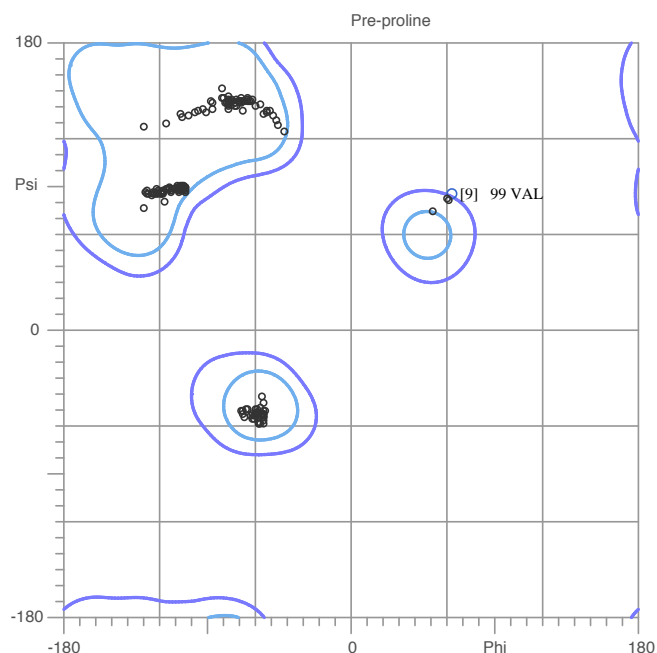
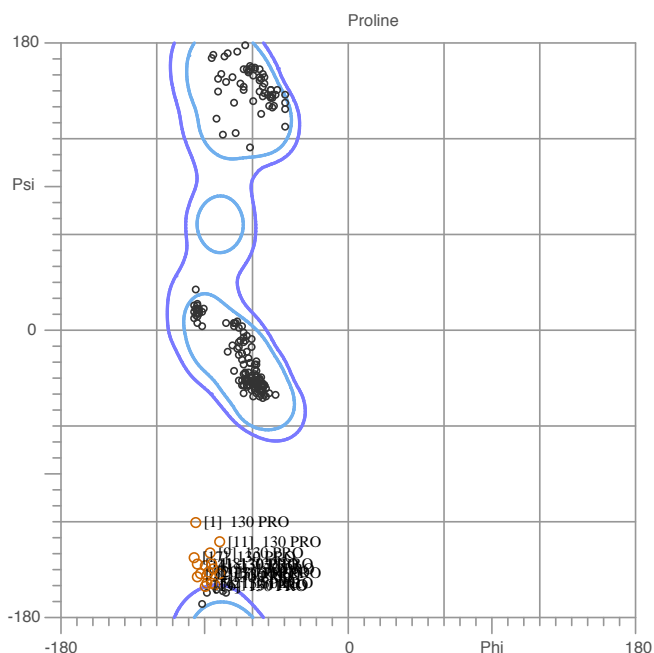
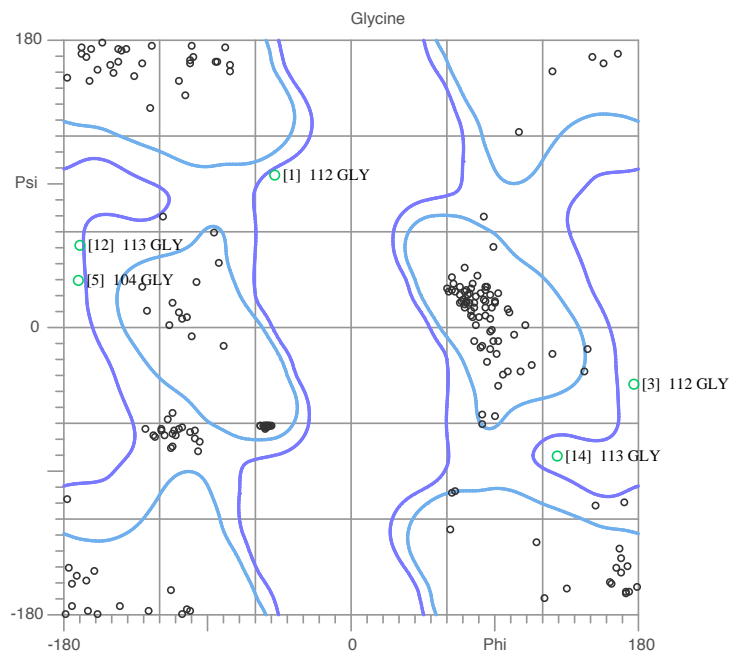
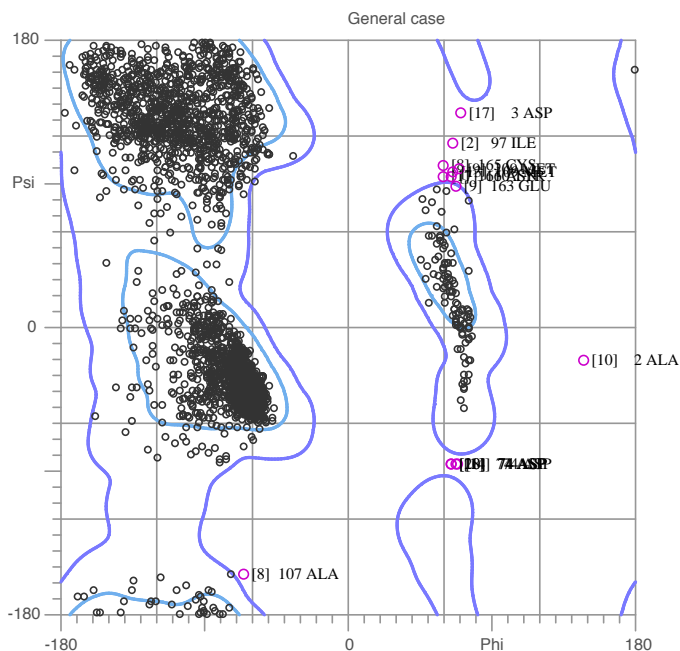


MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, all models



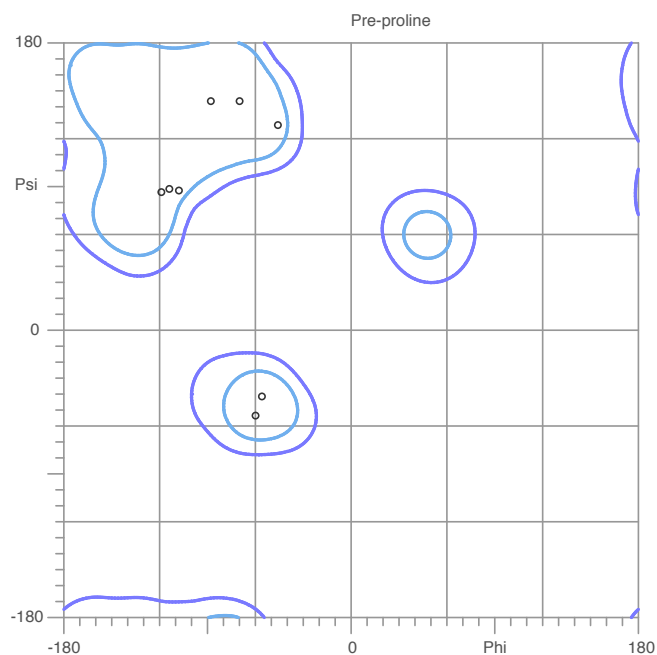
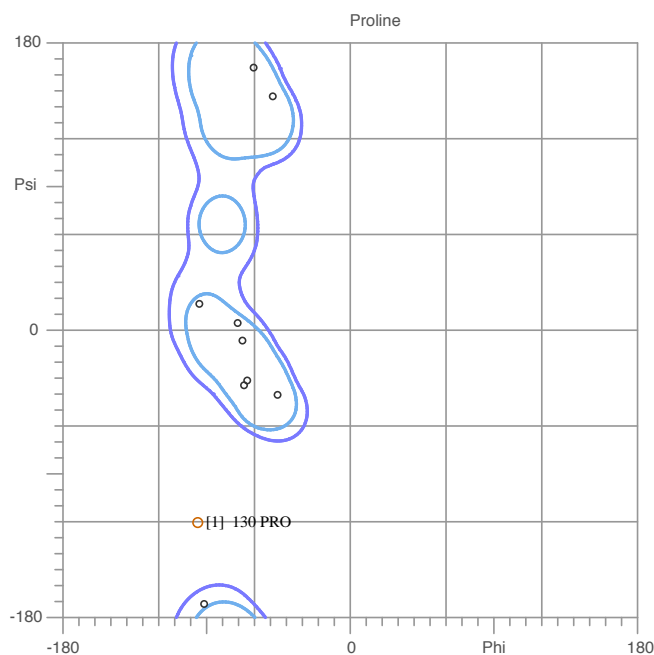
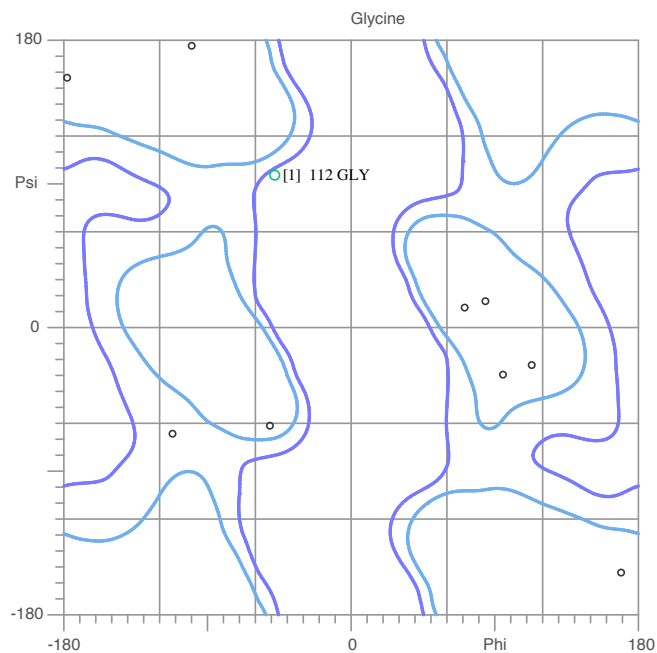
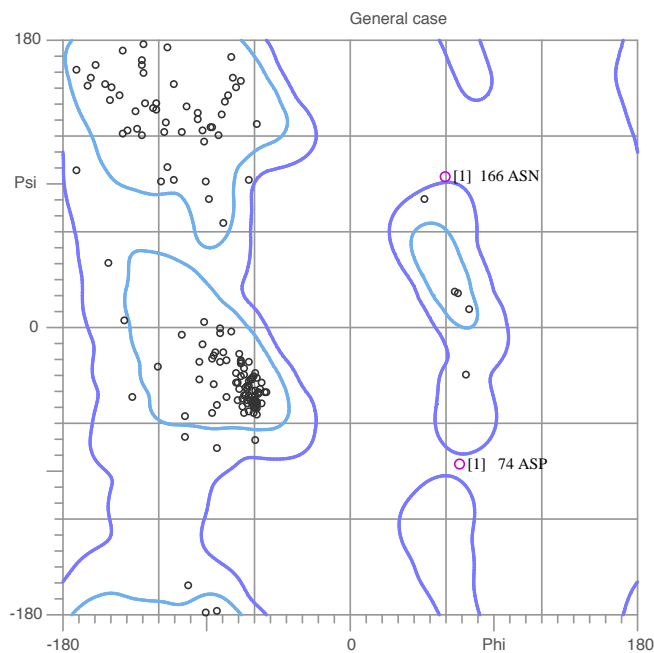
94.1% (3257/3460) of all residues were in favored (98%) regions.
98.9% (3423/3460) of all residues were in allowed (>99.8%) regions.

There were 37 outliers (phi, psi):

- | | |
|-----------------------------|------------------------------|
| [1] 74 ASP (68.3, -86.0) | [9] 99 VAL (63.5, 86.6) |
| [1] 112 GLY (-49.0, 96.6) | [9] 109 MET (69.5, 100.1) |
| [1] 130 PRO (-96.7, -120.1) | [9] 130 PRO (-87.9, -139.8) |
| [1] 166 ASN (59.7, 95.0) | [9] 163 GLU (67.6, 89.7) |
| [2] 97 ILE (65.9, 116.2) | [10] 2 ALA (147.0, -20.2) |
| [2] 130 PRO (-89.0, -153.3) | [11] 130 PRO (-81.9, -132.4) |
| [3] 112 GLY (177.3, -35.3) | [12] 113 GLY (-170.0, 52.9) |
| [3] 130 PRO (-93.4, -152.9) | [12] 130 PRO (-86.4, -158.3) |
| [4] 130 PRO (-90.4, -147.5) | [13] 109 MET (65.6, 98.7) |
| [5] 104 GLY (-171.7, 30.2) | [13] 130 PRO (-81.5, -152.4) |
| [5] 130 PRO (-90.0, -158.3) | [14] 74 ASP (67.6, -85.8) |
| [6] 130 PRO (-84.3, -159.5) | [14] 113 GLY (129.1, -80.1) |
| [7] 110 TYR (64.2, 95.6) | [14] 130 PRO (-95.6, -146.2) |
| [7] 130 PRO (-96.0, -154.7) | [15] 130 PRO (-85.0, -149.6) |
| [8] 107 ALA (-67.0, -154.8) | [17] 3 ASP (70.3, 135.1) |
| [8] 165 CYS (59.6, 102.1) | [17] 130 PRO (-97.1, -142.2) |
| | [18] 74 ASP (64.4, -85.0) |
| | [18] 130 PRO (-86.5, -146.6) |
| | [19] 130 PRO (-90.8, -160.9) |
| | [20] 74 ASP (64.5, -85.9) |
| | [20] 130 PRO (-88.6, -151.6) |

