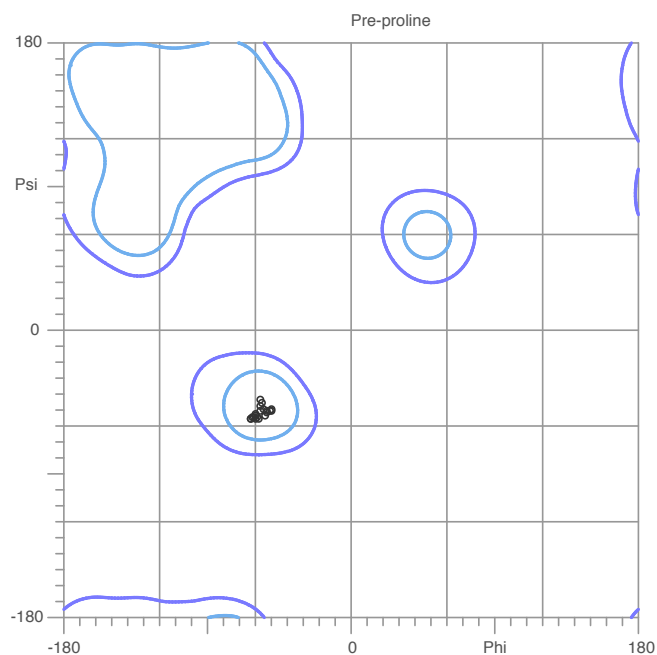
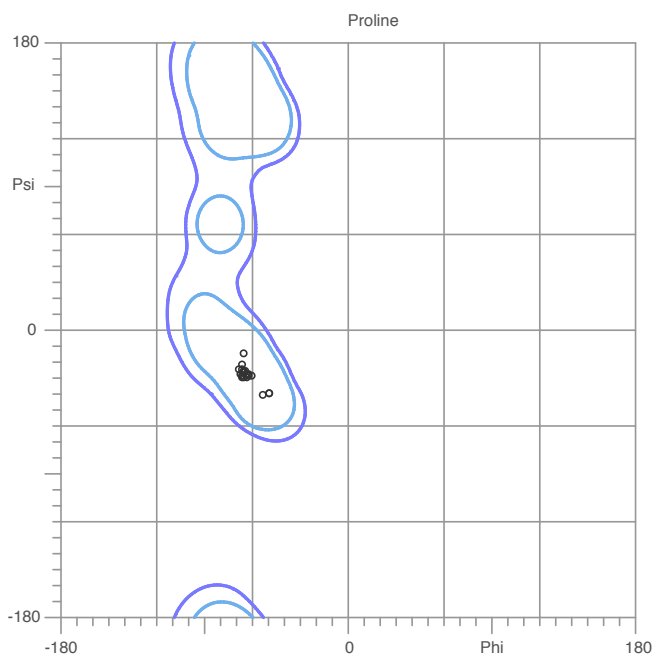
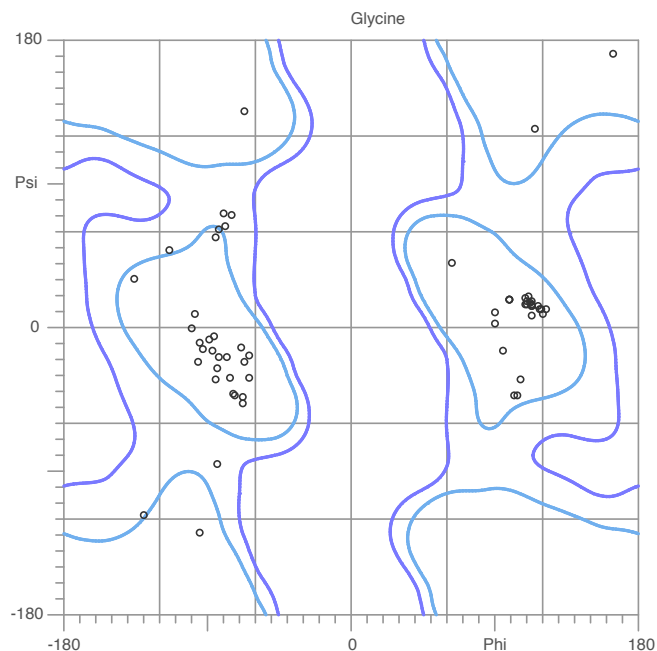
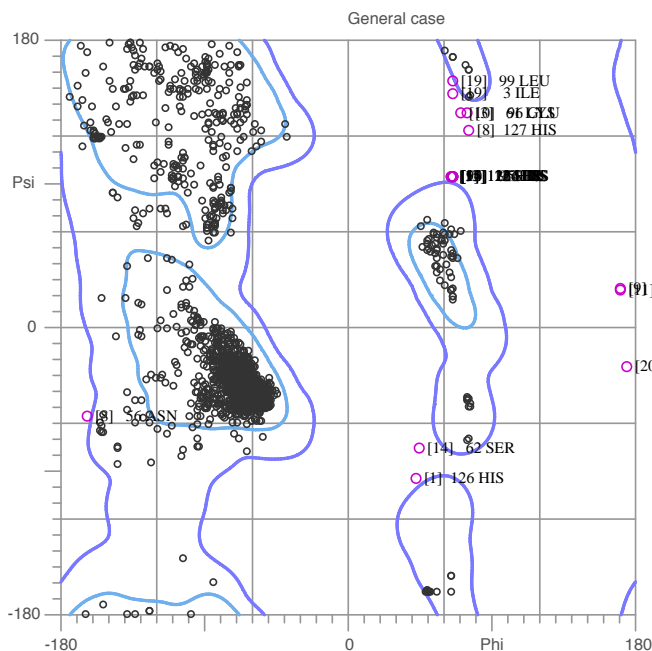


MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, all models



95.4% (2422/2540) of all residues were in favored (98%) regions.
99.3% (2522/2540) of all residues were in allowed (>99.8%) regions.

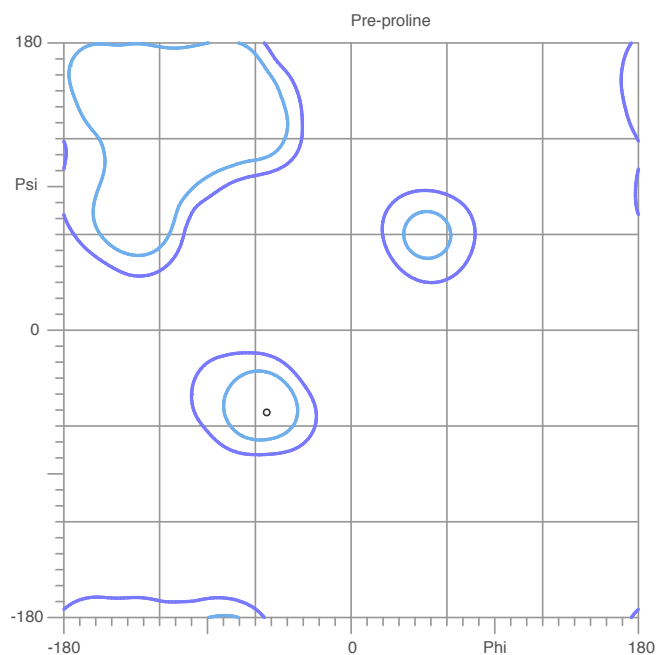
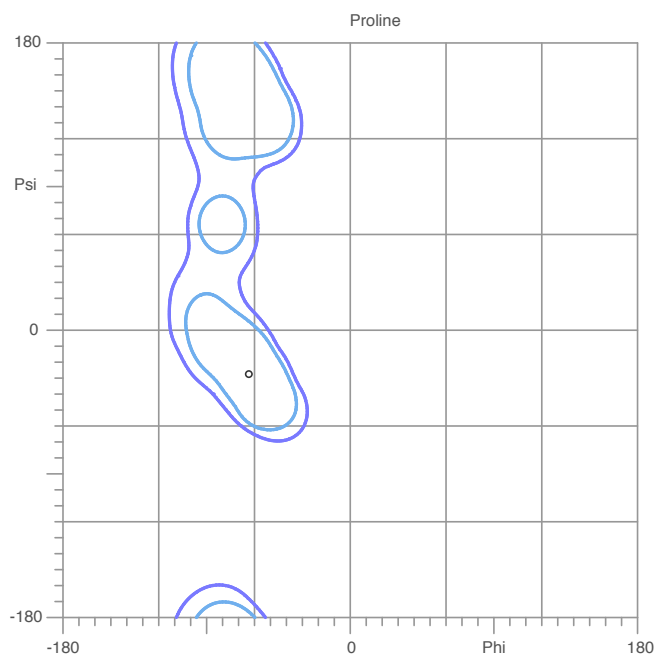
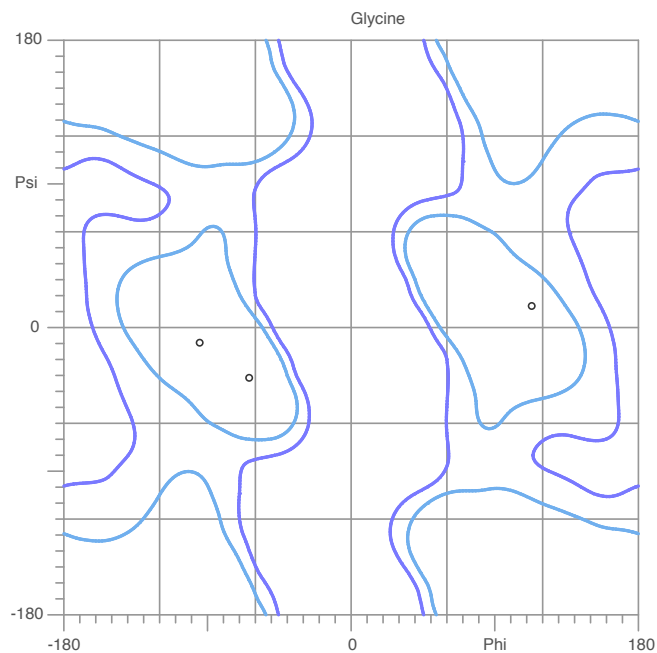
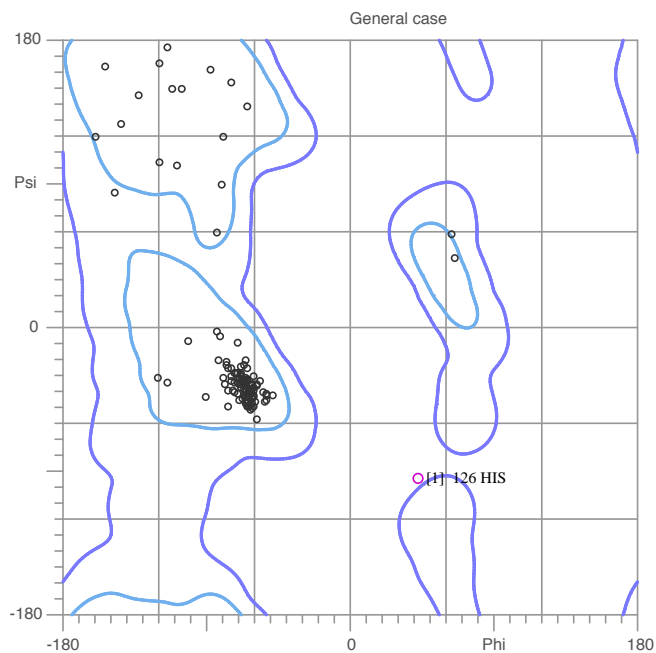
There were 18 outliers (phi, psi):

- [1] 126 HIS (42.5, -95.0)
- [3] 61 LYS (74.9, 135.1)
- [5] 125 HIS (65.1, 95.0)
- [8] 56 ASN (-165.0, -55.0)
- [8] 127 HIS (75.0, 125.0)
- [9] 46 ASN (170.1, 25.1)
- [9] 126 HIS (65.0, 95.1)

- [10] 95 HIS (65.1, 95.0)
- [10] 96 GLU (70.2, 135.1)
- [11] 46 ASN (170.4, 24.9)
- [14] 62 SER (45.0, -75.4)
- [14] 126 HIS (65.1, 95.0)
- [15] 124 HIS (65.0, 95.0)
- [15] 127 HIS (64.9, 95.0)
- [17] 4 SER (64.9, 95.0)
- [19] 3 ILE (65.1, 147.2)
- [19] 99 LEU (65.4, 155.0)
- [20] 128 HIS (175.0, -24.9)

MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 1



97.6% (124/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

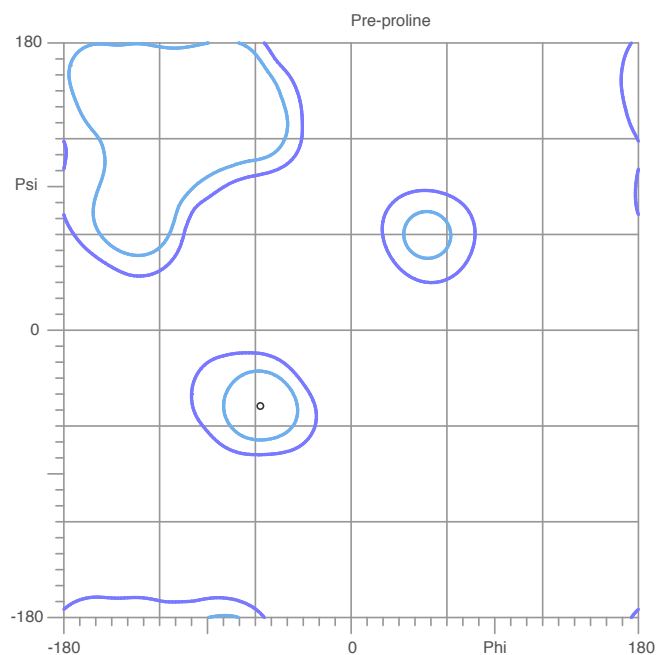
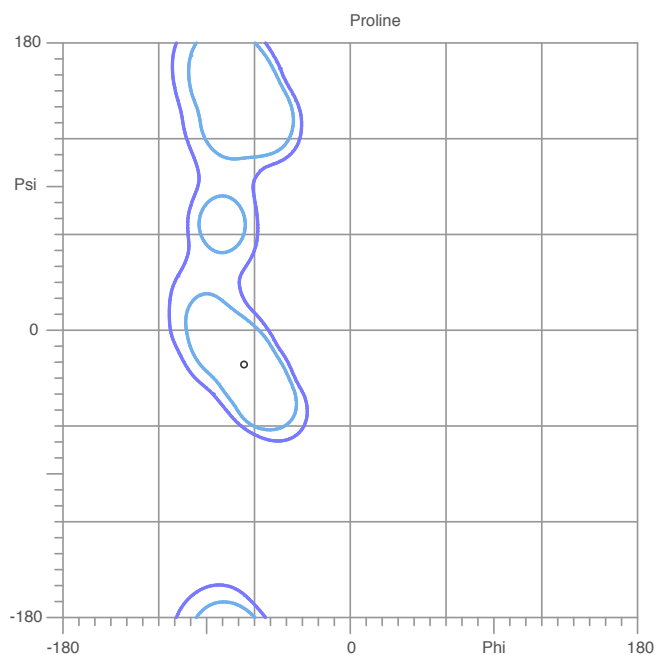
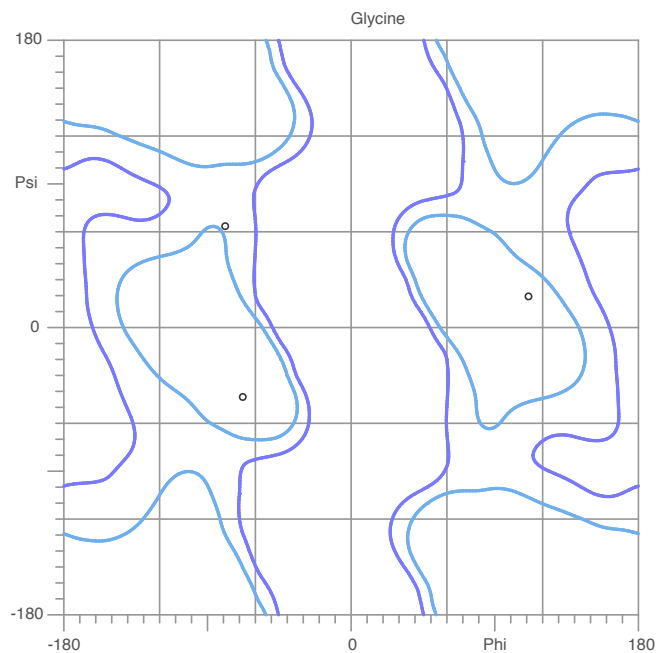
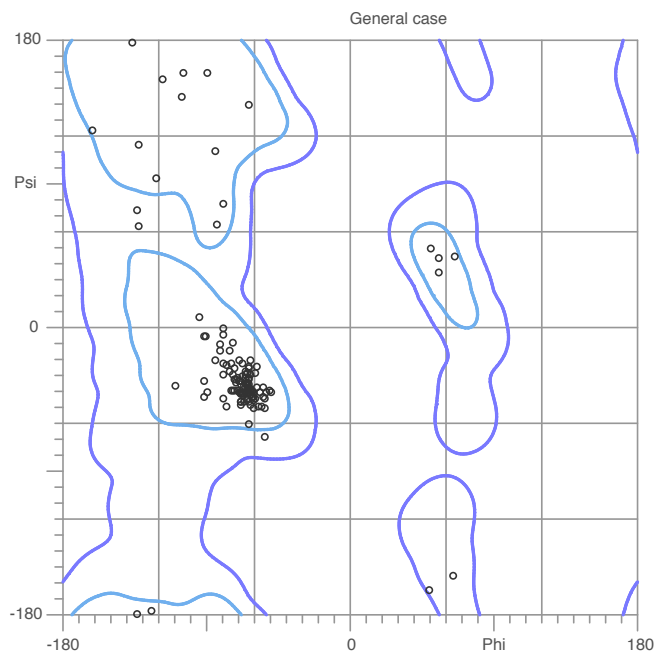
There were 1 outliers (phi, psi):
[1] 126 HIS (42.5, -95.0)

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 2



95.3% (121/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

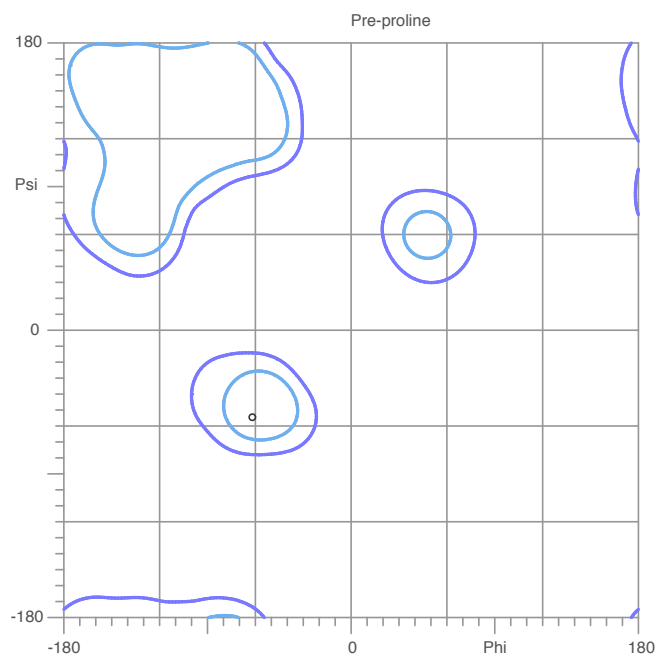
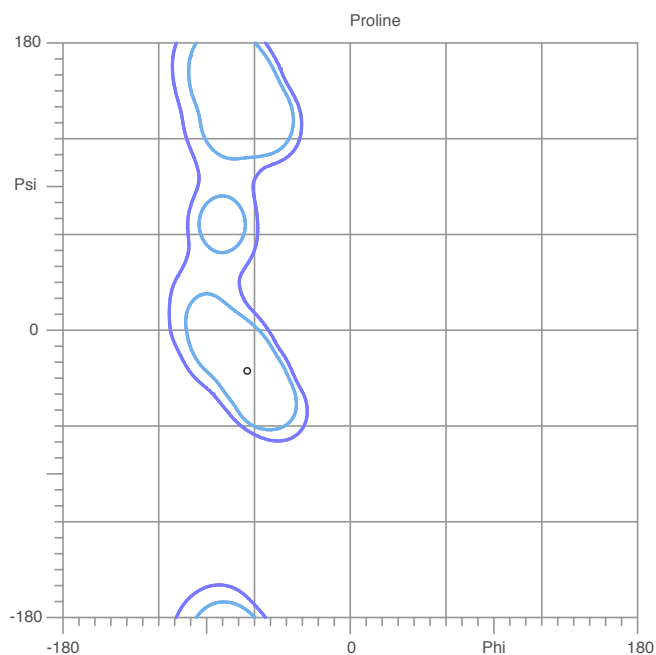
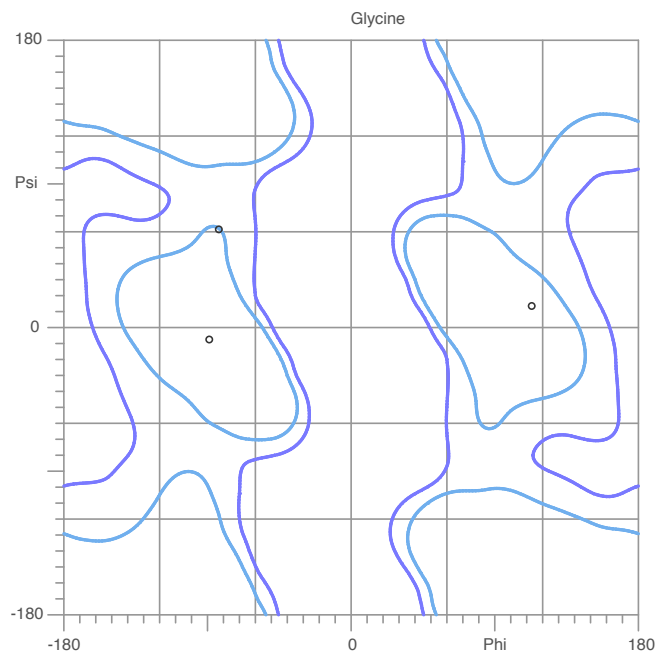
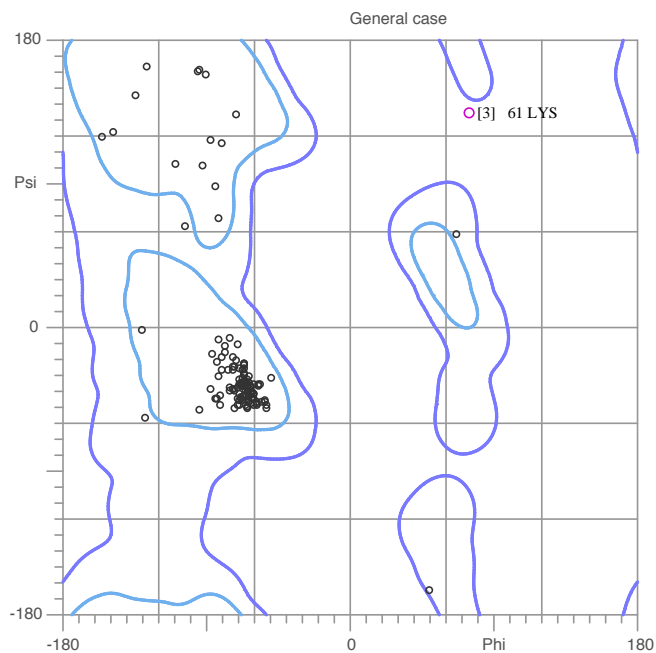
There were no outliers.

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

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

MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 3



95.3% (121/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

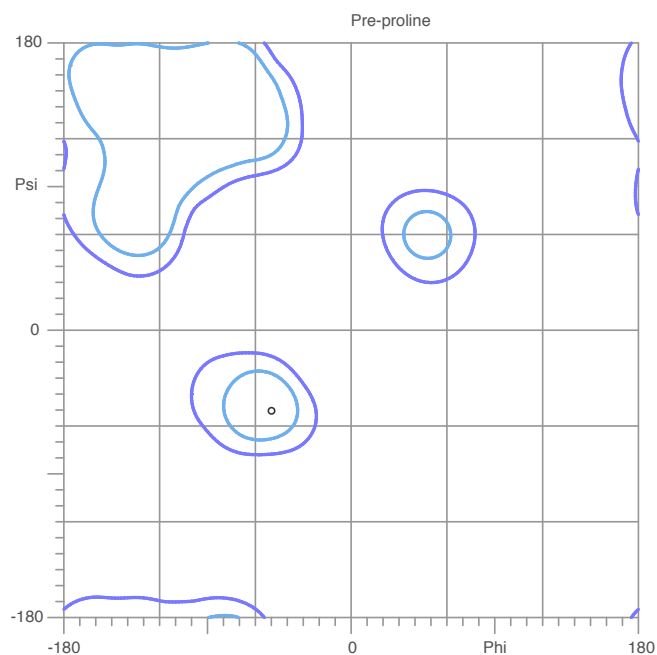
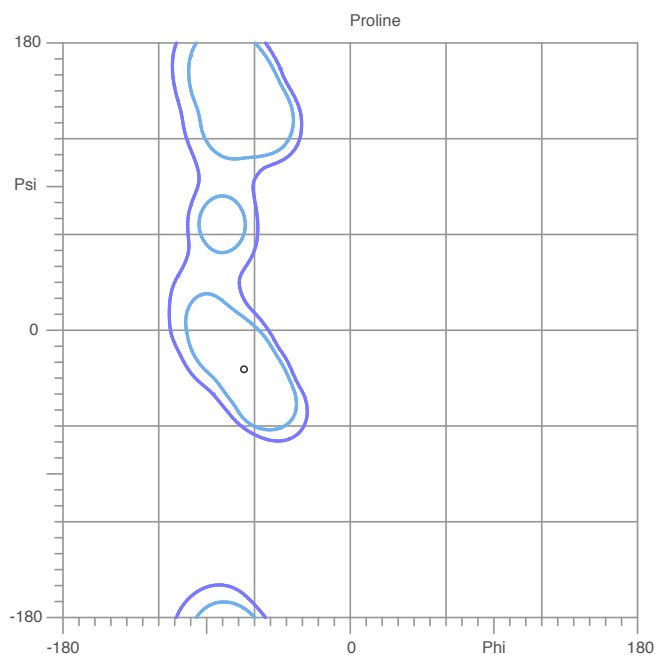
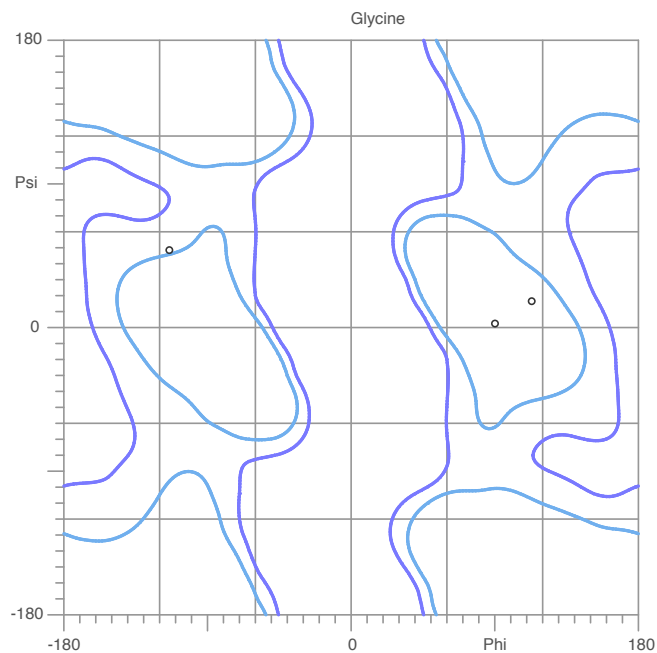
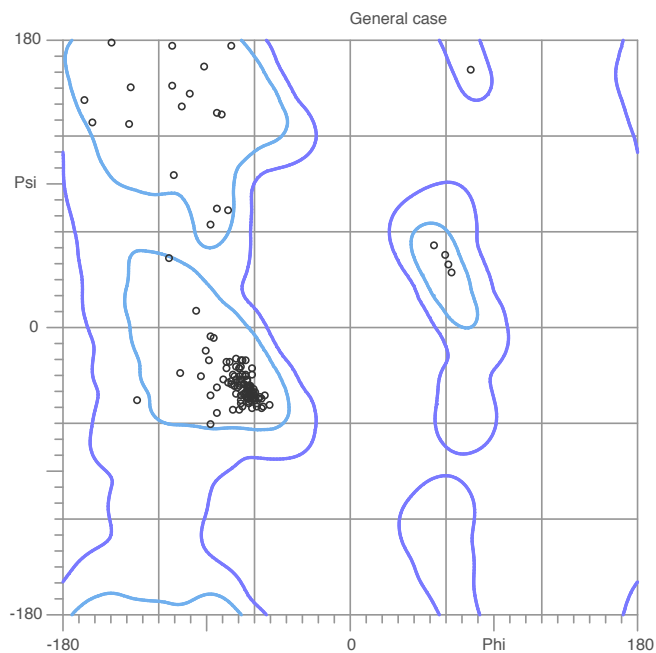
There were 1 outliers (phi, psi):
[3] 61 LYS (74.9, 135.1)

