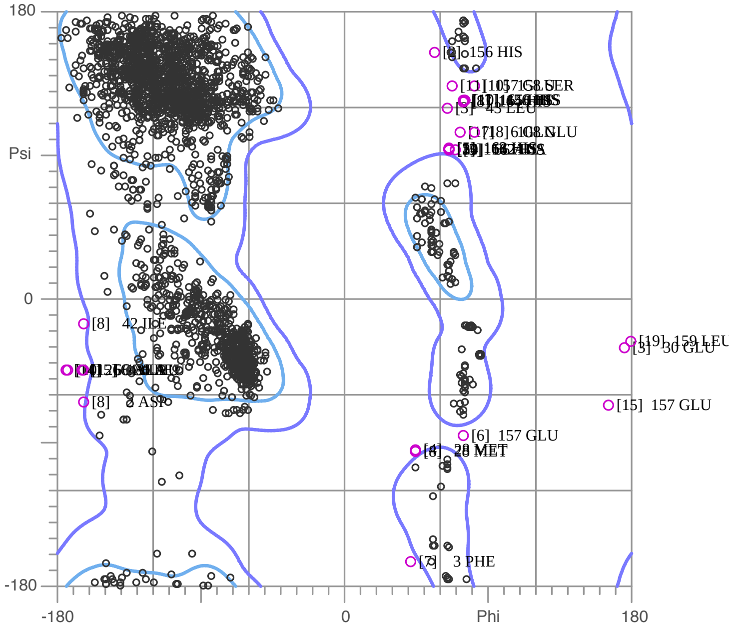
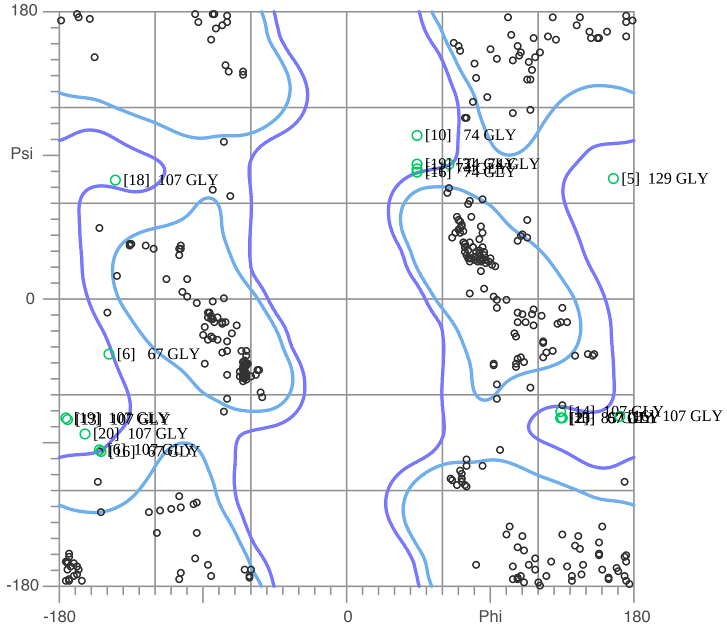
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, all models

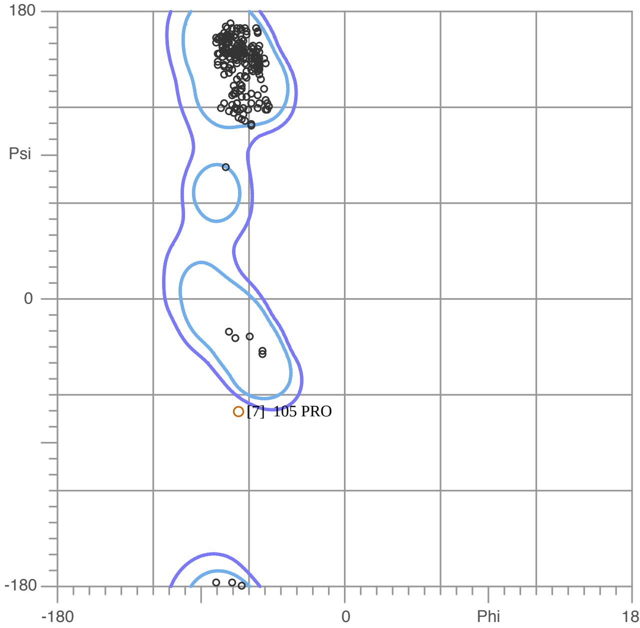
General case



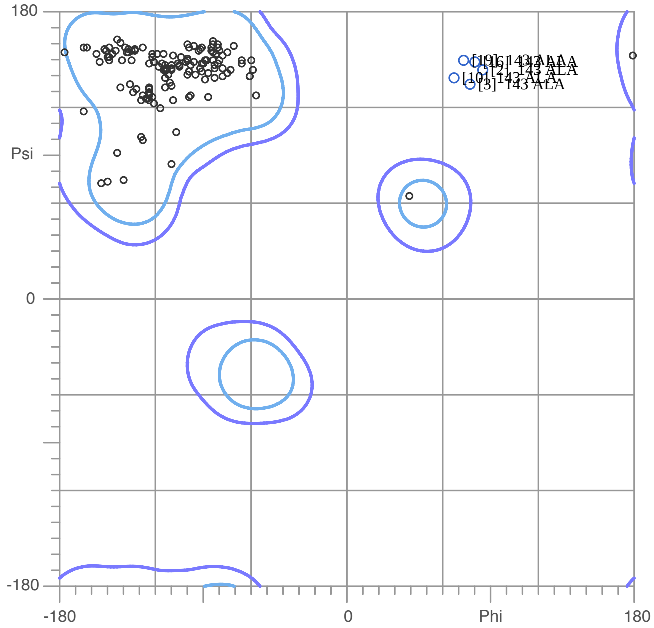
Glycine



Proline



Pre-proline



92.4% (3032/3280) of all residues were in favored (98%) regions.
98.4% (3227/3280) of all residues were in allowed (>99.8%) regions.

```
There were 53 outliers (phi, psi):
   [1]   74 GLY (45.0, 82.8)
   [1]  161 HIS (75.0, 125.0)
   [1]  163 HIS (65.0, 95.0)
   [2]   85 GLY (135.0, -75.0)
   [2]  143 ALA (85.1, 144.5)
   [2]  156 HIS (56.6, 155.0)
   [3]   30 GLU (175.1, -30.7)
   [3]   43 LEU (65.0, 120.1)
   [3]   74 GLY (65.0, 85.9)
   [3]  143 ALA (77.8, 135.4)
   [3]  164 HIS (65.0, 95.0)
   [4]   28 MET (44.9, -95.0)
   [5]   66 ALA (69.3, 95.0)
   [5]  129 GLY (167.4, 76.3)
   [5]  163 HIS (65.0, 95.0)
   [6]   67 GLY (-149.2, -34.9)
   [6]  107 GLY (-155.1, -95.0)
   [6]  157 GLU (74.9, -85.1)
   [7]    3 PHE (41.9, -165.0)
   [7]  105 PRO (-67.6, -70.6)
   [8]    2 ASP (-164.7, -65.0)
   [8]   28 MET (45.0, -95.0)
   [8]   42 ILE (-165.0, -15.0)
   [8]  164 HIS (75.0, 125.0)
   [10]   66 ALA (-175.0, -45.0)
   [10]   74 GLY (44.9, 103.1)
   [10]  143 ALA (67.2, 139.7)
   [10]  156 HIS (75.0, 125.1)
   [10]  158 SER (81.5, 134.9)
   [11]  157 GLU (67.1, 135.0)
   [12]  136 LEU (-164.9, -45.0)
   [13]   67 GLY (135.0, -75.0)
   [13]  107 GLY (-175.1, -75.0)
   [14]   66 ALA (-175.1, -44.9)
   [14]  107 GLY (135.0, -70.9)
   [14]  162 HIS (65.0, 95.0)
   [15]   43 LEU (-165.0, -45.0)
   [15]  157 GLU (165.0, -66.7)
   [16]   67 GLY (-155.0, -95.0)
   [16]   74 GLY (45.0, 80.6)
   [16]  107 GLY (171.8, -73.7)
   [16]  143 ALA (80.7, 149.8)
   [17]    6 GLN (72.1, 105.5)
   [17]  156 HIS (75.0, 125.0)
   [18]  107 GLY (-145.0, 75.0)
   [18]  108 GLU (81.9, 105.0)
   [19]   74 GLY (45.0, 86.0)
   [19]  107 GLY (-176.5, -75.0)
   [19]  143 ALA (73.2, 150.1)
   [19]  159 LEU (179.6, -26.5)
   [20]   67 GLY (135.0, -74.9)
   [20]  107 GLY (-165.0, -85.0)
   [20]  162 HIS (65.1, 95.0)
```

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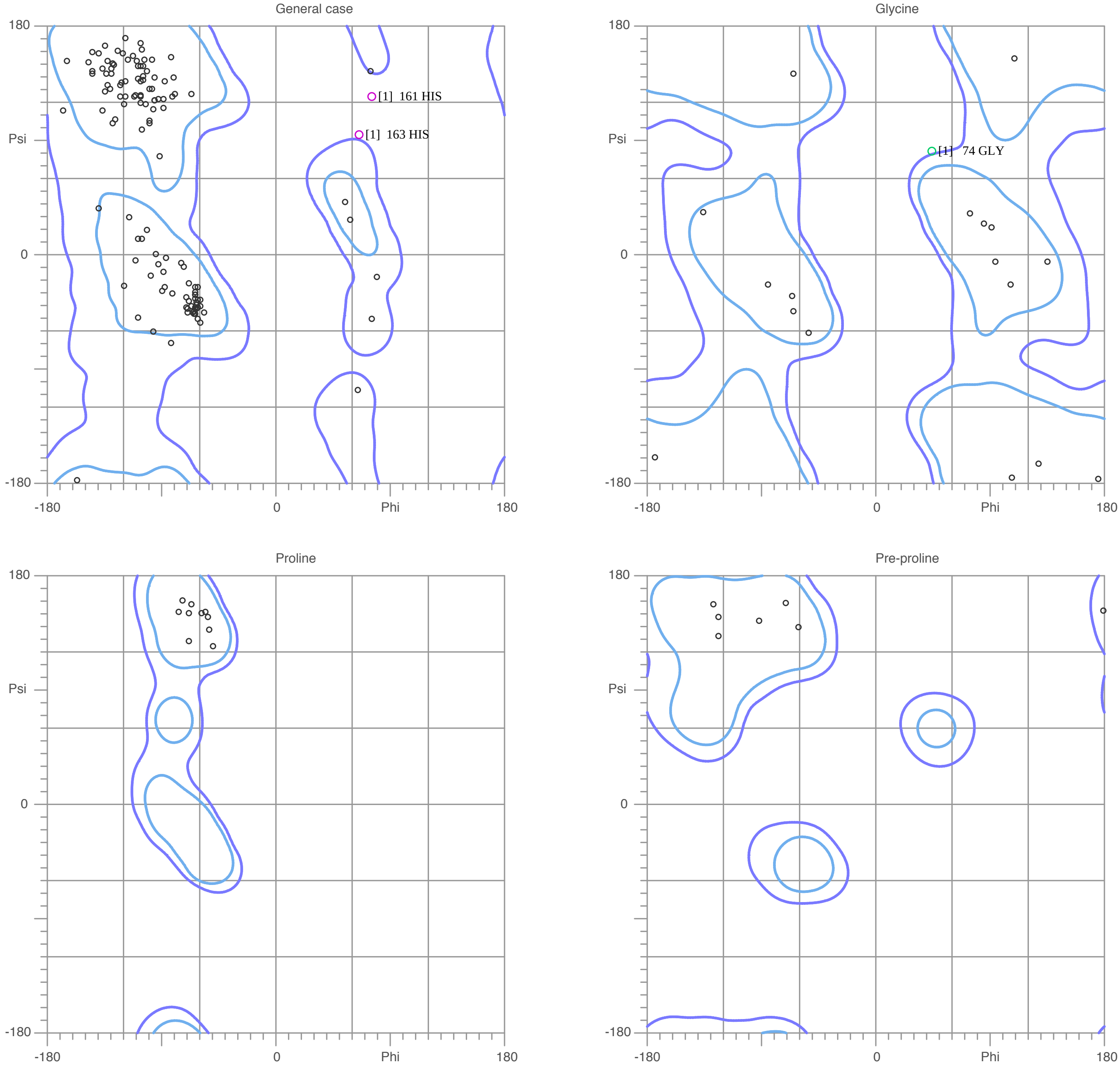
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 1



