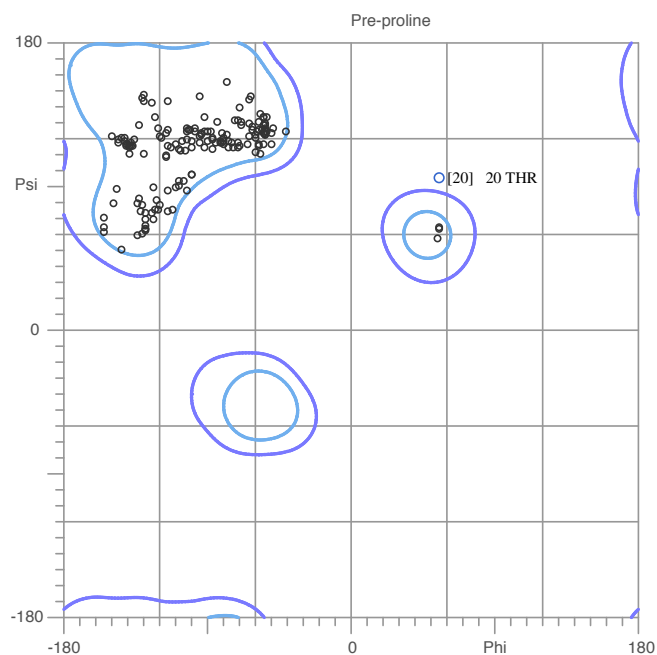
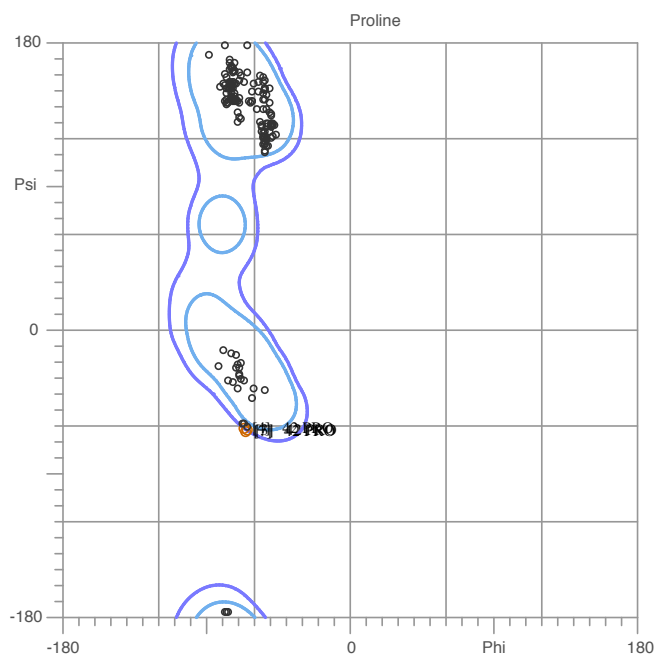
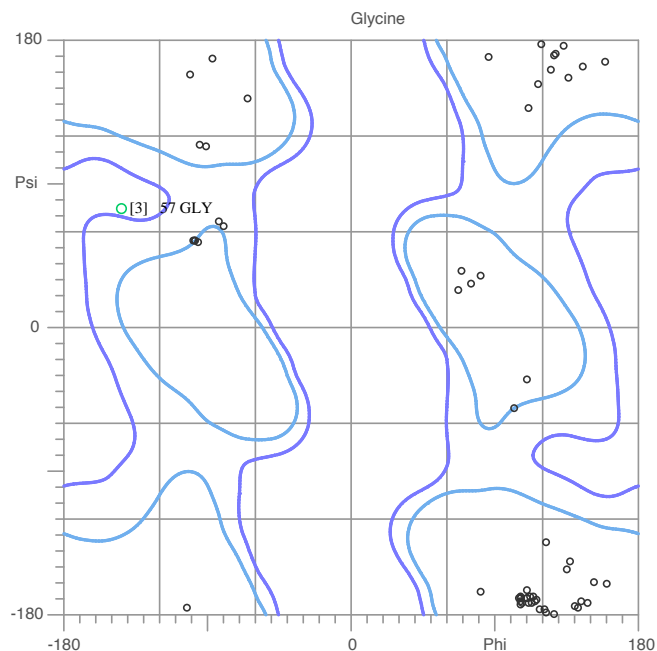
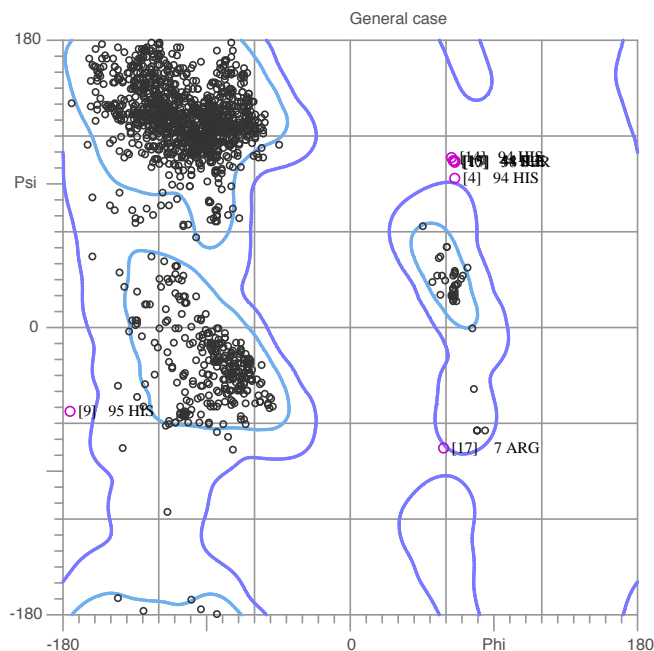


MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, all models



96.4% (1812/1880) of all residues were in favored (98%) regions.
99.4% (1868/1880) of all residues were in allowed (>99.8%) regions.

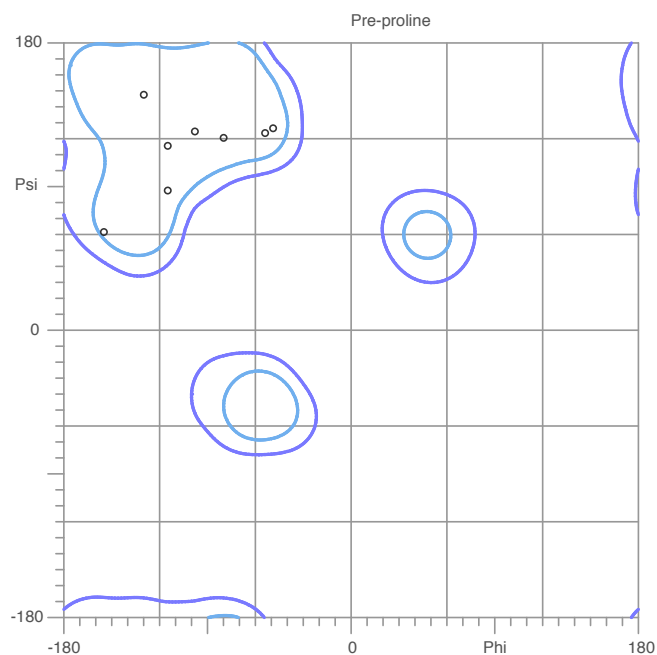
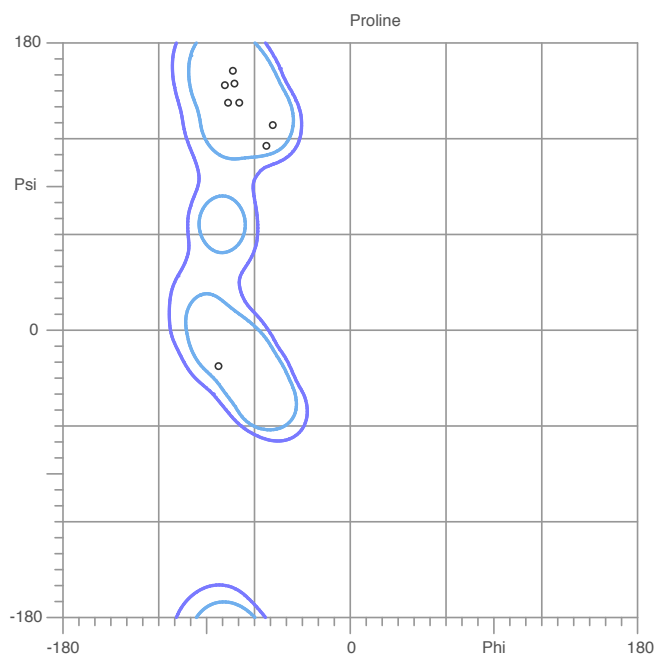
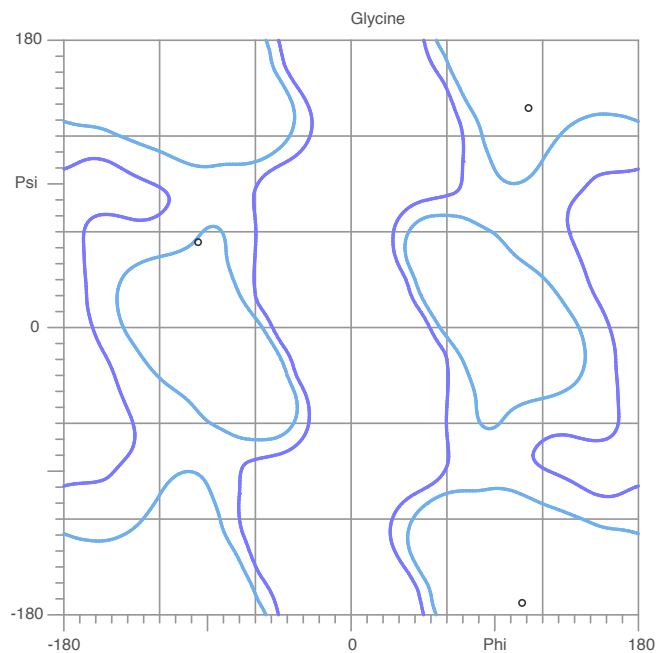
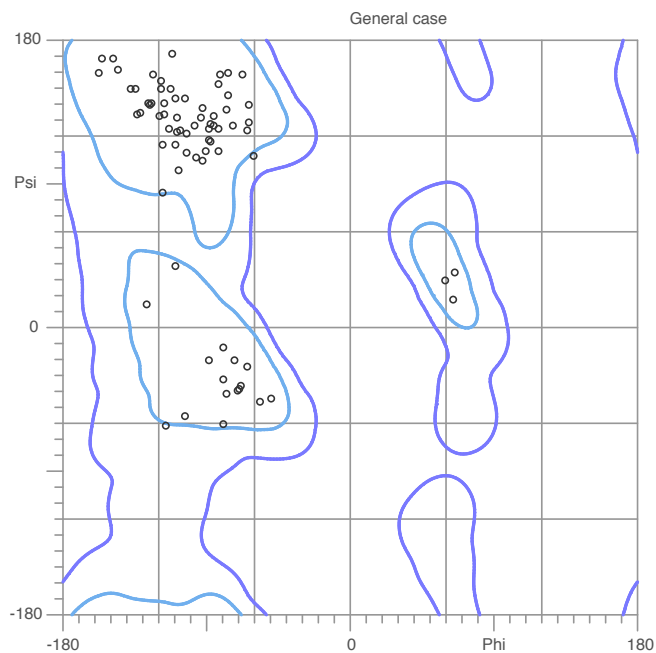
There were 12 outliers (phi, psi):

- [3] 42 PRO (-65.0, -62.9)
- [3] 57 GLY (-145.0, 75.6)
- [4] 42 PRO (-67.6, -61.9)
- [4] 94 HIS (65.0, 95.0)

- [7] 42 PRO (-66.0, -63.8)
- [9] 95 HIS (-176.8, -52.9)
- [10] 44 ILE (64.9, 105.0)
- [14] 94 HIS (63.5, 107.3)
- [15] 58 SER (65.1, 105.0)
- [17] 7 ARG (58.9, -75.6)
- [17] 44 ILE (65.0, 105.0)
- [20] 20 THR (55.2, 96.9)

MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 1



97.9% (92/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

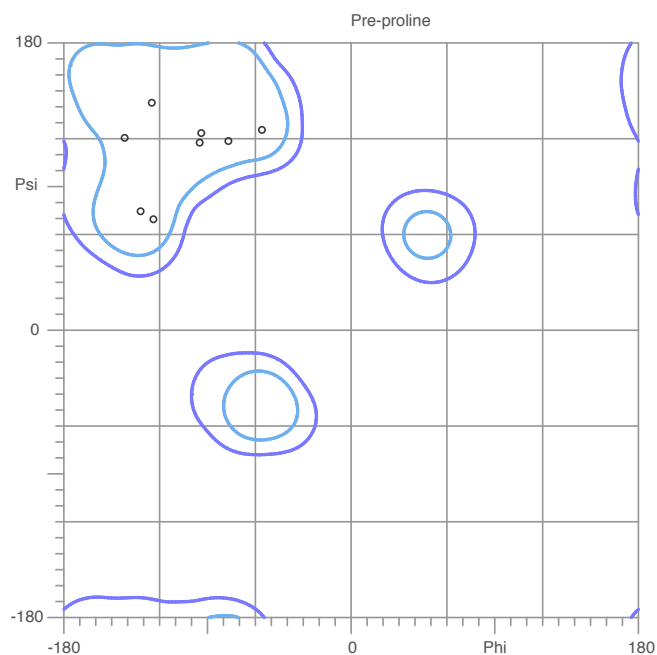
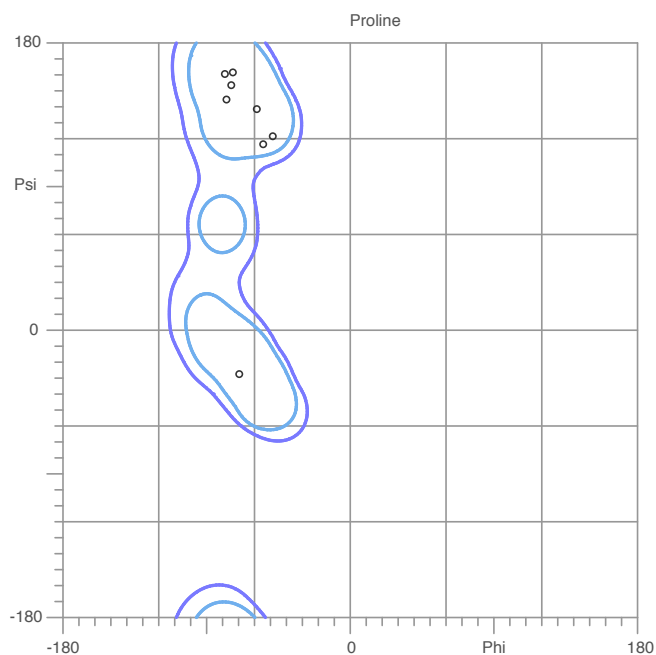
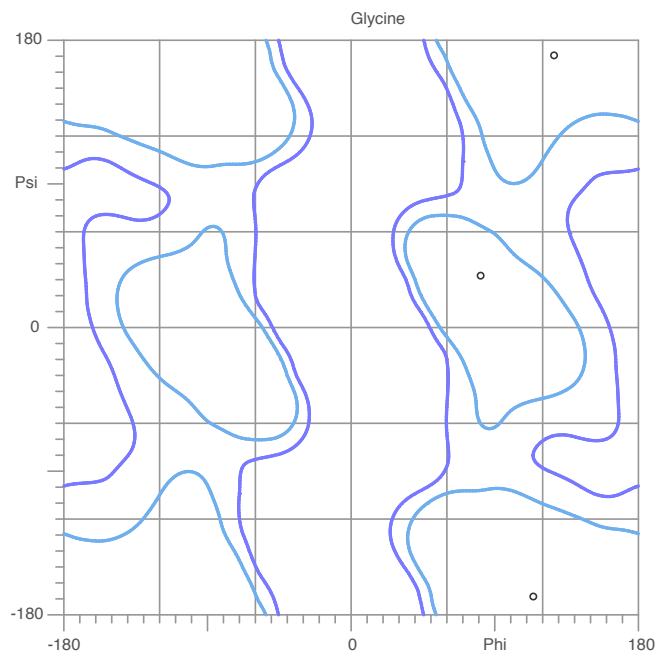
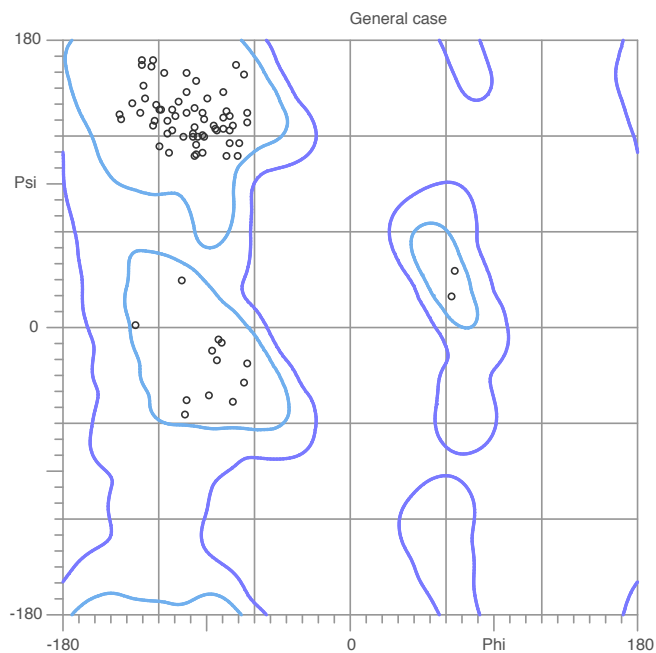
There were no outliers.

