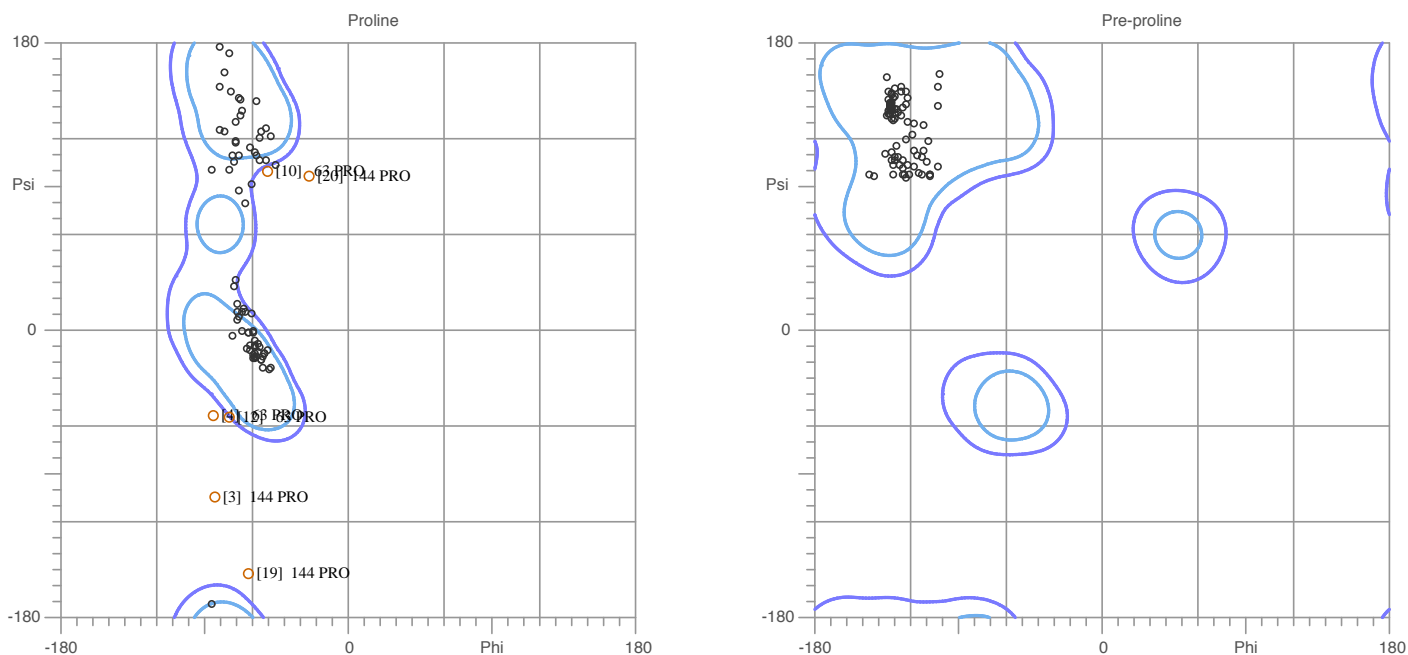
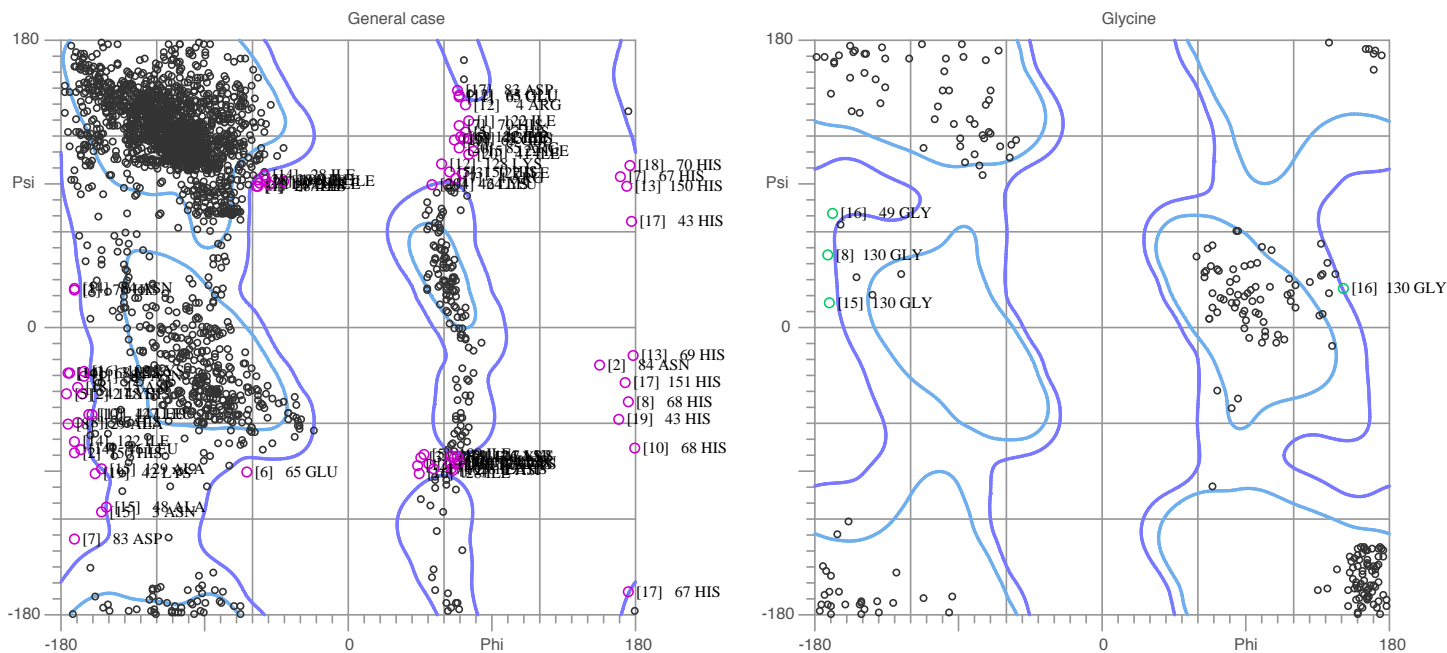


MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, all models



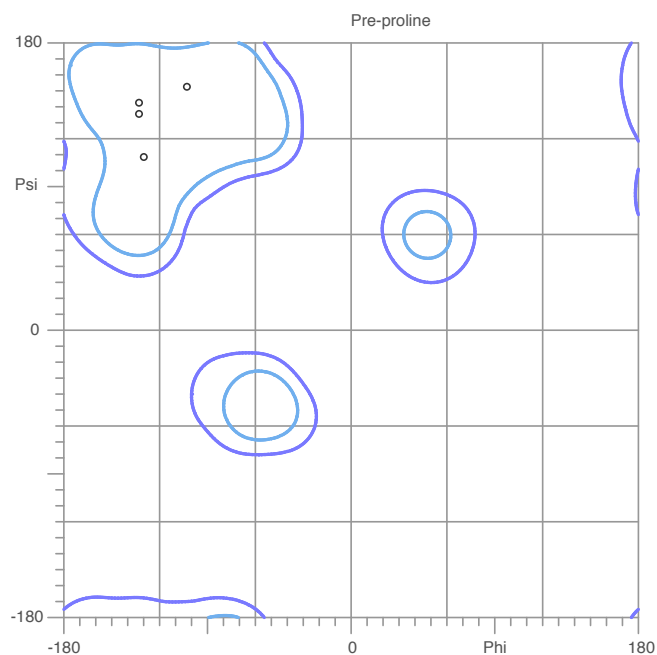
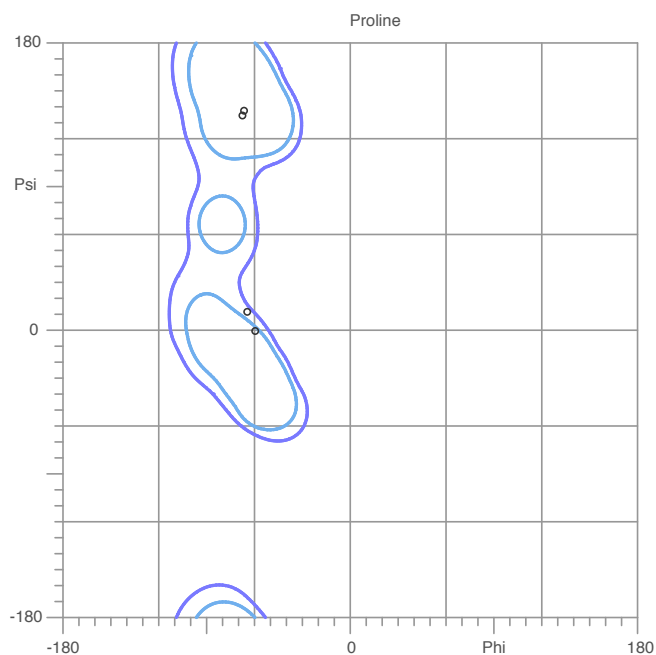
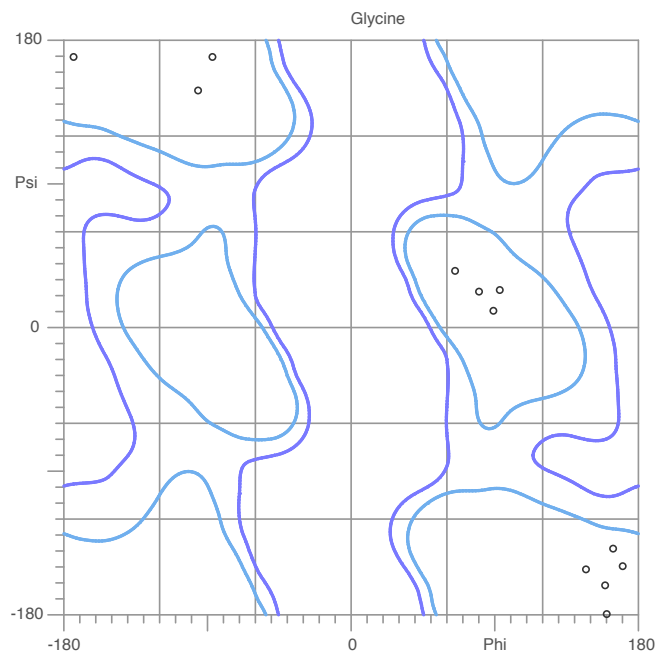
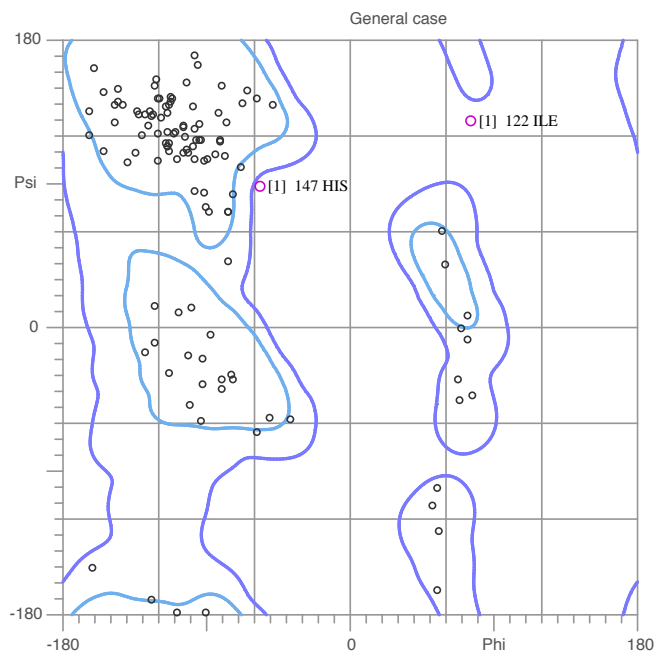
86.6% (1216/1393) of all residues were in favored (98%) regions.
 96.9% (1271/1311) of all residues were in allowed (98%) regions.

There were 87 outliers (phi, psi):

111	109 LEU (31.6, 85.8)
112	2 ASP (6.6, 90.0)
113	4 MET (34.0, 87.0)
114	28 ARG (43.3, 86.6)
115	82 PRO (1.0, 86.0)
116	65 LEU (70.0, 140.0)
117	120 ARG (70.0, 150.0)
118	47 LYS (67.4, 85.3)
119	69 HIS (57.4, 87.0)
120	125 LYS (67.4, 85.3)
121	129 ARG (57.4, 85.3)
122	130 HIS (67.4, 85.3)
123	131 HIS (67.4, 85.3)
124	132 HIS (67.4, 85.3)
125	133 HIS (67.4, 85.3)
126	134 HIS (67.4, 85.3)
127	135 HIS (67.4, 85.3)
128	136 HIS (67.4, 85.3)
129	137 HIS (67.4, 85.3)
130	138 HIS (67.4, 85.3)
131	139 HIS (67.4, 85.3)
132	140 HIS (67.4, 85.3)
133	141 HIS (67.4, 85.3)
134	142 HIS (67.4, 85.3)
135	143 HIS (67.4, 85.3)
136	144 HIS (67.4, 85.3)
137	145 HIS (67.4, 85.3)
138	146 HIS (67.4, 85.3)
139	147 HIS (67.4, 85.3)
140	148 HIS (67.4, 85.3)
141	149 HIS (67.4, 85.3)
142	150 HIS (67.4, 85.3)
143	151 HIS (67.4, 85.3)
144	152 HIS (67.4, 85.3)
145	153 HIS (67.4, 85.3)
146	154 HIS (67.4, 85.3)
147	155 HIS (67.4, 85.3)
148	156 HIS (67.4, 85.3)
149	157 HIS (67.4, 85.3)
150	158 HIS (67.4, 85.3)
151	159 HIS (67.4, 85.3)
152	160 HIS (67.4, 85.3)
153	161 HIS (67.4, 85.3)
154	162 HIS (67.4, 85.3)
155	163 HIS (67.4, 85.3)
156	164 HIS (67.4, 85.3)
157	165 HIS (67.4, 85.3)
158	166 HIS (67.4, 85.3)
159	167 HIS (67.4, 85.3)
160	168 HIS (67.4, 85.3)
161	169 HIS (67.4, 85.3)
162	170 HIS (67.4, 85.3)
163	171 HIS (67.4, 85.3)
164	172 HIS (67.4, 85.3)
165	173 HIS (67.4, 85.3)
166	174 HIS (67.4, 85.3)
167	175 HIS (67.4, 85.3)
168	176 HIS (67.4, 85.3)
169	177 HIS (67.4, 85.3)
170	178 HIS (67.4, 85.3)
171	179 HIS (67.4, 85.3)
172	180 HIS (67.4, 85.3)
173	181 HIS (67.4, 85.3)
174	182 HIS (67.4, 85.3)
175	183 HIS (67.4, 85.3)
176	184 HIS (67.4, 85.3)
177	185 HIS (67.4, 85.3)
178	186 HIS (67.4, 85.3)
179	187 HIS (67.4, 85.3)
180	188 HIS (67.4, 85.3)
181	189 HIS (67.4, 85.3)
182	190 HIS (67.4, 85.3)
183	191 HIS (67.4, 85.3)
184	192 HIS (67.4, 85.3)
185	193 HIS (67.4, 85.3)
186	194 HIS (67.4, 85.3)
187	195 HIS (67.4, 85.3)
188	196 HIS (67.4, 85.3)
189	197 HIS (67.4, 85.3)
190	198 HIS (67.4, 85.3)
191	199 HIS (67.4, 85.3)
192	200 HIS (67.4, 85.3)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 1



