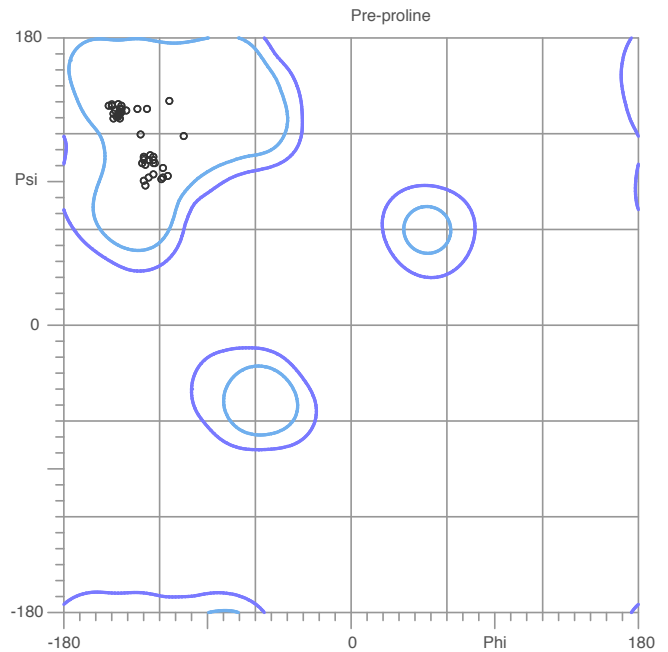
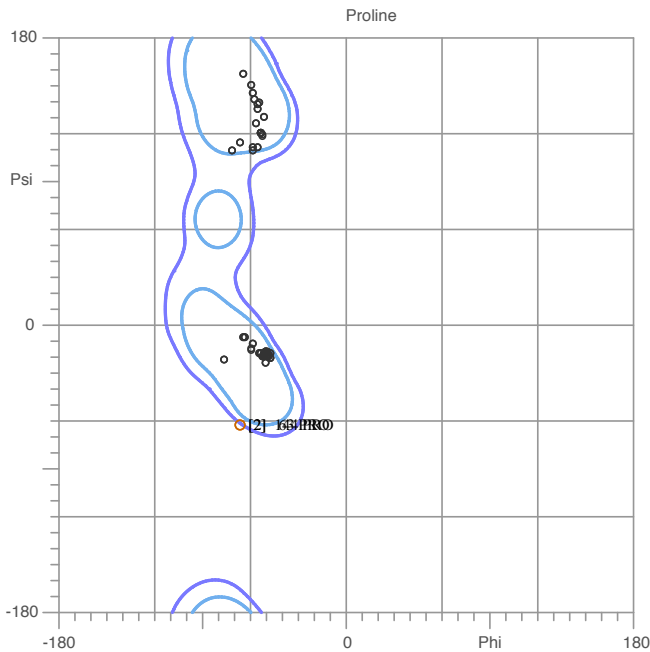
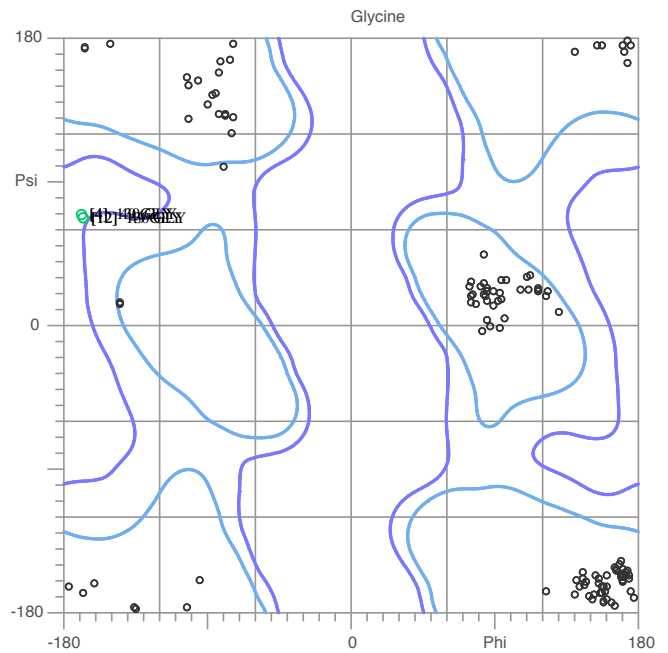
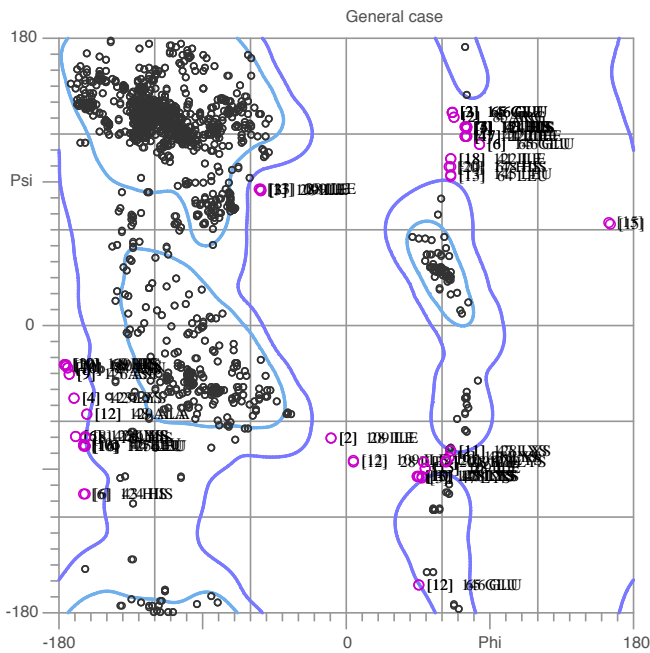


MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, all models



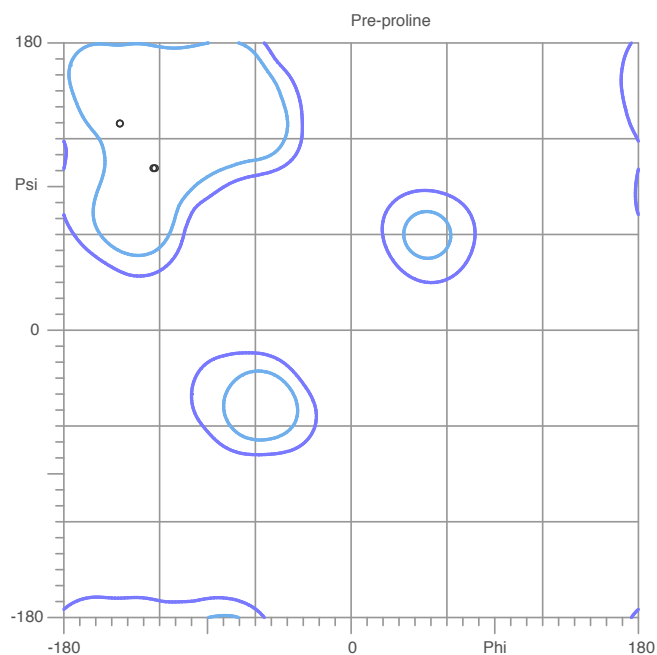
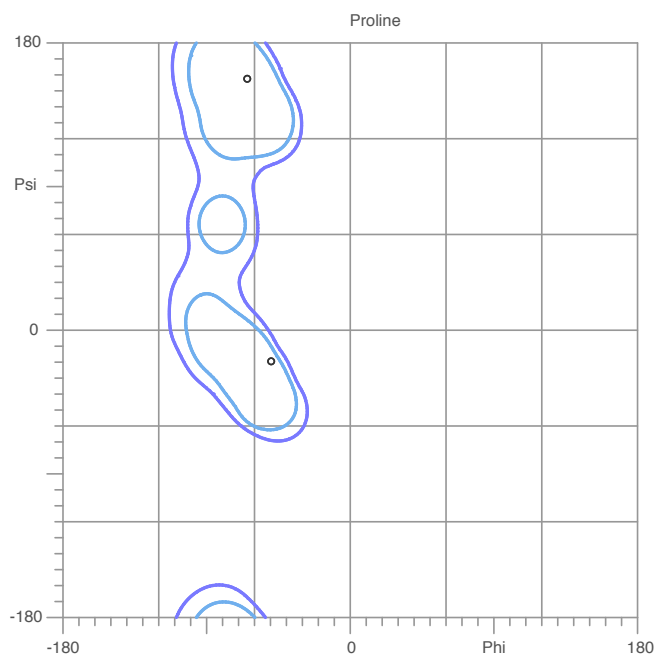
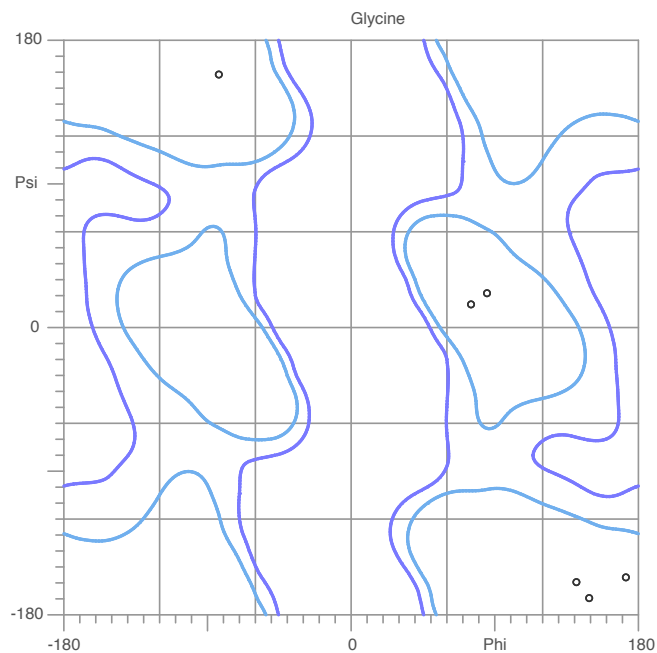
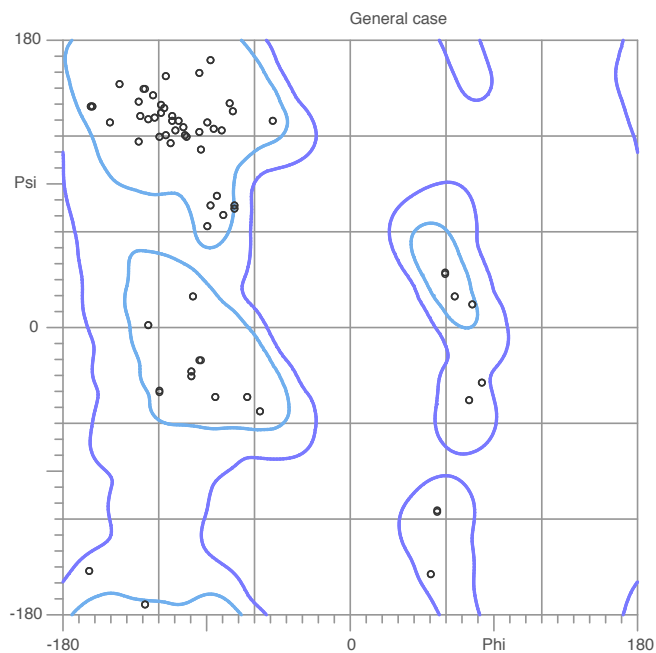
89.7% (246/276) of all residues were in favored (98%) regions.
97.7% (248/276) of all residues were in allowed (98%) regions.

There were 80 outliers (Phi, Psi):

- [1] 4 ARG (67.0, 11.46)
- [2] 28 LEU (66.2, 70.1)
- [3] 63 PRO (67.8, 62.2)
- [4] 65 LEU (66.1, 110.0)
- [5] 85 ARG (67.1, 131.6)
- [6] 109 LEU (62.2, 70.1)
- [7] 144 PRO (67.8, 62.2)
- [8] 146 GLU (66.2, 110.0)
- [9] 28 LEU (64.9, 85.9)
- [10] 47 LYS (67.2, 90.0)
- [11] 65 GLU (66.7, 13.0)
- [12] 108 LEU (66.9, 85.0)
- [13] 128 LYS (67.1, 85.0)
- [14] 146 GLU (66.7, 110.0)
- [15] 41 LEU (74.9, 119.2)
- [16] 42 LYS (71.7, 41.0)
- [17] 43 HIS (79.0, 123.0)
- [18] 49 LEU (59.4, 70.9)
- [19] 122 LEU (74.9, 119.1)
- [20] 123 LYS (71.7, 41.0)
- [21] 124 HIS (79.0, 123.0)
- [22] 138 LEU (69.5, 70.9)
- [23] 43 HIS (79.0, 123.0)
- [24] 124 HIS (79.0, 123.0)
- [25] 138 LEU (69.5, 70.9)
- [26] 43 HIS (79.0, 123.0)
- [27] 124 HIS (79.0, 123.0)
- [28] 128 LYS (67.1, 85.0)
- [29] 146 GLU (66.7, 110.0)
- [30] 124 HIS (79.0, 123.0)
- [31] 47 LYS (67.1, 85.0)
- [32] 65 GLU (66.3, 114.0)
- [33] 128 LYS (67.1, 85.0)
- [34] 124 HIS (79.0, 123.0)
- [35] 146 GLU (66.7, 114.0)
- [36] 70 HIS (79.0, 123.0)
- [37] 135 HIS (74.9, 123.1)
- [38] 64 HIS (64.6, 49.9)
- [39] 149 HIS (64.9, 70.0)
- [40] 42 ASP (174.3, 30.6)
- [41] 126 ASP (174.3, 30.5)
- [42] 61 ASN (170.0, 26.6)
- [43] 64 LEU (166.2, 75.0)
- [44] 47 LYS (45.4, 95.0)
- [45] 40 HIS (177.1, 25.0)
- [46] 41 ASN (170.0, 26.7)
- [47] 40 HIS (166.2, 75.0)
- [48] 44 ASN (170.0, 26.7)
- [49] 47 LYS (45.4, 95.0)
- [50] 40 HIS (177.1, 25.0)
- [51] 47 LYS (45.4, 95.0)
- [52] 40 HIS (166.2, 75.0)
- [53] 28 LEU (59.4, 85.9)
- [54] 40 ARG (65.3, 85.9)
- [55] 49 GLY (108.4, 48.9)
- [56] 65 GLU (66.7, 131.0)
- [57] 49 LEU (50.0, 85.0)
- [58] 40 HIS (166.3, 85.0)
- [59] 40 HIS (166.3, 85.0)
- [60] 49 GLY (108.4, 48.9)
- [61] 56 GLU (65.1, 102.0)
- [62] 49 LEU (50.0, 85.0)
- [63] 28 LEU (59.4, 85.9)
- [64] 40 HIS (166.3, 85.0)
- [65] 40 HIS (166.3, 85.0)
- [66] 44 LEU (164.4, 94.9)
- [67] 44 LEU (164.4, 94.9)
- [68] 28 LEU (59.4, 85.9)
- [69] 40 HIS (166.3, 85.0)
- [70] 40 HIS (166.3, 85.0)
- [71] 44 LEU (164.4, 94.9)
- [72] 44 LEU (164.4, 94.9)
- [73] 40 HIS (166.3, 85.0)
- [74] 40 HIS (166.3, 85.0)
- [75] 40 HIS (166.3, 85.0)
- [76] 44 LEU (164.4, 94.9)
- [77] 44 LEU (164.4, 94.9)
- [78] 40 HIS (166.3, 85.0)
- [79] 40 HIS (166.3, 85.0)
- [80] 40 HIS (166.3, 85.0)
- [81] 40 HIS (166.3, 85.0)
- [82] 40 HIS (166.3, 85.0)
- [83] 40 HIS (166.3, 85.0)
- [84] 40 HIS (166.3, 85.0)
- [85] 40 HIS (166.3, 85.0)
- [86] 40 HIS (166.3, 85.0)
- [87] 40 HIS (166.3, 85.0)
- [88] 40 HIS (166.3, 85.0)
- [89] 40 HIS (166.3, 85.0)
- [90] 40 HIS (166.3, 85.0)
- [91] 40 HIS (166.3, 85.0)
- [92] 40 HIS (166.3, 85.0)
- [93] 40 HIS (166.3, 85.0)
- [94] 40 HIS (166.3, 85.0)
- [95] 40 HIS (166.3, 85.0)
- [96] 40 HIS (166.3, 85.0)
- [97] 40 HIS (166.3, 85.0)
- [98] 40 HIS (166.3, 85.0)
- [99] 40 HIS (166.3, 85.0)
- [100] 40 HIS (166.3, 85.0)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 1



92.8% (128/138) of all residues were in favored (98%) regions.
100.0% (138/138) of all residues were in allowed (>99.8%) regions.

