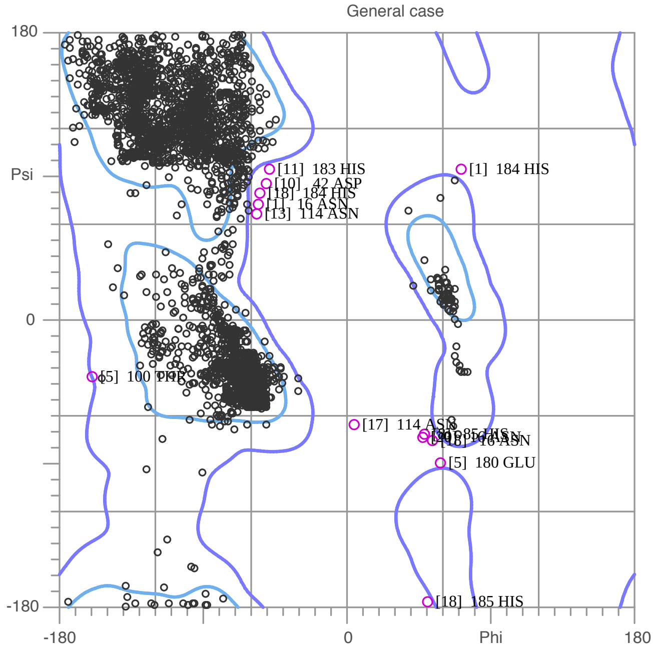
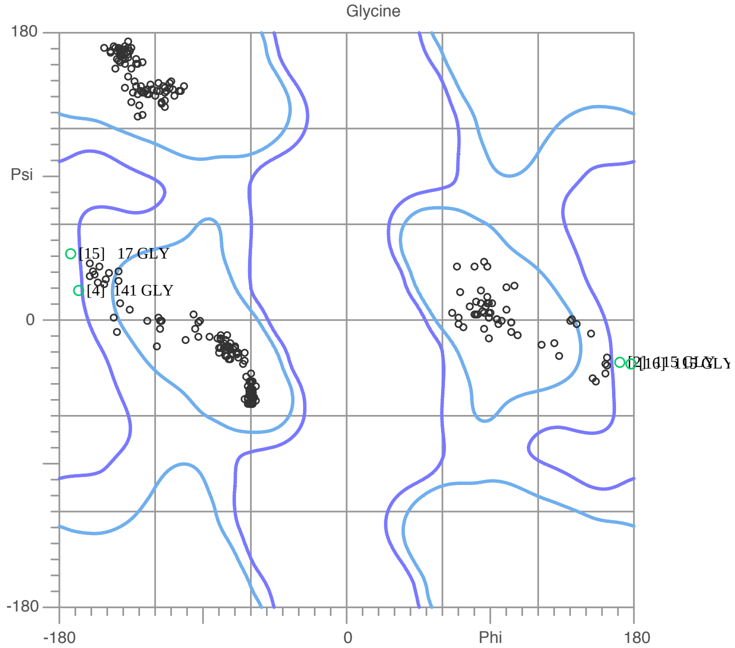
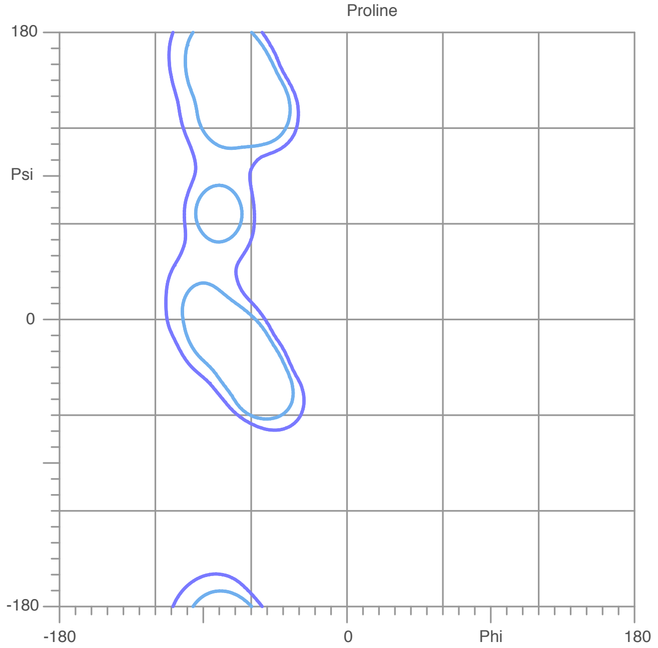
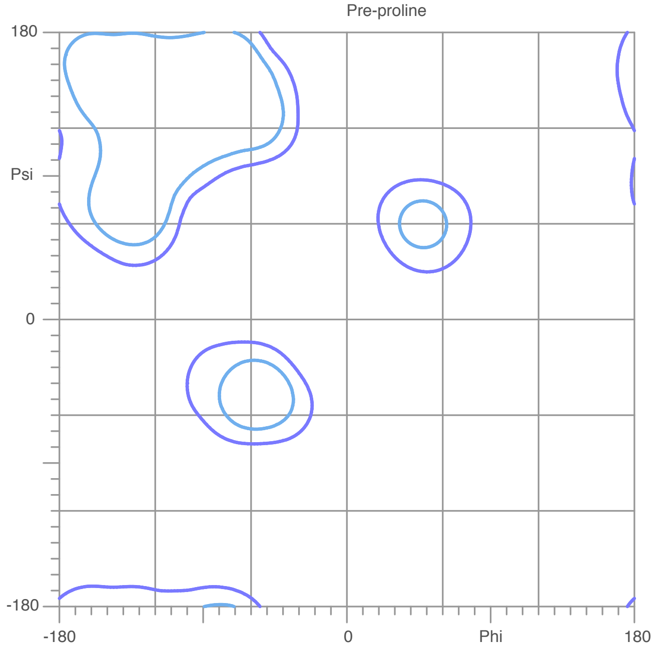
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, all models









95.1% (3270/3440) of all residues were in favored (98%) regions.
99.5% (3423/3440) of all residues were in allowed (>99.8%) regions.

There were 17 outliers (phi, psi):
[1] 16 ASN (-56.1, 74.0)
[1] 184 HIS (71.6, 95.9)
[2] 115 GLY (171.1, -26.4)
[4] 141 GLY (-168.7, 19.2)
[5] 100 THR (-160.9, -35.6)
[5] 180 GLU (58.5, -89.5)
[8] 85 HIS (48.4, -71.1)
[10] 42 ASP (-51.7, 86.6)
[11] 183 HIS (-49.3, 95.7)
[13] 114 ASN (-57.1, 67.3)
[15] 17 GLY (-173.1, 42.3)
[16] 115 GLY (178.1, -27.7)
[17] 114 ASN (4.4, -65.4)
[18] 16 ASN (54.0, -75.4)
[18] 184 HIS (-55.8, 80.6)
[18] 185 HIS (50.1, -176.7)
[20] 16 ASN (48.0, -73.9)

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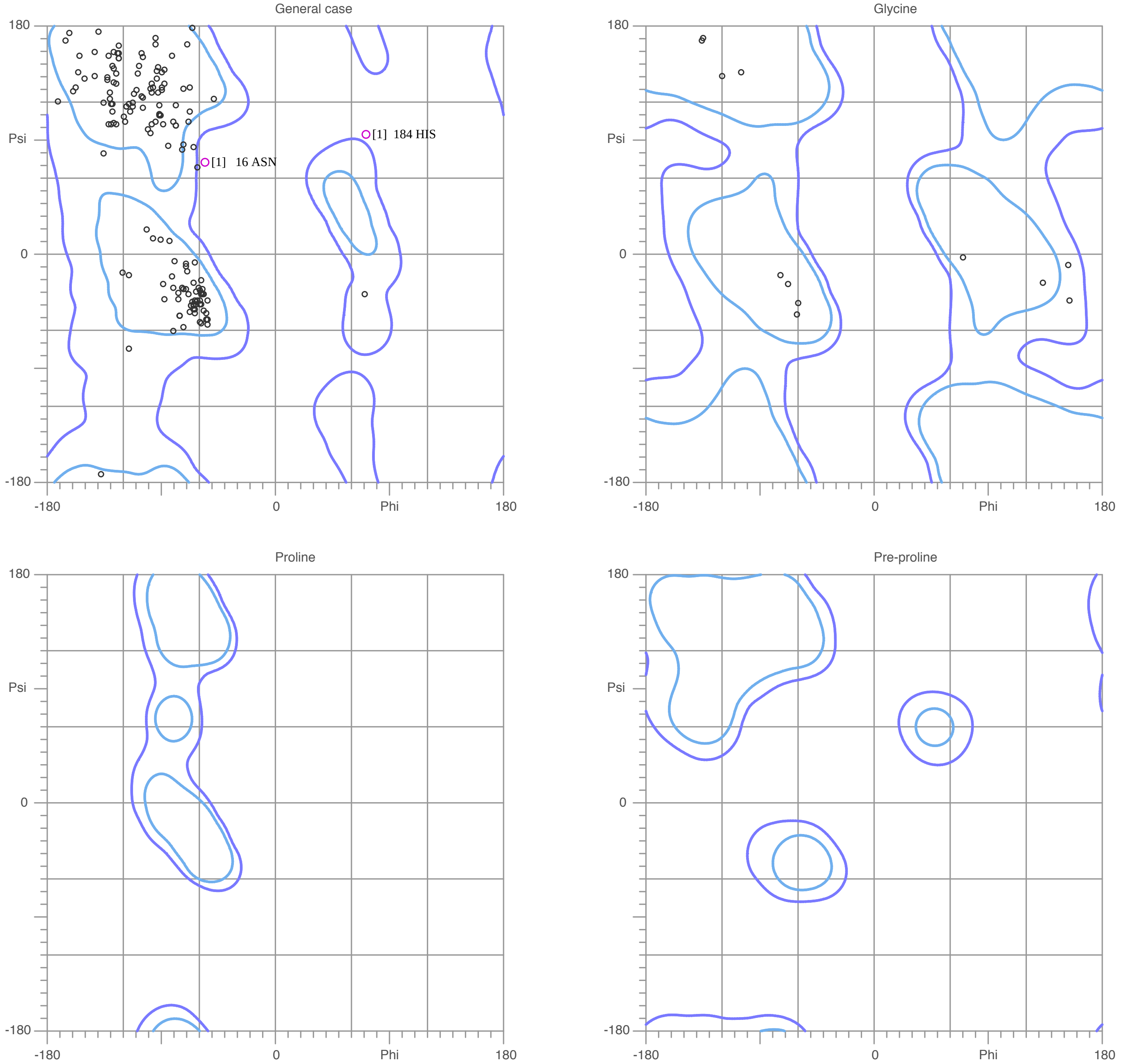
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 1



93.0% (160/172) of all residues were in favored (98%) regions.
98.8% (170/172) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[1] 16 ASN (-56.1, 74.0)
[1] 184 HIS (71.6, 95.9)

