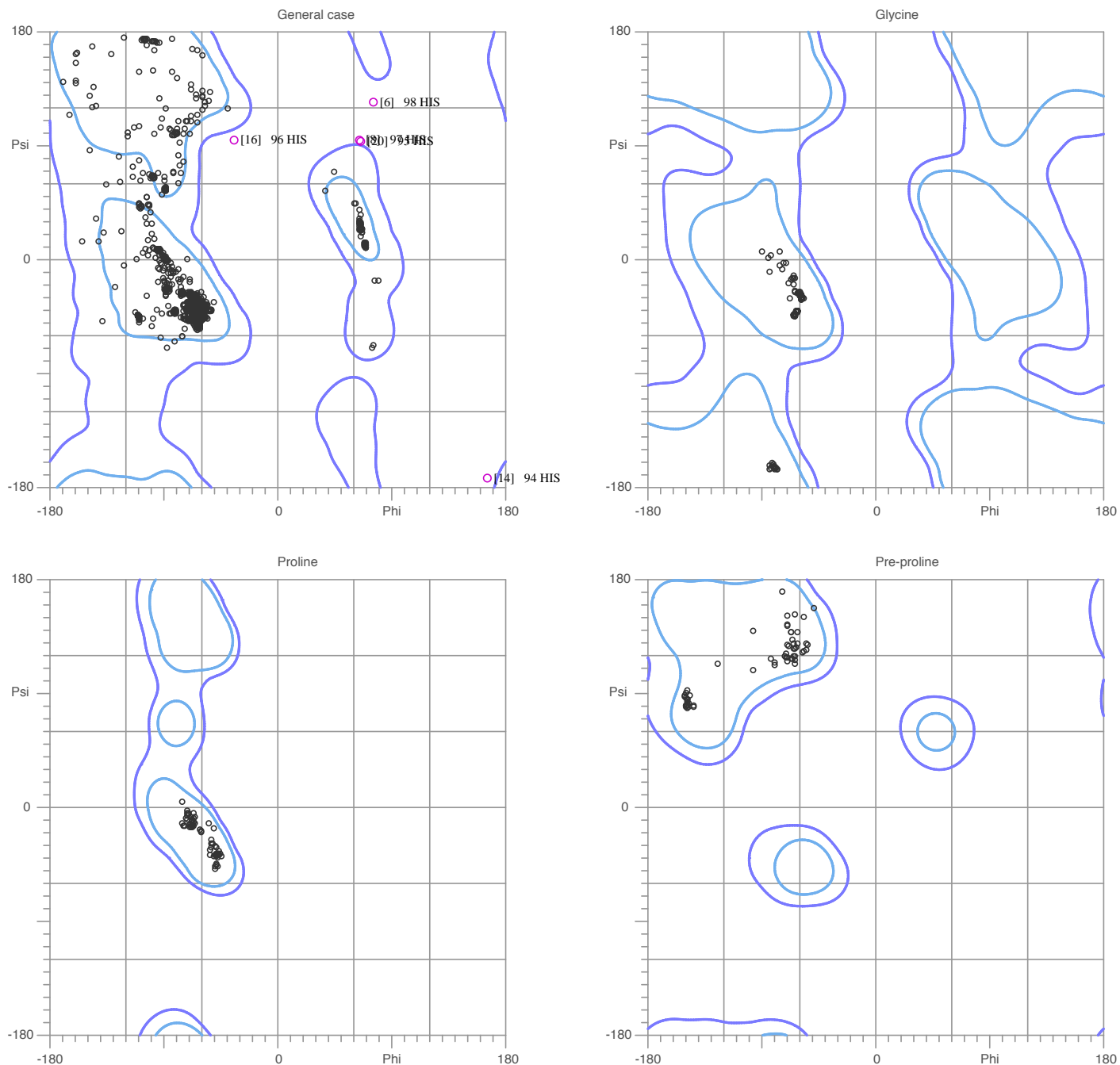


MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, all models



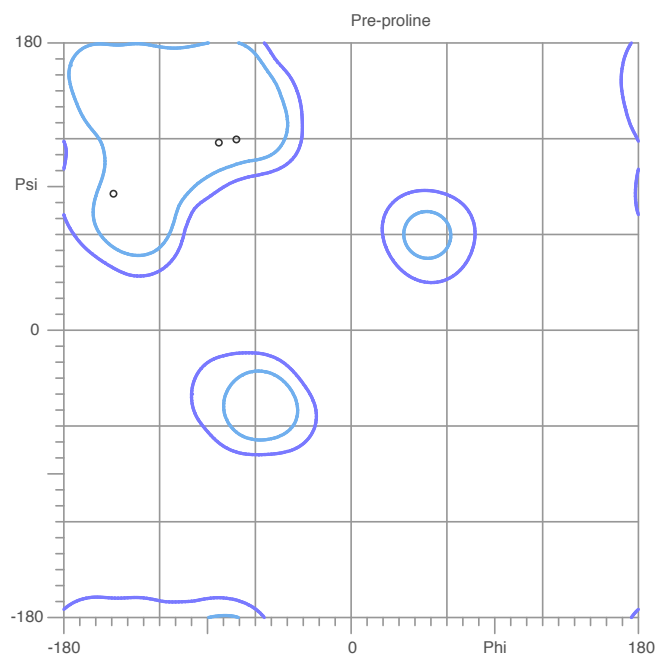
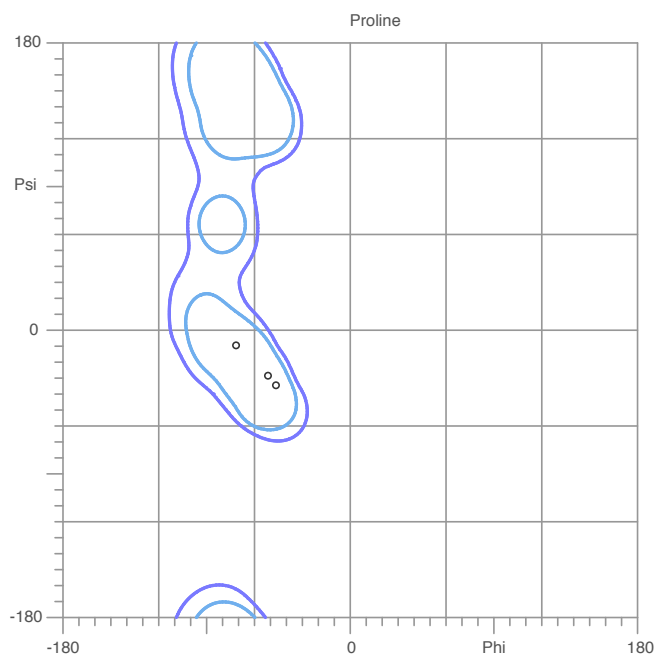
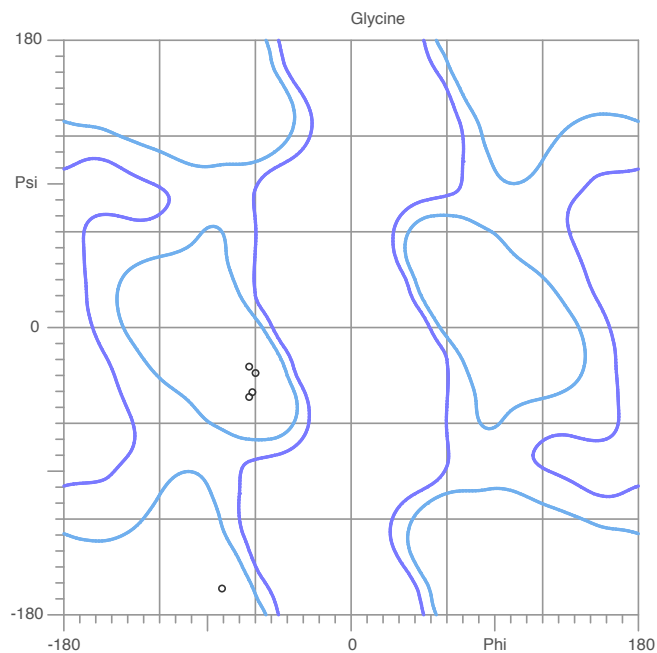
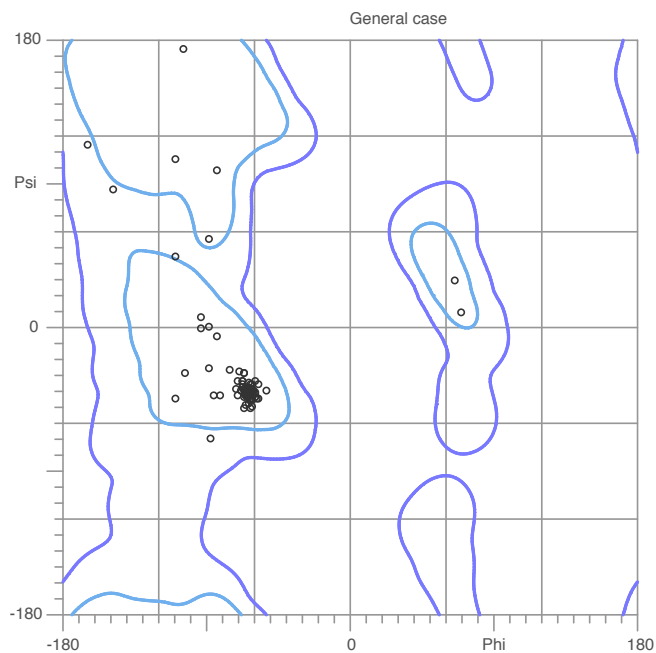
97.5% (1892/1940) of all residues were in favored (98%) regions.
99.7% (1935/1940) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[6] 98 HIS (75.1, 125.2)
[8] 97 HIS (65.0, 95.0)
[14] 94 HIS (165.0, -172.2)
[16] 96 HIS (-35.1, 95.1)
[20] 95 HIS (65.1, 94.9)

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 1



95.9% (93/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

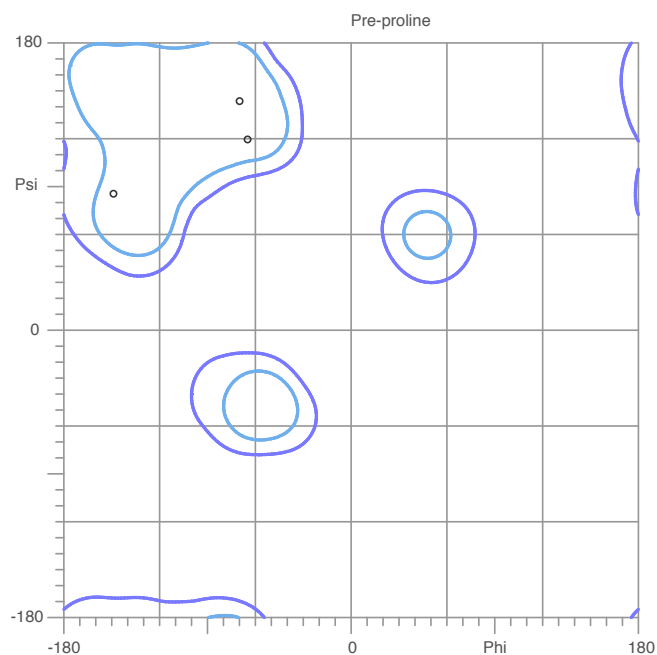
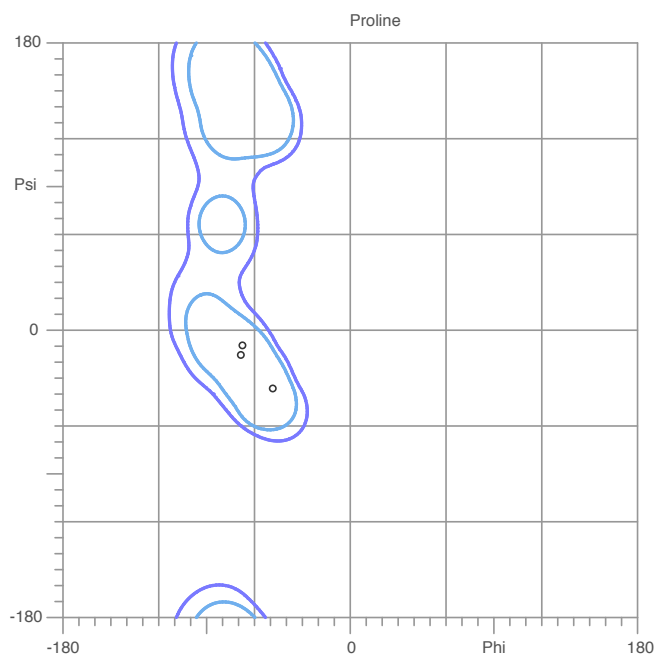
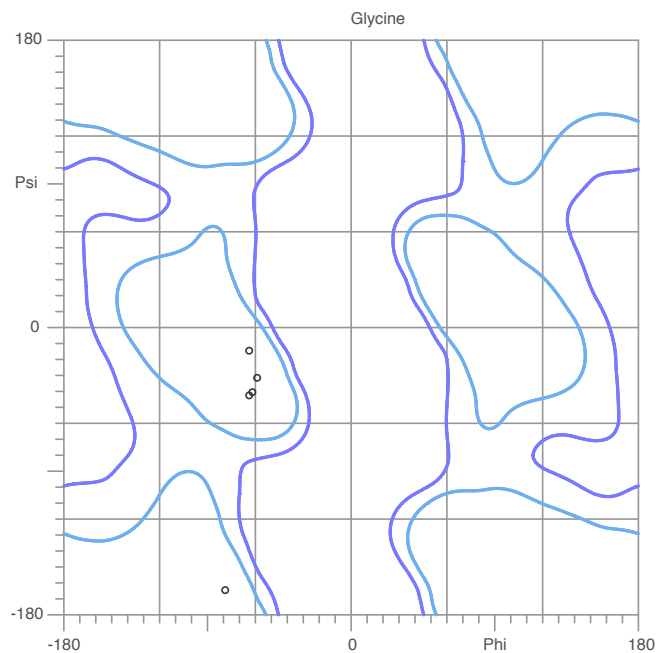
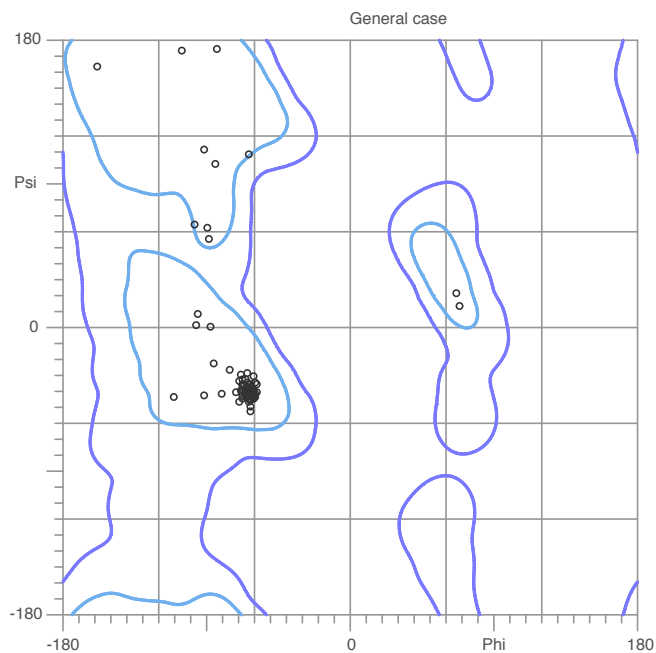
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 2



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.

