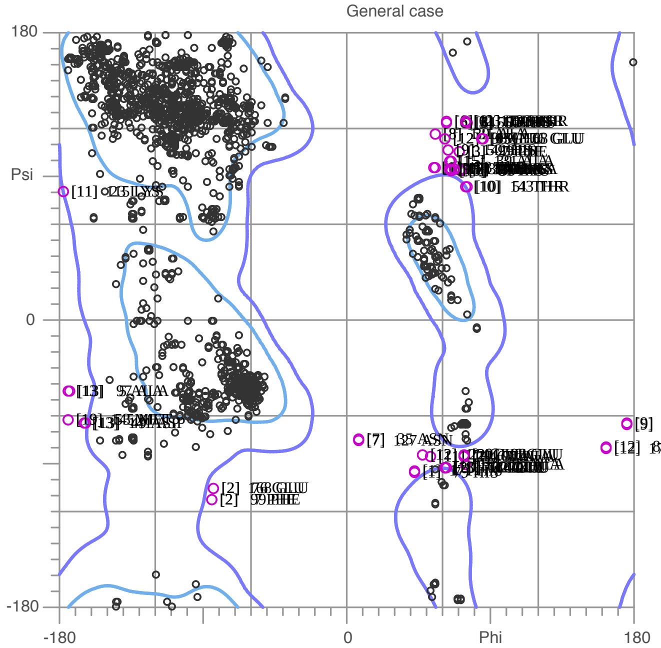
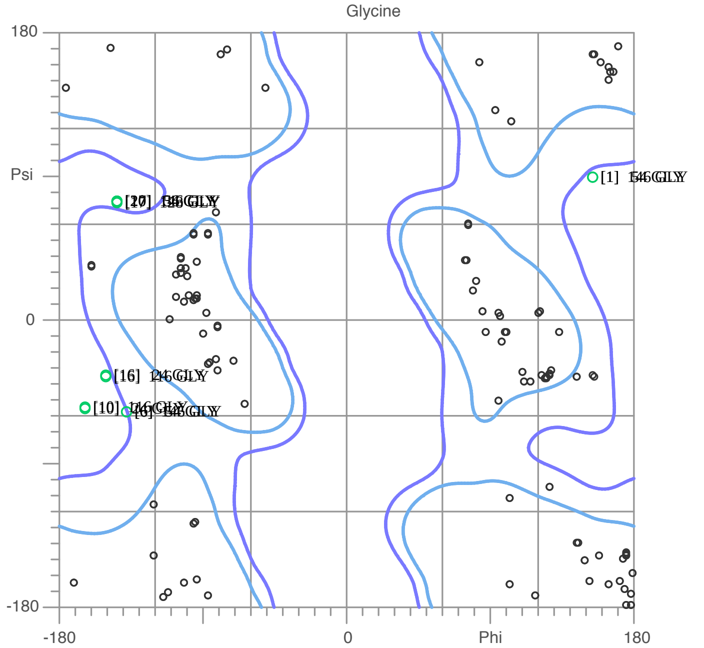
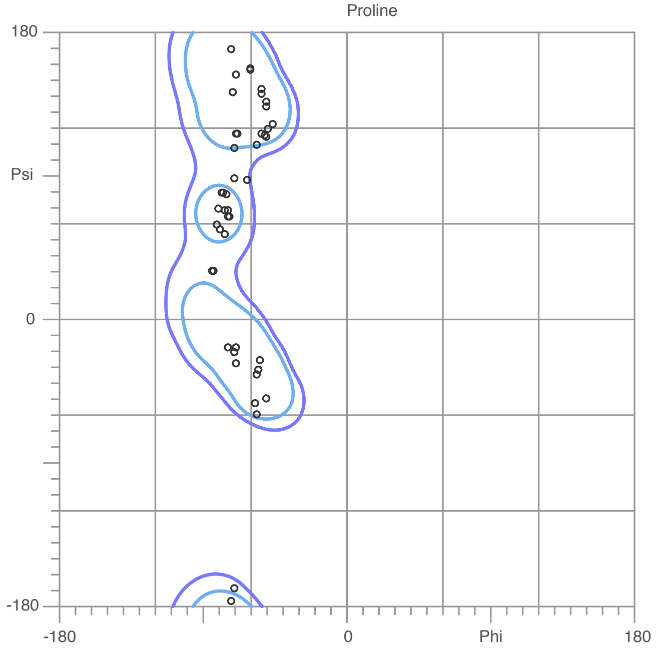
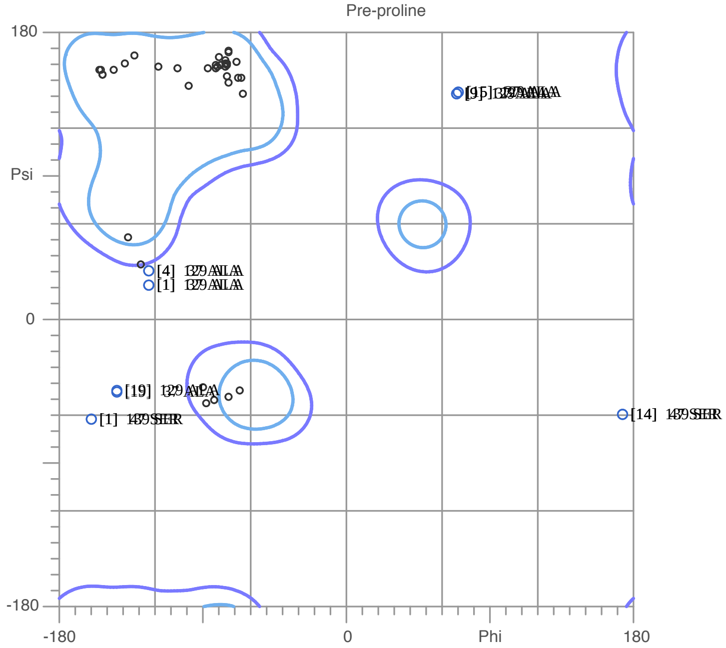
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, all models









89.3% (2859/3200) of all residues were in favored (98%) regions.
97.0% (3104/3200) of all residues were in allowed (>99.8%) regions.

There were 96 outliers (phi, psi):

```
   [1]   5 ALA (73.8, -85.0)
   [1]  37 ALA (-124.8, 22.5)
   [1]  47 SER (-160.6, -62.8)
   [1]  51 THR (55.1, 96.8)
   [1]  54 GLY (155.0, 90.1)
   [1]  55 LYS (71.5, 95.0)
   [1]  76 GLU (61.6, -92.5)
   [1]  79 HIS (42.6, -95.0)
   [1]  97 ALA (73.8, -85.0)
   [1] 129 ALA (-124.8, 22.6)
   [1] 139 SER (-160.6, -62.8)
   [1] 143 THR (55.0, 96.8)
   [1] 146 GLY (155.0, 90.1)
   [1] 147 LYS (71.4, 95.0)
   [1] 168 GLU (61.6, -92.5)
   [1] 171 HIS (42.6, -95.0)
   [2]   7 PHE (-85.0, -112.3)
   [2]  76 GLU (-84.8, -105.4)
   [2]  99 PHE (-85.1, -112.3)
   [2] 168 GLU (-84.8, -105.3)
   [3]   7 PHE (70.4, 106.7)
   [3]  50 HIS (75.0, 125.0)
   [3]  99 PHE (70.3, 106.7)
   [3] 142 HIS (75.0, 125.0)
   [4]  37 ALA (-124.9, 31.5)
   [4] 129 ALA (-125.0, 31.5)
   [6]  23 LYS (62.9, 125.0)
   [6]  54 GLY (-138.4, -57.1)
   [6]  81 HIS (75.1, 125.0)
   [6] 115 LYS (62.9, 125.0)
   [6] 146 GLY (-138.4, -57.1)
   [6] 173 HIS (75.0, 125.0)
   [7]  35 ASN (7.6, -75.0)
   [7] 127 ASN (7.7, -75.1)
   [8]  39 ALA (55.0, 117.1)
   [8] 131 ALA (55.0, 117.0)
   [9]  23 LYS (175.0, -65.0)
   [9]  37 ALA (69.5, 142.0)
   [9]  39 ALA (64.9, 95.1)
   [9]  50 HIS (63.7, 107.1)
   [9] 115 LYS (175.0, -65.0)
   [9] 129 ALA (69.5, 142.0)
   [9] 131 ALA (64.9, 95.2)
   [9] 142 HIS (63.7, 107.1)
   [10]   5 ALA (74.9, -90.4)
   [10]  24 GLY (-165.0, -55.1)
   [10]  51 THR (75.0, 84.9)
   [10]  97 ALA (75.0, -90.4)
   [10] 116 GLY (-165.0, -55.0)
   [10] 143 THR (75.0, 84.9)
   [11]  22 GLU (52.3, -85.1)
   [11]  23 LYS (-178.5, 81.9)
   [11]  51 THR (75.0, 125.0)
   [11] 114 GLU (52.3, -85.1)
   [11] 115 LYS (-178.4, 81.8)
   [11] 143 THR (75.0, 125.0)
   [12]   6 GLU (61.7, 114.0)
   [12]  22 GLU (47.8, -85.0)
   [12]  80 HIS (162.4, -80.0)
   [12]  98 GLU (61.7, 114.1)
   [12] 114 GLU (47.8, -85.0)
   [12] 172 HIS (162.5, -80.0)
   [13]   5 ALA (-175.0, -45.0)
   [13]  49 ASP (-165.0, -64.9)
   [13]  97 ALA (-175.0, -45.0)
   [13] 141 ASP (-165.0, -65.0)
   [14]  47 SER (173.7, -59.5)
   [14] 139 SER (173.7, -59.5)
   [15]  37 ALA (70.8, 143.7)
   [15]  39 ALA (65.0, 100.7)
   [15]  76 GLU (85.0, 114.8)
   [15] 129 ALA (70.8, 143.7)
   [15] 131 ALA (65.0, 100.7)
   [15] 168 GLU (85.0, 114.9)
   [16]  24 GLY (-151.3, -35.0)
   [16]  79 HIS (65.0, 95.0)
   [16] 116 GLY (-151.3, -35.0)
   [16] 171 HIS (65.0, 95.0)
   [17]  36 GLY (-144.4, 75.0)
   [17] 128 GLY (-144.4, 75.0)
   [18]  22 GLU (61.1, -92.7)
   [18]  39 ALA (67.1, 95.3)
   [18]  81 HIS (65.0, 95.0)
   [18] 114 GLU (61.1, -92.7)
   [18] 131 ALA (67.2, 95.2)
   [18] 173 HIS (65.0, 95.0)
   [19]  37 ALA (-145.0, -45.0)
   [19]  53 MET (-175.0, -62.7)
   [19] 129 ALA (-145.0, -45.0)
   [19] 145 MET (-175.0, -62.7)
   [20]   6 GLU (73.3, -85.0)
   [20]  22 GLU (62.1, -92.7)
   [20]  54 GLY (-145.0, 75.0)
   [20]  98 GLU (73.2, -85.0)
   [20] 114 GLU (62.2, -92.7)
   [20] 146 GLY (-145.0, 75.0)
```