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 1



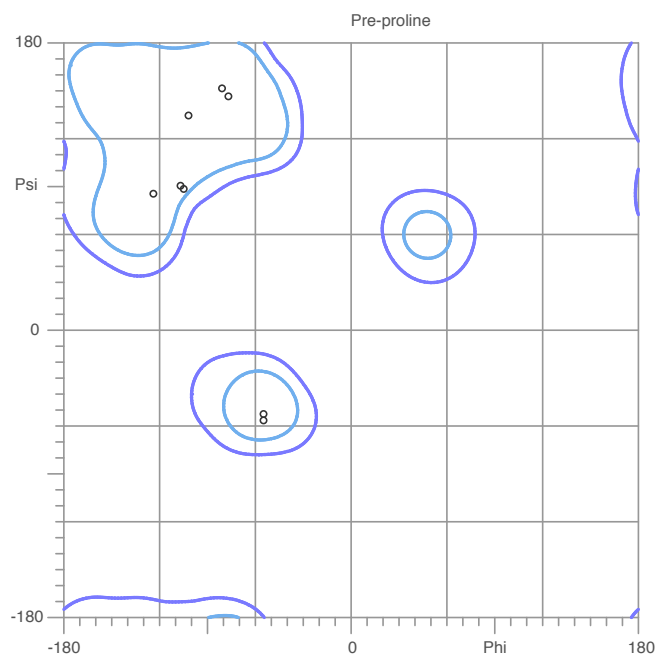
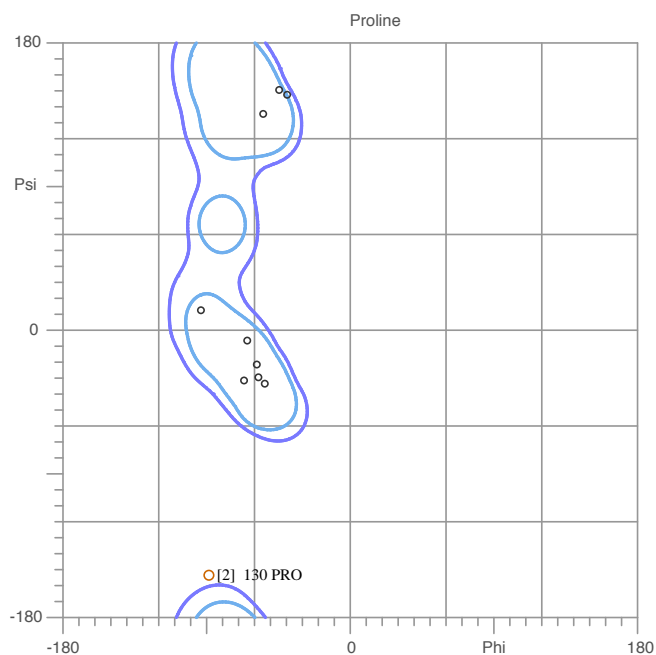
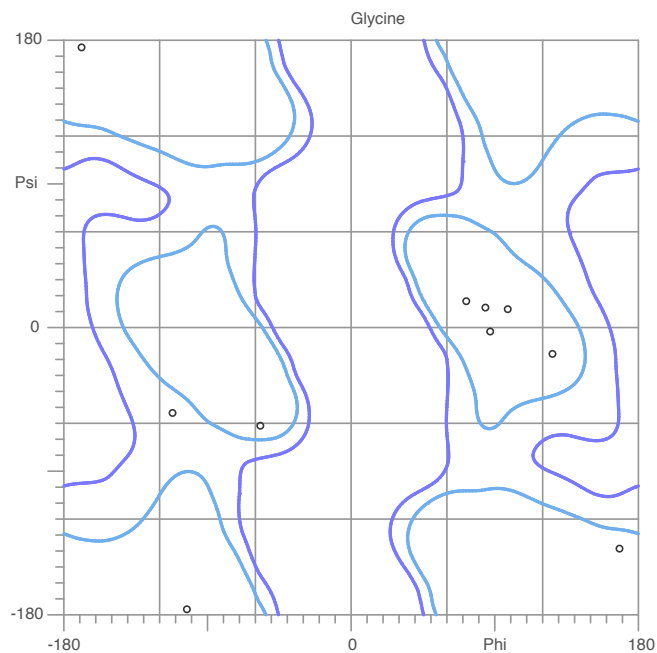
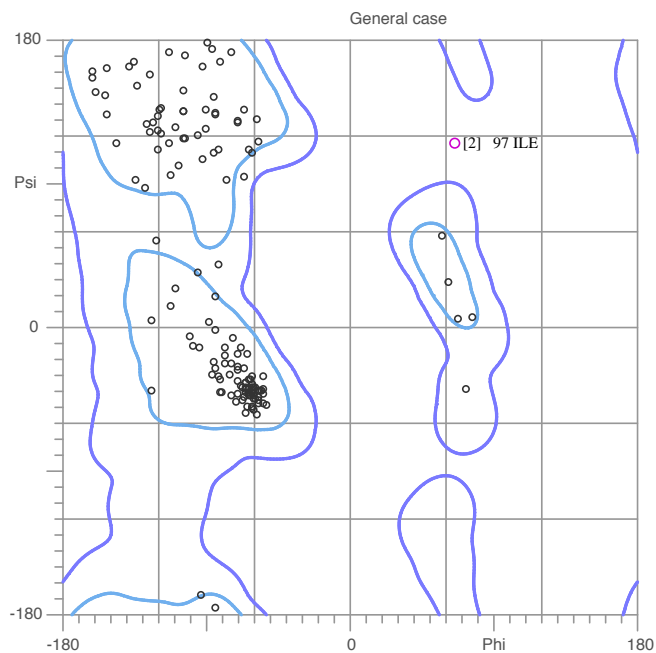
90.2% (156/173) of all residues were in favored (98%) regions.
97.7% (169/173) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [1] 74 ASP (68.3, -86.0)
- [1] 112 GLY (-49.0, 96.6)
- [1] 130 PRO (-96.7, -120.1)
- [1] 166 ASN (59.7, 95.0)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 2



94.8% (164/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

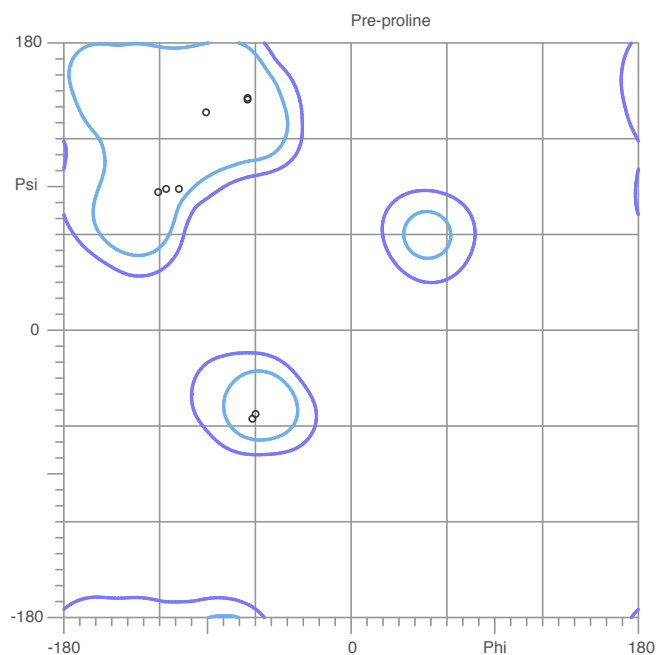
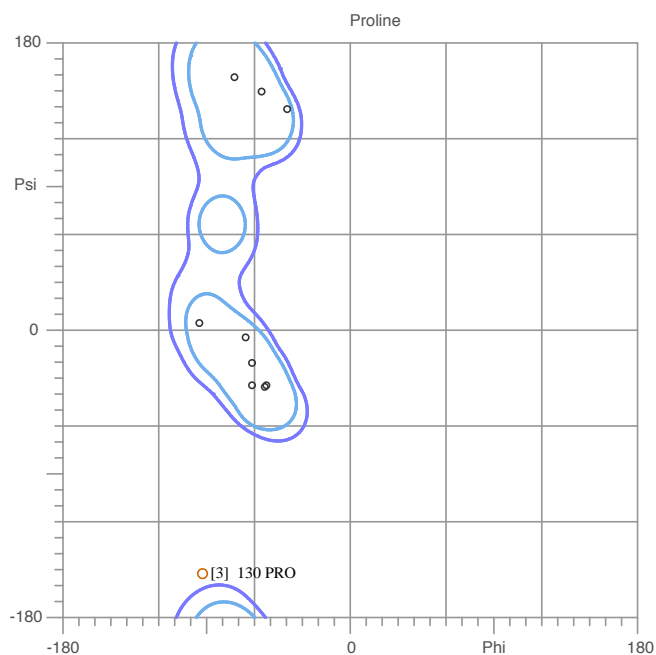
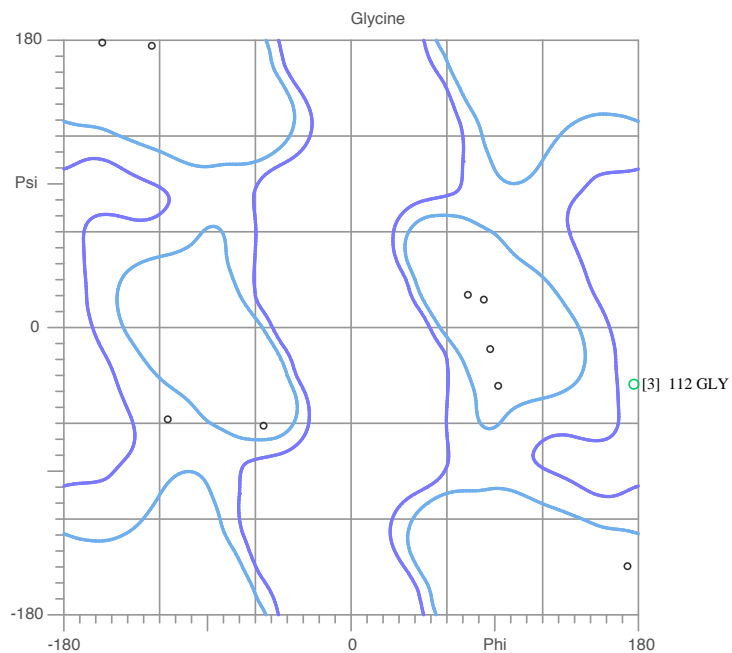
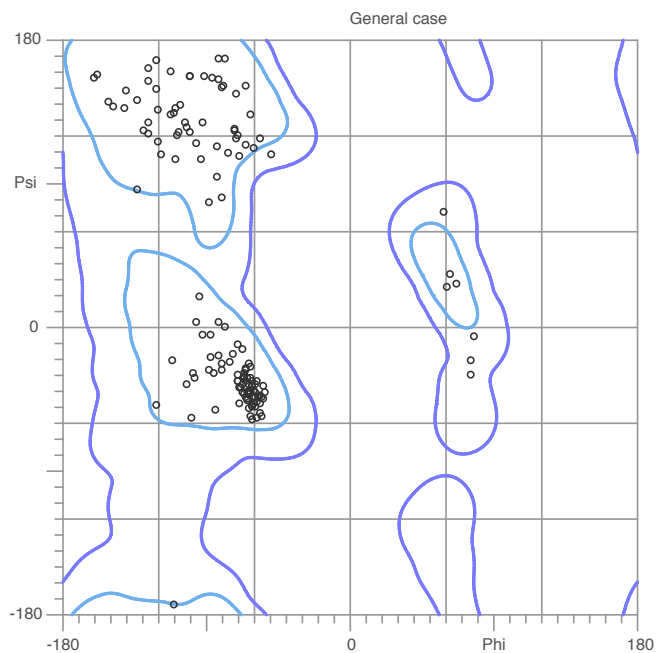
There were 2 outliers (phi, psi):

[2] 97 ILE (65.9, 116.2)

[2] 130 PRO (-89.0, -153.3)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 3

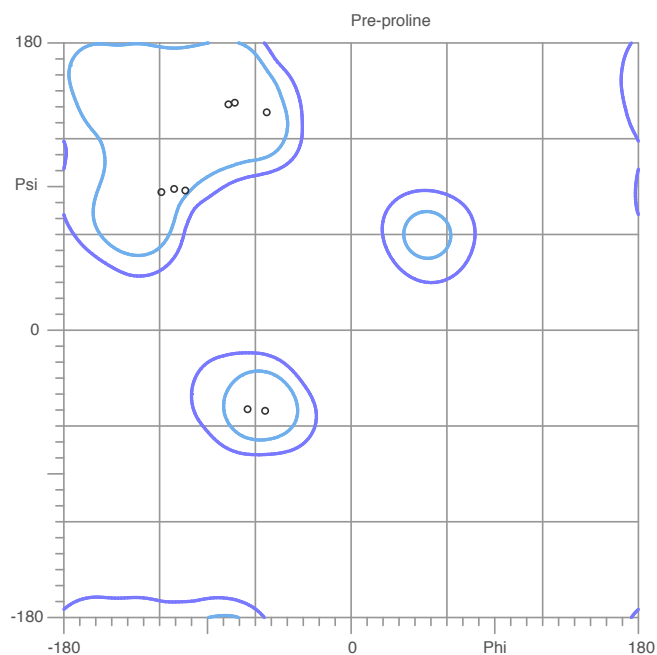
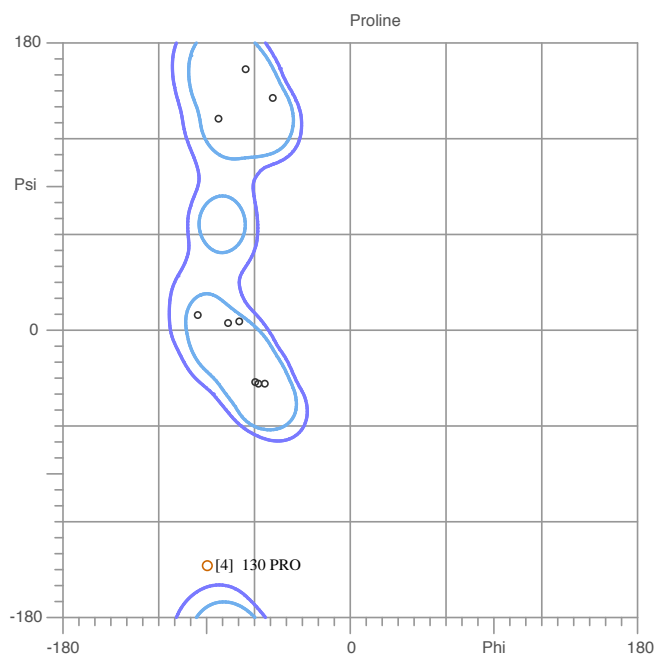
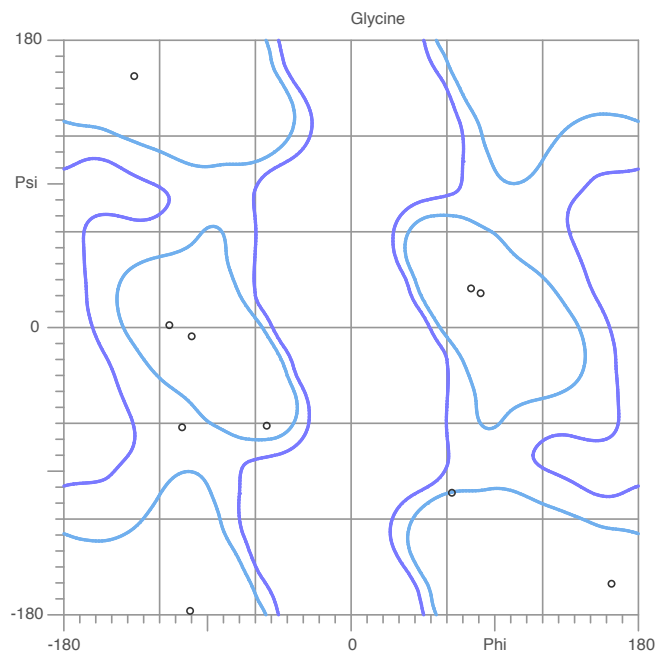
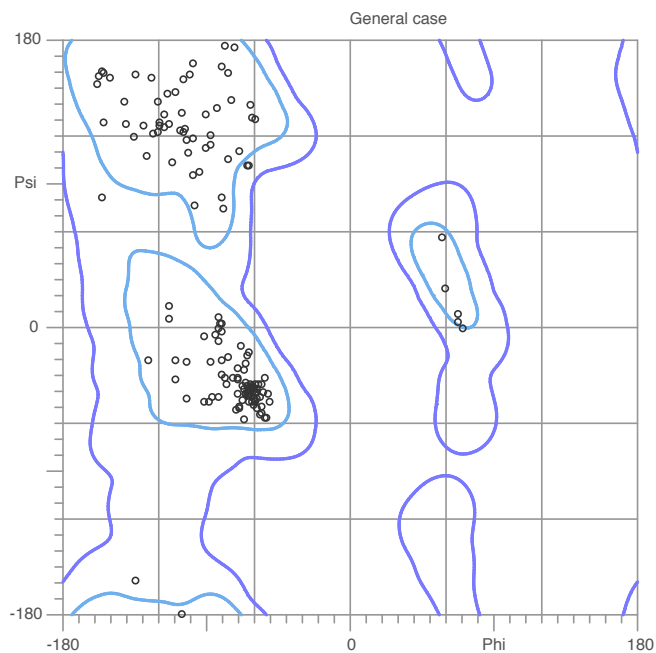


