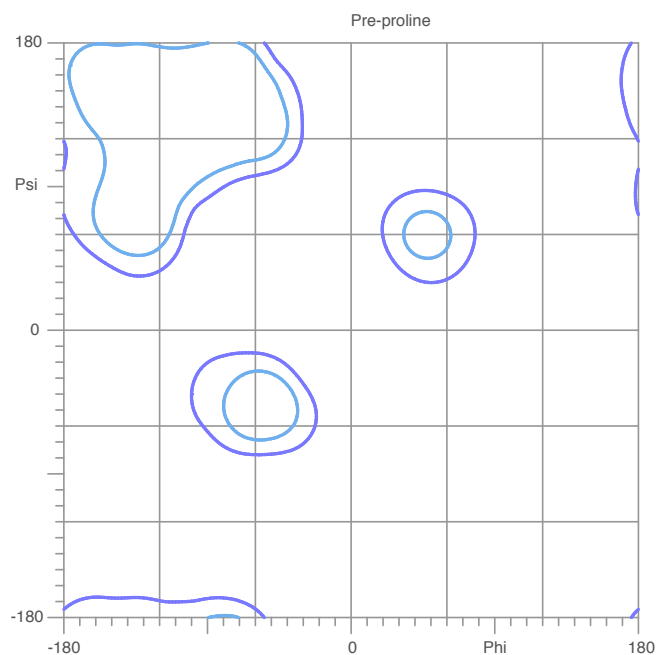
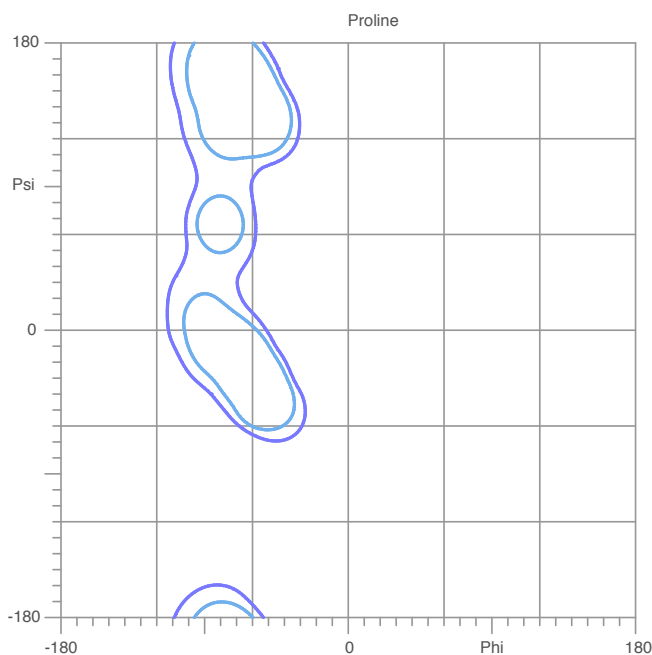
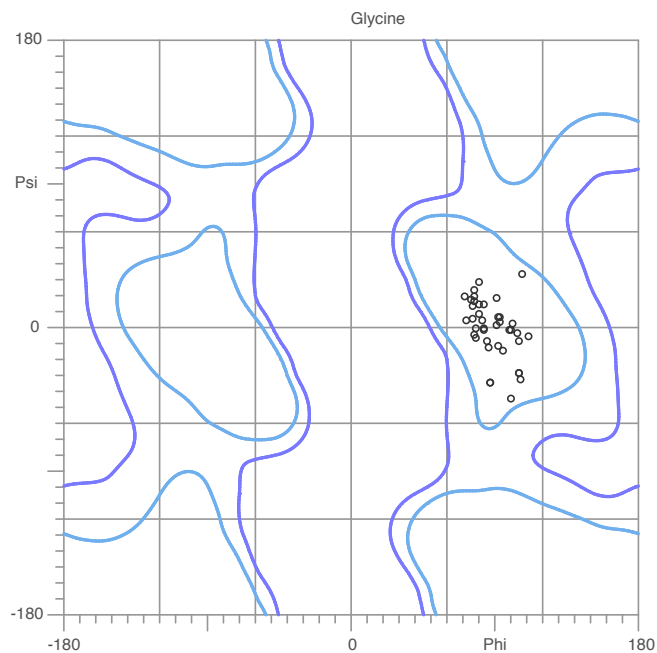
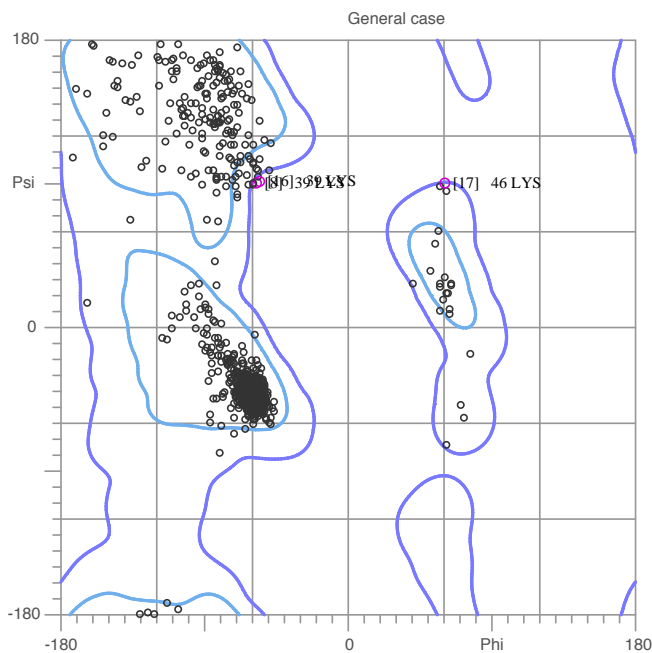


MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, all models



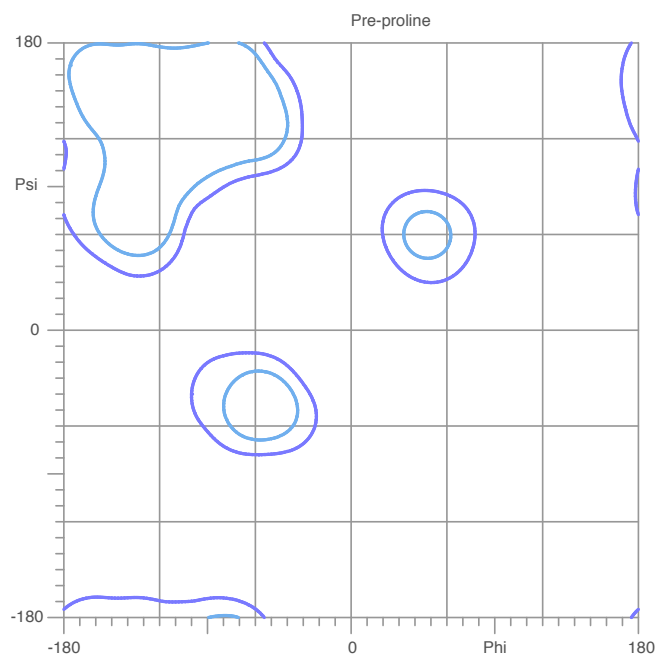
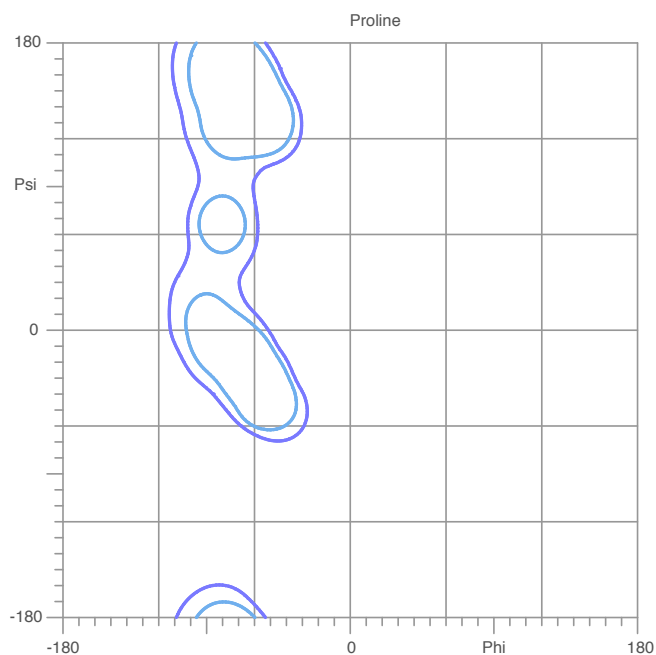
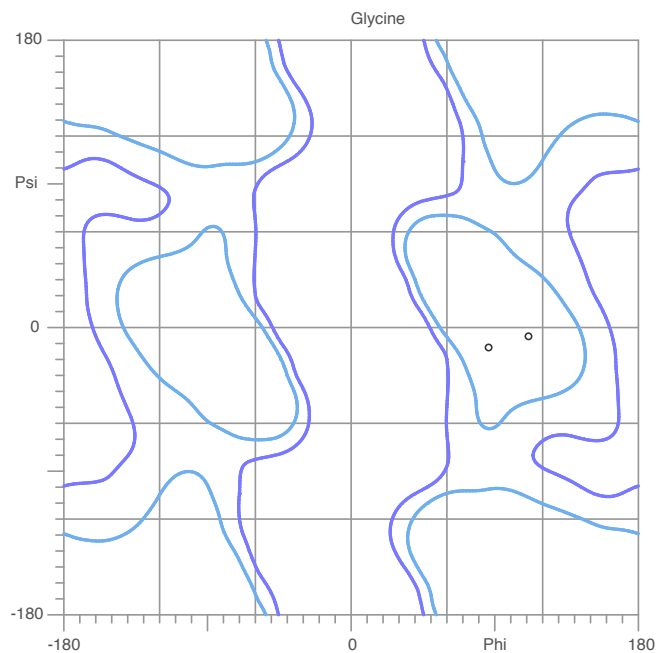
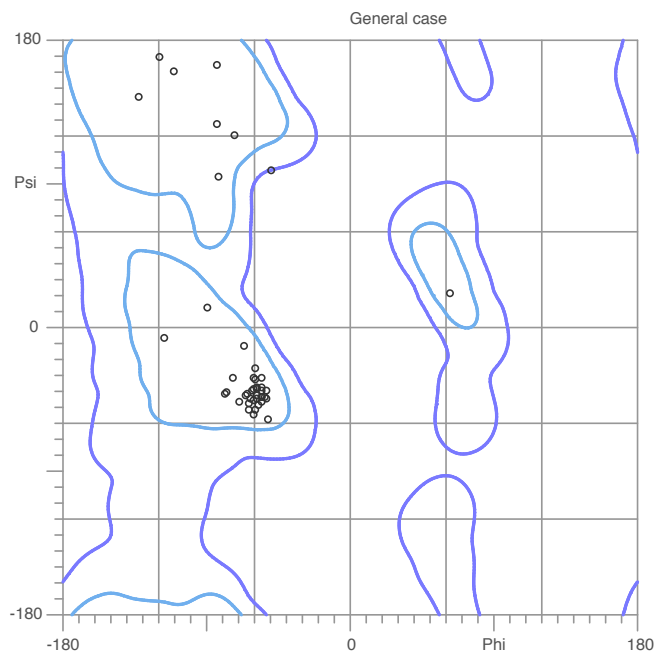
95.9% (882/920) of all residues were in favored (98%) regions.
99.7% (917/920) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 39 LYS (-58.5, 91.9)
- [16] 39 LYS (-56.4, 92.4)
- [17] 46 LYS (60.7, 91.9)

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 1



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

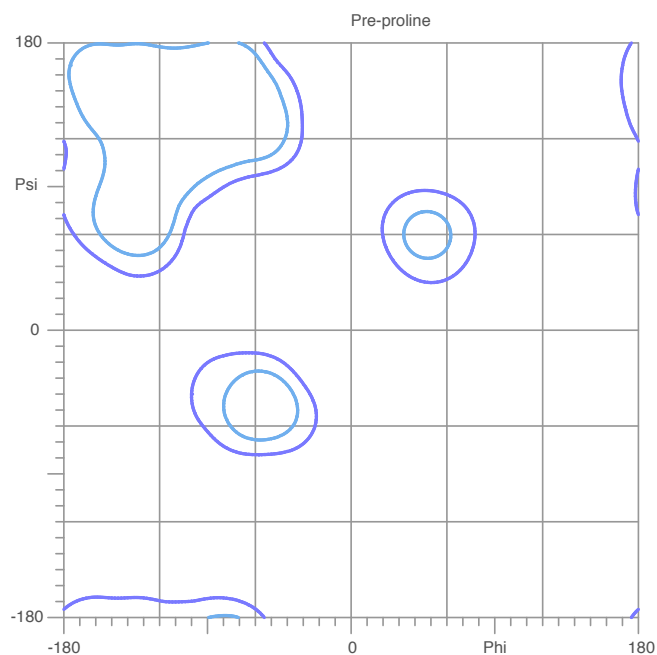
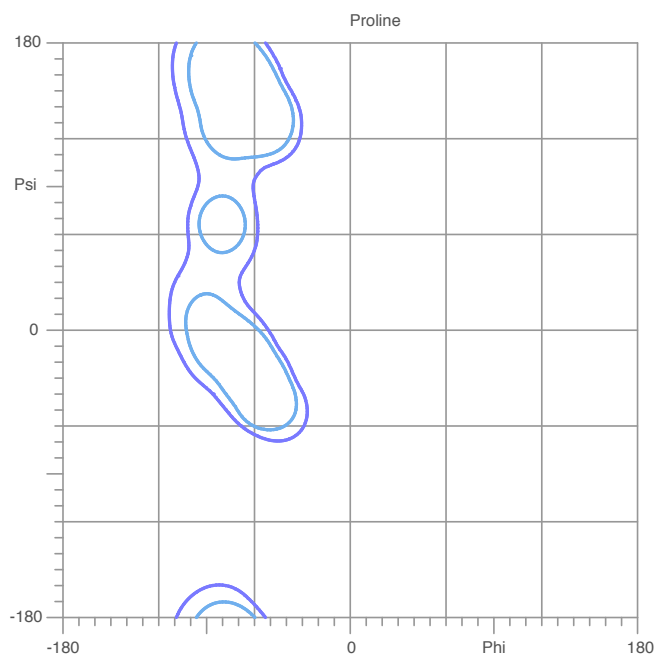
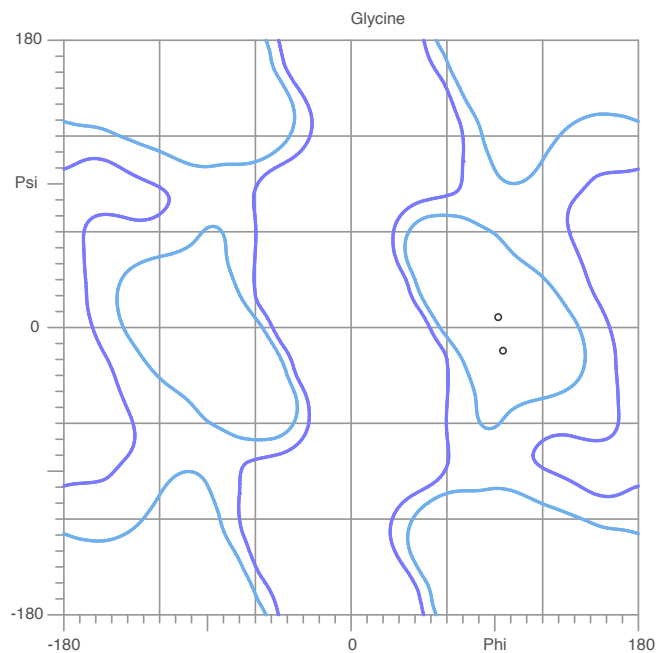
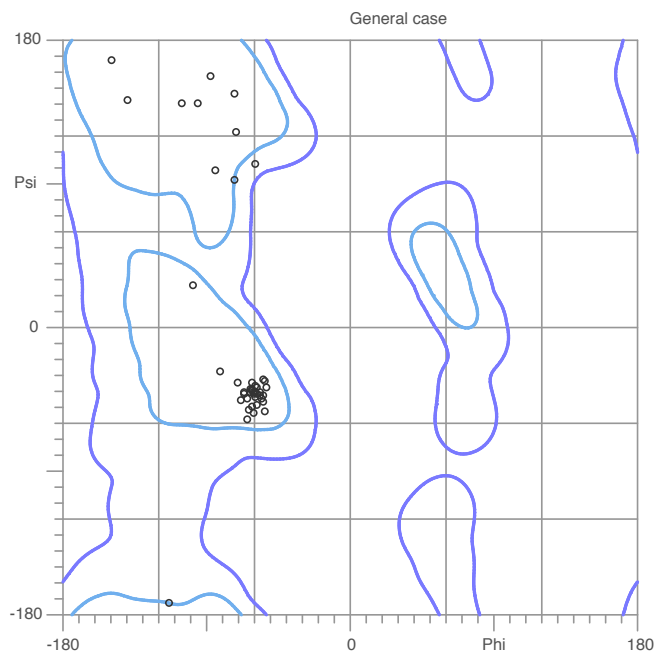
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 2



