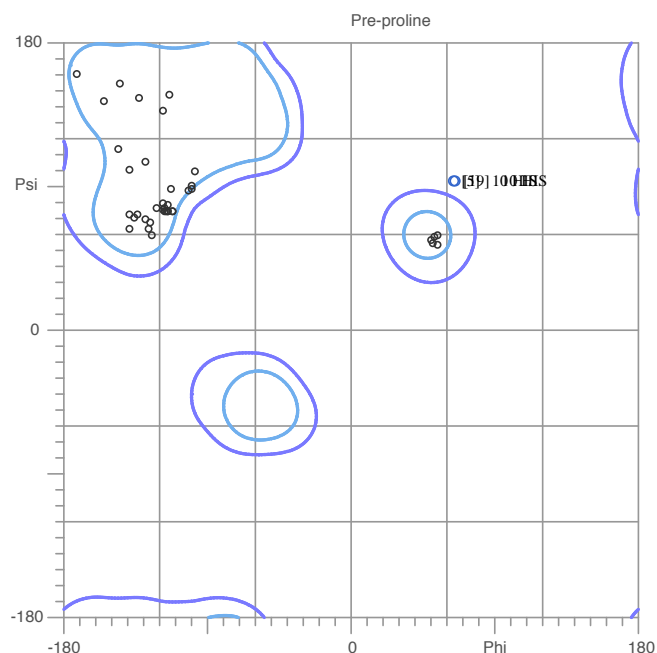
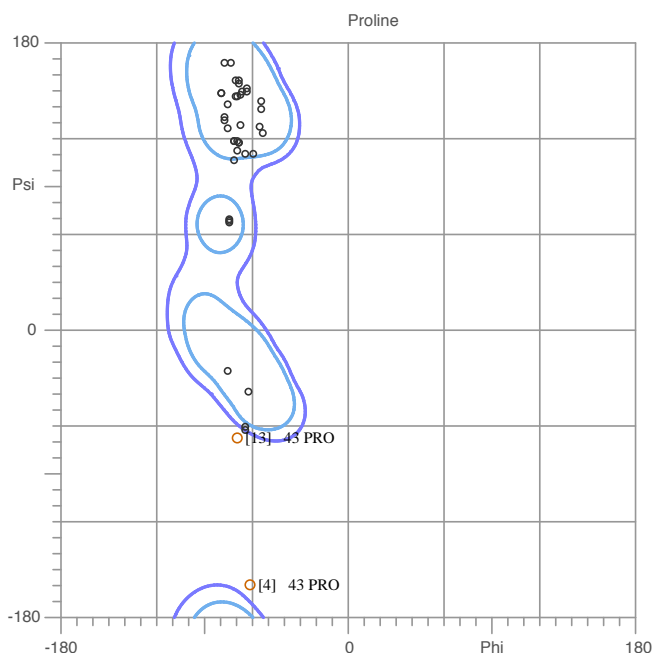
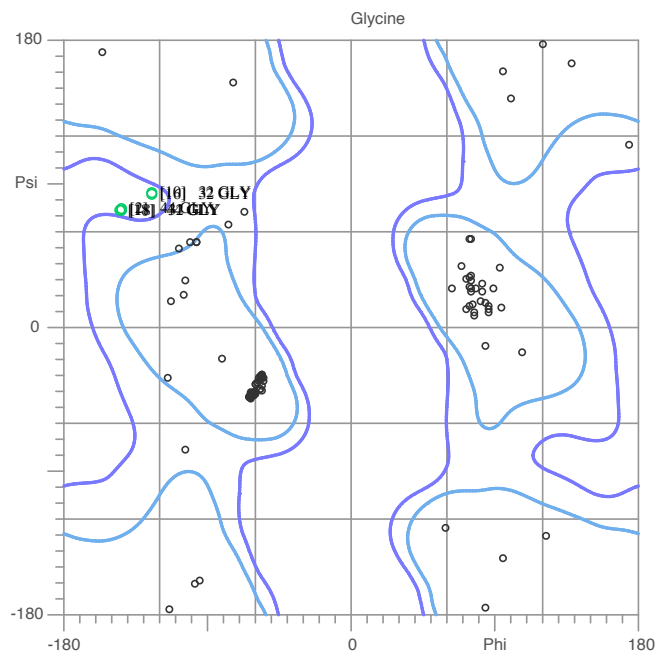
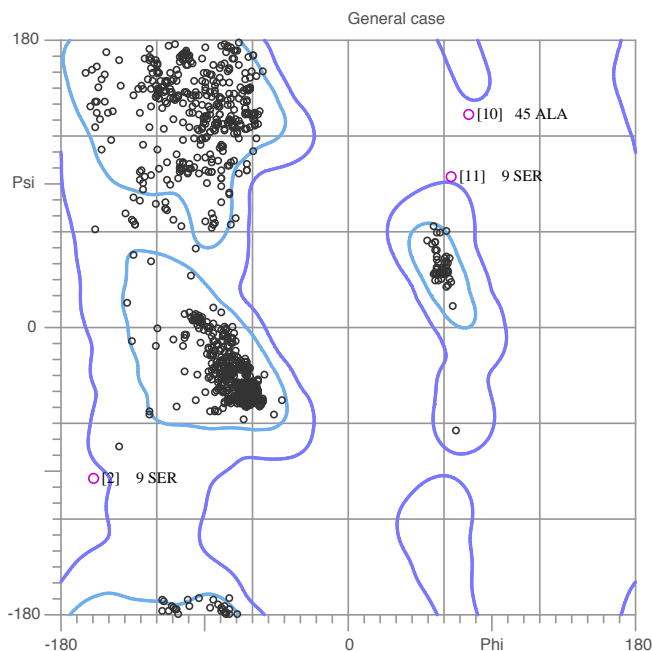


MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, all models



96.8% (1627/1680) of all residues were in favored (98%) regions.
99.3% (1668/1680) of all residues were in allowed (>99.8%) regions.

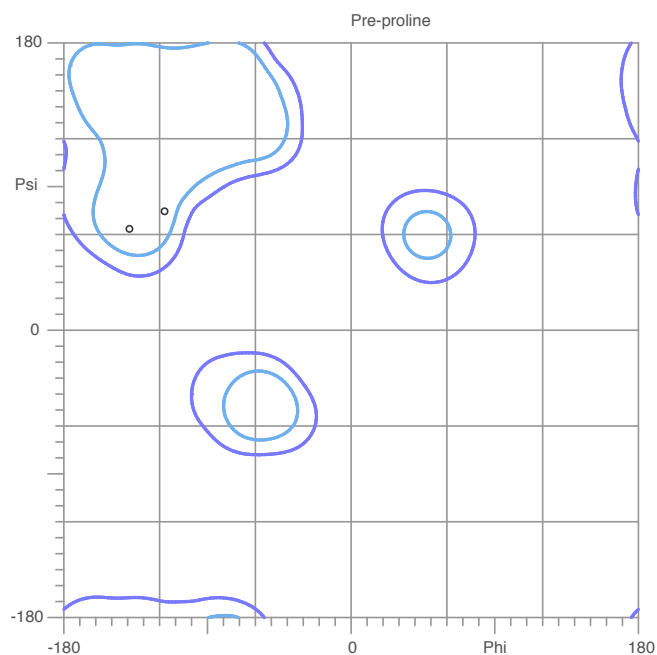
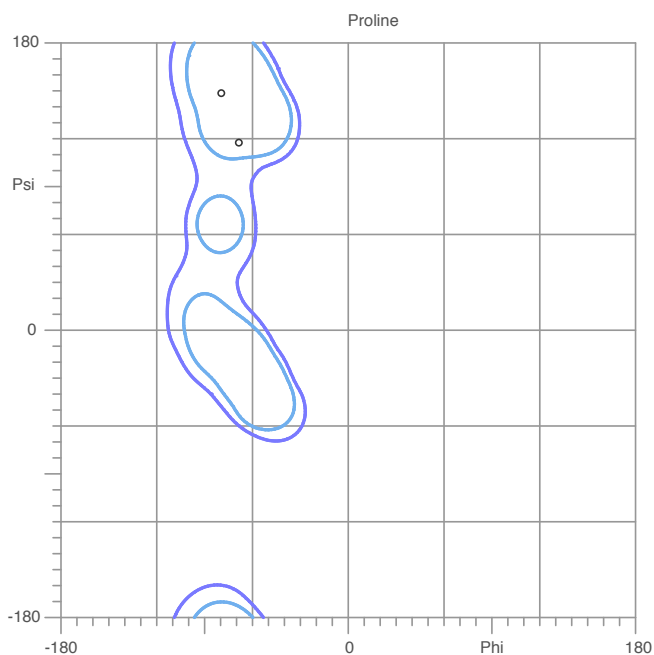
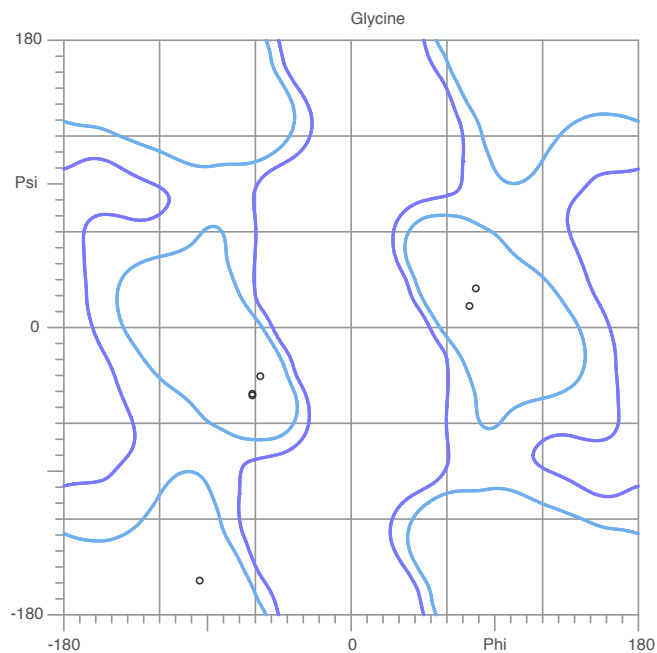
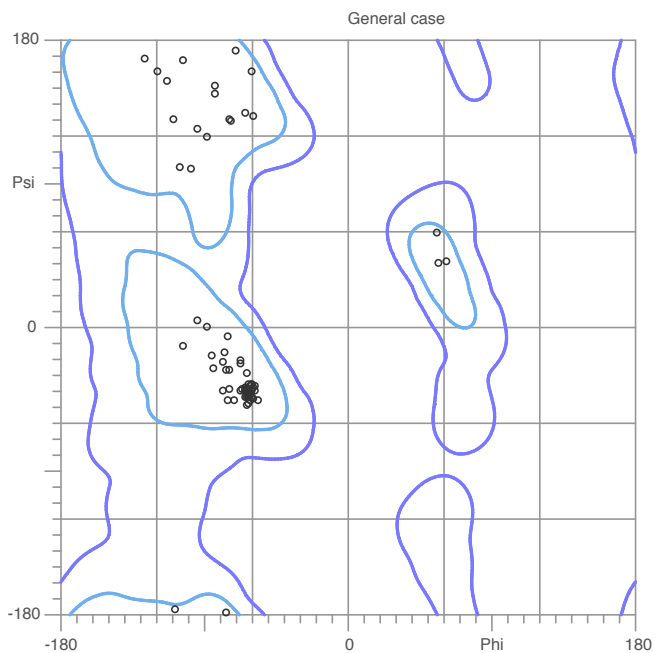
There were 12 outliers (phi, psi):

- [2] 9 SER (-160.1, -94.9)
- [2] 44 GLY (-145.0, 75.0)
- [4] 43 PRO (-62.1, -159.9)
- [5] 10 HIS (65.0, 94.9)

- [10] 32 GLY (-125.2, 85.0)
- [10] 45 ALA (75.7, 135.0)
- [11] 9 SER (64.7, 95.1)
- [13] 43 PRO (-70.9, -67.2)
- [16] 32 GLY (-125.0, 84.9)
- [18] 32 GLY (-145.0, 75.0)
- [18] 44 GLY (-145.0, 75.0)
- [19] 10 HIS (65.0, 94.9)

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 1



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

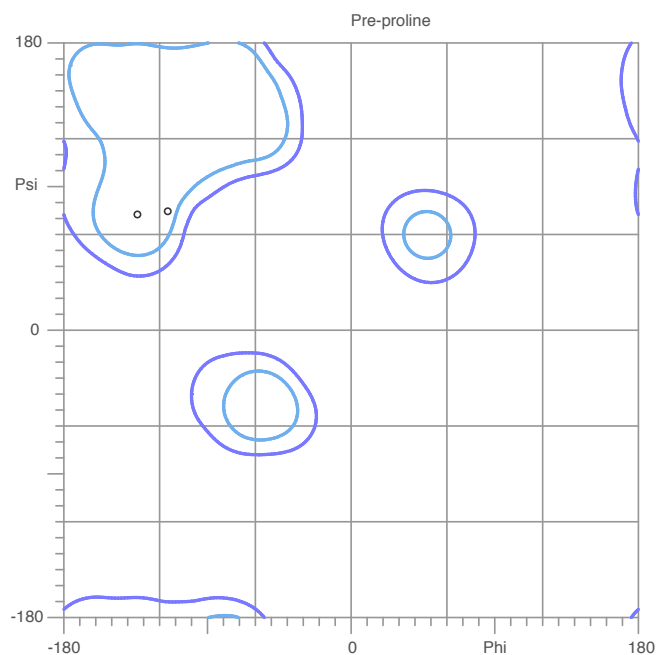
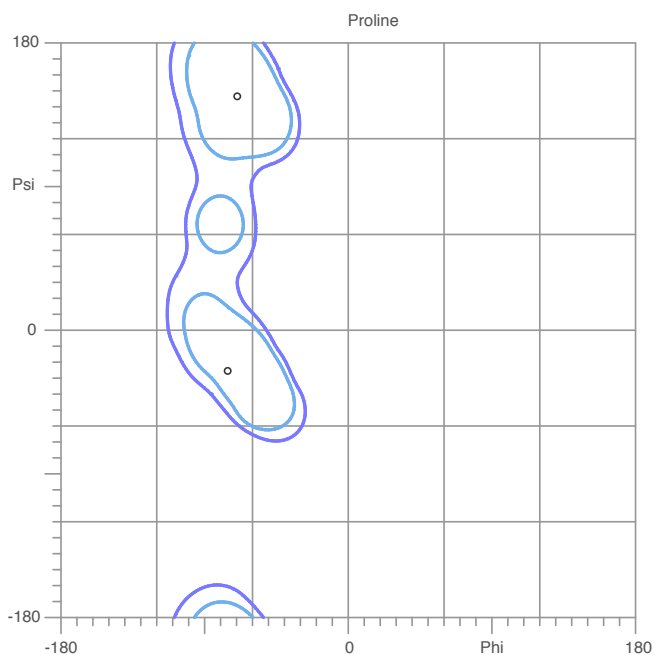
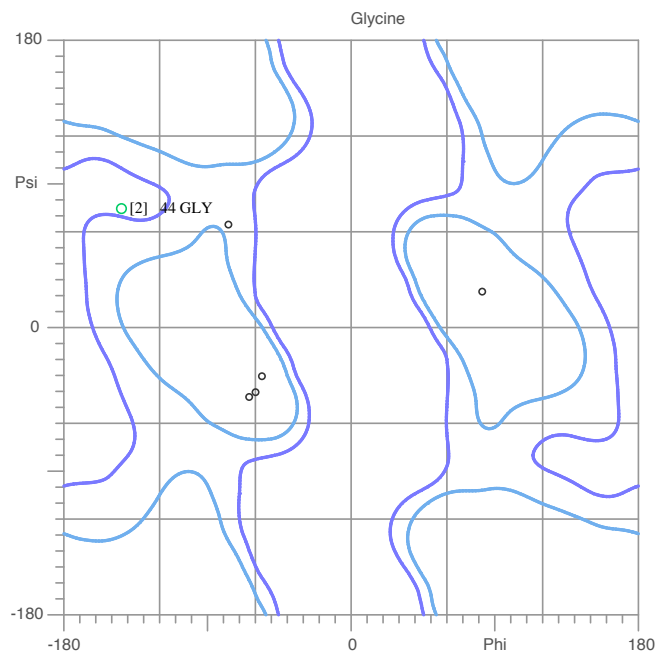
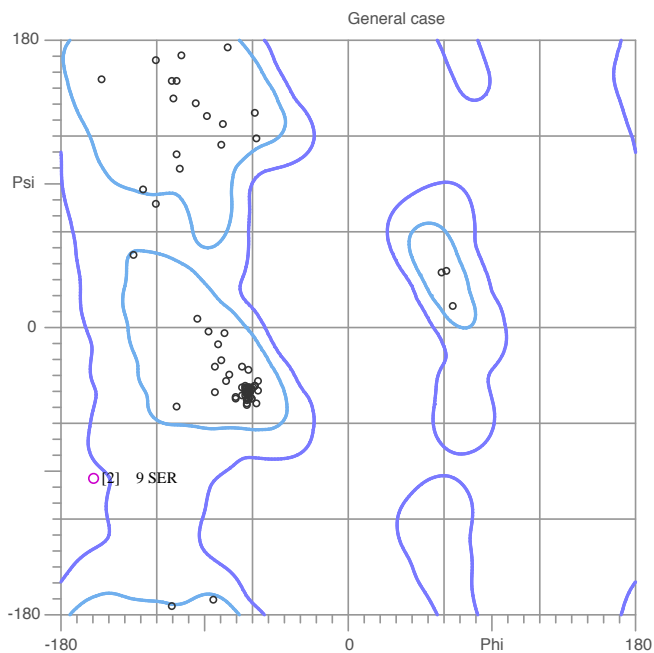
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 2