93.3% (153/164) 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):
 [1] 74 GLY (45.0, 82.8)
 [1] 161 HIS (75.0, 125.0)
 [1] 163 HIS (65.0, 95.0)

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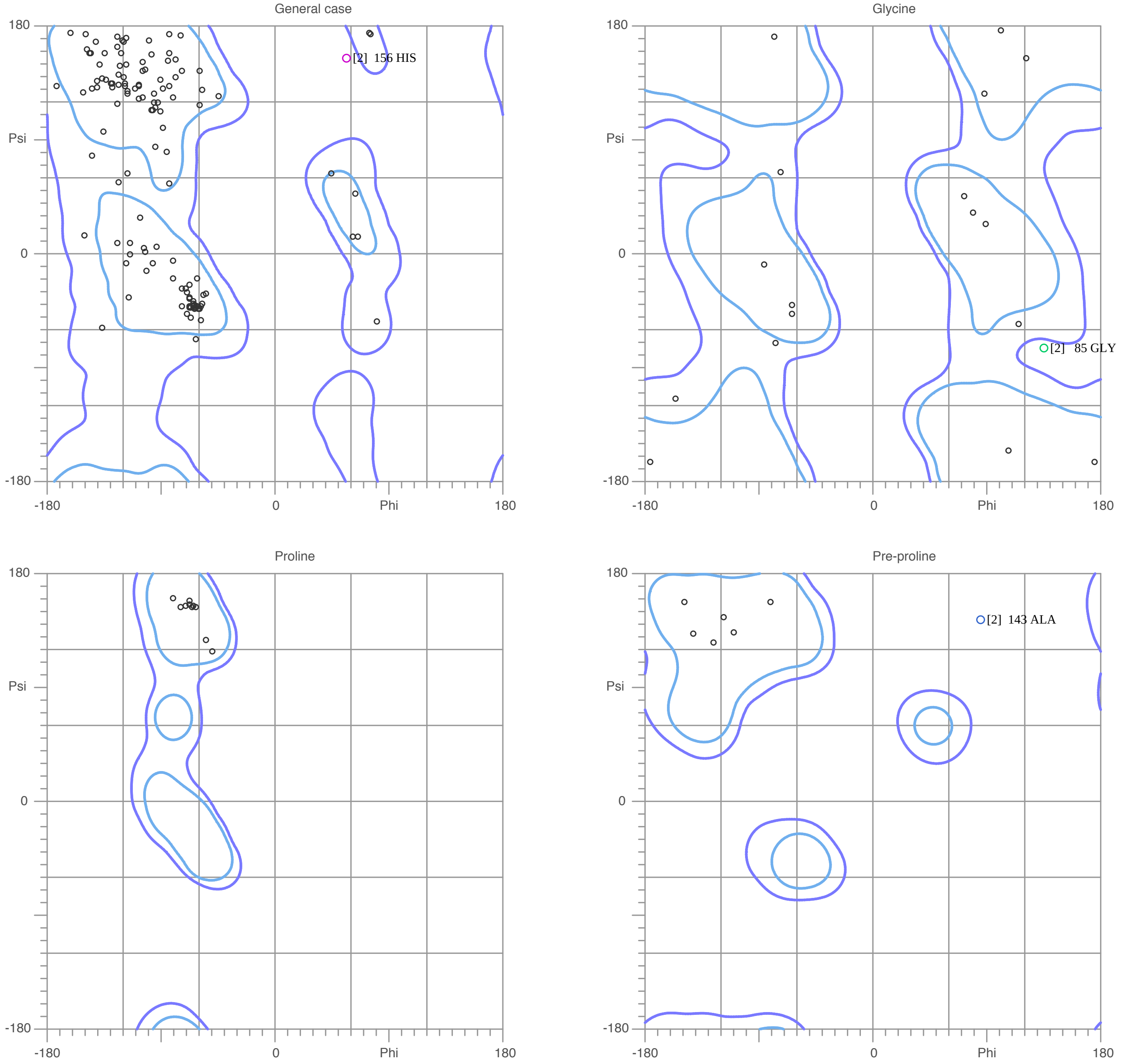
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 2



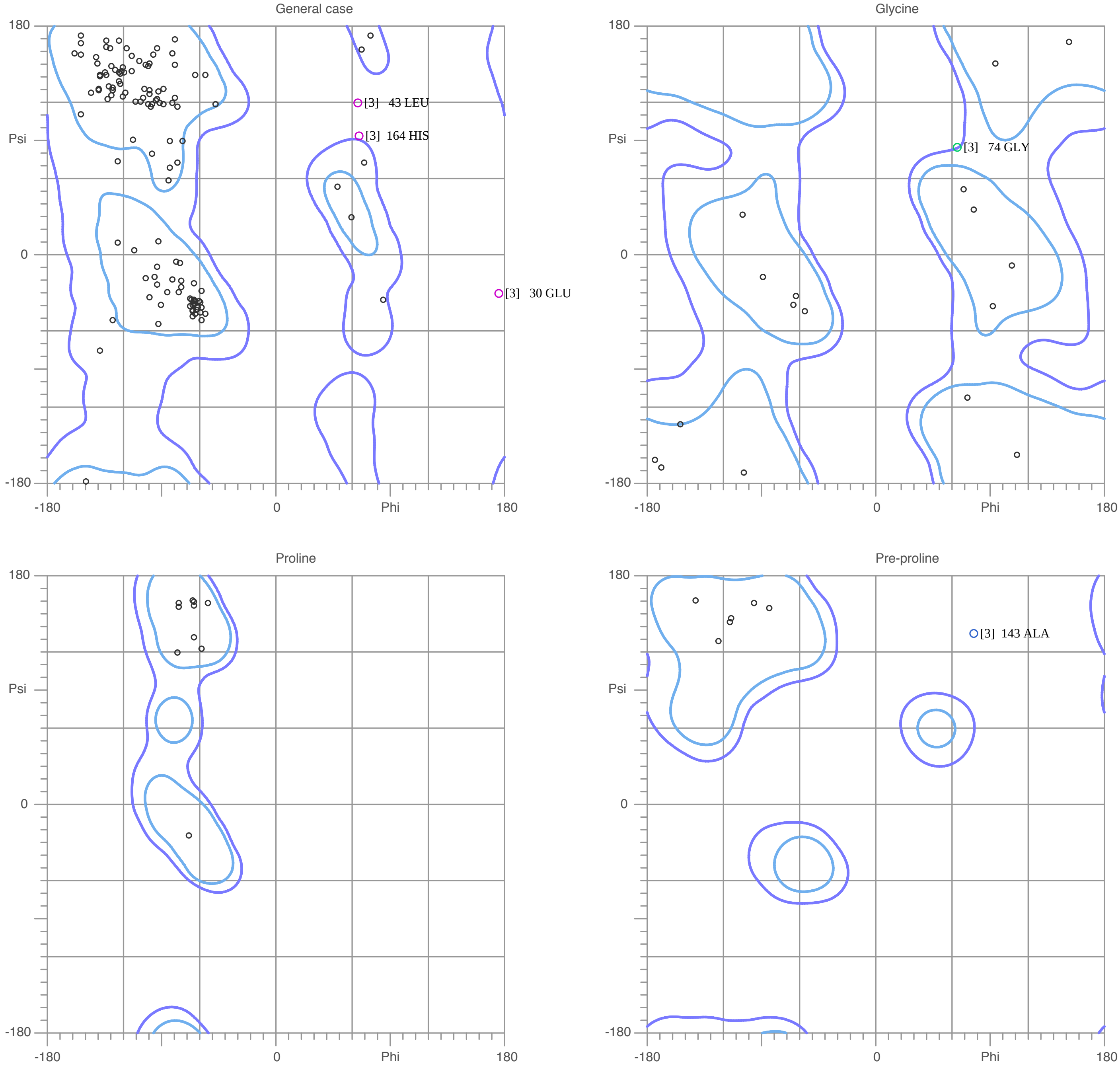
89.0% (146/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[2] 85 GLY (135.0, -75.0)
[2] 143 ALA (85.1, 144.5)
[2] 156 HIS (56.6, 155.0)

MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 3



92.7% (152/164) 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):

[3] 30 GLU (175.1, -30.7)
[3] 43 LEU (65.0, 120.1)
[3] 74 GLY (65.0, 85.9)
[3] 143 ALA (77.8, 135.4)
[3] 164 HIS (65.0, 95.0)

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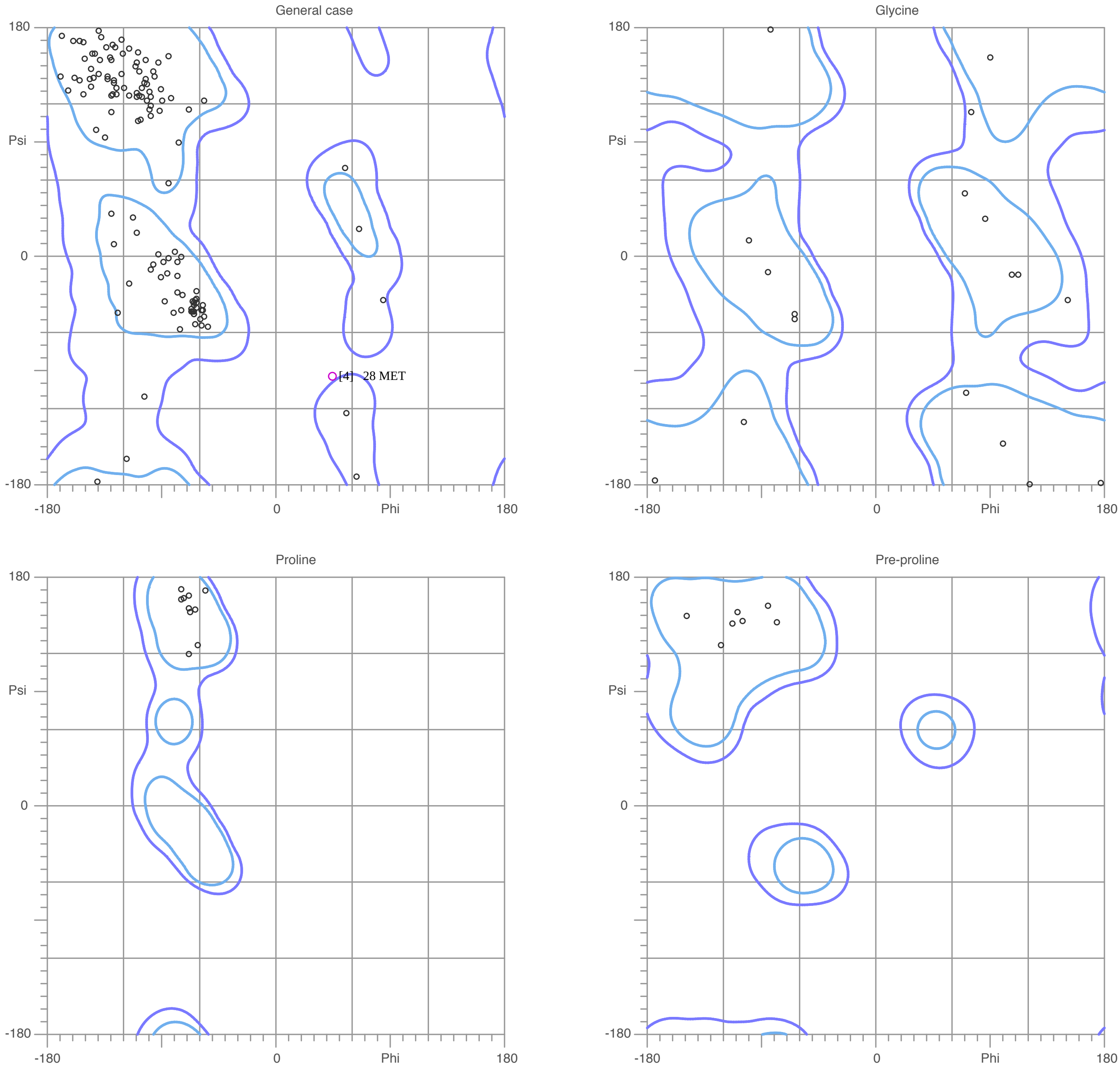
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 4