95.7% (44/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

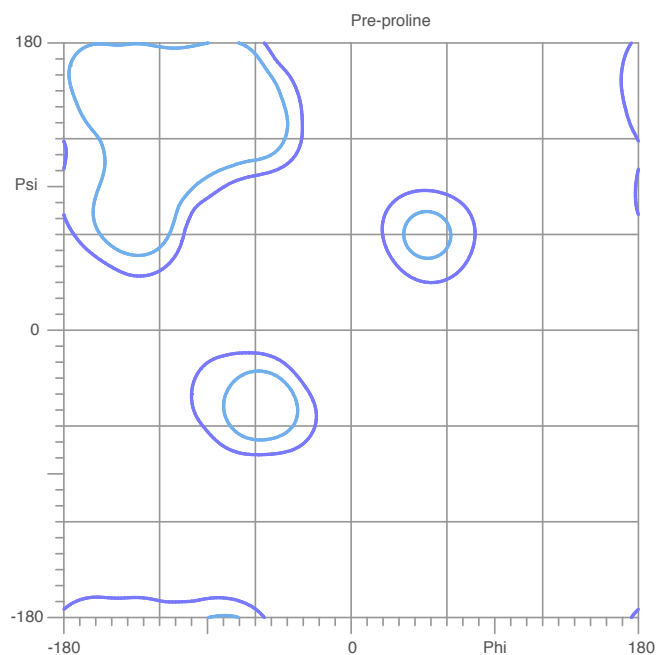
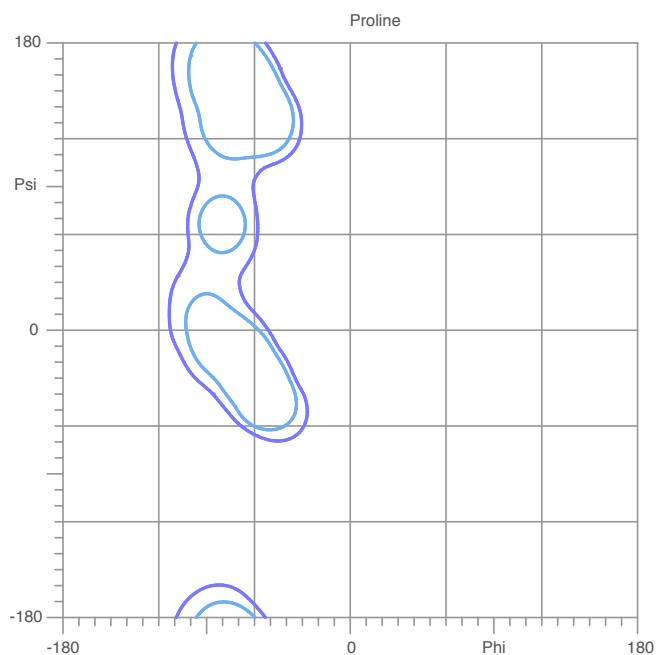
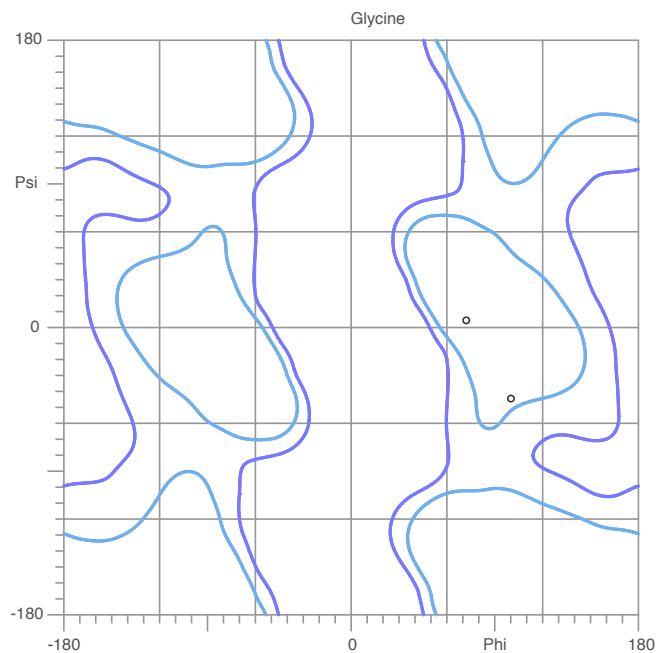
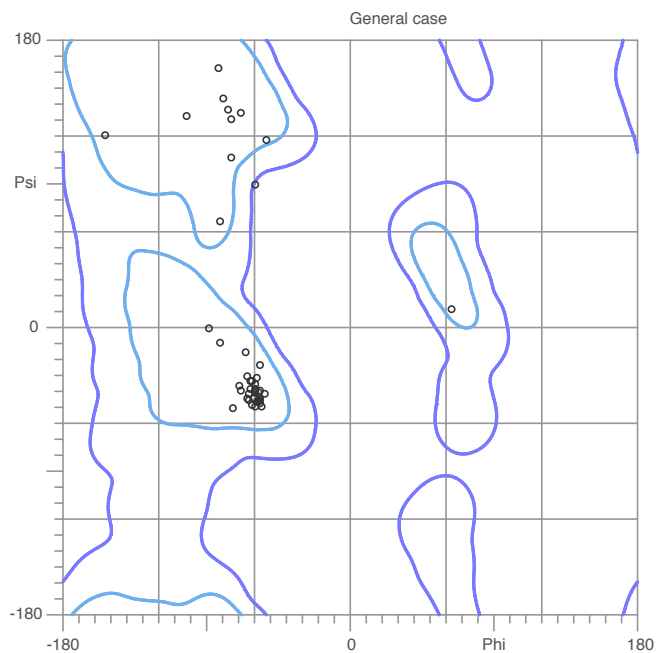
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 3



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

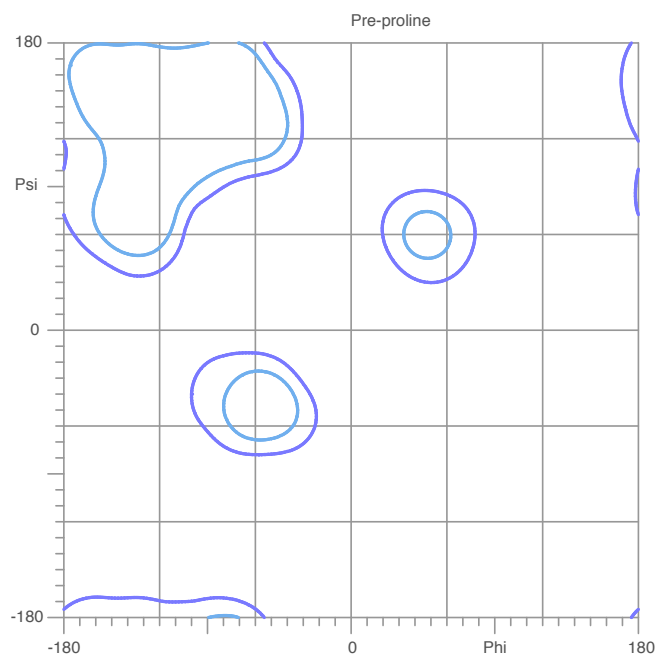
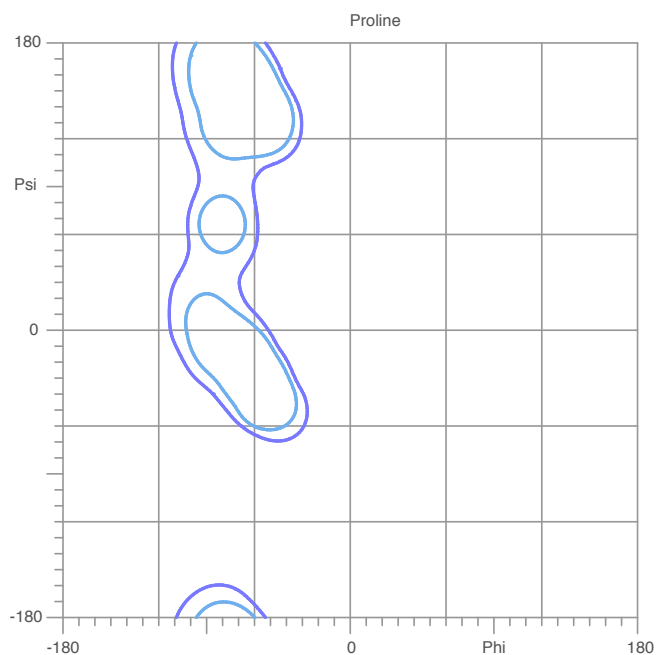
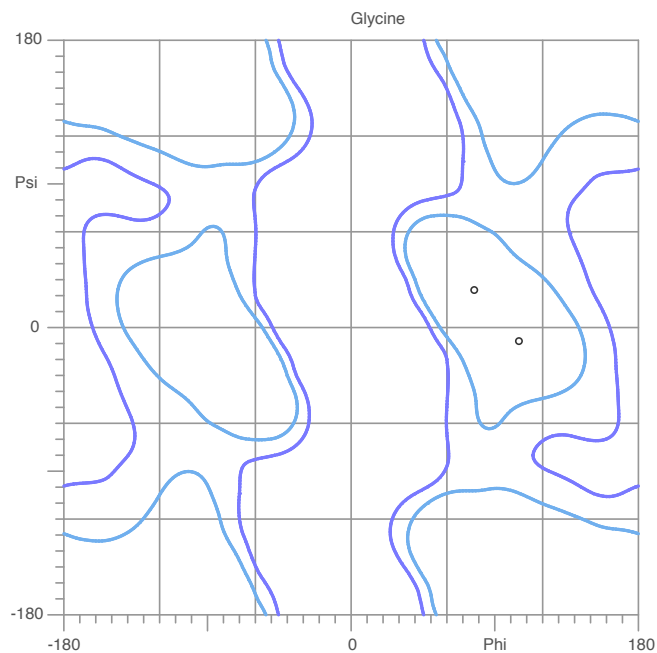
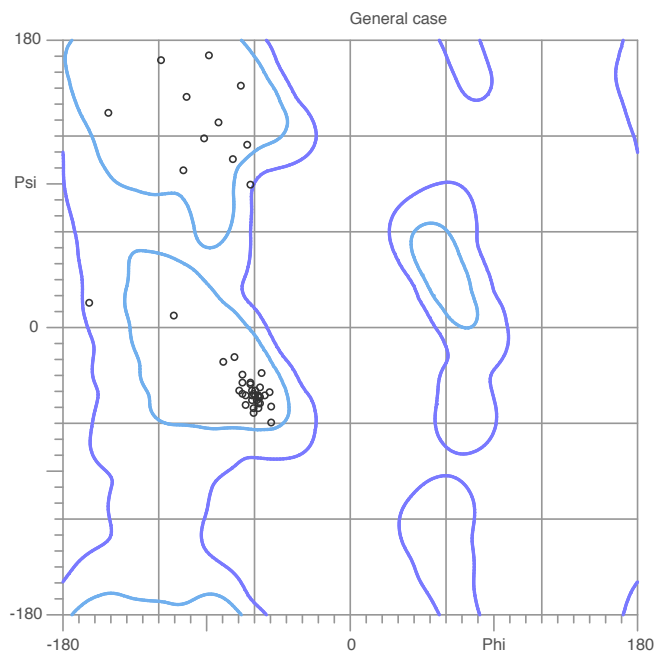
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 4



