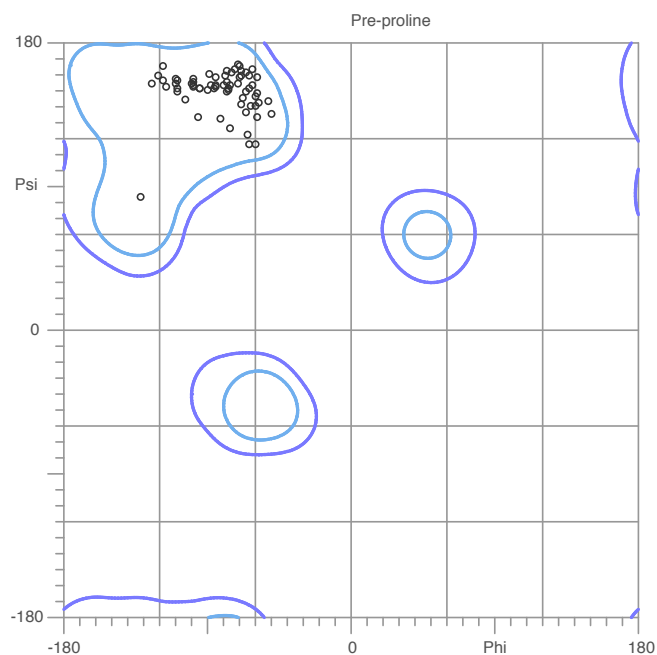
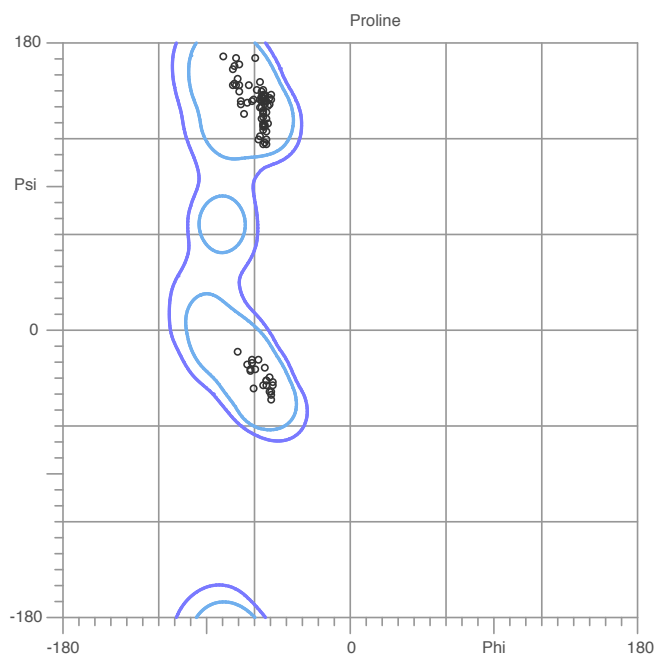
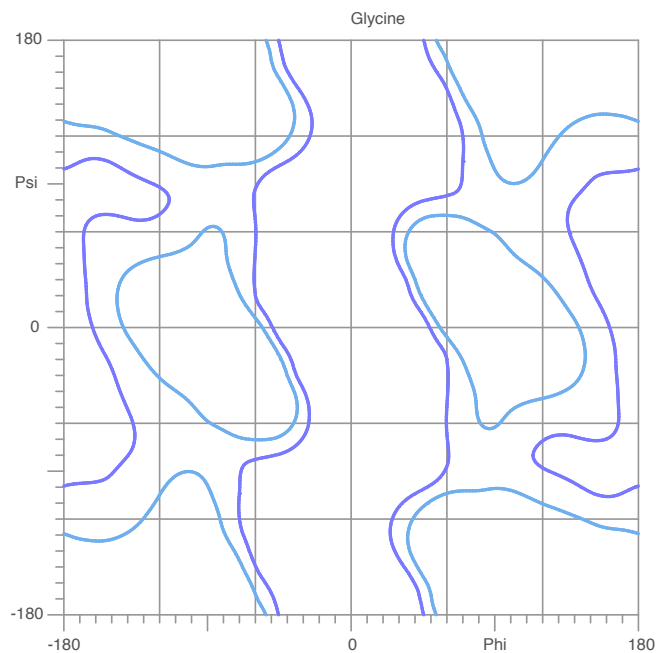
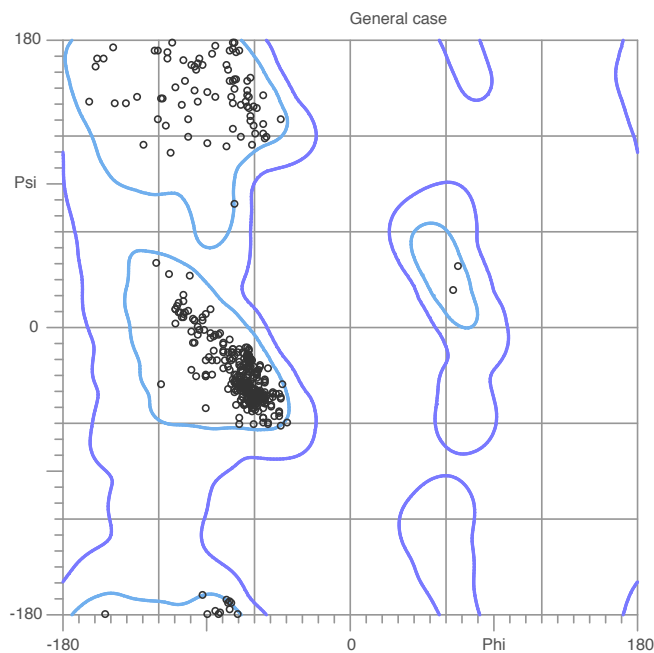


MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, all models



99.5% (569/572) of all residues were in favored (98%) regions.
100.0% (572/572) of all residues were in allowed (>99.8%) regions.

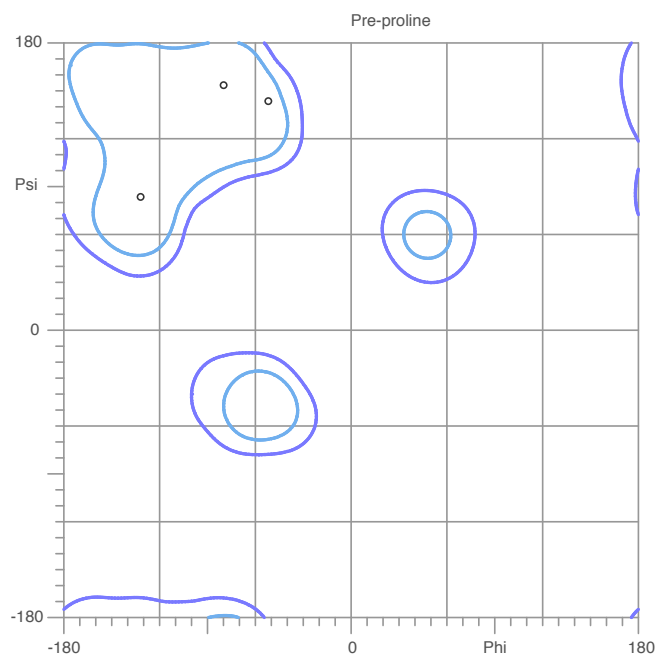
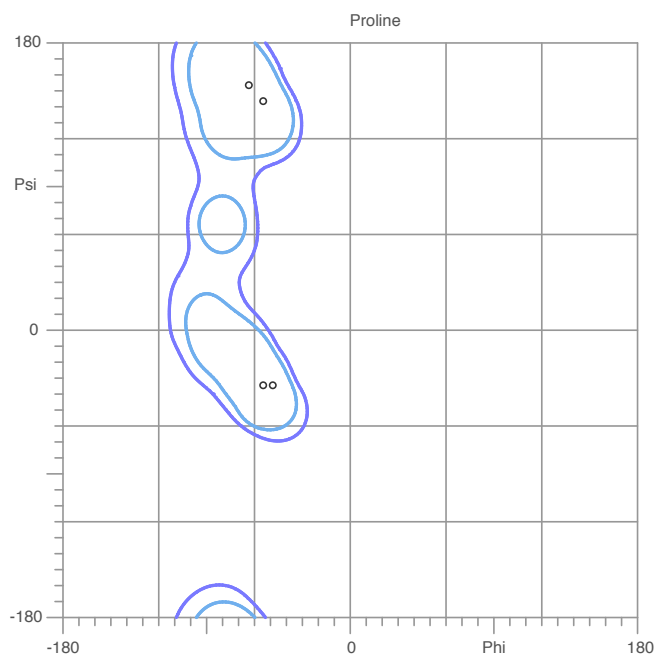
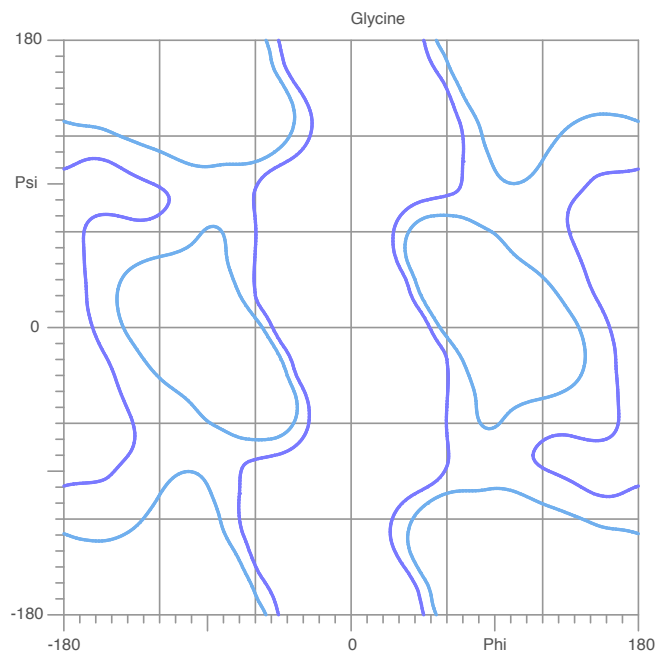
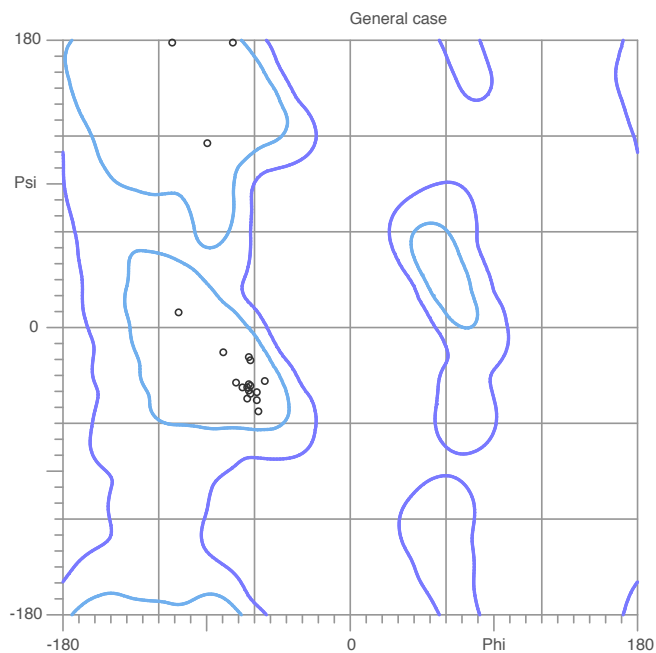
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 1



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

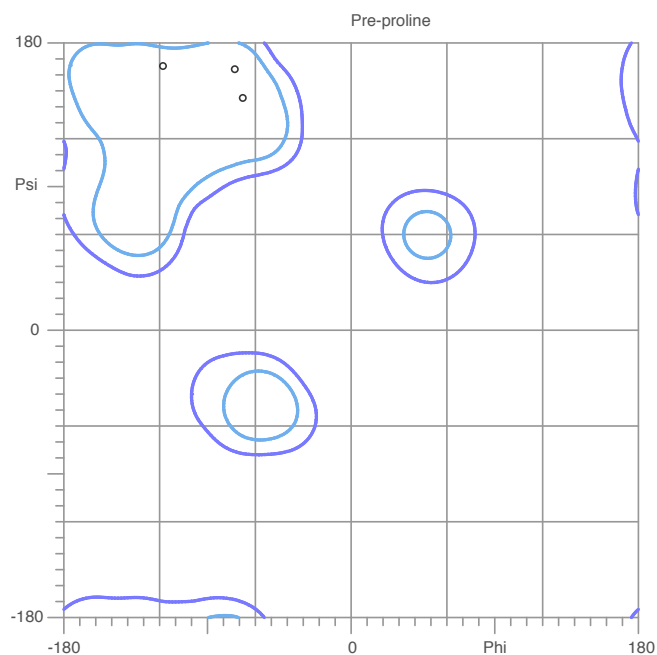
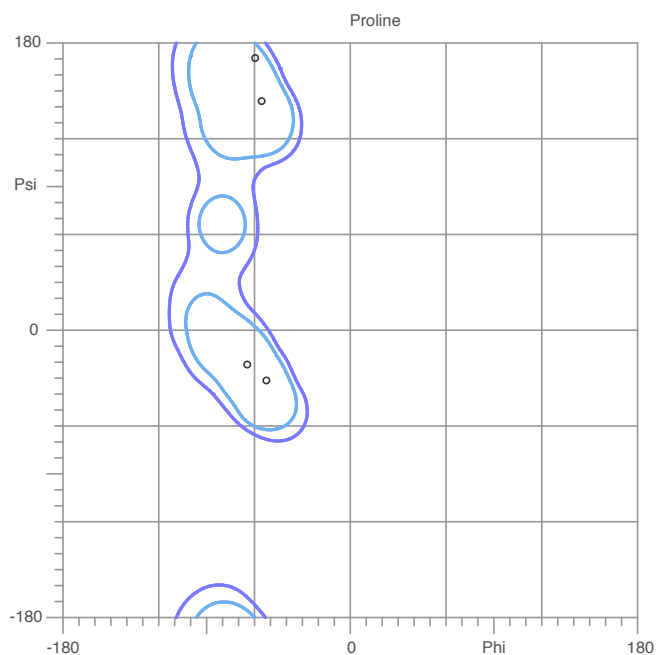
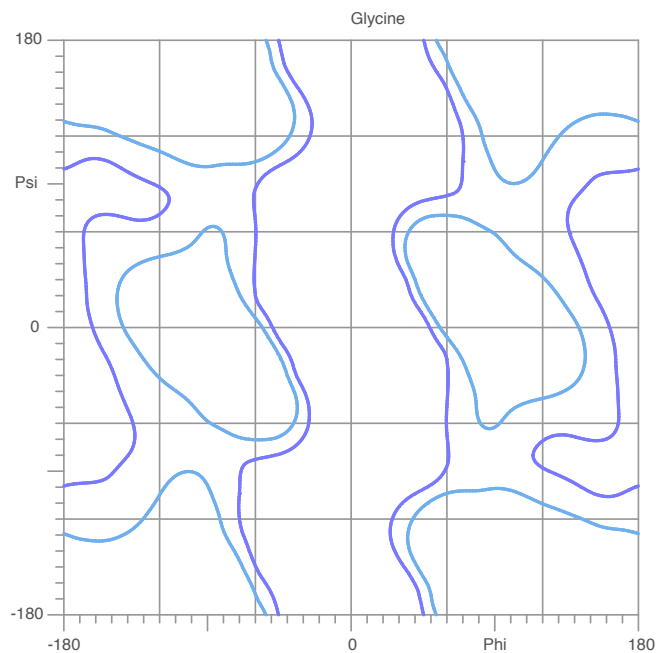
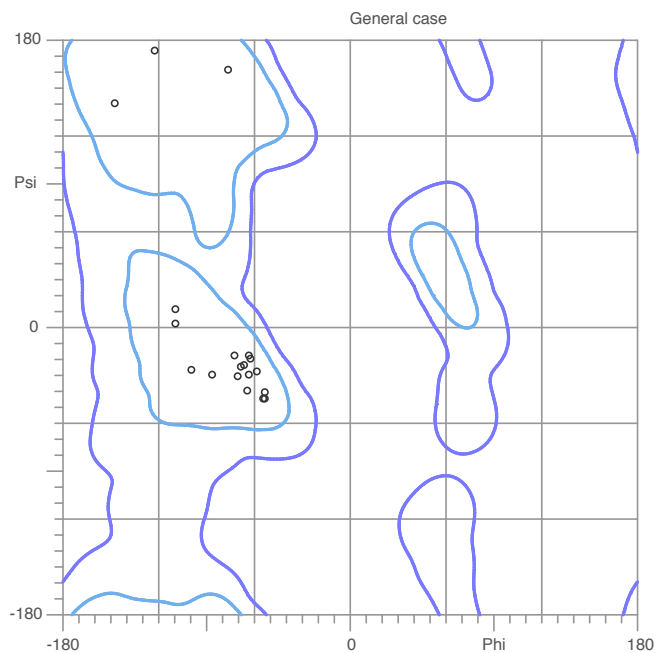
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 2



