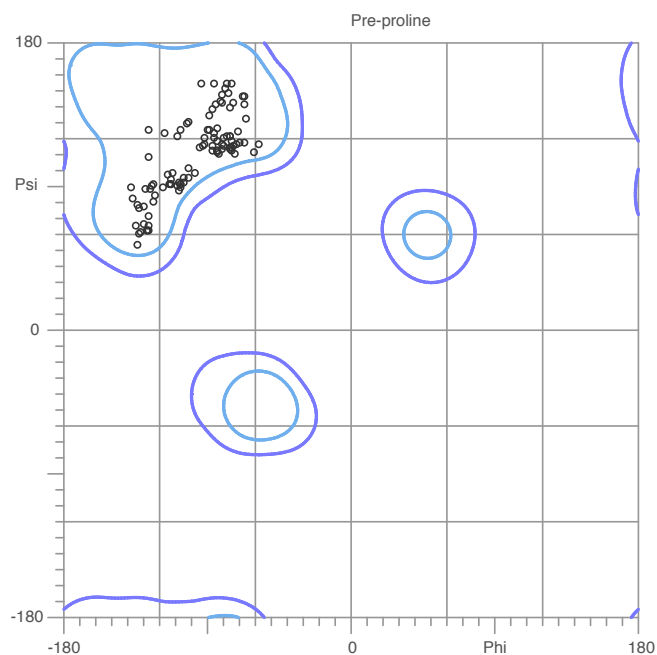
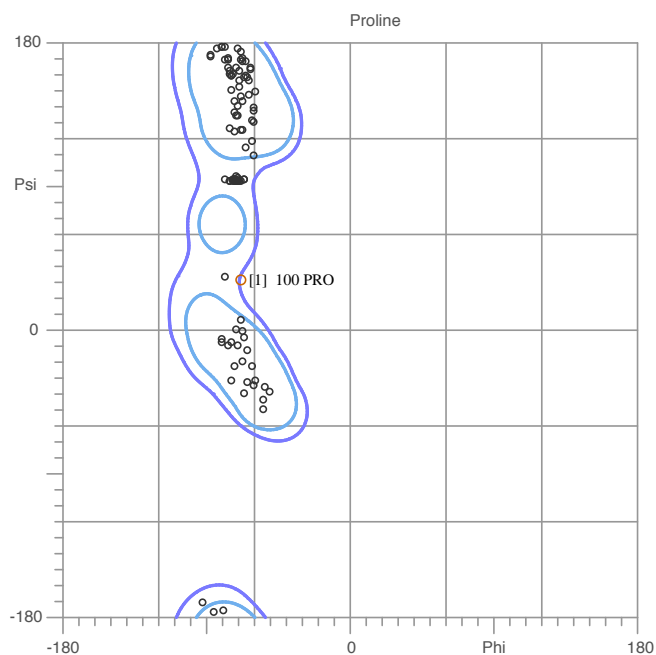
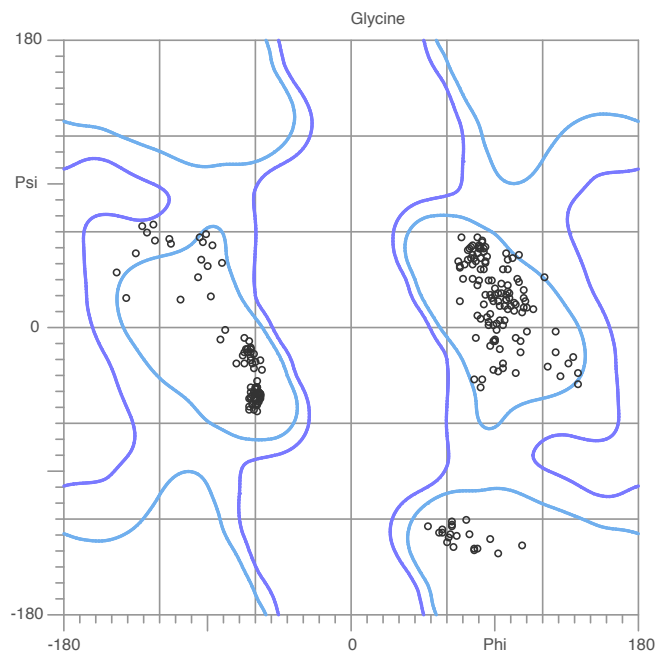
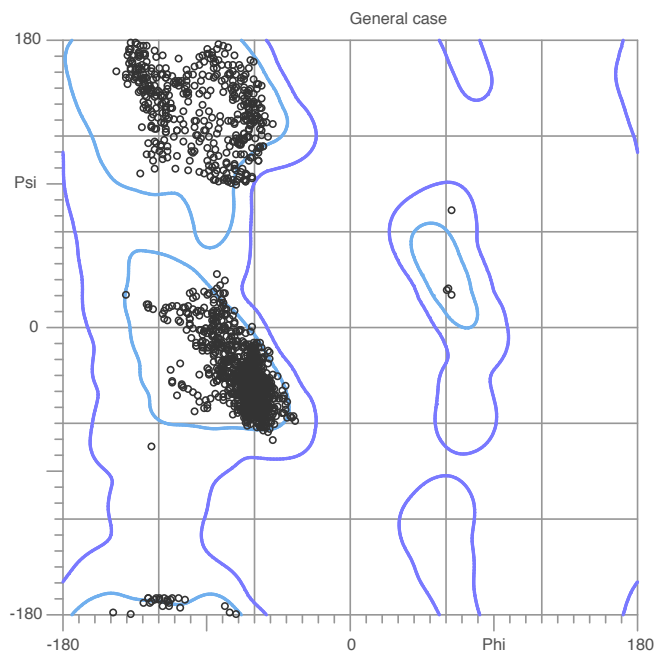


# MolProbity Ramachandran analysis

2KIF.pdb, all models



95.4% (1908/2000) of all residues were in favored (98%) regions.  
100.0% (1999/2000) of all residues were in allowed (>99.8%) regions.

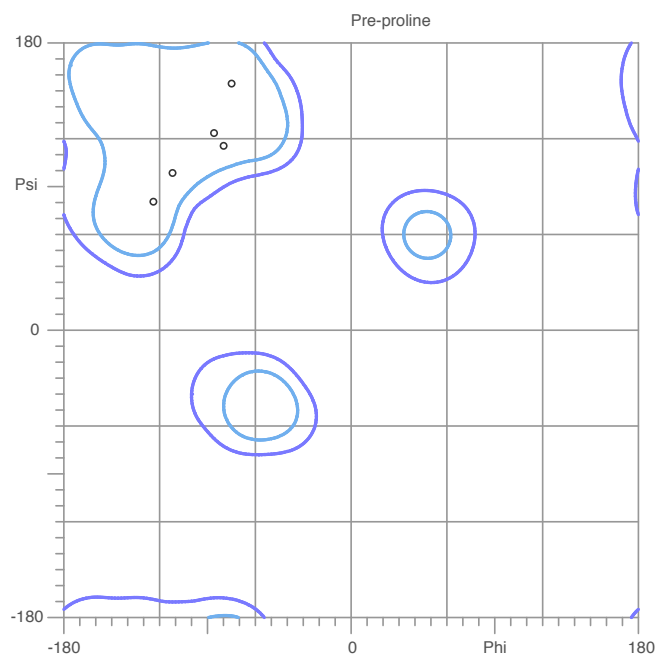
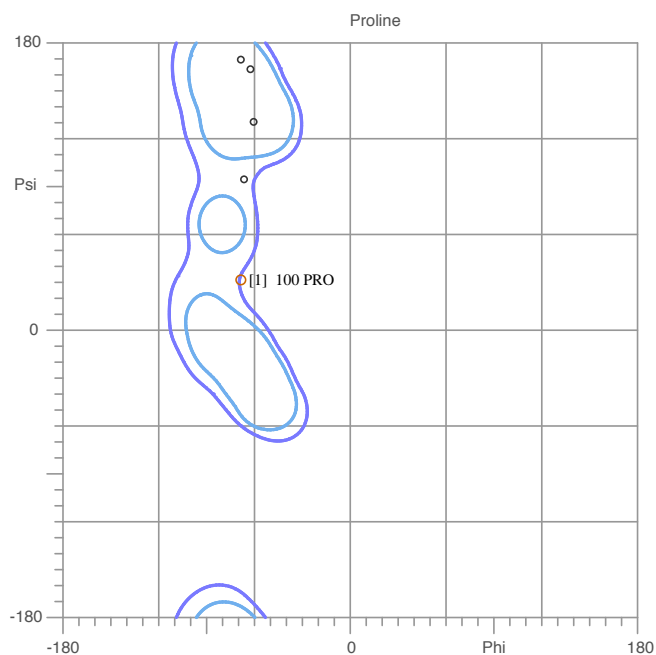
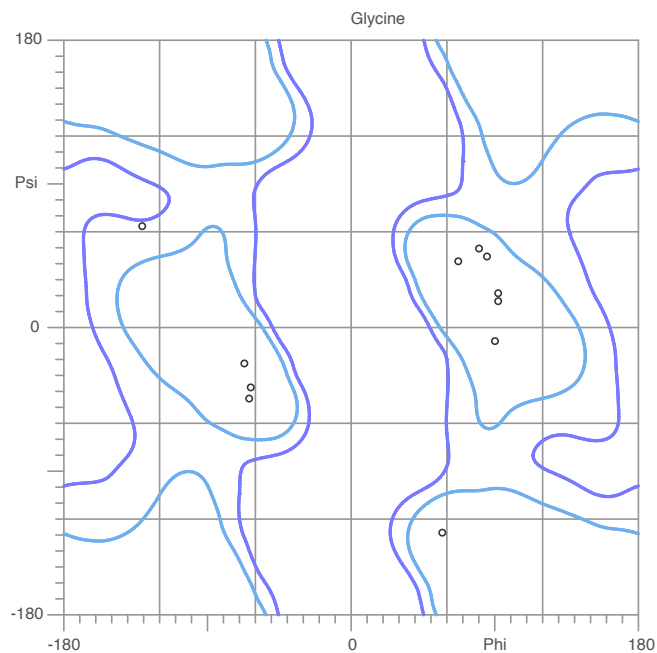
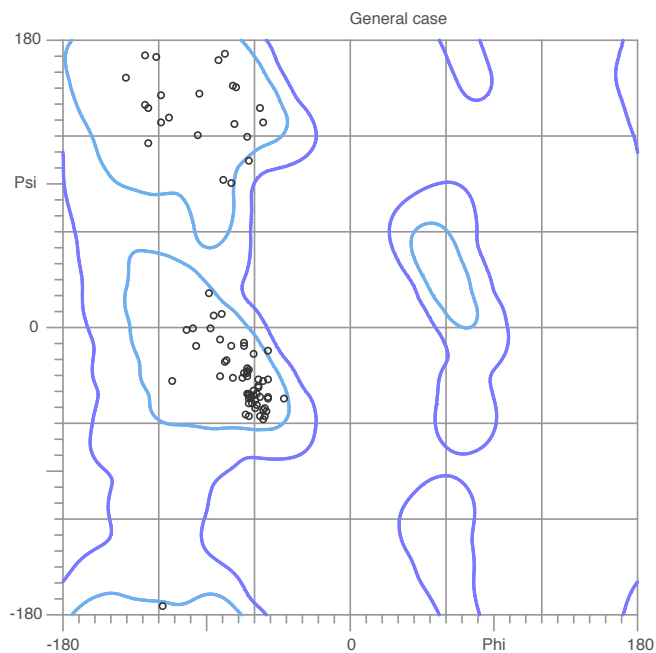
There were 1 outliers (phi, psi):  
[1] 100 PRO (-69.2, 32.2)

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# MolProbity Ramachandran analysis

2KIF.pdb, model 1



95.0% (95/100) of all residues were in favored (98%) regions.  
99.0% (99/100) of all residues were in allowed (>99.8%) regions.

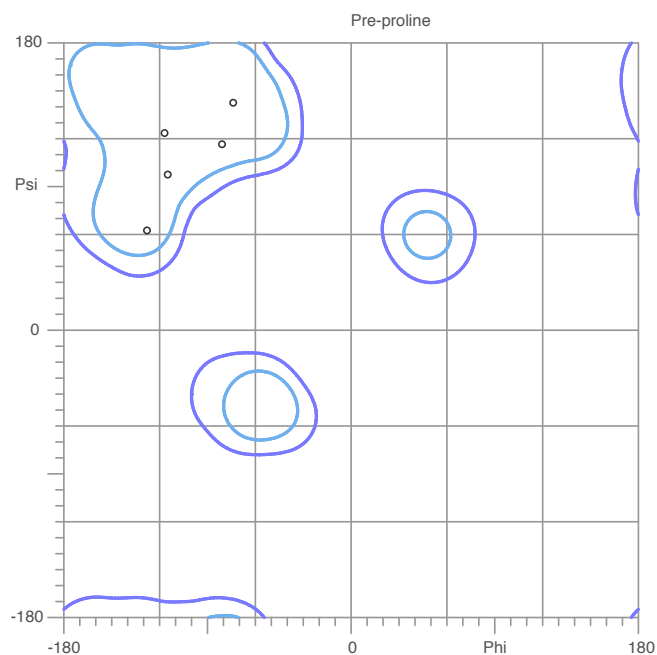
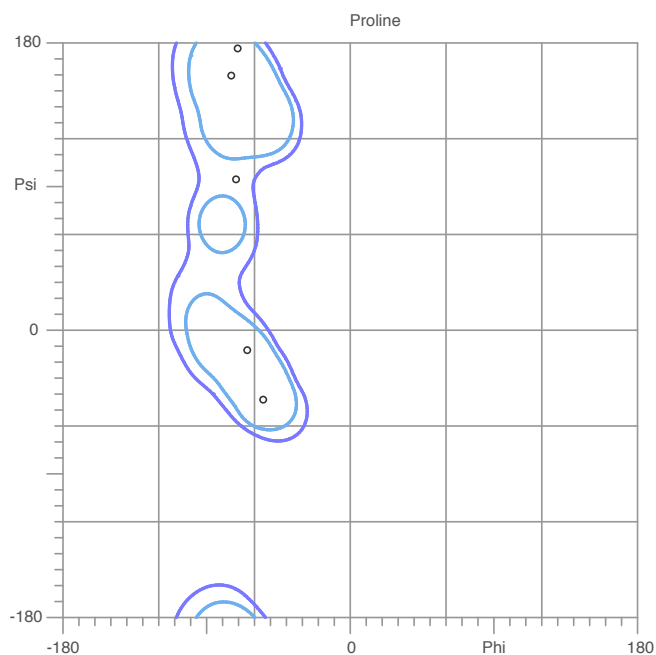
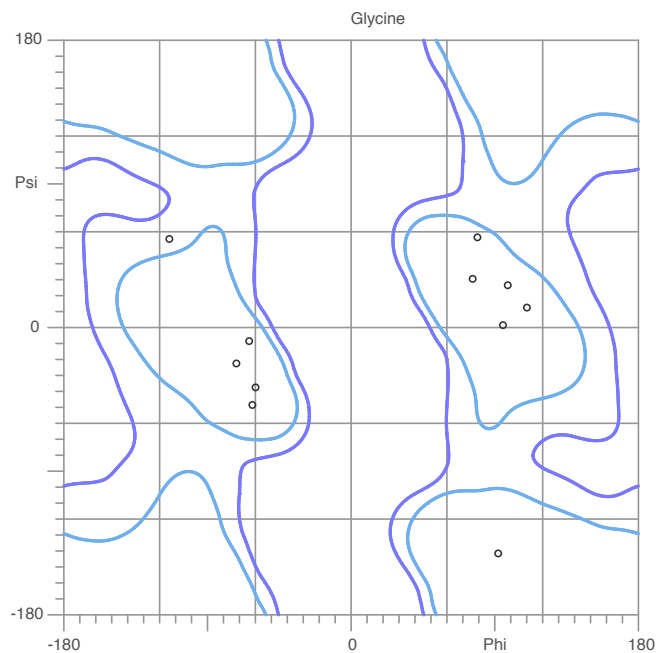
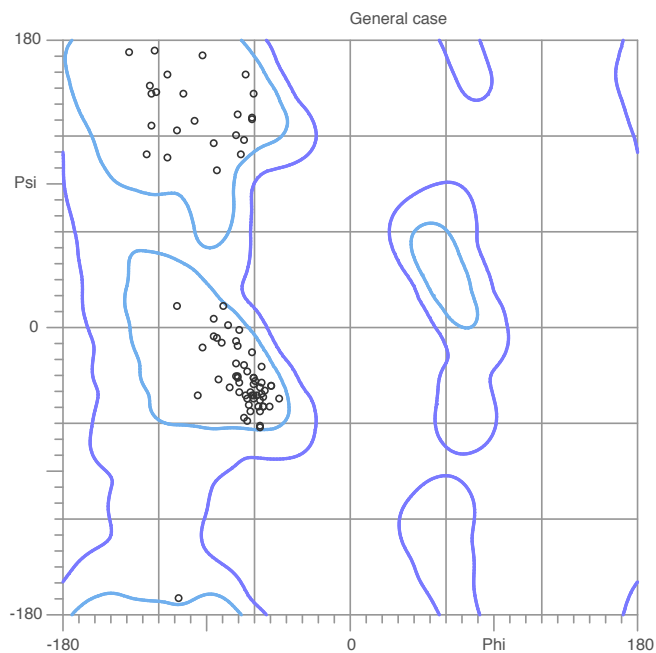
There were 1 outliers (phi, psi):  
[1] 100 PRO (-69.2, 32.2)