95.7% (44/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

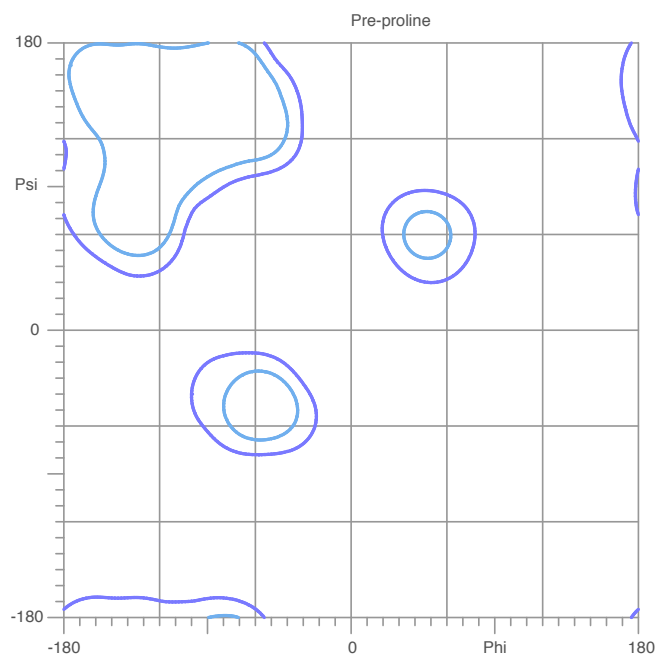
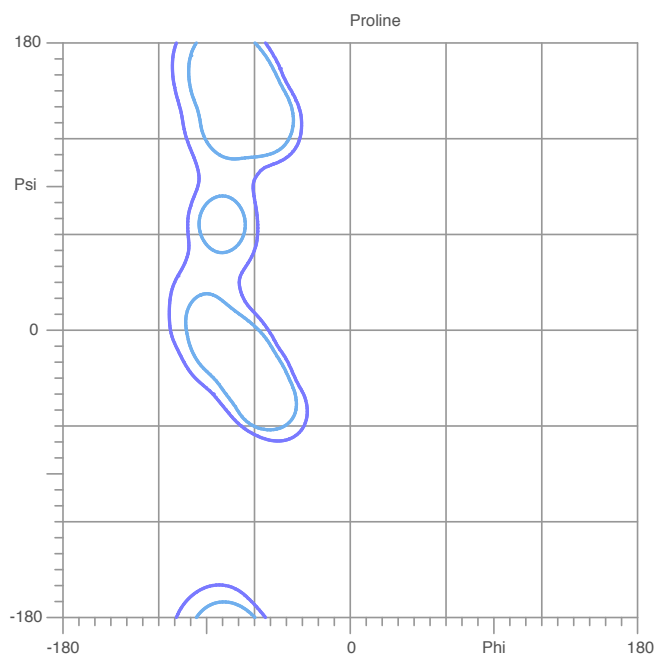
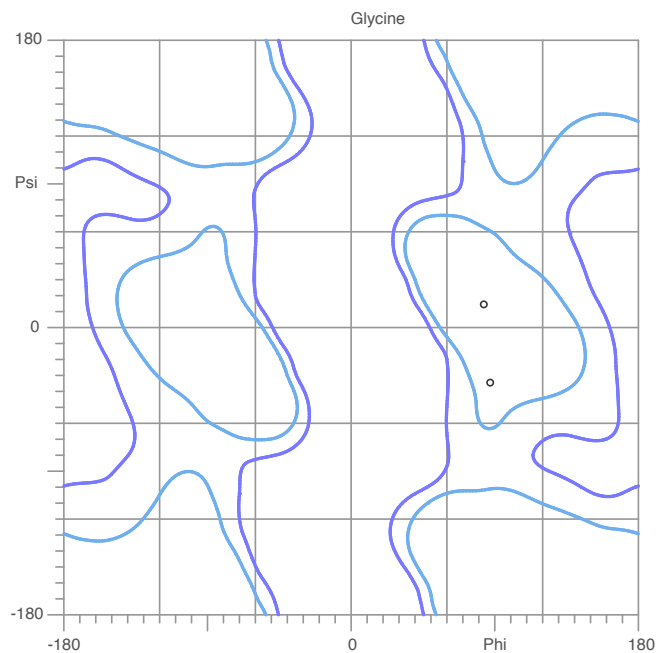
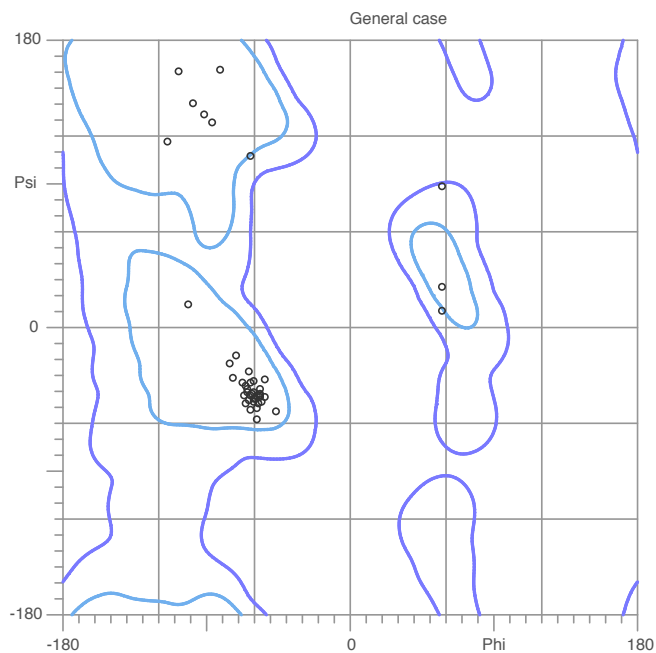
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 5



95.7% (44/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

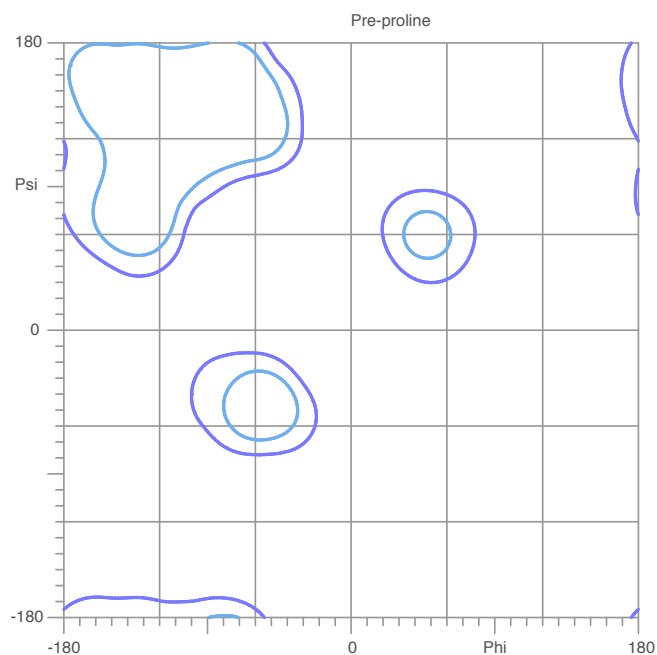
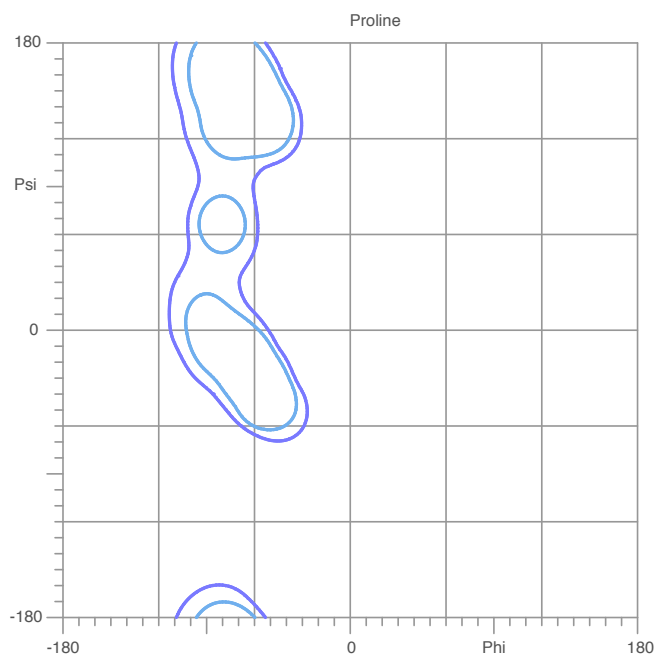
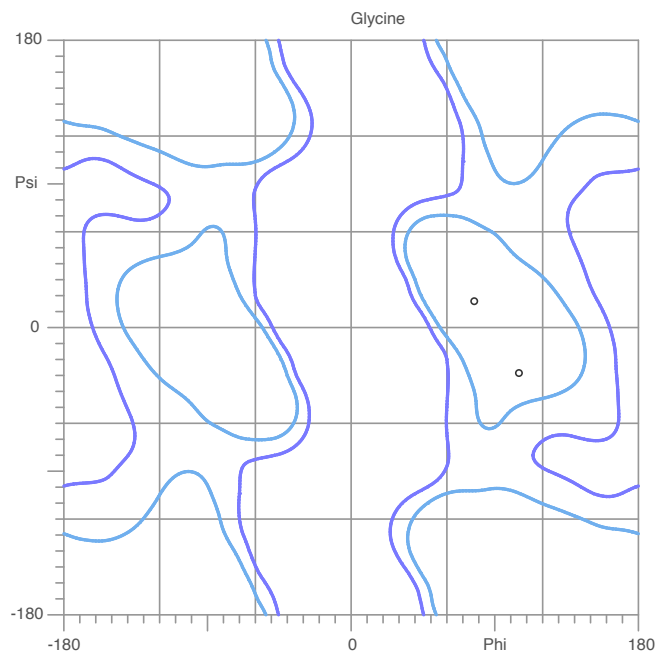
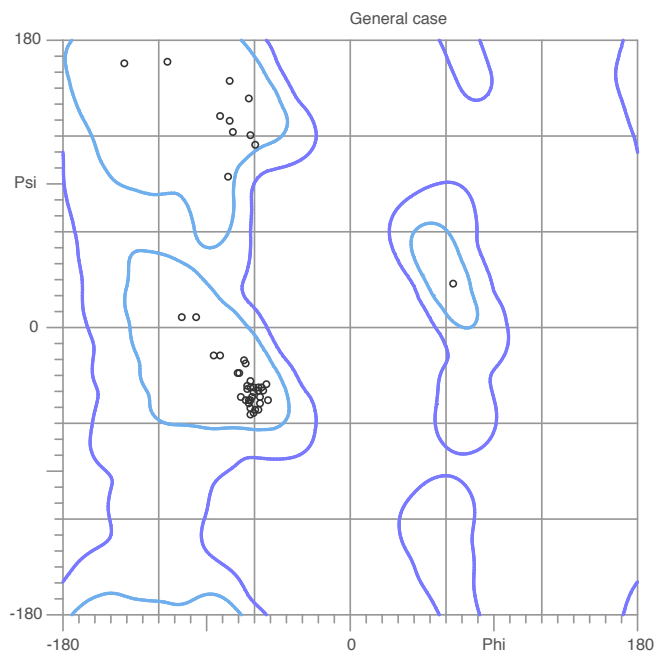
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 6



100.0% (46/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

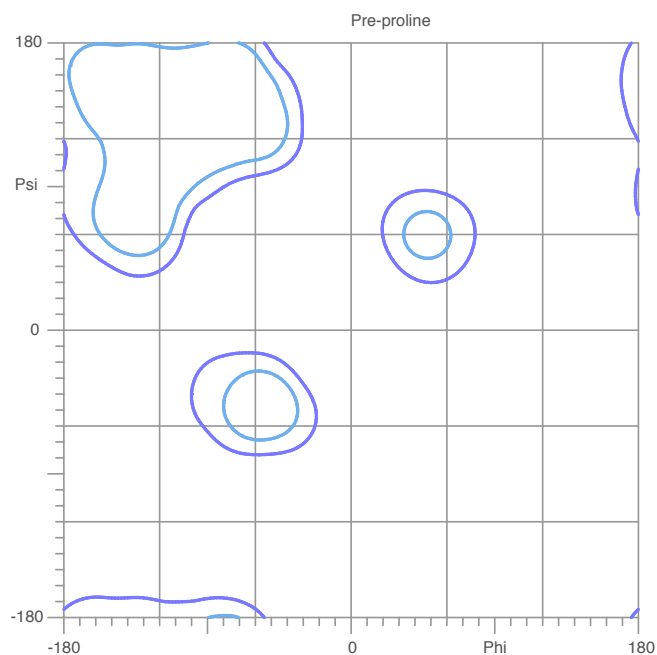
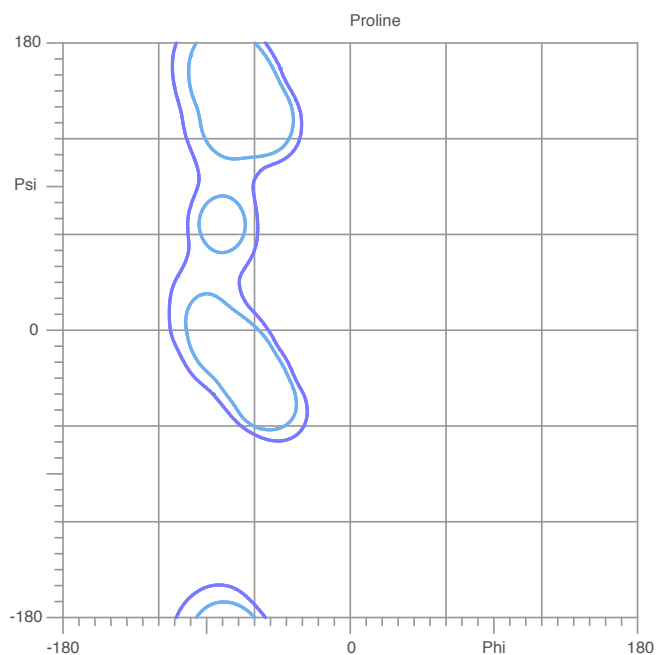
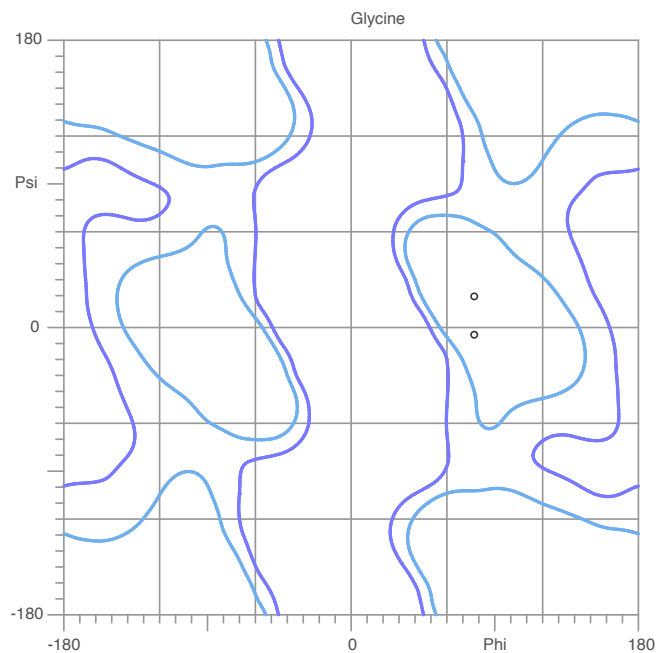
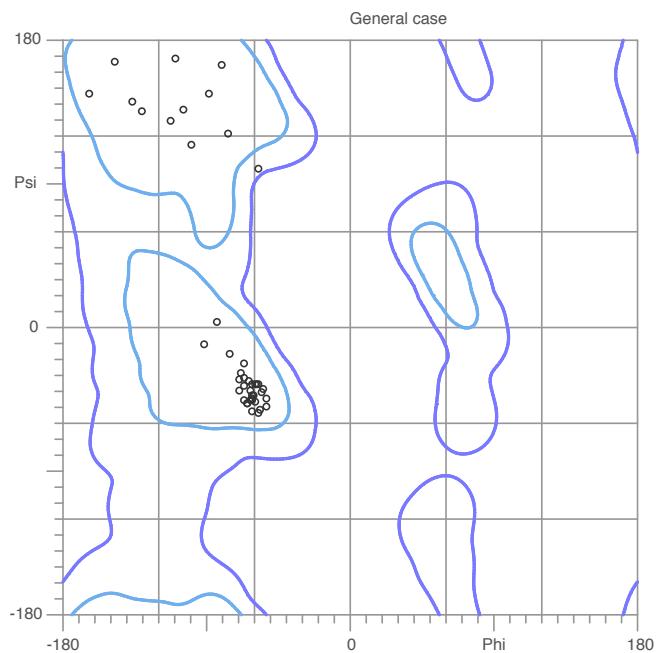
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 7



