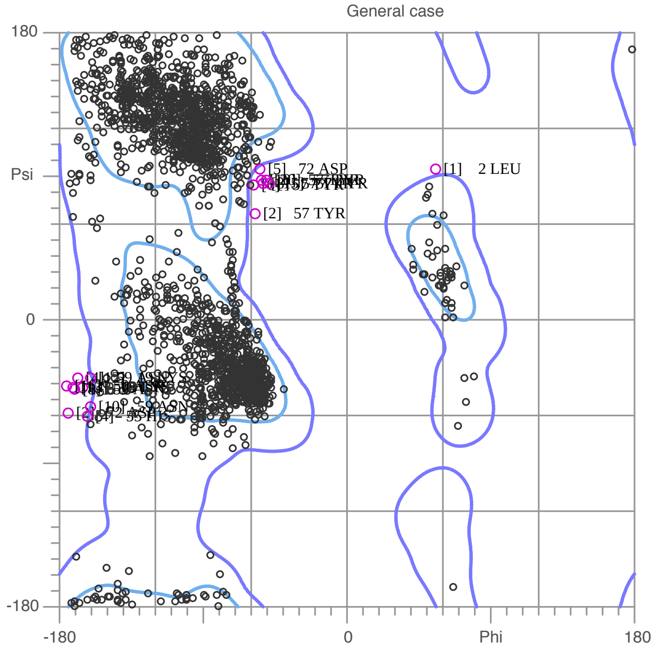
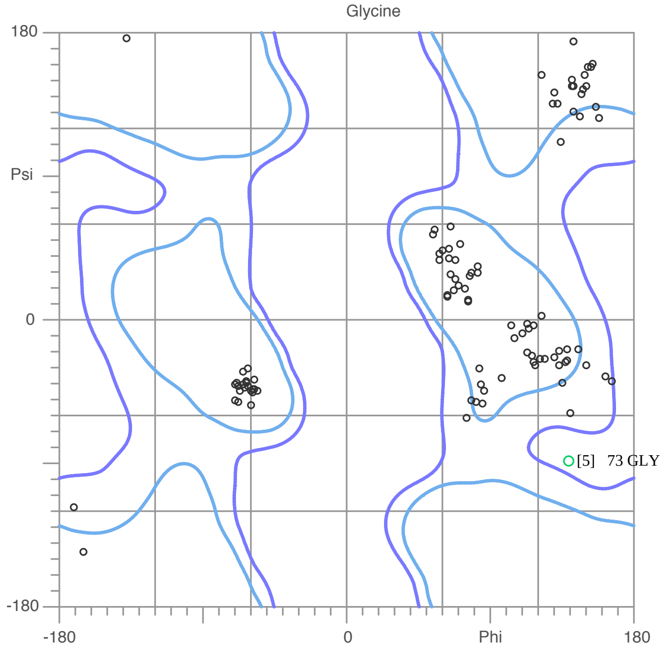
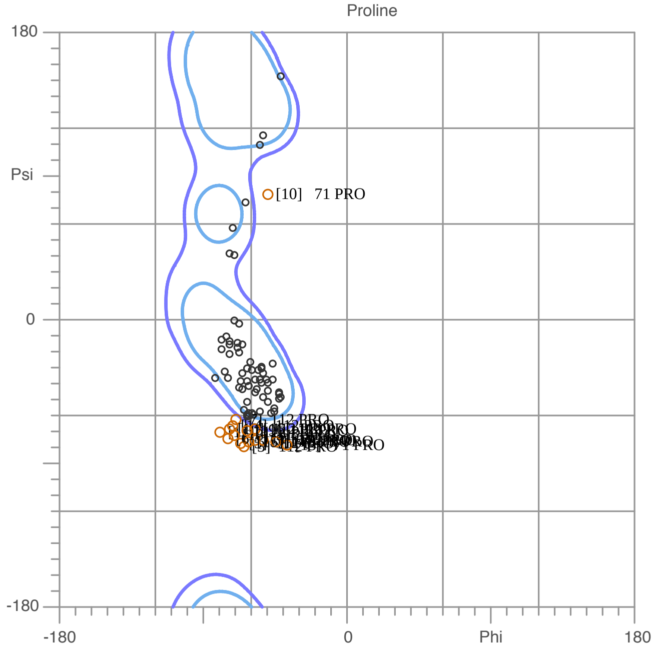
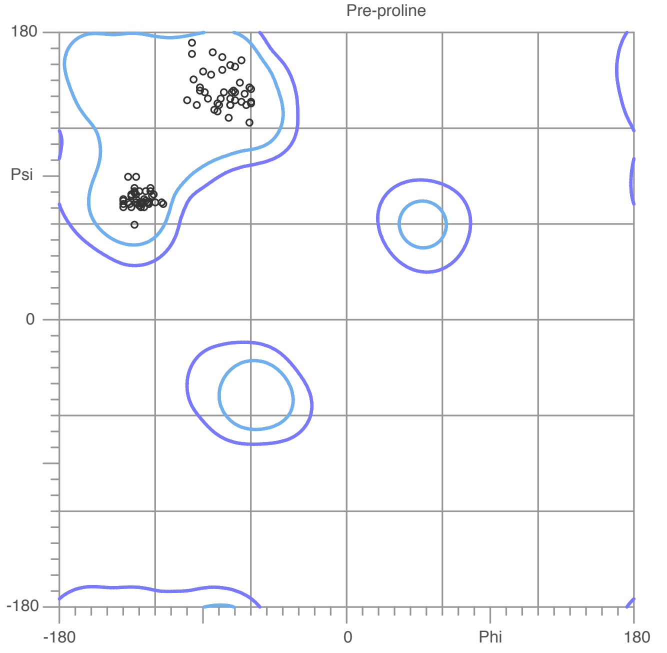
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, all models









91.3% (2174/2380) of all residues were in favored (98%) regions.
98.6% (2346/2380) of all residues were in allowed (>99.8%) regions.

There were 34 outliers (phi, psi):
[1] 2 LEU (55.3, 95.2)
[2] 57 TYR (-58.5, 67.0)
[2] 72 ASP (-175.4, -58.3)
[3] 112 PRO (-65.3, -80.0)
[4] 19 LYS (-167.0, -42.7)
[4] 55 HIS (-163.9, -60.2)
[4] 59 ASN (-169.5, -36.4)
[5] 72 ASP (-55.7, 95.2)
[5] 73 GLY (139.4, -88.4)
[5] 112 PRO (-67.5, -77.3)
[6] 57 TYR (-59.2, 85.0)
[6] 112 PRO (-75.1, -74.5)
[7] 112 PRO (-70.2, -62.4)
[8] 57 TYR (-53.4, 86.7)
[8] 59 ASN (-171.7, -43.4)
[9] 71 PRO (-53.1, -75.2)
[10] 57 TYR (-54.5, 88.9)
[10] 59 ASN (-161.5, -54.2)
[10] 71 PRO (-50.3, 79.5)
[10] 112 PRO (-74.4, -68.1)
[11] 112 PRO (-80.3, -70.8)
[12] 19 LYS (-161.3, -36.8)
[13] 19 LYS (-172.4, -43.0)
[13] 71 PRO (-38.6, -78.2)
[13] 112 PRO (-58.3, -76.0)
[14] 71 PRO (-45.2, -76.8)
[14] 112 PRO (-72.2, -67.0)
[15] 57 TYR (-50.0, 86.1)
[15] 112 PRO (-62.1, -76.9)
[16] 59 ASN (-176.0, -41.3)
[16] 112 PRO (-58.0, -68.5)
[18] 112 PRO (-71.9, -72.7)
[19] 112 PRO (-63.8, -69.3)
[20] 57 TYR (-51.7, 88.8)

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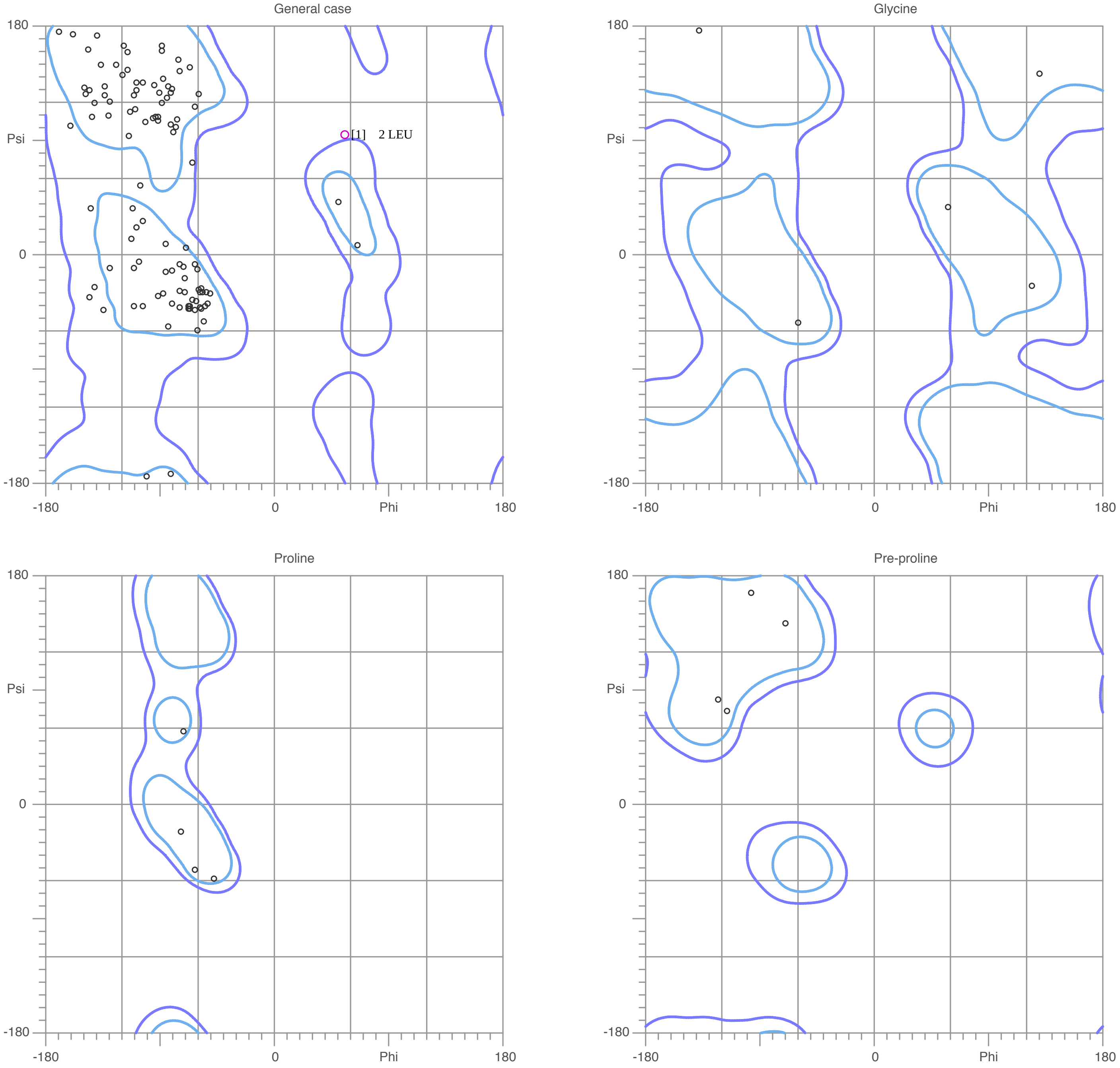
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 1



93.3% (111/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[1] 2 LEU (55.3, 95.2)