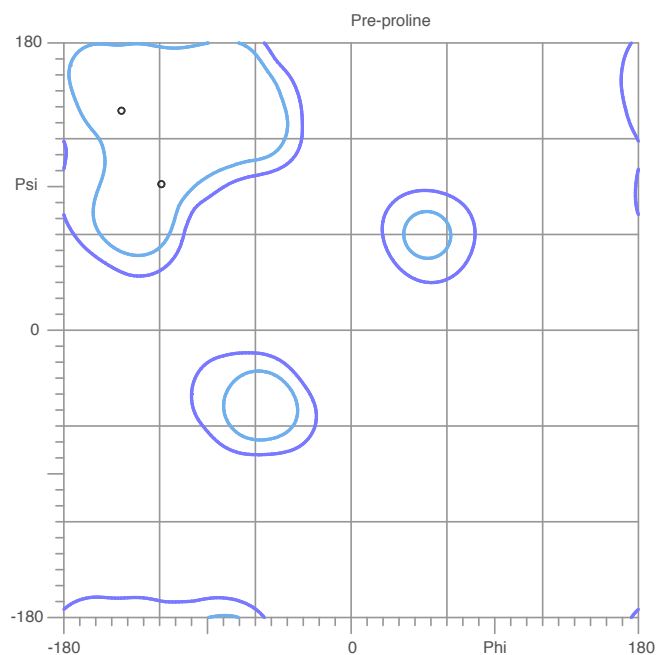
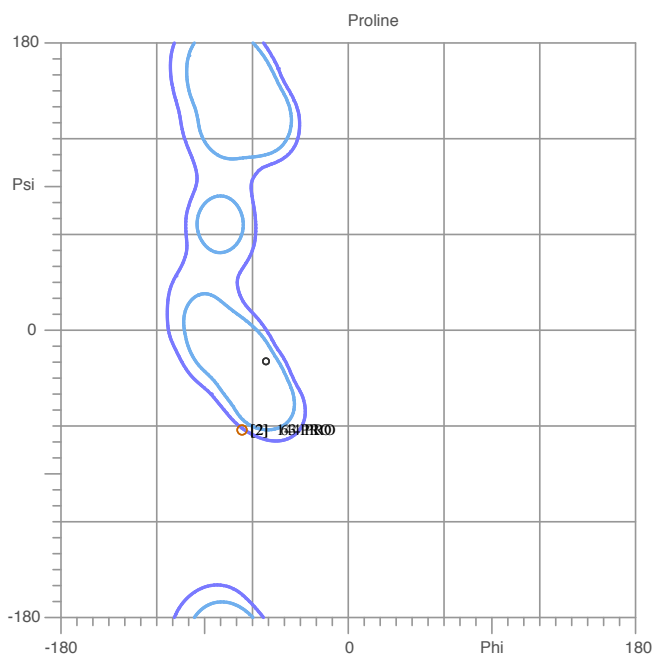
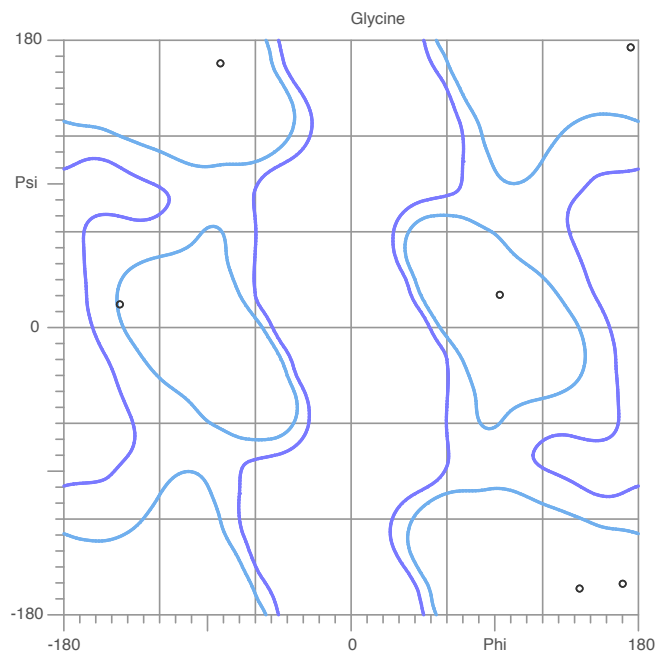
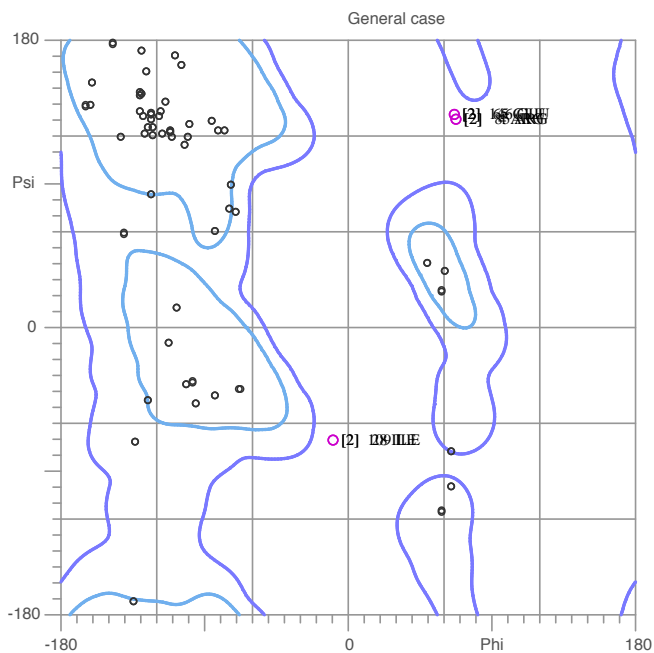
There were no outliers.

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

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

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 2



84.1% (116/138) of all residues were in favored (98%) regions.
94.2% (130/138) of all residues were in allowed (>99.8%) regions.

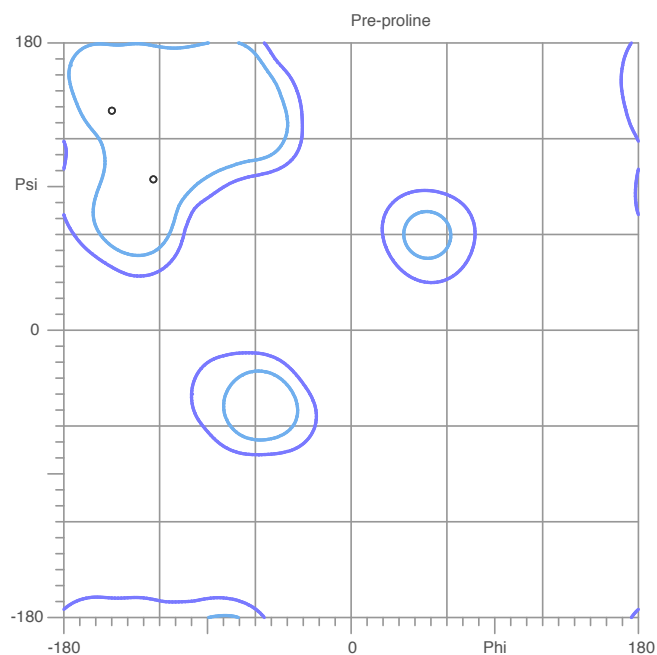
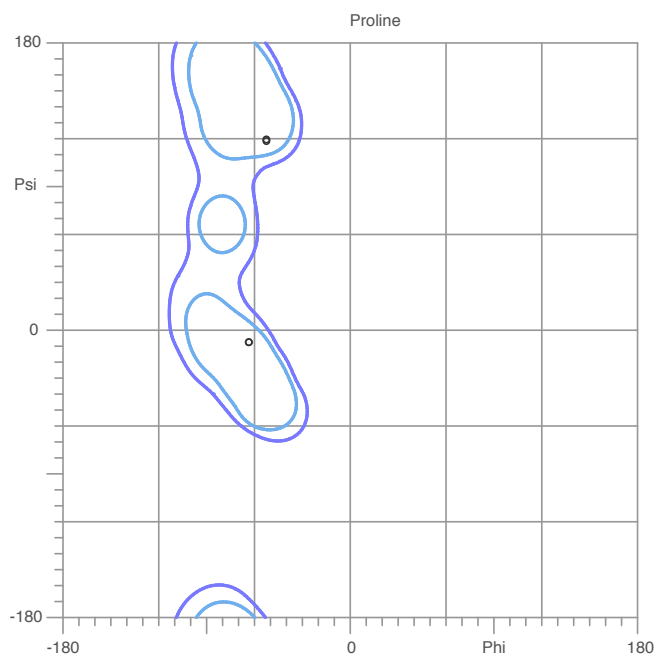
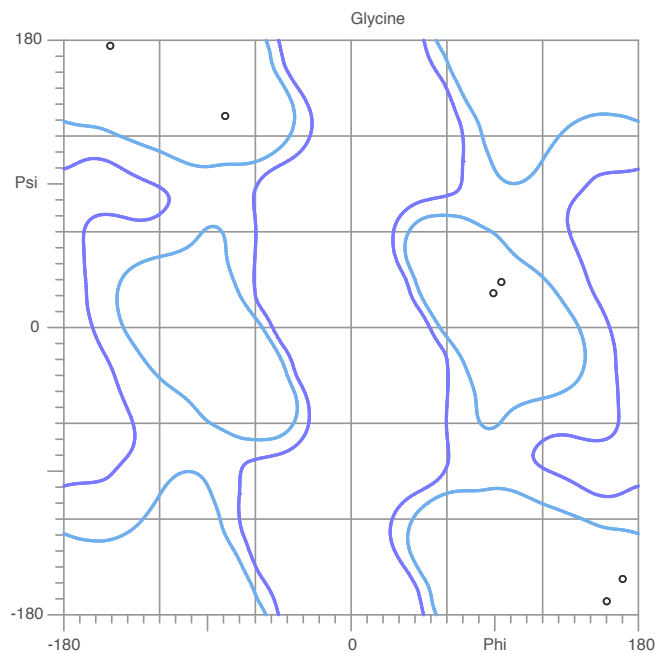
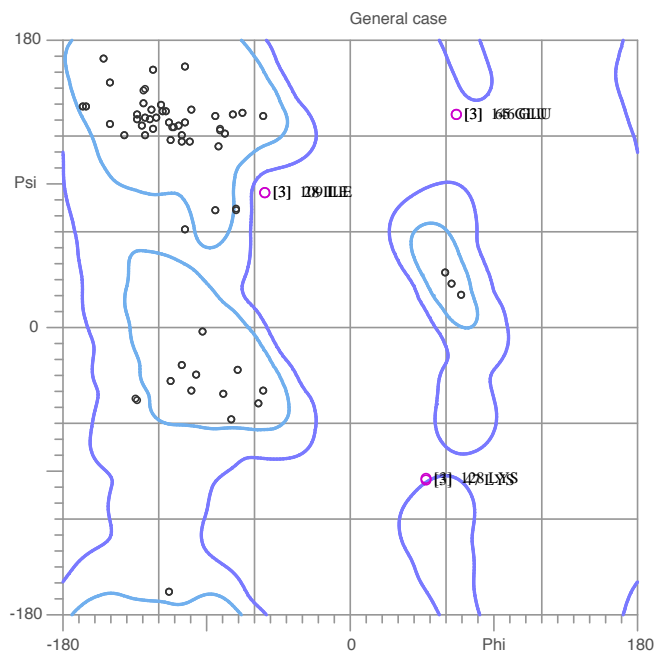
There were 8 outliers (phi, psi):

[2] 4 ARG (67.0, 131.4)
[2] 28 ILE (-10.2, -70.1)

[2] 63 PRO (-67.8, -62.2)
[2] 65 GLU (66.1, 135.0)
[2] 85 ARG (67.1, 131.4)
[2] 109 ILE (-10.2, -70.1)
[2] 144 PRO (-67.8, -62.2)
[2] 146 GLU (66.2, 135.0)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 3



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):

[3] 28 ILE (-54.9, 85.9)

[3] 47 LYS (47.2, -95.0)

[3] 65 GLU (66.7, 135.0)

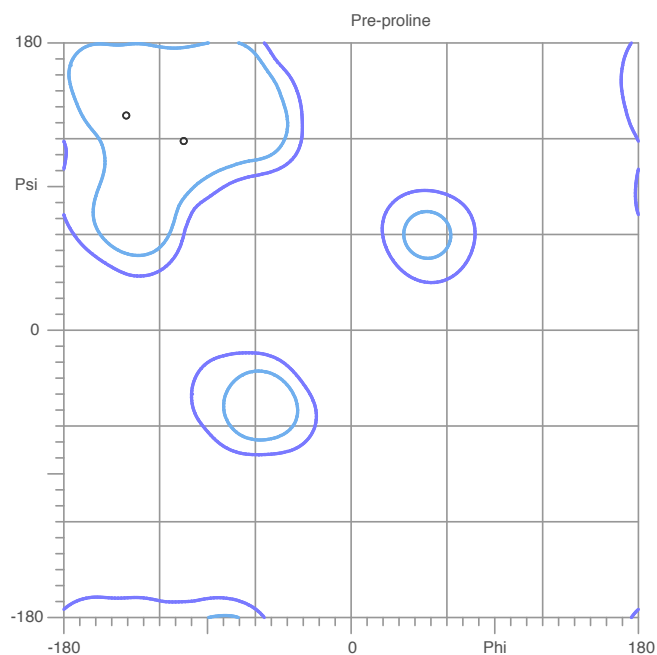
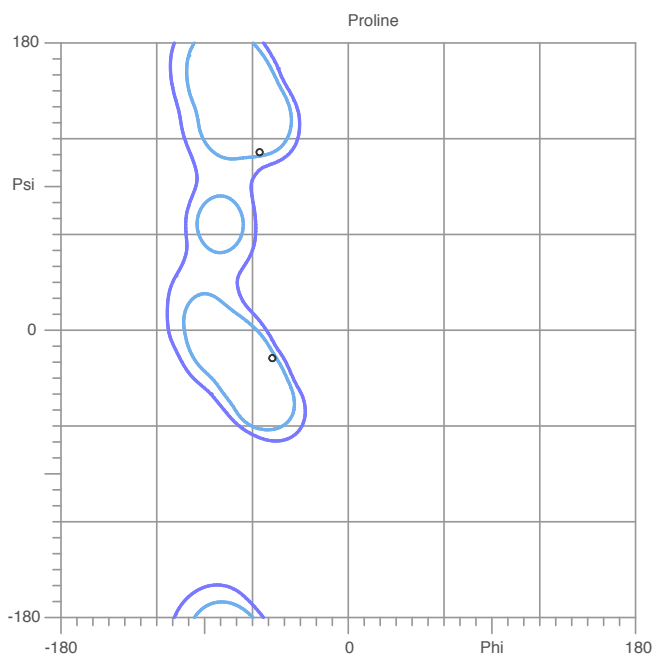
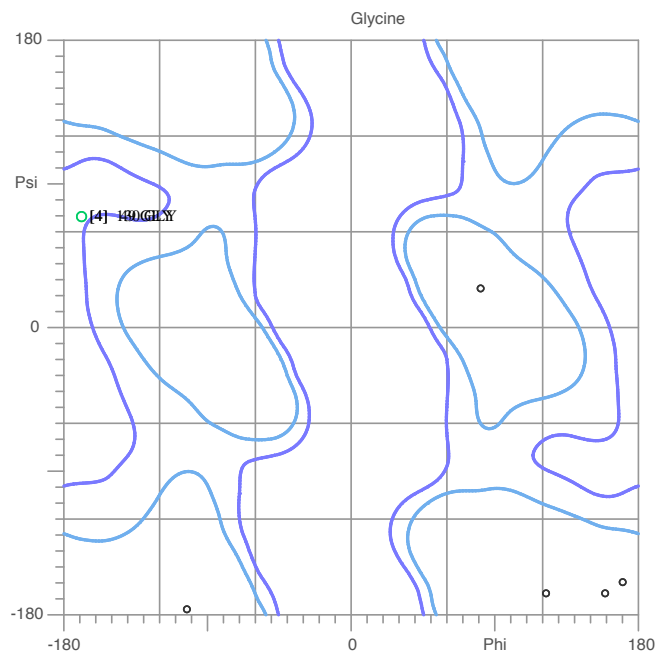
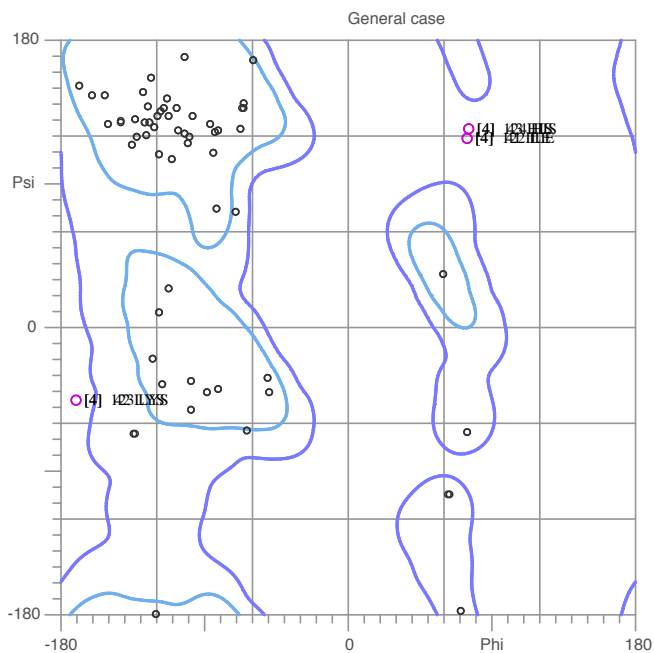
[3] 109 ILE (-54.9, 85.9)

