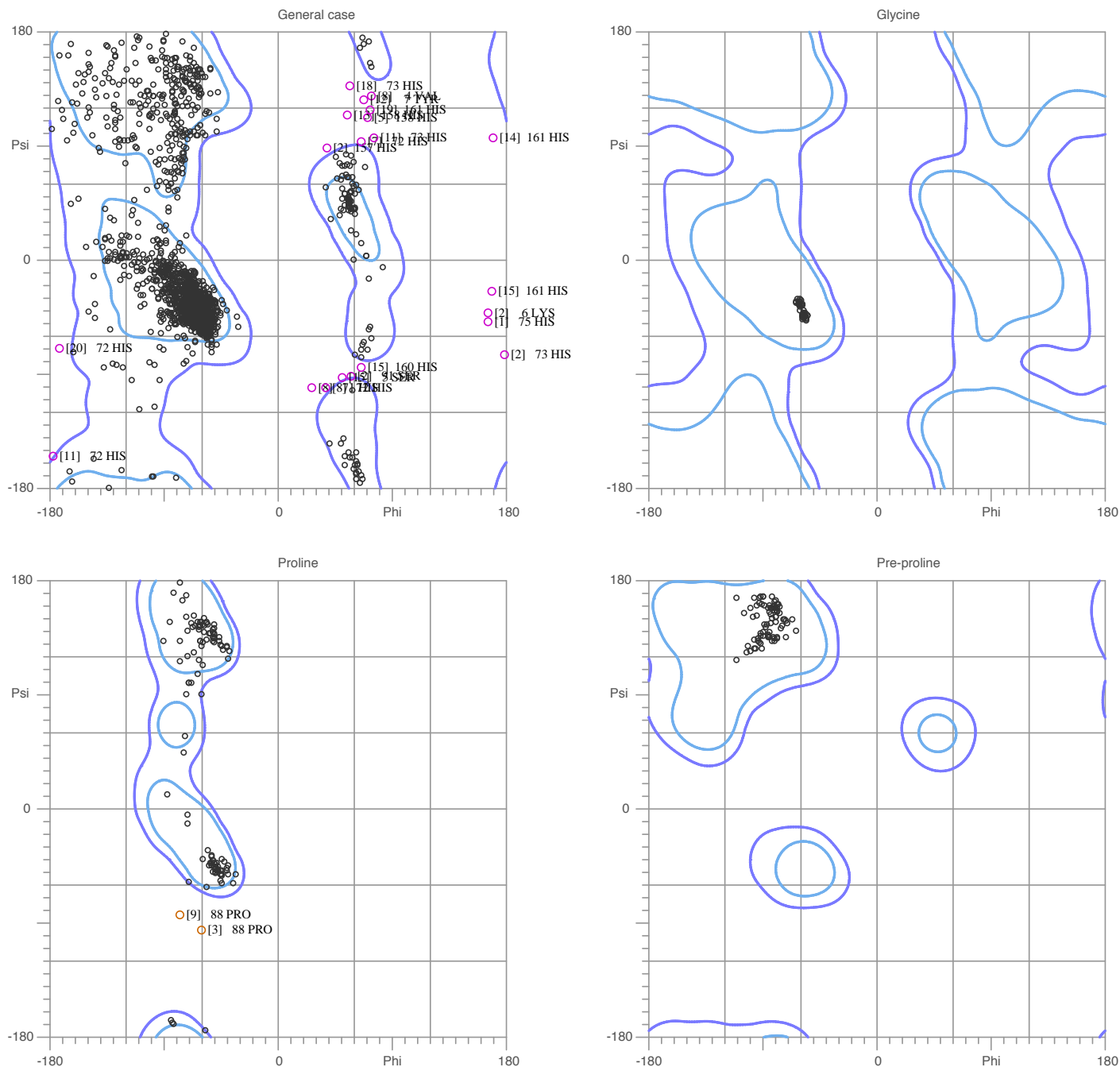


MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, all models



94.5% (2796/2960) of all residues were in favored (98%) regions.
99.2% (2937/2960) of all residues were in allowed (>99.8%) regions.

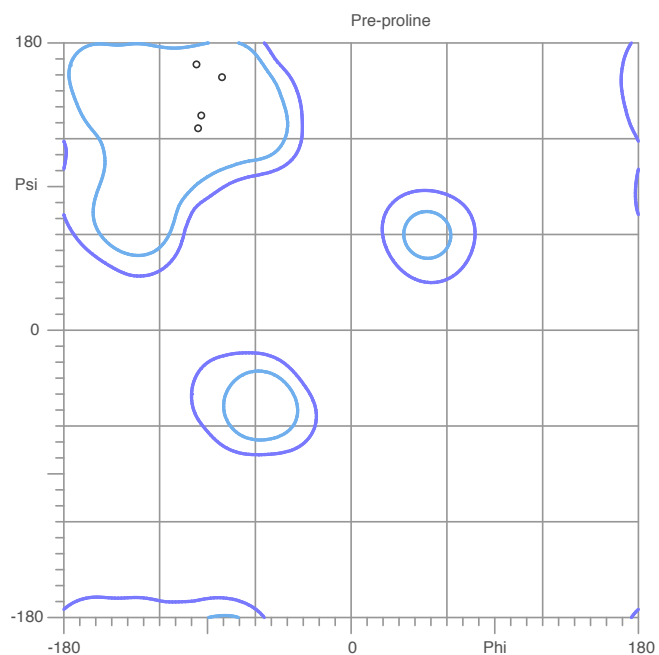
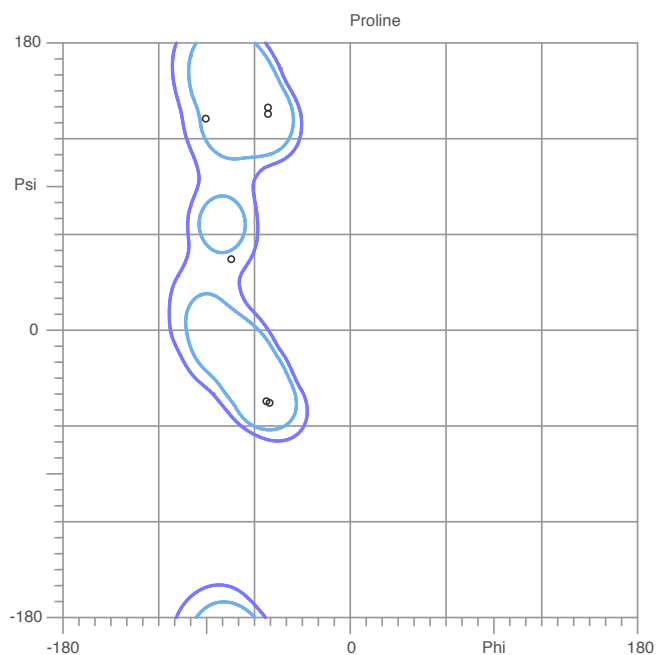
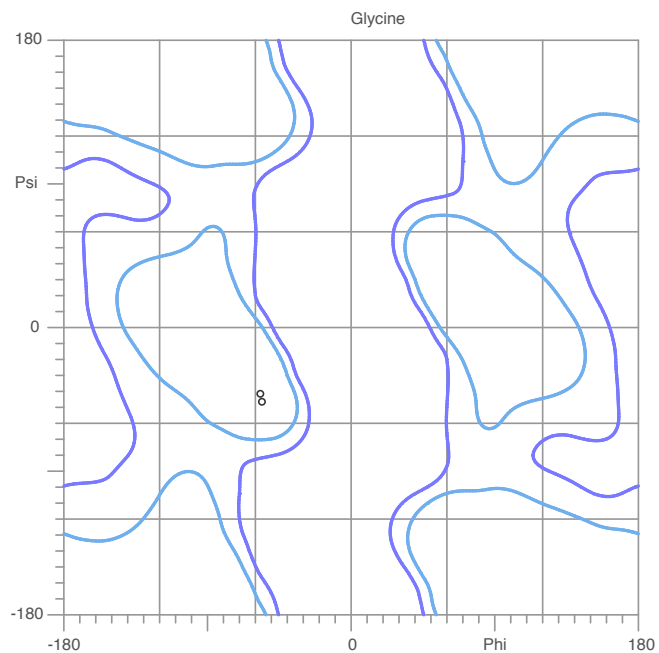
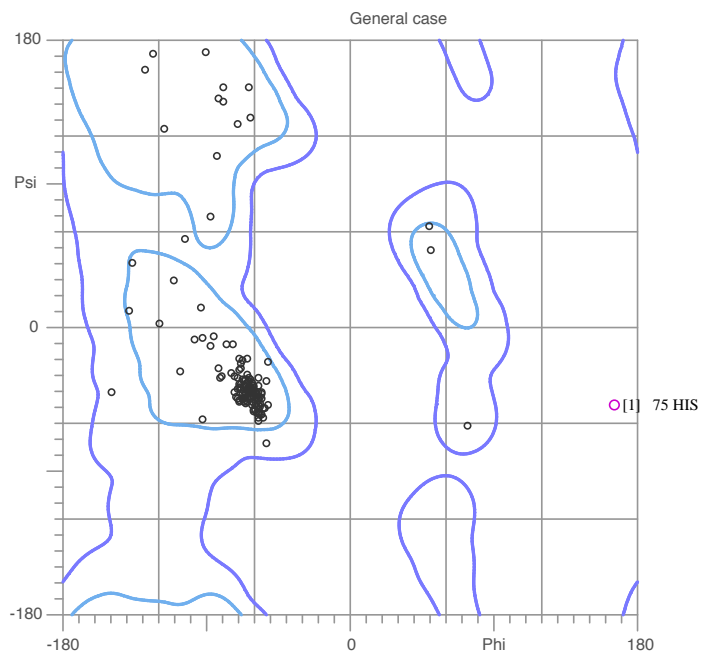
There were 23 outliers (phi, psi):

- [1] 75 HIS (165.4, -48.7)
- [2] 6 LYS (165.4, -41.1)
- [2] 73 HIS (178.9, -74.7)
- [2] 91 SER (58.0, -91.1)
- [2] 157 HIS (38.5, 89.5)
- [3] 88 PRO (-61.8, -95.5)
- [5] 158 HIS (70.1, 113.8)
- [7] 72 HIS (65.8, 94.9)
- [8] 4 VAL (73.1, 130.4)

- [8] 71 HIS (26.5, -100.3)
- [8] 72 HIS (37.7, -101.0)
- [9] 88 PRO (-78.4, -83.5)
- [11] 72 HIS (-178.6, -154.4)
- [11] 73 HIS (75.3, 97.1)
- [12] 7 TYR (67.3, 127.1)
- [13] 158 HIS (54.6, 115.1)
- [14] 161 HIS (169.1, 97.1)
- [15] 5 SER (50.6, -92.2)
- [15] 160 HIS (65.6, -84.0)
- [15] 161 HIS (168.6, -24.7)
- [18] 73 HIS (56.8, 138.3)
- [19] 161 HIS (72.0, 119.5)
- [20] 72 HIS (-173.6, -70.0)

MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 1



95.9% (142/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

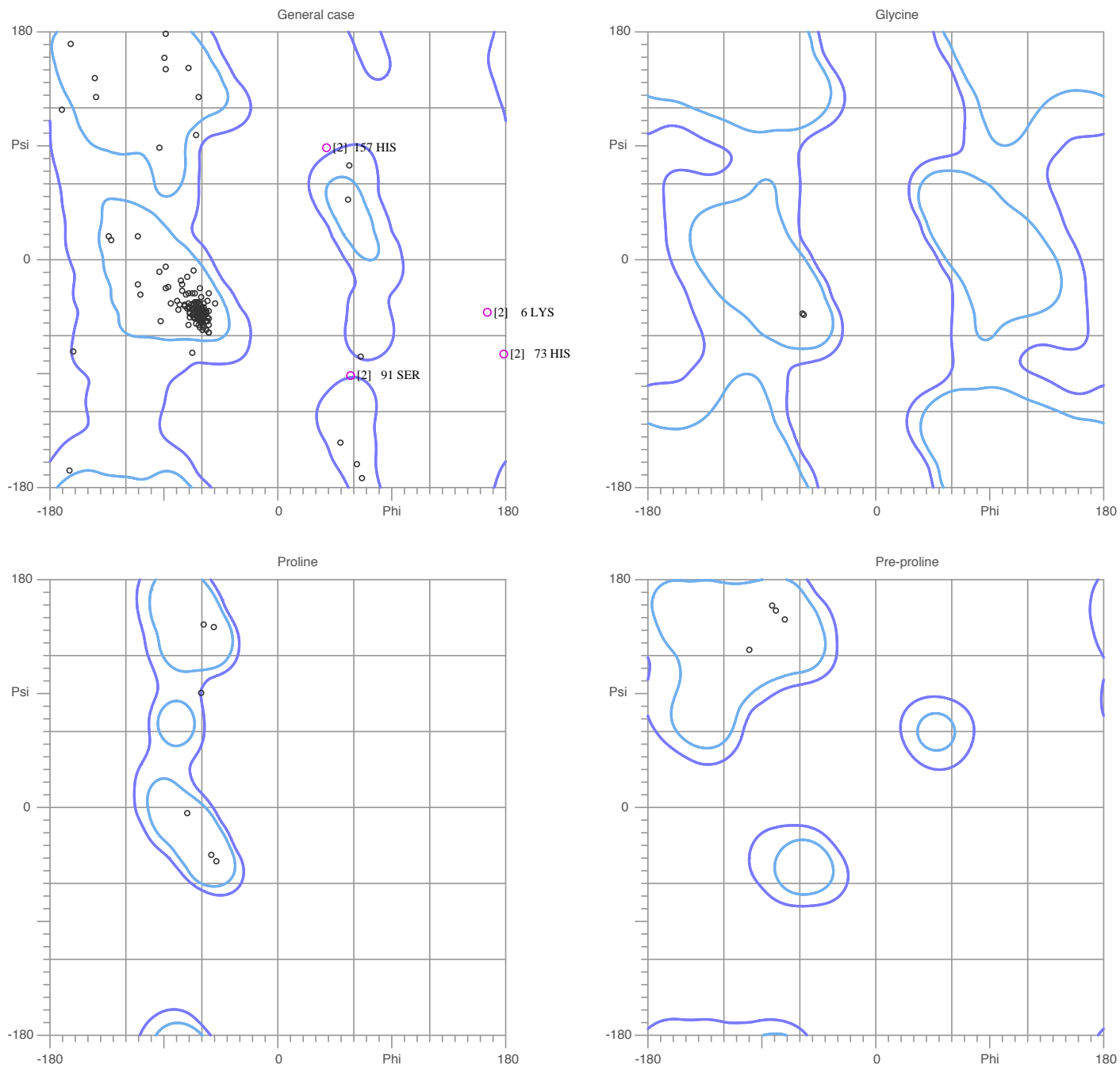
There were 1 outliers (phi, psi):
[1] 75 HIS (165.4, -48.7)