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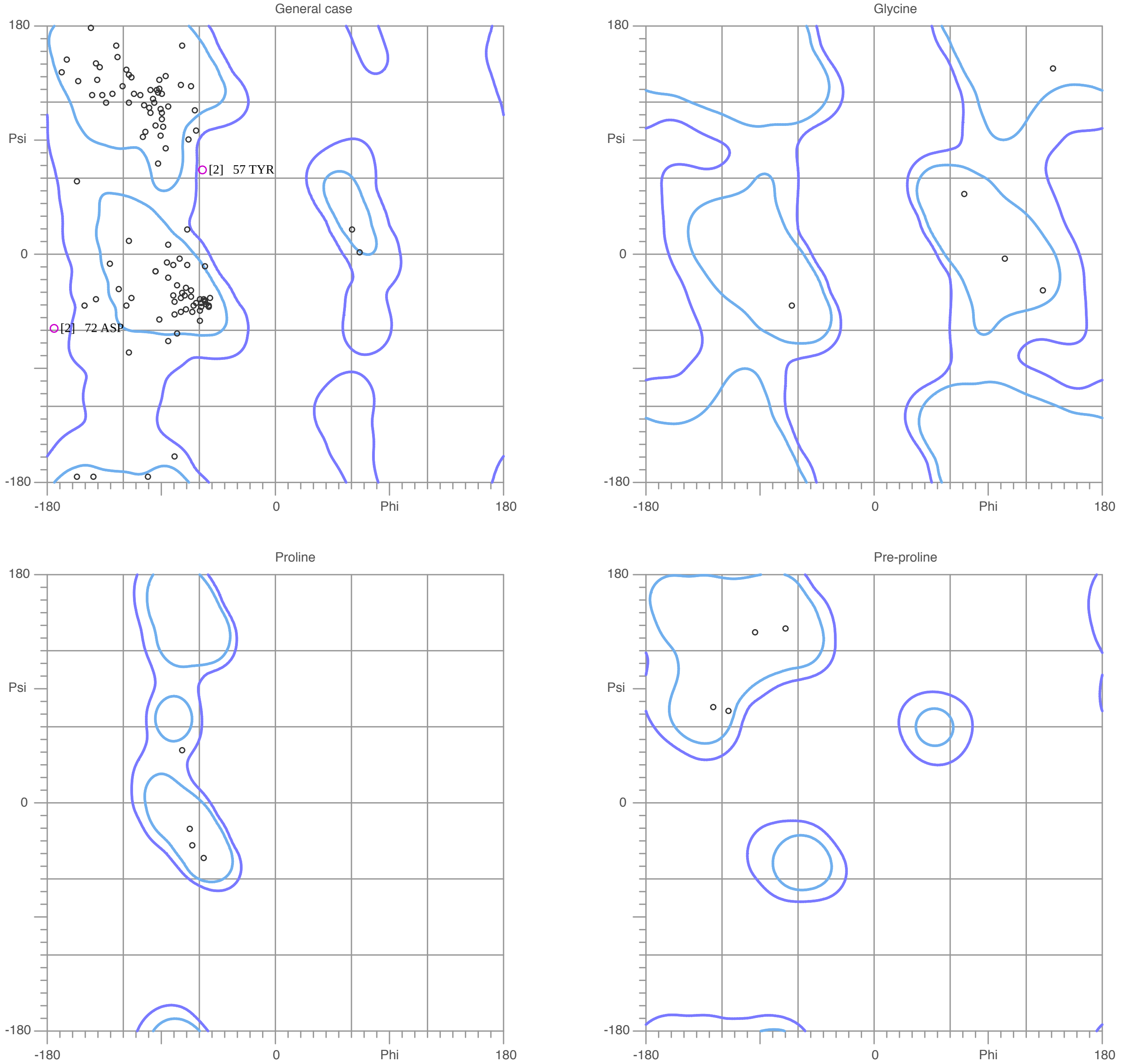
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 2



89.9% (107/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[2] 57 TYR (-58.5, 67.0)
[2] 72 ASP (-175.4, -58.3)

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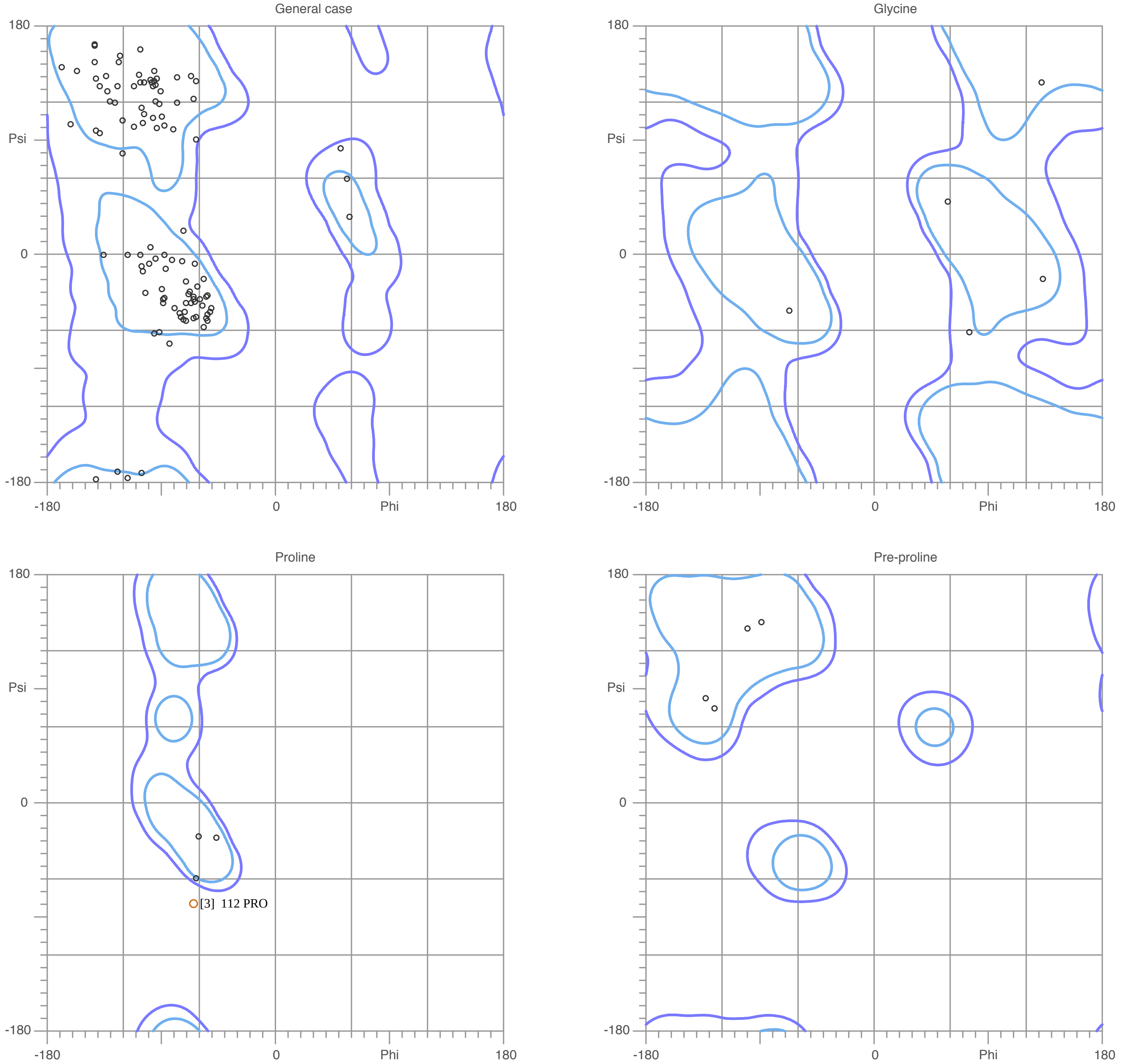
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 3



90.8% (108/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 112 PRO (-65.3, -80.0)

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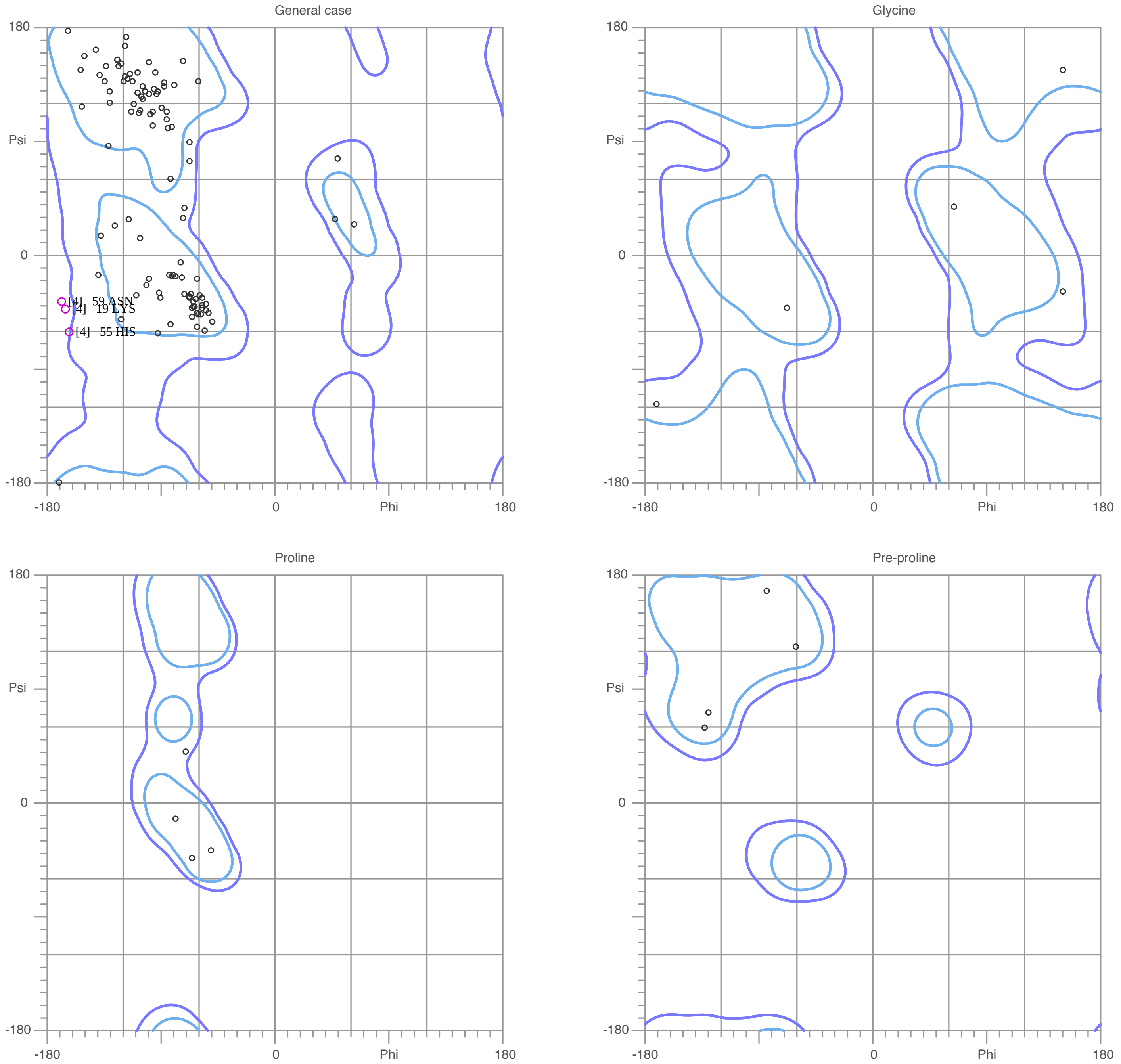
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 4



