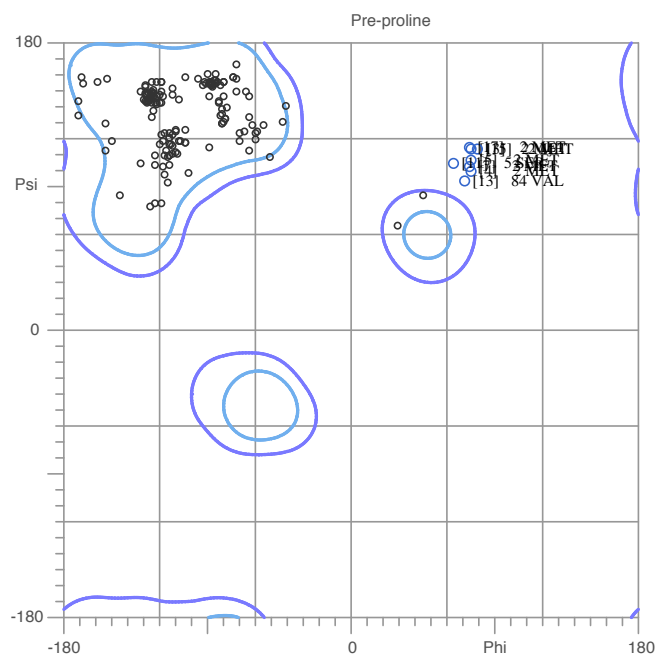
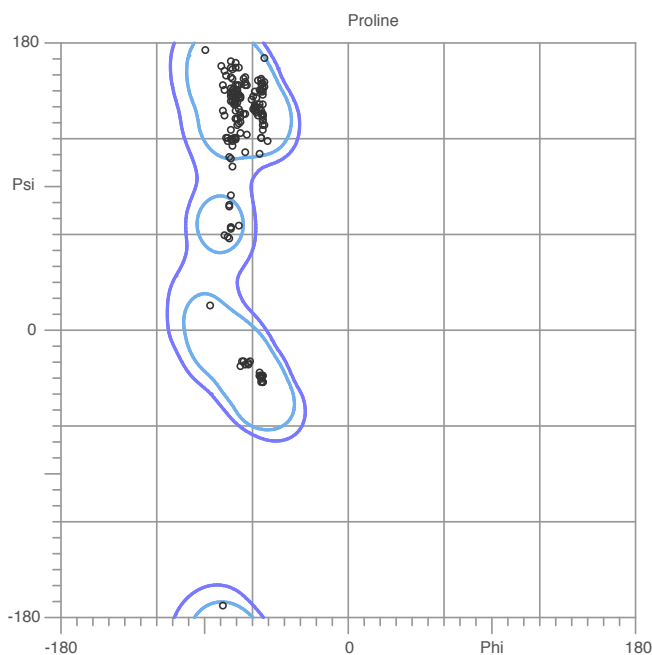
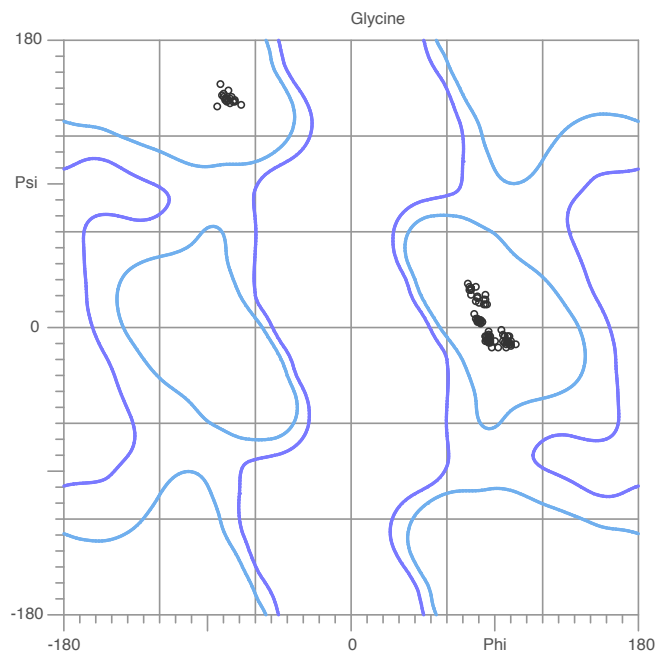
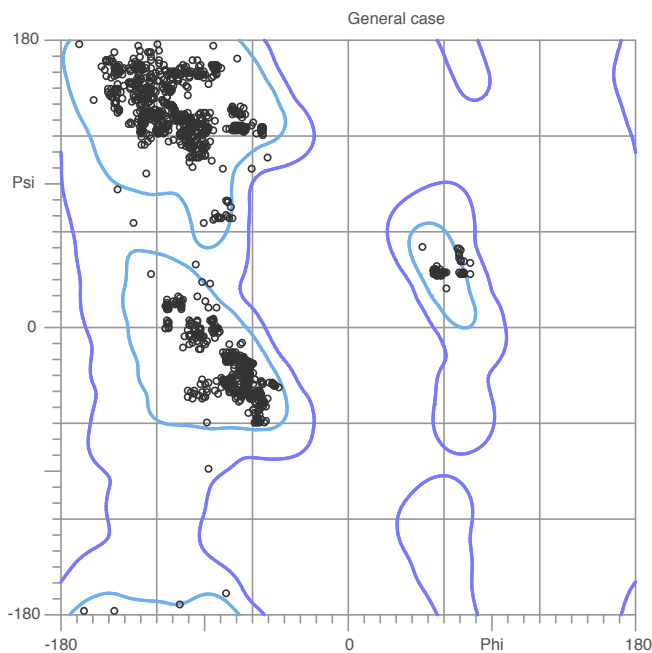


MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, all models



97.9% (1645/1680) of all residues were in favored (98%) regions.
99.5% (1672/1680) of all residues were in allowed (>99.8%) regions.

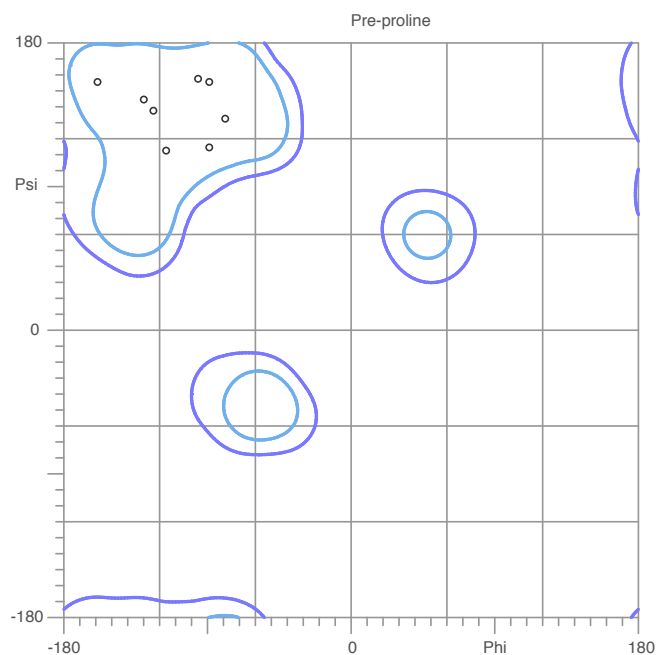
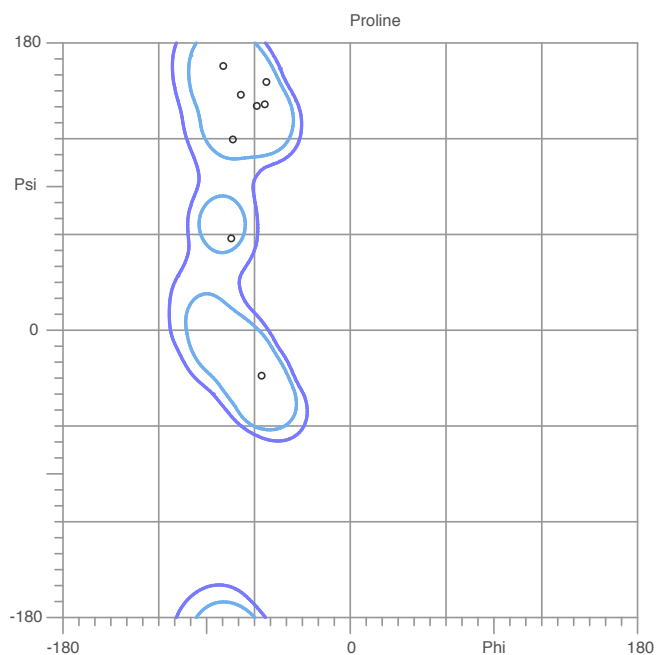
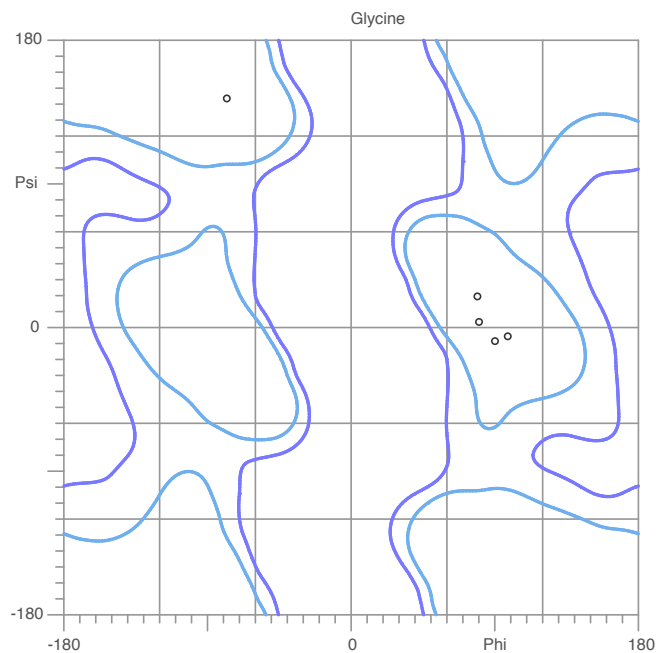
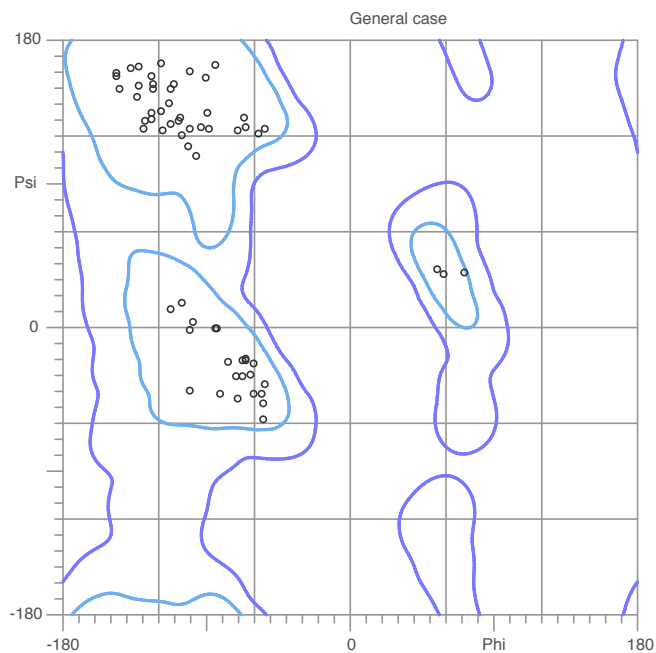
There were 8 outliers (phi, psi):

- [4] 2 MET (75.0, 100.6)
- [5] 2 MET (75.1, 107.0)

- [7] 2 MET (74.9, 103.1)
- [11] 5 SER (64.9, 105.0)
- [13] 2 MET (75.2, 114.7)
- [13] 84 VAL (71.1, 95.0)
- [15] 2 MET (79.0, 114.5)
- [17] 2 MET (75.0, 115.1)

MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 1



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.

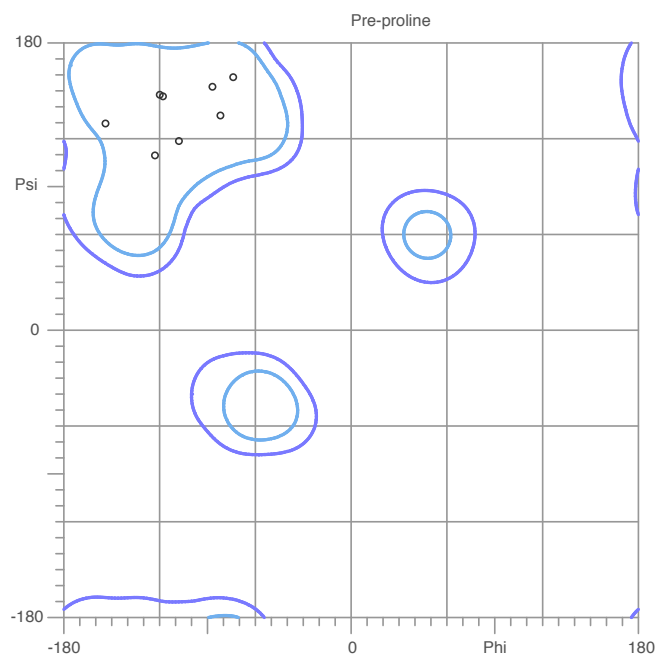
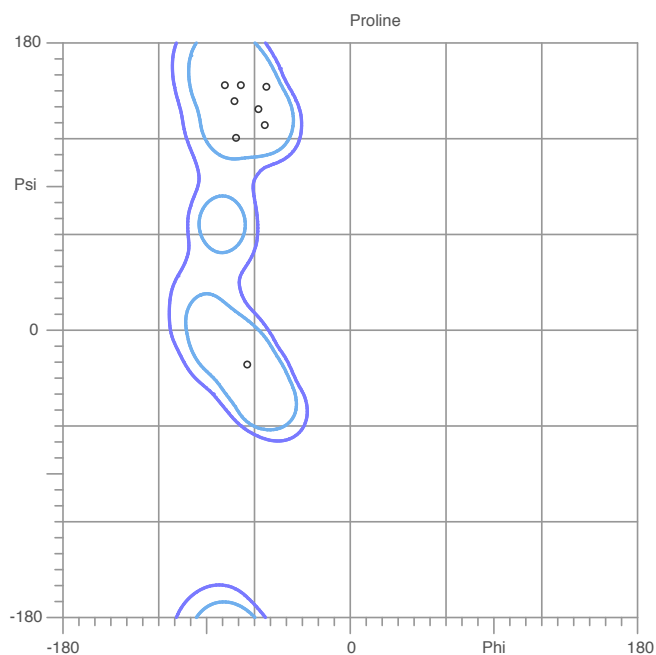
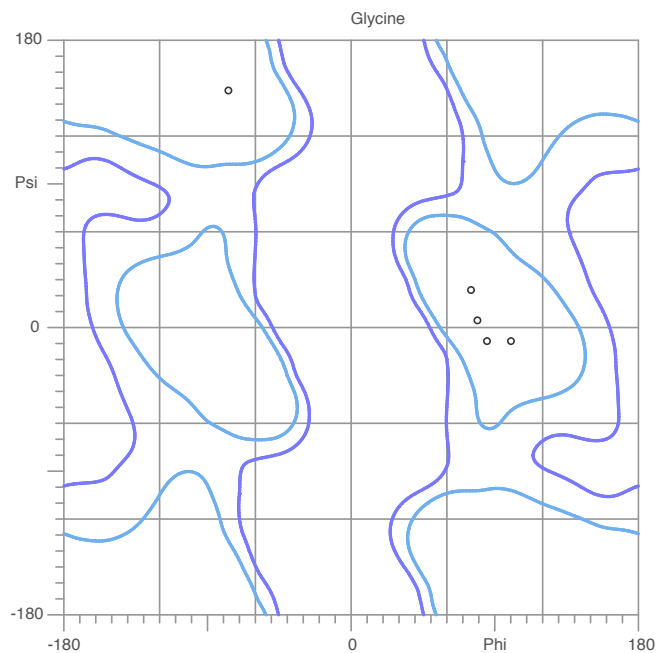
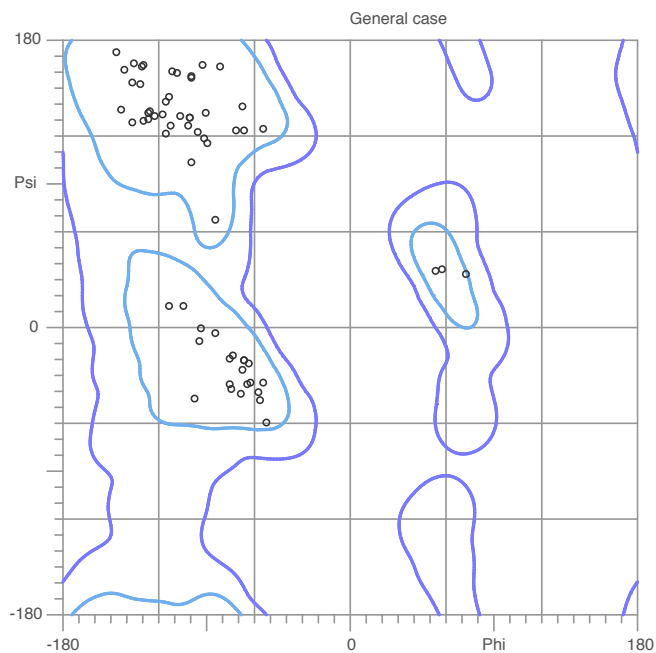
There were no outliers.

