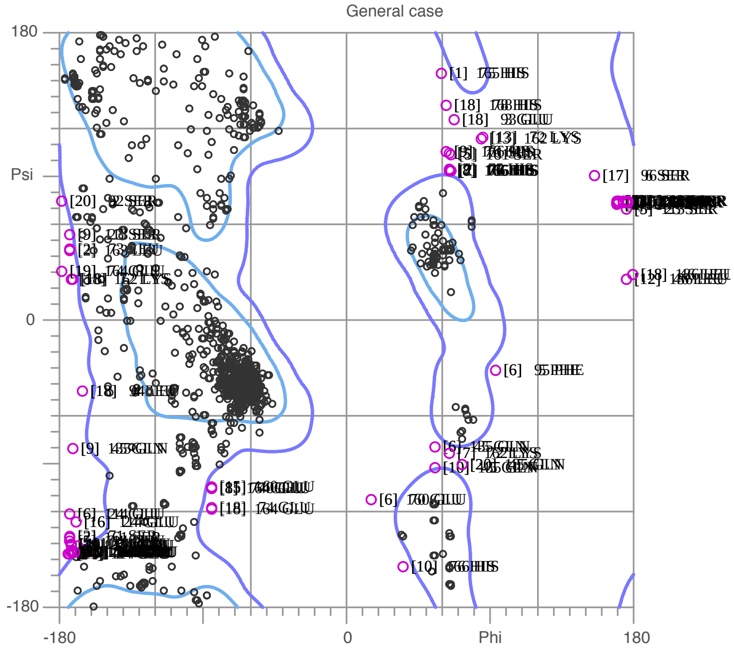
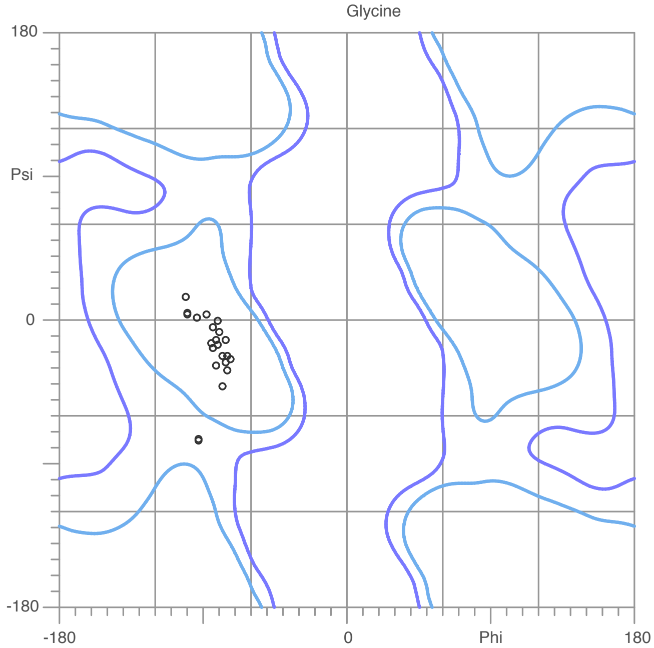
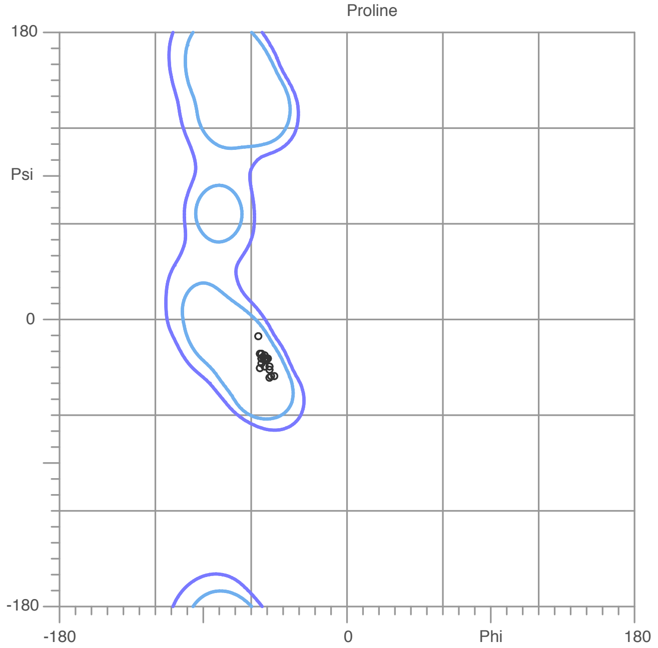
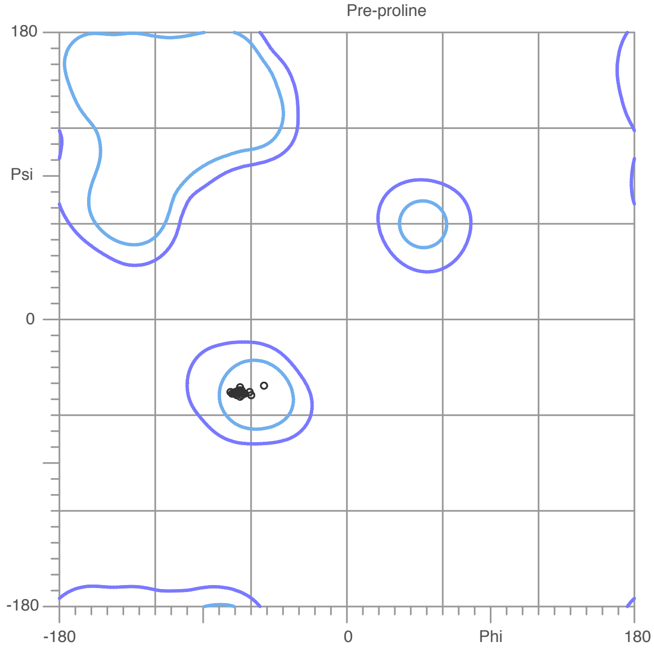
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, all models









```
85.5% (2668/3120) of all residues were in favored (98%) regions.
96.7% (3016/3120) of all residues were in allowed (>99.8%) regions.

There were 104 outliers (phi, psi):
   [1]   75 HIS (59.0, 155.0)
   [1]  165 HIS (59.1, 155.0)
   [2]   23 SER (169.6, 73.6)
   [2]   24 GLU (-172.5, -144.7)
   [2]   71 SER (-174.6, -136.0)
   [2]   73 LEU (-175.0, 45.0)
   [2]   76 HIS (65.0, 95.0)
   [2]  113 SER (169.6, 73.6)
   [2]  114 GLU (-172.4, -144.7)
   [2]  161 SER (-174.6, -136.0)
   [2]  163 LEU (-175.0, 45.0)
   [2]  166 HIS (65.0, 95.0)
   [3]   23 SER (170.5, 75.2)
   [3]  113 SER (170.5, 75.2)
   [4]   23 SER (175.8, 75.0)
   [4]   24 GLU (-173.2, -140.2)
   [4]  113 SER (175.8, 75.1)
   [4]  114 GLU (-173.2, -140.3)
   [5]   23 SER (175.0, 70.2)
   [5]   24 GLU (-175.0, -138.6)
   [5]   71 SER (65.0, 105.0)
   [5]  113 SER (175.0, 70.2)
   [5]  114 GLU (-175.0, -138.6)
   [5]  161 SER (65.0, 105.0)
   [6]    5 PHE (93.5, -31.4)
   [6]   23 SER (173.6, 75.0)
   [6]   24 GLU (-174.0, -121.3)
   [6]   45 GLN (55.1, -79.5)
   [6]   70 GLU (15.5, -112.8)
   [6]   95 PHE (93.4, -31.4)
   [6]  113 SER (173.7, 75.0)
   [6]  114 GLU (-174.0, -121.3)
   [6]  135 GLN (55.0, -79.5)
   [6]  160 GLU (15.6, -112.8)
   [7]   72 LYS (64.1, -83.2)
   [7]   75 HIS (65.0, 95.0)
   [7]  162 LYS (64.2, -83.2)
   [7]  165 HIS (65.0, 95.0)
   [8]   23 SER (175.0, 75.0)
   [8]   24 GLU (-173.3, -145.1)
   [8]   74 GLU (-85.0, -105.0)
   [8]   76 HIS (65.0, 94.9)
   [8]  113 SER (175.1, 75.0)
   [8]  114 GLU (-173.3, -145.1)
   [8]  164 GLU (-85.1, -105.0)
   [8]  166 HIS (64.9, 94.9)
   [9]   23 SER (-174.9, 55.0)
   [9]   24 GLU (-169.9, -141.2)
   [9]   45 GLN (-172.3, -80.5)
   [9]   76 HIS (62.9, 106.3)
   [9]  113 SER (-175.0, 55.0)
