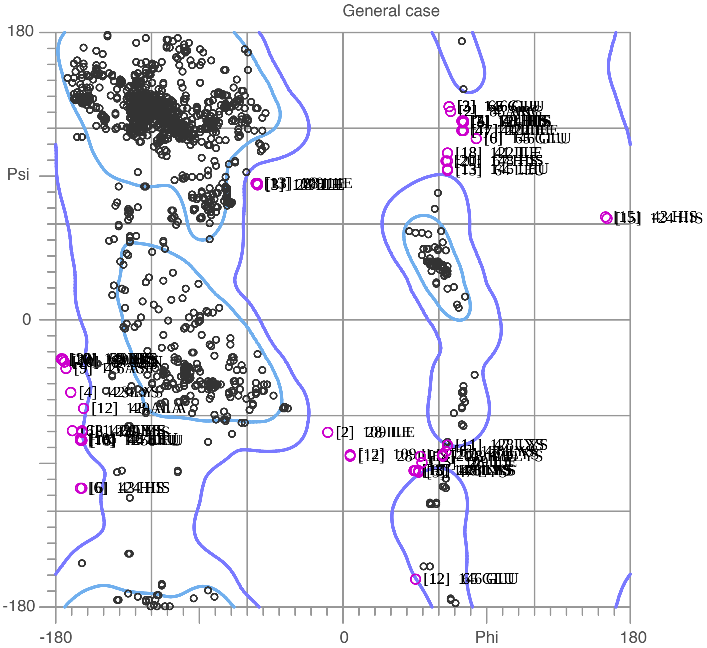
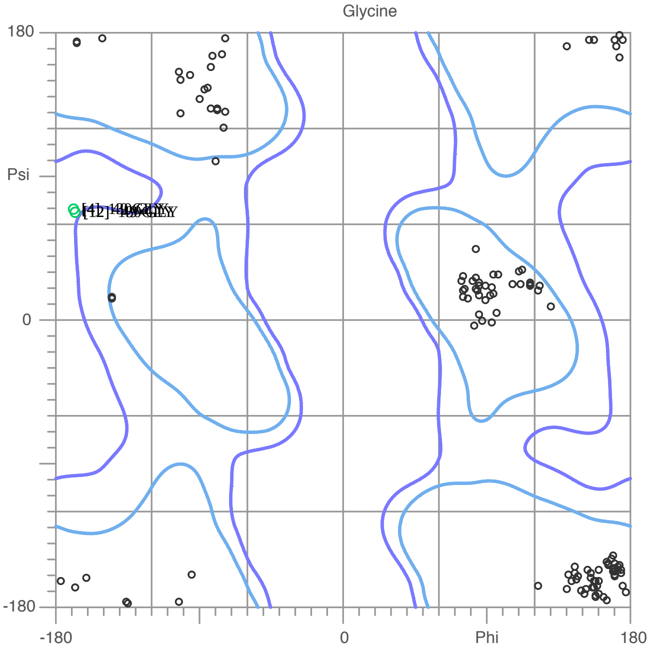
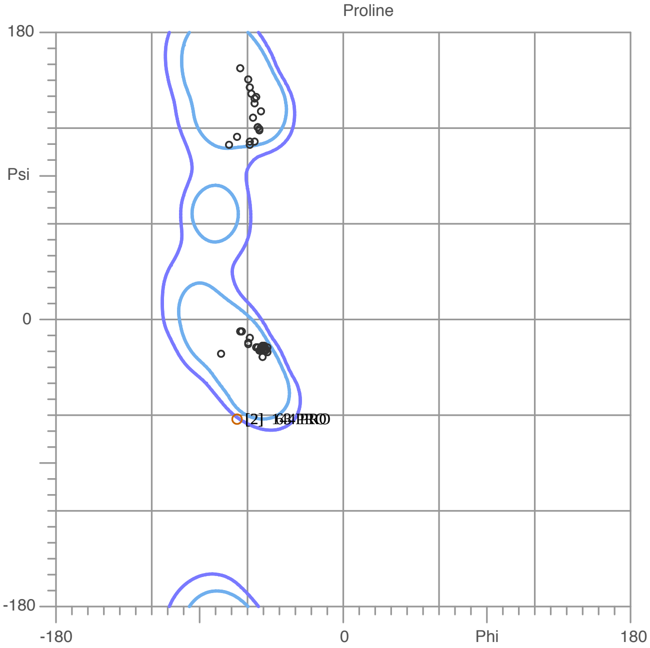
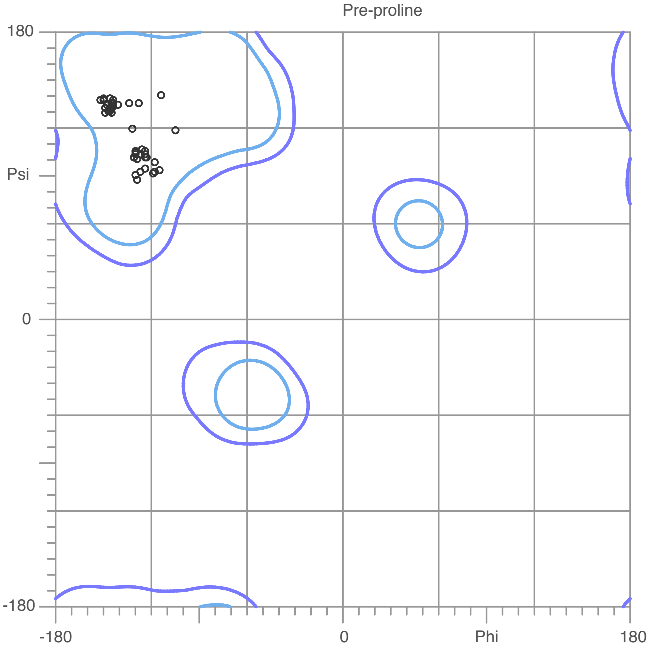
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, all models









```
89.7% (2476/2760) of all residues were in favored (98%) regions.
97.1% (2680/2760) of all residues were in allowed (>99.8%) regions.

There were 80 outliers (phi, psi):
   [2]   4 ARG (67.0, 131.4)
   [2]  28 ILE (-10.2, -70.1)
   [2]  63 PRO (-67.8, -62.2)
   [2]  65 GLU (66.1, 135.0)
   [2]  85 ARG (67.1, 131.4)
   [2] 109 ILE (-10.2, -70.1)
   [2] 144 PRO (-67.8, -62.2)
   [2] 146 GLU (66.2, 135.0)
   [3]  28 ILE (-54.9, 85.9)
   [3]  47 LYS (47.2, -95.0)
   [3]  65 GLU (66.7, 135.0)
   [3] 109 ILE (-54.9, 85.9)
   [3] 128 LYS (47.1, -95.0)
   [3] 146 GLU (66.7, 135.0)
   [4]  41 ILE (74.9, 119.2)
   [4]  42 LYS (-171.9, -45.0)
   [4]  43 HIS (75.0, 125.0)
   [4]  49 GLY (-169.4, 70.5)
   [4] 122 ILE (74.9, 119.1)
   [4] 123 LYS (-171.9, -45.0)
   [4] 124 HIS (75.0, 125.0)
   [4] 130 GLY (-169.5, 70.4)
   [5]  43 HIS (75.0, 125.0)
   [5] 124 HIS (75.0, 125.0)
   [6]  42 LYS (-170.3, -69.8)
   [6]  43 HIS (-165.0, -105.0)
   [6]  47 LYS (64.7, -82.3)
   [6]  65 GLU (83.3, 114.6)
   [6] 123 LYS (-170.3, -69.8)
   [6] 124 HIS (-165.0, -105.0)
   [6] 128 LYS (64.7, -82.3)
   [6] 146 GLU (83.3, 114.6)
   [7]  70 HIS (75.0, 125.0)
   [7] 151 HIS (74.9, 125.1)
   [8]  68 HIS (-164.9, -69.9)
   [8] 149 HIS (-164.9, -70.0)
   [9]  45 ASP (-174.3, -30.4)
   [9] 126 ASP (-174.3, -30.5)
```

```
[10]   3 ASN (-175.0, -26.6)
[10]  46 LEU (-165.2, -75.0)
[10]  47 LYS (45.4, -95.0)
[10]  68 HIS (-177.1, -25.0)
[10]  84 ASN (-175.0, -26.7)
[10] 127 LEU (-165.2, -75.0)
[10] 128 LYS (45.4, -95.0)
[10] 149 HIS (-177.1, -25.0)
[11]  47 LYS (65.4, -78.4)
[11] 128 LYS (65.4, -78.4)
[12]  28 ILE (5.0, -85.0)
[12]  48 ALA (-163.3, -55.9)
[12]  49 GLY (-168.6, 68.9)
[12]  65 GLU (45.1, -162.9)
[12] 109 ILE (5.0, -85.0)
[12] 129 ALA (-163.3, -55.9)
[12] 130 GLY (-168.5, 68.9)
[12] 146 GLU (45.1, -162.9)
[13]  28 ILE (-55.0, 86.6)
[13]  47 LYS (44.4, -94.9)
[13]  64 LEU (65.1, 94.9)
[13] 109 ILE (-55.0, 86.7)
[13] 128 LYS (44.4, -95.0)
[13] 145 LEU (65.1, 95.0)
[14]  28 ILE (48.9, -85.2)
[14] 109 ILE (48.9, -85.2)
[15]  28 ILE (49.2, -89.8)
[15]  43 HIS (165.0, 65.1)
[15] 109 ILE (49.2, -89.8)
[15] 124 HIS (165.0, 65.0)
[16]  44 LEU (-164.8, -75.1)
[16] 125 LEU (-164.8, -75.2)
[17]  41 ILE (75.0, 120.0)
[17] 122 ILE (75.0, 119.9)
[18]  41 ILE (65.2, 105.1)
[18] 122 ILE (65.2, 105.0)
[20]  47 LYS (62.6, -84.9)
[20]  67 HIS (65.0, 100.3)
[20]  69 HIS (-176.7, -25.0)
[20] 128 LYS (62.7, -85.0)
[20] 148 HIS (65.0, 100.3)
[20] 150 HIS (-176.7, -25.0)
```

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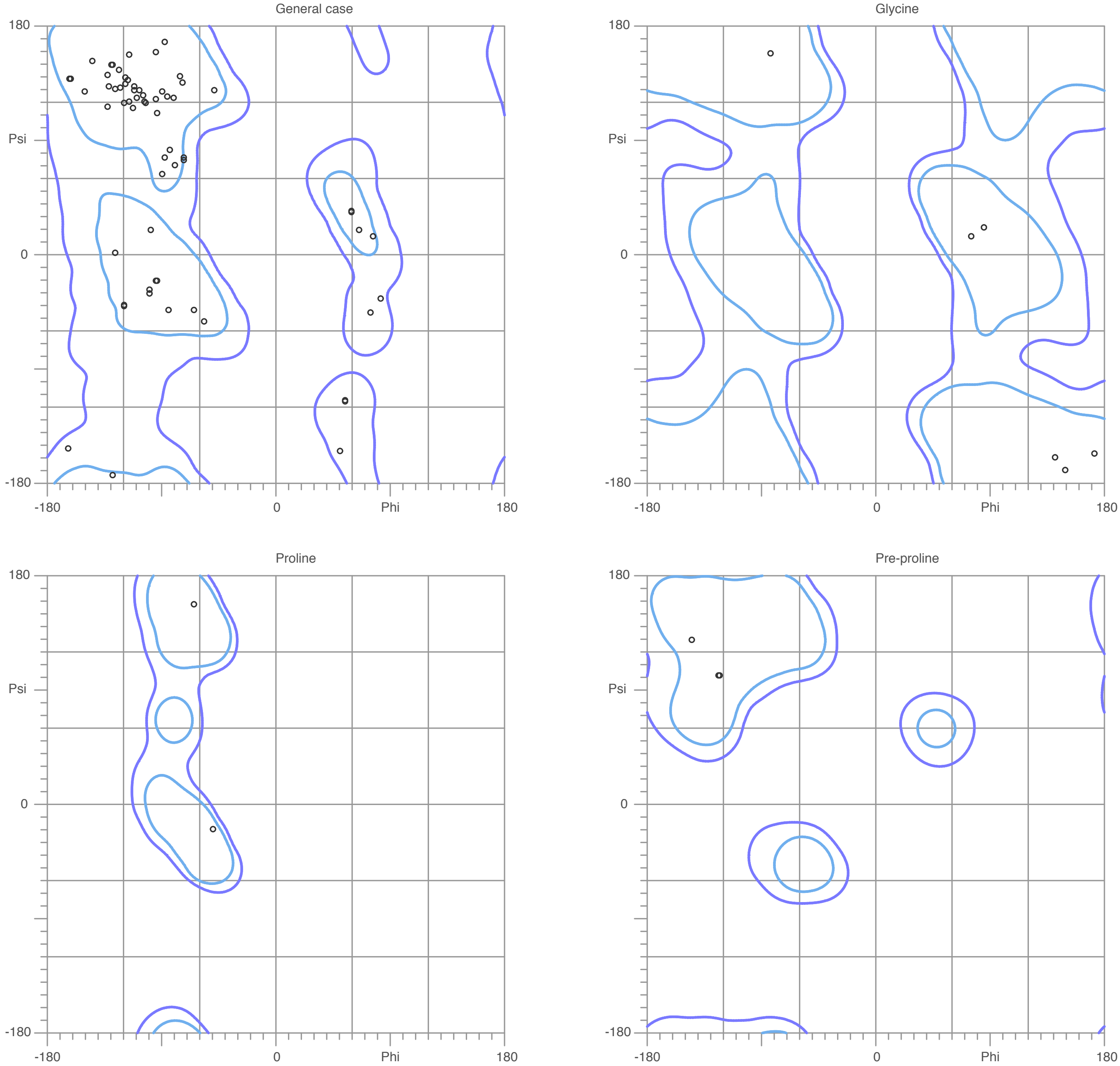
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 1



