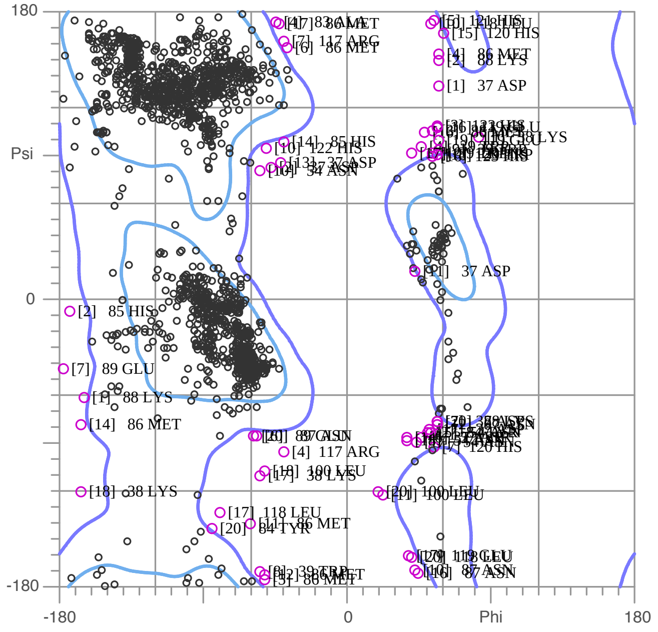
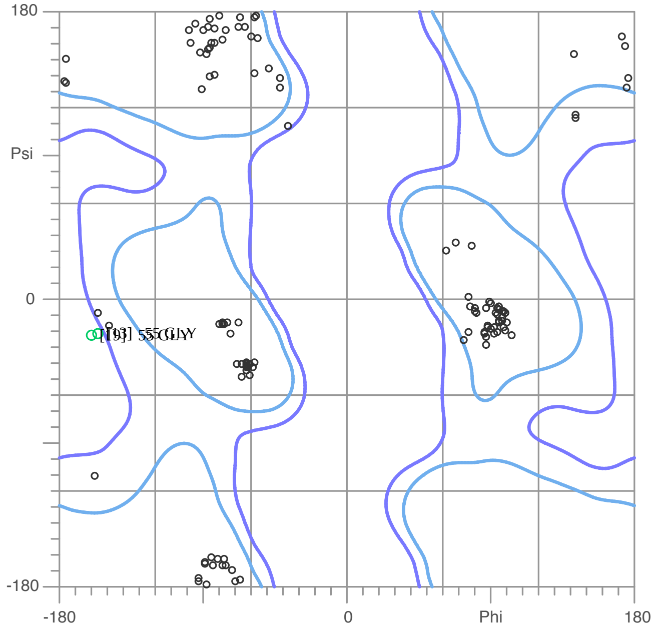
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, all models

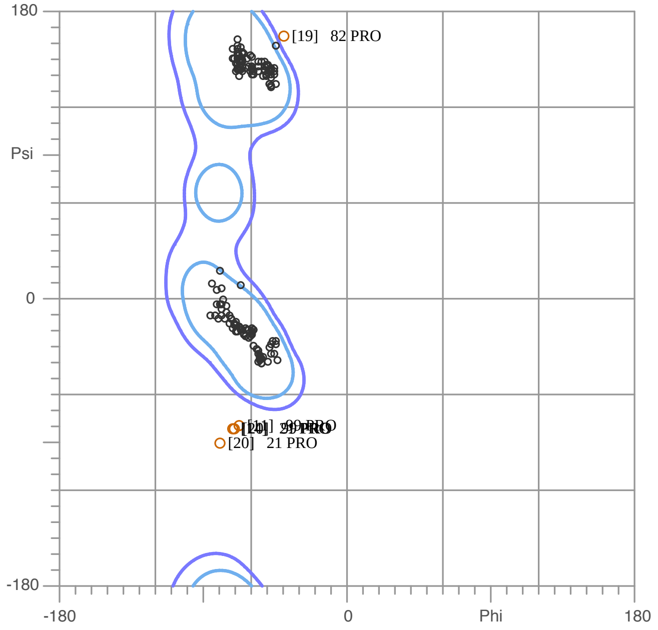
General case



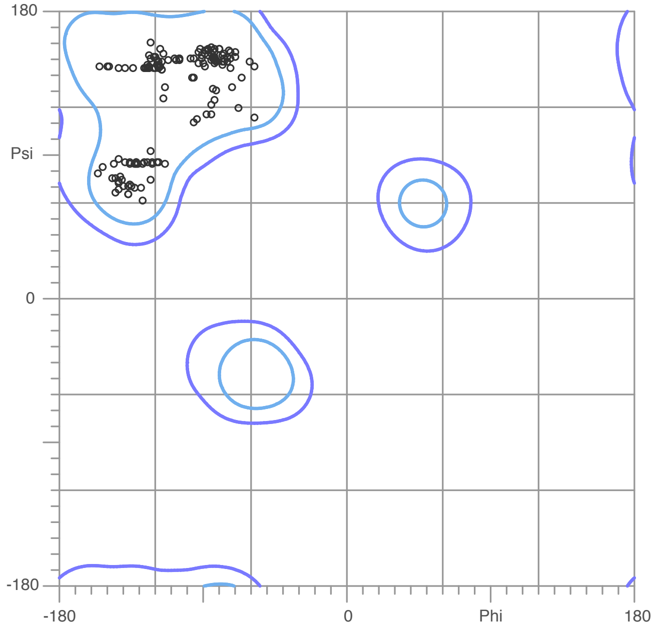
Glycine



Proline



Pre-proline

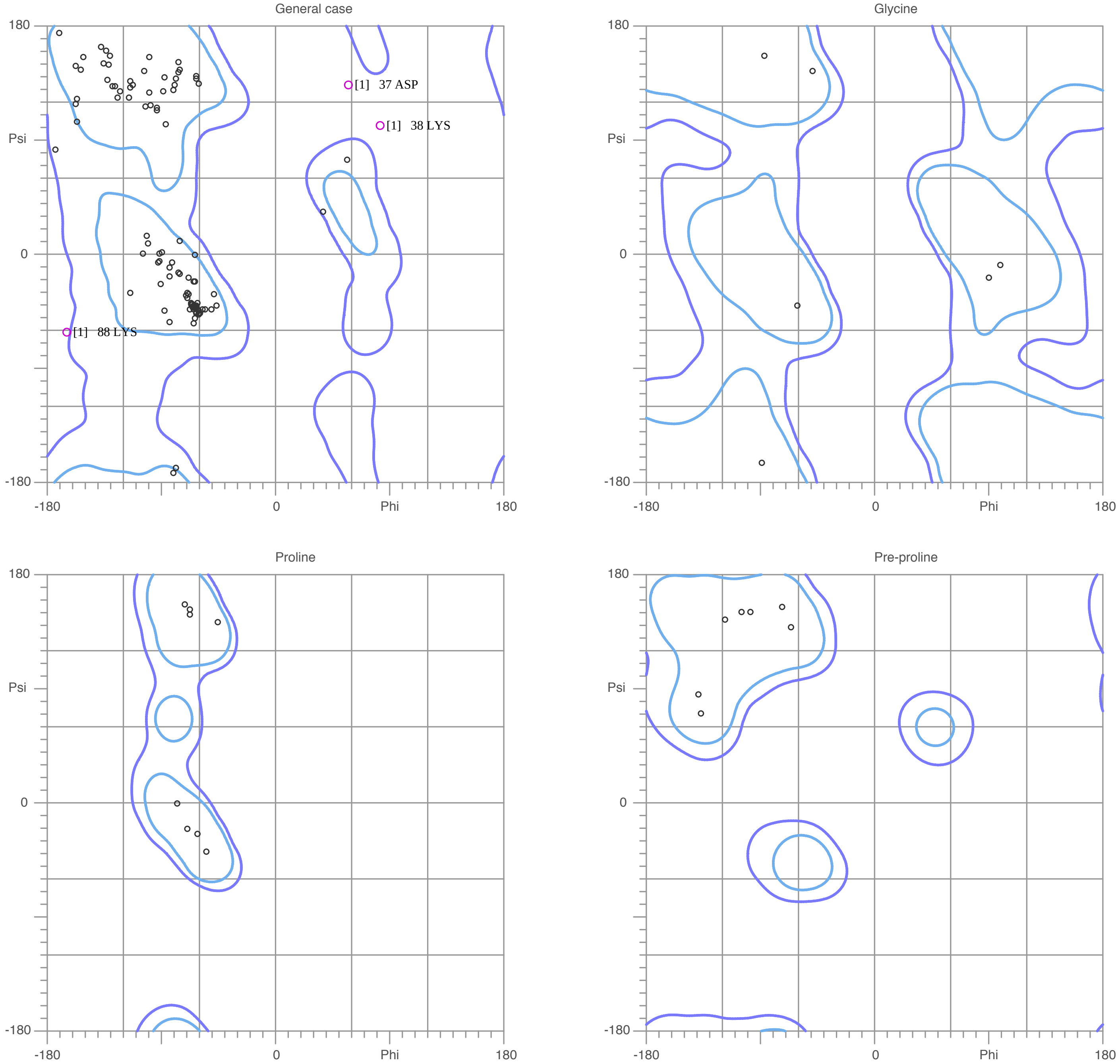


92.4% (2274/2460) of all residues were in favored (98%) regions.
97.2% (2392/2460) of all residues were in allowed (>99.8%) regions.

There were 68 outliers (phi, psi):
[1] 37 ASP (57.7, 134.9)
[1] 38 LYS (82.4, 102.2)
[1] 88 LYS (-165.3, -61.1)
[2] 37 ASP (-48.4, 83.5)
[2] 84 TYR (50.8, -83.5)
[2] 85 HIS (-175.0, -7.7)
[2] 88 LYS (57.9, 150.1)
[3] 38 LYS (53.2, 106.1)
[3] 122 HIS (56.3, 109.2)
[4] 39 TRP (46.5, 96.2)
[4] 83 ALA (-46.0, 174.2)
[4] 86 MET (57.6, 154.1)
[4] 117 ARG (-40.8, -95.6)
[5] 54 ASN (52.8, -83.1)
[5] 86 MET (-52.8, -175.3)
[5] 121 HIS (54.5, 175.4)
[6] 37 ASP (46.7, -86.2)
[6] 86 MET (-38.1, 158.9)
[6] 89 GLU (-57.8, -85.1)
[7] 37 ASP (56.8, -76.8)
[7] 89 GLU (-178.8, -43.4)
[7] 117 ARG (-40.2, 162.1)
[7] 120 HIS (54.3, -92.7)
[8] 39 TRP (-55.6, -170.5)
[9] 39 TRP (57.2, 95.0)
[10] 54 ASN (-55.9, 81.8)
[10] 87 ASN (42.3, -169.9)
[10] 118 LEU (52.7, 173.7)
[10] 120 HIS (53.3, 92.4)
[10] 122 HIS (-51.5, 95.0)
[11] 37 ASP (42.7, 18.1)
[11] 86 MET (-61.6, -140.9)
[11] 99 PRO (-68.0, -79.9)
[11] 100 LEU (22.9, -122.0)
[12] 86 MET (-52.1, -172.9)
[12] 87 ASN (56.3, -78.7)
[13] 37 ASP (-42.5, 87.0)
[13] 55 GLY (-156.9, -21.9)
[14] 21 PRO (-72.3, -81.1)
[14] 37 ASP (37.2, -86.9)
[14] 85 HIS (-40.8, 99.4)
[14] 86 MET (-167.7, -78.2)
[15] 120 HIS (60.3, 167.1)
[16] 86 MET (48.6, 105.7)
[16] 87 ASN (44.0, -171.3)
[16] 119 GLU (56.9, 108.7)
[16] 123 HIS (53.2, 90.7)
[17] 37 ASP (51.3, -81.4)
[17] 38 LYS (-55.9, -110.1)
[17] 39 TRP (40.8, 92.1)
[17] 54 ASN (43.0, -89.2)
[17] 86 MET (-43.7, 173.5)
[17] 118 LEU (-80.8, -133.5)
[17] 119 GLU (38.8, -160.7)
[18] 38 LYS (-167.7, -120.3)
[18] 39 TRP (56.2, 91.6)
[18] 54 ASN (37.2, -88.9)
[18] 100 LEU (-52.6, -108.0)
[19] 55 GLY (-160.1, -22.5)
[19] 82 PRO (-40.6, 165.2)
[19] 119 GLU (57.2, 100.6)
[20] 21 PRO (-80.2, -90.2)
[20] 84 TYR (-85.1, -143.0)
[20] 87 ASN (-59.6, -85.9)
[20] 88 LYS (56.9, -76.7)
[20] 99 PRO (-71.6, -81.2)
[20] 100 LEU (19.2, -120.7)
[20] 118 LEU (40.0, -161.6)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 1