   [9]  114 GLU (-170.0, -141.3)
   [9]  135 GLN (-172.3, -80.5)
   [9]  166 HIS (63.0, 106.3)
   [10]   23 SER (175.3, 75.0)
   [10]   24 GLU (-172.0, -145.3)
   [10]   45 GLN (55.0, -92.8)
   [10]   76 HIS (35.5, -154.9)
   [10]  113 SER (175.2, 75.1)
   [10]  114 GLU (-172.0, -145.4)
   [10]  135 GLN (55.0, -92.8)
   [10]  166 HIS (35.5, -154.9)
   [11]   24 GLU (-175.0, -146.7)
   [11]  114 GLU (-175.0, -146.8)
   [12]   23 SER (169.9, 75.0)
   [12]   24 GLU (-171.6, -145.0)
   [12]   46 LEU (175.1, 26.5)
   [12]  113 SER (170.0, 75.0)
   [12]  114 GLU (-171.6, -145.0)
   [12]  136 LEU (175.1, 26.5)
   [13]   72 LYS (85.0, 115.1)
   [13]  162 LYS (85.0, 115.0)
   [15]   23 SER (176.7, 75.0)
   [15]   24 GLU (-171.8, -145.1)
   [15]   70 GLU (-85.1, -105.0)
   [15]  113 SER (176.8, 75.0)
   [15]  114 GLU (-171.8, -145.0)
   [15]  160 GLU (-85.1, -105.0)
   [16]   24 GLU (-170.0, -126.4)
   [16]  114 GLU (-170.1, -126.4)
   [17]    6 SER (155.1, 91.7)
   [17]   96 SER (155.1, 91.7)
   [18]    3 GLU (67.7, 126.7)
   [18]    4 LEU (-166.1, -45.0)
   [18]   24 GLU (-173.5, -145.0)
   [18]   46 LEU (179.9, 29.1)
   [18]   72 LYS (-173.0, 27.0)
   [18]   74 GLU (-85.9, -118.0)
   [18]   78 HIS (62.2, 135.0)
   [18]   93 GLU (67.6, 126.7)
   [18]   94 LEU (-166.1, -45.0)
   [18]  114 GLU (-173.5, -145.0)
   [18]  136 LEU (179.9, 29.0)
   [18]  162 LYS (-173.0, 27.0)
   [18]  164 GLU (-86.0, -118.0)
   [18]  168 HIS (62.3, 135.0)
   [19]   74 GLU (-179.4, 31.8)
   [19]  164 GLU (-179.4, 31.8)
   [20]    2 SER (-179.0, 75.0)
   [20]   24 GLU (-173.8, -141.0)
   [20]   45 GLN (72.3, -91.0)
   [20]   92 SER (-179.0, 75.0)
   [20]  114 GLU (-173.8, -141.0)
   [20]  135 GLN (72.3, -90.9)
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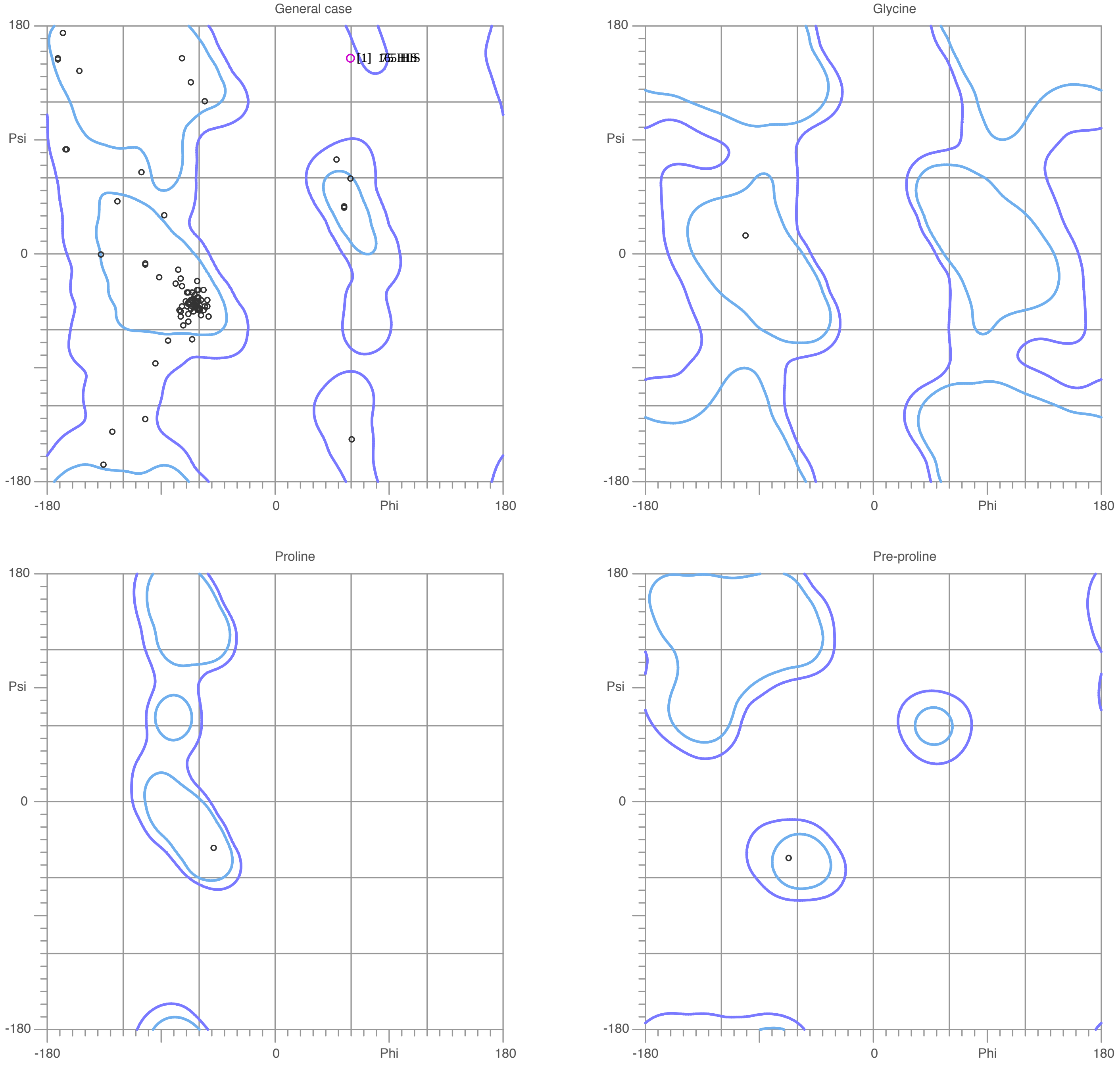
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 1



83.3% (130/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[1] 75 HIS (59.0, 155.0)
[1] 165 HIS (59.1, 155.0)