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 4

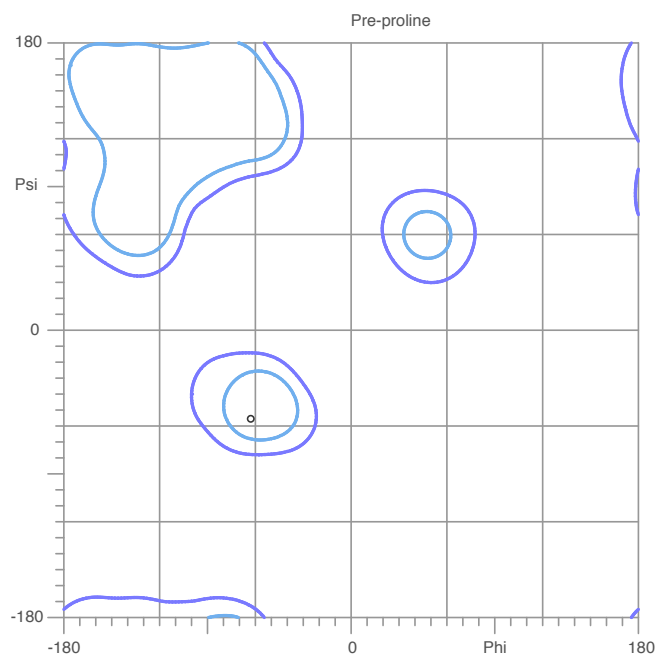
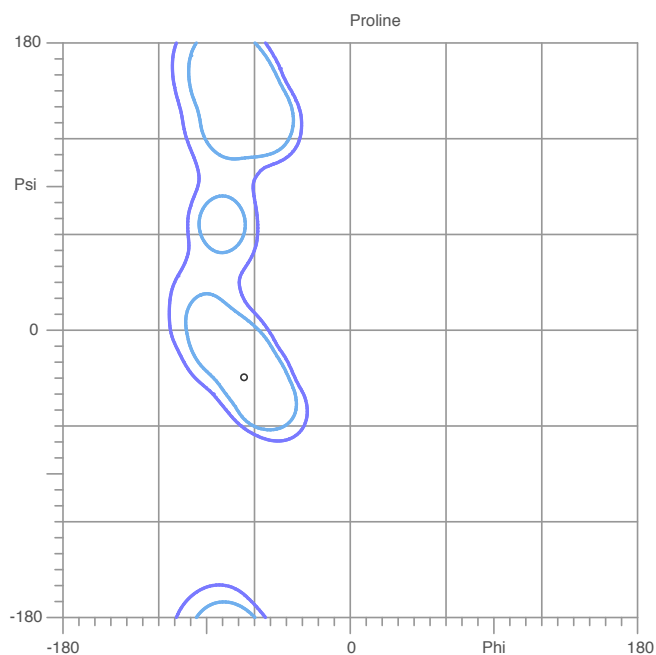
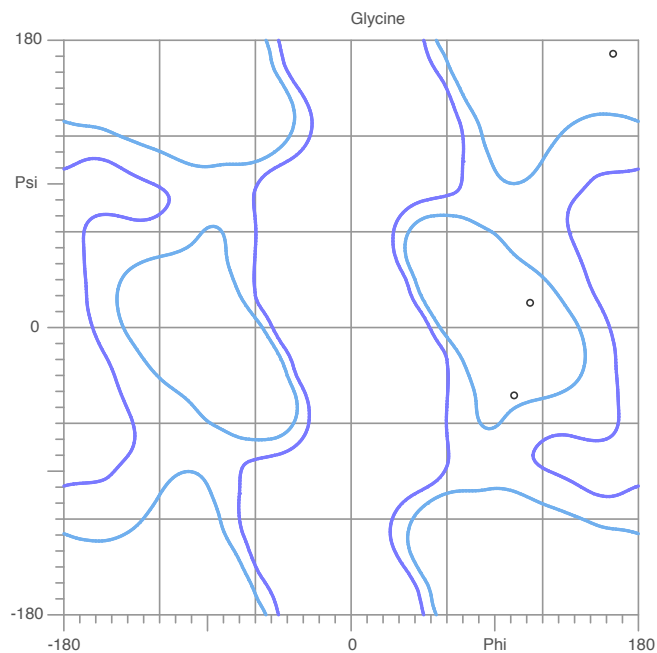
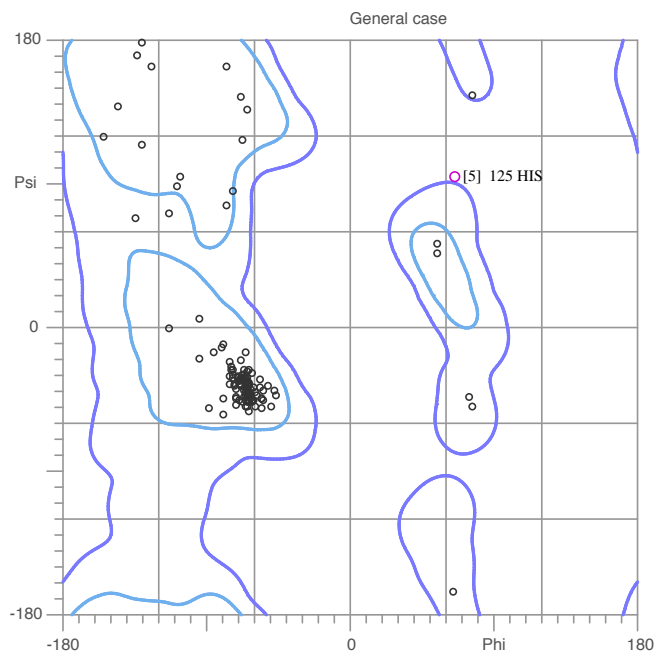


97.6% (124/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 5



94.5% (120/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

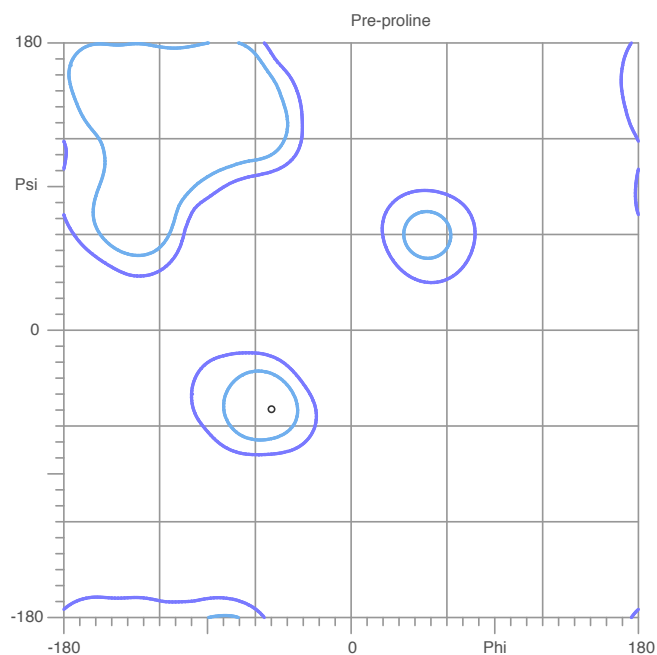
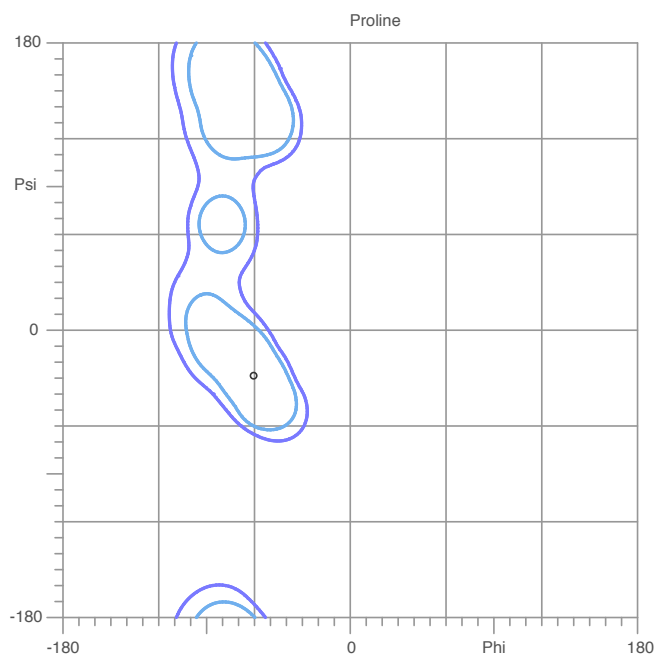
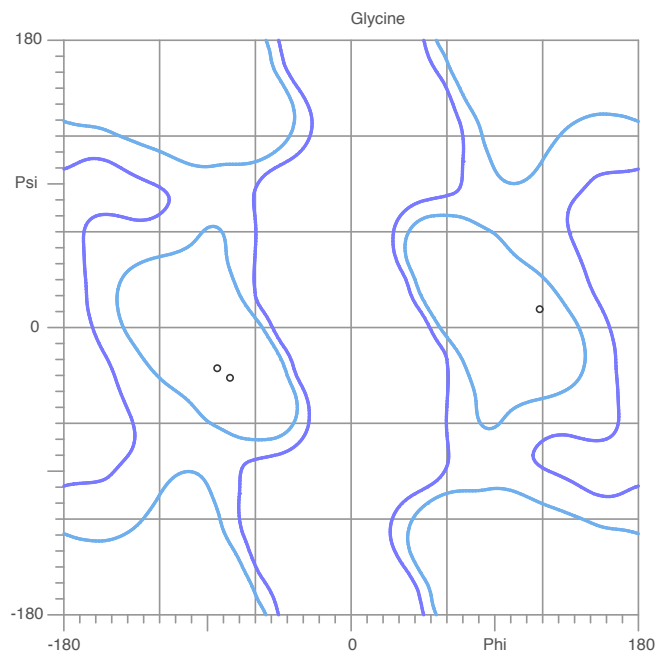
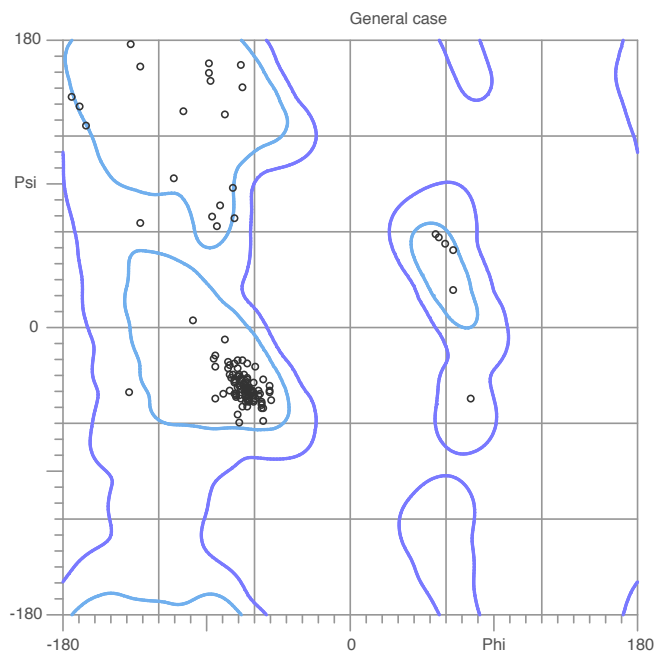
There were 1 outliers (phi, psi):
[5] 125 HIS (65.1, 95.0)

