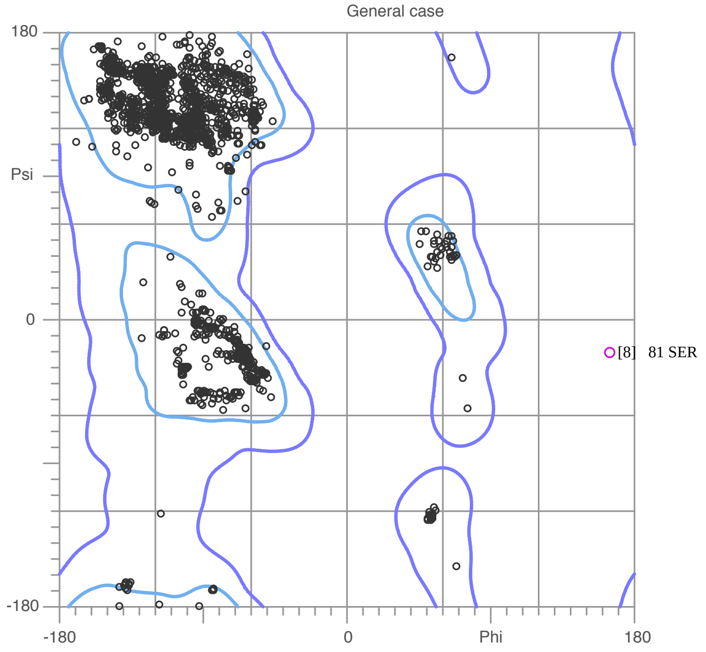
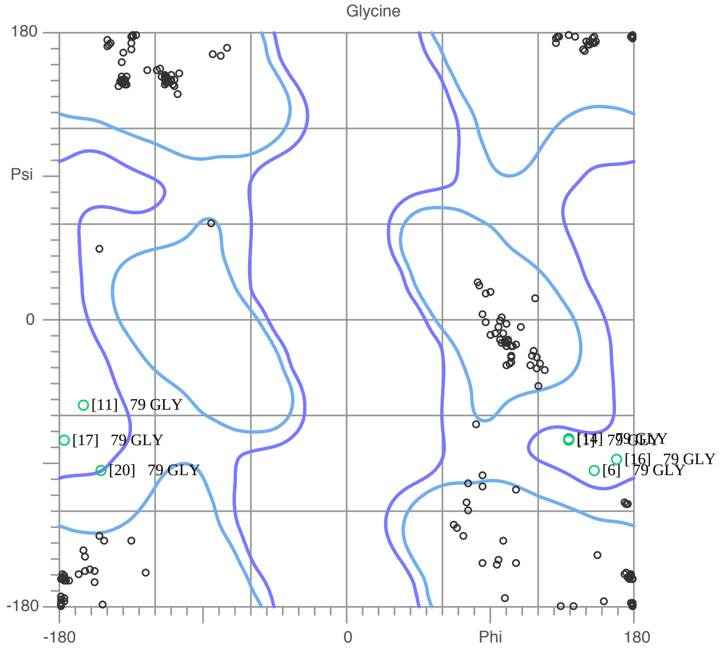
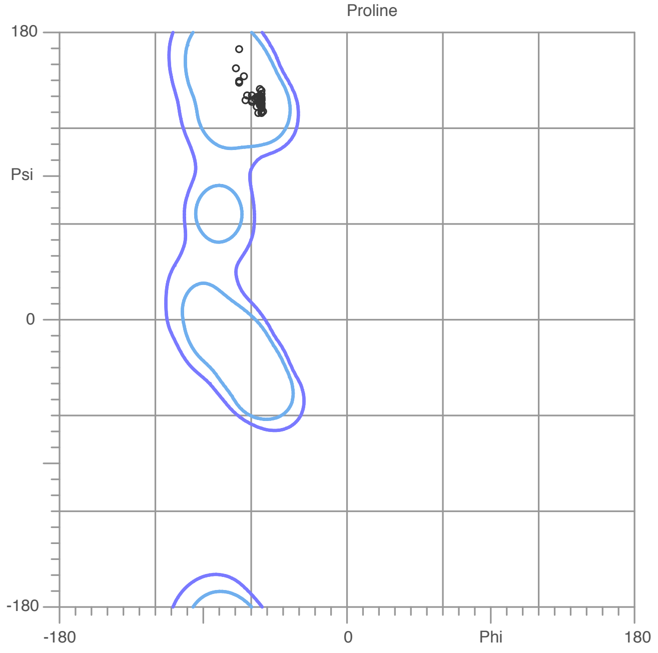
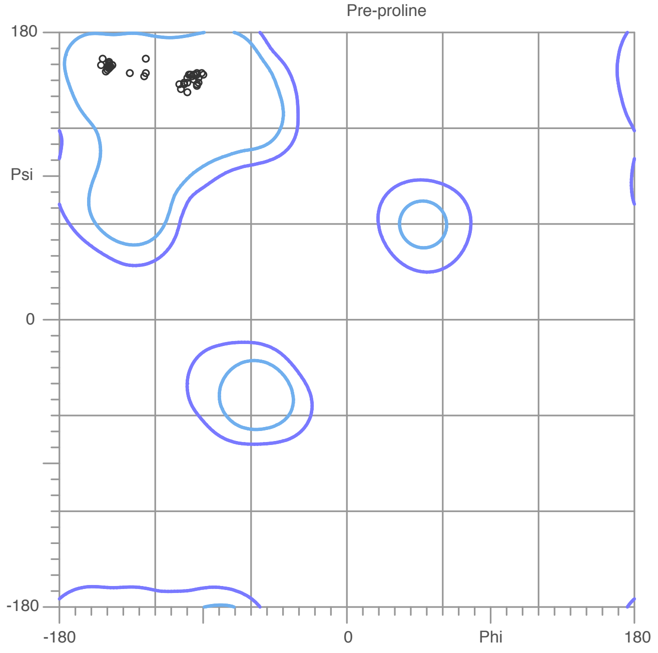
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, all models









96.8% (1859/1920) of all residues were in favored (98%) regions.
99.6% (1912/1920) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):
[1] 79 GLY (139.4, -75.2)
[6] 79 GLY (155.0, -94.0)
[8] 81 SER (165.0, -20.8)
[11] 79 GLY (-165.1, -53.4)
[14] 79 GLY (139.7, -75.0)
[16] 79 GLY (169.5, -87.9)
[17] 79 GLY (-177.7, -75.0)
[20] 79 GLY (-155.0, -95.0)

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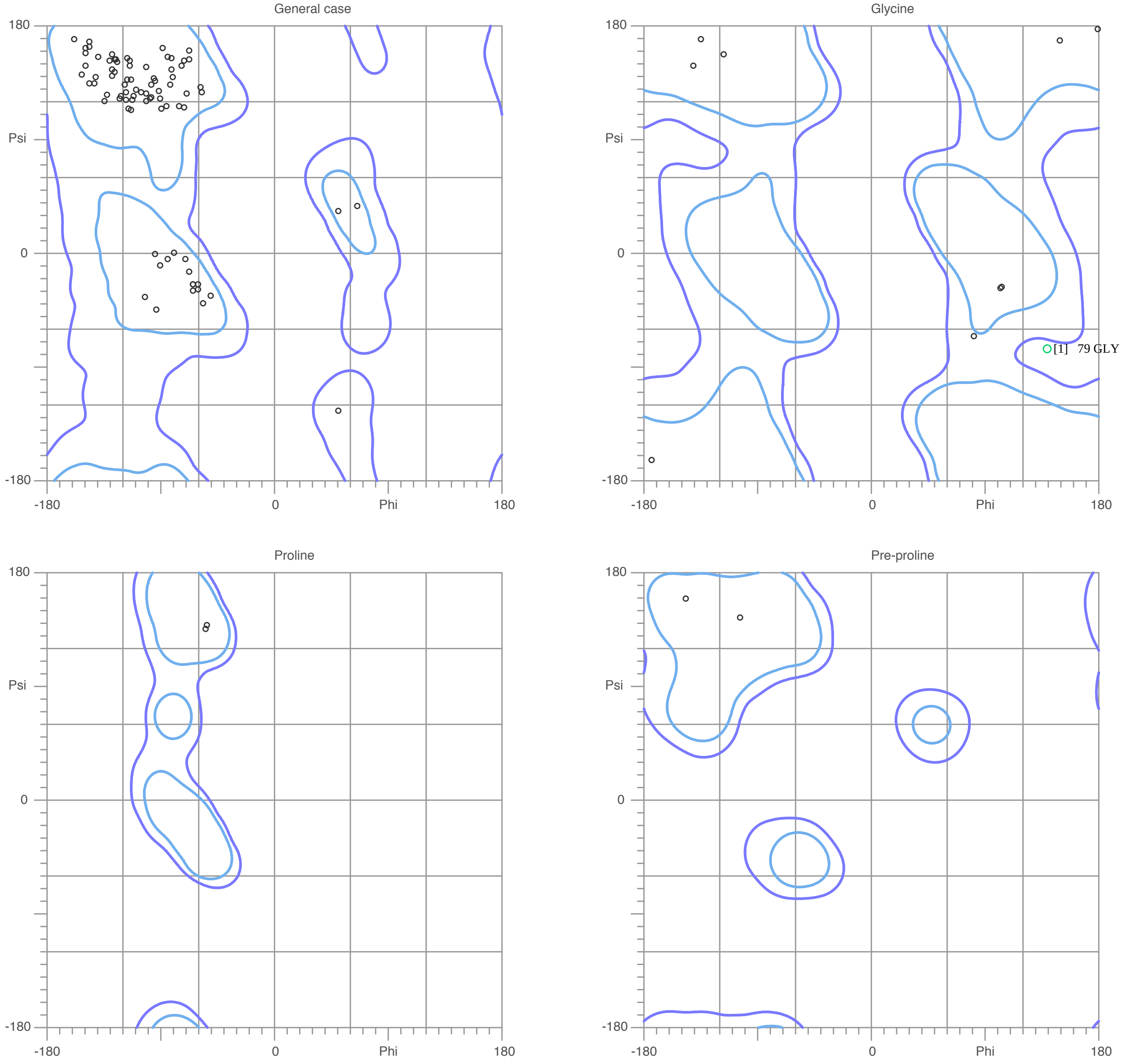
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 1



96.9% (93/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[1] 79 GLY (139.4, -75.2)

