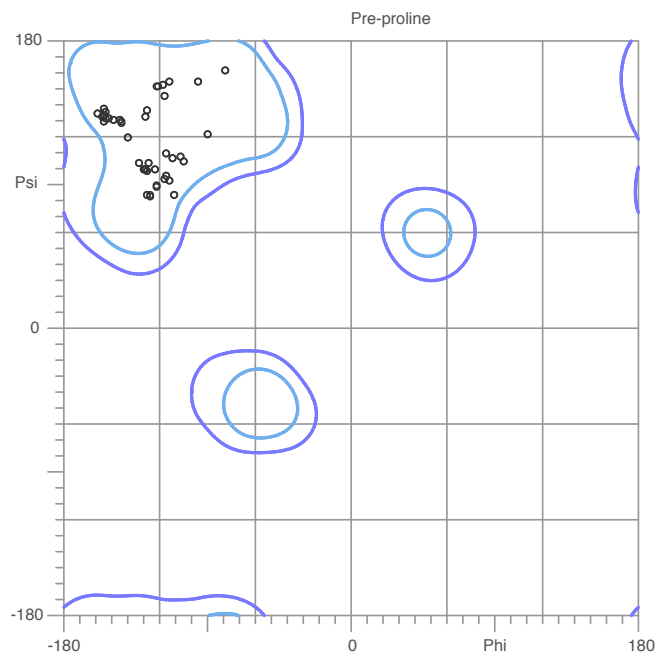
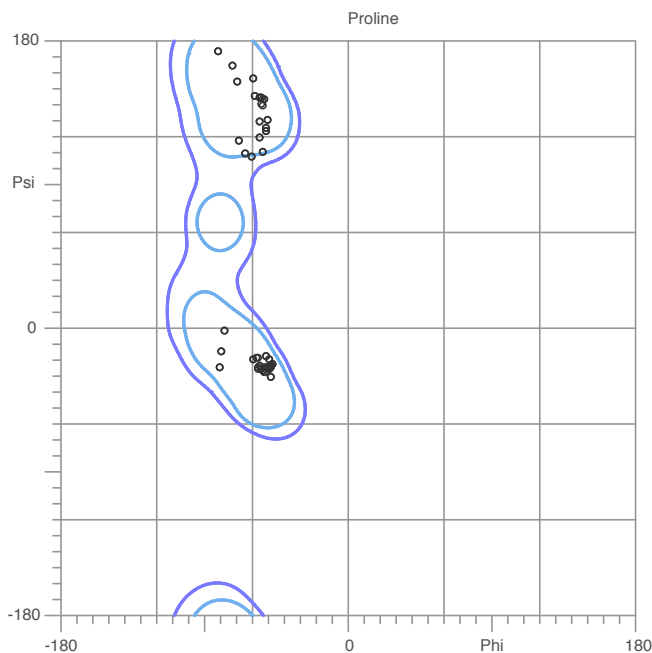
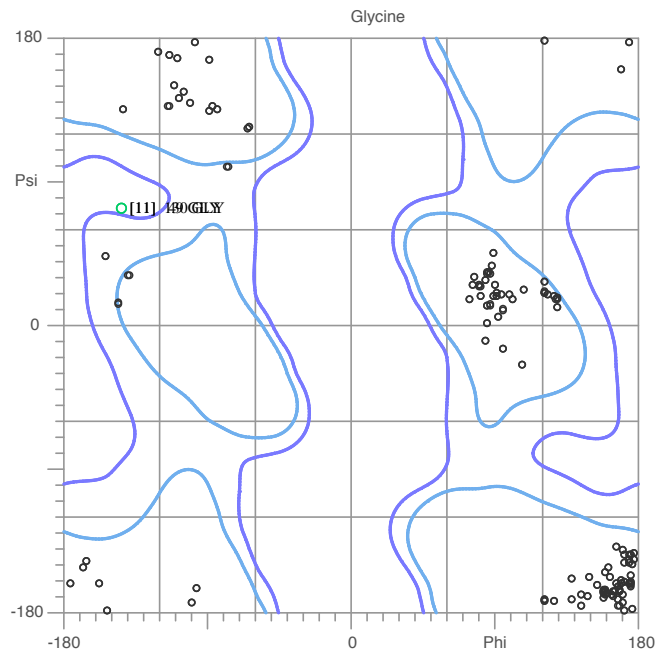
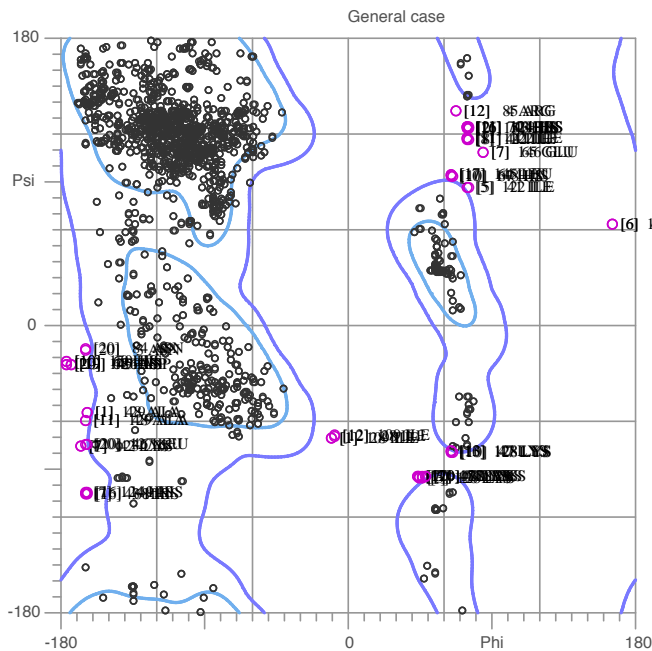


MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, all models



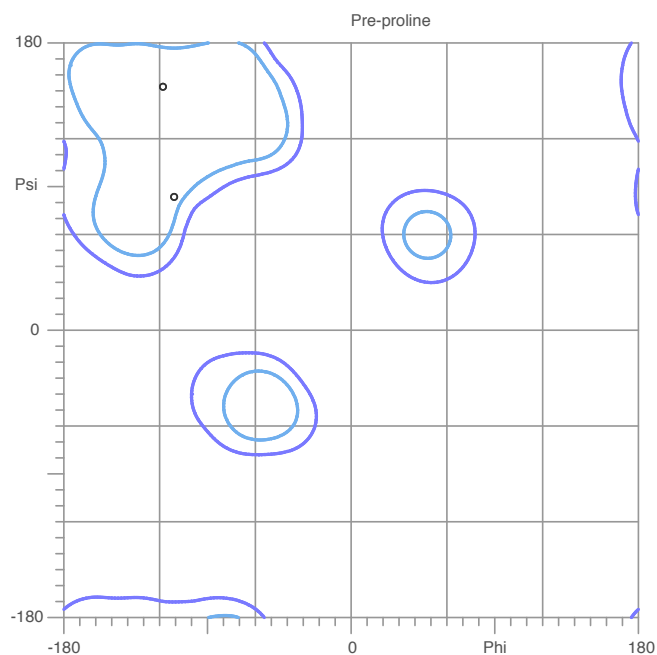
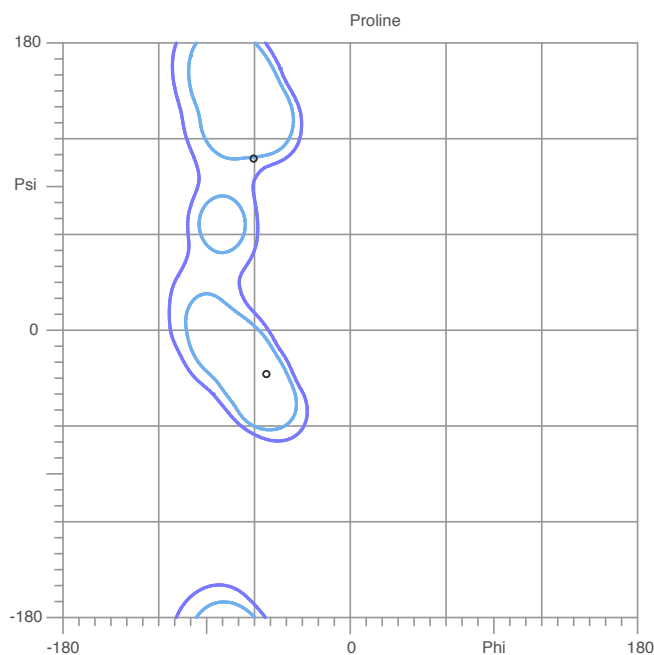
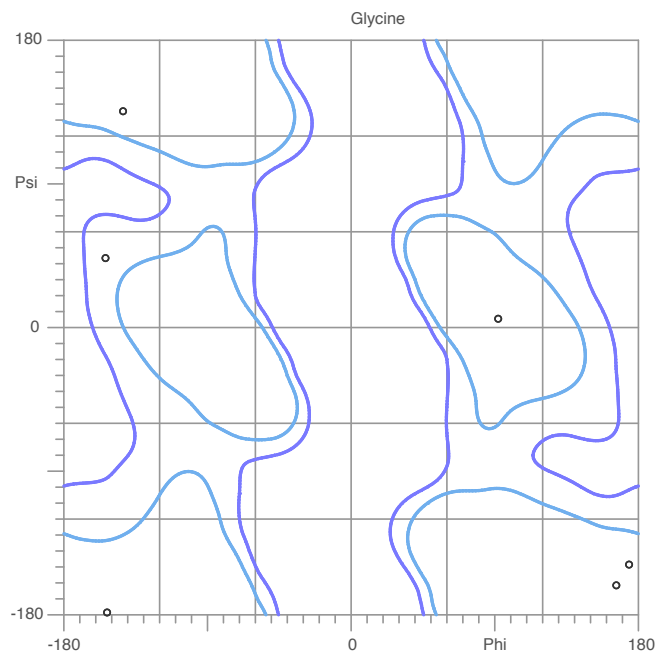
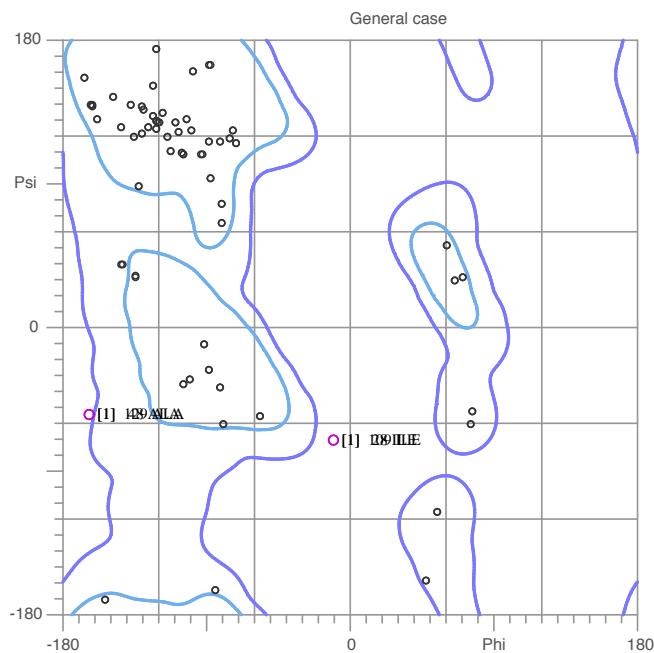
90.1% (2486/2760) of all residues were in favored (98%) regions.
97.8% (2700/2760) of all residues were in allowed (<99.9%) regions.

There were 60 outliers (phi, psi):

- | | |
|------------------------------|------------------------------|
| [1] 28 ILE (-11.7, 70.7) | [11] 41 ILE (74.7, 118.5) |
| [1] 48 ALA (-164.9, 54.9) | [11] 48 ALA (-165.0, 59.8) |
| [1] 109 ILE (-11.7, 70.8) | [11] 49 GLY (-144.9, 74.7) |
| [1] 120 ALA (-164.9, 54.9) | [11] 122 ILE (74.7, 118.5) |
| [2] 70 HIS (75.0, 125.0) | [11] 124 HIS (74.9, 125.1) |
| [2] 151 HIS (75.1, 125.0) | [11] 129 ALA (-165.0, 59.8) |
| [3] 47 LYS (64.8, 95.0) | [11] 130 GLY (-145.0, 74.8) |
| [3] 128 LYS (46.8, 95.0) | [12] 4 ARG (67.4, 135.1) |
| [5] 41 ILE (75.0, 87.6) | [12] 28 ILE (-9.9, 49.1) |
| [7] 42 LYS (-168.2, 75.9) | [12] 85 ARG (67.3, 135.1) |
| [9] 43 HIS (165.7, 64.5) | [12] 109 ILE (-10.0, 49.0) |
| [9] 124 HIS (165.8, 64.8) | [13] 47 LYS (65.0, 78.1) |
| [7] 43 HIS (-165.0, -105.1) | [16] 124 HIS (75.0, 78.3) |
| [7] 47 LYS (44.9, 95.0) | [16] 49 HIS (-165.0, -105.0) |
| [7] 65 GLU (64.9, 109.4) | [17] 47 LYS (43.4, 94.9) |
| [7] 121 LYS (-168.2, 75.9) | [17] 64 LEU (65.0, 95.0) |
| [7] 124 HIS (-165.0, -105.0) | [17] 124 LYS (43.5, 95.0) |
| [7] 128 LYS (45.0, 95.0) | [17] 145 LEU (64.9, 95.1) |
| [7] 146 GLU (64.9, 109.4) | [19] 45 ASP (-174.9, 24.9) |
| [8] 41 ILE (75.0, 117.7) | [19] 126 ASP (-174.9, 24.9) |
| [8] 122 ILE (75.0, 117.7) | [20] 3 ASN (-165.0, -15.1) |
| [10] 47 LYS (65.1, 79.9) | [20] 46 LEU (-165.0, 75.0) |
| [10] 67 HIS (65.0, 95.0) | [20] 47 LYS (48.5, 95.0) |
| [10] 69 HIS (-177.2, -22.8) | [20] 68 HIS (-177.5, 34.9) |
| [10] 128 LYS (65.0, 79.9) | [20] 84 ASN (-165.1, -15.0) |
| [10] 148 HIS (65.1, 94.9) | [20] 171 LEU (-164.9, 75.0) |
| [10] 150 HIS (-177.1, -22.8) | [20] 128 LYS (48.4, 95.0) |
| | [20] 149 HIS (-177.6, 25.0) |

