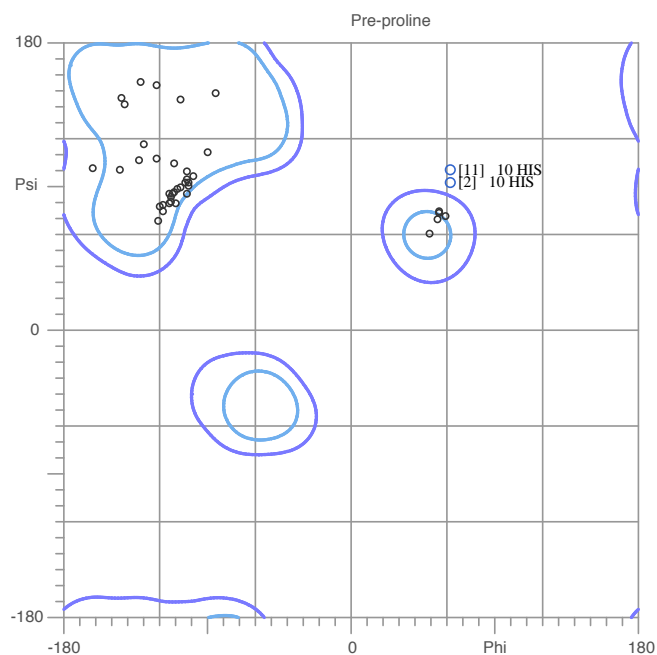
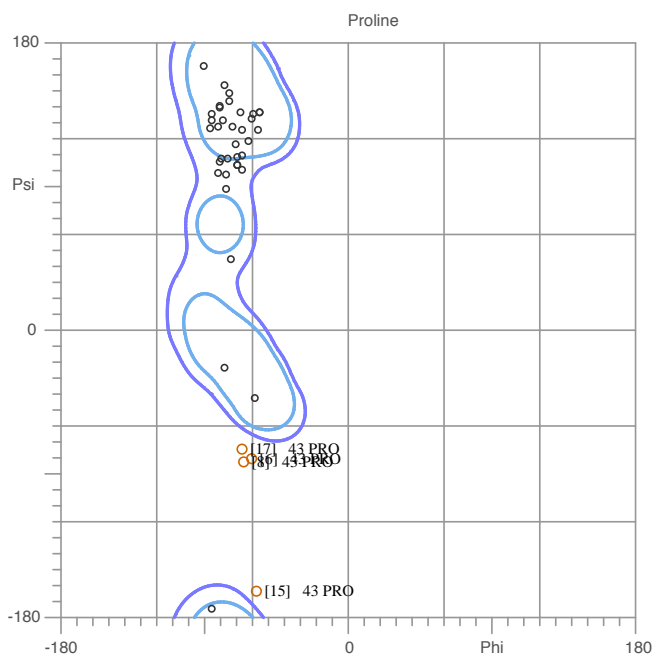
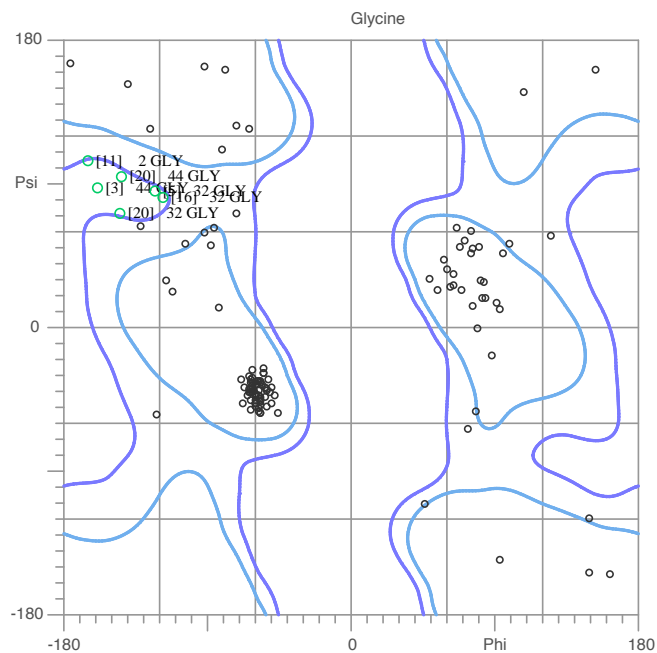
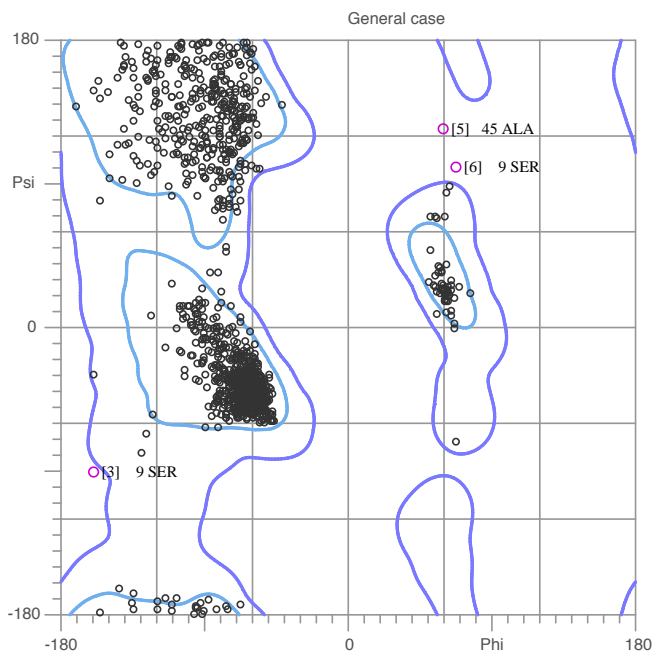


MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, all models



94.8% (1592/1680) of all residues were in favored (98%) regions.
99.1% (1665/1680) of all residues were in allowed (>99.8%) regions.

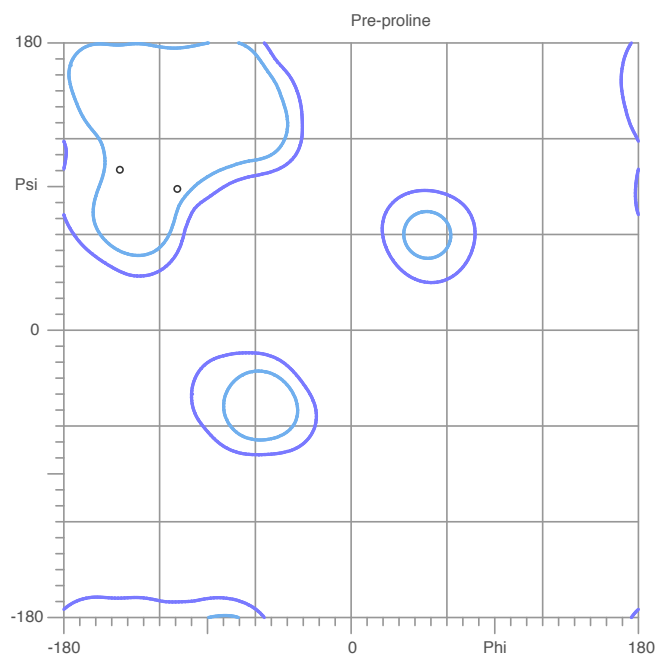
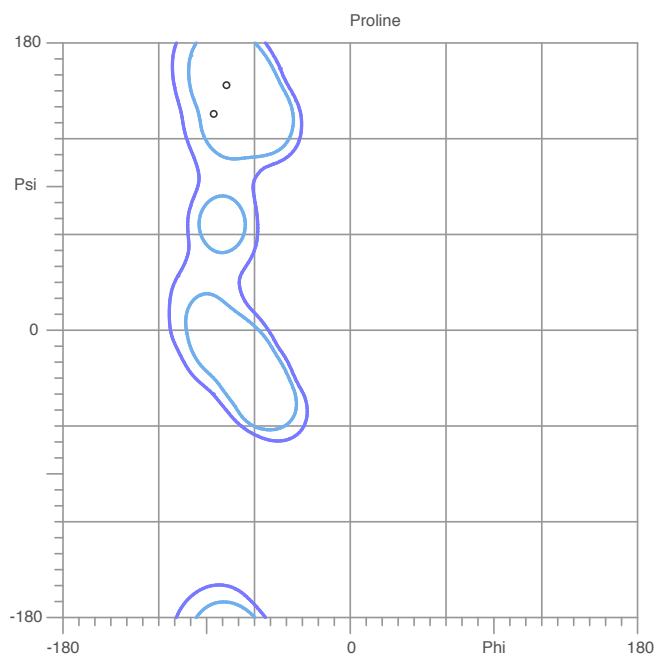
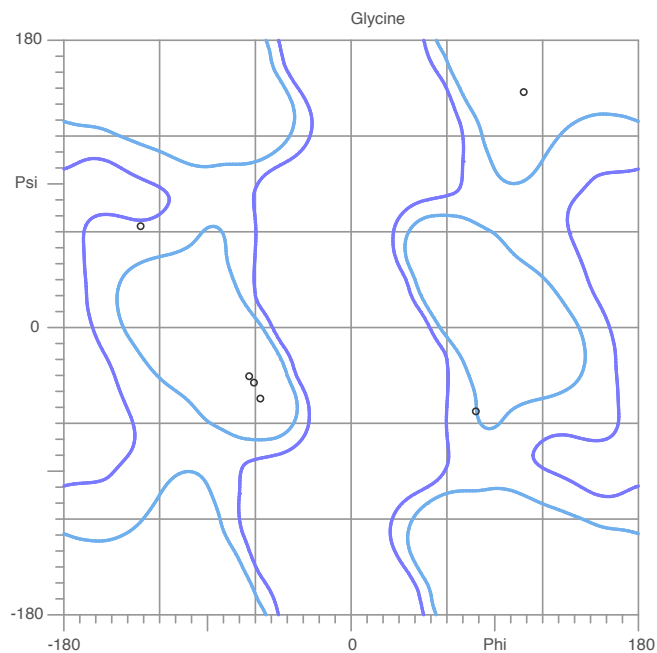
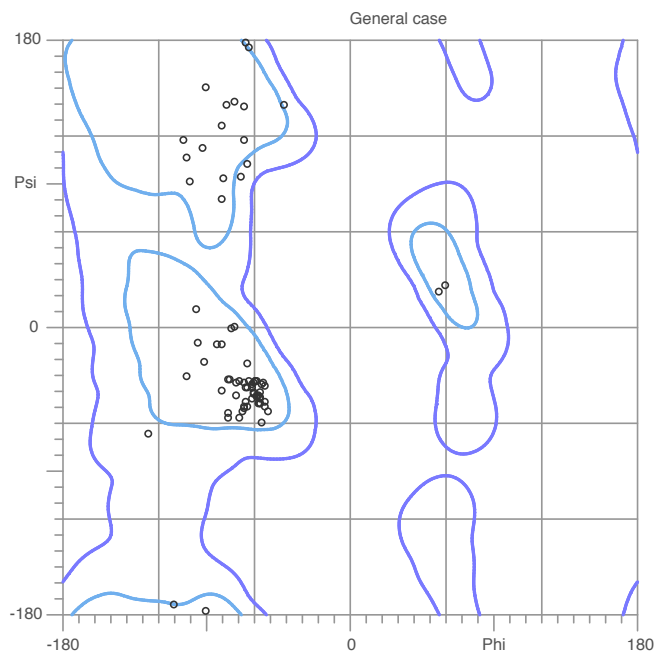
There were 15 outliers (phi, psi):

- [2] 10 HIS (62.4, 93.6)
- [3] 9 SER (-160.4, -90.9)
- [3] 44 GLY (-159.5, 88.1)
- [5] 32 GLY (-123.4, 86.0)
- [5] 45 ALA (60.0, 125.8)

- [6] 9 SER (67.3, 101.7)
- [6] 43 PRO (-61.9, -80.3)
- [8] 43 PRO (-66.9, -82.4)
- [11] 2 GLY (-165.6, 105.3)
- [11] 10 HIS (63.0, 102.0)
- [15] 43 PRO (-58.9, -164.0)
- [16] 32 GLY (-118.7, 82.4)
- [17] 43 PRO (-67.1, -74.1)
- [20] 32 GLY (-145.3, 72.1)
- [20] 44 GLY (-144.3, 95.0)

MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 1



89.3% (75/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

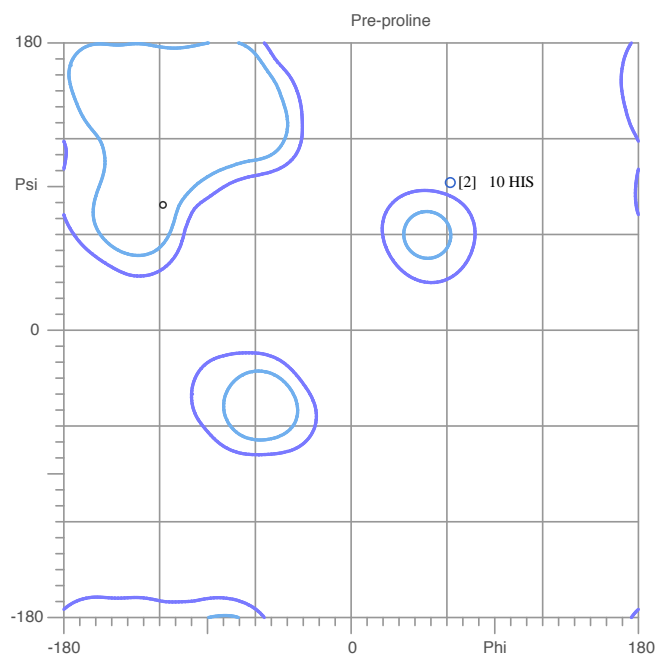
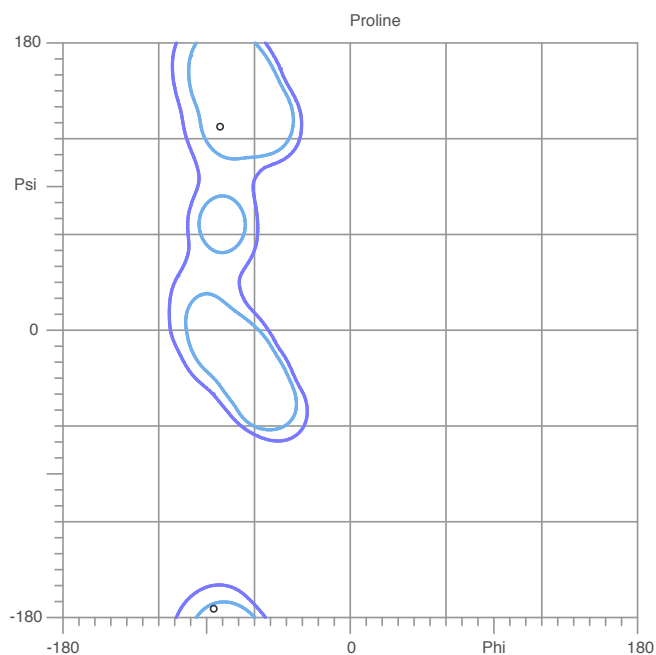
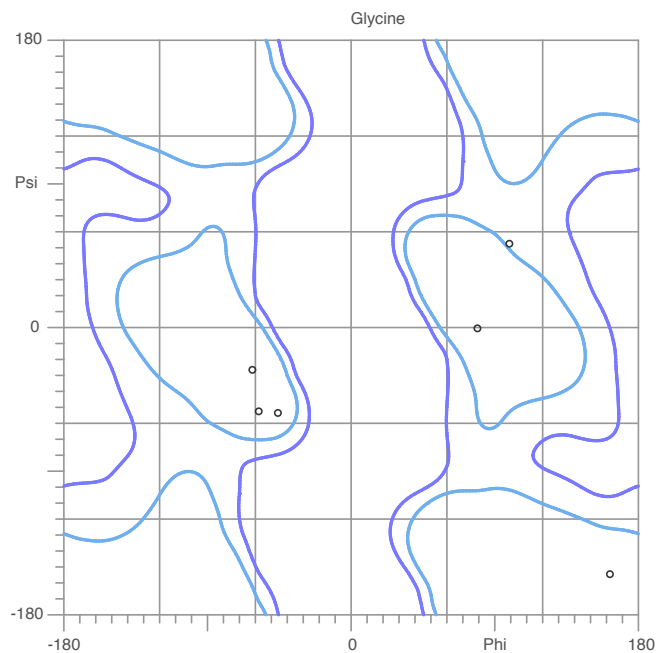
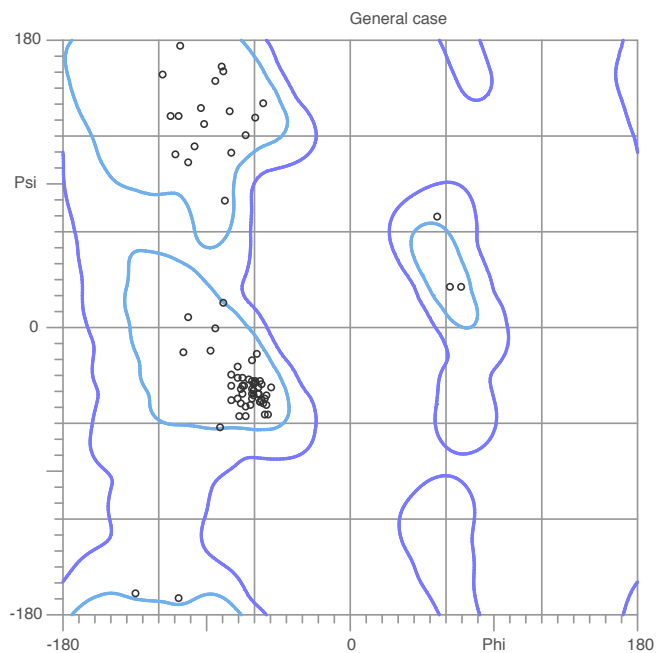
There were no outliers.

