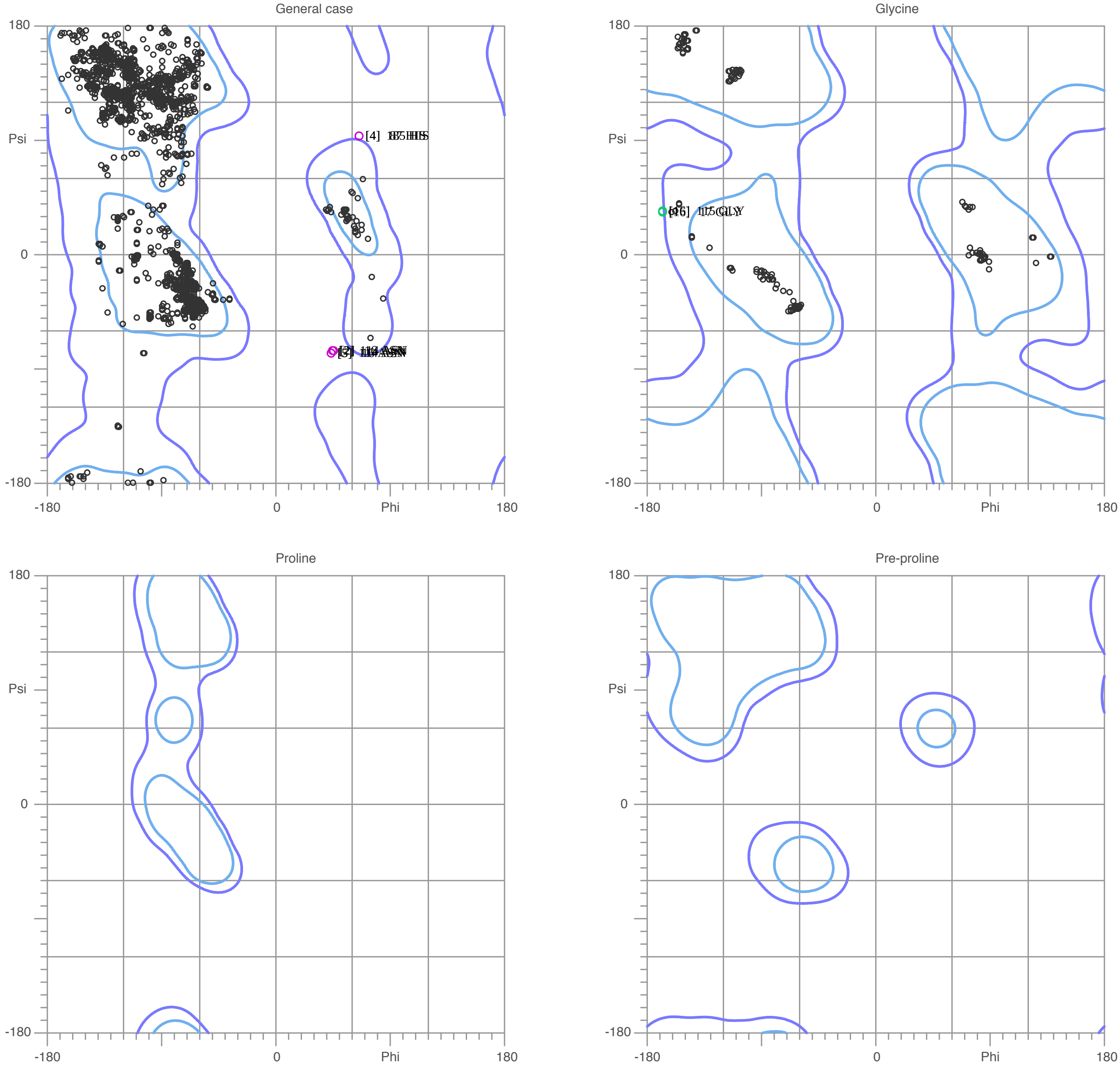
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, all models



97.4% (3352/3440) of all residues were in favored (98%) regions.
99.8% (3432/3440) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[2]	16 ASN (45.0, -75.8)
[2]	114 ASN (45.0, -75.8)
[4]	87 HIS (65.4, 94.4)
[4]	185 HIS (65.5, 94.4)
[5]	16 ASN (43.4, -77.5)
[5]	114 ASN (43.3, -77.5)
[16]	17 GLY (-168.4, 34.9)
[16]	115 GLY (-168.4, 35.0)

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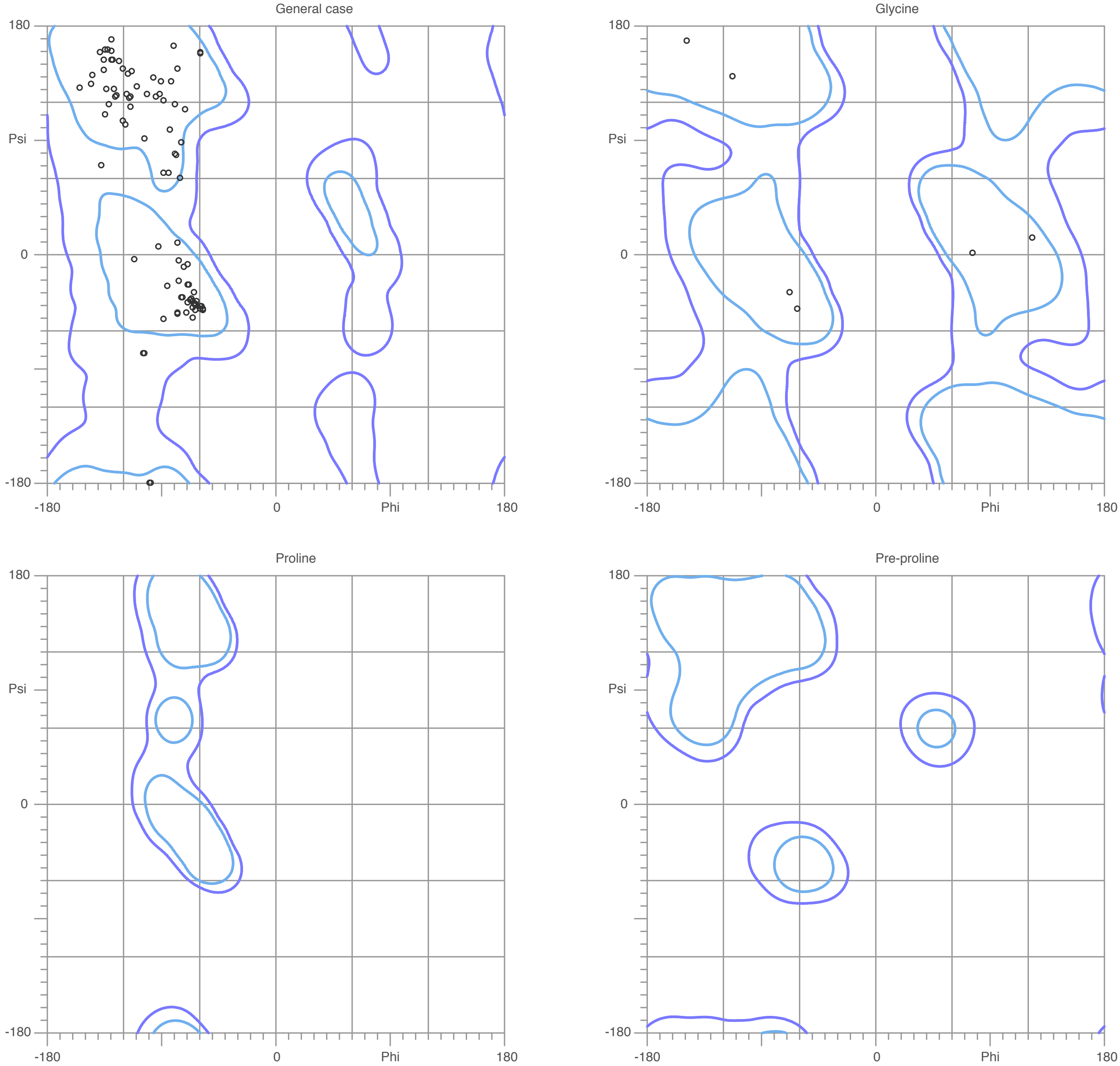
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 1



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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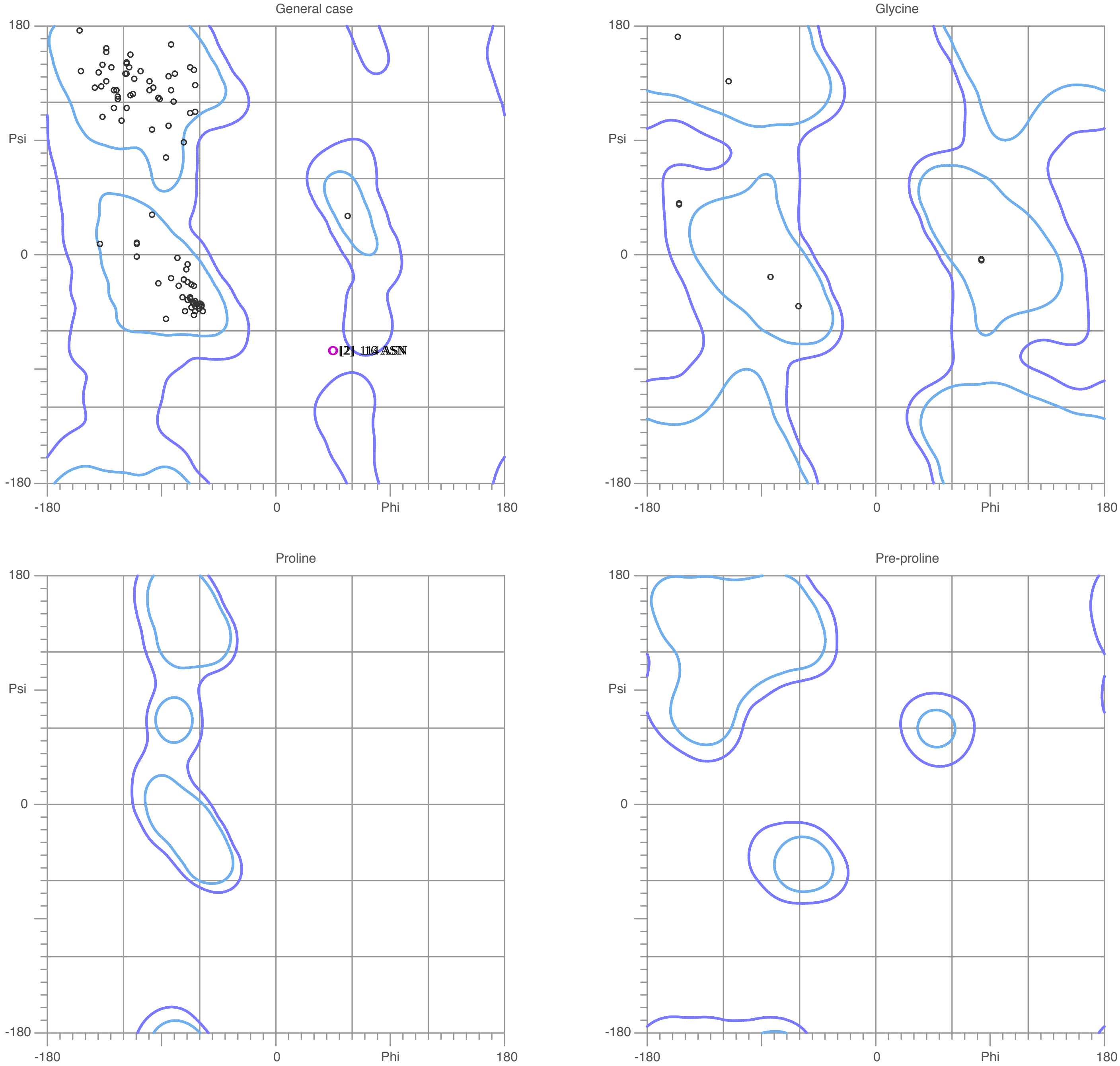
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 2