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 1



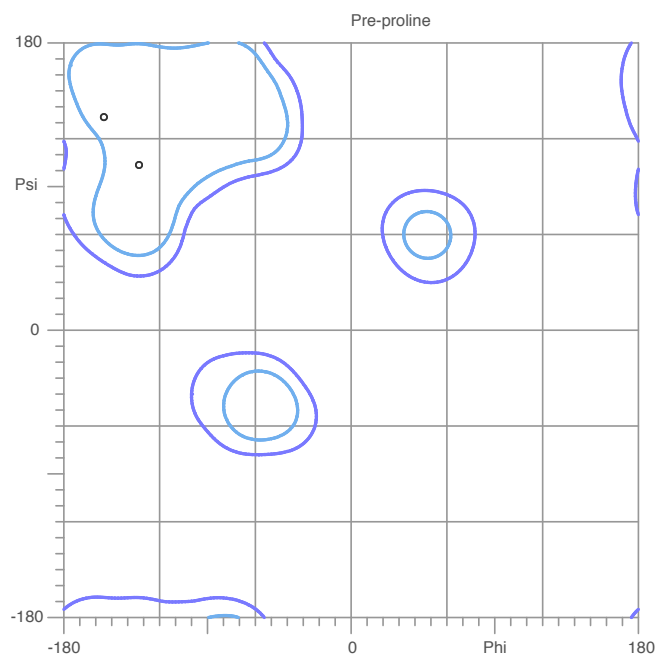
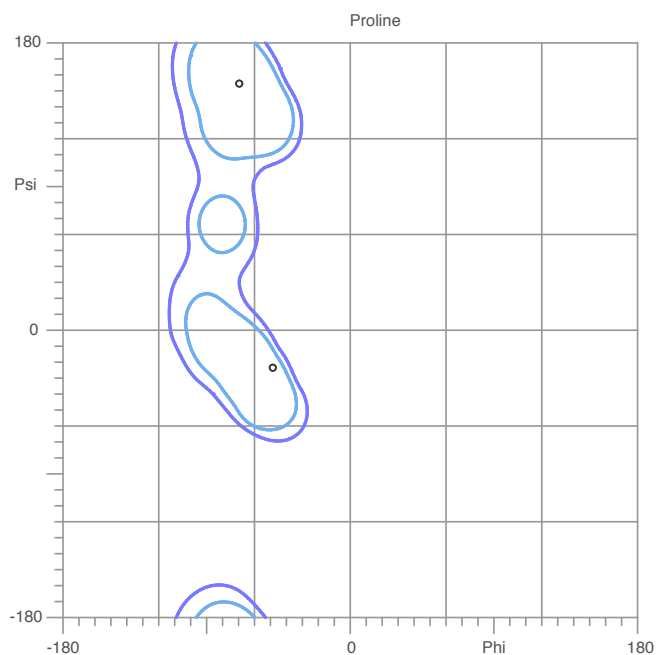
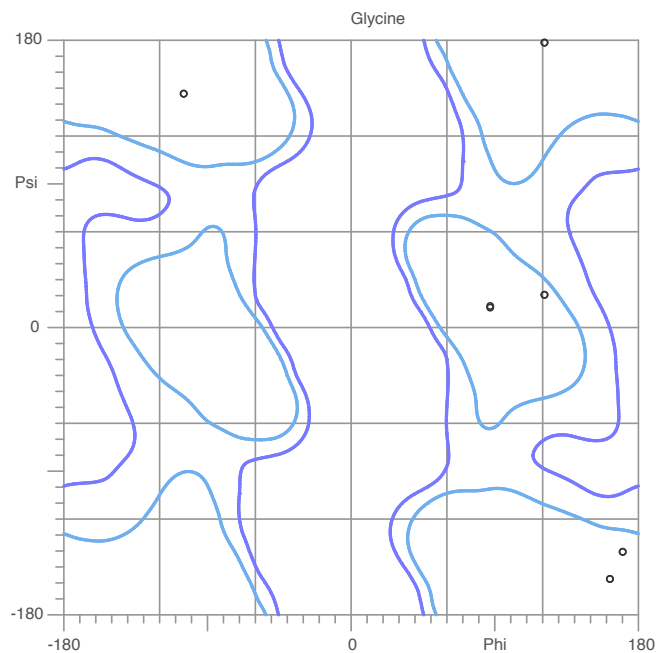
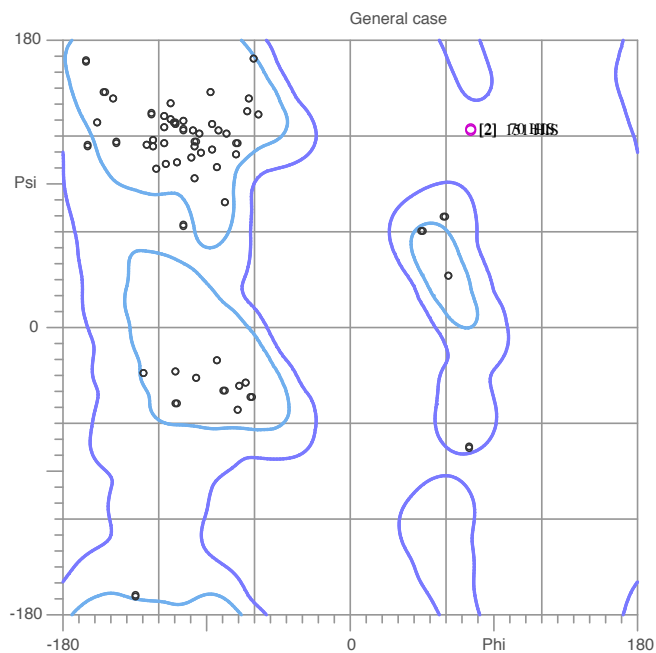
87.0% (120/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [1] 28 ILE (-11.7, -70.7)
- [1] 48 ALA (-164.9, -54.9)
- [1] 109 ILE (-11.7, -70.8)
- [1] 129 ALA (-164.9, -54.9)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 2



91.3% (126/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

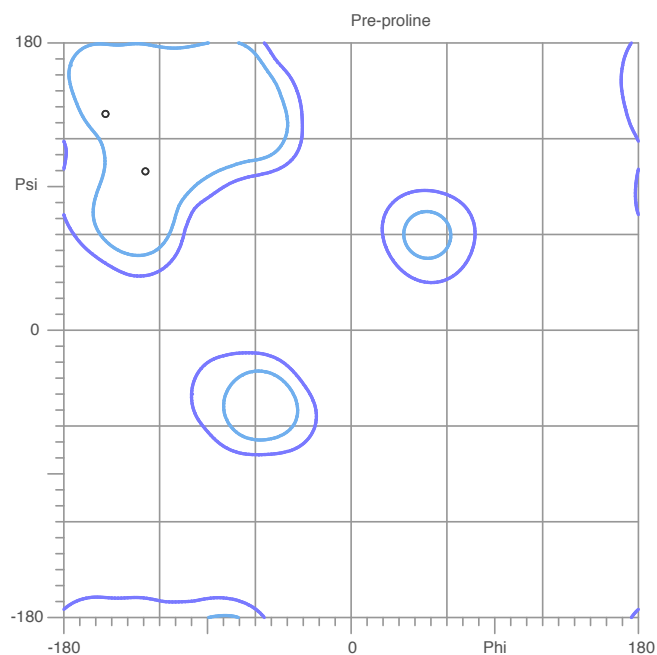
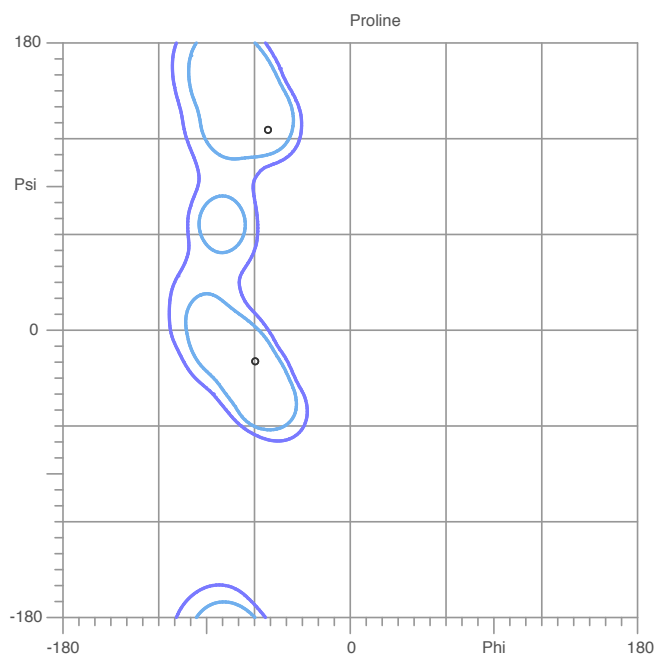
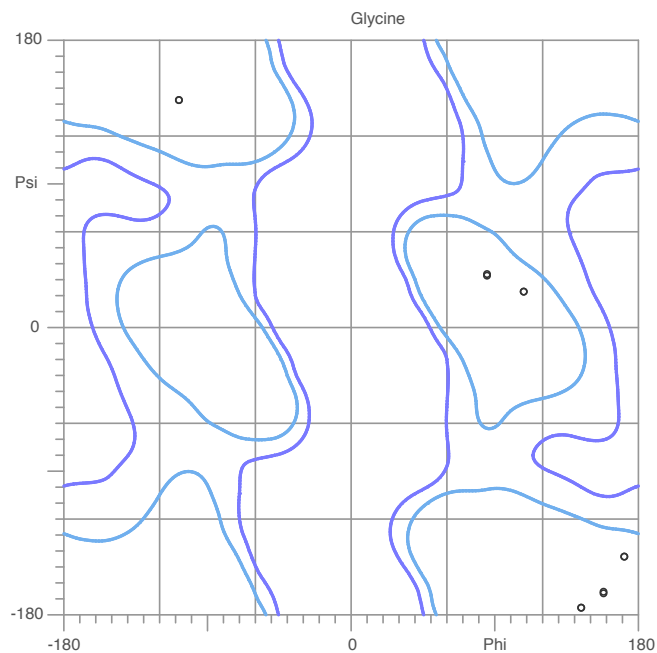
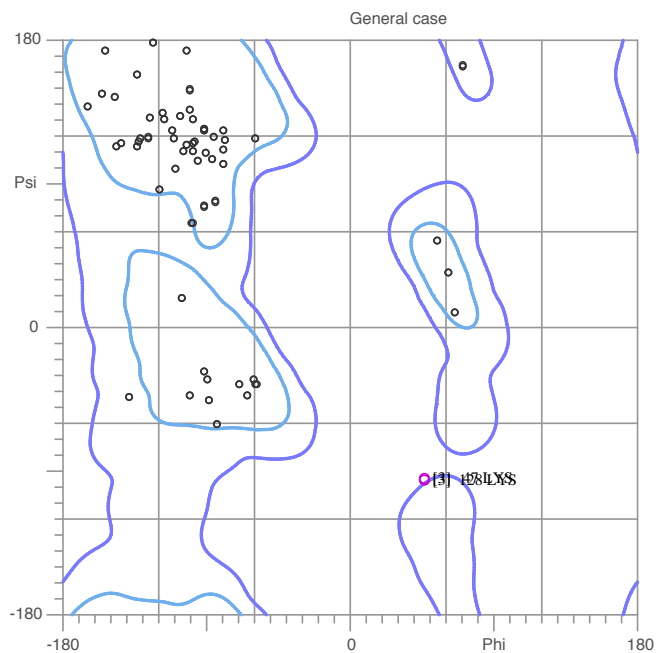
There were 2 outliers (phi, psi):

[2] 70 HIS (75.0, 125.0)

[2] 151 HIS (75.1, 125.0)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 3



94.2% (130/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

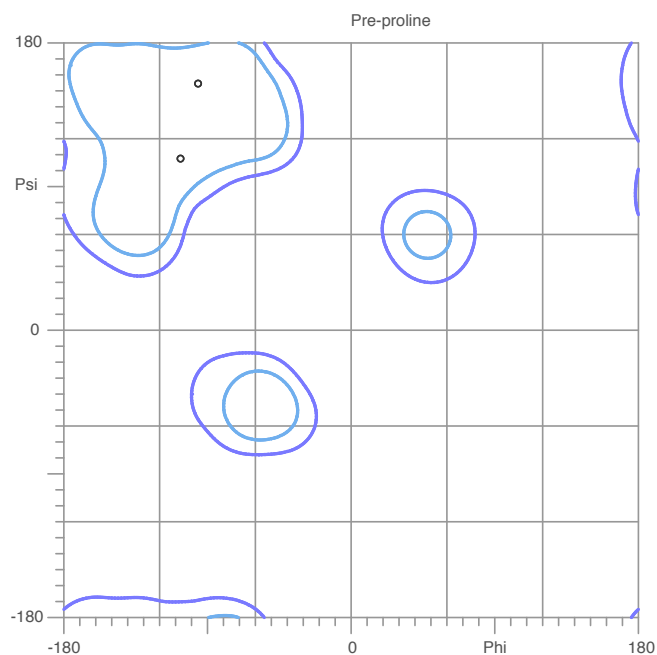
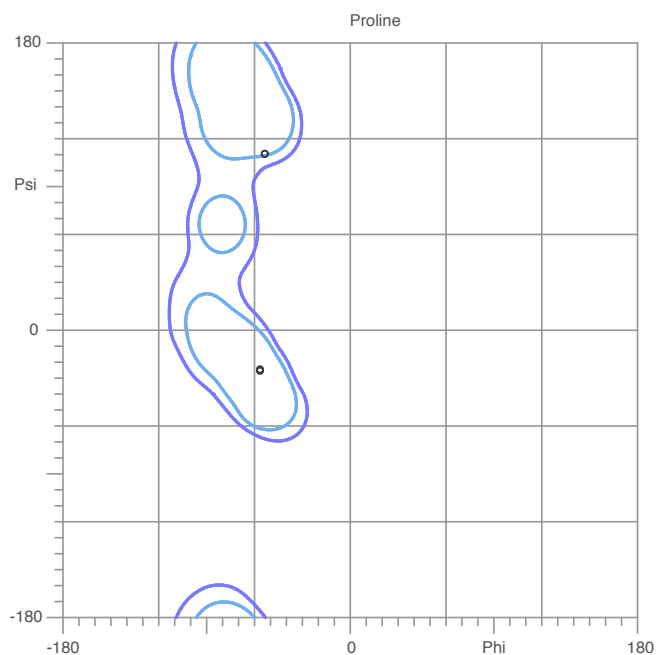
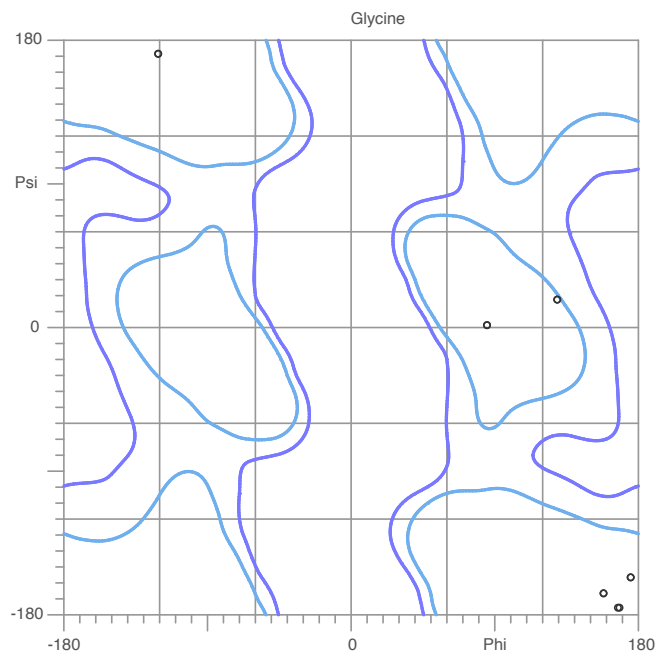
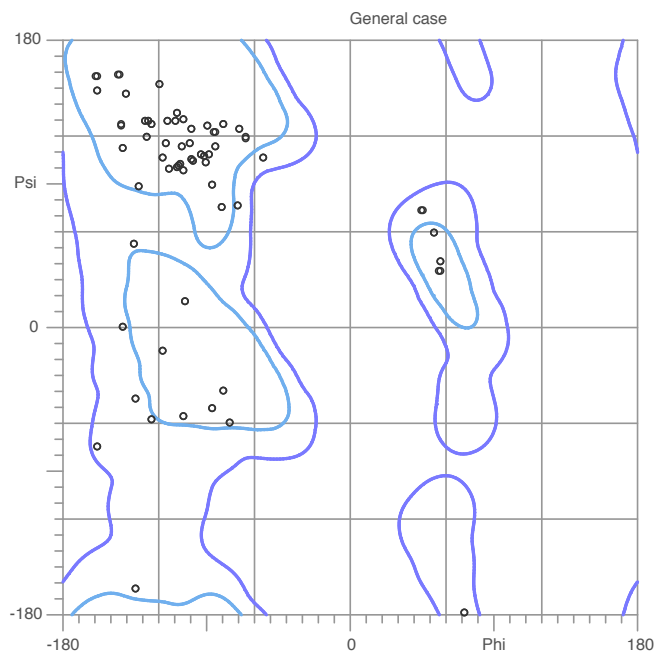
There were 2 outliers (phi, psi):

[3] 47 LYS (46.8, -95.0)

[3] 128 LYS (46.8, -95.0)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 4



85.5% (118/138) of all residues were in favored (98%) regions.
100.0% (138/138) of all residues were in allowed (>99.8%) regions.

