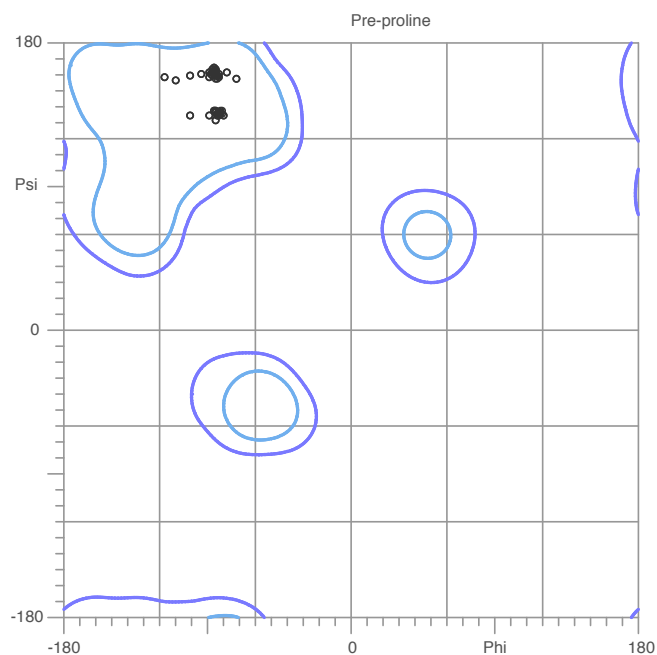
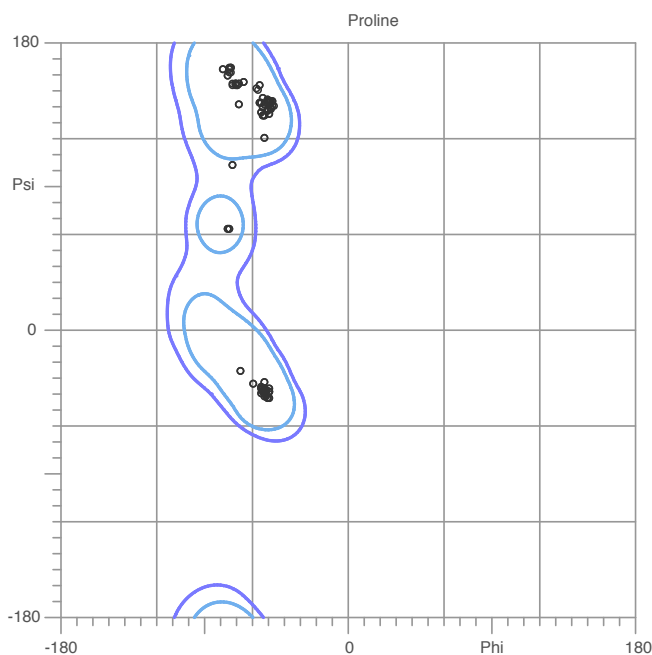
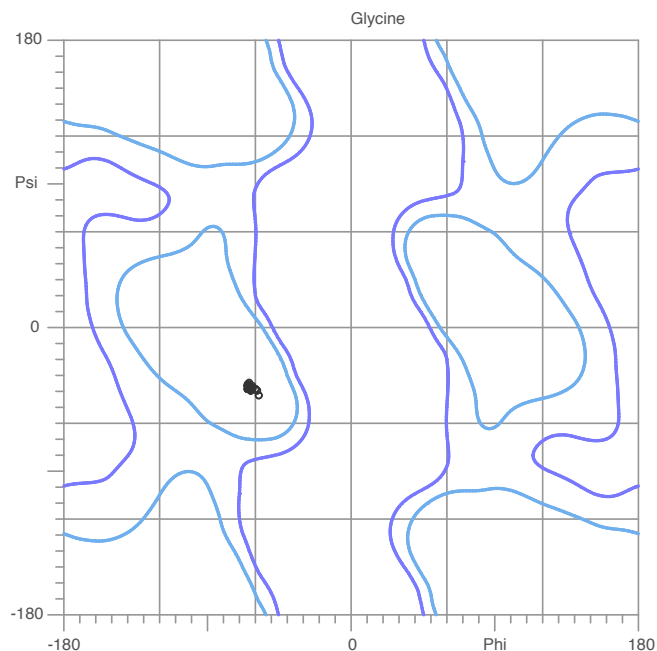
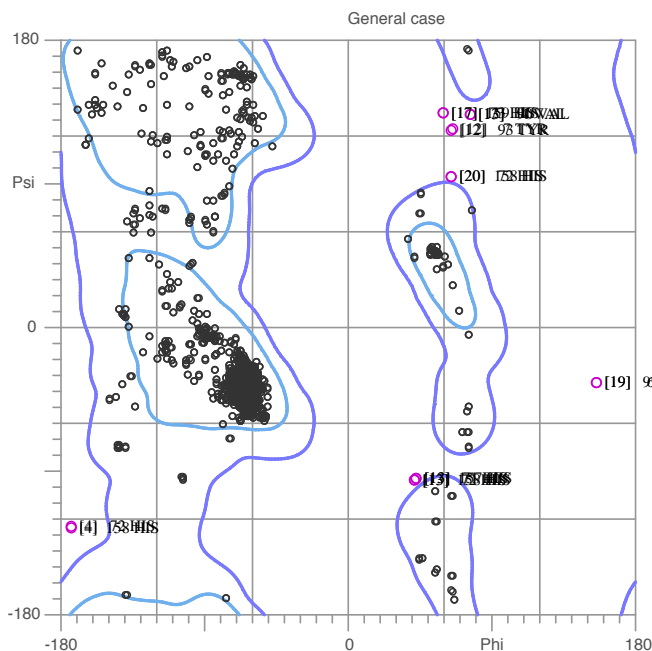


MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, all models



95.0% (2812/2960) of all residues were in favored (98%) regions.
99.5% (2944/2960) of all residues were in allowed (>99.8%) regions.

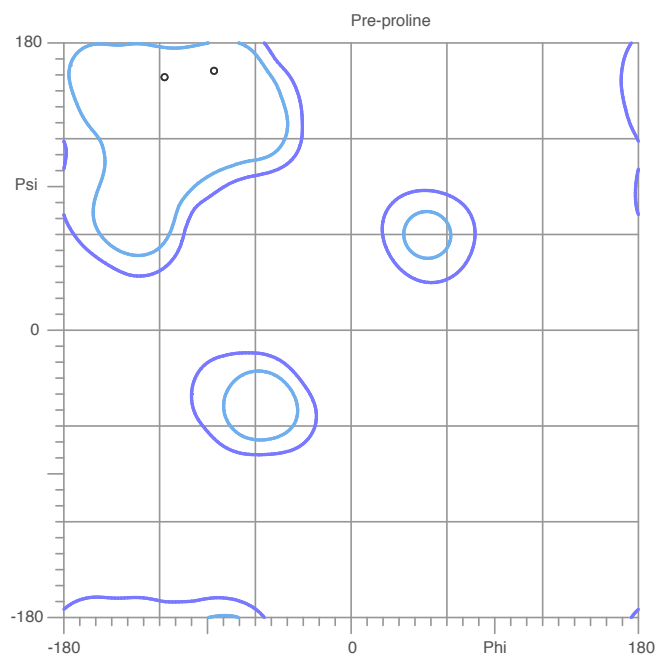
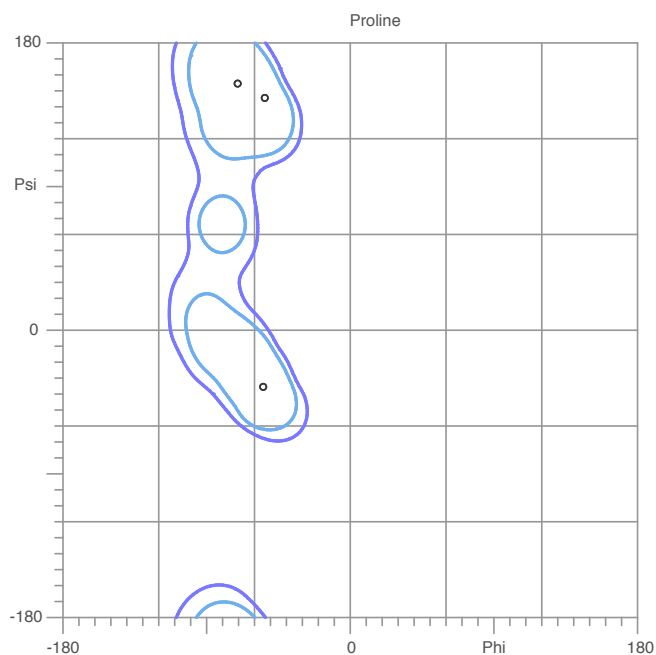
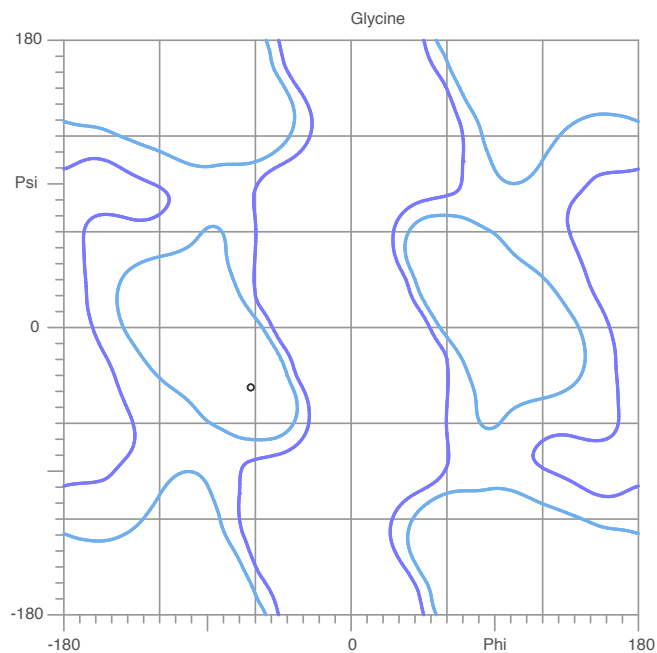
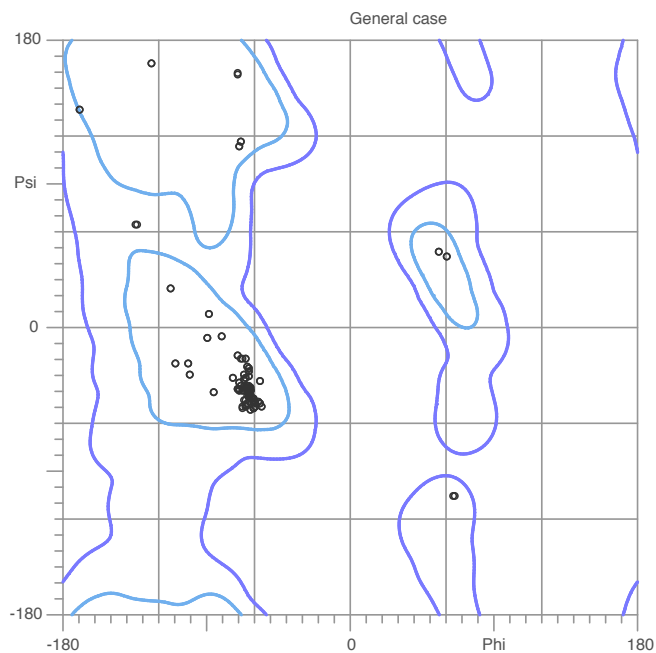
There were 16 outliers (phi, psi):

- [4] 72 HIS (-174.9, -125.0)
- [4] 158 HIS (-174.8, -125.1)
- [12] 7 TYR (65.0, 125.0)
- [12] 93 TYR (65.0, 125.0)
- [13] 4 VAL (76.1, 134.5)
- [13] 71 HIS (42.4, -94.8)

- [13] 72 HIS (42.0, -95.2)
- [13] 90 VAL (76.2, 134.5)
- [13] 157 HIS (42.4, -94.8)
- [13] 158 HIS (41.9, -95.2)
- [17] 73 HIS (59.7, 135.1)
- [17] 159 HIS (59.7, 135.0)
- [19] 6 LYS (155.1, -35.0)
- [19] 92 LYS (155.1, -35.0)
- [20] 72 HIS (65.0, 95.1)
- [20] 158 HIS (64.9, 95.1)

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 1



95.9% (142/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

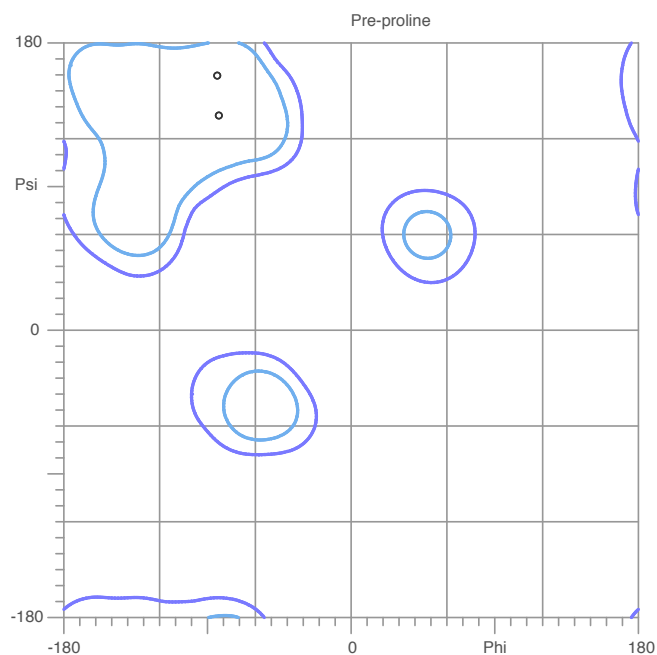
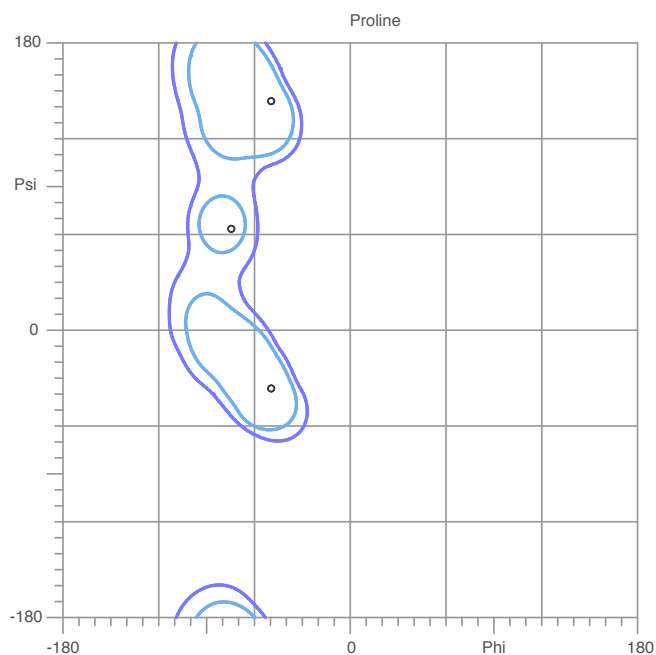
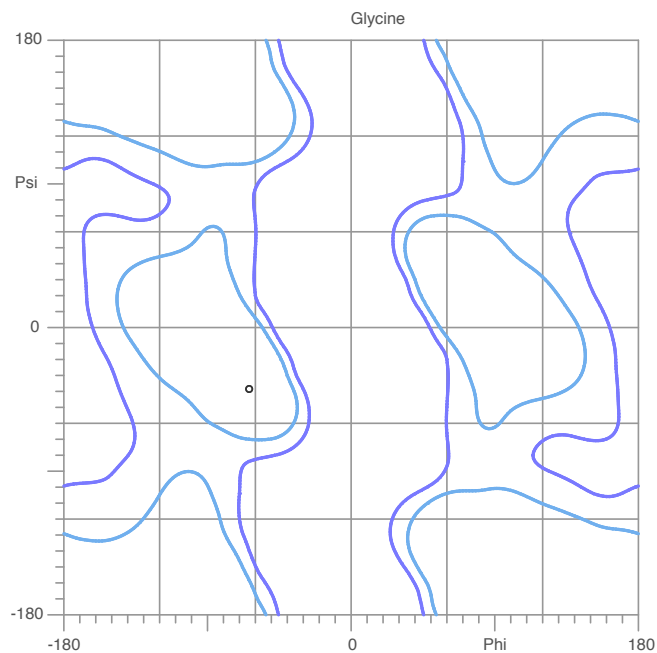
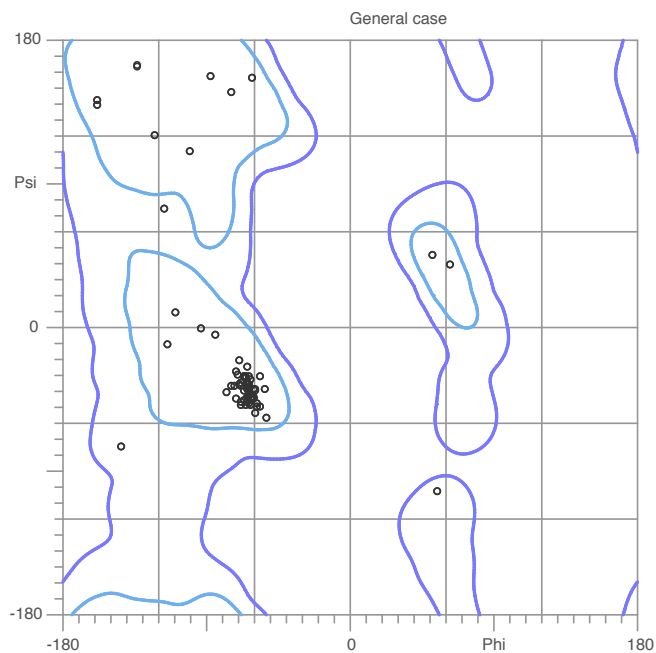
There were no outliers.

