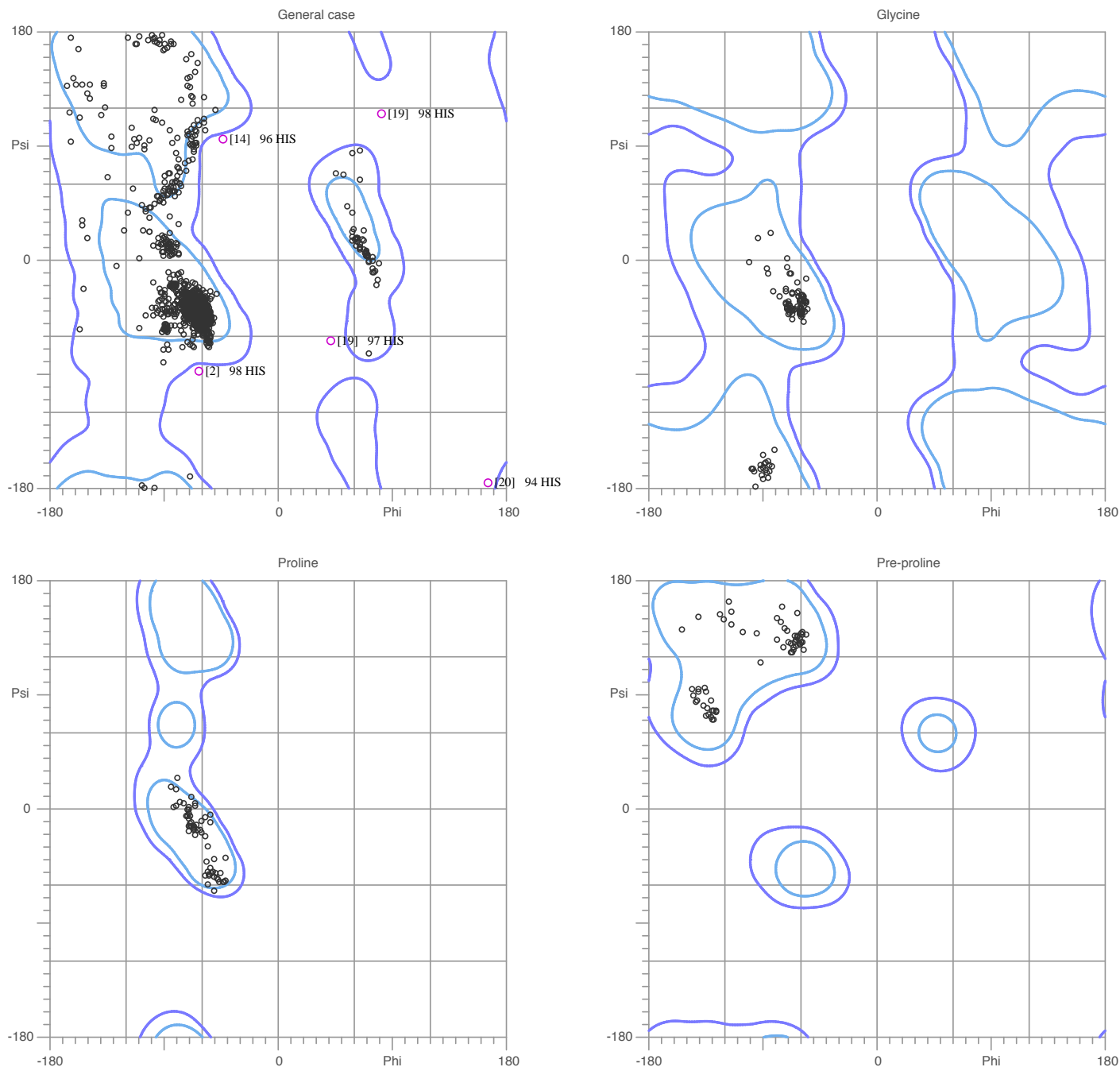


MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, all models



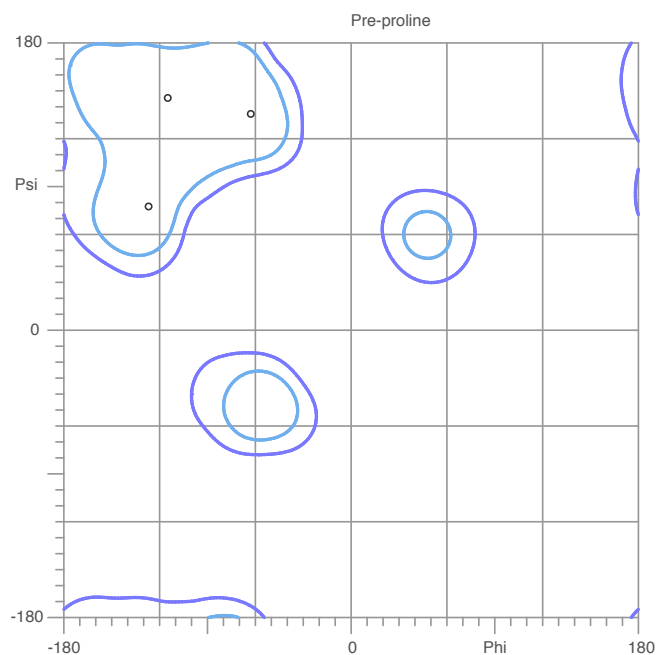
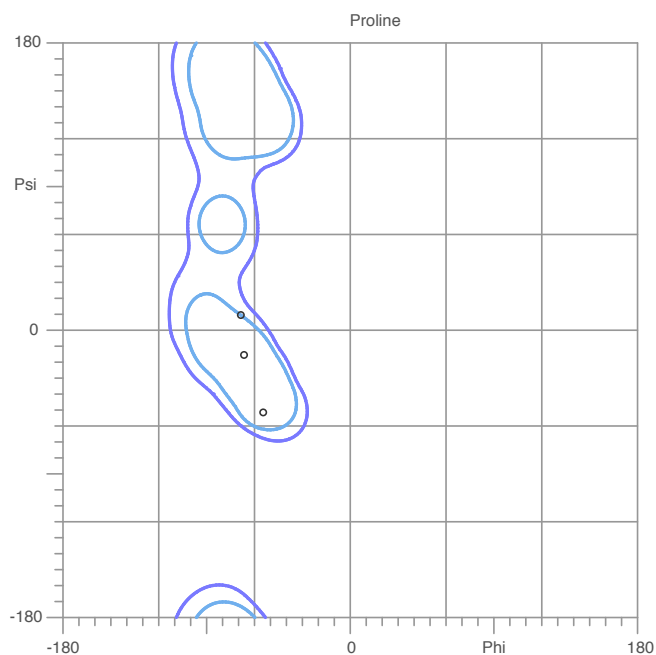
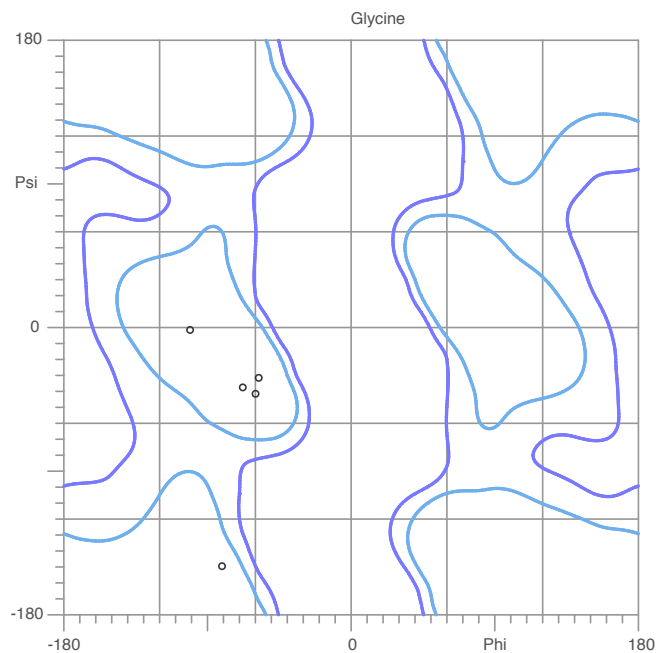
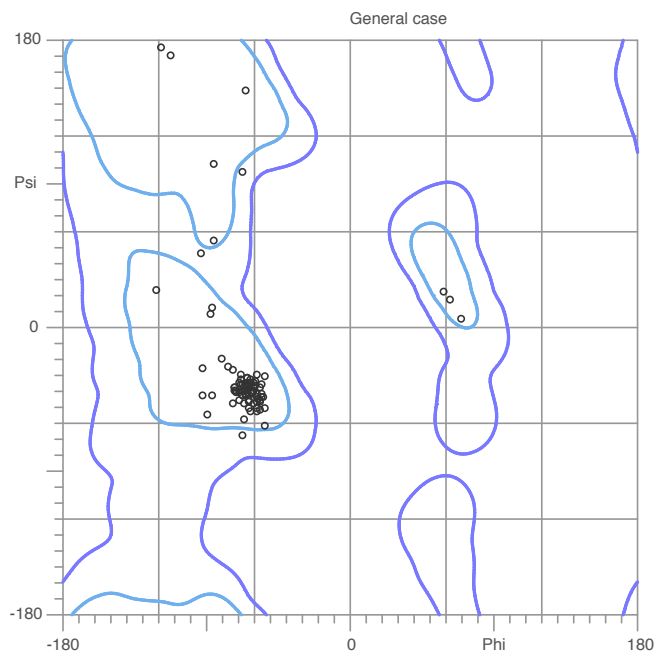
95.7% (1856/1940) of all residues were in favored (98%) regions.
99.7% (1935/1940) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[2] 98 HIS (-63.7, -87.0)
[14] 96 HIS (-44.4, 96.5)
[19] 97 HIS (41.5, -63.5)
[19] 98 HIS (81.9, 116.3)
[20] 94 HIS (165.3, -175.4)

MolProbity Ramachandran analysis

SRR115C_NMR_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.

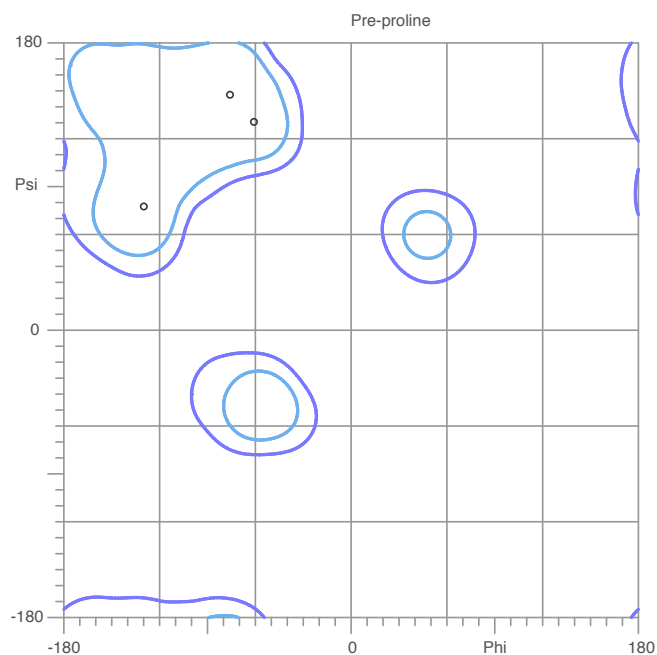
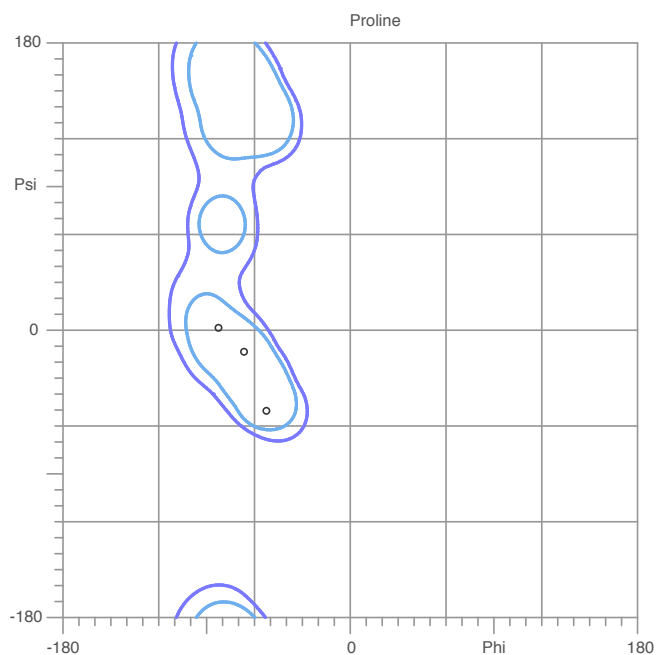
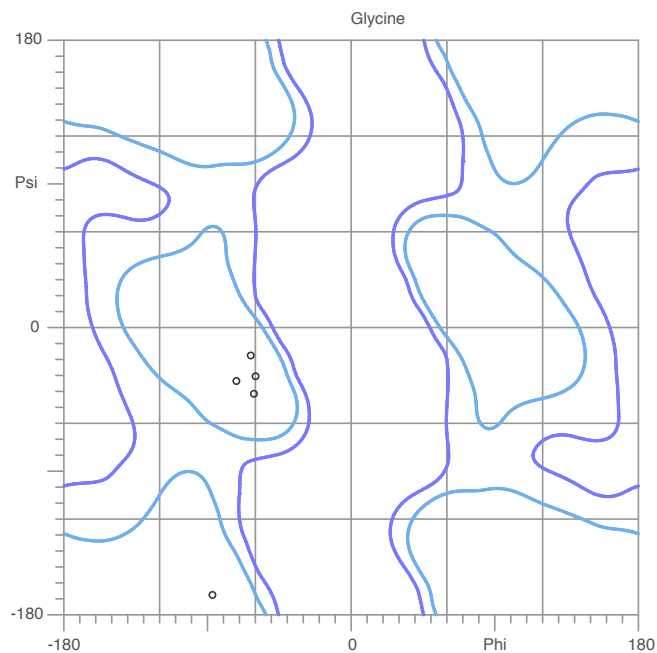
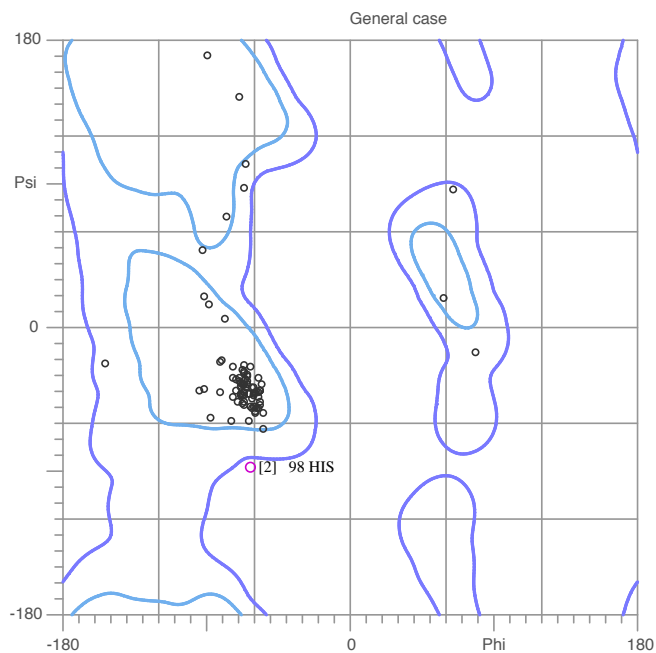
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 2