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

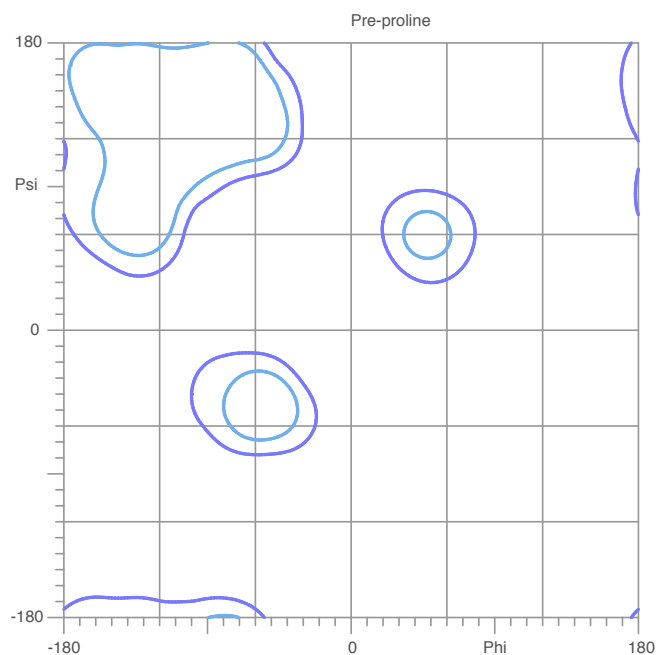
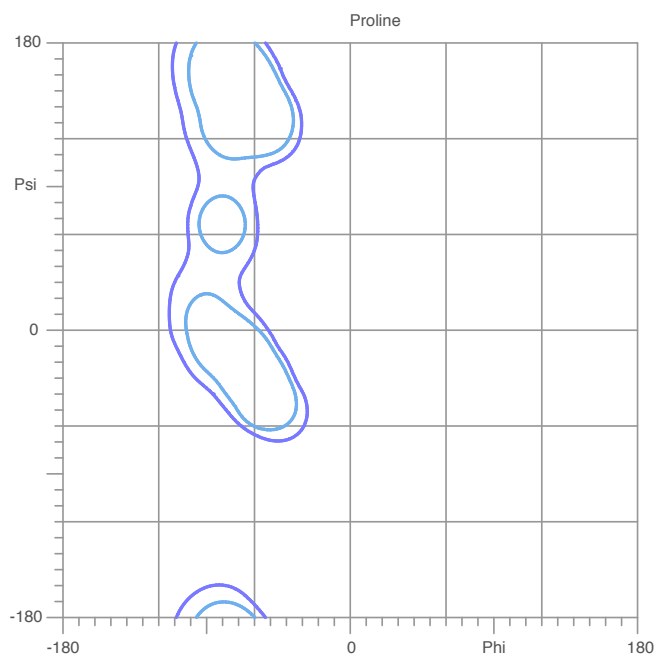
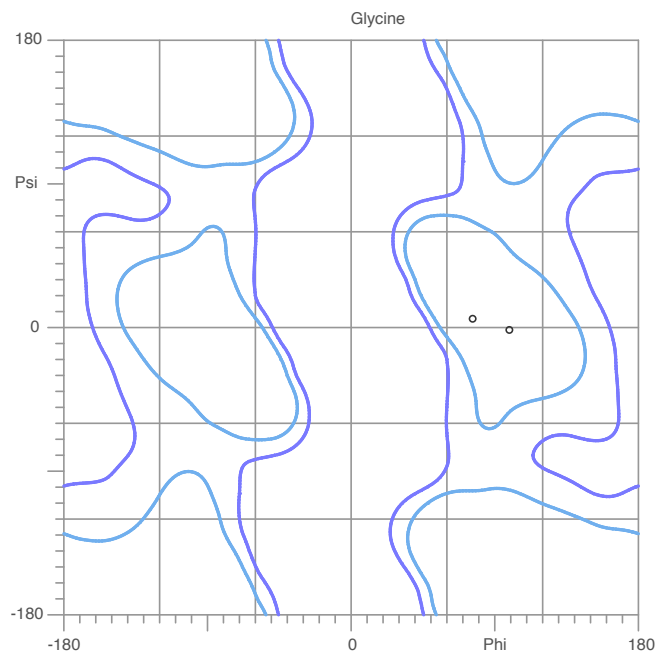
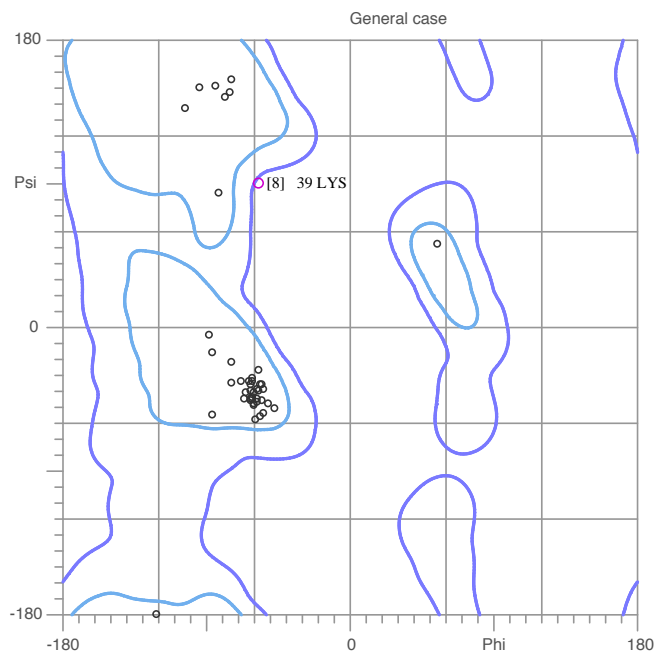
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 8



97.8% (45/46) of all residues were in favored (98%) regions.
97.8% (45/46) of all residues were in allowed (>99.8%) regions.

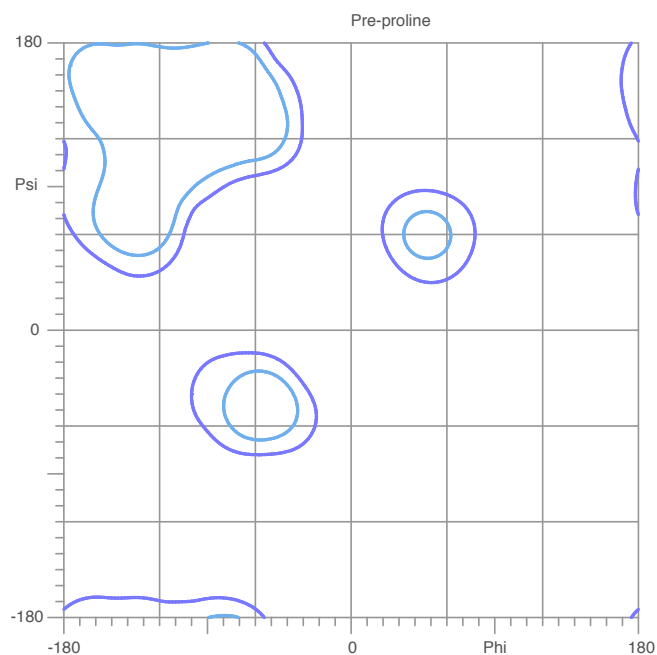
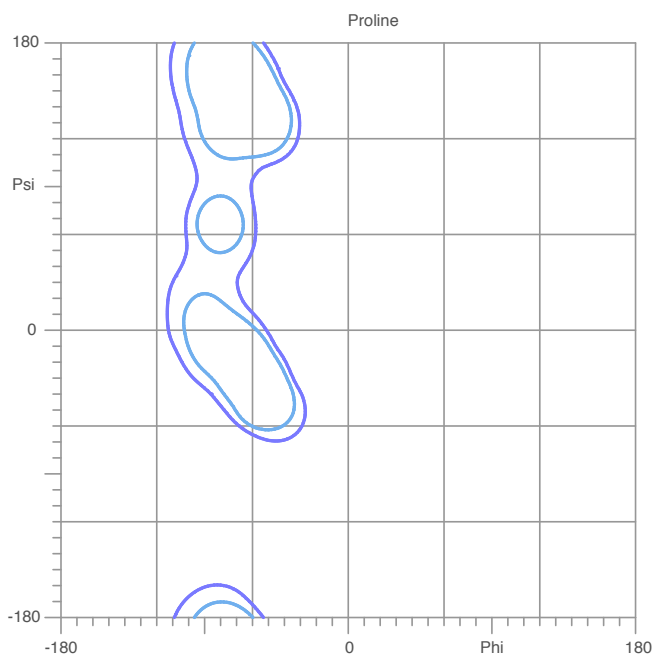
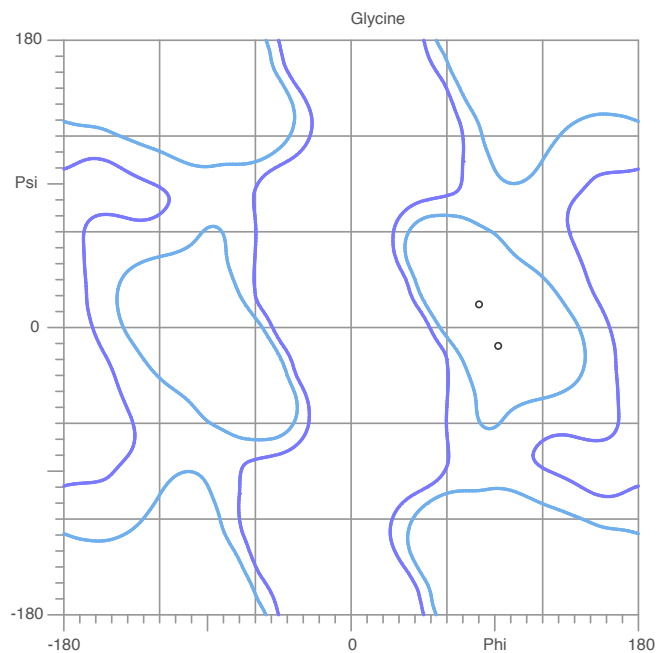
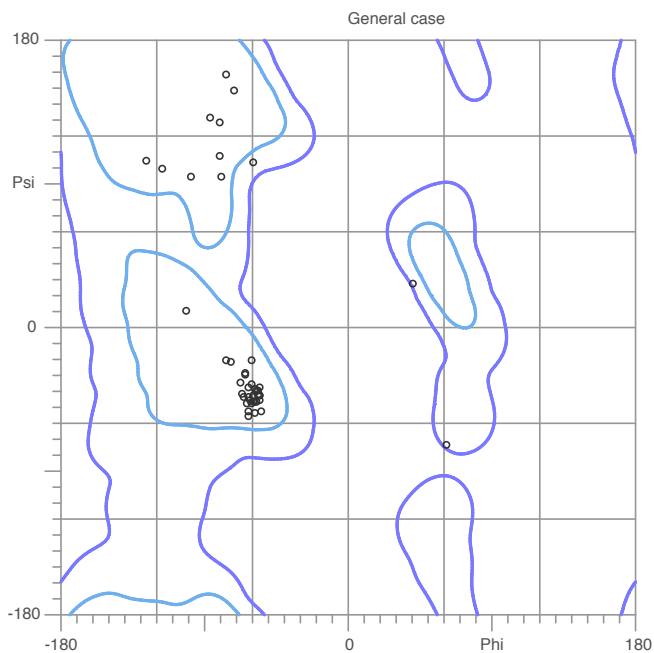
There were 1 outliers (phi, psi):
[8] 39 LYS (-58.5, 91.9)

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 9



93.5% (43/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

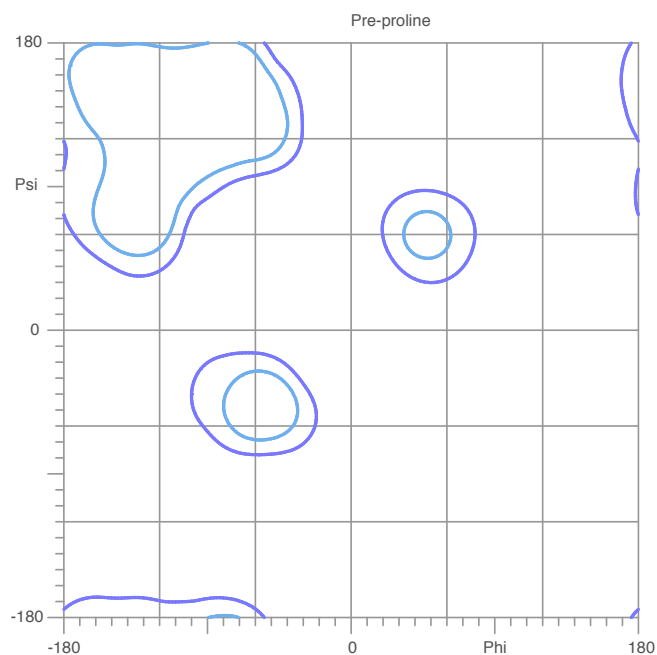
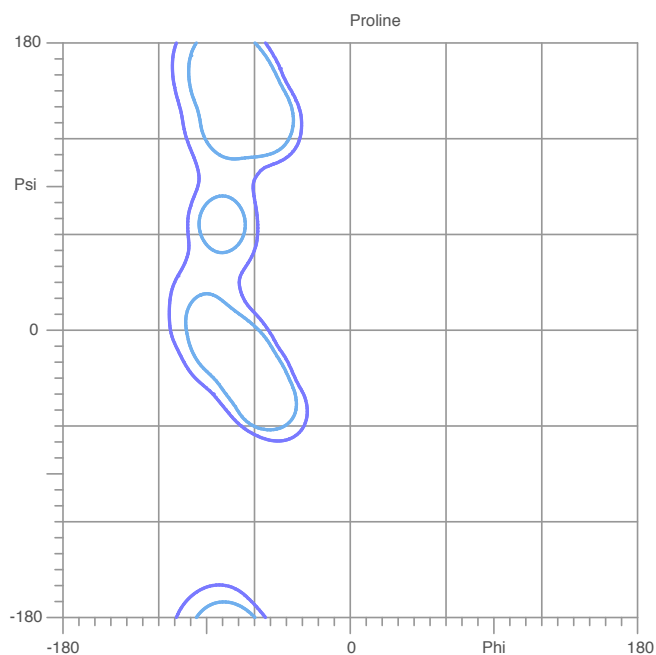
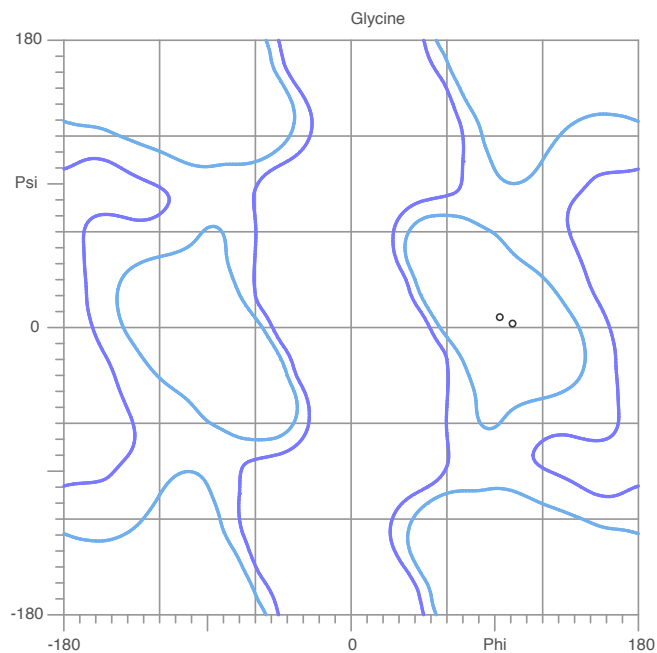
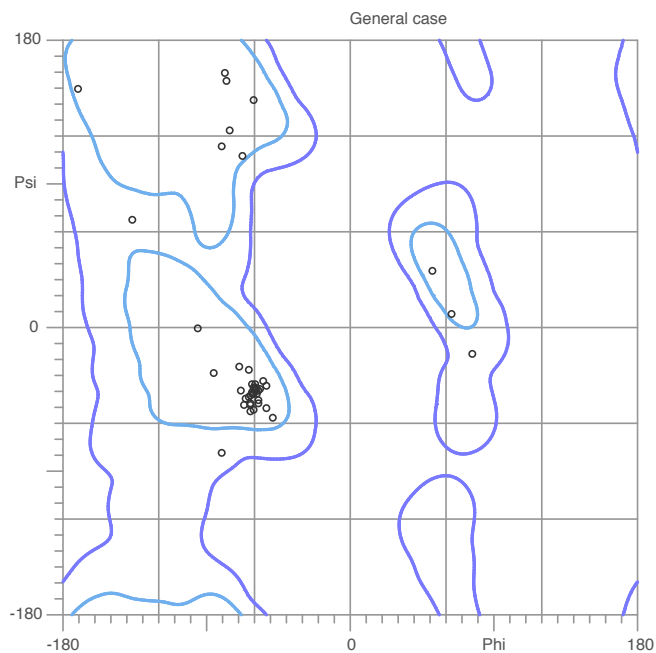
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 10