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

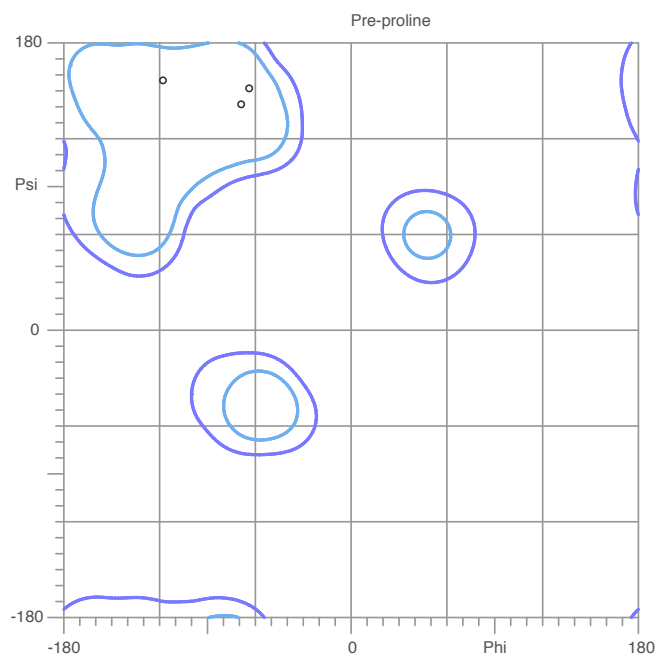
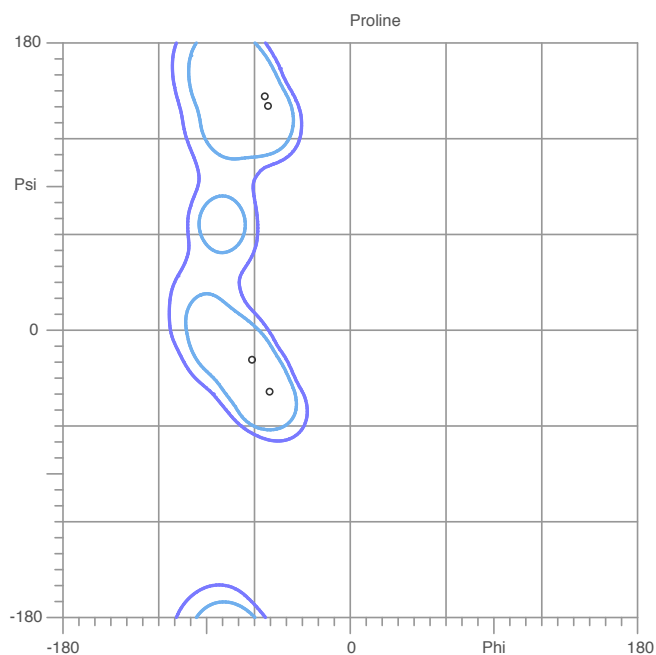
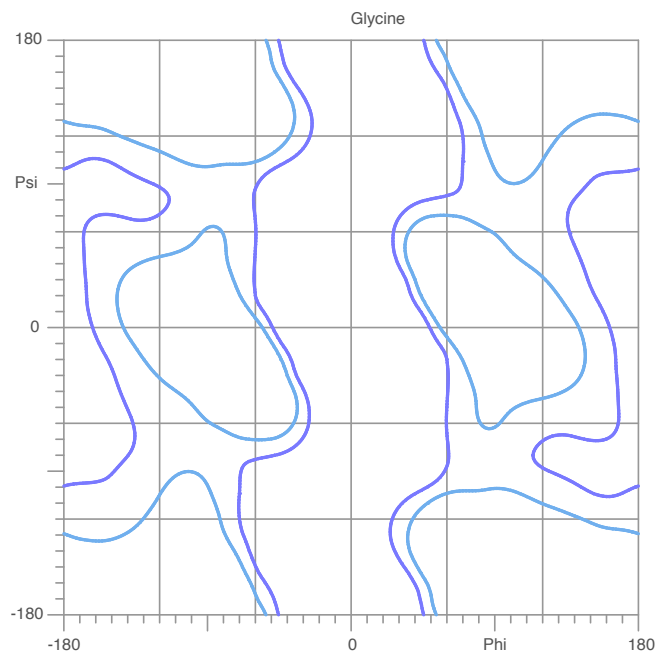
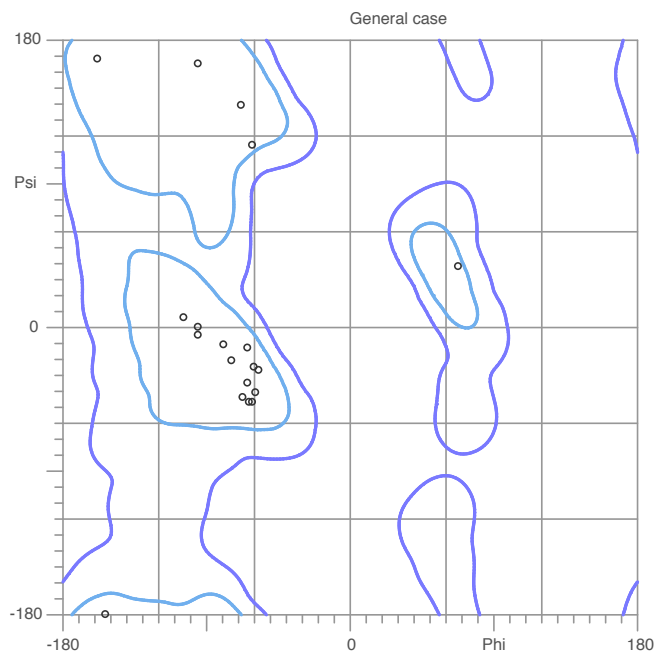
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 3



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

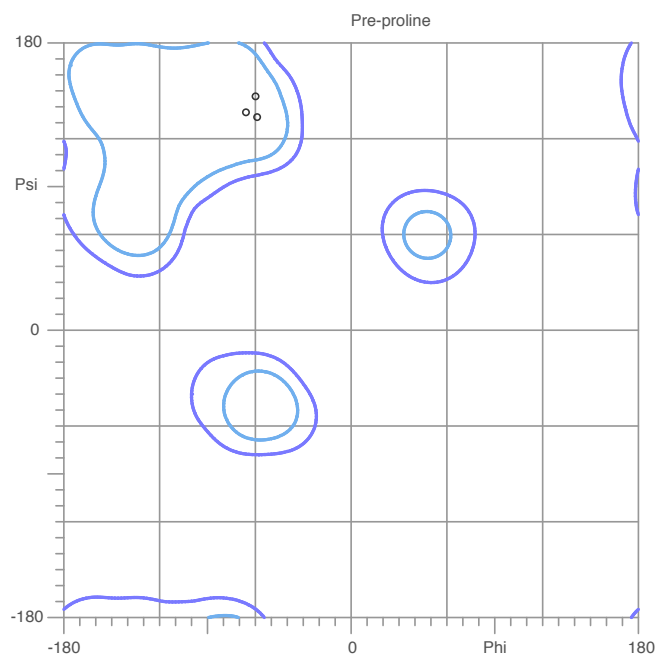
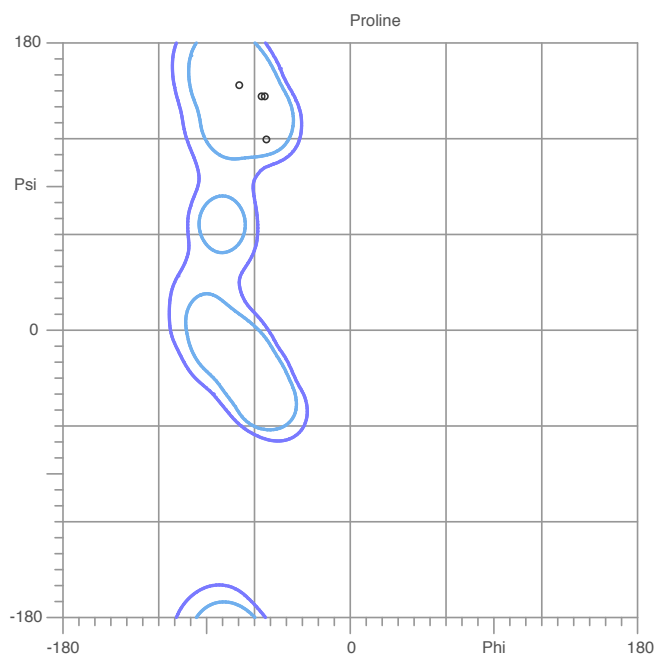
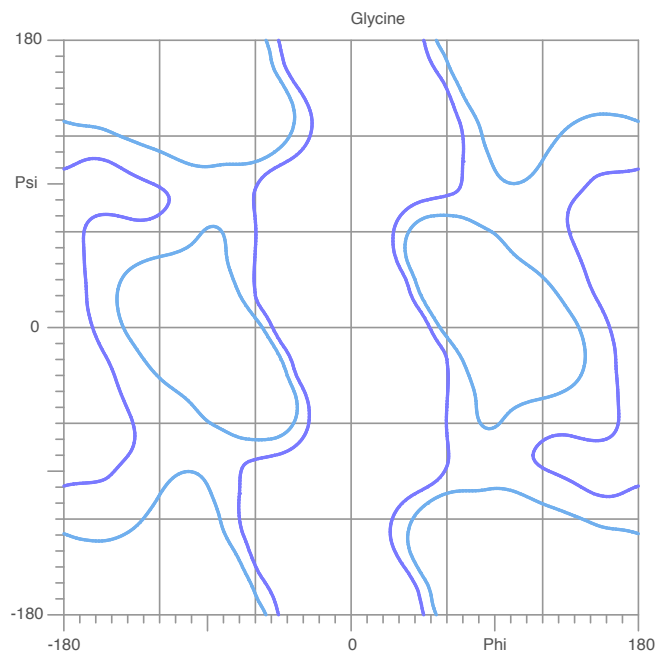
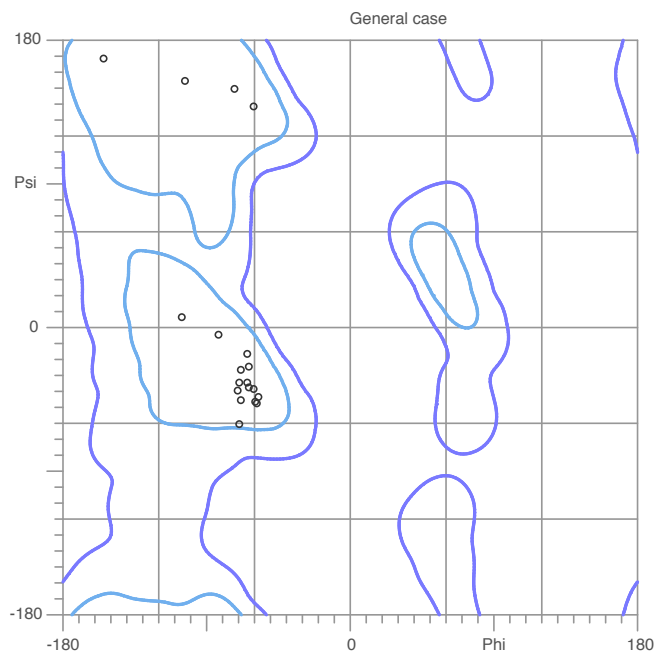
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 4



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

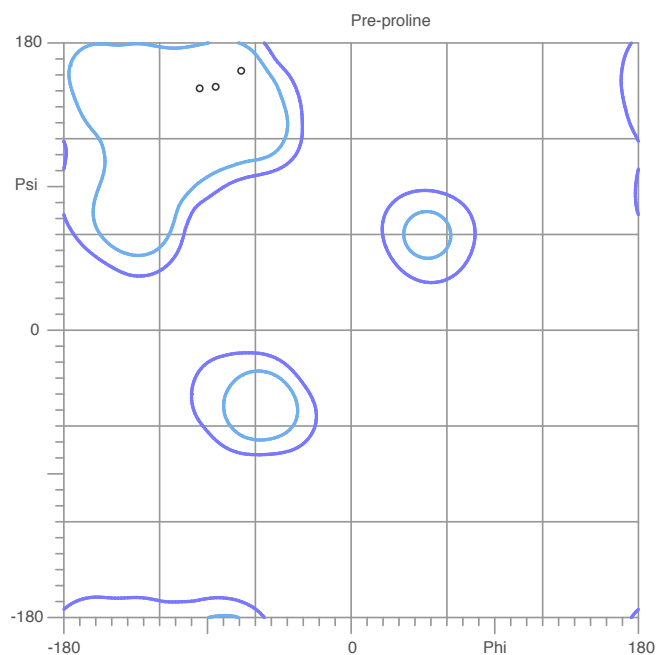
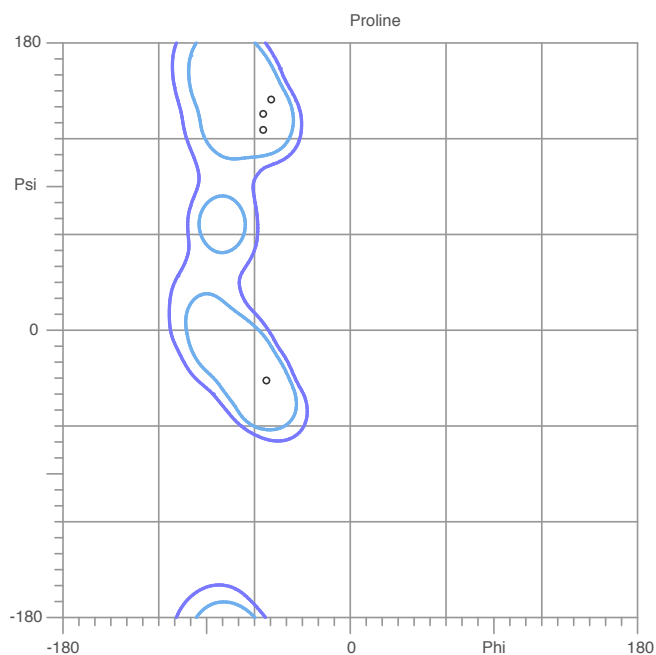
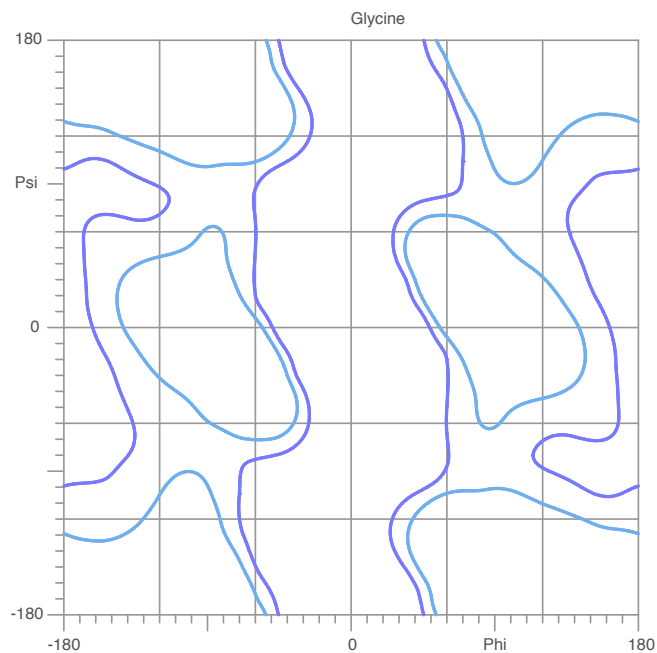
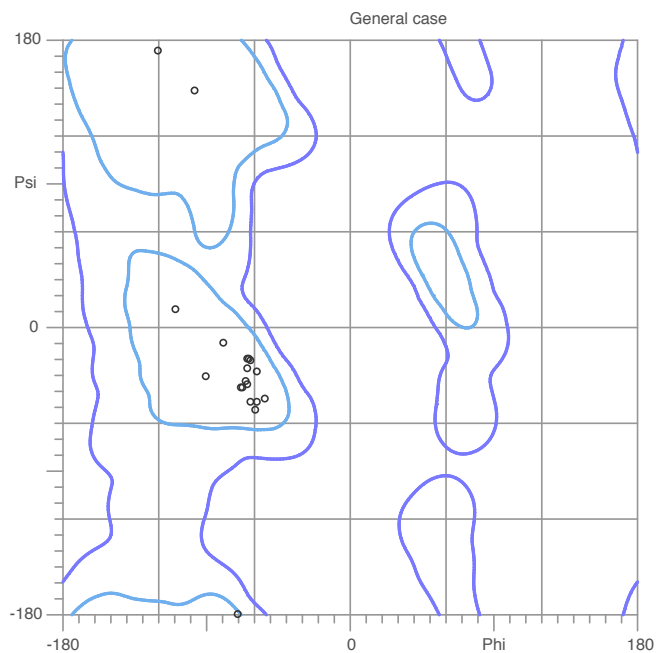
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 5



