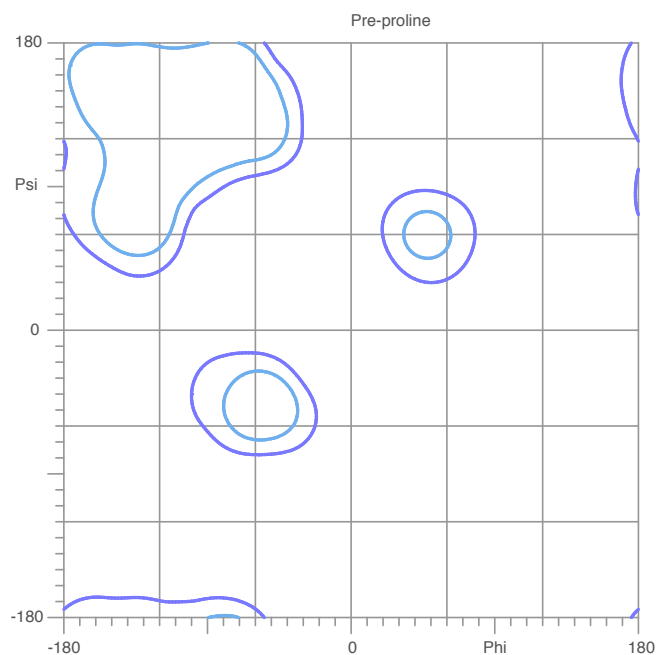
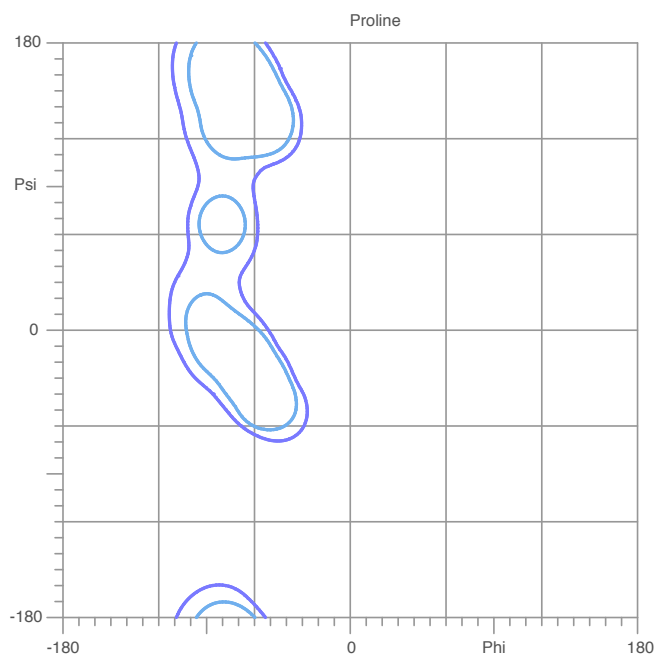
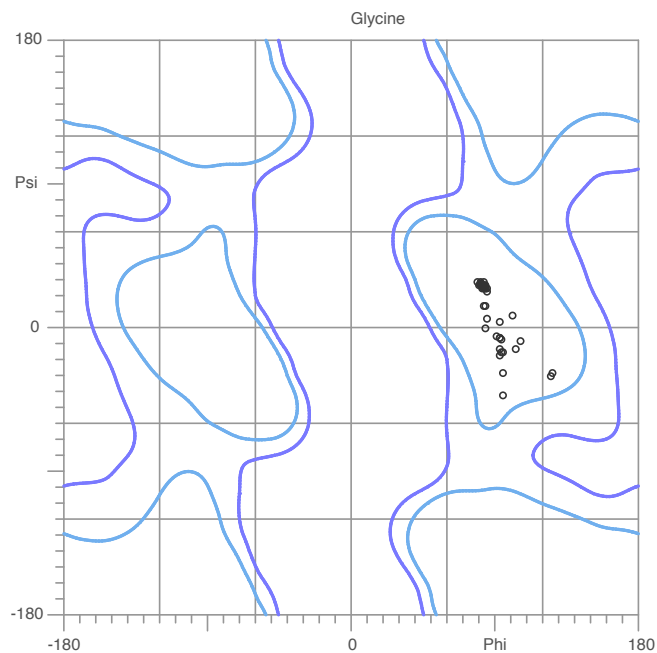
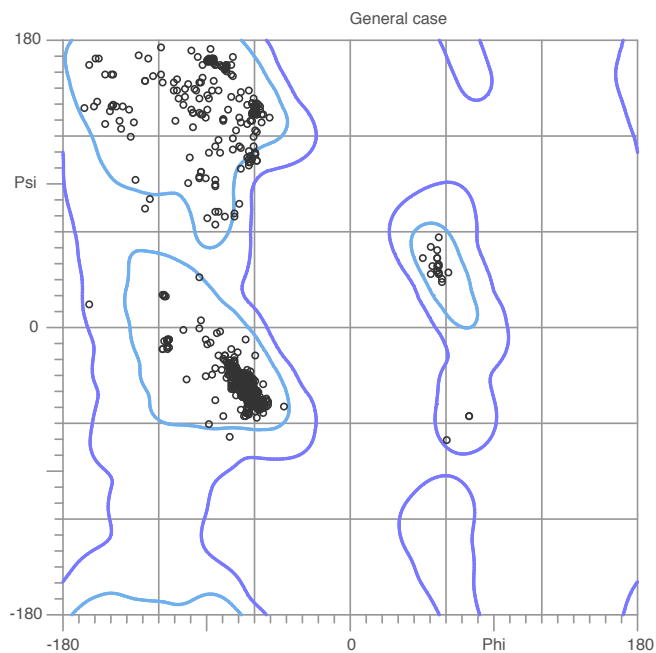


MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, all models



97.8% (900/920) of all residues were in favored (98%) regions.
100.0% (920/920) of all residues were in allowed (>99.8%) regions.

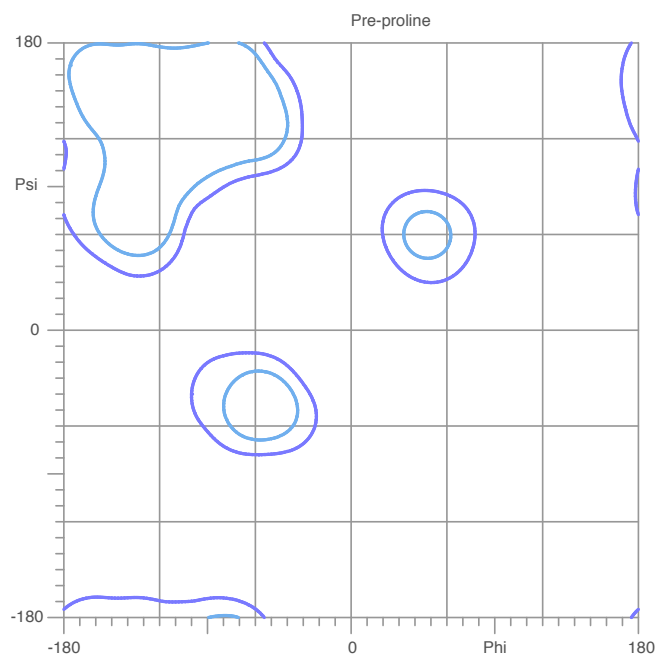
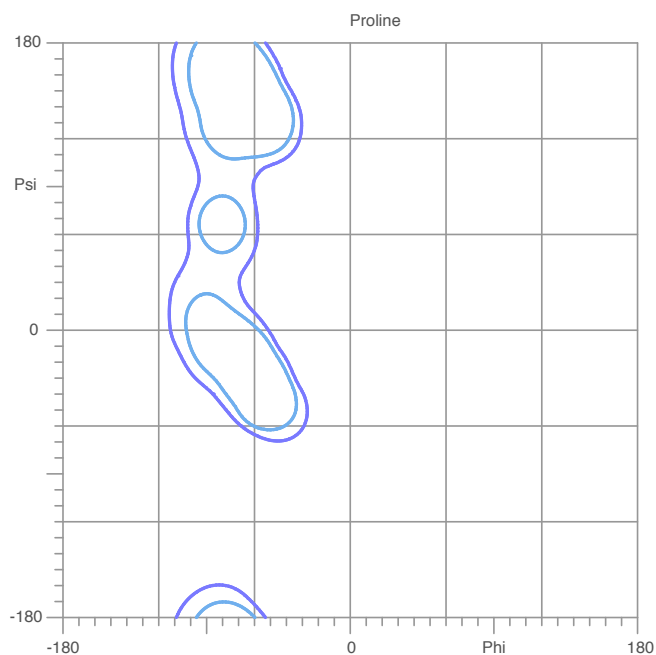
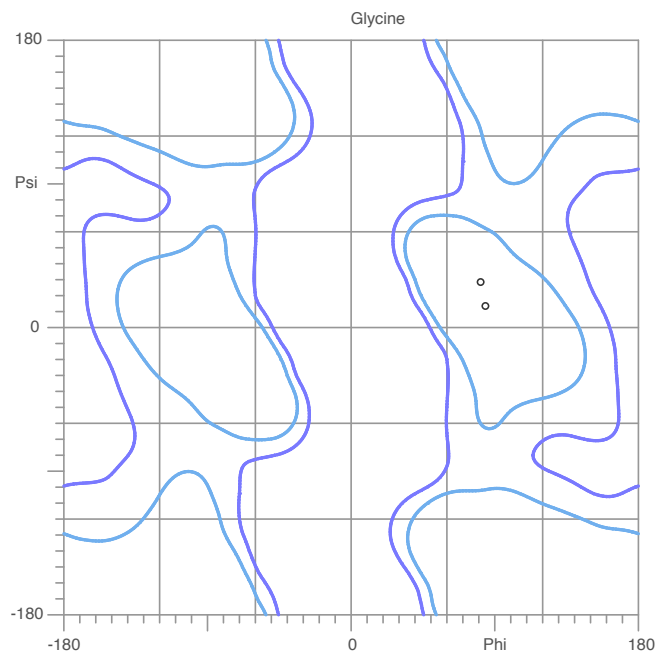
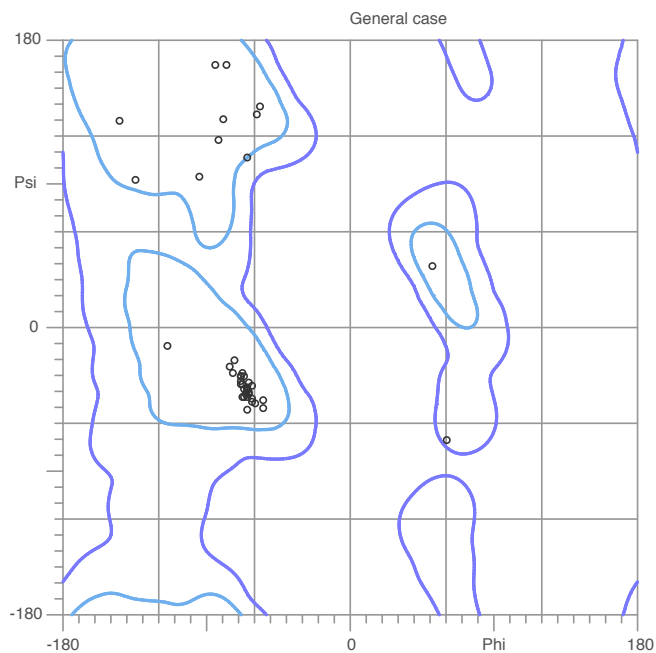
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_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.

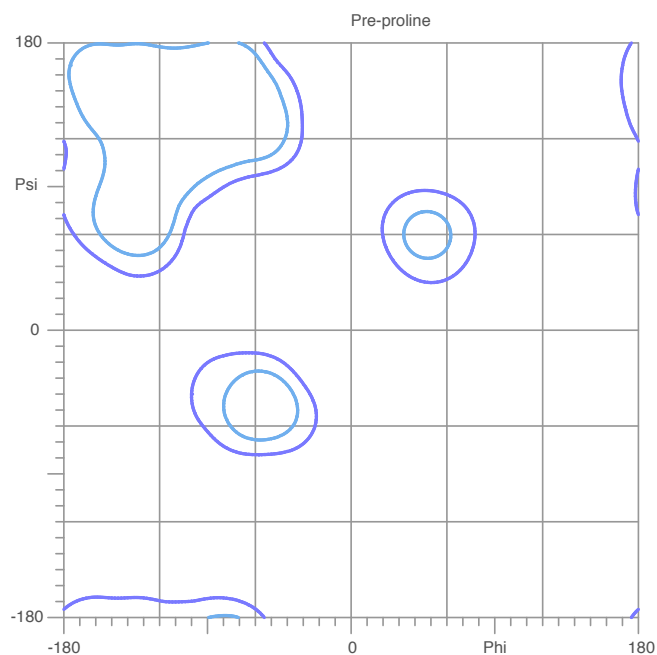
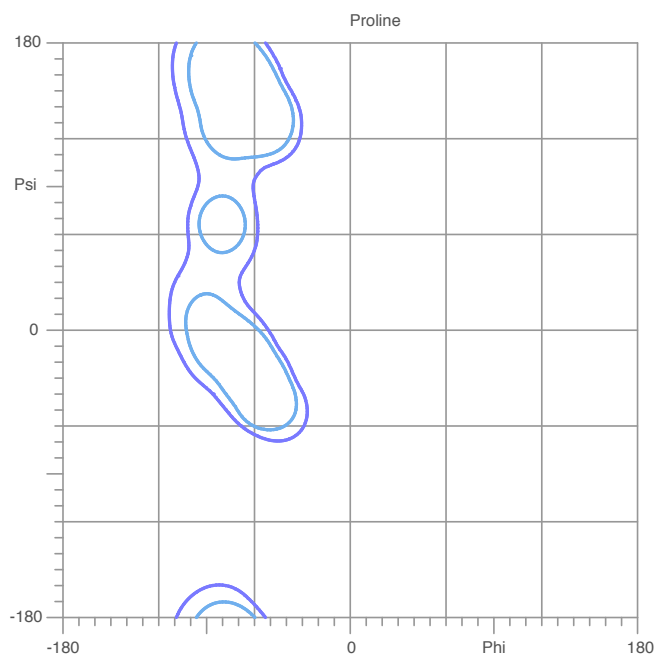
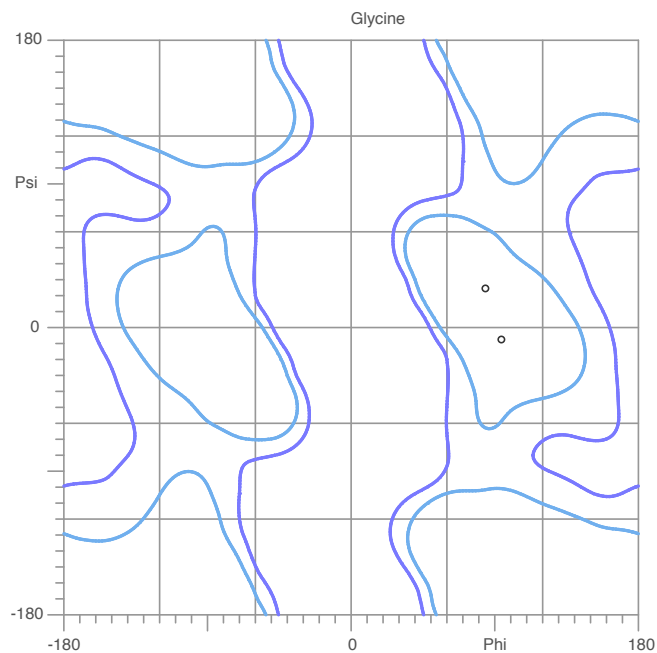
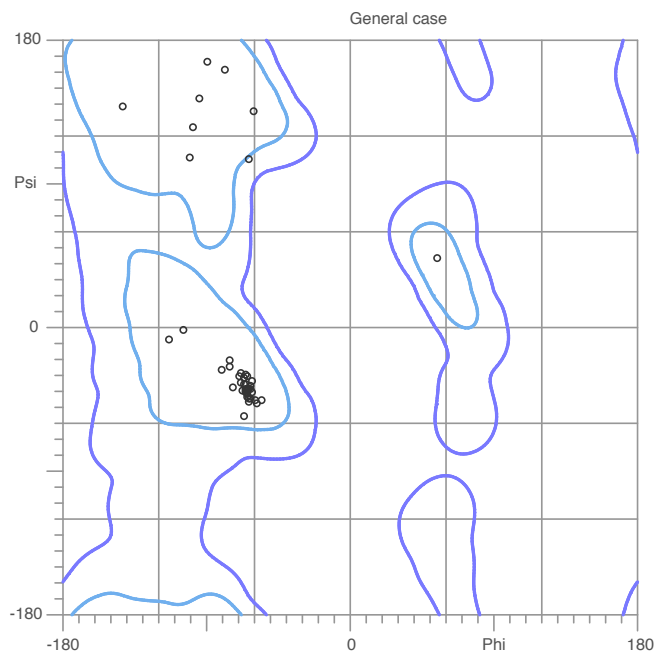
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 2



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.