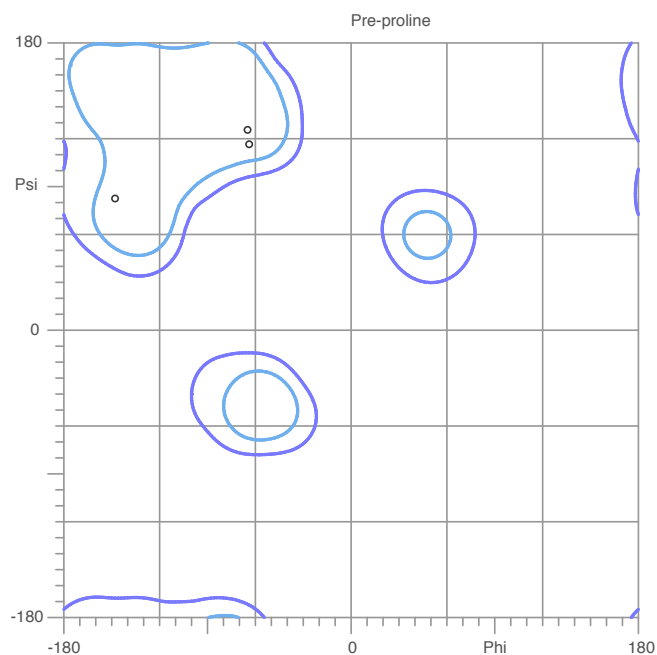
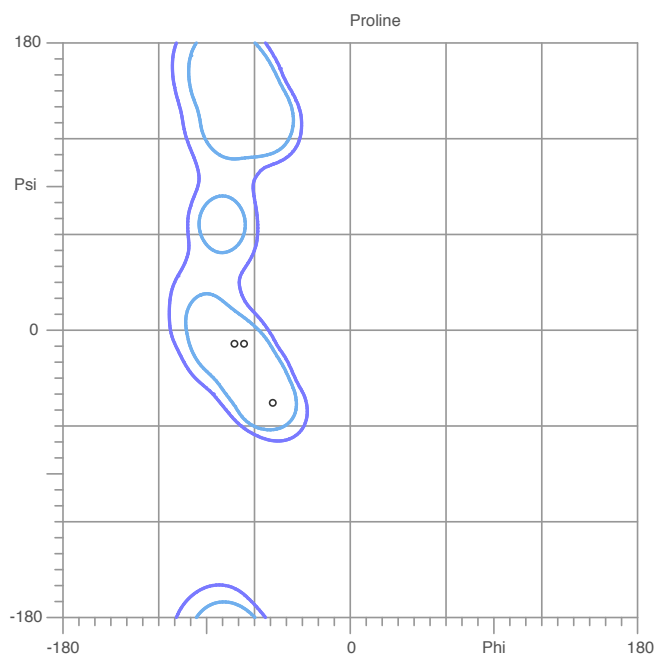
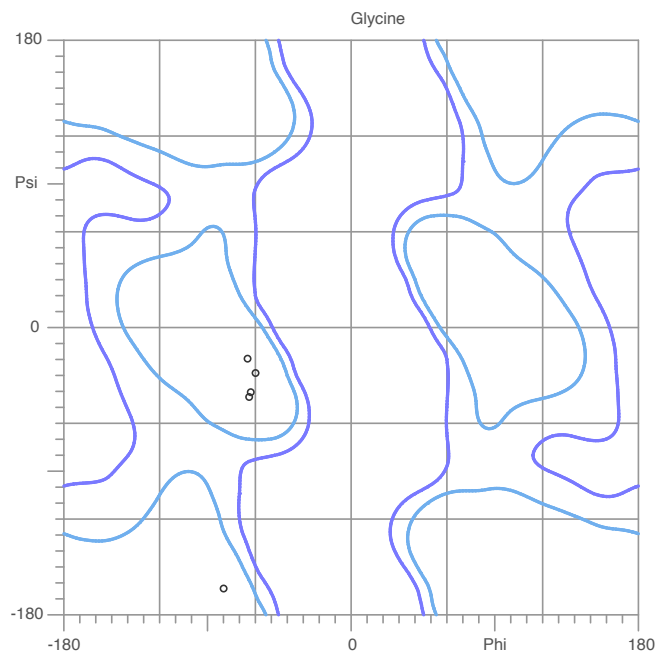
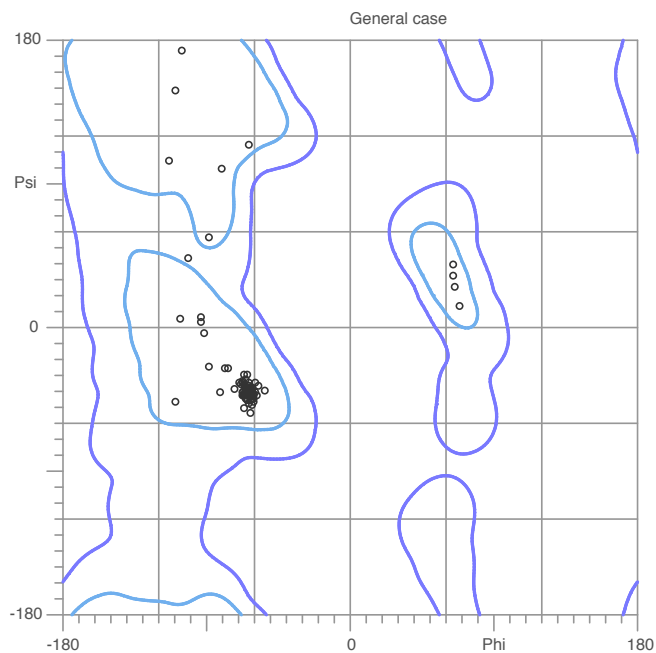
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_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.

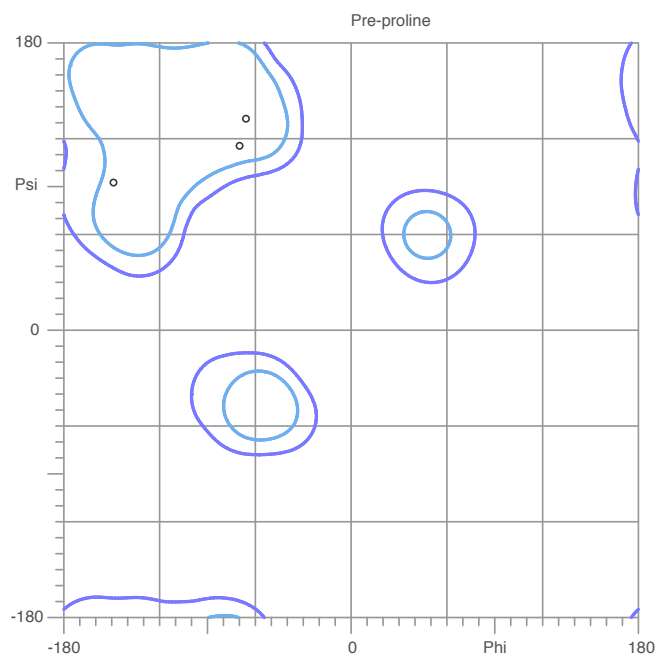
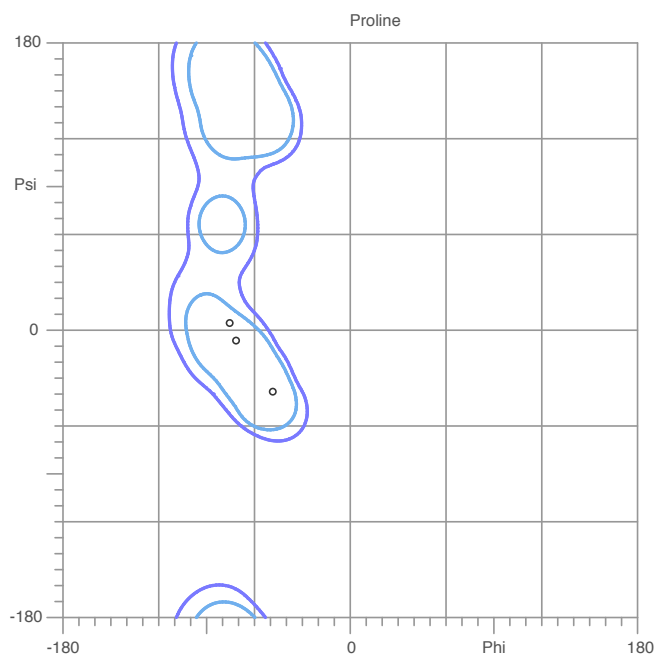
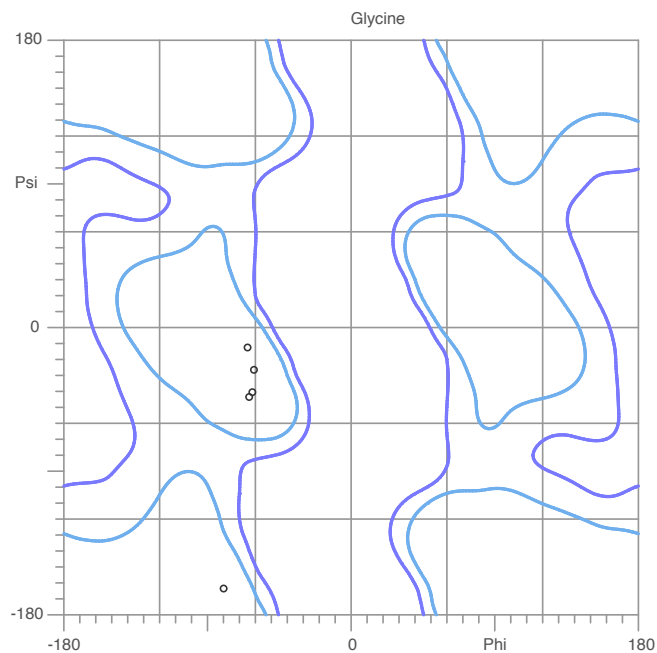
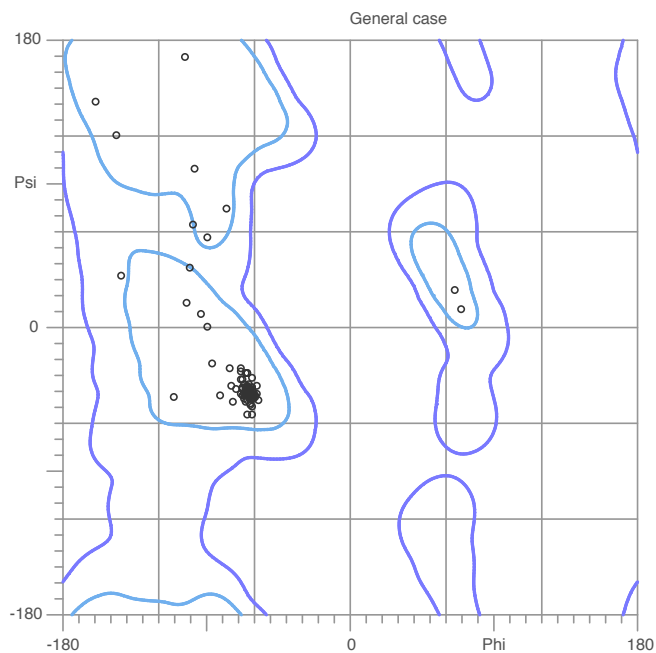
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 4



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.

