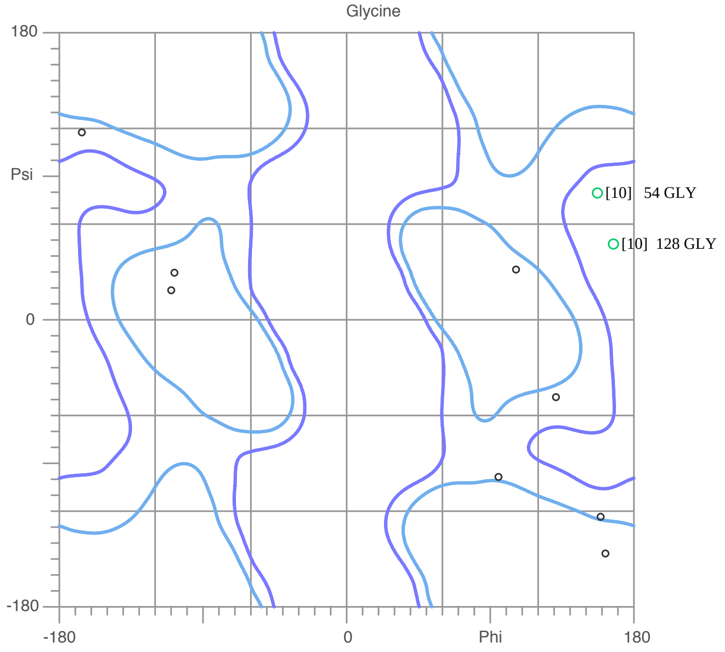
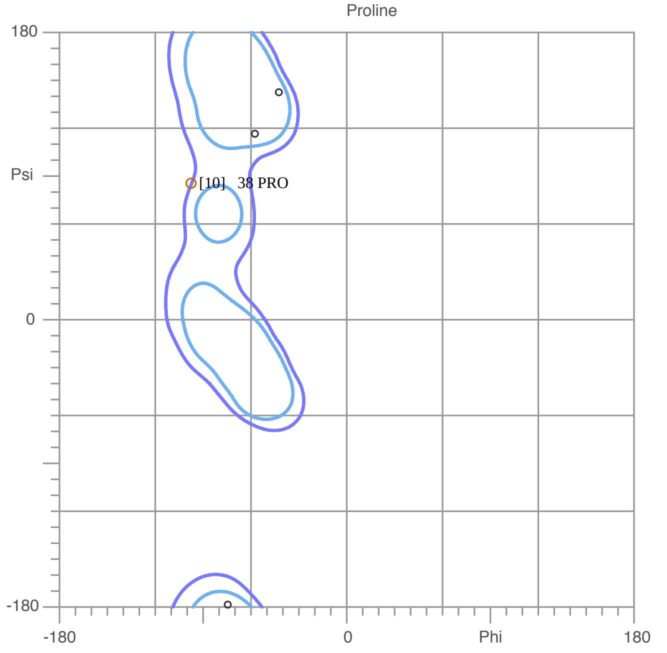
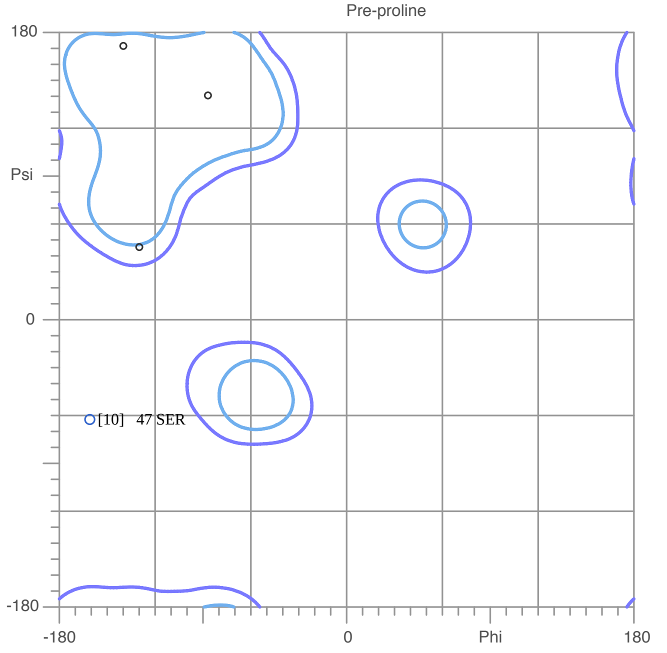
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 10









74.4% (119/160) of all residues were in favored (98%) regions.
91.9% (147/160) of all residues were in allowed (>99.8%) regions.

There were 13 outliers (phi, psi):

- [10] 38 PRO (-98.9, 86.8)
- [10] 47 SER (-161.6, -62.2)
- [10] 51 THR (49.3, 97.5)
- [10] 54 GLY (157.7, 80.6)
- [10] 55 LYS (69.8, 96.8)
- [10] 76 GLU (61.6, -87.3)
- [10] 77 HIS (176.0, -54.1)
- [10] 79 HIS (44.2, -94.9)
- [10] 115 LYS (55.4, 95.8)
- [10] 128 GLY (167.1, 48.3)
- [10] 141 ASP (62.9, -88.1)
- [10] 142 HIS (177.3, -132.3)
- [10] 170 HIS (62.2, -84.1)