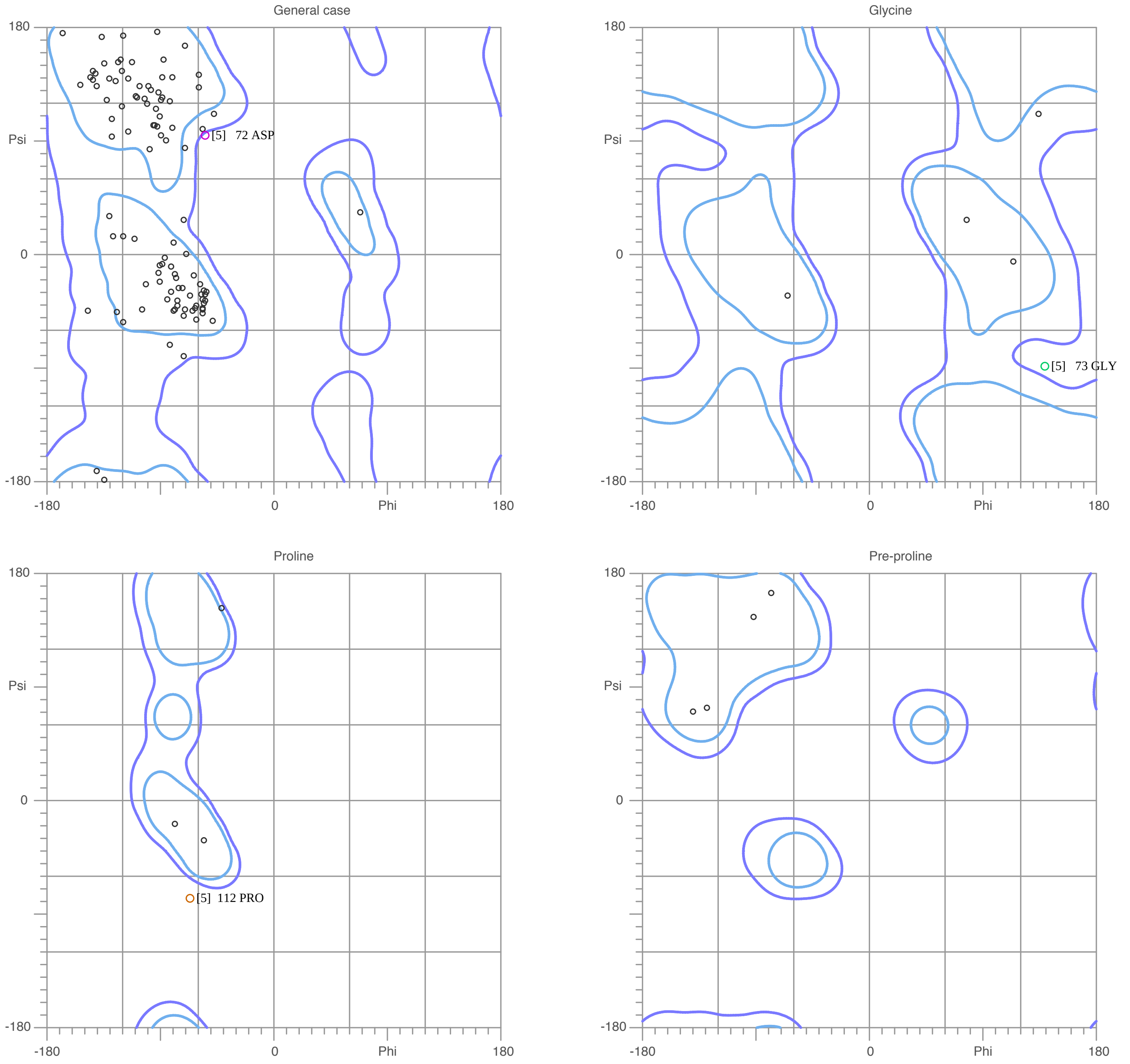
89.1% (106/119) of all residues were in favored (98%) regions.
97.5% (116/119) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[4] 19 LYS (-167.0, -42.7)
[4] 55 HIS (-163.9, -60.2)
[4] 59 ASN (-169.5, -36.4)

MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 5



89.9% (107/119) of all residues were in favored (98%) regions.
97.5% (116/119) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
- [5] 72 ASP (-55.7, 95.2)
- [5] 73 GLY (139.4, -88.4)
- [5] 112 PRO (-67.5, -77.3)

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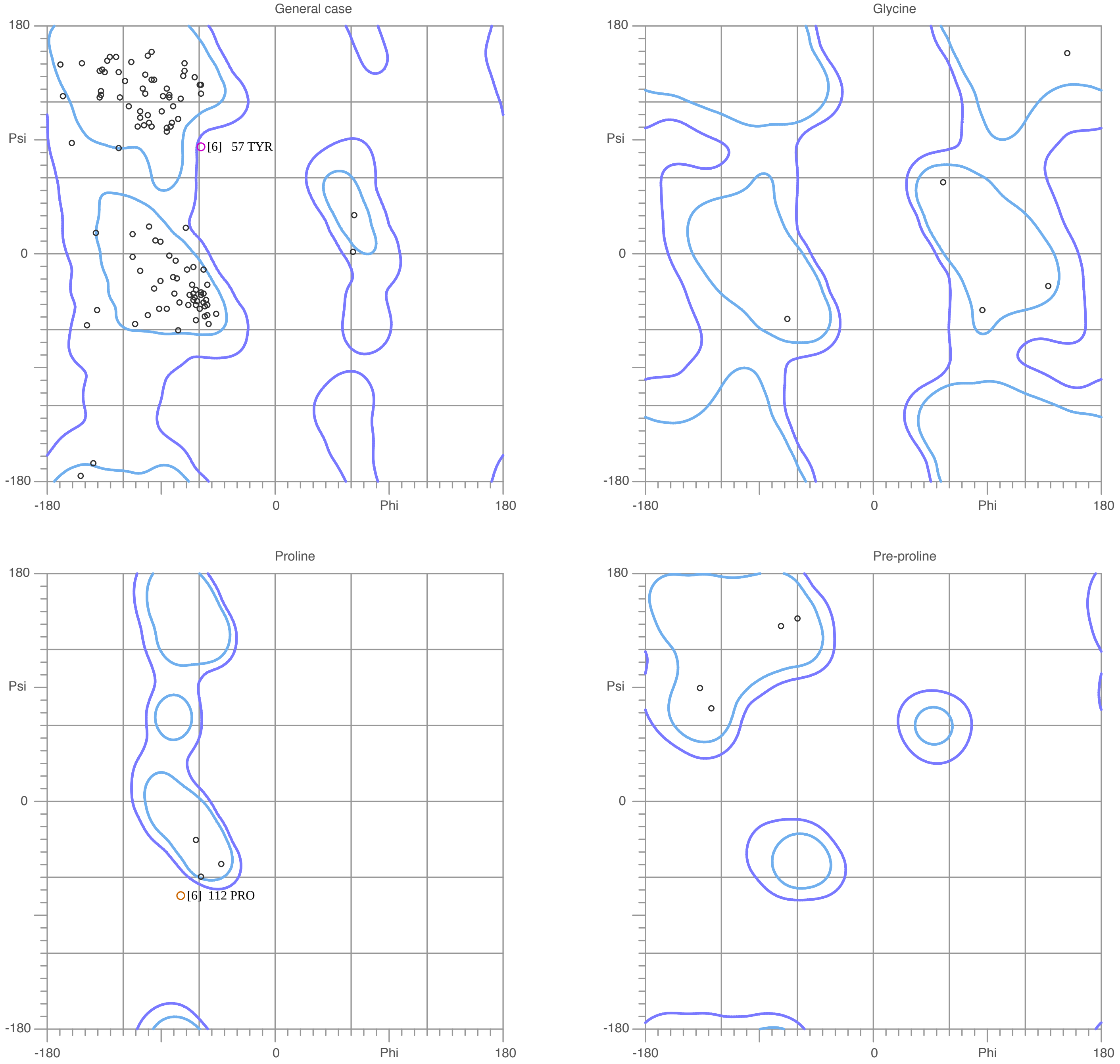
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 6



91.6% (109/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[6] 57 TYR (-59.2, 85.0)
[6] 112 PRO (-75.1, -74.5)

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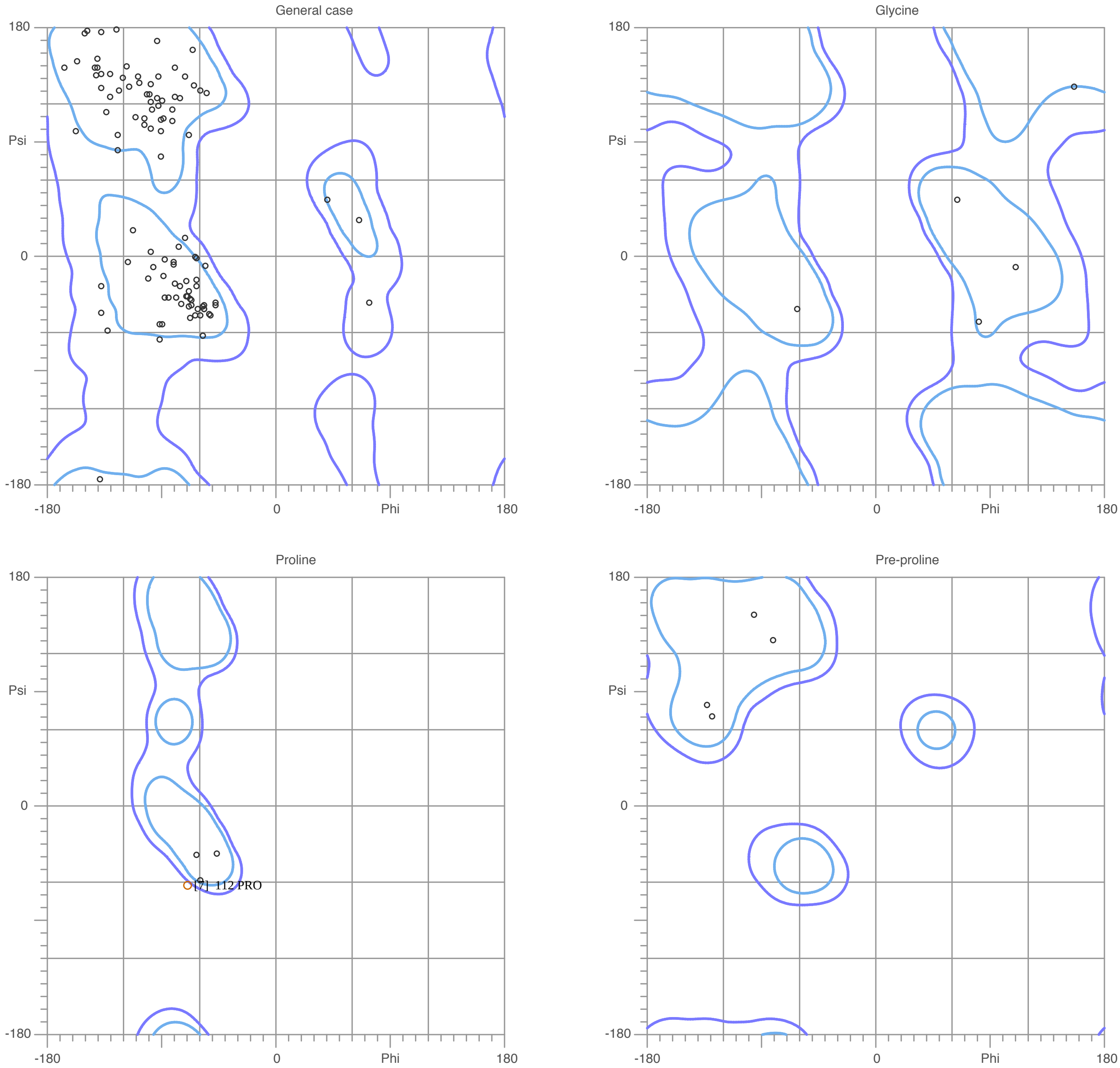
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 7



91.6% (109/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[7] 112 PRO (-70.2, -62.4)

