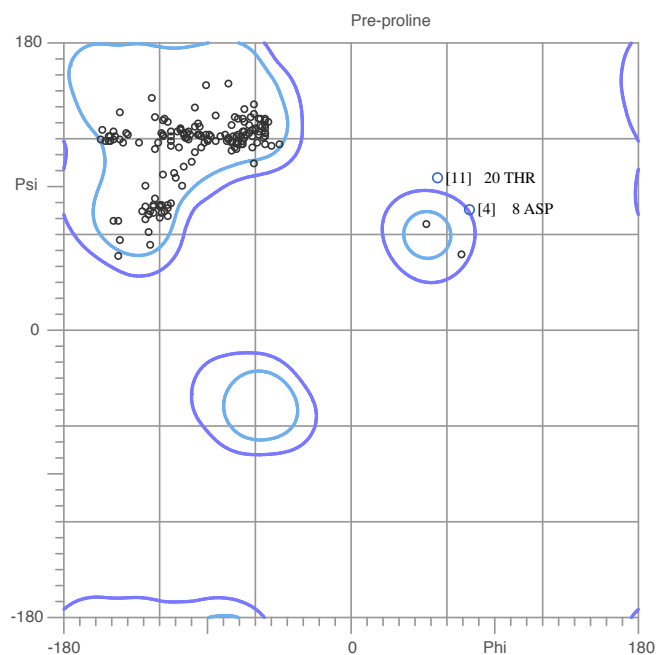
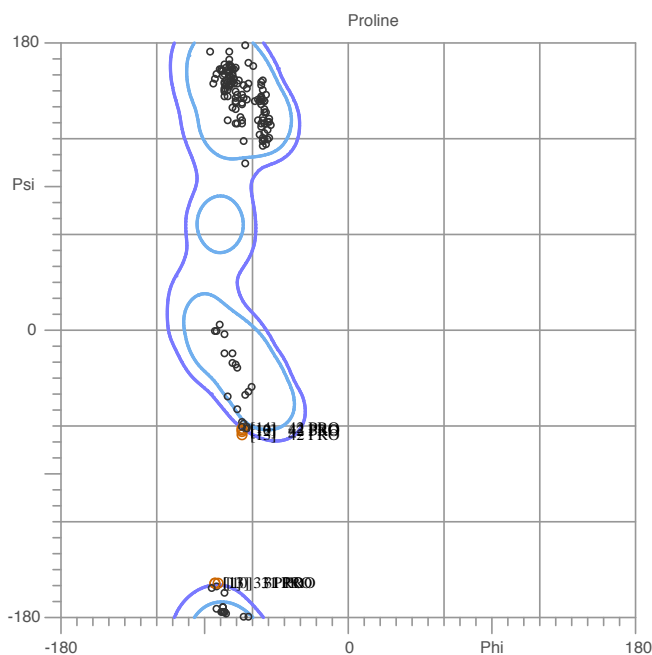
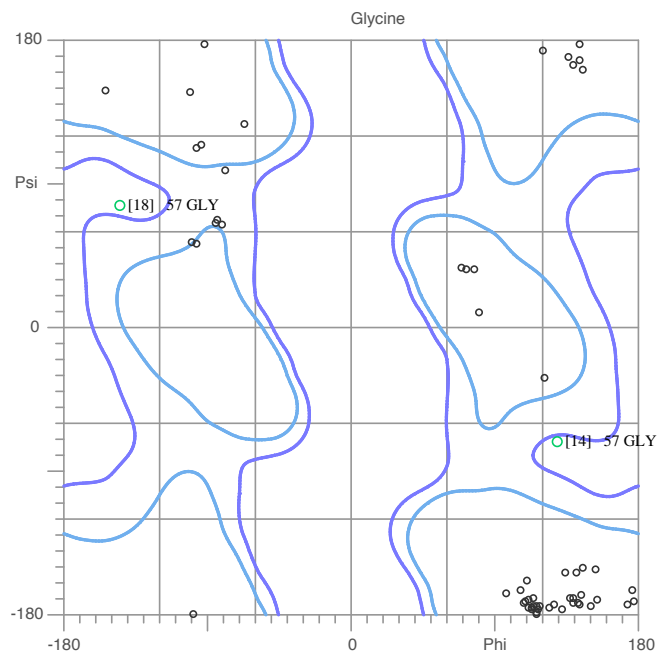
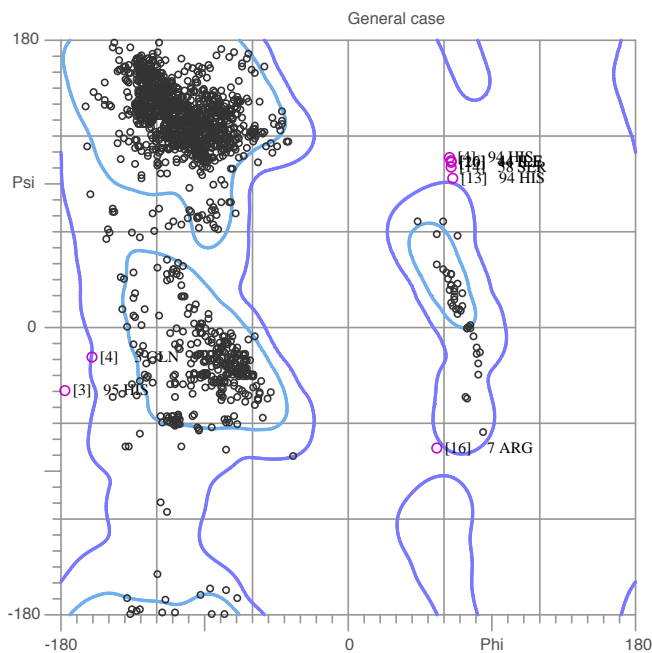


MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, all models



94.5% (1777/1880) of all residues were in favored (98%) regions.
99.0% (1861/1880) of all residues were in allowed (>99.8%) regions.

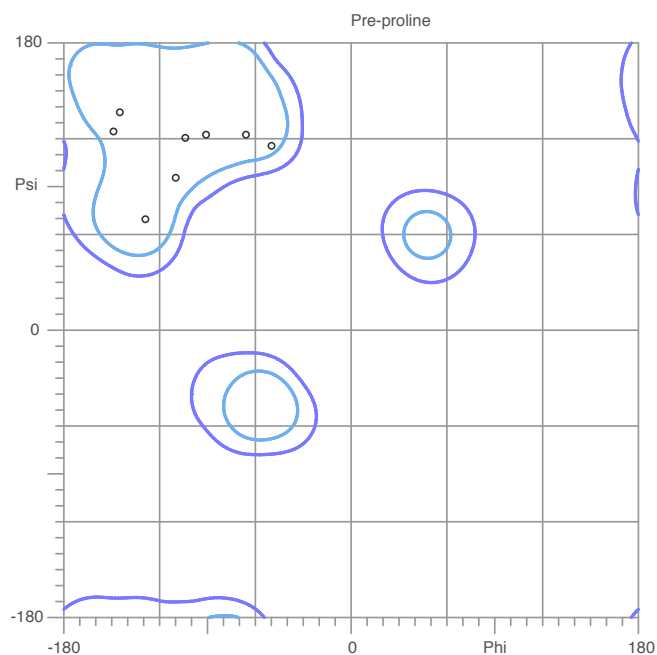
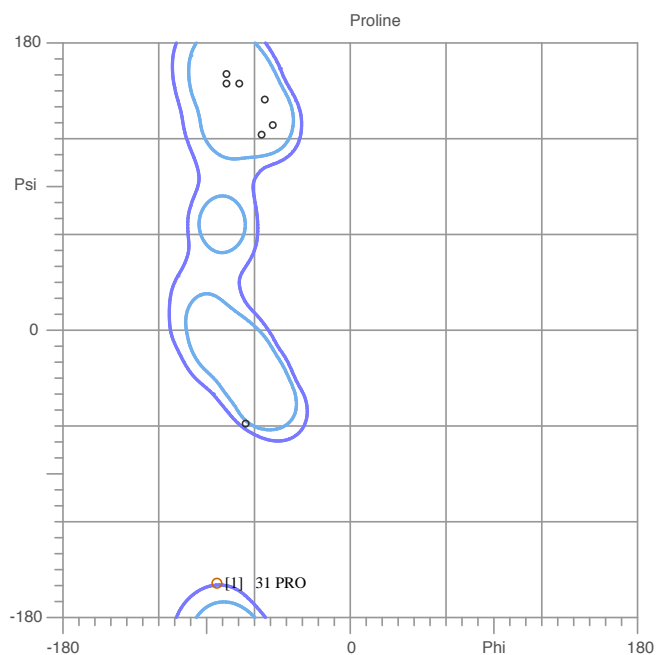
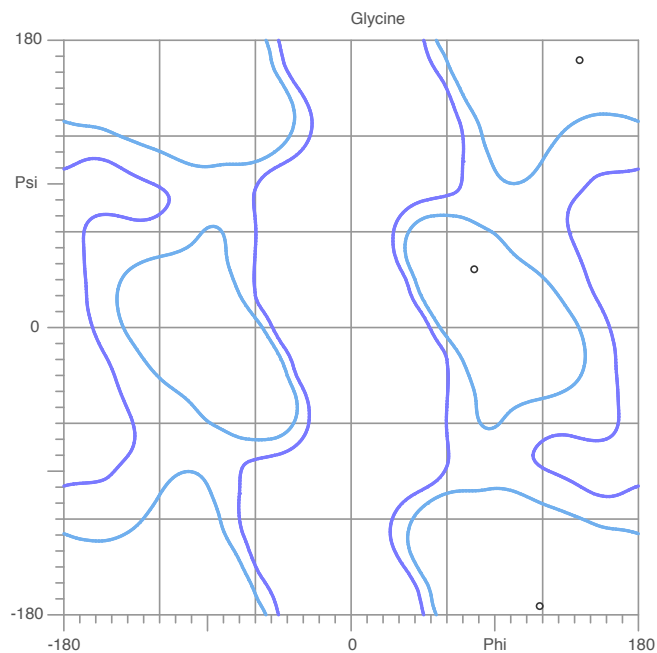
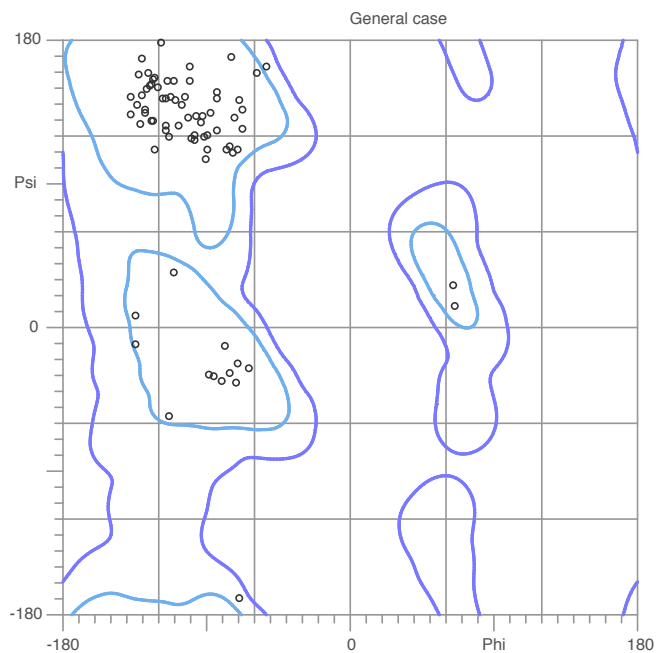
There were 19 outliers (phi, psi):

- [1] 31 PRO (-85.0, -158.1)
- [3] 95 HIS (-178.8, -39.0)
- [4] 3 GLN (-161.8, -18.6)
- [4] 8 ASP (74.7, 76.6)
- [4] 94 HIS (64.0, 107.3)
- [10] 31 PRO (-82.1, -158.4)
- [10] 42 PRO (-67.1, -62.8)

- [11] 20 THR (54.9, 96.9)
- [12] 42 PRO (-67.9, -63.2)
- [13] 31 PRO (-84.8, -158.0)
- [13] 42 PRO (-67.6, -65.9)
- [13] 94 HIS (65.1, 94.8)
- [14] 42 PRO (-67.9, -61.5)
- [14] 57 GLY (129.8, -71.3)
- [14] 58 SER (64.5, 101.1)
- [16] 7 ARG (55.3, -75.3)
- [16] 44 ILE (64.8, 105.0)
- [18] 57 GLY (-145.1, 78.0)
- [20] 44 ILE (64.5, 104.6)

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 1



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.

