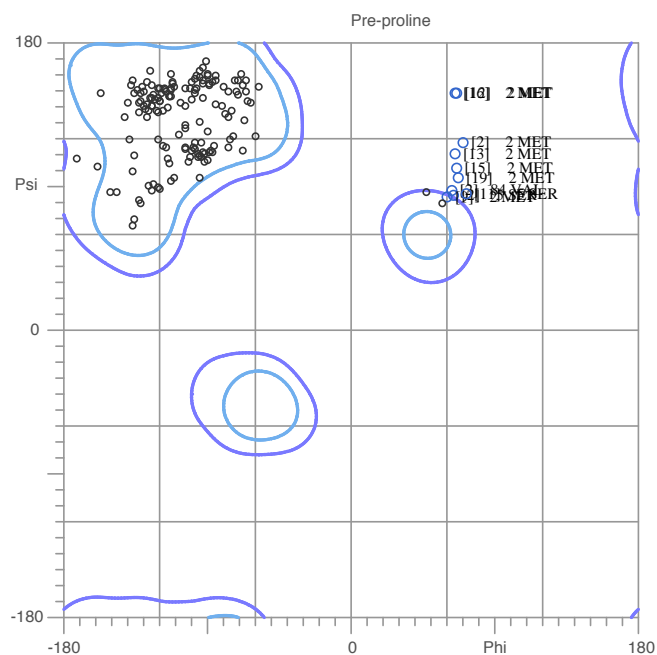
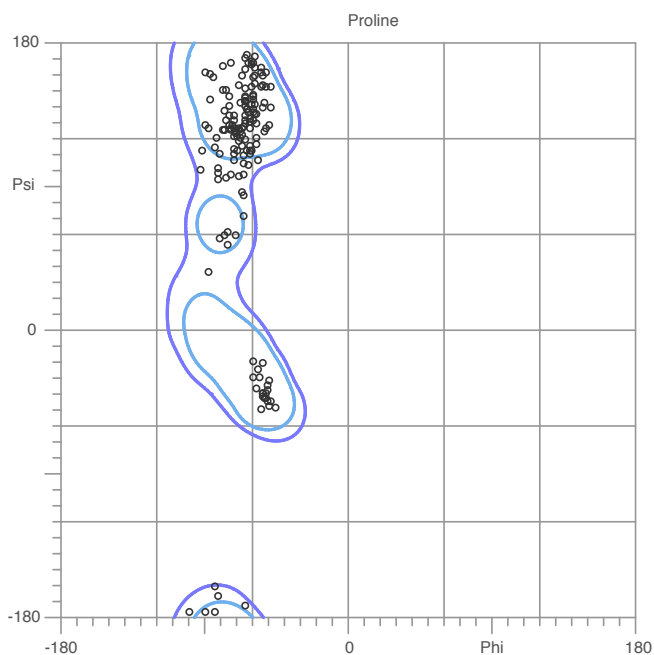
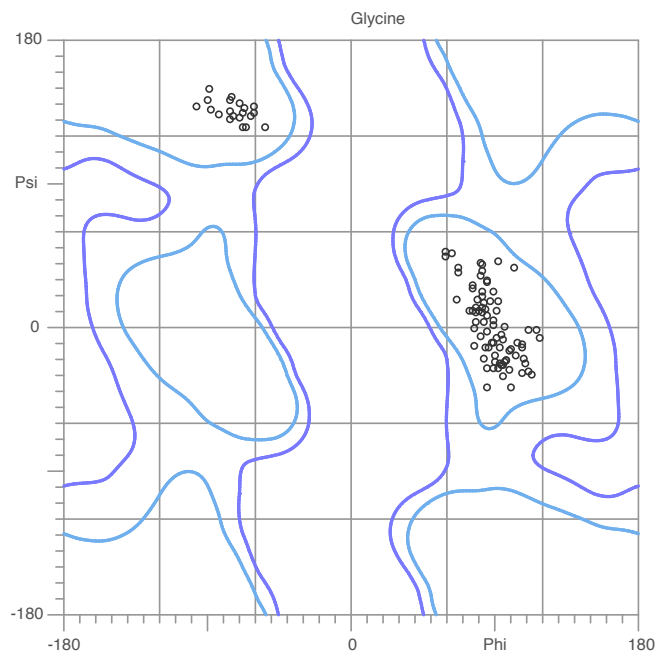
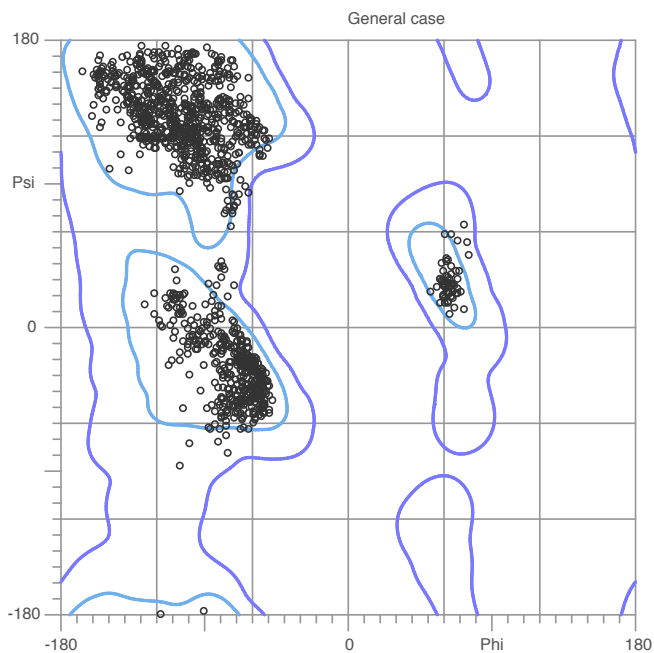


MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, all models



95.8% (1609/1680) of all residues were in favored (98%) regions.
99.4% (1670/1680) of all residues were in allowed (>99.8%) regions.

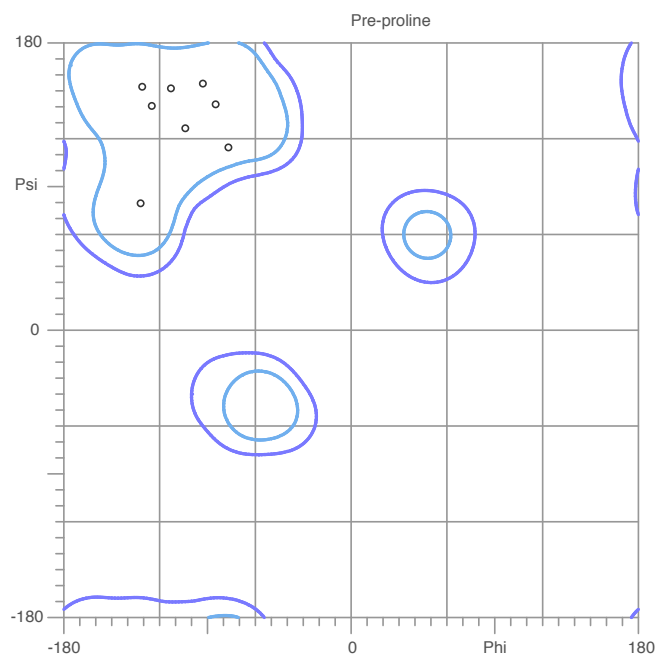
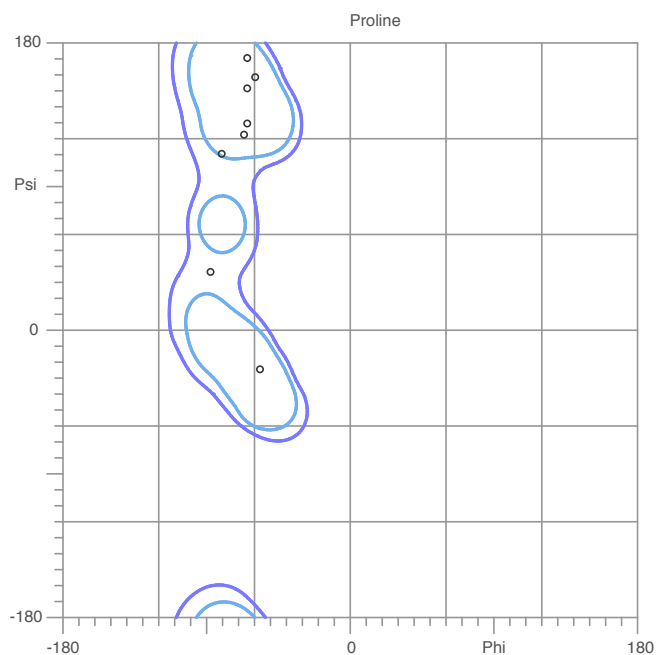
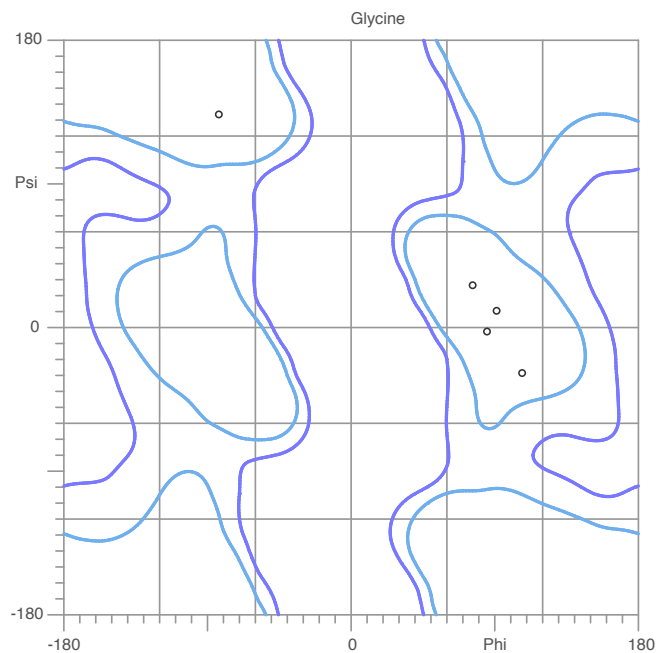
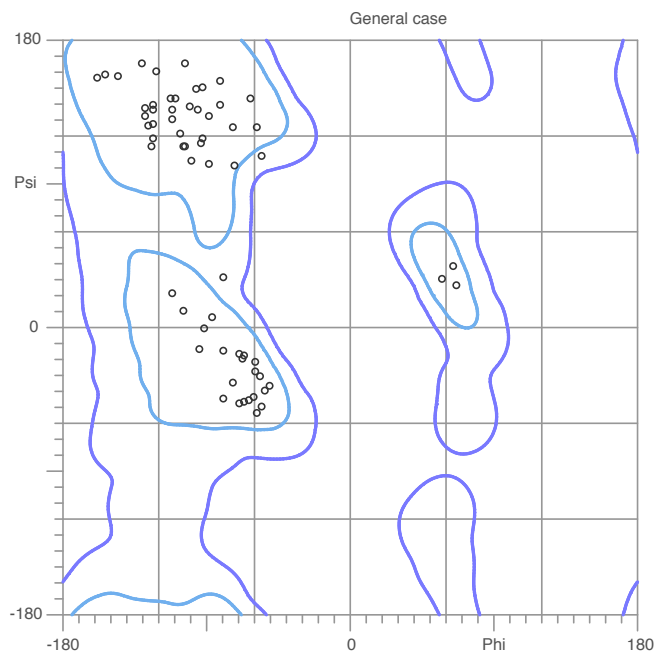
There were 10 outliers (phi, psi):

- [2] 2 MET (70.6, 118.3)
- [2] 5 SER (64.9, 85.2)
- [2] 84 VAL (63.4, 88.1)

- [9] 2 MET (60.8, 84.9)
- [11] 5 SER (72.8, 86.7)
- [12] 2 MET (66.3, 149.4)
- [13] 2 MET (65.5, 111.4)
- [15] 2 MET (66.8, 102.5)
- [16] 2 MET (65.2, 149.8)
- [19] 2 MET (67.3, 96.8)

MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 1



96.4% (81/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

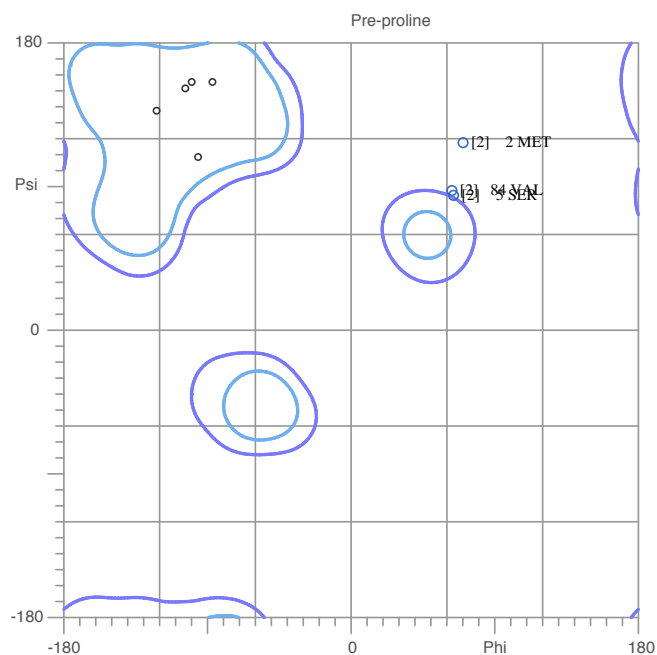
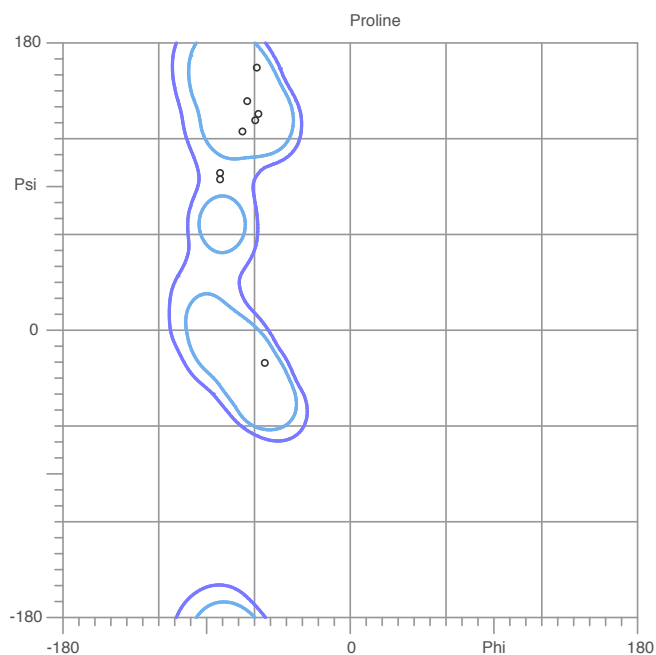
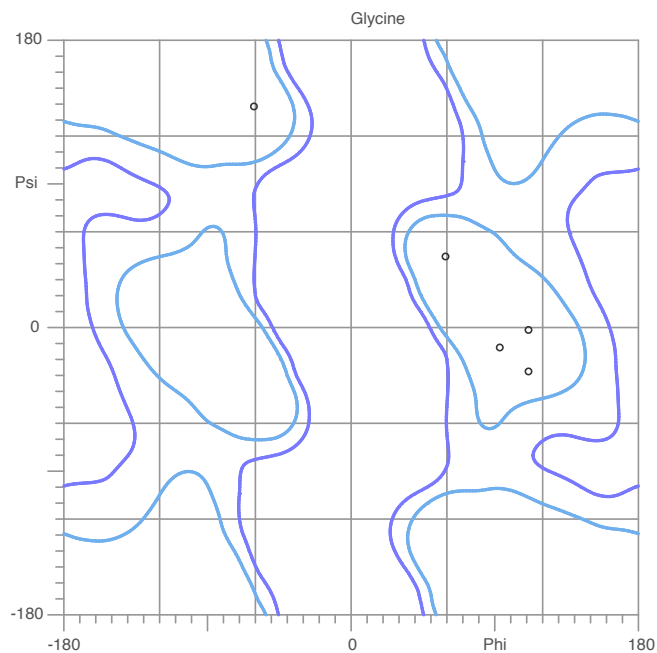
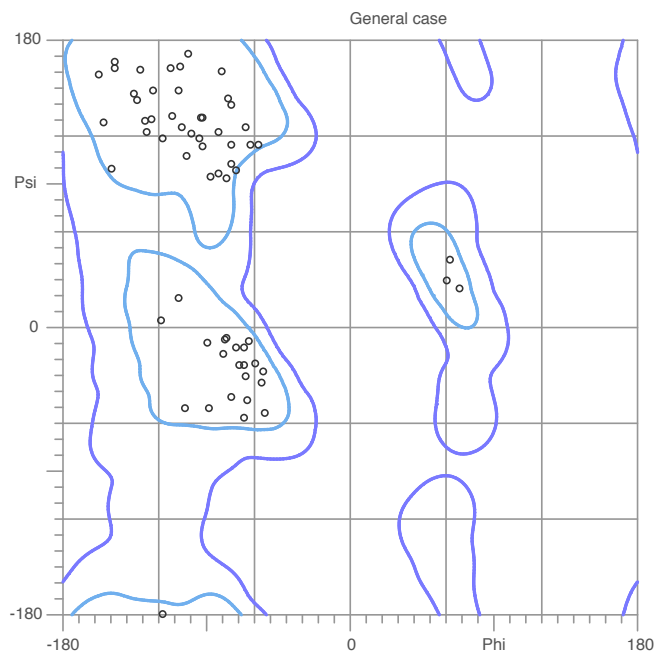
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 2