97.7% (168/172) 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):
[2] 16 ASN (45.0, -75.8)
[2] 114 ASN (45.0, -75.8)

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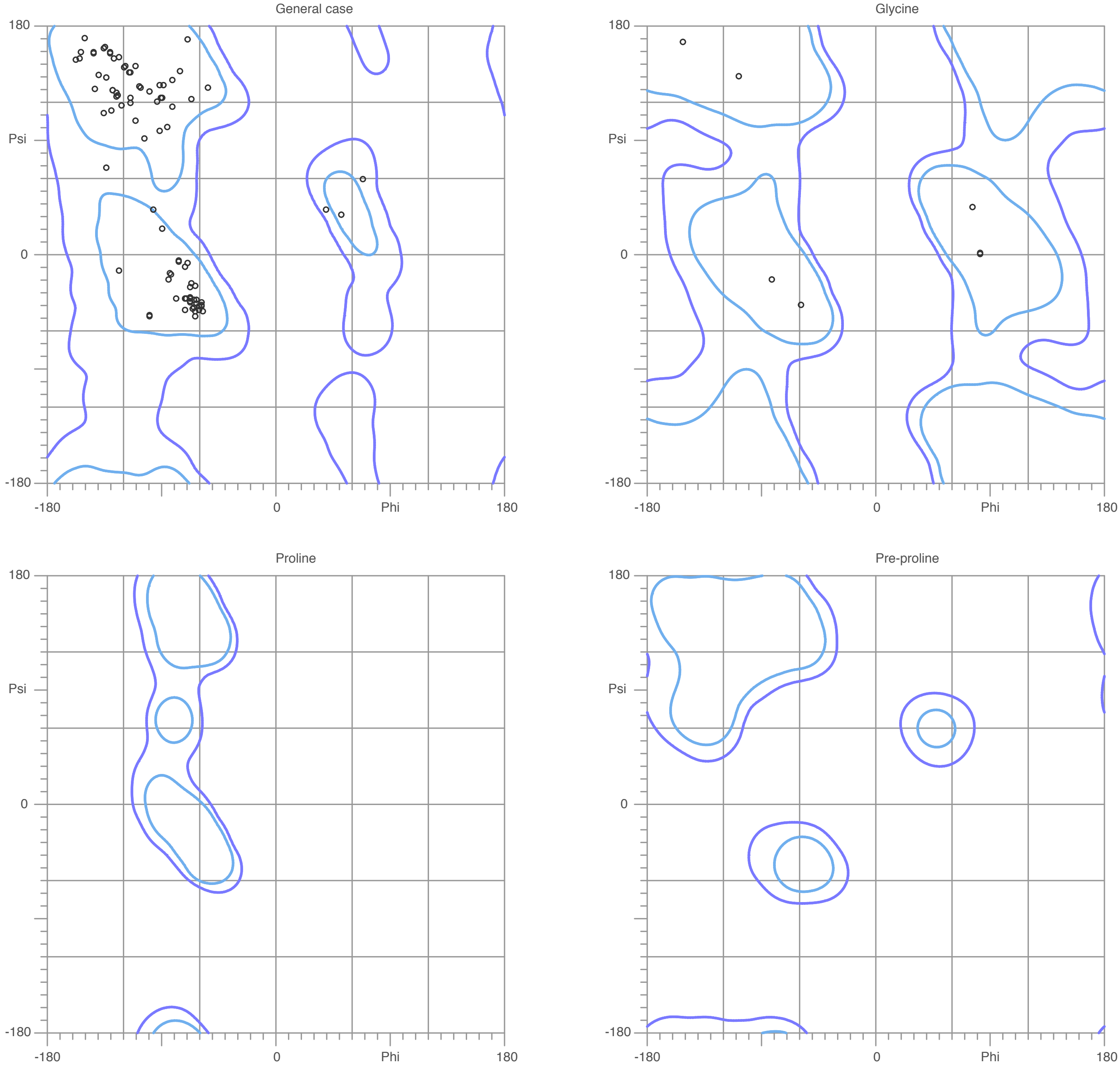
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 3



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.

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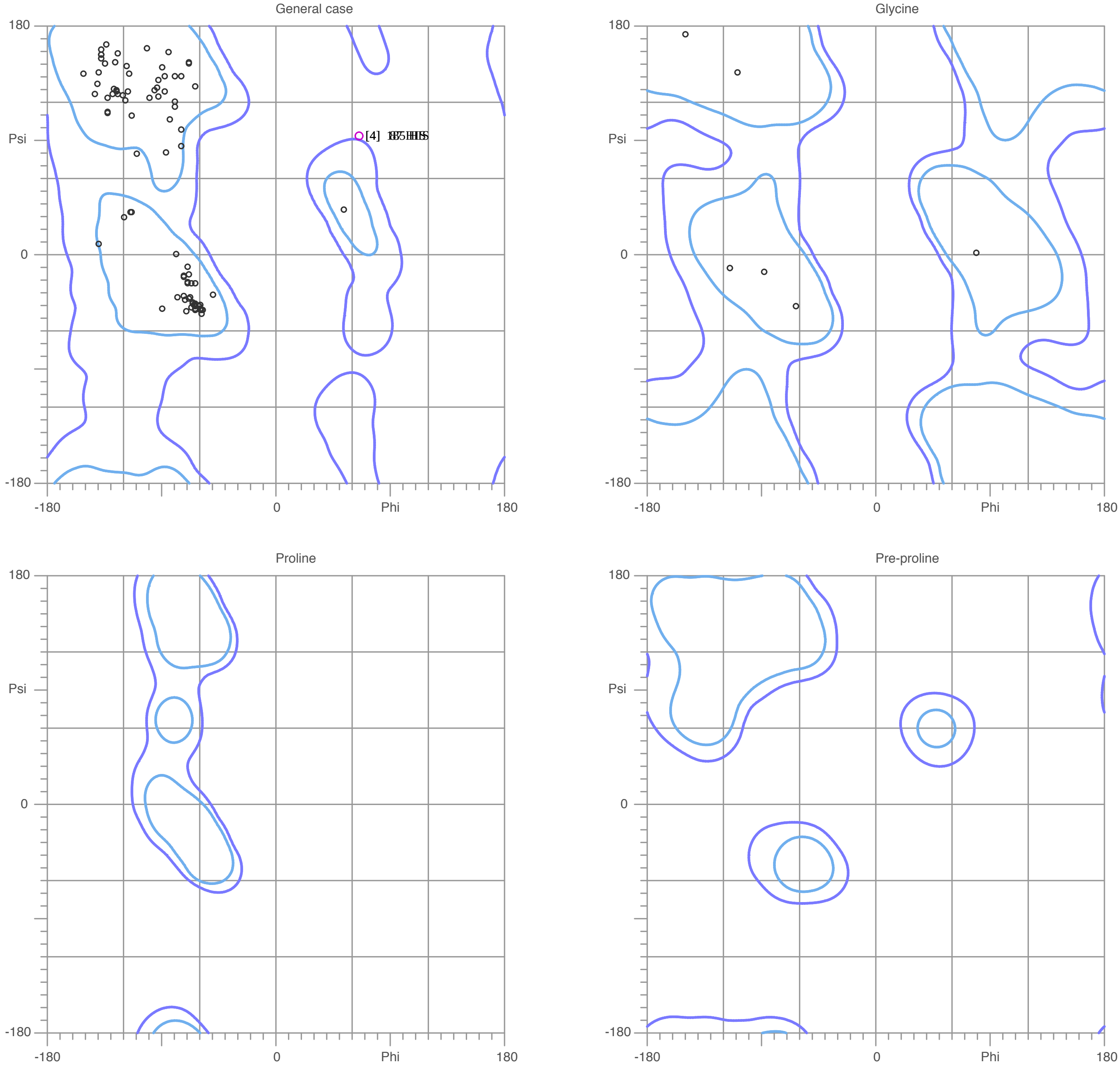
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 4



97.7% (168/172) 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):
[4] 87 HIS (65.4, 94.4)
[4] 185 HIS (65.5, 94.4)