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

# MolProbity Ramachandran analysis

2KIF.pdb, model 2



97.0% (97/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

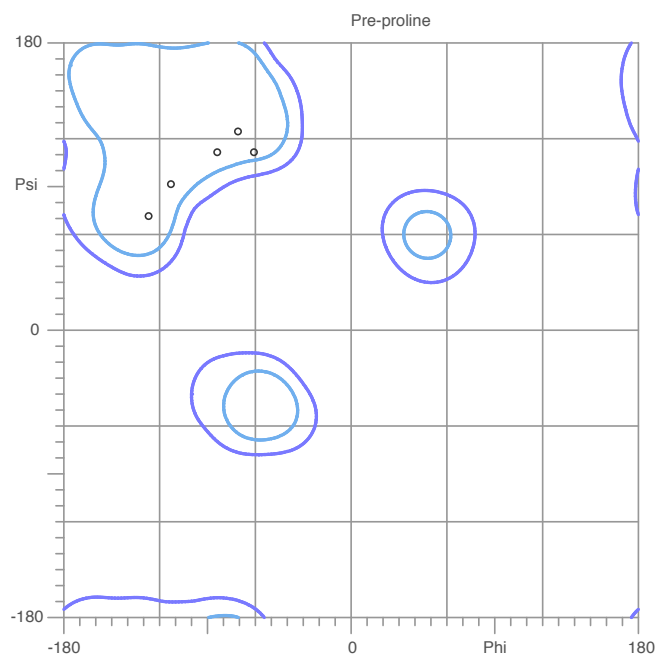
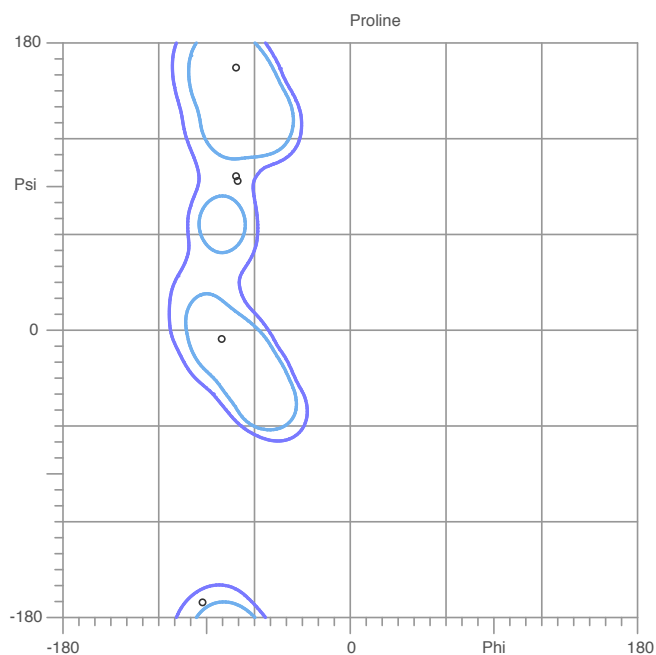
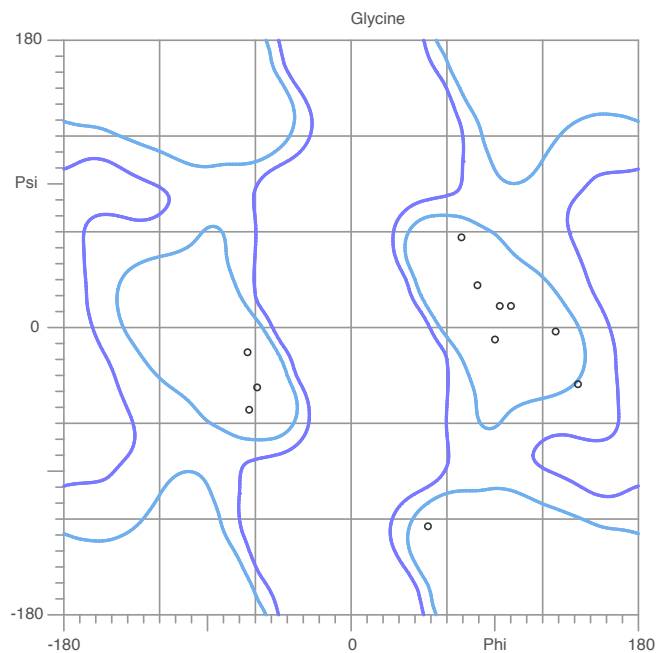
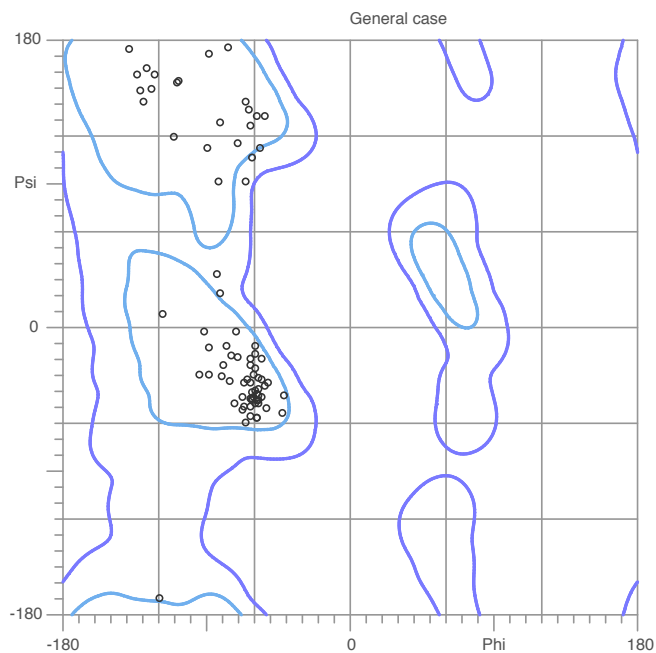
There were no outliers.

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

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# MolProbity Ramachandran analysis

2KIF.pdb, model 3

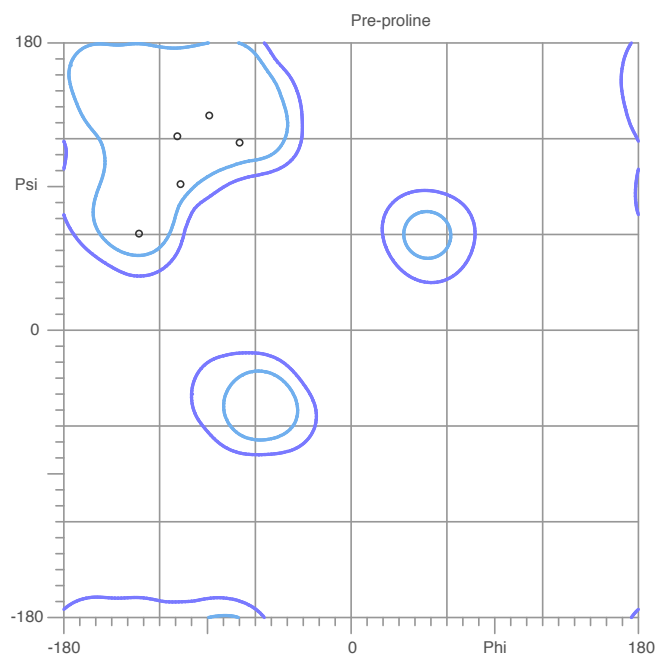
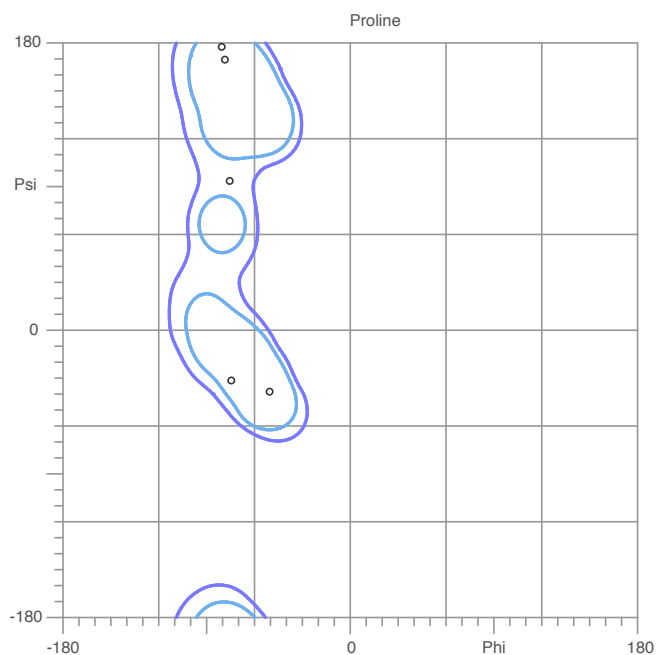
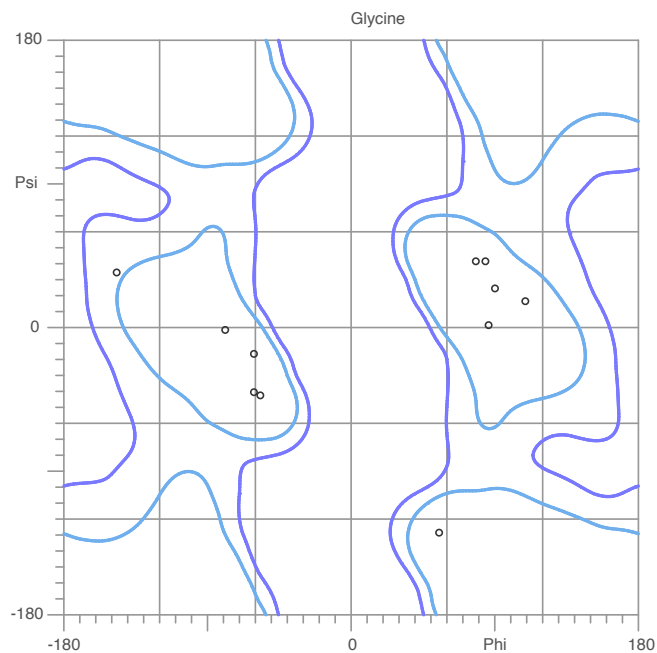
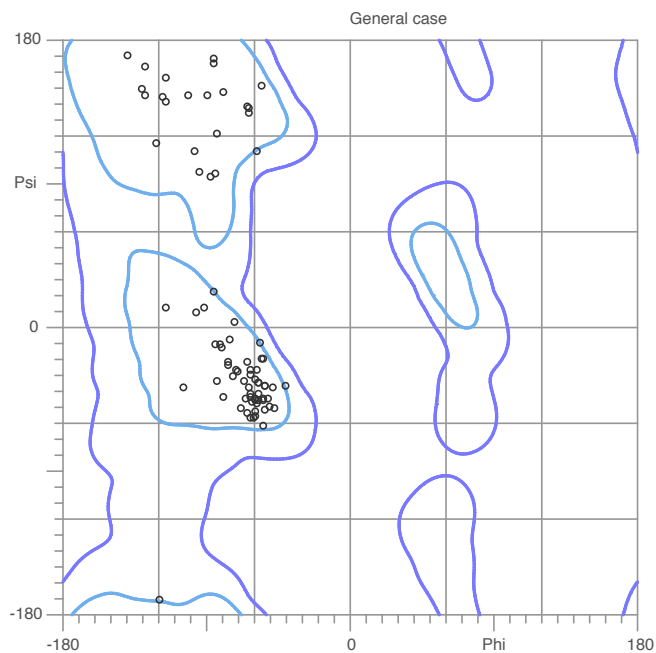