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CSR4_NMR_em_bcr3.pdb, model 2



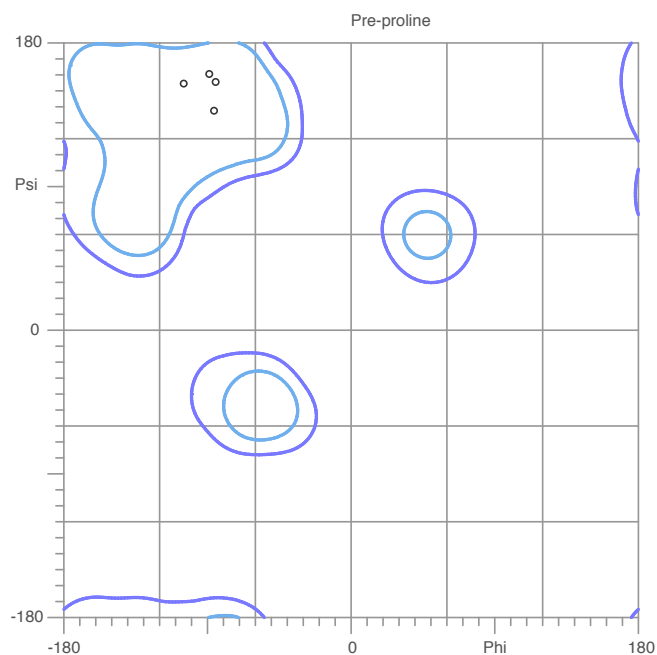
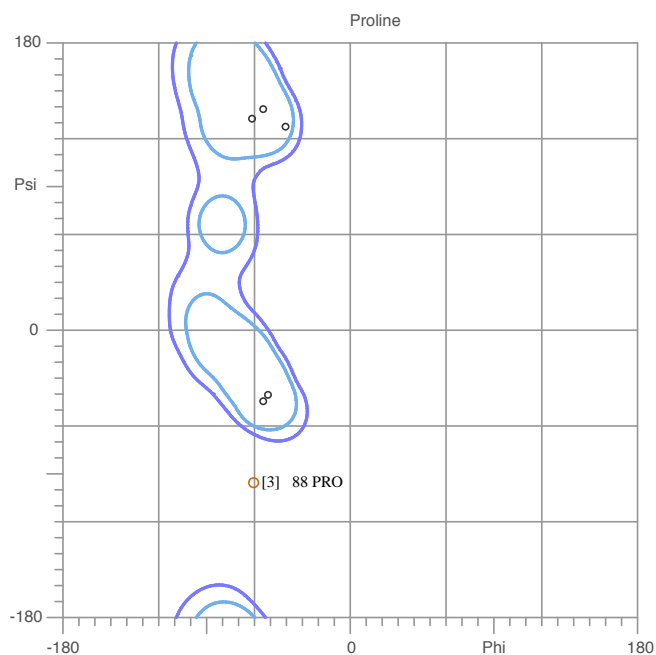
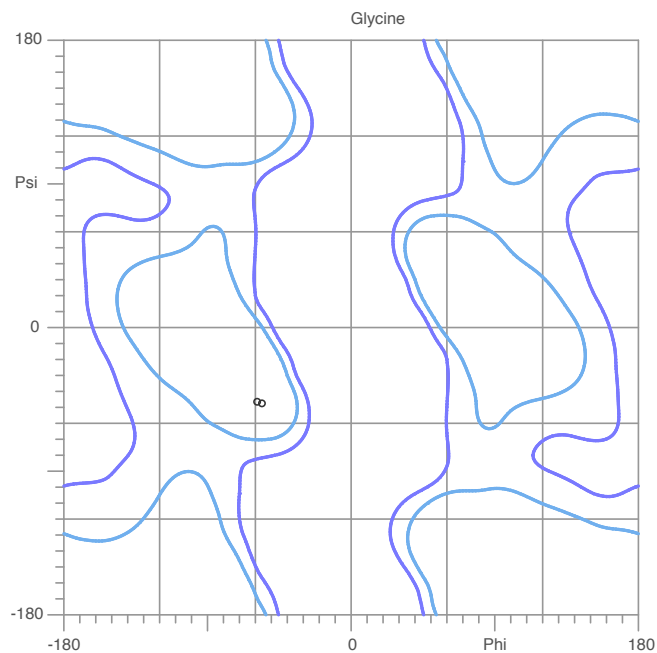
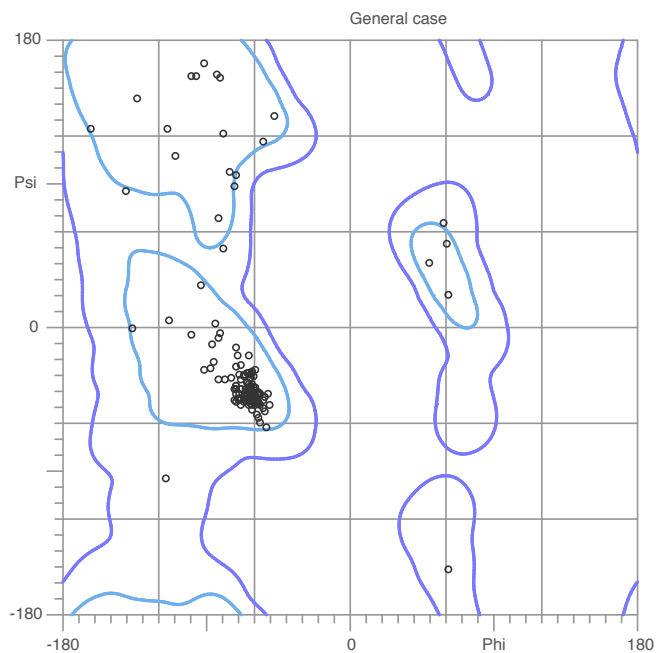
89.9% (133/148) of all residues were in favored (98%) regions.
97.3% (144/148) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [2] 6 LYS (165.4, -41.1)
- [2] 73 HIS (178.9, -74.7)
- [2] 91 SER (58.0, -91.1)
- [2] 157 HIS (38.5, 89.5)

MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 3



95.9% (142/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

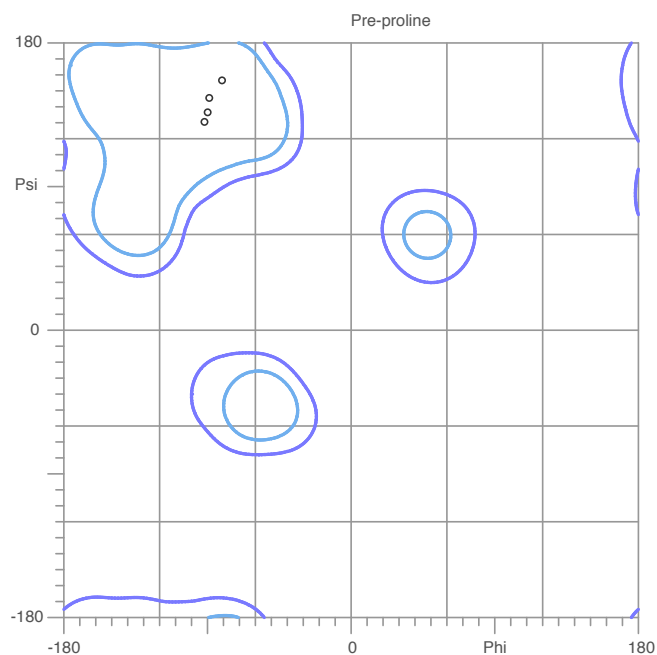
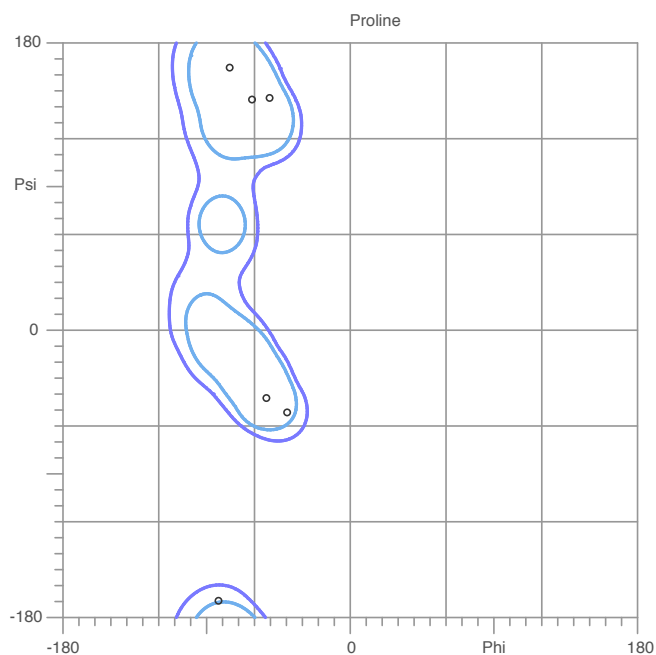
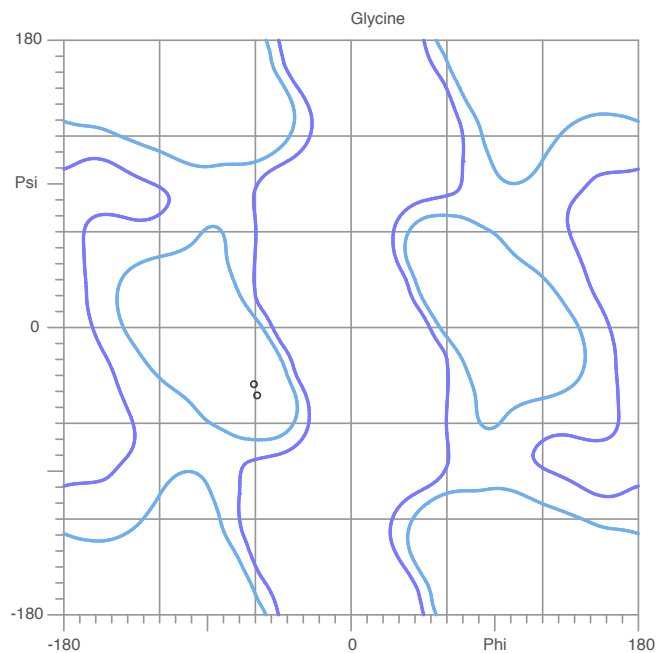
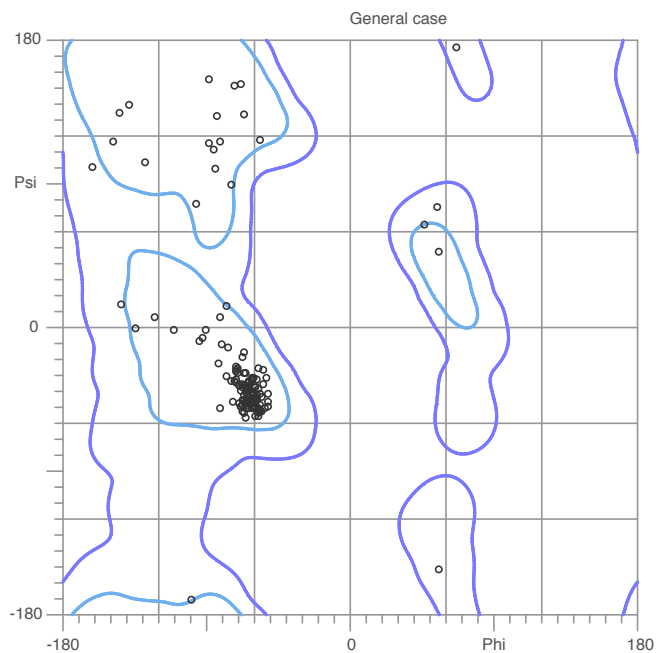
There were 1 outliers (phi, psi):
[3] 88 PRO (-61.8, -95.5)