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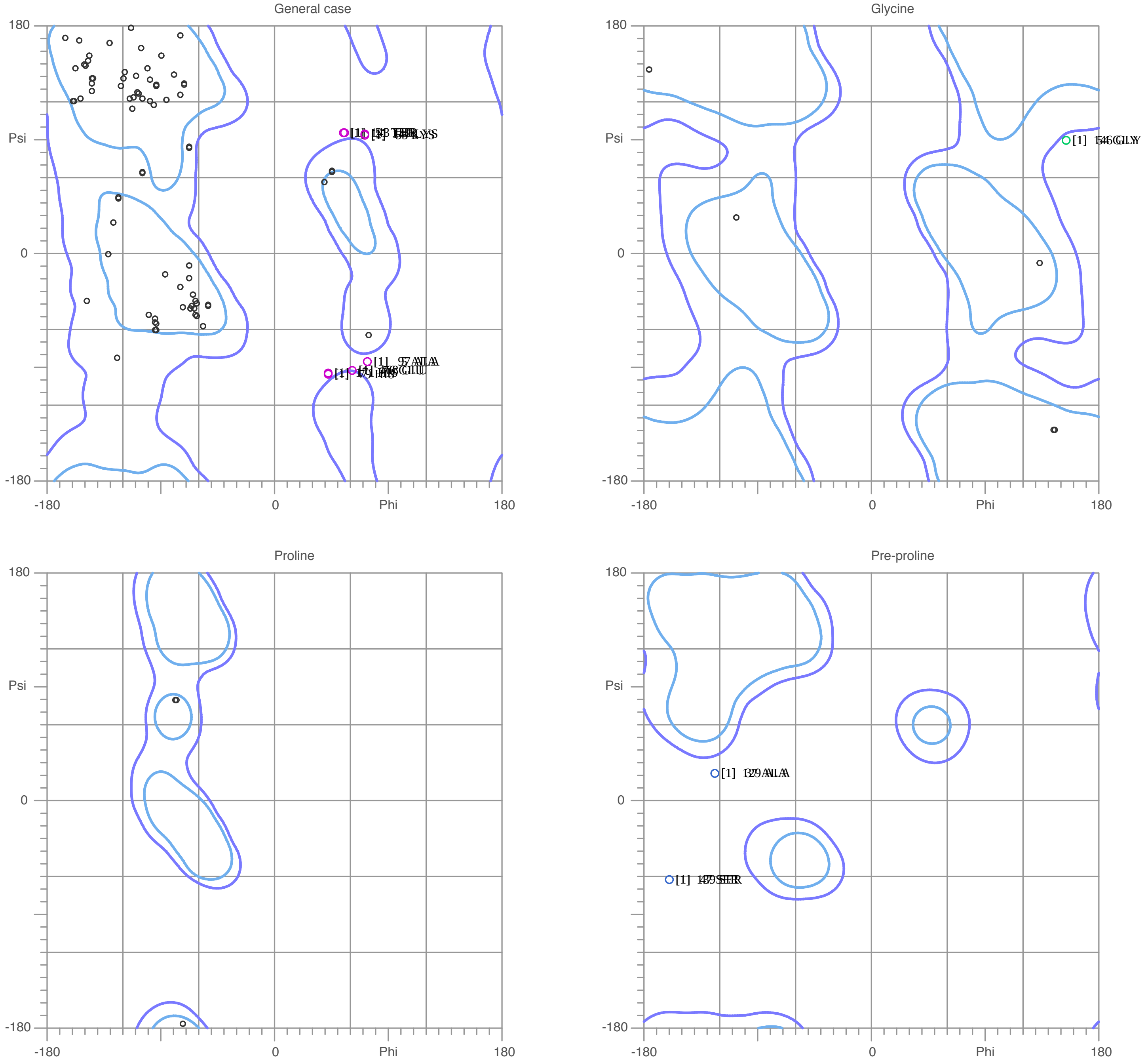
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 1



82.5% (132/160) of all residues were in favored (98%) regions.
90.0% (144/160) of all residues were in allowed (>99.8%) regions.

There were 16 outliers (phi, psi):

[1] 5 ALA (73.8, -85.0)
[1] 37 ALA (-124.8, 22.5)
[1] 47 SER (-160.6, -62.8)
[1] 51 THR (55.1, 96.8)
[1] 54 GLY (155.0, 90.1)
[1] 55 LYS (71.5, 95.0)
[1] 76 GLU (61.6, -92.5)
[1] 79 HIS (42.6, -95.0)
[1] 97 ALA (73.8, -85.0)
[1] 129 ALA (-124.8, 22.6)
[1] 139 SER (-160.6, -62.8)
[1] 143 THR (55.0, 96.8)
[1] 146 GLY (155.0, 90.1)
[1] 147 LYS (71.4, 95.0)
[1] 168 GLU (61.6, -92.5)
[1] 171 HIS (42.6, -95.0)

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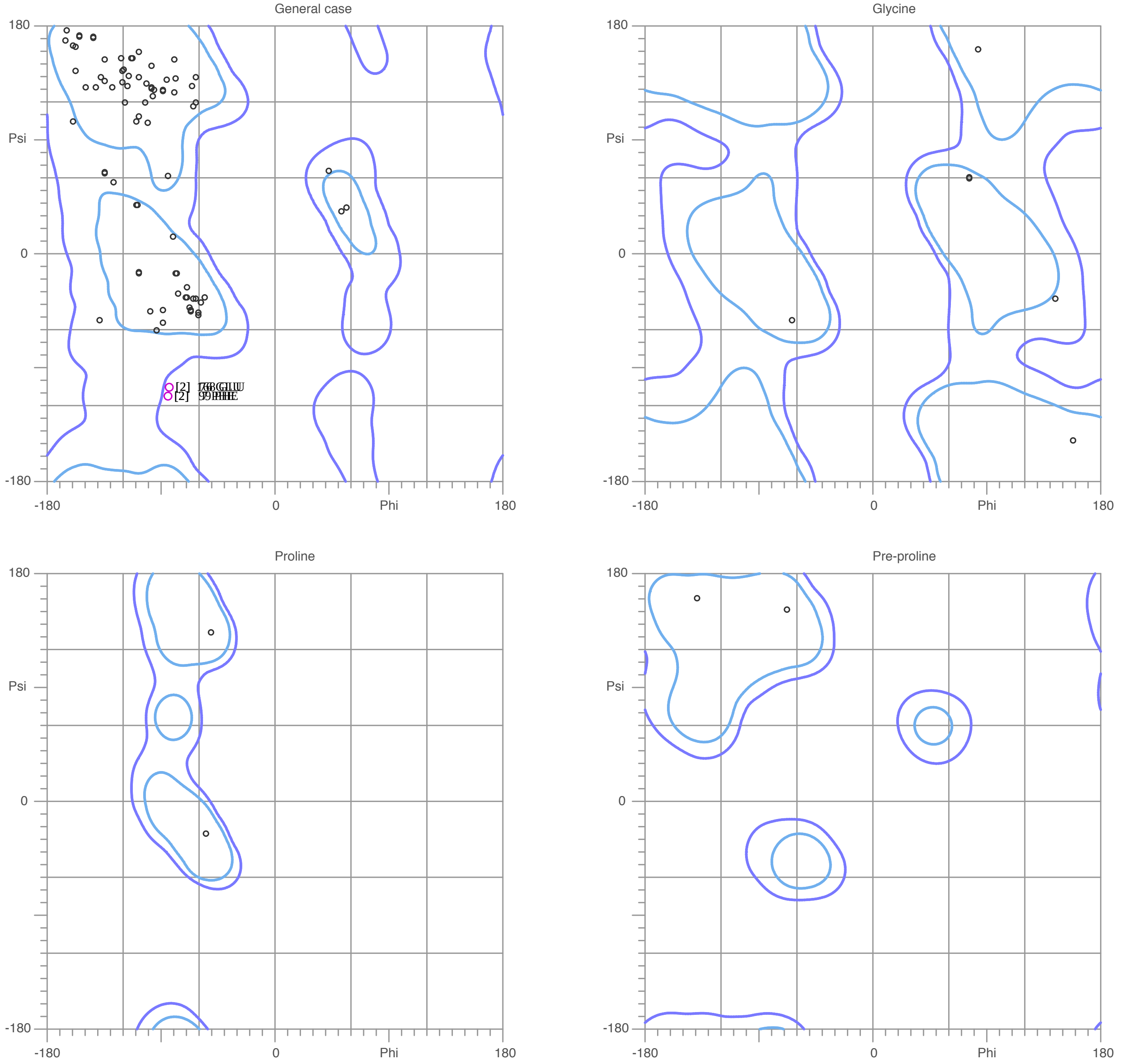
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 2



90.0% (144/160) 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):

- [2] 7 PHE (-85.0, -112.3)
- [2] 76 GLU (-84.8, -105.4)
- [2] 99 PHE (-85.1, -112.3)
- [2] 168 GLU (-84.8, -105.3)

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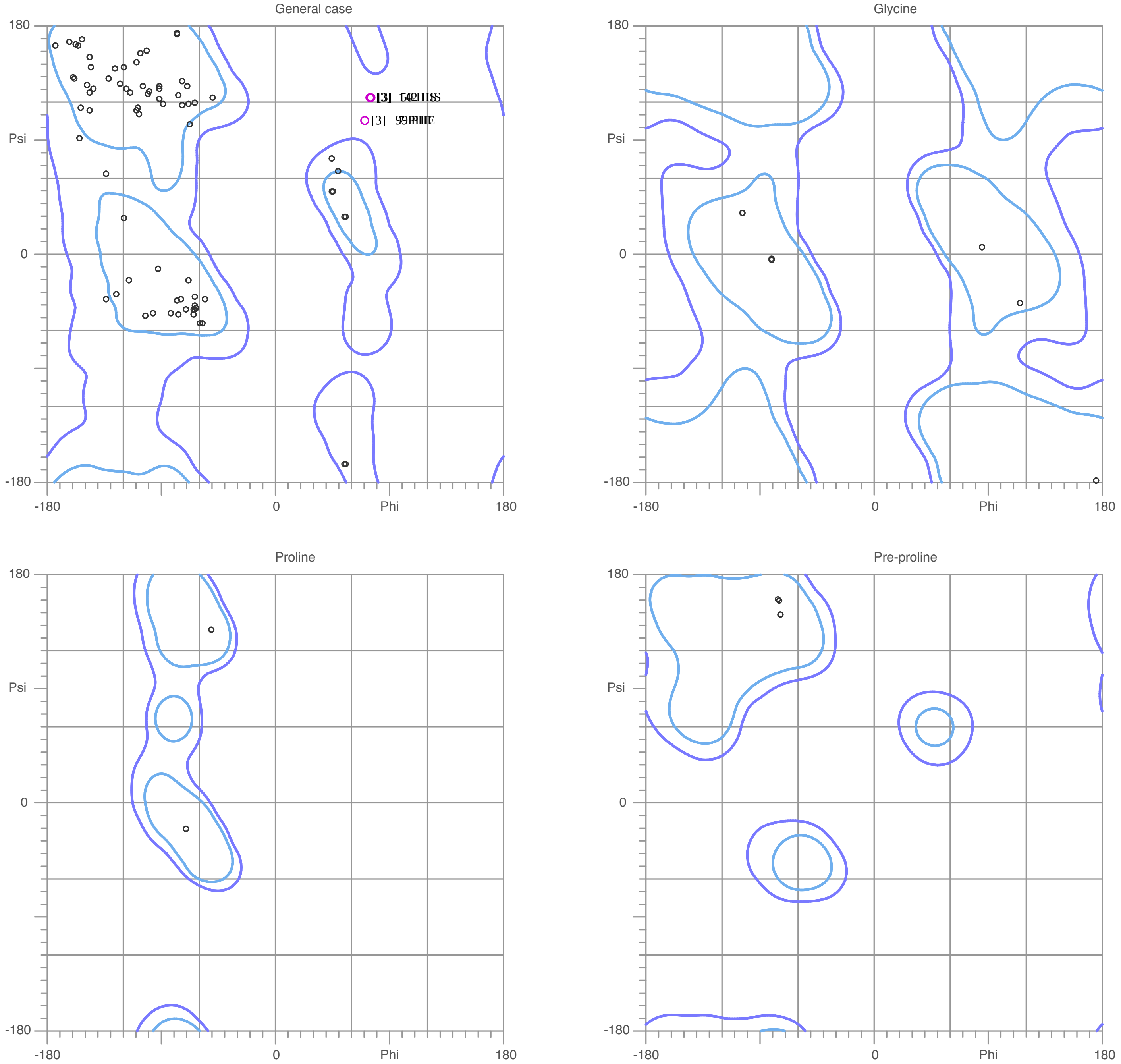
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 3



90.0% (144/160) 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):
[3] 7 PHE (70.4, 106.7)
[3] 50 HIS (75.0, 125.0)
[3] 99 PHE (70.3, 106.7)
[3] 142 HIS (75.0, 125.0)