91.0% (91/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

2KIF.pdb, model 4



97.0% (97/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

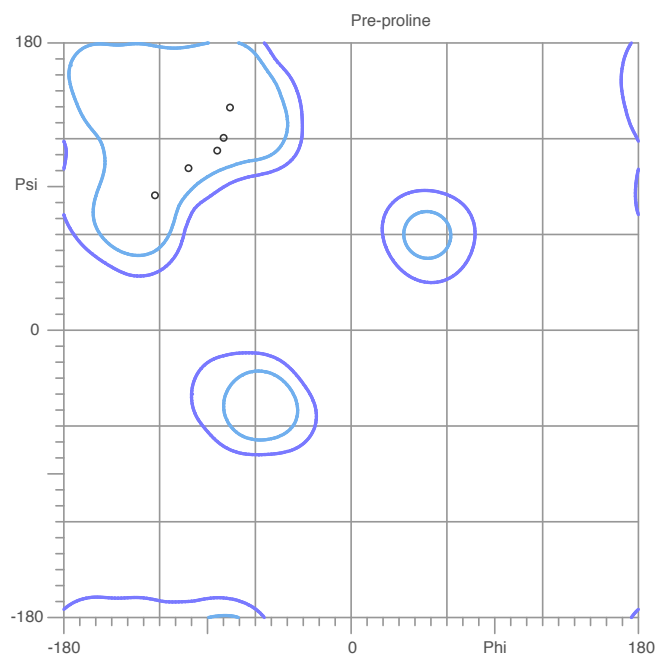
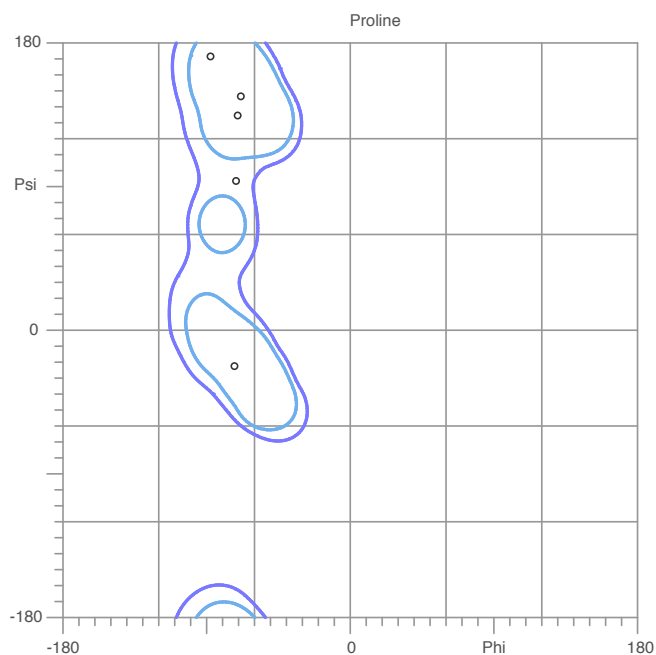
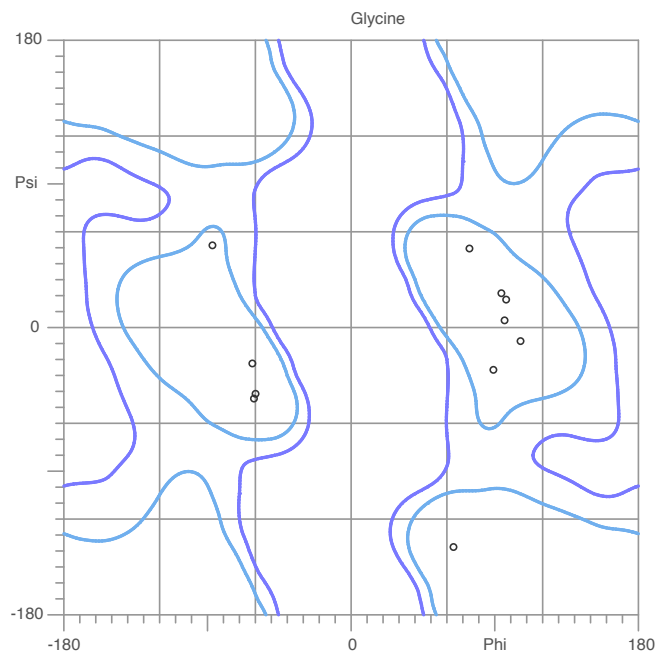
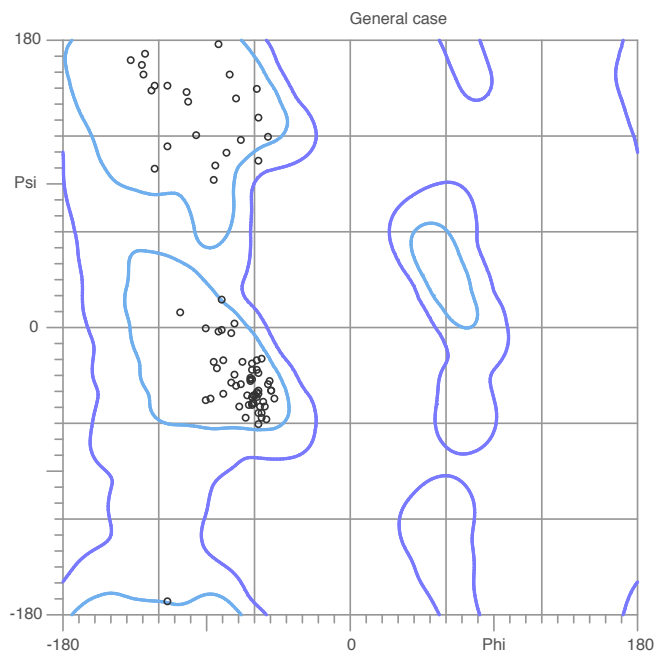
There were no outliers.

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

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# MolProbity Ramachandran analysis

2KIF.pdb, model 5

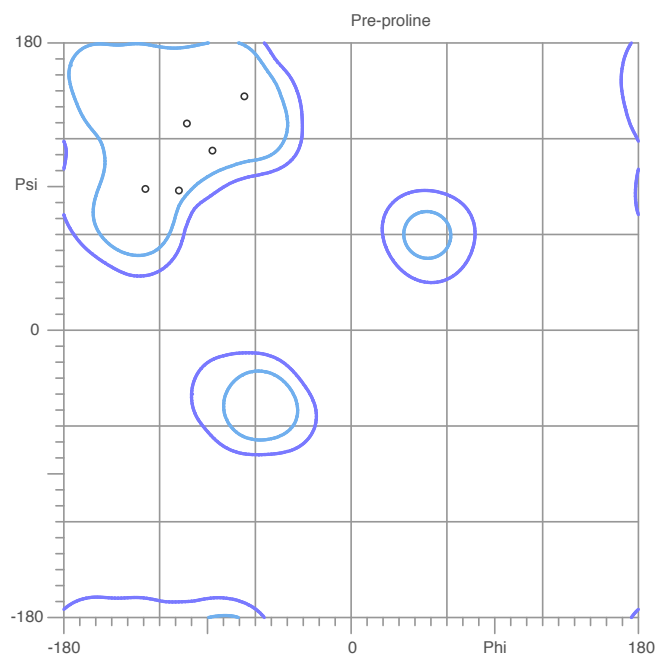
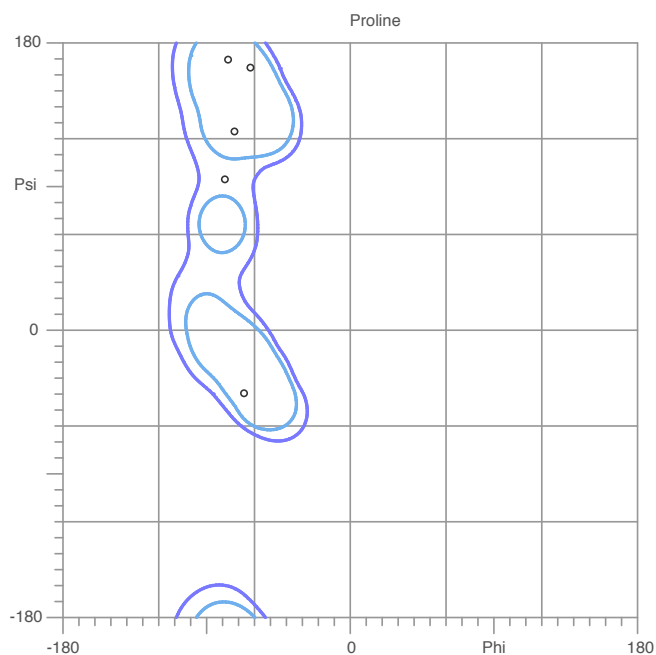
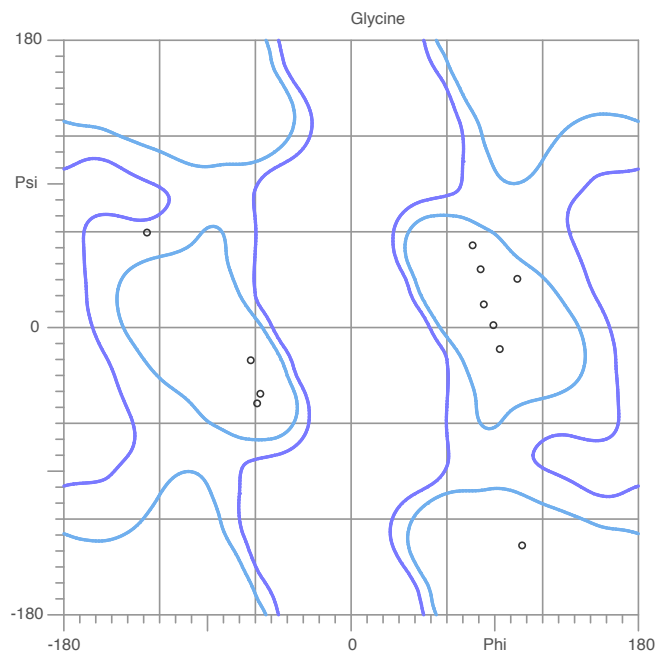
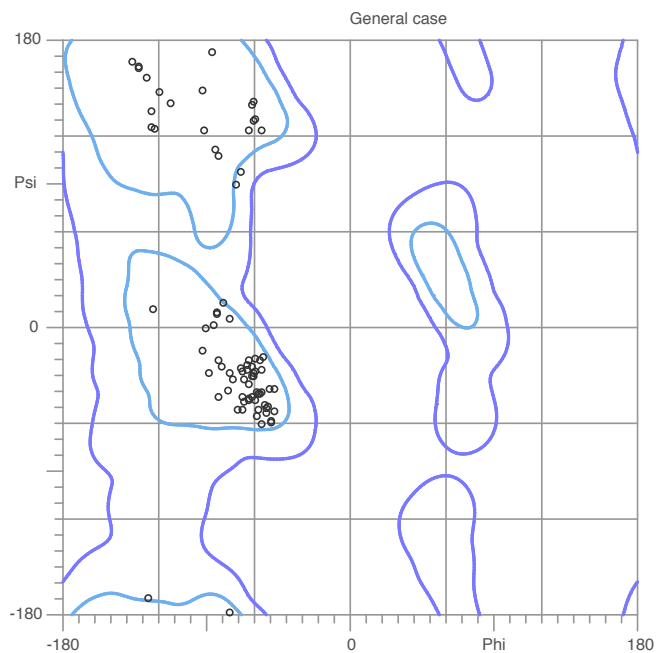


96.0% (96/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

2KIF.pdb, model 6



95.0% (95/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

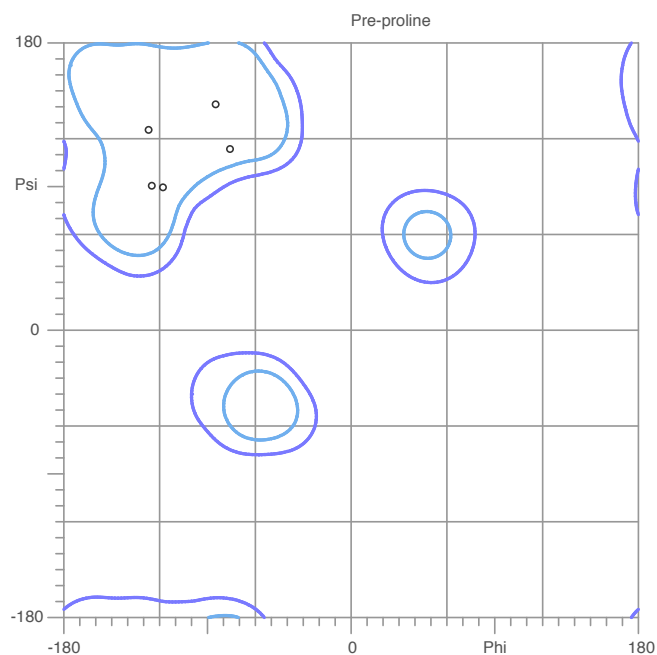
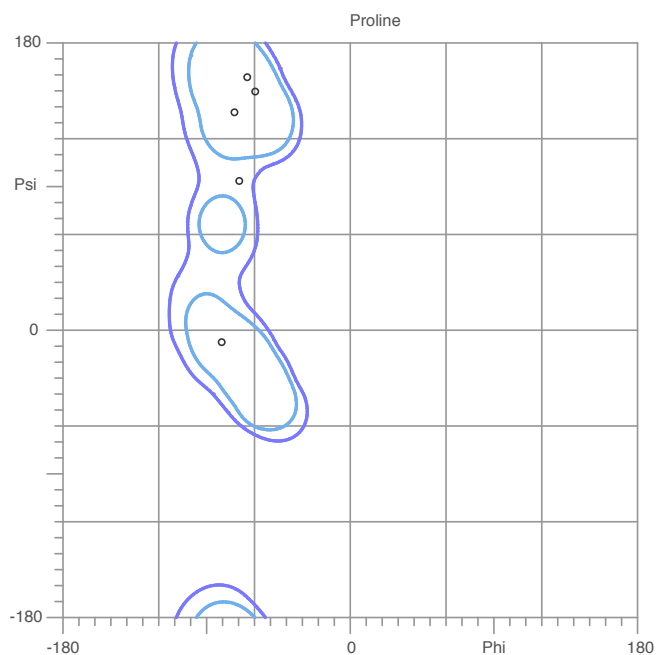
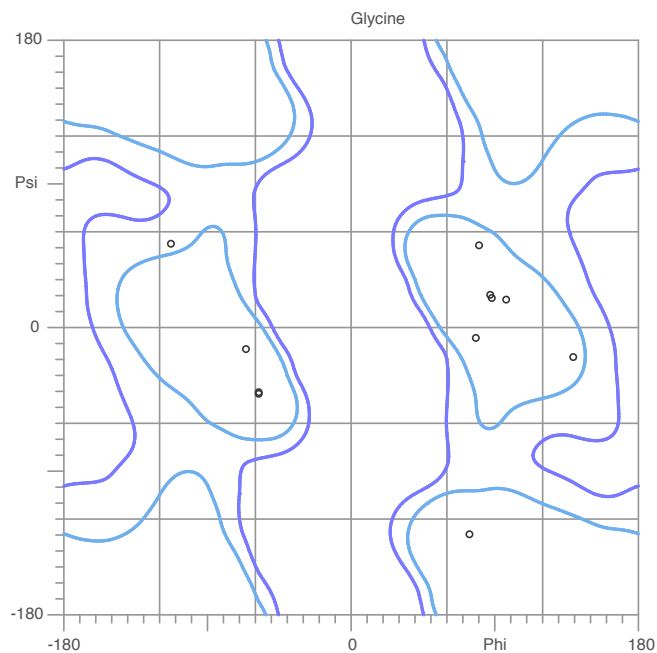
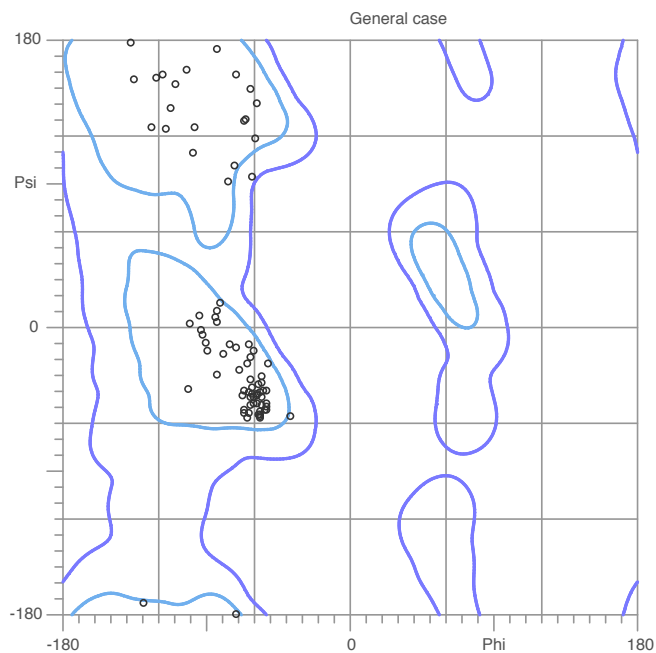
There were no outliers.