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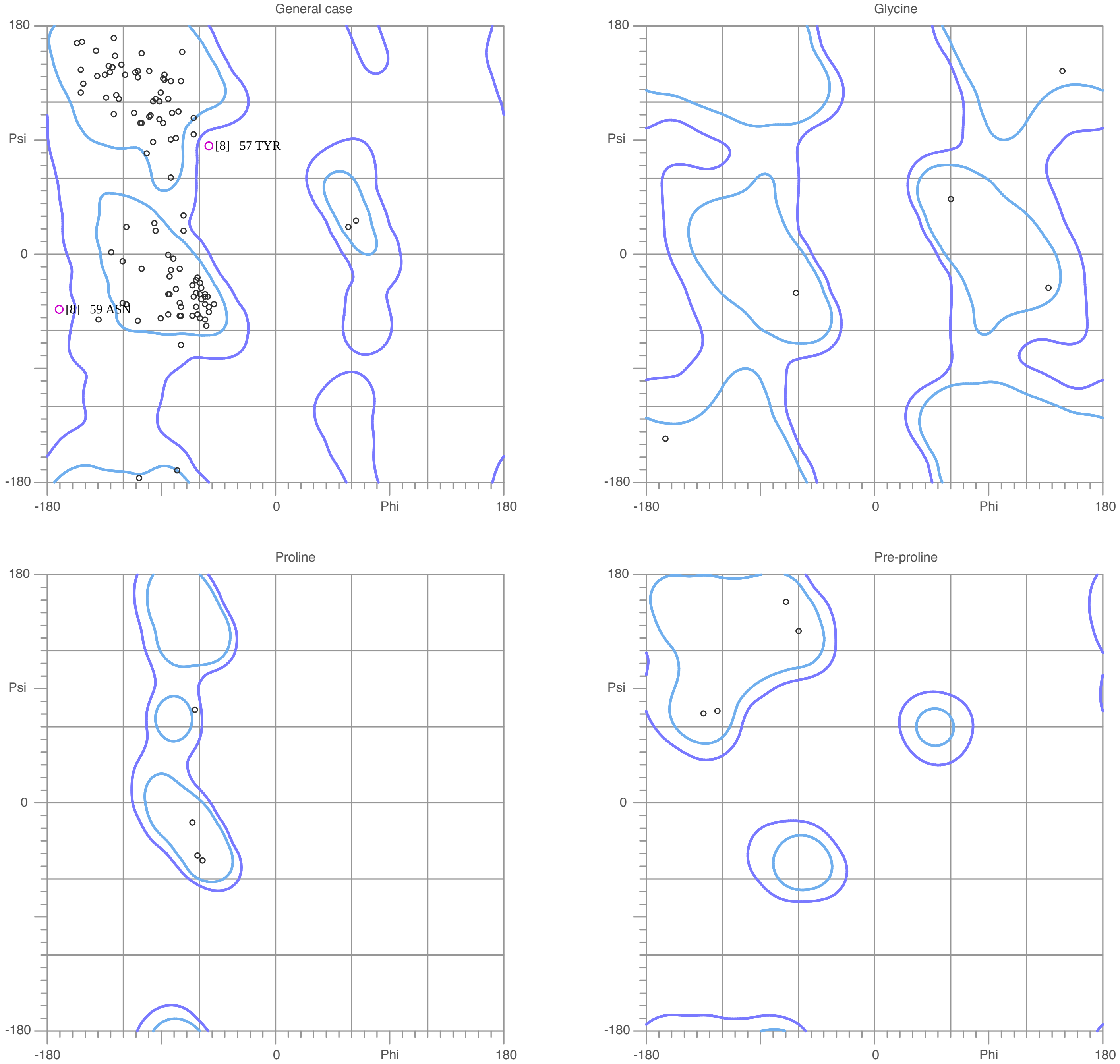
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 8

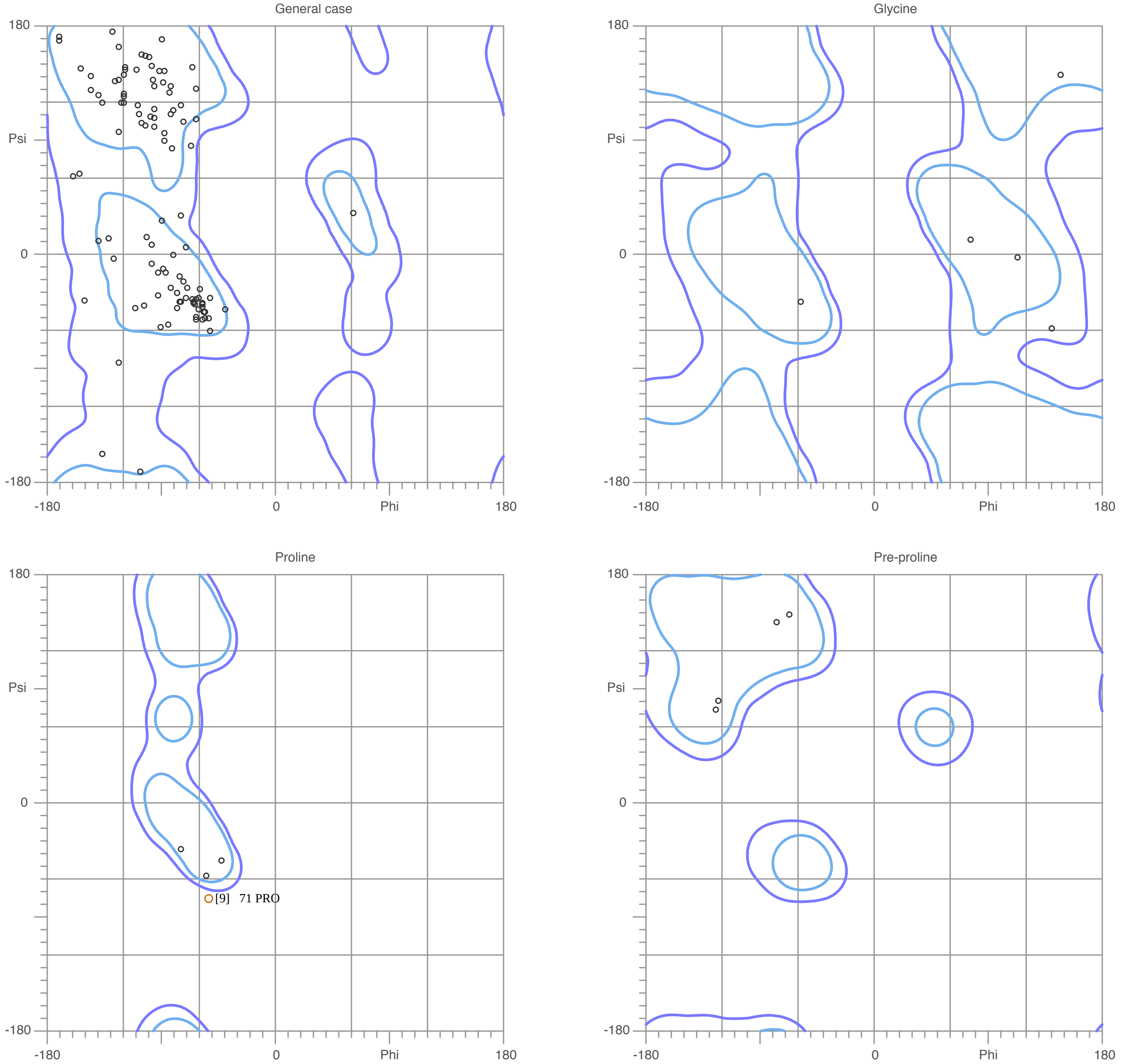


93.3% (111/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[8] 57 TYR (-53.4, 86.7)
[8] 59 ASN (-171.7, -43.4)

MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 9



90.8% (108/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 71 PRO (-53.1, -75.2)

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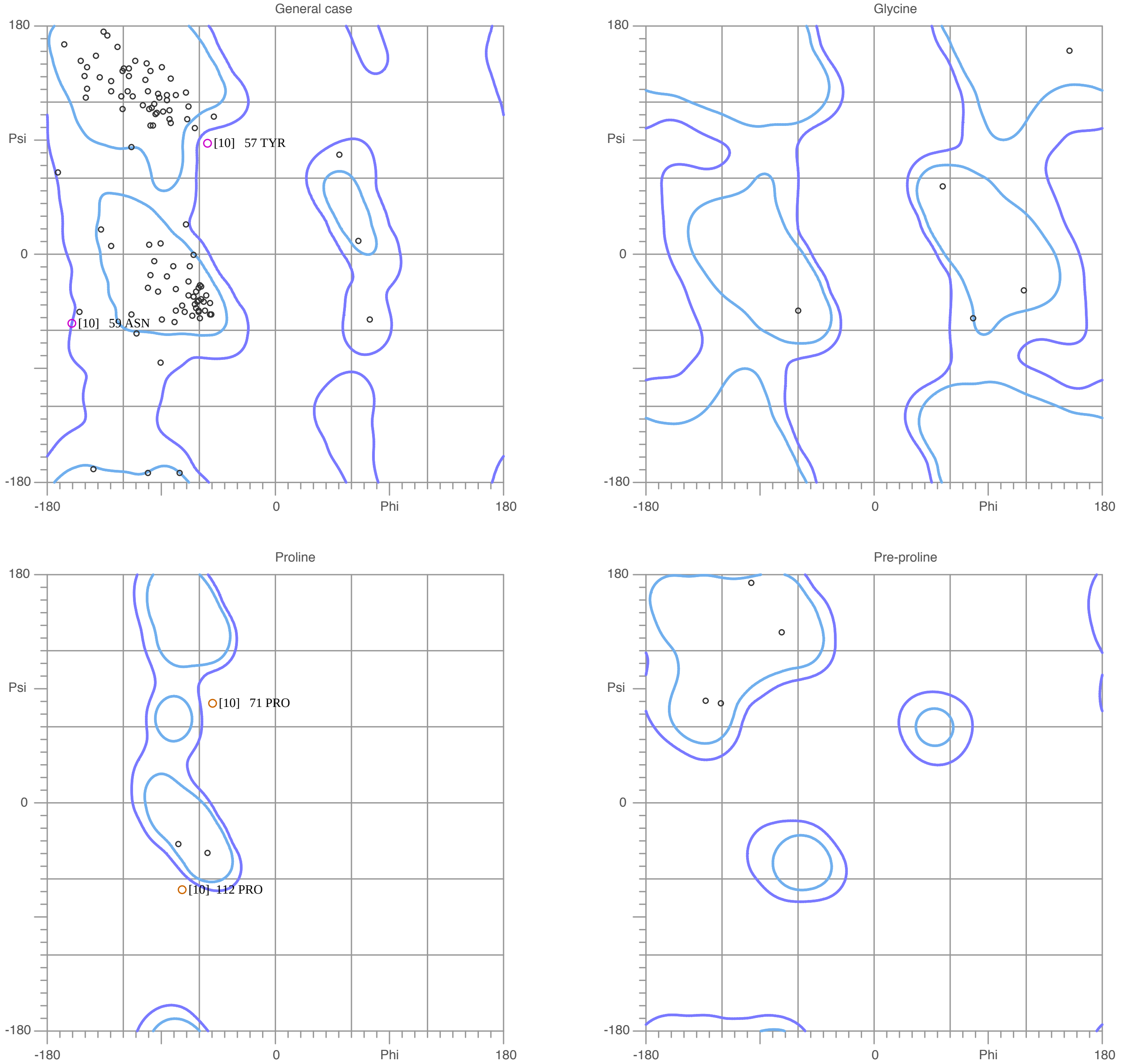
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 10



89.1% (106/119) of all residues were in favored (98%) regions.
96.6% (115/119) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[10] 57 TYR (-54.5, 88.9)
[10] 59 ASN (-161.5, -54.2)
[10] 71 PRO (-50.3, 79.5)
[10] 112 PRO (-74.4, -68.1)