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 6



95.3% (121/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

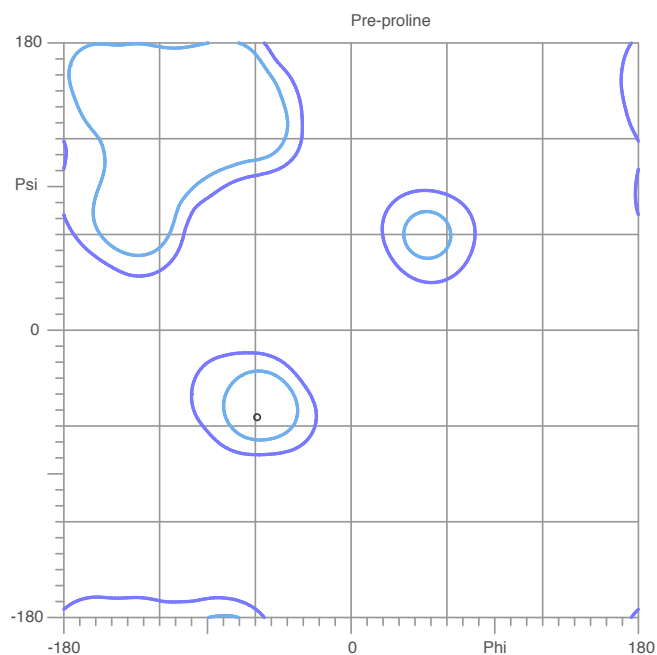
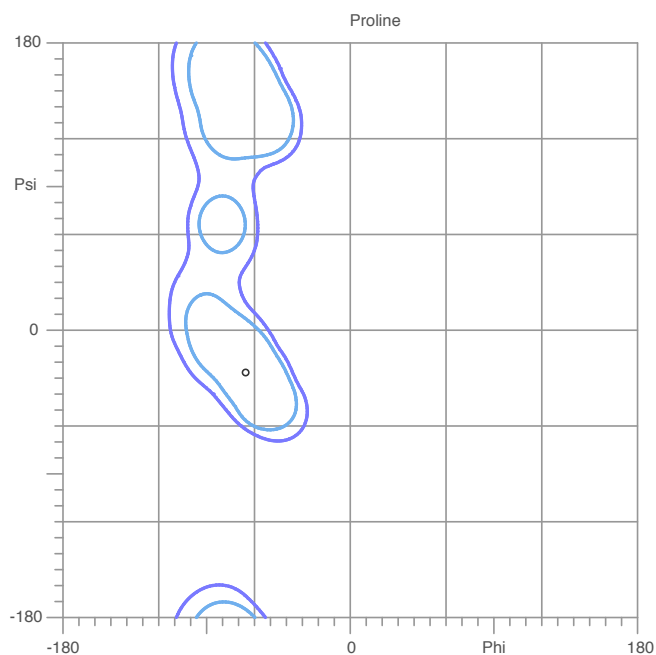
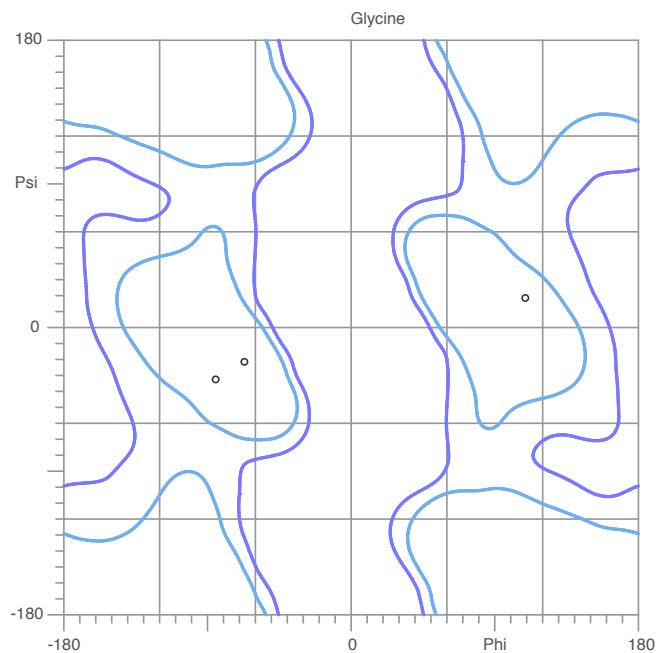
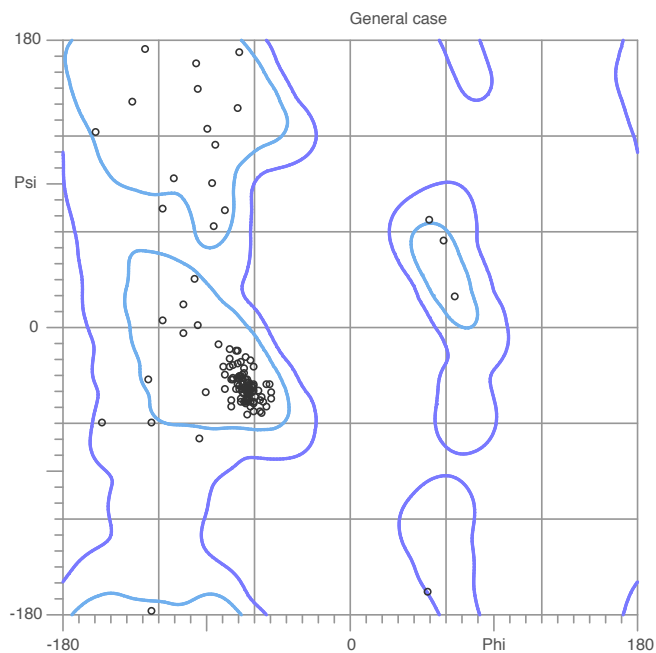
There were no outliers.

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

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 7



95.3% (121/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

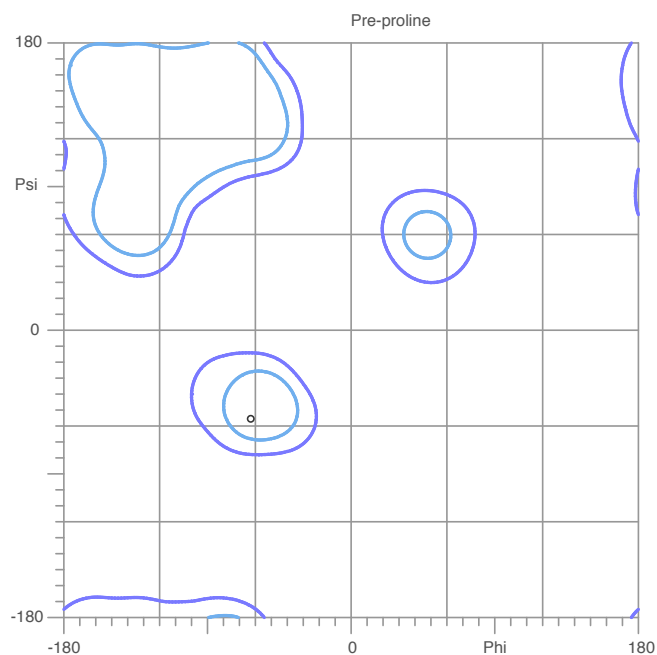
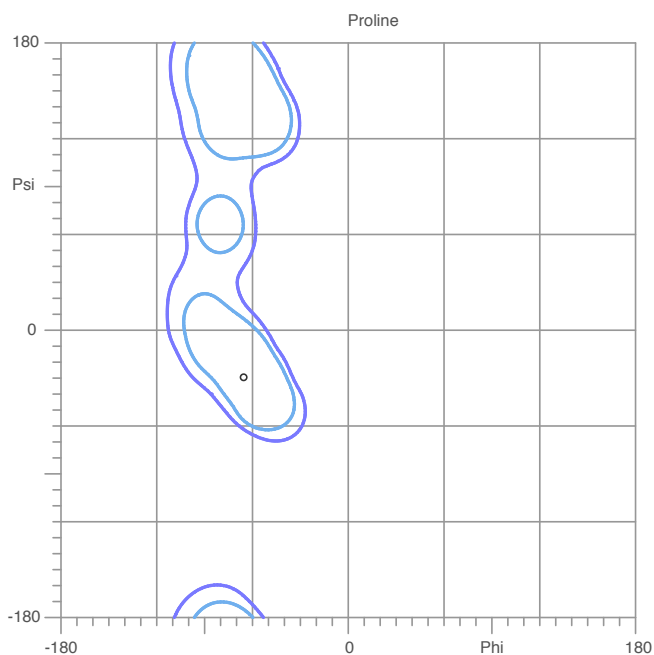
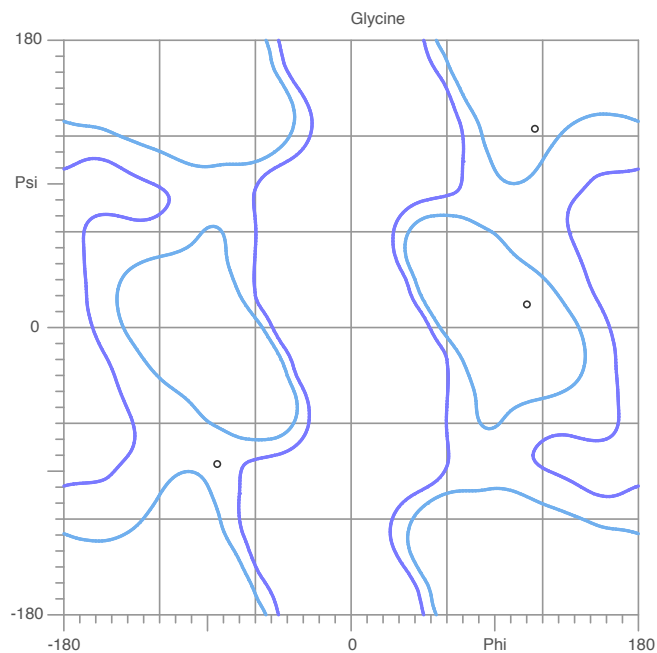
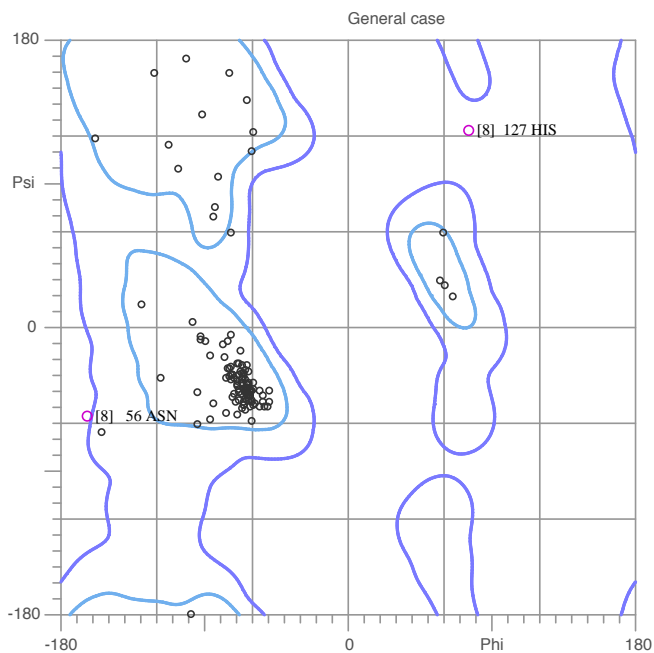
There were no outliers.

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

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 8



96.1% (122/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

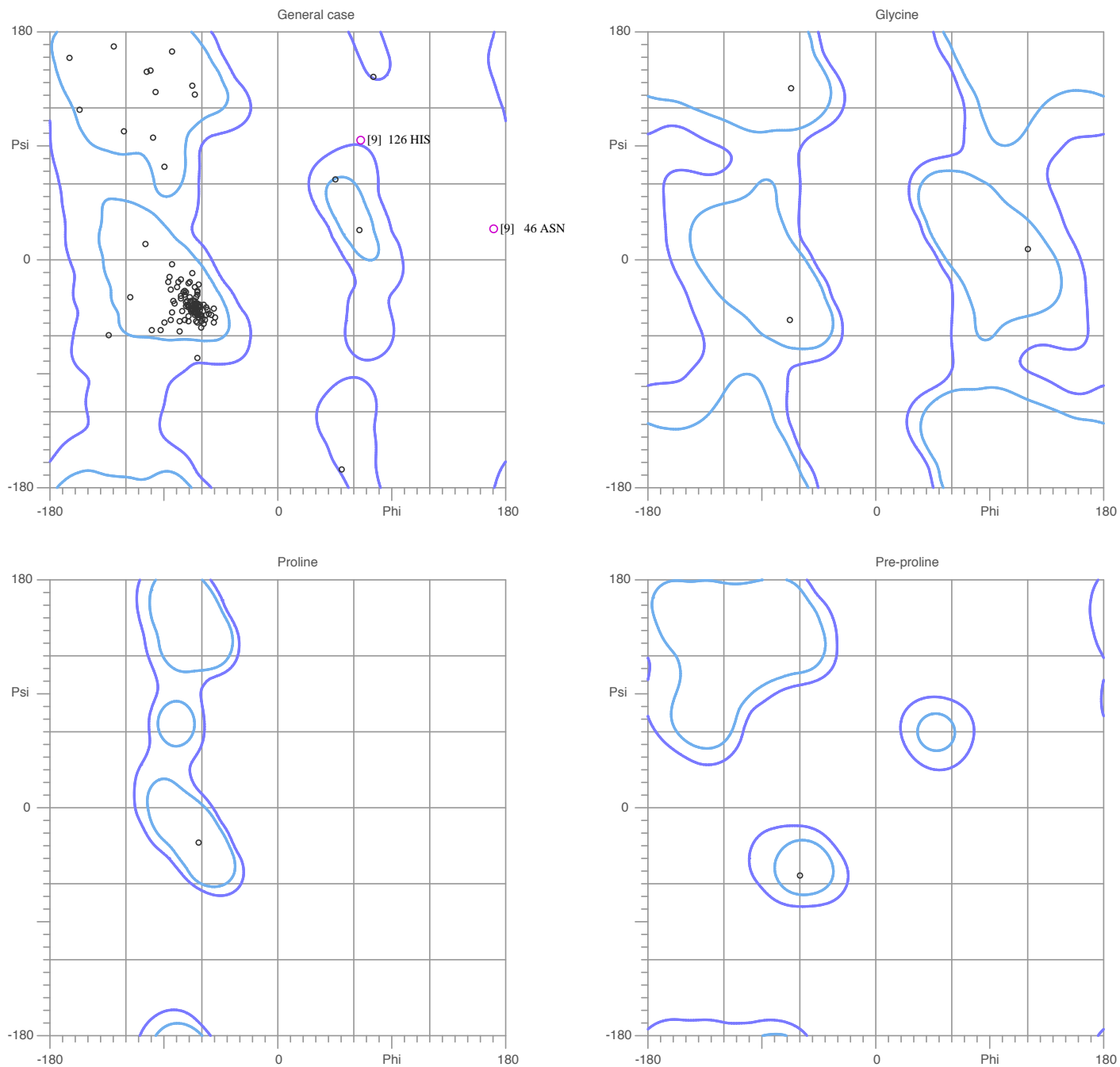
There were 2 outliers (phi, psi):

[8] 56 ASN (-165.0, -55.0)

[8] 127 HIS (75.0, 125.0)

MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 9



94.5% (120/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

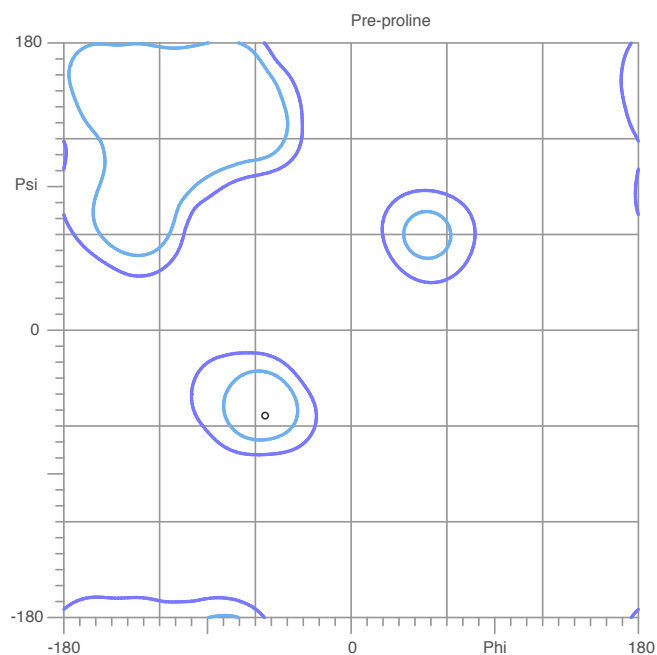
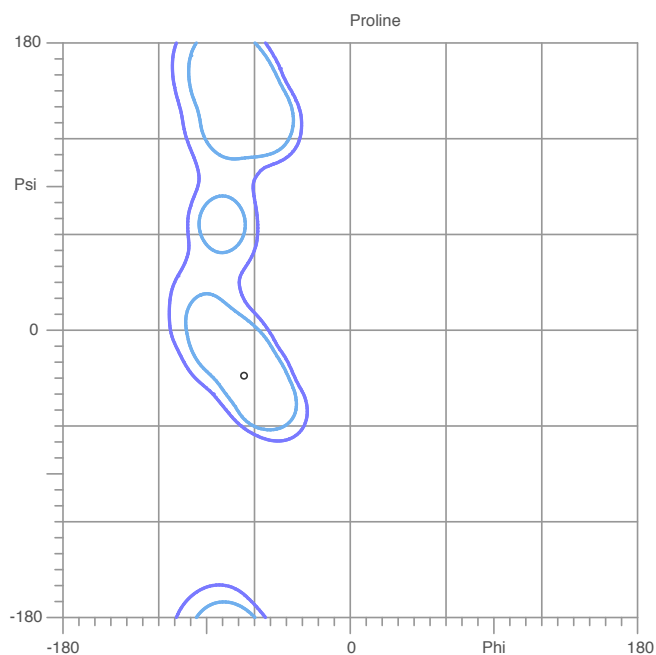
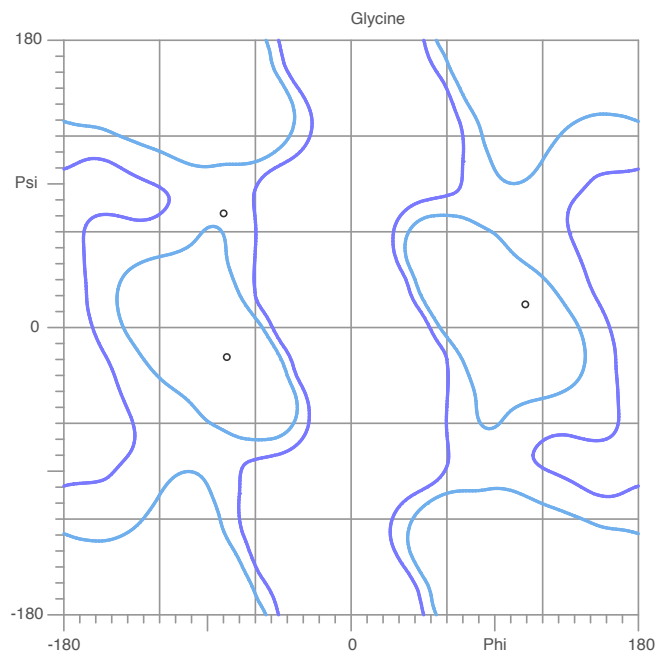
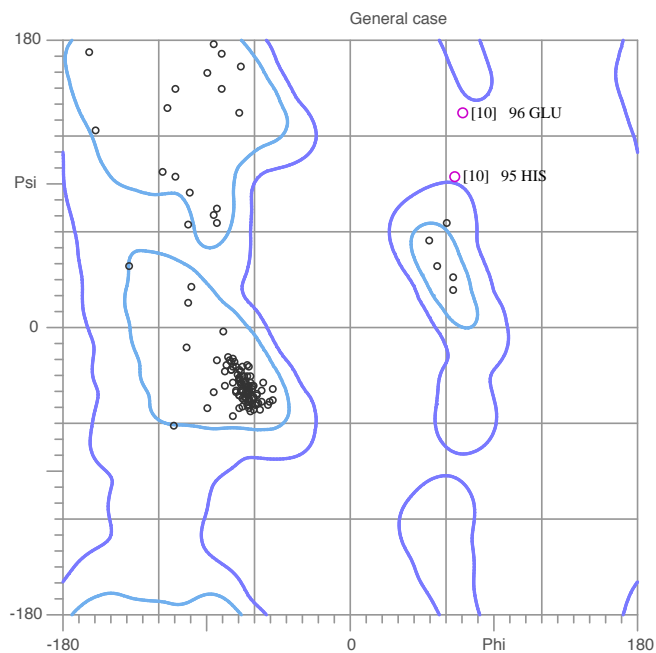
There were 2 outliers (phi, psi):

[9] 46 ASN (170.1, 25.1)

[9] 126 HIS (65.0, 95.1)

MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 10



94.5% (120/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

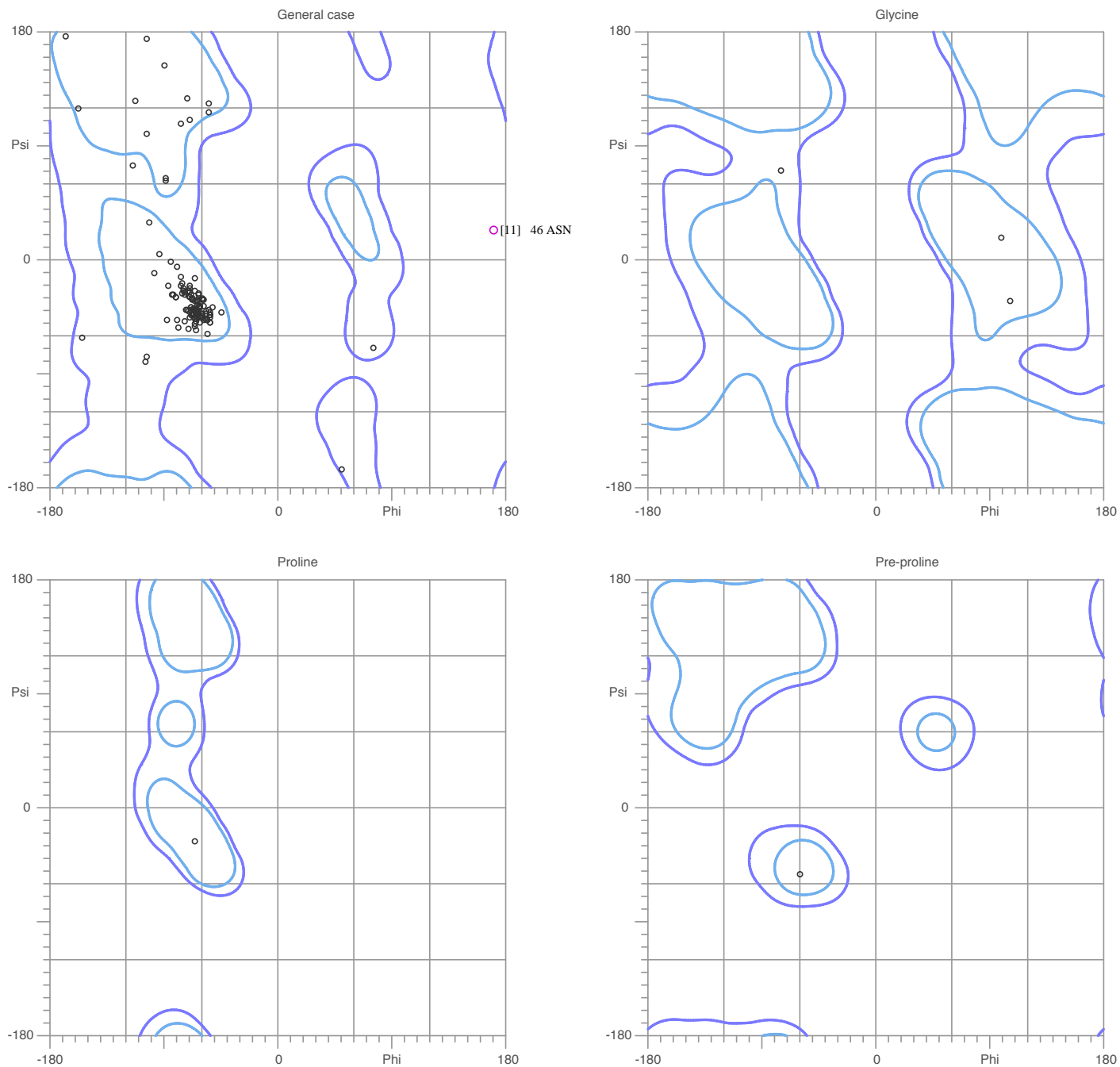
There were 2 outliers (phi, psi):

[10] 95 HIS (65.1, 95.0)

[10] 96 GLU (70.2, 135.1)

MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 11



93.7% (119/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

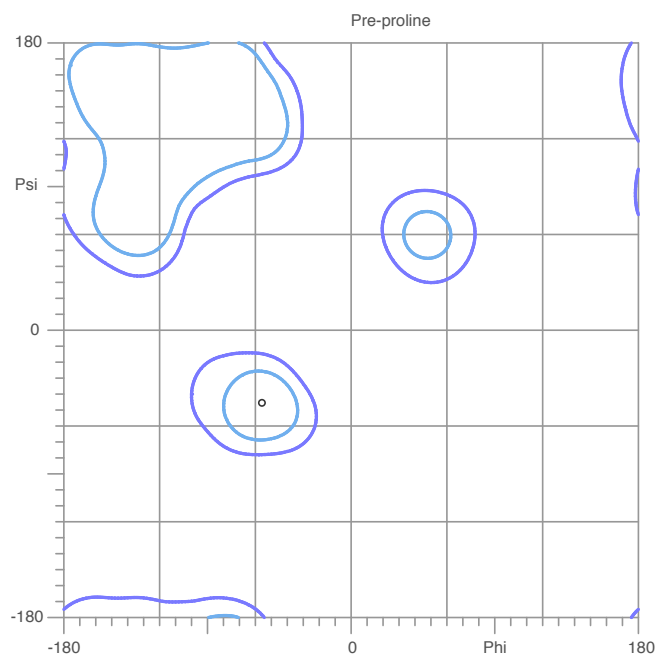
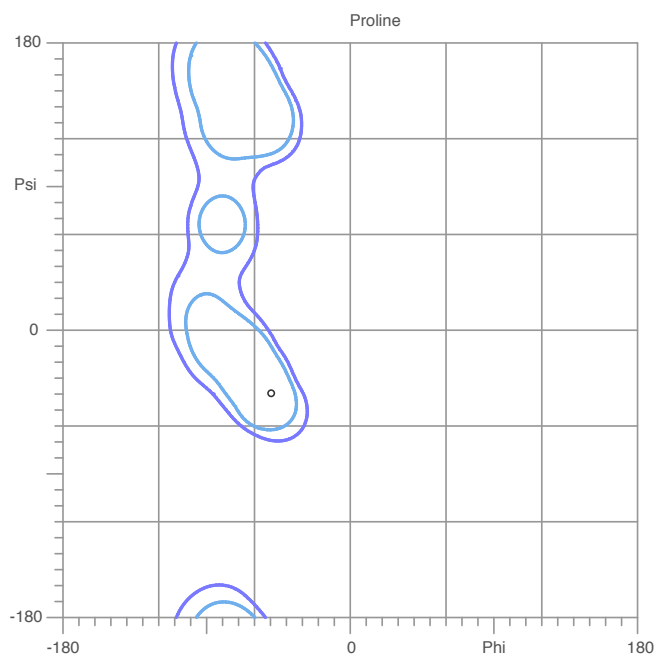
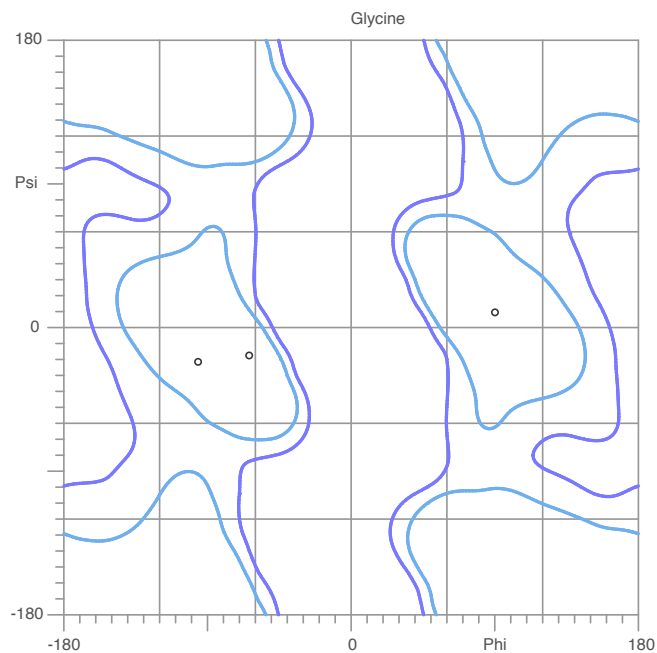
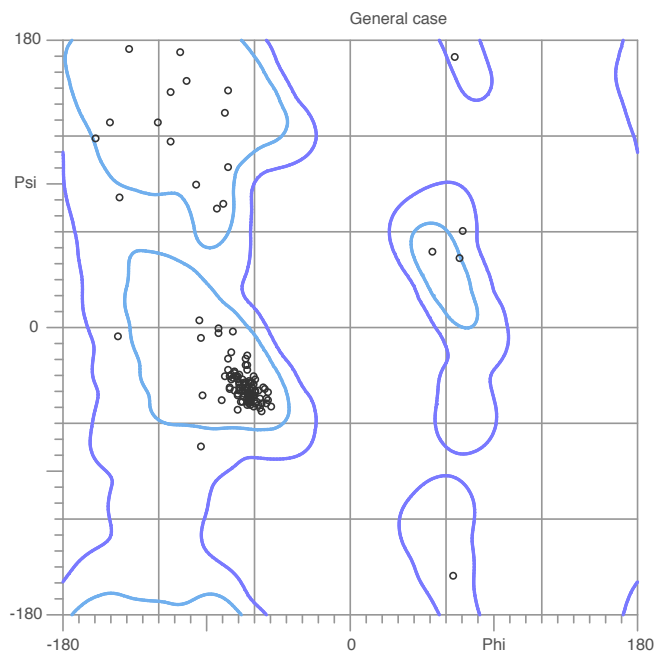
There were 1 outliers (phi, psi):
[11] 46 ASN (170.4, 24.9)