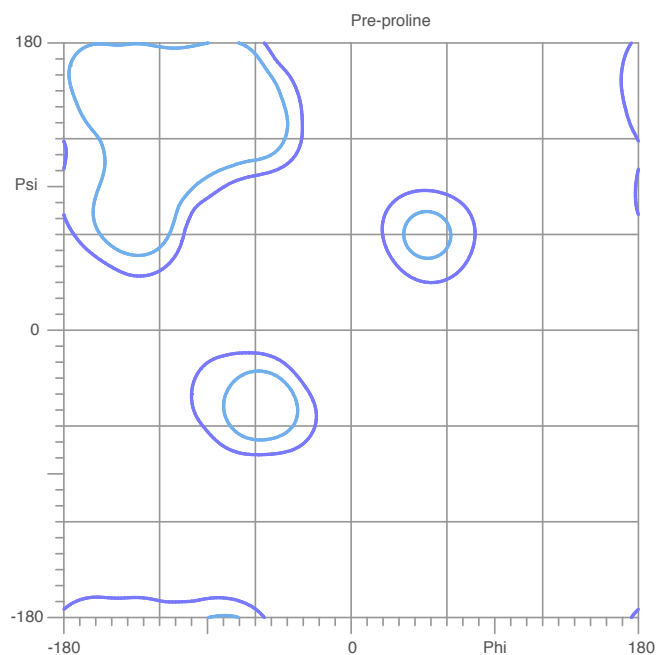
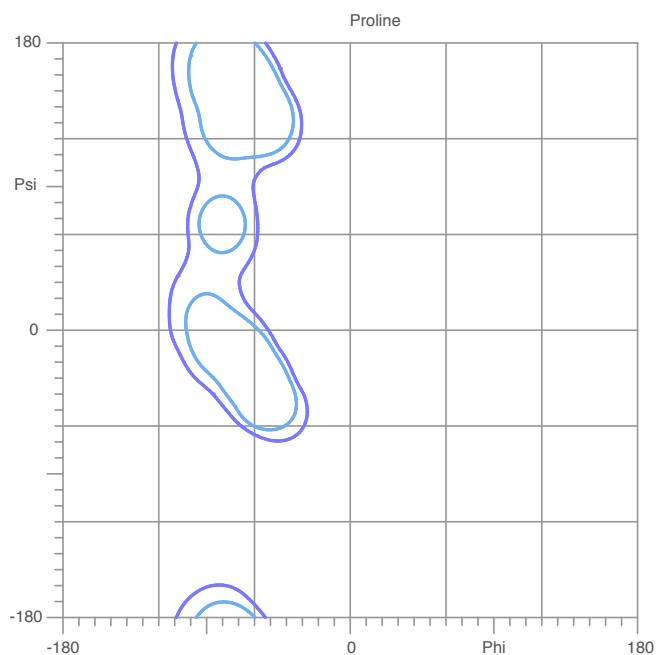
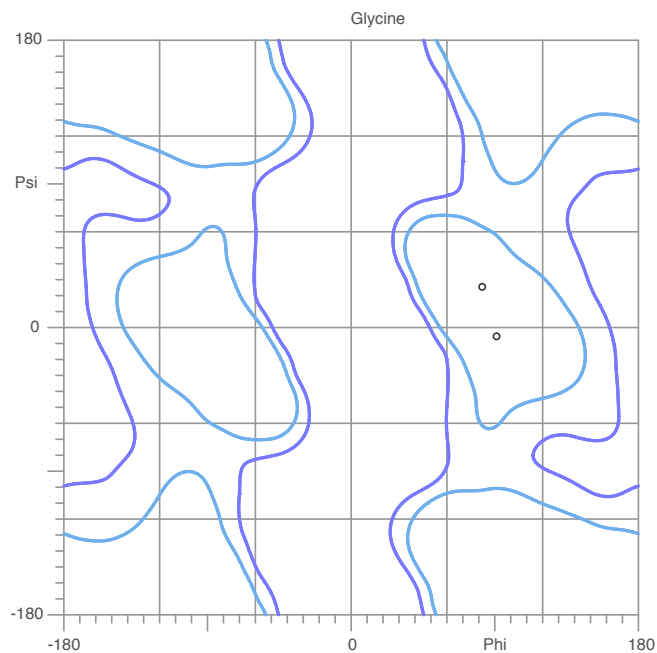
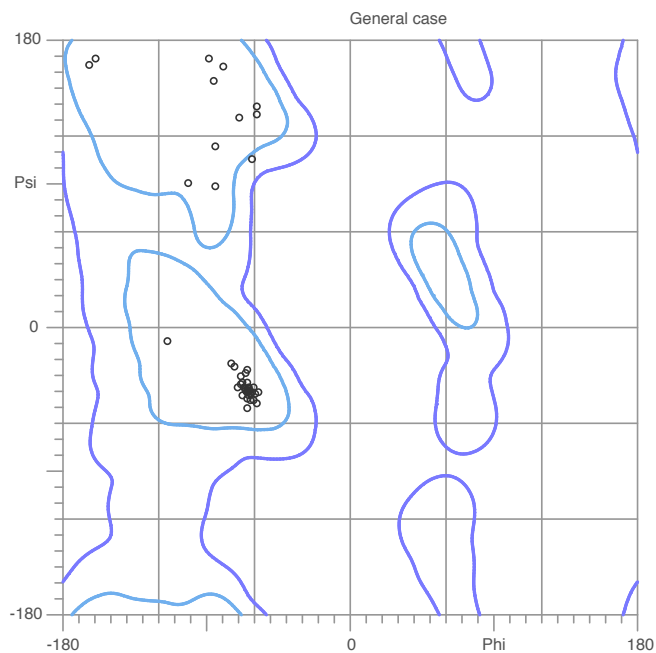
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_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.

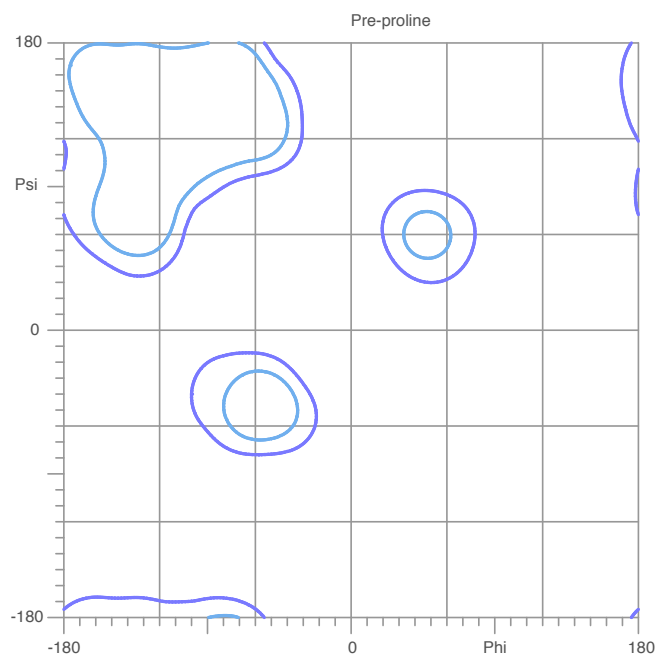
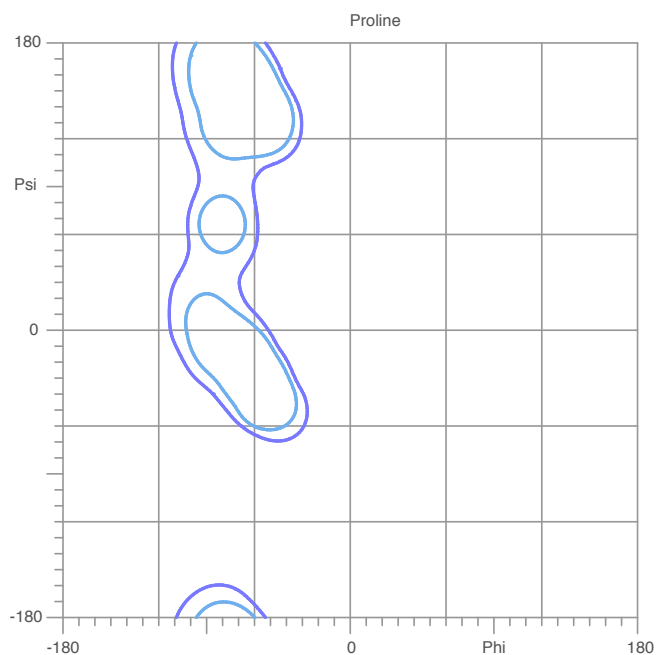
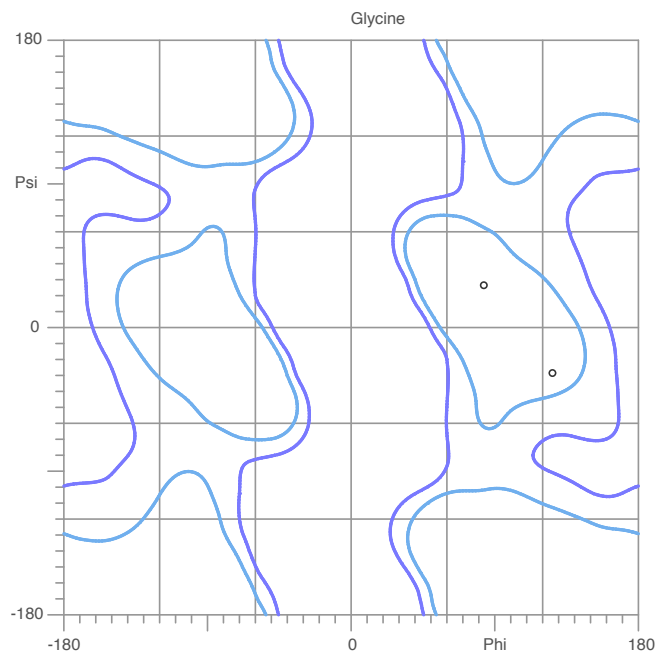
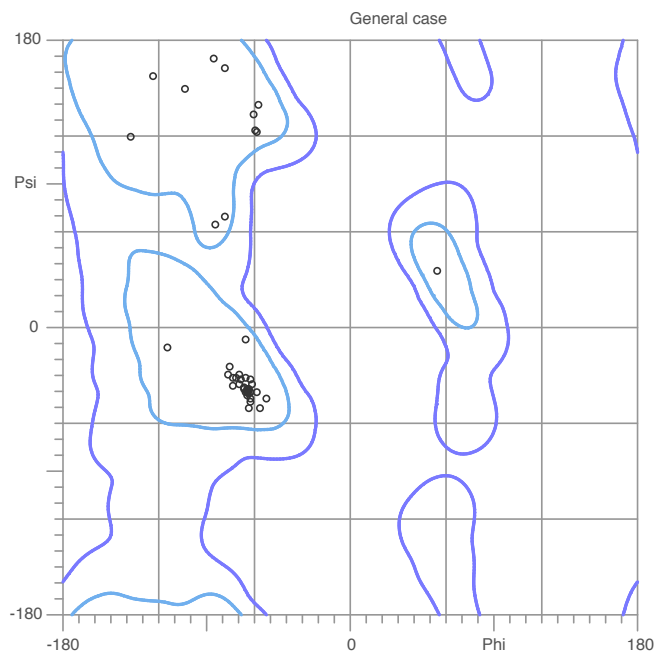
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 4



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.

