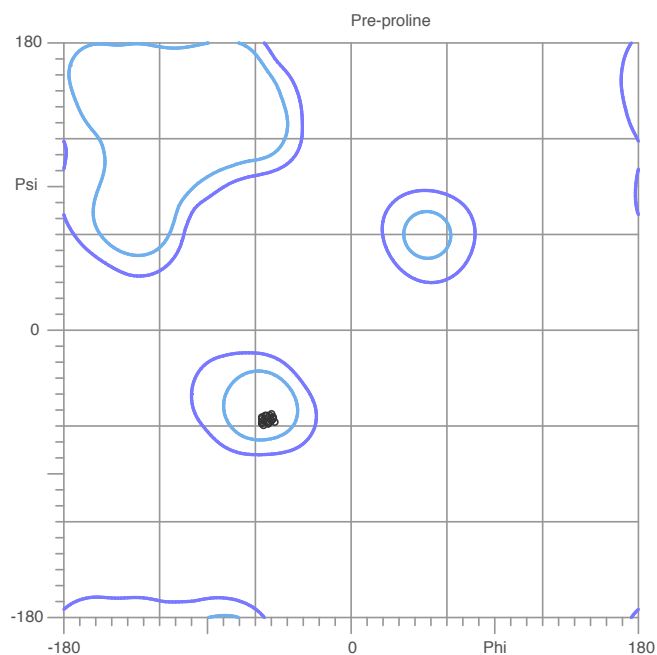
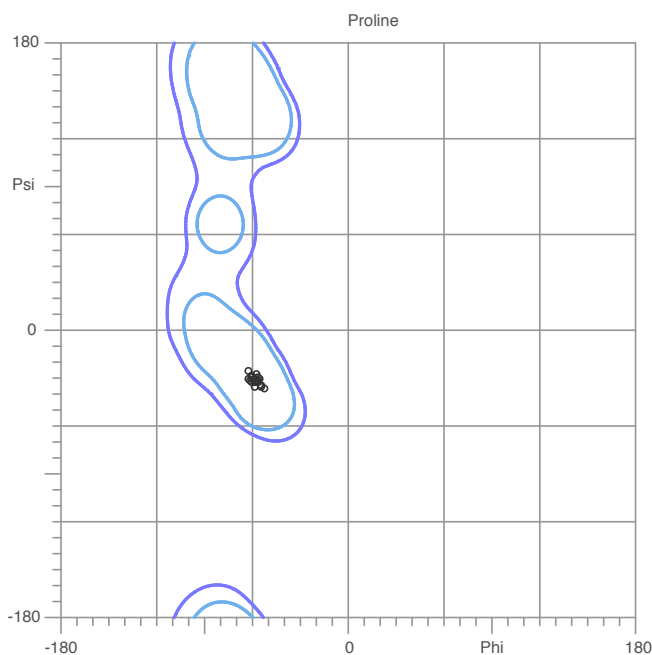
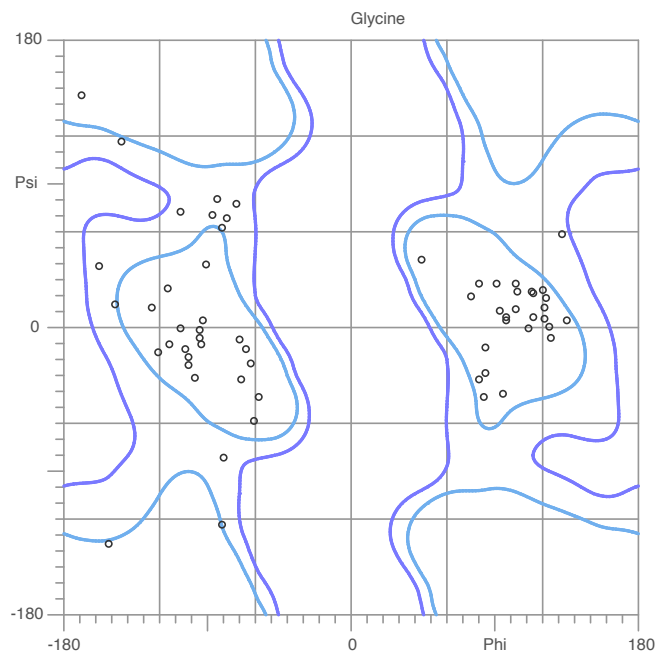
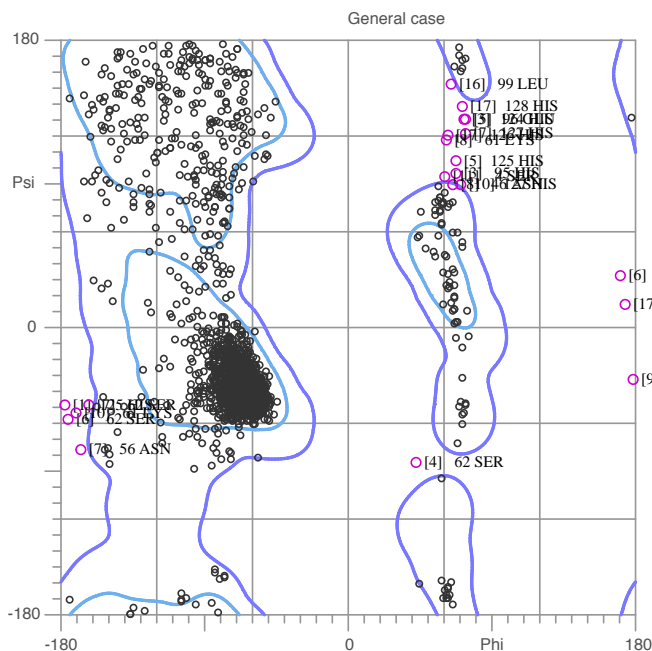


MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, all models



92.4% (2347/2540) of all residues were in favored (98%) regions.
99.2% (2519/2540) of all residues were in allowed (>99.8%) regions.

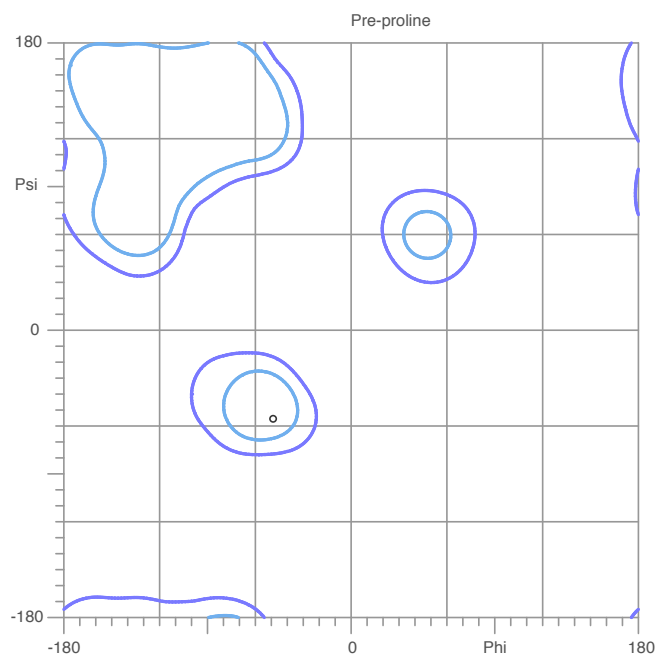
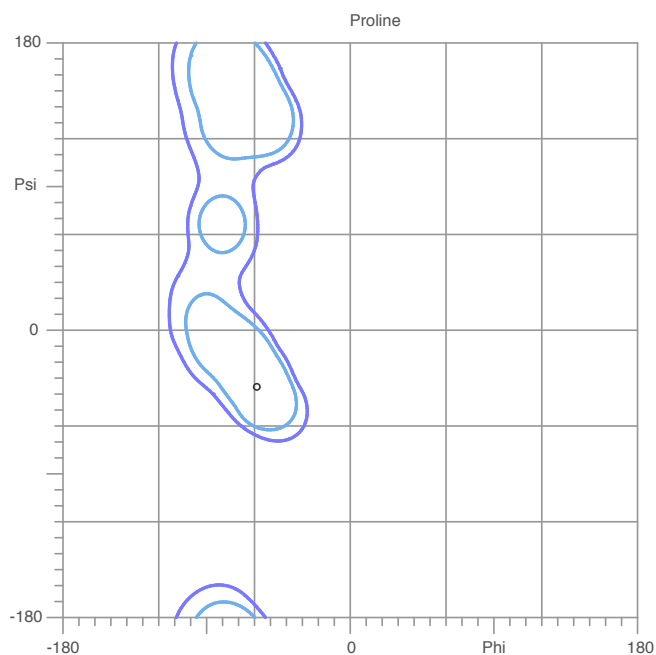
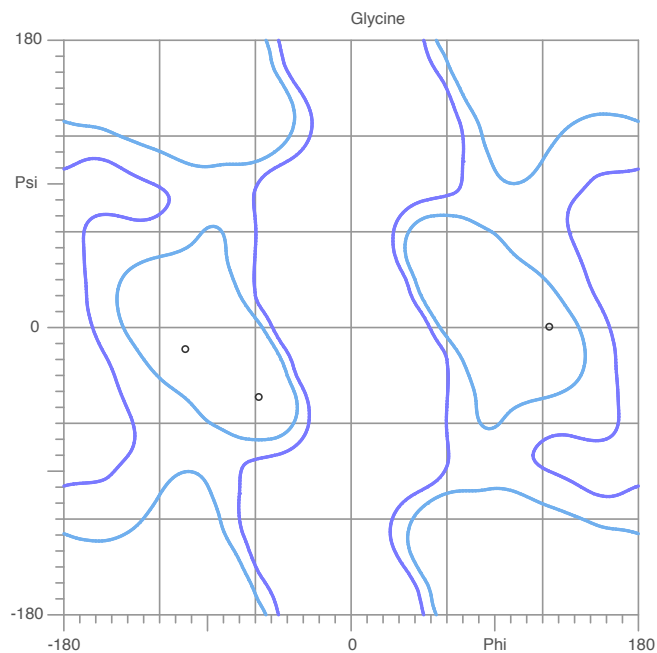
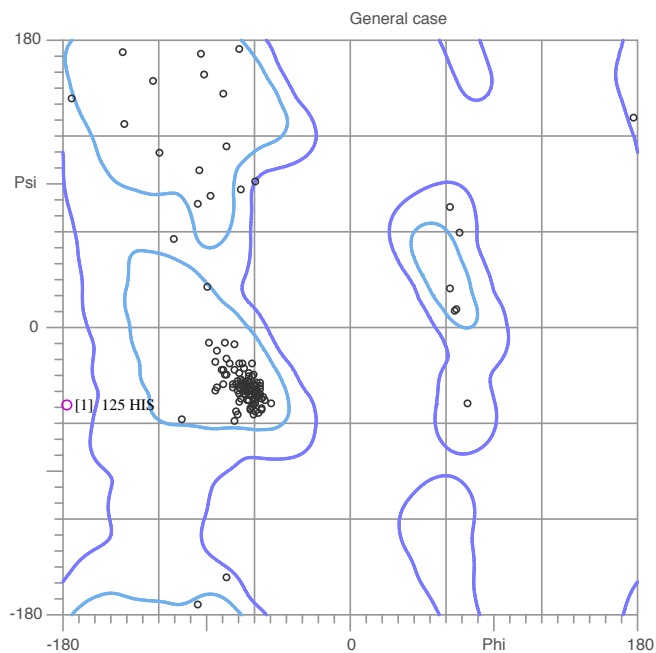
There were 21 outliers (phi, psi):

- [1] 125 HIS (-179.0, -48.4)
- [3] 95 HIS (68.0, 97.1)
- [3] 96 GLU (72.3, 131.5)
- [4] 62 SER (42.0, -84.9)
- [5] 124 HIS (73.1, 131.6)
- [5] 125 HIS (67.9, 105.6)
- [6] 46 ASN (170.7, 33.4)
- [6] 62 SER (-176.9, -57.6)

- [7] 56 ASN (-168.6, -76.4)
- [7] 62 SER (-163.1, -48.7)
- [7] 127 HIS (73.4, 122.6)
- [8] 46 ASN (65.1, 90.9)
- [8] 61 LYS (61.6, 118.3)
- [9] 128 HIS (179.0, -32.3)
- [10] 61 LYS (-171.7, -53.2)
- [10] 127 HIS (70.4, 90.0)
- [11] 4 SER (60.2, 95.5)
- [16] 99 LEU (64.9, 153.4)
- [17] 46 ASN (173.5, 15.3)
- [17] 126 HIS (62.9, 122.0)
- [17] 128 HIS (71.3, 139.7)