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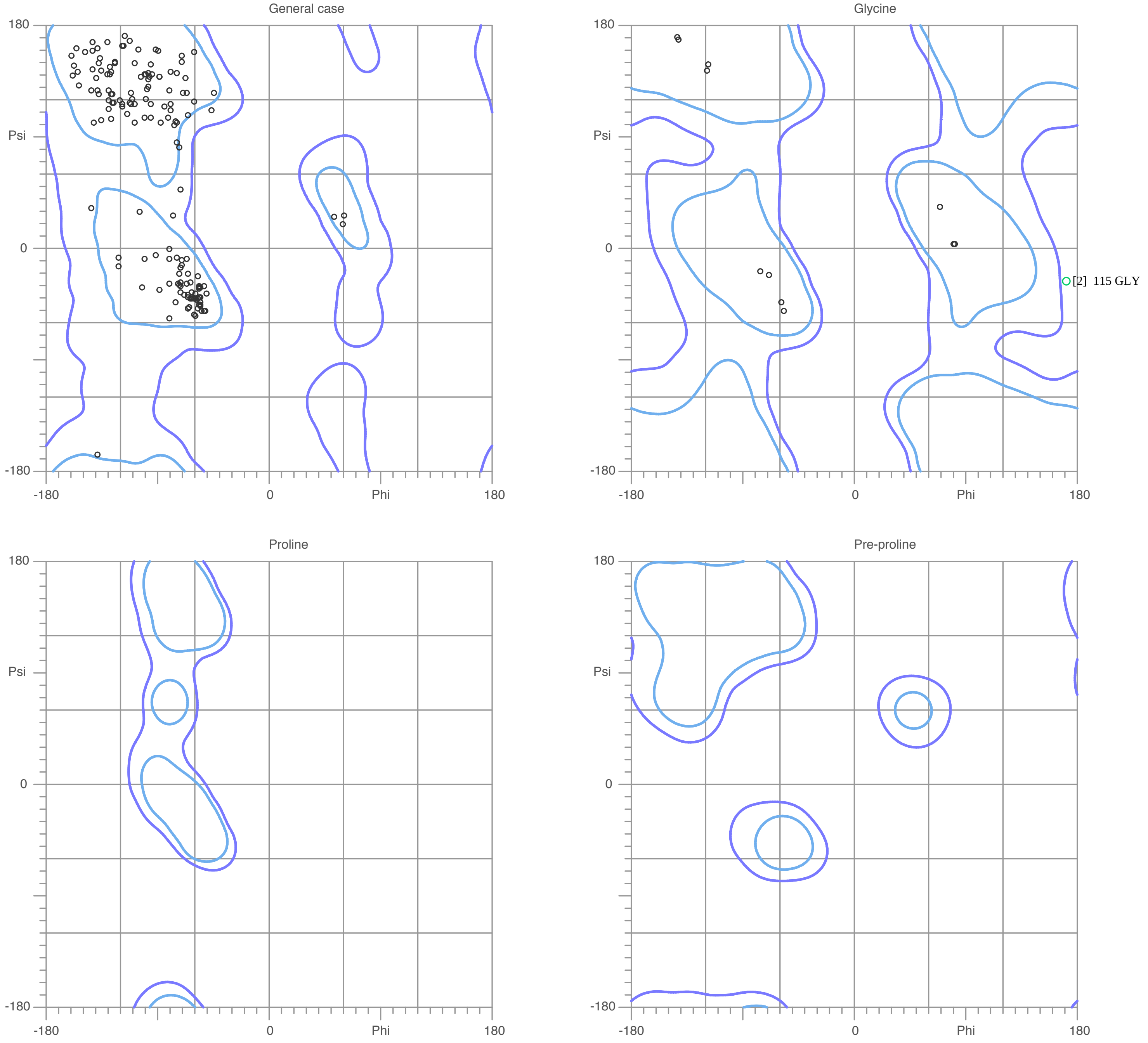
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 2



96.5% (166/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[2] 115 GLY (171.1, -26.4)

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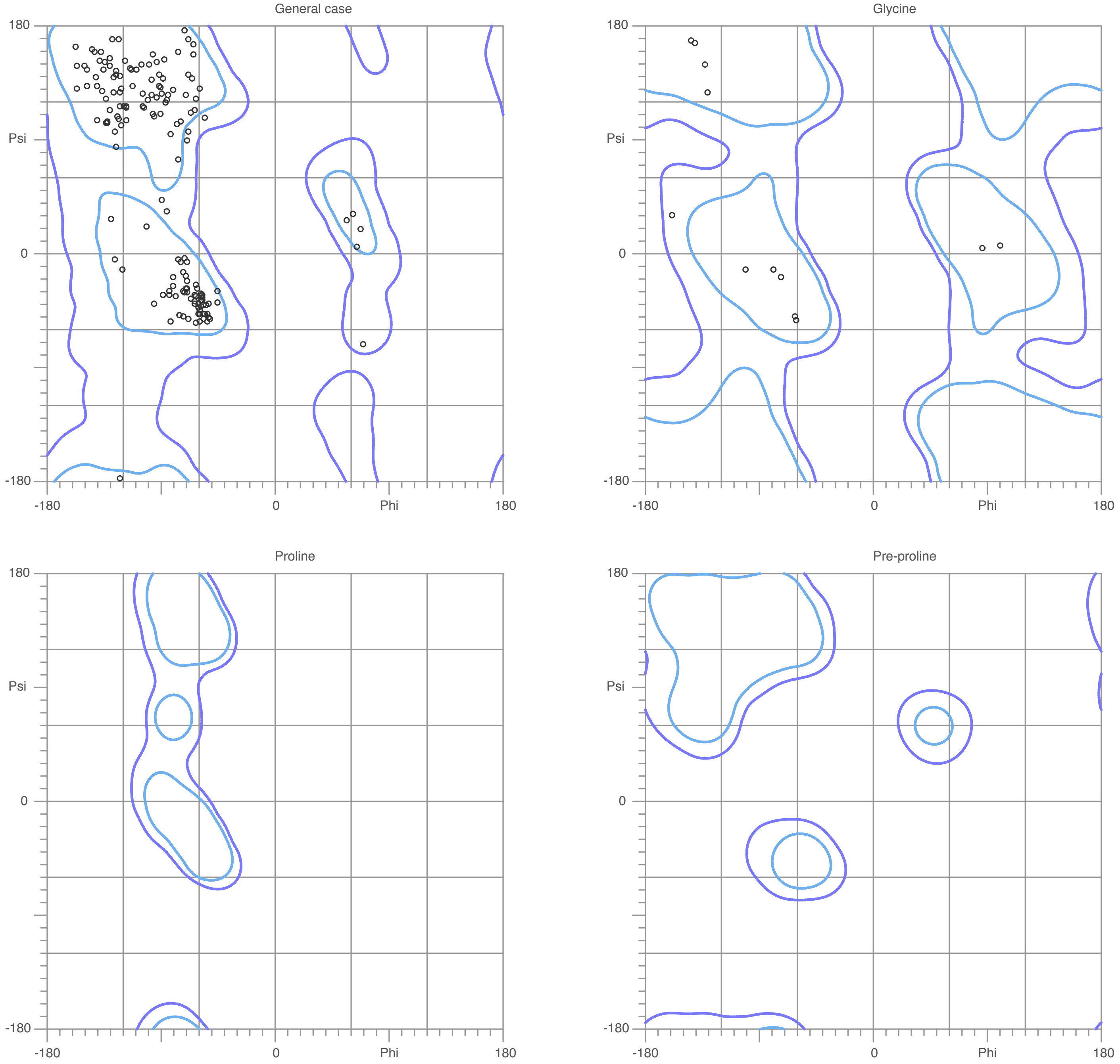
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 3



95.9% (165/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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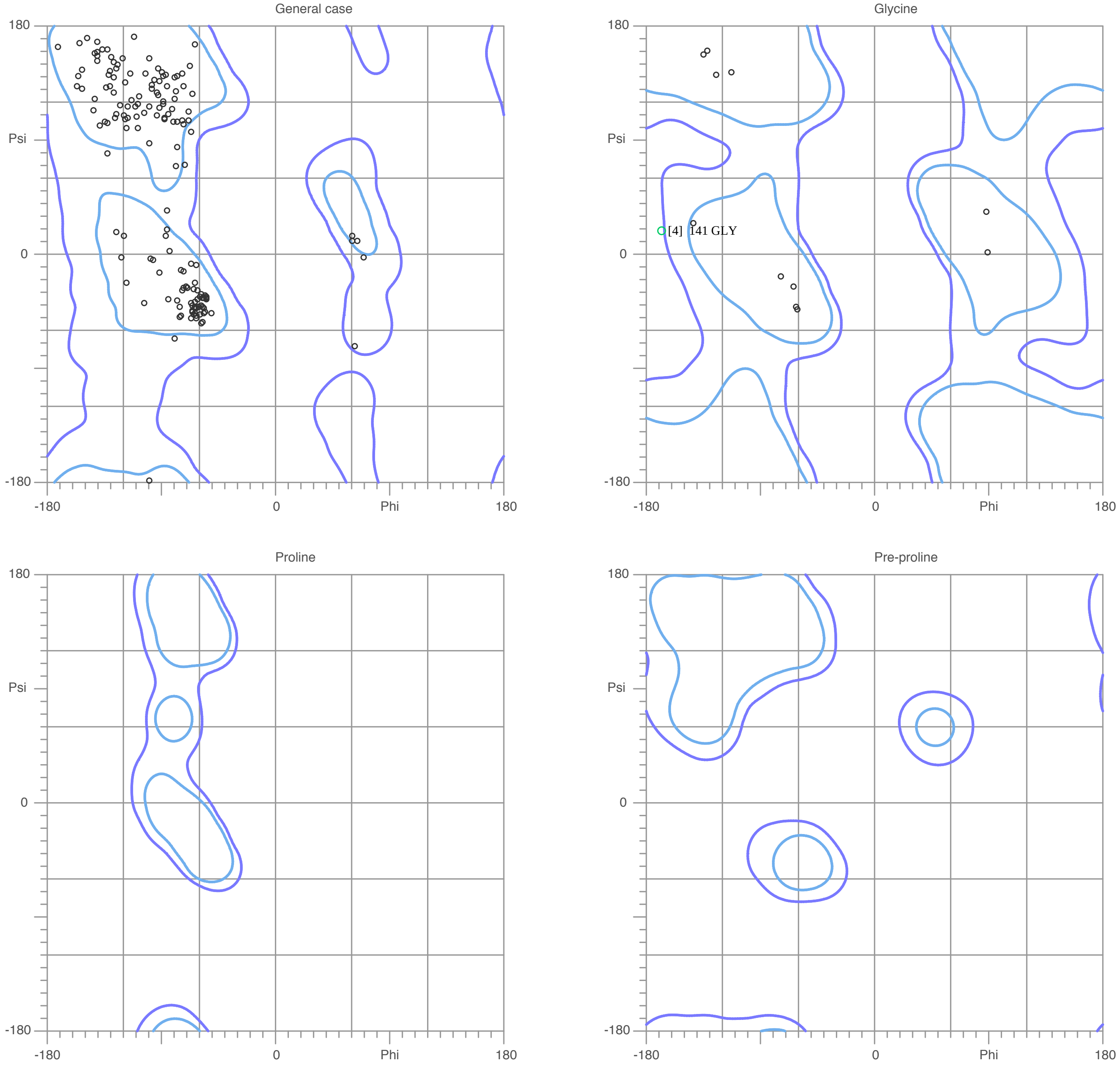
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 4



95.3% (164/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[4] 141 GLY (-168.7, 19.2)

