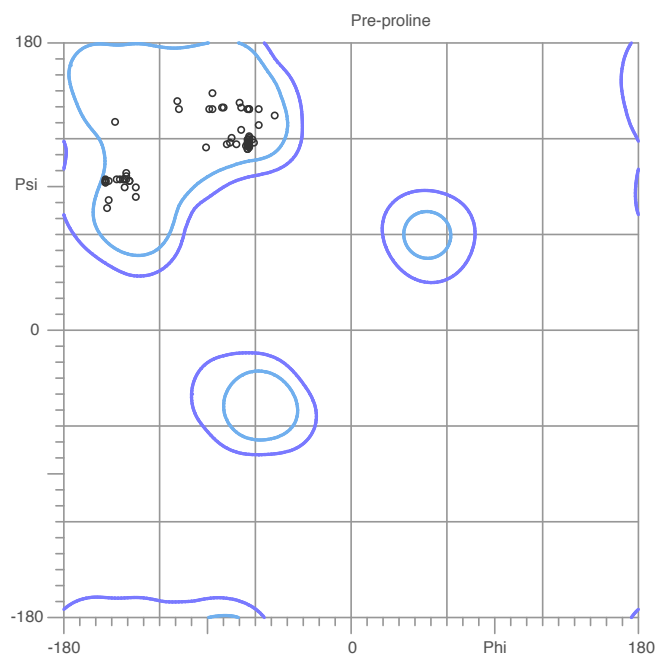
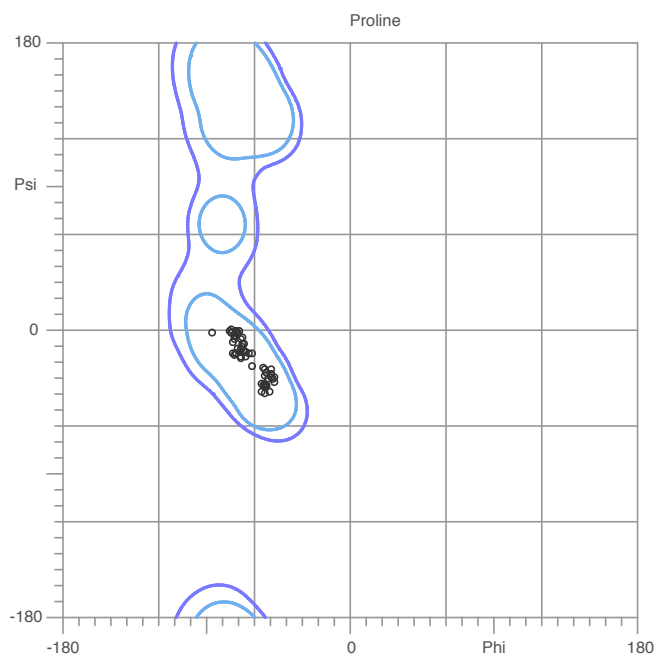
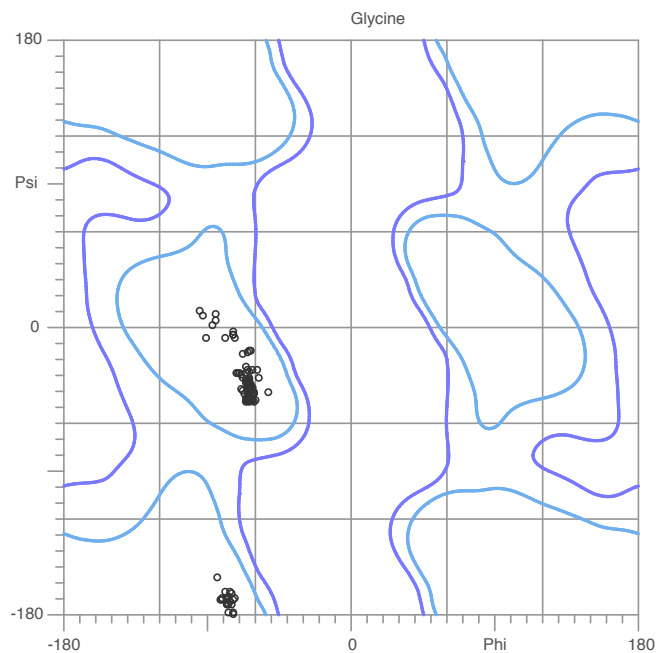
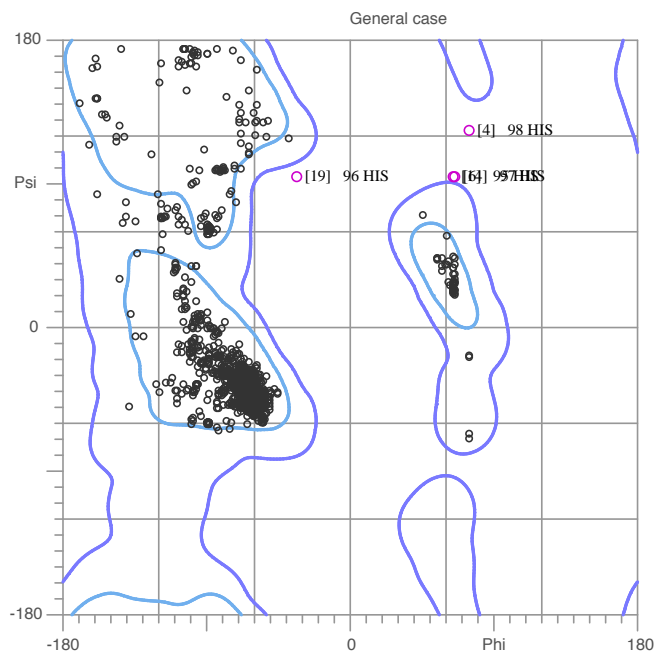


MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, all models



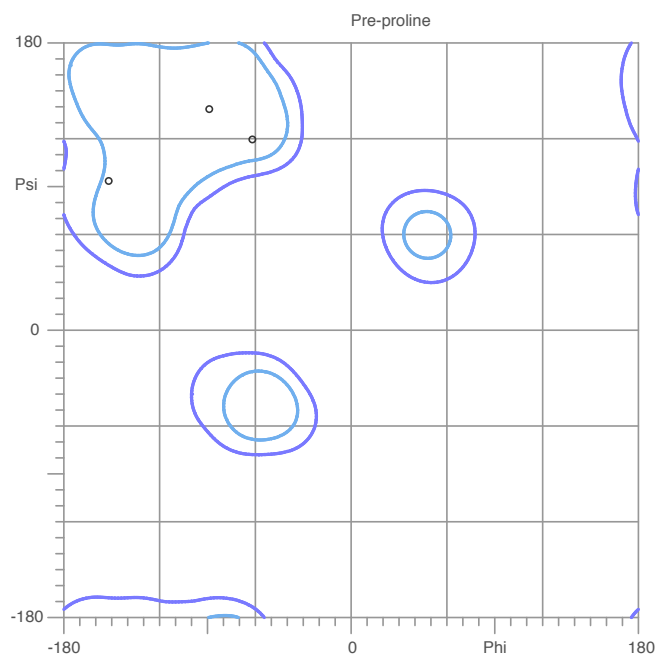
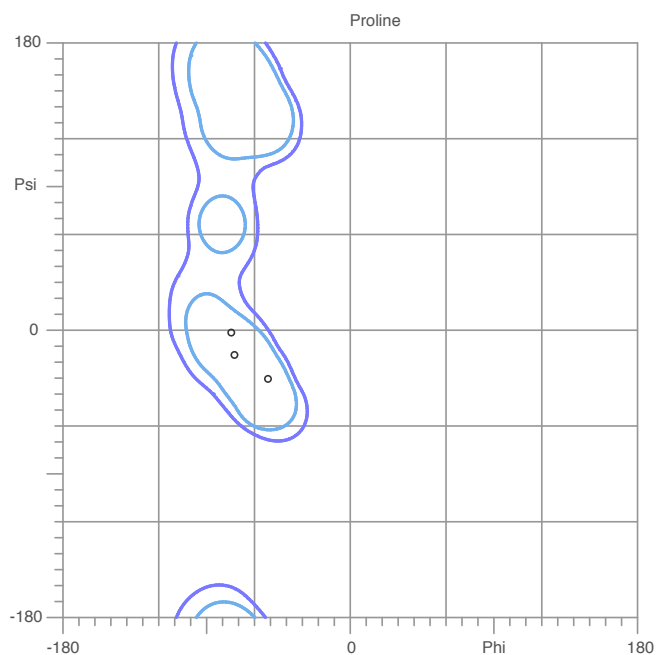
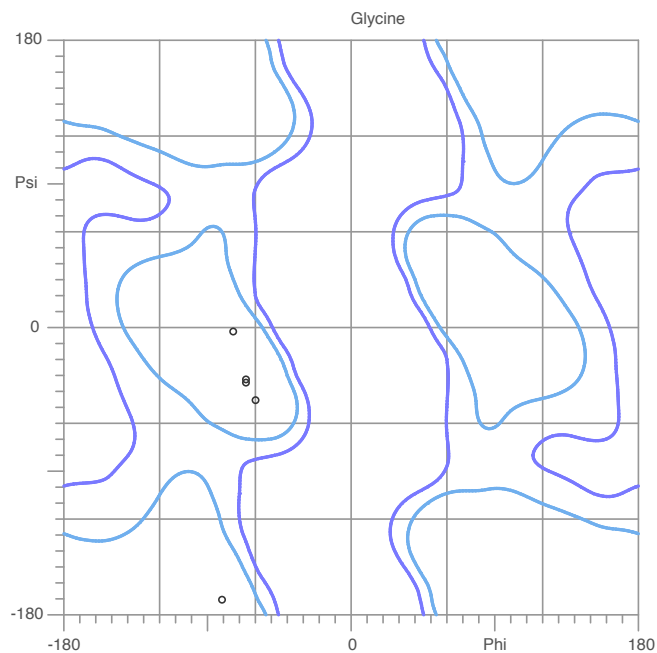
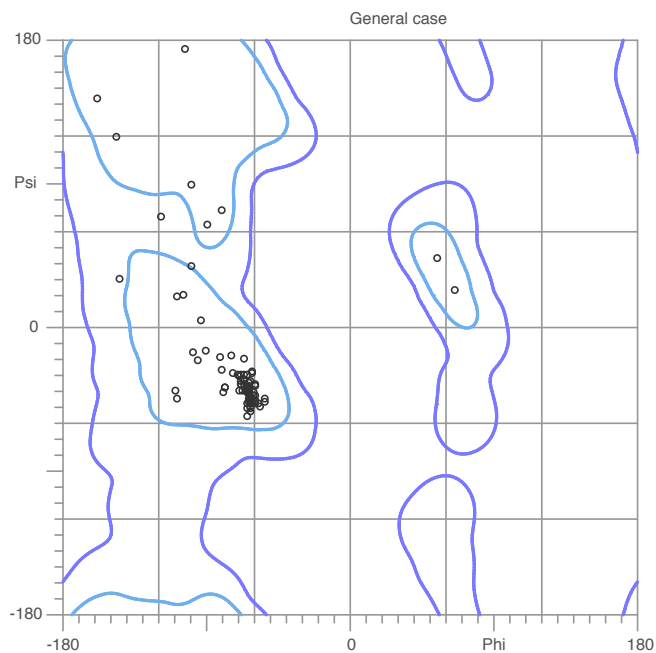
97.8% (1897/1940) of all residues were in favored (98%) regions.
99.8% (1936/1940) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [4] 98 HIS (75.0, 124.9)
- [6] 95 HIS (65.1, 95.1)
- [14] 97 HIS (65.0, 95.0)
- [19] 96 HIS (-34.8, 95.0)

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 1



96.9% (94/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

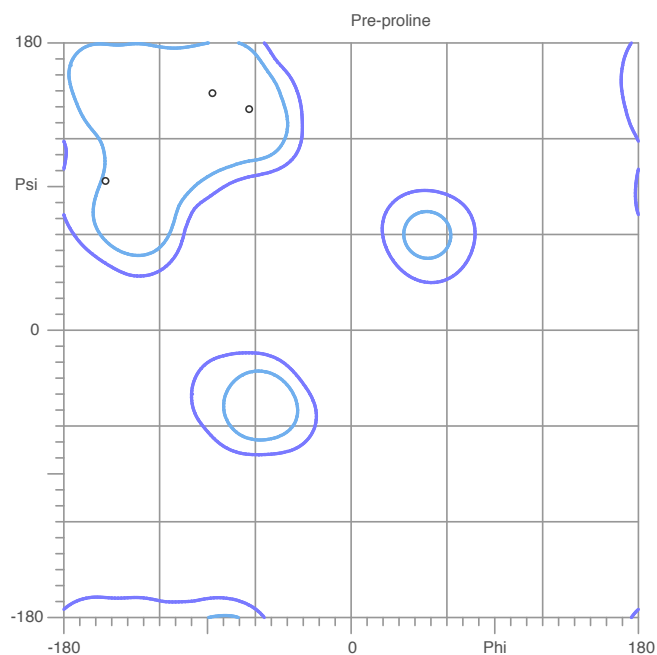
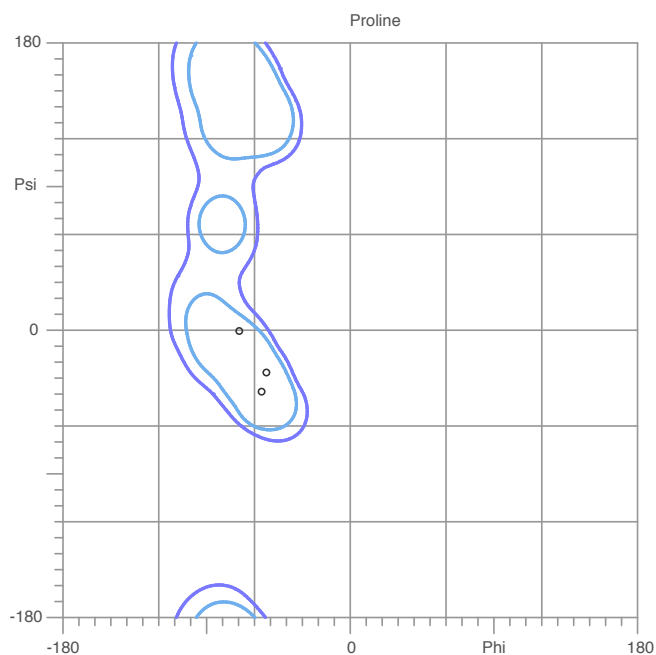
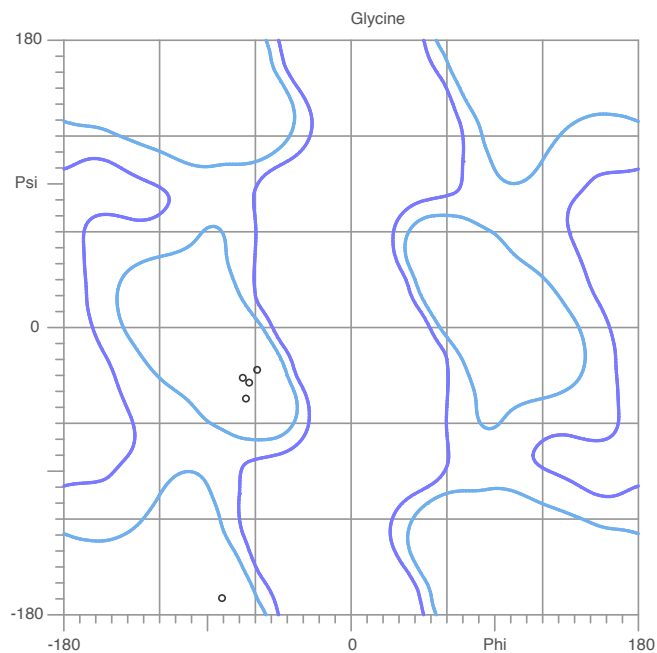
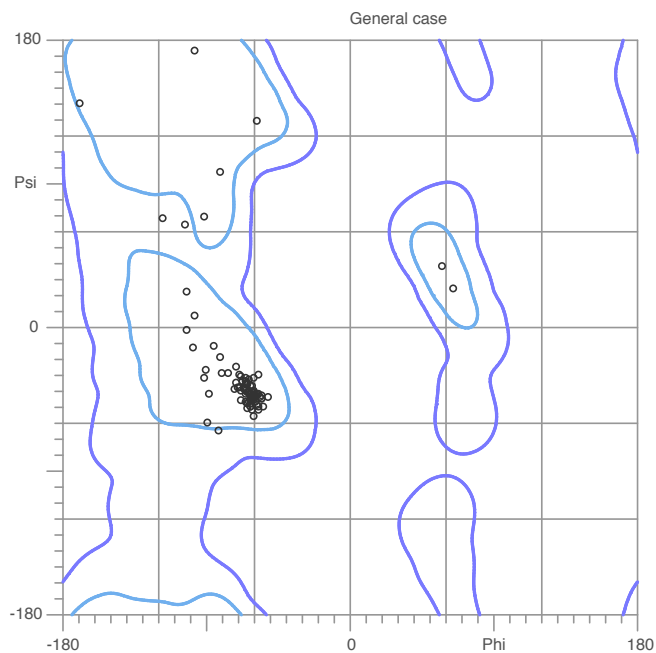
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 2