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

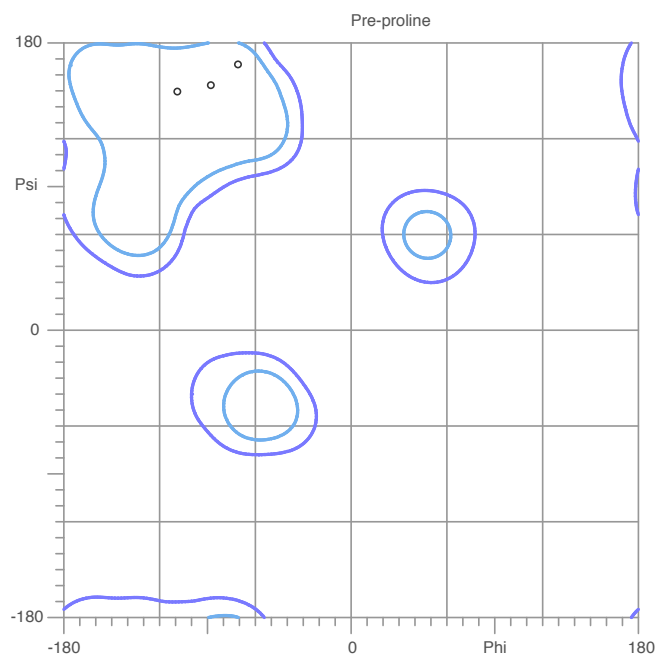
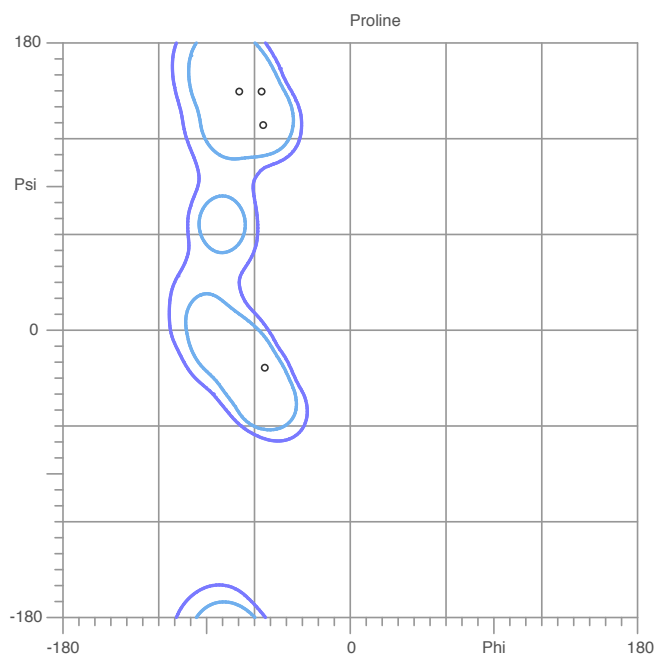
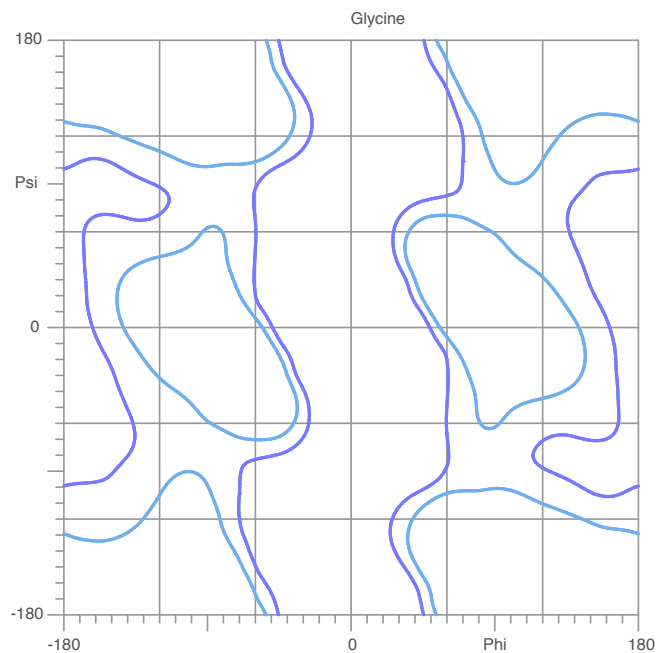
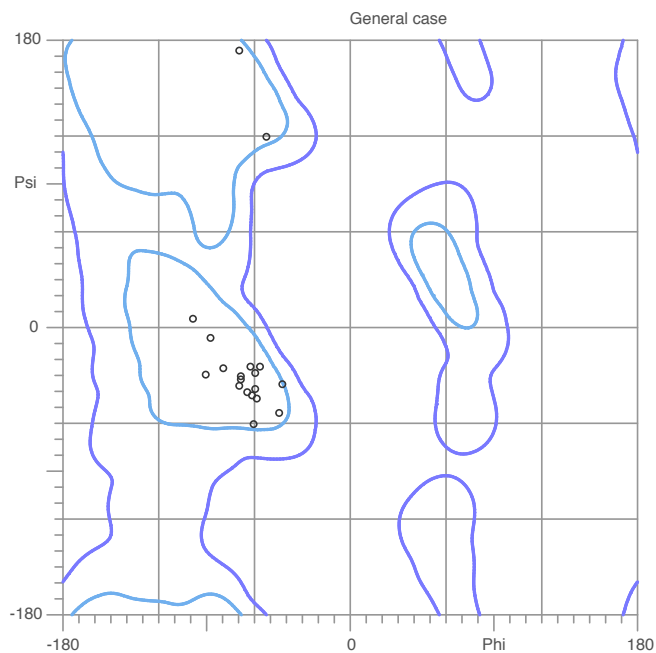
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 6



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

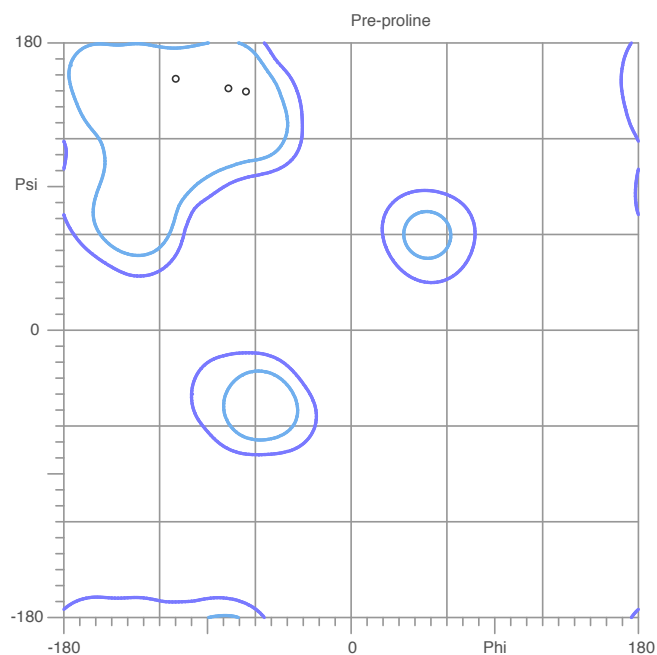
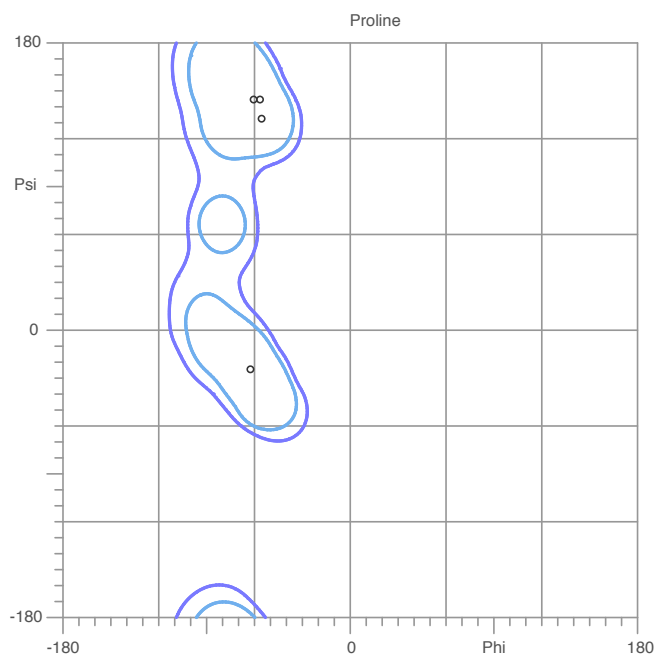
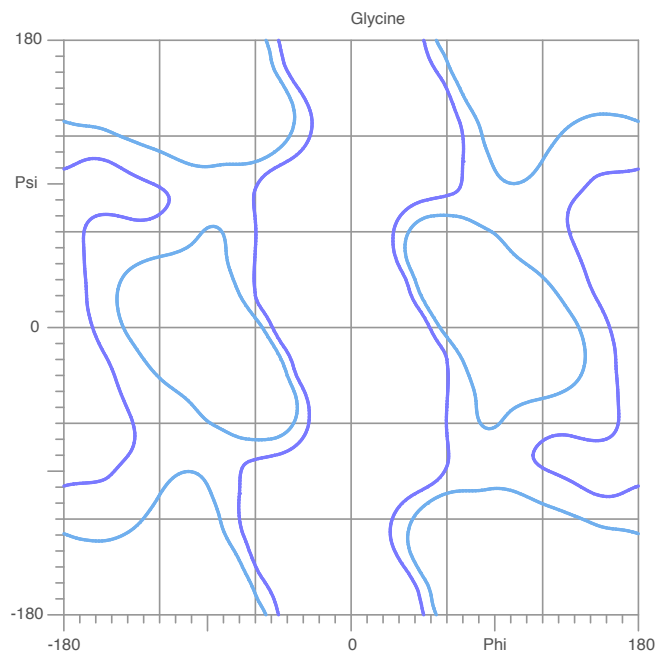
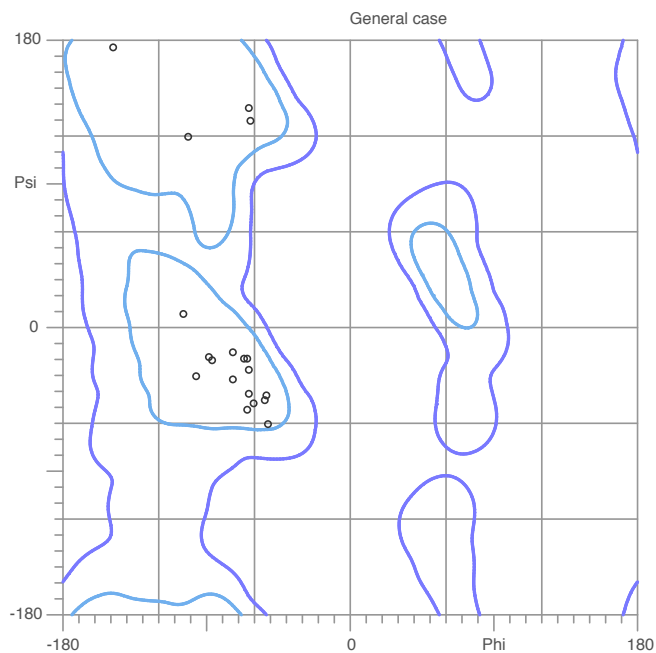
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 7



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

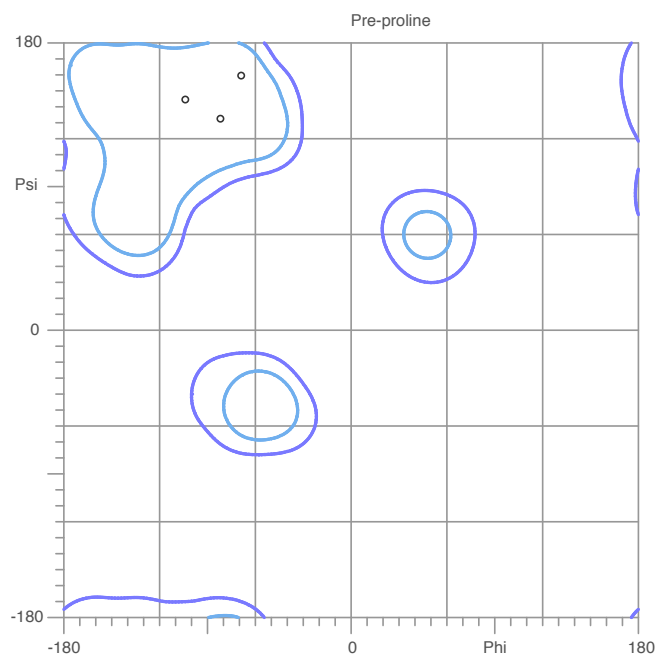
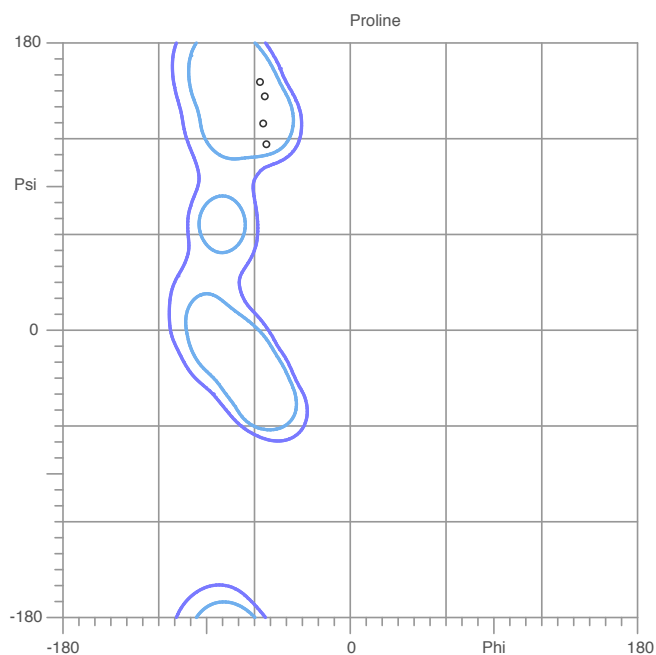
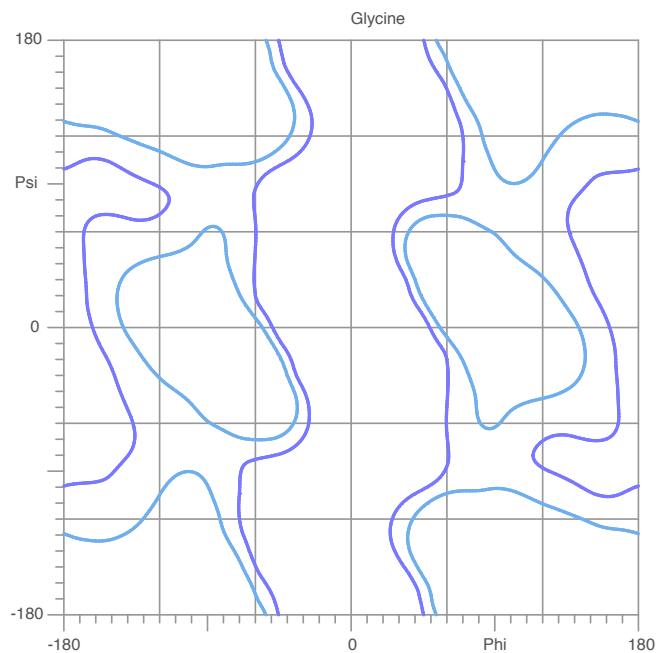
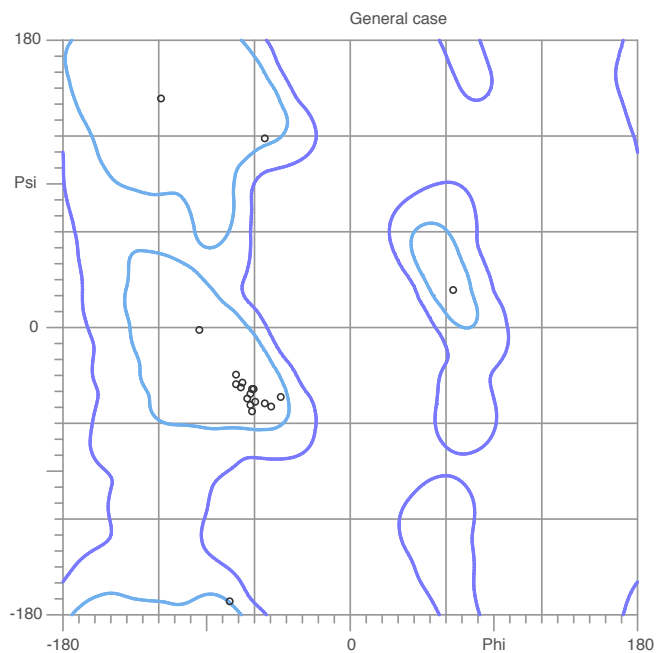
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 8