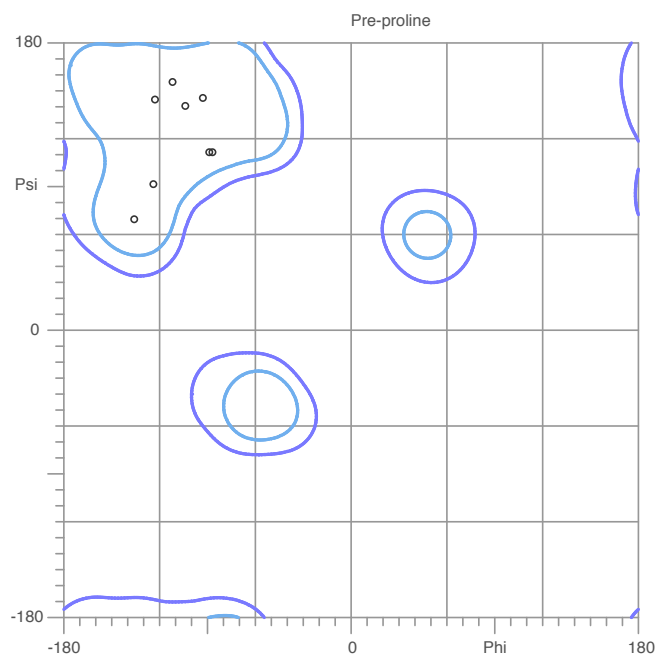
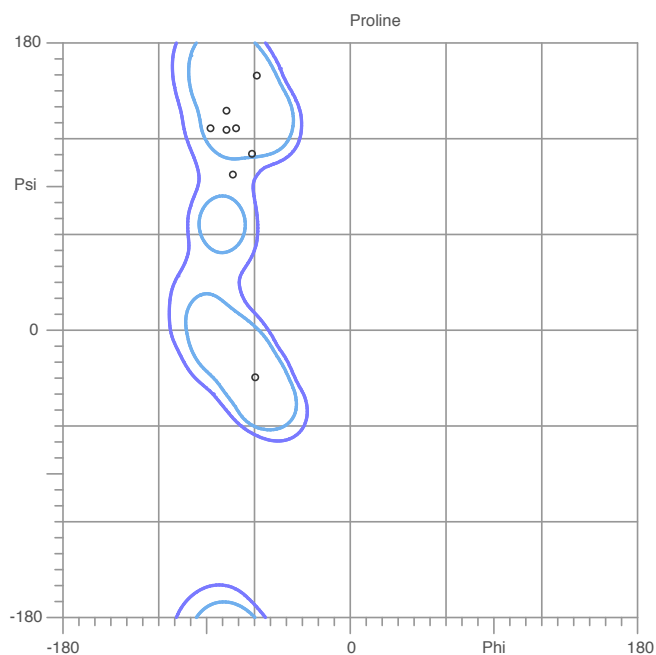
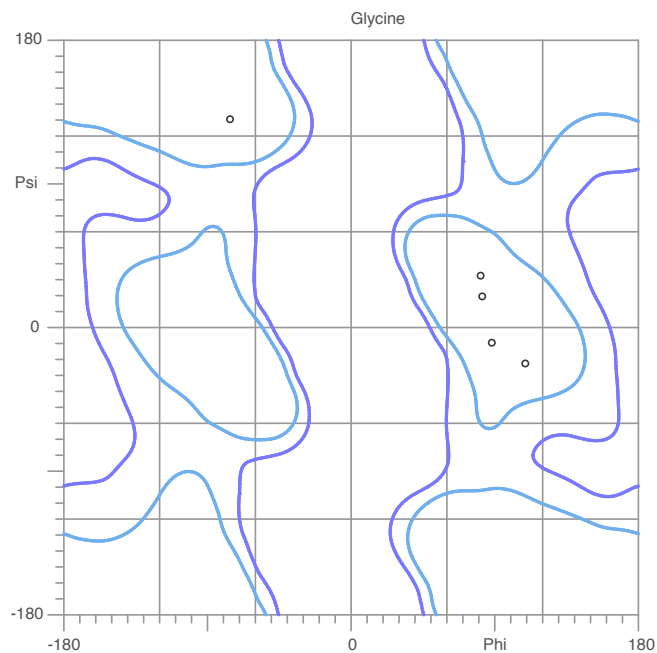
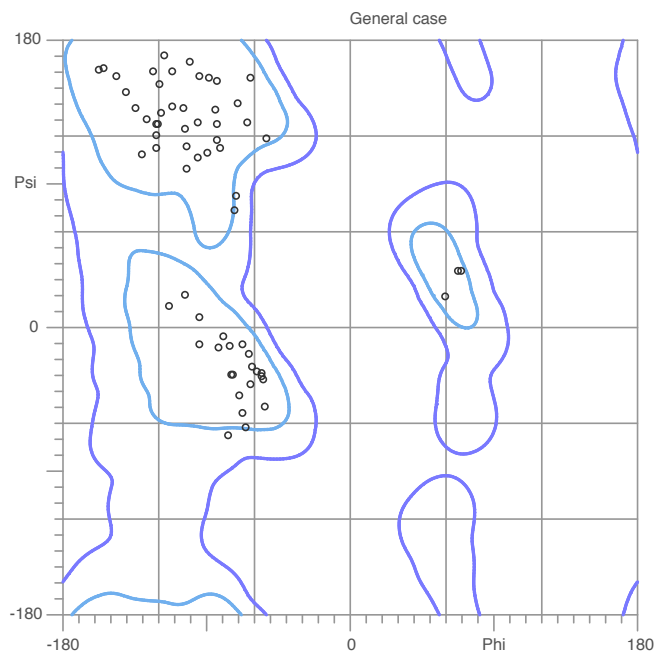
94.0% (79/84) of all residues were in favored (98%) regions.
96.4% (81/84) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 2 MET (70.6, 118.3)
- [2] 5 SER (64.9, 85.2)
- [2] 84 VAL (63.4, 88.1)

MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 3



96.4% (81/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

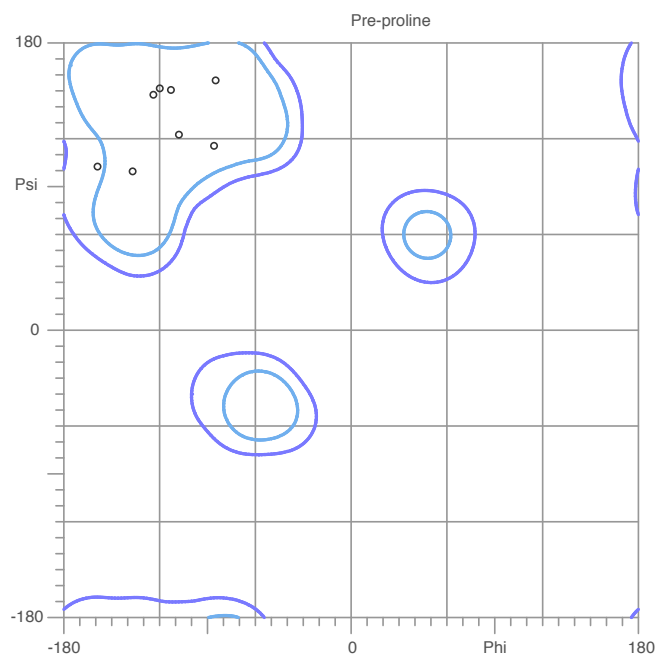
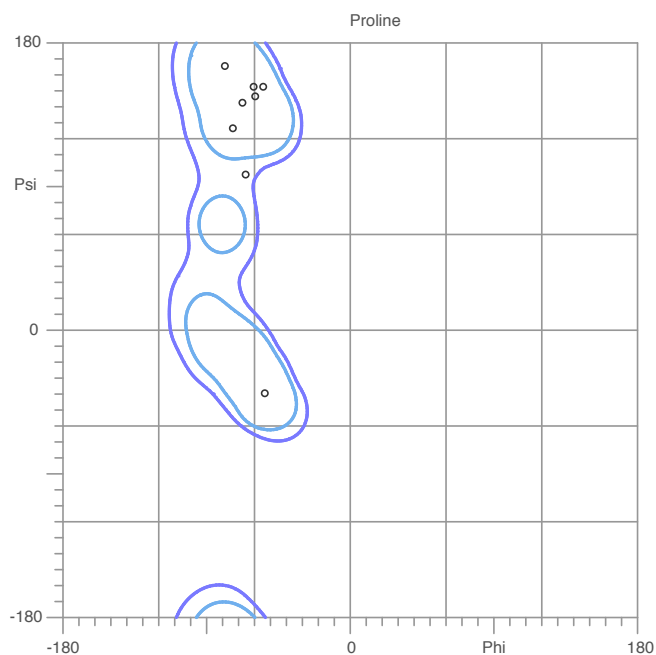
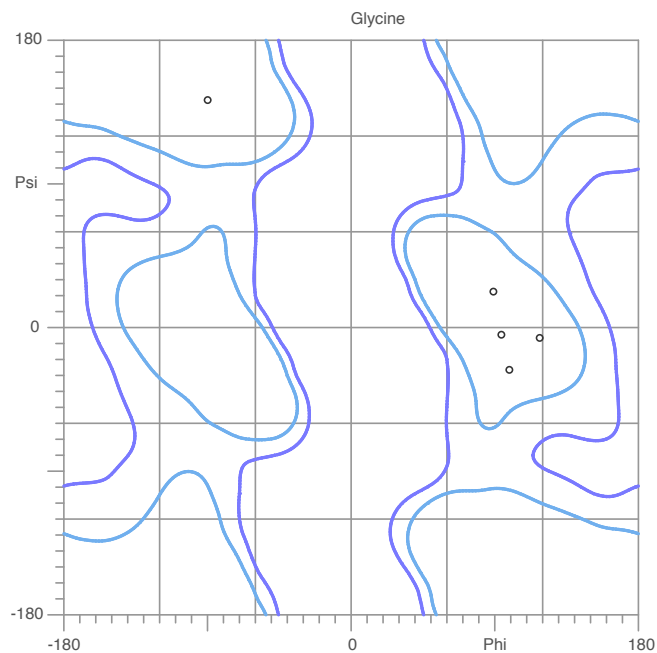
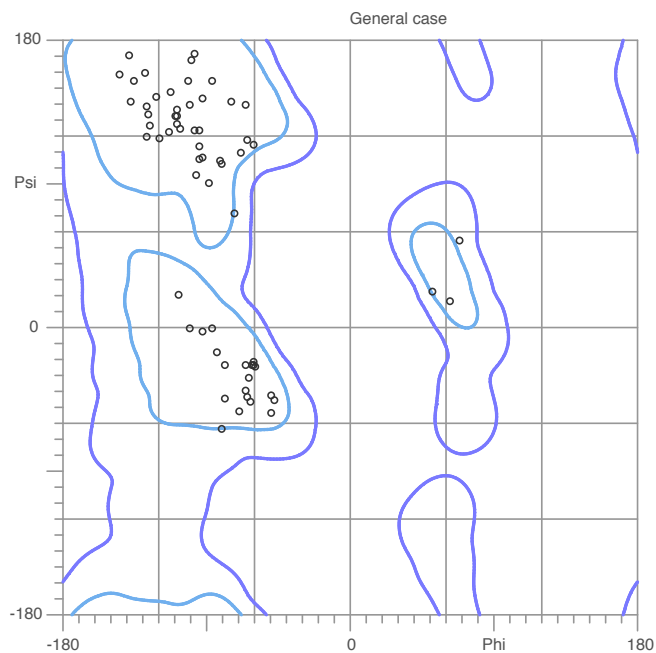
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 4