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 4

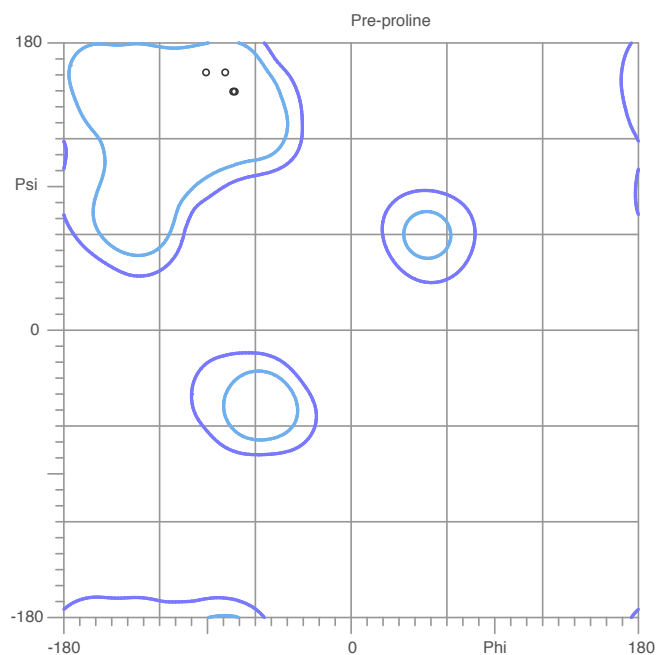
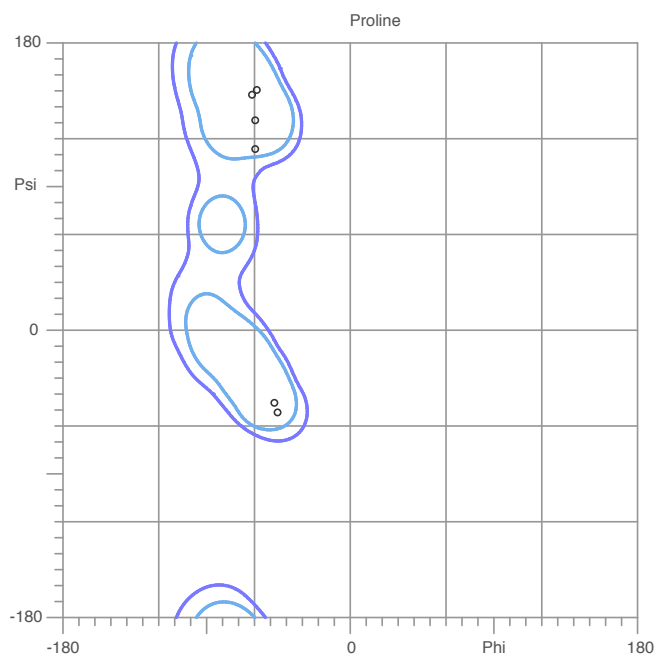
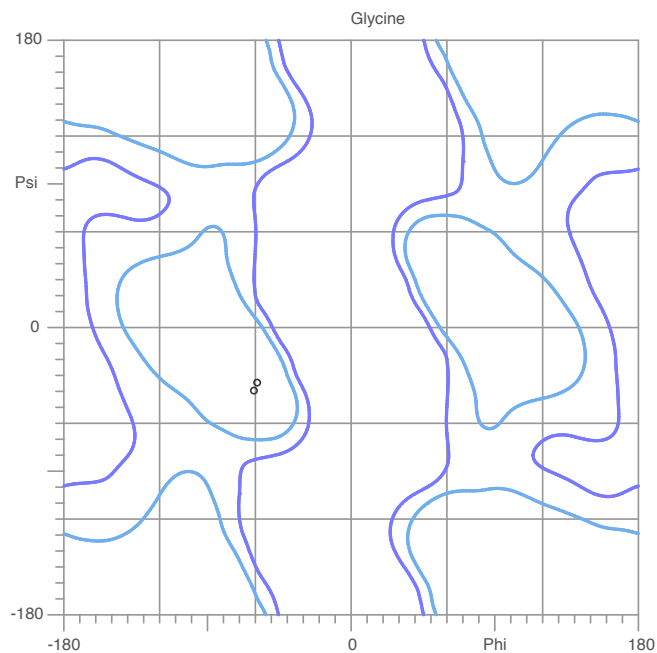
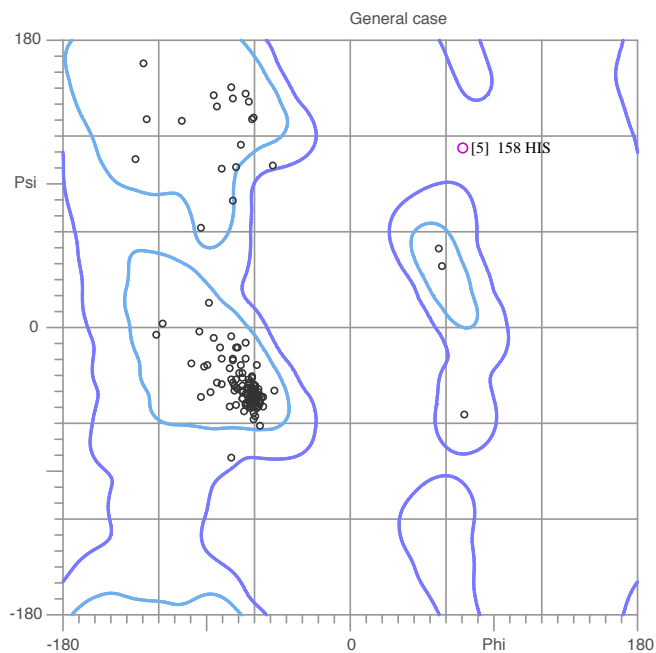


94.6% (140/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 5

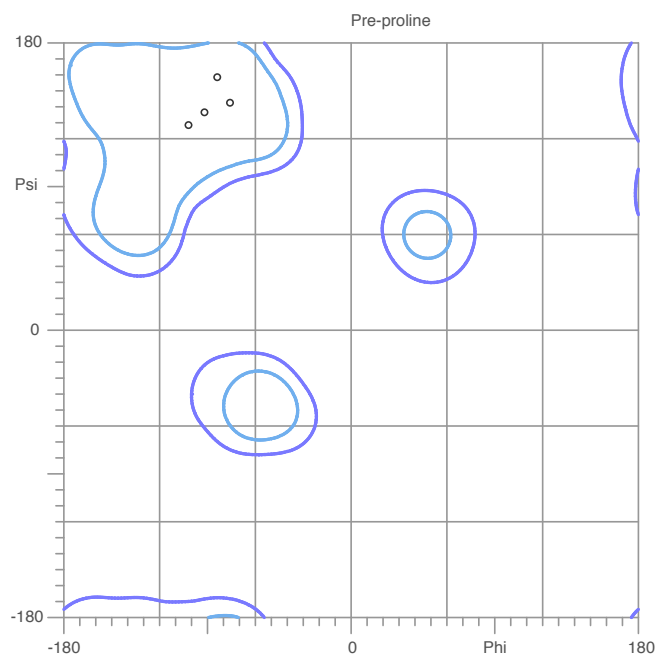
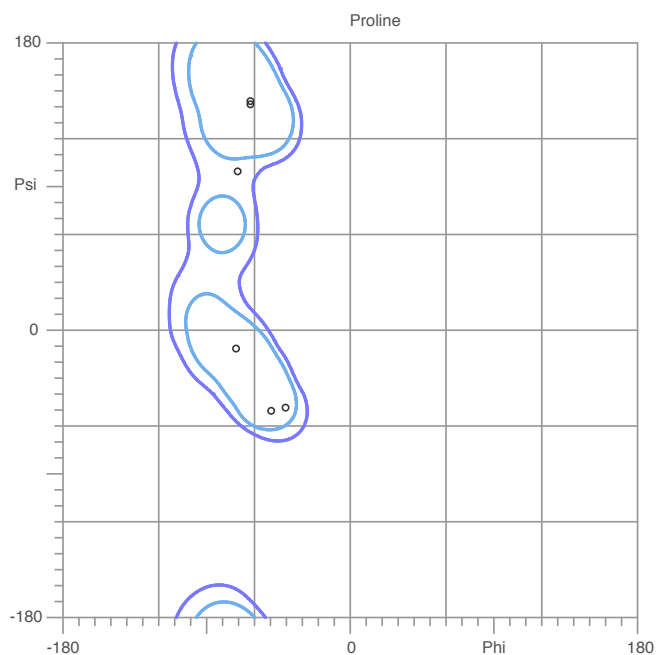
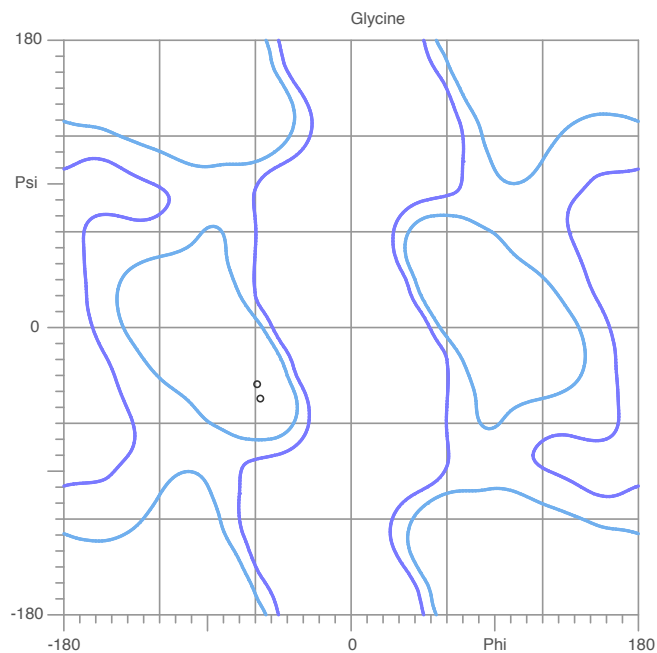
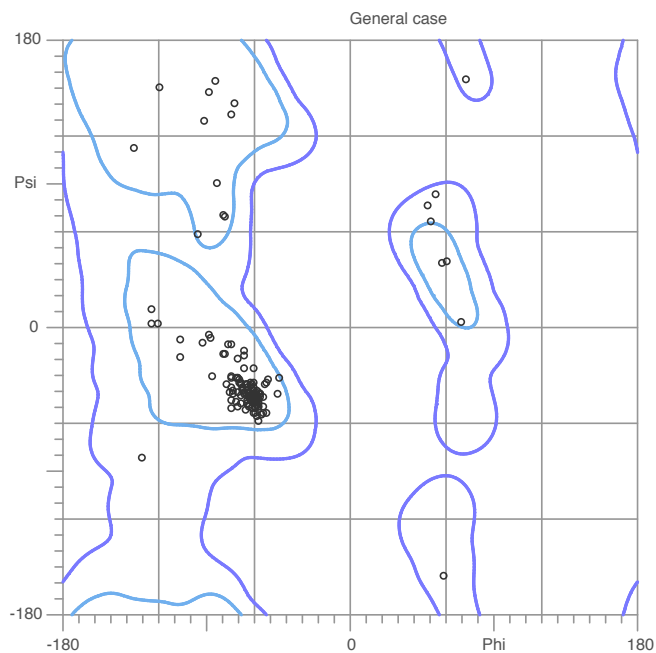


97.3% (144/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 158 HIS (70.1, 113.8)

MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 6



95.3% (141/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

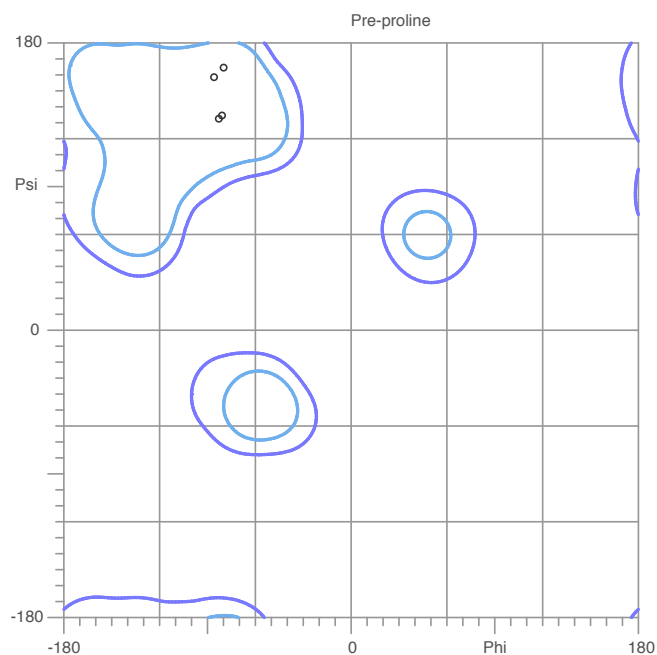
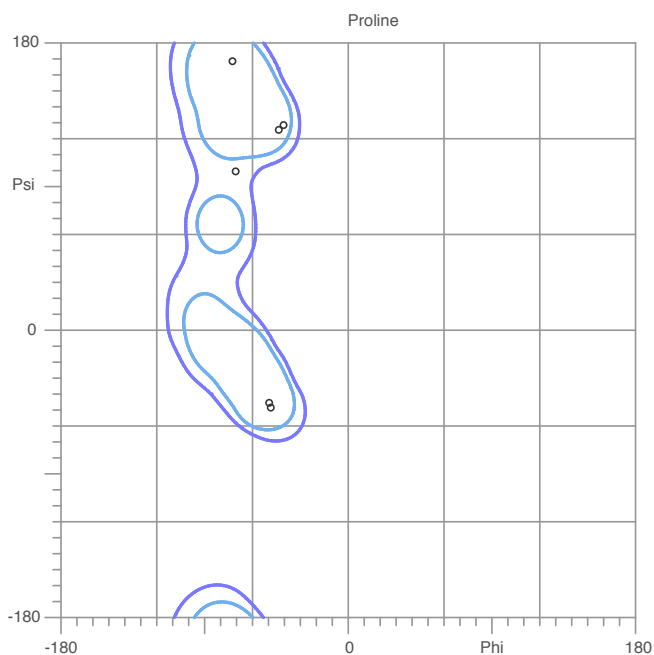
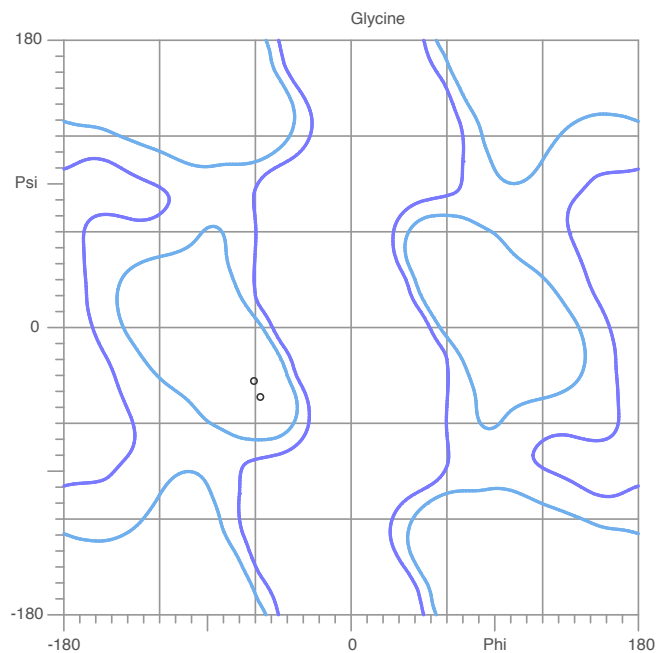
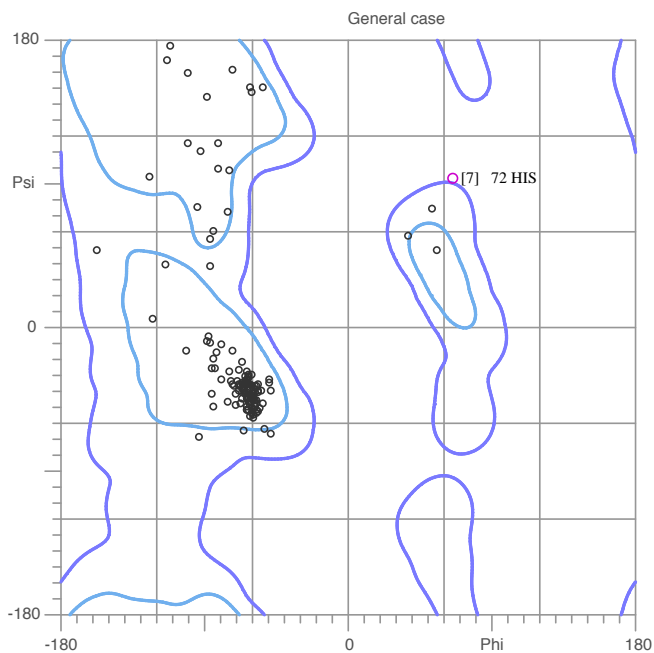
There were no outliers.