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# MolProbity Ramachandran analysis

2KIF.pdb, model 7



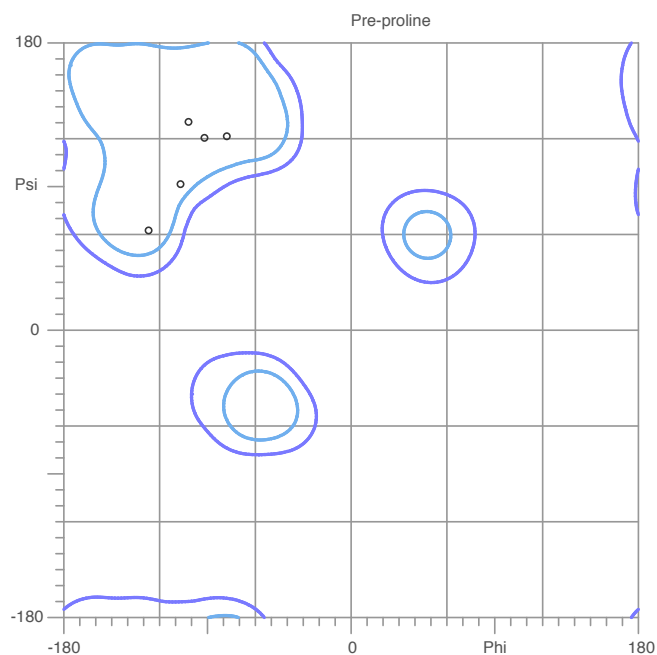
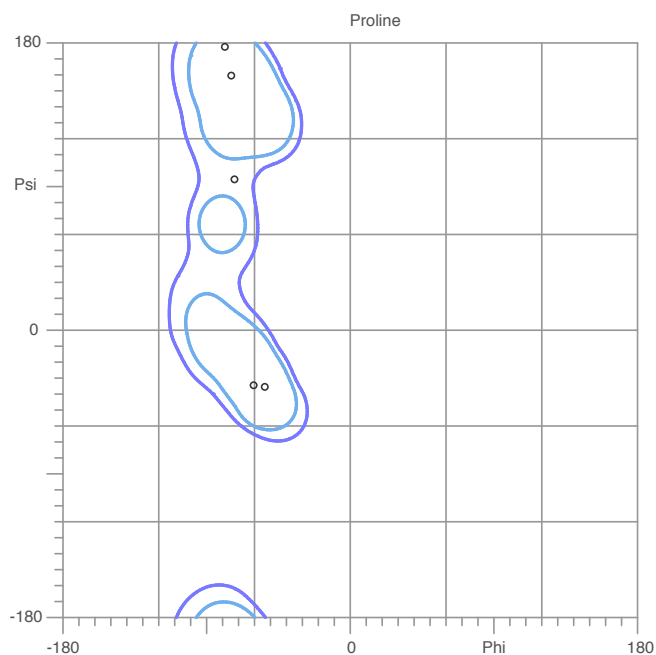
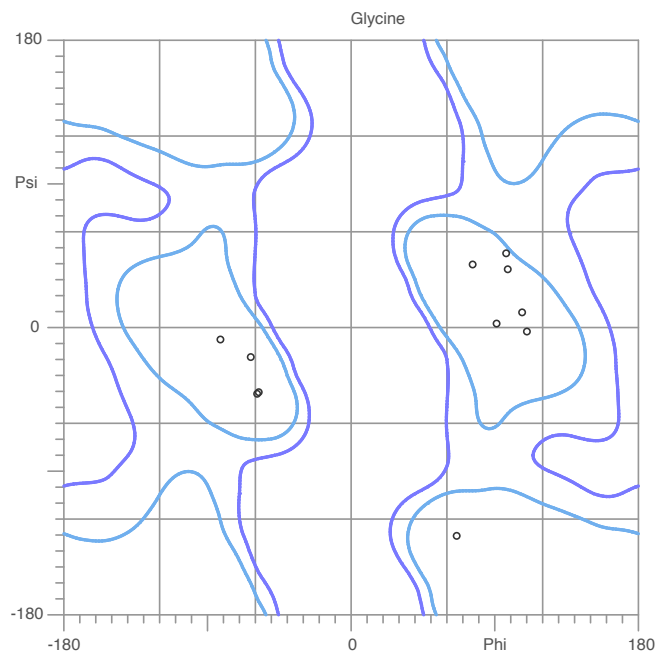
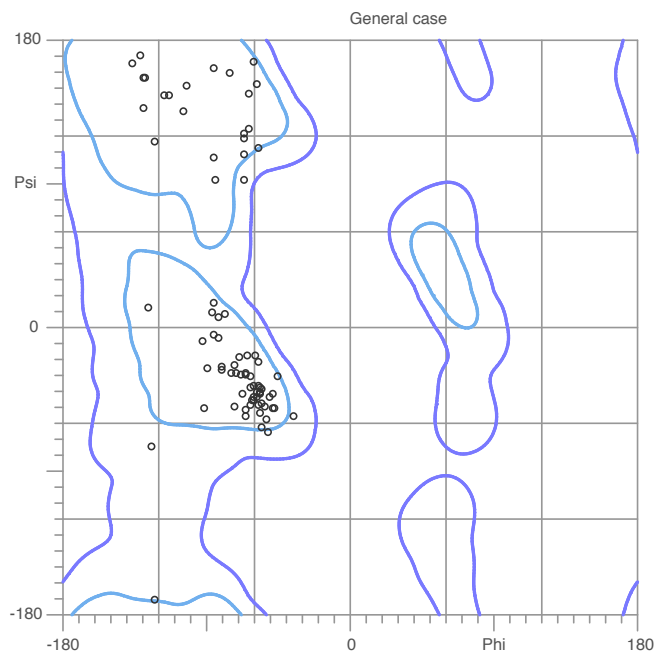
96.0% (96/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

There were no outliers.



# MolProbity Ramachandran analysis

2KIF.pdb, model 8



94.0% (94/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

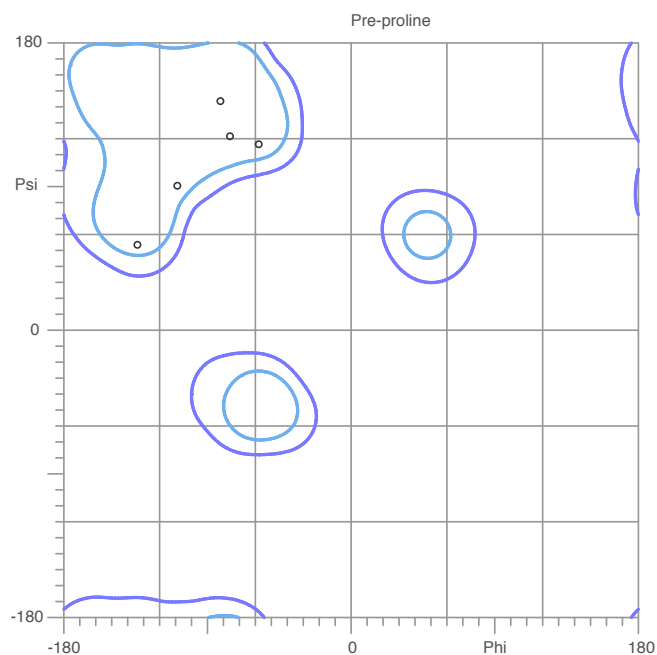
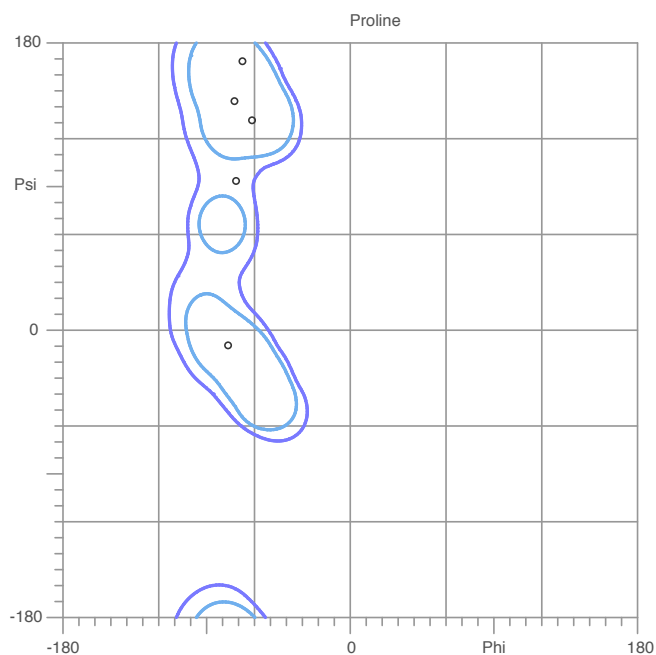
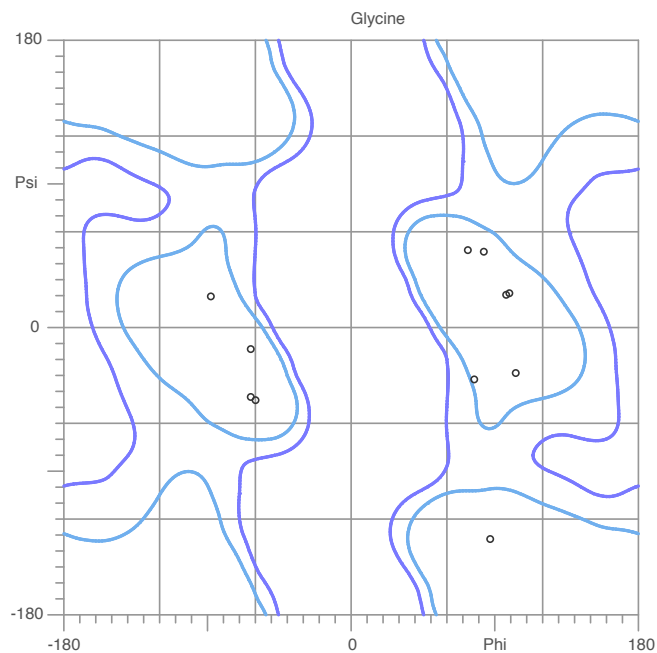
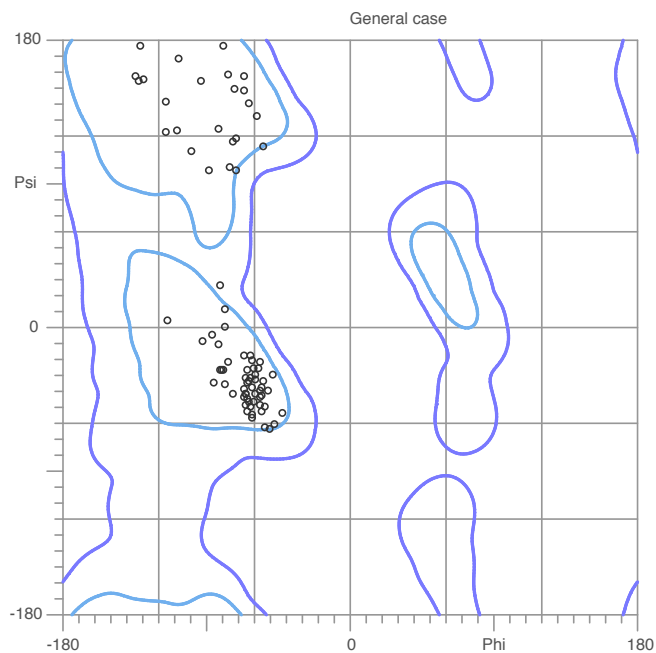
There were no outliers.

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# MolProbity Ramachandran analysis