93.5% (43/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

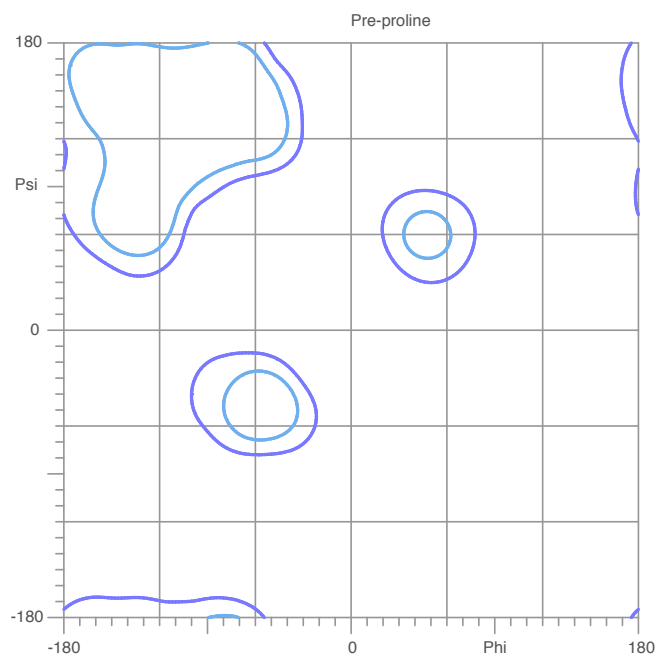
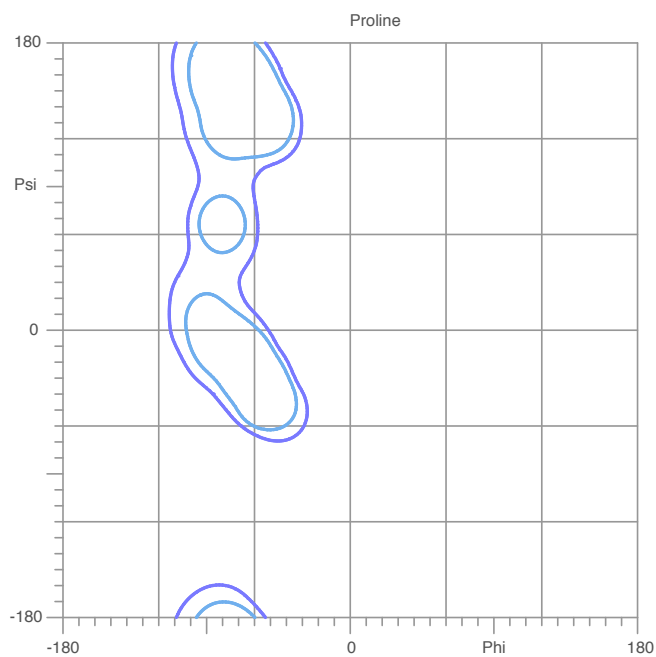
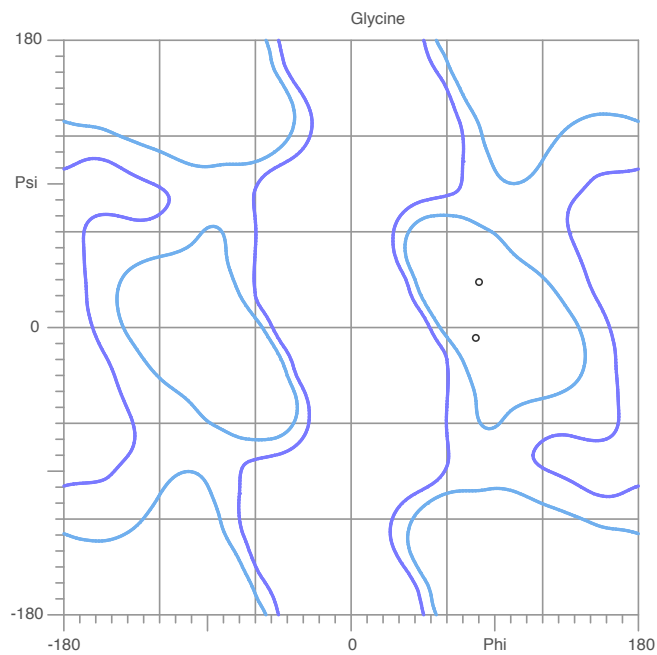
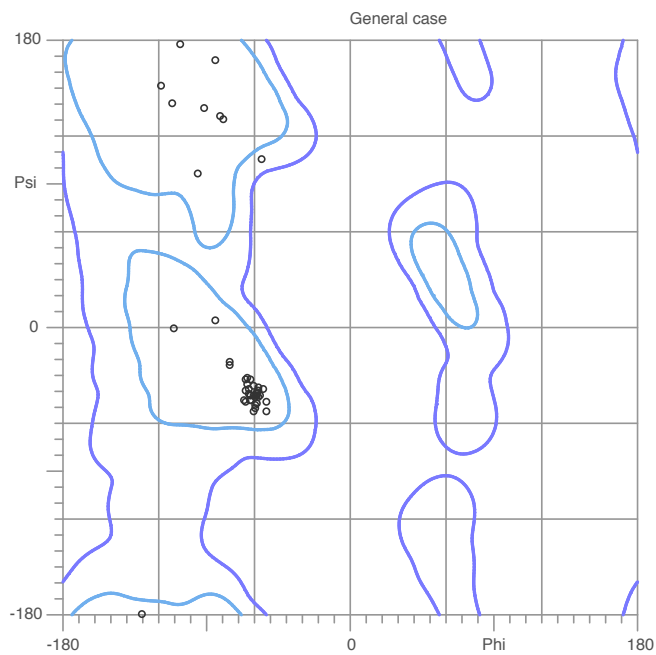
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 11



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

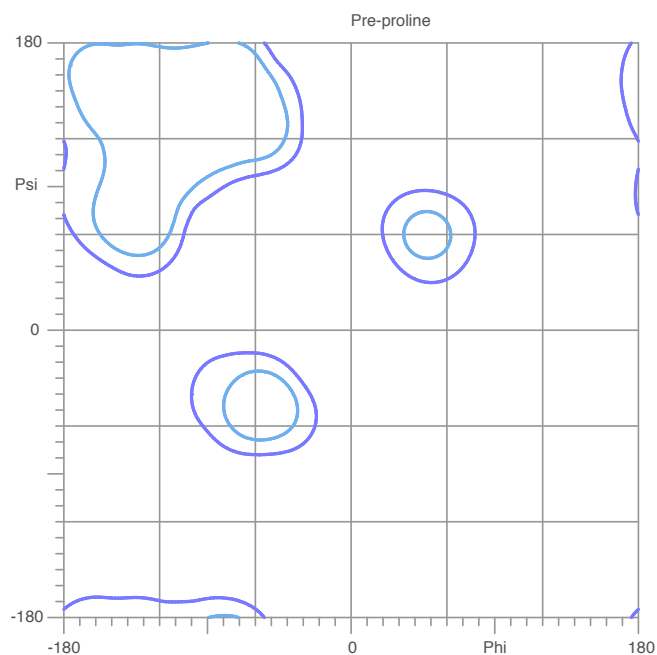
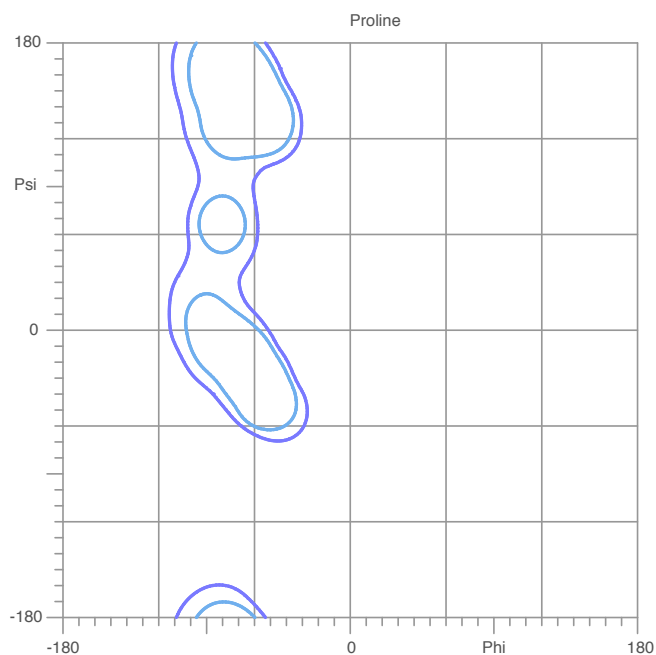
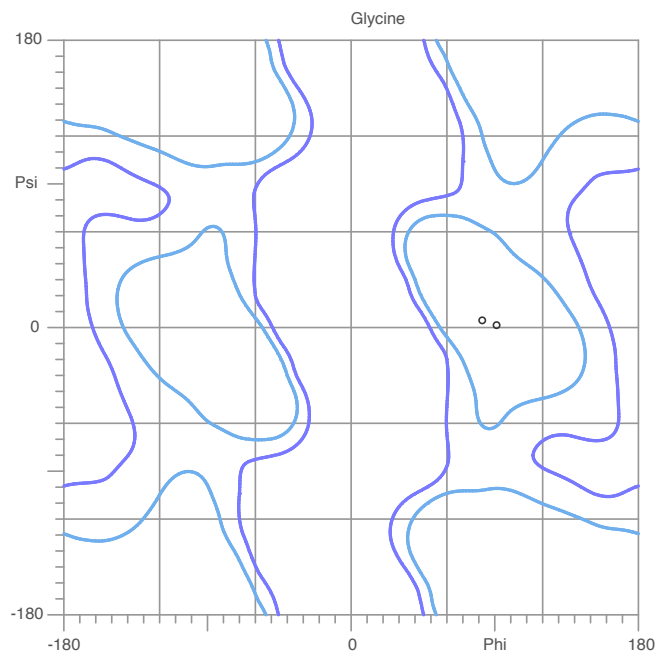
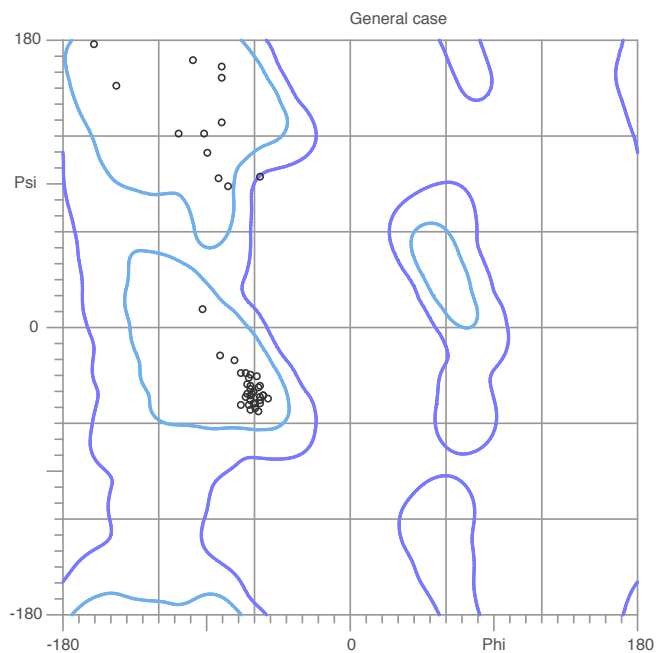
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 12