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 1

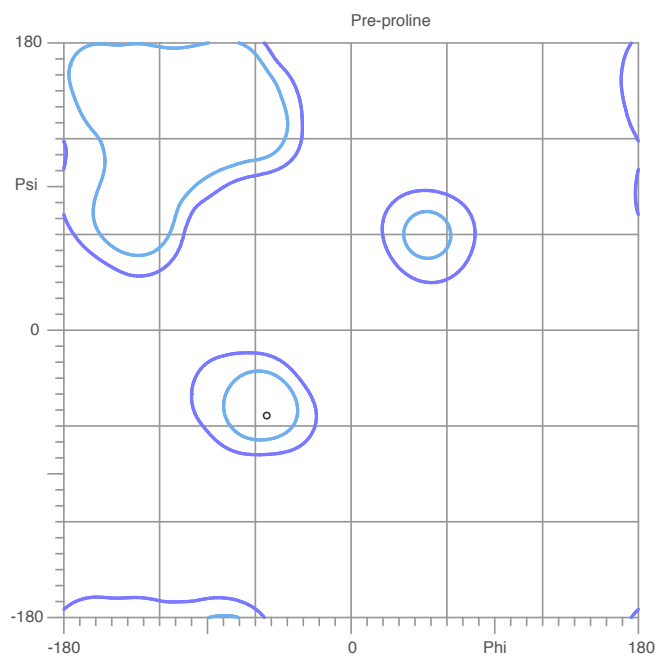
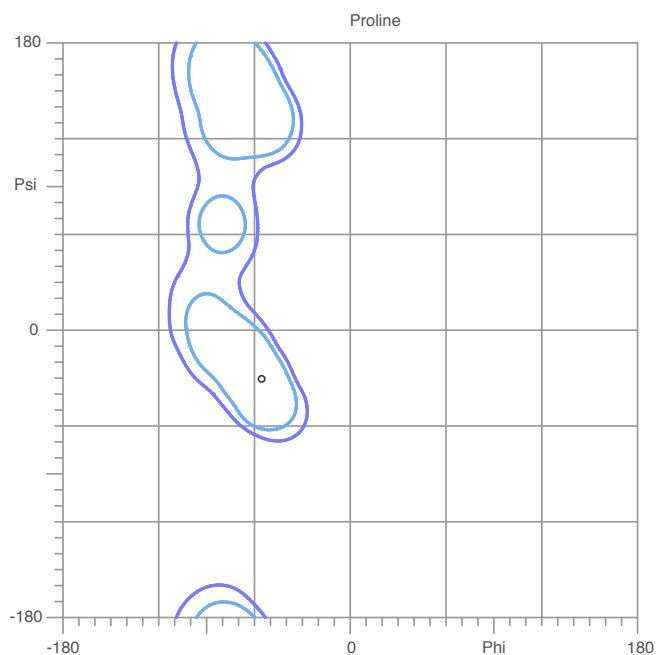
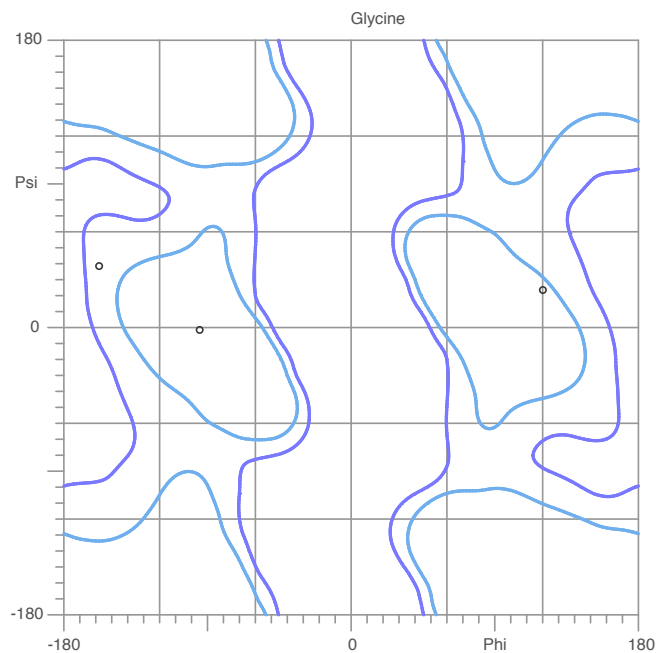
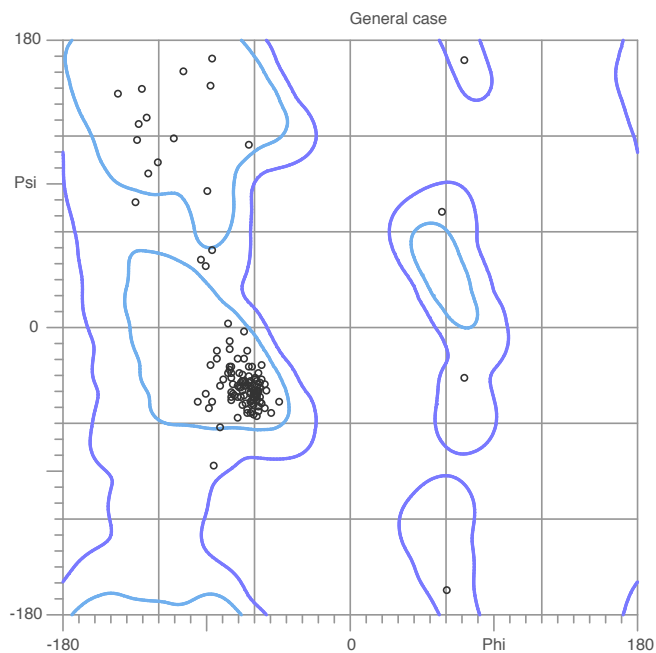


92.1% (117/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[1] 125 HIS (-179.0, -48.4)

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 2



92.1% (117/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

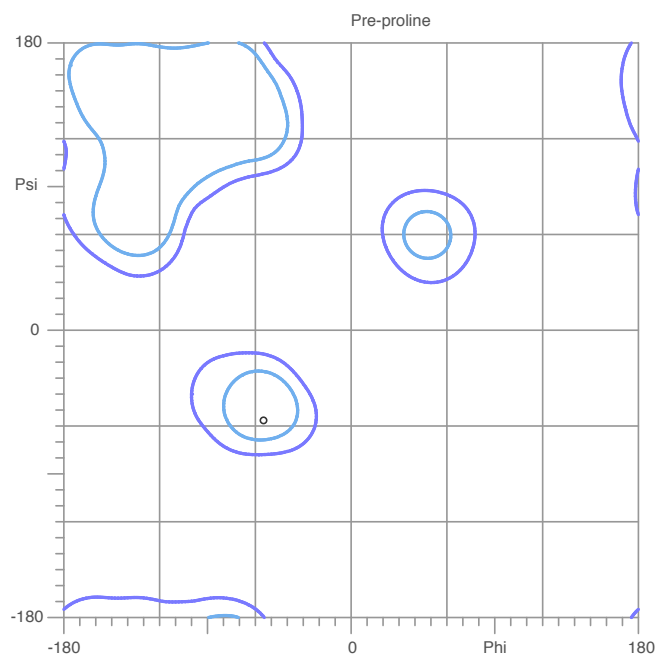
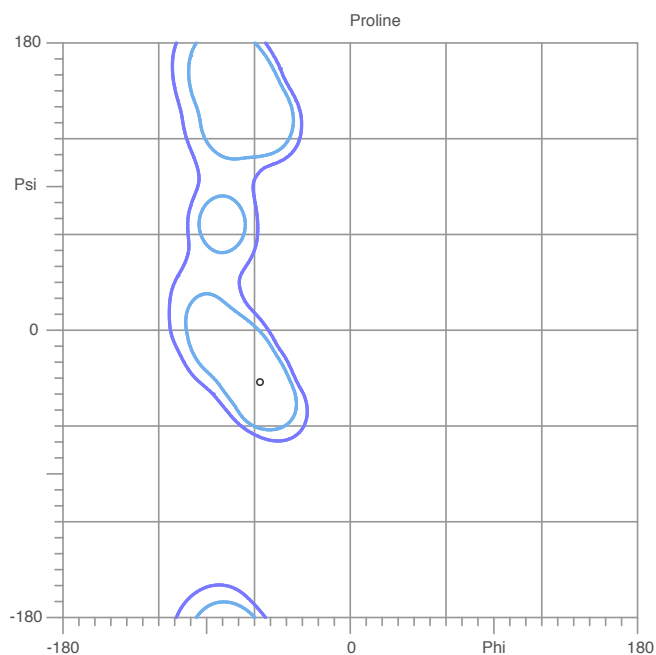
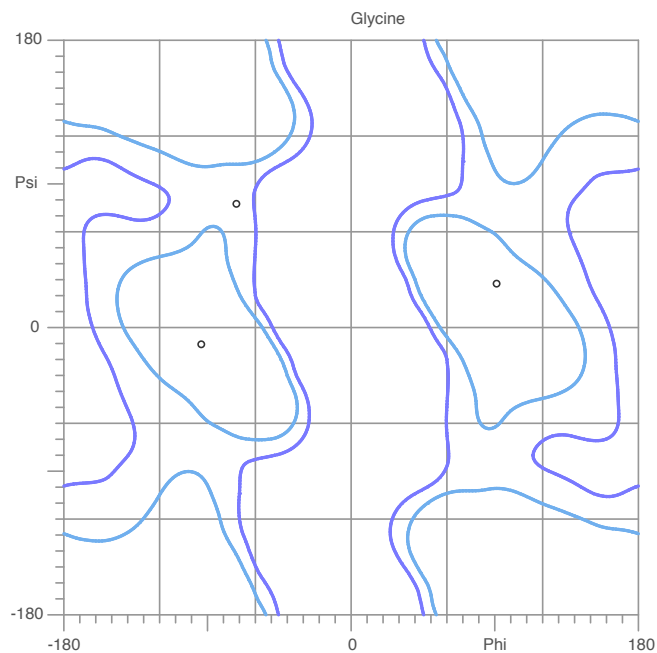
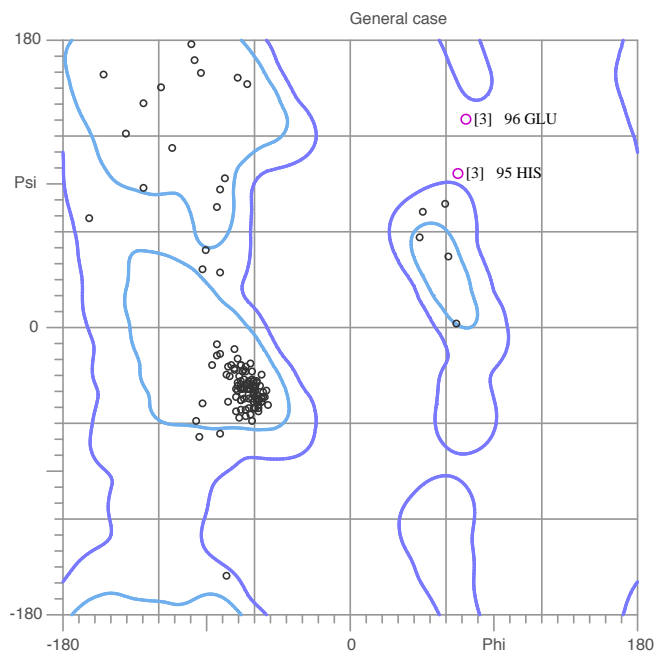
There were no outliers.

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MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 3



90.6% (115/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

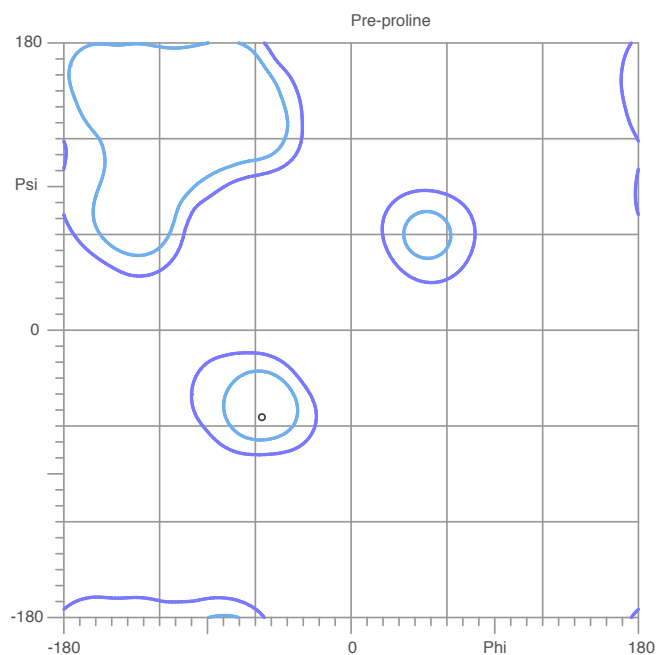
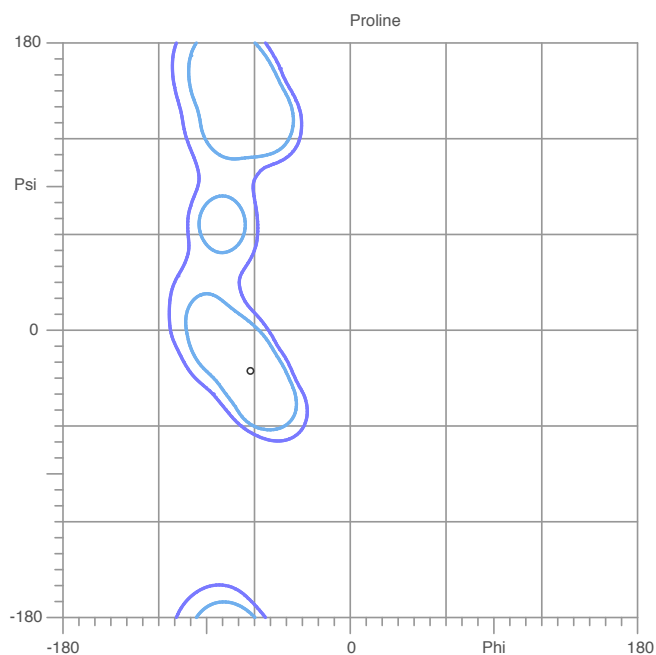
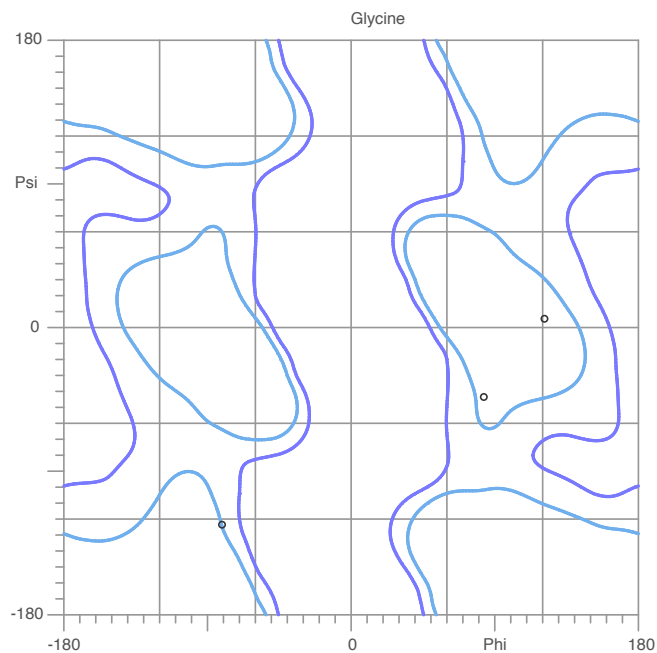
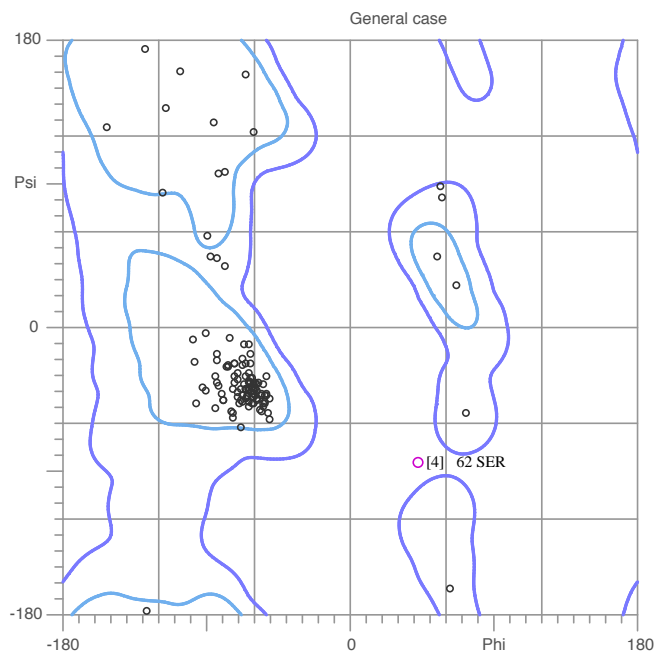
There were 2 outliers (phi, psi):

