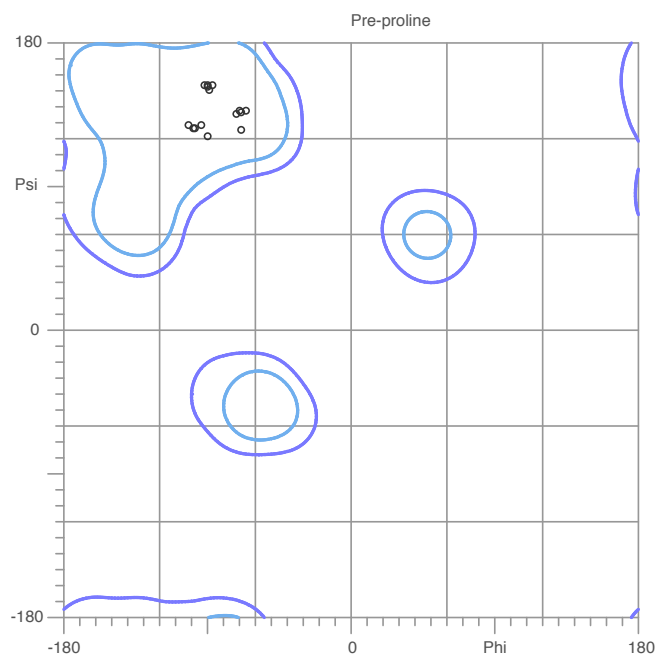
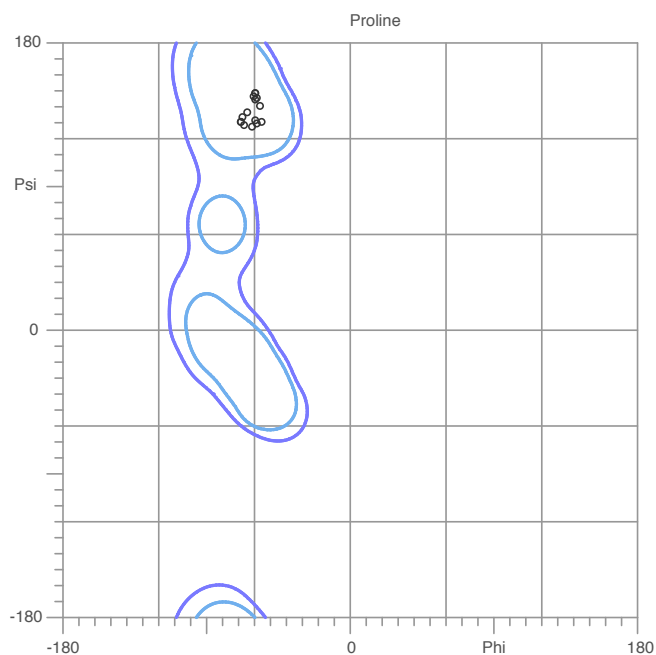
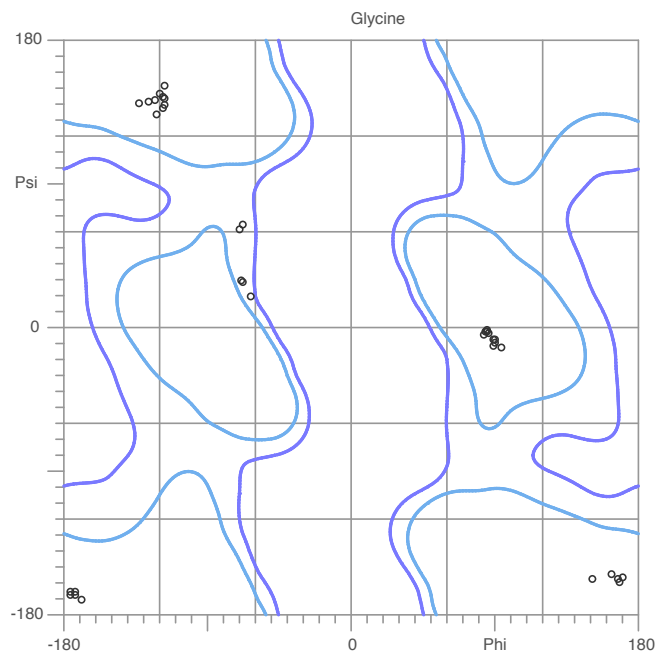
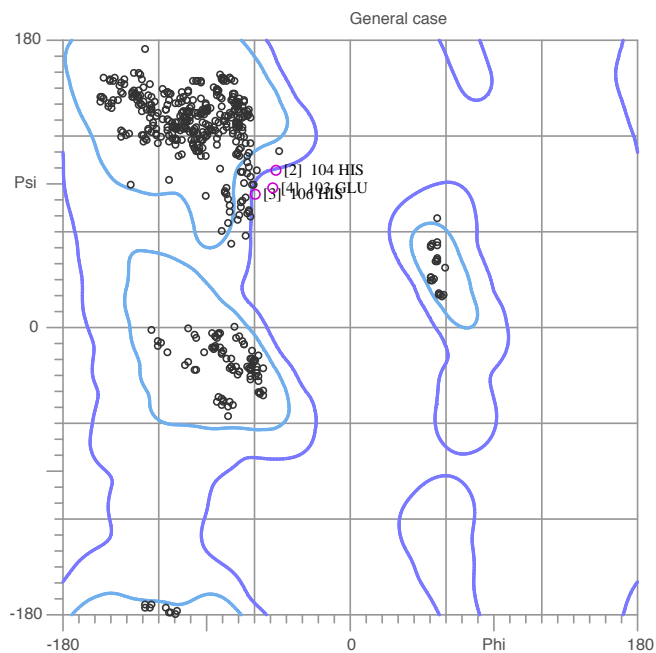