96.9% (94/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

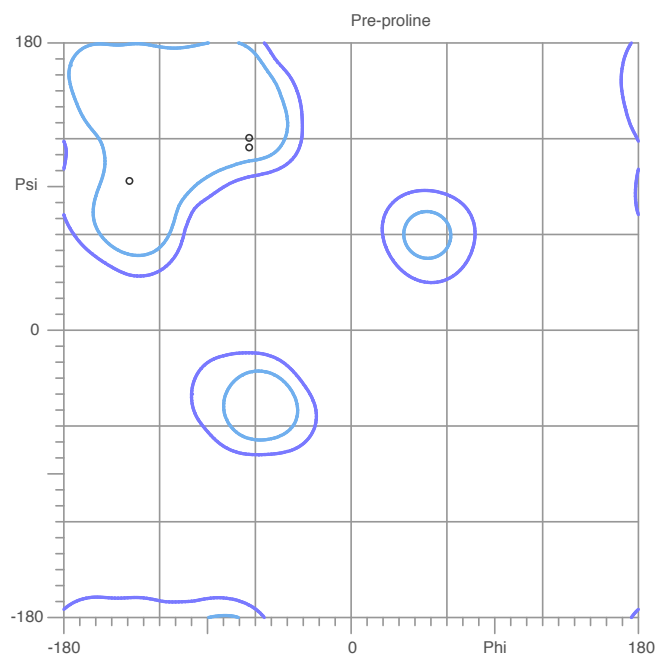
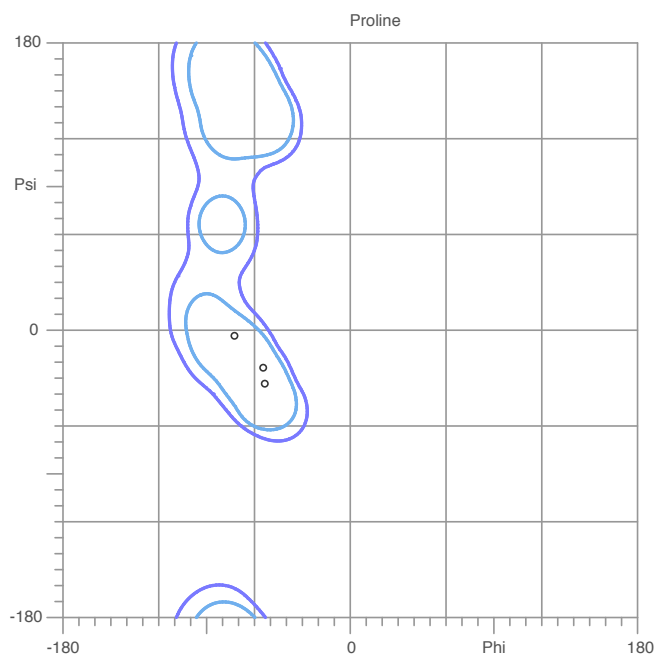
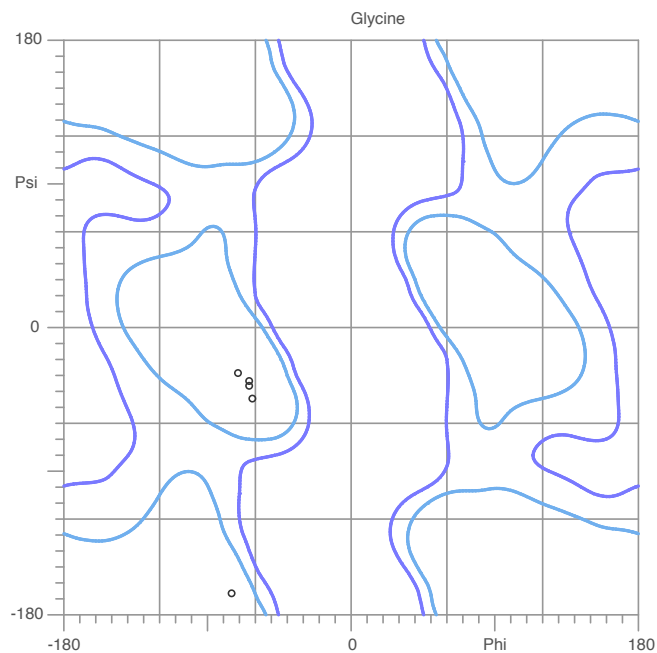
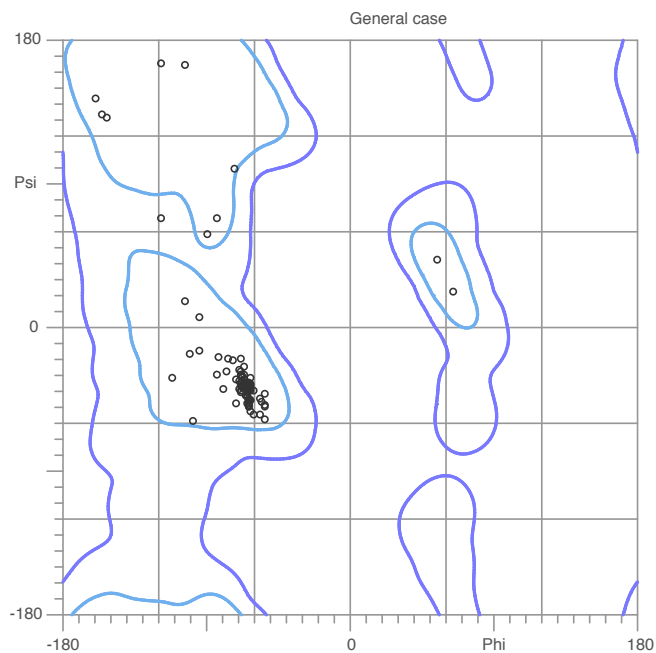
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 3



99.0% (96/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

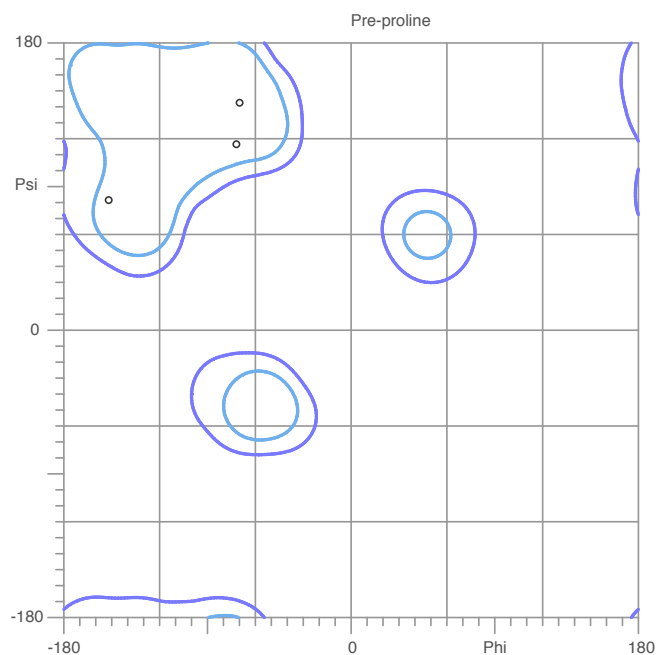
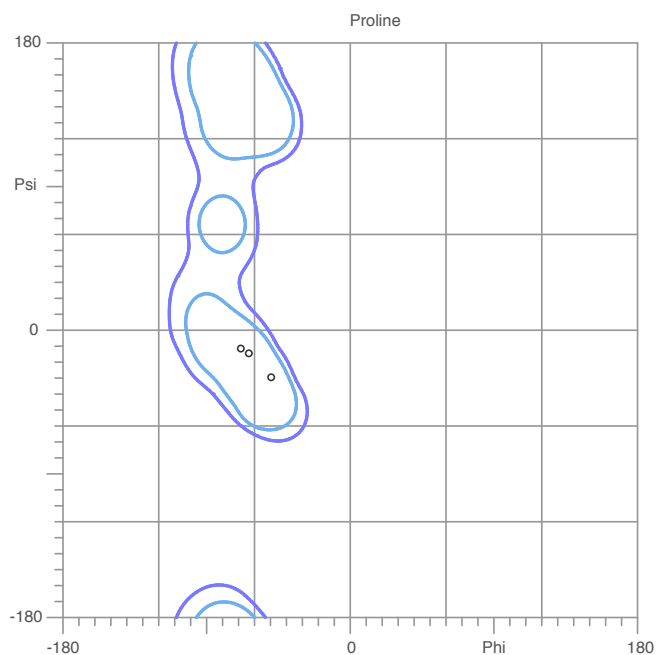
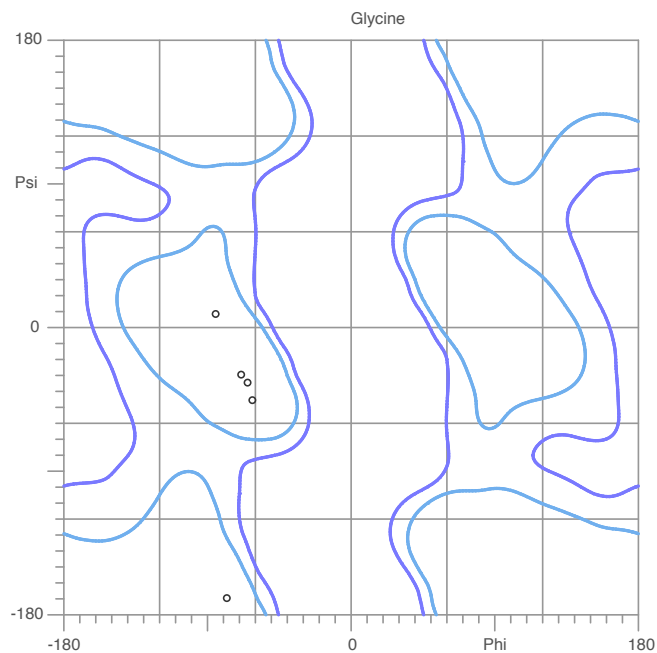
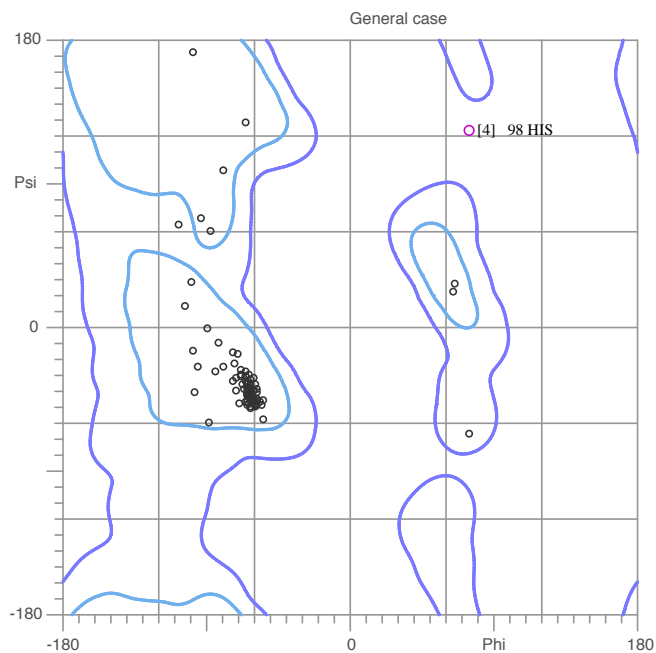
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 4



96.9% (94/97) of all residues were in favored (98%) regions.
99.0% (96/97) of all residues were in allowed (>99.8%) regions.