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

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

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 2



95.9% (142/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

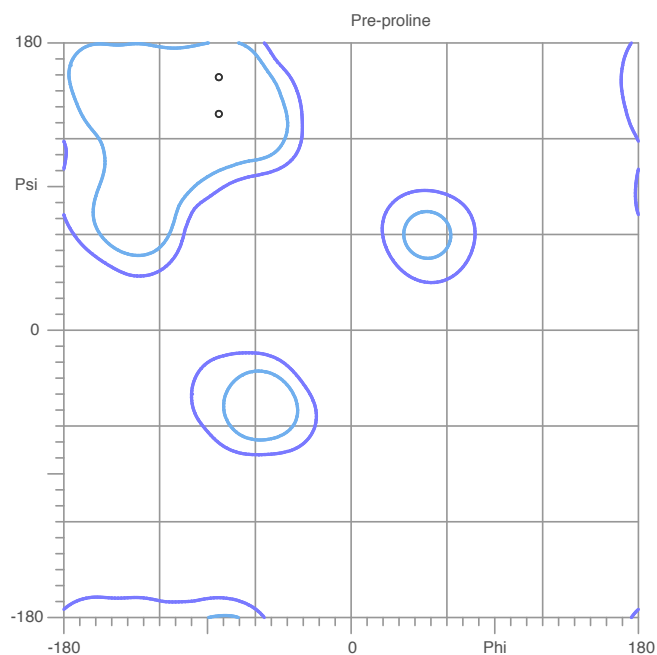
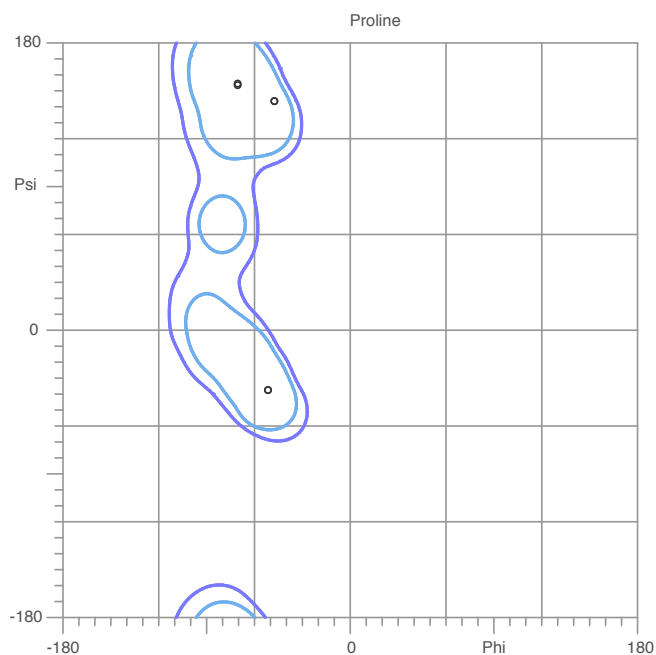
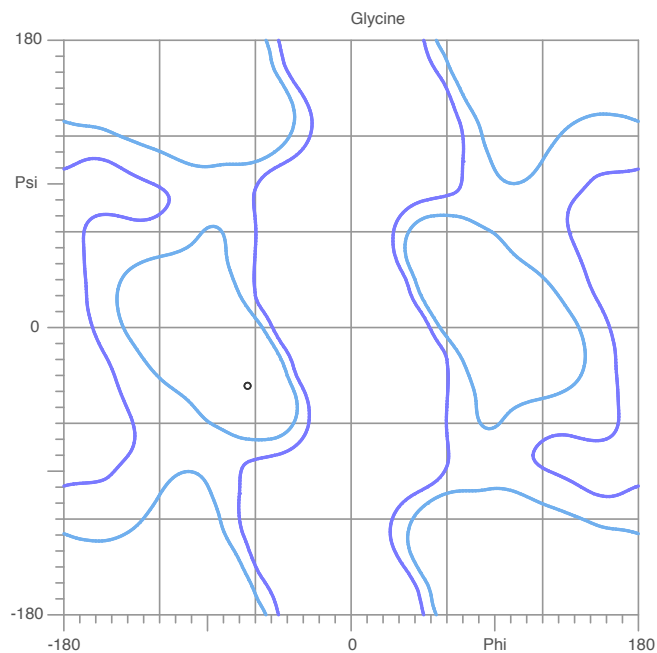
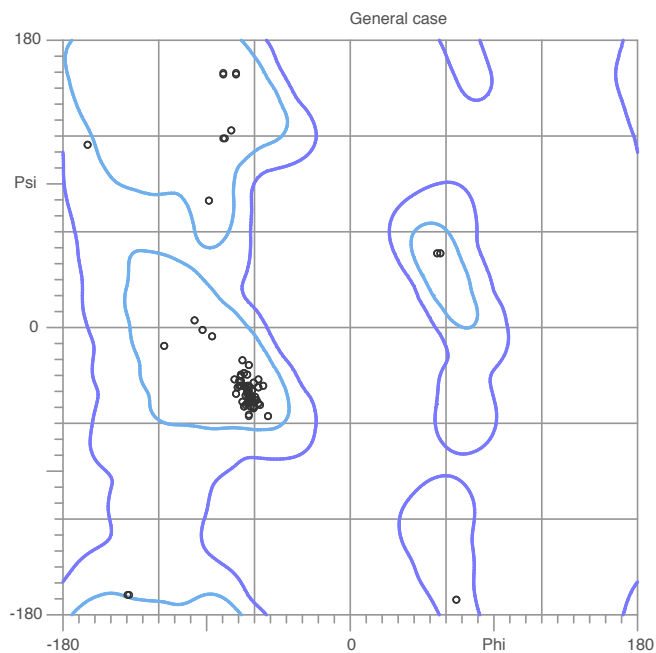
There were no outliers.

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

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

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 3



95.9% (142/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

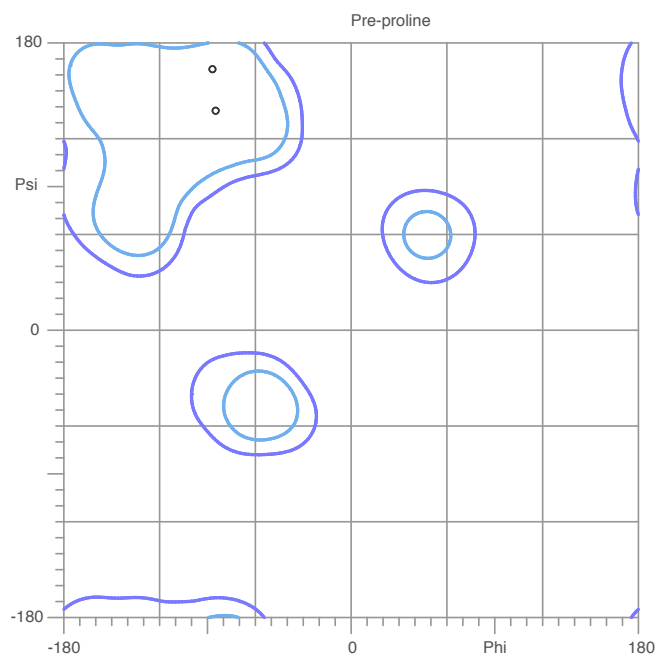
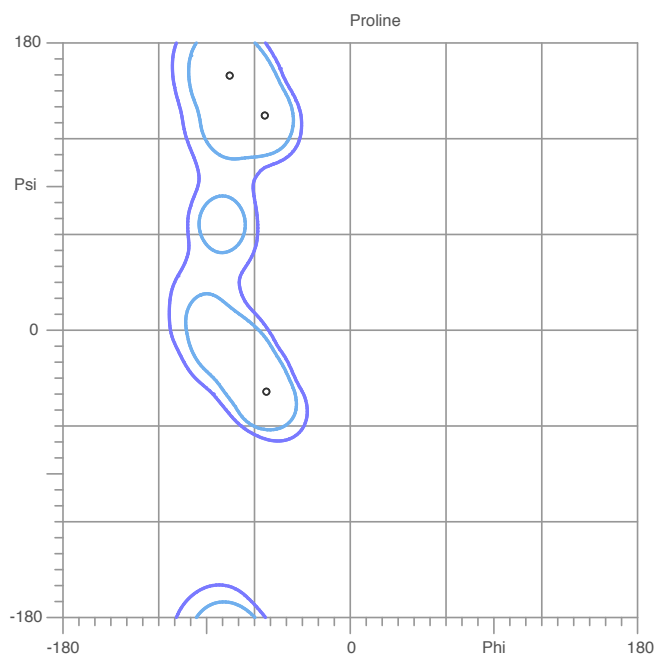
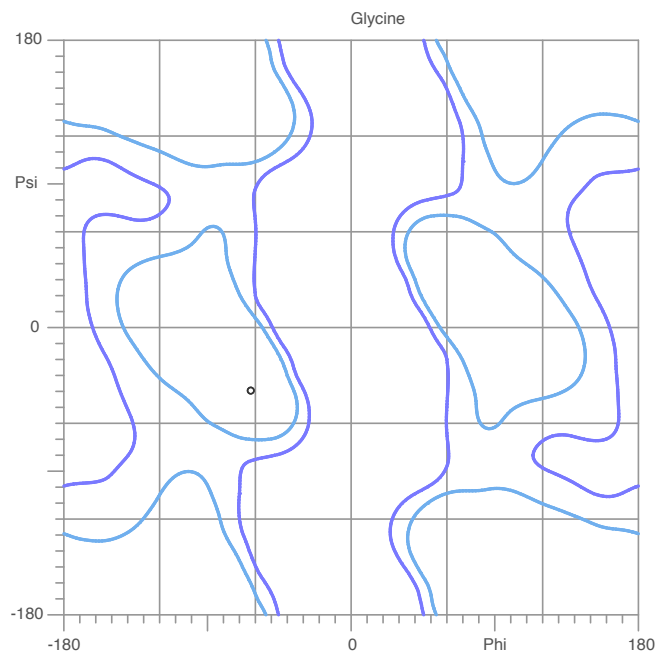
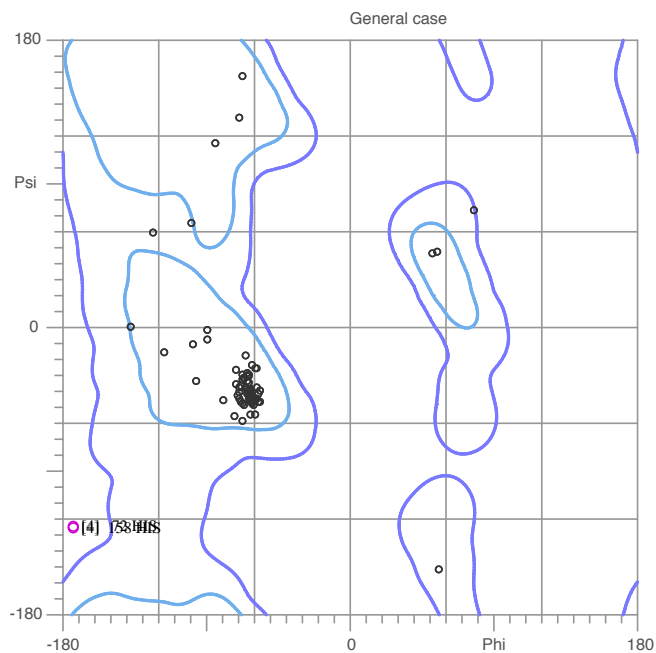
There were no outliers.

