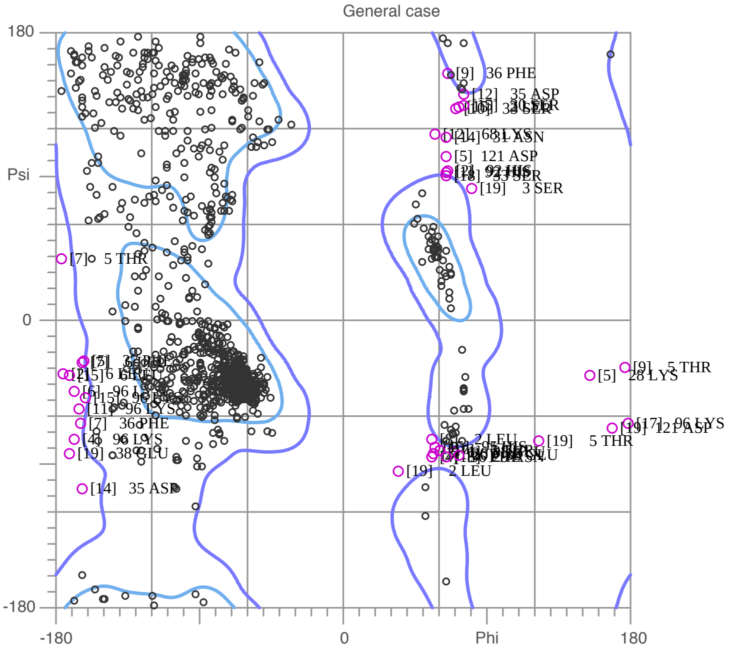
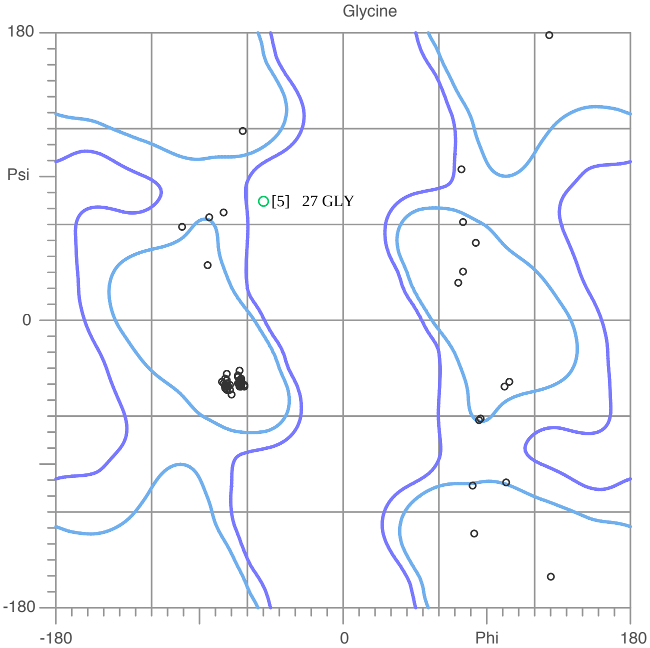
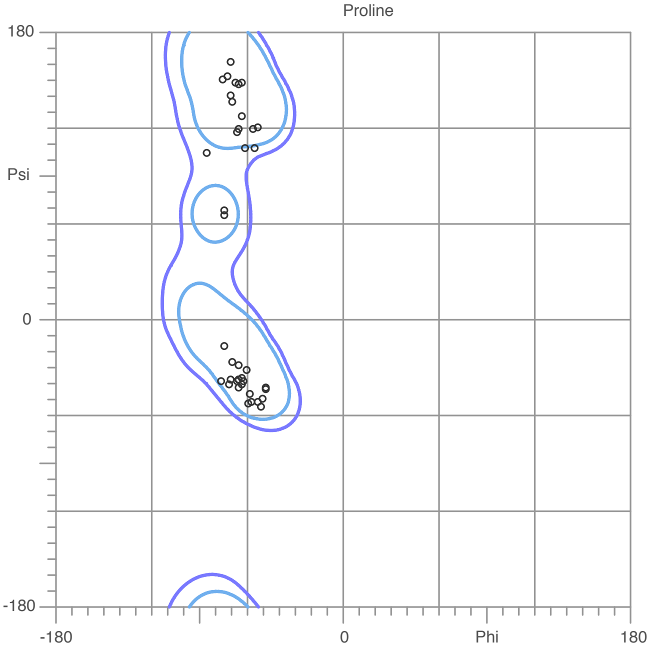
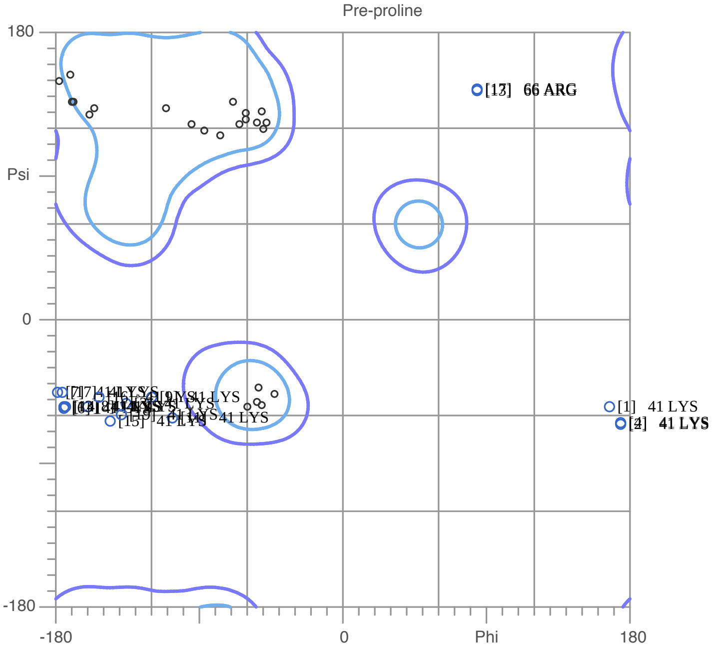
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, all models


General case


Glycine


Proline


Pre-proline

92.2% (2232/2420) of all residues were in favored (98%) regions.
97.7% (2364/2420) of all residues were in allowed (>99.8%) regions.

```
There were 56 outliers (phi, psi):
   [1]   38 GLU (69.5, -82.6)
   [1]   41 LYS (167.5, -55.0)
   [1]   92 HIS (64.9, 93.7)
   [2]    6 LEU (-176.3, -33.5)
   [2]   41 LYS (175.0, -65.1)
   [2]   92 HIS (65.0, 95.0)
   [3]   36 PHE (56.5, -83.6)
   [3]   41 LYS (-136.7, -52.8)
   [4]   36 PHE (55.0, -85.1)
   [4]   41 LYS (175.0, -64.9)
   [4]   96 LYS (-169.3, -74.9)
   [5]   27 GLY (-50.4, 75.7)
   [5]   28 LYS (155.0, -35.0)
   [5]   37 PHE (-163.6, -25.2)
   [5]  121 ASP (64.9, 103.4)
   [6]   41 LYS (-175.0, -55.1)
   [6]   96 LYS (-169.1, -45.0)
   [7]    5 THR (-177.5, 39.4)
   [7]    6 LEU (-164.9, -26.3)
   [7]   36 PHE (-165.1, -64.9)
   [7]   41 LYS (-179.7, -45.1)
   [8]    2 LEU (55.7, -74.7)
   [8]   41 LYS (-160.9, -54.9)