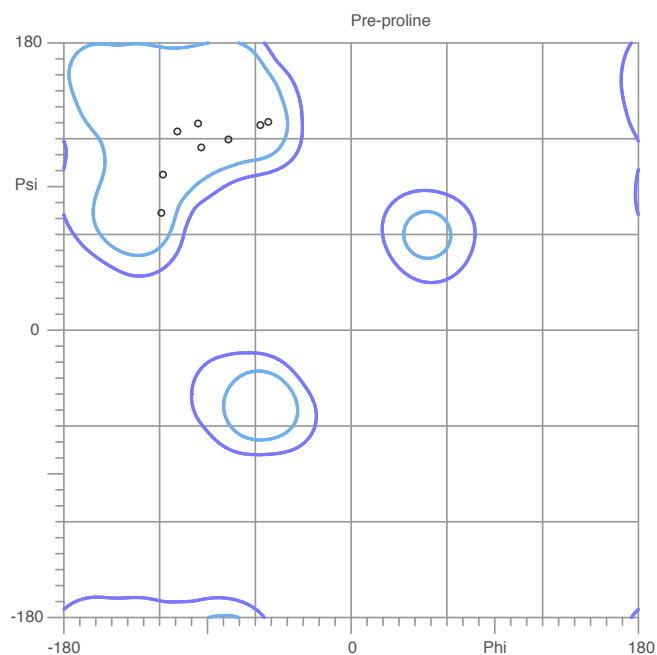
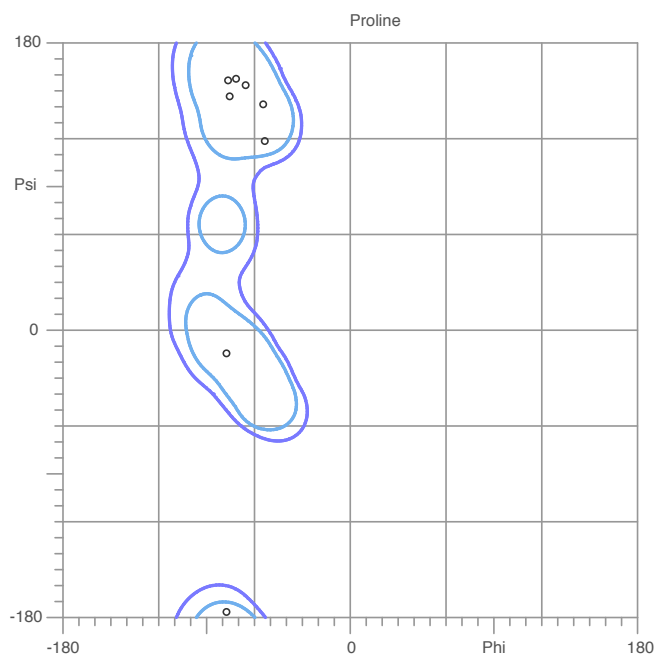
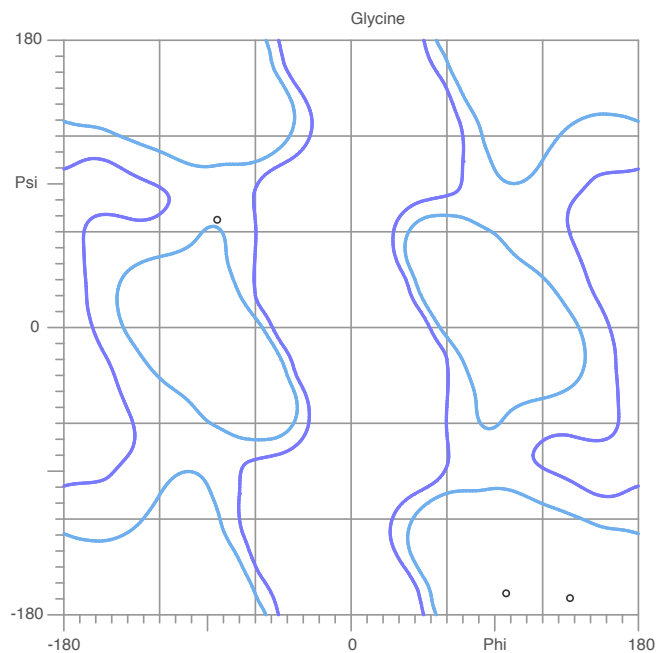
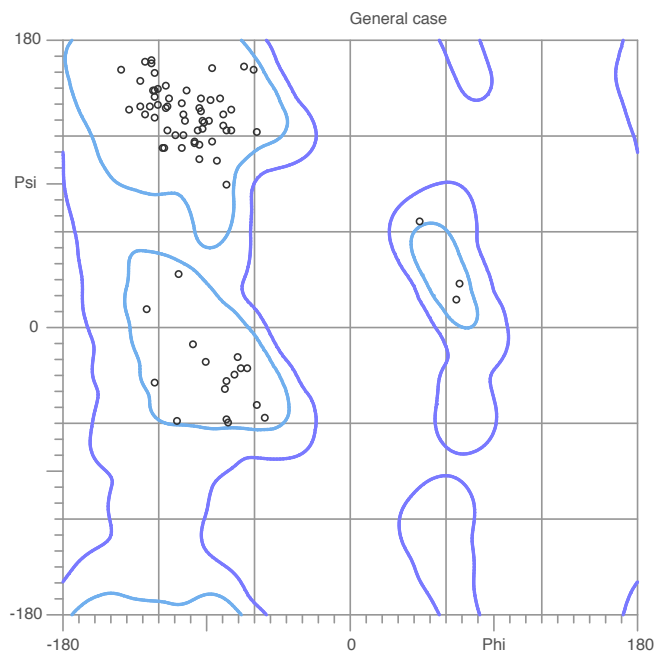
There were 1 outliers (phi, psi):
[1] 31 PRO (-85.0, -158.1)

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 2



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.

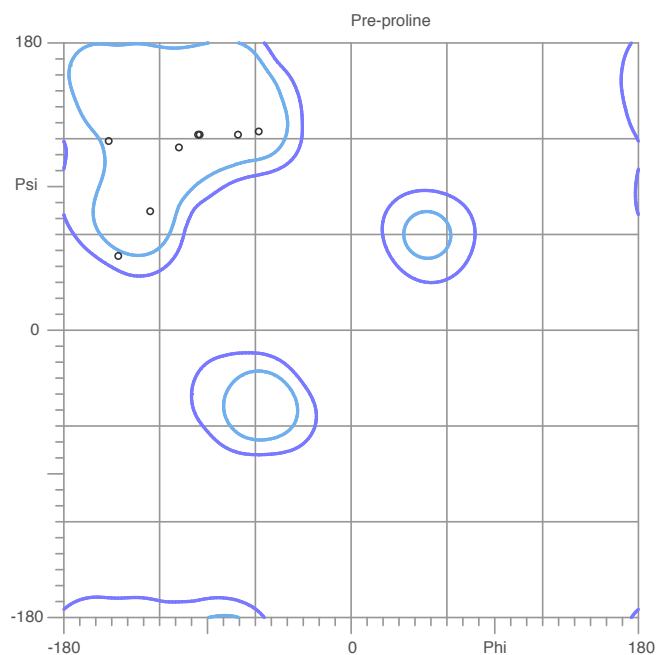
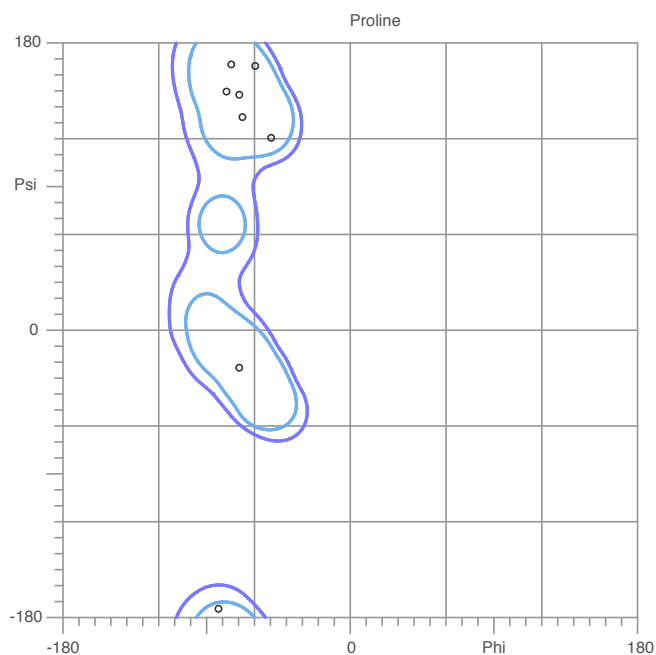
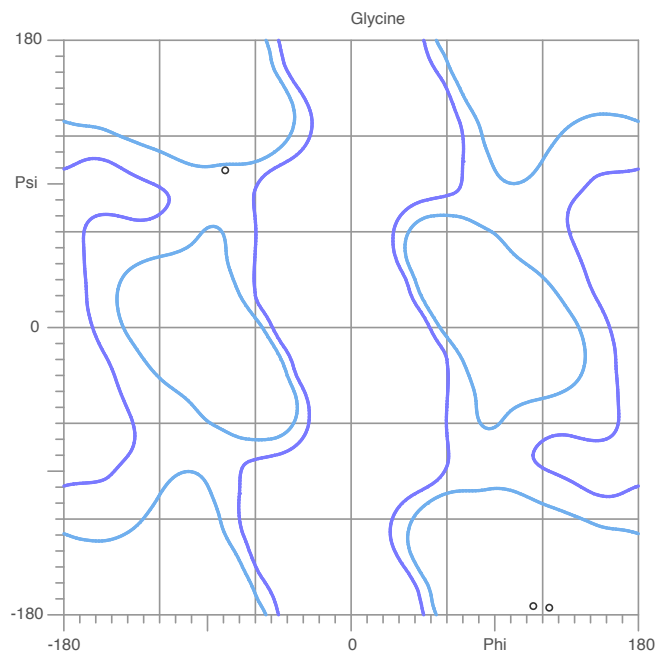
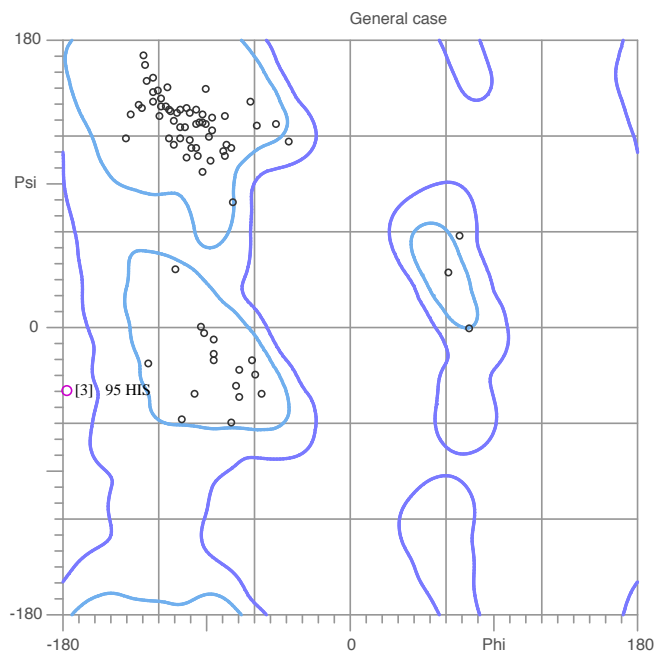
There were no outliers.

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

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 3



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.

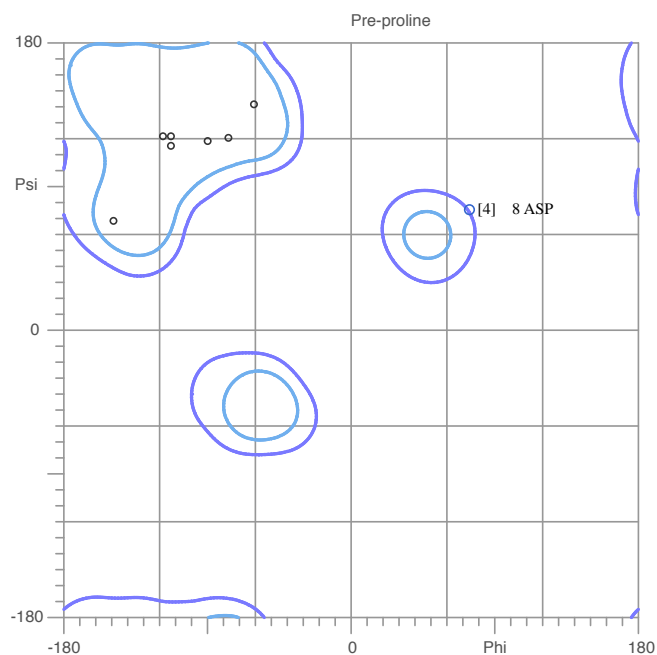
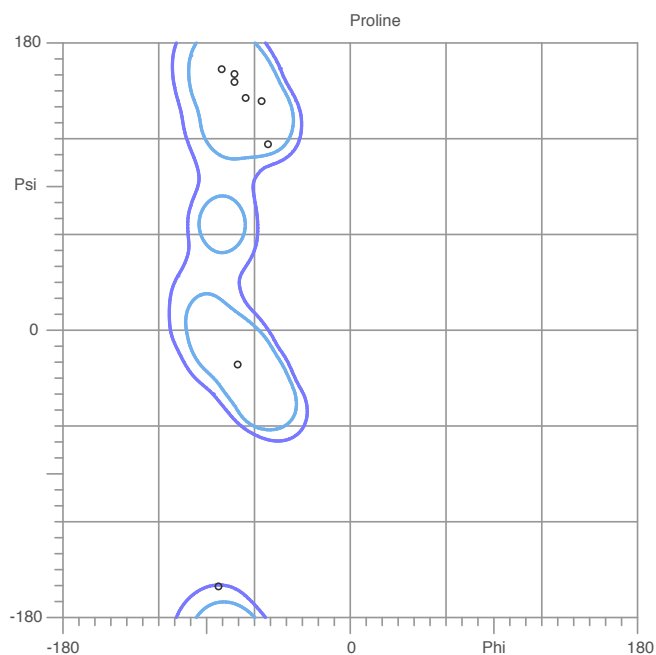
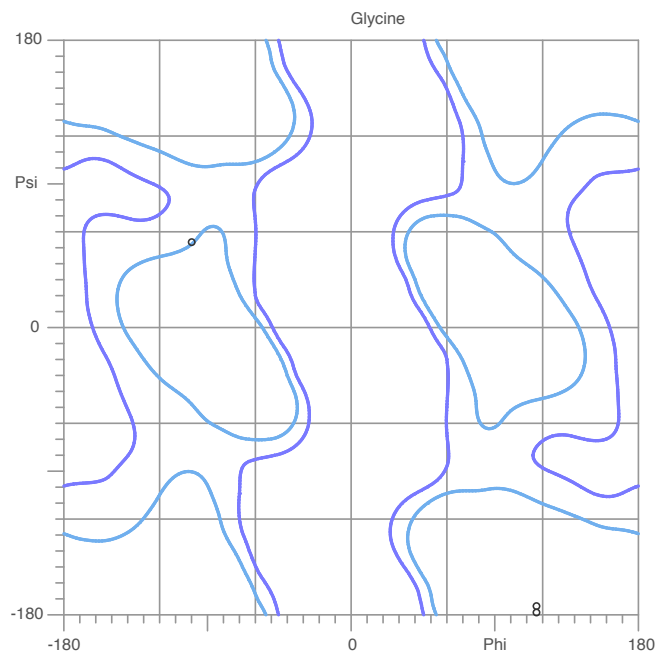
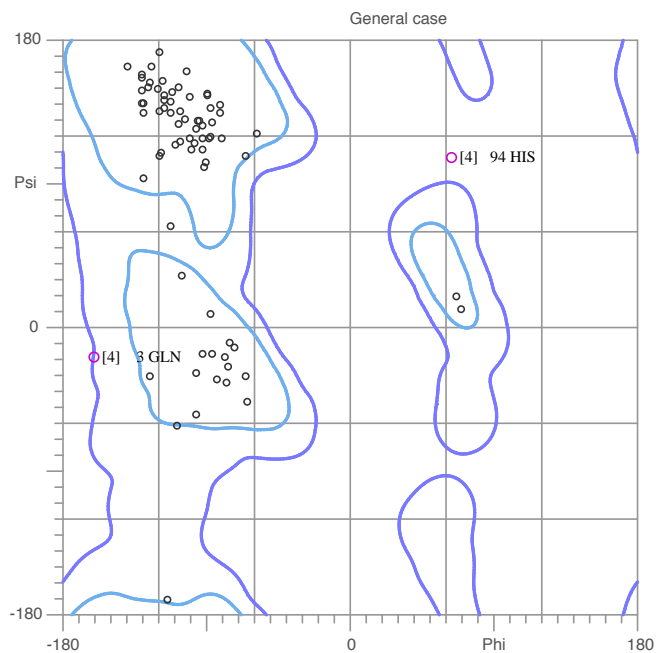
There were 1 outliers (phi, psi):
[3] 95 HIS (-178.8, -39.0)