96.4% (81/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

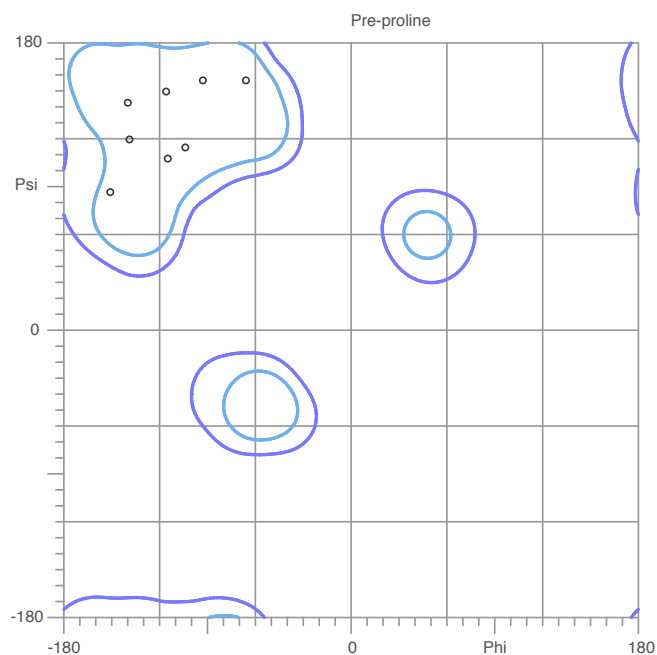
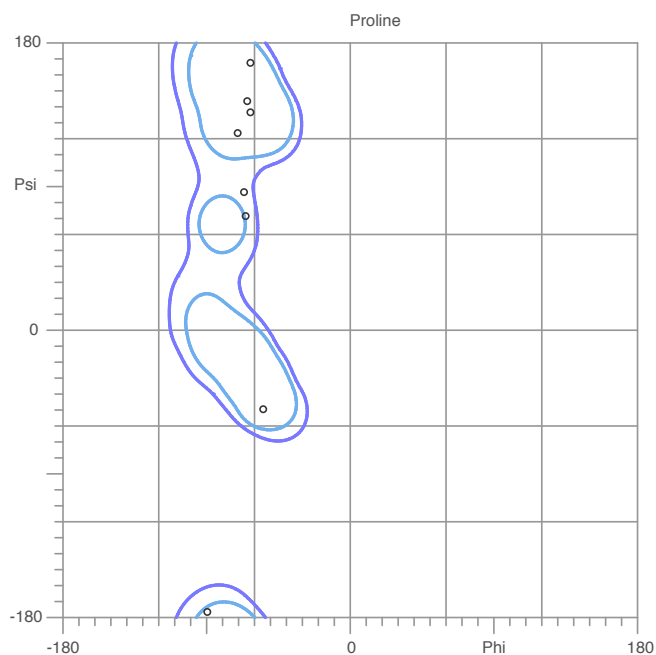
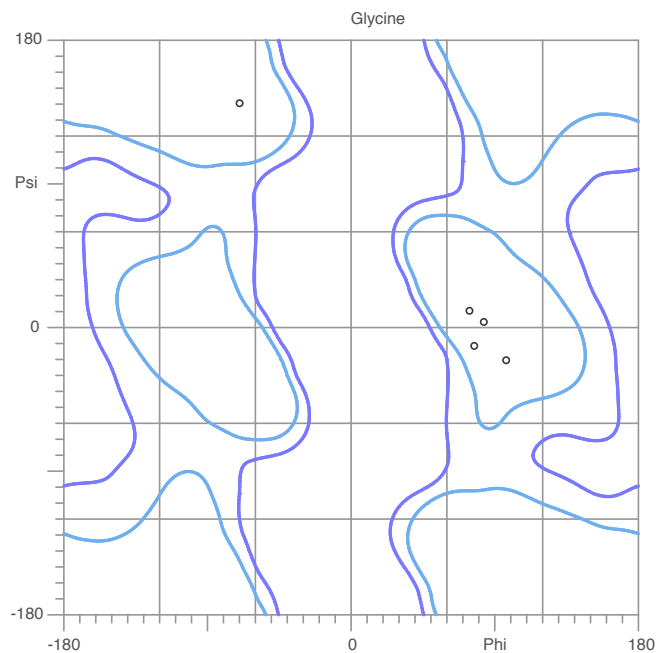
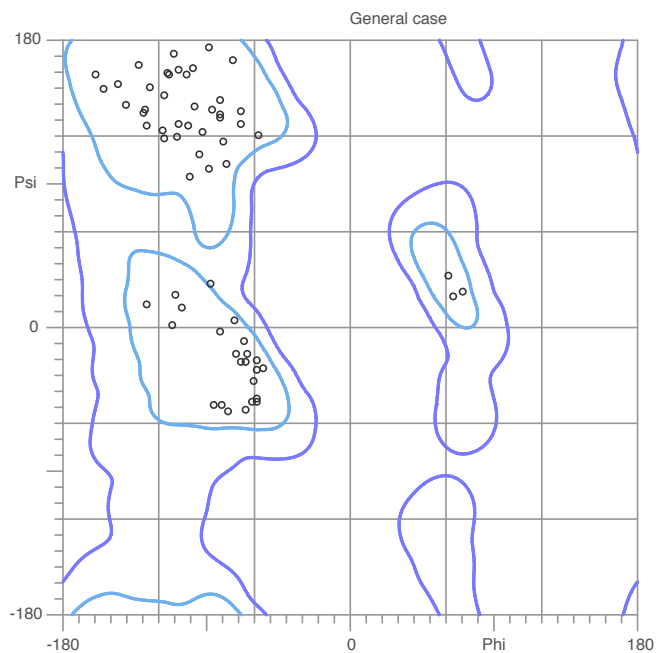
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 5



96.4% (81/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

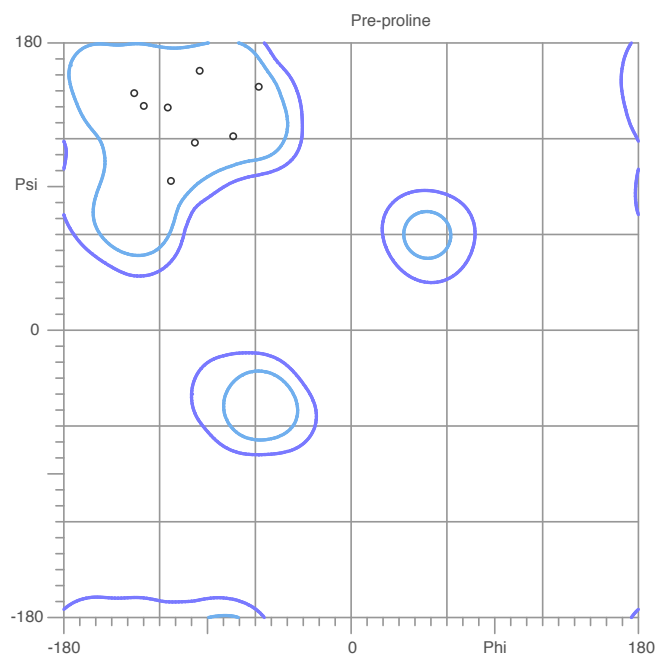
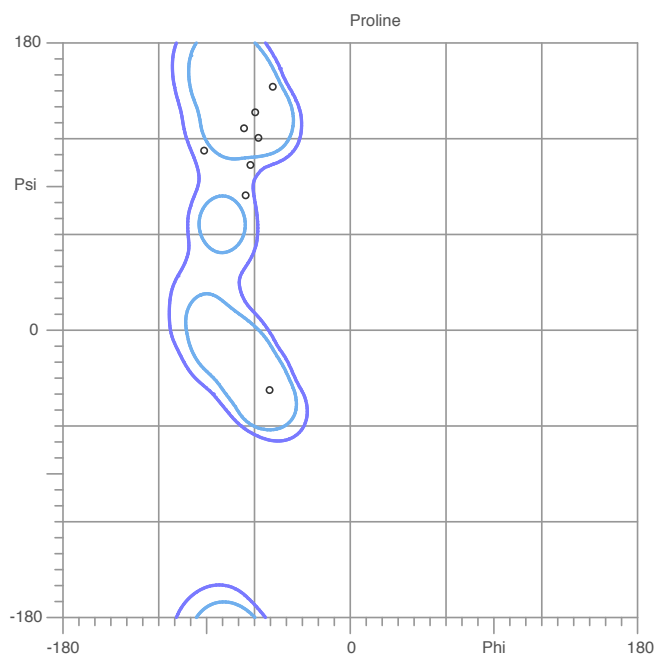
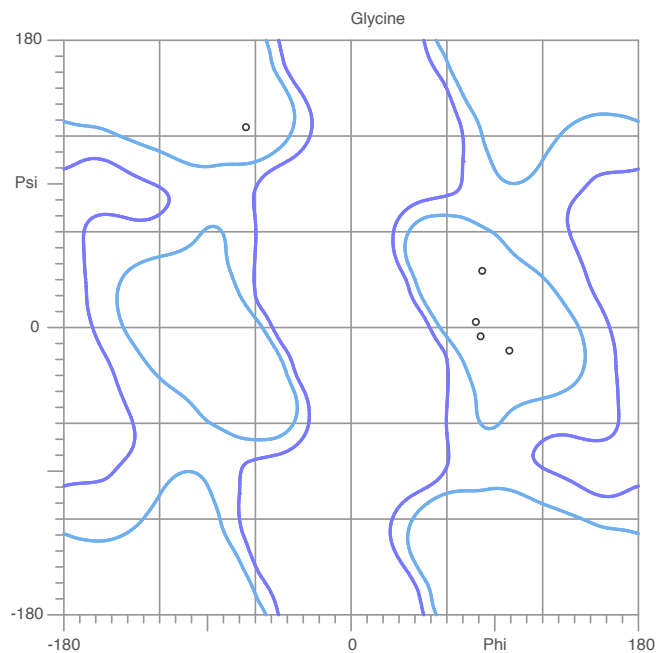
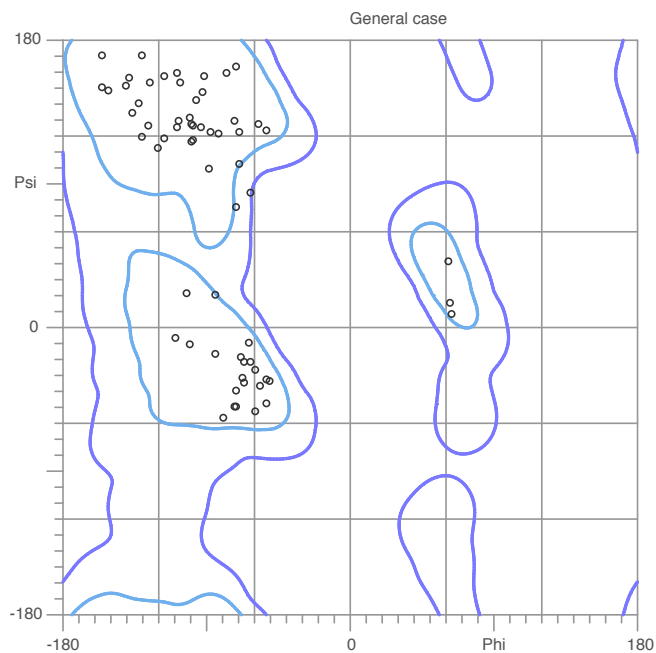
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 6



94.0% (79/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

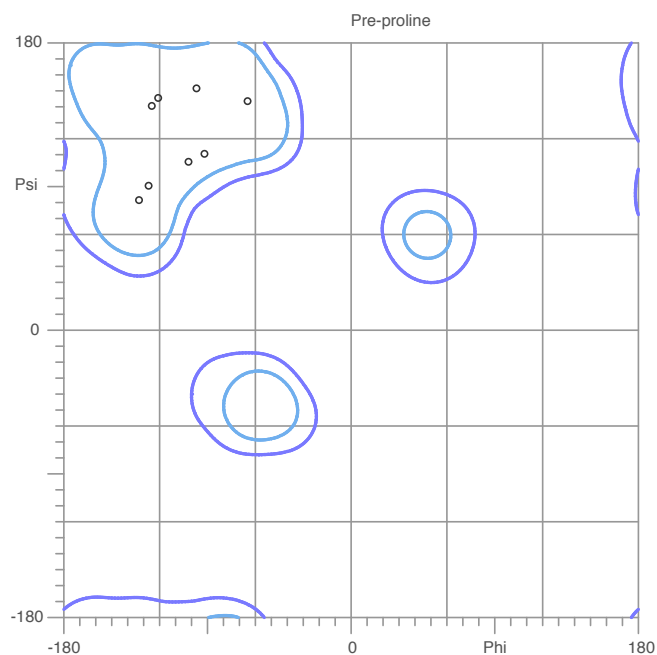
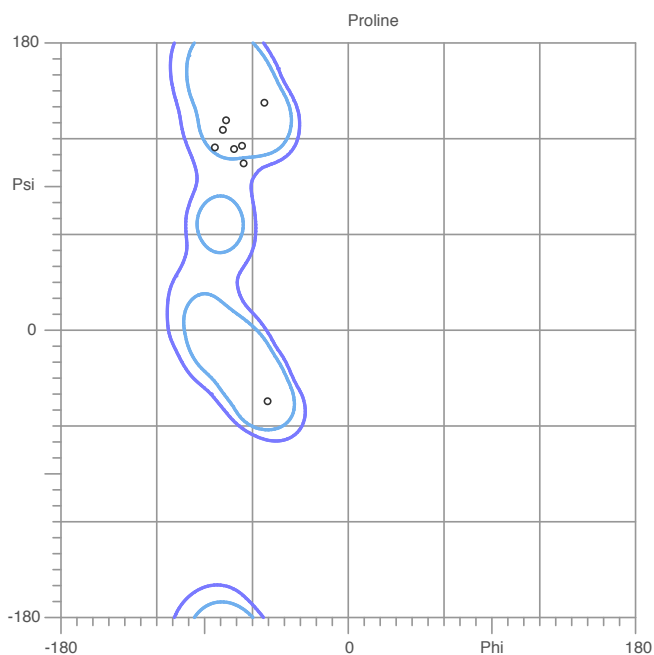
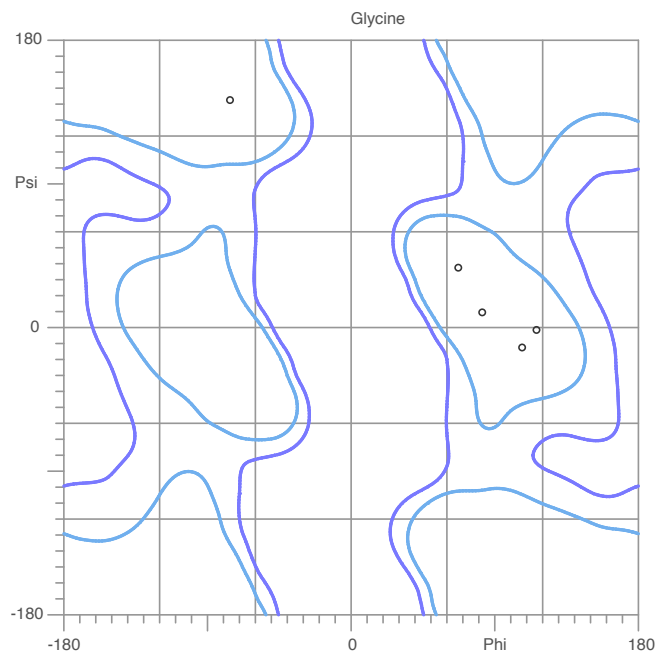
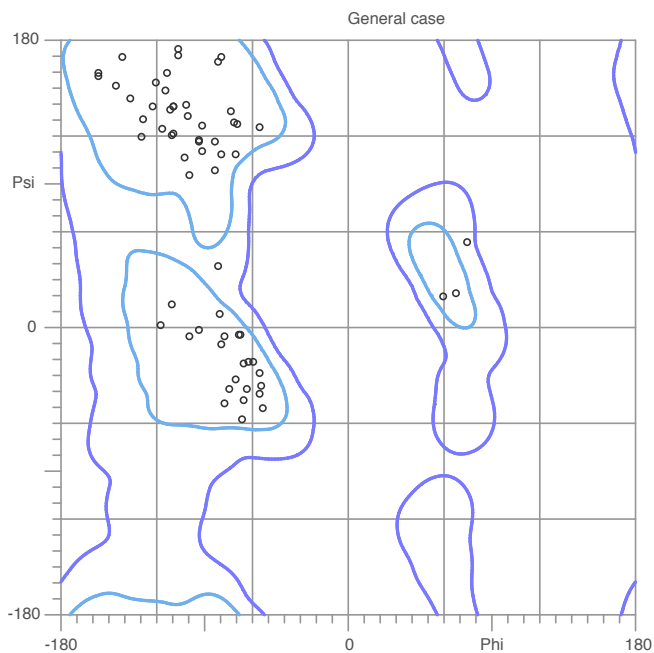
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 7