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

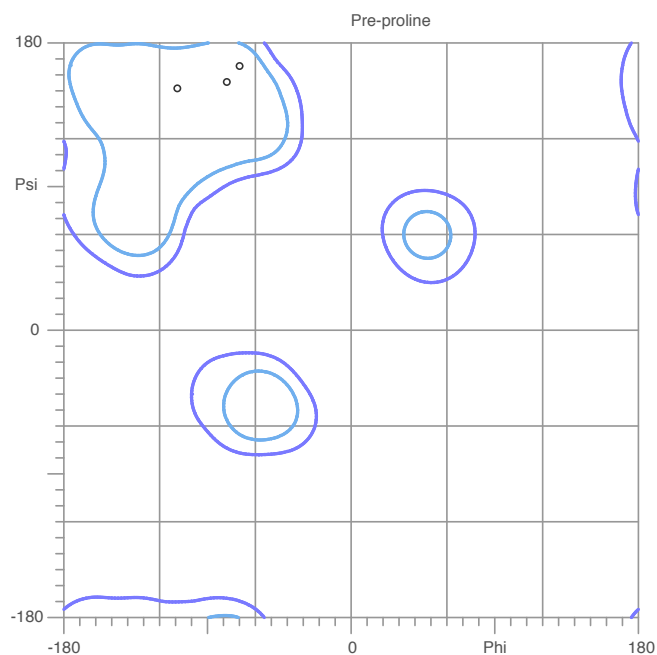
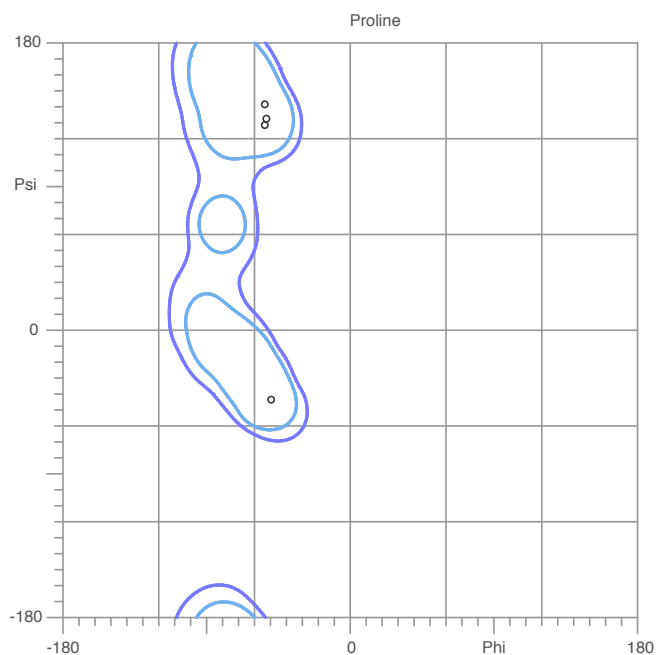
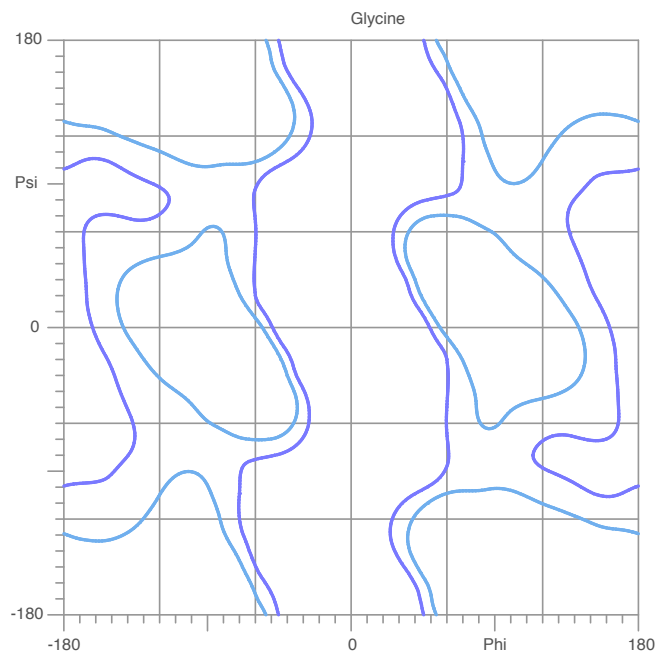
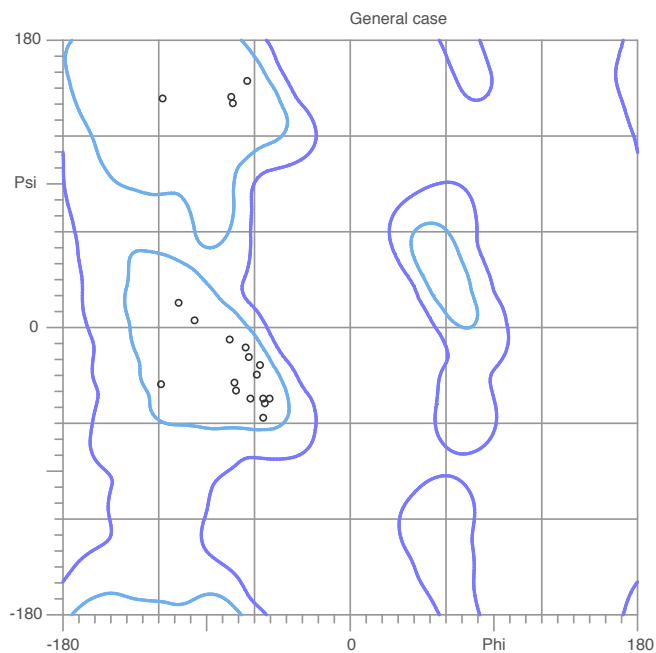
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 9



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

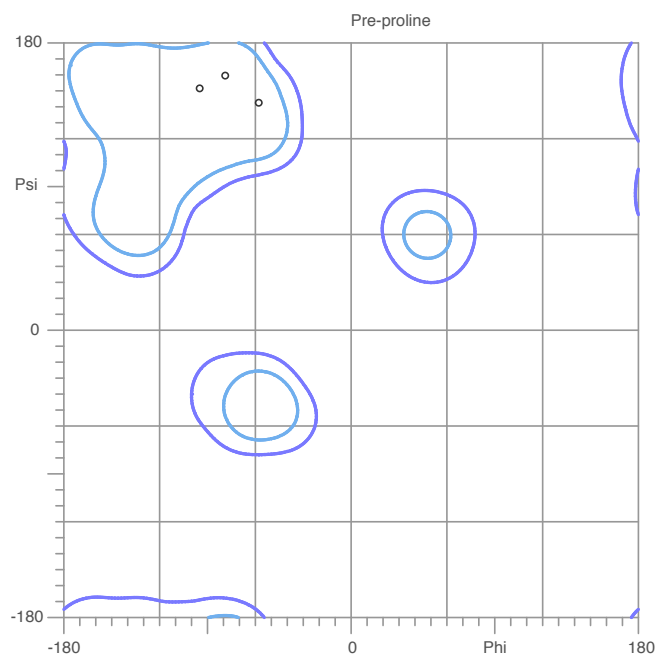
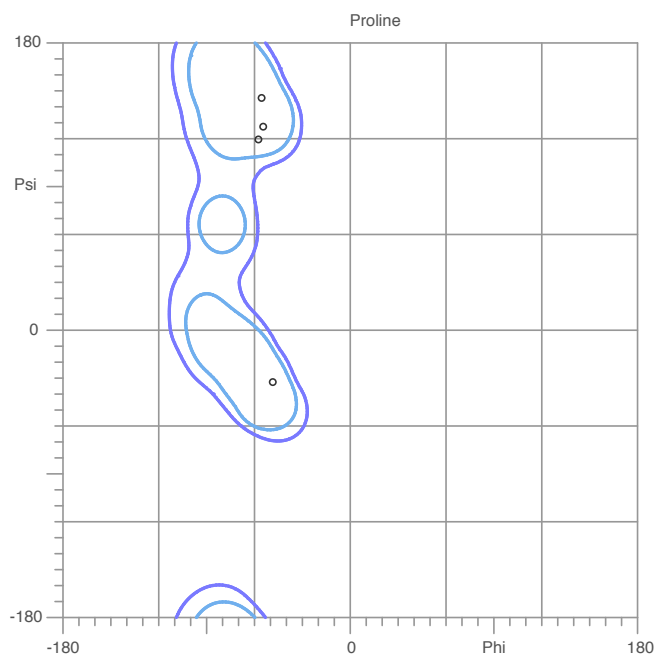
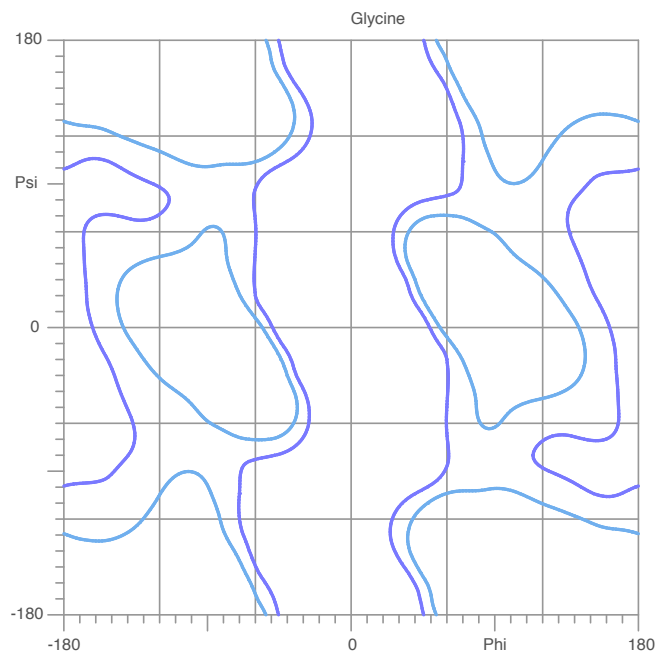
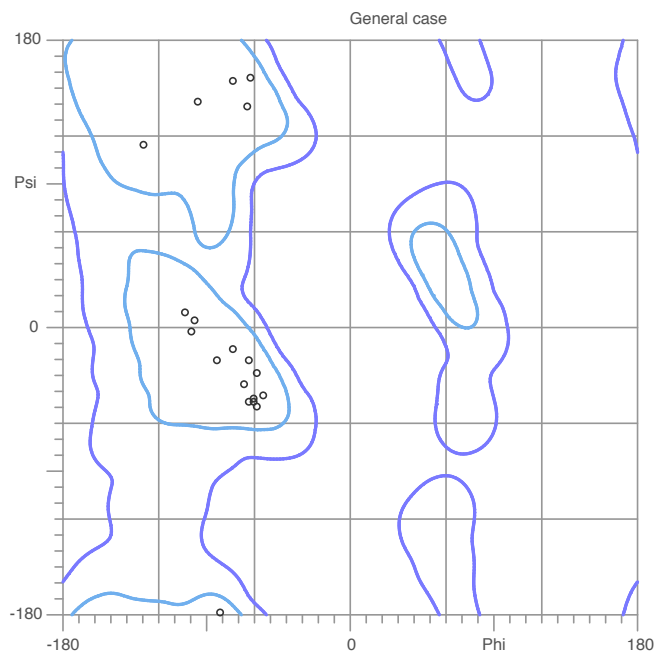
There were no outliers.

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 10



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

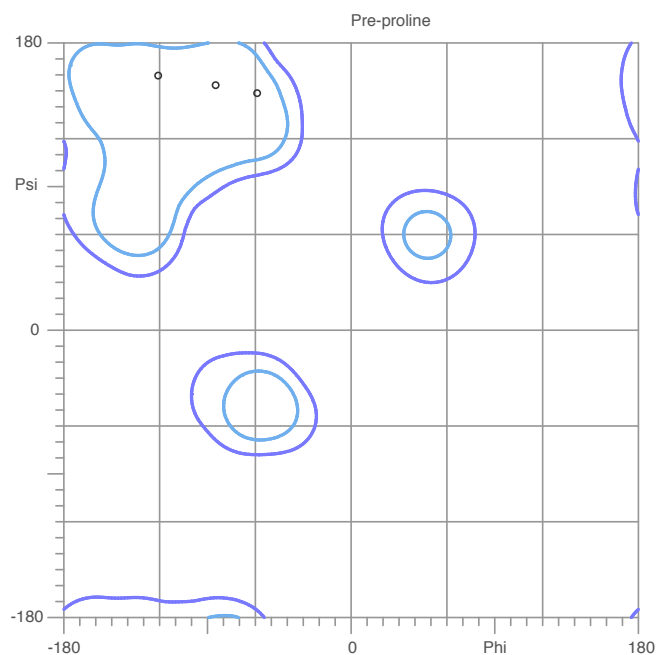
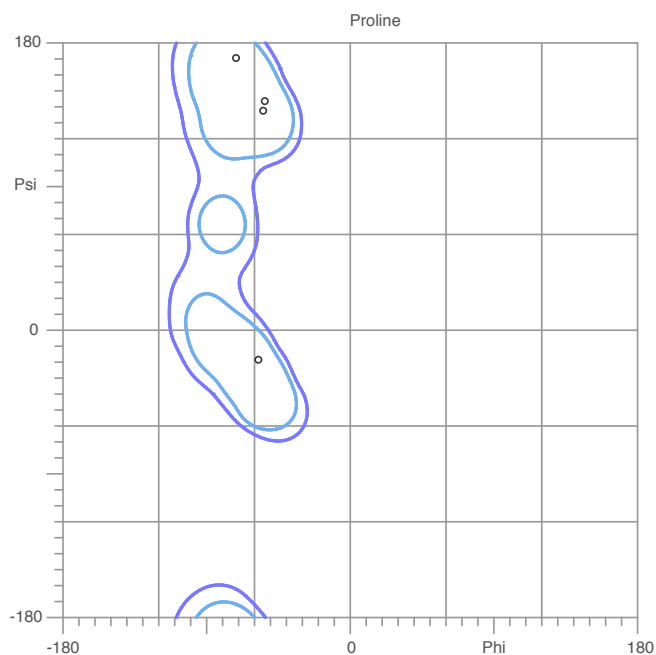
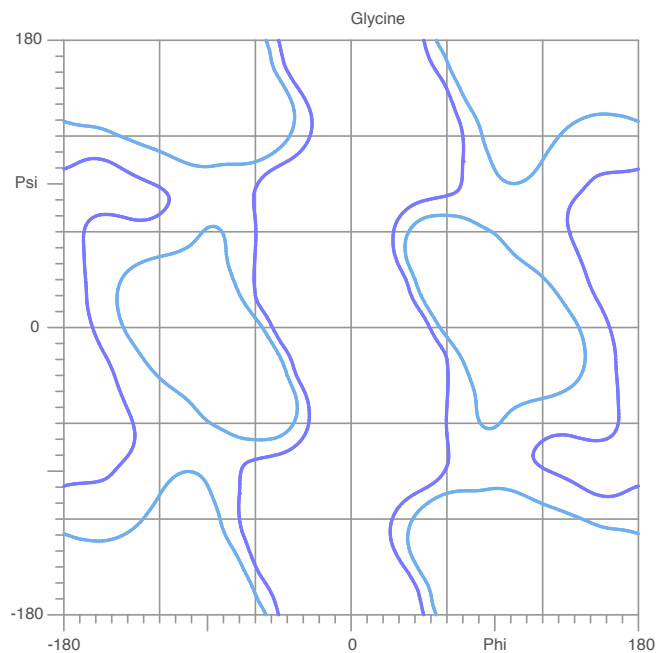
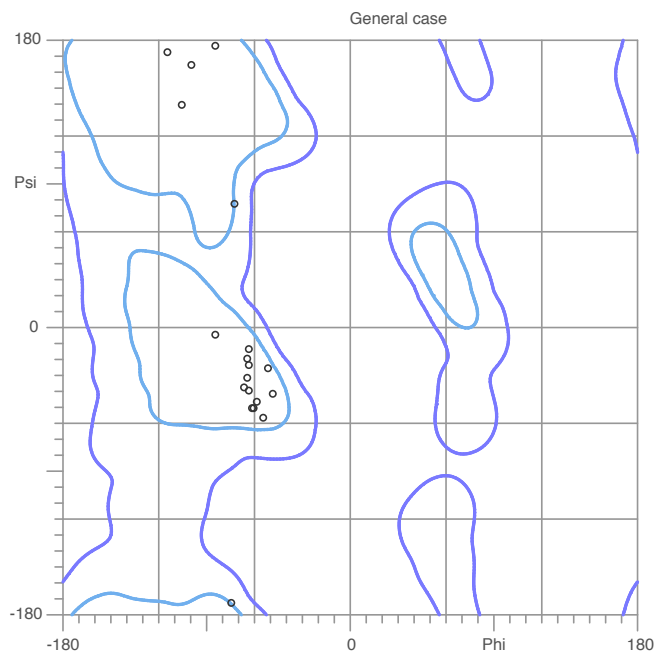
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 11