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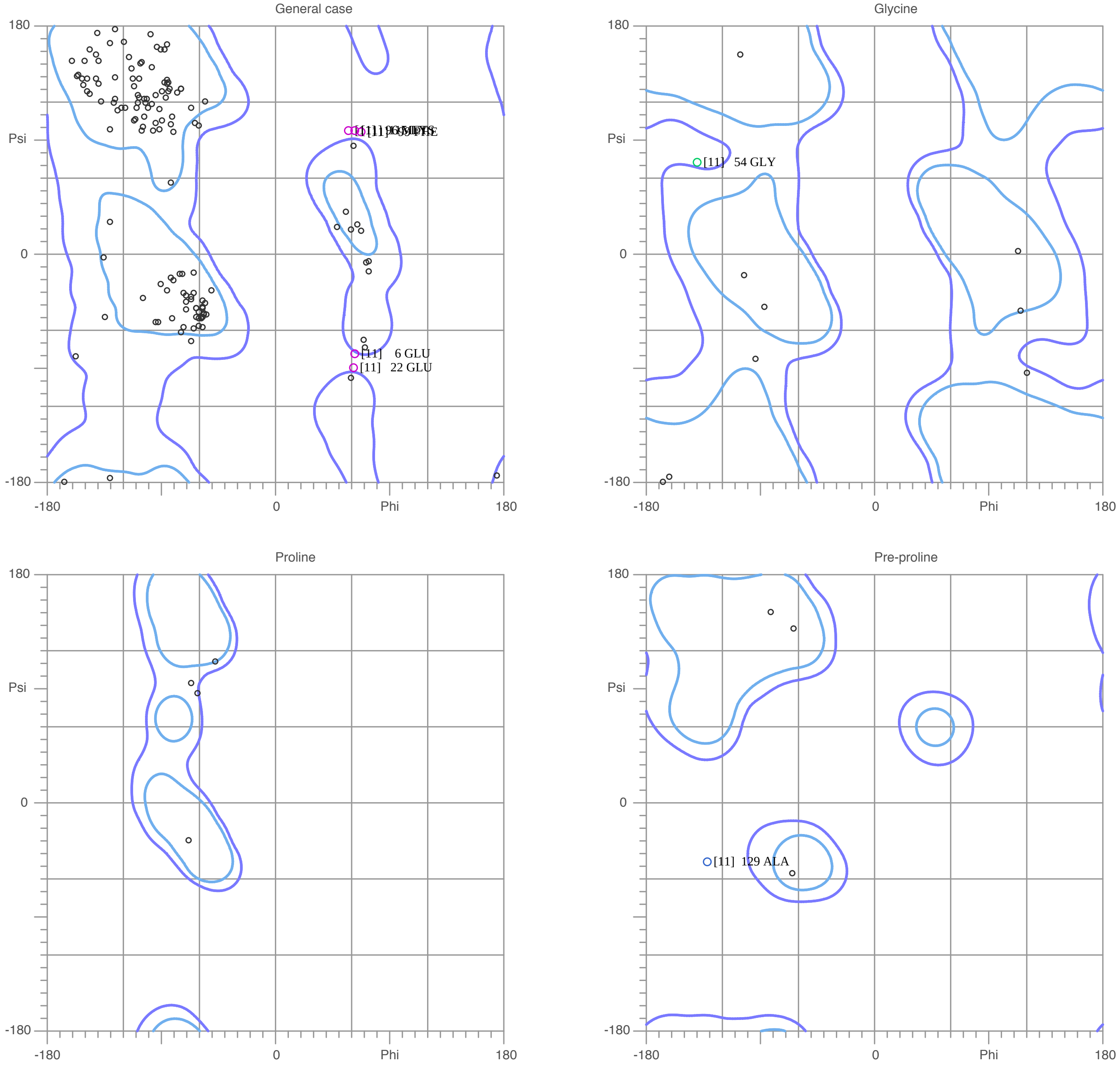
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 11

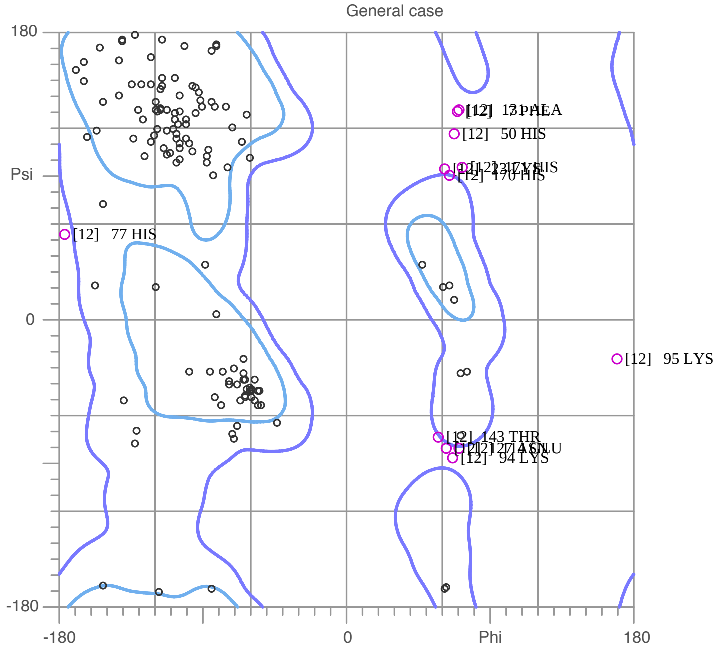


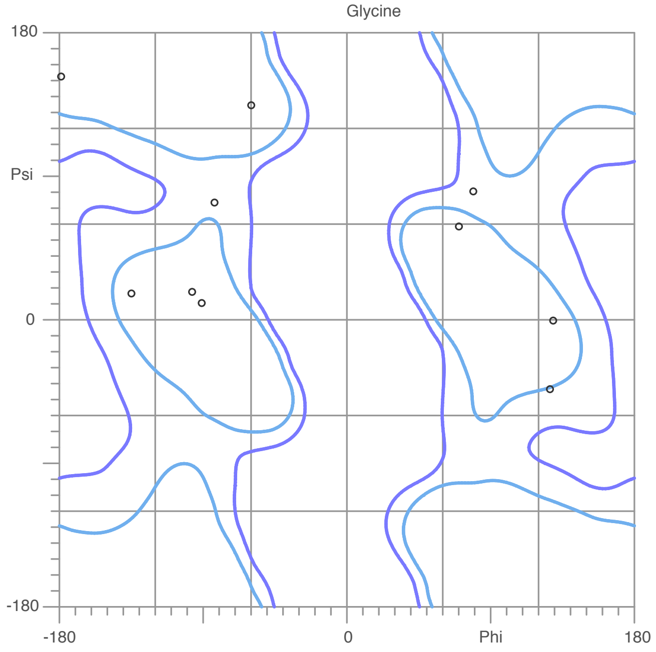
84.4% (135/160) of all residues were in favored (98%) regions.
95.6% (153/160) of all residues were in allowed (>99.8%) regions.

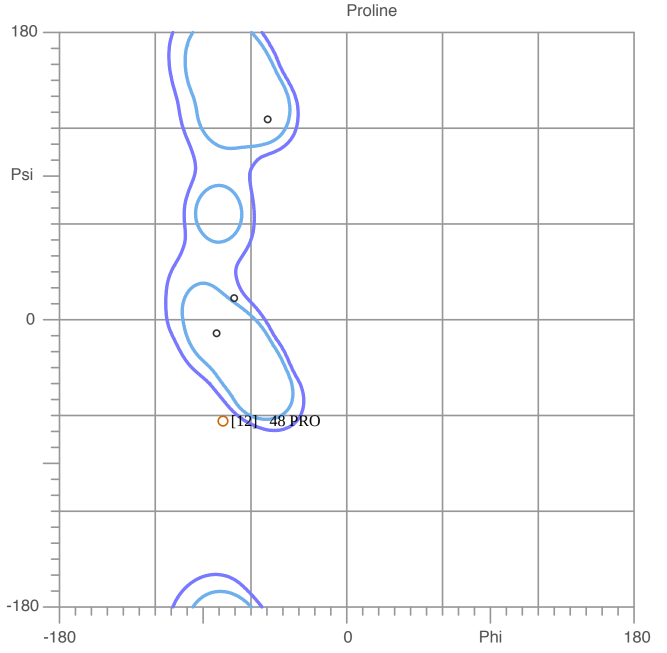
There were 7 outliers (phi, psi):
[11] 6 GLU (62.8, -78.5)
[11] 22 GLU (61.4, -89.3)
[11] 54 GLY (-140.3, 73.2)
[11] 96 MET (57.9, 98.1)
[11] 99 PHE (67.1, 97.9)
[11] 115 LYS (62.2, 98.8)
[11] 129 ALA (-132.4, -46.5)