MolProbity Ramachandran analysis

2KBN_AF.pdb, all models



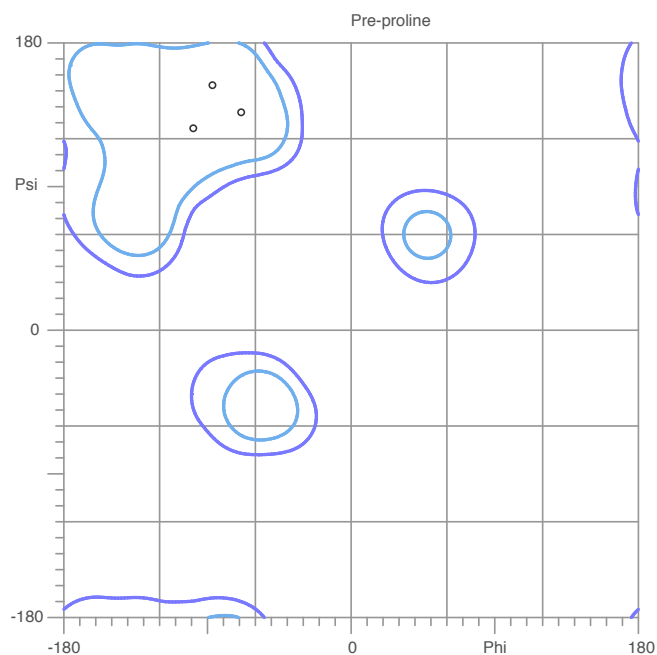
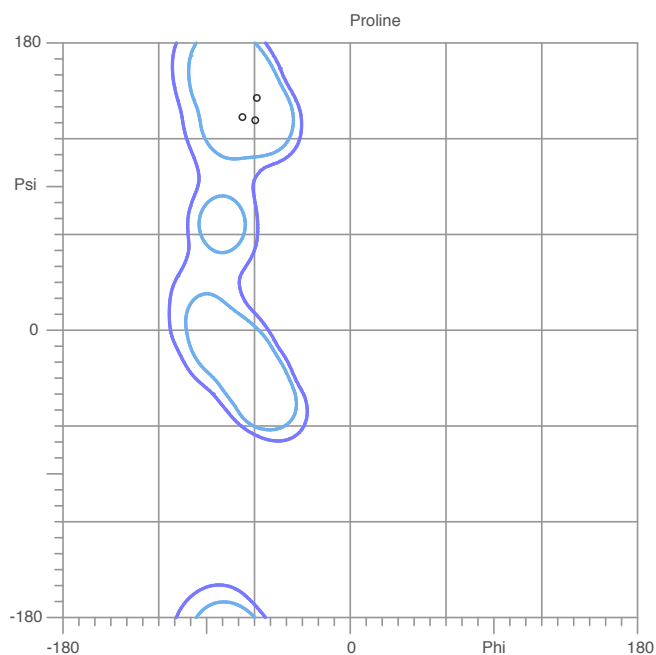
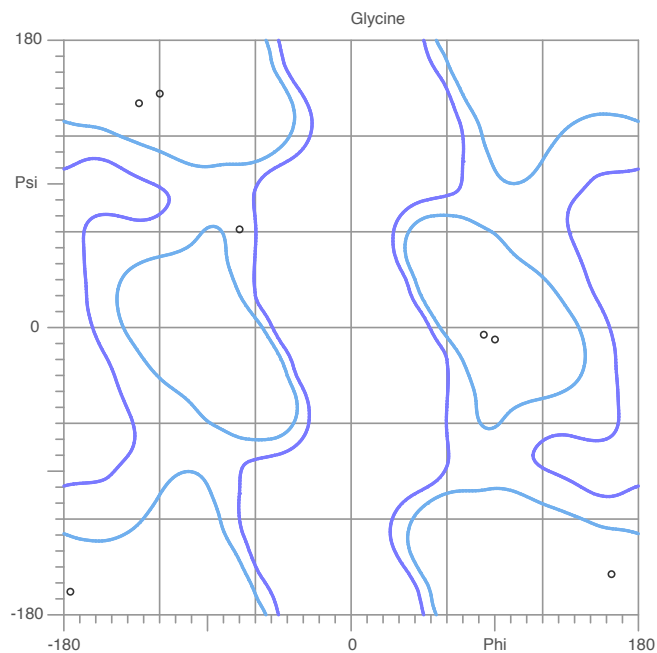
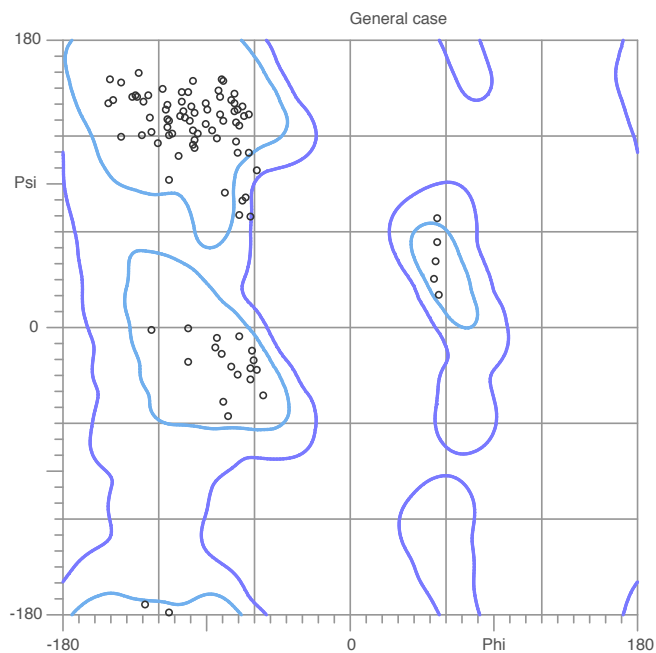
94.0% (503/535) of all residues were in favored (98%) regions.
99.4% (532/535) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 104 HIS (-47.2, 99.1)
- [3] 106 HIS (-60.8, 84.6)
- [4] 103 GLU (-49.8, 88.5)