96.4% (81/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

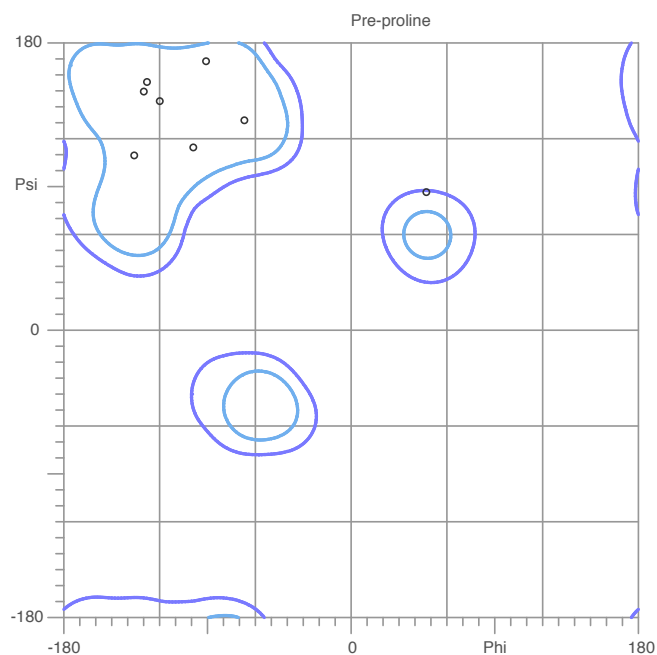
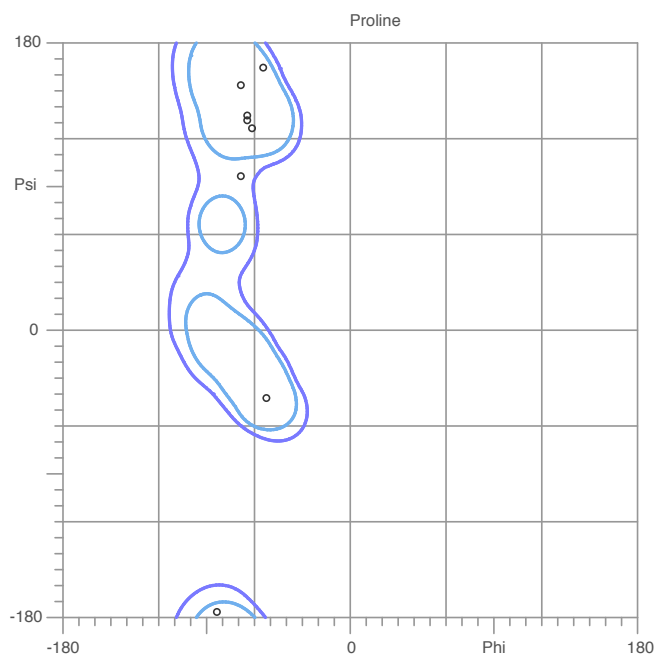
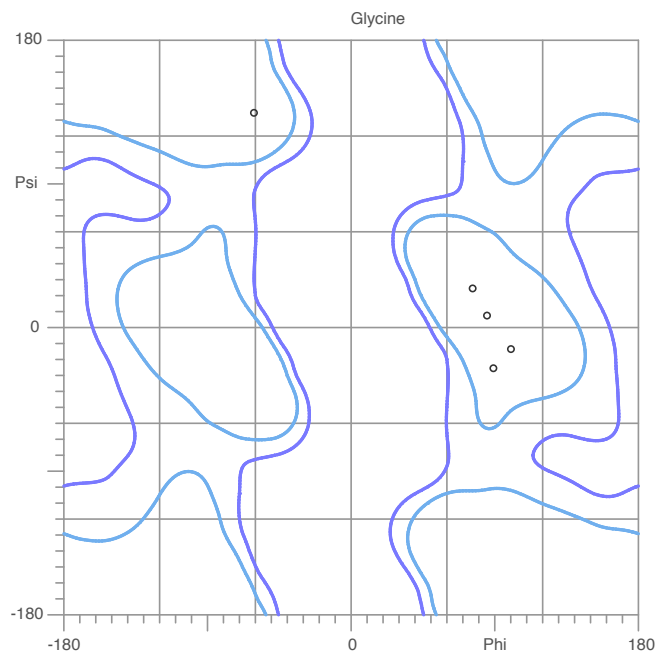
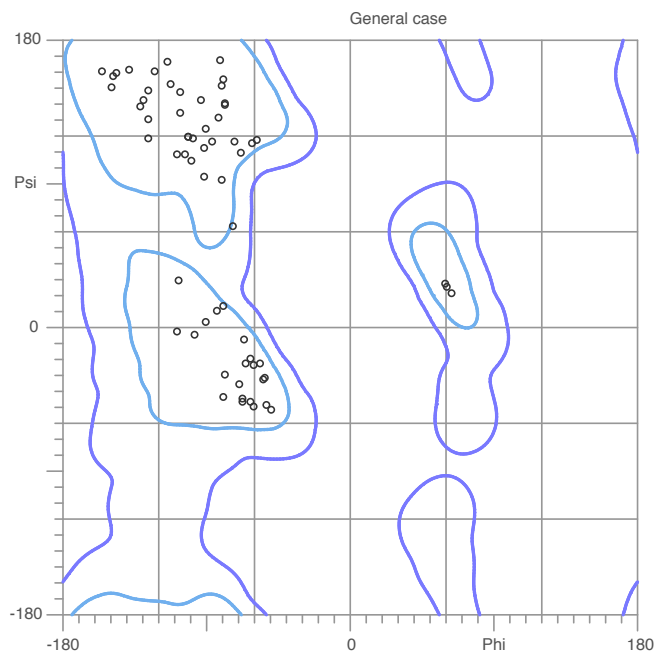
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4694F_NMR_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.

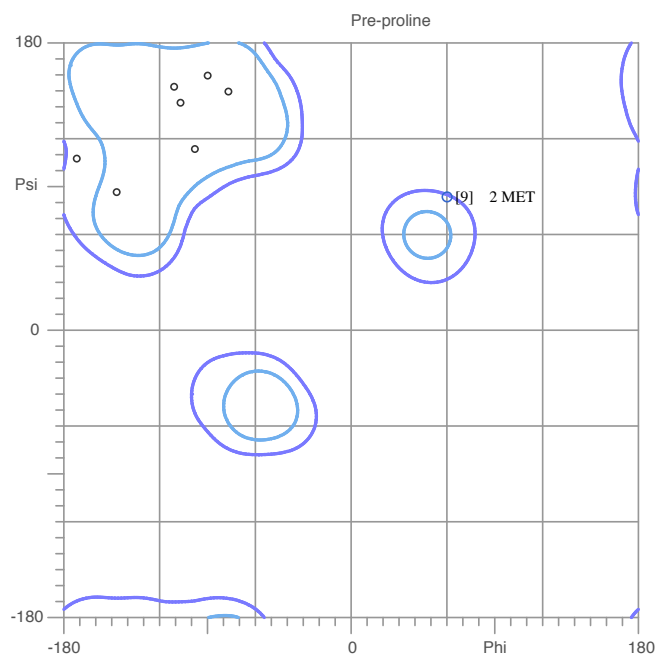
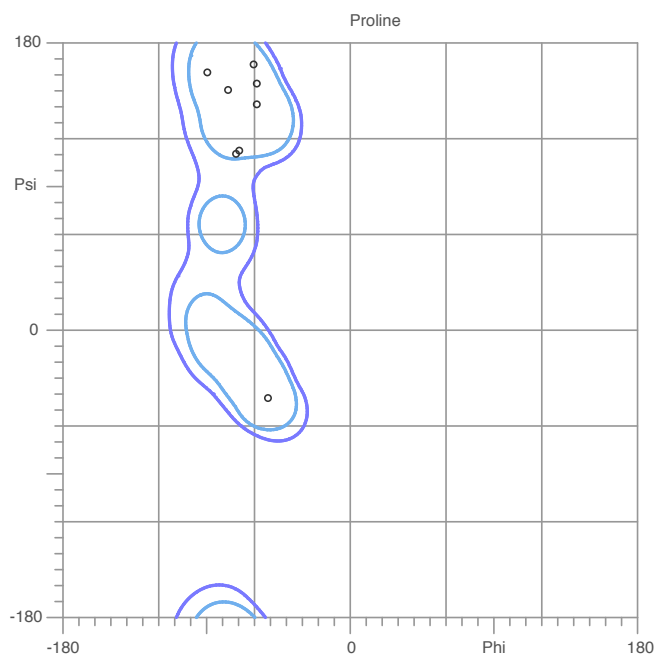
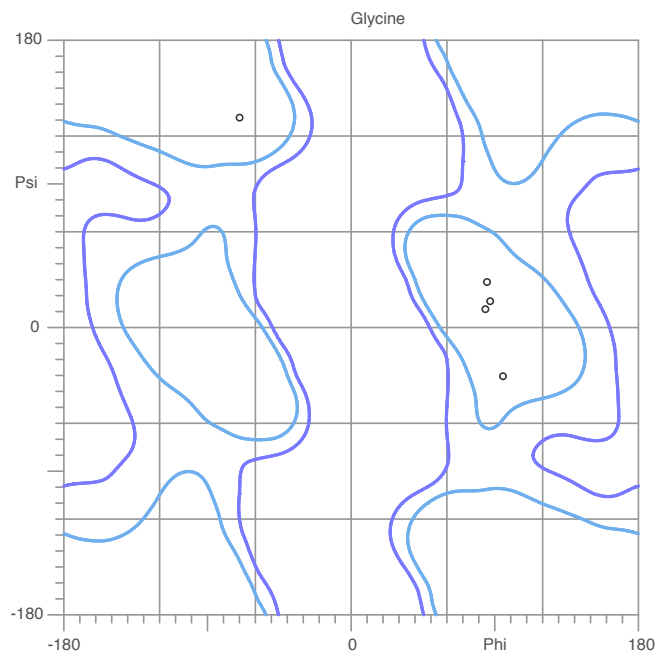
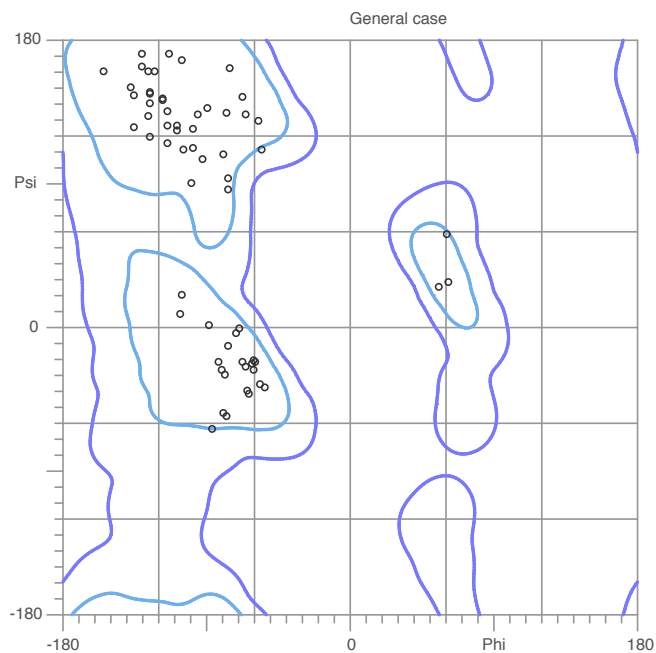
There were no outliers.