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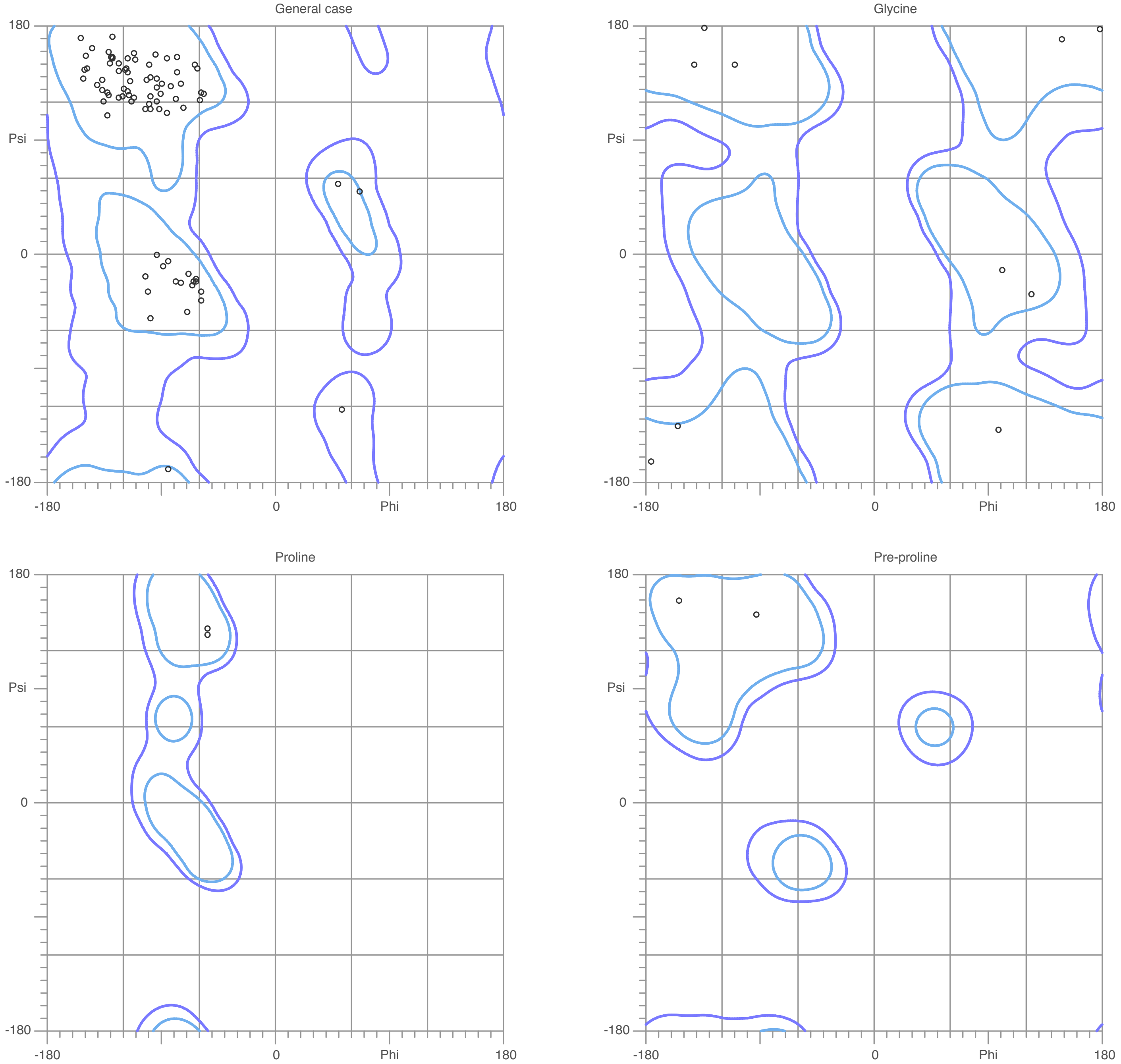
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 2



97.9% (94/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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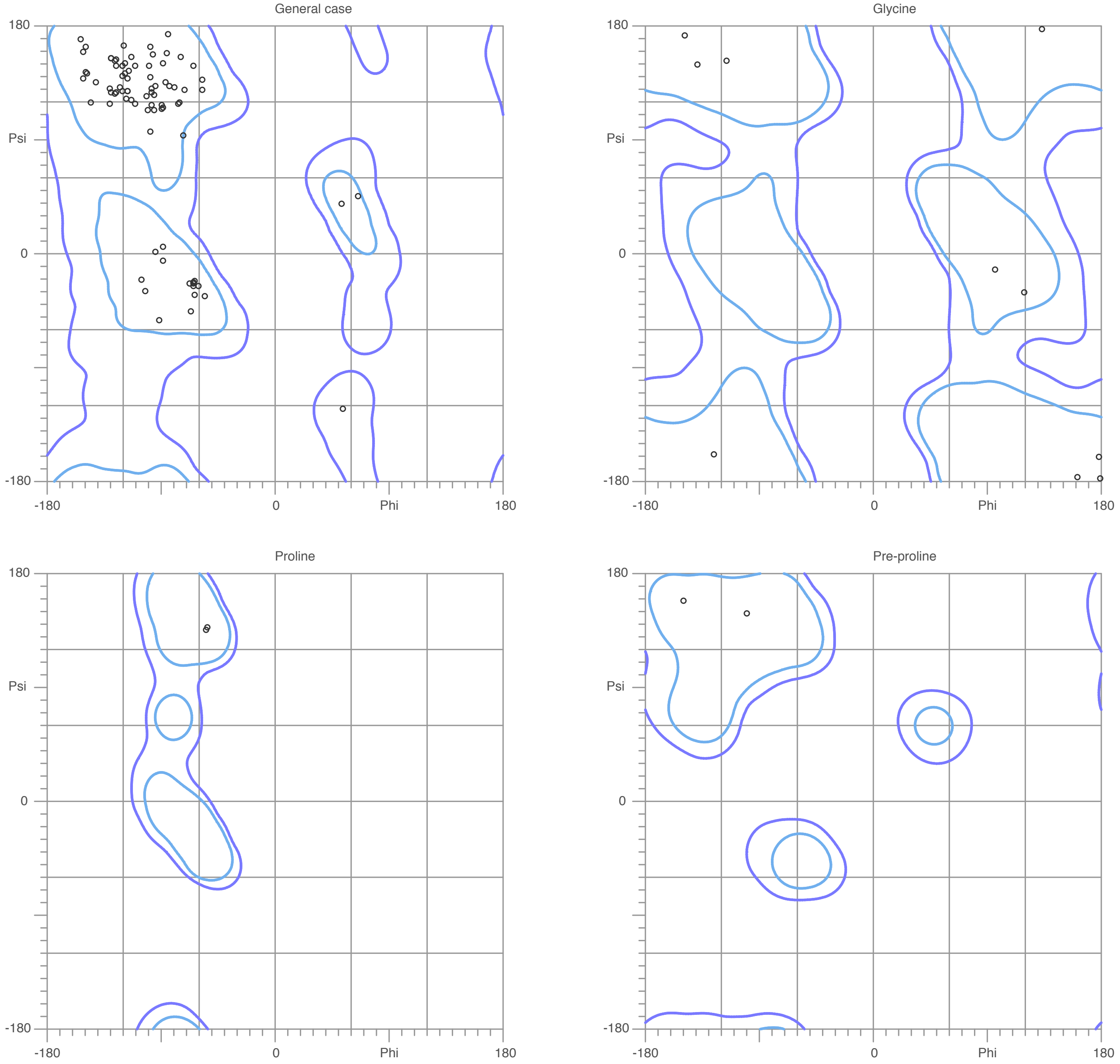
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 3



99.0% (95/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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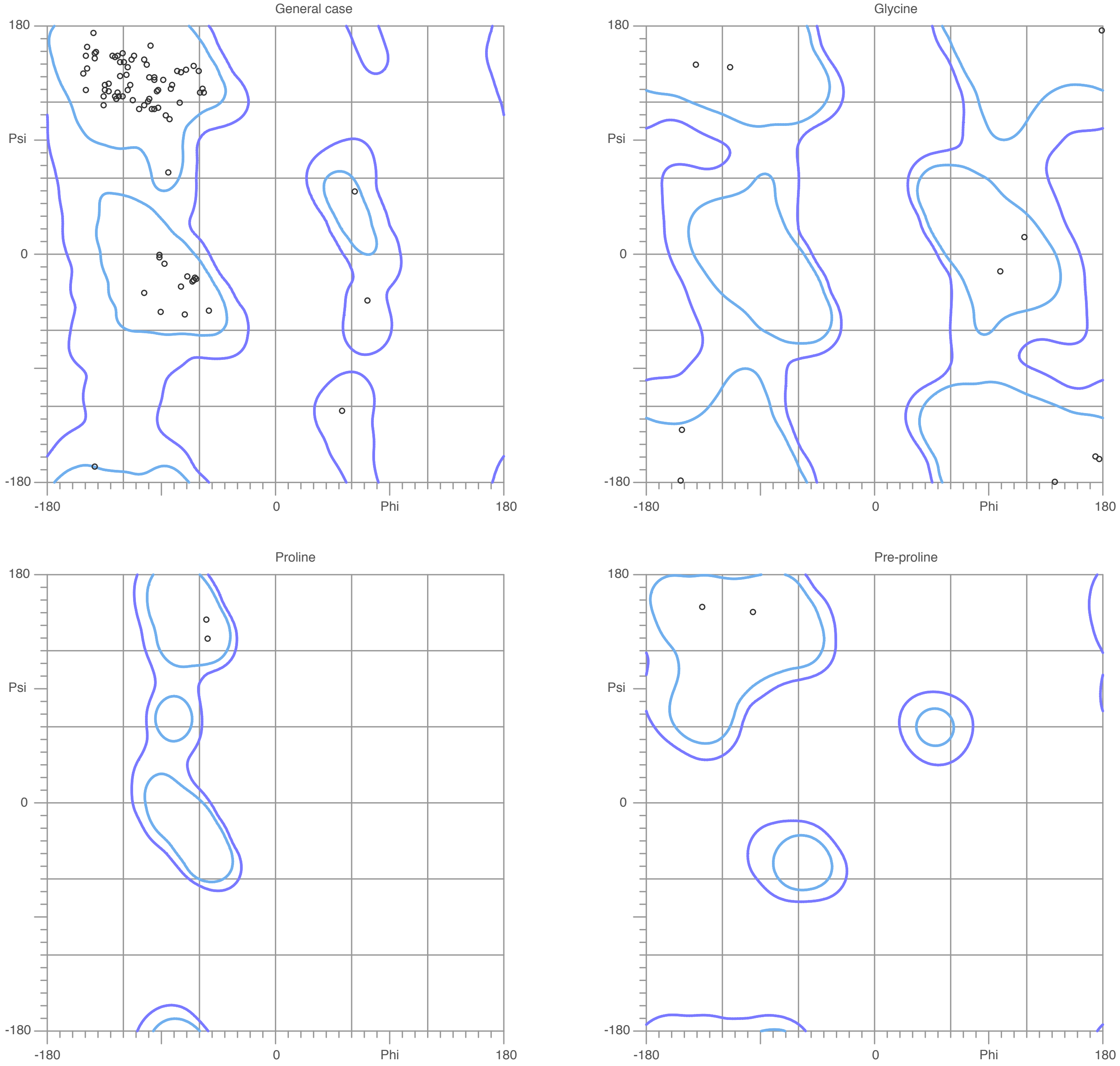
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 4