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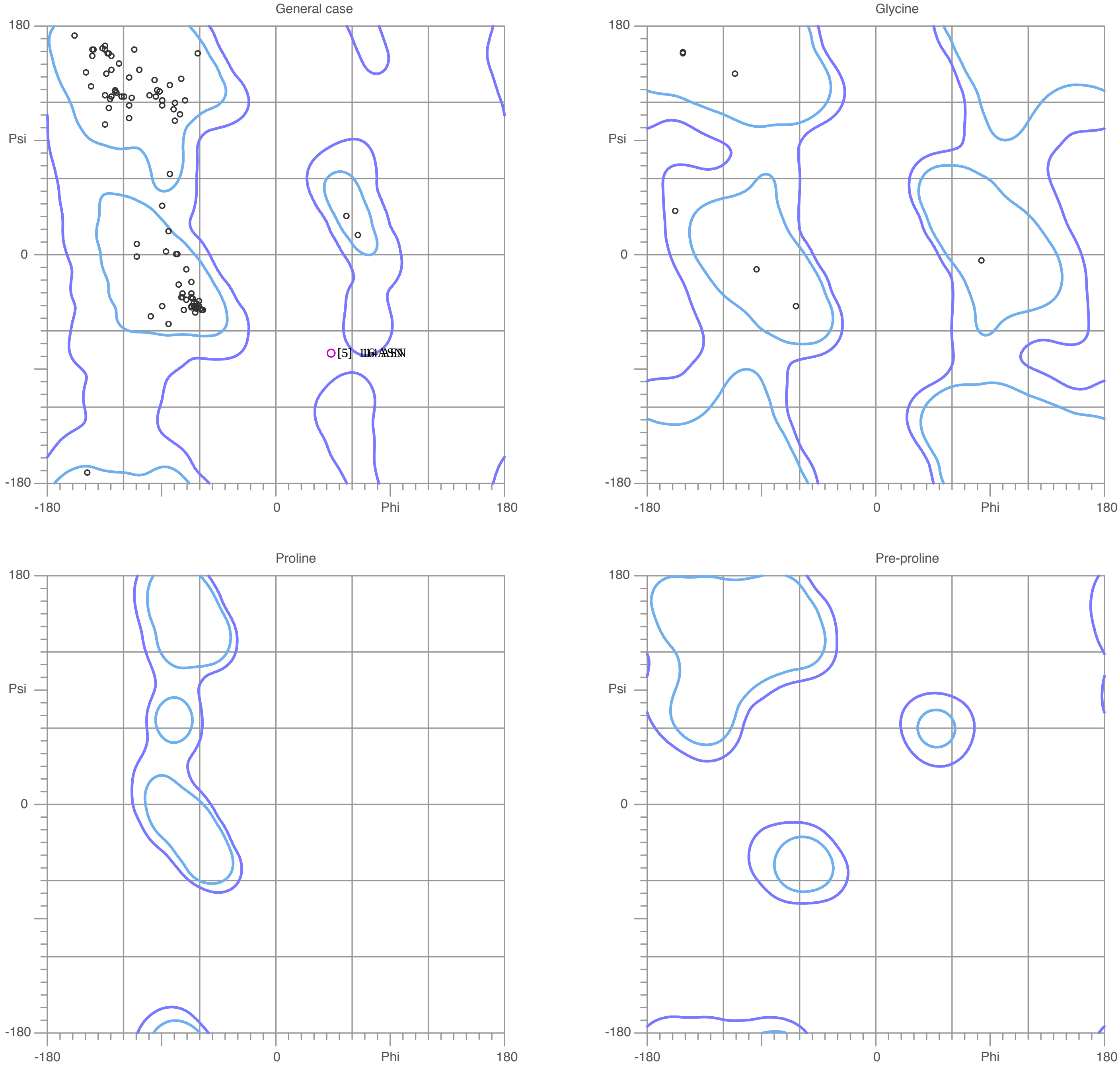
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 5

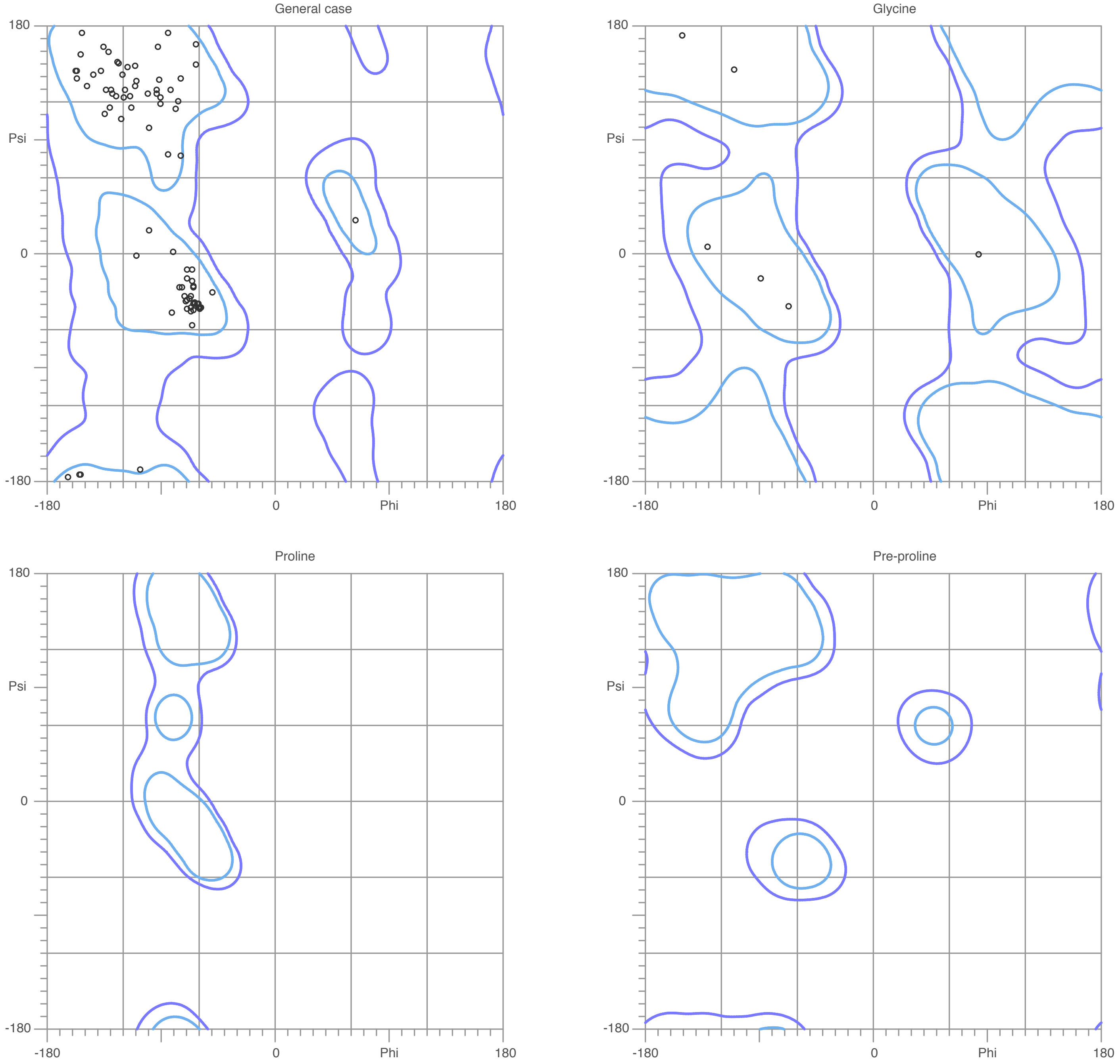


96.5% (166/172) of all residues were in favored (98%) regions.
98.8% (170/172) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[5] 16 ASN (43.4, -77.5)
[5] 114 ASN (43.3, -77.5)

MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 6

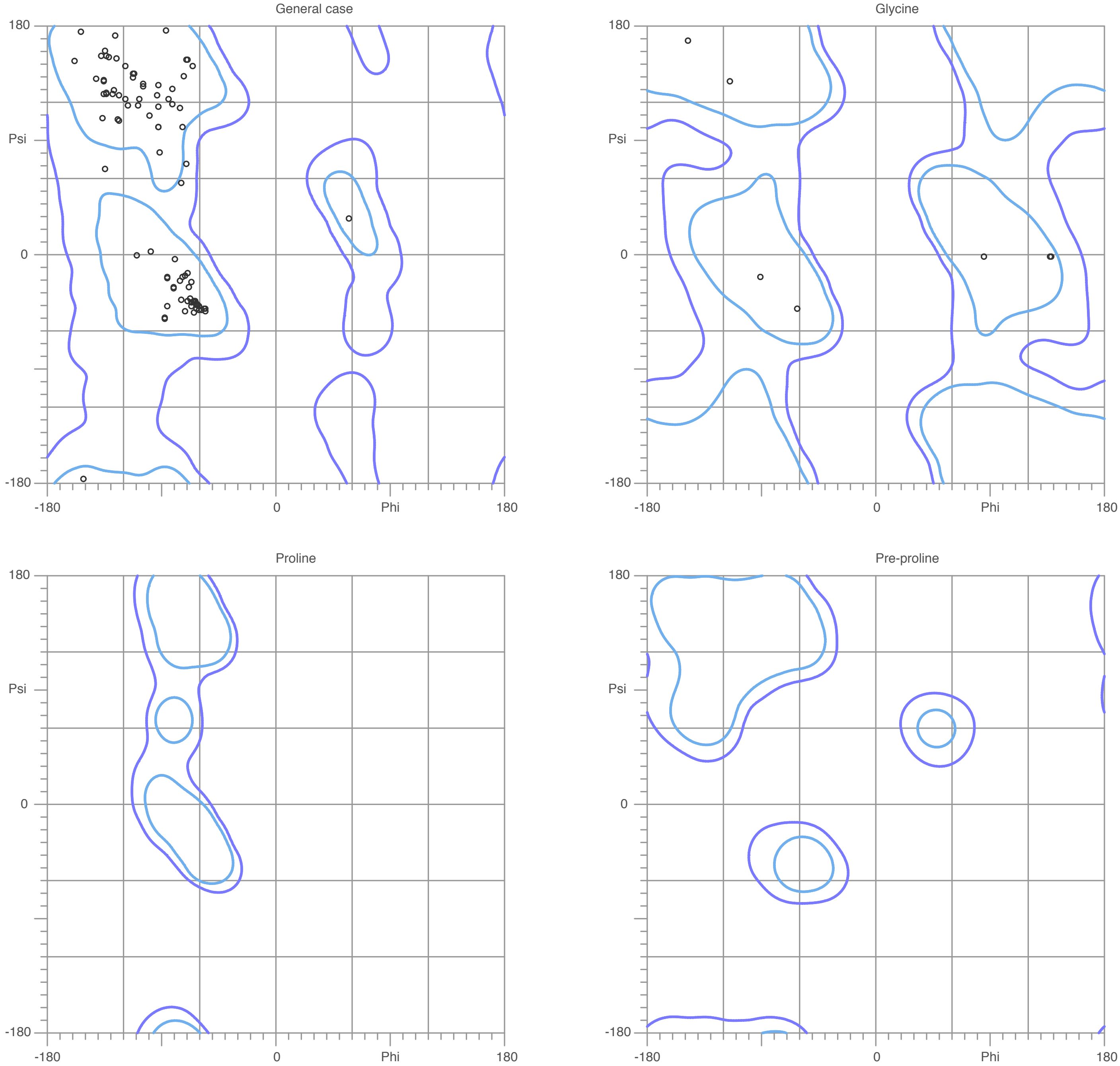


98.8% (170/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_R3Cons_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.