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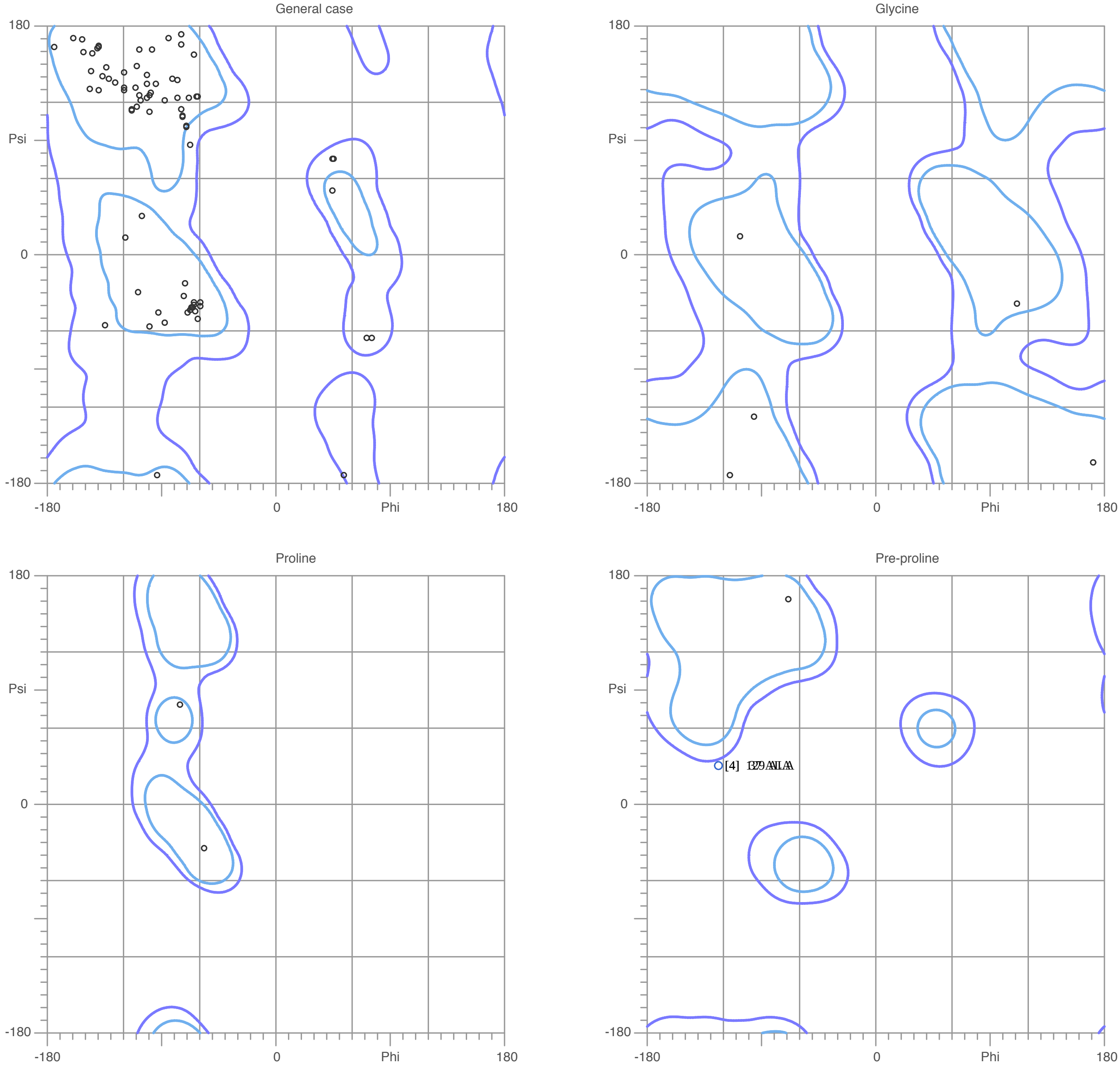
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 4



91.2% (146/160) 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):

[4] 37 ALA (-124.9, 31.5)
[4] 129 ALA (-125.0, 31.5)

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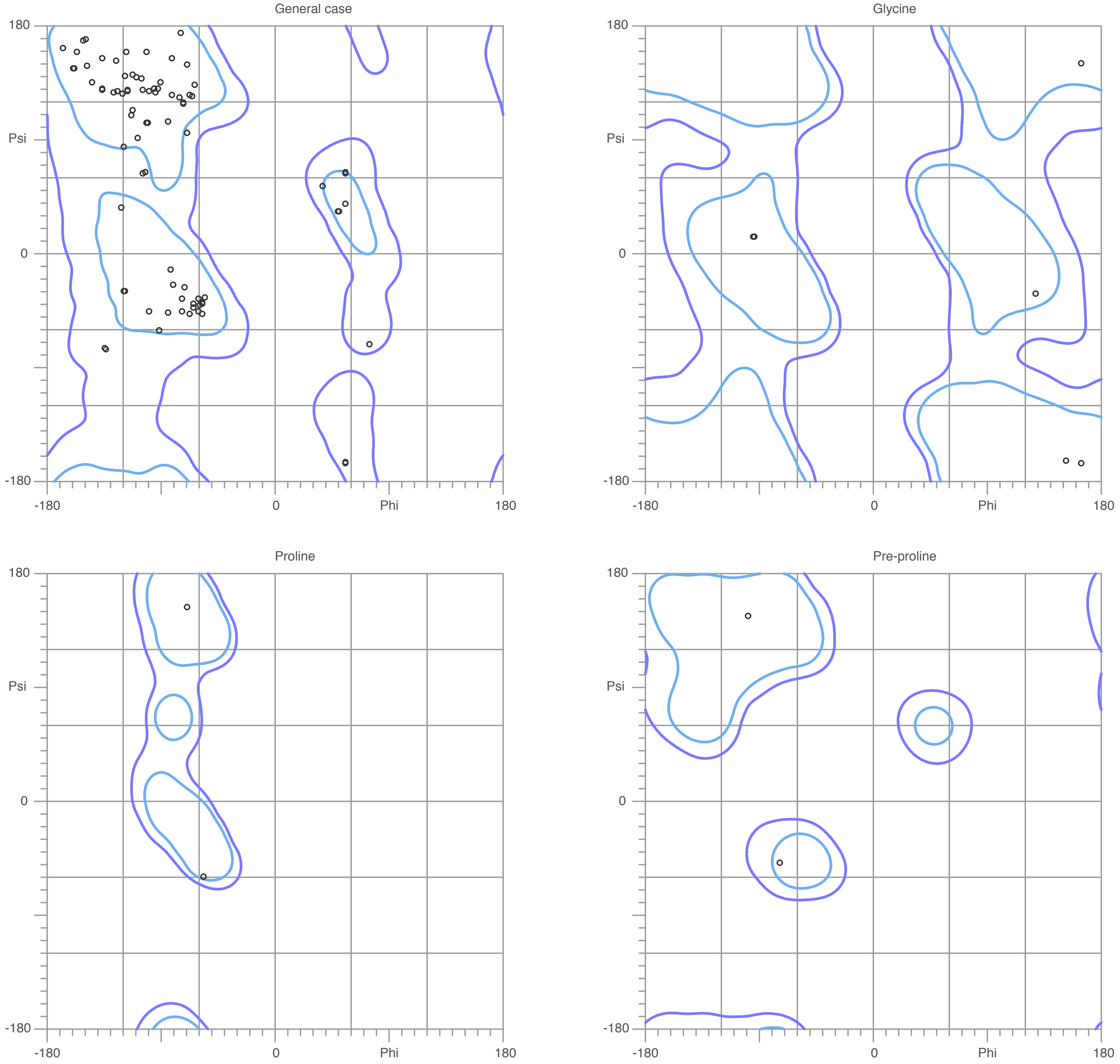
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 5



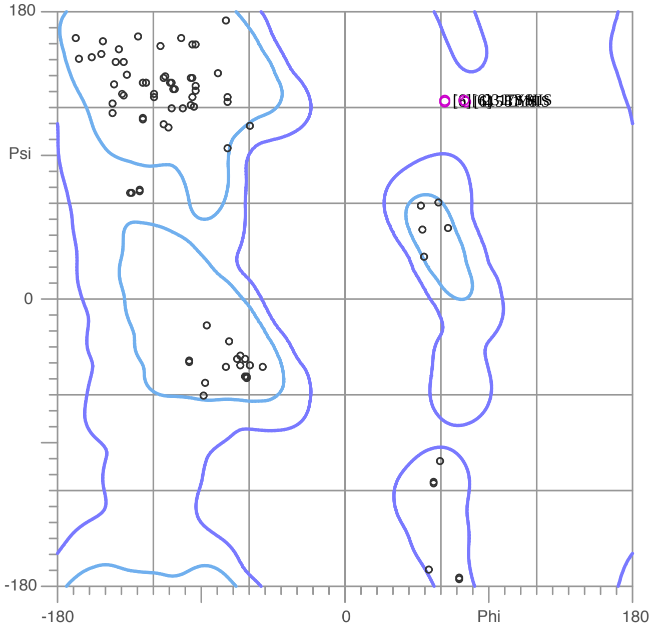
90.0% (144/160) of all residues were in favored (98%) regions.
100.0% (160/160) of all residues were in allowed (>99.8%) regions.

There were no outliers.

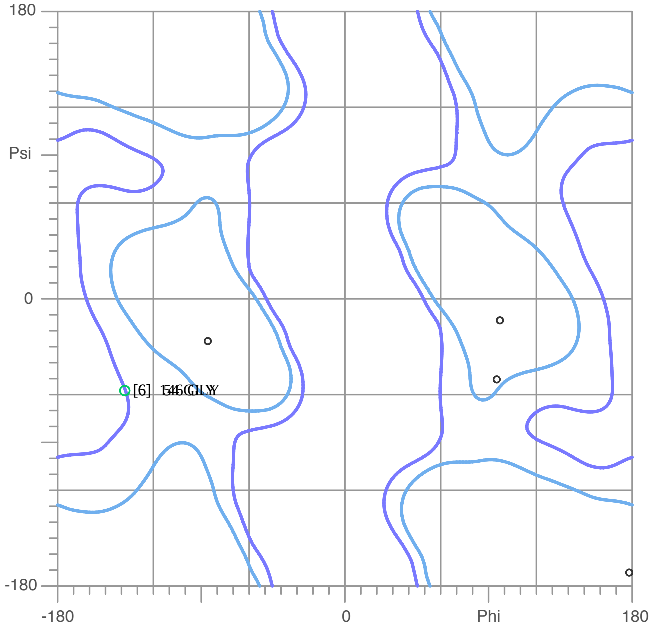
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 6

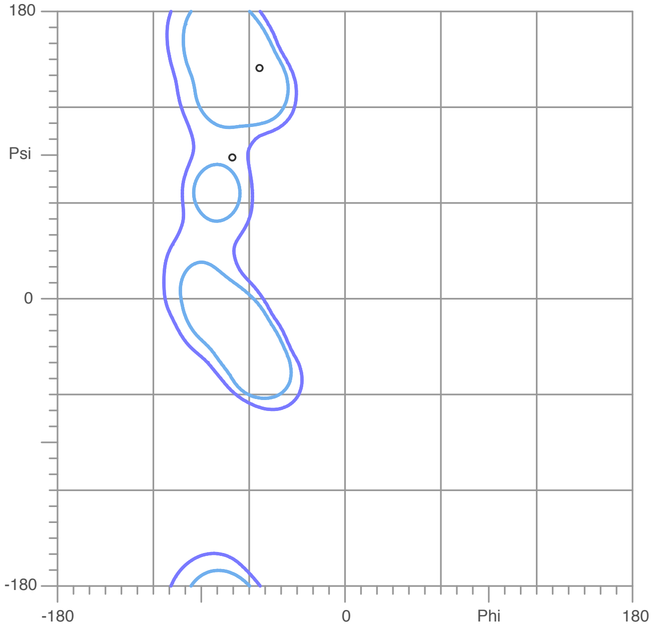
General case



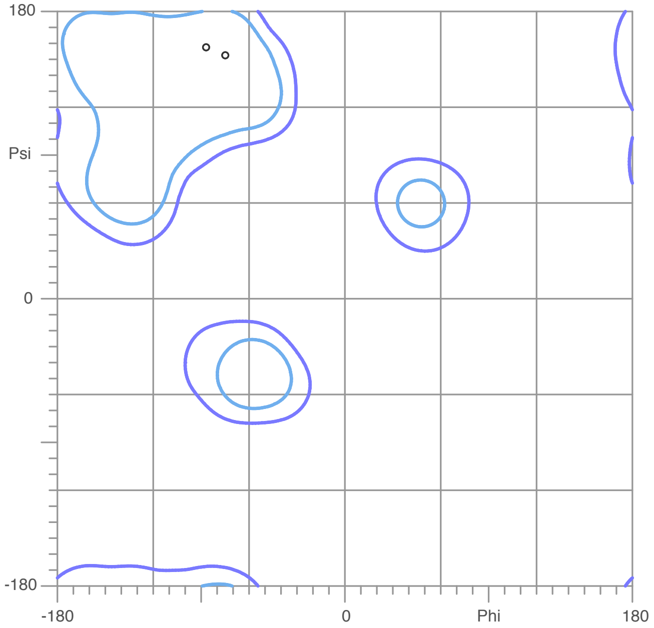
Glycine



Proline



Pre-proline



86.2% (138/160) 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] 23 LYS (62.9, 125.0)
[6] 54 GLY (-138.4, -57.1)
[6] 81 HIS (75.1, 125.0)
[6] 115 LYS (62.9, 125.0)
[6] 146 GLY (-138.4, -57.1)
[6] 173 HIS (75.0, 125.0)