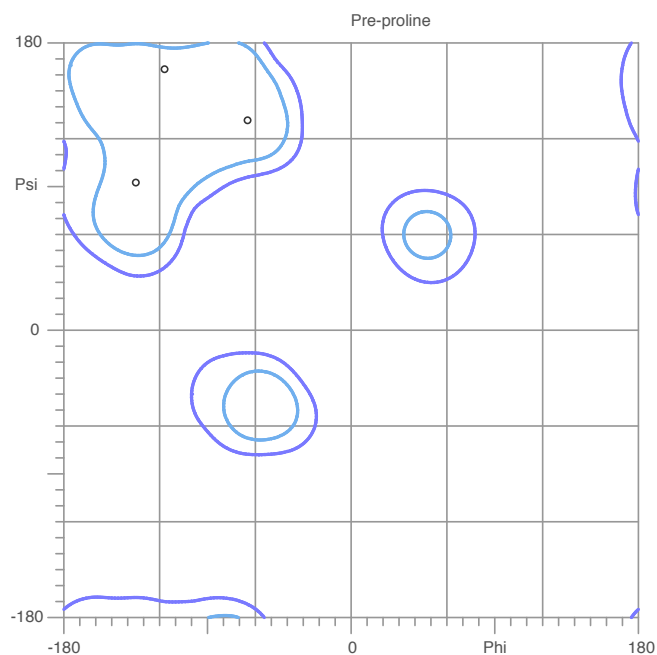
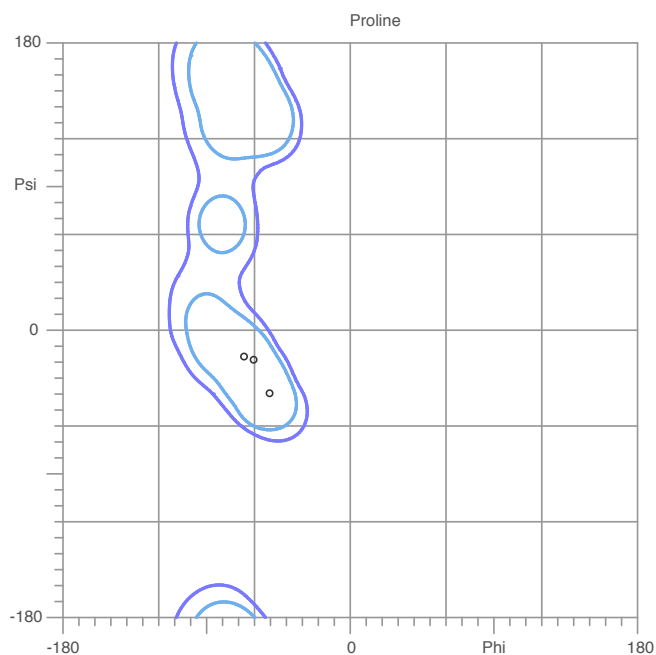
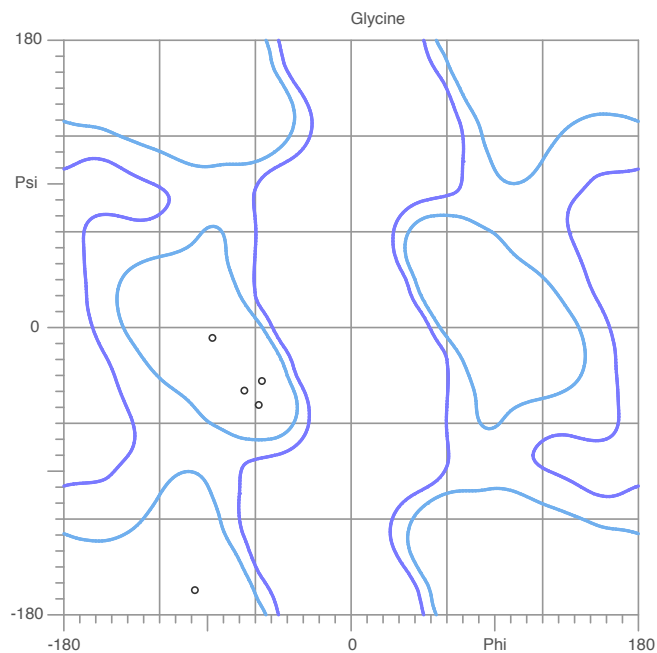
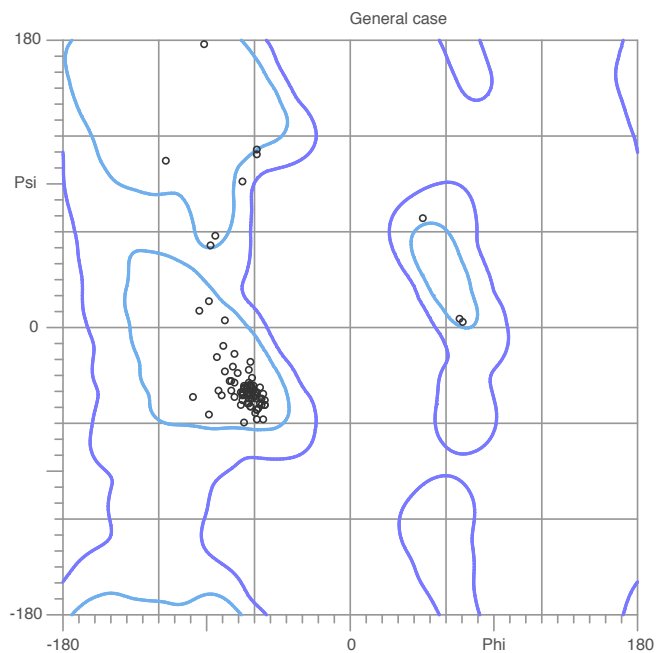


92.8% (90/97) of all residues were in favored (98%) regions.
99.0% (96/97) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[2] 98 HIS (-63.7, -87.0)

MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 3



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.

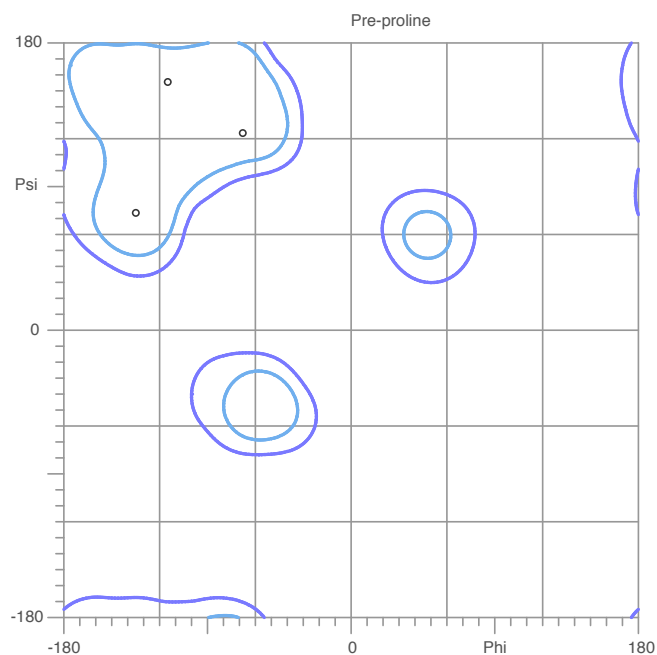
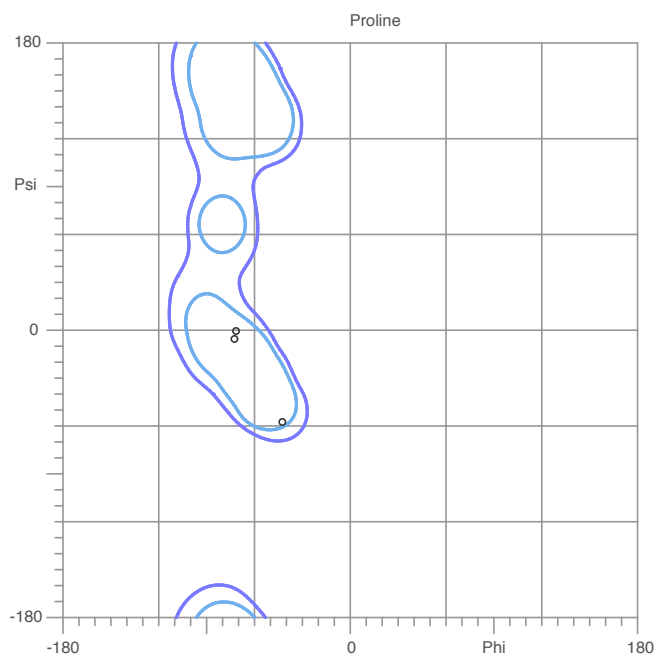
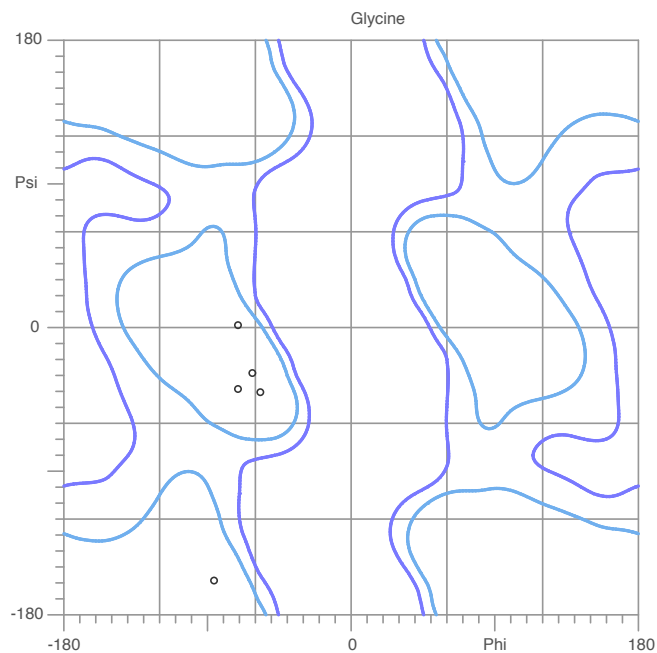
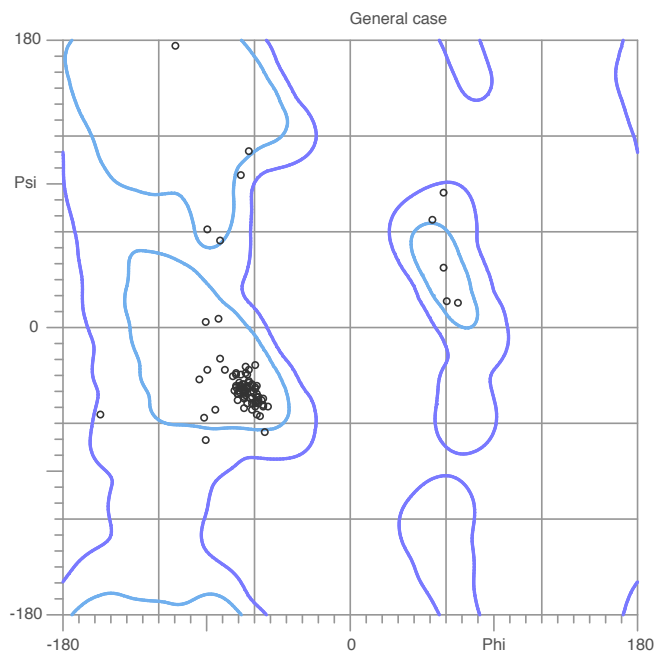
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 4