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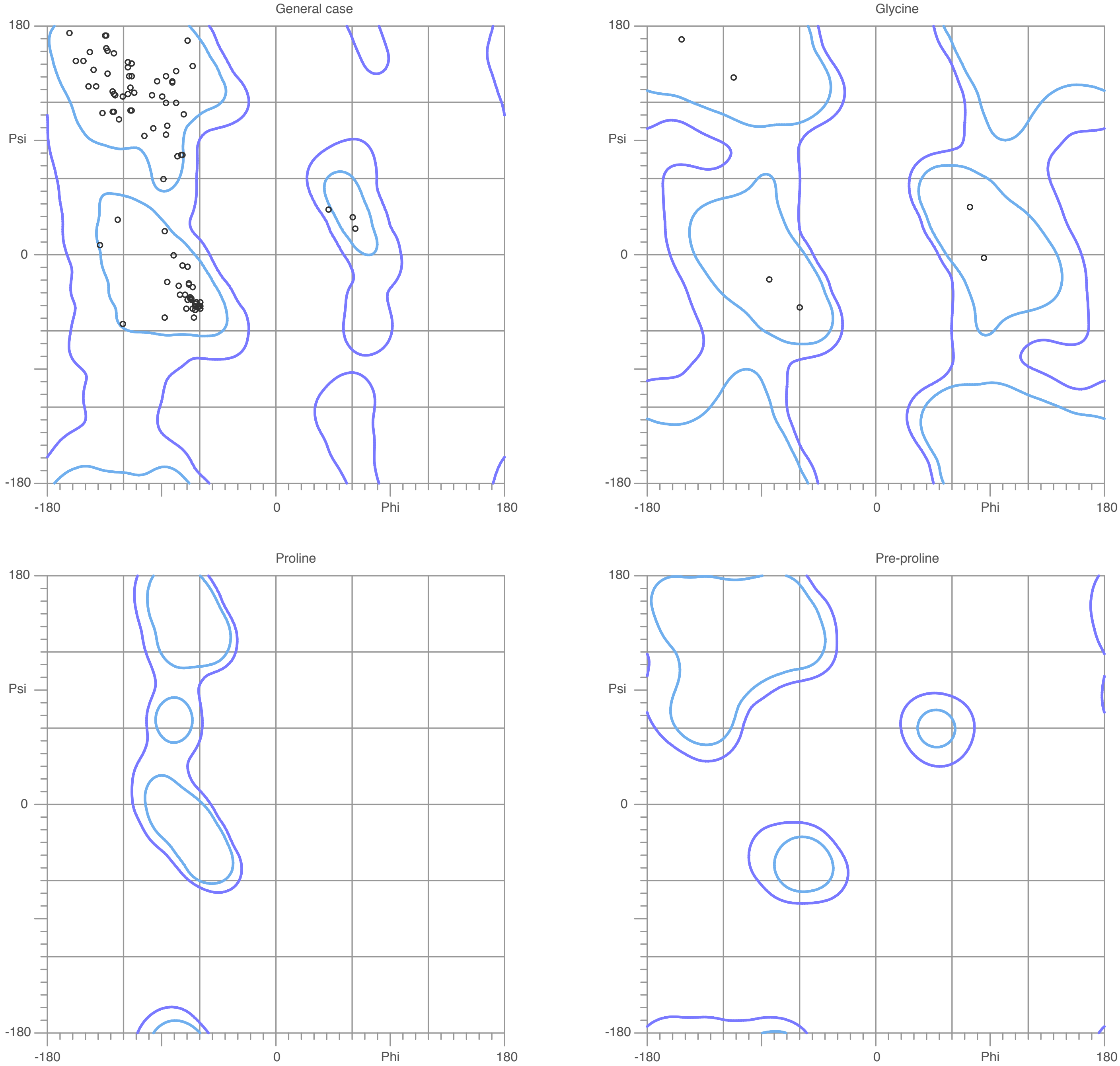
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 8

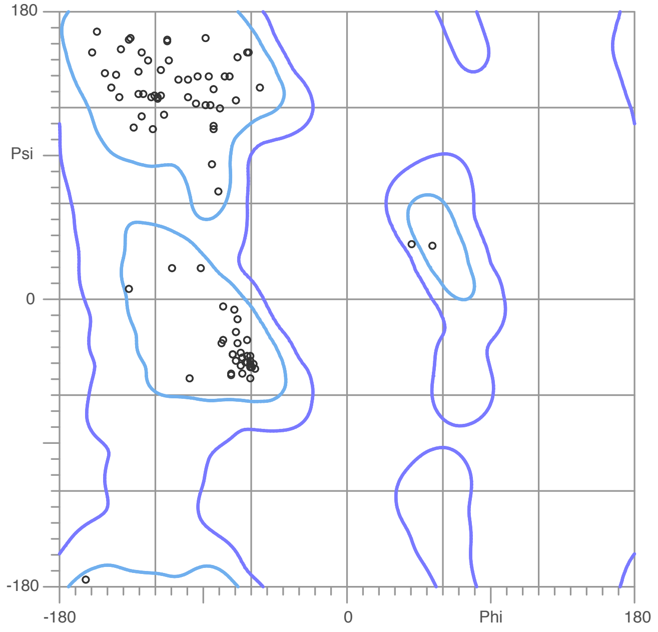


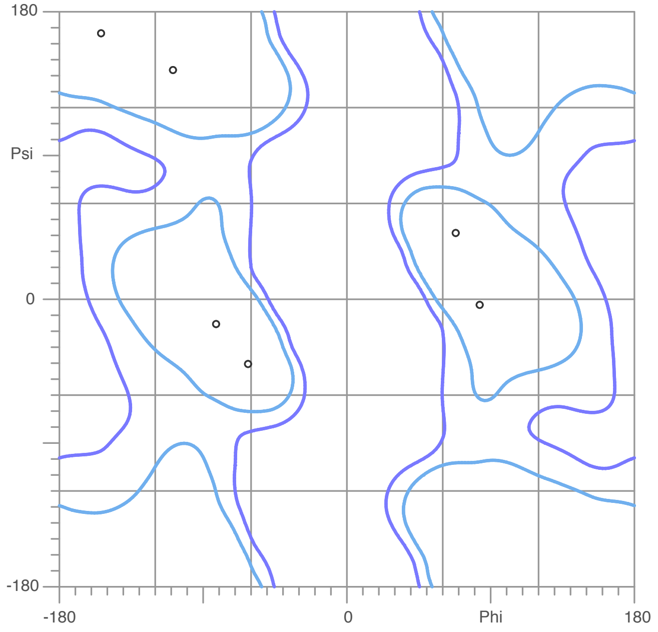
98.8% (170/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

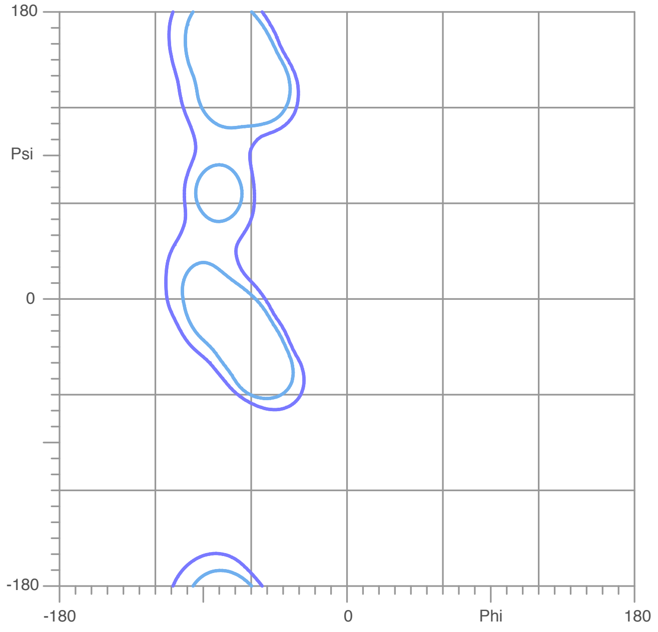
There were no outliers.

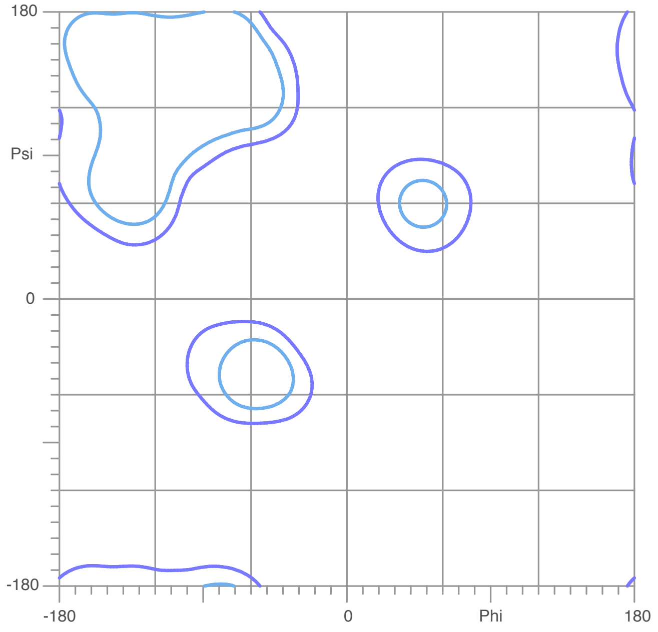
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 9


General case


Glycine


Proline


Pre-proline

98.8% (170/172) 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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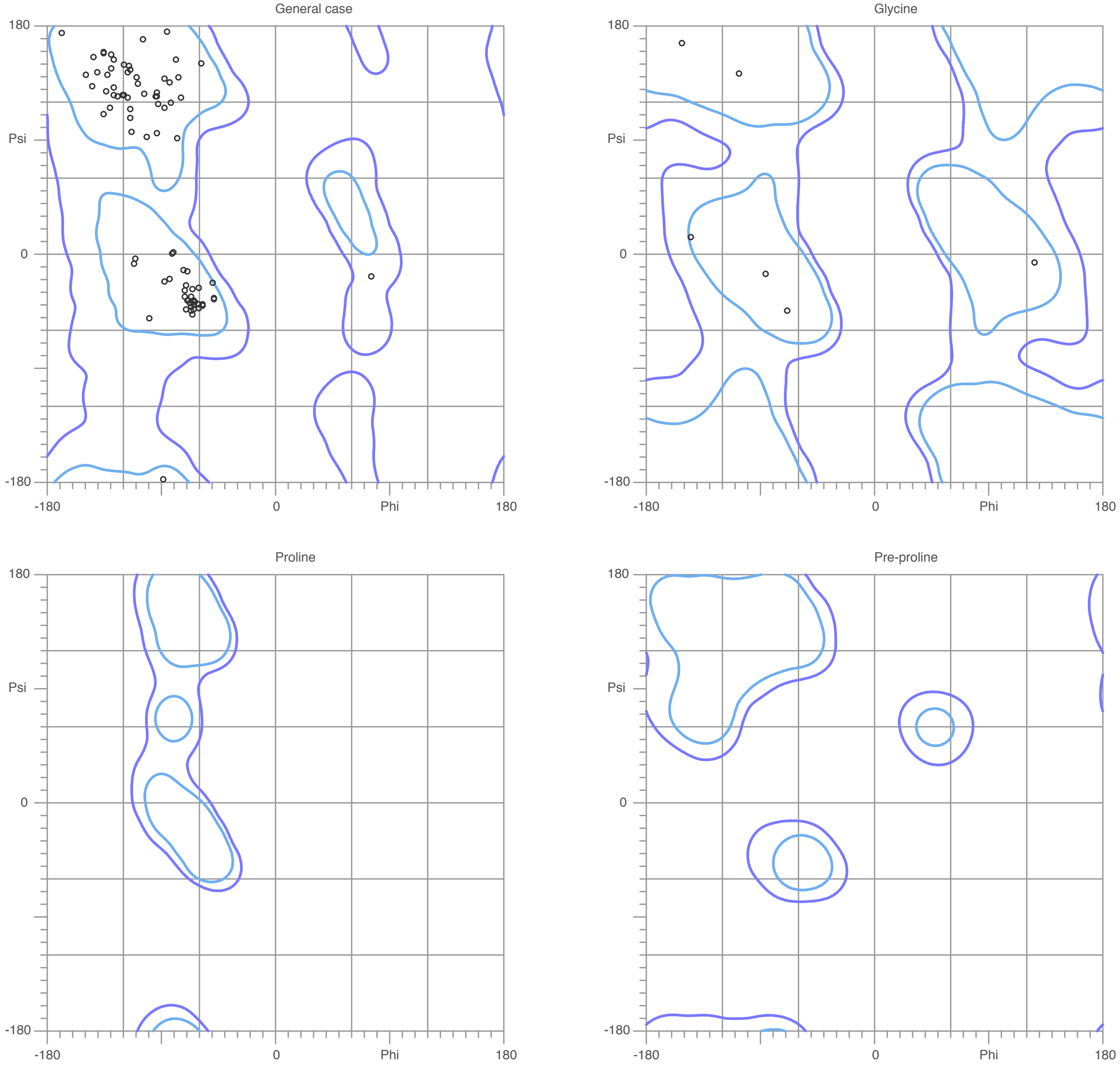
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 10