[3] 128 LYS (47.1, -95.0)

[3] 146 GLU (66.7, 135.0)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 4



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.

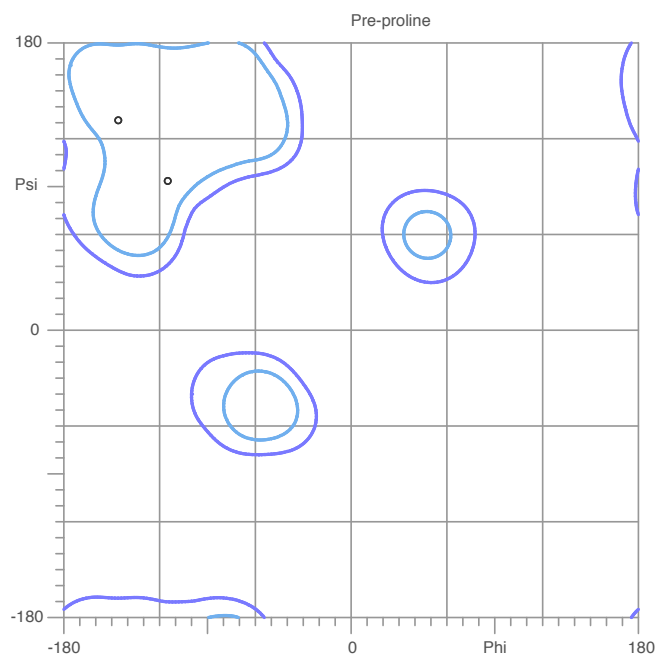
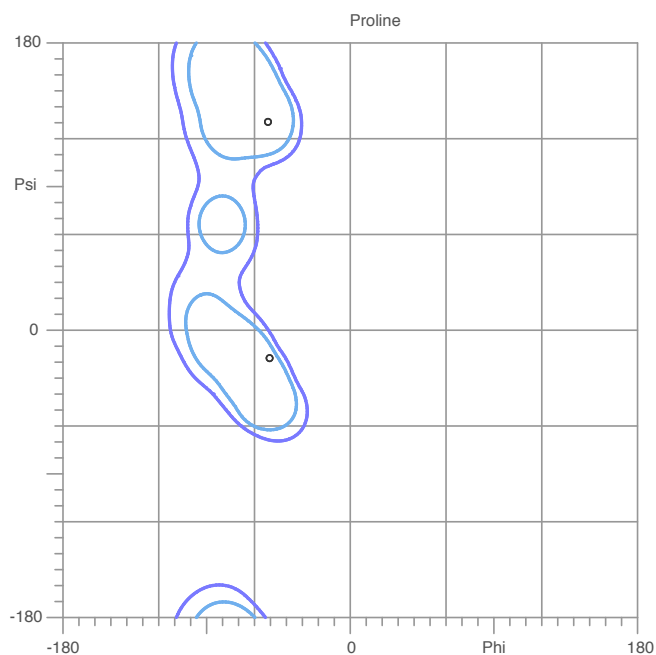
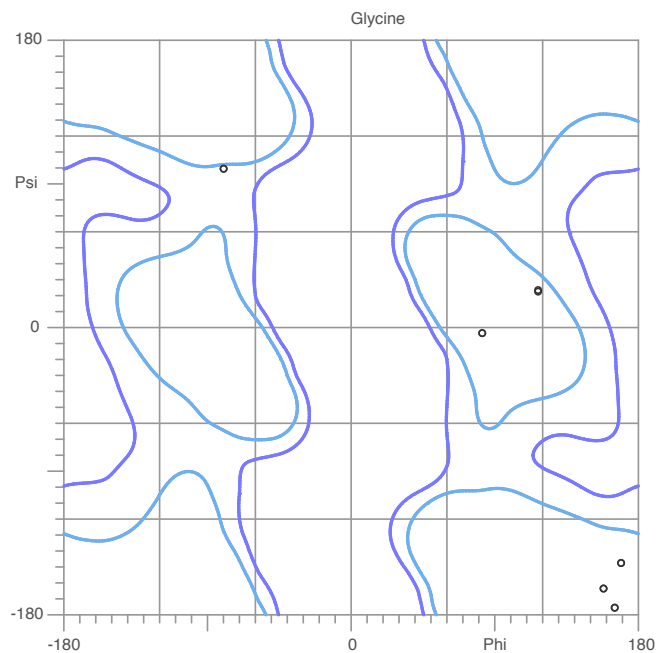
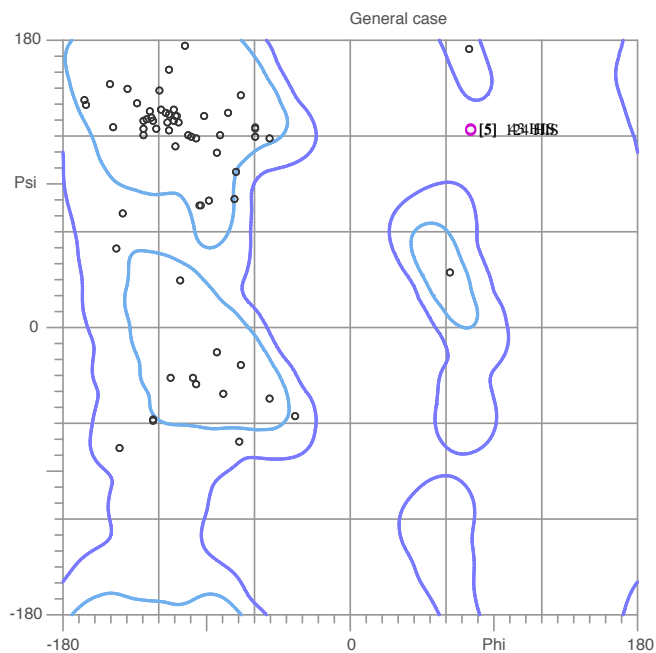
There were 8 outliers (phi, psi):

- [4] 41 ILE (74.9, 119.2)
- [4] 42 LYS (-171.9, -45.0)

- [4] 43 HIS (75.0, 125.0)
- [4] 49 GLY (-169.4, 70.5)
- [4] 122 ILE (74.9, 119.1)
- [4] 123 LYS (-171.9, -45.0)
- [4] 124 HIS (75.0, 125.0)
- [4] 130 GLY (-169.5, 70.4)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 5



87.0% (120/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

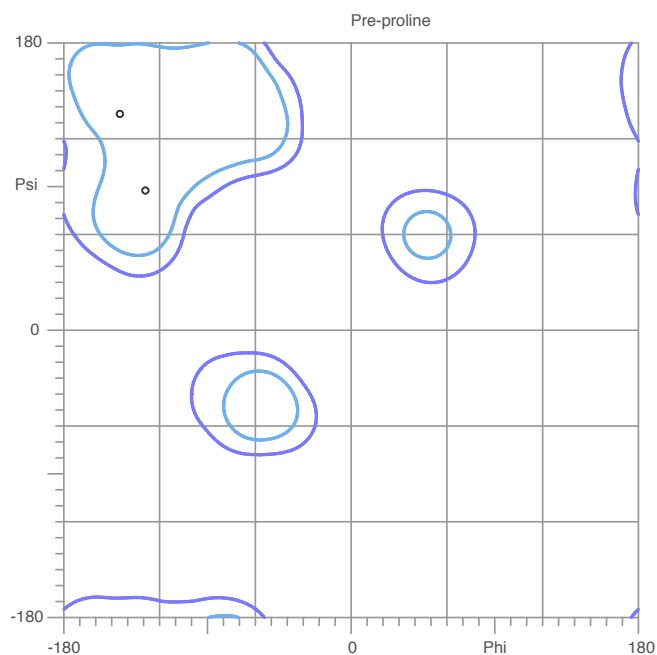
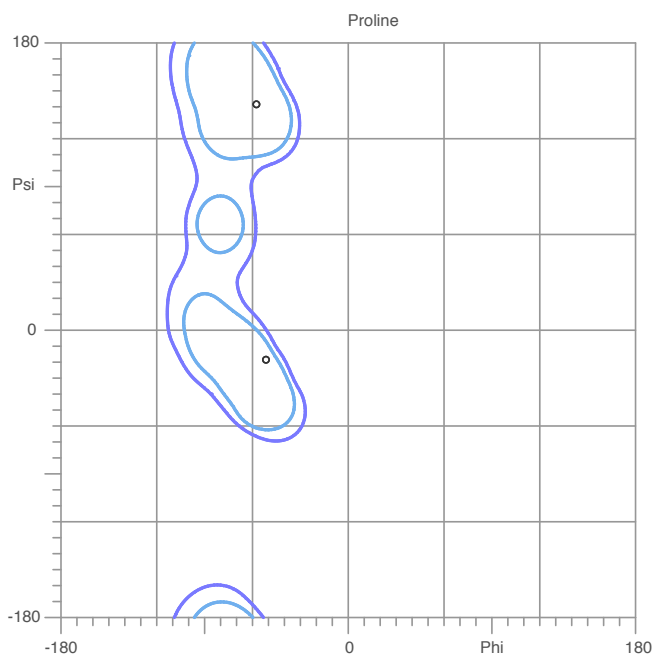
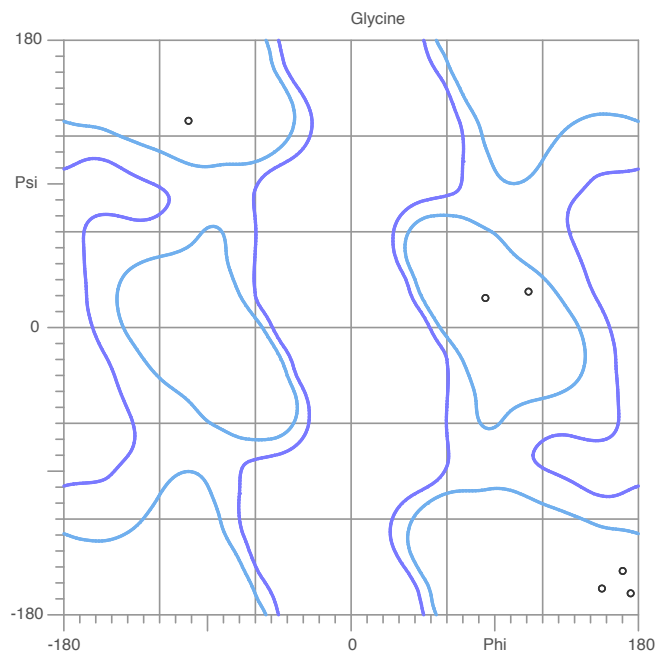
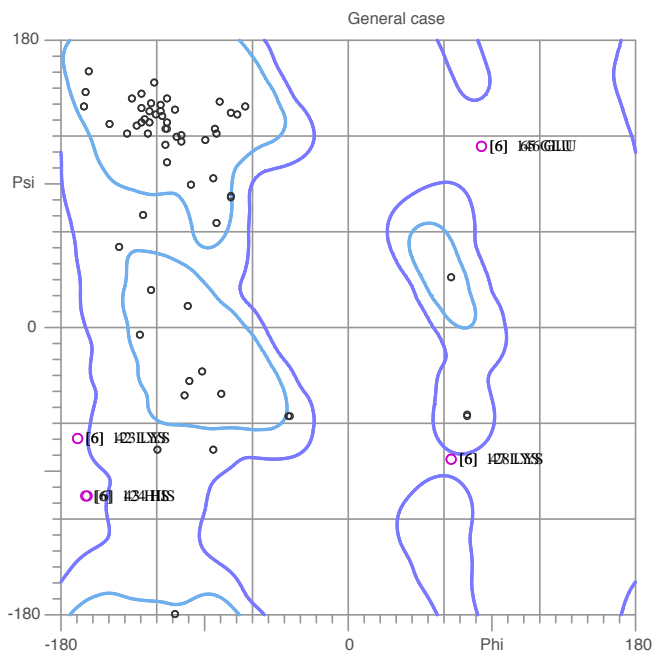
There were 2 outliers (phi, psi):

[5] 43 HIS (75.0, 125.0)

[5] 124 HIS (75.0, 125.0)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 6



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.