<http://kinemage.biochem.duke.edu>

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MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 2



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.

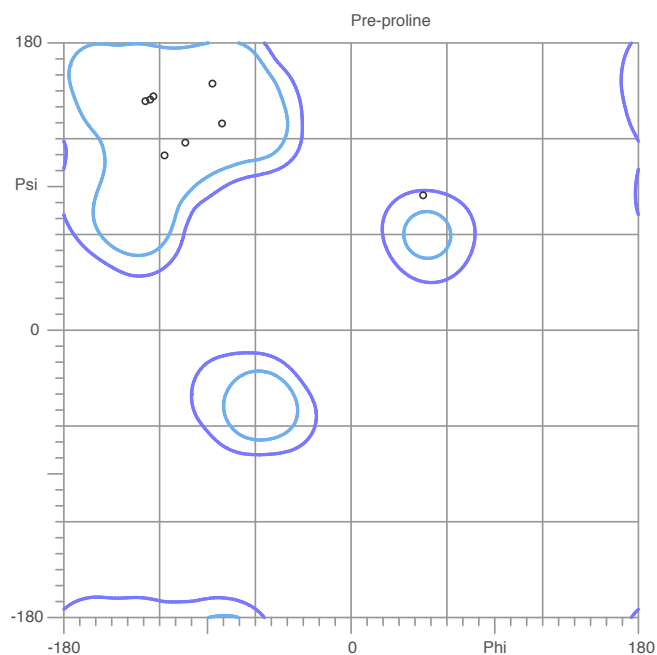
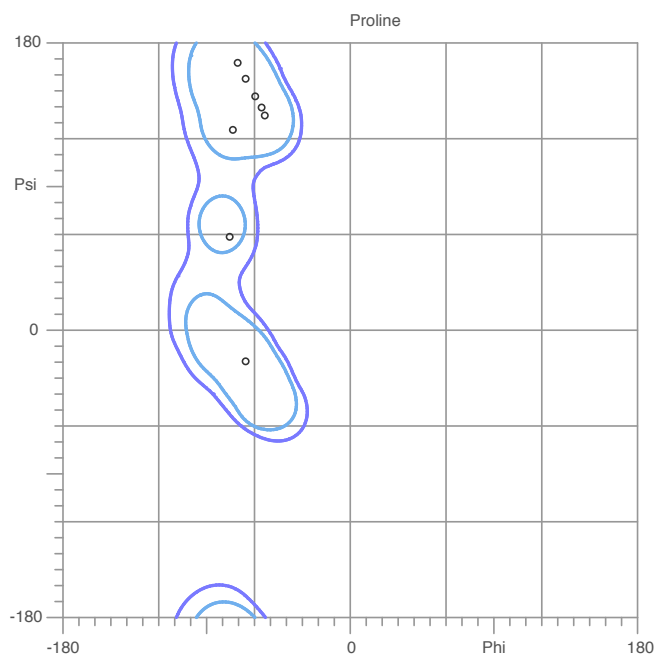
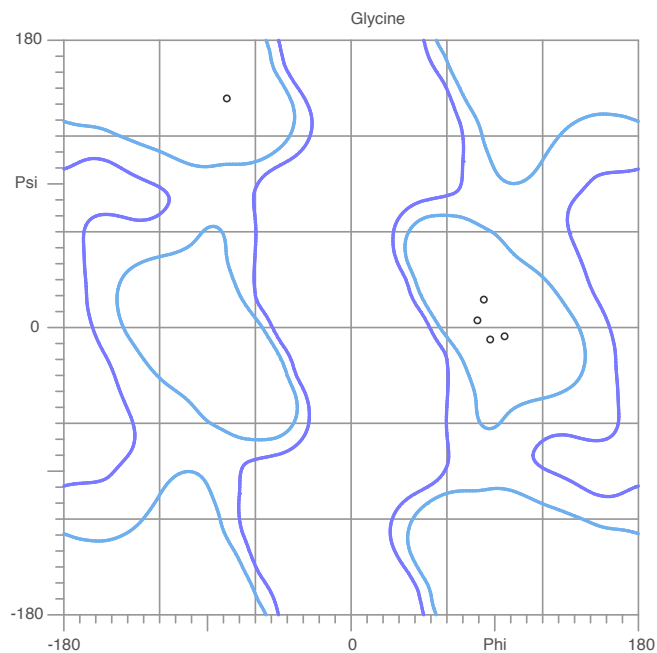
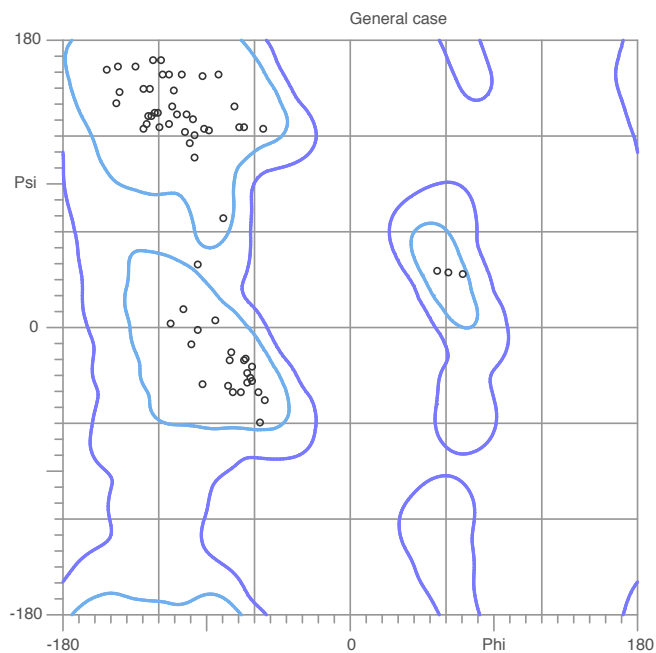
There were no outliers.

<http://kinemage.biochem.duke.edu>

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

MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 3



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.

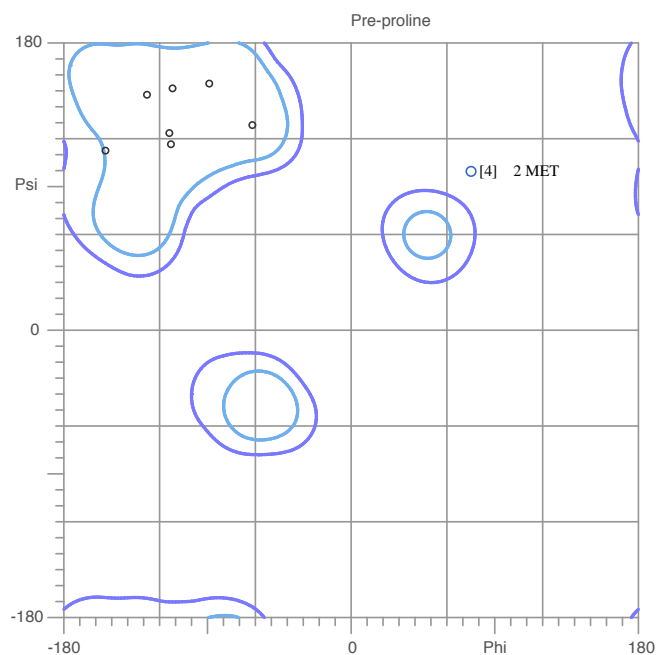
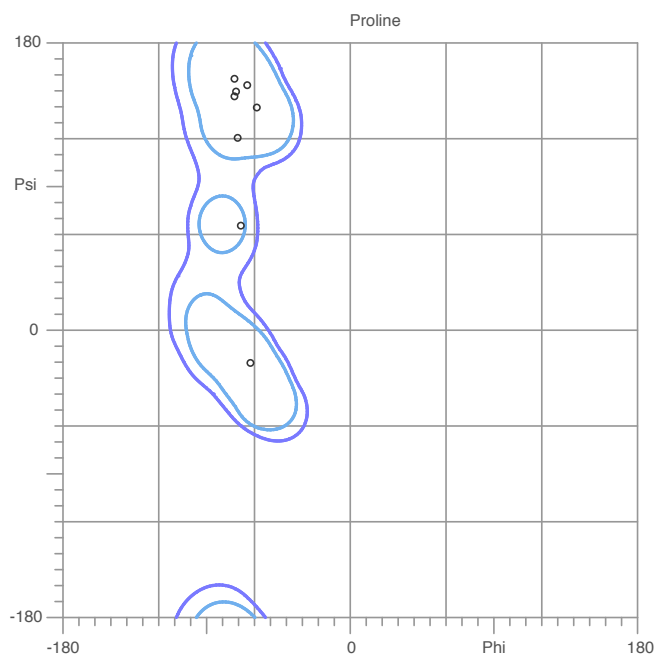
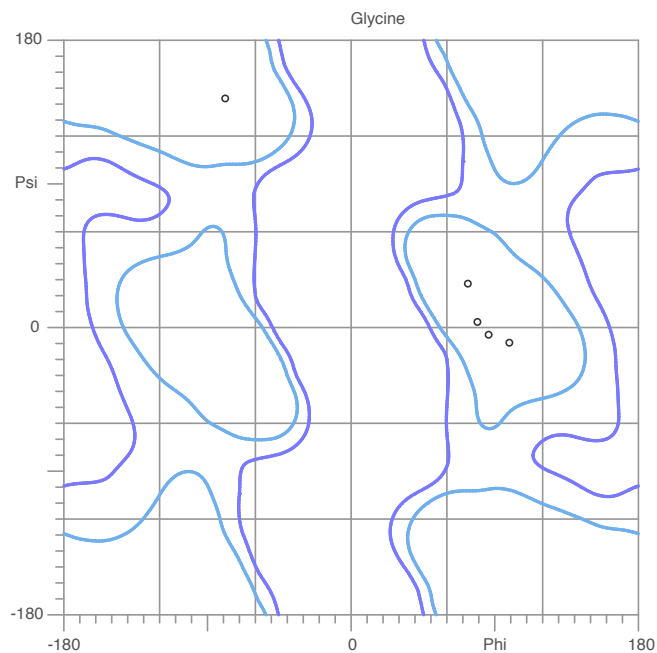
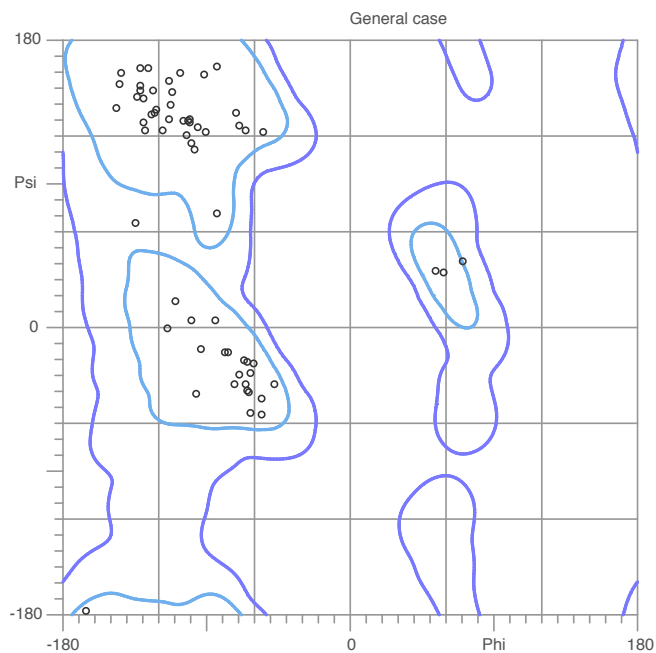
There were no outliers.