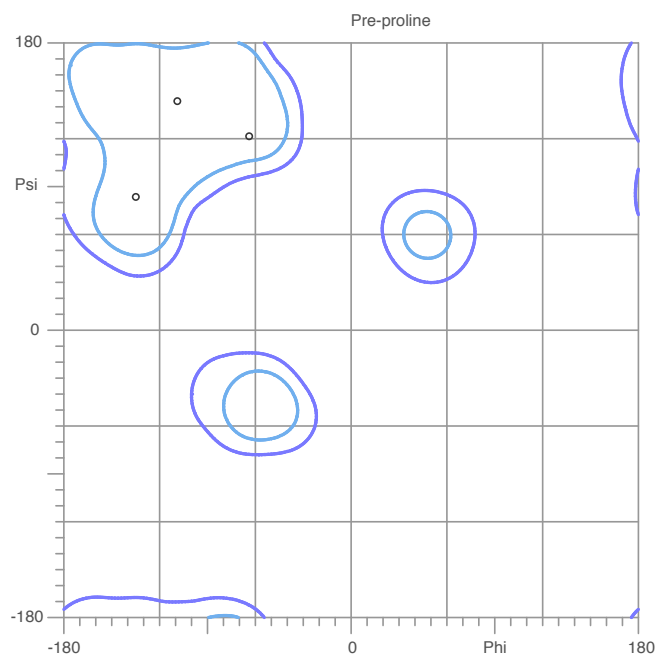
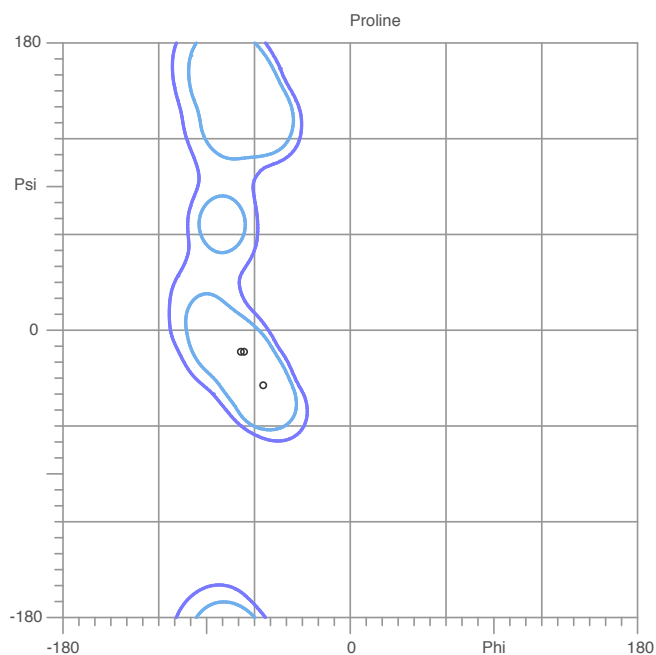
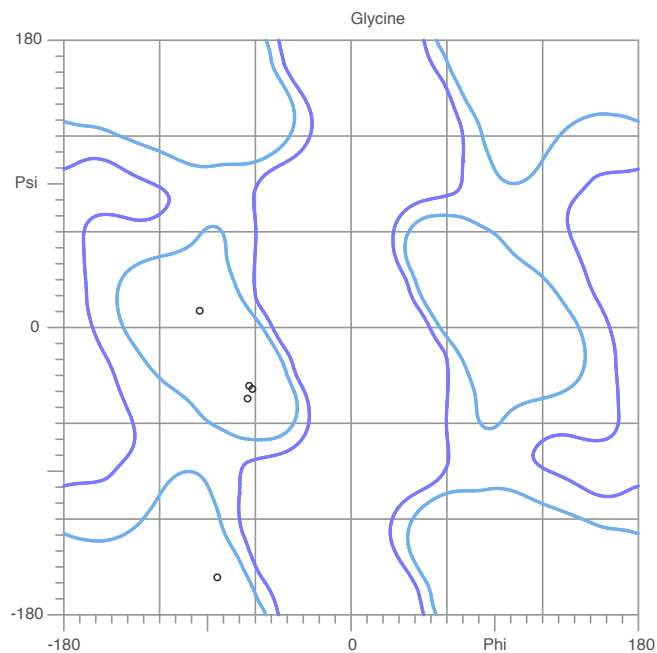
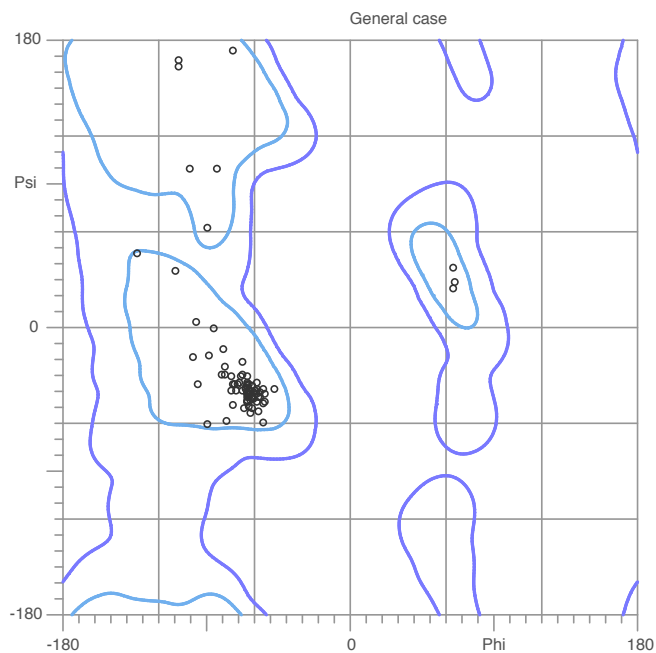
There were 1 outliers (phi, psi):
[4] 98 HIS (75.0, 124.9)

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

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 5



100.0% (97/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

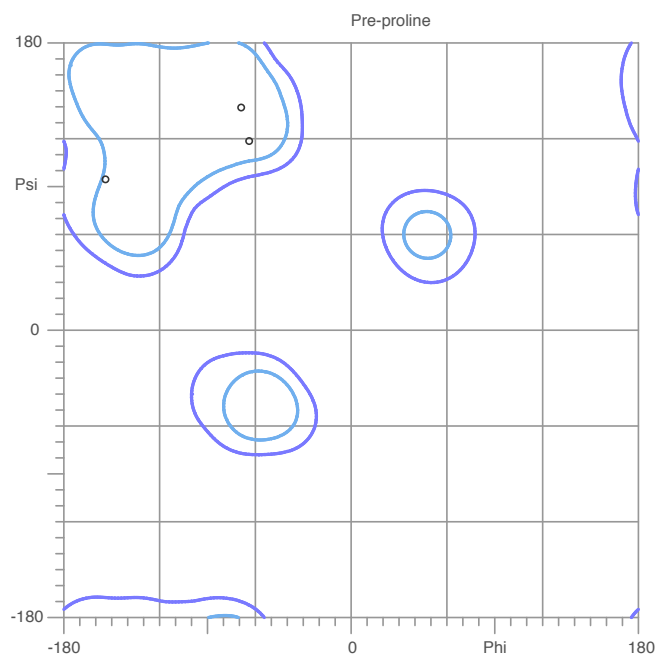
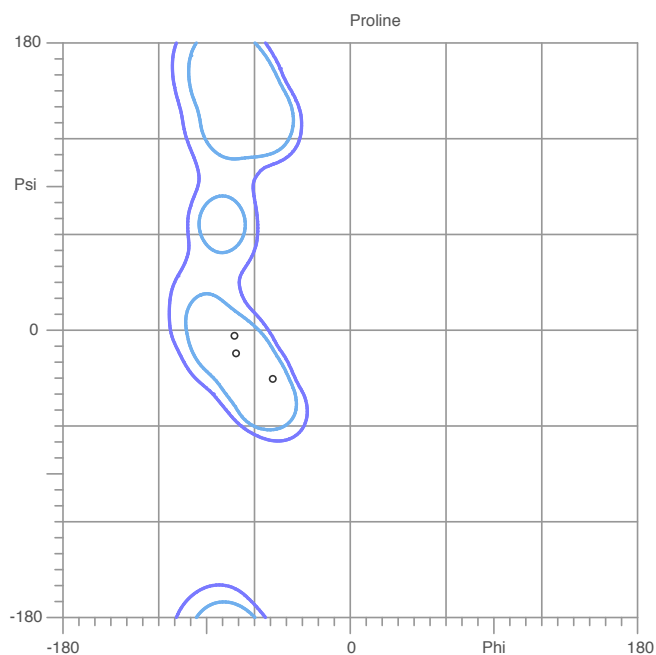
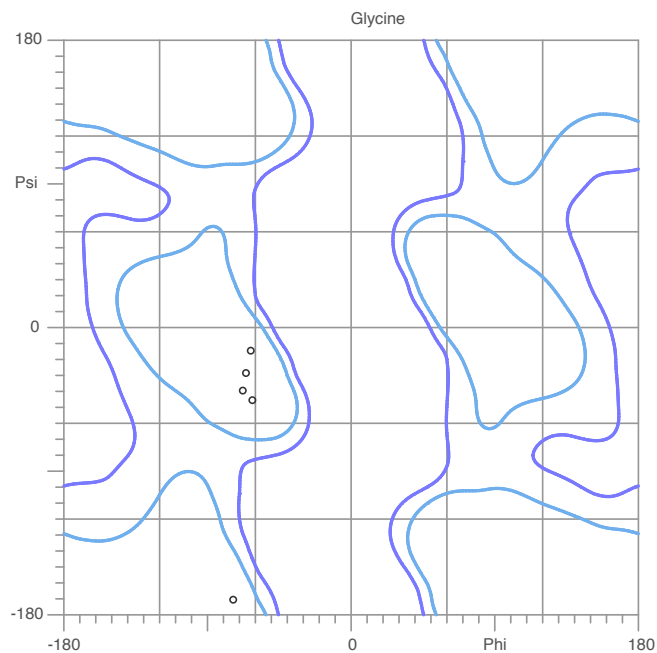
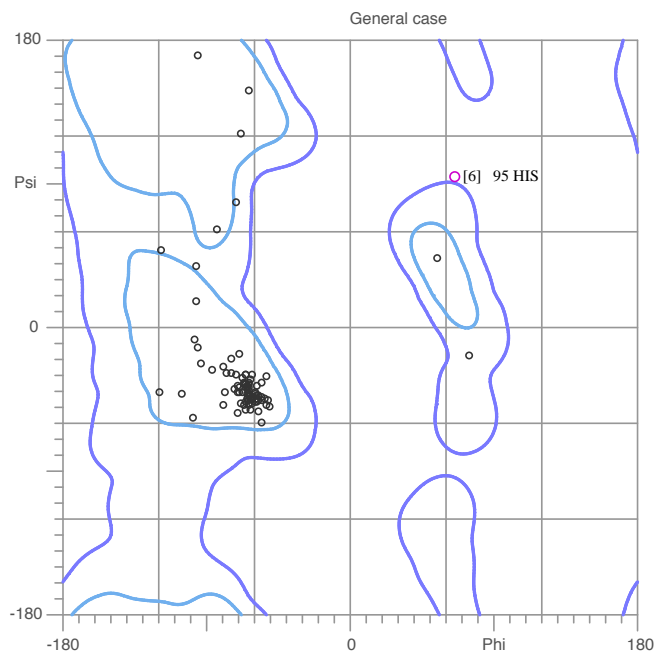
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 6

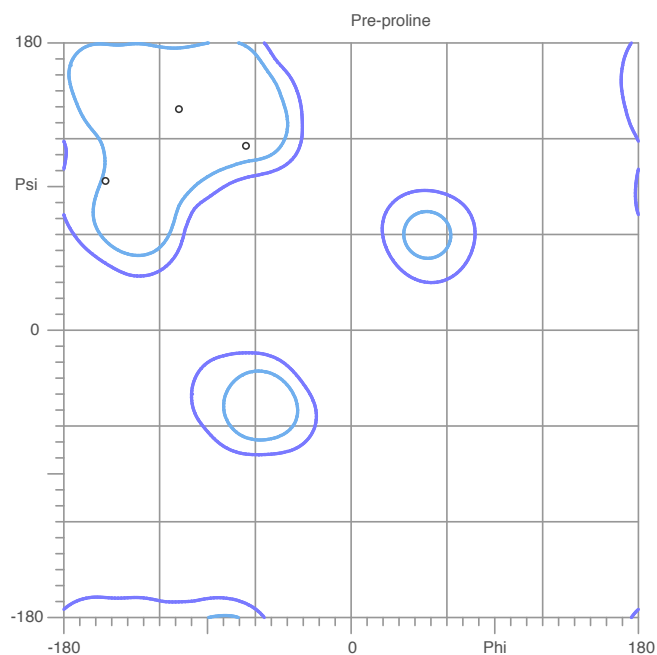
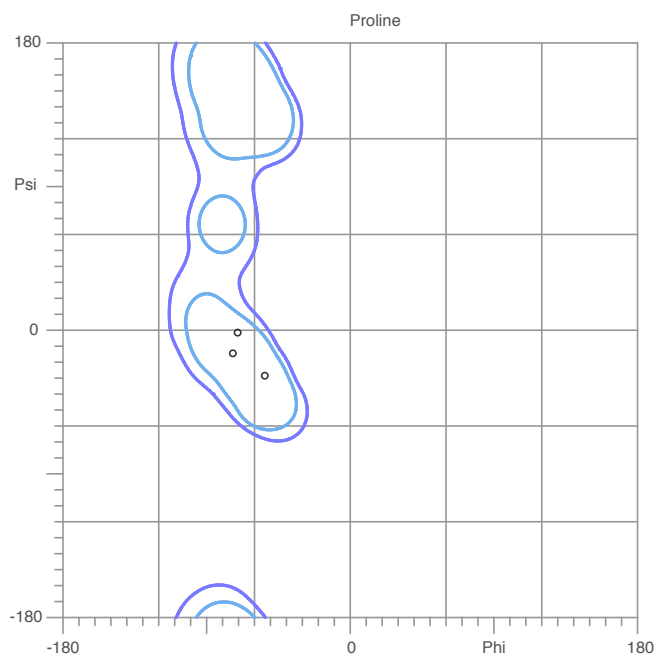
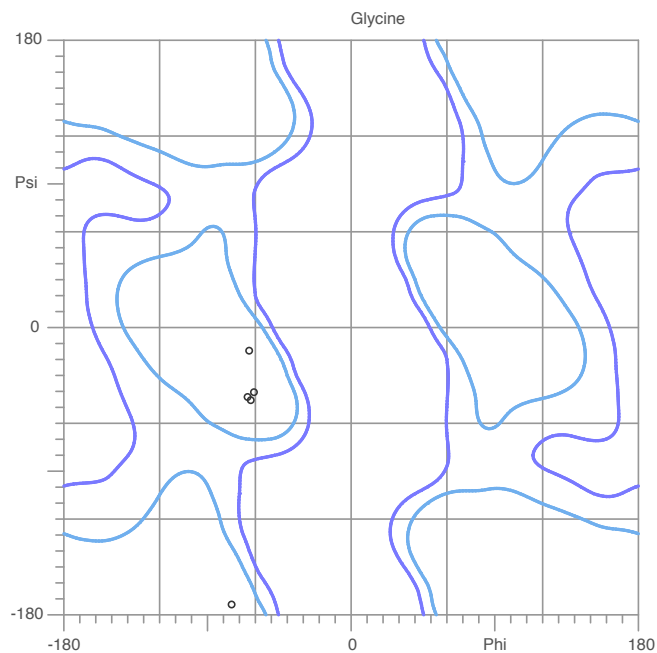
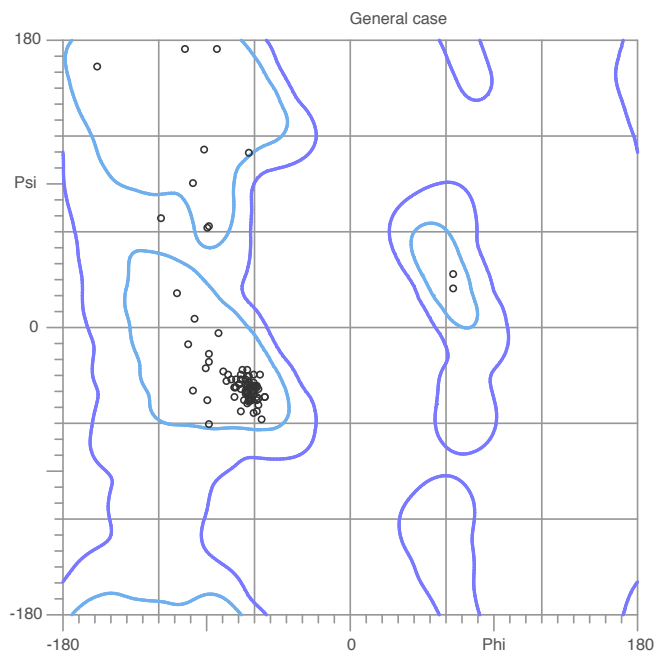