93.5% (115/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[1] 37 ASP (57.7, 134.9)
[1] 38 LYS (82.4, 102.2)
[1] 88 LYS (-165.3, -61.1)

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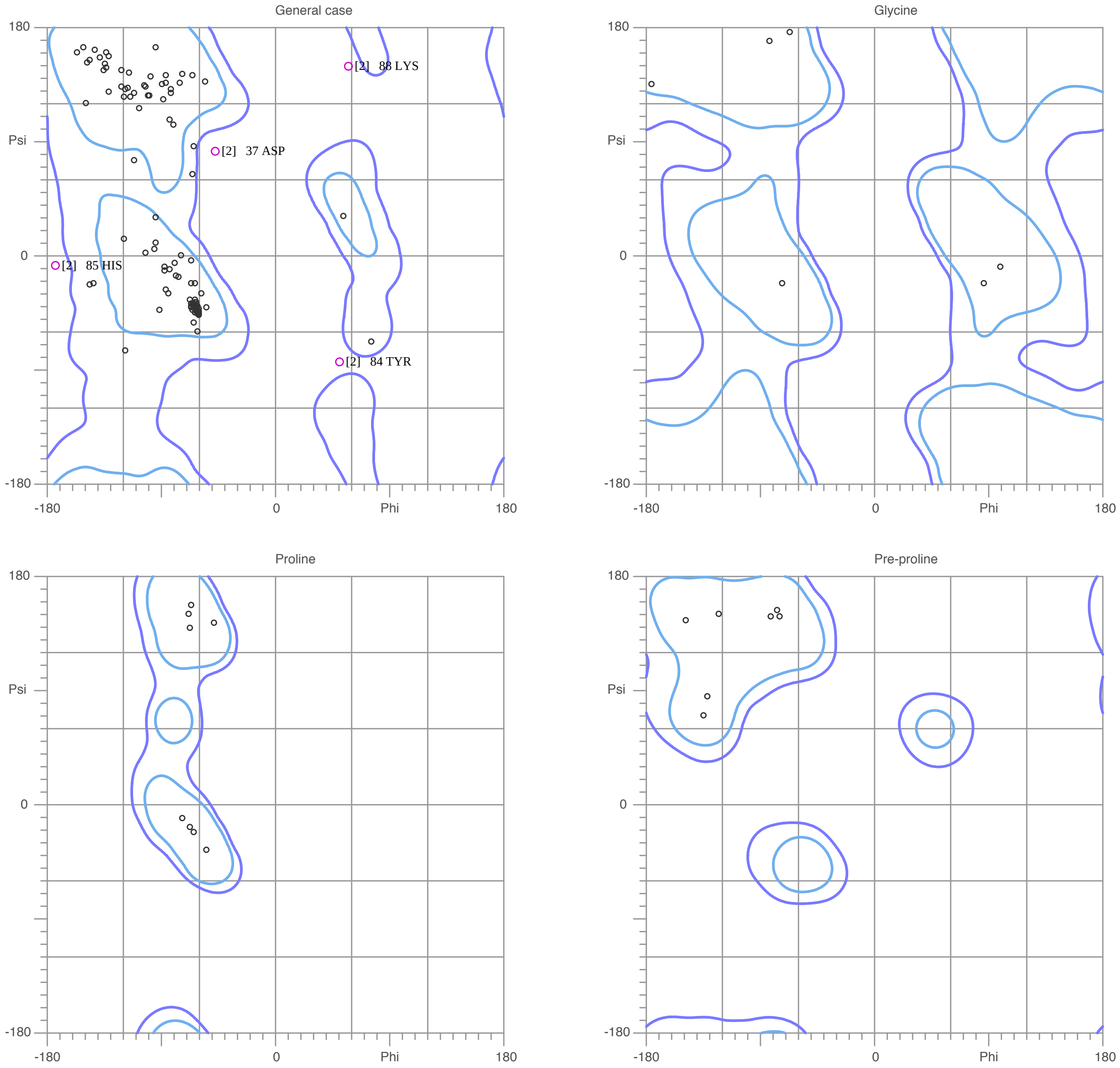
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 2



91.1% (112/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[2] 37 ASP (-48.4, 83.5)
[2] 84 TYR (50.8, -83.5)
[2] 85 HIS (-175.0, -7.7)
[2] 88 LYS (57.9, 150.1)

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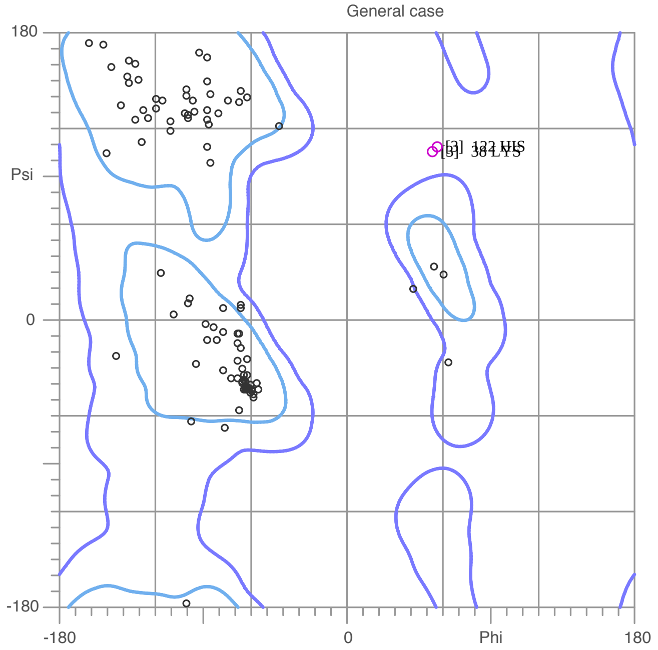
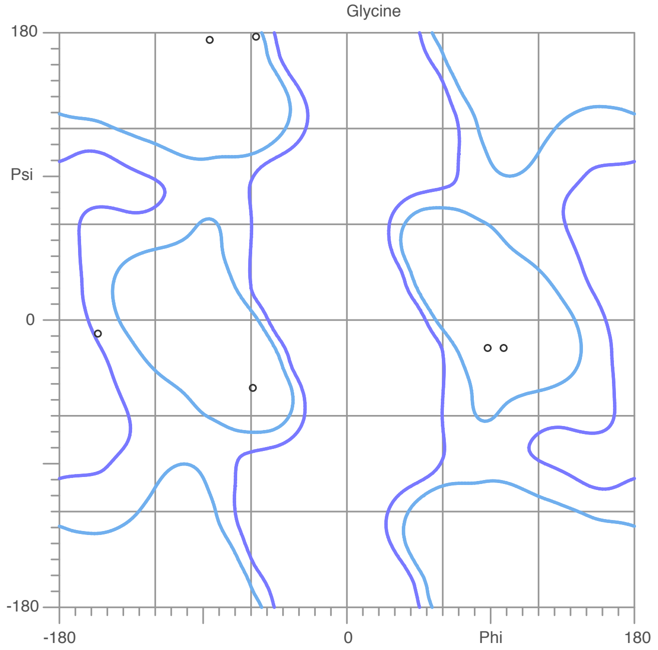
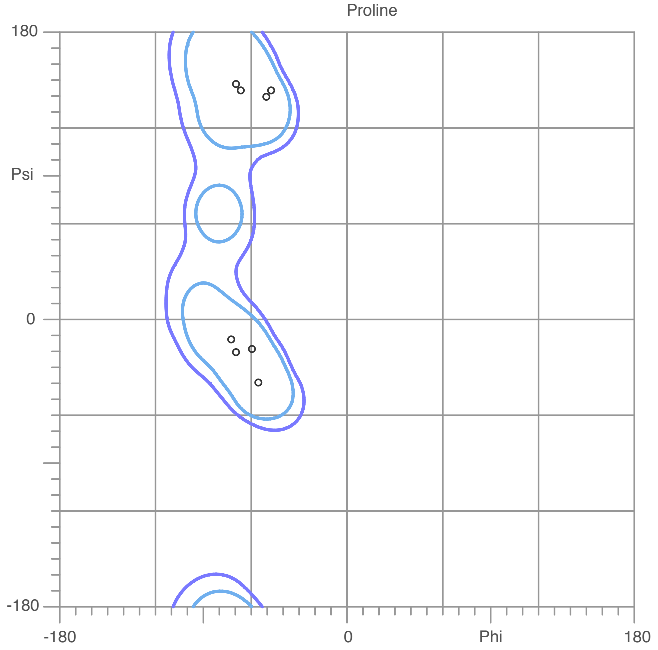
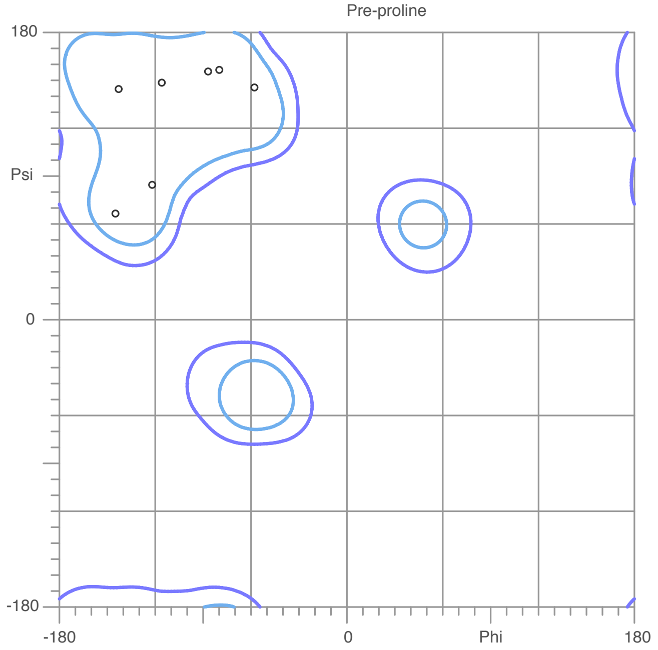
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 3