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

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 2



94.0% (79/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

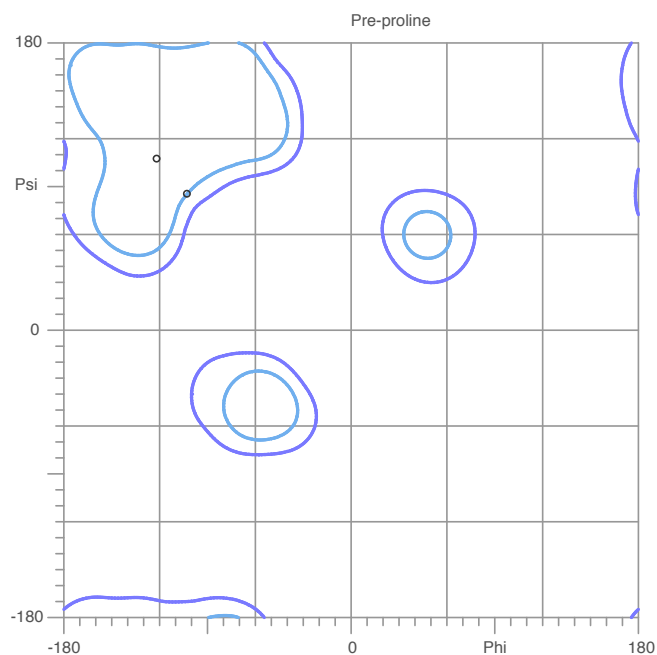
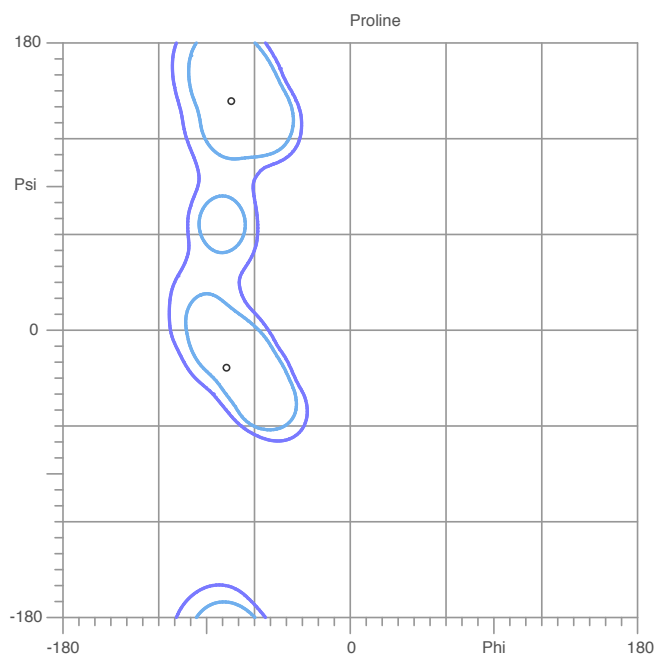
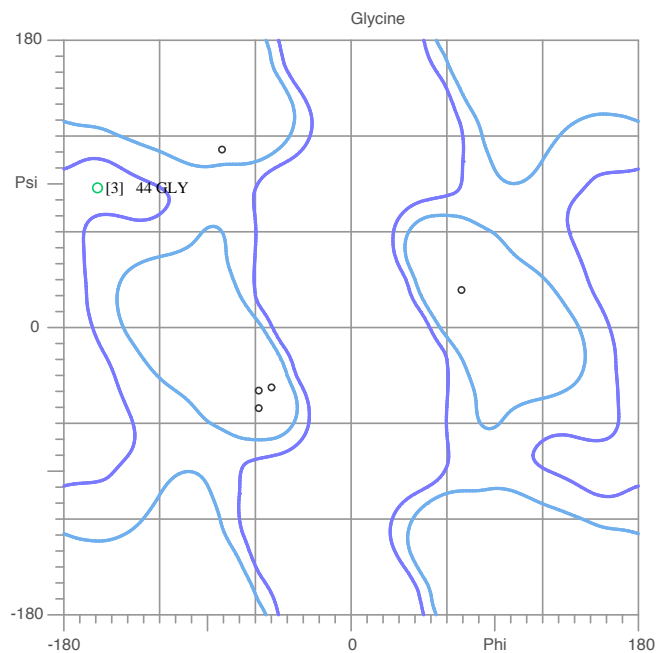
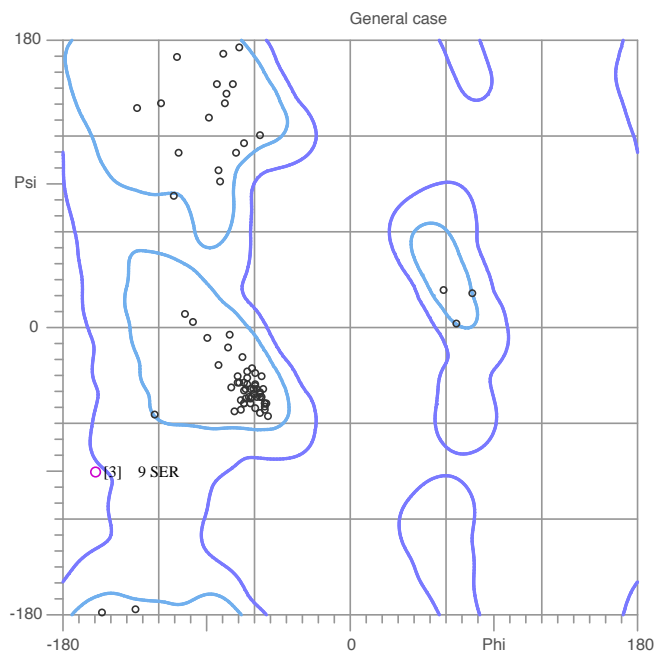
There were 1 outliers (phi, psi):
[2] 10 HIS (62.4, 93.6)

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

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 3



95.2% (80/84) of all residues were in favored (98%) regions.
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

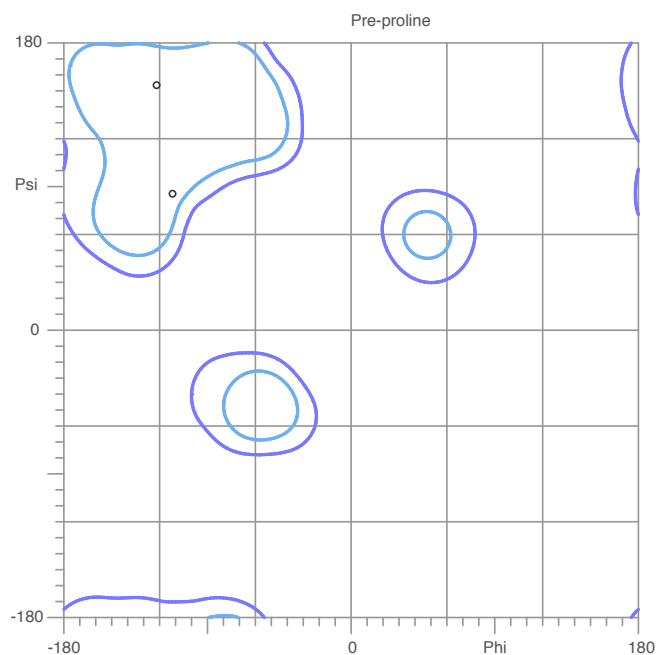
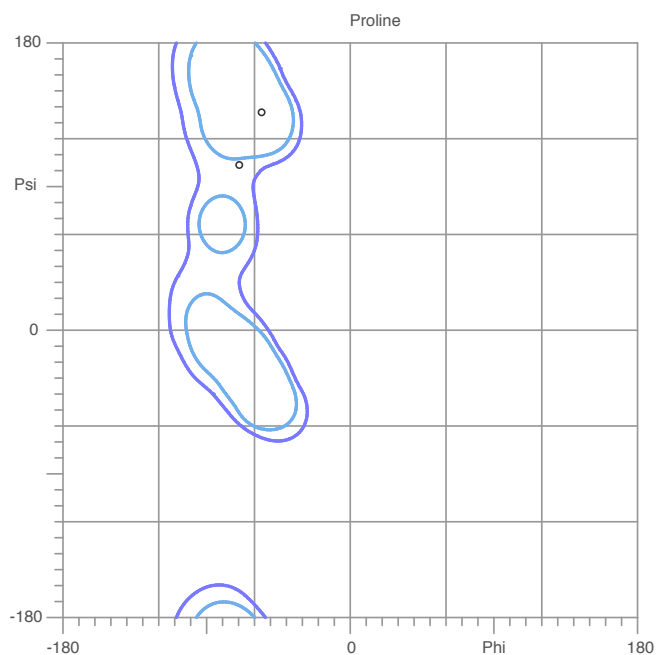
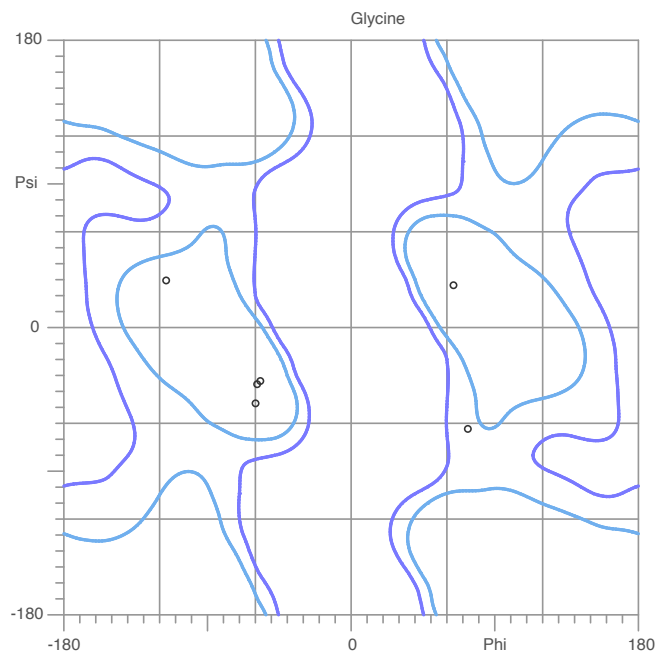
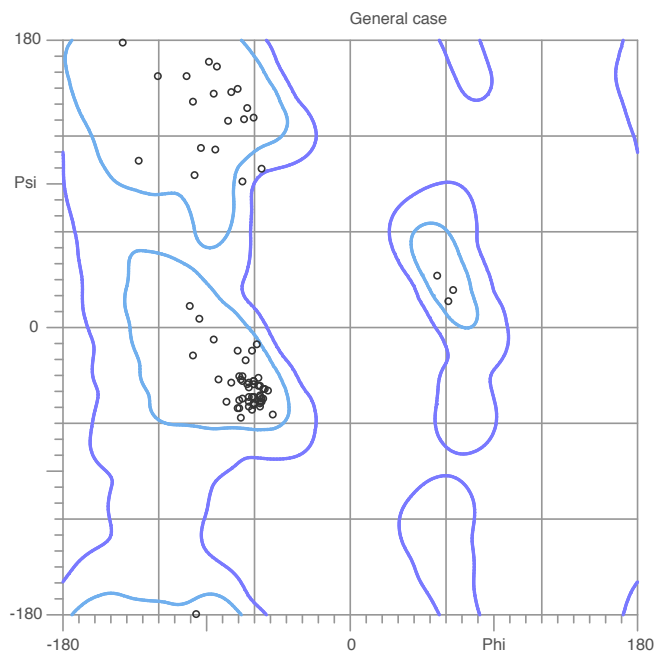
There were 2 outliers (phi, psi):

[3] 9 SER (-160.4, -90.9)

[3] 44 GLY (-159.5, 88.1)

MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 4



95.2% (80/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

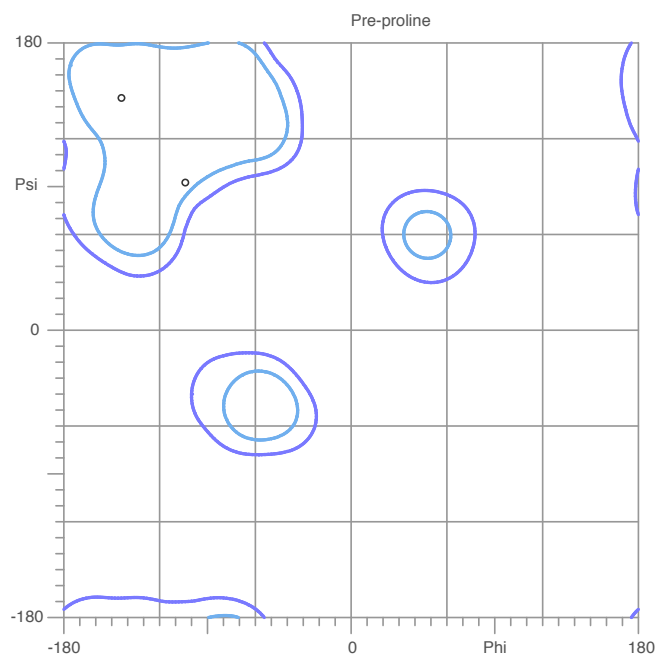
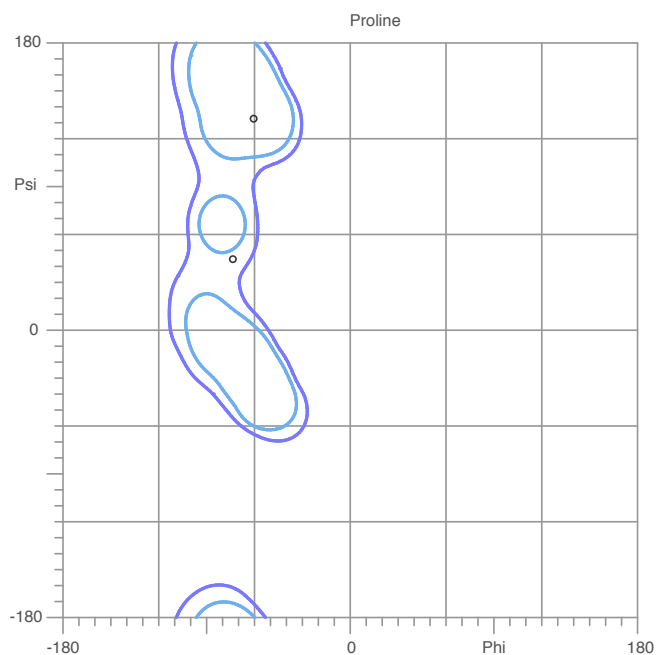
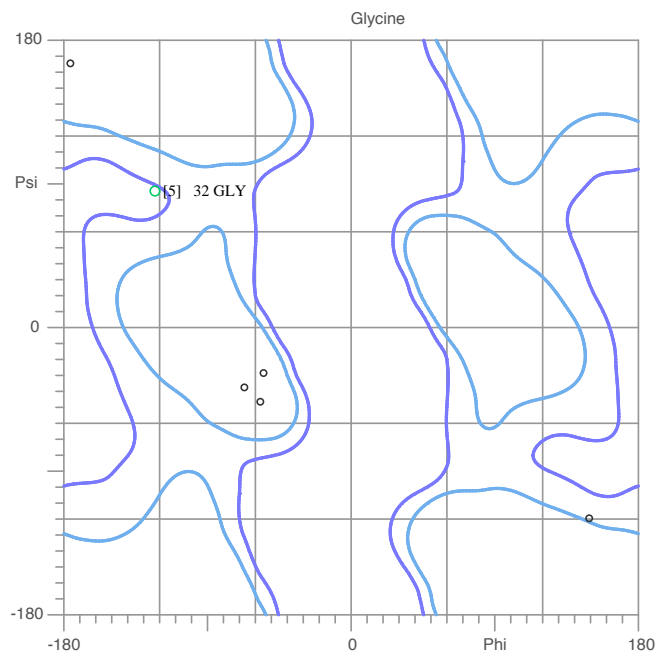
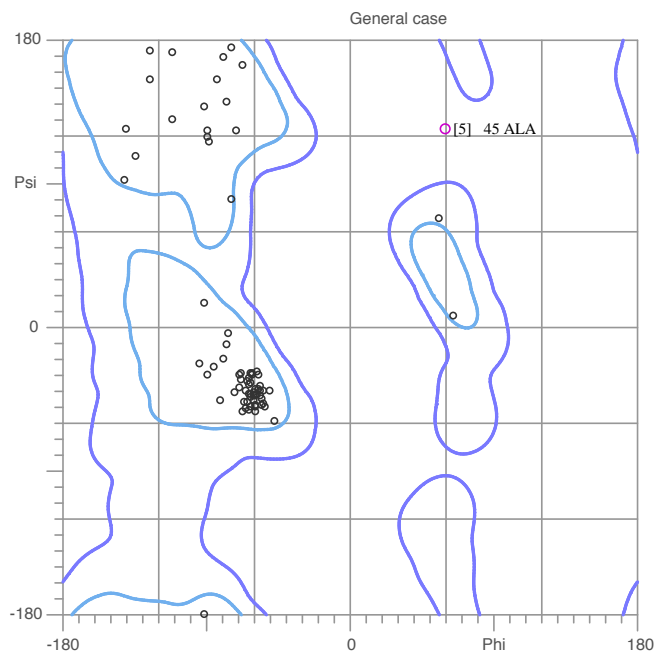
There were no outliers.

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

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 5



94.0% (79/84) of all residues were in favored (98%) regions.
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

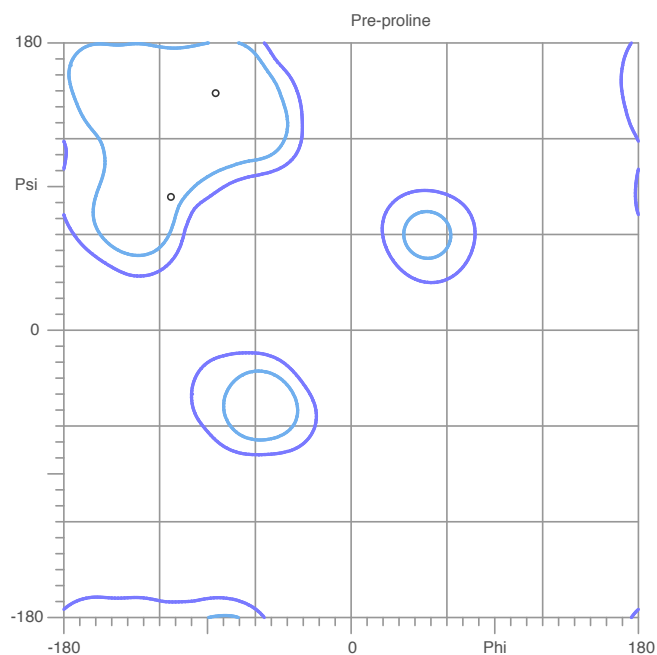
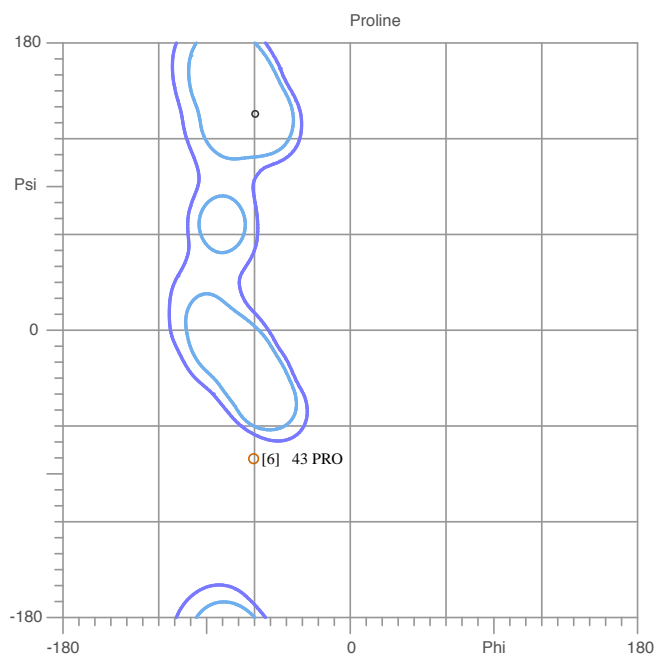
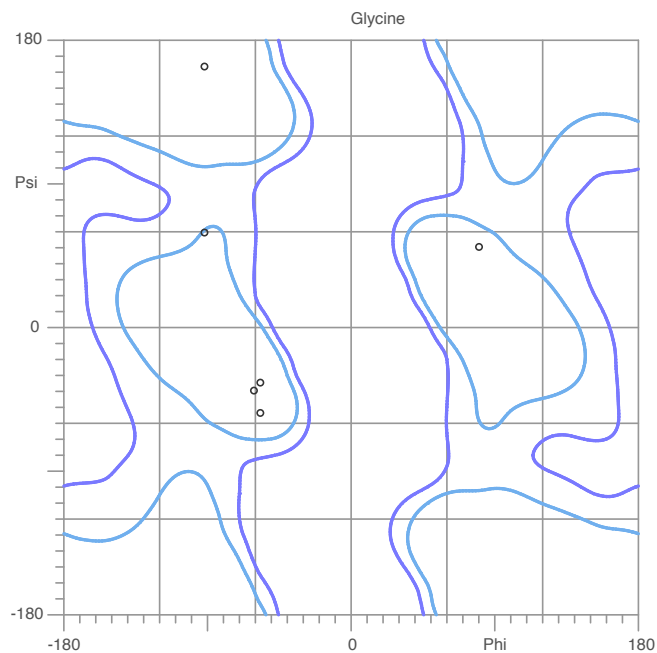
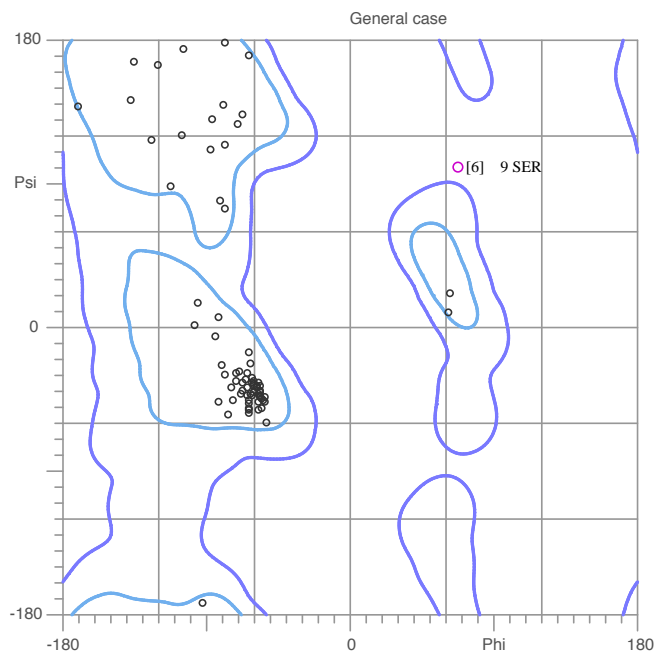
There were 2 outliers (phi, psi):

[5] 32 GLY (-123.4, 86.0)

[5] 45 ALA (60.0, 125.8)

MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 6



96.4% (81/84) of all residues were in favored (98%) regions.
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

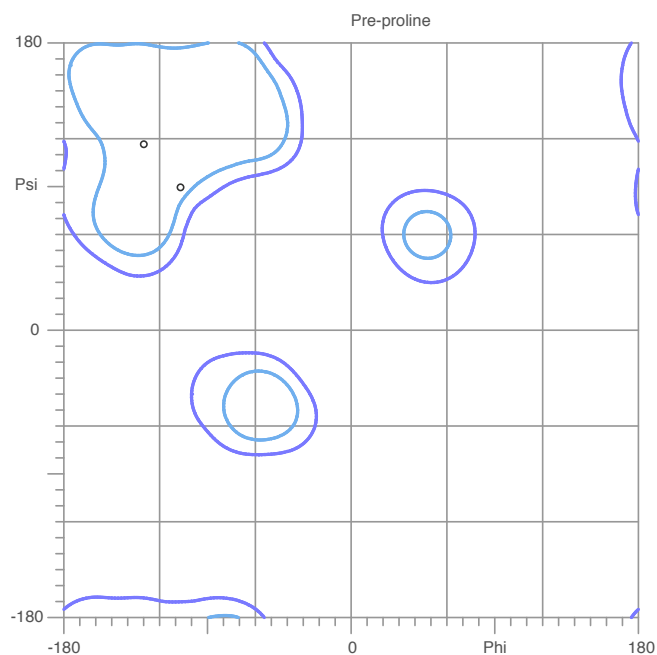
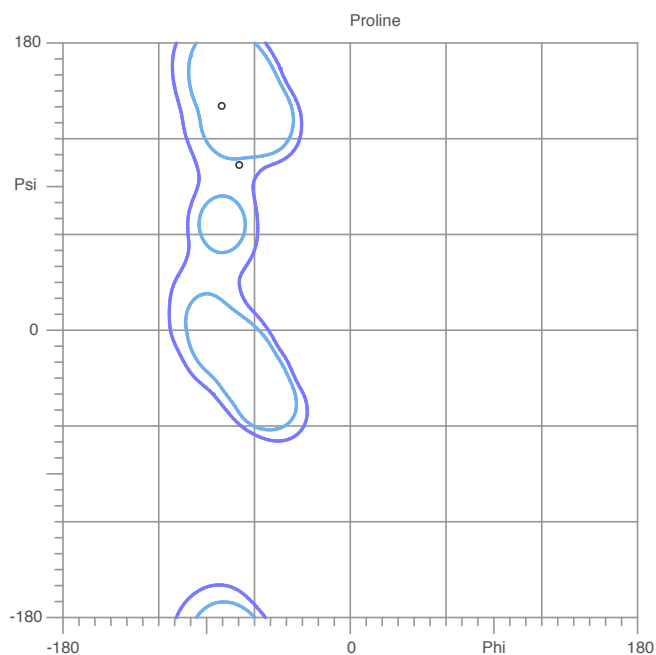
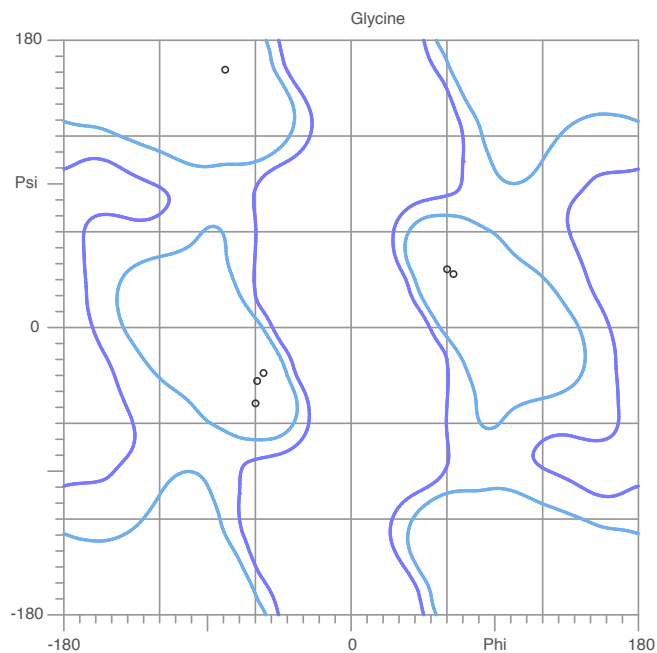
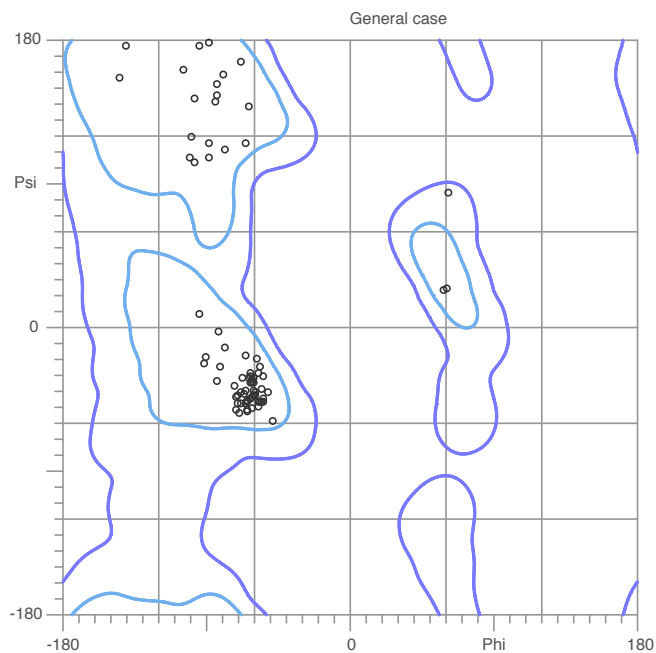
There were 2 outliers (phi, psi):