94.5% (155/164) 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):
   [4]   28 MET (44.9, -95.0)

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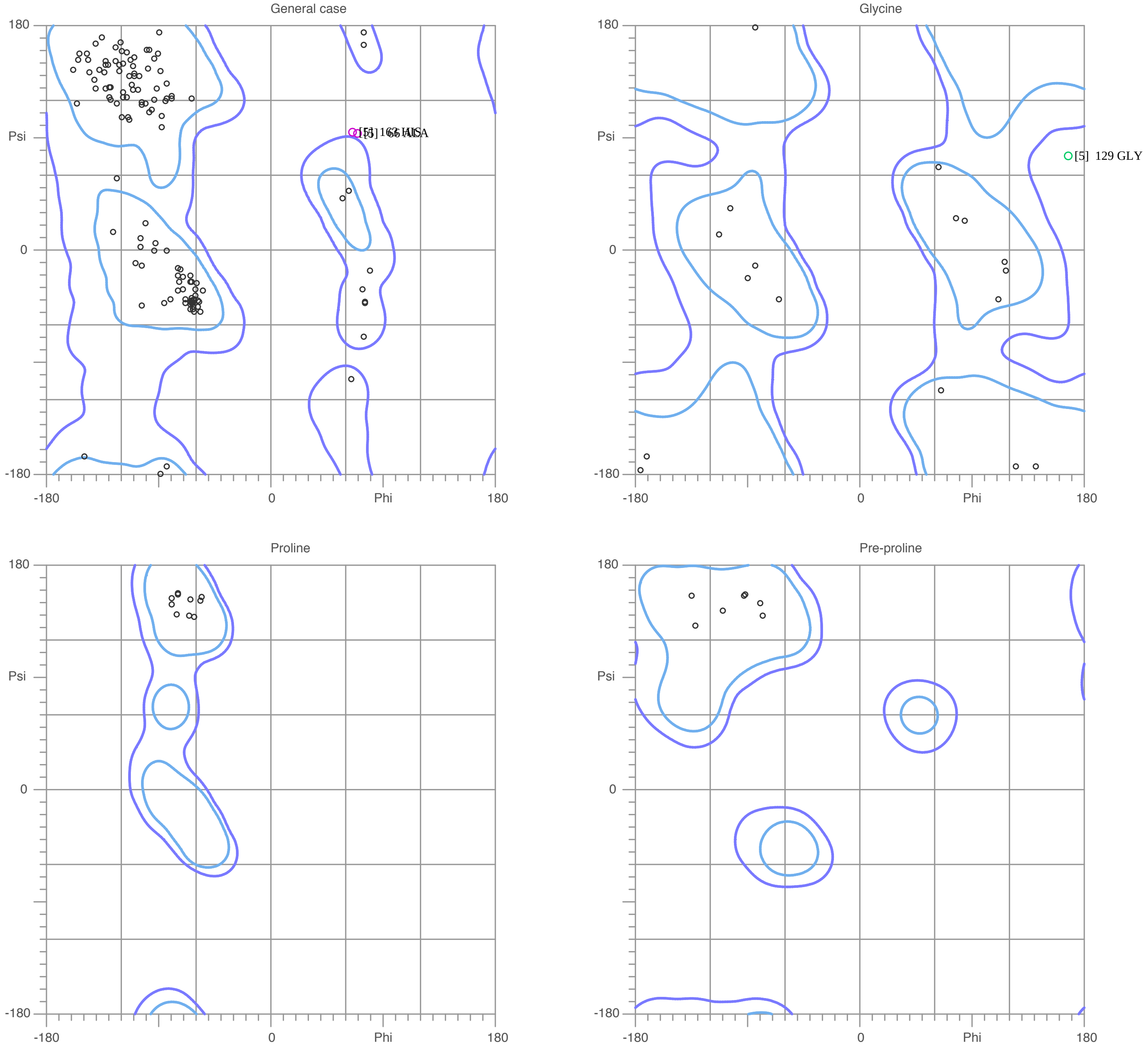
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 5



92.1% (151/164) 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):
- [5] 66 ALA (69.3, 95.0)
- [5] 129 GLY (167.4, 76.3)
- [5] 163 HIS (65.0, 95.0)

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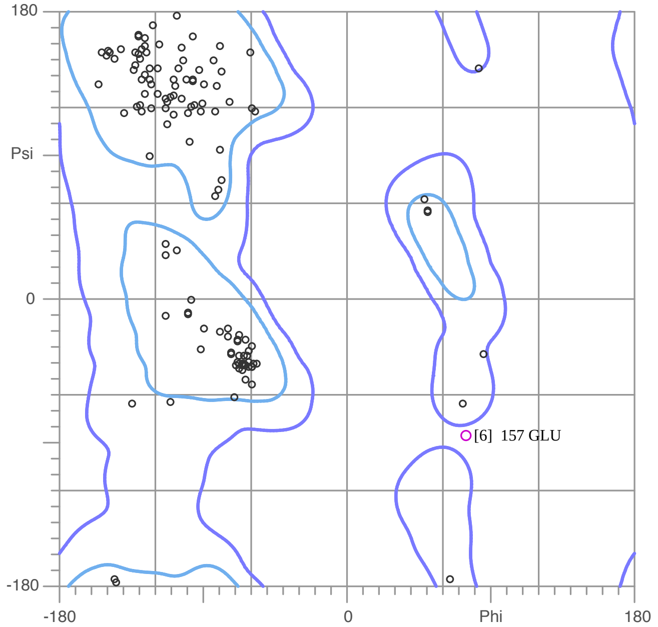
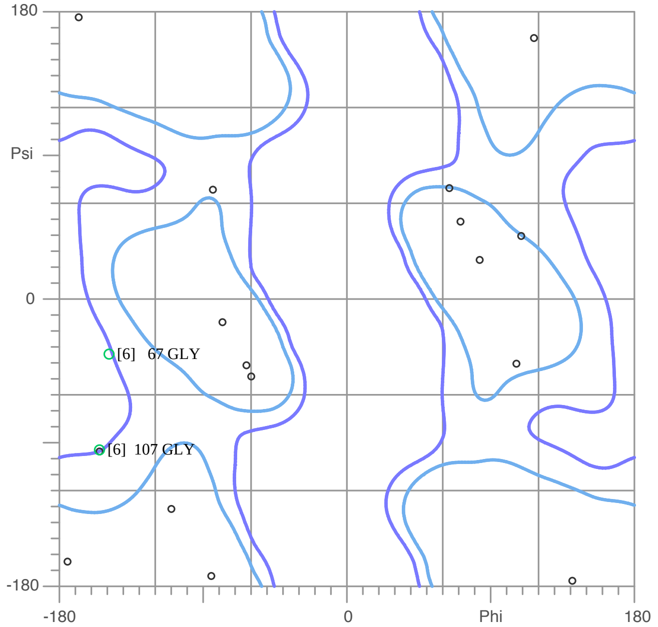
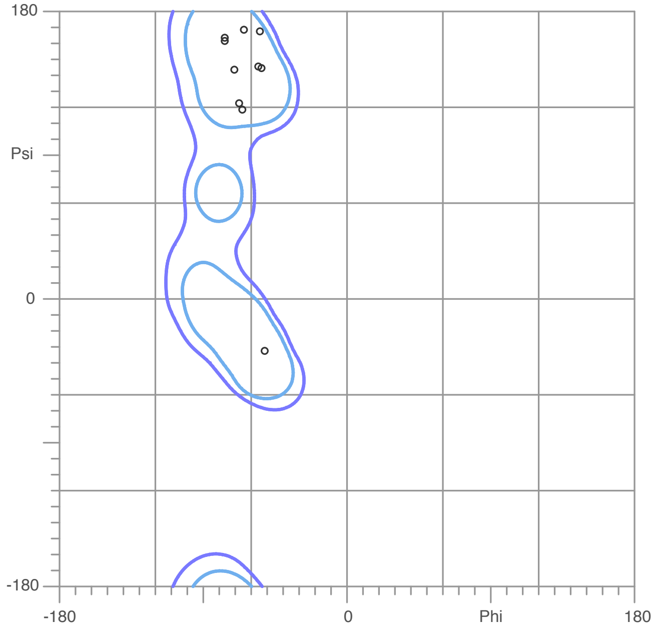
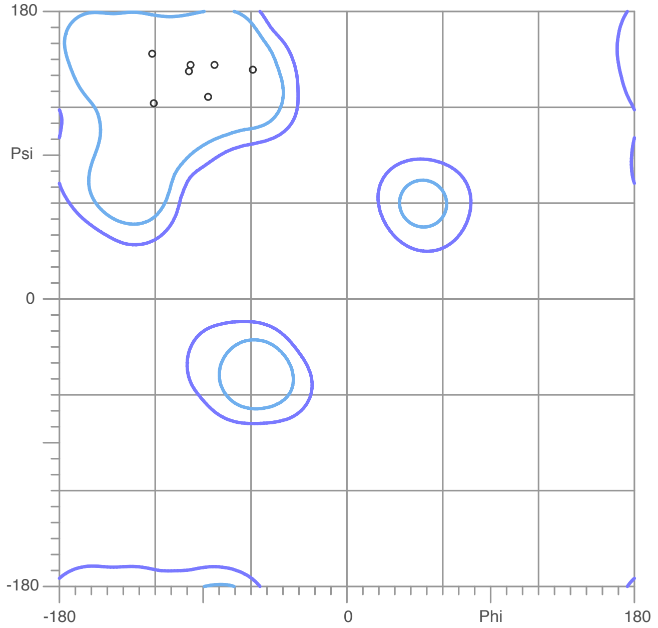
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 6


General case


Glycine


Proline

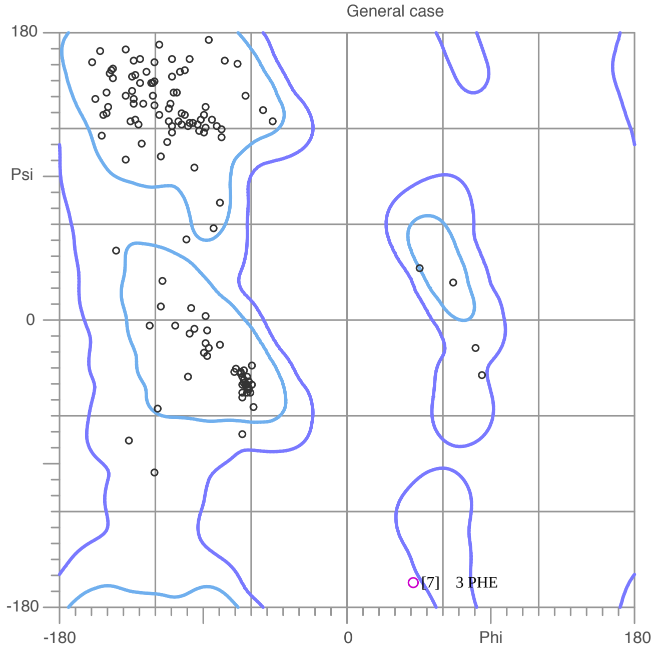

Pre-proline

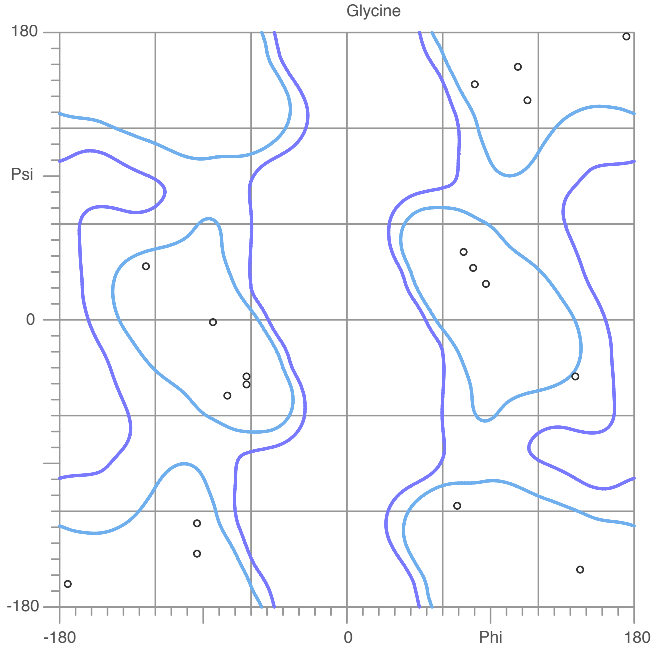
92.1% (151/164) of all residues were in favored (98%) regions.
98.2% (161/164) of all residues were in allowed (>99.8%) regions.