94.8% (92/97) of all residues were in favored (98%) regions.
99.0% (96/97) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[6] 95 HIS (65.1, 95.1)

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 7



99.0% (96/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

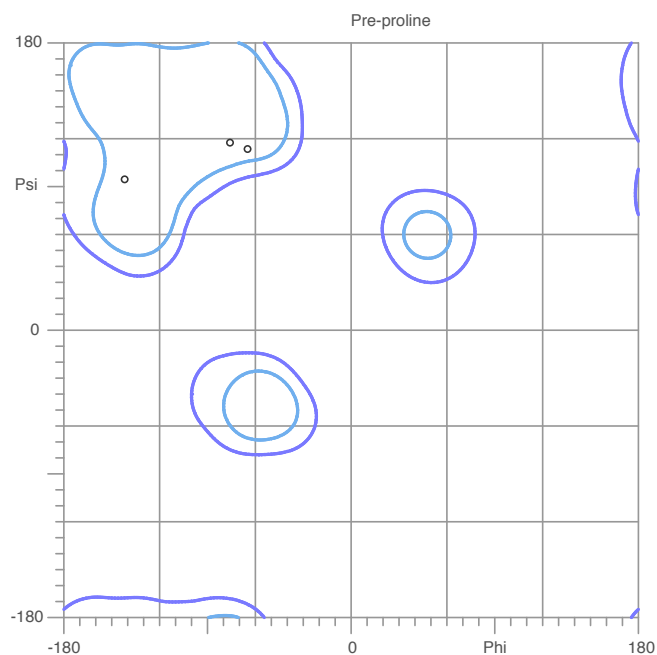
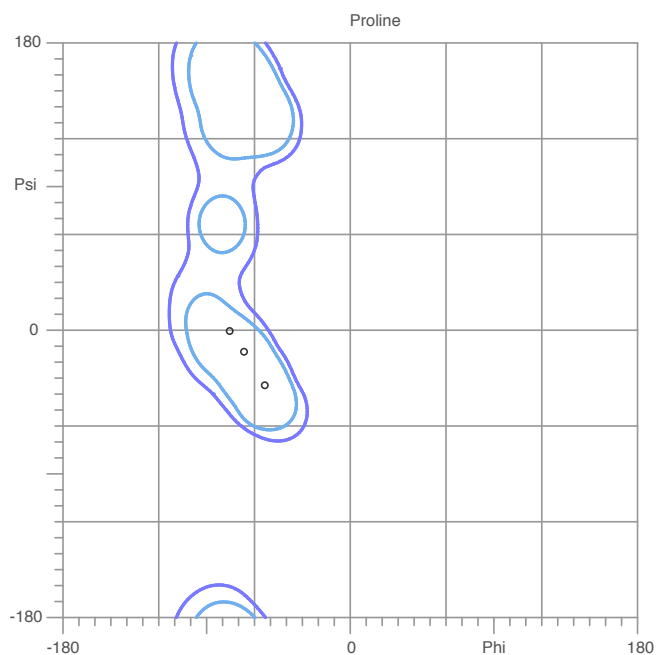
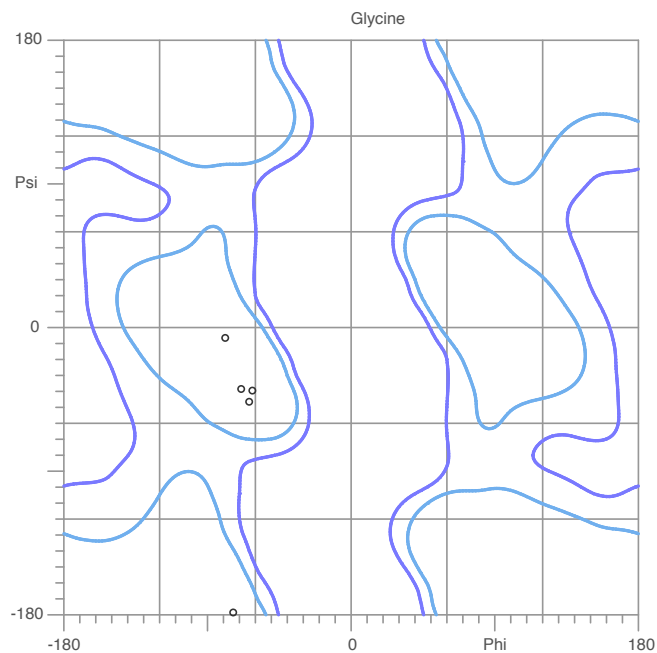
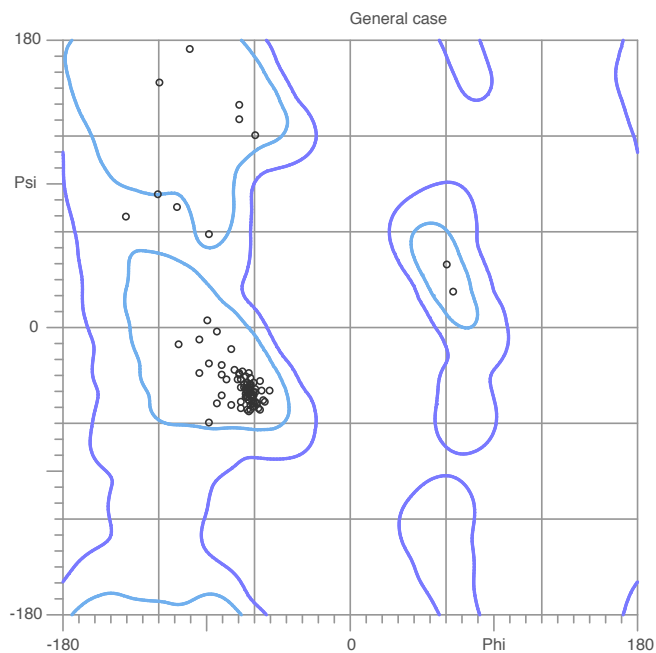
There were no outliers.

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 8



97.9% (95/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

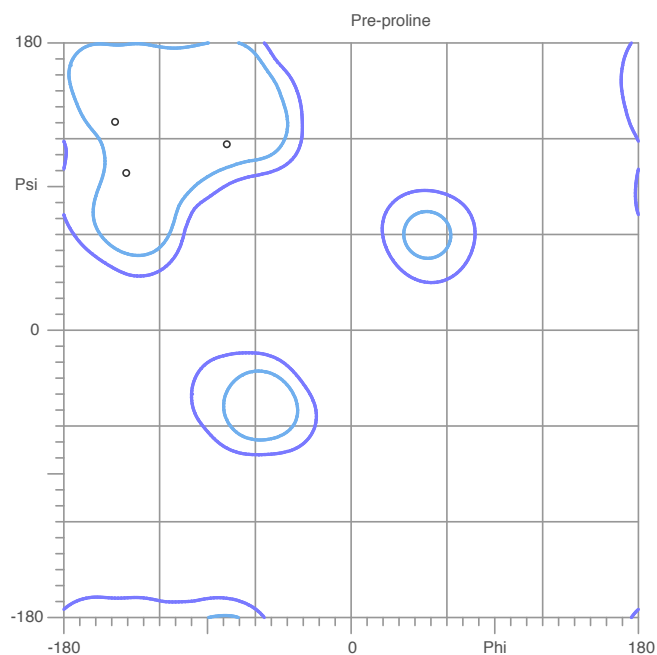
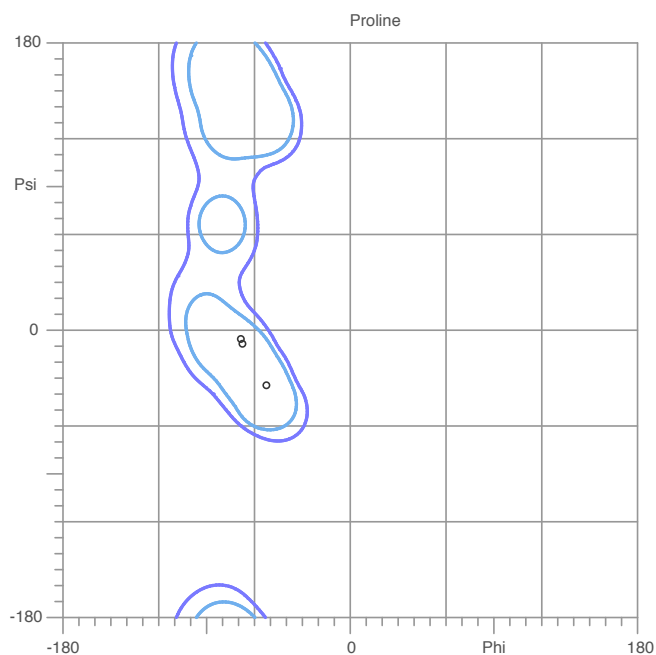
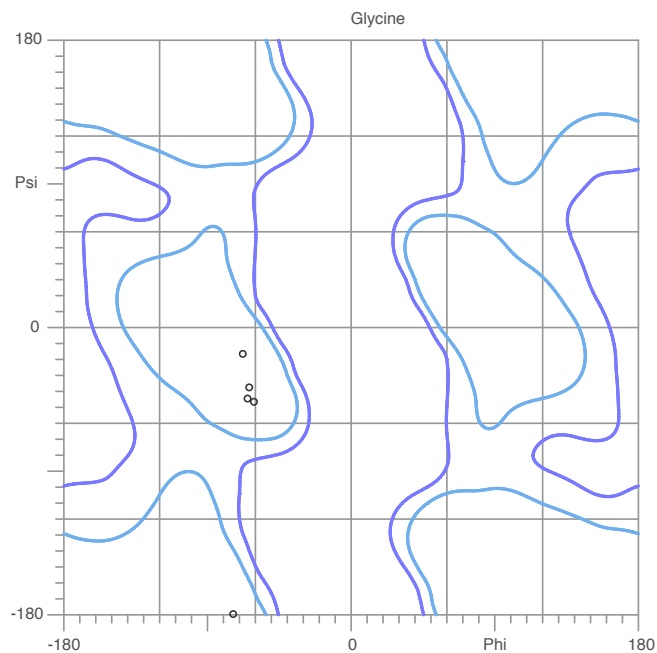
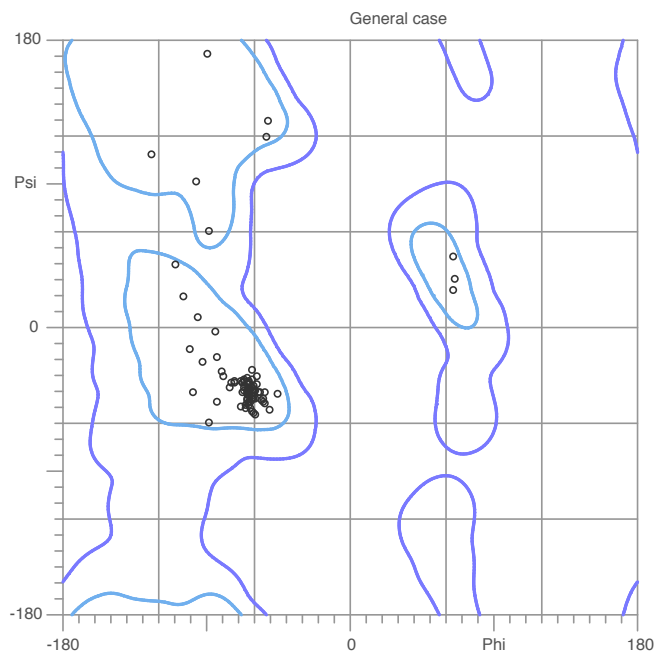
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 9