96.9% (93/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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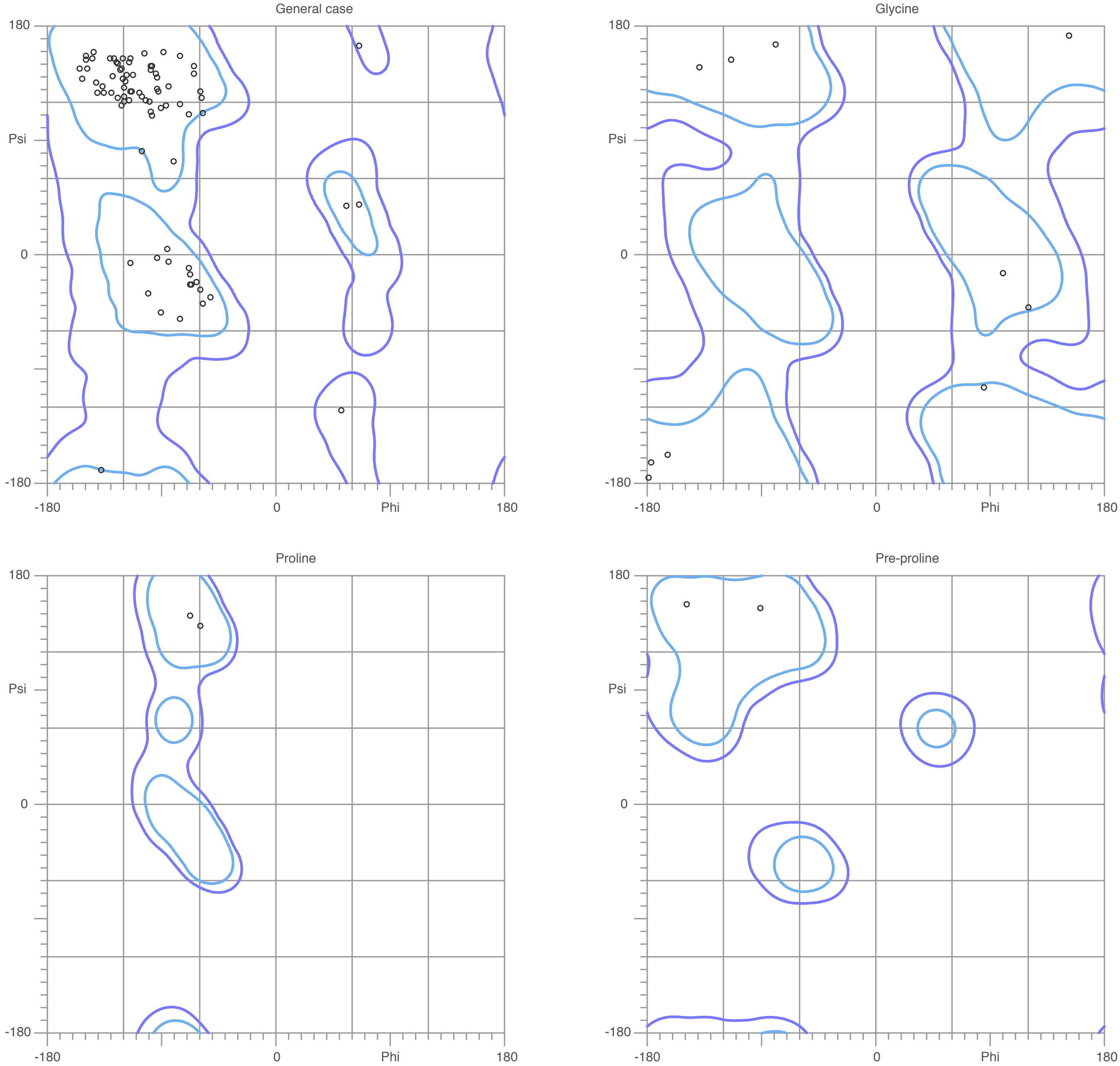
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 5



95.8% (92/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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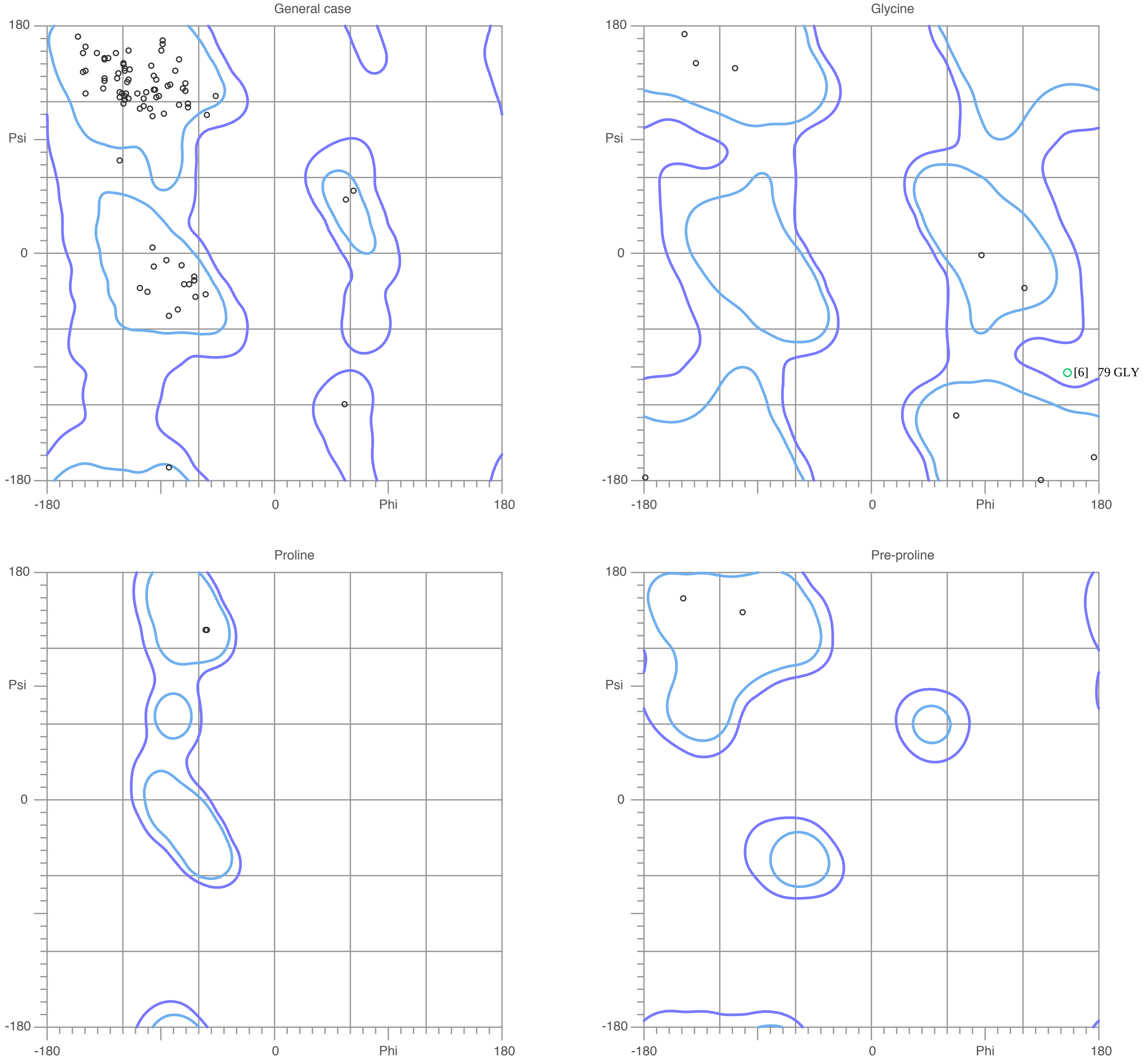
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 6



95.8% (92/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[6] 79 GLY (155.0, -94.0)

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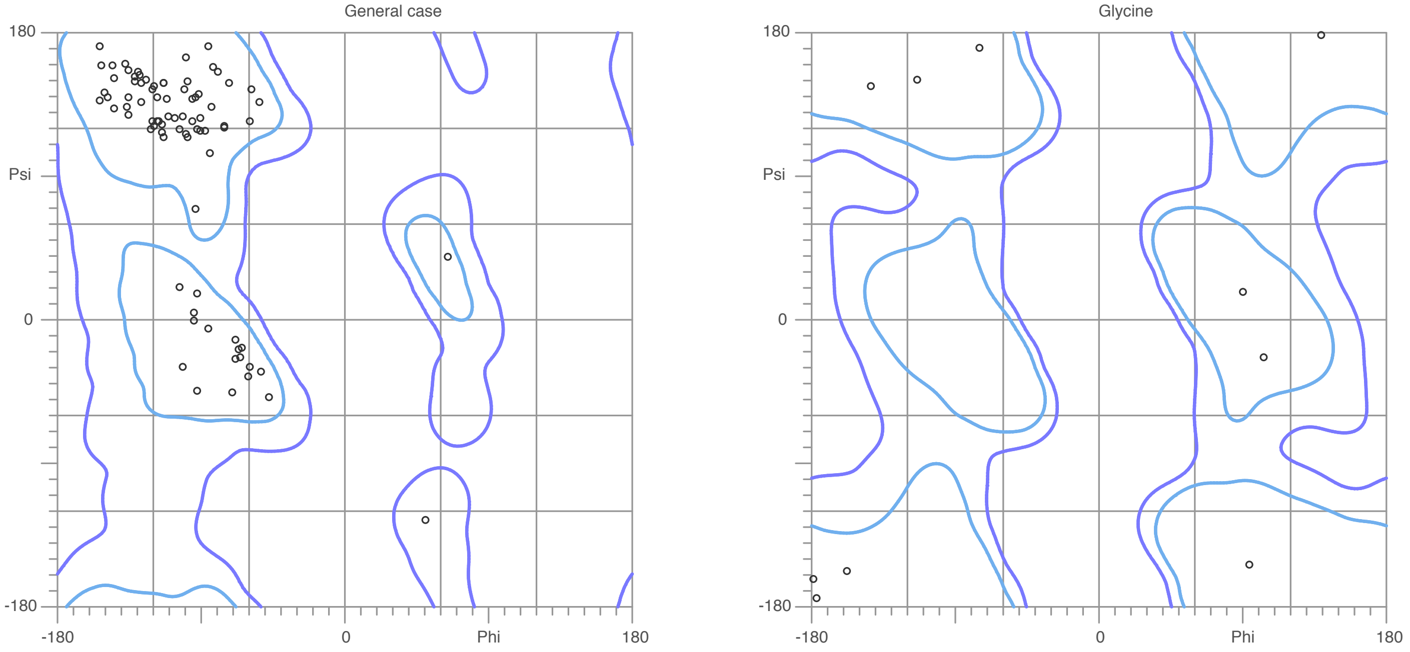
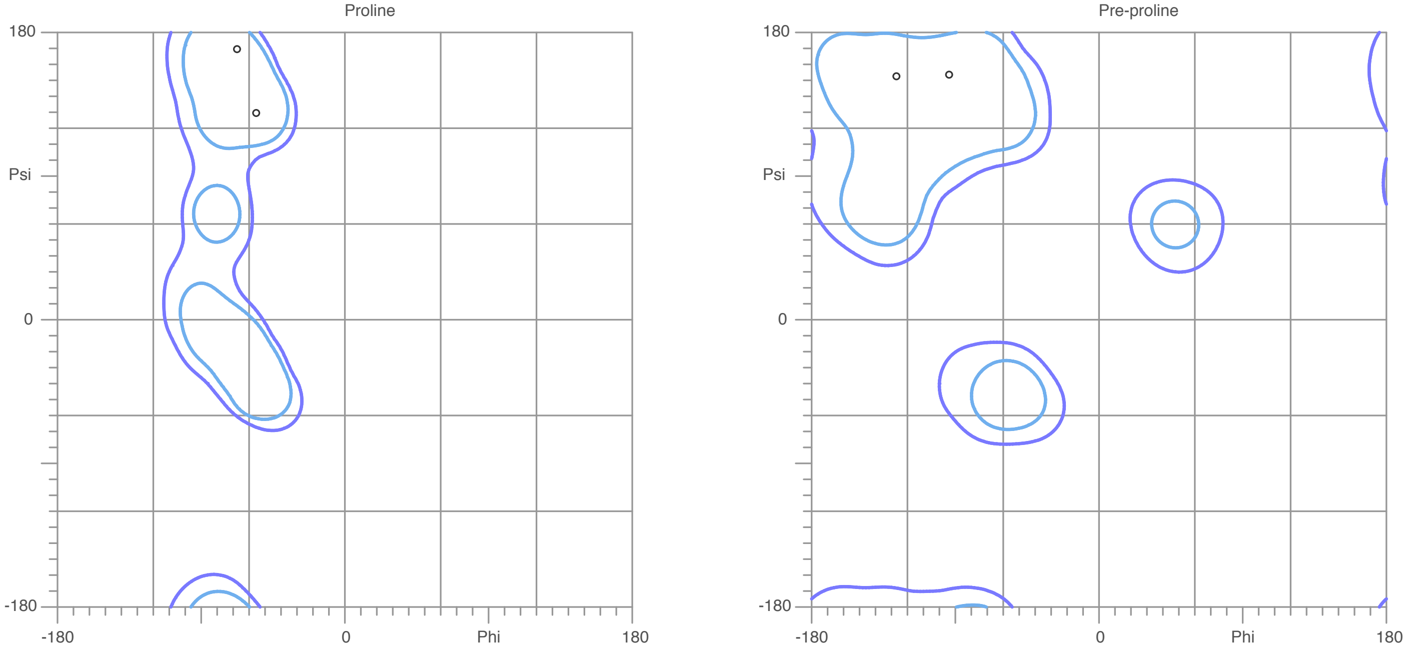
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 7