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 7

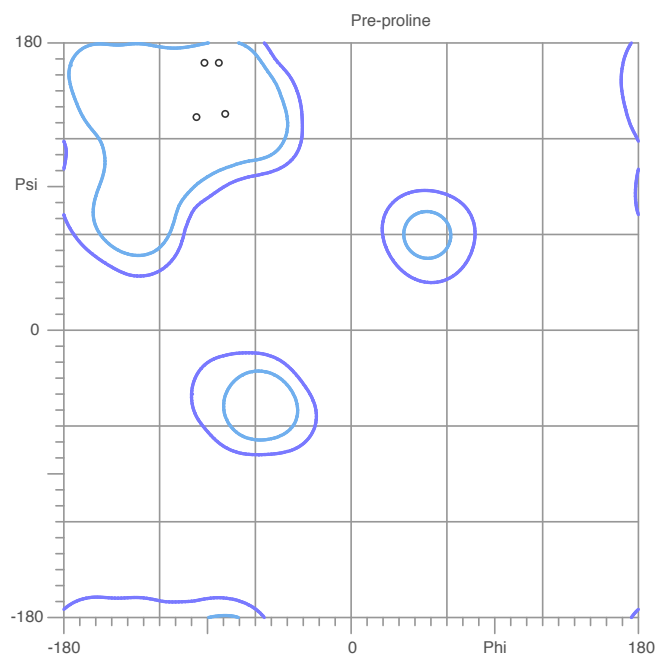
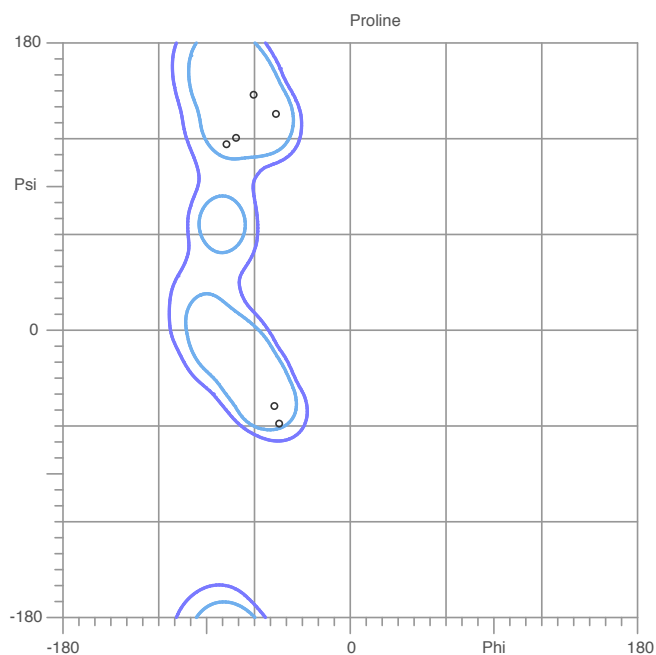
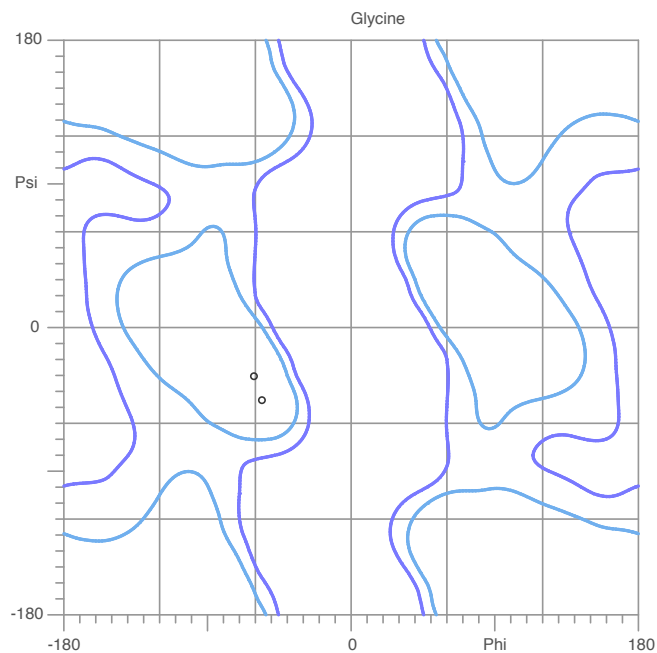
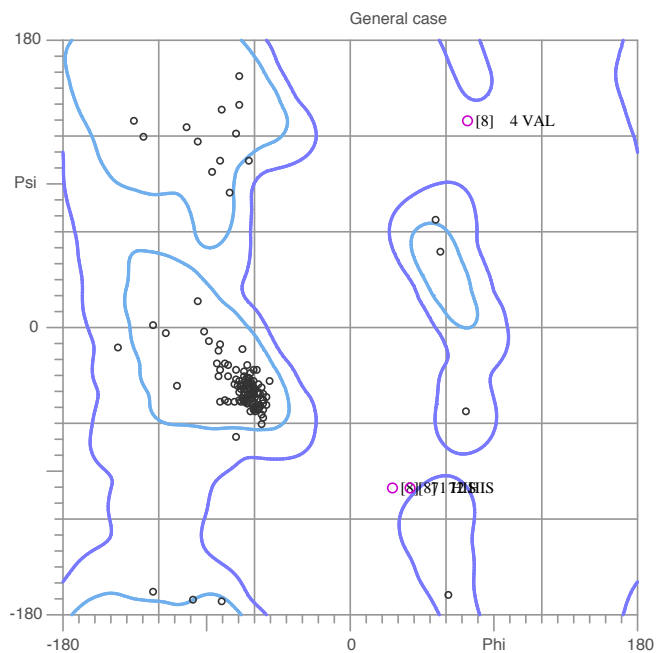


93.9% (139/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[7] 72 HIS (65.8, 94.9)

MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 8



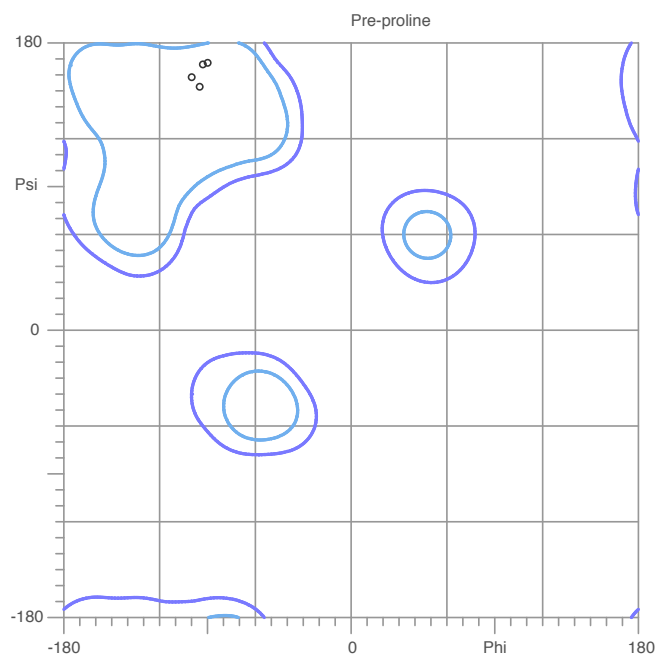
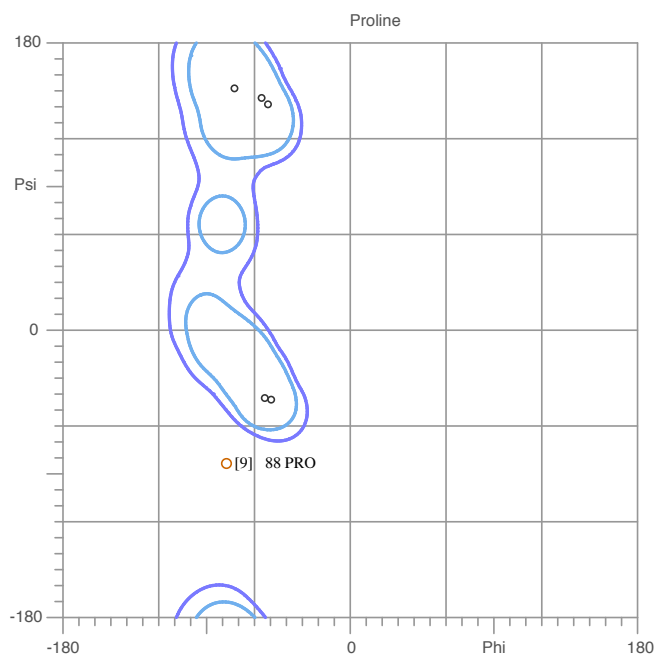
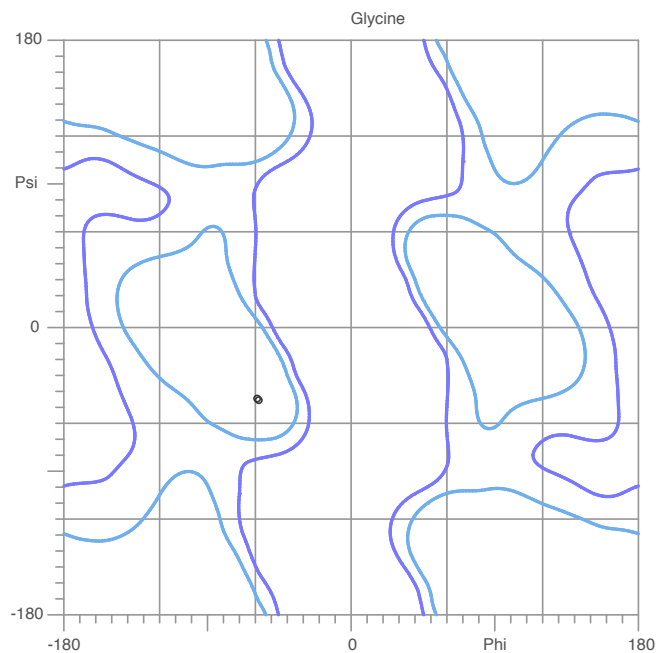
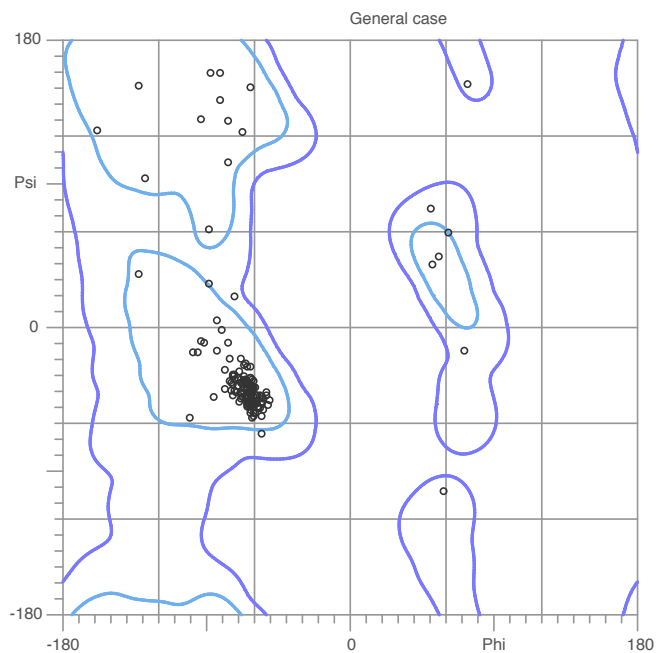
92.6% (137/148) of all residues were in favored (98%) regions.
98.0% (145/148) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 4 VAL (73.1, 130.4)
- [8] 71 HIS (26.5, -100.3)
- [8] 72 HIS (37.7, -101.0)

MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 9



93.9% (139/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

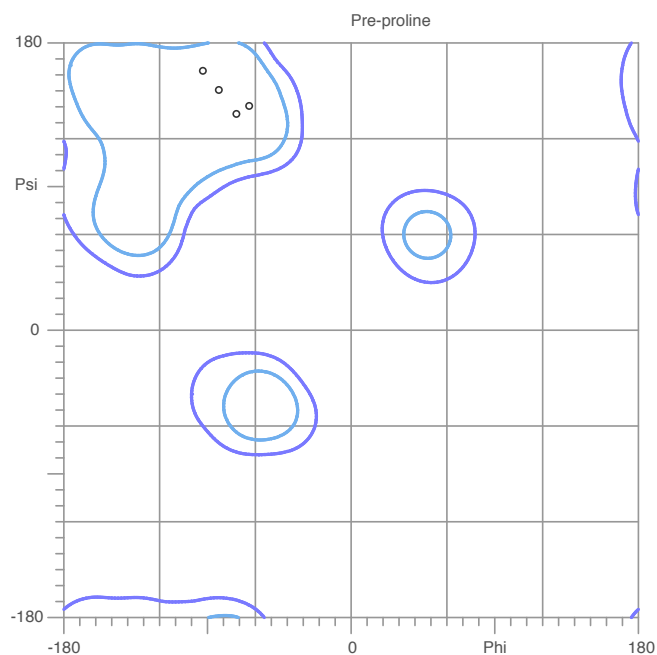
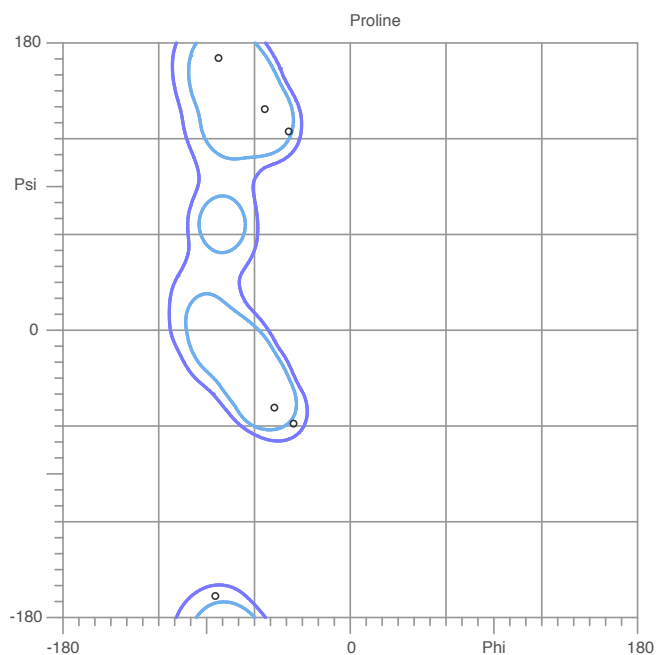
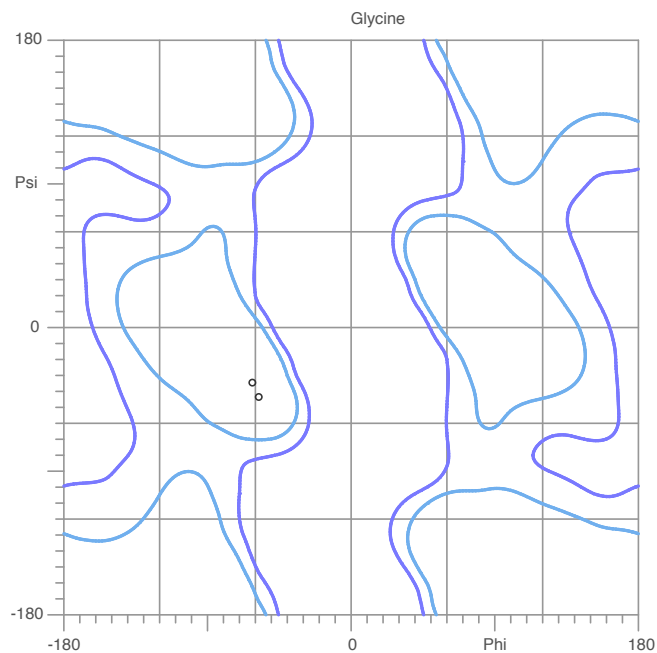
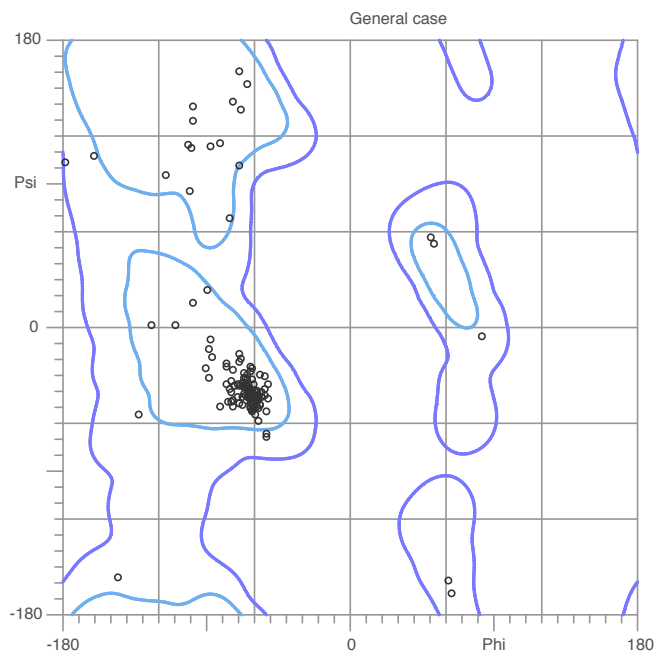
There were 1 outliers (phi, psi):
[9] 88 PRO (-78.4, -83.5)

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 10



92.6% (137/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

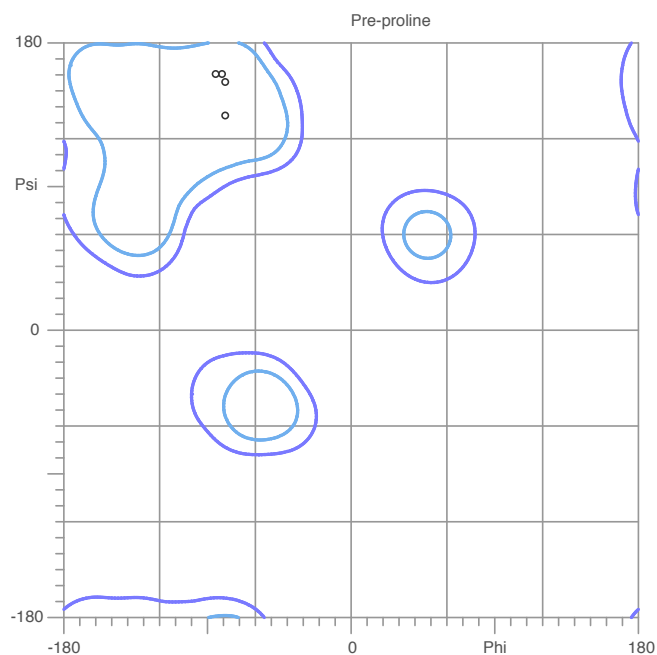
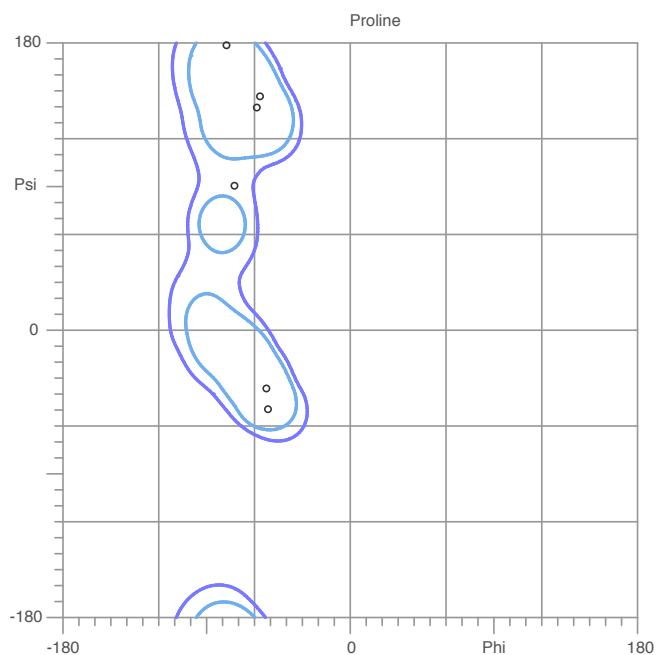
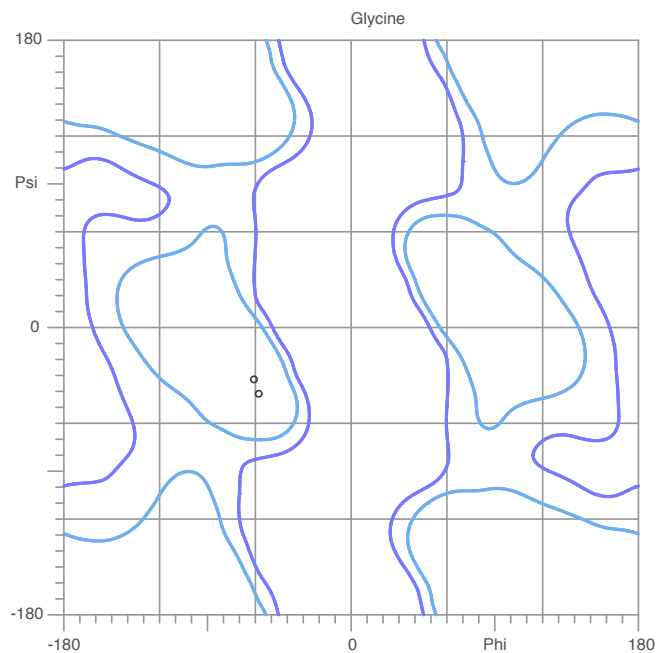
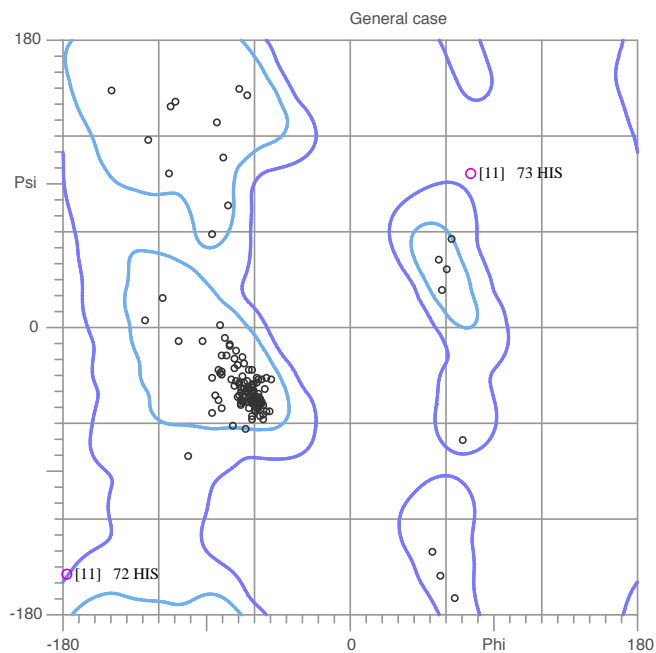
There were no outliers.

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 11

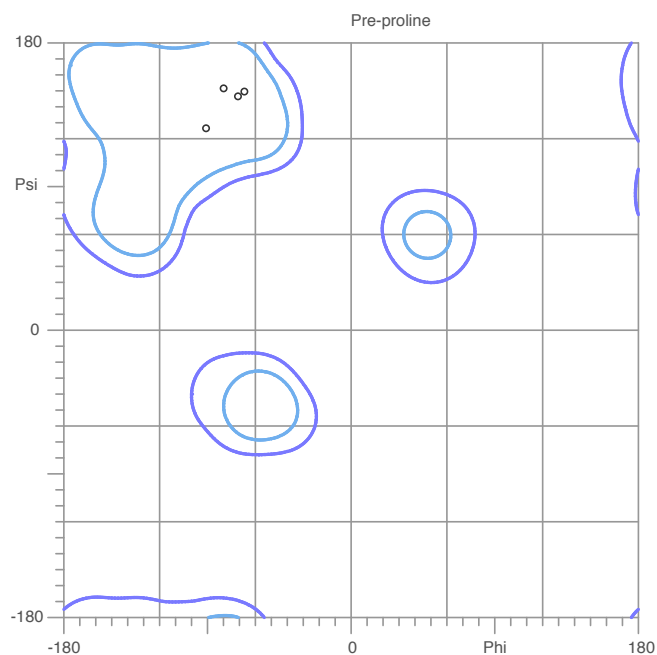
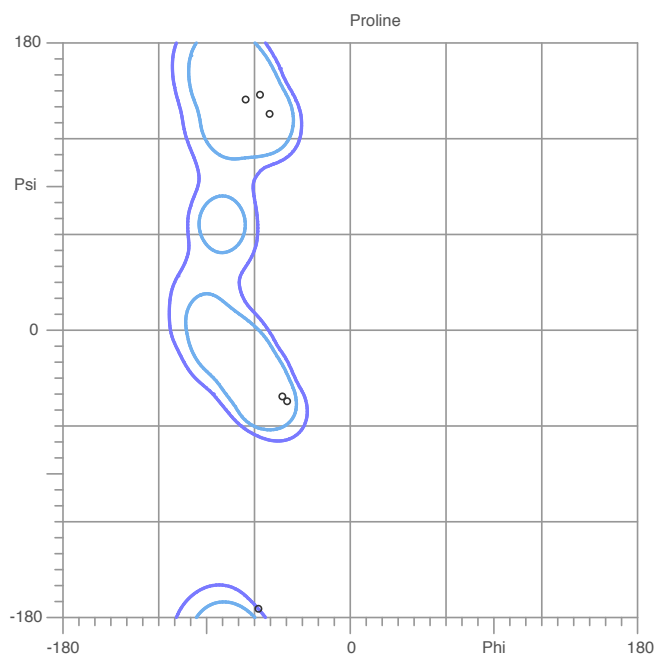
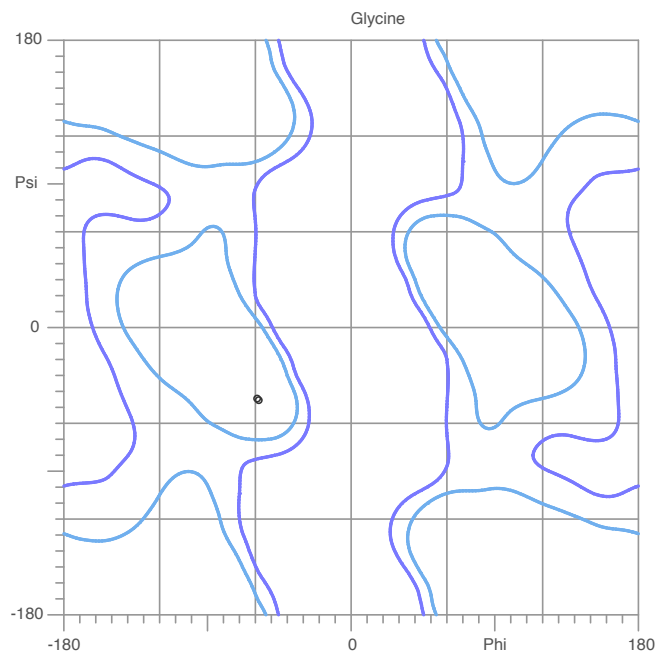
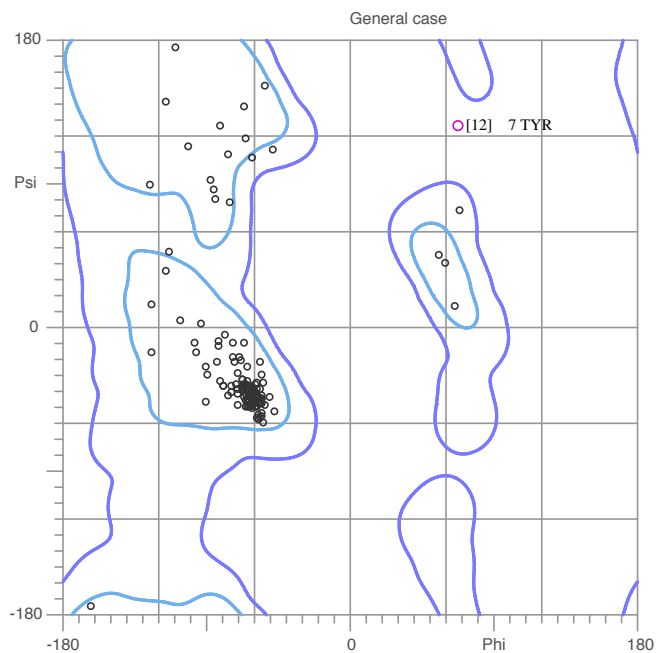