2KIF.pdb, model 9



98.0% (98/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

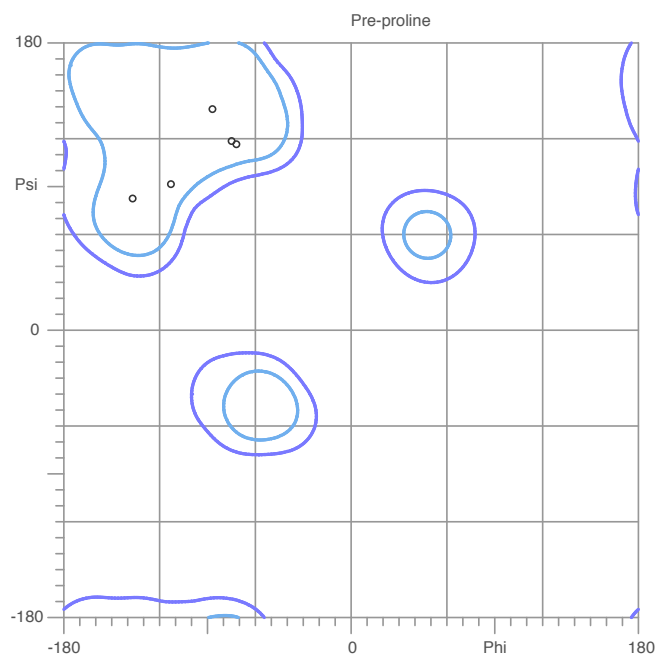
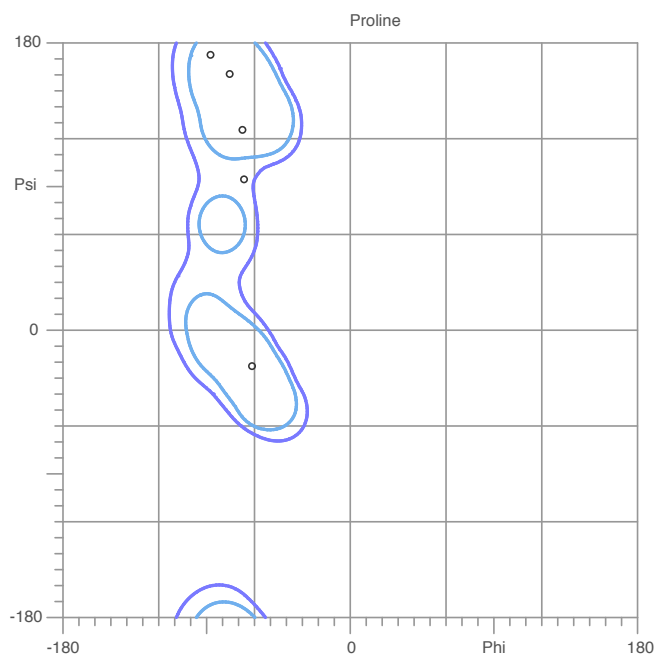
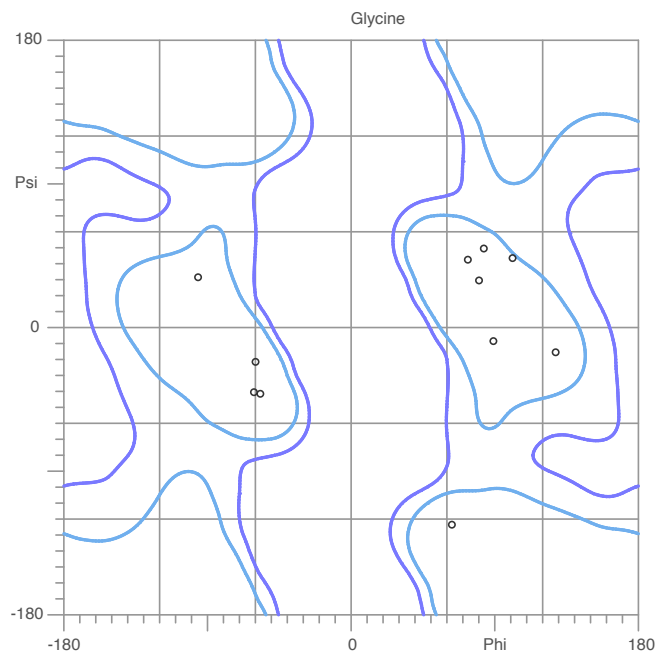
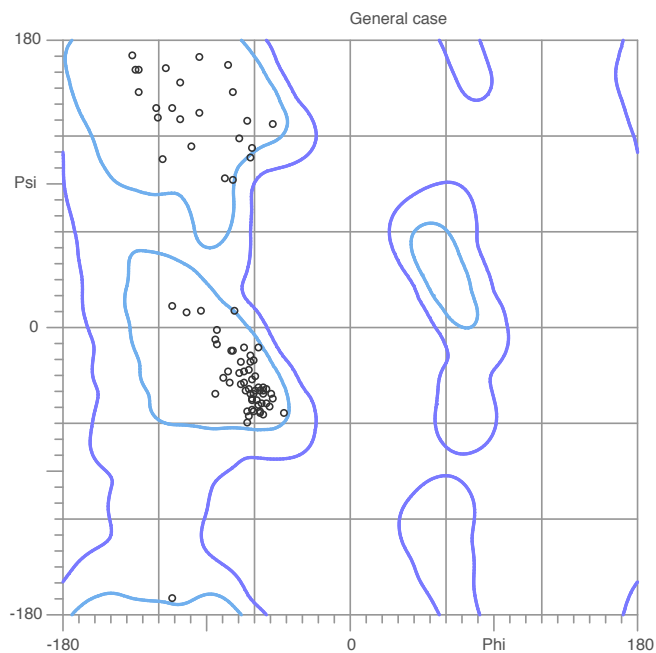
There were no outliers.

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# MolProbity Ramachandran analysis

2KIF.pdb, model 10



97.0% (97/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

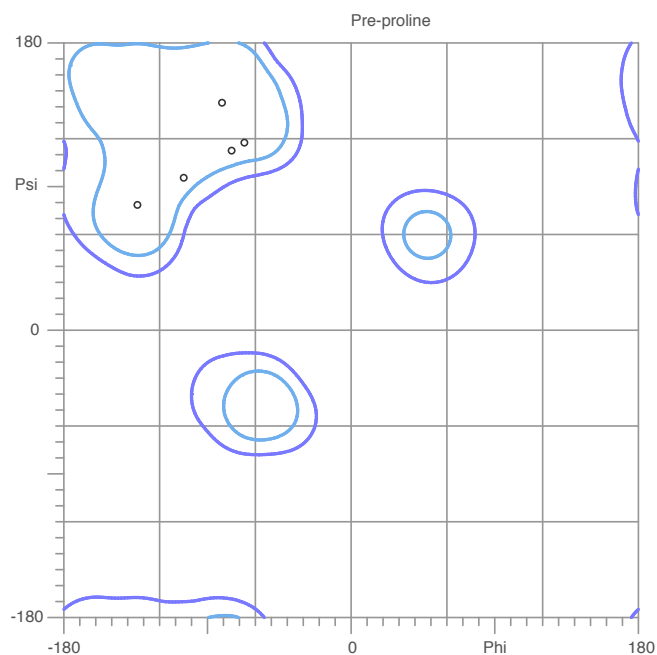
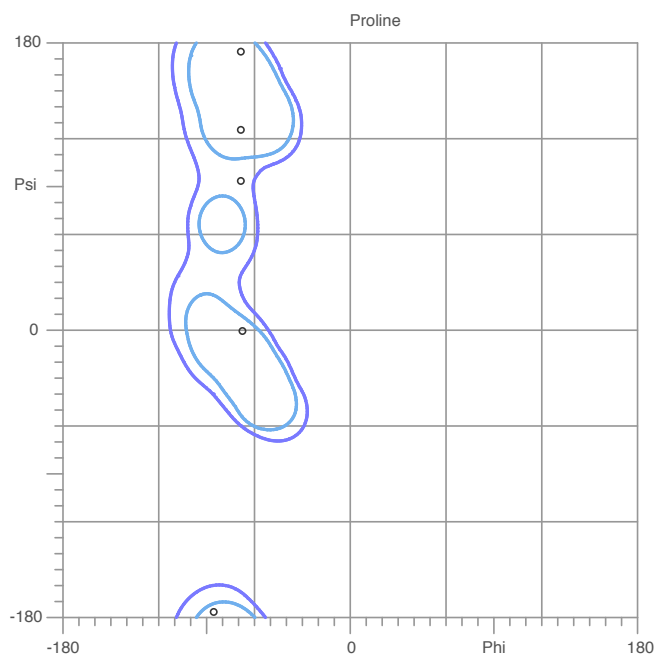
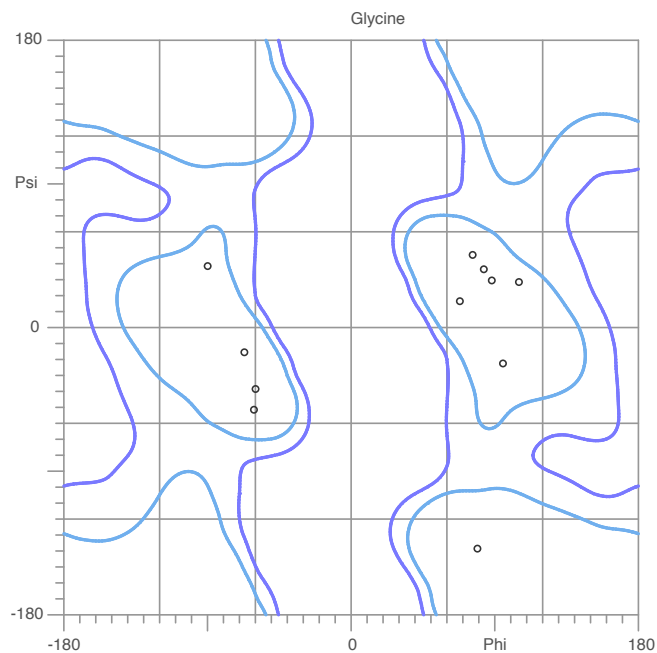
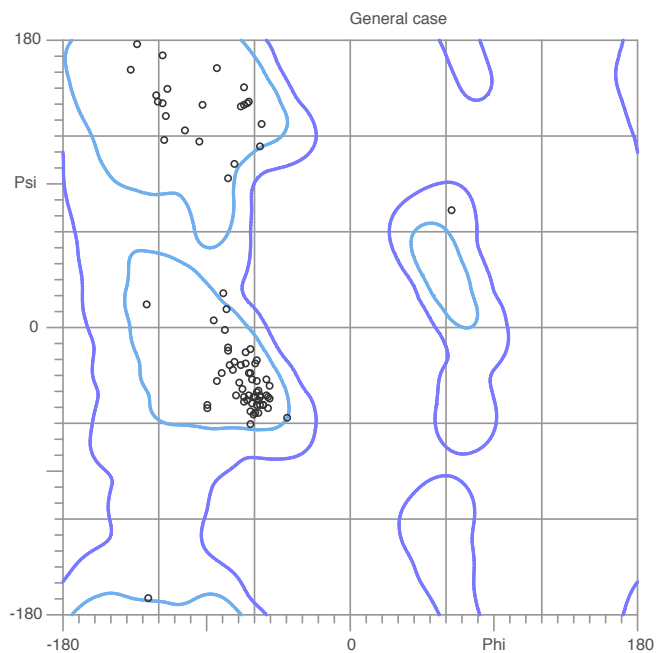
There were no outliers.

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# MolProbity Ramachandran analysis

2KIF.pdb, model 11



96.0% (96/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

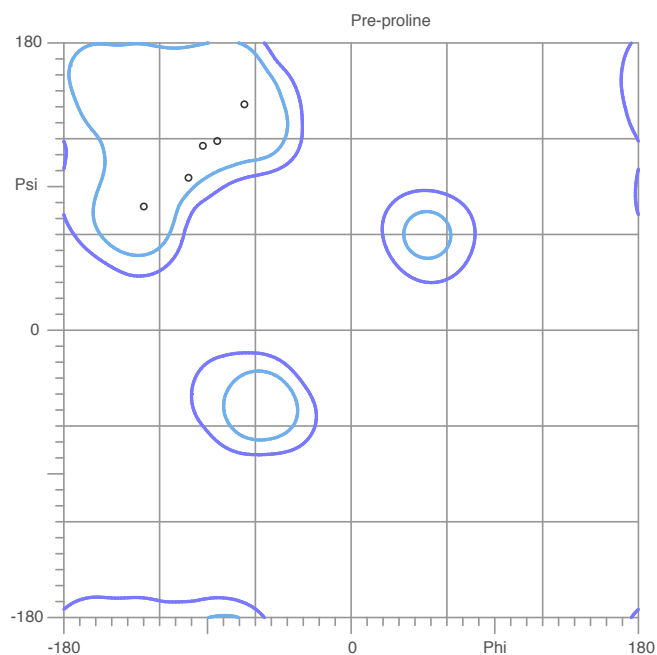
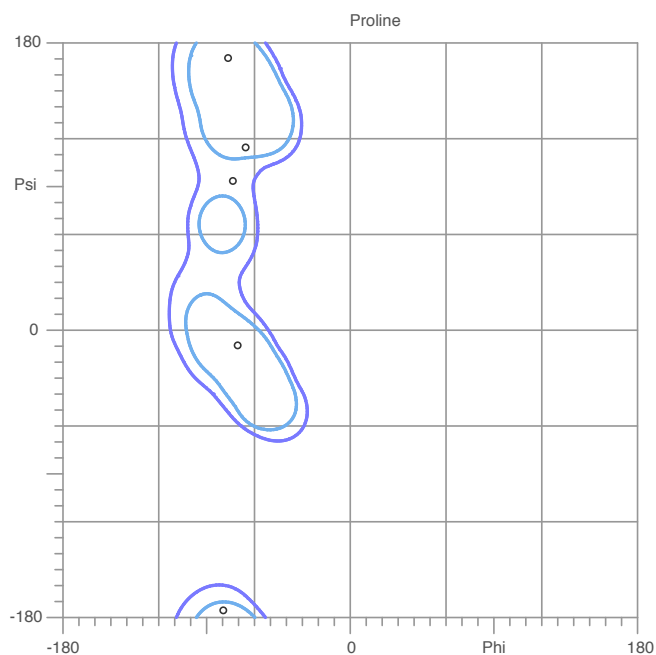
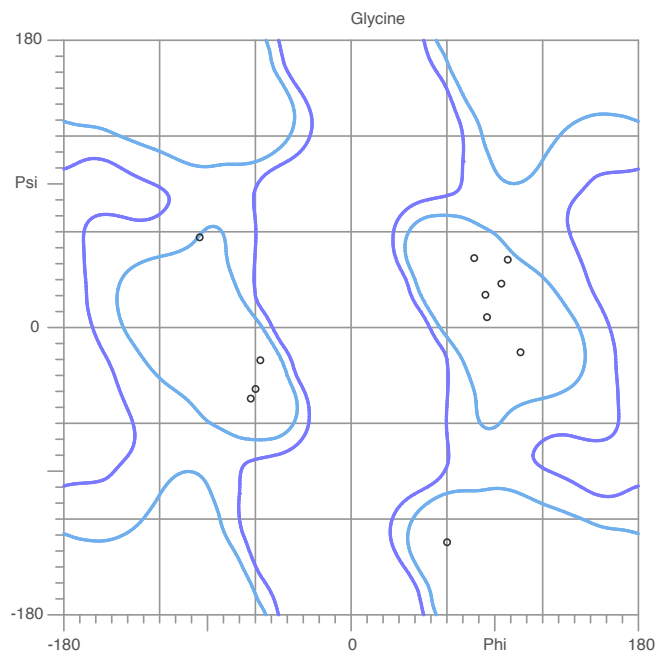
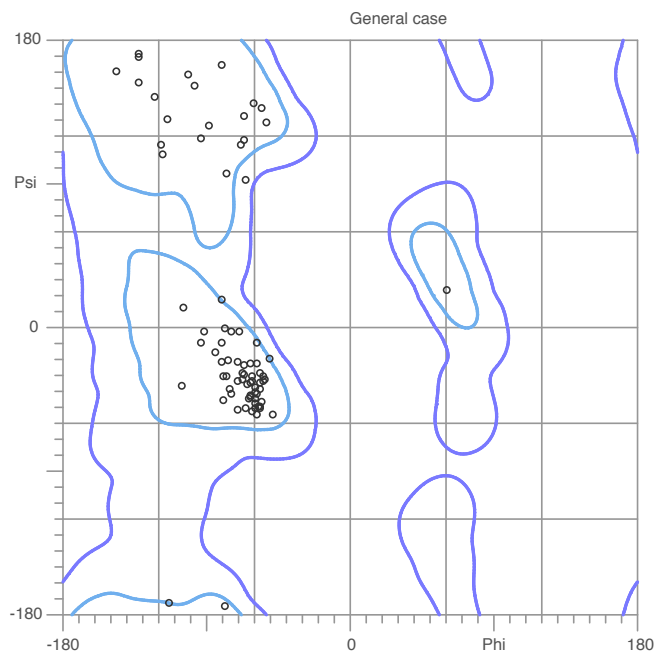
There were no outliers.