99.0% (95/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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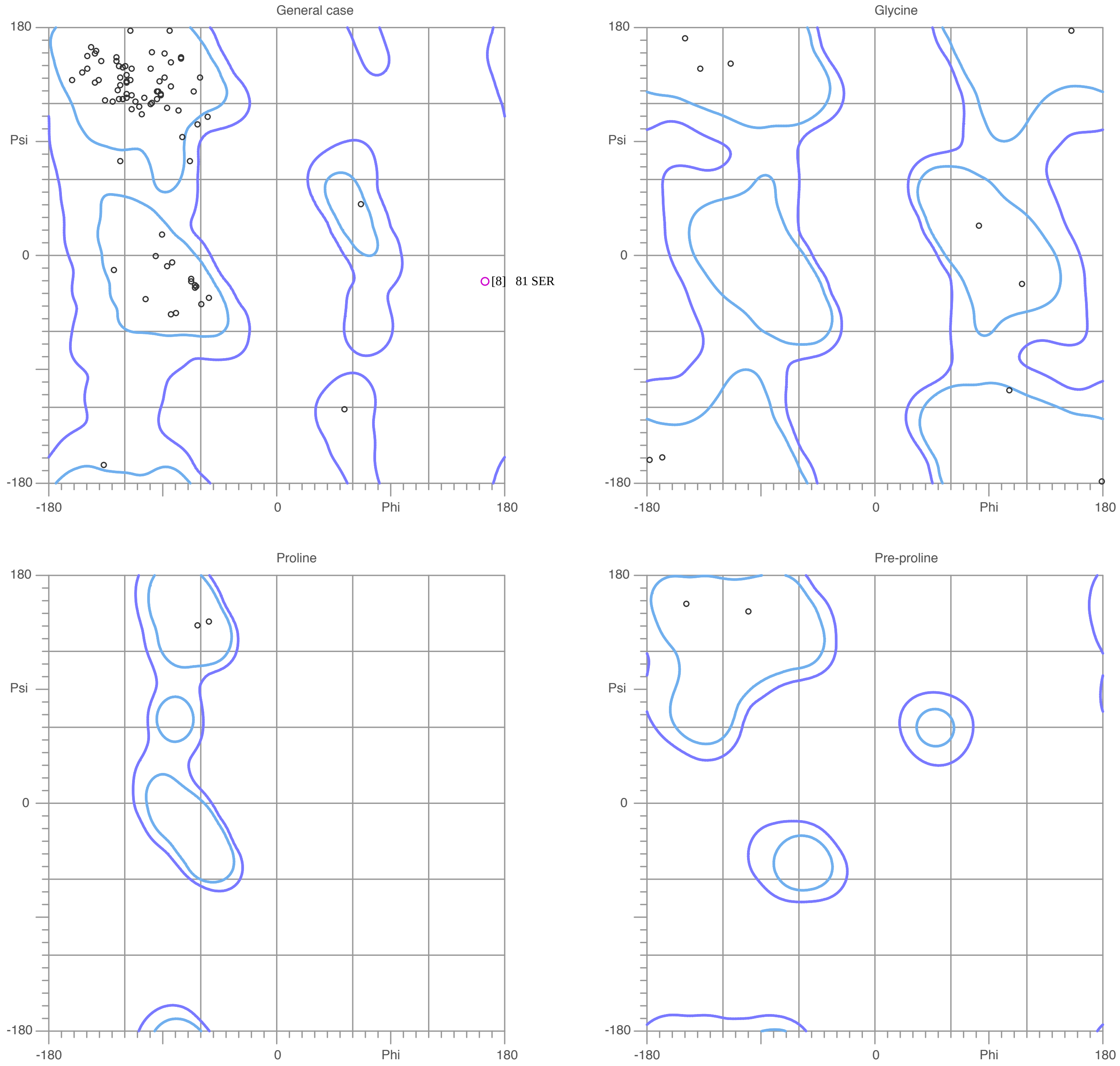
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 8



92.7% (89/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 81 SER (165.0, -20.8)

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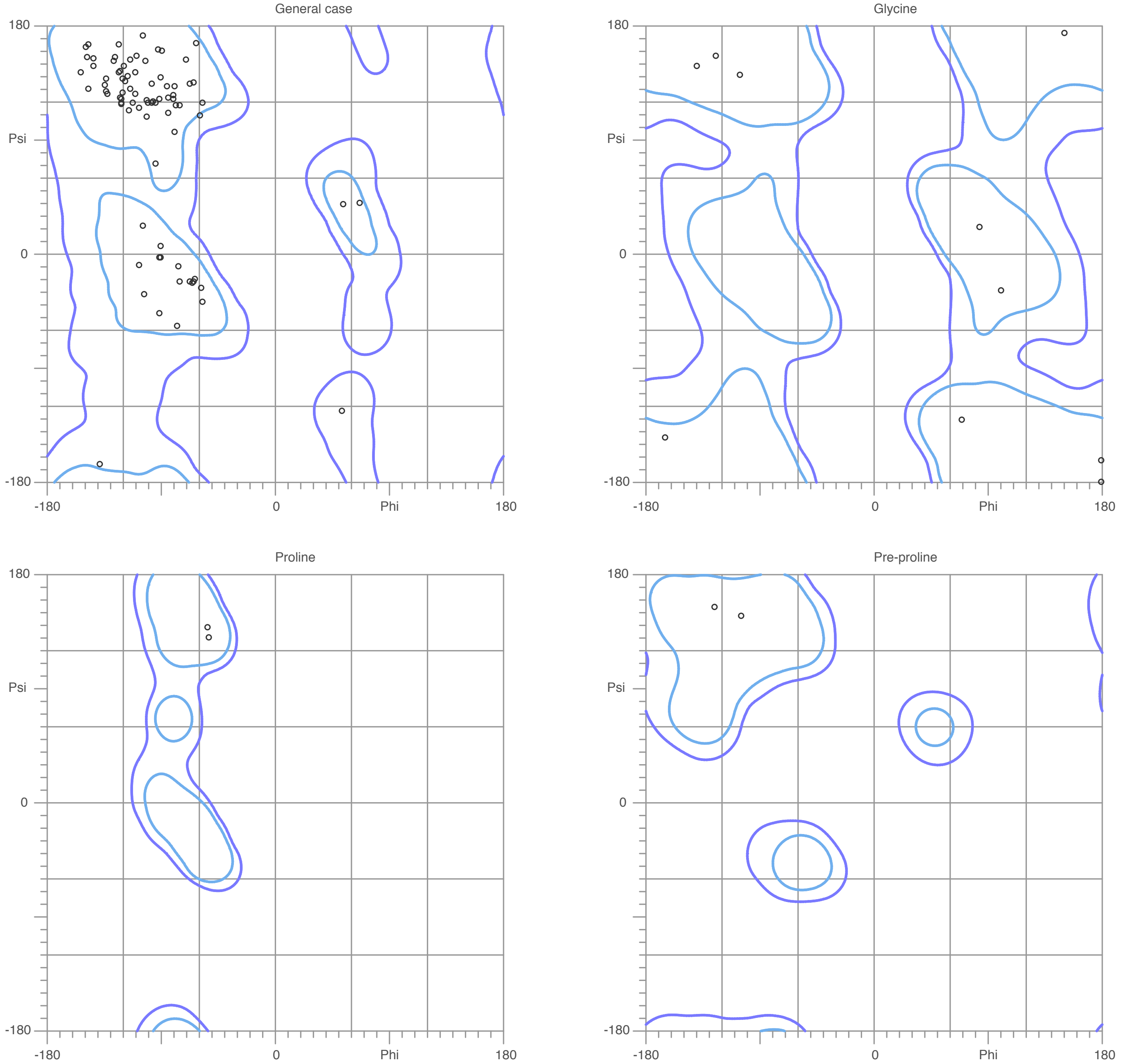
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 9