[3] 95 HIS (68.0, 97.1)

[3] 96 GLU (72.3, 131.5)

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 4

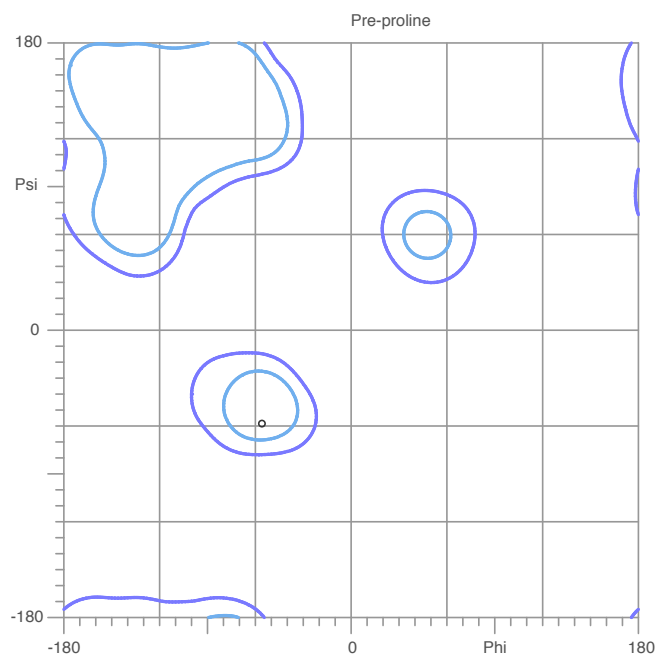
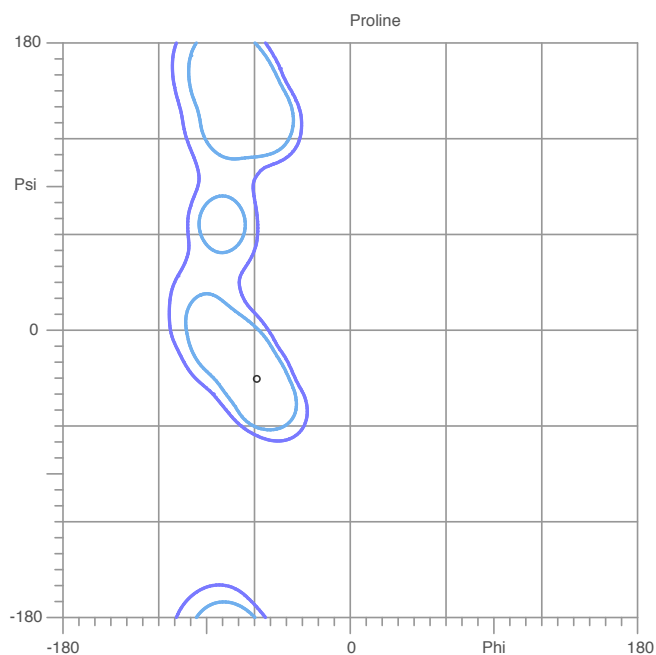
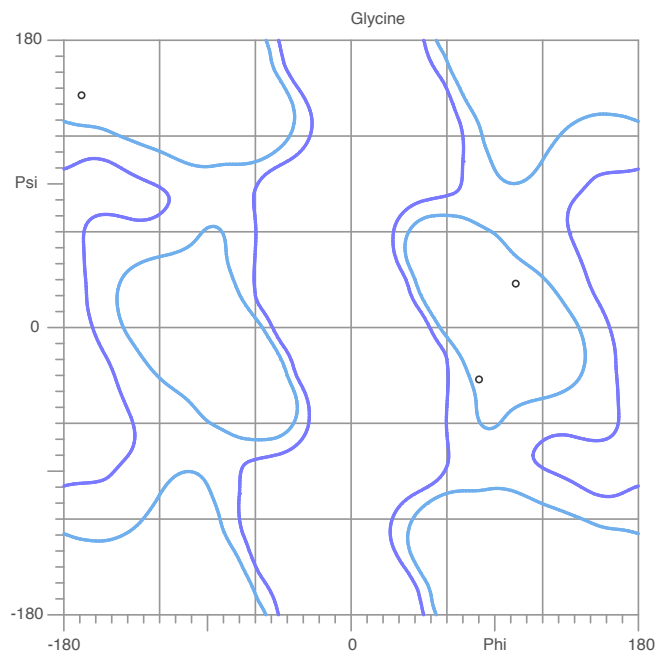
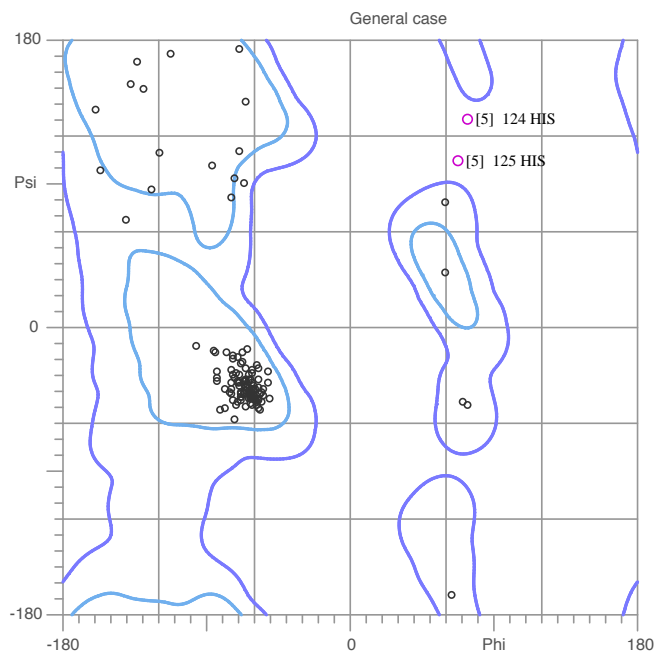


93.7% (119/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[4] 62 SER (42.0, -84.9)

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 5



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.

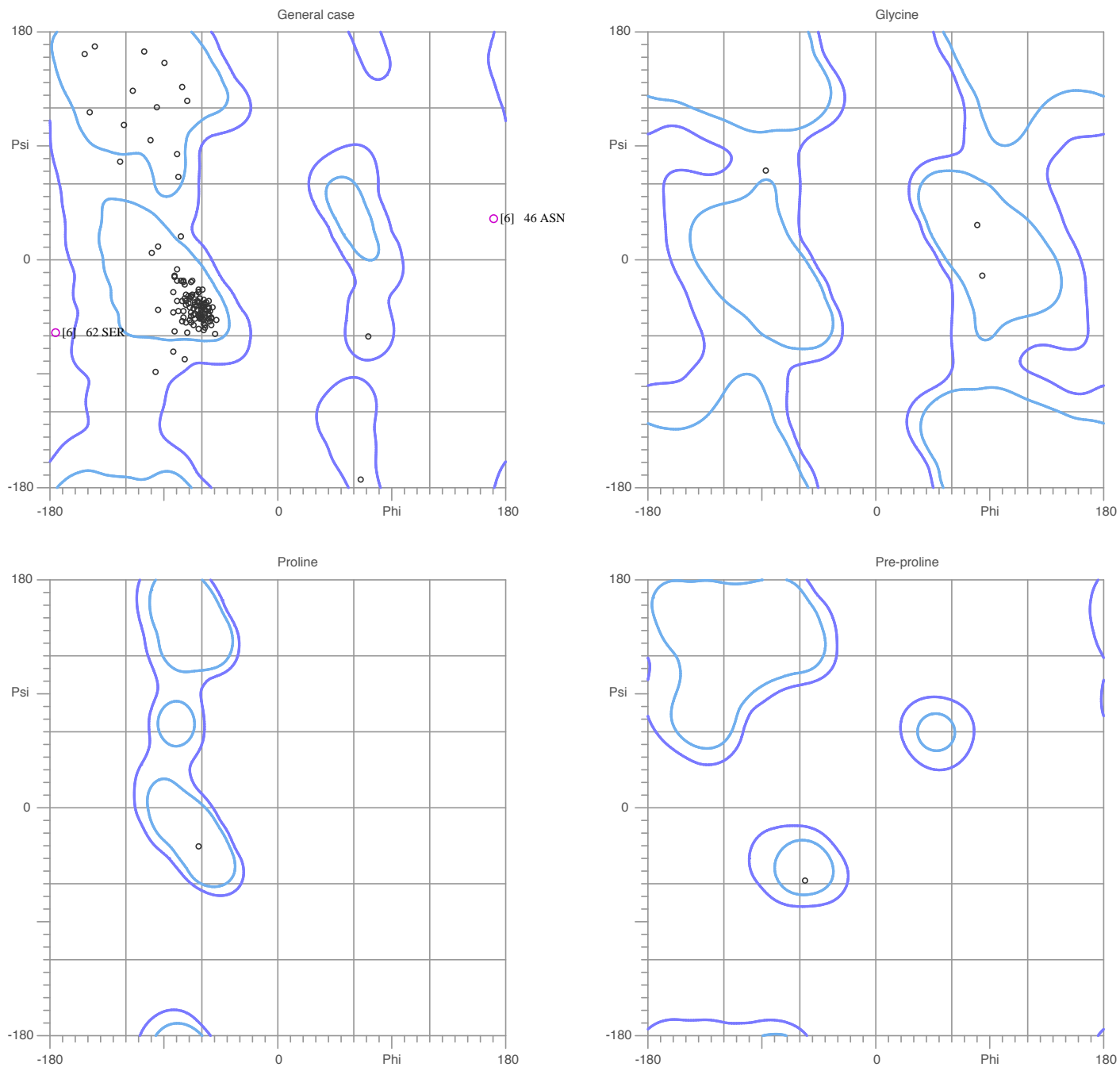
There were 2 outliers (phi, psi):

[5] 124 HIS (73.1, 131.6)

[5] 125 HIS (67.9, 105.6)

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 6



92.1% (117/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

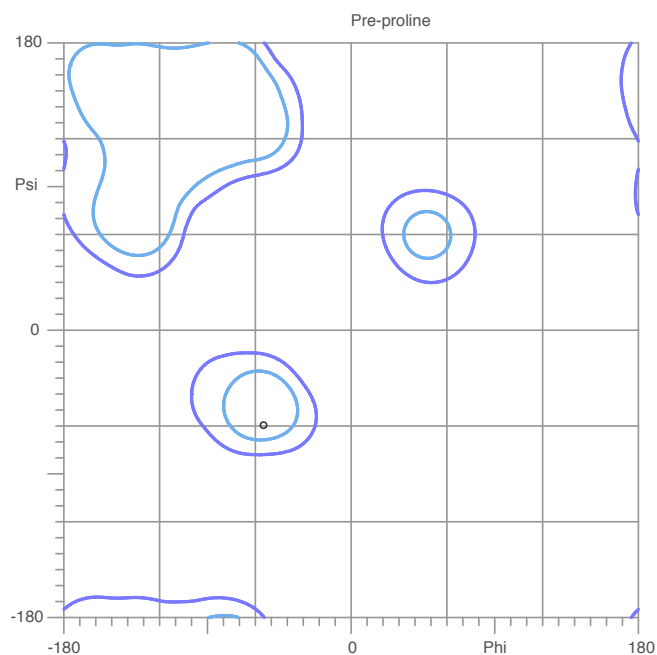
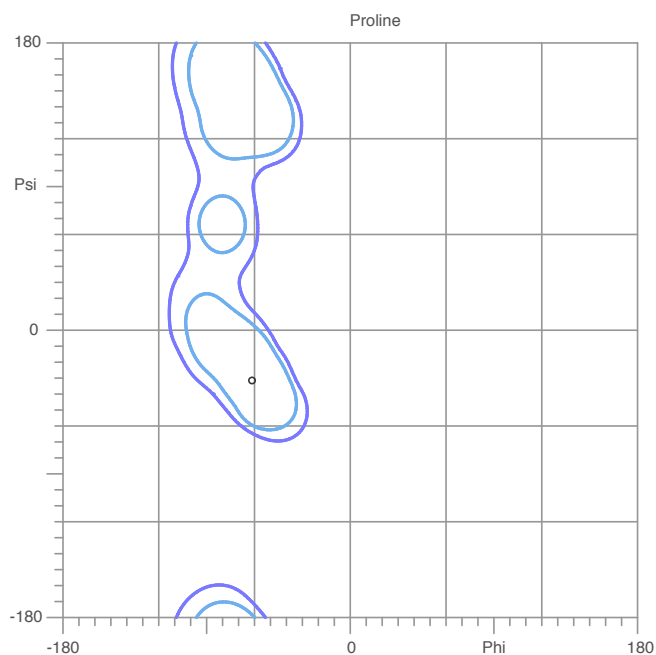
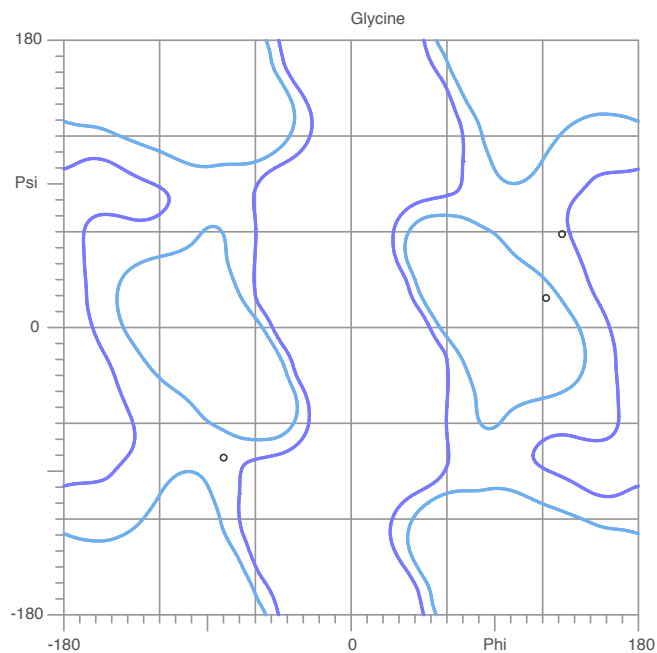
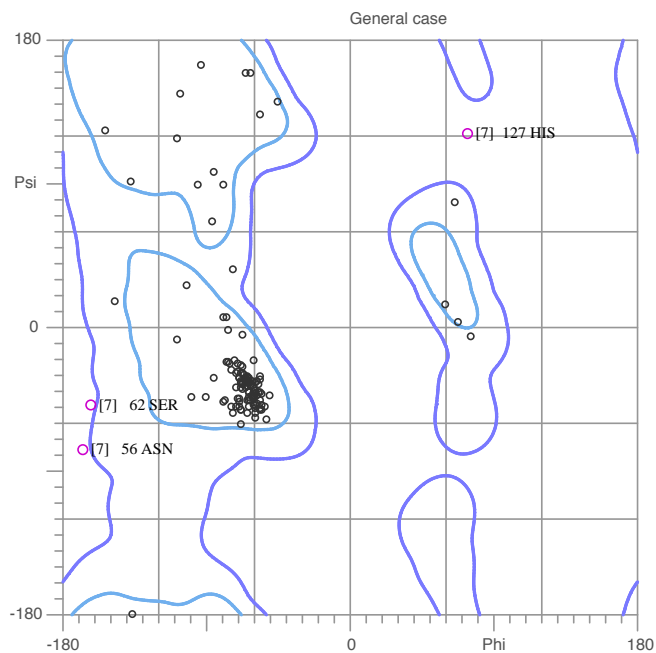
There were 2 outliers (phi, psi):