98.8% (170/172) 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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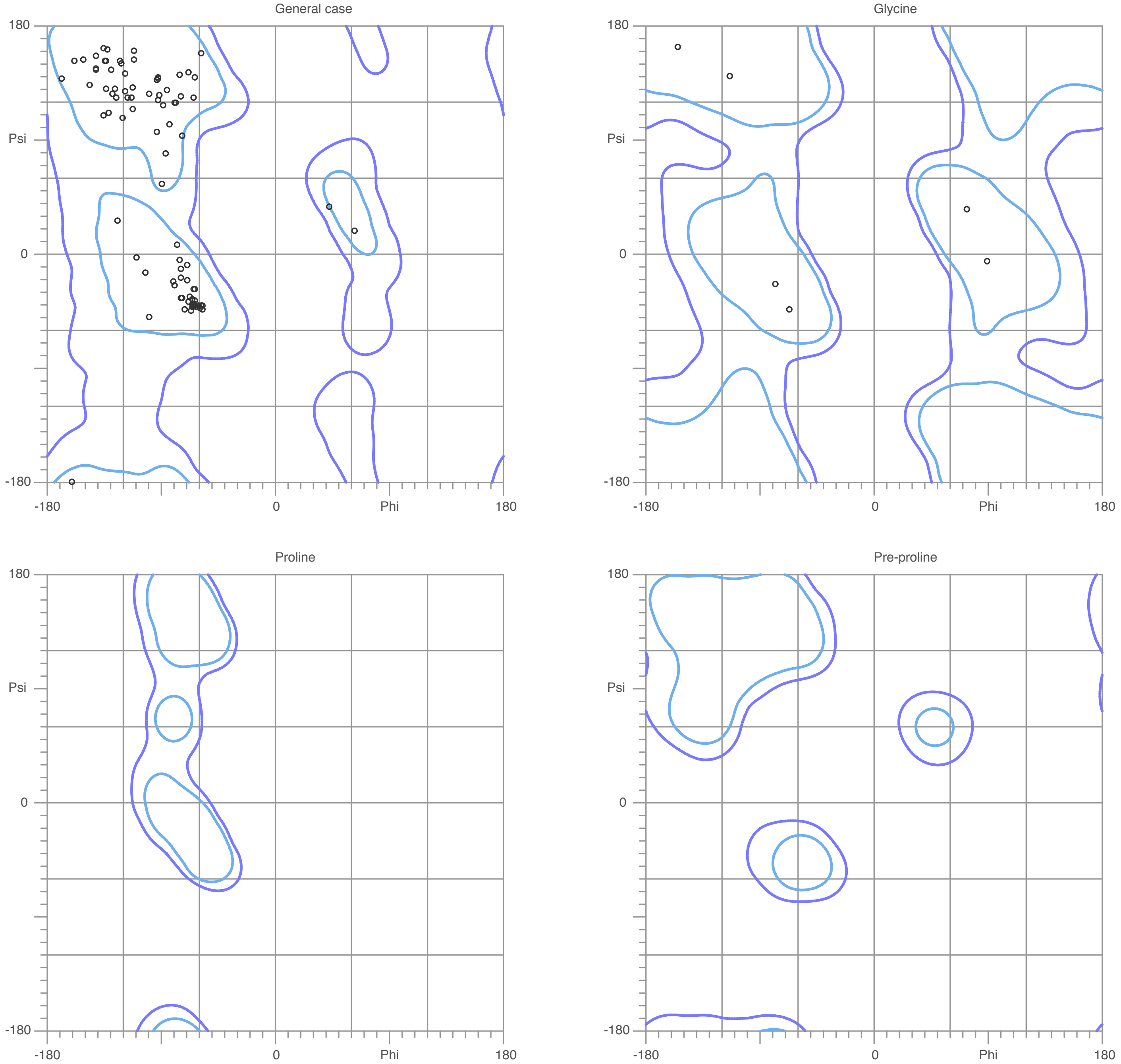
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 11



100.0% (172/172) 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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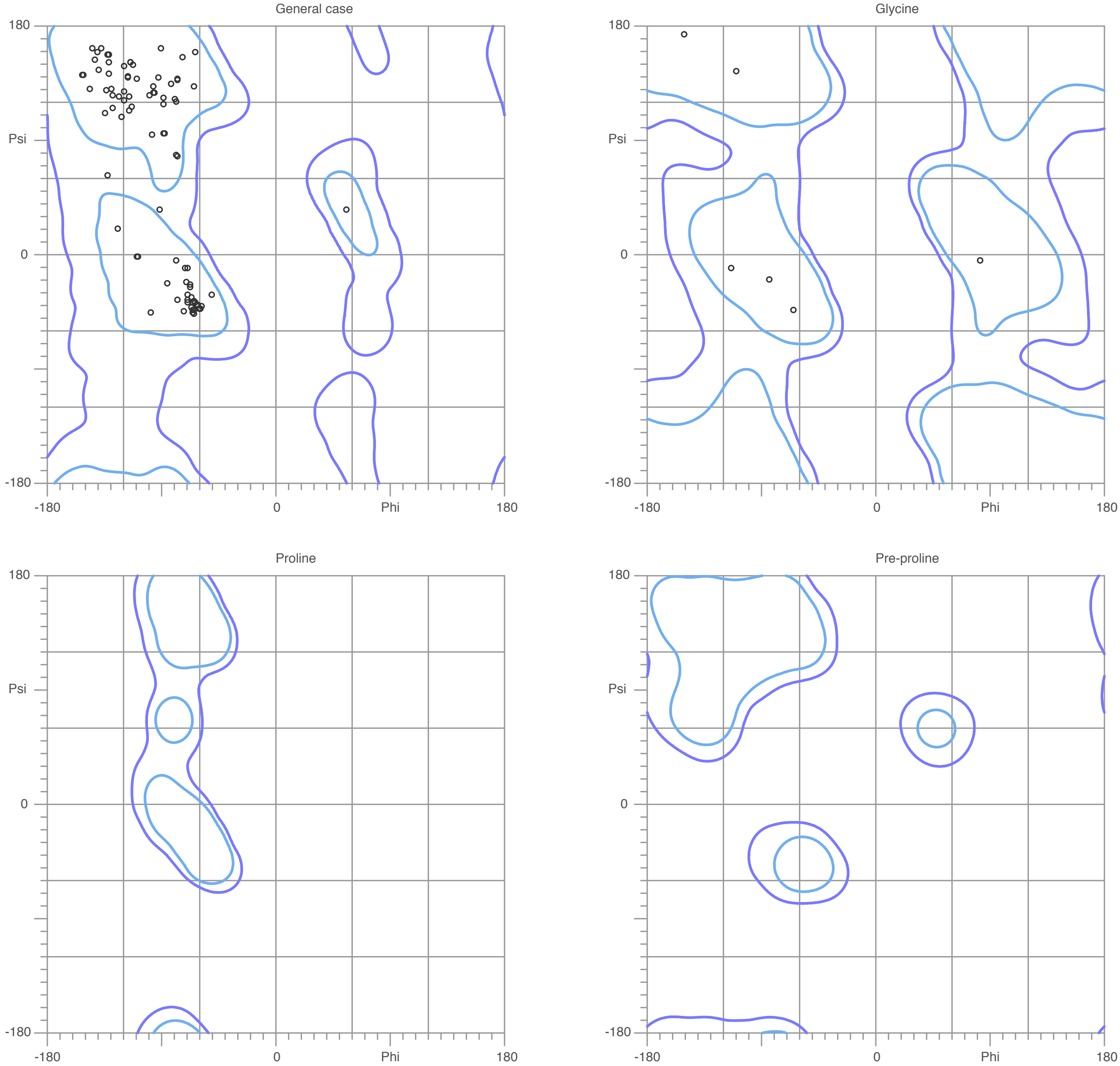
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 12