MolProbity Ramachandran analysis

2KBN_AF.pdb, model 1



93.5% (100/107) of all residues were in favored (98%) regions.
100.0% (107/107) of all residues were in allowed (>99.8%) regions.

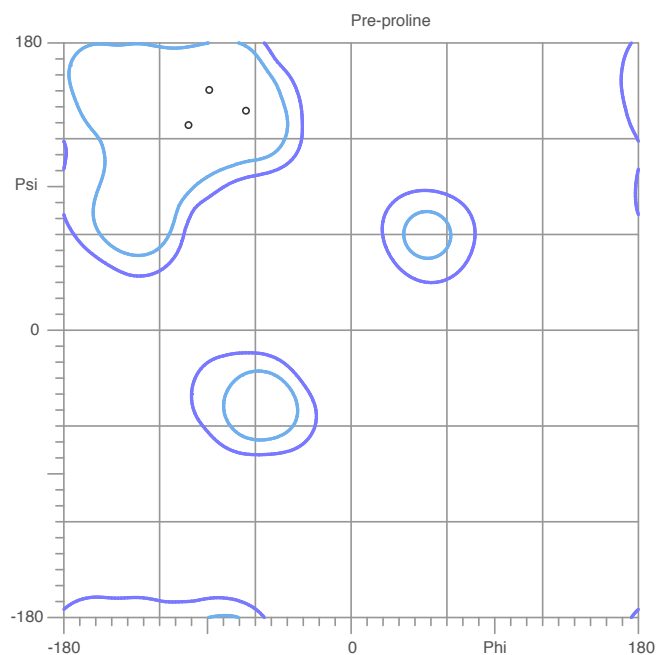
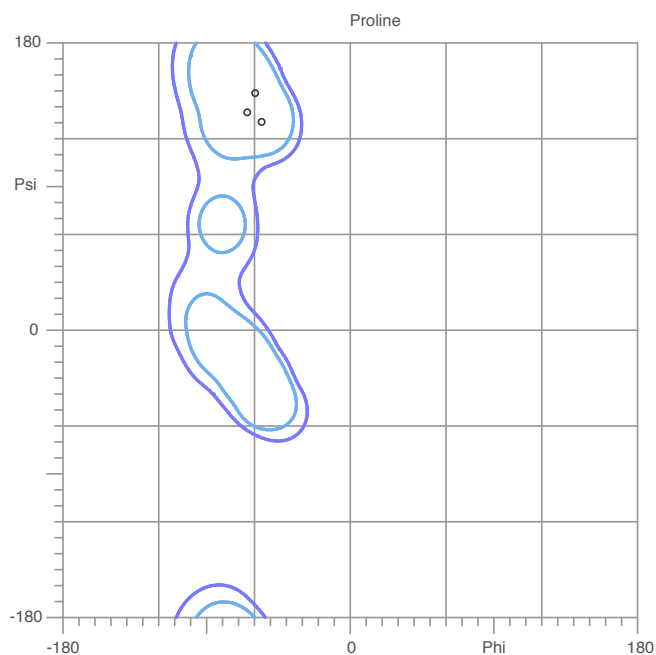
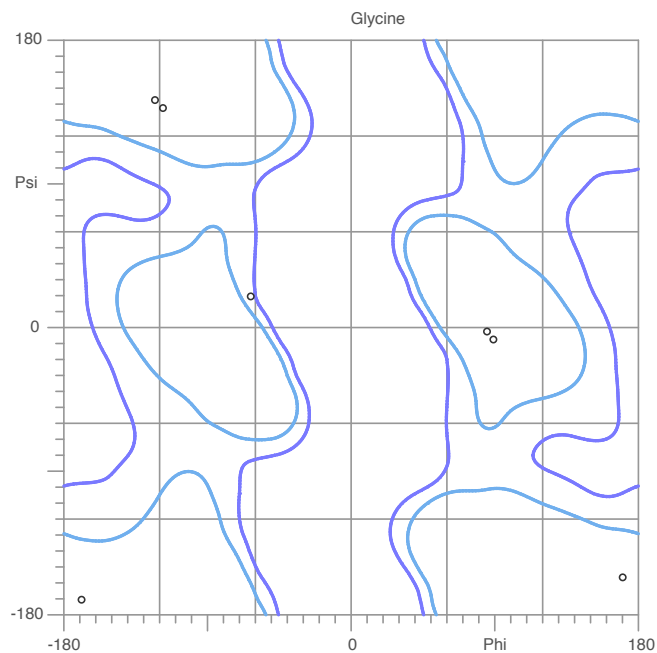
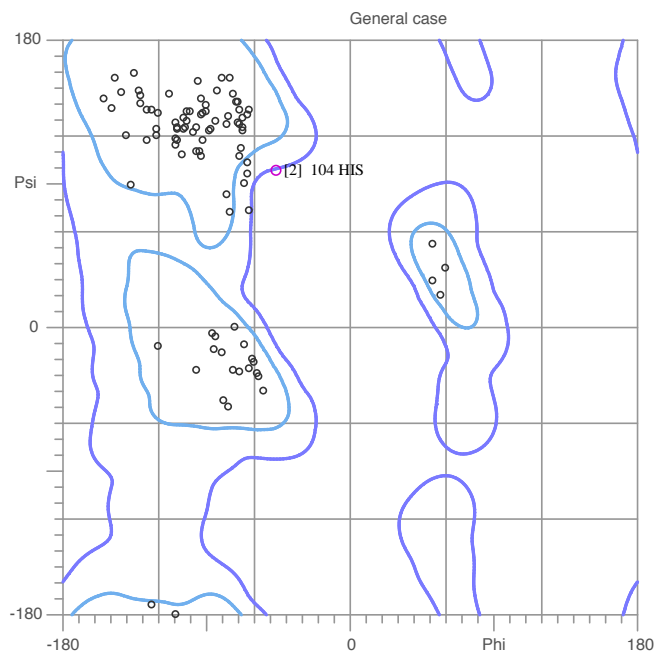
There were no outliers.

