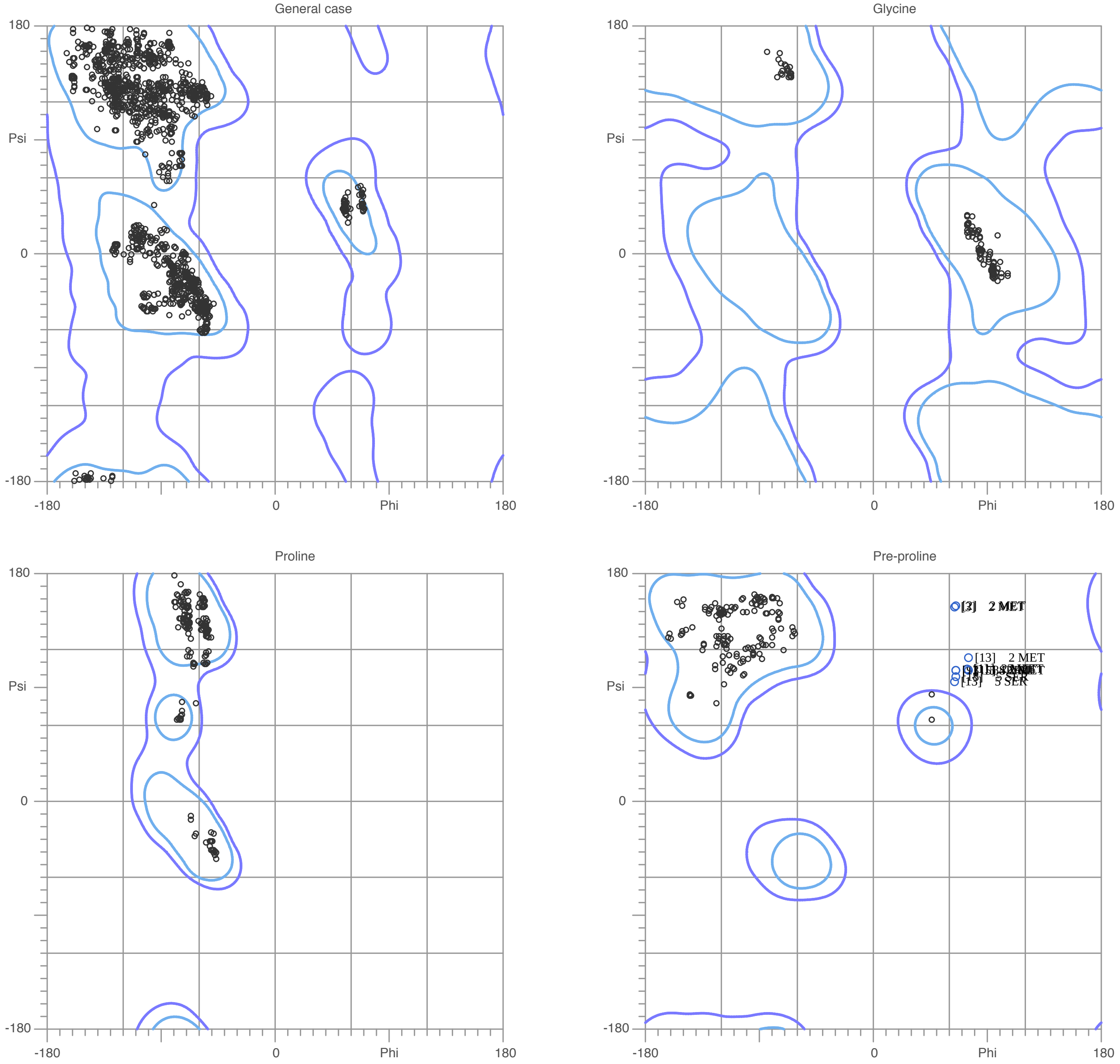
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, all models



98.8% (1660/1680) of all residues were in favored (98%) regions.
99.4% (1670/1680) of all residues were in allowed (>99.8%) regions.

There were 10 outliers (phi, psi):

[1] 2 MET (74.9, 105.8)
[2] 2 MET (65.0, 155.1)
[3] 2 MET (65.0, 155.0)
[9] 5 SER (65.1, 105.0)
[11] 2 MET (75.0, 105.4)
[13] 2 MET (75.1, 115.0)
[13] 5 SER (65.0, 95.0)
[13] 84 VAL (65.1, 105.0)
[15] 2 MET (75.1, 105.0)
[18] 5 SER (65.0, 99.2)

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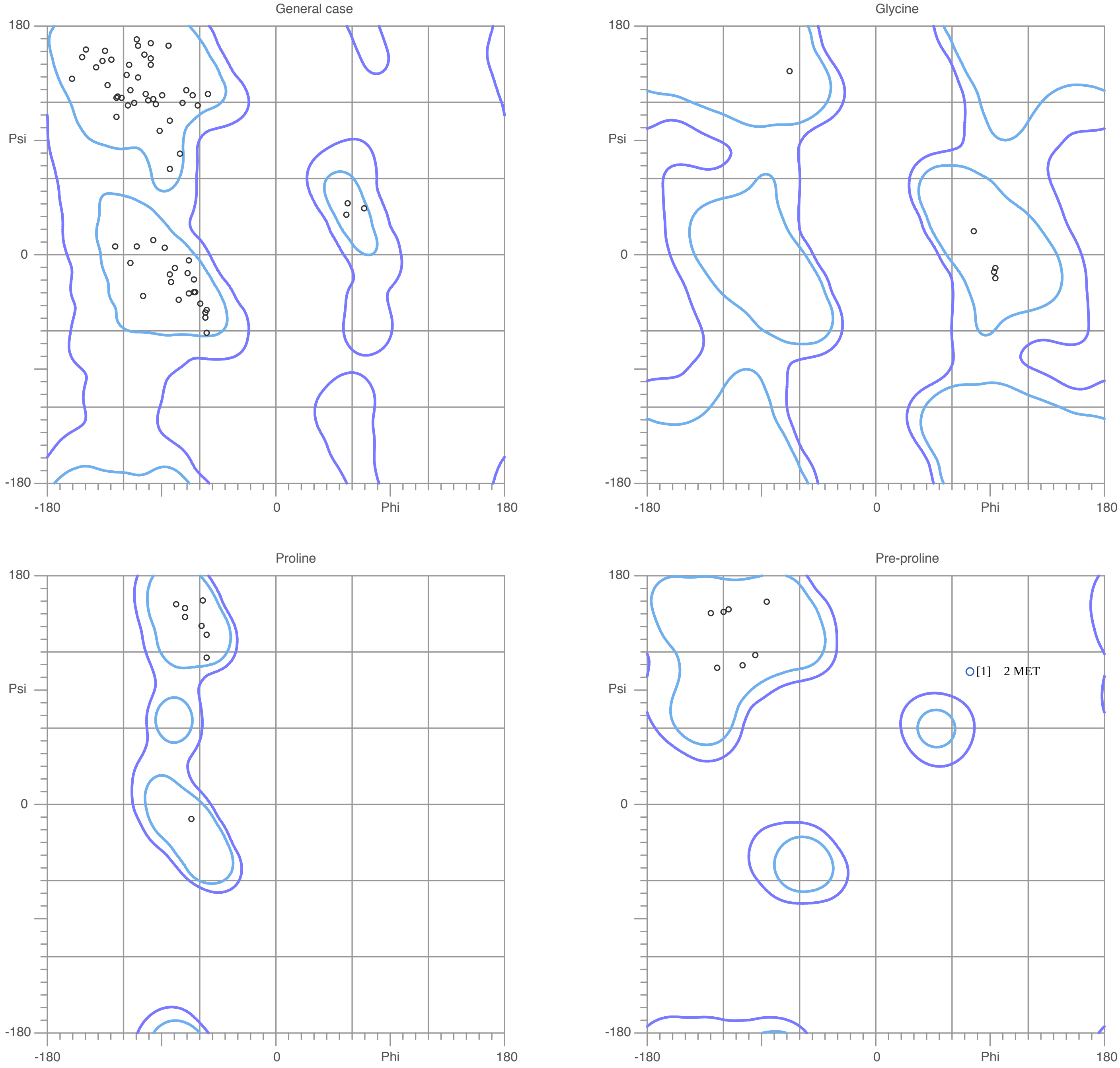
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 1



98.8% (83/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[1] 2 MET (74.9, 105.8)

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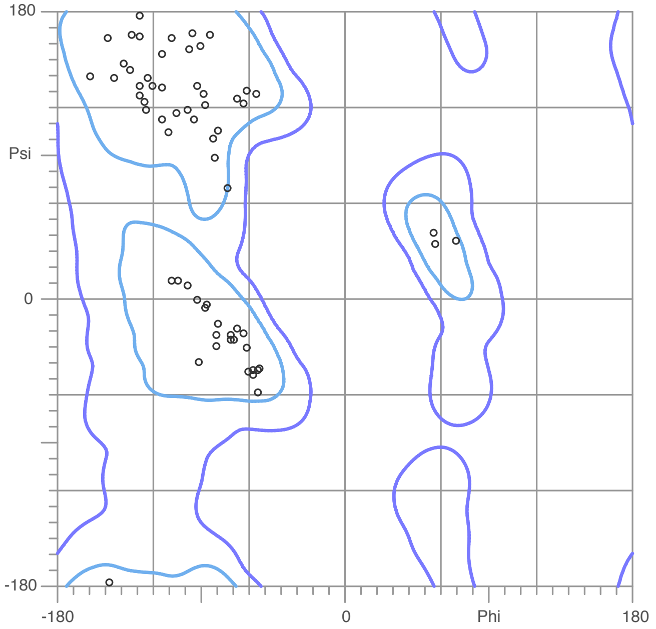
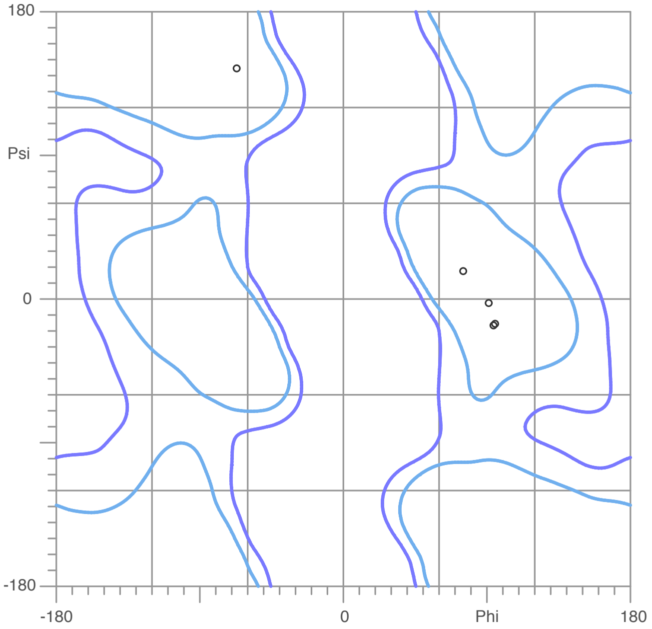
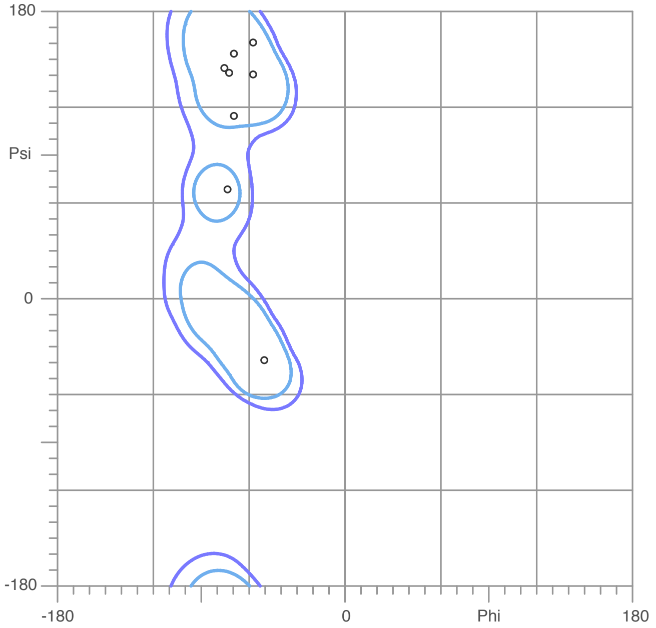
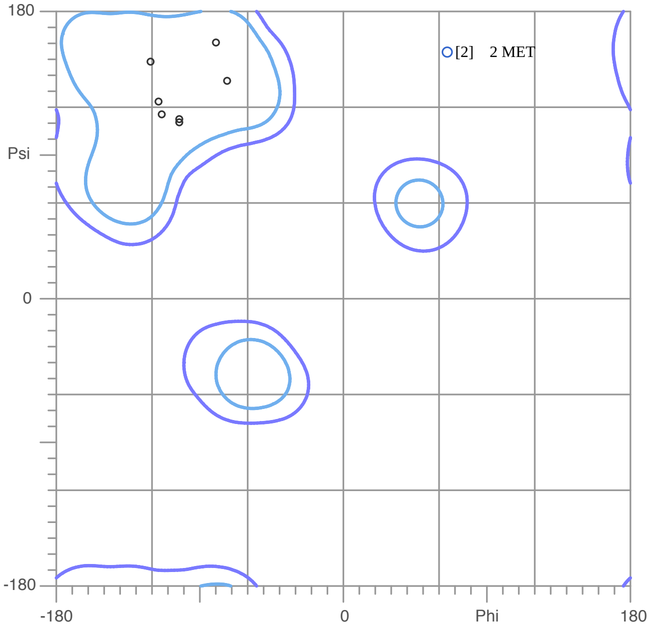
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 2