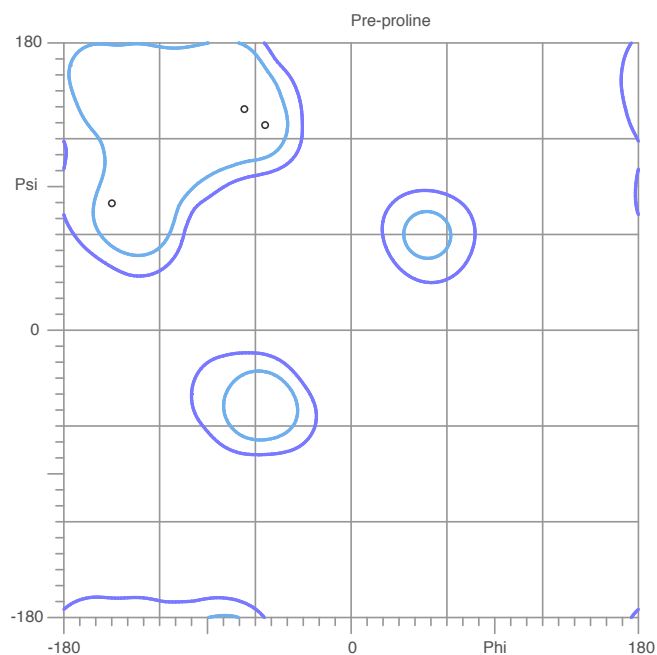
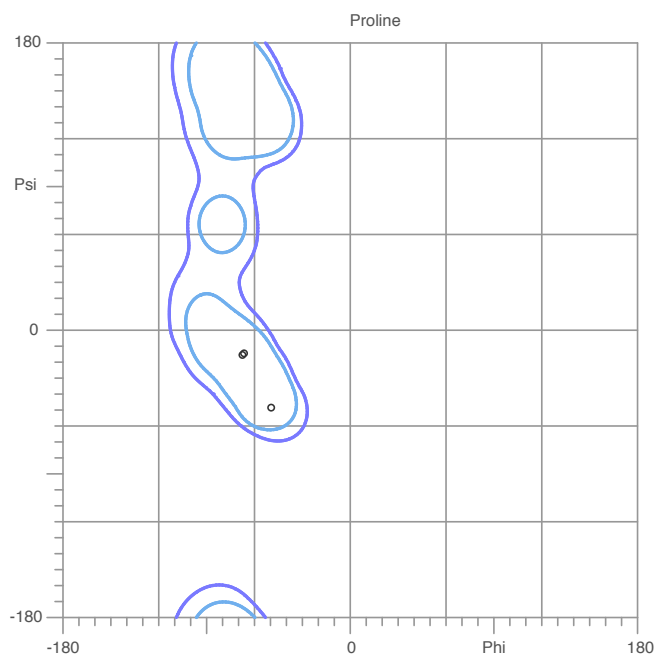
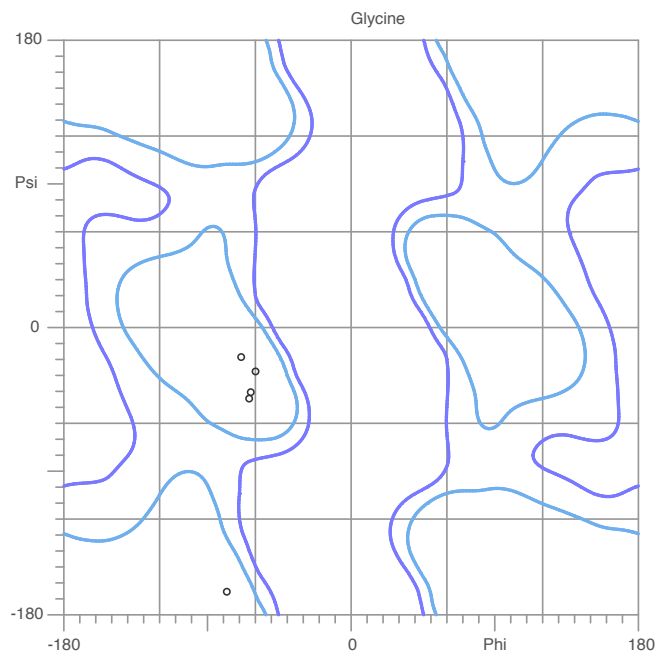
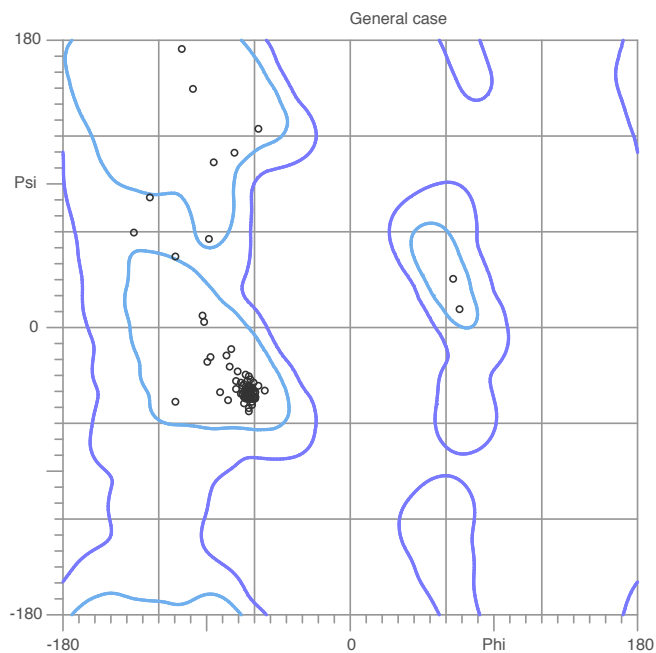
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 5



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.

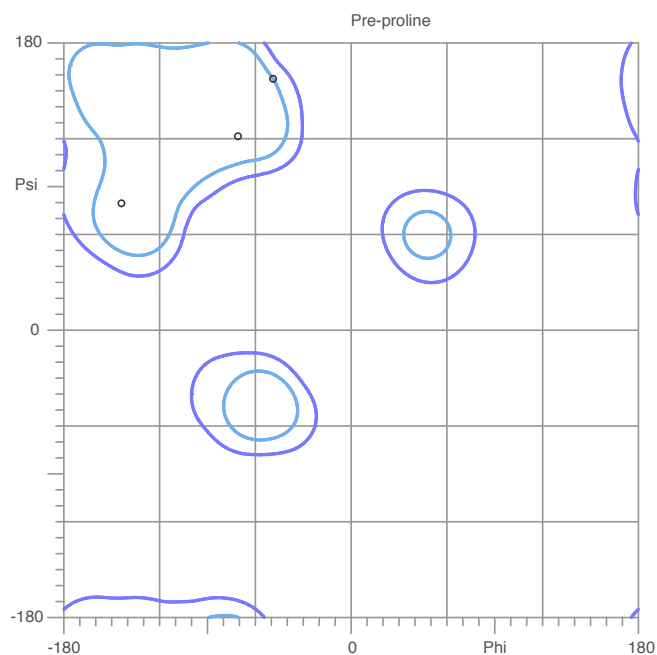
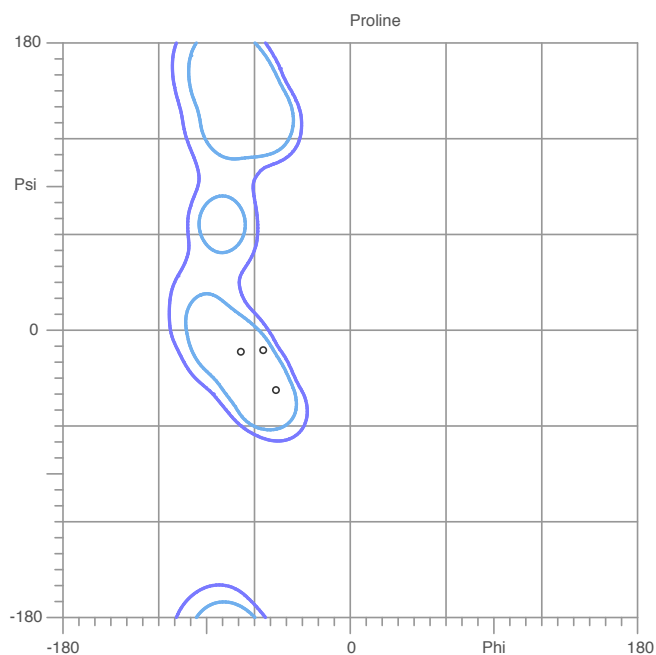
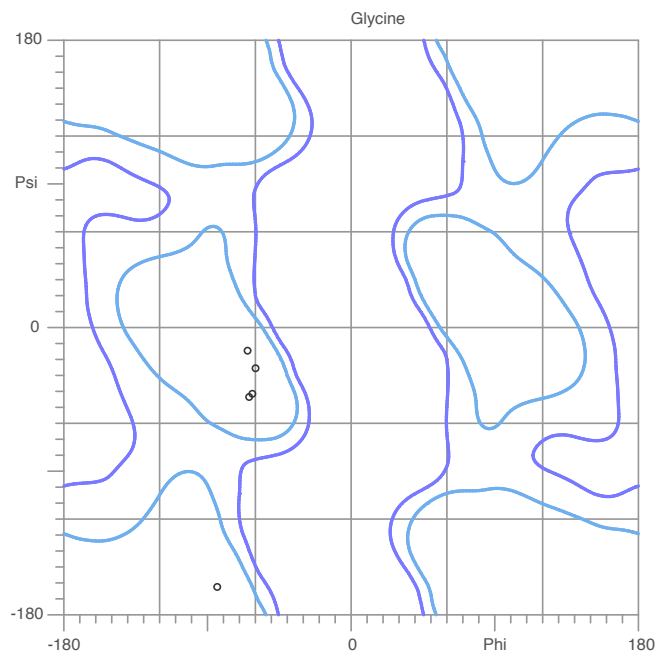
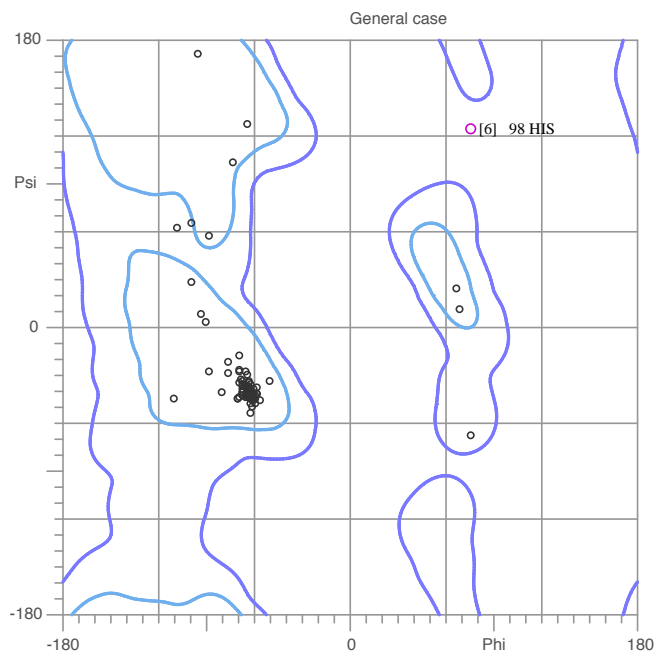
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 6



95.9% (93/97) of all residues were in favored (98%) regions.
99.0% (96/97) of all residues were in allowed (>99.8%) regions.

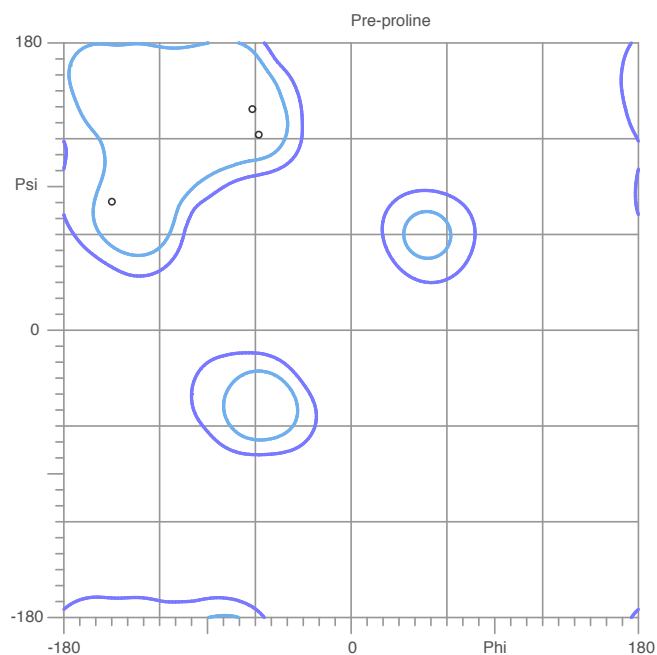
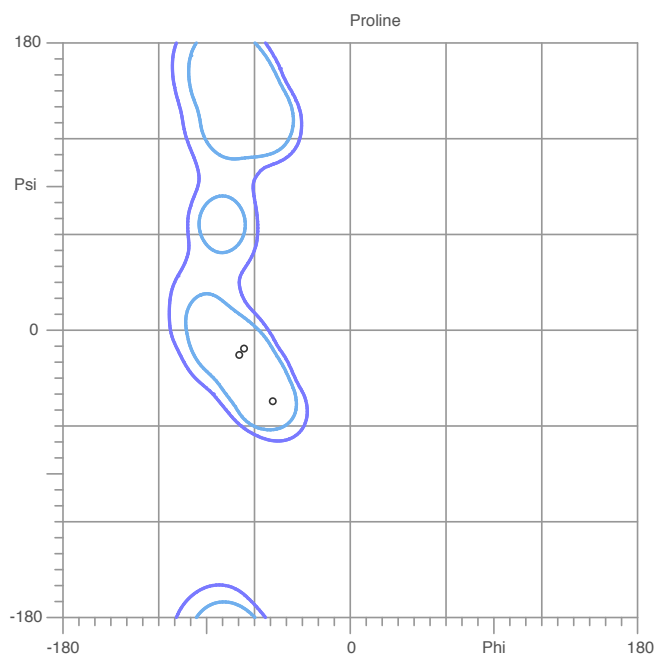
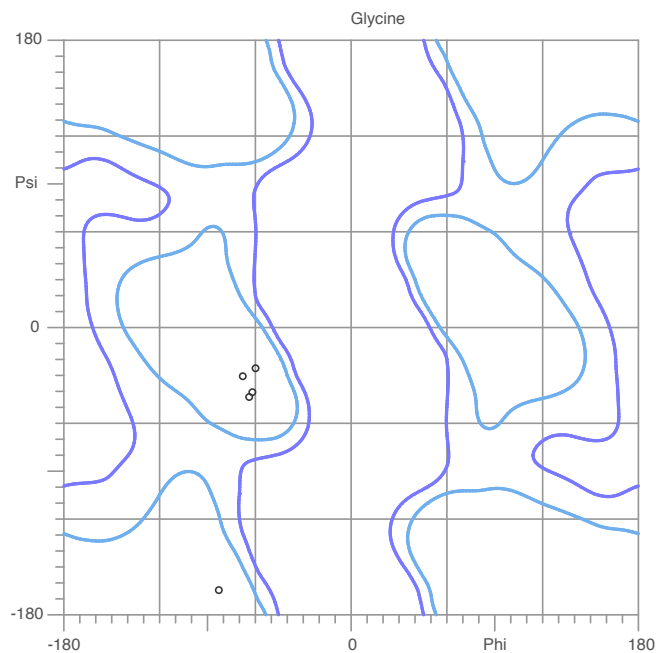
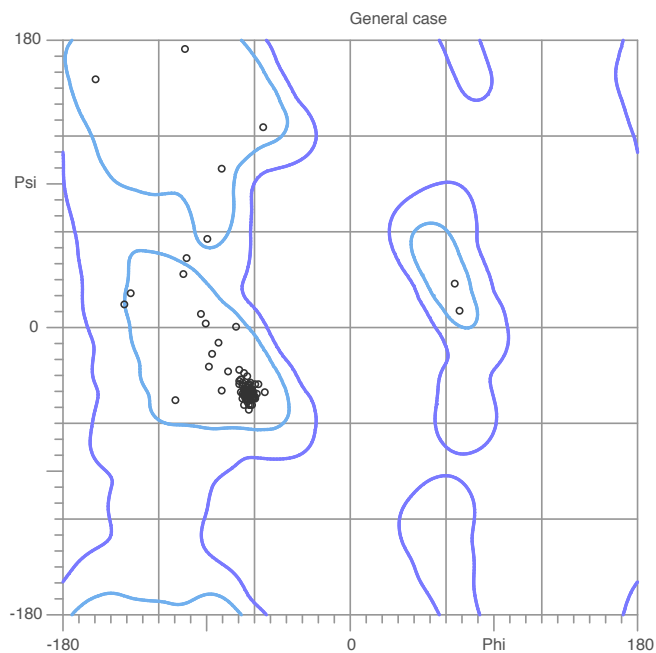
There were 1 outliers (phi, psi):
[6] 98 HIS (75.1, 125.2)

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

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MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 7



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.