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

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 2



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

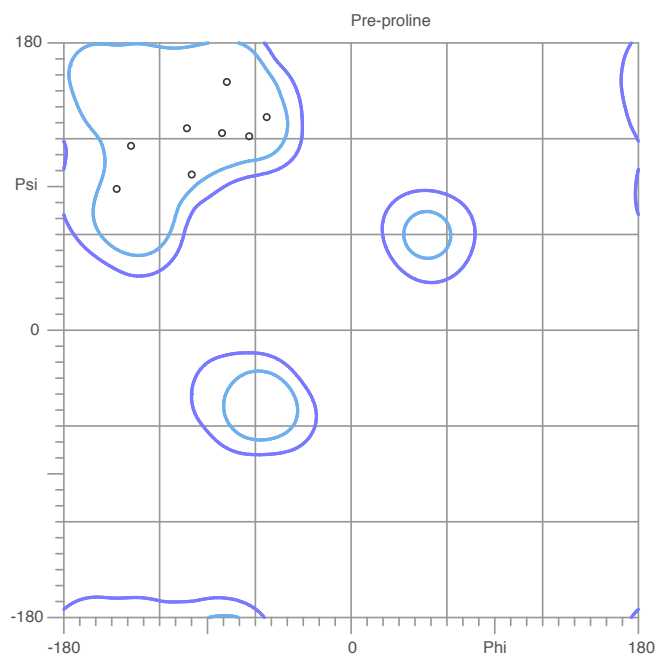
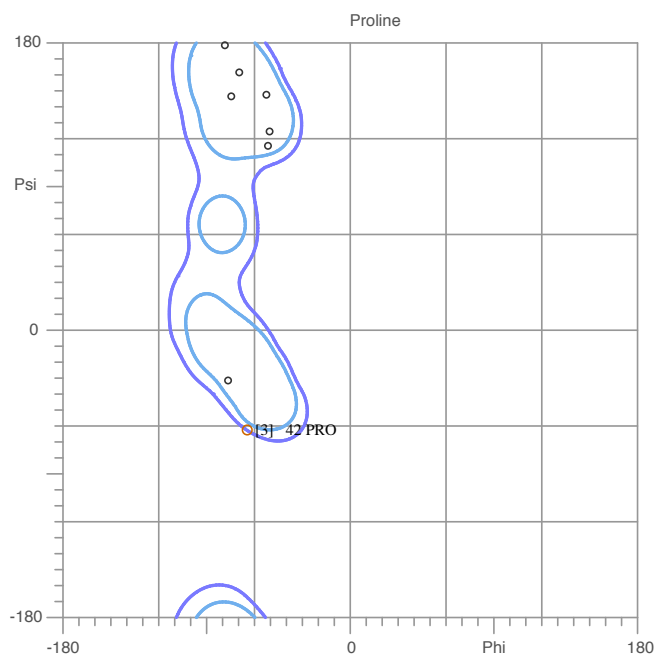
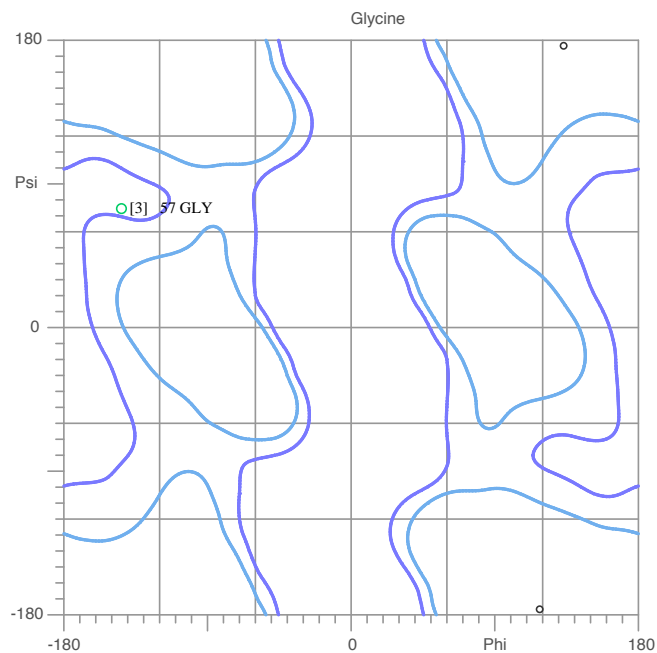
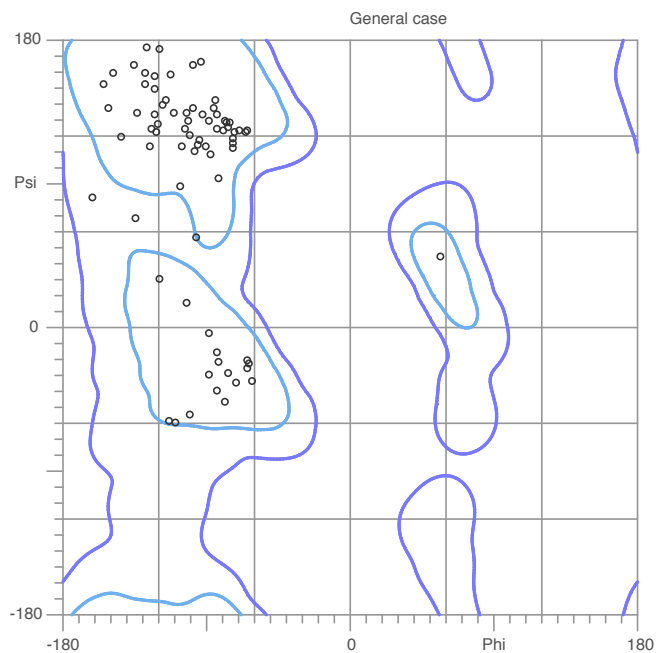
There were no outliers.

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

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 3



94.7% (89/94) of all residues were in favored (98%) regions.
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

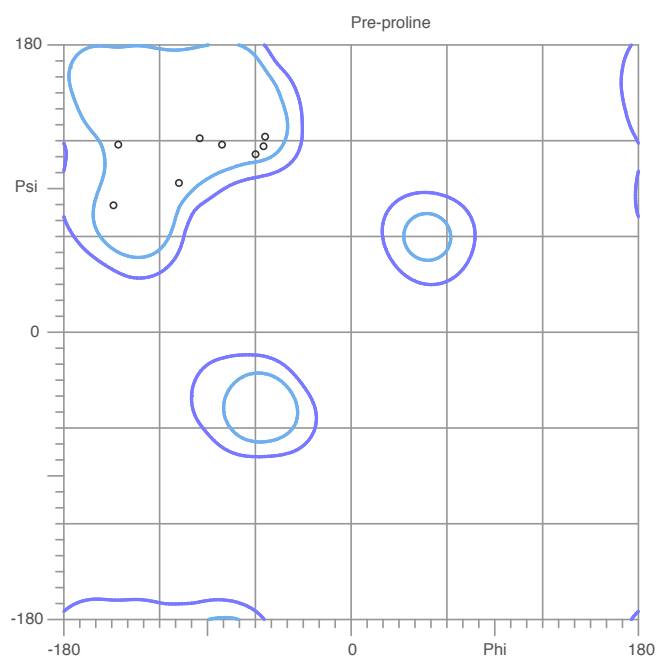
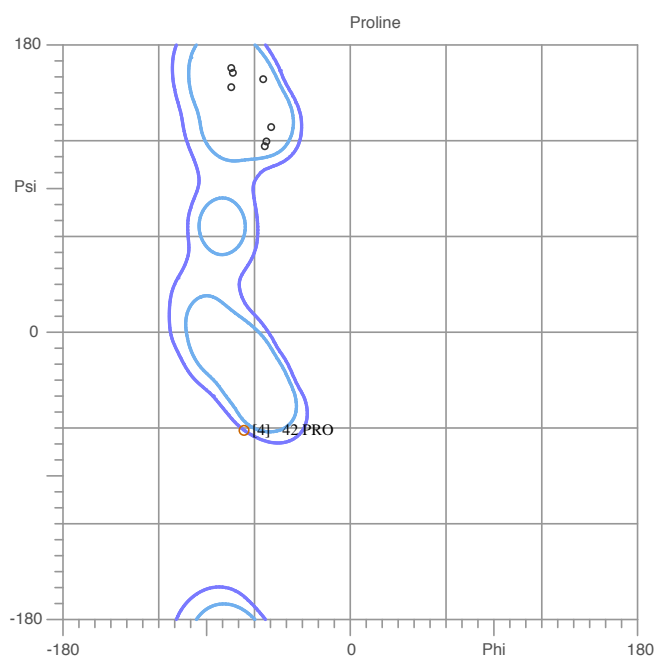
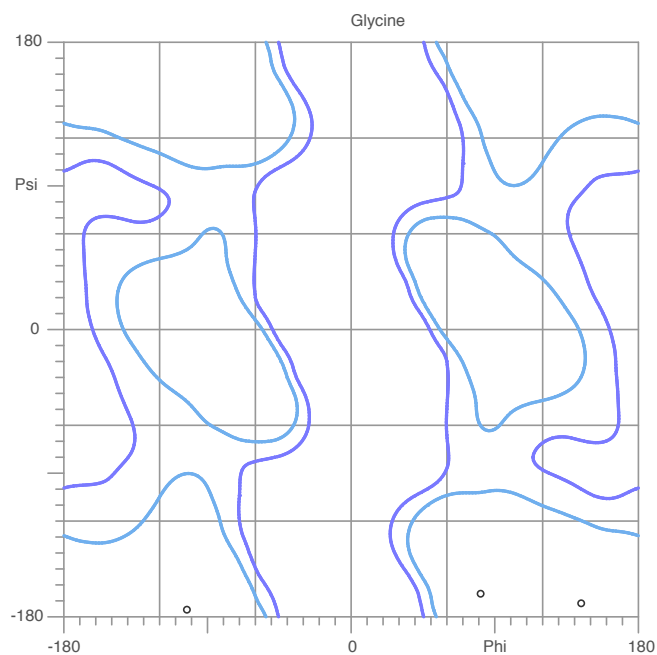
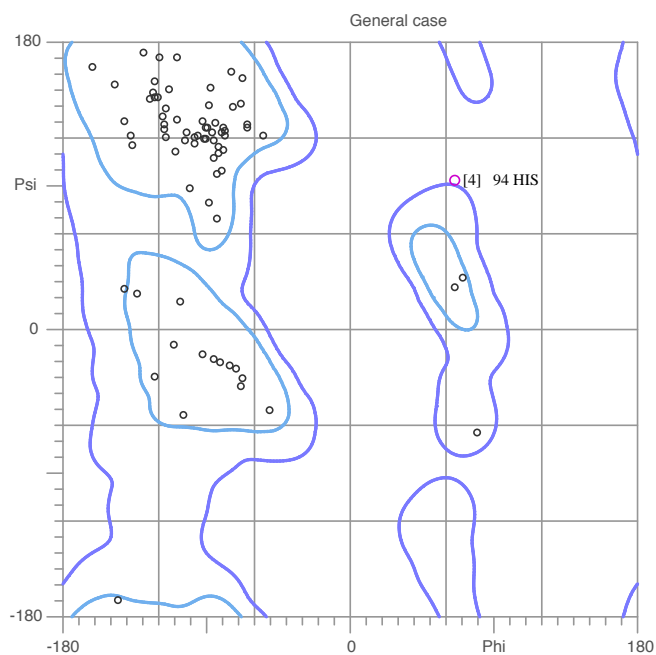
There were 2 outliers (phi, psi):

[3] 42 PRO (-65.0, -62.9)

[3] 57 GLY (-145.0, 75.6)

MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 4



95.7% (90/94) of all residues were in favored (98%) regions.
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