93.8% (91/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

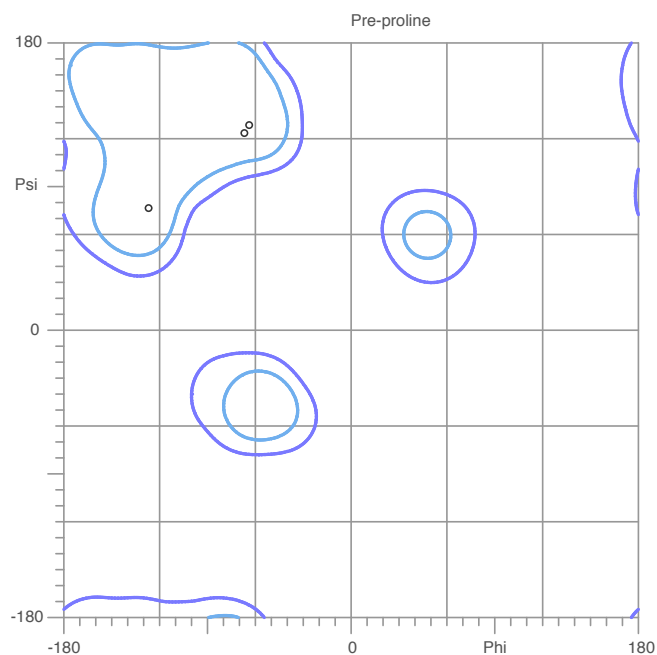
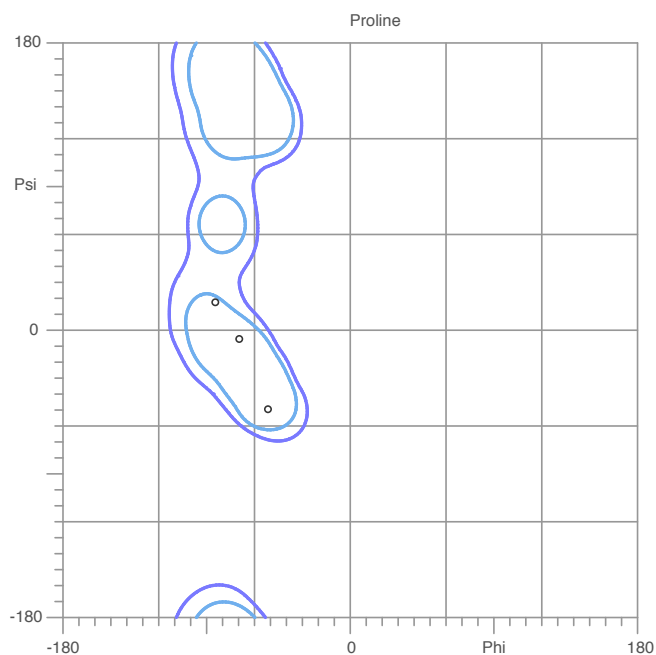
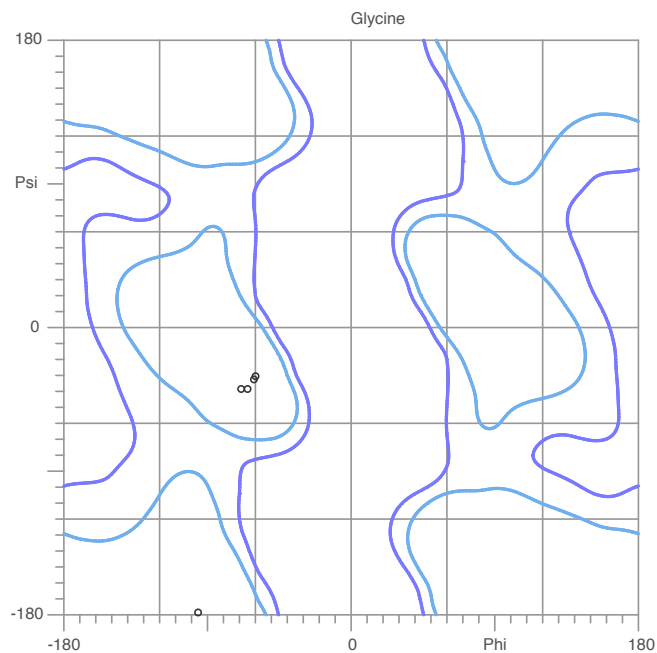
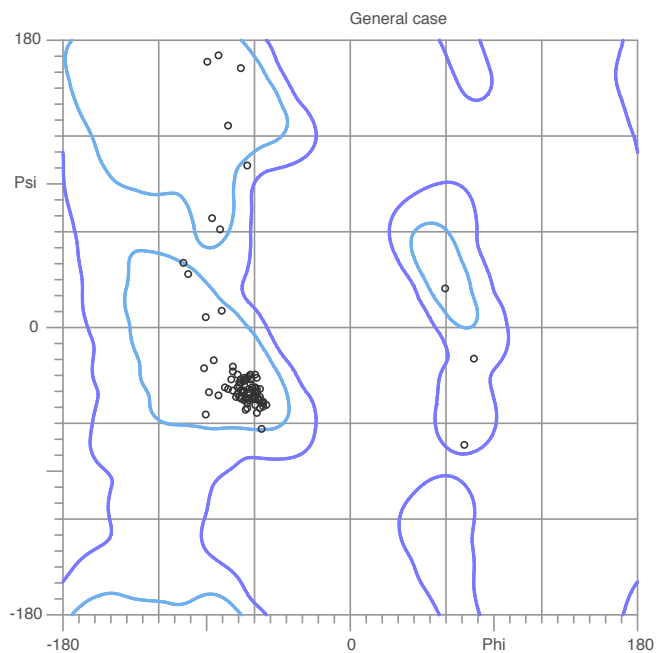
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 5



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.

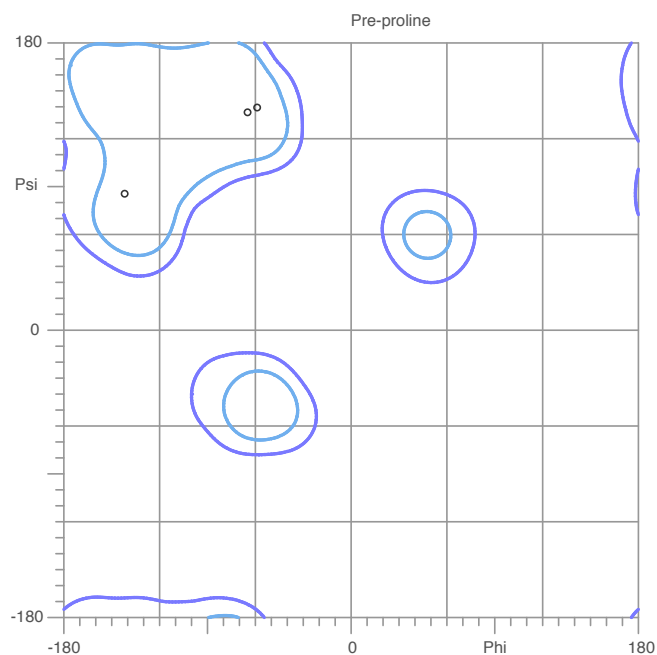
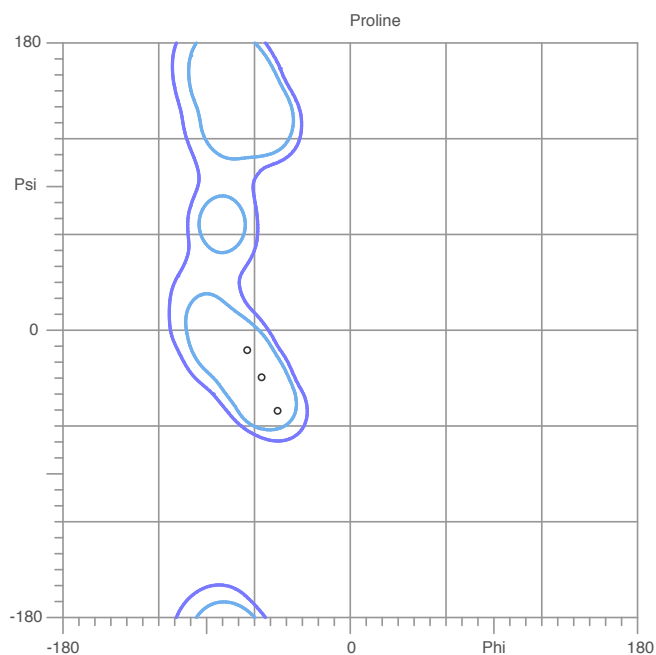
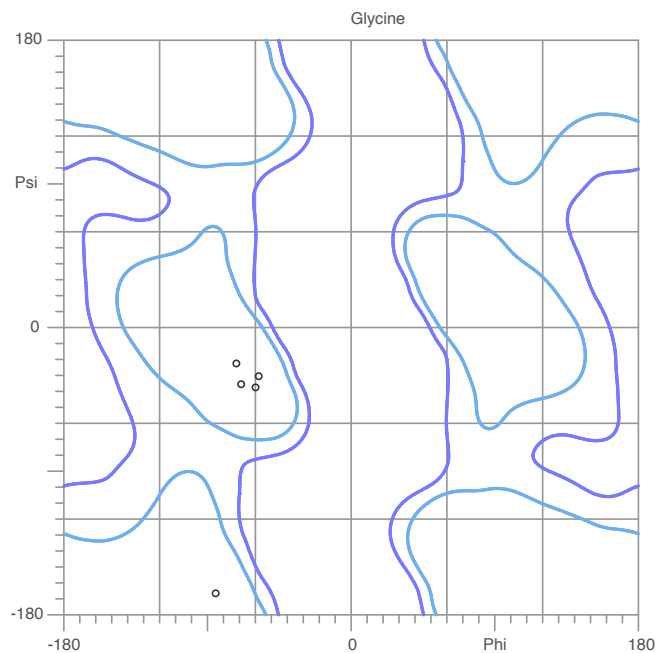
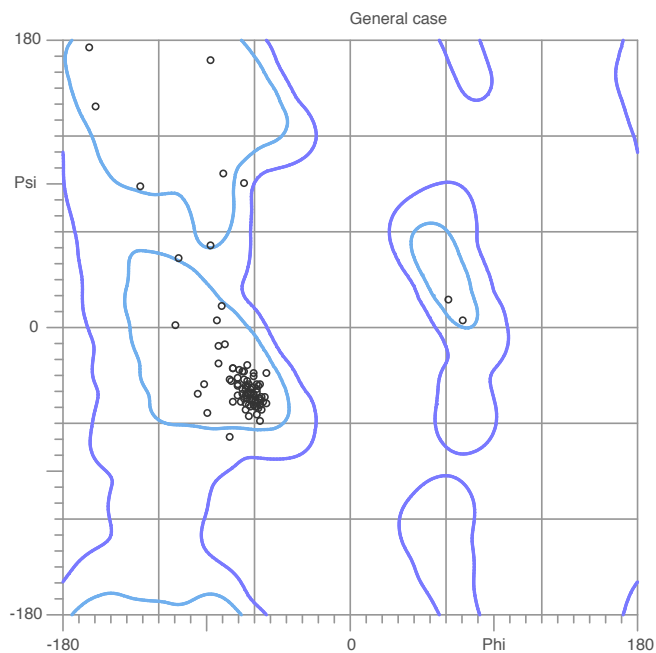
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 6



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.

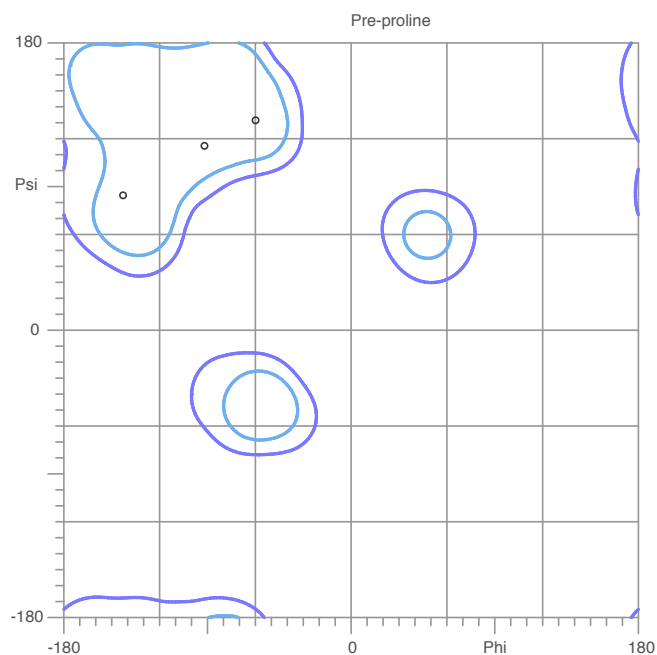
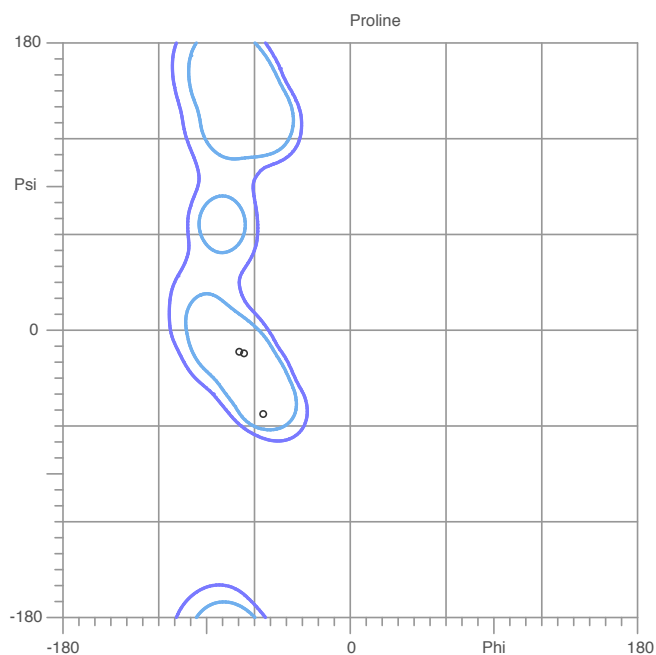
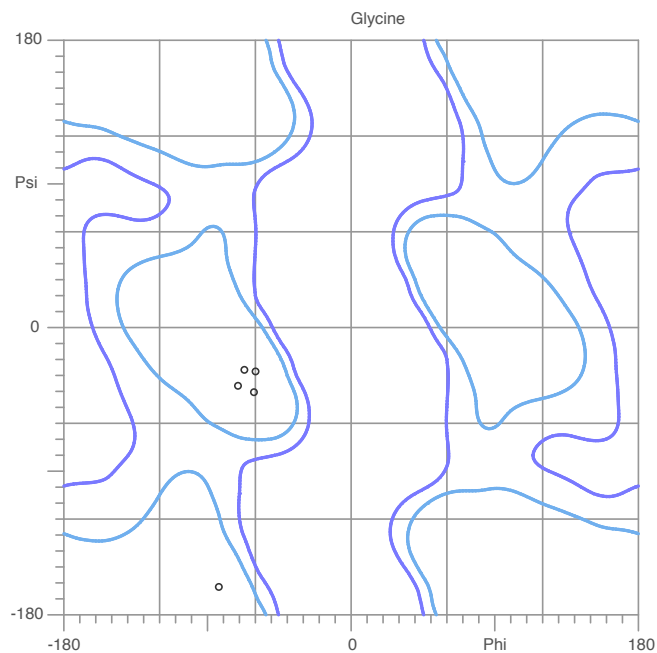
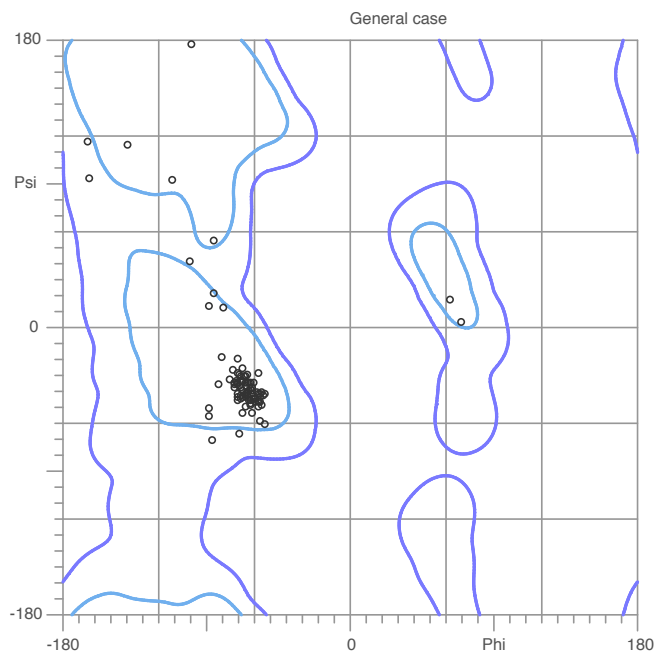
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 7