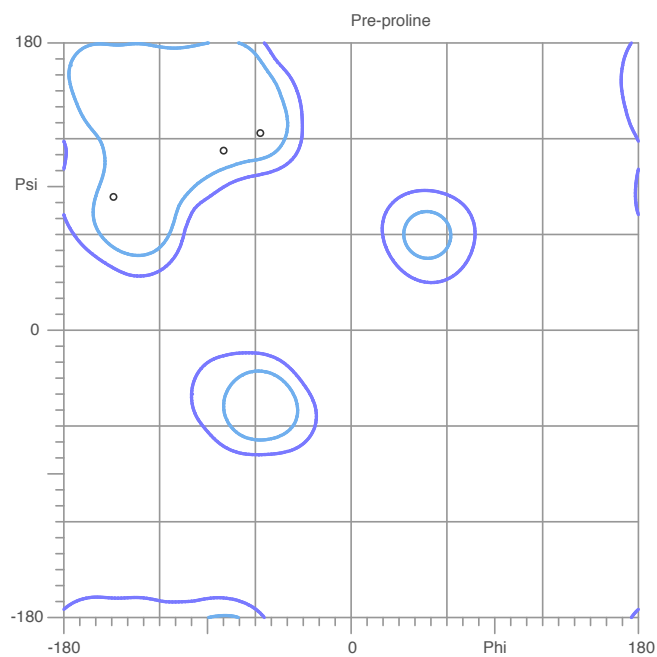
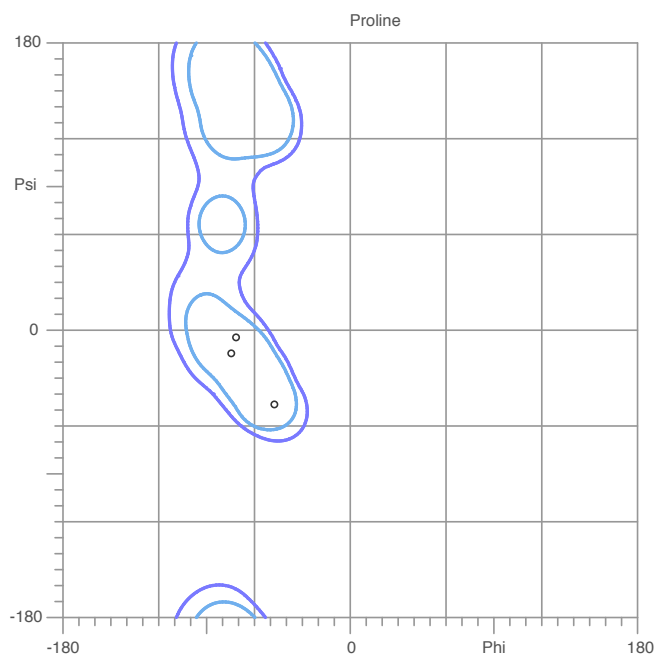
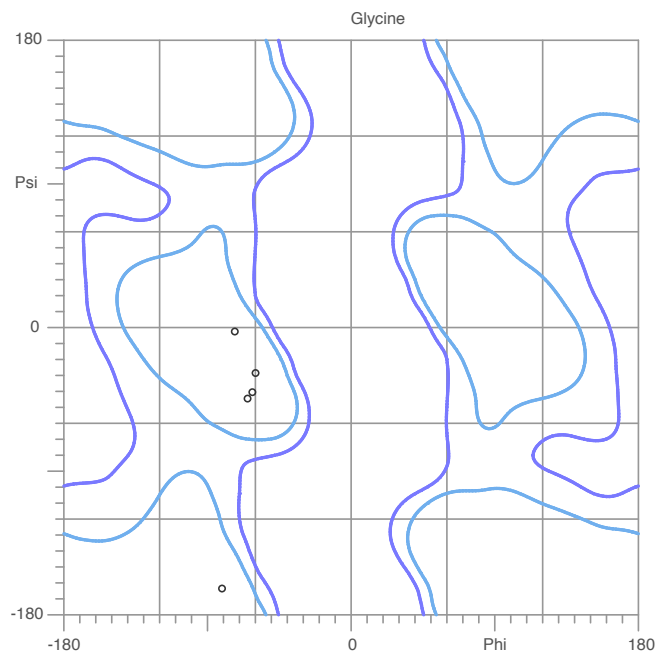
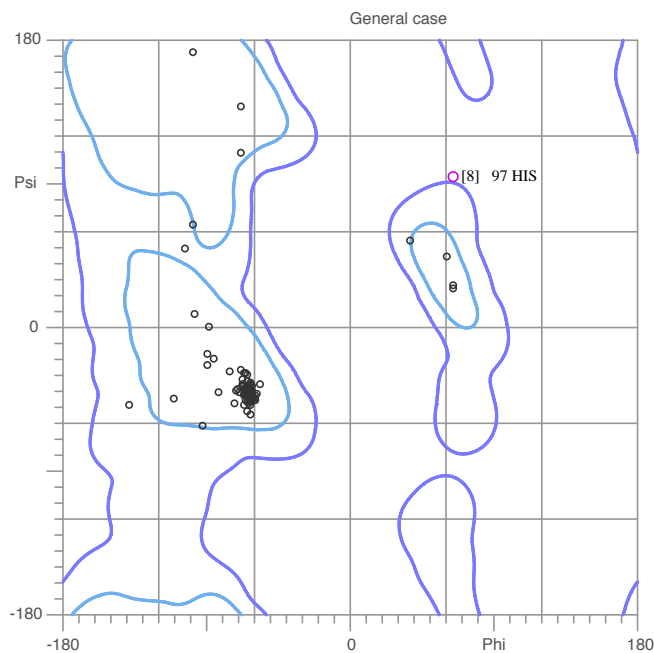
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 8

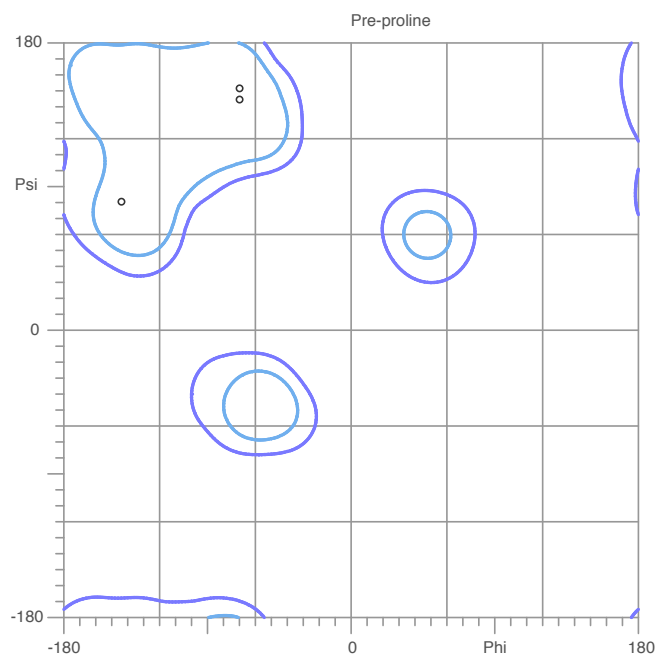
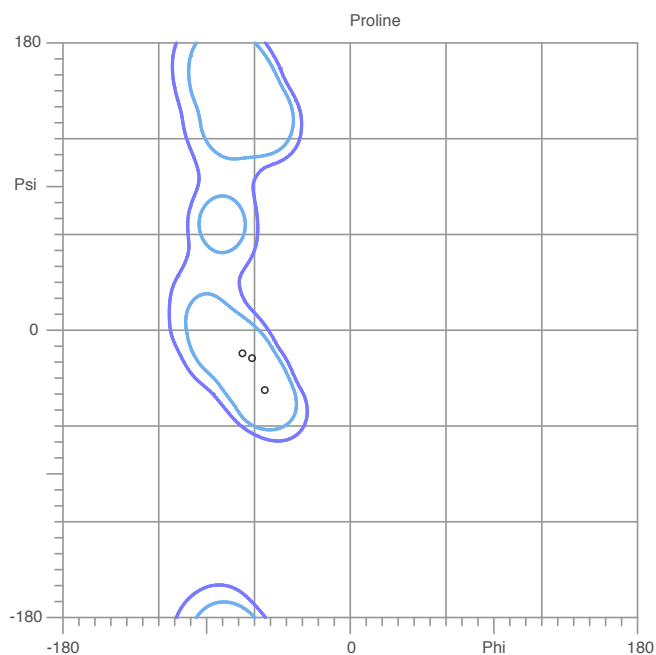
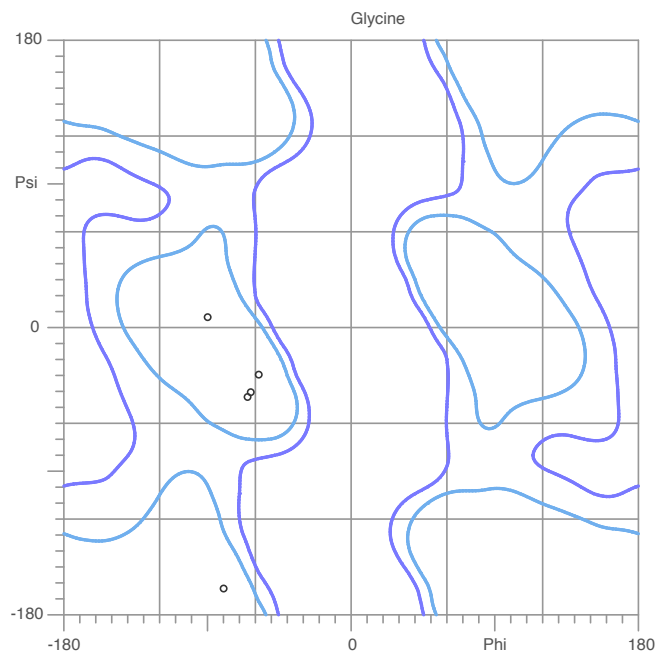
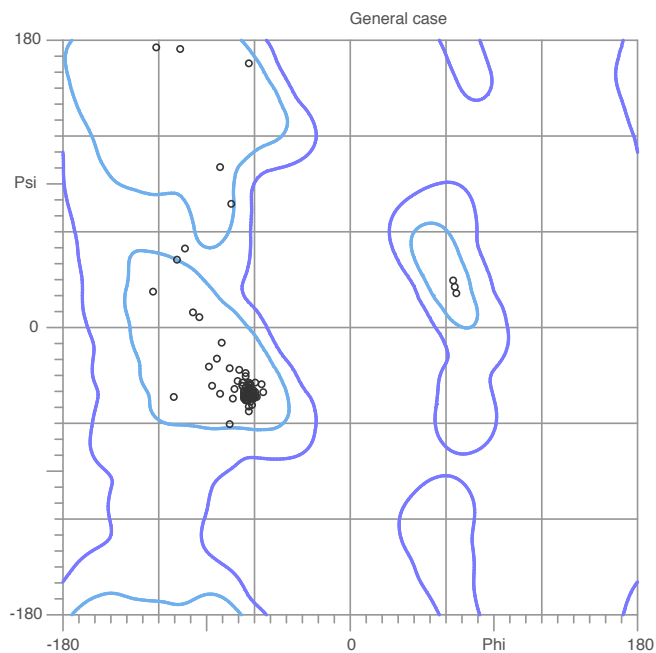


94.8% (92/97) of all residues were in favored (98%) regions.
99.0% (96/97) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 97 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 9



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.