[6] 46 ASN (170.7, 33.4)

[6] 62 SER (-176.9, -57.6)

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 7



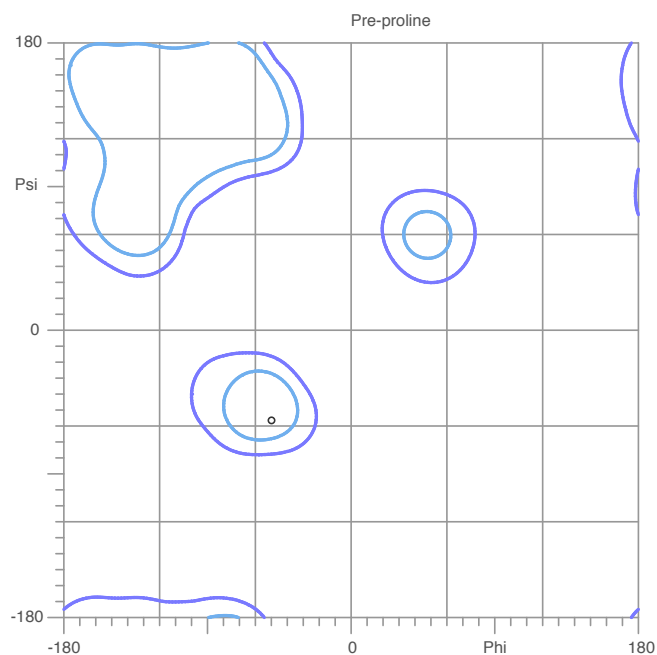
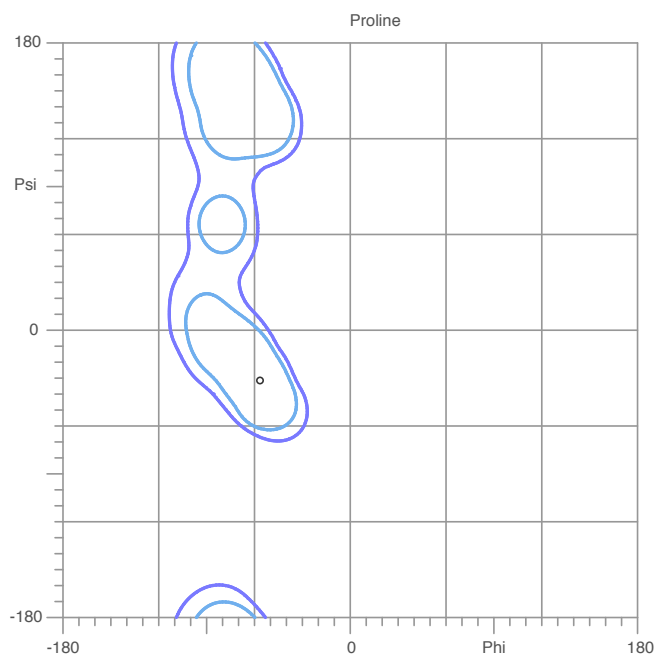
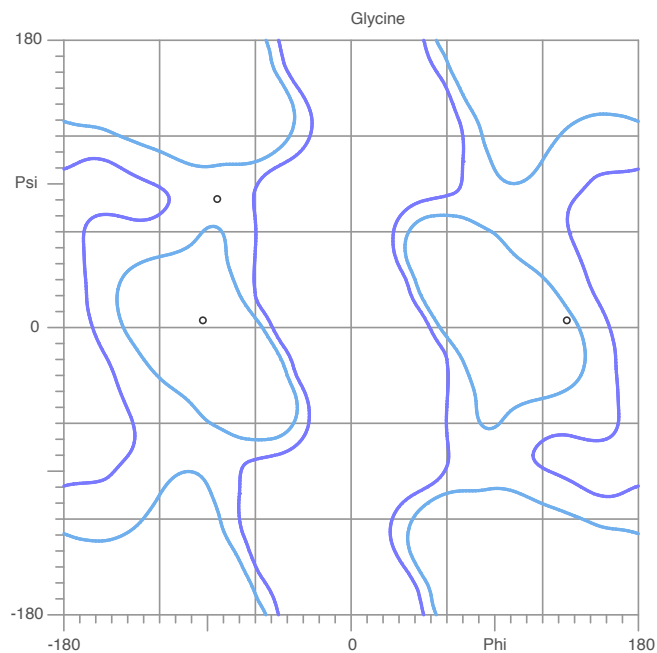
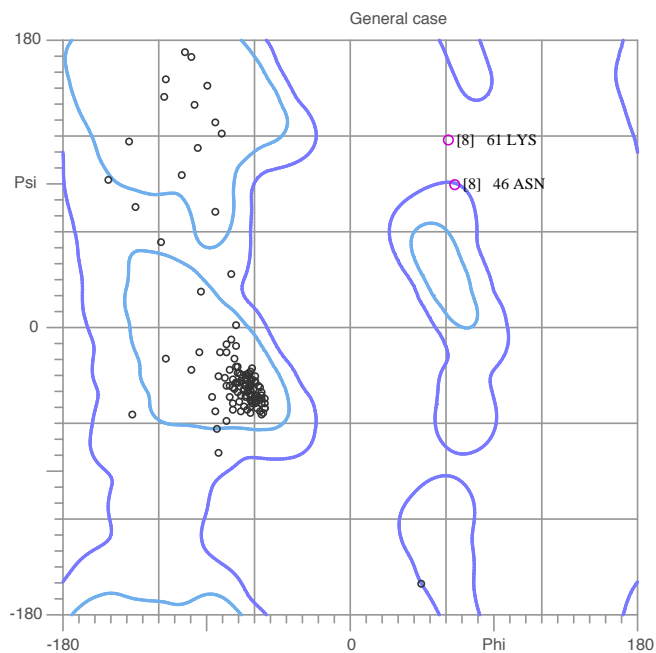
92.9% (118/127) of all residues were in favored (98%) regions.
97.6% (124/127) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [7] 56 ASN (-168.6, -76.4)
- [7] 62 SER (-163.1, -48.7)
- [7] 127 HIS (73.4, 122.6)

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 8



92.1% (117/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

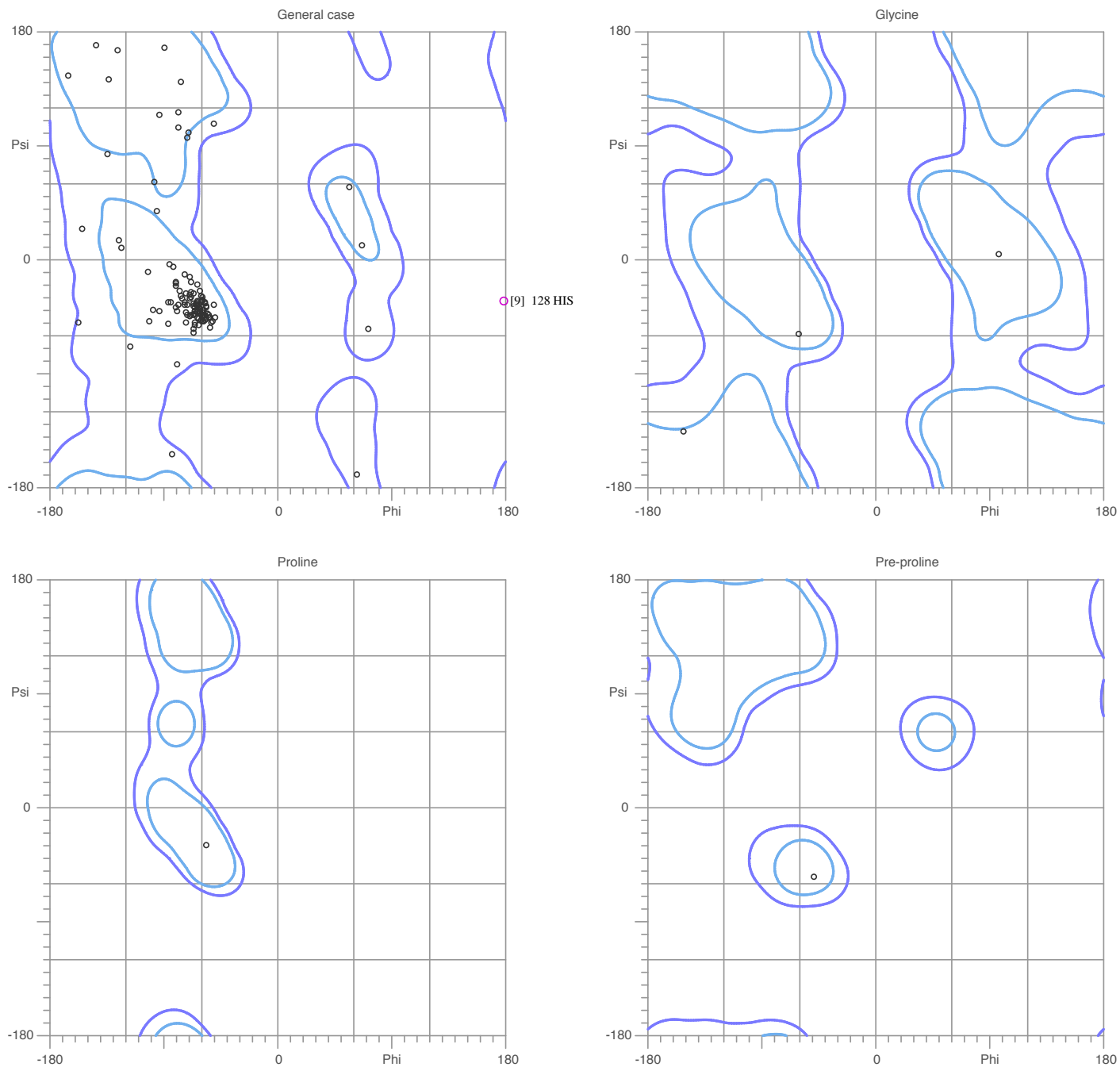
There were 2 outliers (phi, psi):

[8] 46 ASN (65.1, 90.9)

[8] 61 LYS (61.6, 118.3)

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 9



90.6% (115/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

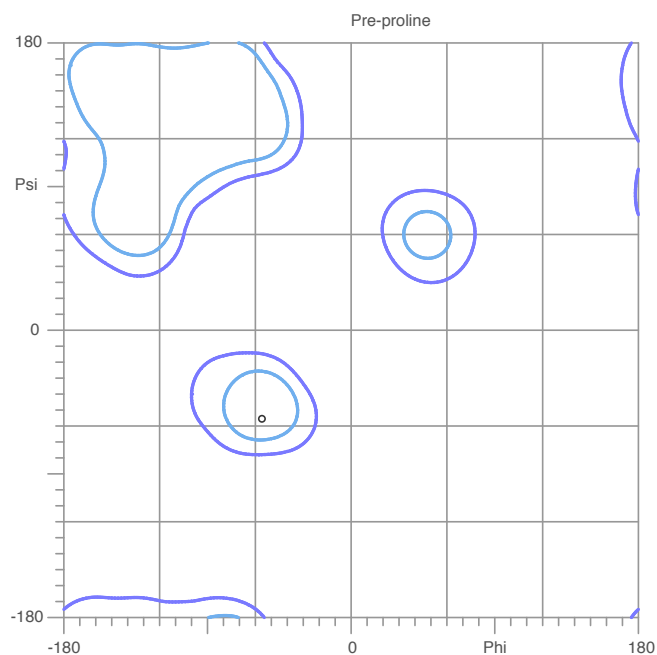
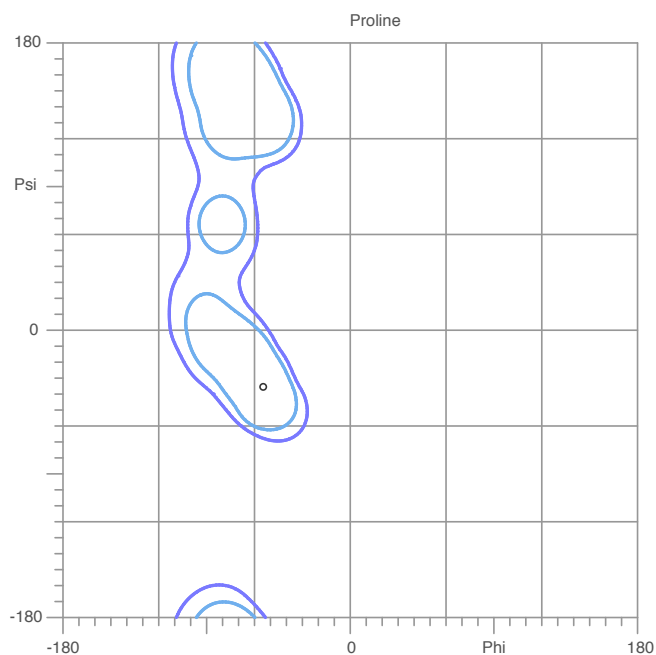
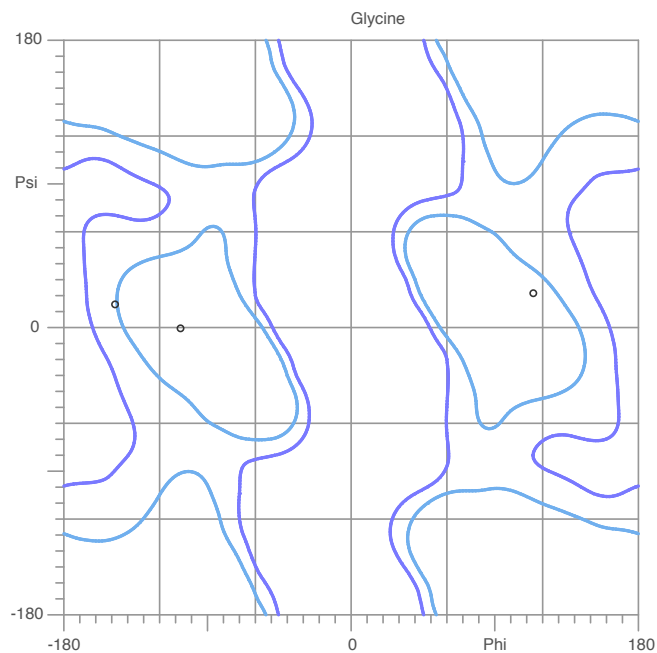
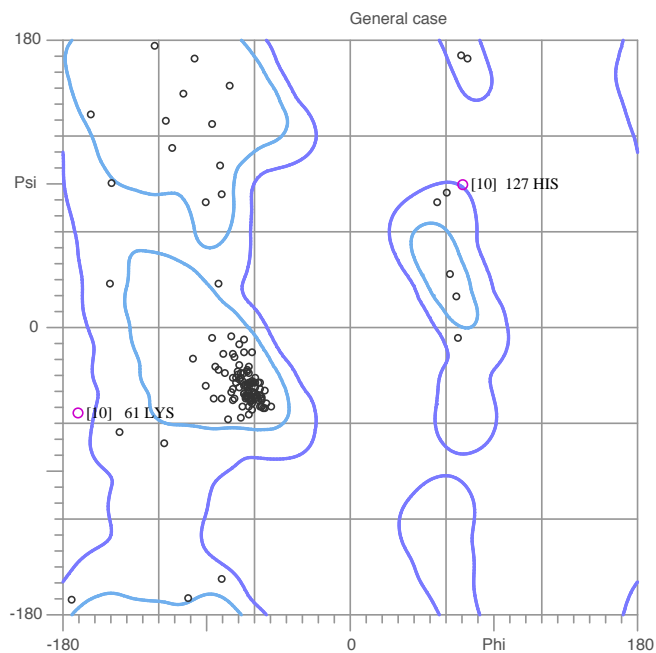
There were 1 outliers (phi, psi):
[9] 128 HIS (179.0, -32.3)