96.2% (25/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

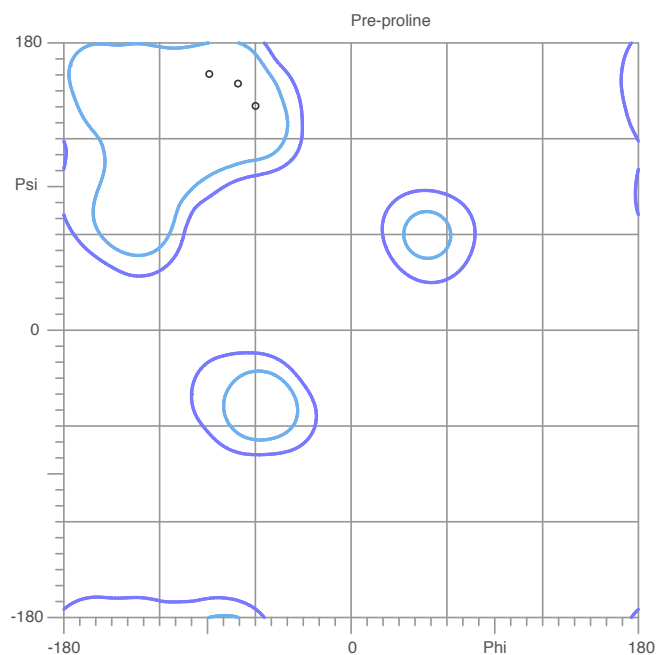
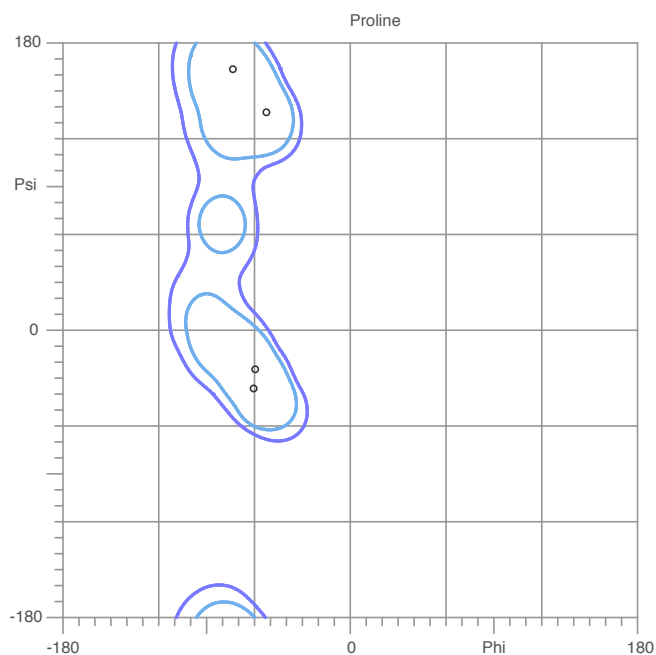
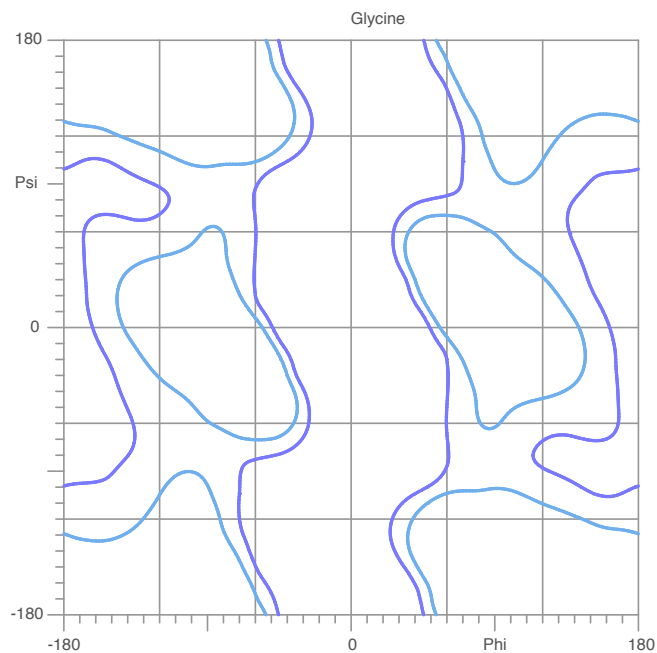
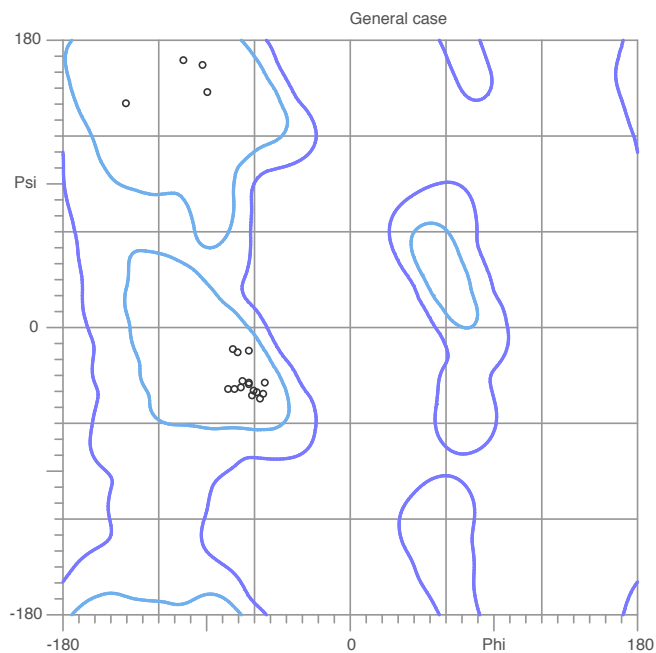
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 12



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

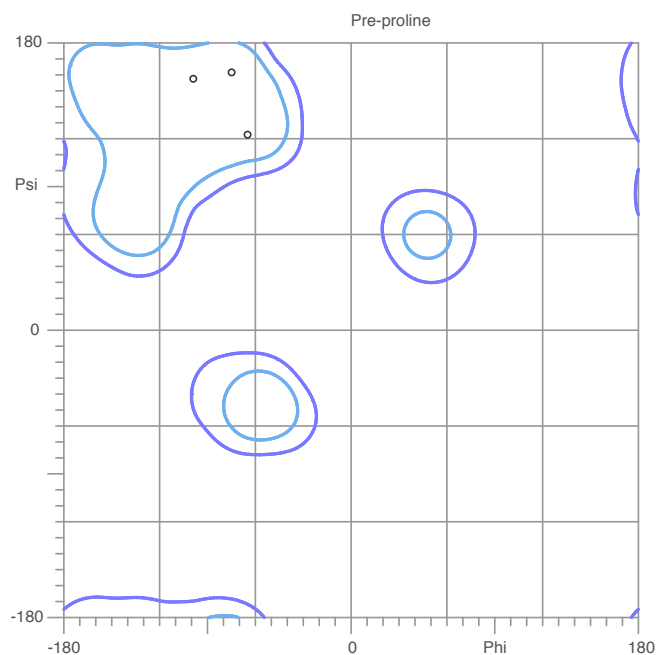
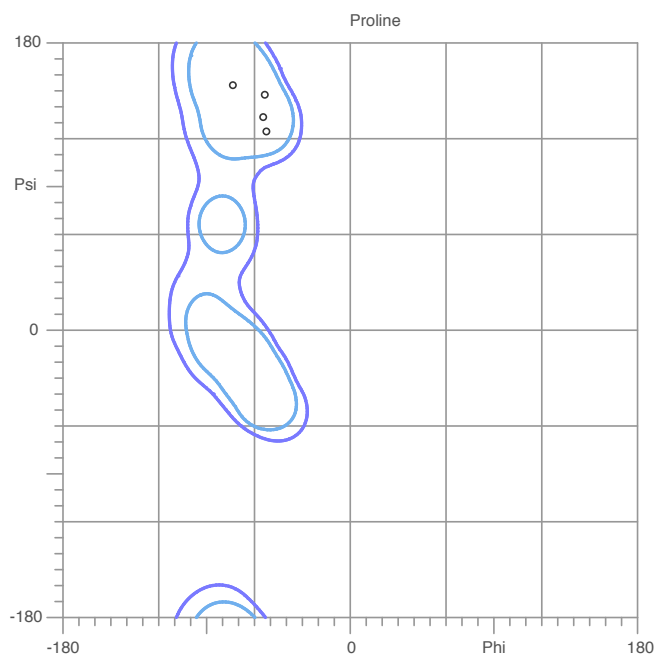
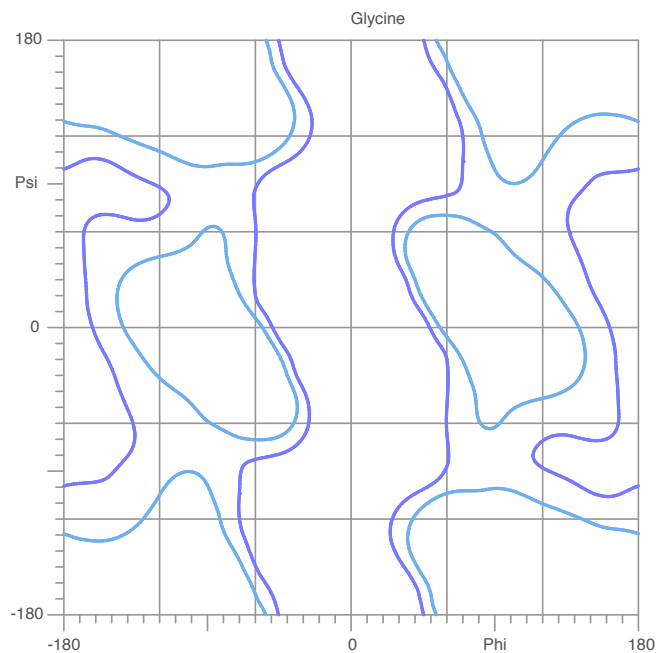
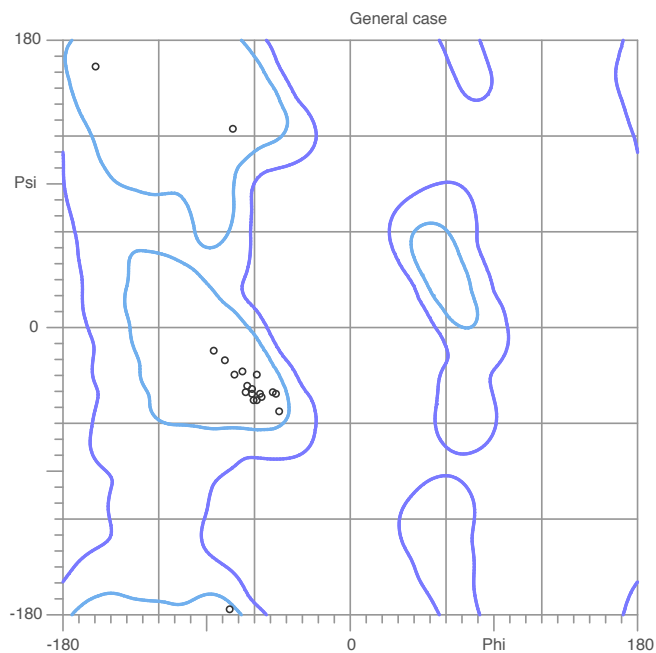
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 13