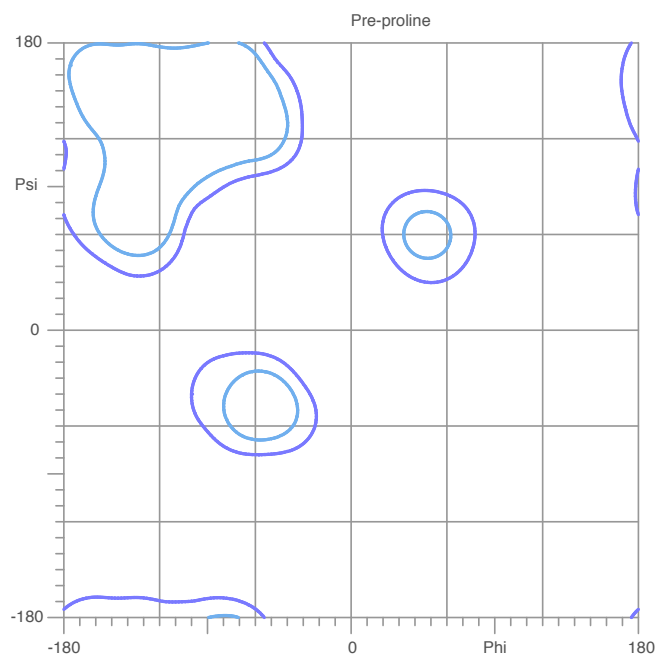
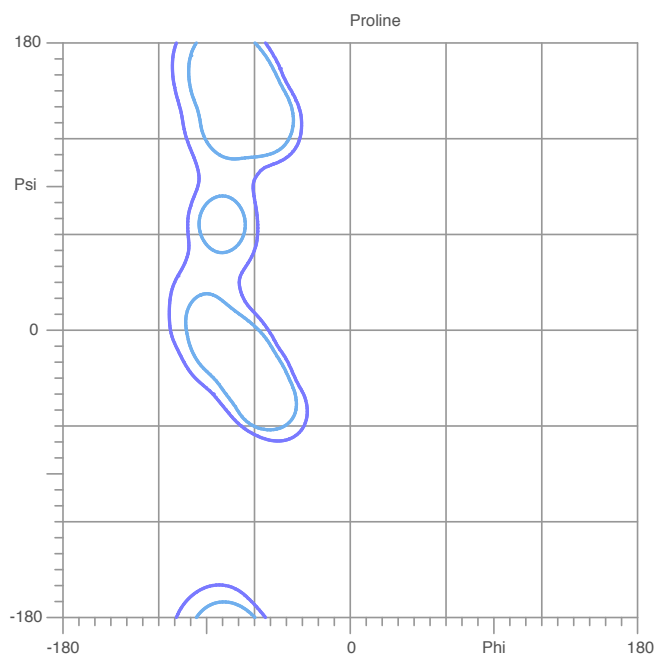
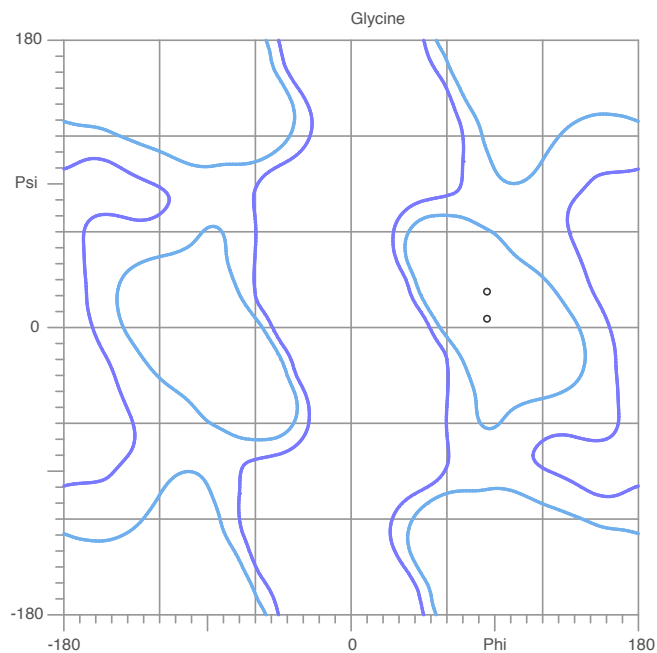
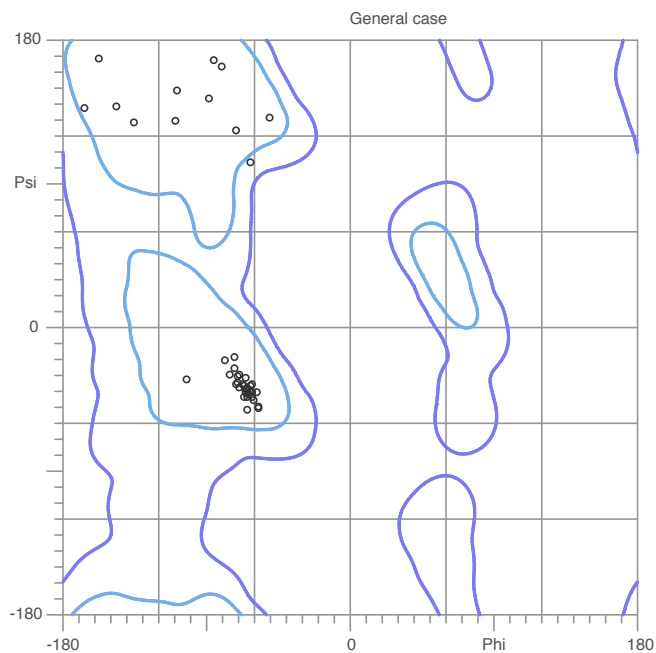
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 5



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.

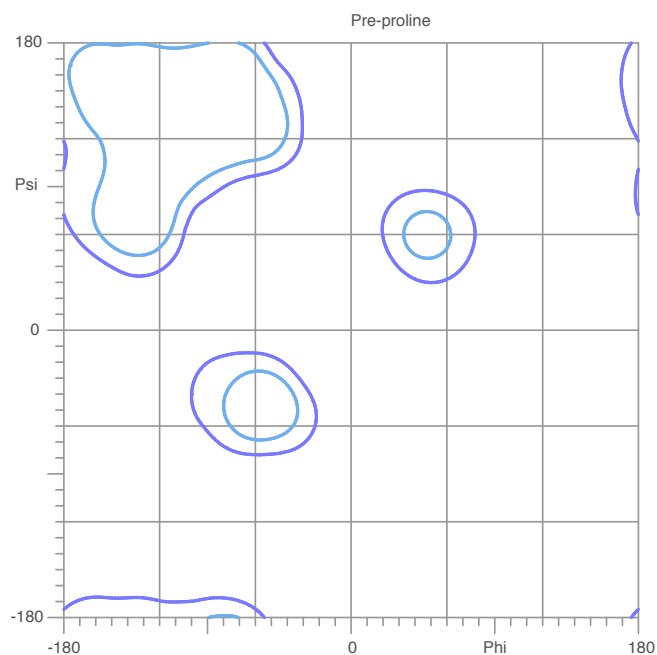
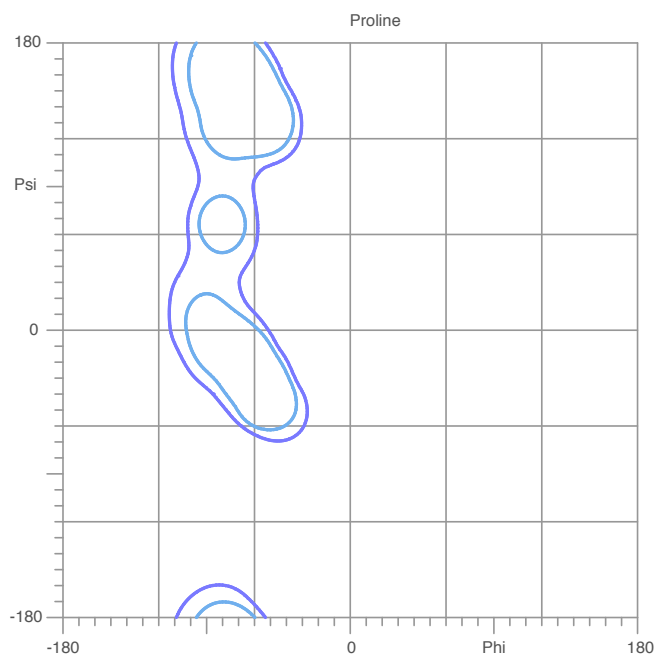
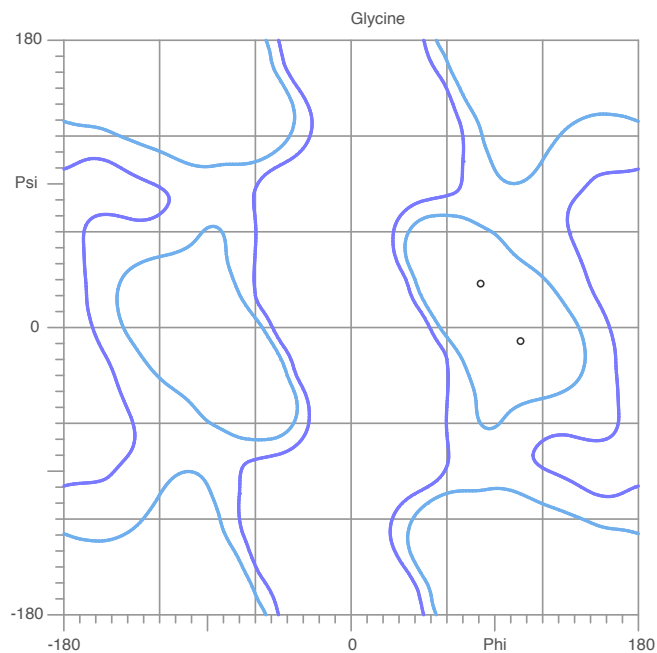
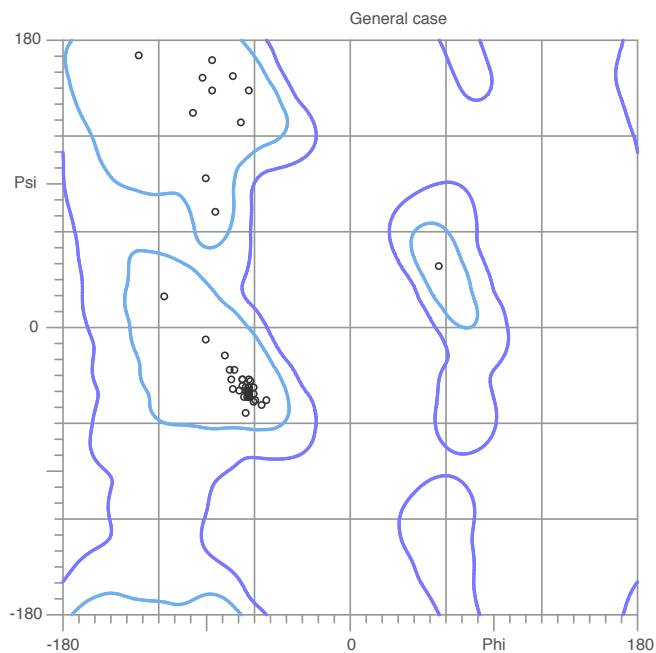
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_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.

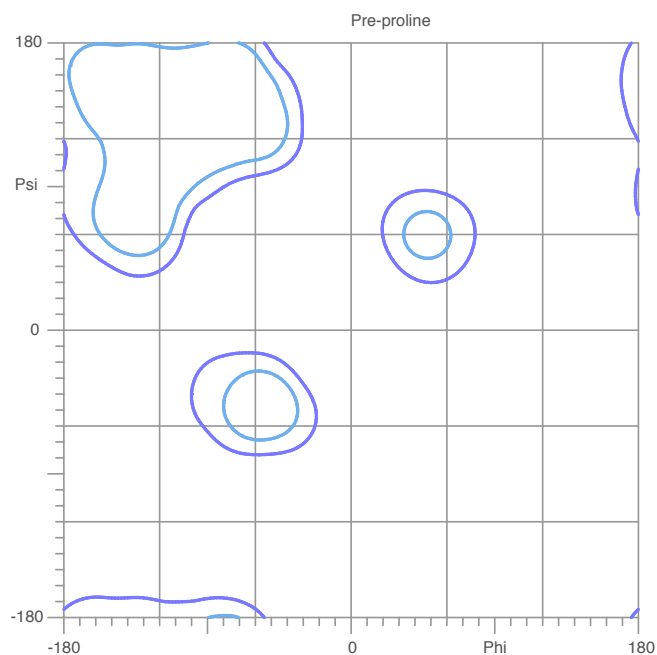
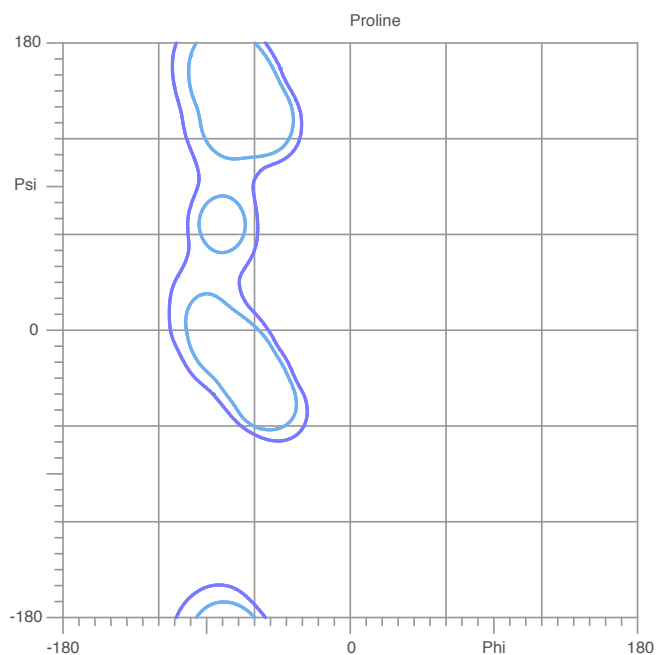
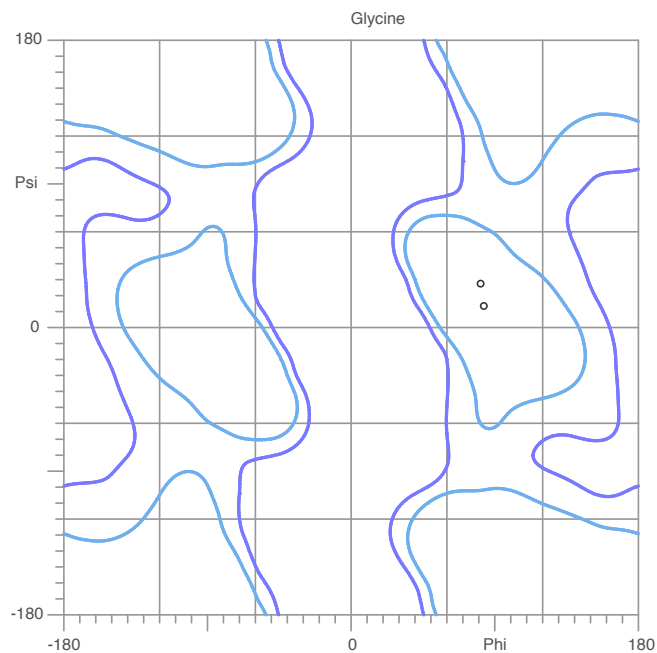
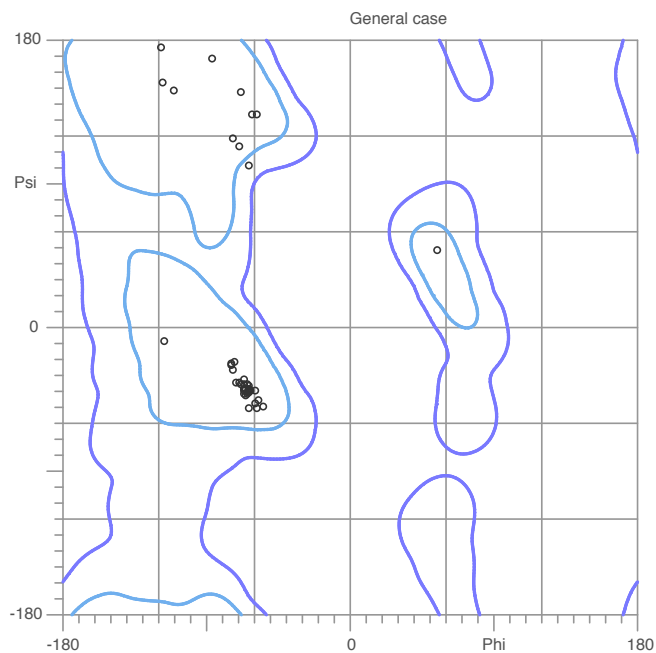
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_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.