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

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MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 4



91.9% (136/148) of all residues were in favored (98%) regions.
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

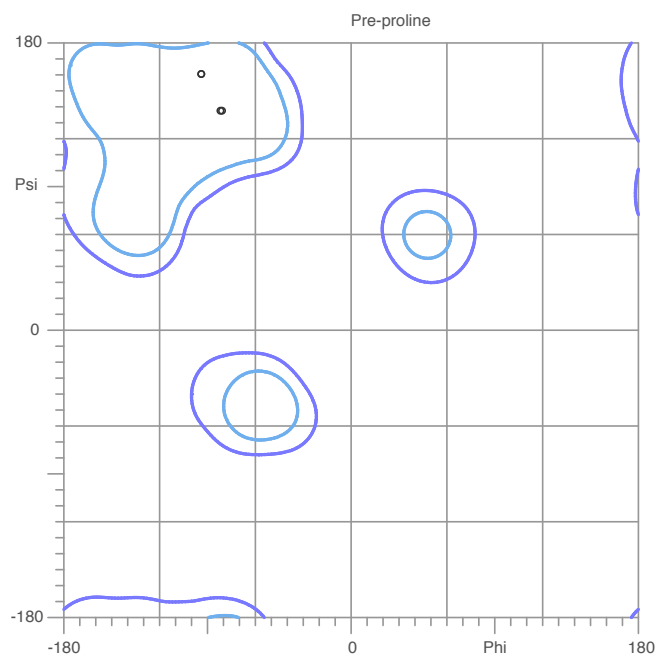
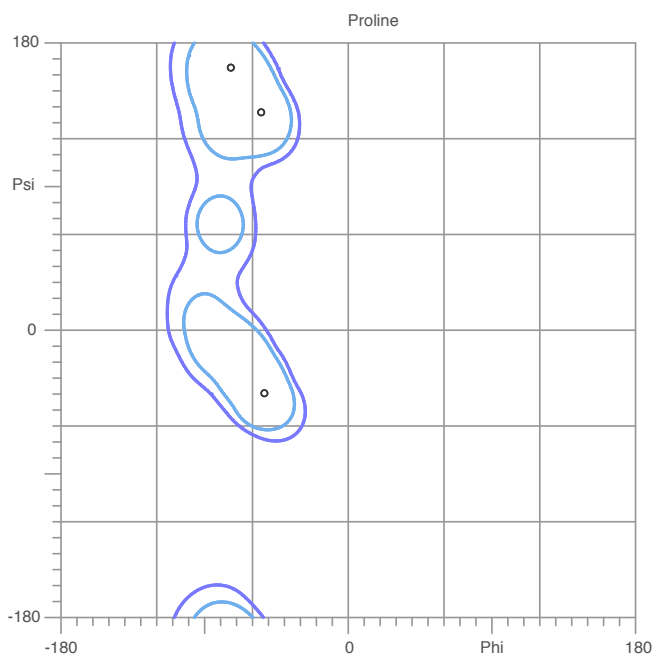
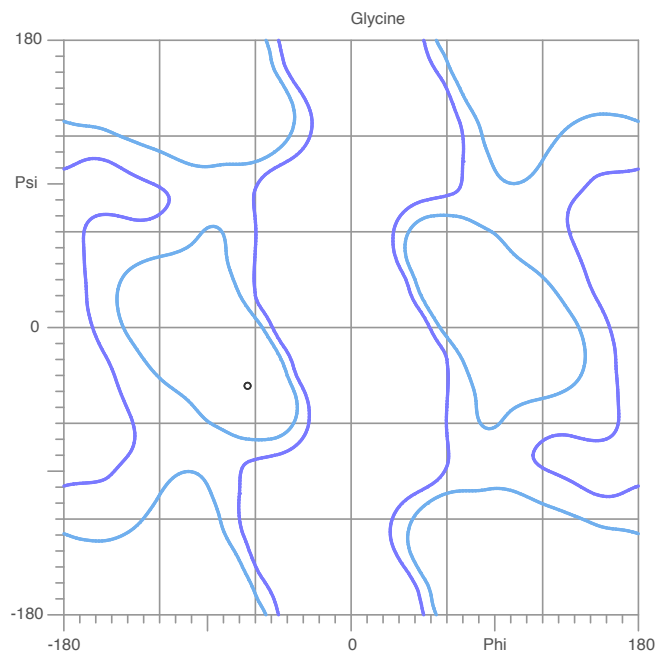
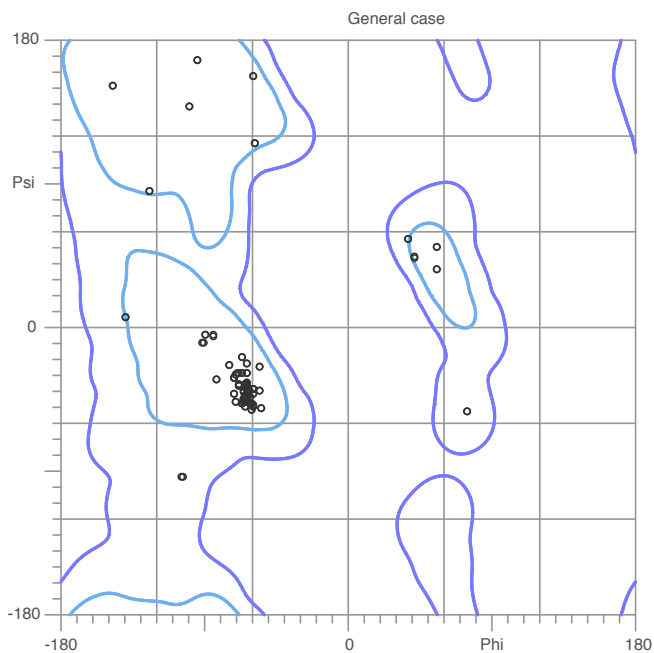
There were 2 outliers (phi, psi):

[4] 72 HIS (-174.9, -125.0)

[4] 158 HIS (-174.8, -125.1)

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 5

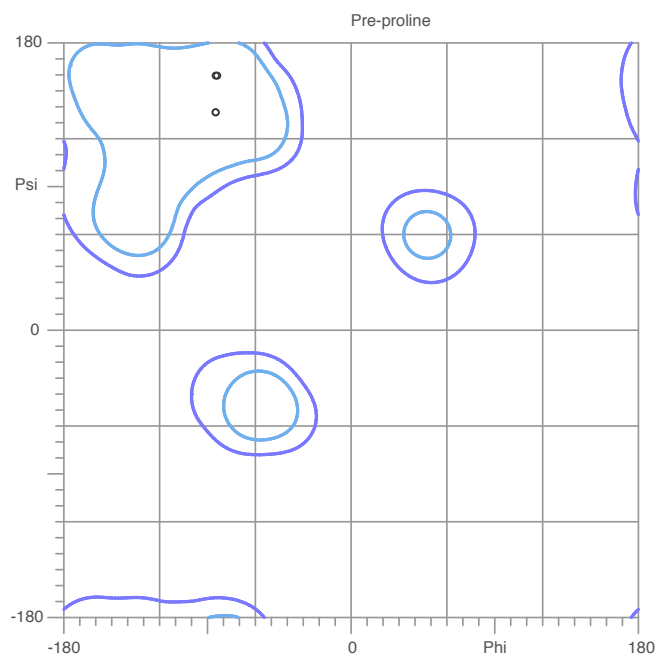
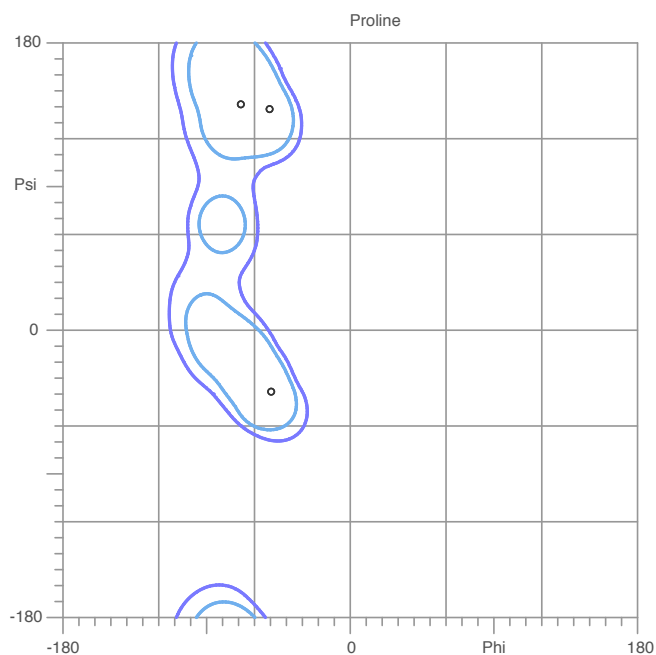
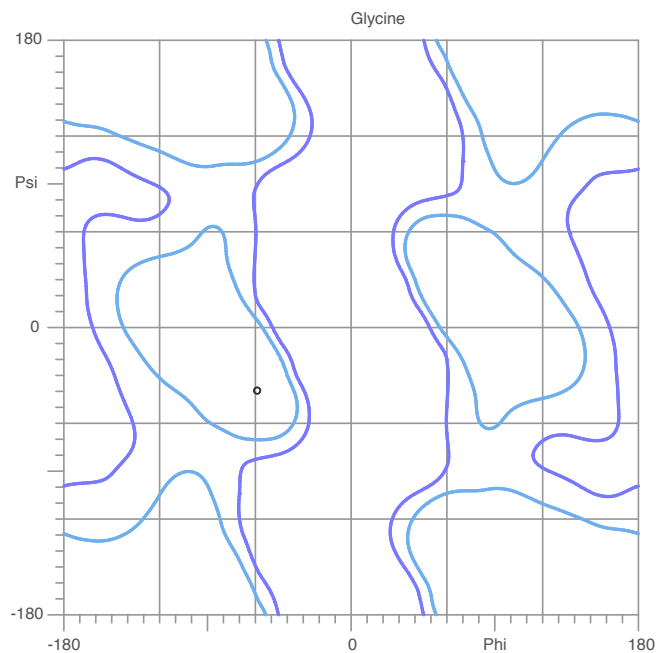
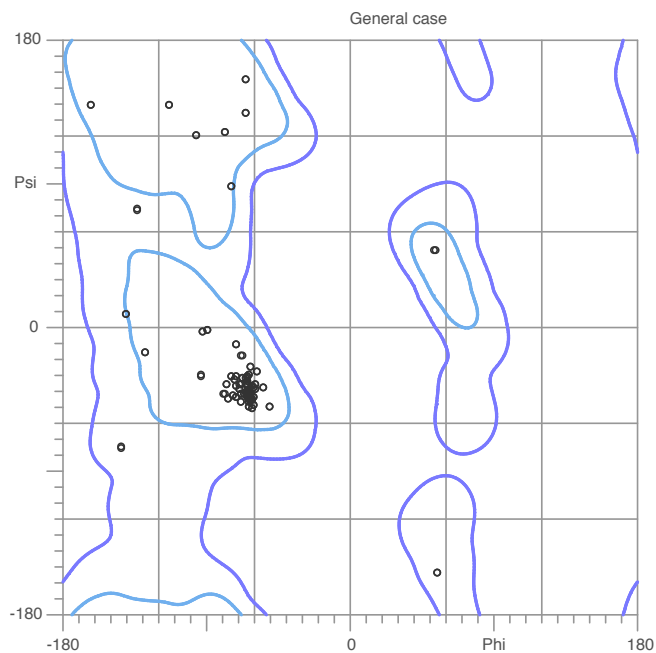


94.6% (140/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 6

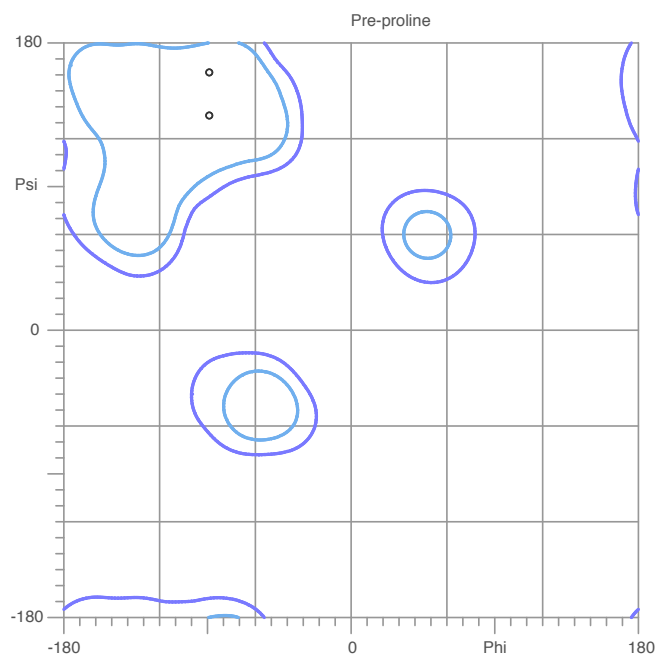
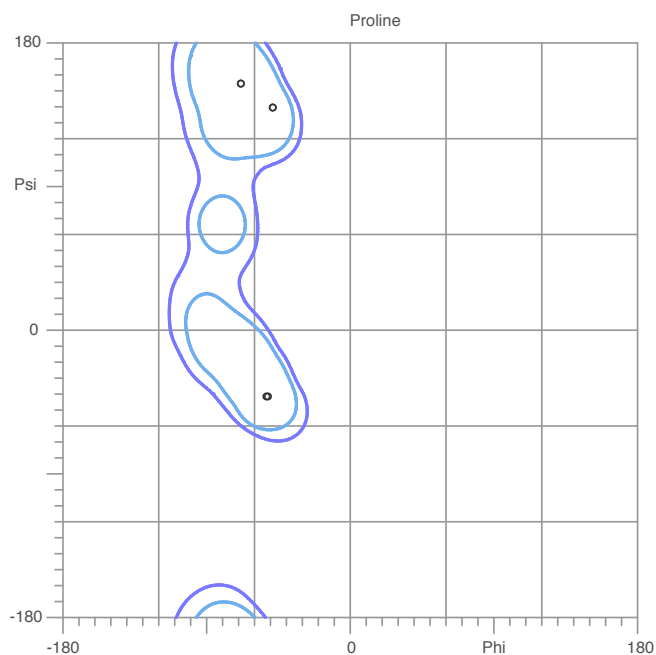
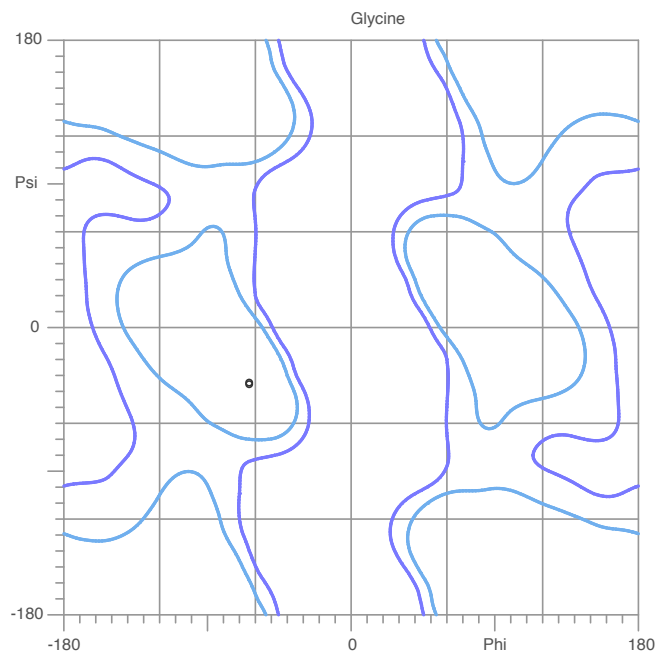
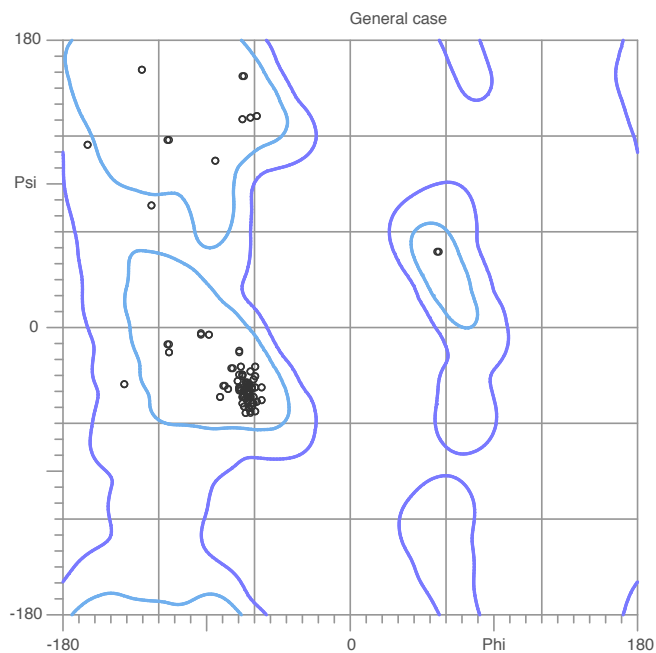