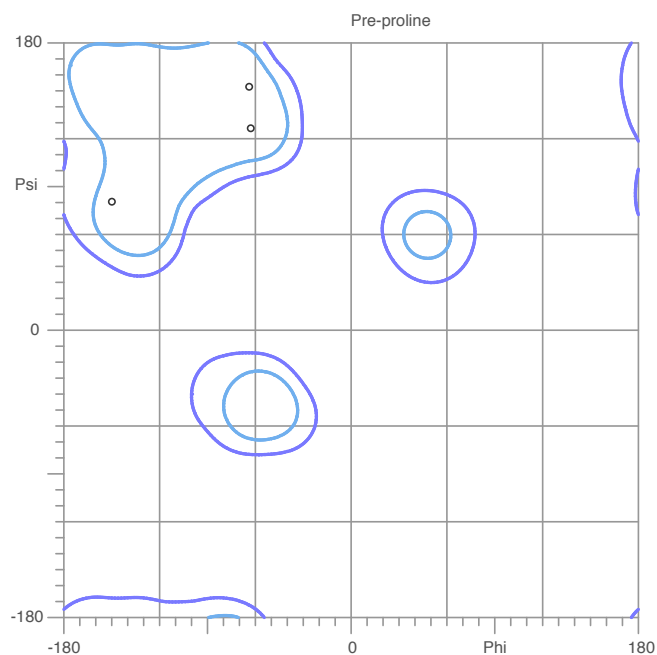
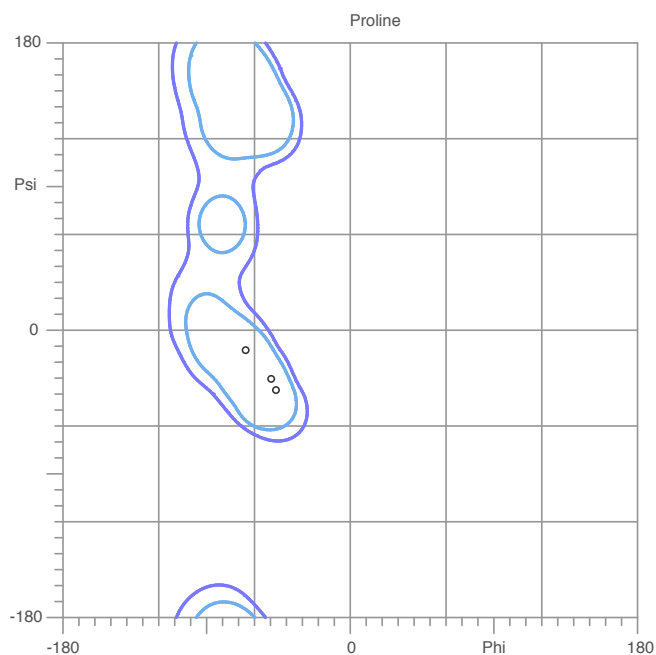
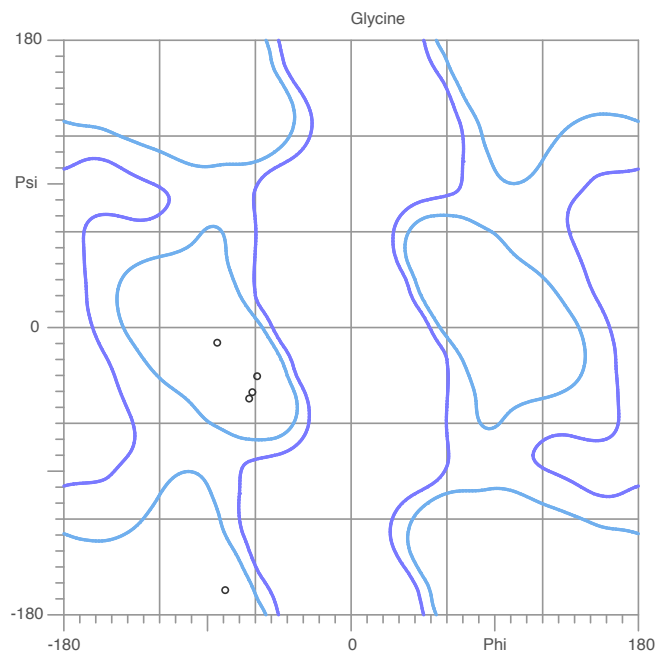
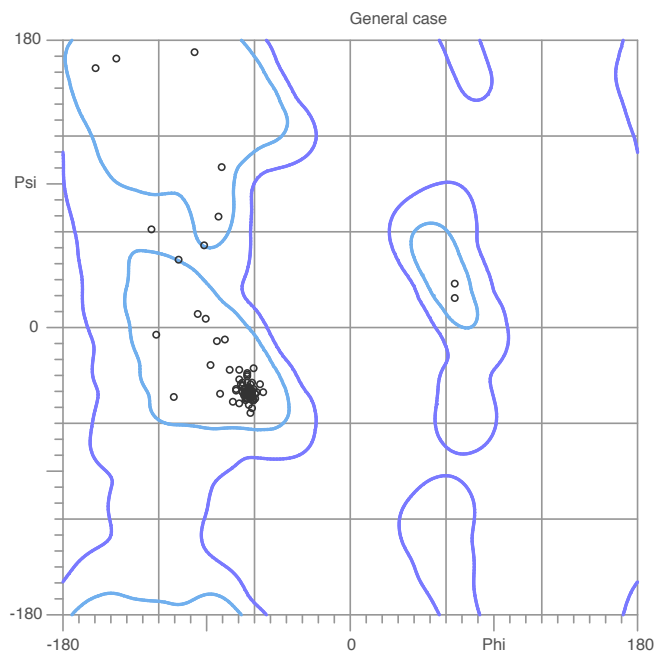
There were no outliers.

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MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 10



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.

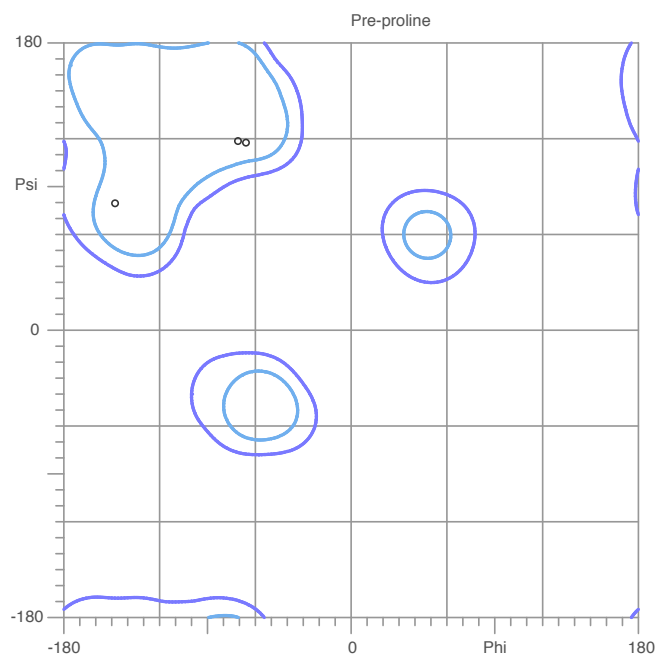
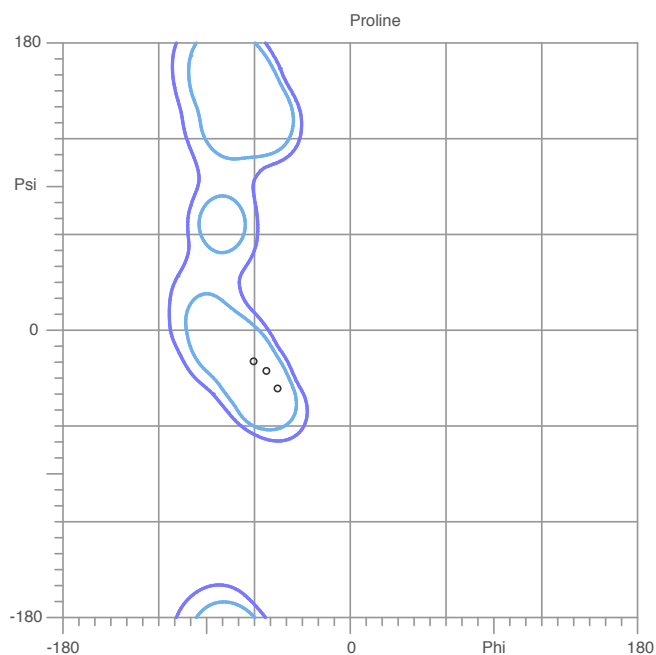
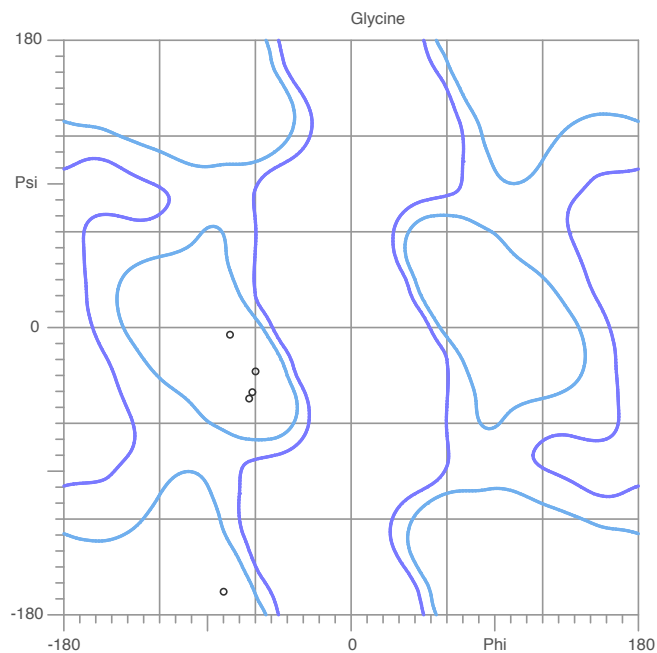
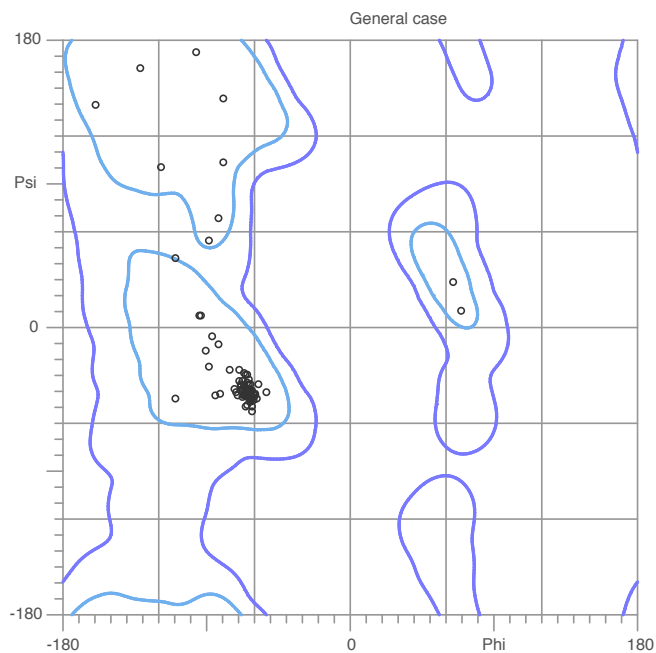
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 11



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.

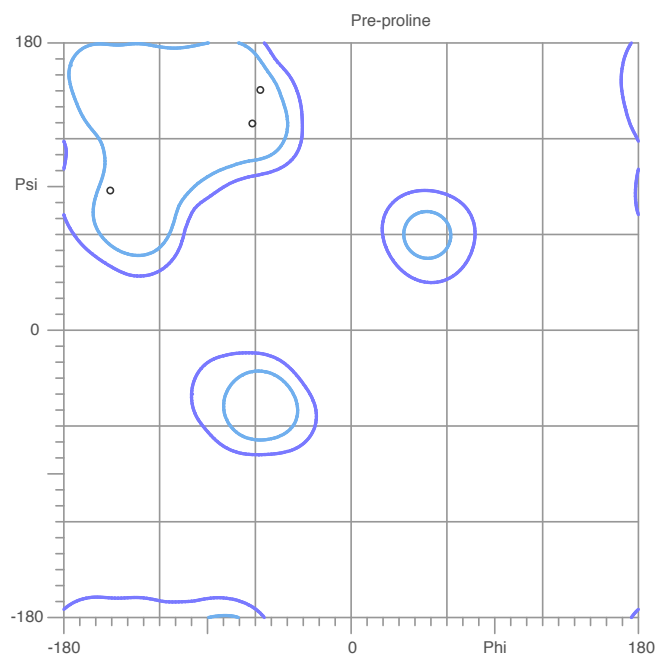
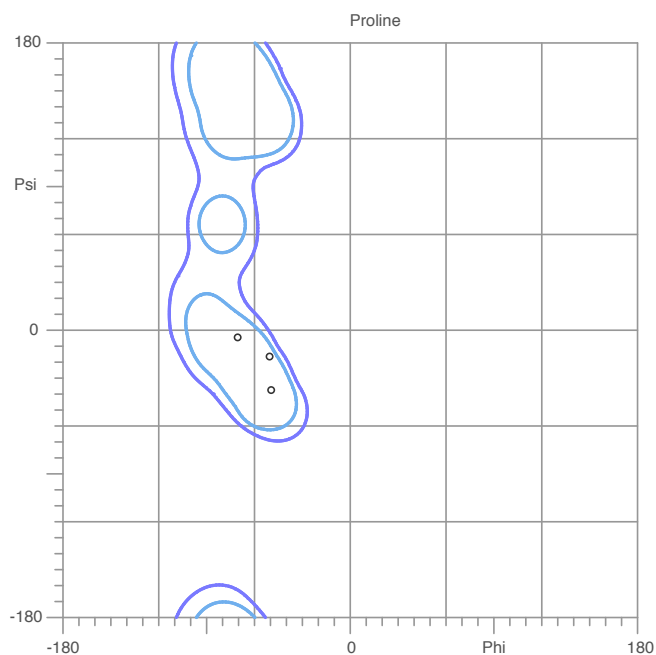
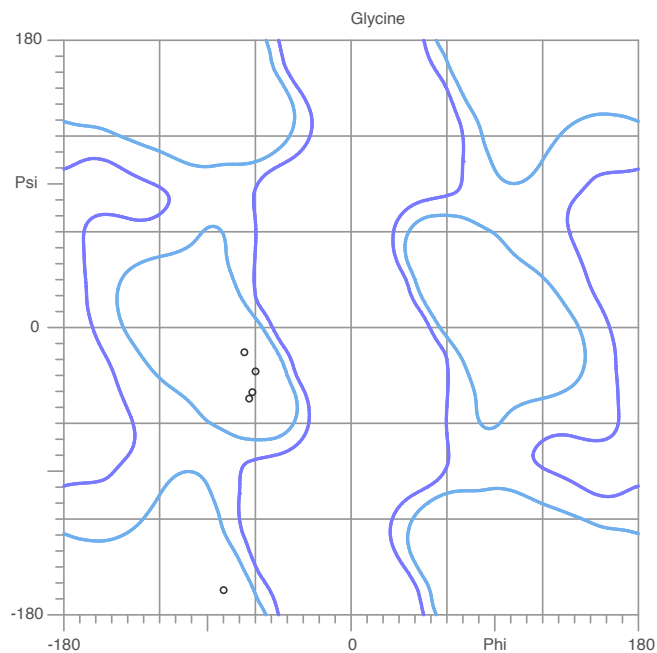
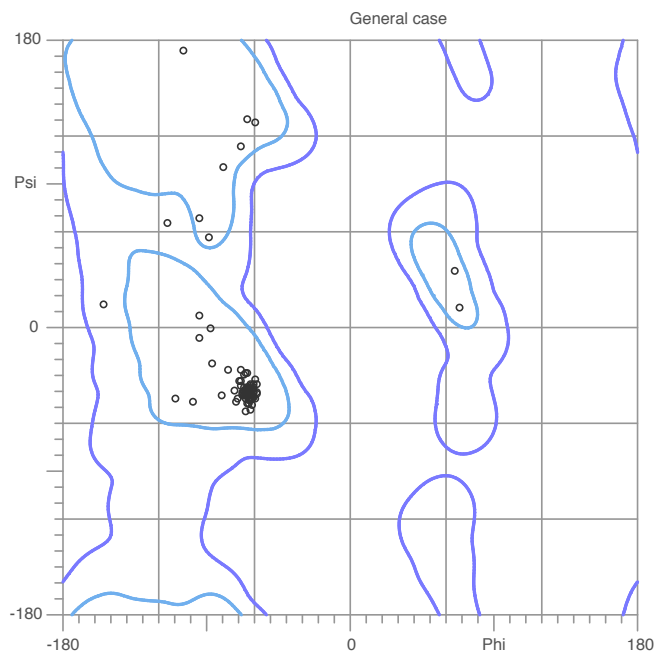
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_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.