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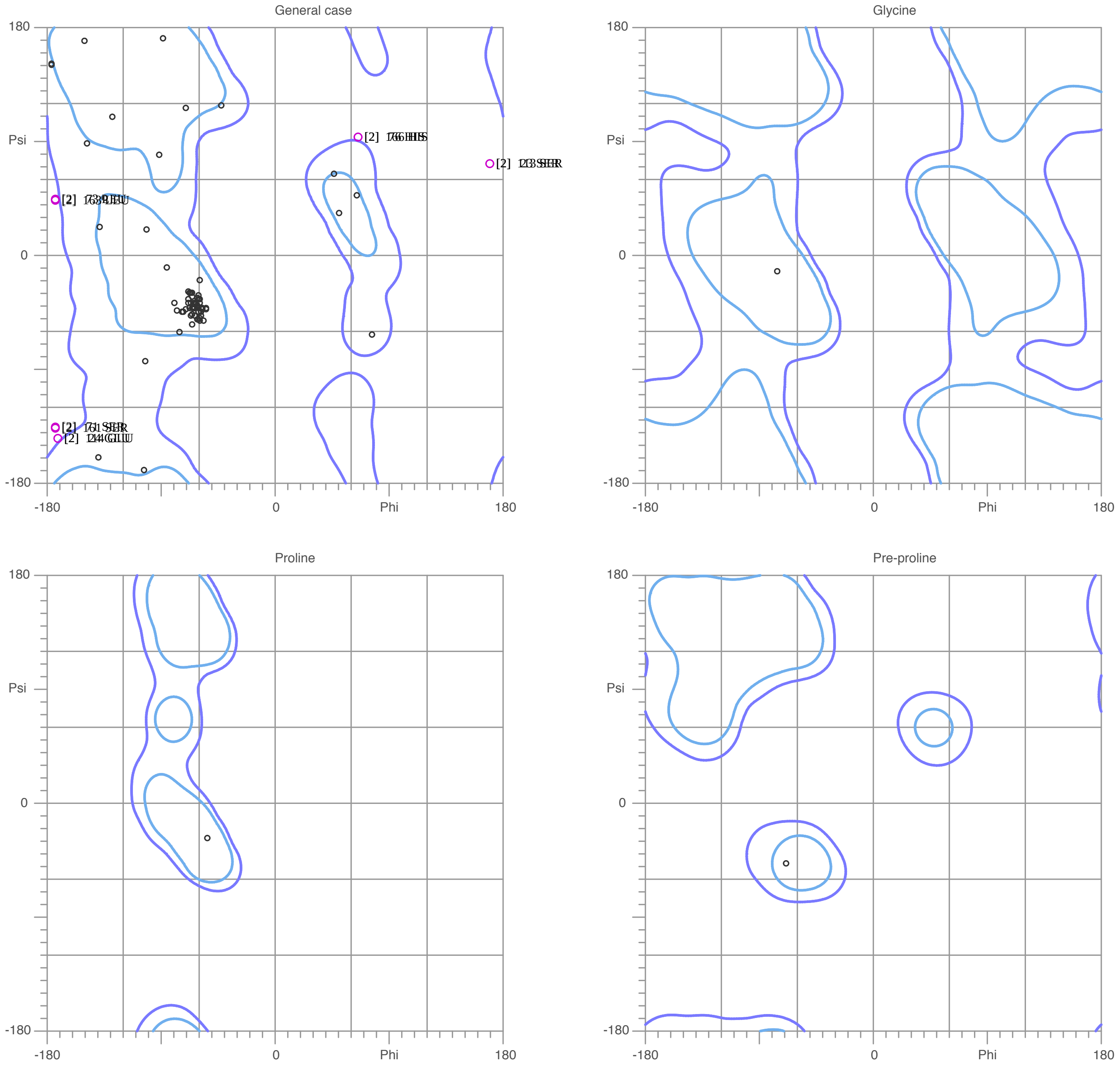
SR478_R3Cons_em_bcr3.pdb, model 2



84.6% (132/156) of all residues were in favored (98%) regions.
93.6% (146/156) of all residues were in allowed (>99.8%) regions.

There were 10 outliers (phi, psi):

[2]	23 SER (169.6, 73.6)
[2]	24 GLU (-172.5, -144.7)
[2]	71 SER (-174.6, -136.0)
[2]	73 LEU (-175.0, 45.0)
[2]	76 HIS (65.0, 95.0)
[2]	113 SER (169.6, 73.6)
[2]	114 GLU (-172.4, -144.7)
[2]	161 SER (-174.6, -136.0)
[2]	163 LEU (-175.0, 45.0)
[2]	166 HIS (65.0, 95.0)

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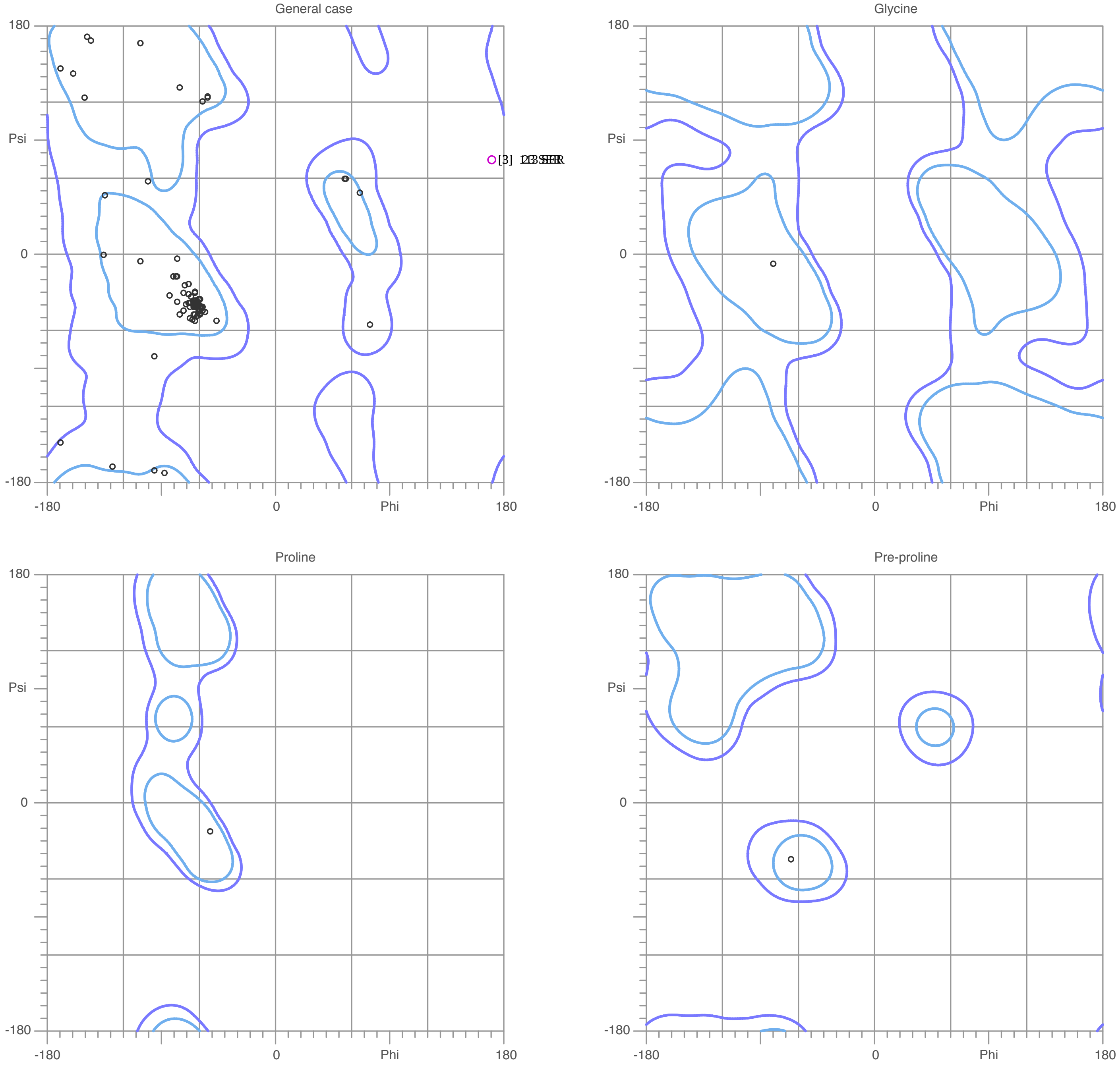
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 3



91.0% (142/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[3] 23 SER (170.5, 75.2)
[3] 113 SER (170.5, 75.2)

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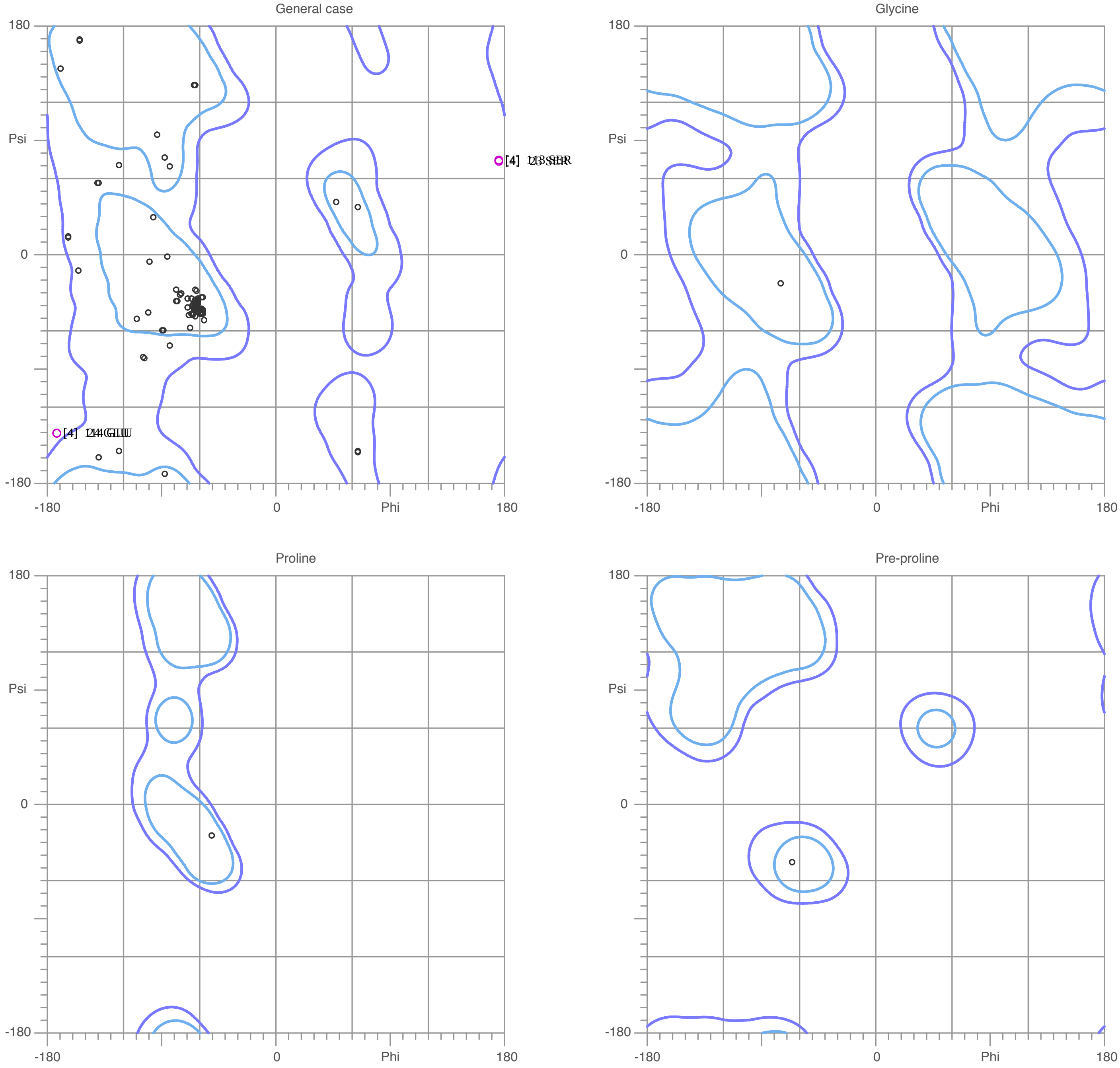
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 4



85.9% (134/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[4] 23 SER (175.8, 75.0)
[4] 24 GLU (-173.2, -140.2)
[4] 113 SER (175.8, 75.1)
[4] 114 GLU (-173.2, -140.3)

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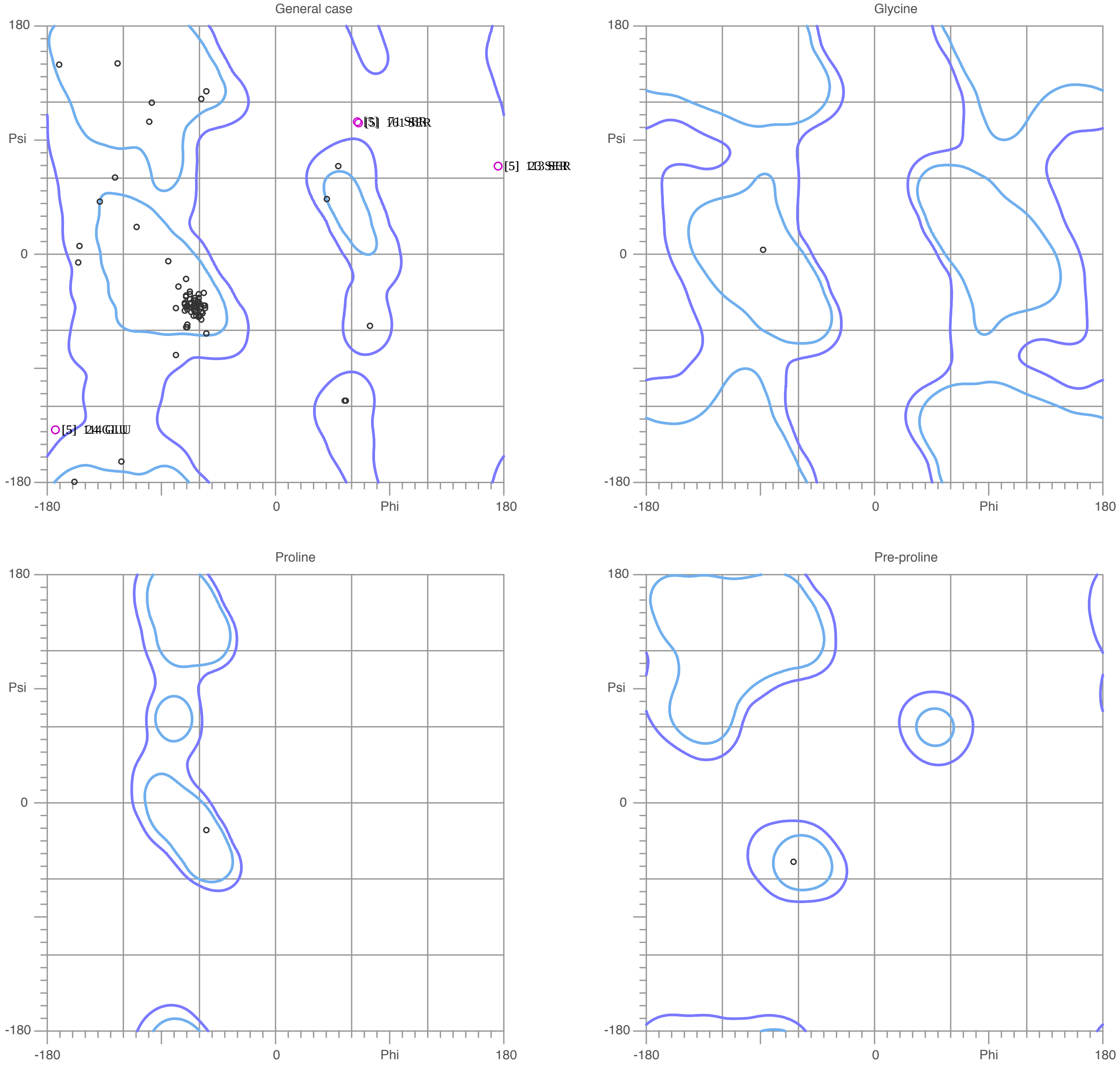
SR478_R3Cons_em_bcr3.pdb, model 5



84.6% (132/156) of all residues were in favored (98%) regions.
96.2% (150/156) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[5] 23 SER (175.0, 70.2)
[5] 24 GLU (-175.0, -138.6)
[5] 71 SER (65.0, 105.0)
[5] 113 SER (175.0, 70.2)
[5] 114 GLU (-175.0, -138.6)
[5] 161 SER (65.0, 105.0)

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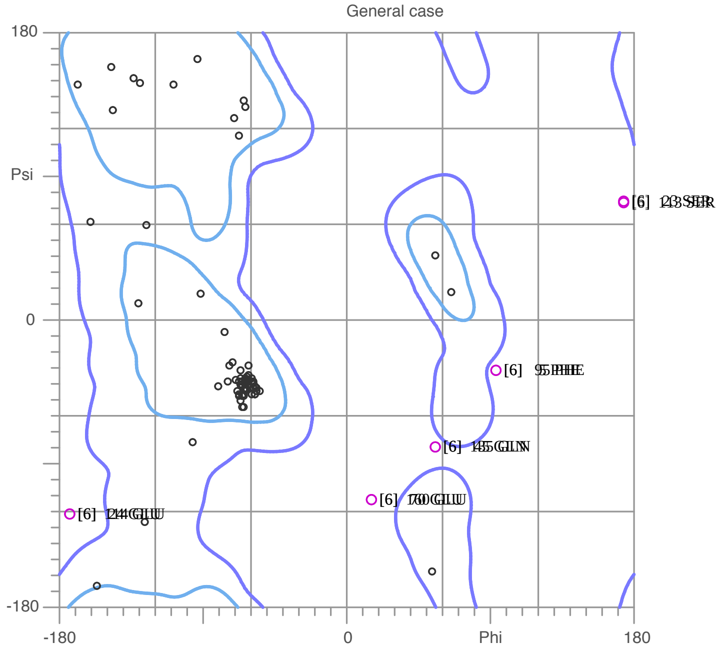
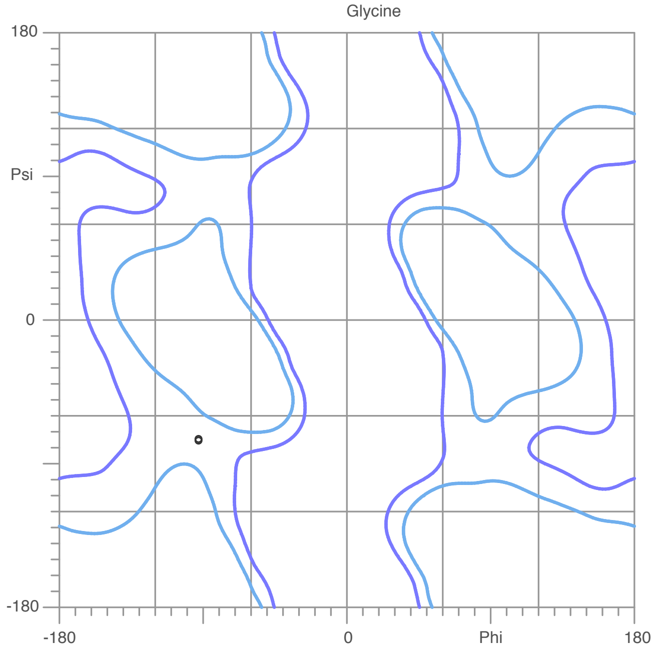
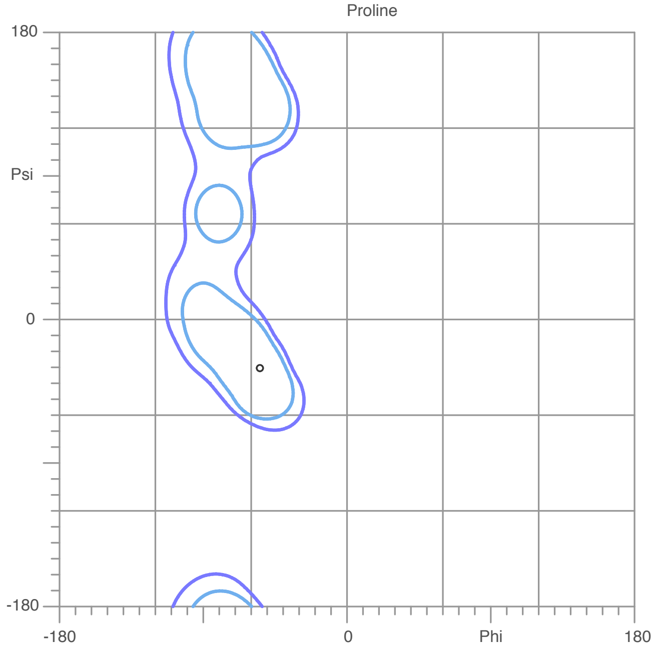
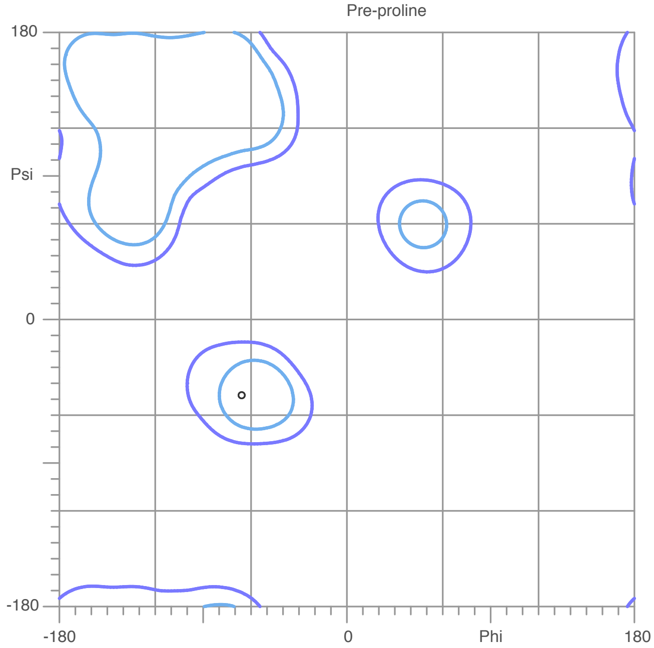
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 6


General case


Glycine


Proline


Pre-proline

84.6% (132/156) of all residues were in favored (98%) regions.
93.6% (146/156) of all residues were in allowed (>99.8%) regions.