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

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

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 4



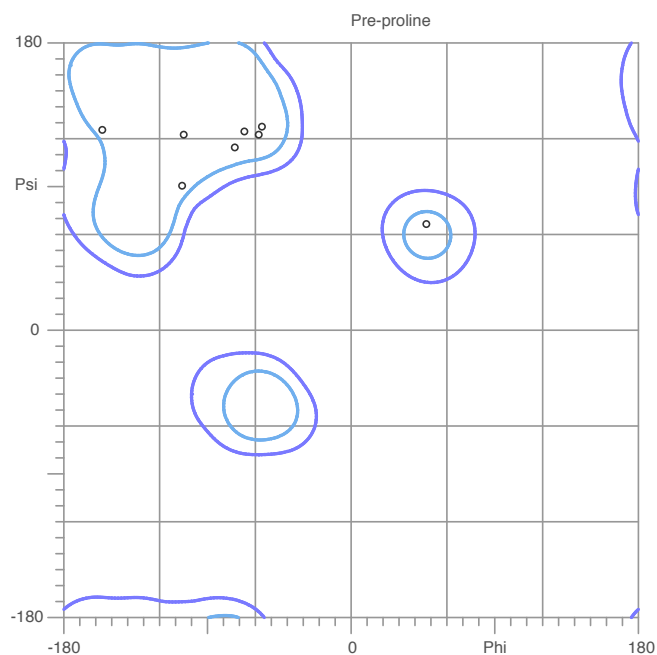
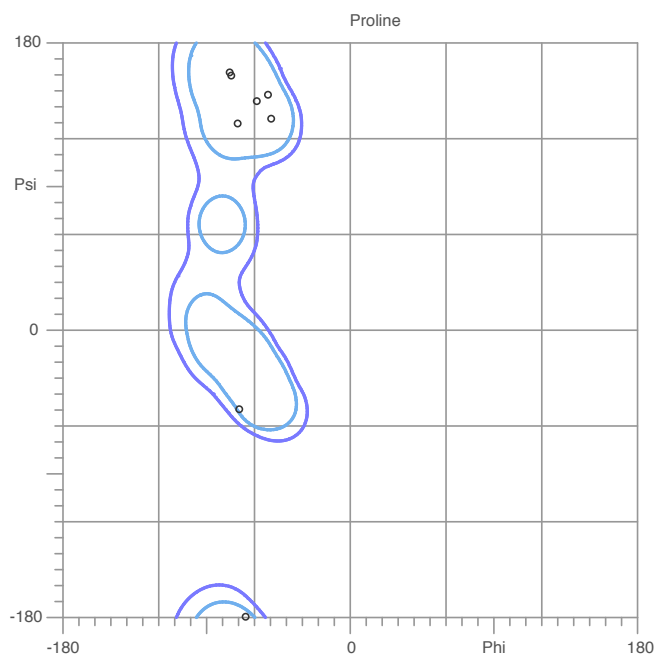
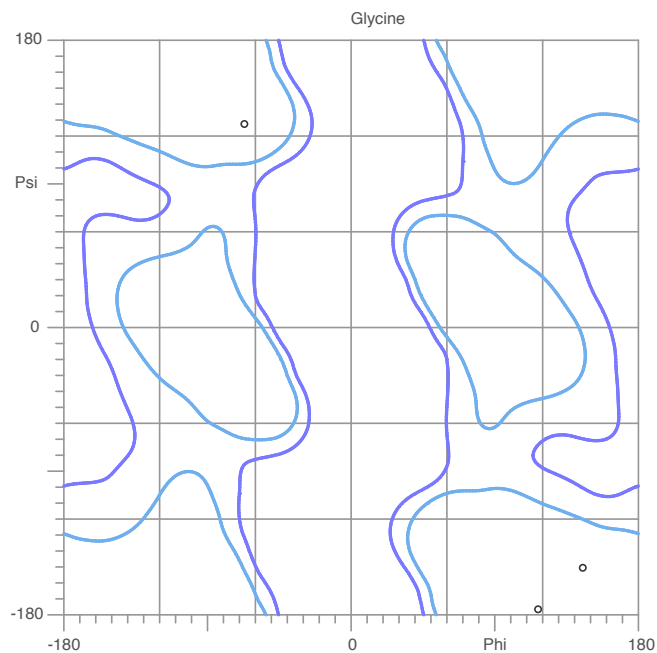
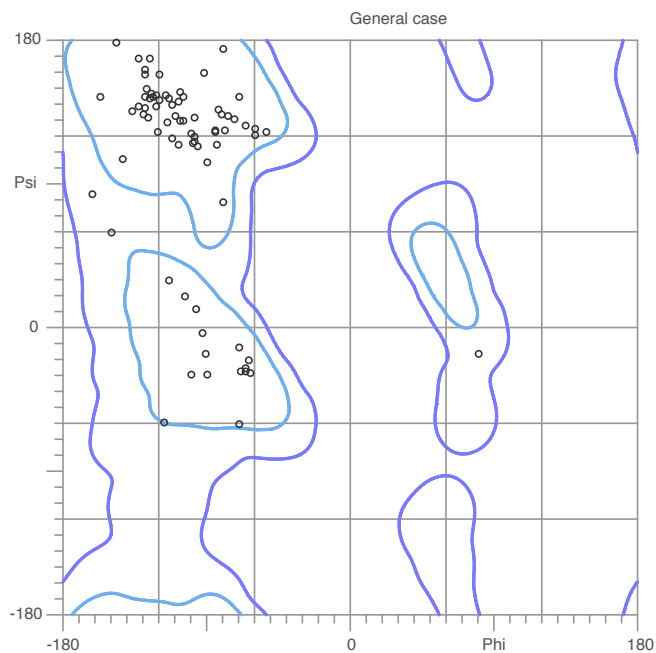
91.5% (86/94) of all residues were in favored (98%) regions.
96.8% (91/94) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [4] 3 GLN (-161.8, -18.6)
- [4] 8 ASP (74.7, 76.6)
- [4] 94 HIS (64.0, 107.3)

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 5



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.

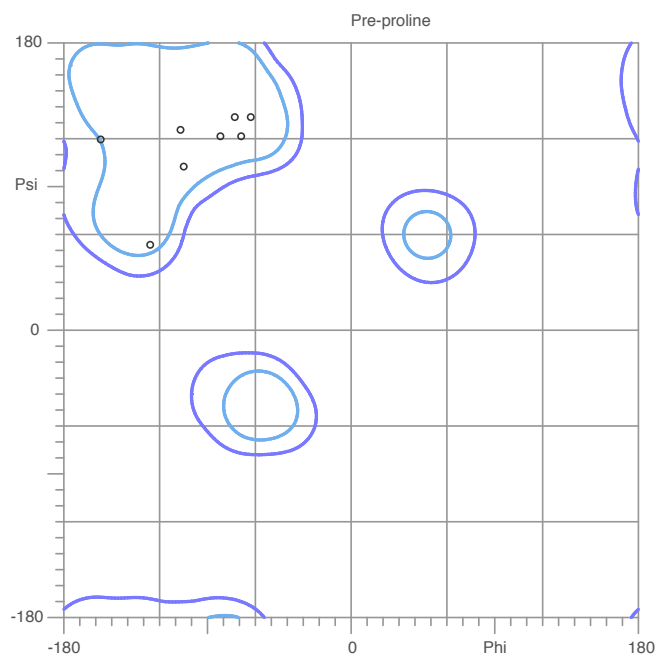
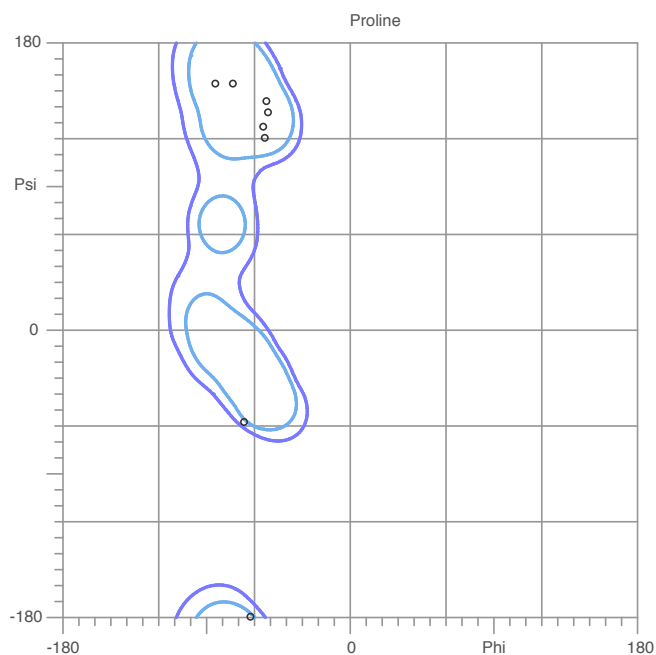
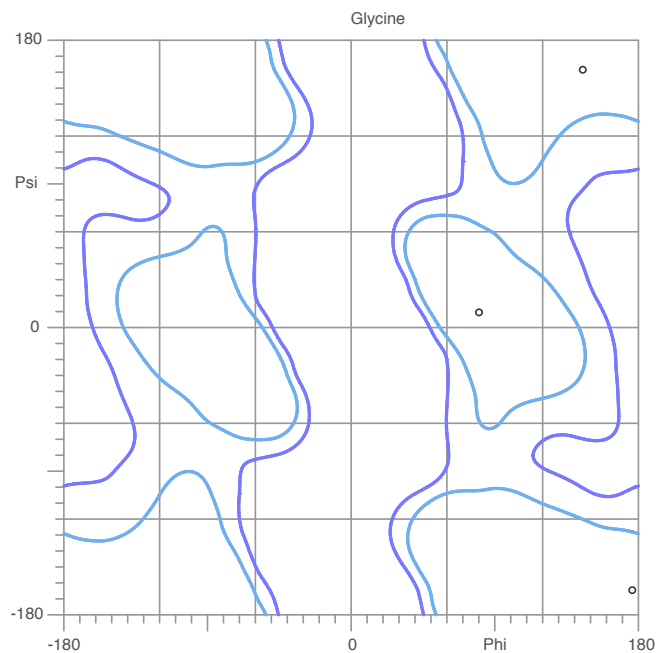
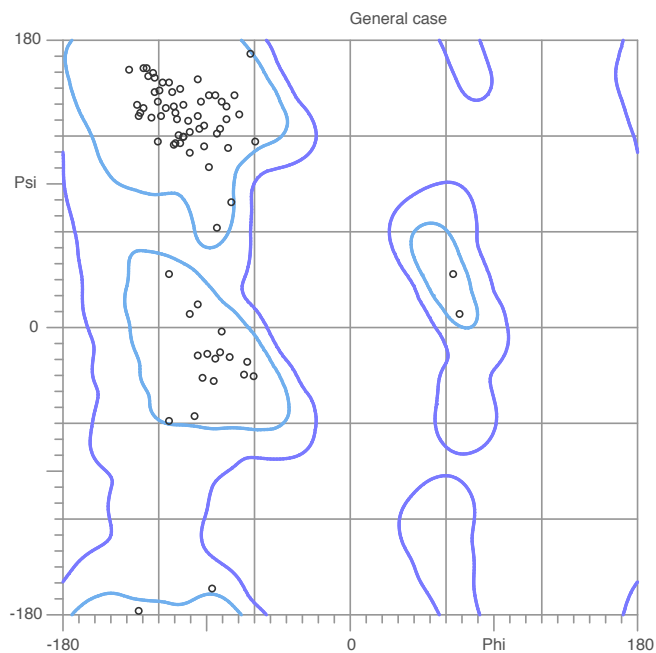
There were no outliers.

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 6



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.

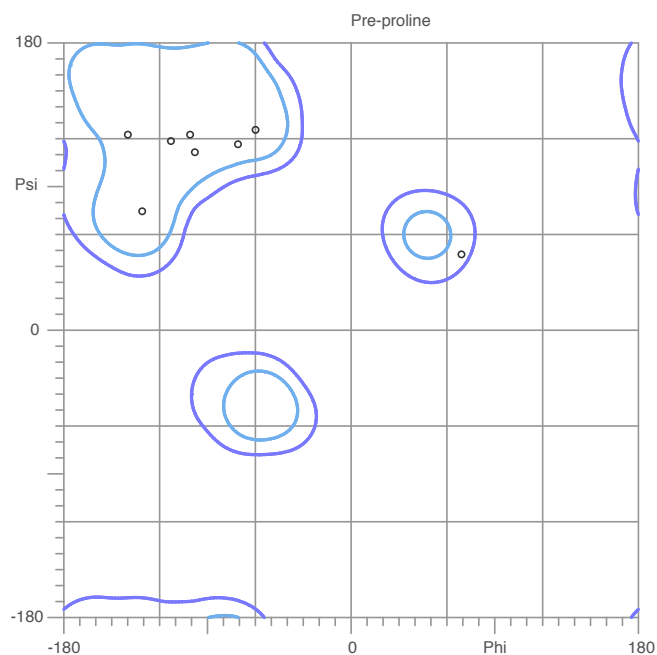
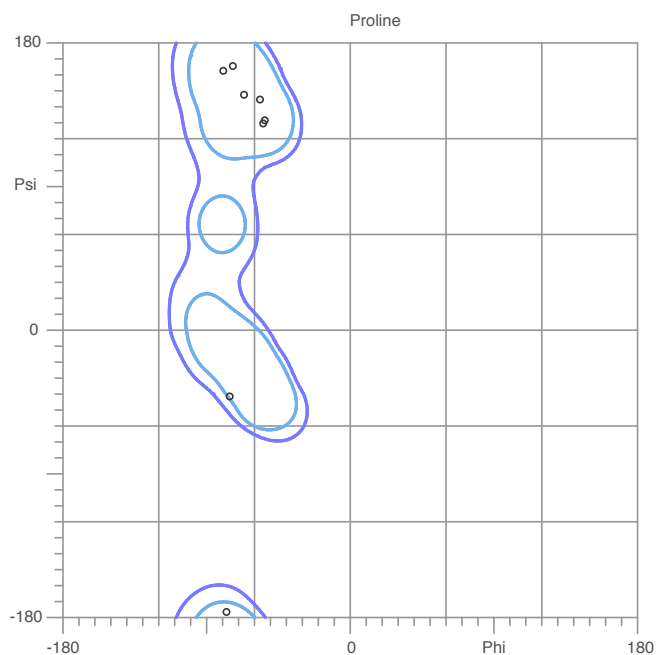
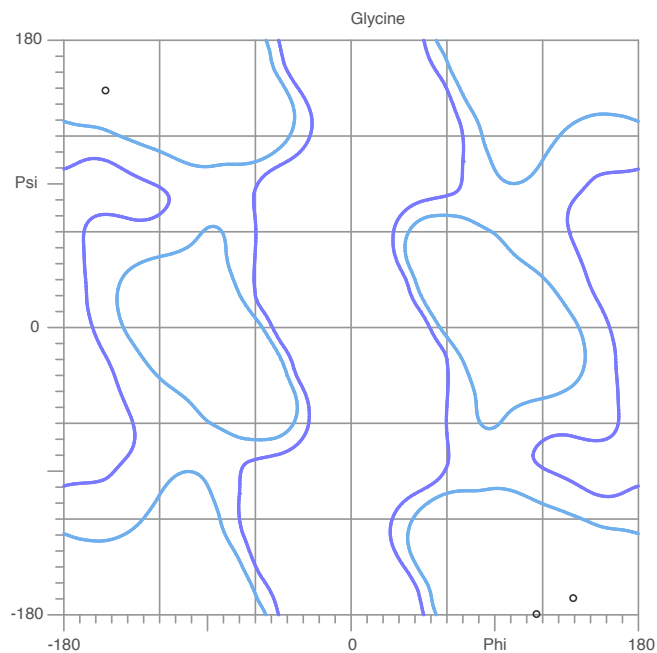
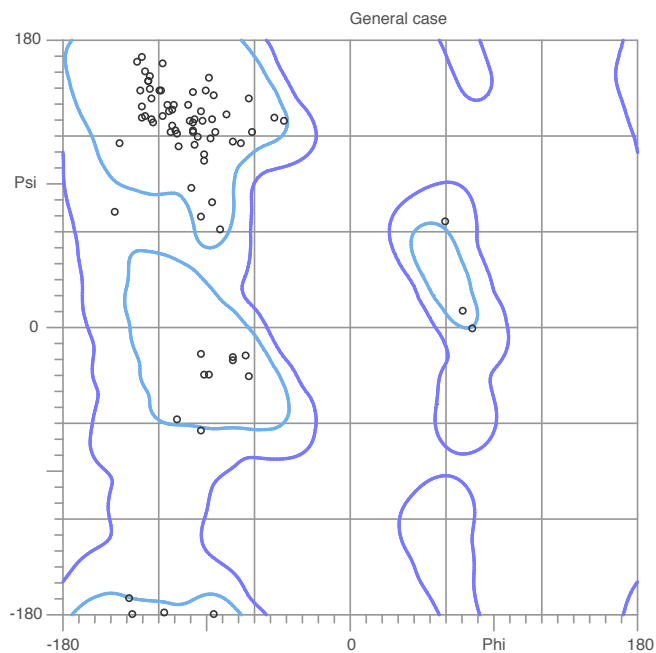
There were no outliers.