92.8% (128/138) of all residues were in favored (98%) regions.
100.0% (138/138) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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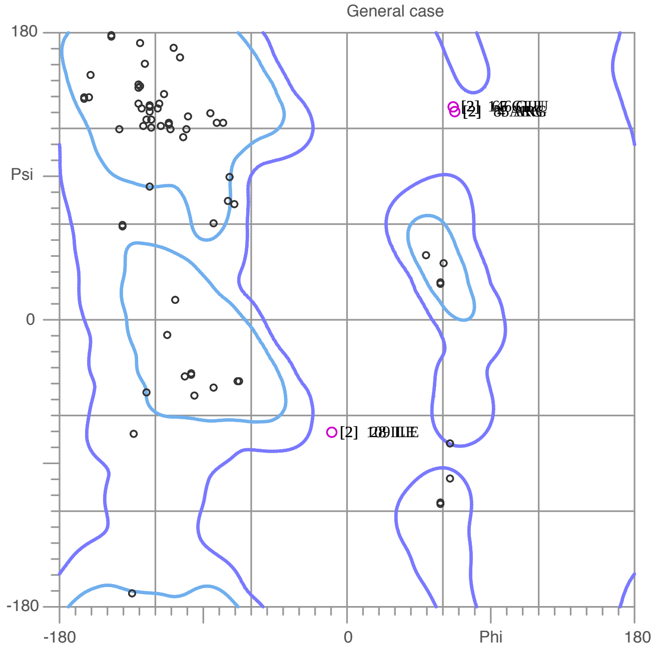
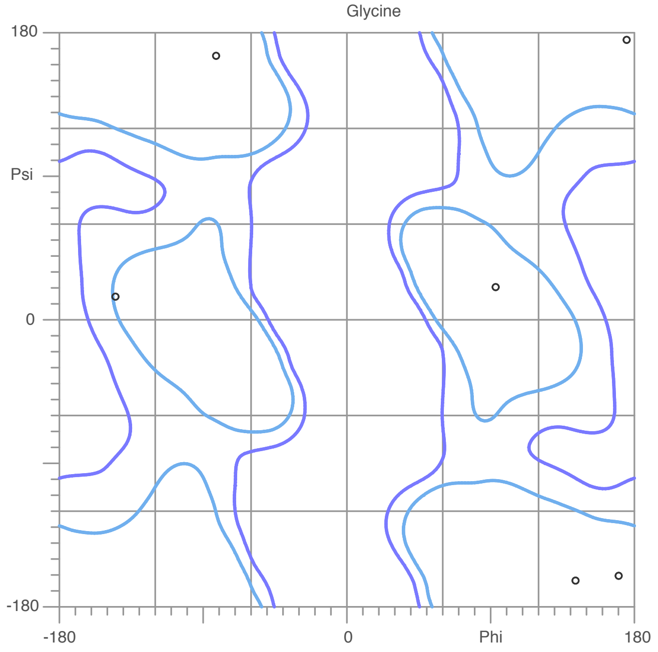
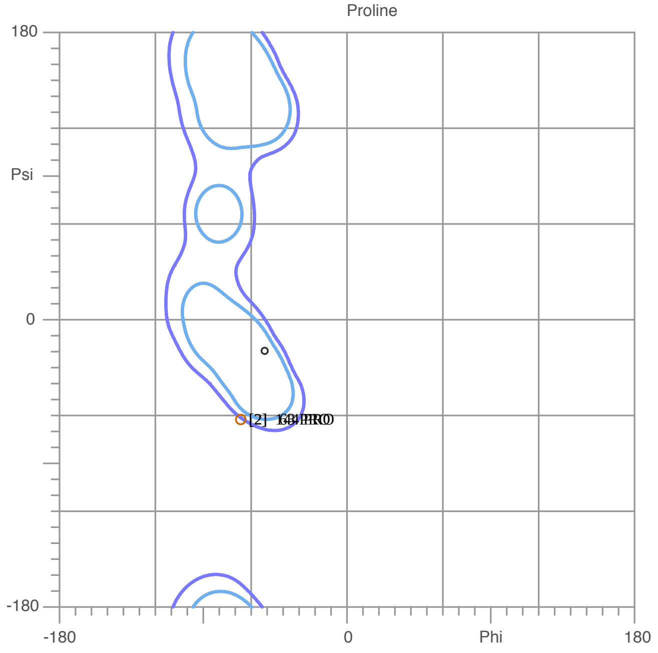
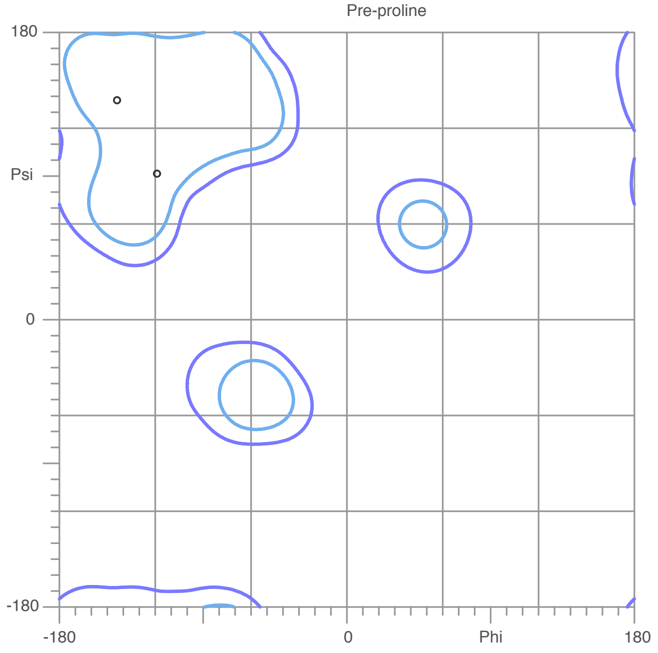
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 2


General case


Glycine


Proline


Pre-proline

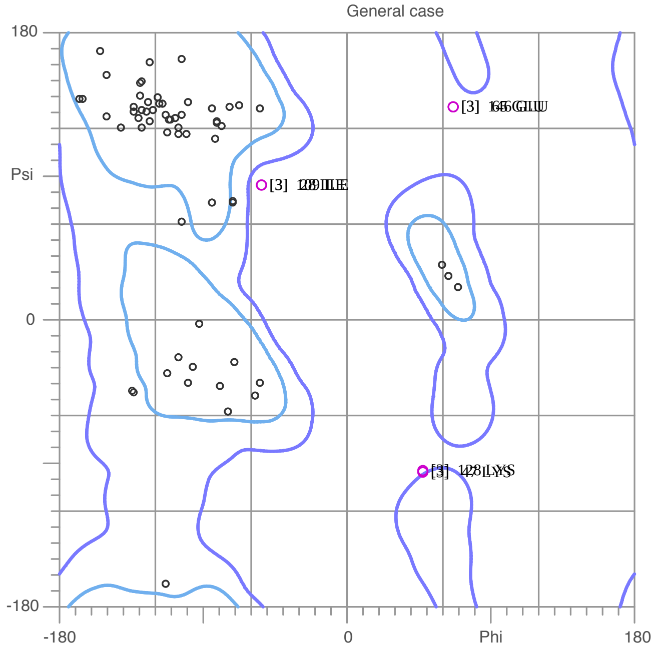
84.1% (116/138) of all residues were in favored (98%) regions.
94.2% (130/138) of all residues were in allowed (>99.8%) regions.

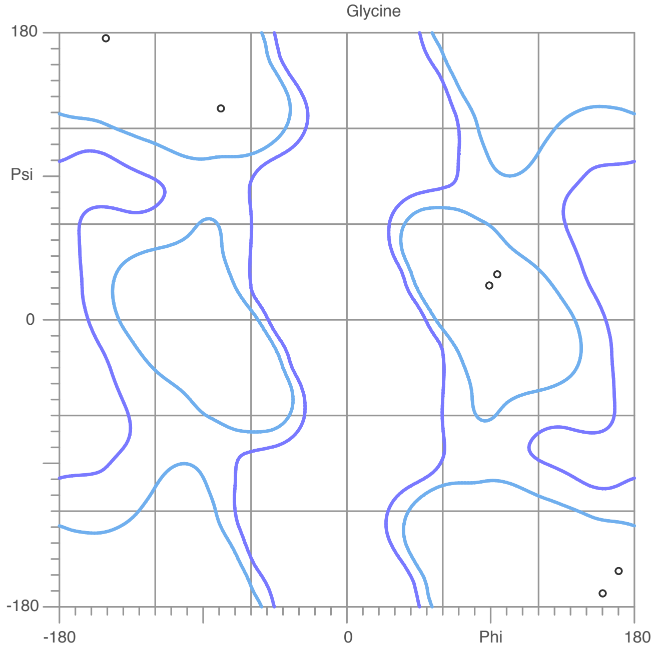
There were 8 outliers (phi, psi):

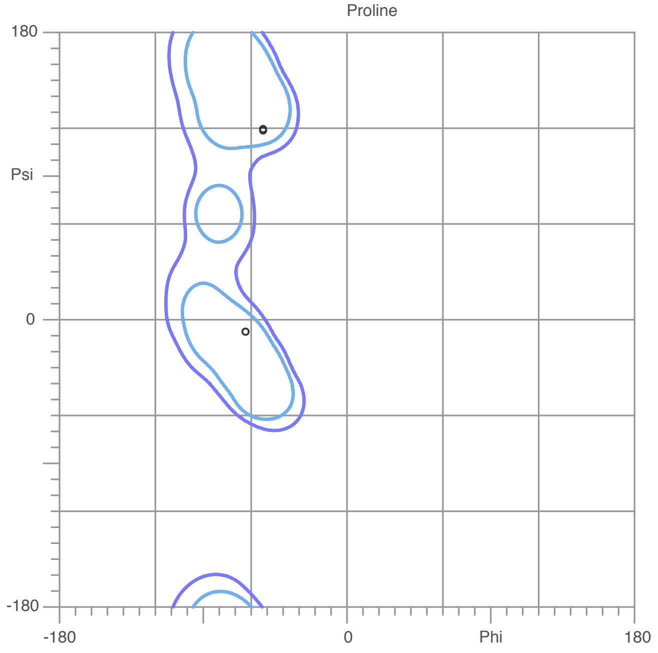
[2] 4 ARG (67.0, 131.4)
[2] 28 ILE (-10.2, -70.1)
[2] 63 PRO (-67.8, -62.2)
[2] 65 GLU (66.1, 135.0)
[2] 85 ARG (67.1, 131.4)
[2] 109 ILE (-10.2, -70.1)
[2] 144 PRO (-67.8, -62.2)
[2] 146 GLU (66.2, 135.0)

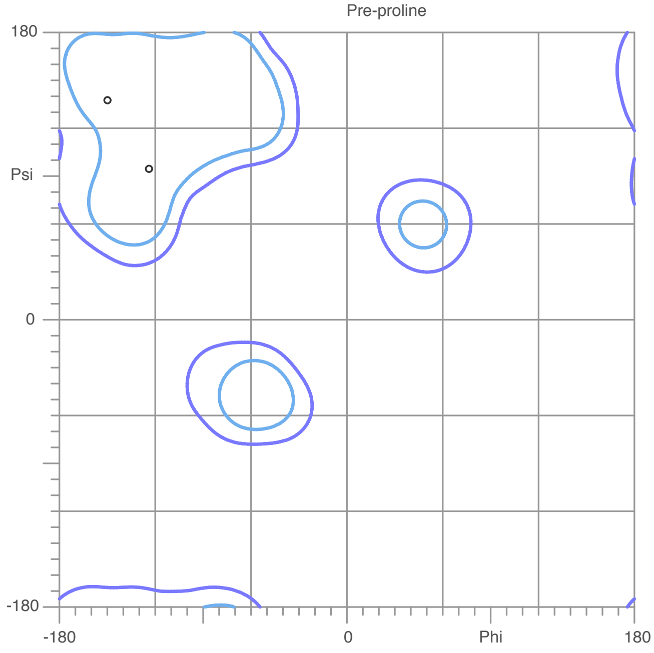
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 3