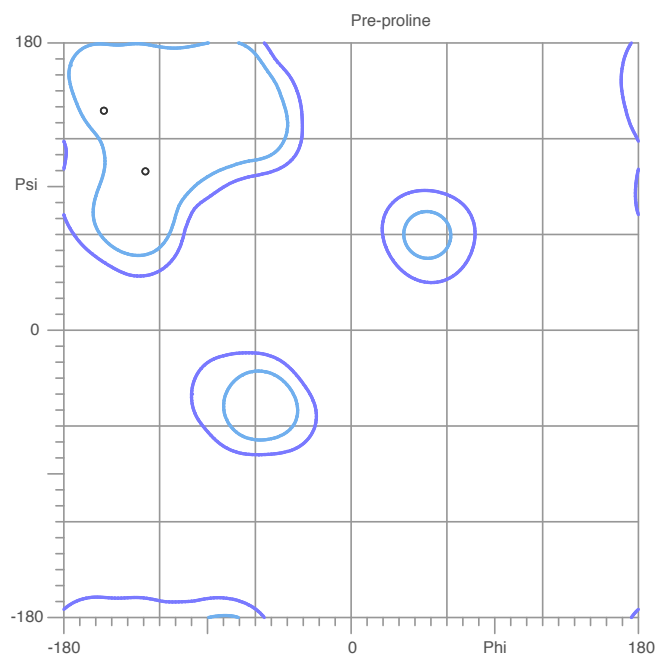
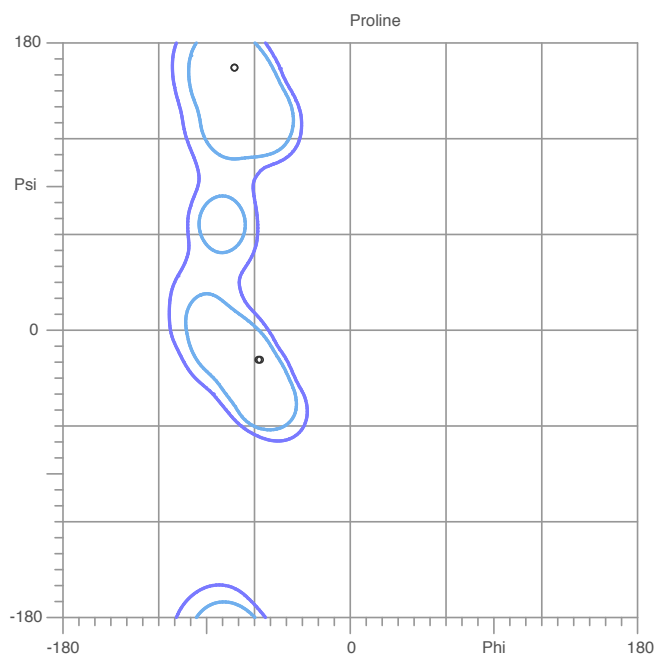
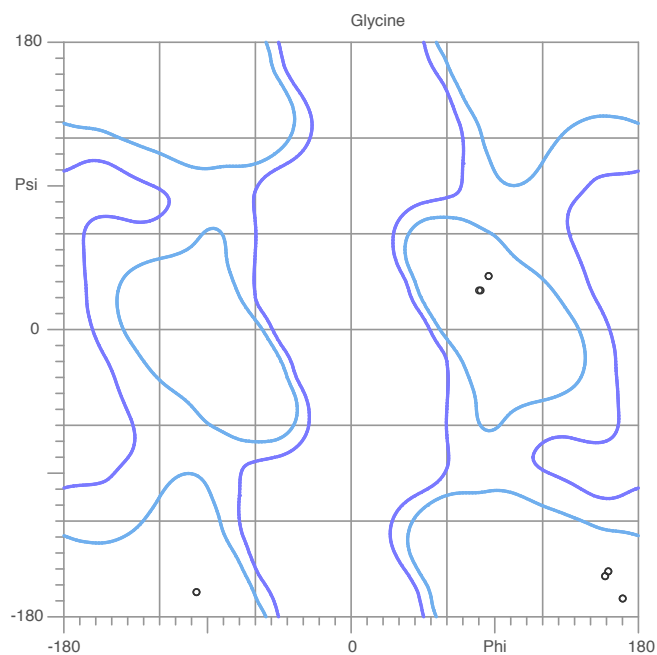
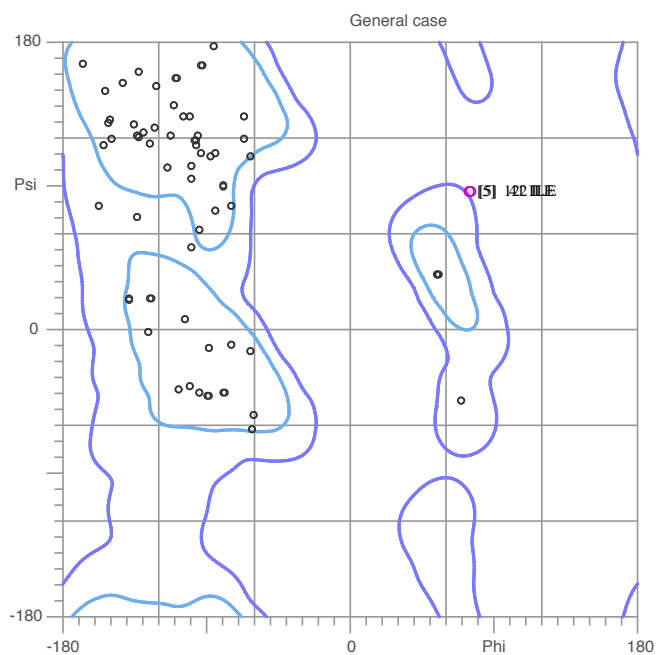
There were no outliers.

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MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 5



92.8% (128/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

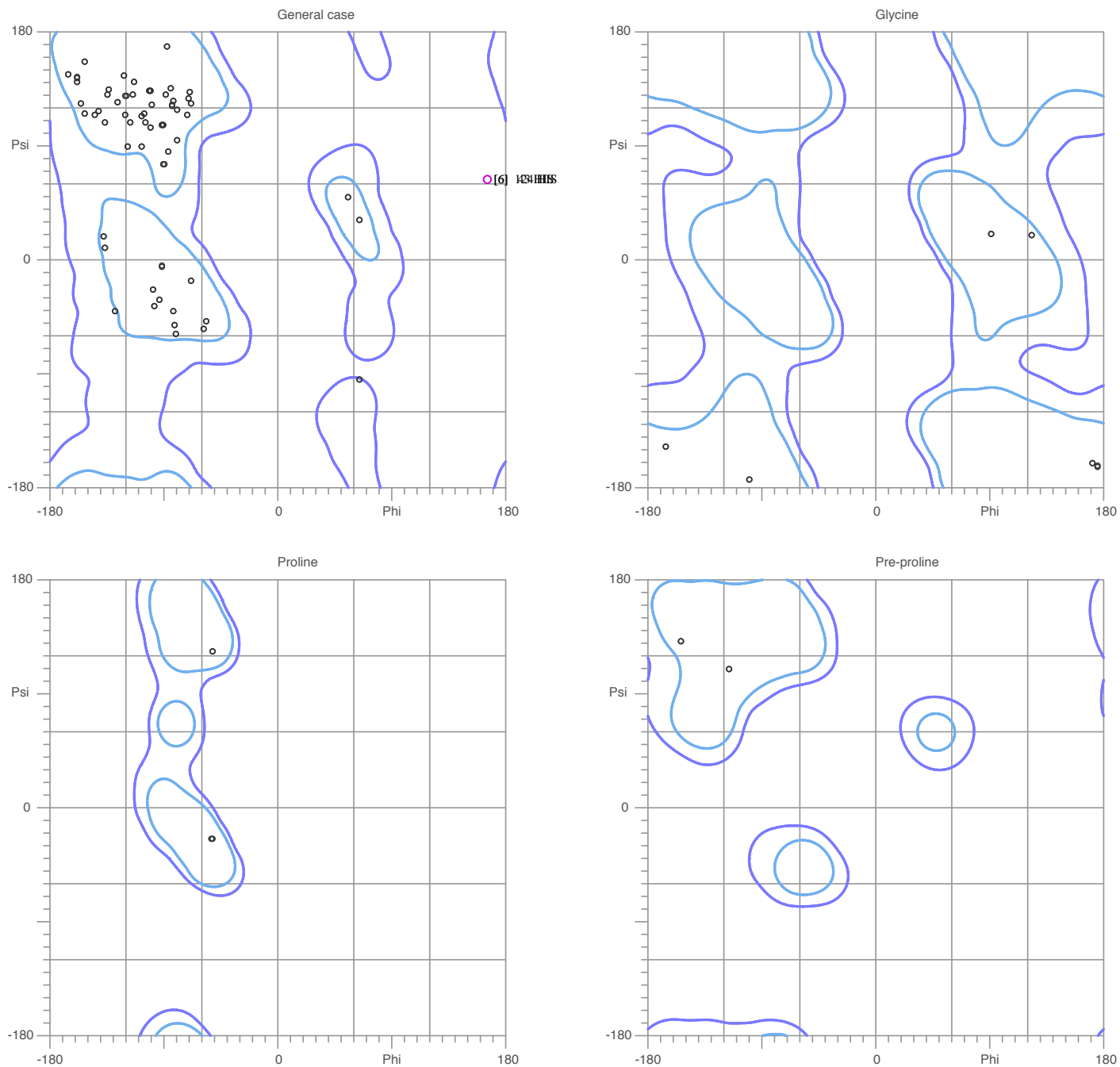
There were 2 outliers (phi, psi):

[5] 41 ILE (75.0, 87.6)

[5] 122 ILE (75.0, 87.7)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 6



95.7% (132/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

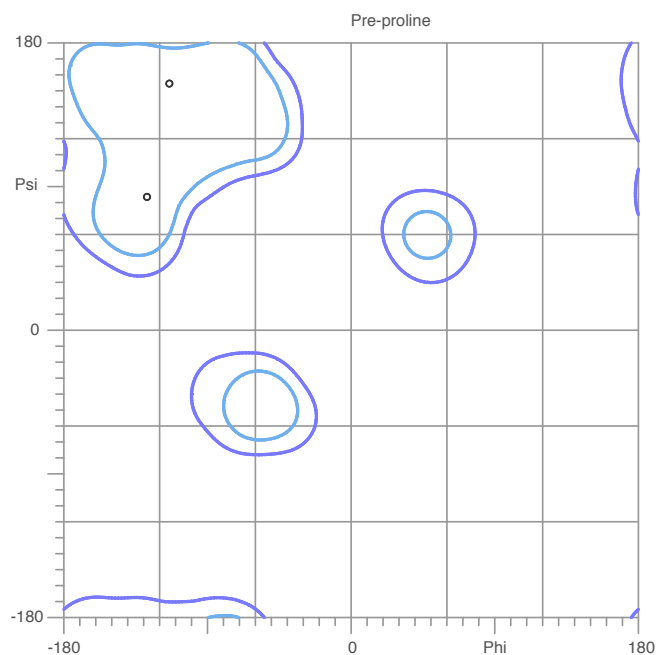
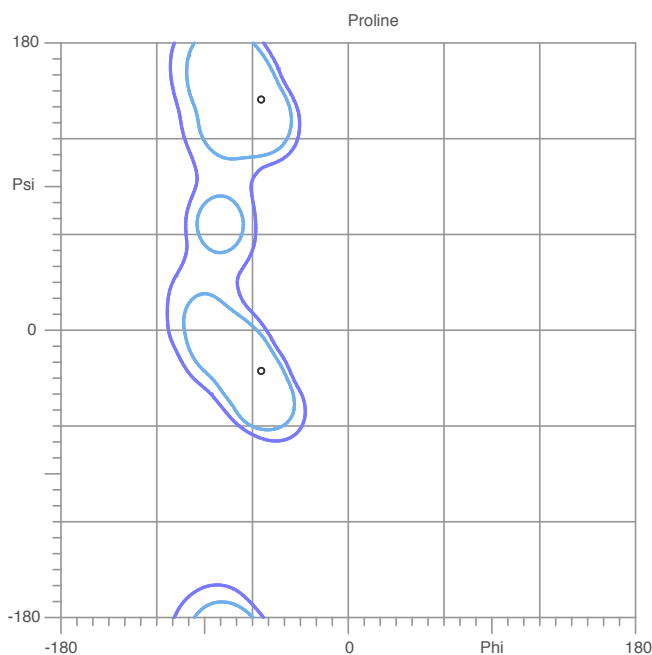
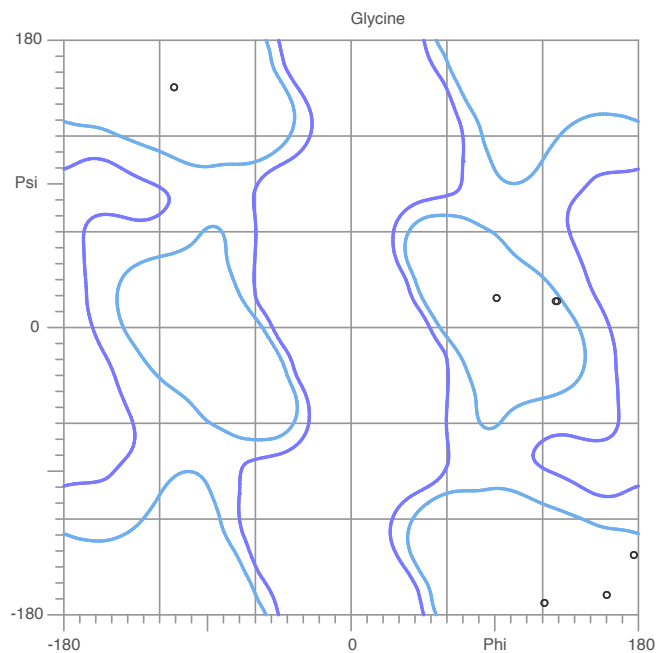
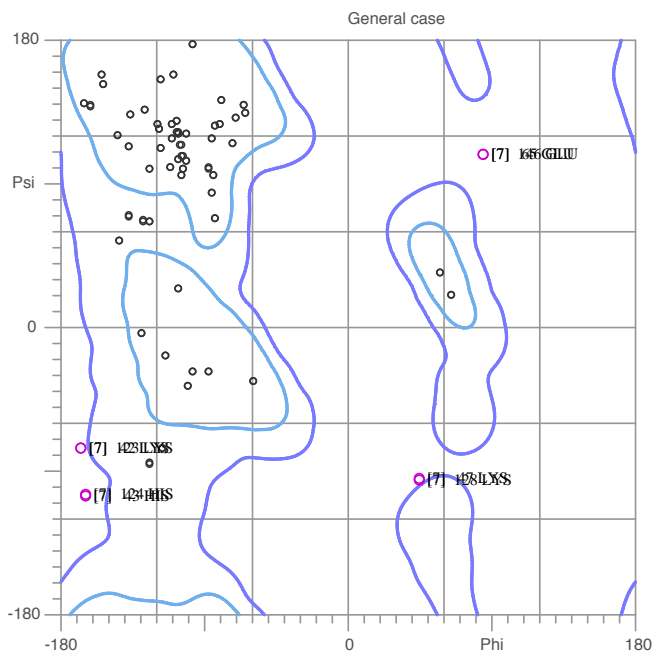
There were 2 outliers (phi, psi):

[6] 43 HIS (165.7, 64.9)

[6] 124 HIS (165.8, 64.8)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 7



85.5% (118/138) of all residues were in favored (98%) regions.
94.2% (130/138) of all residues were in allowed (>99.8%) regions.