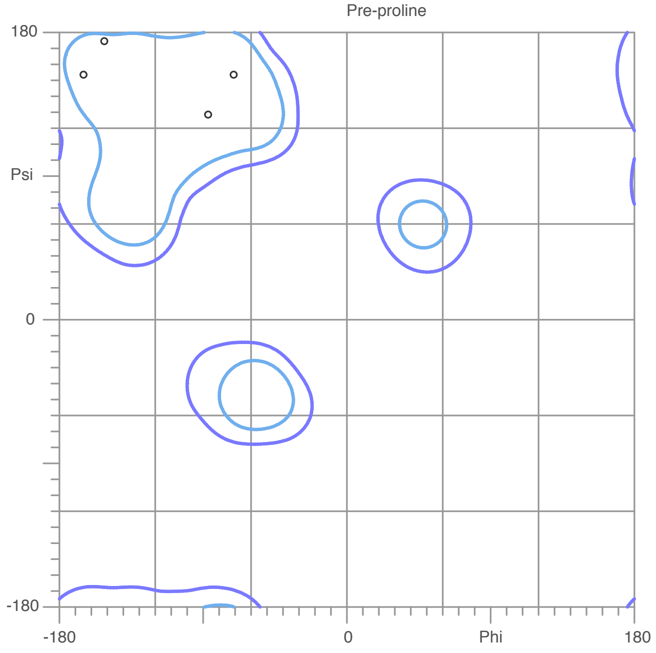
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 12


General case


Glycine


Proline


Pre-proline

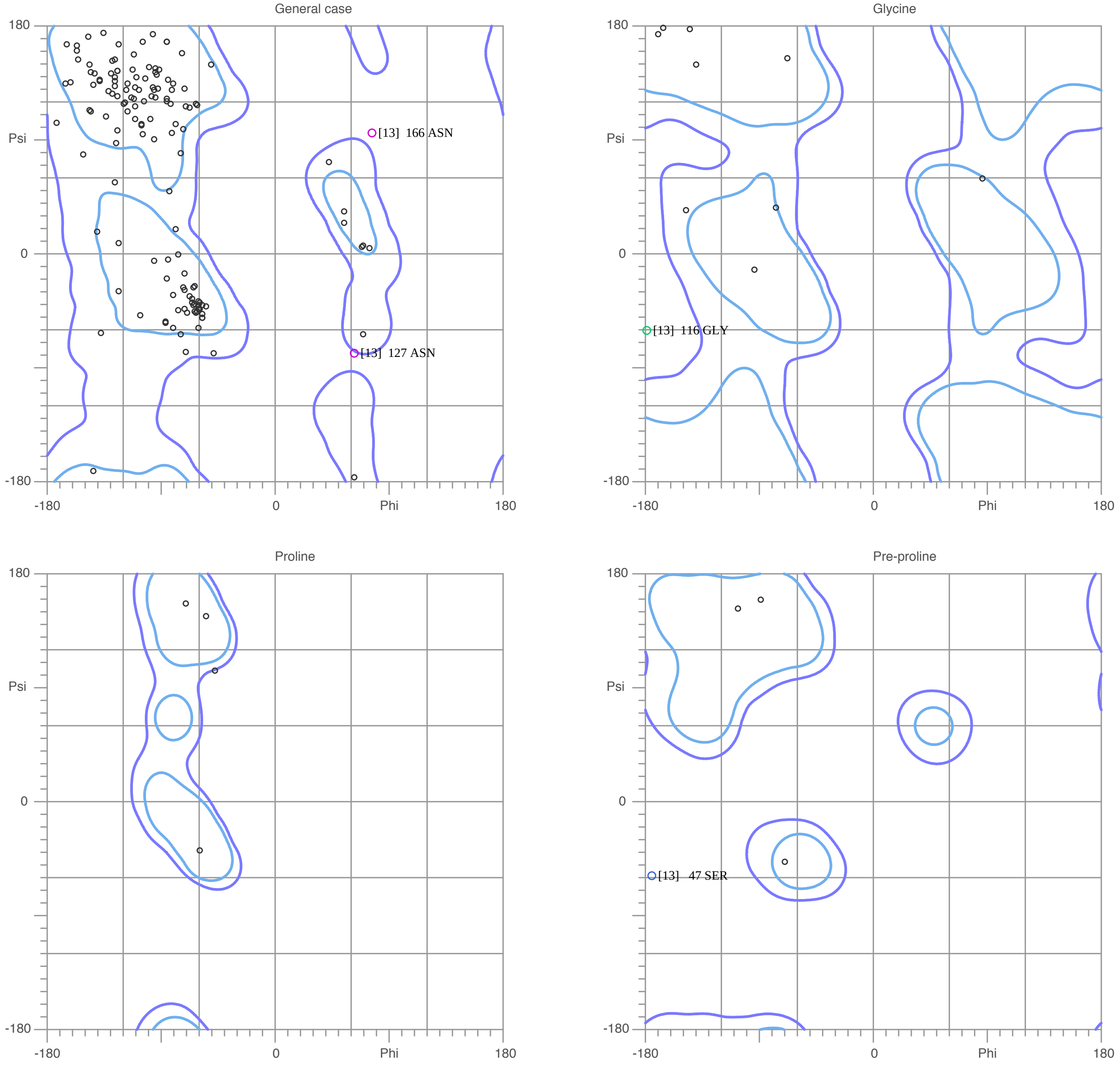
77.5% (124/160) of all residues were in favored (98%) regions.
91.9% (147/160) of all residues were in allowed (>99.8%) regions.

There were 13 outliers (phi, psi):

[12] 7 PHE (69.9, 131.9)
[12] 23 LYS (61.4, 95.6)
[12] 48 PRO (-78.5, -63.5)
[12] 50 HIS (67.8, 117.3)
[12] 77 HIS (-177.1, 55.0)
[12] 94 LYS (66.1, -86.5)
[12] 95 LYS (169.3, -24.5)
[12] 114 GLU (70.7, -80.2)
[12] 127 ASN (62.9, -80.6)
[12] 131 ALA (70.3, 133.0)
[12] 143 THR (57.8, -73.2)
[12] 170 HIS (64.9, 91.3)
[12] 171 HIS (72.0, 96.2)

MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 13



87.5% (140/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[13] 47 SER (-175.9, -58.9)
[13] 116 GLY (-179.6, -60.5)
[13] 127 ASN (62.1, -78.8)
[13] 166 ASN (76.9, 97.0)