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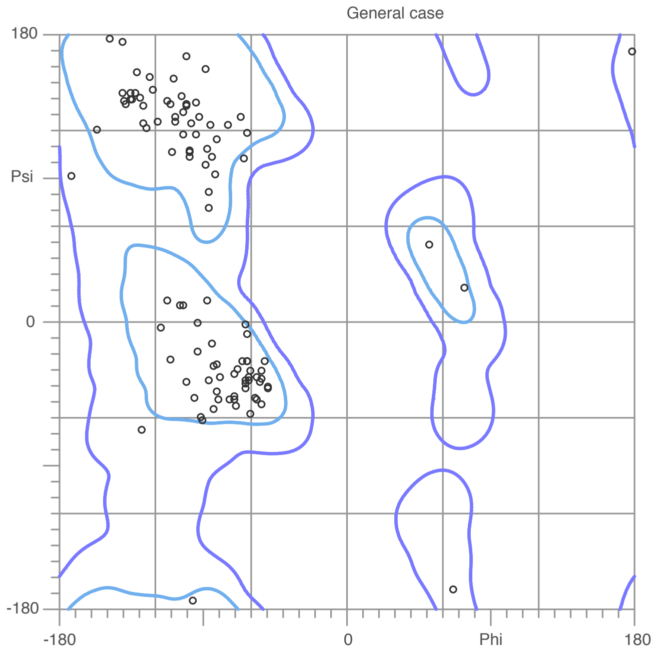
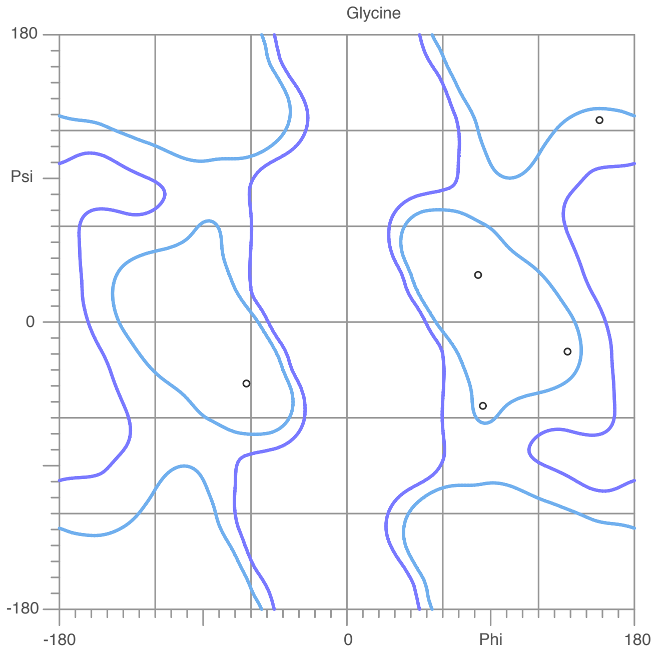
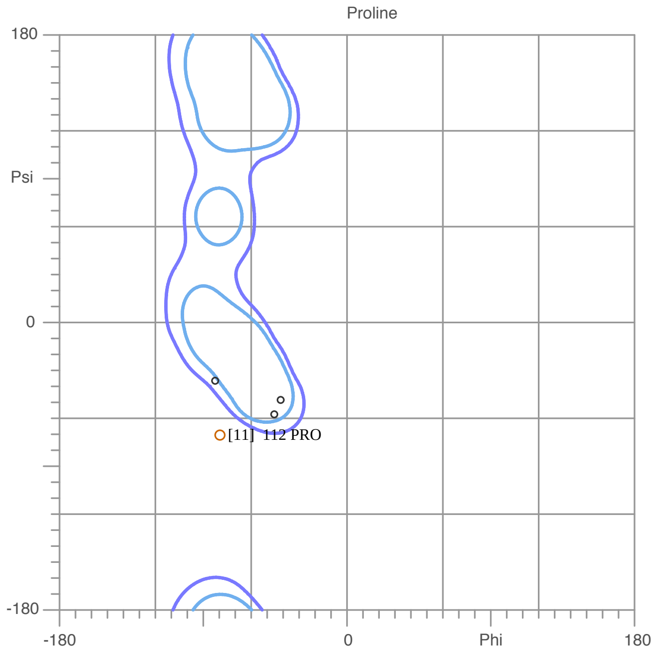
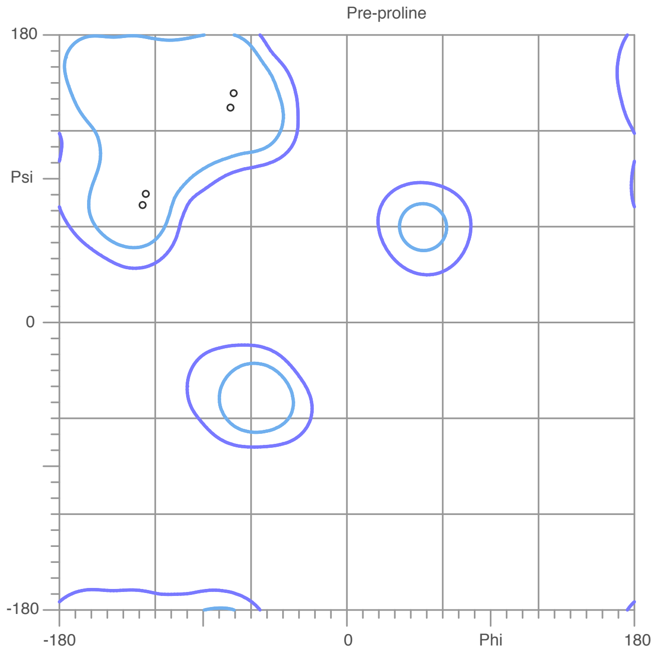
UUR17A_NMR_em_bcr3.pdb, model 11


General case


Glycine


Proline


Pre-proline

93.3% (111/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[11] 112 PRO (-80.3, -70.8)

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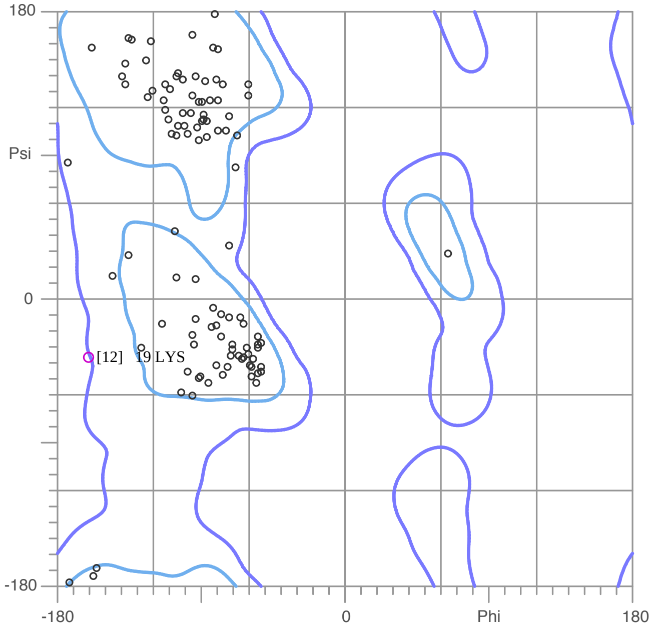
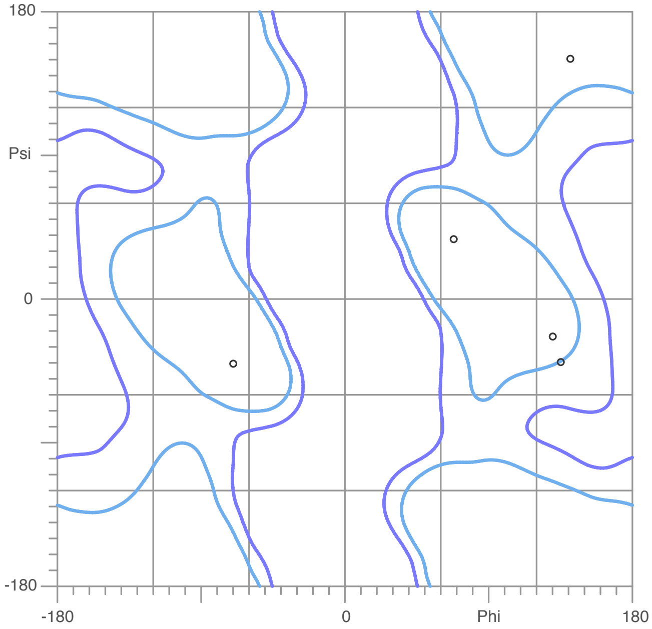
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 12

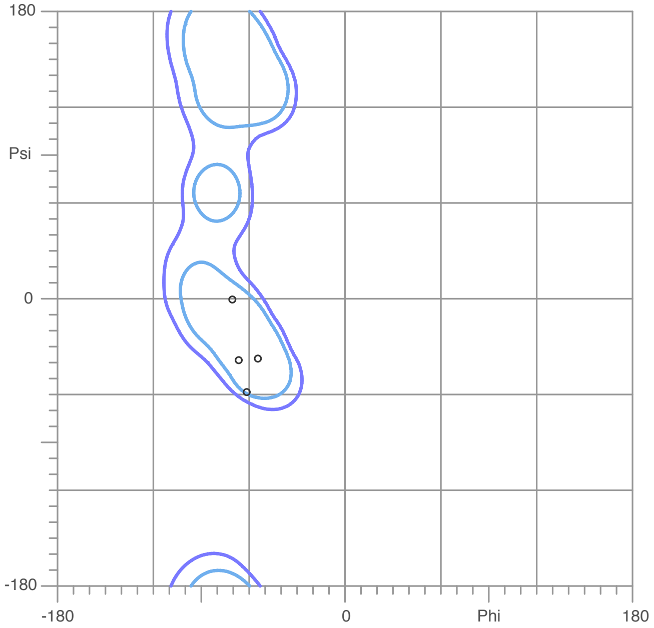
General case



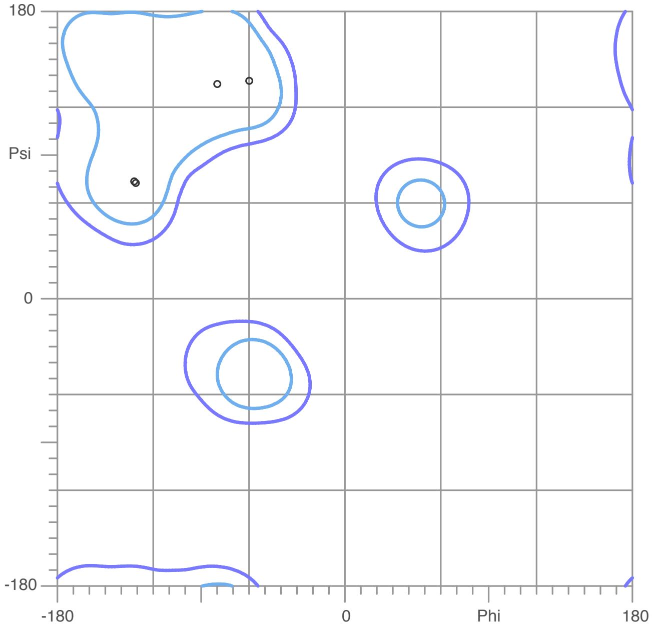
Glycine



Proline



Pre-proline



93.3% (111/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[12] 19 LYS (-161.3, -36.8)

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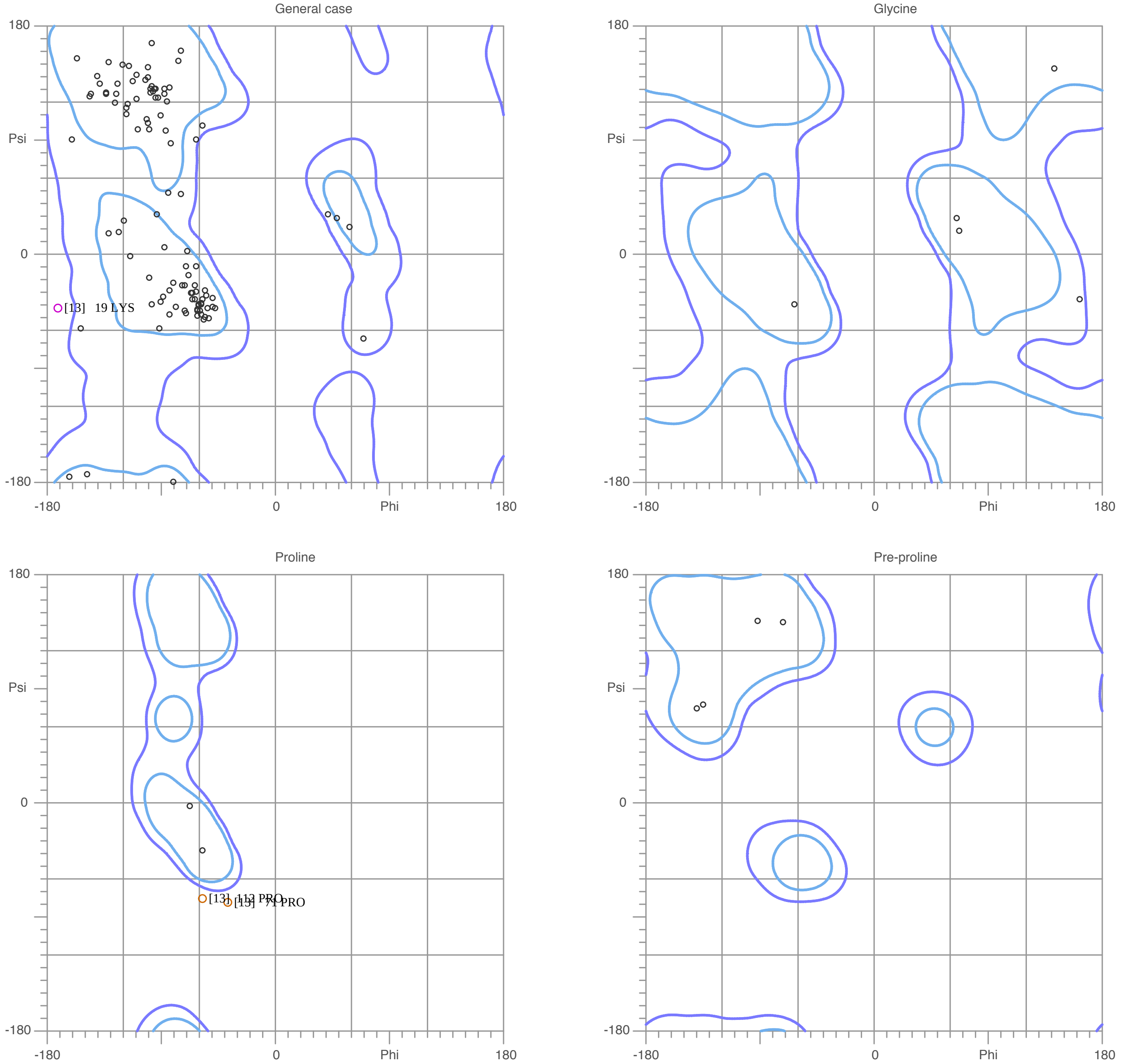
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 13