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MolProbity Ramachandran analysis

2KBN_AF.pdb, model 2



94.4% (101/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

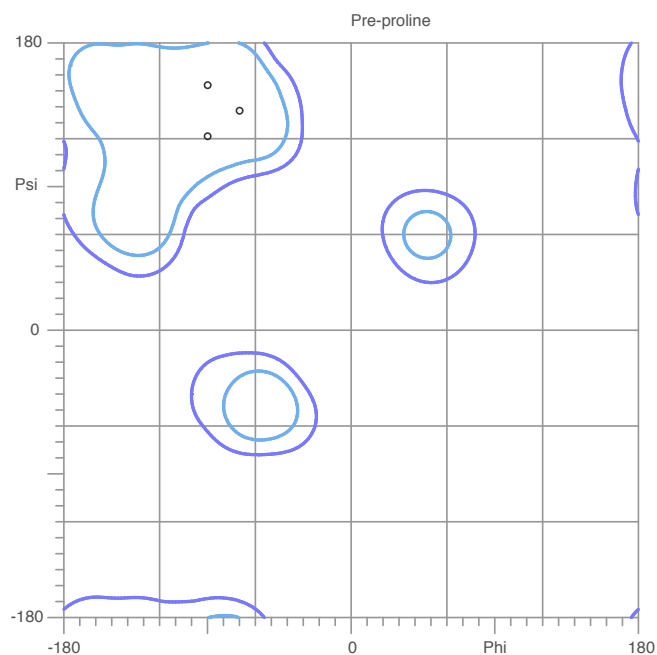
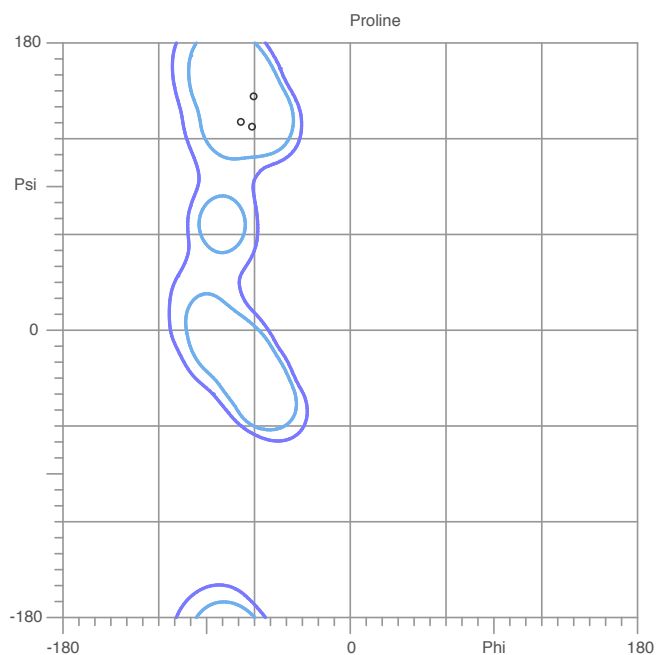
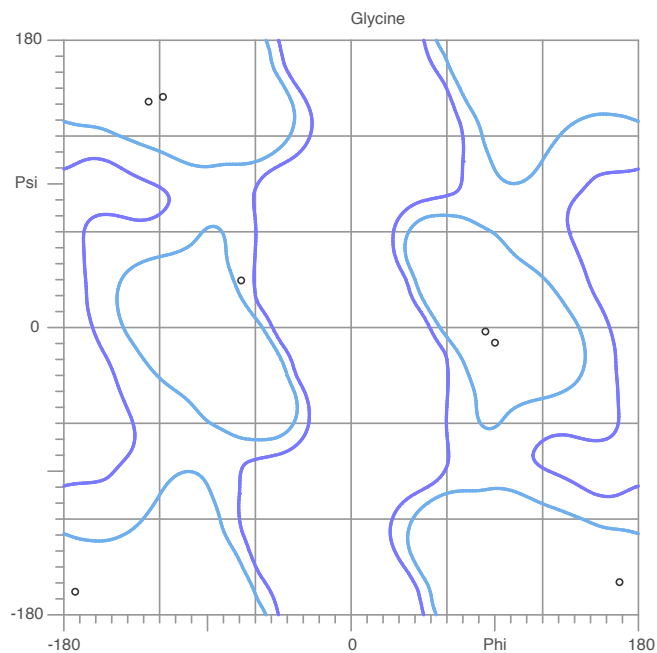
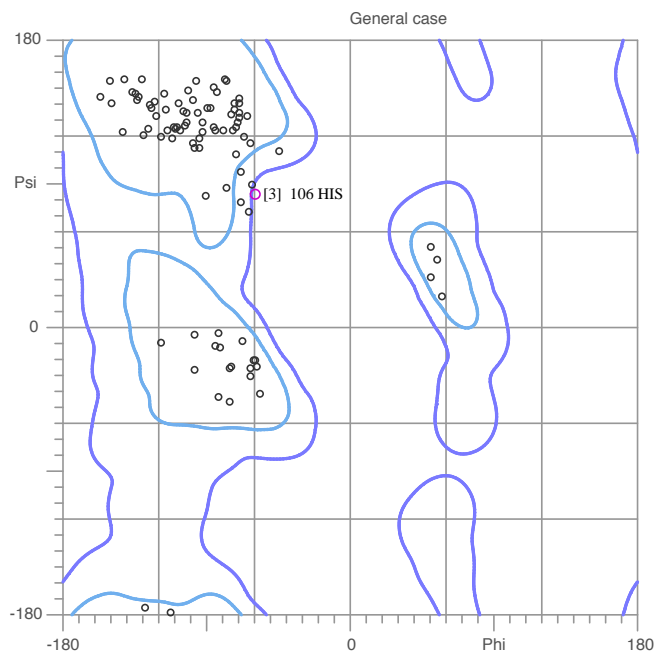
There were 1 outliers (phi, psi):
[2] 104 HIS (-47.2, 99.1)