94.8% (92/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

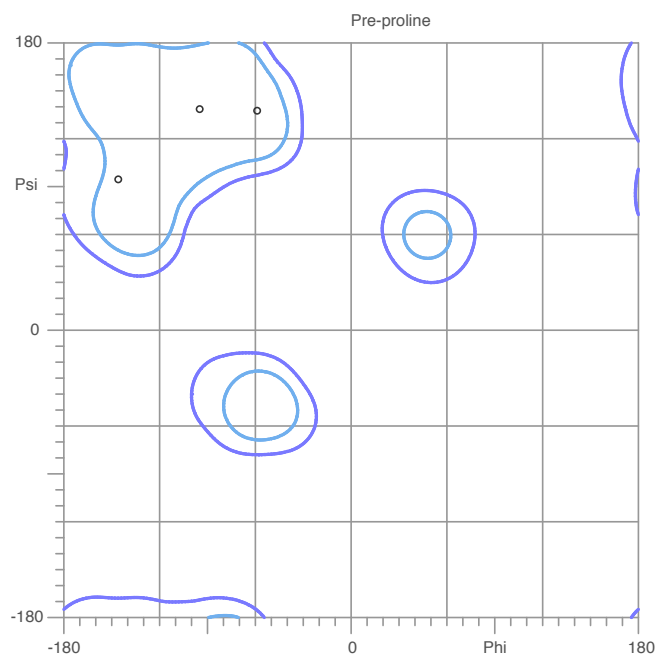
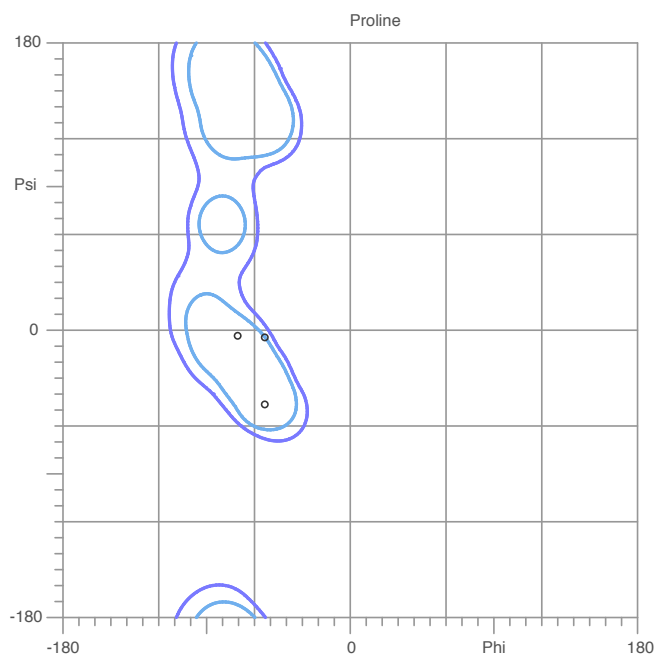
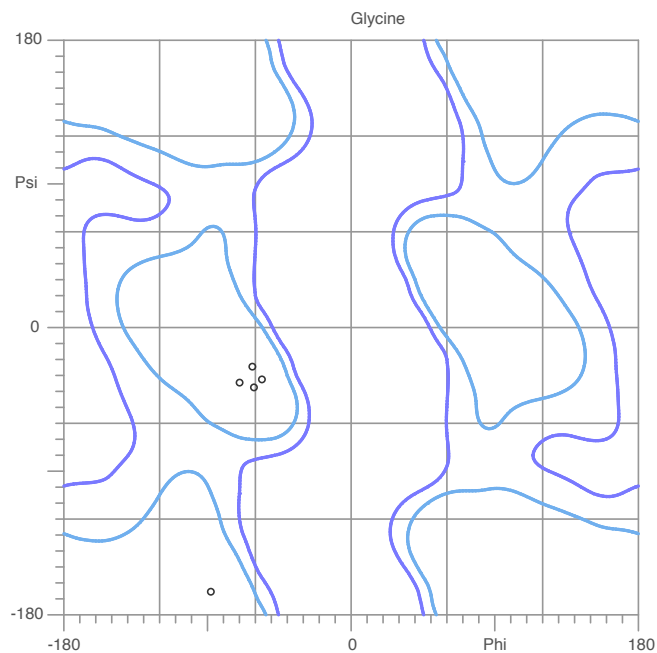
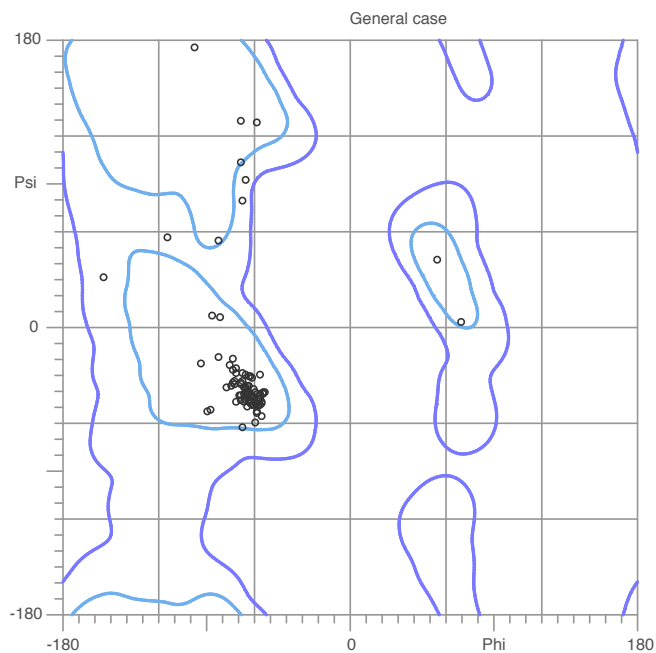
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 8



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.

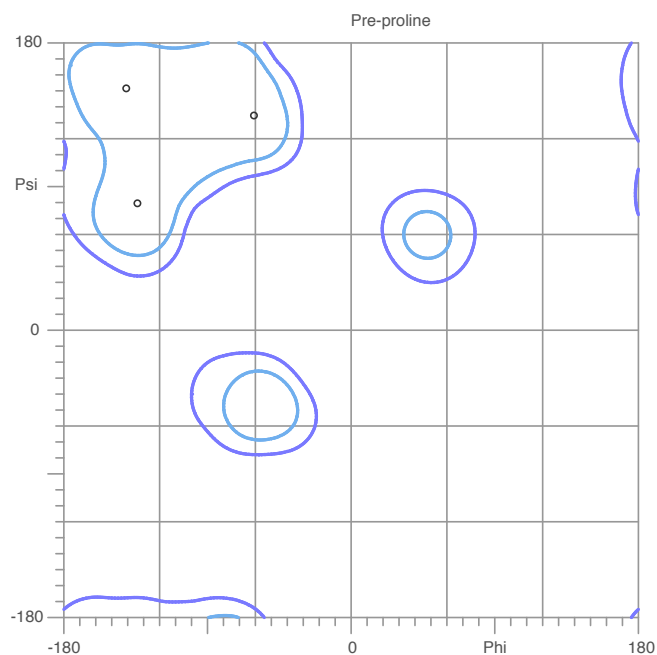
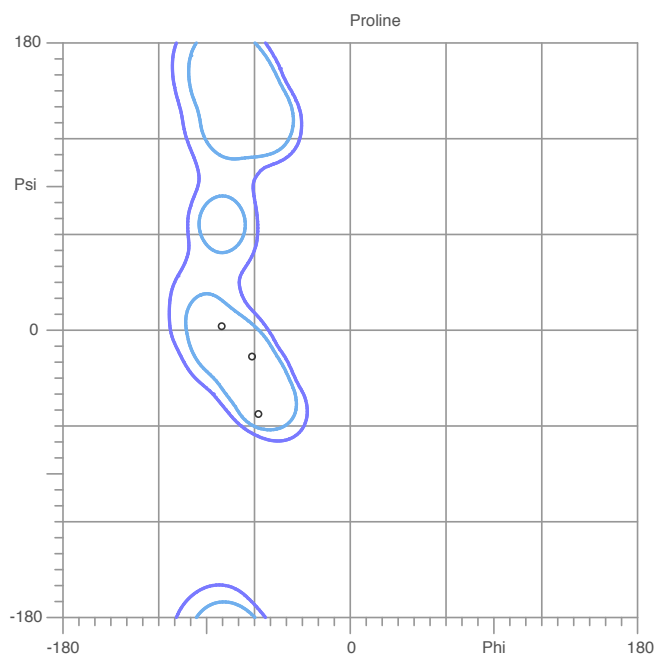
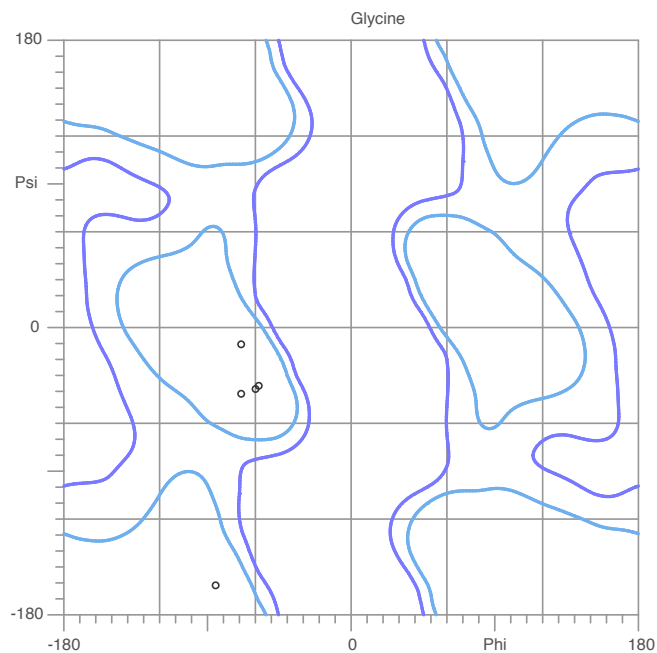
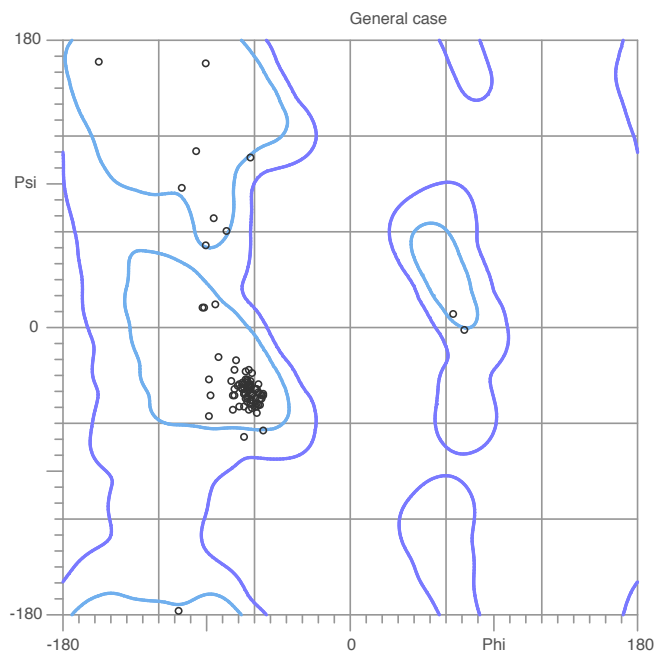
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 9



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.

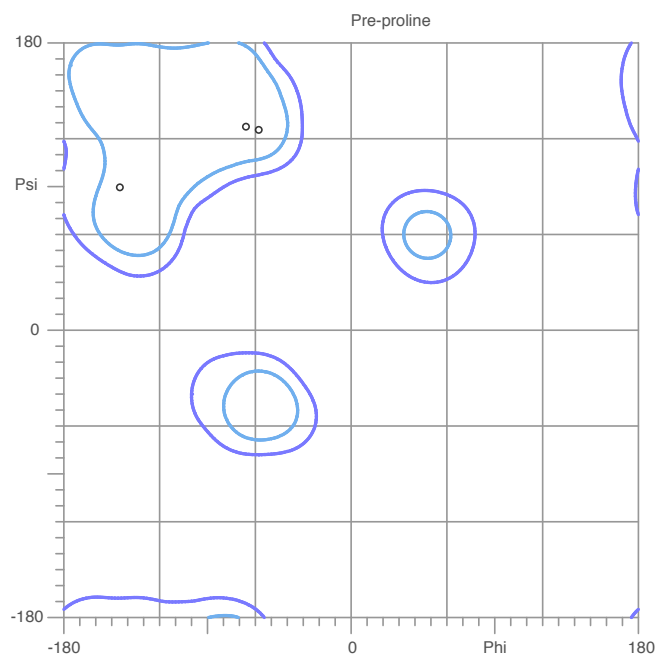
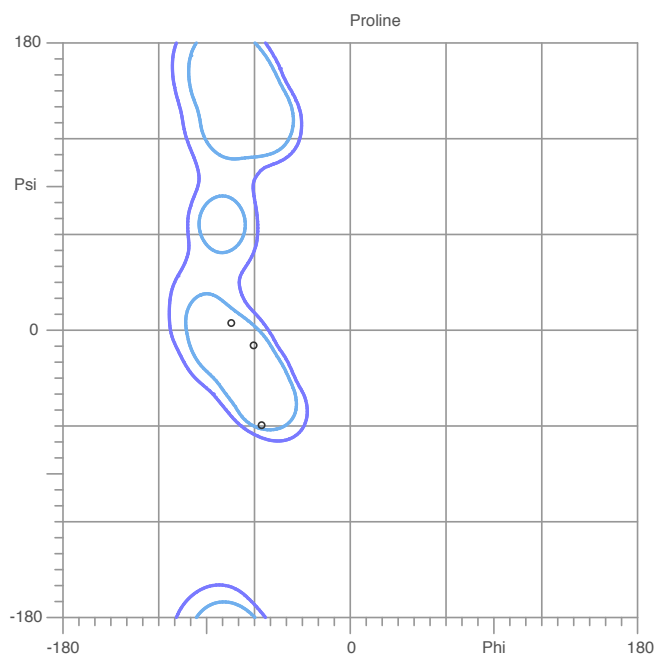
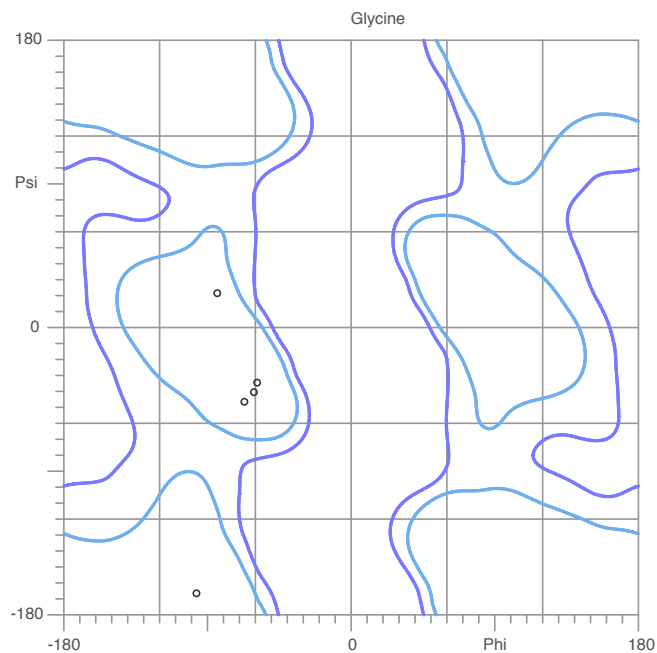
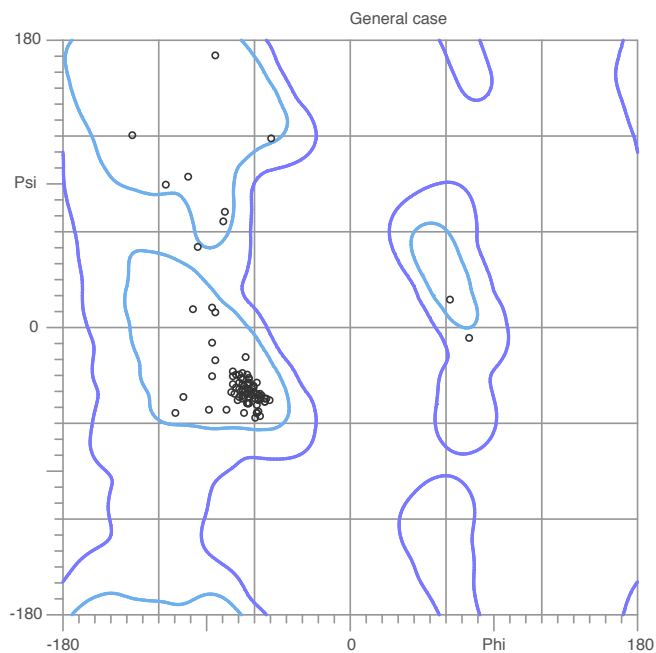
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_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.