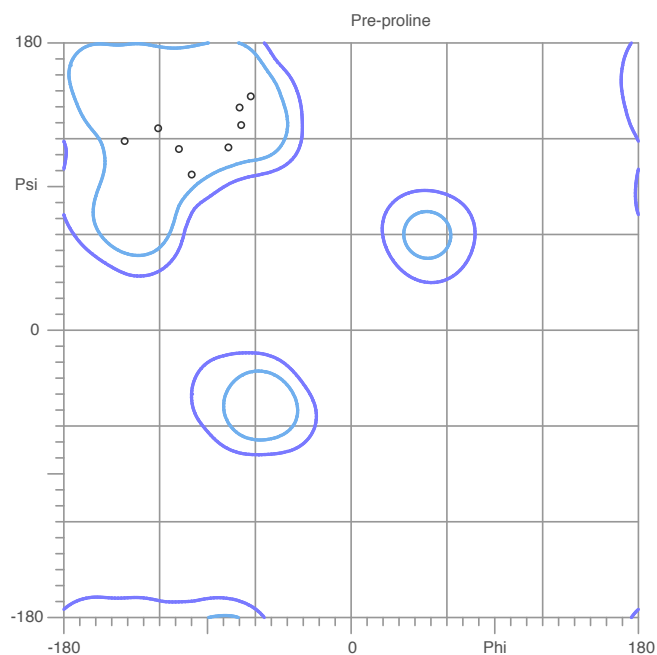
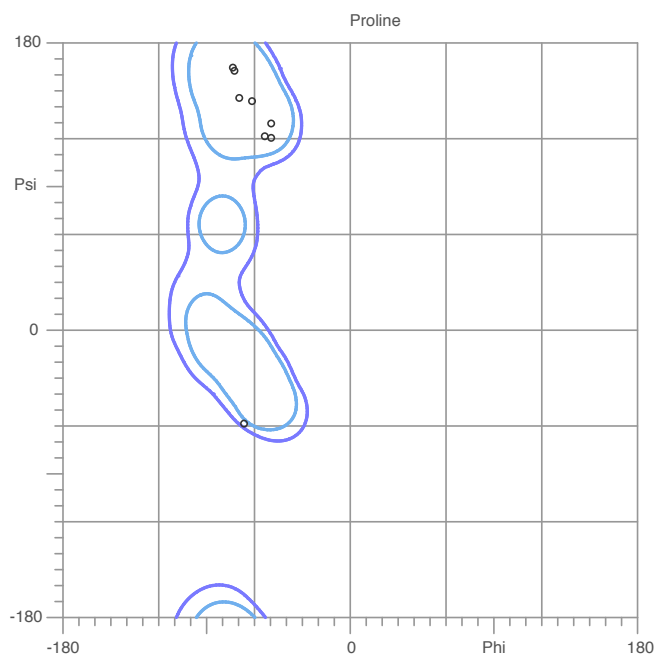
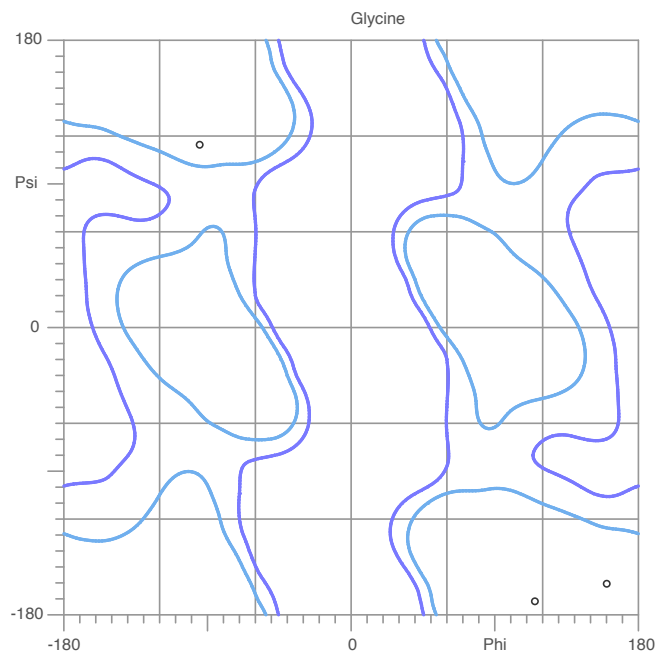
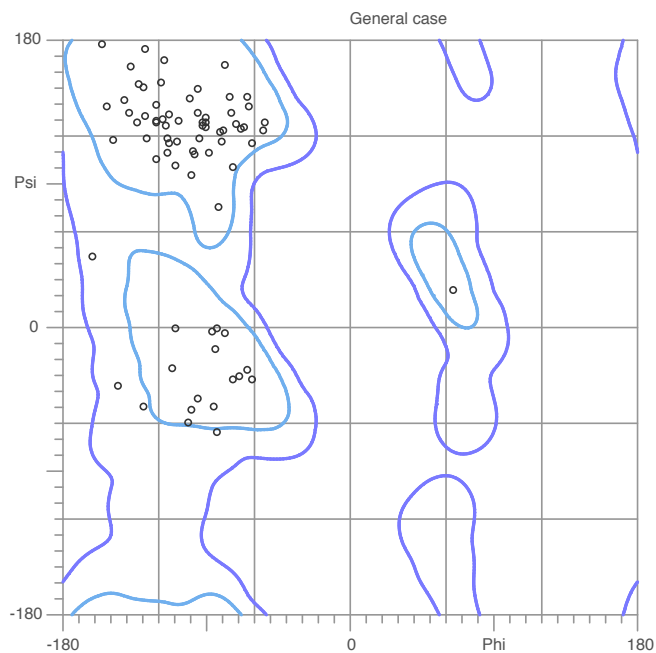
There were 2 outliers (phi, psi):

[4] 42 PRO (-67.6, -61.9)

[4] 94 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 5

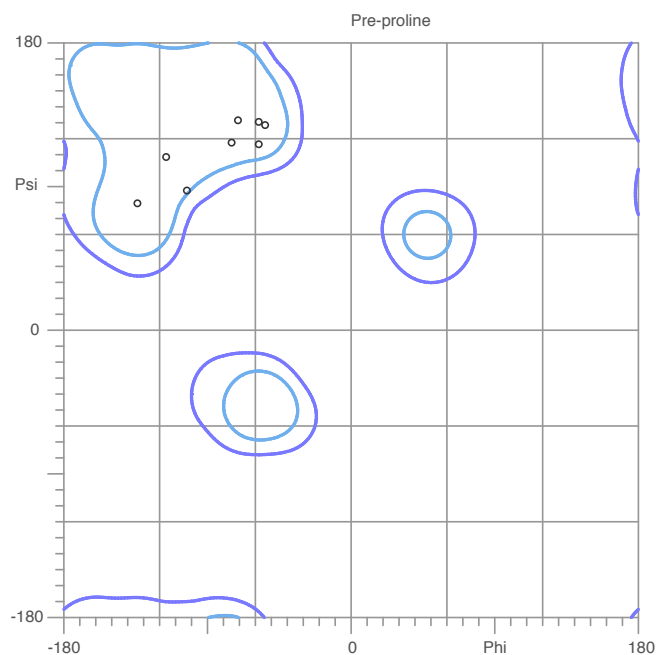
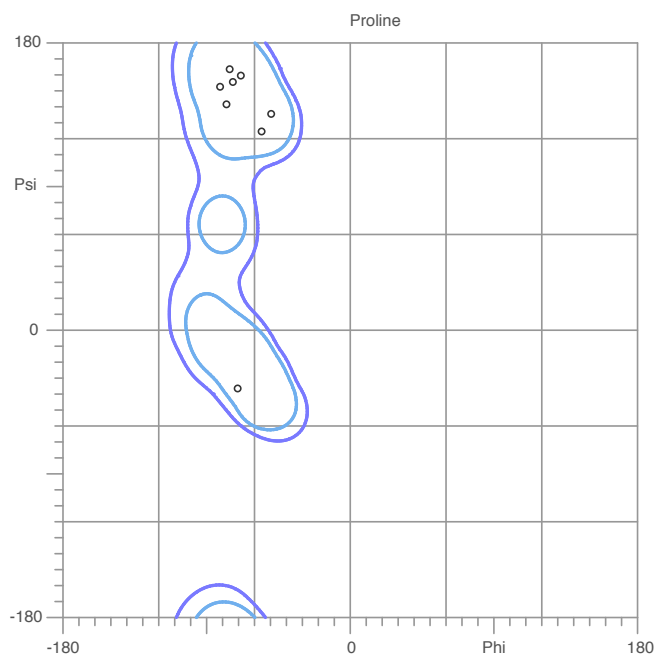
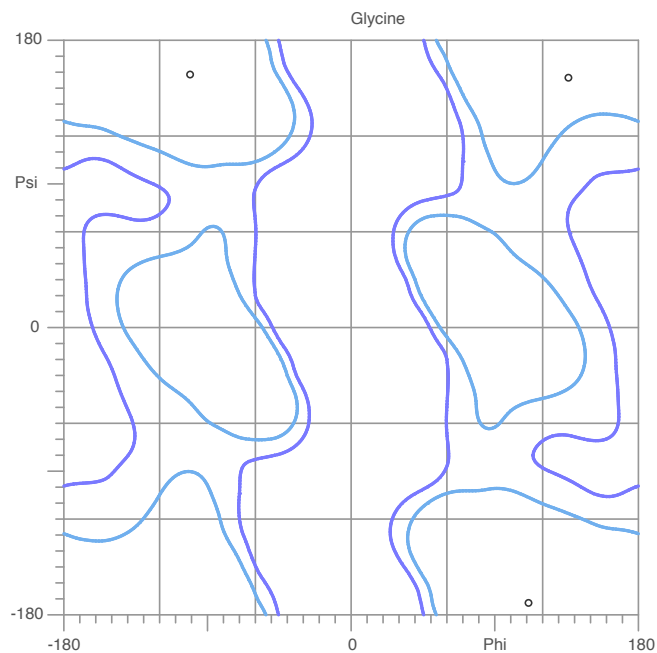
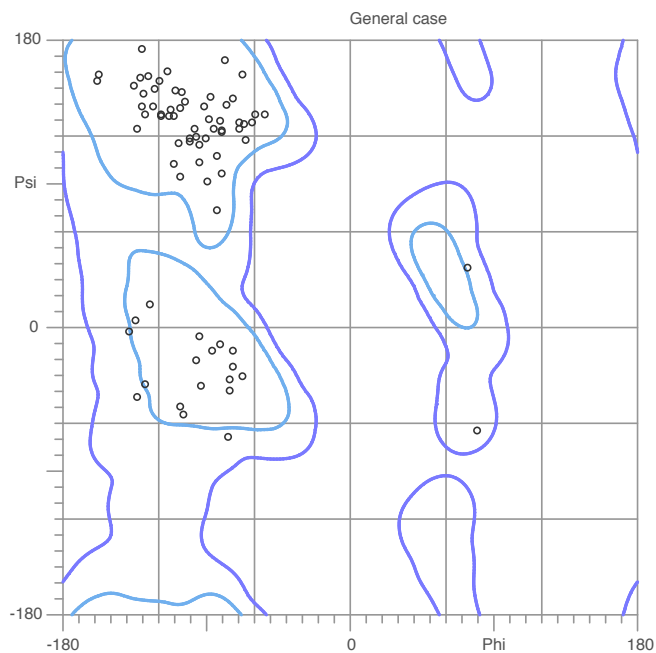


94.7% (89/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 6



94.7% (89/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

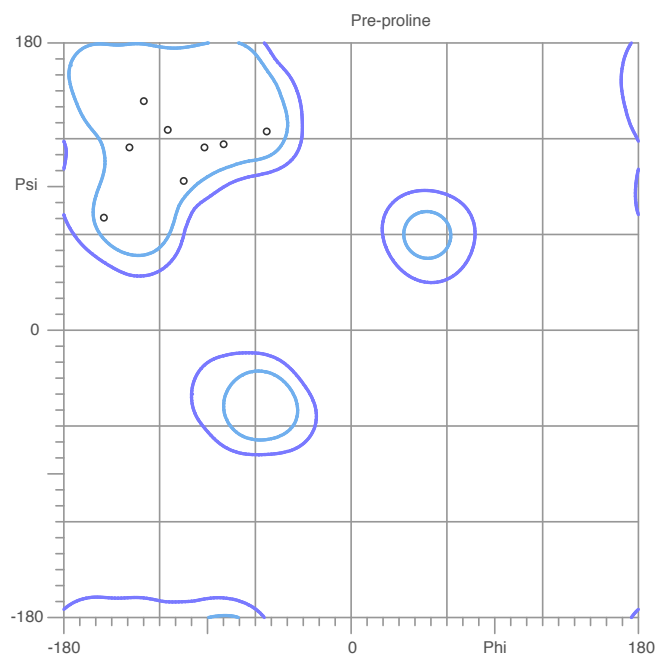
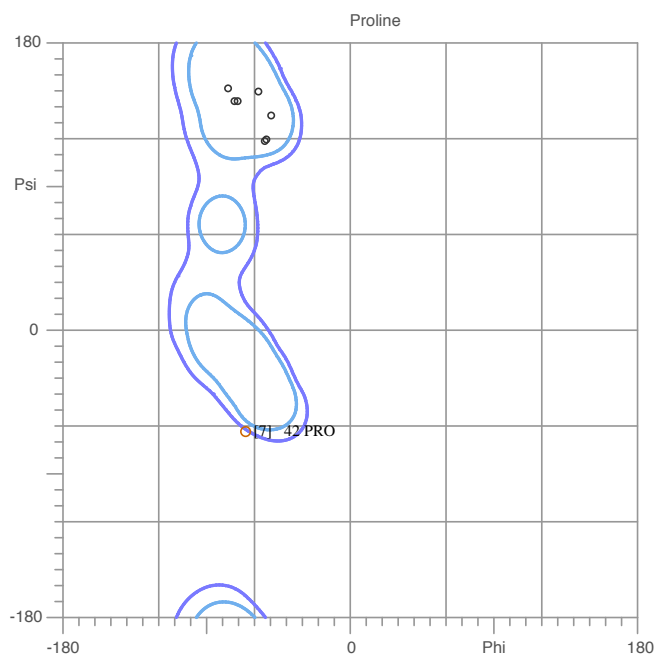
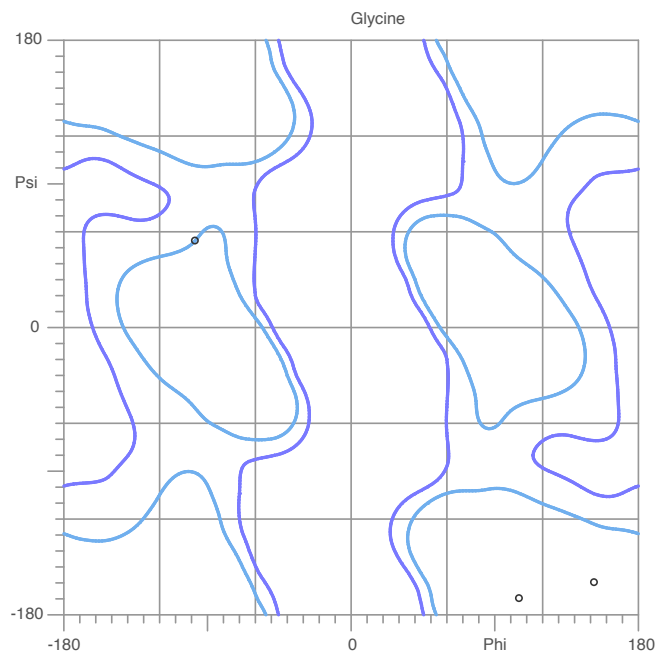
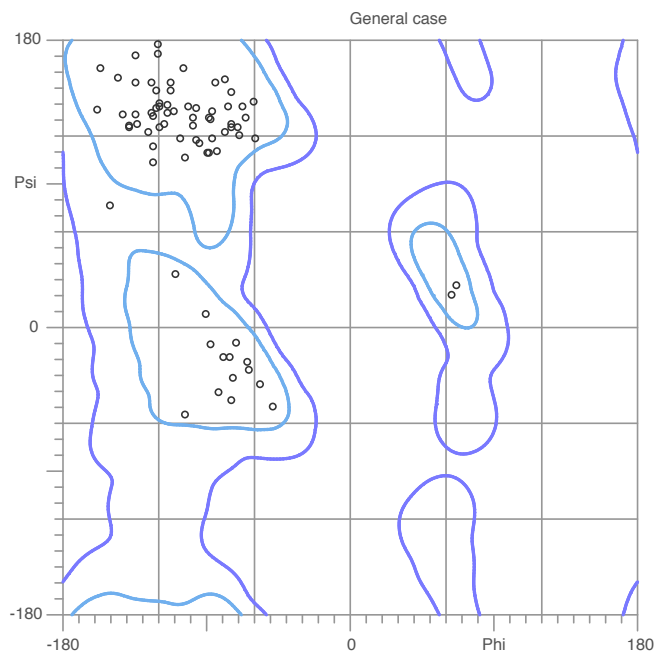
There were no outliers.