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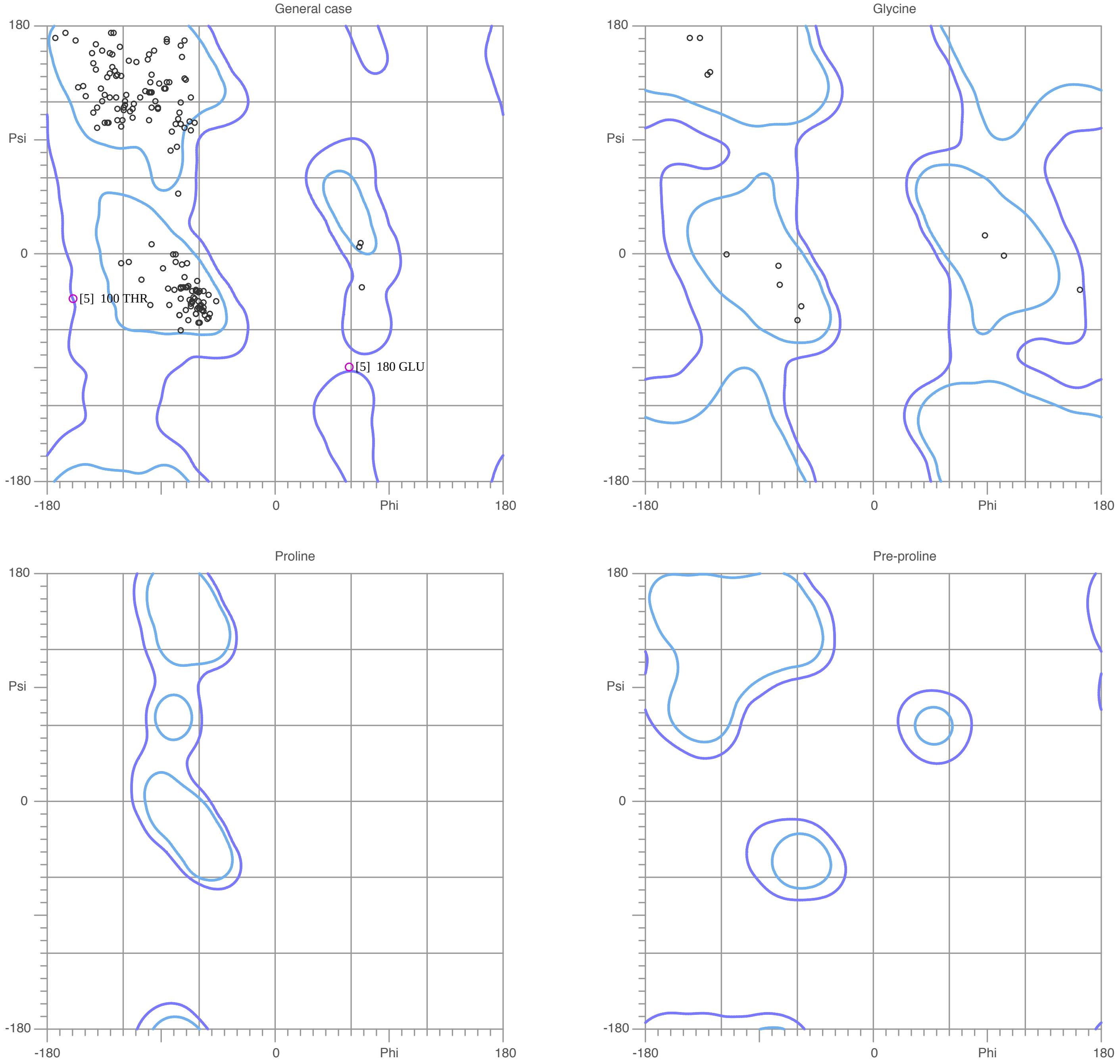
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 5



95.9% (165/172) of all residues were in favored (98%) regions.
98.8% (170/172) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
- [5] 100 THR (-160.9, -35.6)
- [5] 180 GLU (58.5, -89.5)

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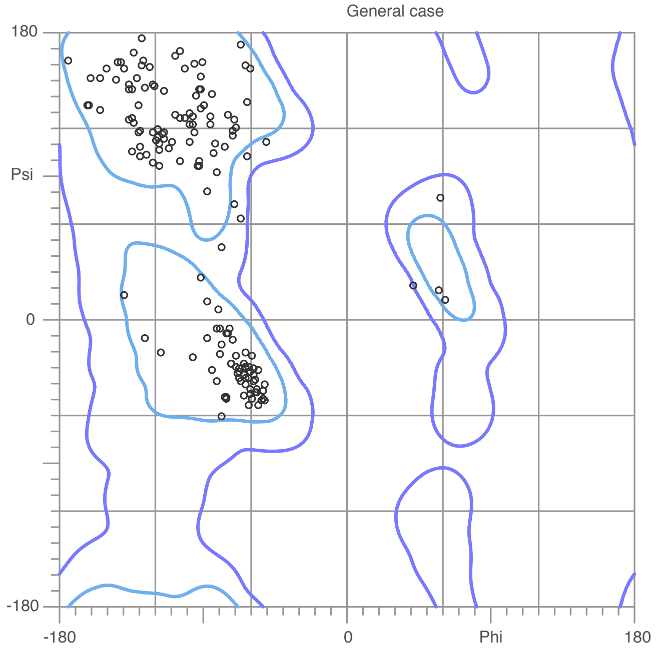
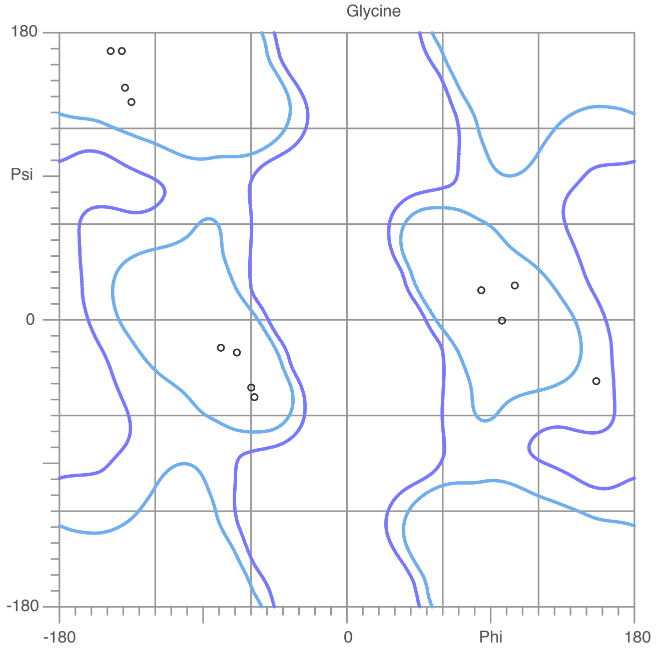
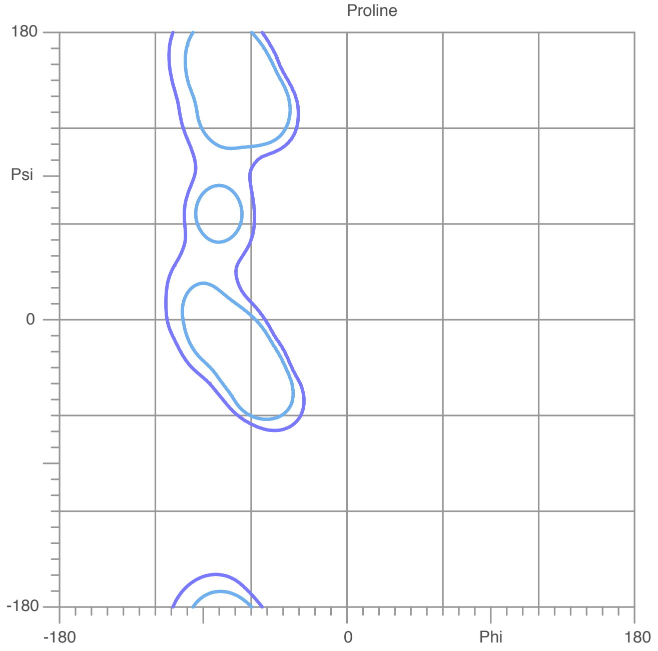
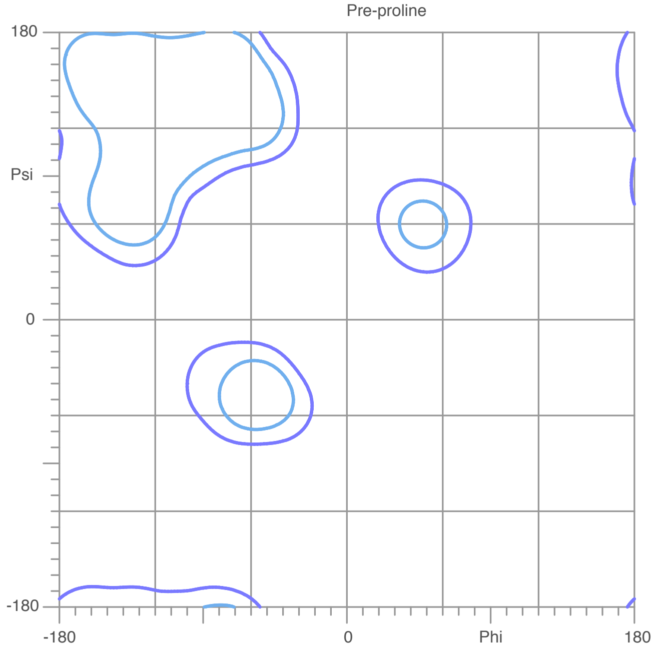
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 6