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MolProbity Ramachandran analysis

2KBN_AF.pdb, model 3



93.5% (100/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

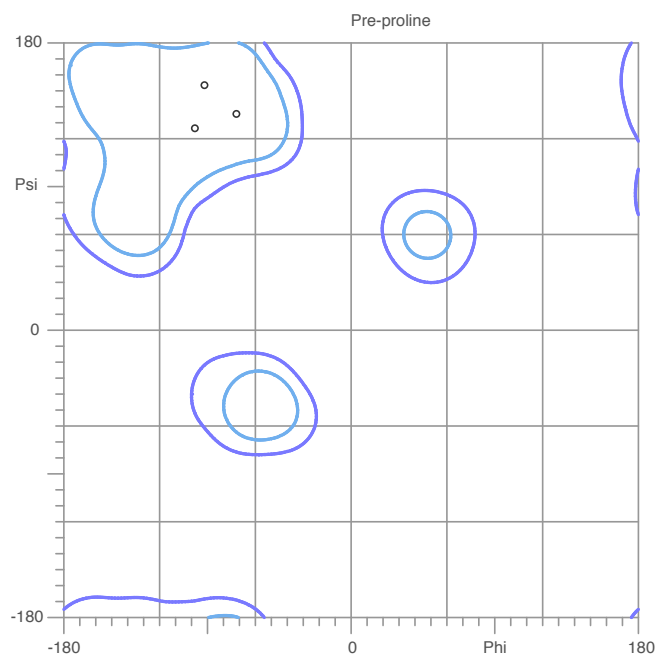
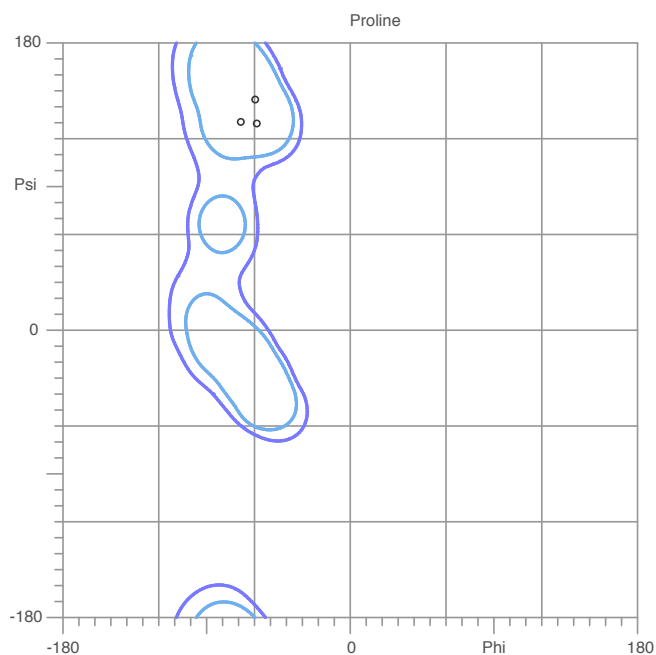
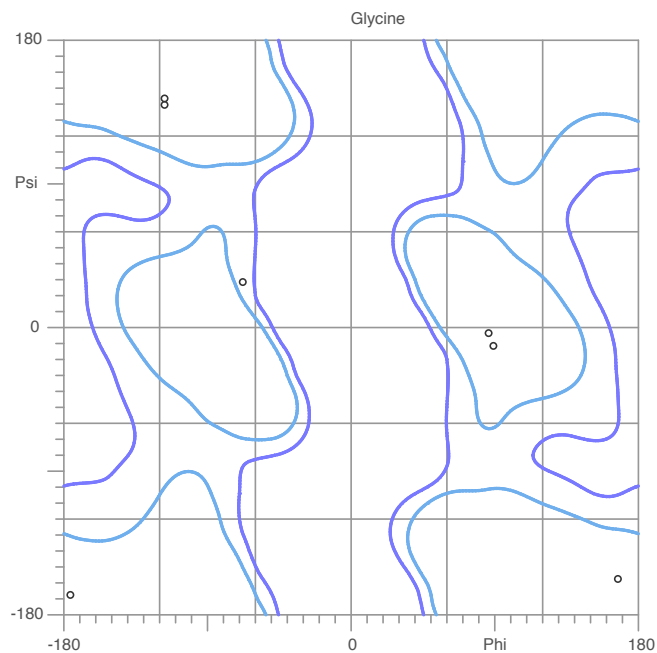
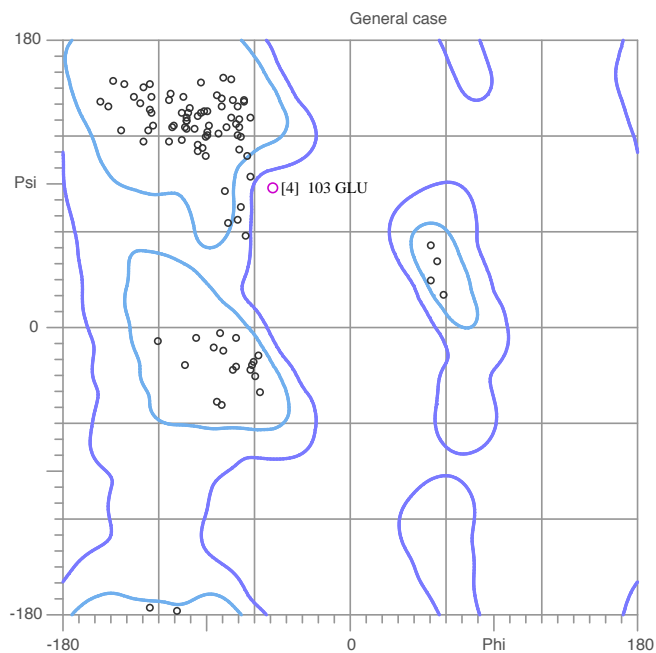
[3] 106 HIS (-60.8, 84.6)