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MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 10

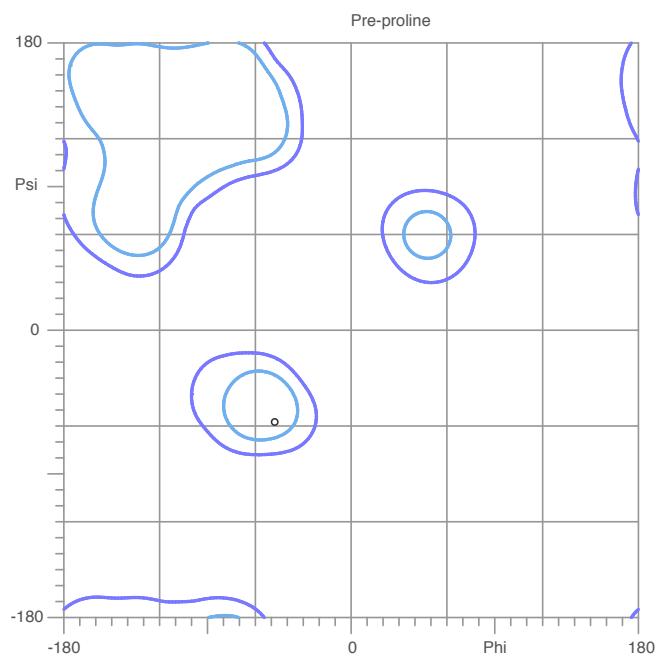
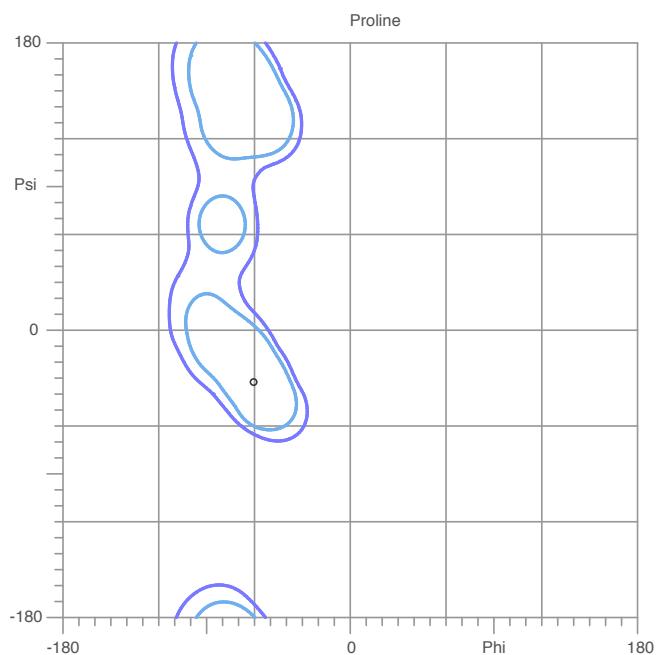
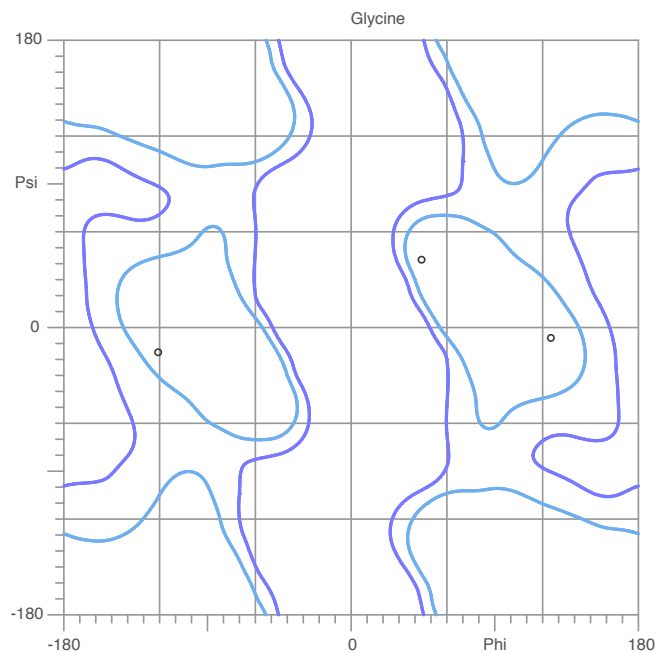
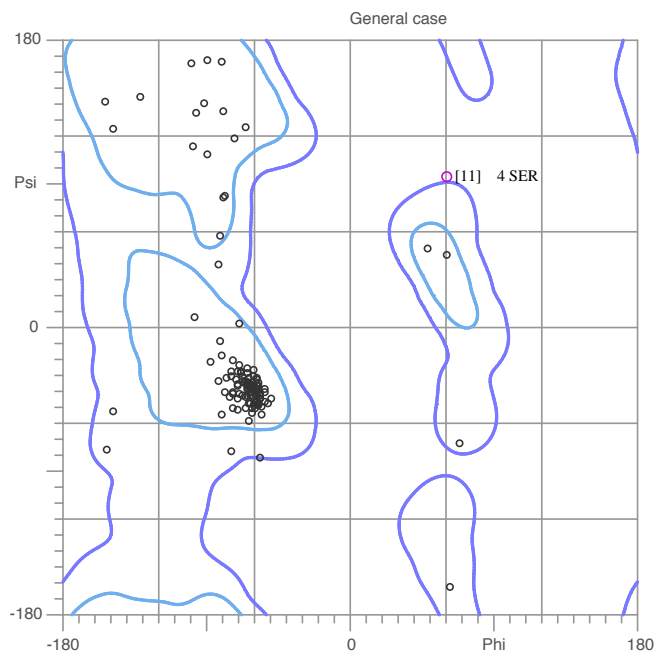


87.4% (111/127) of all residues were in favored (98%) regions.
98.4% (125/127) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[10] 61 LYS (-171.7, -53.2)
[10] 127 HIS (70.4, 90.0)

MolProbity Ramachandran analysis

SSR10_NMR_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.

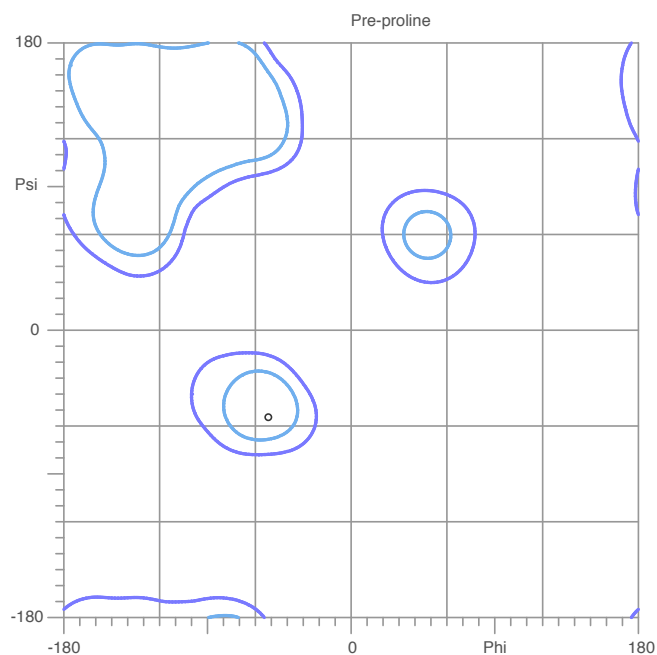
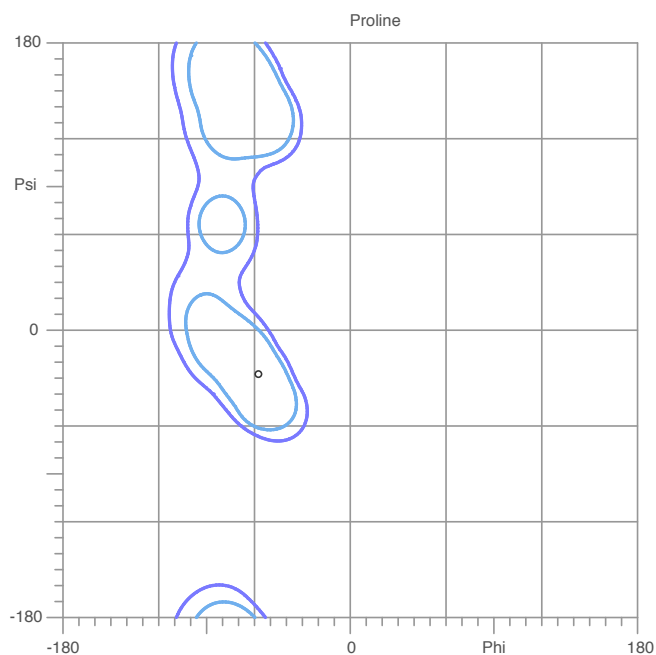
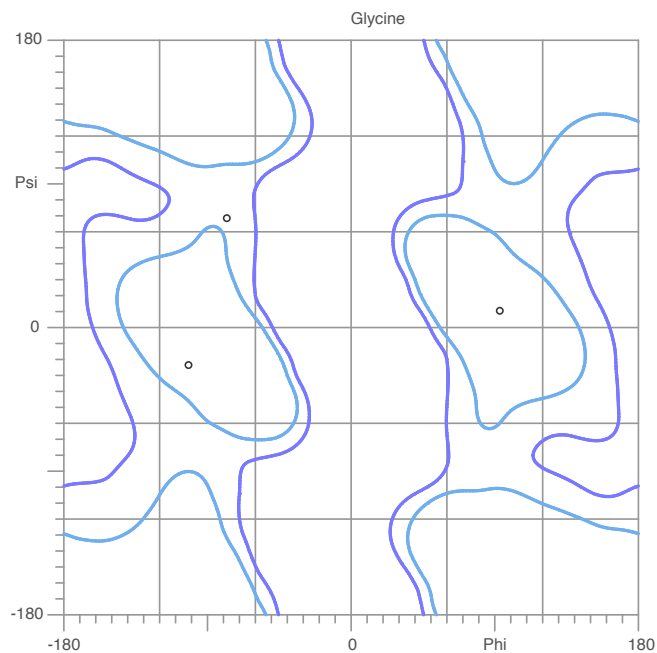
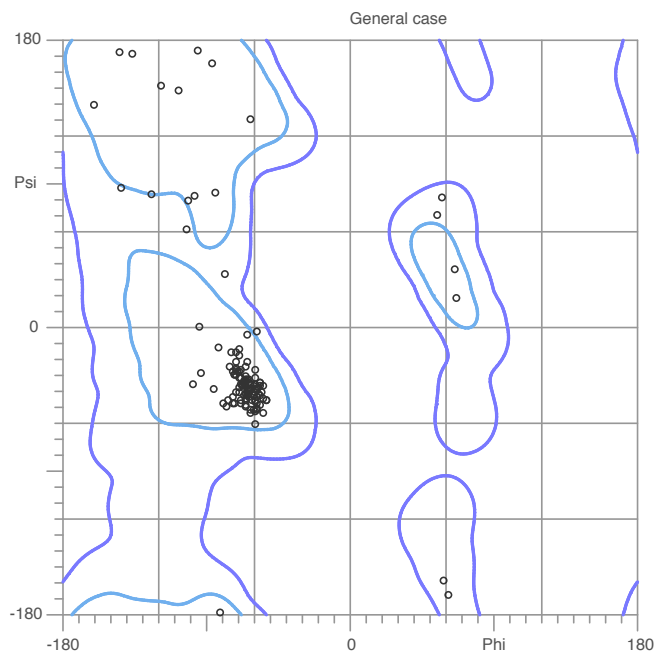
There were 1 outliers (phi, psi):
[11] 4 SER (60.2, 95.5)

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MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 12