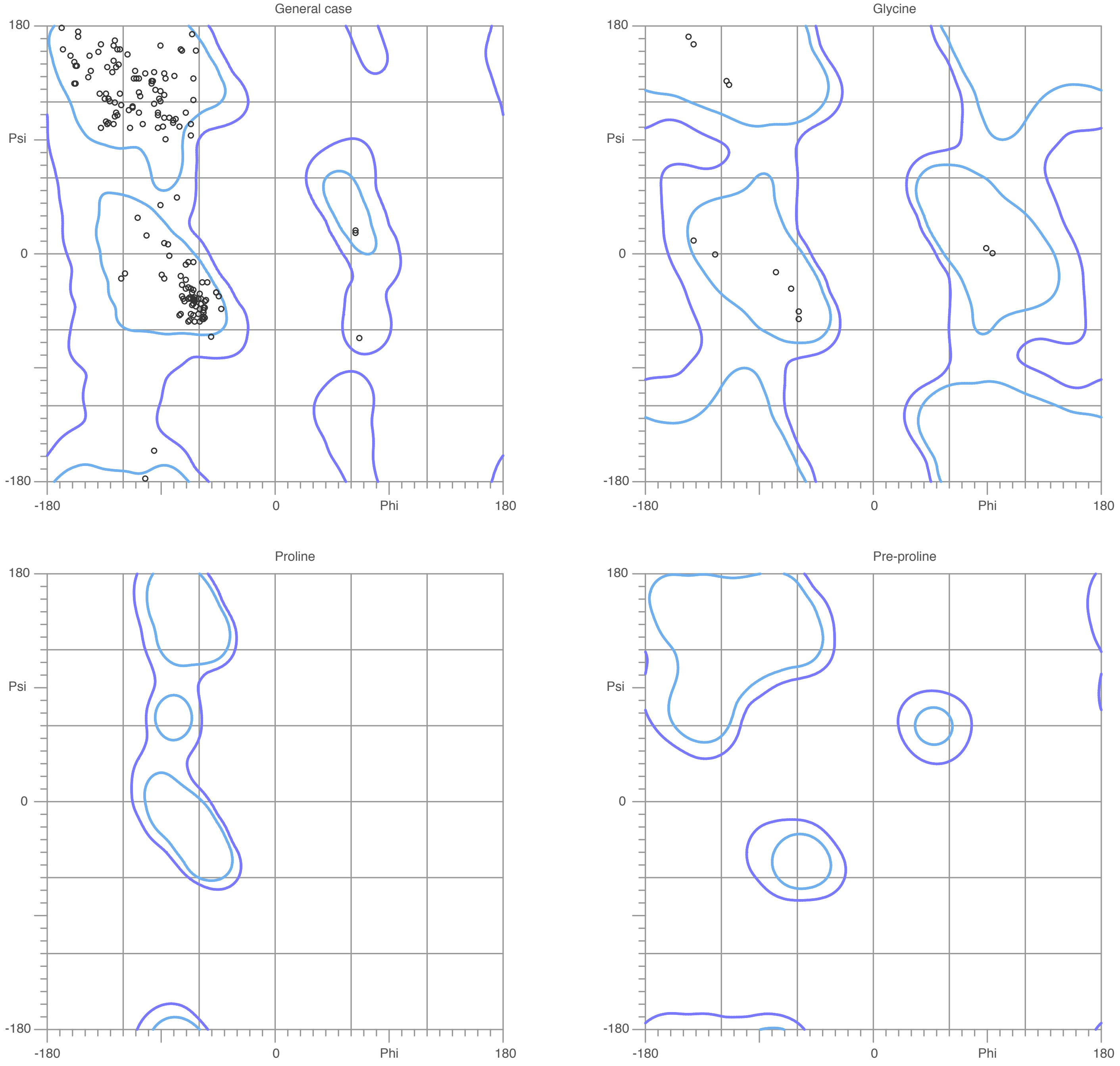


95.3% (164/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 7

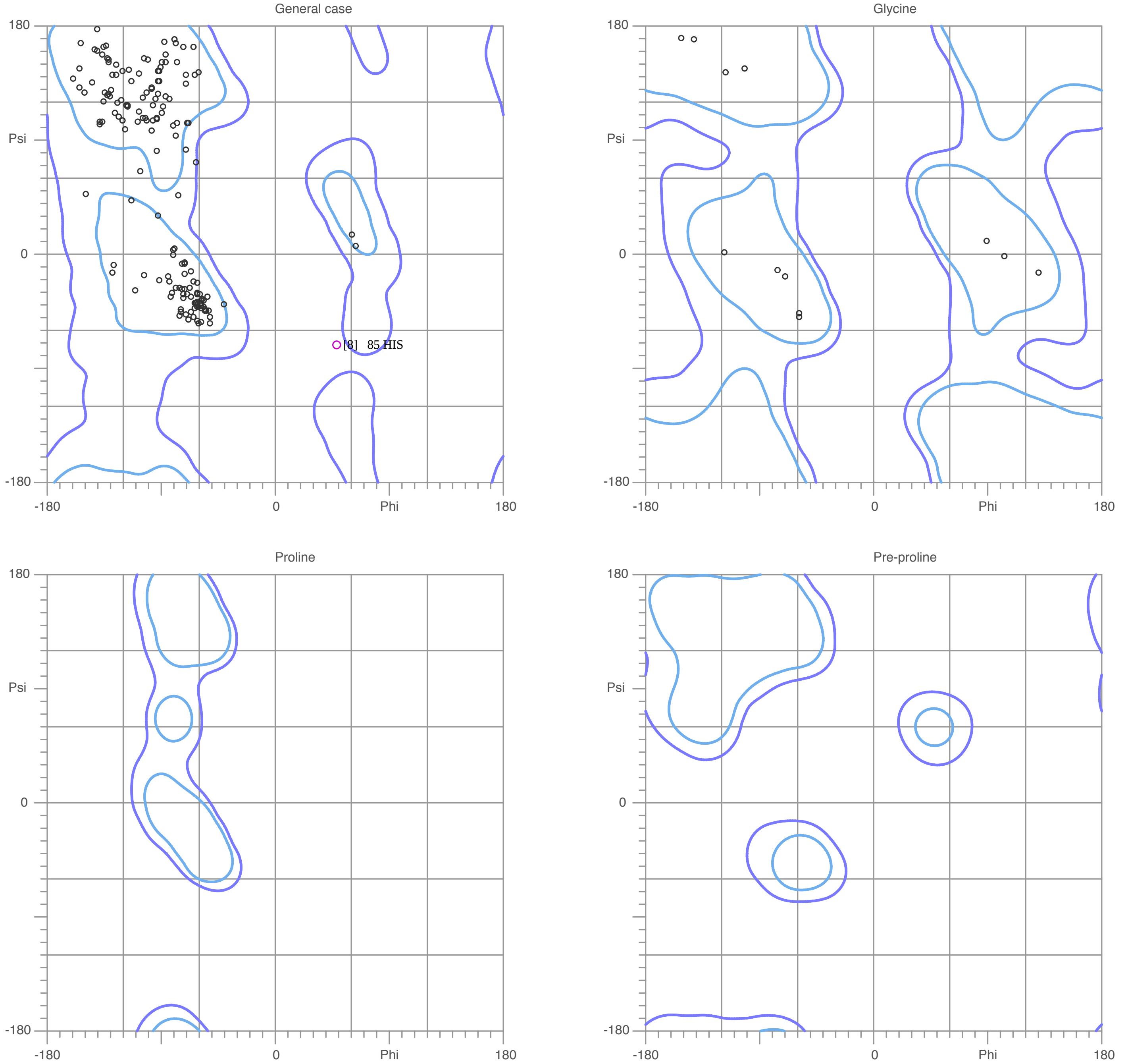


96.5% (166/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 8



95.9% (165/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 85 HIS (48.4, -71.1)

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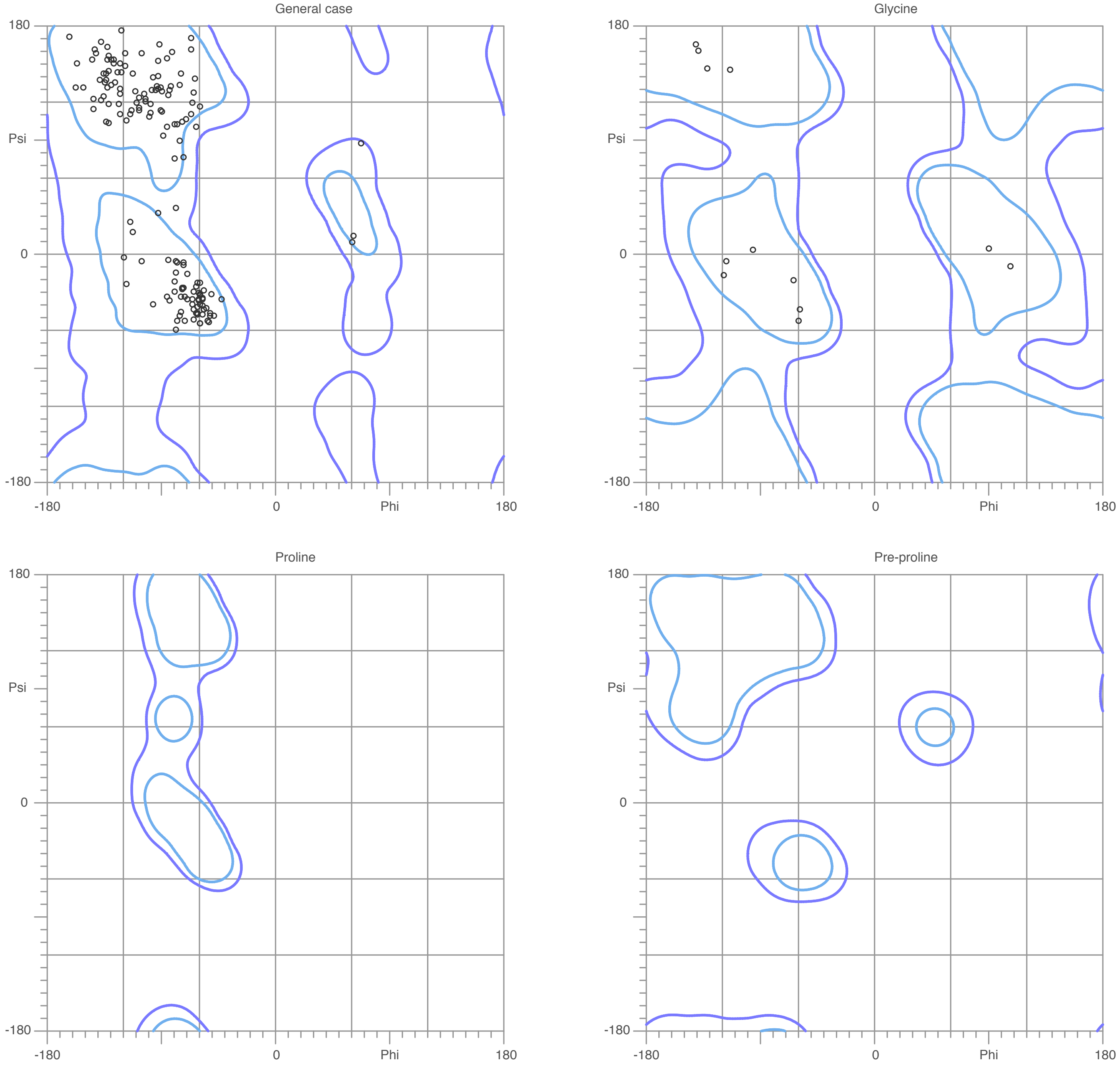
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 9



97.7% (168/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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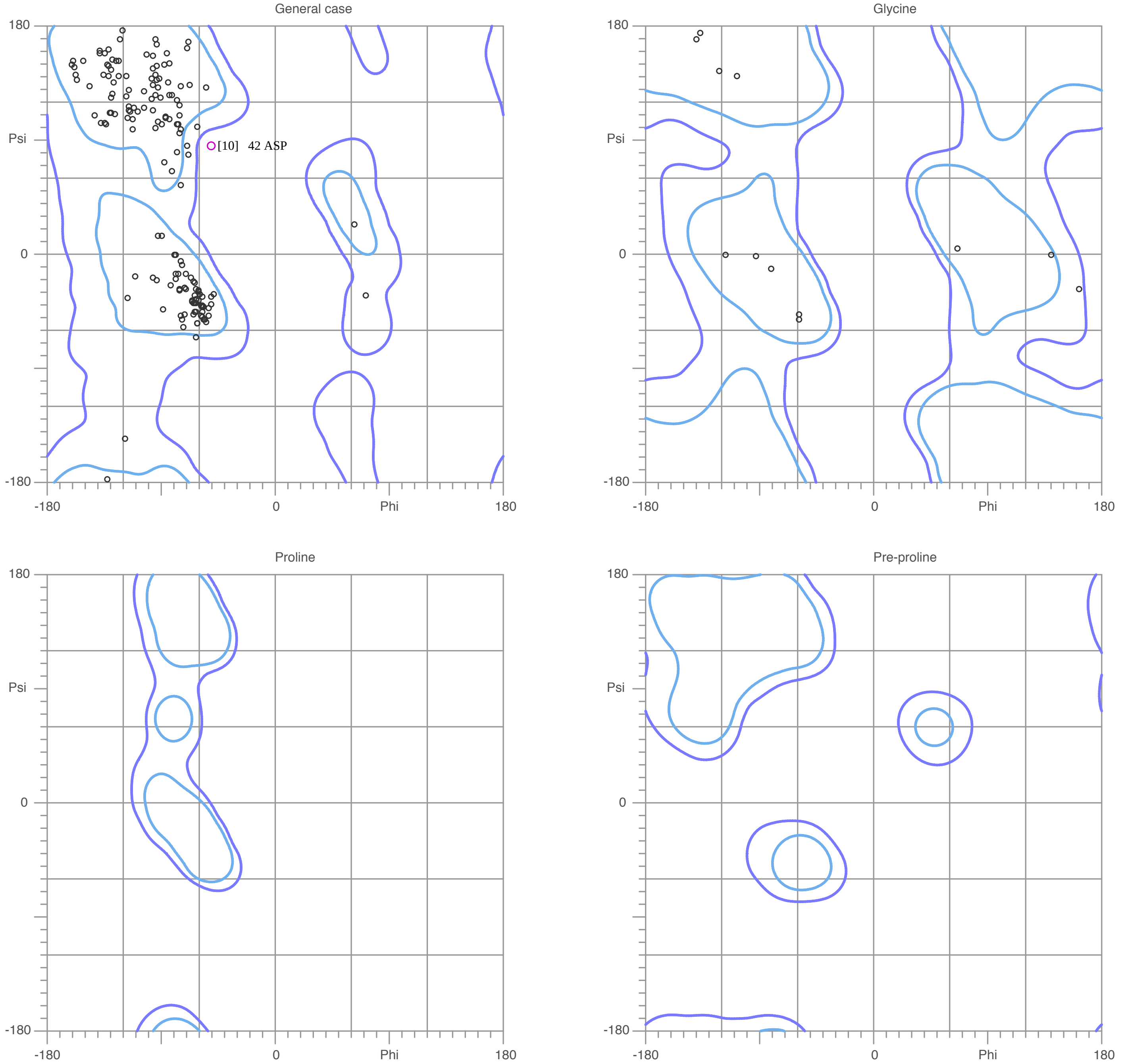
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 10