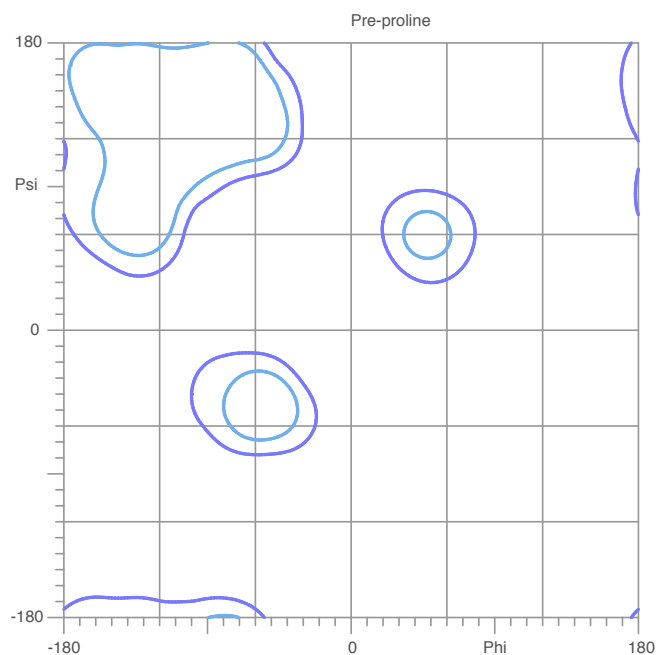
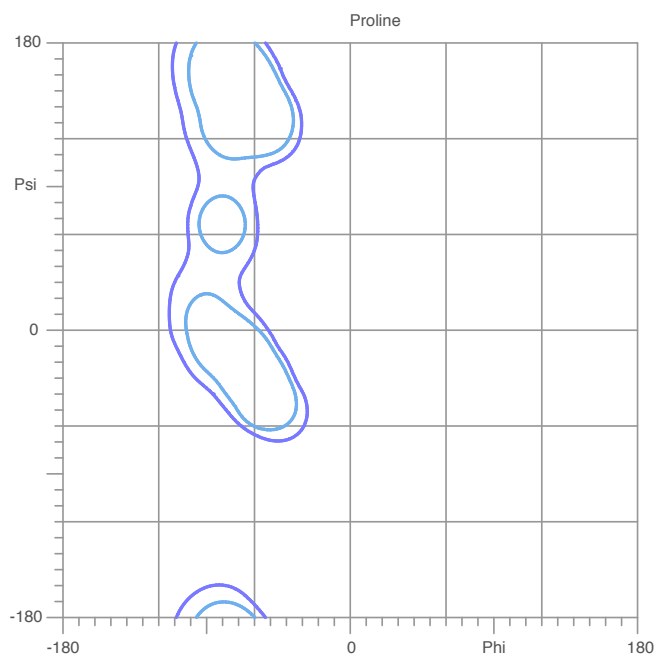
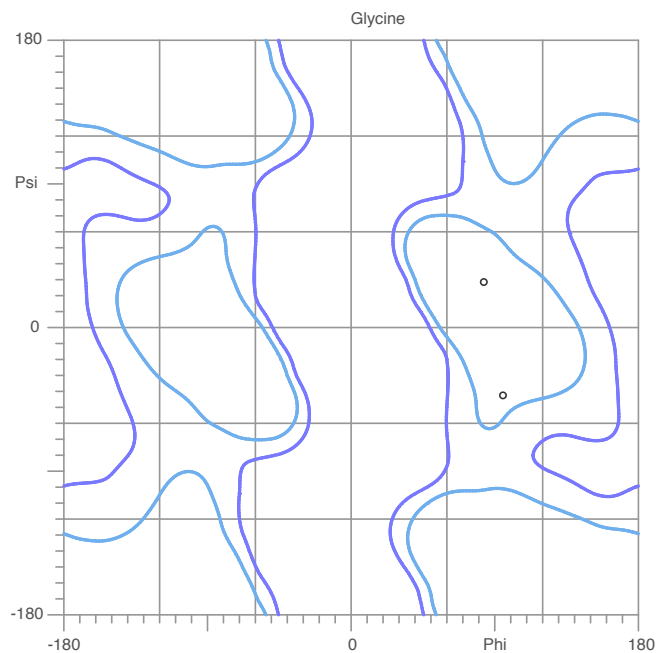
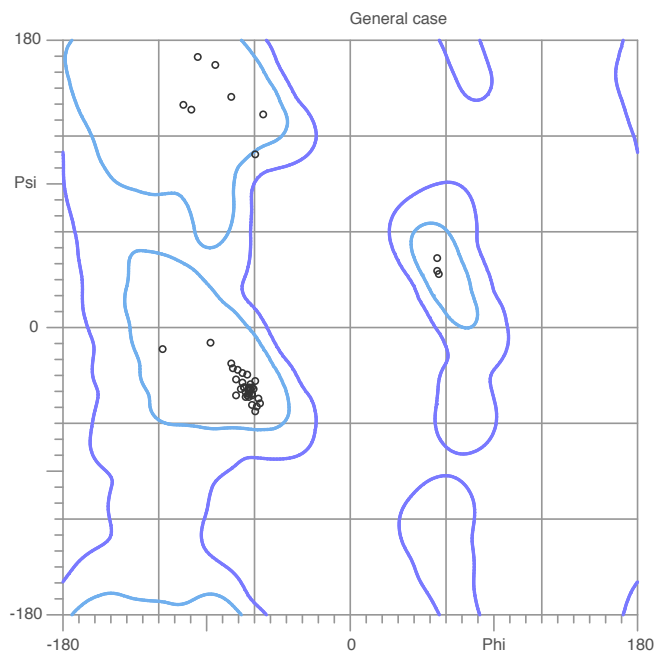
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 8



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.

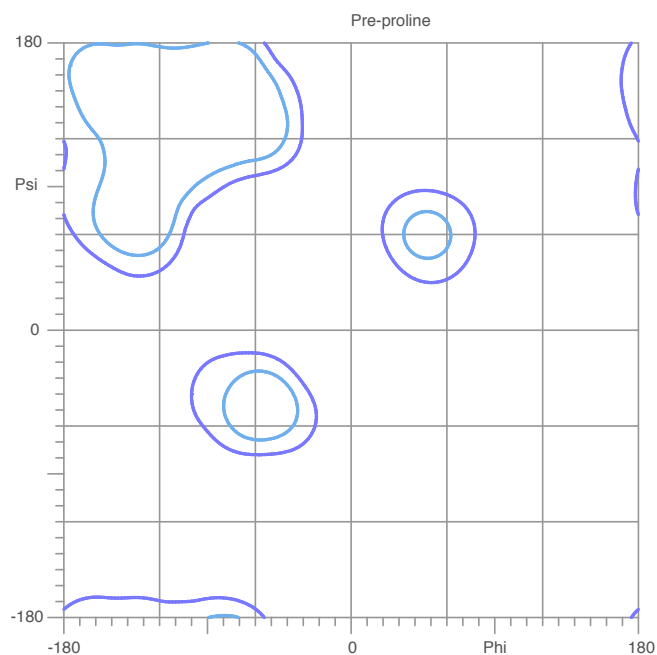
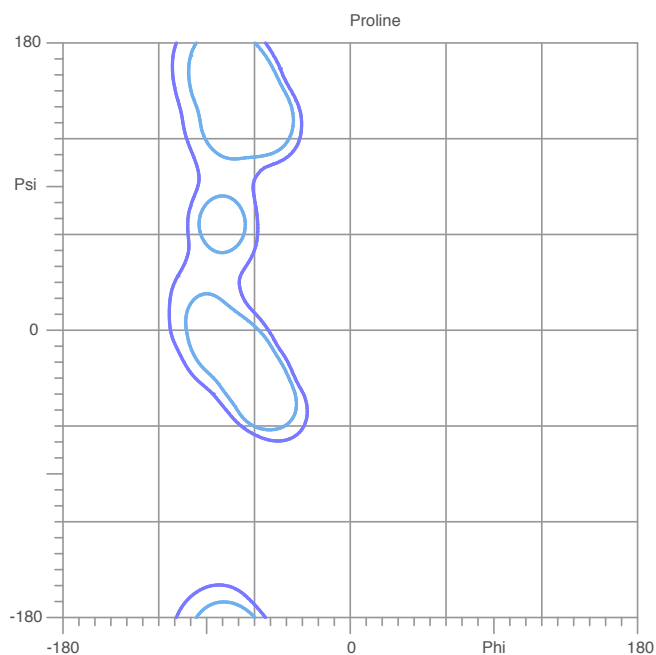
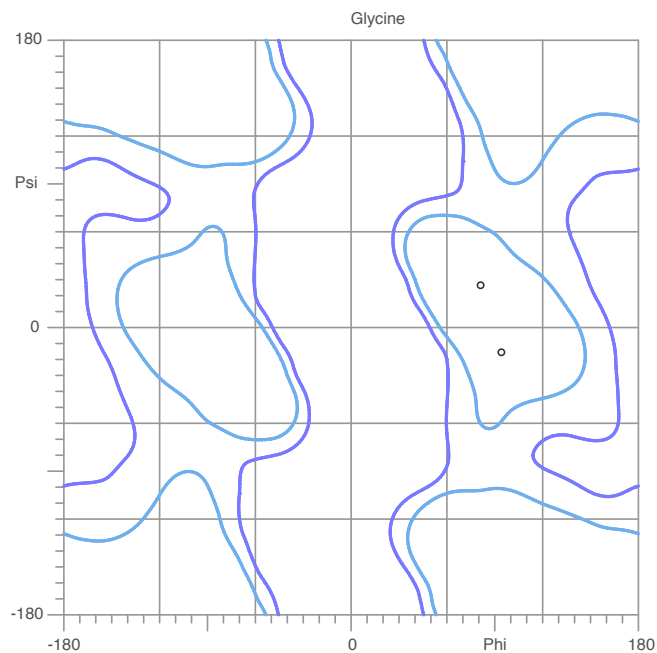
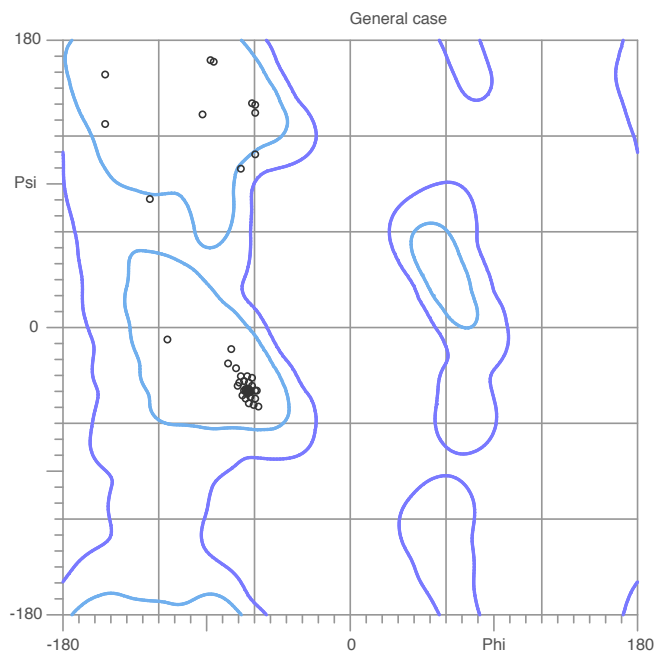
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_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.

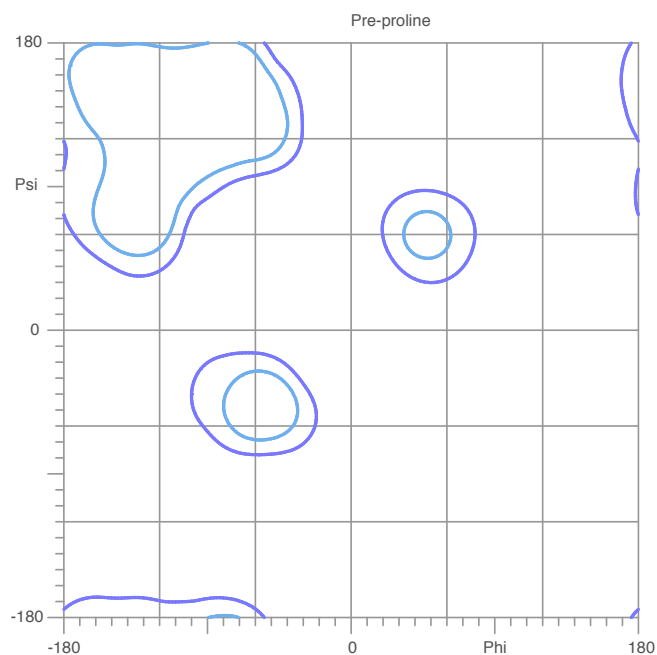
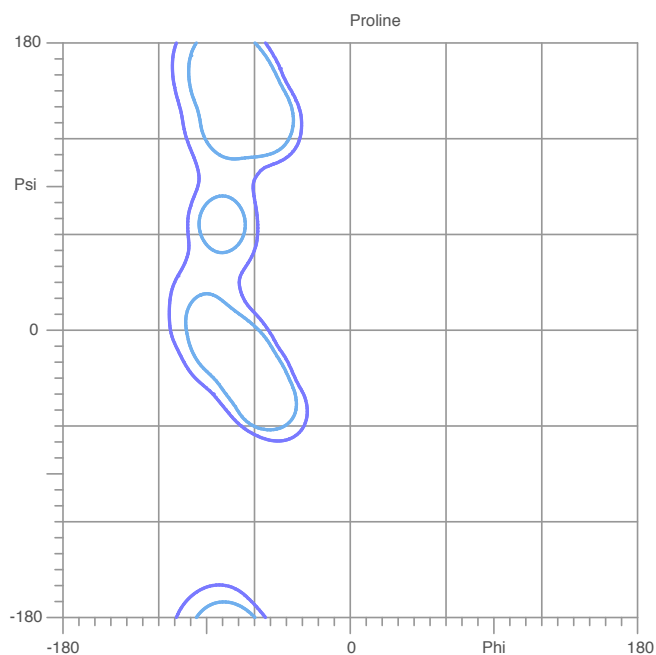
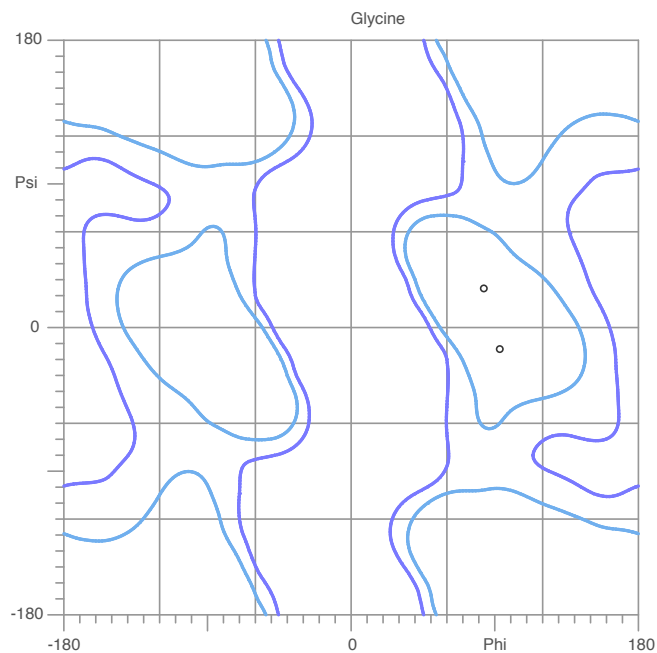
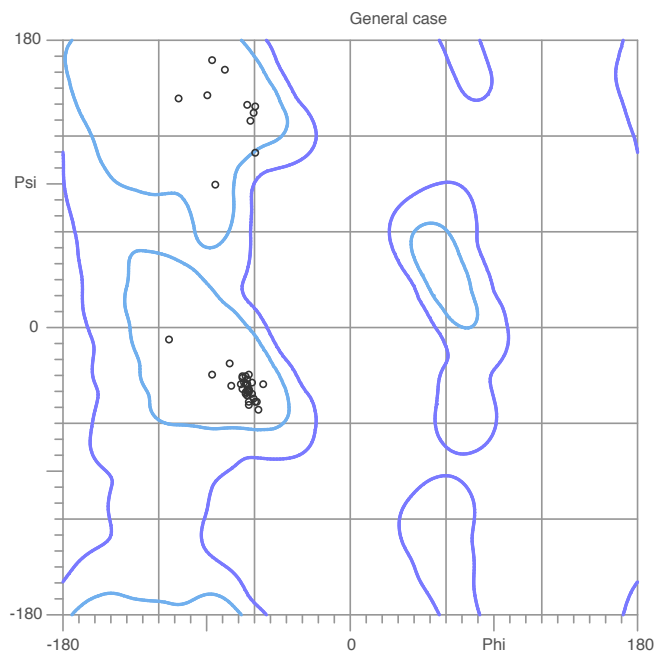
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 10