100.0% (97/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

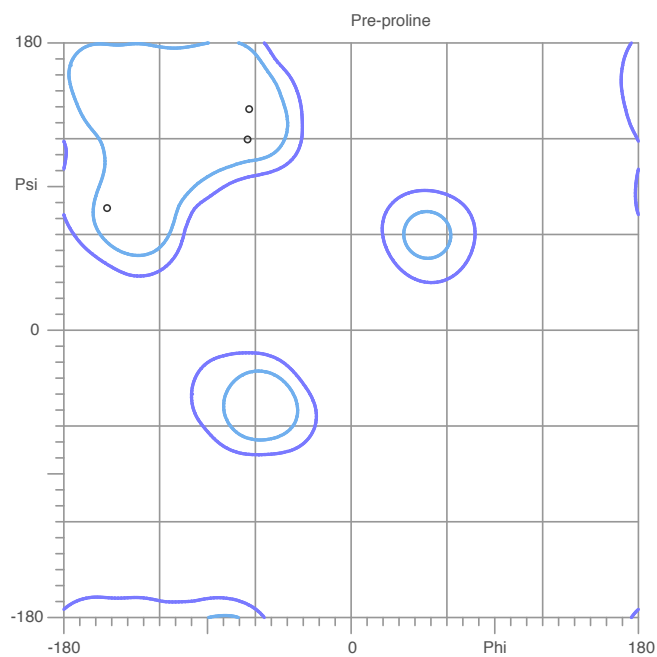
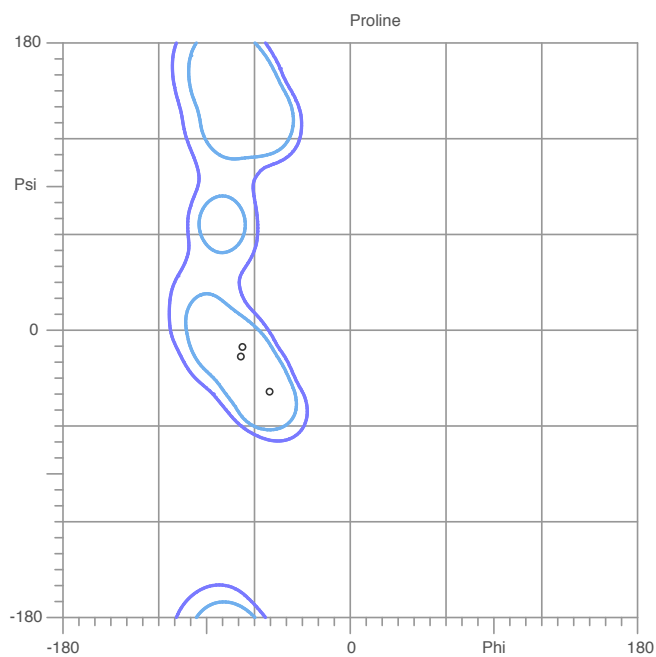
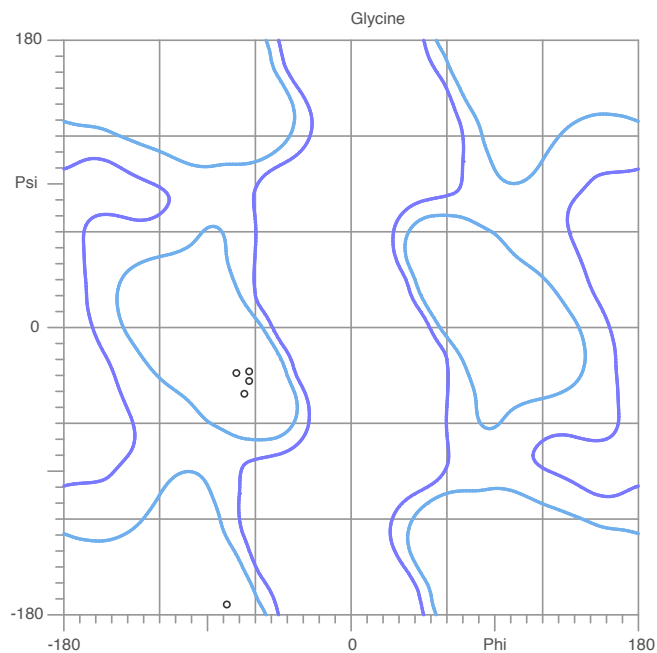
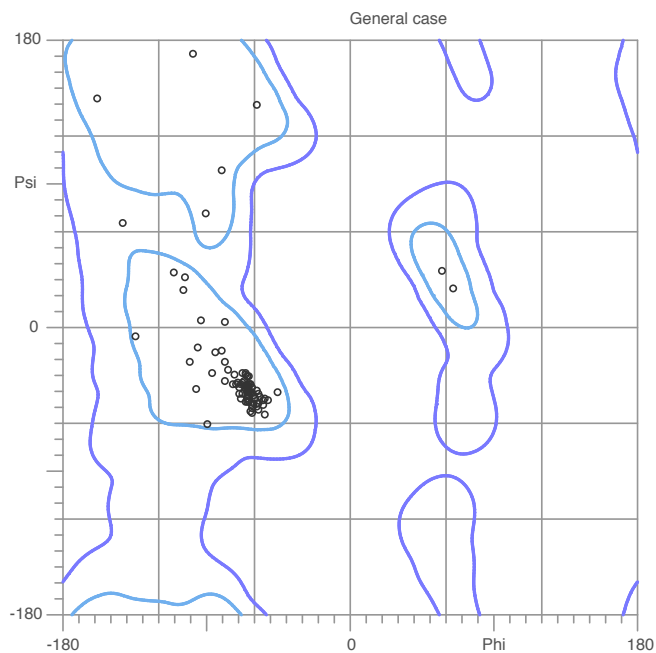
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 10



99.0% (96/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

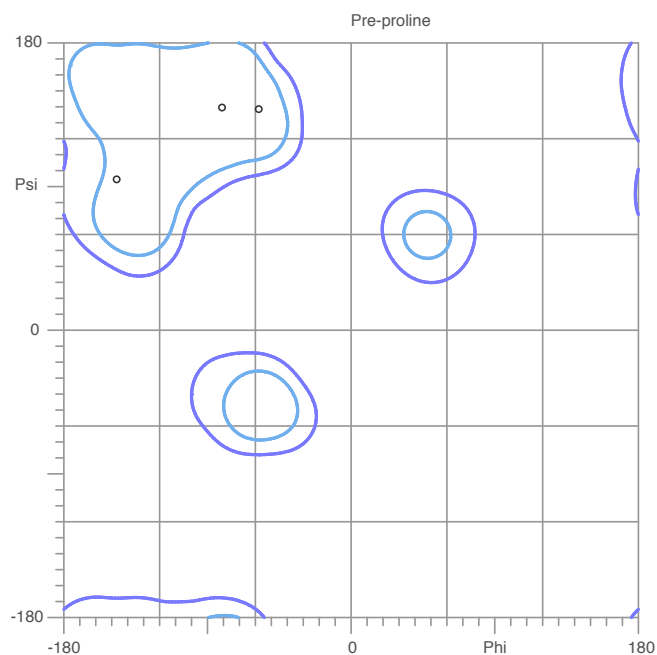
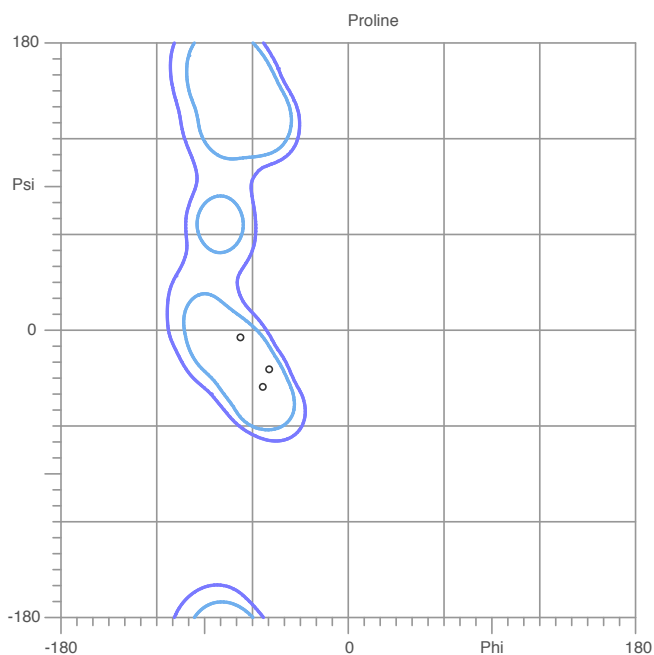
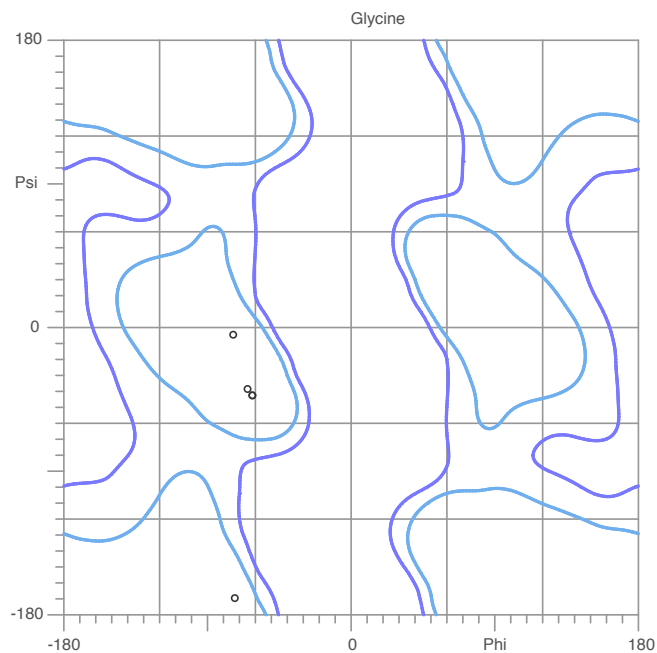
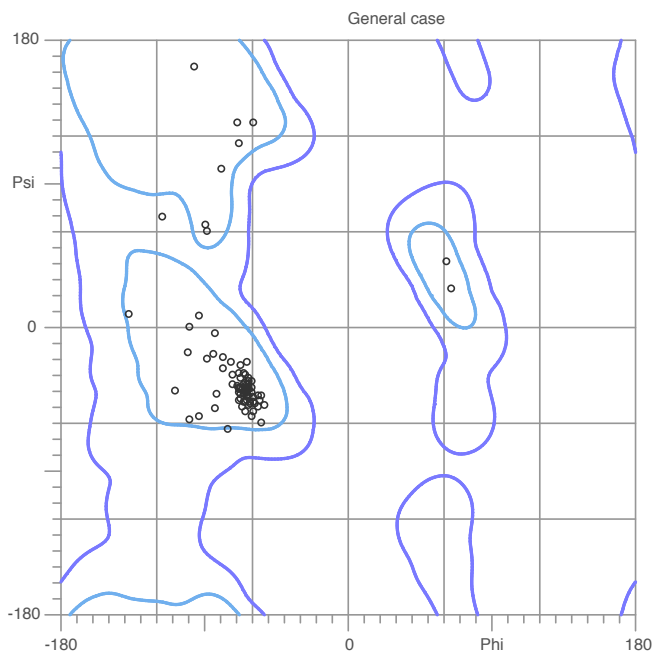
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 11



97.9% (95/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

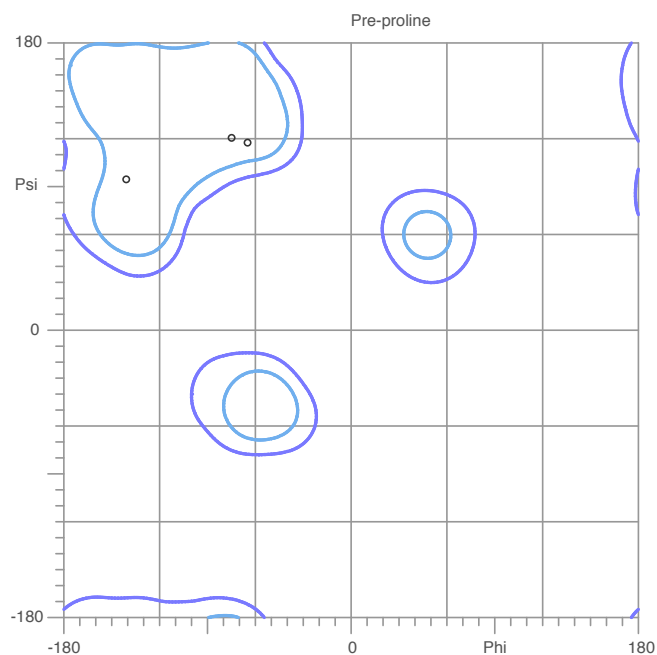
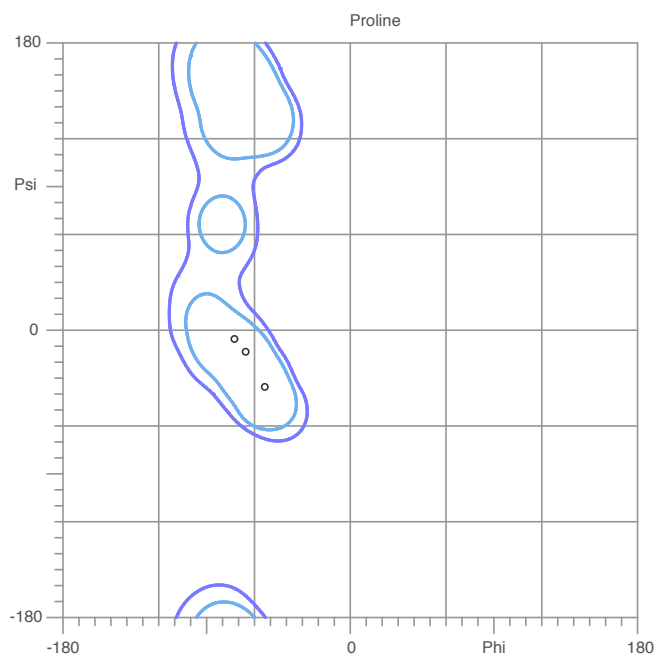
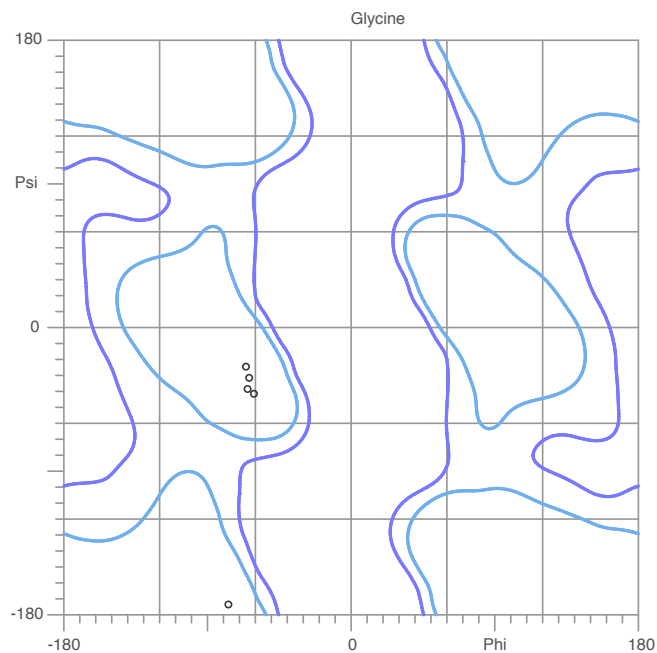
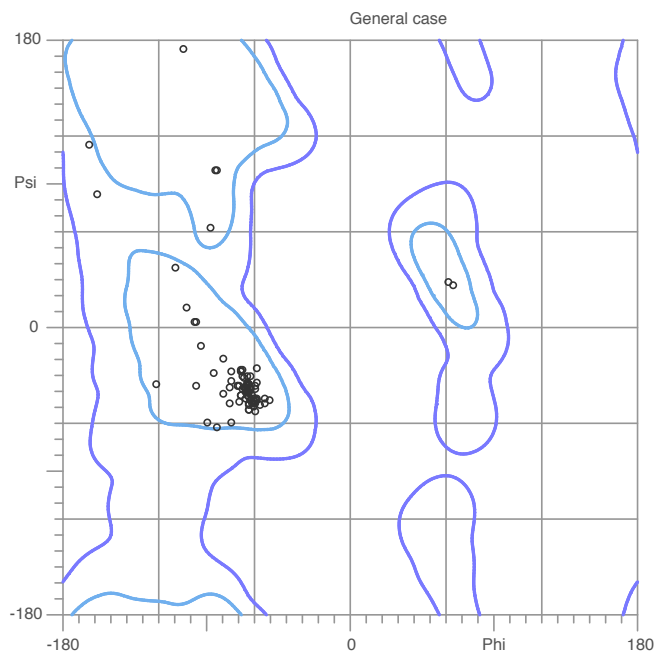
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 12