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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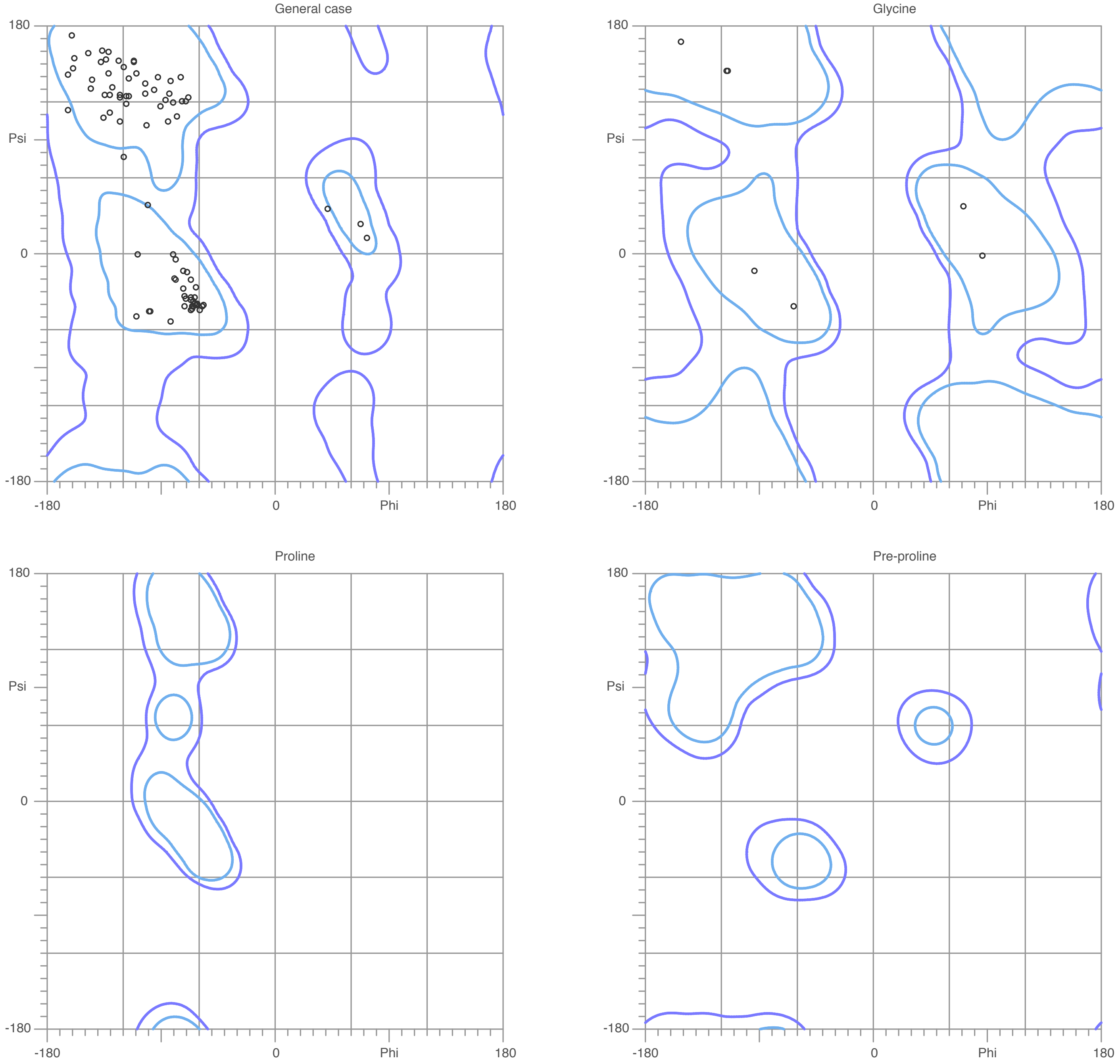
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 13

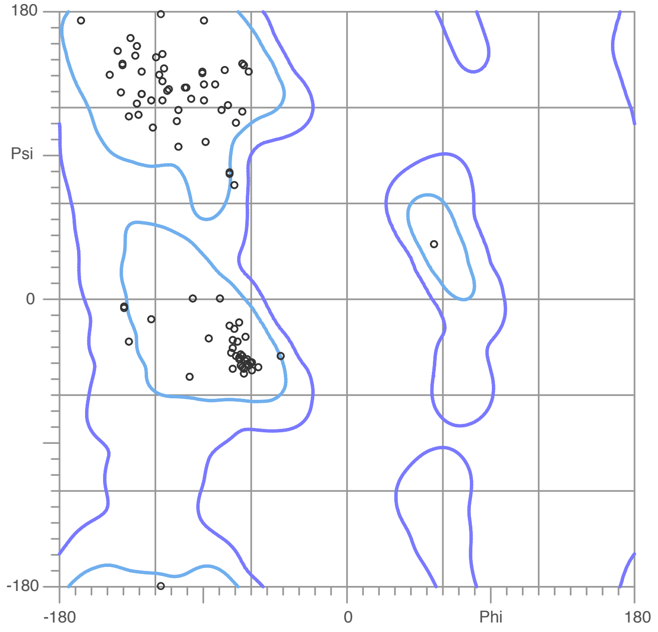


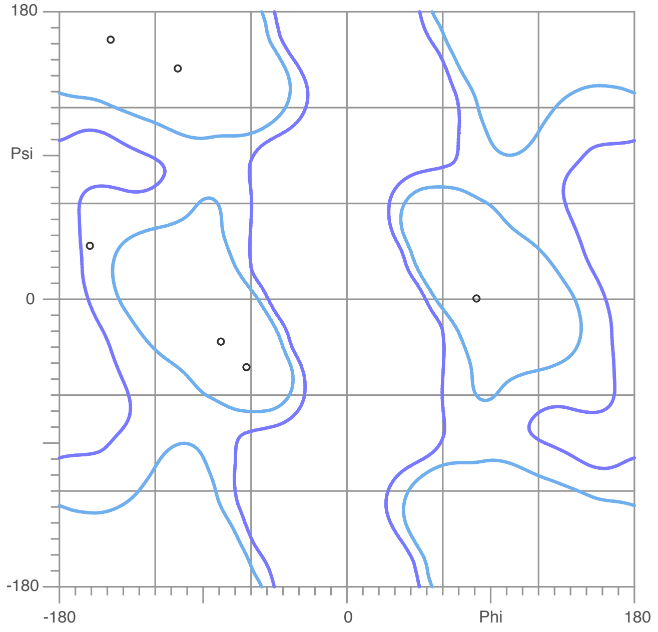
95.3% (164/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

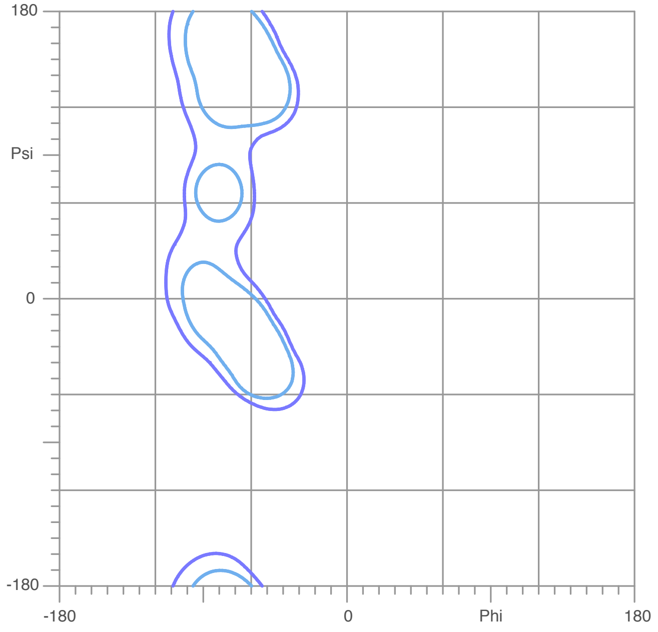
There were no outliers.

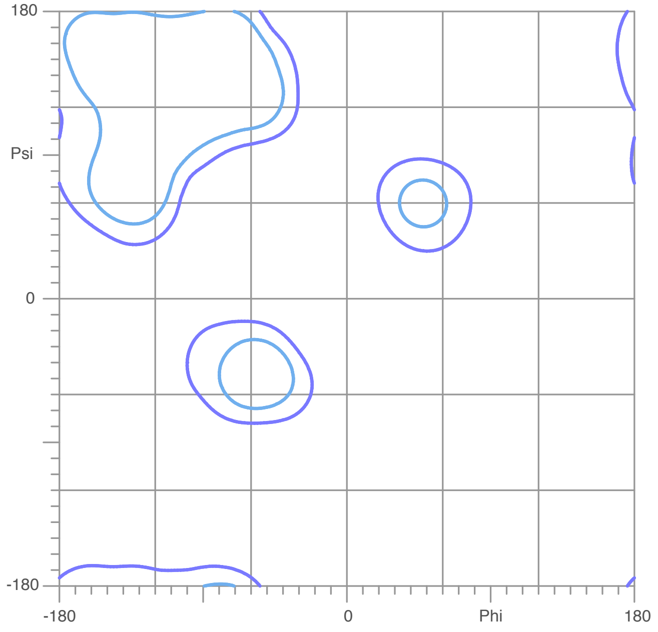
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 14


General case


Glycine


Proline


Pre-proline

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.

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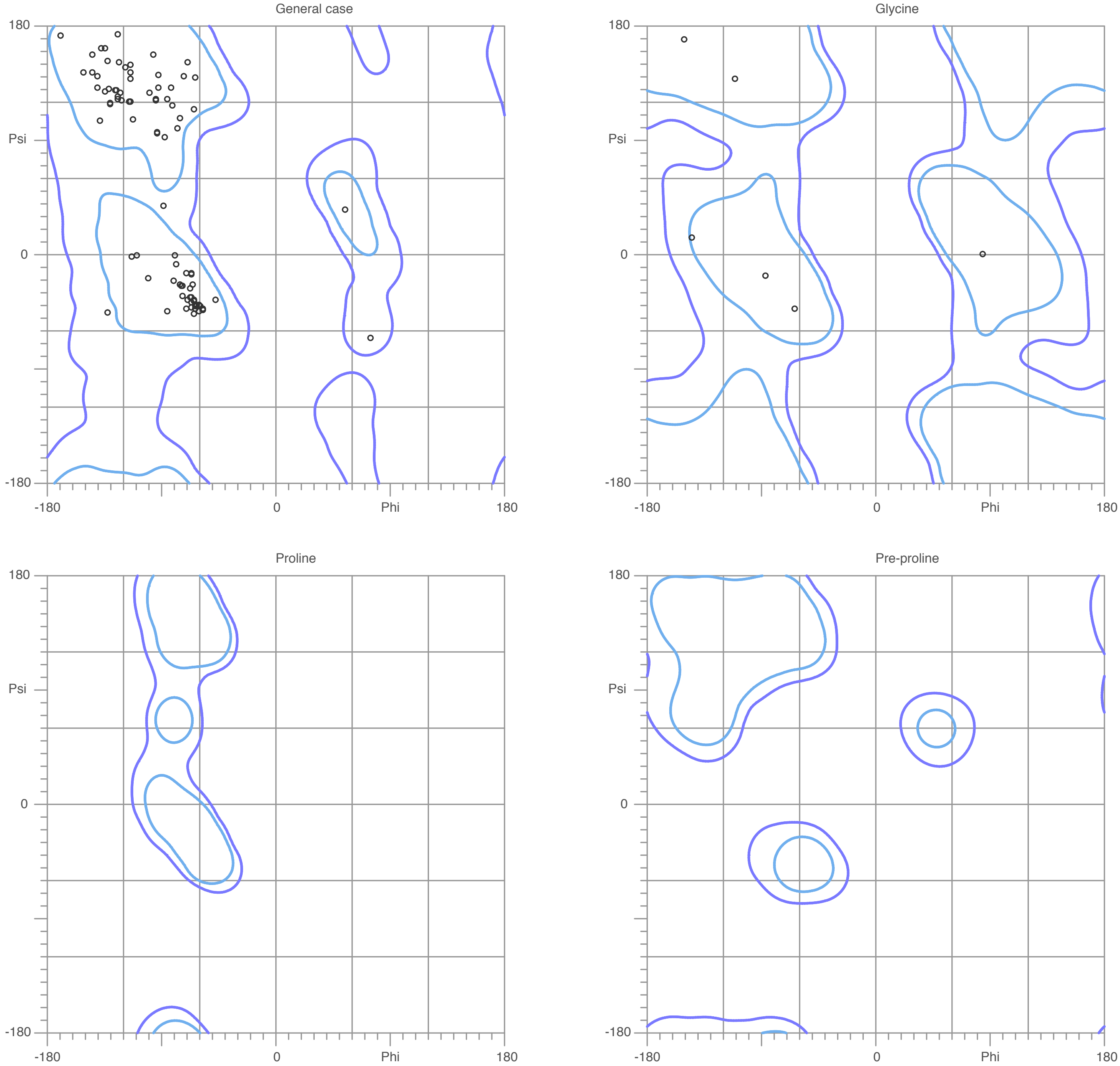
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 15