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.

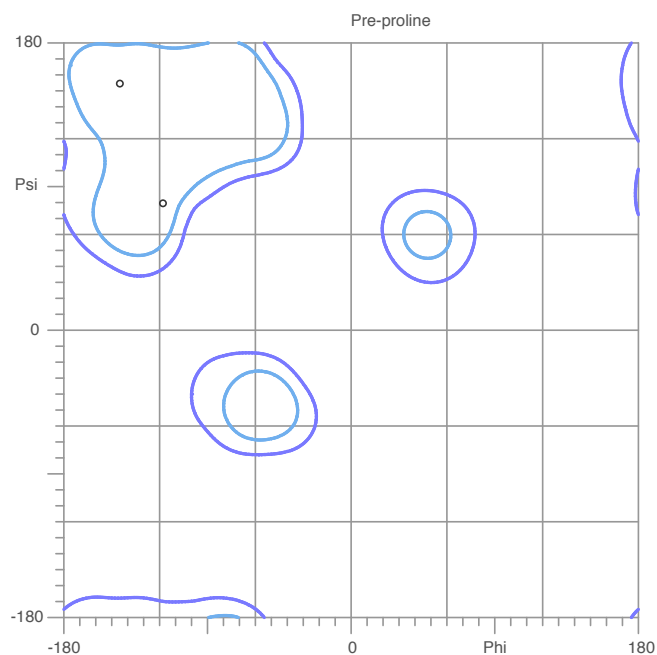
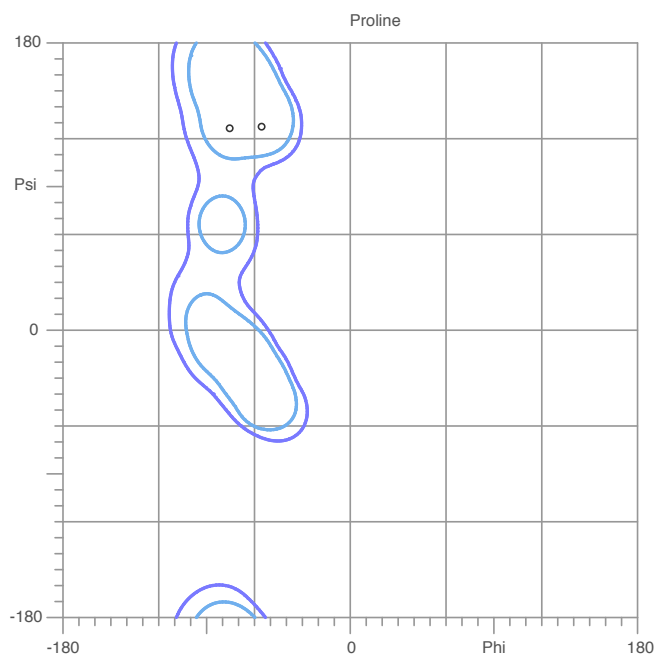
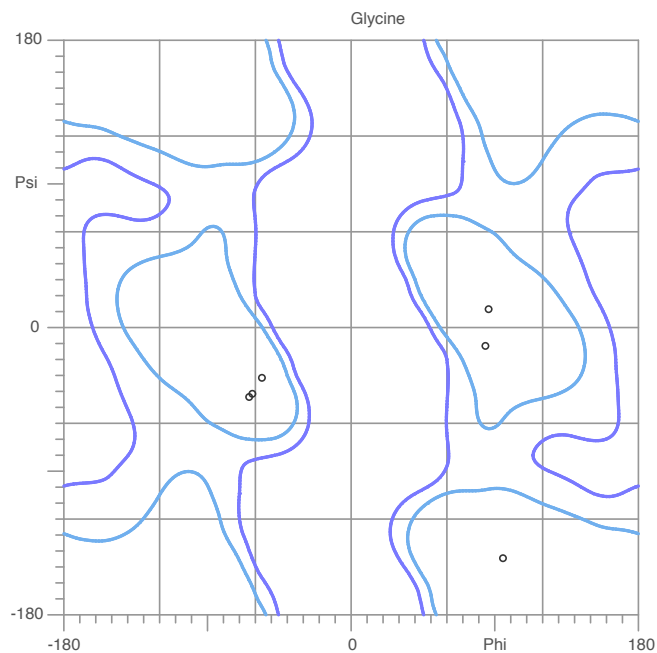
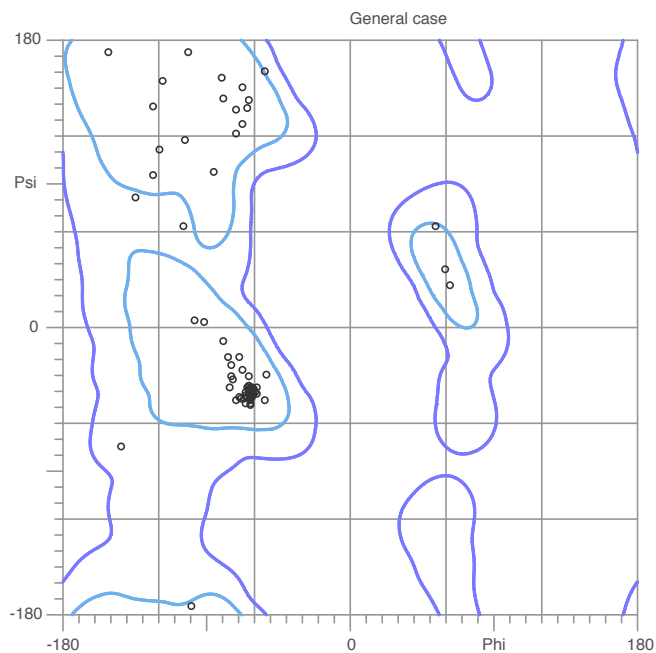
There were 2 outliers (phi, psi):

[2] 9 SER (-160.1, -94.9)

[2] 44 GLY (-145.0, 75.0)

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 3



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.

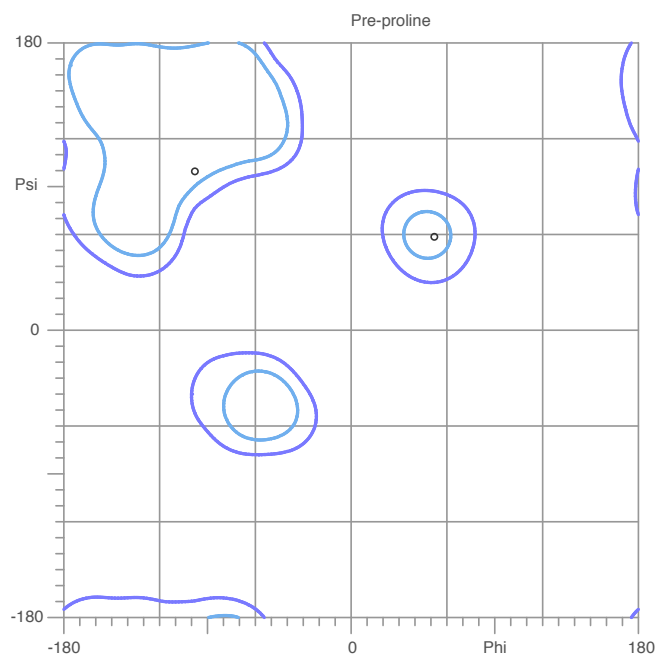
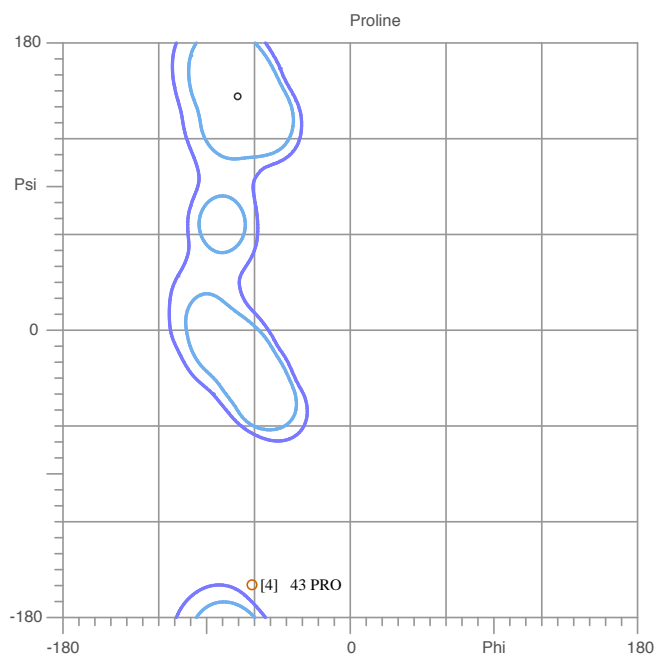
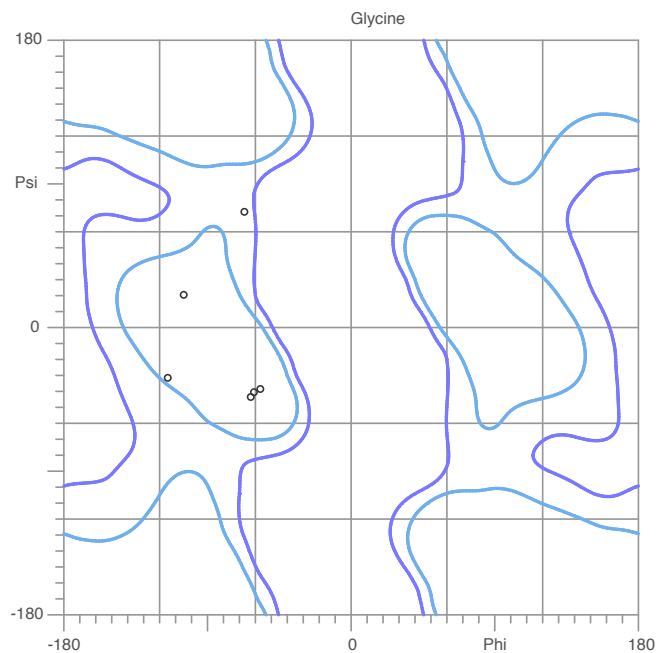
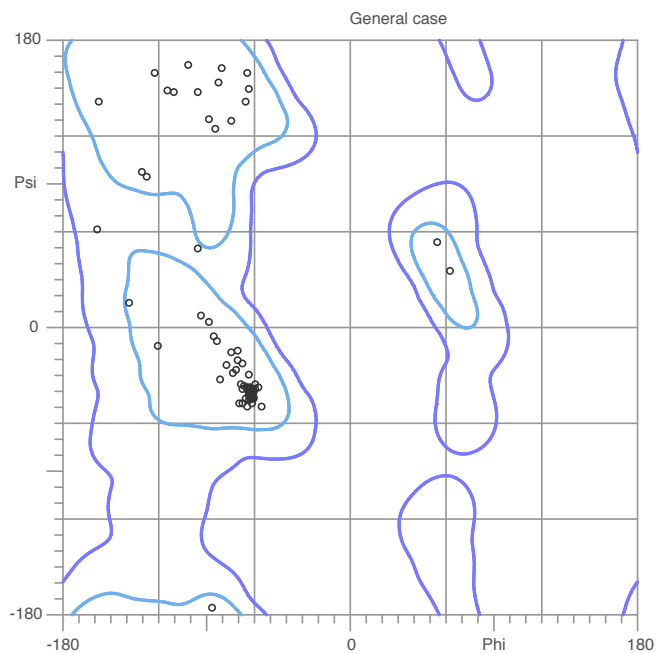
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 4