97.9% (95/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

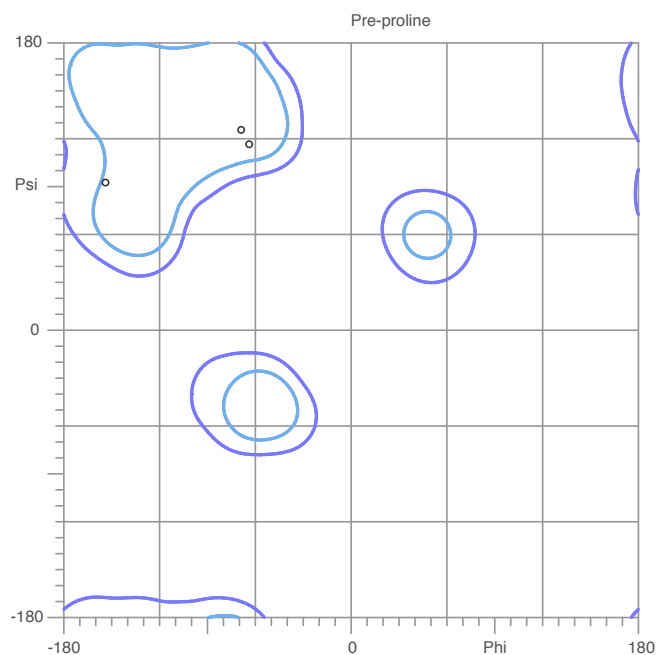
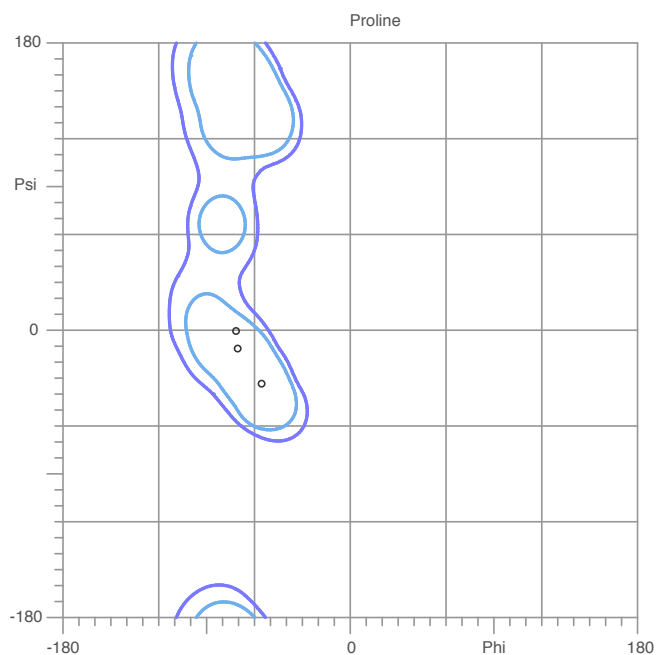
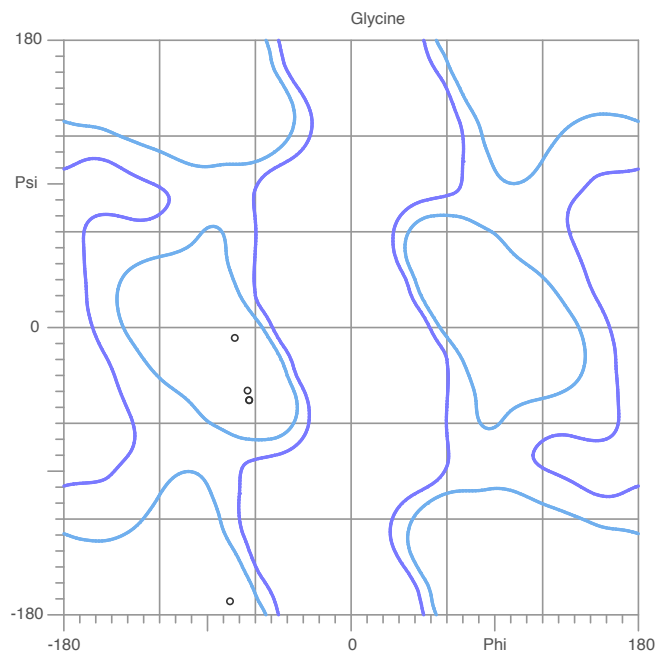
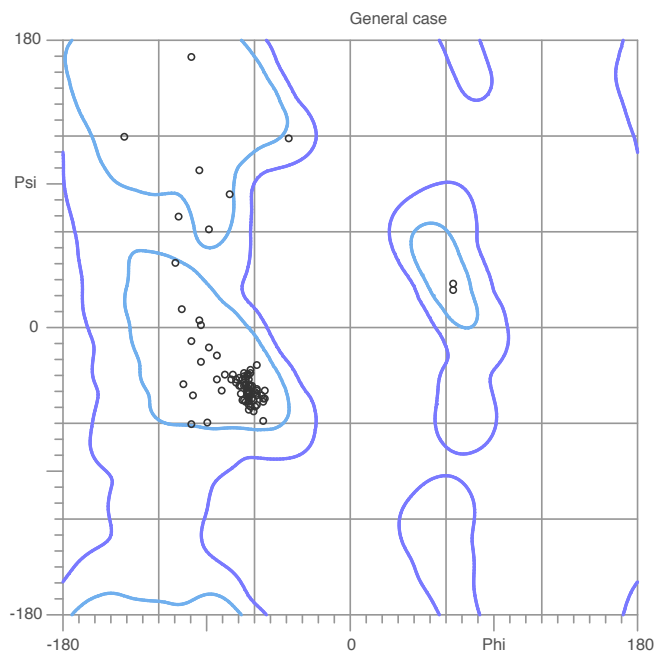
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 13



97.9% (95/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

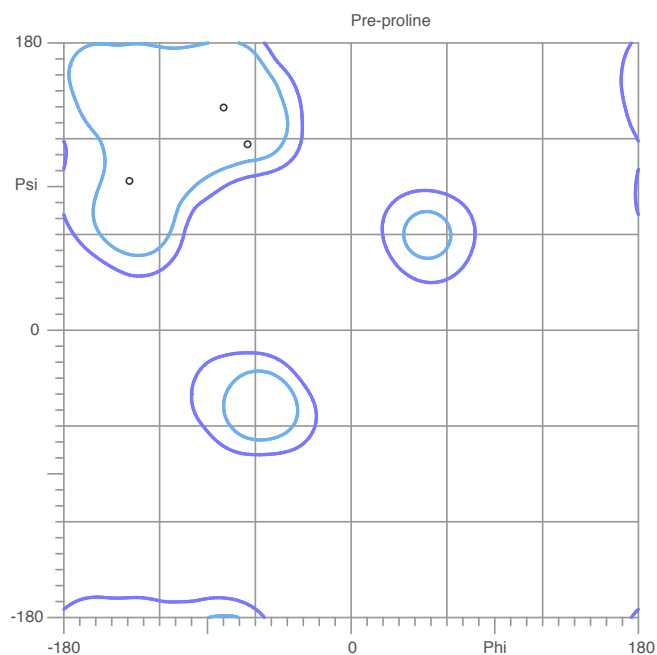
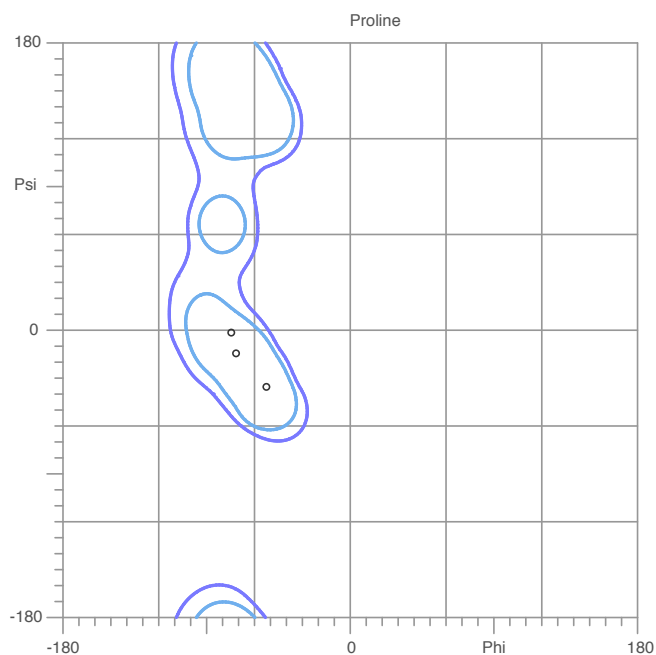
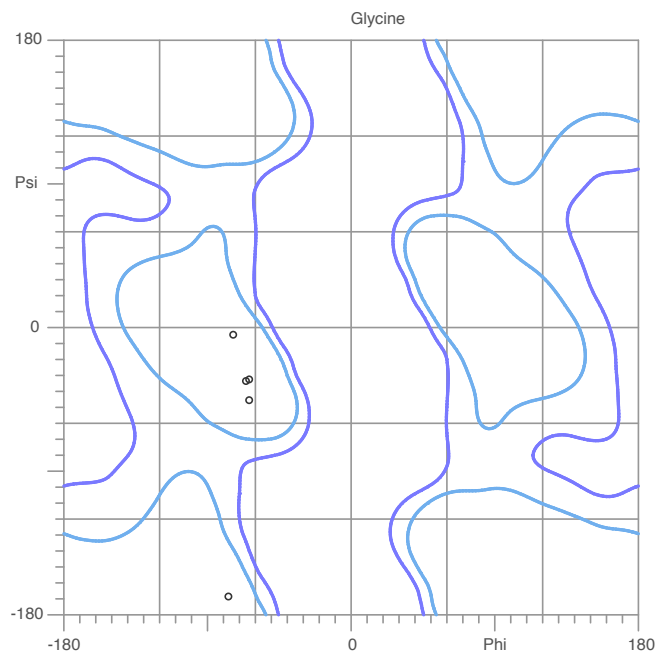
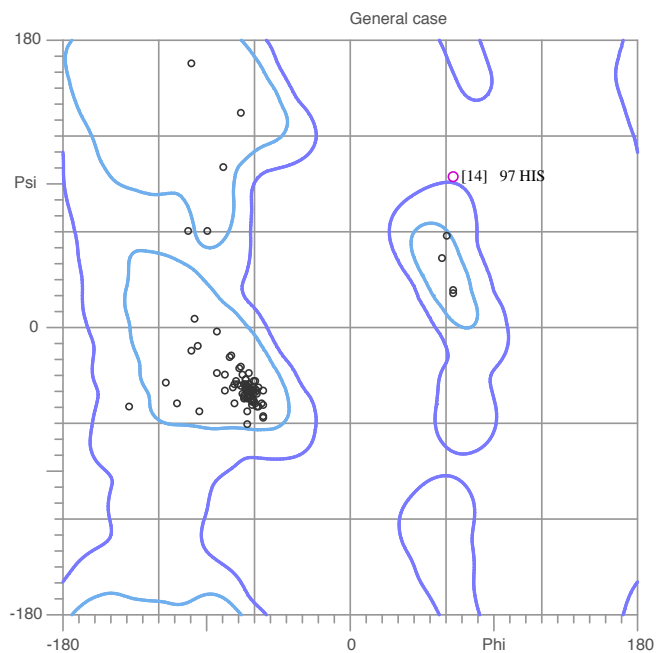
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 14



96.9% (94/97) of all residues were in favored (98%) regions.
99.0% (96/97) of all residues were in allowed (>99.8%) regions.

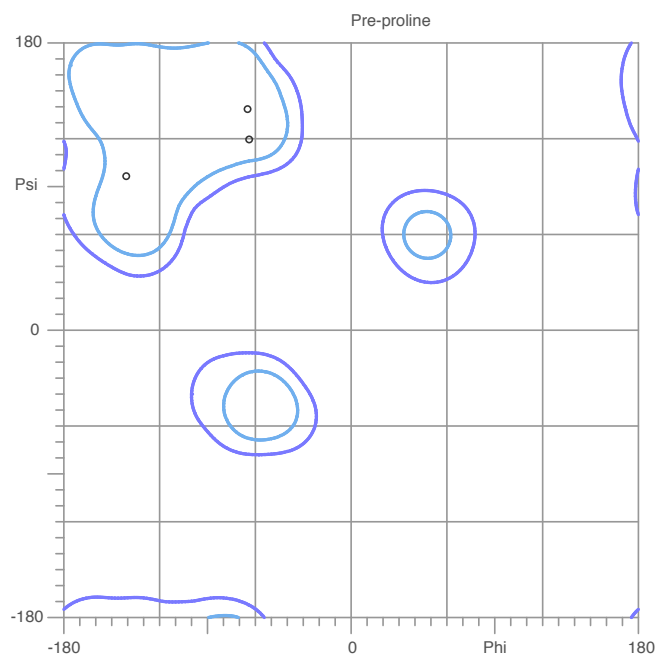
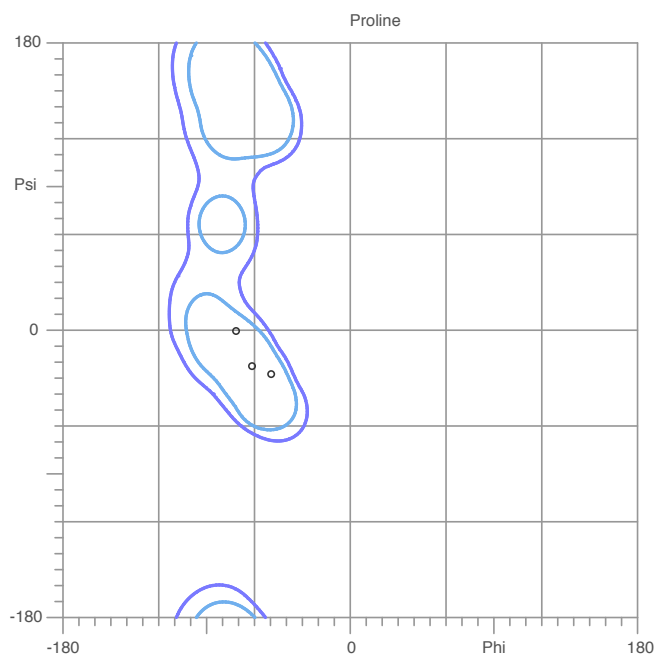
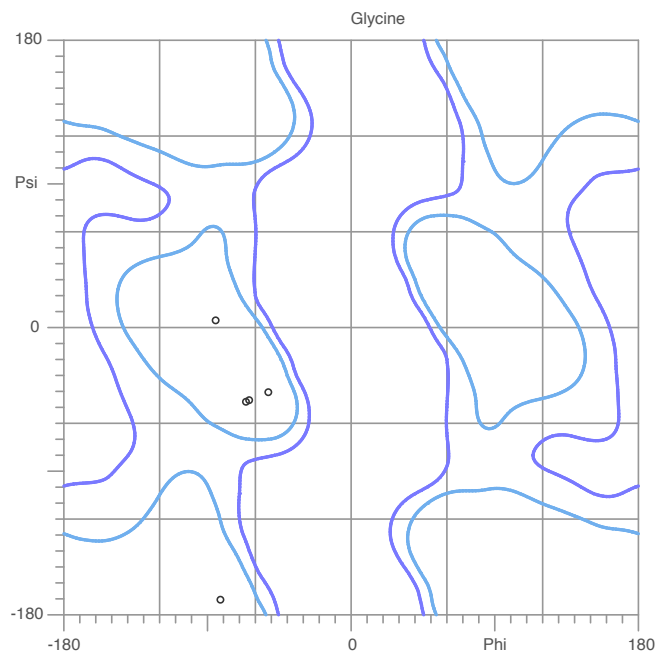
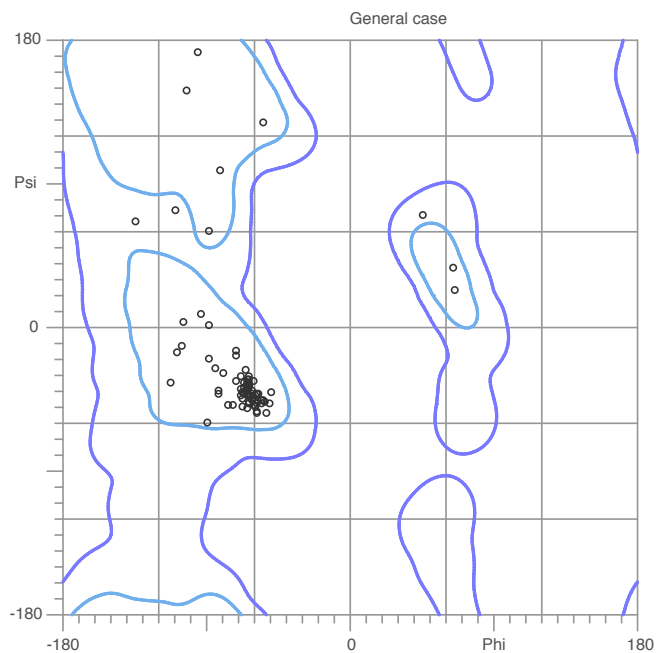
There were 1 outliers (phi, psi):
[14] 97 HIS (65.0, 95.0)