94.6% (140/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 7



95.9% (142/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

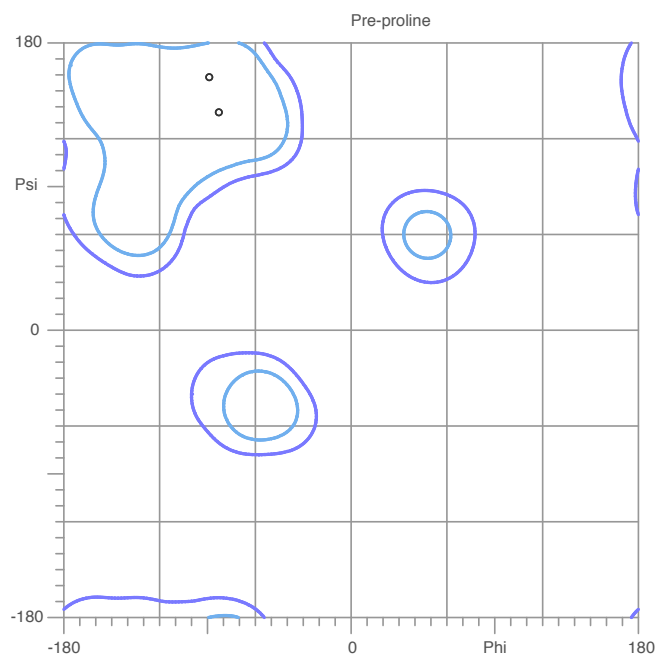
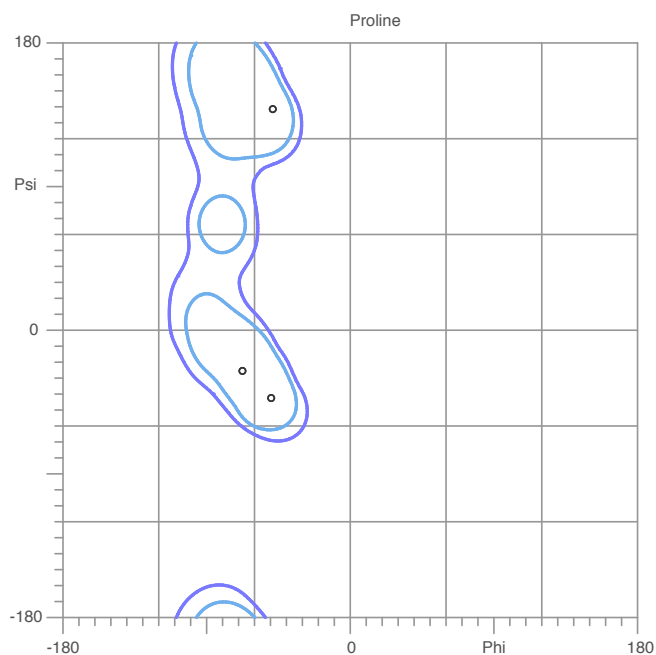
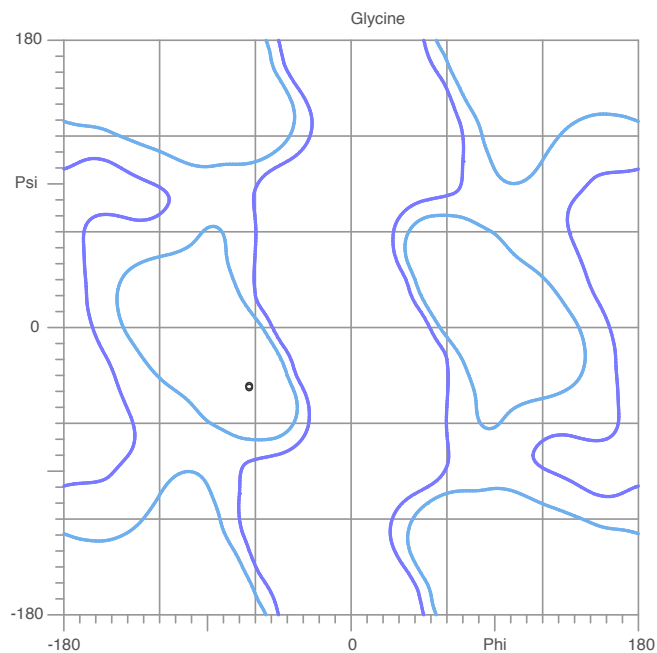
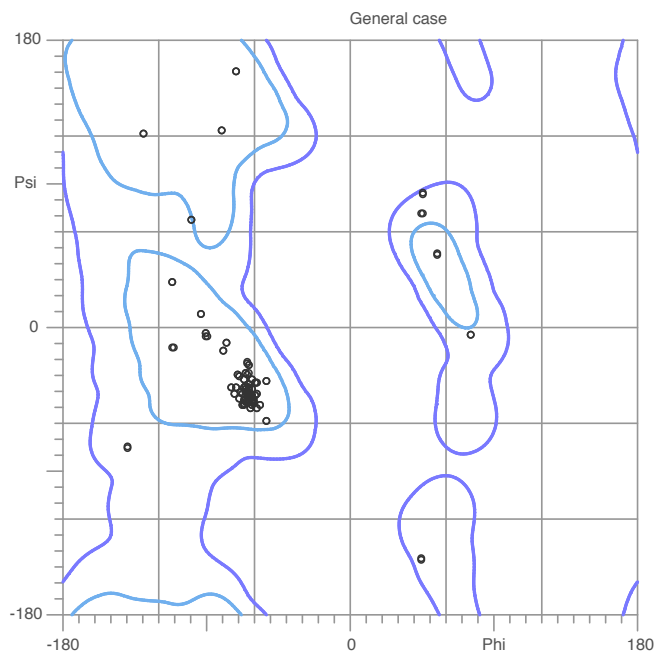
There were no outliers.

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

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MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 8



91.9% (136/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

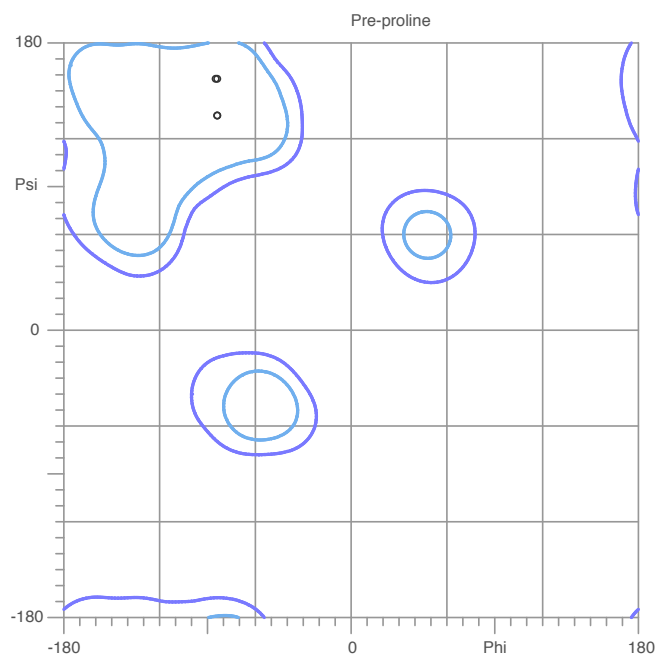
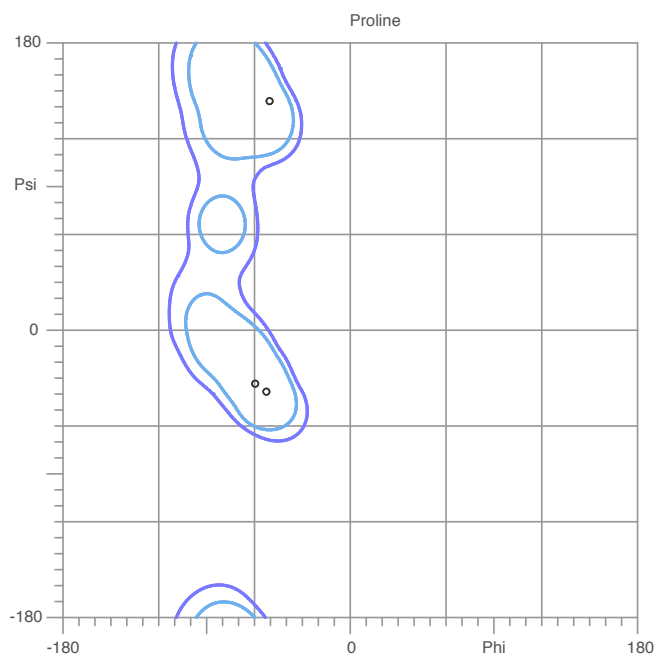
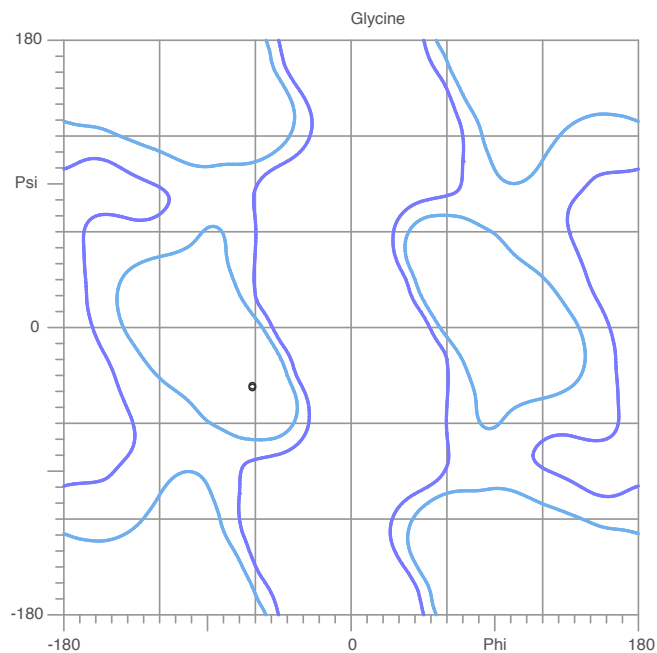
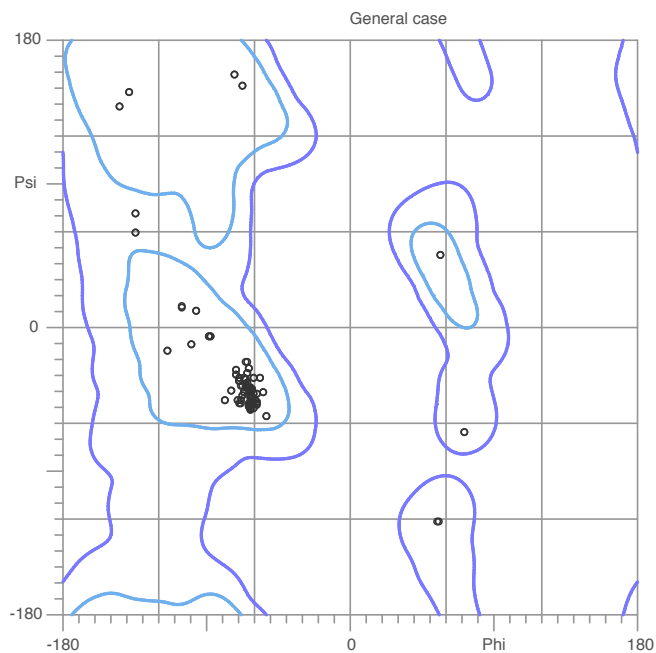
There were no outliers.

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

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MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 9

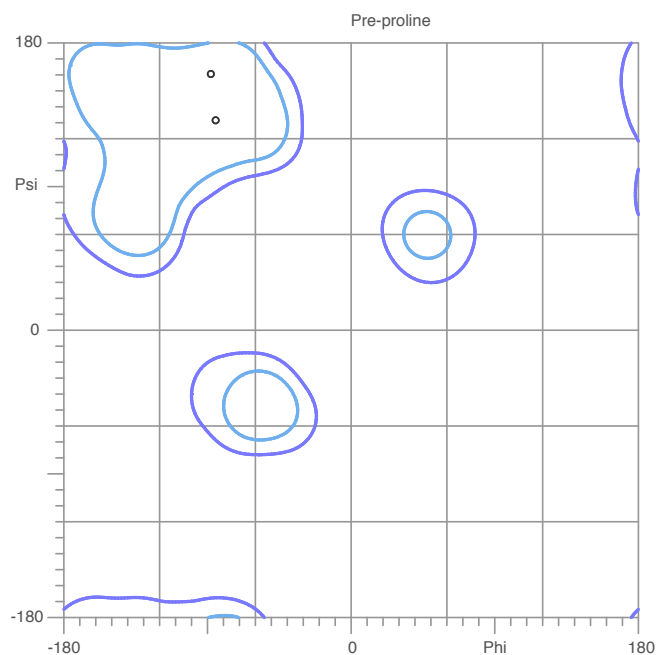
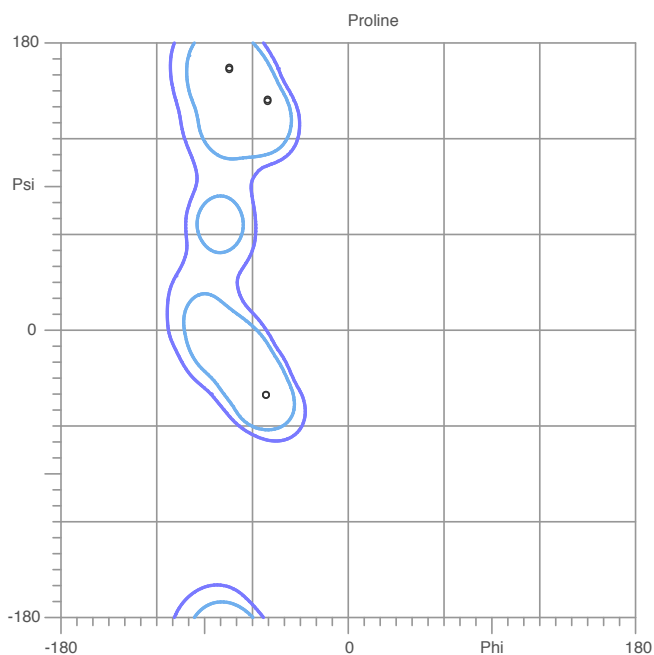
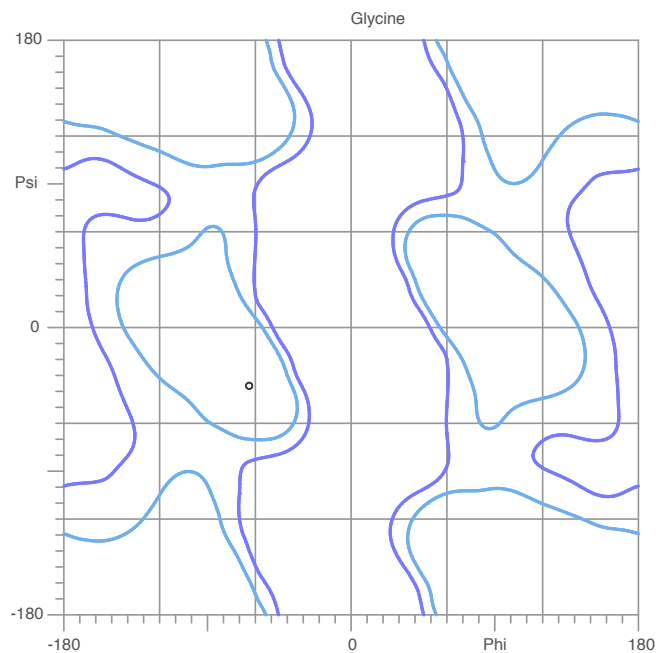
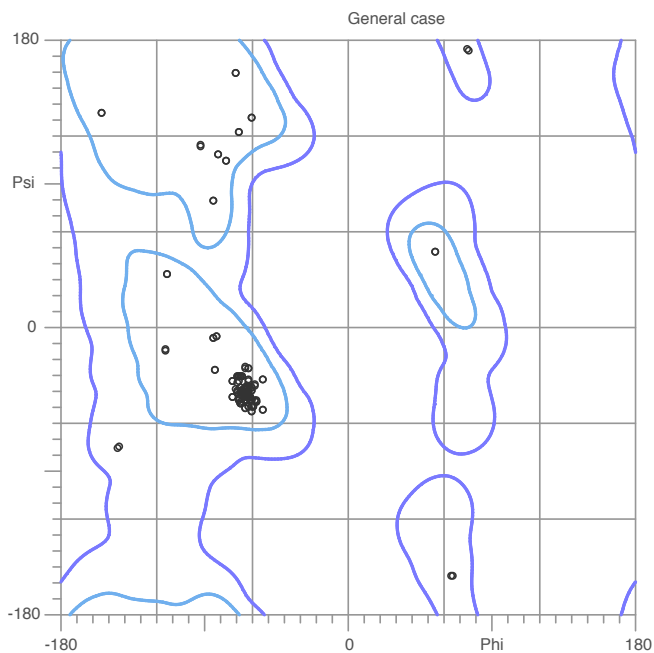