94.8% (163/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[10] 42 ASP (-51.7, 86.6)

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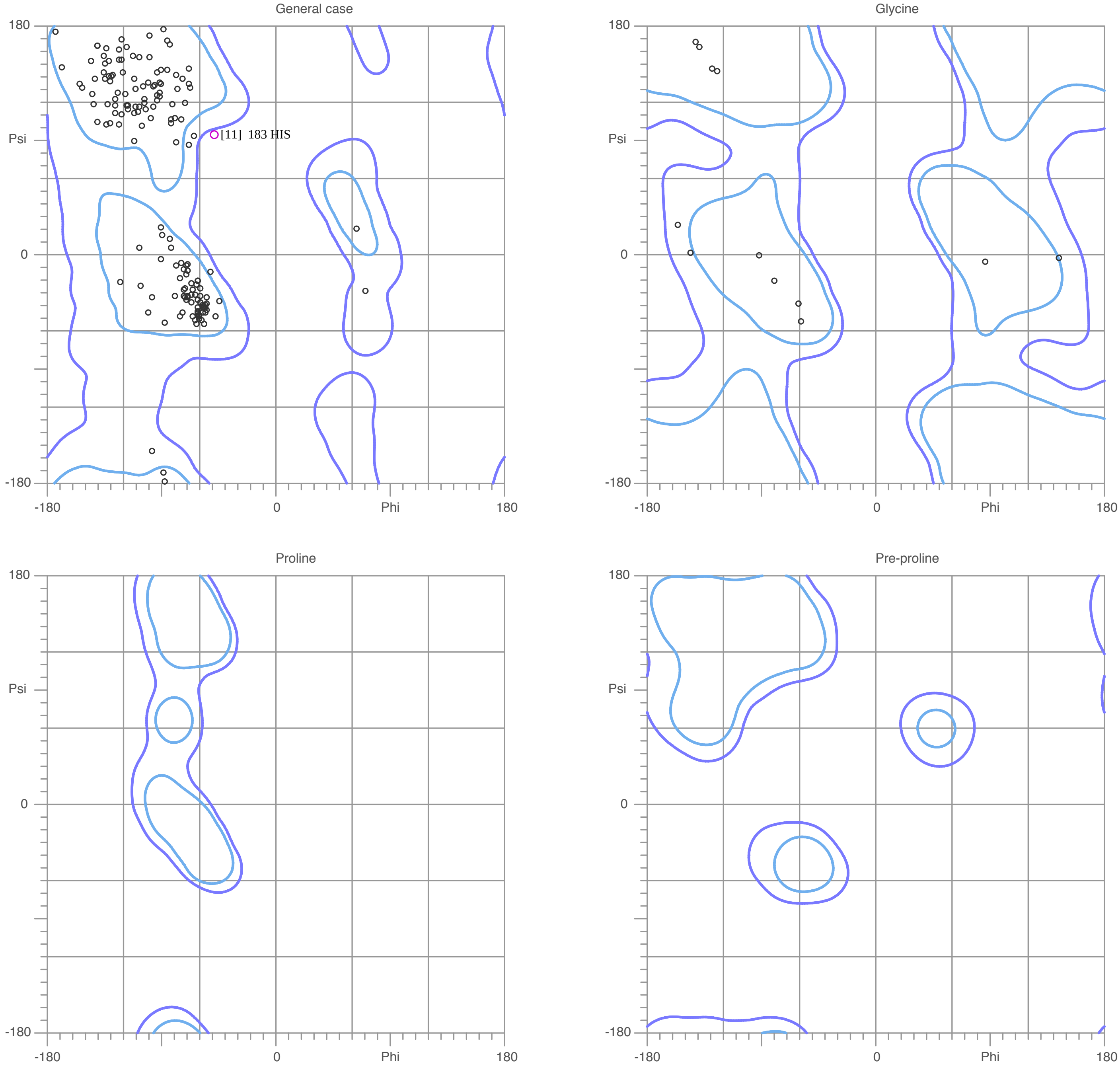
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 11

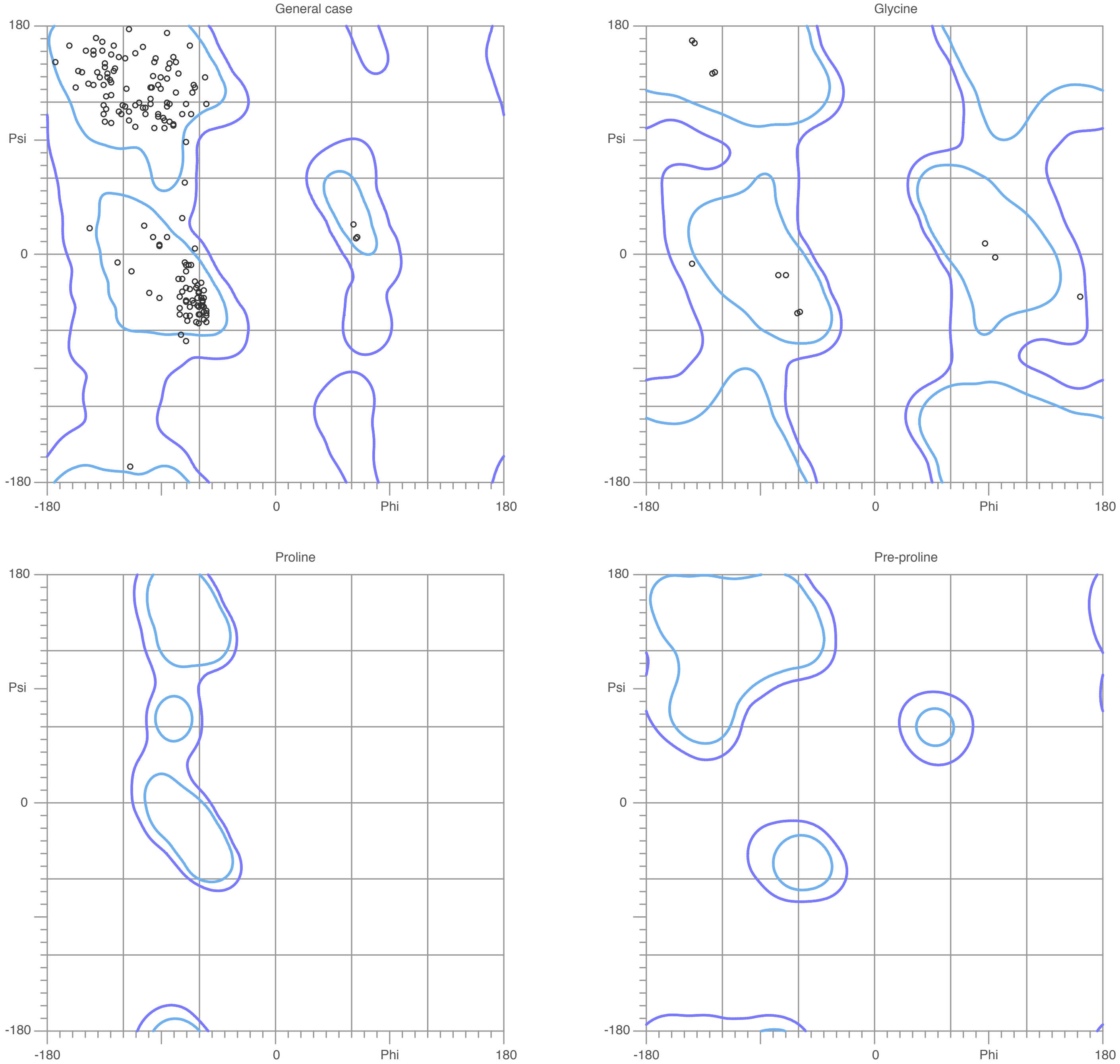


94.8% (163/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[11] 183 HIS (-49.3, 95.7)

MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 12



94.2% (162/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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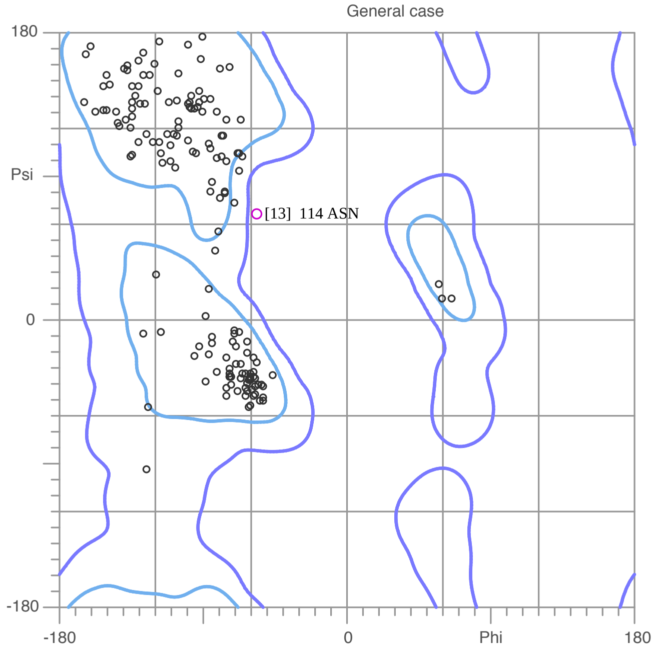
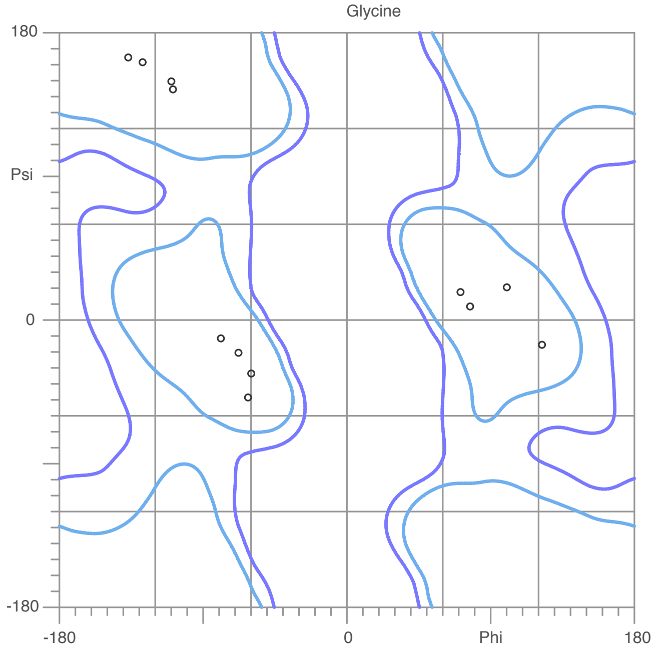
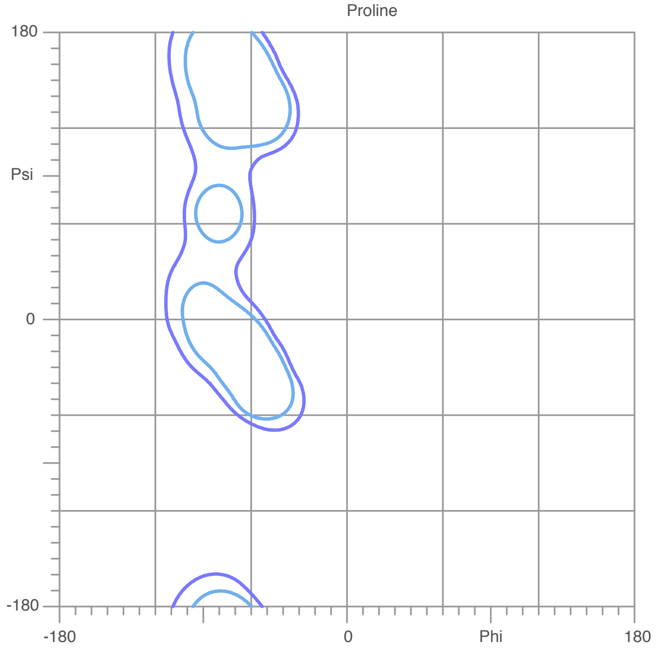
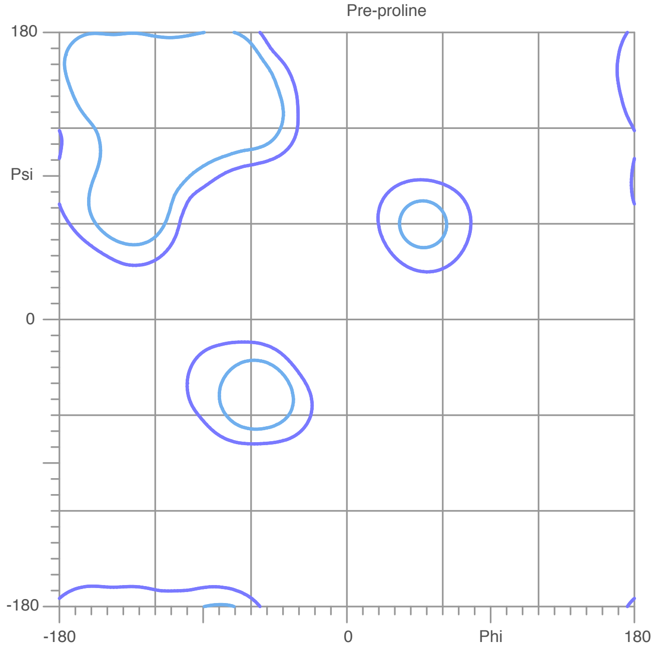
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 13







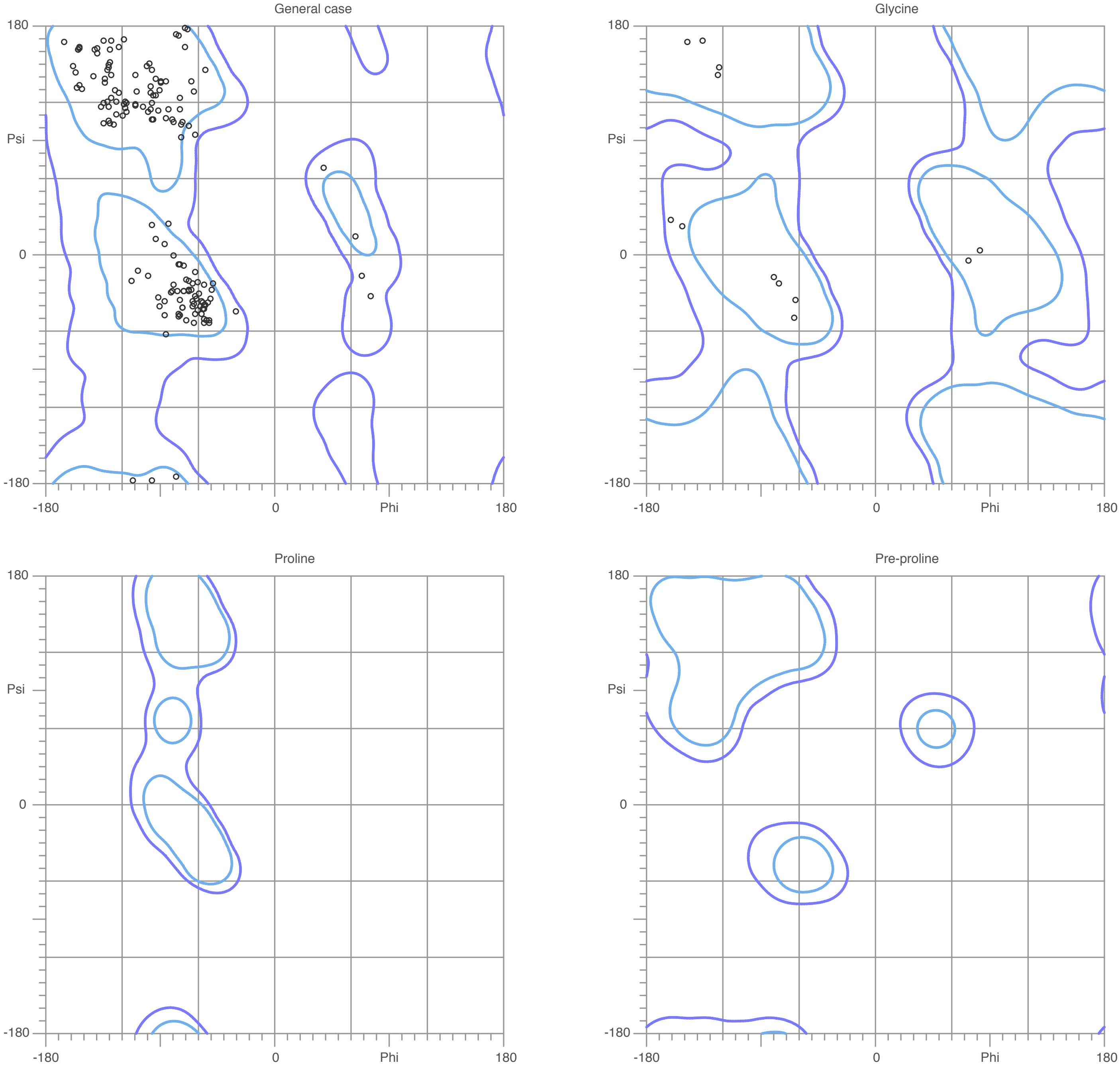


95.9% (165/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[13] 114 ASN (-57.1, 67.3)

MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 14



94.8% (163/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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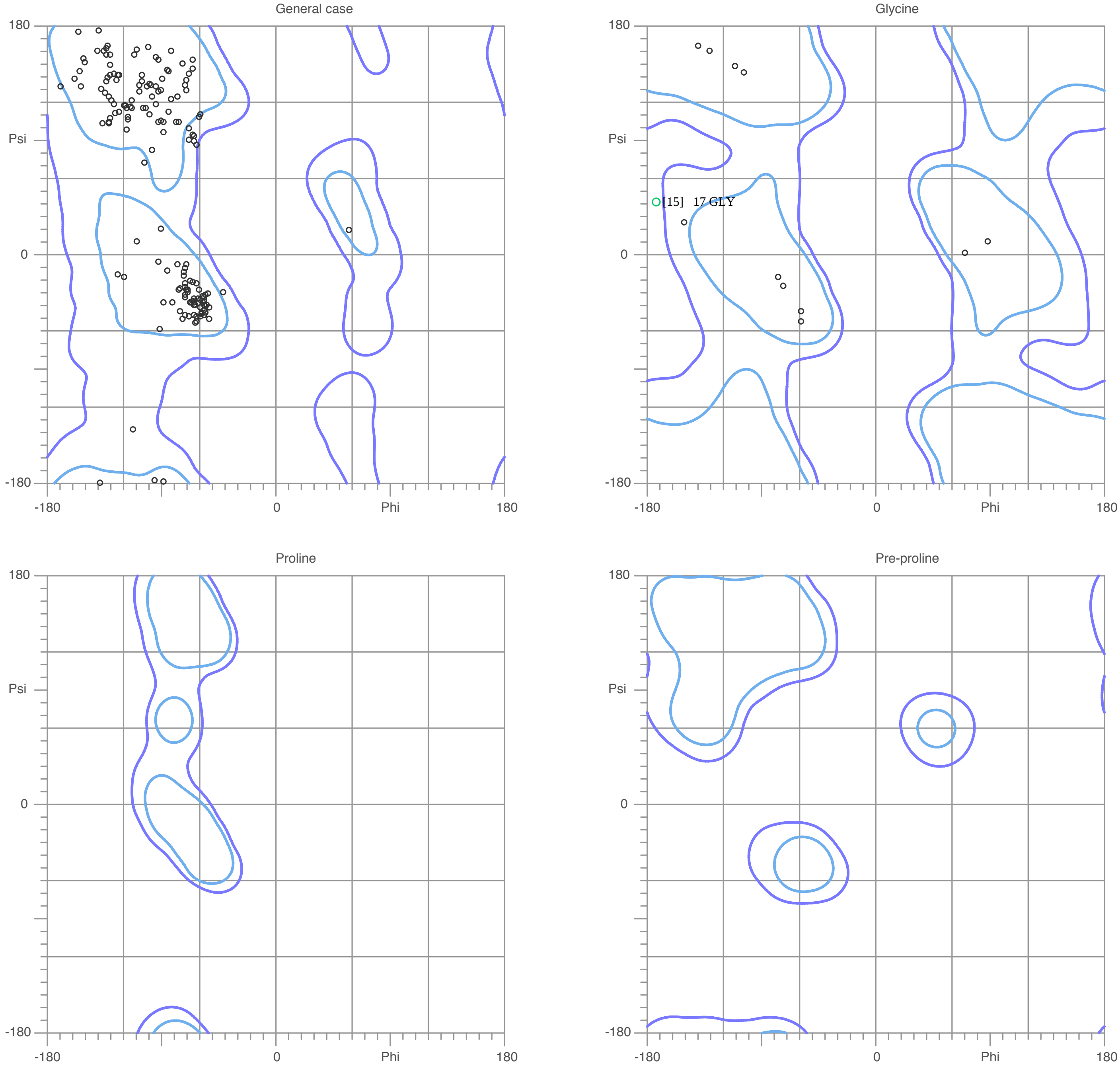
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 15