86.2% (119/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

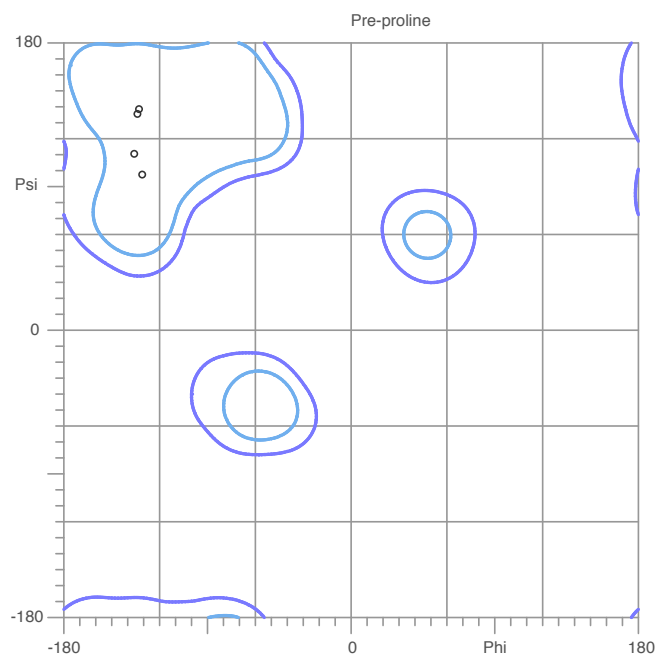
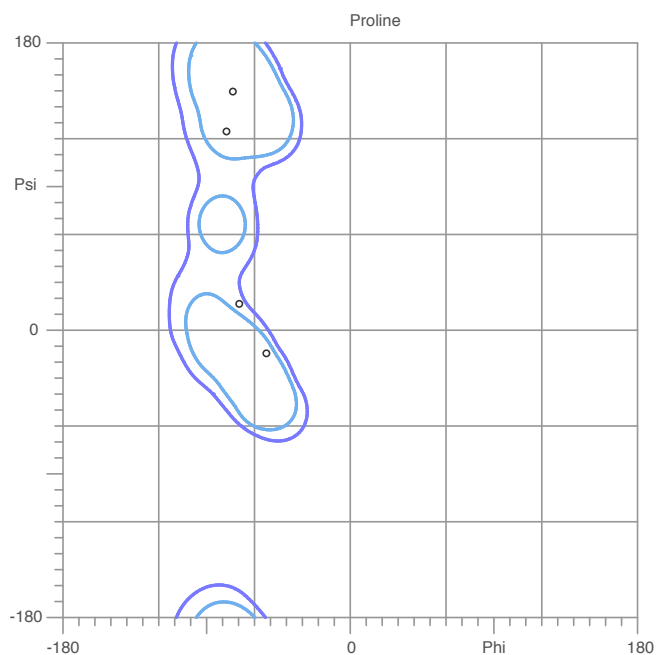
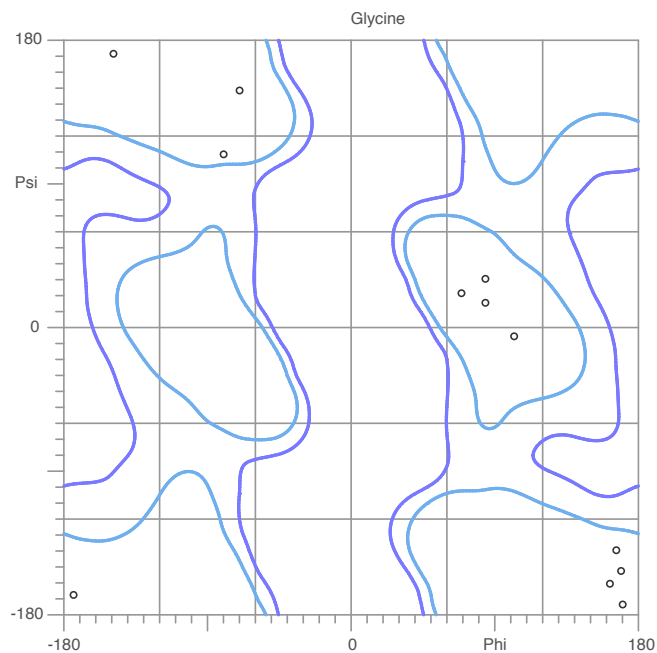
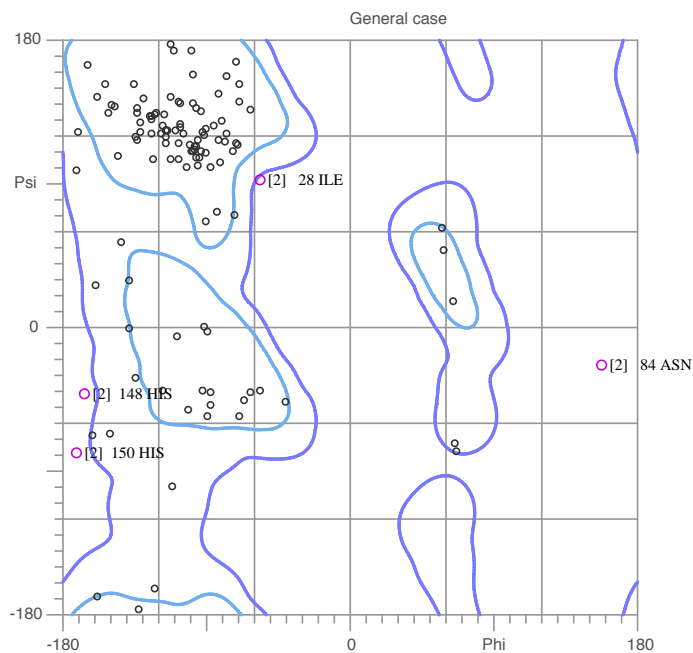
There were 2 outliers (phi, psi):

[1] 122 ILE (75.5, 130.9)

[1] 147 HIS (-57.3, 89.5)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 2



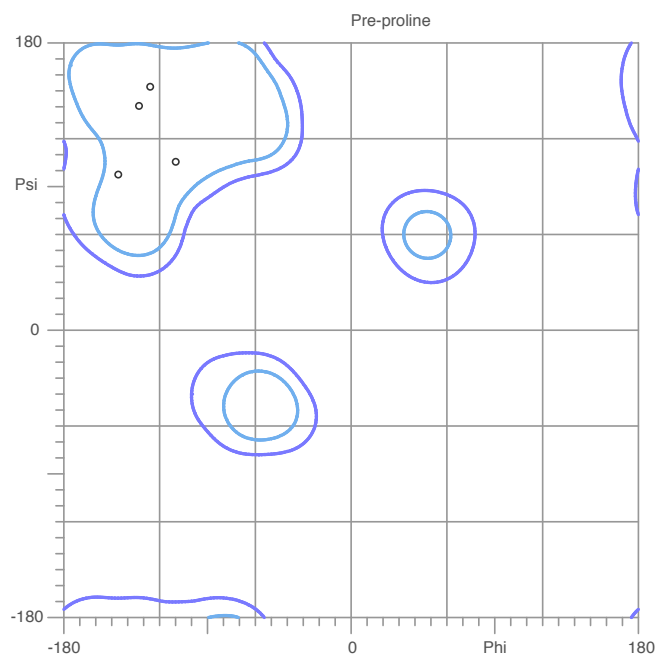
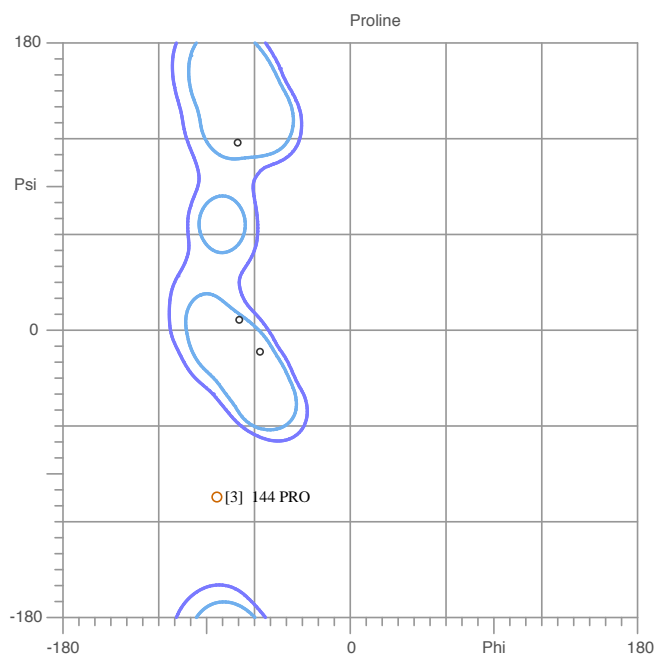
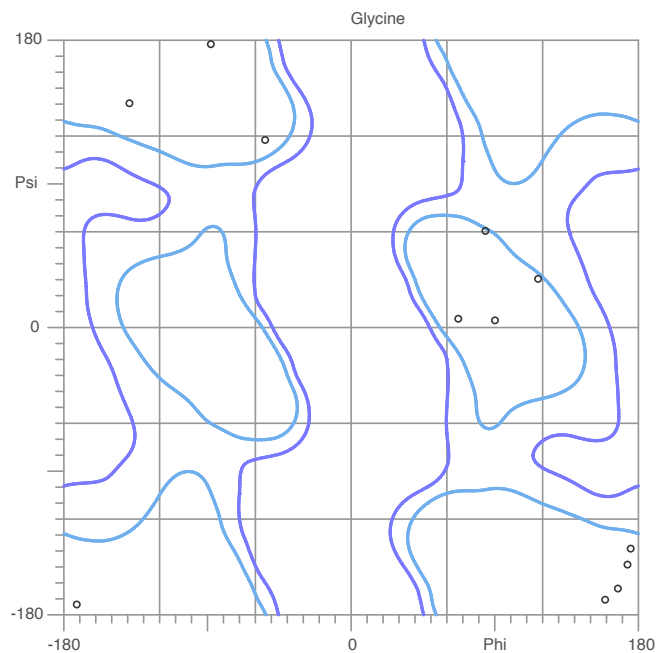
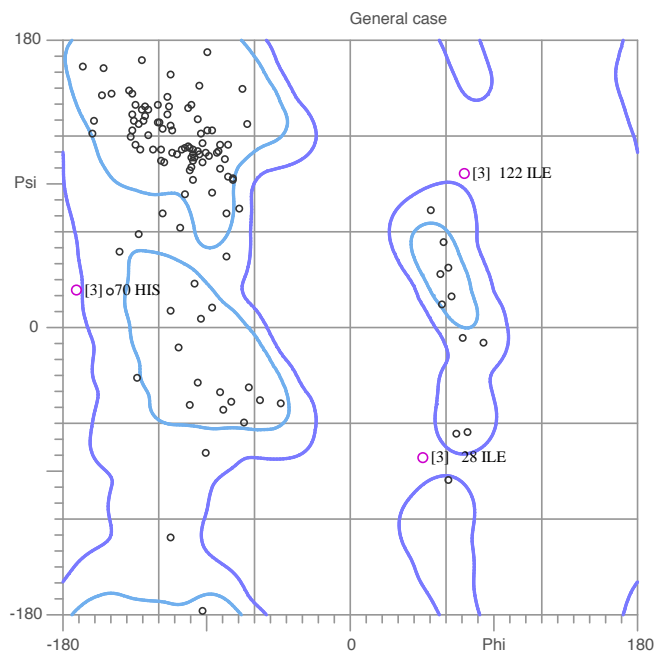
84.8% (117/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [2] 28 ILE (-57.8, 93.1)
- [2] 84 ASN (157.6, -23.7)
- [2] 148 HIS (-167.9, -41.7)
- [2] 150 HIS (-172.7, -78.0)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 3