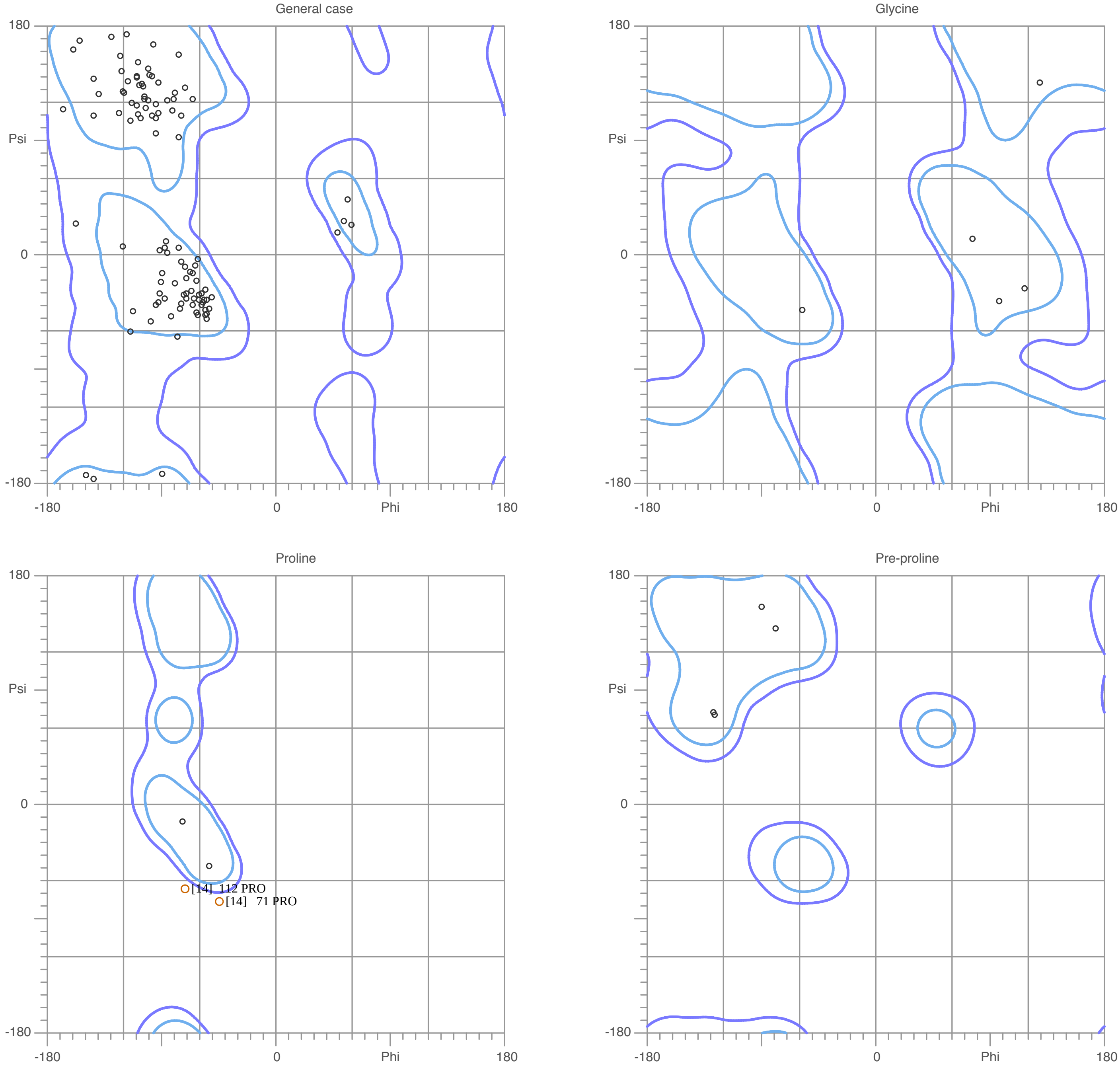


89.9% (107/119) of all residues were in favored (98%) regions.
97.5% (116/119) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[13] 19 LYS (-172.4, -43.0)
[13] 71 PRO (-38.6, -78.2)
[13] 112 PRO (-58.3, -76.0)

MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 14

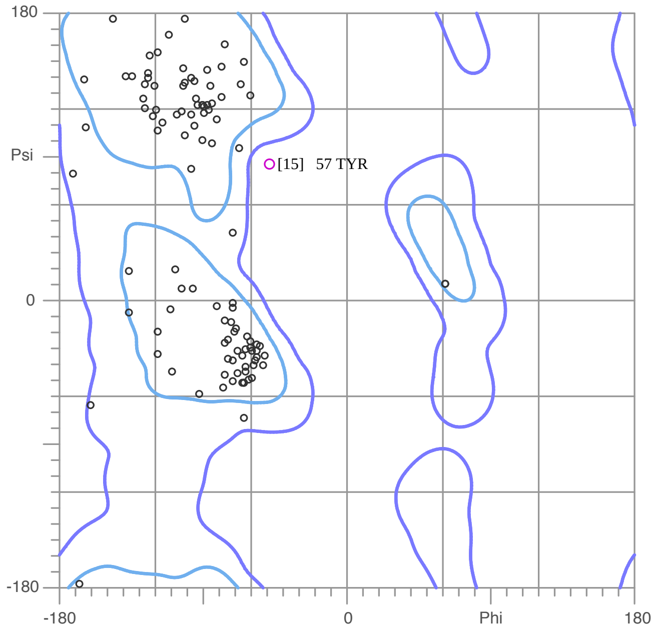


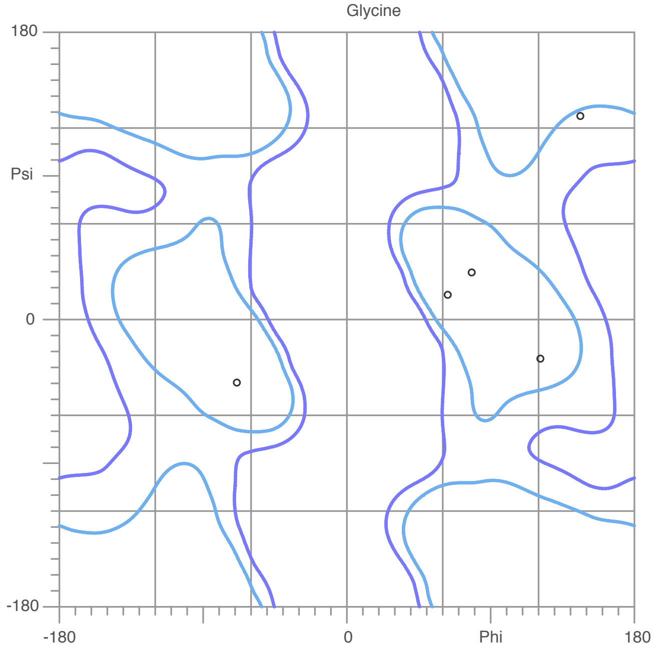
94.1% (112/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

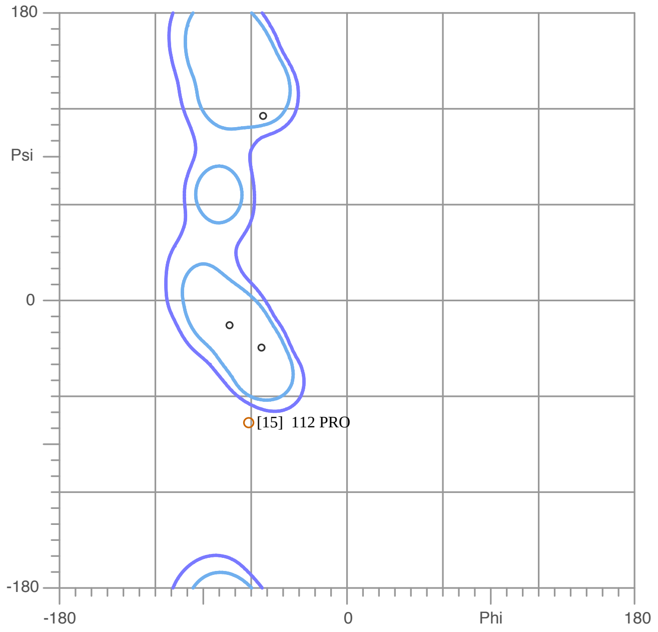
There were 2 outliers (phi, psi):
[14] 71 PRO (-45.2, -76.8)
[14] 112 PRO (-72.2, -67.0)

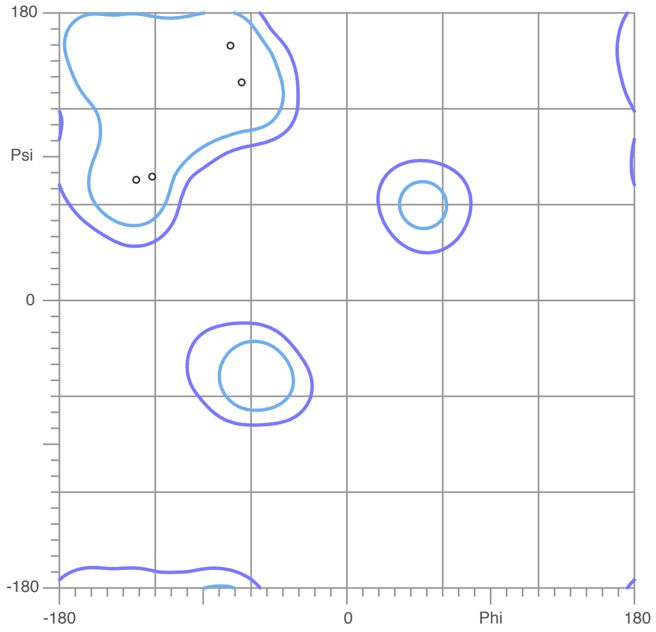
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 15