96.9% (93/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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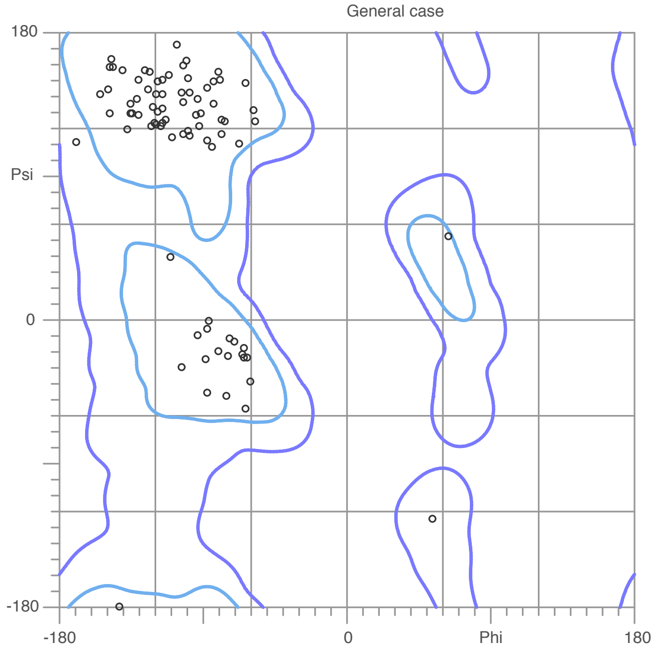
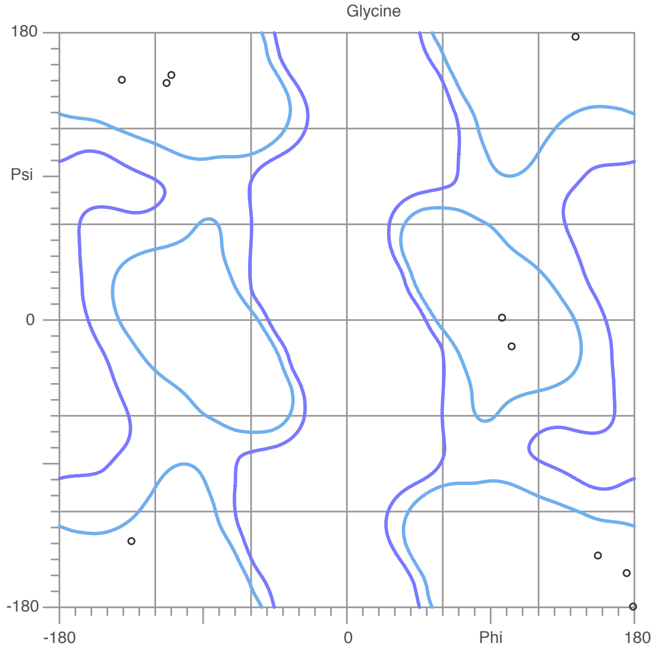
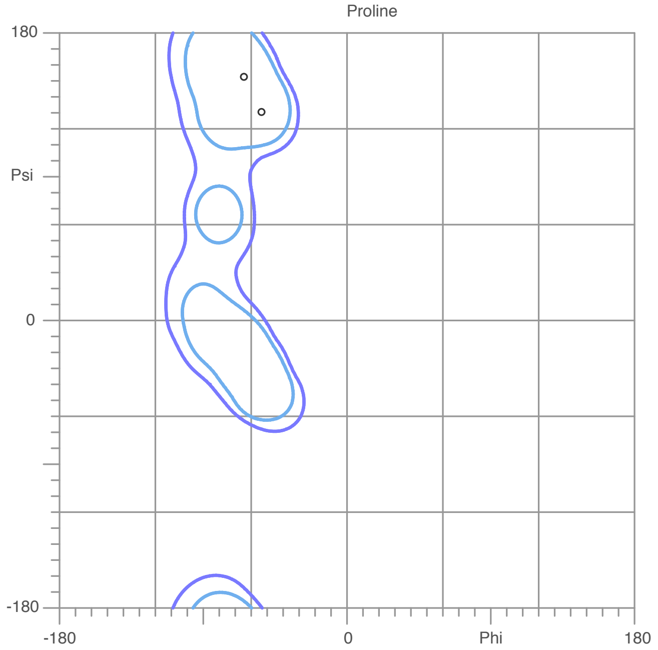
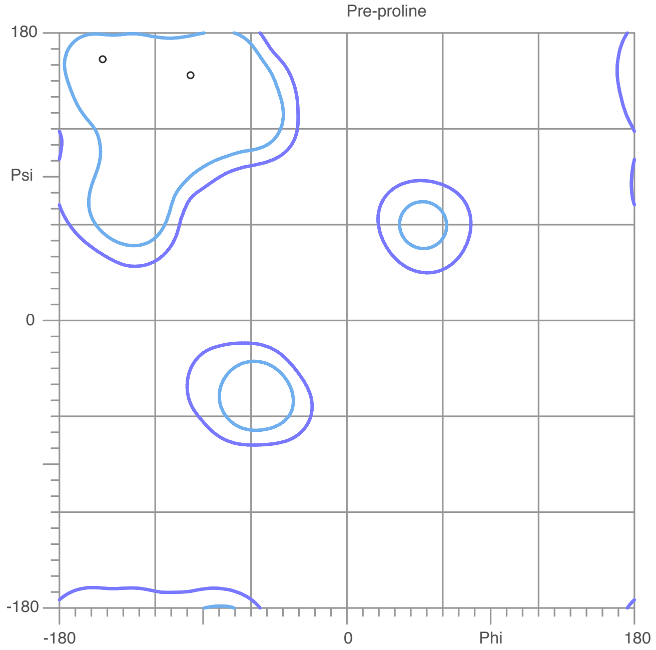
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 10


General case


Glycine


Proline


Pre-proline

97.9% (94/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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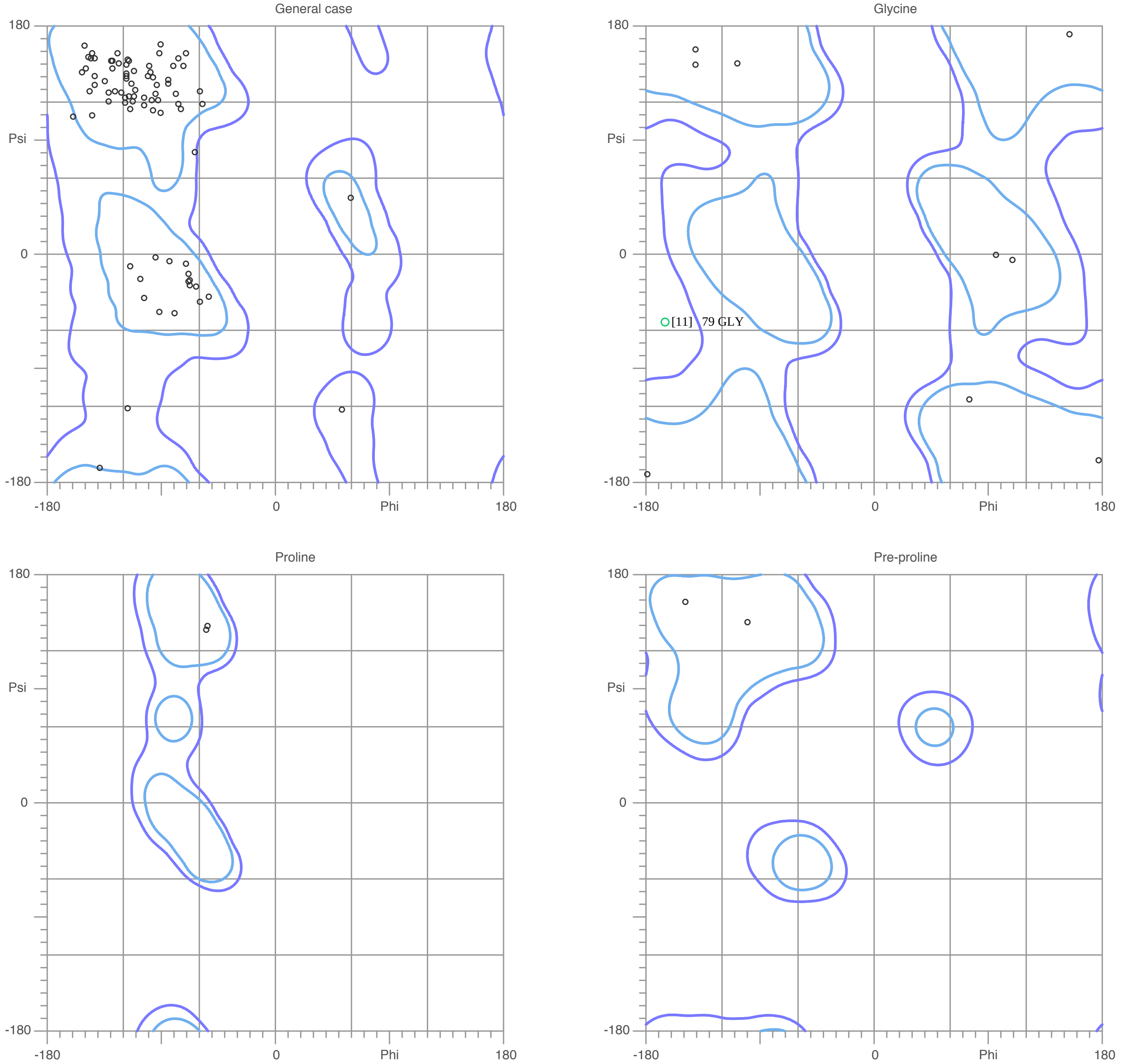
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 11



93.8% (90/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[11] 79 GLY (-165.1, -53.4)

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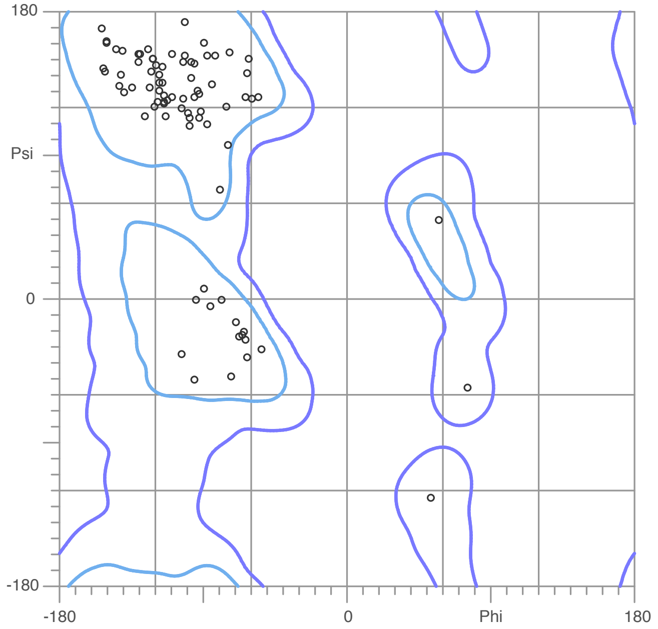
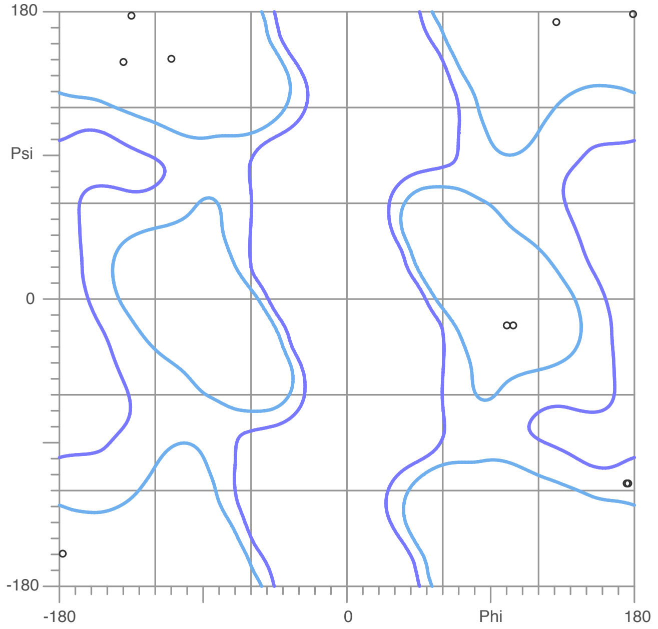
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 12