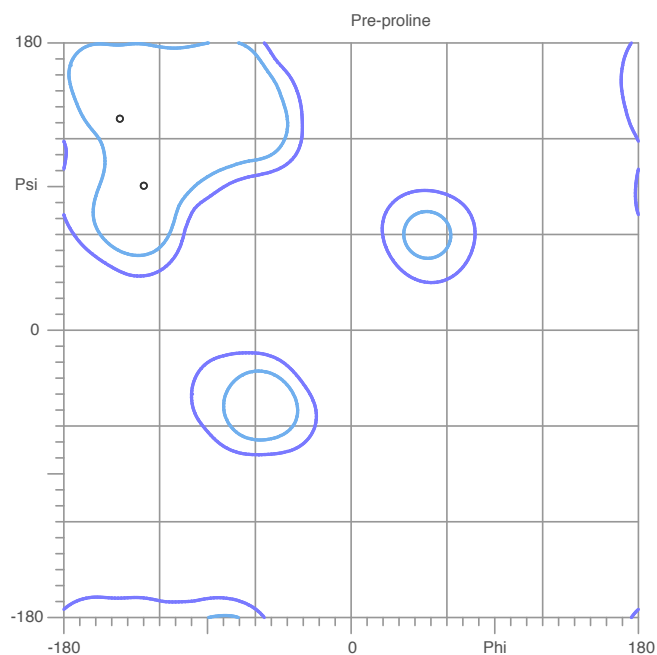
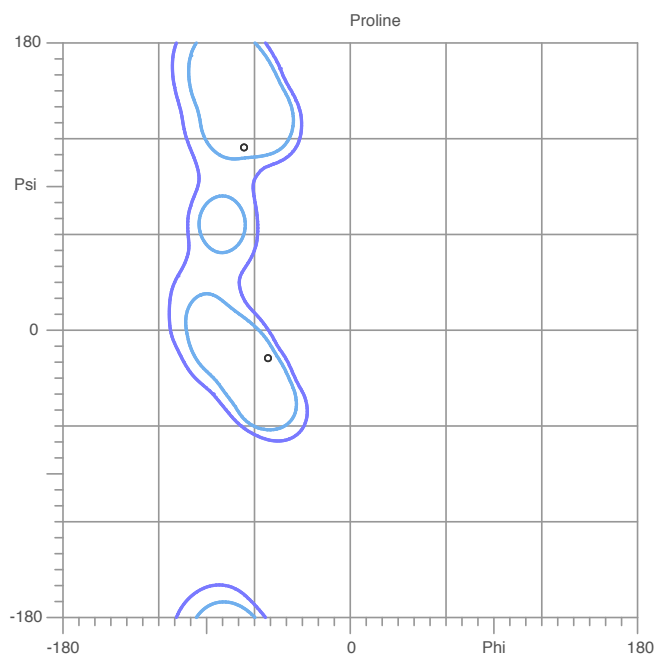
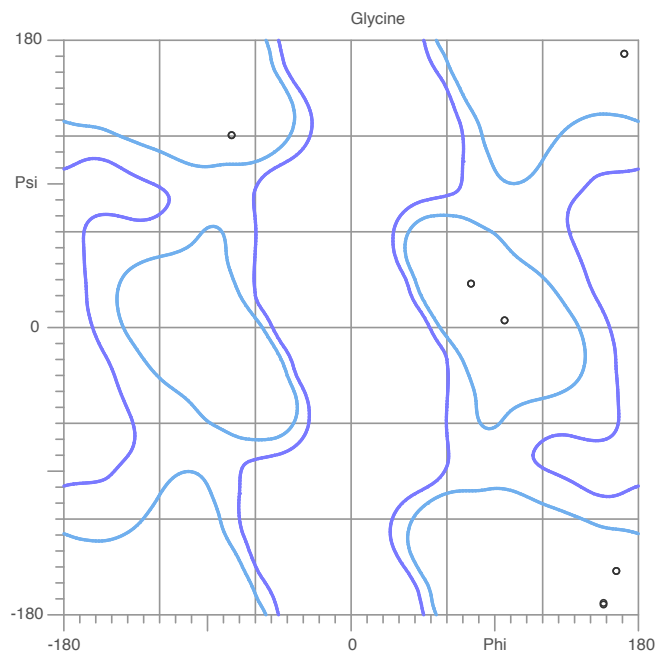
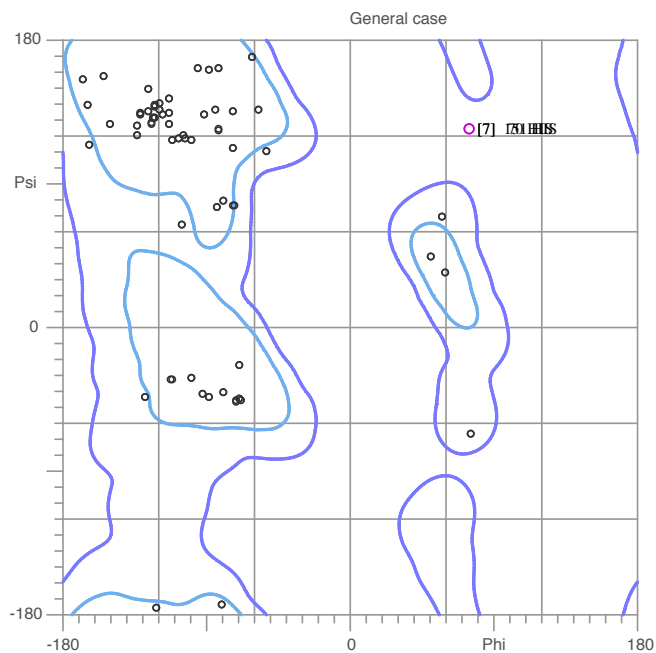
There were 8 outliers (phi, psi):

[6] 42 LYS (-170.3, -69.8)
[6] 43 HIS (-165.0, -105.0)

[6] 47 LYS (64.7, -82.3)
[6] 65 GLU (83.3, 114.6)
[6] 123 LYS (-170.3, -69.8)
[6] 124 HIS (-165.0, -105.0)
[6] 128 LYS (64.7, -82.3)
[6] 146 GLU (83.3, 114.6)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 7



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.

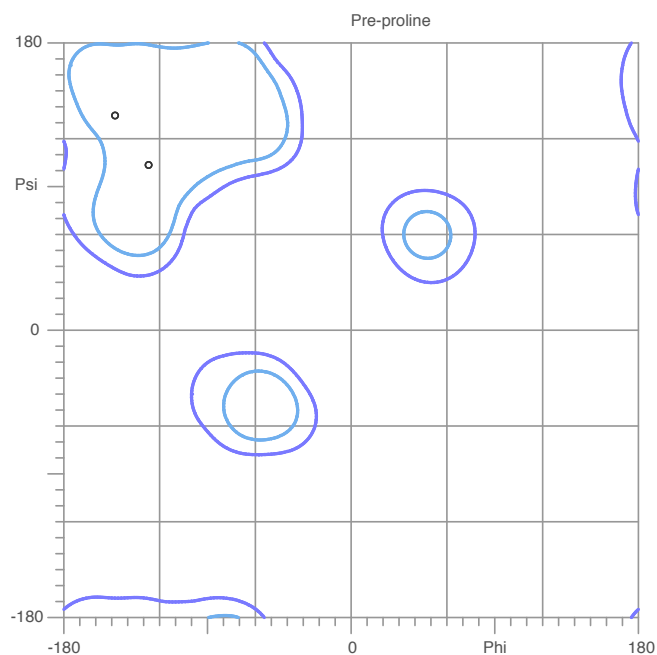
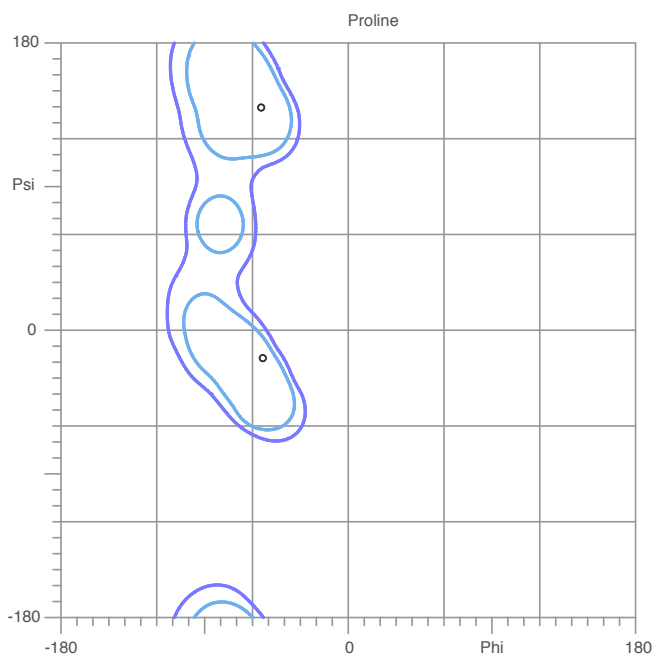
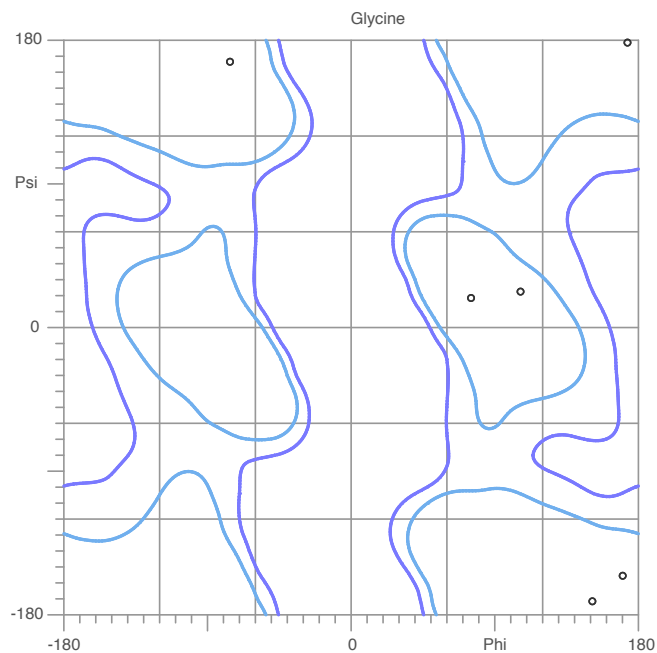
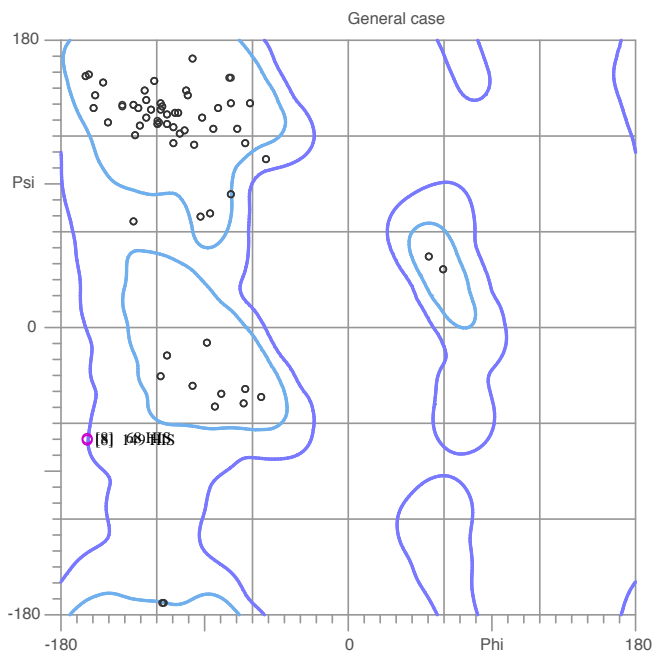
There were 2 outliers (phi, psi):

[7] 70 HIS (75.0, 125.0)

[7] 151 HIS (74.9, 125.1)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 8



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.

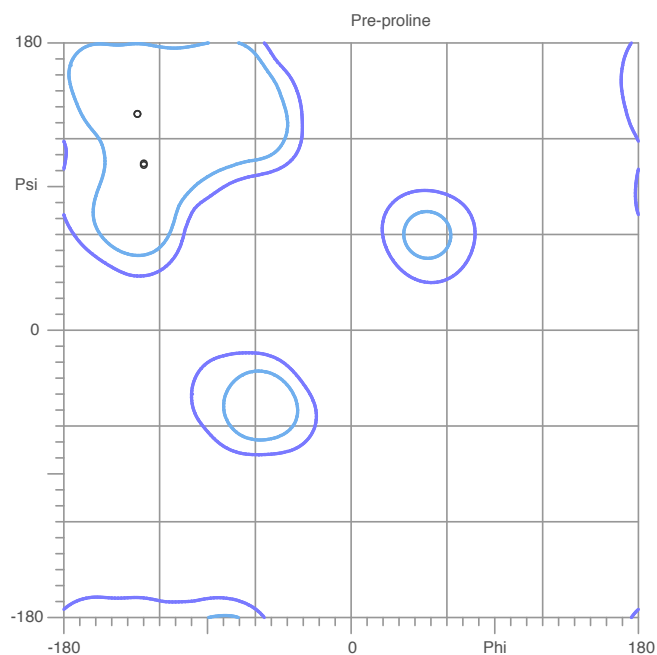
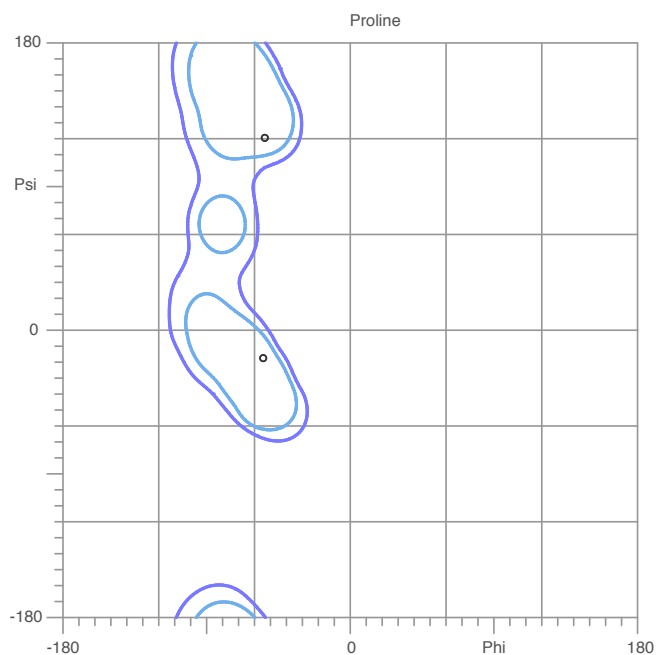
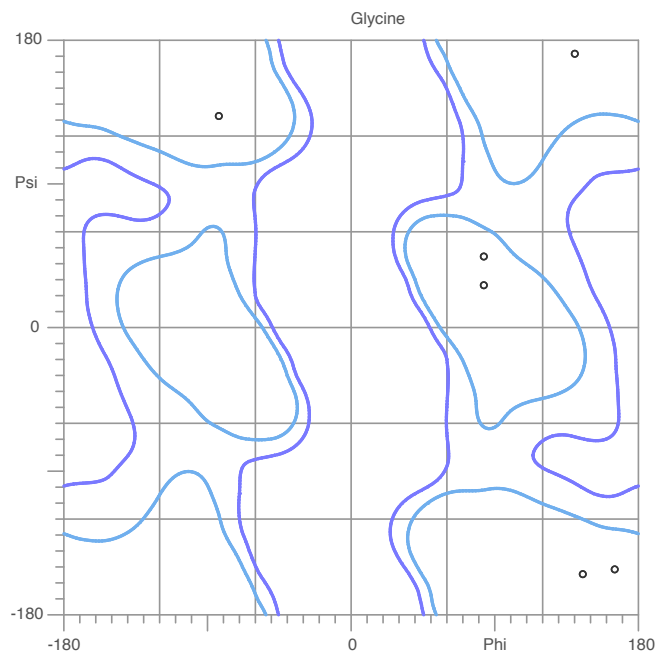
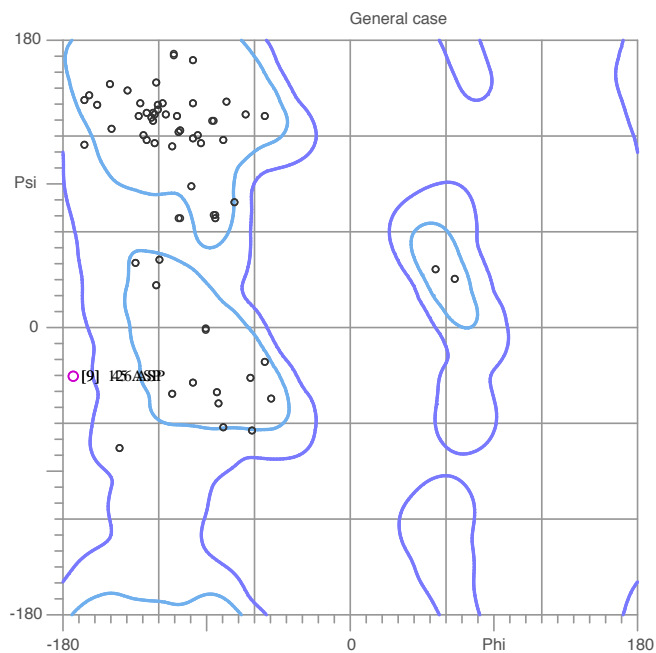
There were 2 outliers (phi, psi):

[8] 68 HIS (-164.9, -69.9)

[8] 149 HIS (-164.9, -70.0)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 9



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.