[6] 9 SER (67.3, 101.7)

[6] 43 PRO (-61.9, -80.3)

MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 7



97.6% (82/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

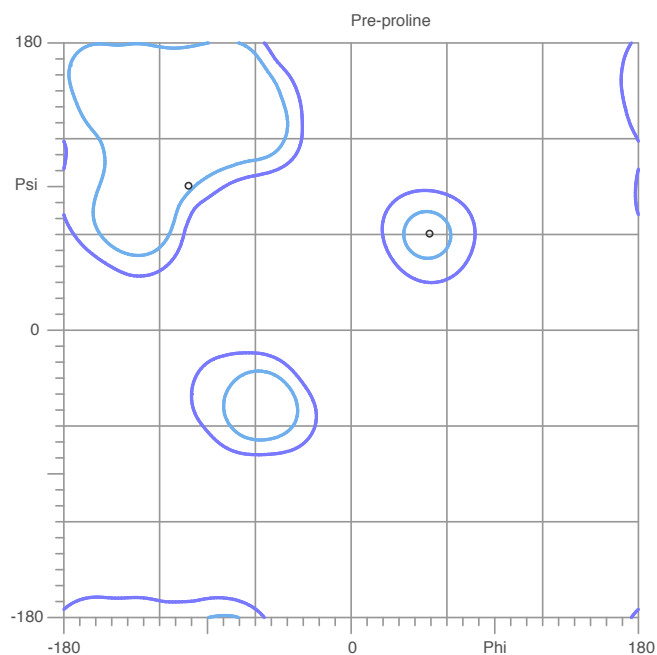
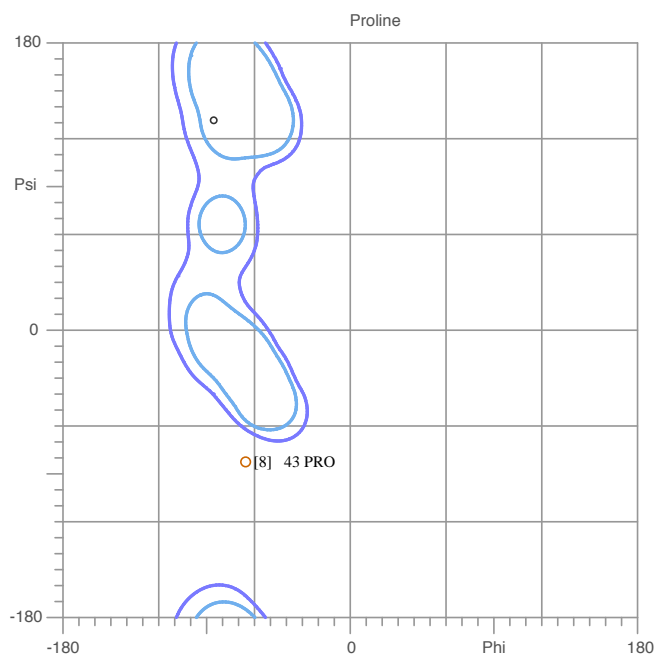
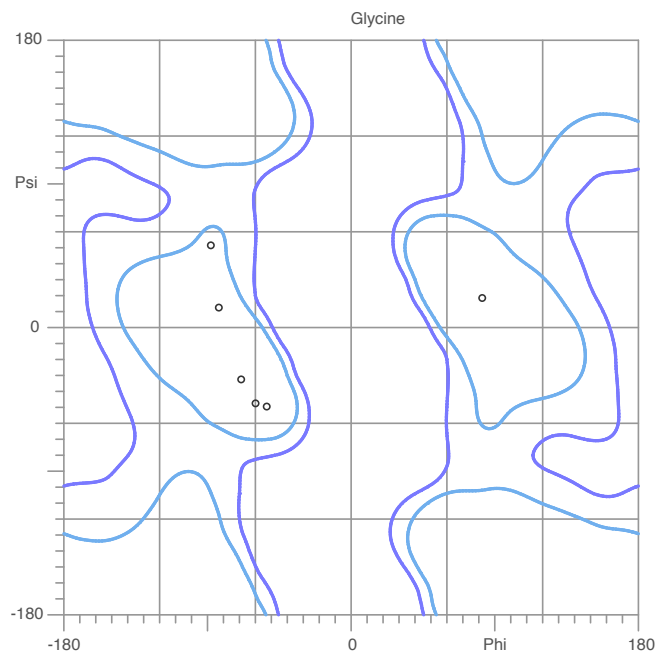
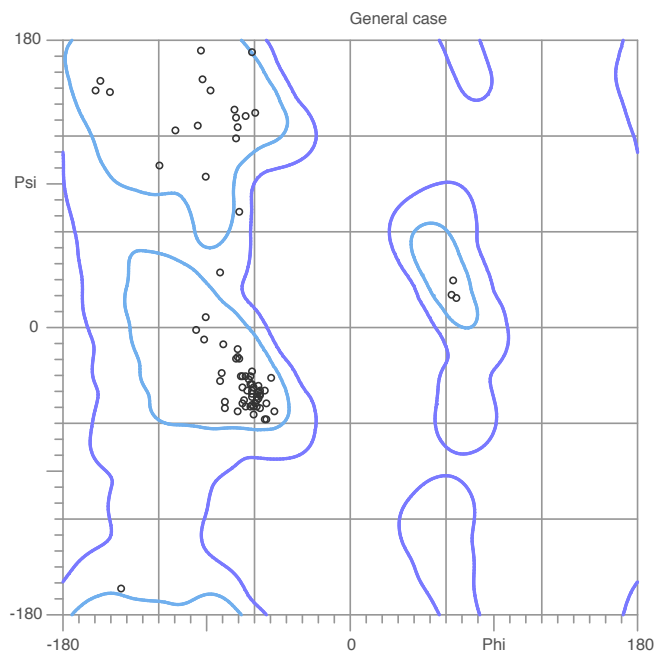
There were no outliers.

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

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 8



94.0% (79/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

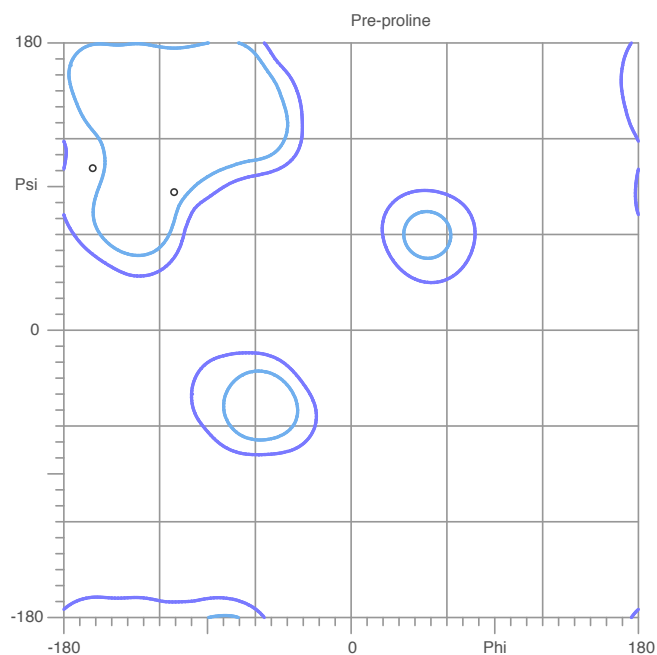
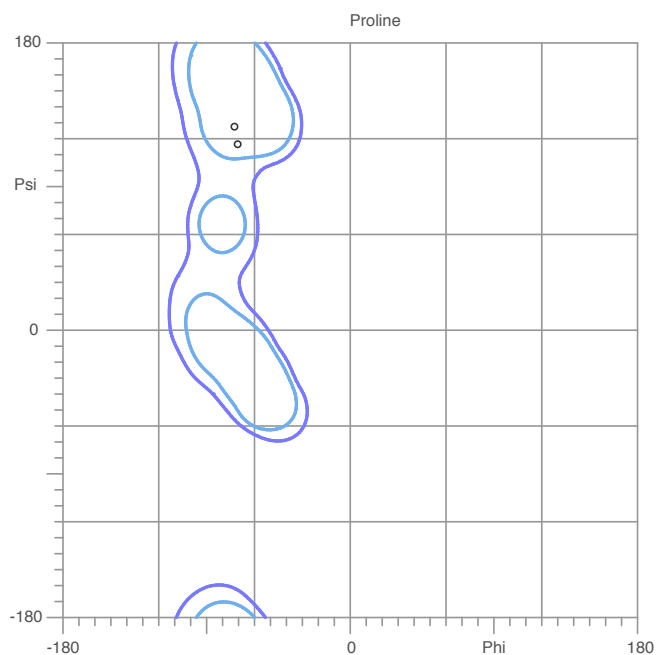
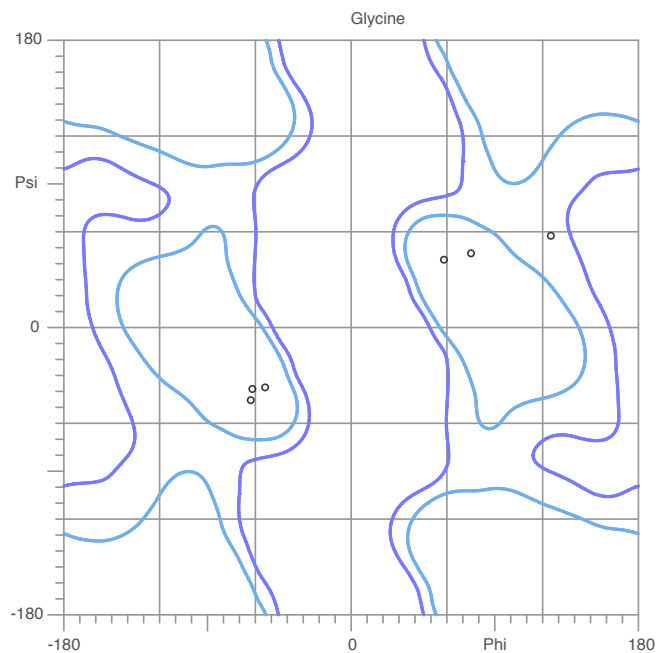
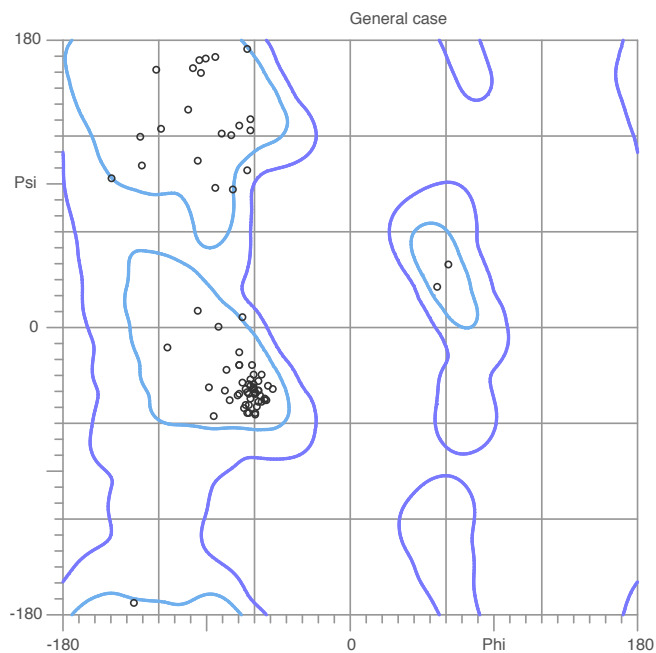
There were 1 outliers (phi, psi):
[8] 43 PRO (-66.9, -82.4)