95.4% (165/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[3] 112 GLY (177.3, -35.3)
[3] 130 PRO (-93.4, -152.9)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 4



96.0% (166/173) of all residues were in favored (98%) regions.
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

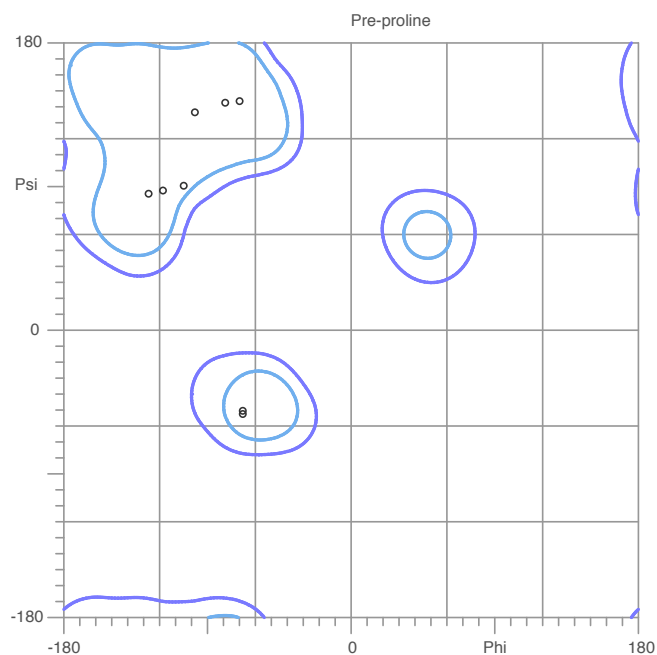
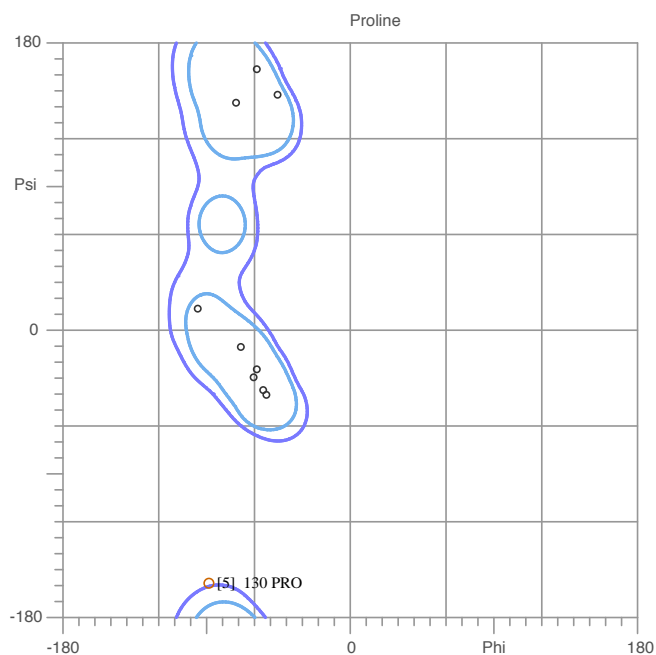
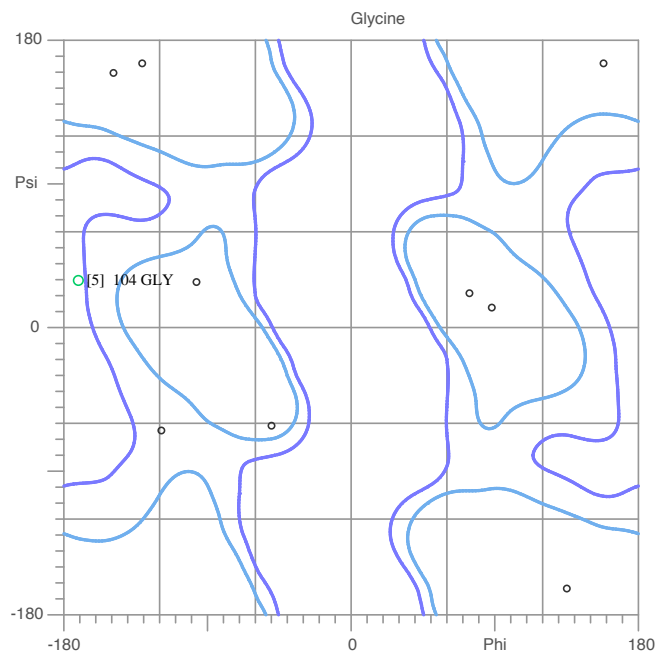
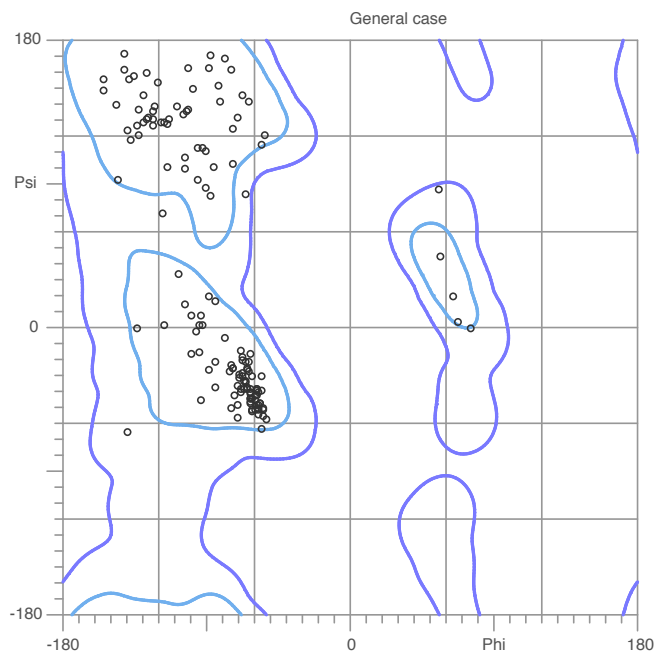
There were 1 outliers (phi, psi):
[4] 130 PRO (-90.4, -147.5)

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MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 5

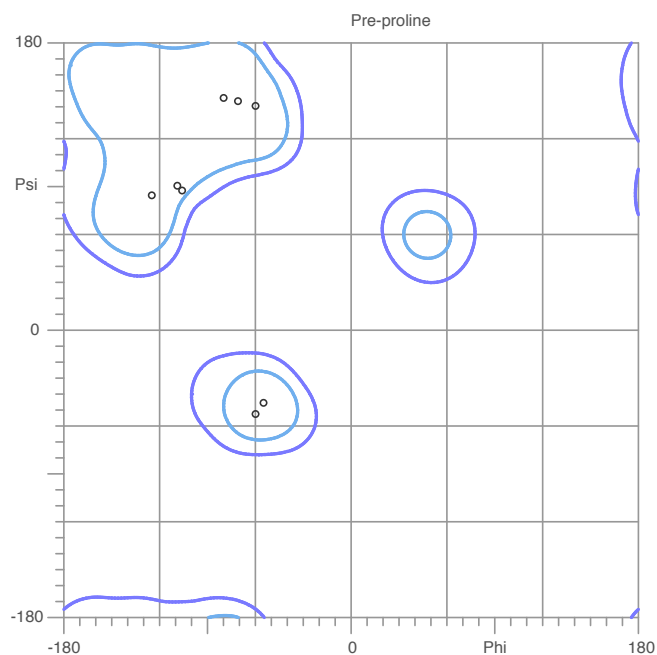
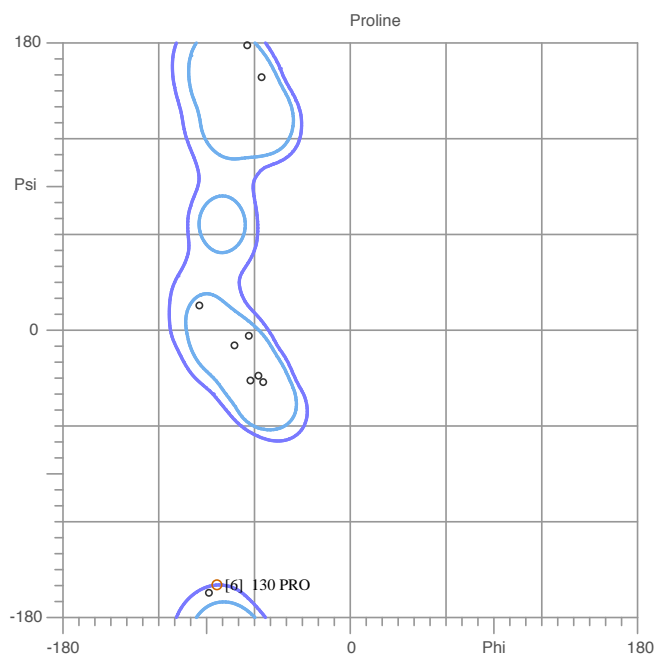
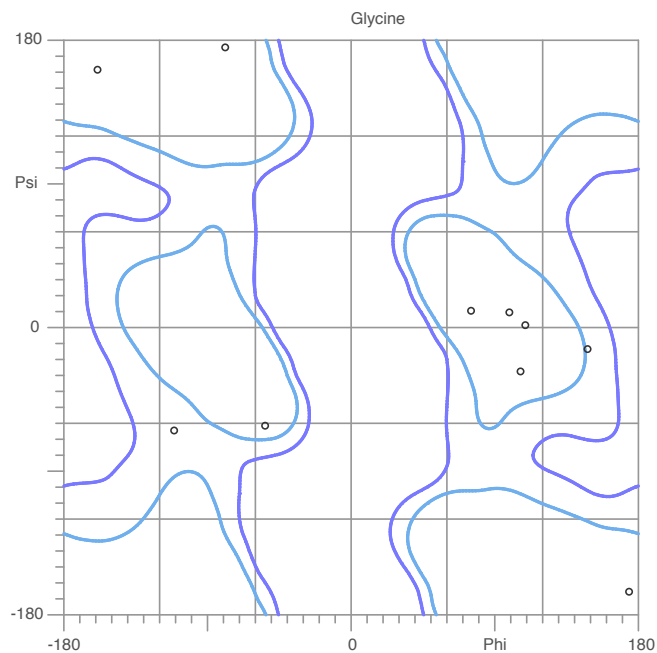
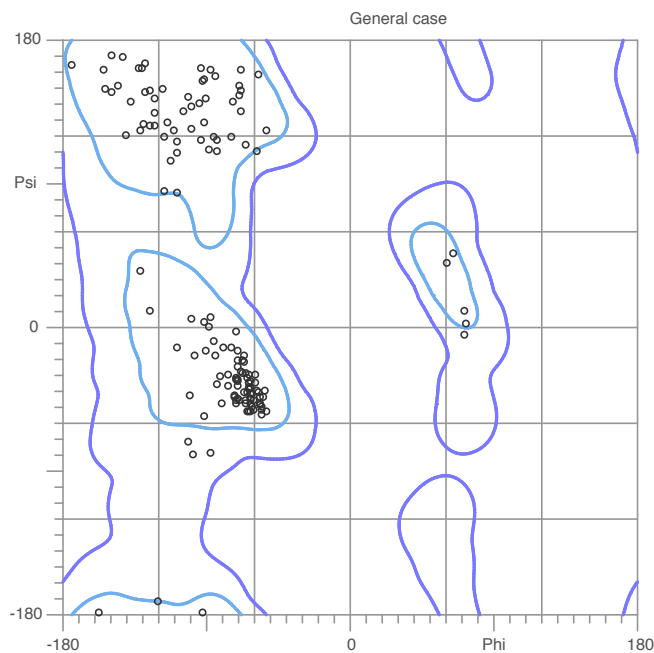


96.0% (166/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[5] 104 GLY (-171.7, 30.2)
[5] 130 PRO (-90.0, -158.3)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 6



95.4% (165/173) of all residues were in favored (98%) regions.
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

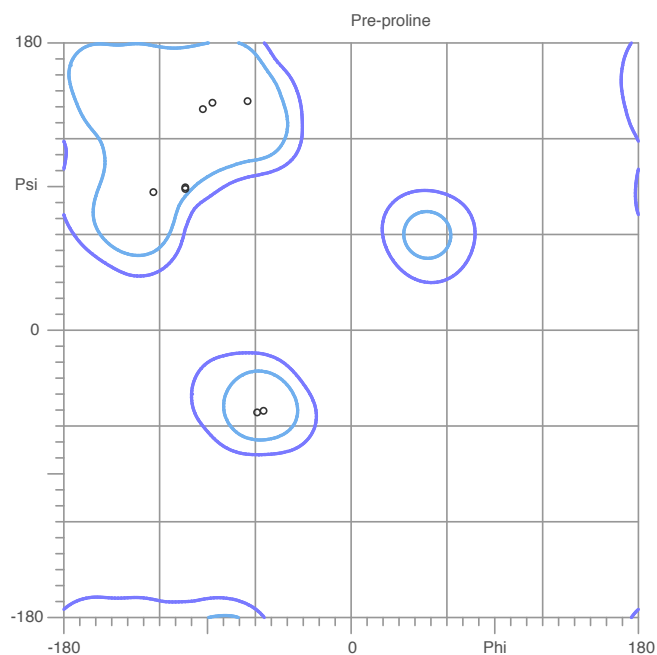
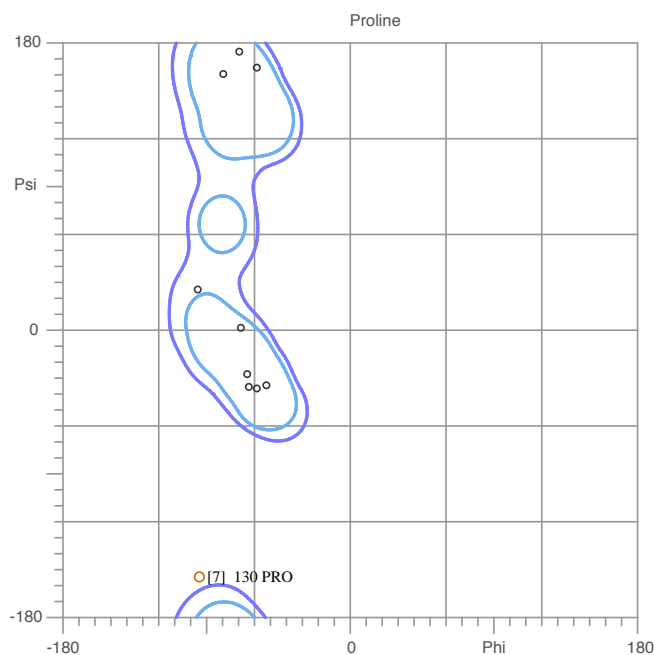
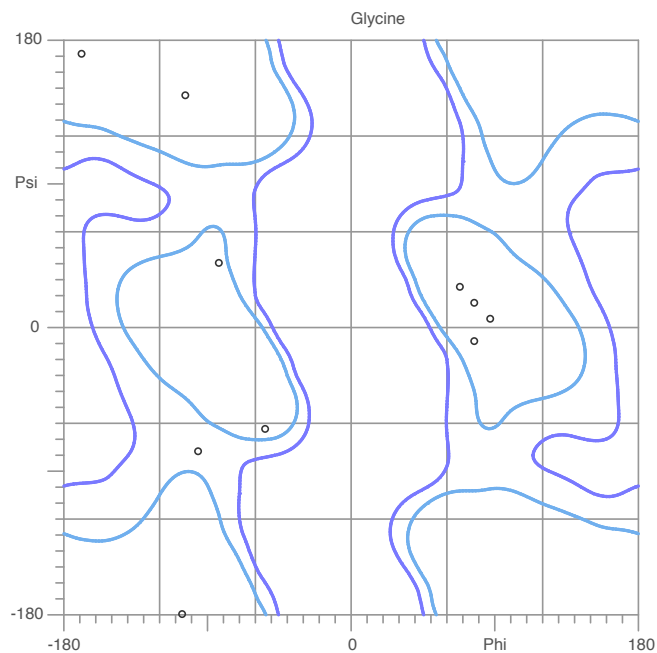
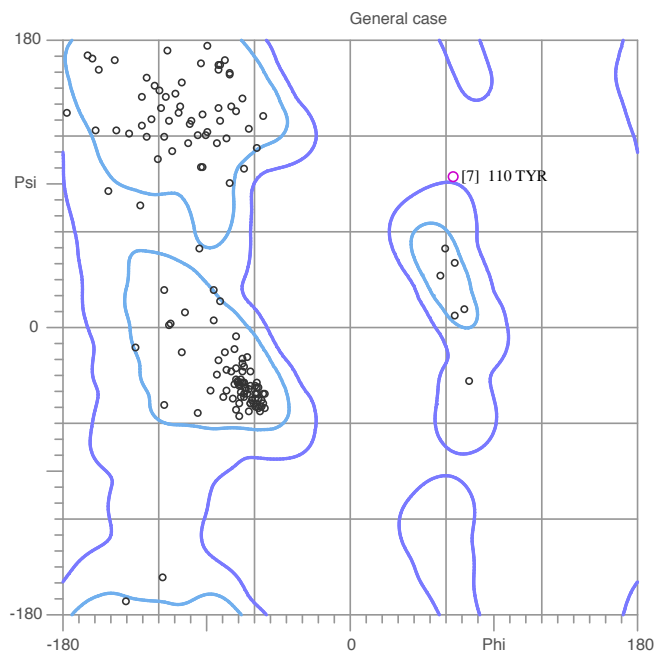
There were 1 outliers (phi, psi):
[6] 130 PRO (-84.3, -159.5)