94.6% (140/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 10

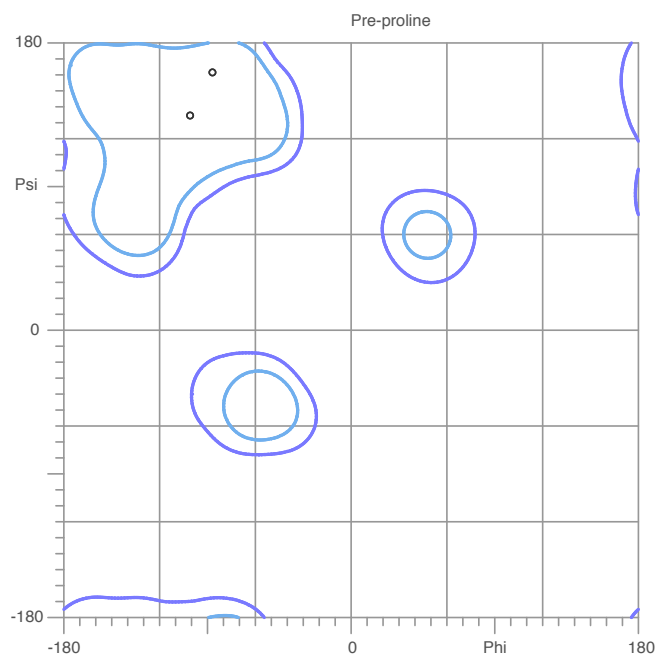
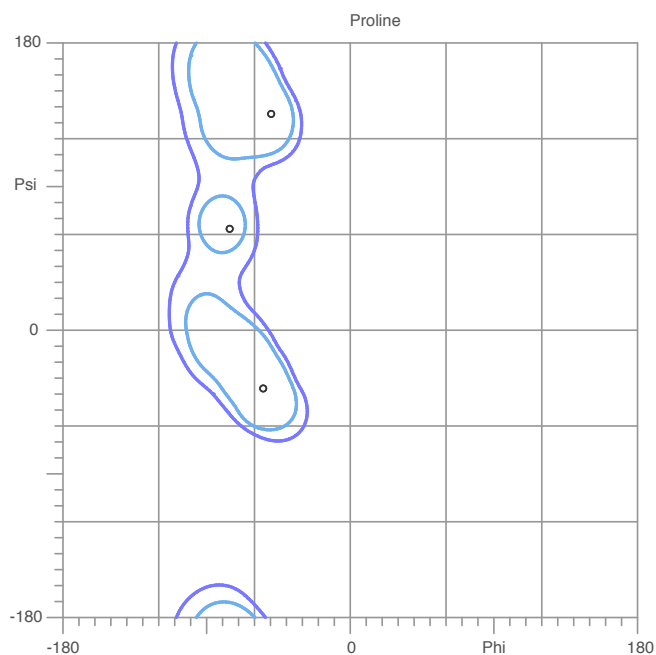
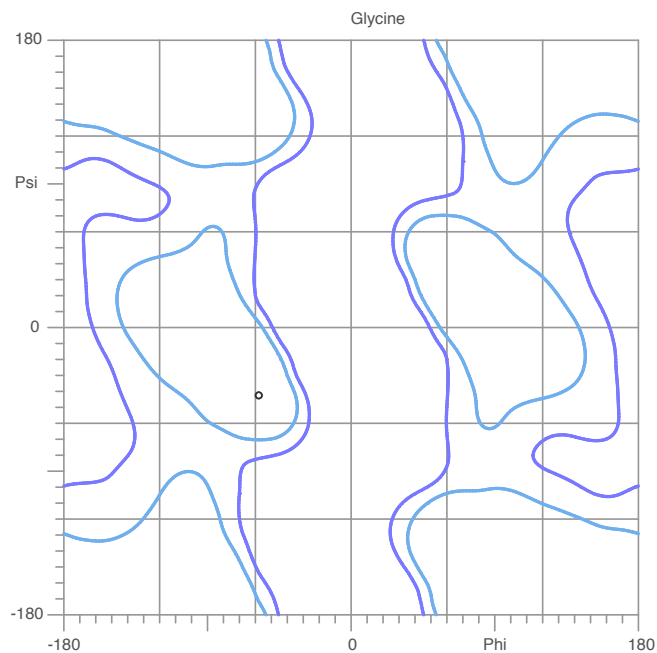
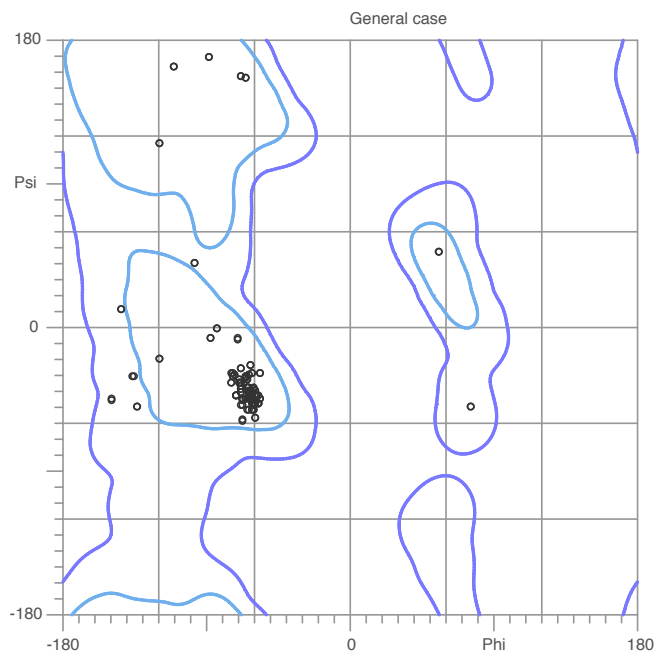


95.9% (142/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 11



91.9% (136/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

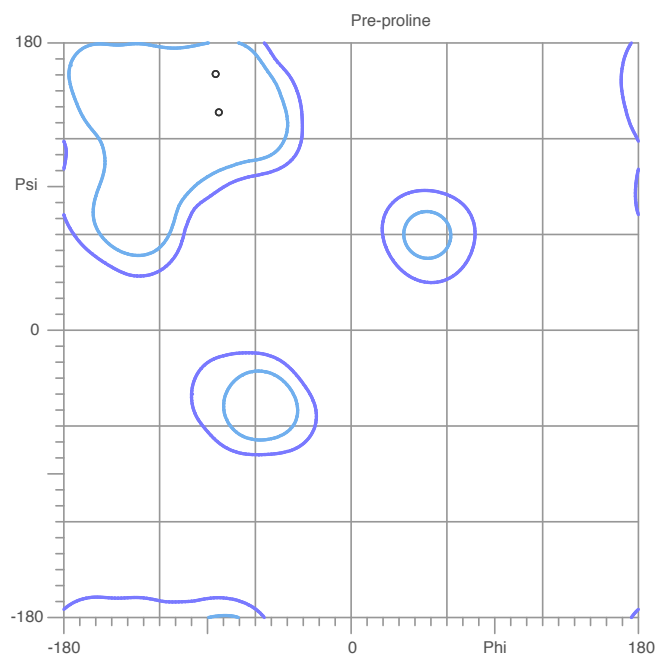
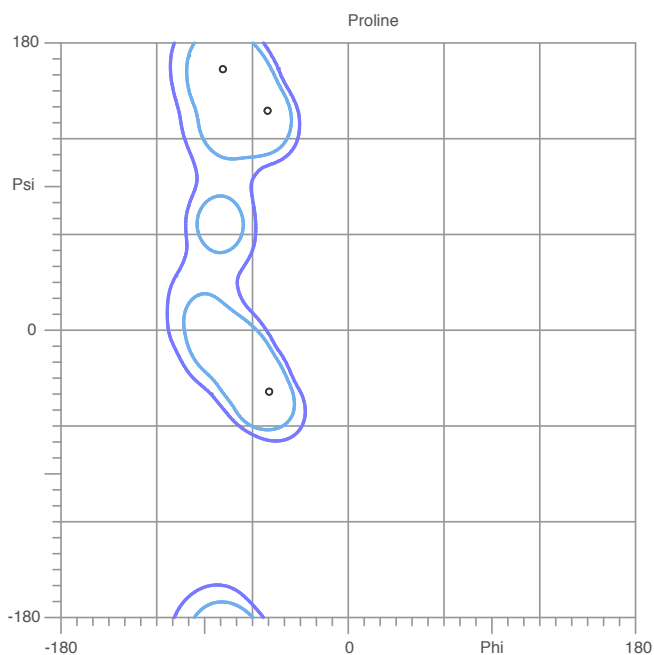
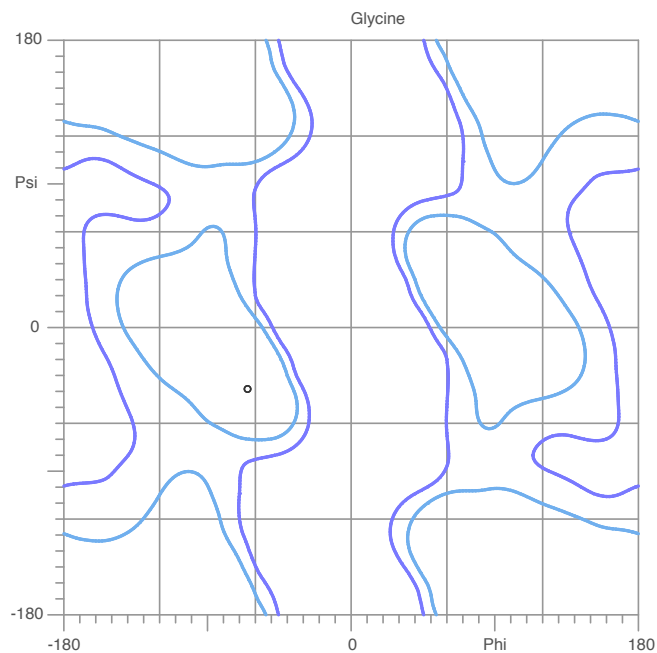
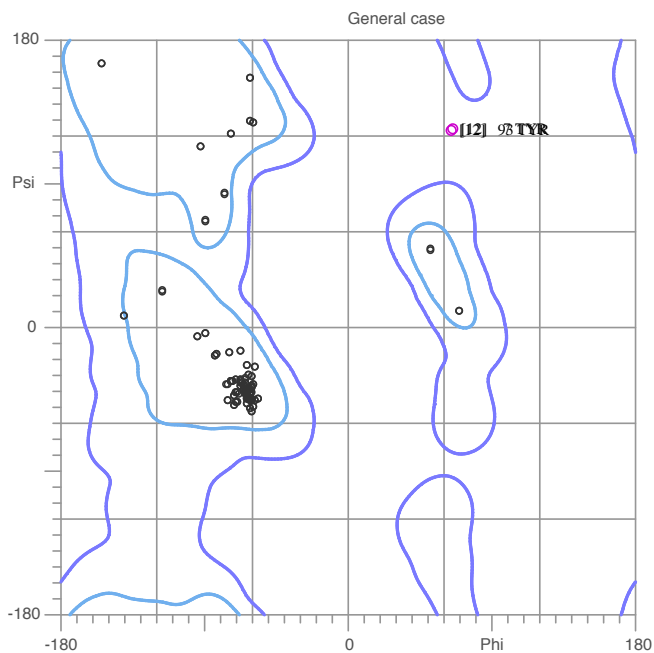
There were no outliers.