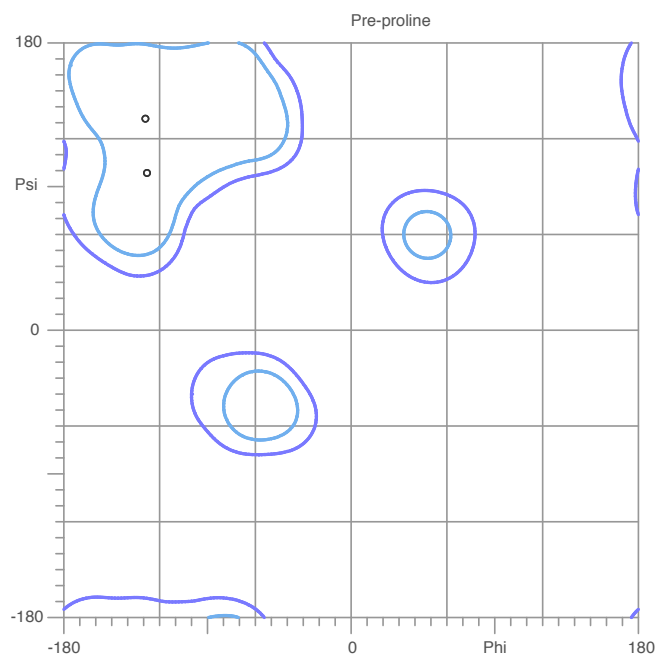
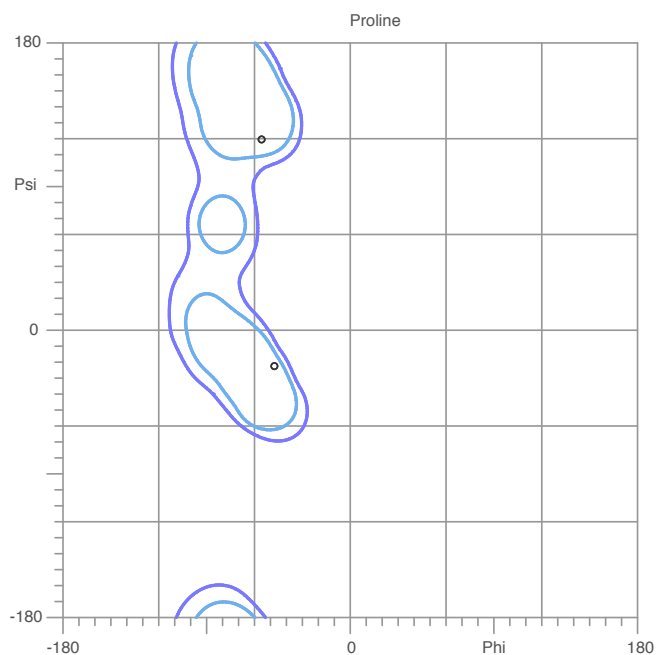
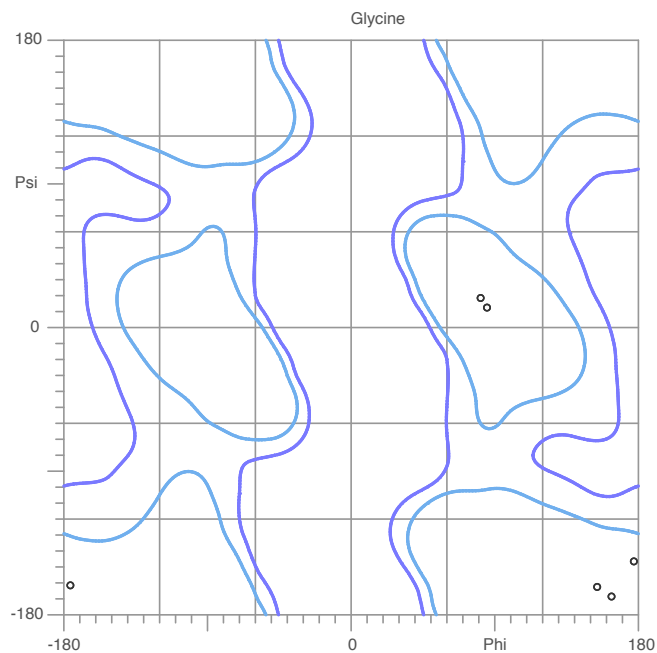
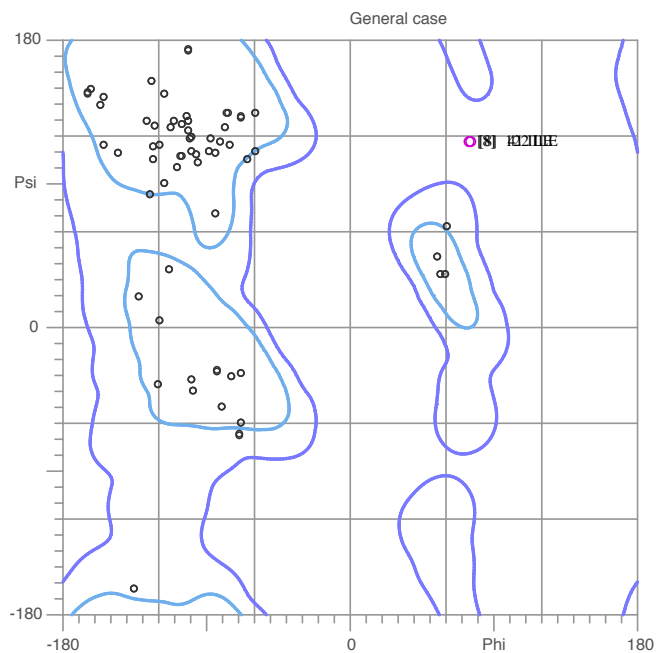
There were 8 outliers (phi, psi):

[7] 42 LYS (-168.2, -75.9)
[7] 43 HIS (-165.0, -105.1)

[7] 47 LYS (44.9, -95.0)
[7] 65 GLU (84.9, 109.4)
[7] 123 LYS (-168.2, -75.9)
[7] 124 HIS (-165.0, -105.0)
[7] 128 LYS (45.0, -95.0)
[7] 146 GLU (84.9, 109.4)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 8



94.2% (130/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

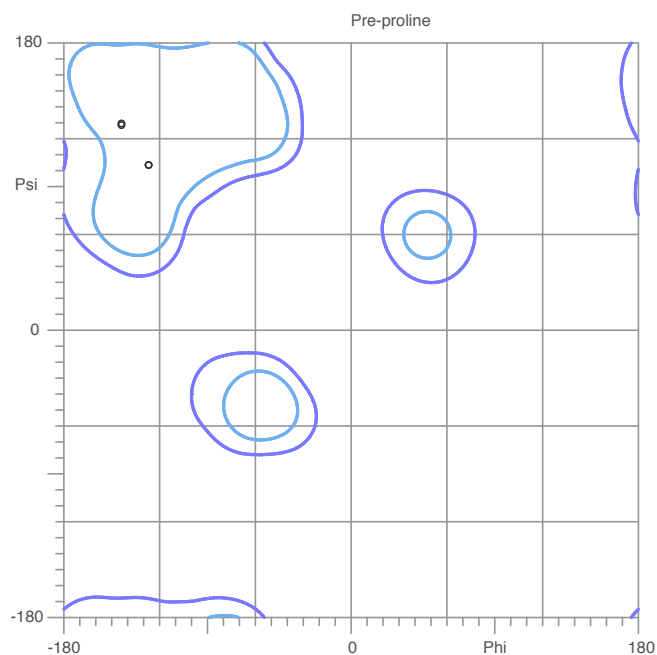
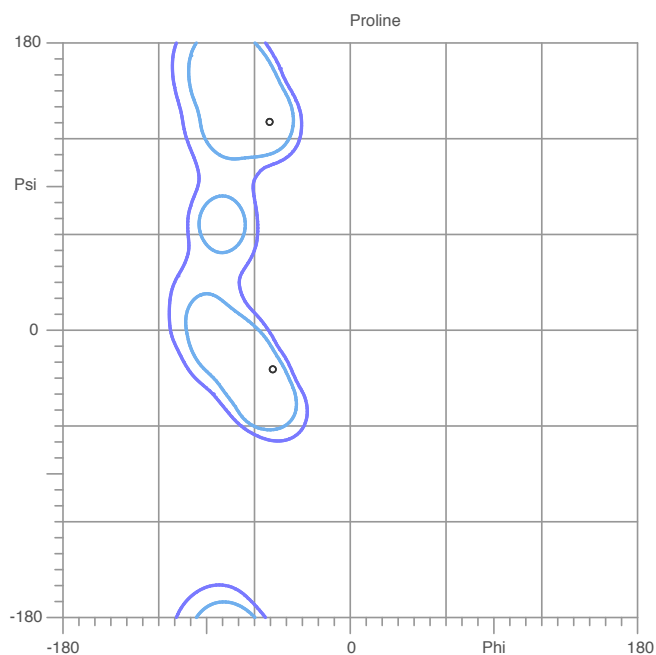
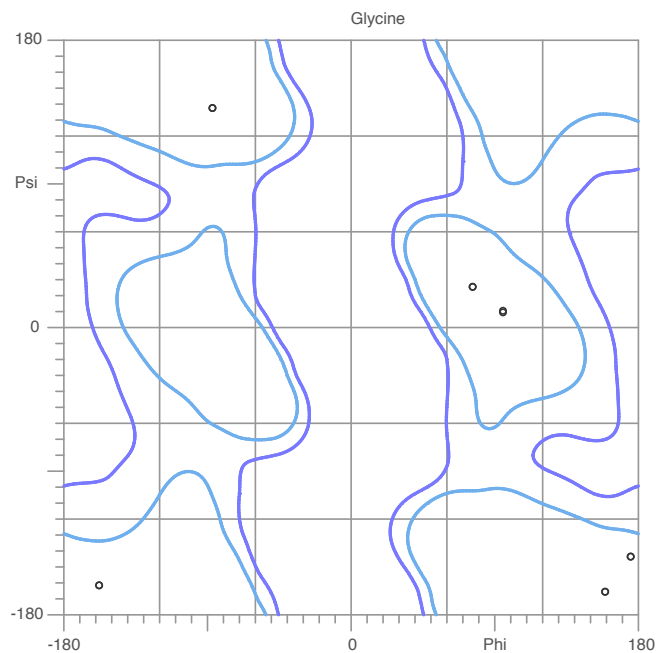
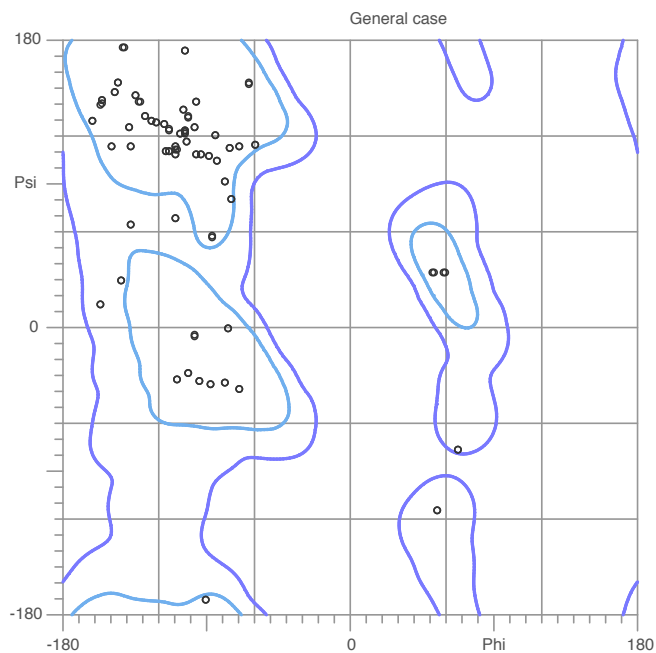
There were 2 outliers (phi, psi):

[8] 41 ILE (75.0, 117.7)

[8] 122 ILE (75.0, 117.7)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 9



91.3% (126/138) of all residues were in favored (98%) regions.
100.0% (138/138) of all residues were in allowed (>99.8%) regions.