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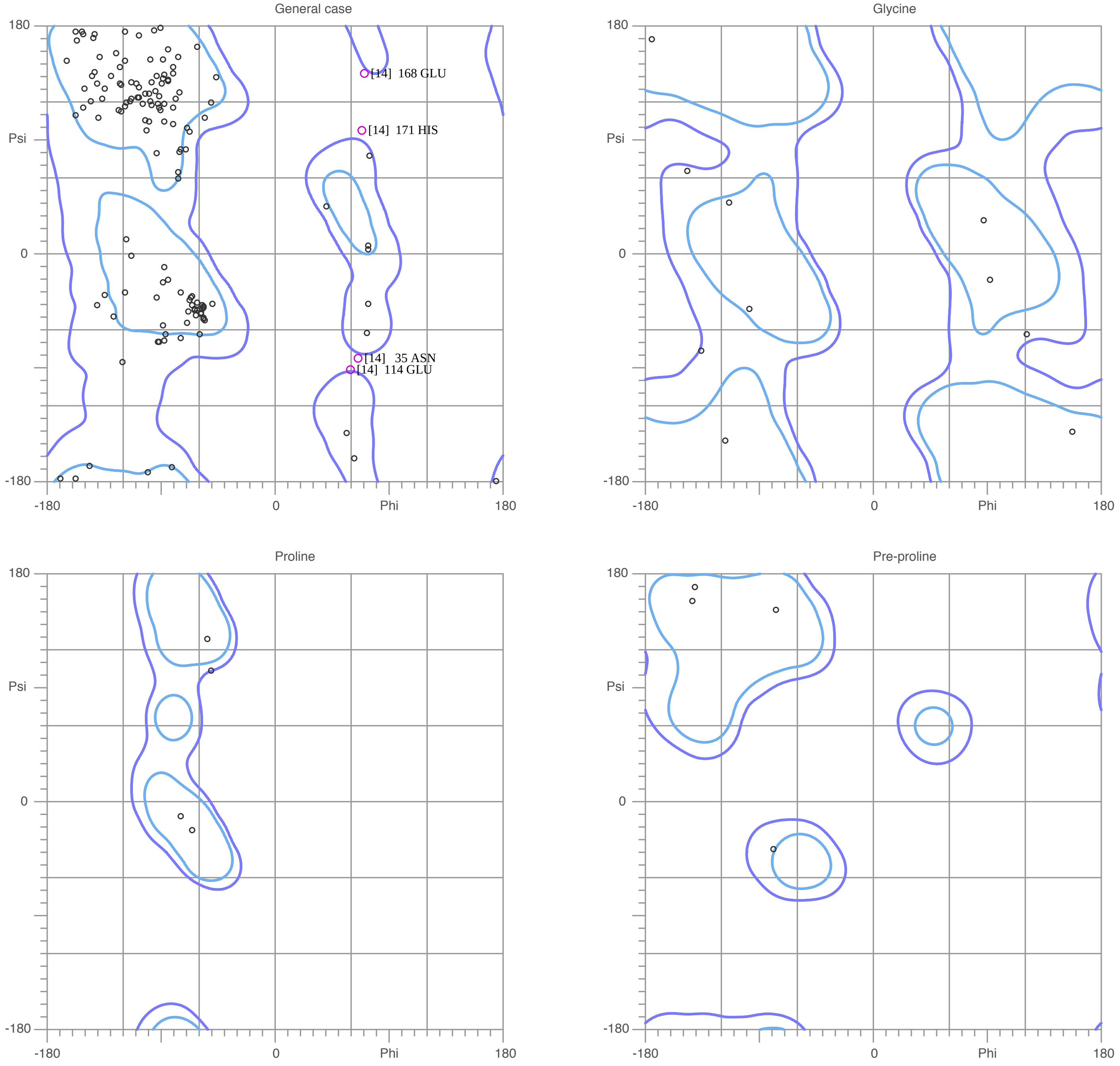
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 14



81.2% (130/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
- [14] 35 ASN (65.5, -82.4)
- [14] 114 GLU (59.3, -91.3)
- [14] 168 GLU (70.3, 143.1)
- [14] 171 HIS (68.1, 98.0)

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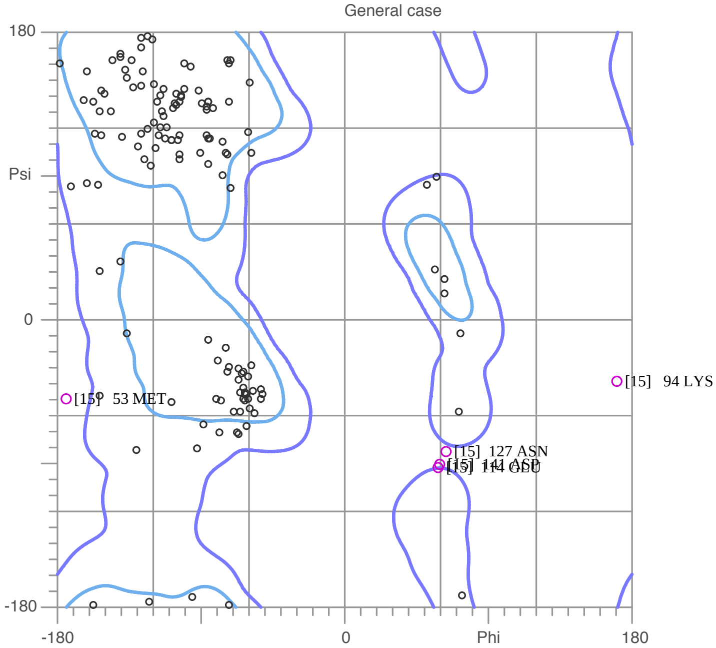
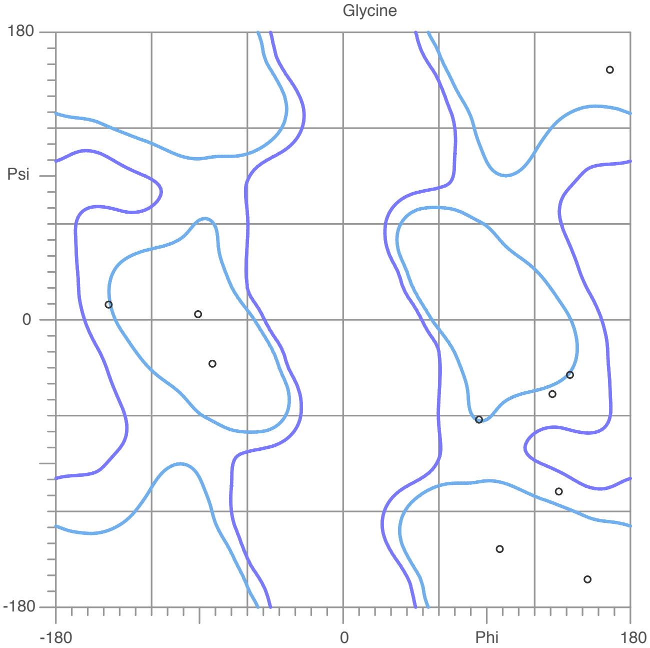
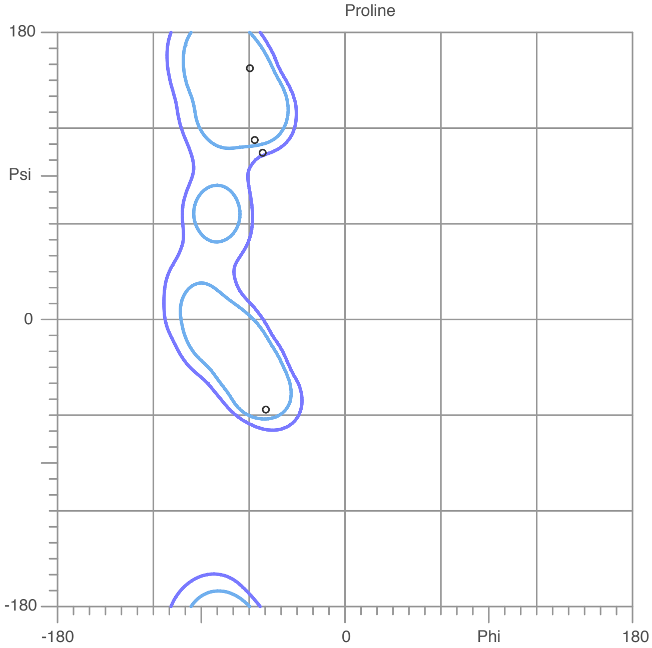
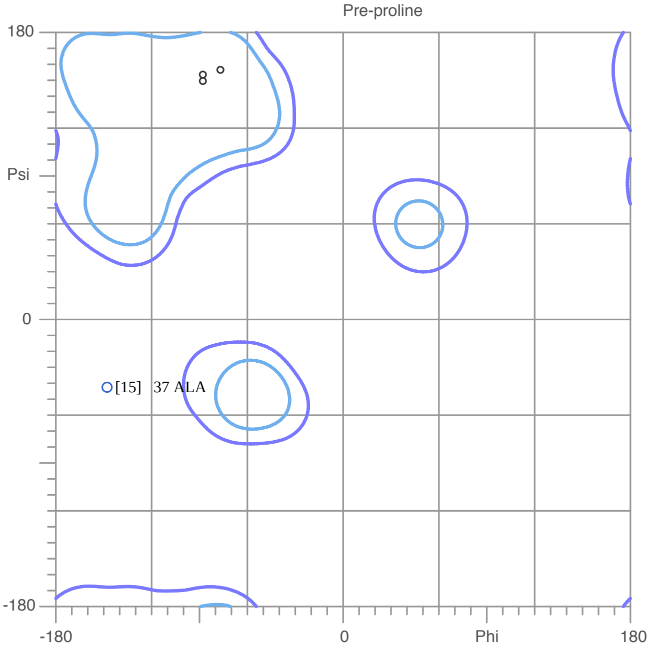
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 15