General case


Glycine


Proline


Pre-proline

89.9% (124/138) of all residues were in favored (98%) regions.
95.7% (132/138) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[3] 28 ILE (-54.9, 85.9)
[3] 47 LYS (47.2, -95.0)
[3] 65 GLU (66.7, 135.0)
[3] 109 ILE (-54.9, 85.9)
[3] 128 LYS (47.1, -95.0)
[3] 146 GLU (66.7, 135.0)

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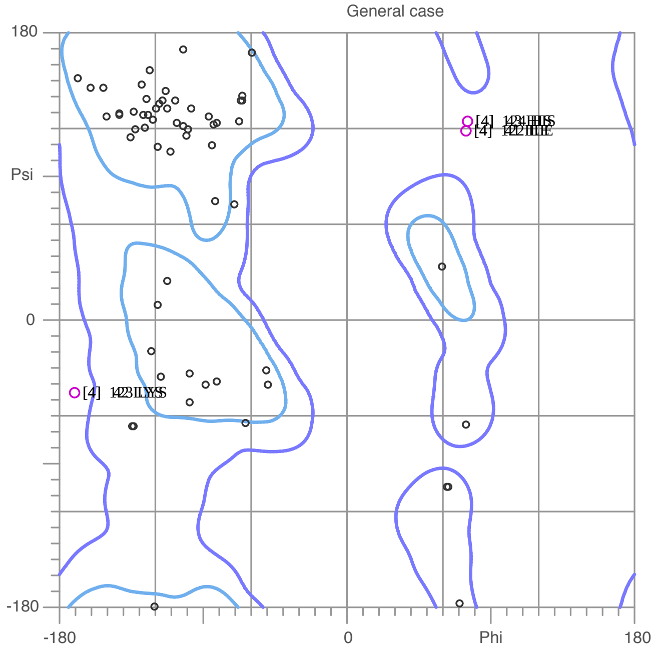
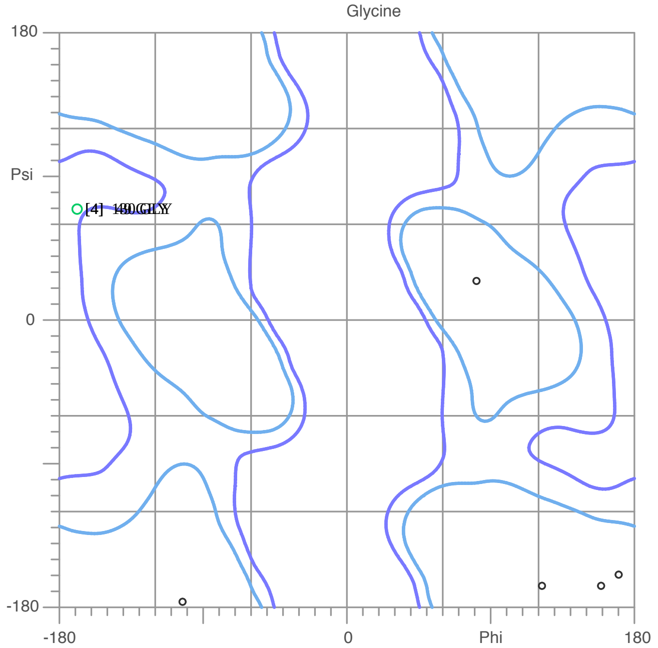
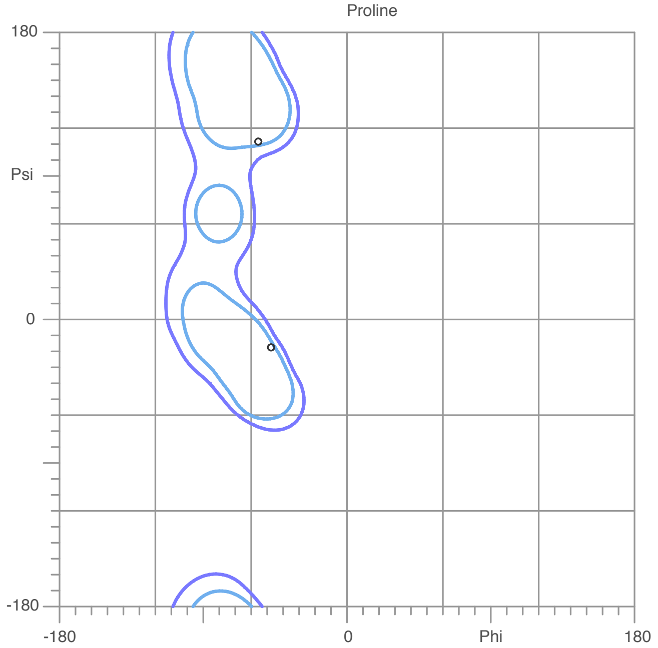
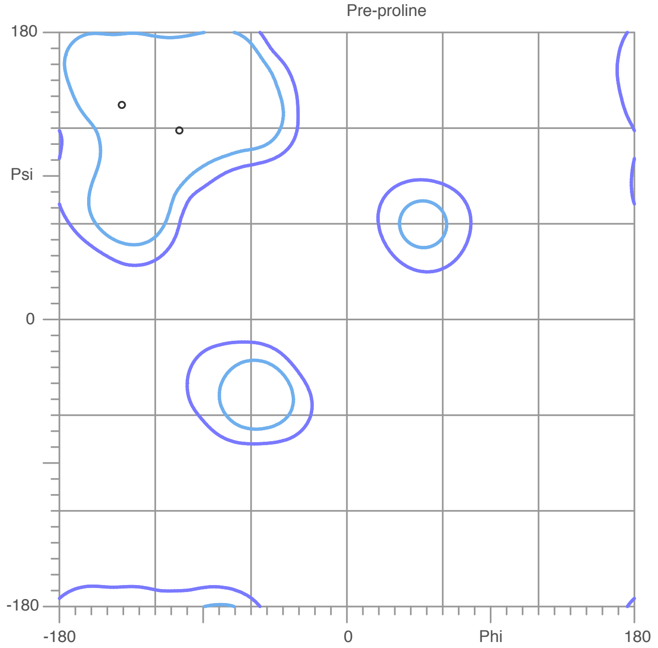
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 4









85.5% (118/138) of all residues were in favored (98%) regions.
94.2% (130/138) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[4] 41 ILE (74.9, 119.2)
[4] 42 LYS (-171.9, -45.0)
[4] 43 HIS (75.0, 125.0)
[4] 49 GLY (-169.4, 70.5)
[4] 122 ILE (74.9, 119.1)
[4] 123 LYS (-171.9, -45.0)
[4] 124 HIS (75.0, 125.0)
[4] 130 GLY (-169.5, 70.4)

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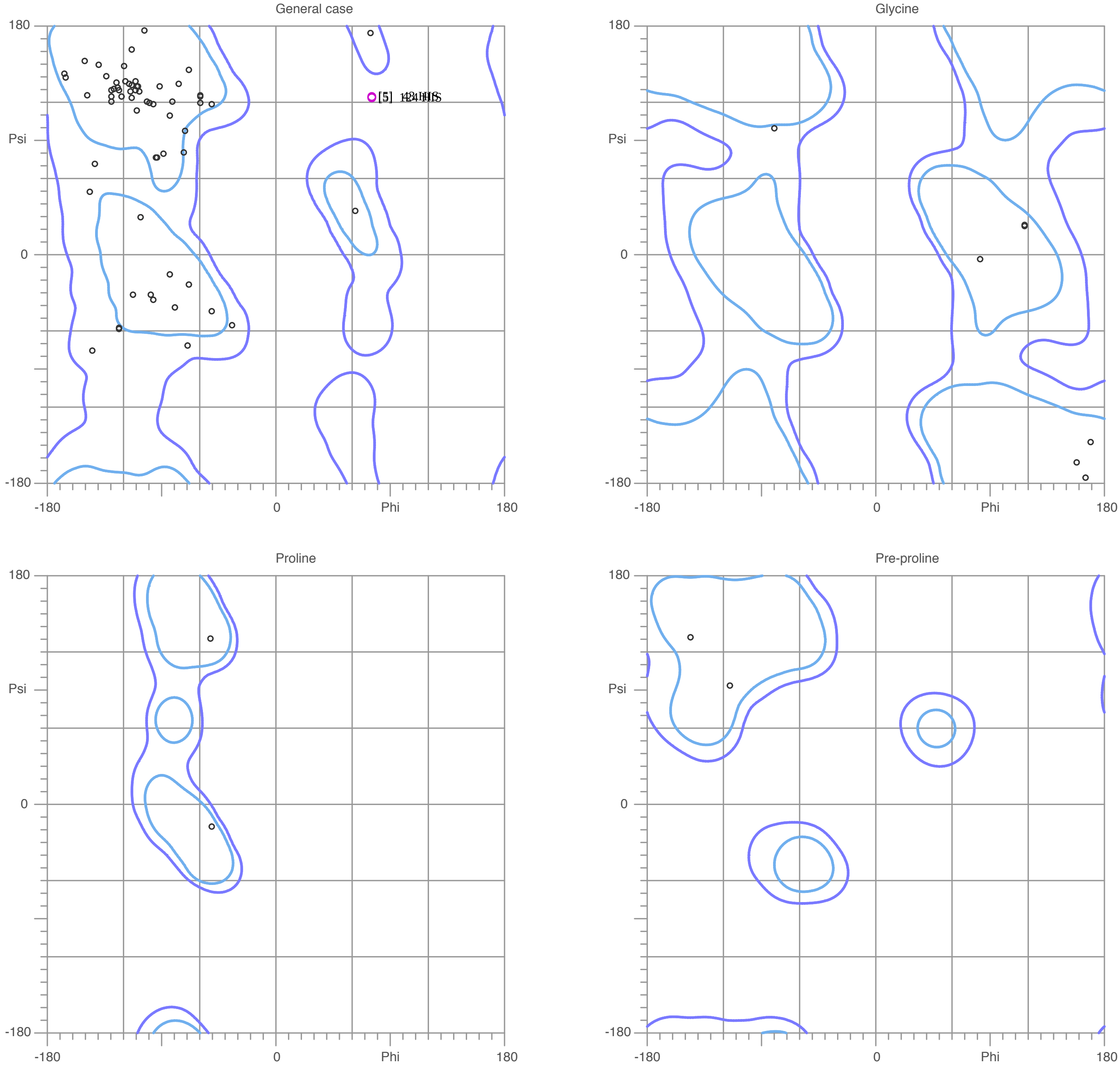
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 5



87.0% (120/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
- [5] 43 HIS (75.0, 125.0)
- [5] 124 HIS (75.0, 125.0)

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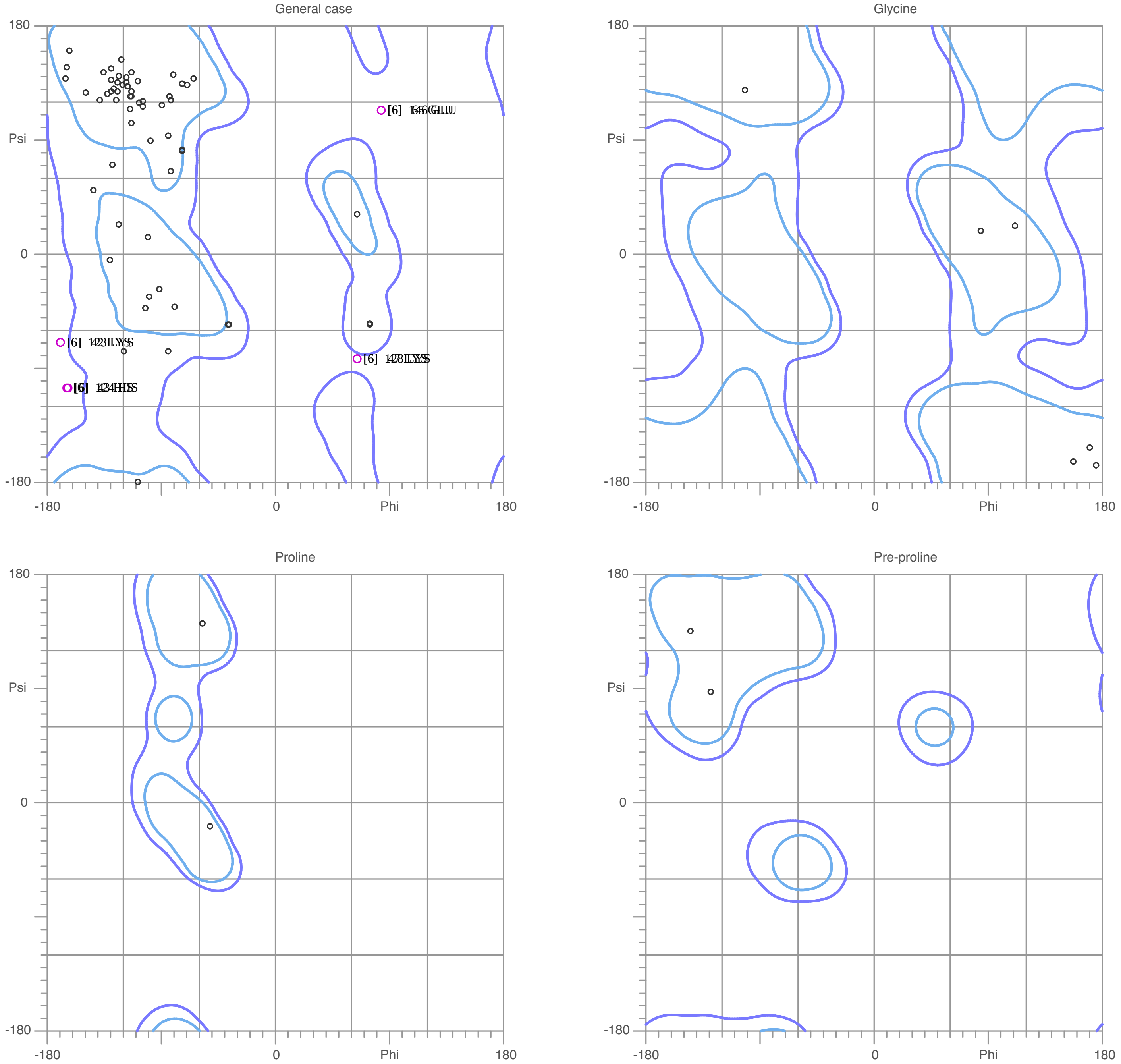
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 6