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MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 7

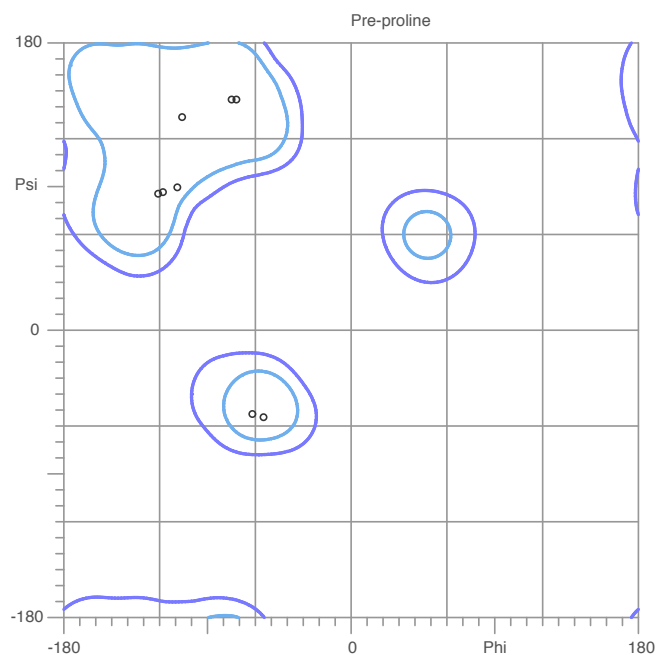
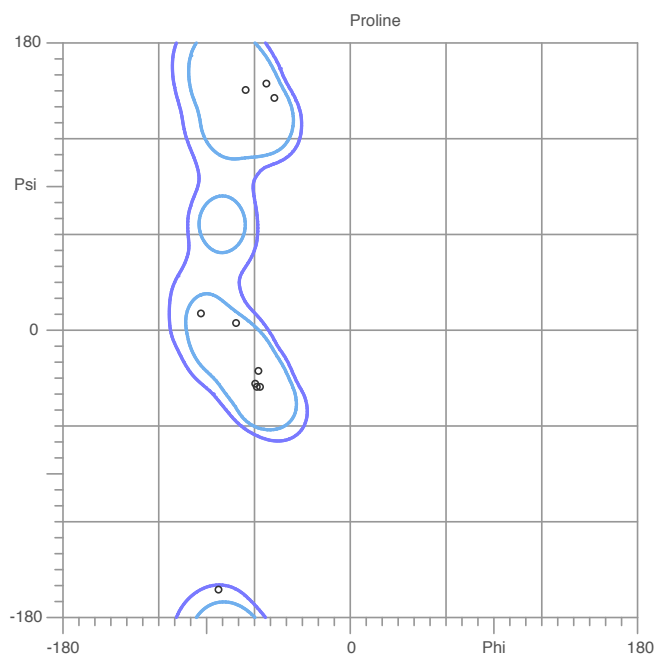
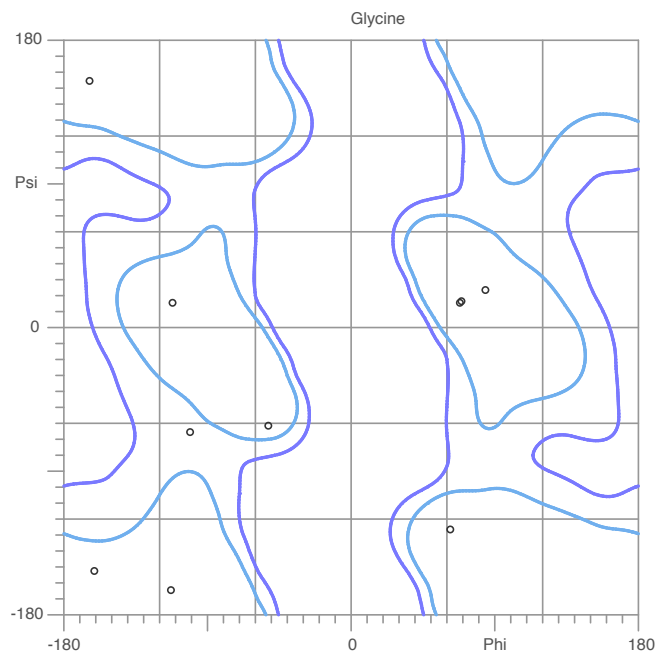
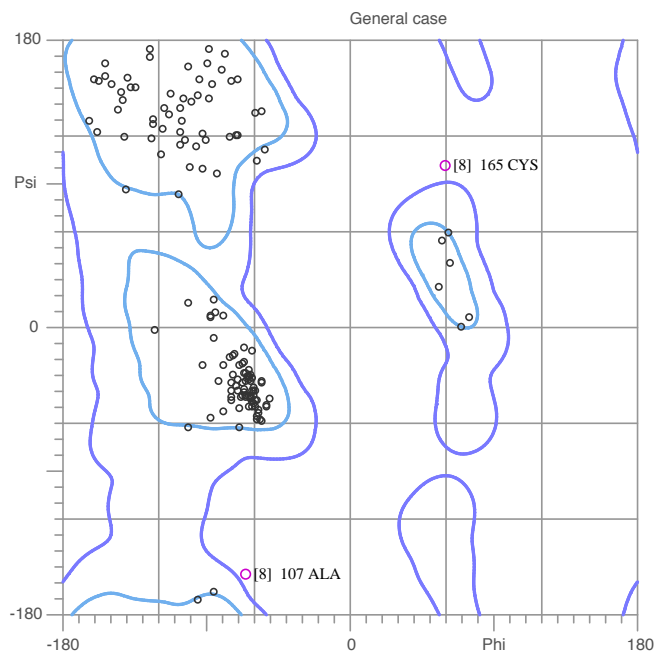


93.1% (161/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[7] 110 TYR (64.2, 95.6)
[7] 130 PRO (-96.0, -154.7)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 8

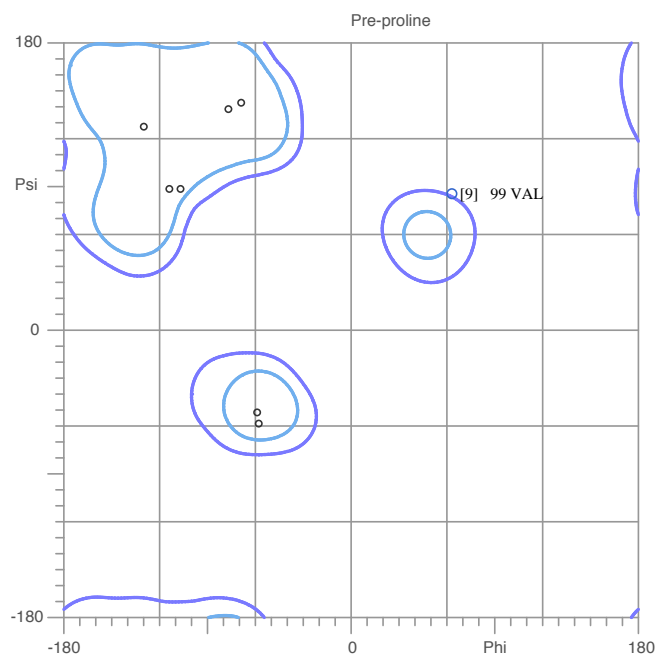
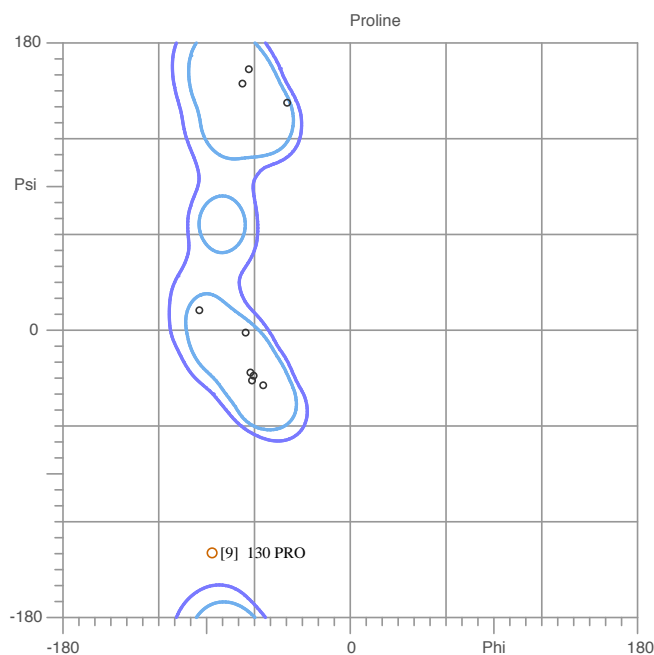
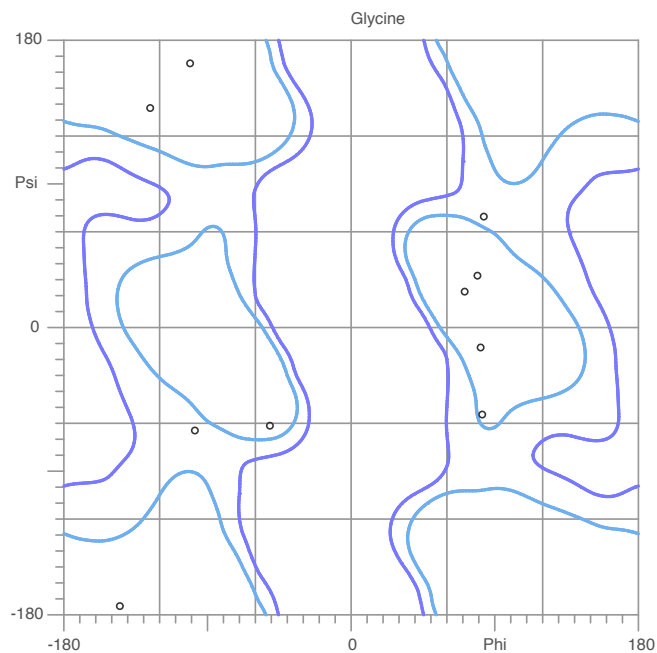
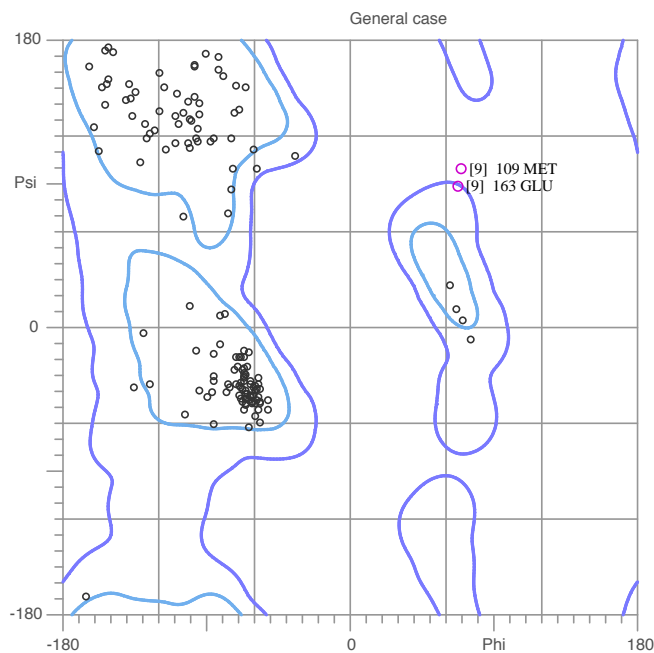


94.2% (163/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[8] 107 ALA (-67.0, -154.8)
[8] 165 CYS (59.6, 102.1)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 9