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

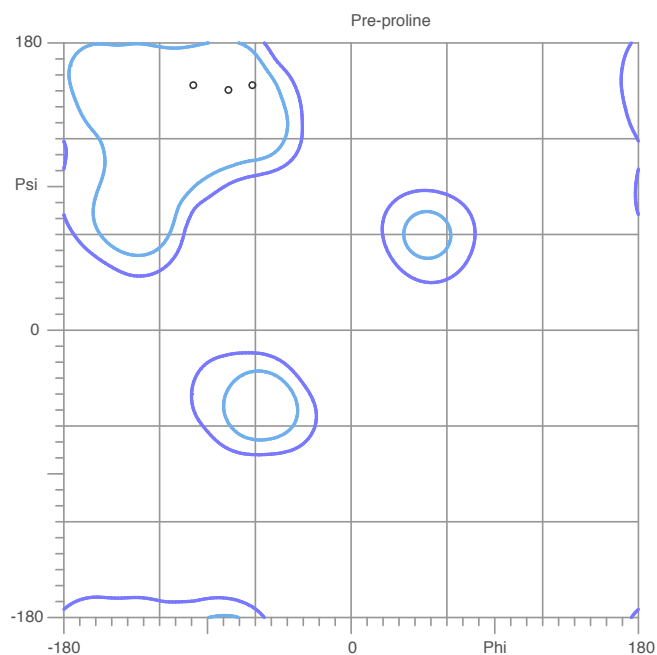
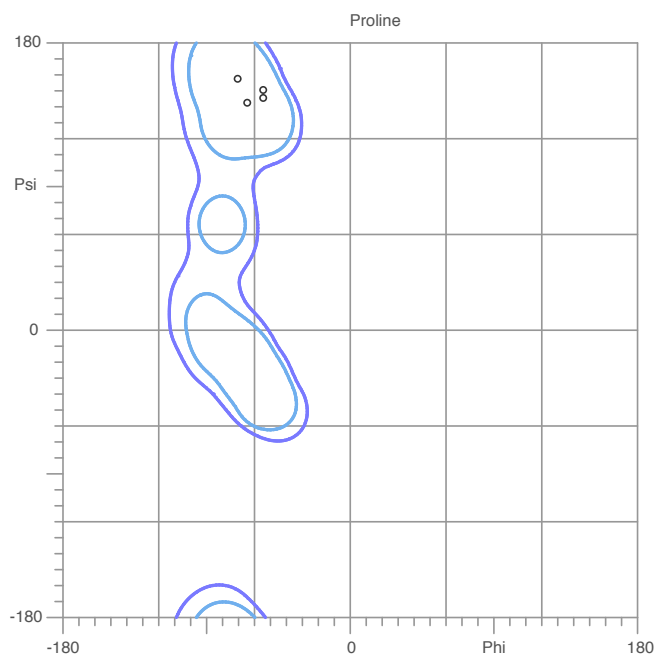
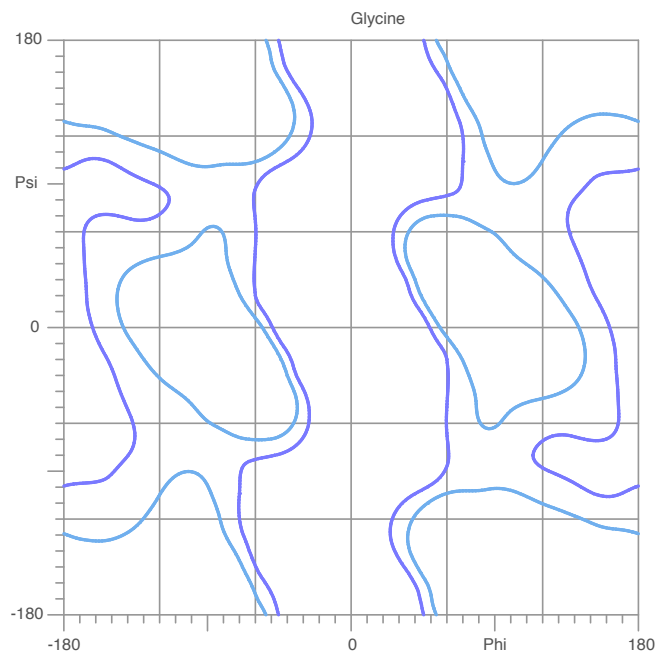
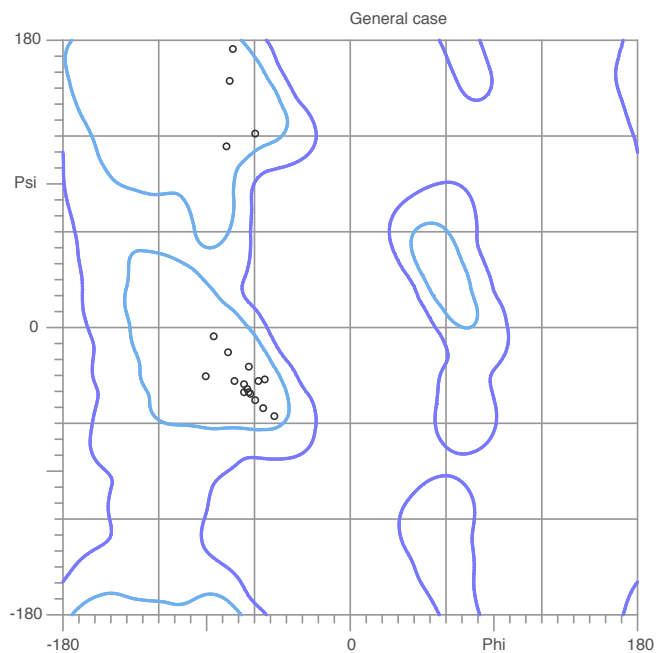
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 14



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

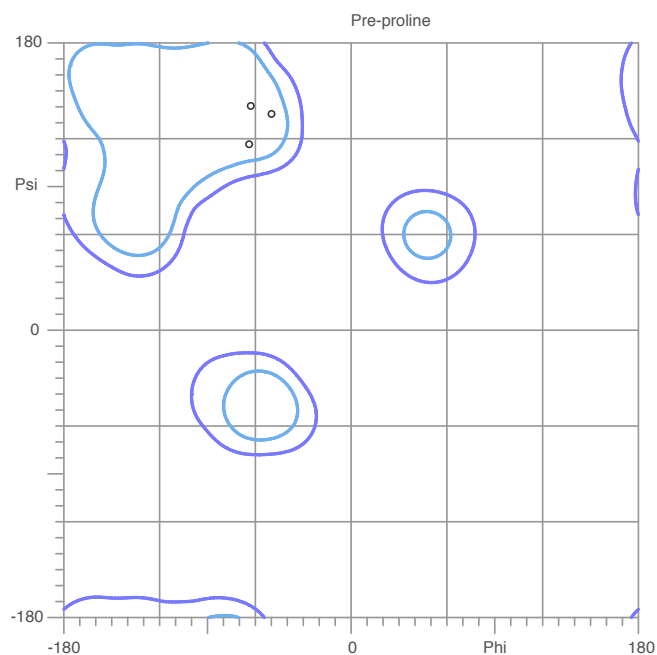
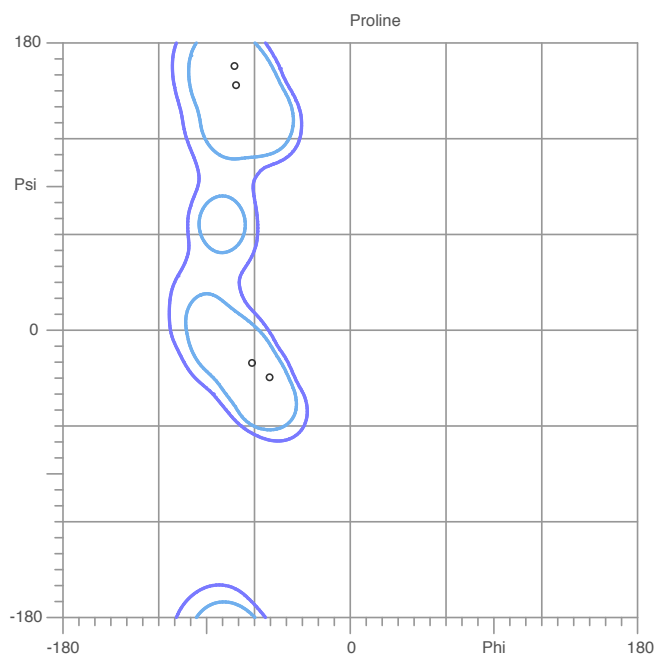
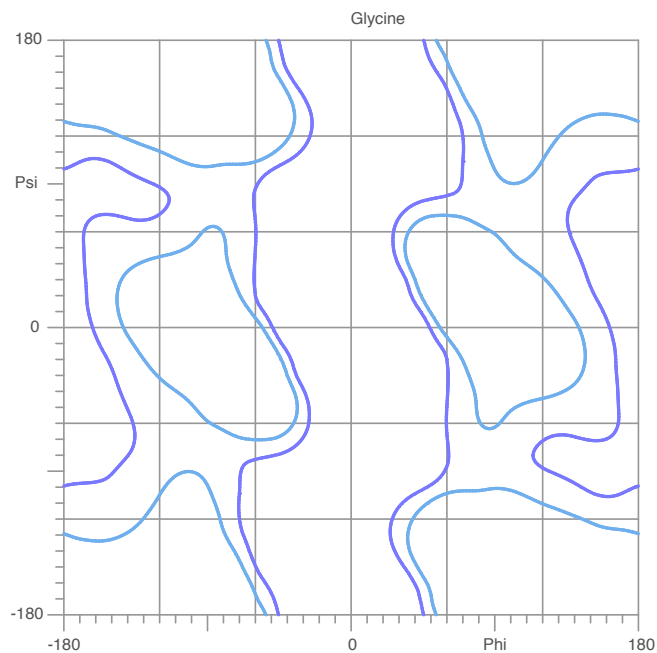
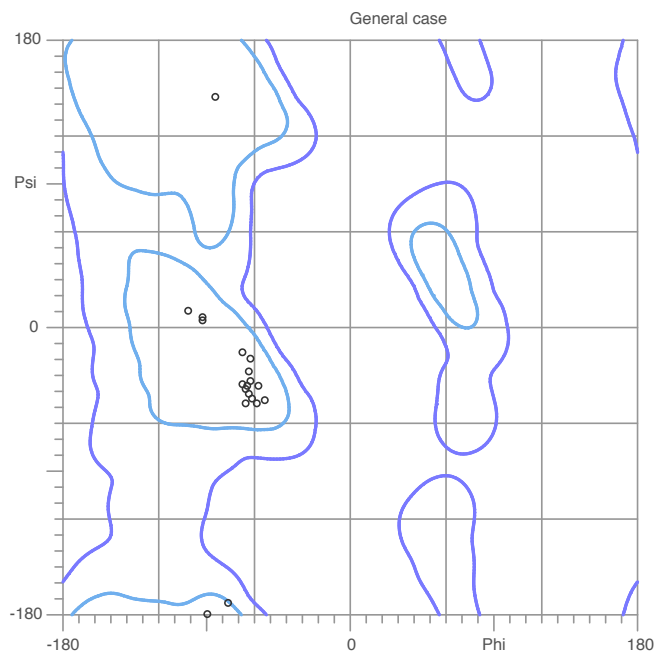
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 15



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

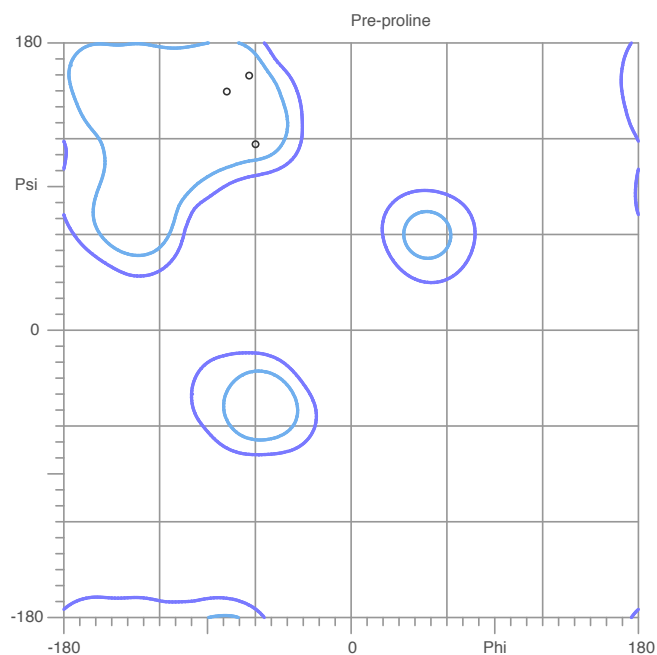
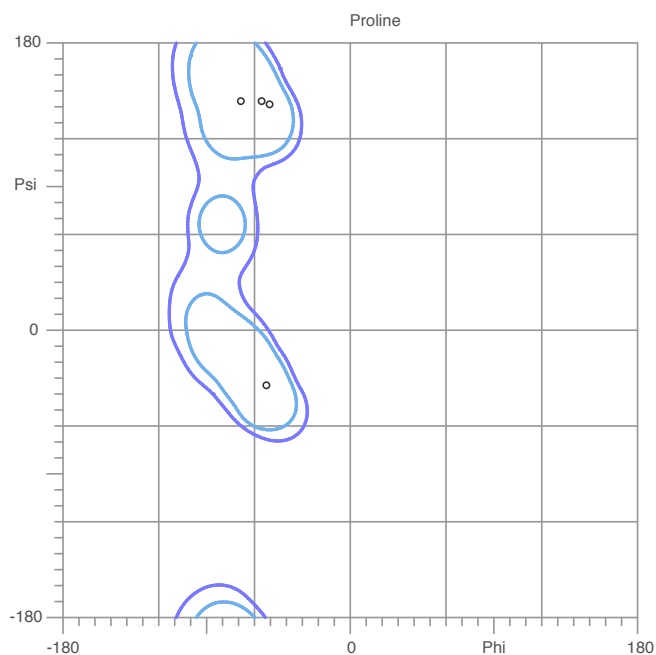
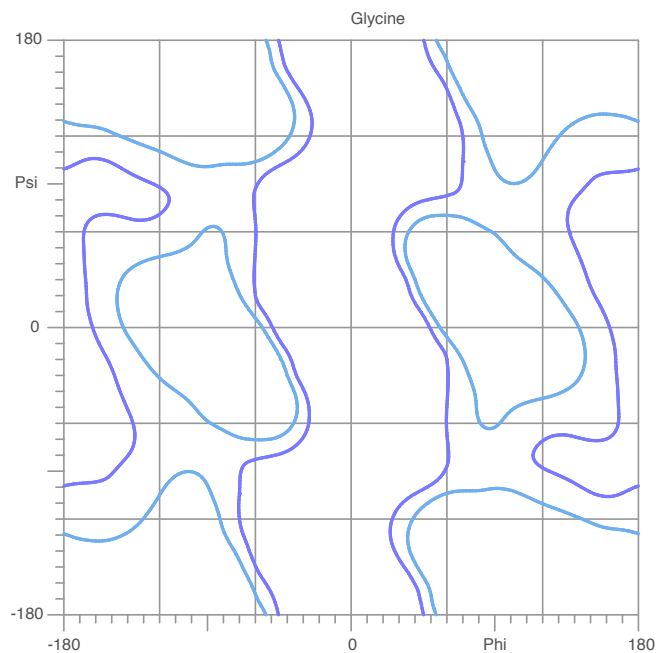
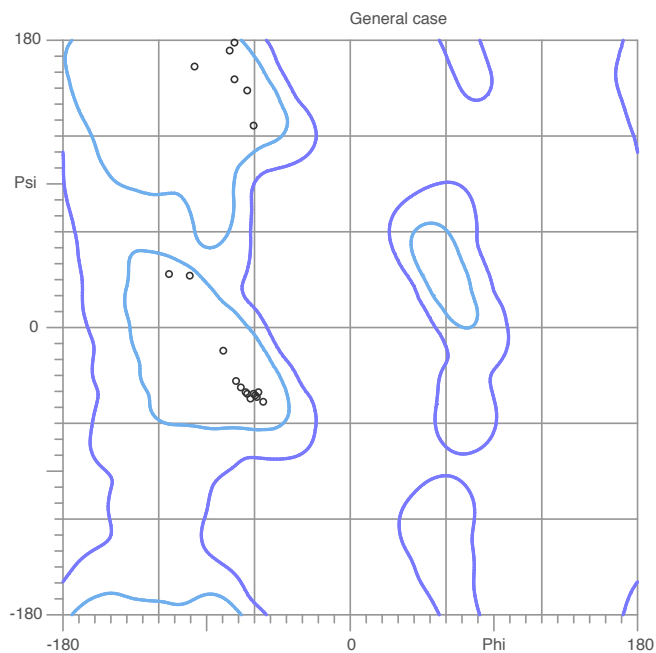
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 16