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 9



94.0% (79/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

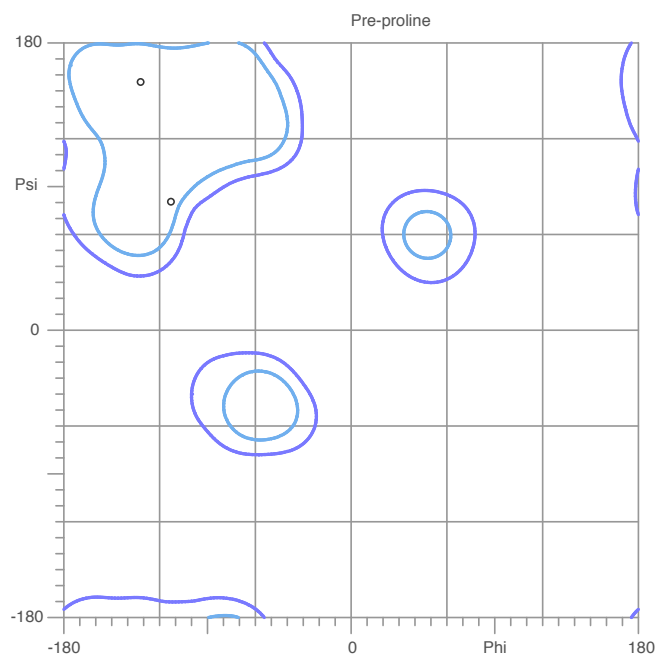
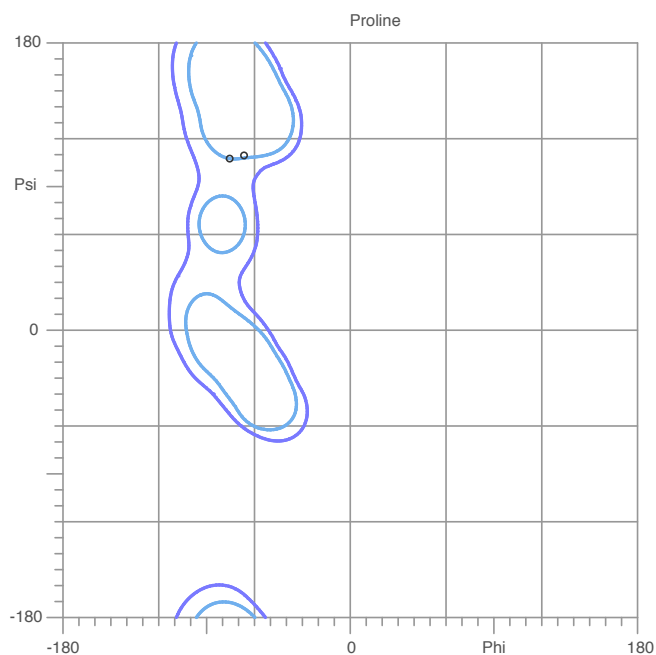
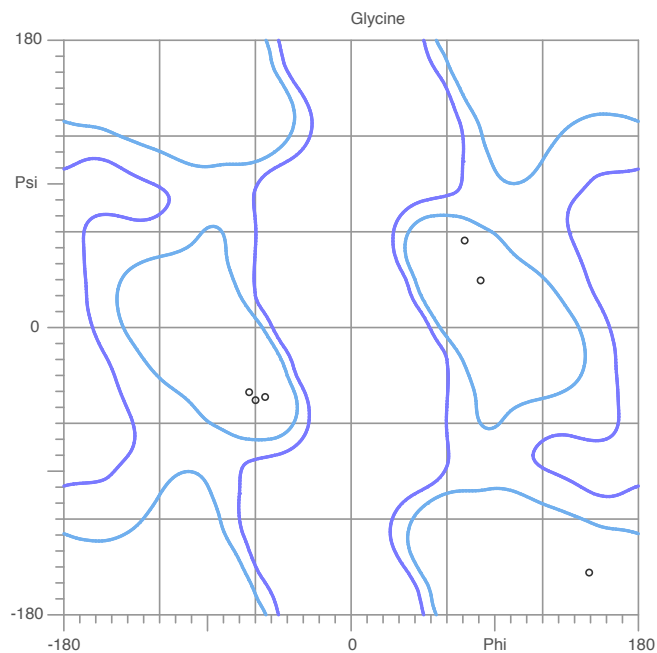
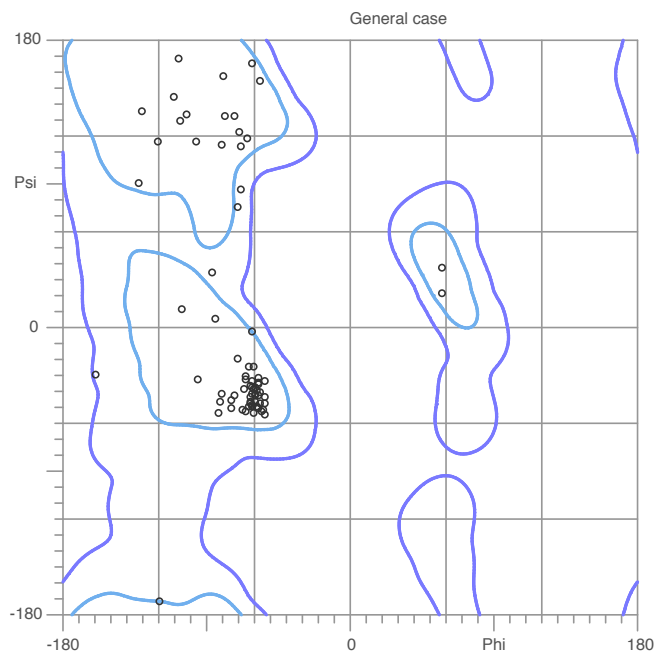
There were no outliers.

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

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 10



94.0% (79/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

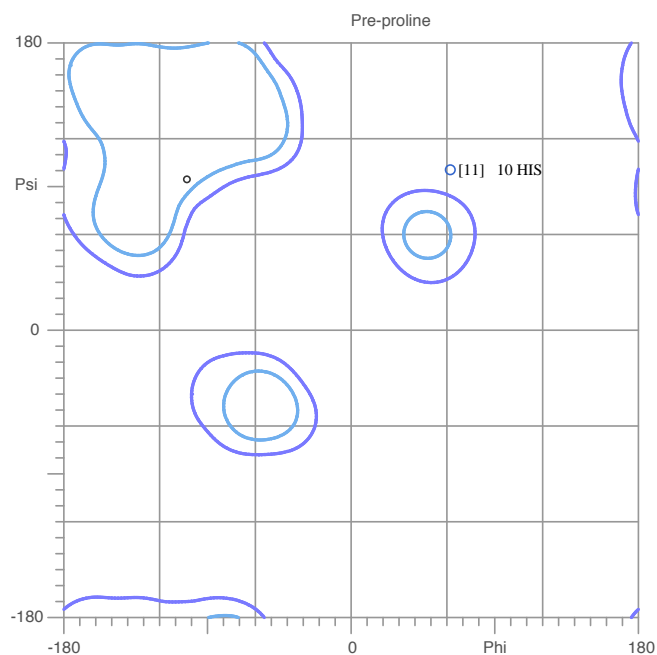
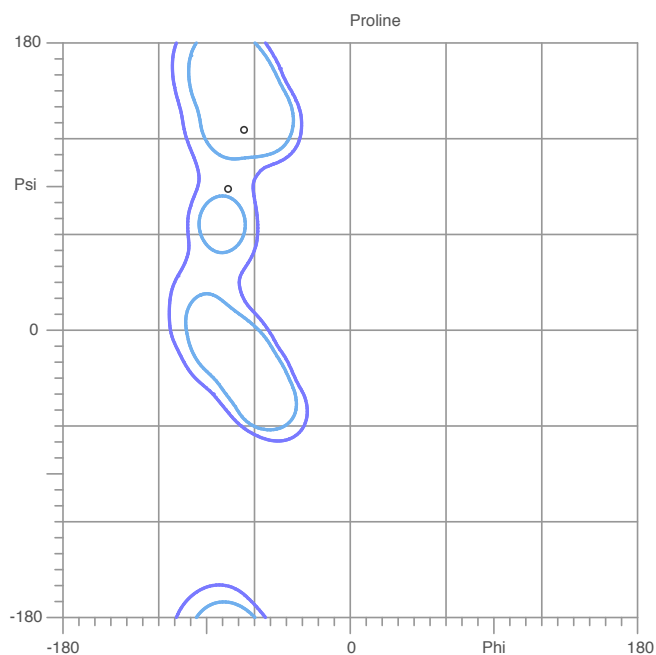
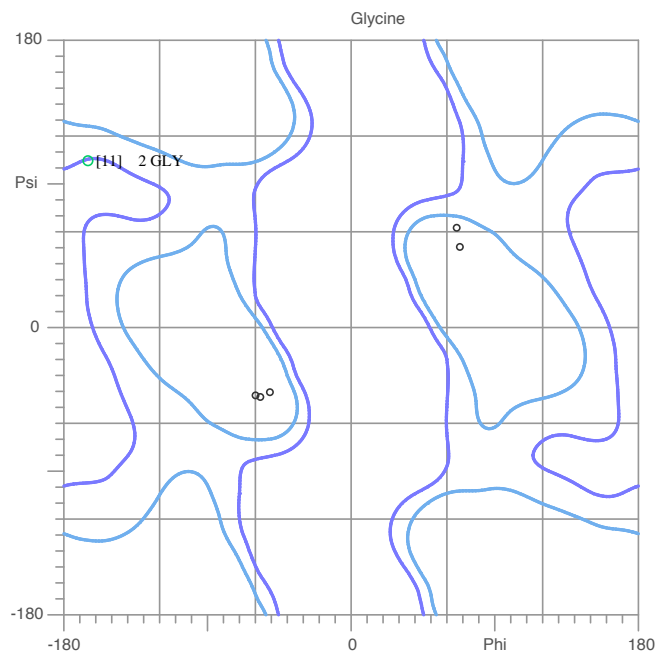
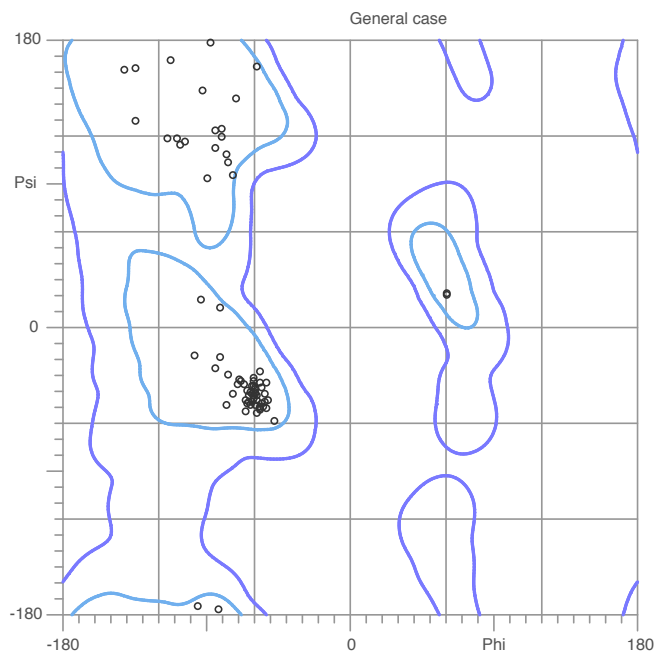
There were no outliers.

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

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 11

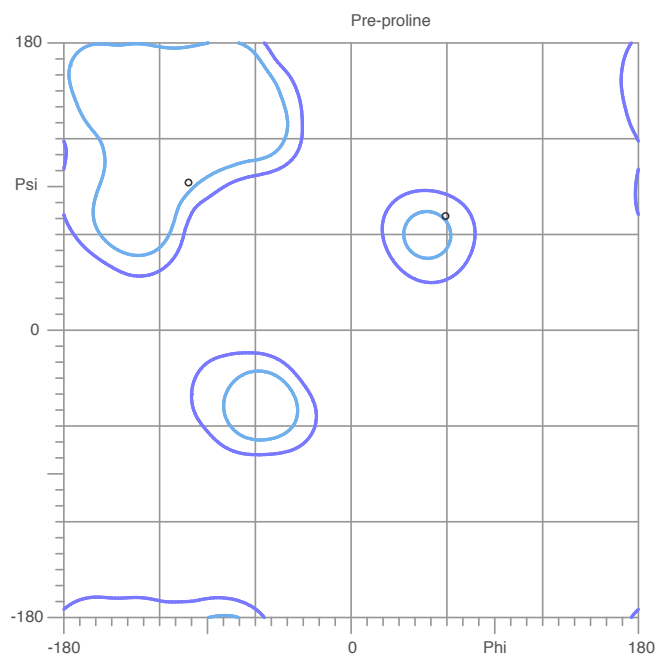
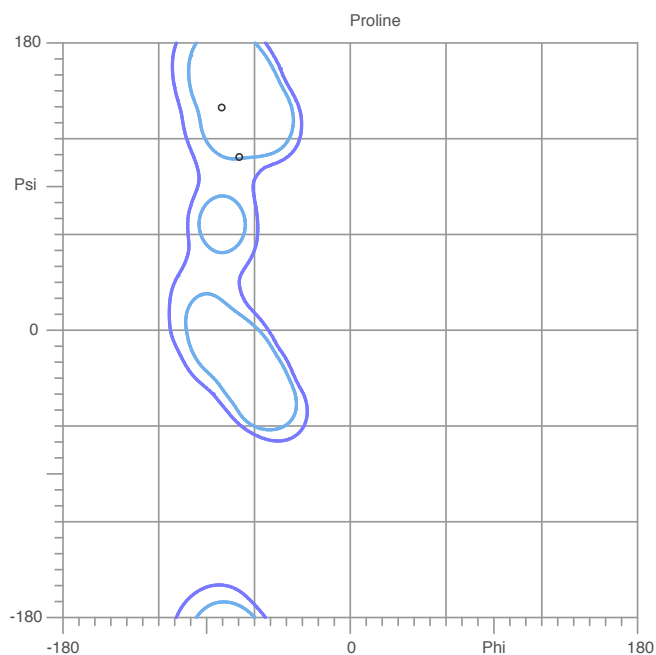
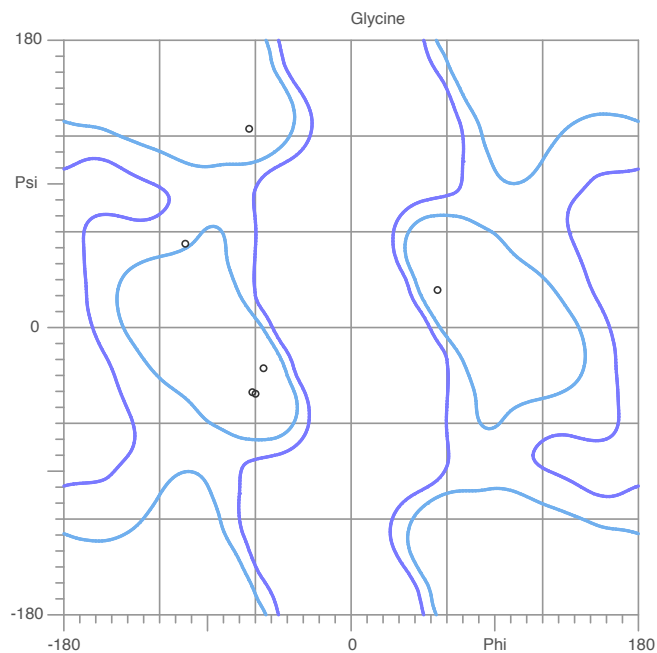
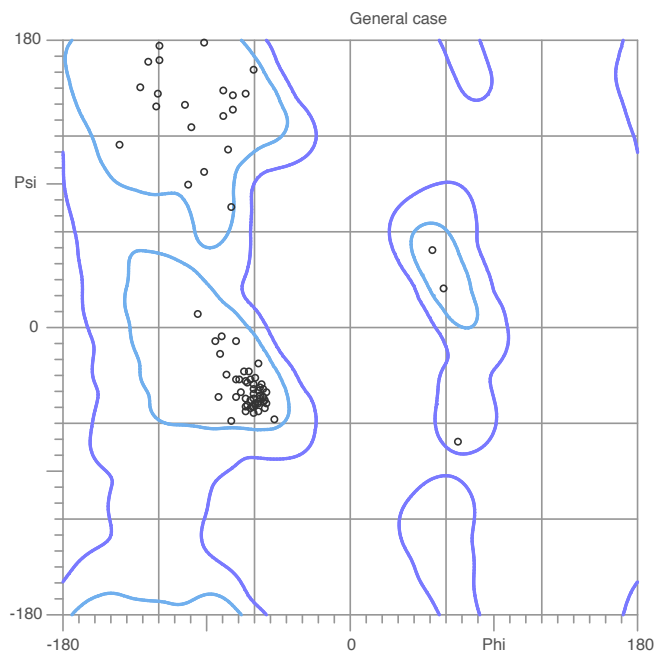


96.4% (81/84) of all residues were in favored (98%) regions.
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[11] 2 GLY (-165.6, 105.3)
[11] 10 HIS (63.0, 102.0)

MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 12



96.4% (81/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

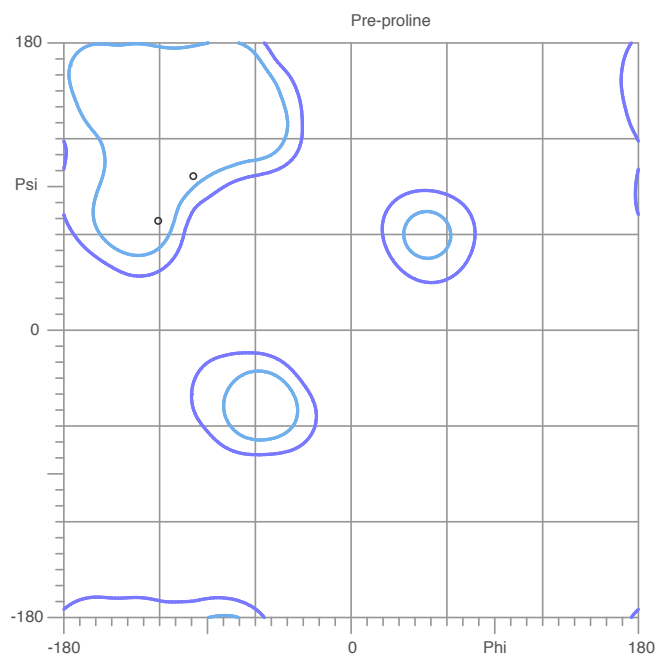
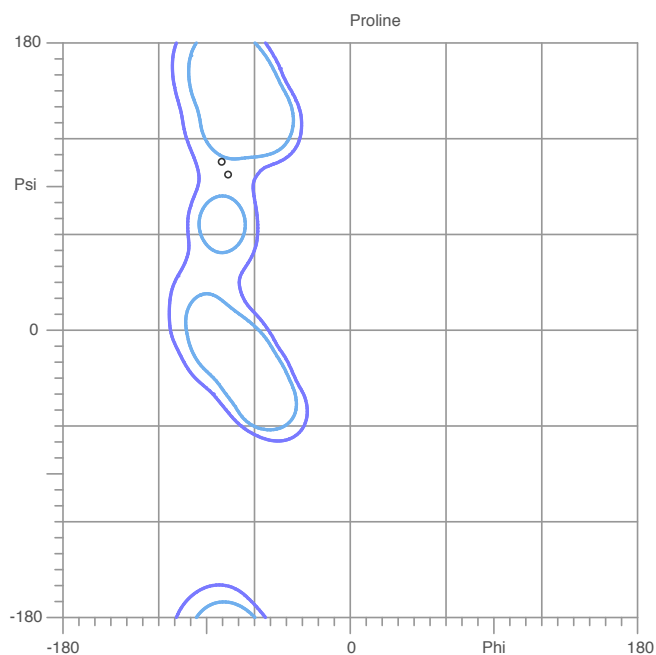
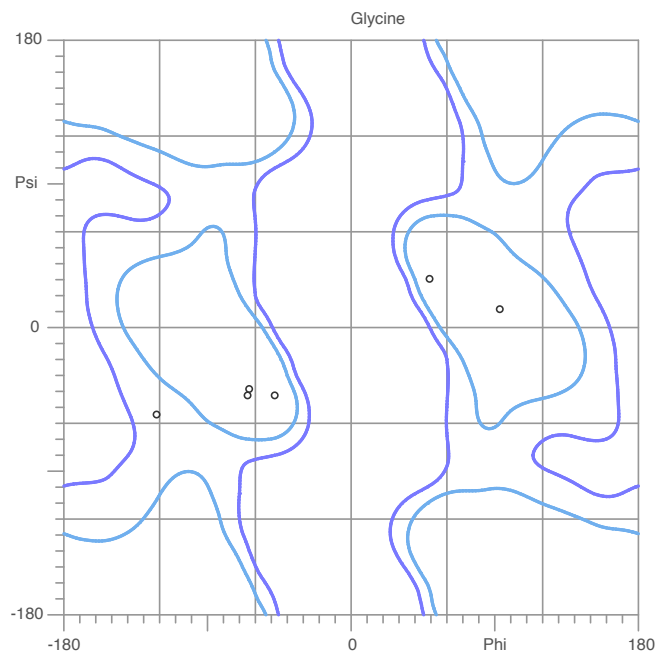
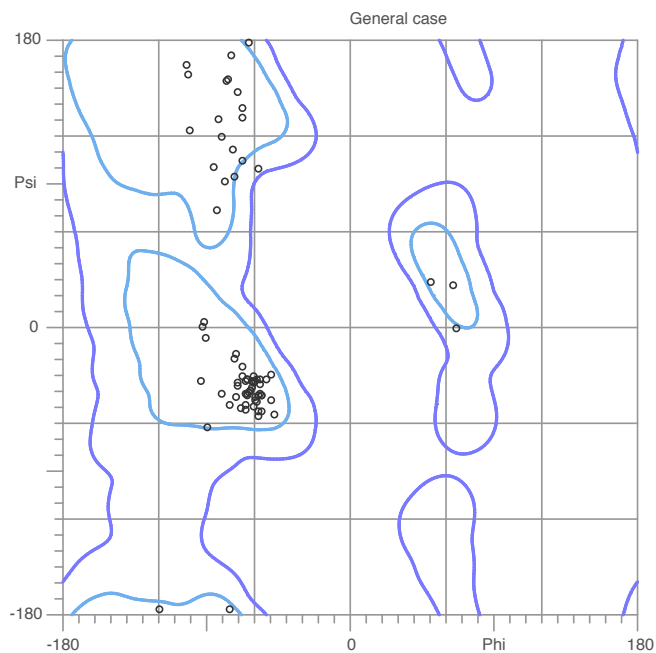
There were no outliers.

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 13

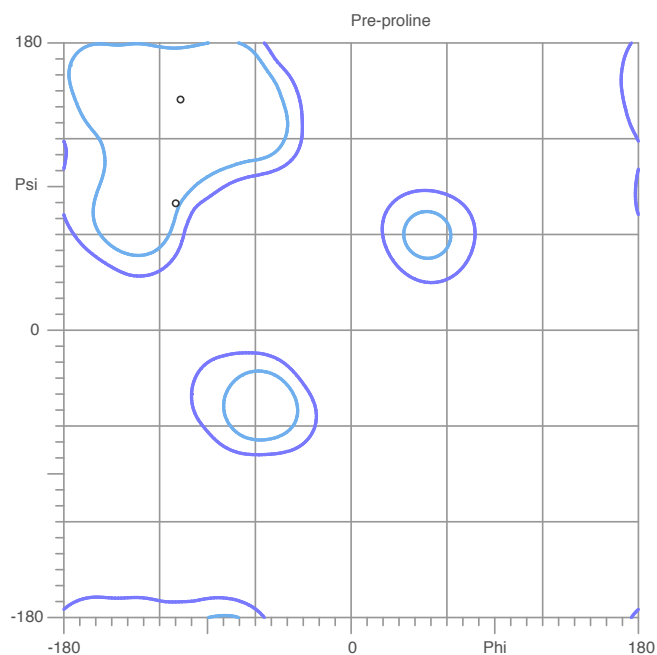
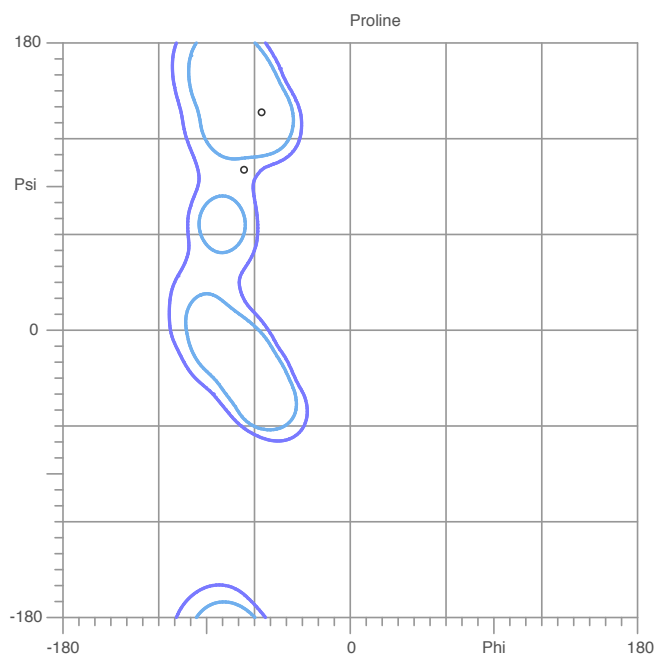
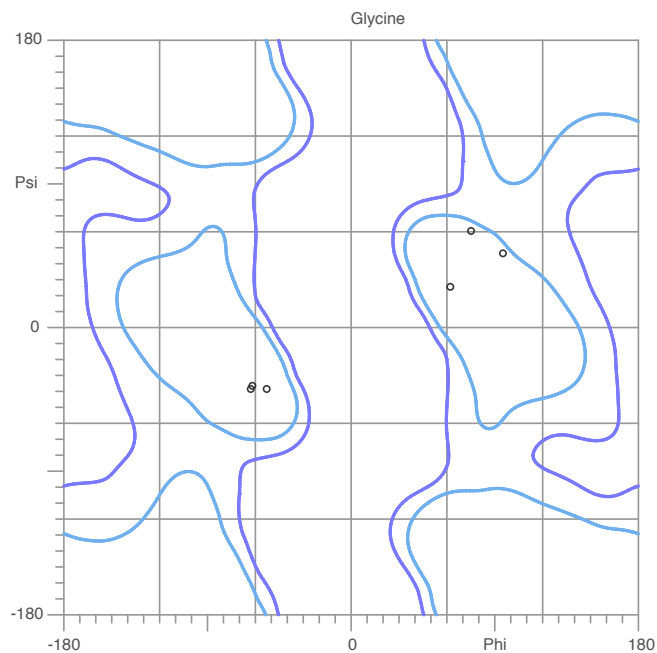
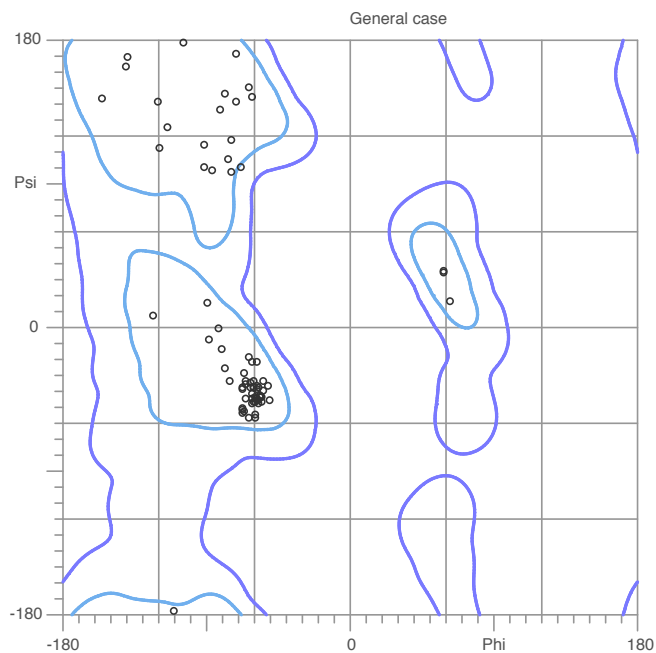


92.9% (78/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 14



98.8% (83/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

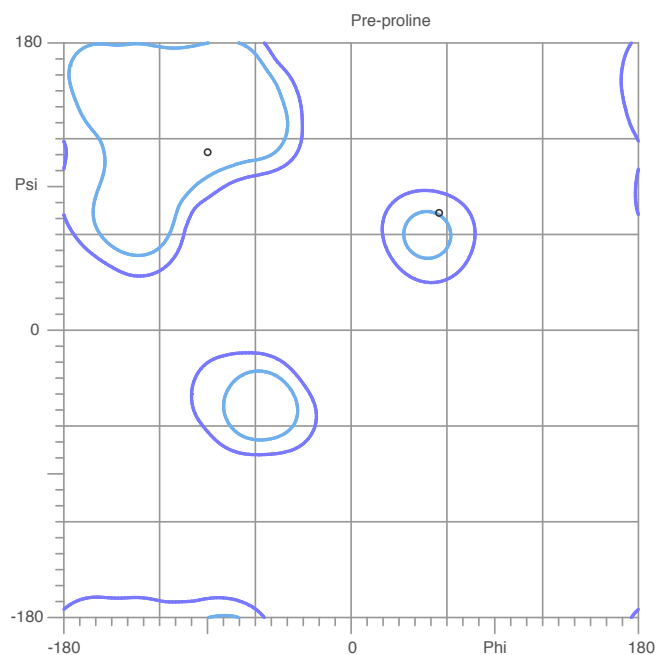
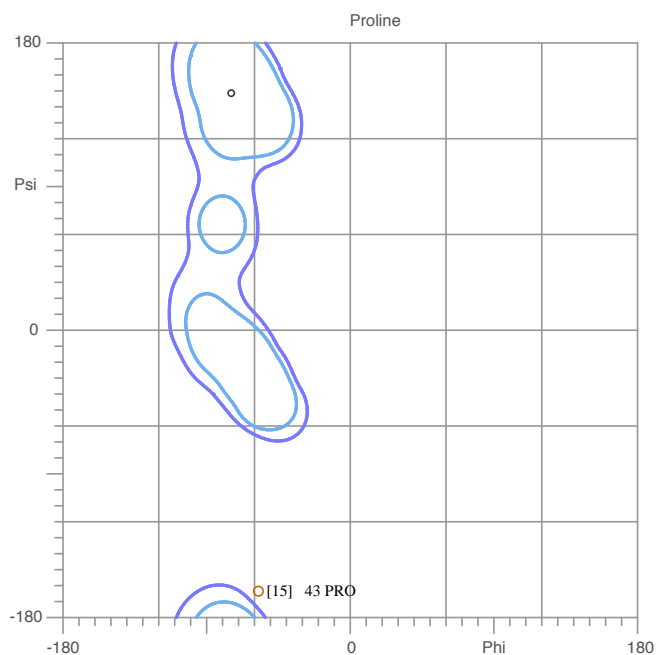
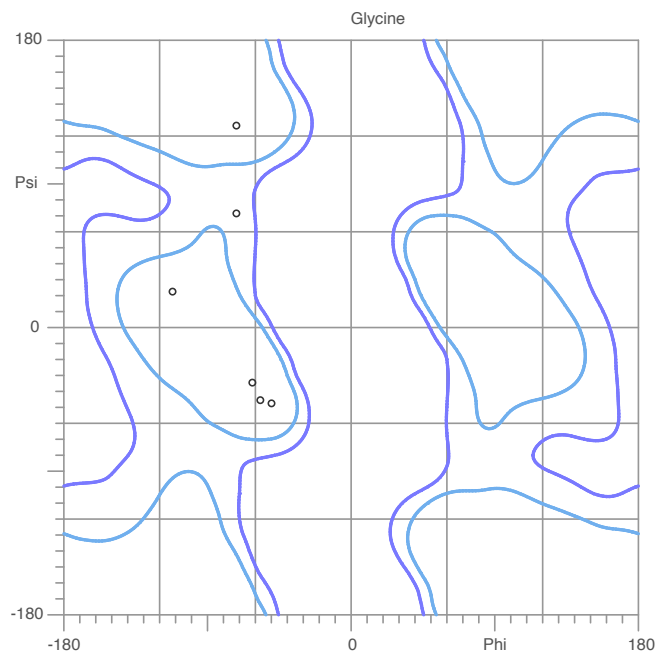
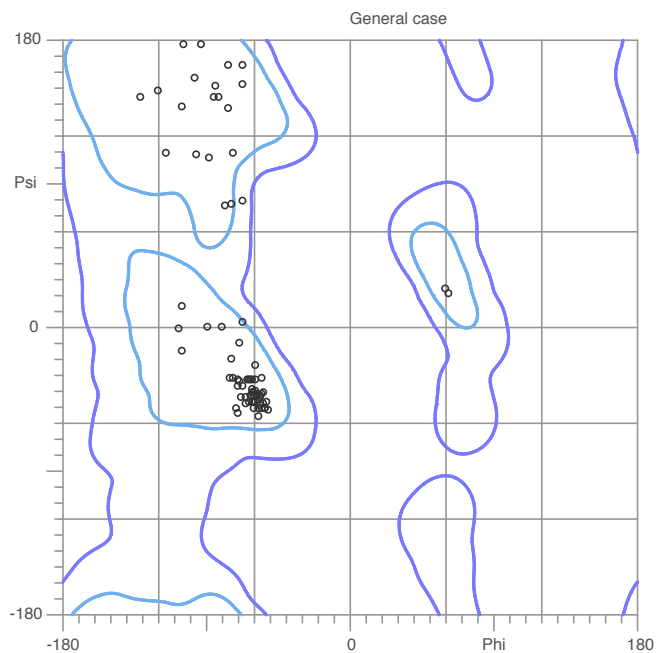
There were no outliers.