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

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

MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 7



96.8% (91/94) of all residues were in favored (98%) regions.
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

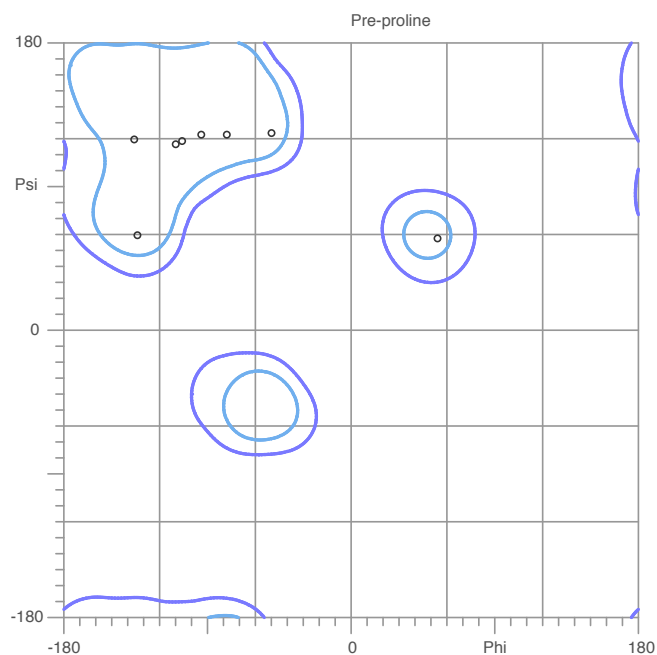
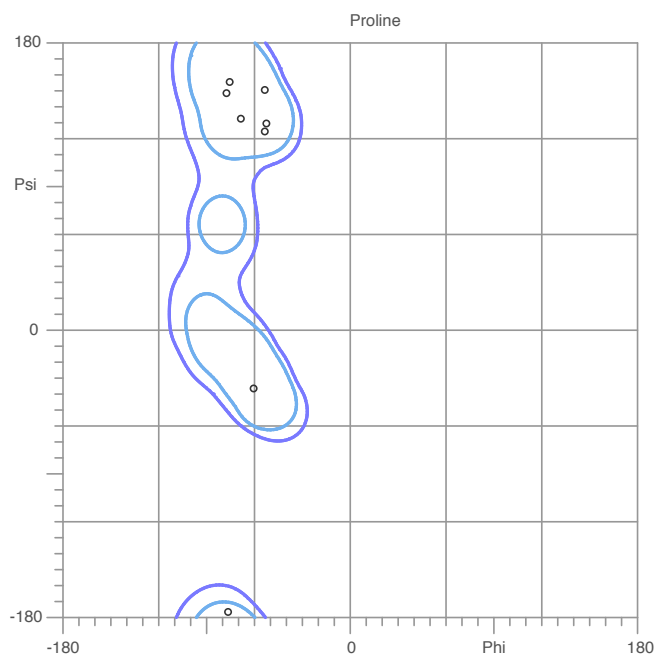
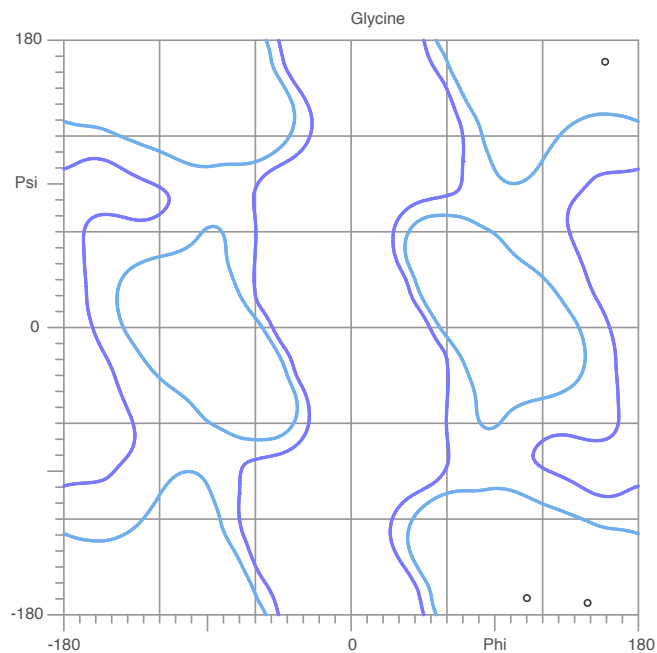
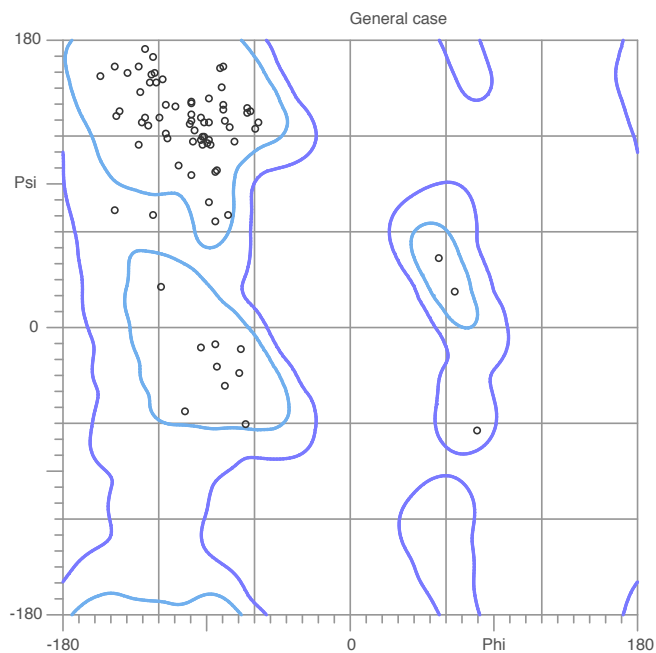
There were 1 outliers (phi, psi):
[7] 42 PRO (-66.0, -63.8)

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 8



96.8% (91/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

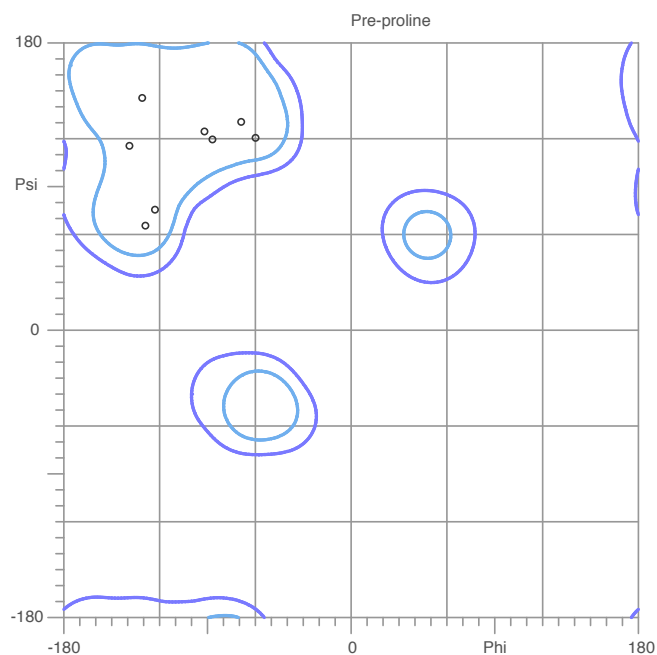
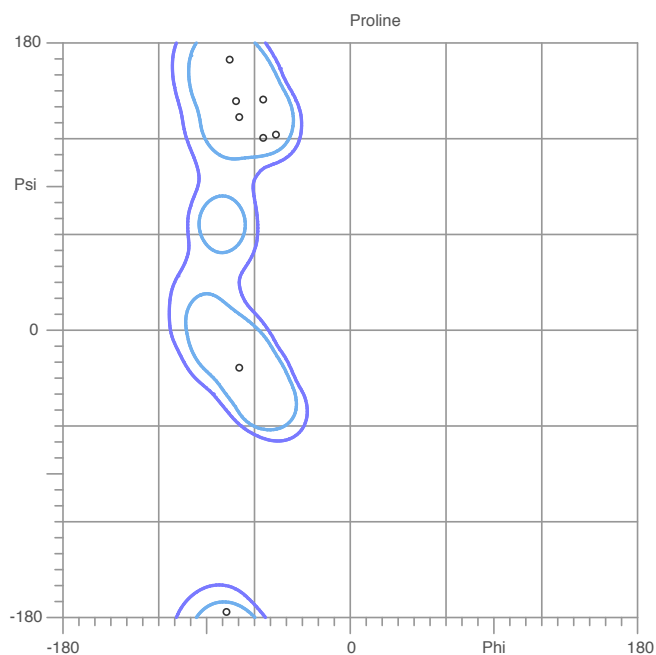
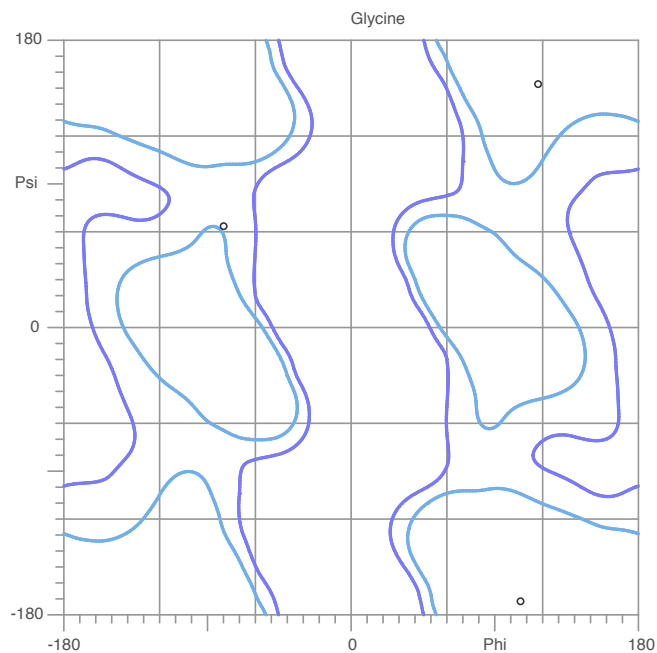
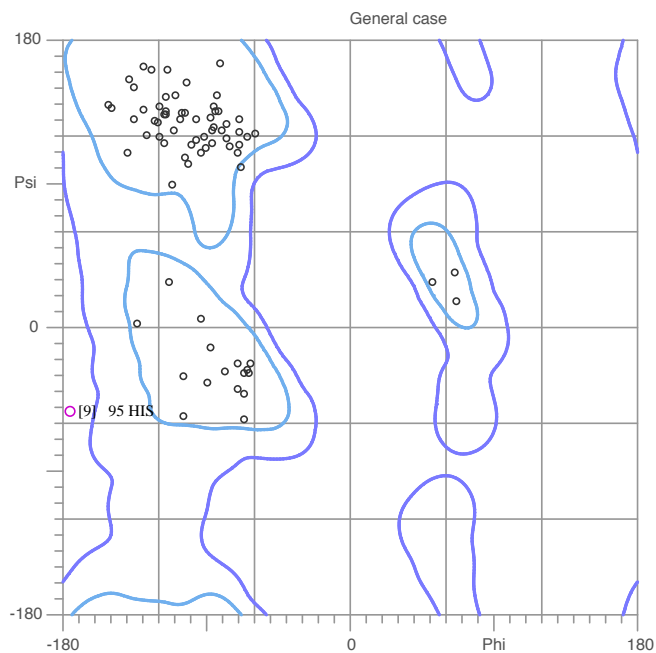
There were no outliers.