   [9]    5 THR (176.9, -29.7)
   [9]   36 PHE (65.7, 155.3)
   [9]   41 LYS (-120.1, -48.1)
   [10]   33 SER (70.8, 133.2)
   [11]   41 LYS (-107.4, -61.0)
   [11]   96 LYS (-166.4, -55.8)
   [12]   35 ASP (75.0, 142.9)
   [12]   68 LYS (57.6, 117.5)
   [13]   41 LYS (-175.6, -55.0)
   [13]   66 ARG (85.0, 145.0)
   [14]   31 ASN (65.0, 115.1)
   [14]   35 ASP (-165.0, -105.0)
   [14]   41 LYS (-175.0, -54.8)
   [15]    2 LEU (72.3, 135.0)
   [15]    6 LEU (-172.5, -34.2)
   [15]   30 SER (75.8, 135.0)
   [15]   41 LYS (-146.8, -63.6)
   [15]   95 HIS (57.1, -79.1)
   [15]   96 LYS (-162.5, -48.8)
   [16]   41 LYS (-153.1, -48.2)
   [17]    5 THR (60.7, -81.6)
   [17]   41 LYS (-176.7, -45.0)
   [17]   66 ARG (84.5, 145.0)
   [17]   96 LYS (178.6, -65.0)
   [18]   29 ASN (64.1, -85.2)
   [18]   33 SER (65.0, 92.0)
   [19]    2 LEU (34.6, -94.8)
   [19]    3 SER (80.2, 83.6)
   [19]    5 THR (122.7, -75.7)
   [19]   38 GLU (-172.9, -83.9)
   [19]   41 LYS (-140.0, -59.5)
   [19]  121 ASP (168.0, -67.6)
   [20]   38 GLU (72.8, -85.0)
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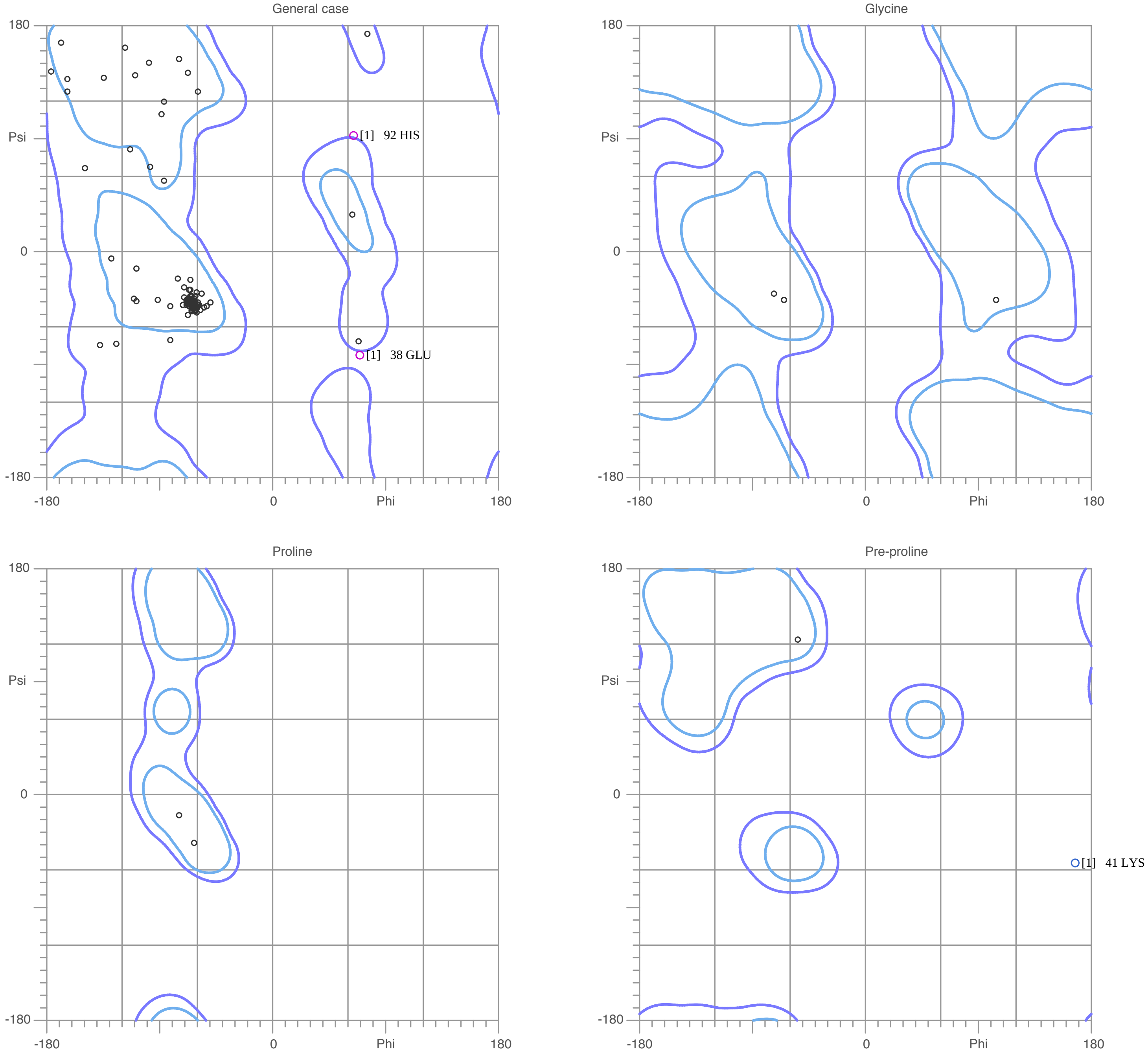
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 1