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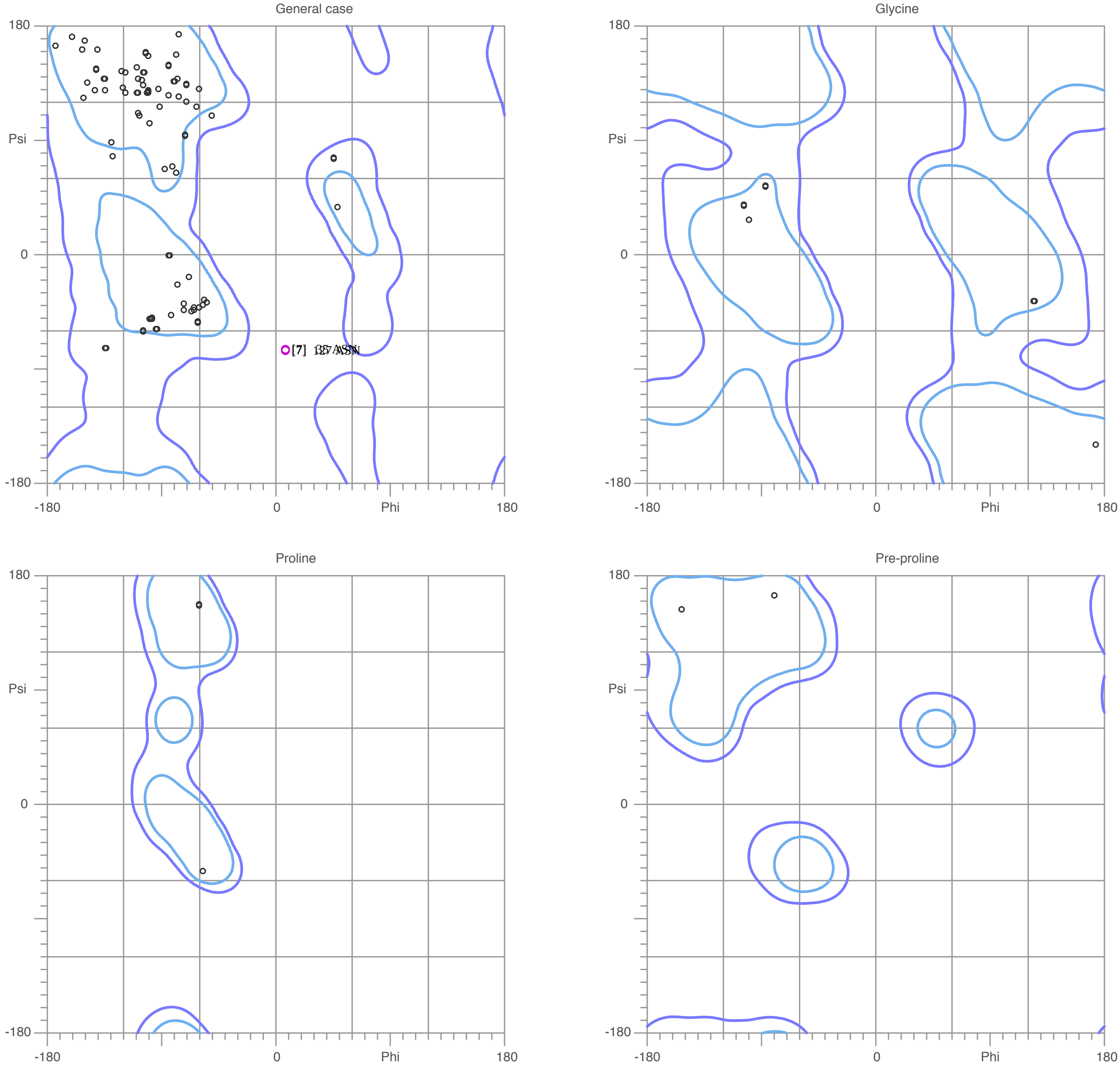
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 7



93.8% (150/160) 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):
[7] 35 ASN (7.6, -75.0)
[7] 127 ASN (7.7, -75.1)

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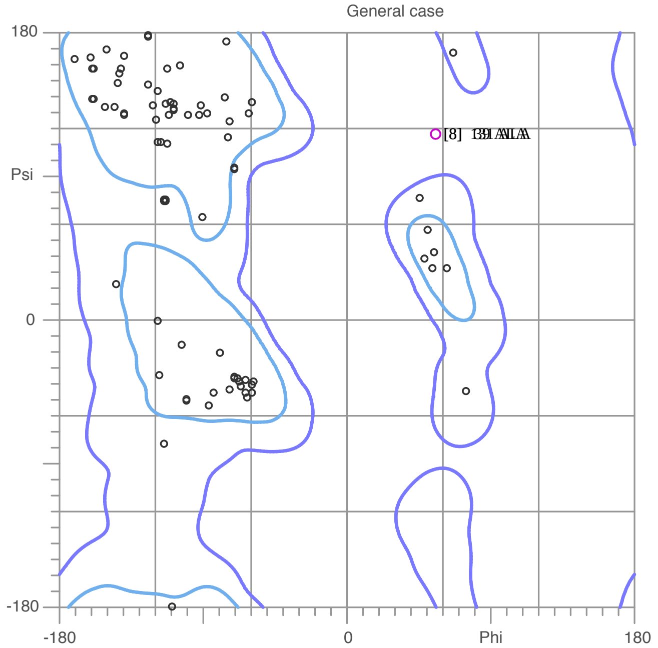
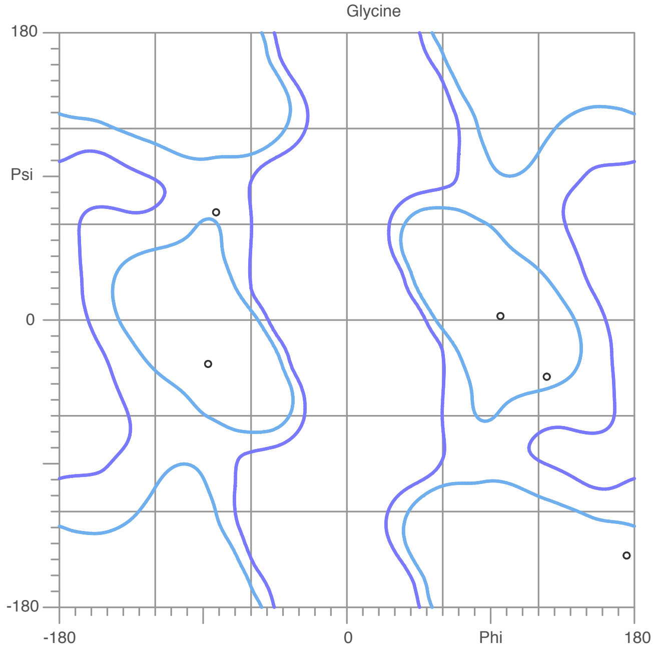
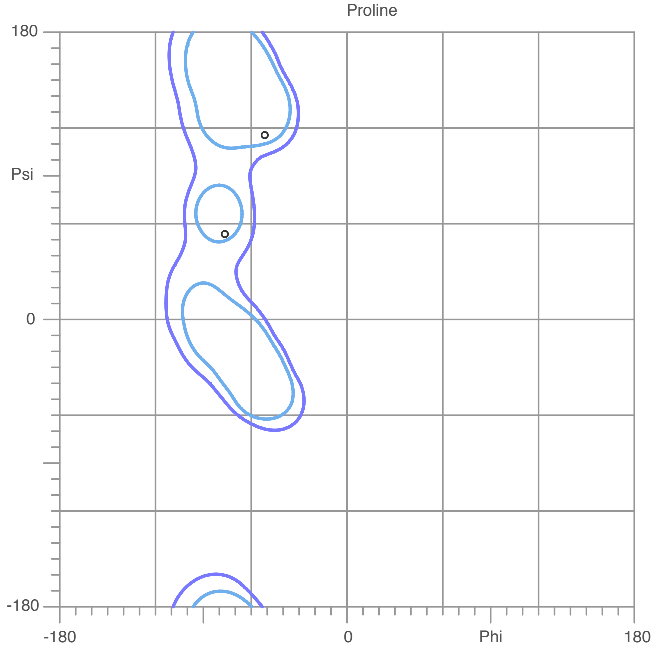
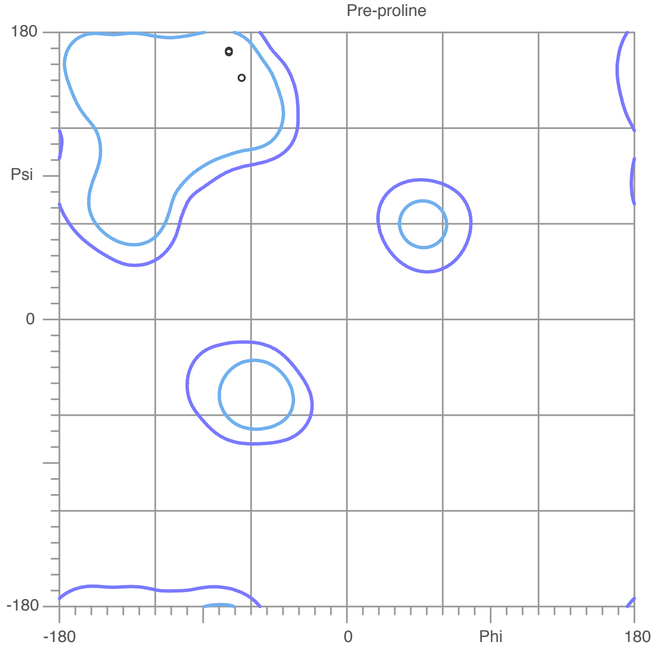
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 8