<http://kinemage.biochem.duke.edu>

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MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 4

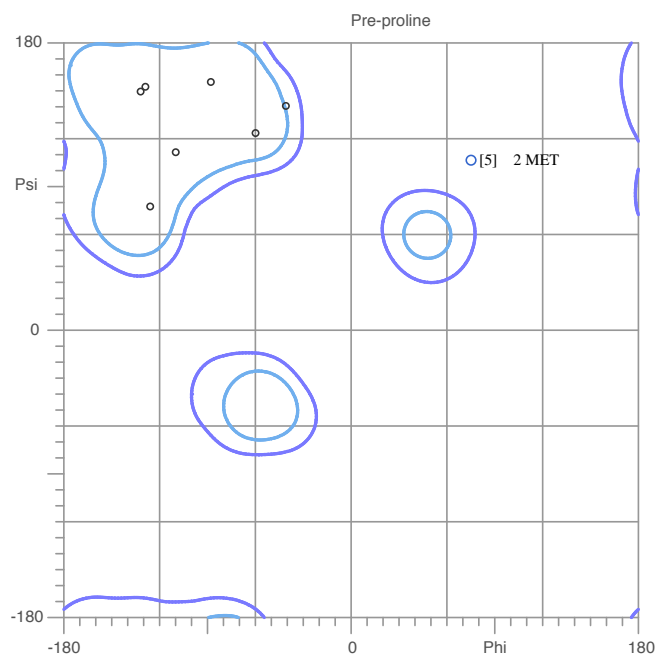
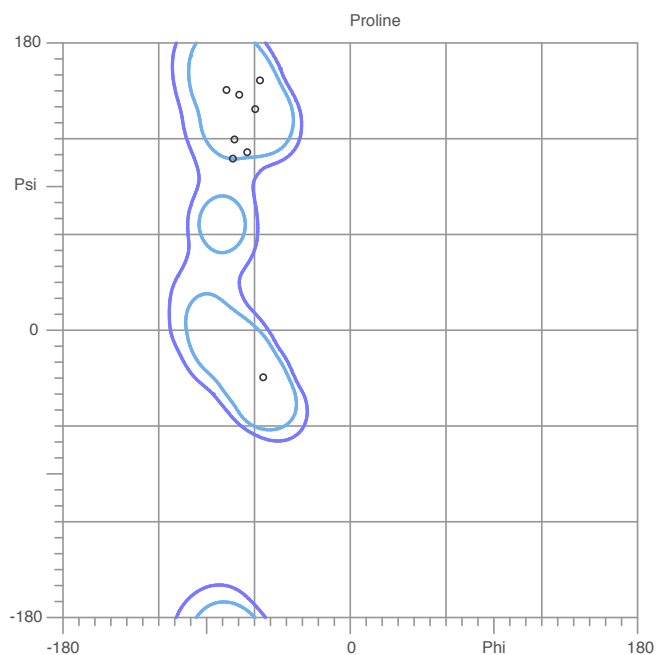
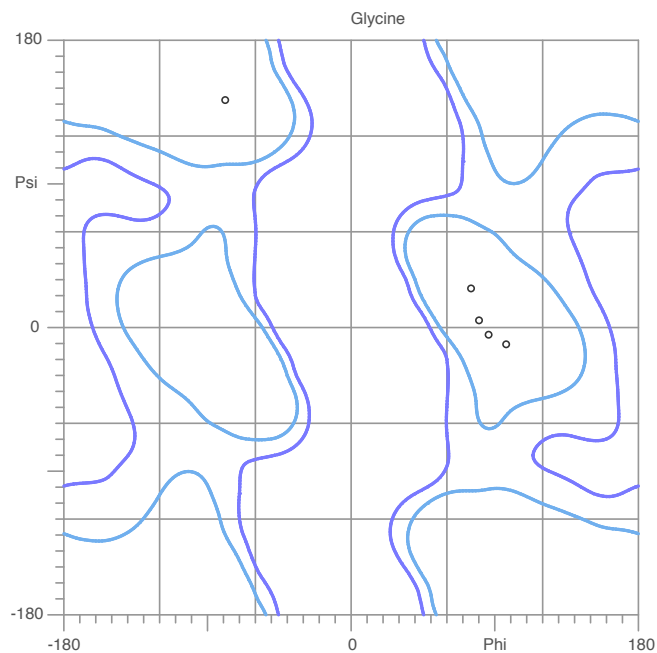
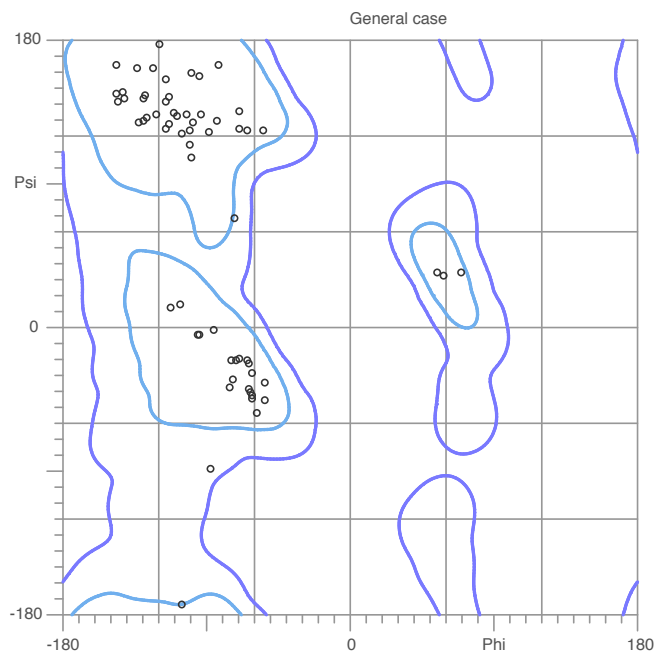


96.4% (81/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[4] 2 MET (75.0, 100.6)

MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 5

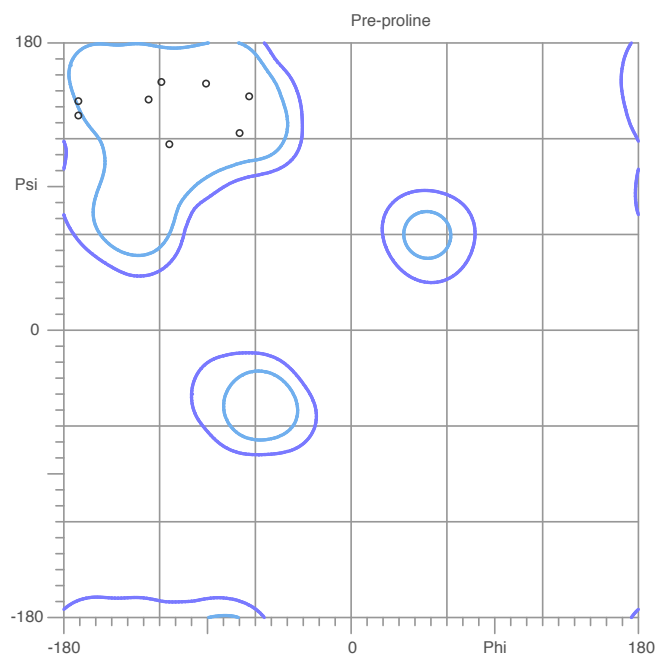
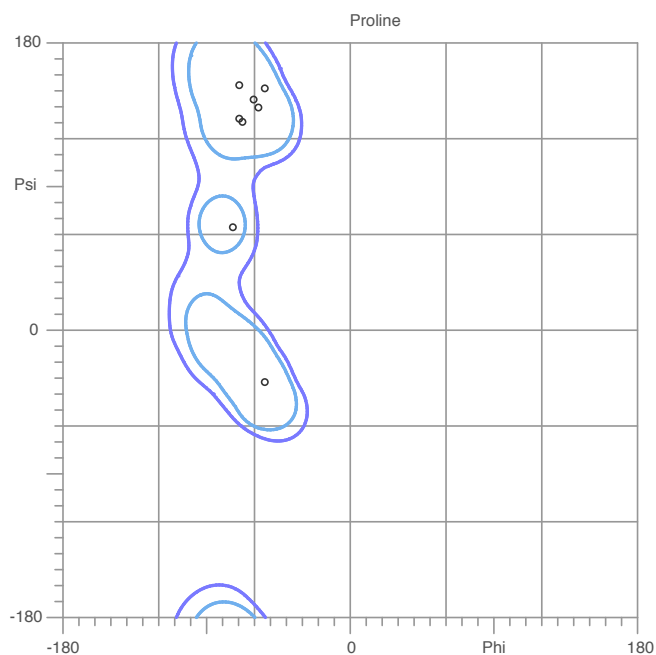
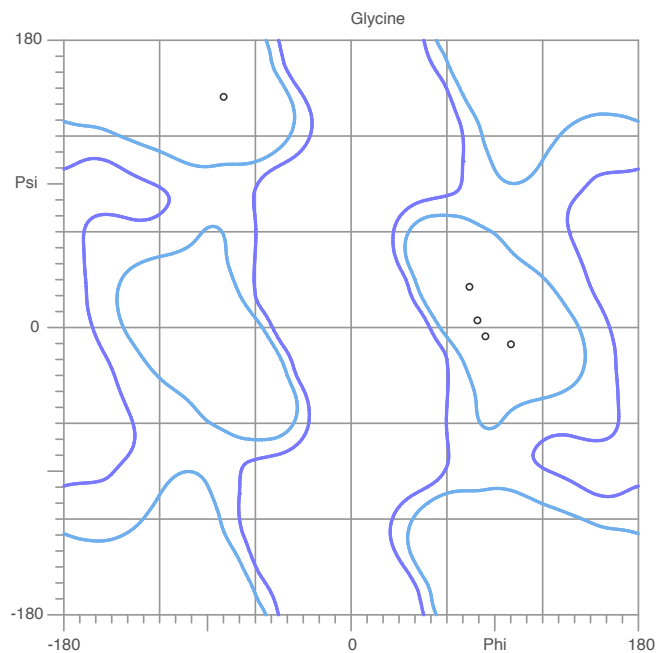
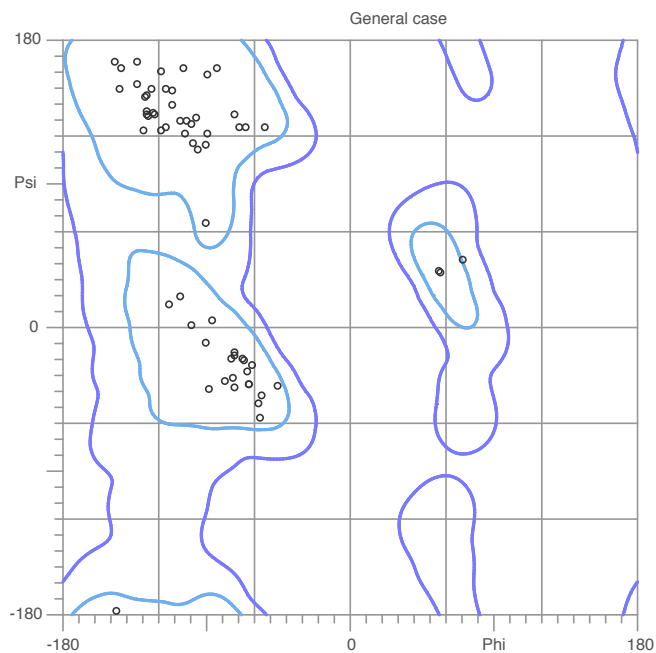


95.2% (80/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 2 MET (75.1, 107.0)

MolProbity Ramachandran analysis

HR4694F_R3Cons_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.

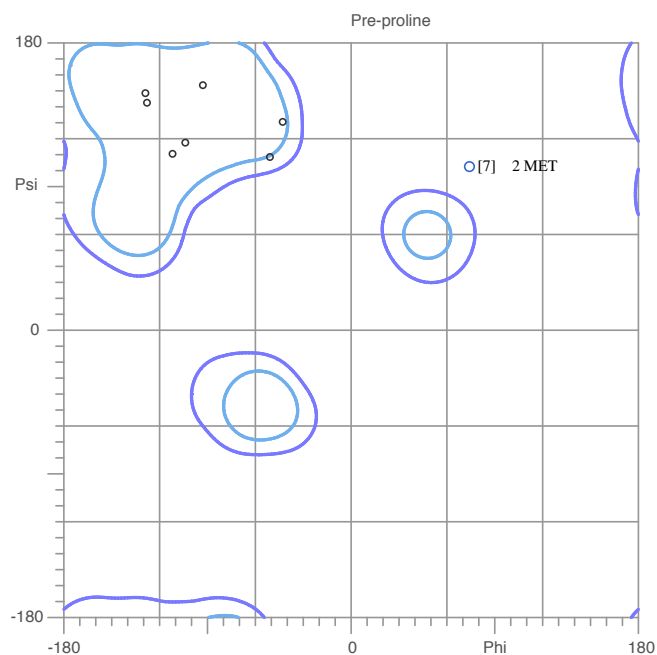
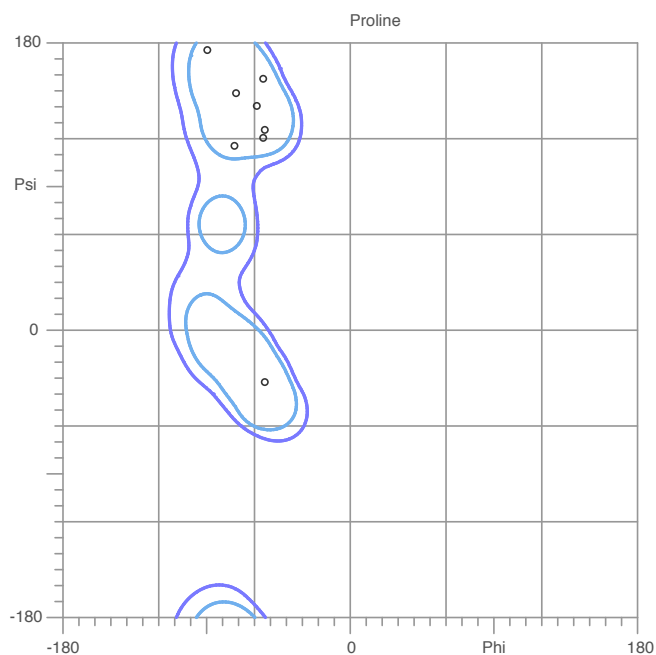
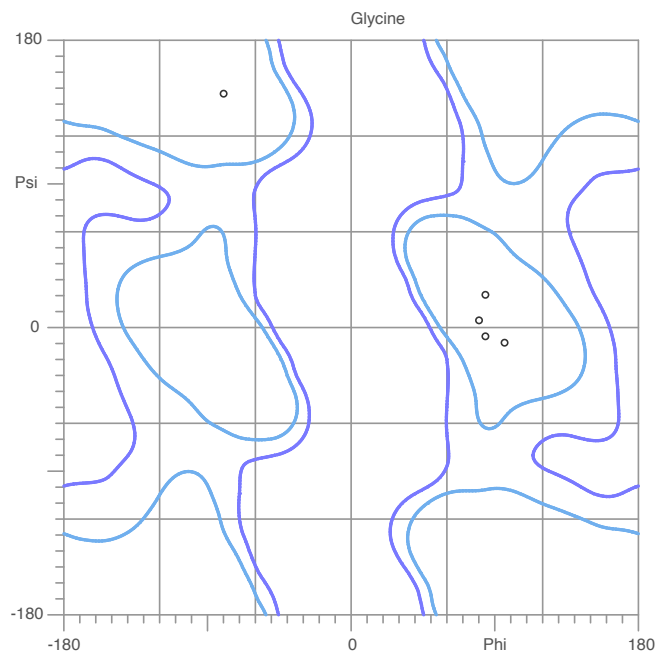
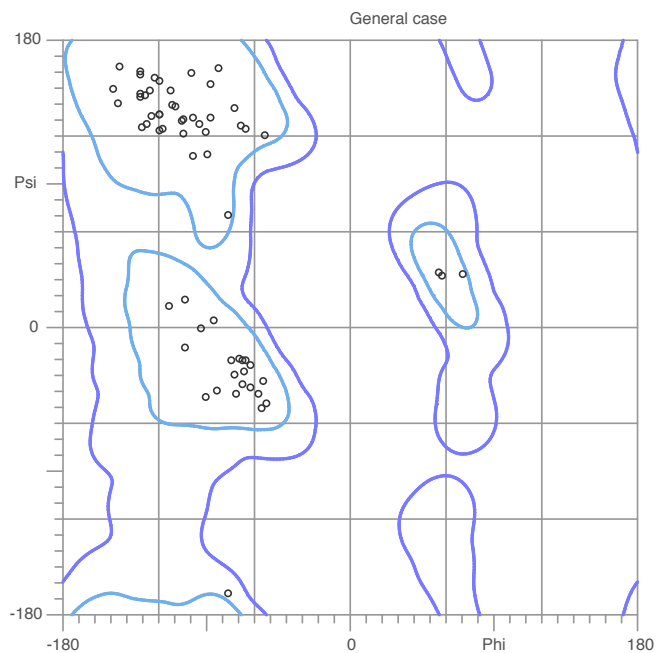
There were no outliers.