85.5% (118/138) of all residues were in favored (98%) regions.

94.2% (130/138) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[6] 42 LYS (-170.3, -69.8)
[6] 43 HIS (-165.0, -105.0)
[6] 47 LYS (64.7, -82.3)
[6] 65 GLU (83.3, 114.6)
[6] 123 LYS (-170.3, -69.8)
[6] 124 HIS (-165.0, -105.0)
[6] 128 LYS (64.7, -82.3)
[6] 146 GLU (83.3, 114.6)

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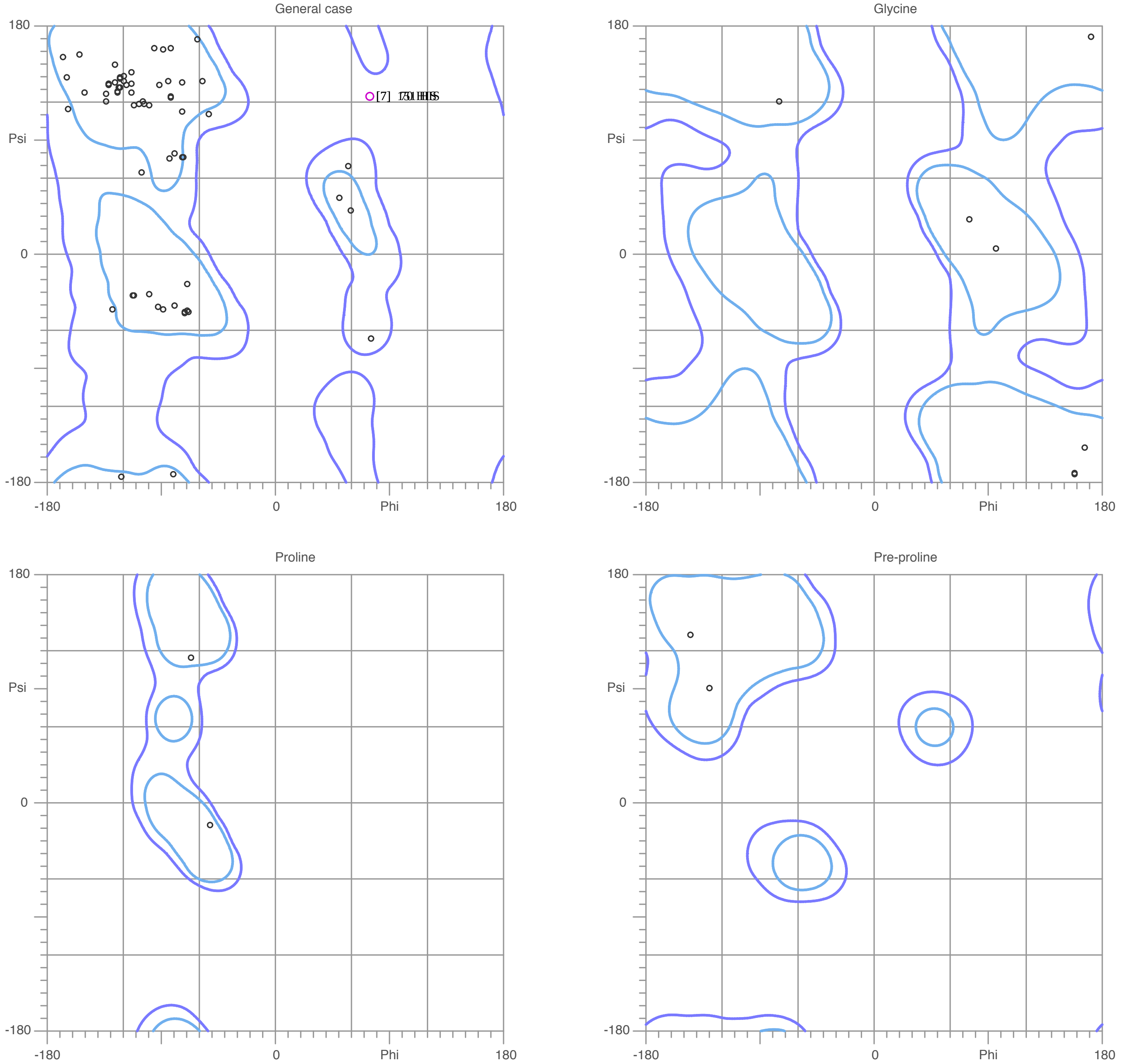
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 7

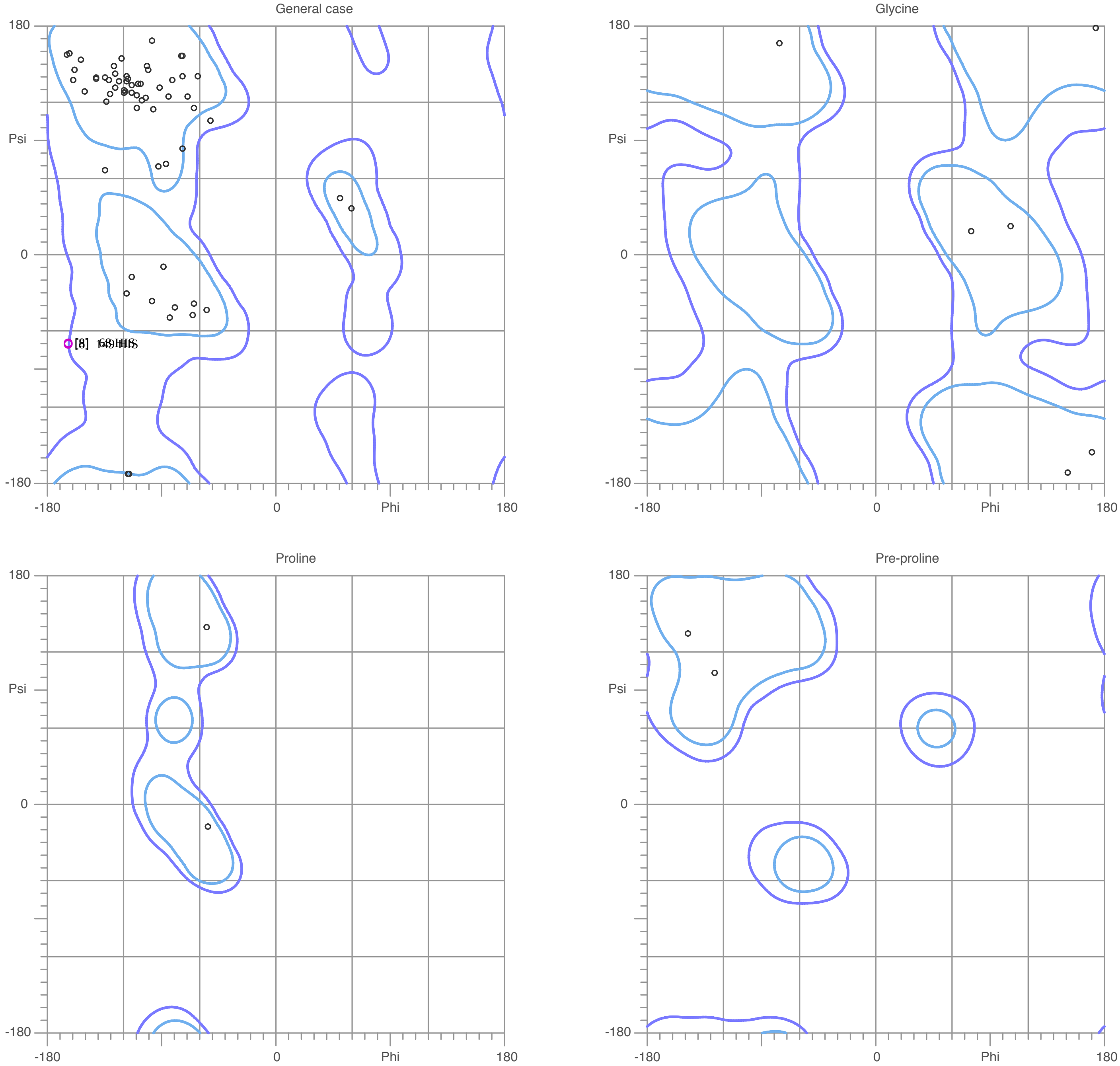


89.9% (124/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[7] 70 HIS (75.0, 125.0)
[7] 151 HIS (74.9, 125.1)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 8



95.7% (132/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[8] 68 HIS (-164.9, -69.9)
[8] 149 HIS (-164.9, -70.0)