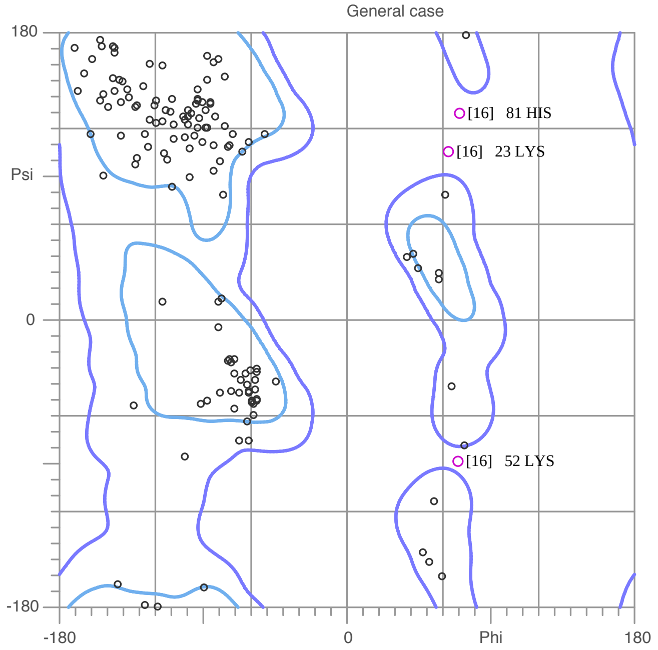
79.4% (127/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

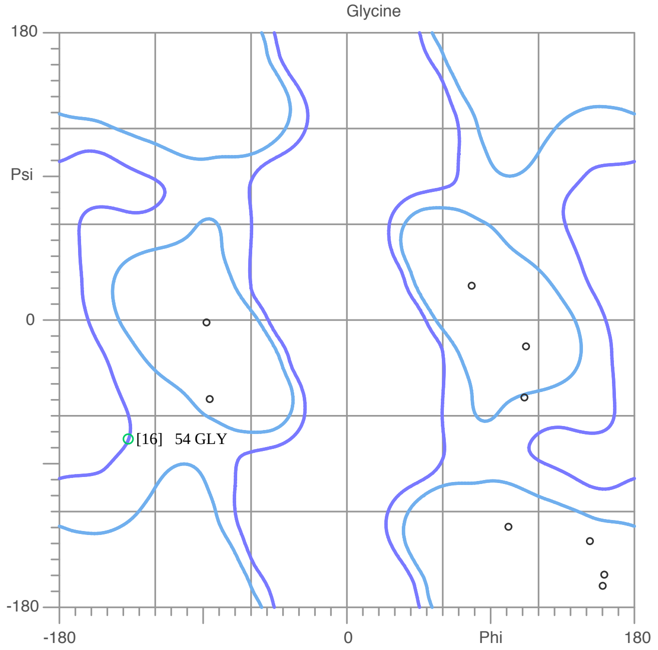
There were 6 outliers (phi, psi):

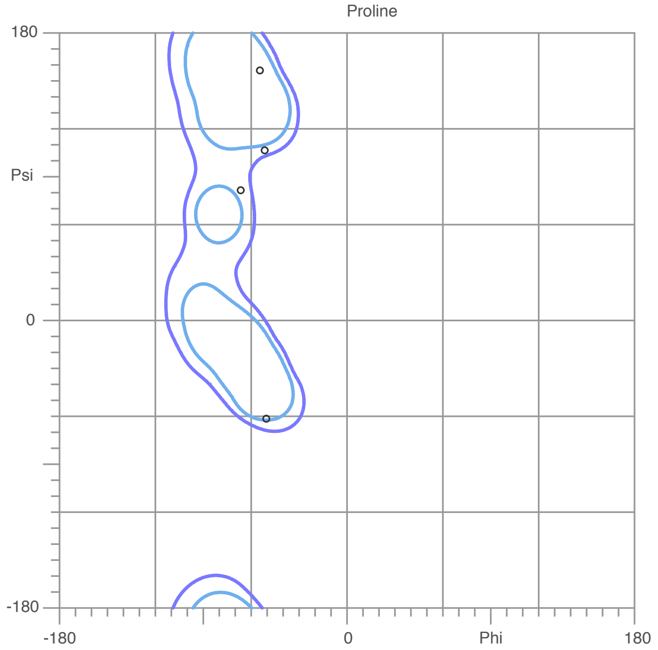
[15] 37 ALA (-148.6, -42.5)
[15] 53 MET (-175.9, -49.2)
[15] 94 LYS (170.5, -38.3)
[15] 114 GLU (58.2, -92.3)
[15] 127 ASN (63.3, -82.0)
[15] 141 ASP (59.7, -90.0)