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MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 7

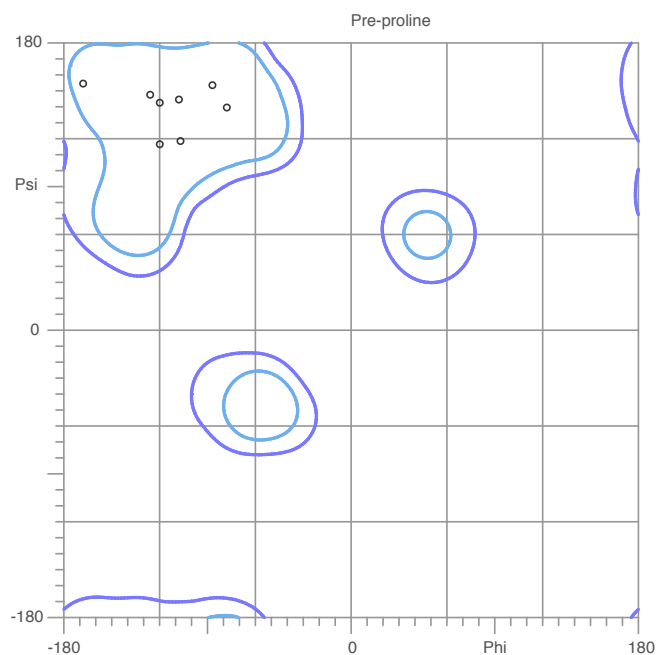
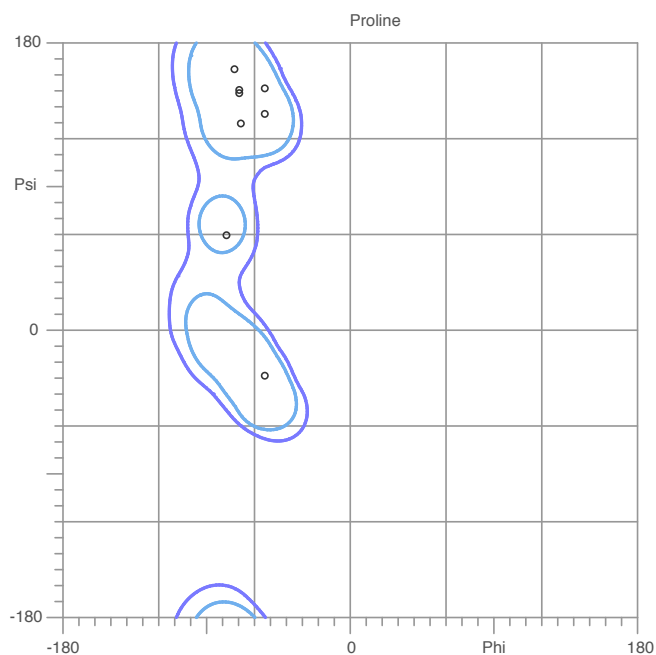
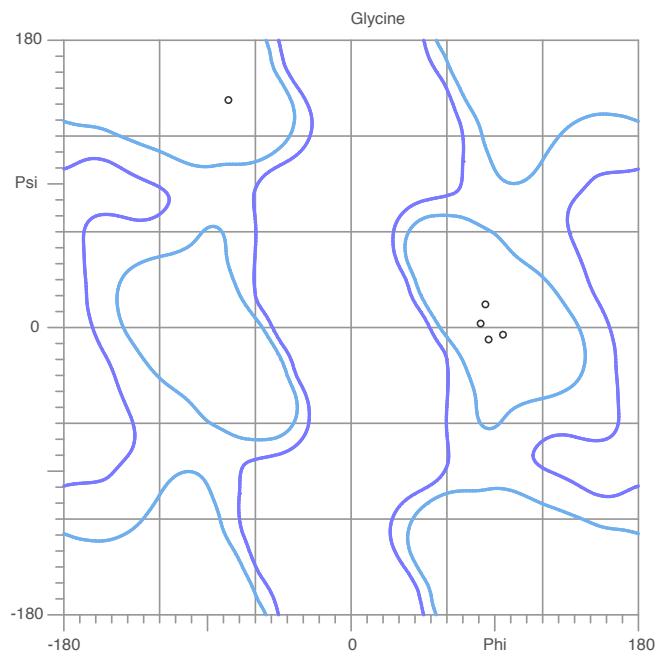
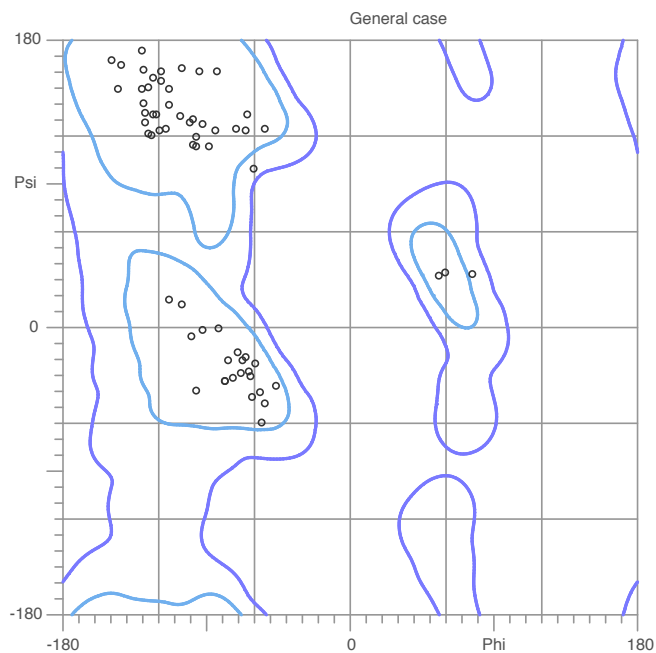


97.6% (82/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[7] 2 MET (74.9, 103.1)

MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 8



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.

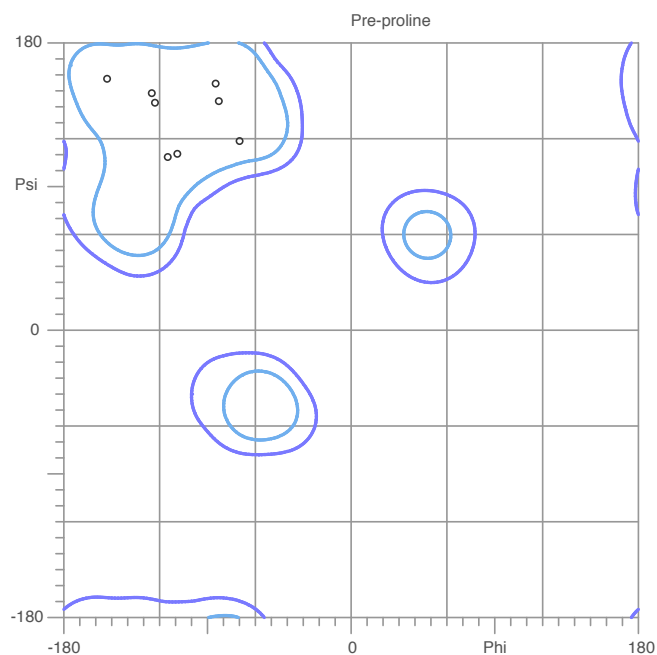
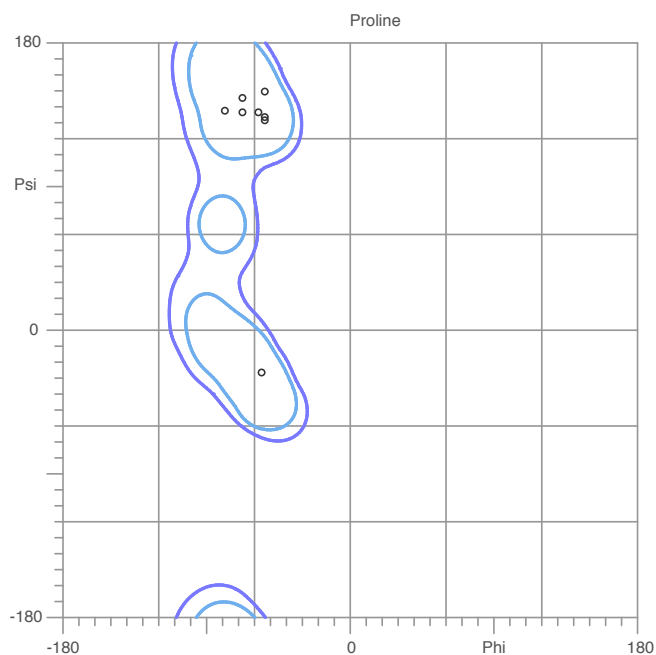
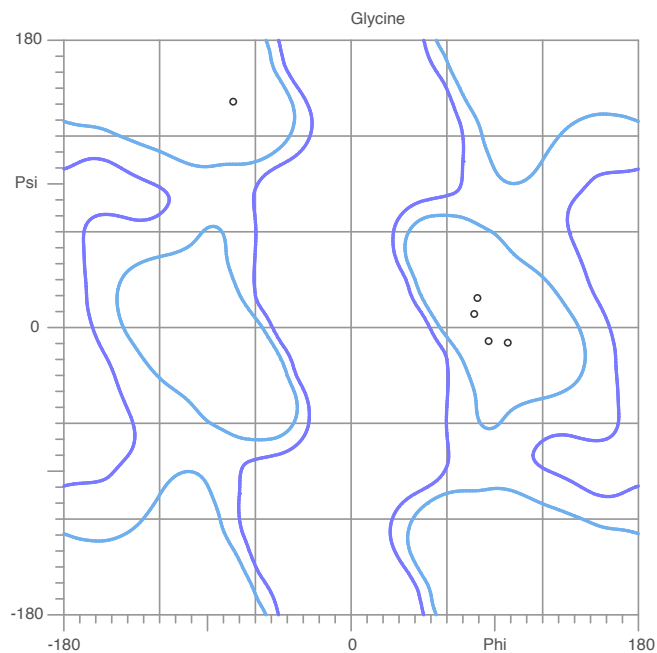
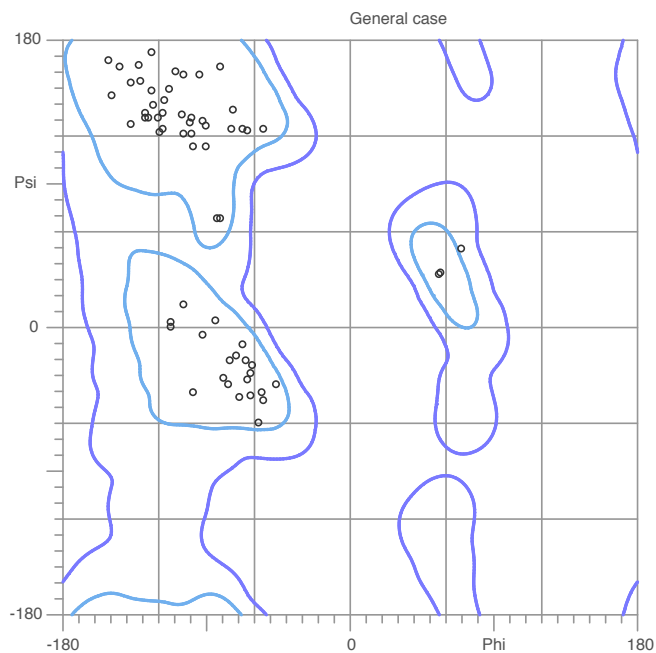
There were no outliers.

<http://kinemage.biochem.duke.edu>

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MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 9



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.