92.9% (118/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

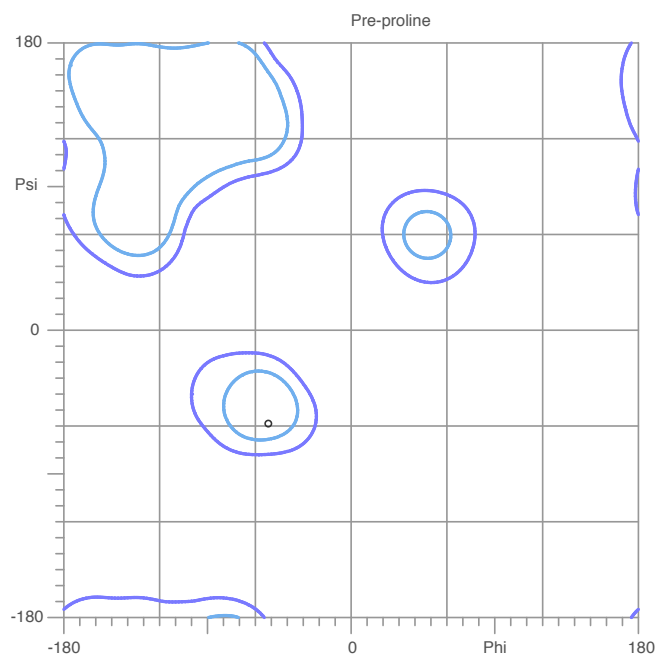
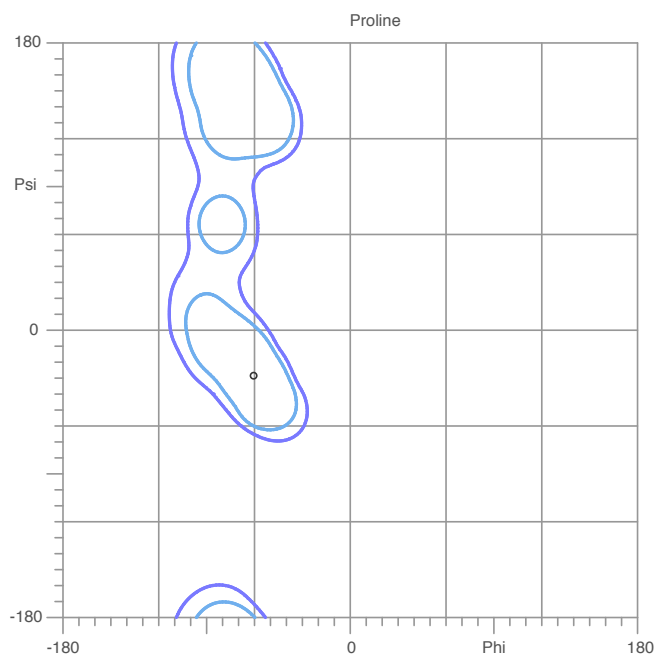
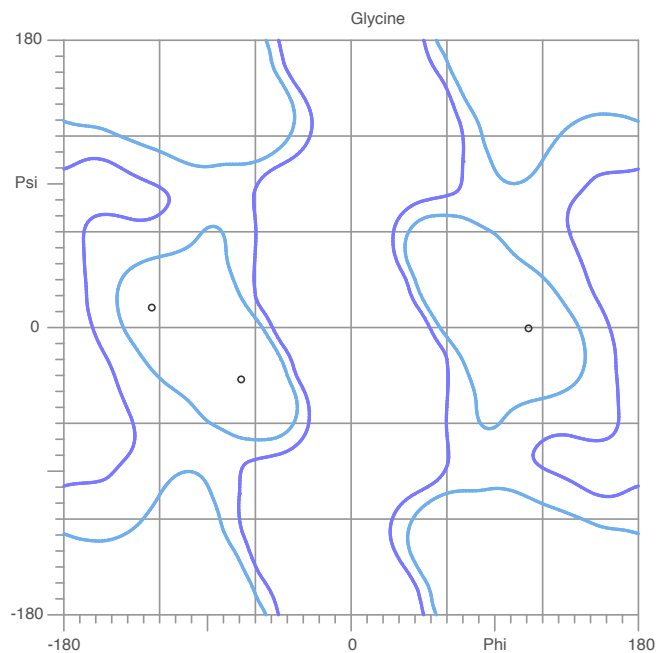
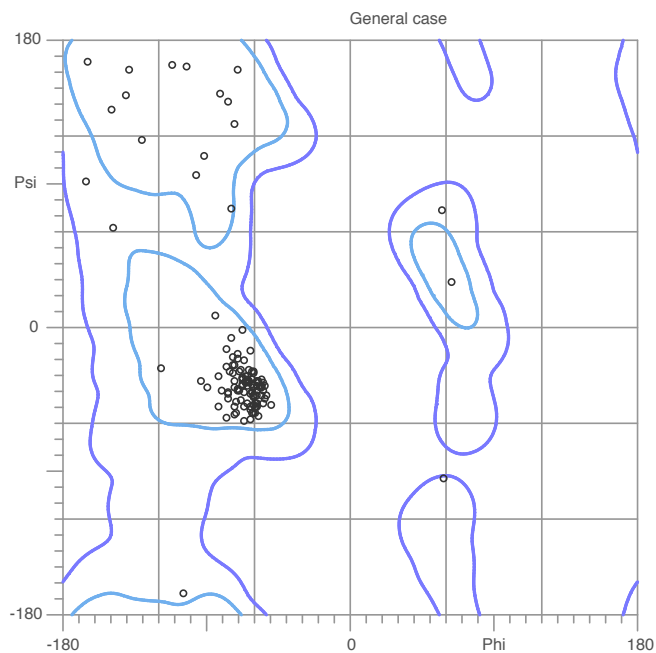
There were no outliers.

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MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 13



96.1% (122/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

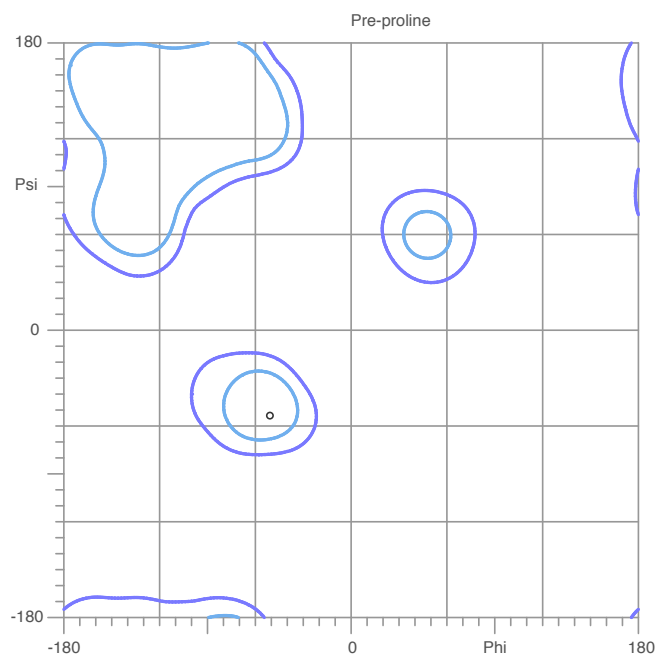
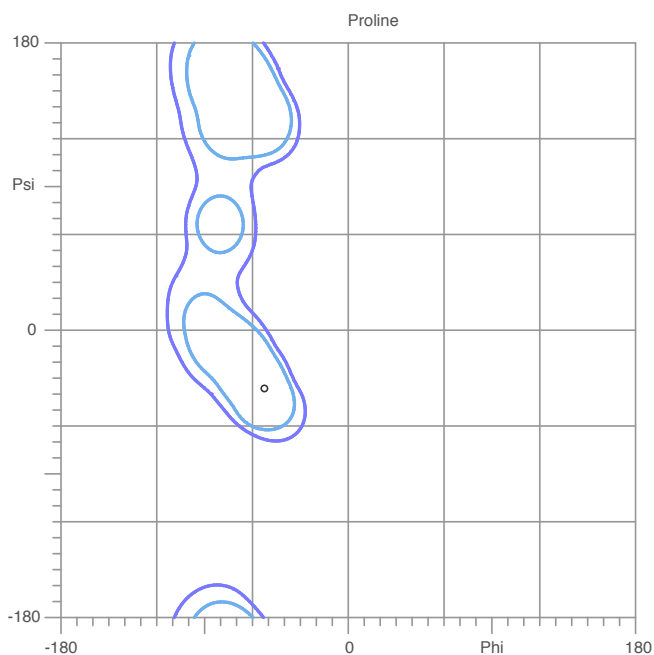
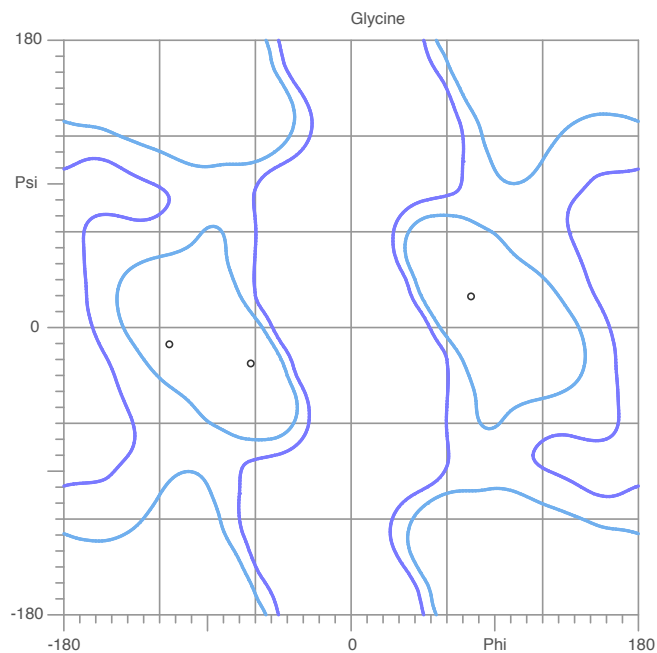
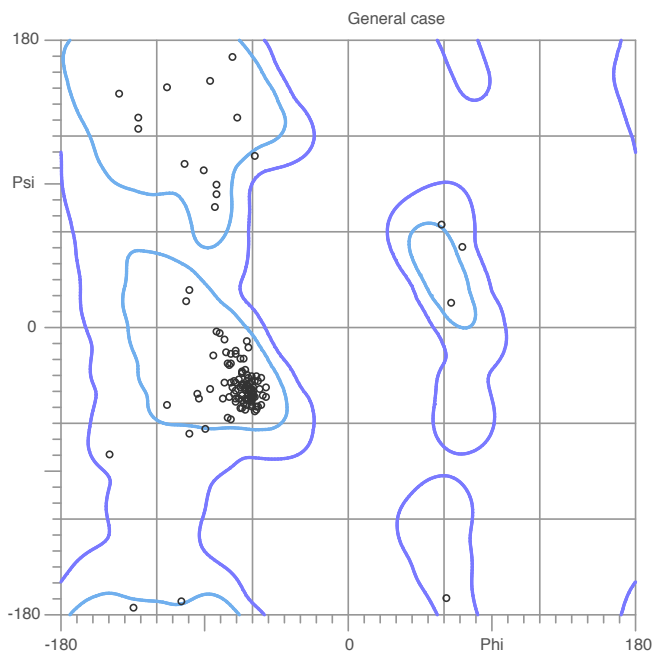
There were no outliers.

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MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 14



93.7% (119/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

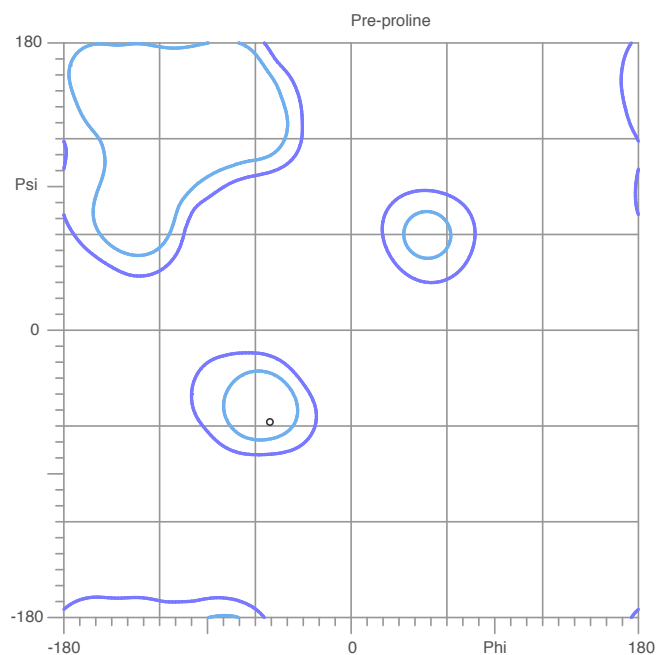
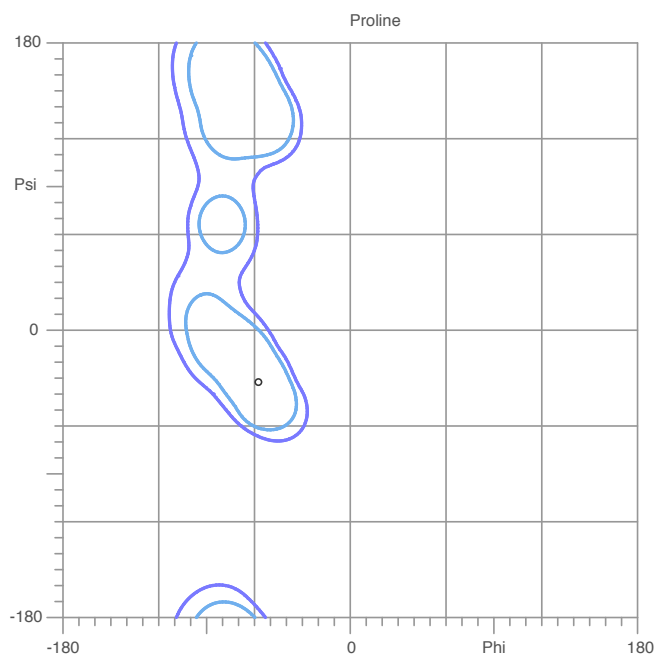
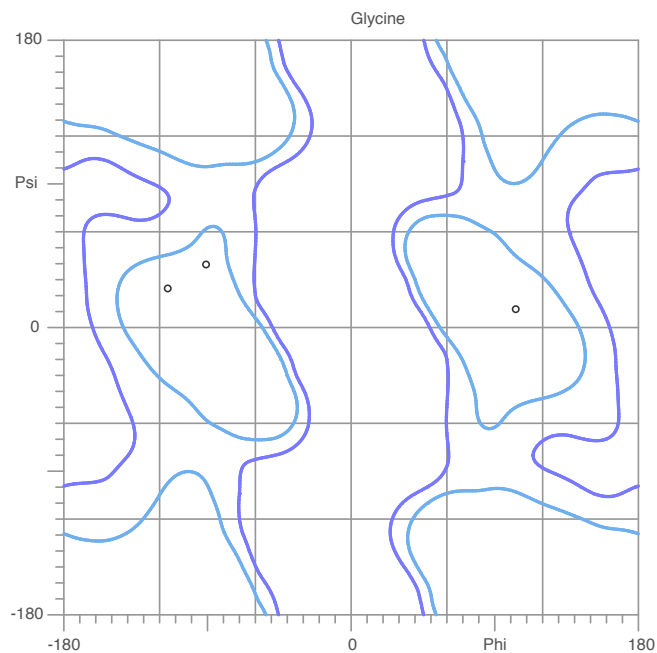
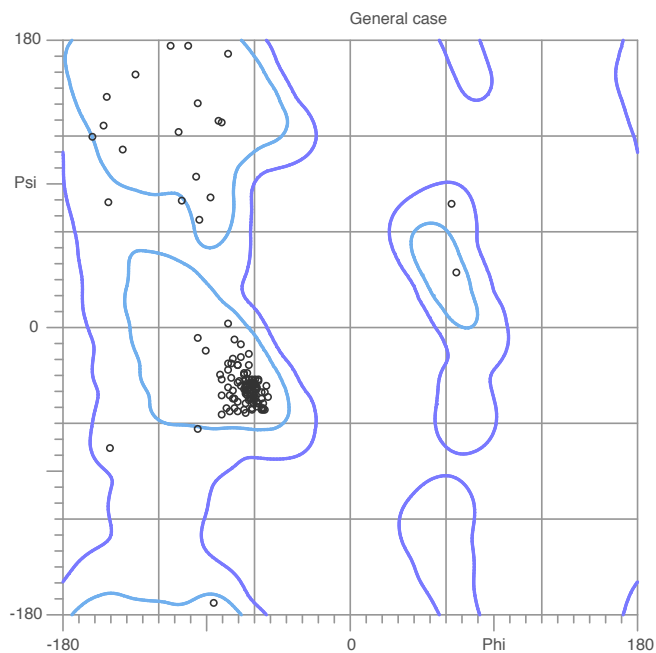
There were no outliers.