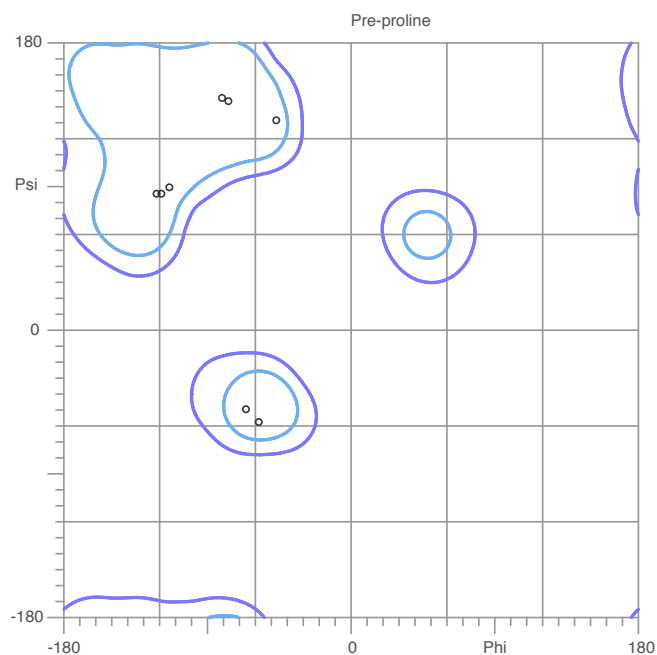
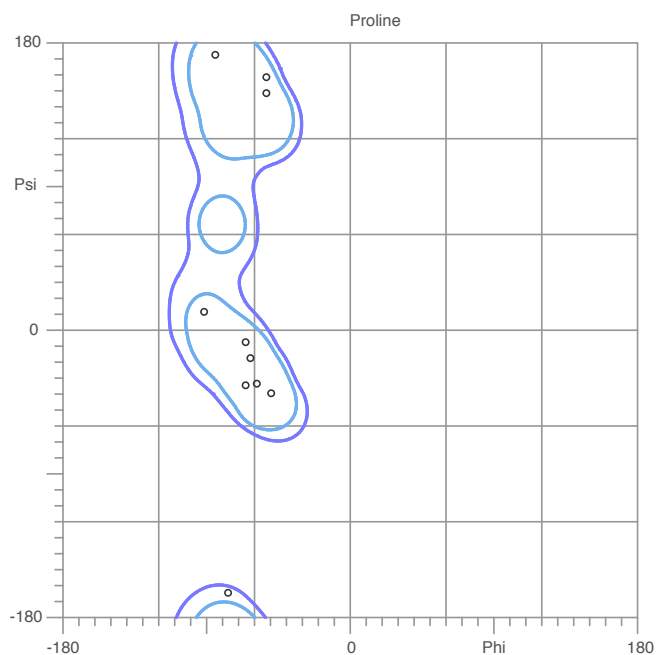
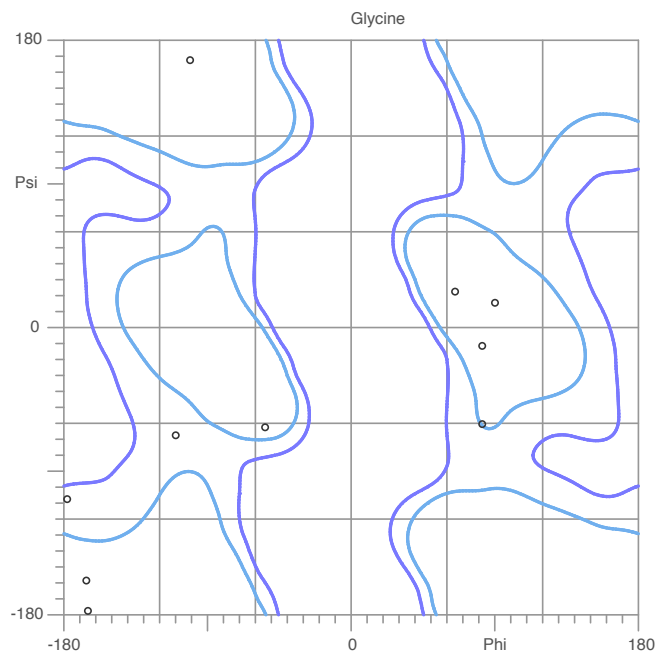
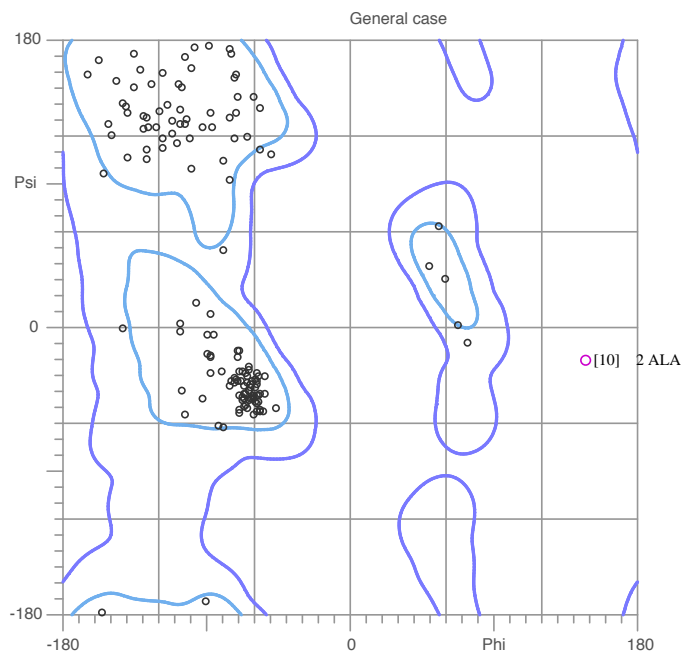
93.1% (161/173) of all residues were in favored (98%) regions.
97.7% (169/173) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [9] 99 VAL (63.5, 86.6)
- [9] 109 MET (69.5, 100.1)
- [9] 130 PRO (-87.9, -139.8)
- [9] 163 GLU (67.6, 89.7)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 10



94.2% (163/173) of all residues were in favored (98%) regions.
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

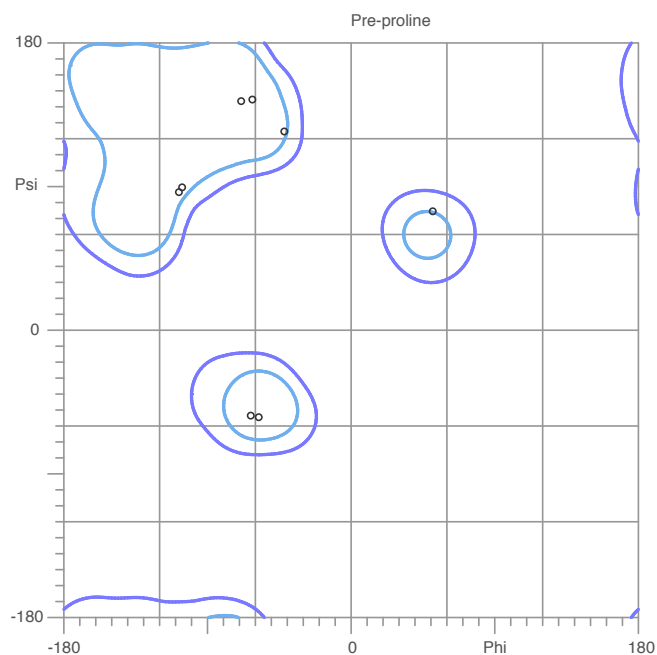
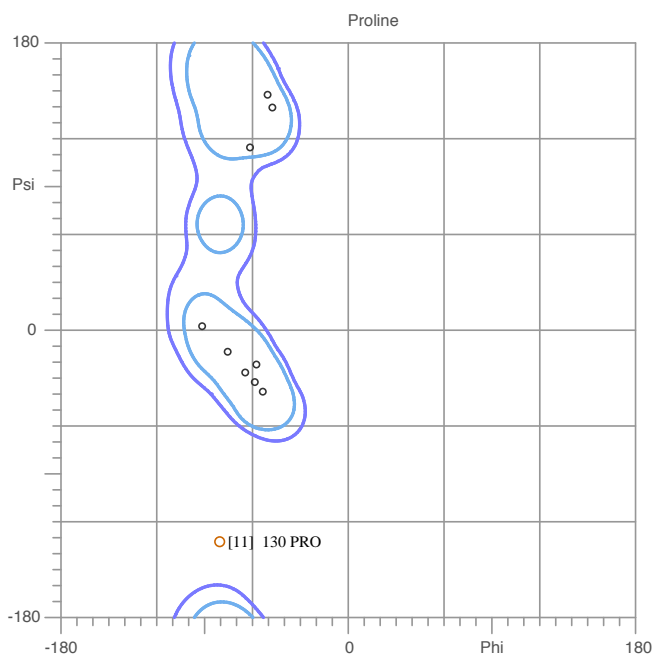
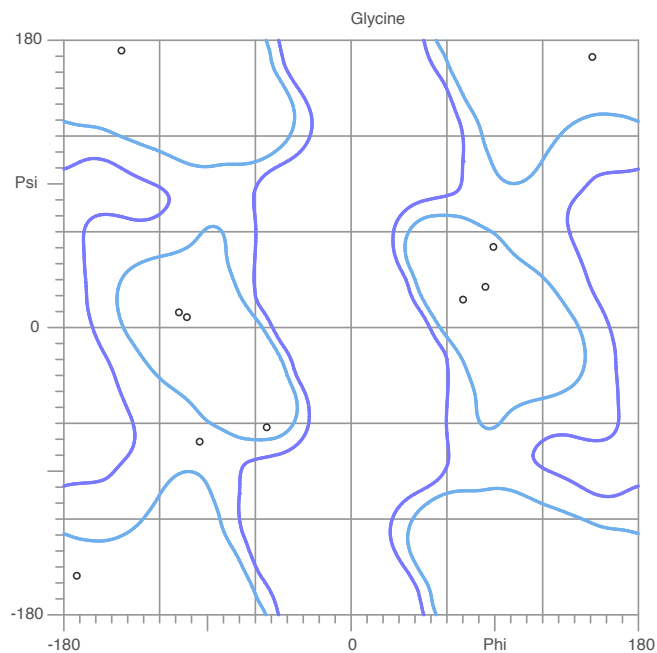
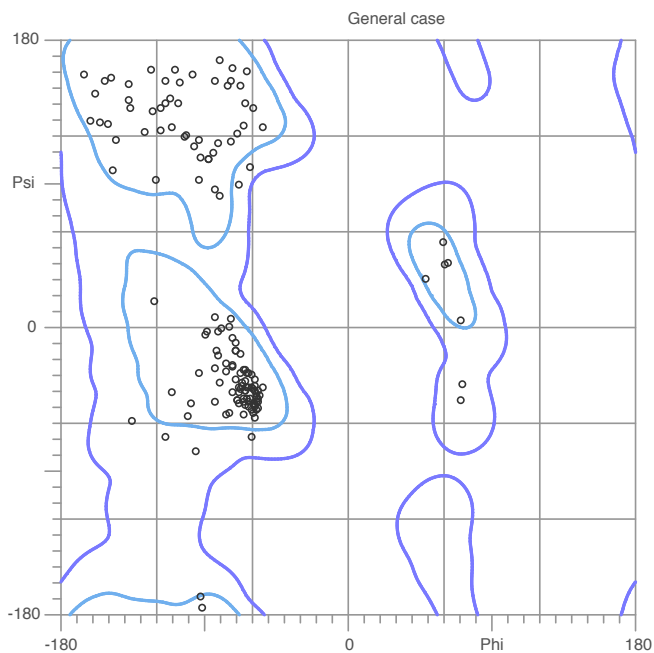
There were 1 outliers (phi, psi):
[10] 2 ALA (147.0, -20.2)

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MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 11

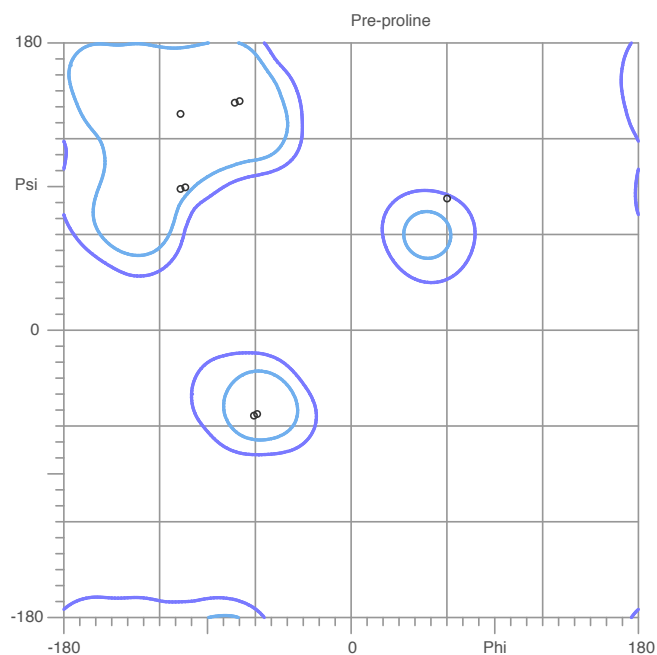
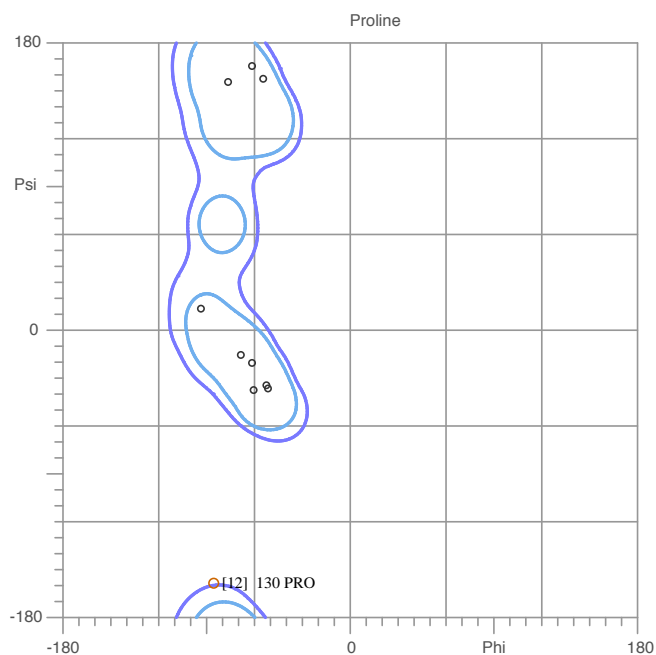
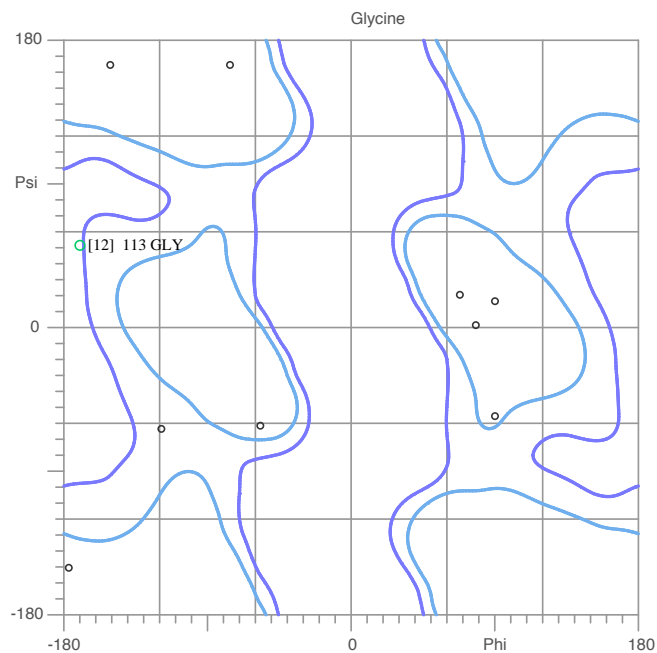
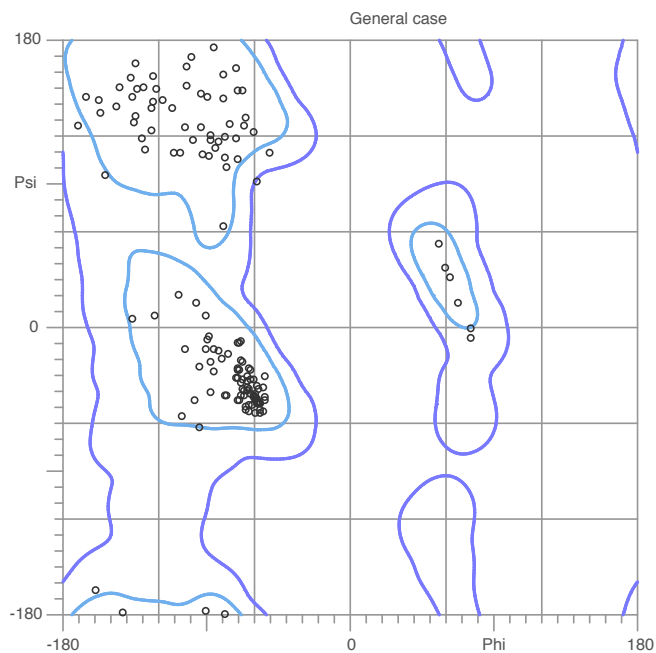


93.1% (161/173) of all residues were in favored (98%) regions.
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[11] 130 PRO (-81.9, -132.4)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 12