There were 10 outliers (phi, psi):

[6] 5 PHE (93.5, -31.4)
[6] 23 SER (173.6, 75.0)
[6] 24 GLU (-174.0, -121.3)
[6] 45 GLN (55.1, -79.5)
[6] 70 GLU (15.5, -112.8)
[6] 95 PHE (93.4, -31.4)
[6] 113 SER (173.7, 75.0)
[6] 114 GLU (-174.0, -121.3)
[6] 135 GLN (55.0, -79.5)
[6] 160 GLU (15.6, -112.8)

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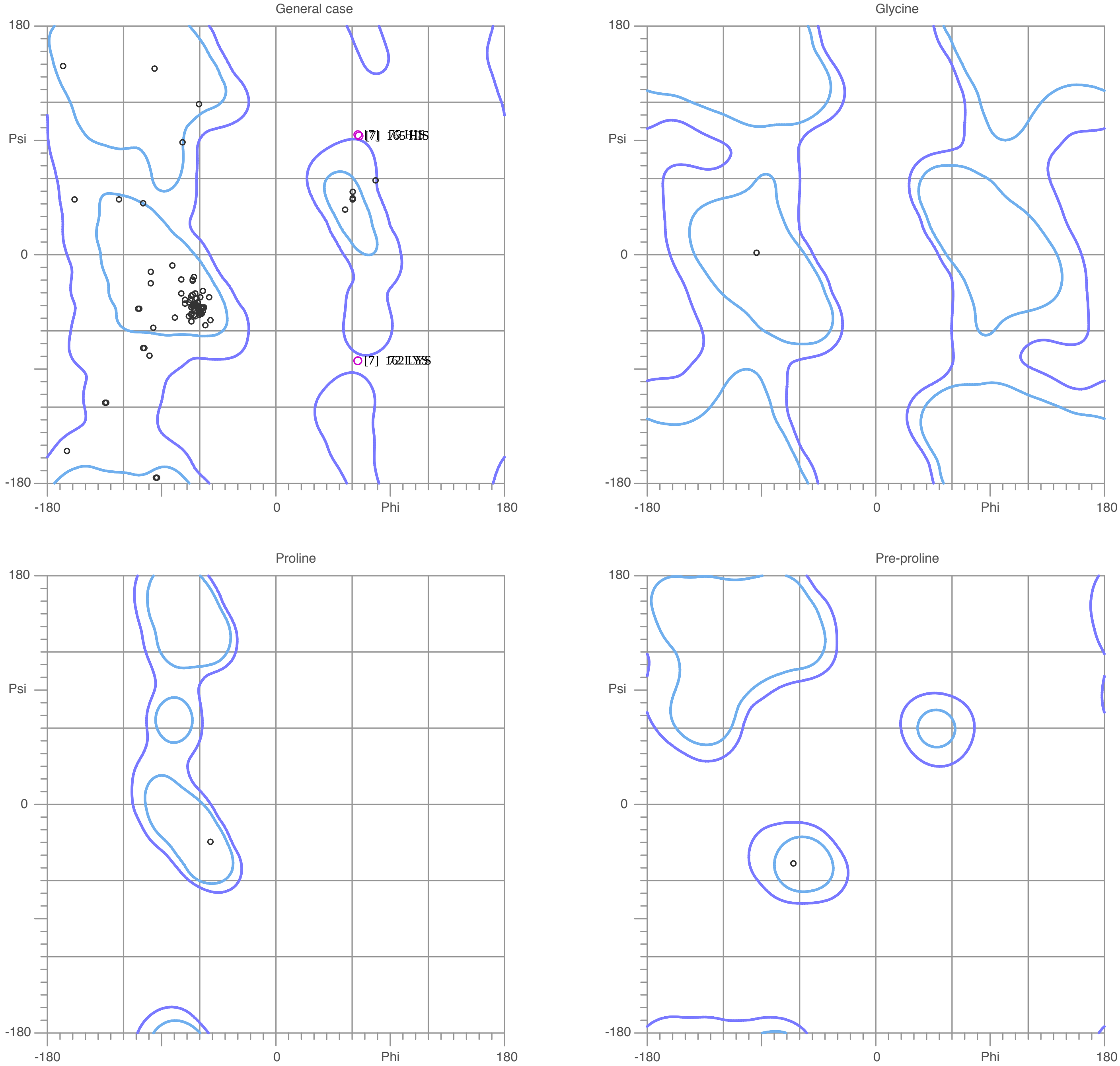
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 7



88.5% (138/156) of all residues were in favored (98%) regions.
97.4% (152/156) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[7] 72 LYS (64.1, -83.2)
[7] 75 HIS (65.0, 95.0)
[7] 162 LYS (64.2, -83.2)
[7] 165 HIS (65.0, 95.0)

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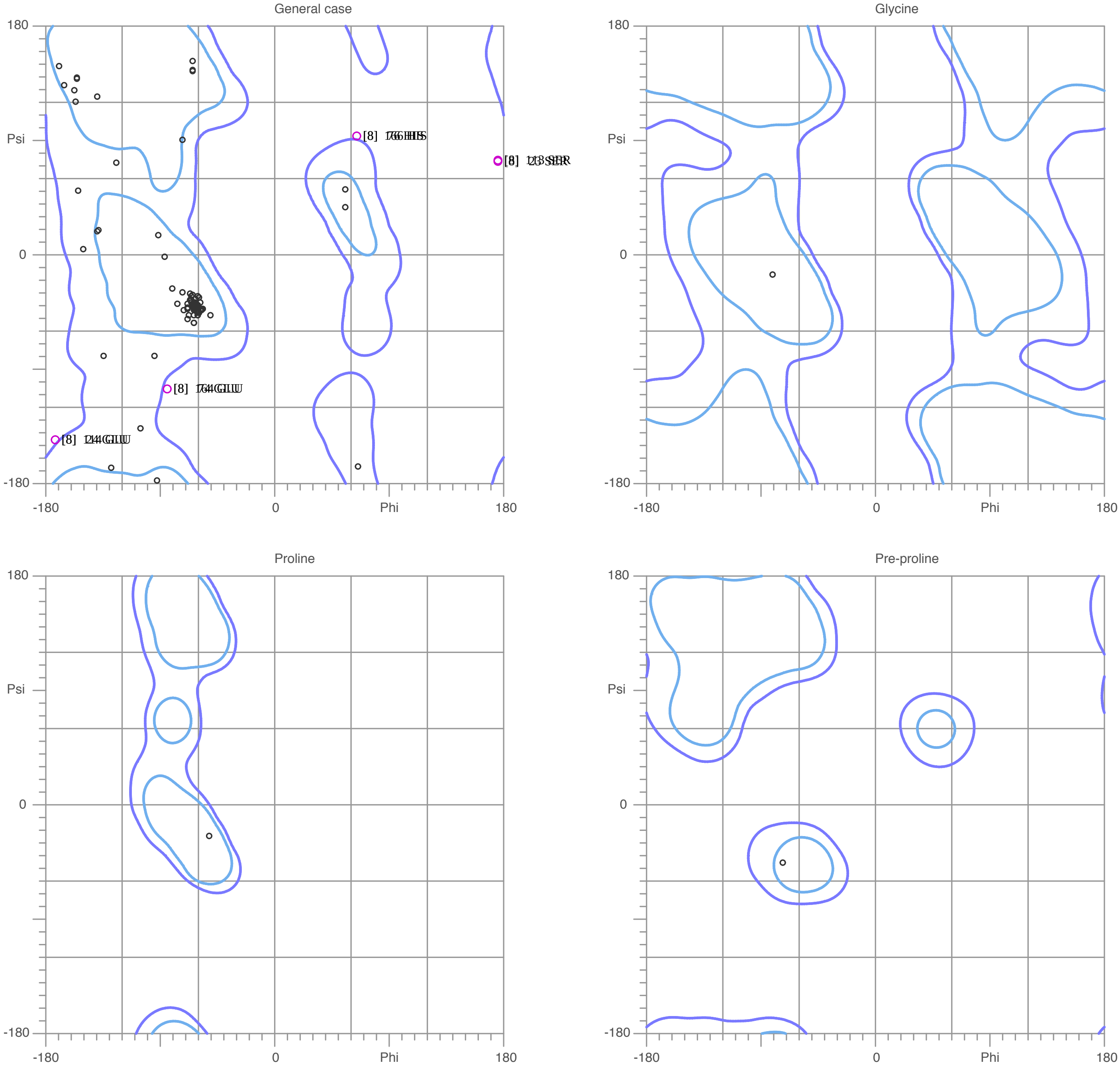
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 8



84.6% (132/156) of all residues were in favored (98%) regions.
94.9% (148/156) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):
[8] 23 SER (175.0, 75.0)
[8] 24 GLU (-173.3, -145.1)
[8] 74 GLU (-85.0, -105.0)
[8] 76 HIS (65.0, 94.9)
[8] 113 SER (175.1, 75.0)
[8] 114 GLU (-173.3, -145.1)
[8] 164 GLU (-85.1, -105.0)
[8] 166 HIS (64.9, 94.9)

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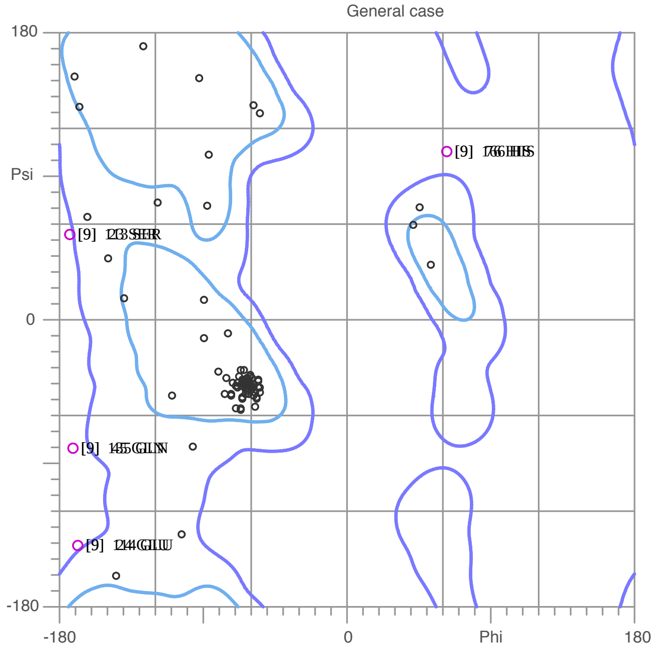
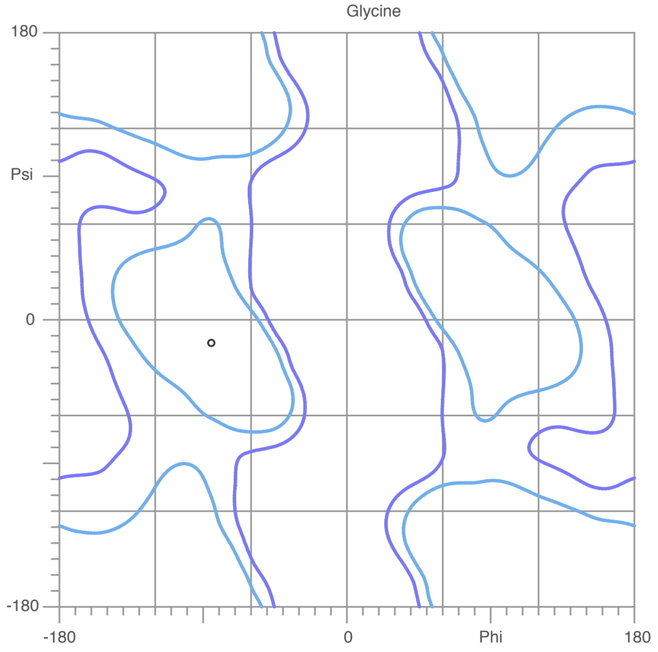
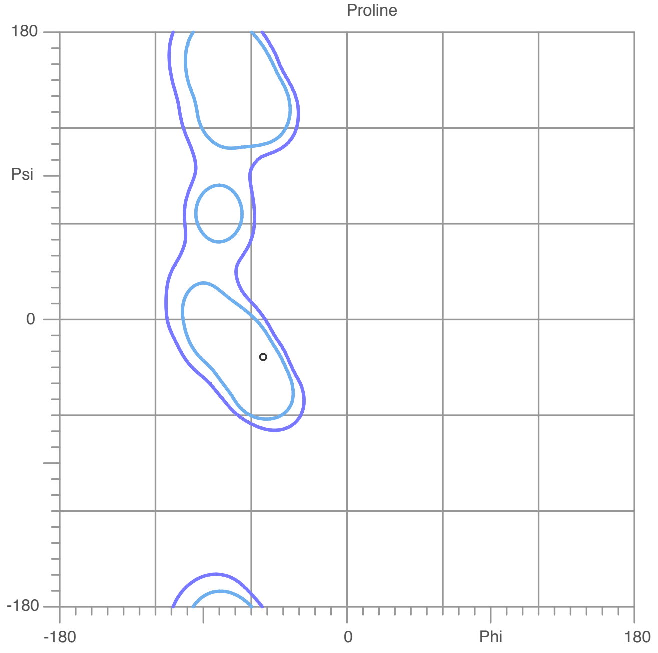
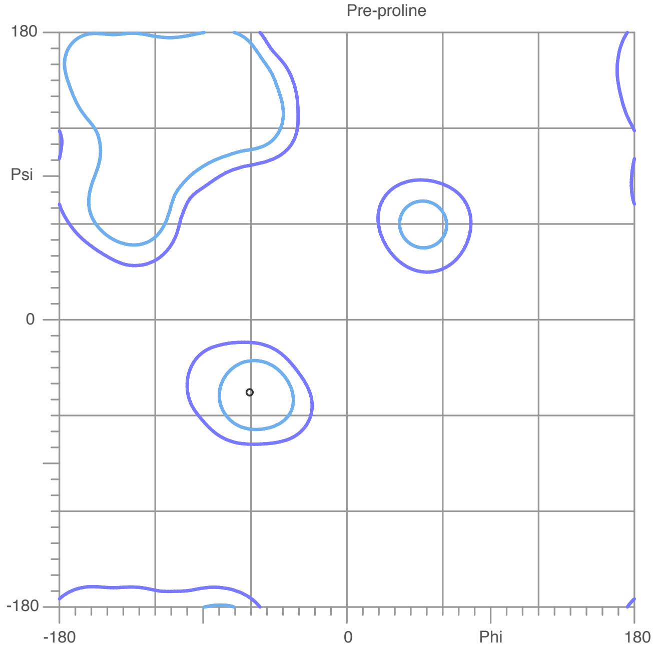
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 9









85.9% (134/156) of all residues were in favored (98%) regions.