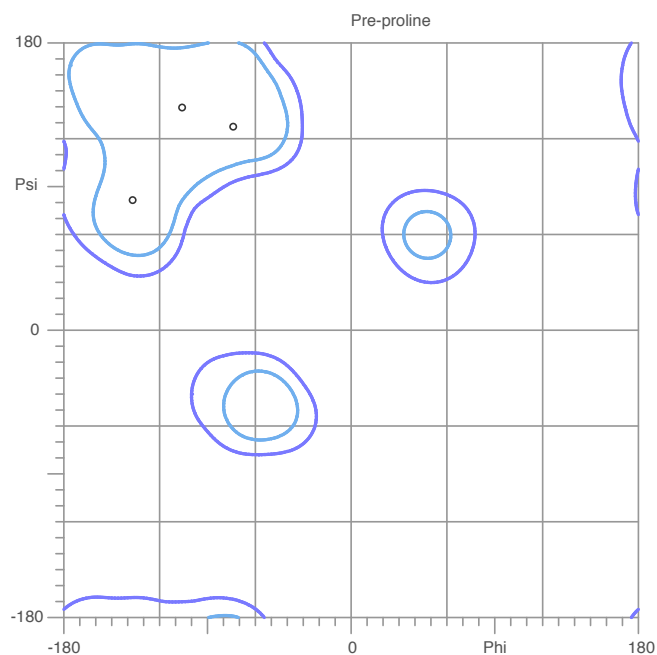
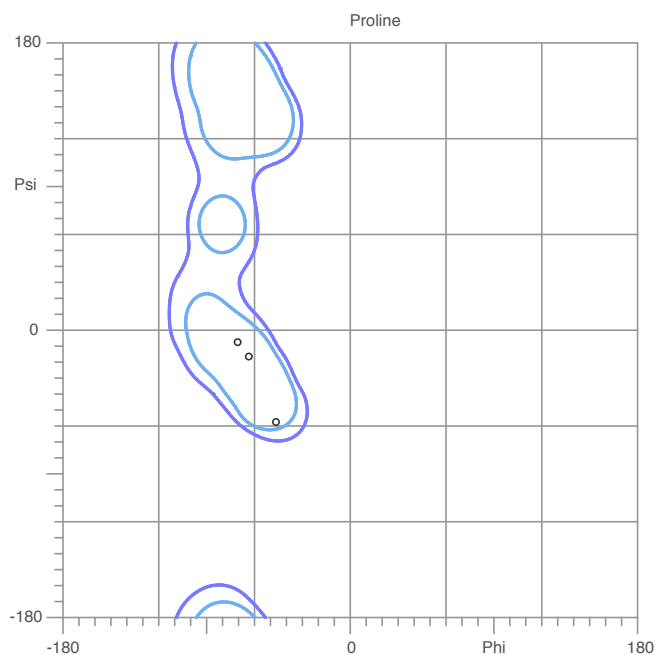
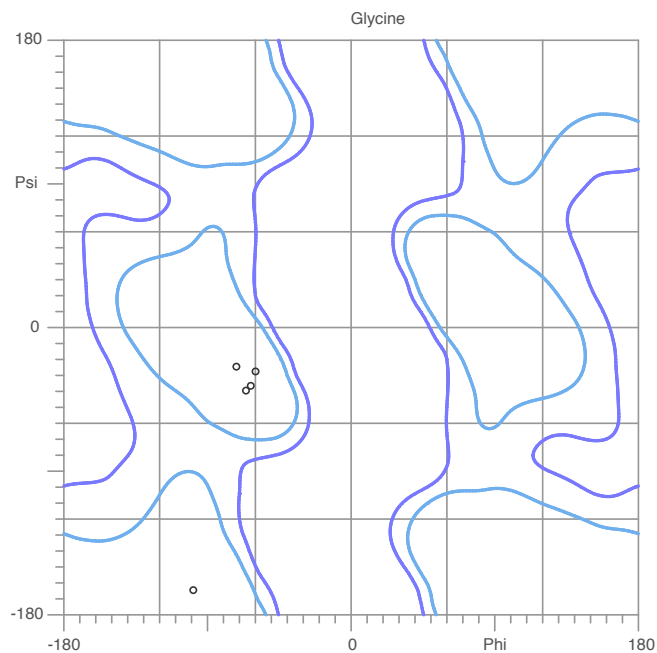
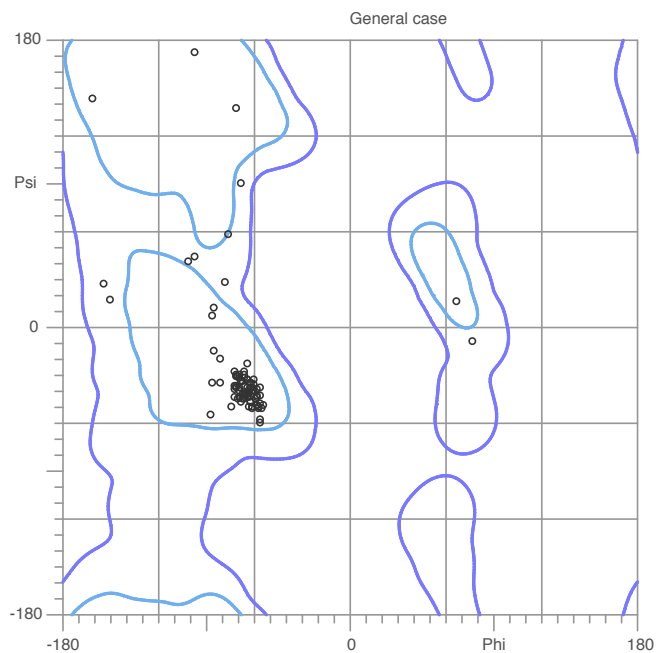
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 11



92.8% (90/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

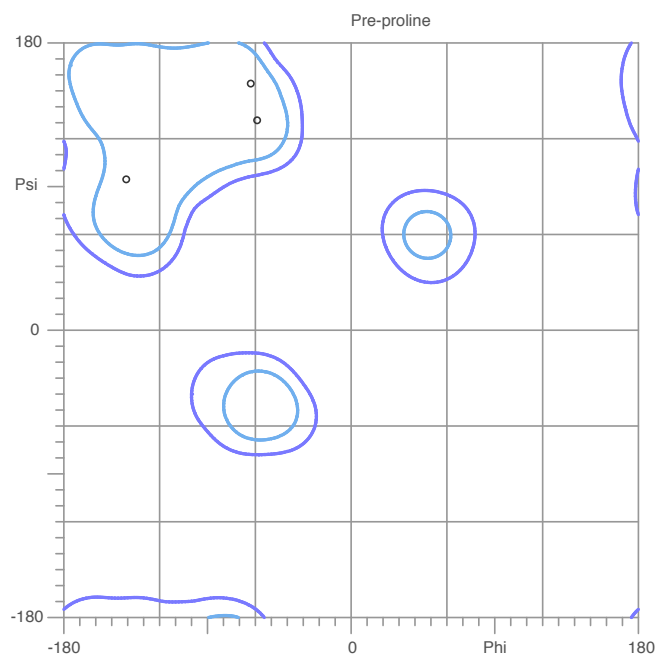
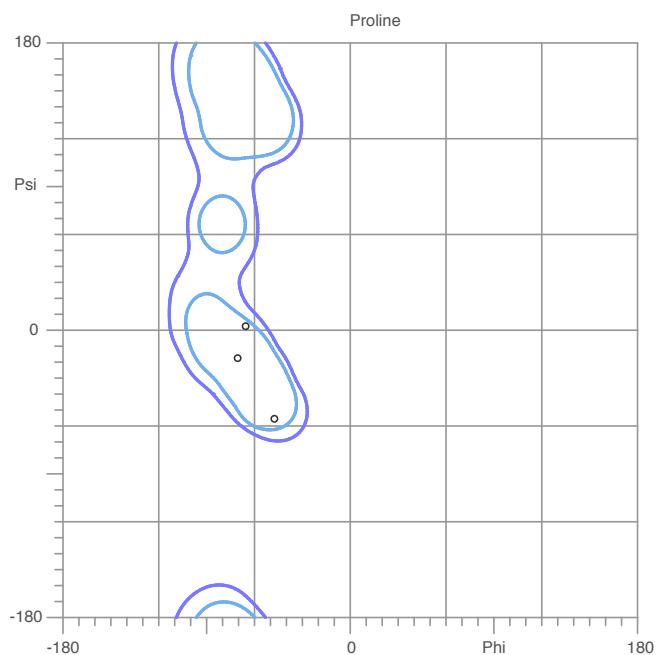
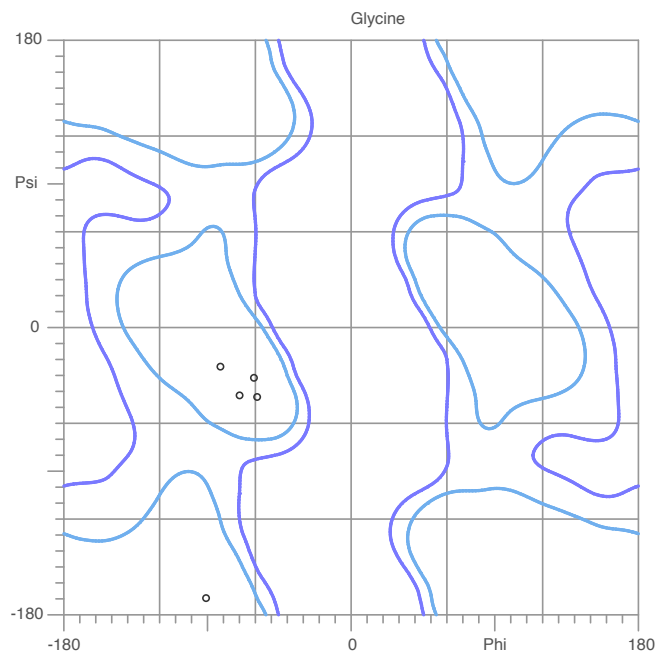
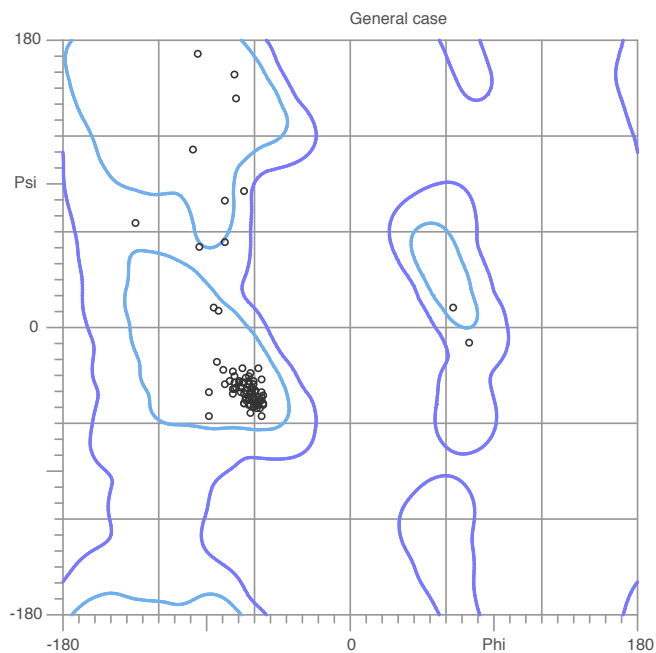
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 12