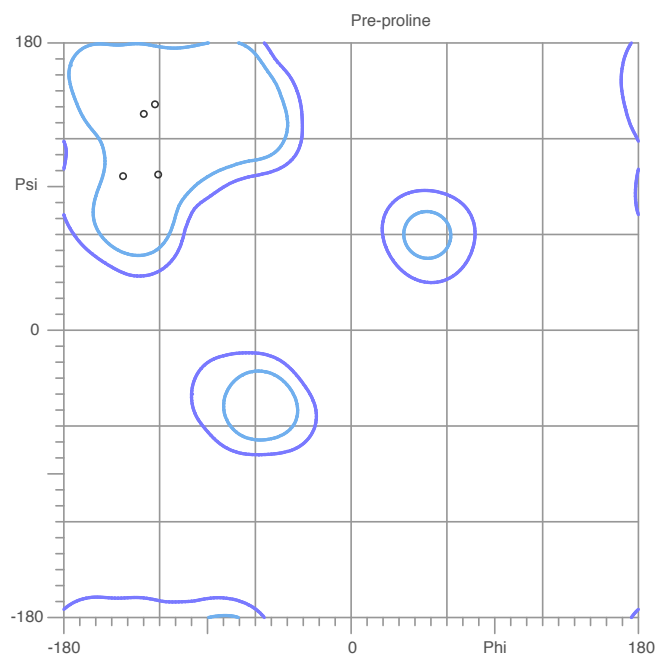
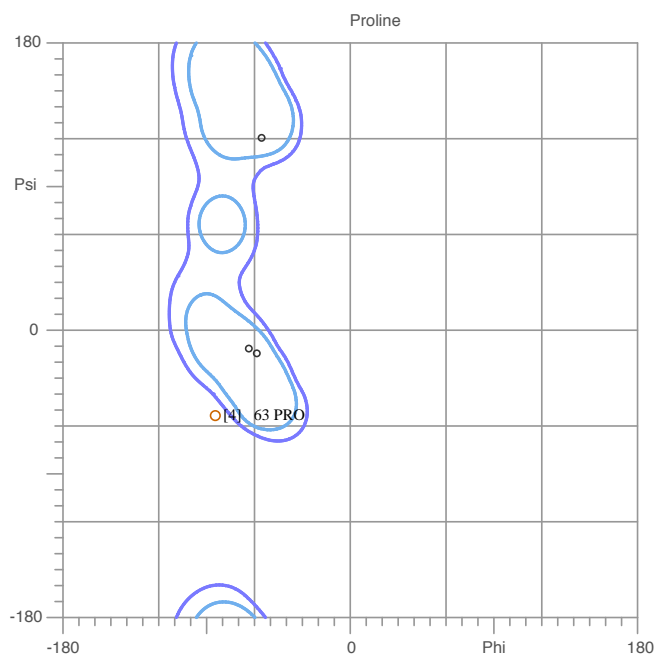
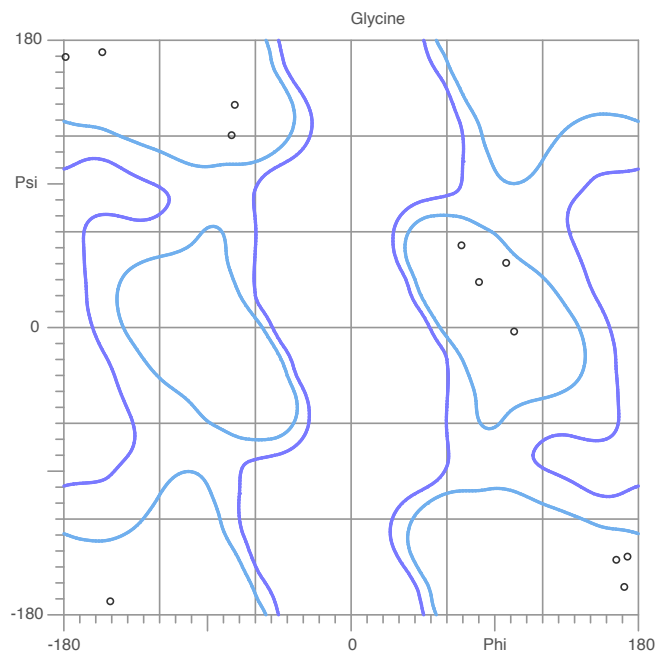
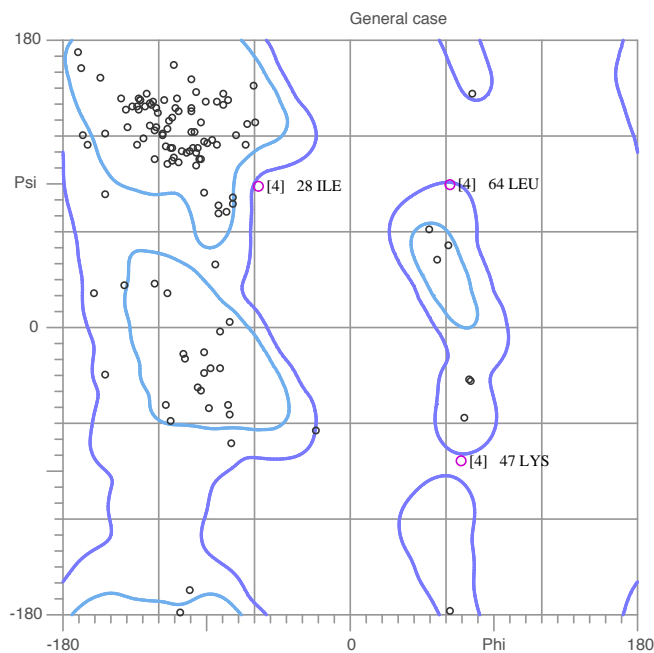
85.5% (118/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [3] 28 ILE (45.5, -81.4)
- [3] 70 HIS (-172.8, 24.7)
- [3] 122 ILE (71.3, 97.1)
- [3] 144 PRO (-84.9, -104.4)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 4