94.9% (148/156) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[9] 23 SER (-174.9, 55.0)
[9] 24 GLU (-169.9, -141.2)
[9] 45 GLN (-172.3, -80.5)
[9] 76 HIS (62.9, 106.3)
[9] 113 SER (-175.0, 55.0)
[9] 114 GLU (-170.0, -141.3)
[9] 135 GLN (-172.3, -80.5)
[9] 166 HIS (63.0, 106.3)

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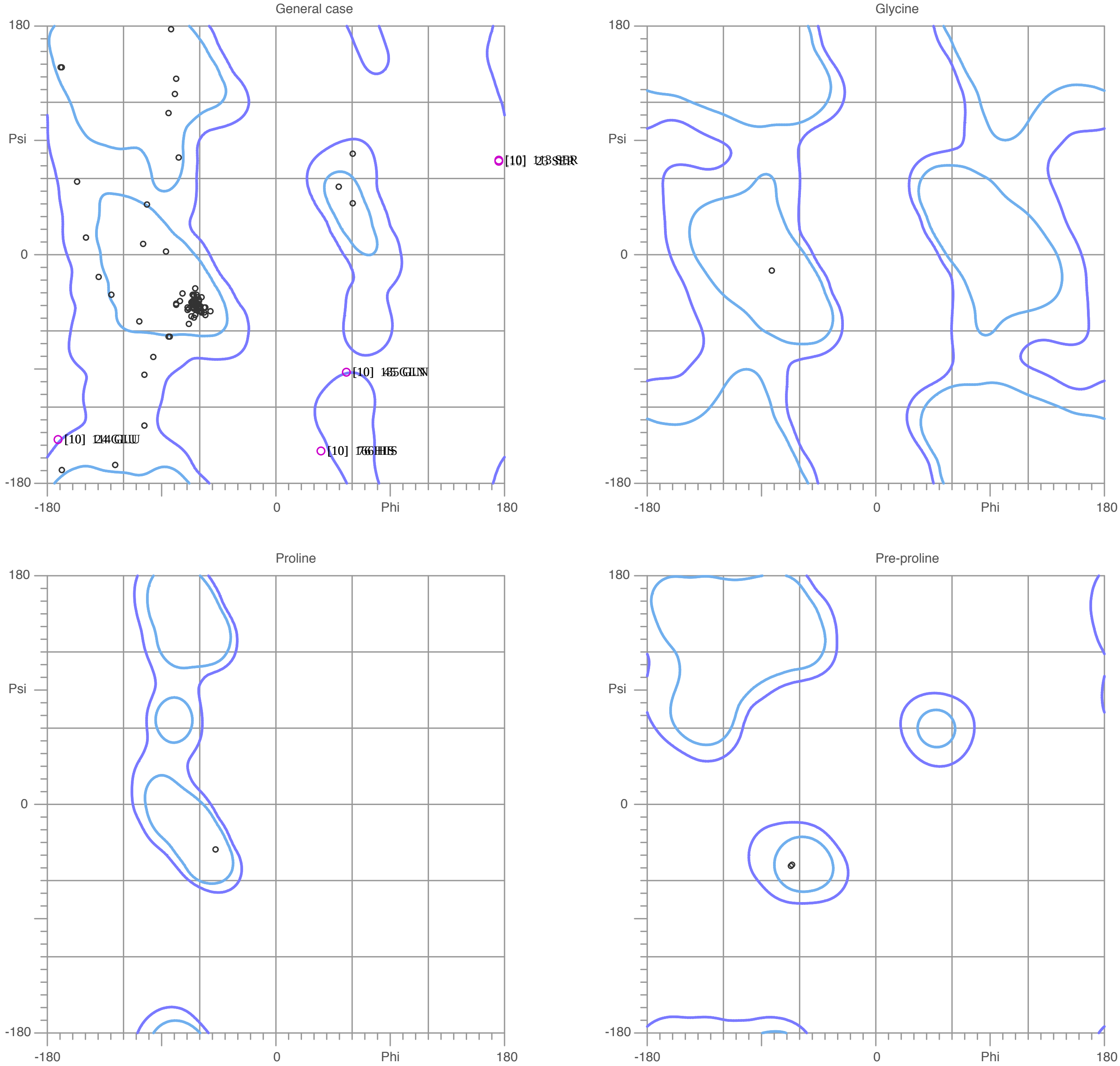
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 10



80.8% (126/156) of all residues were in favored (98%) regions.
94.9% (148/156) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[10]	23 SER (175.3, 75.0)
[10]	24 GLU (-172.0, -145.3)
[10]	45 GLN (55.0, -92.8)
[10]	76 HIS (35.5, -154.9)
[10]	113 SER (175.2, 75.1)
[10]	114 GLU (-172.0, -145.4)
[10]	135 GLN (55.0, -92.8)
[10]	166 HIS (35.5, -154.9)

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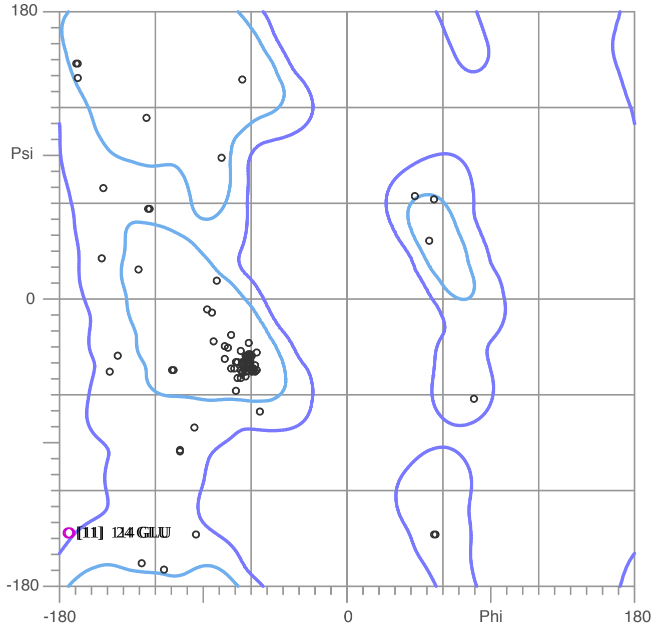
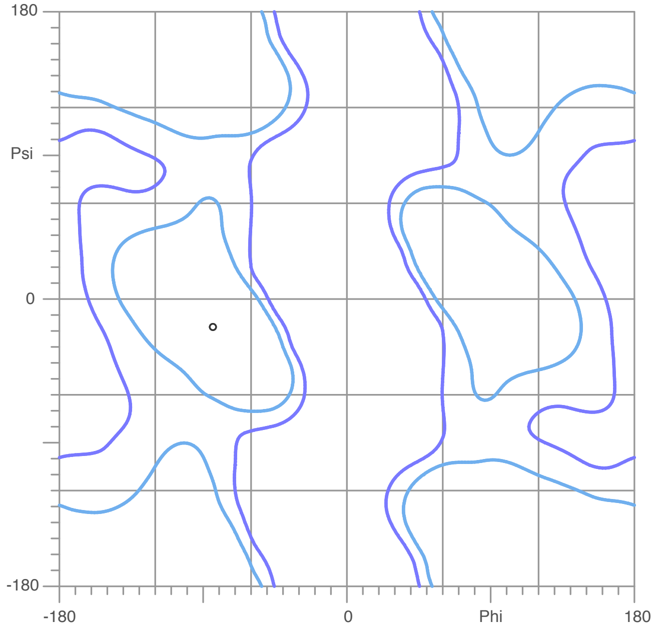
MolProbity Ramachandran analysis

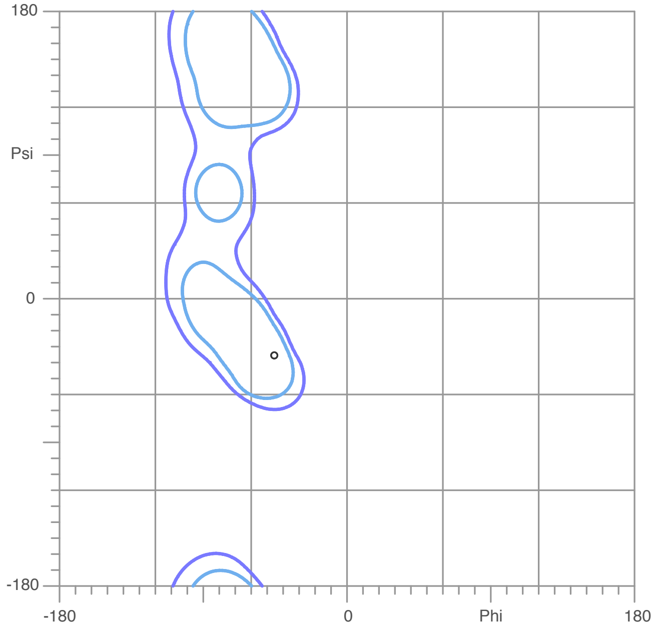
SR478_R3Cons_em_bcr3.pdb, model 11



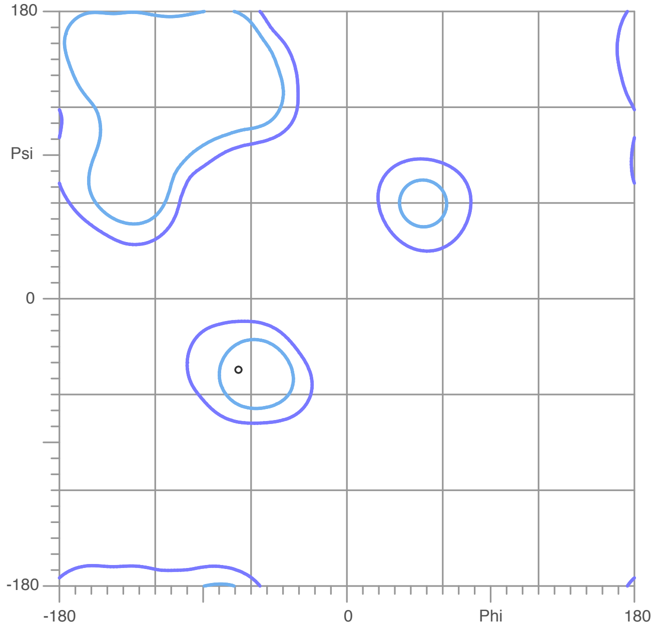
General case



Glycine



Proline



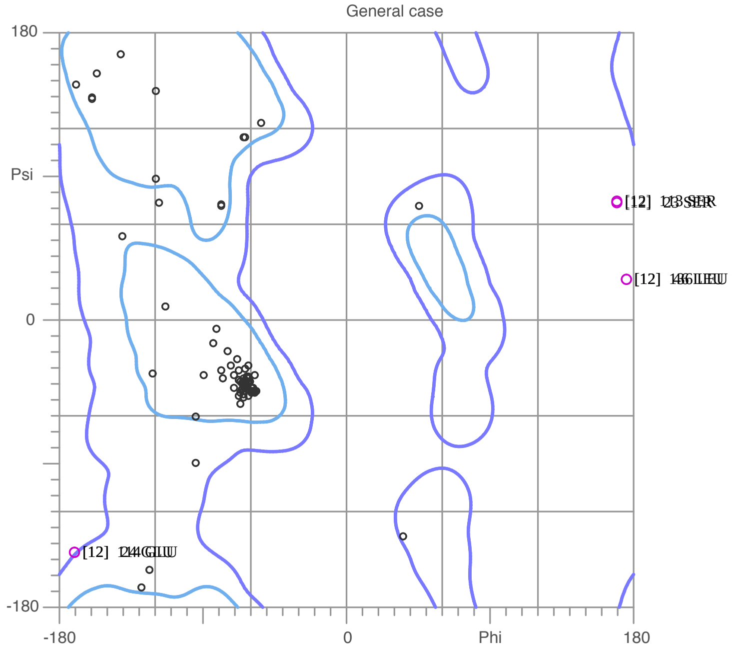
Pre-proline

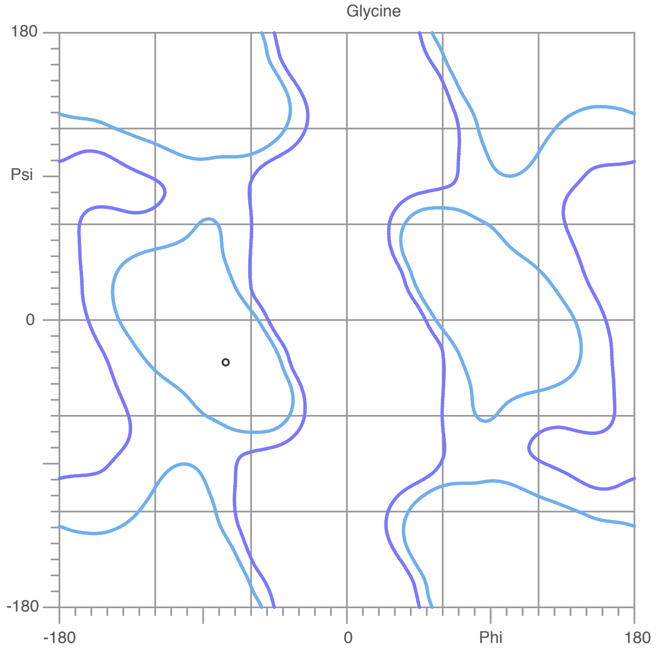
80.8% (126/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

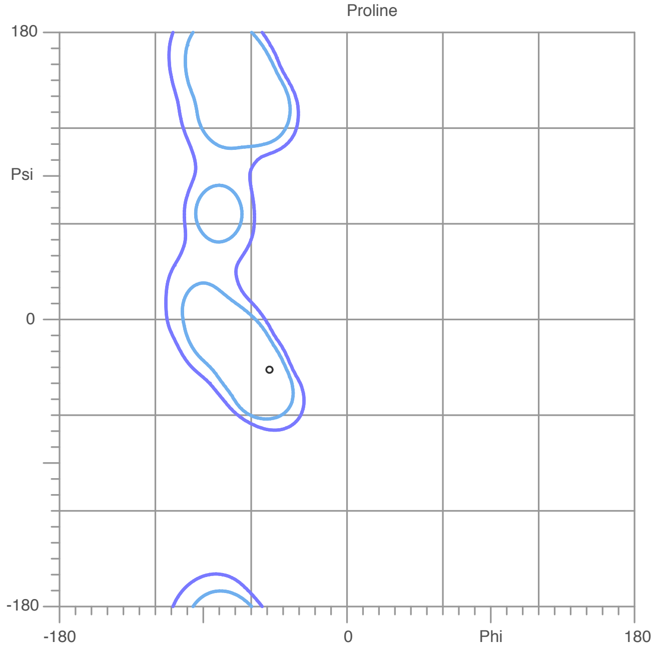
There were 2 outliers (phi, psi):
[11] 24 GLU (-175.0, -146.7)
[11] 114 GLU (-175.0, -146.8)

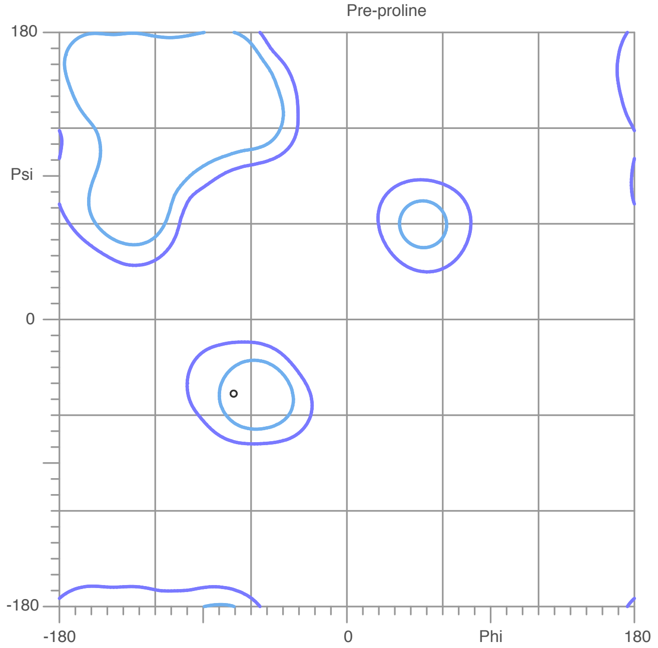
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 12









87.2% (136/156) of all residues were in favored (98%) regions.