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 9

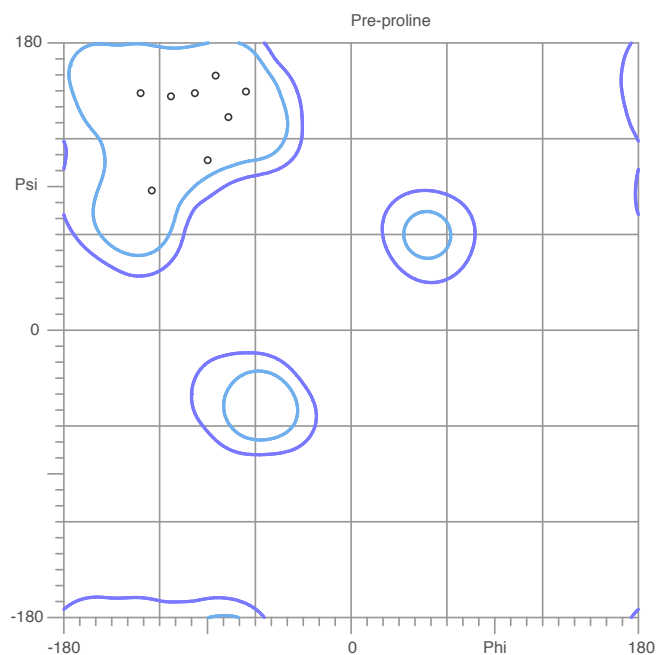
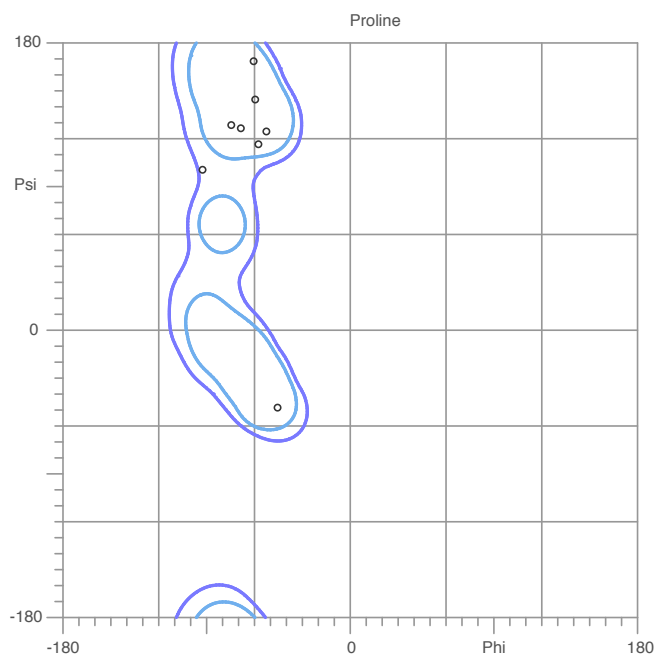
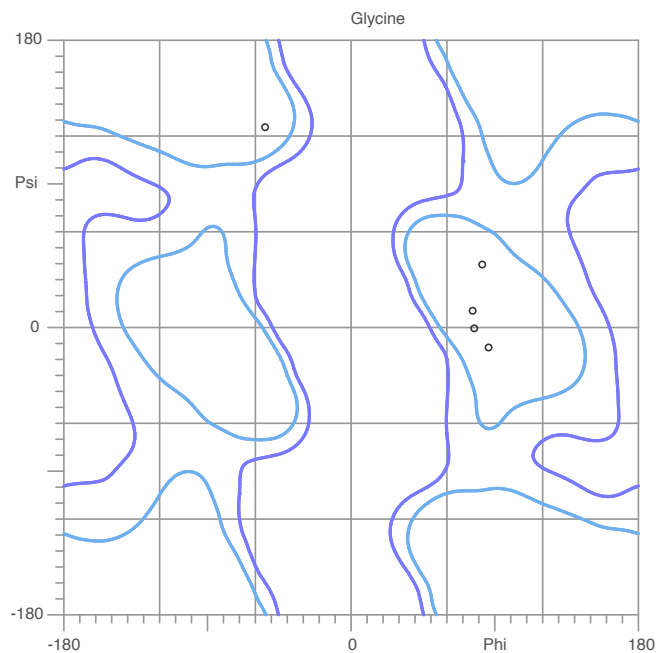
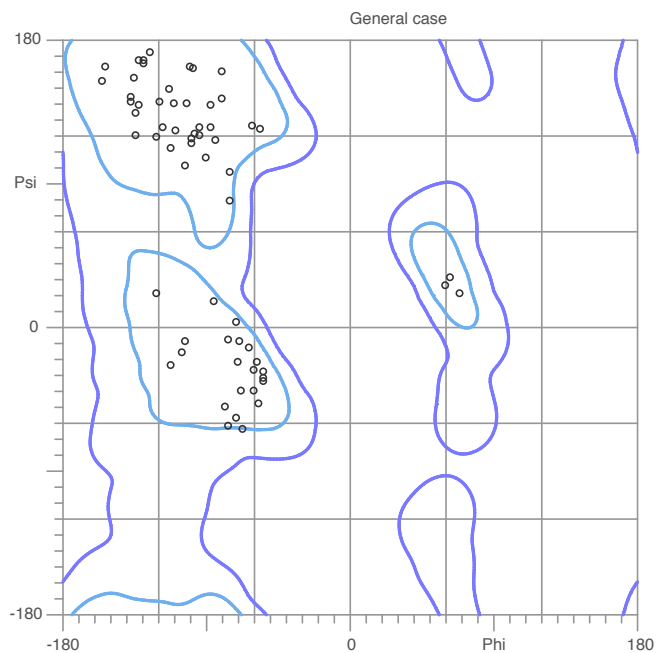


95.2% (80/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 2 MET (60.8, 84.9)

MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 10



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.

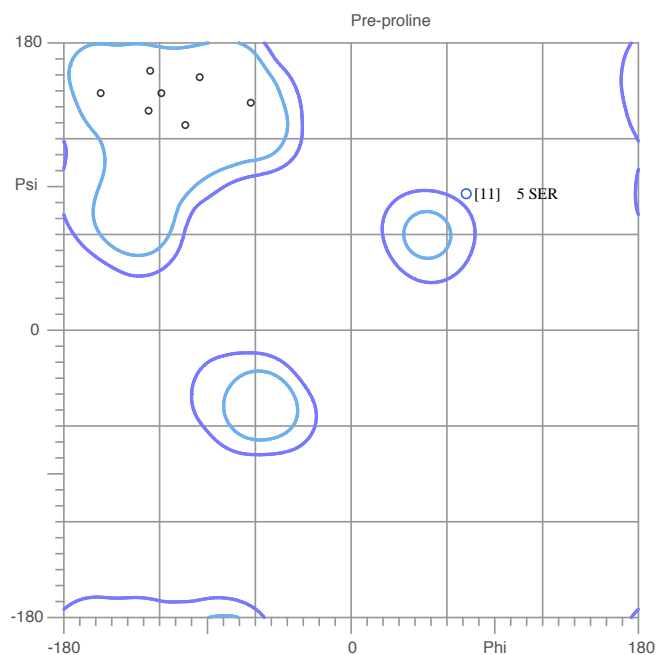
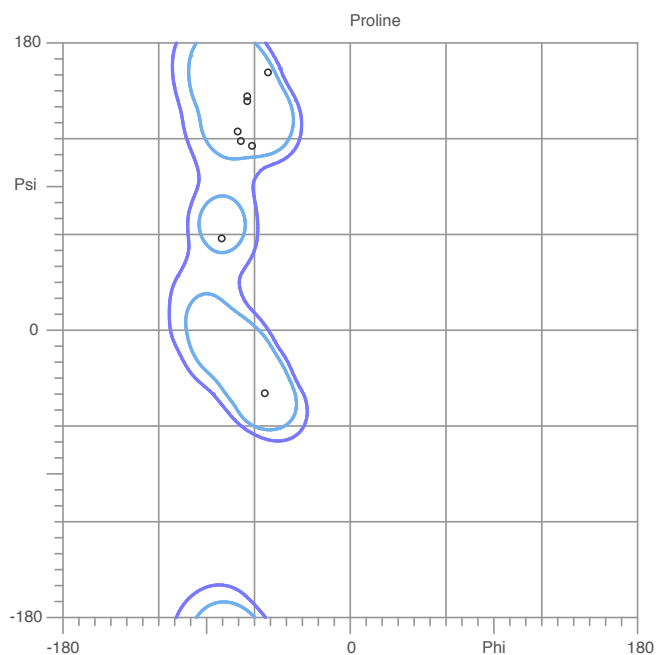
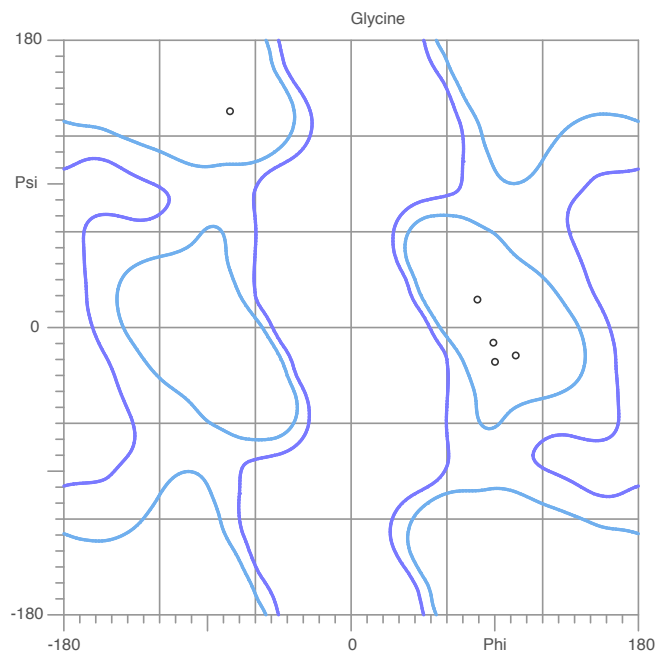
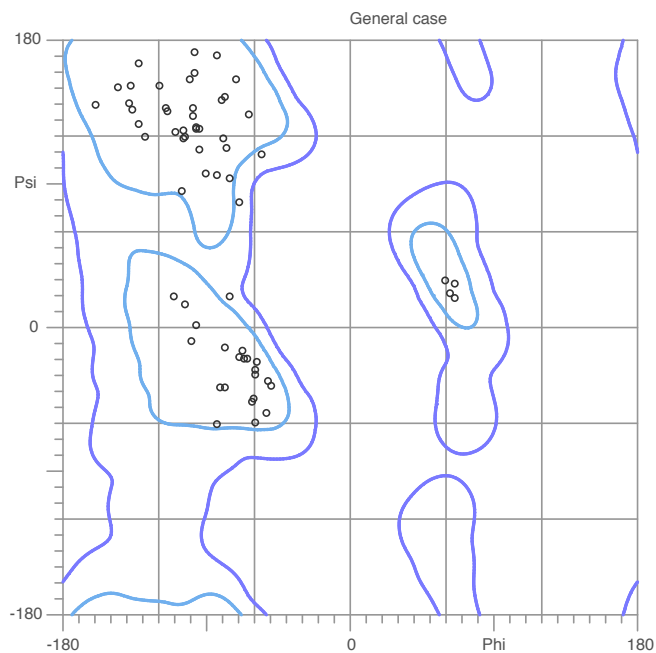
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 11



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.

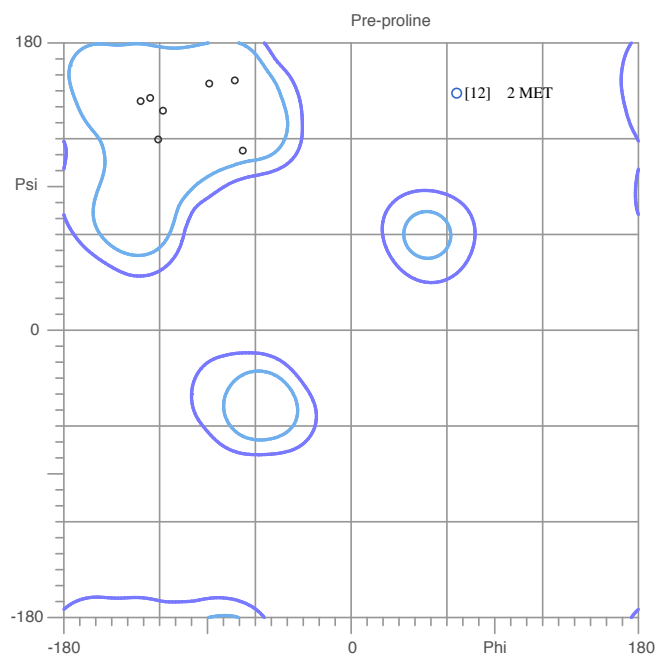
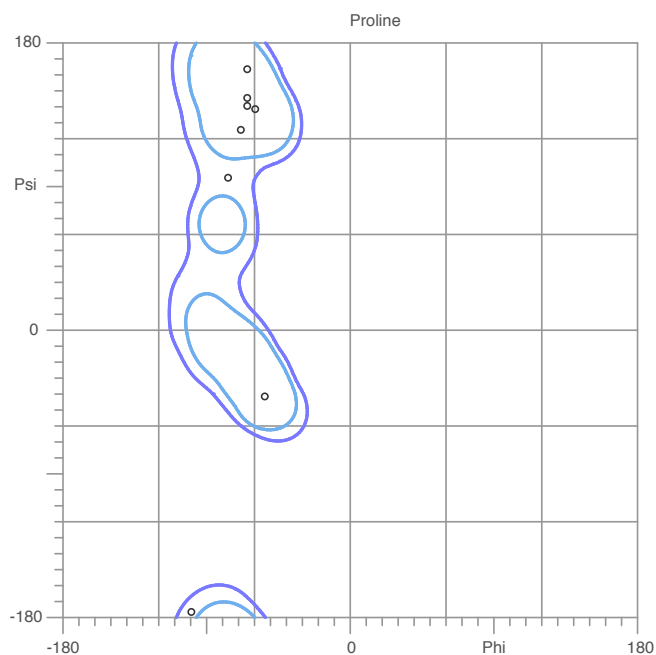
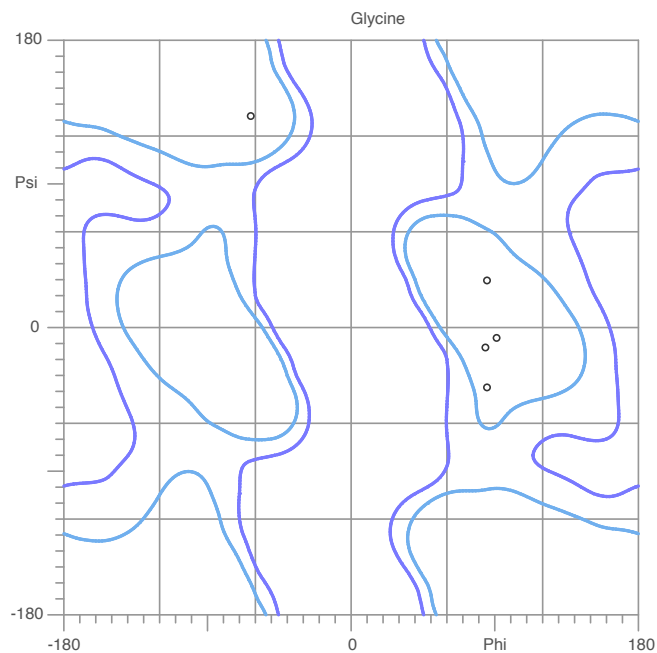
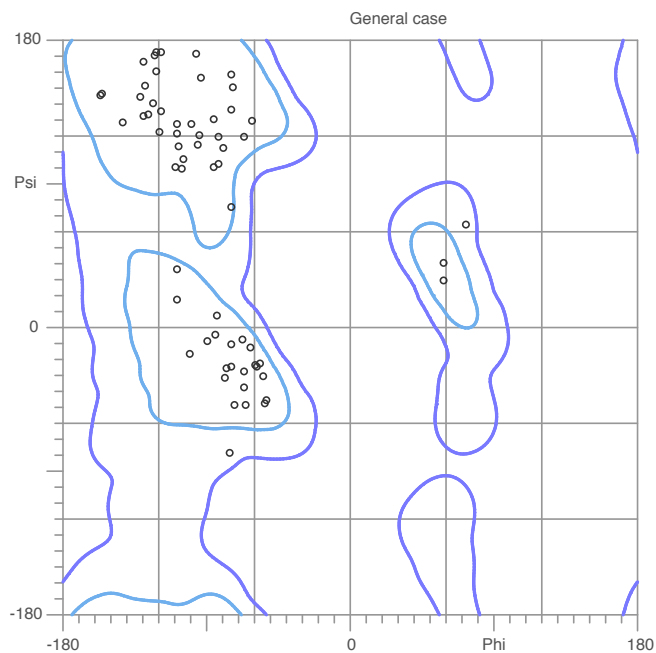
There were 1 outliers (phi, psi):
[11] 5 SER (72.8, 86.7)