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

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

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 15



96.9% (94/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

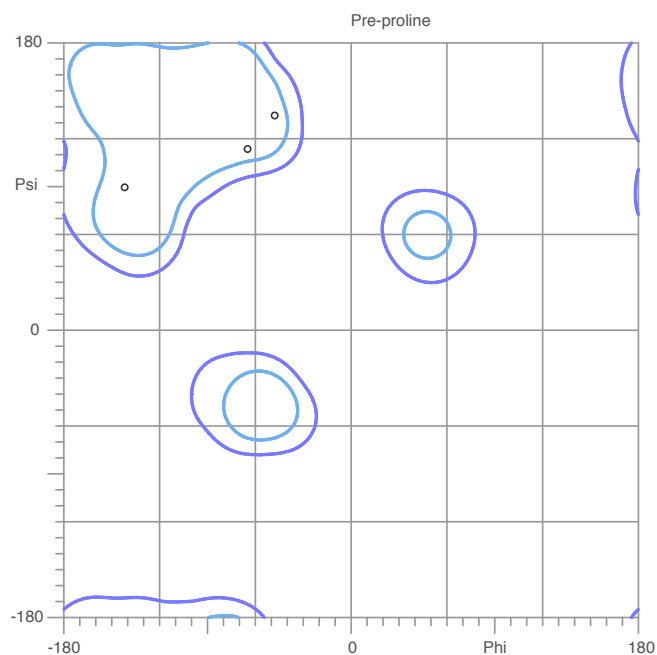
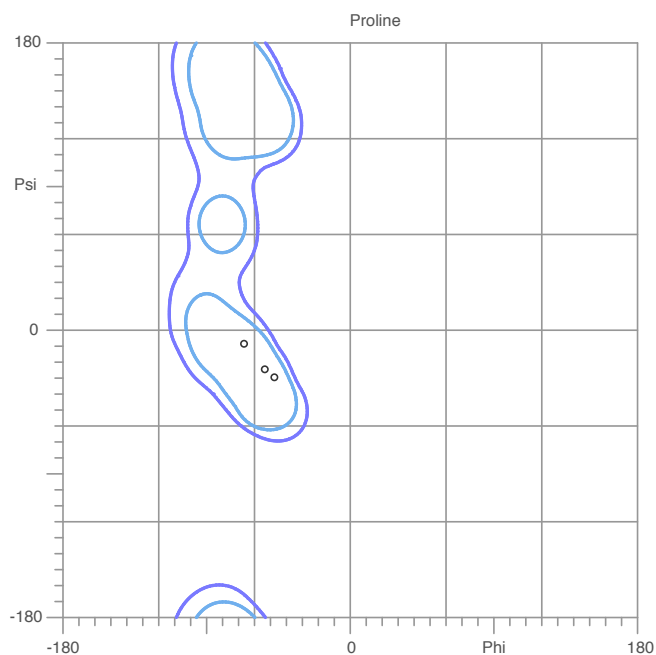
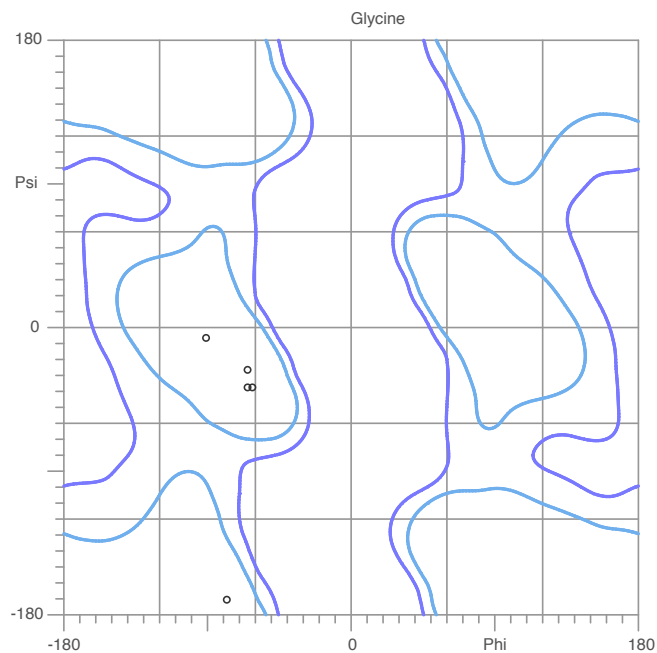
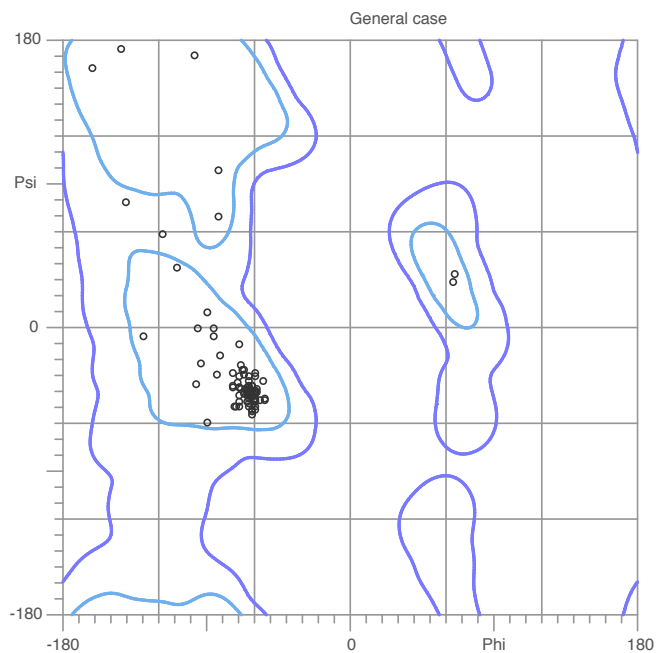
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 16

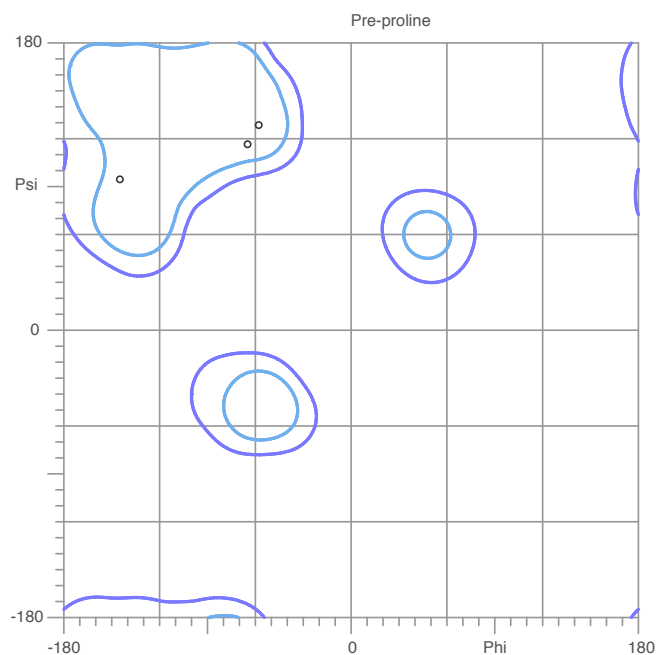
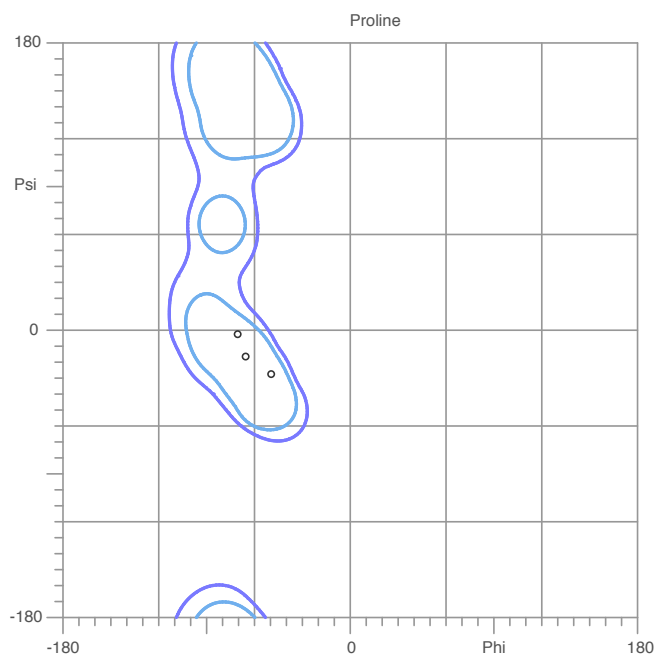
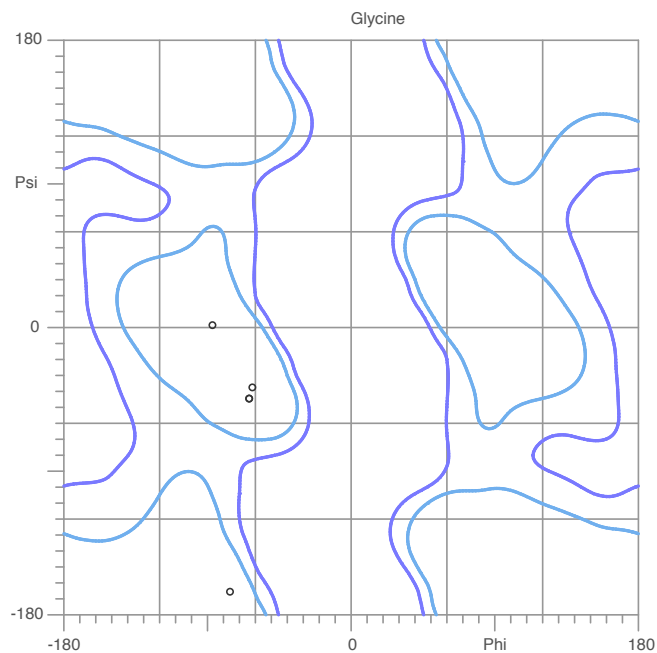
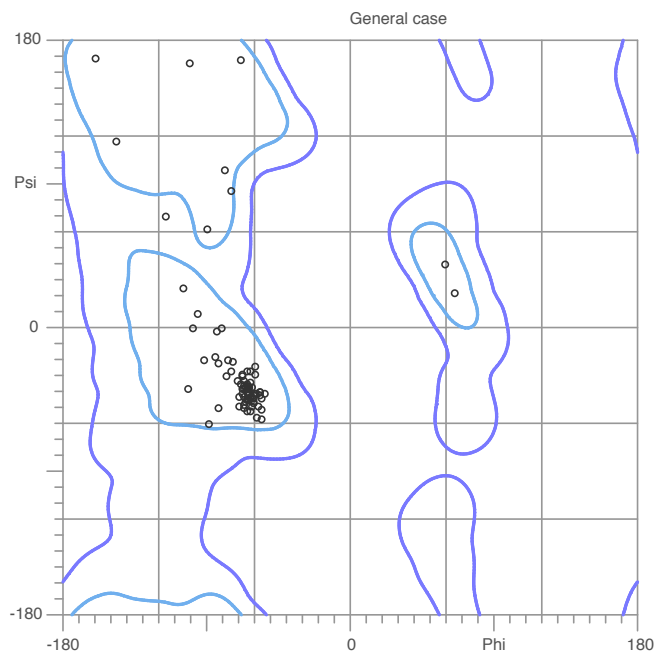