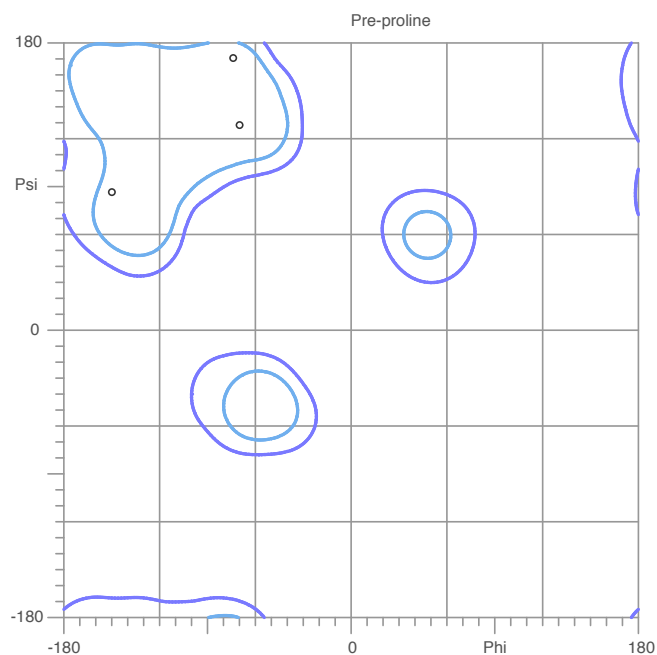
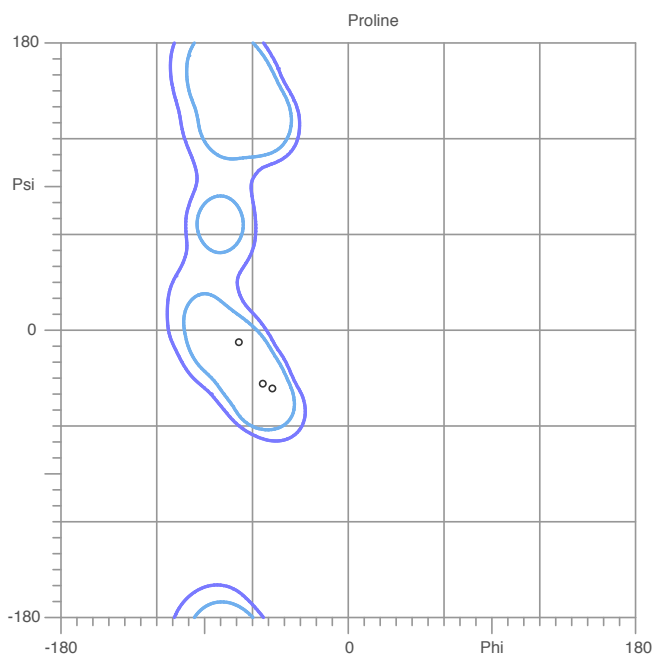
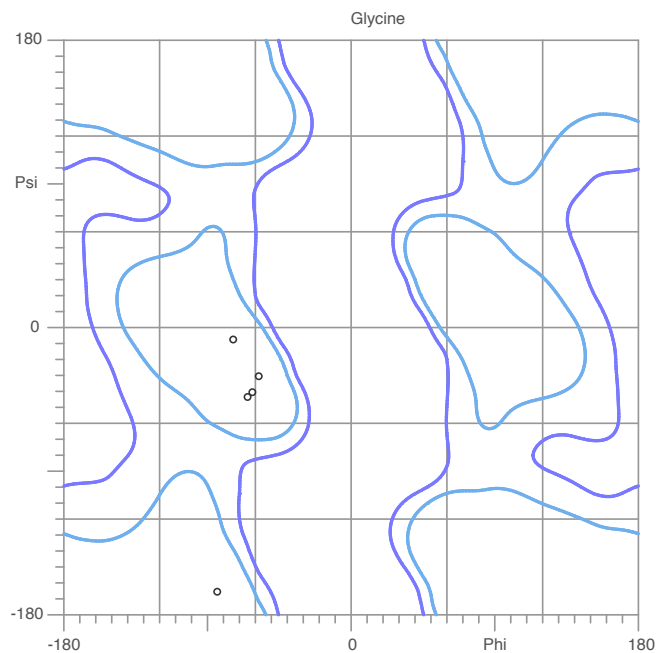
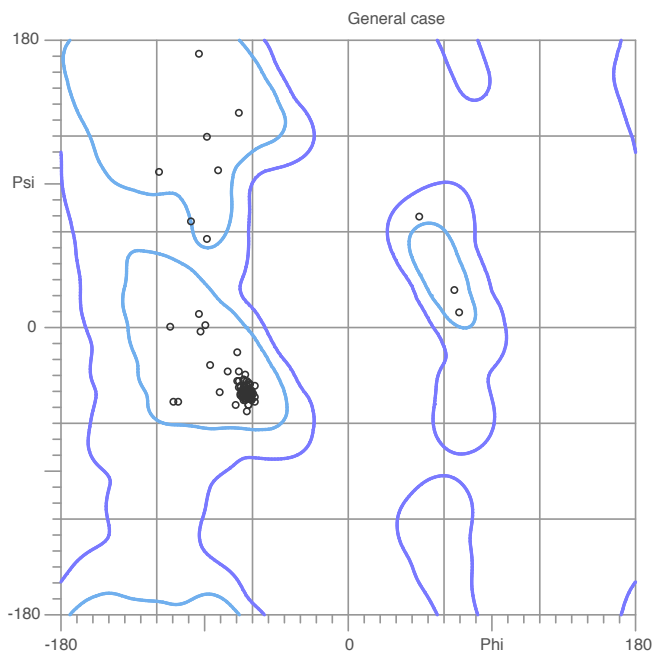
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_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.

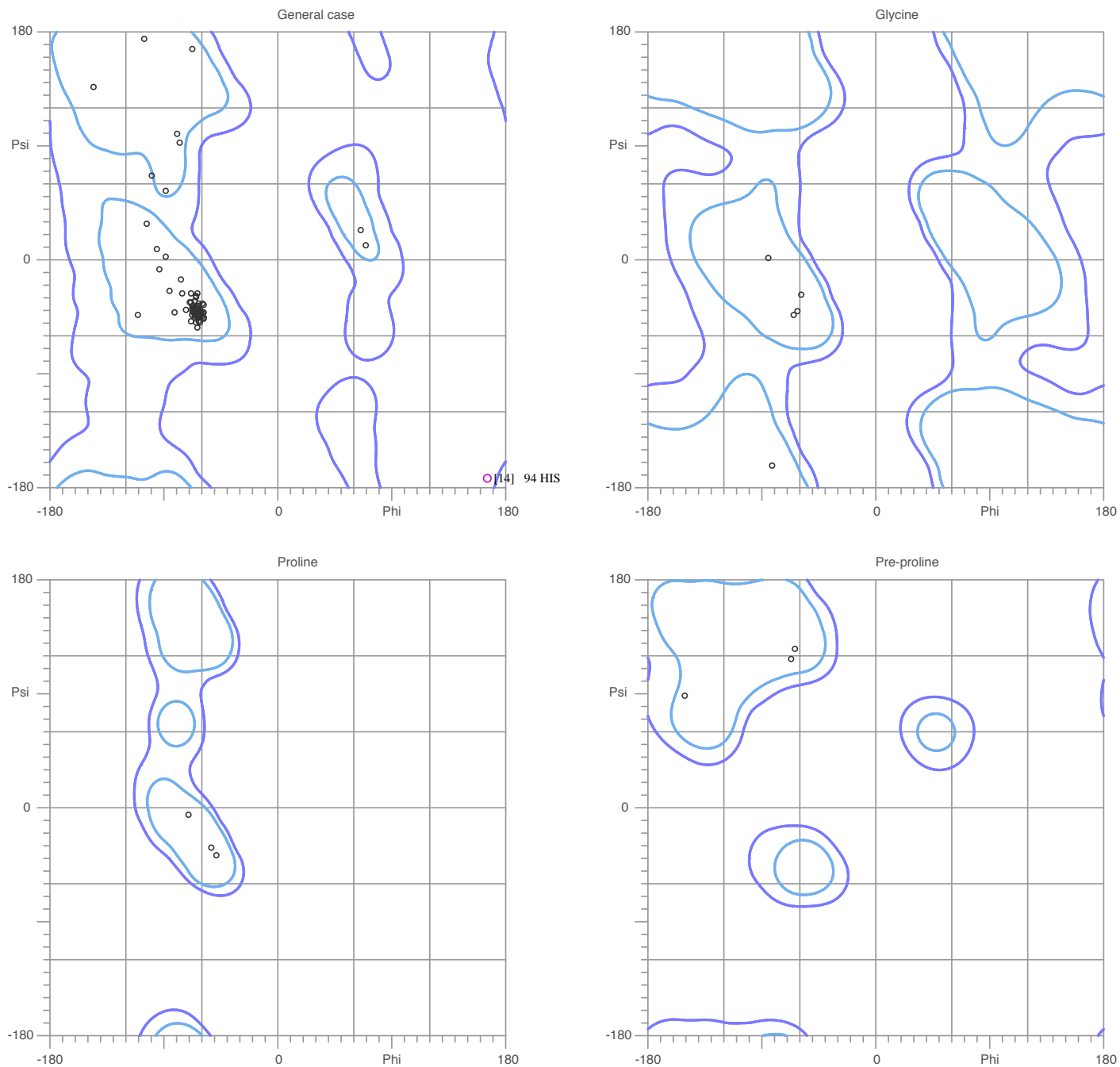
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 14



97.9% (95/97) of all residues were in favored (98%) regions.
99.0% (96/97) of all residues were in allowed (>99.8%) regions.

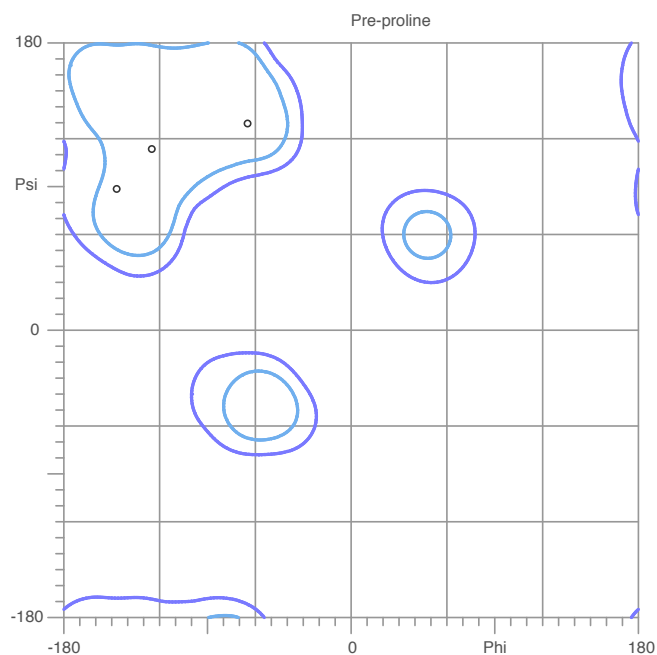
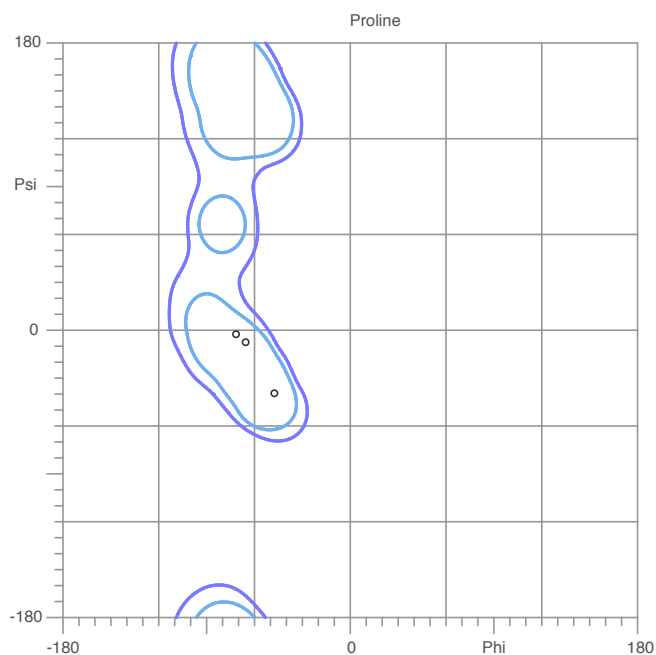
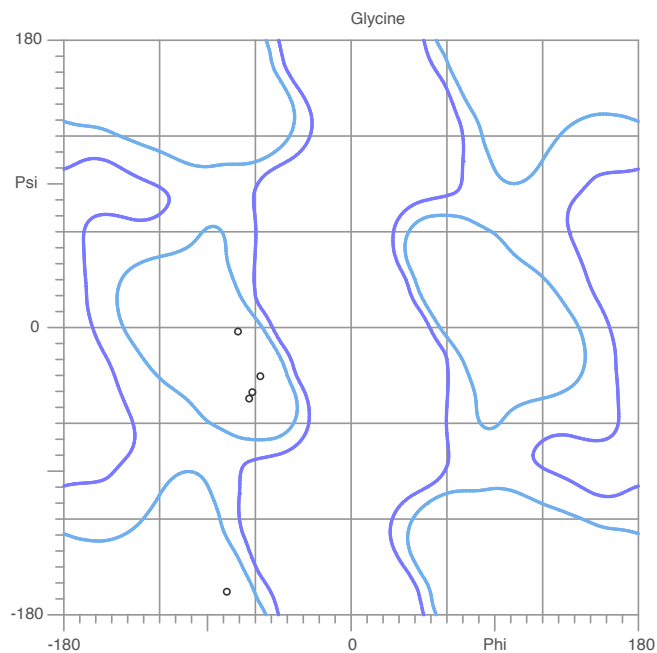
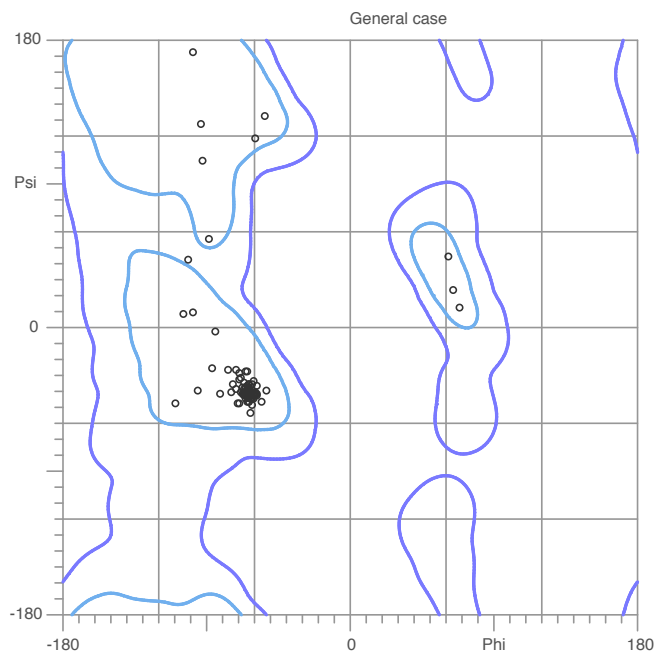
There were 1 outliers (phi, psi):
[14] 94 HIS (165.0, -172.2)

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 15



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.