93.2% (138/148) of all residues were in favored (98%) regions.
98.6% (146/148) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[11] 72 HIS (-178.6, -154.4)
[11] 73 HIS (75.3, 97.1)

MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 12



95.9% (142/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

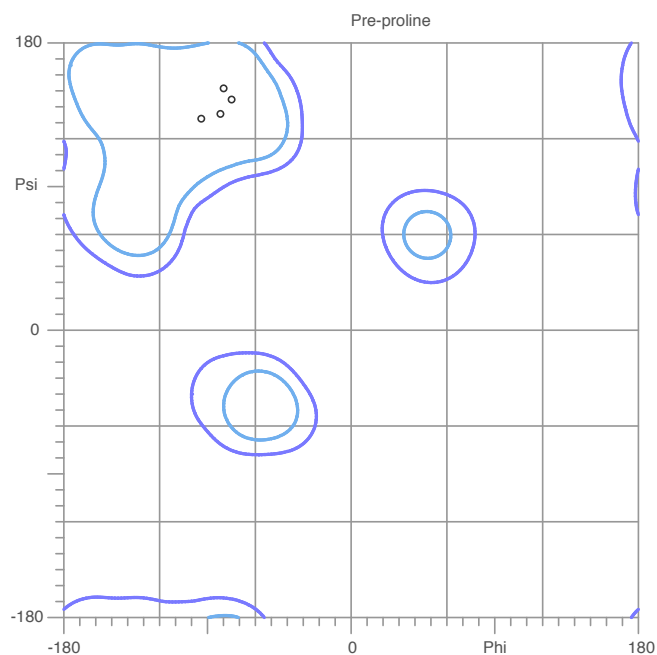
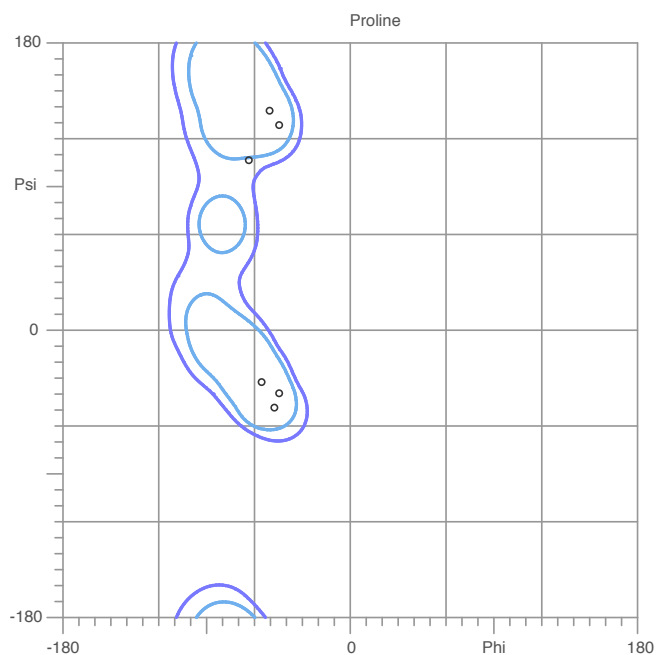
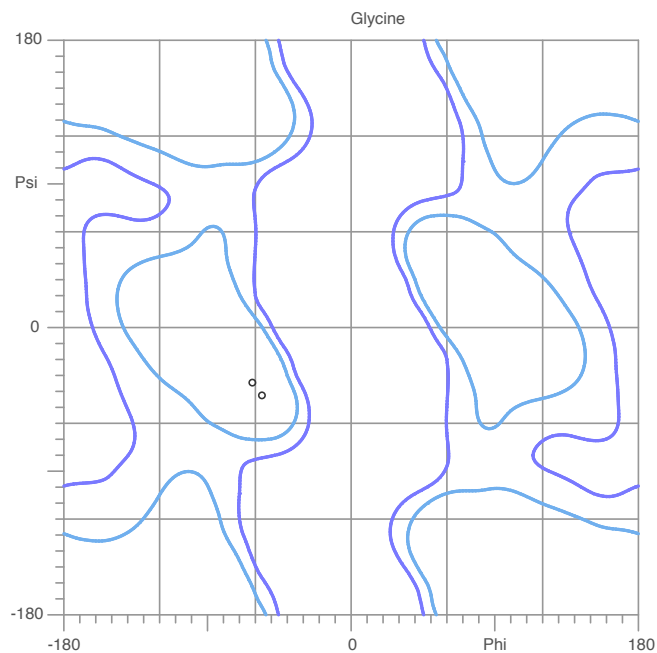
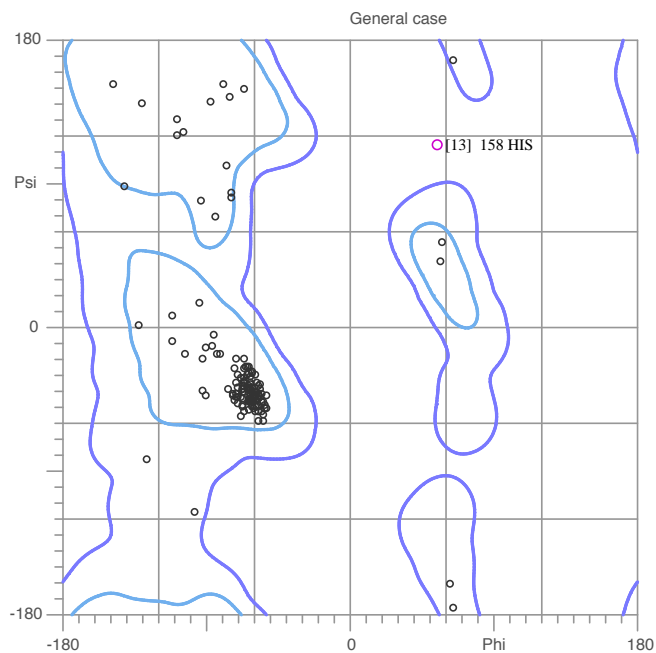
There were 1 outliers (phi, psi):
[12] 7 TYR (67.3, 127.1)

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 13



95.3% (141/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

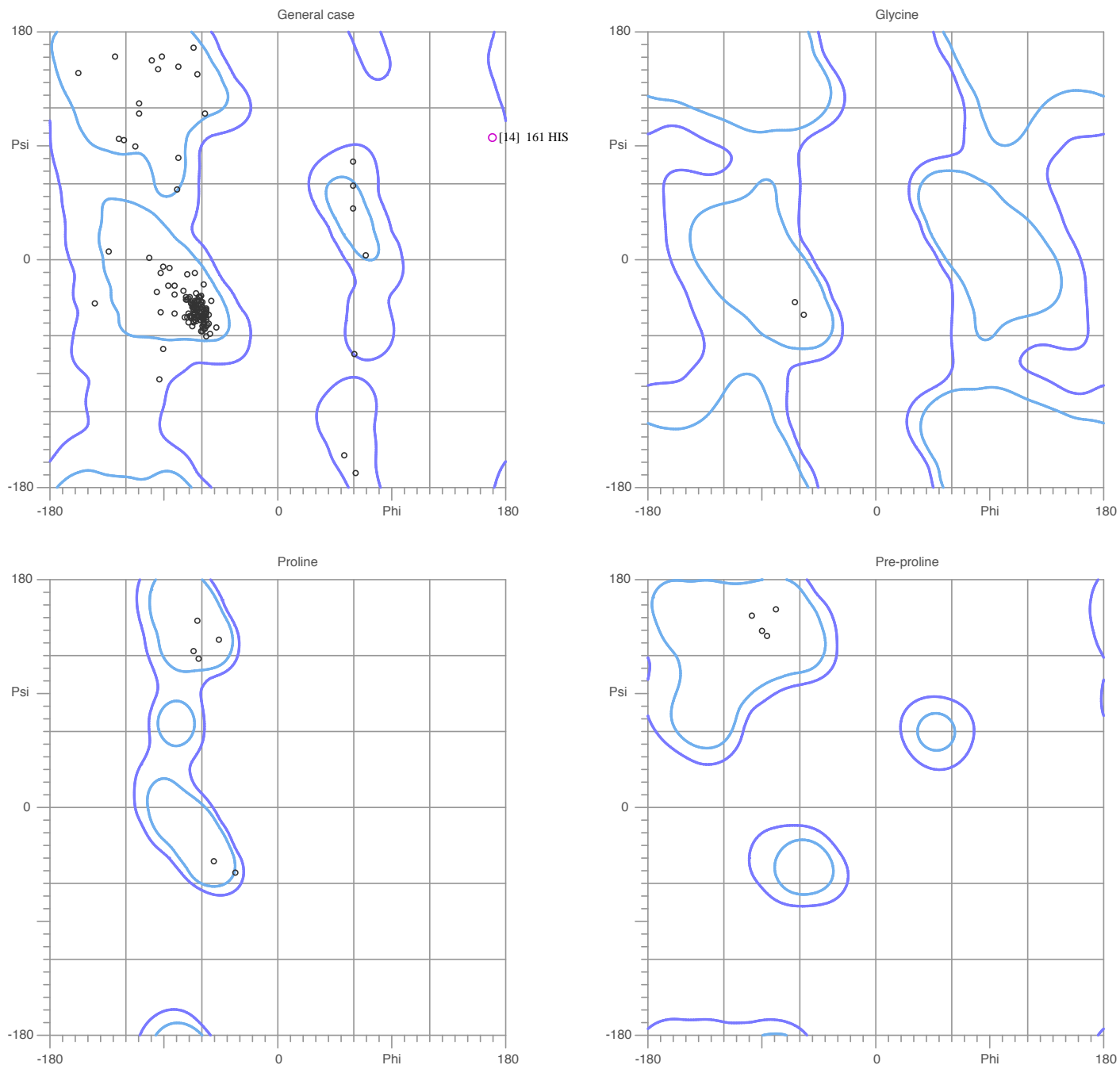
There were 1 outliers (phi, psi):
[13] 158 HIS (54.6, 115.1)

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 14



93.9% (139/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

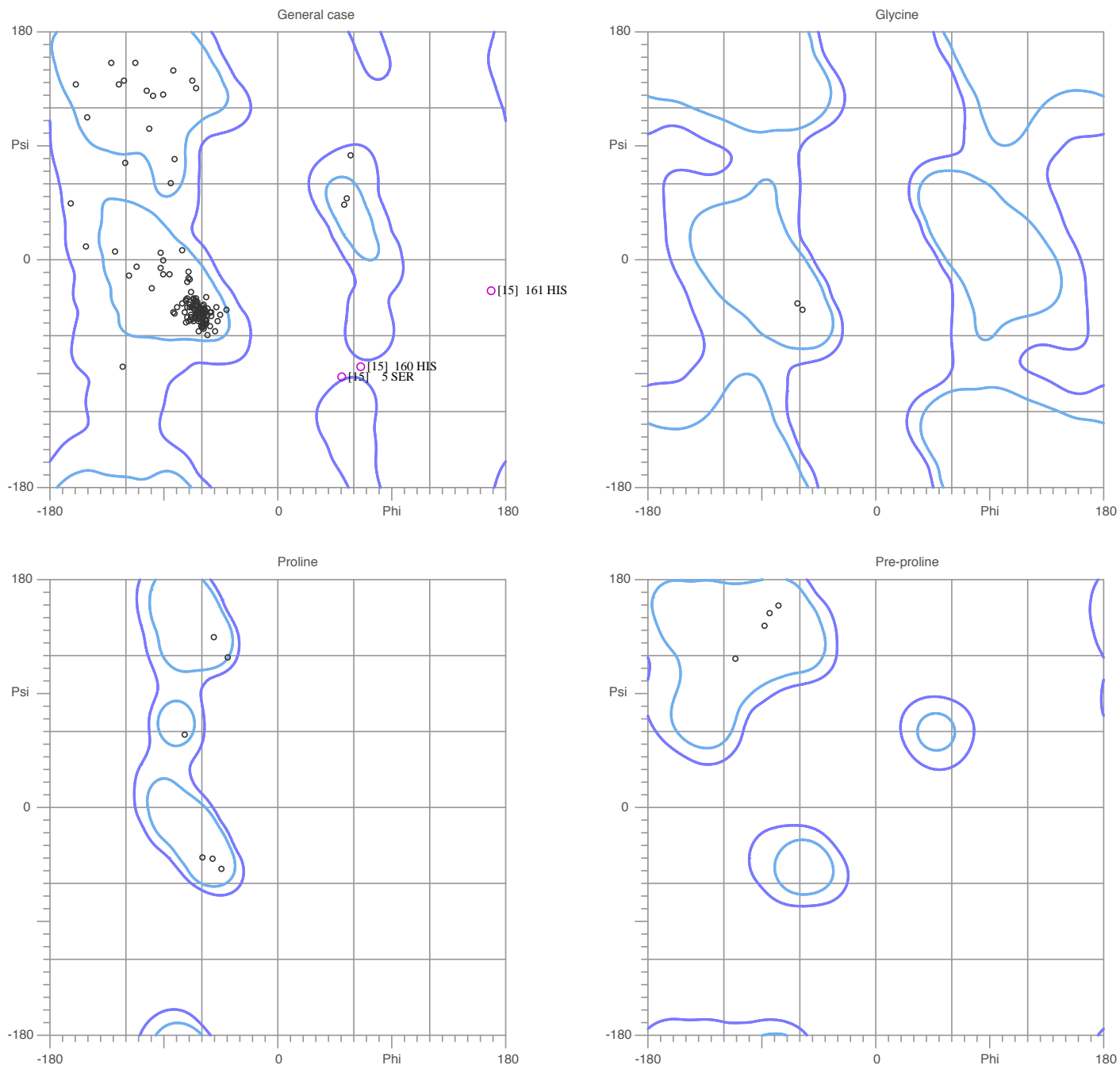
There were 1 outliers (phi, psi):
[14] 161 HIS (169.1, 97.1)

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 15



94.6% (140/148) of all residues were in favored (98%) regions.
98.0% (145/148) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