General case


Glycine


Proline


Pre-proline

98.8% (83/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[2] 2 MET (65.0, 155.1)

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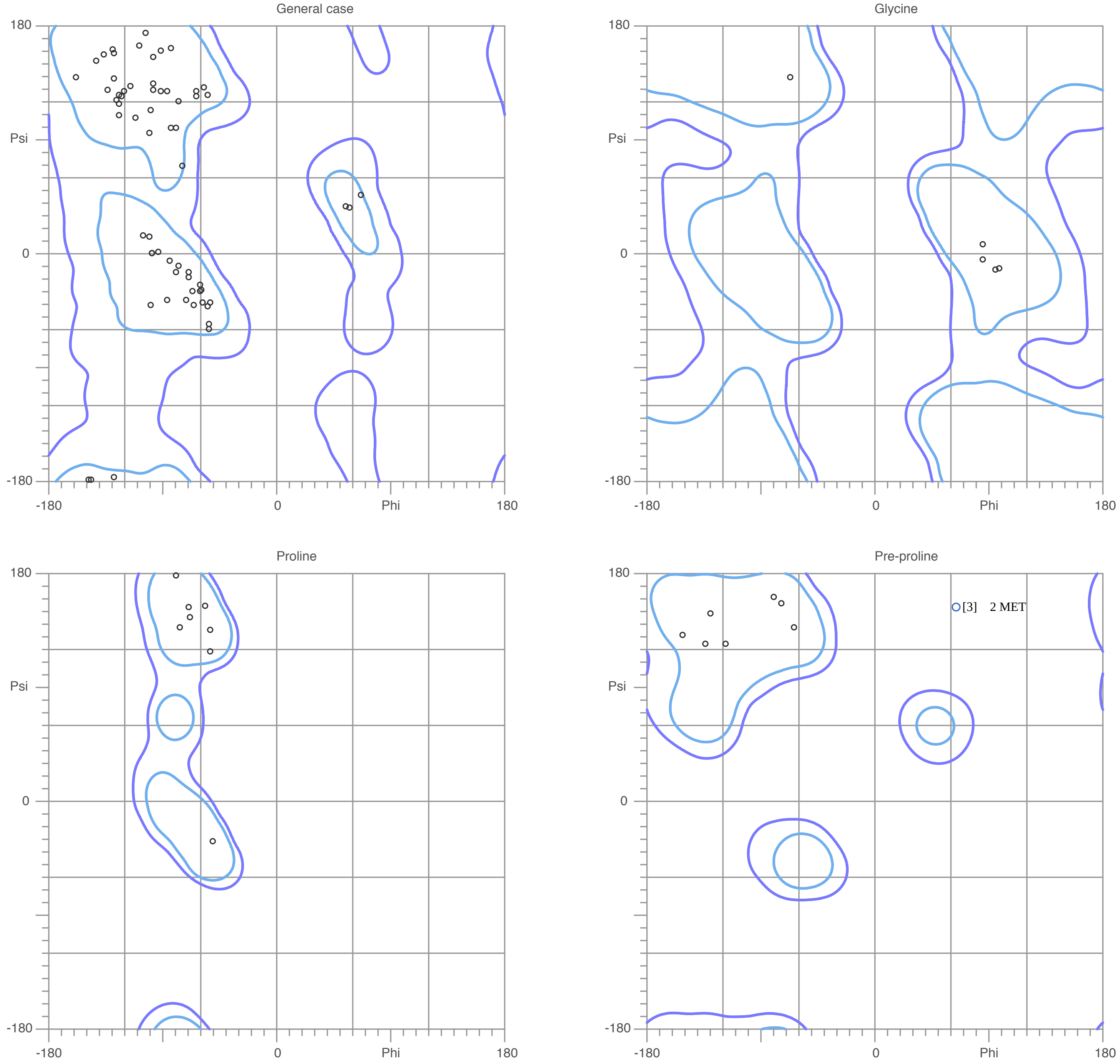
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 3

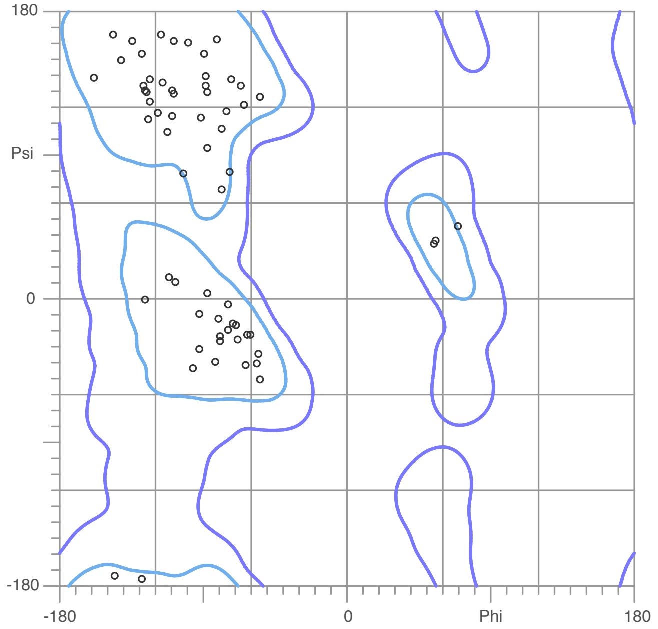


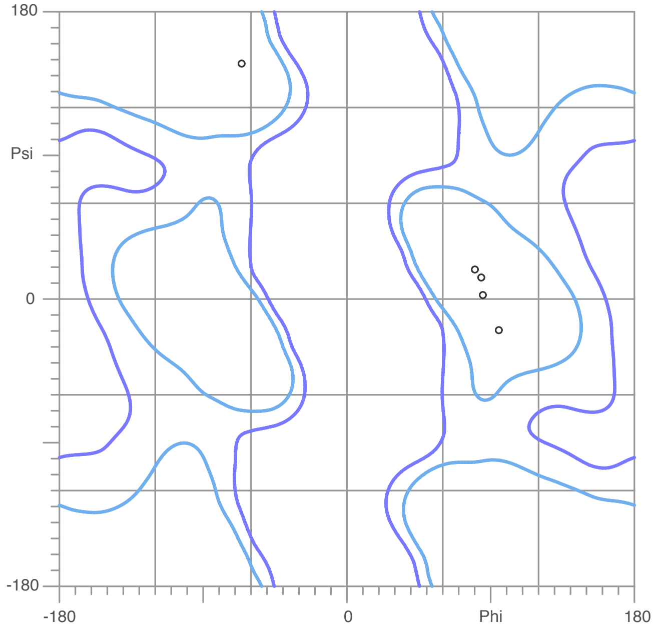
98.8% (83/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

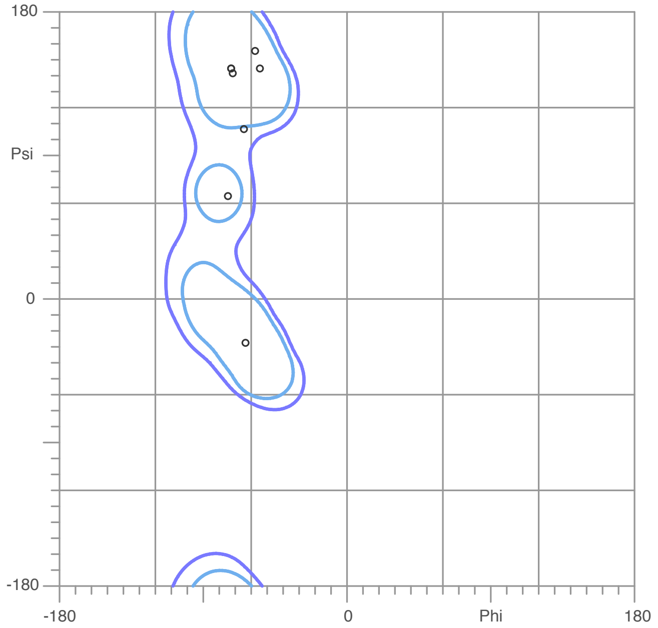
There were 1 outliers (phi, psi):
[3] 2 MET (65.0, 155.0)

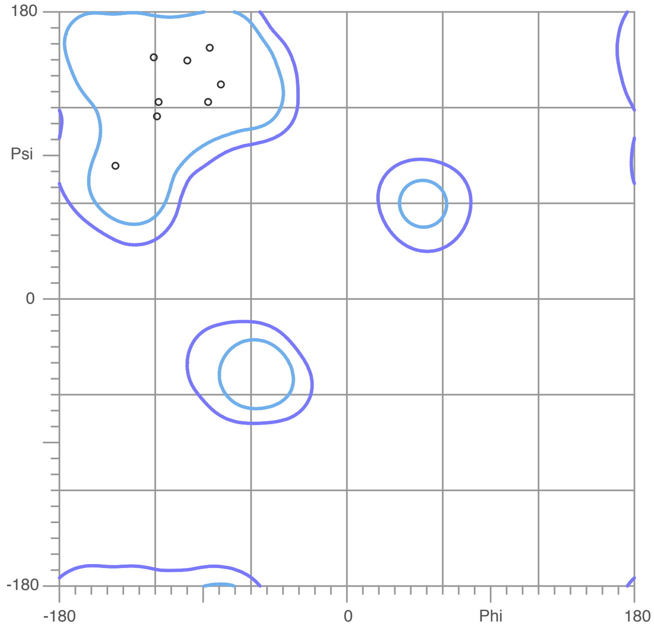
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 4