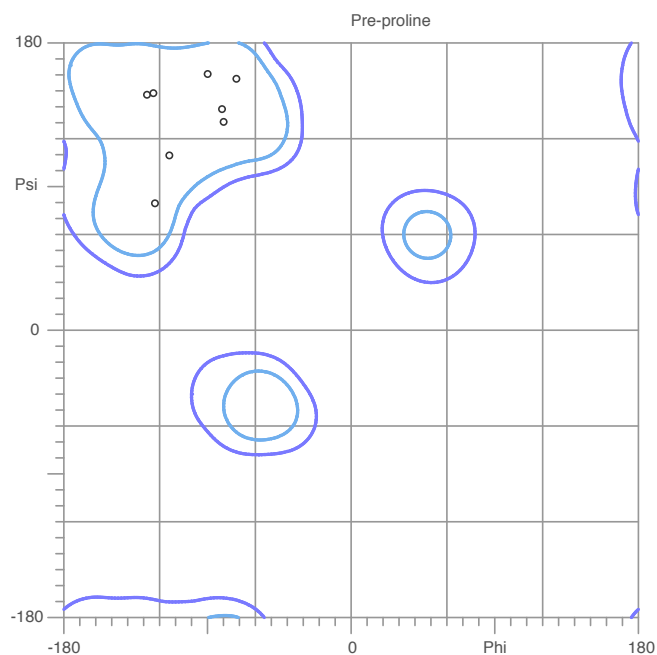
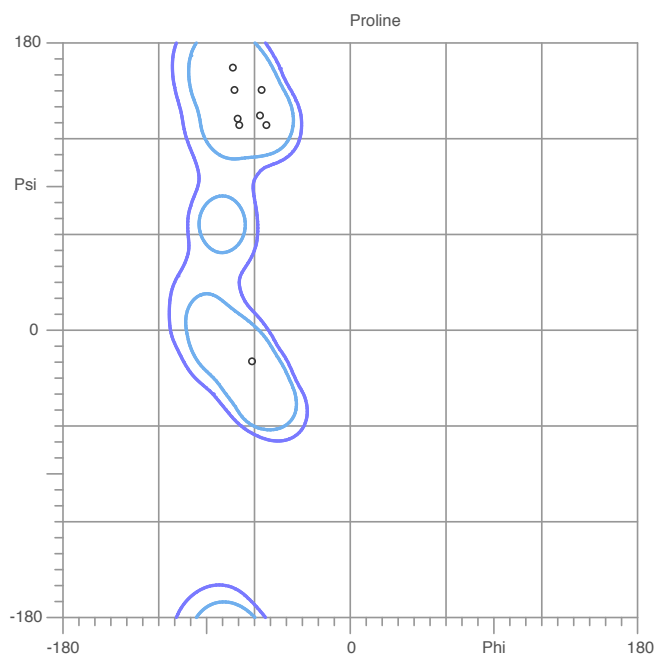
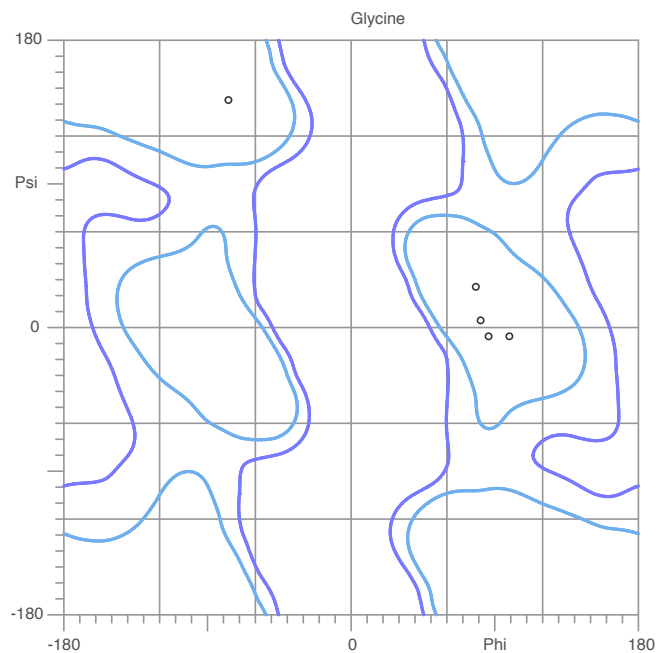
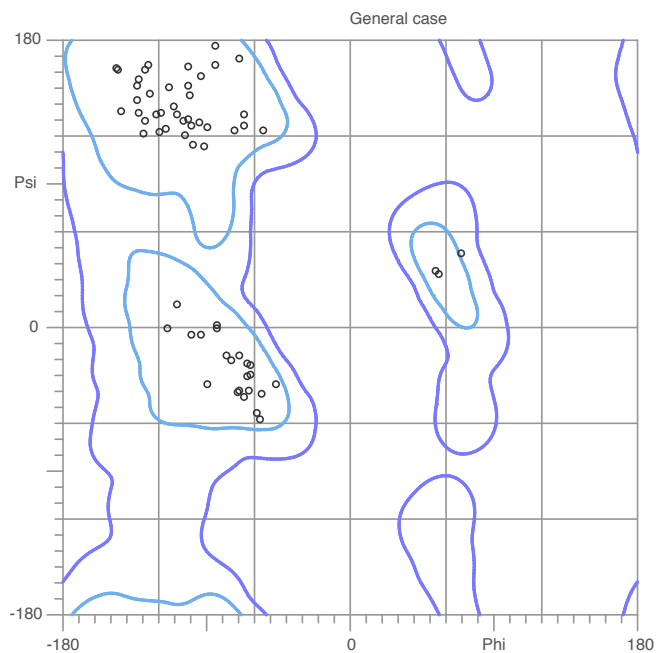
There were no outliers.

<http://kinemage.biochem.duke.edu>

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MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 10

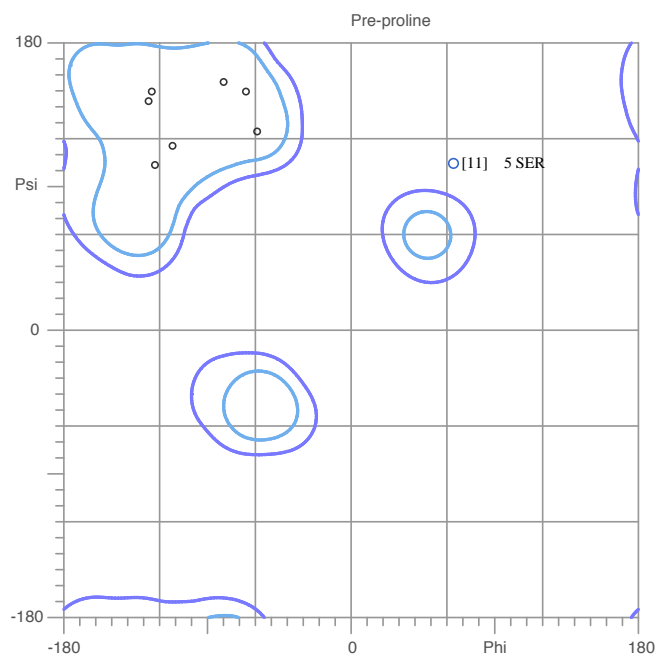
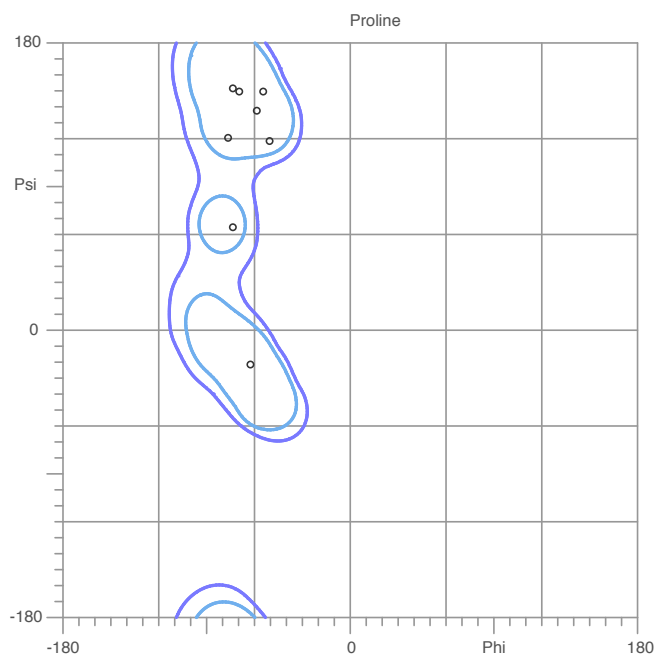
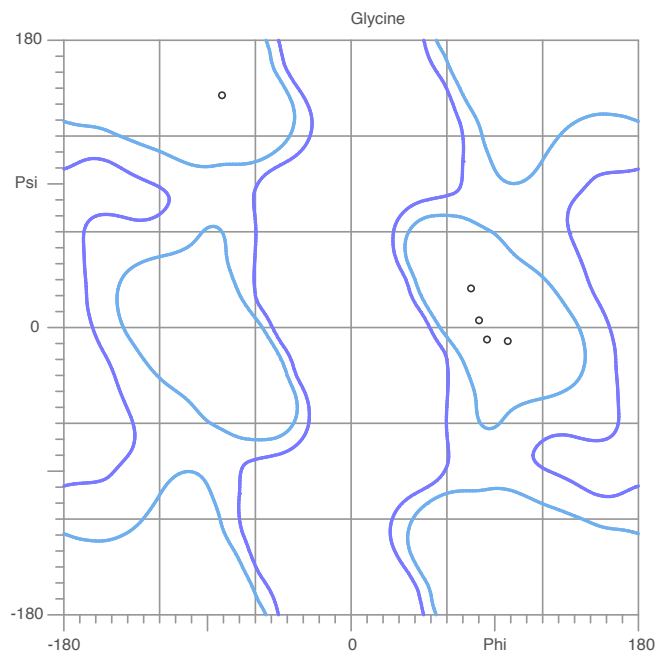
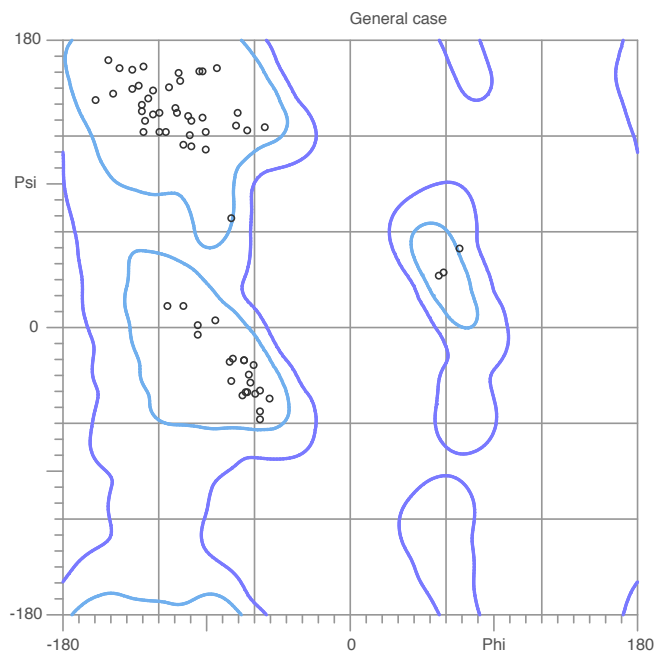


98.8% (83/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 11



97.6% (82/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

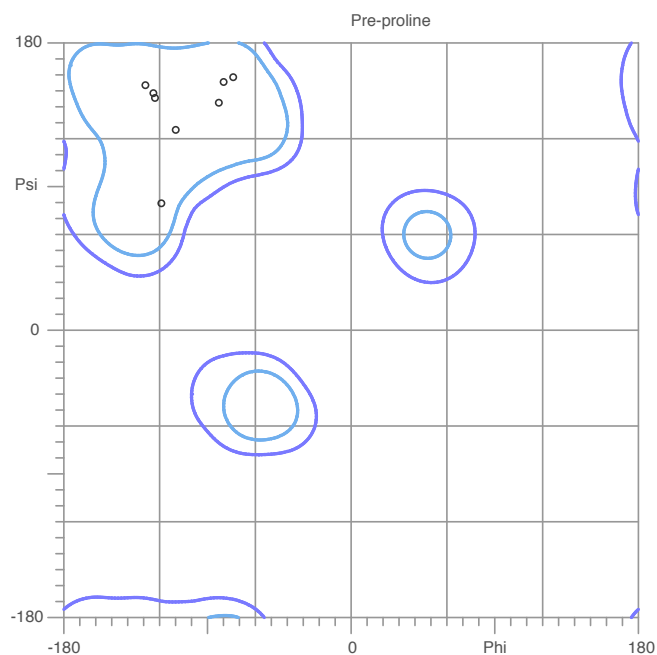
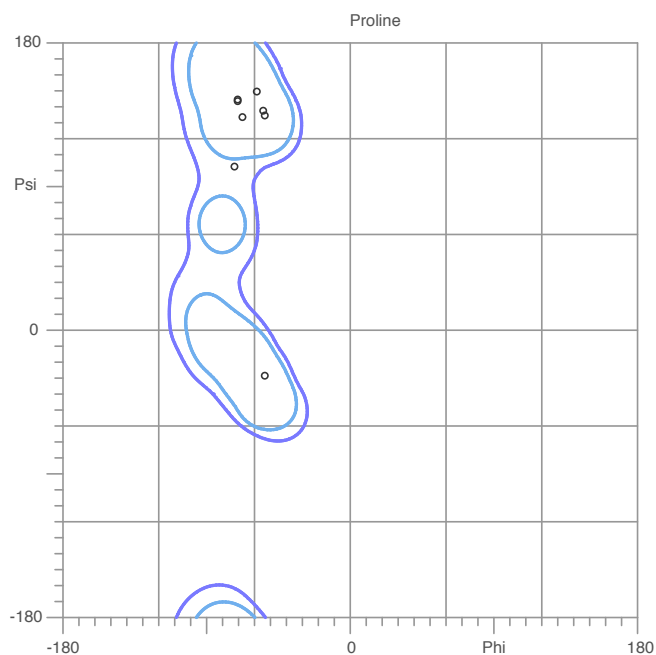
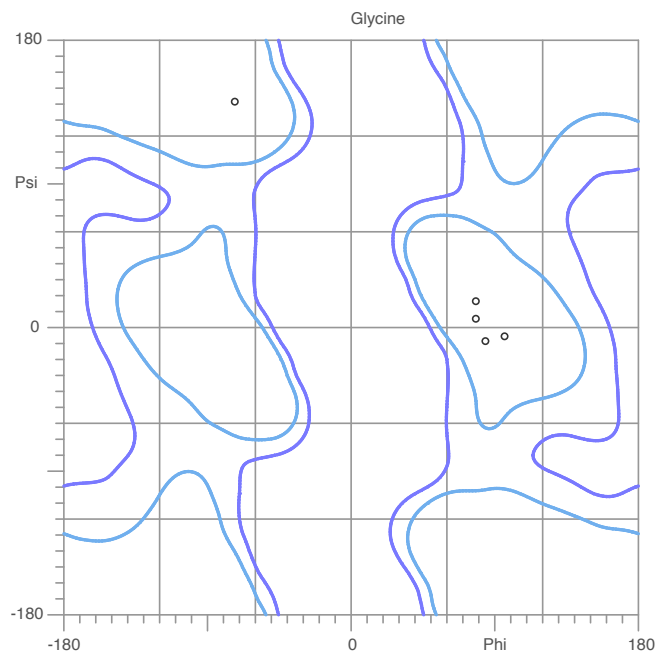
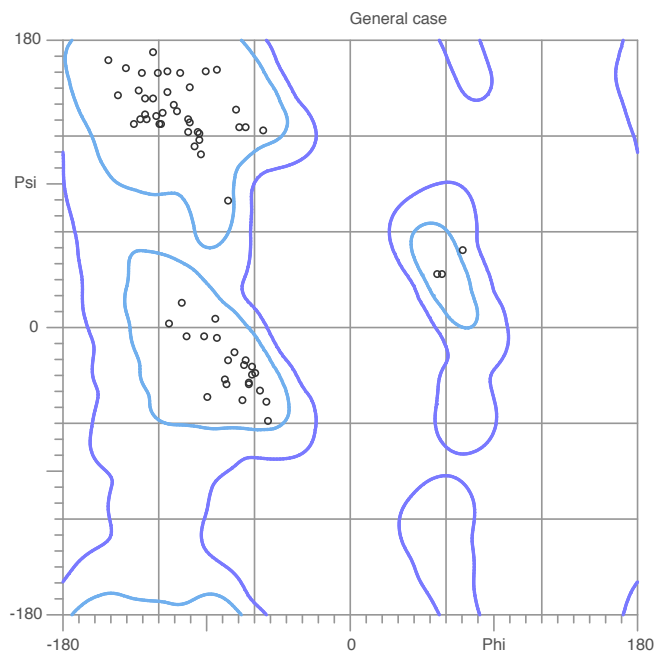
There were 1 outliers (phi, psi):
[11] 5 SER (64.9, 105.0)

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MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 12