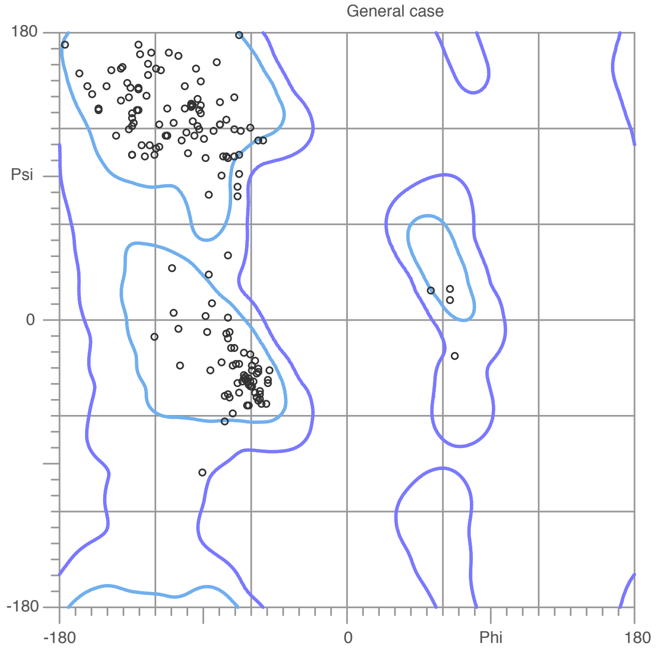


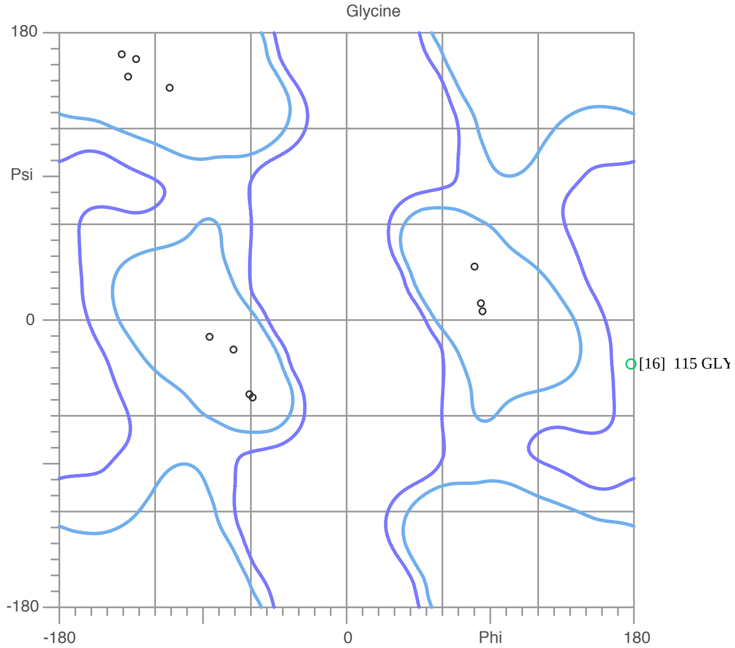
93.0% (160/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

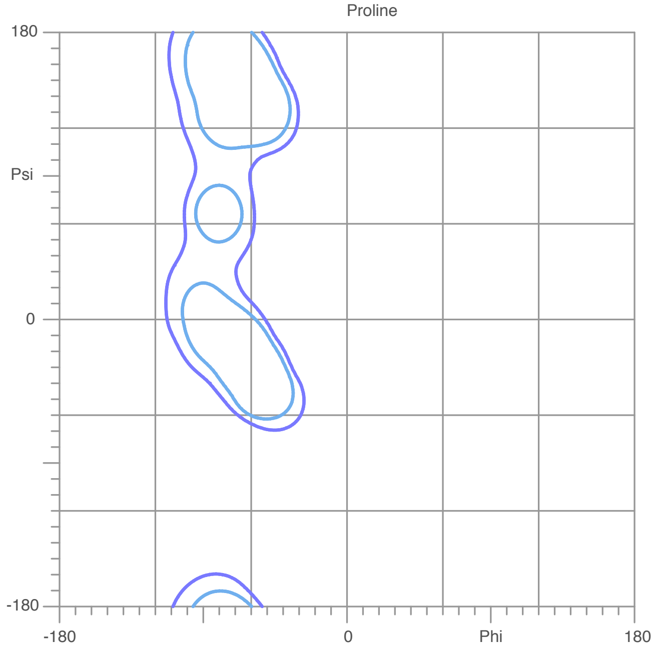
There were 1 outliers (phi, psi):
[15] 17 GLY (-173.1, 42.3)

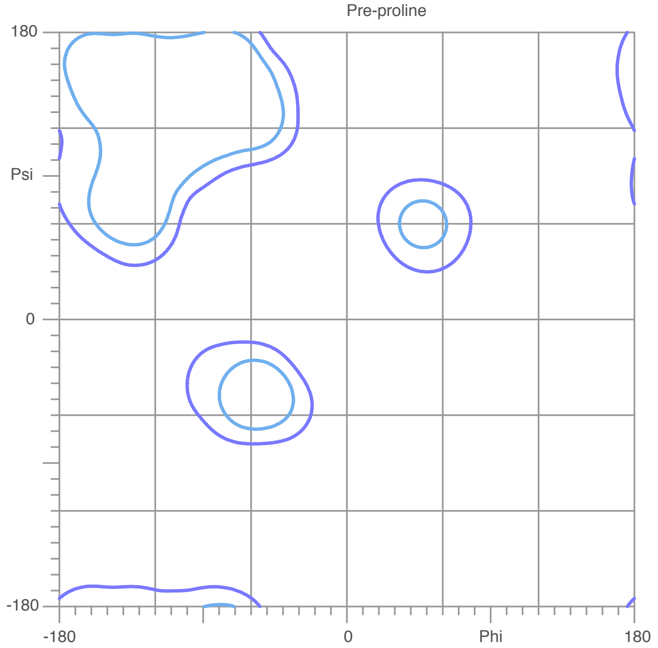
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 16









93.6% (161/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[16] 115 GLY (178.1, -27.7)

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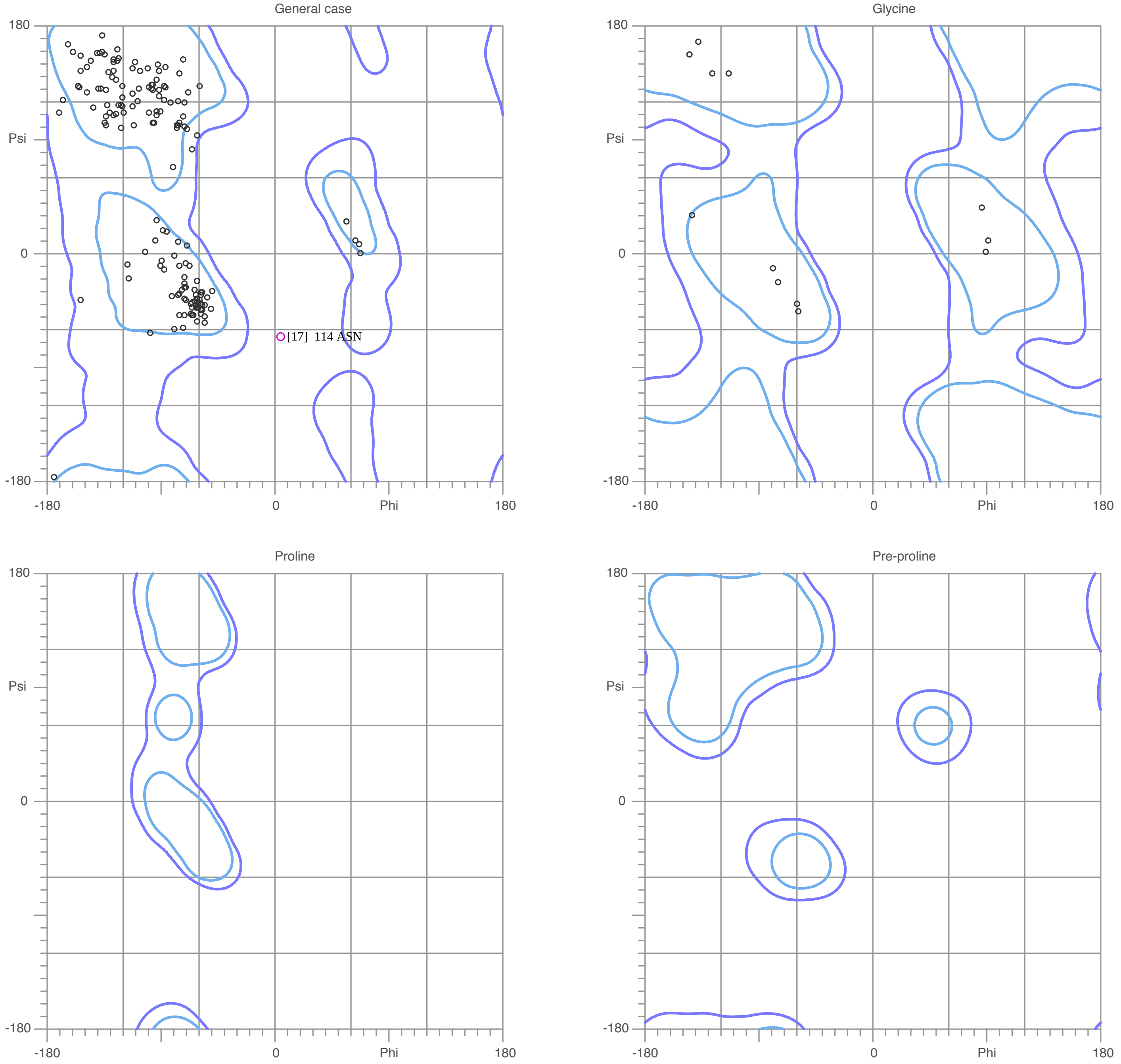
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 17



93.6% (161/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[17] 114 ASN (4.4, -65.4)

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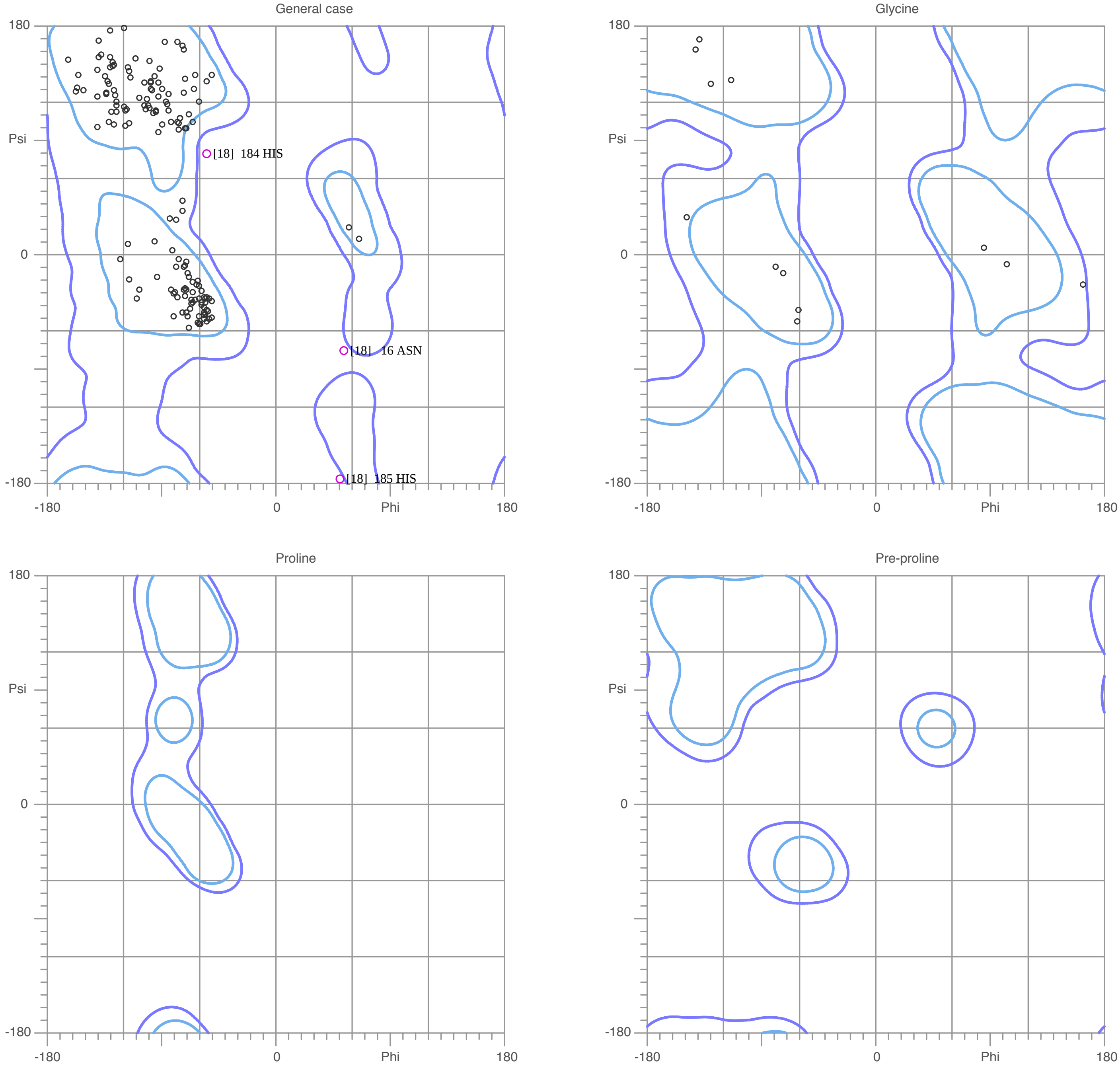
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 18