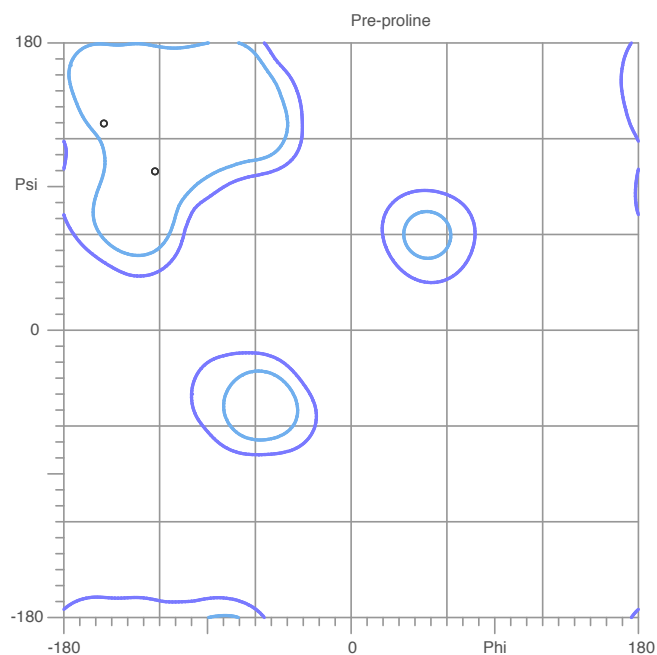
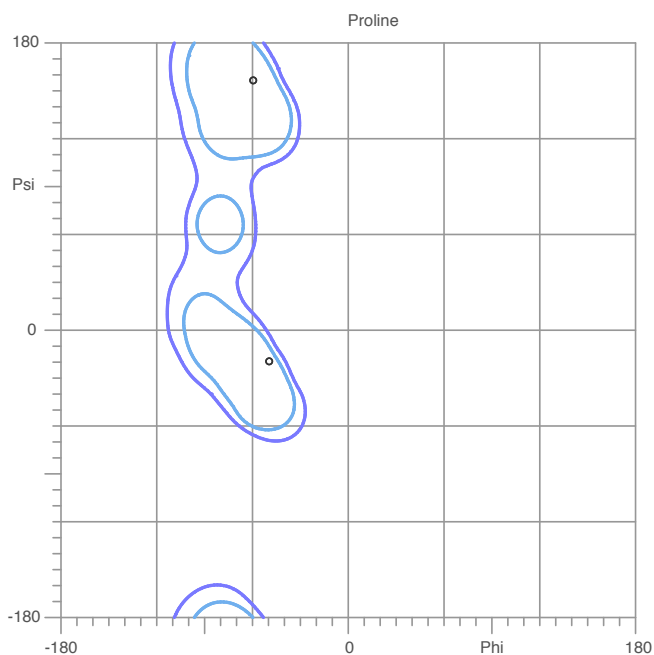
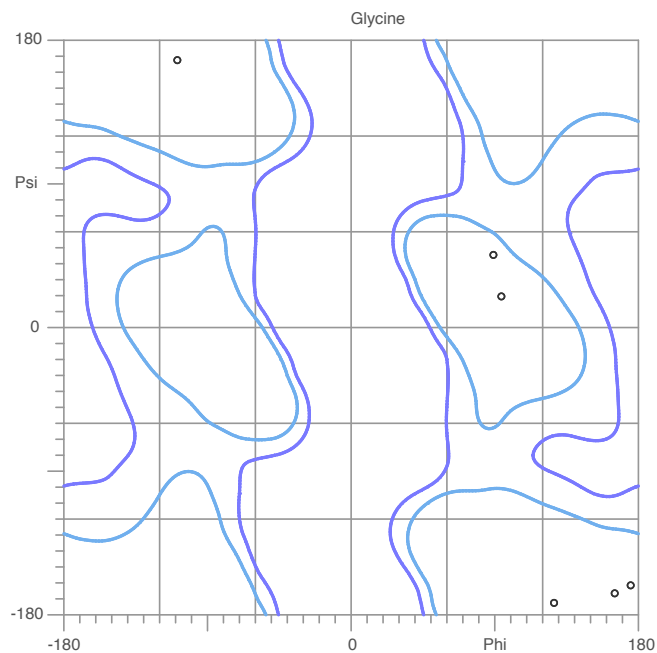
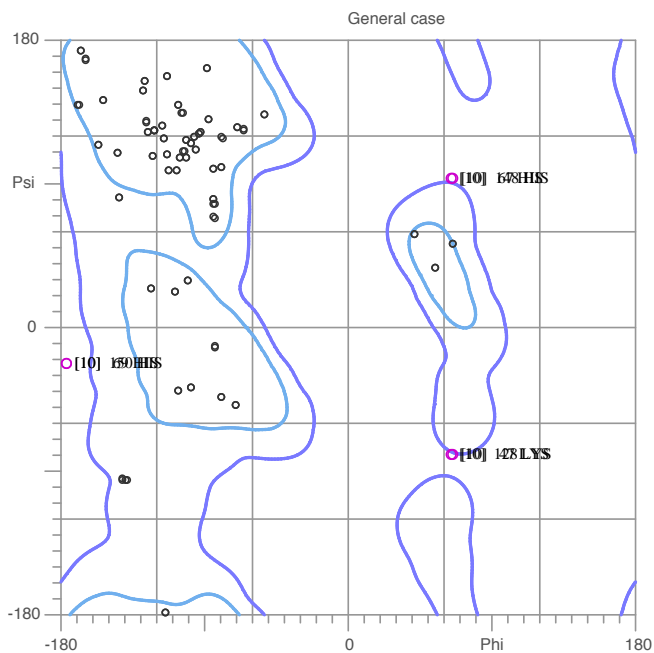
There were no outliers.

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

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MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 10



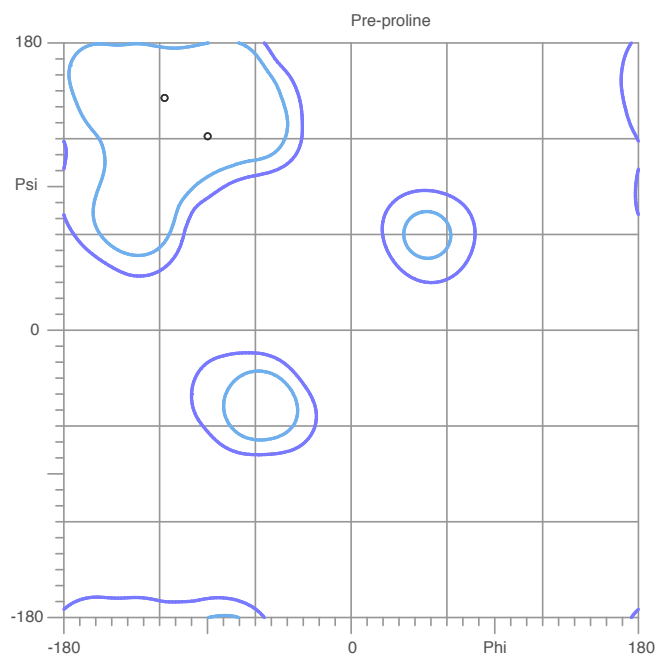
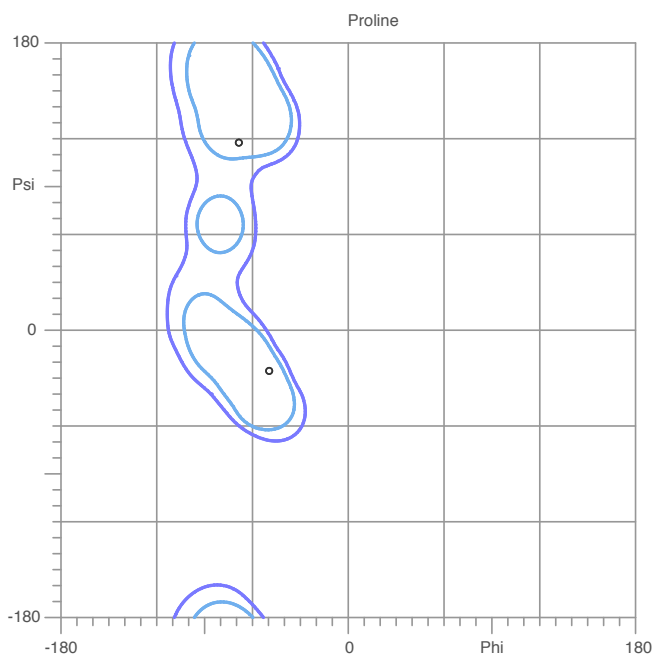
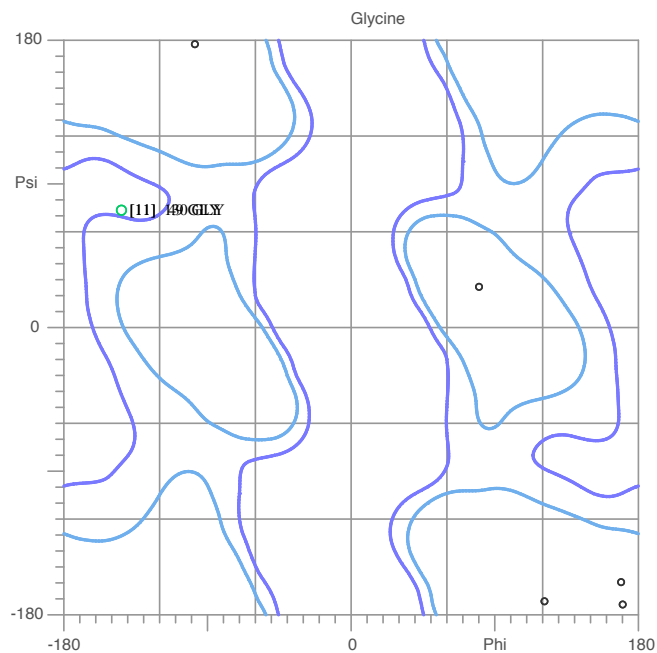
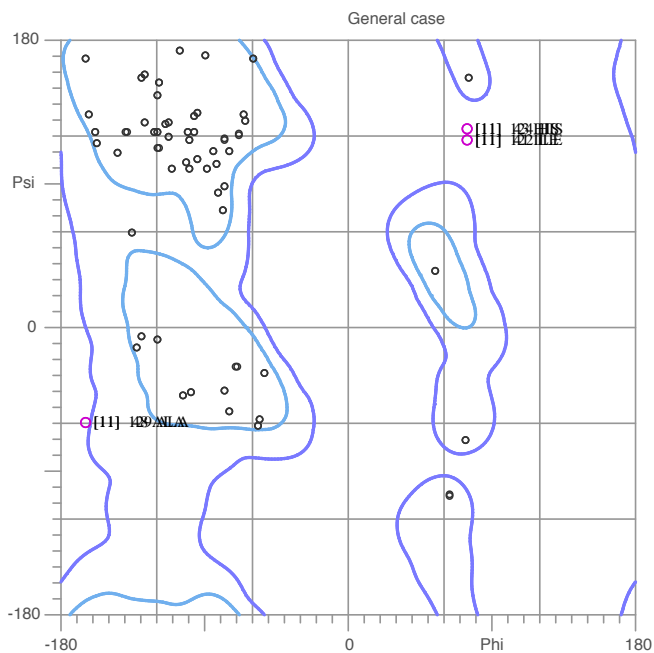
89.9% (124/138) of all residues were in favored (98%) regions.
95.7% (132/138) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[10] 47 LYS (65.1, -79.9)

[10] 67 HIS (65.0, 95.0)
[10] 69 HIS (-177.2, -22.8)
[10] 128 LYS (65.0, -79.9)
[10] 148 HIS (65.1, 94.9)
[10] 150 HIS (-177.1, -22.8)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 11



88.4% (122/138) of all residues were in favored (98%) regions.
94.2% (130/138) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[11] 41 ILE (74.7, 118.5)

[11] 43 HIS (74.9, 125.0)

[11] 48 ALA (-165.0, -59.8)

[11] 49 GLY (-144.9, 74.7)

[11] 122 ILE (74.7, 118.5)

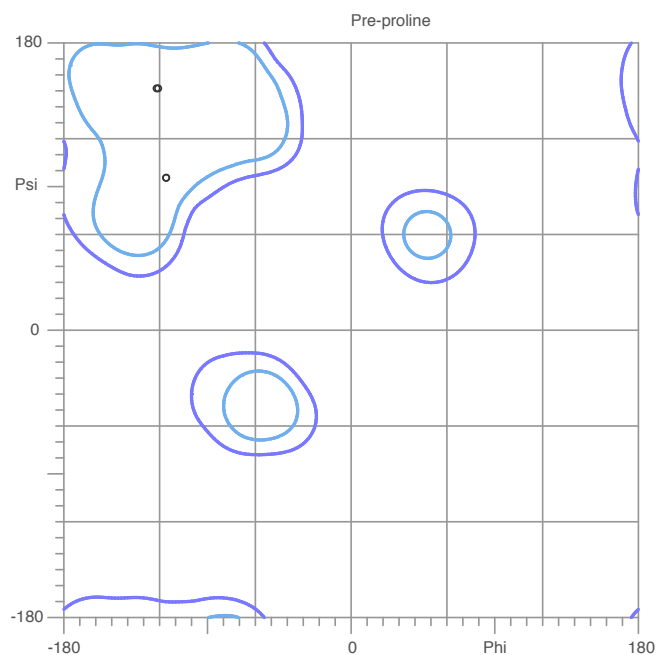
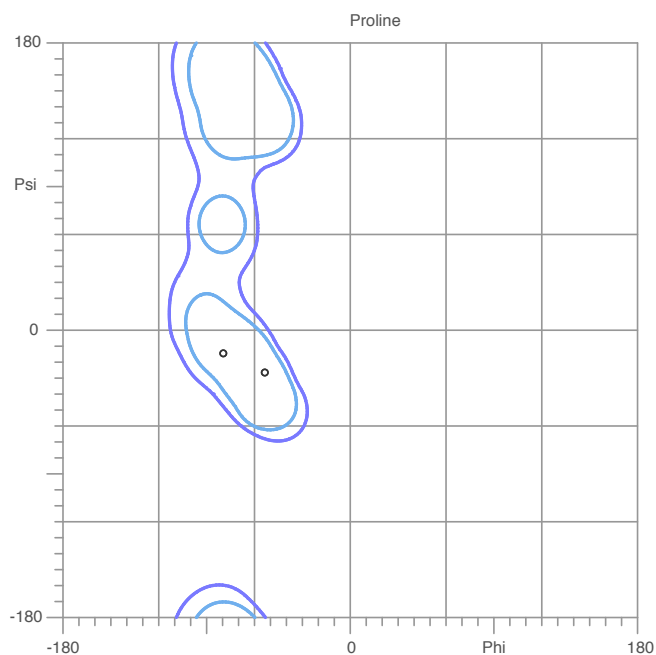
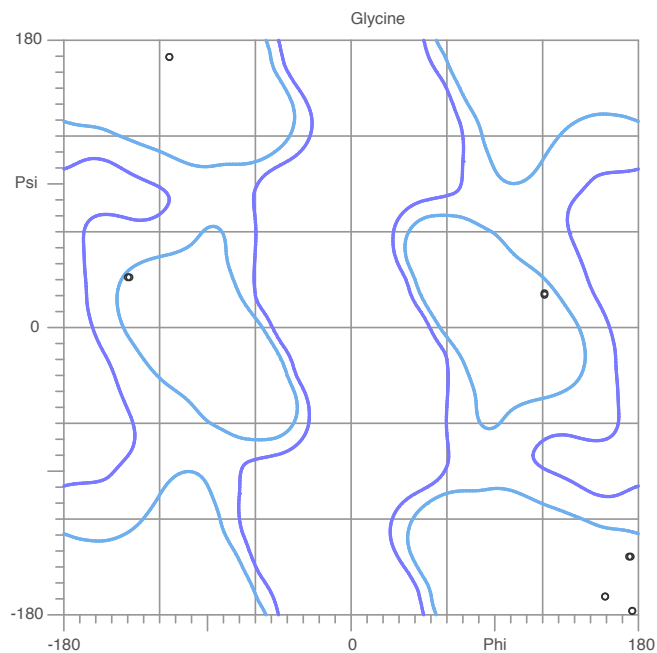
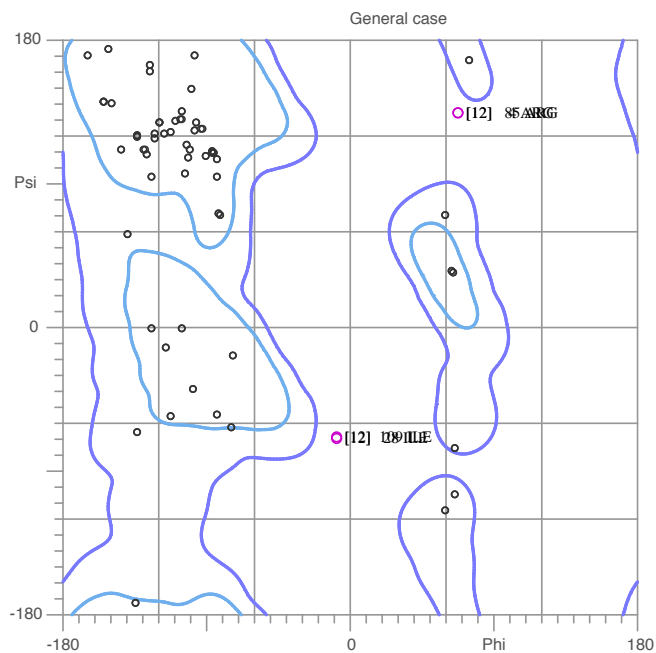
[11] 124 HIS (74.9, 125.1)

[11] 129 ALA (-165.0, -59.8)

[11] 130 GLY (-145.0, 74.8)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 12