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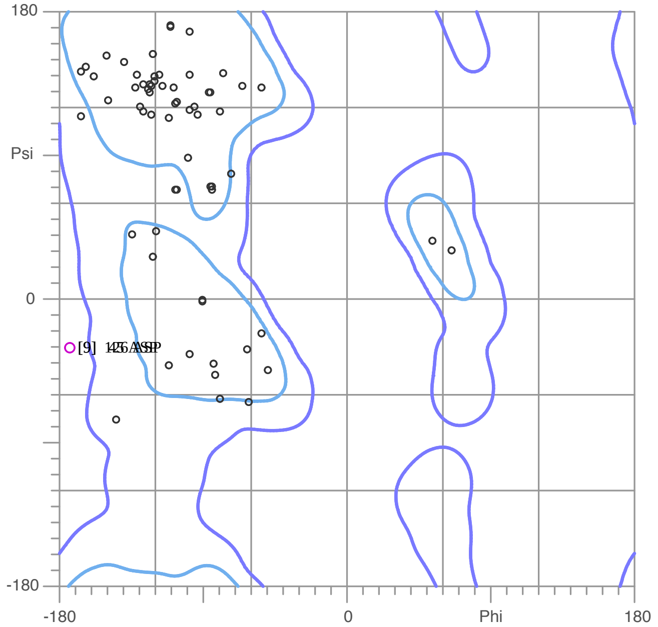
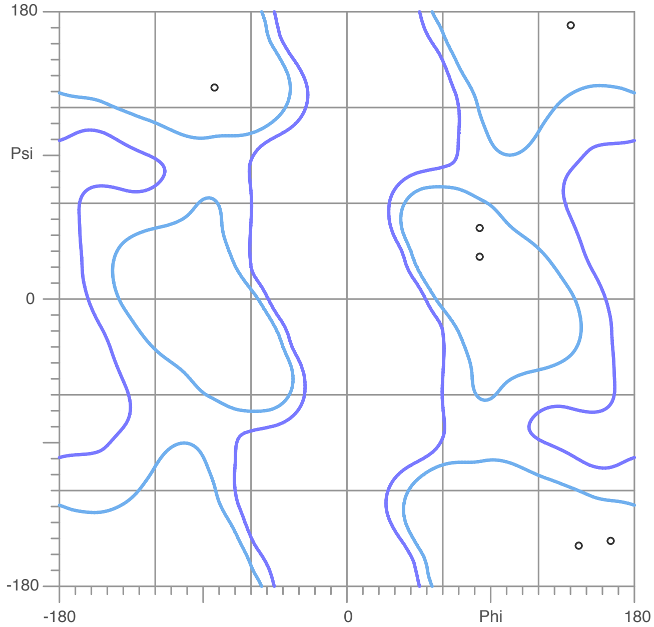
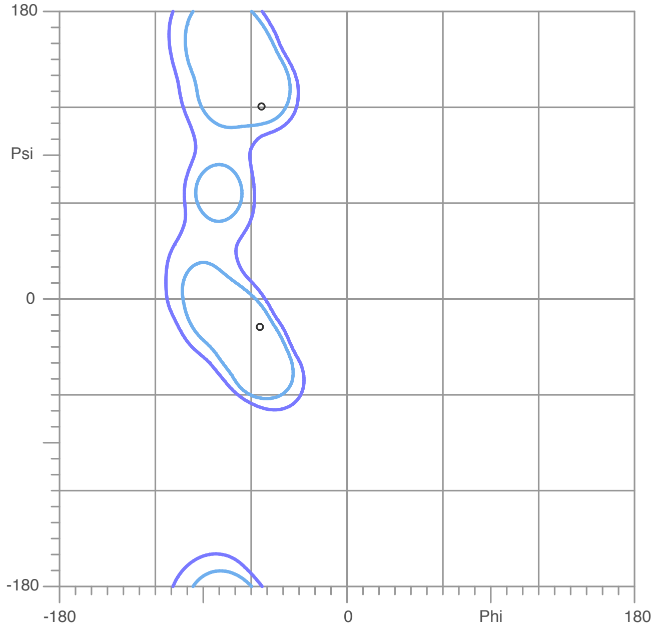
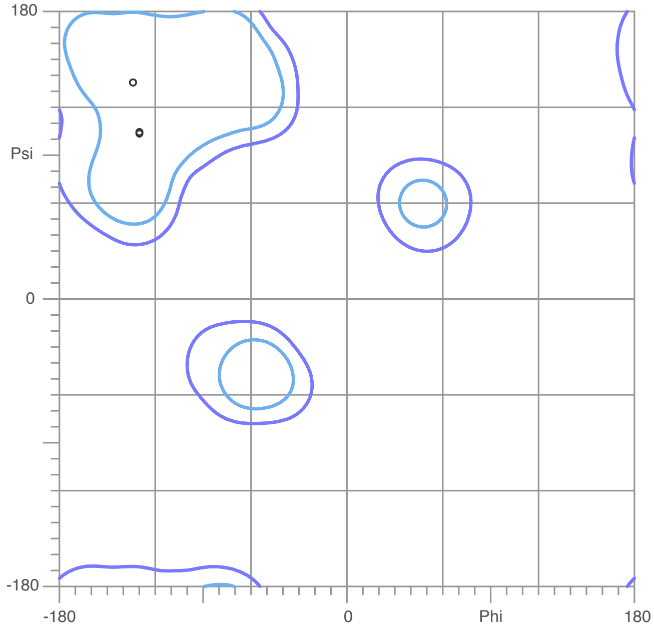
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 9


General case


Glycine


Proline


Pre-proline

92.8% (128/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
- [9] 45 ASP (-174.3, -30.4)
- [9] 126 ASP (-174.3, -30.5)

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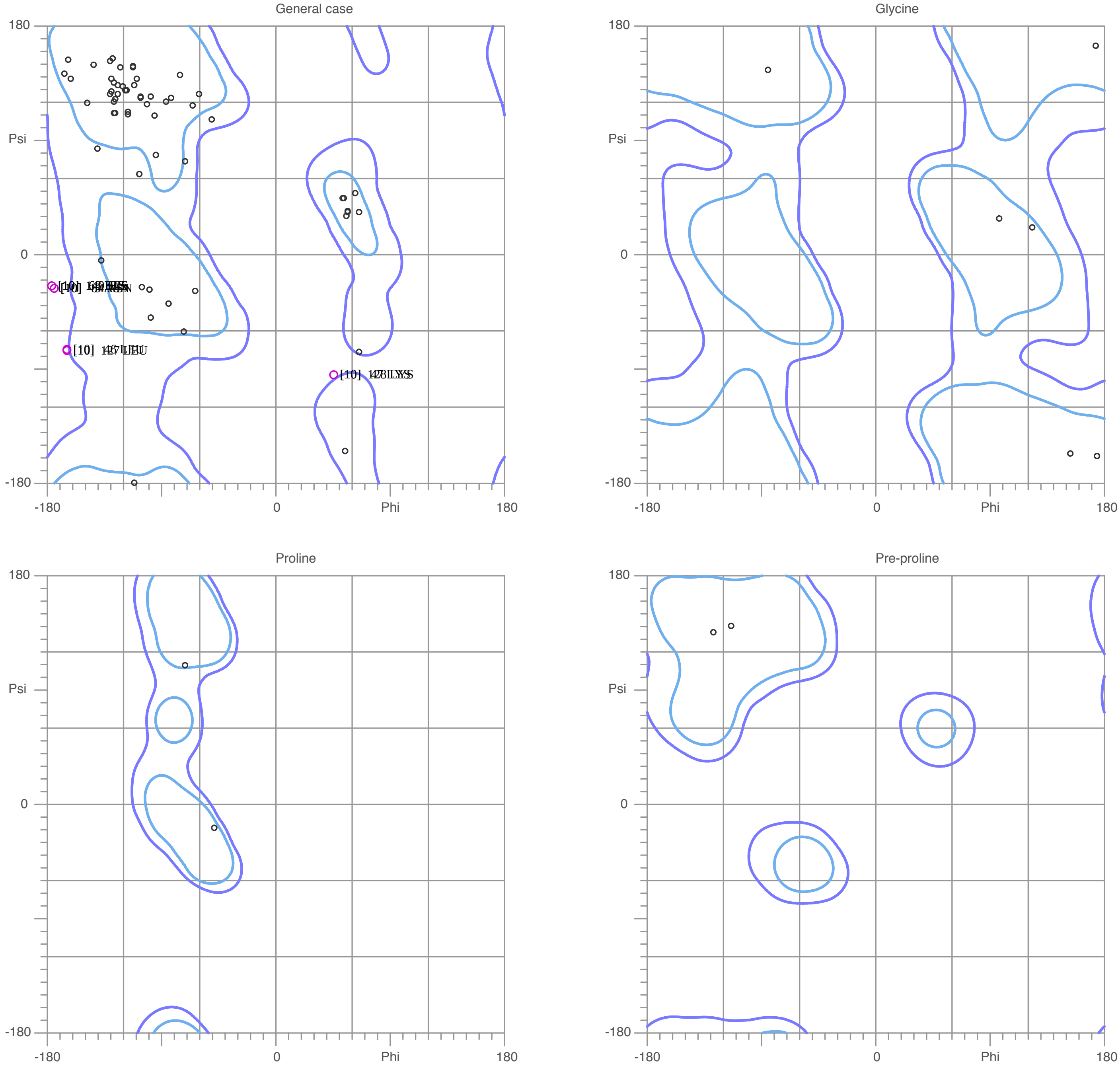
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 10



84.1% (116/138) of all residues were in favored (98%) regions.
94.2% (130/138) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[10] 3 ASN (-175.0, -26.6)
[10] 46 LEU (-165.2, -75.0)
[10] 47 LYS (45.4, -95.0)
[10] 68 HIS (-177.1, -25.0)
[10] 84 ASN (-175.0, -26.7)
[10] 127 LEU (-165.2, -75.0)
[10] 128 LYS (45.4, -95.0)
[10] 149 HIS (-177.1, -25.0)

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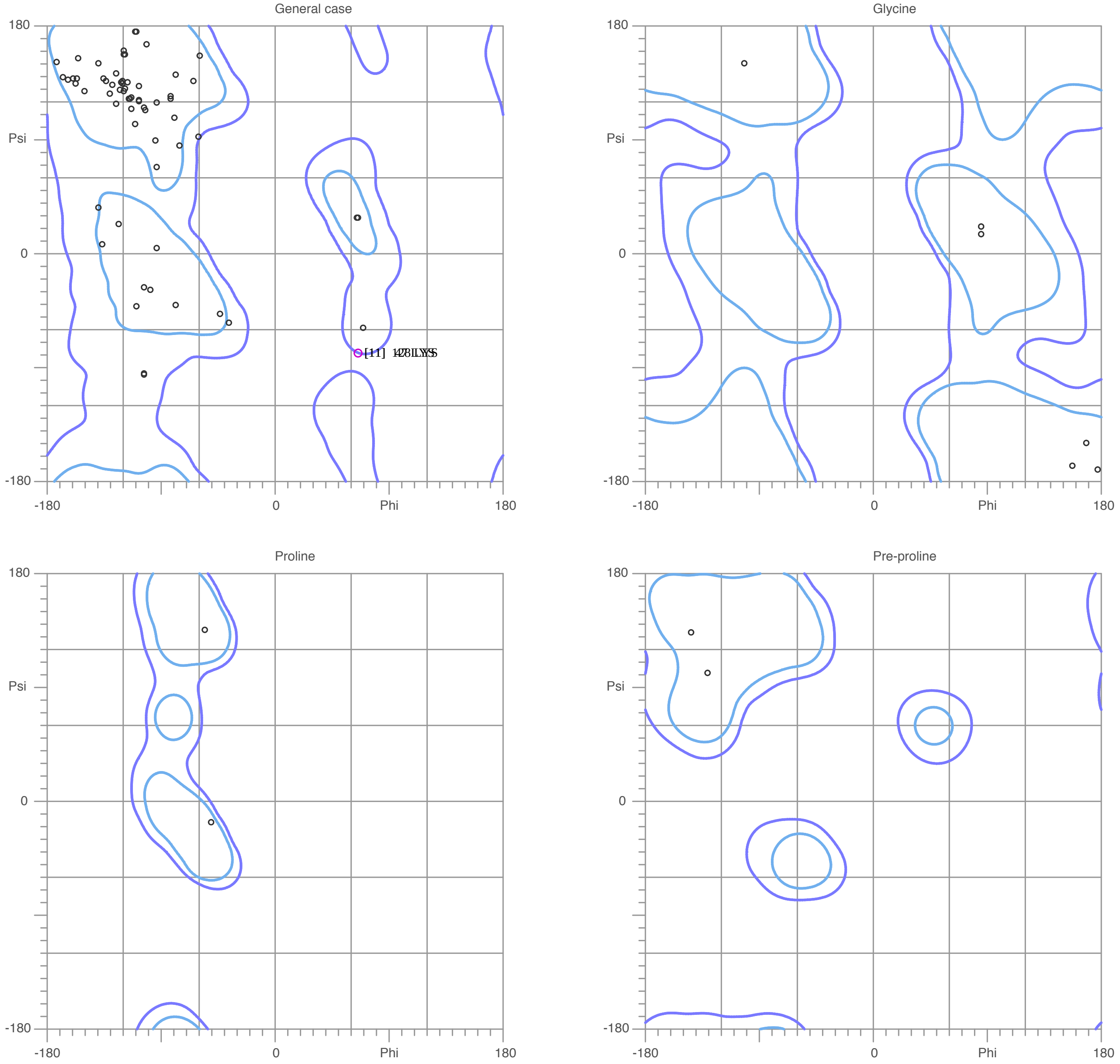
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 11



91.3% (126/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
- [11] 47 LYS (65.4, -78.4)
- [11] 128 LYS (65.4, -78.4)