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

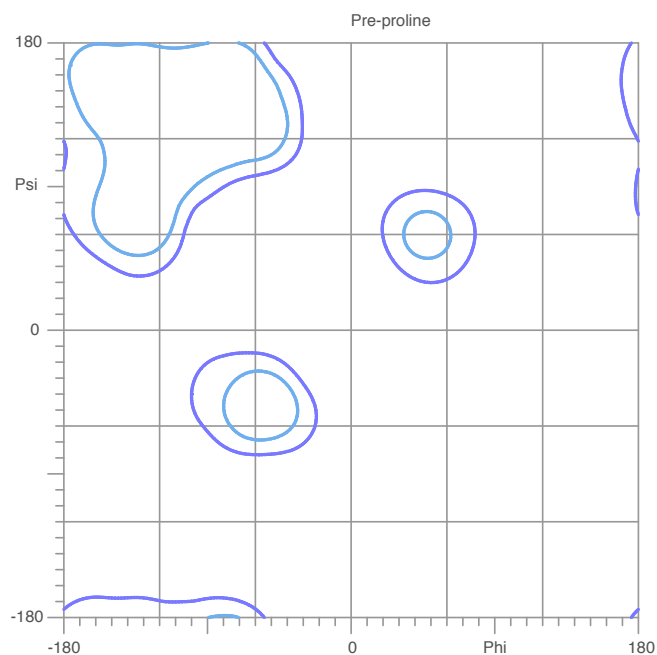
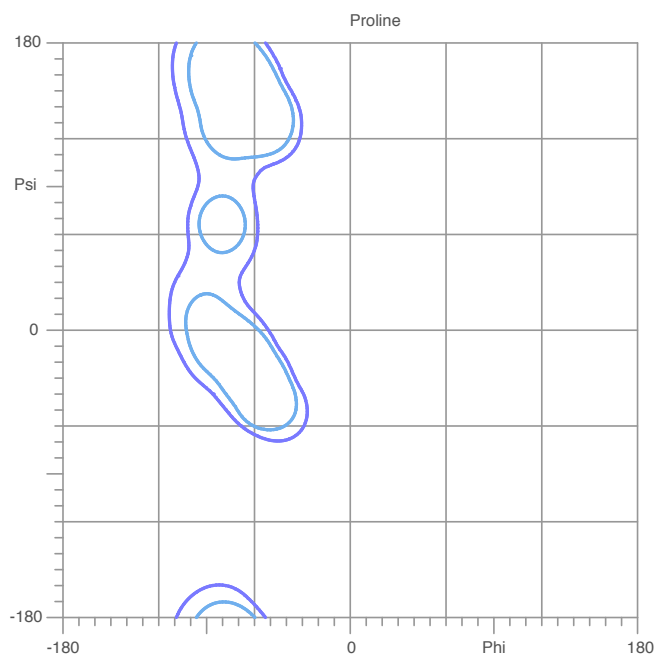
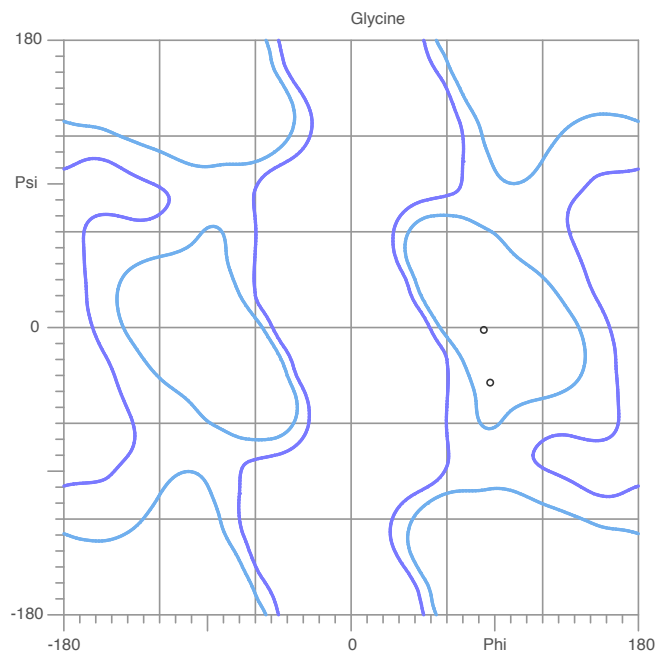
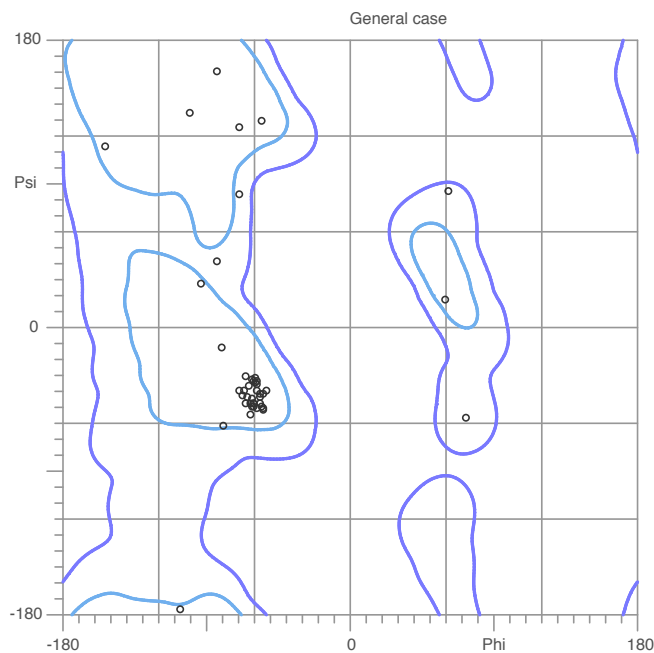
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 13



91.3% (42/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

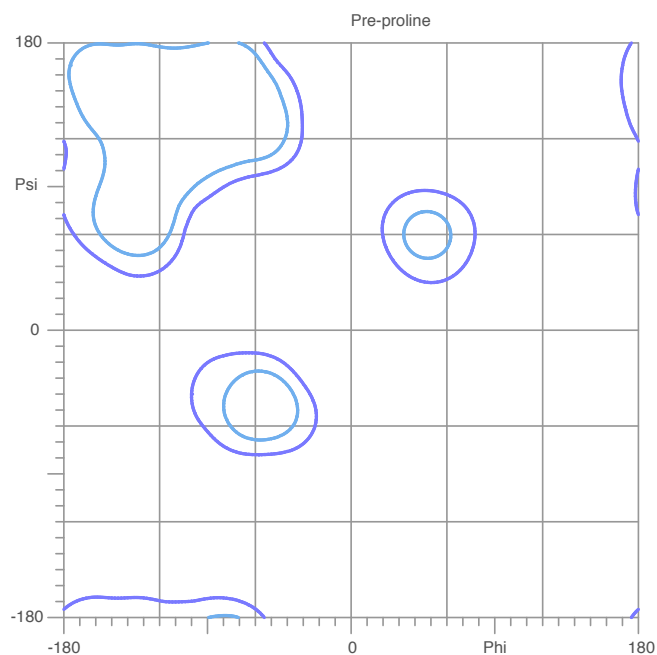
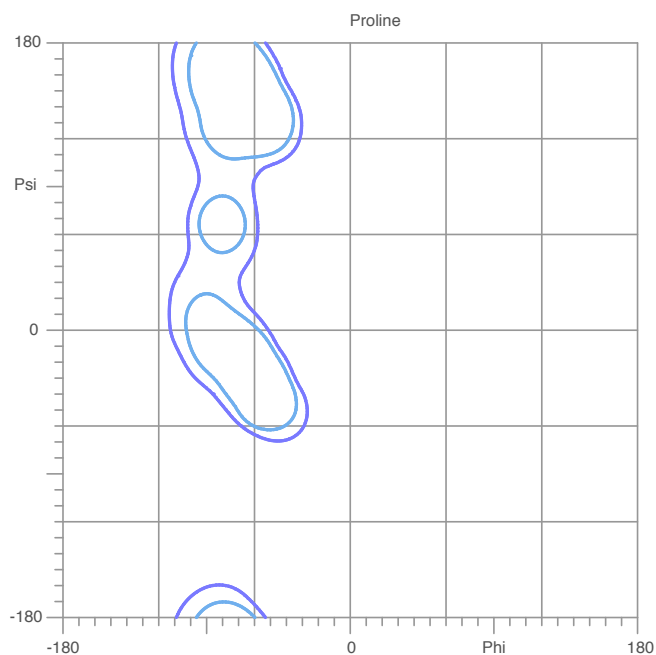
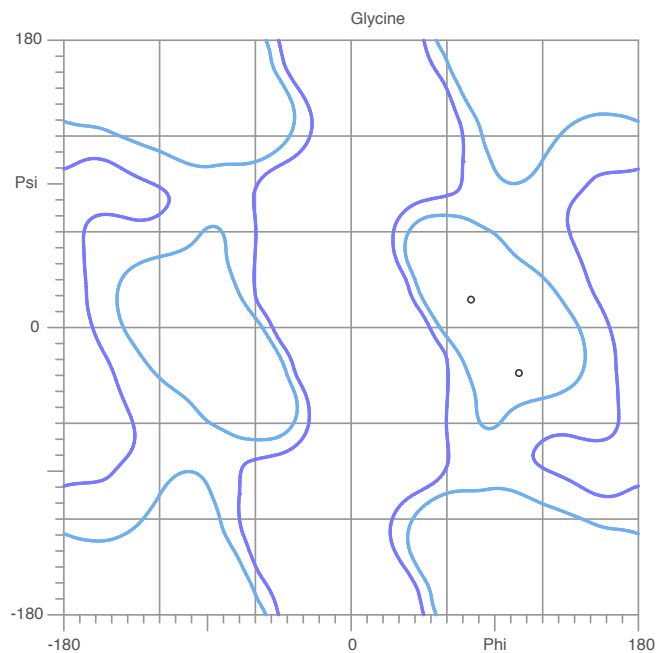
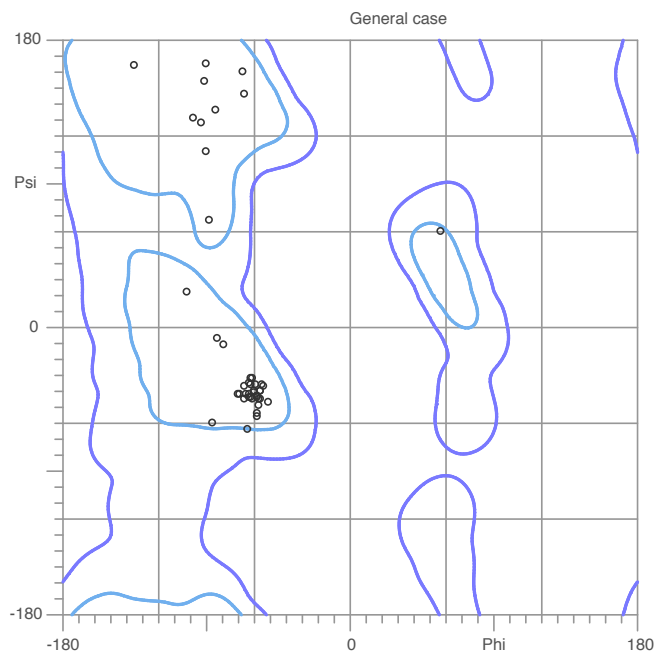
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 14



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

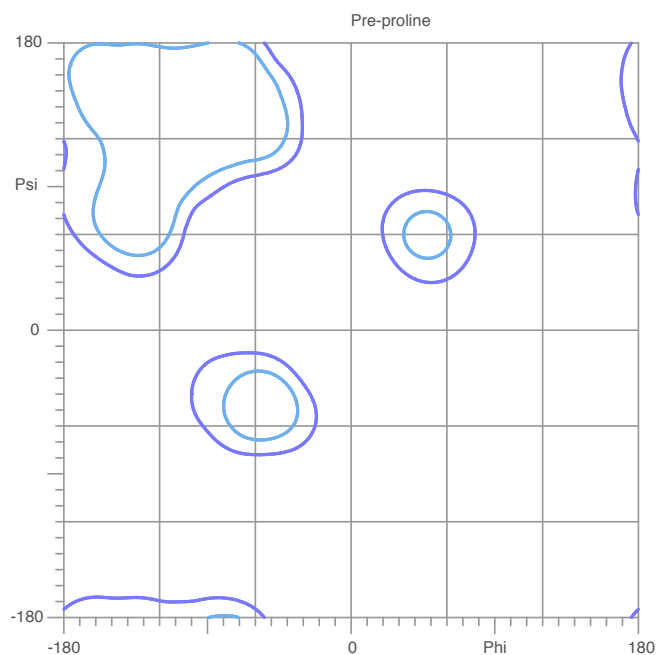
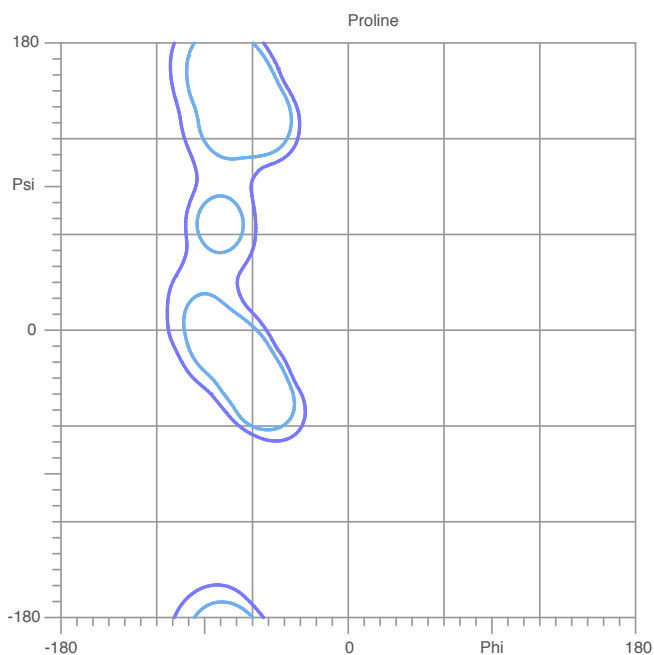
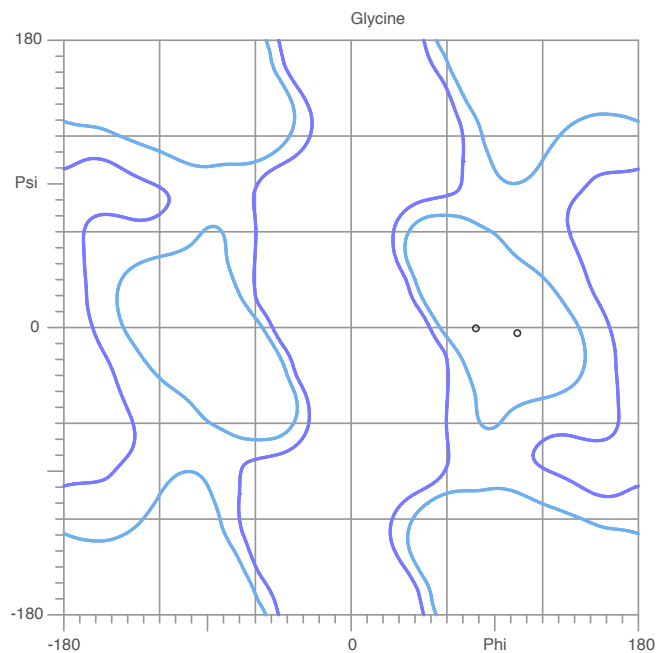
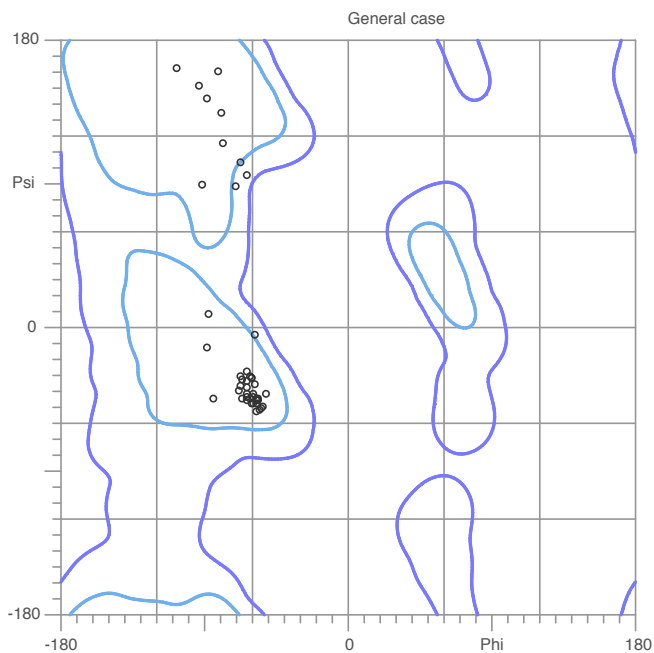
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 15