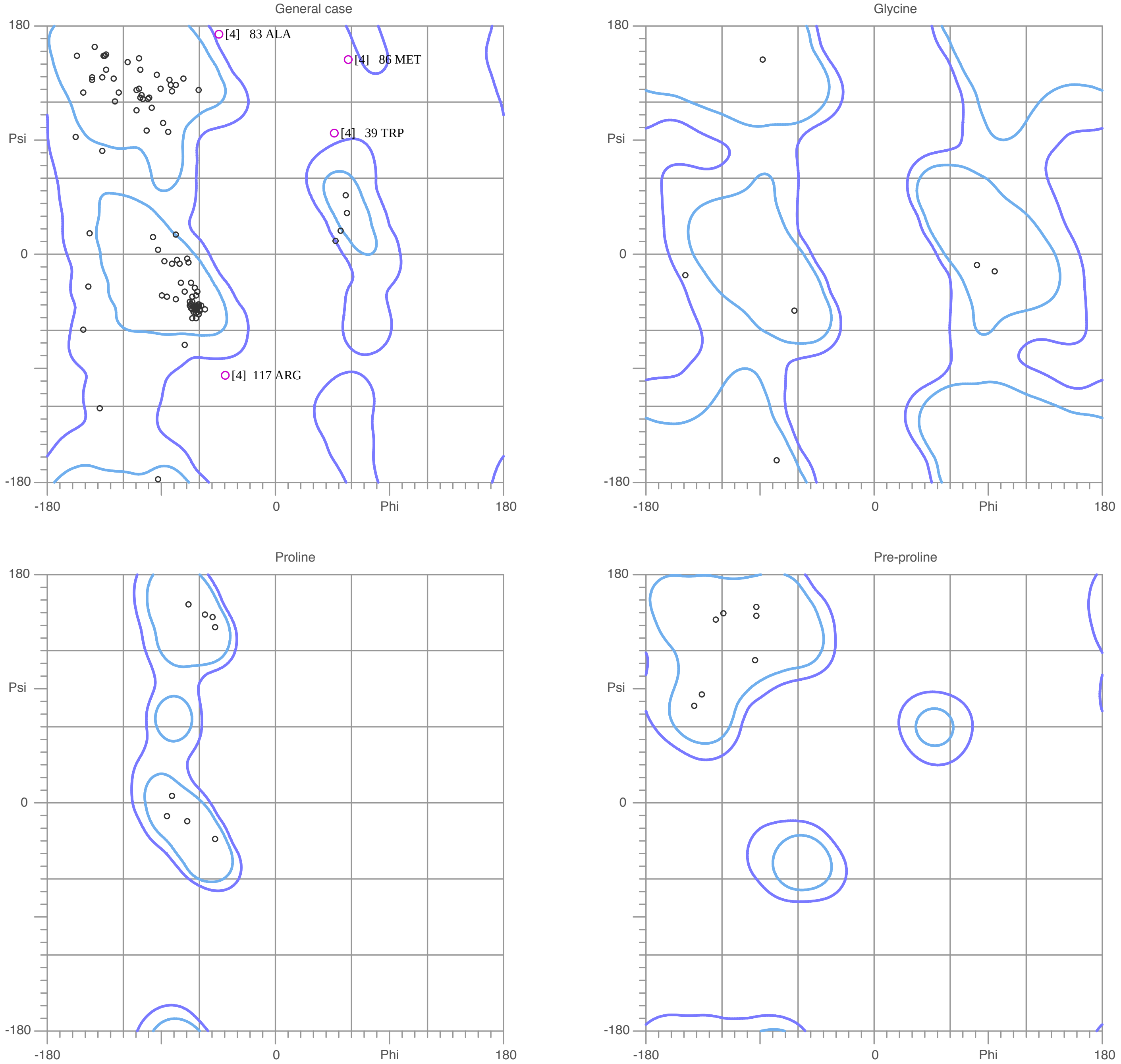


91.9% (113/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[3] 38 LYS (53.2, 106.1)
[3] 122 HIS (56.3, 109.2)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 4



87.8% (108/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
- [4] 39 TRP (46.5, 96.2)
- [4] 83 ALA (-46.0, 174.2)
- [4] 86 MET (57.6, 154.1)
- [4] 117 ARG (-40.8, -95.6)

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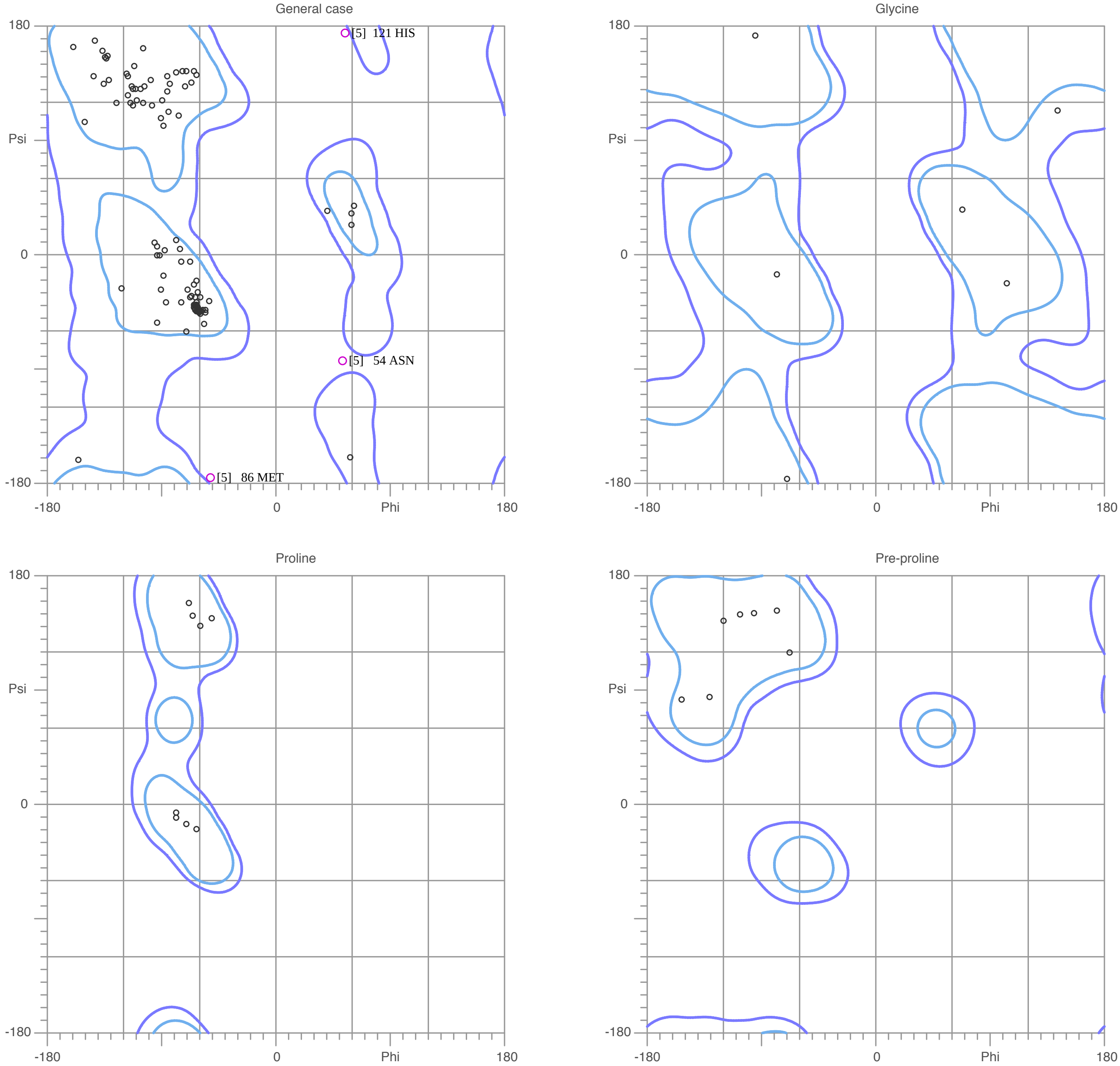
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 5



94.3% (116/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[5] 54 ASN (52.8, -83.1)
[5] 86 MET (-52.8, -175.3)
[5] 121 HIS (54.5, 175.4)

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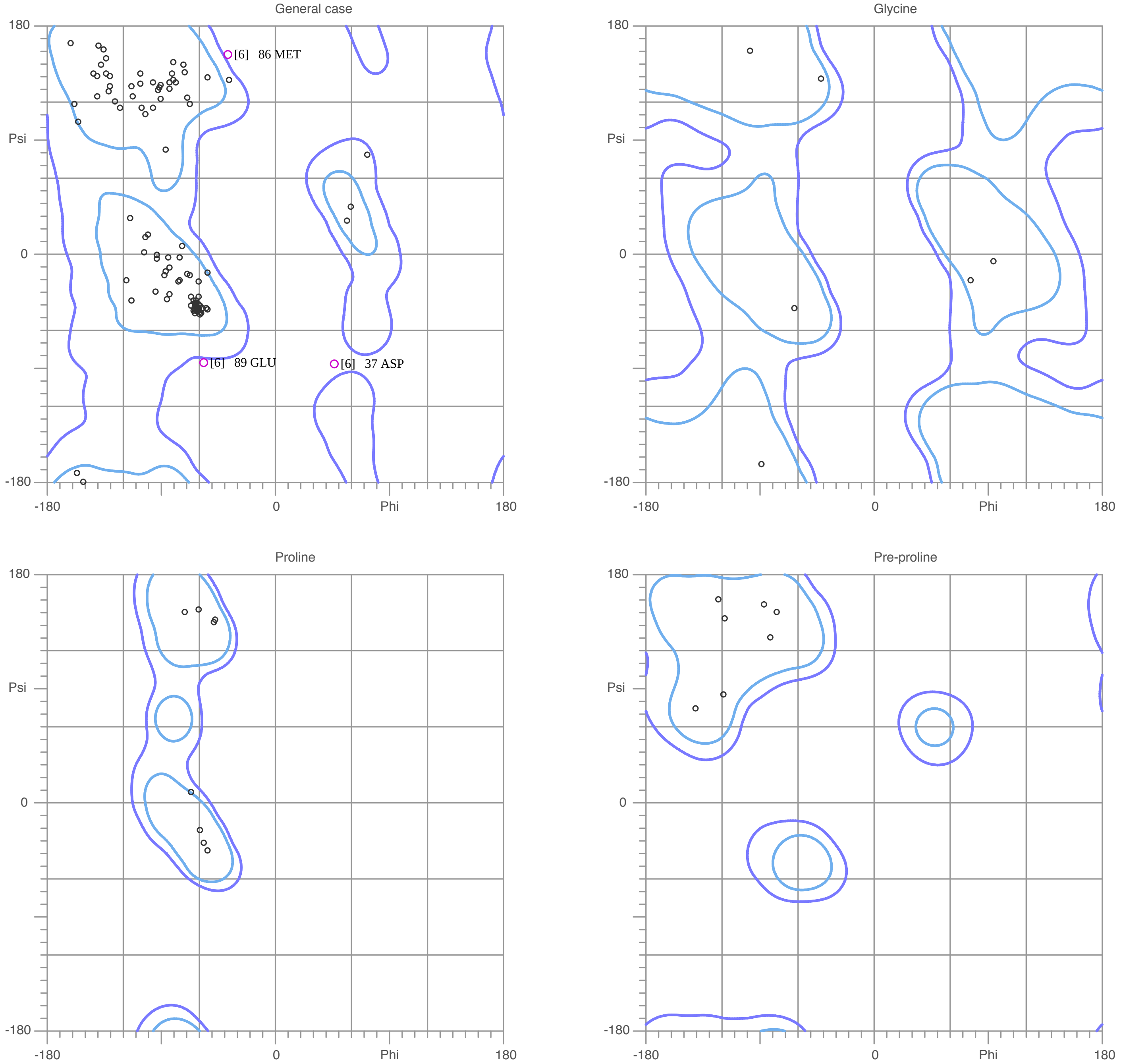
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 6