96.2% (150/156) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[12] 23 SER (169.9, 75.0)
[12] 24 GLU (-171.6, -145.0)
[12] 46 LEU (175.1, 26.5)
[12] 113 SER (170.0, 75.0)
[12] 114 GLU (-171.6, -145.0)
[12] 136 LEU (175.1, 26.5)

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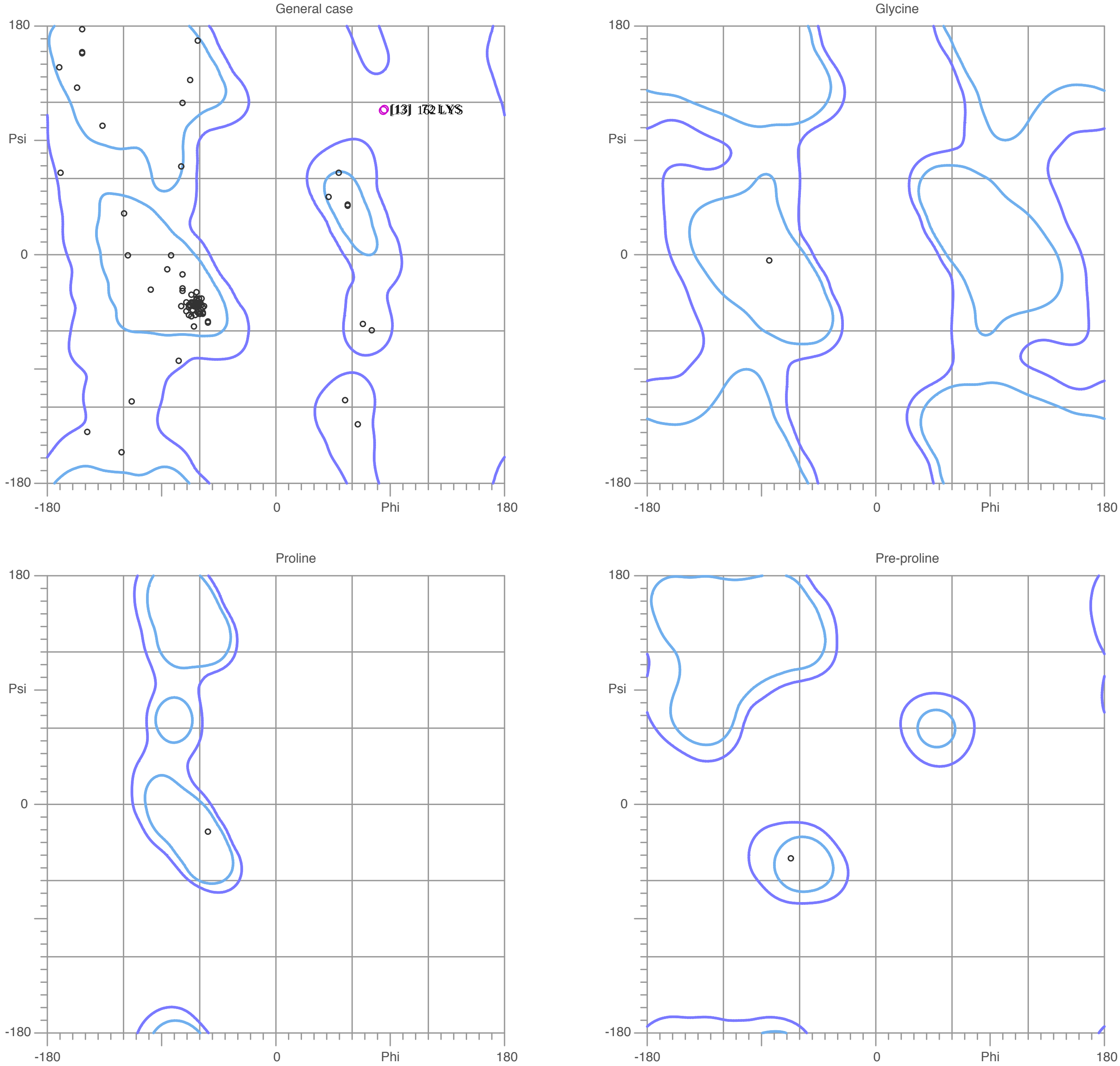
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 13

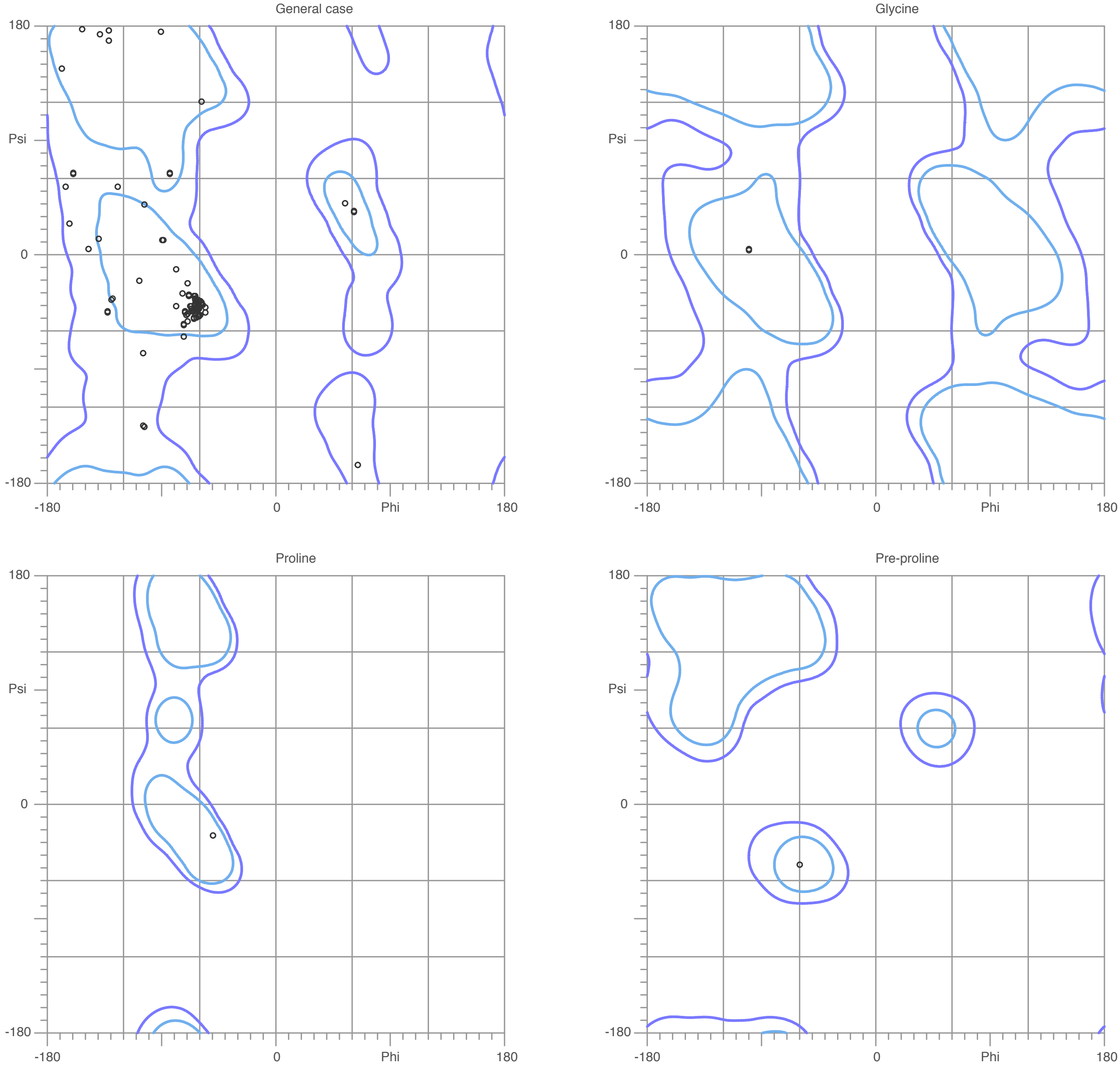


85.9% (134/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[13] 72 LYS (85.0, 115.1)
[13] 162 LYS (85.0, 115.0)

MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 14



84.6% (132/156) of all residues were in favored (98%) regions.