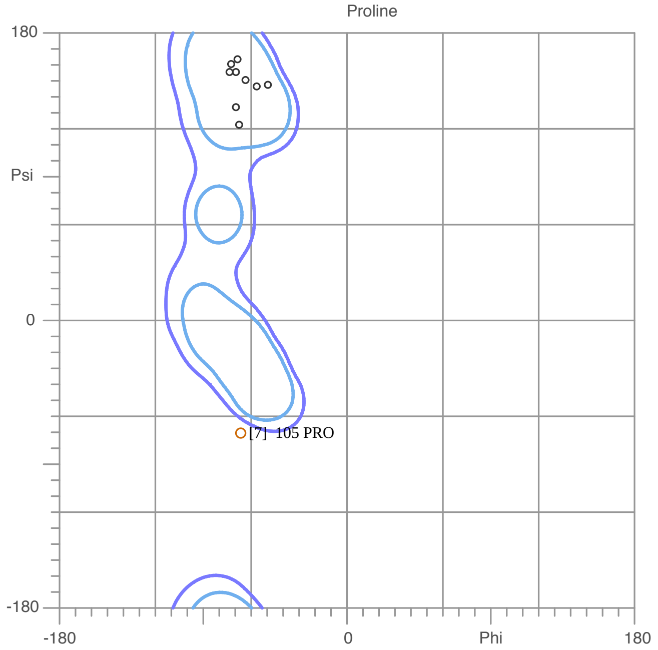
There were 3 outliers (phi, psi):
[6] 67 GLY (-149.2, -34.9)
[6] 107 GLY (-155.1, -95.0)
[6] 157 GLU (74.9, -85.1)

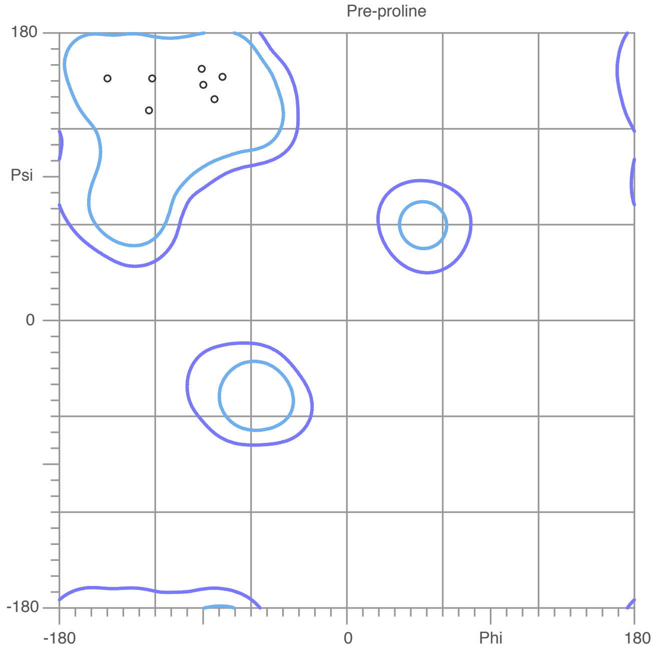
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 7







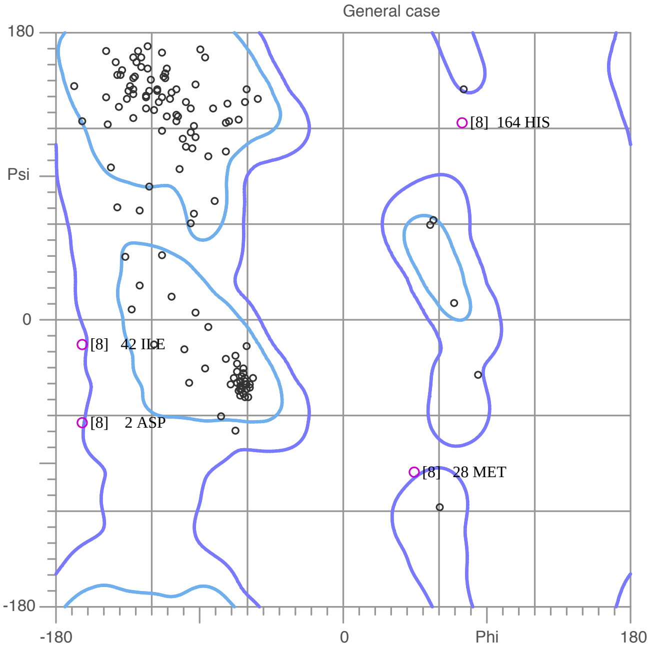


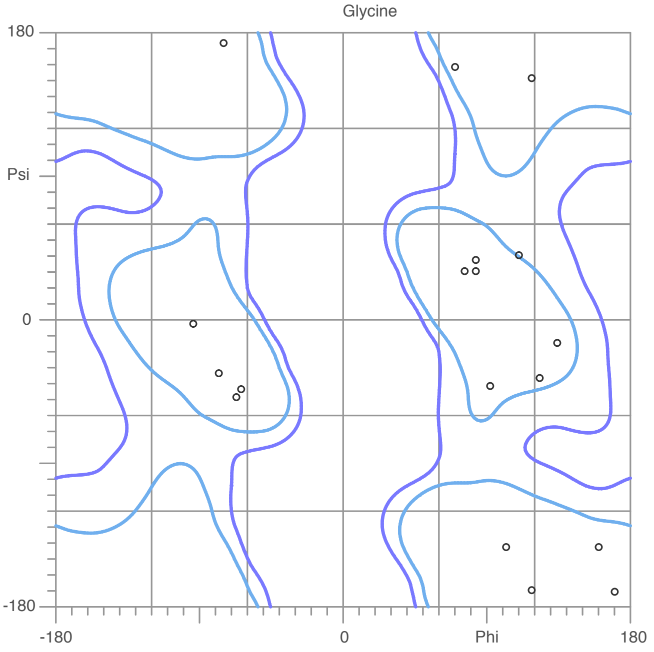
93.9% (154/164) of all residues were in favored (98%) regions.
98.8% (162/164) of all residues were in allowed (>99.8%) regions.

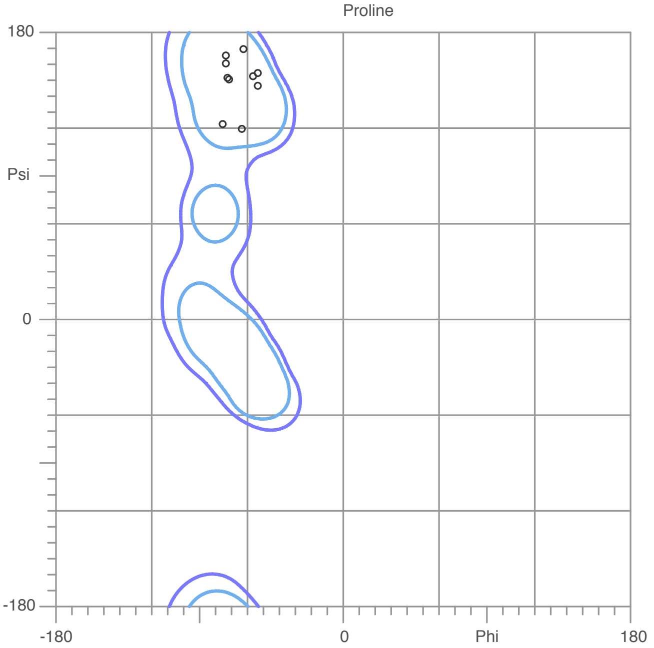
There were 2 outliers (phi, psi):
[7] 3 PHE (41.9, -165.0)
[7] 105 PRO (-67.6, -70.6)

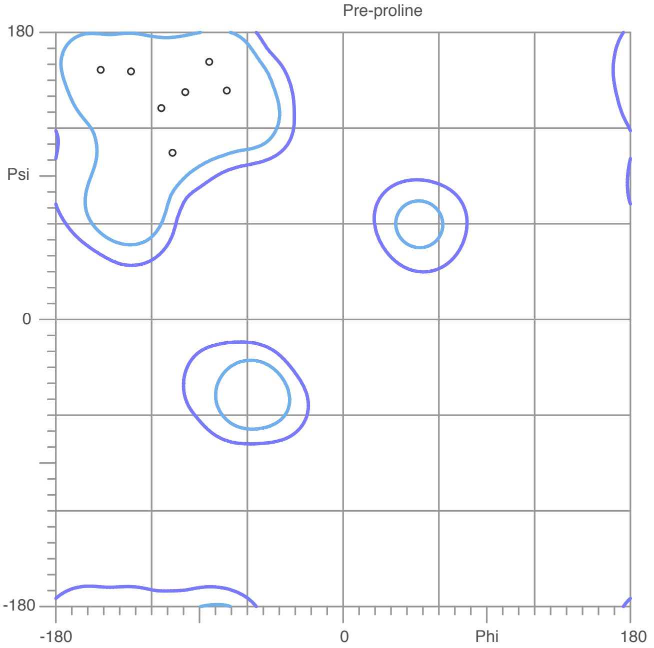
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 8


General case


Glycine


Proline

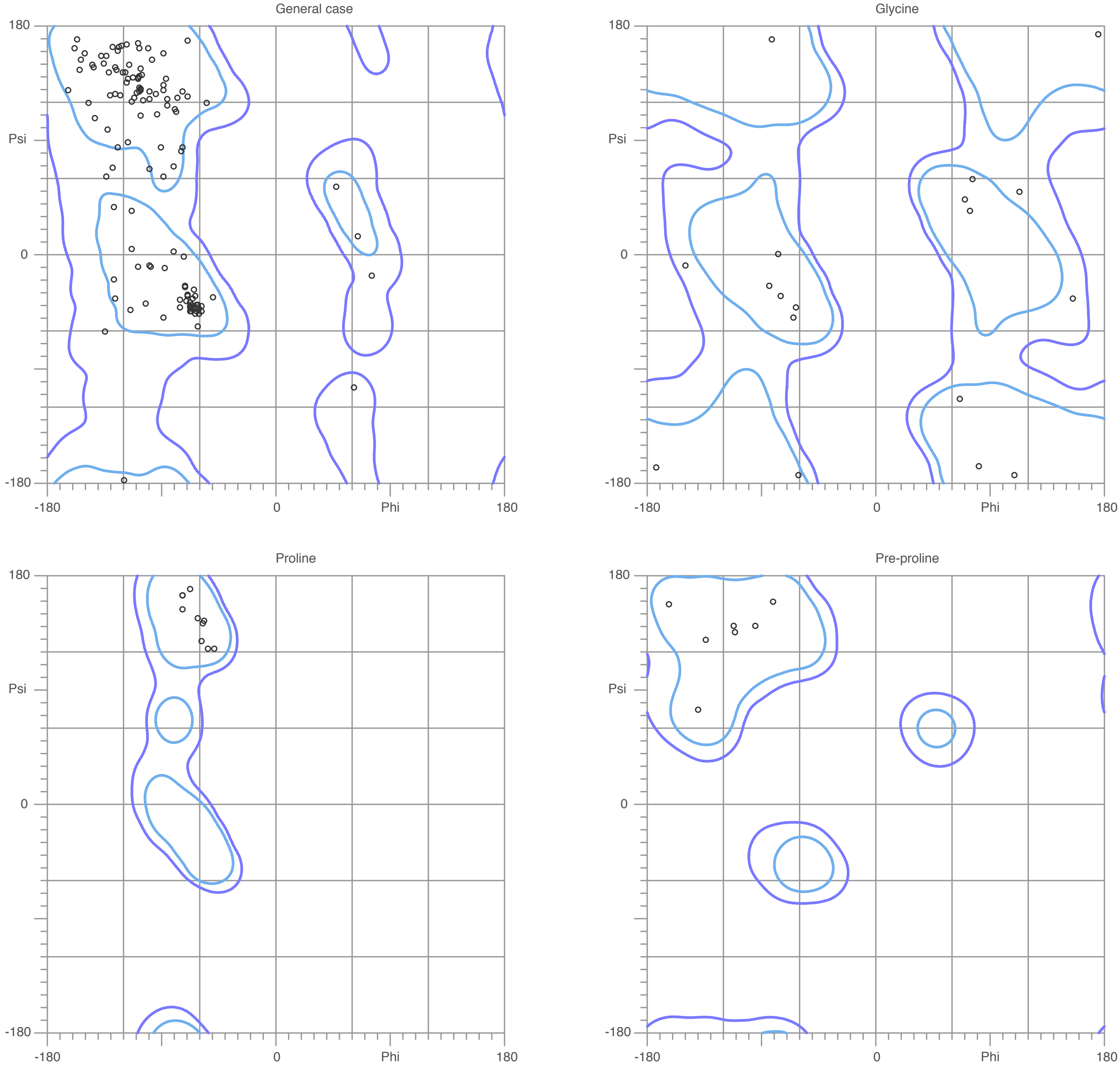

Pre-proline

92.1% (151/164) 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 (-164.7, -65.0)
[8] 28 MET (45.0, -95.0)
[8] 42 ILE (-165.0, -15.0)
[8] 164 HIS (75.0, 125.0)

MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 9



94.5% (155/164) of all residues were in favored (98%) regions.
100.0% (164/164) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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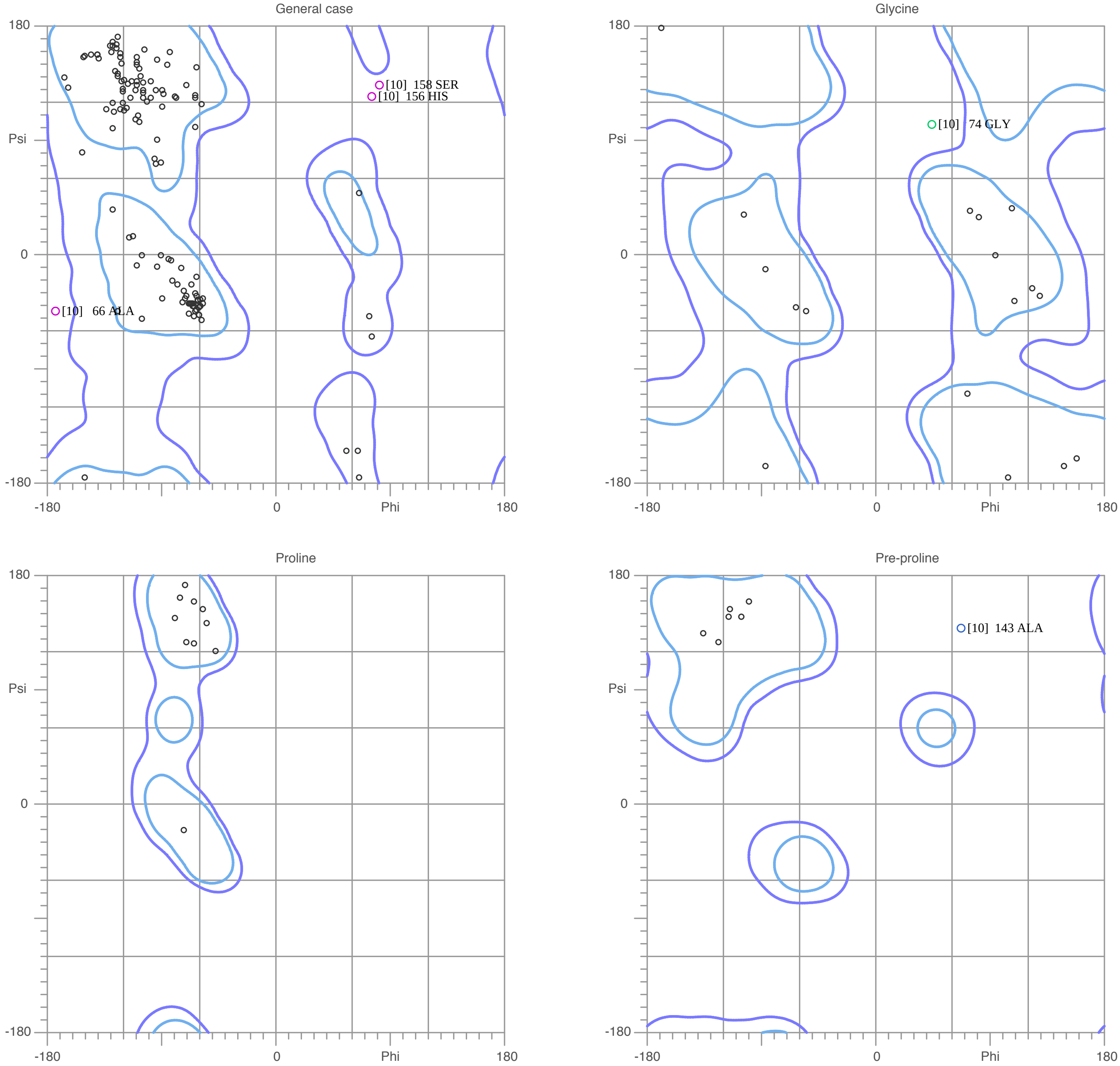
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 10



92.7% (152/164) 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):

[10] 66 ALA (-175.0, -45.0)
[10] 74 GLY (44.9, 103.1)
[10] 143 ALA (67.2, 139.7)
[10] 156 HIS (75.0, 125.1)
[10] 158 SER (81.5, 134.9)

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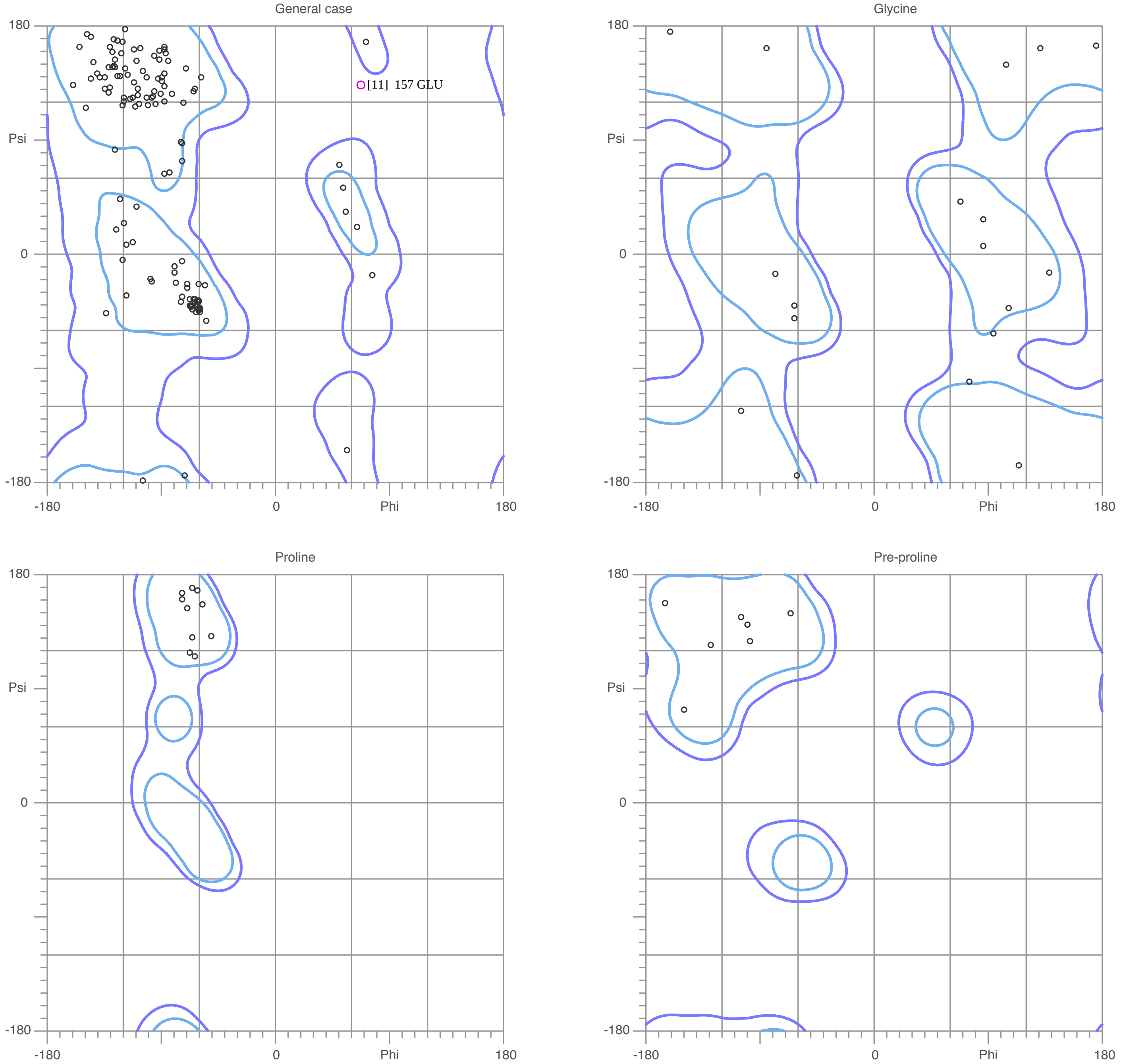
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 11



94.5% (155/164) 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):
[11] 157 GLU (67.1, 135.0)

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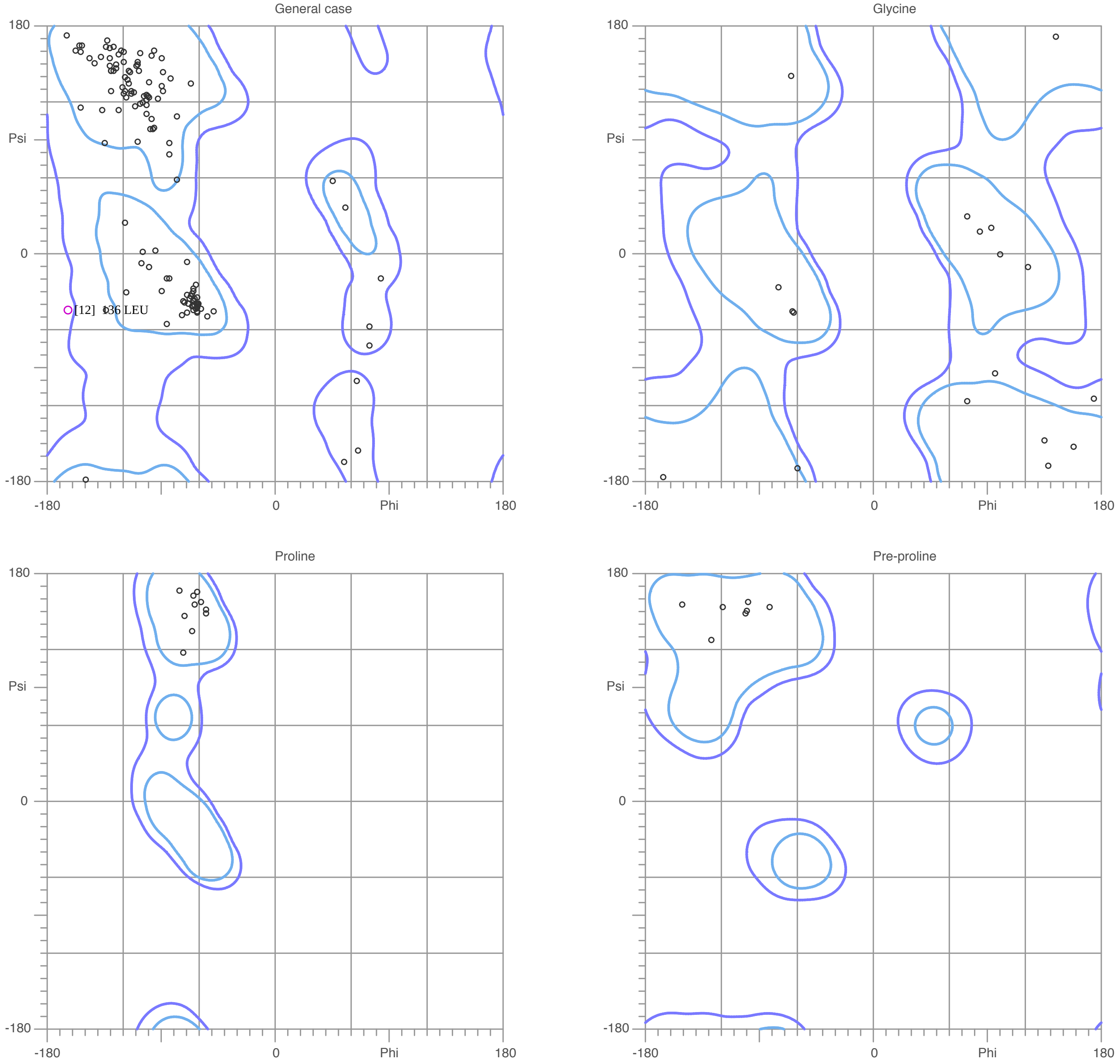
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 12