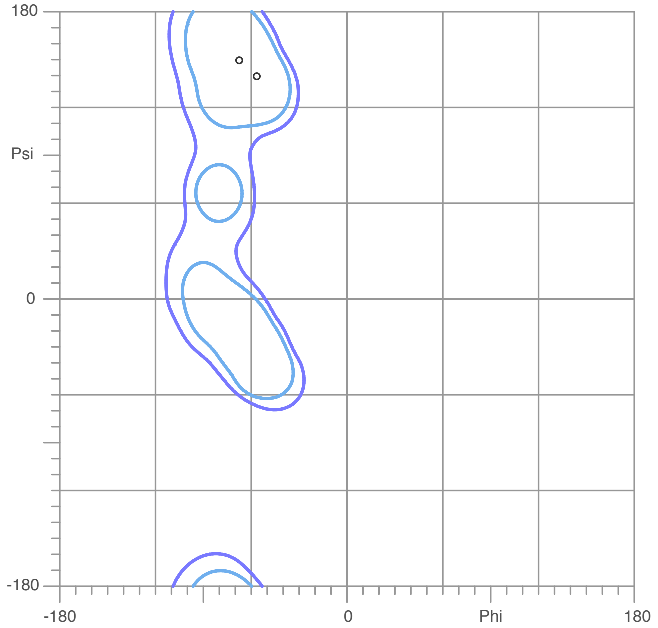
General case



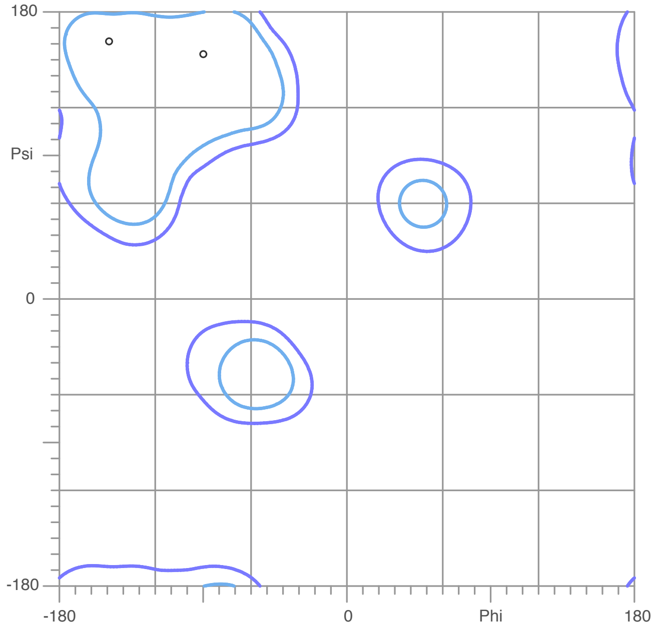
Glycine



Proline



Pre-proline



95.8% (92/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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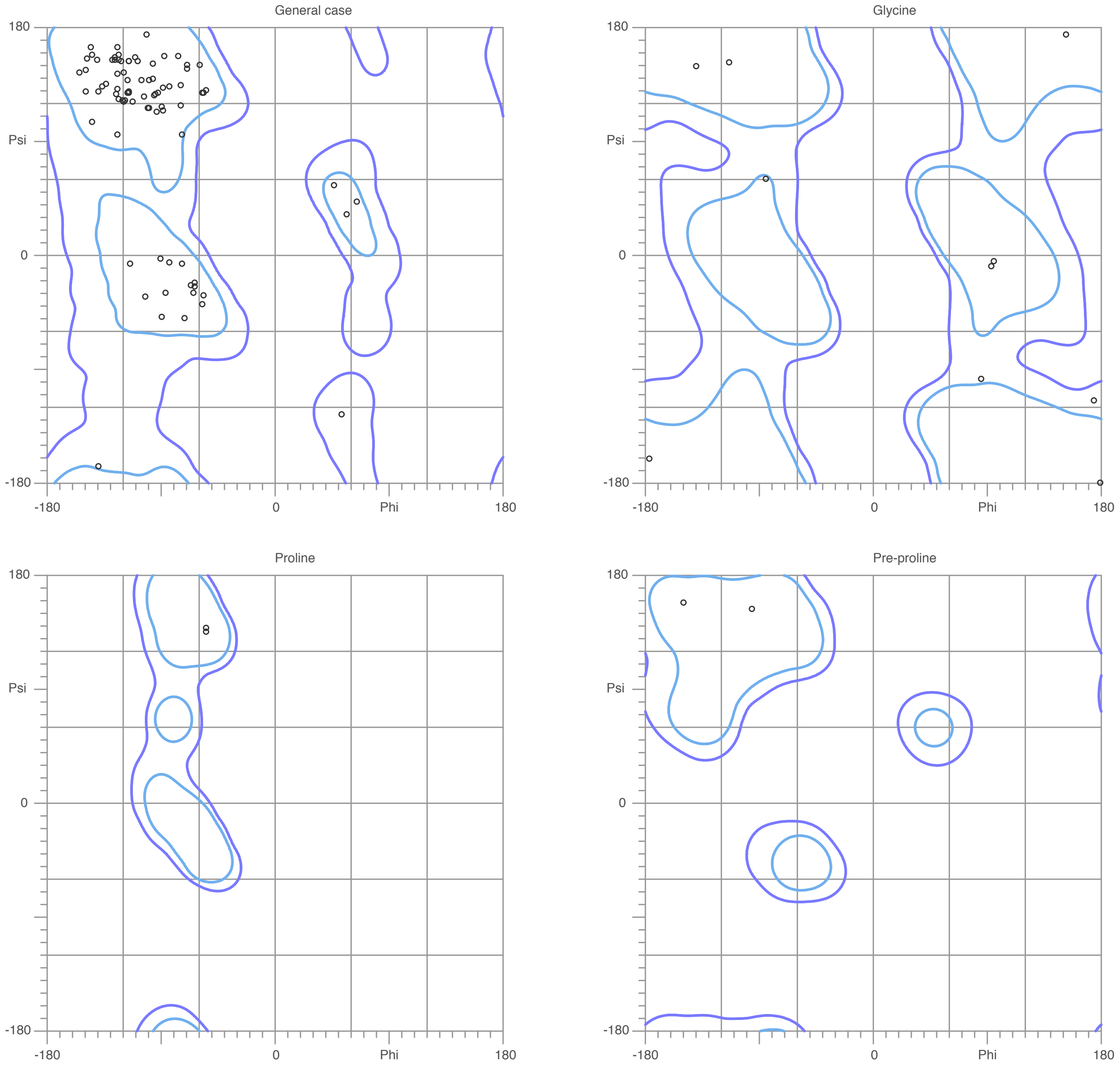
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 13



95.8% (92/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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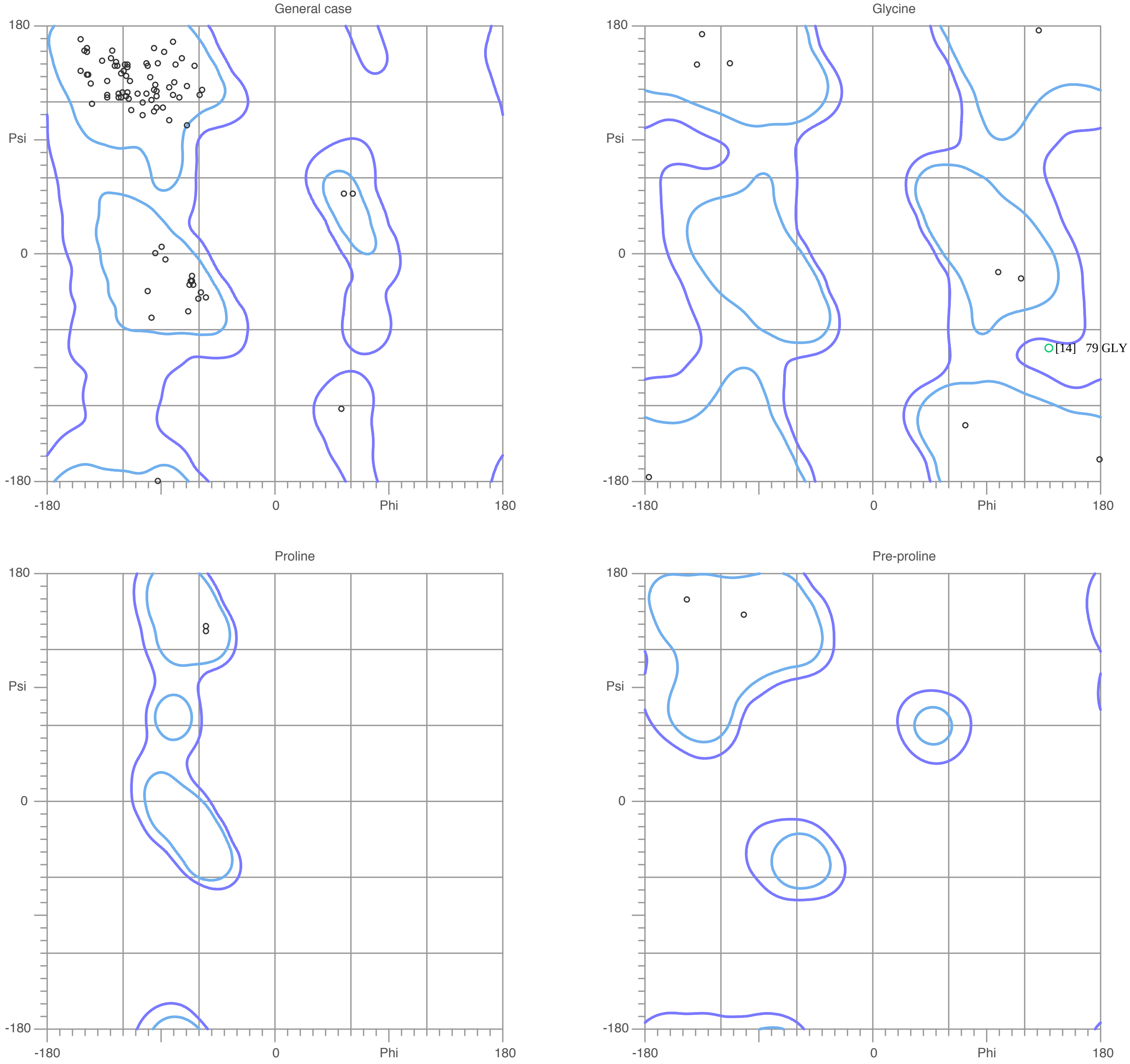
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 14



97.9% (94/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[14] 79 GLY (139.7, -75.0)

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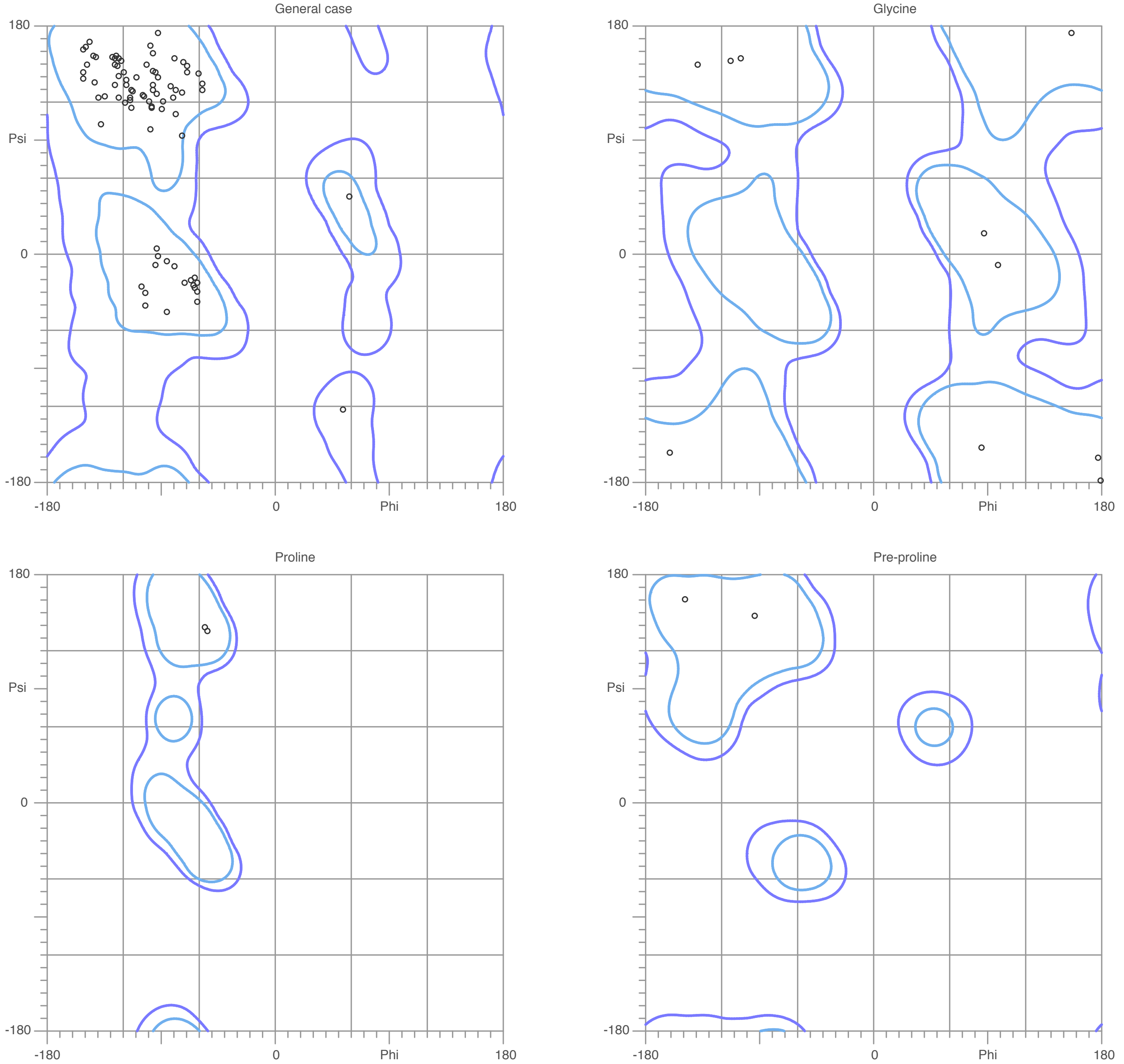
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 15