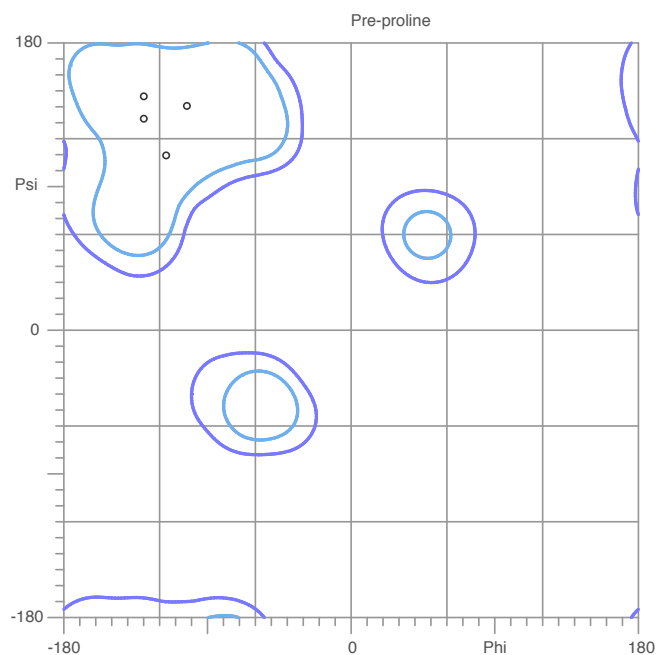
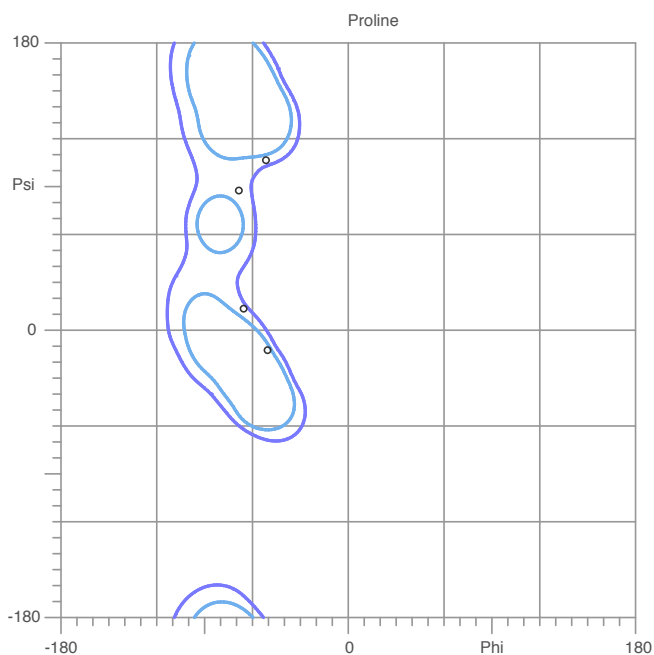
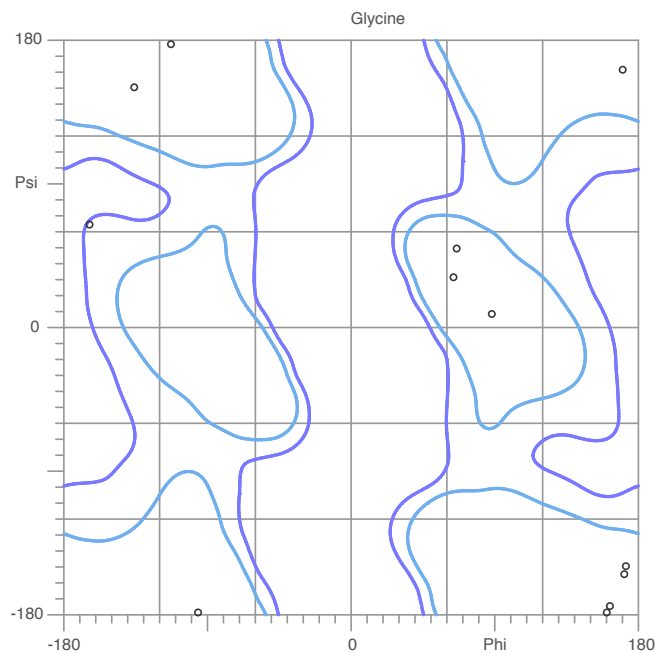
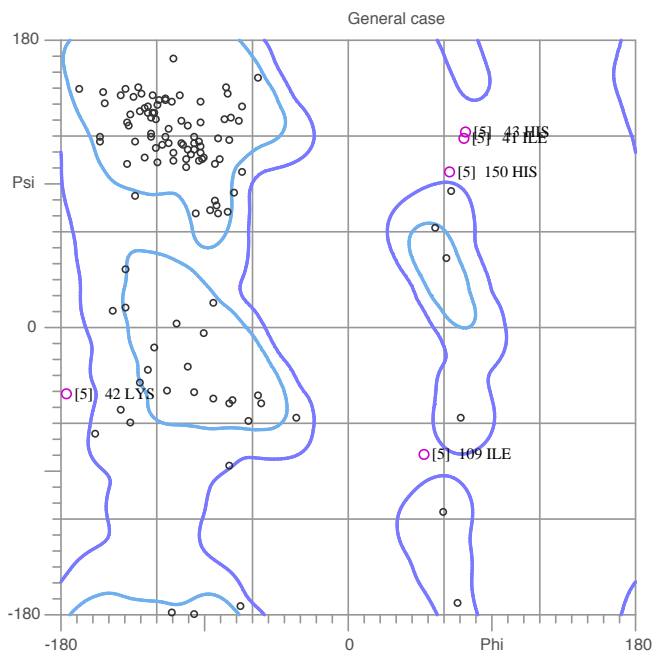
86.2% (119/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [4] 28 ILE (-58.4, 89.5)
- [4] 47 LYS (69.2, -83.3)
- [4] 63 PRO (-86.0, -53.7)
- [4] 64 LEU (62.3, 90.9)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 5



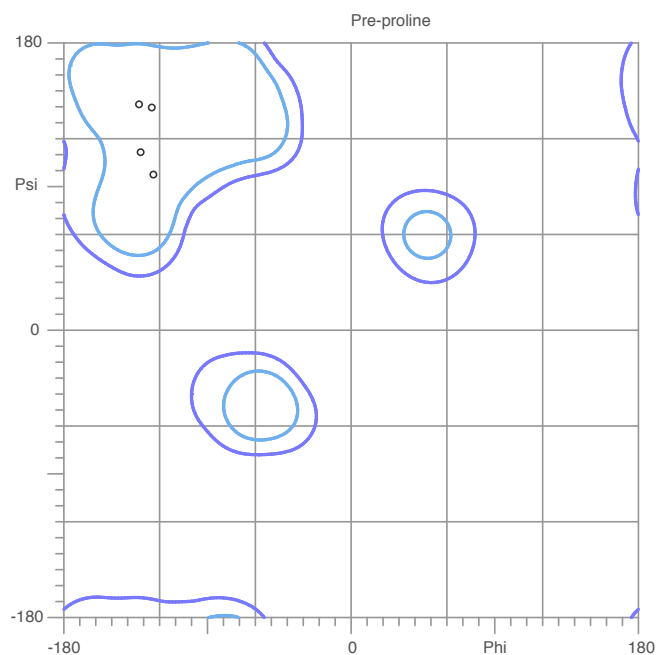
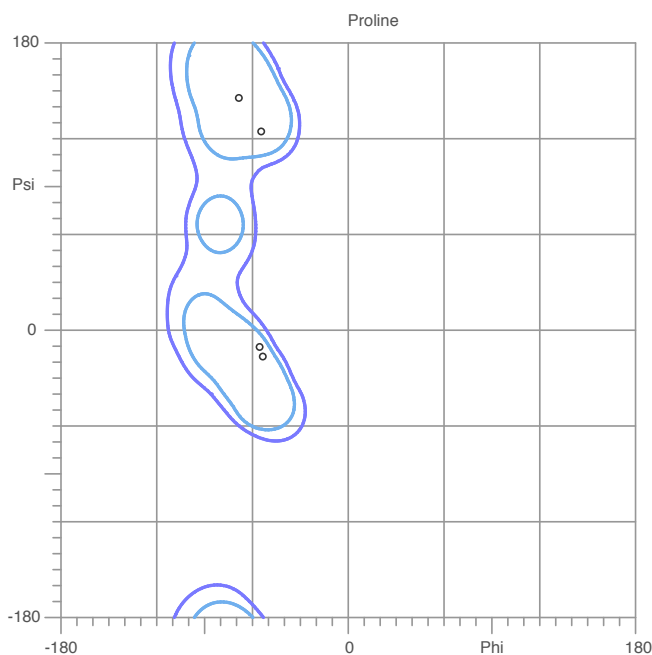
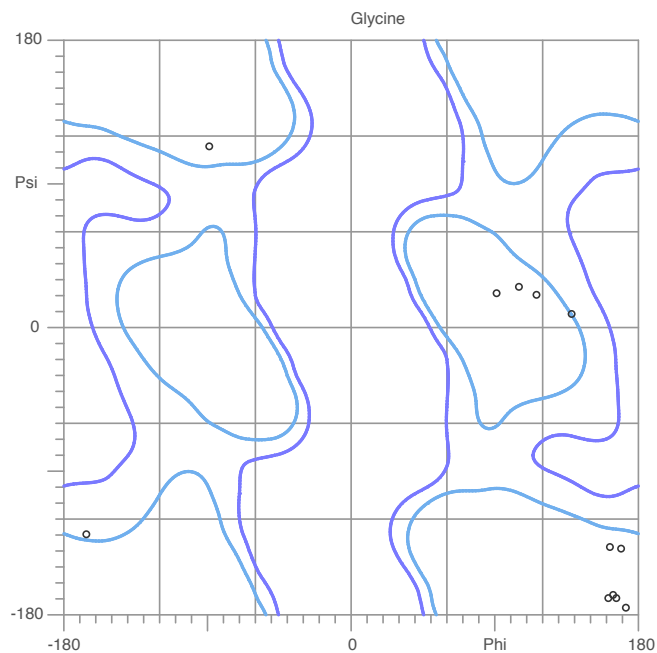
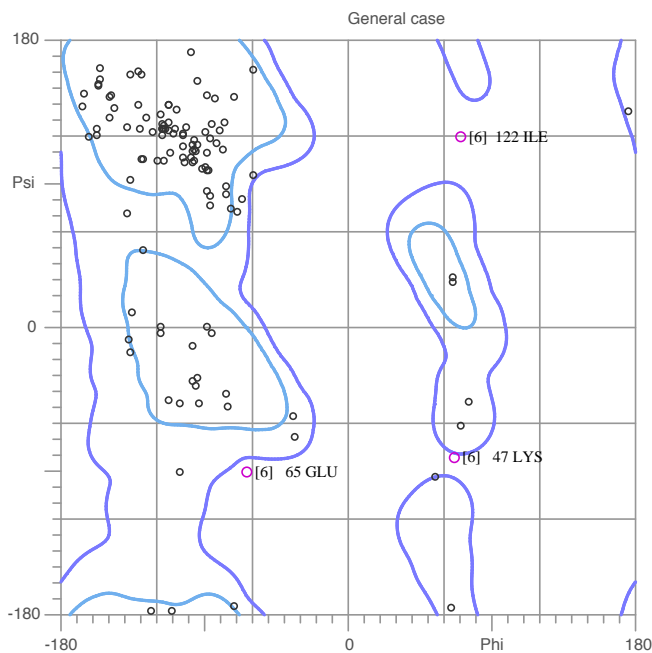
81.9% (113/138) of all residues were in favored (98%) regions.
96.4% (133/138) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[5] 41 ILE (72.4, 119.2)
[5] 42 LYS (-177.8, -41.4)
[5] 43 HIS (73.5, 123.5)
[5] 109 ILE (47.4, -79.4)
[5] 150 HIS (63.4, 98.5)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 6