90.9% (110/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
- [1] 38 GLU (69.5, -82.6)
- [1] 41 LYS (167.5, -55.0)
- [1] 92 HIS (64.9, 93.7)

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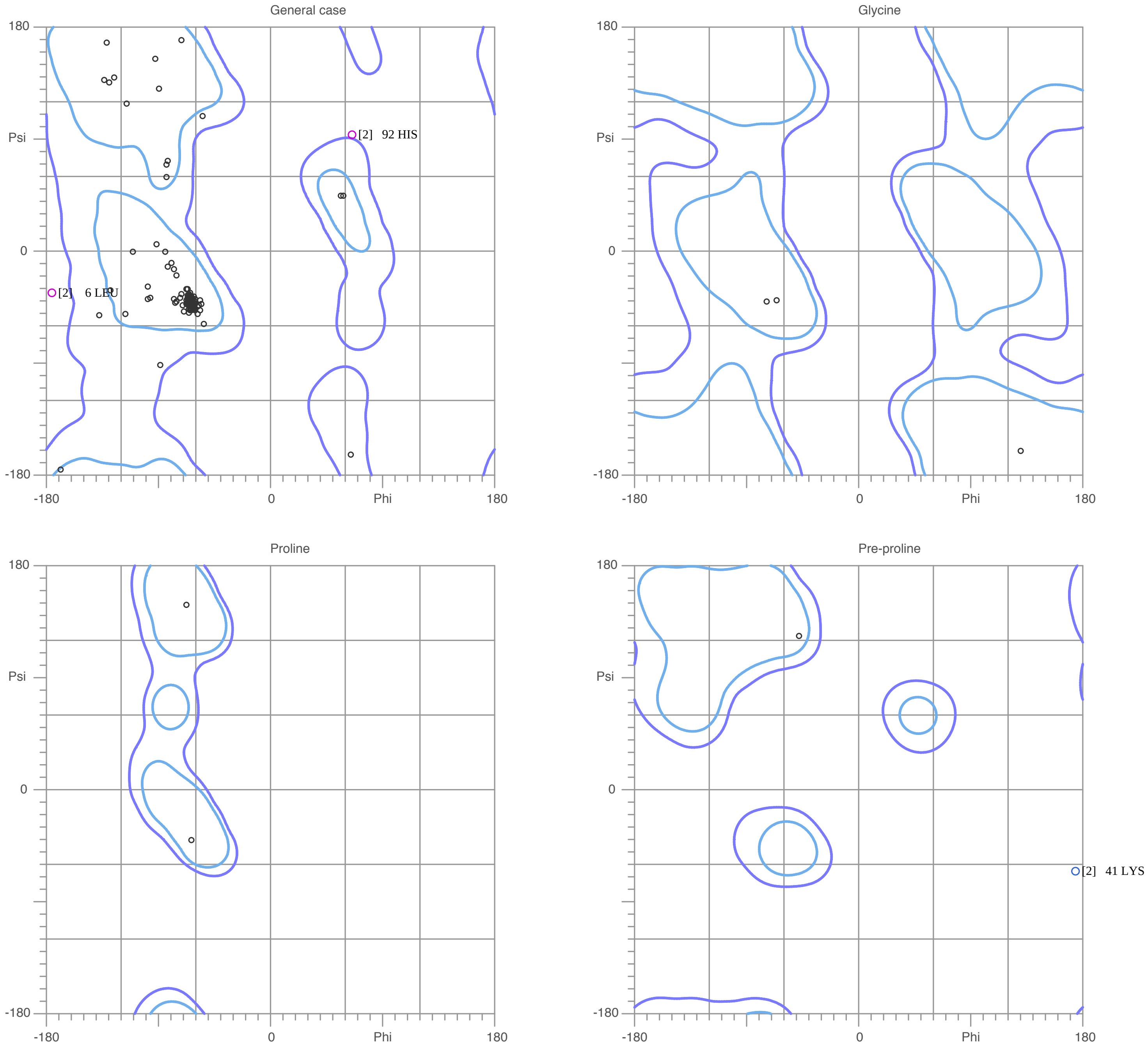
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 2

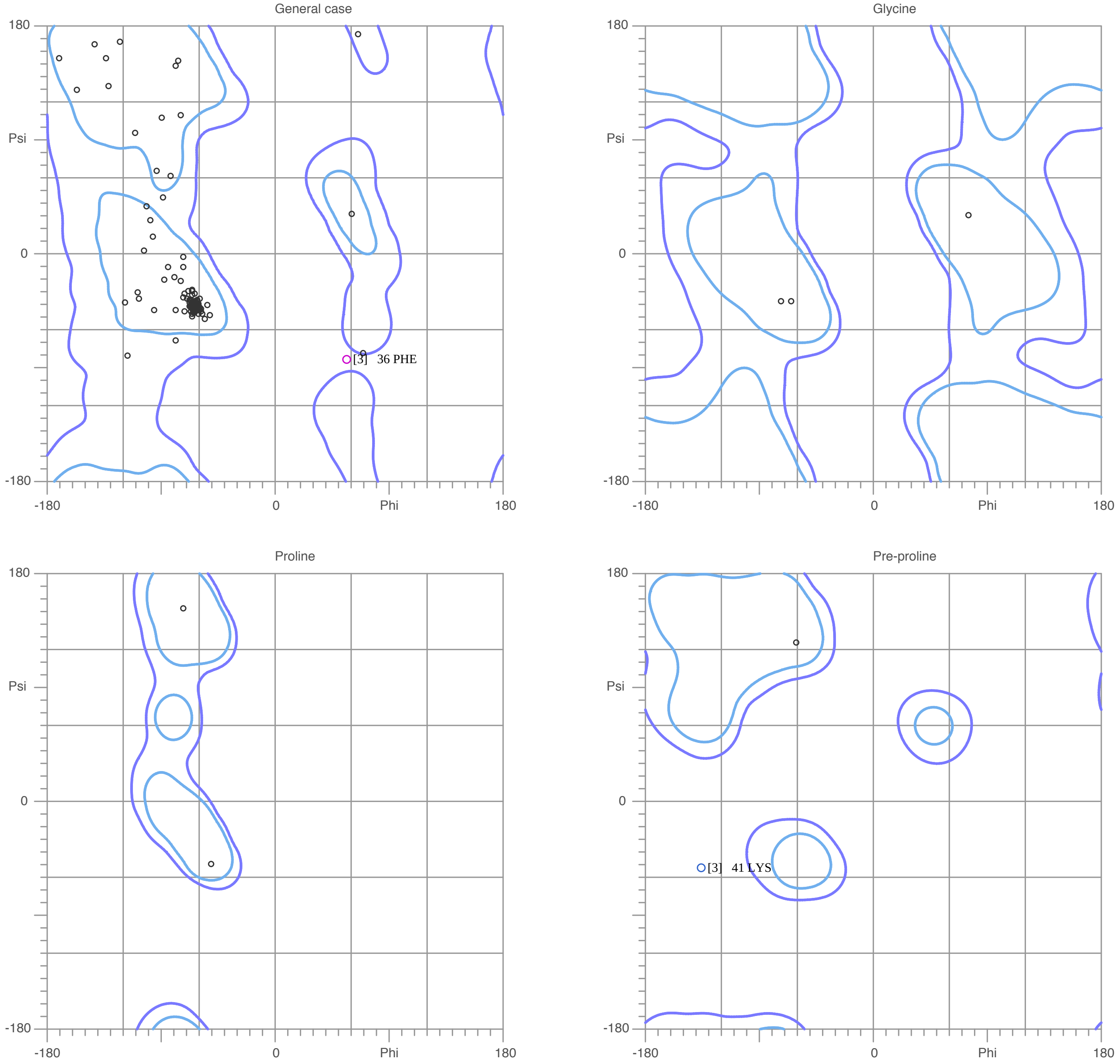


94.2% (114/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[2] 6 LEU (-176.3, -33.5)
[2] 41 LYS (175.0, -65.1)
[2] 92 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 3

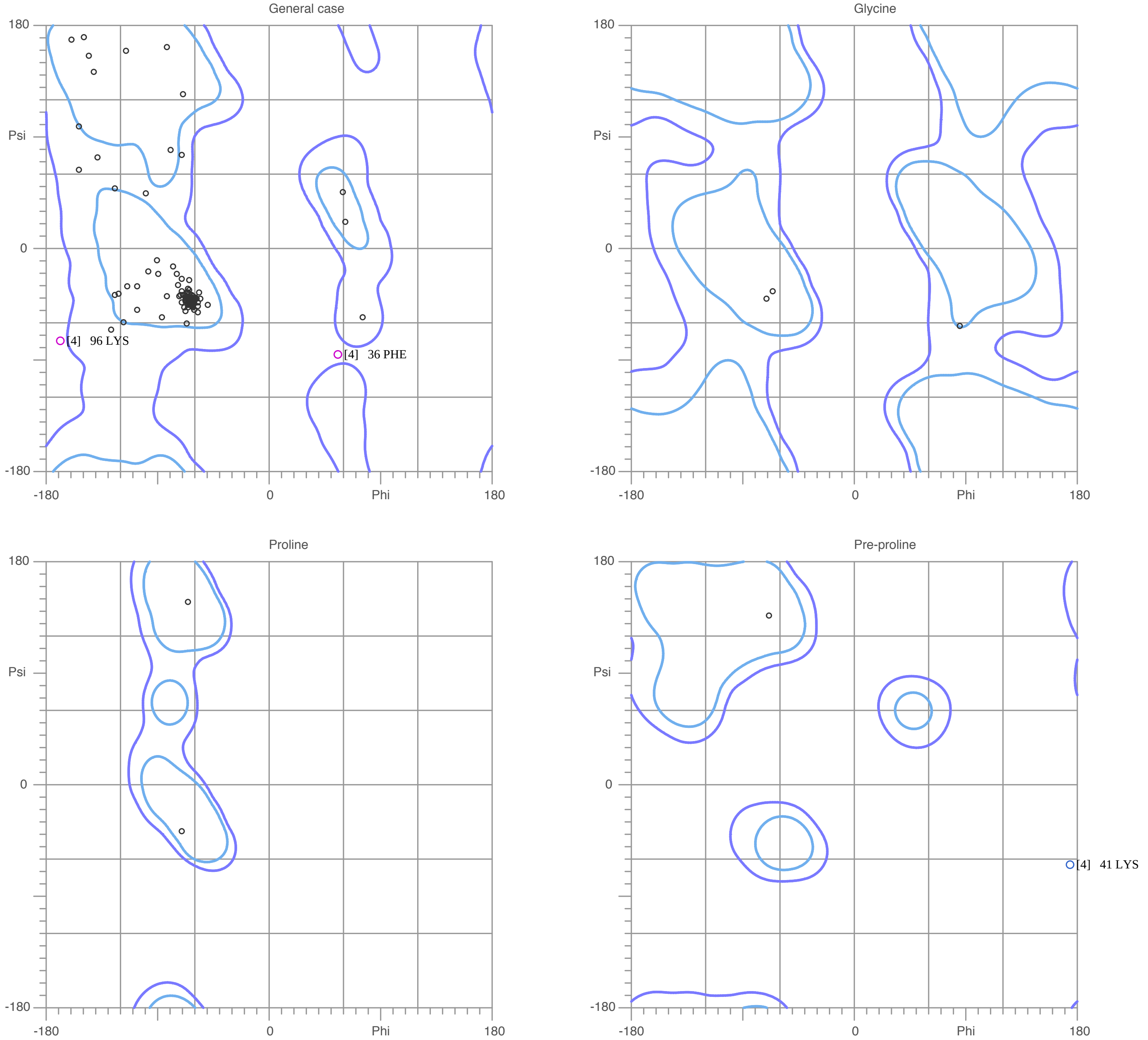


94.2% (114/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
- [3] 36 PHE (56.5, -83.6)
- [3] 41 LYS (-136.7, -52.8)

MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 4



90.1% (109/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
- [4] 36 PHE (55.0, -85.1)
- [4] 41 LYS (175.0, -64.9)
- [4] 96 LYS (-169.3, -74.9)

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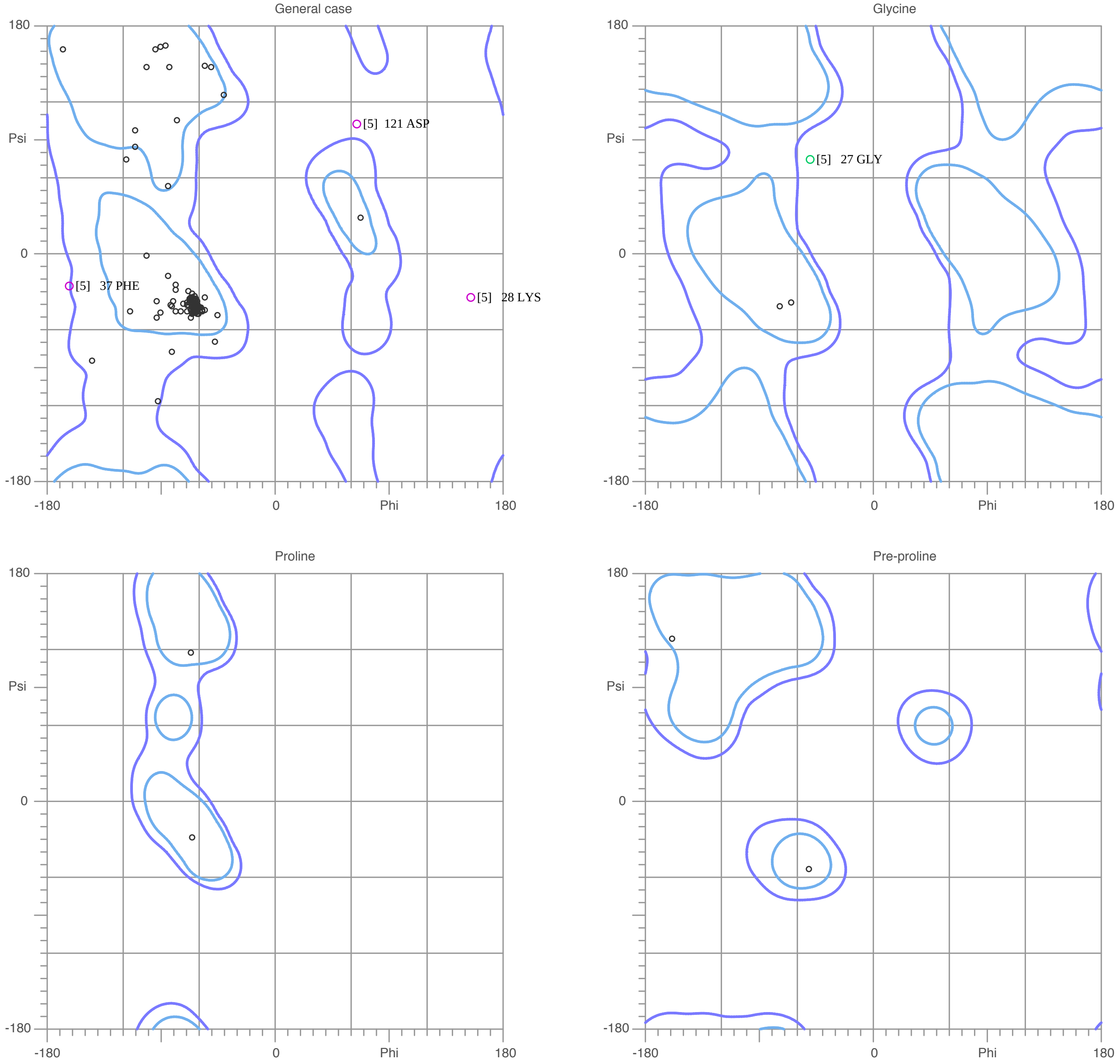
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 5



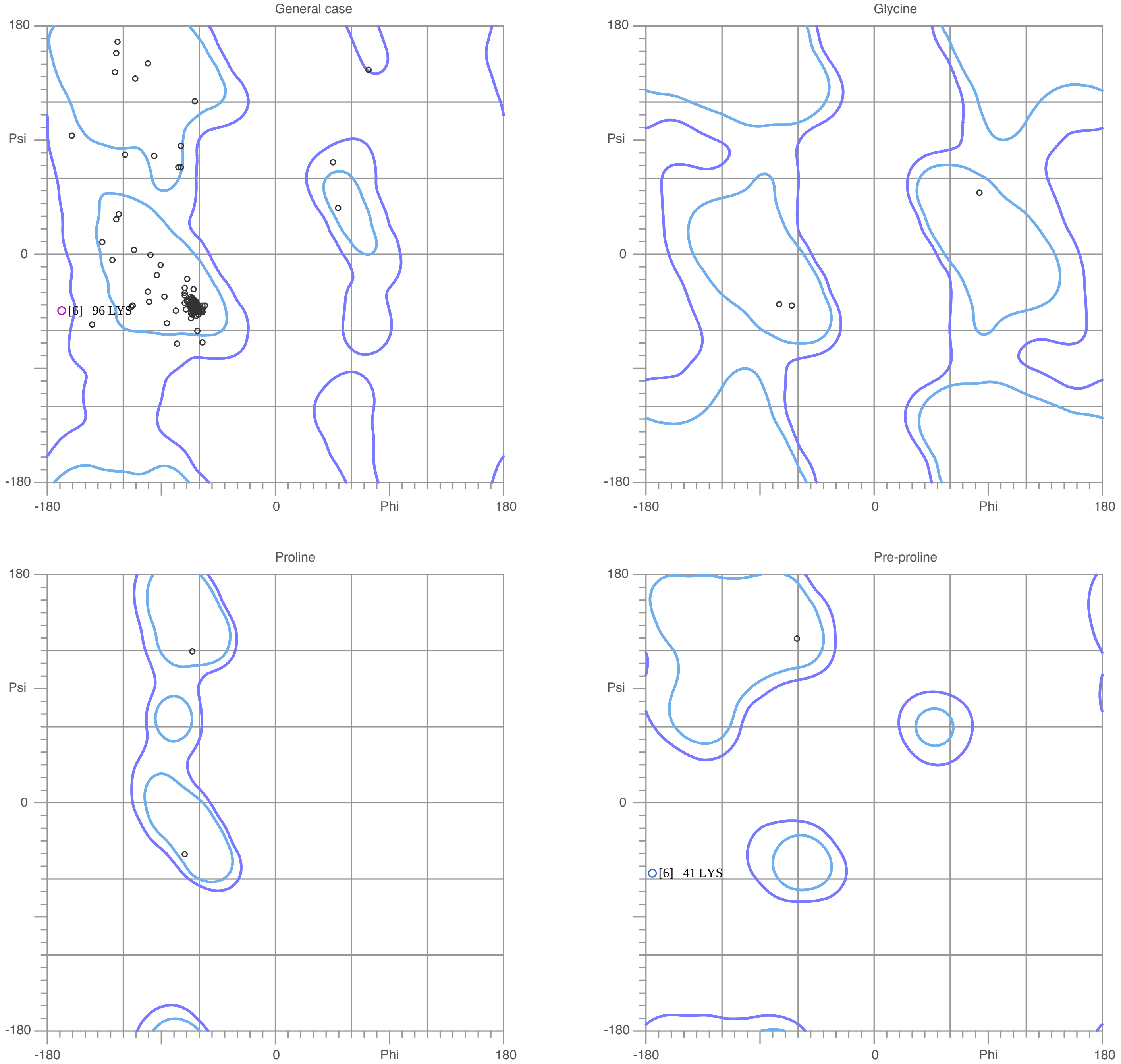
92.6% (112/121) of all residues were in favored (98%) regions.