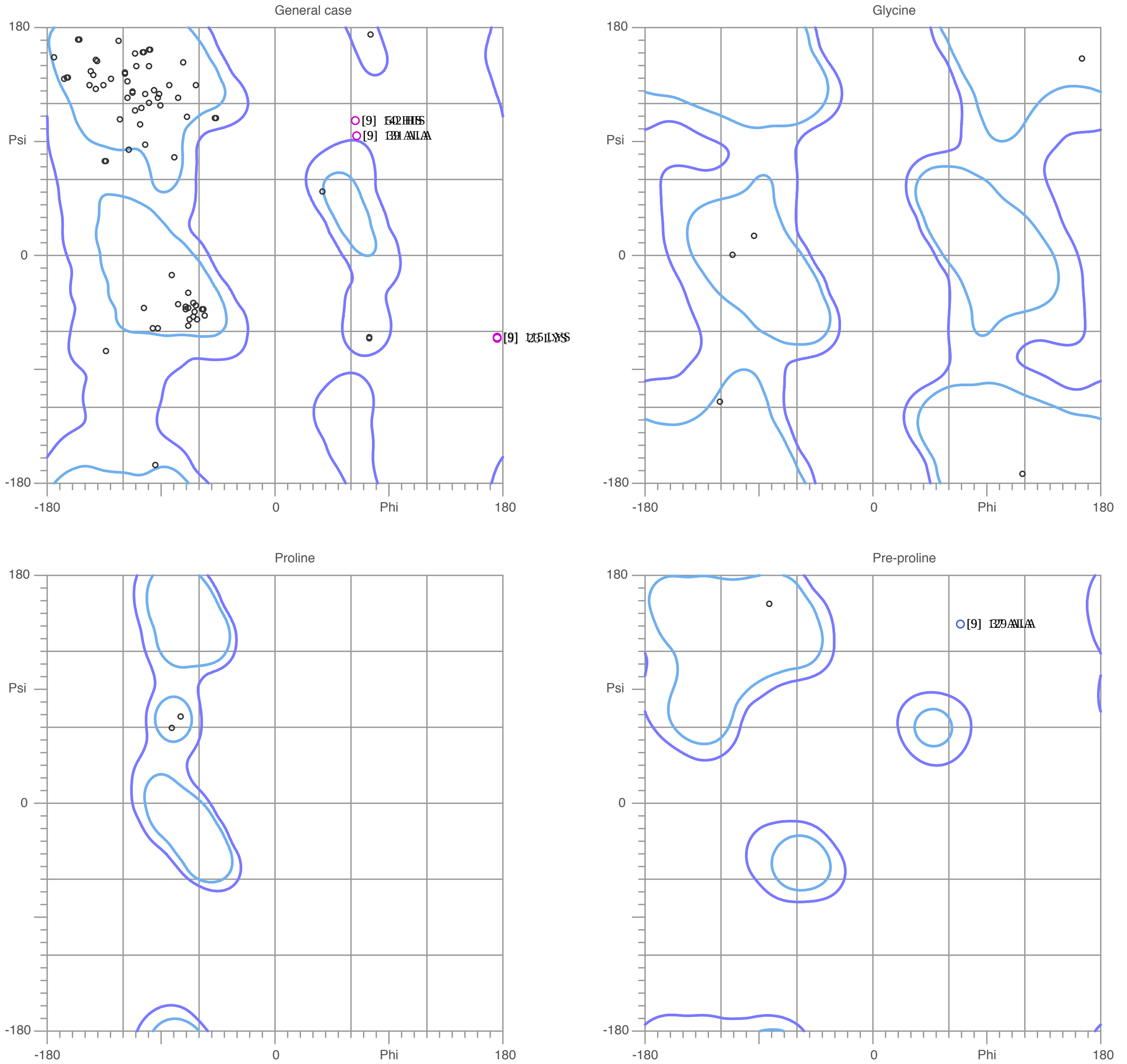


87.5% (140/160) of all residues were in favored (98%) regions.
98.8% (158/160) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[8] 39 ALA (55.0, 117.1)
[8] 131 ALA (55.0, 117.0)

MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 9



86.2% (138/160) 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):
[9] 23 LYS (175.0, -65.0)
[9] 37 ALA (69.5, 142.0)
[9] 39 ALA (64.9, 95.1)
[9] 50 HIS (63.7, 107.1)
[9] 115 LYS (175.0, -65.0)
[9] 129 ALA (69.5, 142.0)
[9] 131 ALA (64.9, 95.2)
[9] 142 HIS (63.7, 107.1)

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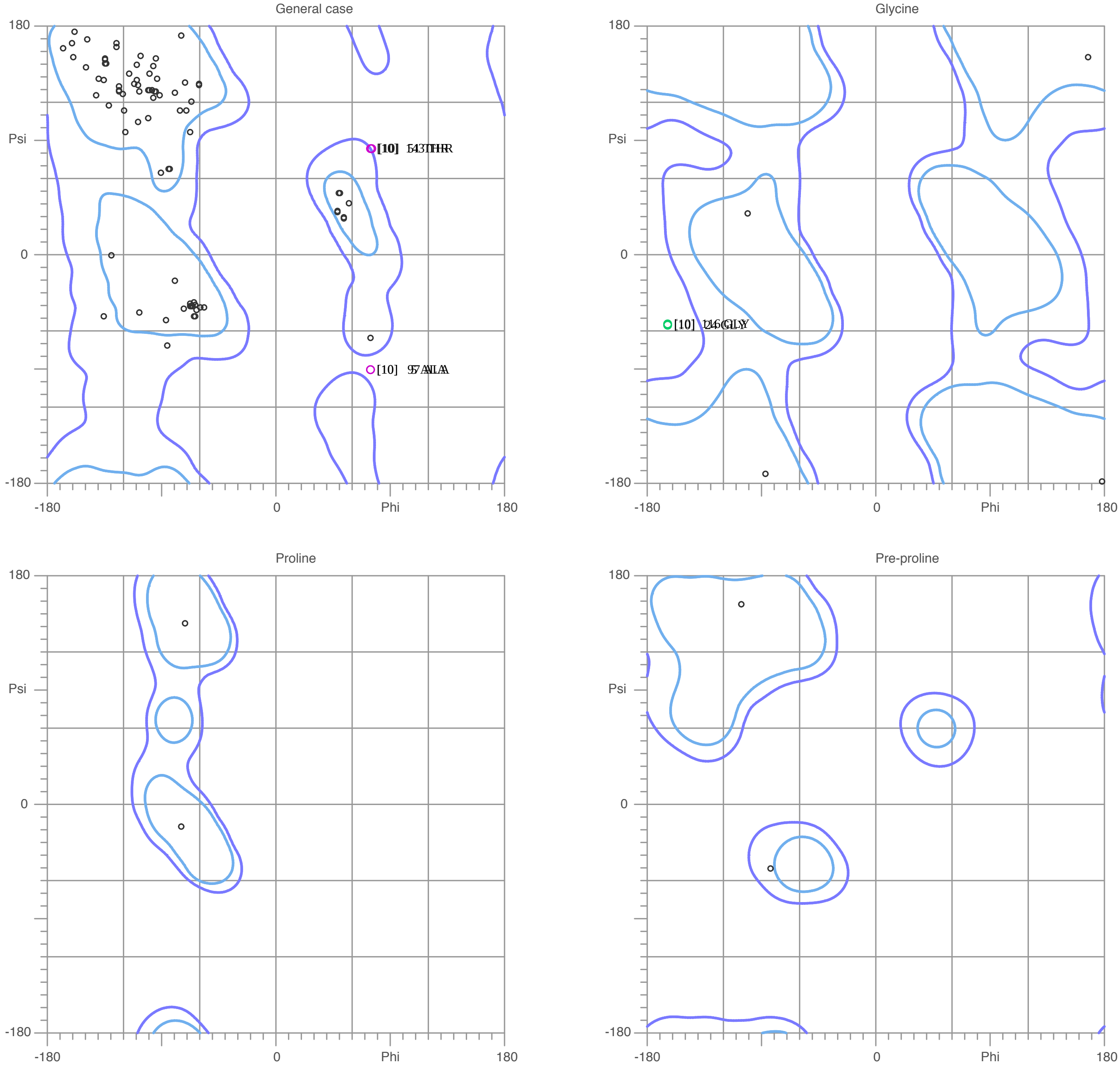
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 10



90.0% (144/160) 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):

[10] 5 ALA (74.9, -90.4)
[10] 24 GLY (-165.0, -55.1)
[10] 51 THR (75.0, 84.9)
[10] 97 ALA (75.0, -90.4)
[10] 116 GLY (-165.0, -55.0)
[10] 143 THR (75.0, 84.9)

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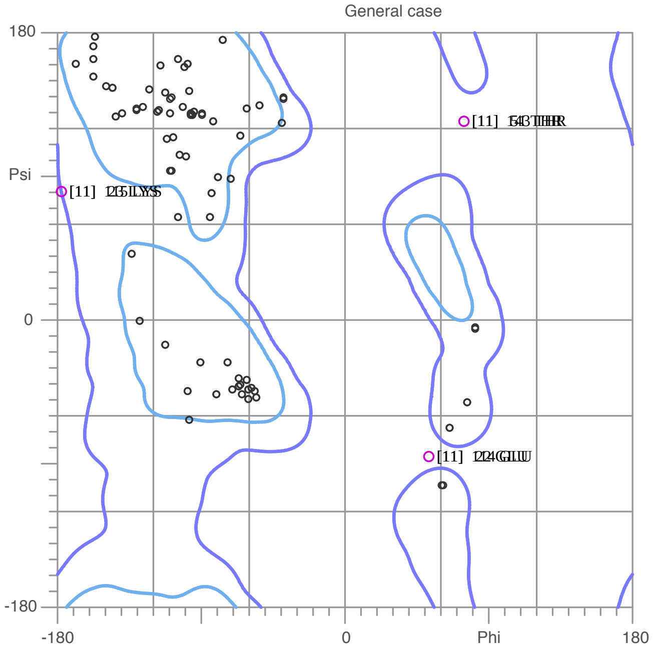
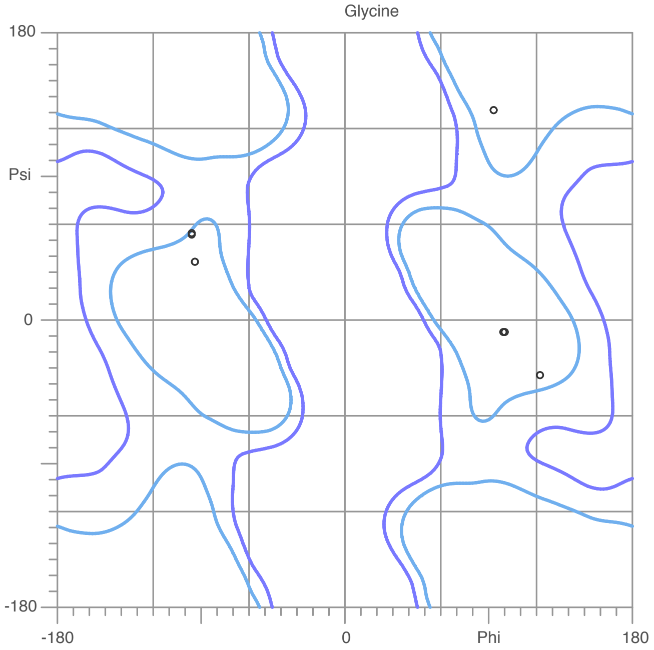
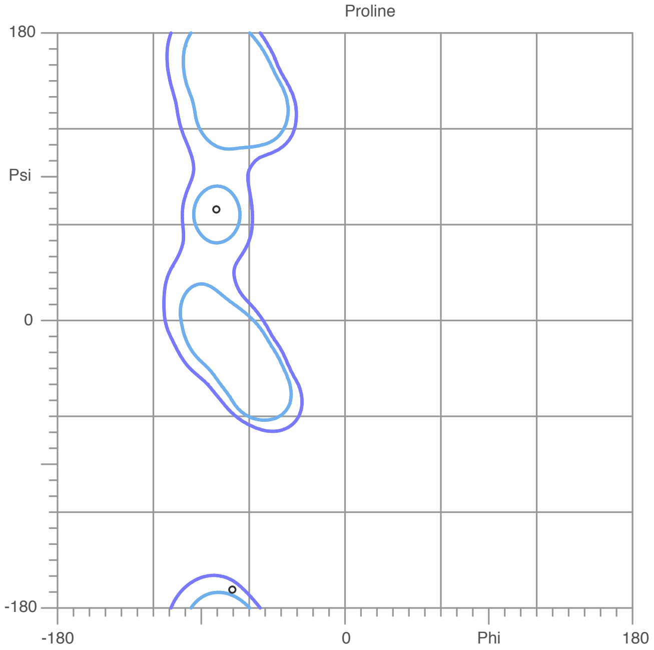
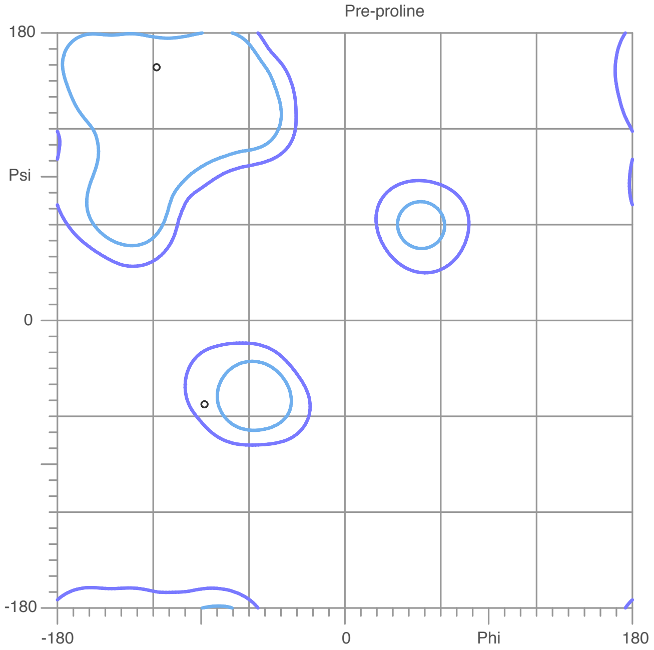
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 11