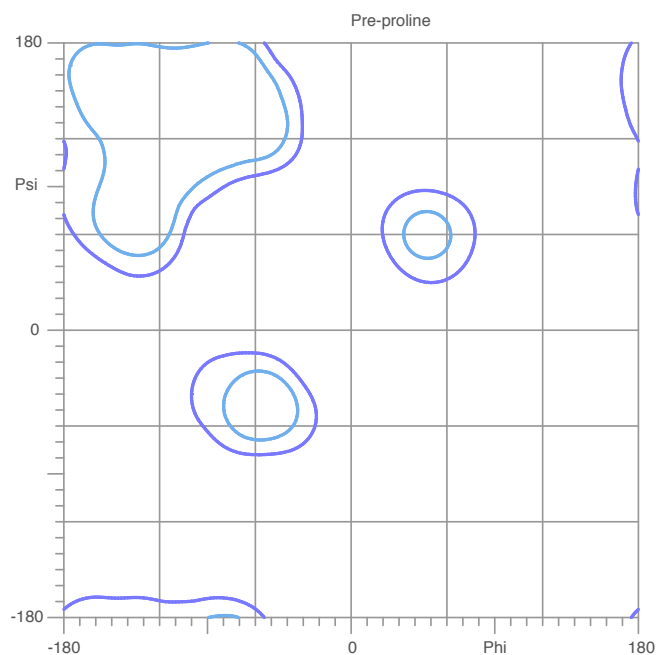
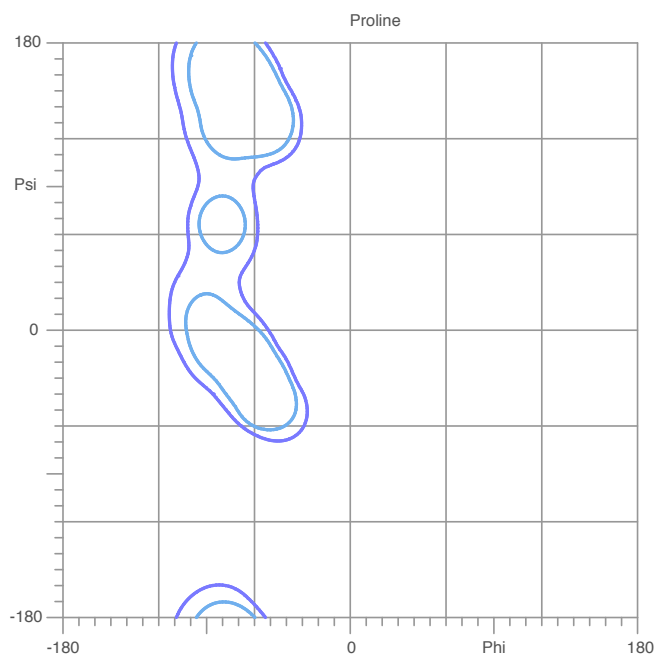
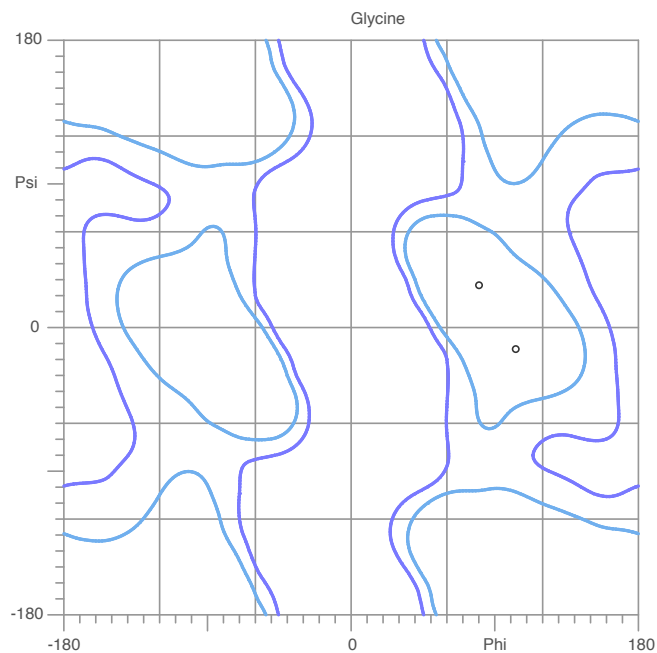
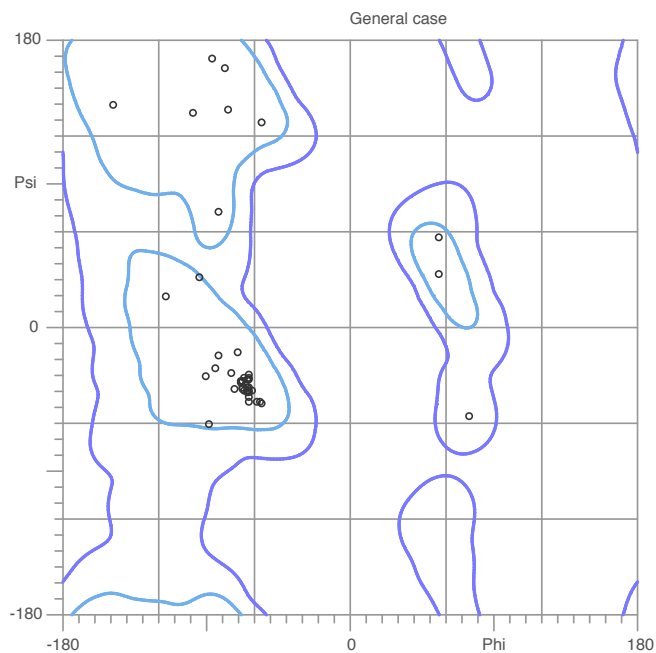


97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

SR384_R3_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.

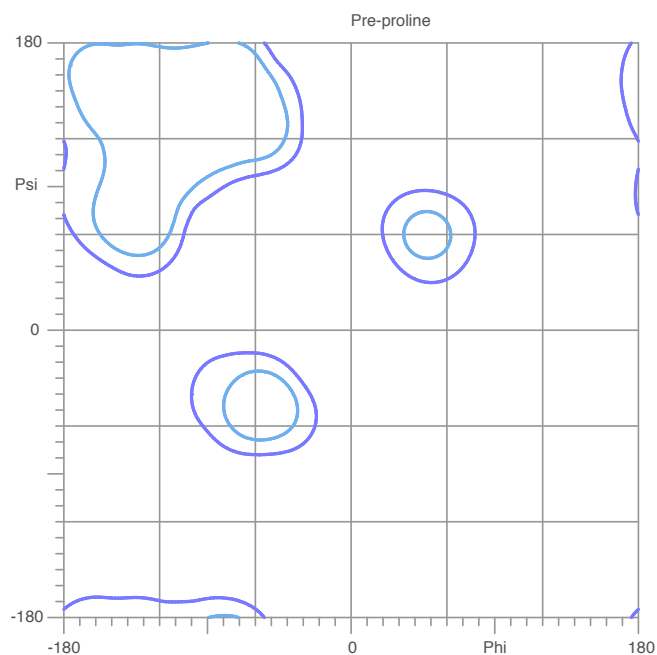
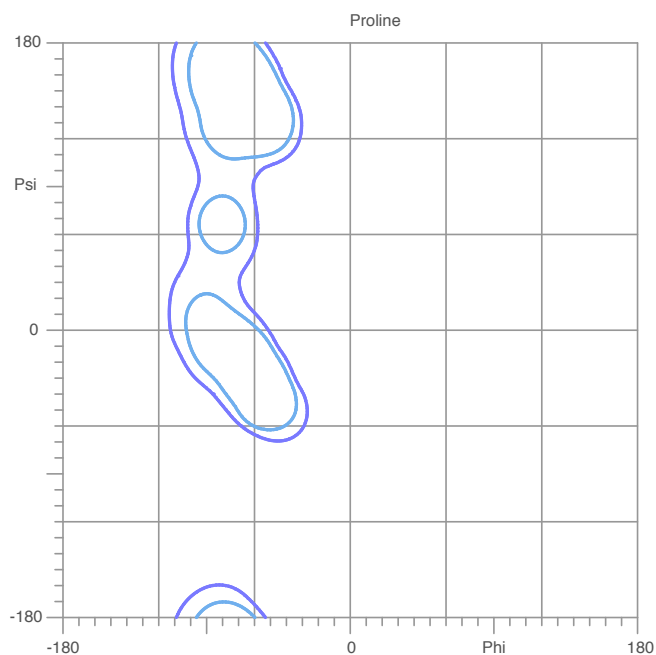
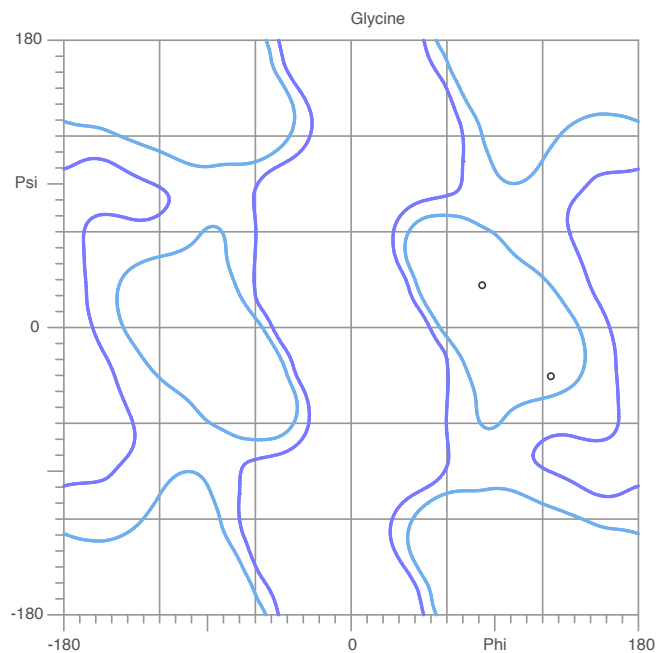
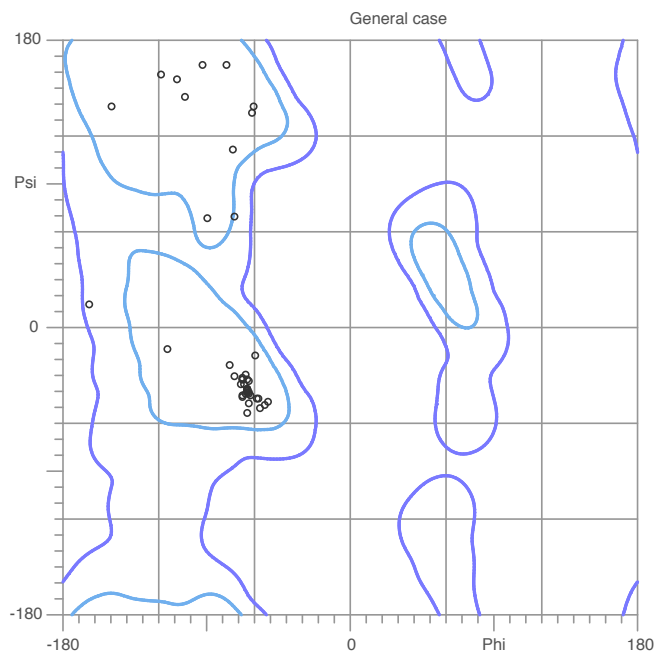
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 12



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.