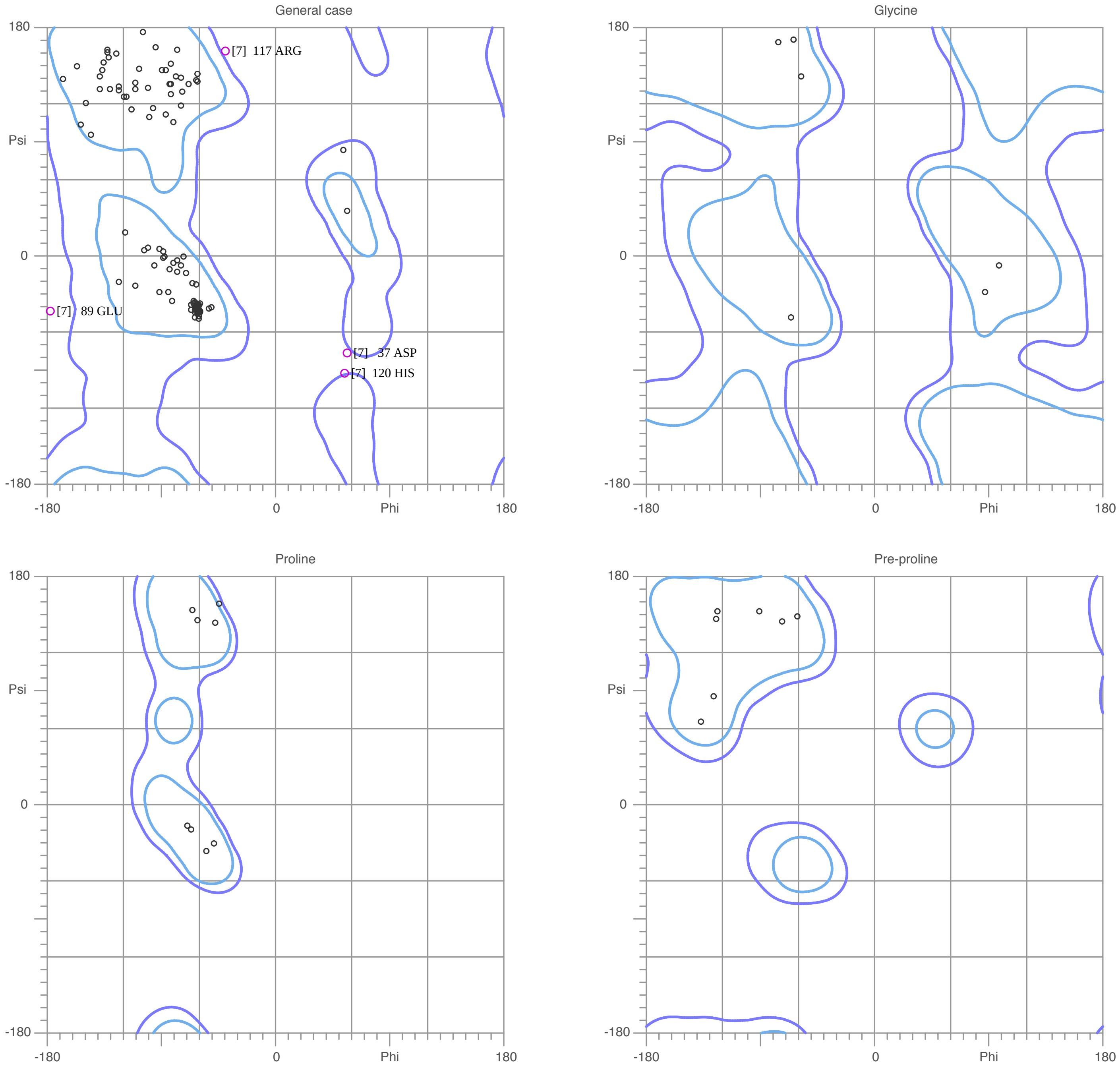
94.3% (116/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[6] 37 ASP (46.7, -86.2)
[6] 86 MET (-38.1, 158.9)
[6] 89 GLU (-57.8, -85.1)

MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 7



95.1% (117/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[7] 37 ASP (56.8, -76.8)
[7] 89 GLU (-178.8, -43.4)
[7] 117 ARG (-40.2, 162.1)
[7] 120 HIS (54.3, -92.7)

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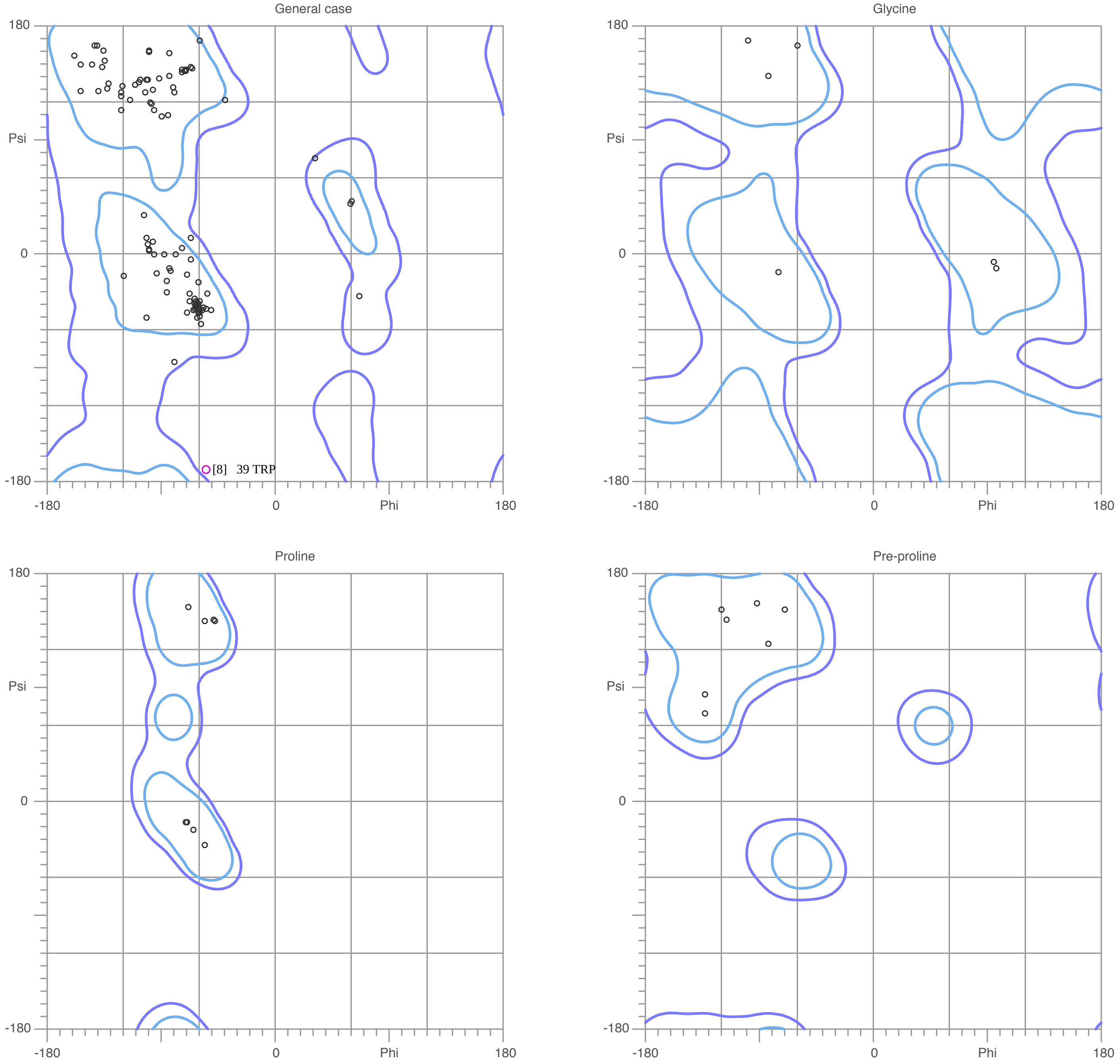
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 8



95.1% (117/123) of all residues were in favored (98%) regions.
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 39 TRP (-55.6, -170.5)

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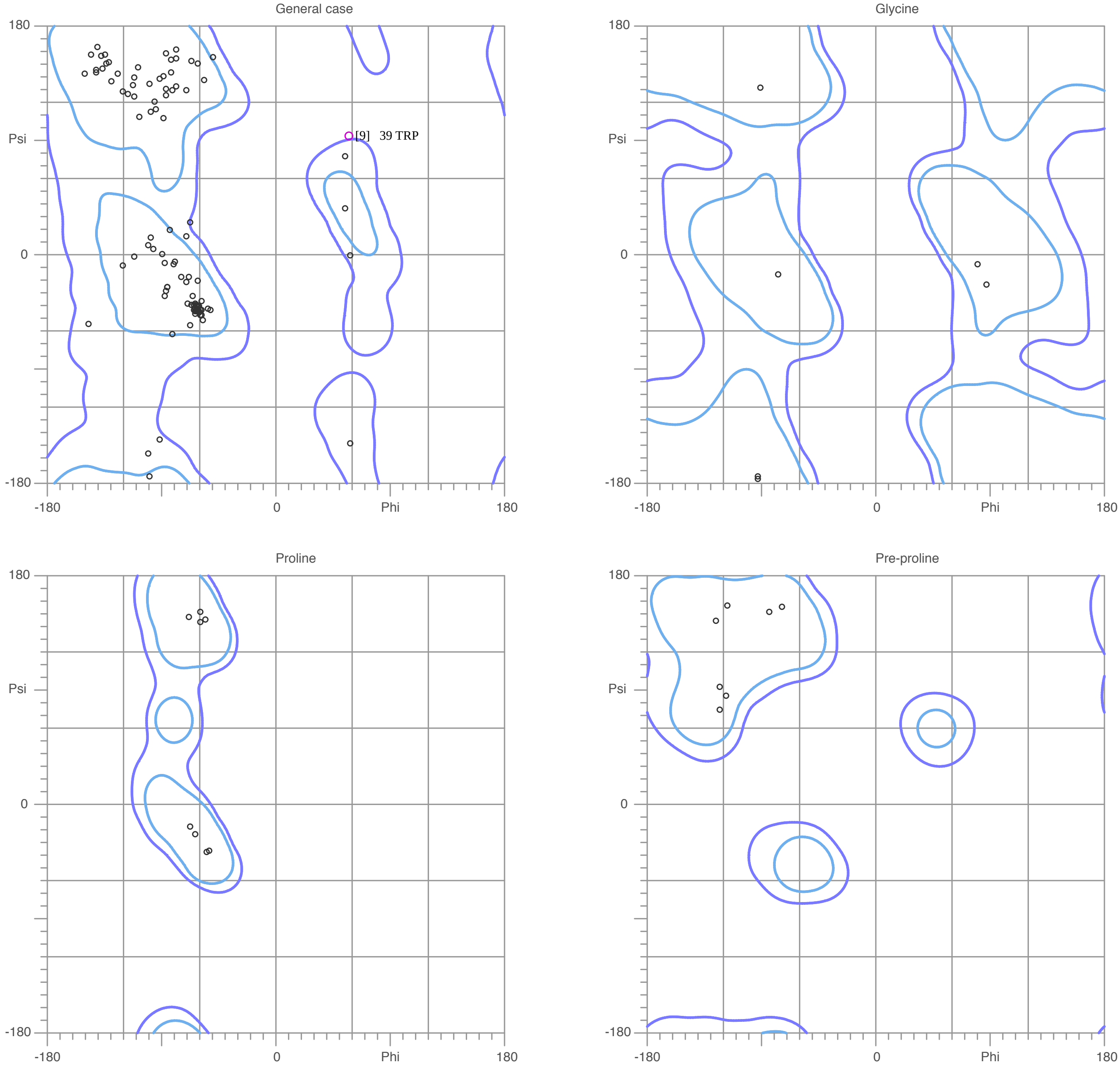
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 9



91.9% (113/123) of all residues were in favored (98%) regions.
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 39 TRP (57.2, 95.0)