93.9% (154/164) 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):
[12] 136 LEU (-164.9, -45.0)

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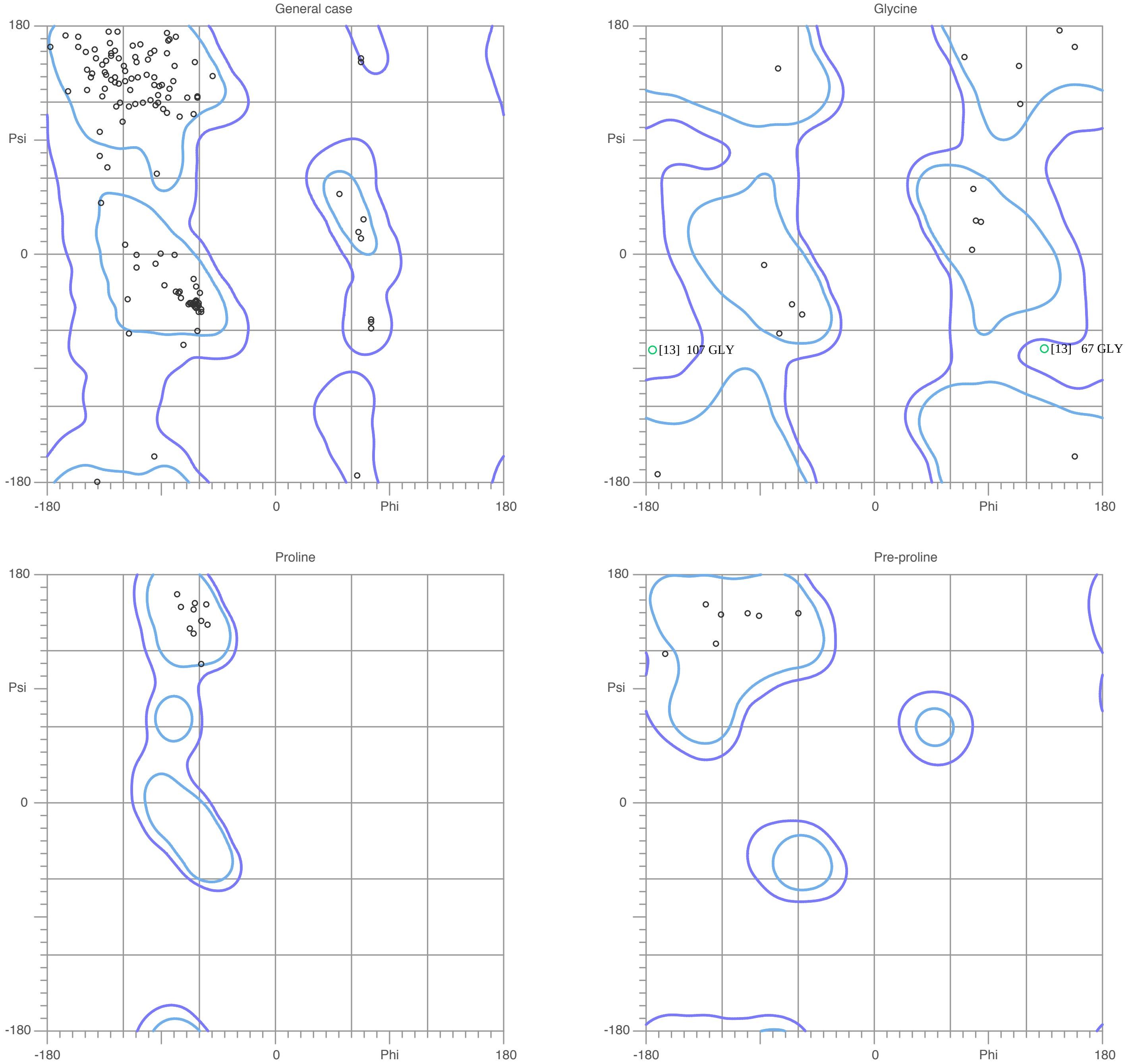
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 13



90.9% (149/164) 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):
[13] 67 GLY (135.0, -75.0)
[13] 107 GLY (-175.1, -75.0)

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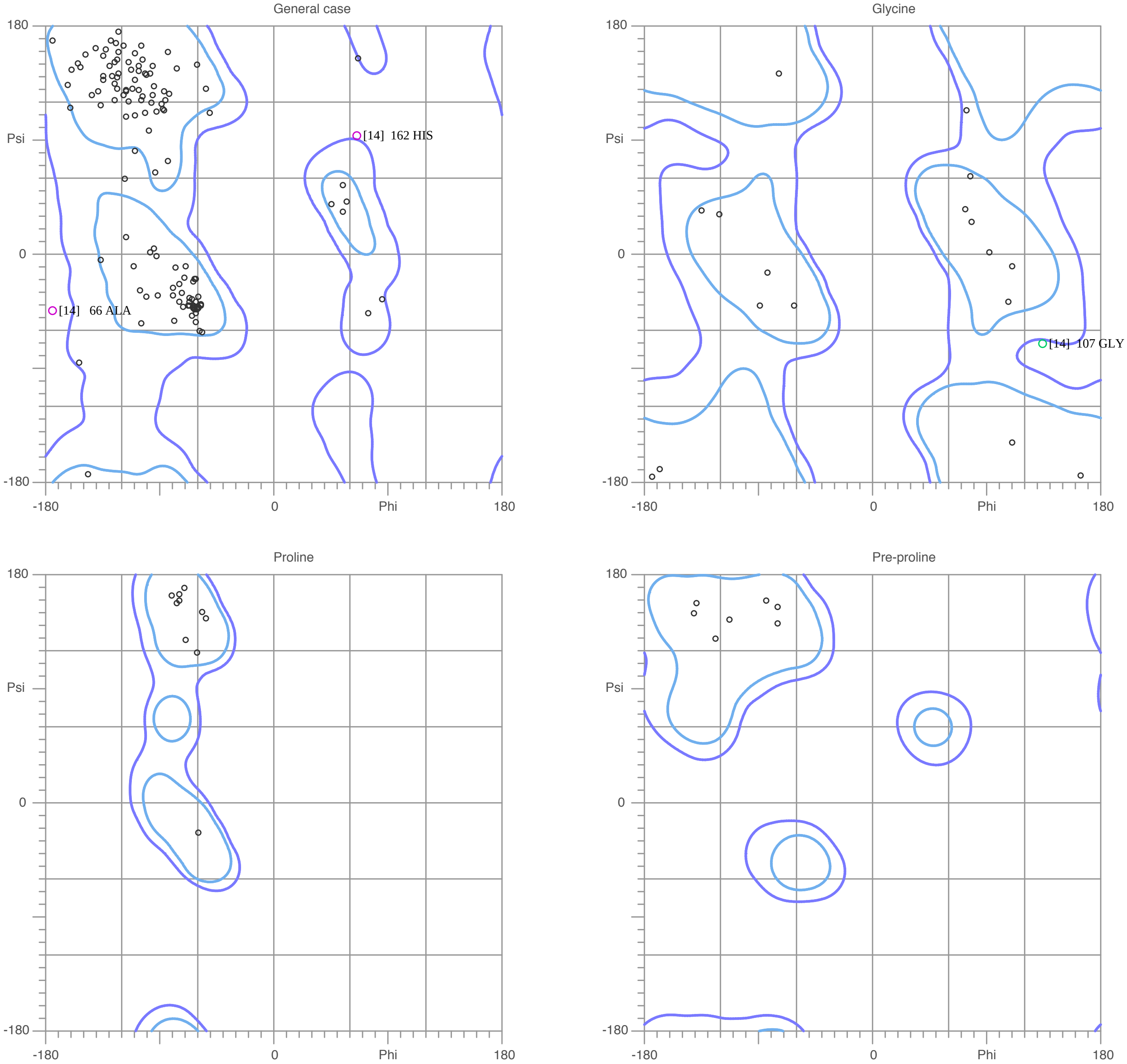
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 14



92.1% (151/164) 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):
[14] 66 ALA (-175.1, -44.9)
[14] 107 GLY (135.0, -70.9)
[14] 162 HIS (65.0, 95.0)

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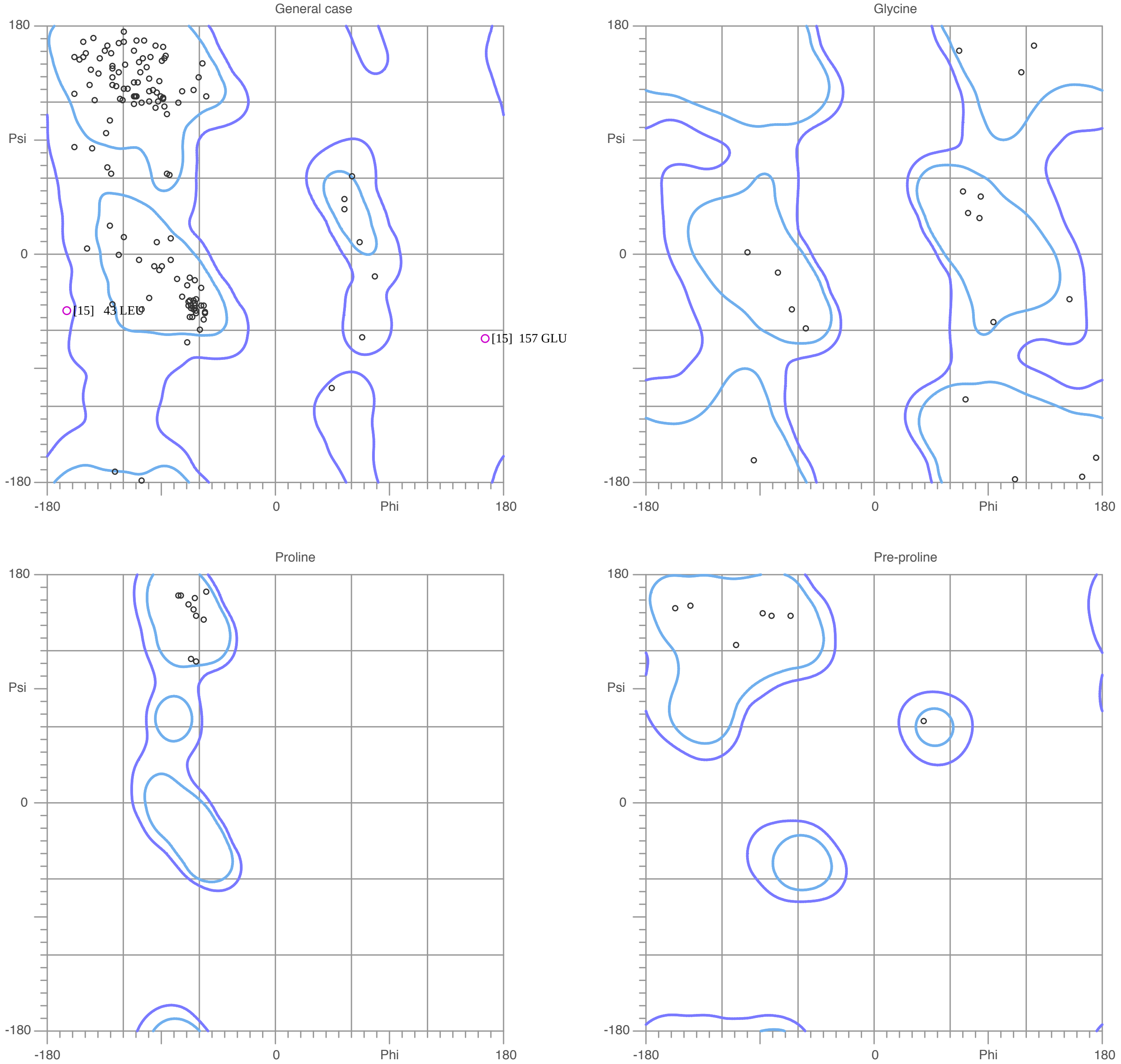
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 15