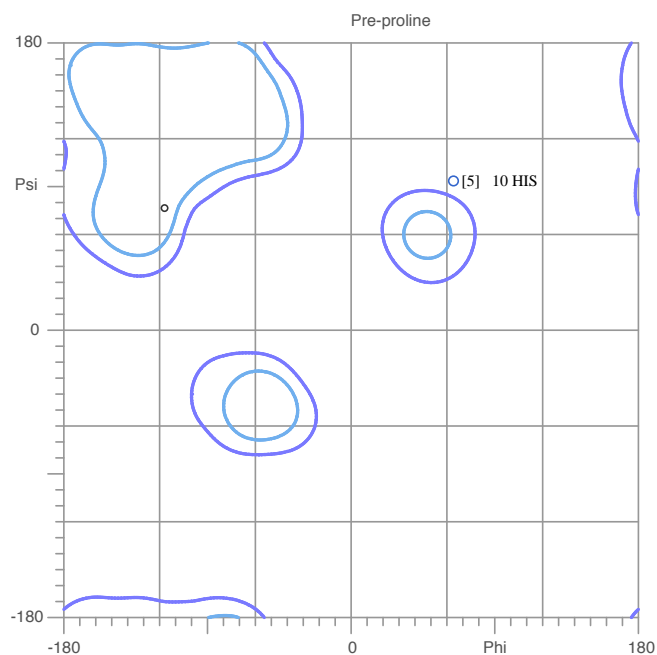
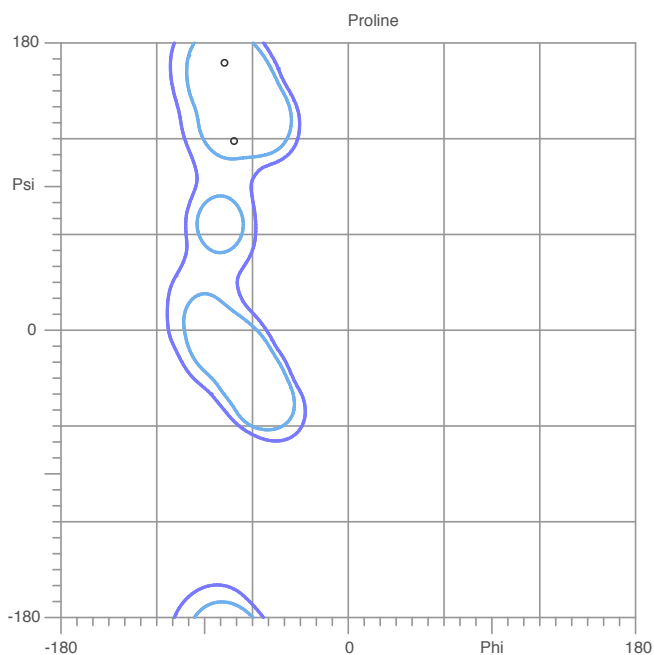
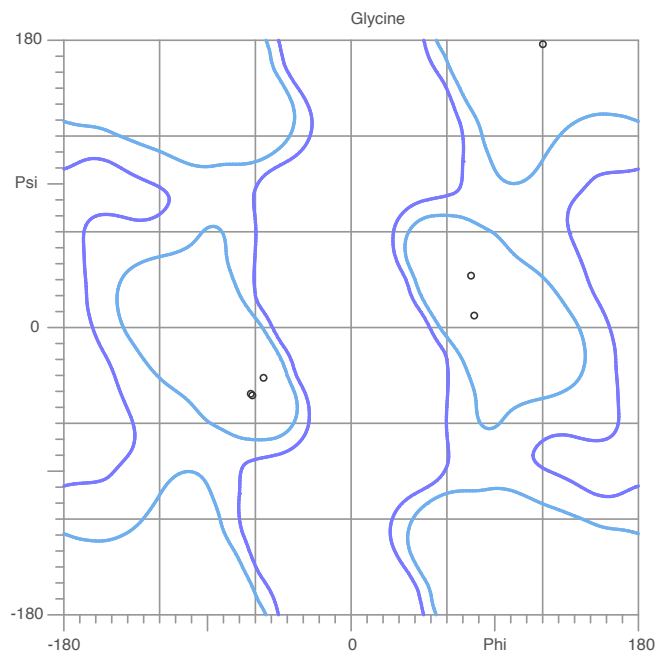
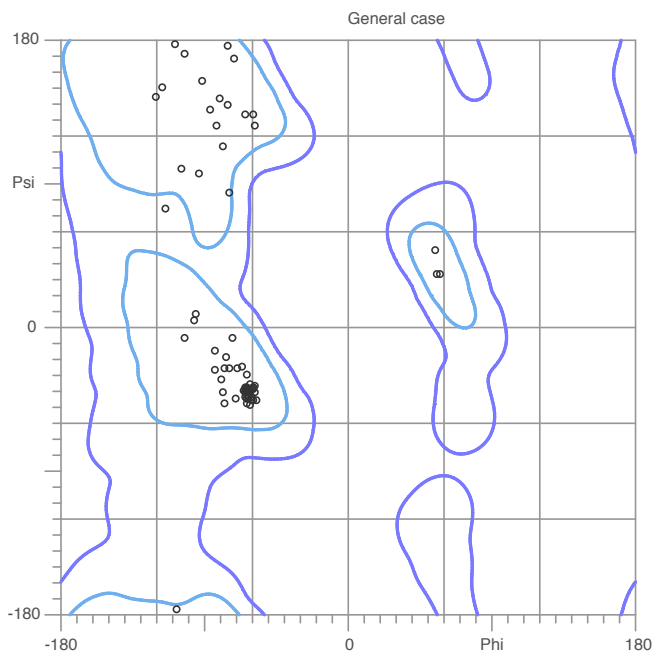


95.2% (80/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[4] 43 PRO (-62.1, -159.9)

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 5

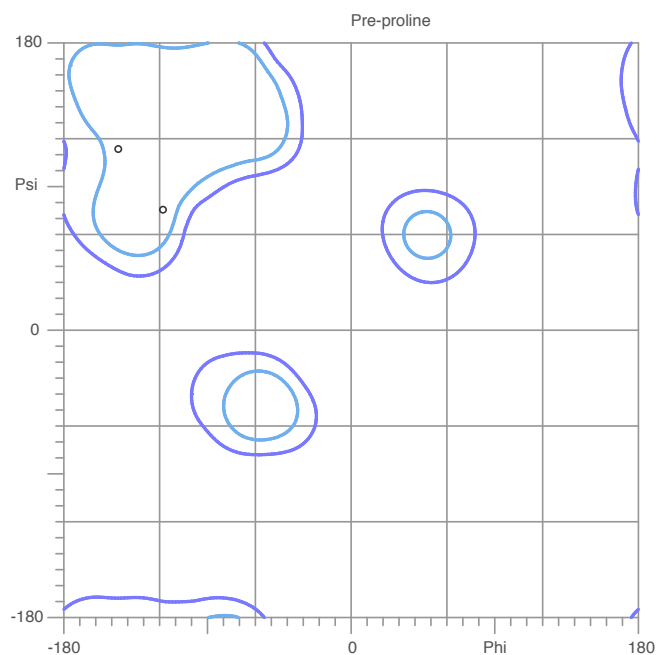
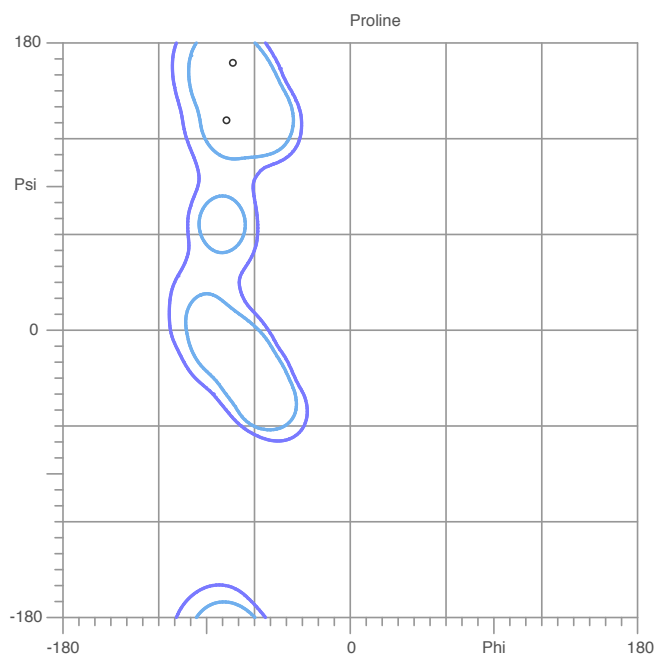
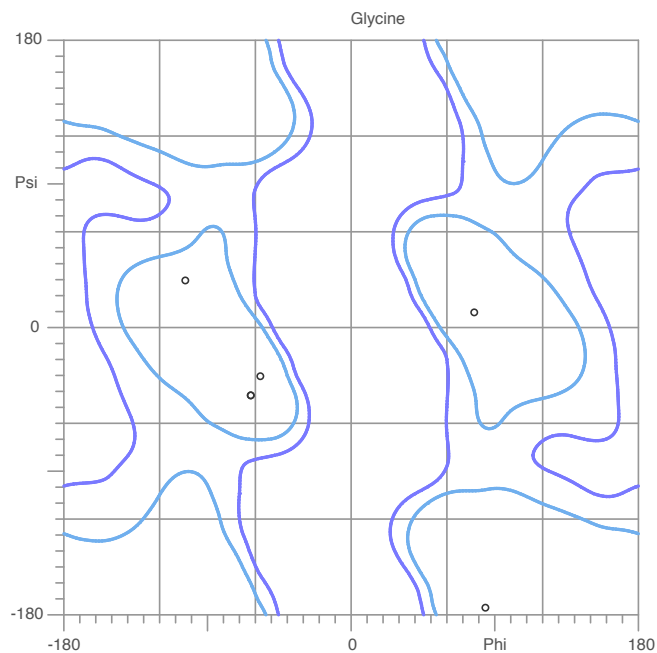
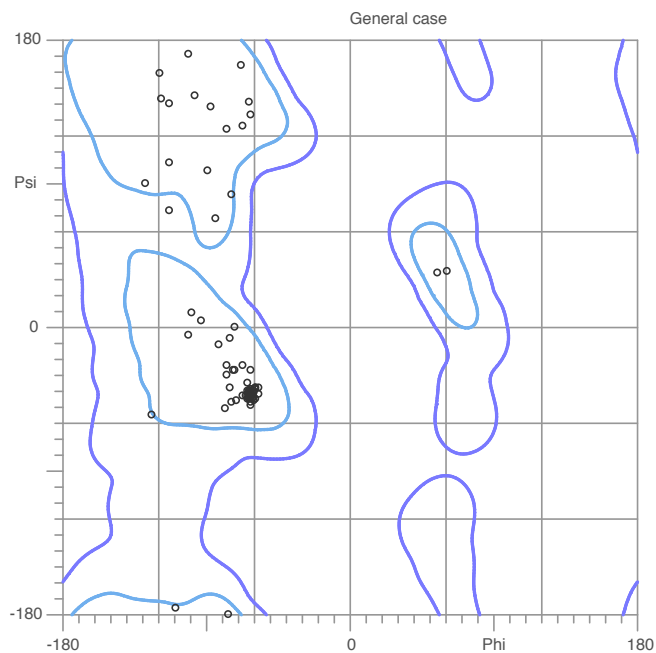


97.6% (82/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 10 HIS (65.0, 94.9)

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 6



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.

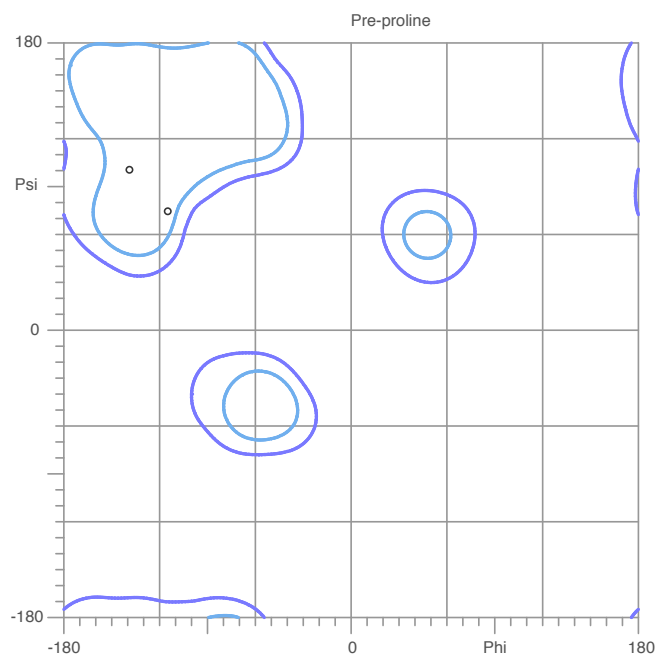
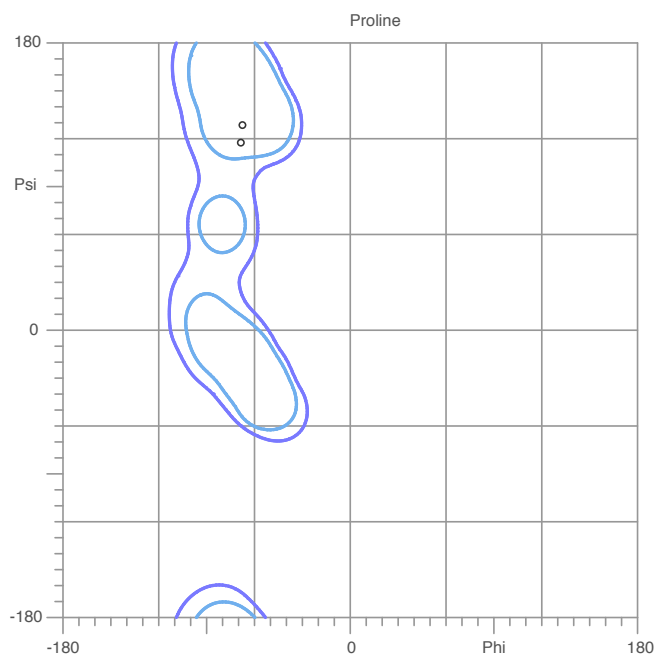
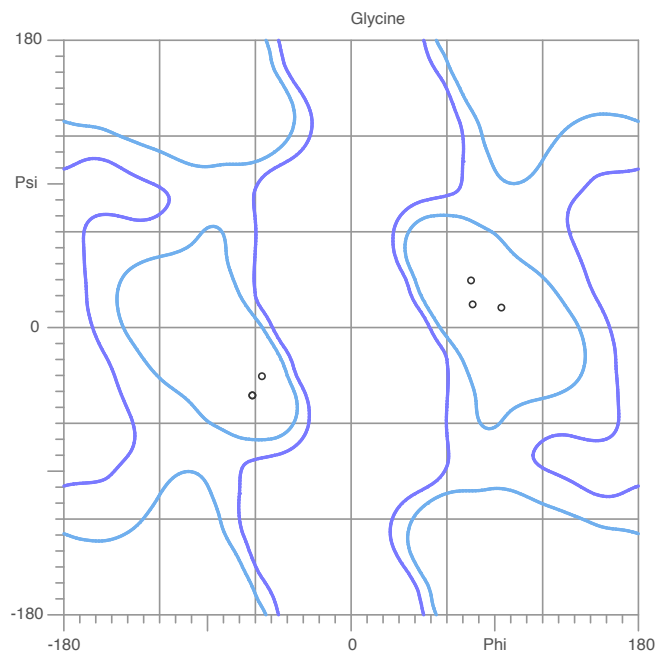
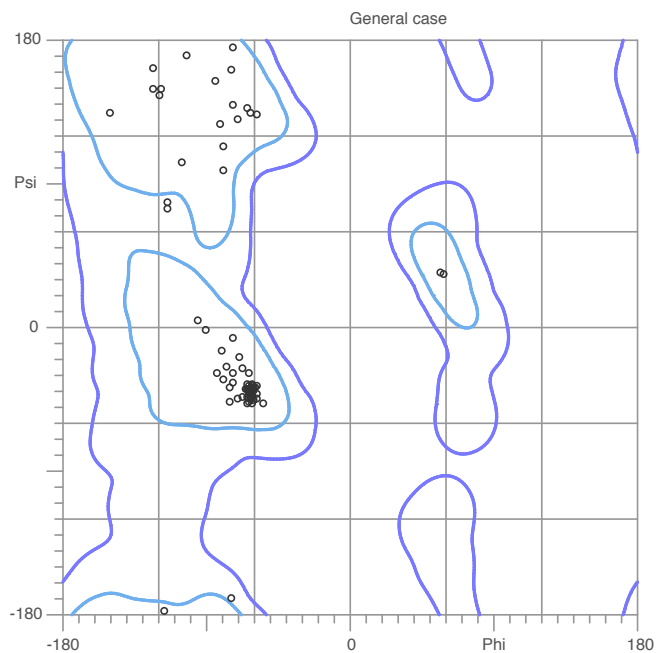
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 7



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.