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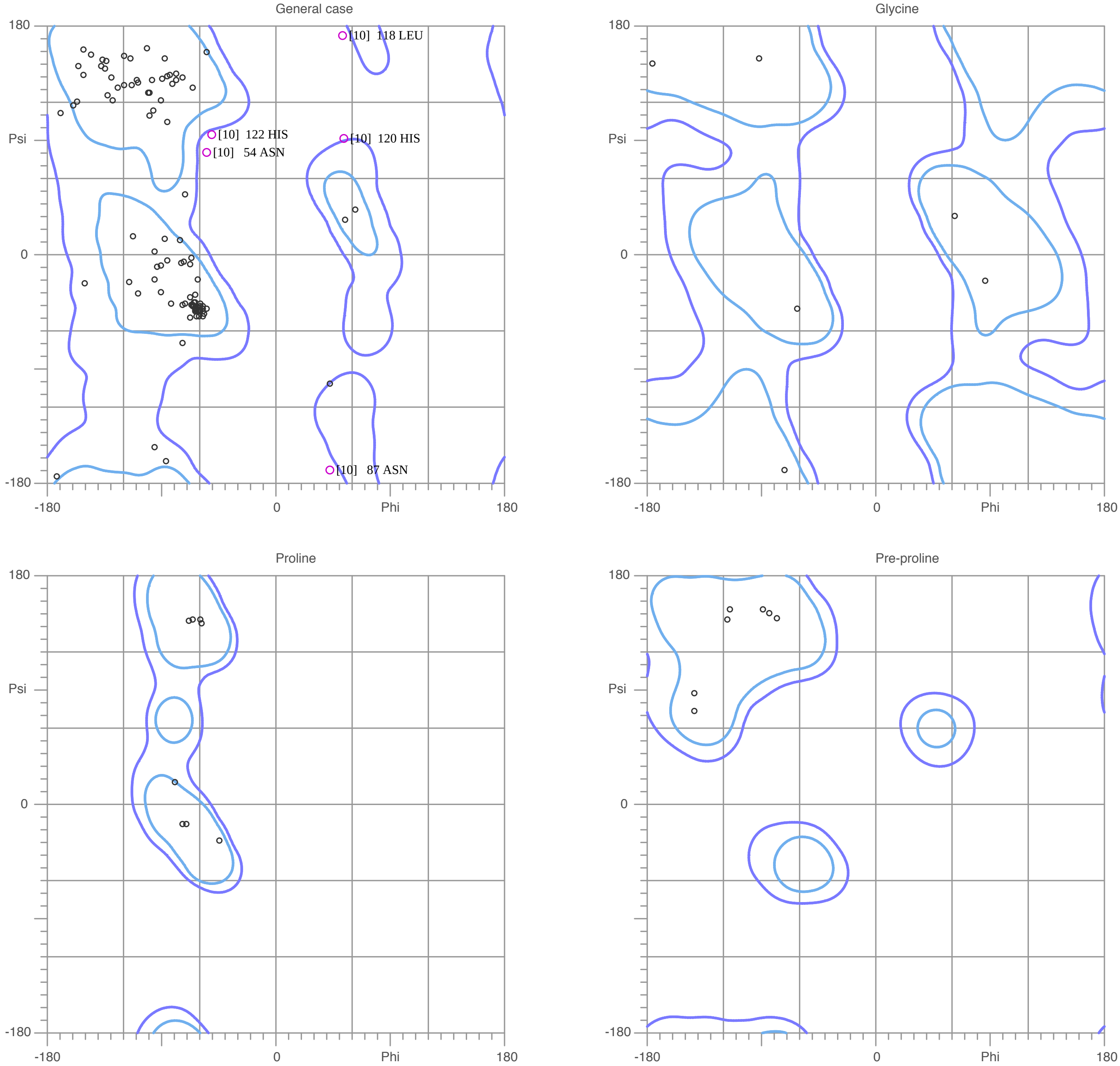
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 10



89.4% (110/123) of all residues were in favored (98%) regions.
95.9% (118/123) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[10] 54 ASN (-55.9, 81.8)
[10] 87 ASN (42.3, -169.9)
[10] 118 LEU (52.7, 173.7)
[10] 120 HIS (53.3, 92.4)
[10] 122 HIS (-51.5, 95.0)

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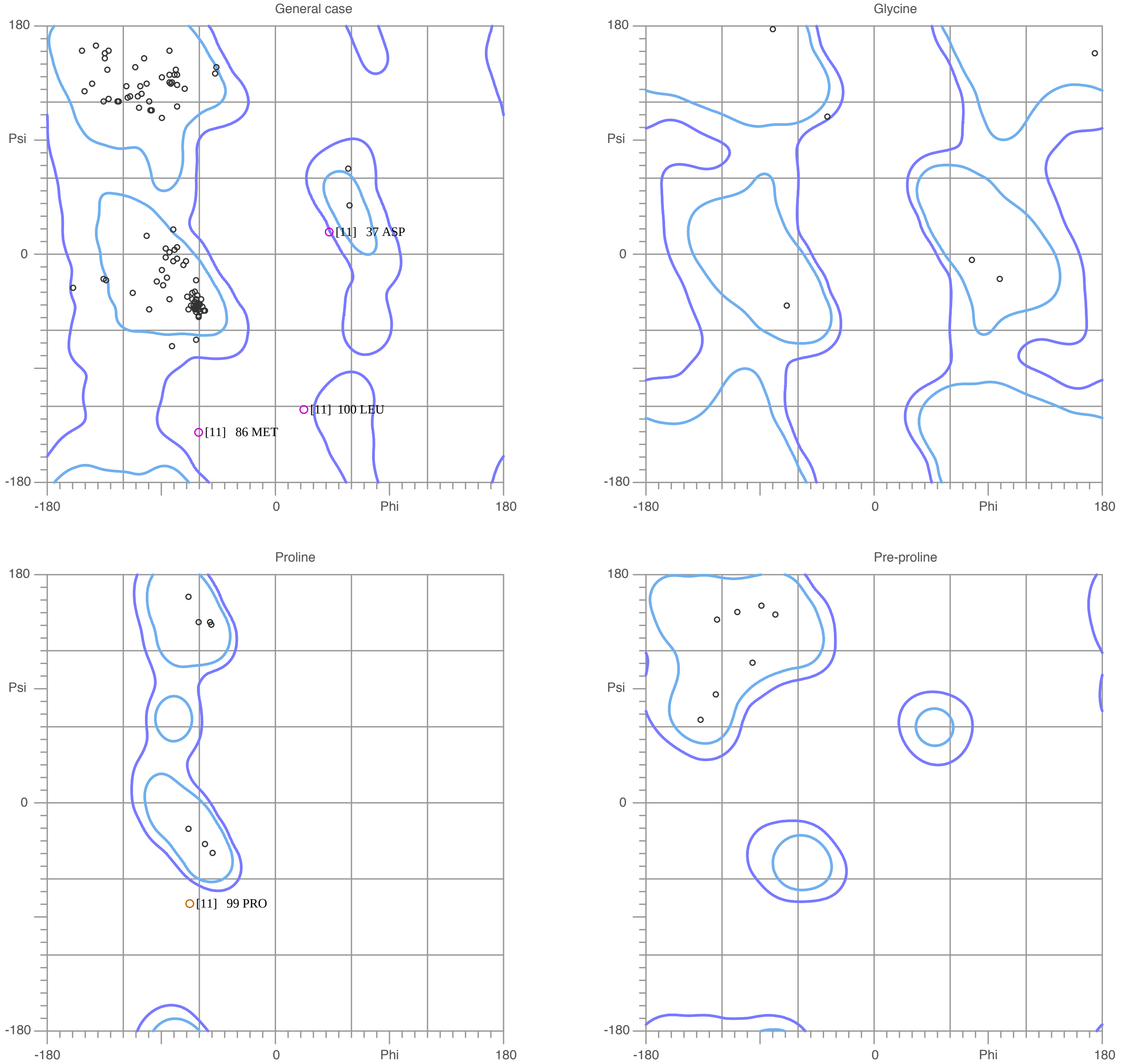
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 11



90.2% (111/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[11] 37 ASP (42.7, 18.1)
[11] 86 MET (-61.6, -140.9)
[11] 99 PRO (-68.0, -79.9)
[11] 100 LEU (22.9, -122.0)

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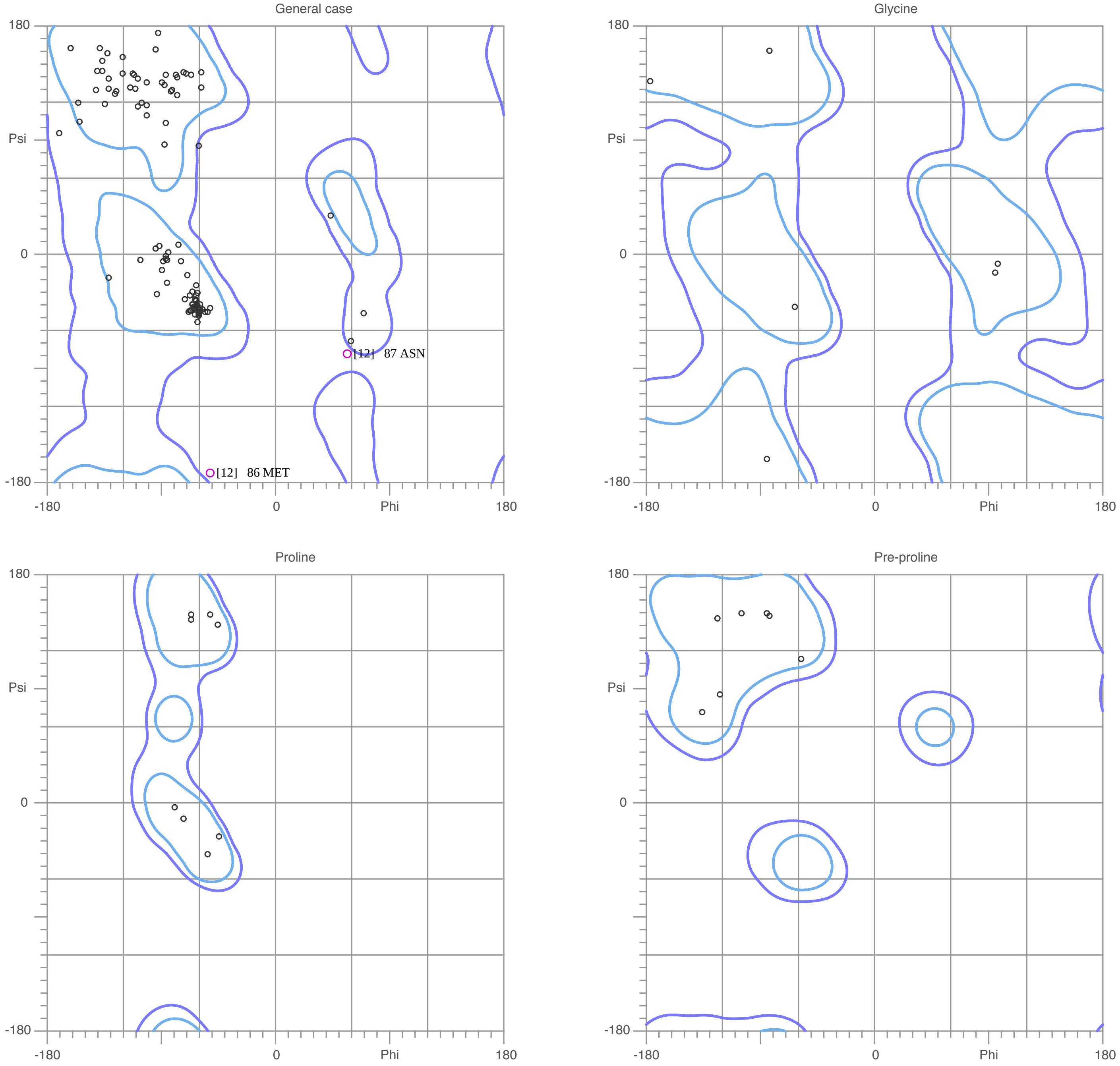
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 12



94.3% (116/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 86 MET (-52.1, -172.9)
[12] 87 ASN (56.3, -78.7)