96.7% (117/121) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[5]	27 GLY (-50.4, 75.7)
[5]	28 LYS (155.0, -35.0)
[5]	37 PHE (-163.6, -25.2)
[5]	121 ASP (64.9, 103.4)

MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 6

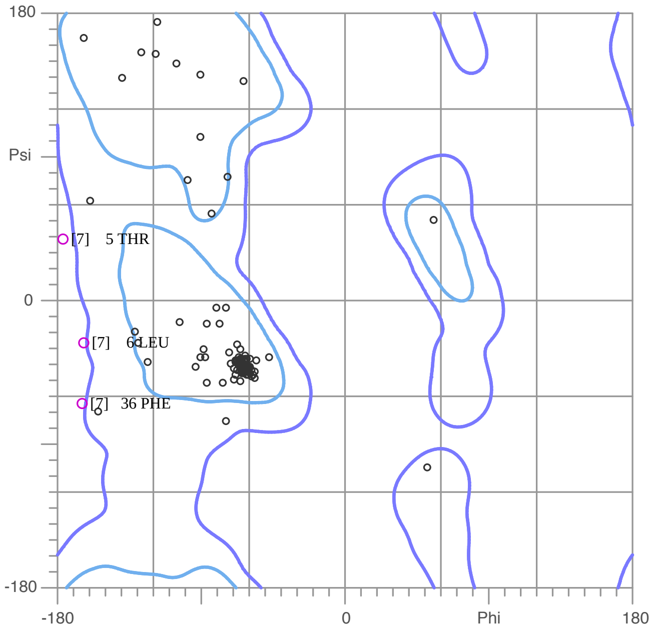


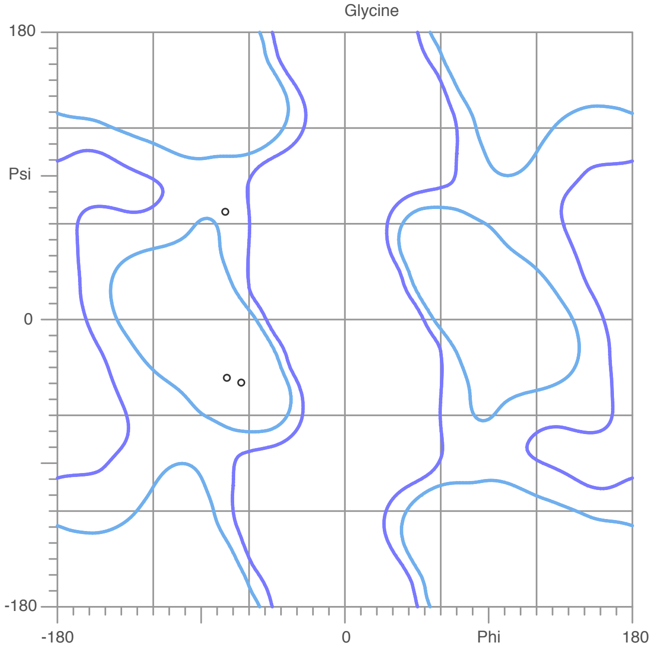
92.6% (112/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

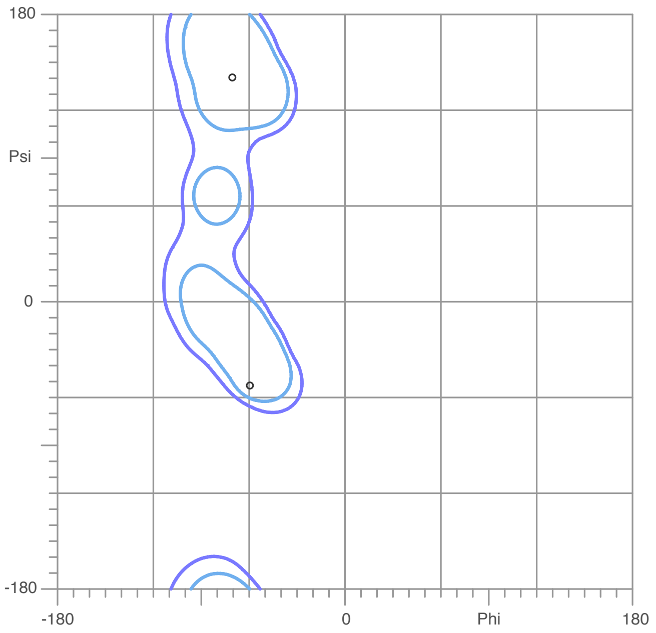
There were 2 outliers (phi, psi):
[6] 41 LYS (-175.0, -55.1)
[6] 96 LYS (-169.1, -45.0)

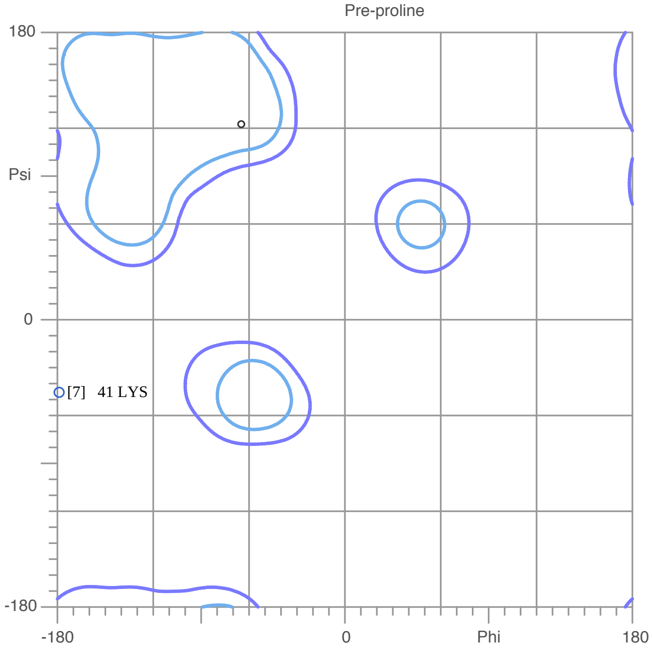
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 7


General case


Glycine


Proline


Pre-proline

91.7% (111/121) of all residues were in favored (98%) regions.
96.7% (117/121) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[7]	5 THR (-177.5, 39.4)
[7]	6 LEU (-164.9, -26.3)