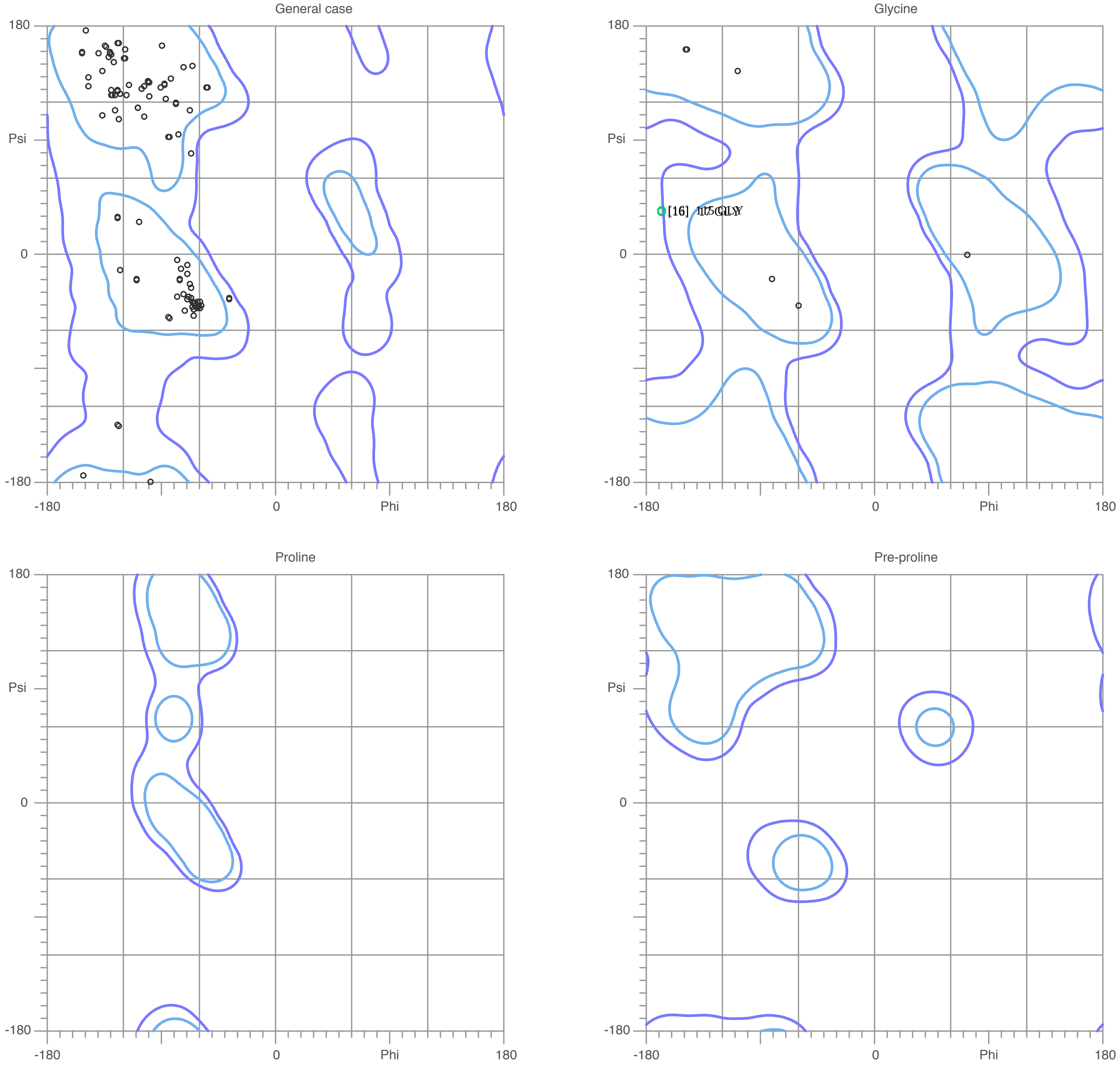


96.5% (166/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 16



95.3% (164/172) 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):
[16] 17 GLY (-168.4, 34.9)
[16] 115 GLY (-168.4, 35.0)

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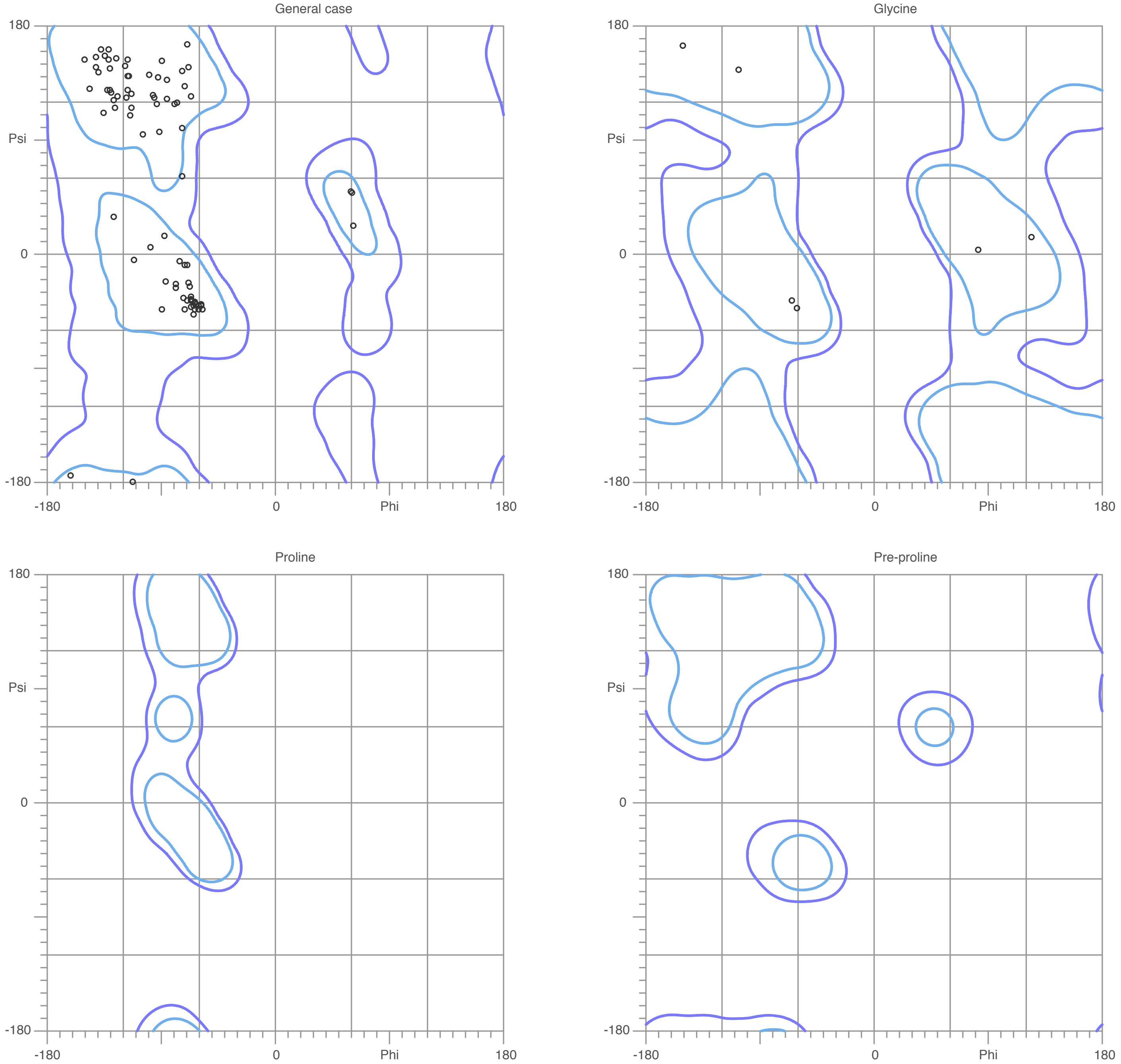
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 17

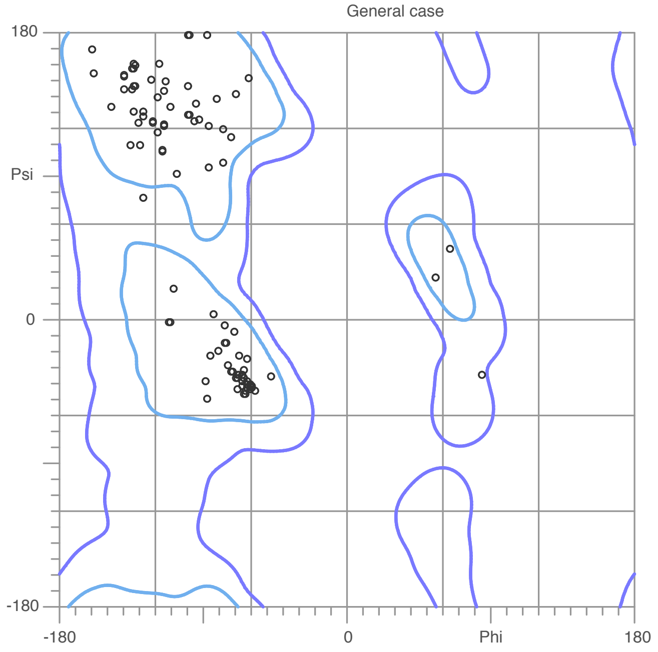


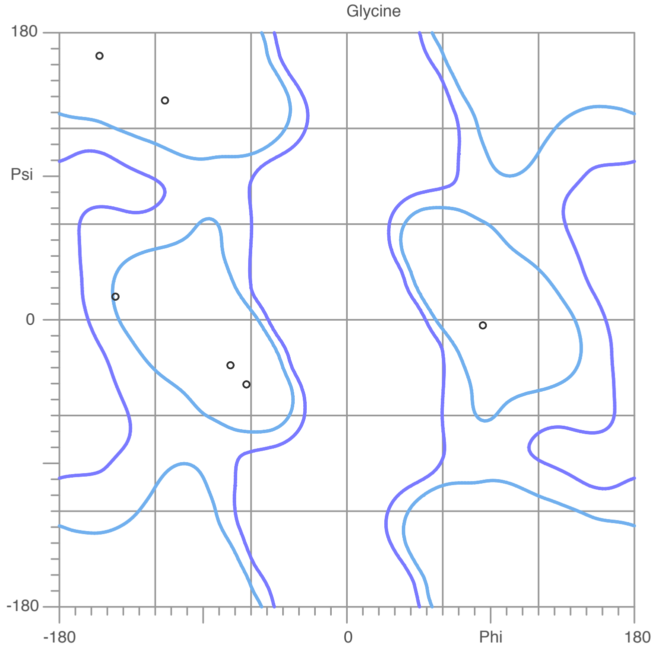
98.8% (170/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