93.5% (43/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

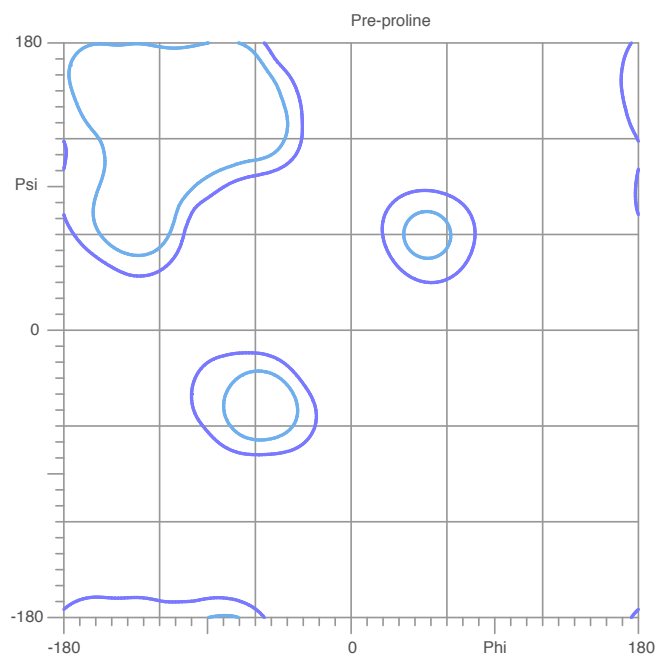
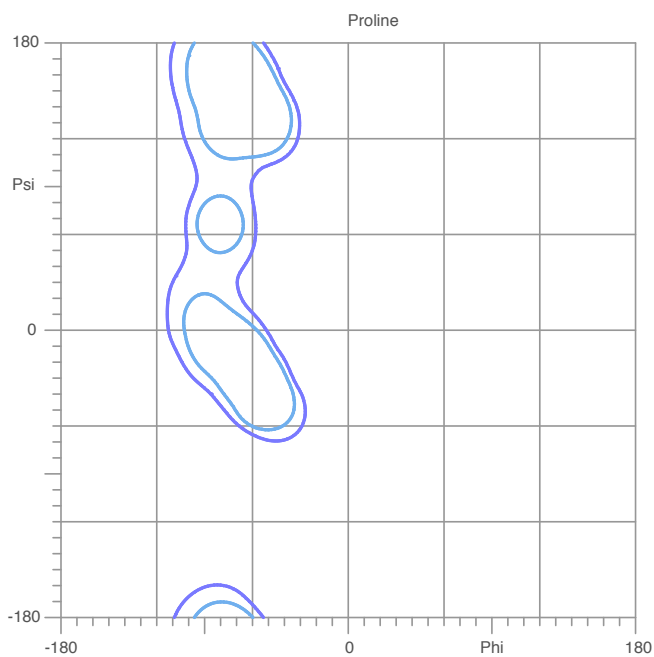
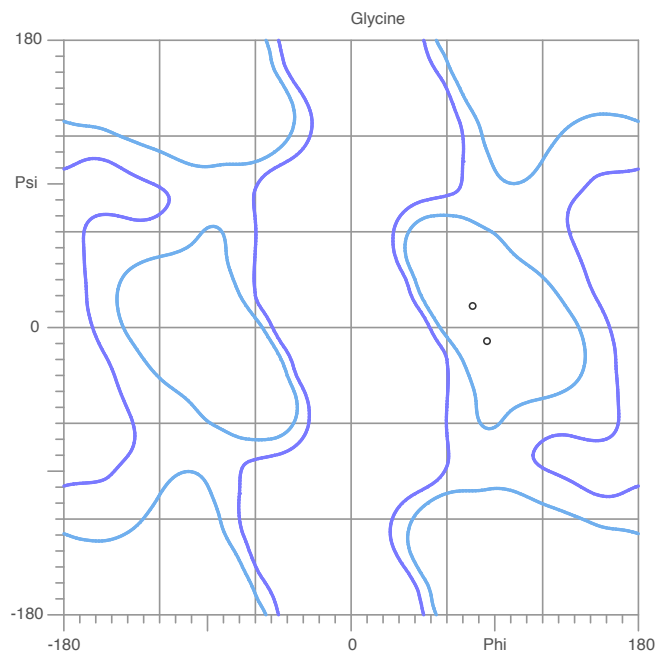
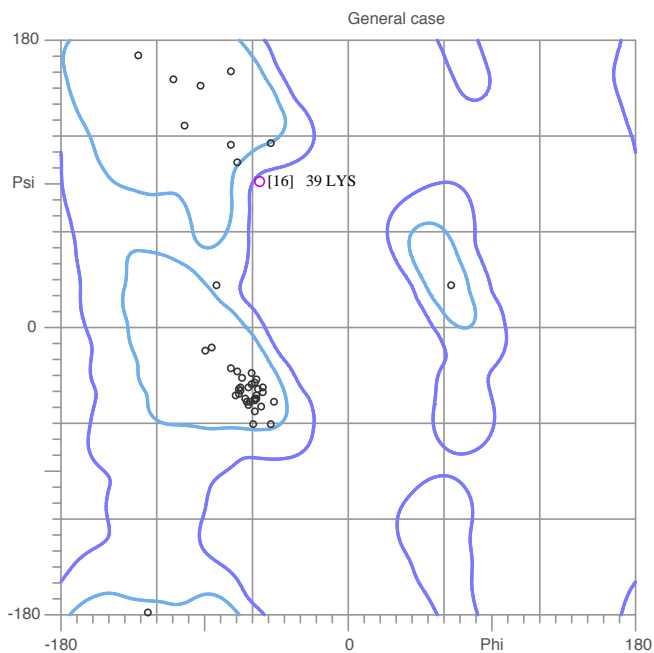
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 16



95.7% (44/46) of all residues were in favored (98%) regions.
97.8% (45/46) of all residues were in allowed (>99.8%) regions.

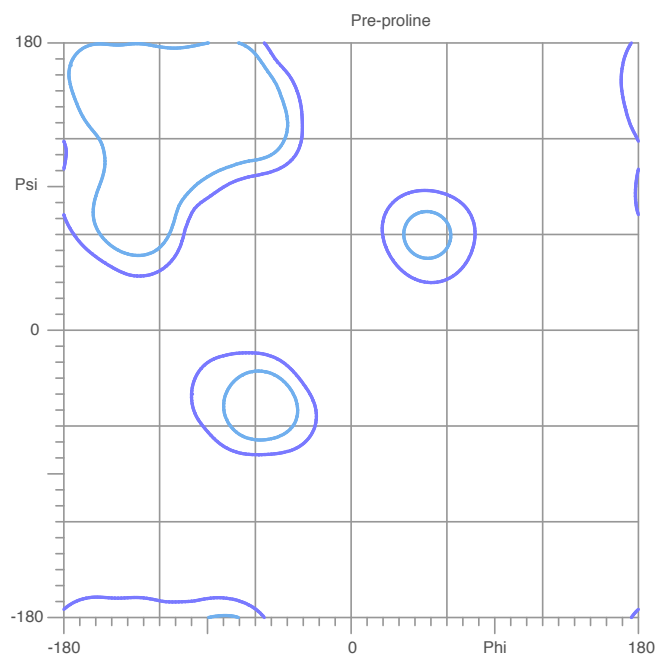
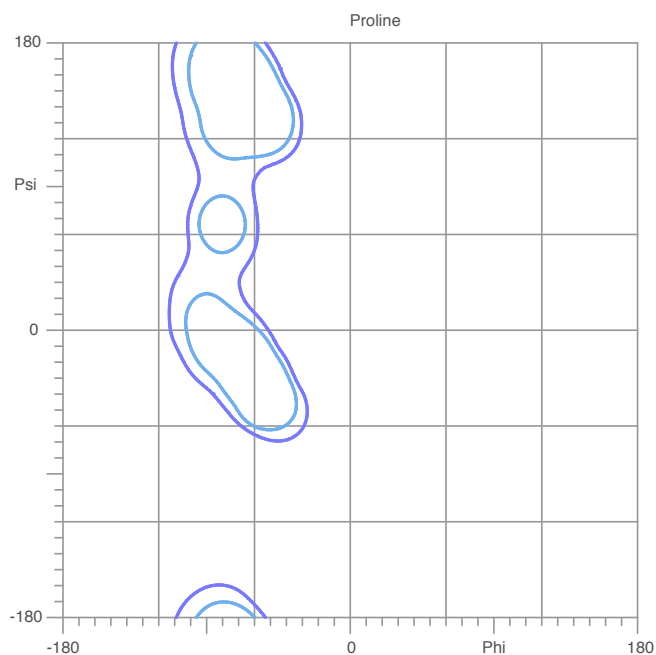
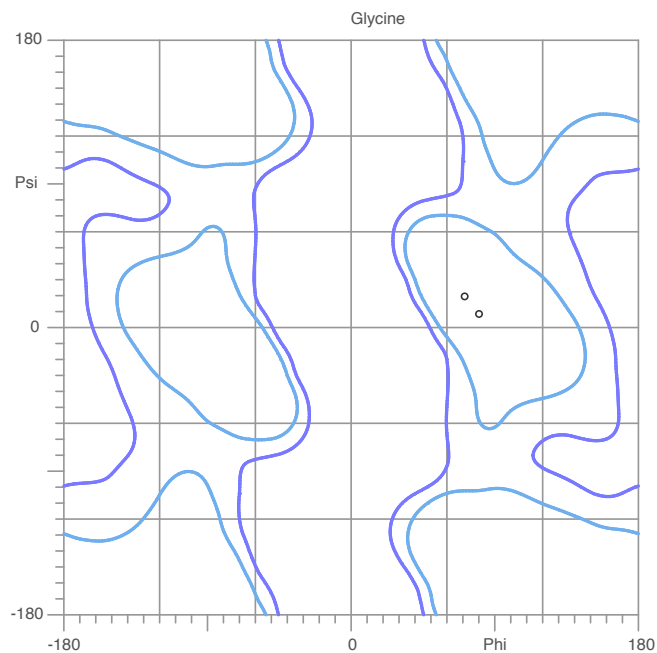
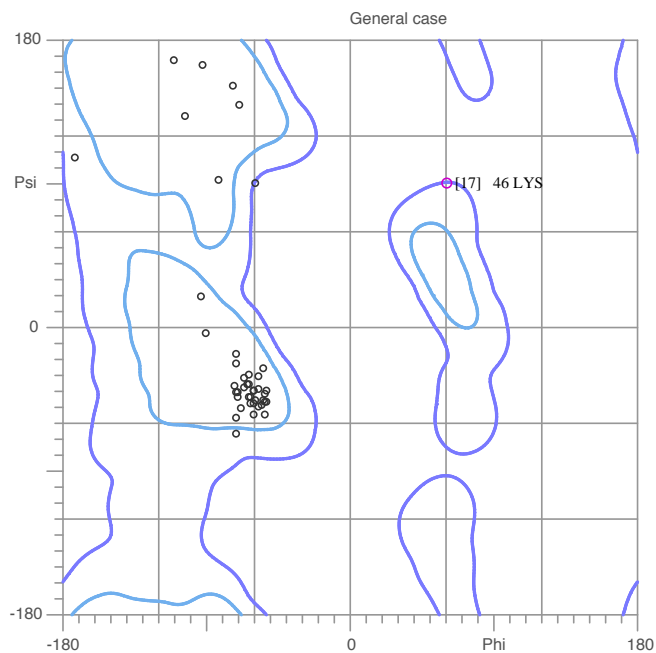
There were 1 outliers (phi, psi):
[16] 39 LYS (-56.4, 92.4)

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 17



91.3% (42/46) of all residues were in favored (98%) regions.
97.8% (45/46) of all residues were in allowed (>99.8%) regions.