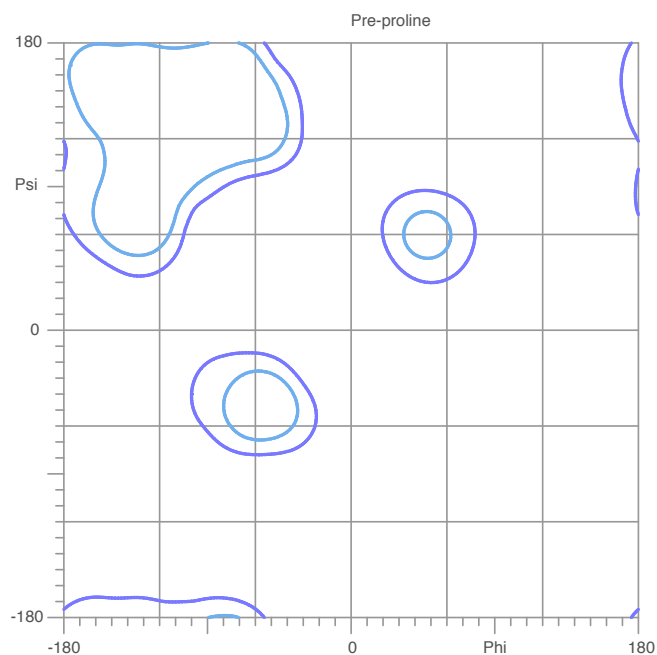
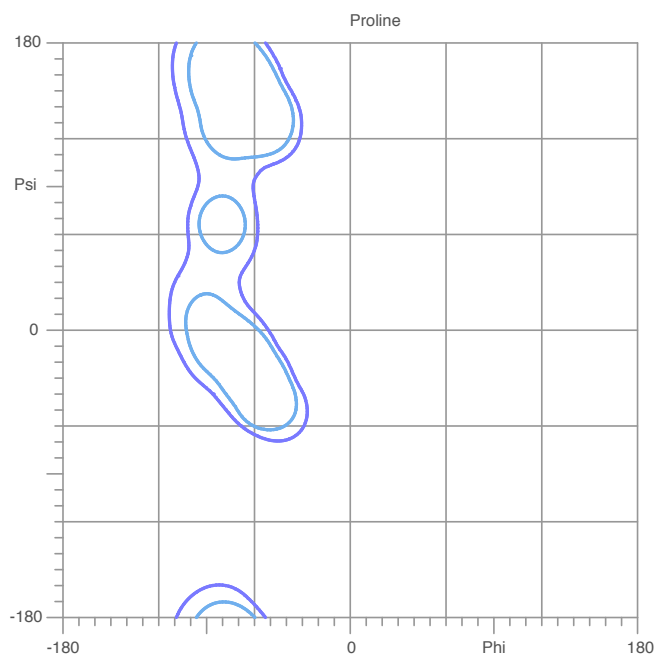
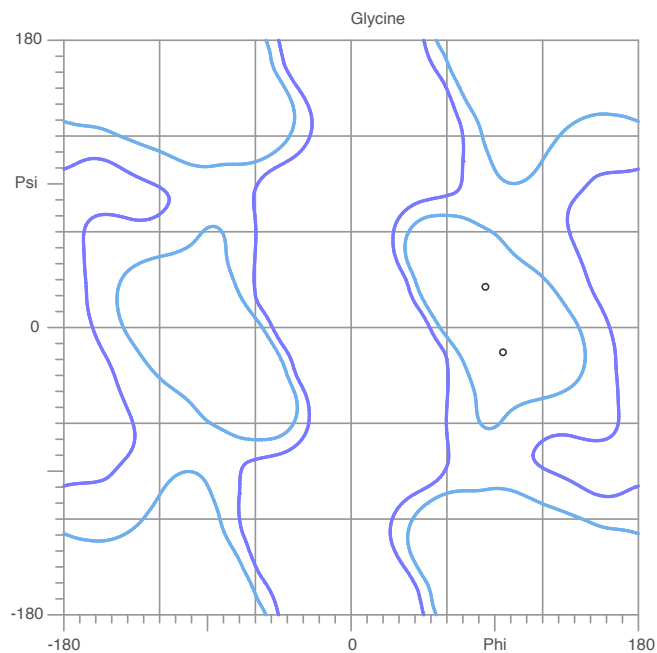
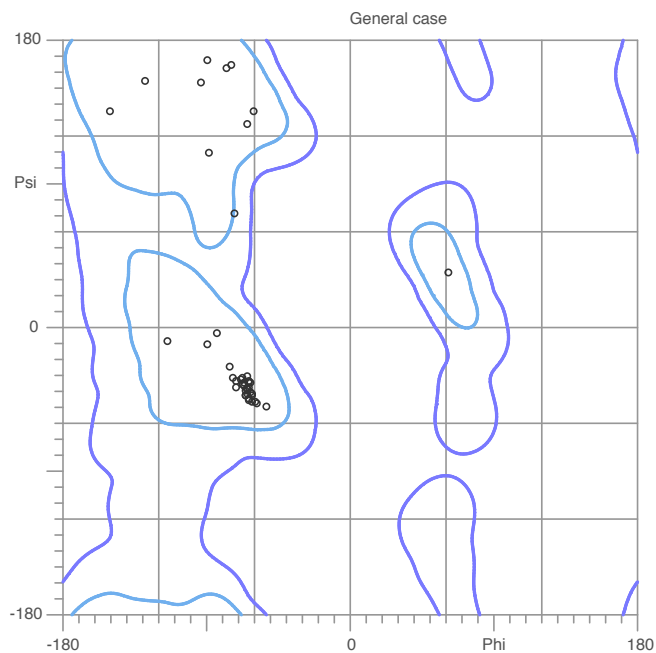
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 13



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.

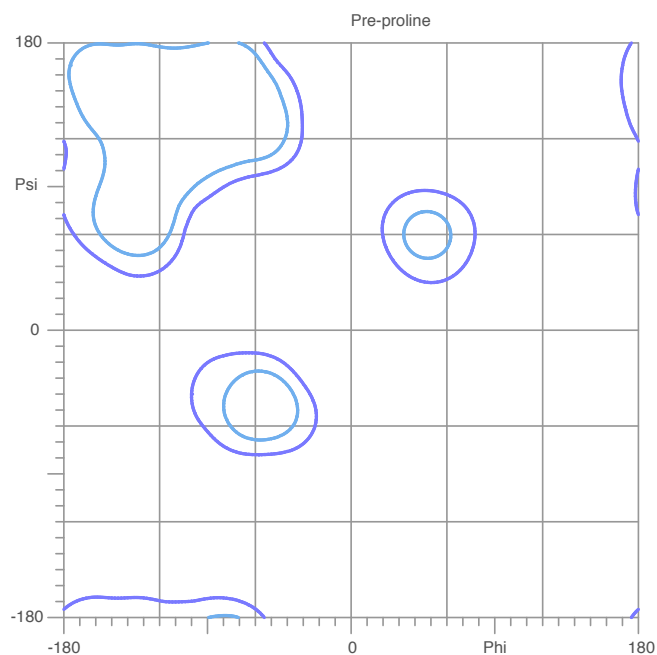
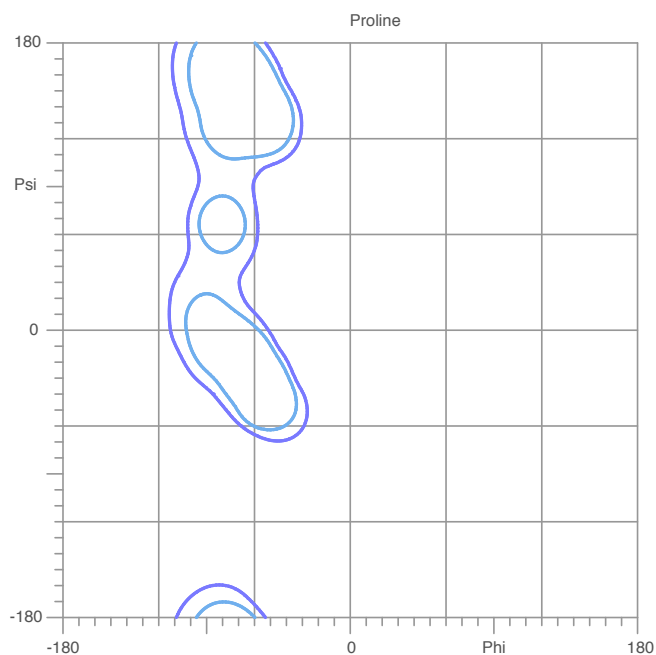
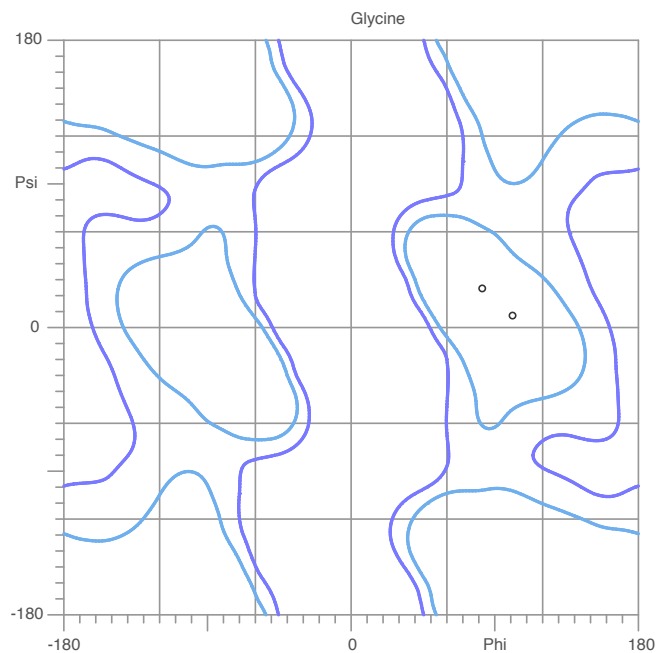
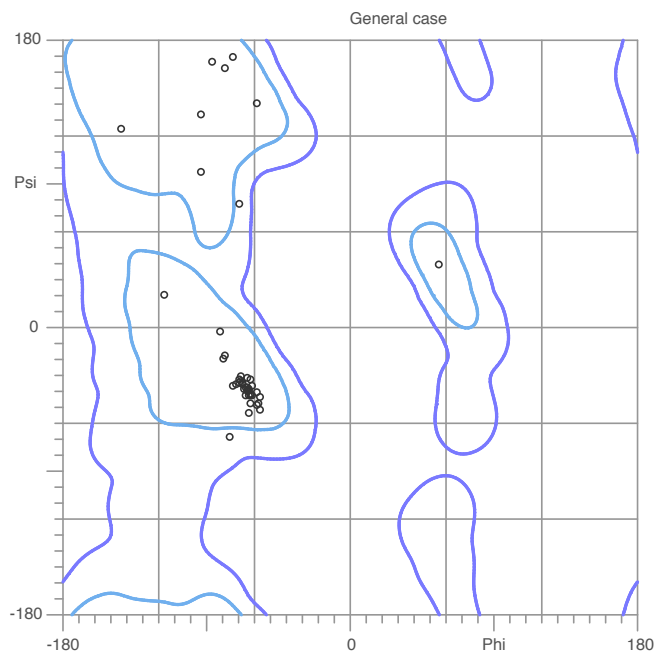
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 14



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.

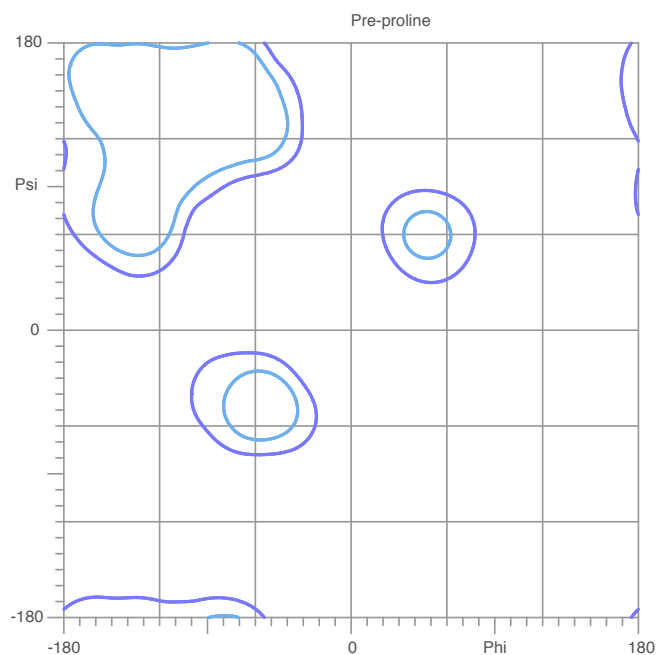
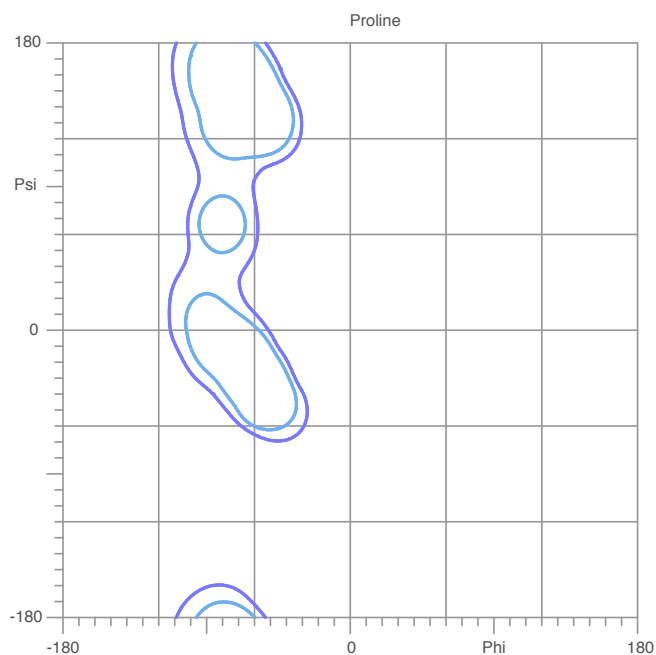
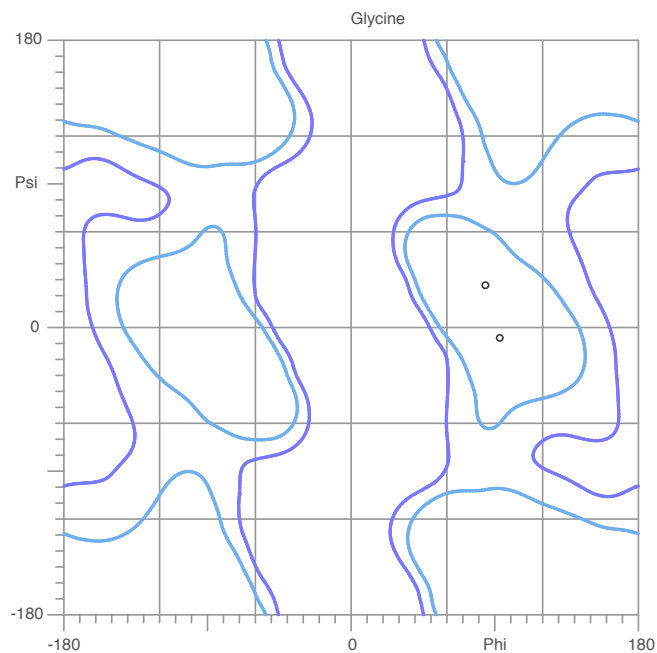
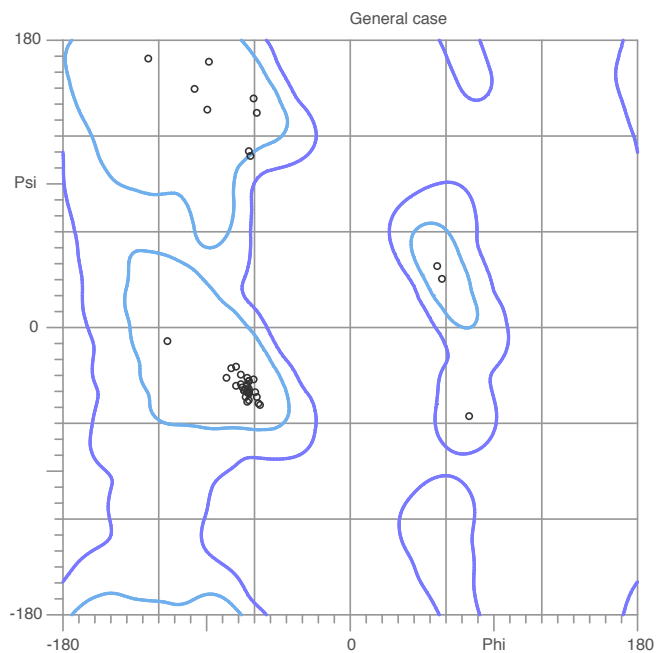
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 15



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.