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 12



95.3% (121/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

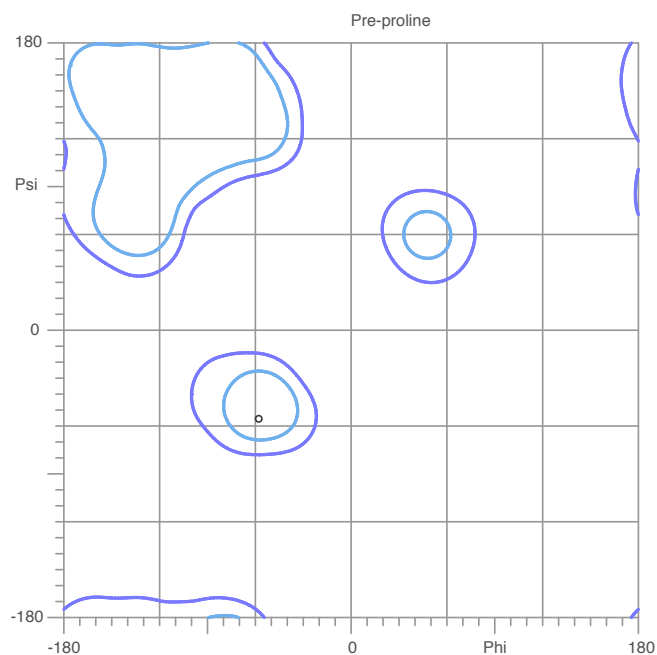
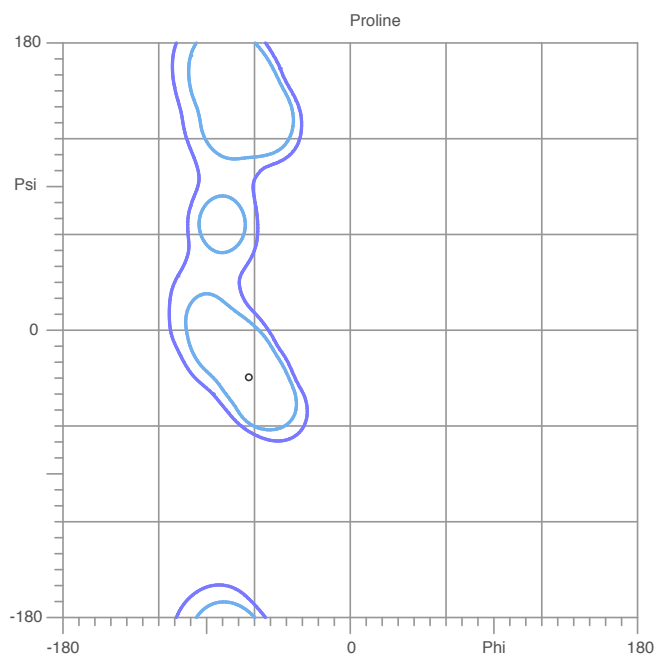
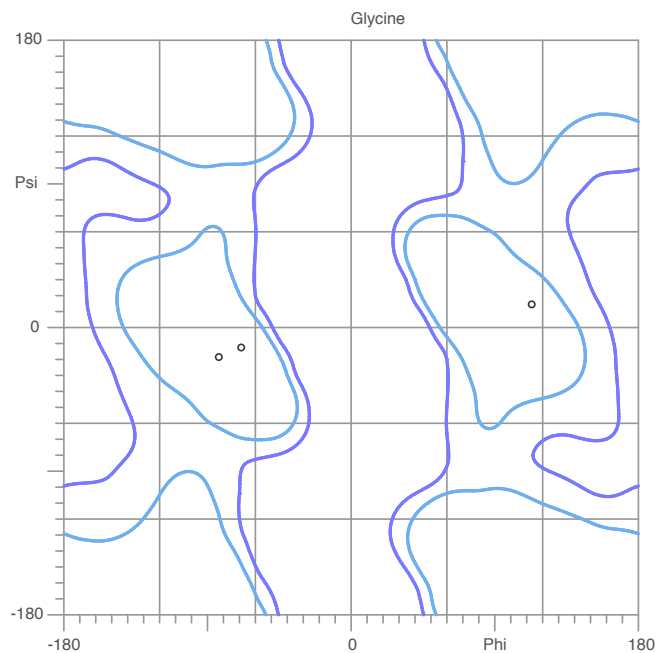
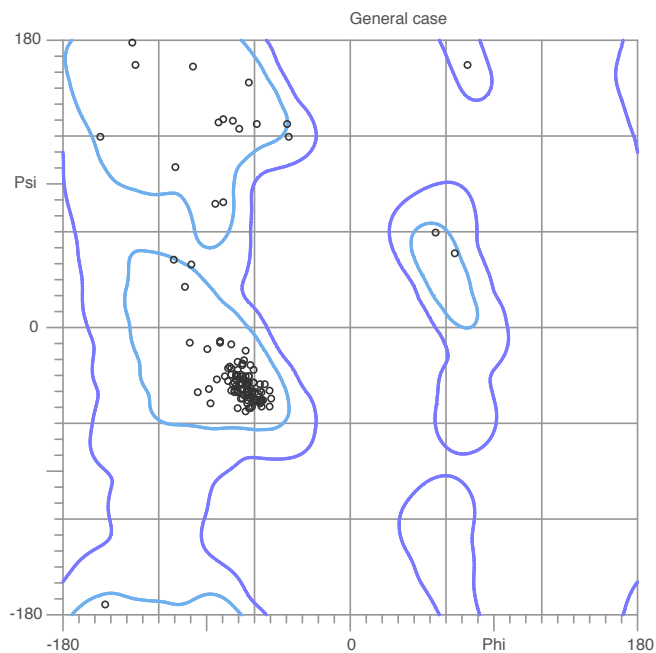
There were no outliers.

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

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 13



97.6% (124/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

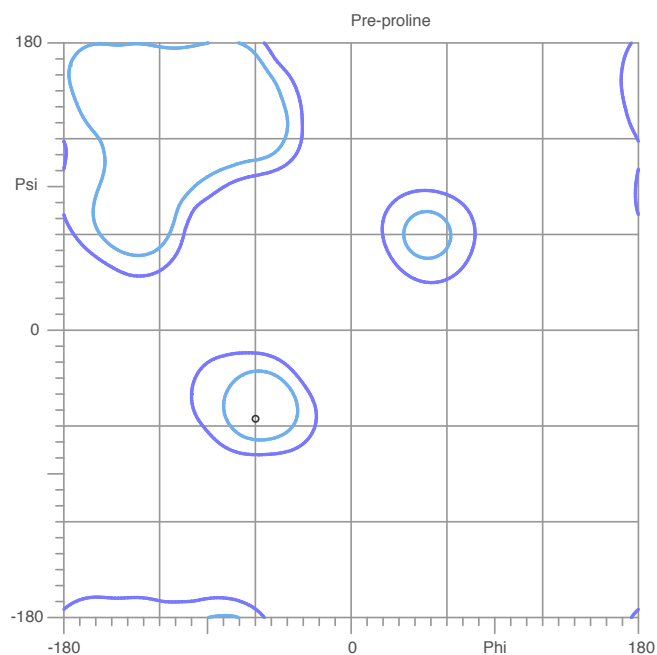
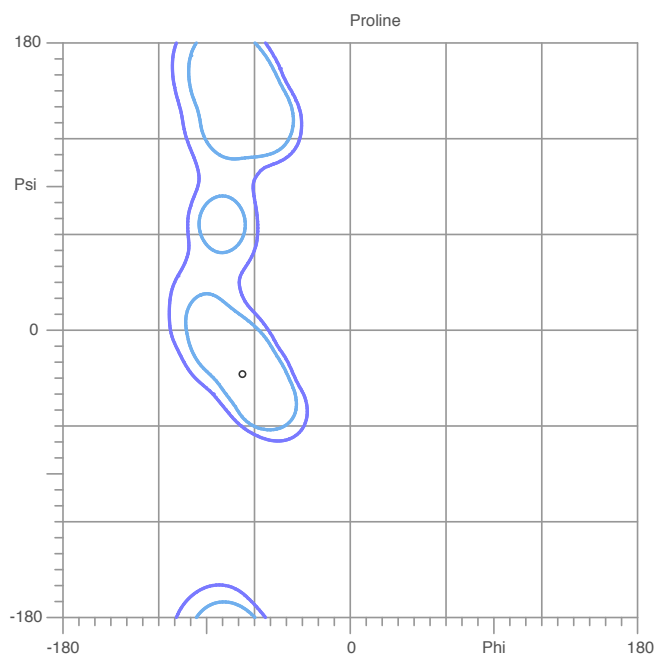
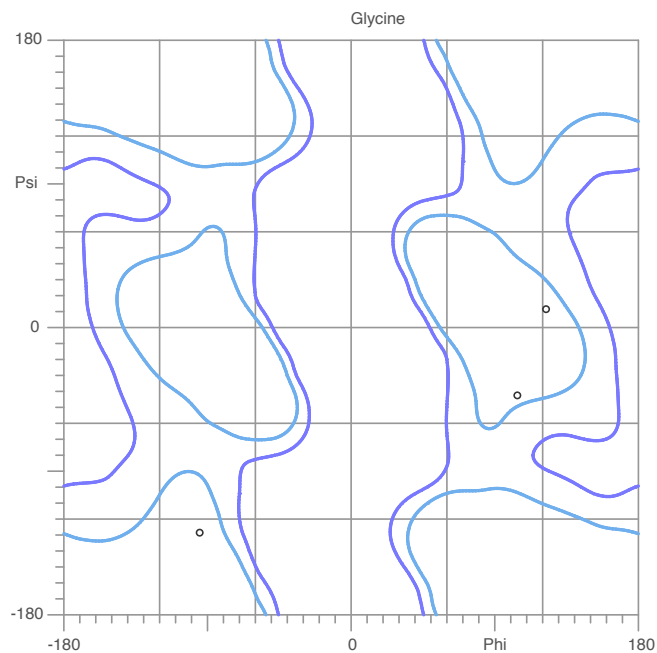
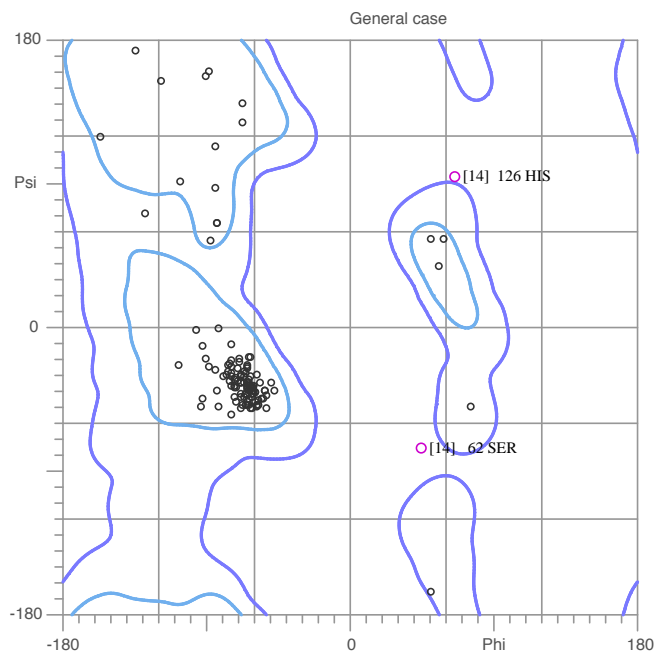
There were no outliers.

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

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 14



96.1% (122/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

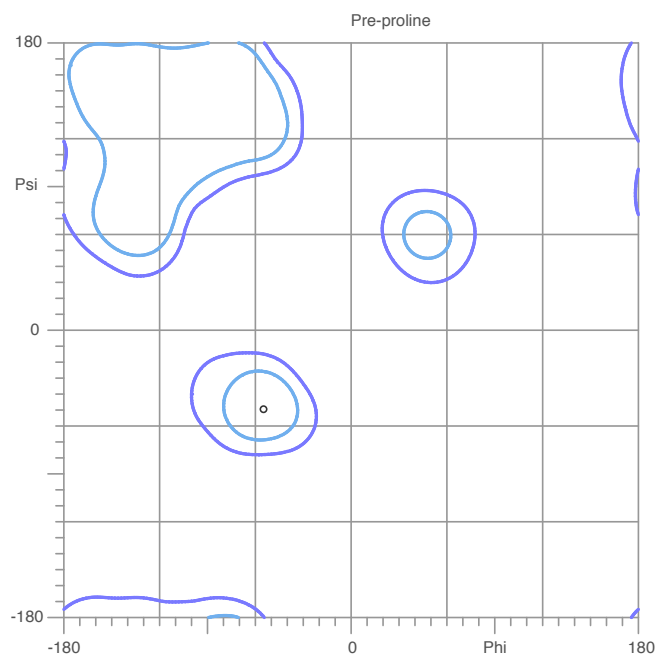
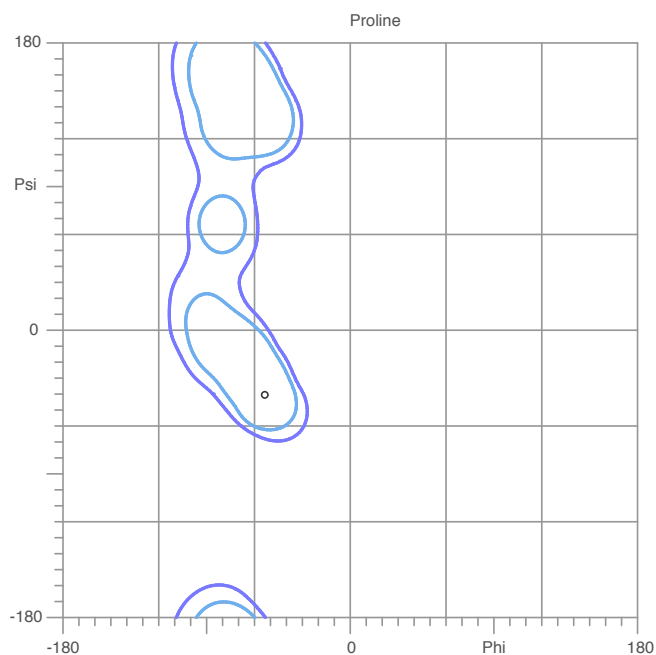
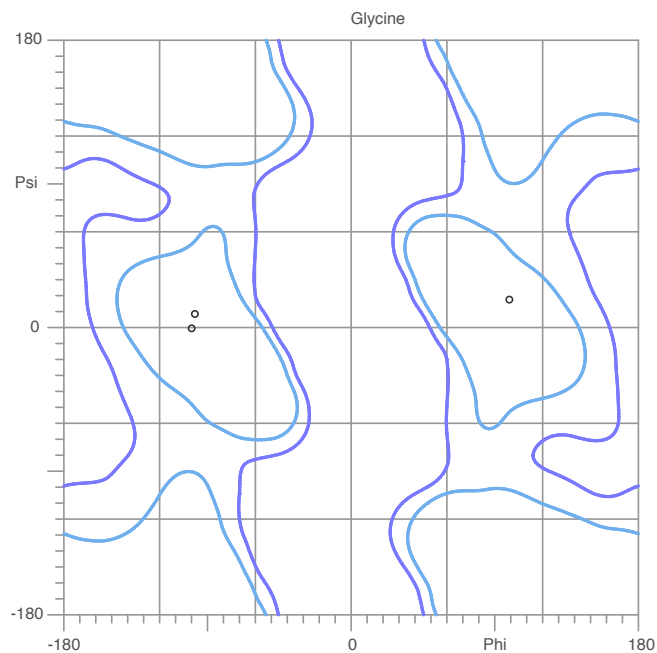
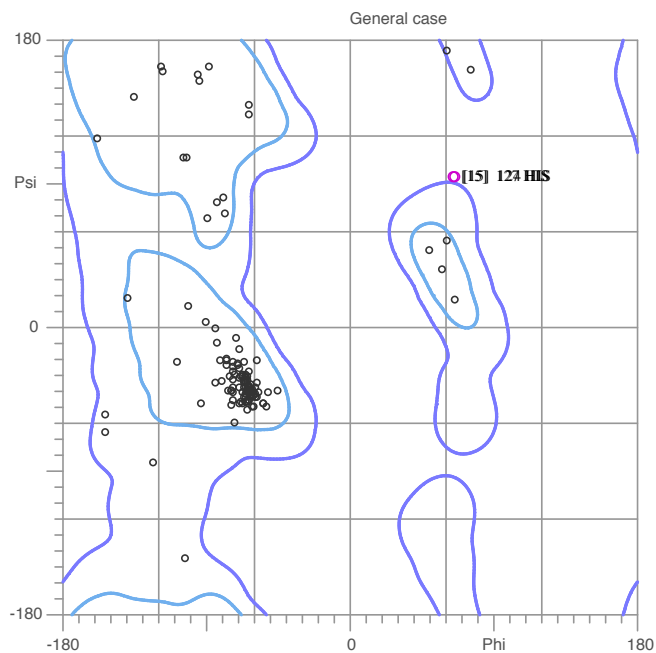
There were 2 outliers (phi, psi):