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

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MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 12

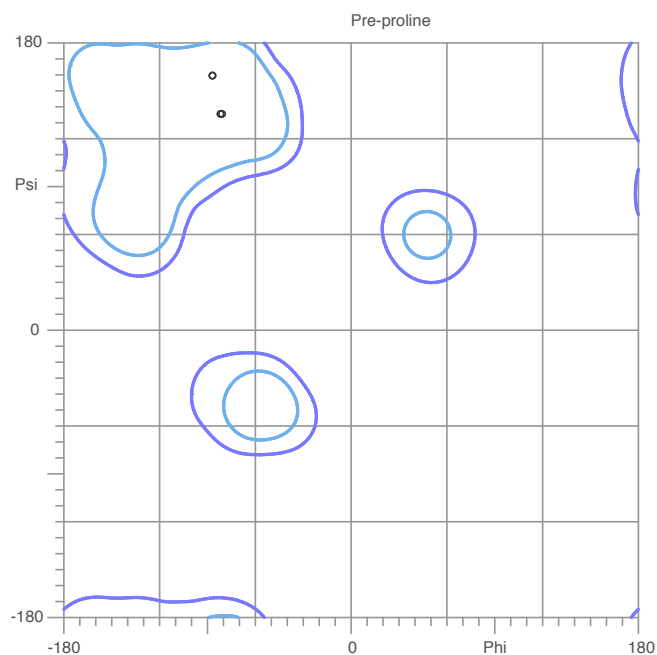
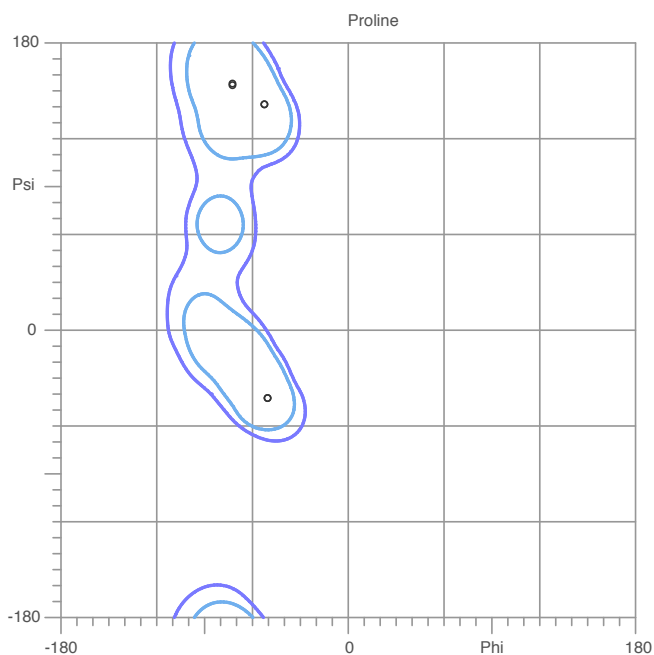
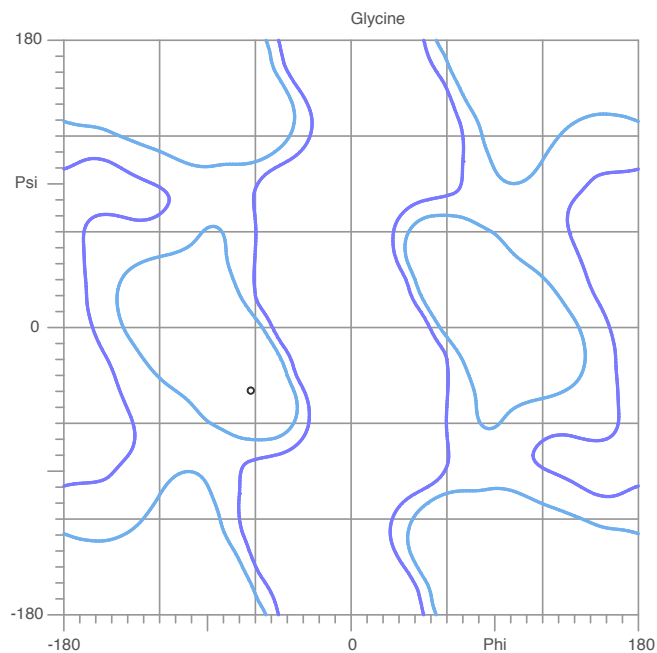
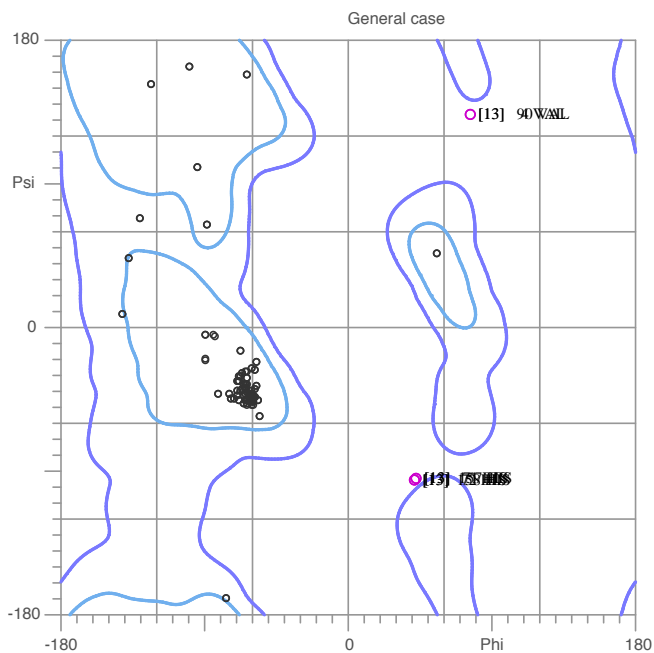


97.3% (144/148) of all residues were in favored (98%) regions.
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 7 TYR (65.0, 125.0)
[12] 93 TYR (65.0, 125.0)

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 13



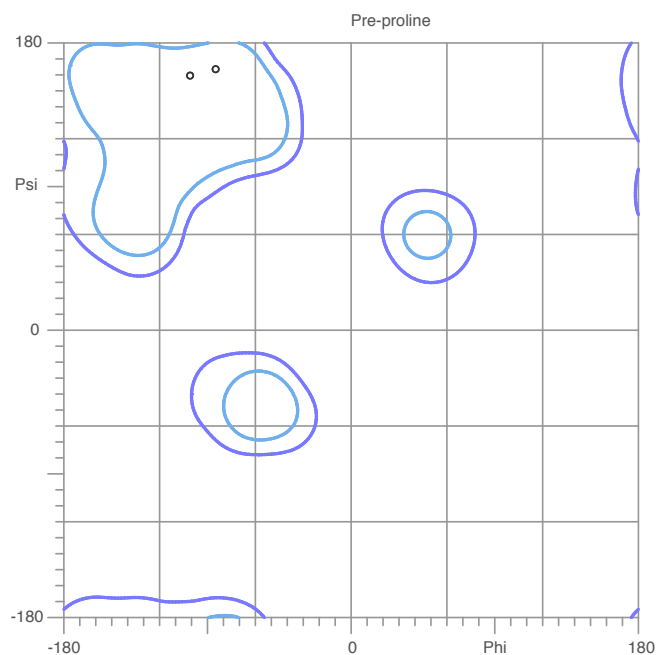
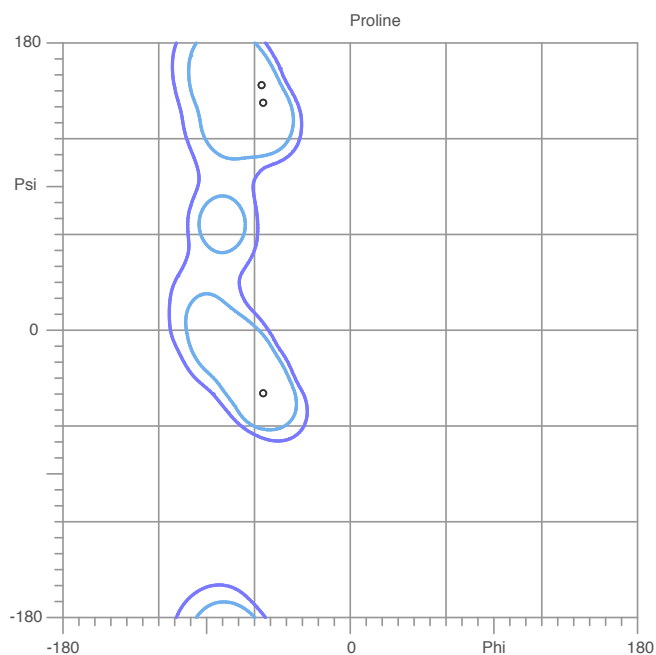
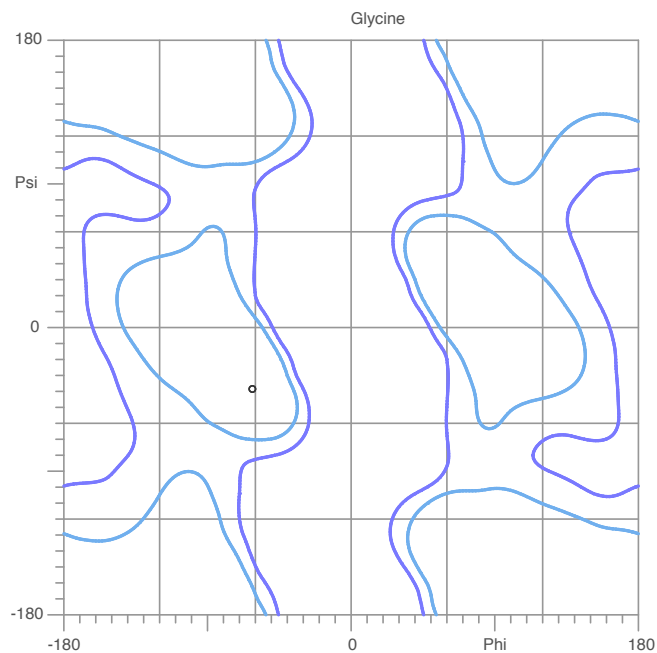
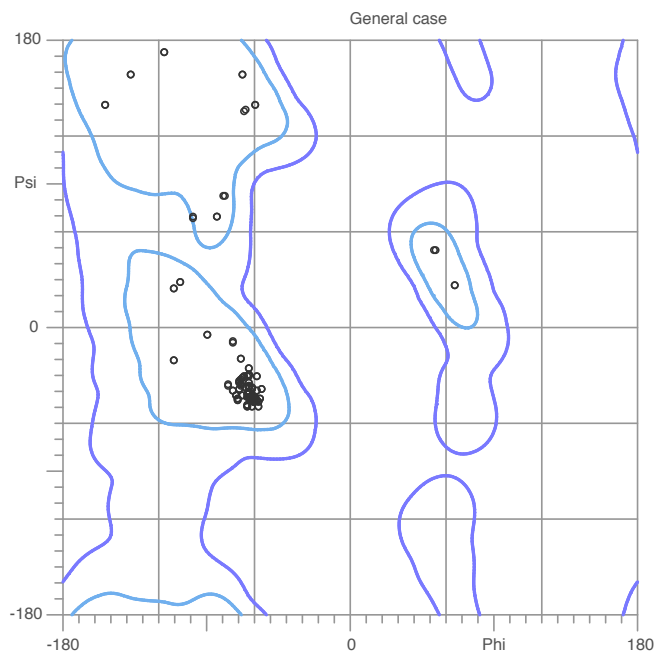
90.5% (134/148) of all residues were in favored (98%) regions.
95.9% (142/148) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[13] 4 VAL (76.1, 134.5)

[13] 71 HIS (42.4, -94.8)
[13] 72 HIS (42.0, -95.2)
[13] 90 VAL (76.2, 134.5)
[13] 157 HIS (42.4, -94.8)
[13] 158 HIS (41.9, -95.2)

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 14



98.6% (146/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

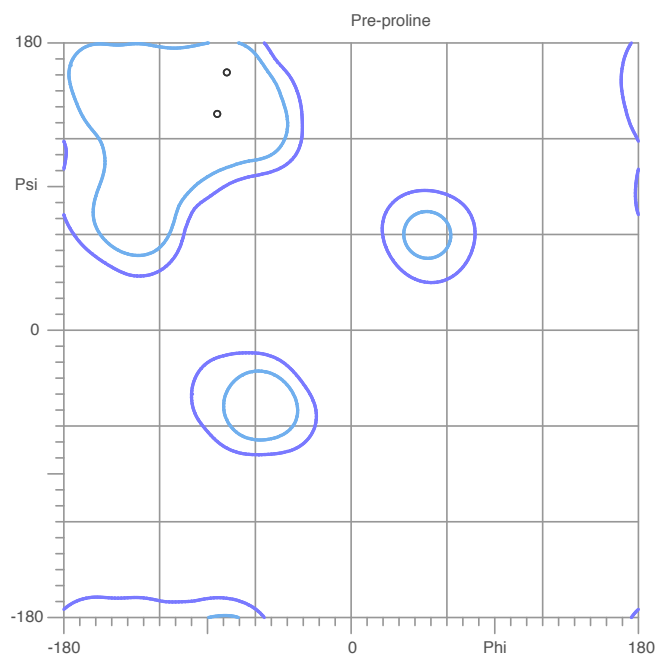
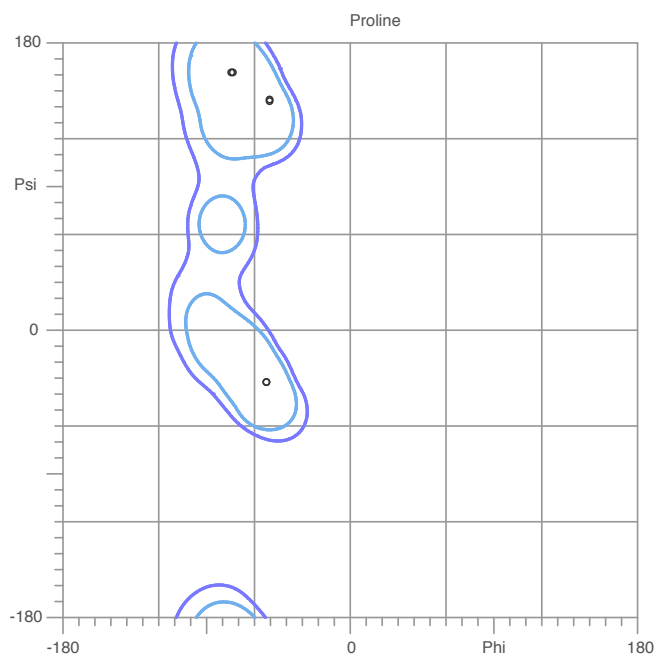
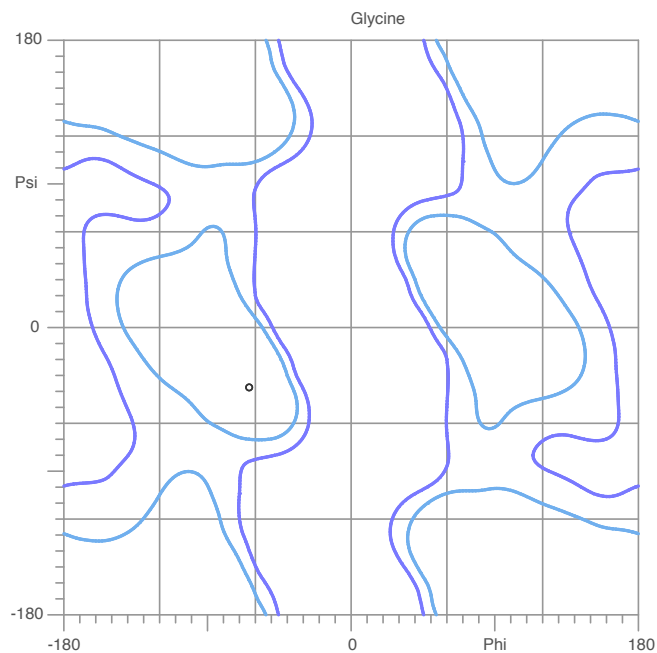
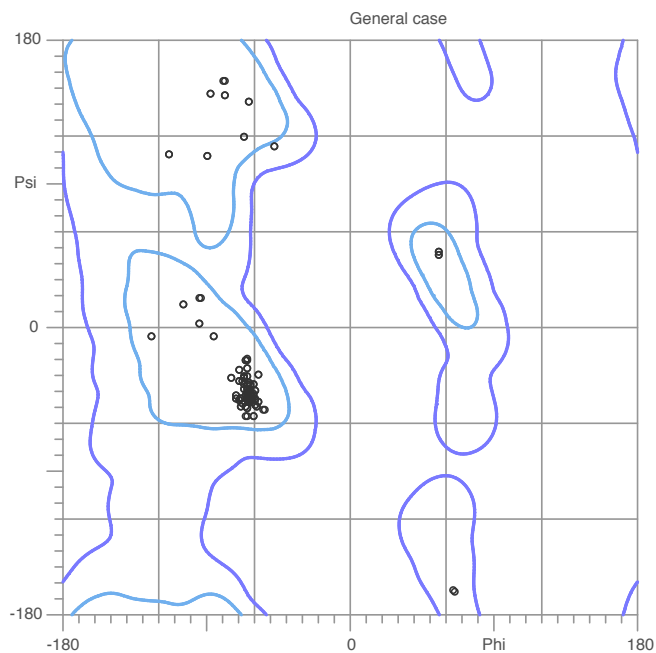
There were no outliers.