[7]	36 PHE (-165.1, -64.9)
[7]	41 LYS (-179.7, -45.1)

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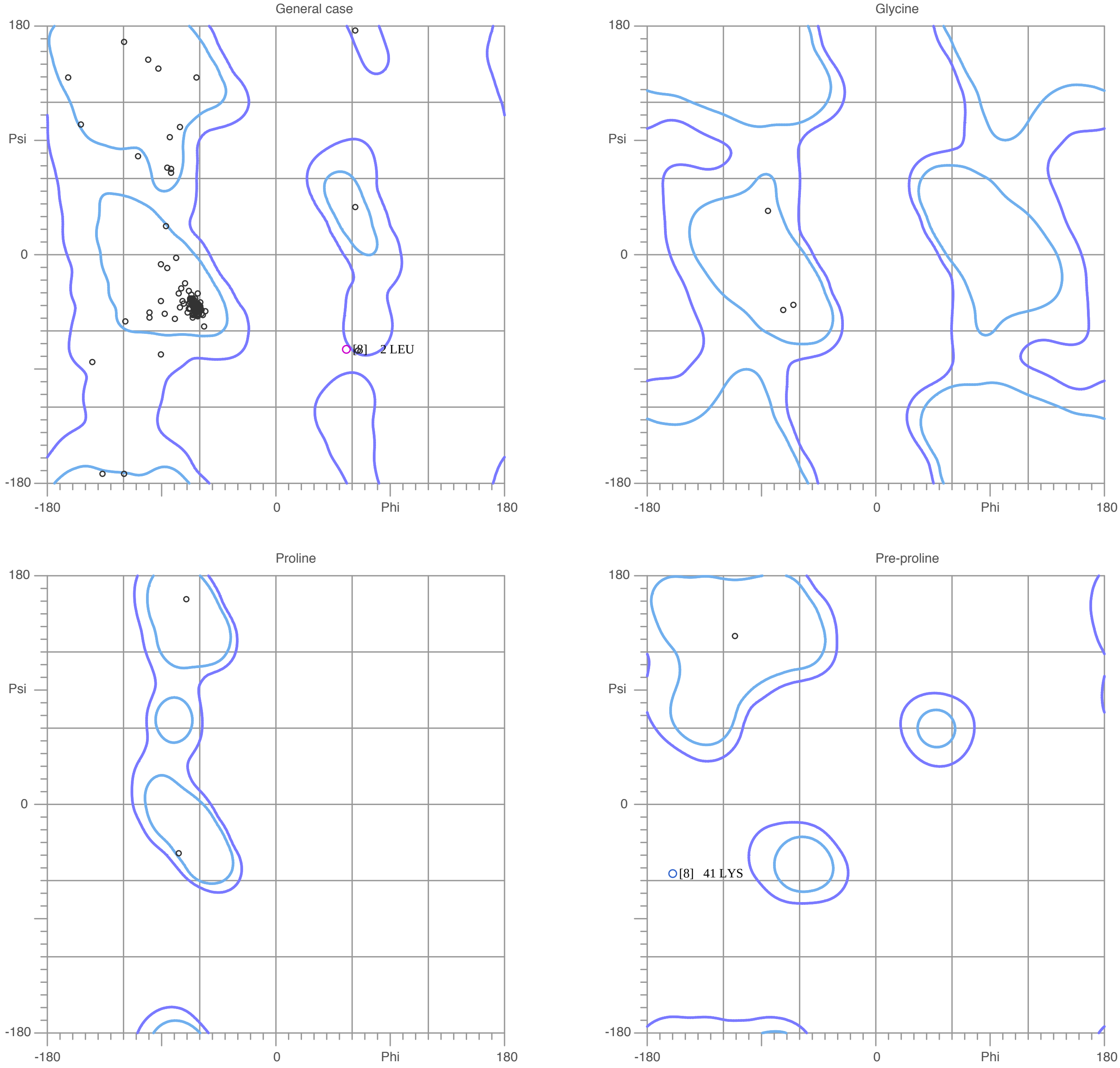
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 8

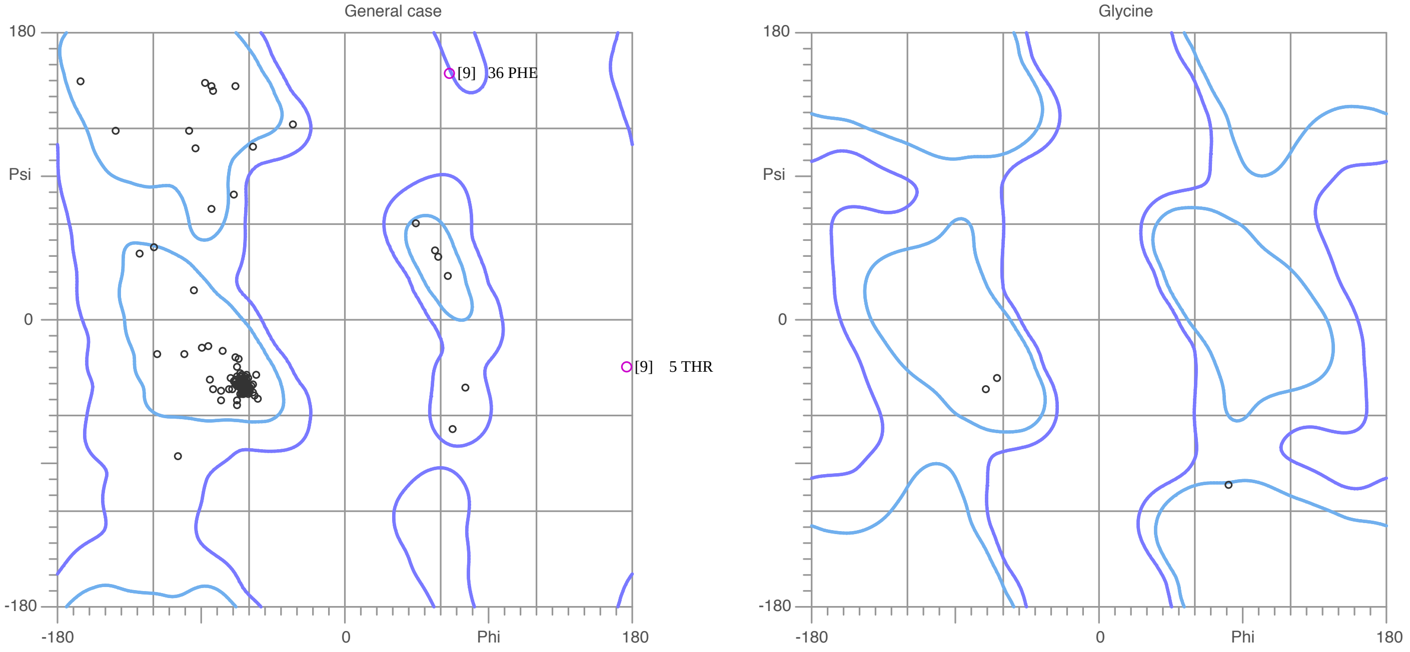


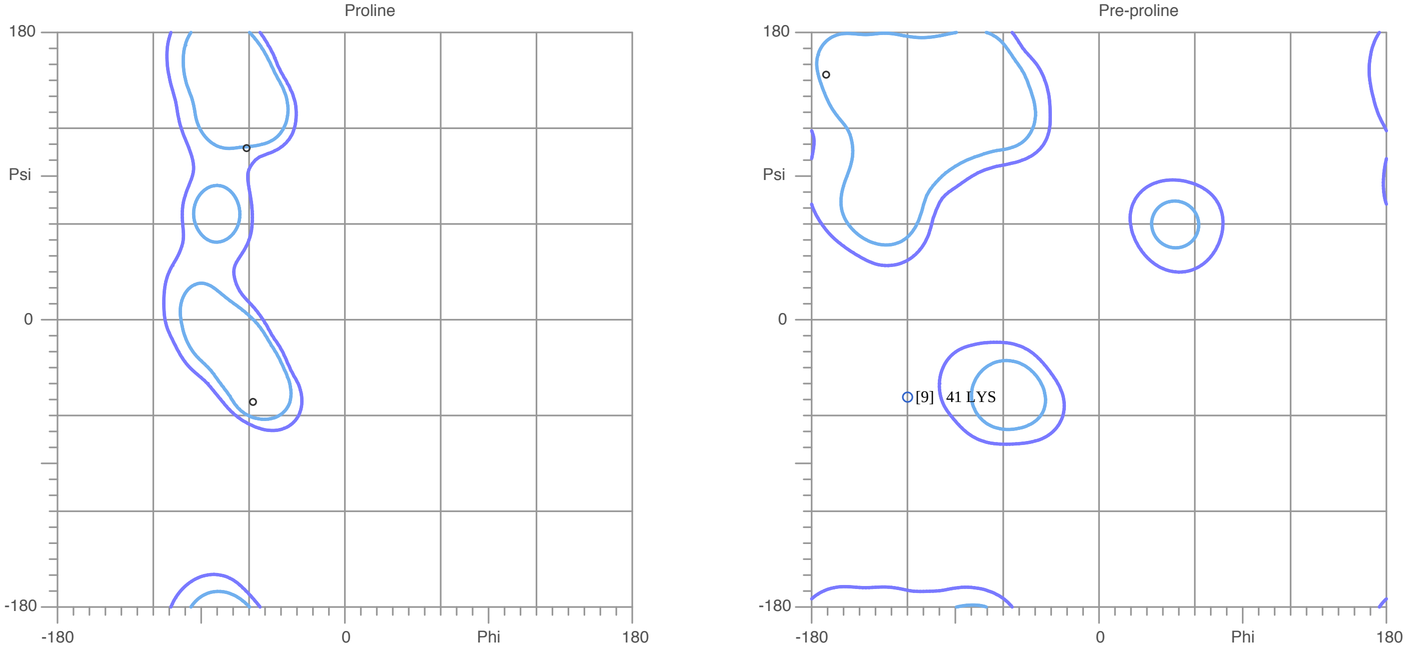
94.2% (114/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
- [8] 2 LEU (55.7, -74.7)
- [8] 41 LYS (-160.9, -54.9)

MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 9





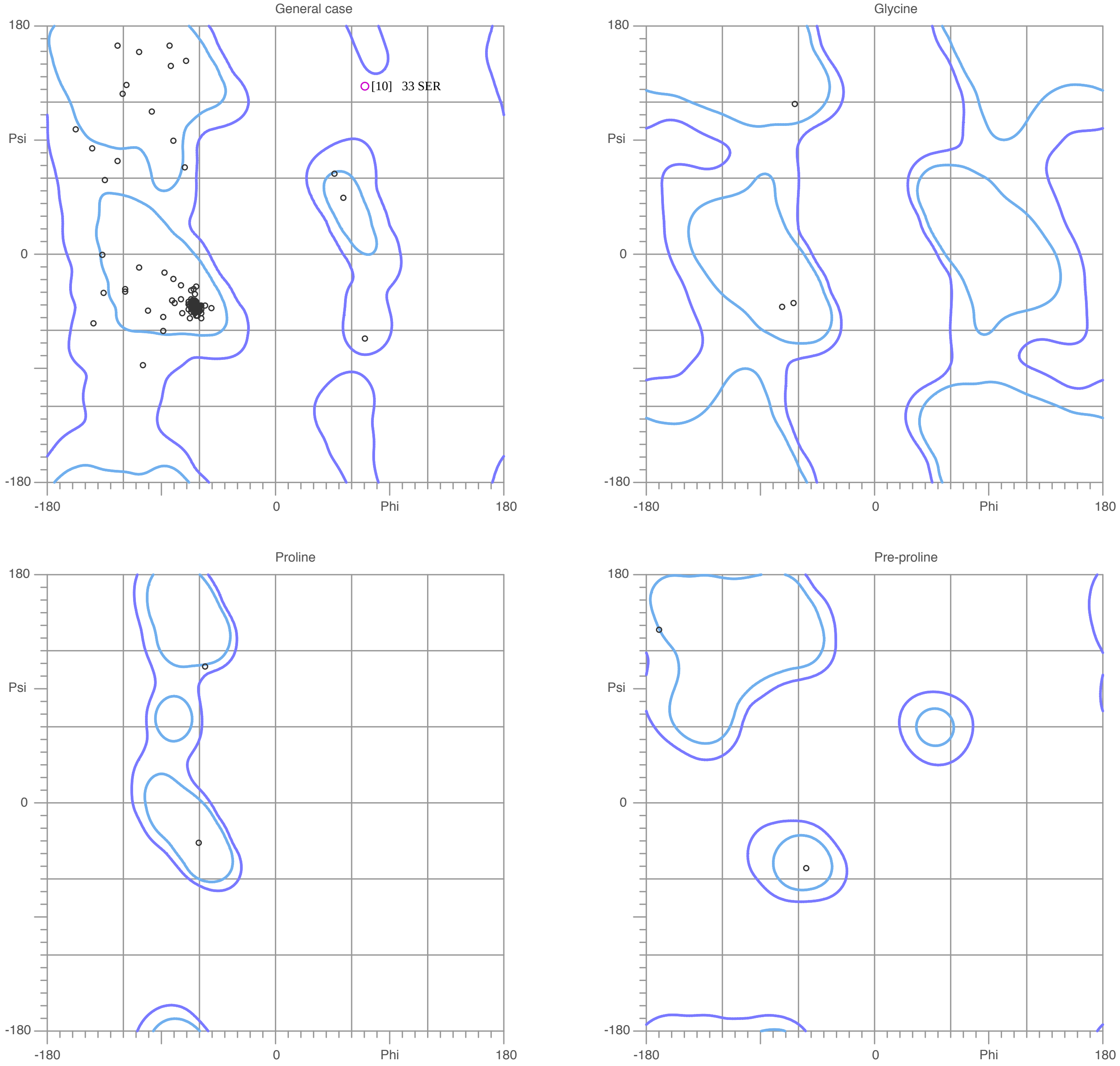
90.9% (110/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[9] 5 THR (176.9, -29.7)
[9] 36 PHE (65.7, 155.3)
[9] 41 LYS (-120.1, -48.1)

MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 10

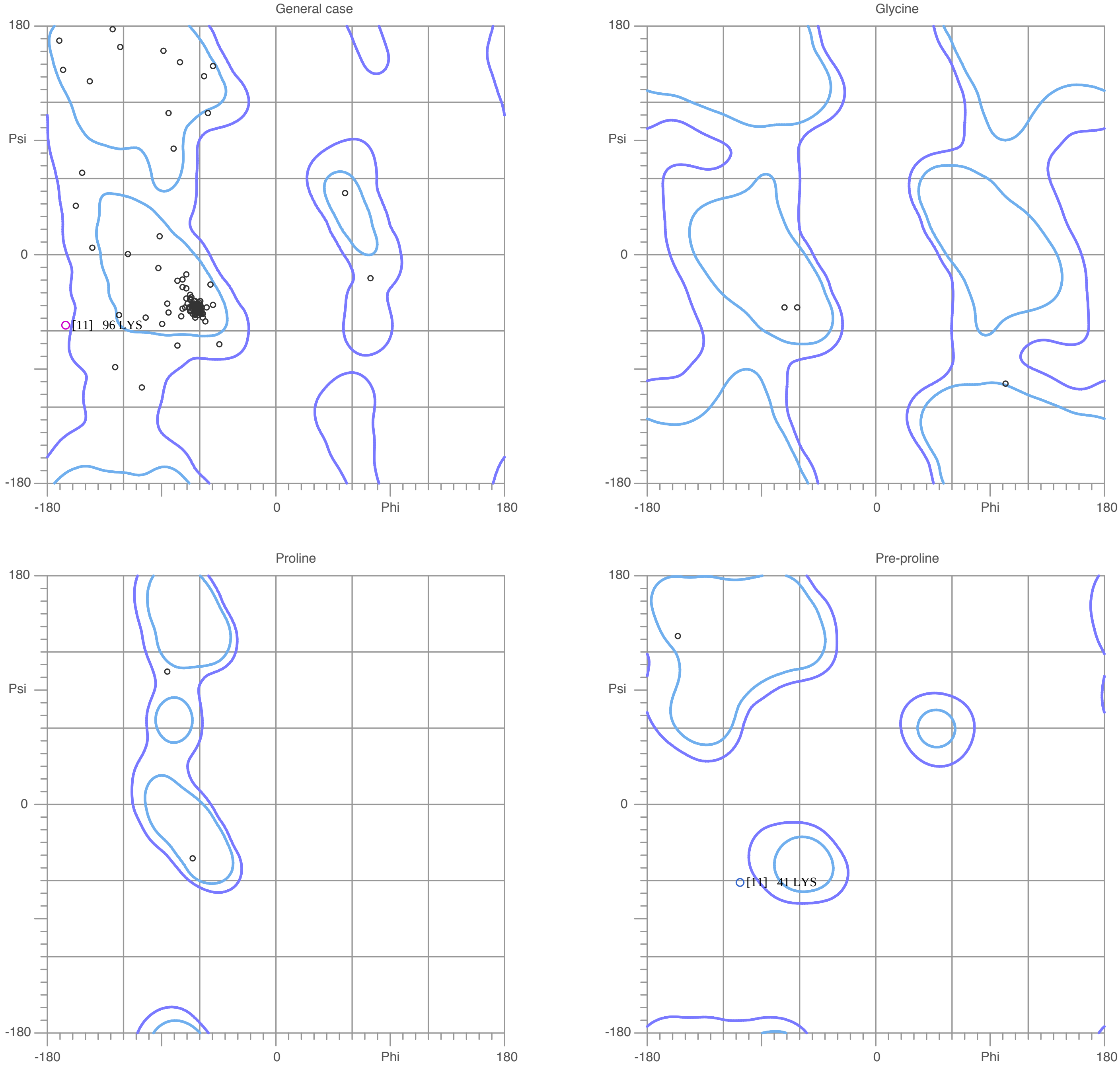


90.1% (109/121) of all residues were in favored (98%) regions.