General case


Glycine


Proline


Pre-proline

97.6% (82/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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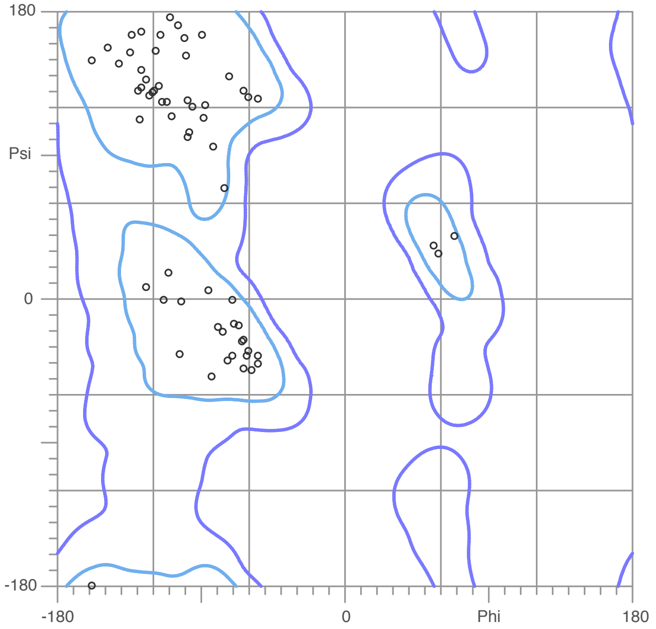
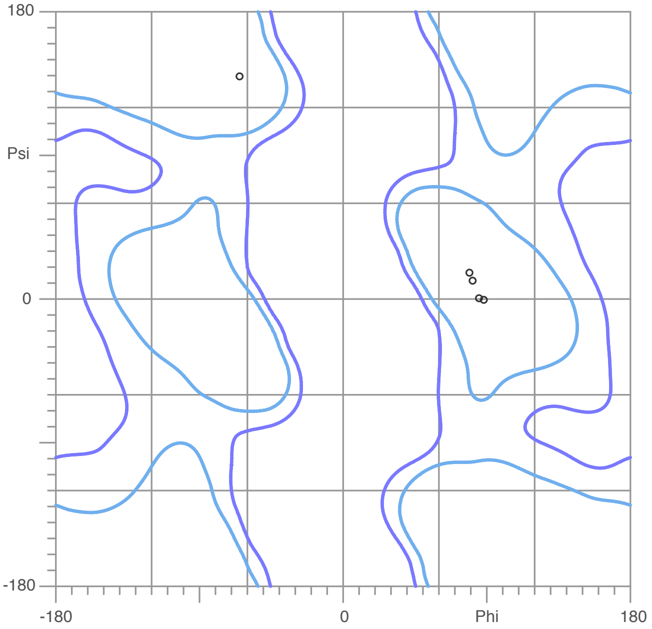
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 5

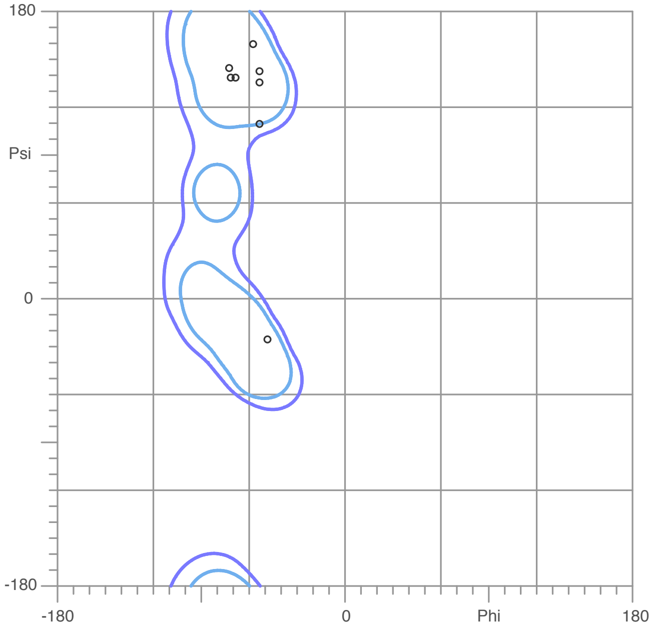
General case



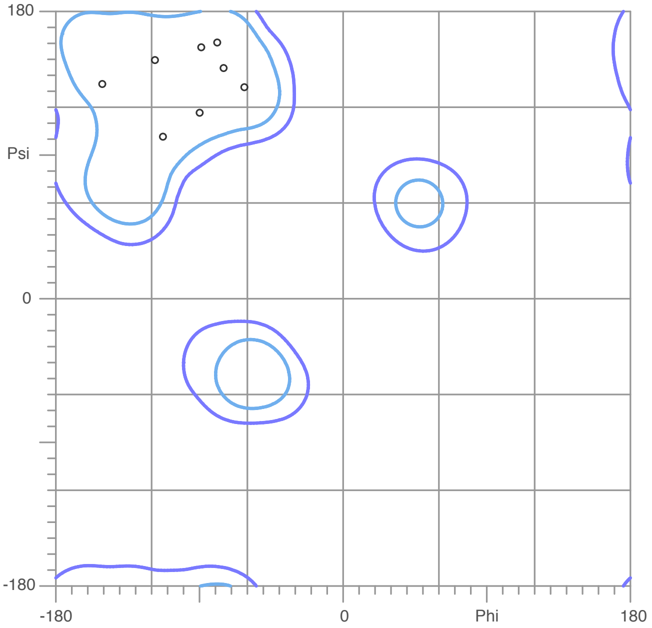
Glycine



Proline



Pre-proline

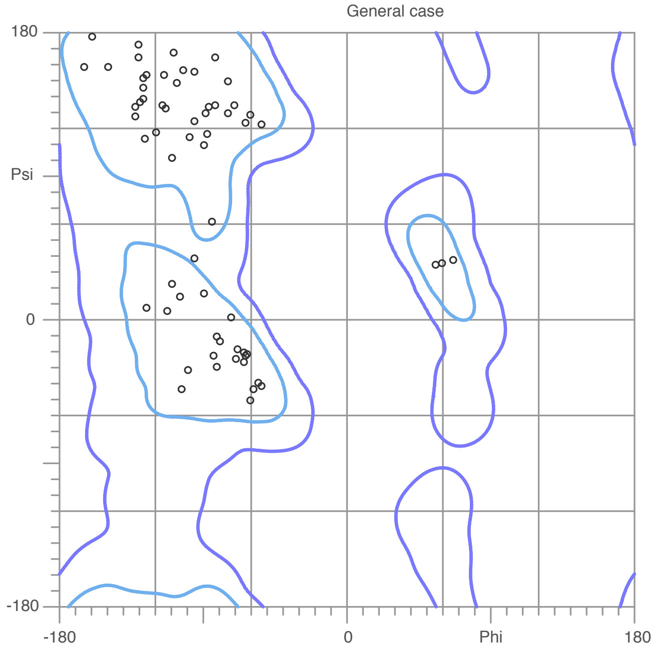


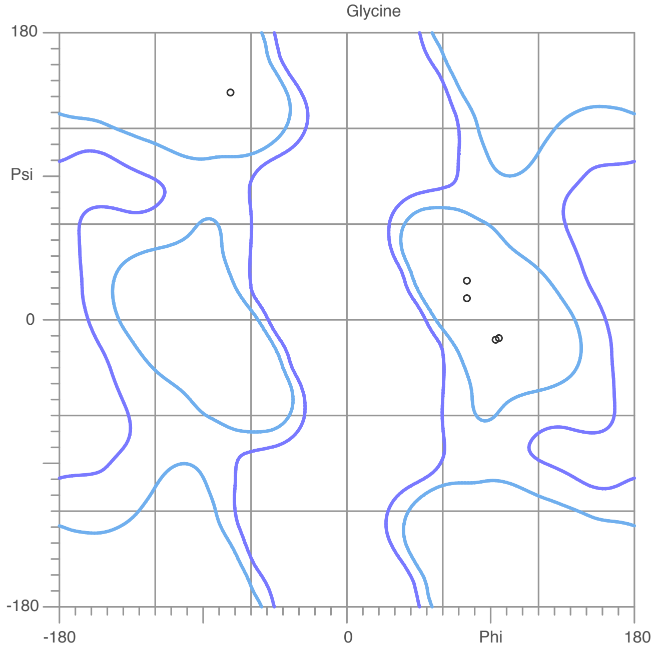
100.0% (84/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

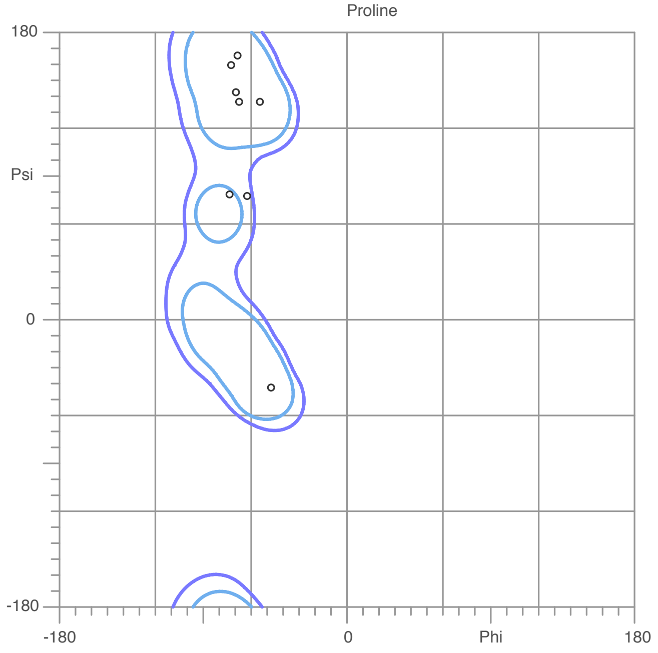
There were no outliers.

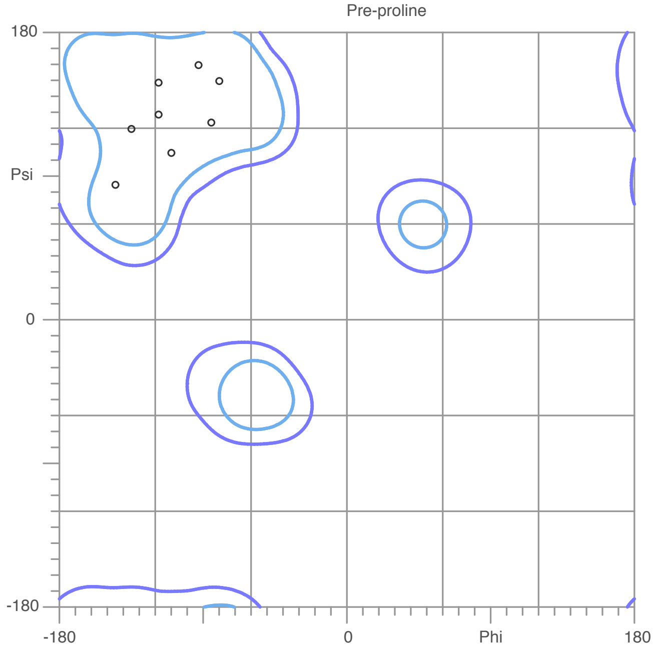
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 6









97.6% (82/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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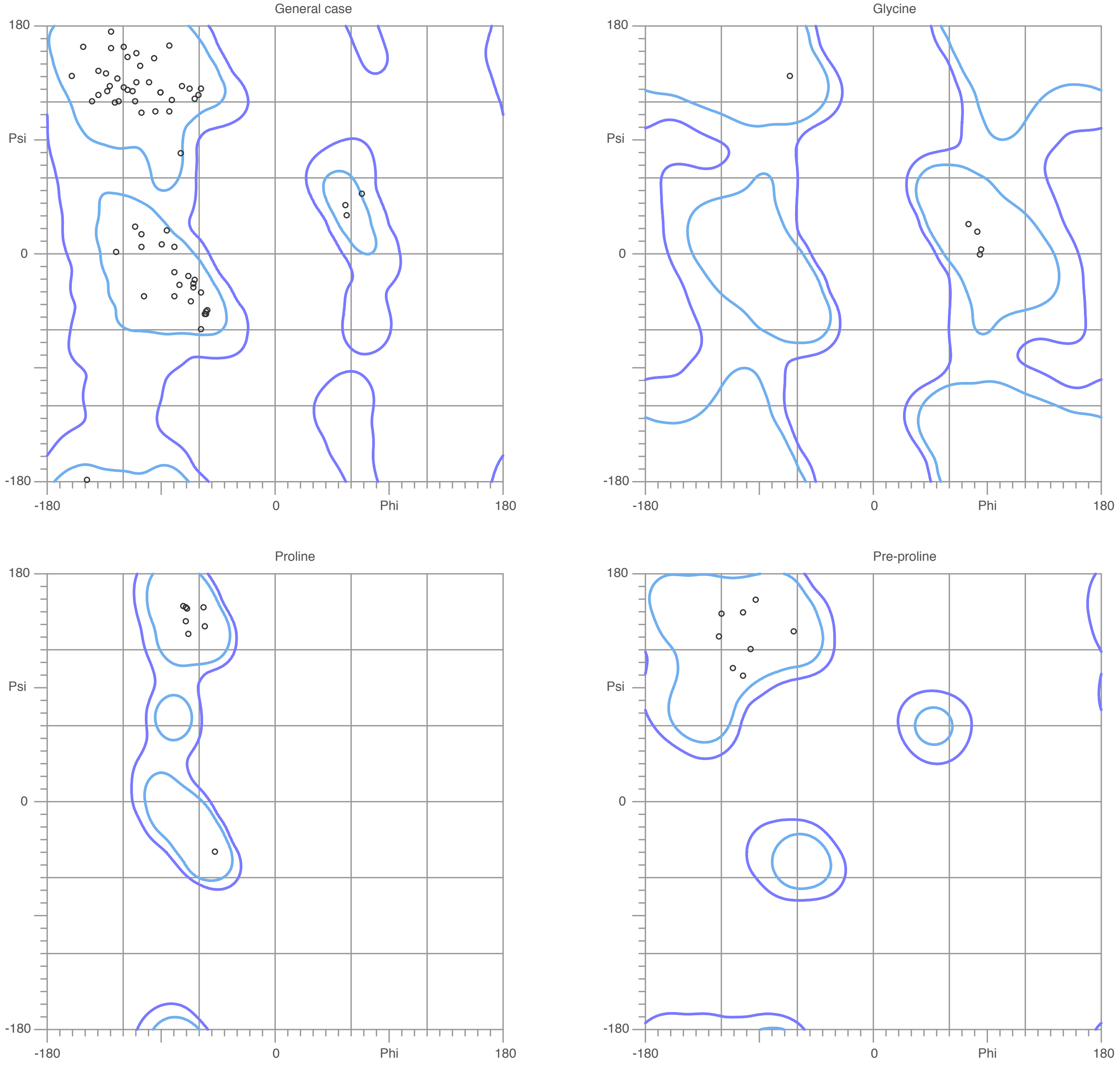
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 7