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MolProbity Ramachandran analysis

2KBN_AF.pdb, model 4



94.4% (101/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

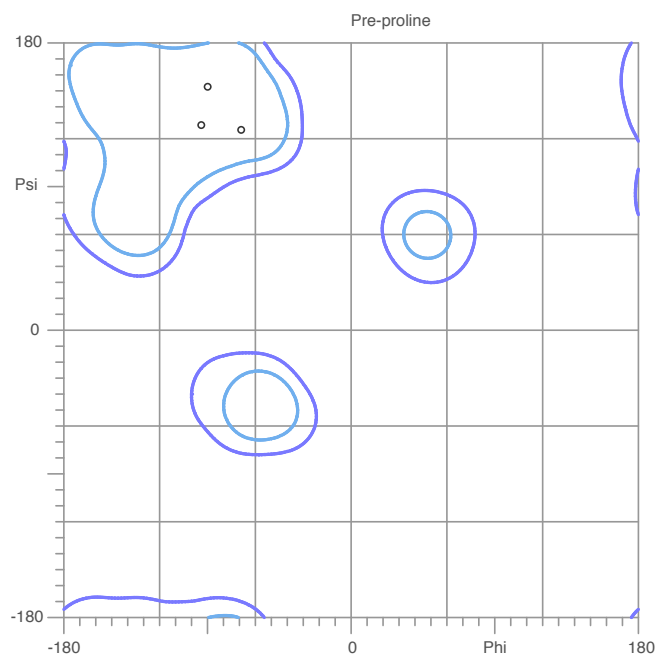
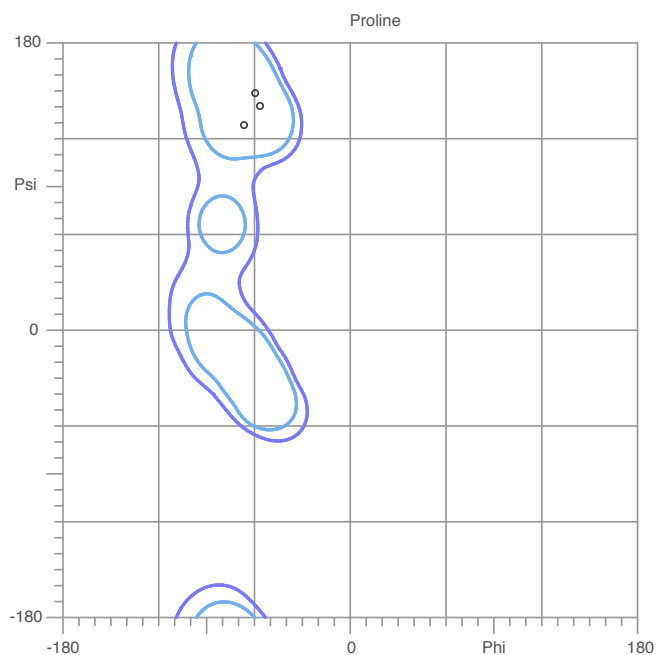
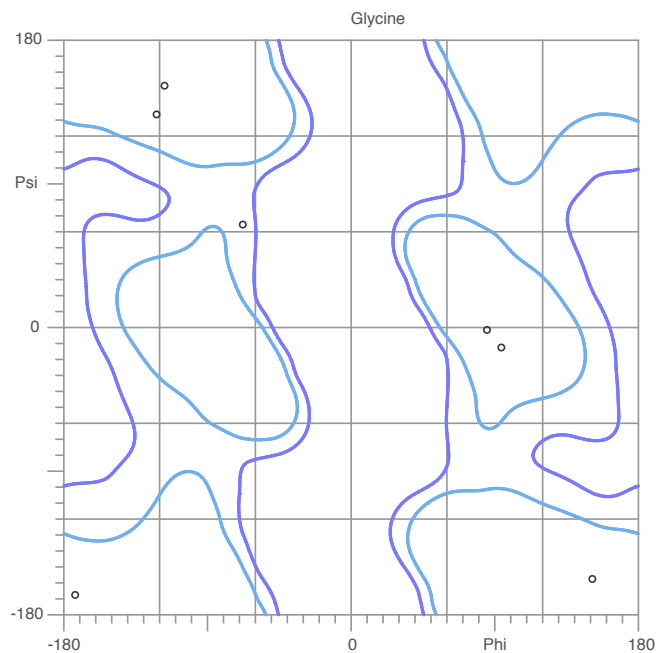
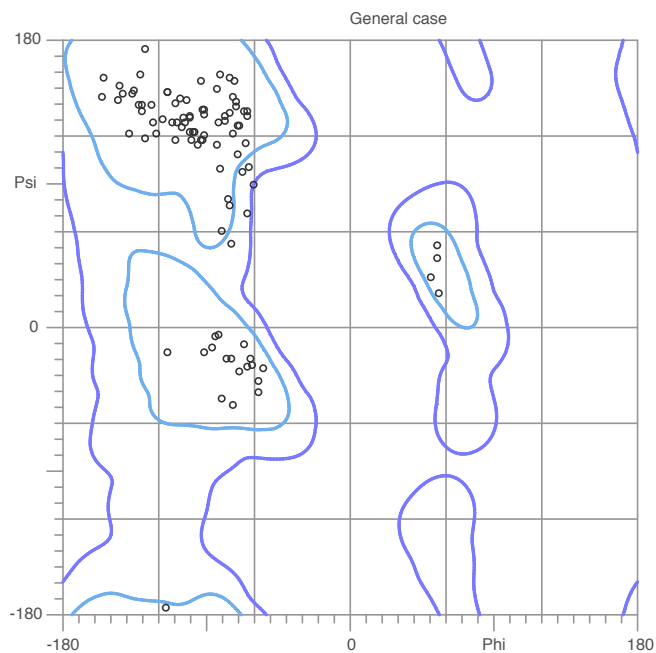
There were 1 outliers (phi, psi):
[4] 103 GLU (-49.8, 88.5)

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MolProbity Ramachandran analysis

2KBN_AF.pdb, model 5



94.4% (101/107) of all residues were in favored (98%) regions.
100.0% (107/107) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

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