[14] 62 SER (45.0, -75.4)

[14] 126 HIS (65.1, 95.0)

MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 15



93.7% (119/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

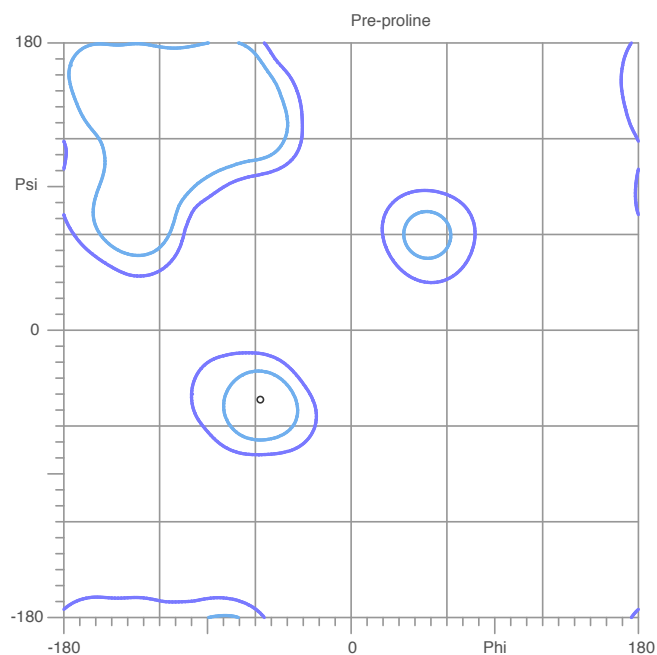
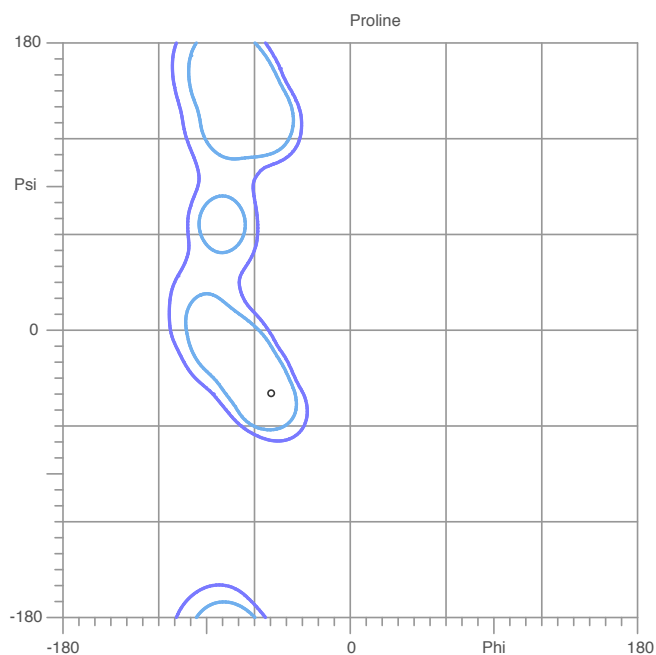
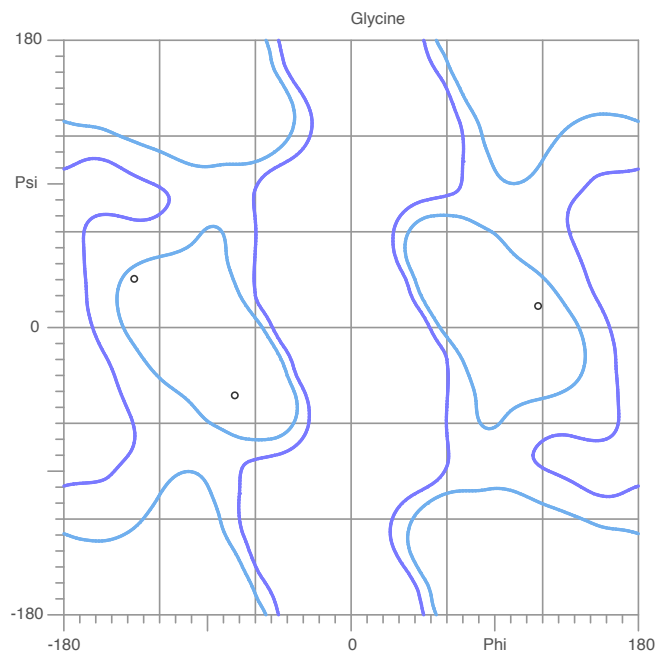
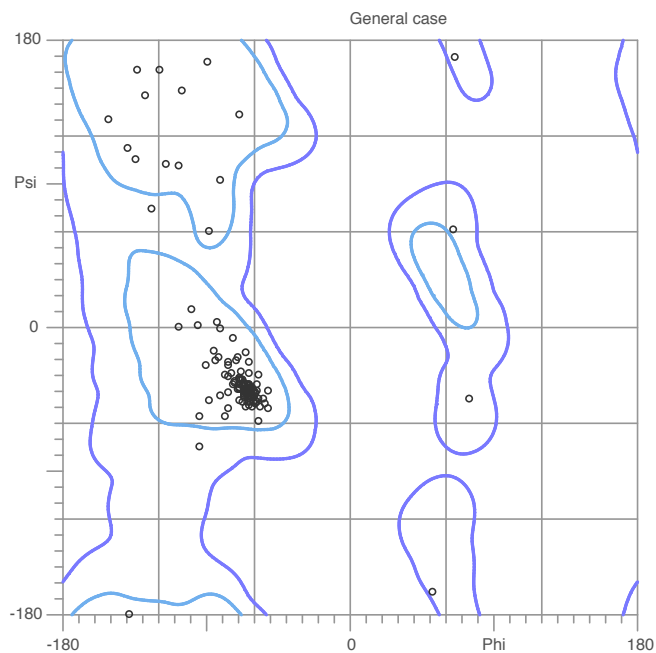
There were 2 outliers (phi, psi):

[15] 124 HIS (65.0, 95.0)

[15] 127 HIS (64.9, 95.0)

MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 16



95.3% (121/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

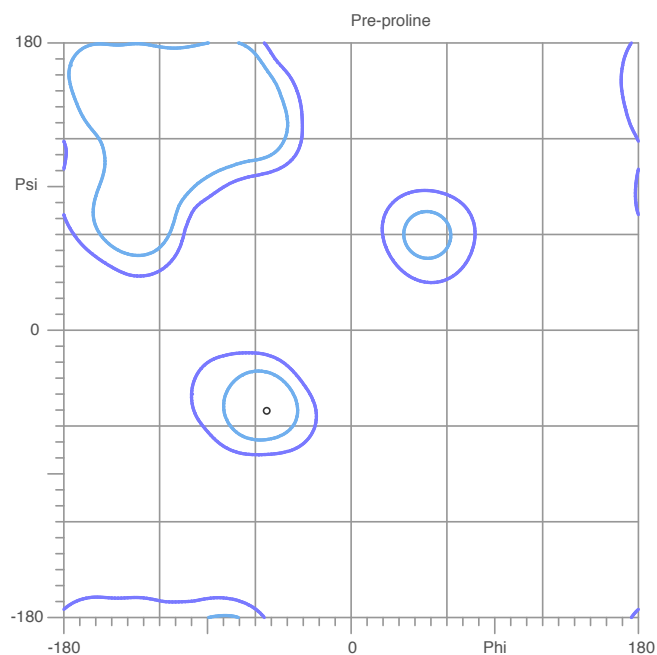
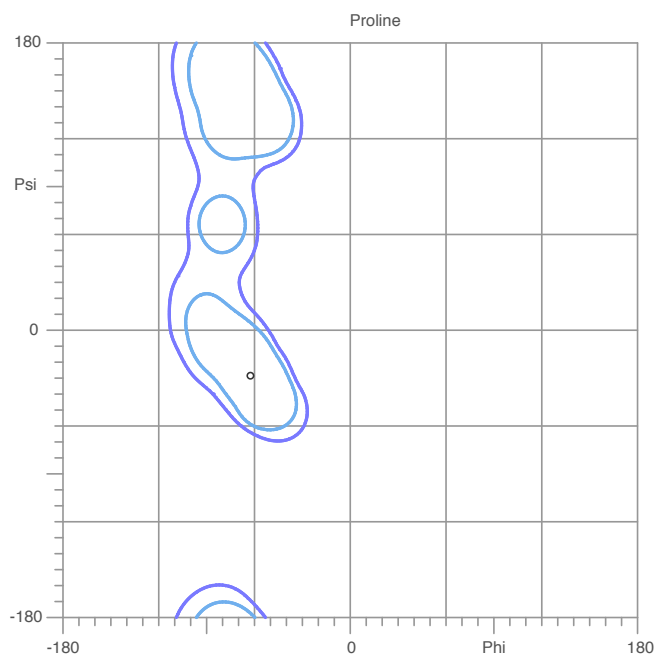
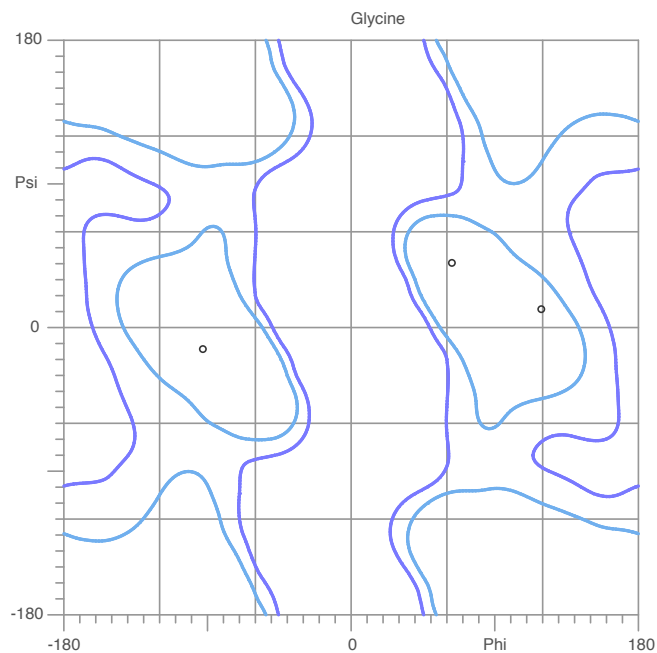
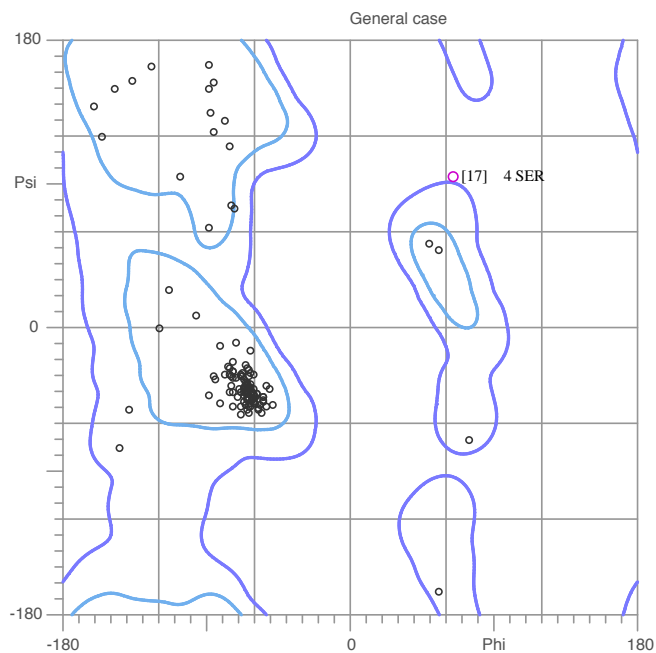
There were no outliers.