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

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 15



95.2% (80/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

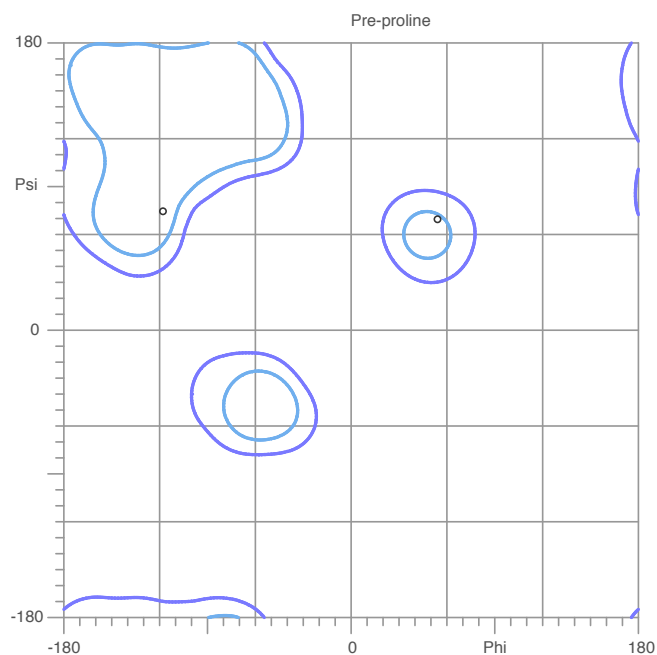
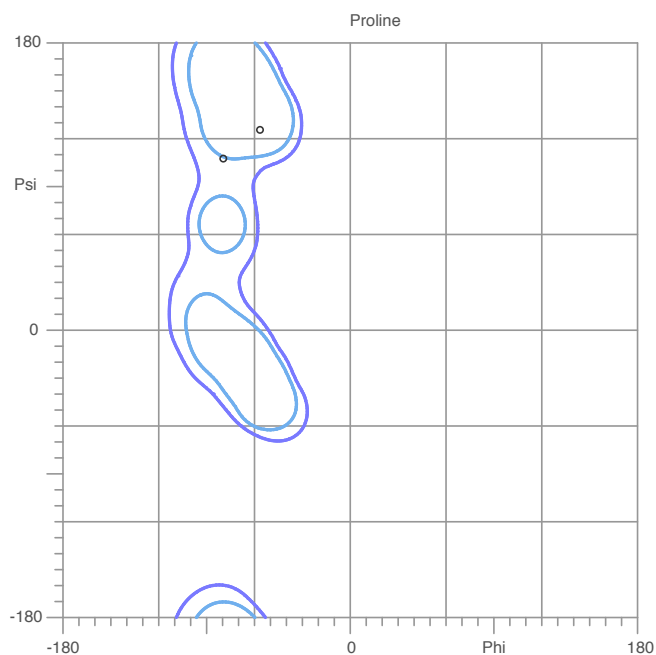
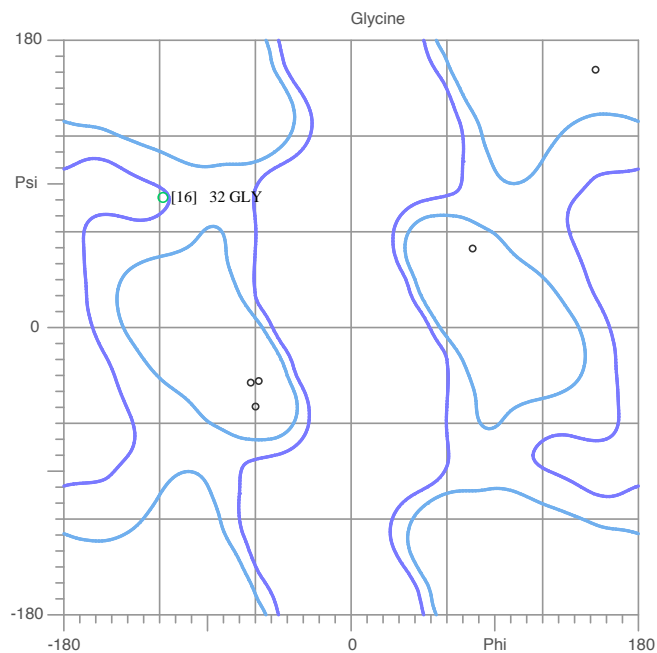
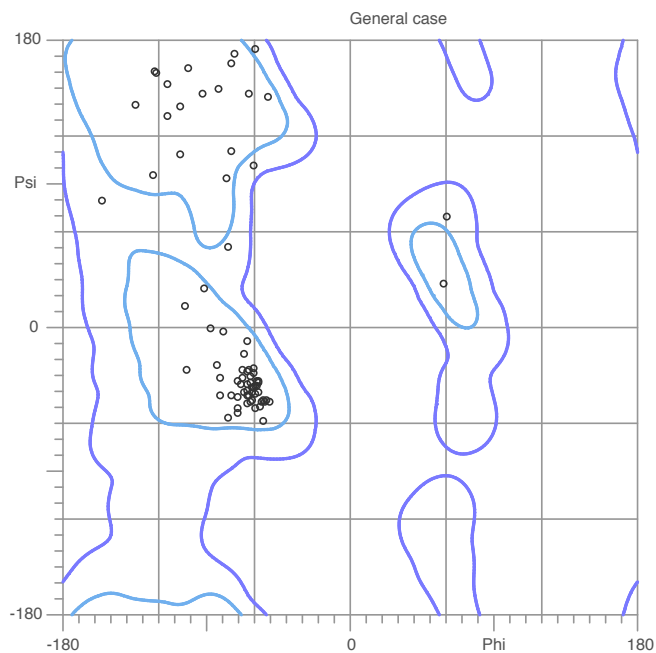
There were 1 outliers (phi, psi):
[15] 43 PRO (-58.9, -164.0)

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

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 16



91.7% (77/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

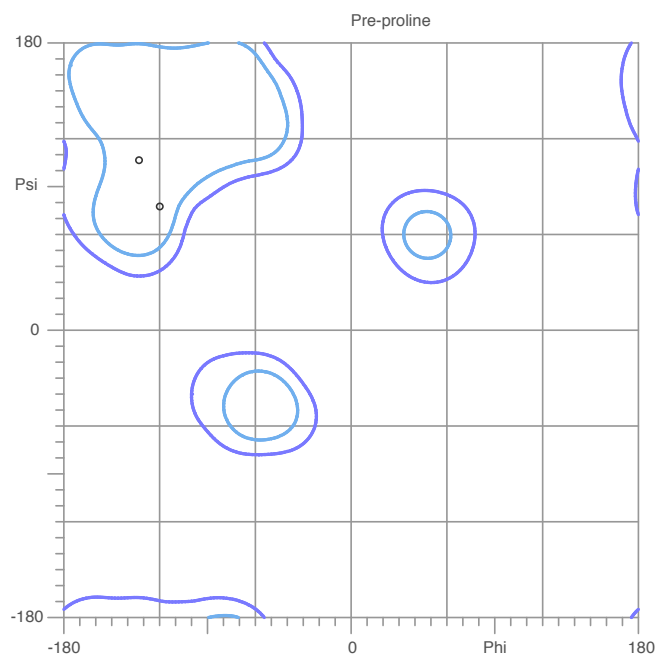
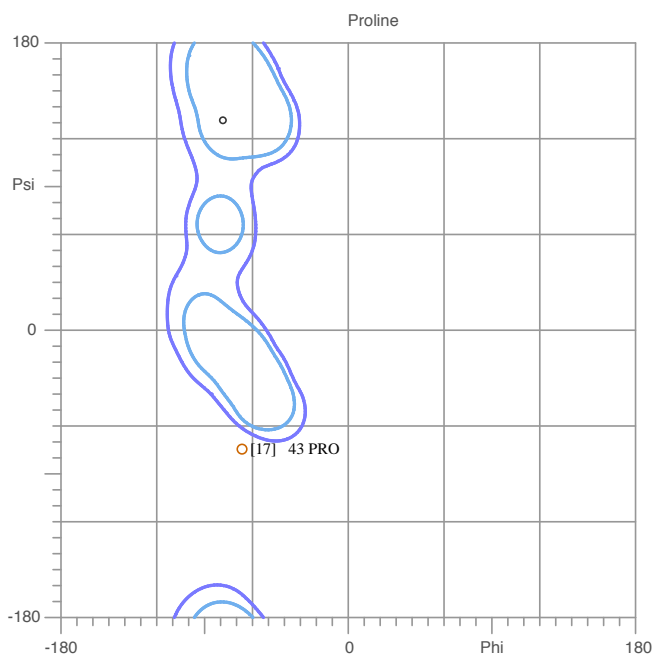
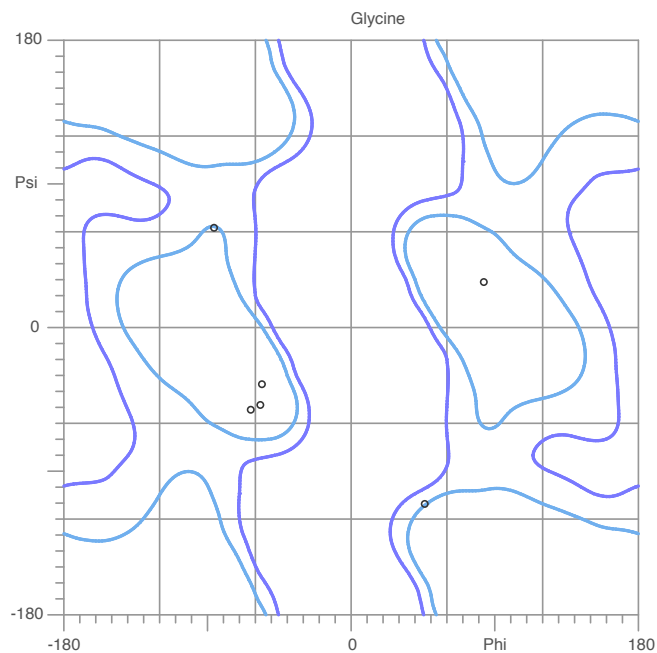
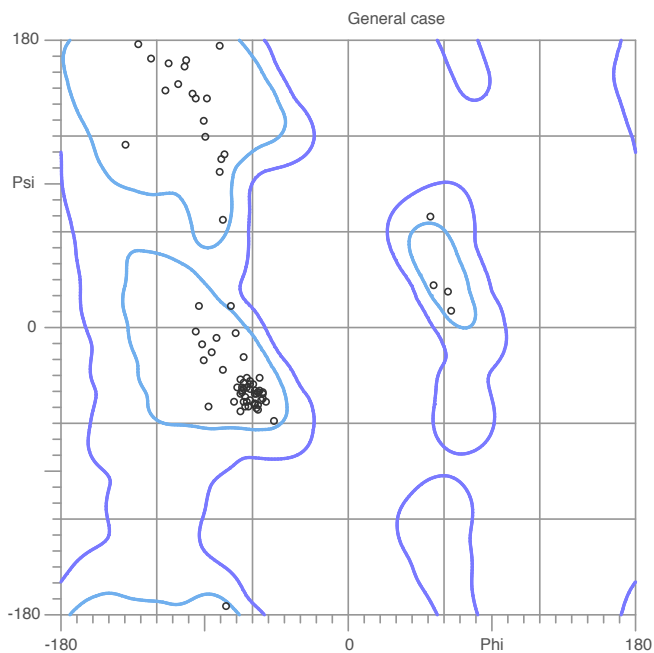
There were 1 outliers (phi, psi):
[16] 32 GLY (-118.7, 82.4)