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MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 15



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.

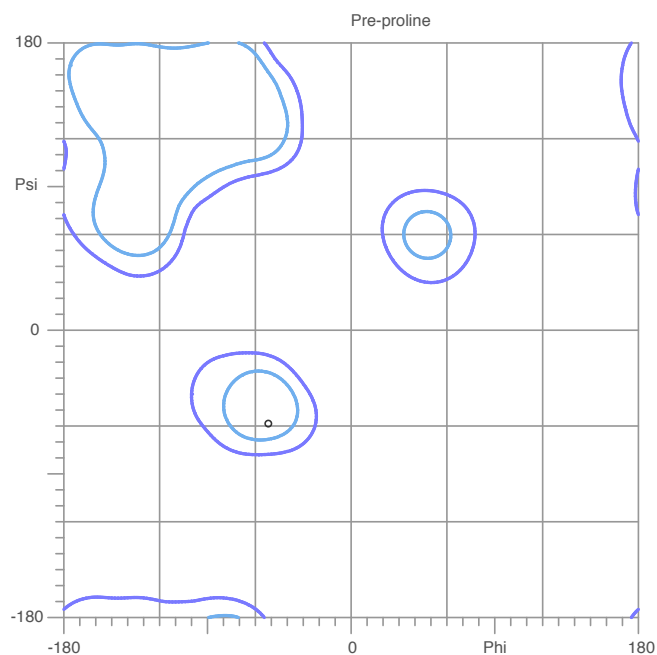
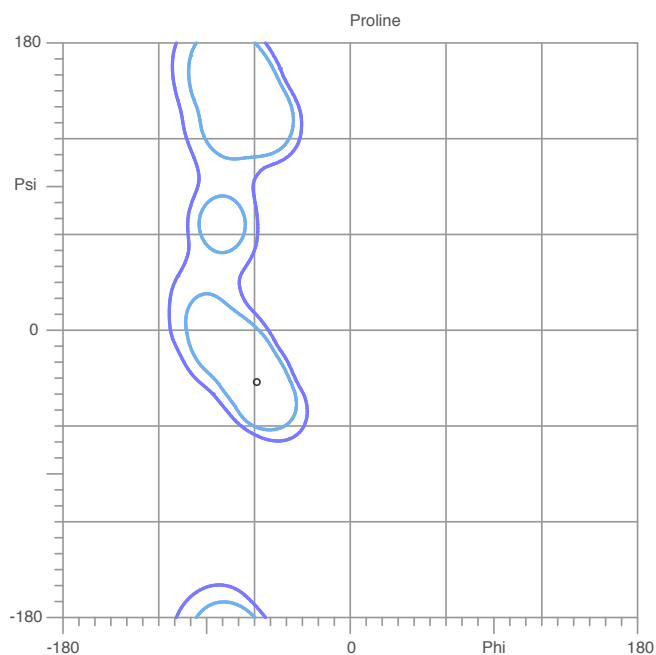
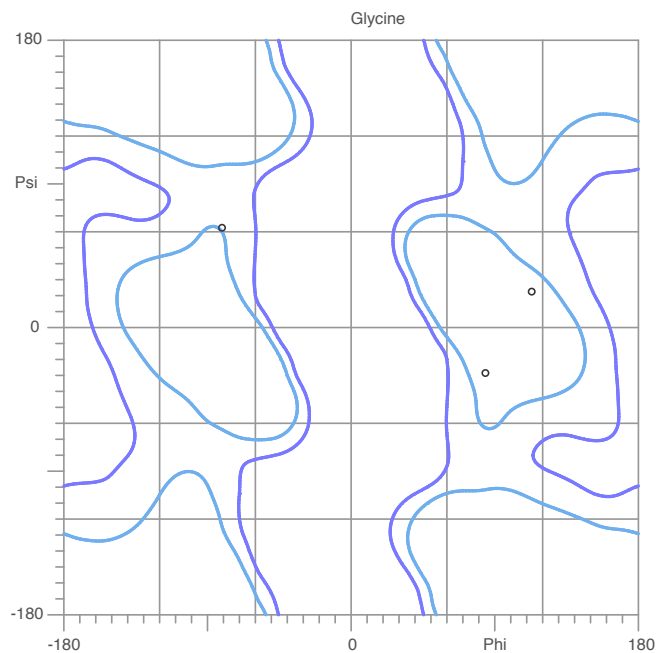
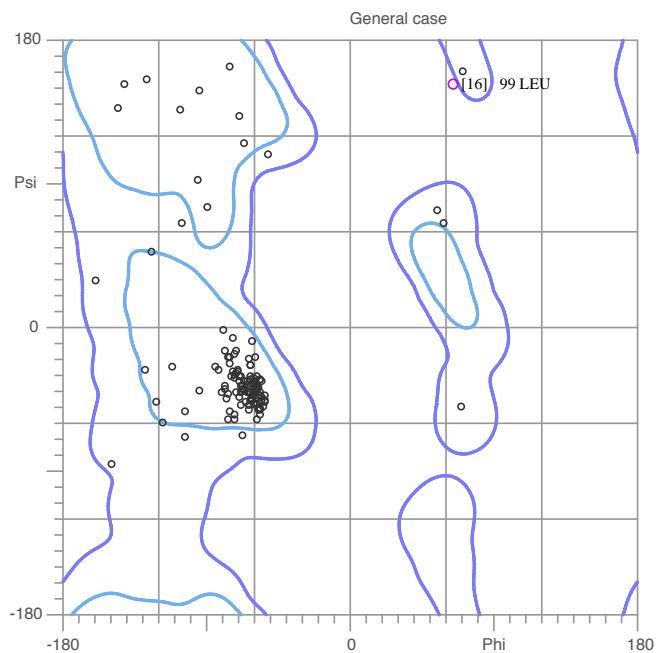
There were no outliers.

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MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 16



89.0% (113/127) of all residues were in favored (98%) regions.
99.2% (126/127) of all residues were in allowed (>99.8%) regions.

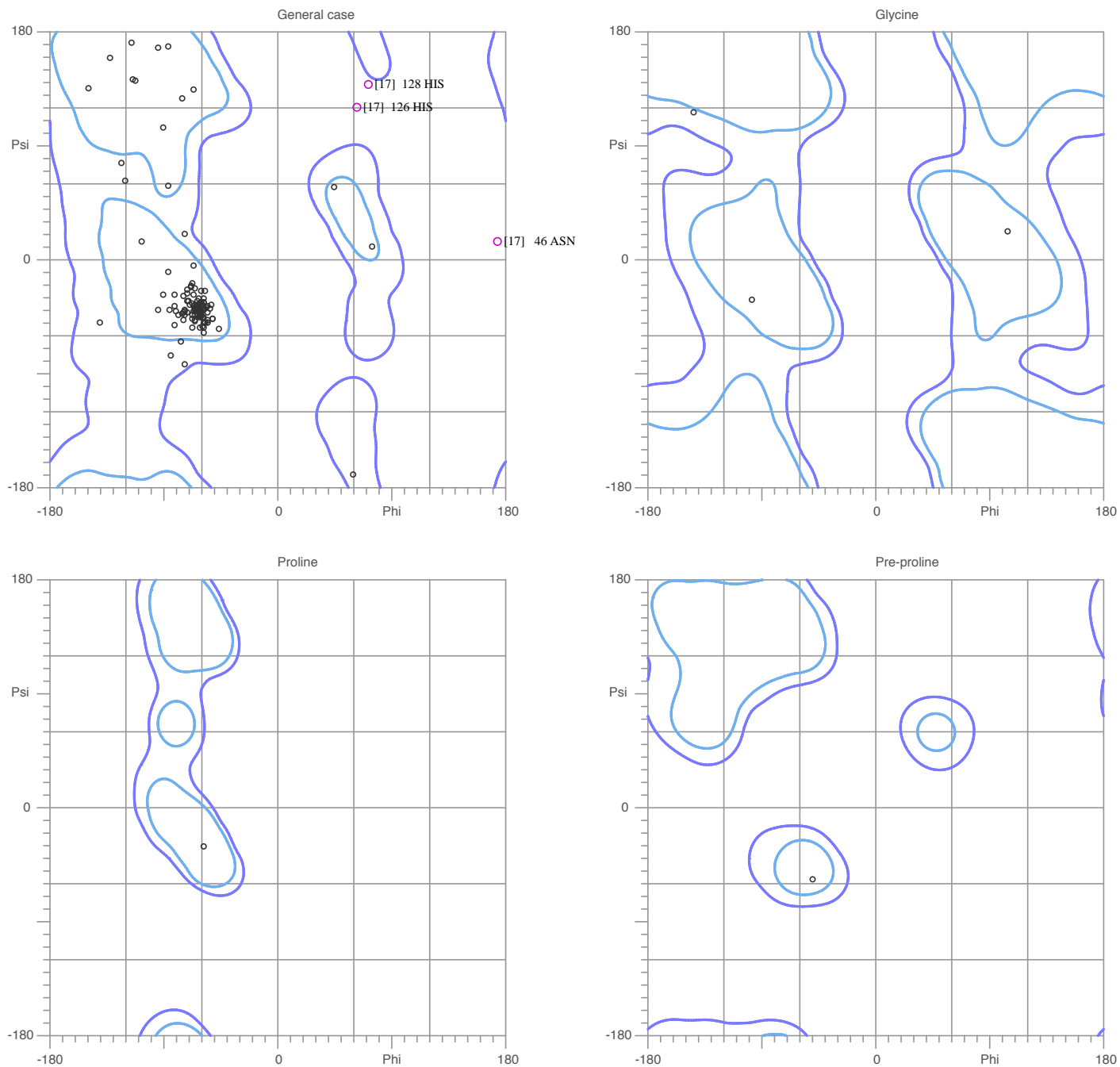
There were 1 outliers (phi, psi):
[16] 99 LEU (64.9, 153.4)

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

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MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 17