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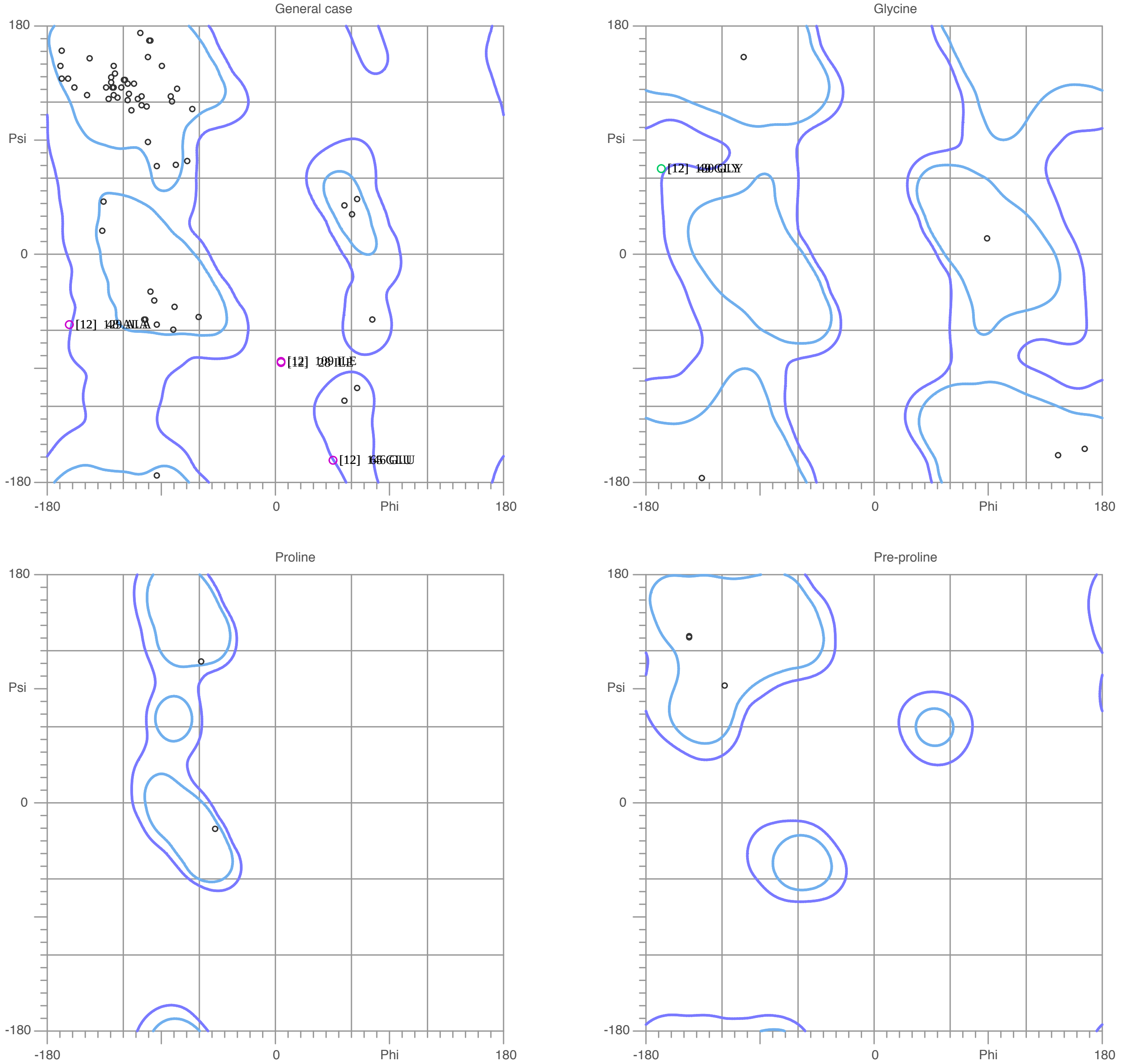
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 12



88.4% (122/138) of all residues were in favored (98%) regions.
94.2% (130/138) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[12] 28 ILE (5.0, -85.0)
[12] 48 ALA (-163.3, -55.9)
[12] 49 GLY (-168.6, 68.9)
[12] 65 GLU (45.1, -162.9)
[12] 109 ILE (5.0, -85.0)
[12] 129 ALA (-163.3, -55.9)
[12] 130 GLY (-168.5, 68.9)
[12] 146 GLU (45.1, -162.9)

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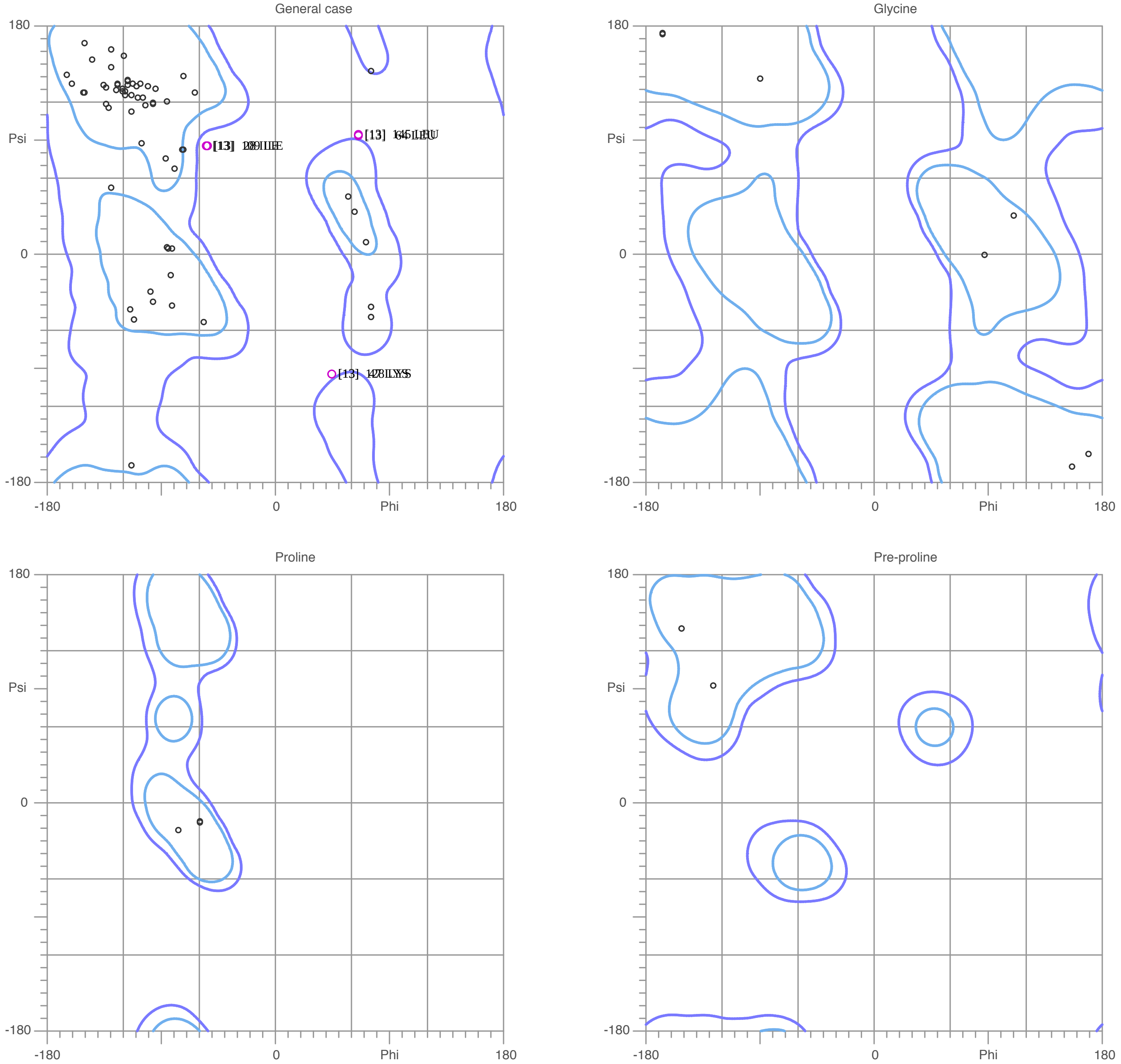
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 13



88.4% (122/138) of all residues were in favored (98%) regions.
95.7% (132/138) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[13] 28 ILE (-55.0, 86.6)
[13] 47 LYS (44.4, -94.9)
[13] 64 LEU (65.1, 94.9)
[13] 109 ILE (-55.0, 86.7)
[13] 128 LYS (44.4, -95.0)
[13] 145 LEU (65.1, 95.0)

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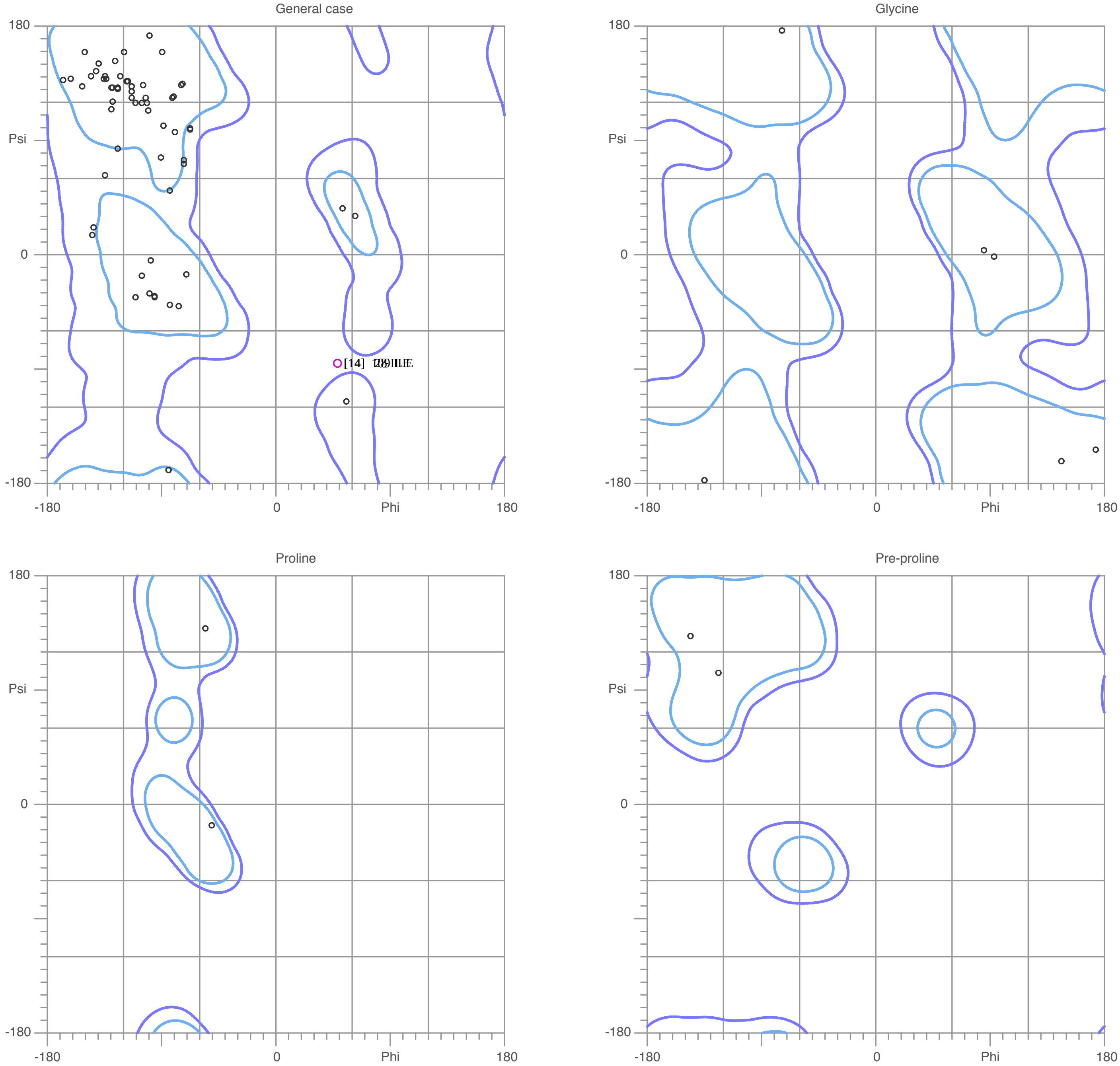
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 14



91.3% (126/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[14] 28 ILE (48.9, -85.2)
[14] 109 ILE (48.9, -85.2)