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 17



94.0% (79/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

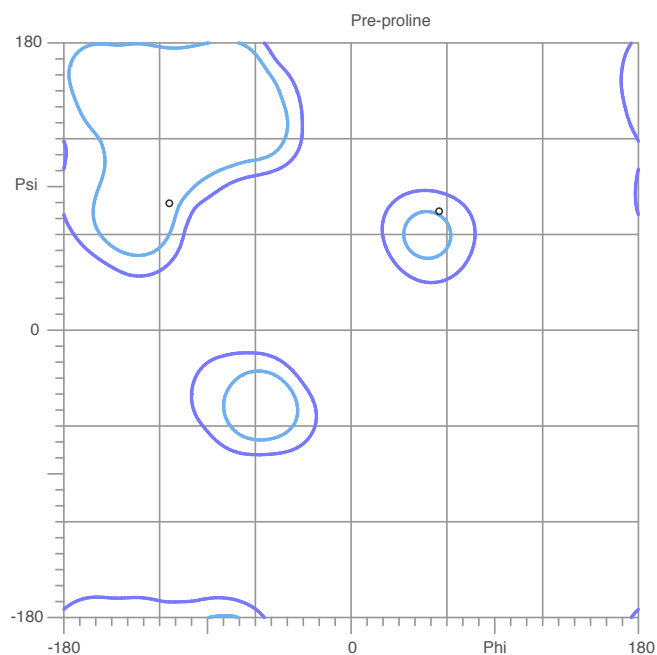
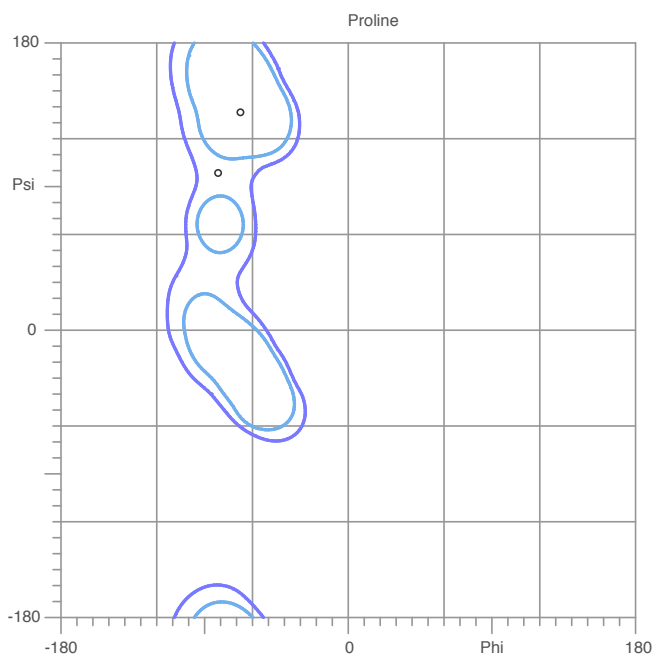
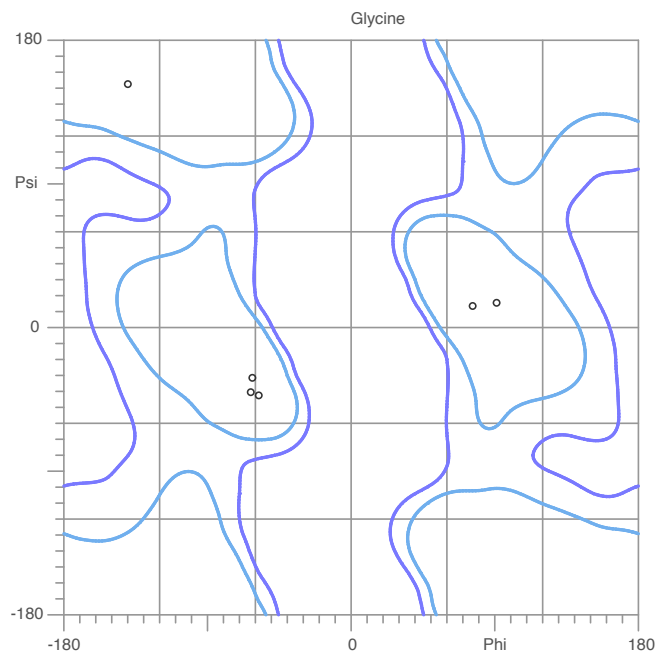
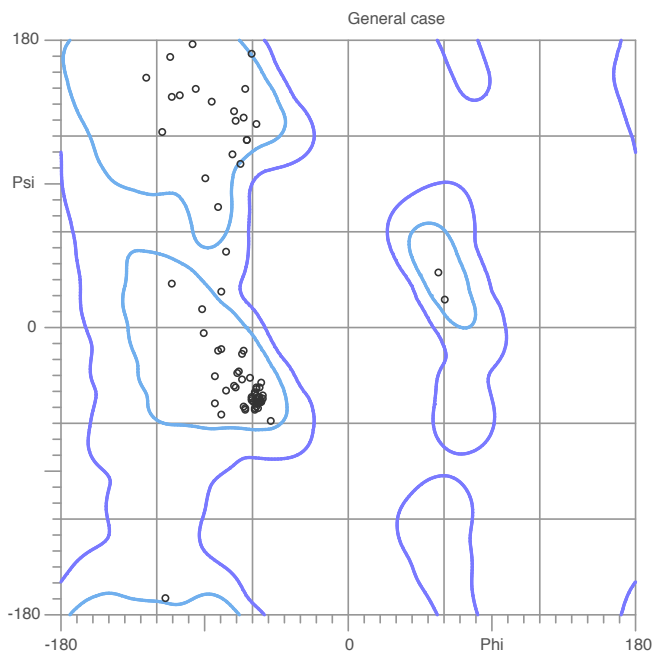
There were 1 outliers (phi, psi):
[17] 43 PRO (-67.1, -74.1)

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 18



92.9% (78/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

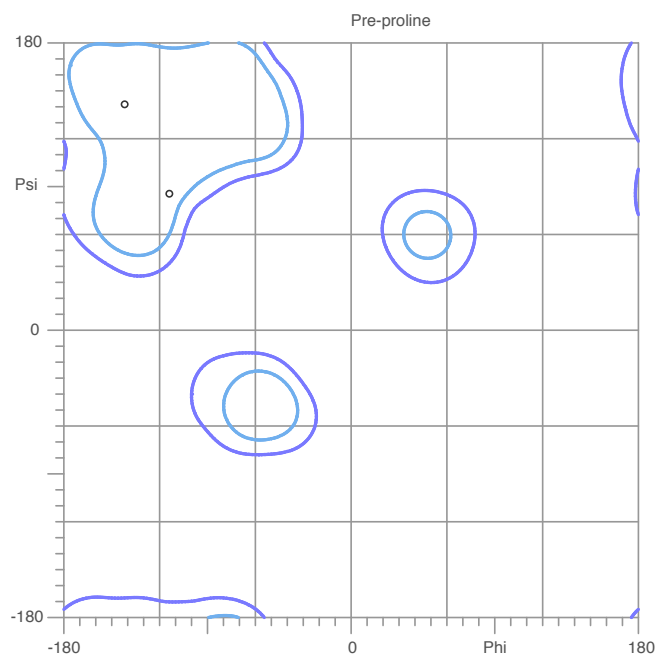
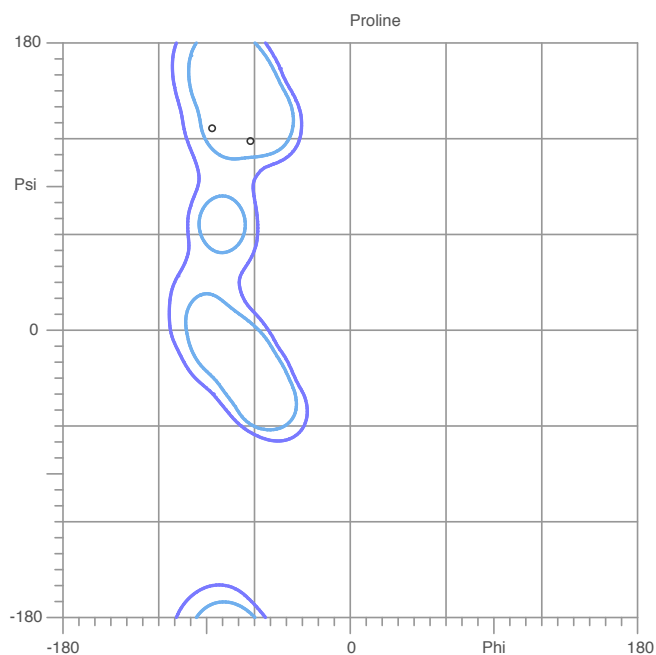
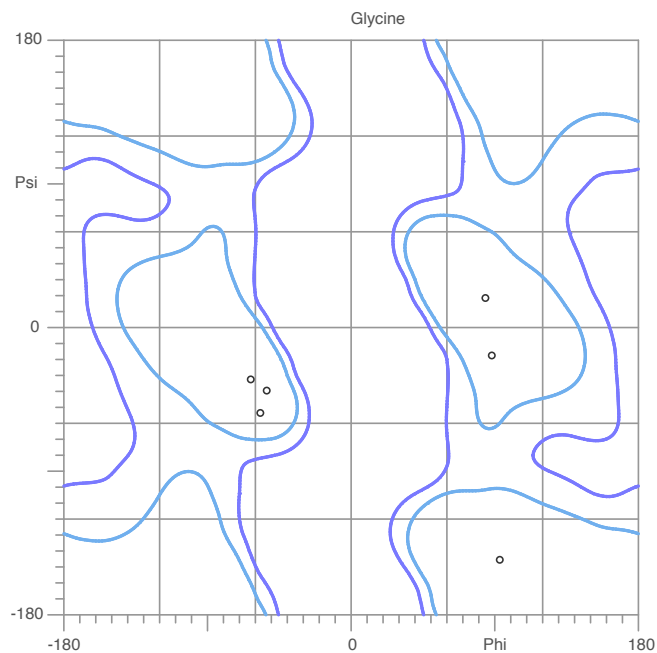
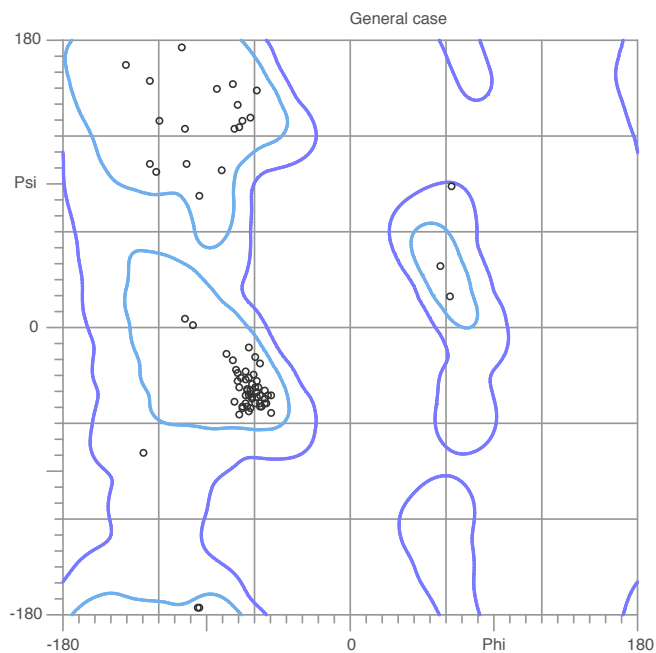
There were no outliers.

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 19



97.6% (82/84) of all residues were in favored (98%) regions.
100.0% (84/84) of all residues were in allowed (>99.8%) regions.

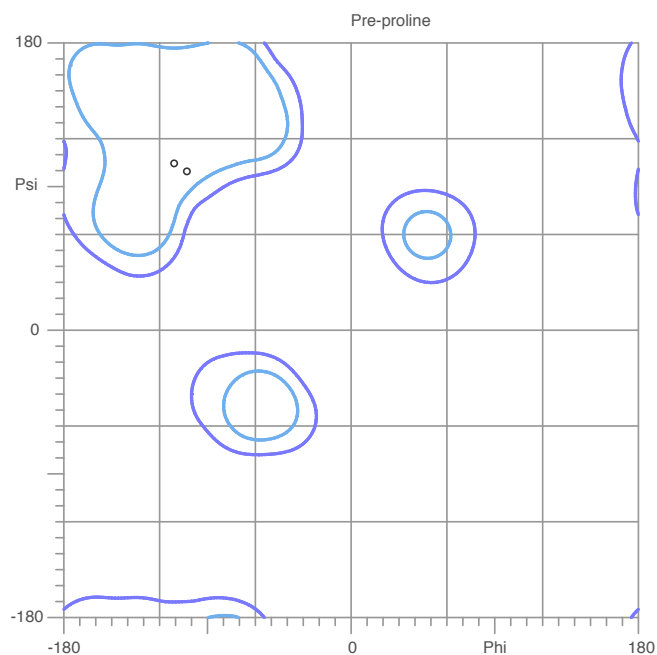
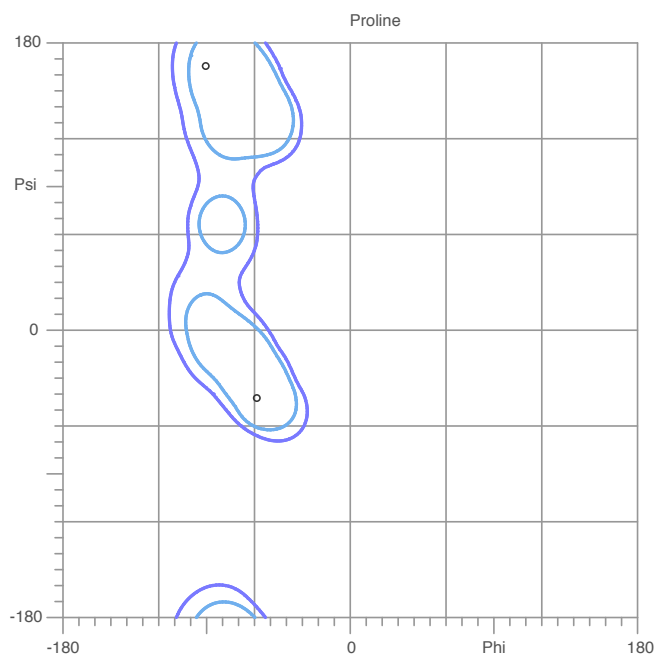
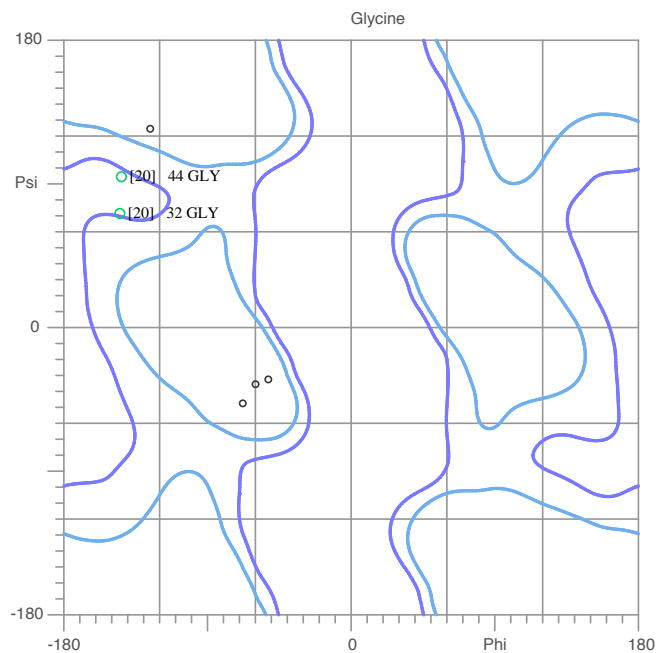
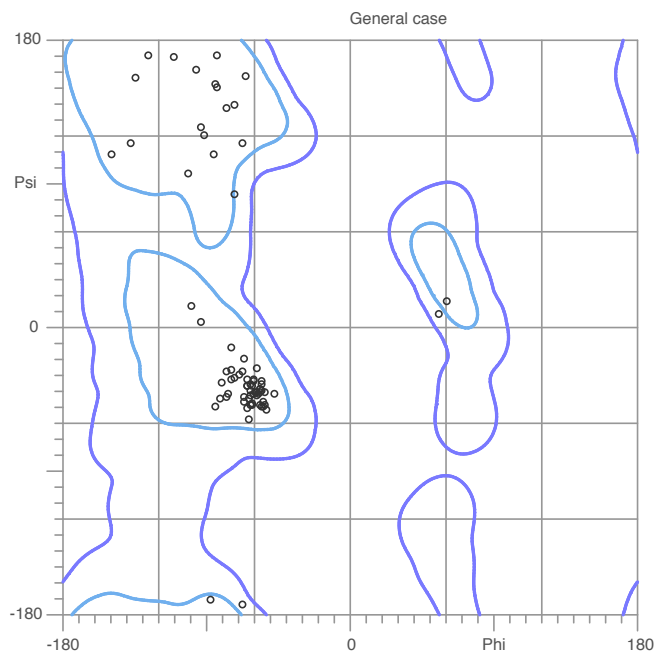
There were no outliers.

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

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MolProbity Ramachandran analysis

HR3102A_NMR_em_bcr3.pdb, model 20



95.2% (80/84) of all residues were in favored (98%) regions.
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[20] 32 GLY (-145.3, 72.1)
[20] 44 GLY (-144.3, 95.0)