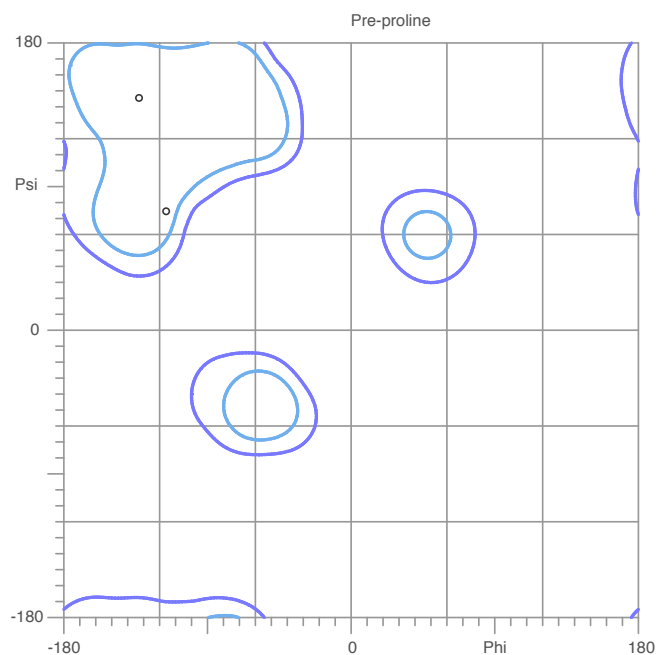
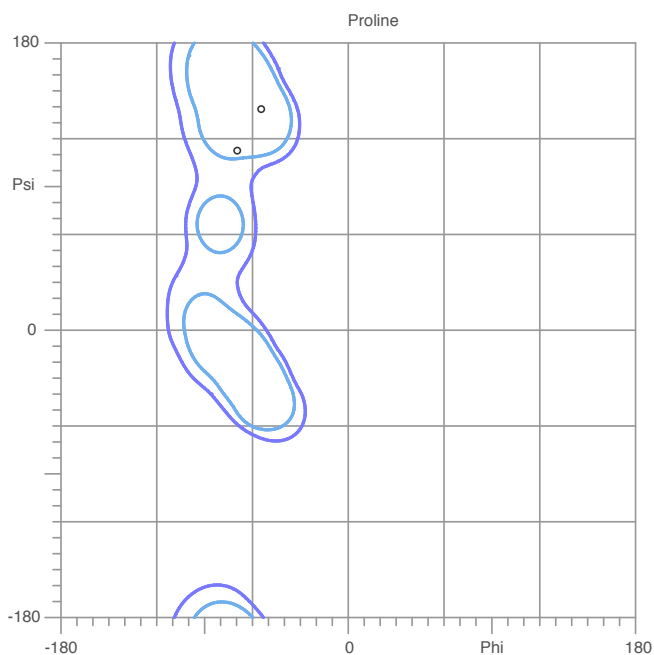
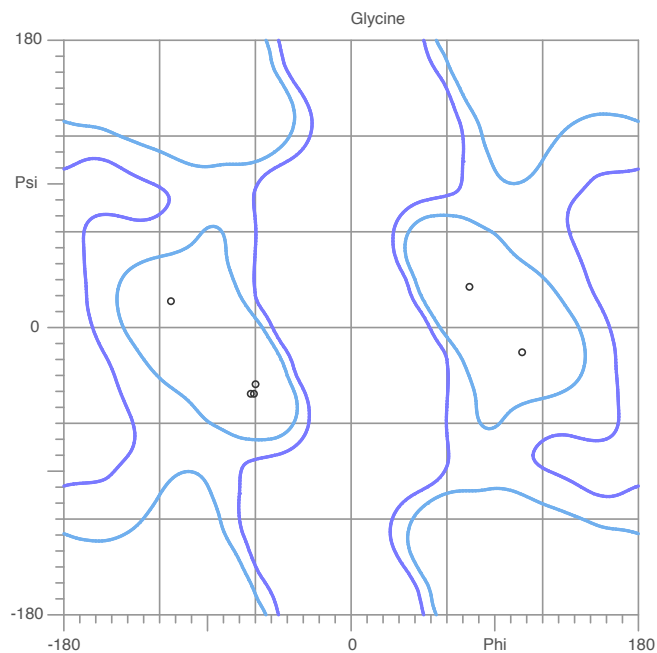
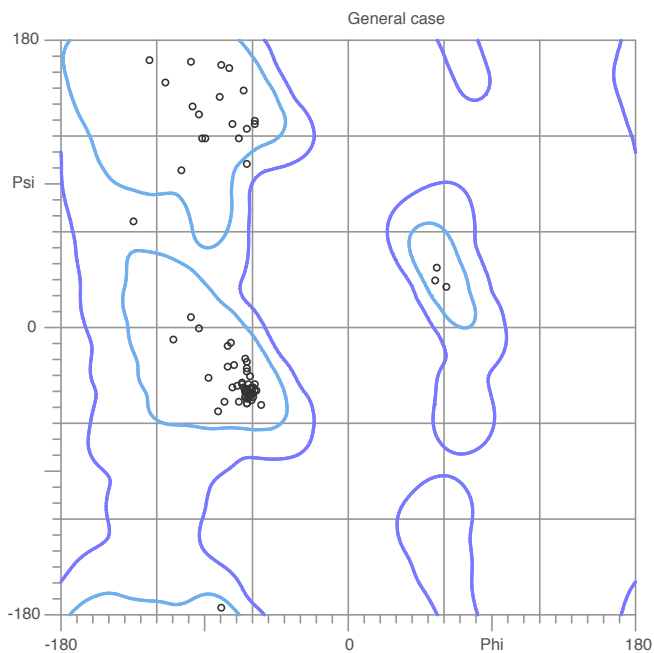
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 8



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.

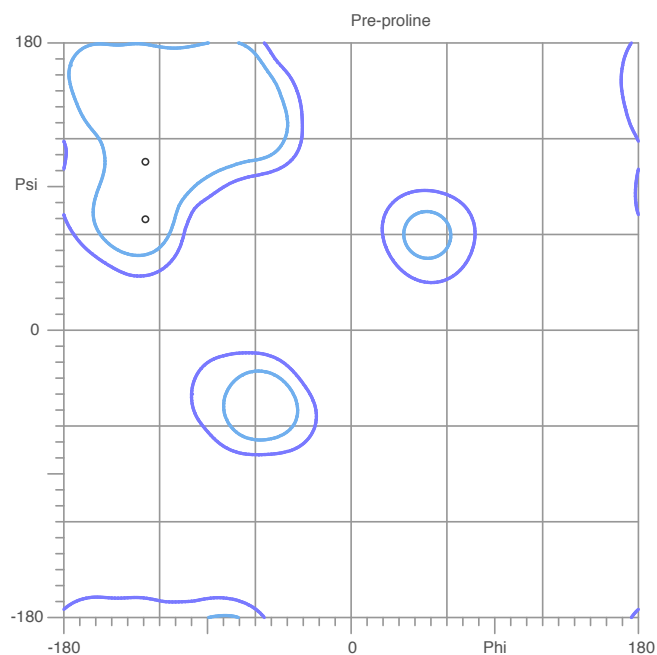
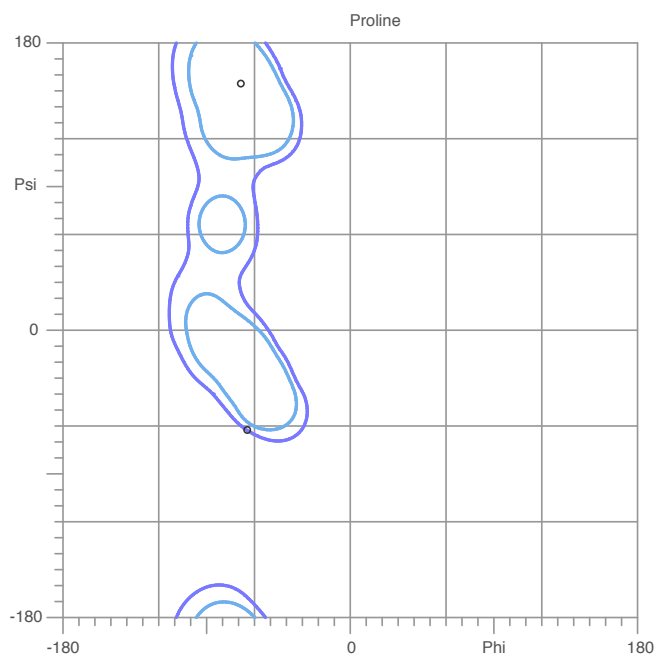
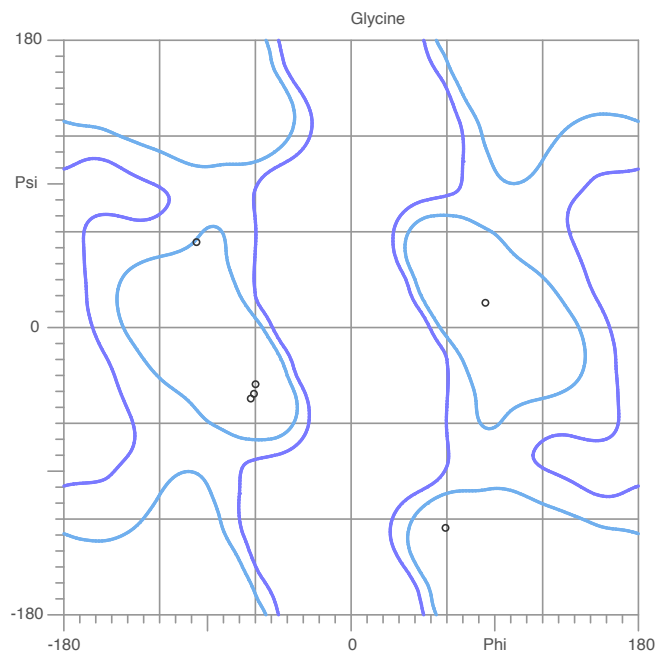
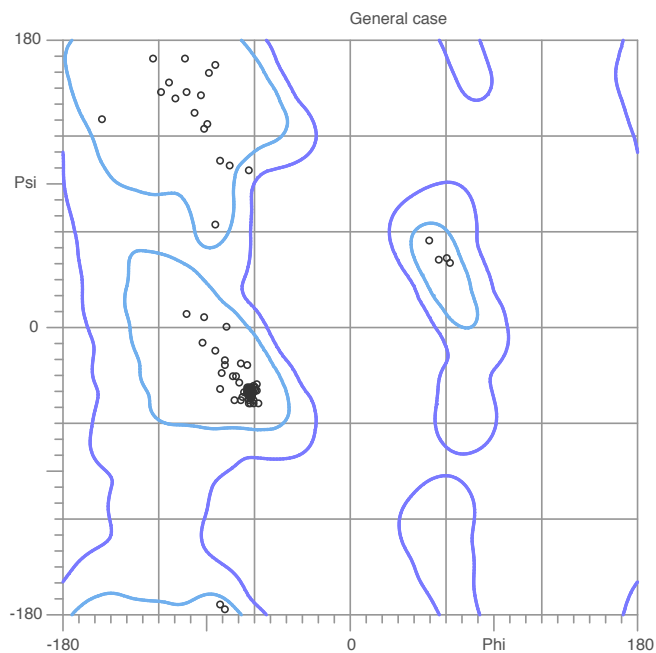
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 9



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.