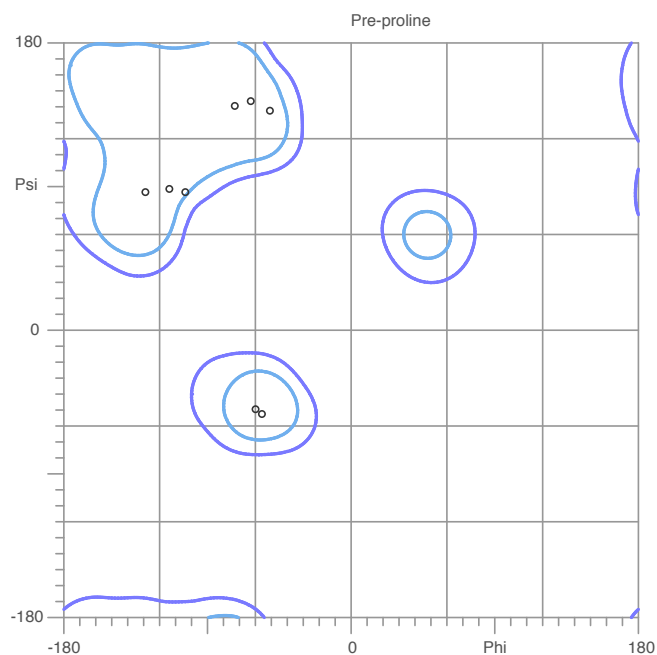
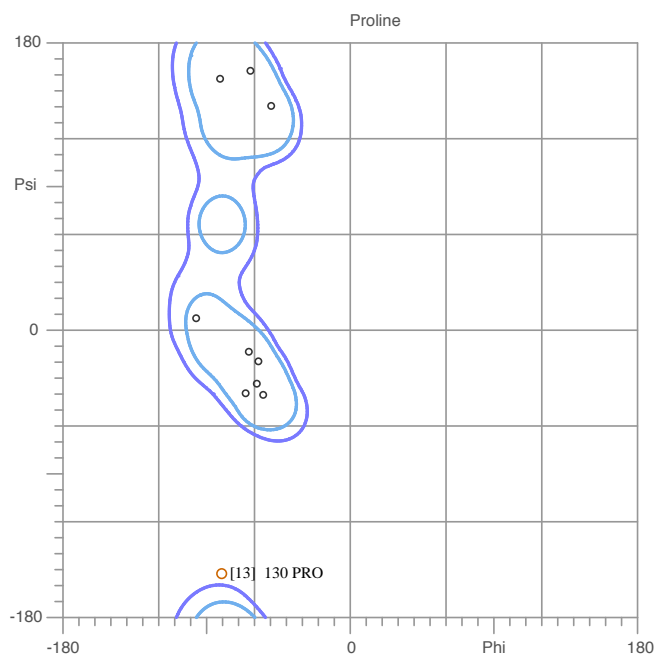
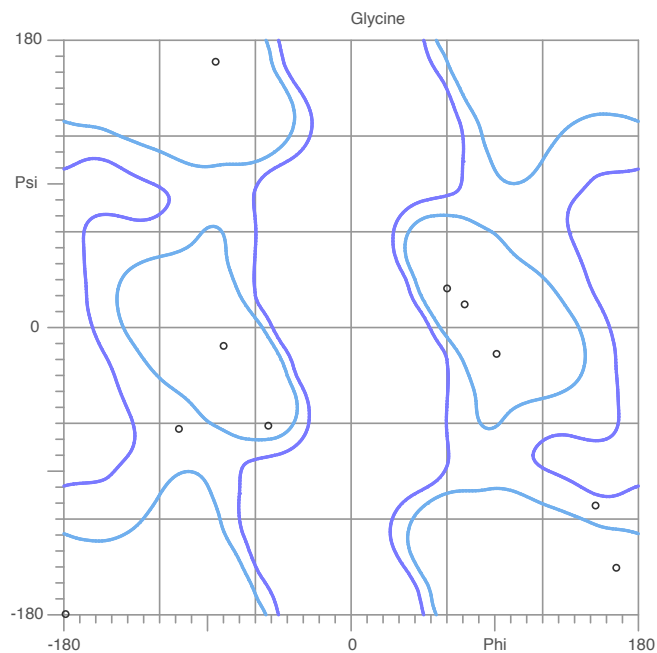
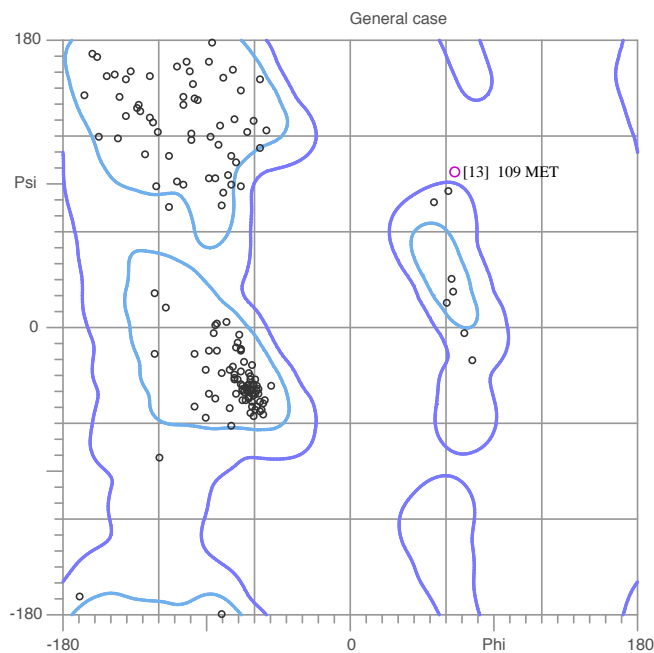


93.1% (161/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 113 GLY (-170.0, 52.9)
[12] 130 PRO (-86.4, -158.3)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 13

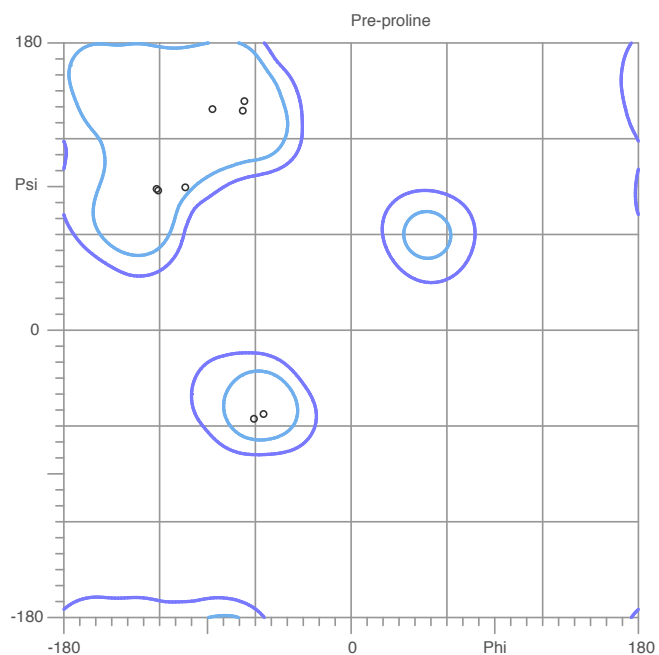
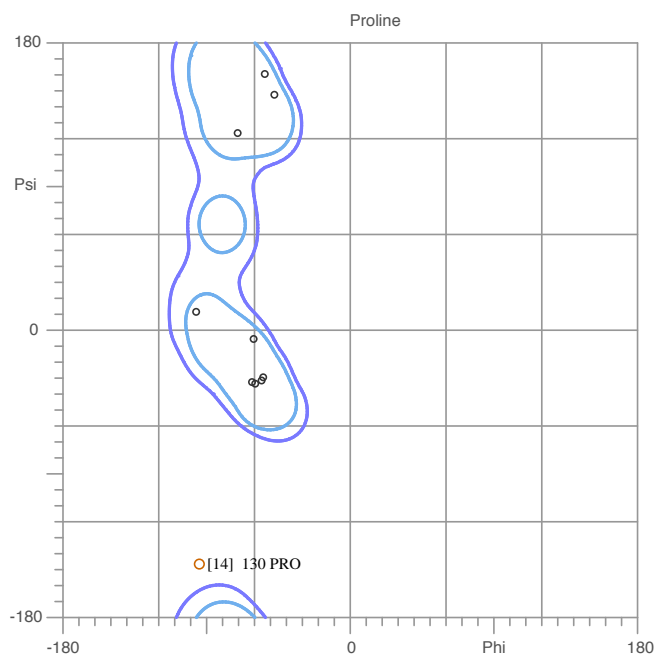
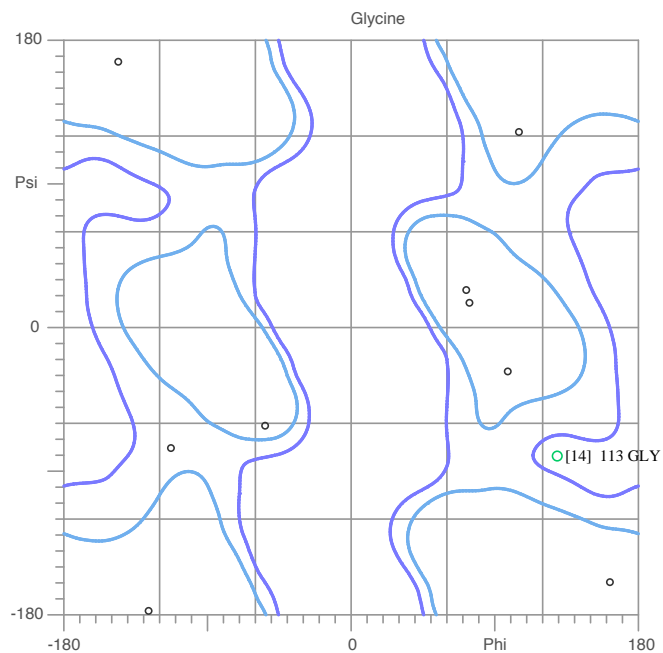
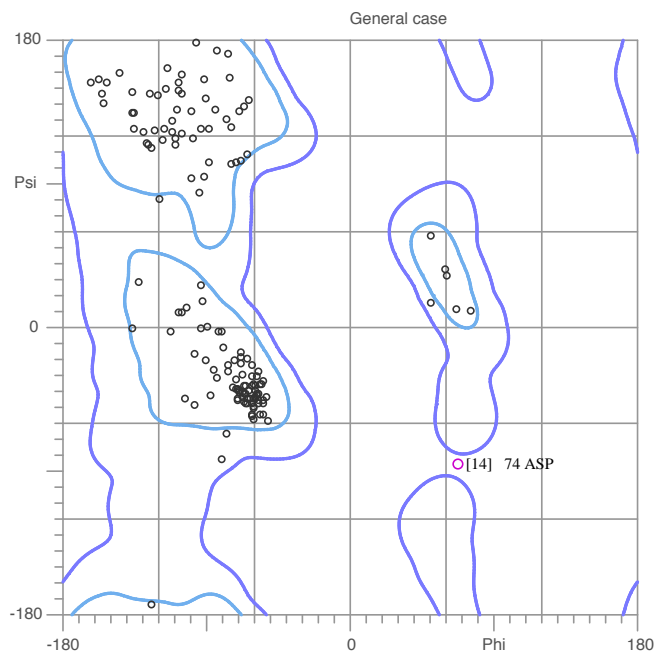


93.1% (161/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[13] 109 MET (65.6, 98.7)
[13] 130 PRO (-81.5, -152.4)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 14



95.4% (165/173) of all residues were in favored (98%) regions.
98.3% (170/173) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

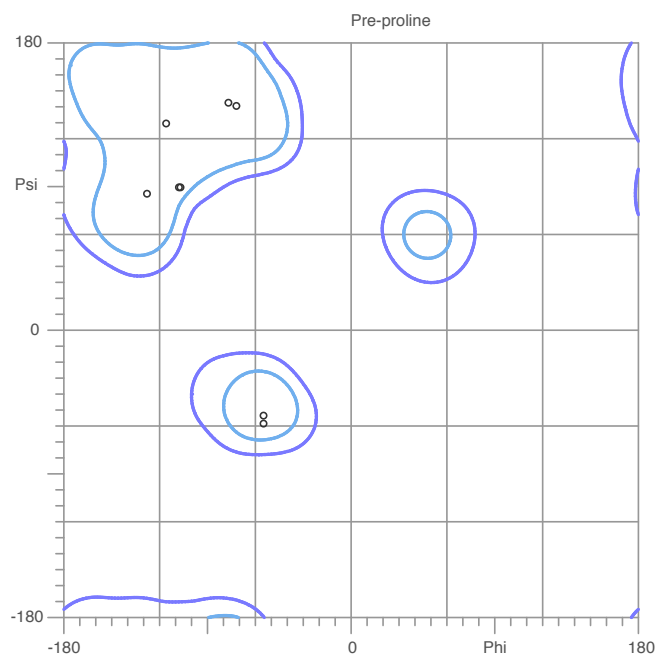
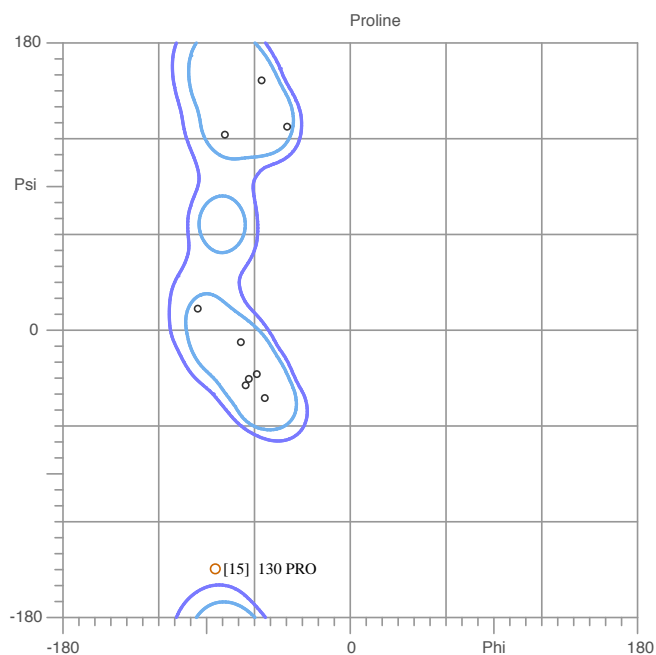
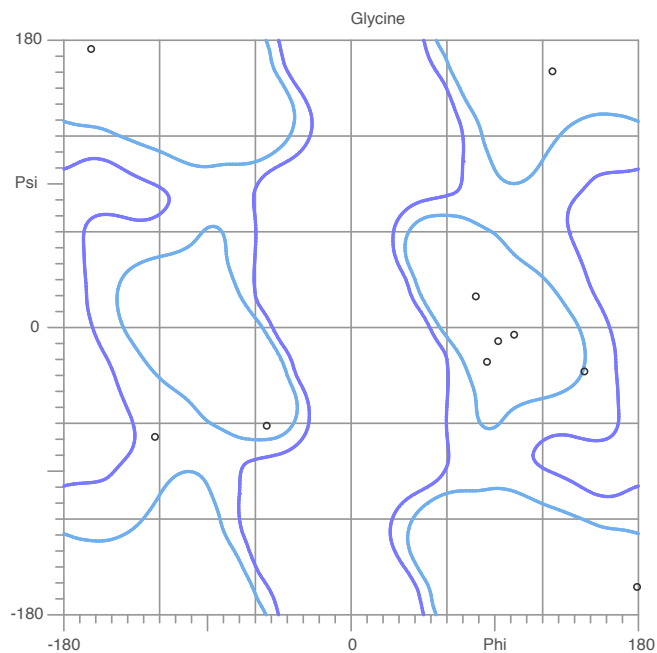
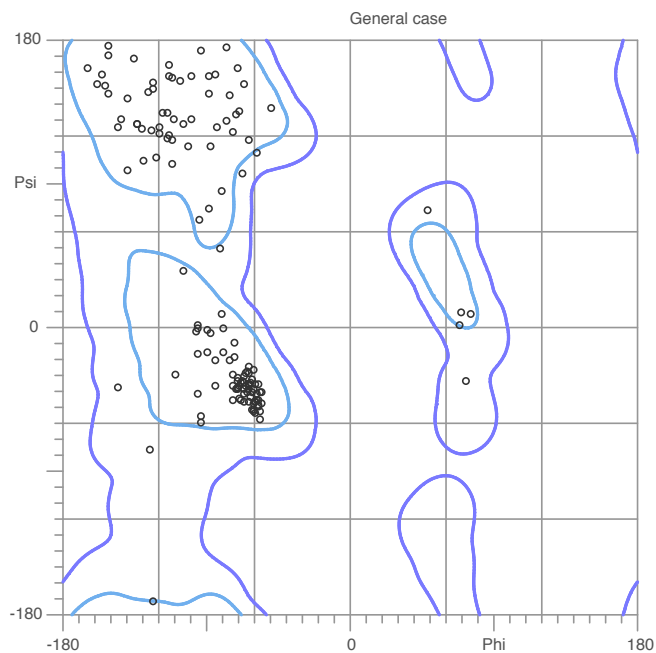
[14] 74 ASP (67.6, -85.8)