100.0% (156/156) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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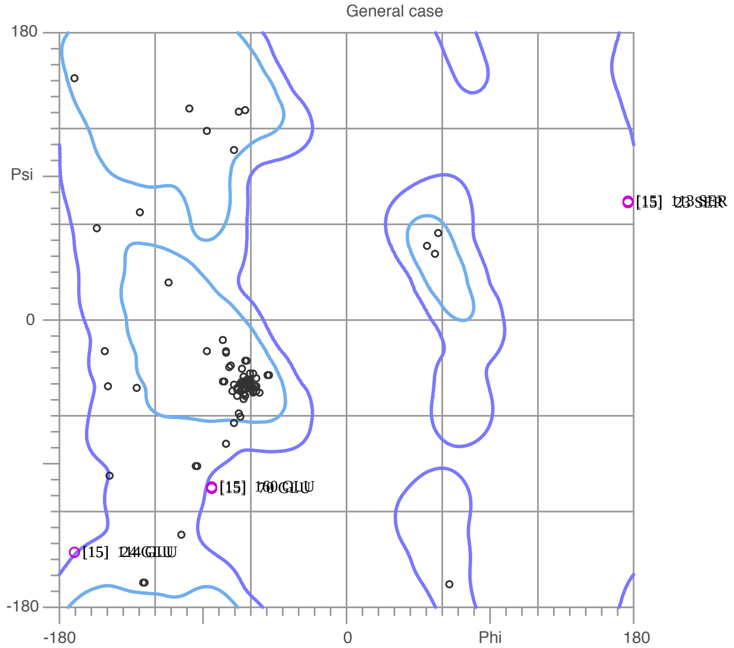
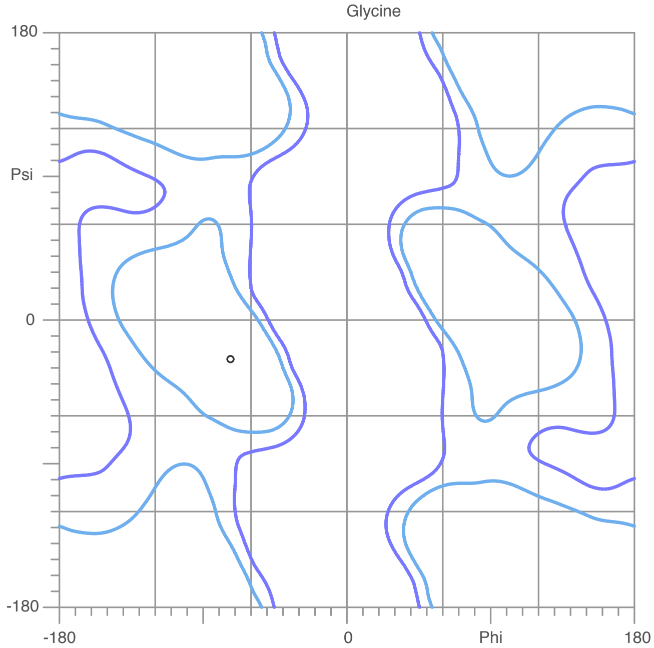
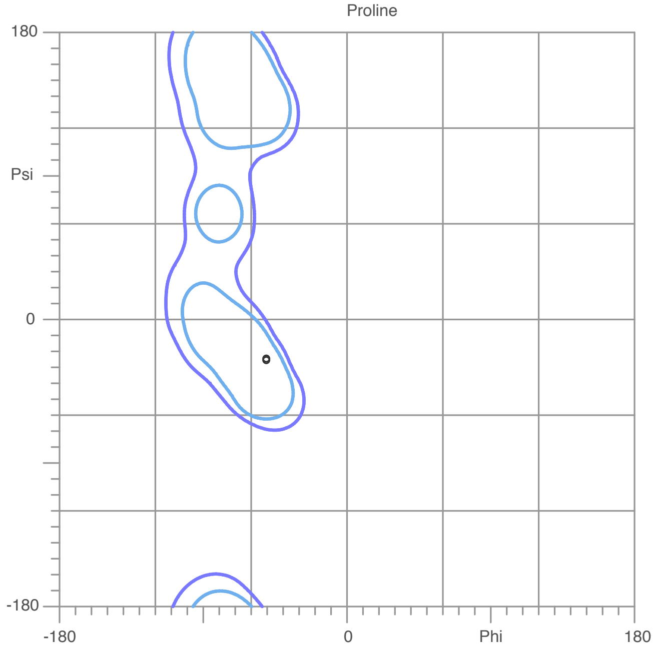
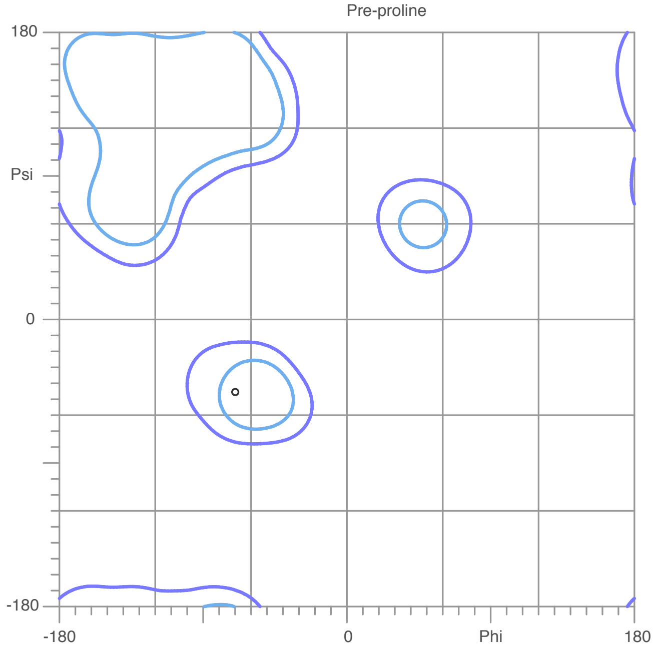
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 15


General case


Glycine


Proline


Pre-proline

80.8% (126/156) of all residues were in favored (98%) regions.
96.2% (150/156) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[15] 23 SER (176.7, 75.0)
[15] 24 GLU (-171.8, -145.1)
[15] 70 GLU (-85.1, -105.0)
[15] 113 SER (176.8, 75.0)
[15] 114 GLU (-171.8, -145.0)
[15] 160 GLU (-85.1, -105.0)

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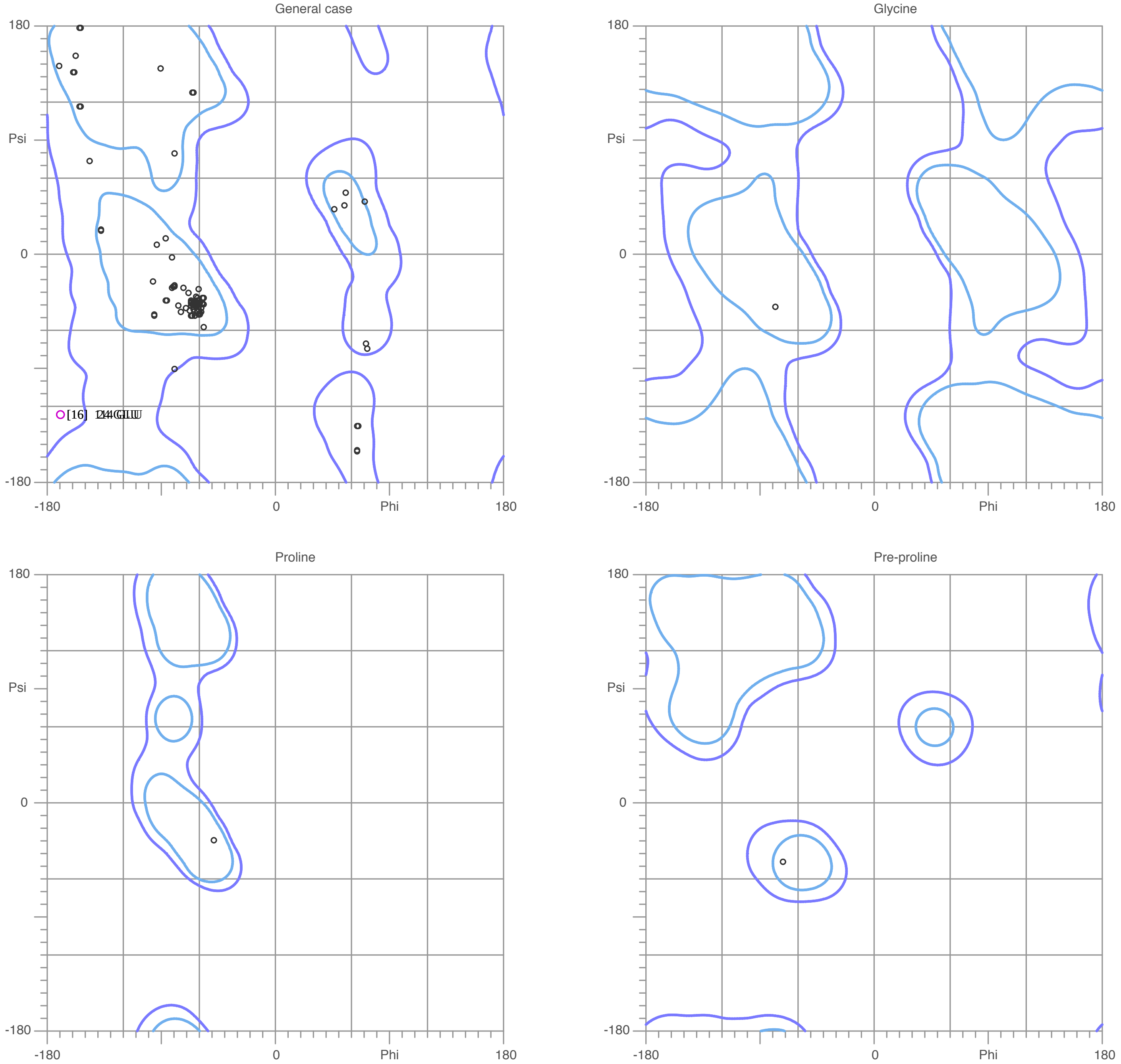
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 16



89.7% (140/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
- [16] 24 GLU (-170.0, -126.4)
- [16] 114 GLU (-170.1, -126.4)

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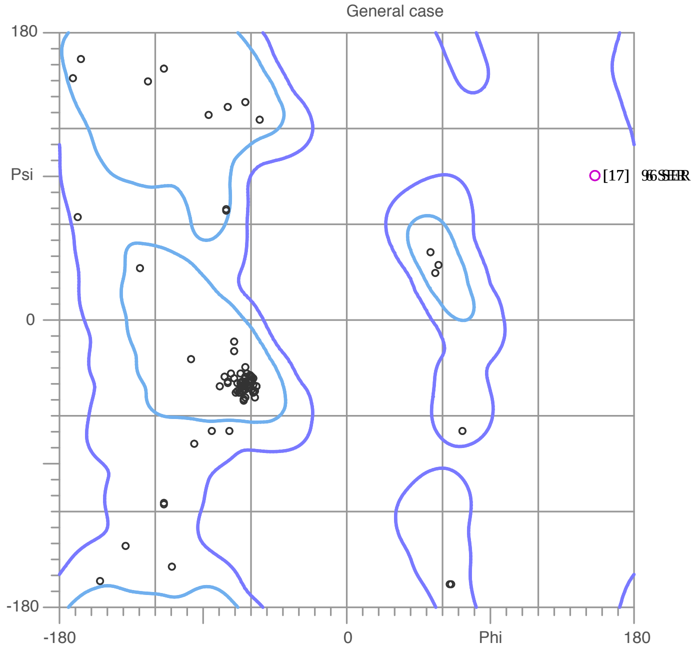
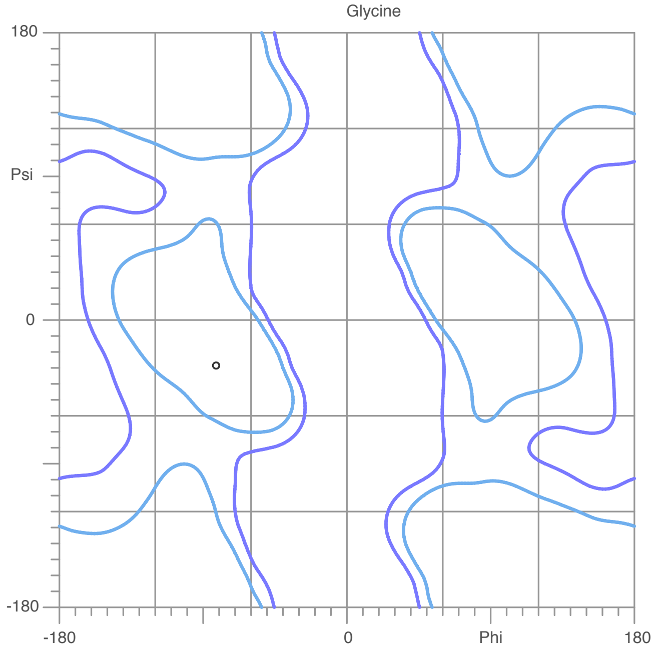
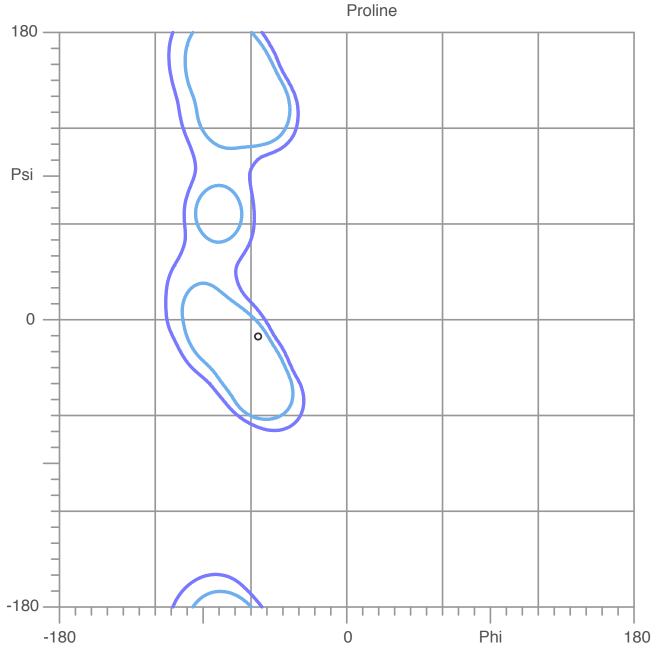
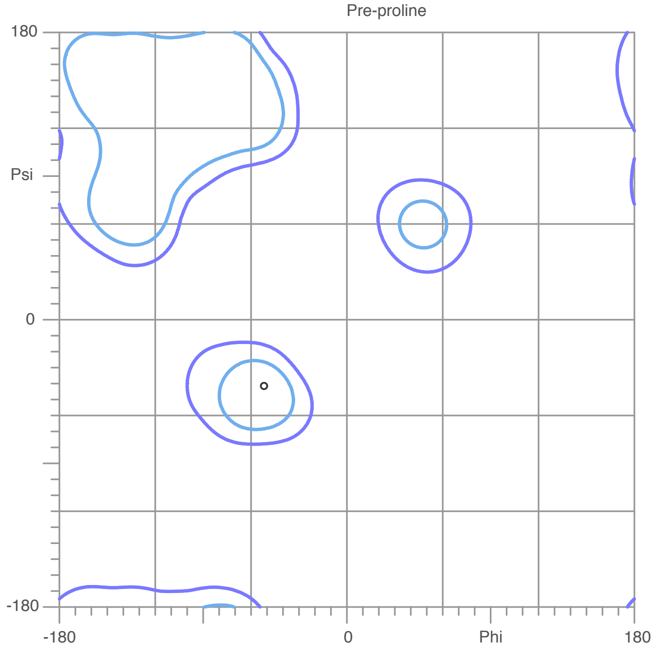
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 17







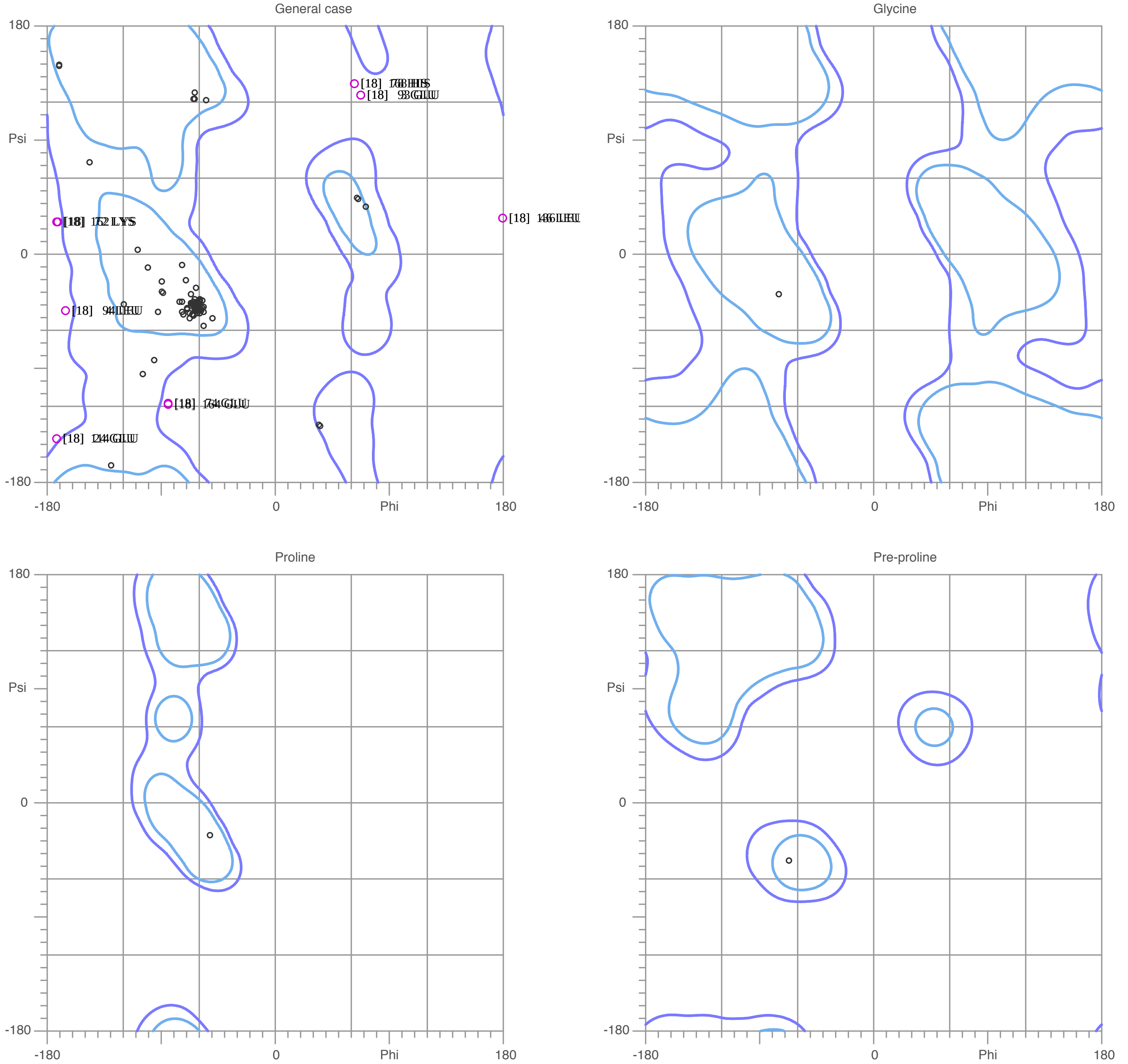


85.9% (134/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[17] 6 SER (155.1, 91.7)
[17] 96 SER (155.1, 91.7)

MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 18



83.3% (130/156) of all residues were in favored (98%) regions.
91.0% (142/156) of all residues were in allowed (>99.8%) regions.

There were 14 outliers (phi, psi):

[18] 3 GLU (67.7, 126.7)
[18] 4 LEU (-166.1, -45.0)
[18] 24 GLU (-173.5, -145.0)
[18] 46 LEU (179.9, 29.1)
[18] 72 LYS (-173.0, 27.0)
[18] 74 GLU (-85.9, -118.0)
[18] 78 HIS (62.2, 135.0)
[18] 93 GLU (67.6, 126.7)
[18] 94 LEU (-166.1, -45.0)
[18] 114 GLU (-173.5, -145.0)
[18] 136 LEU (179.9, 29.0)
[18] 162 LYS (-173.0, 27.0)
[18] 164 GLU (-86.0, -118.0)
[18] 168 HIS (62.3, 135.0)

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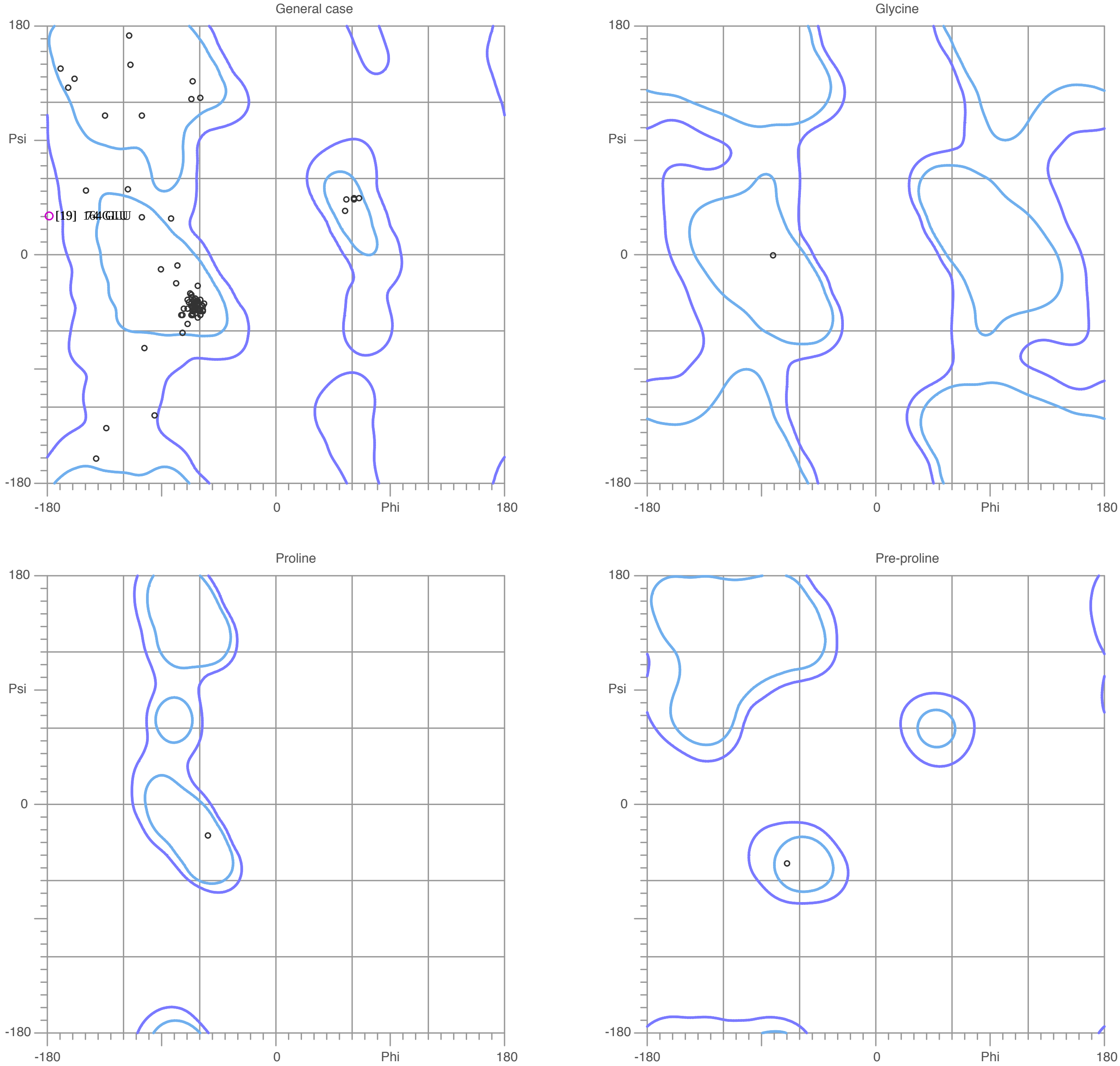
MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 19

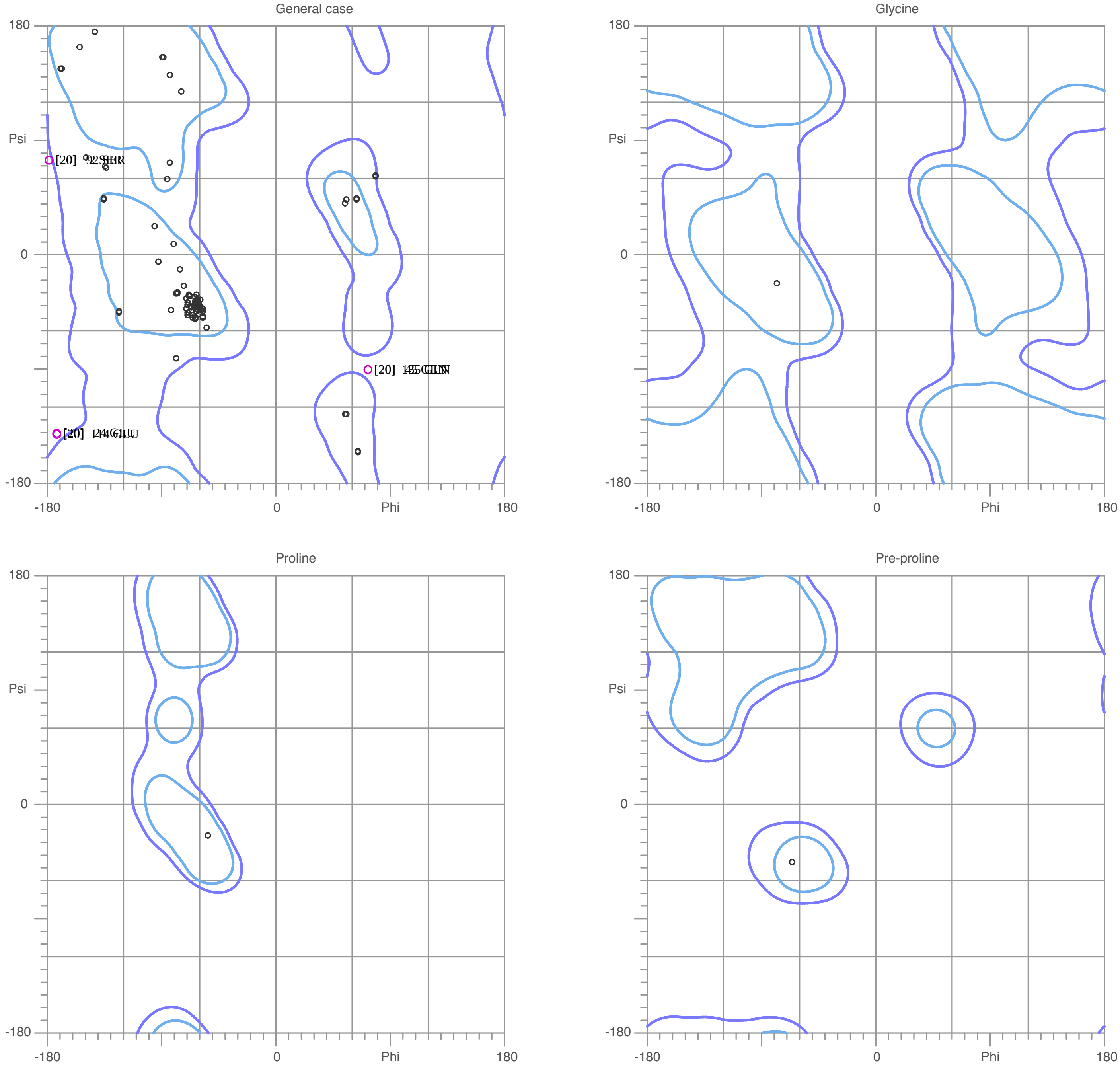


89.7% (140/156) of all residues were in favored (98%) regions.
98.7% (154/156) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 74 GLU (-179.4, 31.8)
[19] 164 GLU (-179.4, 31.8)

MolProbity Ramachandran analysis

SR478_R3Cons_em_bcr3.pdb, model 20



88.5% (138/156) of all residues were in favored (98%) regions.
96.2% (150/156) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[20] 2 SER (-179.0, 75.0)
[20] 24 GLU (-173.8, -141.0)
[20] 45 GLN (72.3, -91.0)
[20] 92 SER (-179.0, 75.0)
[20] 114 GLU (-173.8, -141.0)
[20] 135 GLN (72.3, -90.9)

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