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

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 9

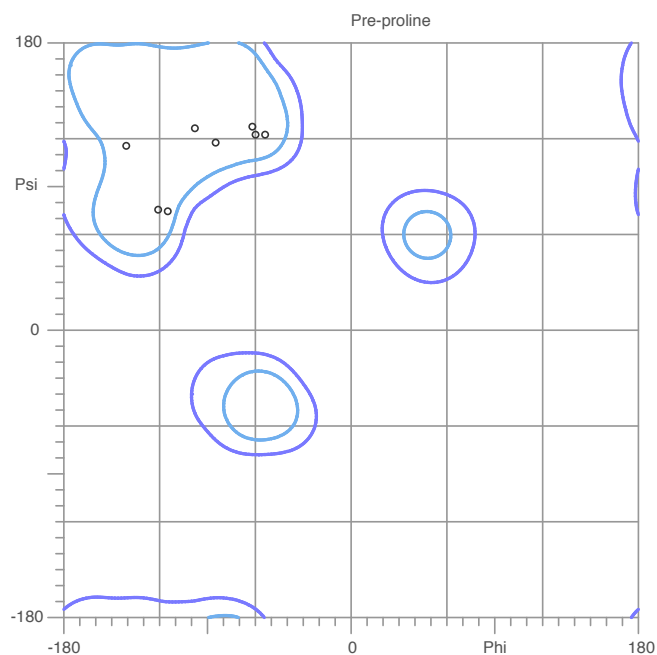
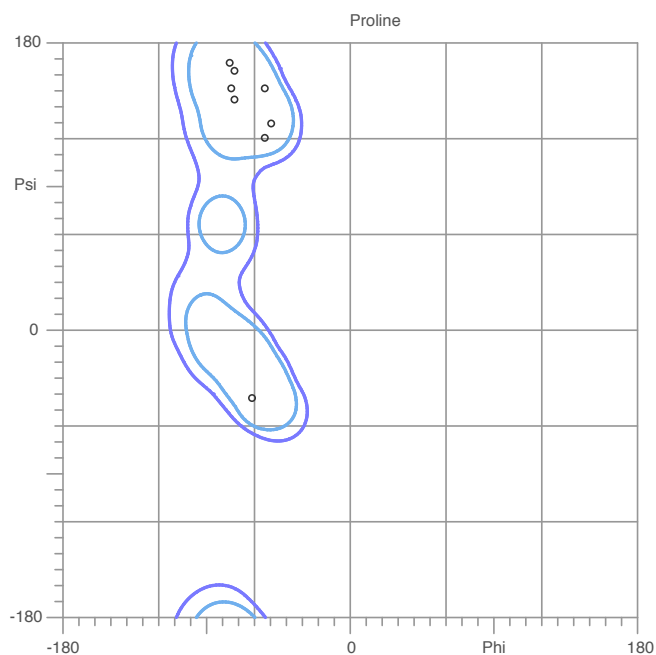
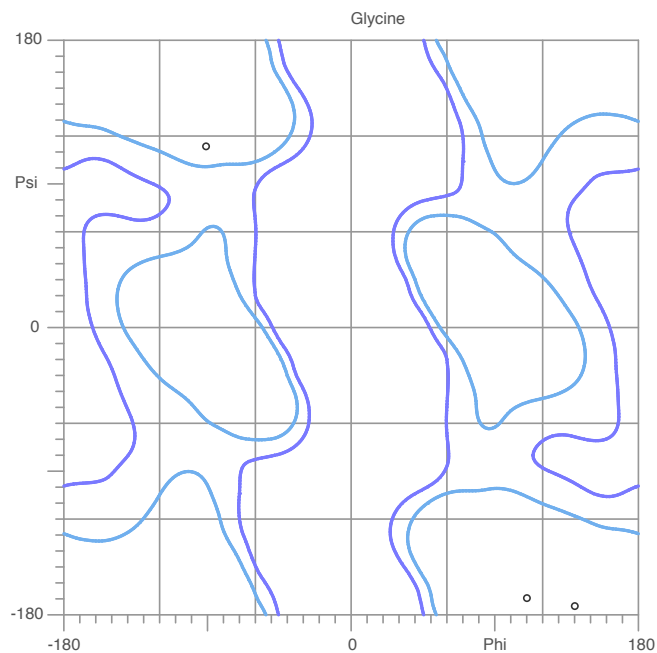
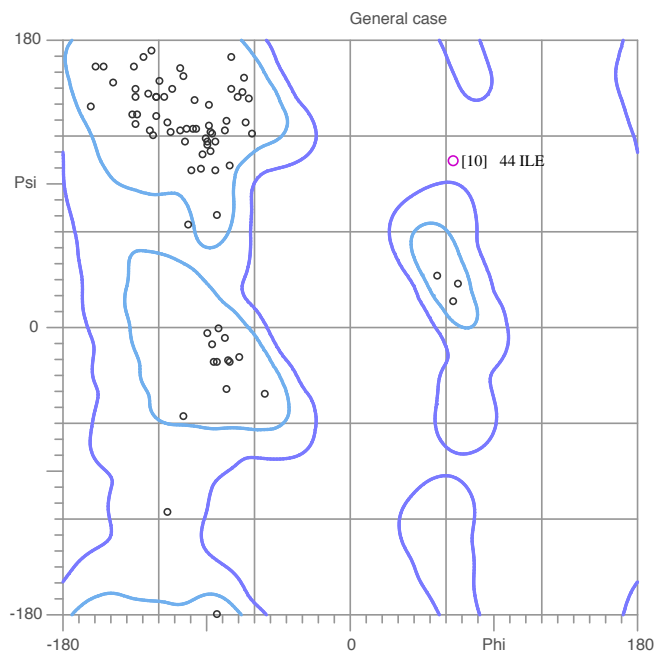


97.9% (92/94) of all residues were in favored (98%) regions.
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 95 HIS (-176.8, -52.9)

MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 10



96.8% (91/94) of all residues were in favored (98%) regions.
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

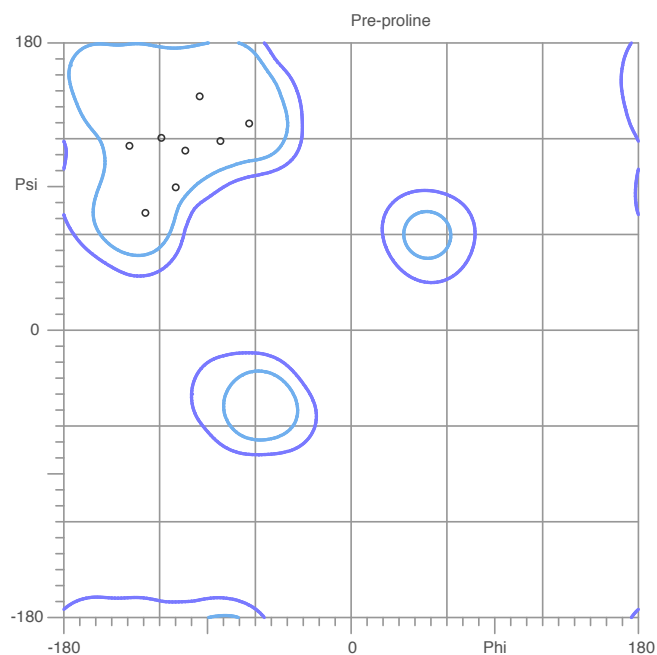
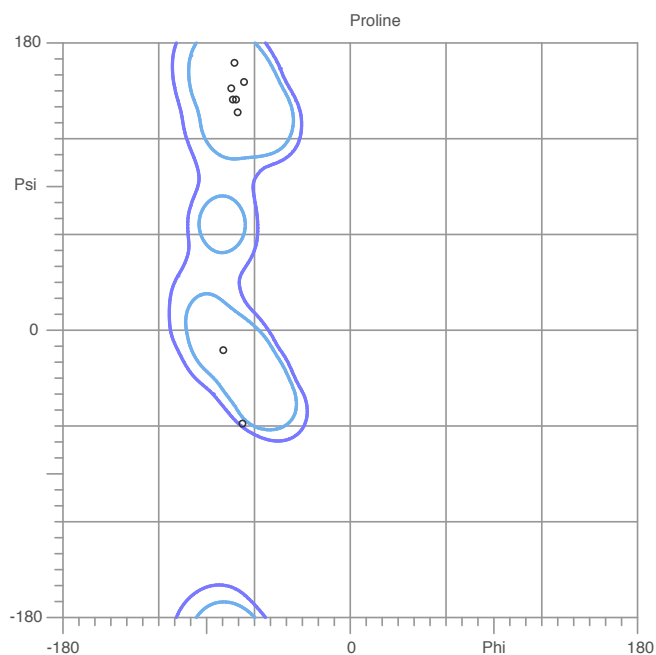
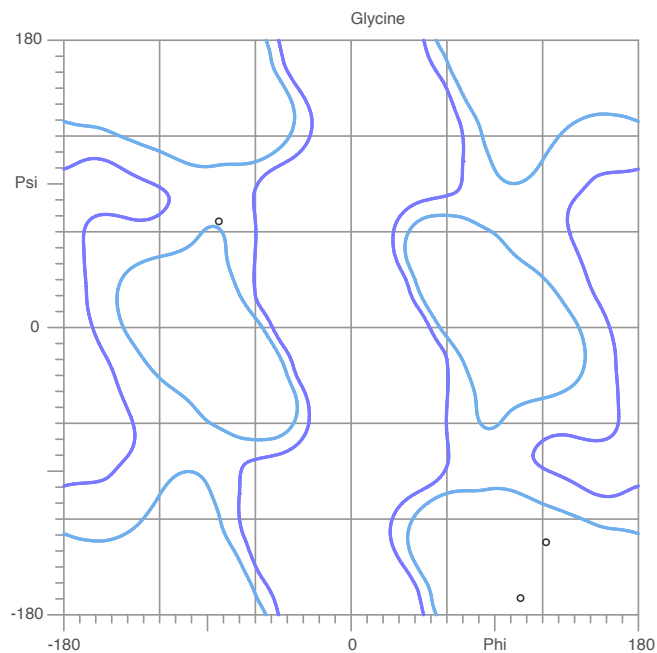
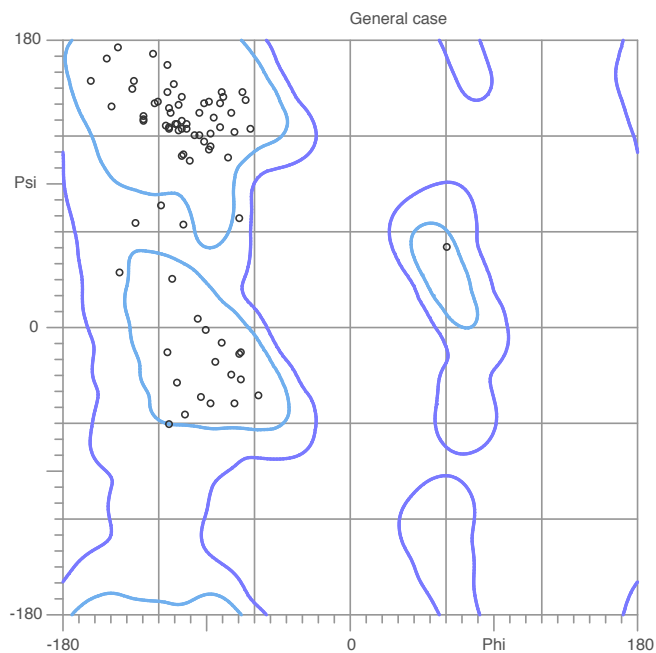
There were 1 outliers (phi, psi):
[10] 44 ILE (64.9, 105.0)

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 11



92.6% (87/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

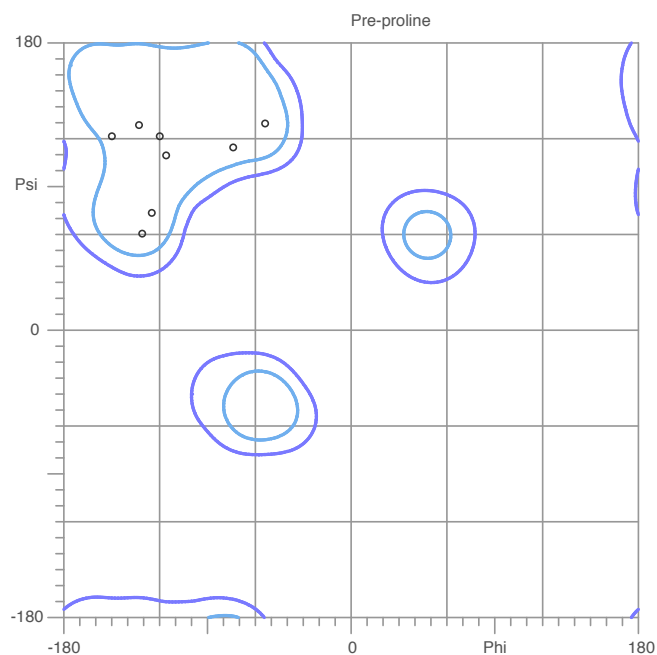
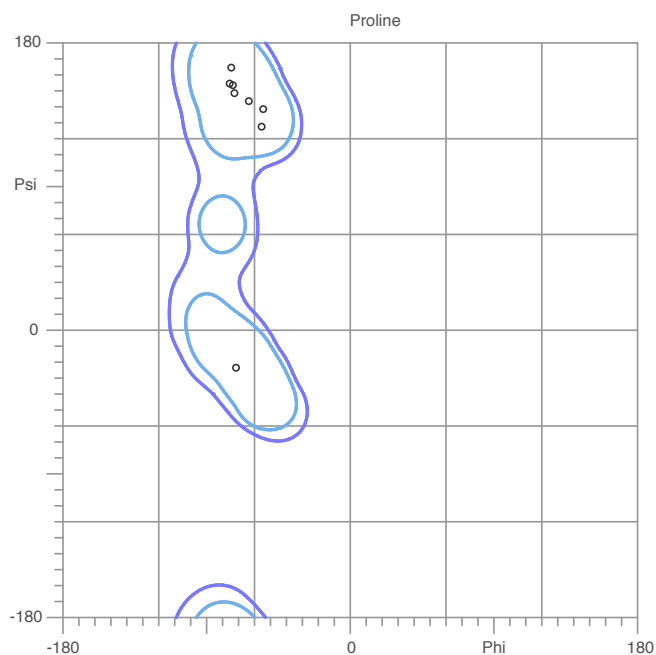
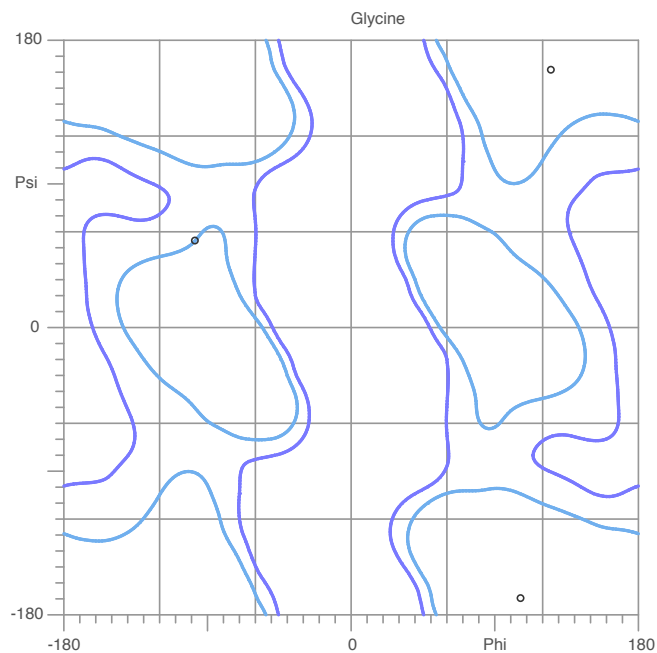
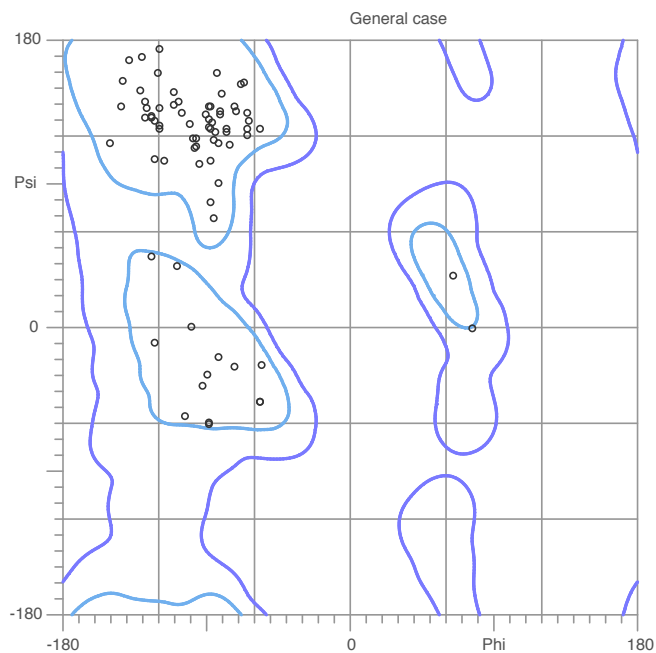
There were no outliers.