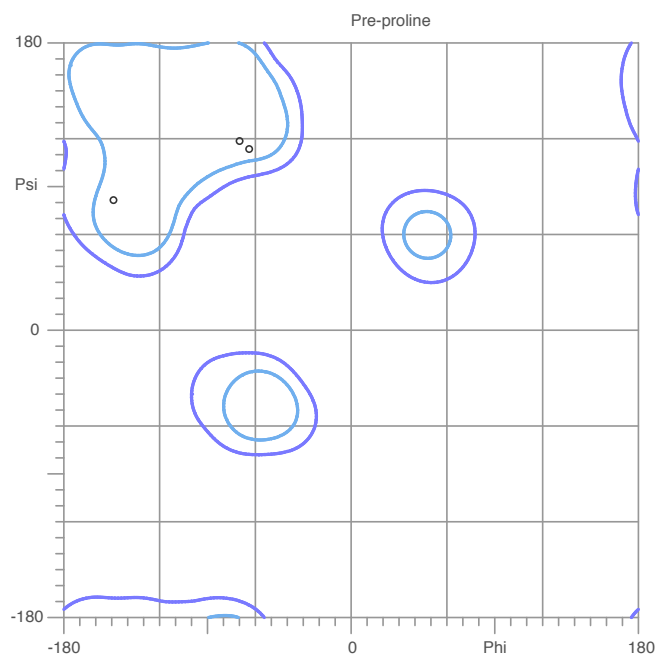
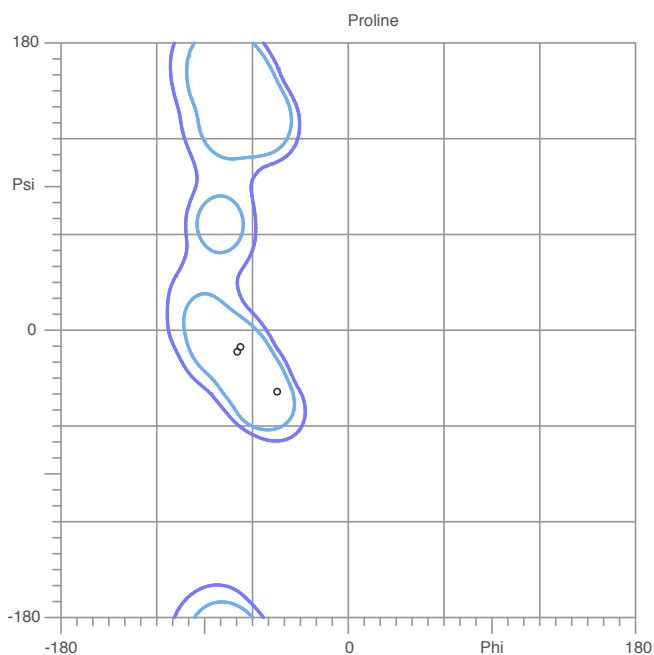
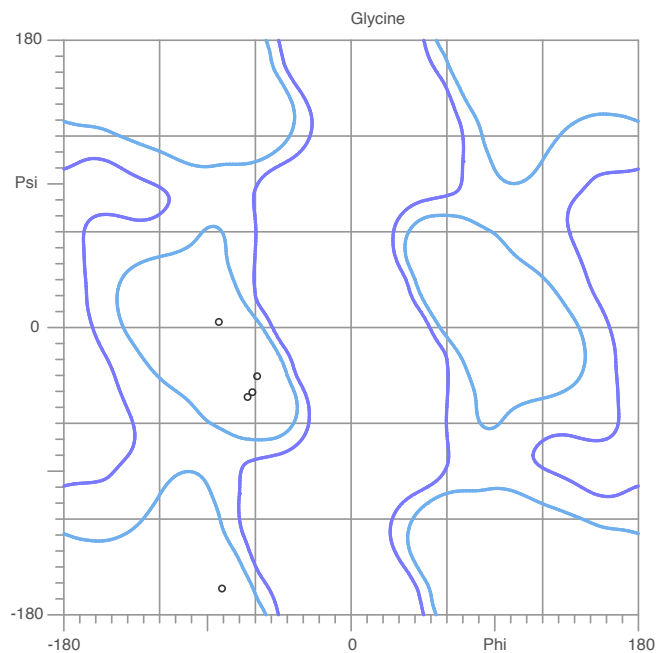
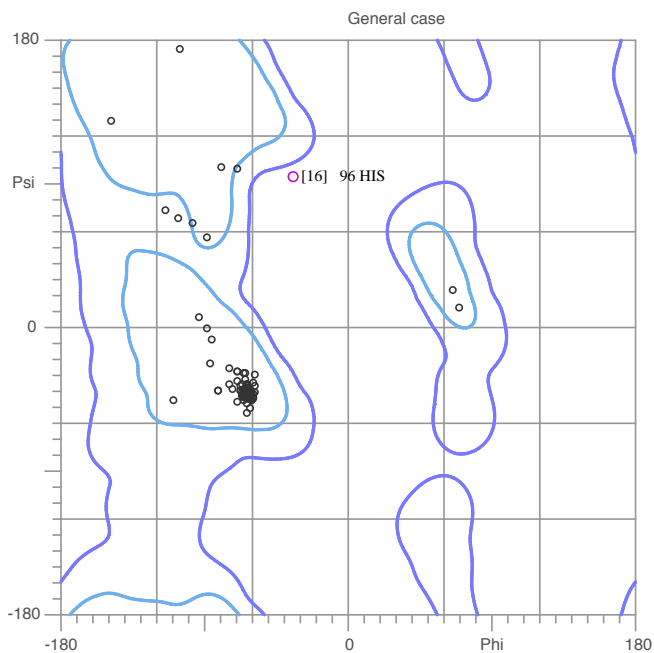
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 16



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.

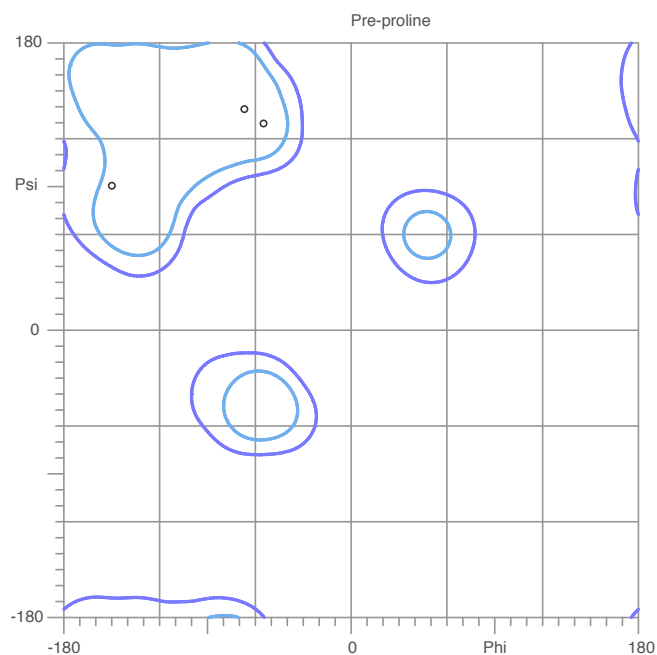
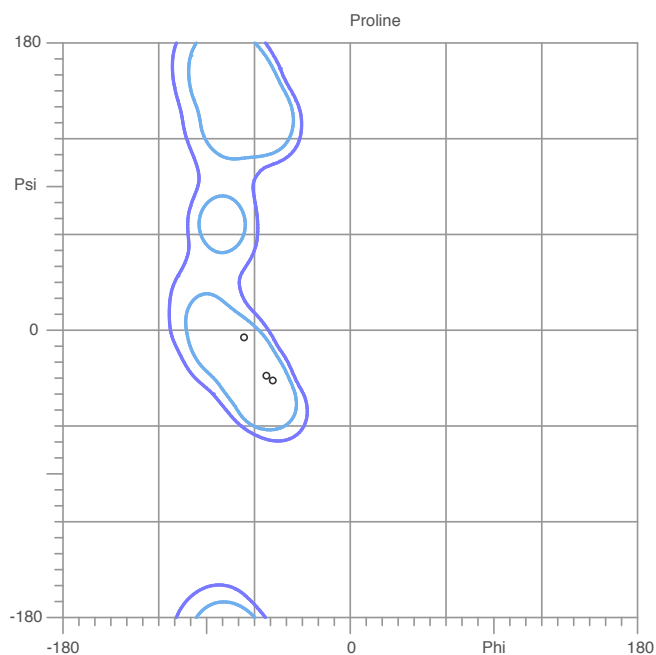
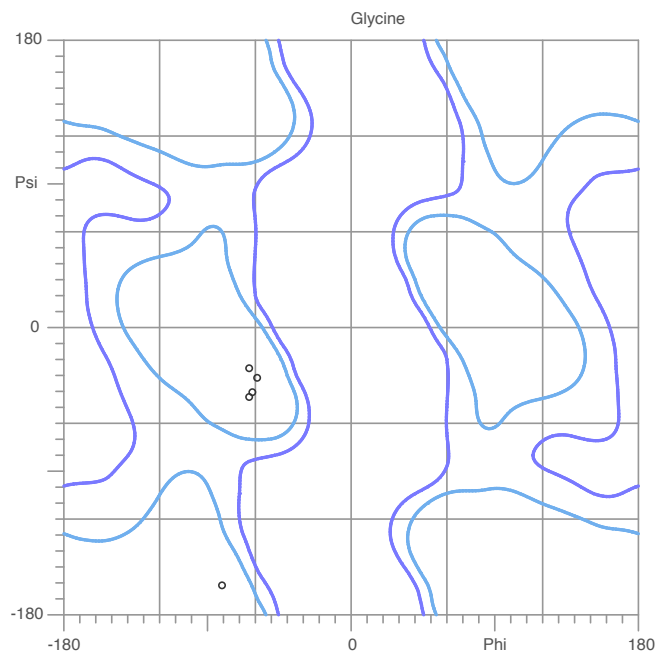
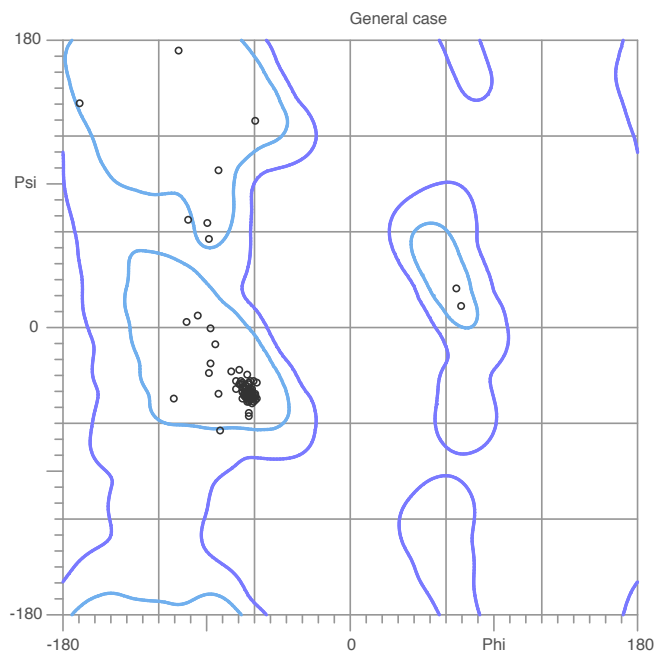
There were 1 outliers (phi, psi):
[16] 96 HIS (-35.1, 95.1)

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 17



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.