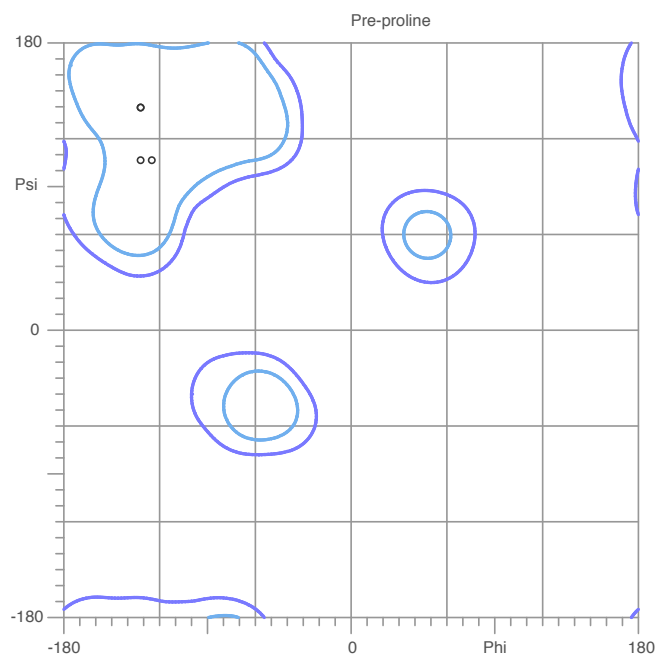
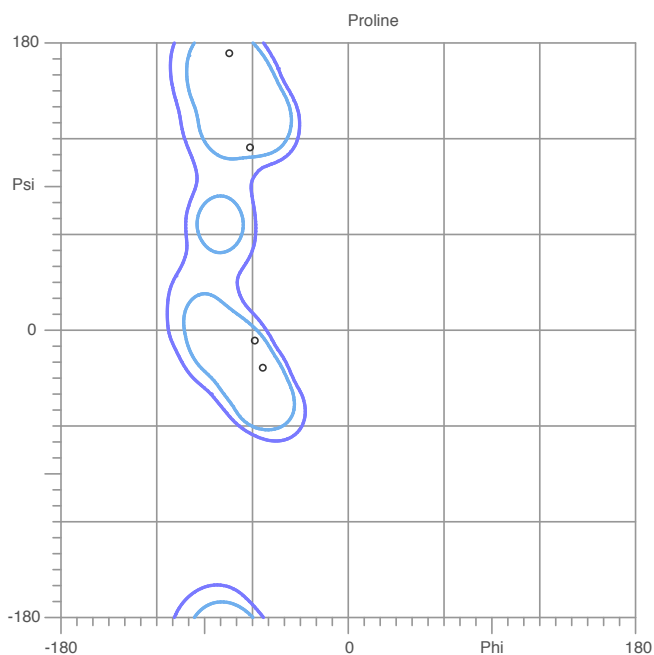
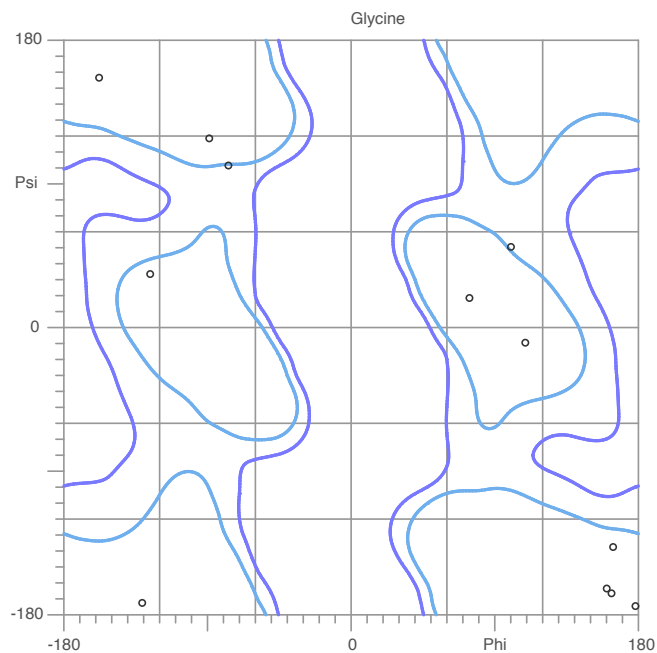
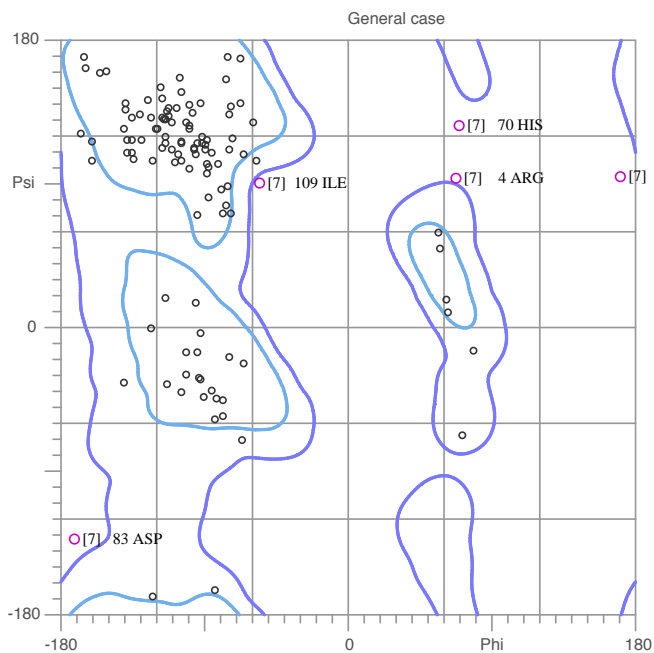
84.1% (116/138) of all residues were in favored (98%) regions.
97.8% (135/138) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 47 LYS (66.9, -81.1)
- [6] 65 GLU (-64.4, -90.3)
- [6] 122 ILE (70.7, 120.1)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 7