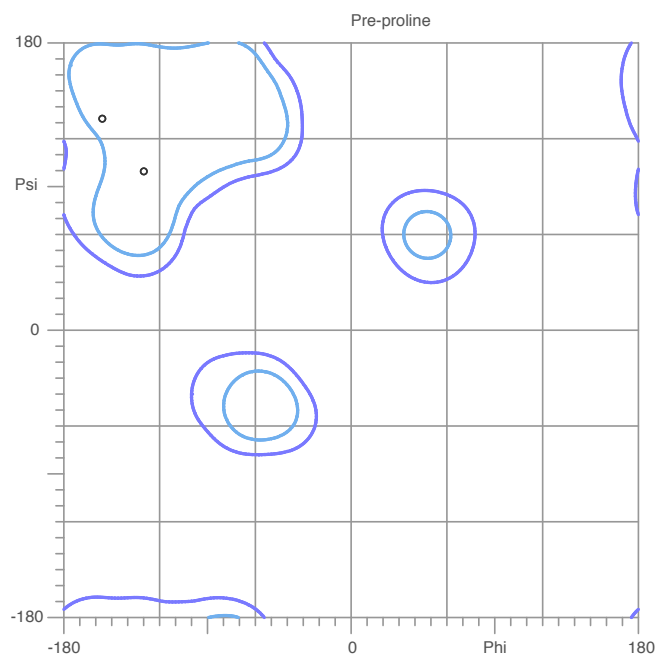
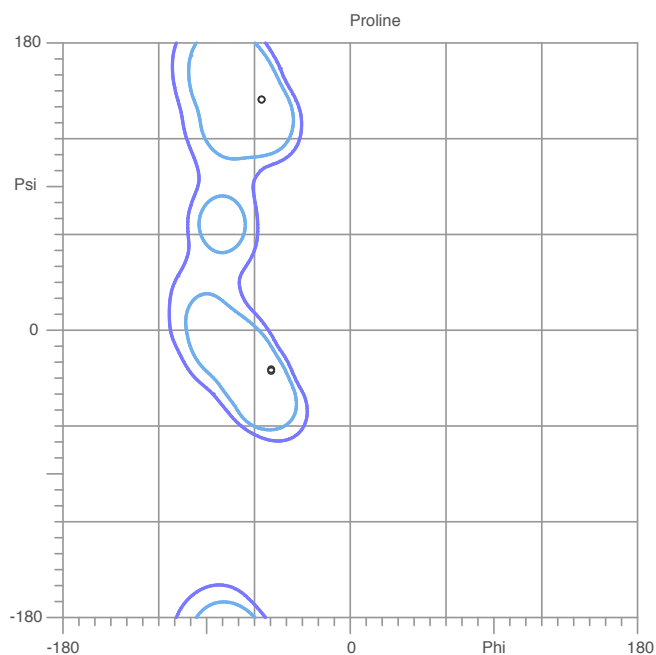
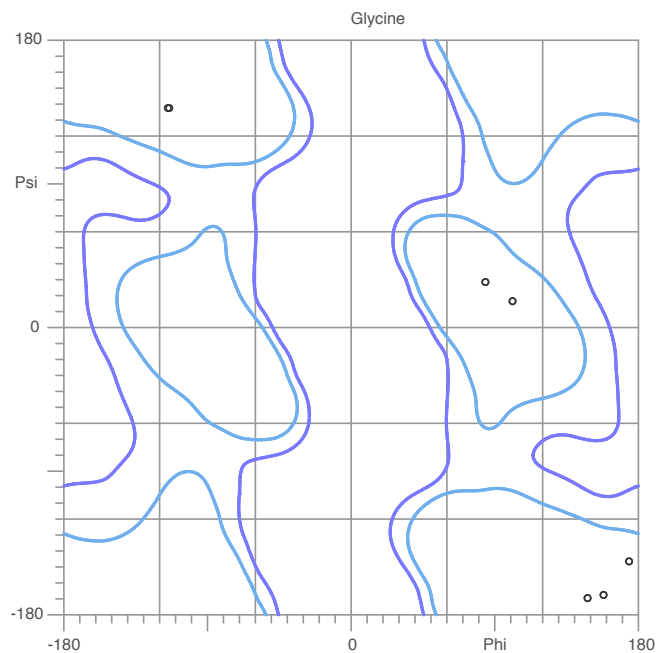
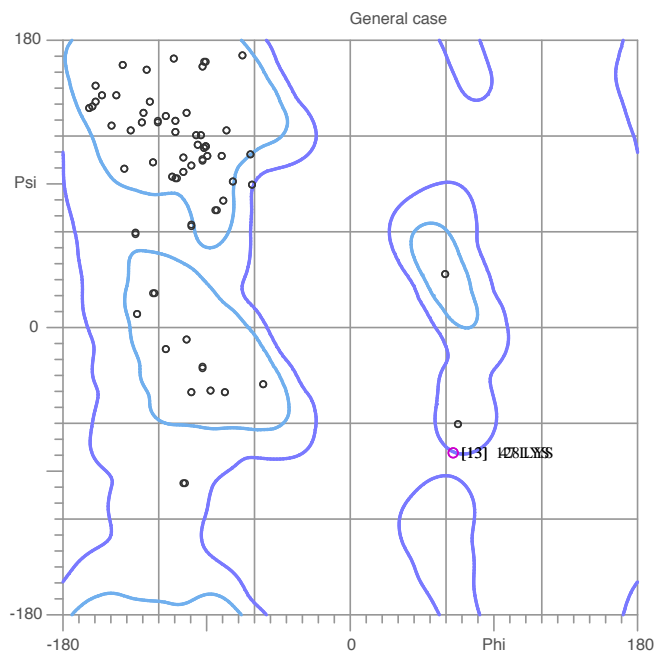
85.5% (118/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [12] 4 ARG (67.4, 135.1)
- [12] 28 ILE (-9.9, -69.1)
- [12] 85 ARG (67.3, 135.1)
- [12] 109 ILE (-10.0, -69.0)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 13



91.3% (126/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

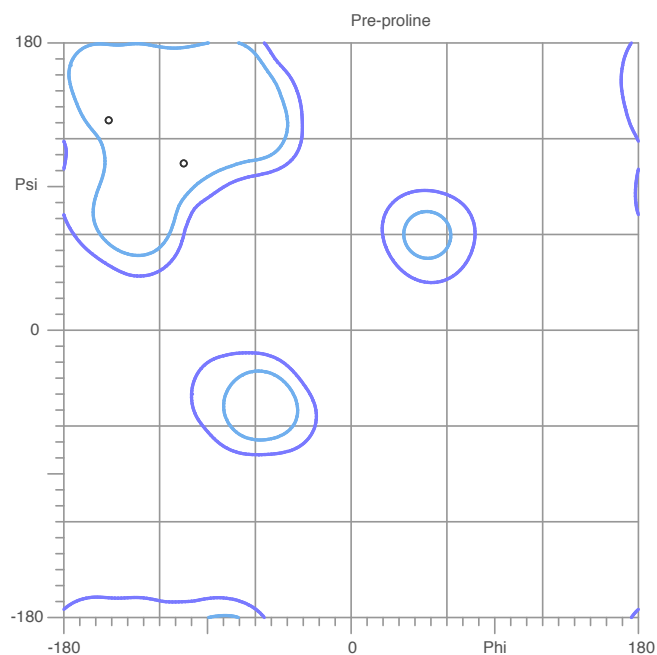
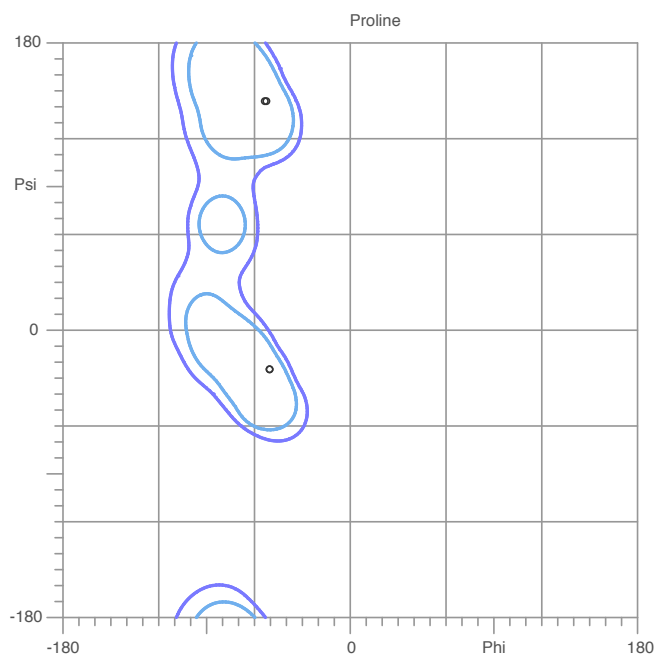
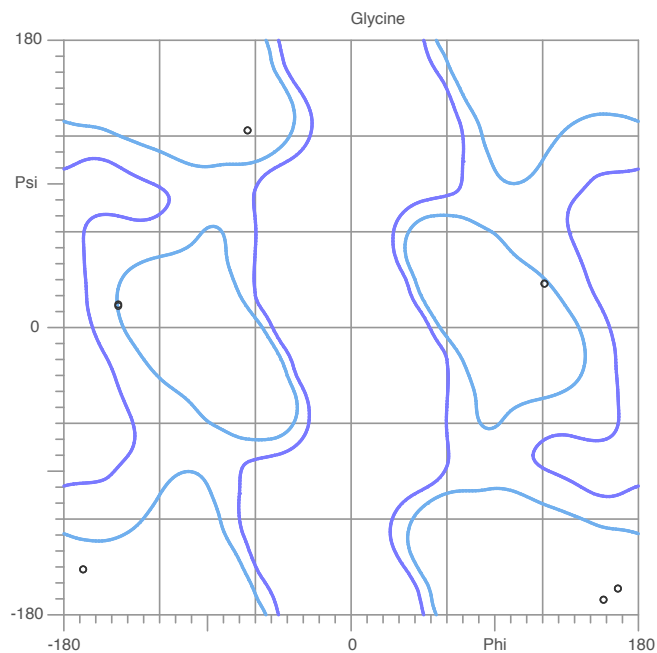
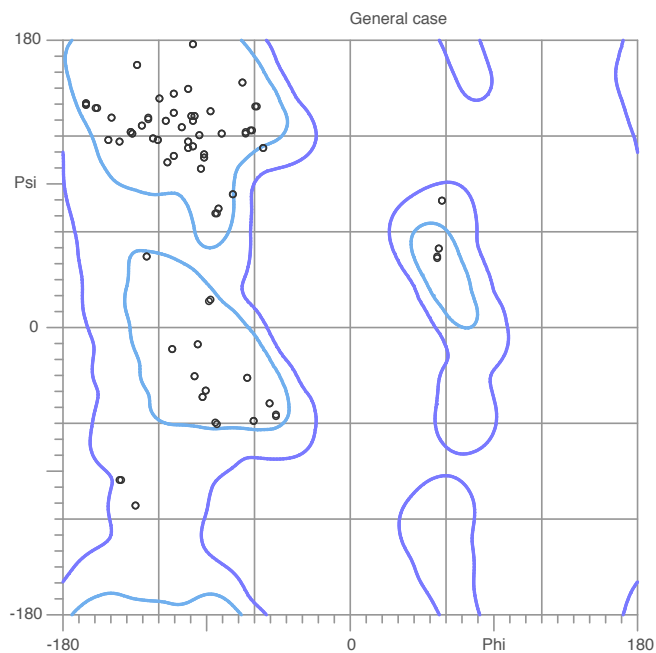
There were 2 outliers (phi, psi):

[13] 47 LYS (65.0, -78.1)

[13] 128 LYS (65.0, -78.1)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 14



95.7% (132/138) of all residues were in favored (98%) regions.
100.0% (138/138) of all residues were in allowed (>99.8%) regions.

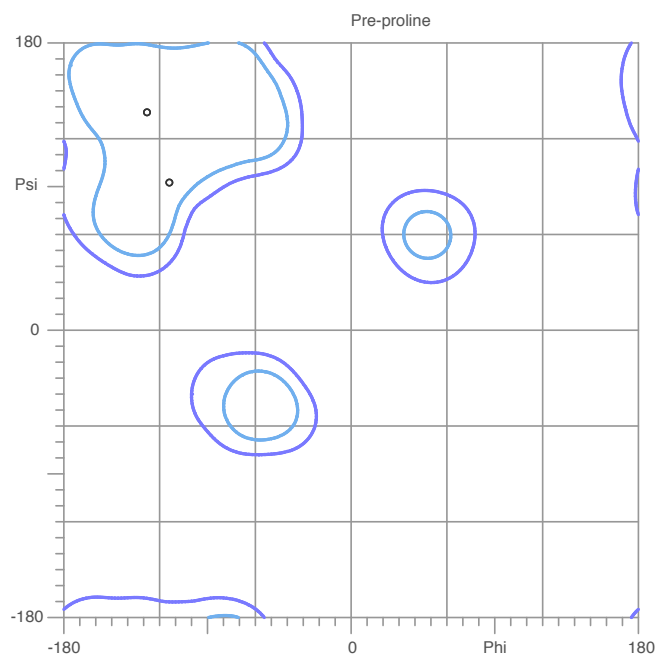
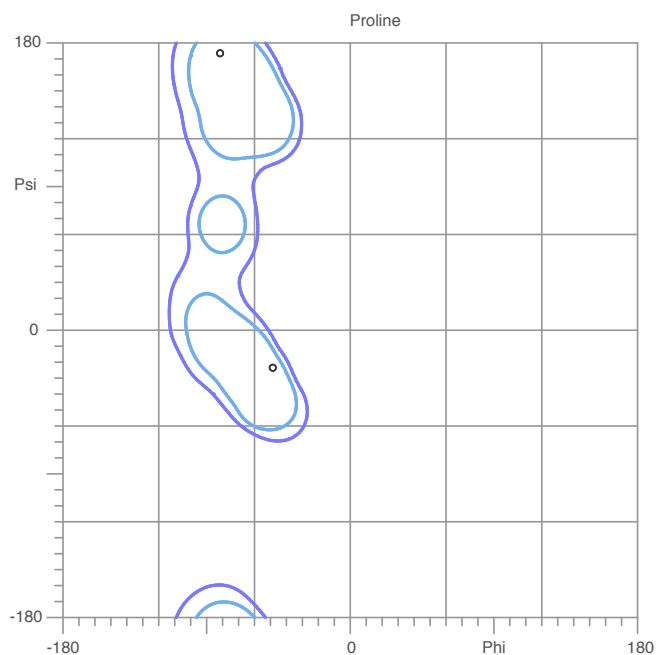
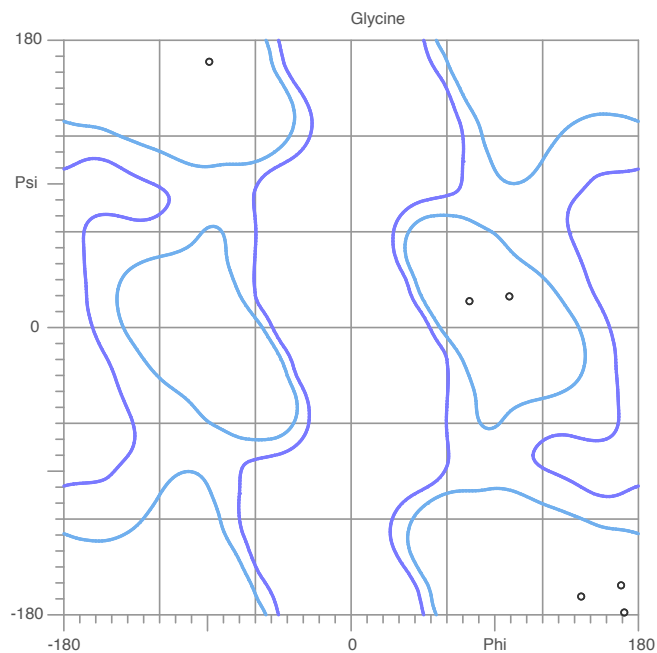
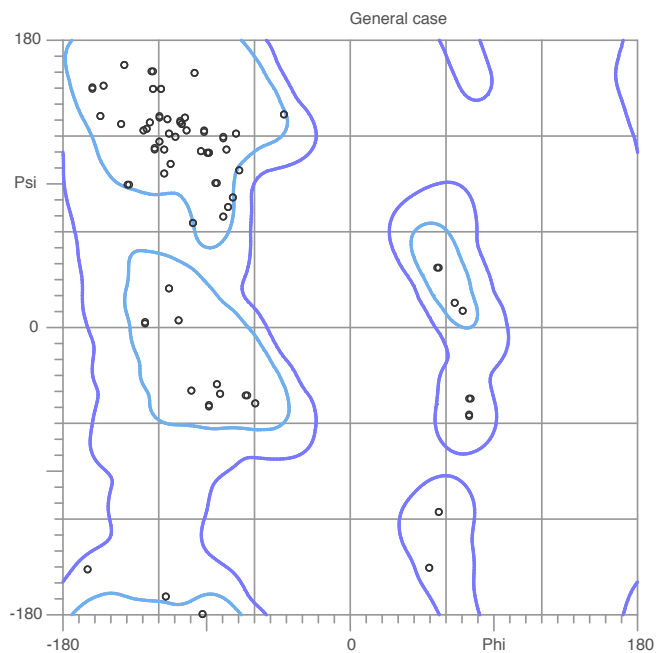
There were no outliers.