98.8% (83/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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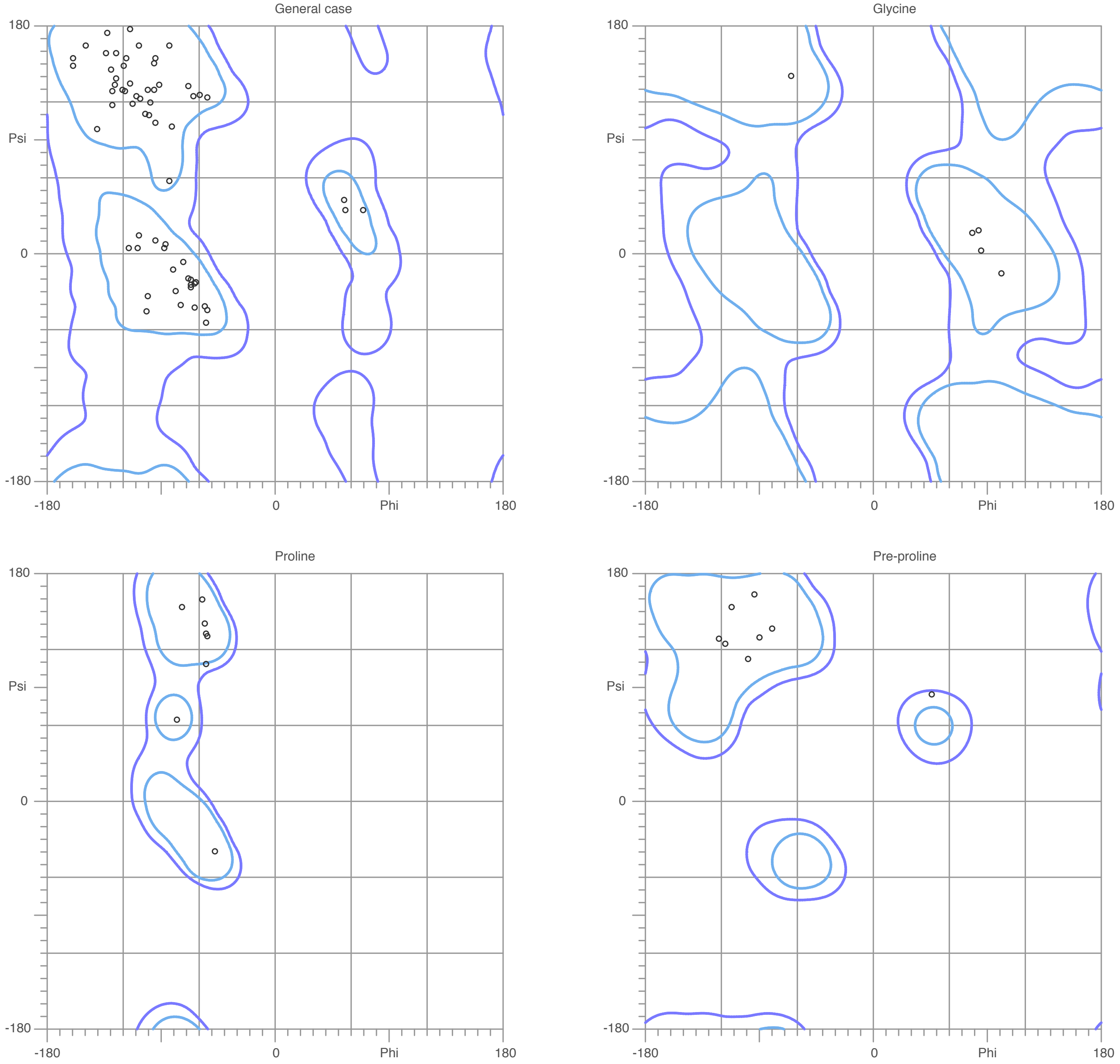
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 8



98.8% (83/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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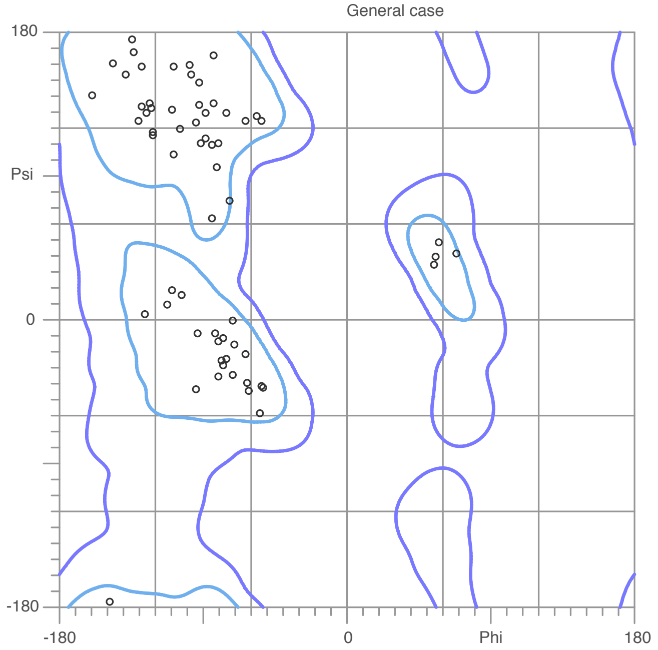
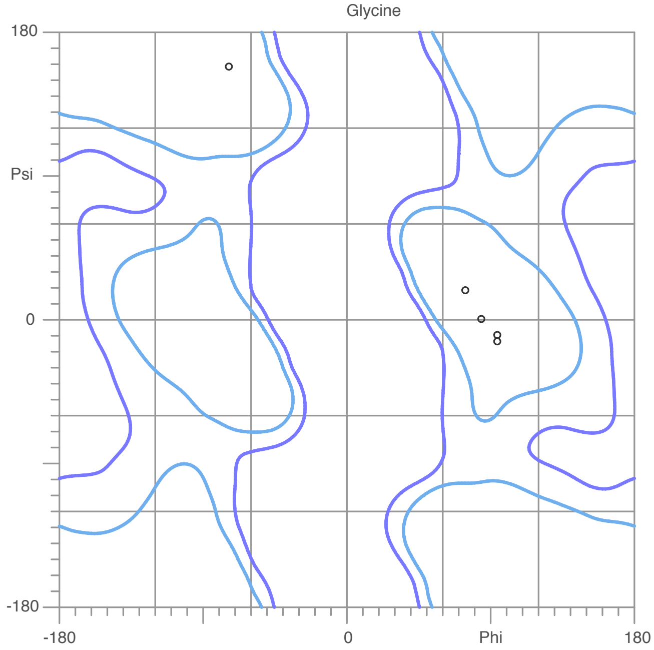
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 9

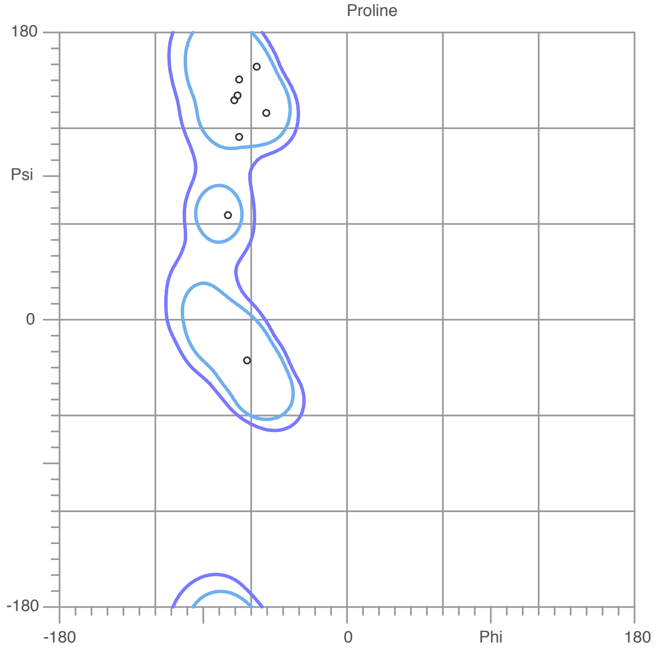
General case



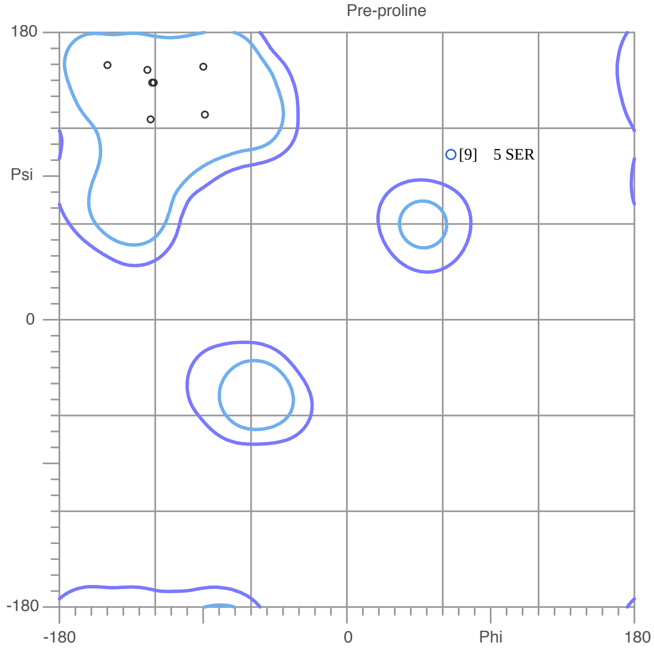
Glycine



Proline



Pre-proline

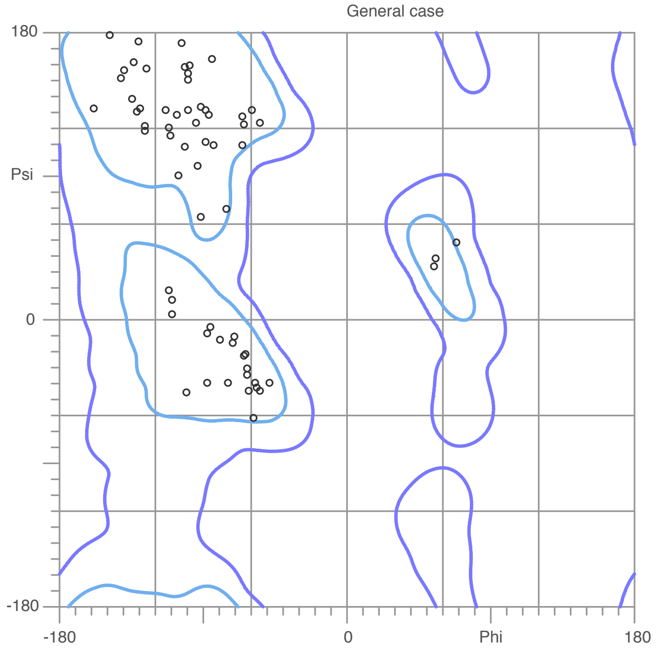


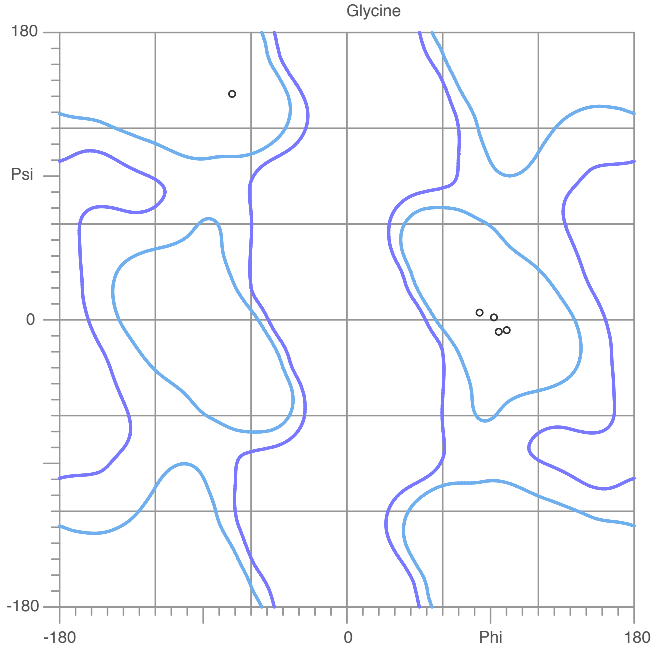
98.8% (83/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