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[10] 33 SER (70.8, 133.2)

MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 11



89.3% (108/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
  [11] 41 LYS (-107.4, -61.0)
  [11] 96 LYS (-166.4, -55.8)

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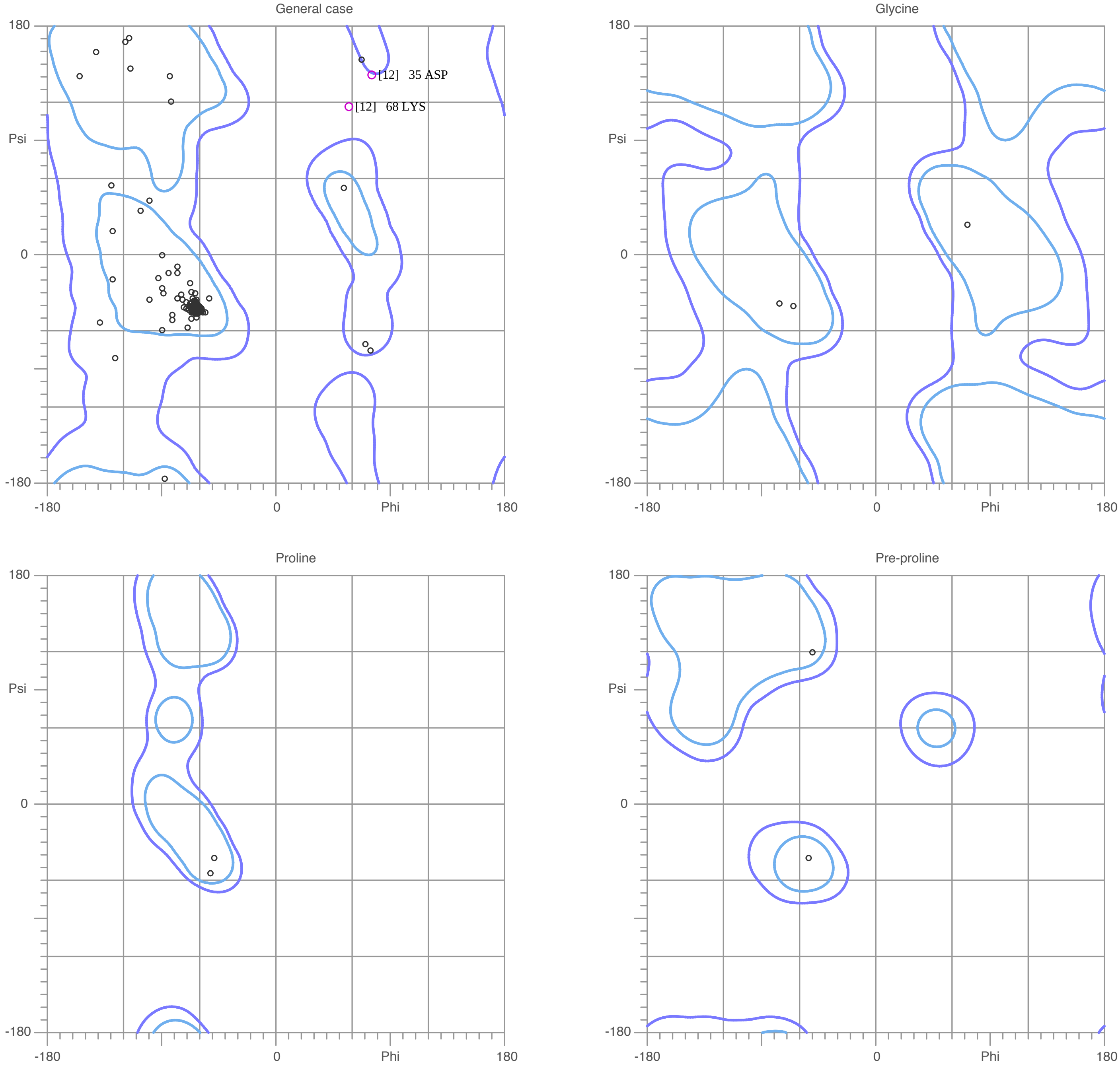
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 12



92.6% (112/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 35 ASP (75.0, 142.9)
[12] 68 LYS (57.6, 117.5)

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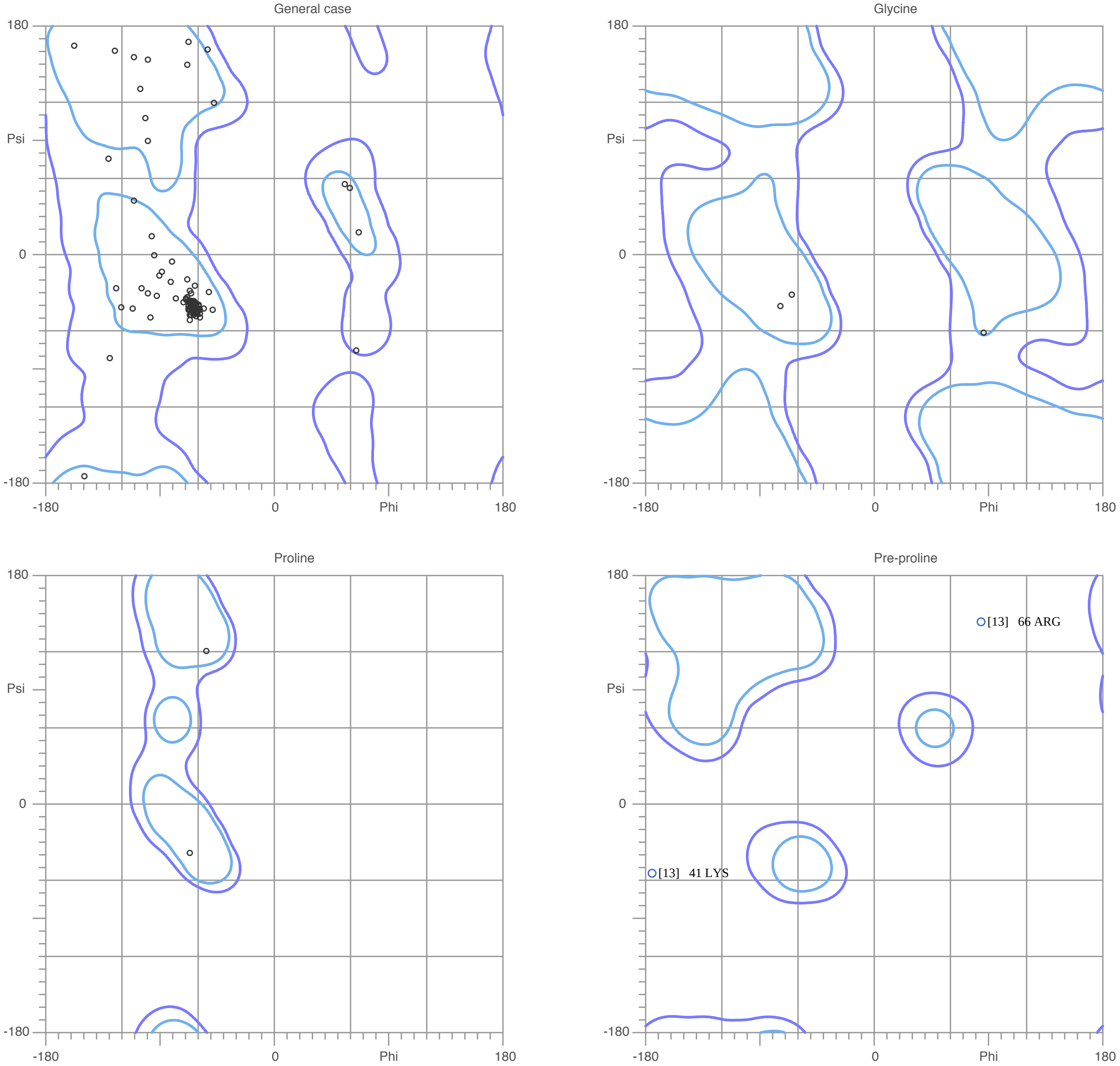
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 13



95.0% (115/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[13] 41 LYS (-175.6, -55.0)
[13] 66 ARG (85.0, 145.0)

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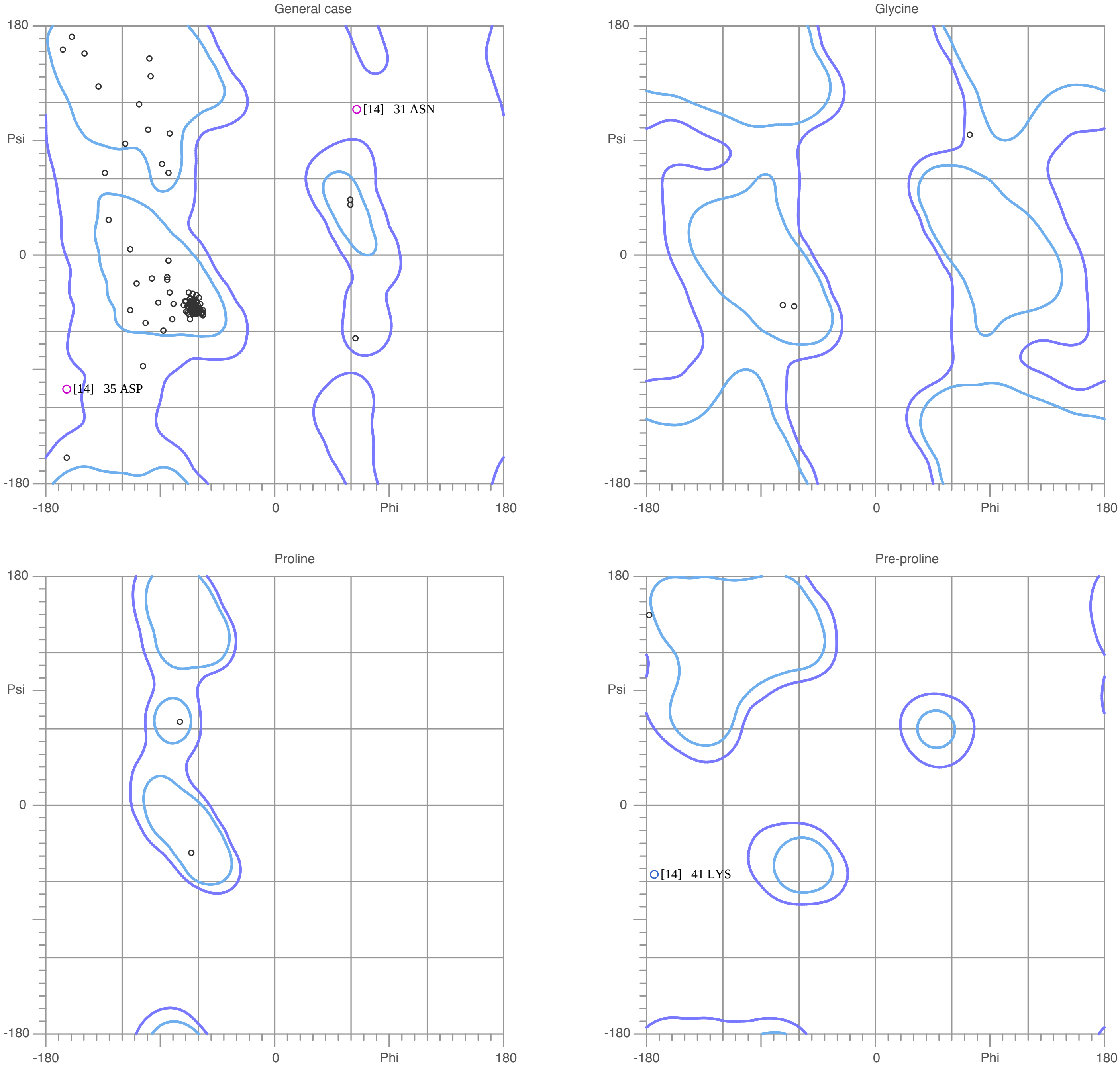
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 14



92.6% (112/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
- [14] 31 ASN (65.0, 115.1)
- [14] 35 ASP (-165.0, -105.0)
- [14] 41 LYS (-175.0, -54.8)

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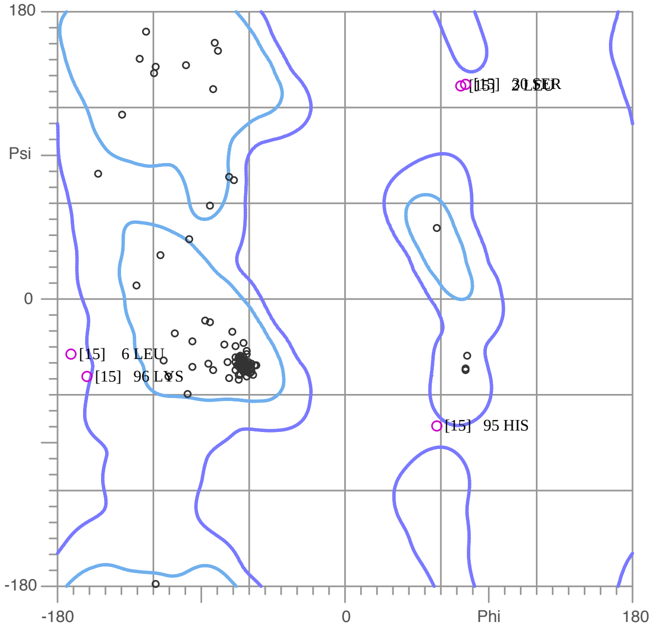
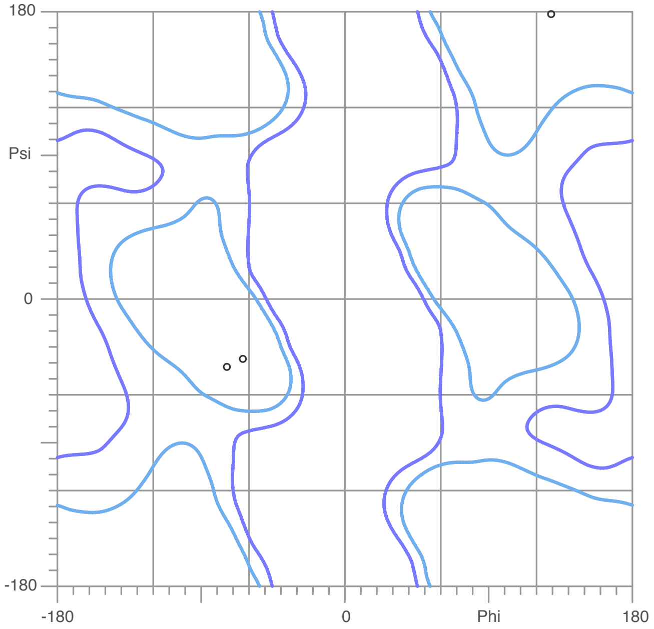
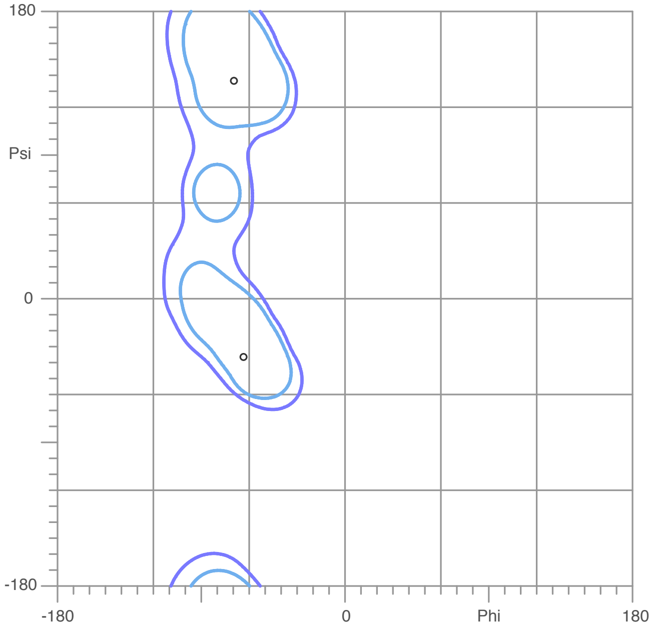
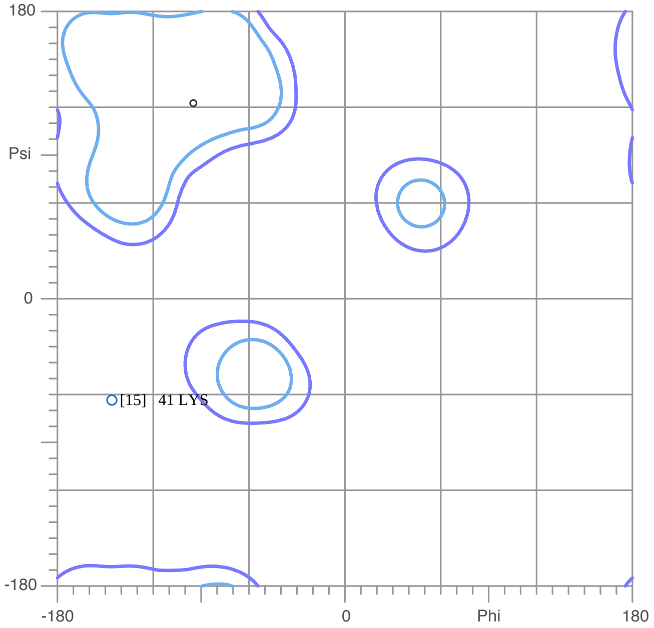
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 15


General case


Glycine


Proline


Pre-proline

90.1% (109/121) of all residues were in favored (98%) regions.