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

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

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 15



88.4% (122/138) of all residues were in favored (98%) regions.
100.0% (138/138) of all residues were in allowed (>99.8%) regions.

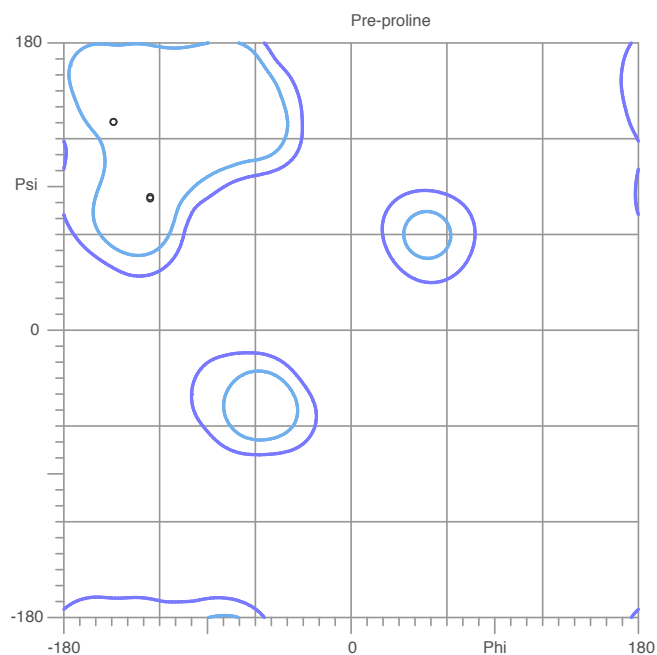
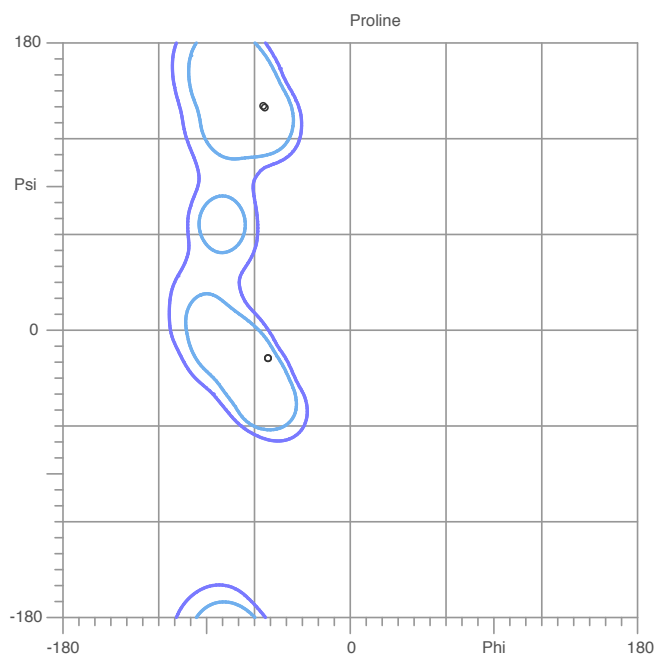
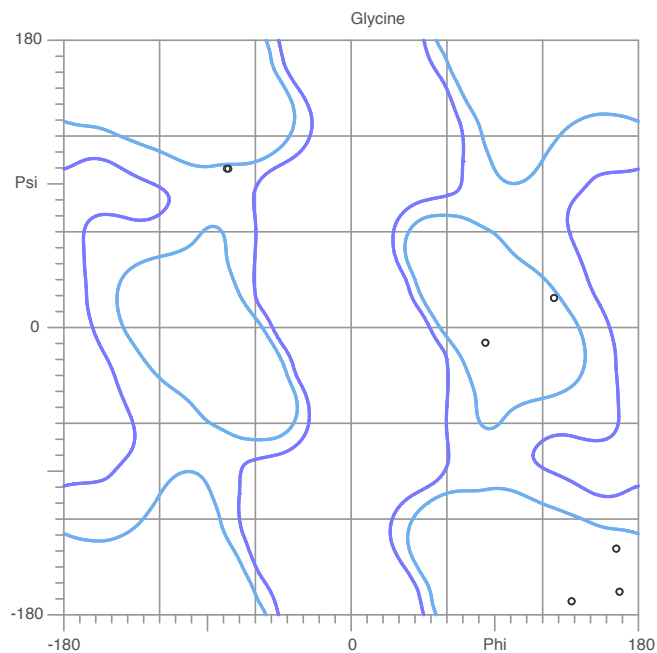
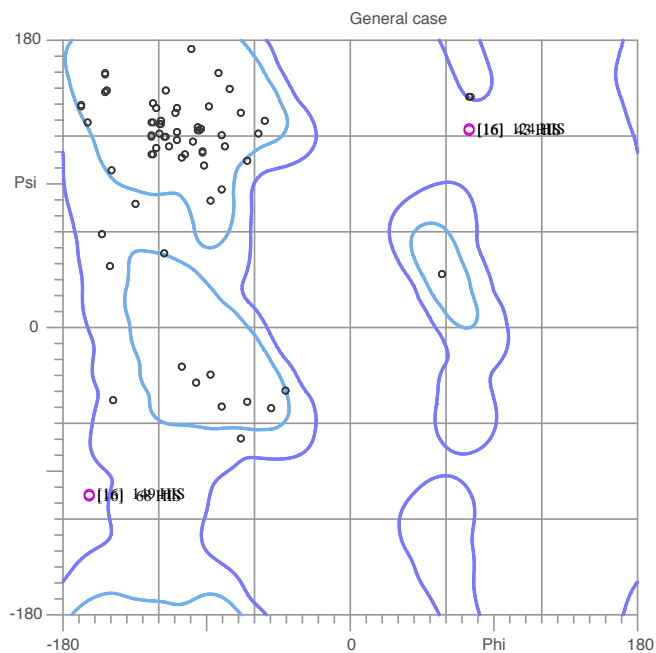
There were no outliers.

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

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

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 16



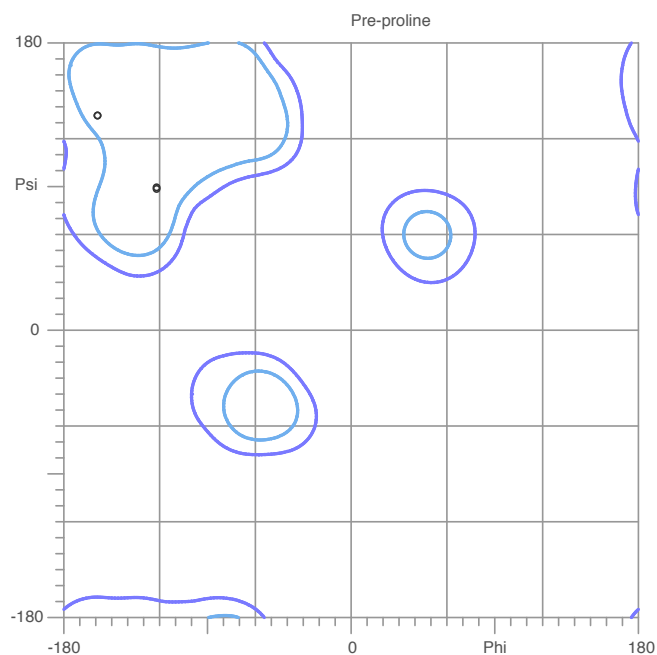
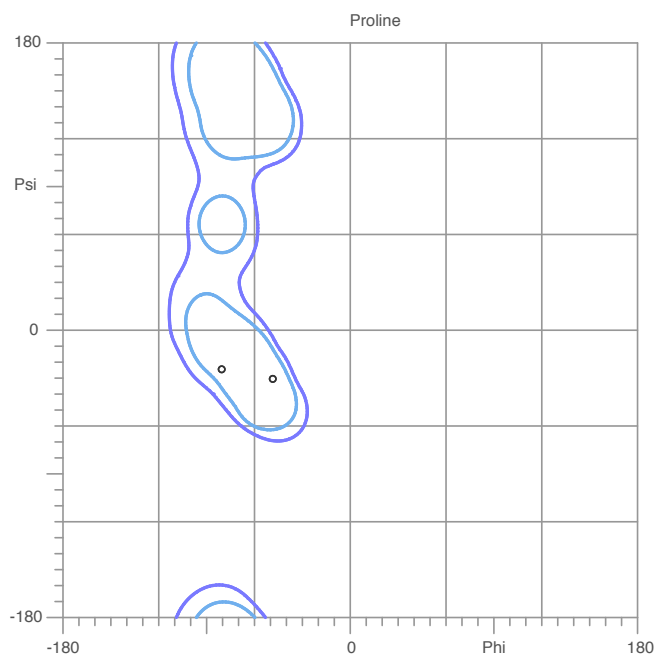
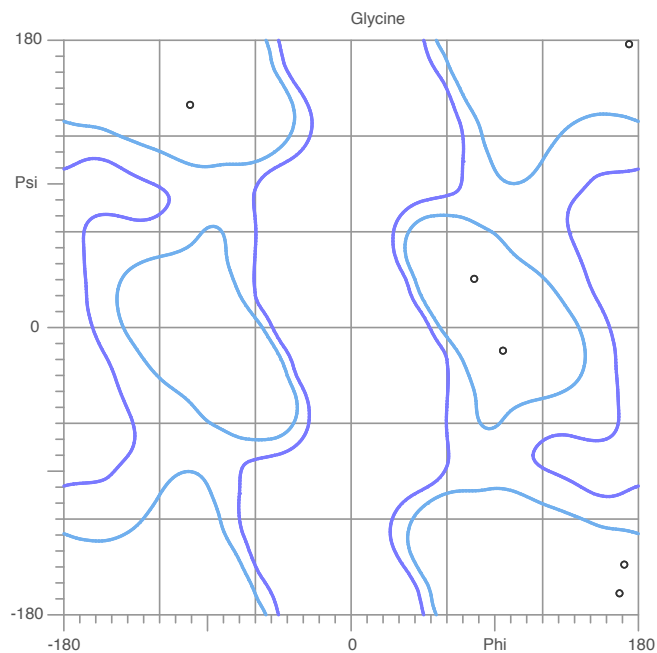
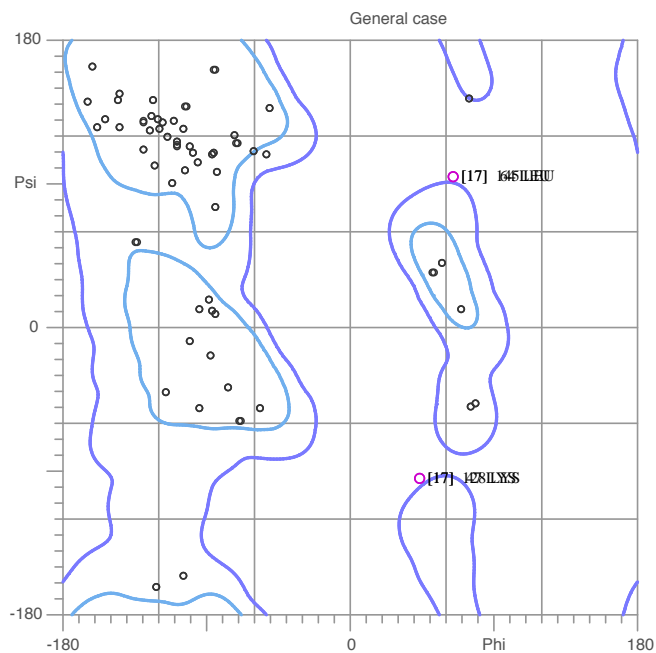
84.1% (116/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [16] 43 HIS (75.0, 125.0)
- [16] 68 HIS (-164.9, -105.0)
- [16] 124 HIS (75.0, 125.0)
- [16] 149 HIS (-165.0, -105.0)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 17