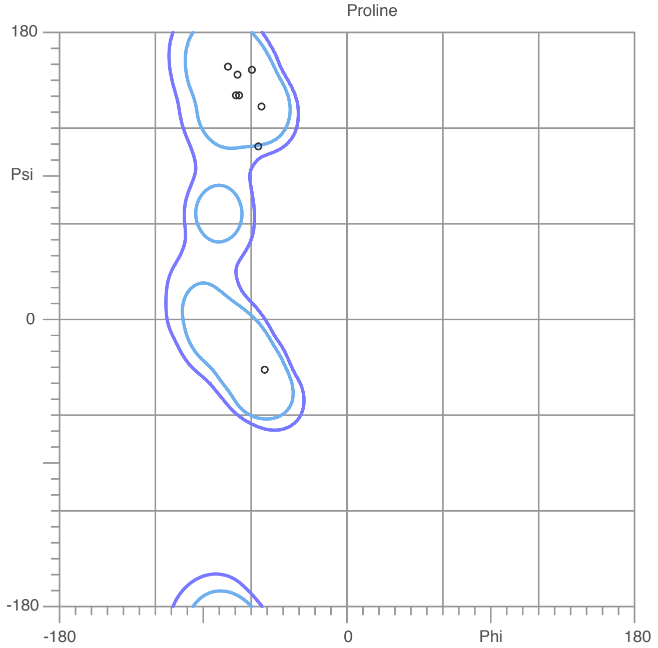
There were 1 outliers (phi, psi):
[9] 5 SER (65.1, 105.0)

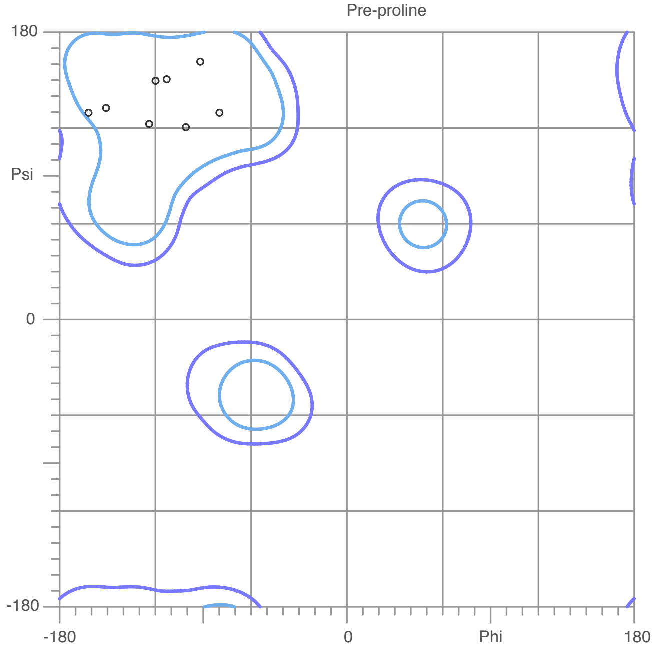
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 10









98.8% (83/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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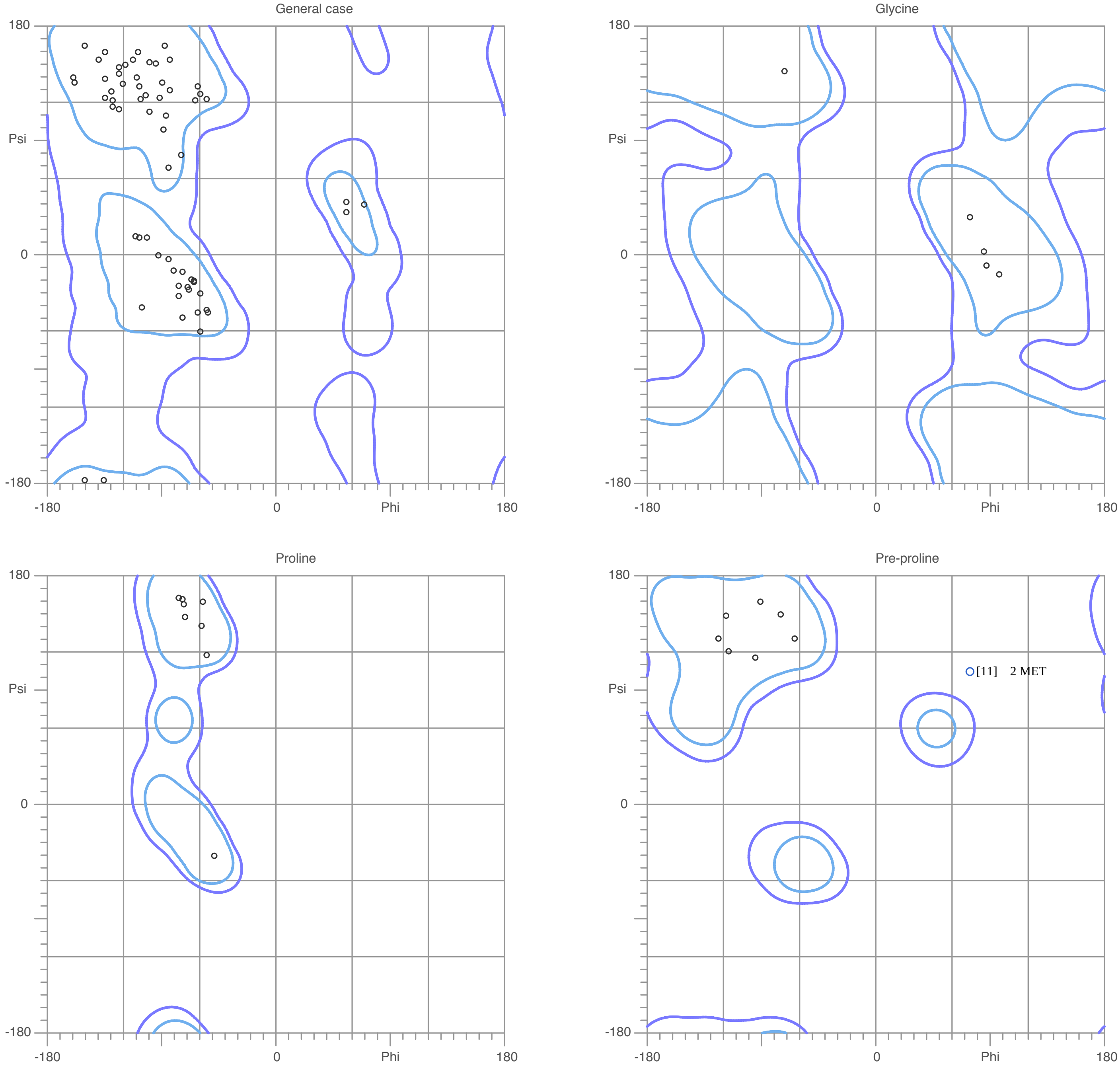
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 11



98.8% (83/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[11]   2 MET (75.0, 105.4)

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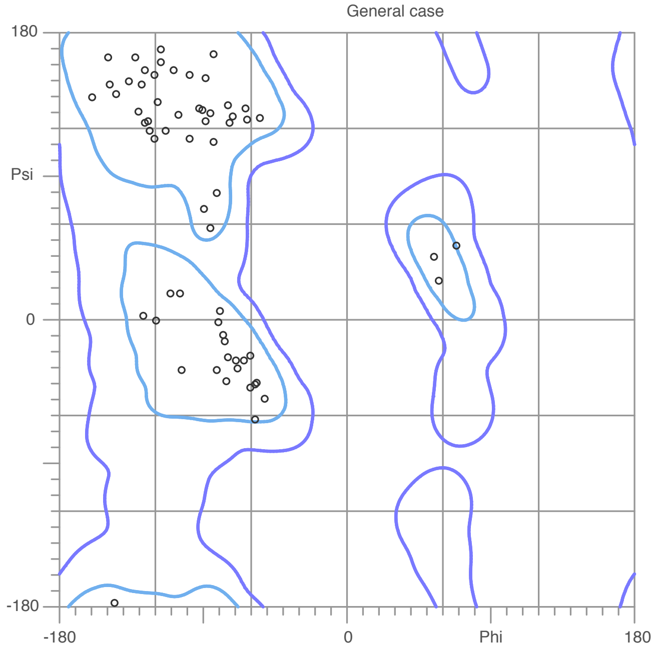
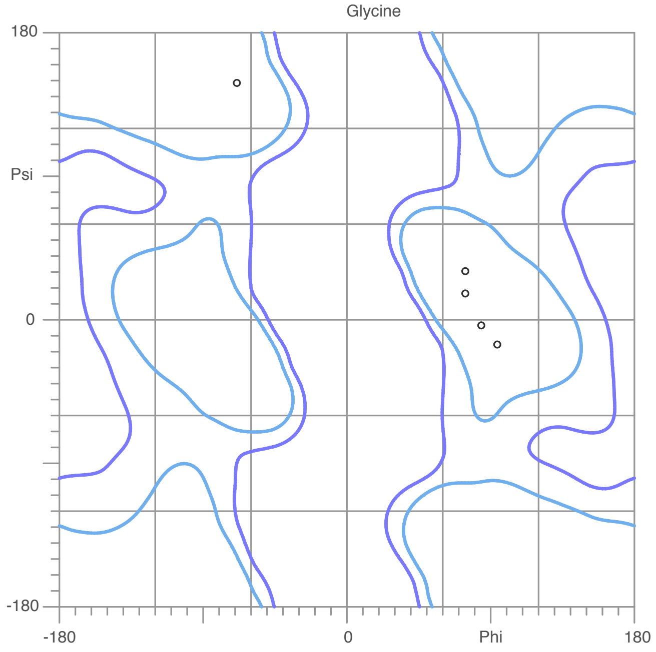
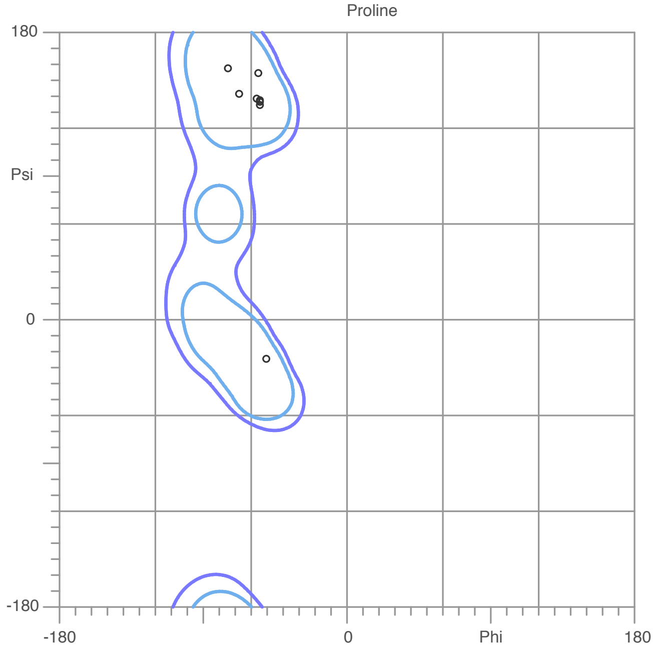
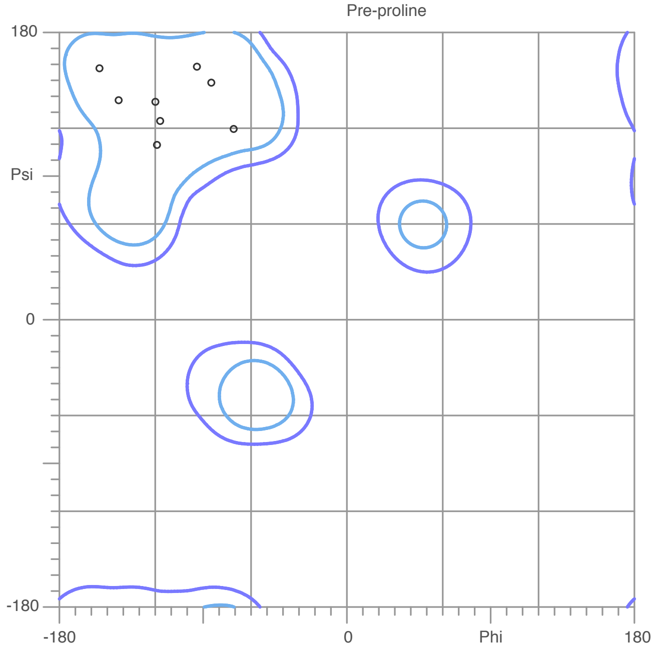
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 12