[14] 113 GLY (129.1, -80.1)

[14] 130 PRO (-95.6, -146.2)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 15

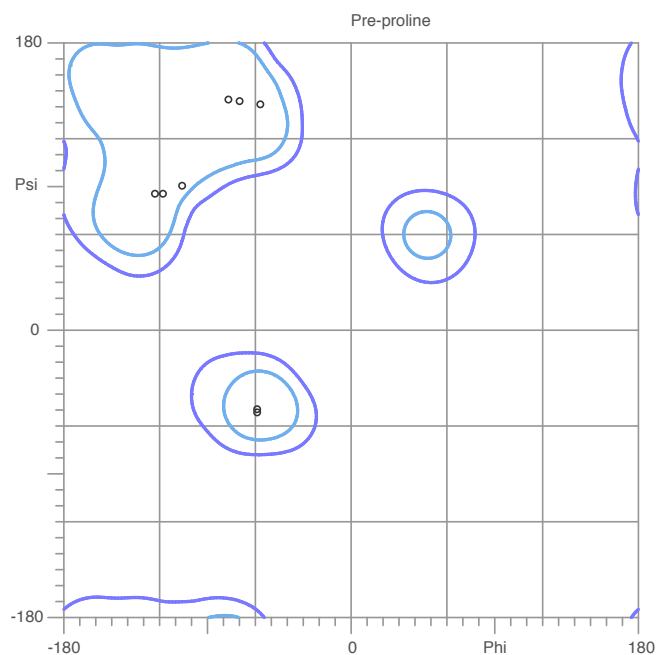
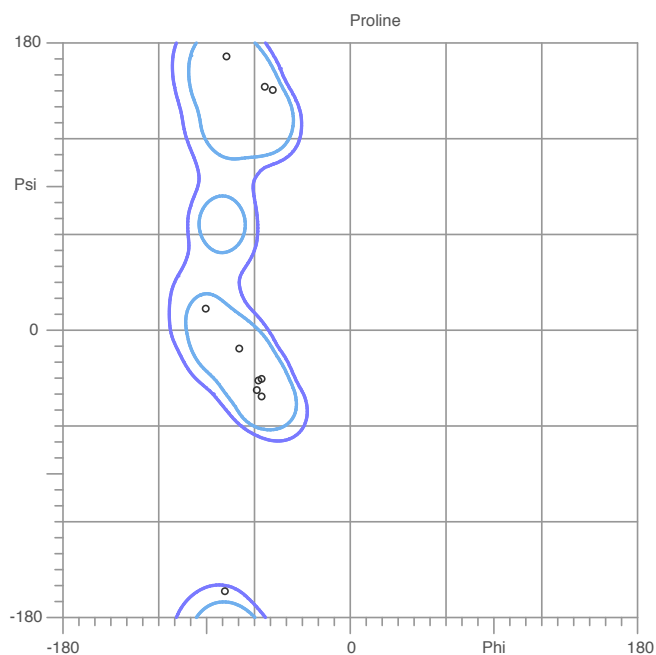
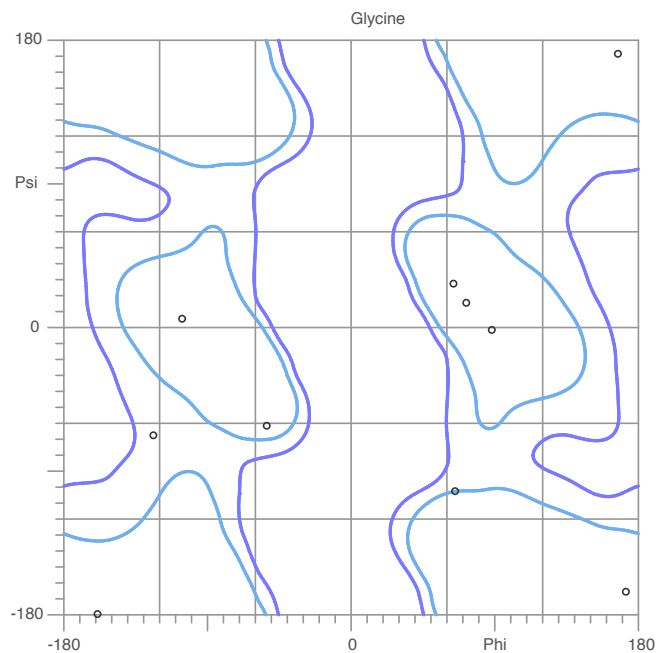
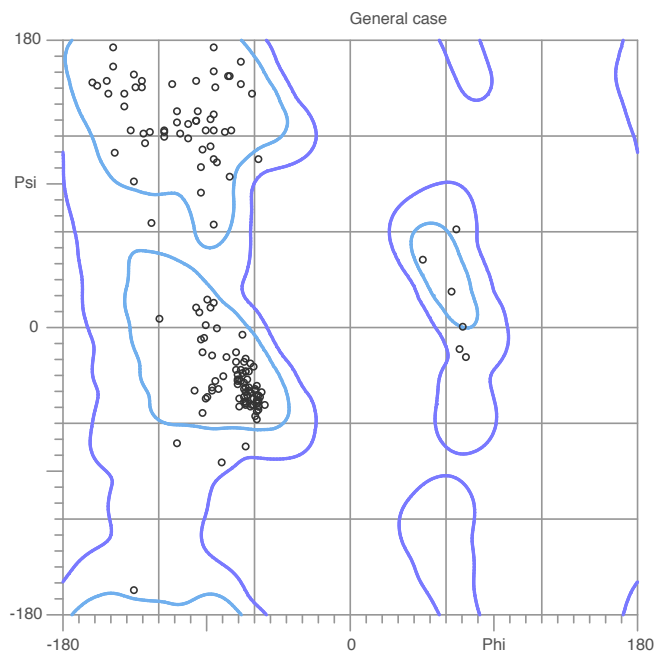


94.2% (163/173) of all residues were in favored (98%) regions.
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[15] 130 PRO (-85.0, -149.6)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 16



93.1% (161/173) of all residues were in favored (98%) regions.
100.0% (173/173) of all residues were in allowed (>99.8%) regions.

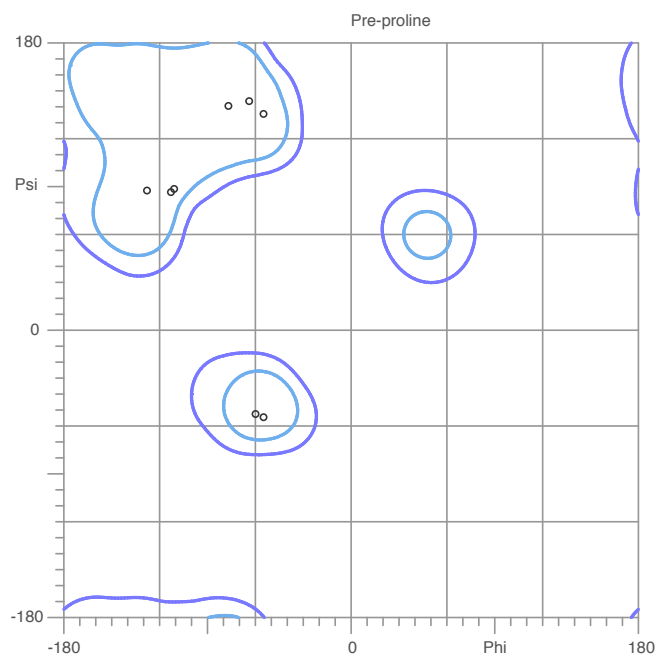
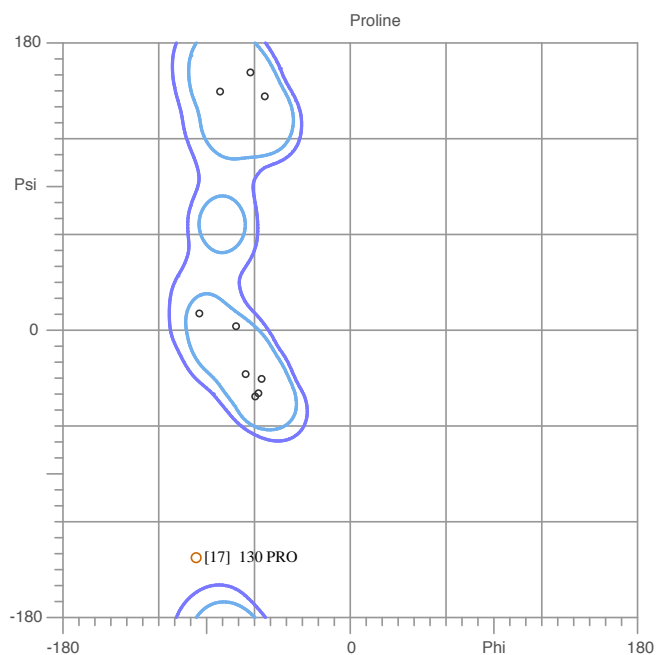
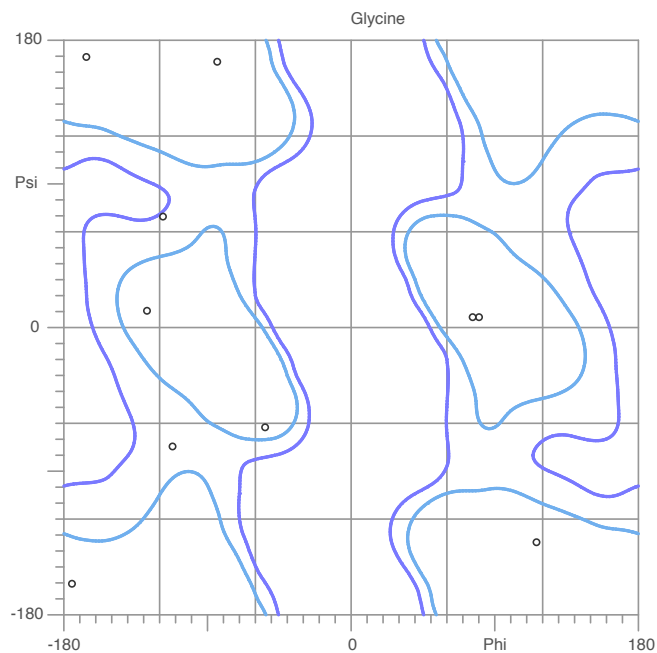
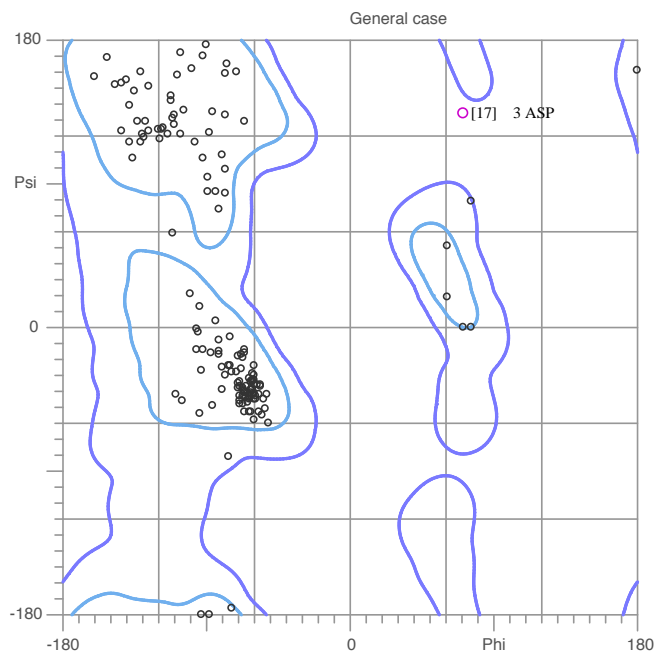
There were no outliers.