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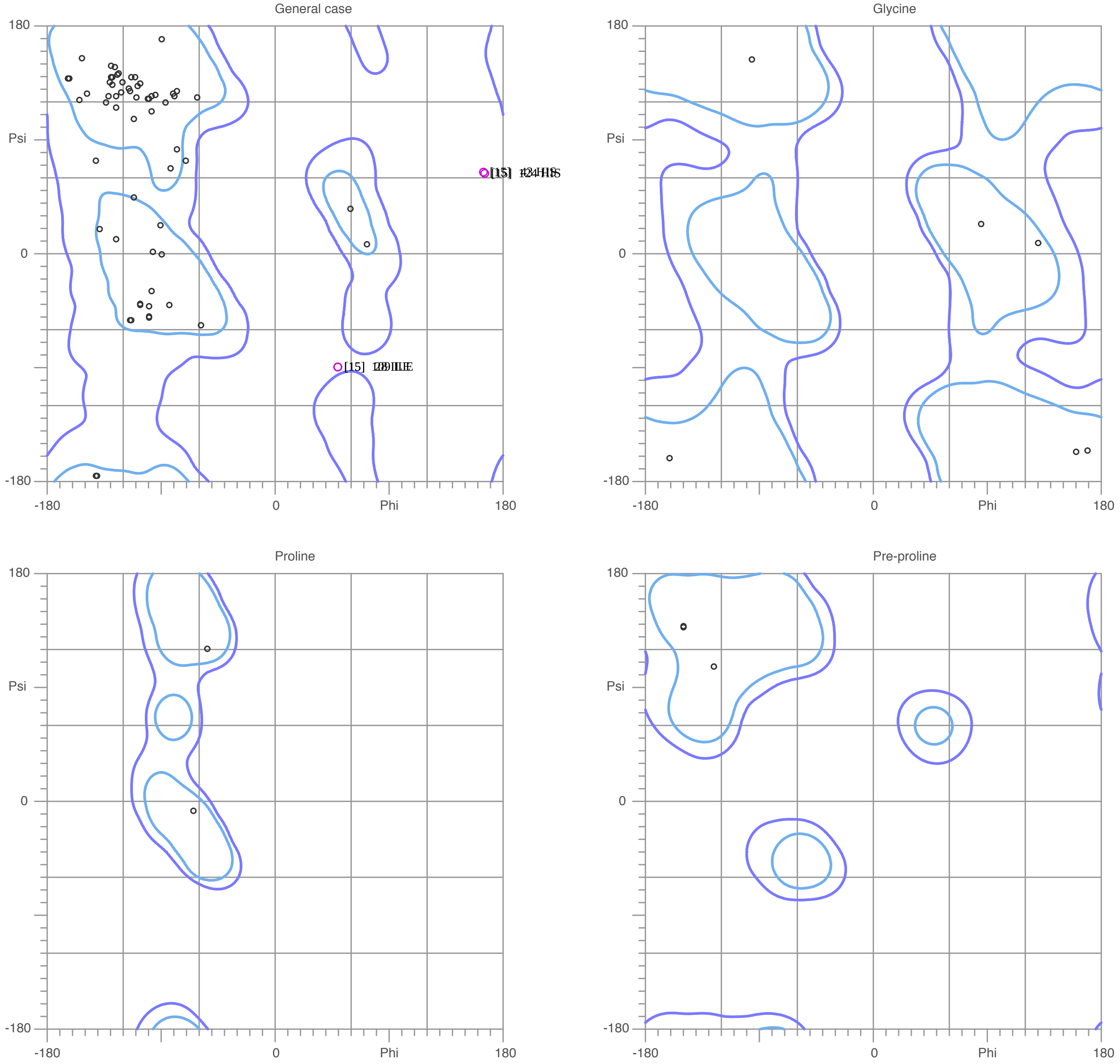
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 15



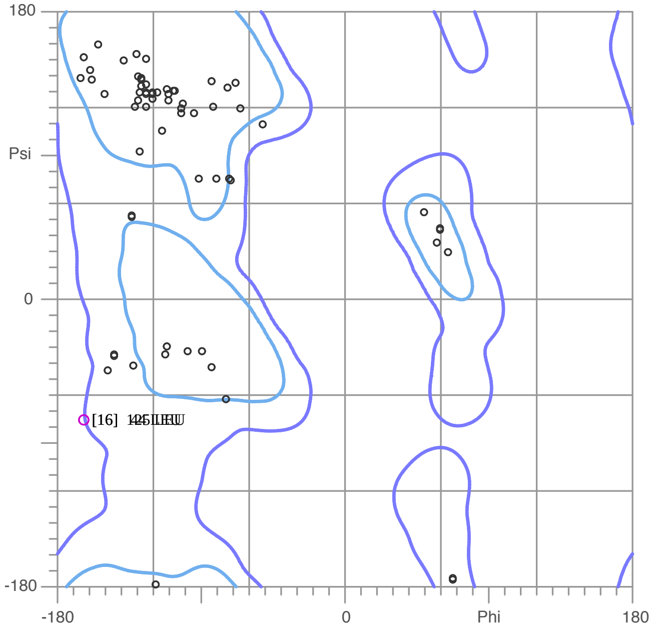
92.8% (128/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[15] 28 ILE (49.2, -89.8)
[15] 43 HIS (165.0, 65.1)
[15] 109 ILE (49.2, -89.8)
[15] 124 HIS (165.0, 65.0)

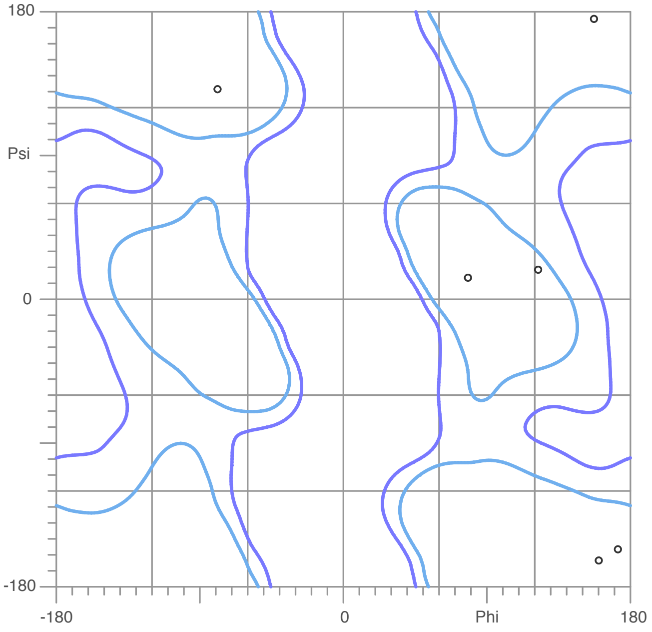
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 16

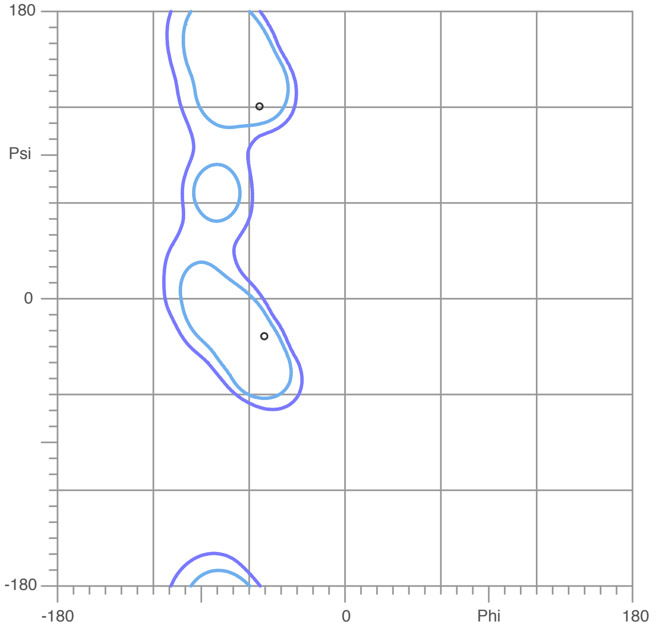
General case



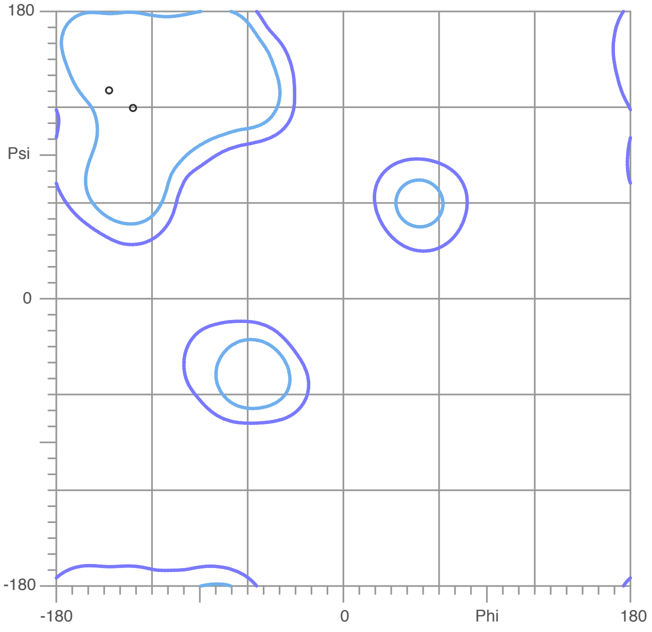
Glycine



Proline



Pre-proline



88.4% (122/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[16] 44 LEU (-164.8, -75.1)
[16] 125 LEU (-164.8, -75.2)

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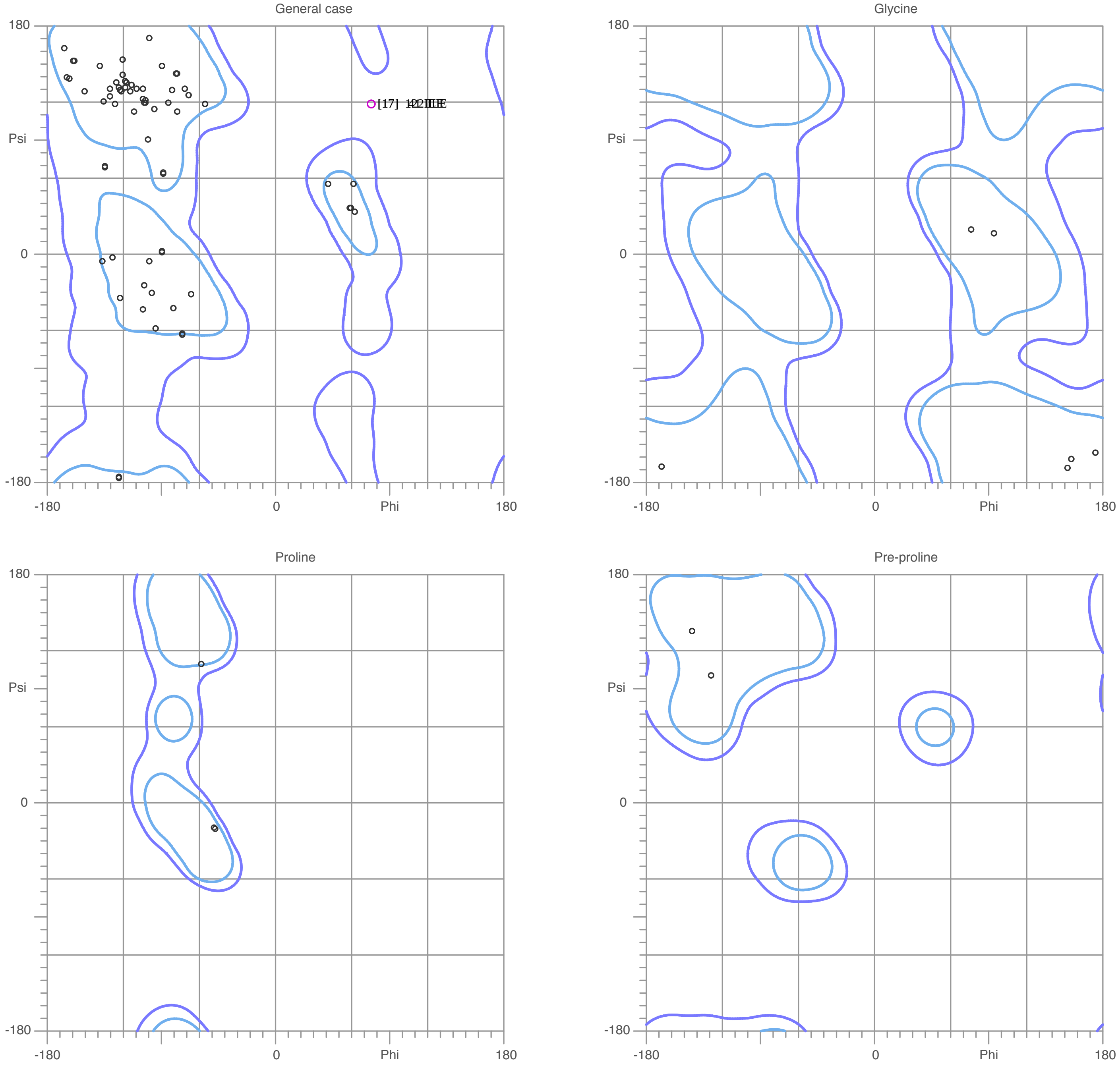
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 17



94.2% (130/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[17] 41 ILE (75.0, 120.0)
[17] 122 ILE (75.0, 119.9)