98.8% (83/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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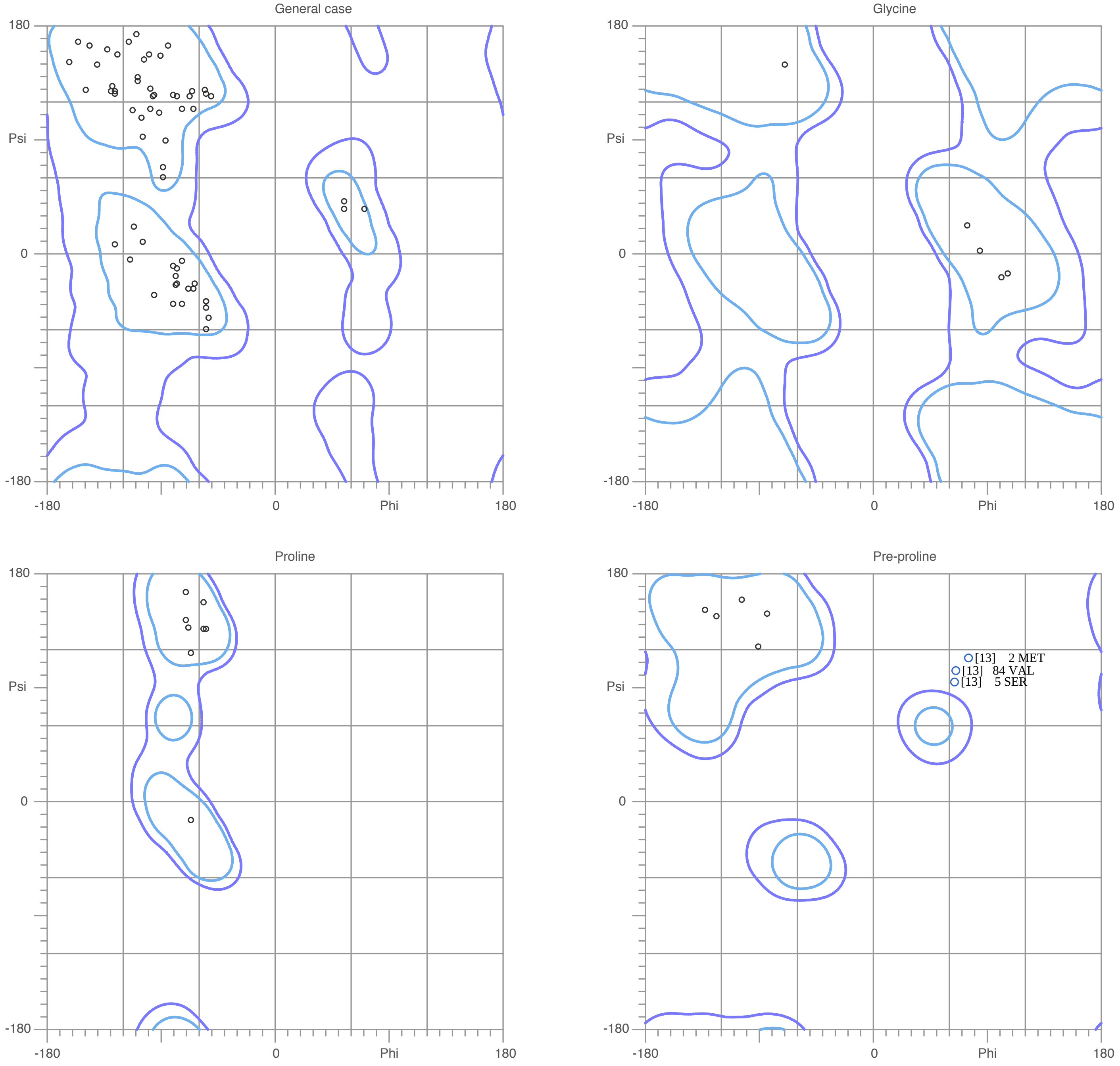
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 13



96.4% (81/84) of all residues were in favored (98%) regions.
96.4% (81/84) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
- [13] 2 MET (75.1, 115.0)
- [13] 5 SER (65.0, 95.0)
- [13] 84 VAL (65.1, 105.0)

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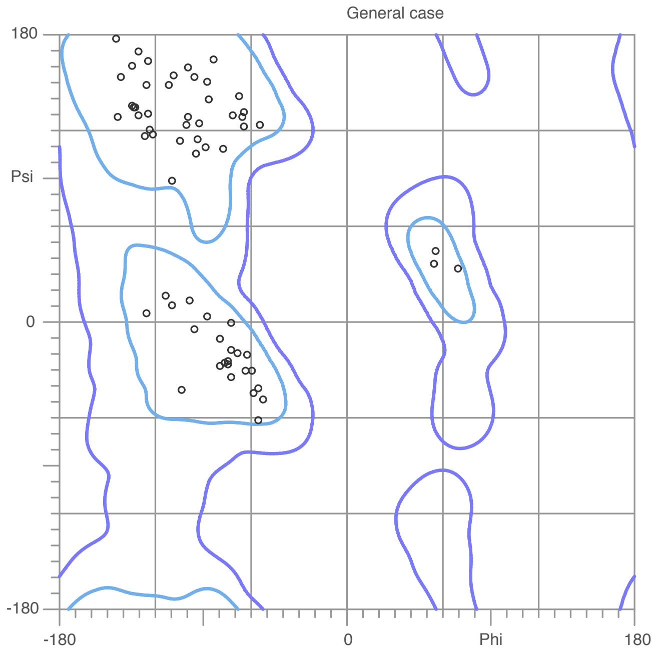
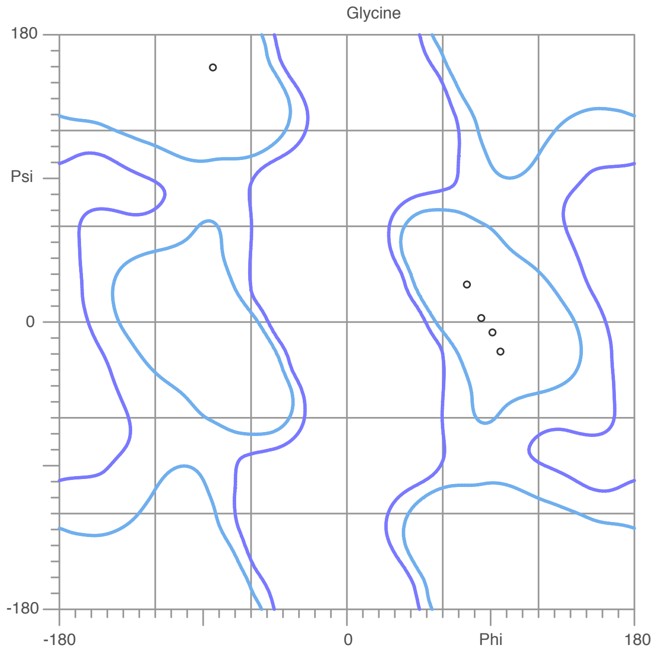
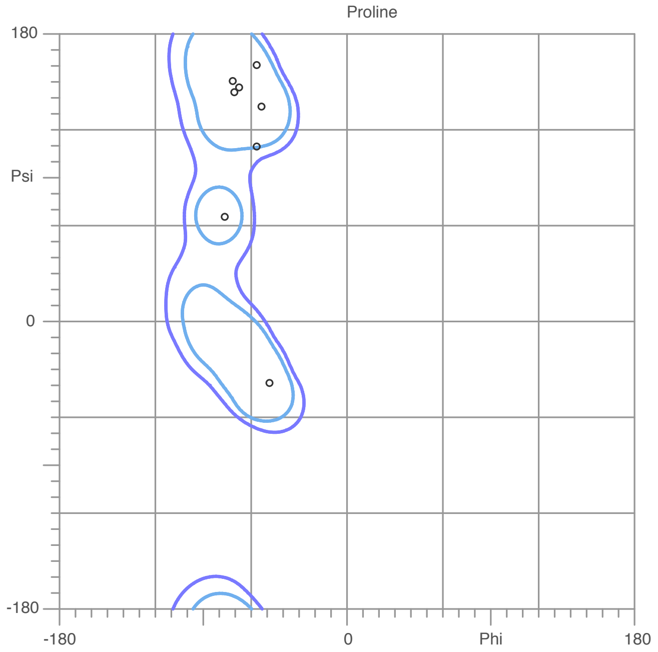
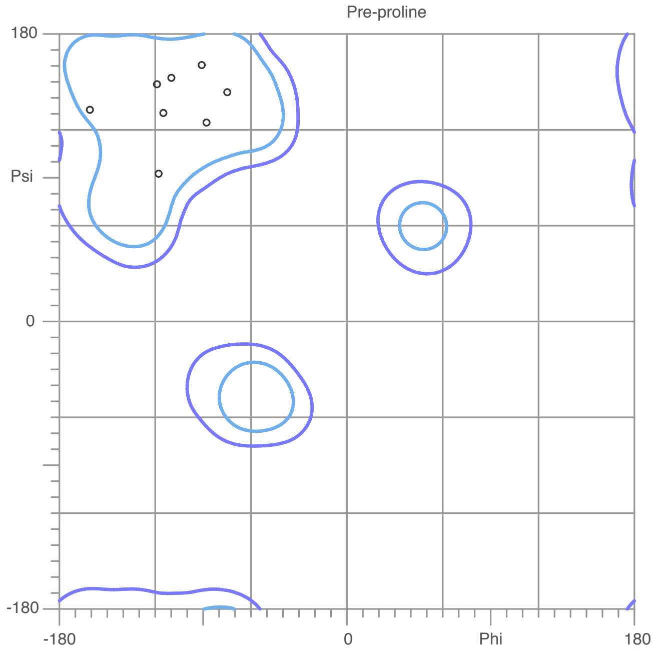
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 14