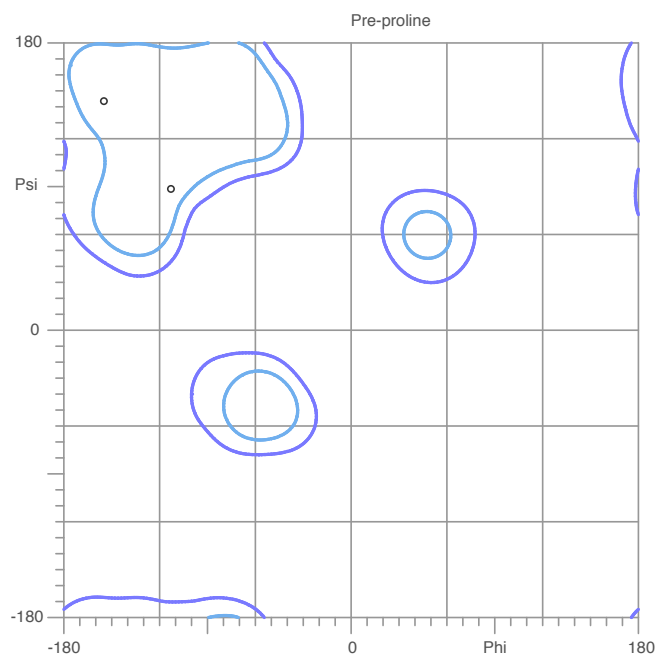
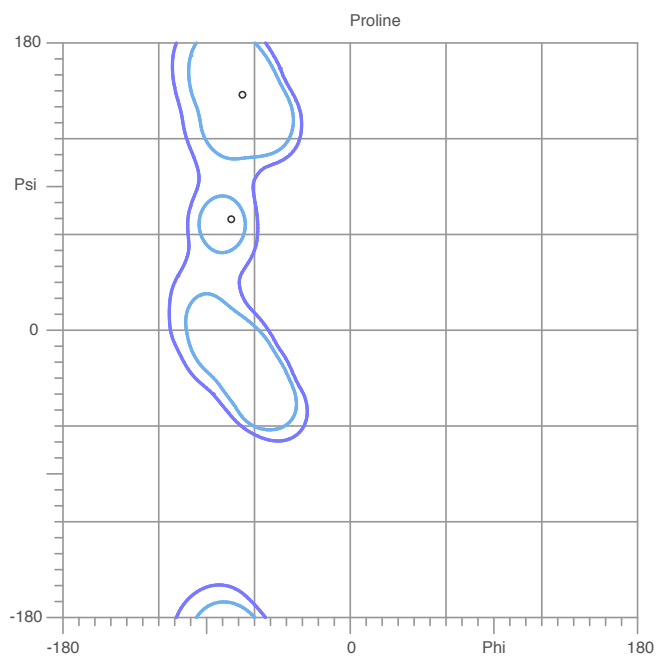
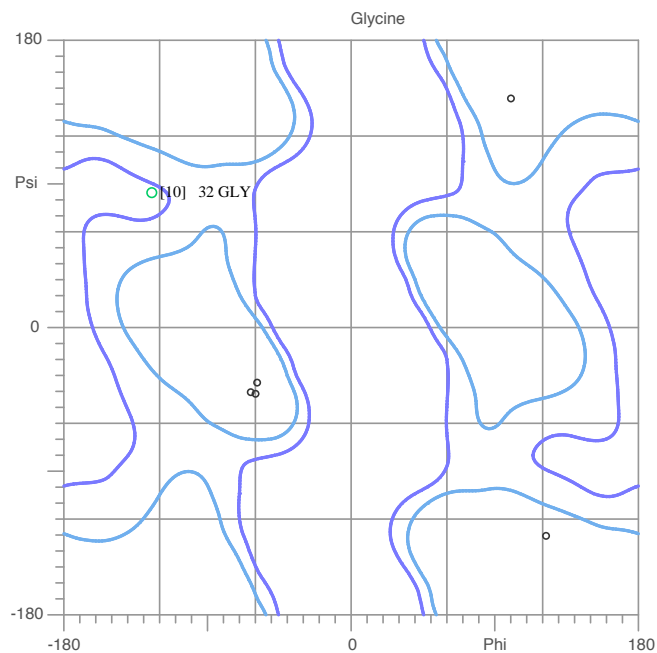
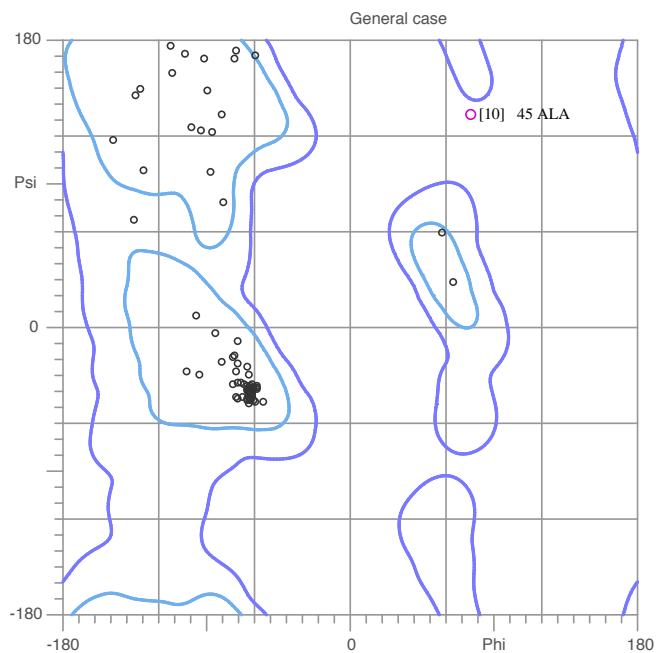
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 10

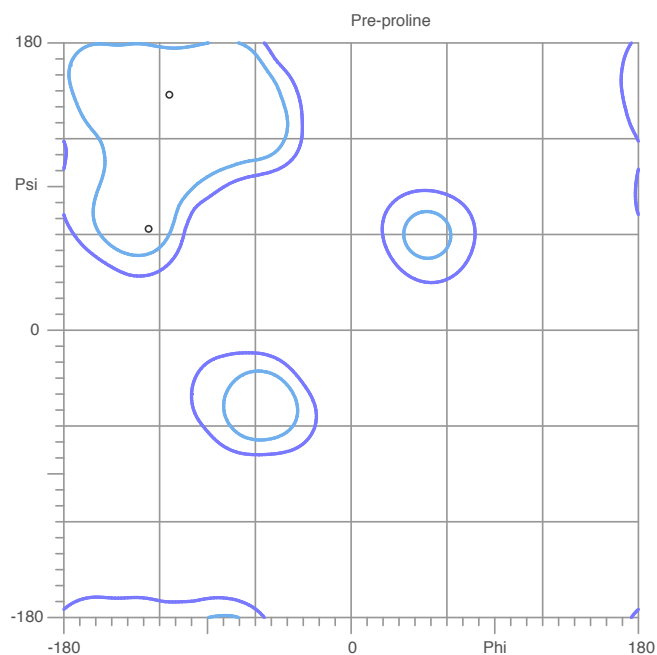
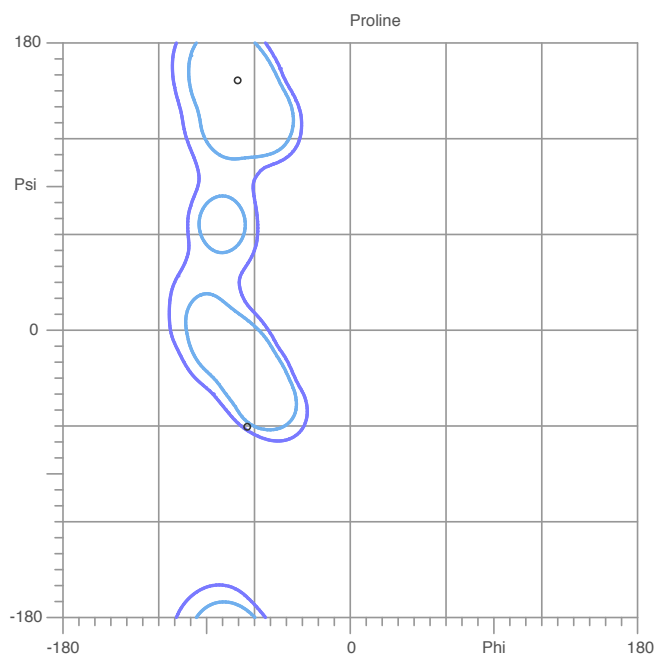
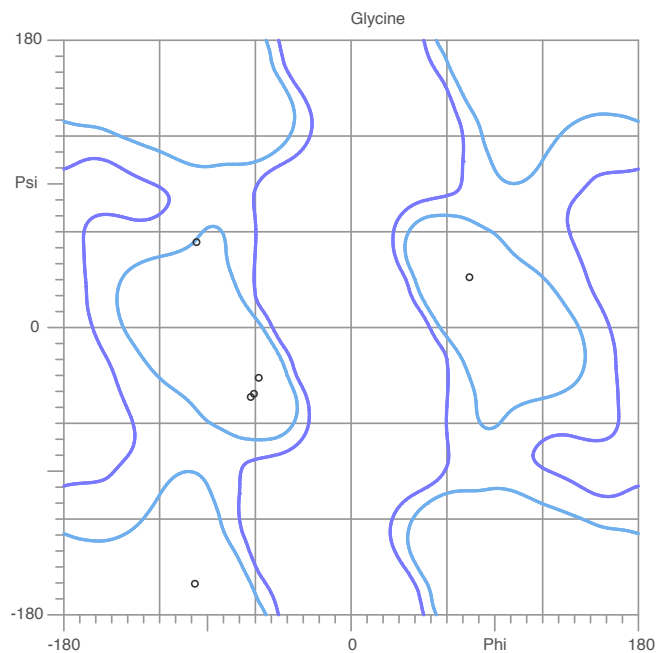
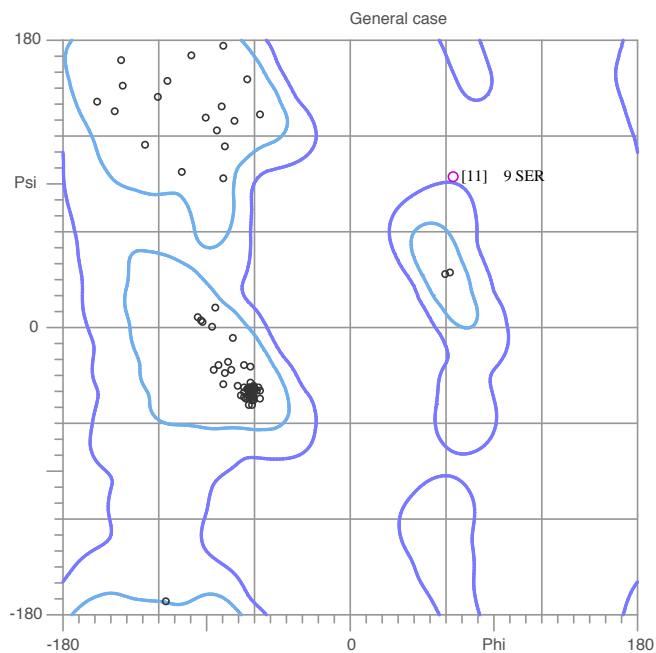


95.2% (80/84) of all residues were in favored (98%) regions.
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[10] 32 GLY (-125.2, 85.0)
[10] 45 ALA (75.7, 135.0)

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 11



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.

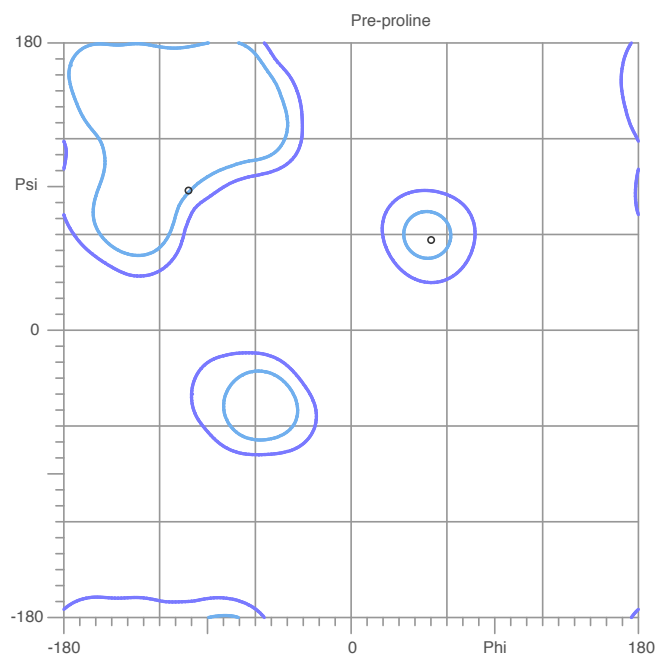
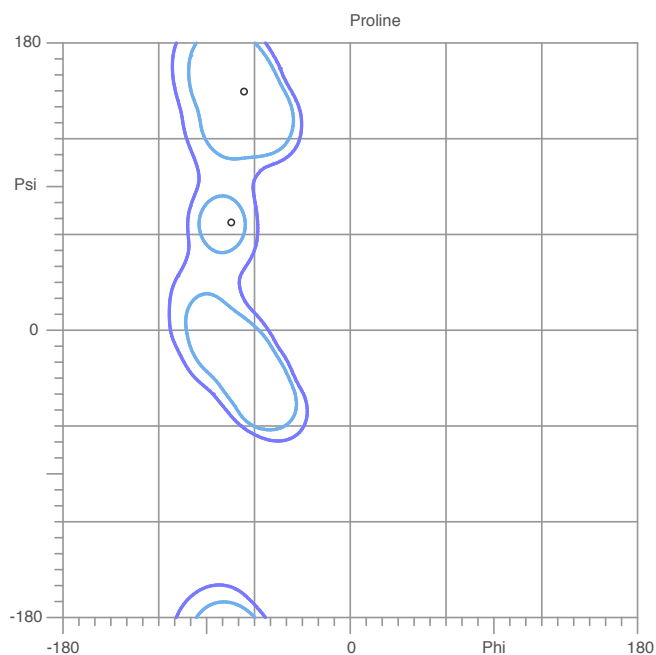
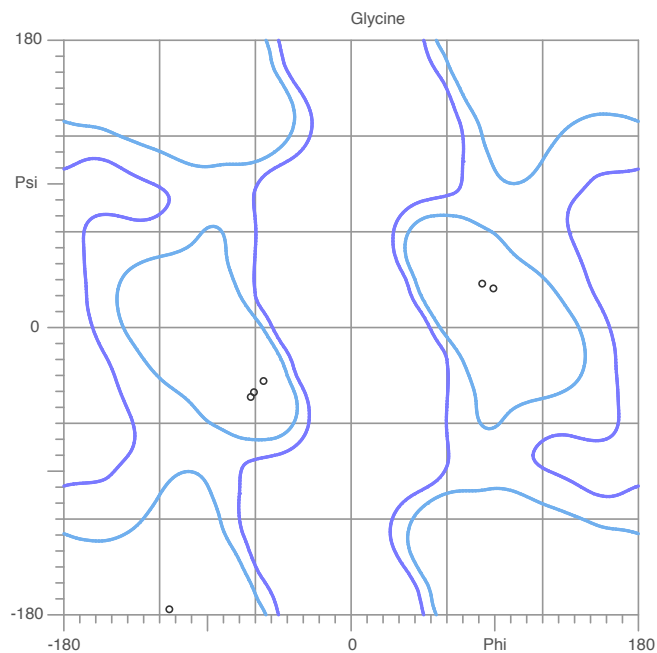
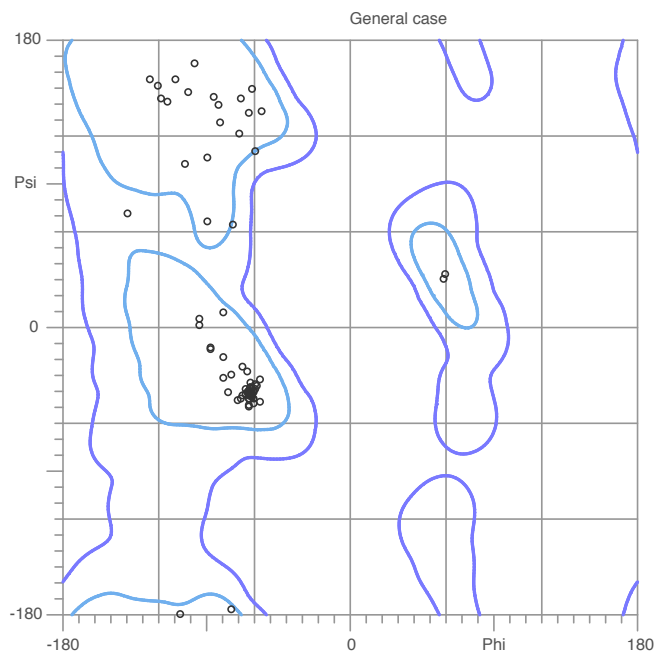
There were 1 outliers (phi, psi):
[11] 9 SER (64.7, 95.1)

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MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 12



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.