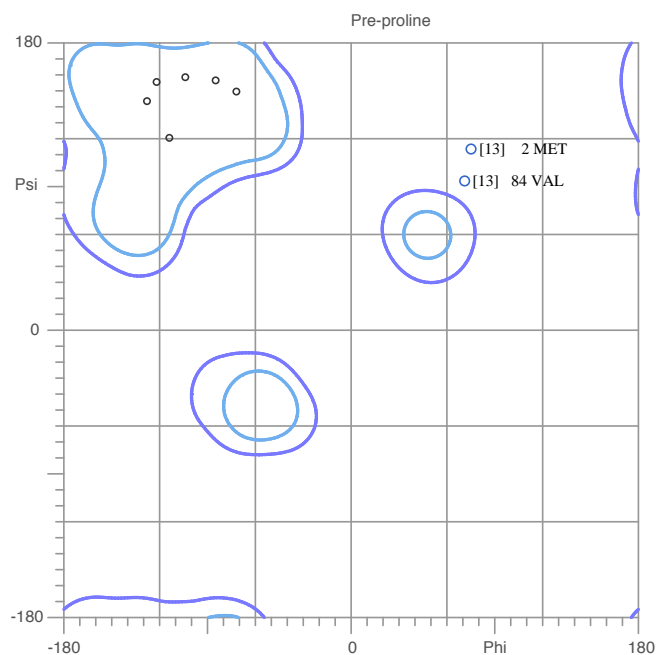
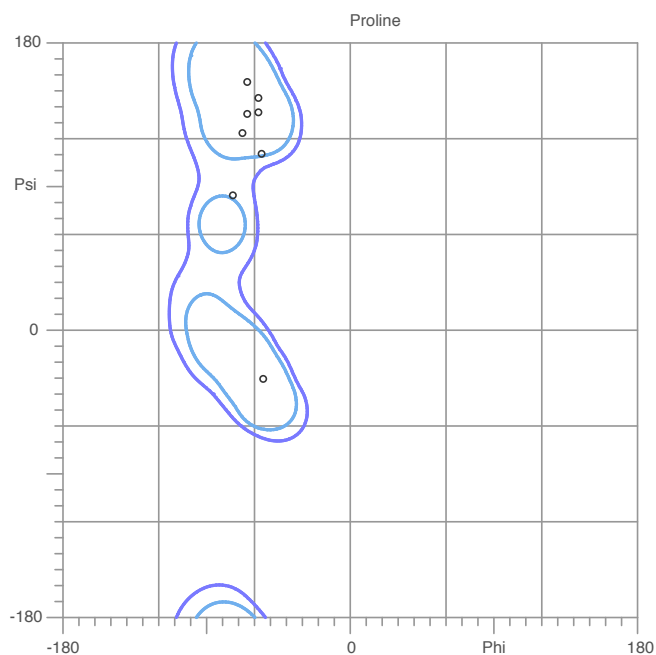
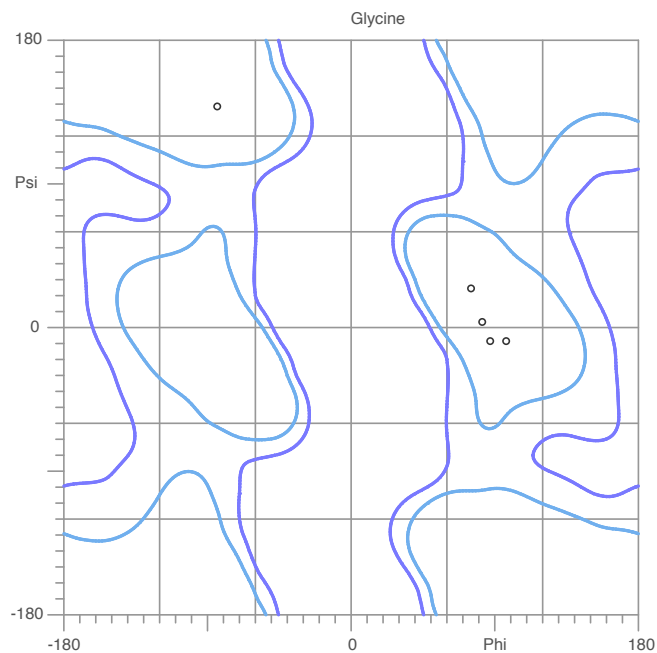
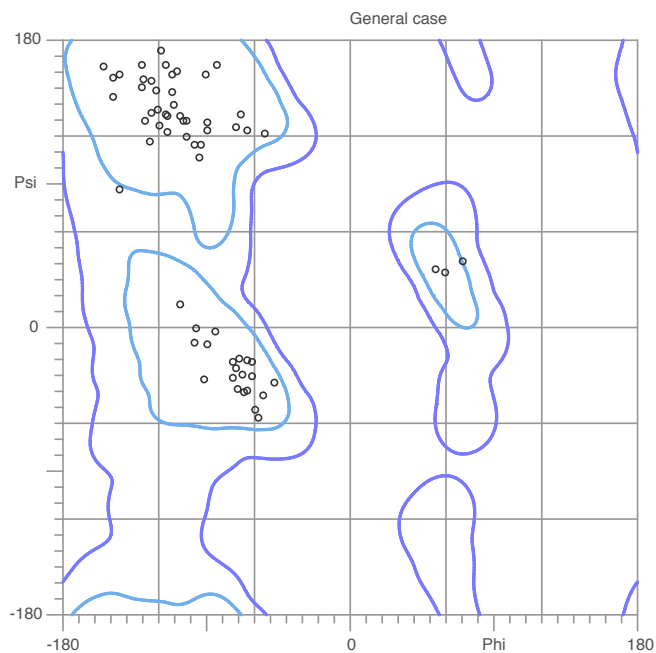


97.6% (82/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 13



94.0% (79/84) of all residues were in favored (98%) regions.
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

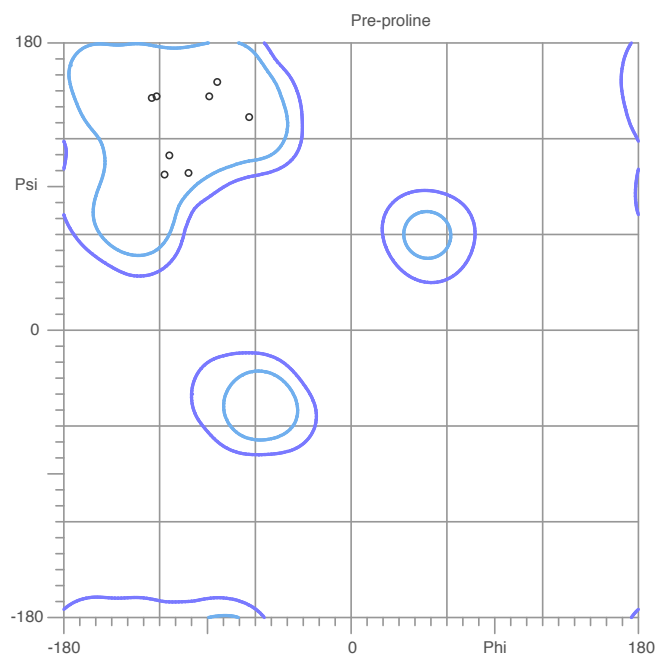
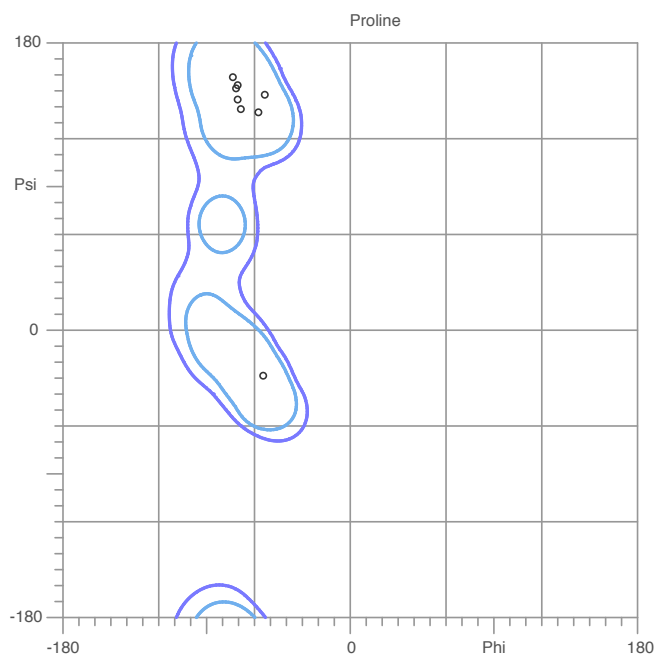
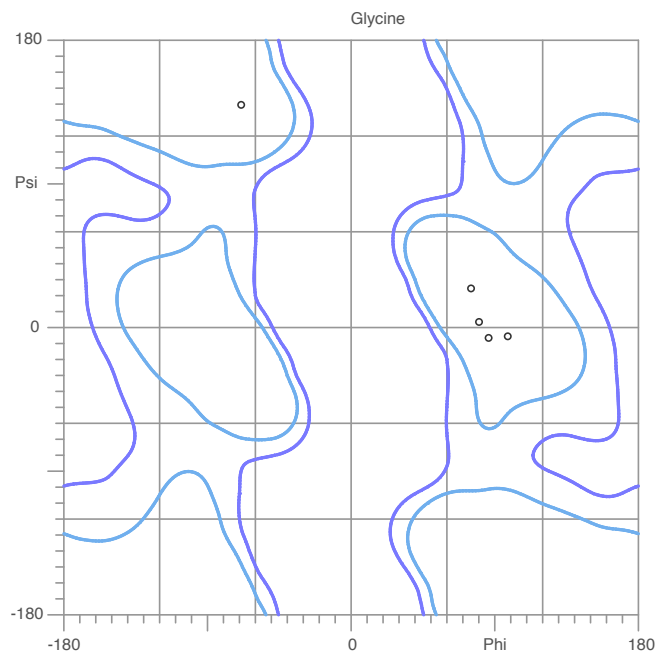
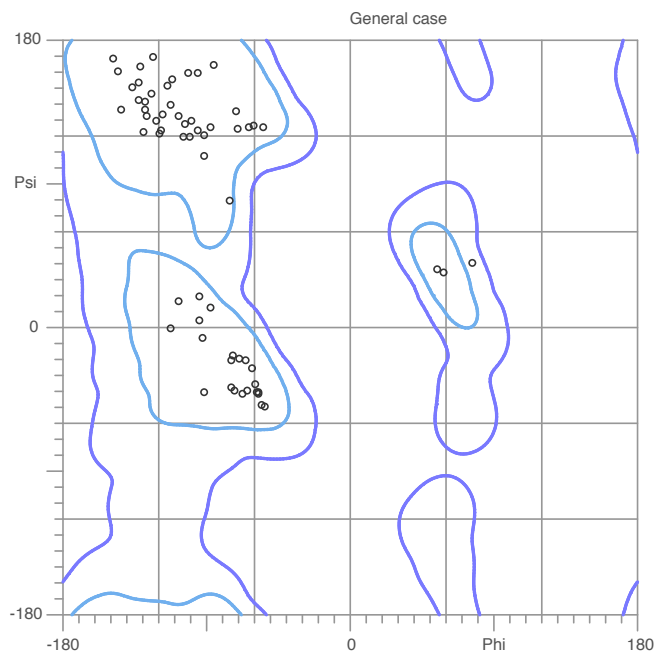
There were 2 outliers (phi, psi):

[13] 2 MET (75.2, 114.7)

[13] 84 VAL (71.1, 95.0)

MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 14



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.

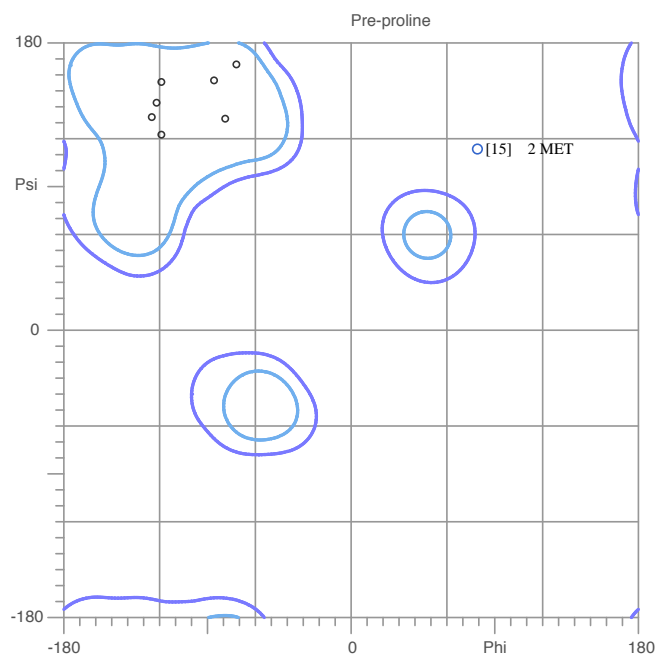
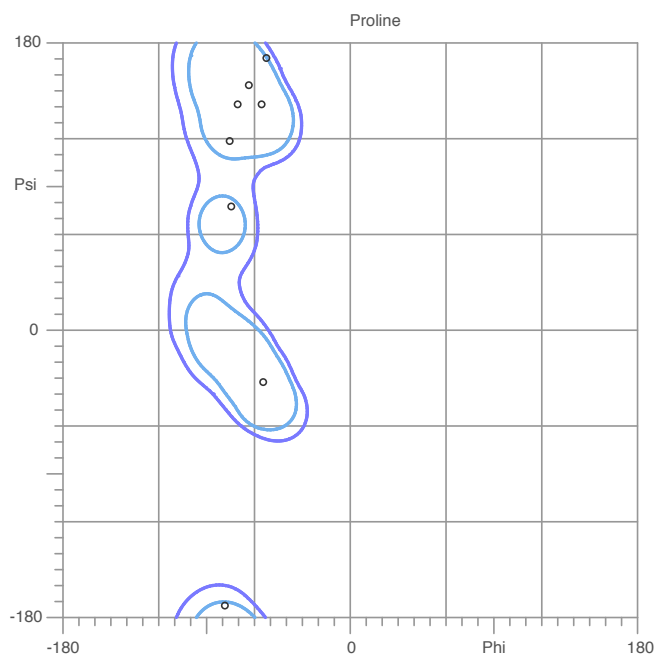
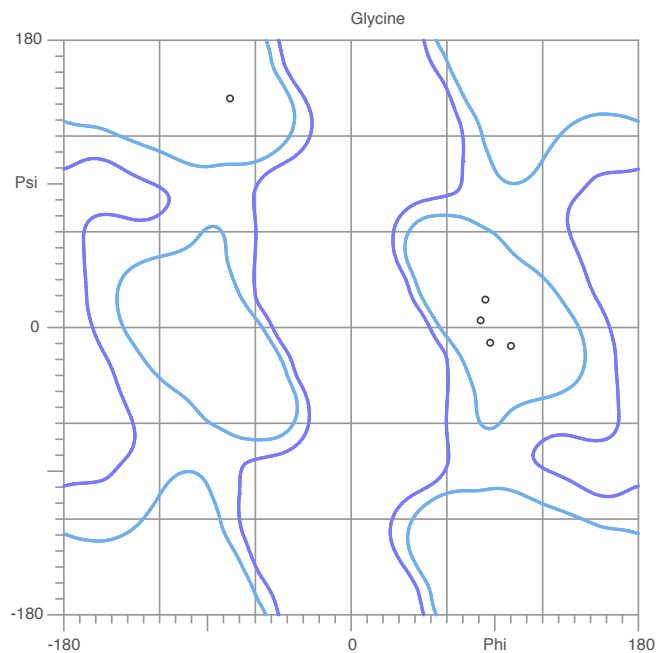
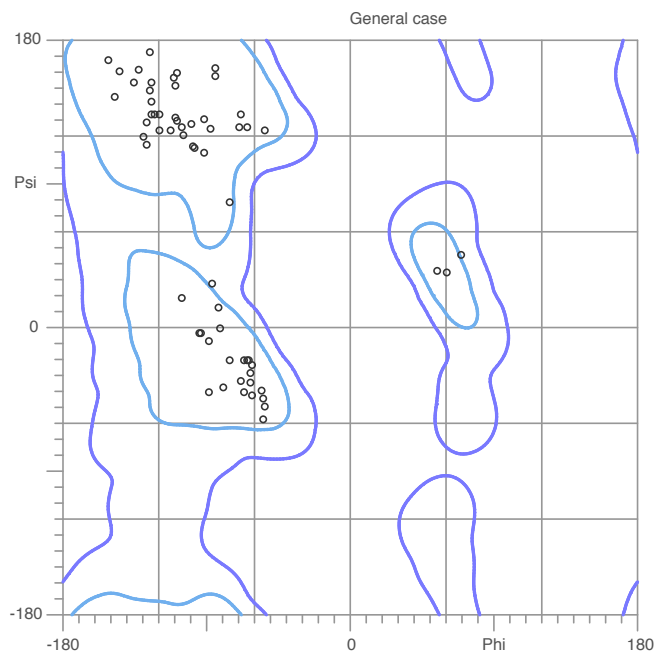
There were no outliers.