99.0% (95/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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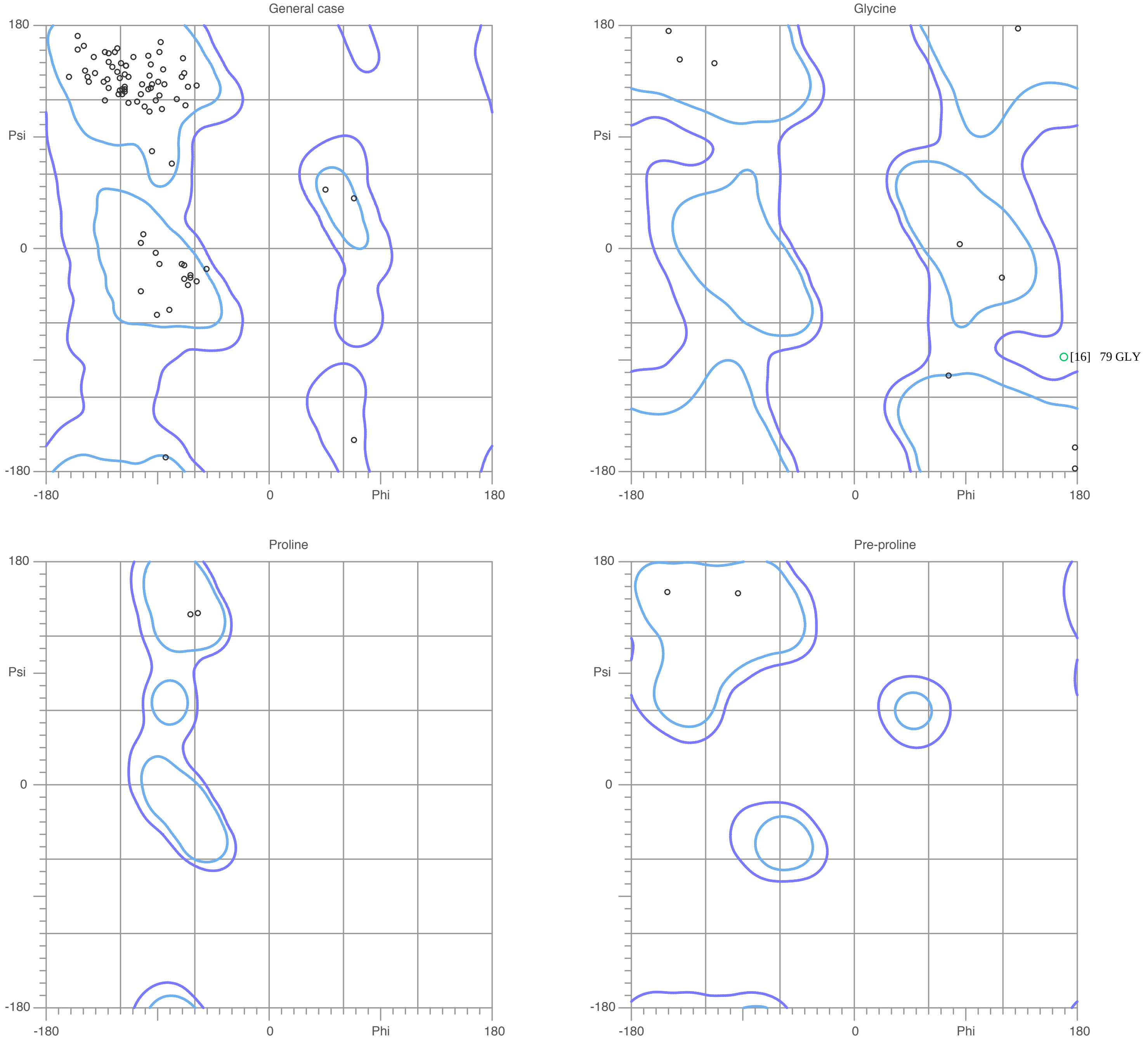
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 16



96.9% (93/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[16] 79 GLY (169.5, -87.9)

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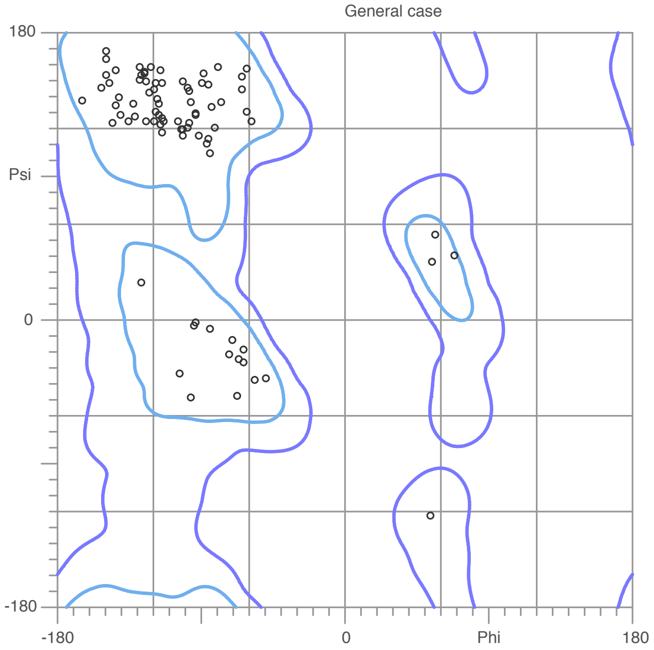
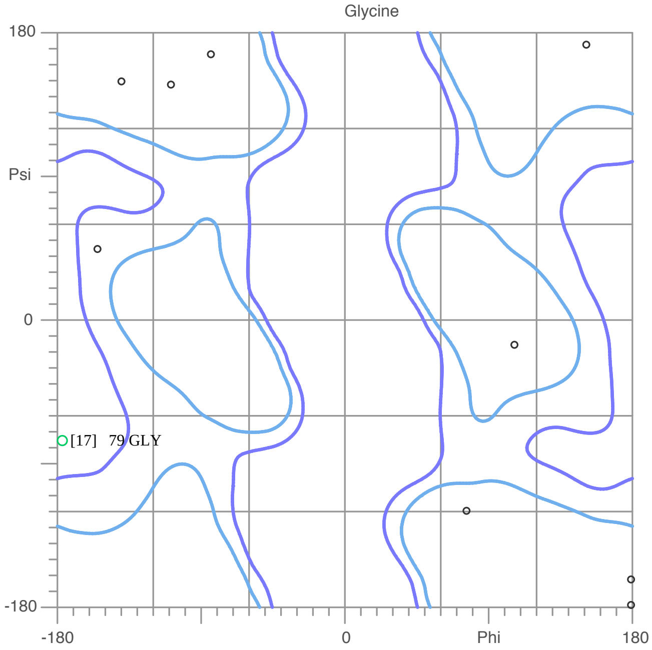
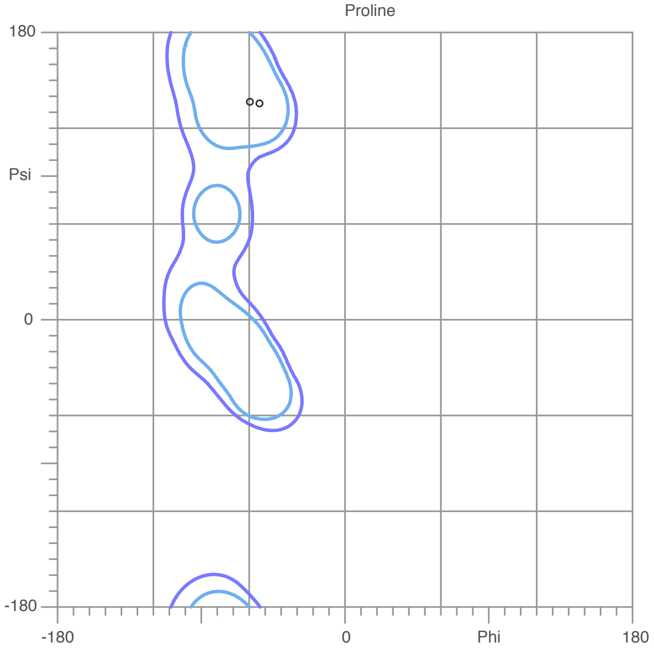
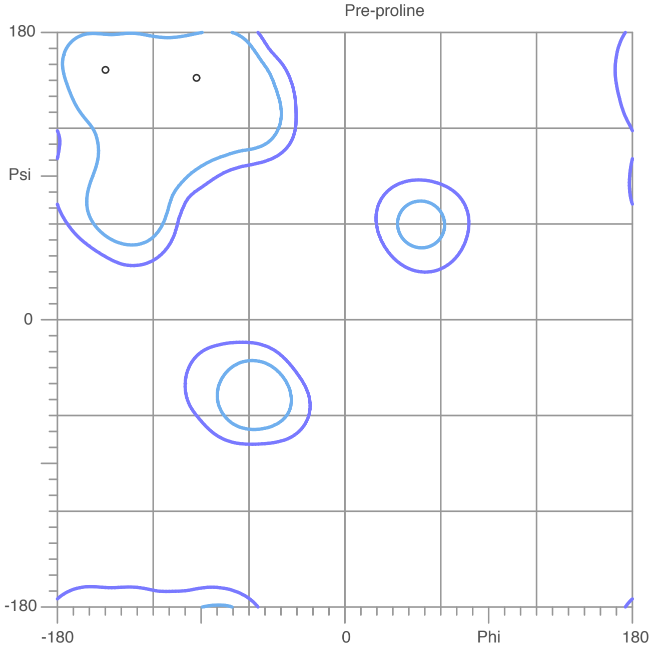
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 17


General case


Glycine


Proline


Pre-proline

96.9% (93/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[17] 79 GLY (-177.7, -75.0)