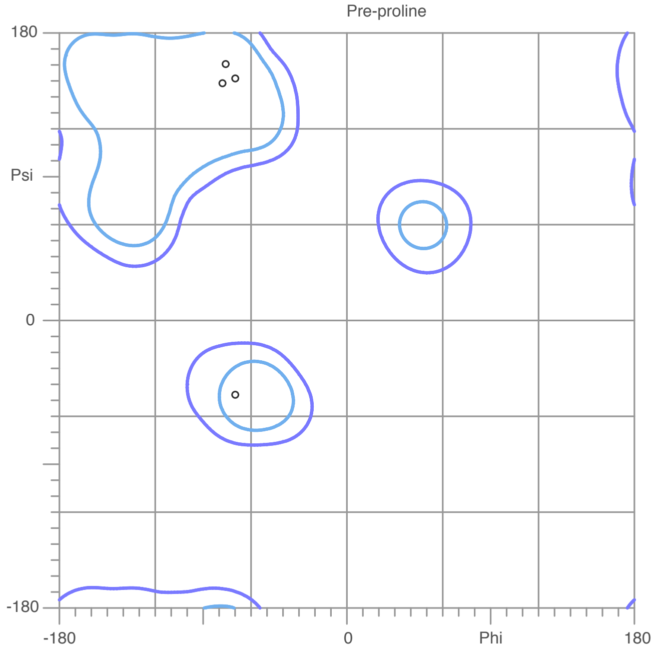
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 16









85.0% (136/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[16] 23 LYS (63.0, 106.0)
[16] 52 LYS (69.6, -88.4)
[16] 54 GLY (-137.7, -74.8)
[16] 81 HIS (70.8, 130.4)

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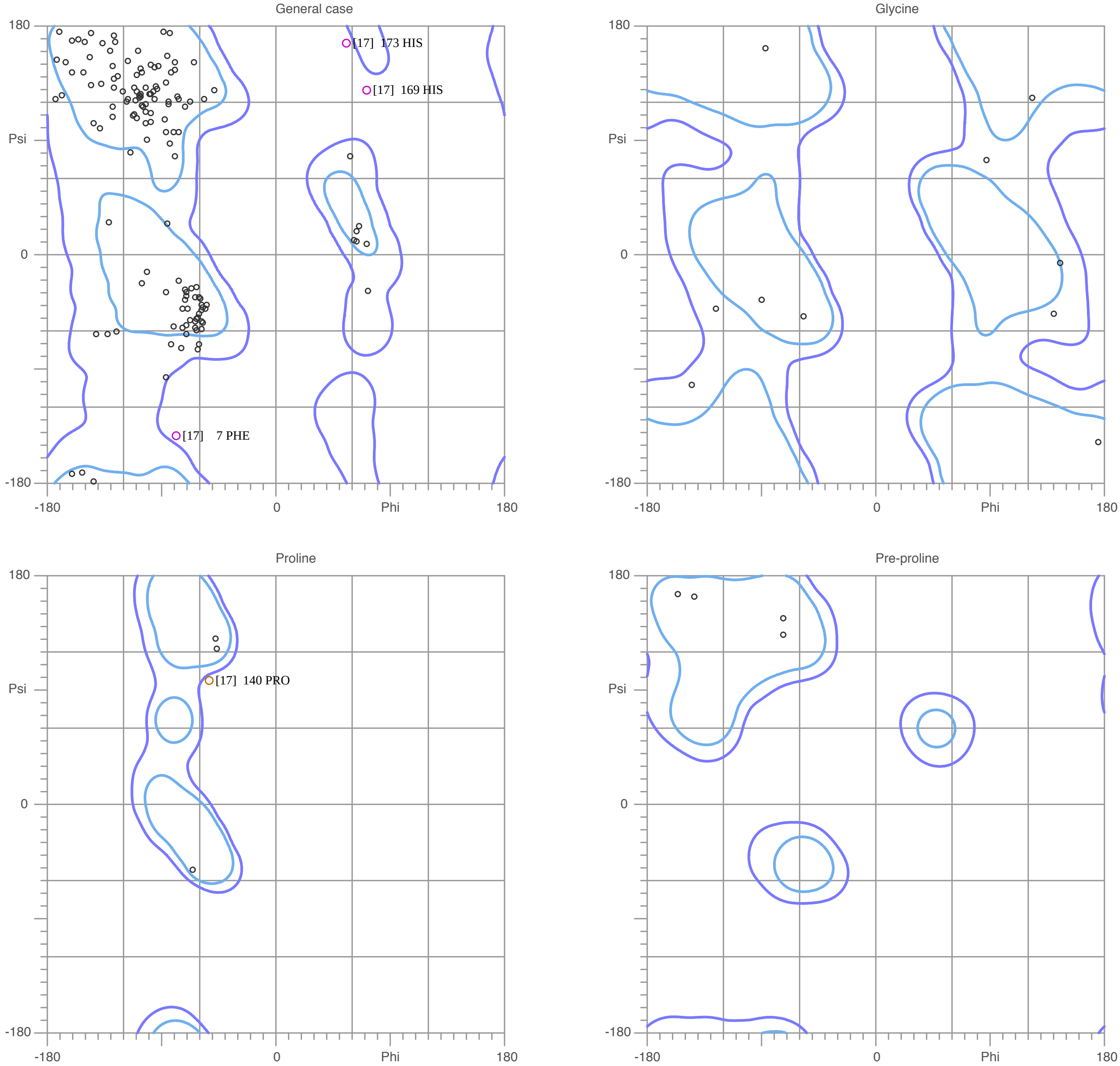
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 17



85.6% (137/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[17] 7 PHE (-79.7, -142.3)
[17] 140 PRO (-53.0, 98.4)
[17] 169 HIS (71.2, 130.6)
[17] 173 HIS (55.0, 167.6)