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

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MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 15



97.3% (144/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

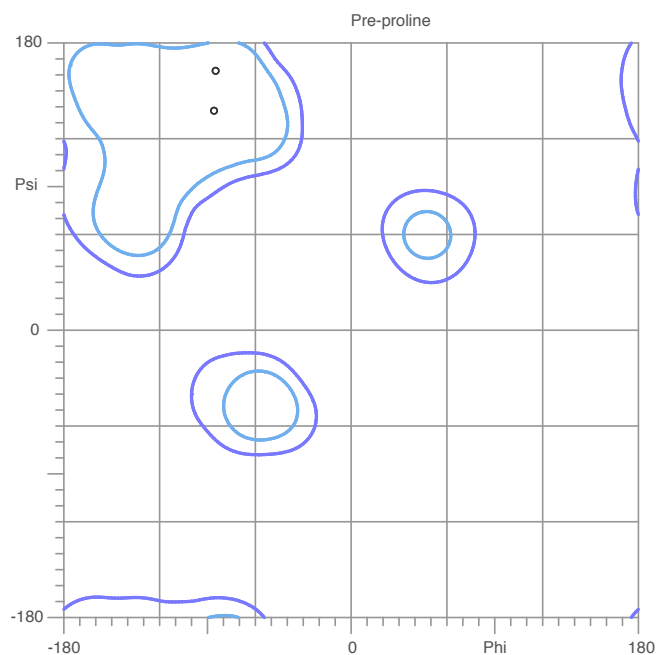
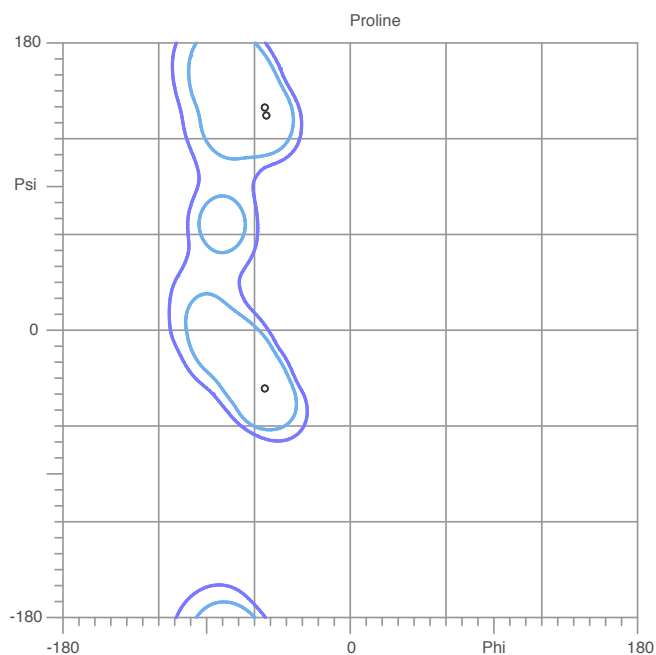
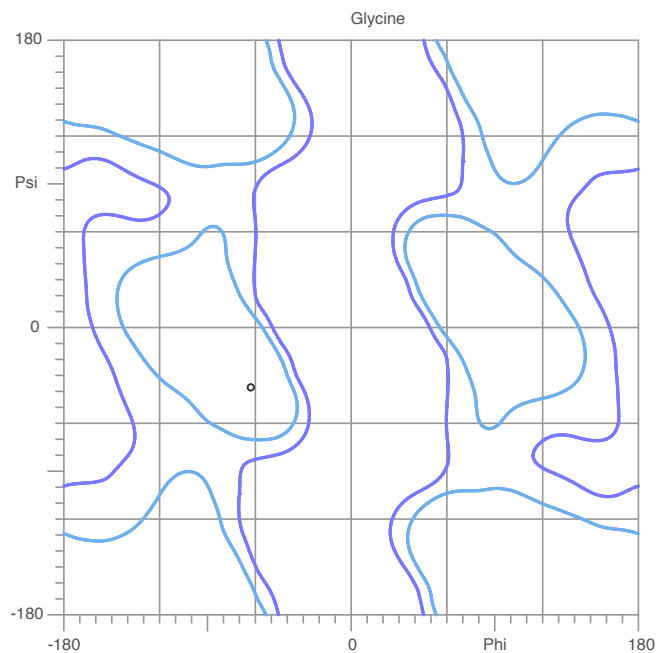
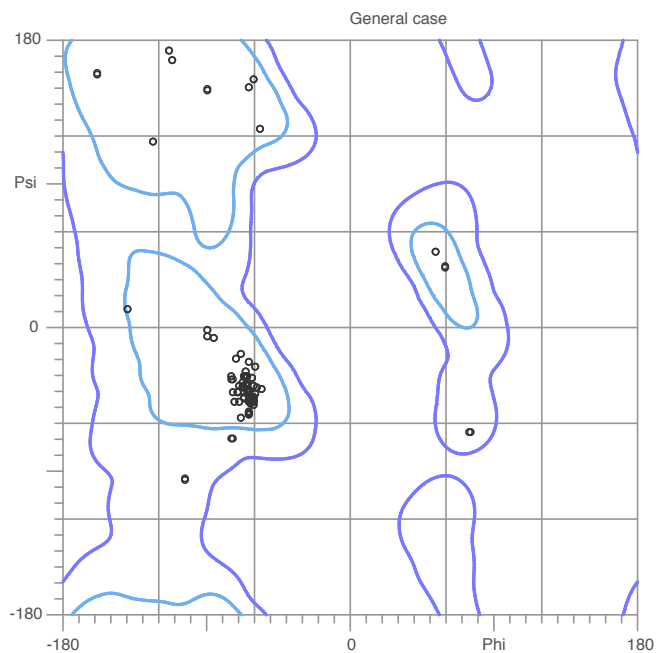
There were no outliers.

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

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MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 16

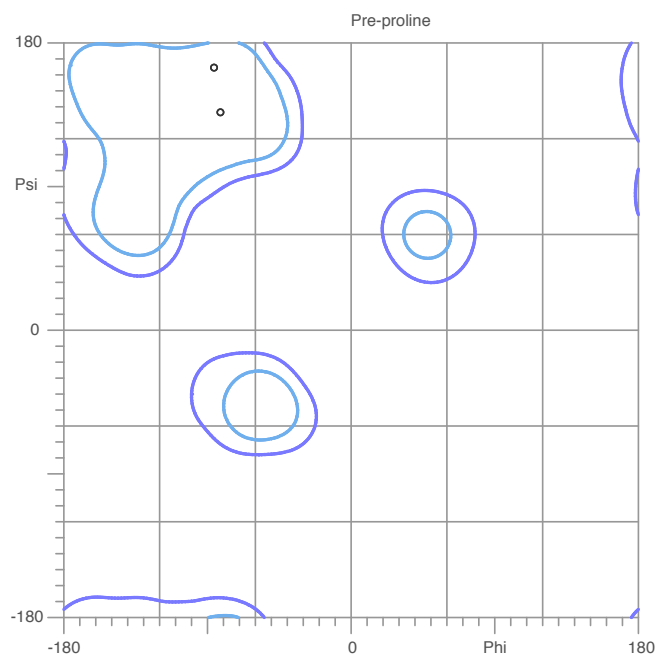
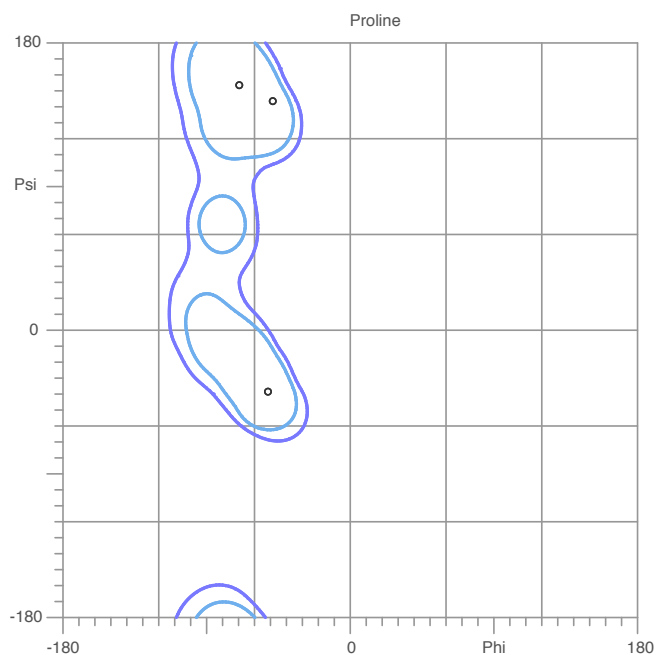
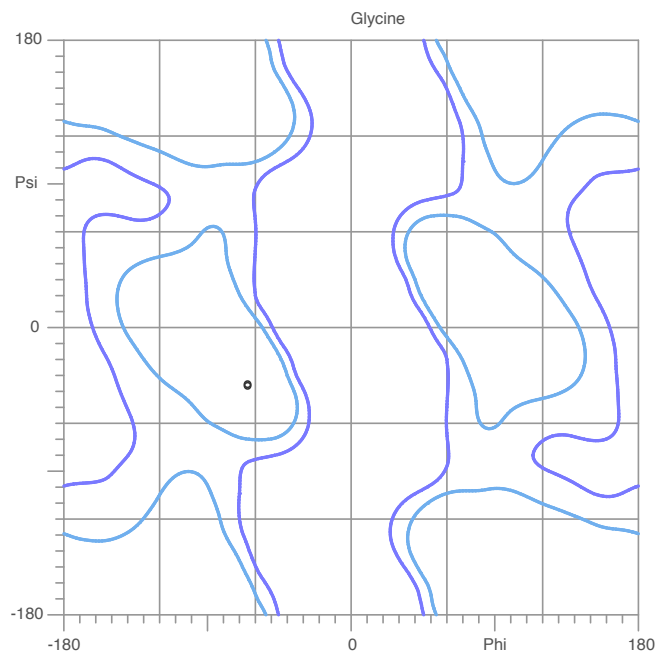
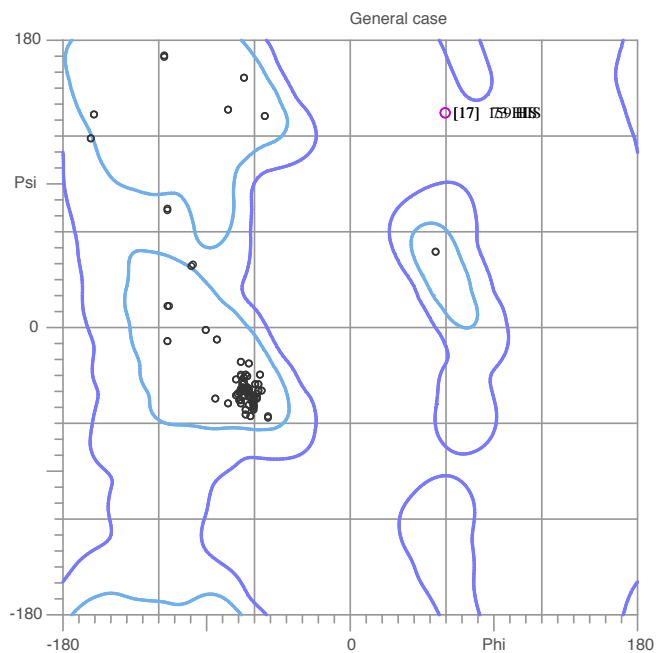


95.9% (142/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 17



94.6% (140/148) of all residues were in favored (98%) regions.
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