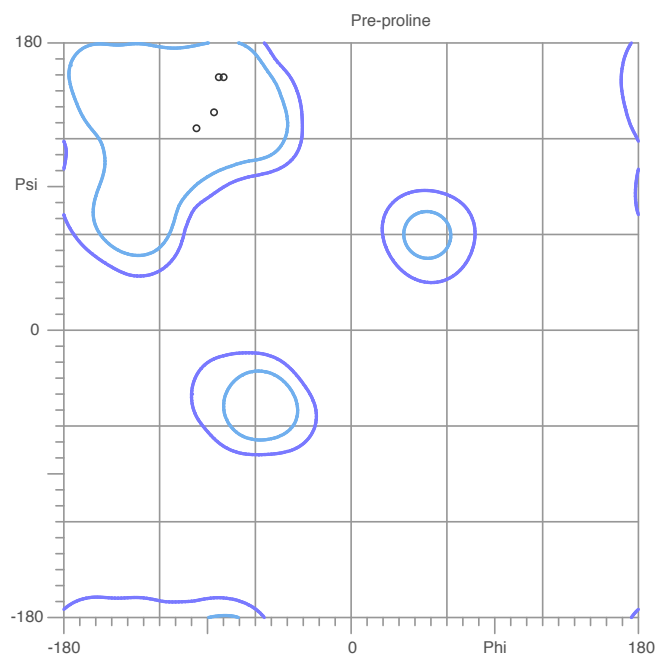
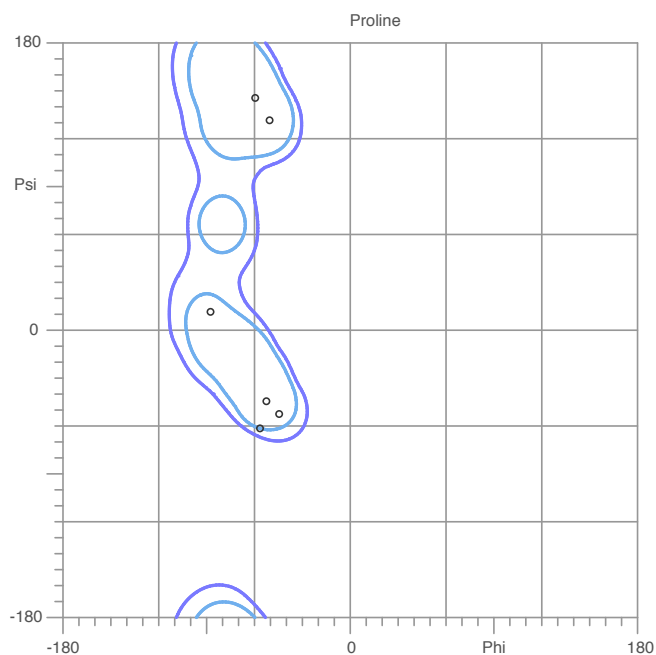
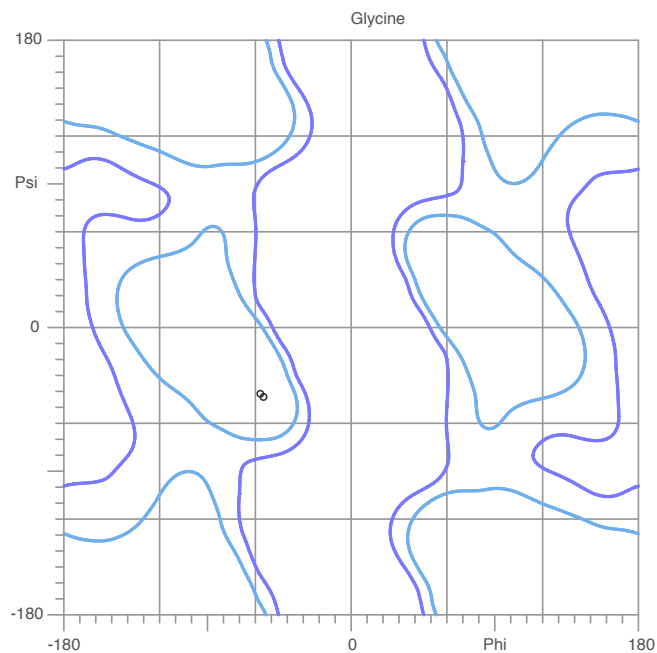
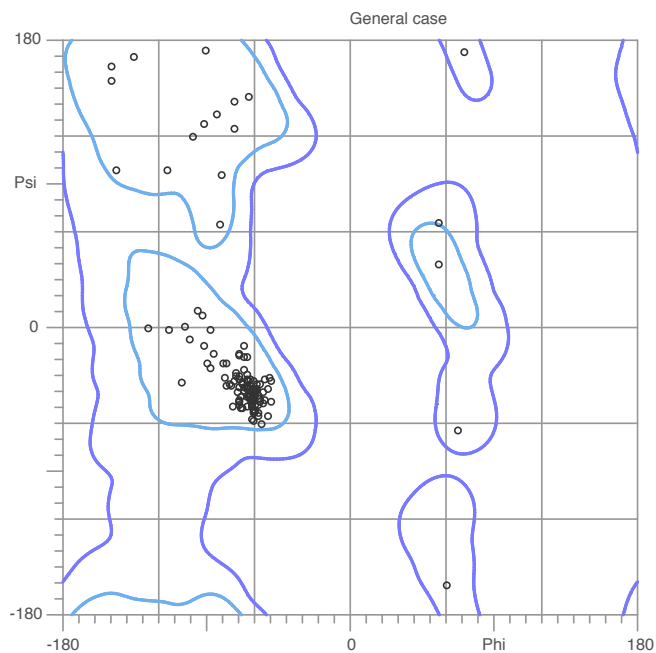
[15] 5 SER (50.6, -92.2)

[15] 160 HIS (65.6, -84.0)

[15] 161 HIS (168.6, -24.7)

MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 16



96.6% (143/148) of all residues were in favored (98%) regions.
100.0% (148/148) of all residues were in allowed (>99.8%) regions.

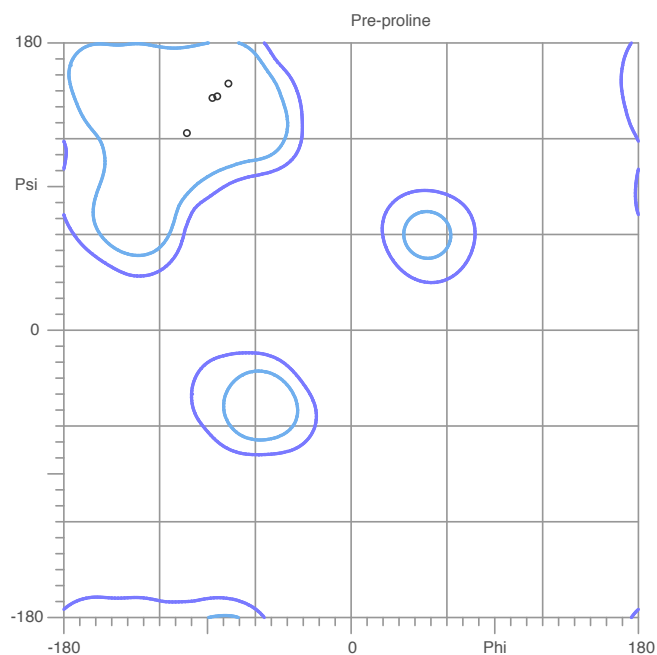
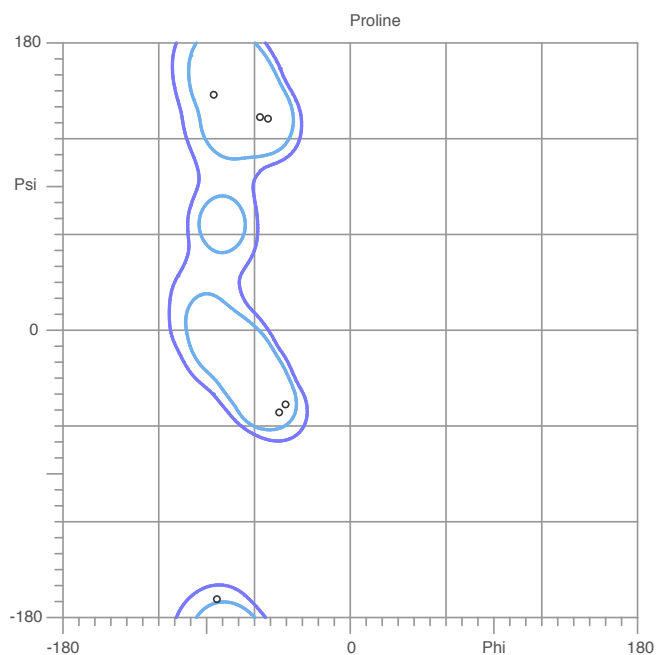
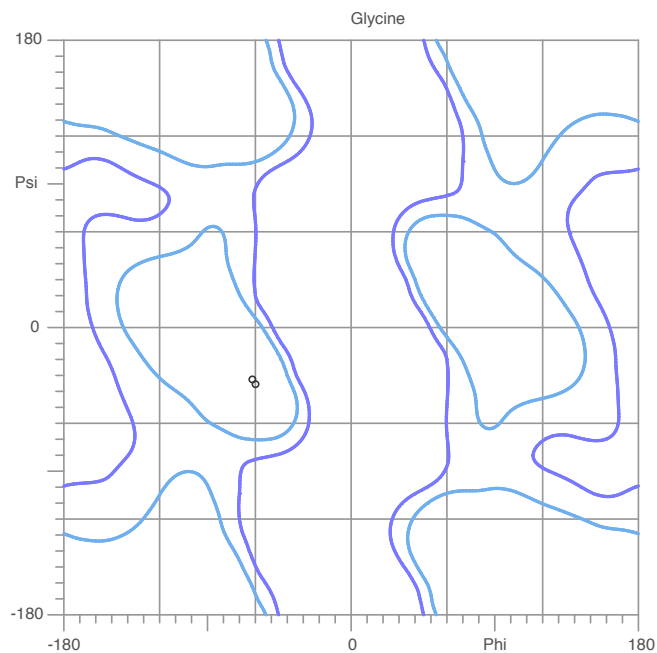
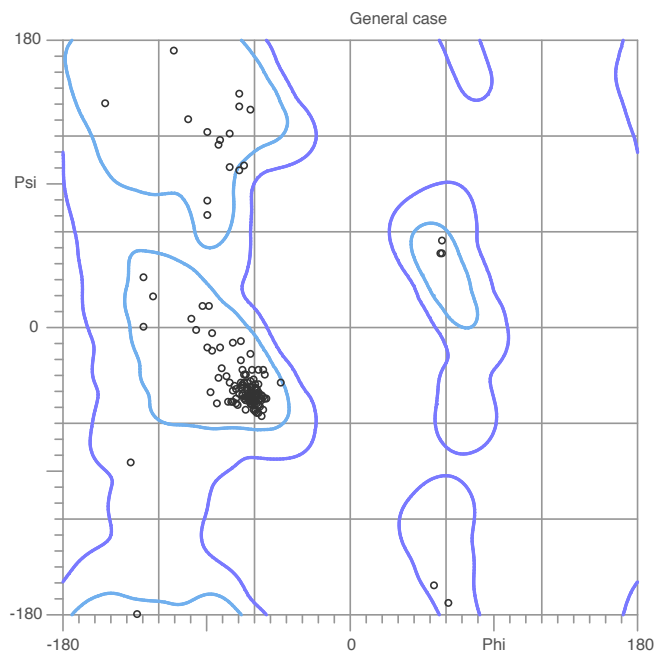
There were no outliers.

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 17



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.

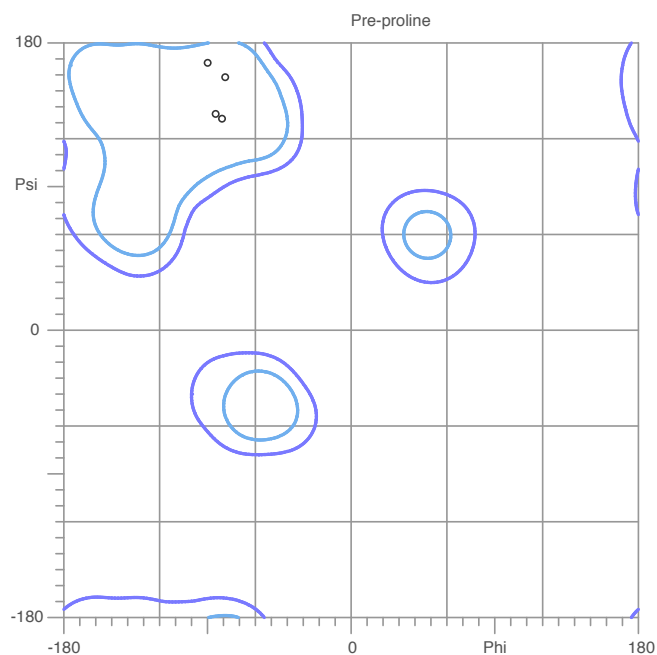
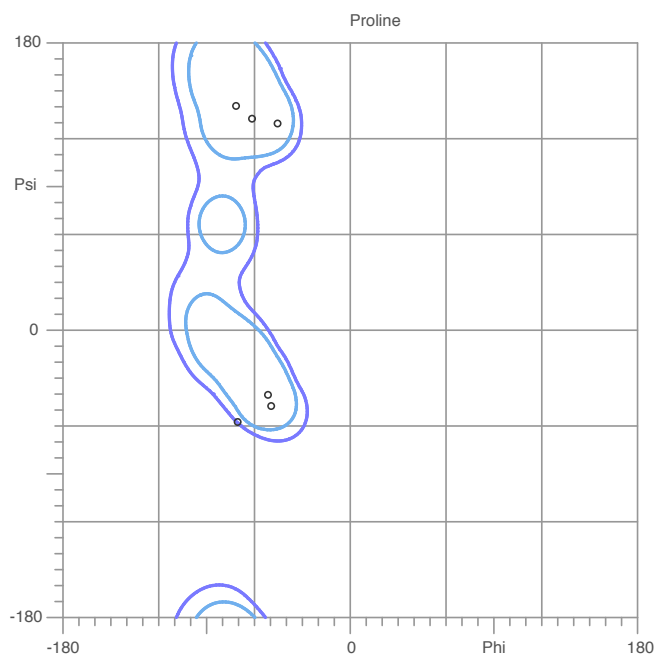
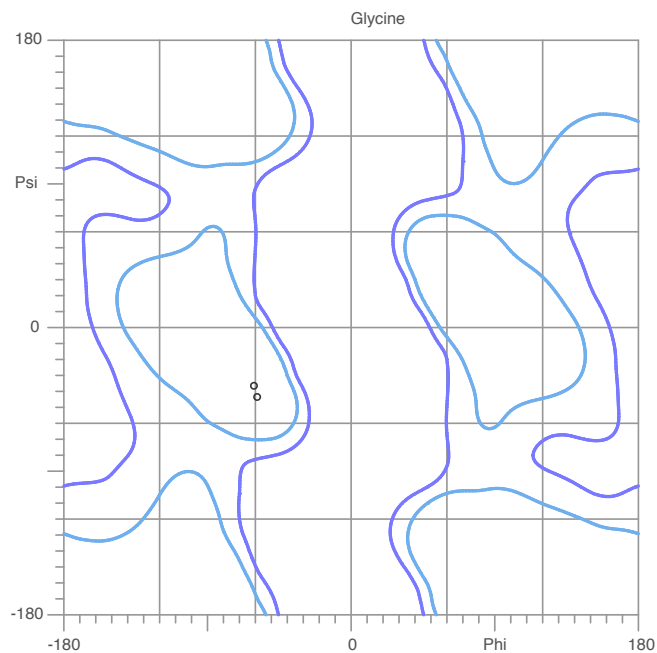
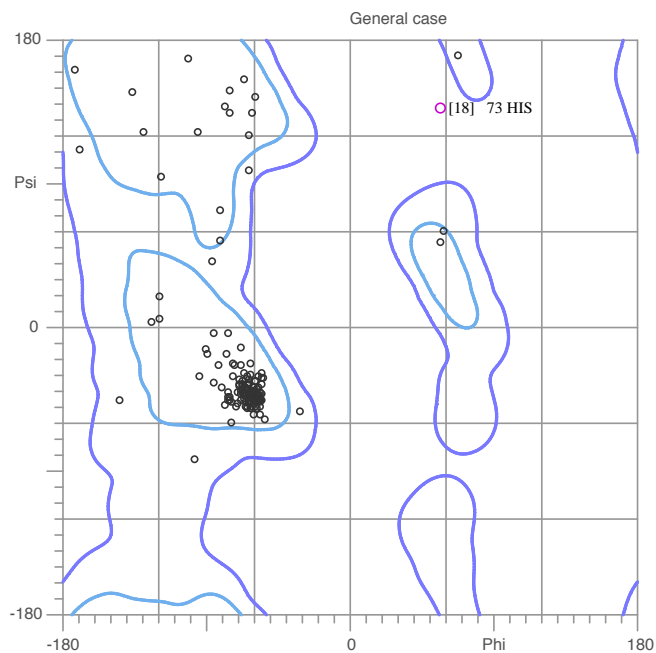
There were no outliers.