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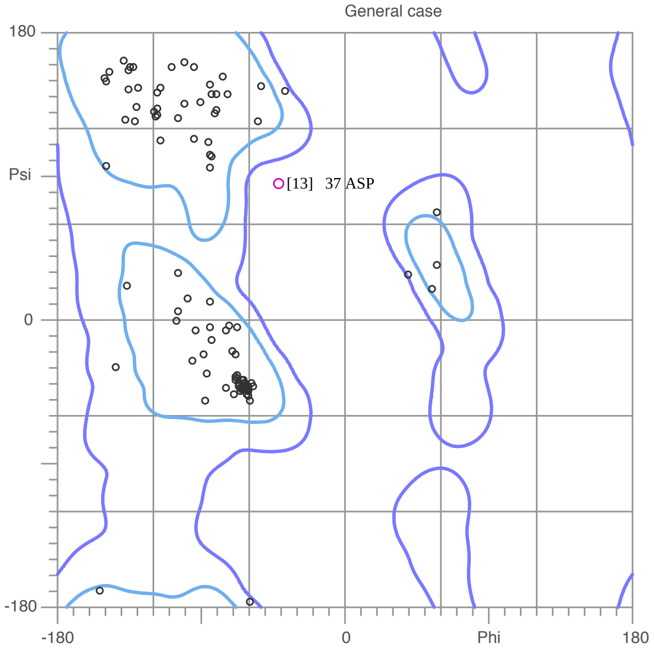
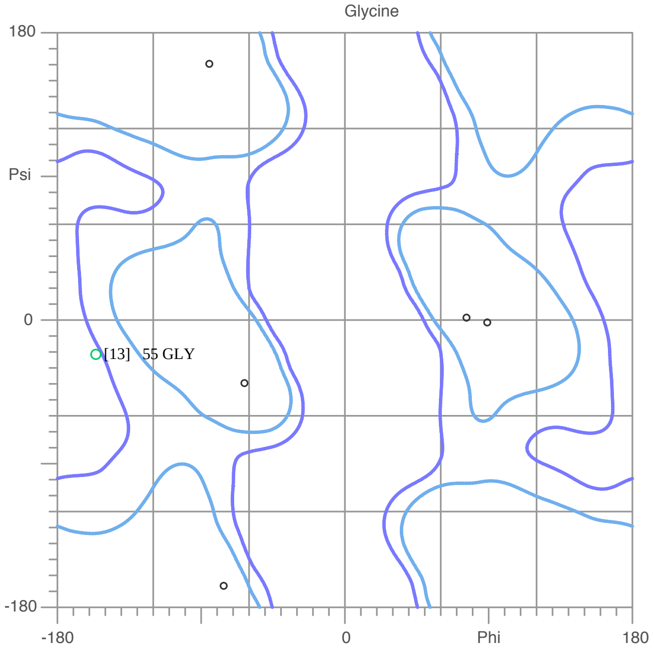
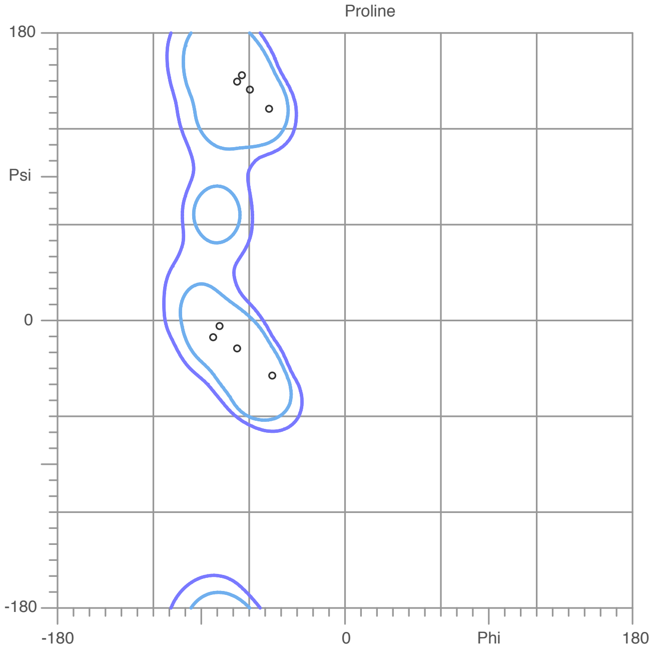
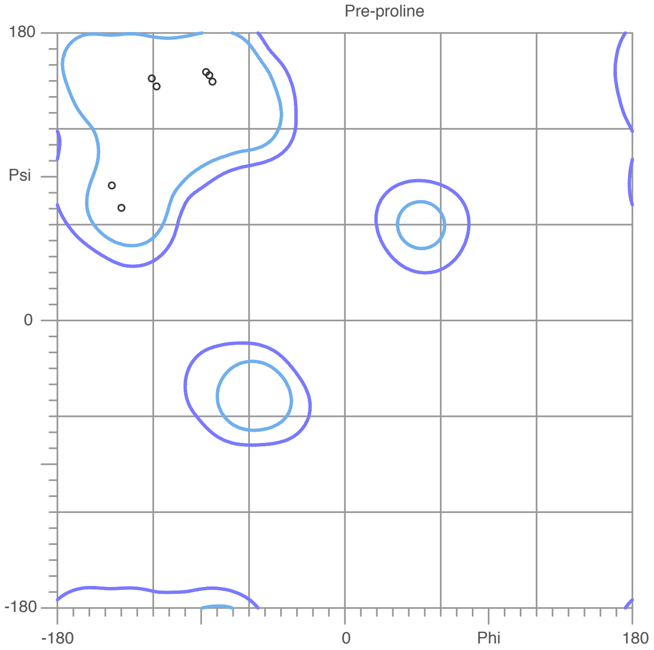
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 13









94.3% (116/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[13] 37 ASP (-42.5, 87.0)
[13] 55 GLY (-156.9, -21.9)

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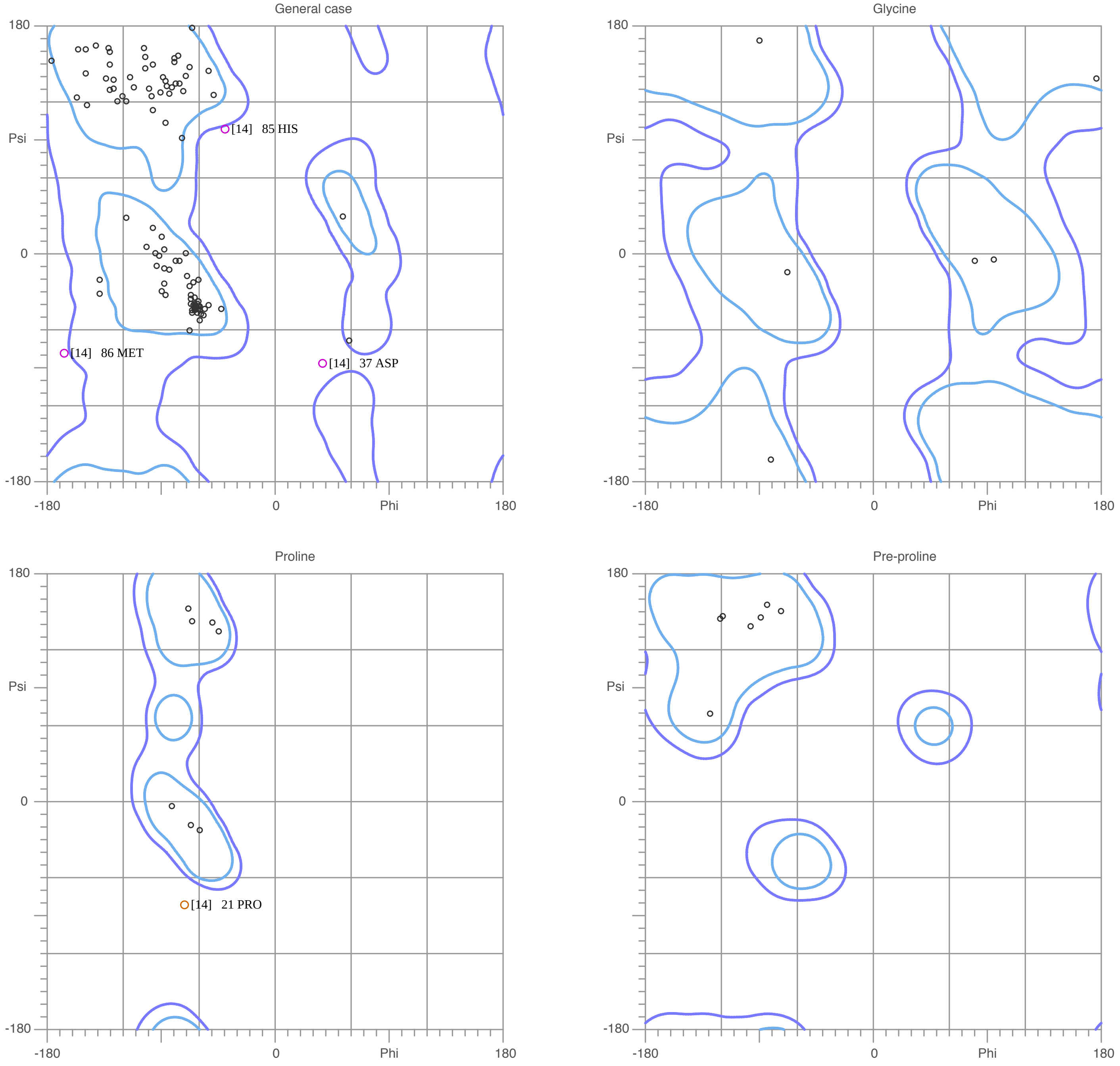
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 14



92.7% (114/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[14] 21 PRO (-72.3, -81.1)
[14] 37 ASP (37.2, -86.9)
[14] 85 HIS (-40.8, 99.4)
[14] 86 MET (-167.7, -78.2)

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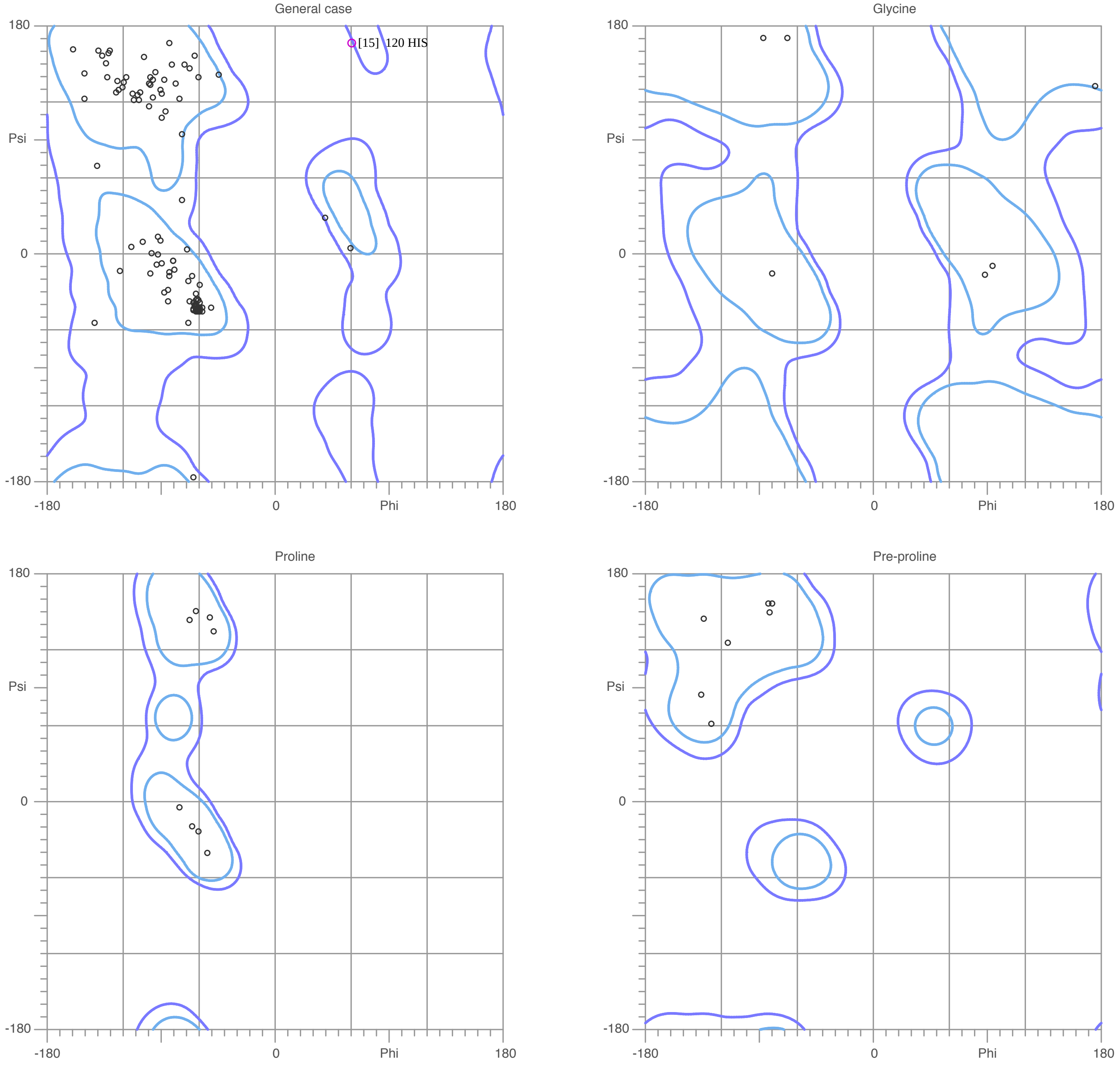
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 15