<http://kinemage.biochem.duke.edu>

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MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 15

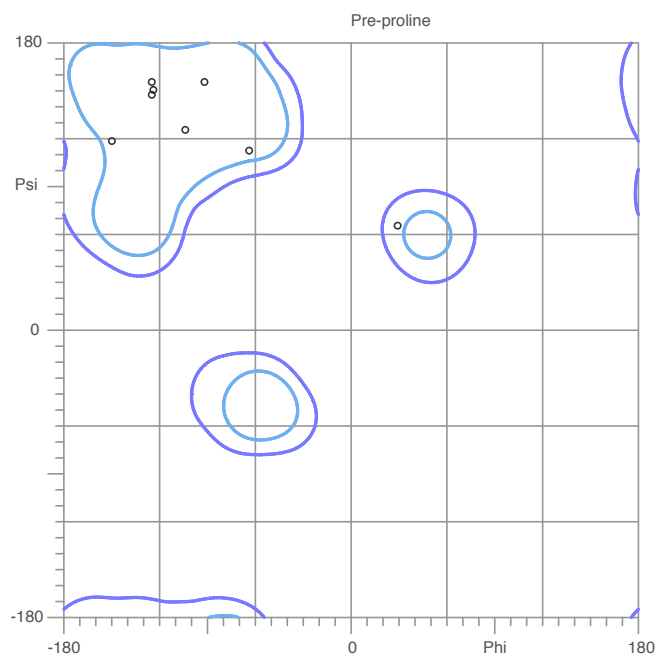
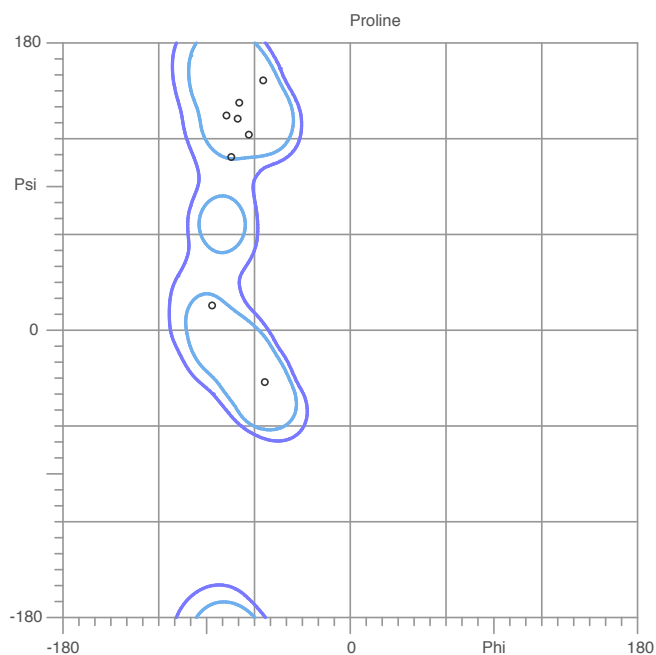
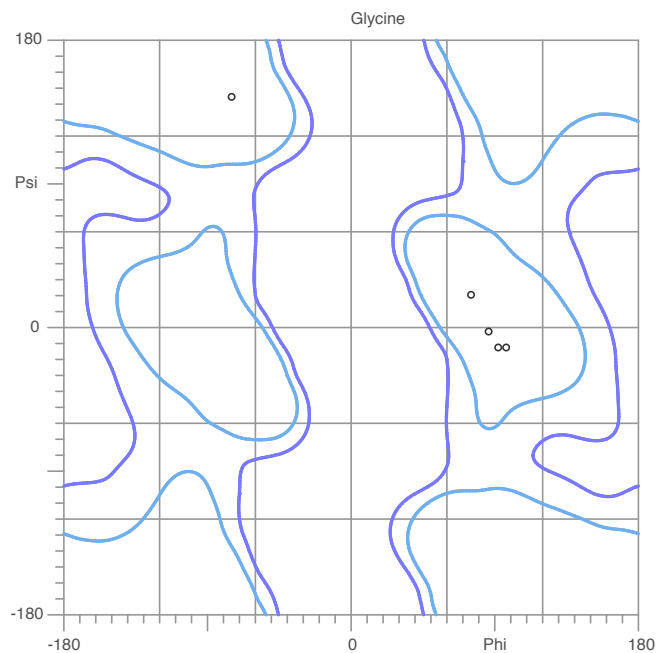
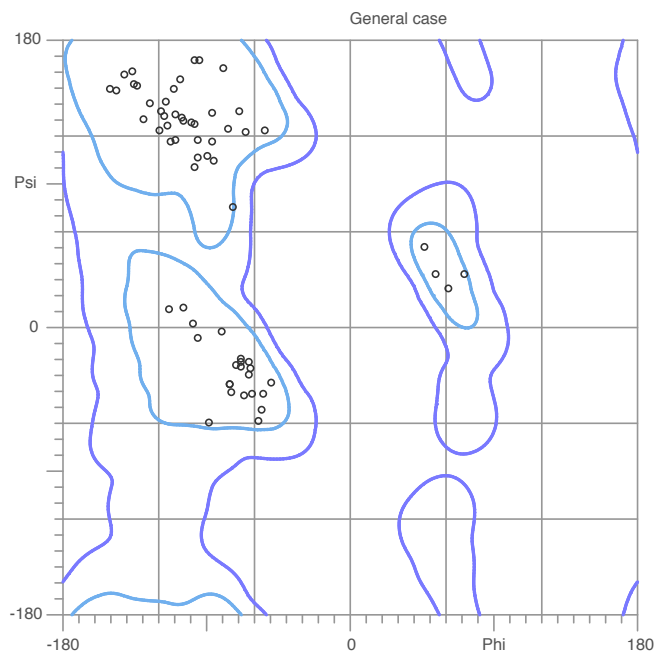


96.4% (81/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[15] 2 MET (79.0, 114.5)

MolProbity Ramachandran analysis

HR4694F_R3Cons_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.

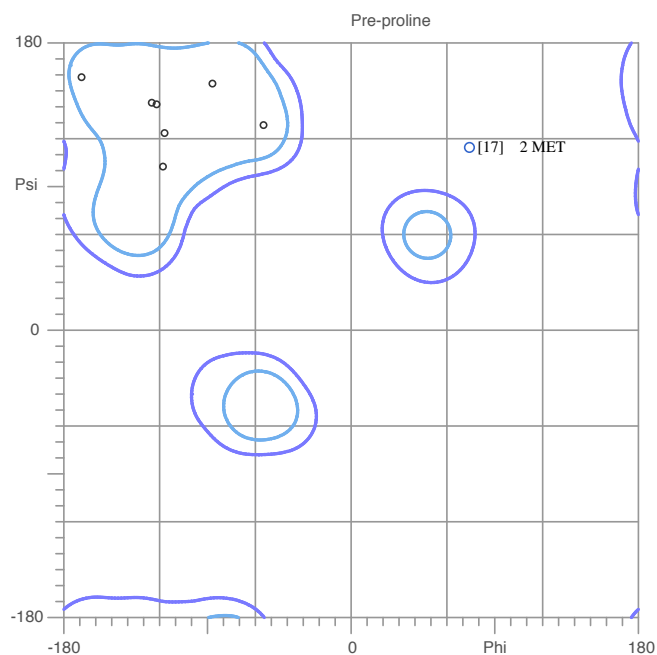
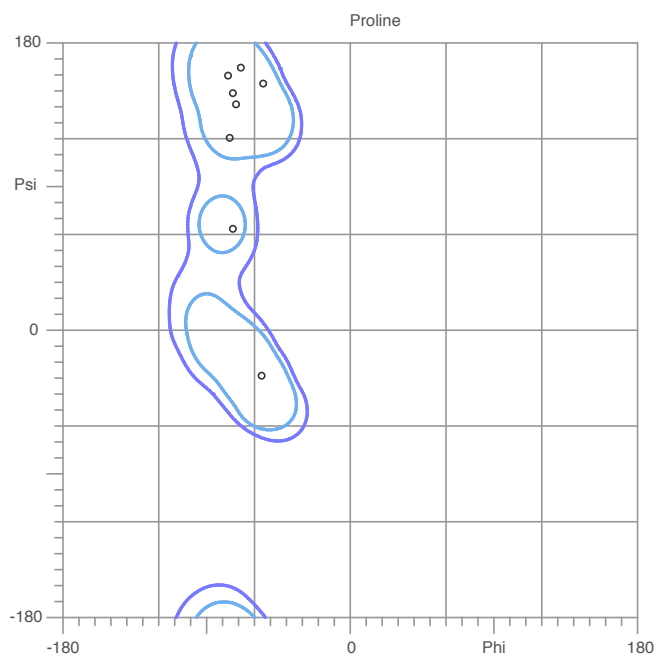
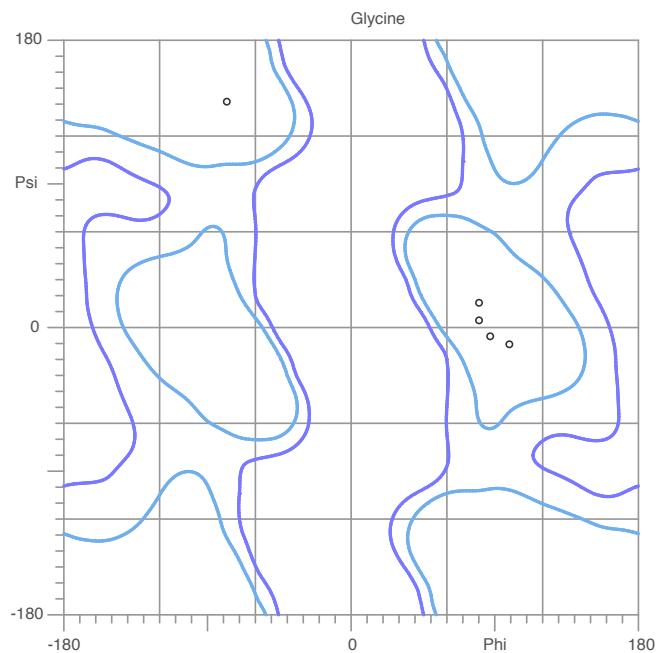
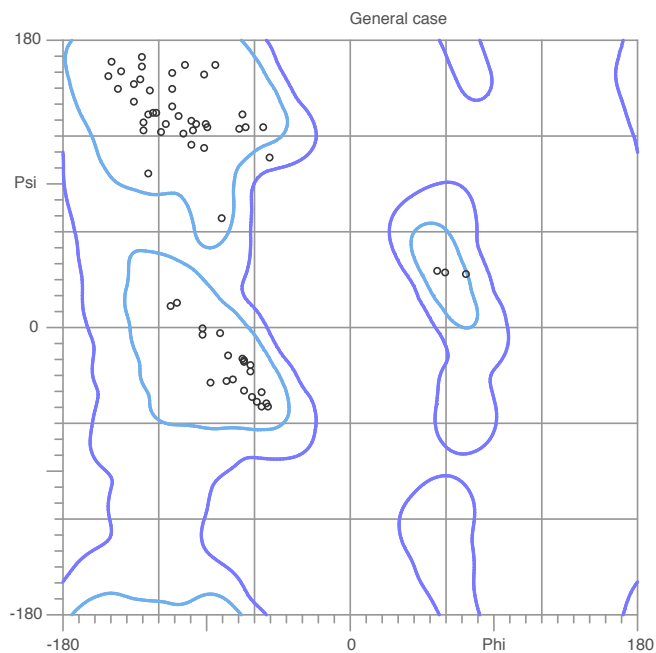
There were no outliers.

<http://kinemage.biochem.duke.edu>

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MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 17