94.8% (92/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

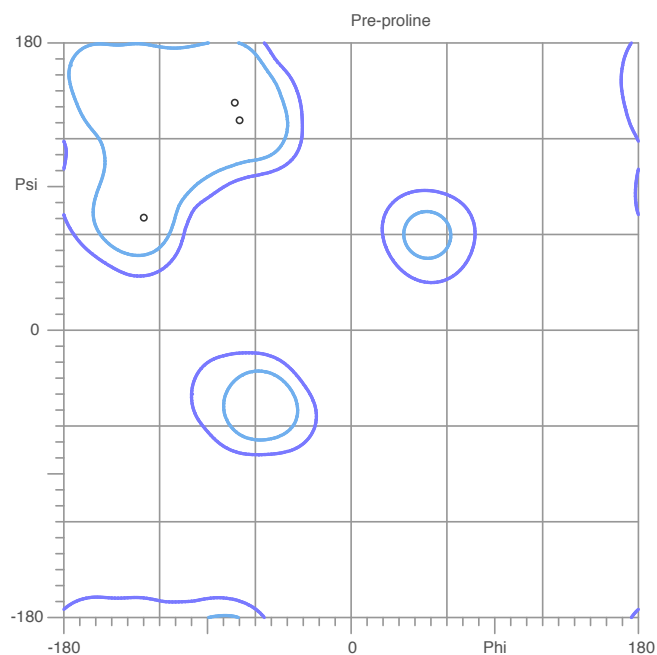
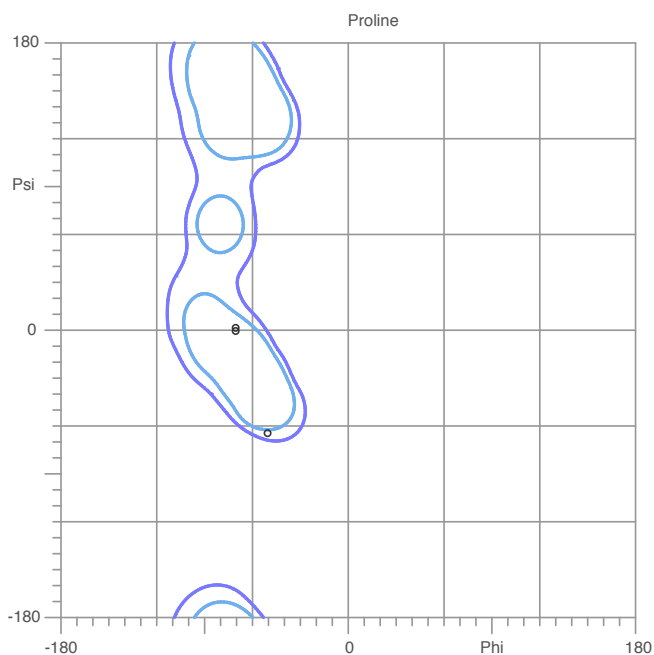
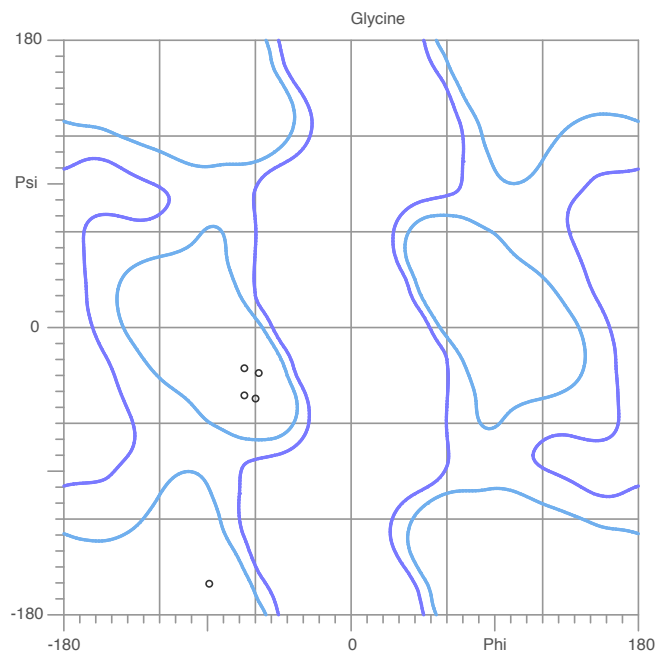
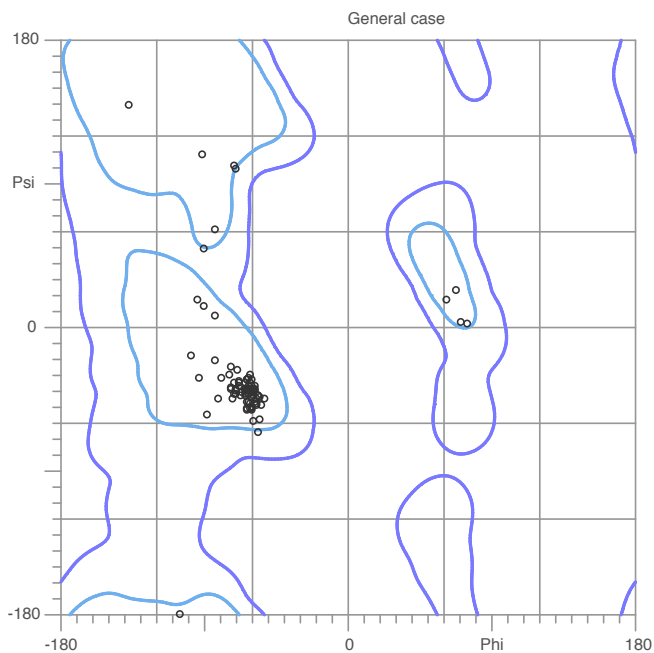
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 13



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.

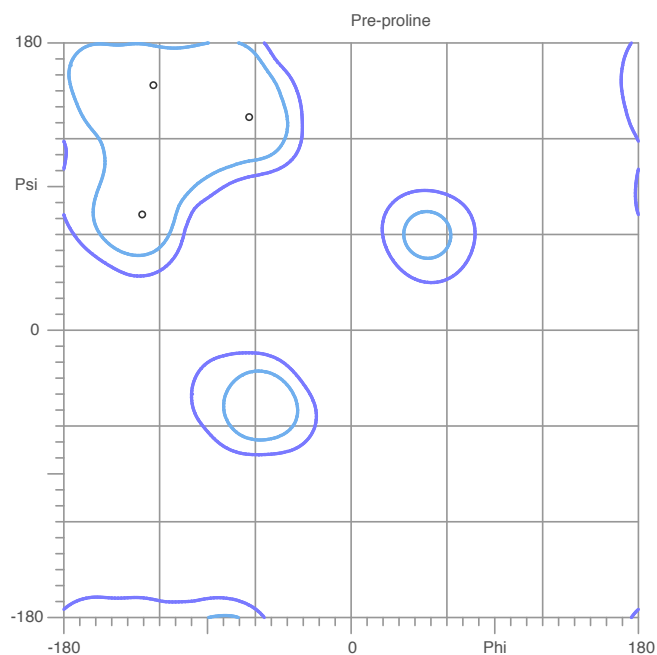
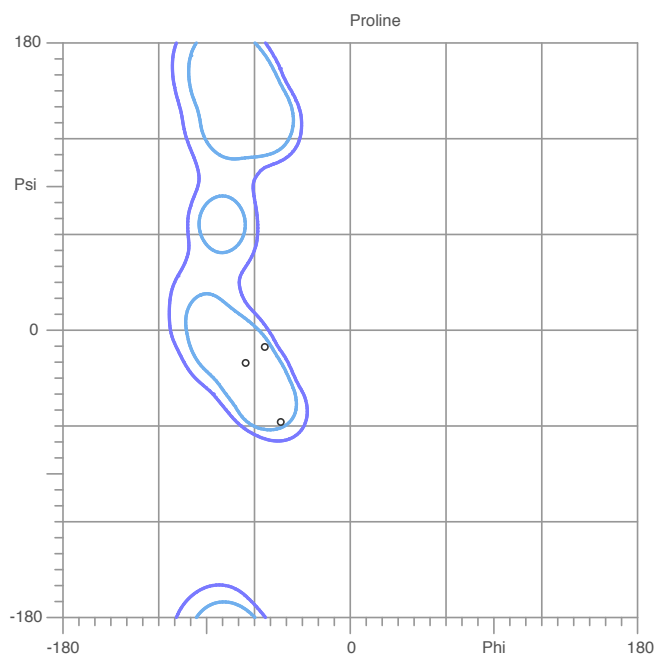
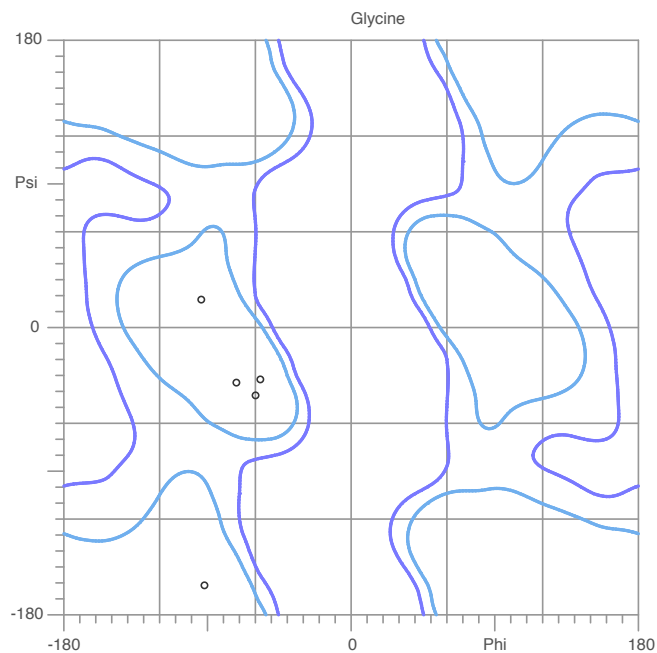
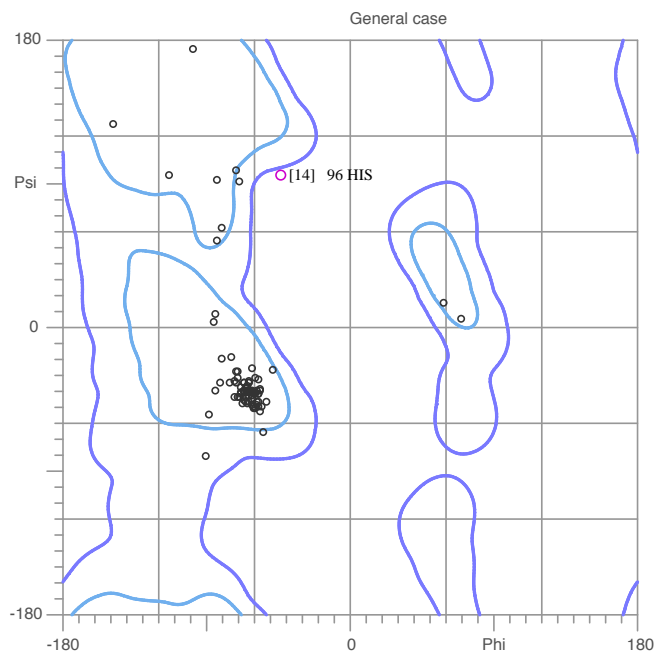
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 14



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.

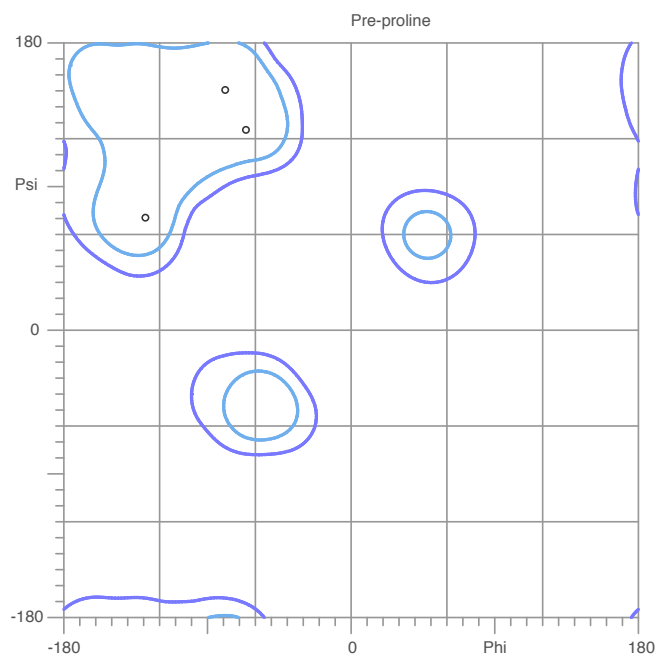
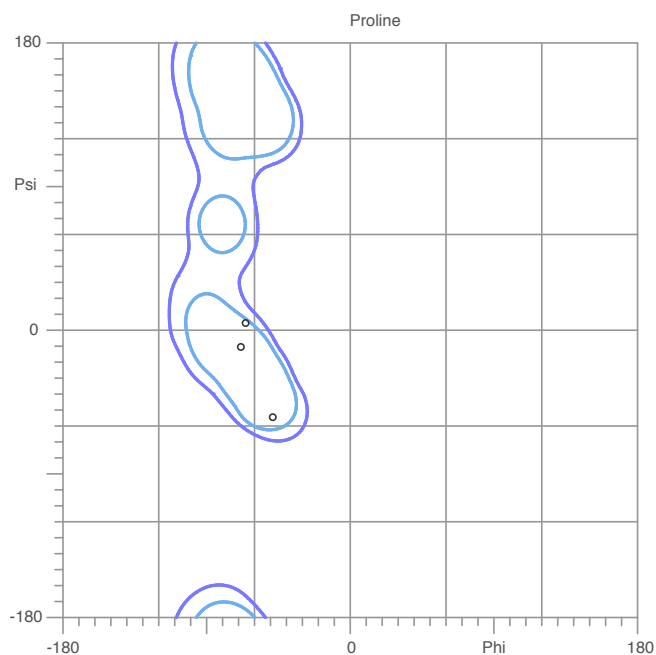
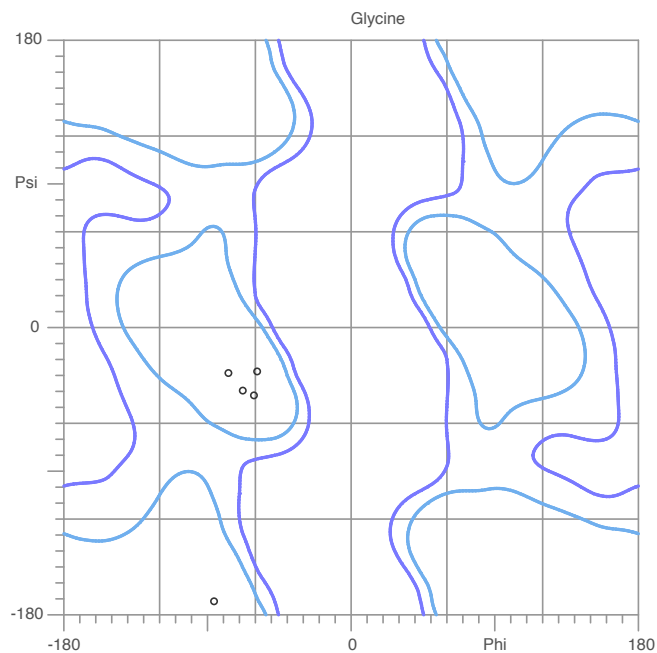
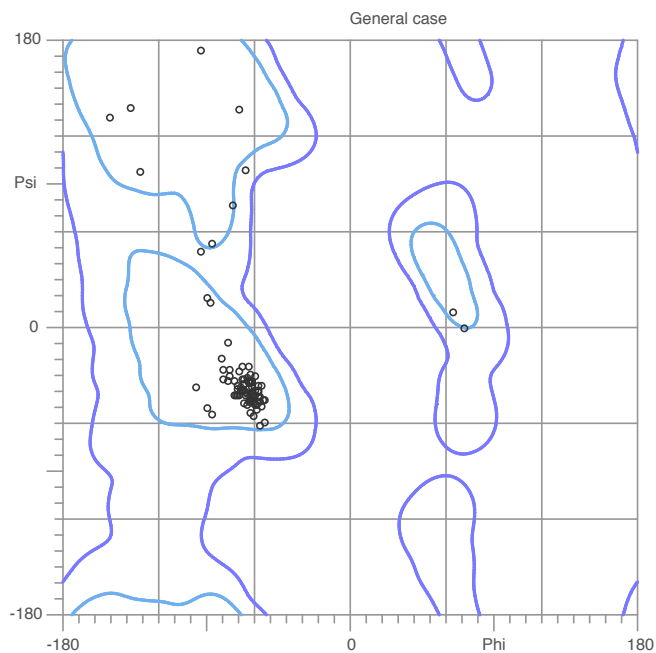
There were 1 outliers (phi, psi):
[14] 96 HIS (-44.4, 96.5)

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

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

MolProbity Ramachandran analysis

SRR115C_NMR_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.