General case


Glycine


Proline

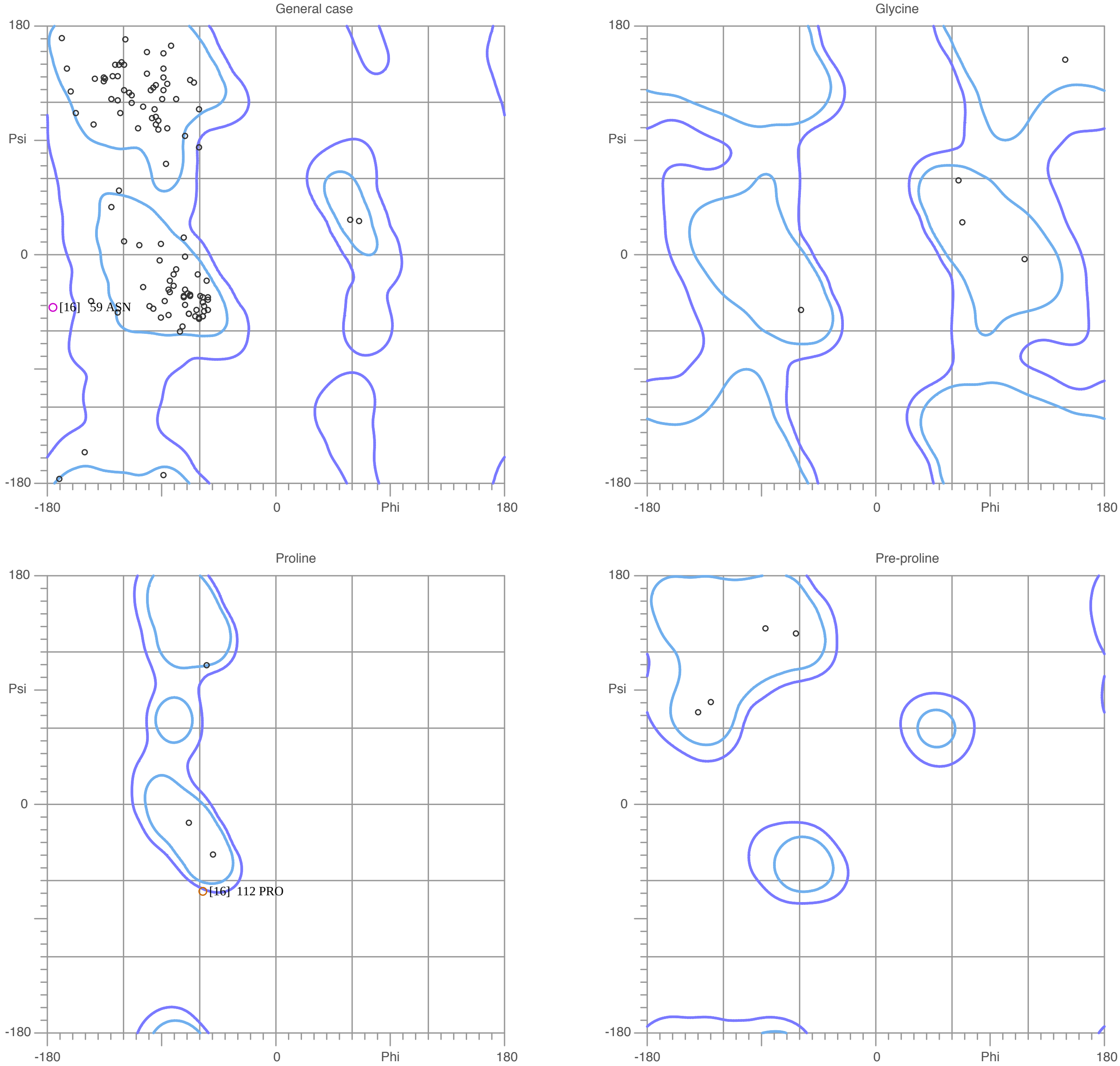

Pre-proline

91.6% (109/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[15] 57 TYR (-50.0, 86.1)
[15] 112 PRO (-62.1, -76.9)

MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 16



93.3% (111/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[16] 59 ASN (-176.0, -41.3)
[16] 112 PRO (-58.0, -68.5)

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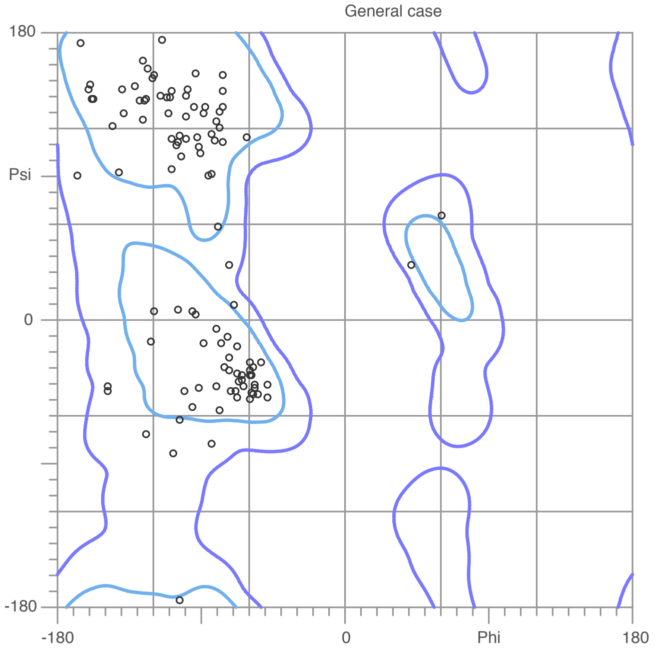
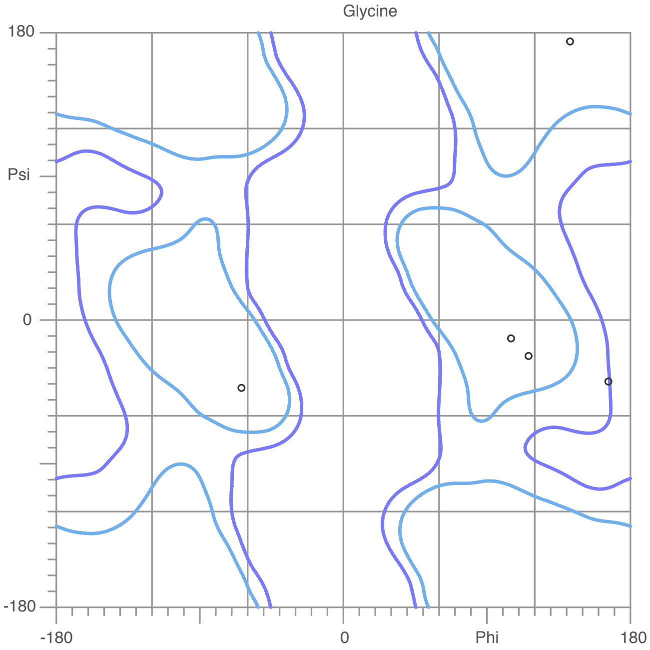
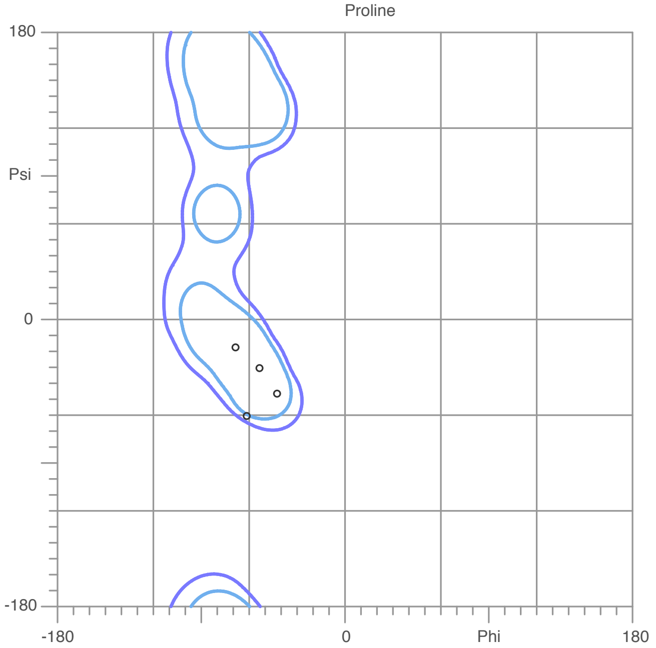
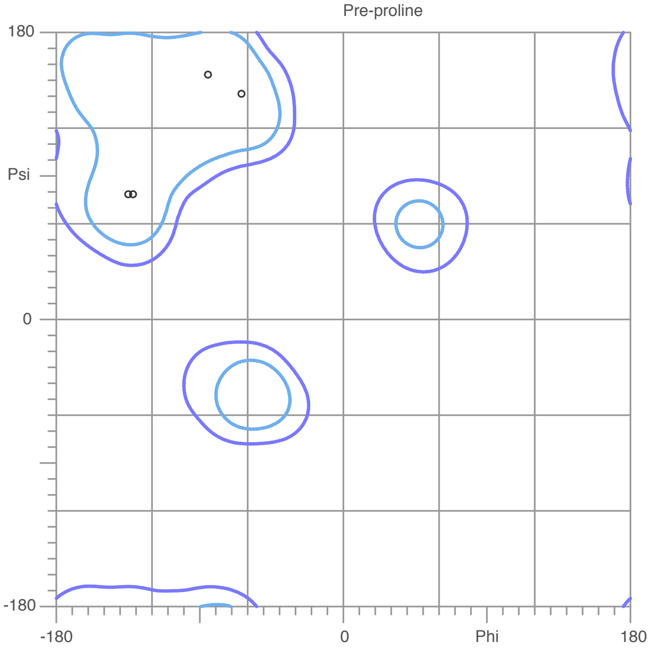
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 17









89.1% (106/119) of all residues were in favored (98%) regions.
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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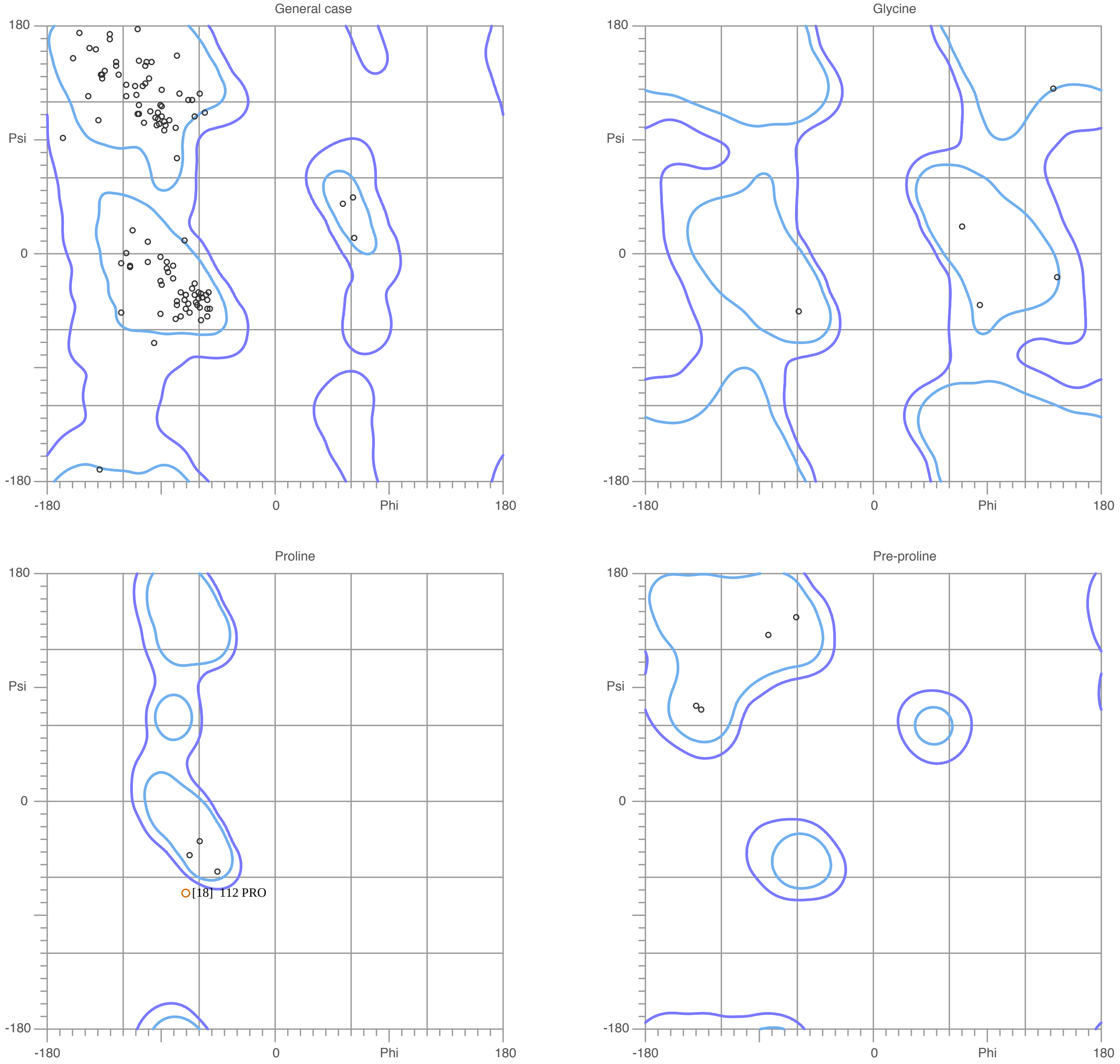
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 18