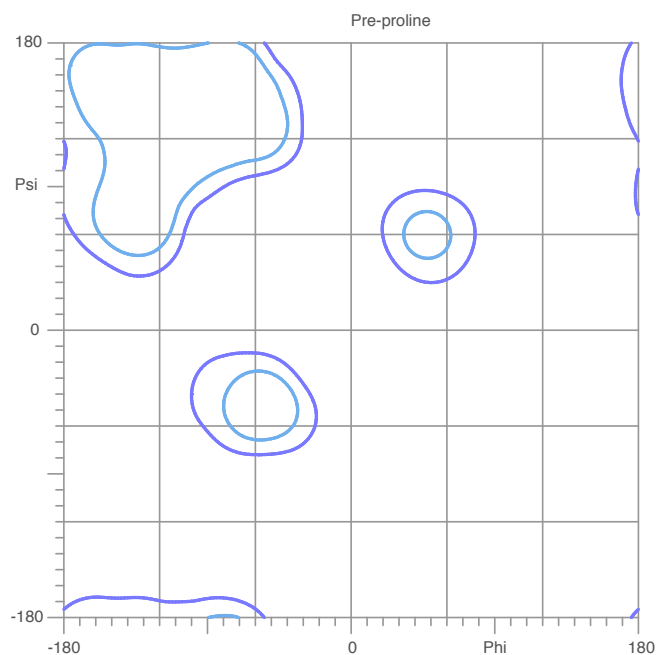
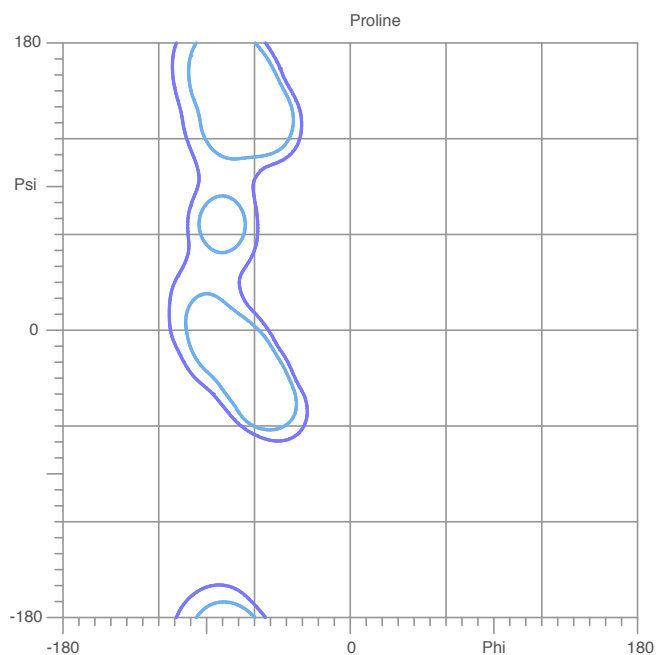
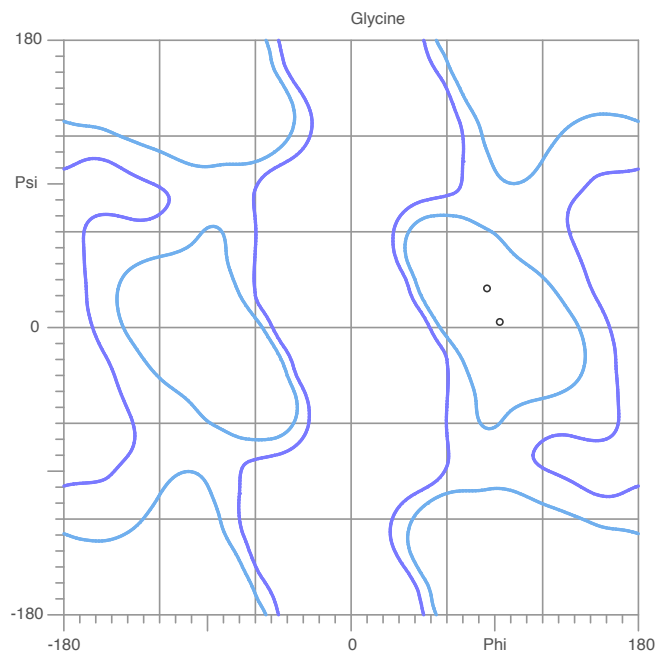
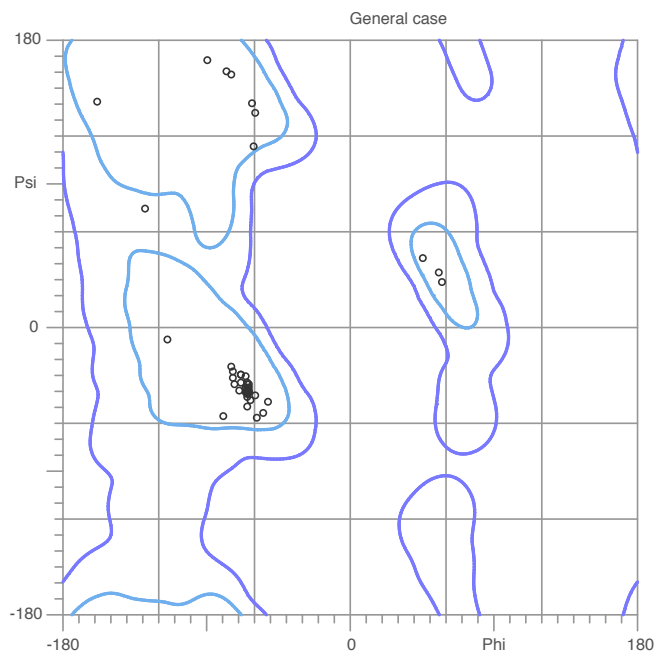
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 16



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.

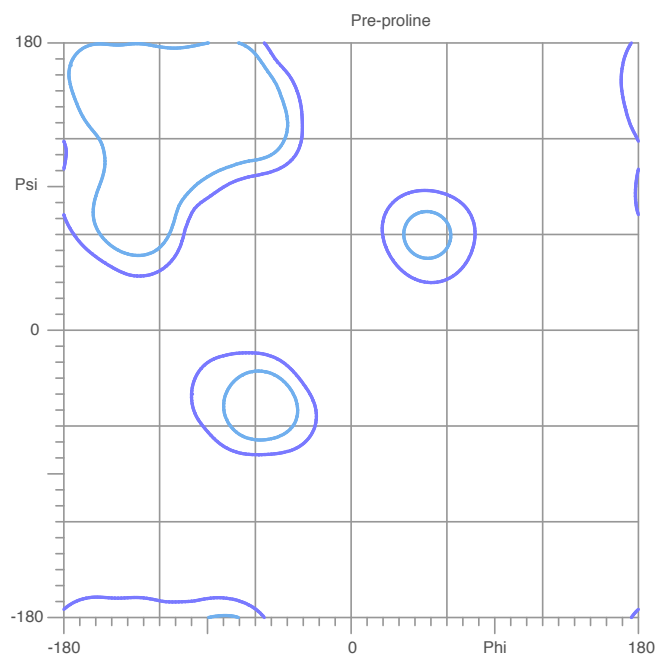
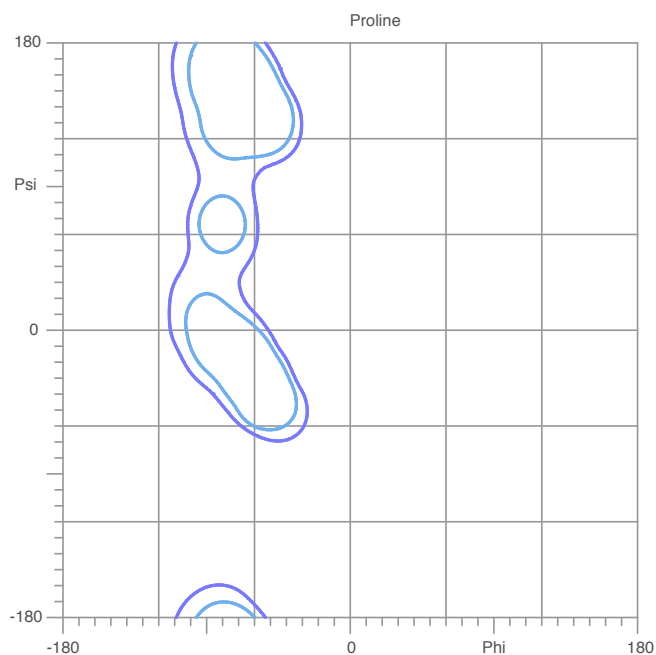
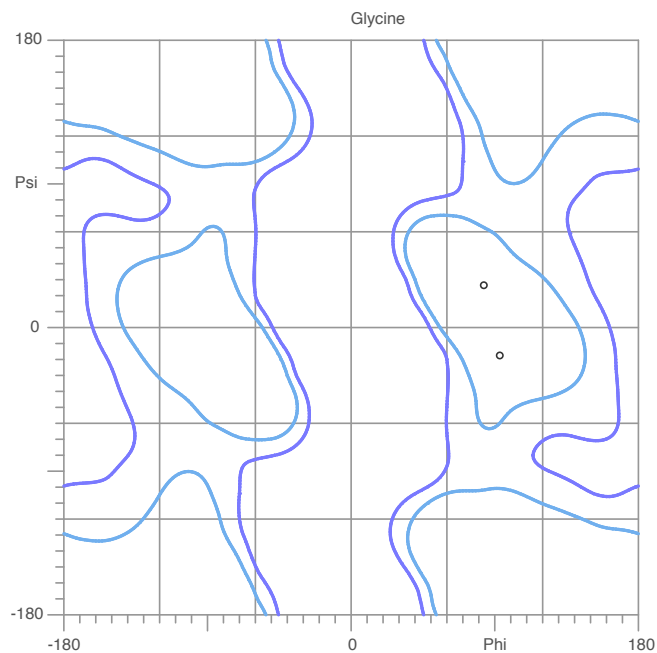
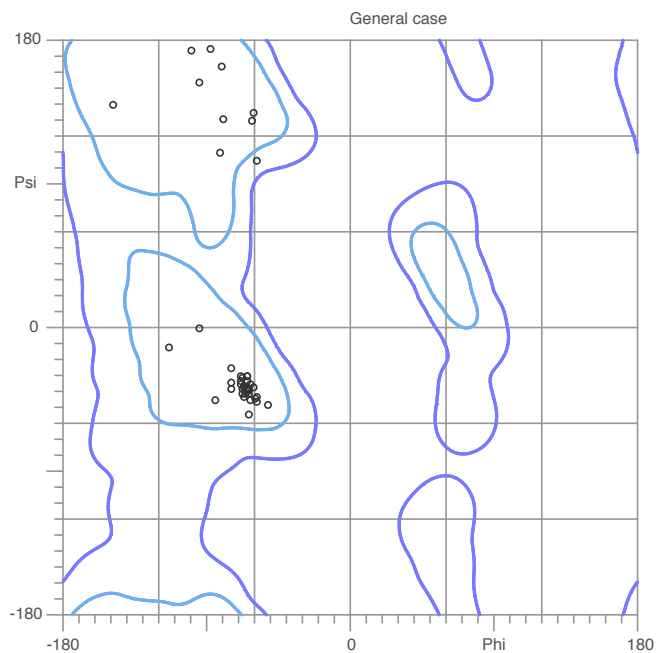
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 17



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.