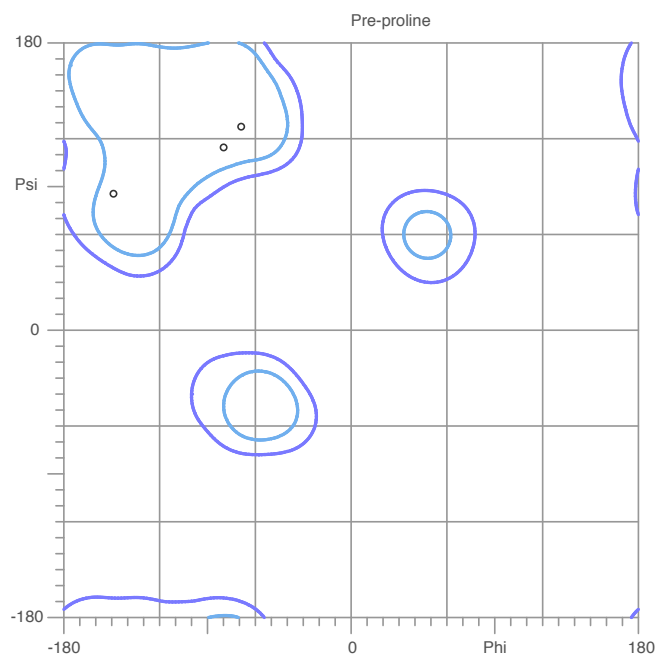
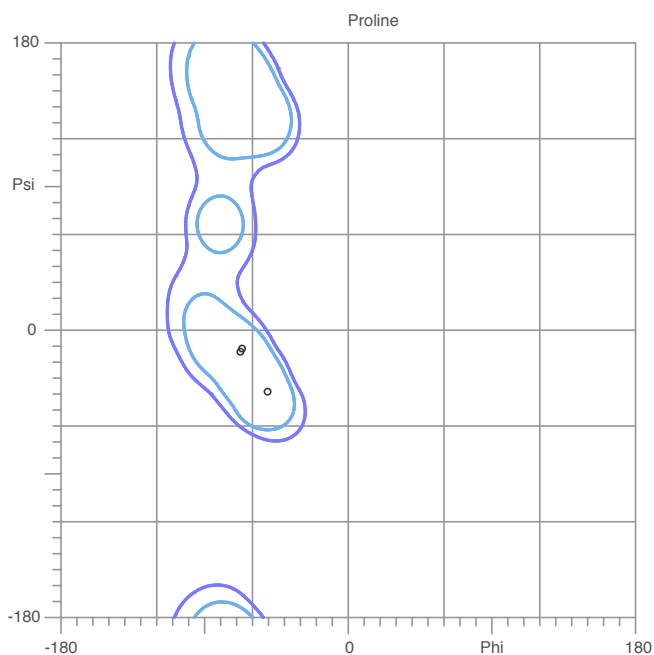
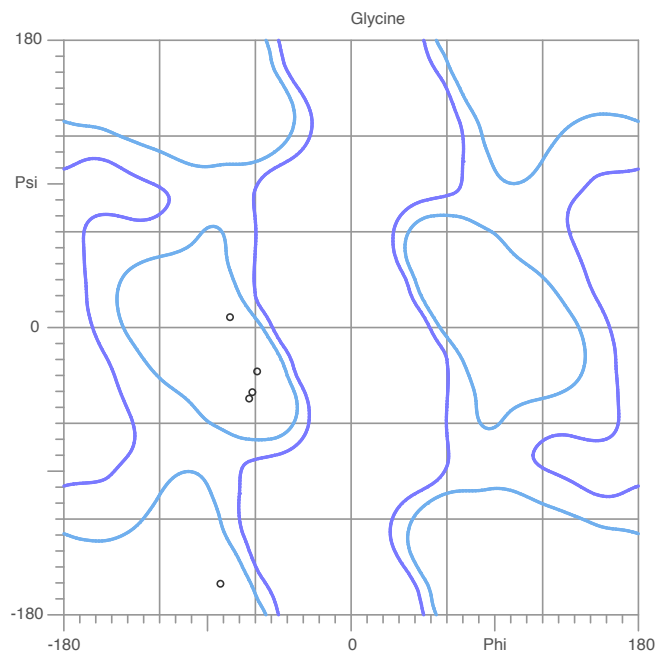
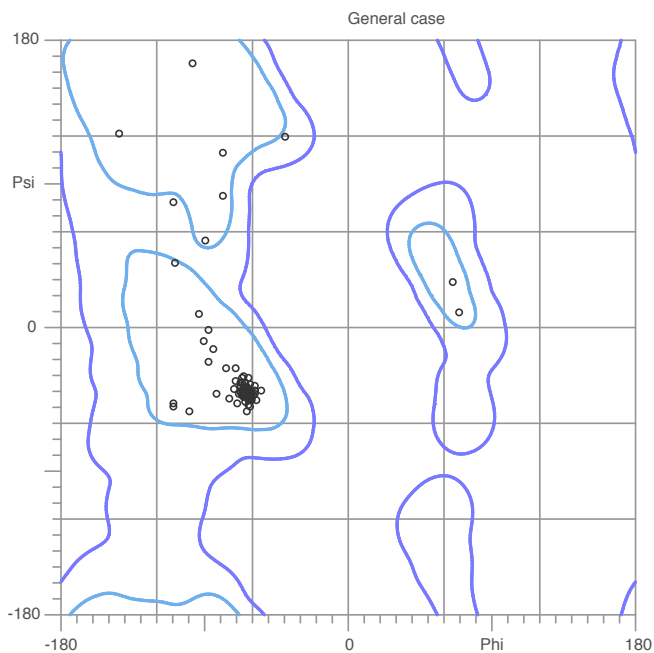
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 18



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.

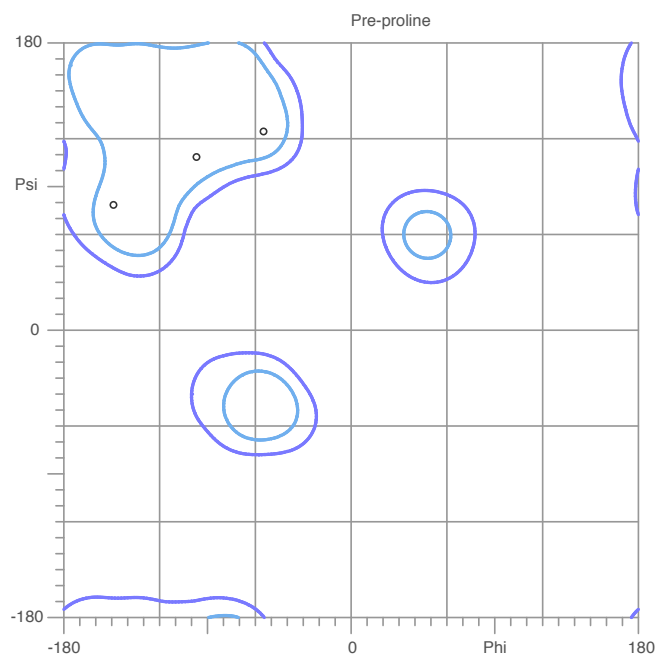
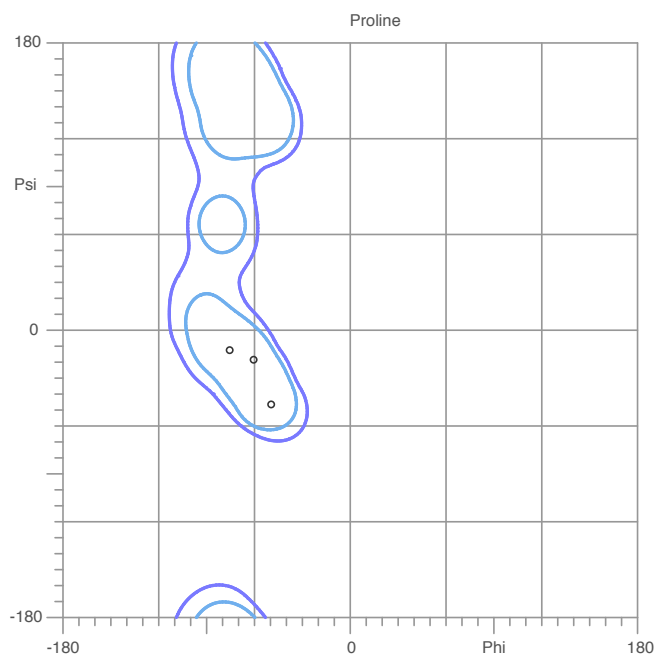
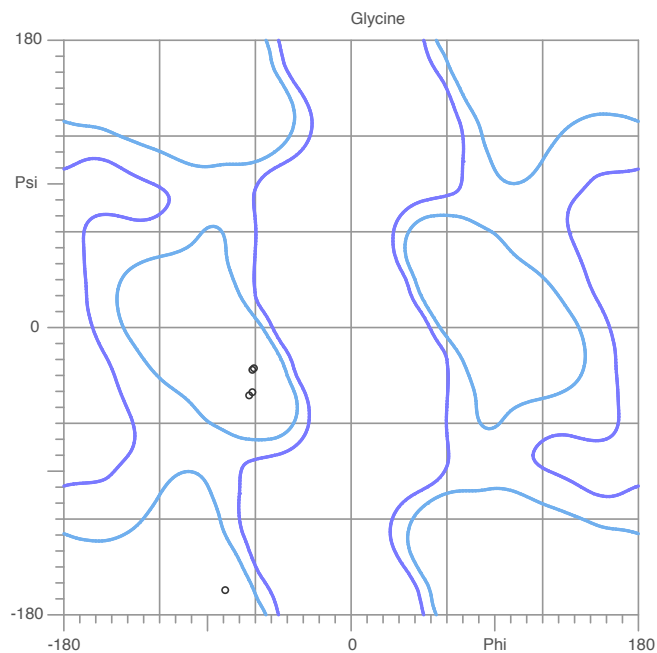
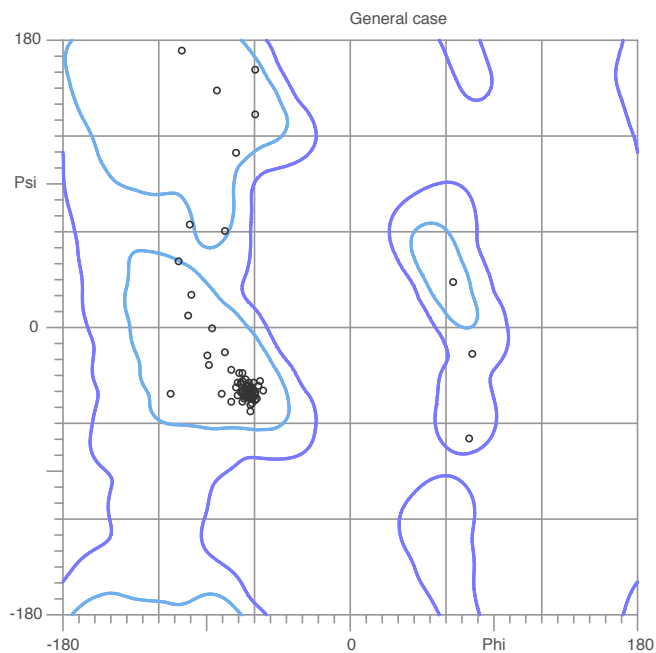
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 19



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.

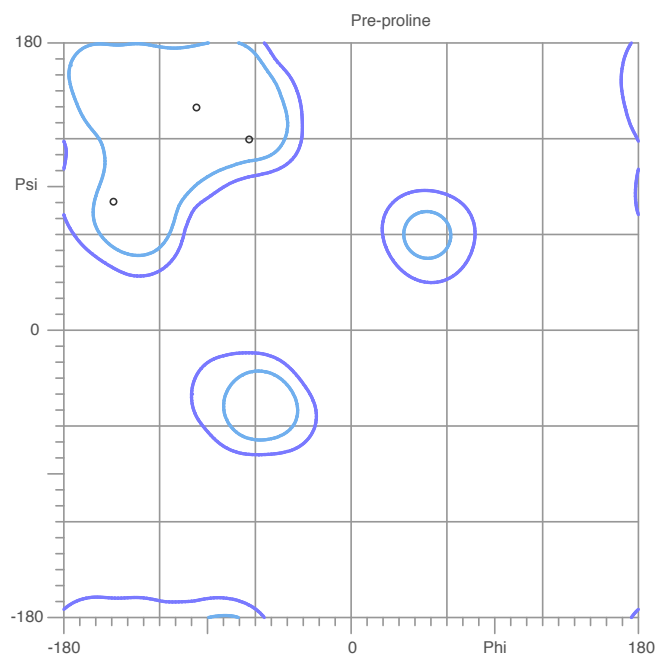
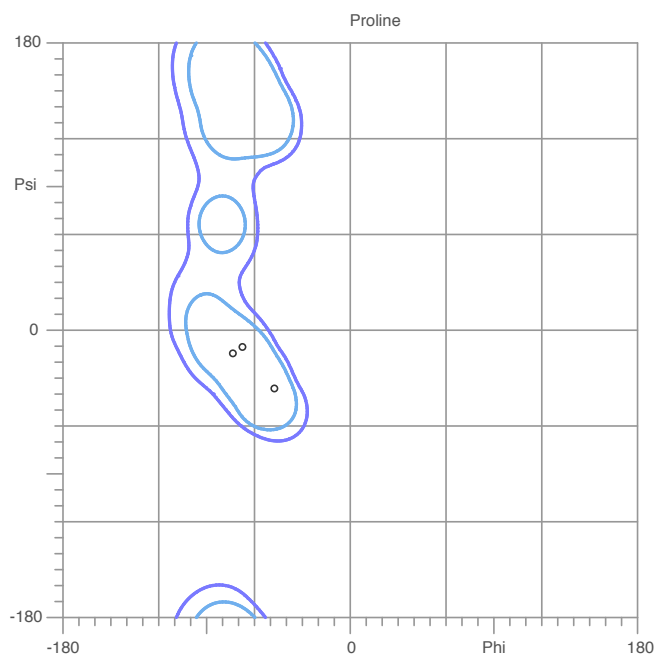
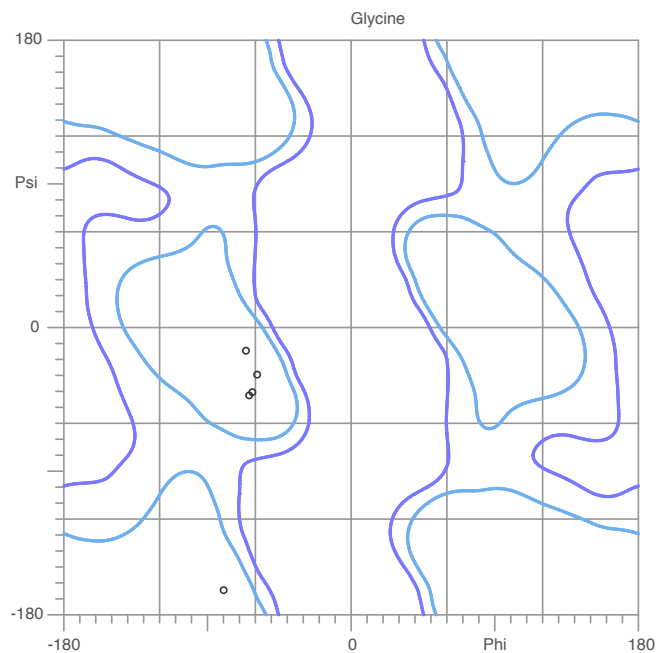
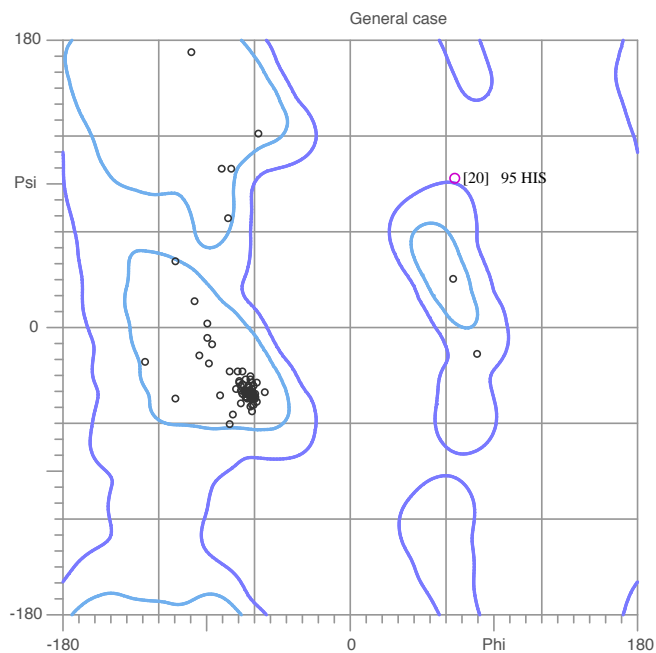
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_R3Cons_em_bcr3.pdb, model 20



97.9% (95/97) 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):
[20] 95 HIS (65.1, 94.9)

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

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