95.0% (115/121) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[15] 2 LEU (72.3, 135.0)
[15] 6 LEU (-172.5, -34.2)
[15] 30 SER (75.8, 135.0)
[15] 41 LYS (-146.8, -63.6)
[15] 95 HIS (57.1, -79.1)
[15] 96 LYS (-162.5, -48.8)

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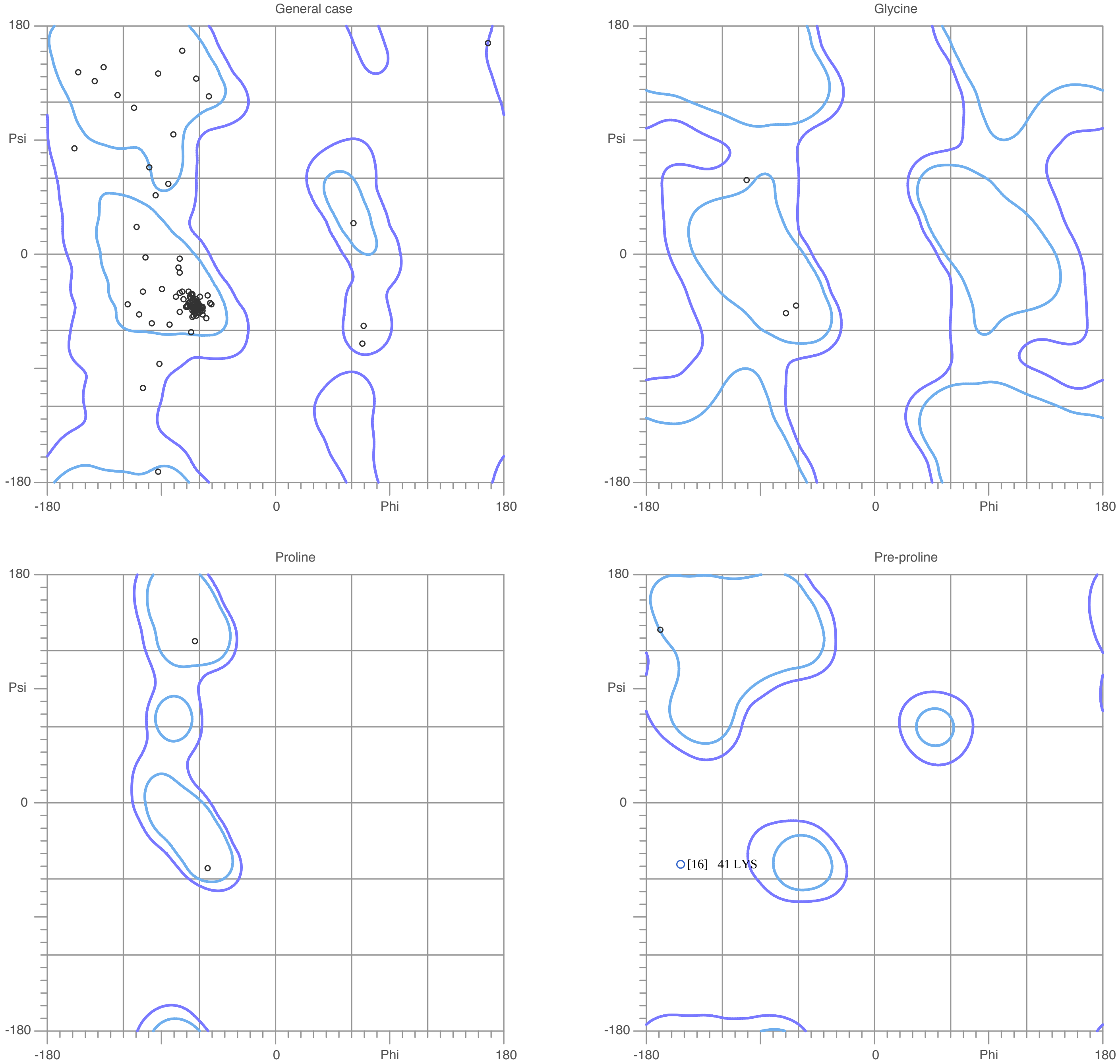
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 16



91.7% (111/121) of all residues were in favored (98%) regions.
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[16] 41 LYS (-153.1, -48.2)

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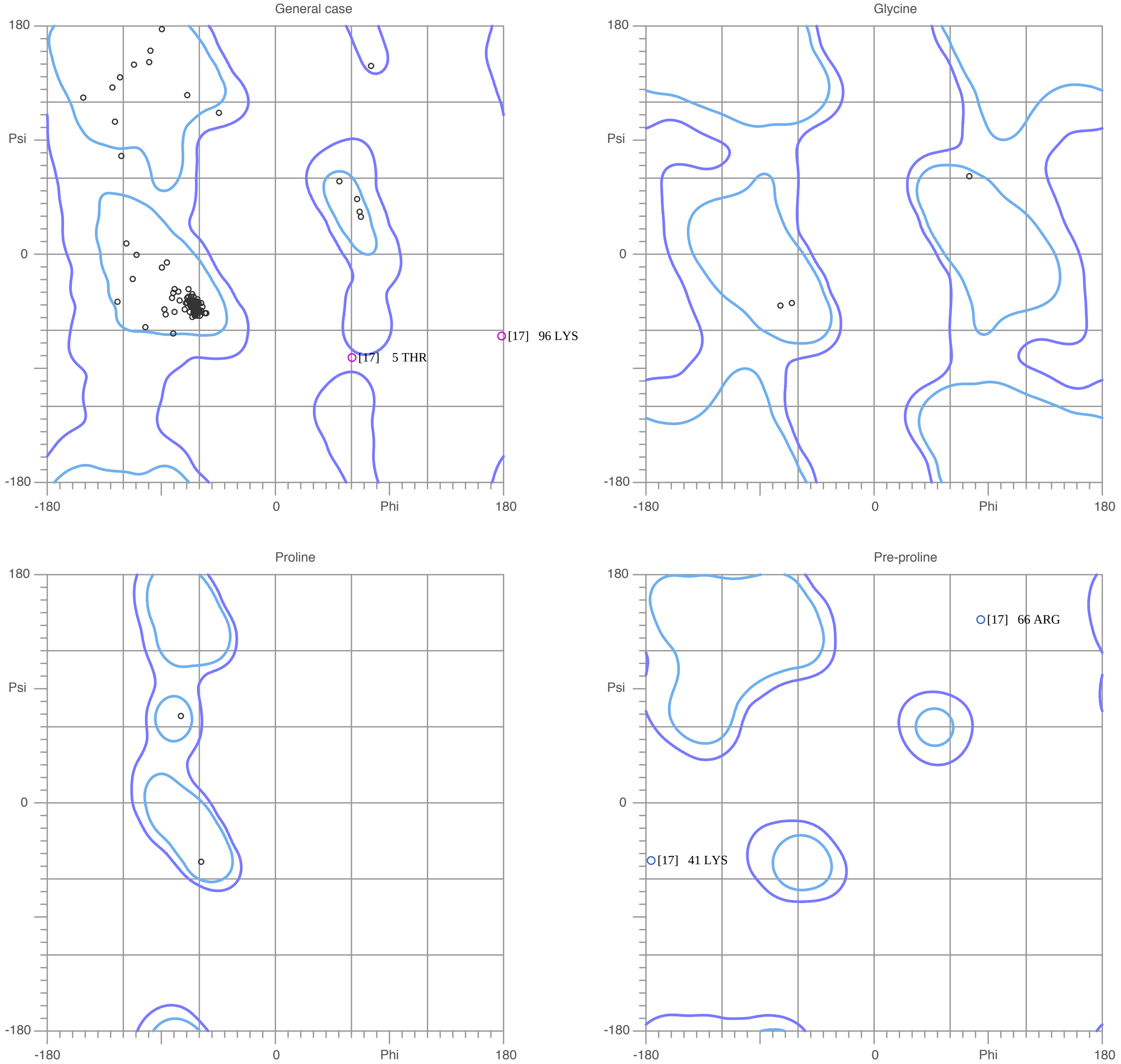
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 17



94.2% (114/121) of all residues were in favored (98%) regions.