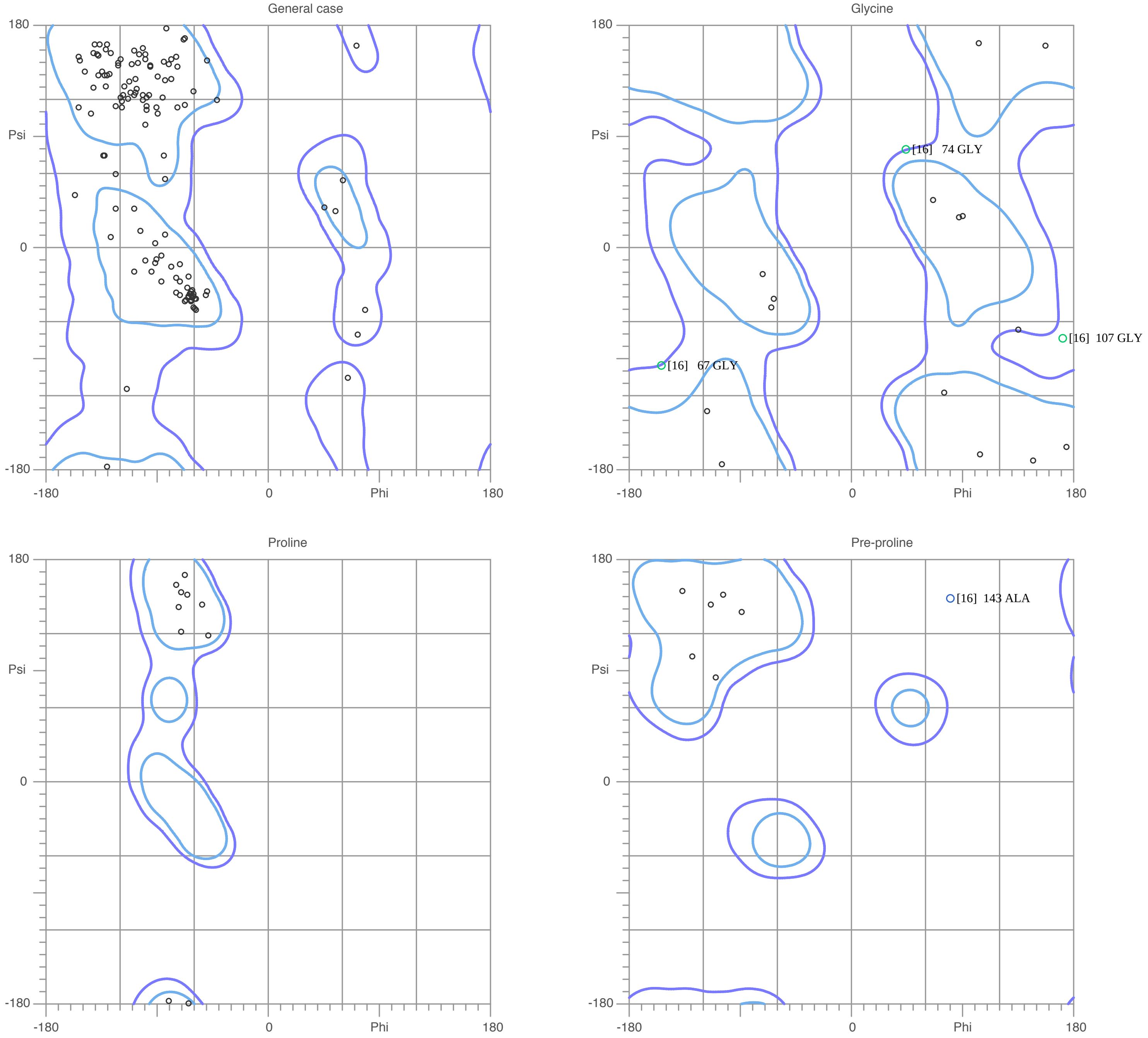


91.5% (150/164) of all residues were in favored (98%) regions.
98.8% (162/164) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[15] 43 LEU (-165.0, -45.0)
[15] 157 GLU (165.0, -66.7)

MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 16



91.5% (150/164) 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 (-155.0, -95.0)
- [16] 74 GLY (45.0, 80.6)
- [16] 107 GLY (171.8, -73.7)
- [16] 143 ALA (80.7, 149.8)

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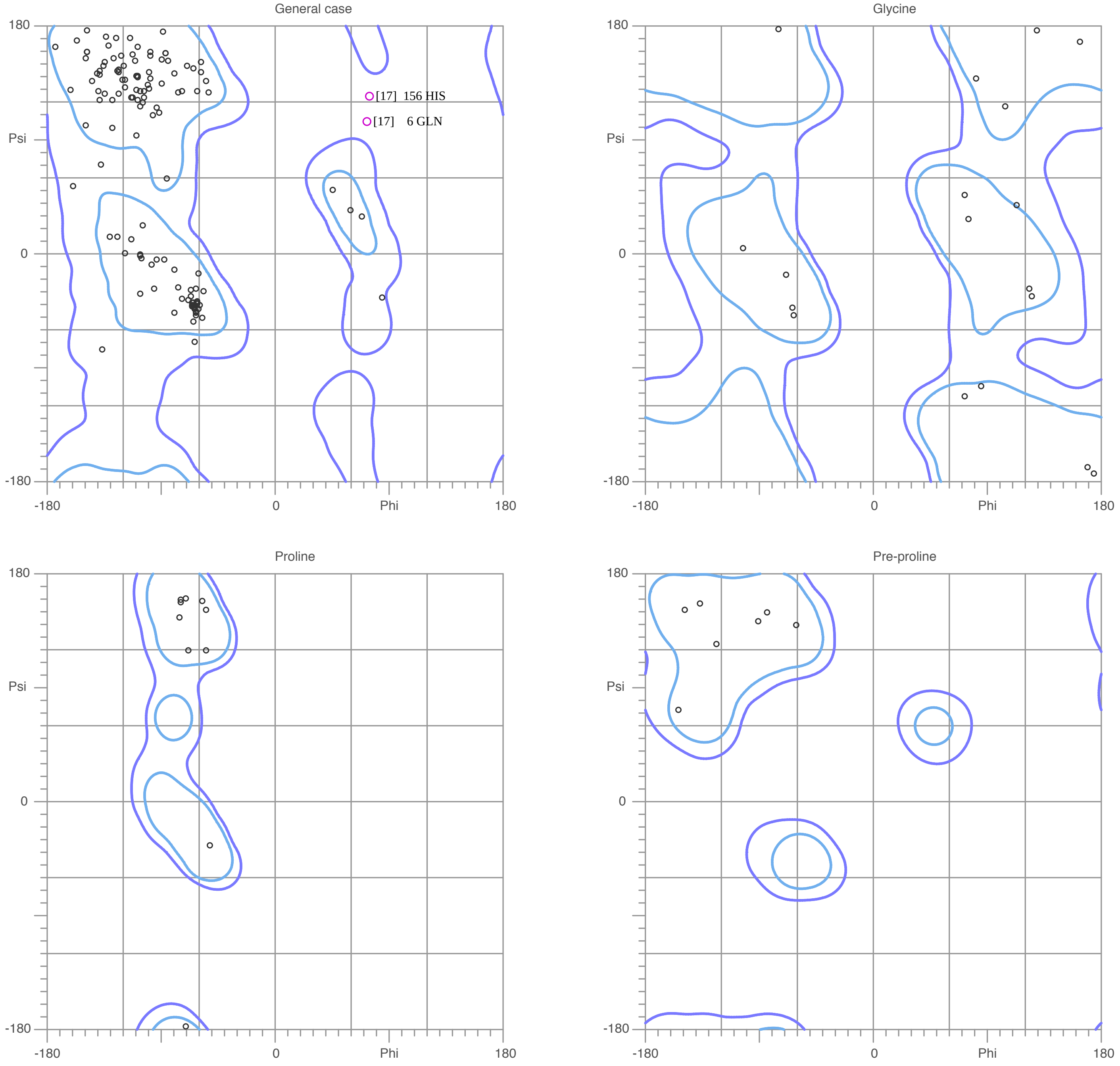
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 17

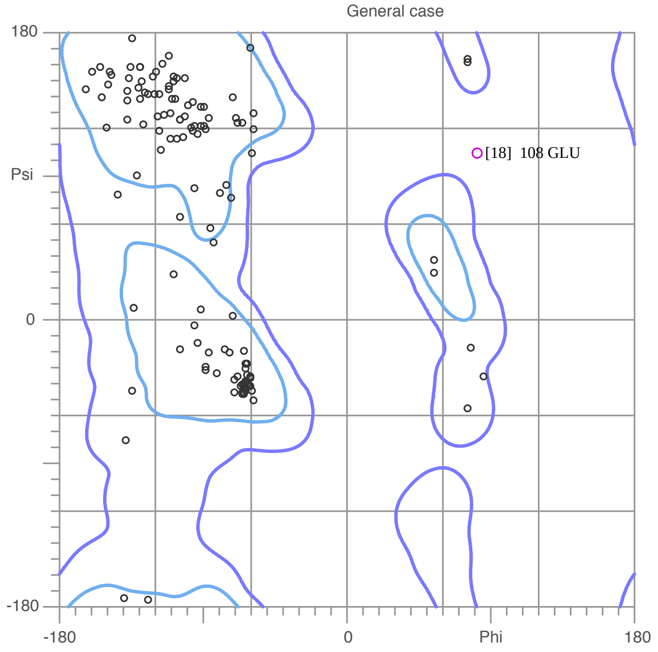


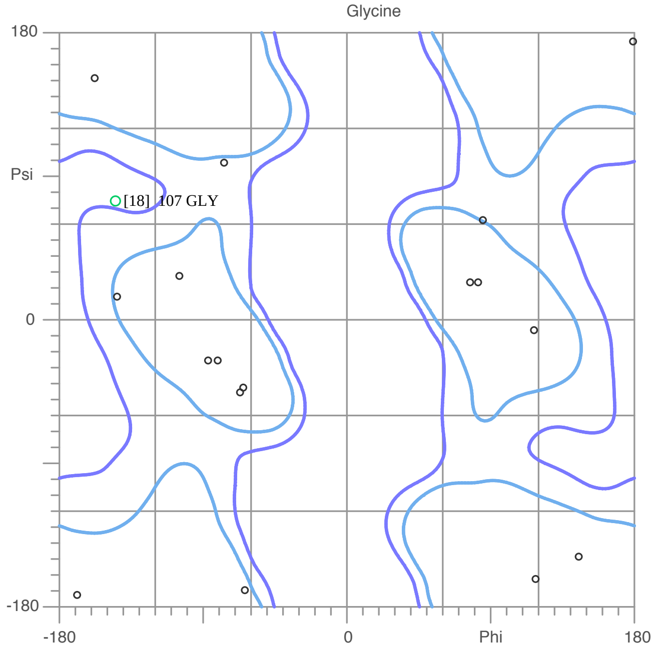
95.1% (156/164) of all residues were in favored (98%) regions.
98.8% (162/164) of all residues were in allowed (>99.8%) regions.