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

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MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 17

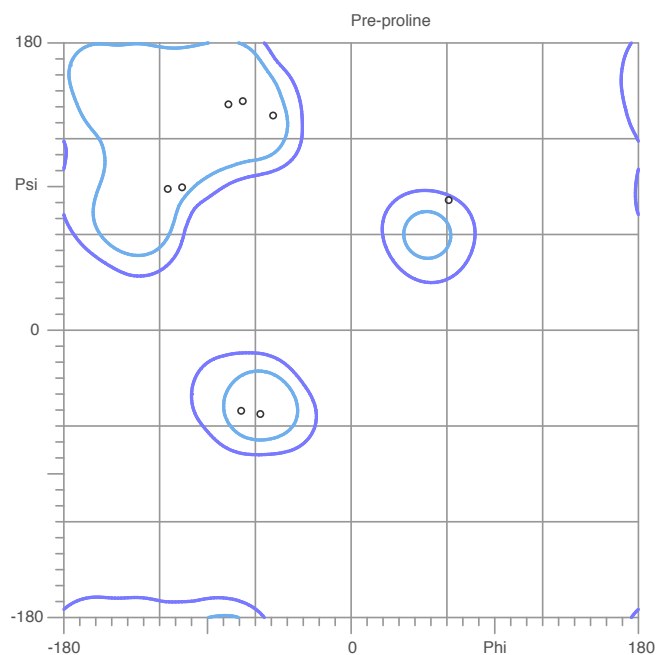
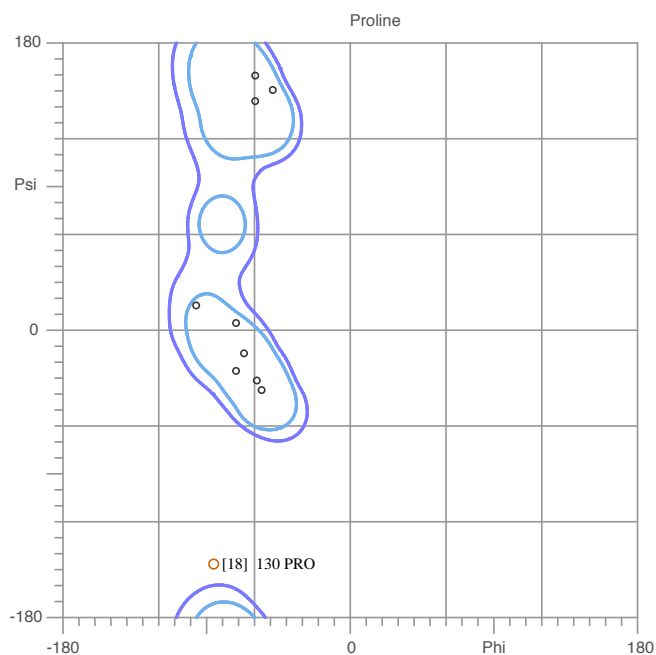
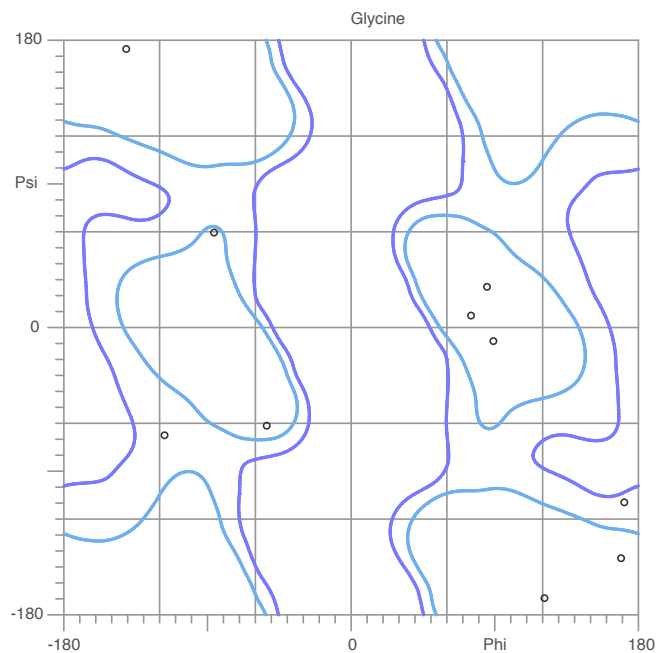
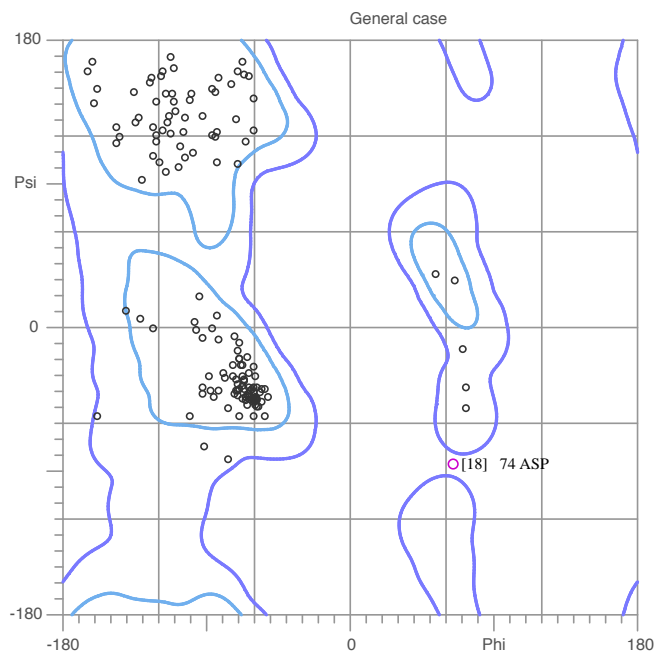


95.4% (165/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[17] 3 ASP (70.3, 135.1)
[17] 130 PRO (-97.1, -142.2)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 18

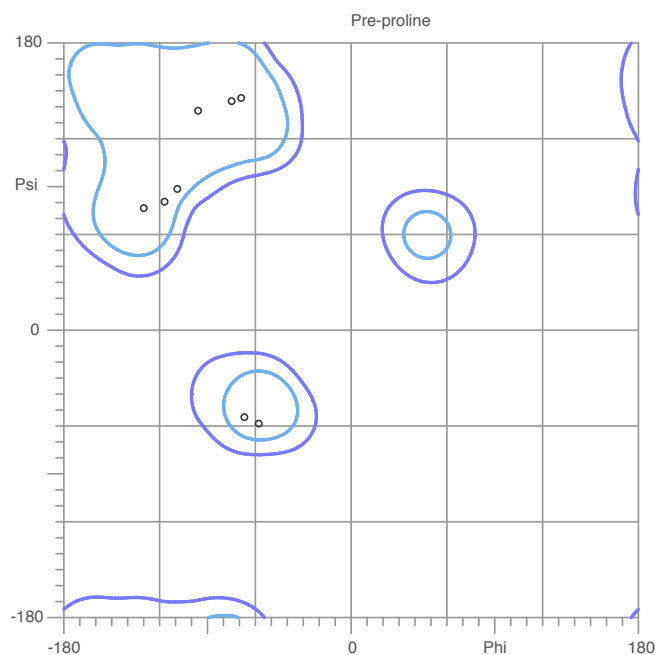
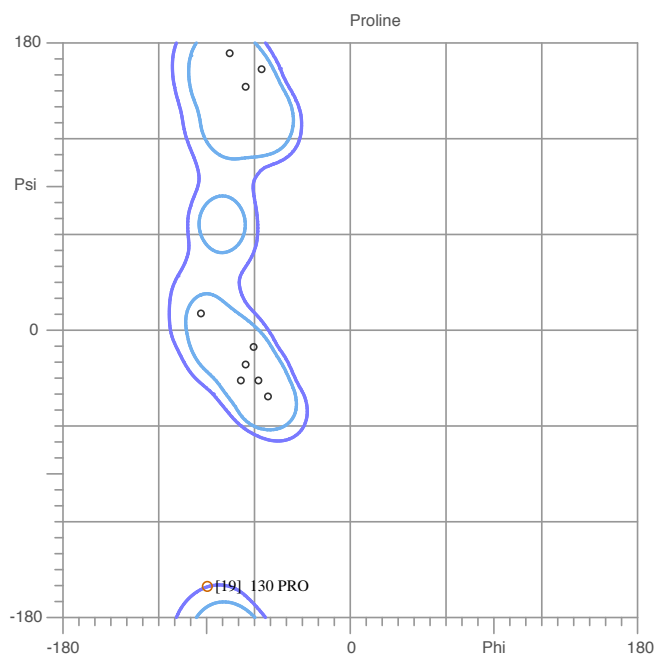
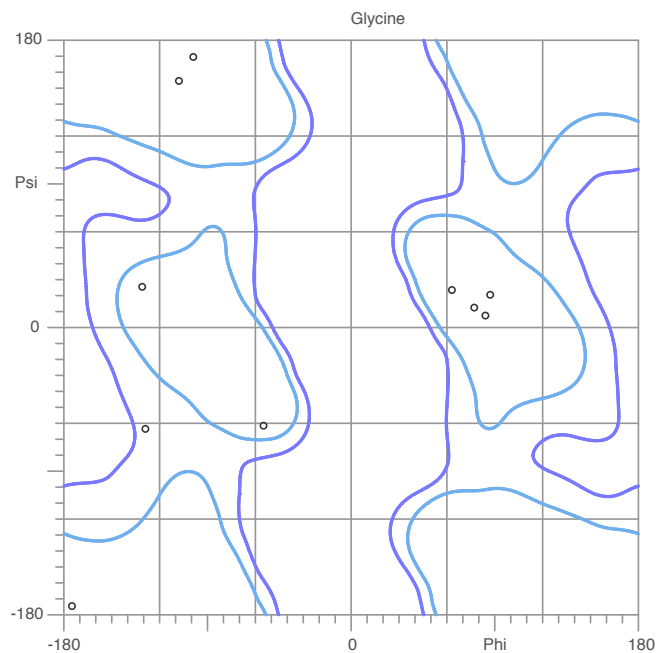
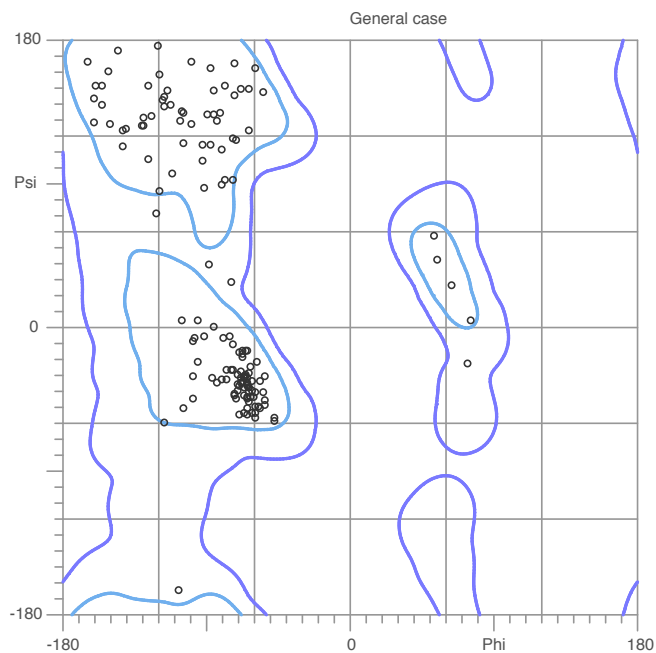


93.1% (161/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 74 ASP (64.4, -85.0)
[18] 130 PRO (-86.5, -146.6)

MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 19



95.4% (165/173) of all residues were in favored (98%) regions.
99.4% (172/173) of all residues were in allowed (>99.8%) regions.

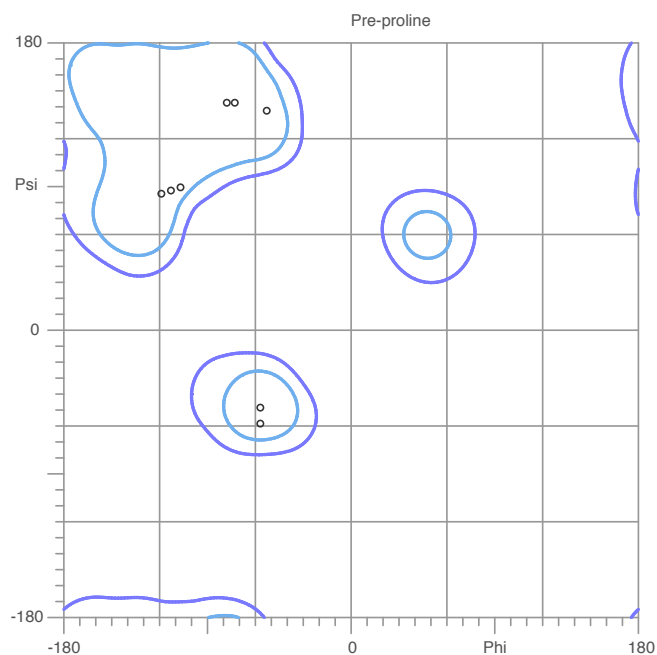
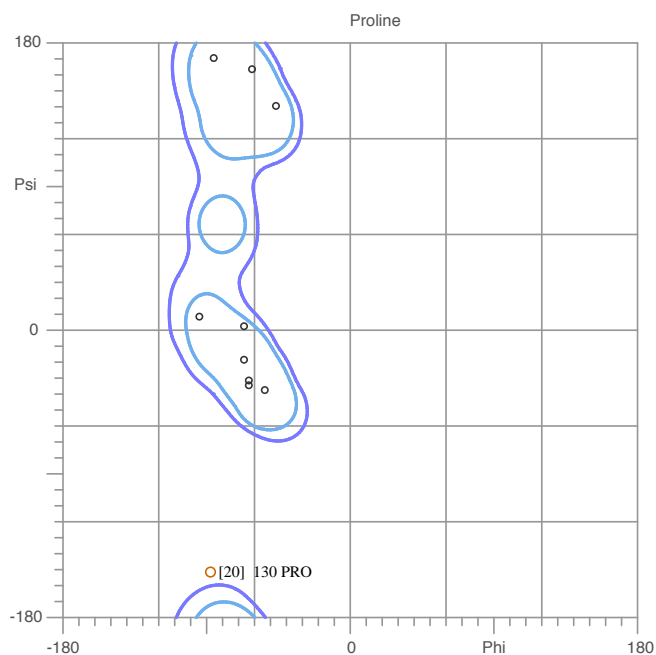
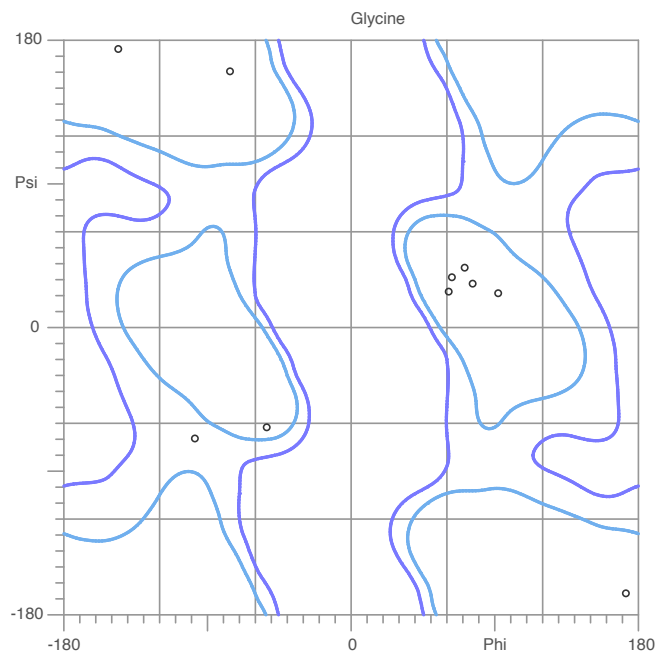
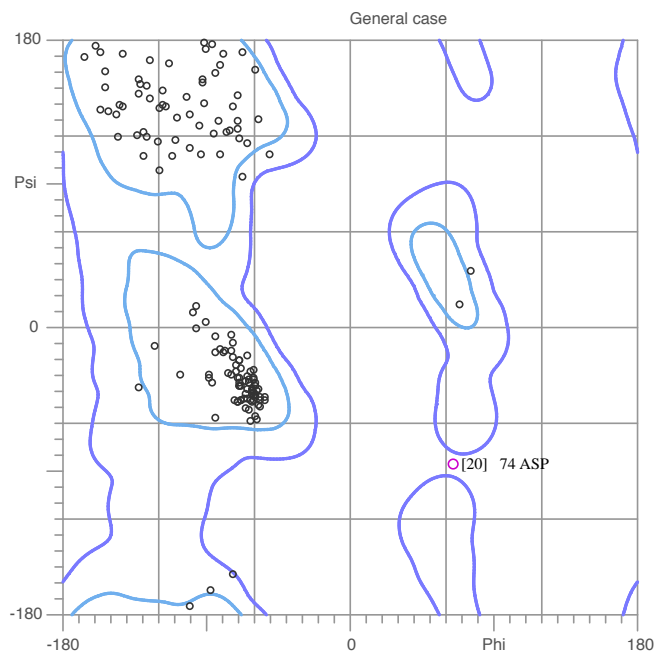
There were 1 outliers (phi, psi):
[19] 130 PRO (-90.8, -160.9)

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MolProbity Ramachandran analysis

HR41_NMR_em_bcr3.pdb, model 20



94.8% (164/173) of all residues were in favored (98%) regions.
98.8% (171/173) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[20] 74 ASP (64.5, -85.9)
[20] 130 PRO (-88.6, -151.6)