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

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 18



93.9% (139/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

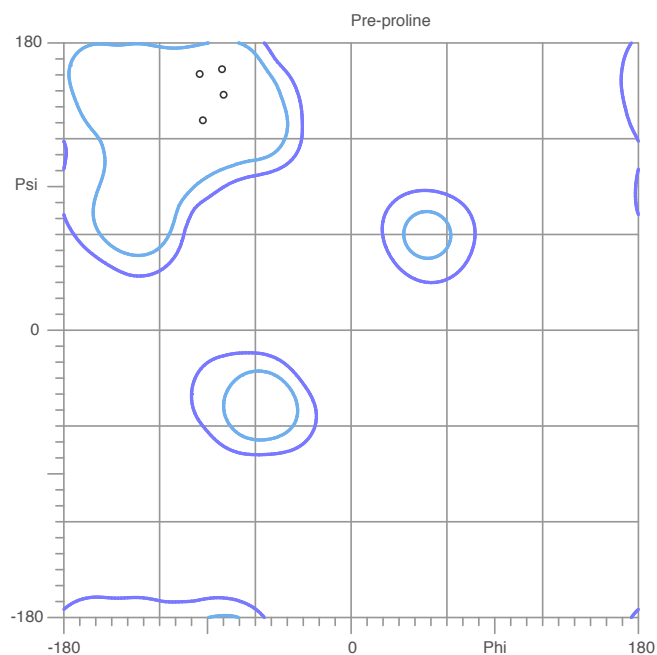
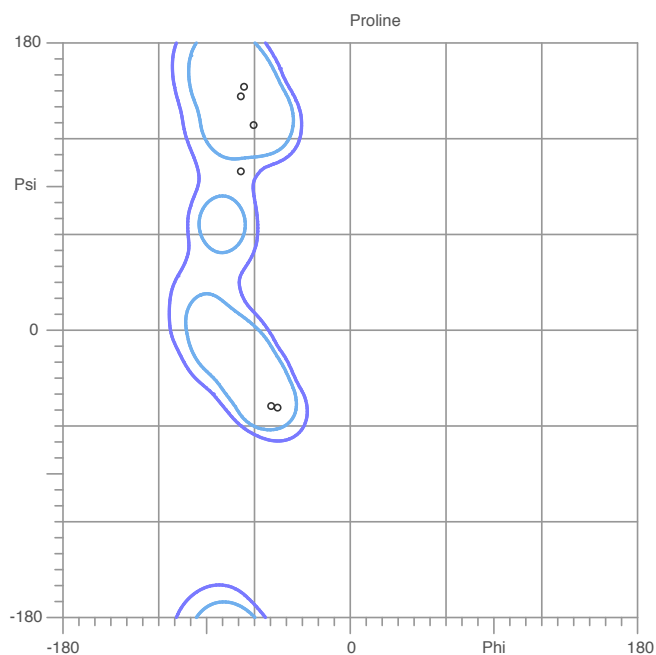
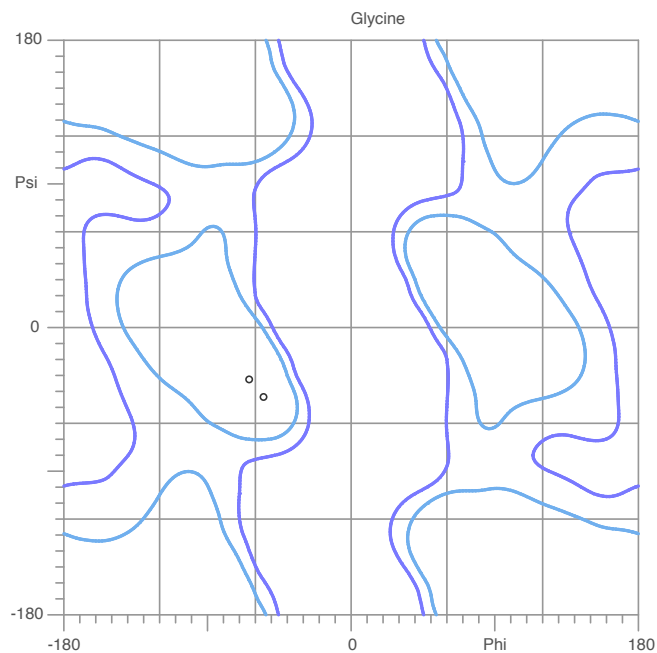
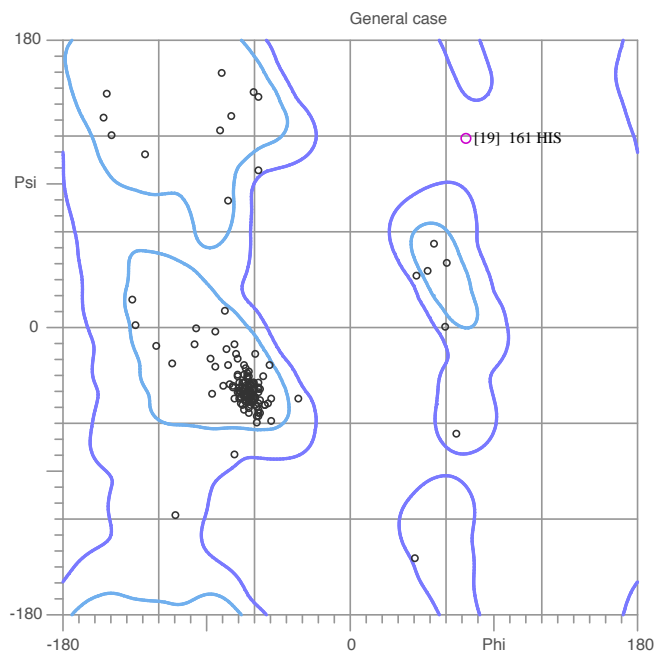
There were 1 outliers (phi, psi):
[18] 73 HIS (56.8, 138.3)

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

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 19



93.2% (138/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

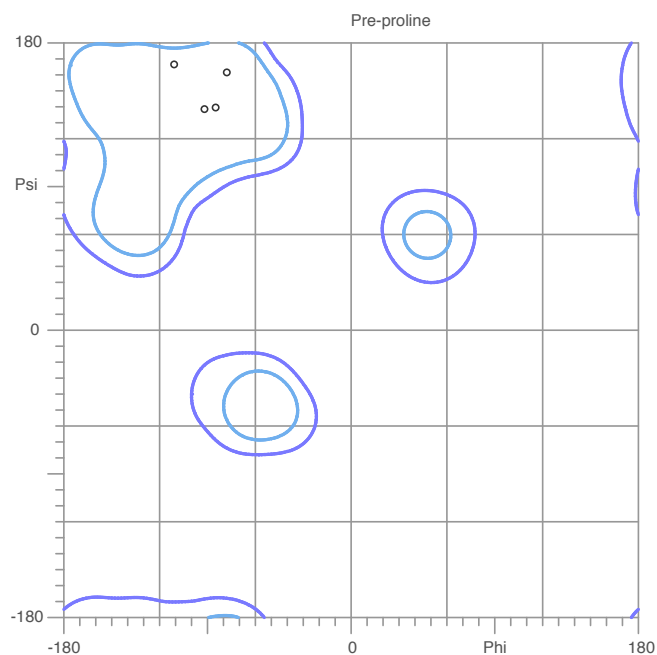
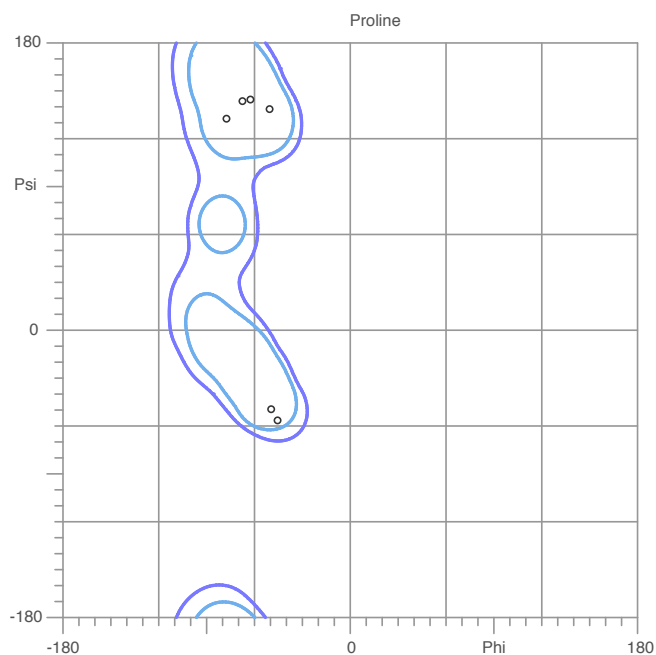
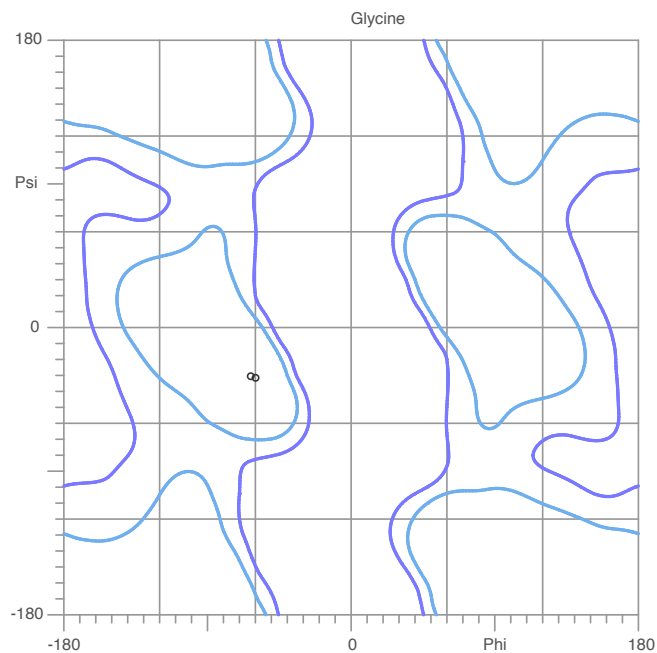
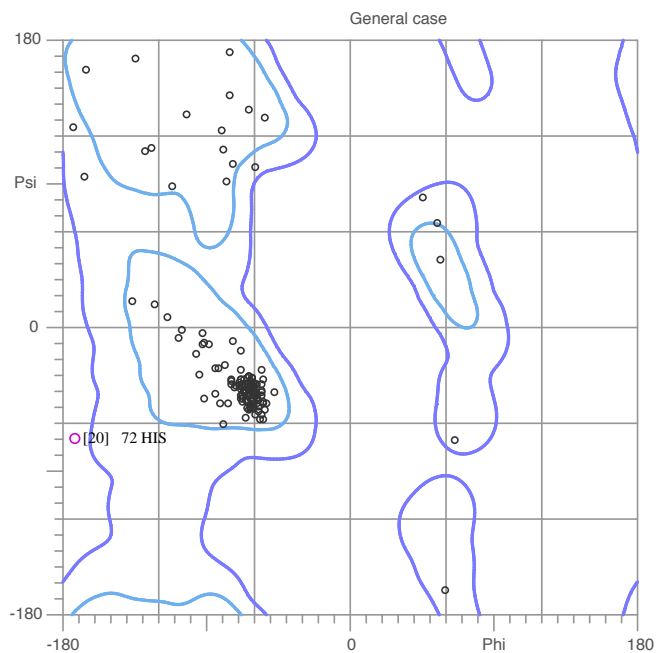
There were 1 outliers (phi, psi):
[19] 161 HIS (72.0, 119.5)

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

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MolProbity Ramachandran analysis

CSR4_NMR_em_bcr3.pdb, model 20



94.6% (140/148) of all residues were in favored (98%) regions.
99.3% (147/148) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 72 HIS (-173.6, -70.0)