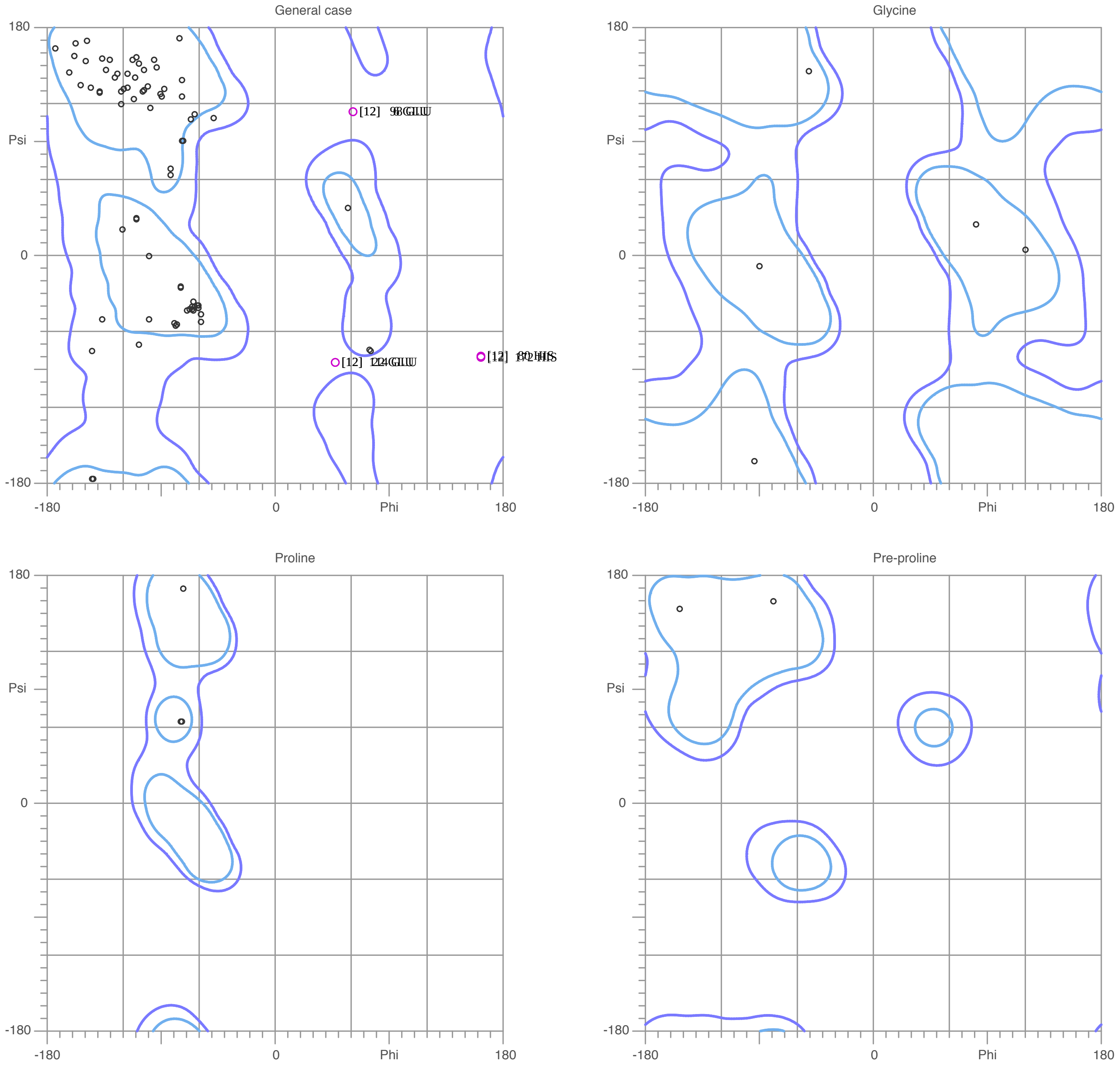


83.1% (133/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[11] 22 GLU (52.3, -85.1)
[11] 23 LYS (-178.5, 81.9)
[11] 51 THR (75.0, 125.0)
[11] 114 GLU (52.3, -85.1)
[11] 115 LYS (-178.4, 81.8)
[11] 143 THR (75.0, 125.0)

MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 12

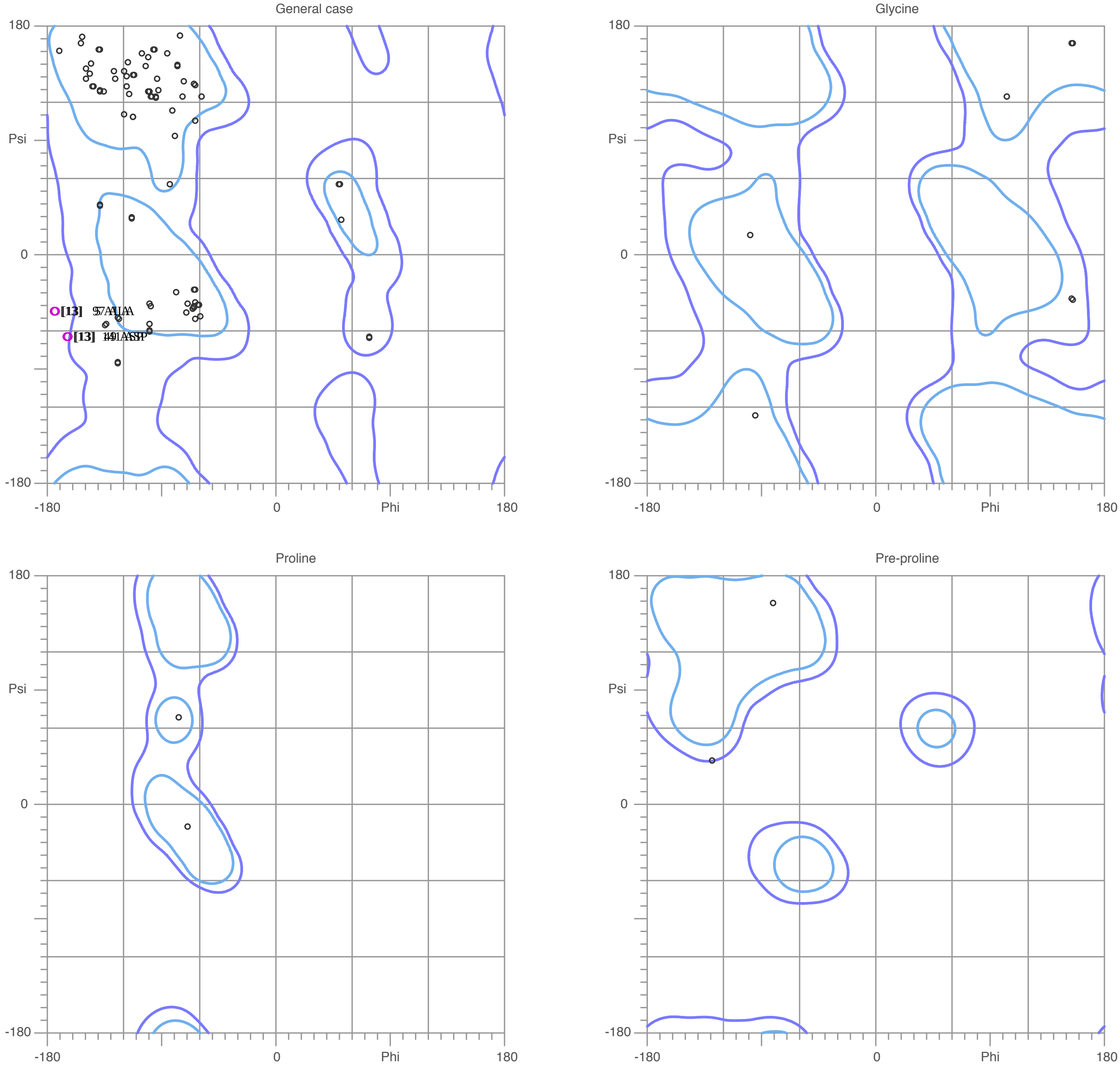


90.0% (144/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[12] 6 GLU (61.7, 114.0)
[12] 22 GLU (47.8, -85.0)
[12] 80 HIS (162.4, -80.0)
[12] 98 GLU (61.7, 114.1)
[12] 114 GLU (47.8, -85.0)
[12] 172 HIS (162.5, -80.0)

MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 13



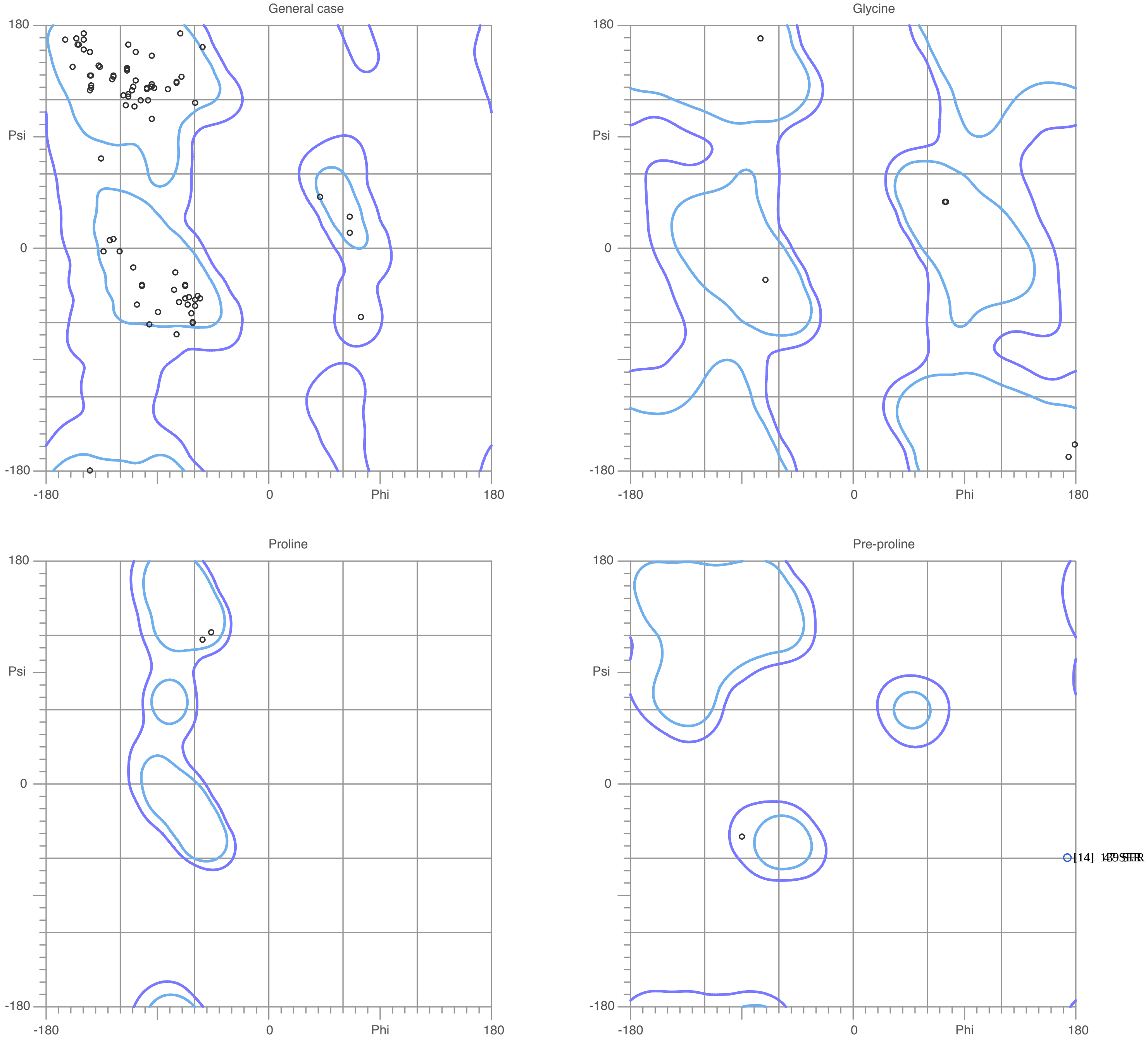
88.8% (142/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[13] 5 ALA (-175.0, -45.0)
[13] 49 ASP (-165.0, -64.9)
[13] 97 ALA (-175.0, -45.0)
[13] 141 ASP (-165.0, -65.0)

MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 14



92.5% (148/160) 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):
[14] 47 SER (173.7, -59.5)
[14] 139 SER (173.7, -59.5)

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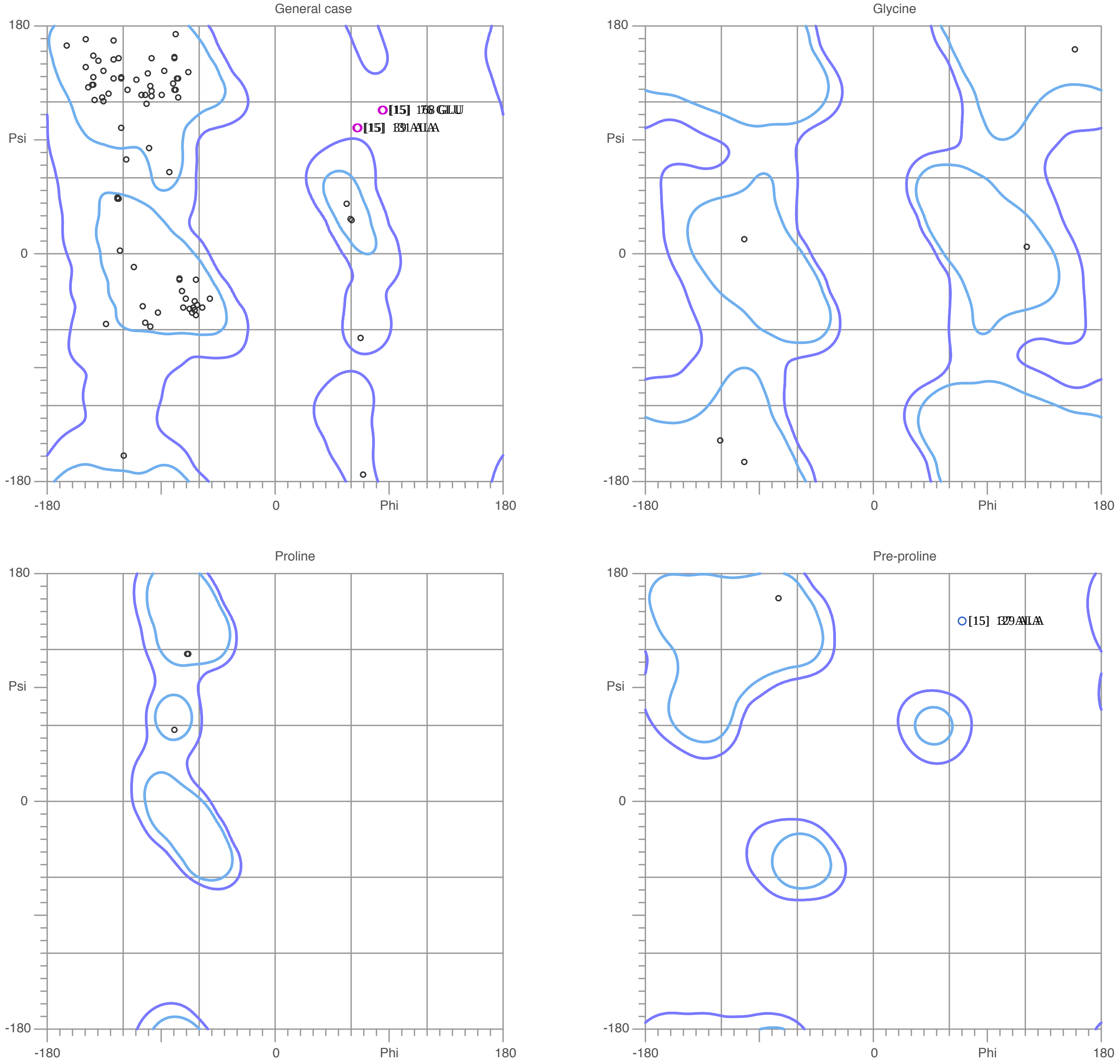
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 15



90.0% (144/160) 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 (70.8, 143.7)
[15]	39 ALA (65.0, 100.7)
[15]	76 GLU (85.0, 114.8)
[15]	129 ALA (70.8, 143.7)
[15]	131 ALA (65.0, 100.7)
[15]	168 GLU (85.0, 114.9)

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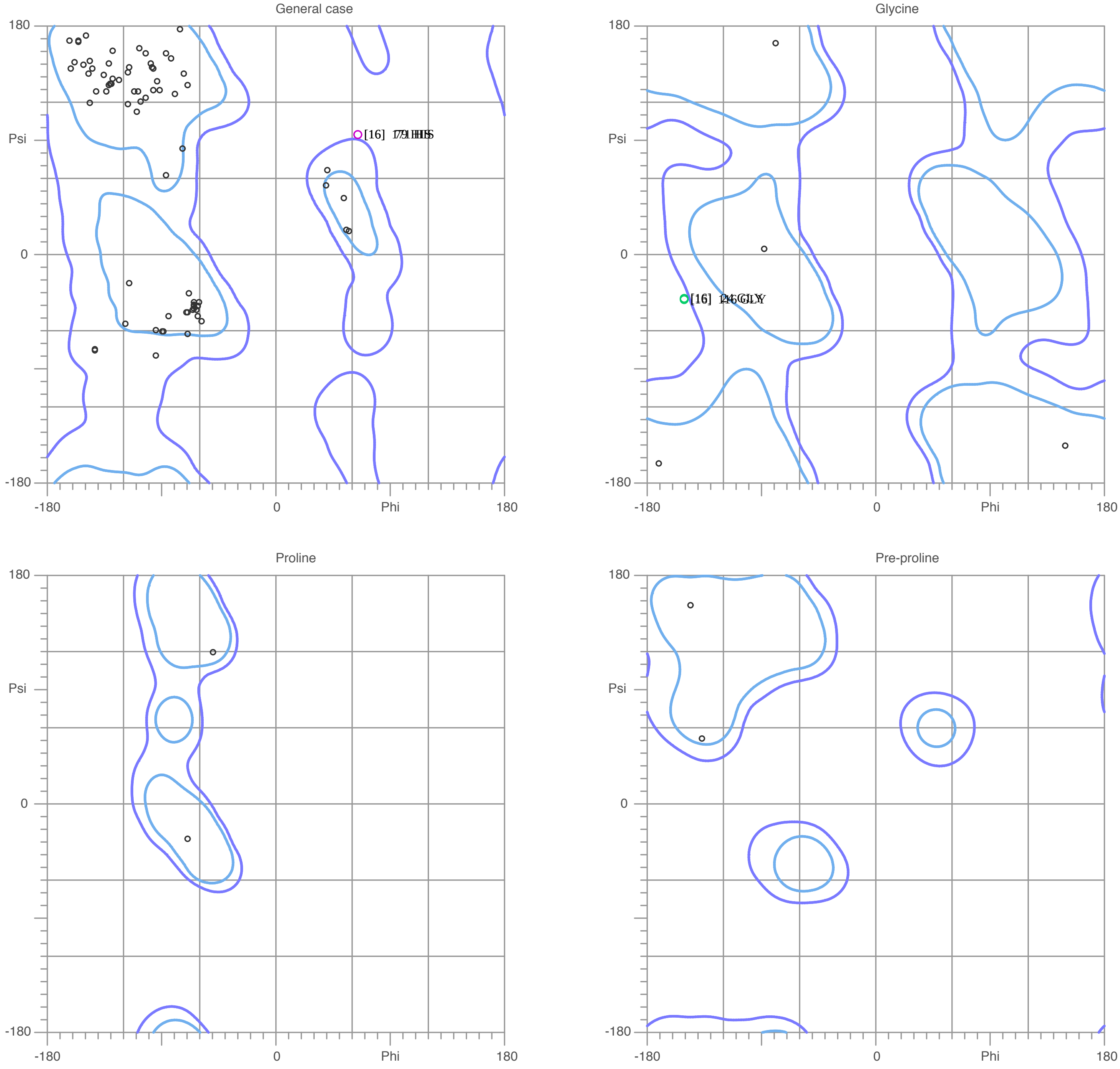
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 16



93.8% (150/160) 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] 24 GLY (-151.3, -35.0)
[16] 79 HIS (65.0, 95.0)
[16] 116 GLY (-151.3, -35.0)
[16] 171 HIS (65.0, 95.0)

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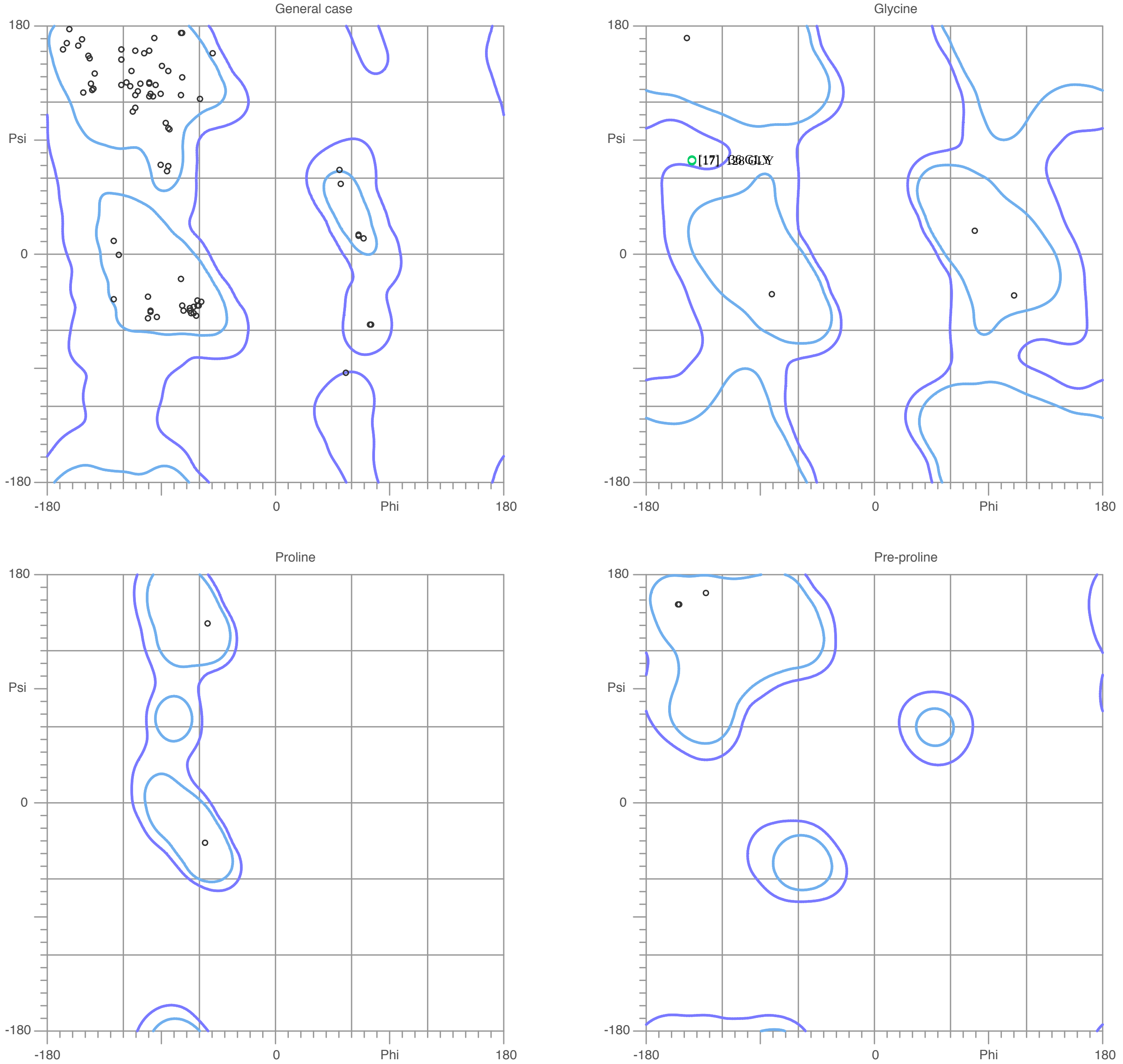
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 17



93.8% (150/160) 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):
[17] 36 GLY (-144.4, 75.0)
[17] 128 GLY (-144.4, 75.0)