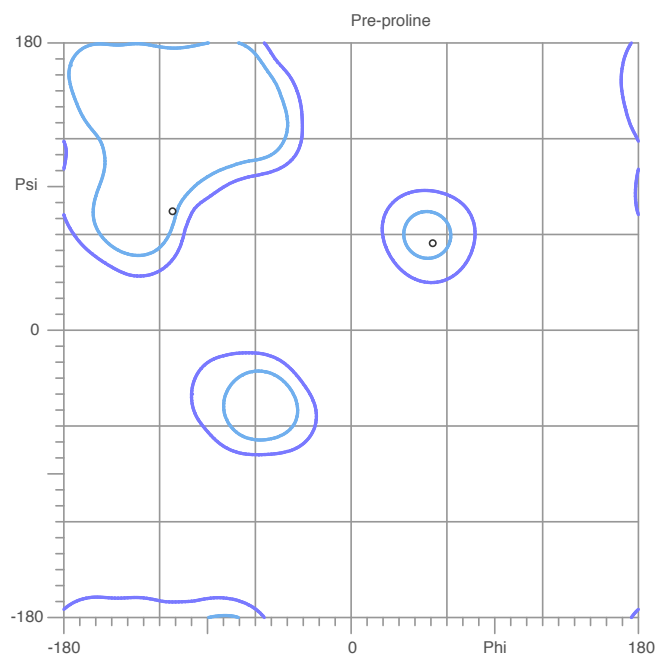
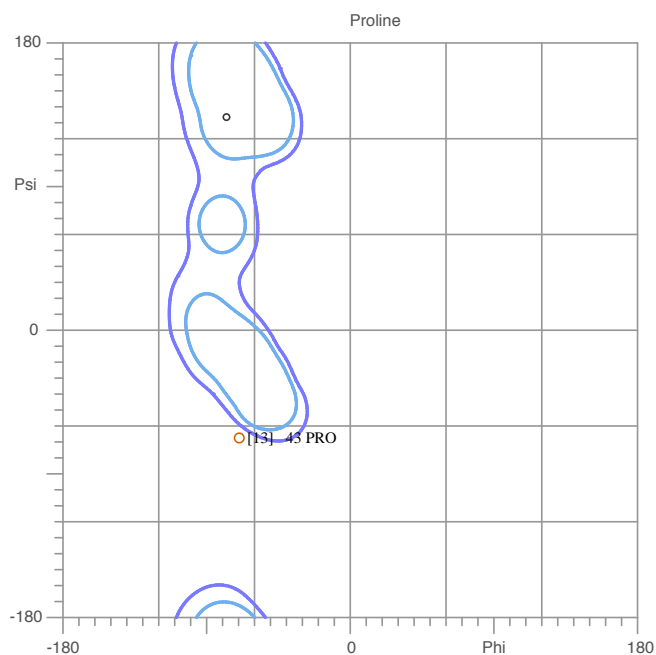
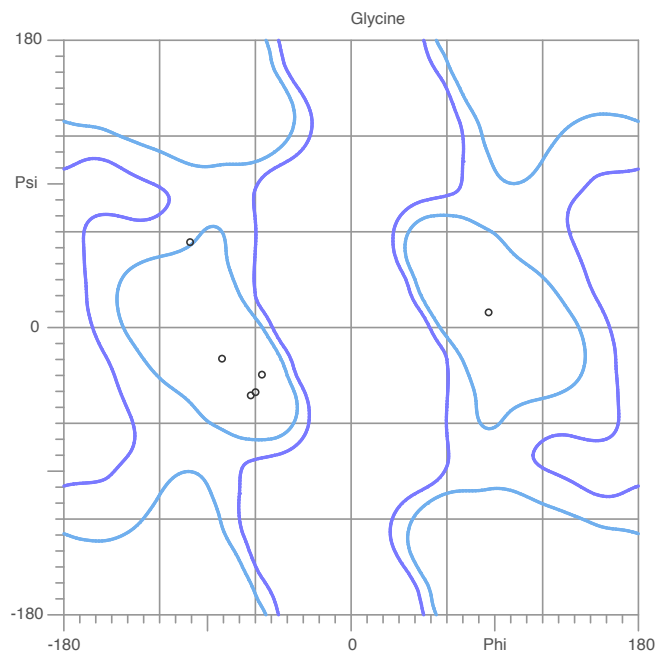
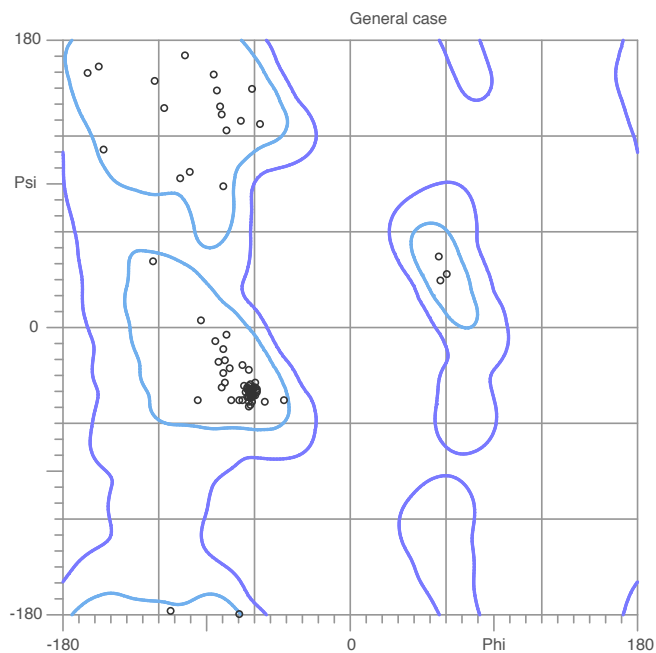
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 13

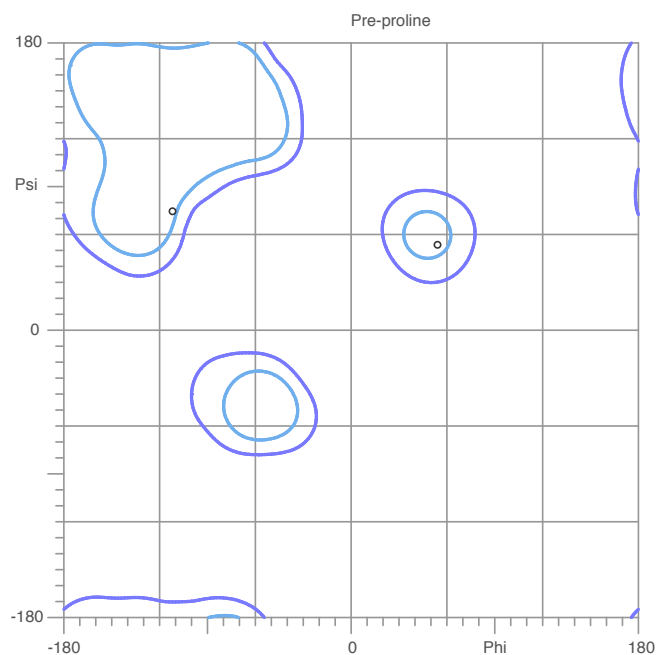
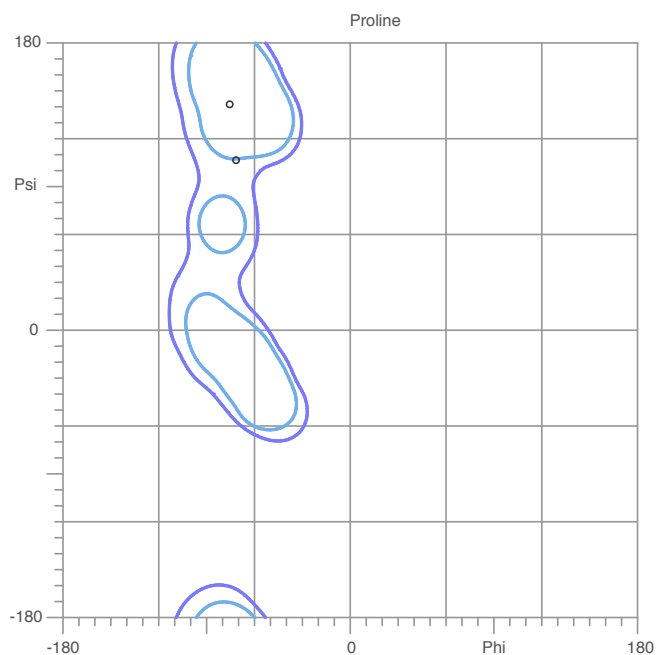
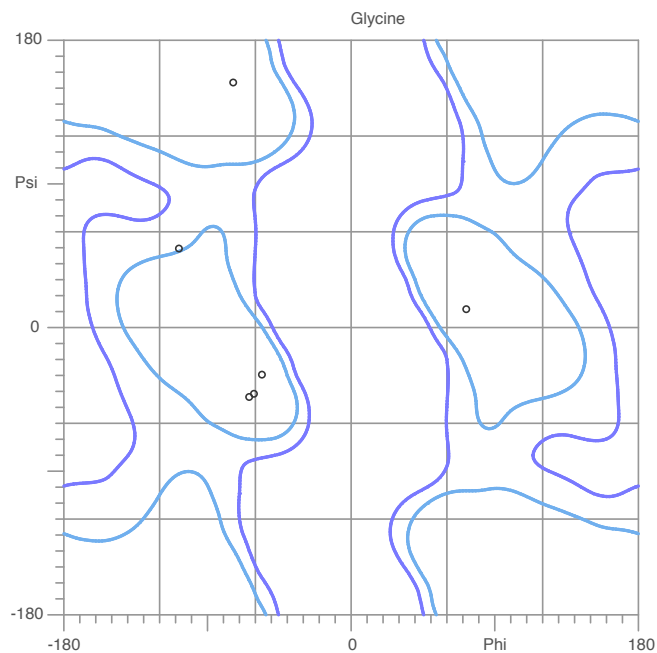
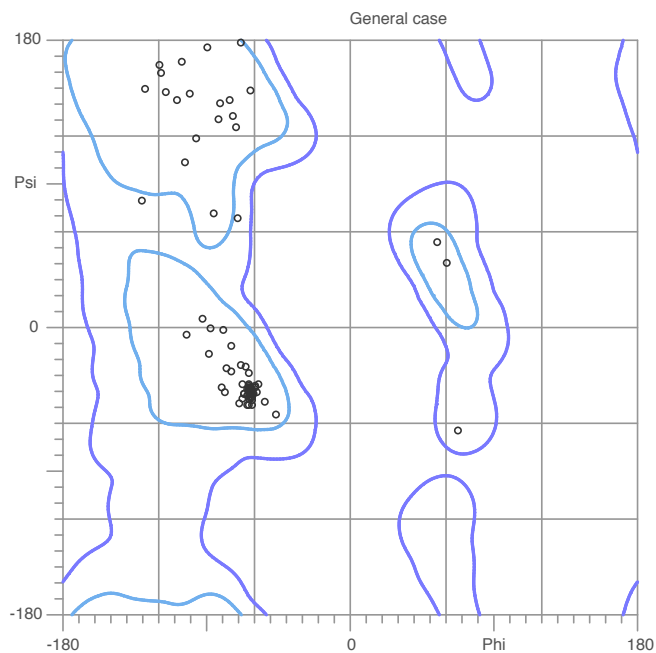


97.6% (82/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[13] 43 PRO (-70.9, -67.2)

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 14



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.

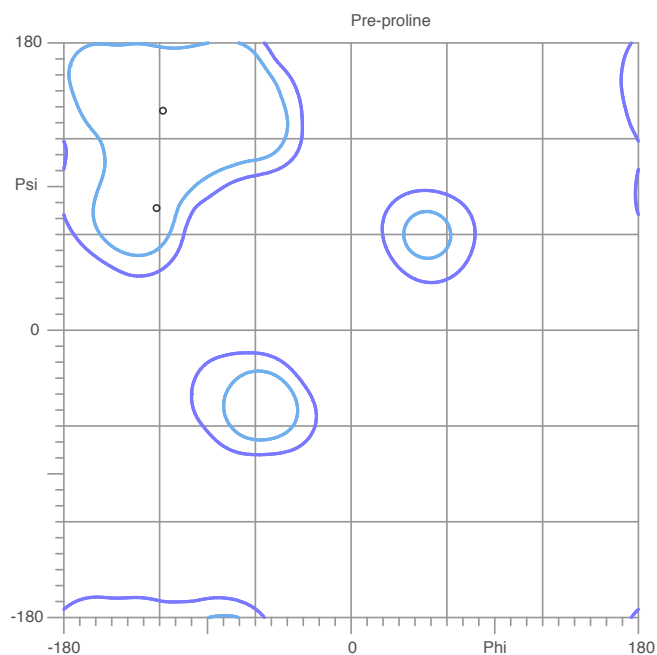
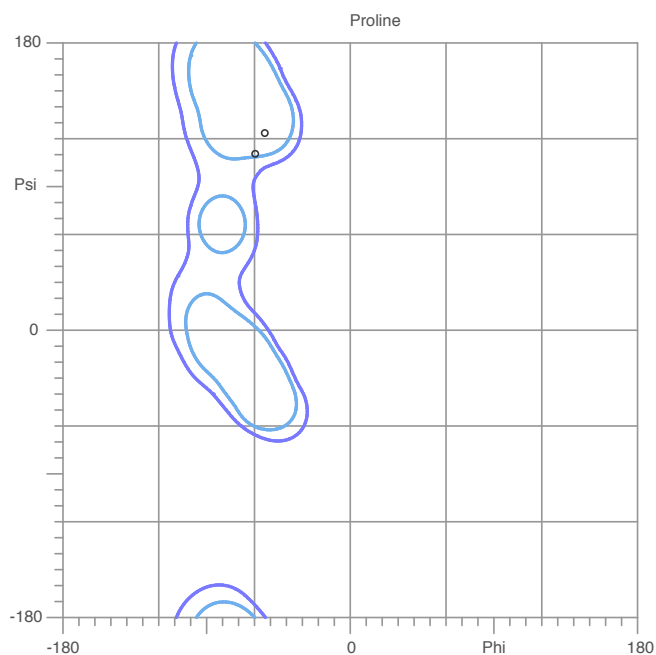
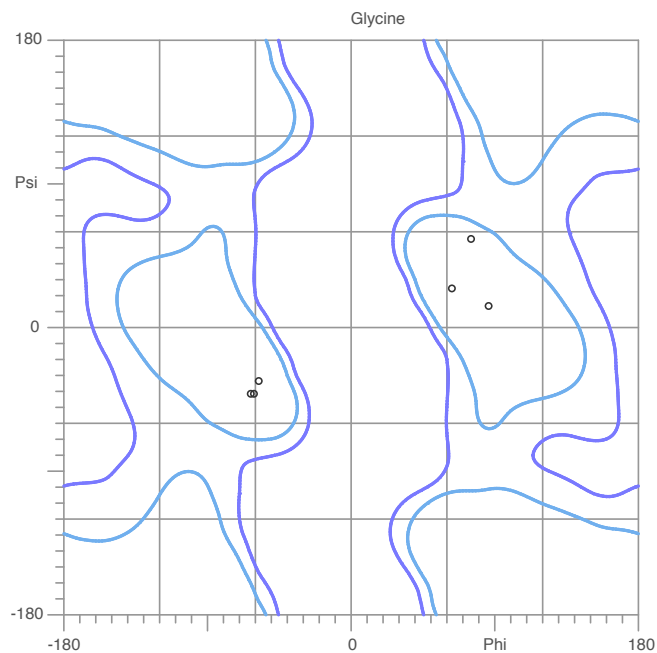
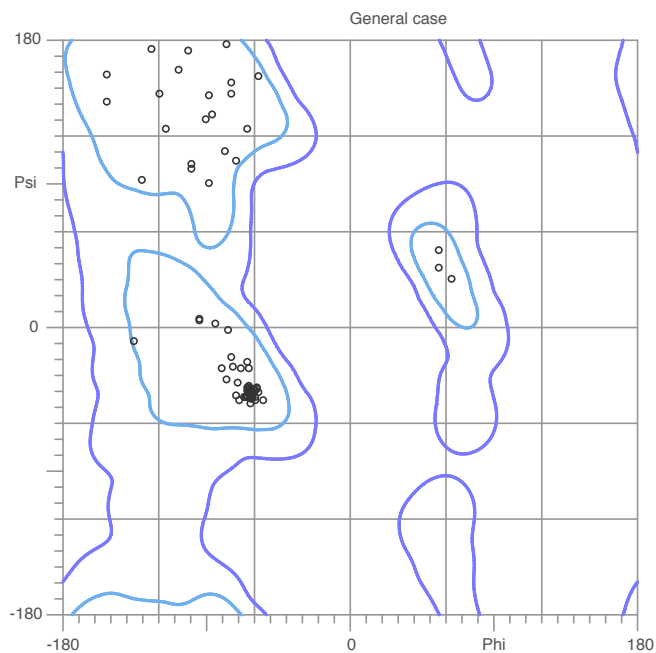
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 15