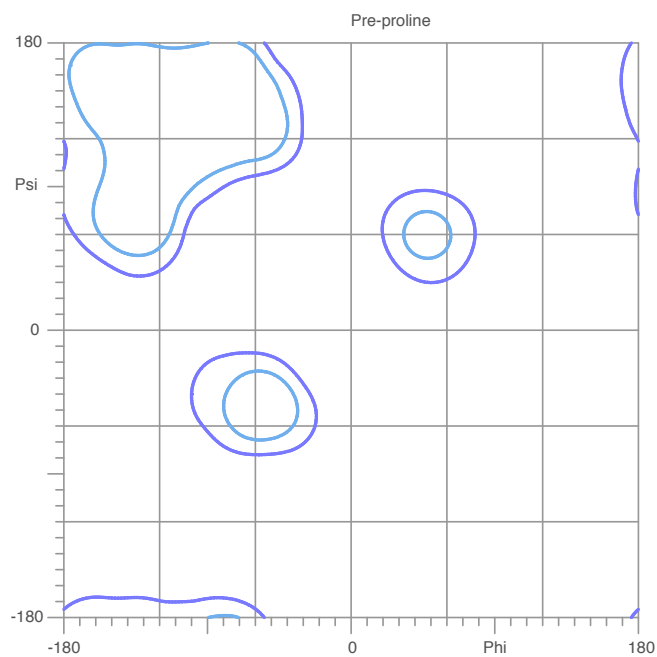
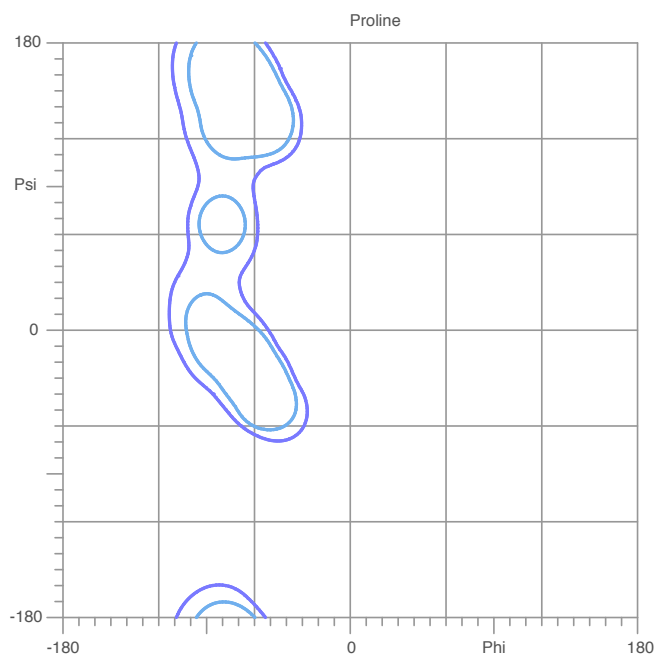
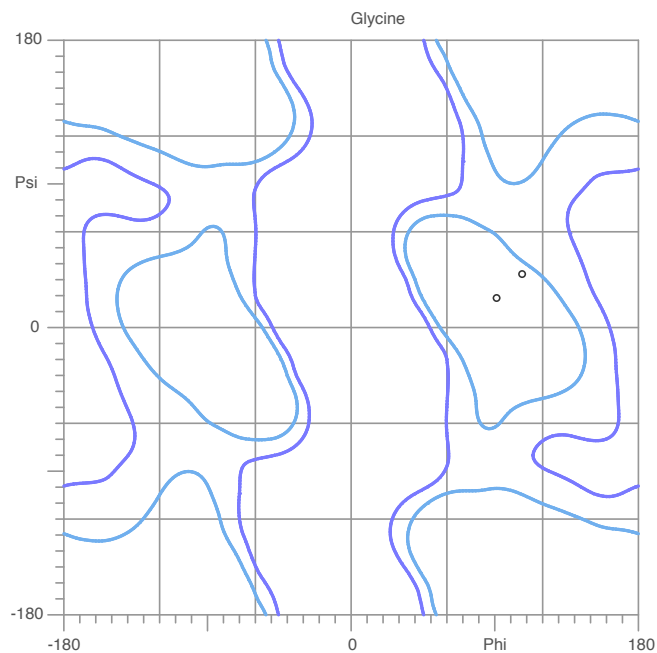
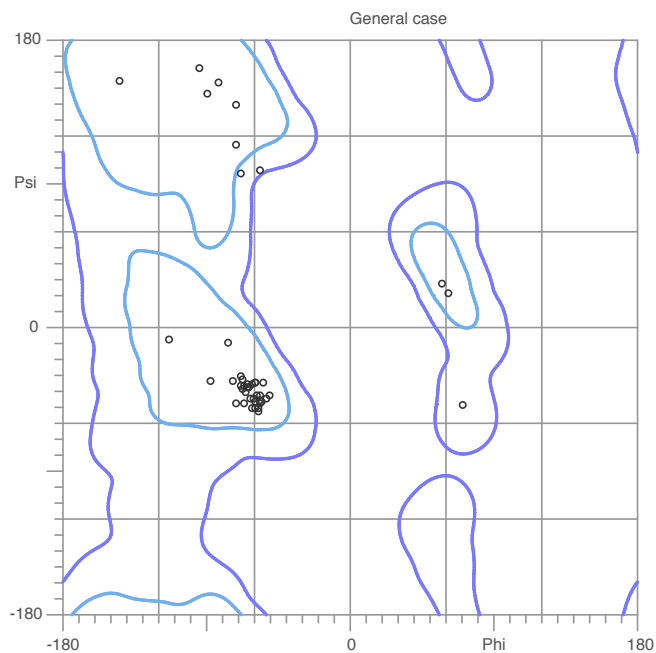
There were 1 outliers (phi, psi):
[17] 46 LYS (60.7, 91.9)

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 18



93.5% (43/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

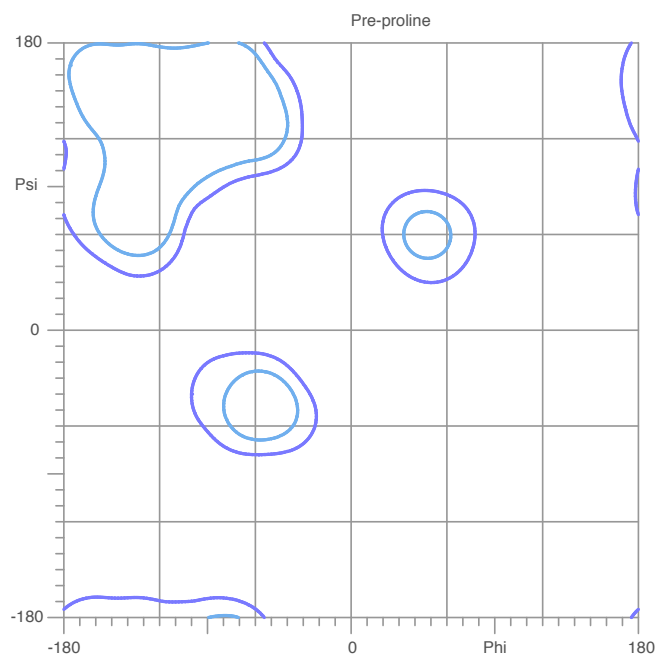
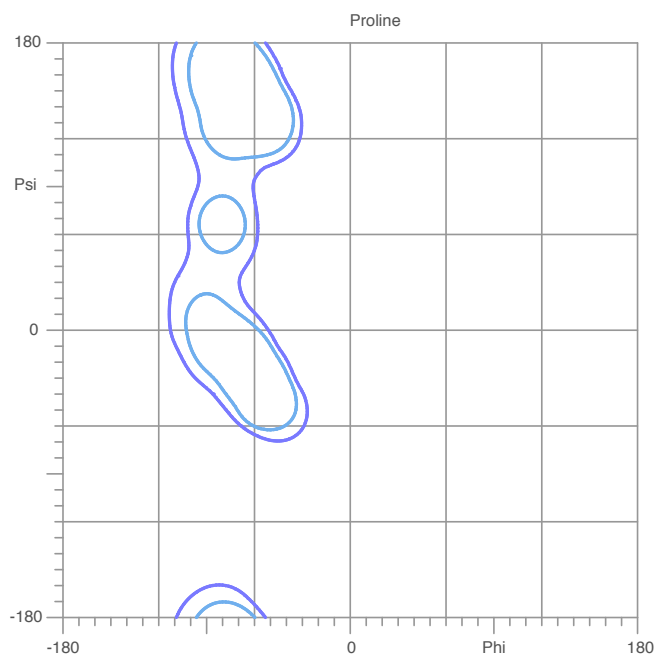
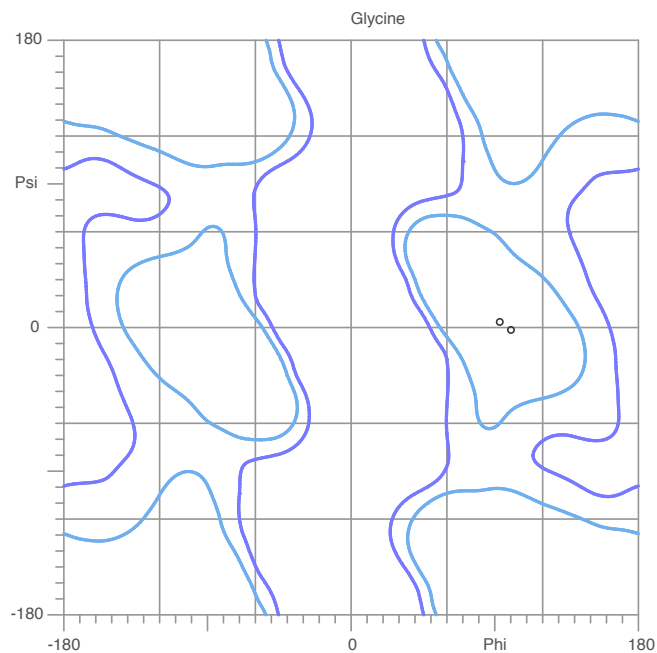
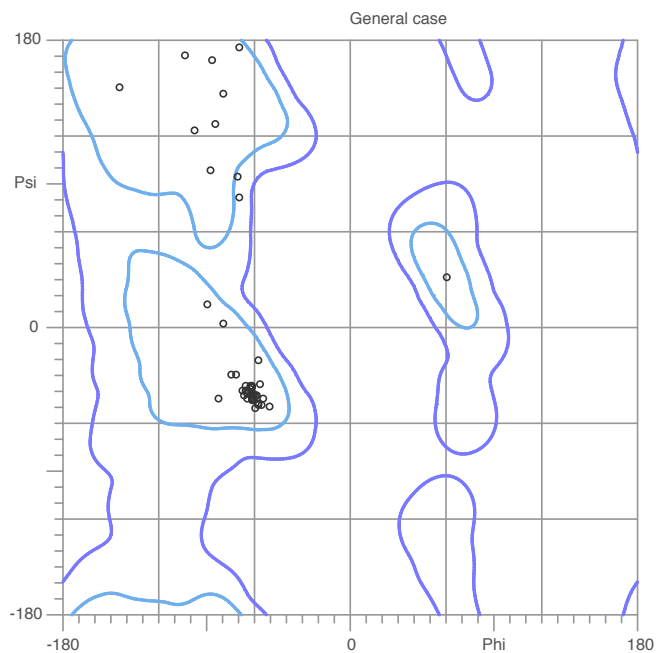
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 19



95.7% (44/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

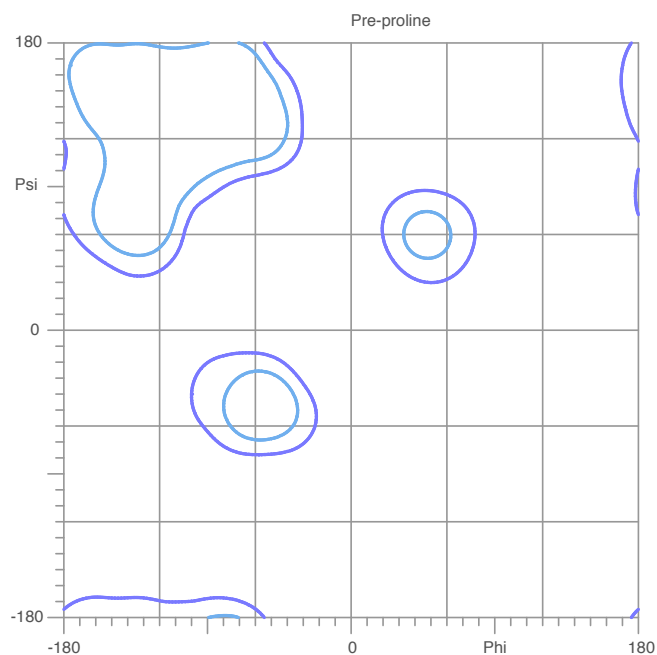
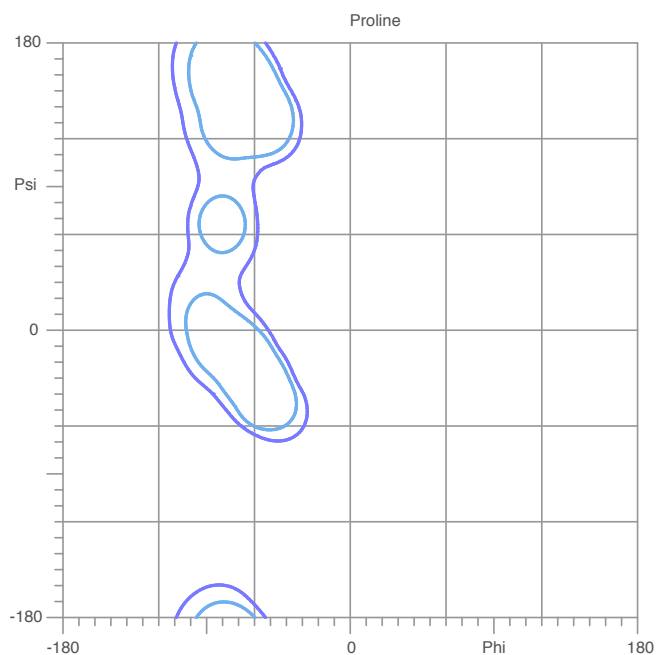
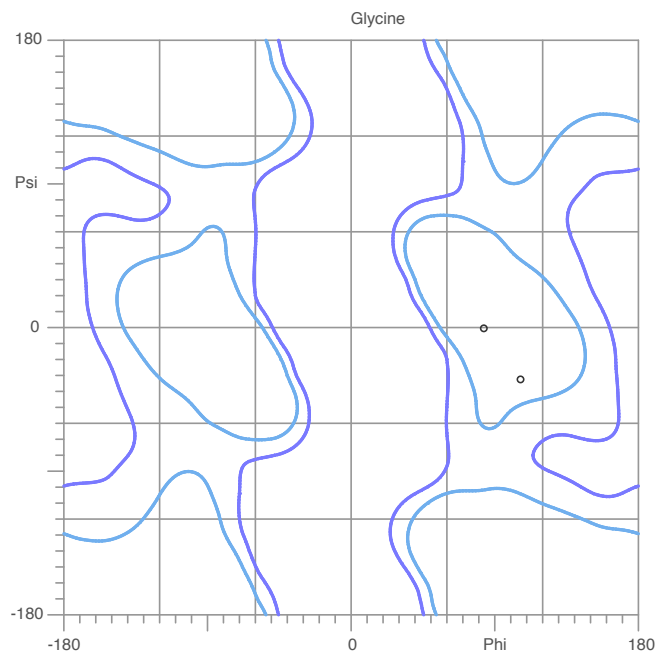
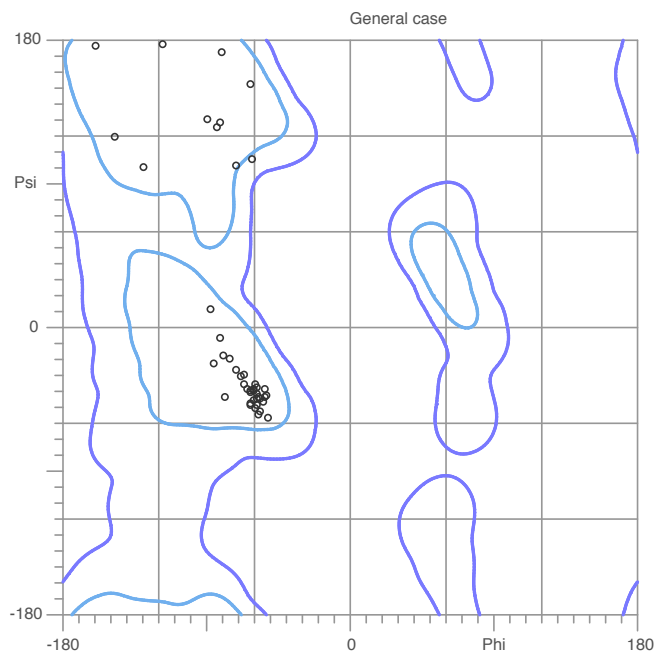
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_NMR_em_bcr3.pdb, model 20



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) 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)