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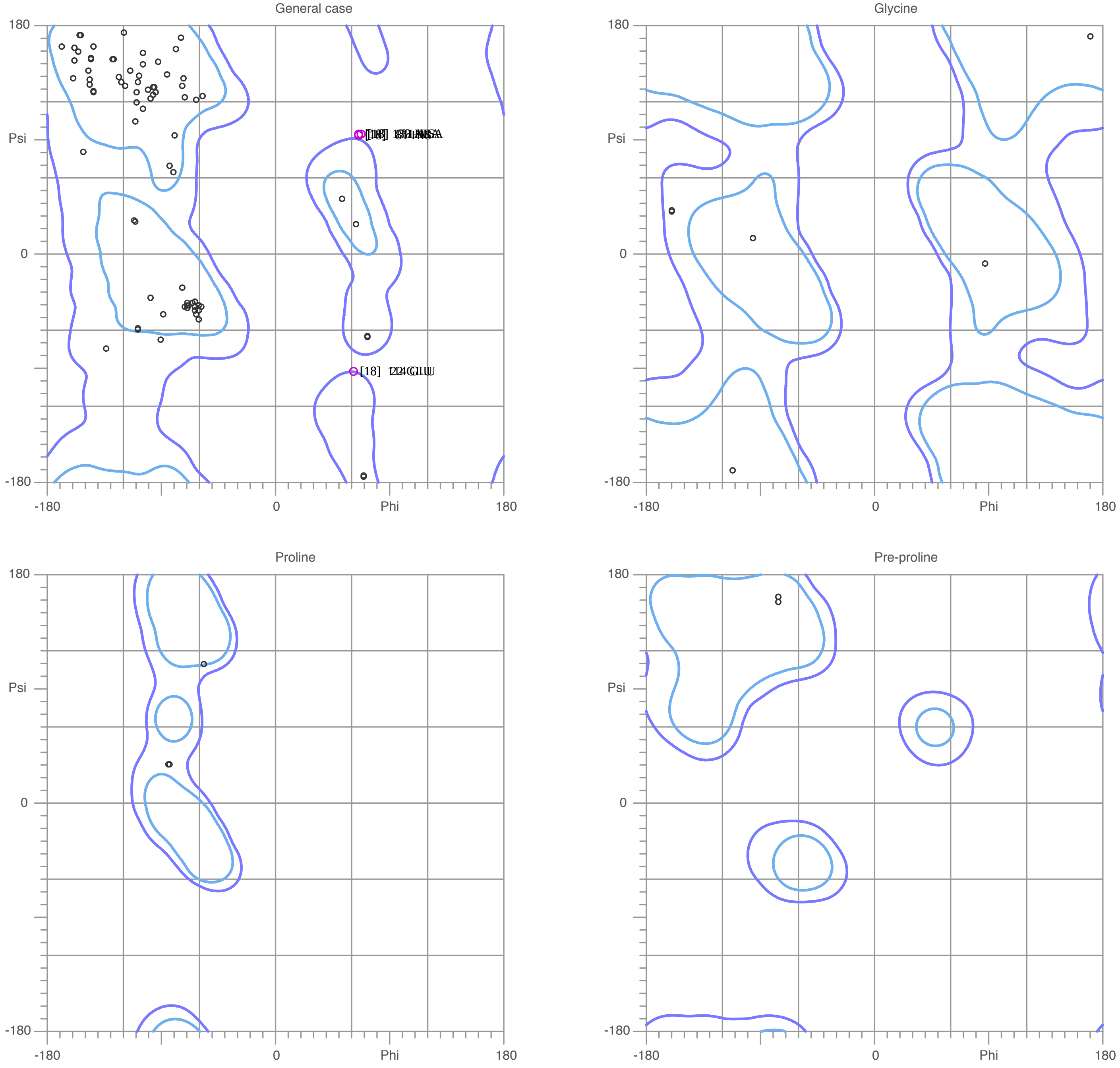
MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 18

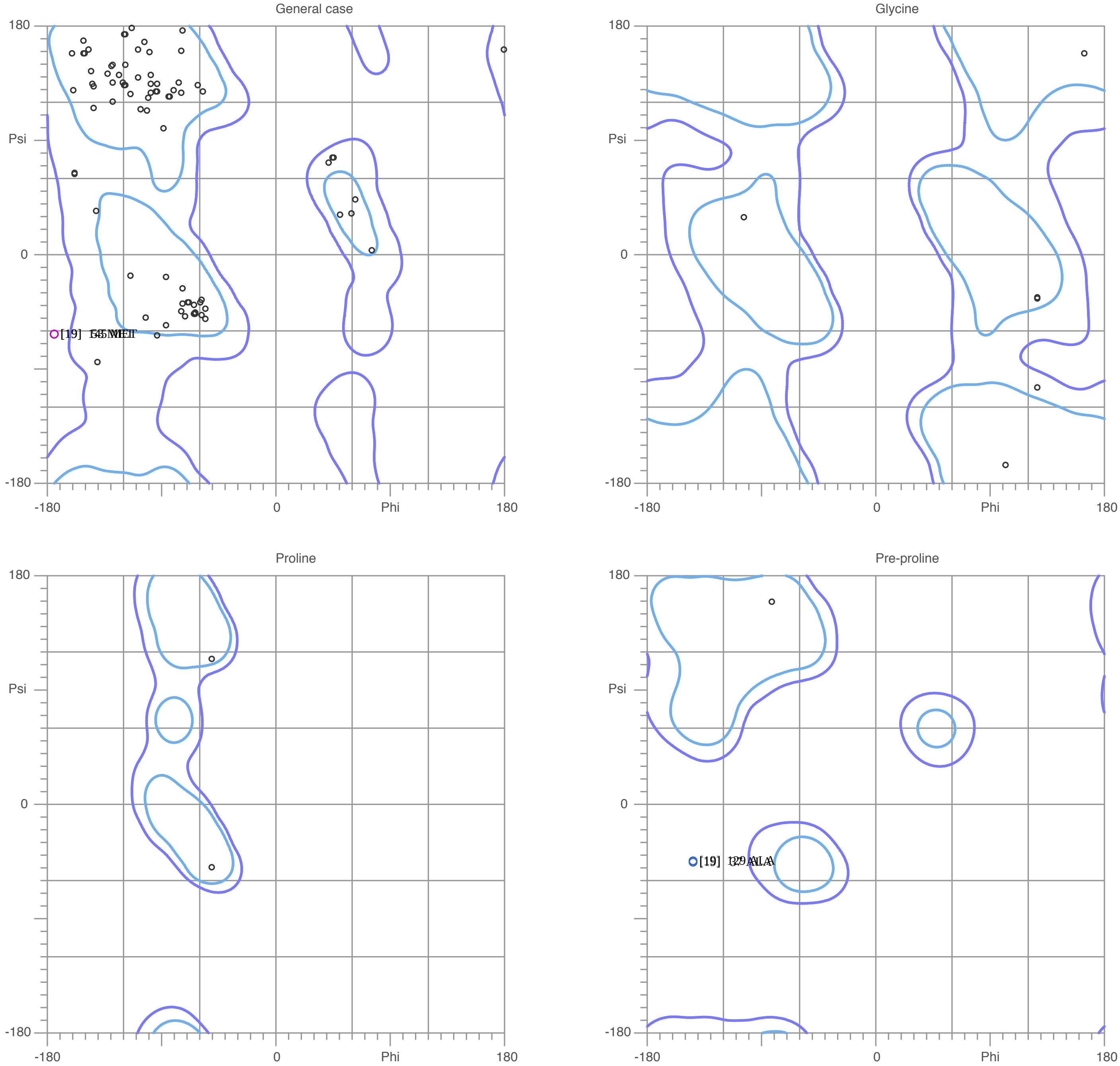


87.5% (140/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[18] 22 GLU (61.1, -92.7)
[18] 39 ALA (67.1, 95.3)
[18] 81 HIS (65.0, 95.0)
[18] 114 GLU (61.1, -92.7)
[18] 131 ALA (67.2, 95.2)
[18] 173 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 19



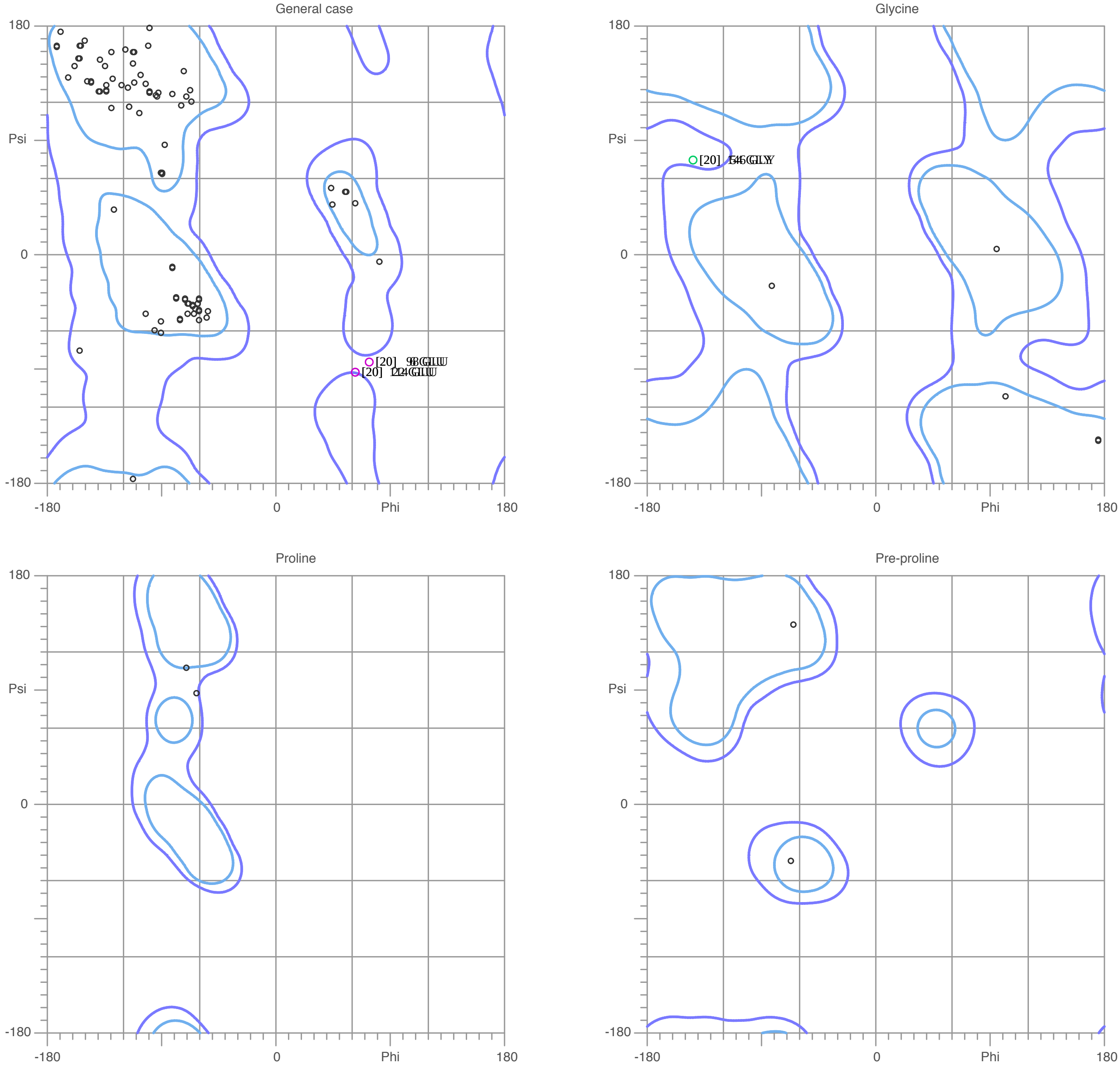
87.5% (140/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[19] 37 ALA (-145.0, -45.0)
[19] 53 MET (-175.0, -62.7)
[19] 129 ALA (-145.0, -45.0)
[19] 145 MET (-175.0, -62.7)

MolProbity Ramachandran analysis

SPR104_R3Cons_em_bcr3.pdb, model 20



92.5% (148/160) 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):
[20] 6 GLU (73.3, -85.0)
[20] 22 GLU (62.1, -92.7)
[20] 54 GLY (-145.0, 75.0)
[20] 98 GLU (73.2, -85.0)
[20] 114 GLU (62.2, -92.7)
[20] 146 GLY (-145.0, 75.0)

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