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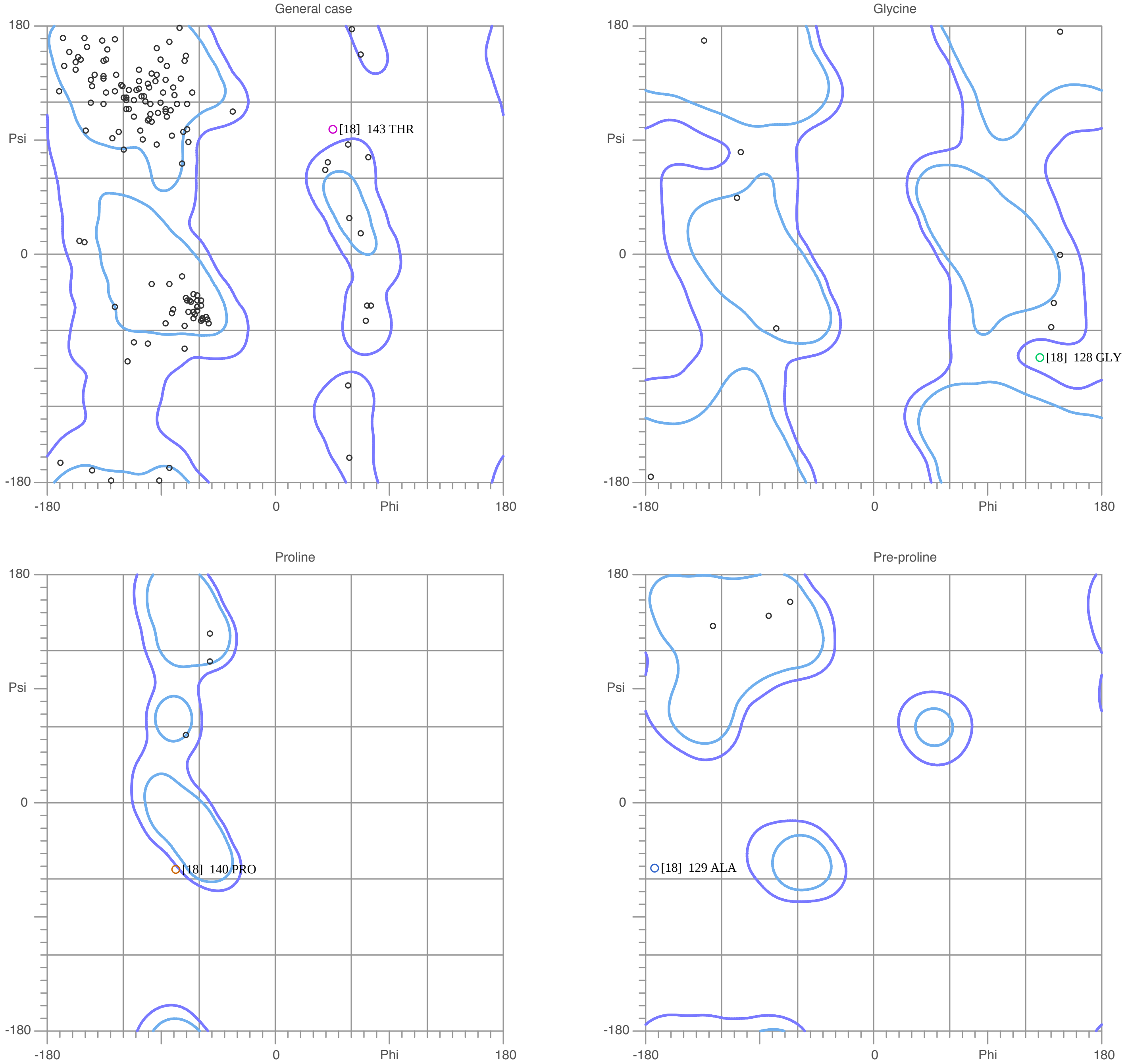
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 18



81.2% (130/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[18] 128 GLY (131.3, -81.5)
[18] 129 ALA (-174.0, -51.8)
[18] 140 PRO (-79.5, -52.2)
[18] 143 THR (45.4, 99.3)

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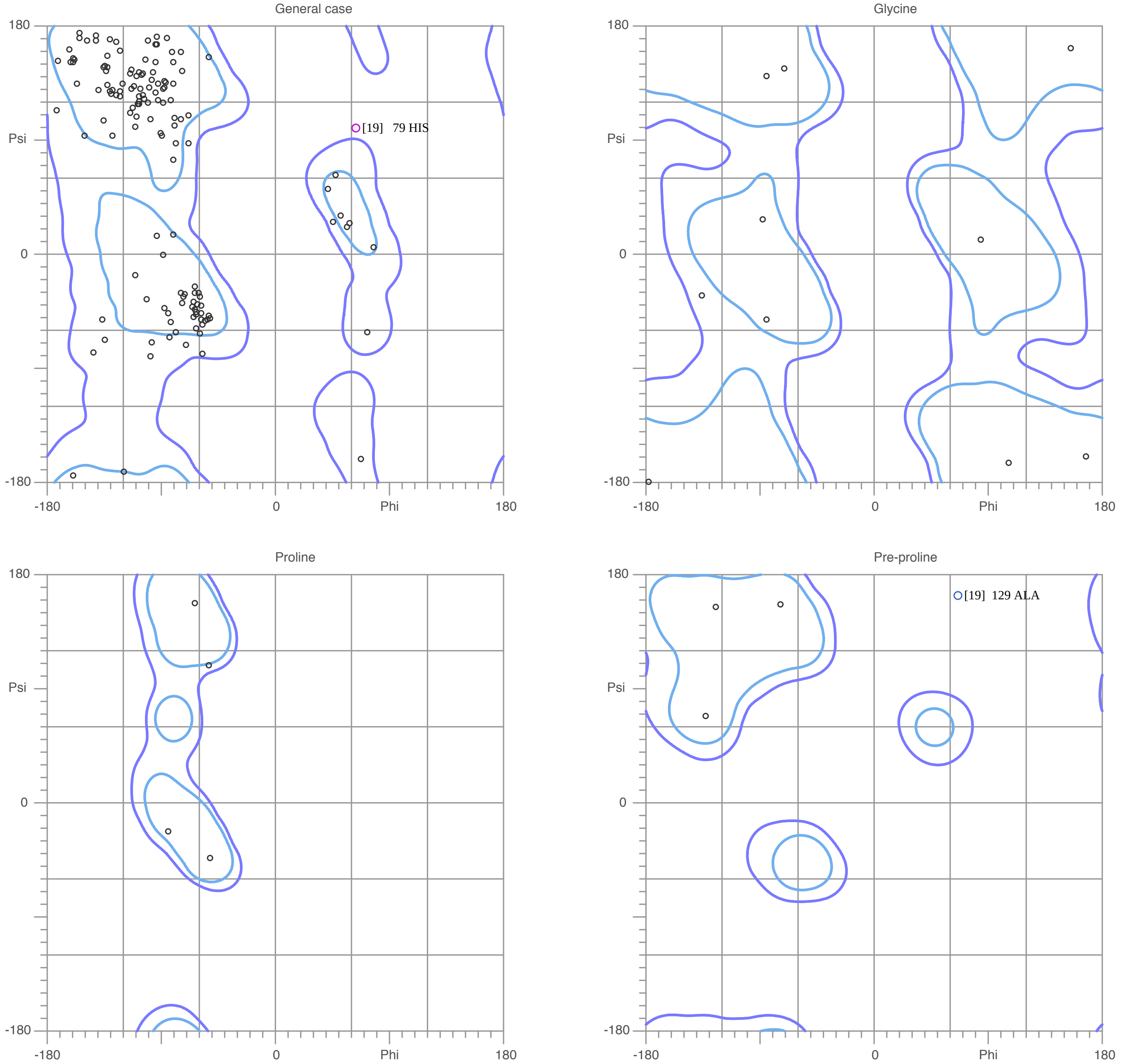
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 19