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# MolProbity Ramachandran analysis

2KIF.pdb, model 12



96.0% (96/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

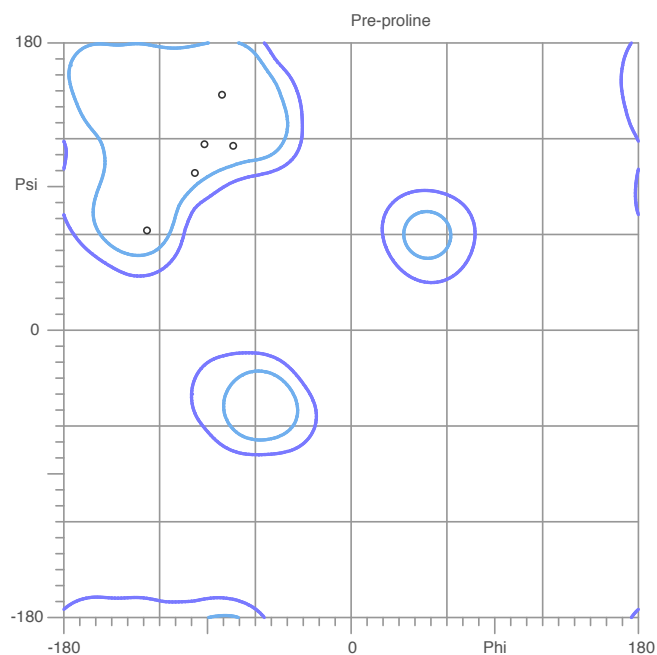
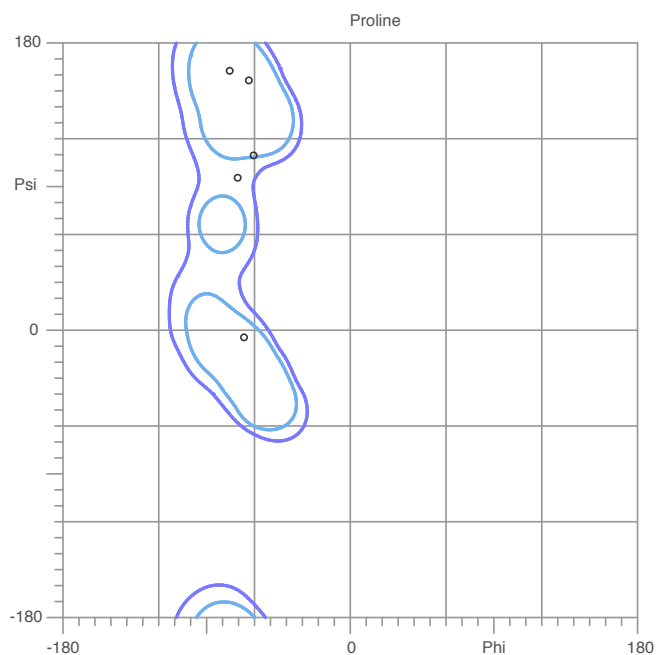
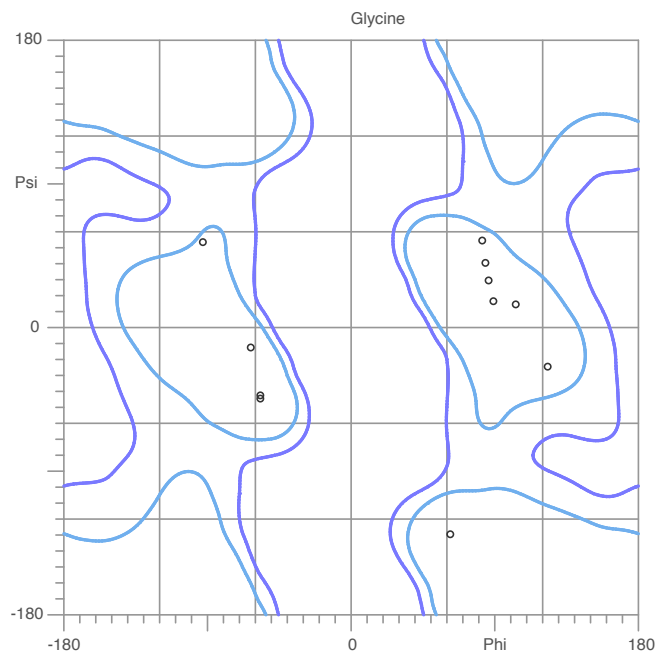
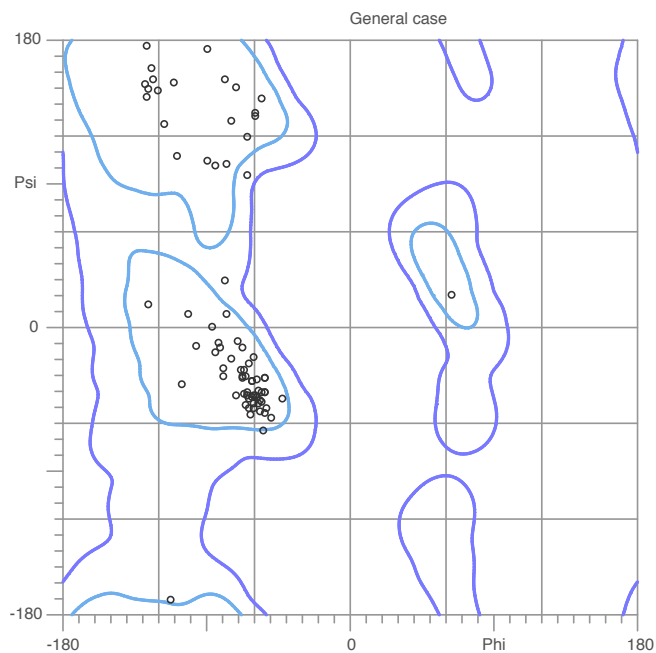
There were no outliers.

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# MolProbity Ramachandran analysis

2KIF.pdb, model 13

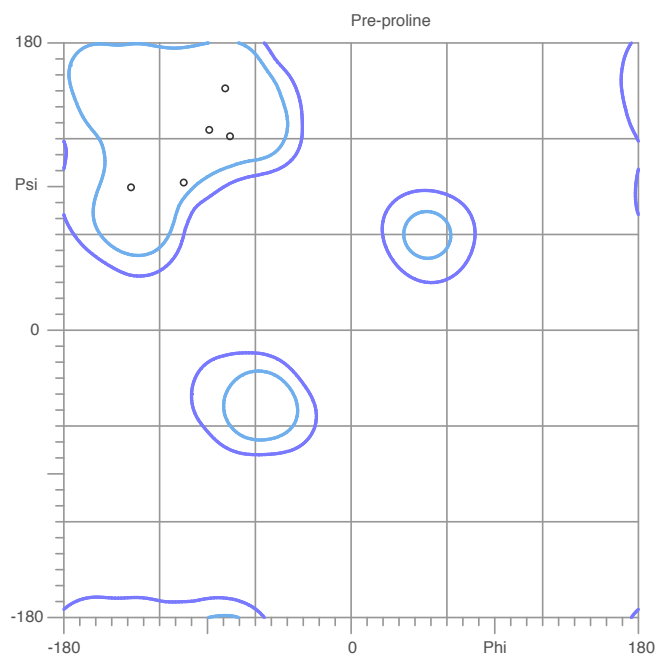
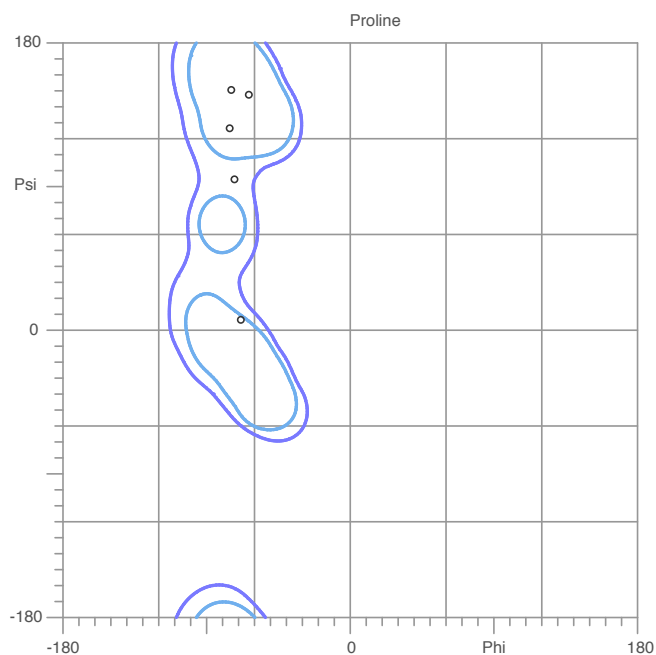
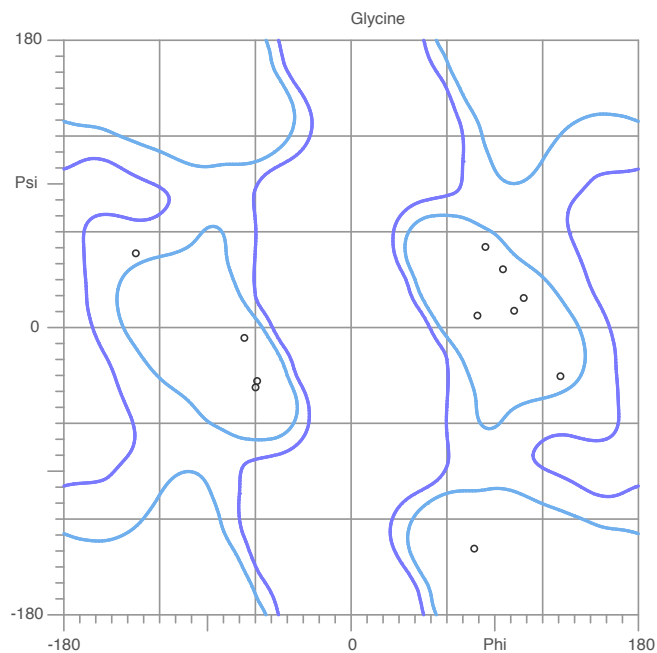
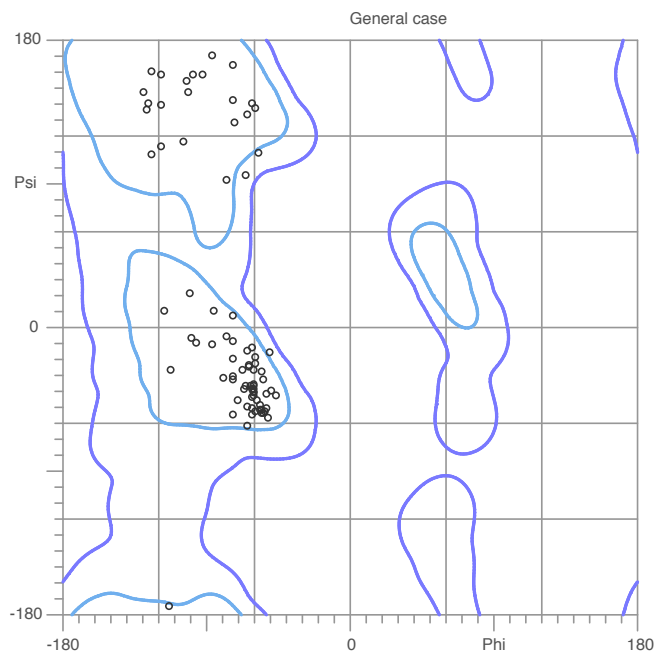


95.0% (95/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

2KIF.pdb, model 14



95.0% (95/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

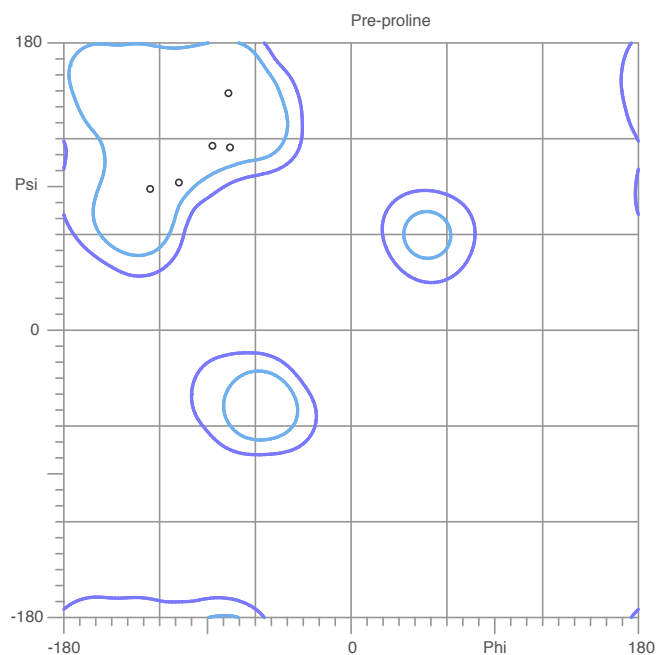
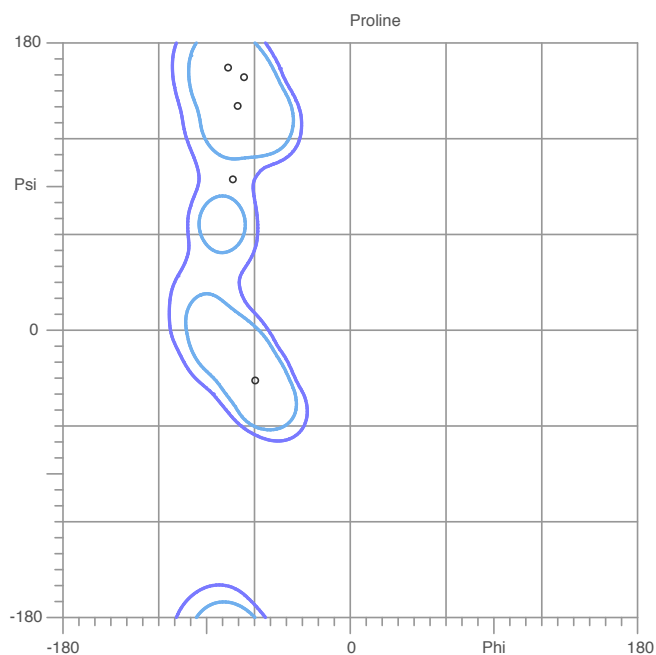
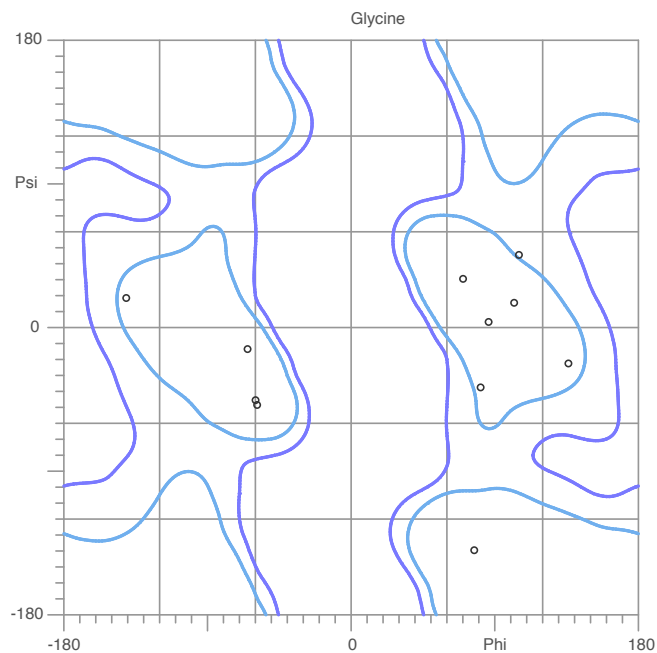
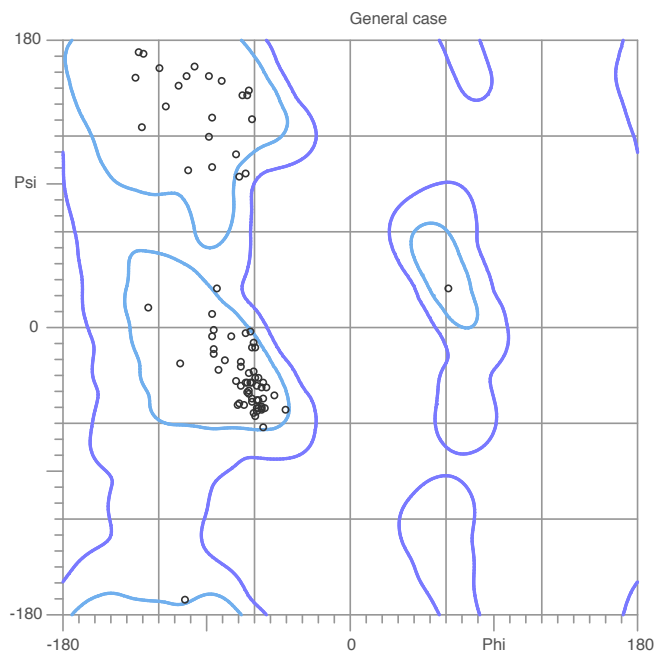
There were no outliers.