97.9% (95/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 17



99.0% (96/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

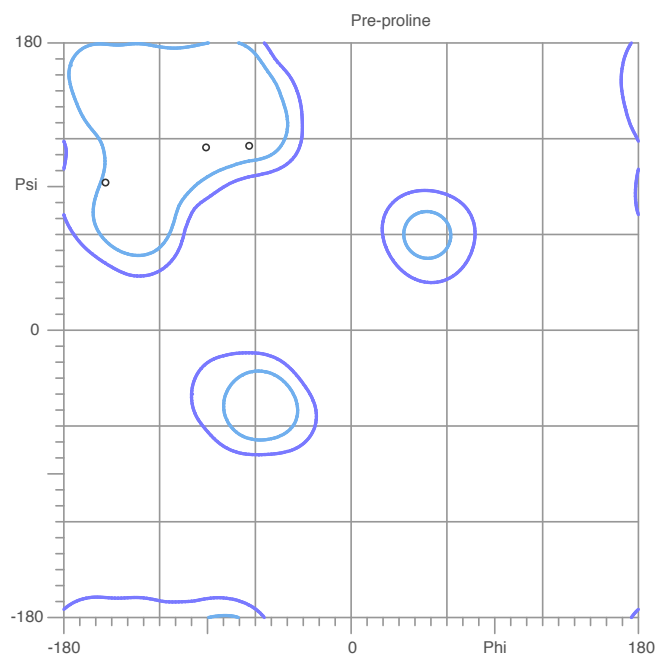
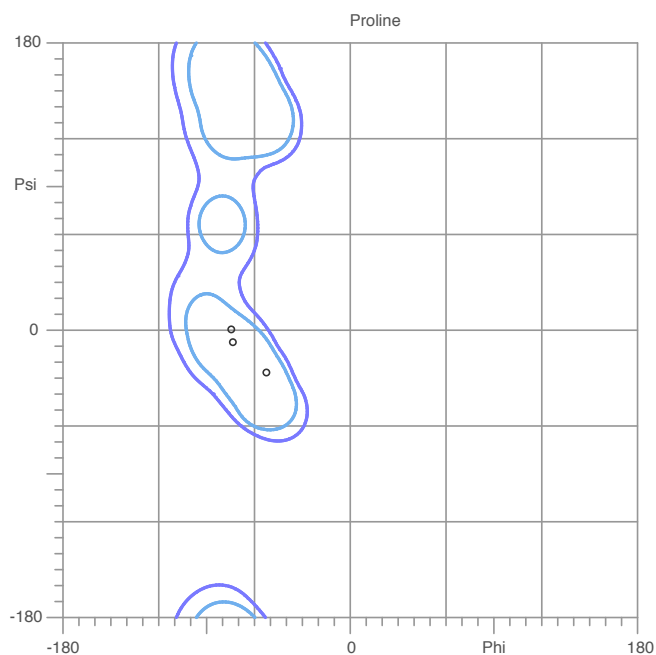
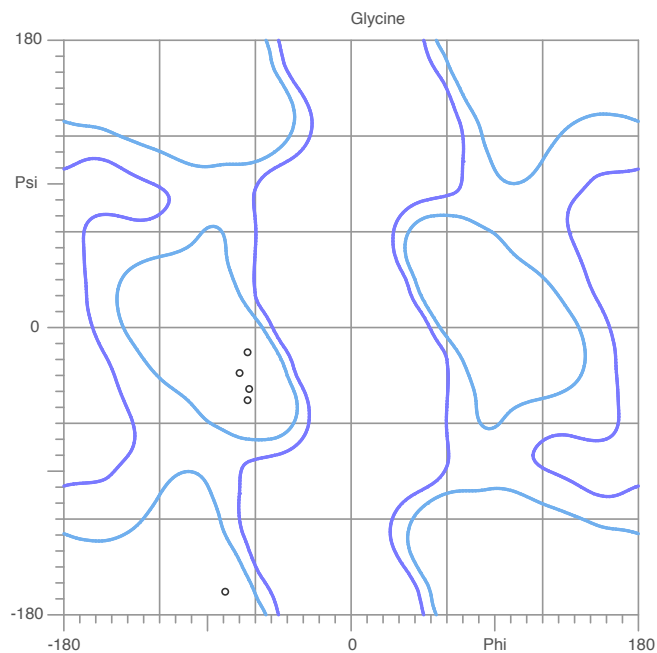
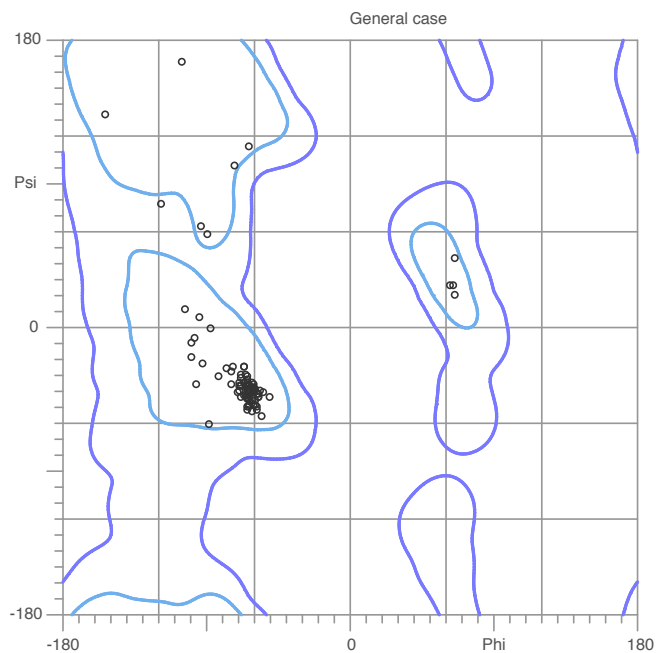
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 18



99.0% (96/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

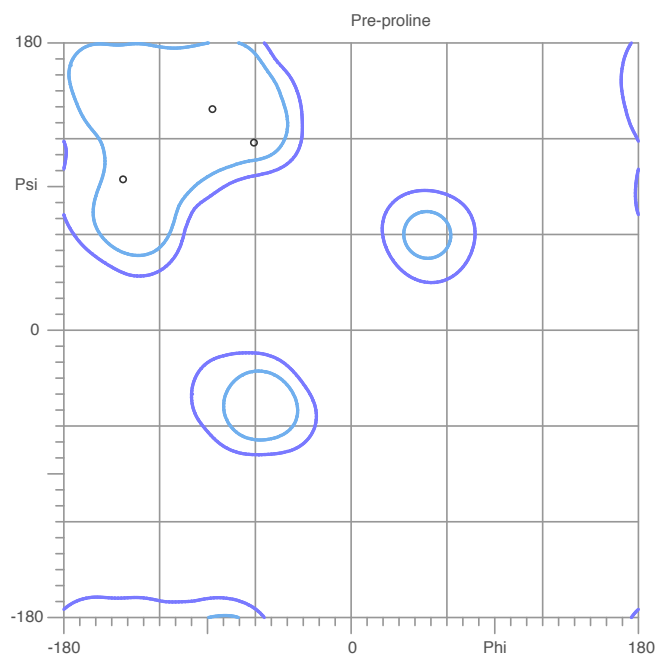
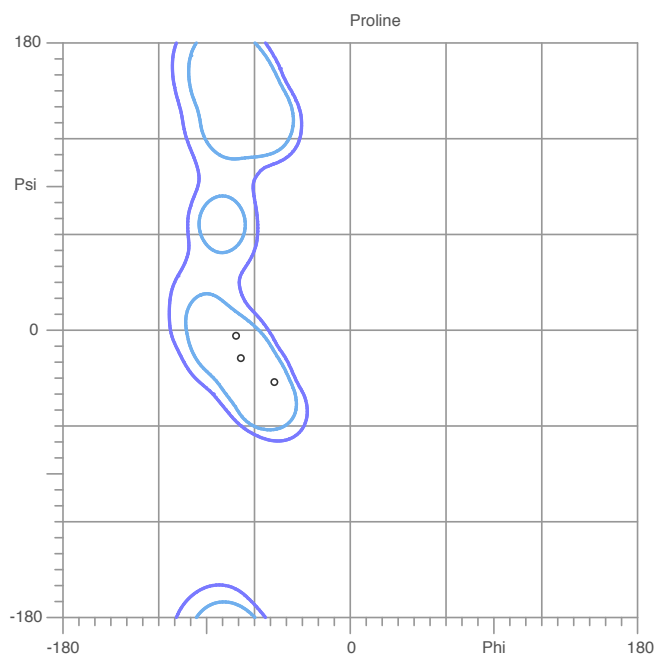
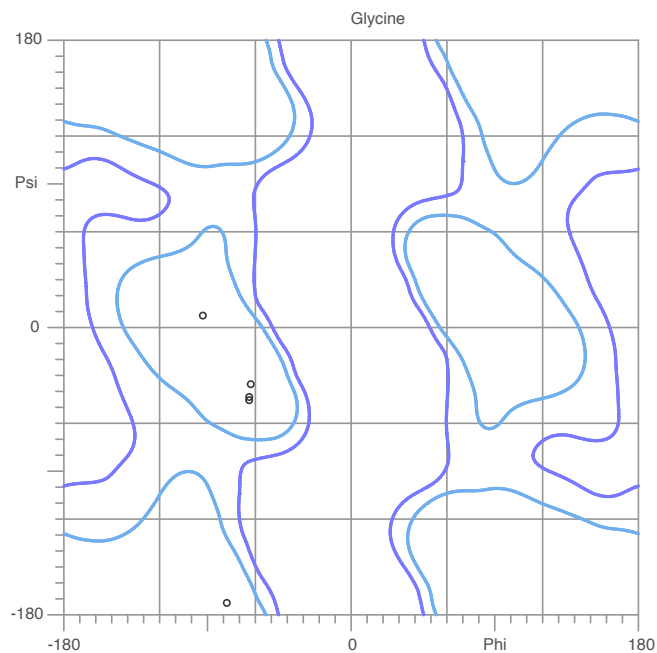
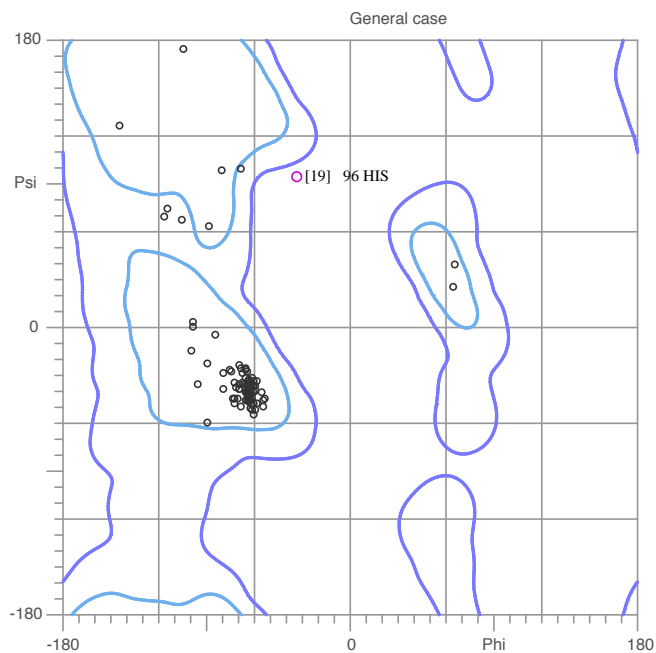
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 19



94.8% (92/97) of all residues were in favored (98%) regions.
99.0% (96/97) of all residues were in allowed (>99.8%) regions.

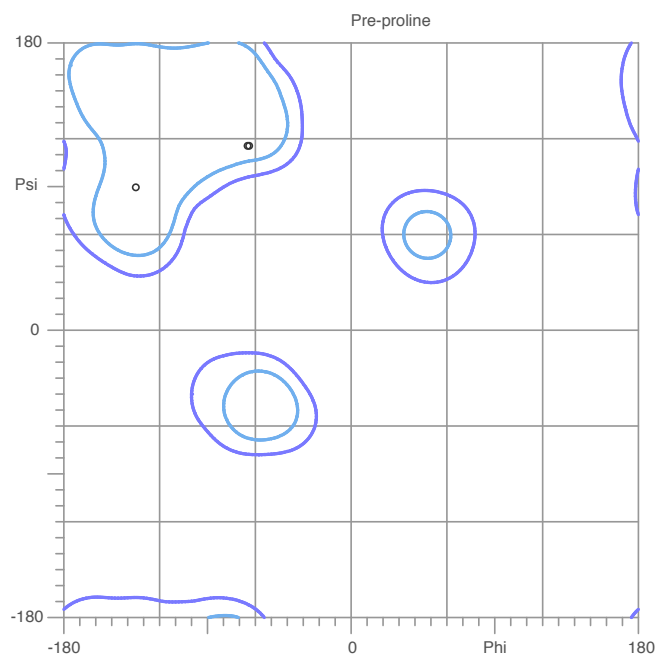
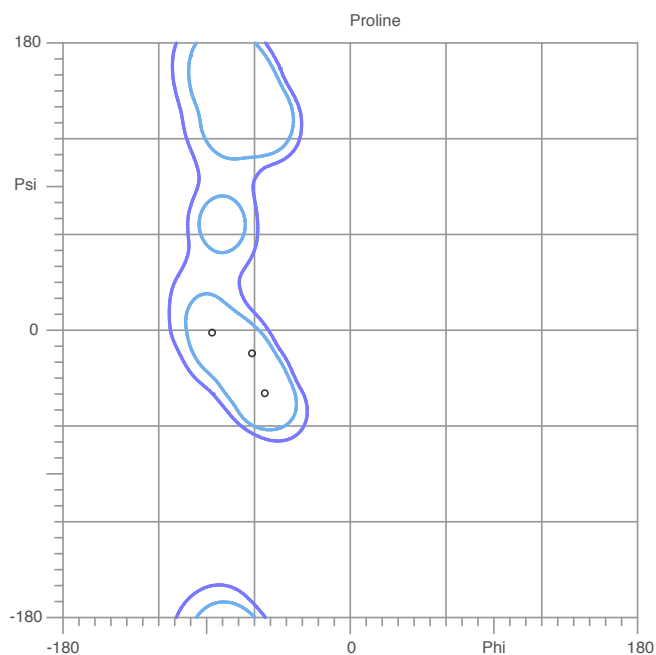
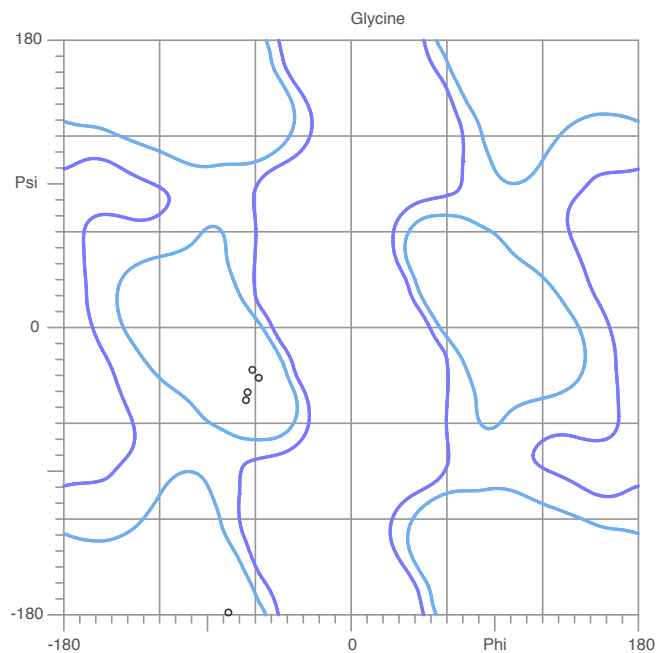
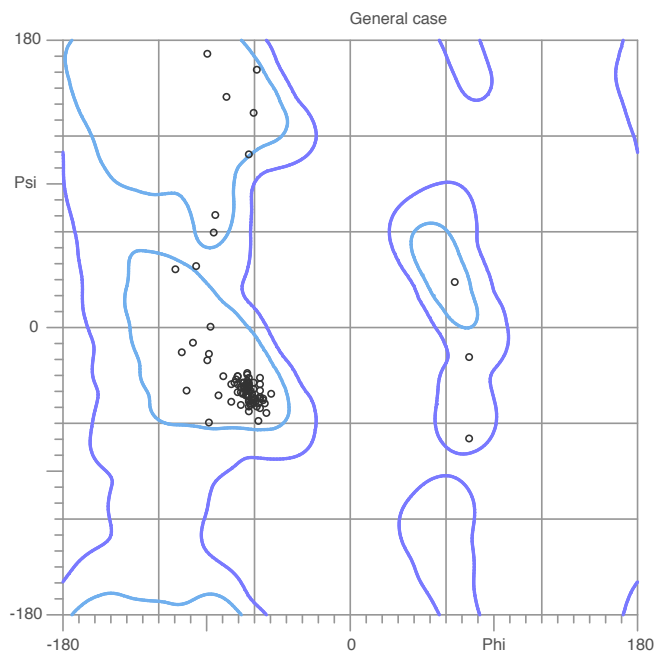
There were 1 outliers (phi, psi):
[19] 96 HIS (-34.8, 95.0)

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MolProbity Ramachandran analysis

SRR115C_R3_em_bcr3.pdb, model 20



96.9% (94/97) of all residues were in favored (98%) regions.
100.0% (97/97) 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)