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

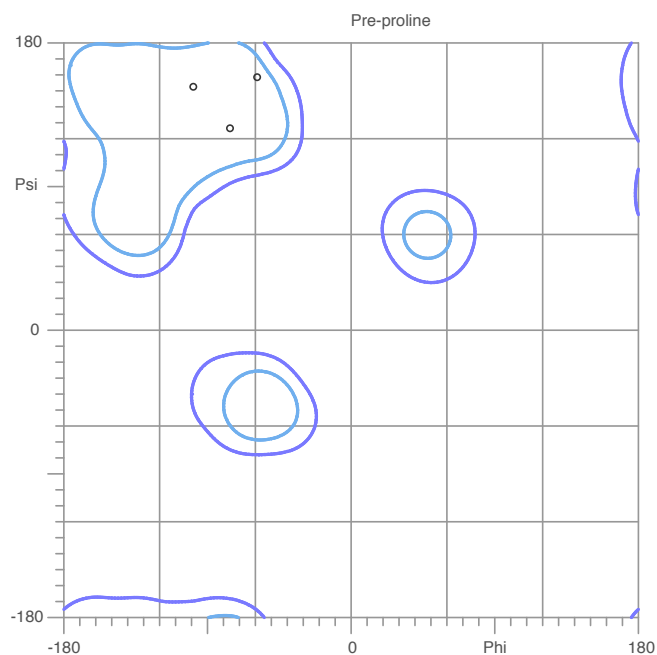
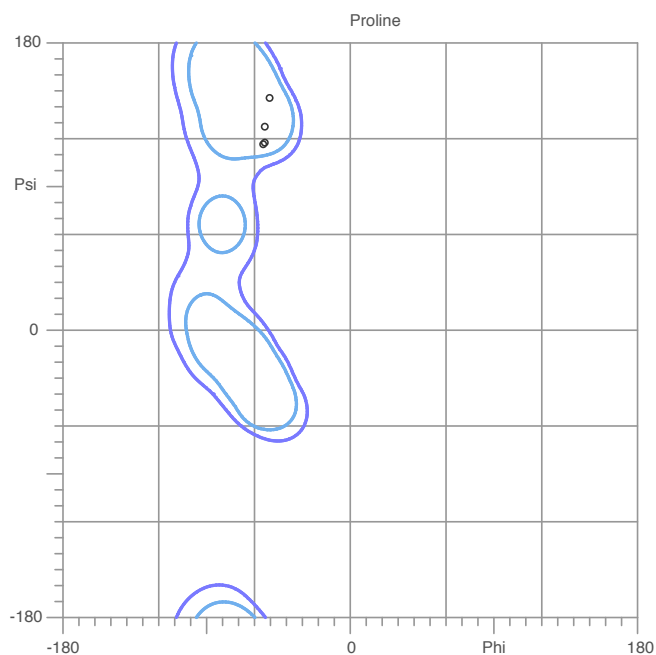
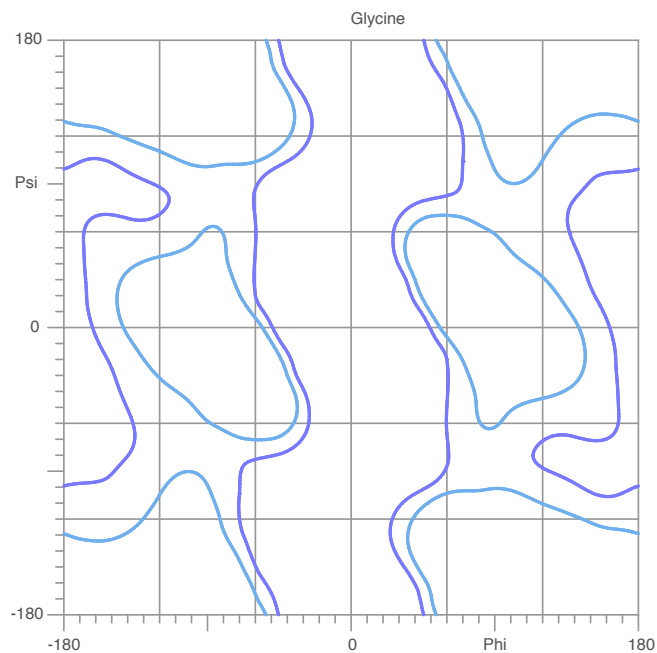
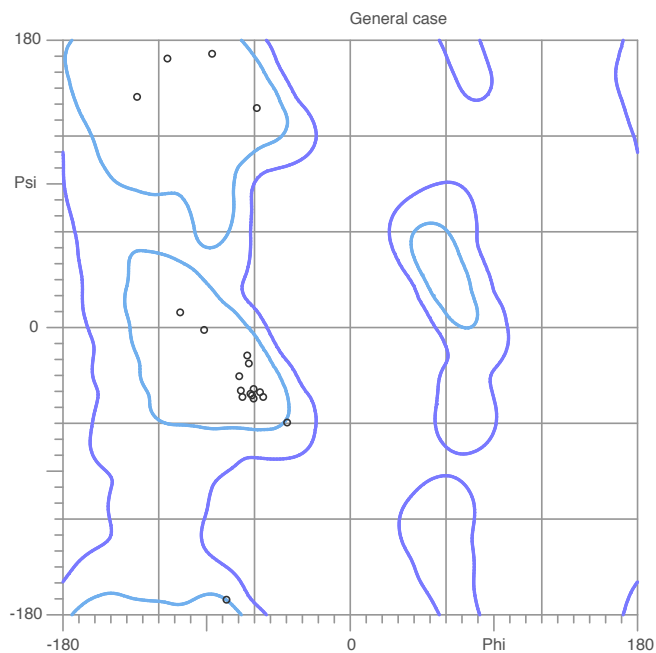
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 17



96.2% (25/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

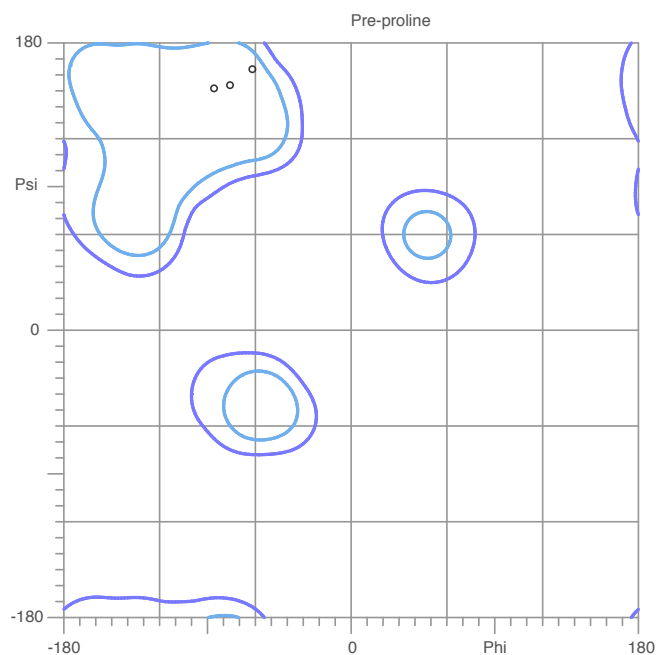
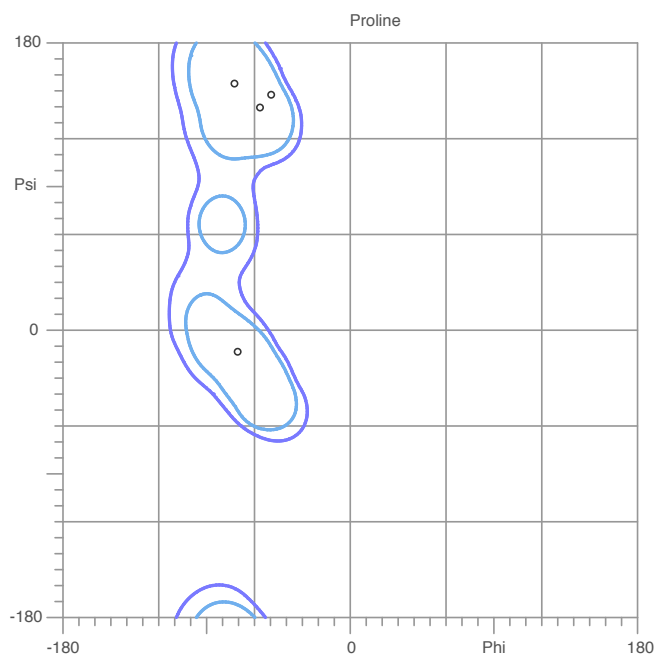
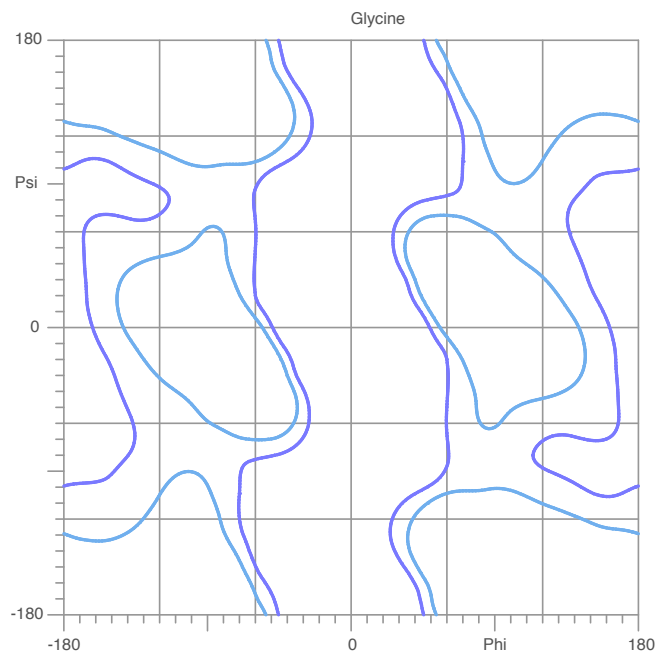
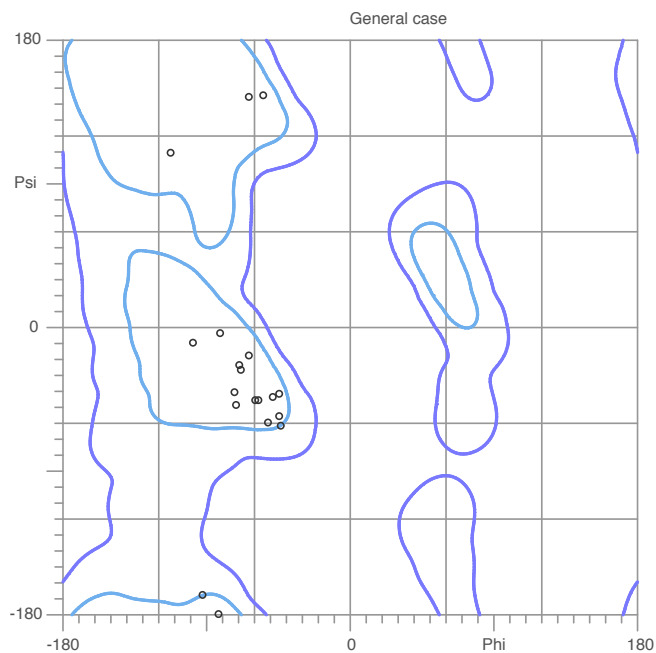
There were no outliers.

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 18



96.2% (25/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

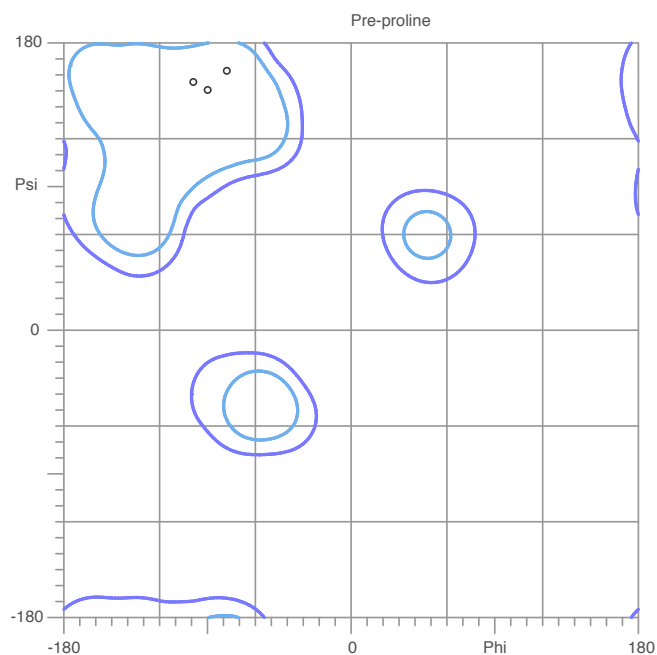
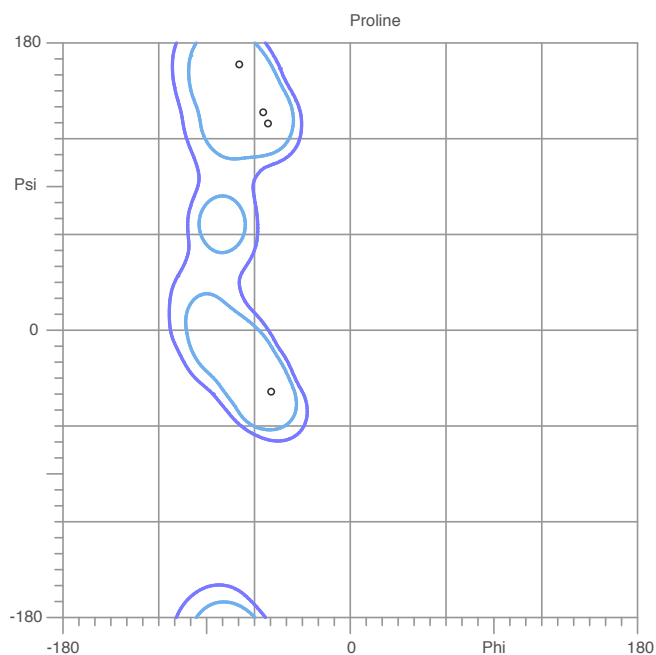
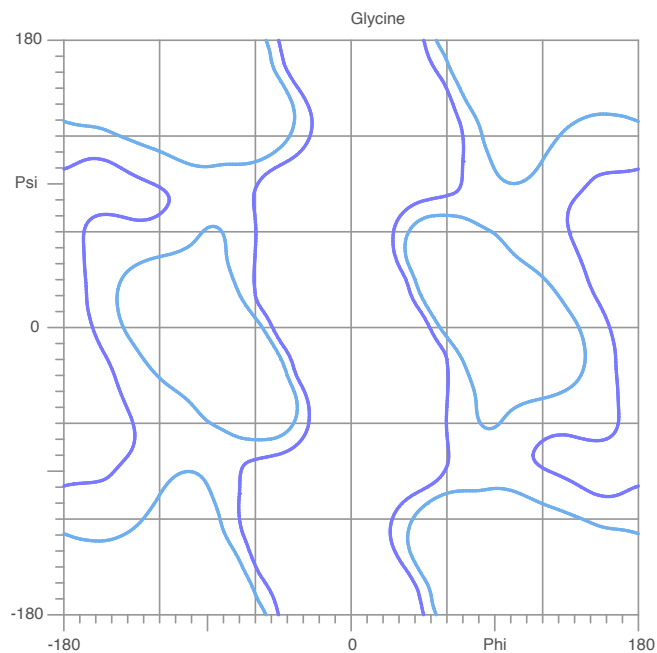
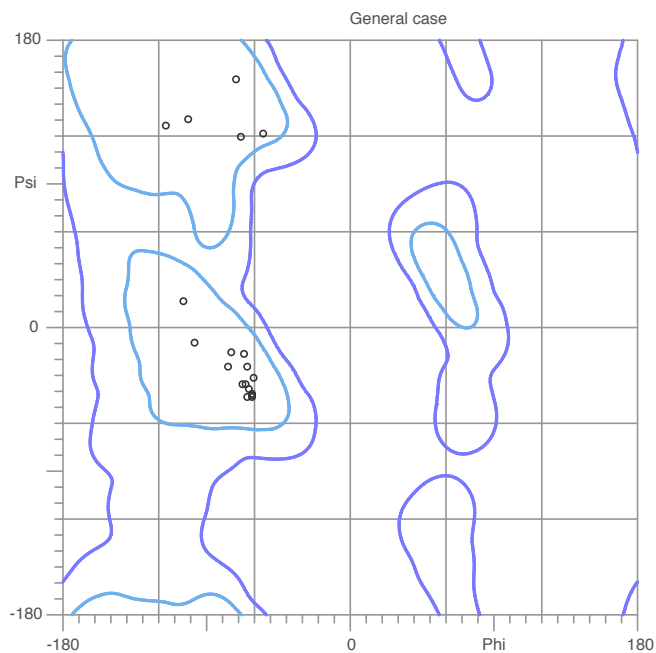
There were no outliers.