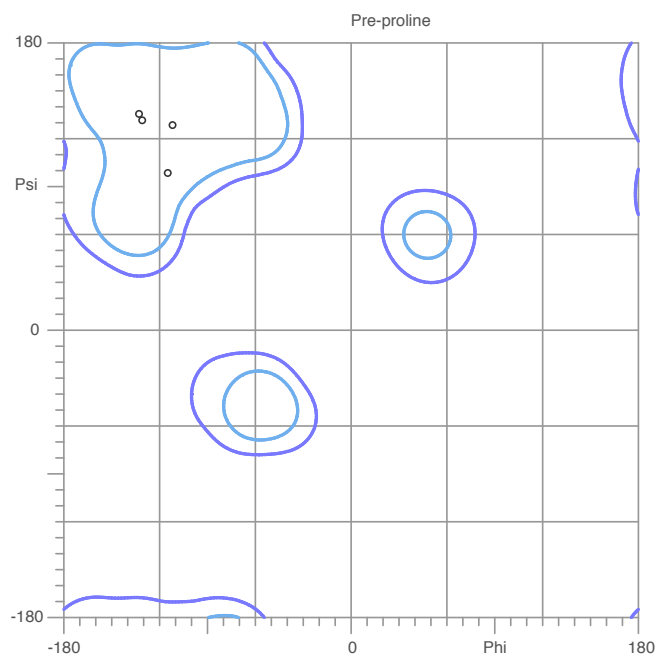
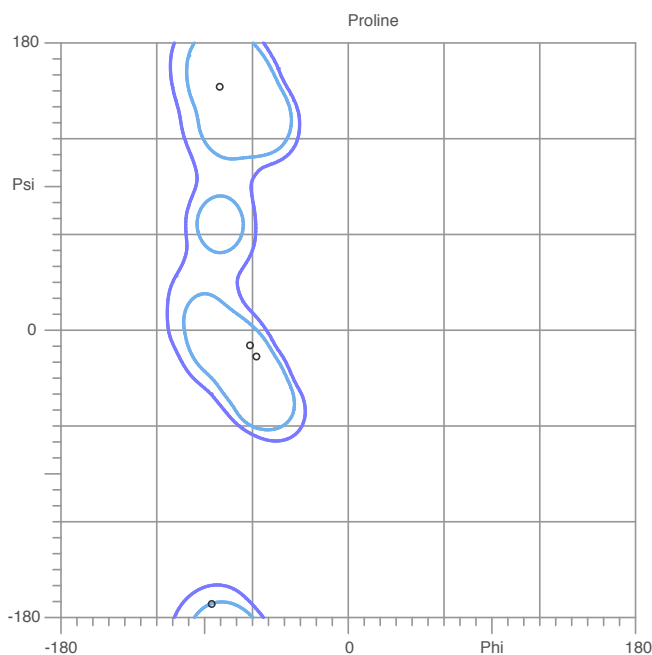
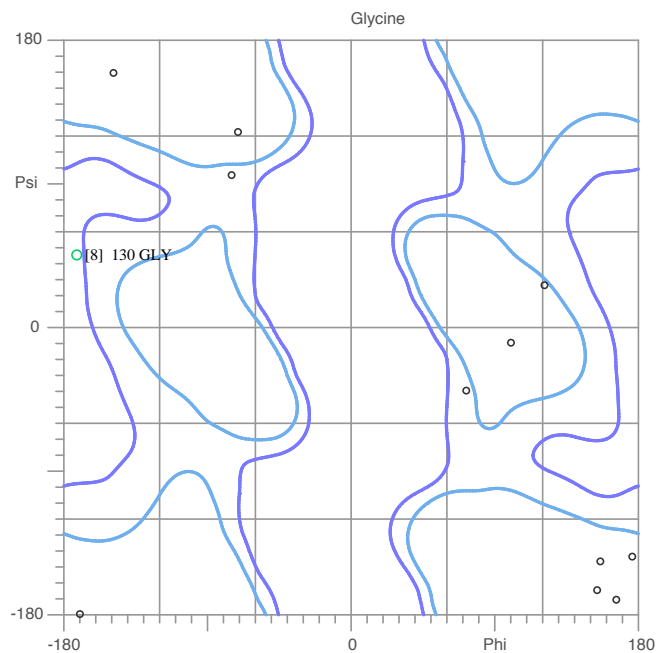
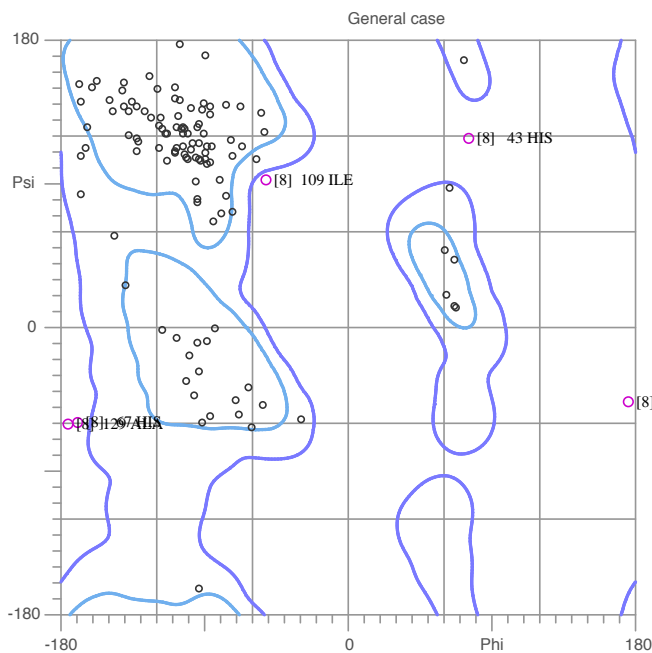
88.4% (122/138) of all residues were in favored (98%) regions.
96.4% (133/138) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[7] 4 ARG (67.3, 95.0)
[7] 67 HIS (170.5, 95.6)
[7] 70 HIS (69.1, 127.7)
[7] 83 ASP (-172.7, -133.0)
[7] 109 ILE (-56.3, 91.4)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 8



87.0% (120/138) 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):

[8] 43 HIS (75.2, 119.7)

[8] 67 HIS (-170.7, -59.5)

[8] 68 HIS (176.0, -46.7)

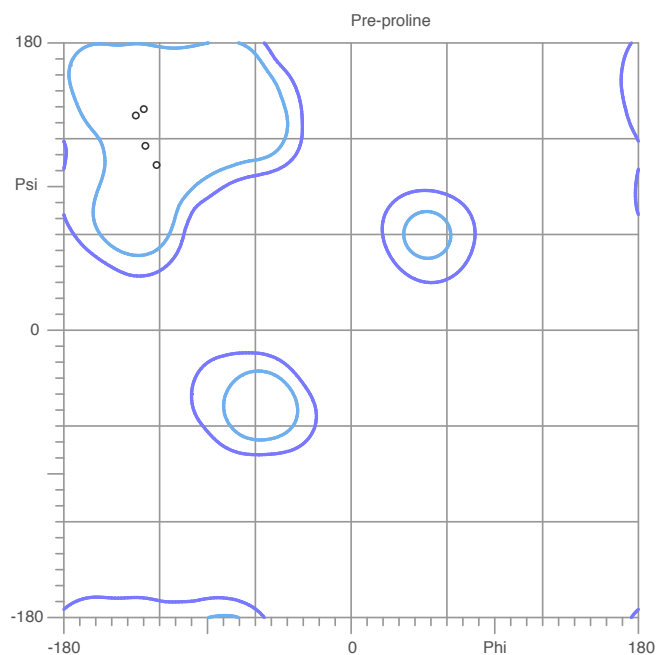
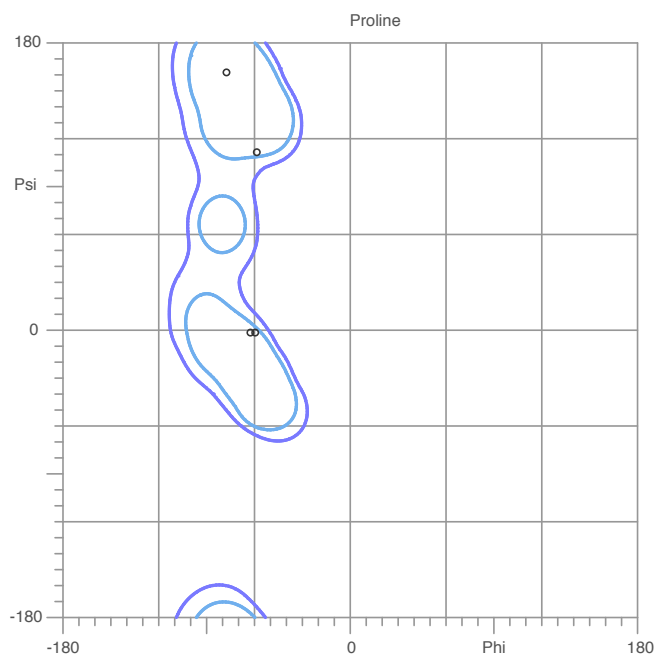
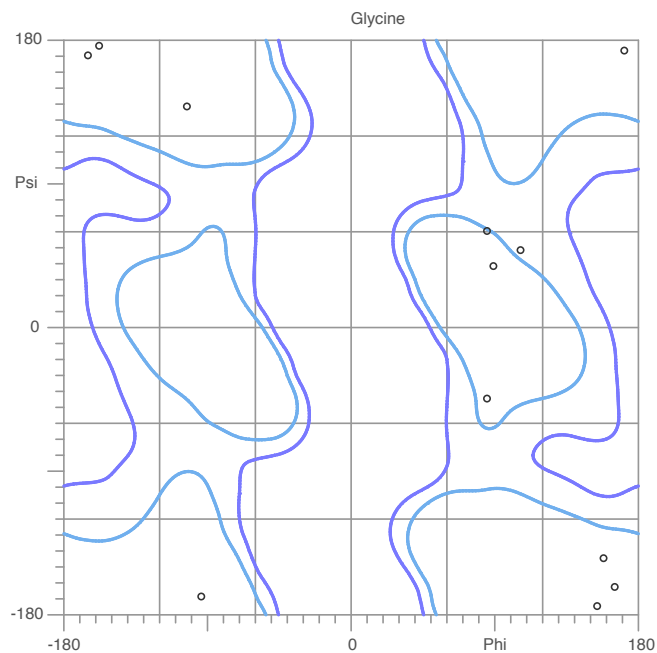
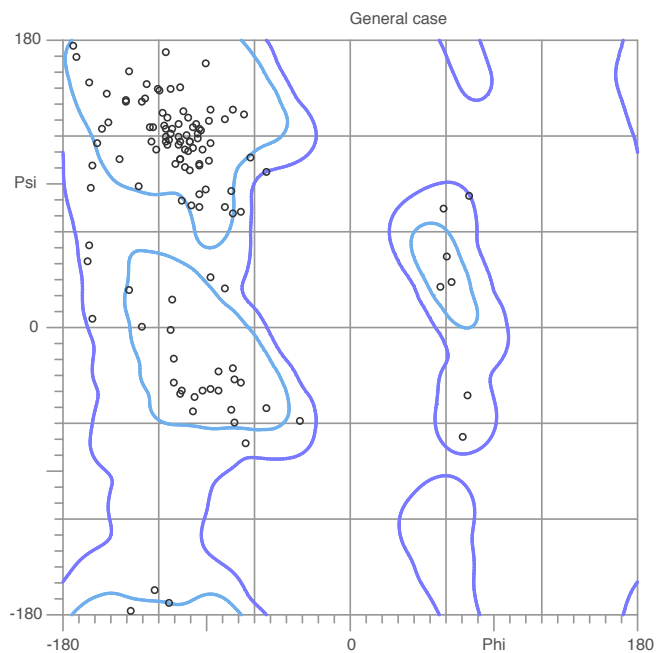
[8] 109 ILE (-52.4, 93.3)