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

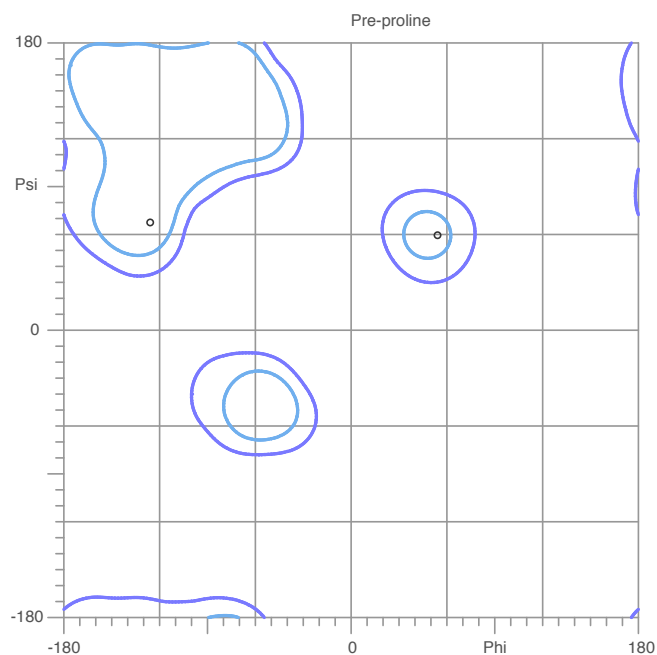
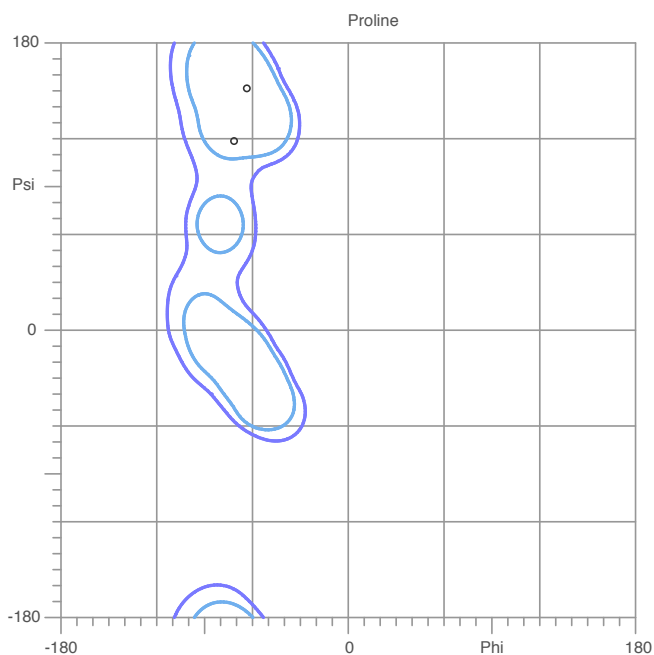
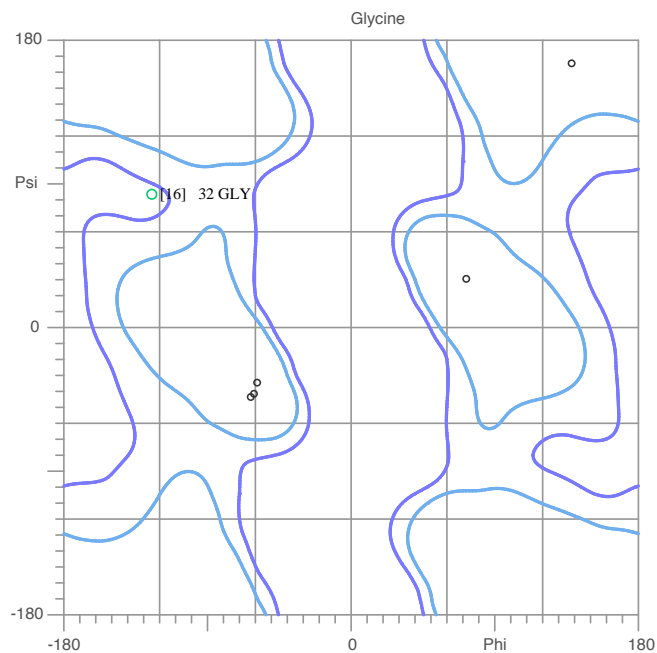
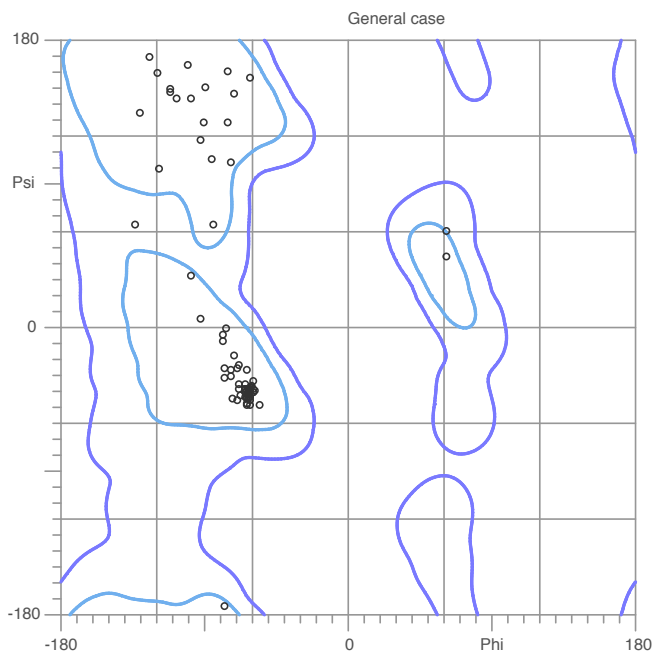
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 16



96.4% (81/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

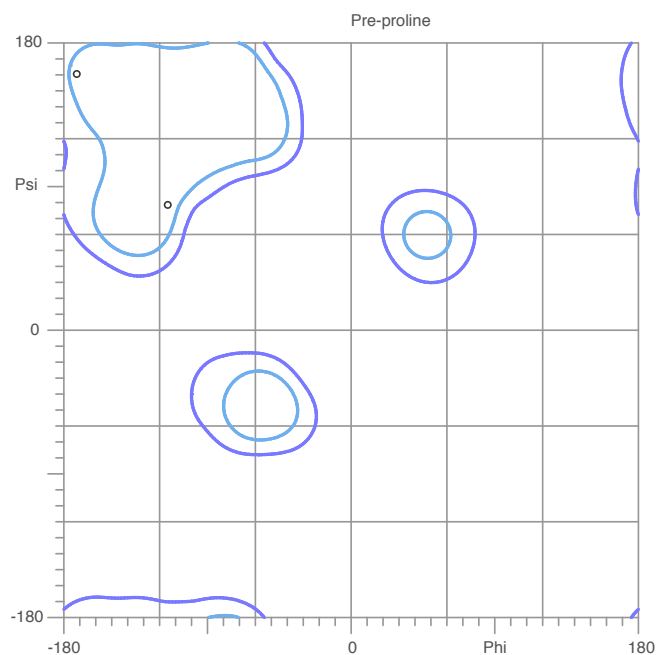
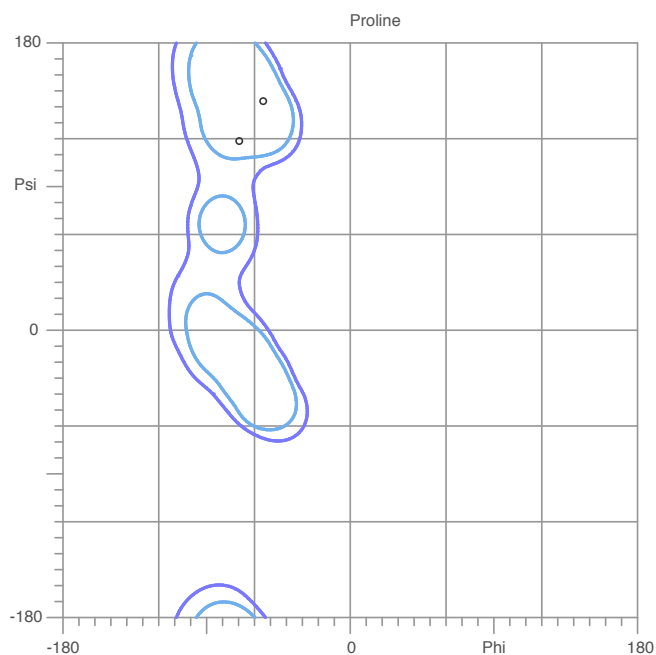
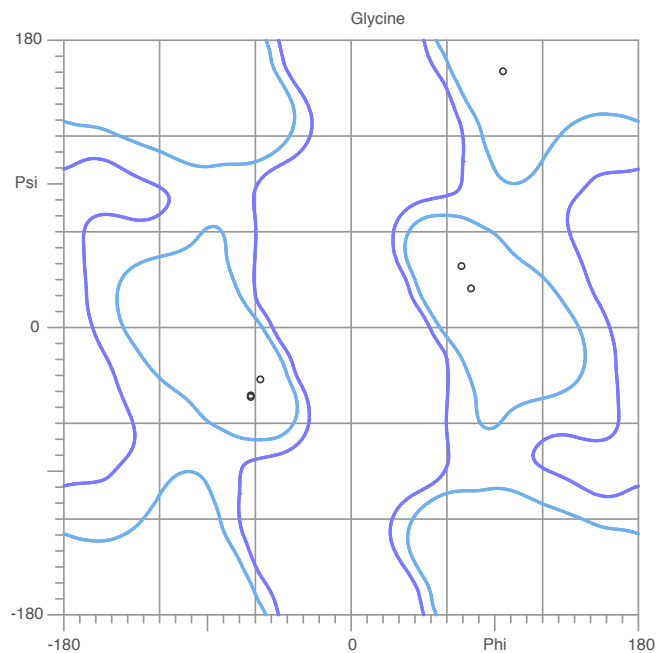
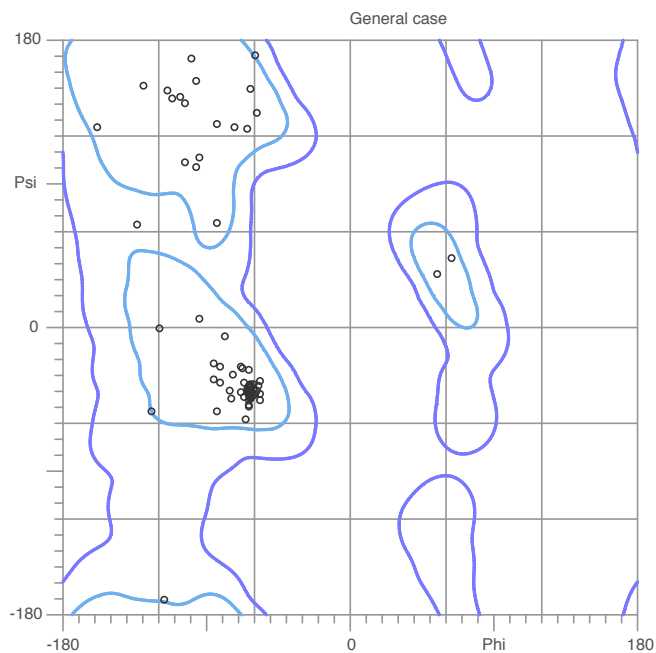
There were 1 outliers (phi, psi):
[16] 32 GLY (-125.0, 84.9)

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 17



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.