96.7% (117/121) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[17] 5 THR (60.7, -81.6)
[17] 41 LYS (-176.7, -45.0)
[17] 66 ARG (84.5, 145.0)
[17] 96 LYS (178.6, -65.0)

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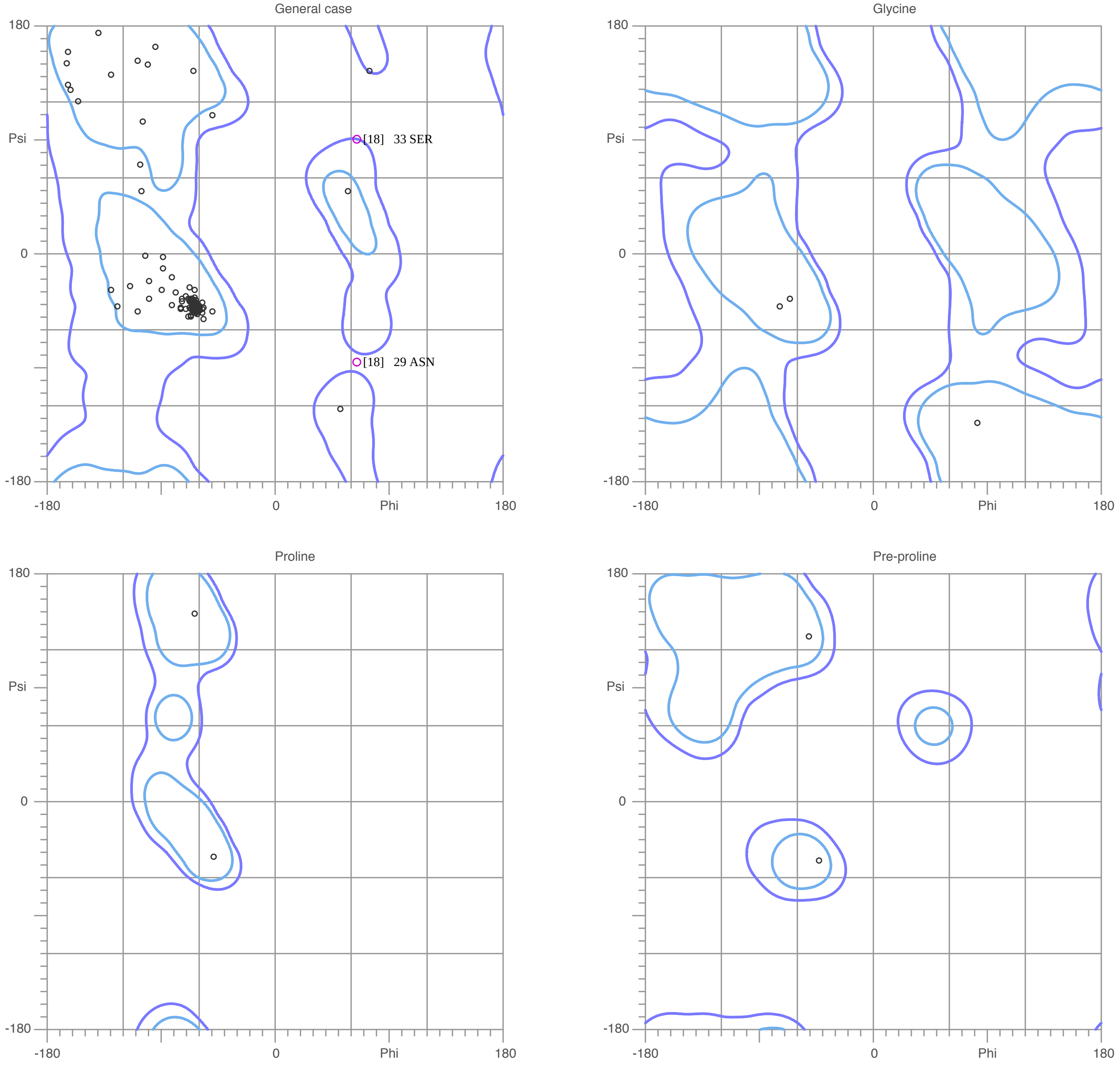
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 18



94.2% (114/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
- [18] 29 ASN (64.1, -85.2)
- [18] 33 SER (65.0, 92.0)

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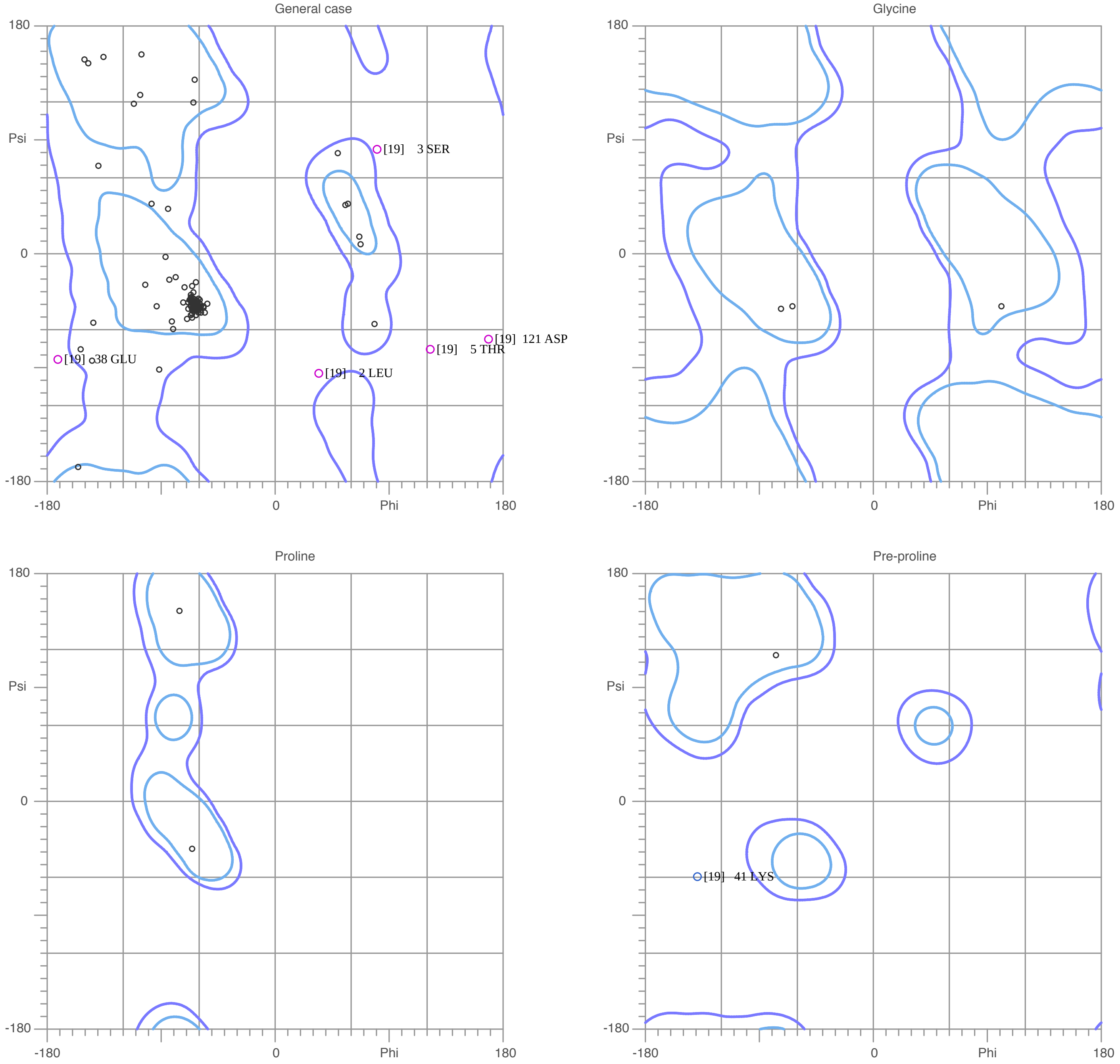
MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 19

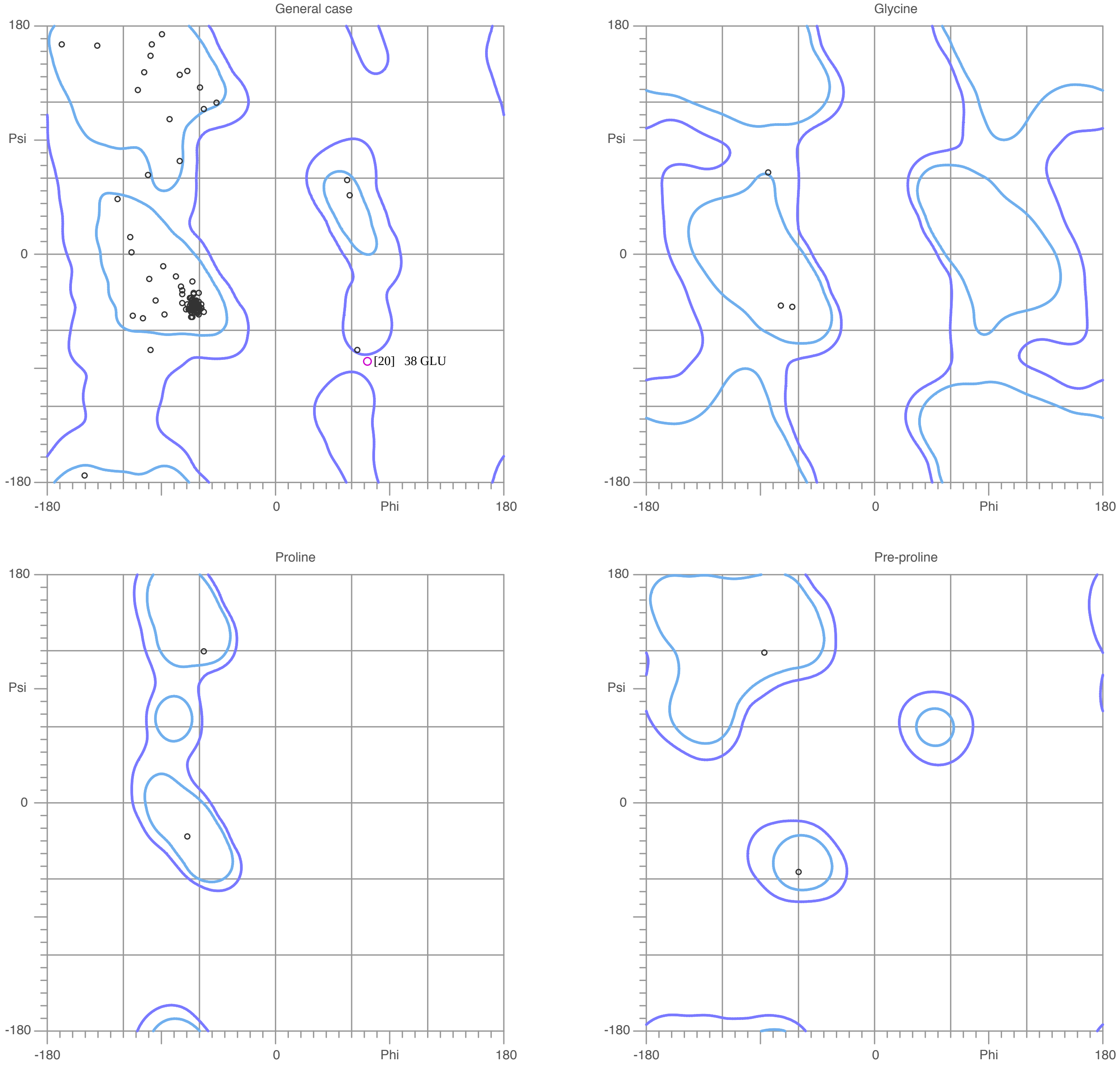


87.6% (106/121) of all residues were in favored (98%) regions.
95.0% (115/121) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[19] 2 LEU (34.6, -94.8)
[19] 3 SER (80.2, 83.6)
[19] 5 THR (122.7, -75.7)
[19] 38 GLU (-172.9, -83.9)
[19] 41 LYS (-140.0, -59.5)
[19] 121 ASP (168.0, -67.6)

MolProbity Ramachandran analysis

SR213_R3Cons_em_bcr3.pdb, model 20



95.9% (116/121) of all residues were in favored (98%) regions.
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 38 GLU (72.8, -85.0)

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