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

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 17



96.1% (122/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

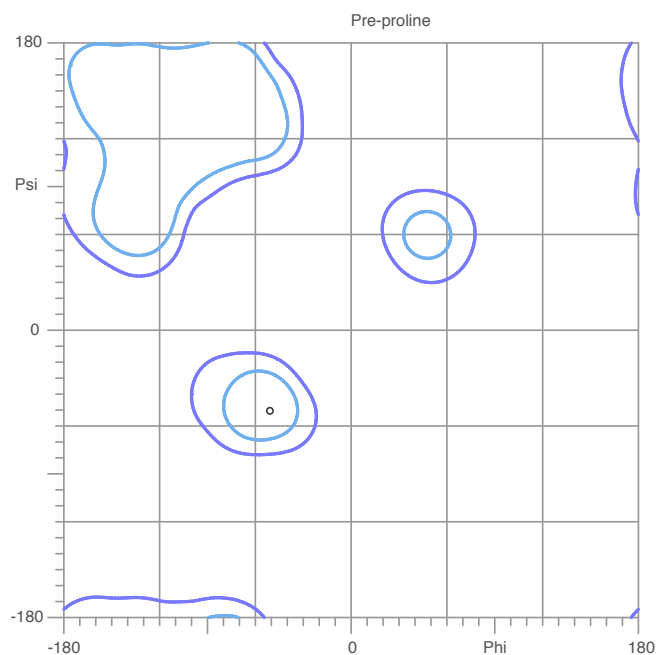
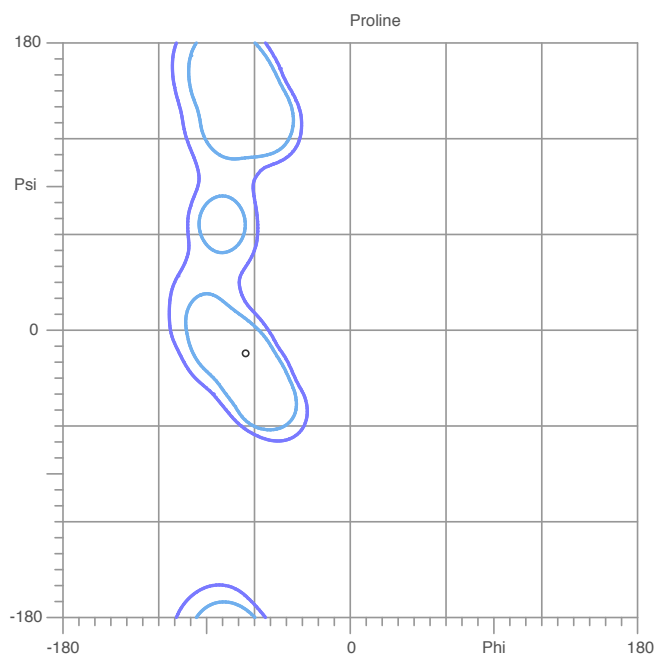
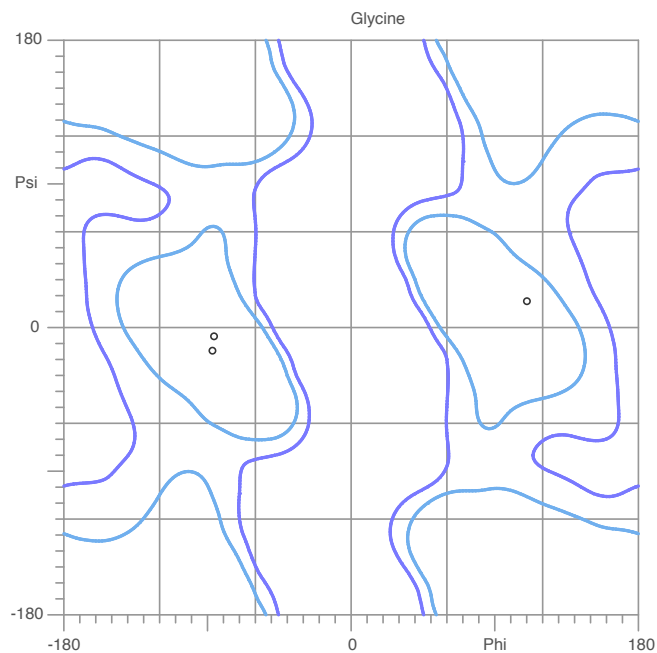
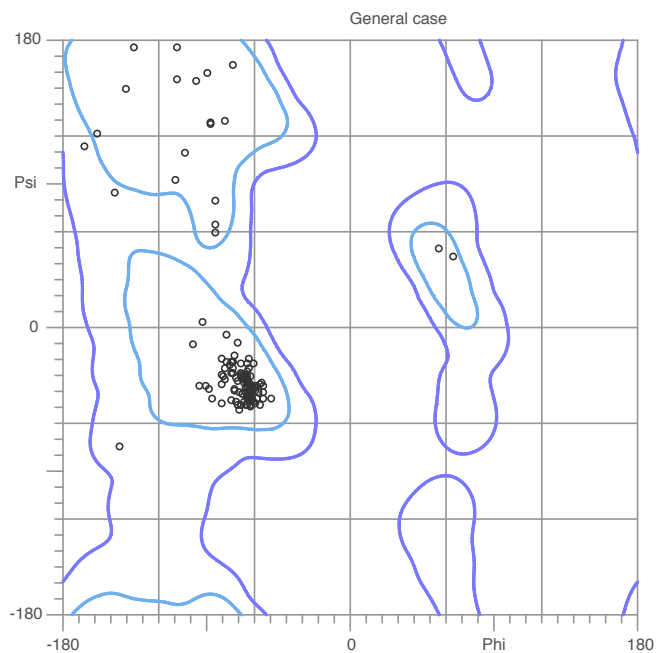
There were 1 outliers (phi, psi):
[17] 4 SER (64.9, 95.0)

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 18



97.6% (124/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

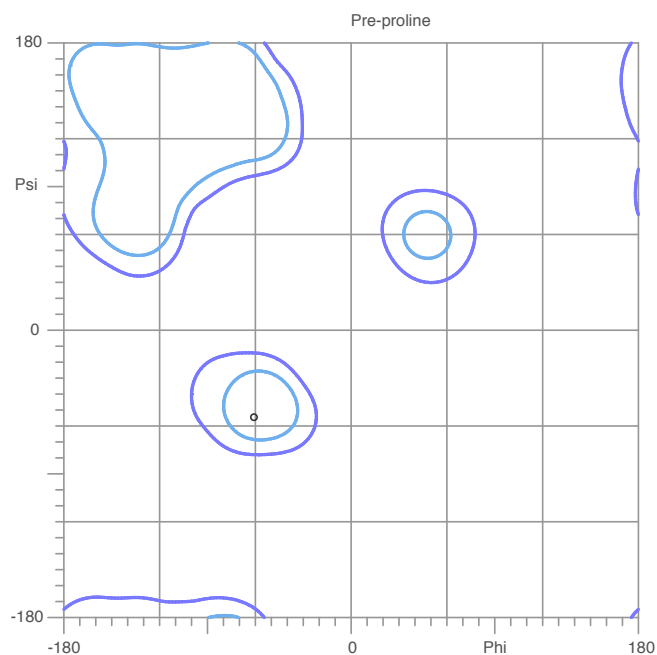
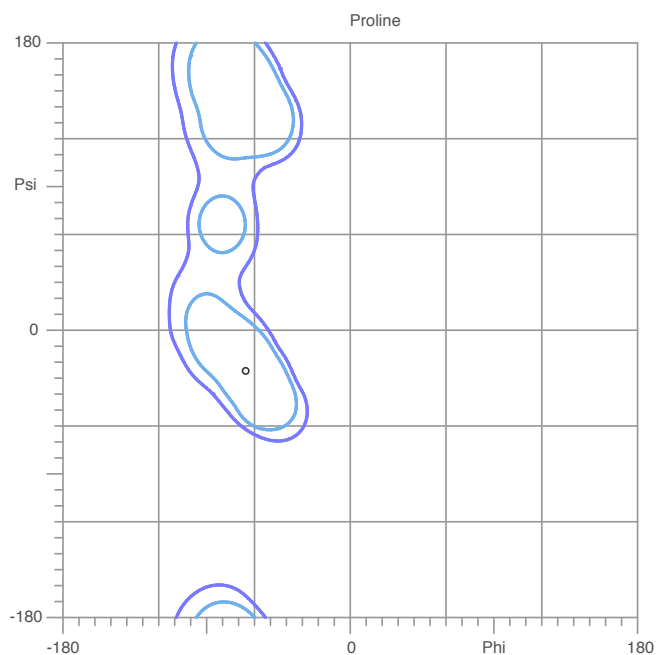
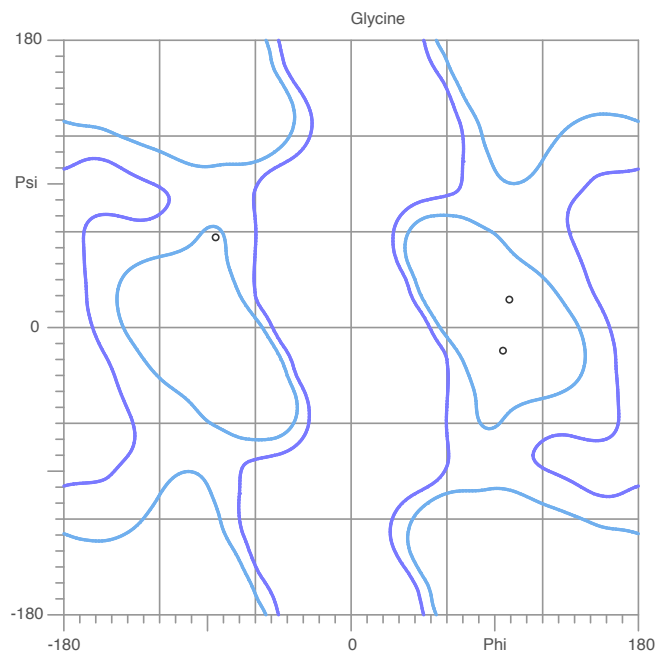
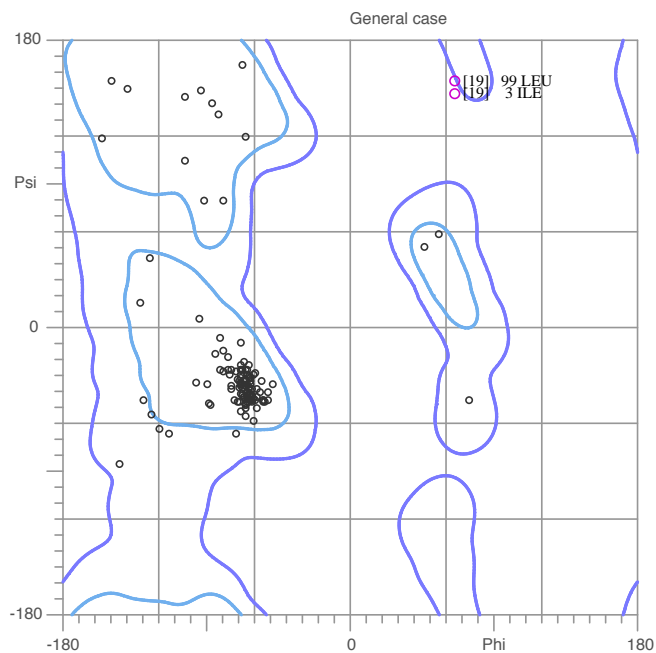
There were no outliers.

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MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 19



92.9% (118/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

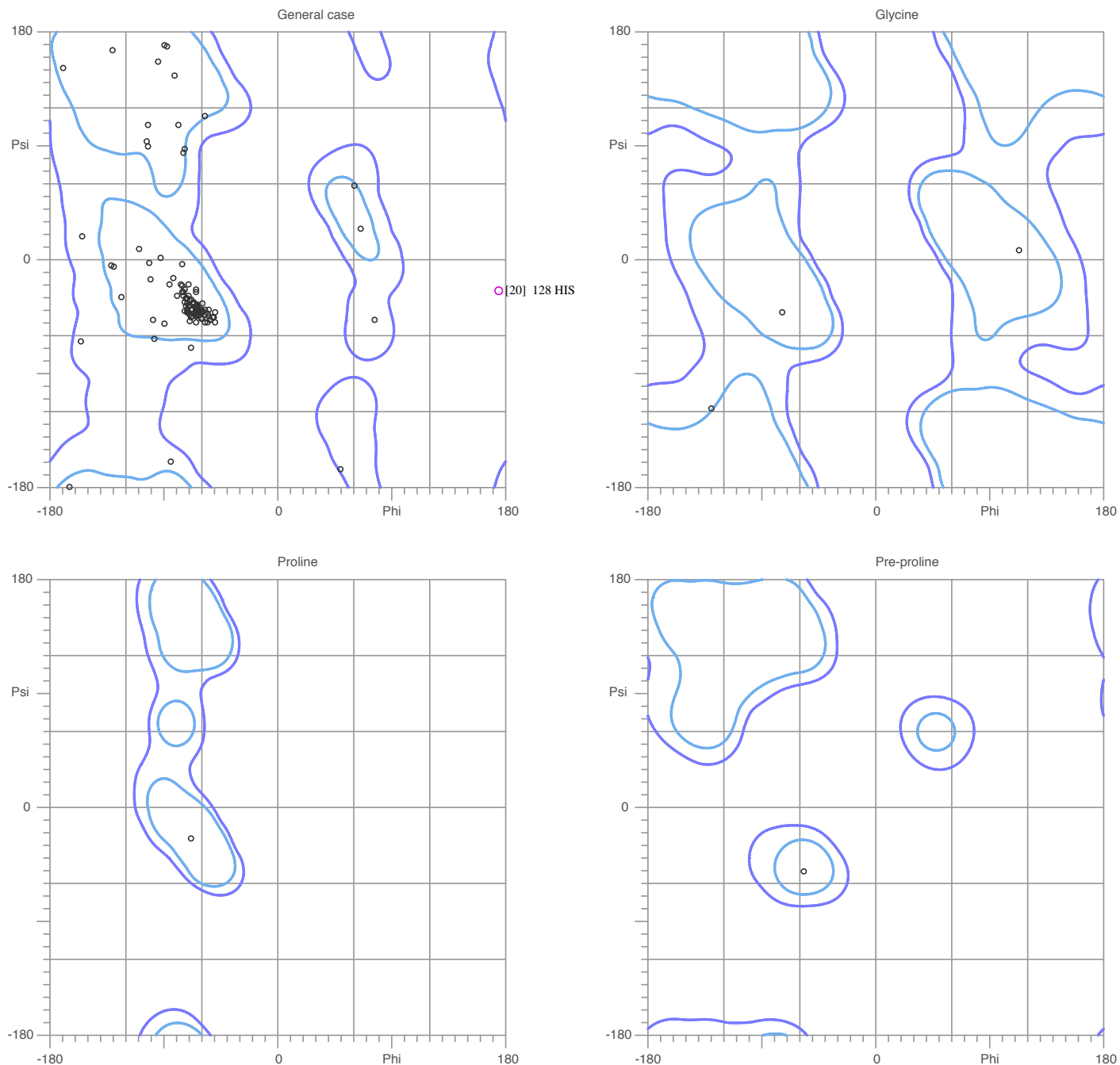
There were 2 outliers (phi, psi):

[19] 3 ILE (65.1, 147.2)

[19] 99 LEU (65.4, 155.0)

MolProbity Ramachandran analysis

SSR10_R3_em_bcr3.pdb, model 20



92.9% (118/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 128 HIS (175.0, -24.9)

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

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