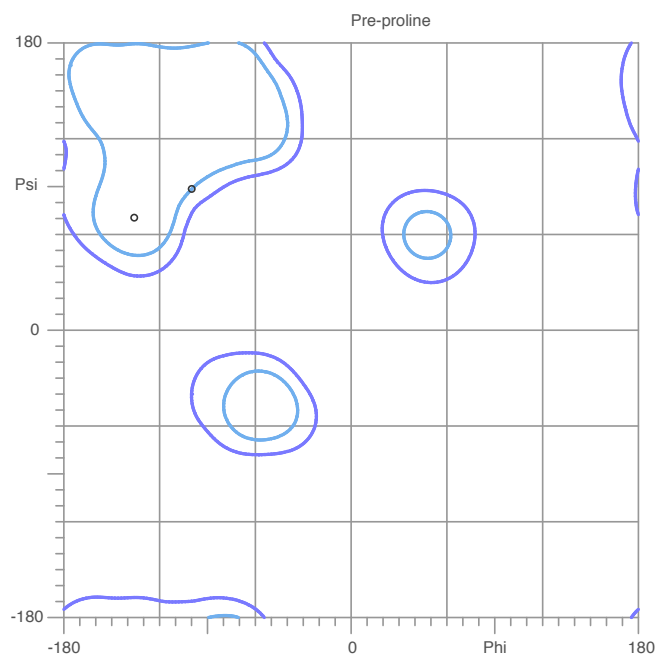
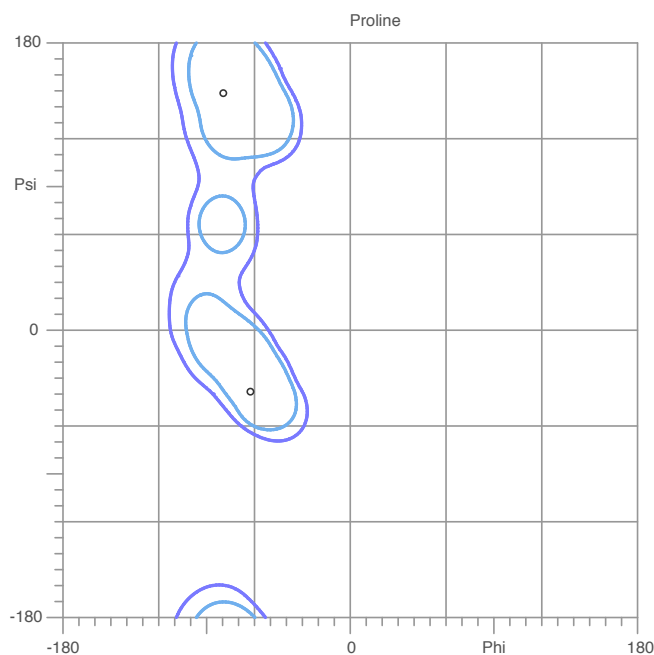
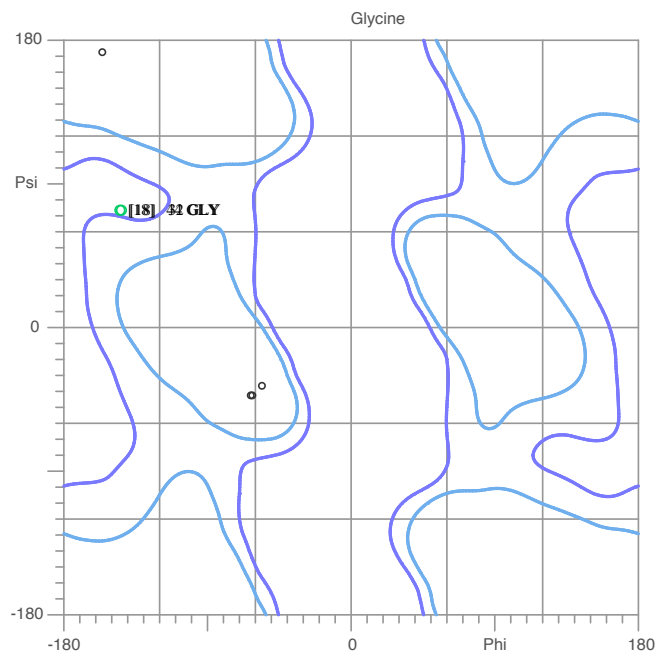
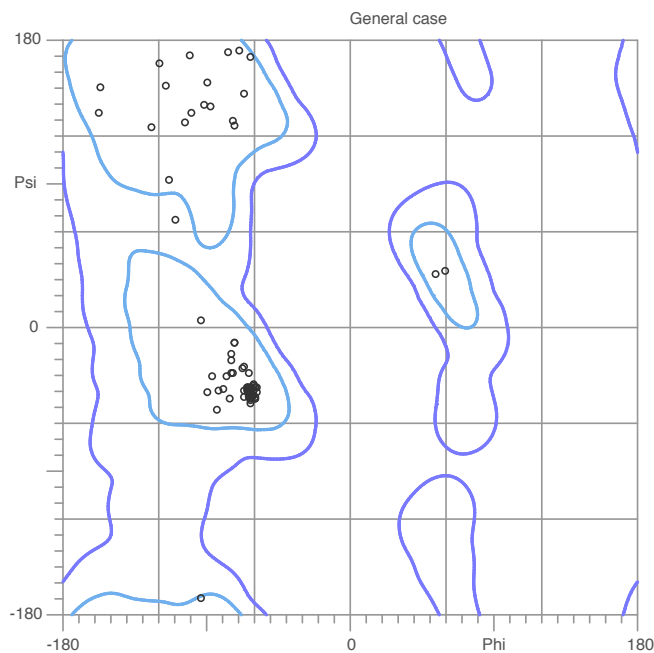
There were no outliers.

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

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 18

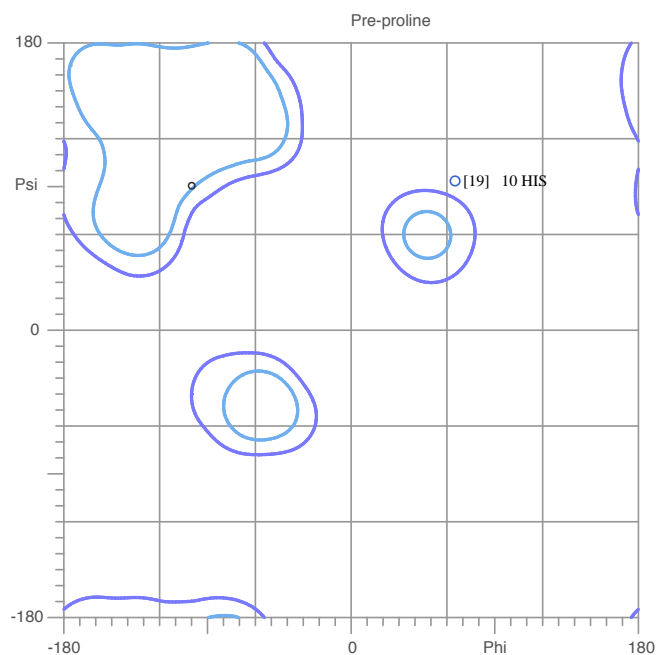
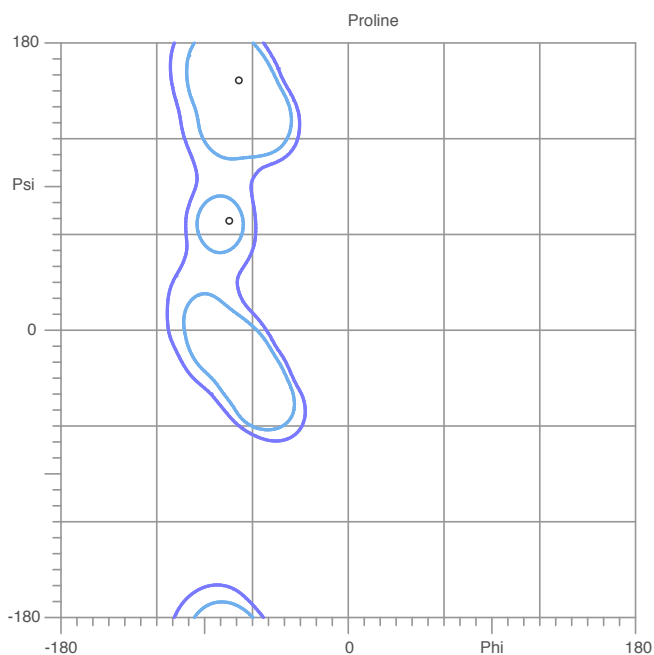
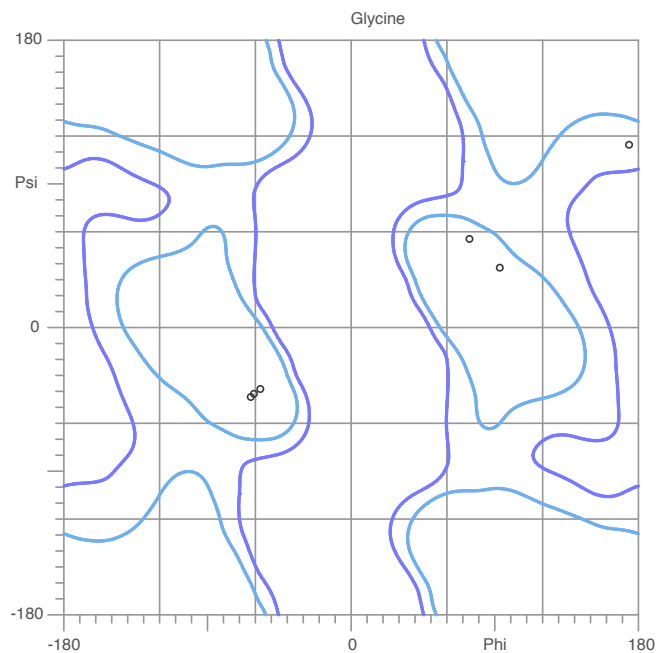
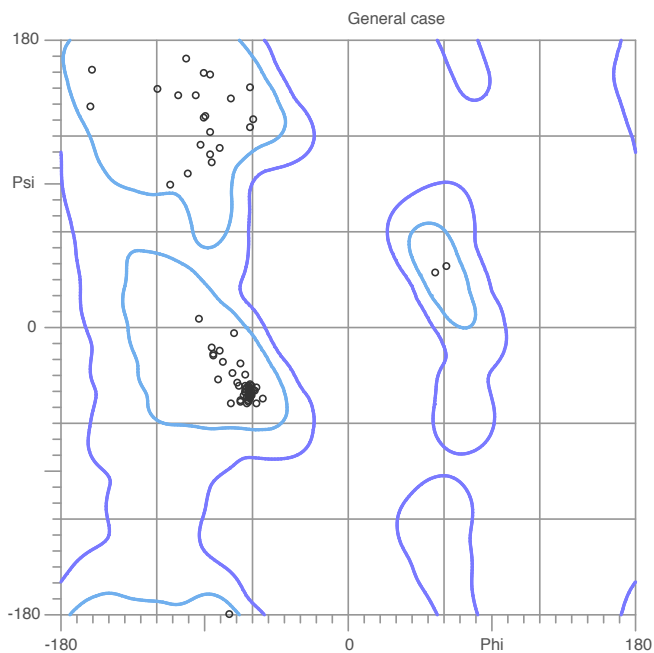


96.4% (81/84) of all residues were in favored (98%) regions.
97.6% (82/84) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 32 GLY (-145.0, 75.0)
[18] 44 GLY (-145.0, 75.0)

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 19

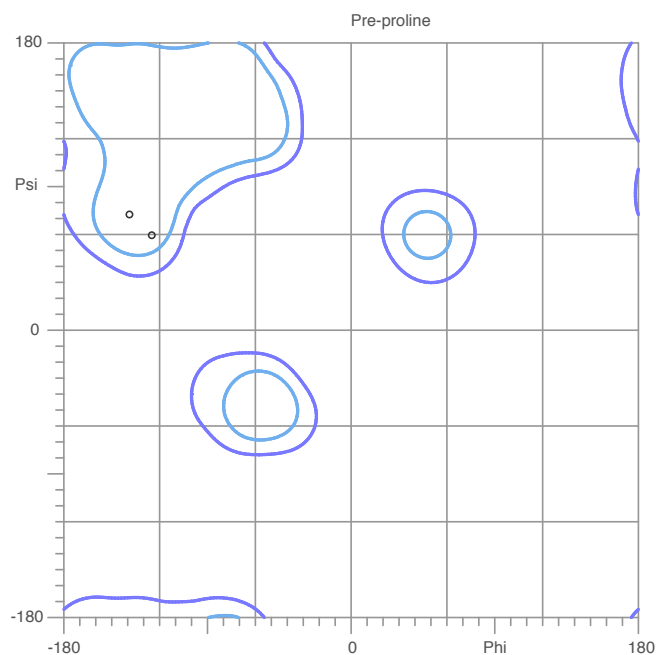
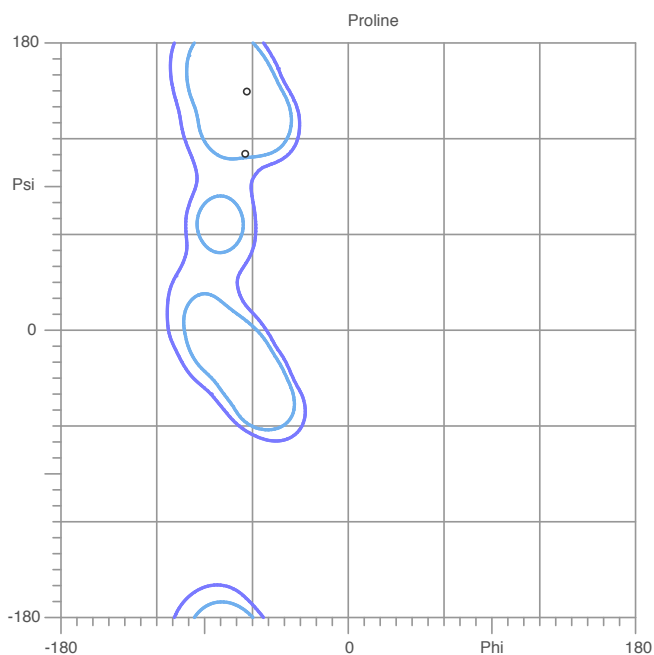
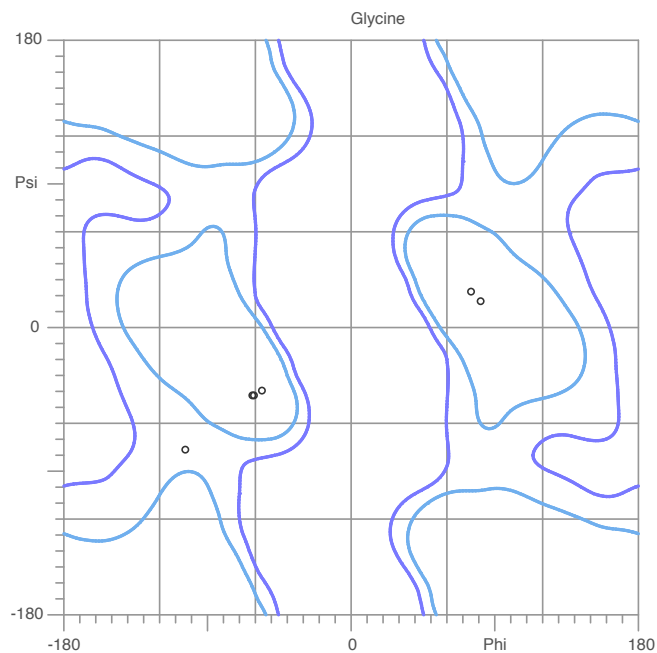
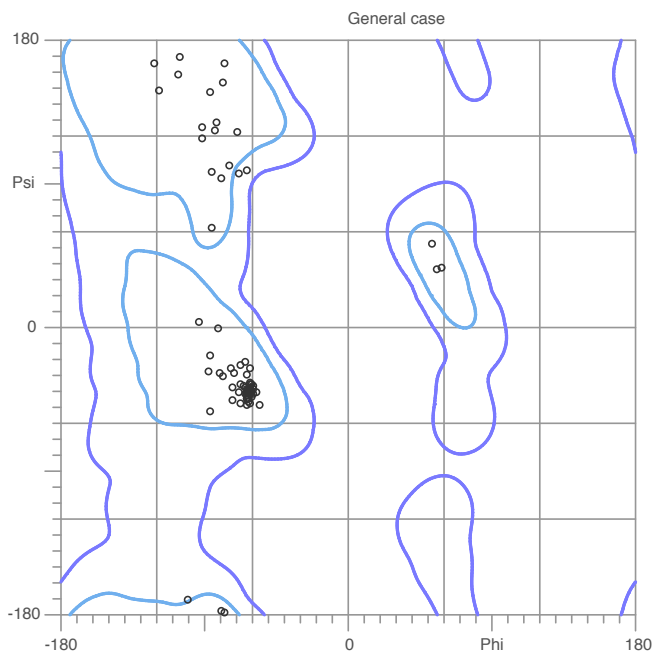


97.6% (82/84) of all residues were in favored (98%) regions.
98.8% (83/84) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[19] 10 HIS (65.0, 94.9)

MolProbity Ramachandran analysis

HR3102A_R3Cons_em_bcr3.pdb, model 20



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.

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