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# MolProbity Ramachandran analysis

2KIF.pdb, model 15



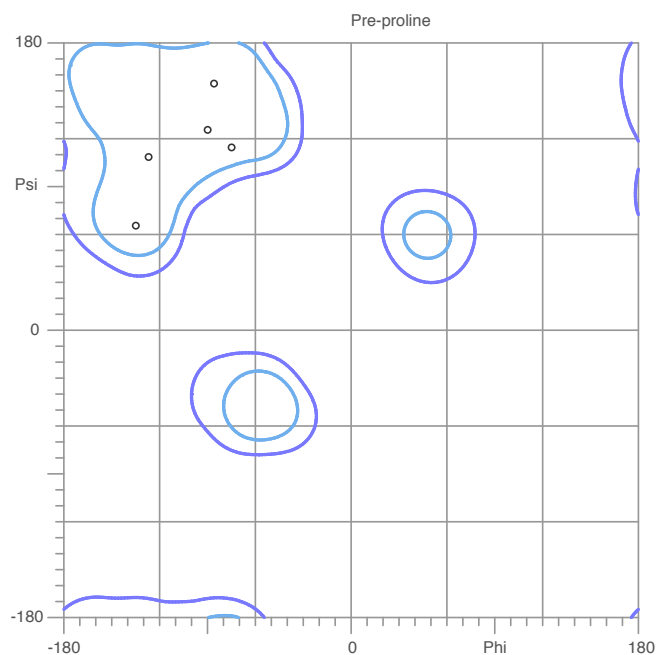
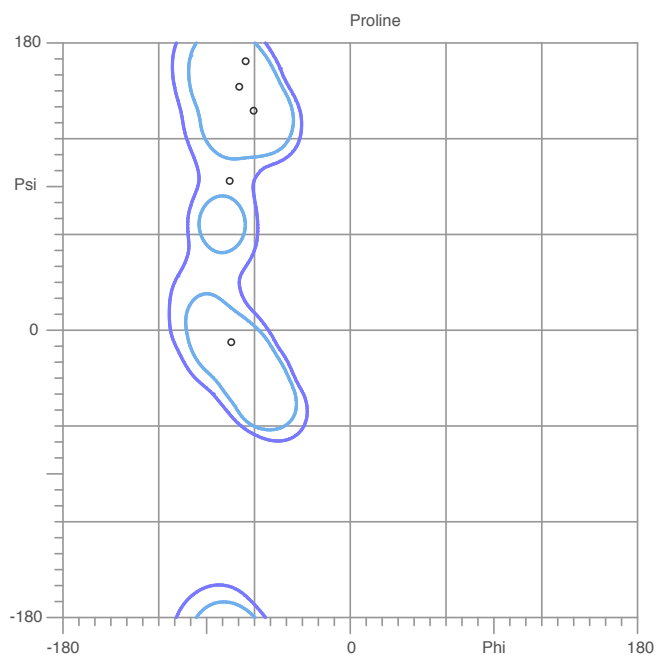
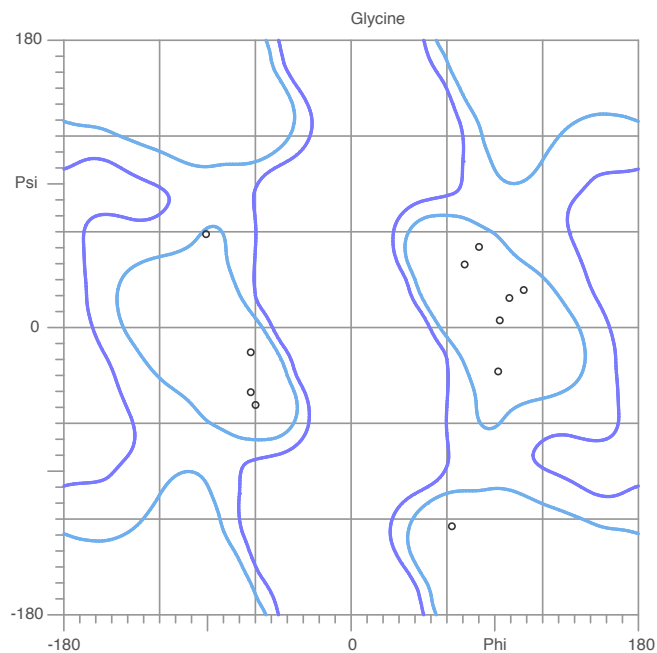
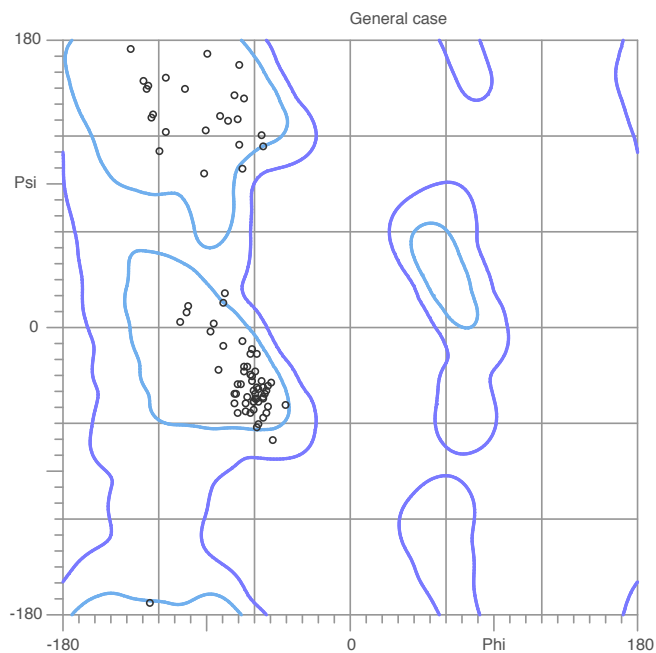
94.0% (94/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

There were no outliers.



# MolProbity Ramachandran analysis

2KIF.pdb, model 16



96.0% (96/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

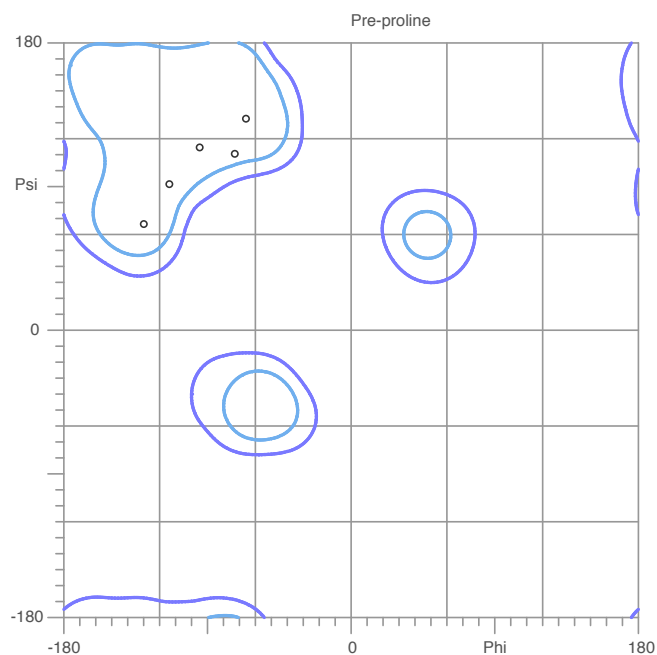
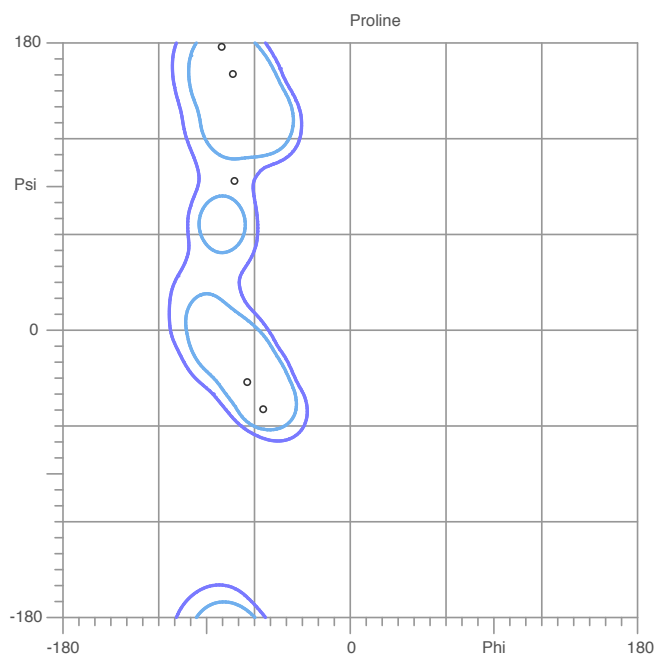
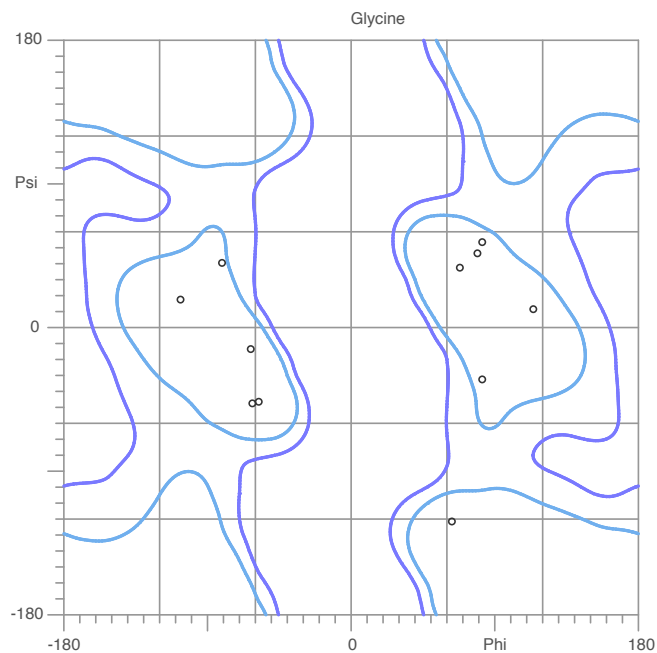
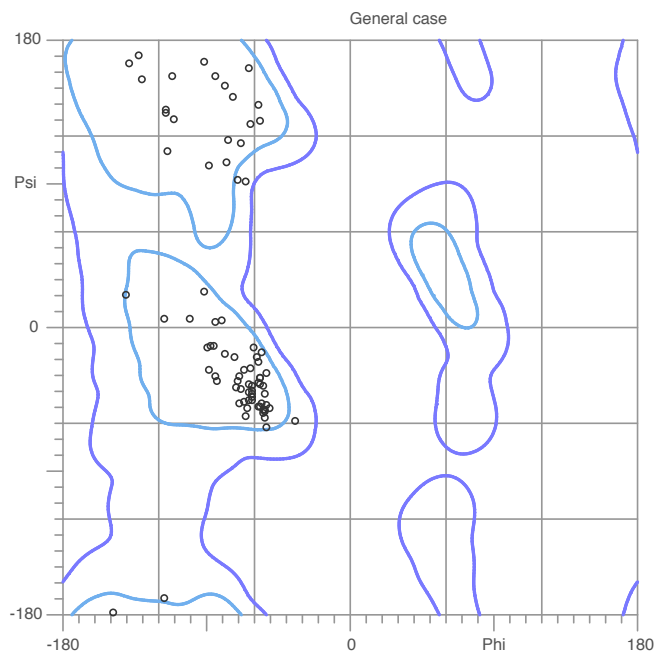
There were no outliers.

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

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# MolProbity Ramachandran analysis