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 7



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.

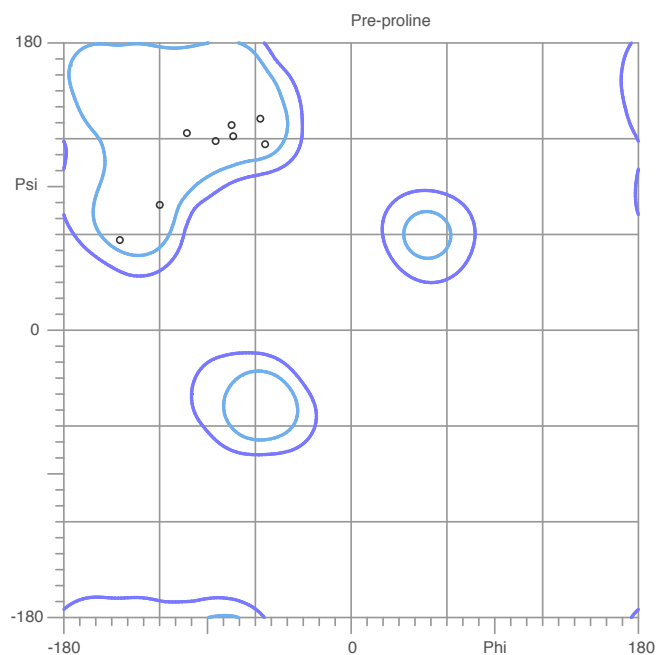
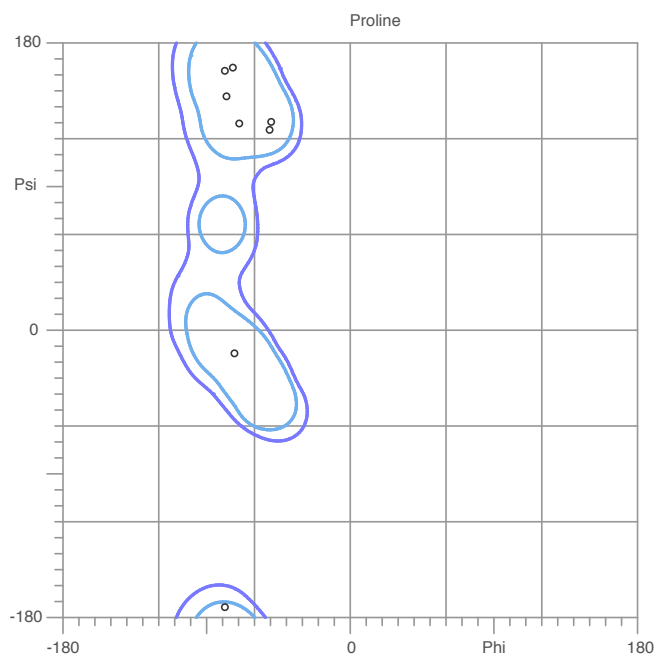
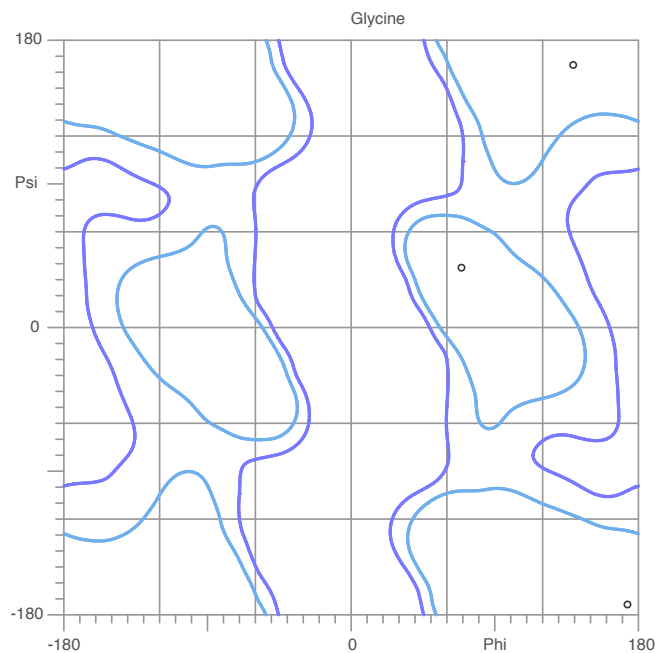
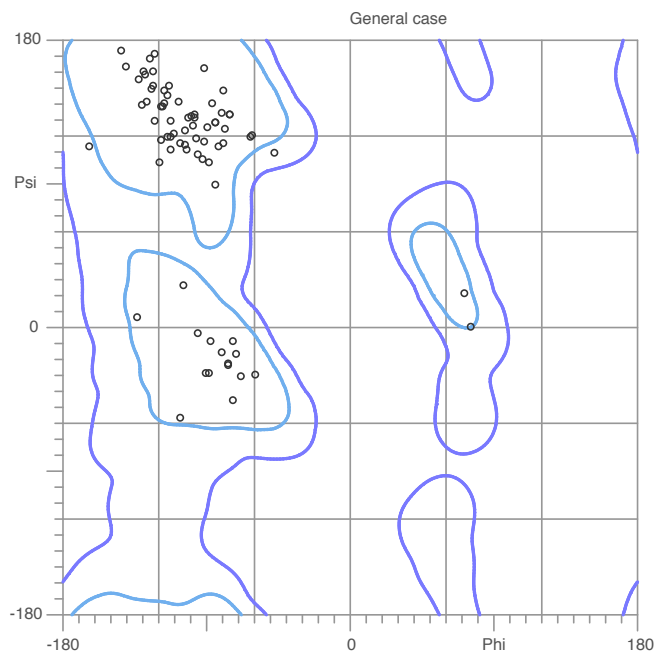
There were no outliers.

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

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 8



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.

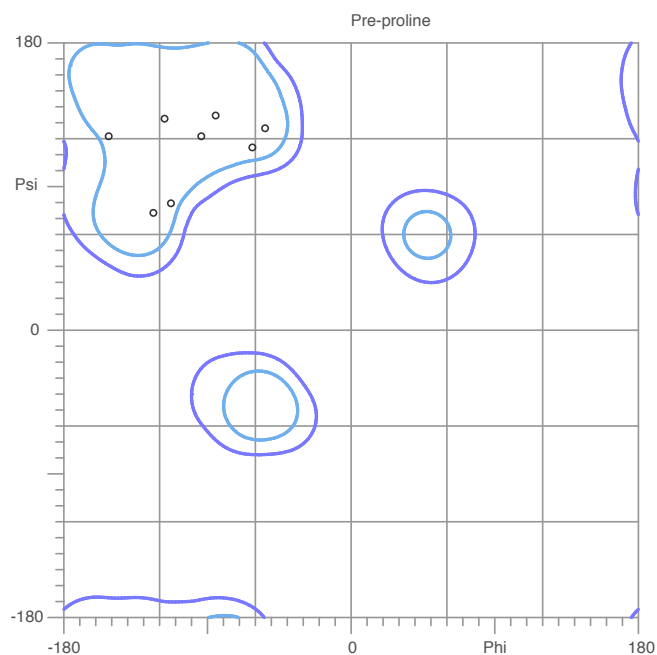
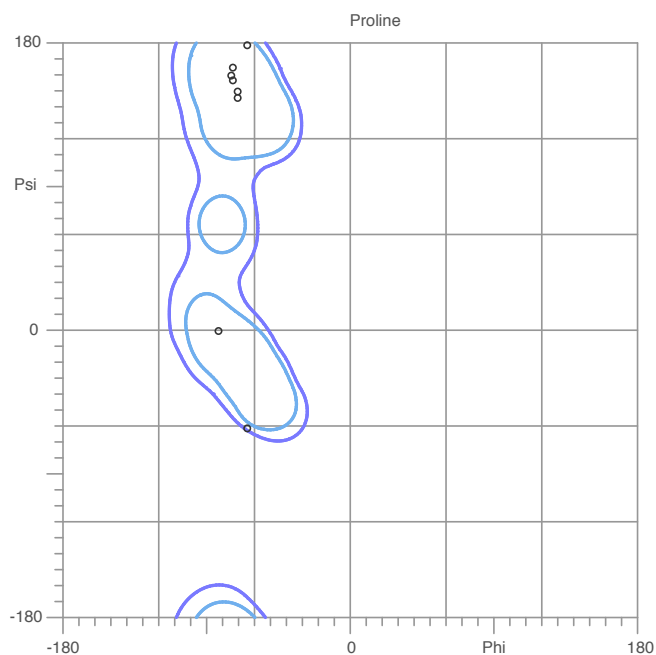
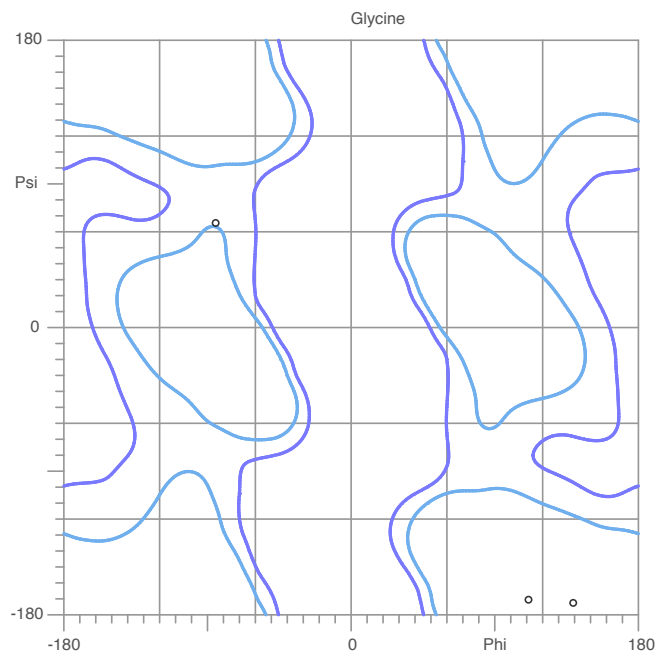
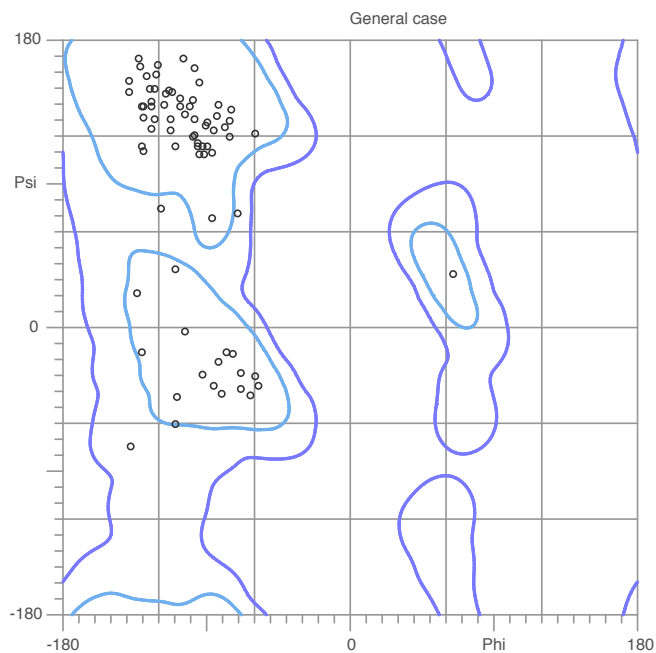
There were no outliers.