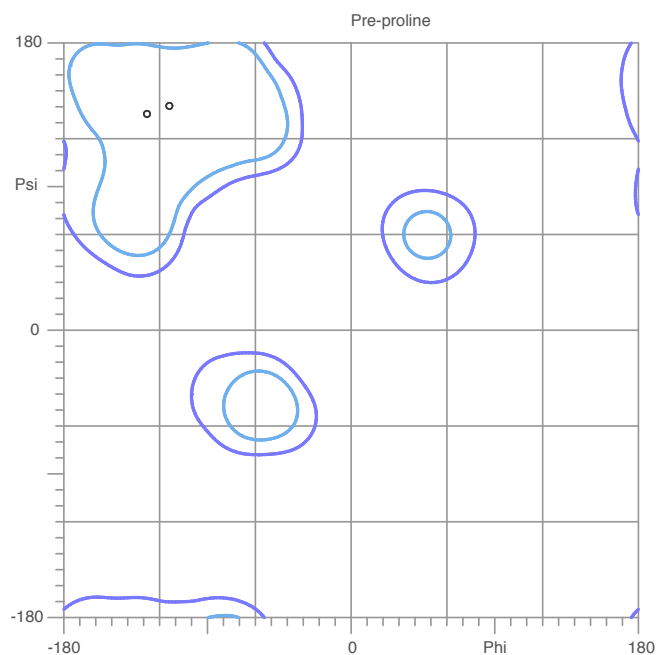
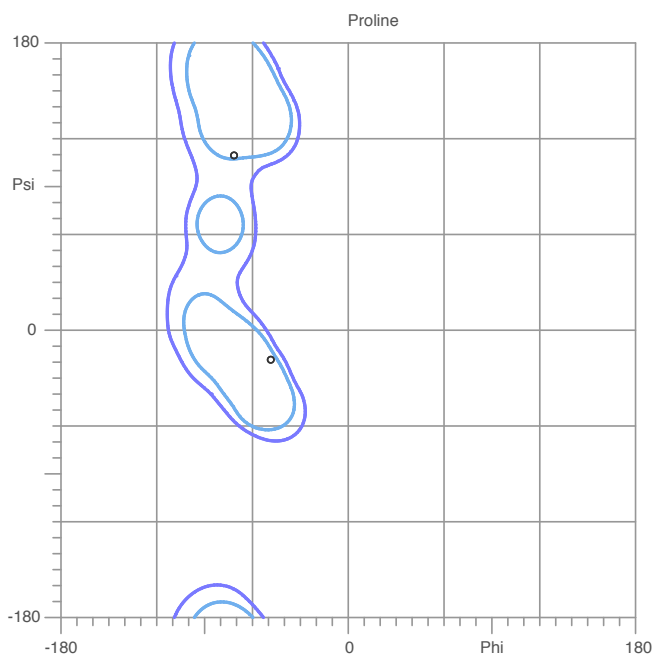
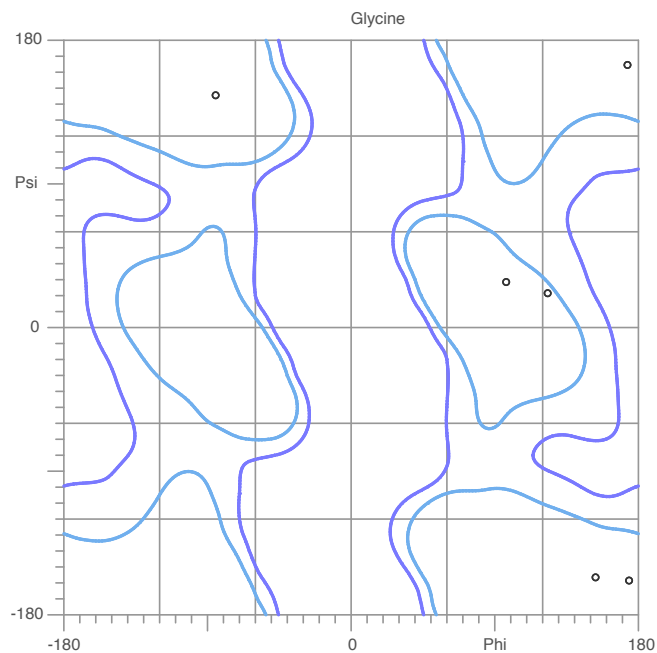
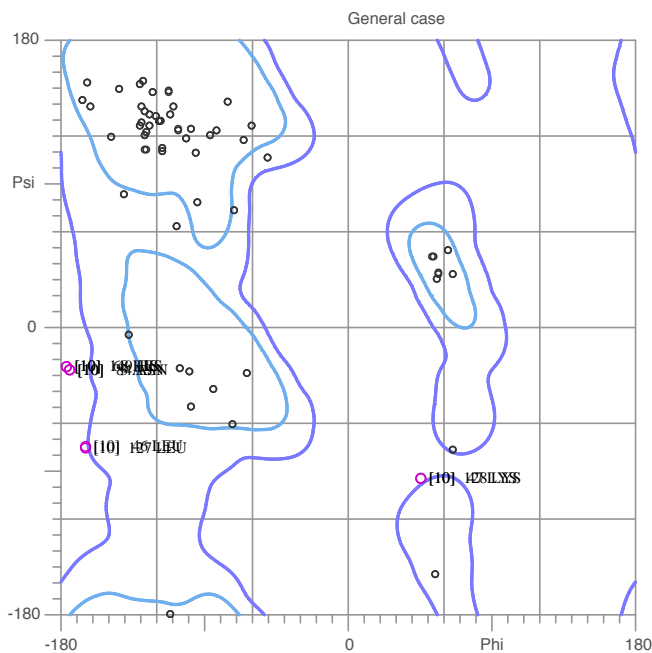
There were 2 outliers (phi, psi):

[9] 45 ASP (-174.3, -30.4)

[9] 126 ASP (-174.3, -30.5)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 10



84.1% (116/138) 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):

[10] 3 ASN (-175.0, -26.6)

[10] 46 LEU (-165.2, -75.0)

[10] 47 LYS (45.4, -95.0)

[10] 68 HIS (-177.1, -25.0)

[10] 84 ASN (-175.0, -26.7)

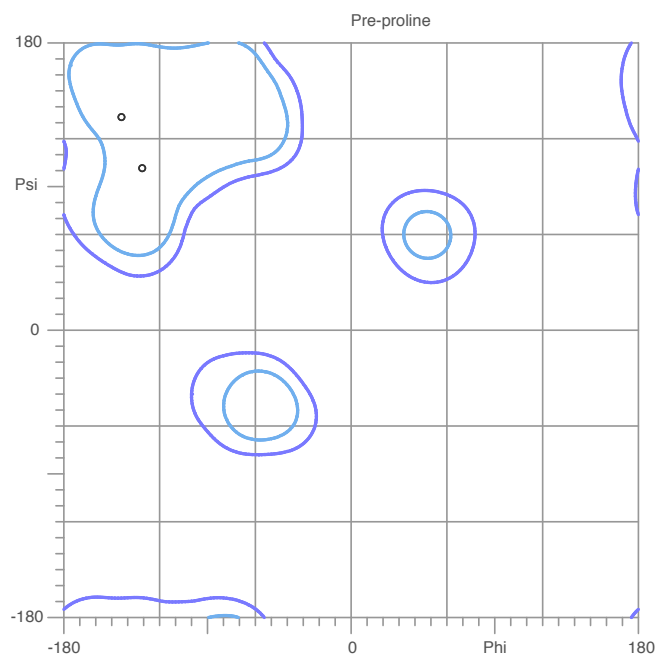
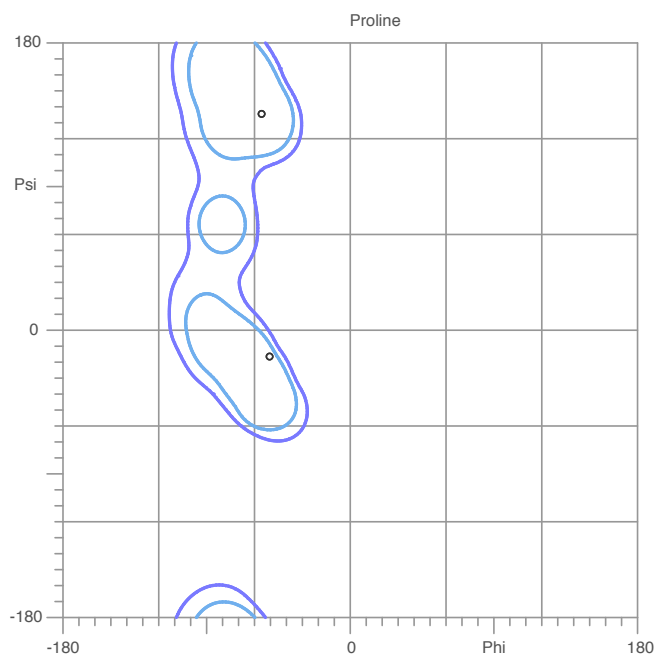
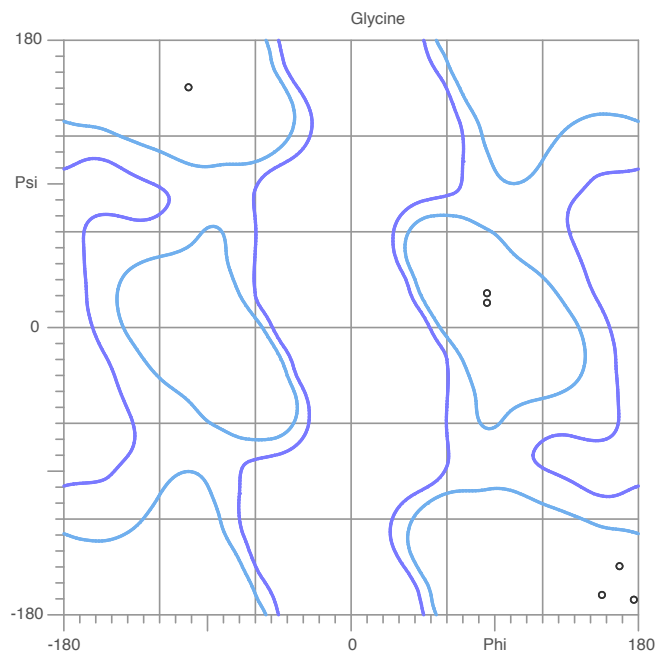
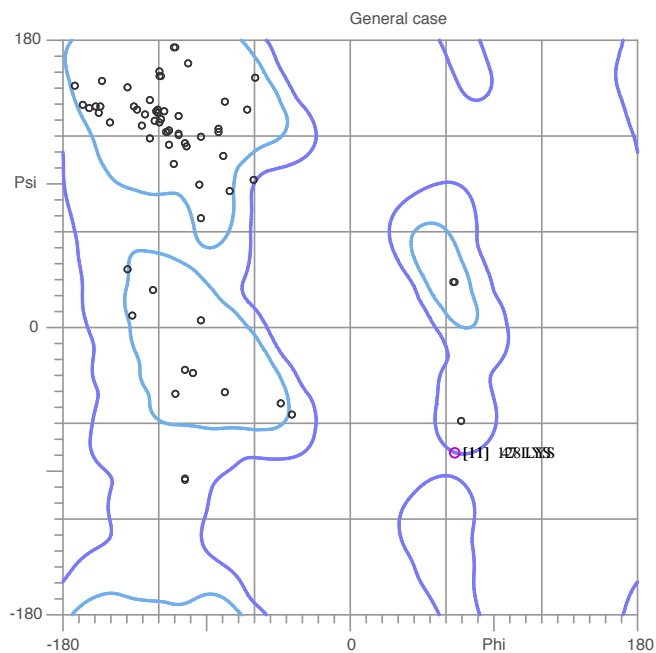
[10] 127 LEU (-165.2, -75.0)

[10] 128 LYS (45.4, -95.0)

[10] 149 HIS (-177.1, -25.0)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 11



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.

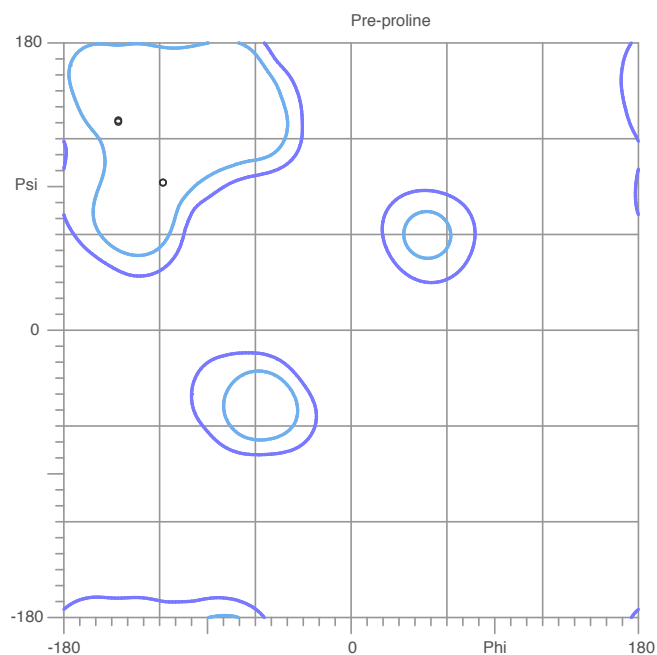
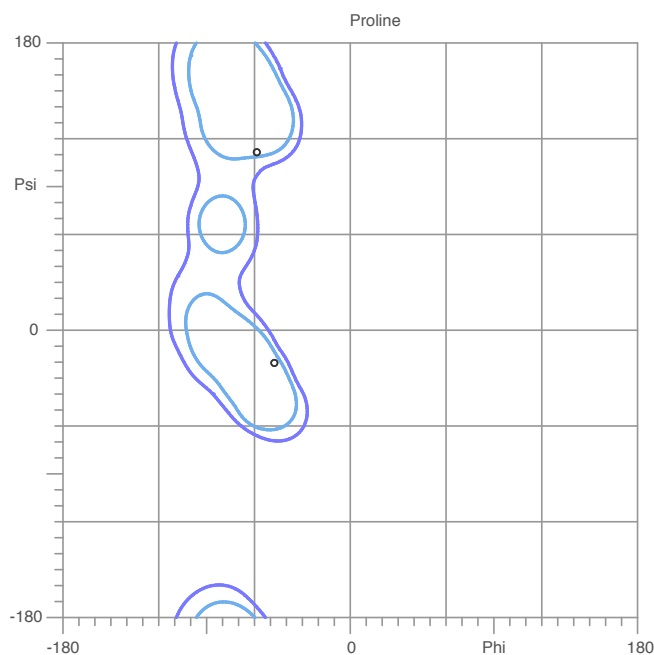
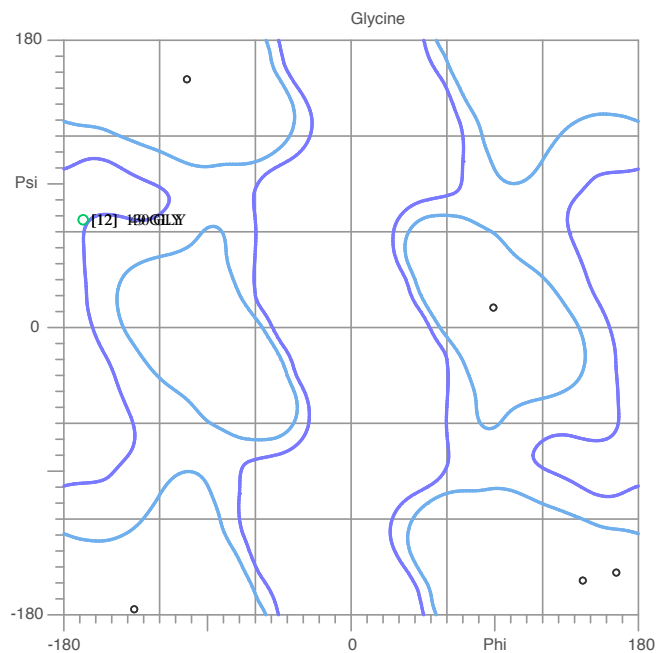
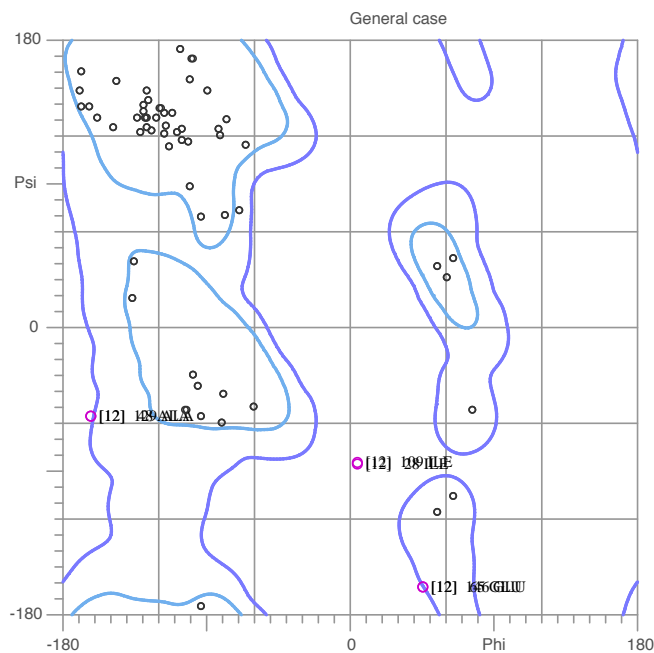
There were 2 outliers (phi, psi):

[11] 47 LYS (65.4, -78.4)

[11] 128 LYS (65.4, -78.4)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 12



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.