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 12



94.0% (79/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

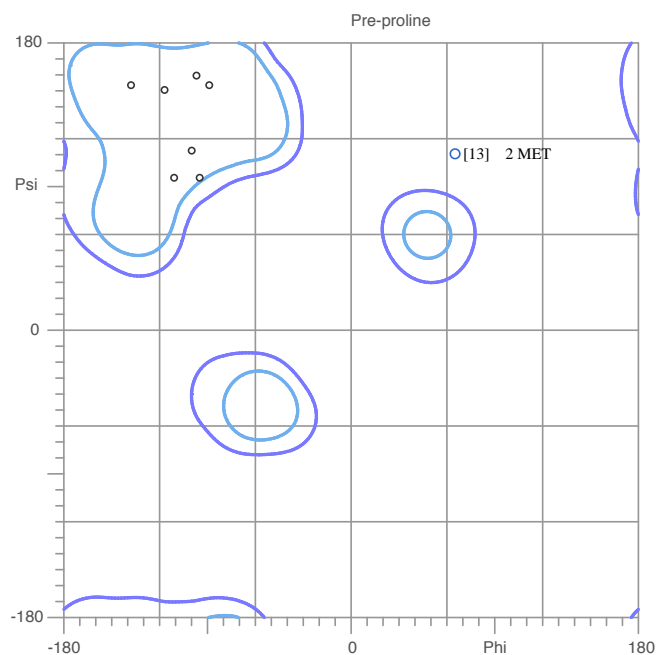
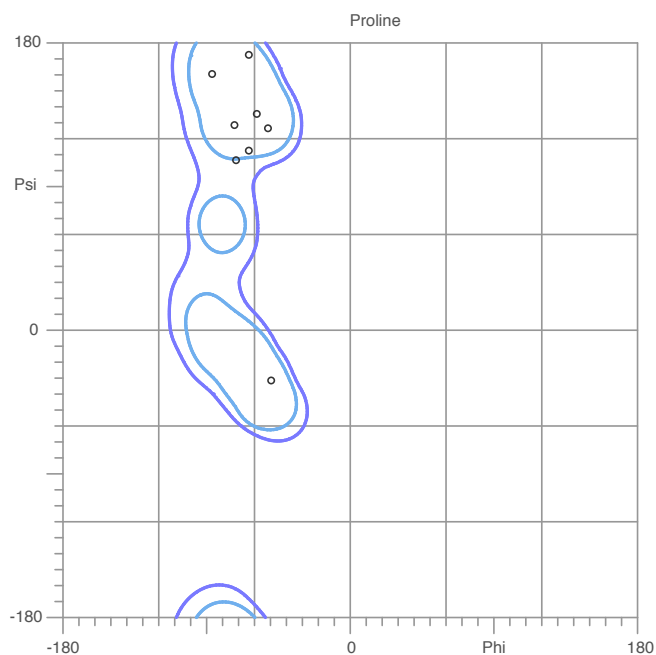
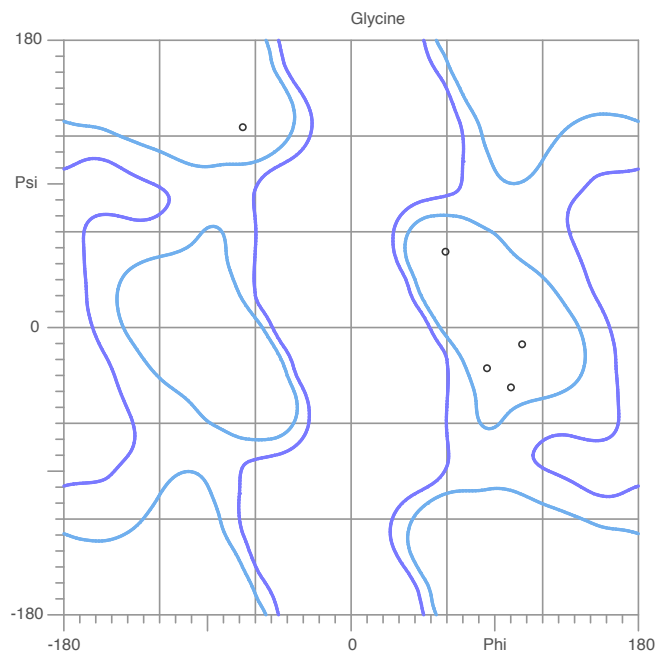
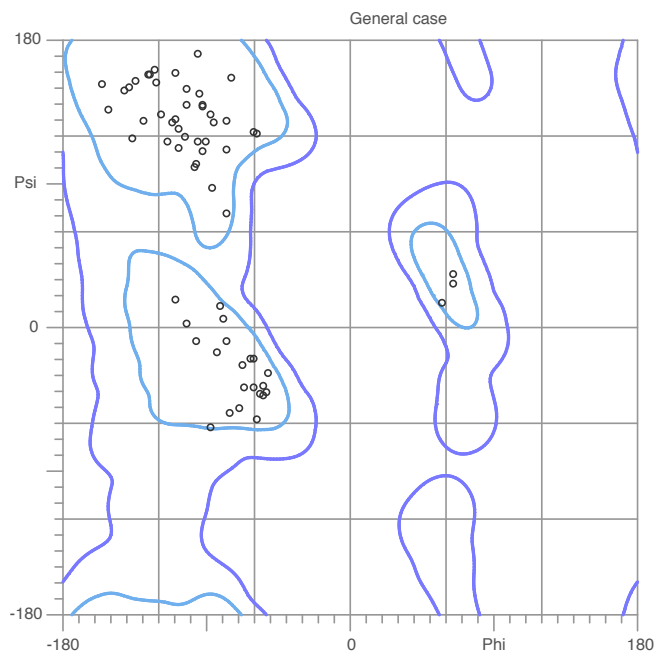
There were 1 outliers (phi, psi):
[12] 2 MET (66.3, 149.4)

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

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

MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 13



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.

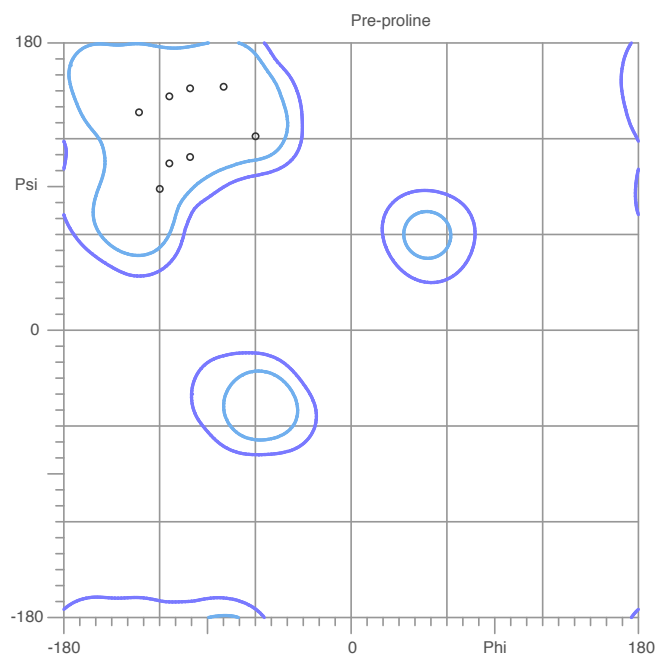
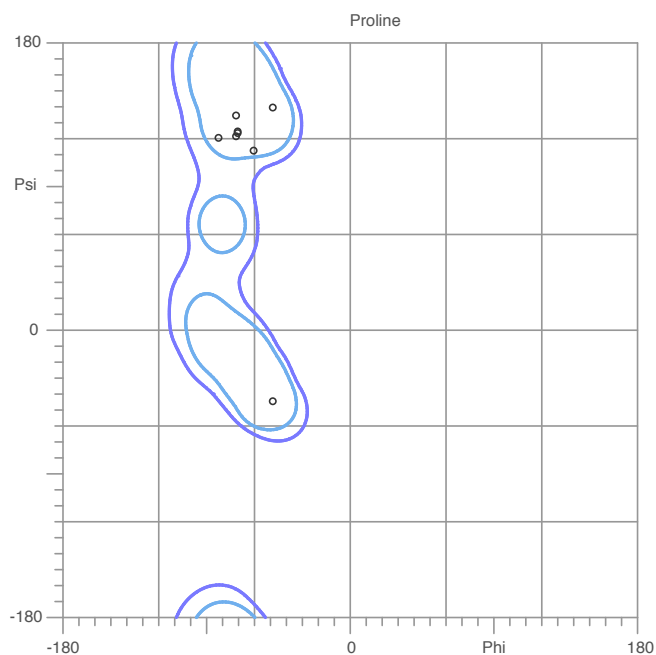
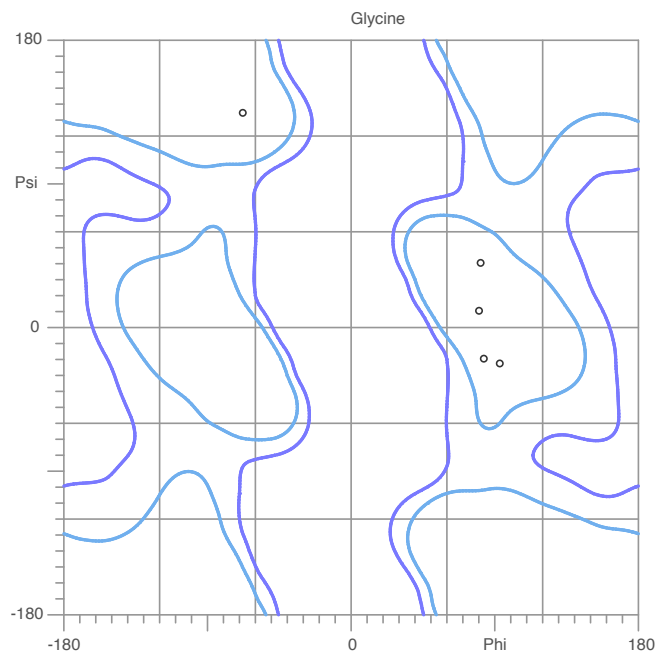
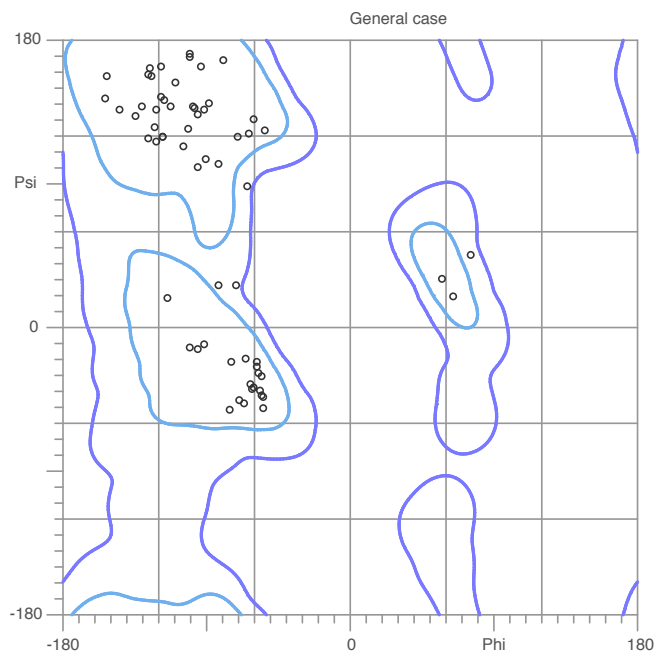
There were 1 outliers (phi, psi):
[13] 2 MET (65.5, 111.4)

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

MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 14



95.2% (80/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

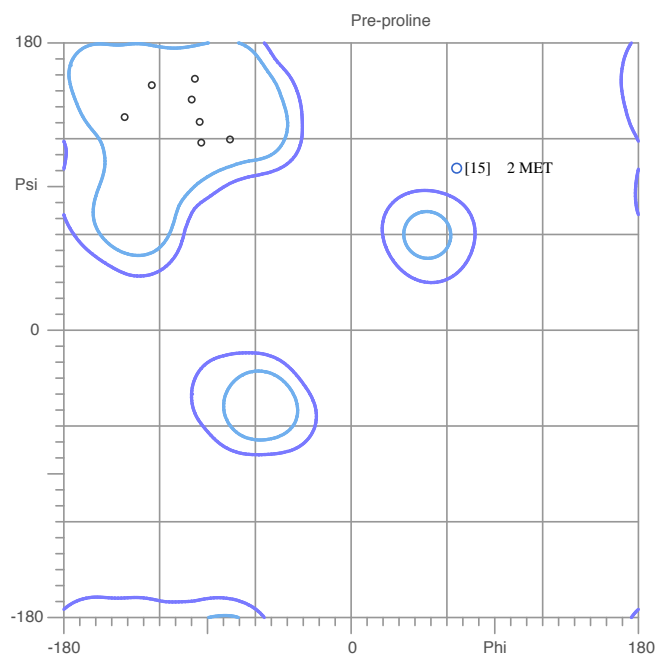
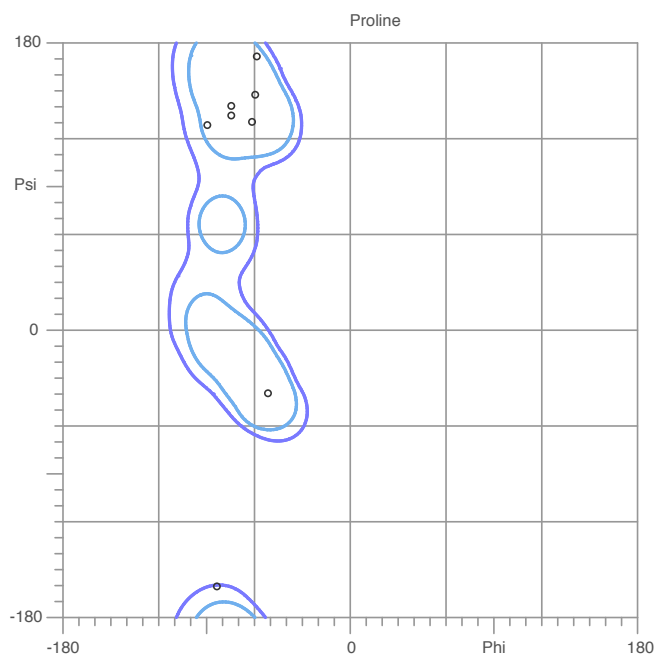
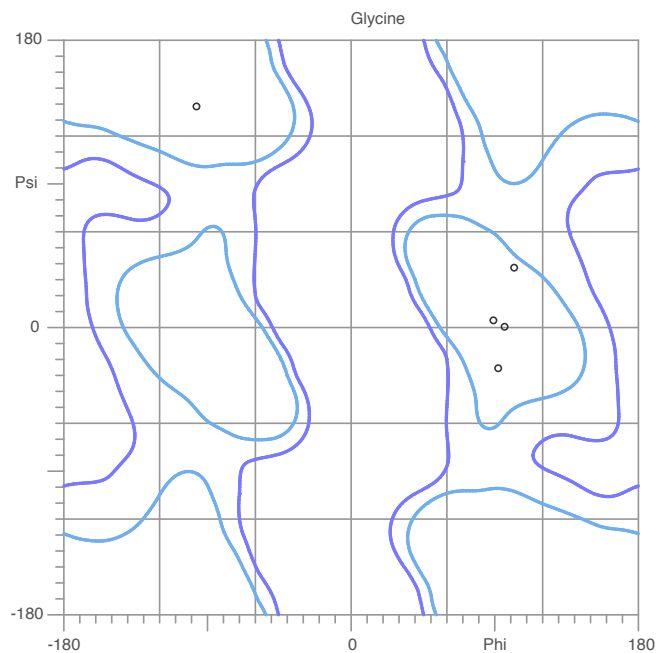
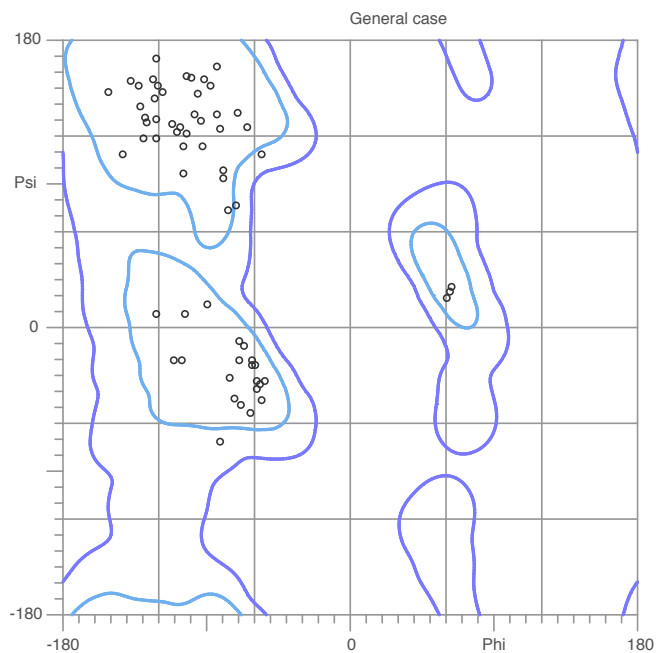
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 15