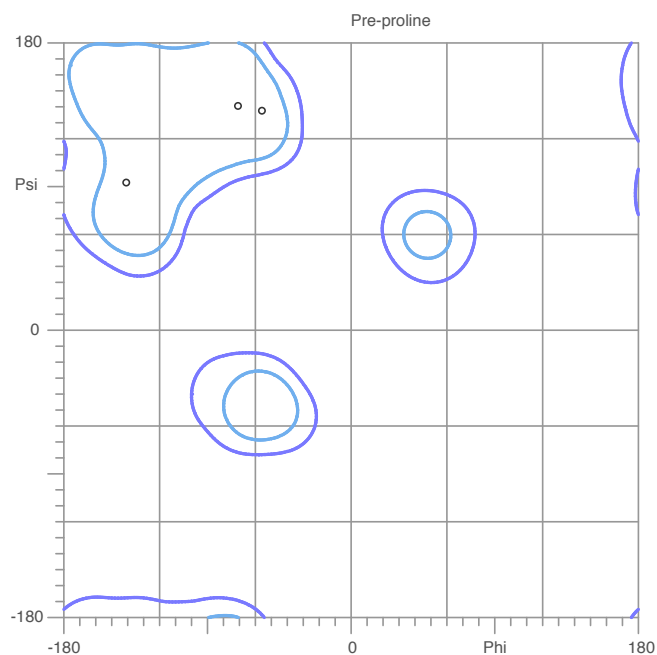
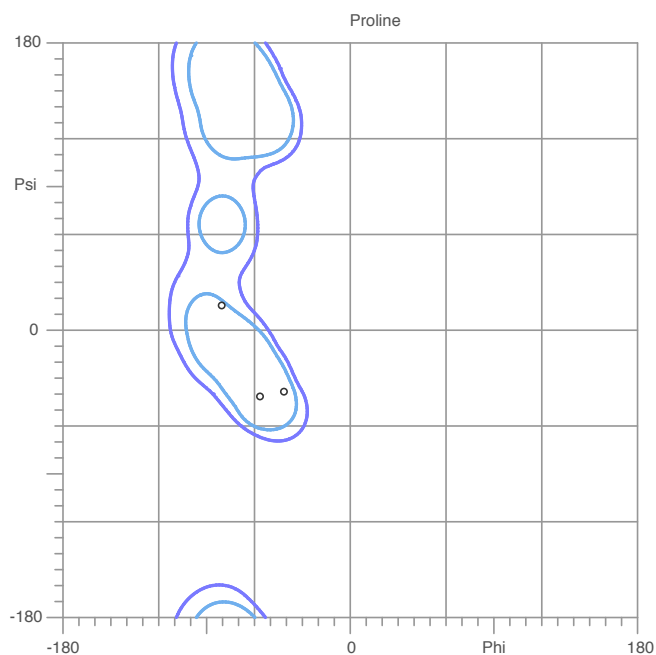
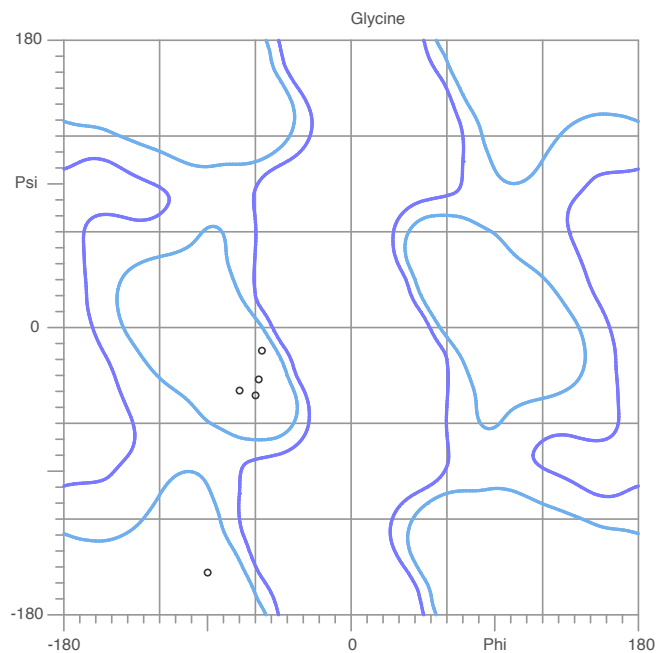
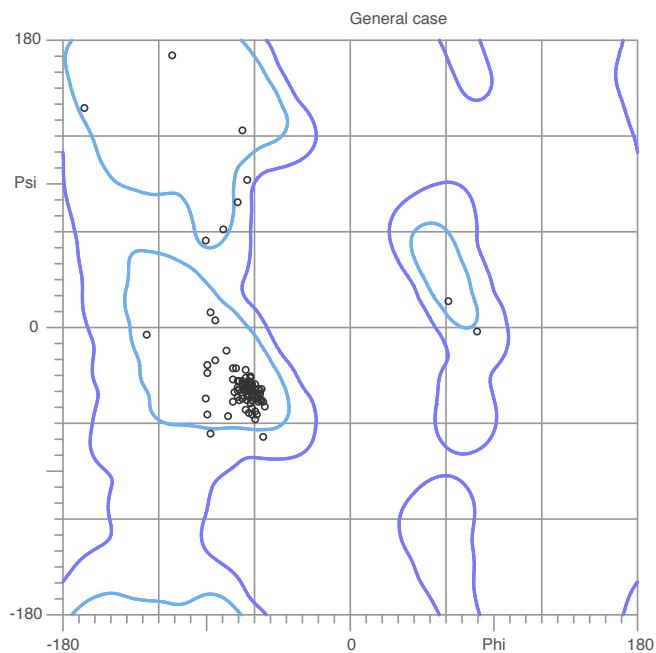
There were no outliers.

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

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MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 16



94.8% (92/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

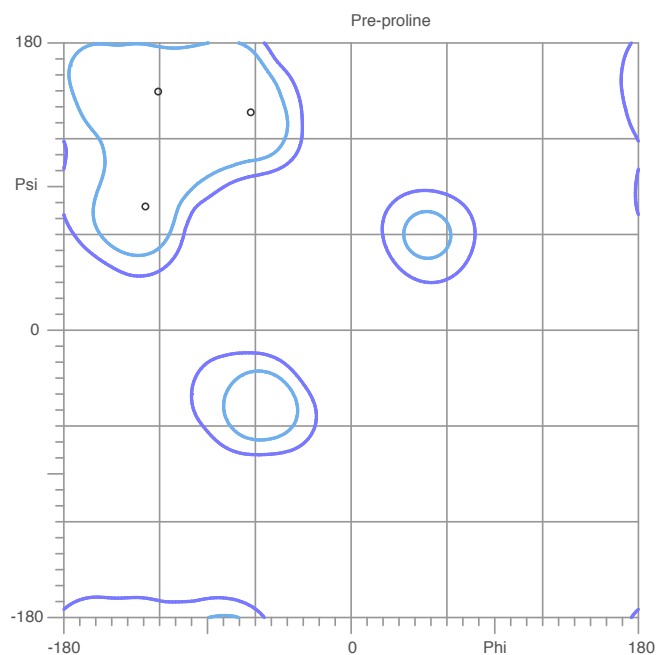
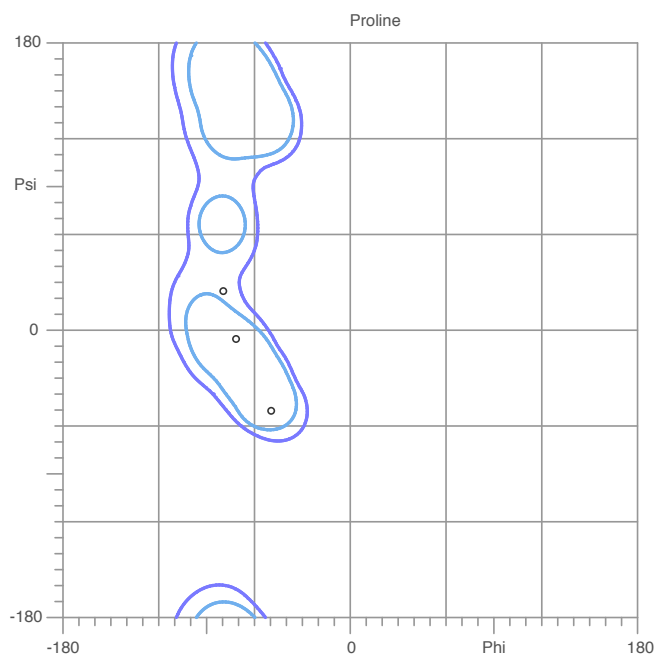
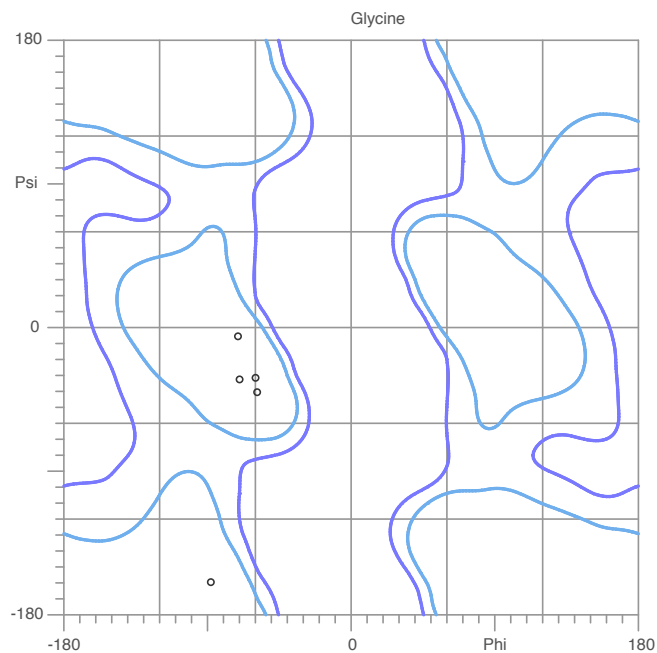
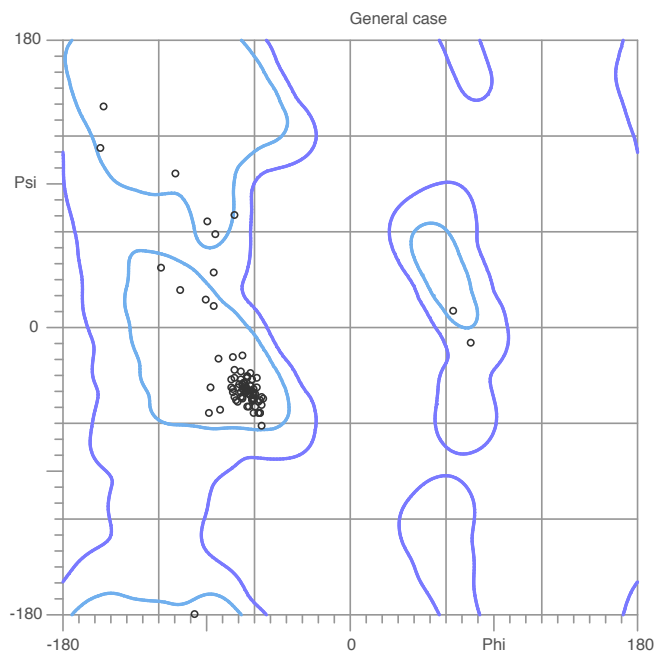
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 17



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.