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

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 9



93.6% (88/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

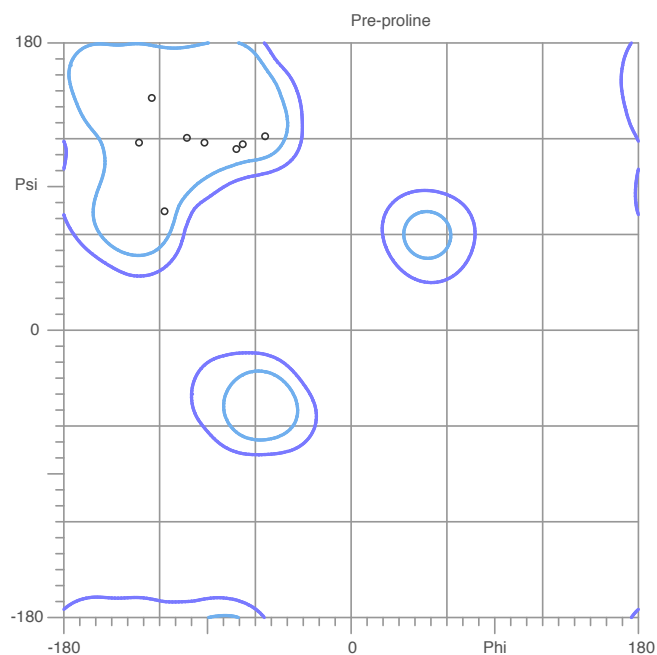
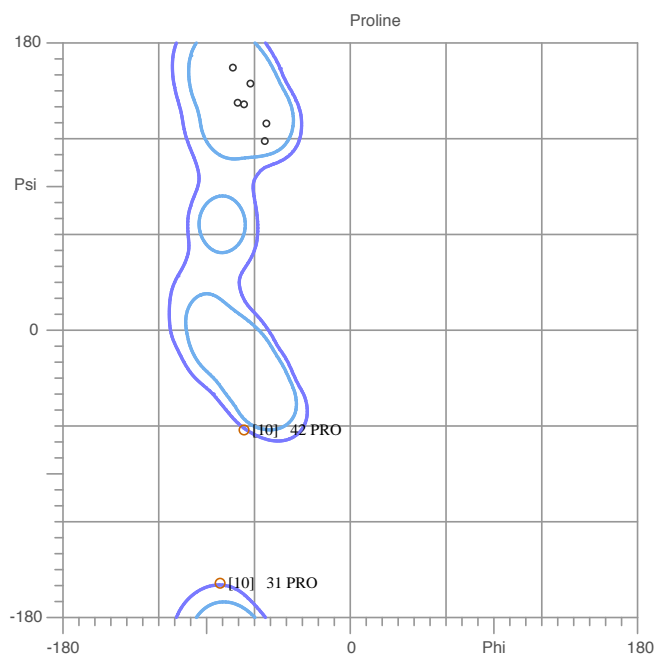
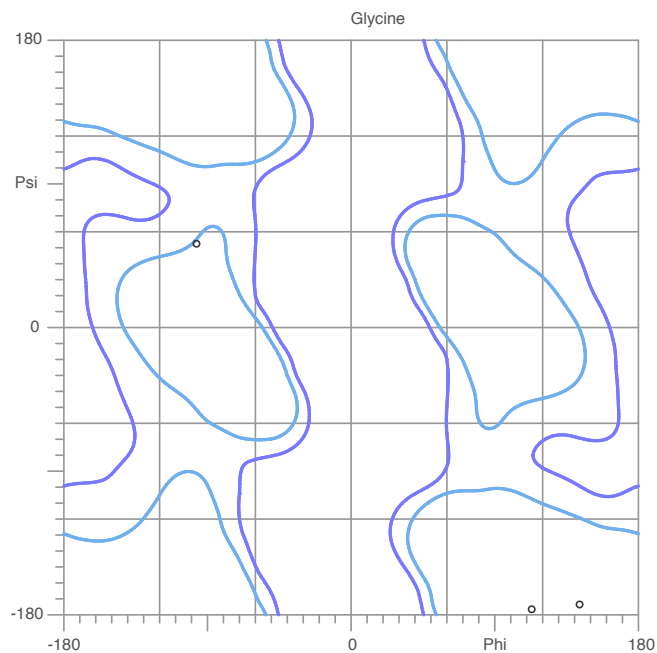
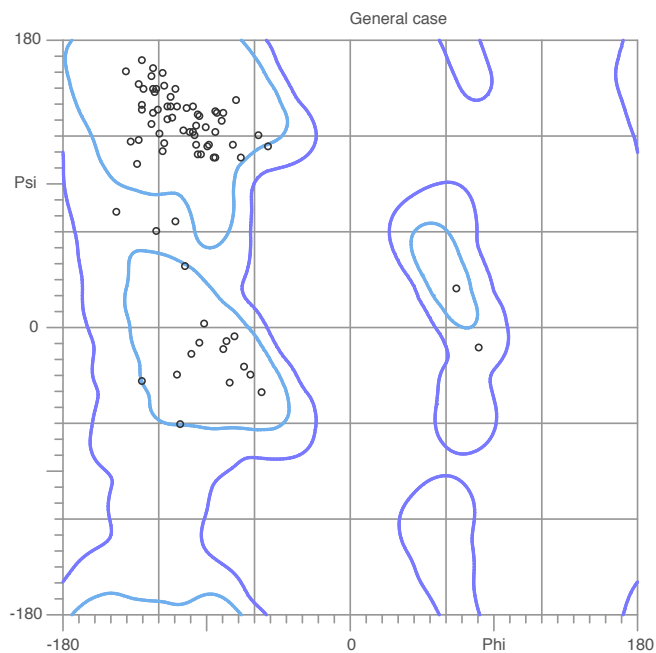
There were no outliers.

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

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

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 10

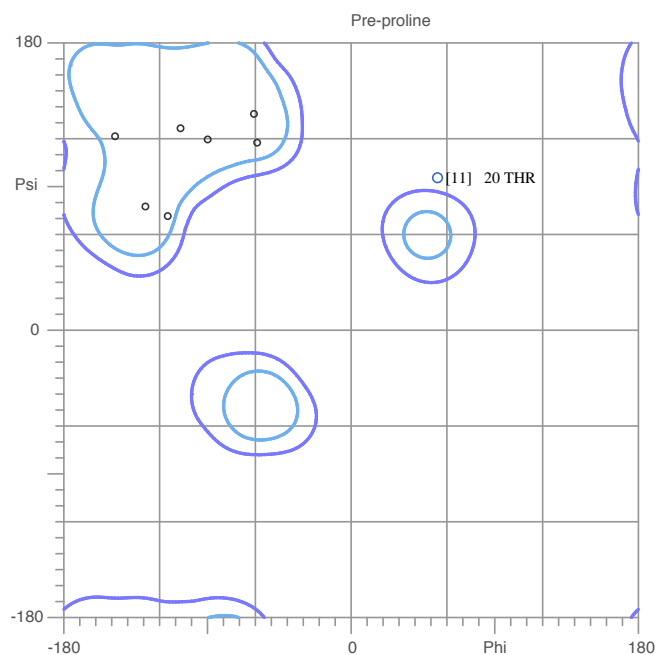
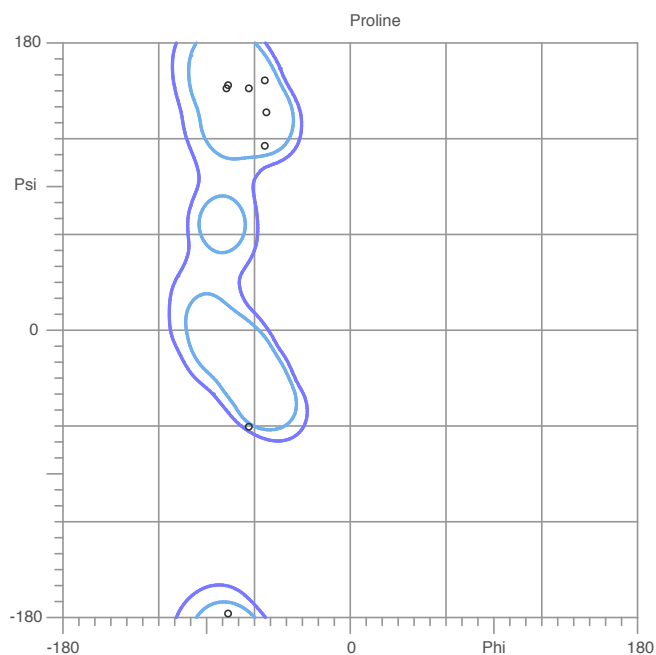
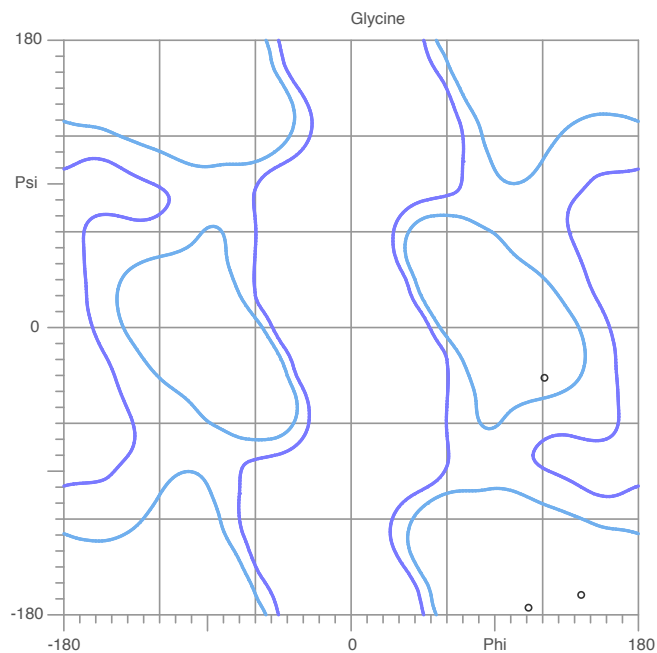
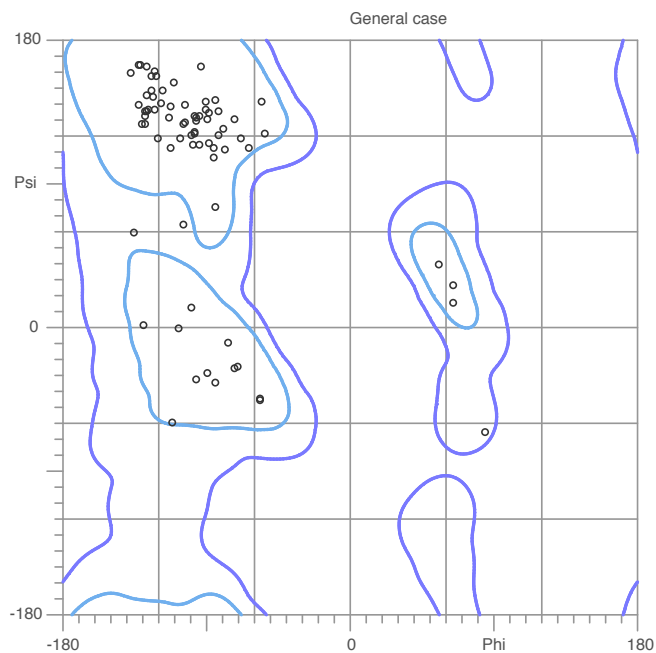


92.6% (87/94) of all residues were in favored (98%) regions.
97.9% (92/94) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[10] 31 PRO (-82.1, -158.4)
[10] 42 PRO (-67.1, -62.8)

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 11



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.

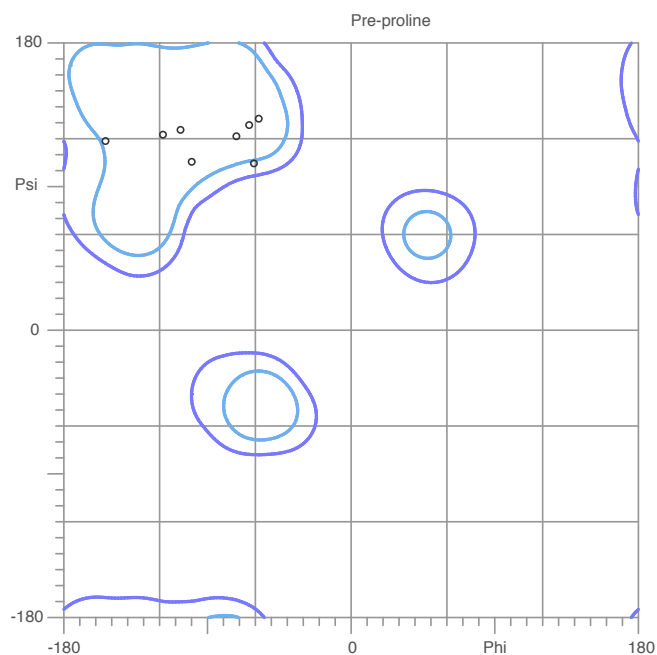
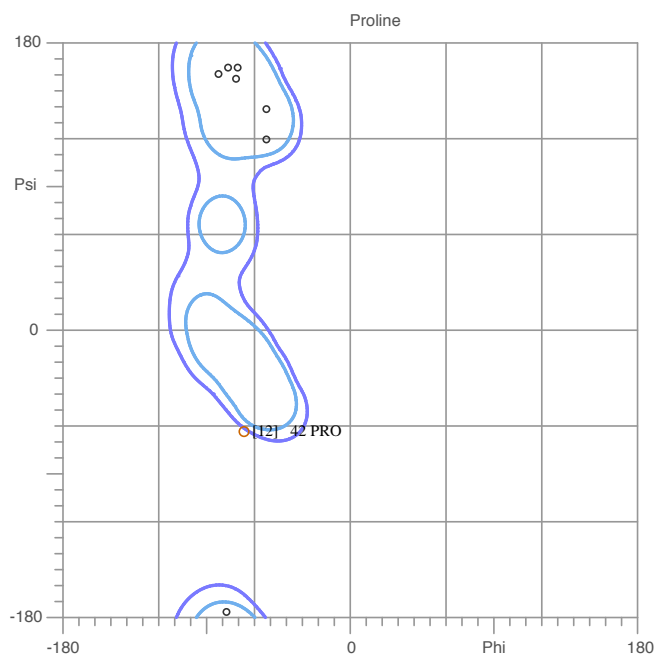
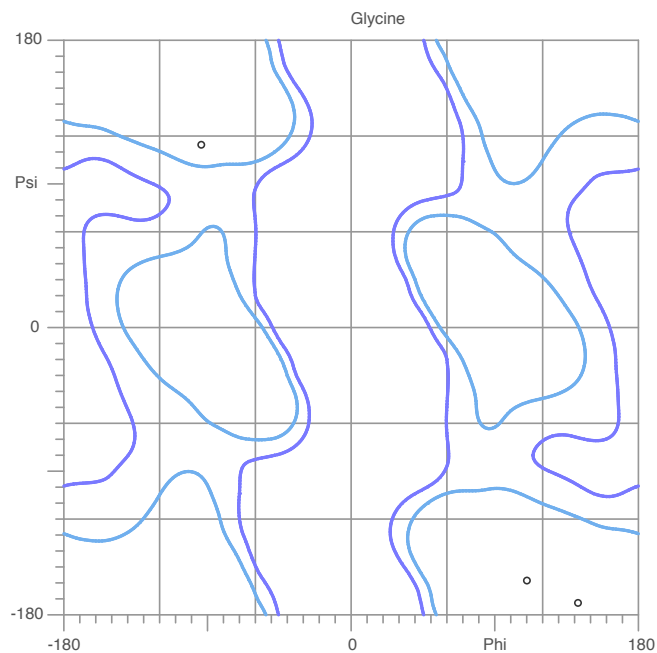
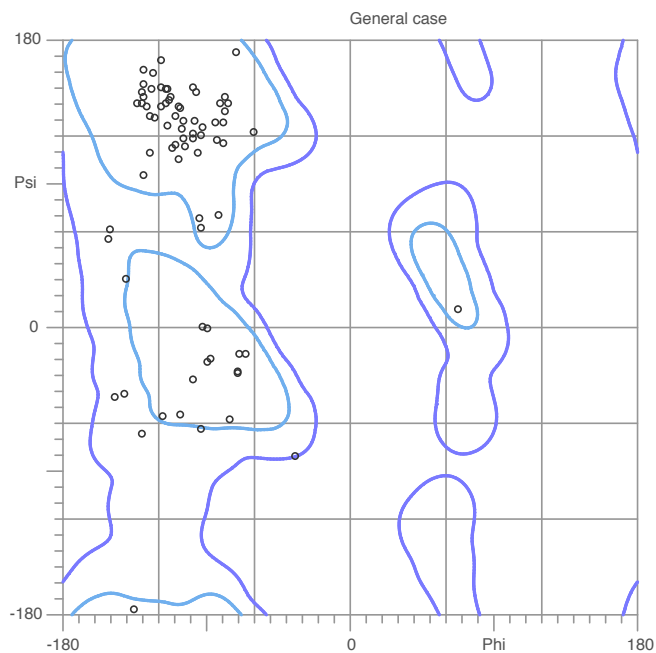
There were 1 outliers (phi, psi):
[11] 20 THR (54.9, 96.9)