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 12



97.9% (92/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

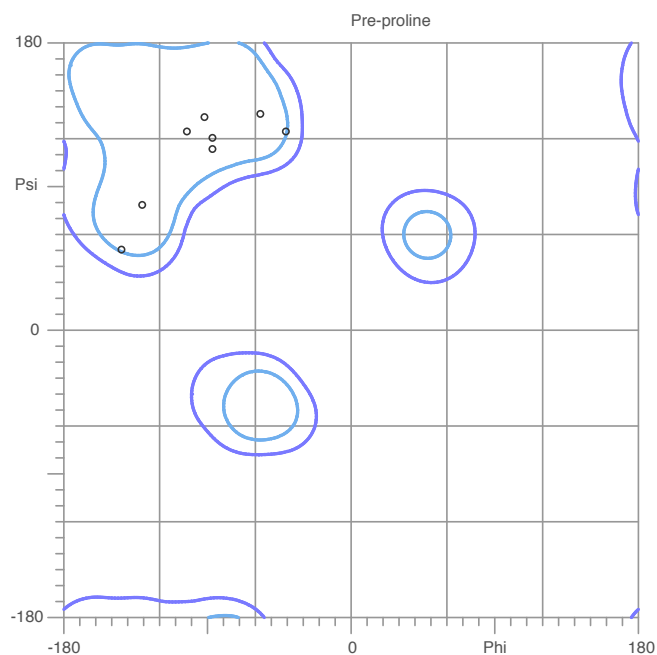
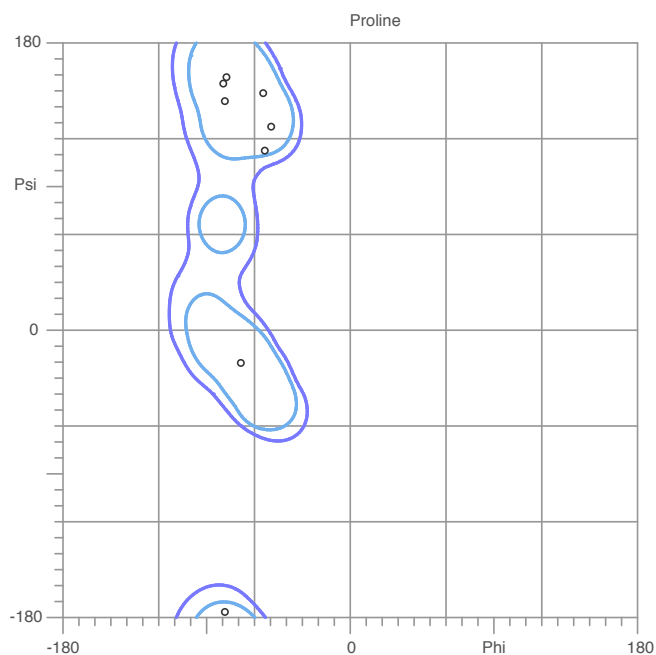
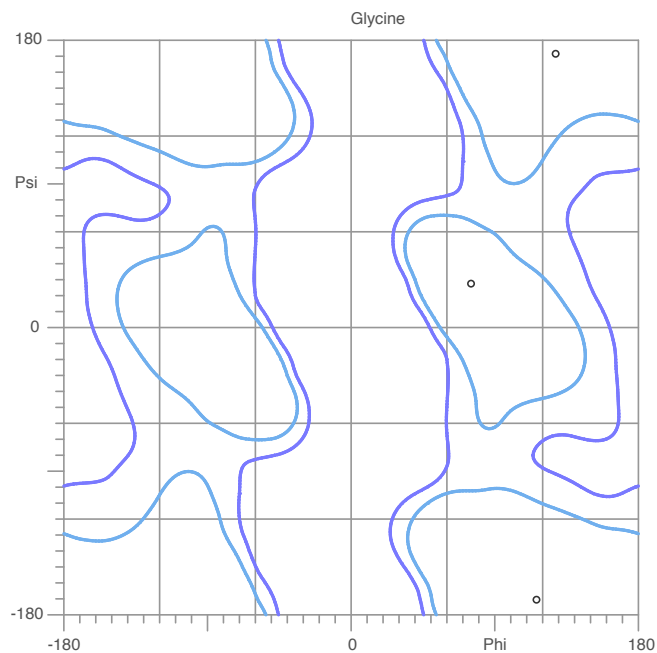
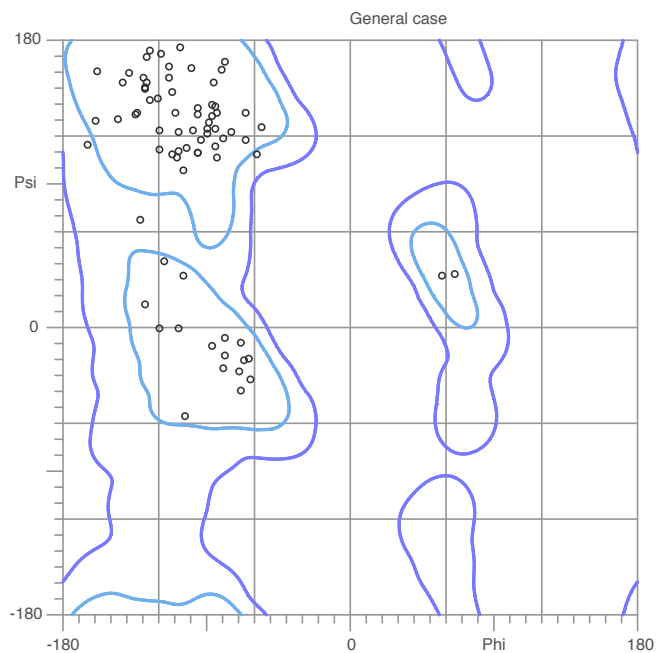
There were no outliers.

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

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 13



96.8% (91/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

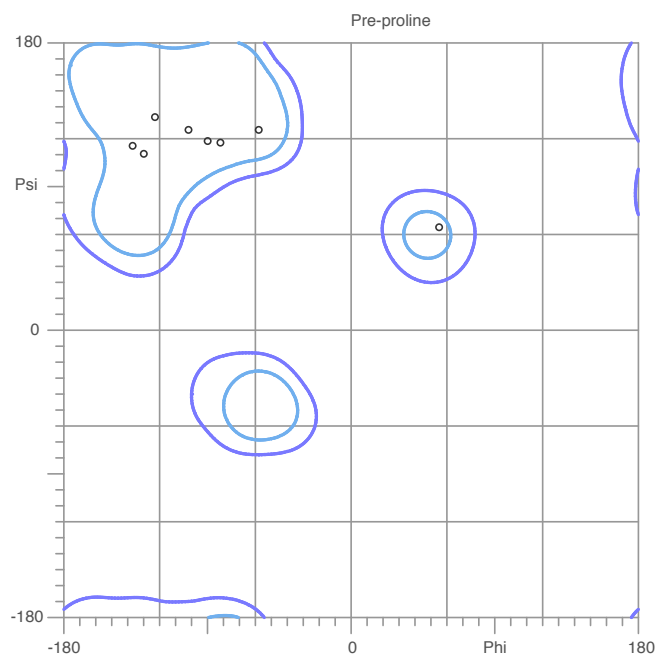
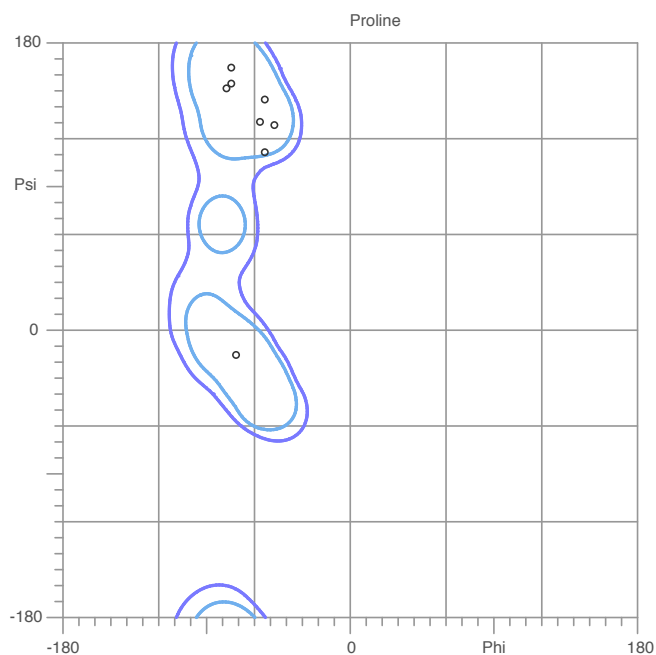
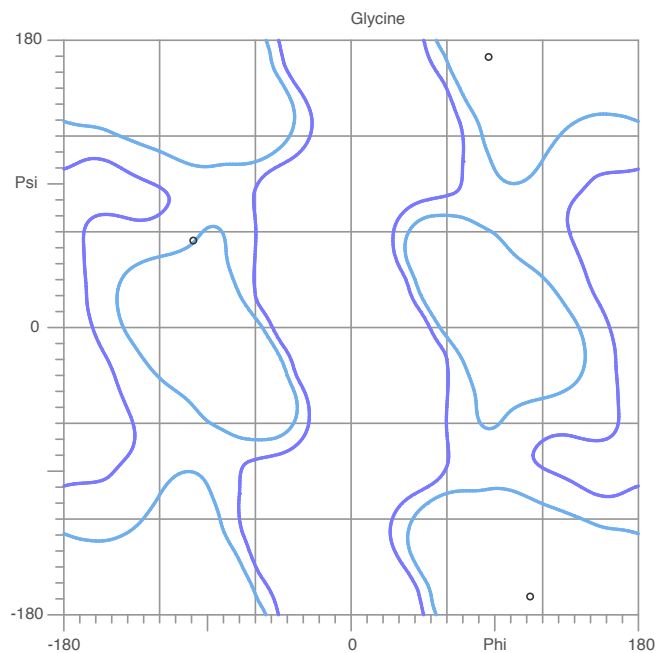
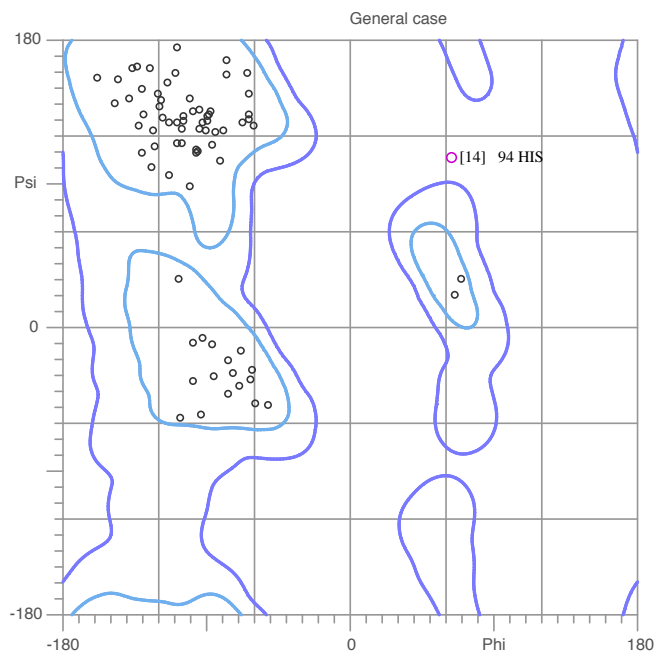
There were no outliers.

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

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 14



97.9% (92/94) of all residues were in favored (98%) regions.
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

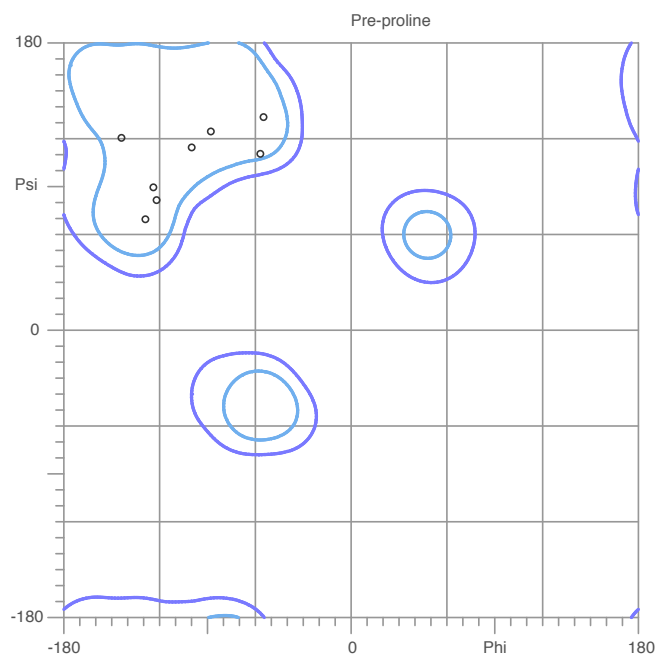
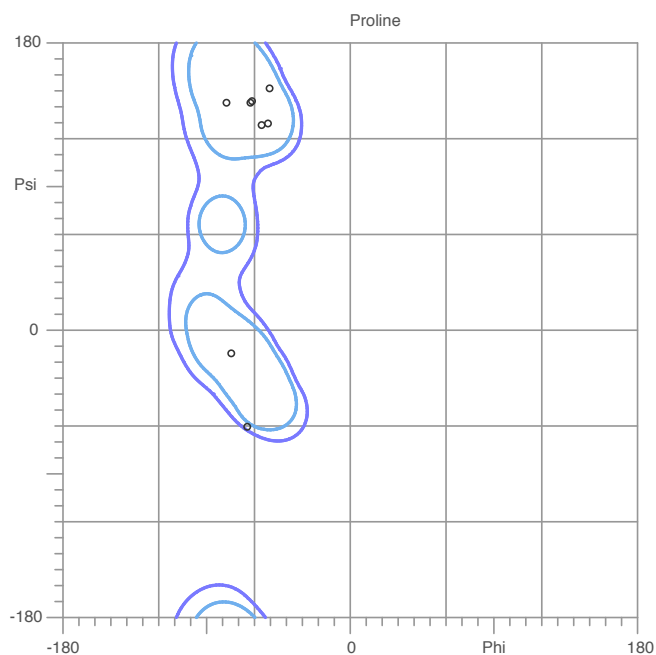
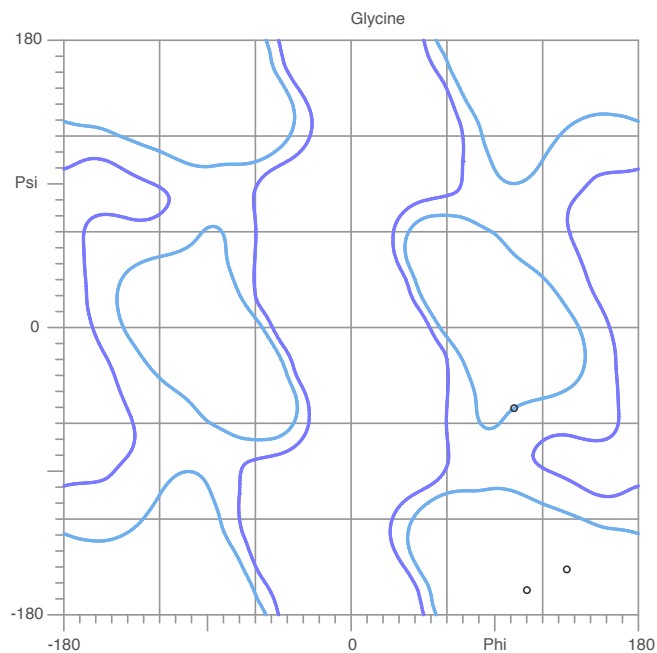
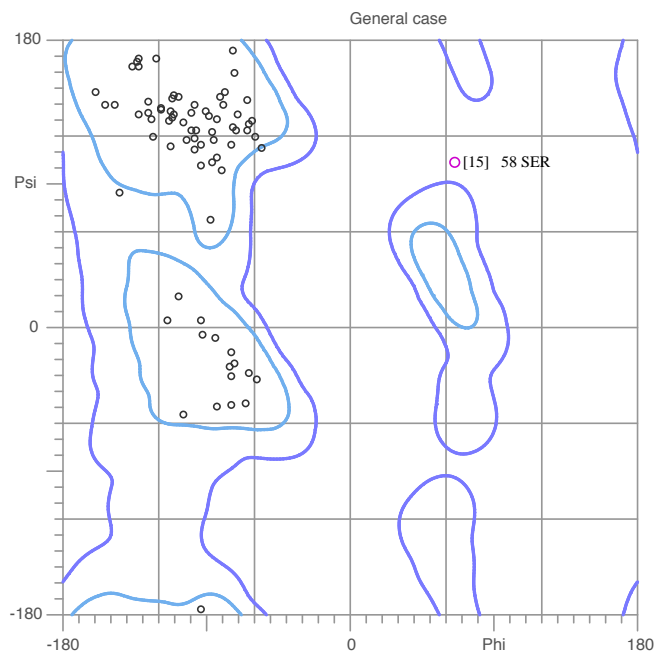
There were 1 outliers (phi, psi):
[14] 94 HIS (63.5, 107.3)