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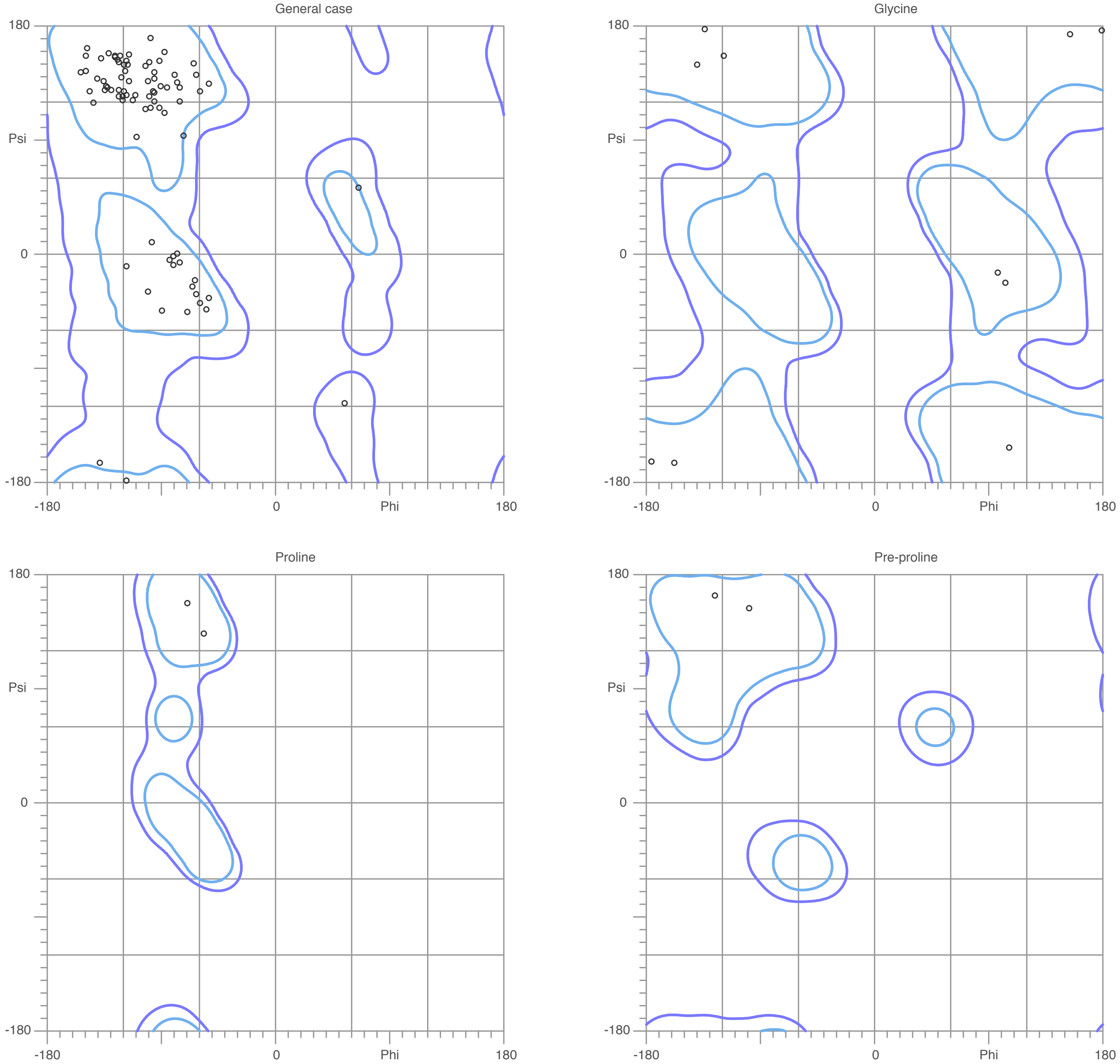
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 18



97.9% (94/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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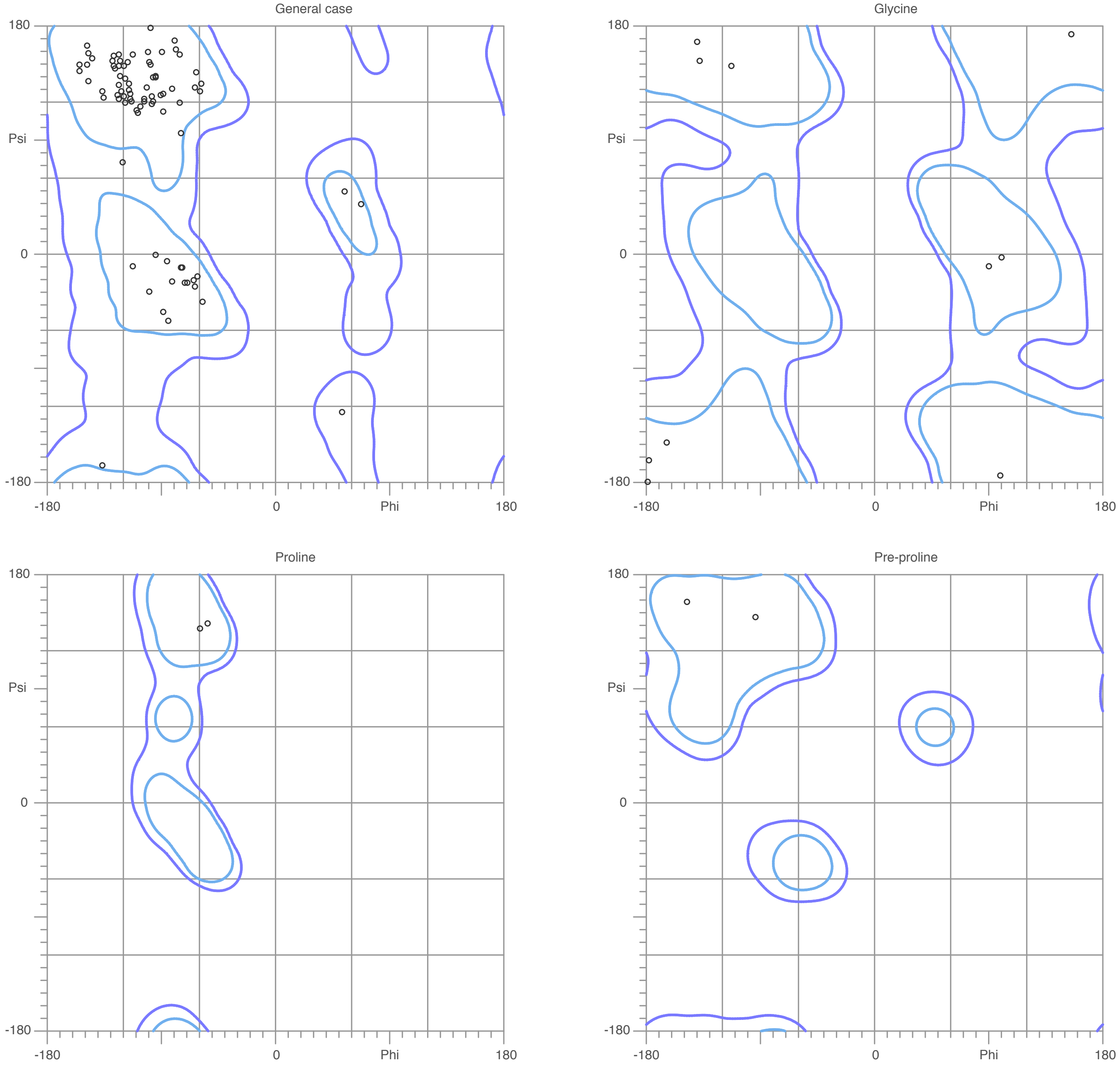
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 19



96.9% (93/96) of all residues were in favored (98%) regions.
100.0% (96/96) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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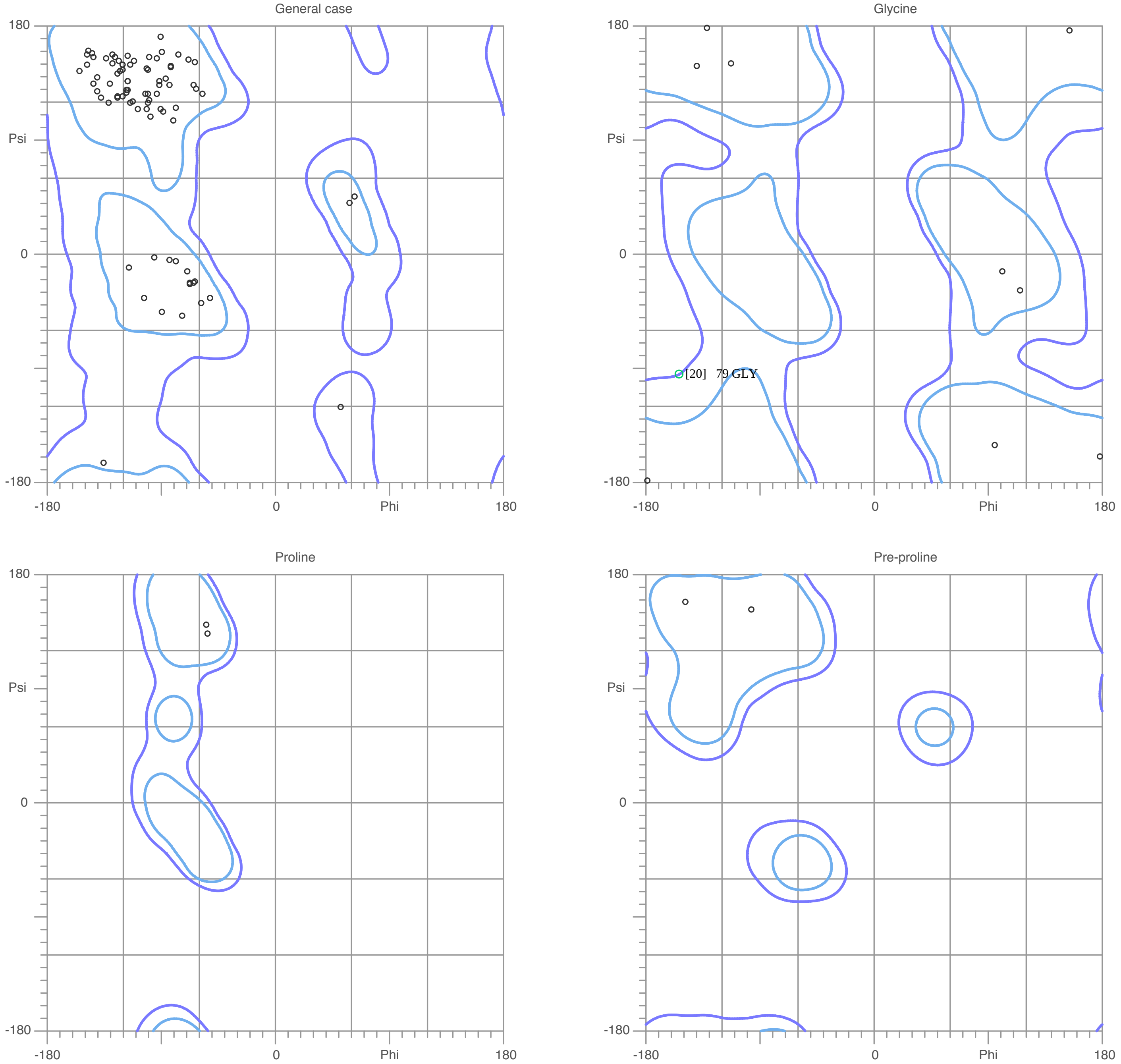
MolProbity Ramachandran analysis

MRR110B_R3Cons_em_bcr3.pdb, model 20



96.9% (93/96) of all residues were in favored (98%) regions.
99.0% (95/96) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 79 GLY (-155.0, -95.0)

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