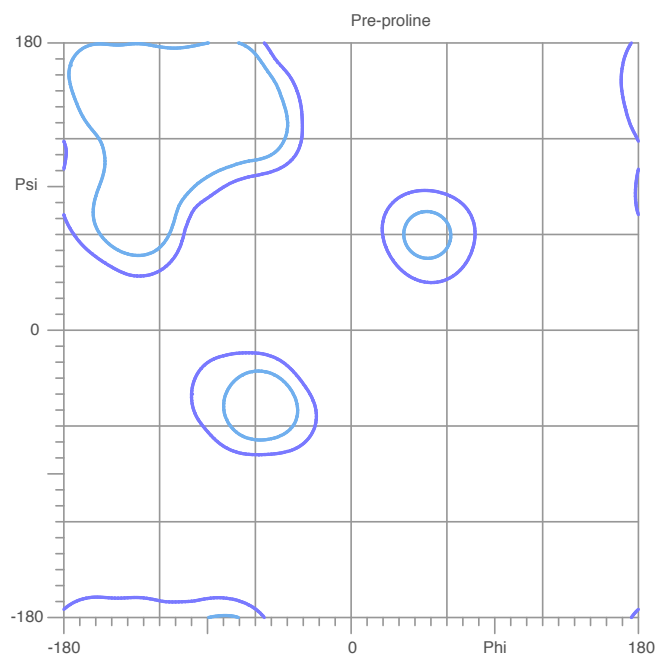
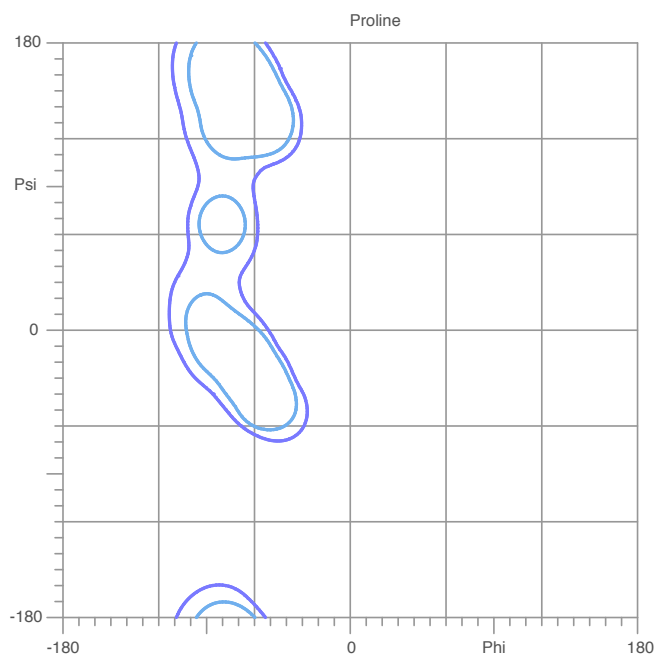
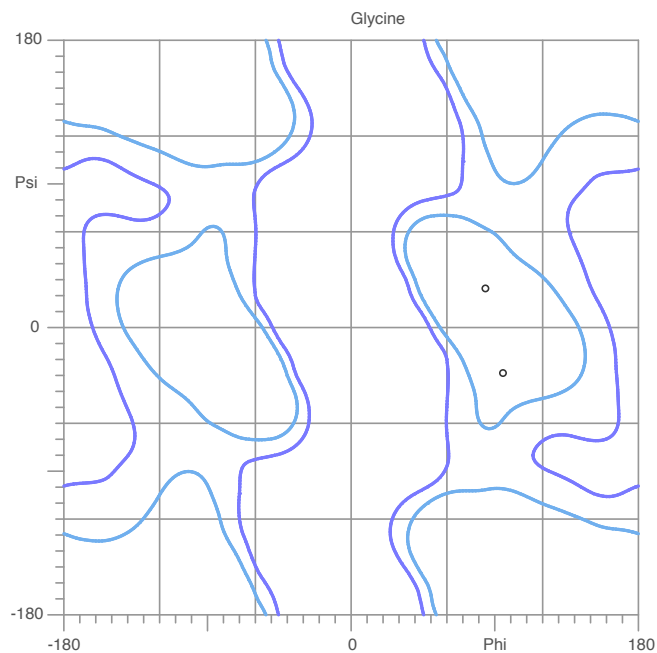
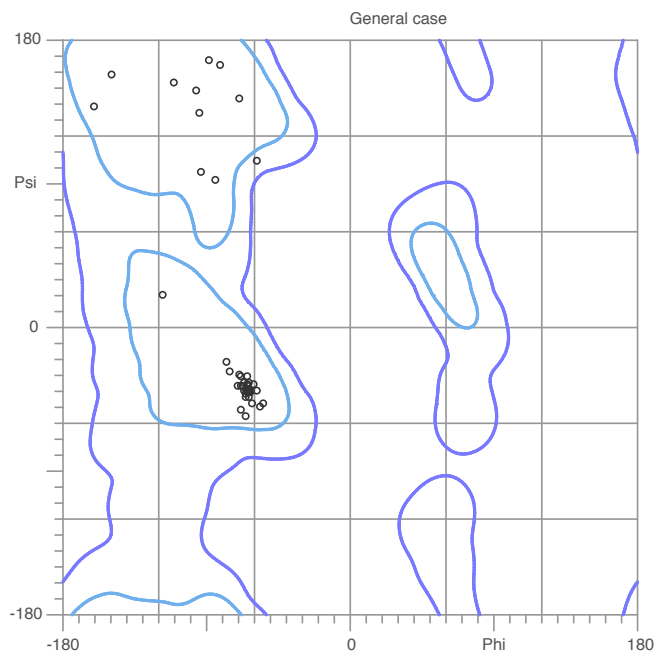
There were no outliers.

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

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MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 18



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.

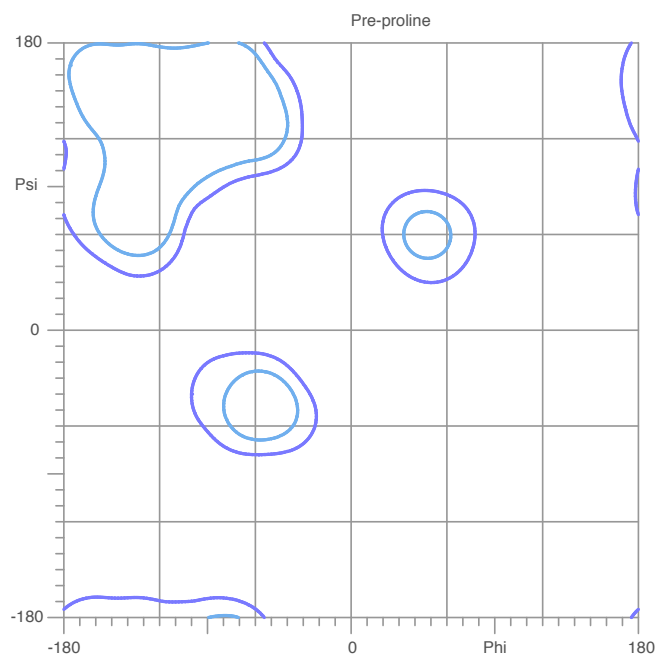
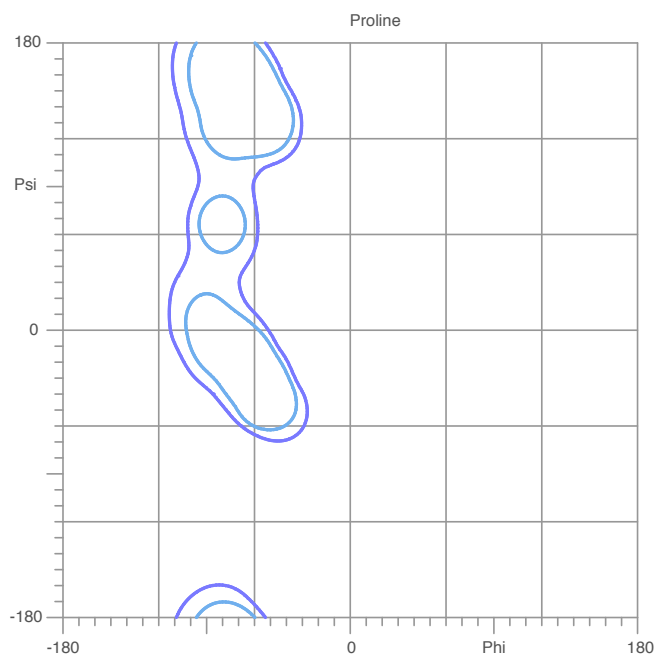
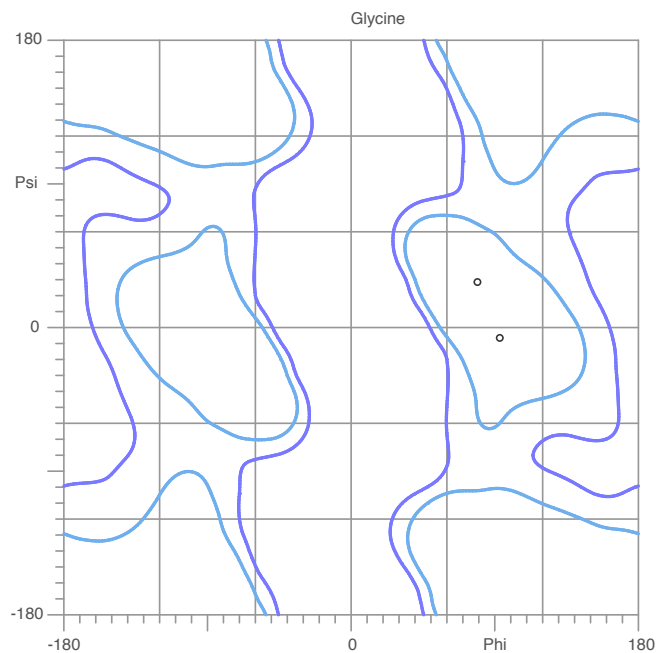
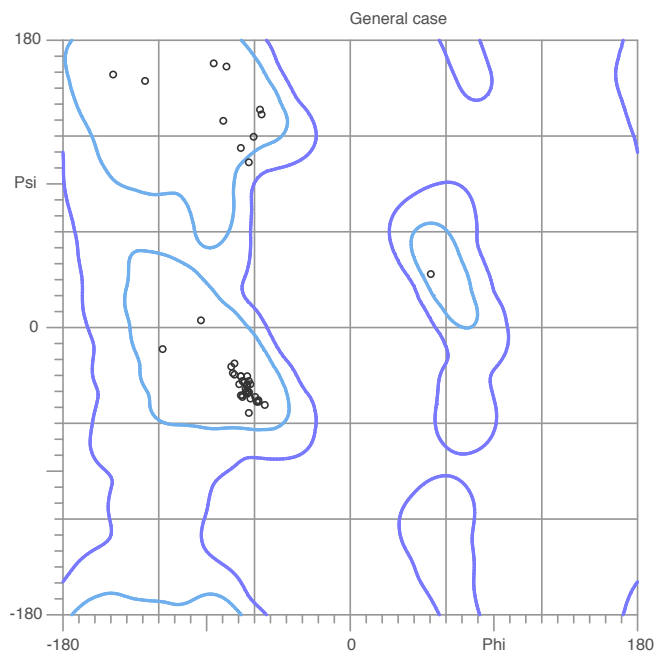
There were no outliers.

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

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

MolProbity Ramachandran analysis

SR384_R3_em_bcr3.pdb, model 19



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.

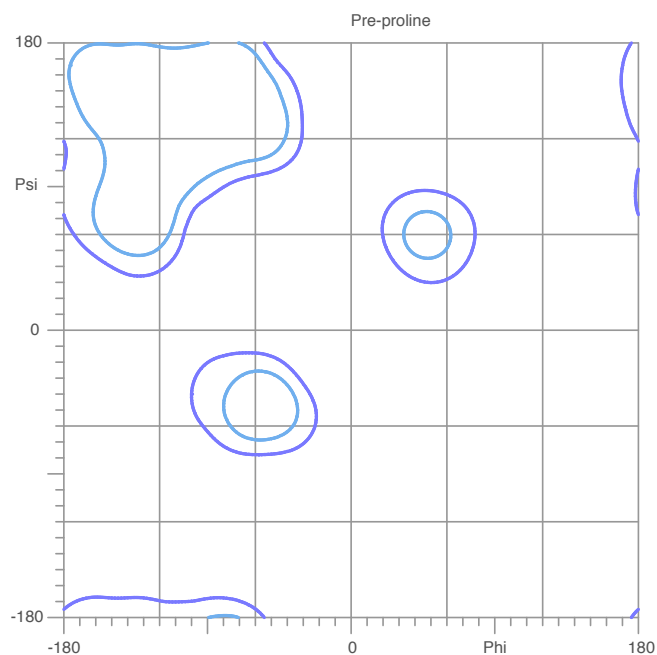
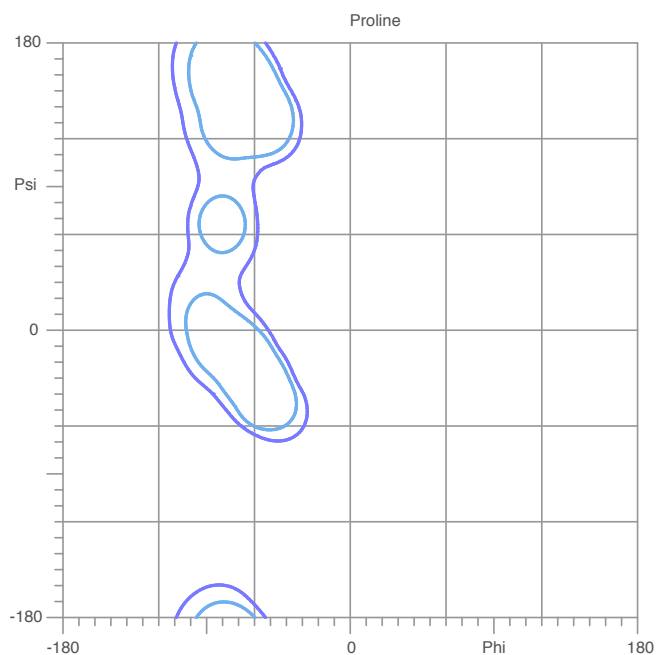
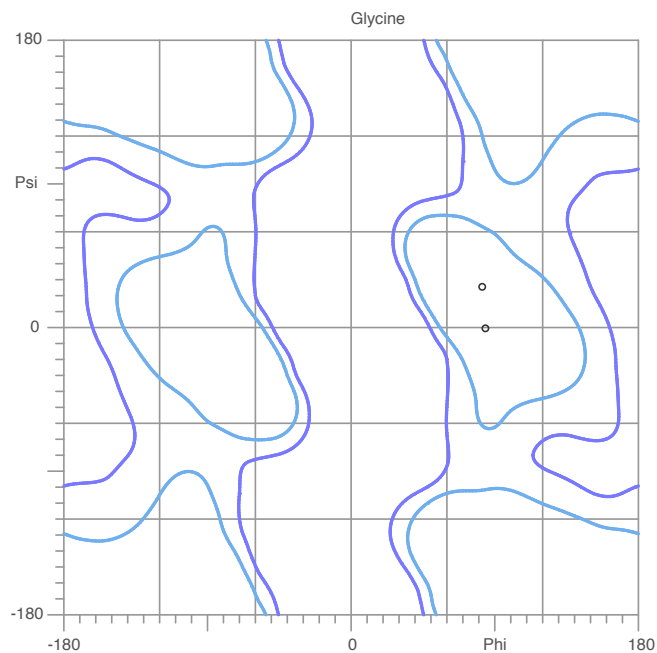
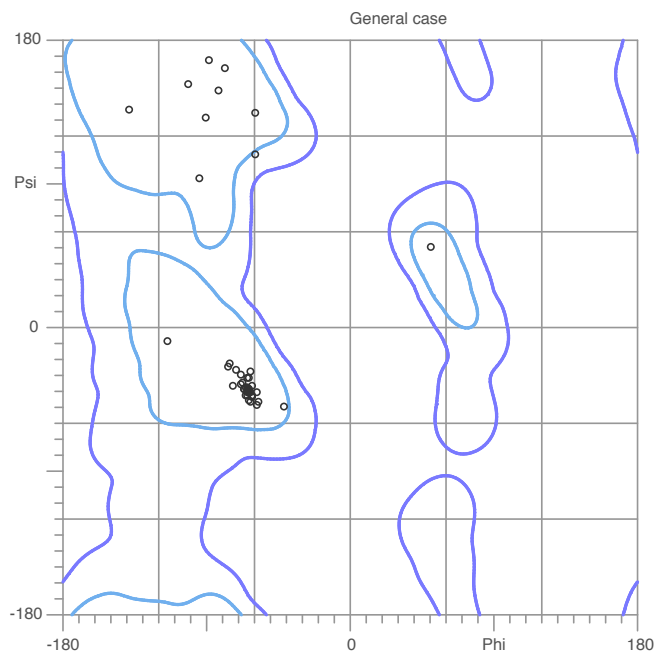
There were no outliers.

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

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MolProbity Ramachandran analysis

SR384_R3_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)