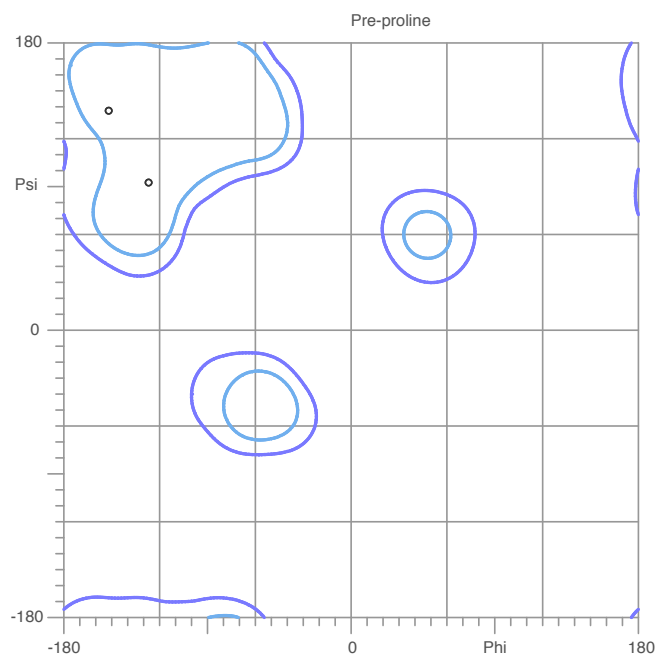
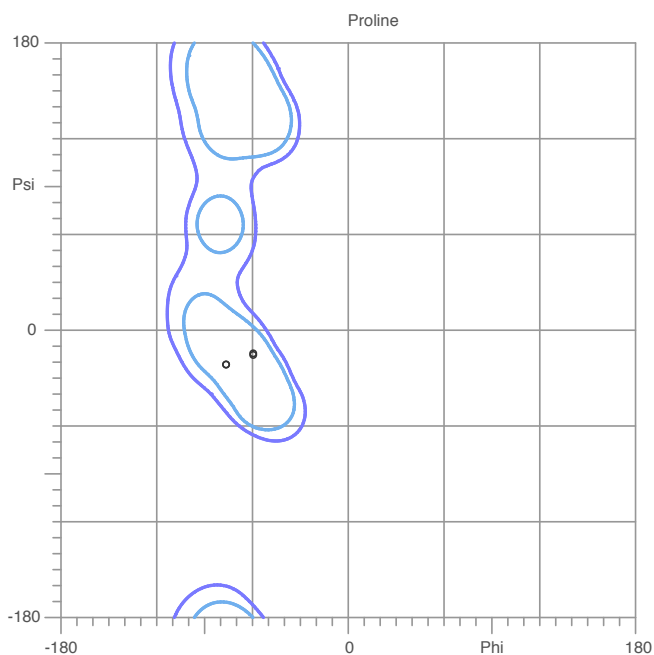
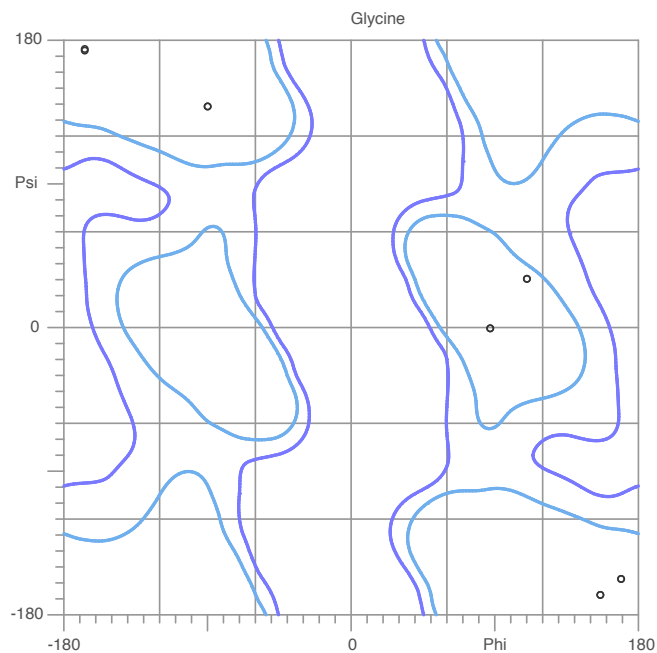
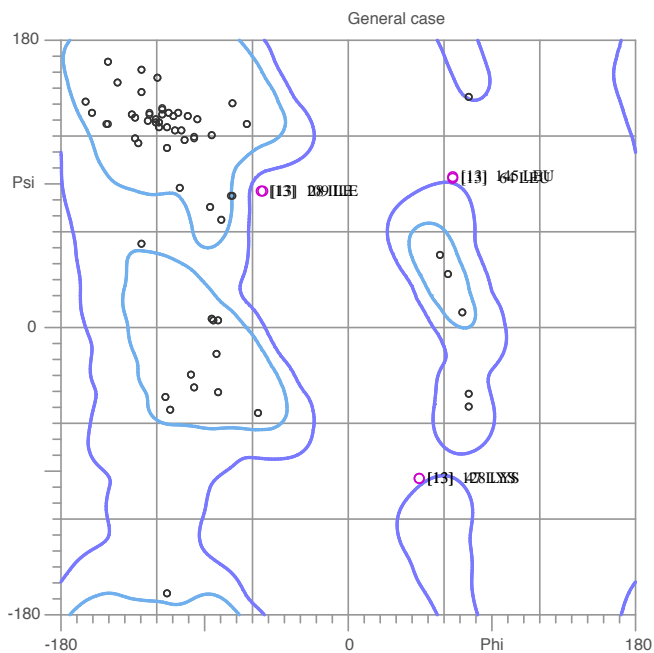
There were 8 outliers (phi, psi):

[12] 28 ILE (5.0, -85.0)
[12] 48 ALA (-163.3, -55.9)

[12] 49 GLY (-168.6, 68.9)
[12] 65 GLU (45.1, -162.9)
[12] 109 ILE (5.0, -85.0)
[12] 129 ALA (-163.3, -55.9)
[12] 130 GLY (-168.5, 68.9)
[12] 146 GLU (45.1, -162.9)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 13



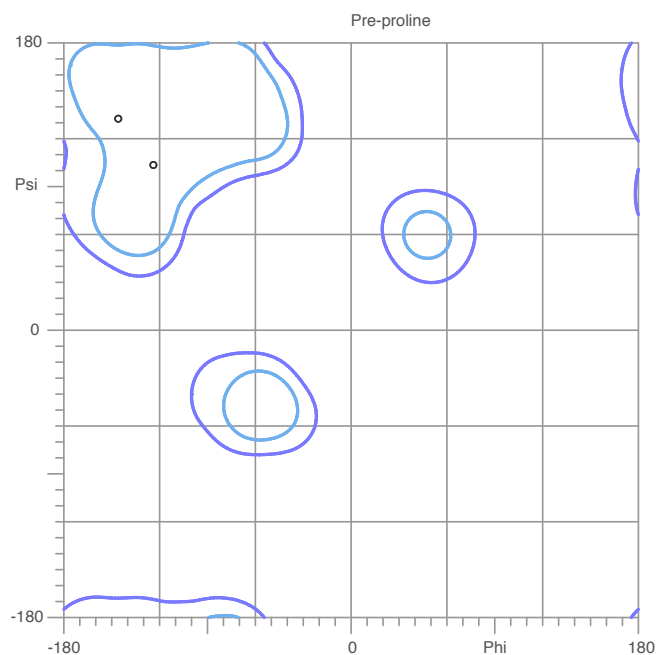
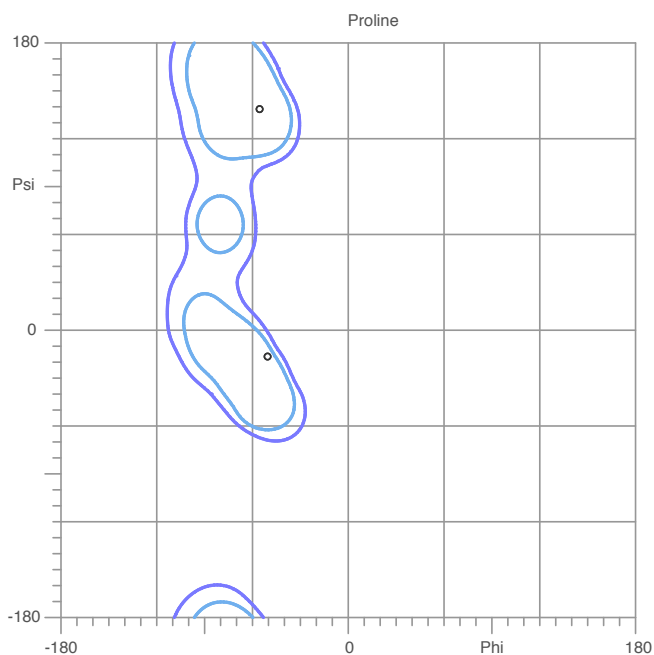
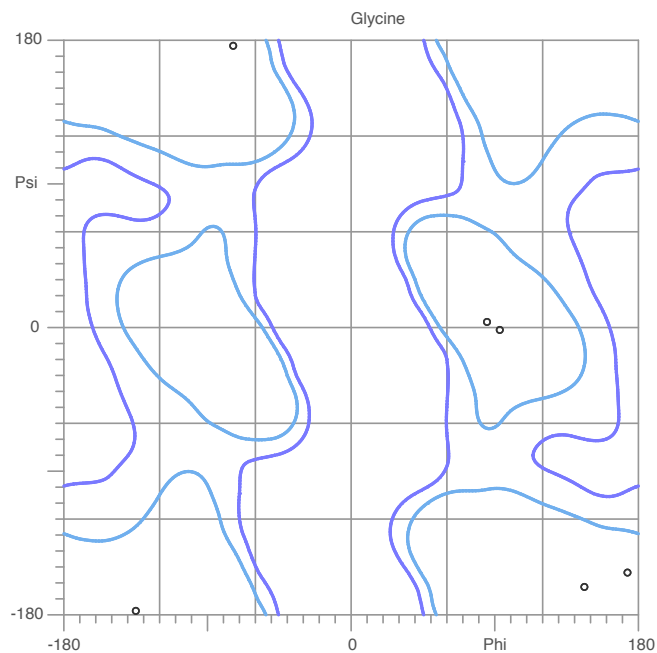
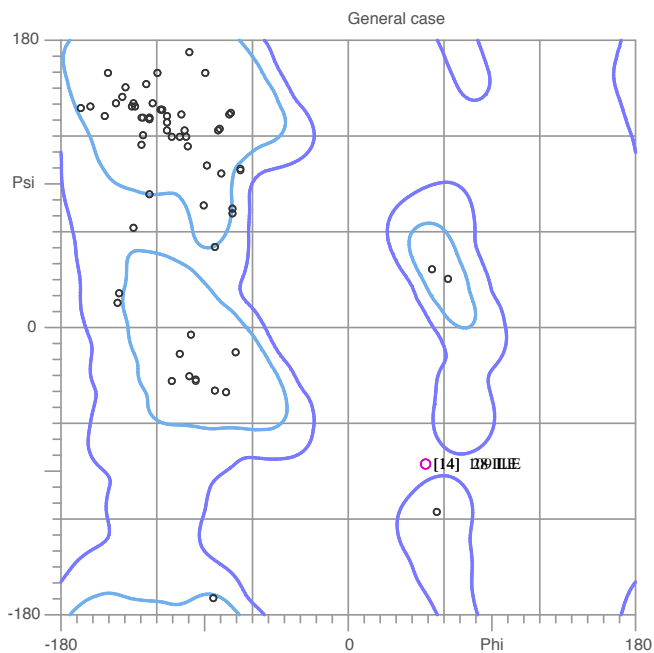
88.4% (122/138) of all residues were in favored (98%) regions.
95.7% (132/138) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[13] 28 ILE (-55.0, 86.6)

[13] 47 LYS (44.4, -94.9)
[13] 64 LEU (65.1, 94.9)
[13] 109 ILE (-55.0, 86.7)
[13] 128 LYS (44.4, -95.0)
[13] 145 LEU (65.1, 95.0)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 14



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.