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 19



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

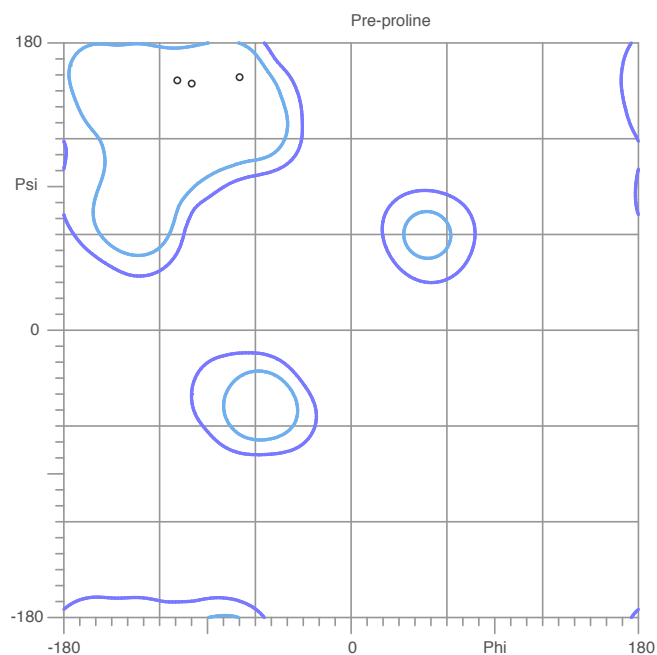
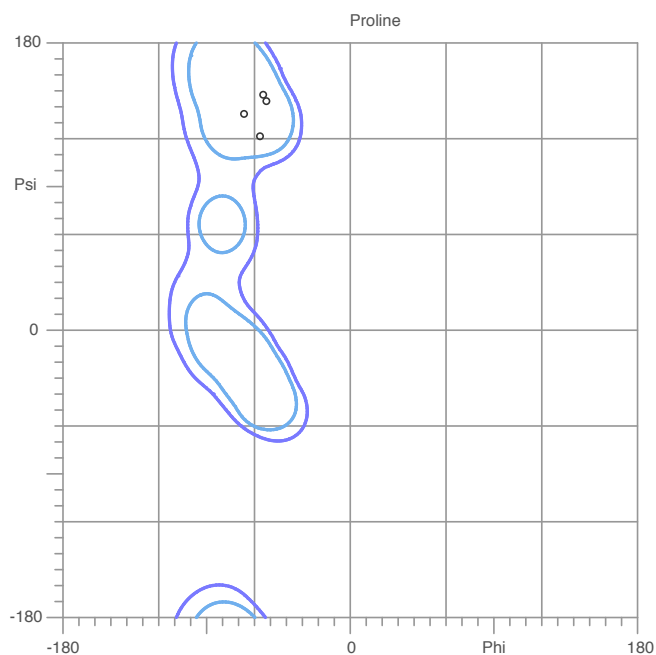
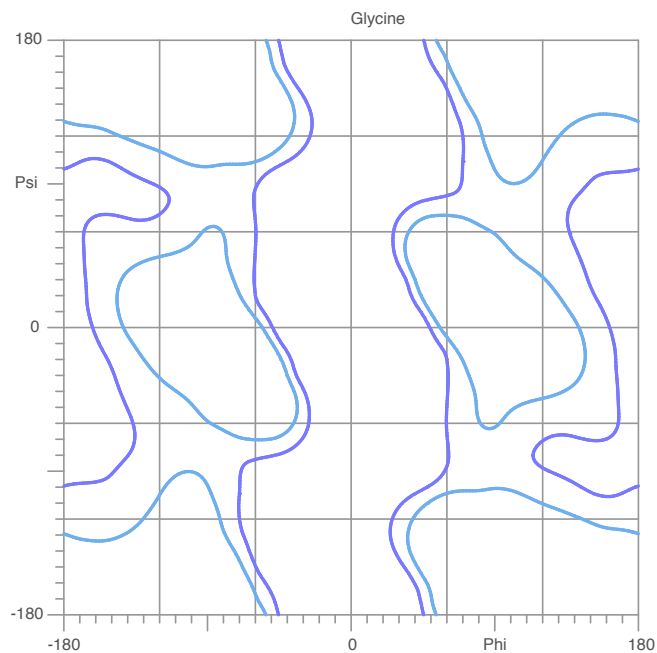
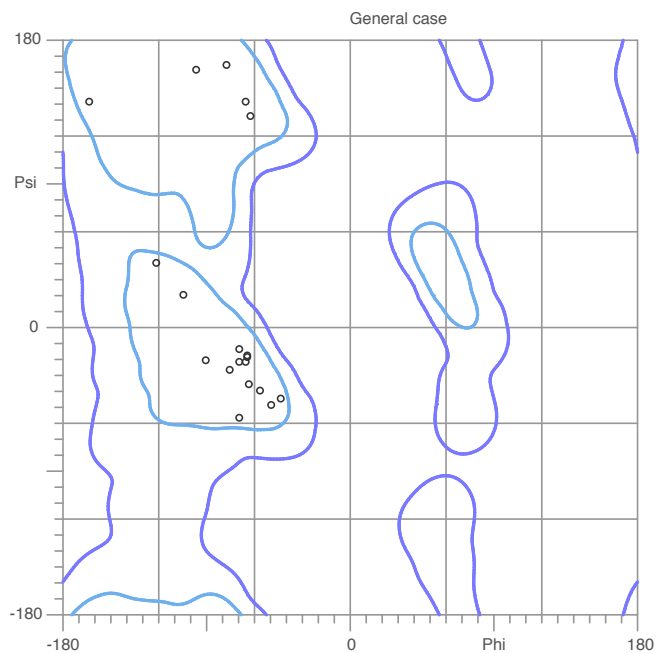
There were no outliers.

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 20



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

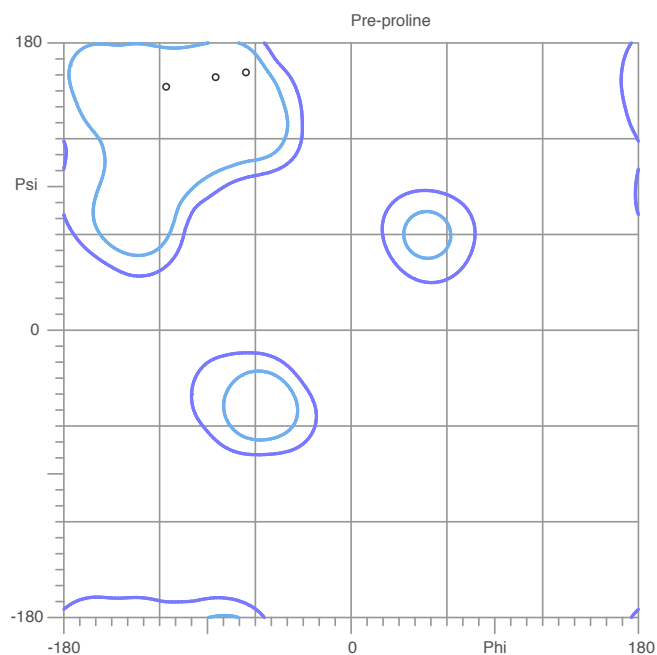
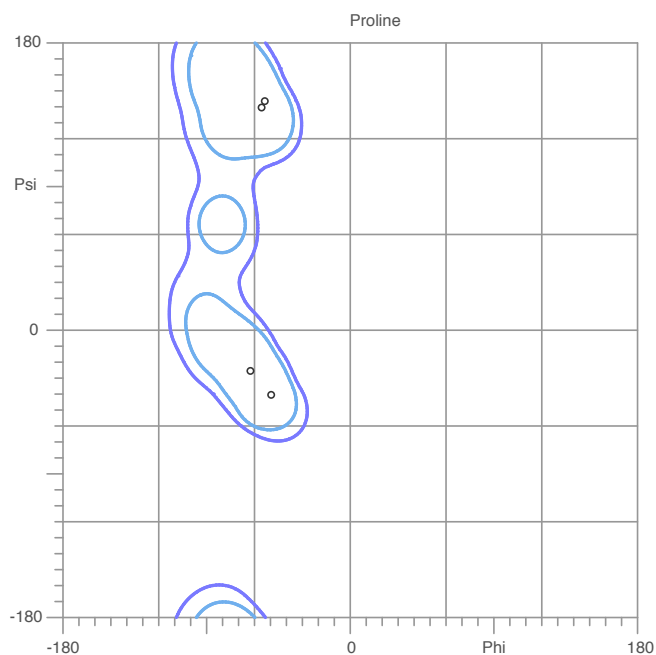
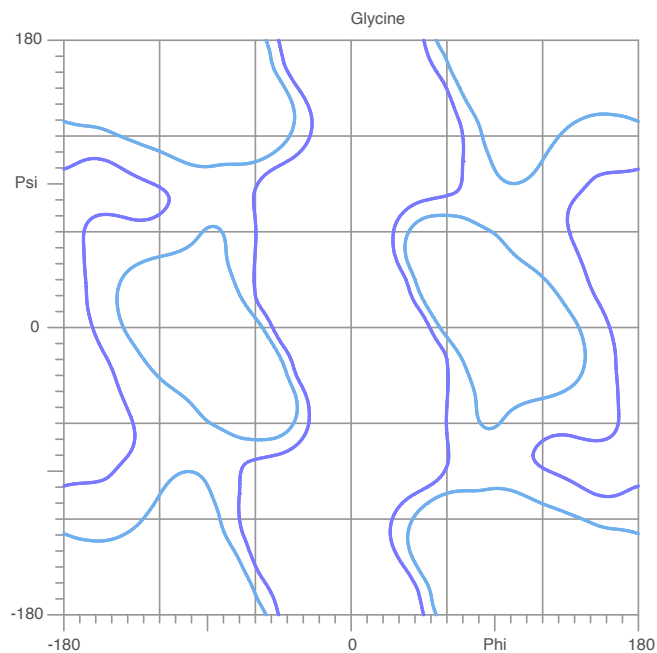
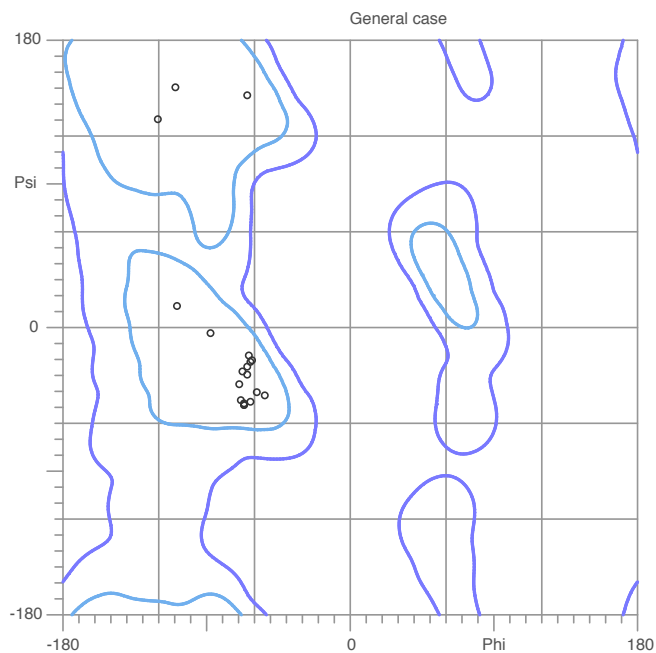
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 21



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) of all residues were in allowed (>99.8%) regions.

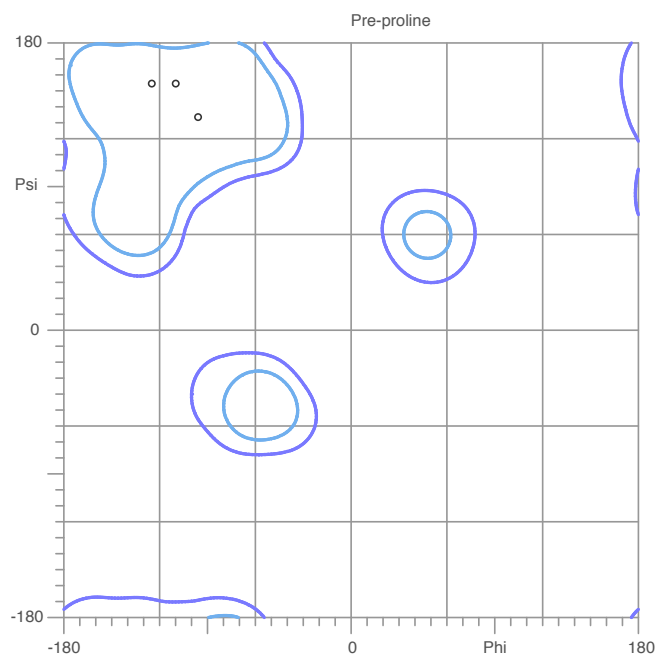
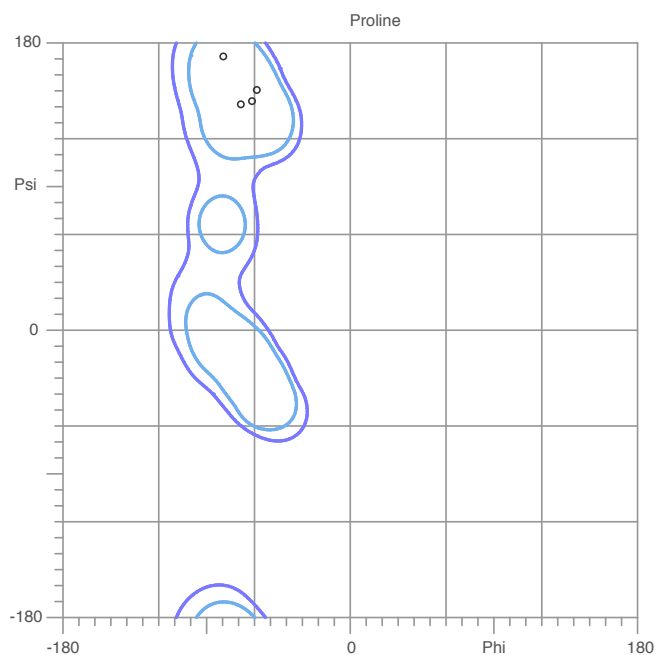
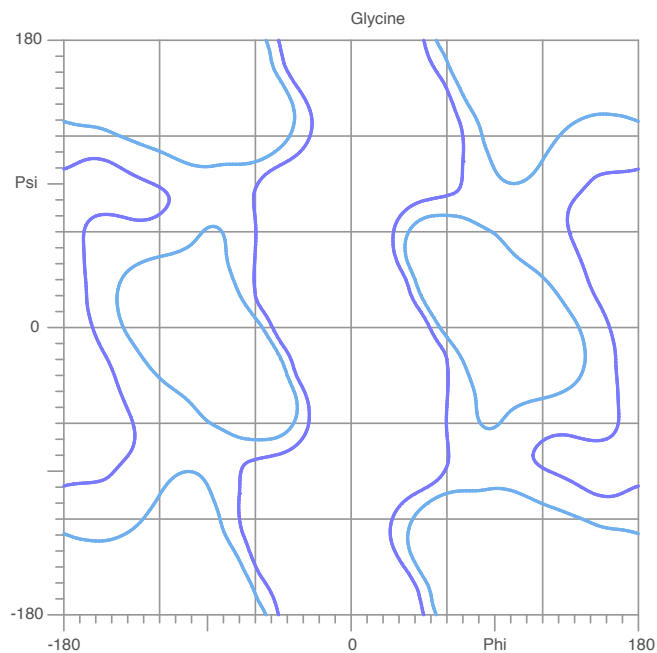
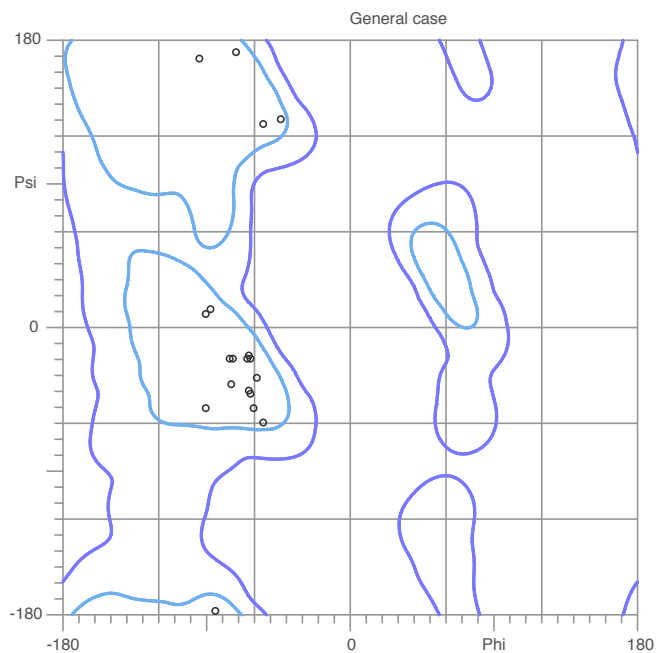
There were no outliers.

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

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

MolProbity Ramachandran analysis

GHSRg_top1000pro.pdb, model 22



100.0% (26/26) of all residues were in favored (98%) regions.
100.0% (26/26) 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)