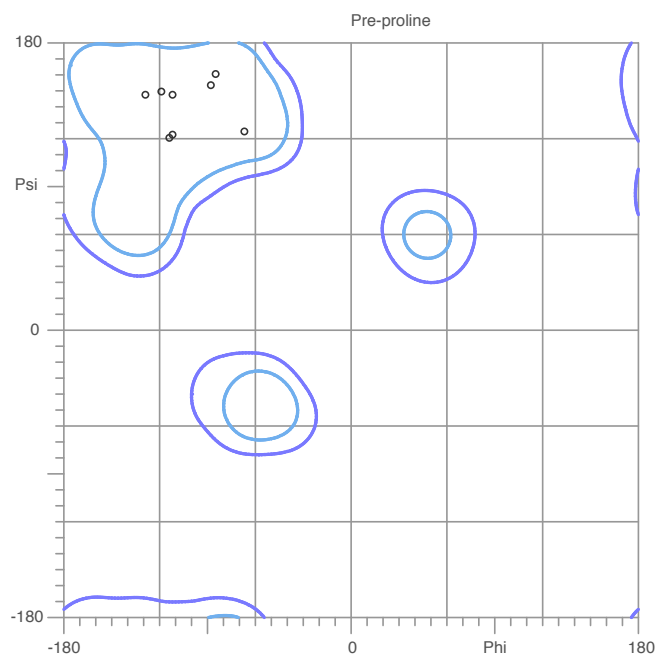
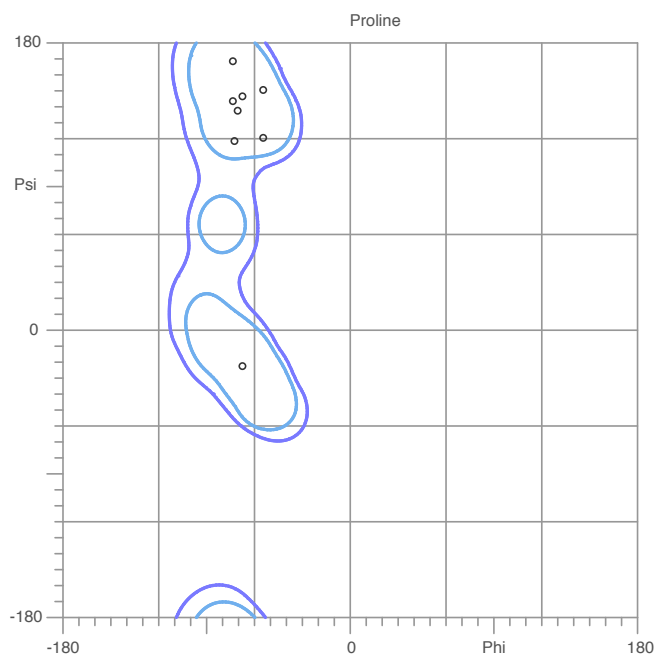
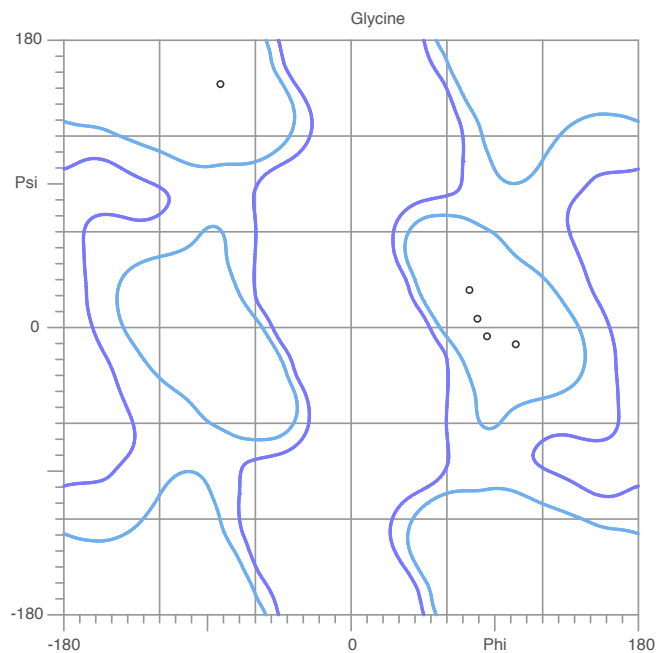
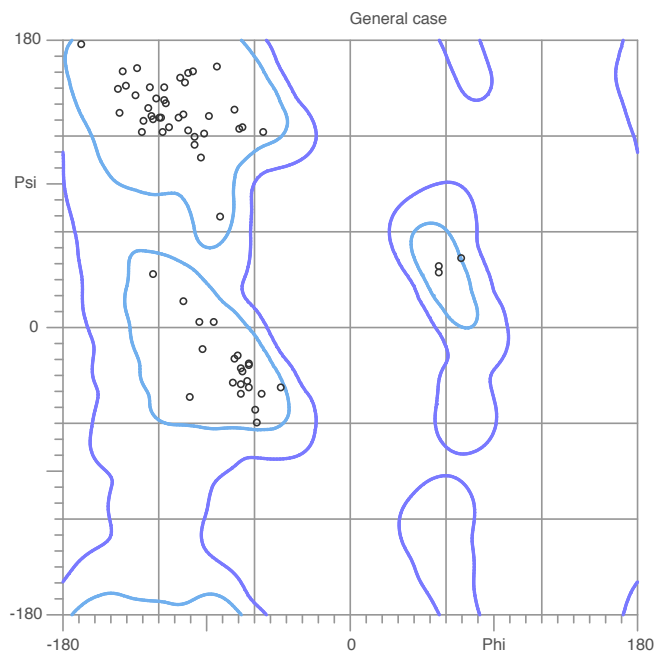


97.6% (82/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[17] 2 MET (75.0, 115.1)

MolProbity Ramachandran analysis

HR4694F_R3Cons_em_bcr3.pdb, model 18



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.

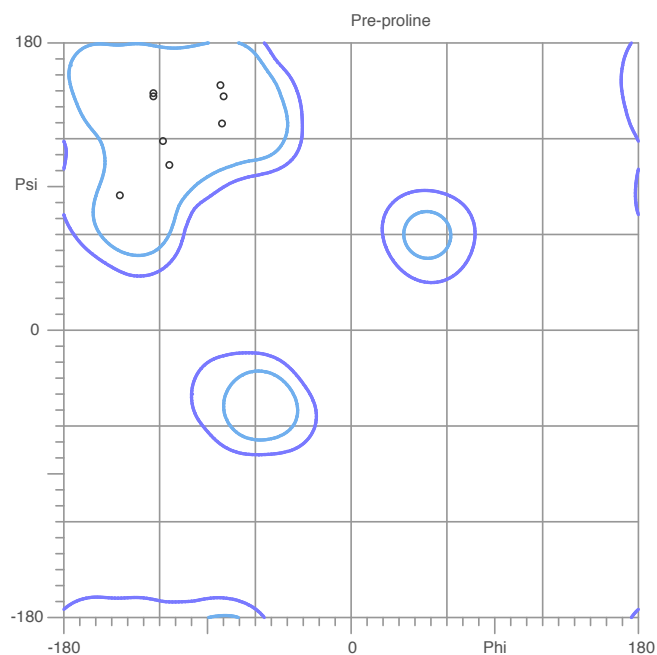
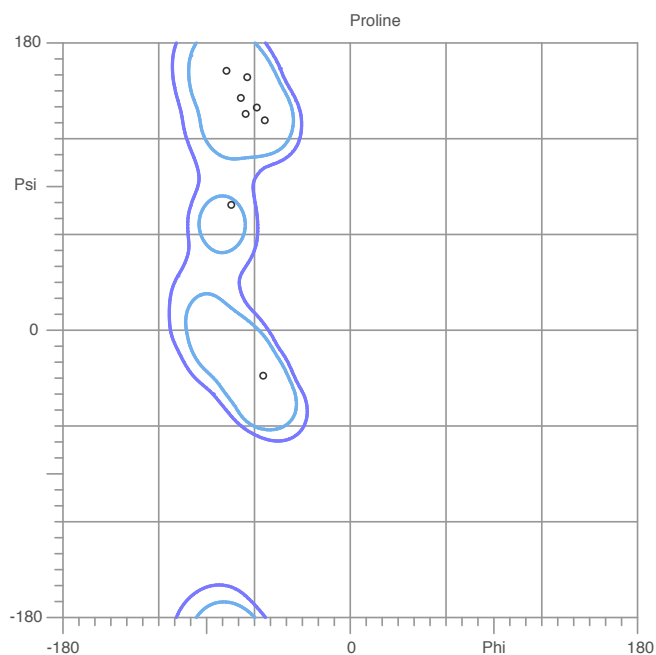
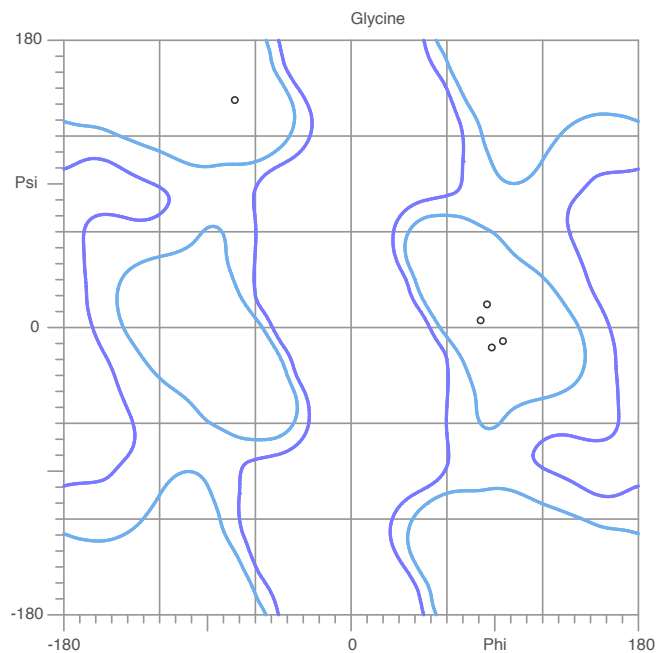
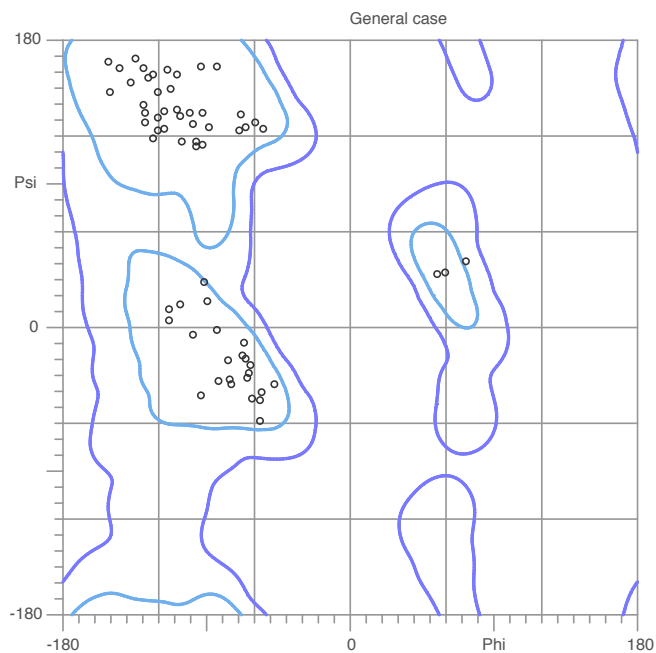
There were no outliers.

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MolProbity Ramachandran analysis

HR4694F_R3Cons_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.

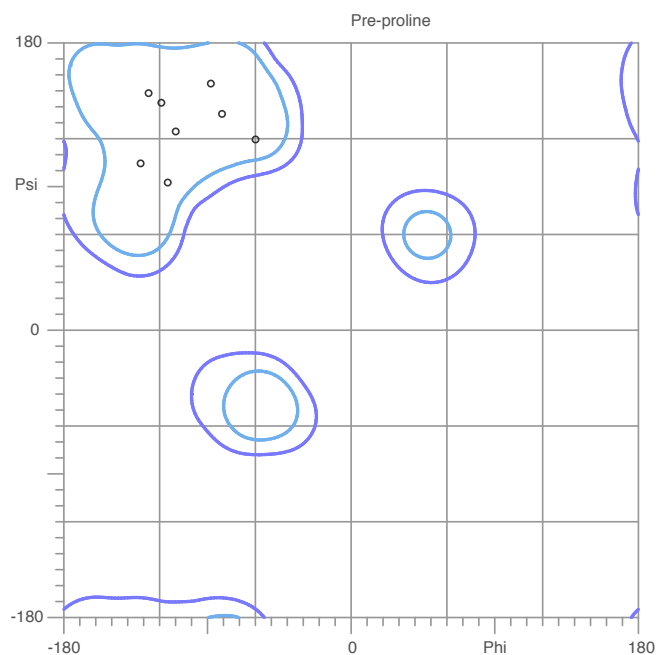
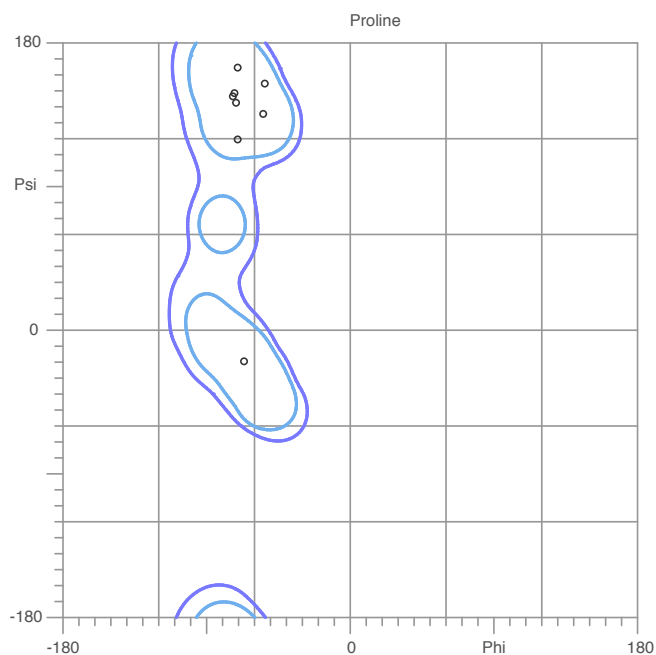
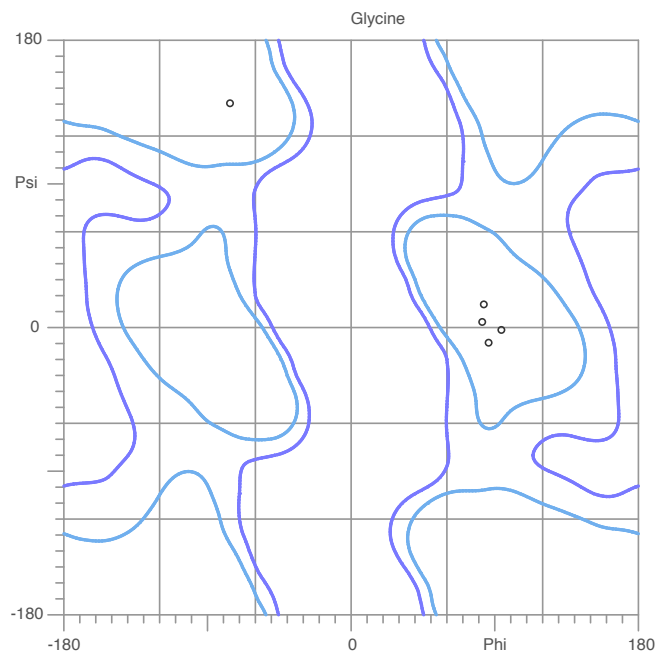
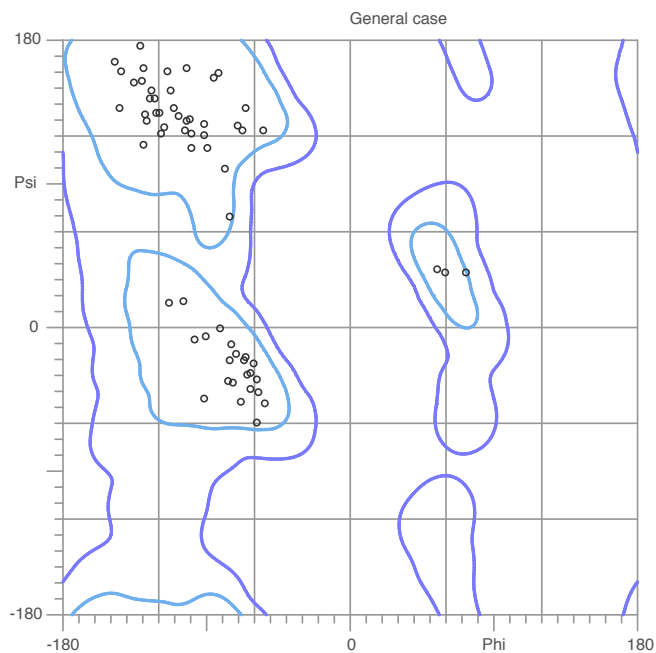
There were no outliers.

<http://kinemage.biochem.duke.edu>

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MolProbity Ramachandran analysis

HR4694F_R3Cons_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>

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