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

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

MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 15



95.7% (90/94) of all residues were in favored (98%) regions.
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

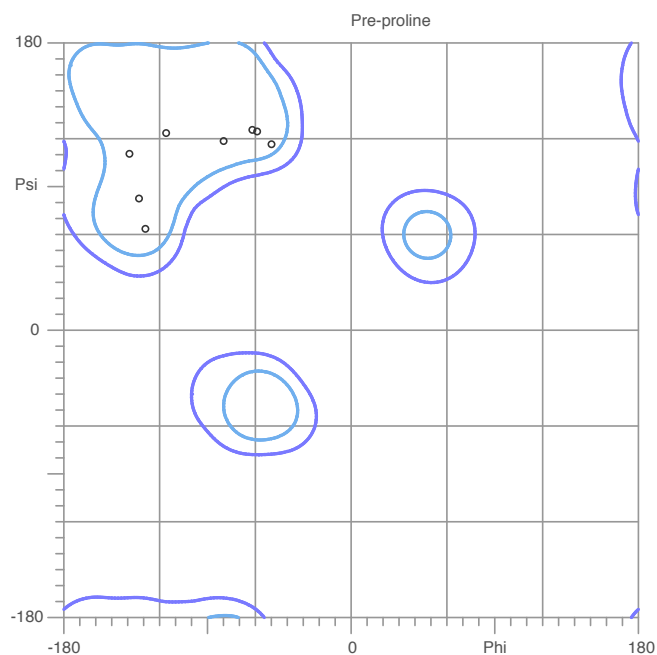
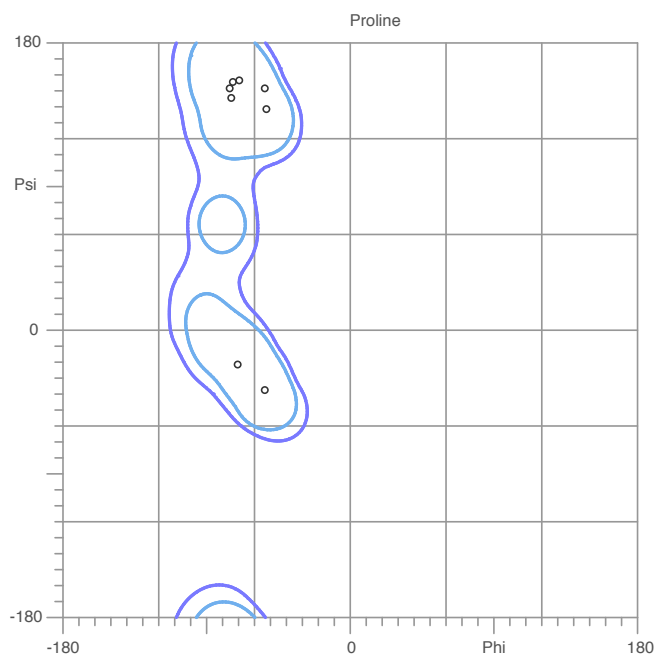
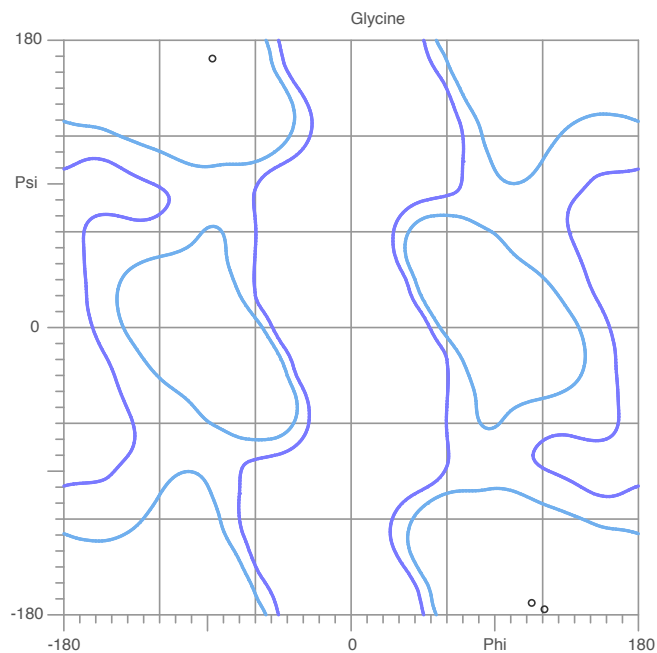
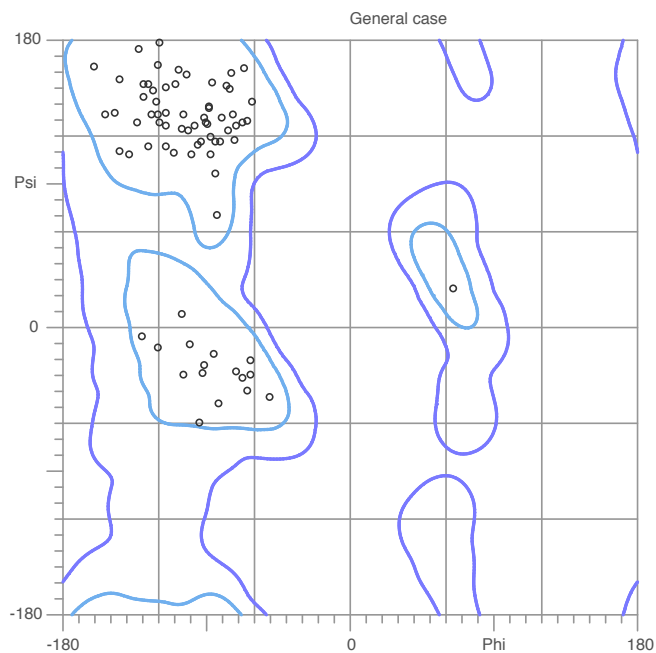
There were 1 outliers (phi, psi):
[15] 58 SER (65.1, 105.0)

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

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 16



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

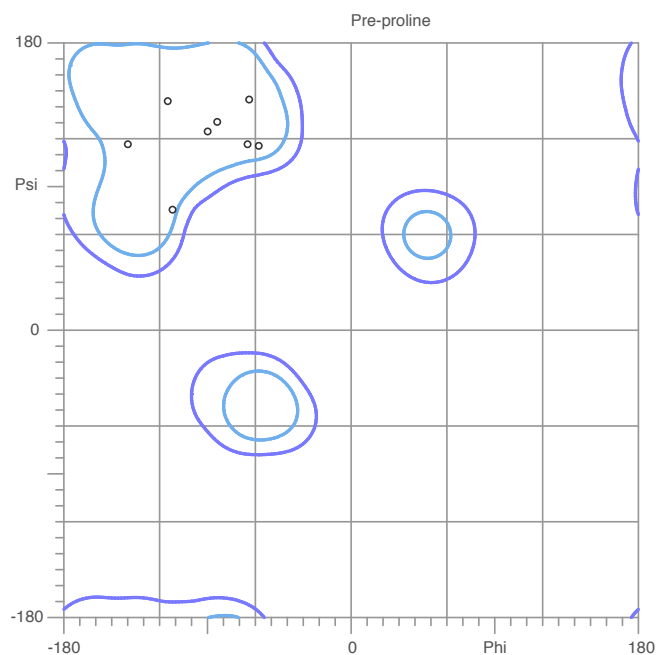
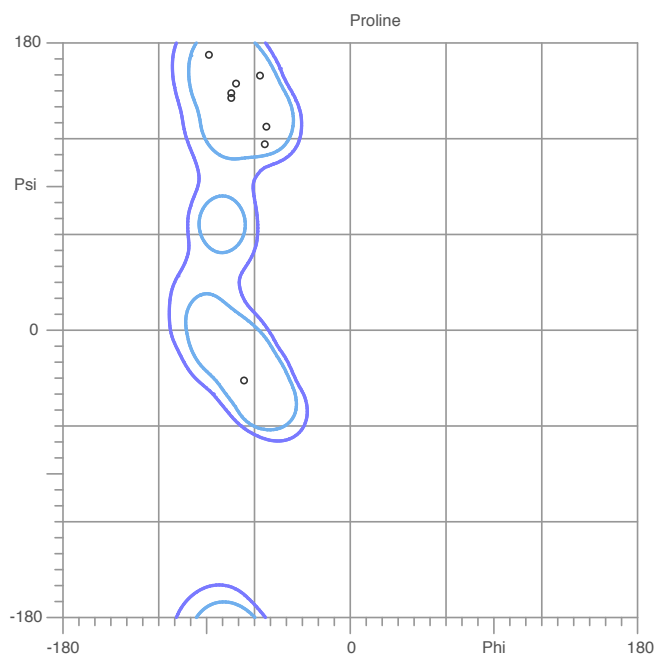
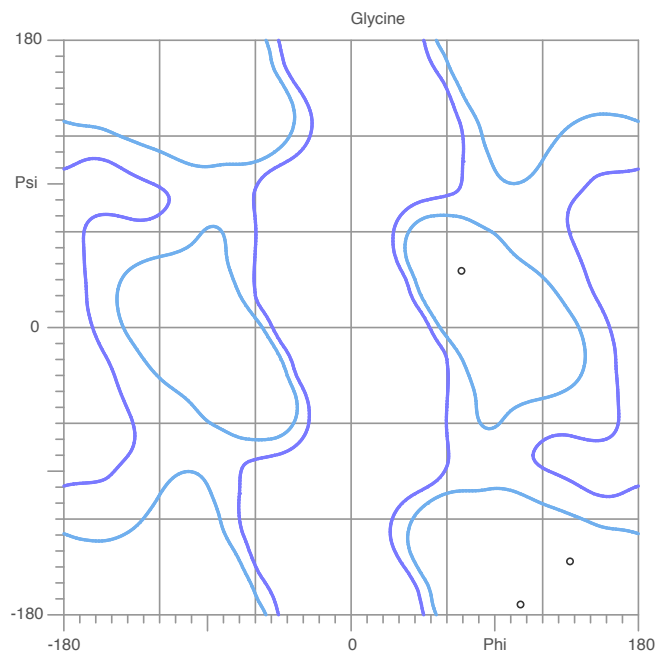
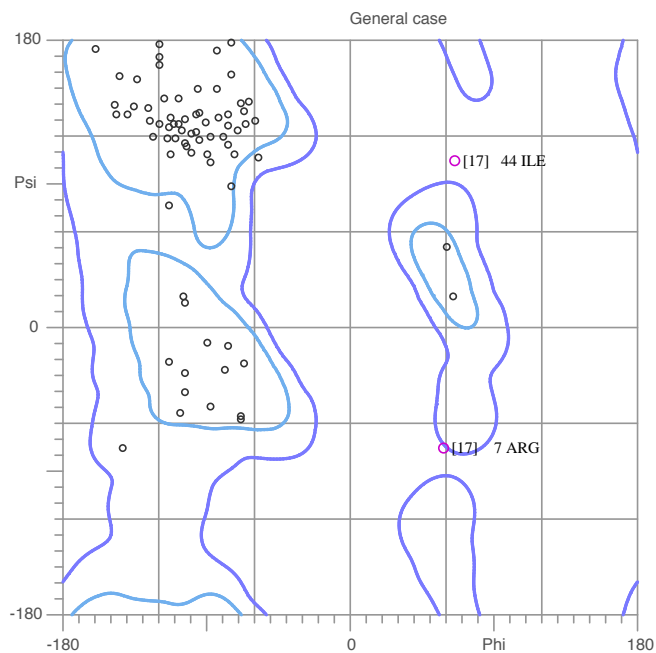
There were no outliers.