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 12

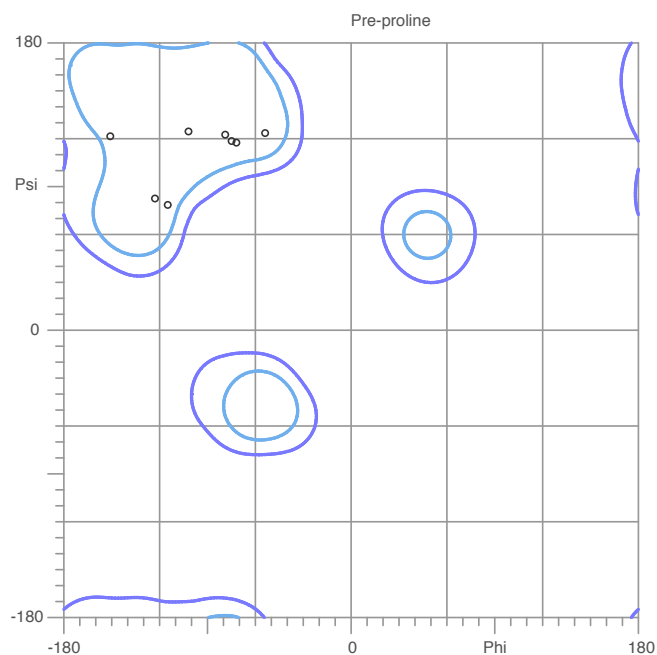
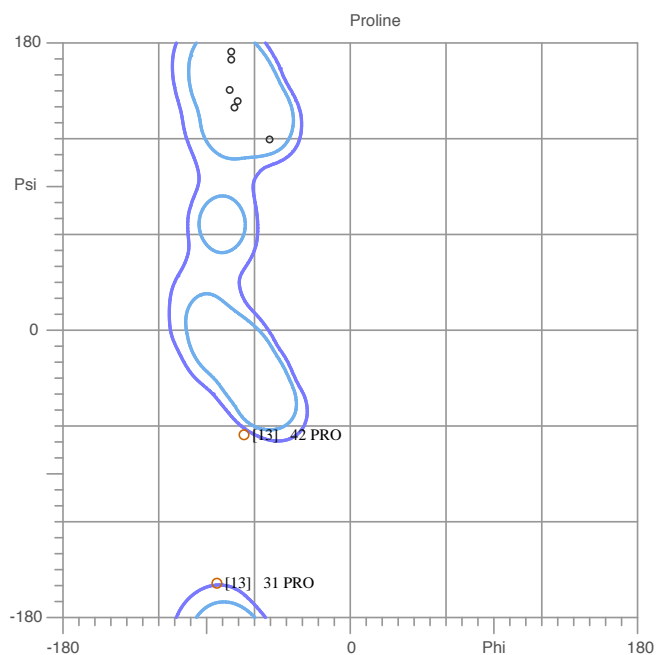
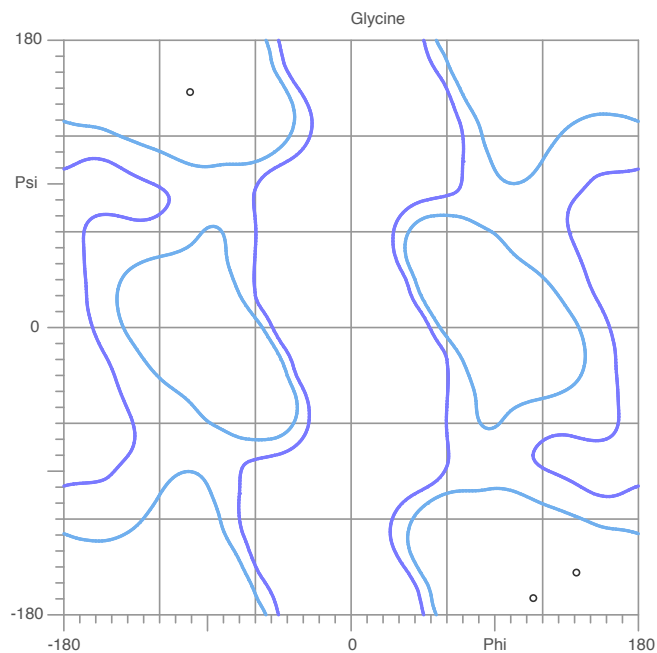
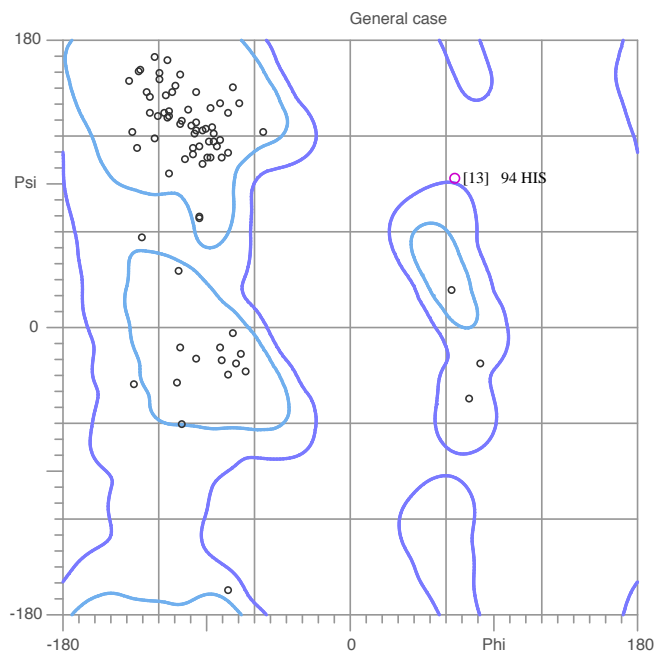


89.4% (84/94) of all residues were in favored (98%) regions.
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[12] 42 PRO (-67.9, -63.2)

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 13



91.5% (86/94) of all residues were in favored (98%) regions.
96.8% (91/94) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

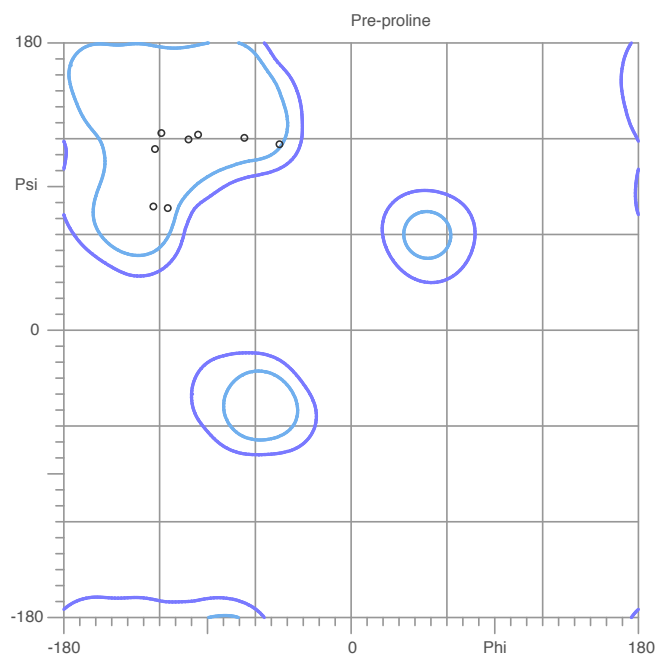
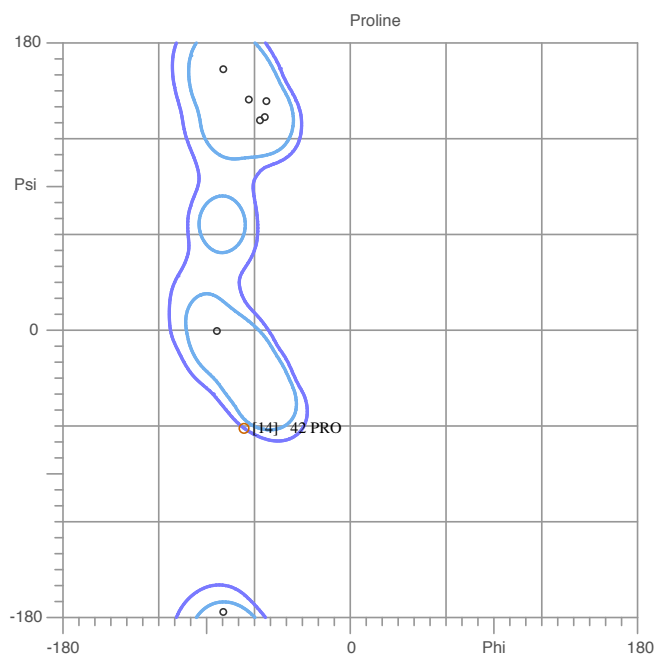
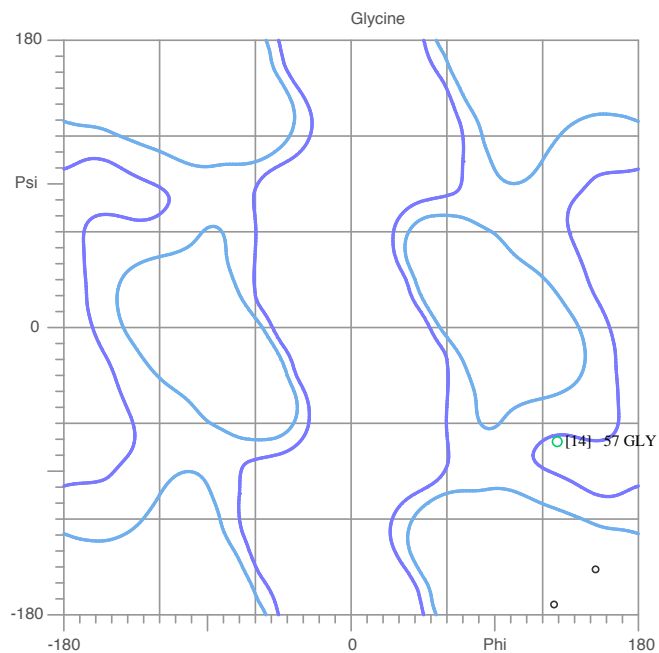
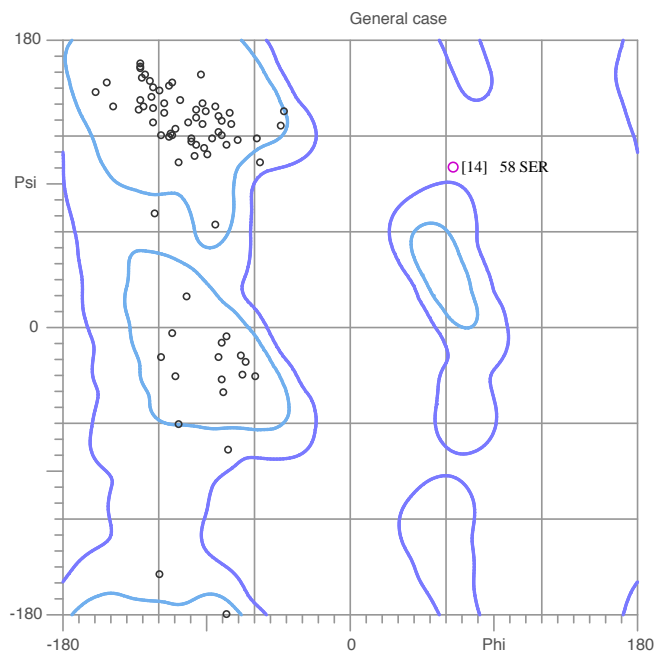
[13] 31 PRO (-84.8, -158.0)

[13] 42 PRO (-67.6, -65.9)

[13] 94 HIS (65.1, 94.8)

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 14



92.6% (87/94) of all residues were in favored (98%) regions.
96.8% (91/94) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

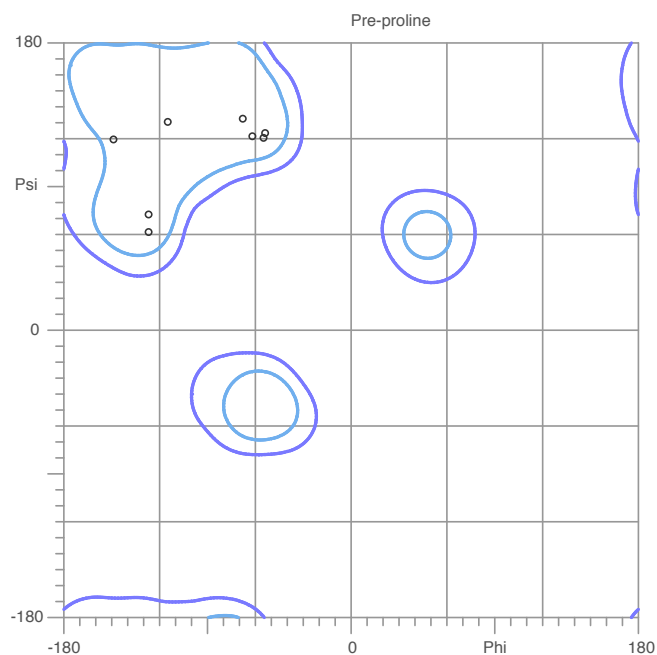
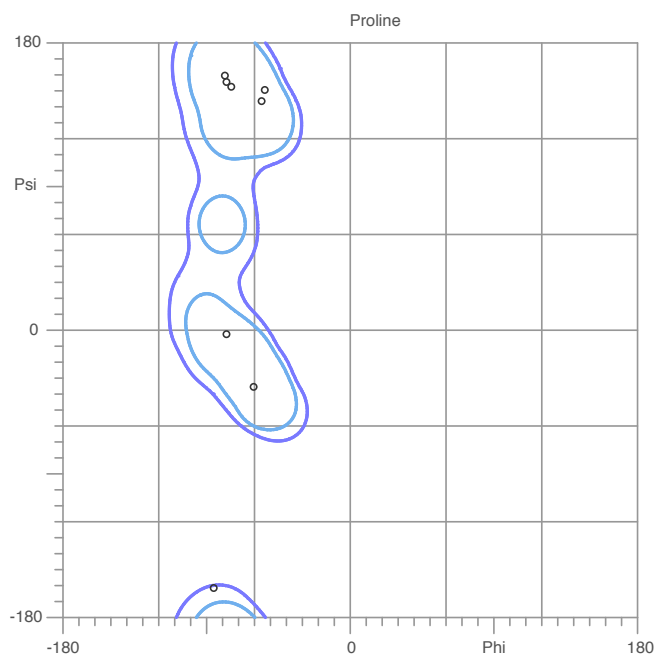
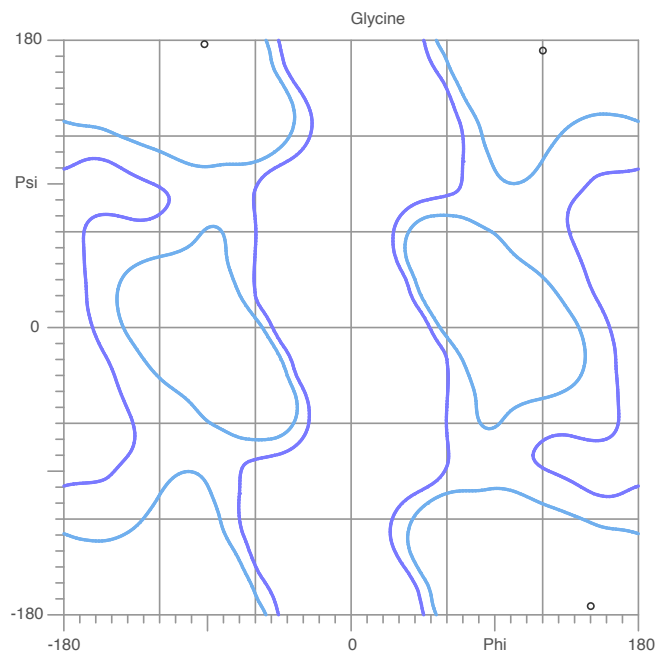
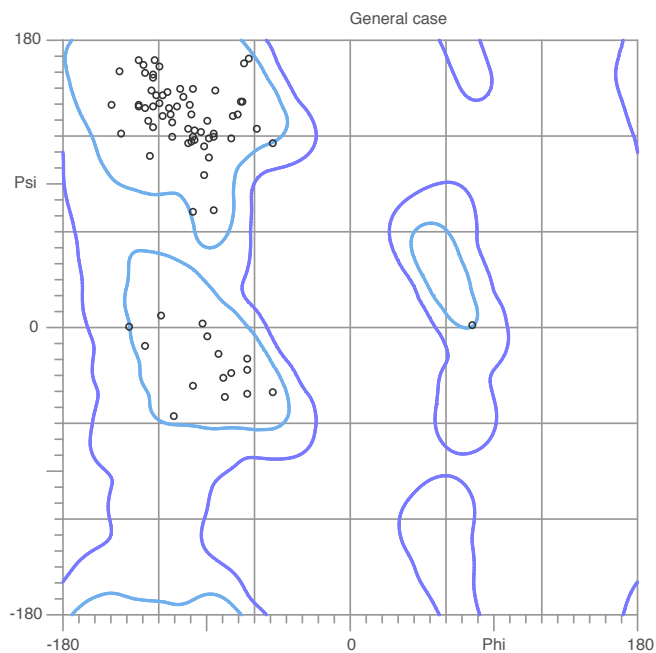
[14] 42 PRO (-67.9, -61.5)

[14] 57 GLY (129.8, -71.3)

[14] 58 SER (64.5, 101.1)

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 15



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.