94.8% (163/172) of all residues were in favored (98%) regions.
98.3% (169/172) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[18] 16 ASN (54.0, -75.4)
[18] 184 HIS (-55.8, 80.6)
[18] 185 HIS (50.1, -176.7)

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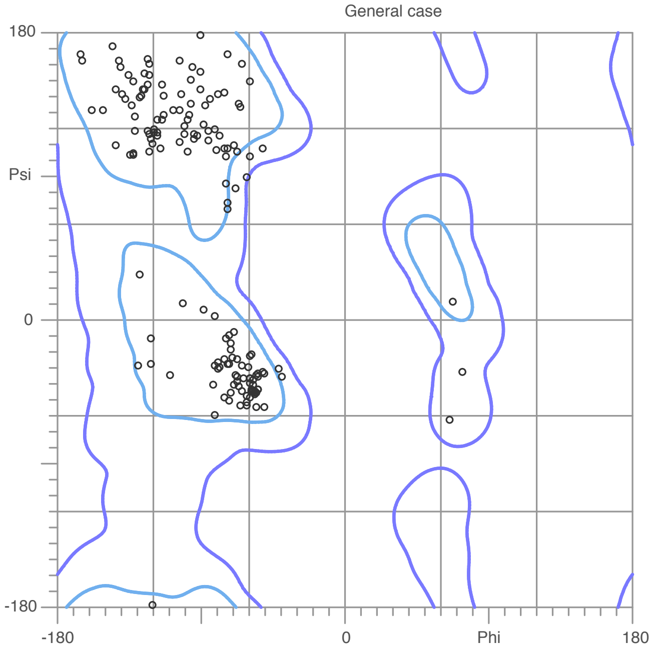
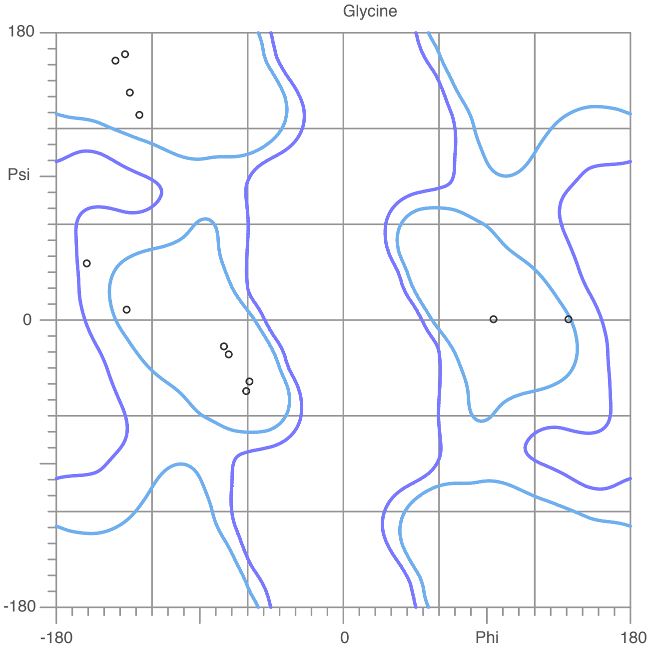
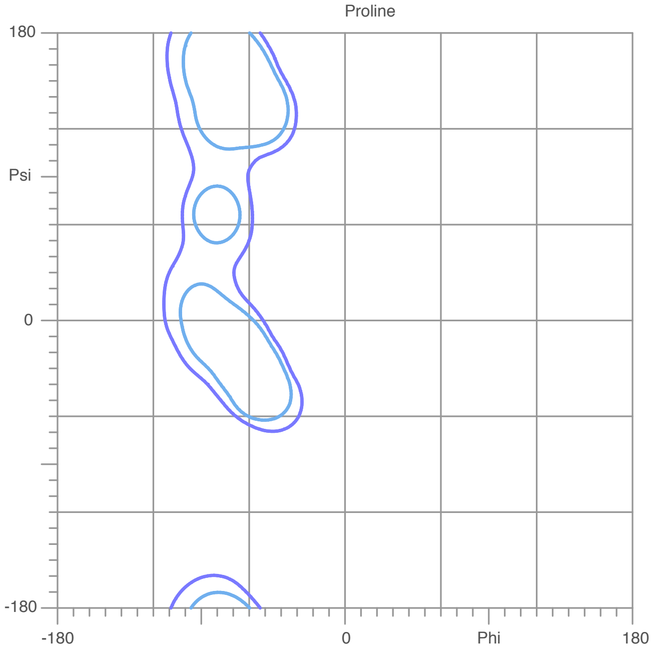
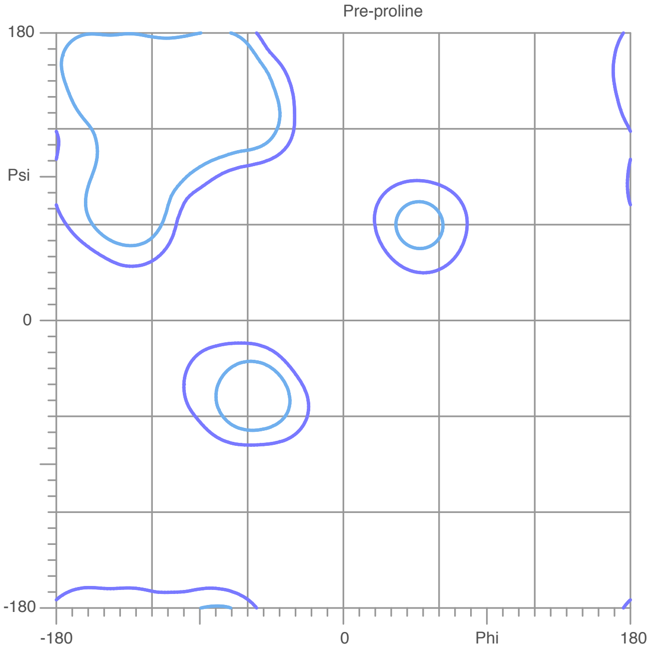
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 19









94.8% (163/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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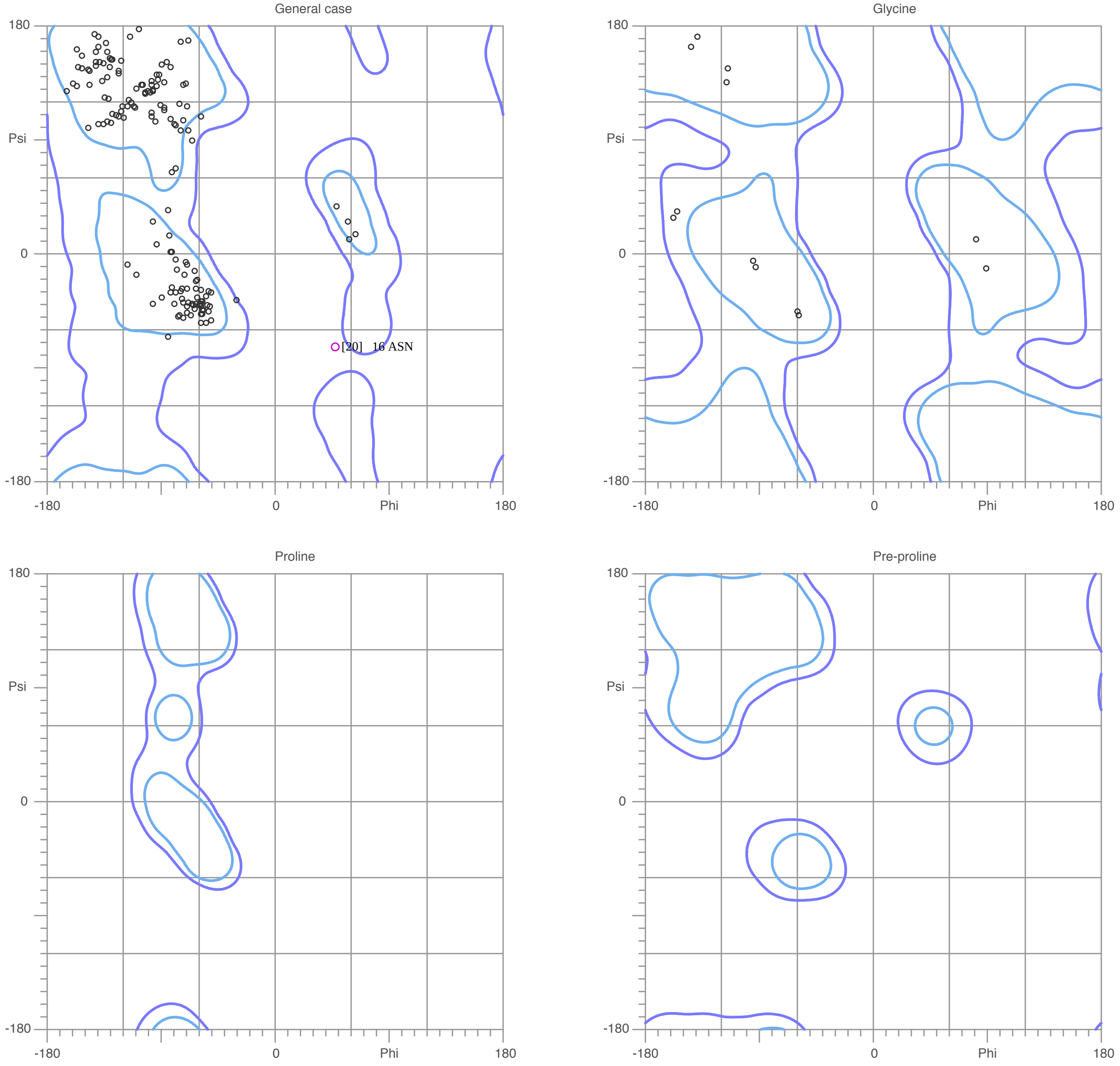
MolProbity Ramachandran analysis

CTR148A_NMR_em_bcr3.pdb, model 20



94.8% (163/172) of all residues were in favored (98%) regions.
99.4% (171/172) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 16 ASN (48.0, -73.9)

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