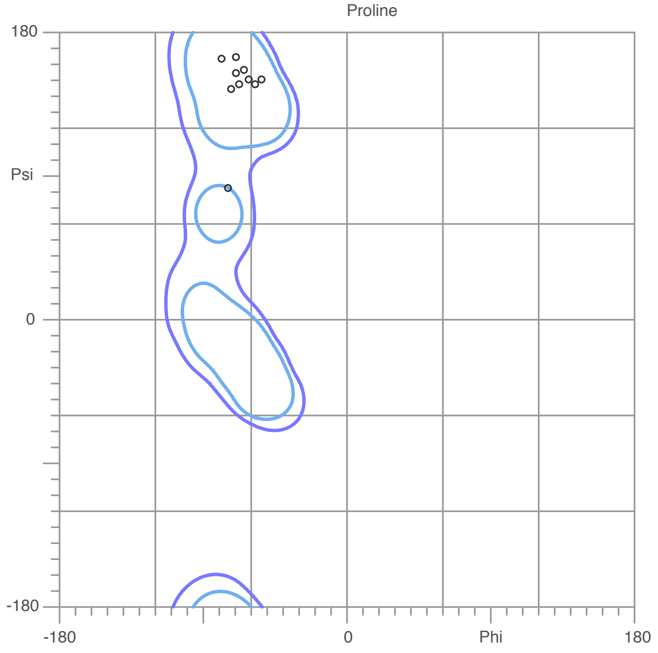
There were 2 outliers (phi, psi):
[17] 6 GLN (72.1, 105.5)
[17] 156 HIS (75.0, 125.0)

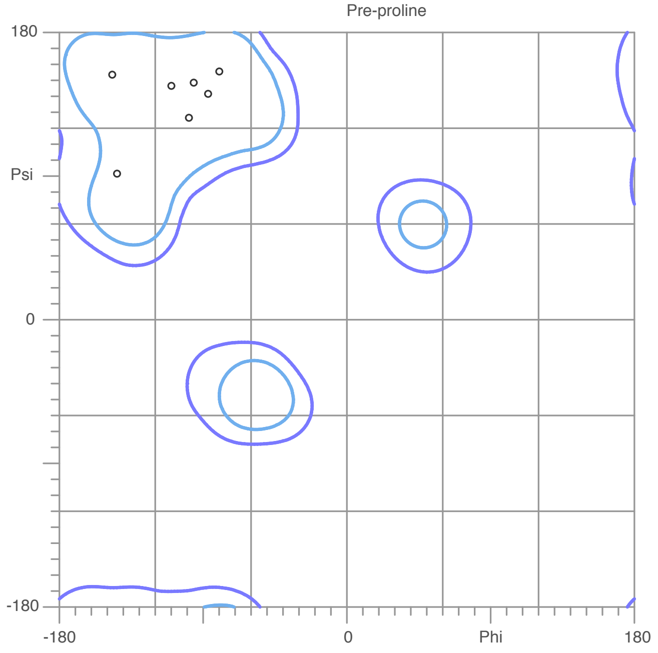
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 18









90.2% (148/164) 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):
[18] 107 GLY (-145.0, 75.0)
[18] 108 GLU (81.9, 105.0)

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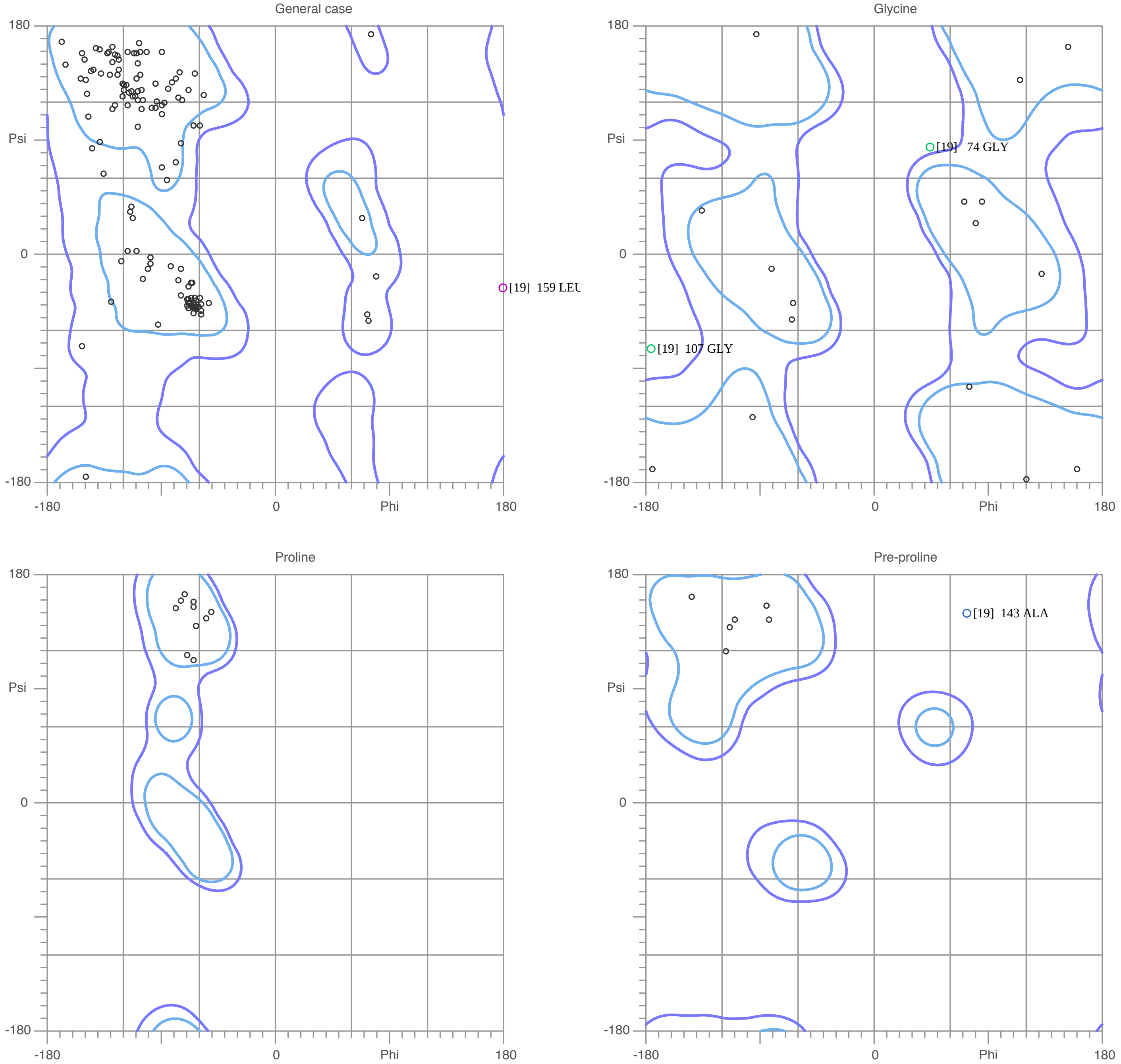
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 19



91.5% (150/164) 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):
[19] 74 GLY (45.0, 86.0)
[19] 107 GLY (-176.5, -75.0)
[19] 143 ALA (73.2, 150.1)
[19] 159 LEU (179.6, -26.5)

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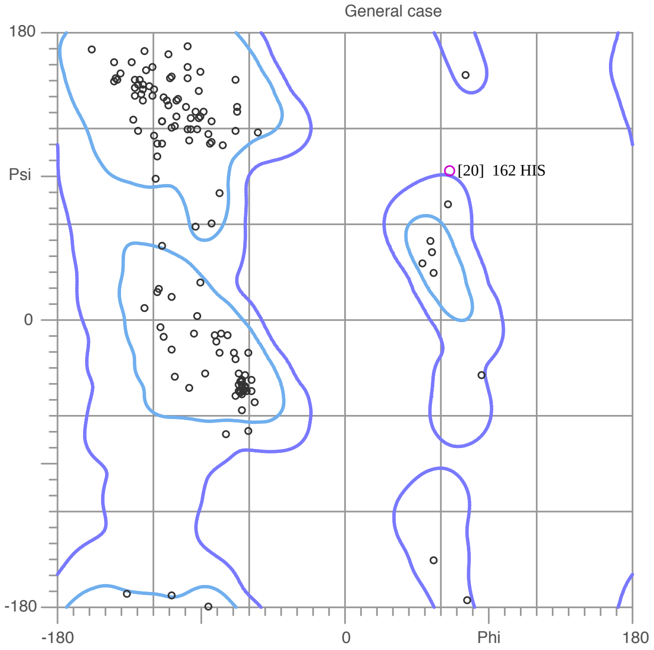
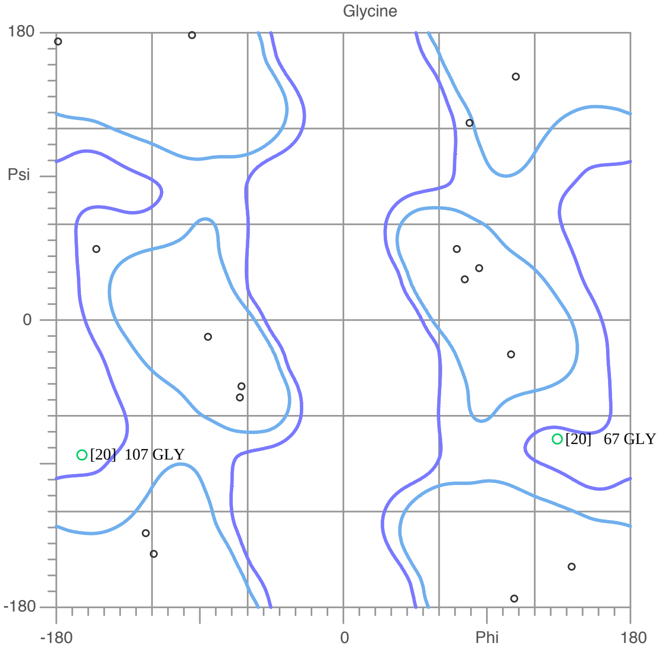
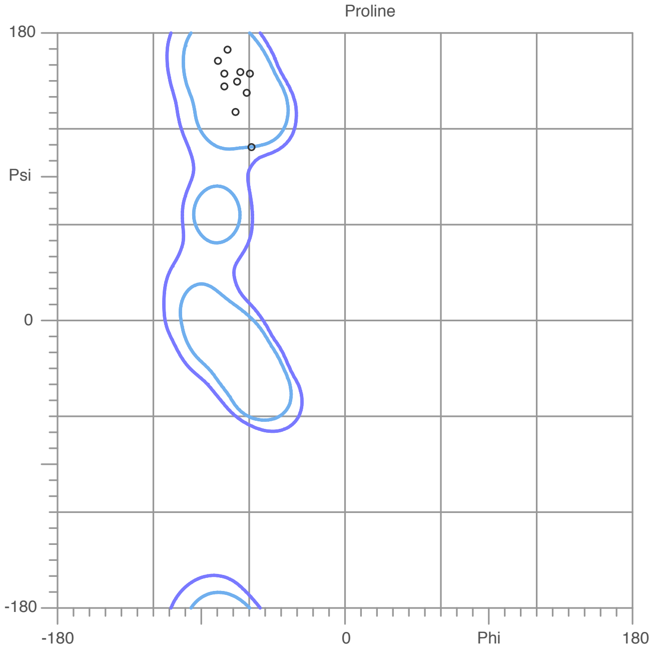
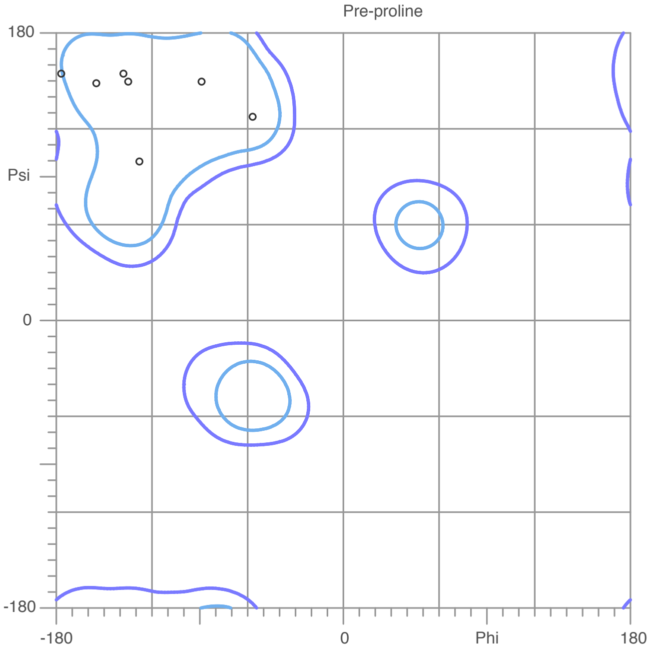
MolProbity Ramachandran analysis

CTR107_R3Cons_em_bcr3.pdb, model 20









90.9% (149/164) 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):
- [20] 67 GLY (135.0, -74.9)
- [20] 107 GLY (-165.0, -85.0)
- [20] 162 HIS (65.1, 95.0)

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