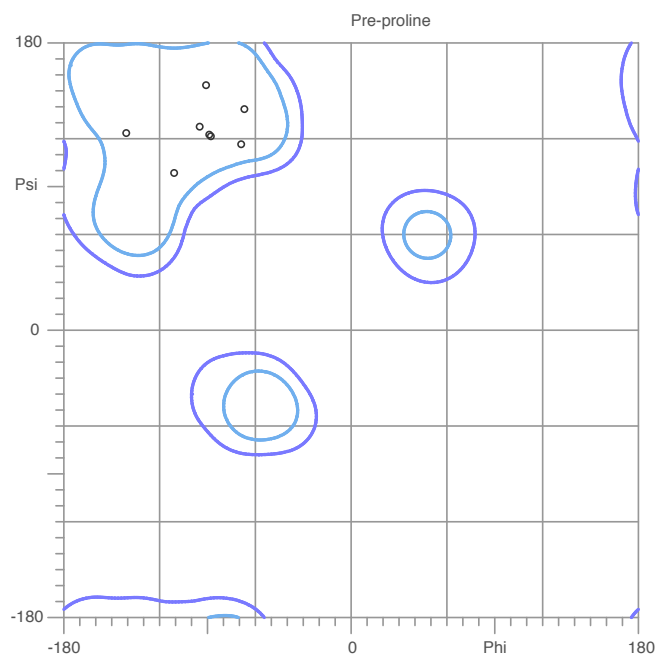
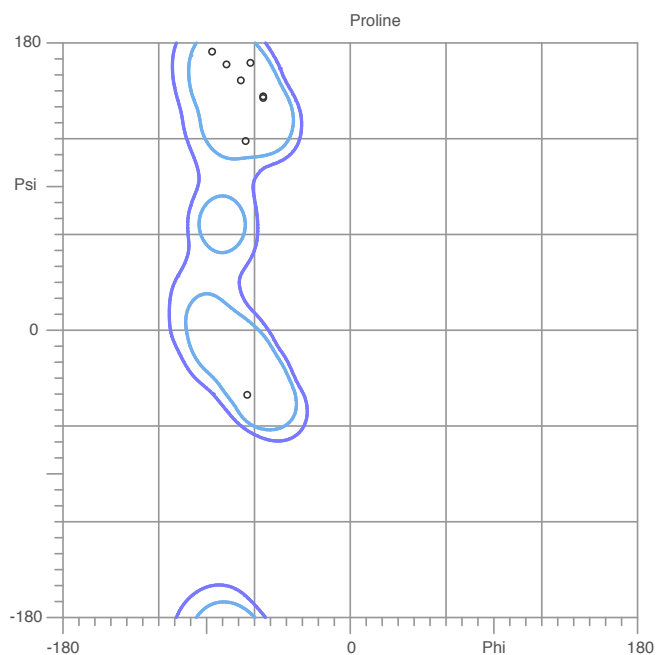
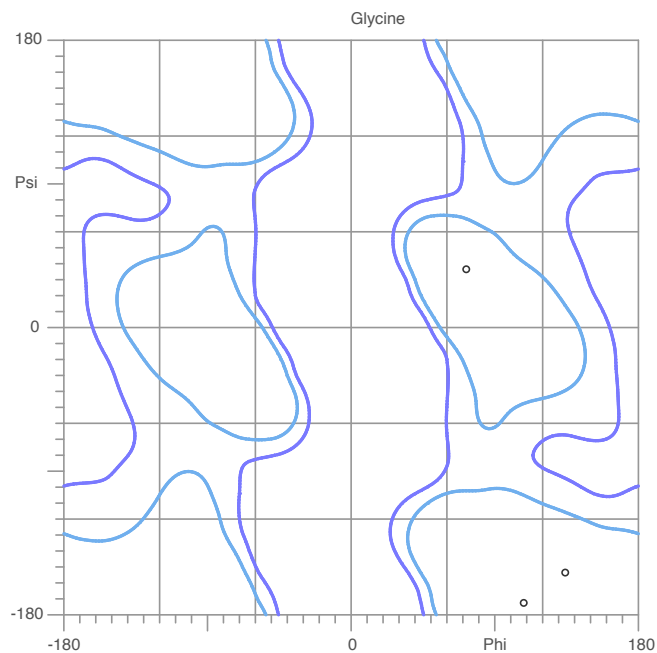
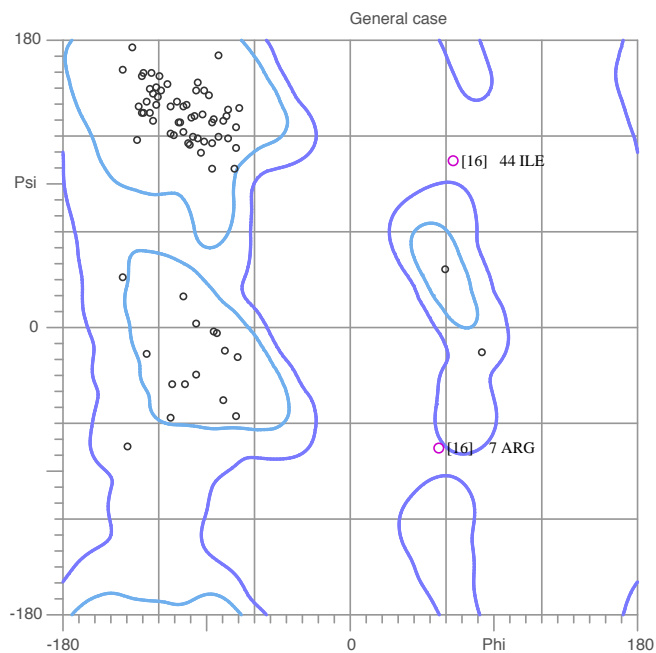
There were no outliers.

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 16



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.

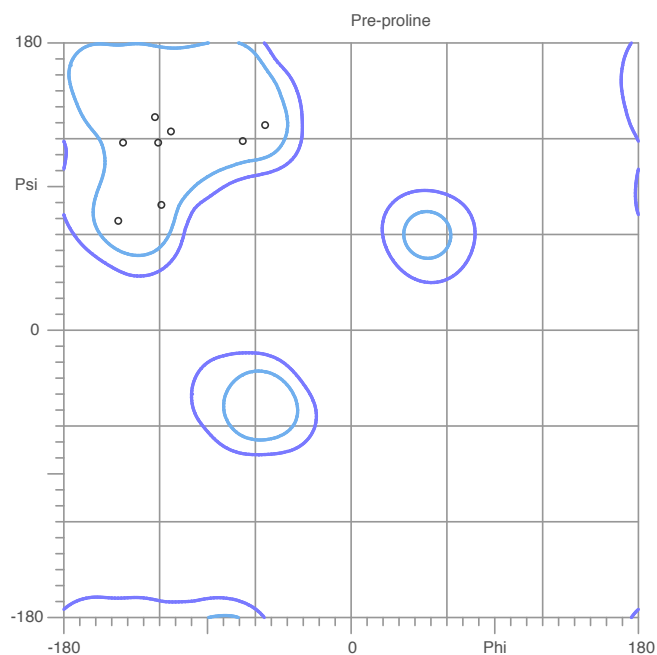
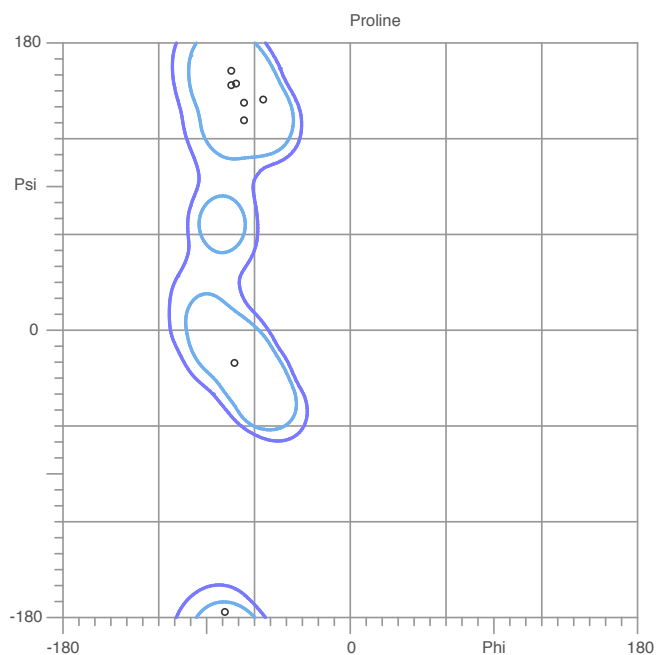
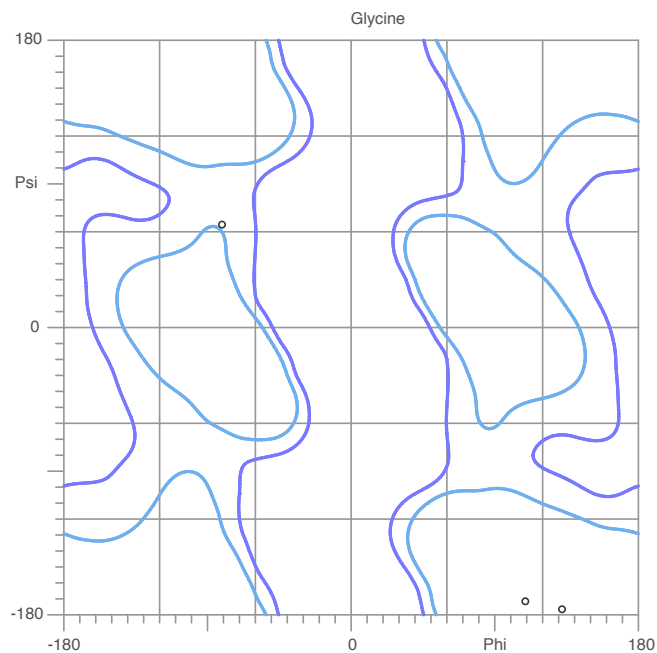
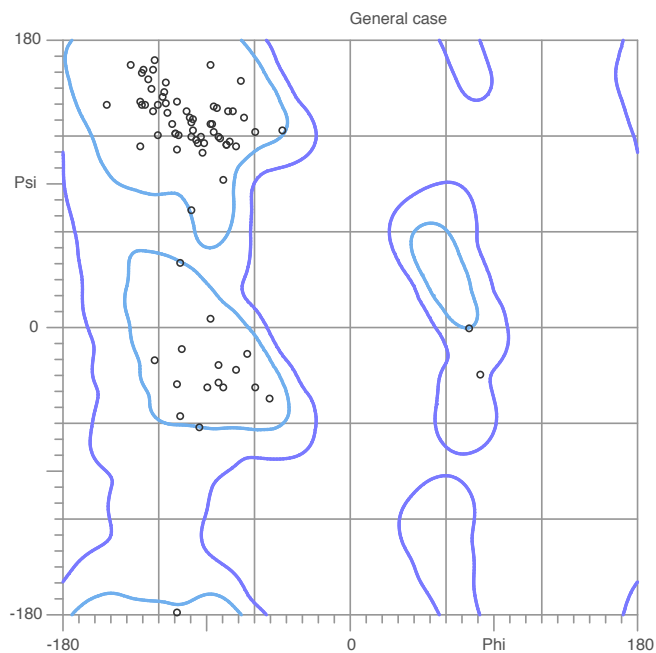
There were 2 outliers (phi, psi):

[16] 7 ARG (55.3, -75.3)

[16] 44 ILE (64.8, 105.0)

MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 17



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.