94.3% (116/123) of all residues were in favored (98%) regions.
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[15] 120 HIS (60.3, 167.1)

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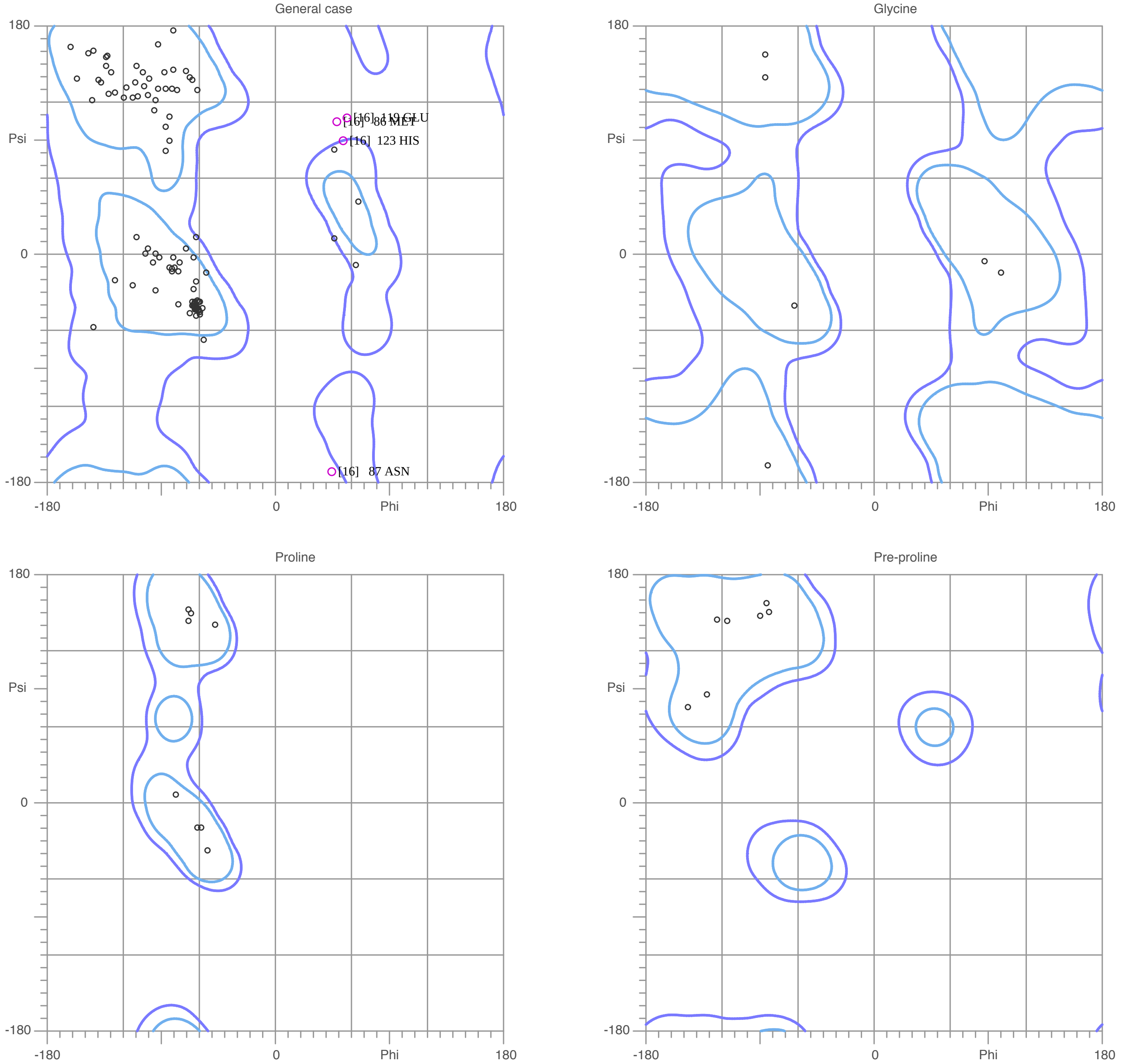
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 16



91.9% (113/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[16] 86 MET (48.6, 105.7)
[16] 87 ASN (44.0, -171.3)
[16] 119 GLU (56.9, 108.7)
[16] 123 HIS (53.2, 90.7)

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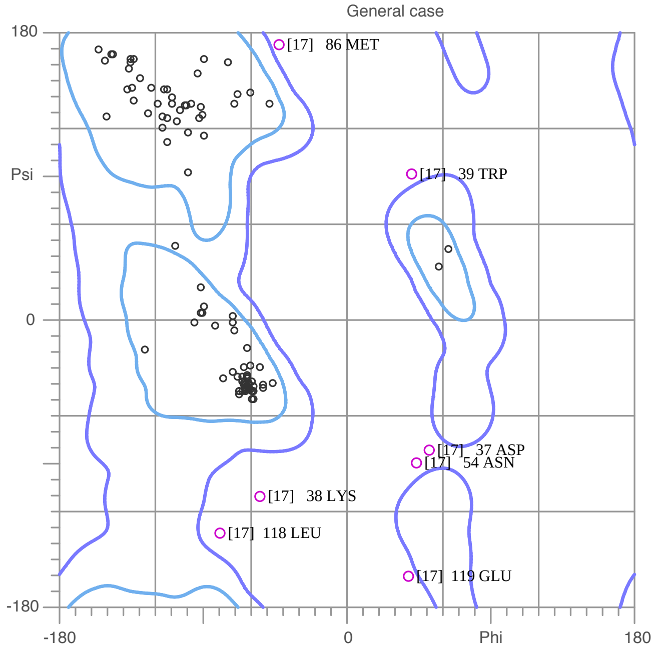
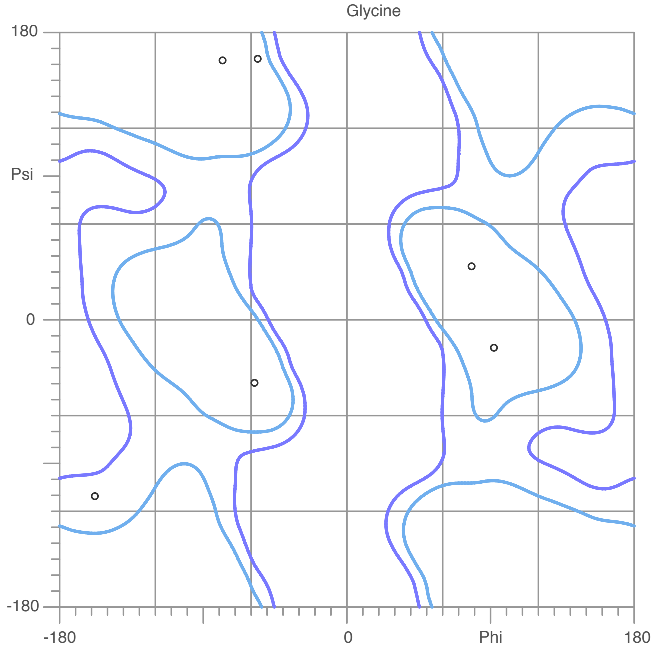
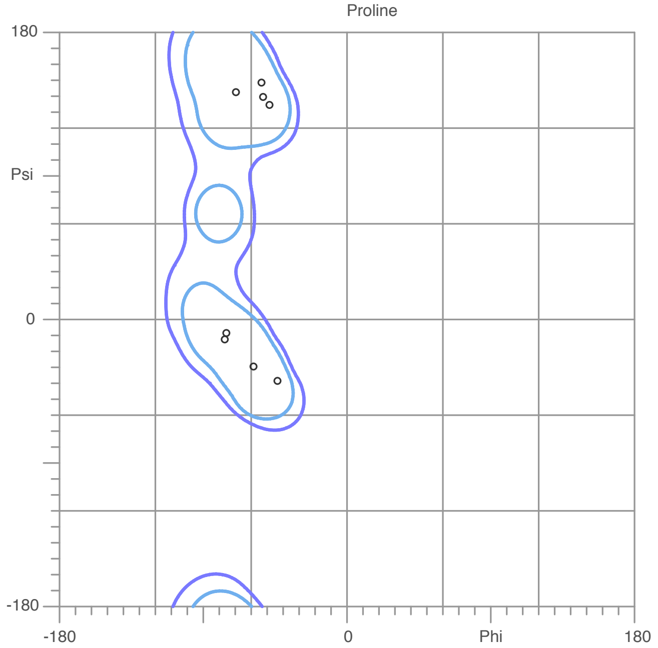
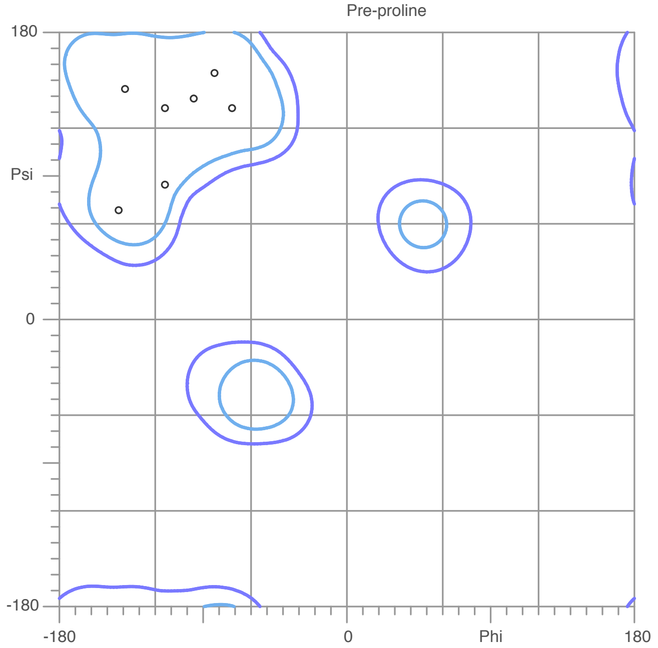
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 17


General case


Glycine


Proline


Pre-proline

92.7% (114/123) of all residues were in favored (98%) regions.
94.3% (116/123) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):

[17] 37 ASP (51.3, -81.4)
[17] 38 LYS (-55.9, -110.1)
[17] 39 TRP (40.8, 92.1)
[17] 54 ASN (43.0, -89.2)
[17] 86 MET (-43.7, 173.5)
[17] 118 LEU (-80.8, -133.5)
[17] 119 GLU (38.8, -160.7)