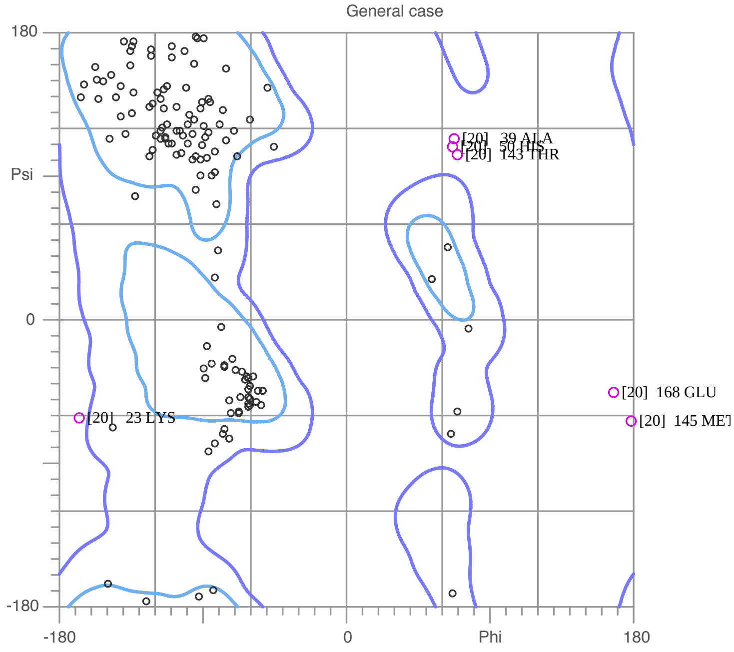


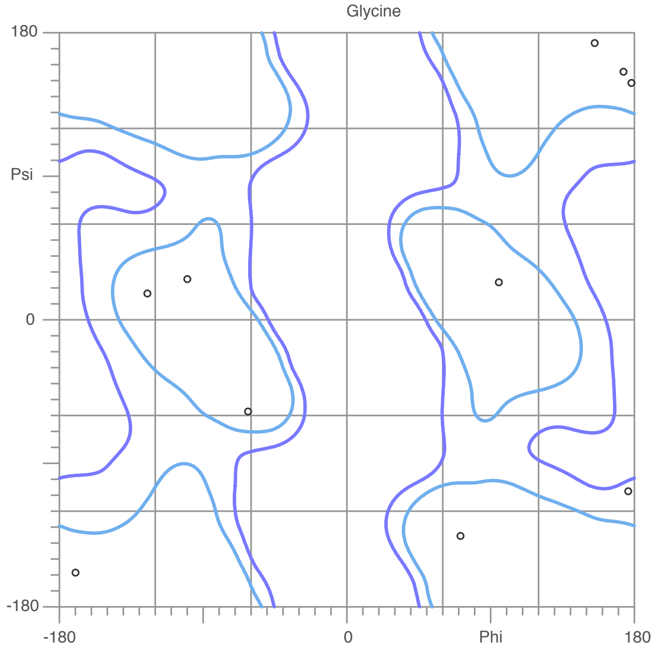
89.4% (143/160) of all residues were in favored (98%) regions.
98.8% (158/160) of all residues were in allowed (>99.8%) regions.

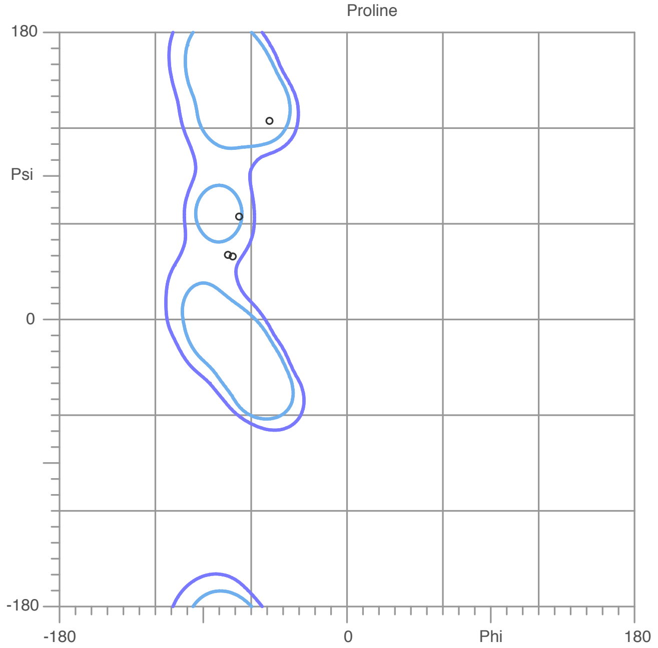
There were 2 outliers (phi, psi):
- [19] 79 HIS (63.5, 100.2)
- [19] 129 ALA (66.8, 165.0)

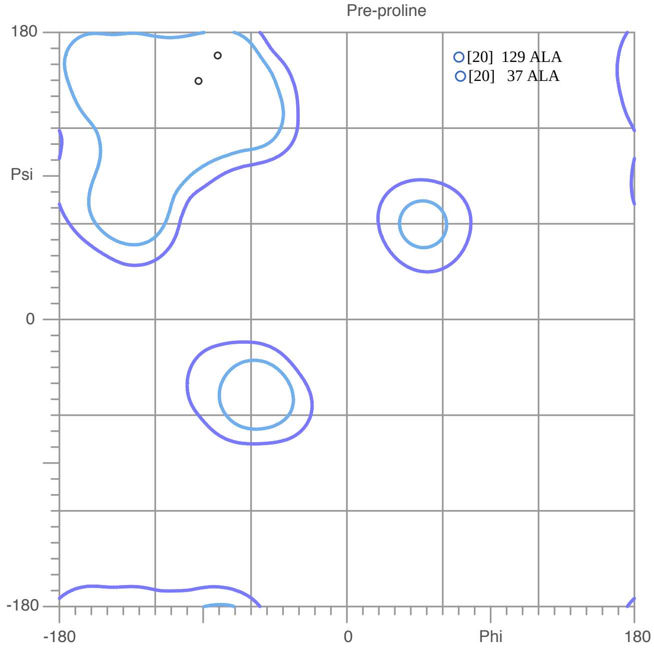
MolProbity Ramachandran analysis

SPR104_NMR_em_bcr3.pdb, model 20









83.8% (134/160) of all residues were in favored (98%) regions.
95.0% (152/160) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[20] 23 LYS (-169.0, -61.3)
[20] 37 ALA (71.0, 153.1)
[20] 39 ALA (67.8, 114.4)
[20] 50 HIS (66.4, 110.0)
[20] 129 ALA (70.7, 166.0)
[20] 143 THR (69.6, 104.8)
[20] 145 MET (178.4, -63.1)
[20] 168 GLU (167.6, -45.4)

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