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 17



94.7% (89/94) of all residues were in favored (98%) regions.
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

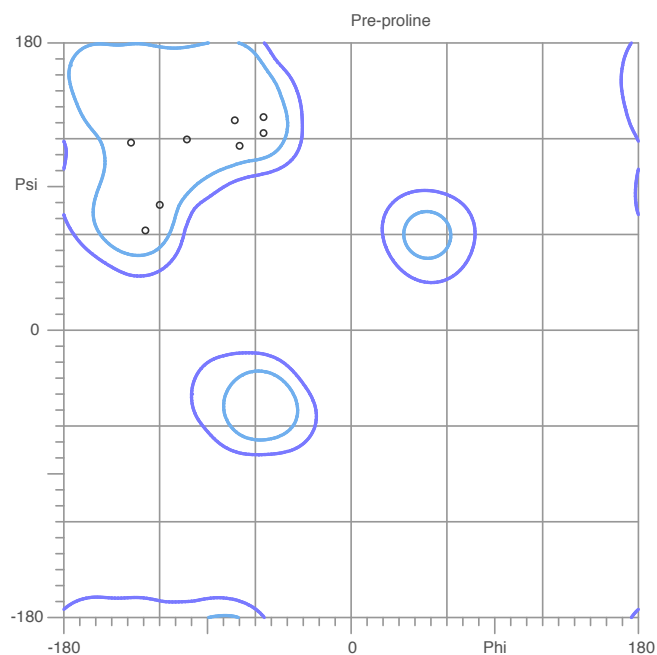
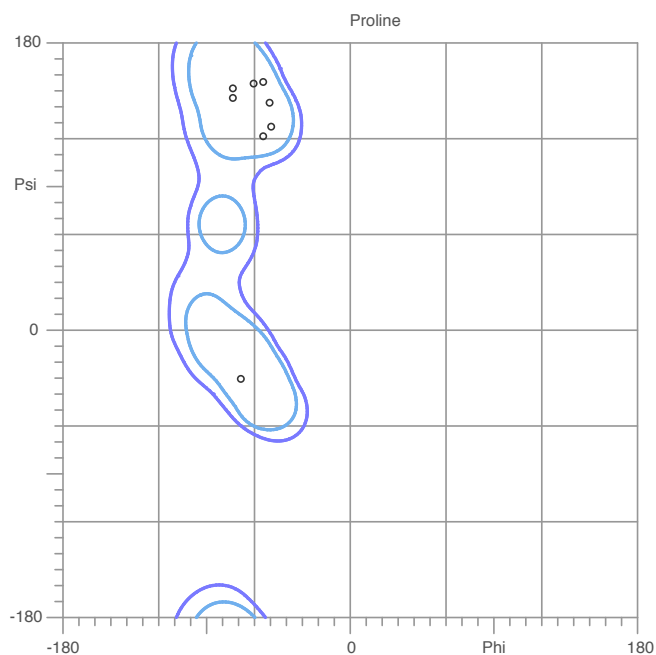
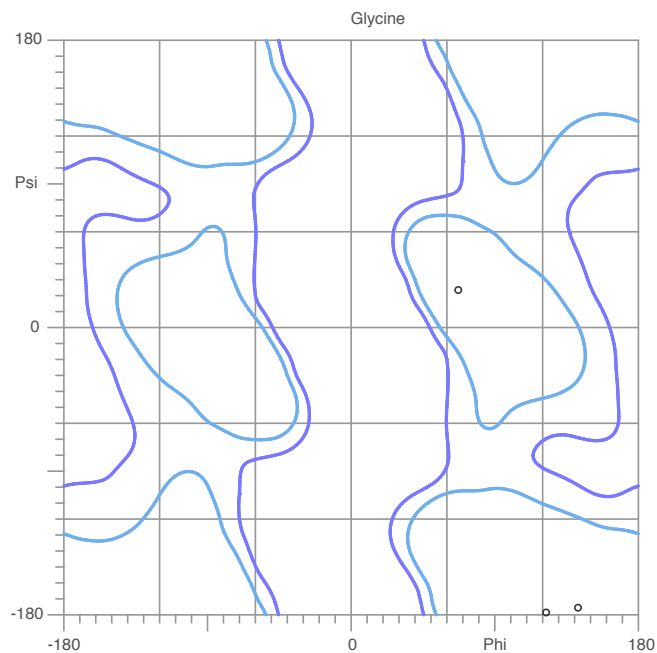
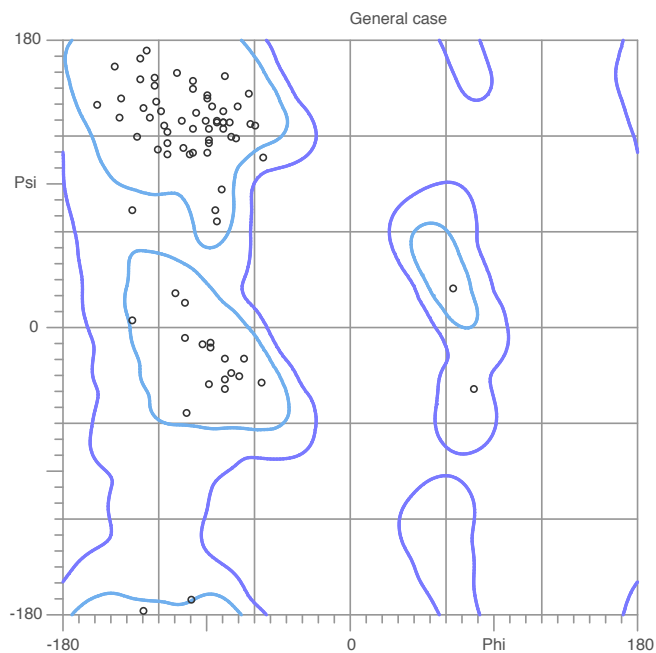
There were 2 outliers (phi, psi):

[17] 7 ARG (58.9, -75.6)

[17] 44 ILE (65.0, 105.0)

MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 18



95.7% (90/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

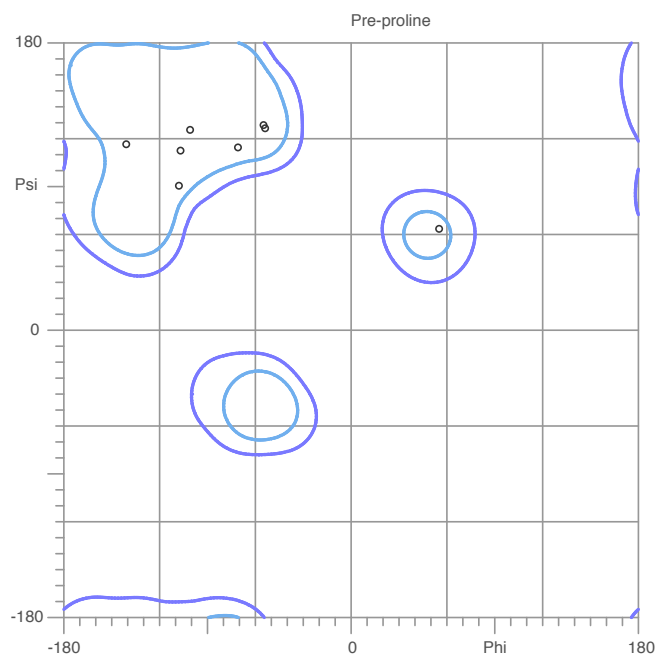
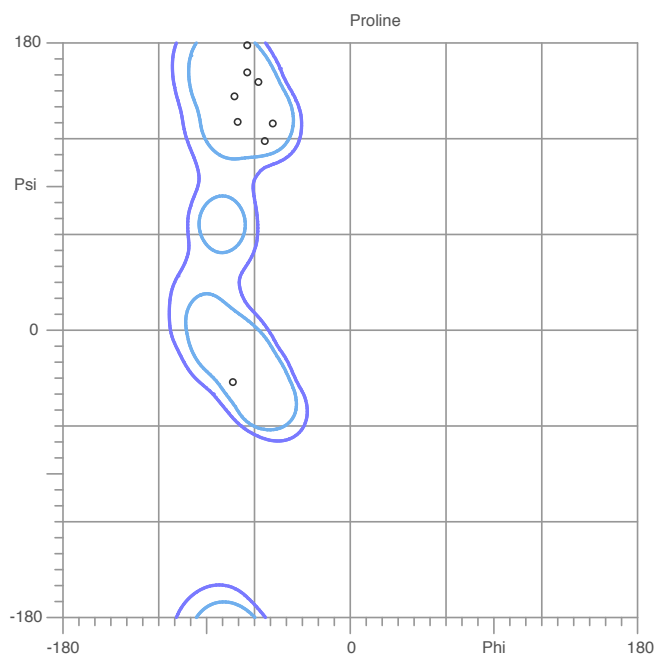
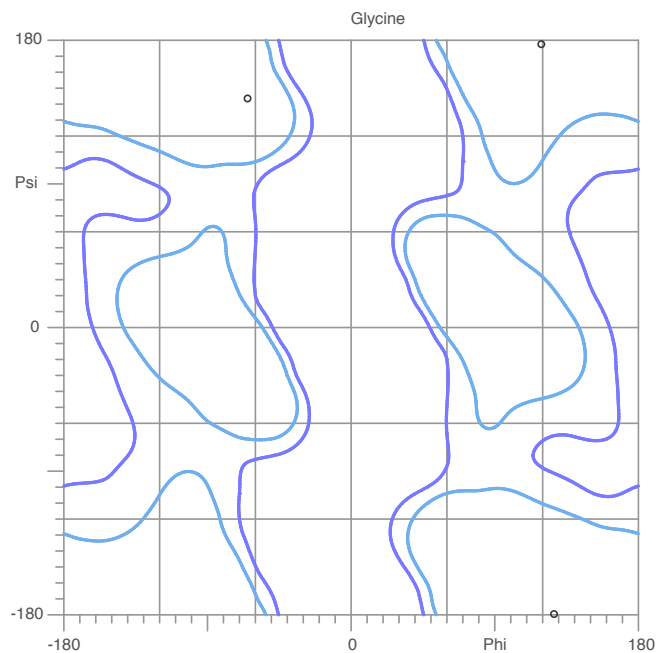
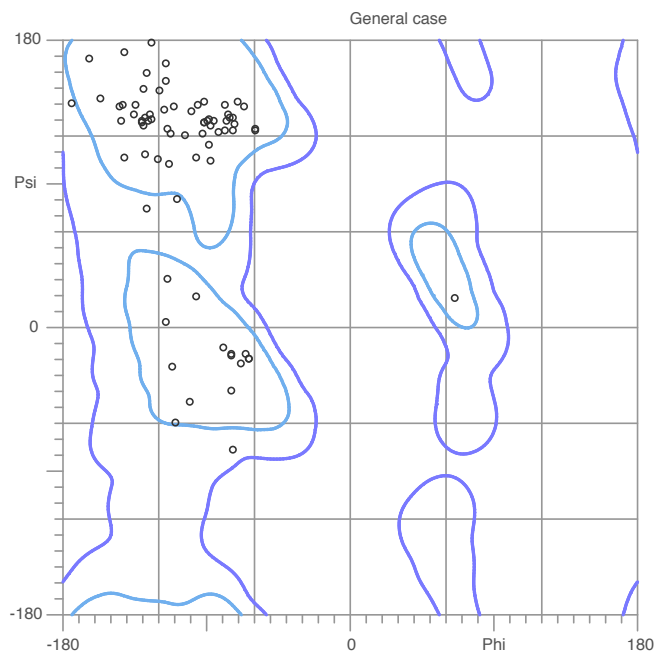
There were no outliers.

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MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 19

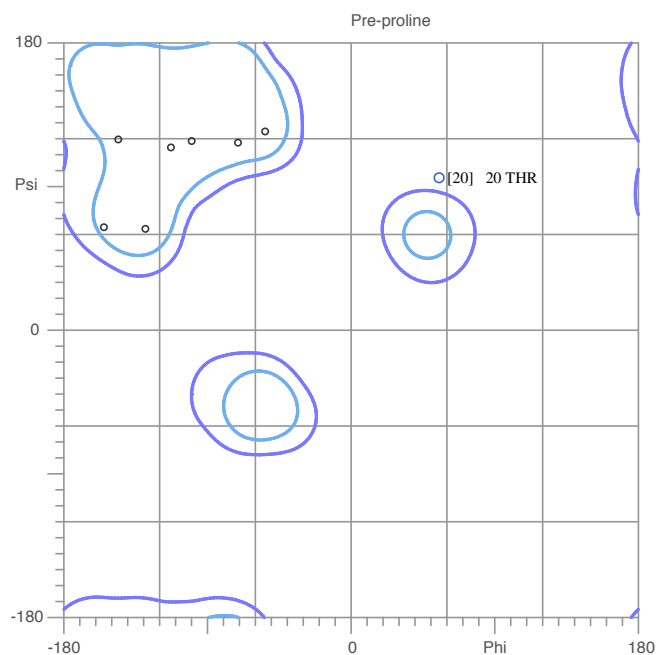
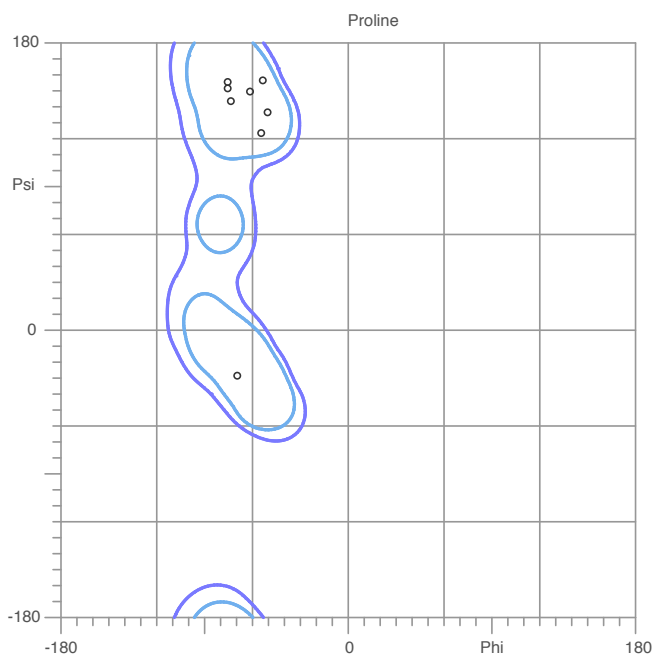
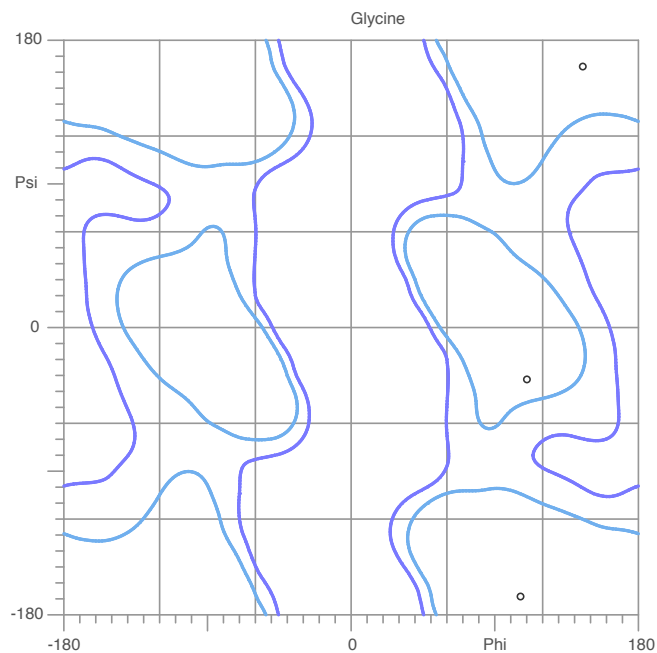
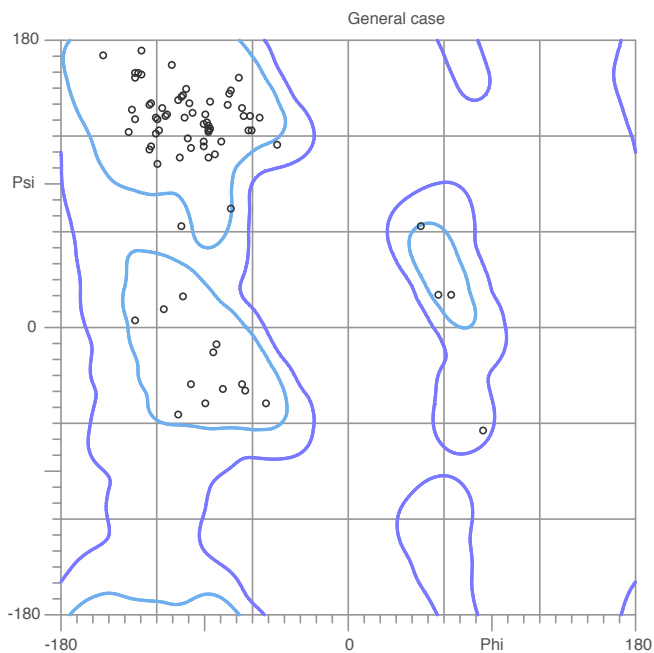


95.7% (90/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

DHR29B_R3_em_bcr3.pdb, model 20



94.7% (89/94) of all residues were in favored (98%) regions.
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 20 THR (55.2, 96.9)

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