2KIF.pdb, model 17



94.0% (94/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

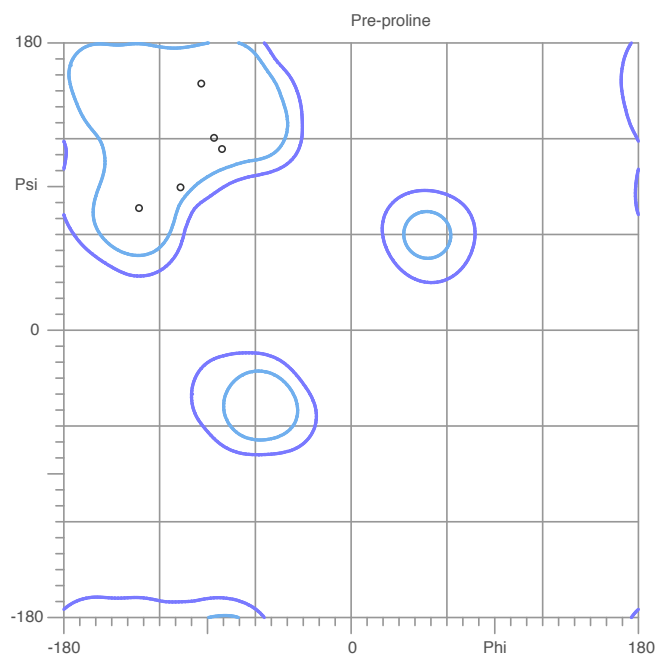
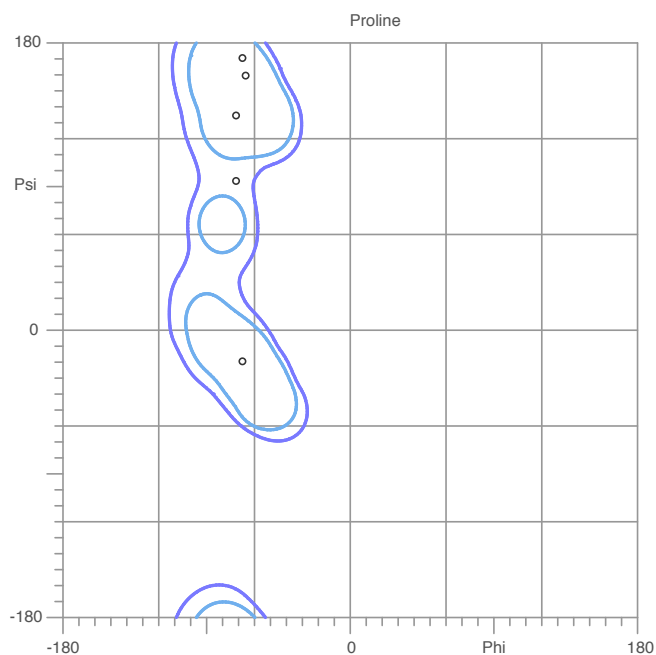
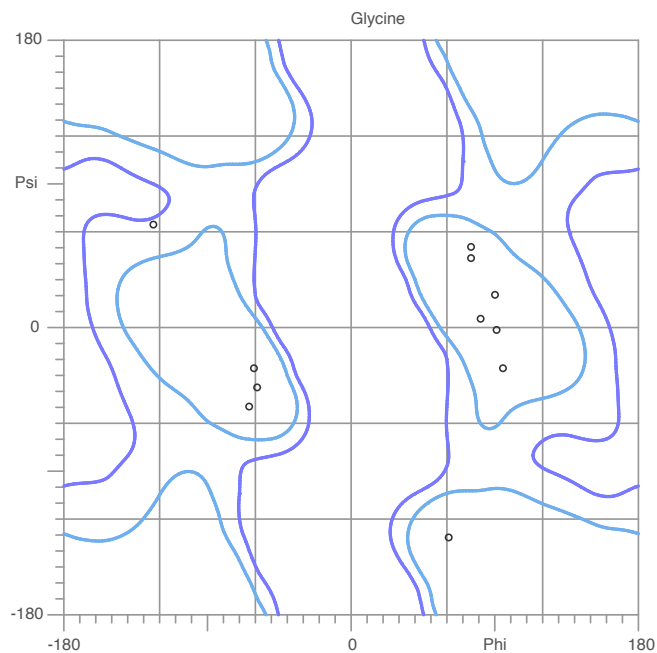
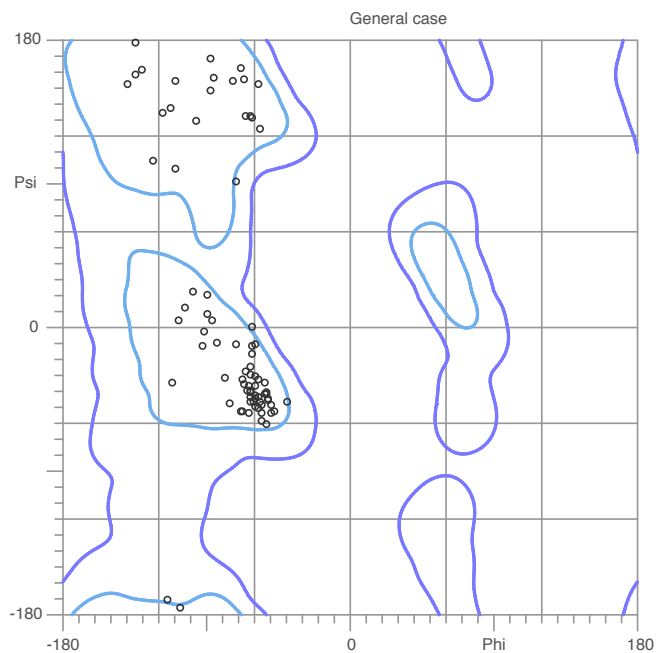
There were no outliers.

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

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# MolProbity Ramachandran analysis

2KIF.pdb, model 18



95.0% (95/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

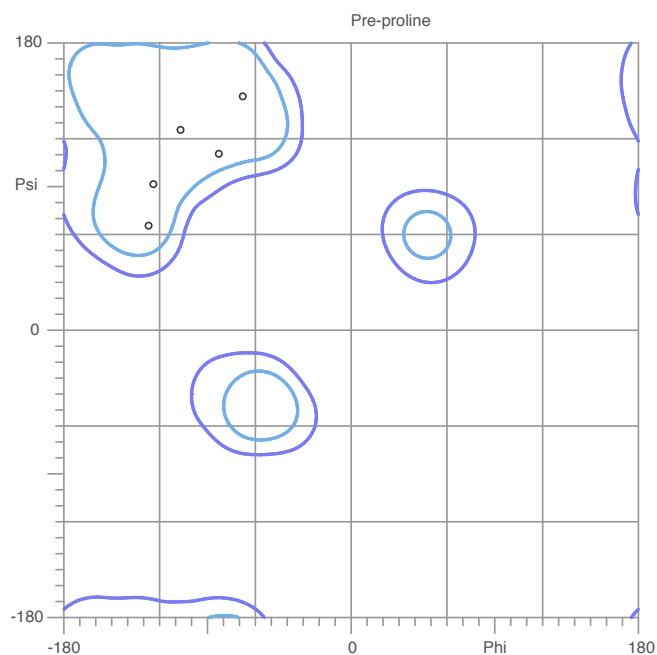
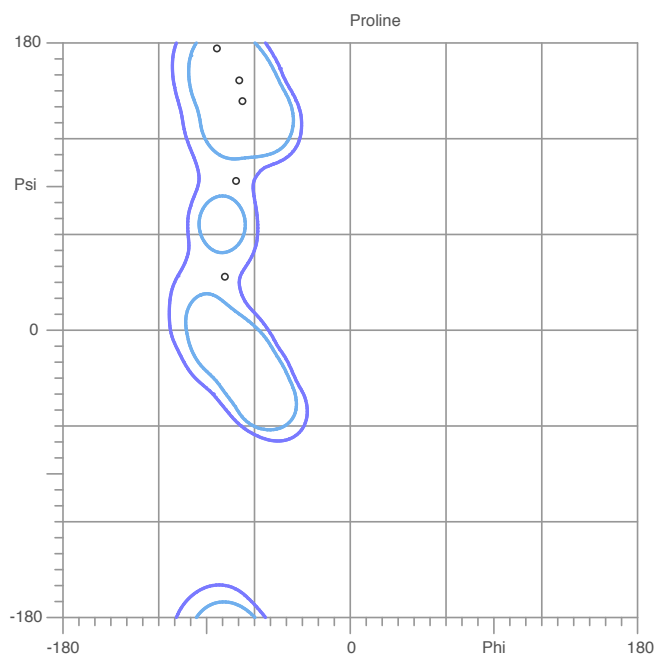
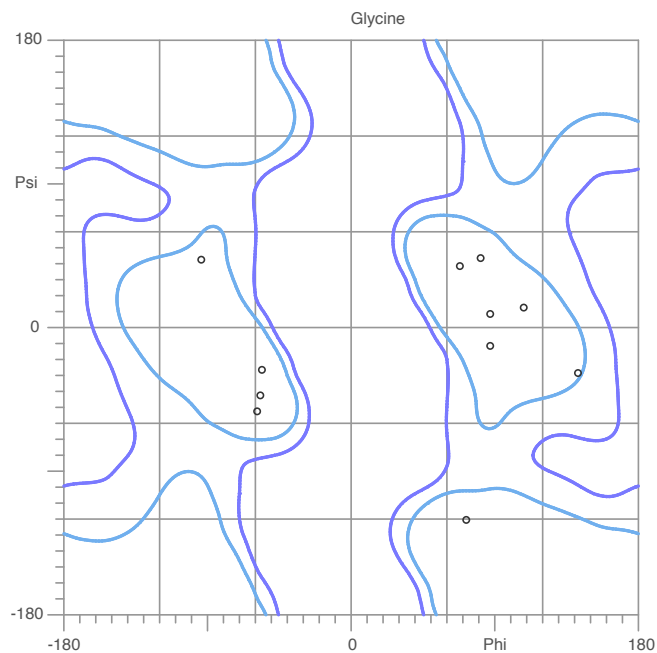
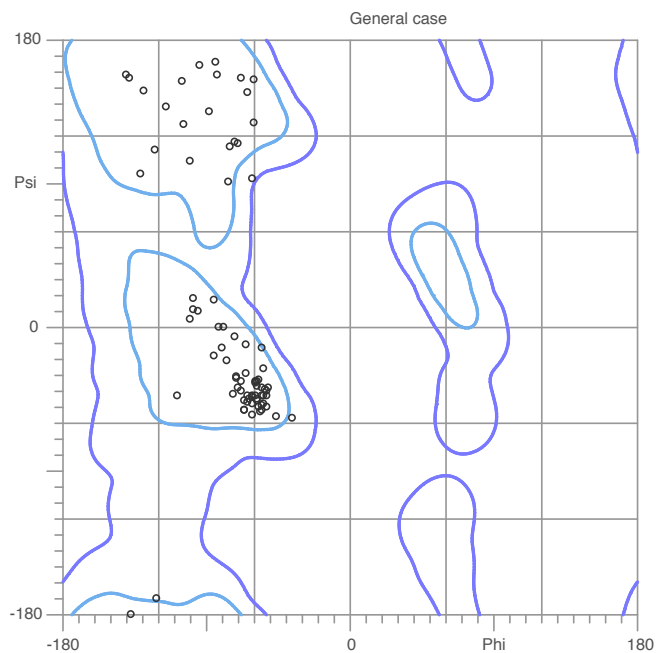
There were no outliers.

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

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

# MolProbity Ramachandran analysis

2KIF.pdb, model 19



95.0% (95/100) of all residues were in favored (98%) regions.  
100.0% (100/100) of all residues were in allowed (>99.8%) regions.

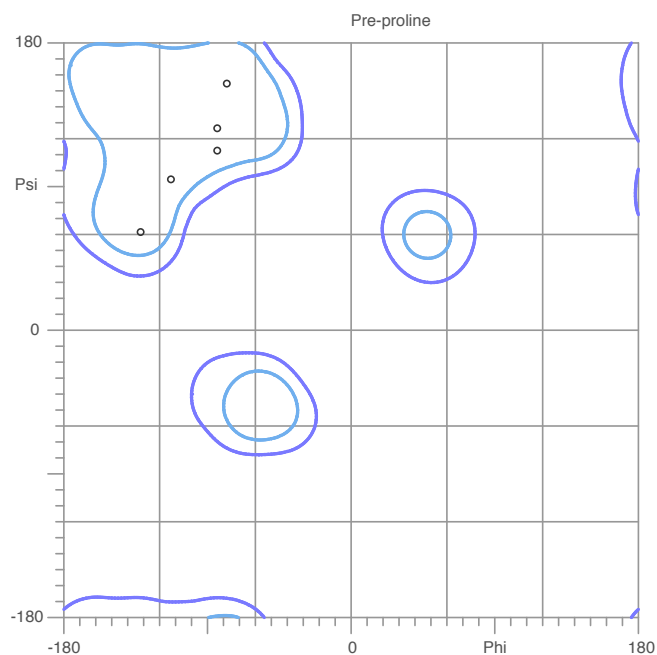
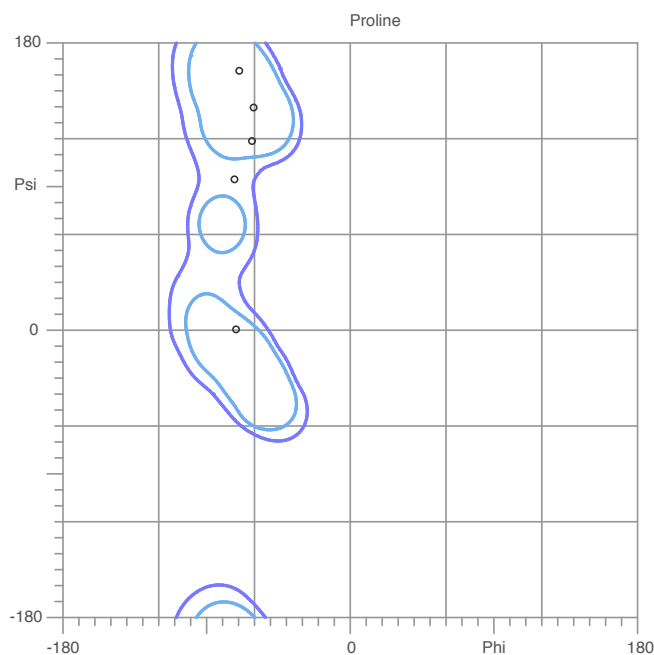
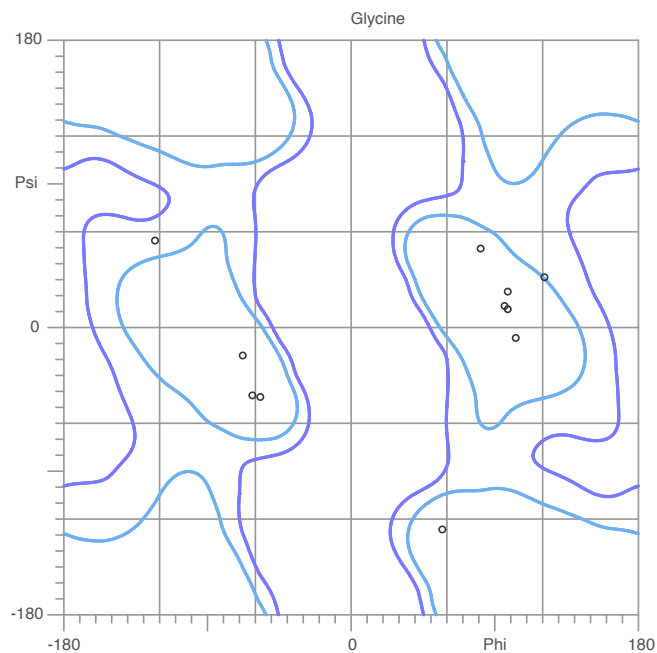
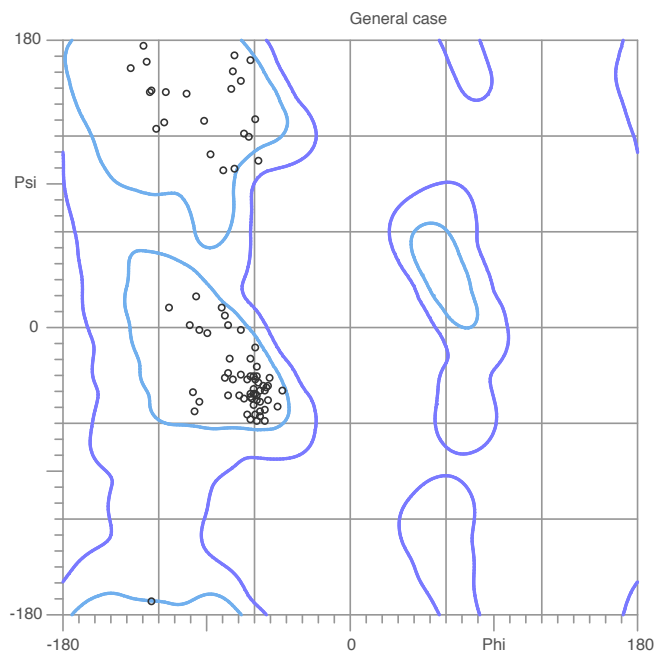
There were no outliers.

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

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

# MolProbity Ramachandran analysis

2KIF.pdb, model 20



96.0% (96/100) of all residues were in favored (98%) regions.  
100.0% (100/100) 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)