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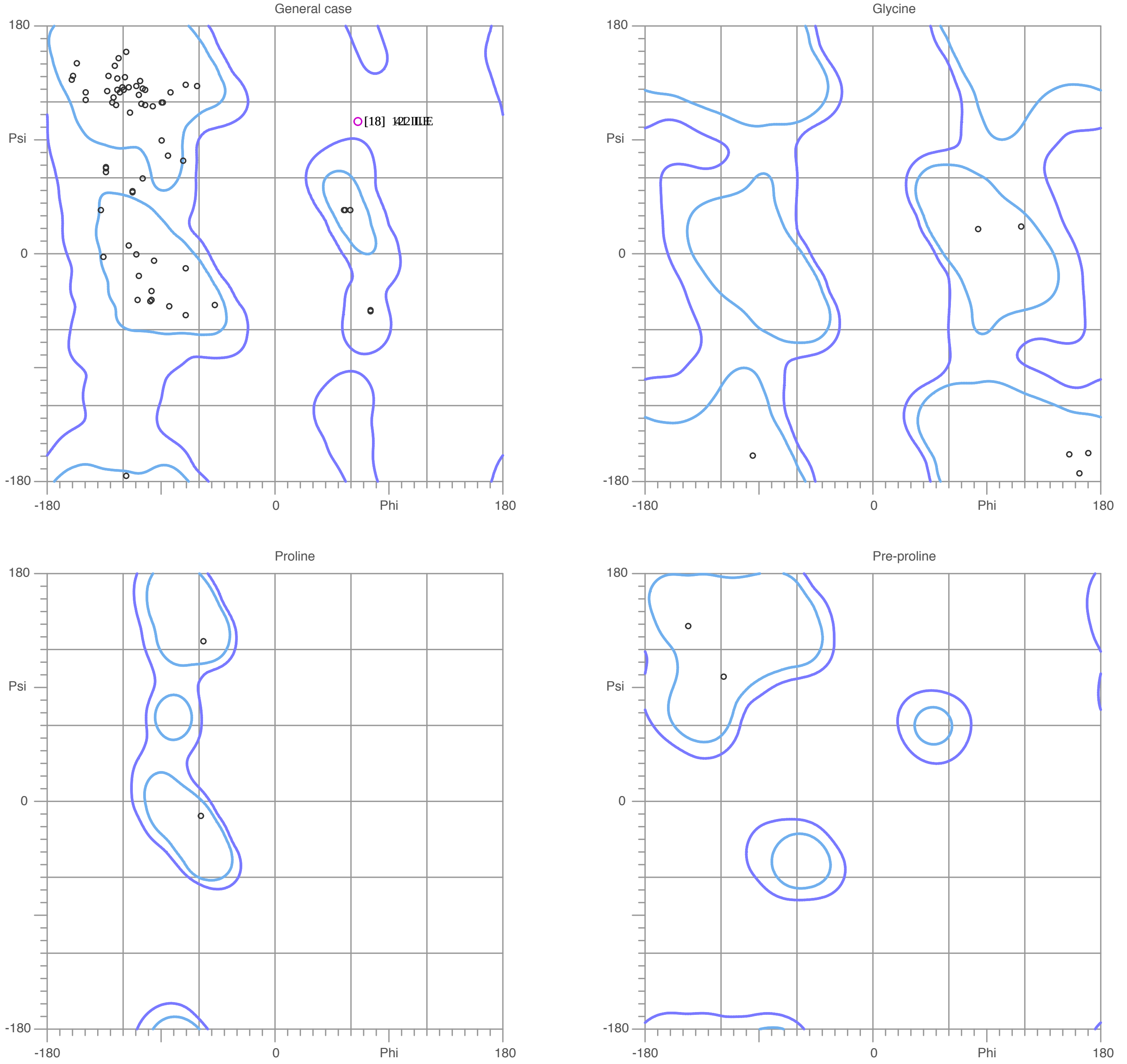
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 18

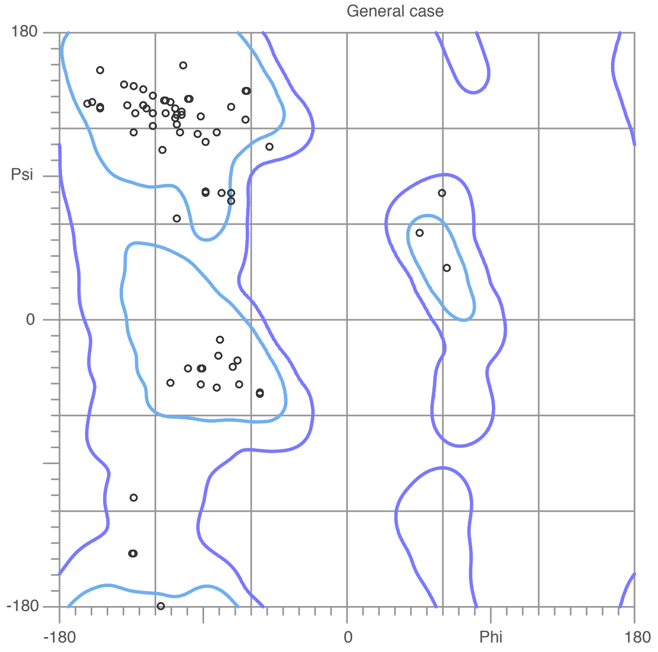


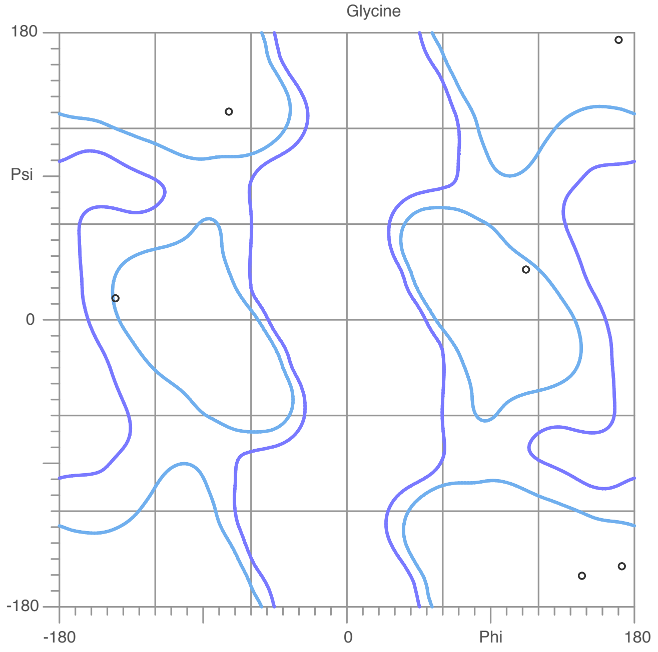
91.3% (126/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

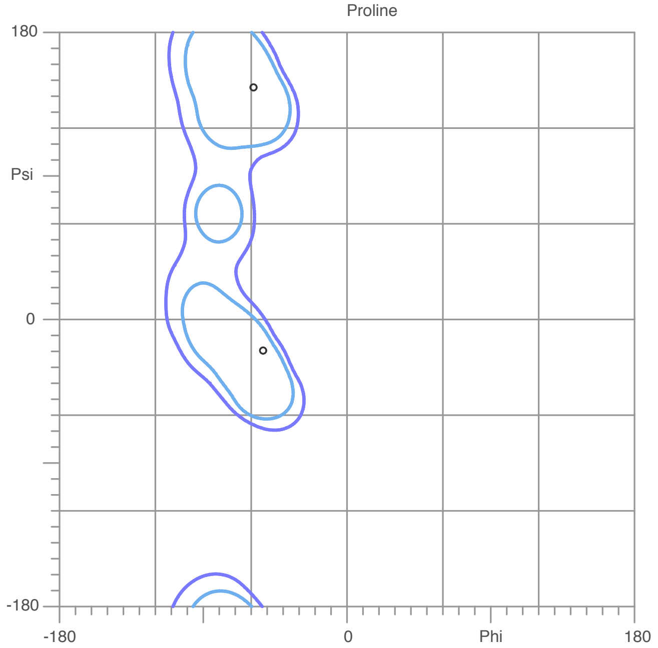
There were 2 outliers (phi, psi):
[18] 41 ILE (65.2, 105.1)
[18] 122 ILE (65.2, 105.0)

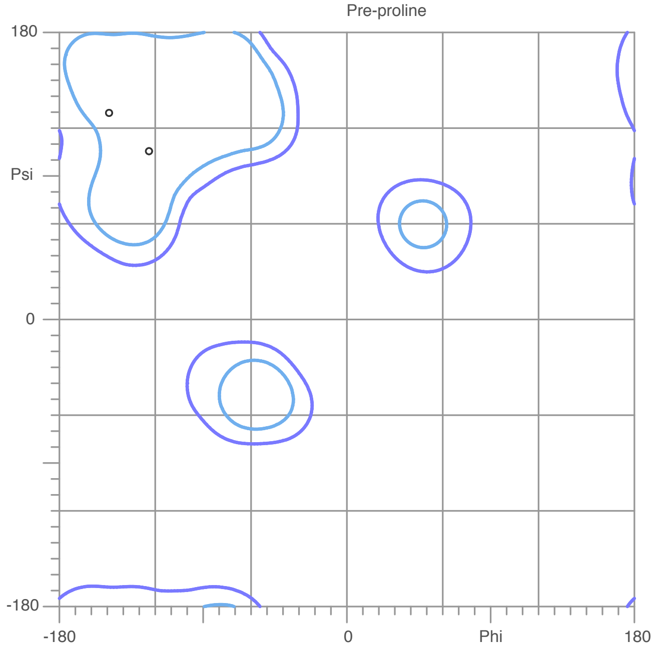
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 19









92.8% (128/138) of all residues were in favored (98%) regions.
100.0% (138/138) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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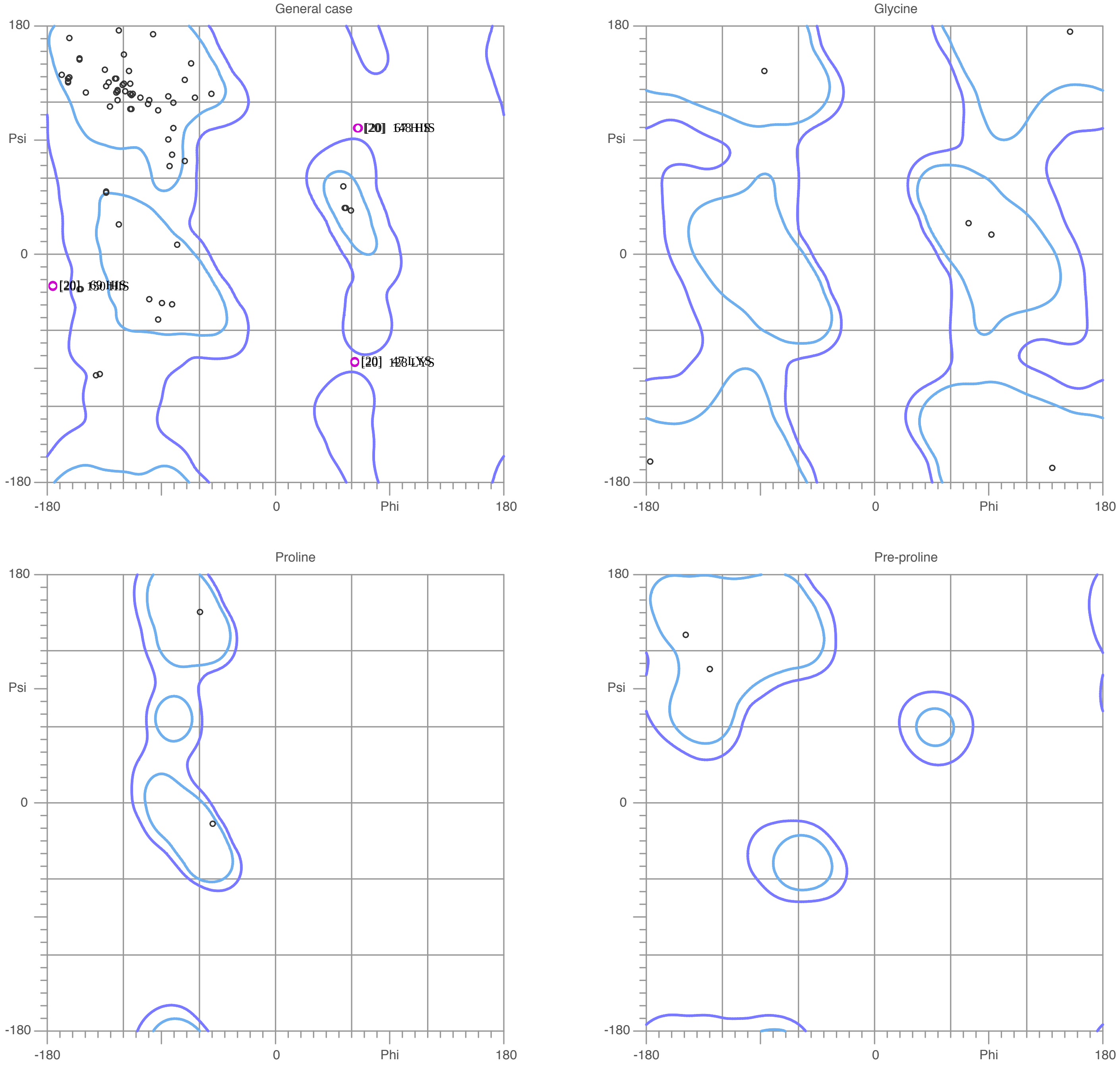
MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 20



88.4% (122/138) of all residues were in favored (98%) regions.
95.7% (132/138) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[20] 47 LYS (62.6, -84.9)
[20] 67 HIS (65.0, 100.3)
[20] 69 HIS (-176.7, -25.0)
[20] 128 LYS (62.7, -85.0)
[20] 148 HIS (65.0, 100.3)
[20] 150 HIS (-176.7, -25.0)

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