100.0% (84/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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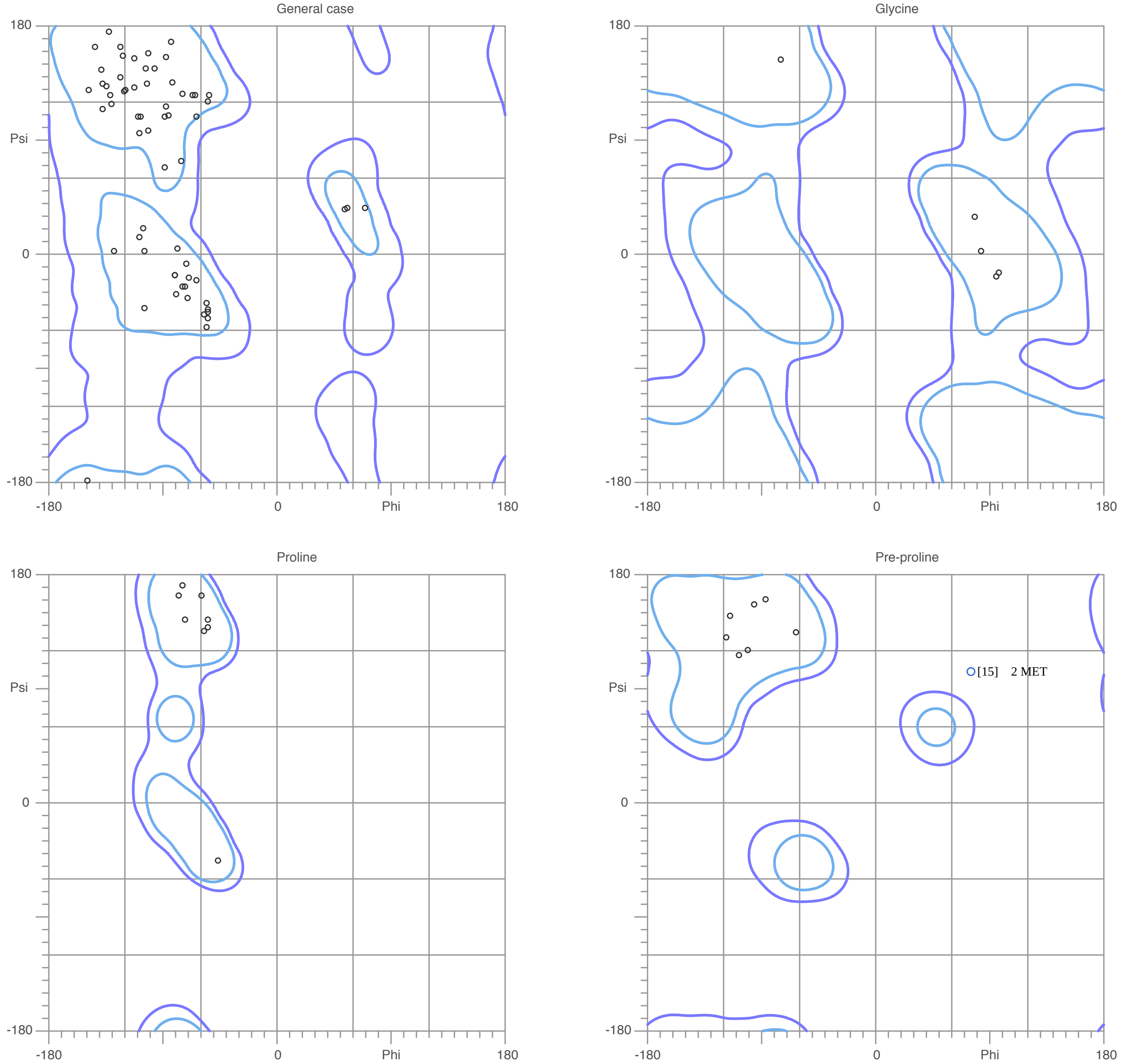
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 15

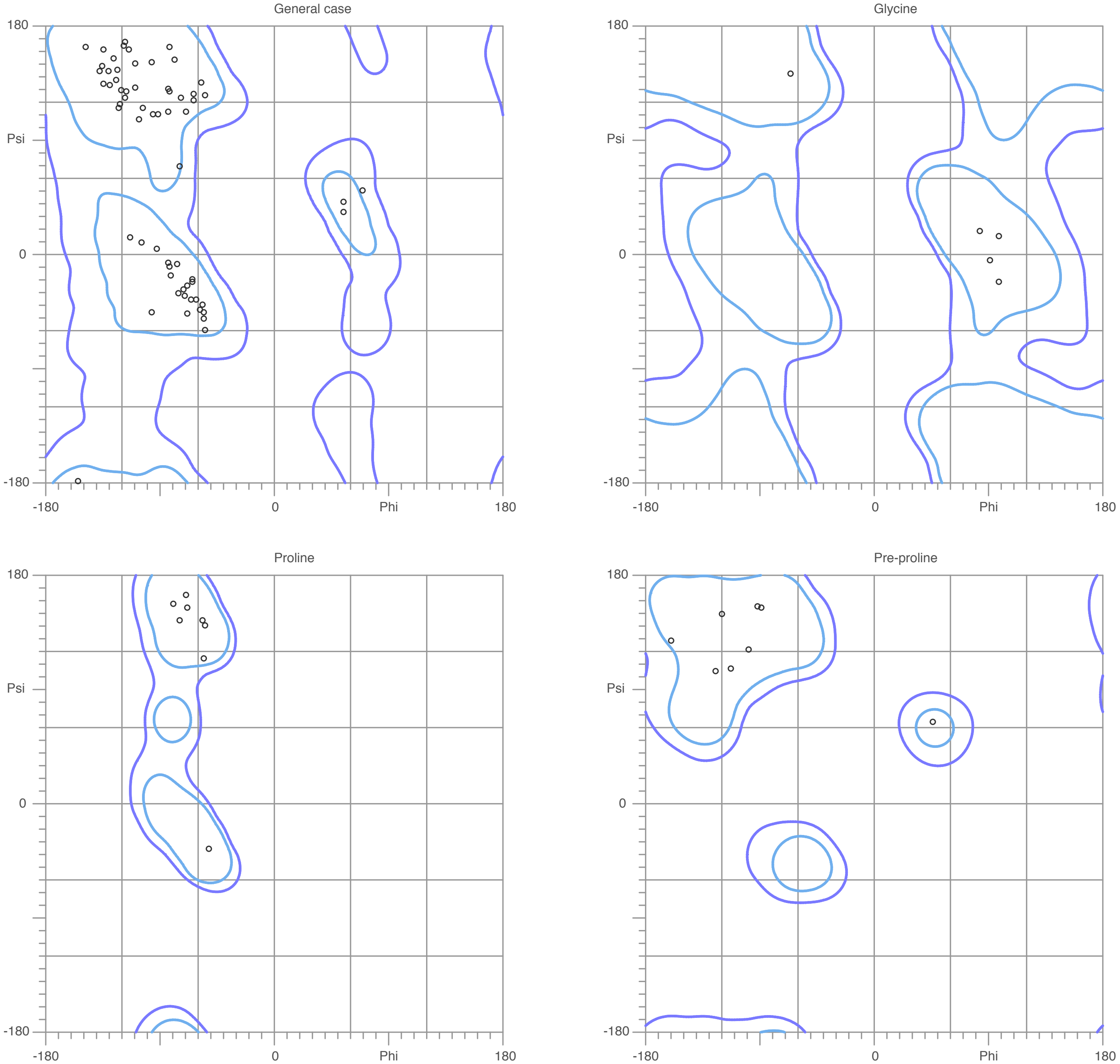


98.8% (83/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[15] 2 MET (75.1, 105.0)

MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 16



98.8% (83/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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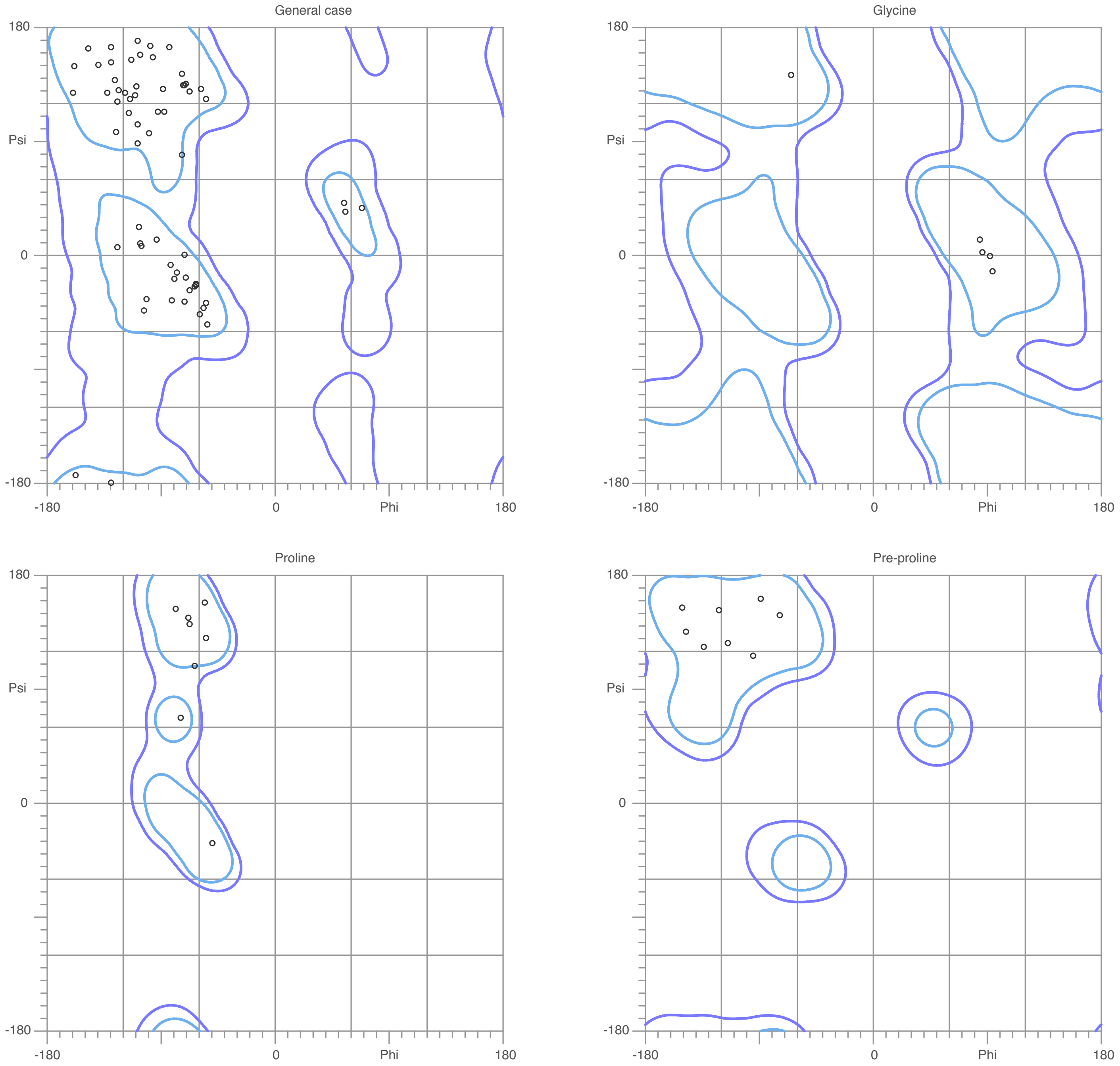
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 17