94.0% (79/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

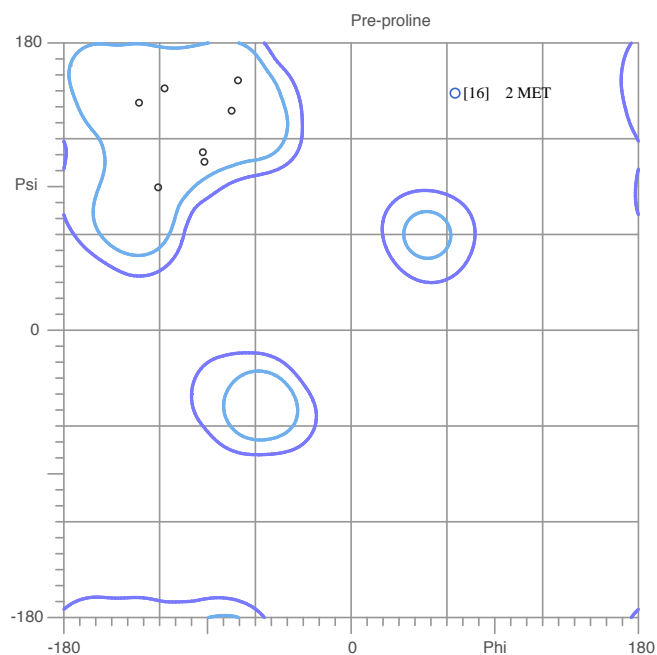
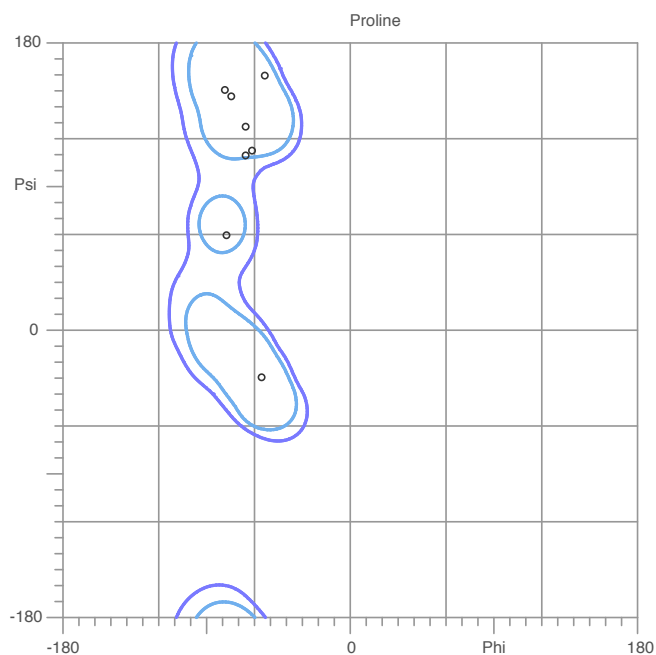
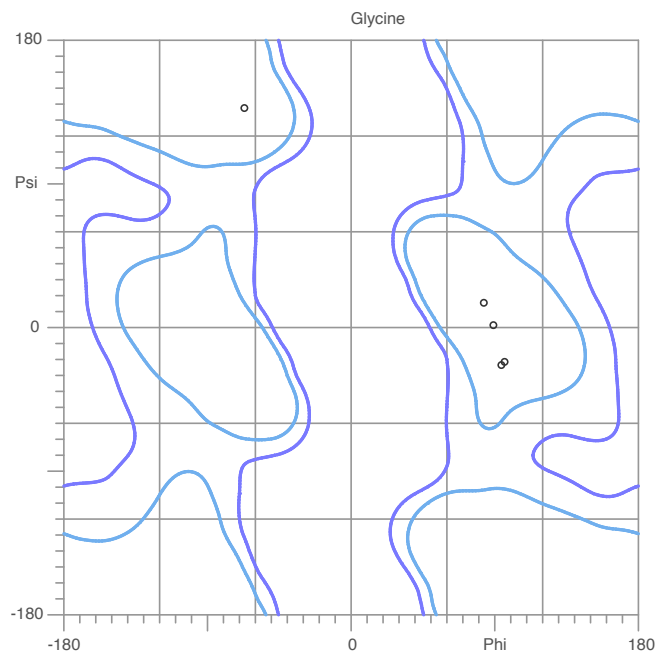
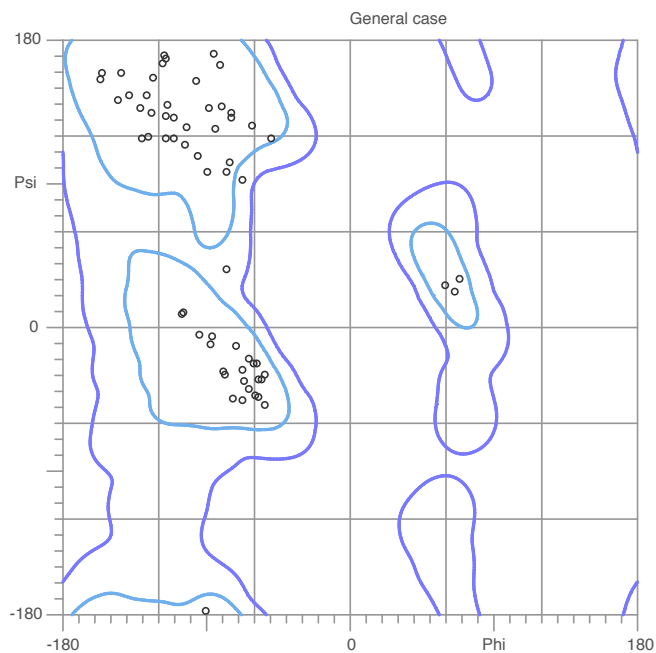
There were 1 outliers (phi, psi):
[15] 2 MET (66.8, 102.5)

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

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

MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 16



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.

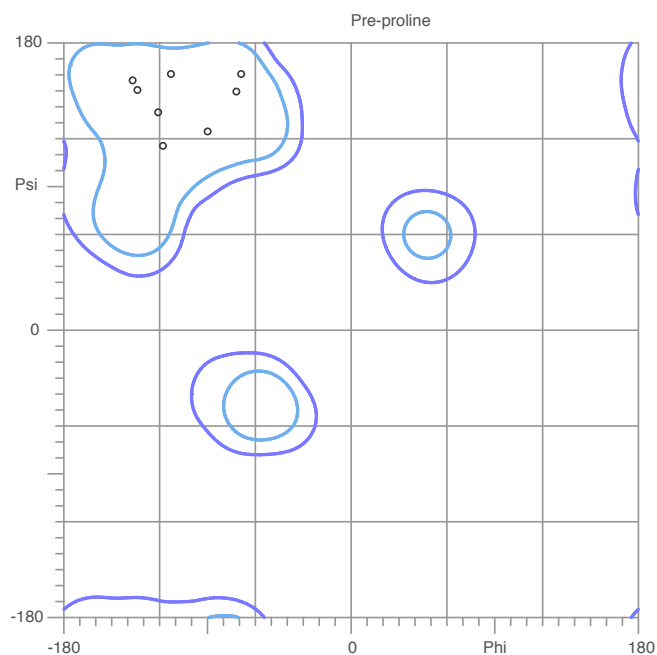
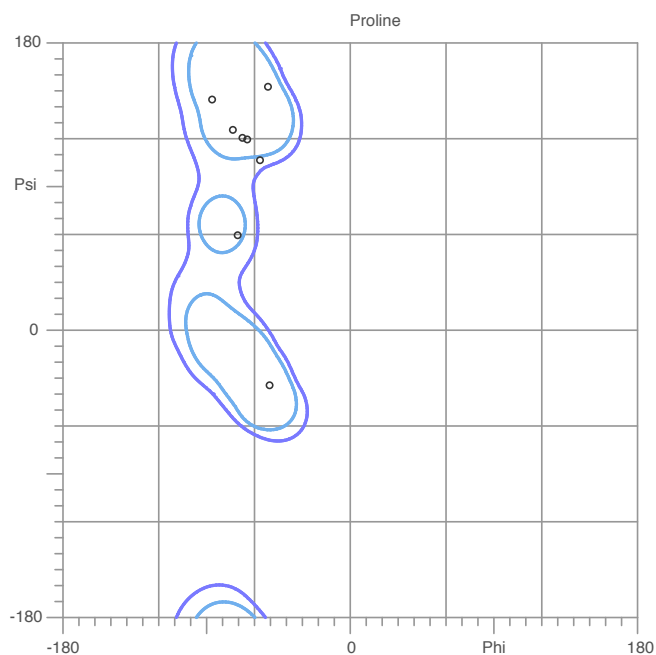
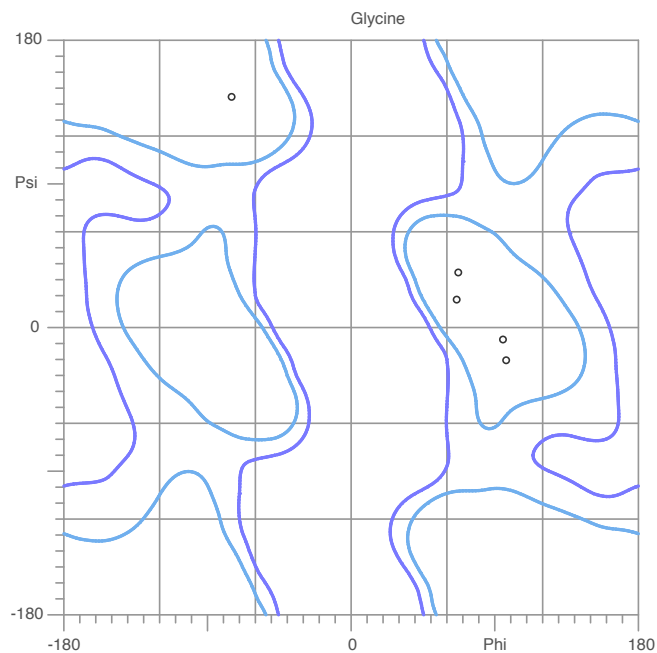
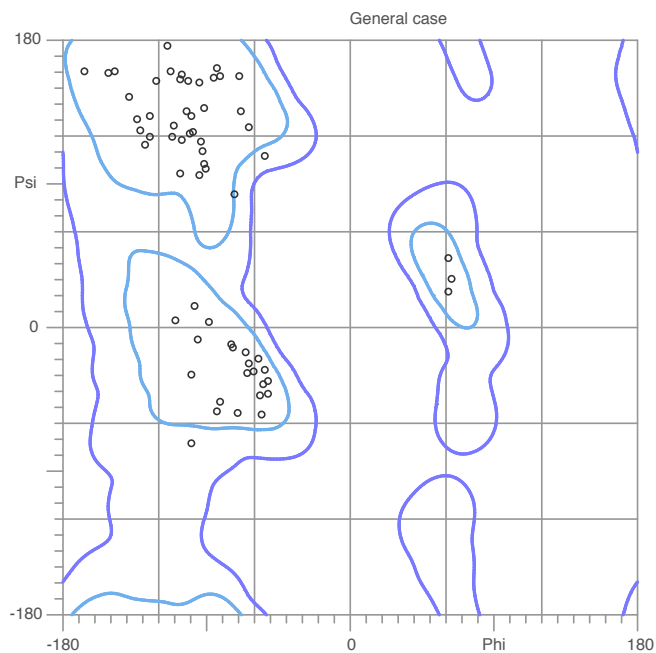
There were 1 outliers (phi, psi):
[16] 2 MET (65.2, 149.8)