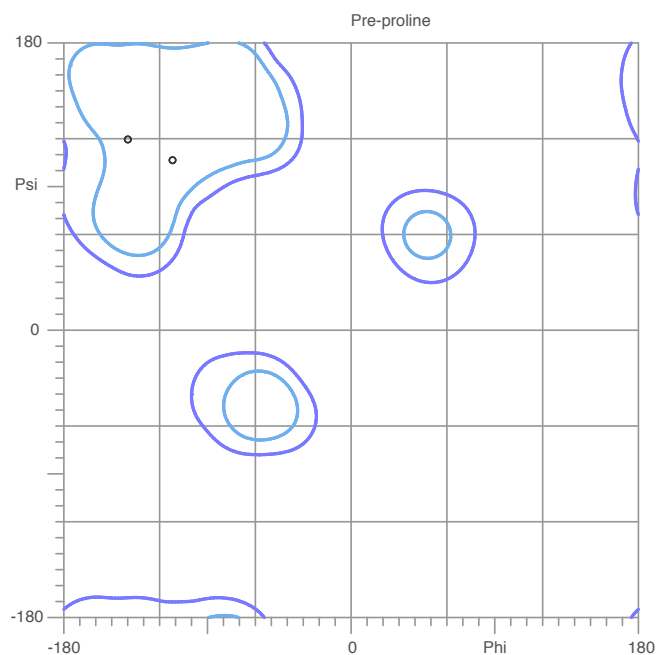
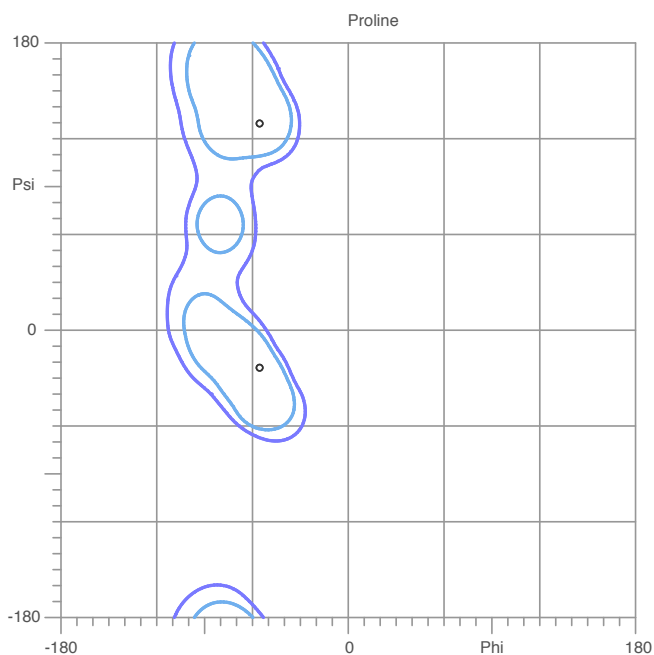
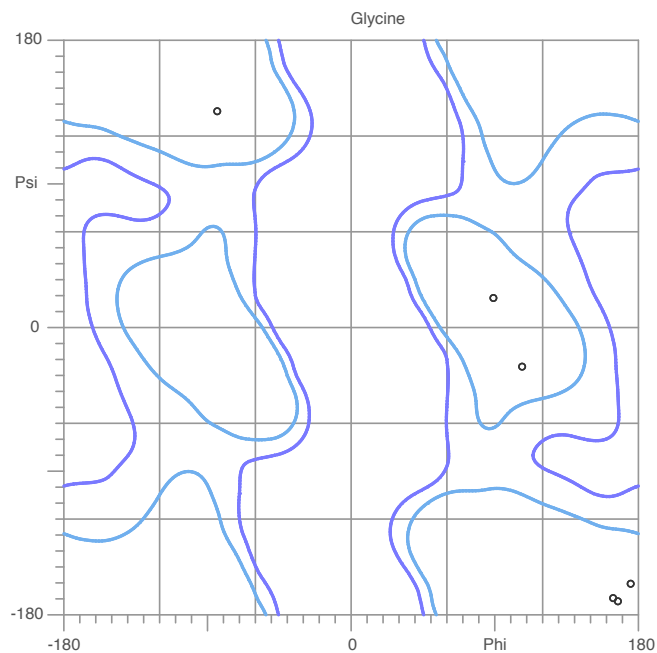
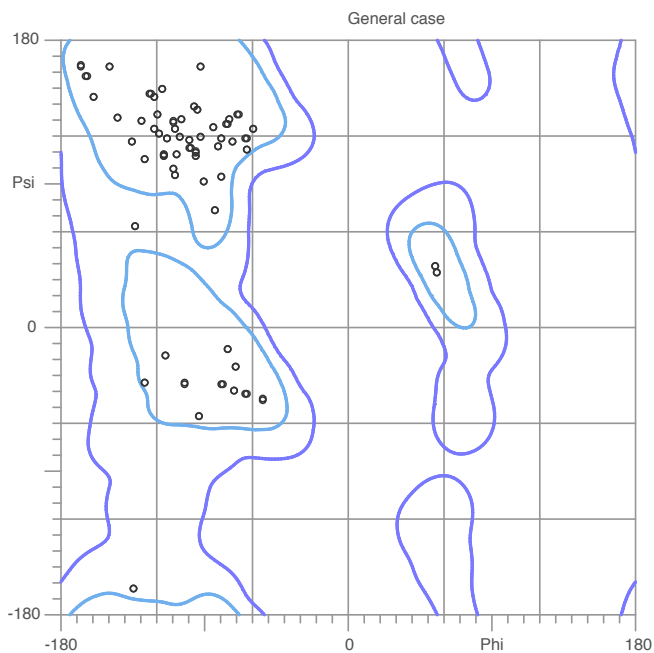
87.0% (120/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [17] 47 LYS (43.4, -94.9)
- [17] 64 LEU (65.0, 95.0)
- [17] 128 LYS (43.5, -95.0)
- [17] 145 LEU (64.9, 95.1)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 18

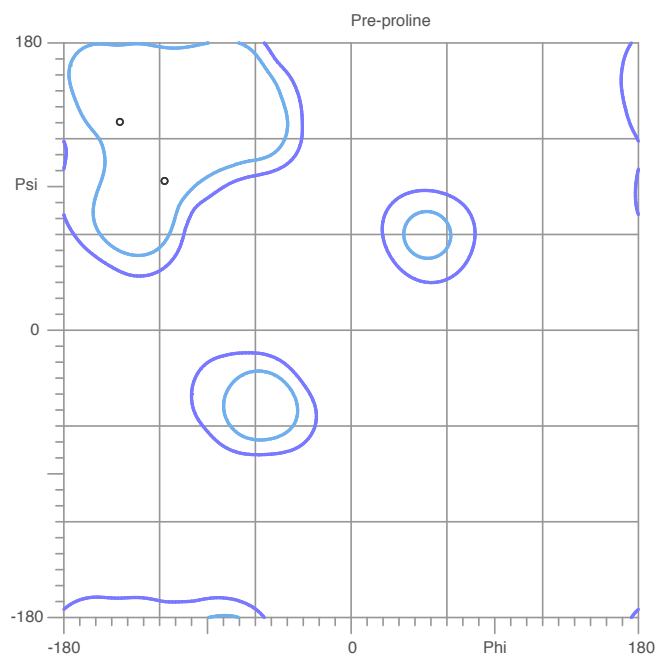
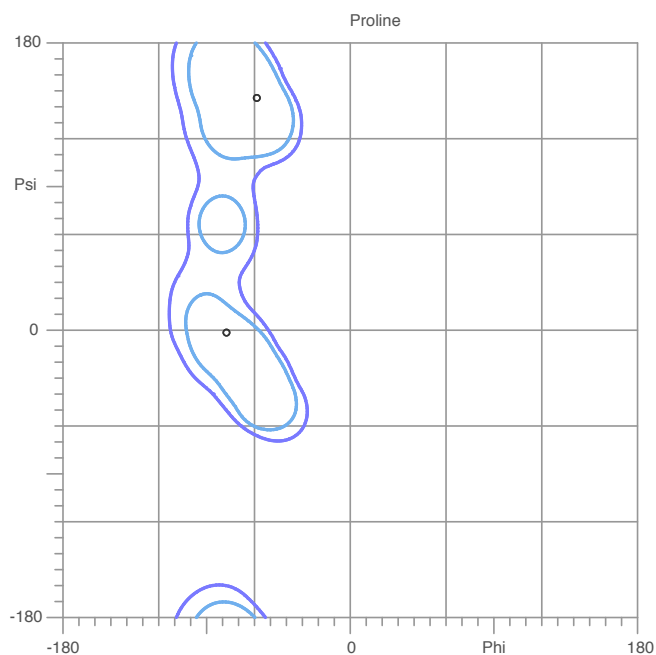
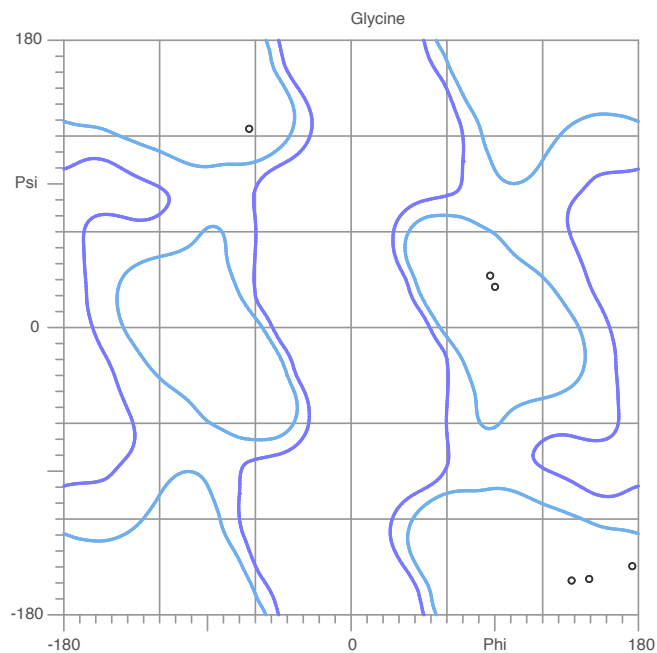
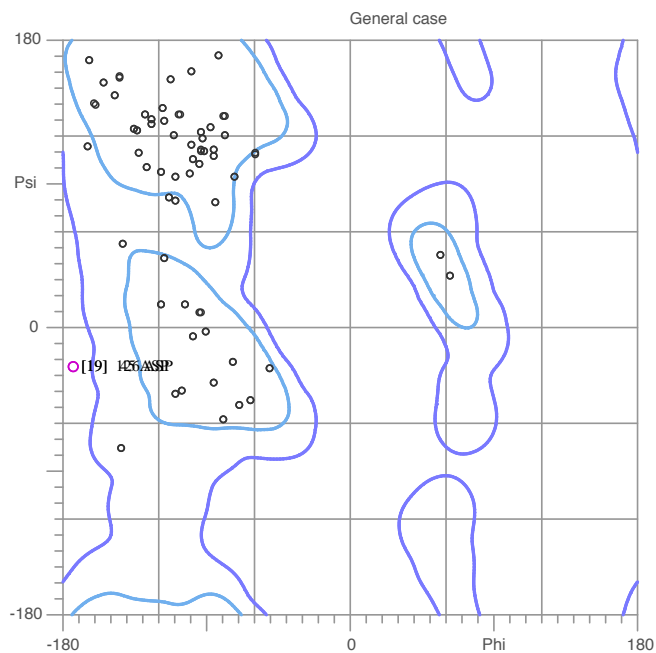


97.1% (134/138) of all residues were in favored (98%) regions.
100.0% (138/138) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 19

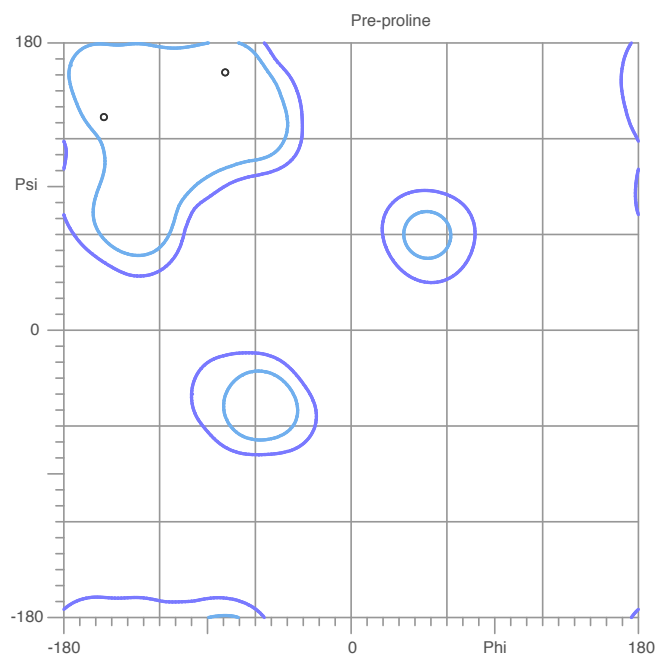
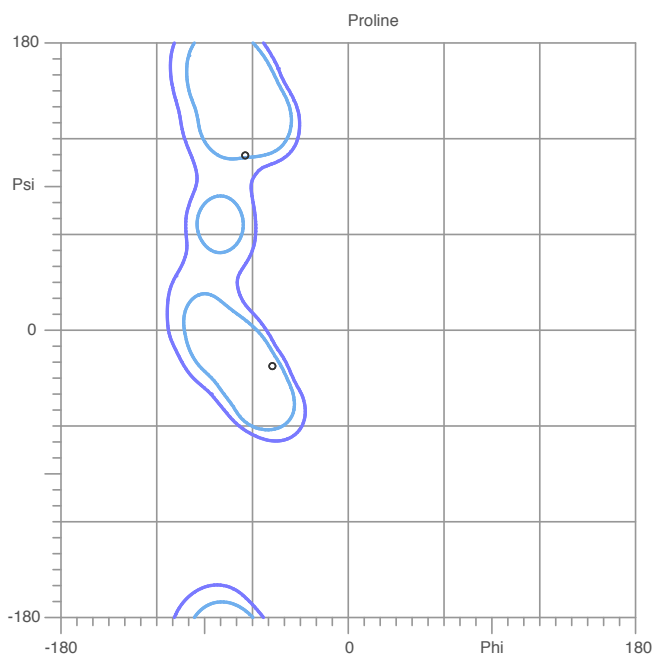
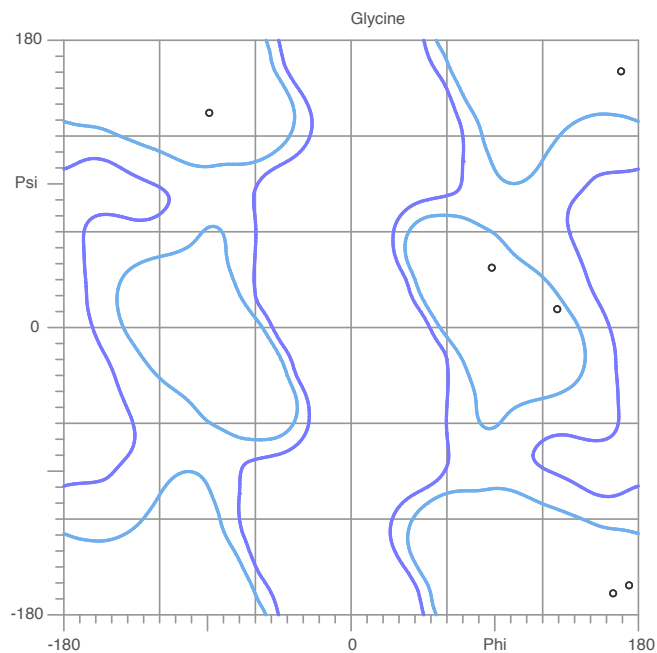
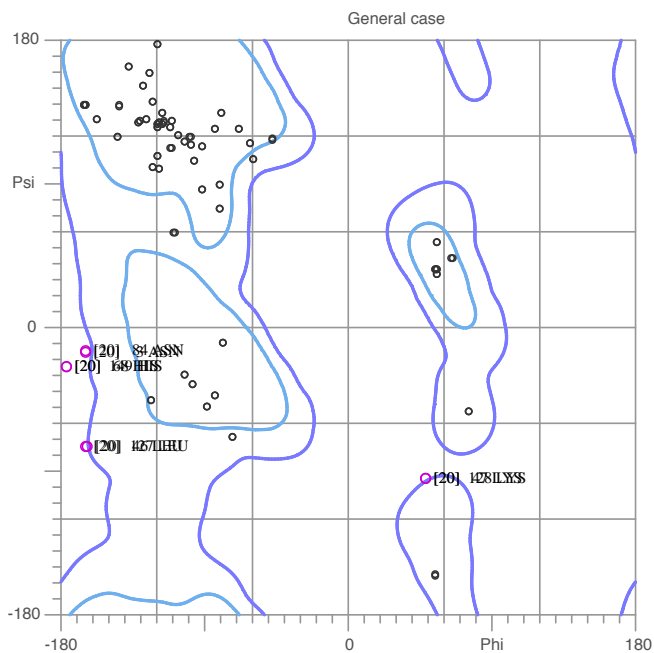


89.9% (124/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 45 ASP (-174.9, -24.9)
[19] 126 ASP (-174.9, -24.9)

MolProbity Ramachandran analysis

DHR8C_R3_em_bcr3.pdb, model 20



87.0% (120/138) of all residues were in favored (98%) regions.
94.2% (130/138) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[20] 3 ASN (-165.0, -15.1)

[20] 46 LEU (-165.0, -75.0)

[20] 47 LYS (48.5, -95.0)

[20] 68 HIS (-177.5, -24.9)

[20] 84 ASN (-165.1, -15.0)

[20] 127 LEU (-164.9, -75.0)

[20] 128 LYS (48.4, -95.0)

[20] 149 HIS (-177.6, -25.0)