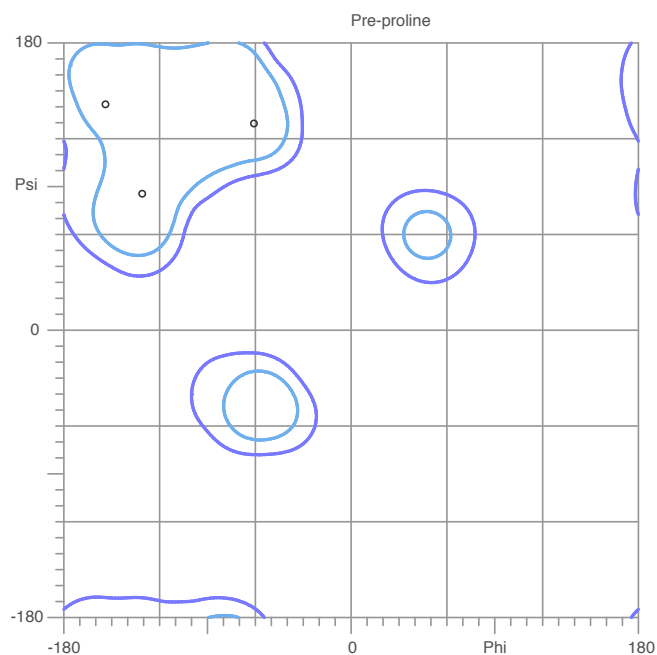
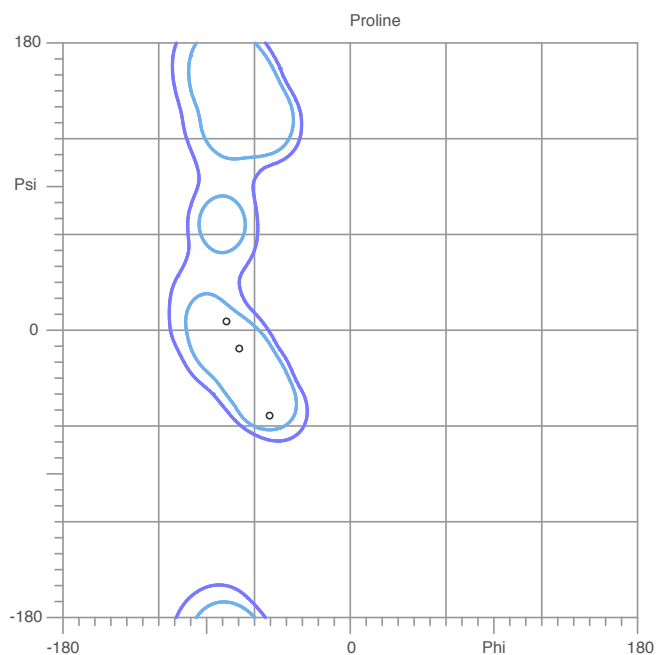
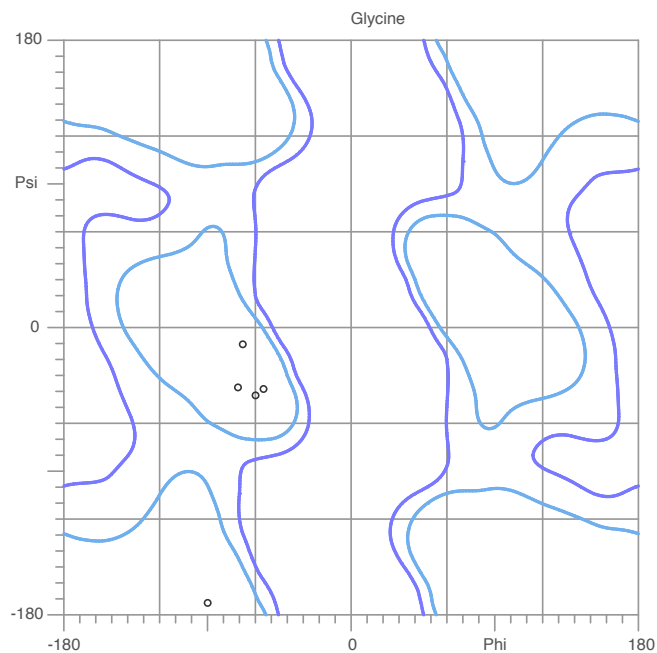
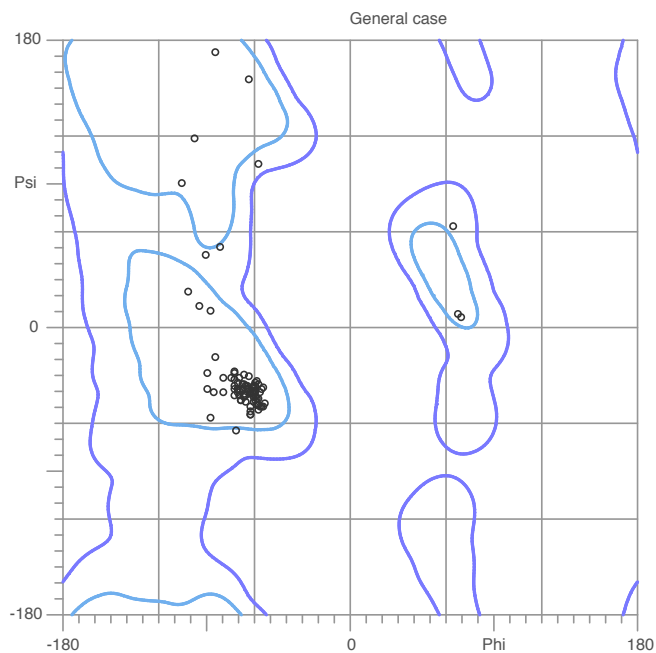
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 18



94.8% (92/97) of all residues were in favored (98%) regions.
100.0% (97/97) of all residues were in allowed (>99.8%) regions.

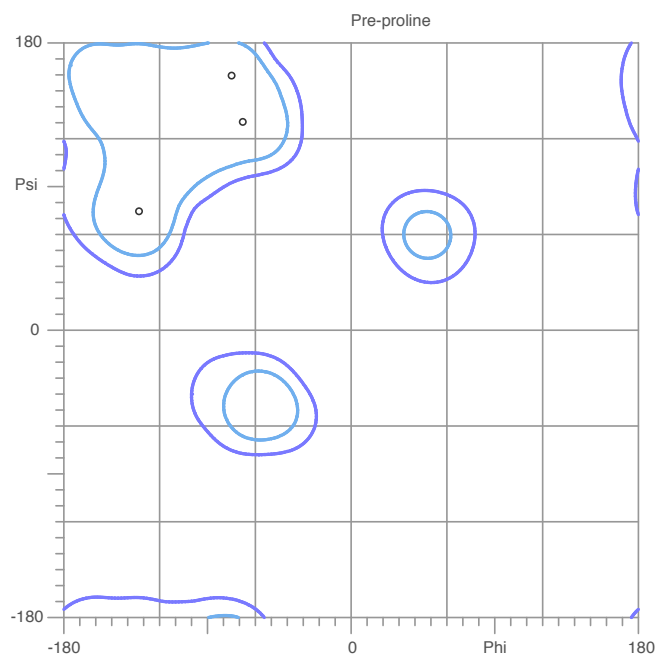
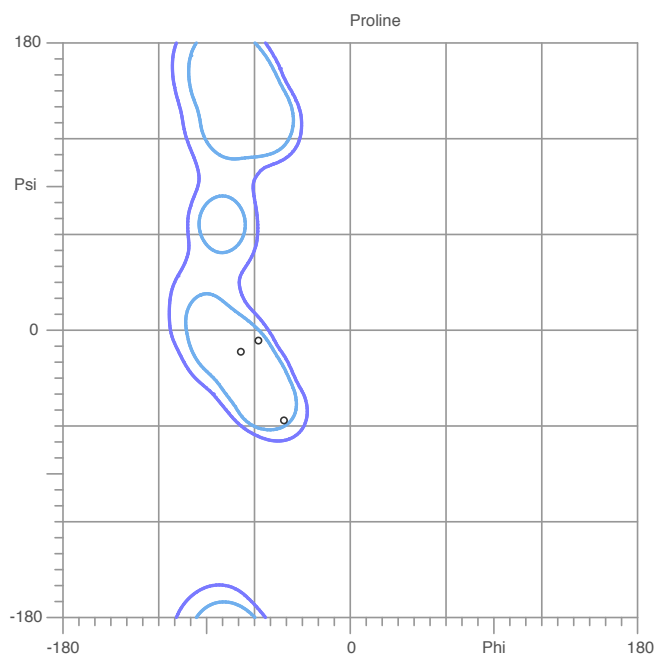
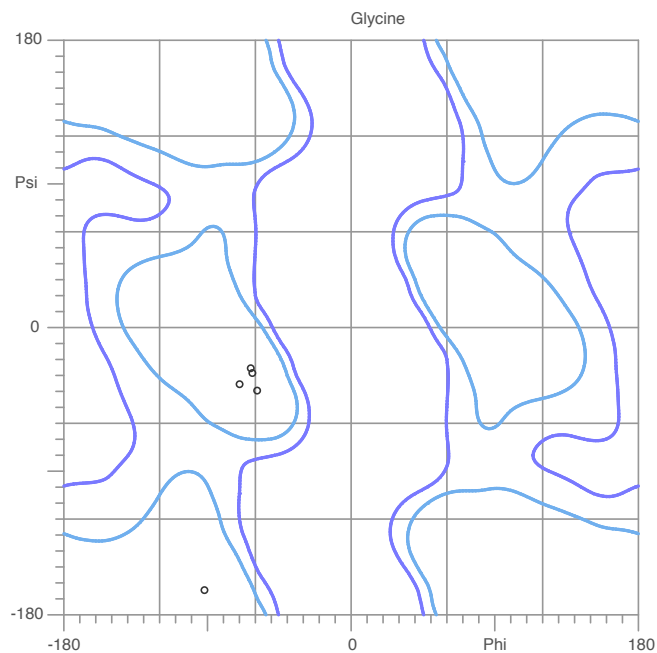
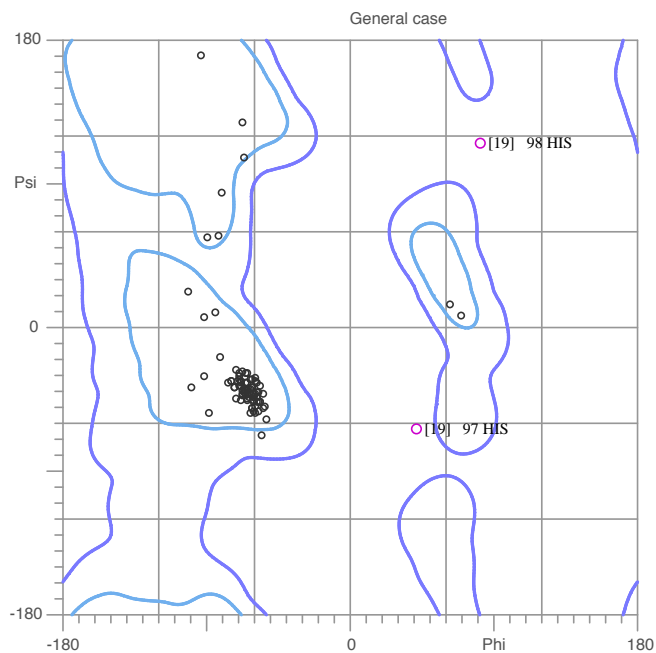
There were no outliers.

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

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

MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 19



96.9% (94/97) of all residues were in favored (98%) regions.
97.9% (95/97) of all residues were in allowed (>99.8%) regions.

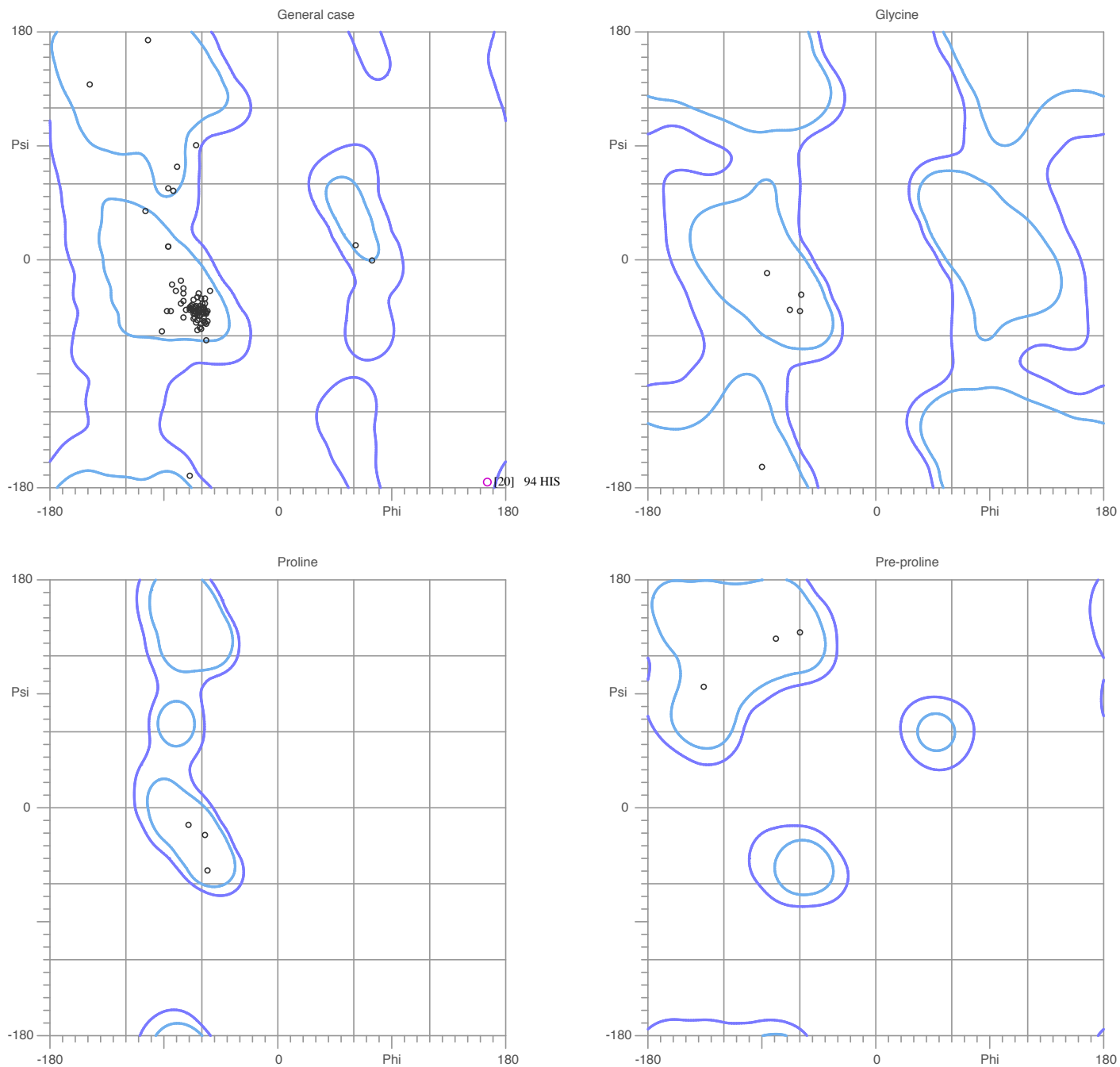
There were 2 outliers (phi, psi):

[19] 97 HIS (41.5, -63.5)

[19] 98 HIS (81.9, 116.3)

MolProbity Ramachandran analysis

SRR115C_NMR_em_bcr3.pdb, model 20



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):
[20] 94 HIS (165.3, -175.4)

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

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