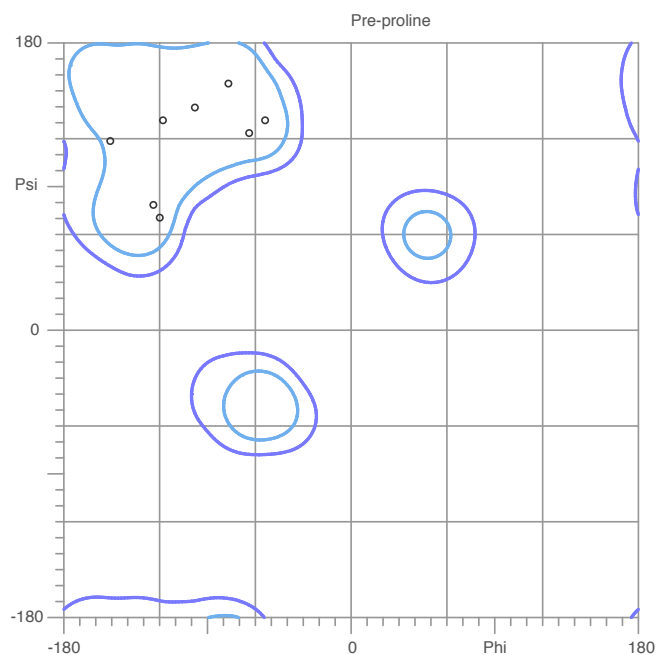
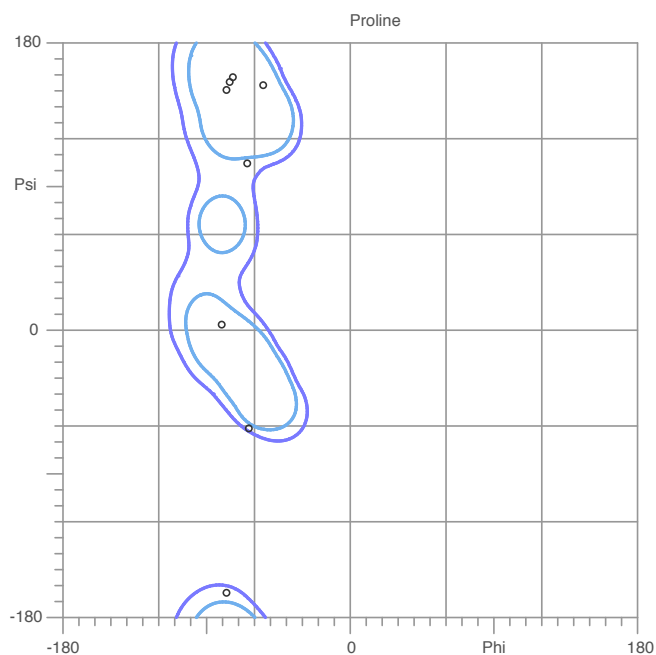
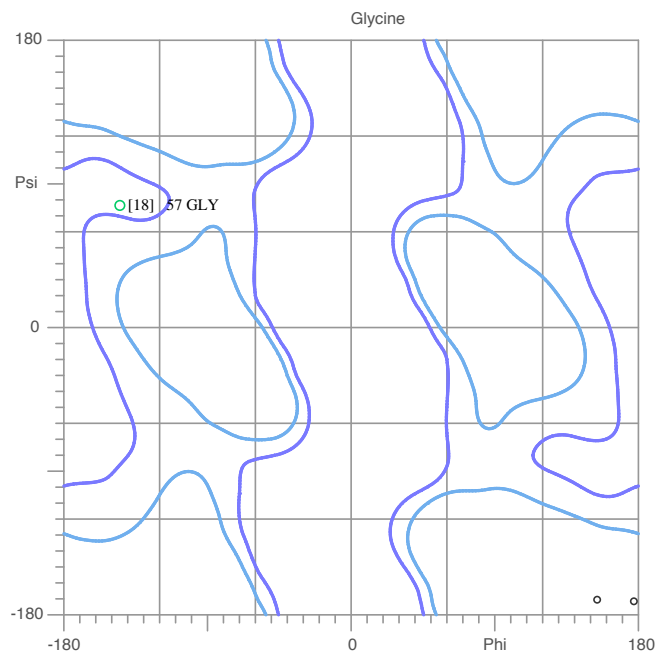
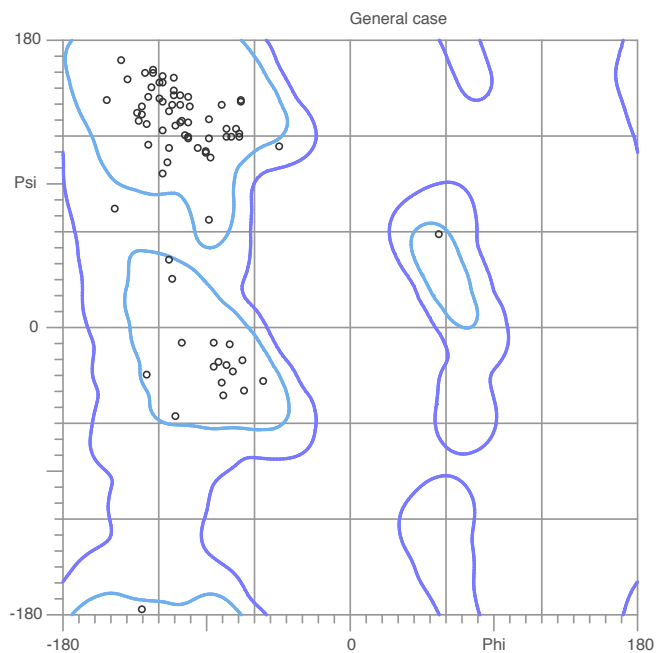
There were no outliers.

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 18



93.6% (88/94) of all residues were in favored (98%) regions.
98.9% (93/94) of all residues were in allowed (>99.8%) regions.

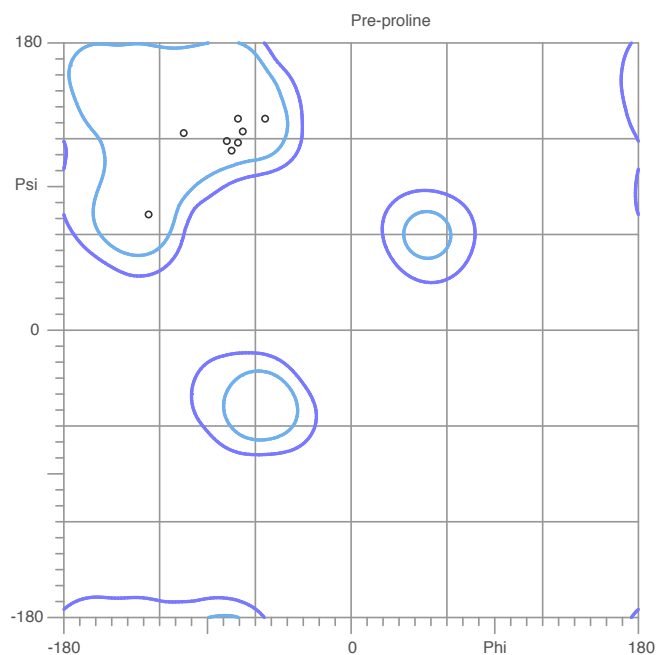
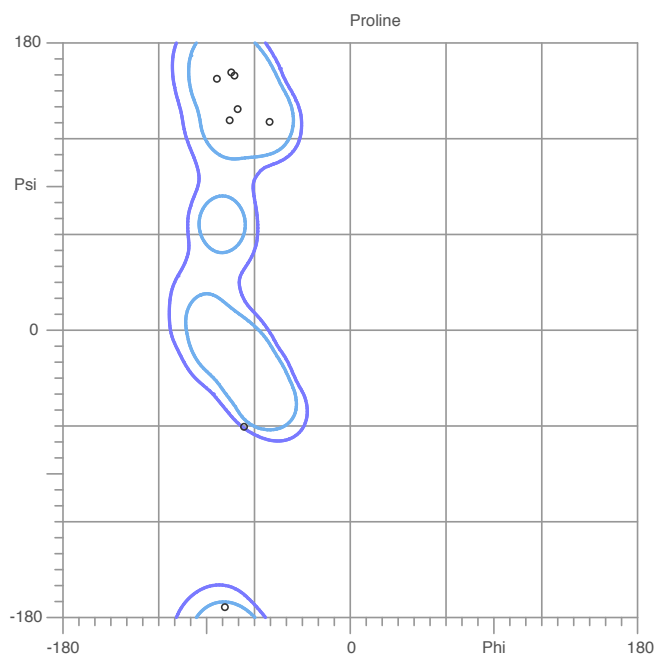
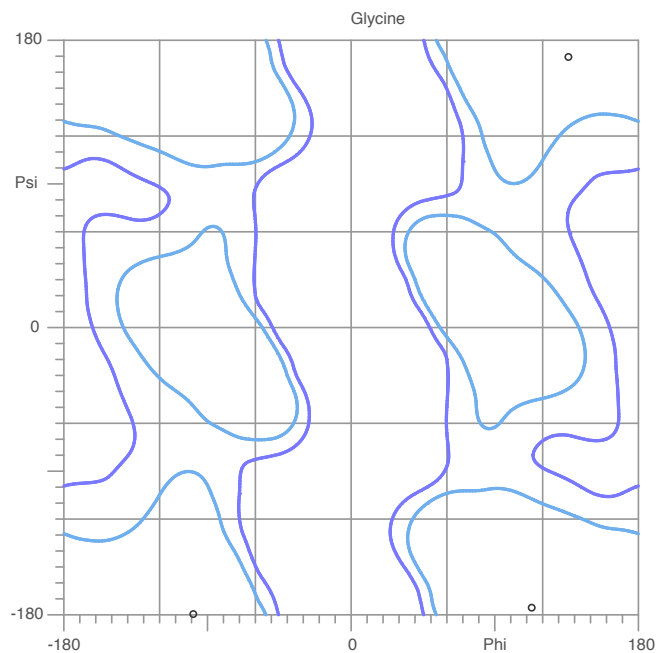
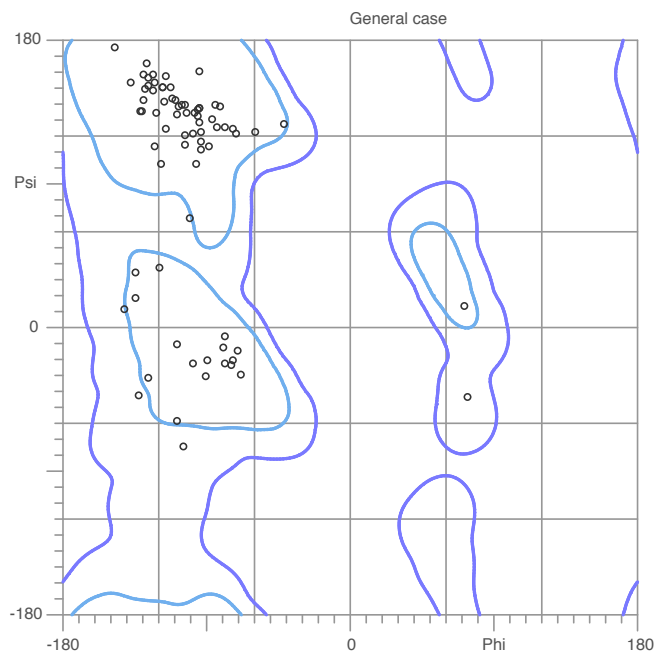
There were 1 outliers (phi, psi):
[18] 57 GLY (-145.1, 78.0)

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 19



93.6% (88/94) of all residues were in favored (98%) regions.
100.0% (94/94) of all residues were in allowed (>99.8%) regions.

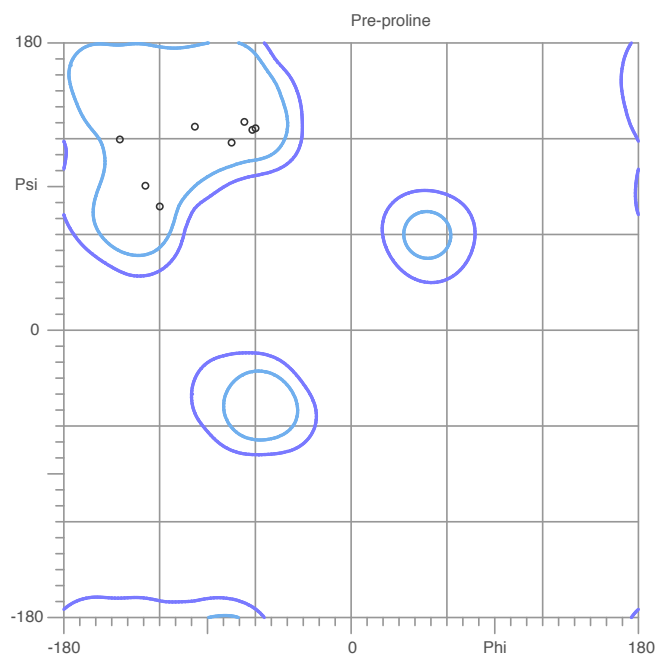
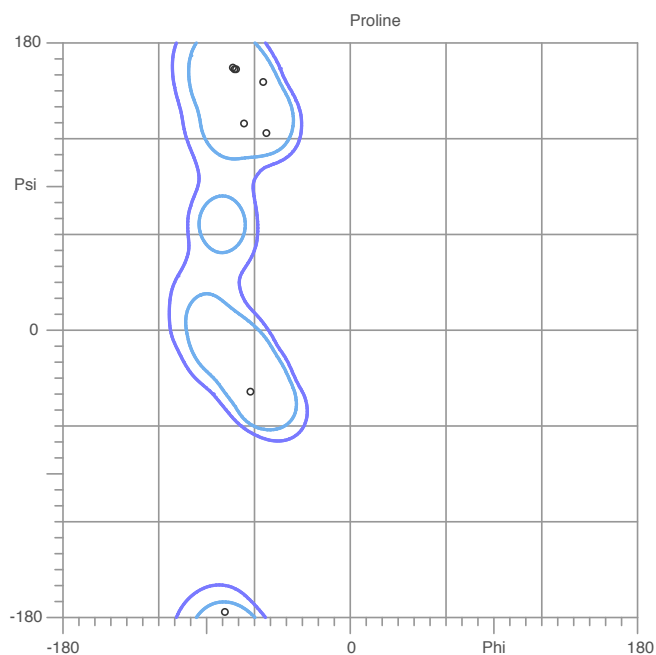
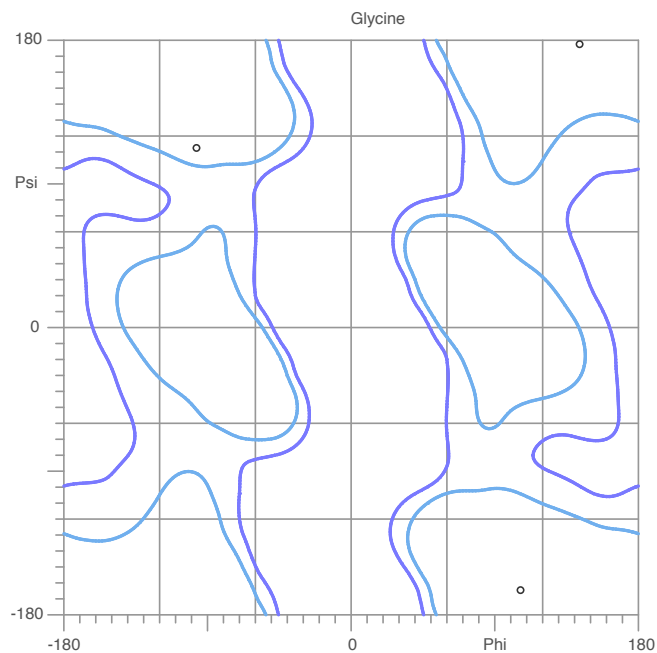
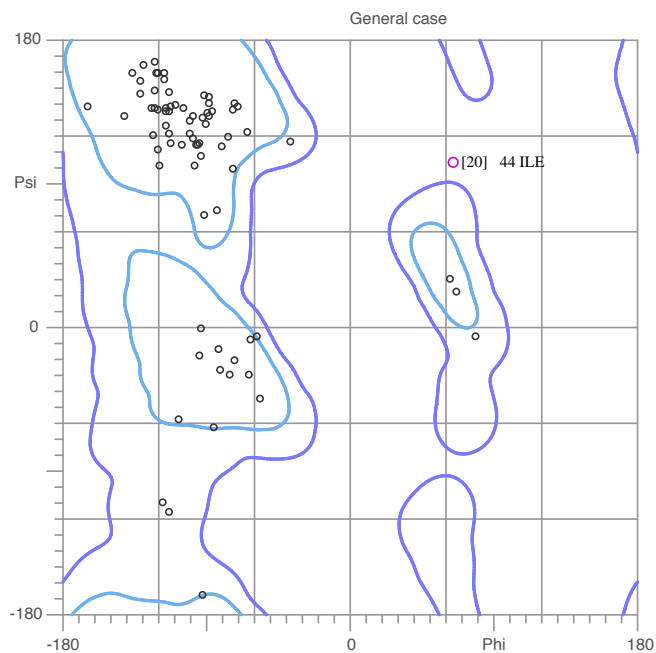
There were no outliers.

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

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MolProbity Ramachandran analysis

DHR29B_R3Cons_em_bcr3.pdb, model 20



93.6% (88/94) 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] 44 ILE (64.5, 104.6)

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