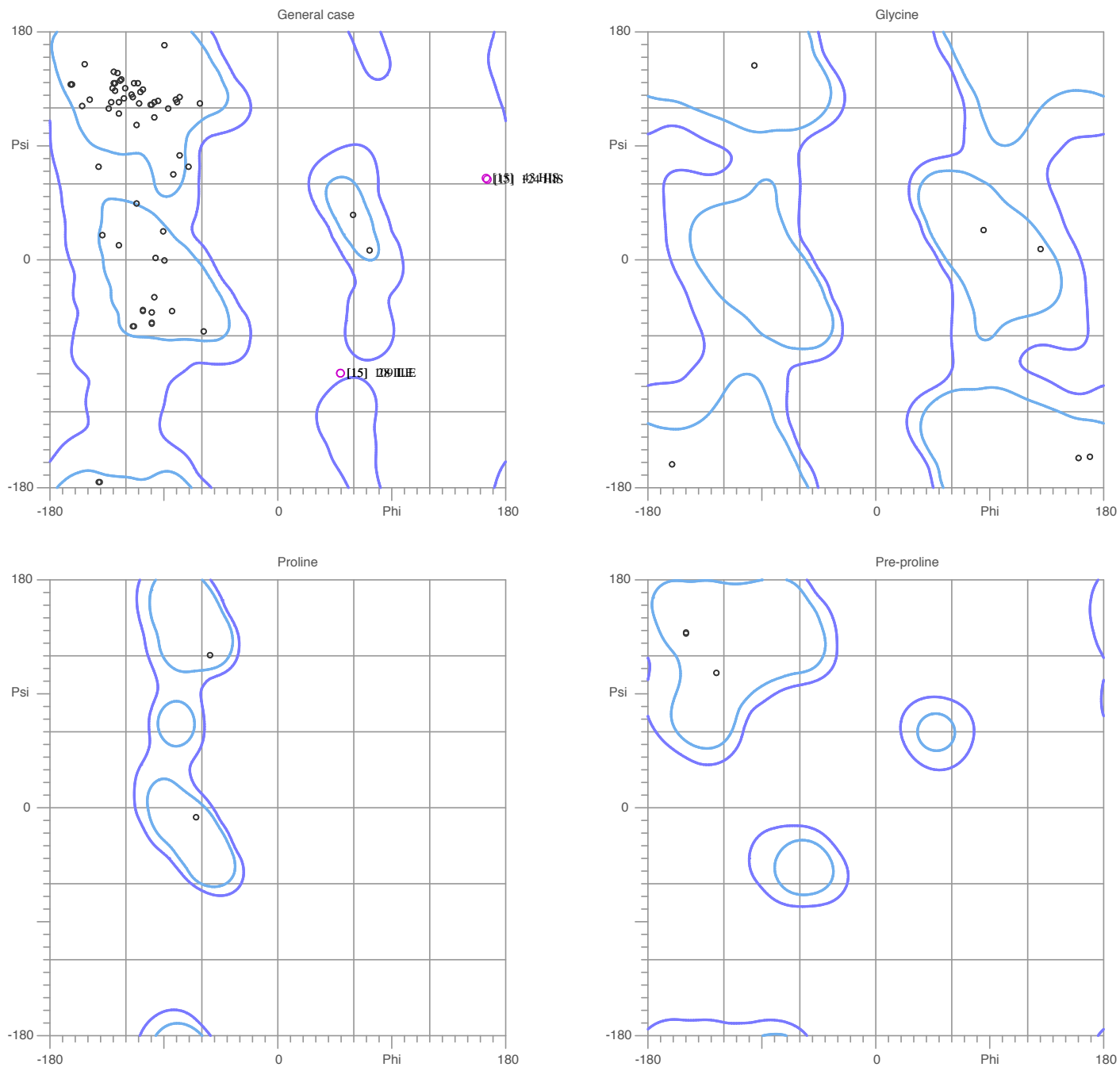
There were 2 outliers (phi, psi):

[14] 28 ILE (48.9, -85.2)

[14] 109 ILE (48.9, -85.2)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 15



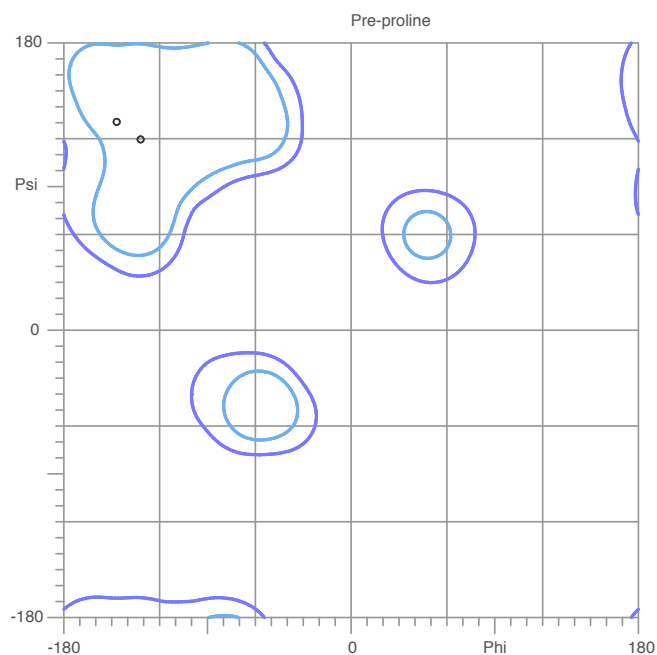
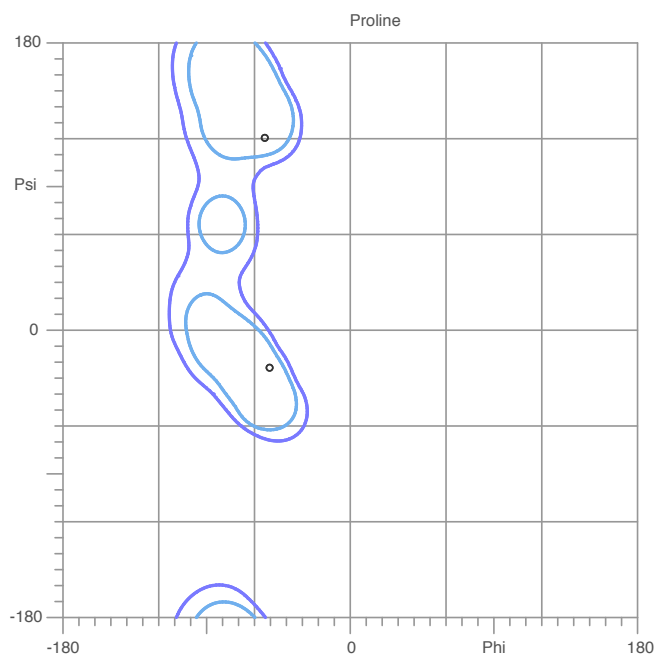
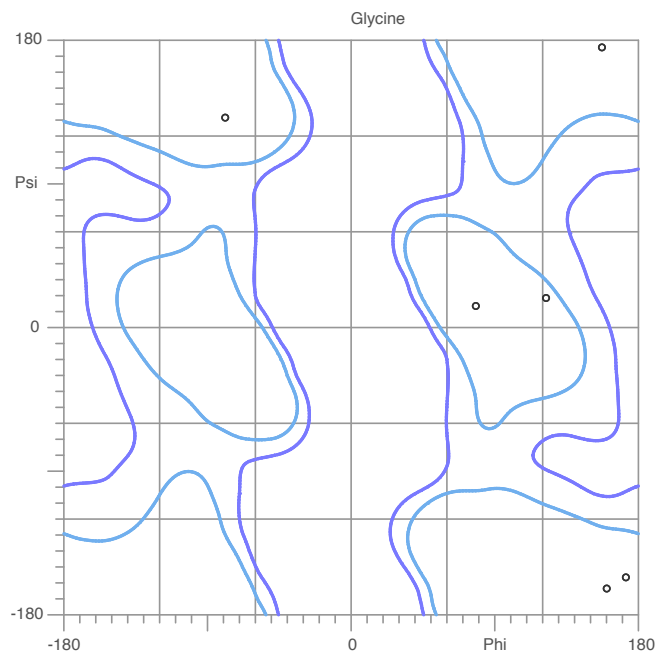
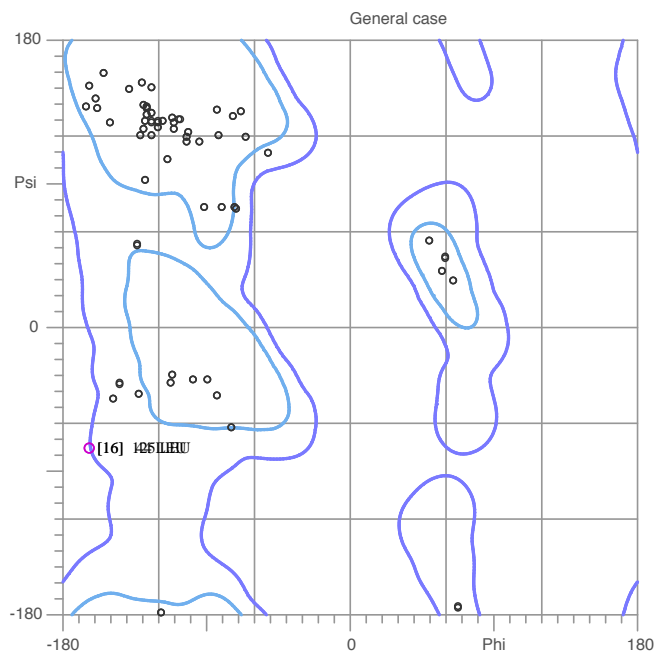
92.8% (128/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [15] 28 ILE (49.2, -89.8)
- [15] 43 HIS (165.0, 65.1)
- [15] 109 ILE (49.2, -89.8)
- [15] 124 HIS (165.0, 65.0)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 16



88.4% (122/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

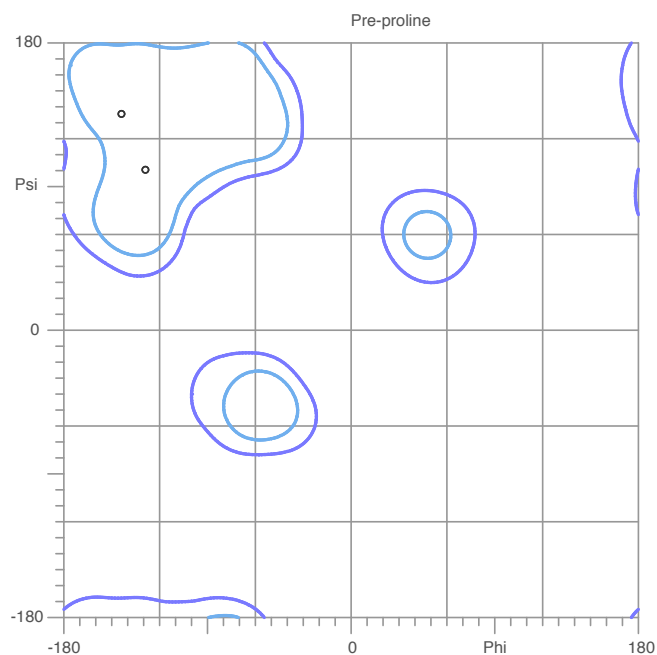
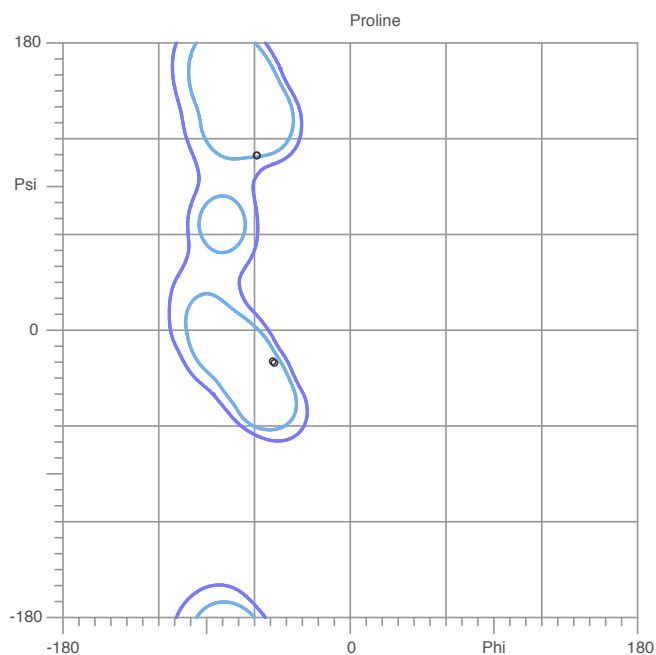
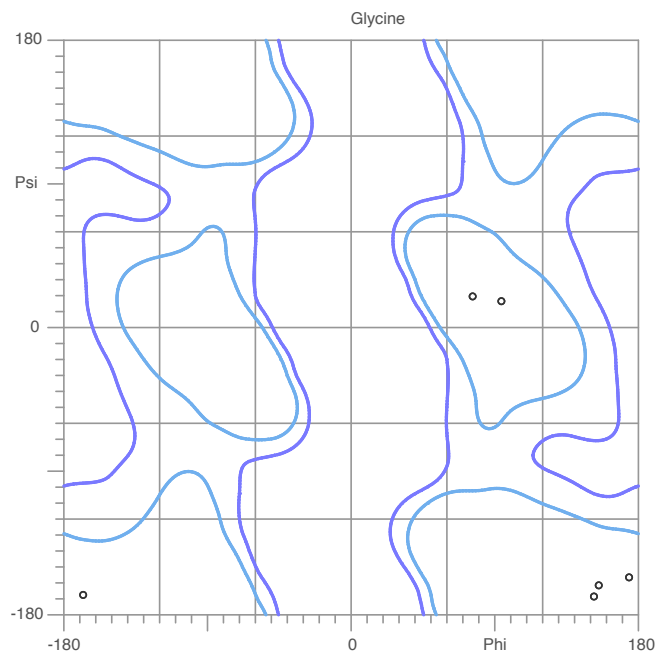
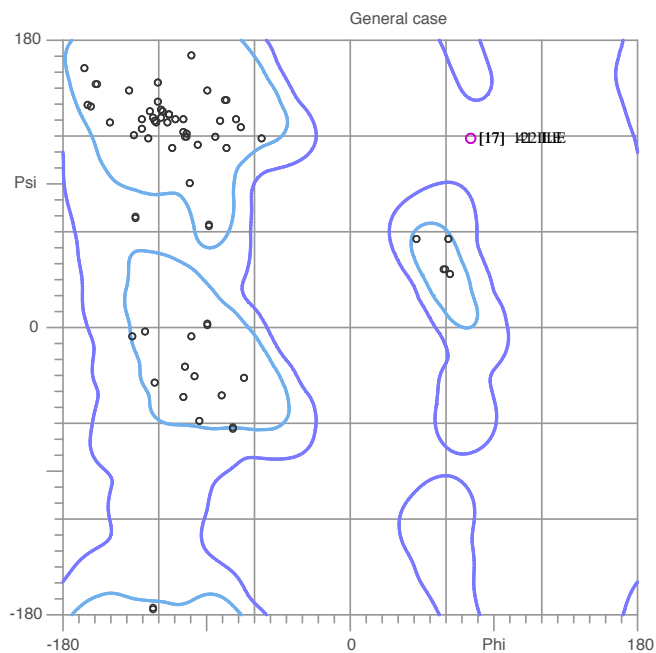
There were 2 outliers (phi, psi):

[16] 44 LEU (-164.8, -75.1)

[16] 125 LEU (-164.8, -75.2)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 17



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.