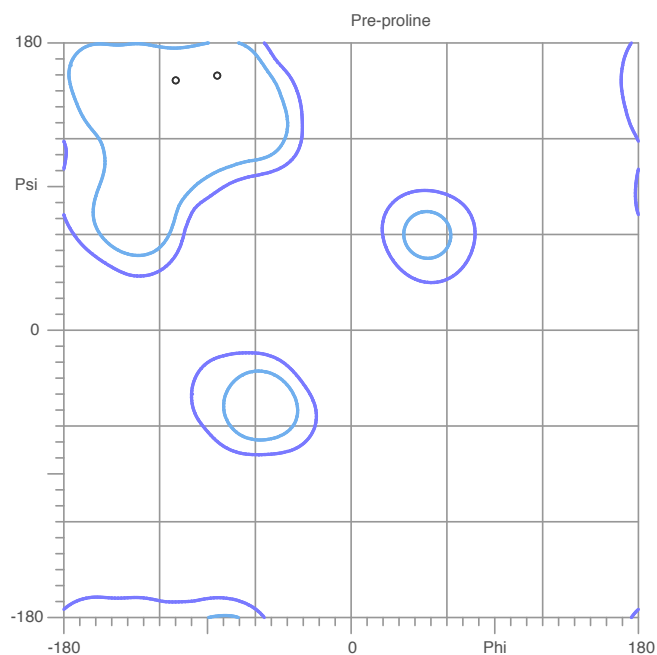
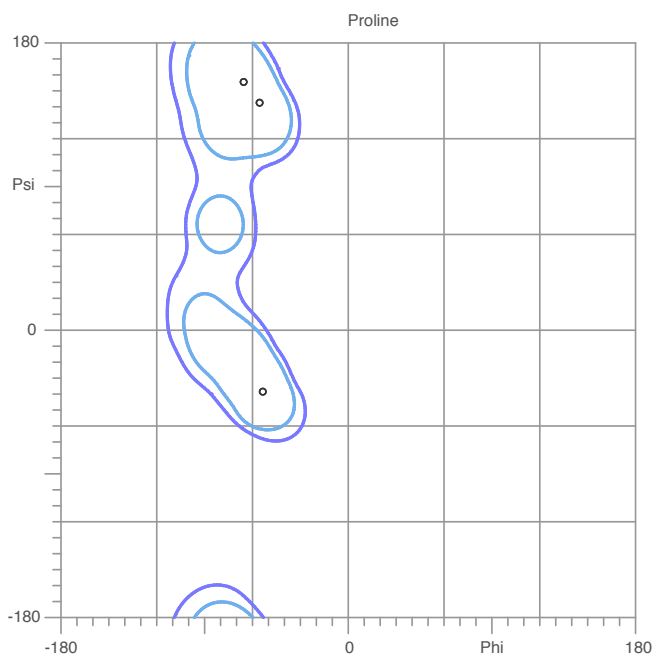
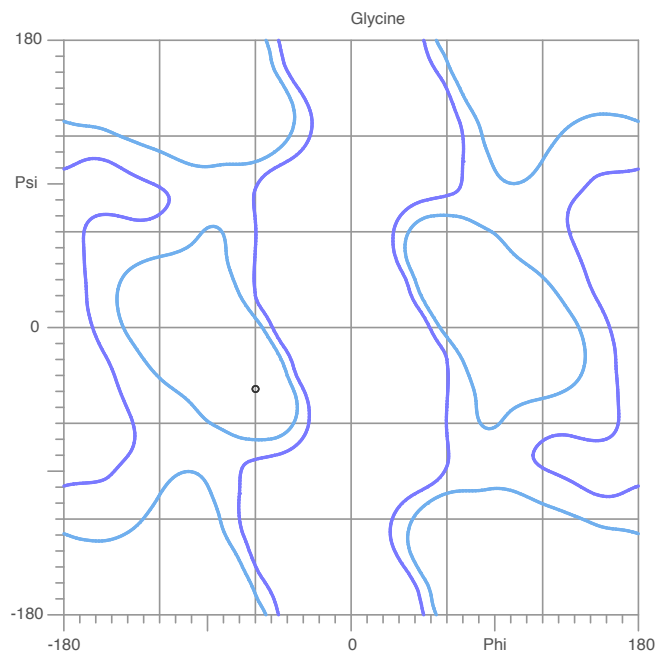
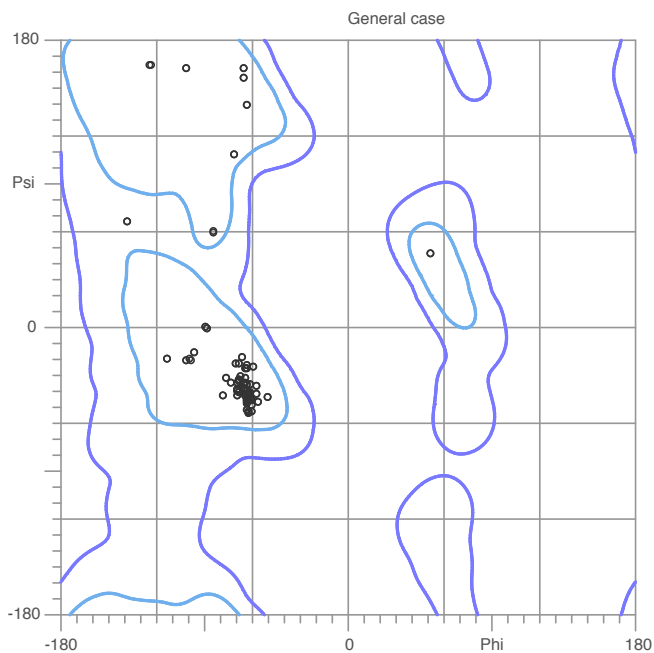
There were 2 outliers (phi, psi):

[17] 73 HIS (59.7, 135.1)

[17] 159 HIS (59.7, 135.0)

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 18



98.6% (146/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

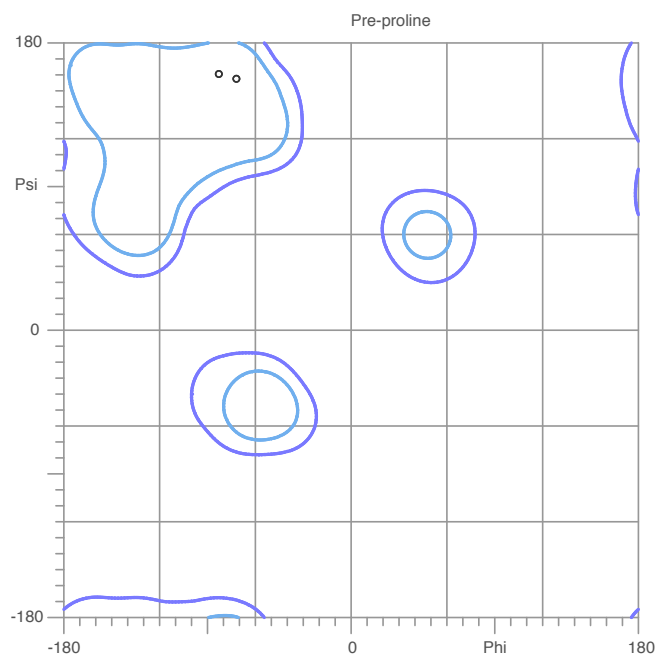
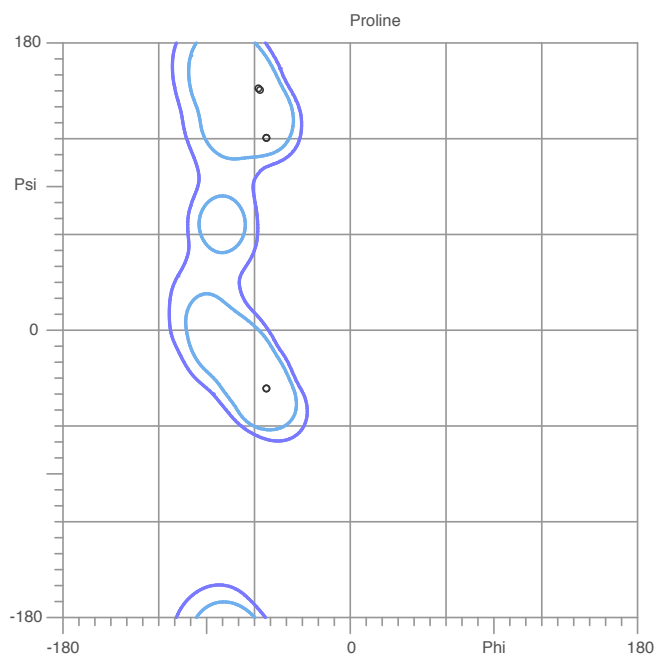
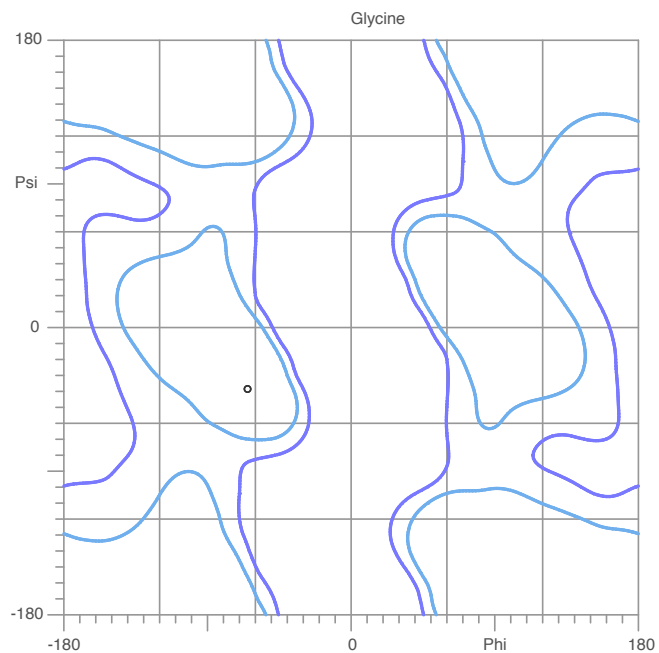
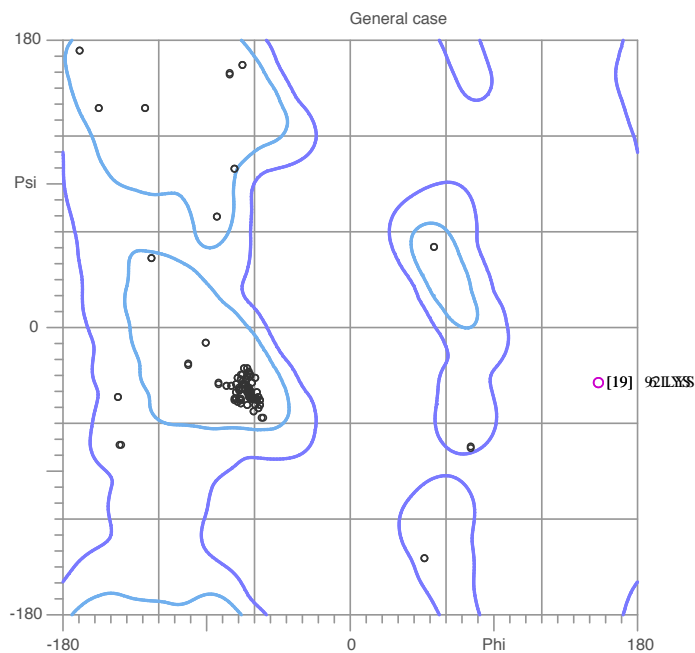
There were no outliers.

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

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

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 19



93.2% (138/148) of all residues were in favored (98%) regions.
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

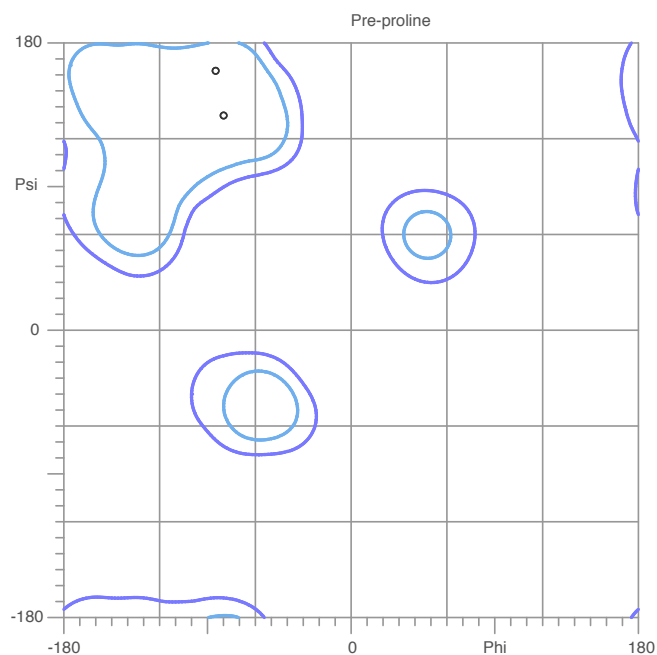
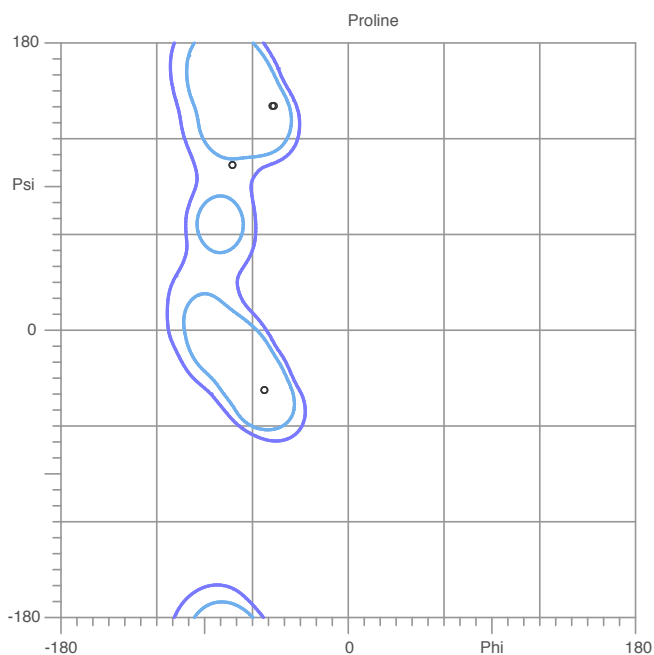
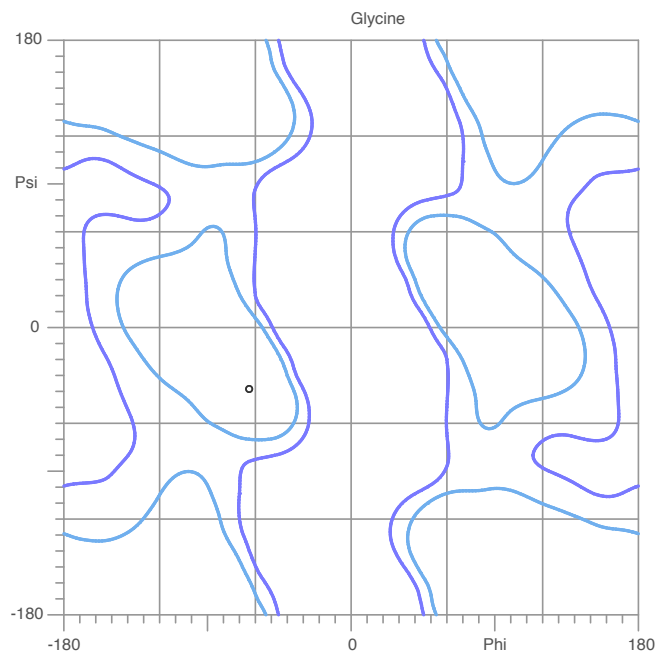
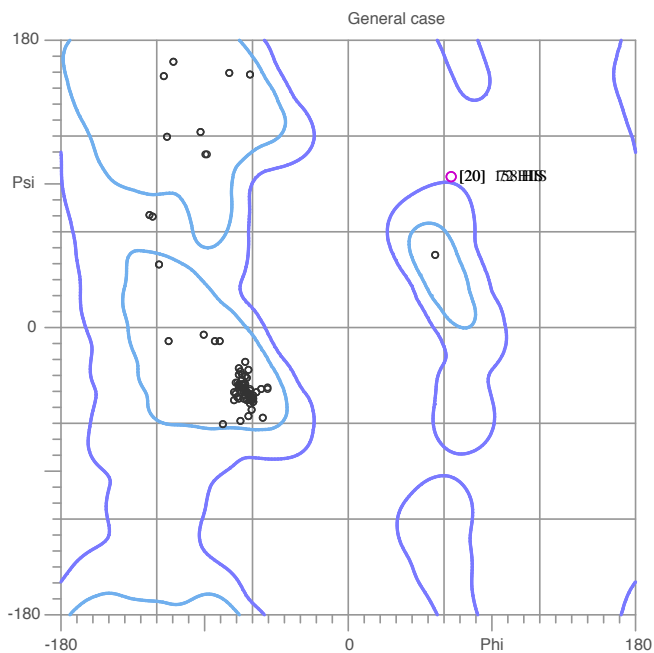
There were 2 outliers (phi, psi):

[19] 6 LYS (155.1, -35.0)

[19] 92 LYS (155.1, -35.0)

MolProbity Ramachandran analysis

CSR4_R3Cons_em_bcr3.pdb, model 20



94.6% (140/148) of all residues were in favored (98%) regions.
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[20] 72 HIS (65.0, 95.1)

[20] 158 HIS (64.9, 95.1)