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 17



96.4% (81/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

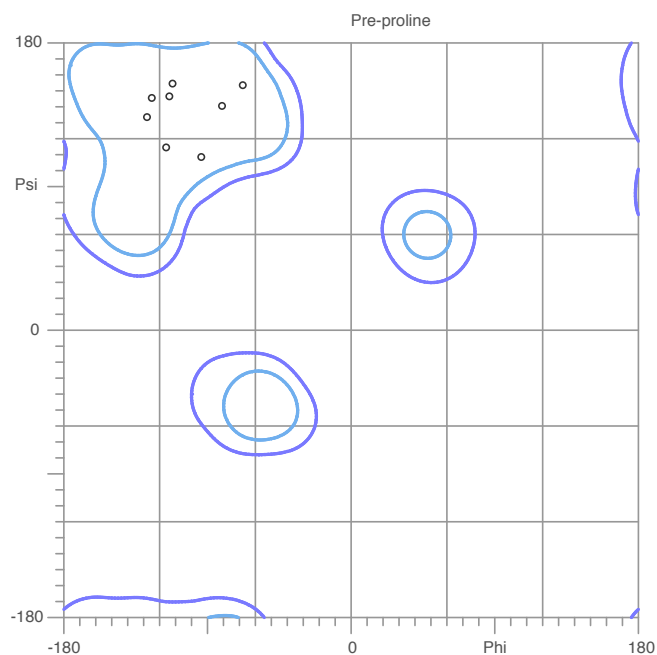
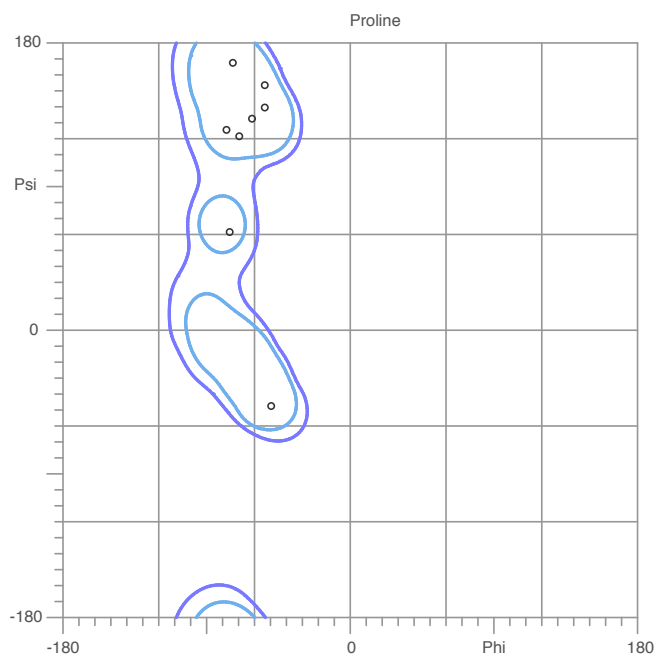
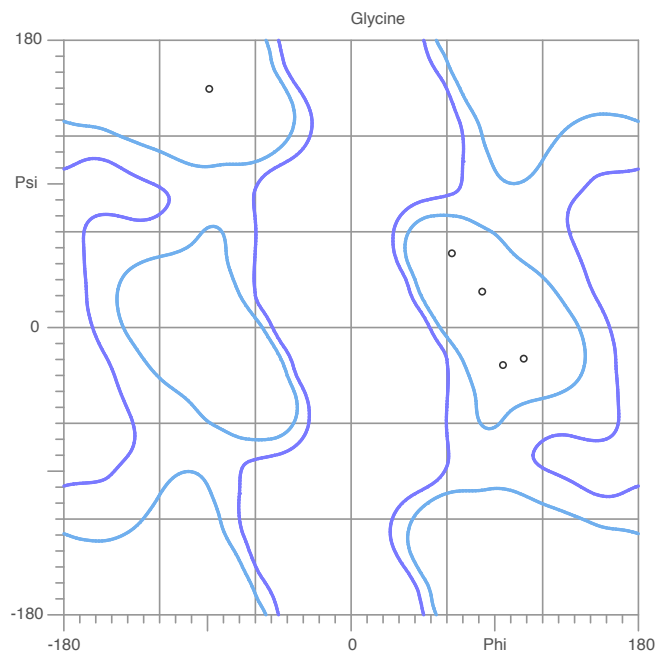
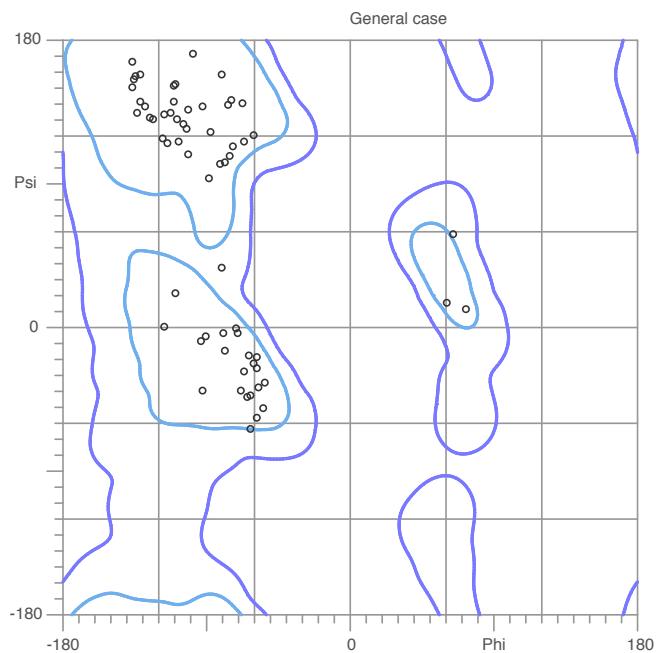
There were no outliers.

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 18



96.4% (81/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

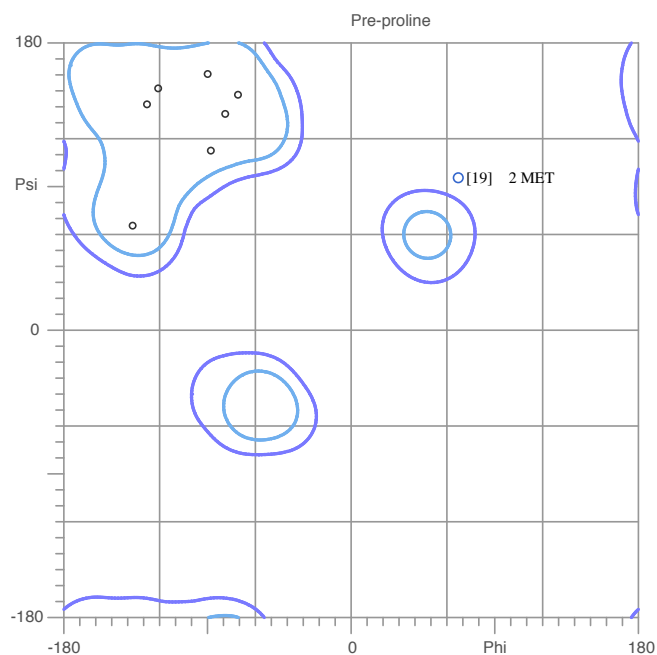
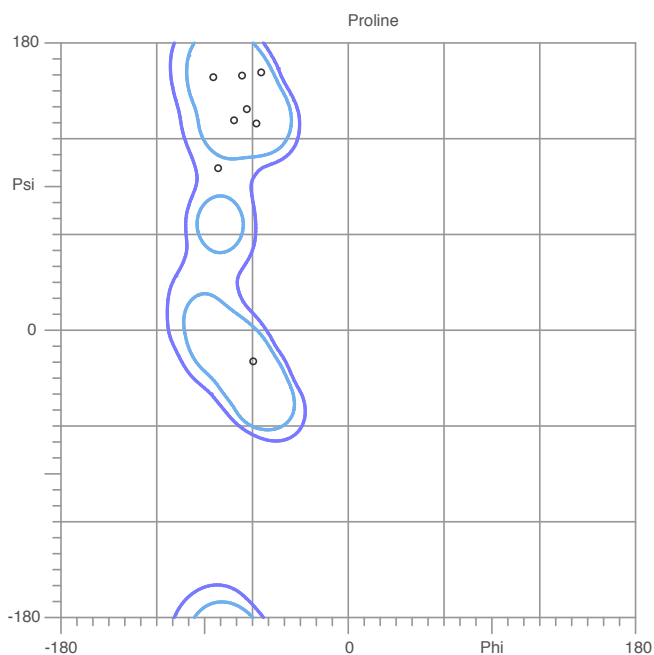
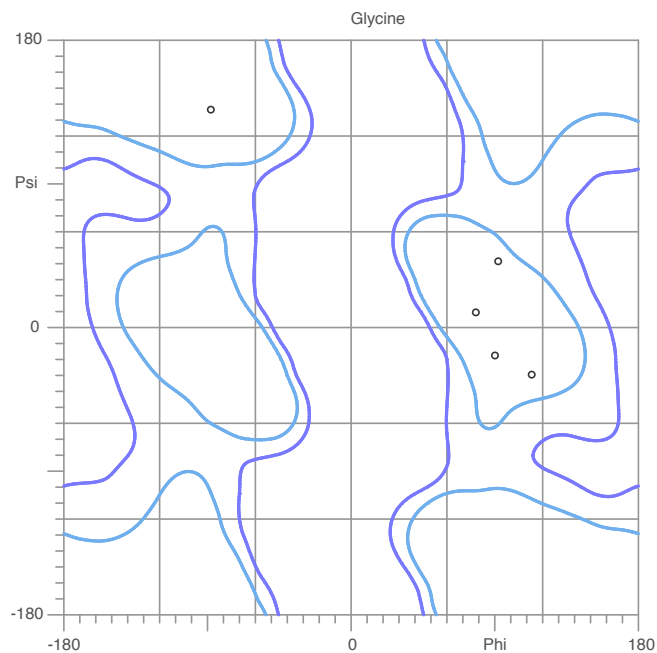
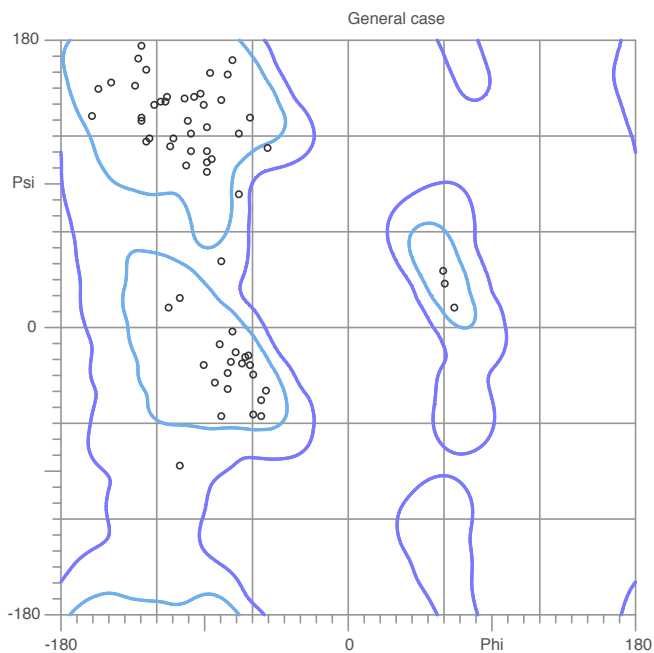
There were no outliers.

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 19



92.9% (78/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

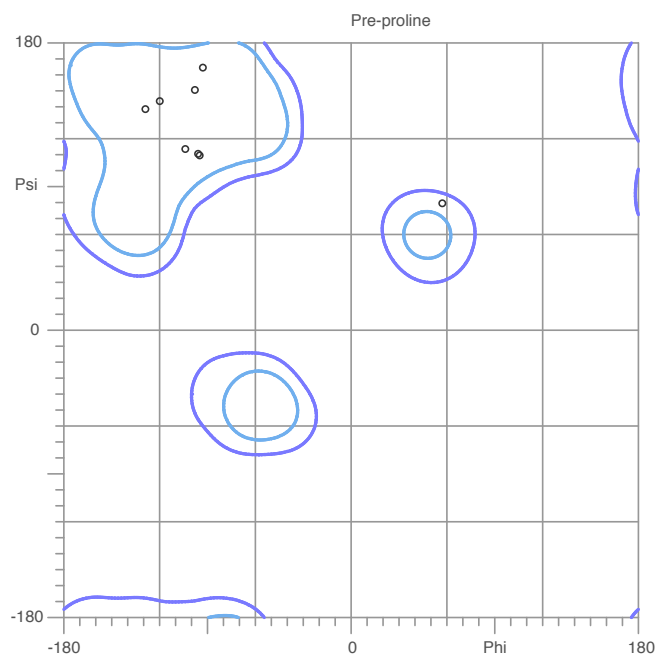
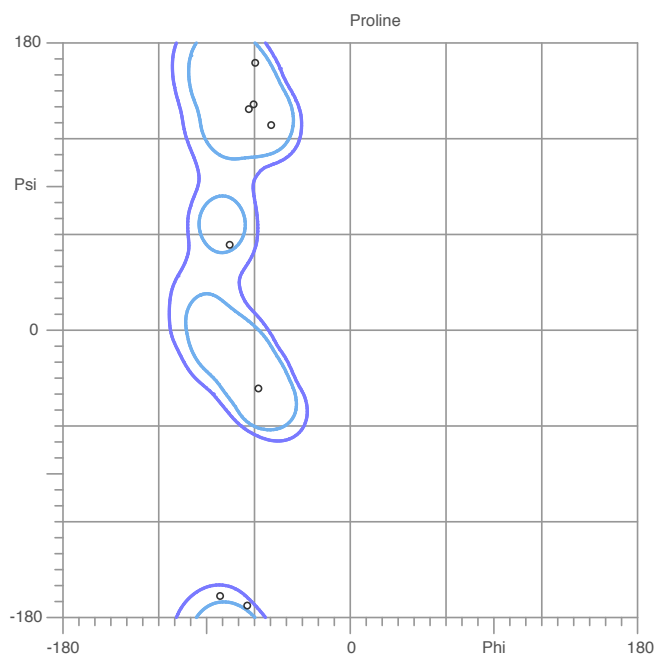
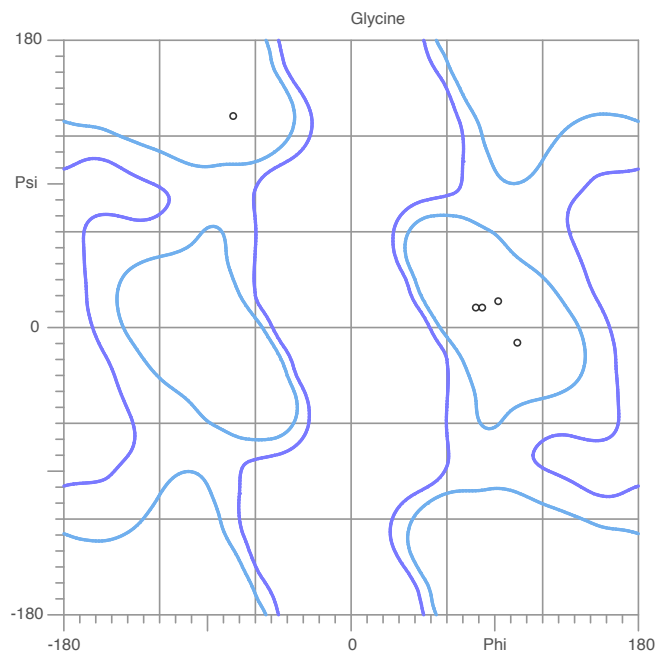
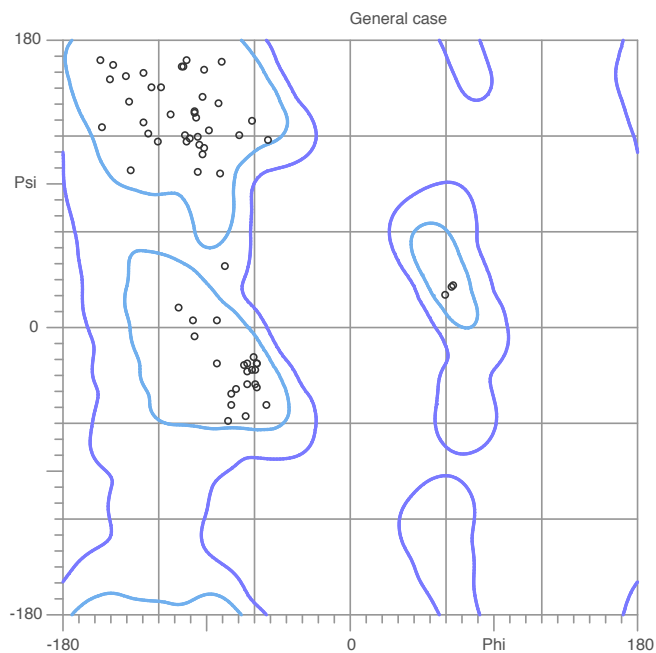
There were 1 outliers (phi, psi):
[19] 2 MET (67.3, 96.8)

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

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MolProbity Ramachandran analysis

HR4694F_NMR_em_bcr3.pdb, model 20



95.2% (80/84) 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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