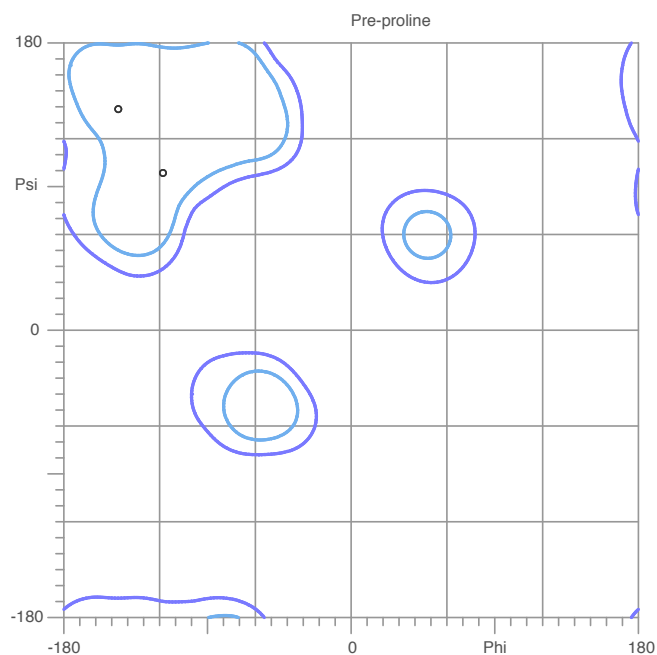
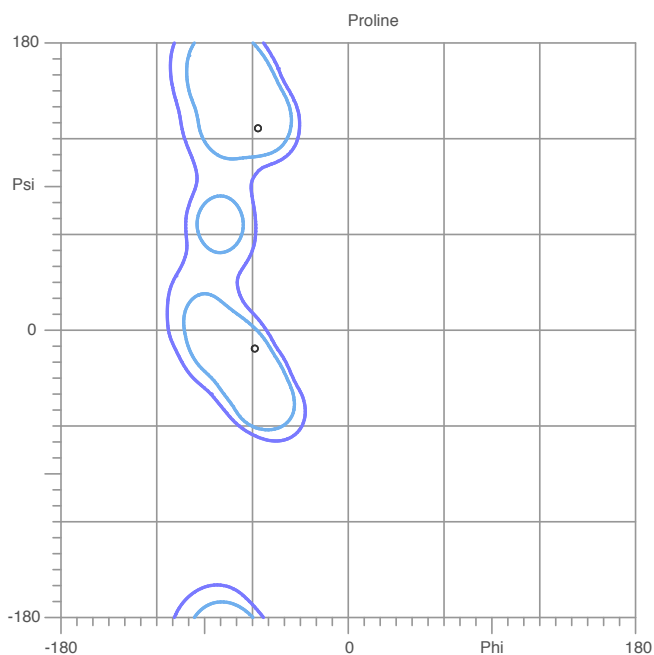
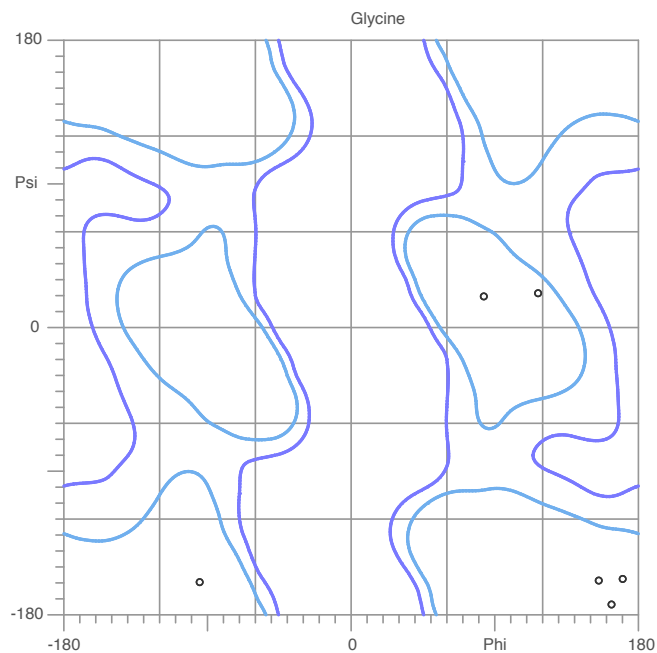
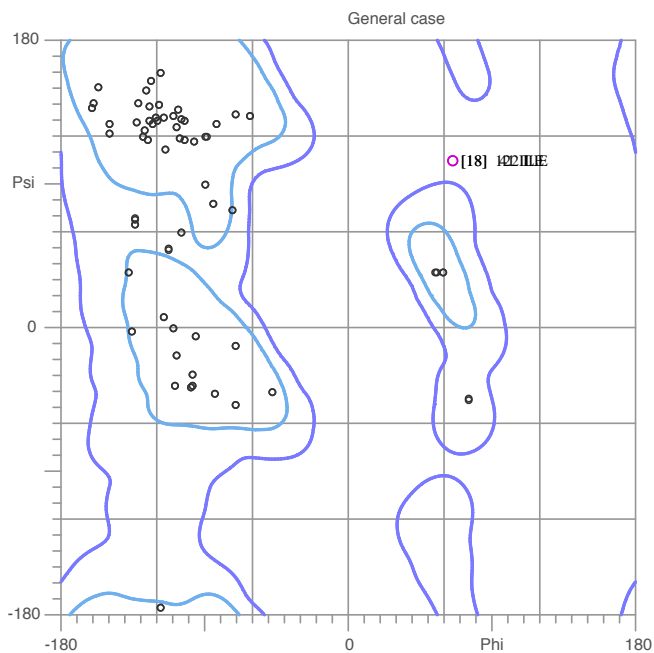
There were 2 outliers (phi, psi):

[17] 41 ILE (75.0, 120.0)

[17] 122 ILE (75.0, 119.9)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 18



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.

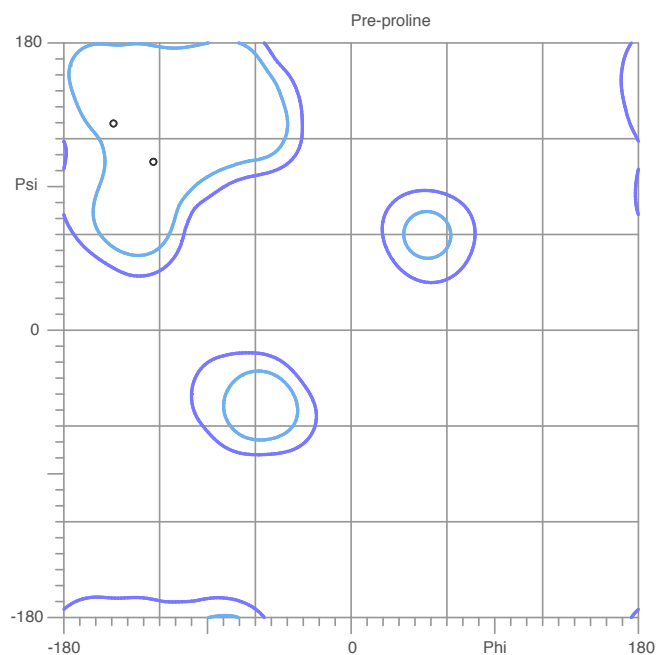
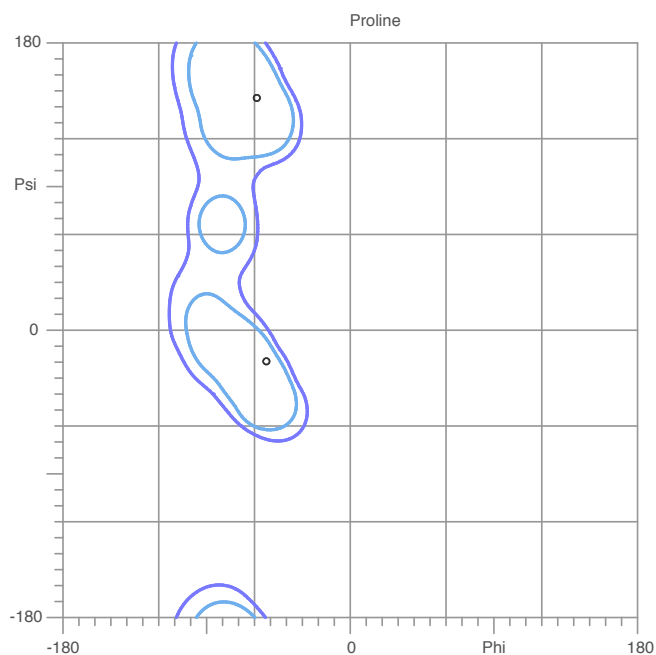
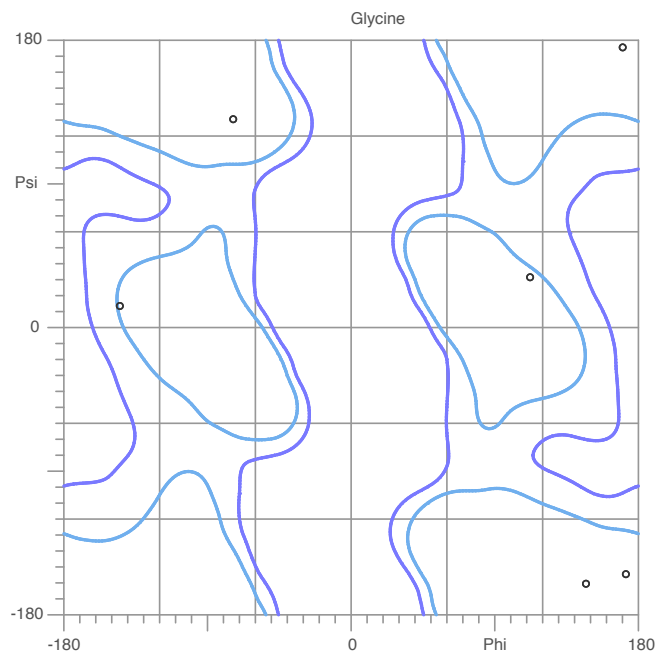
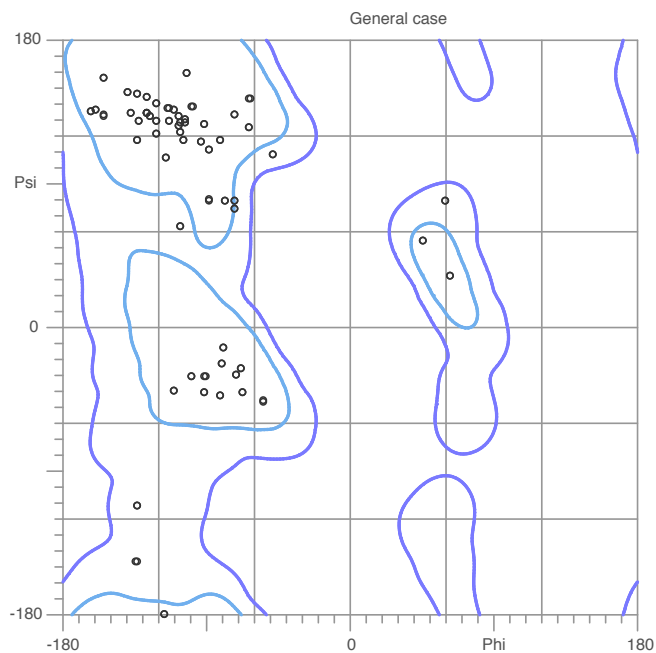
There were 2 outliers (phi, psi):

[18] 41 ILE (65.2, 105.1)

[18] 122 ILE (65.2, 105.0)

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 19



92.8% (128/138) of all residues were in favored (98%) regions.

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

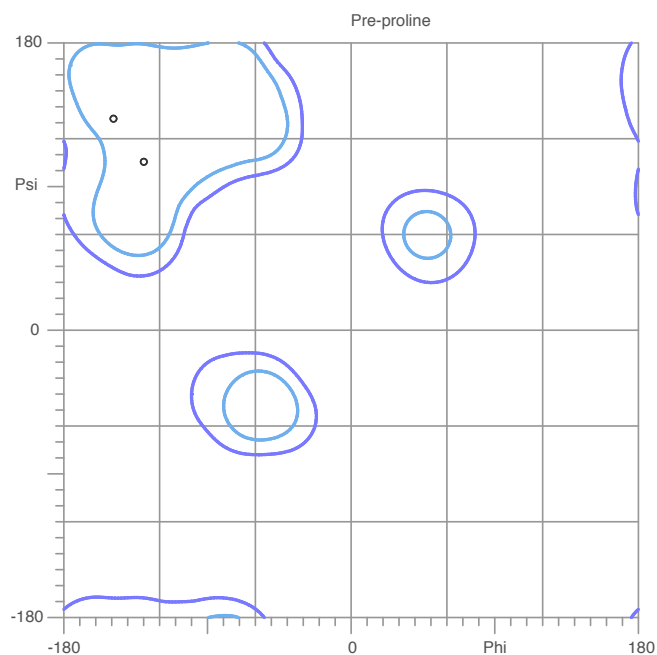
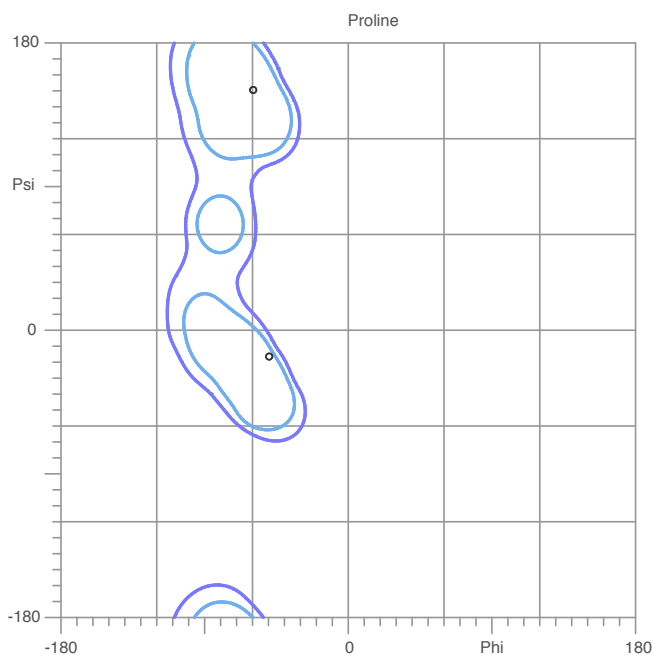
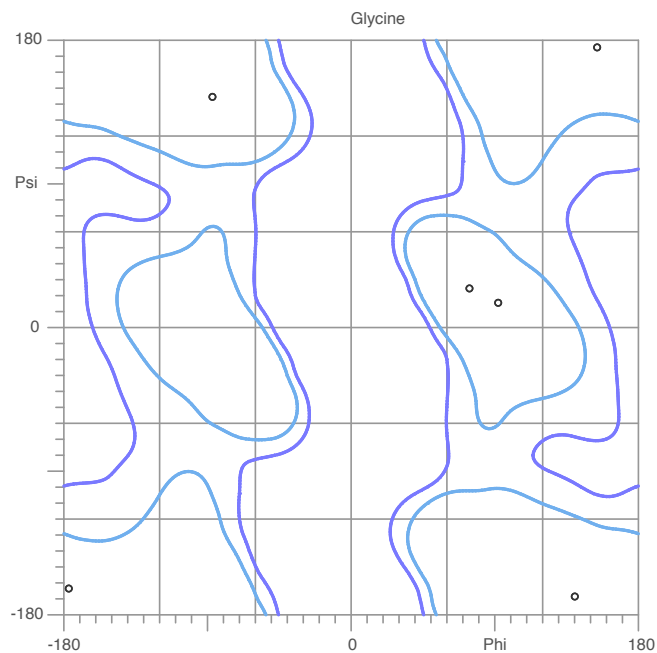
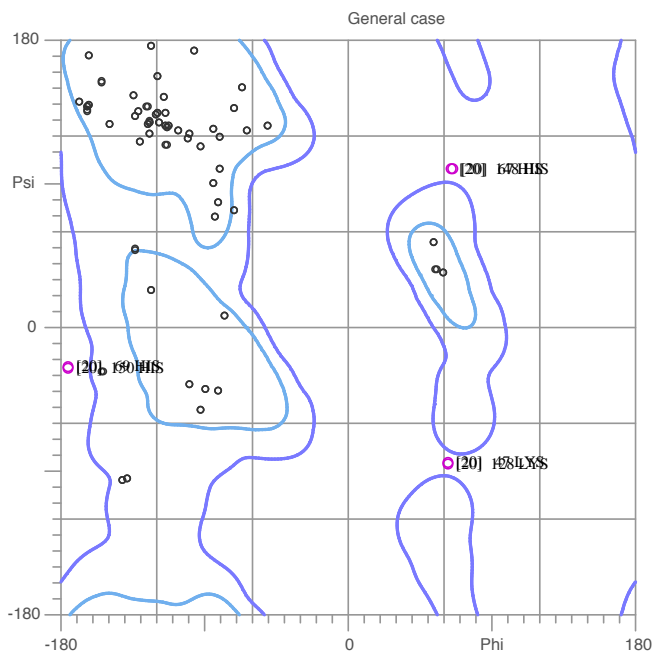
There were no outliers.

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

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

MolProbity Ramachandran analysis

DHR8C_R3Cons_em_bcr3.pdb, model 20



88.4% (122/138) 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):
[20] 47 LYS (62.6, -84.9)

[20] 67 HIS (65.0, 100.3)
[20] 69 HIS (-176.7, -25.0)
[20] 128 LYS (62.7, -85.0)
[20] 148 HIS (65.0, 100.3)
[20] 150 HIS (-176.7, -25.0)