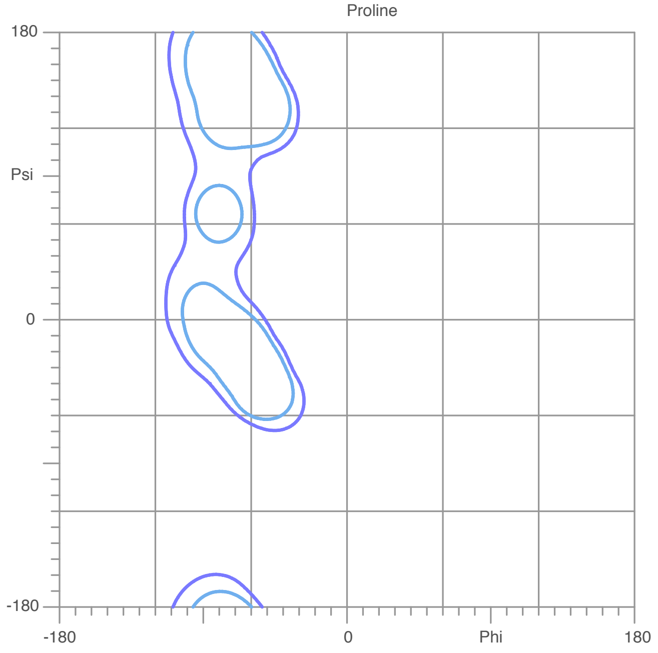
There were no outliers.

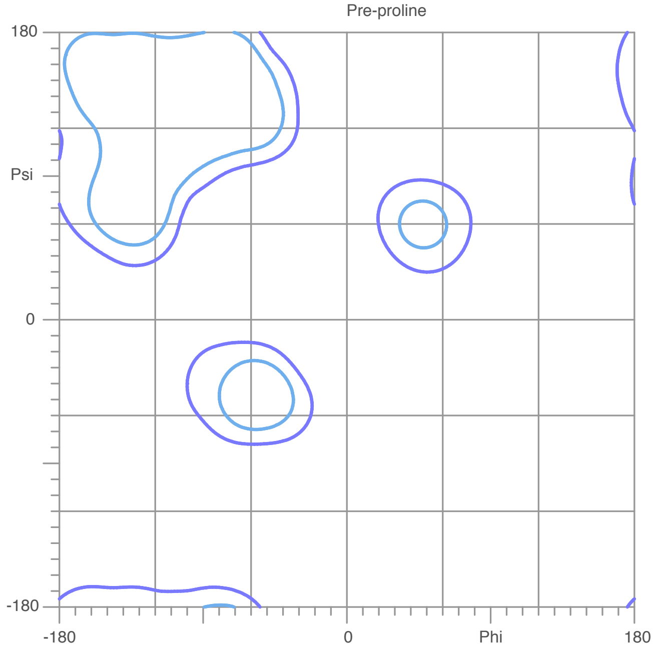
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 18









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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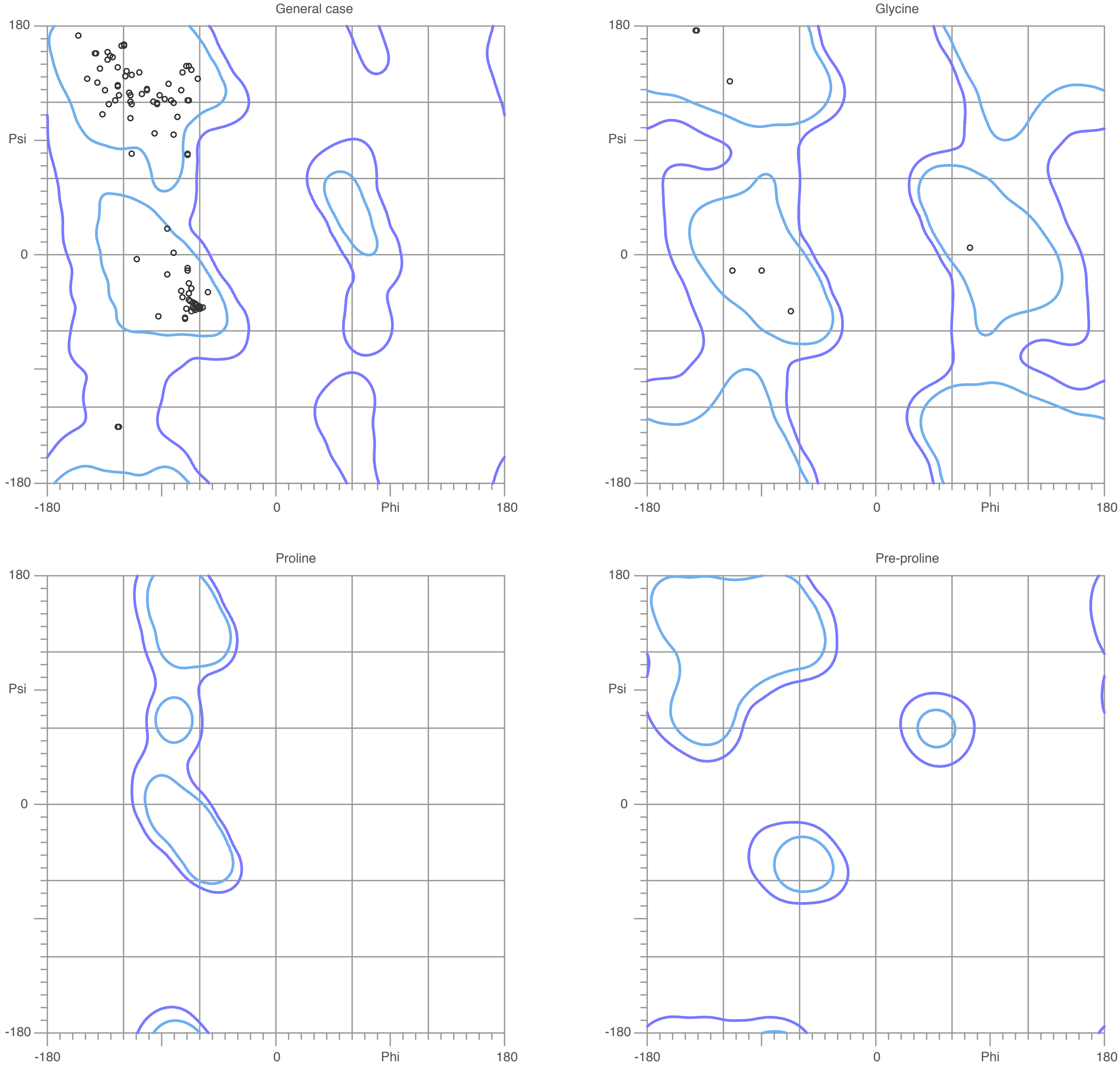
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 19



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.

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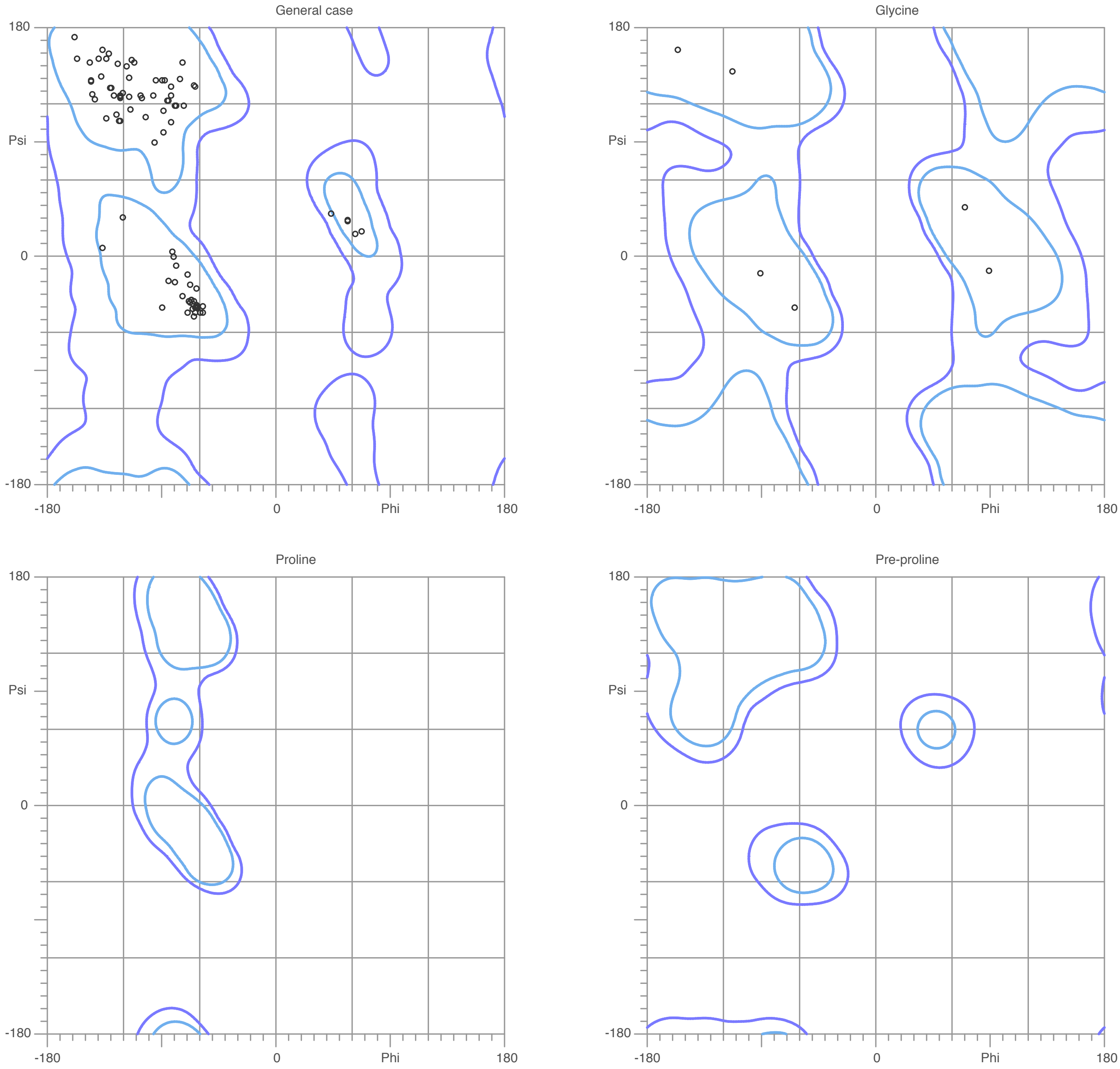
MolProbity Ramachandran analysis

CTR148A_R3Cons_em_bcr3.pdb, model 20



98.8% (170/172) 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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