100.0% (84/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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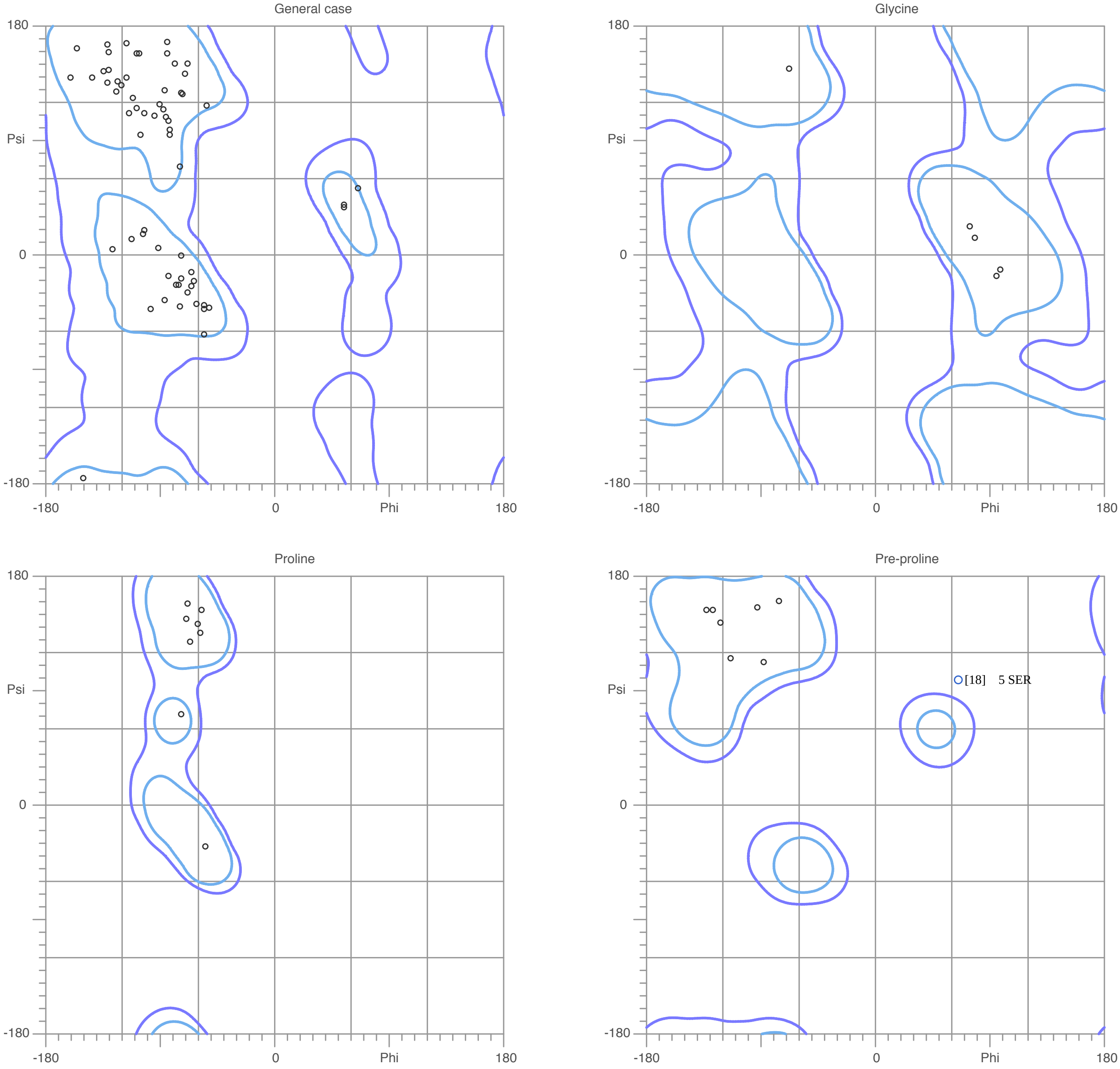
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 18

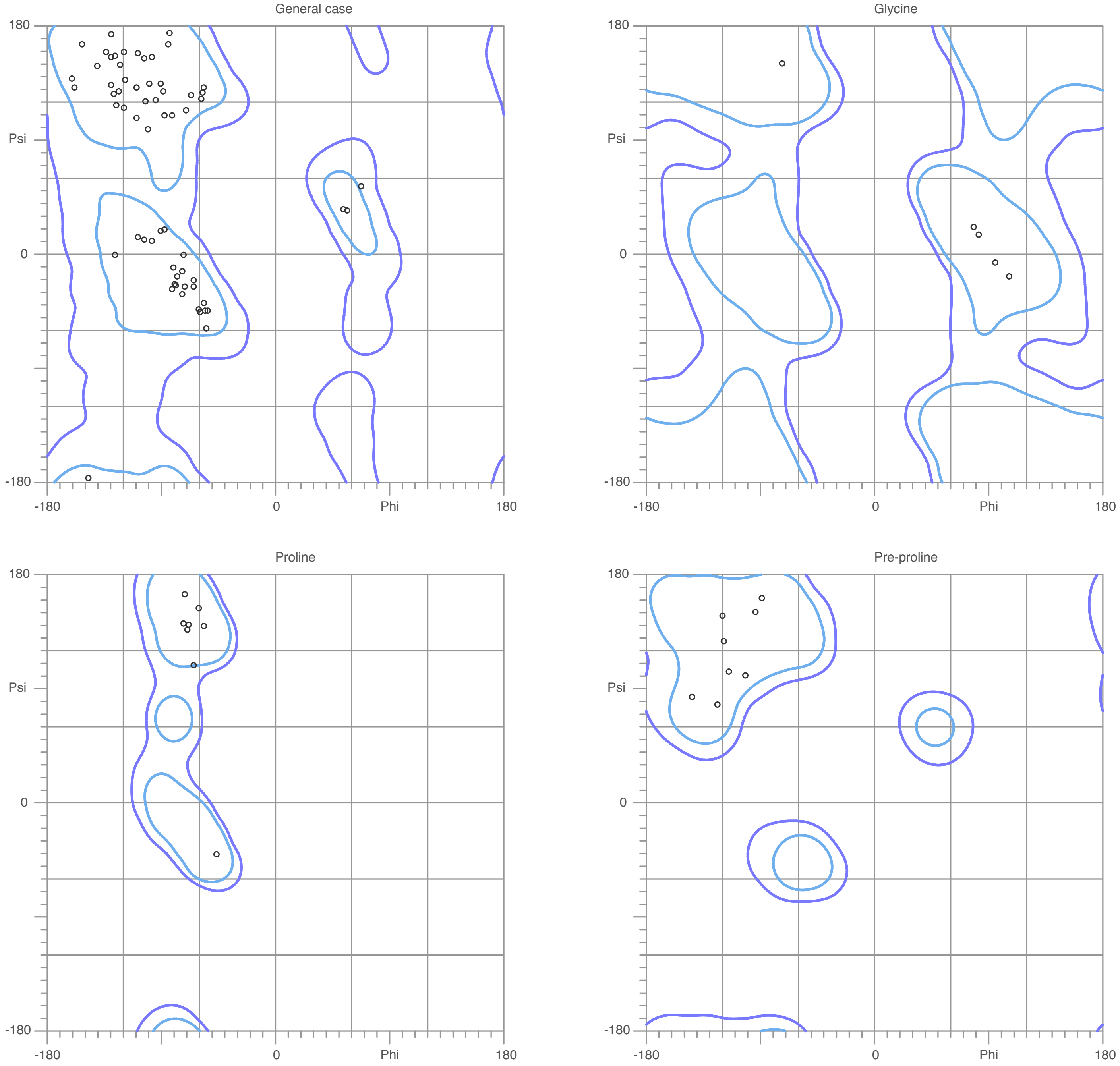


98.8% (83/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[18] 5 SER (65.0, 99.2)

MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 19



98.8% (83/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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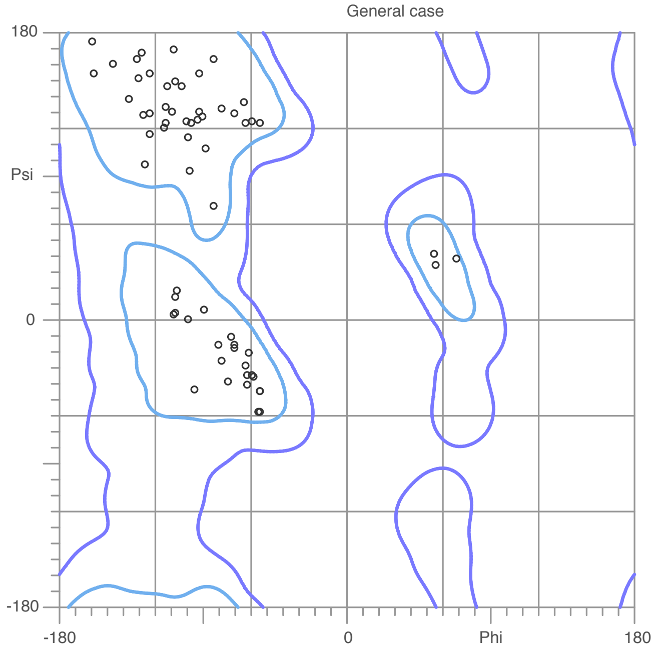
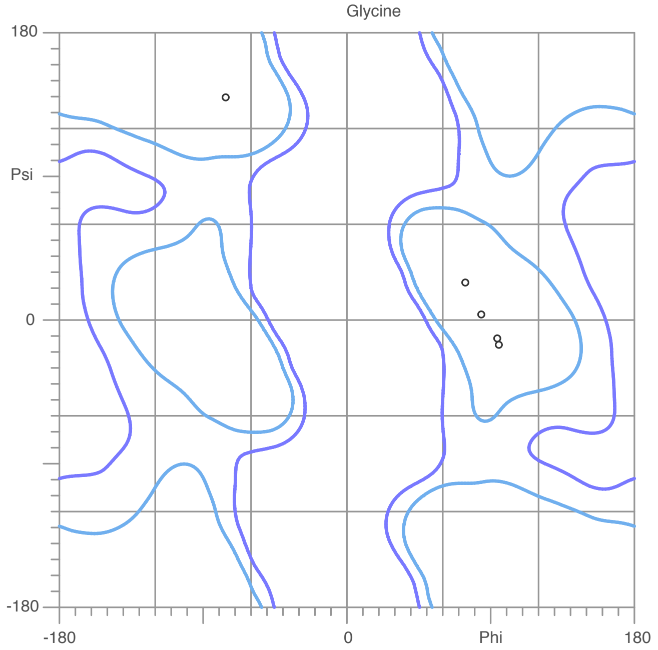
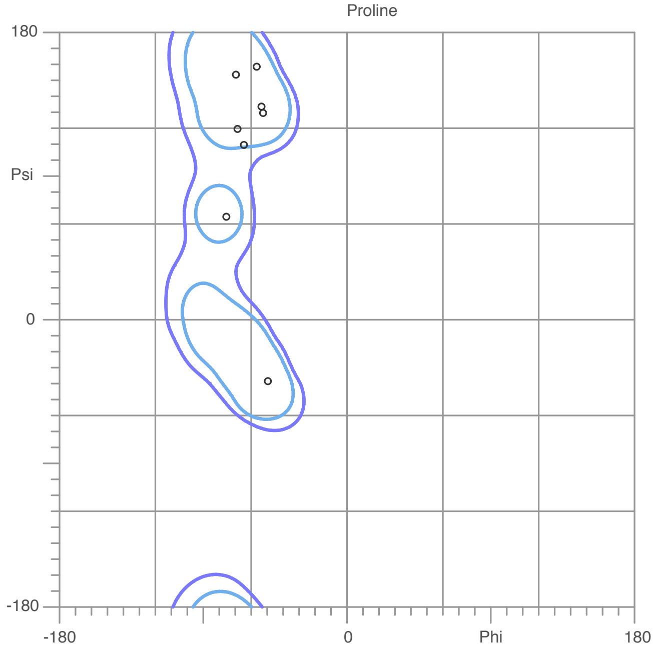
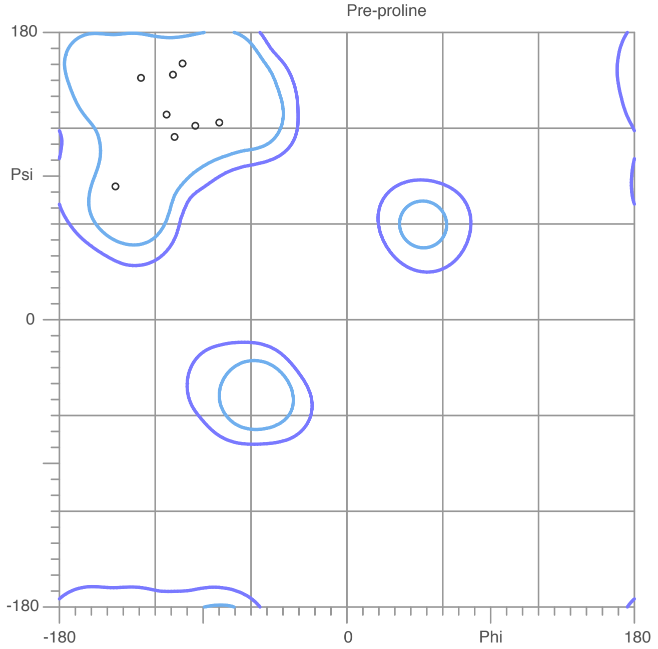
MolProbity Ramachandran analysis

HR4694F_R3_em_bcr3.pdb, model 20









100.0% (84/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

http://kinemage.biochem.duke.edu

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