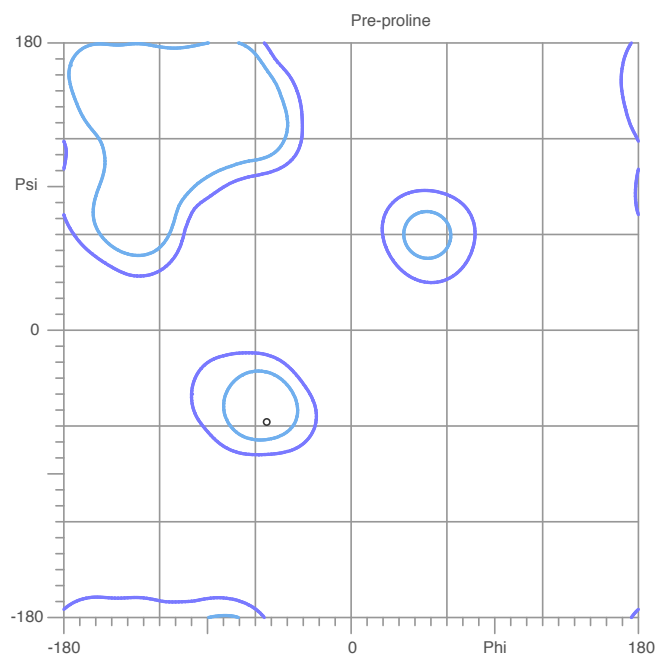
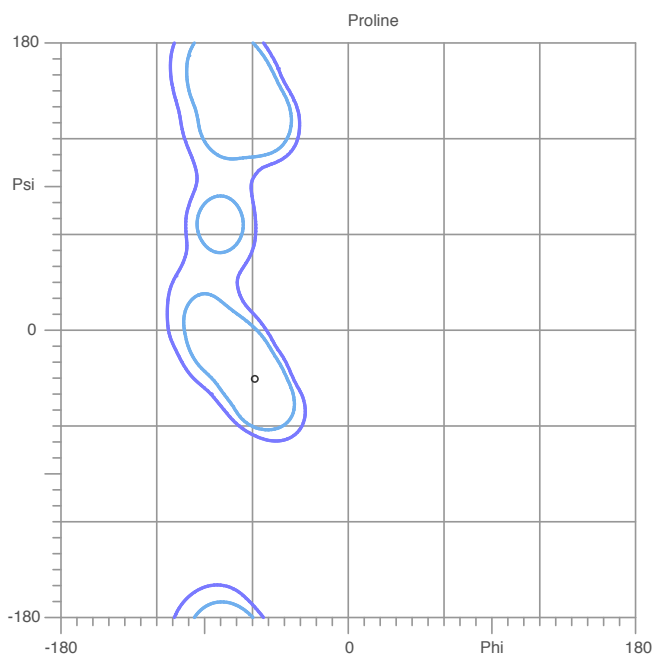
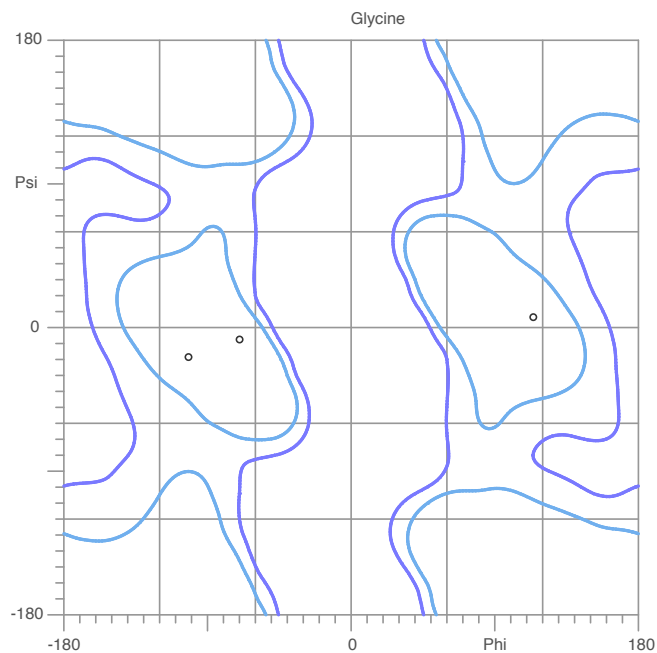
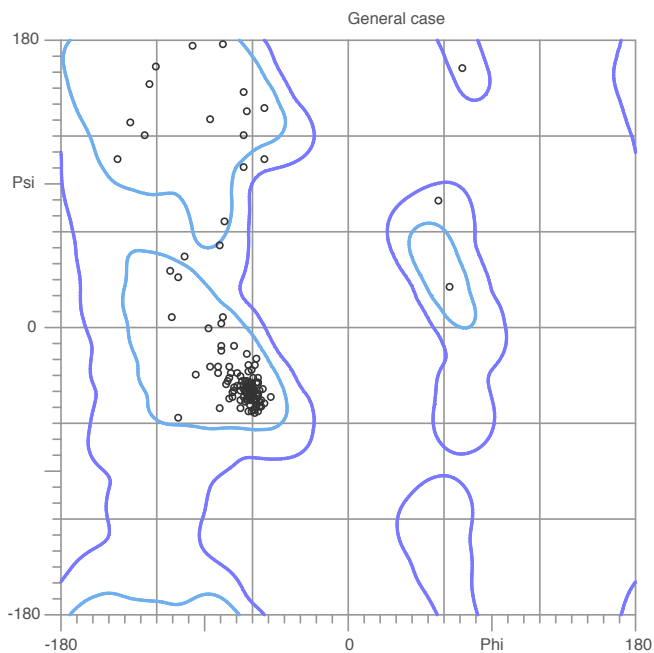
90.6% (115/127) of all residues were in favored (98%) regions.
97.6% (124/127) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[17] 46 ASN (173.5, 15.3)
[17] 126 HIS (62.9, 122.0)
[17] 128 HIS (71.3, 139.7)

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 18



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.

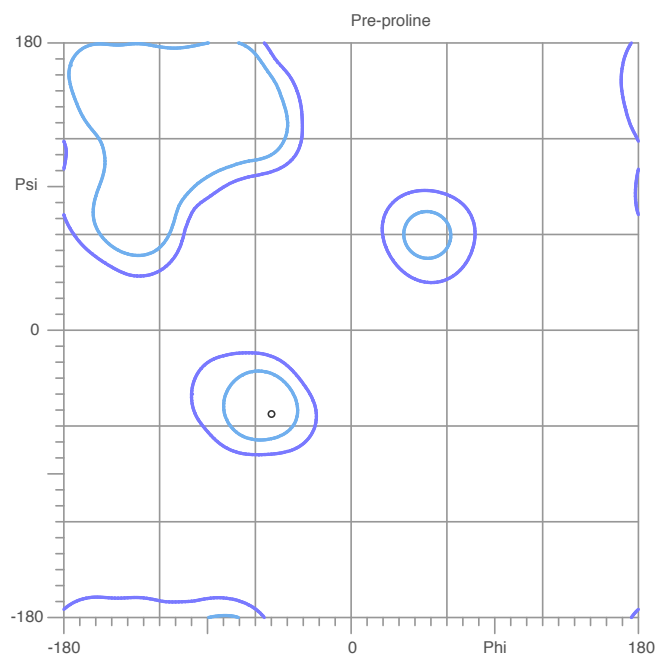
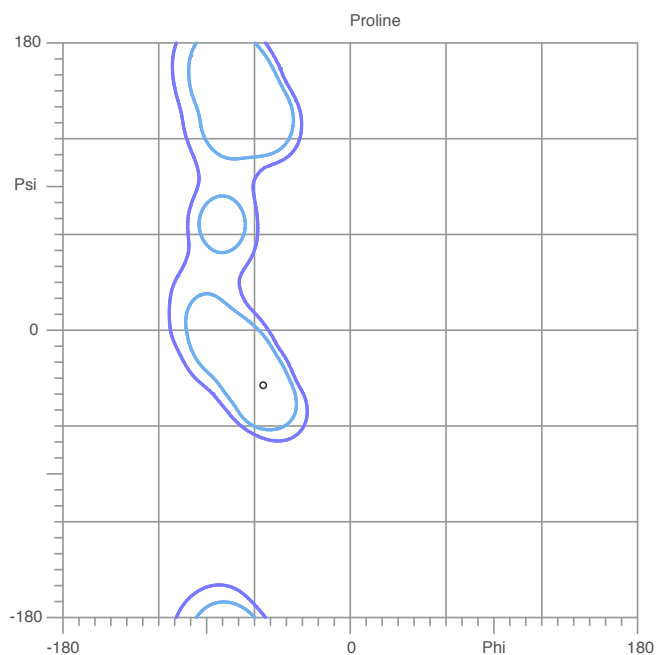
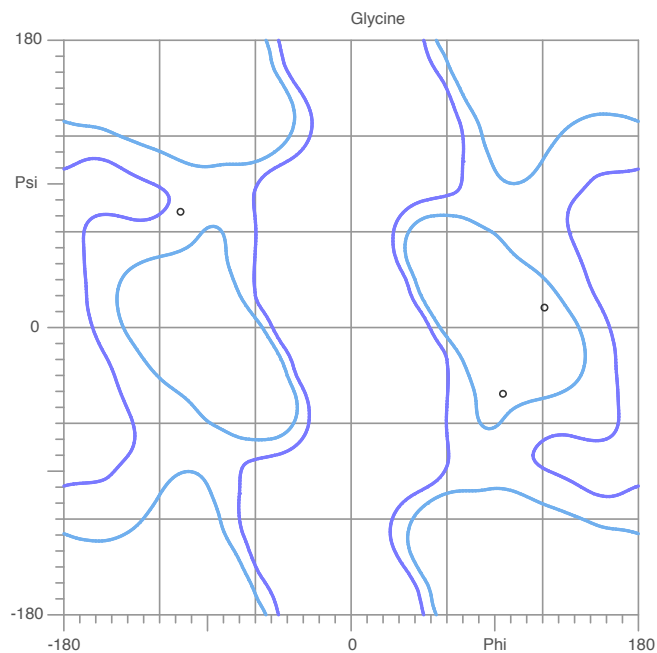
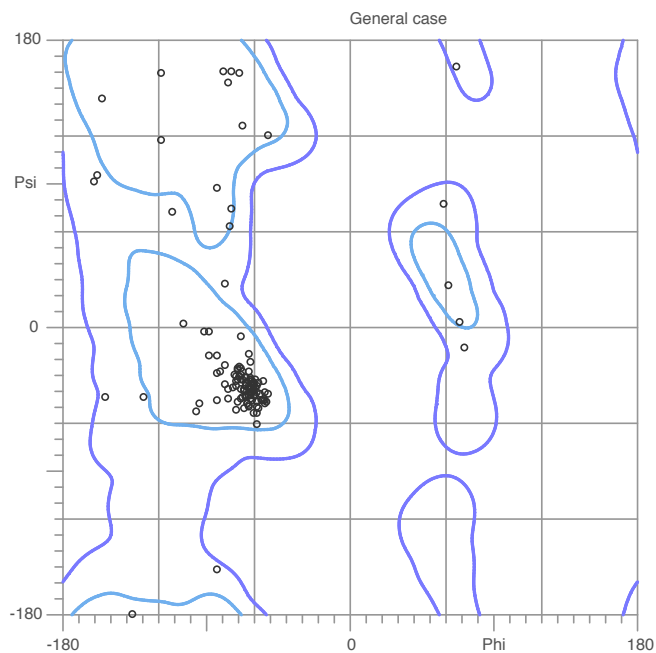
There were no outliers.

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

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

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 19



91.3% (116/127) of all residues were in favored (98%) regions.
100.0% (127/127) of all residues were in allowed (>99.8%) regions.

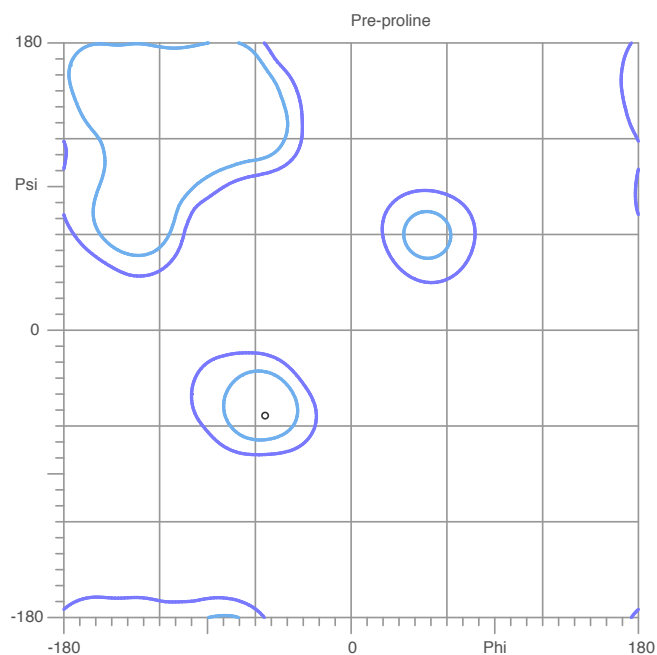
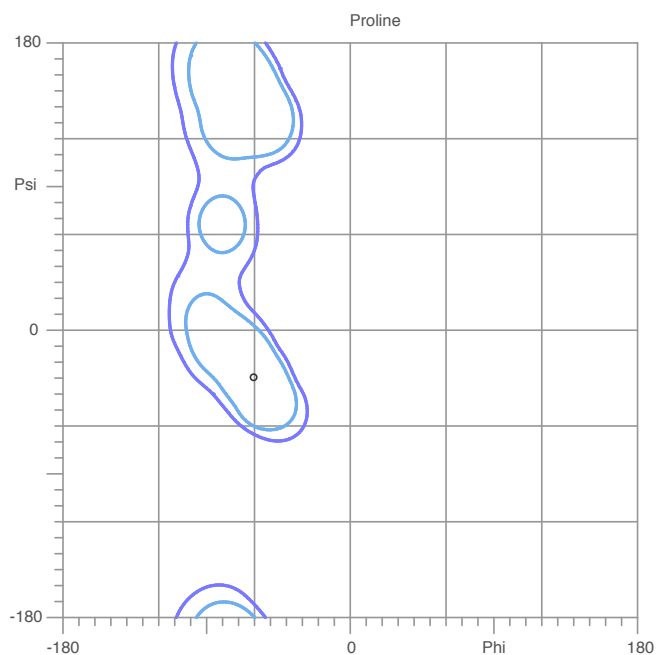
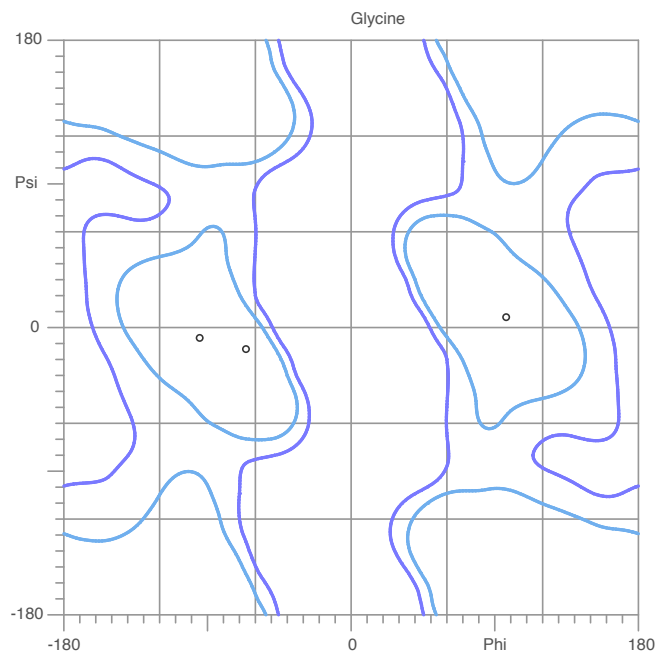
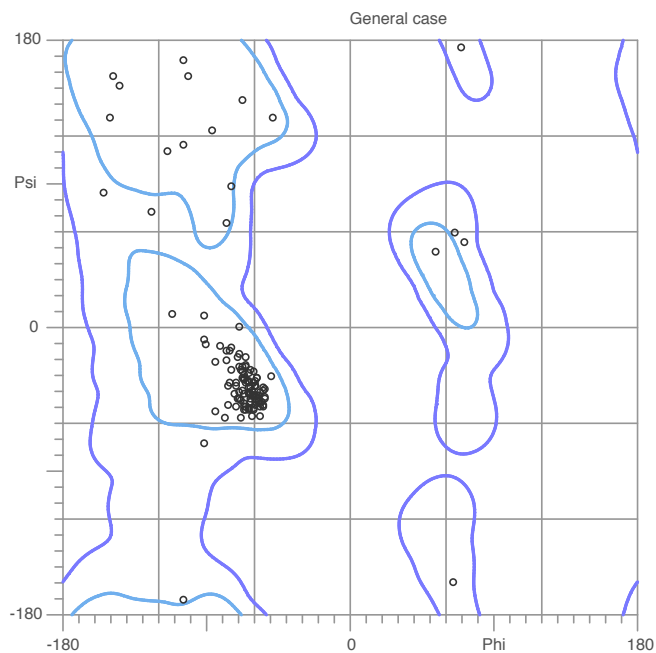
There were no outliers.

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

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

MolProbity Ramachandran analysis

SSR10_NMR_em_bcr3.pdb, model 20



93.7% (119/127) 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)