95.8% (114/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[18] 112 PRO (-71.9, -72.7)

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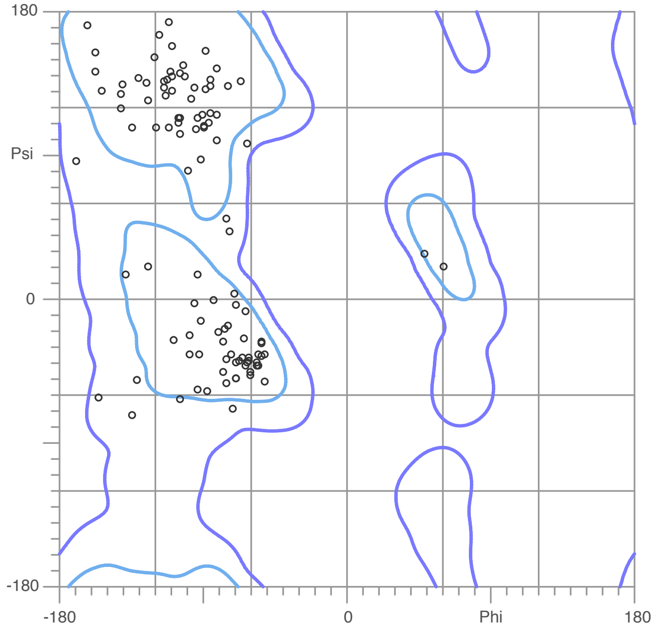
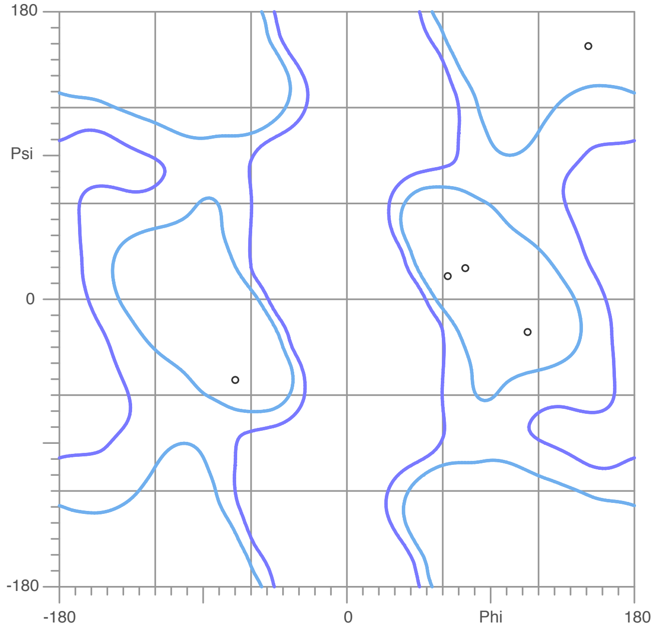
MolProbity Ramachandran analysis

UUR17A_NMR_em_bcr3.pdb, model 19

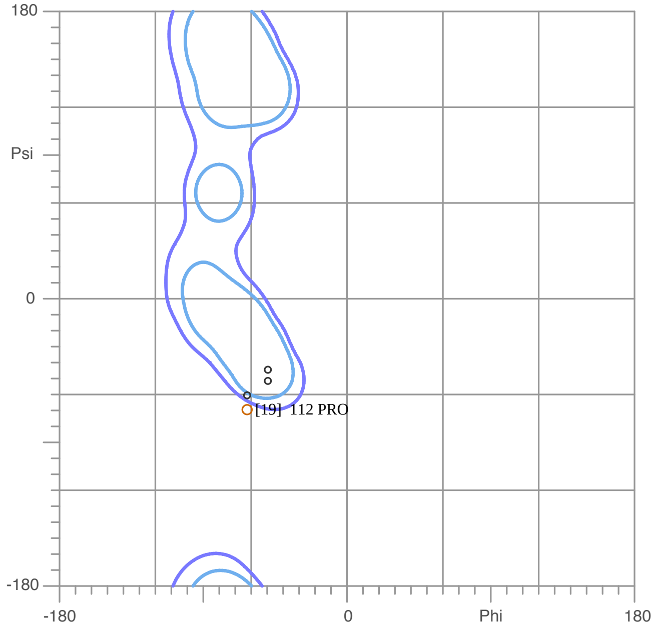
General case



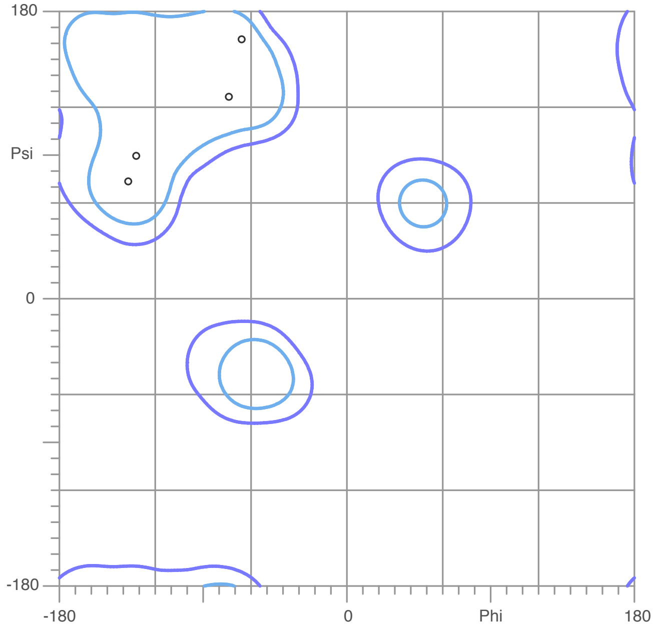
Glycine



Proline



Pre-proline



90.8% (108/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[19] 112 PRO (-63.8, -69.3)

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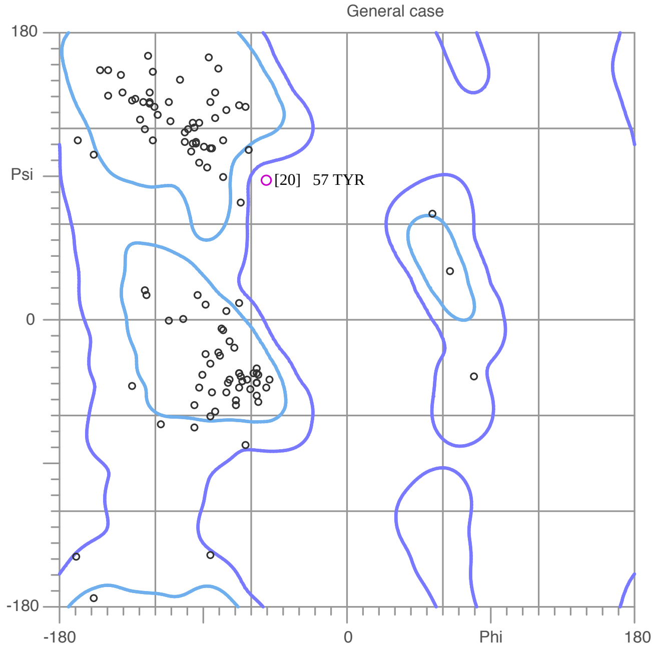
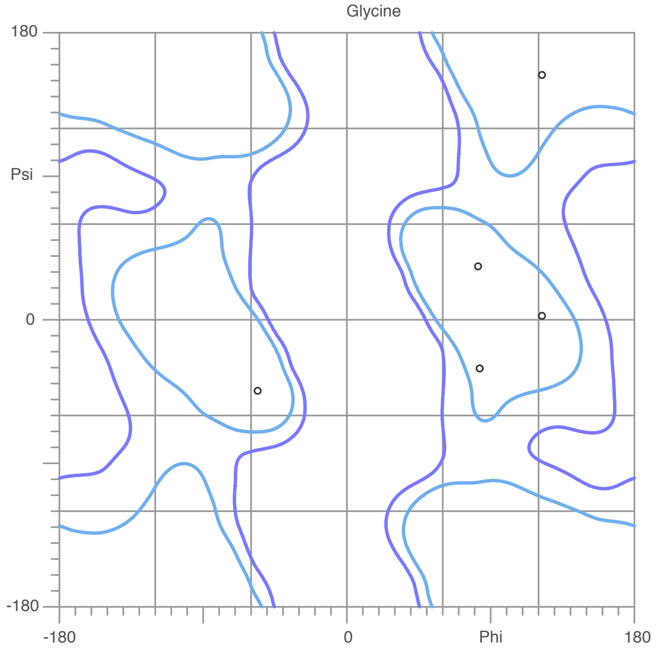
MolProbity Ramachandran analysis

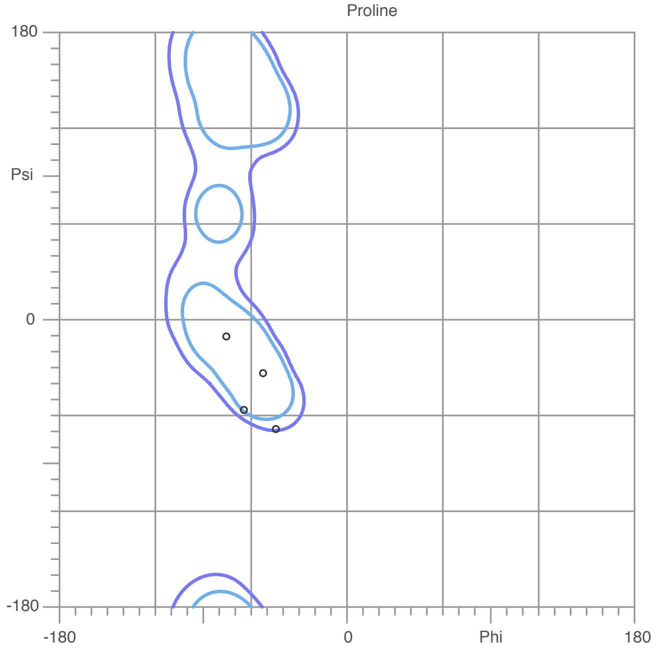
UUR17A_NMR_em_bcr3.pdb, model 20



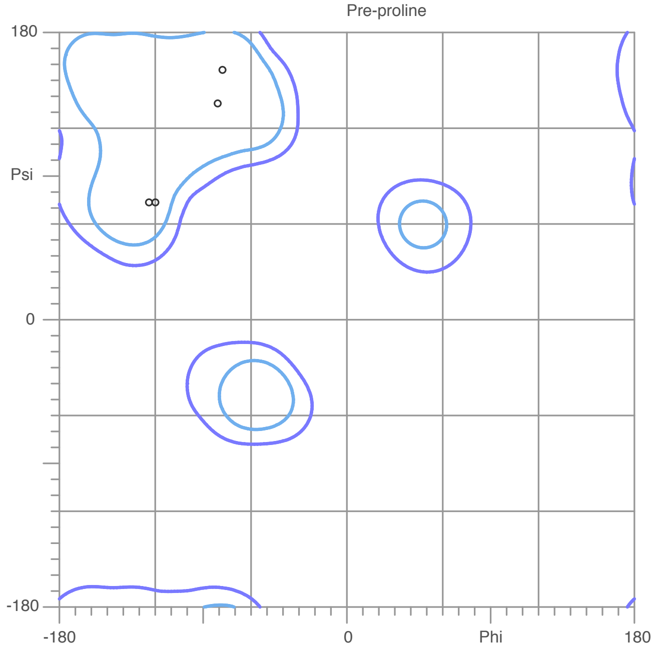
General case



Glycine



Proline



Pre-proline

86.6% (103/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 57 TYR (-51.7, 88.8)

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