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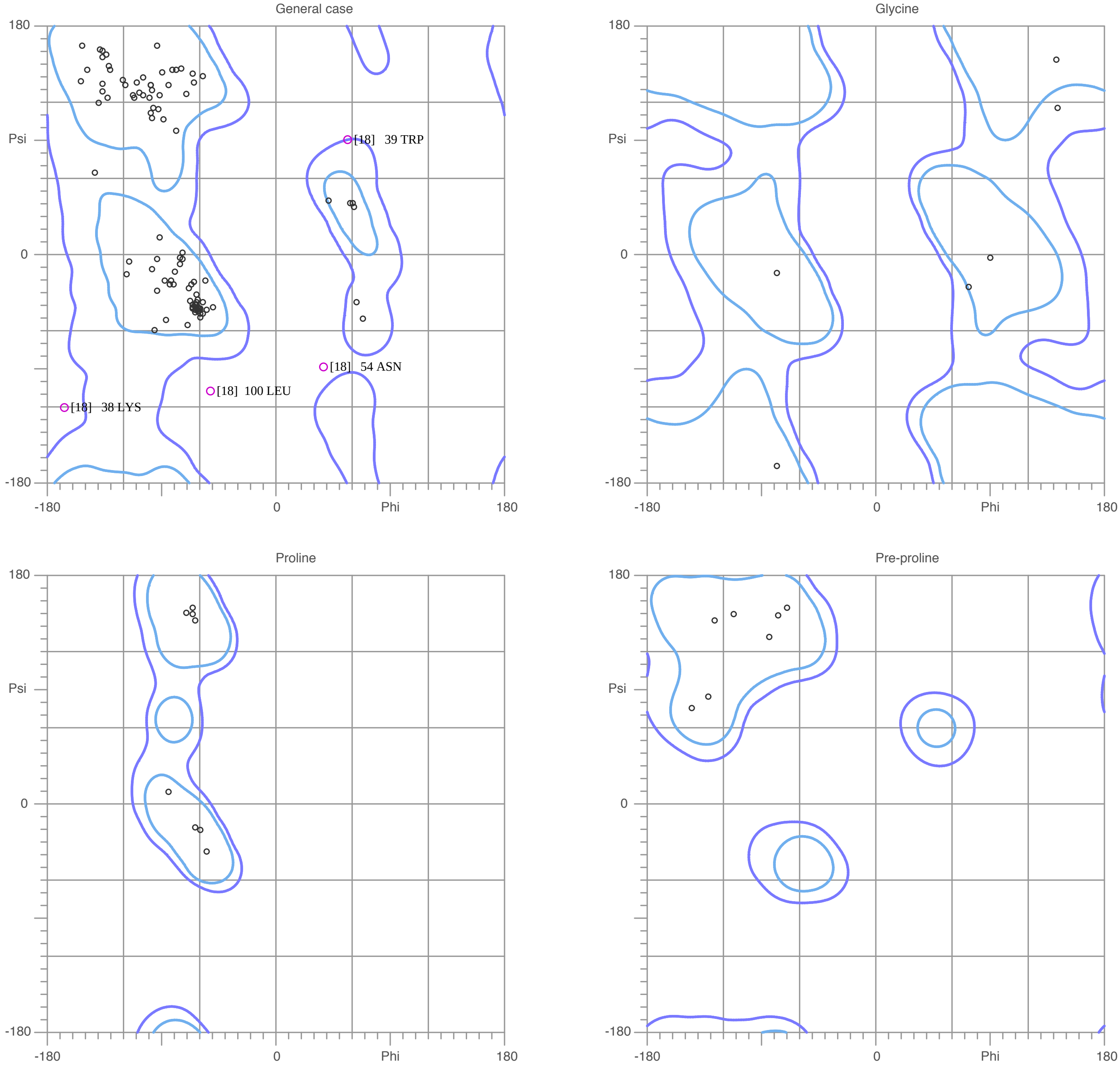
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 18



93.5% (115/123) of all residues were in favored (98%) regions.
96.7% (119/123) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[18] 38 LYS (-167.7, -120.3)
[18] 39 TRP (56.2, 91.6)
[18] 54 ASN (37.2, -88.9)
[18] 100 LEU (-52.6, -108.0)

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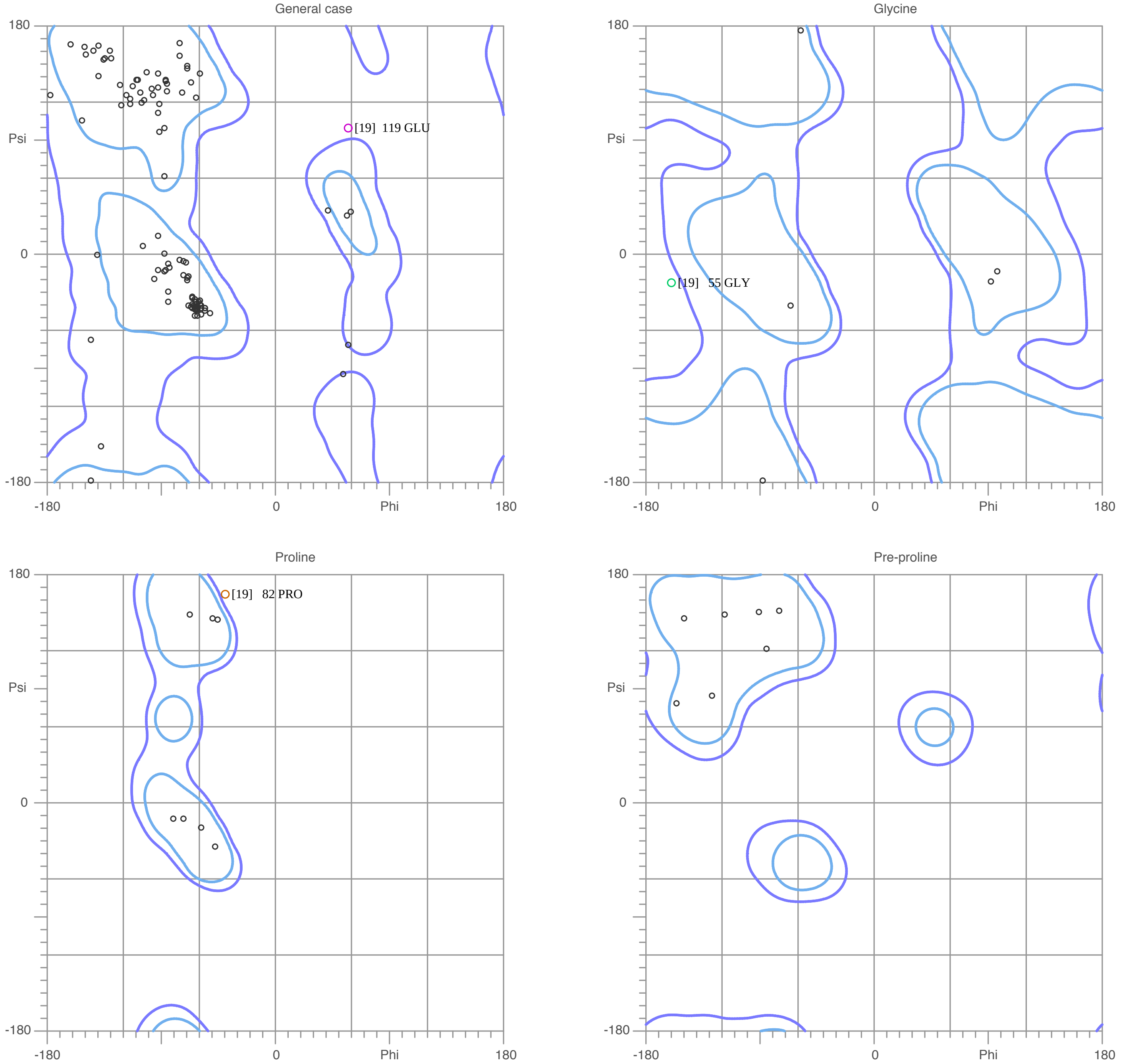
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 19



91.9% (113/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
- [19] 55 GLY (-160.1, -22.5)
- [19] 82 PRO (-40.6, 165.2)
- [19] 119 GLU (57.2, 100.6)

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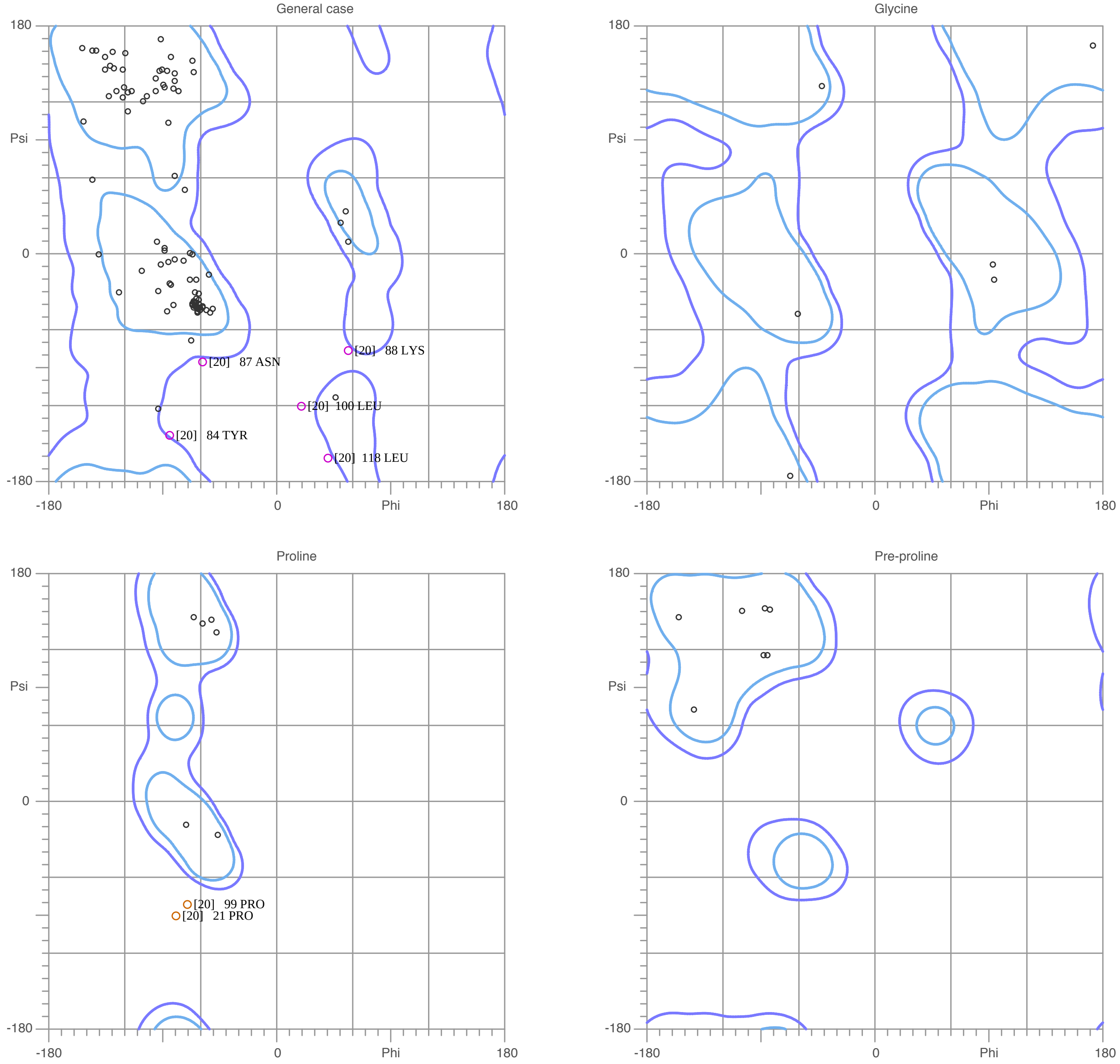
MolProbity Ramachandran analysis

PSR293_NMR_em_bcr3.pdb, model 20



88.6% (109/123) of all residues were in favored (98%) regions.
94.3% (116/123) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[20] 21 PRO (-80.2, -90.2)
[20] 84 TYR (-85.1, -143.0)
[20] 87 ASN (-59.6, -85.9)
[20] 88 LYS (56.9, -76.7)
[20] 99 PRO (-71.6, -81.2)
[20] 100 LEU (19.2, -120.7)
[20] 118 LEU (40.0, -161.6)

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