[8] 129 ALA (-176.0, -60.9)

[8] 130 GLY (-172.9, 46.1)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 9



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.

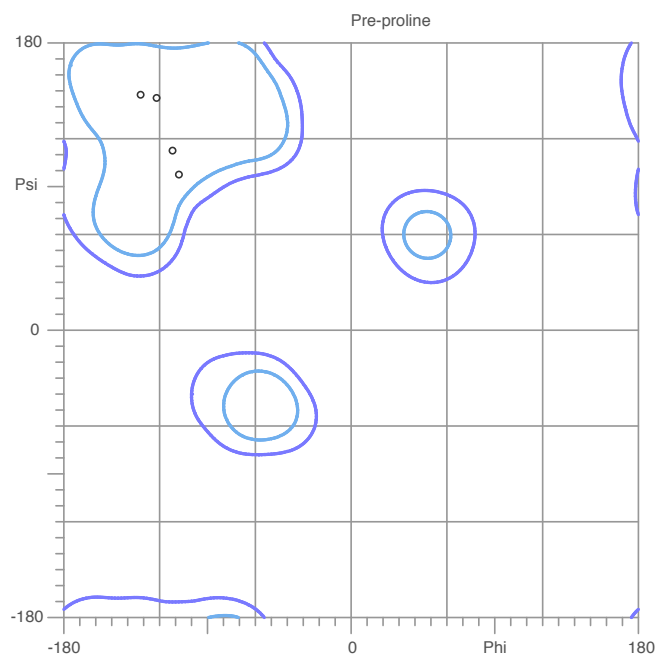
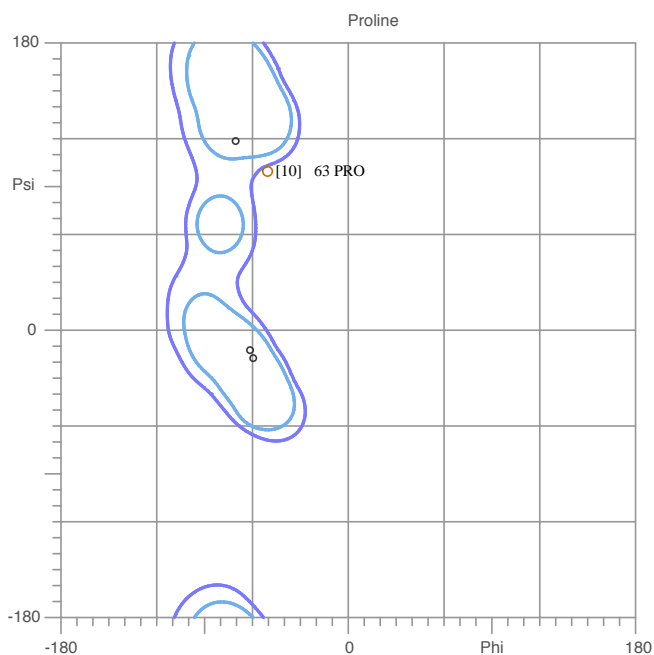
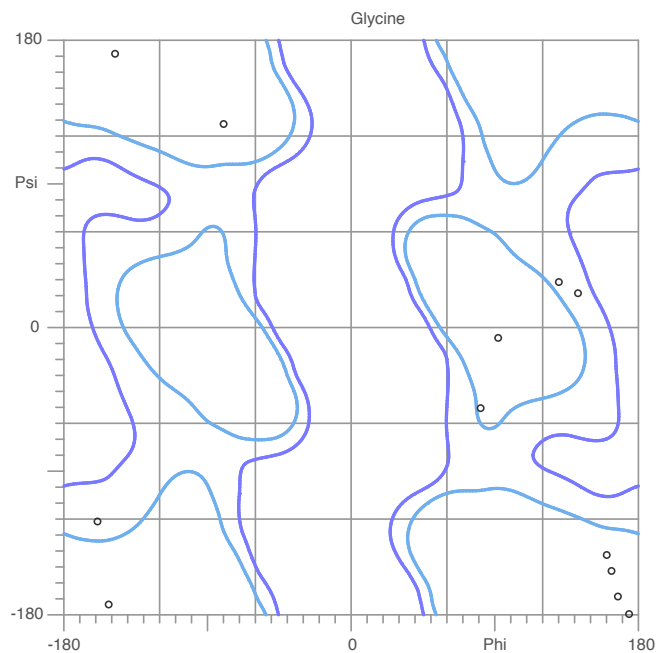
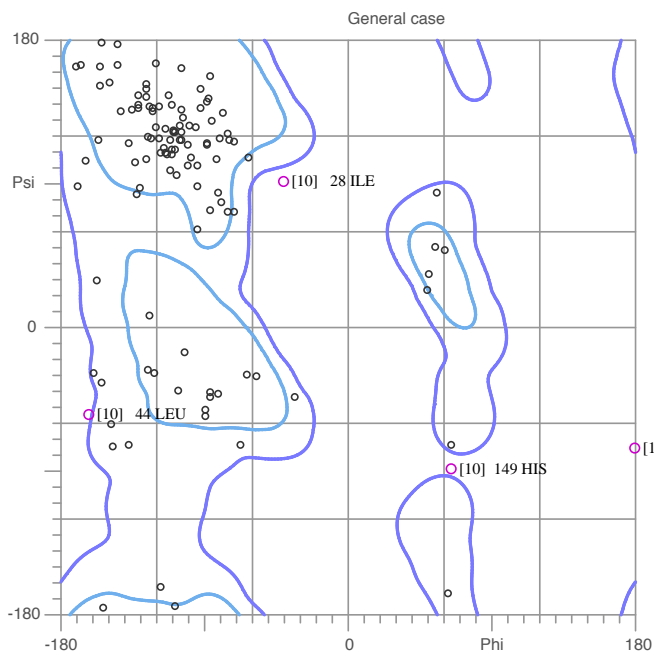
There were no outliers.

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

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

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 10



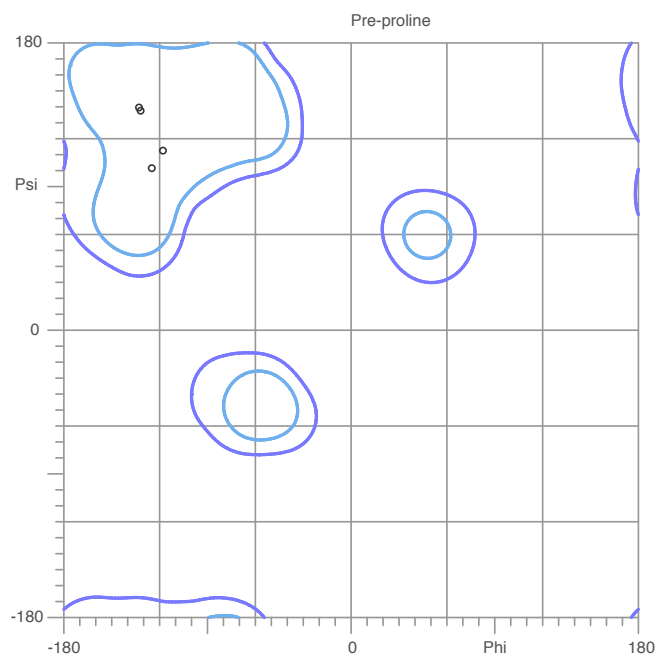
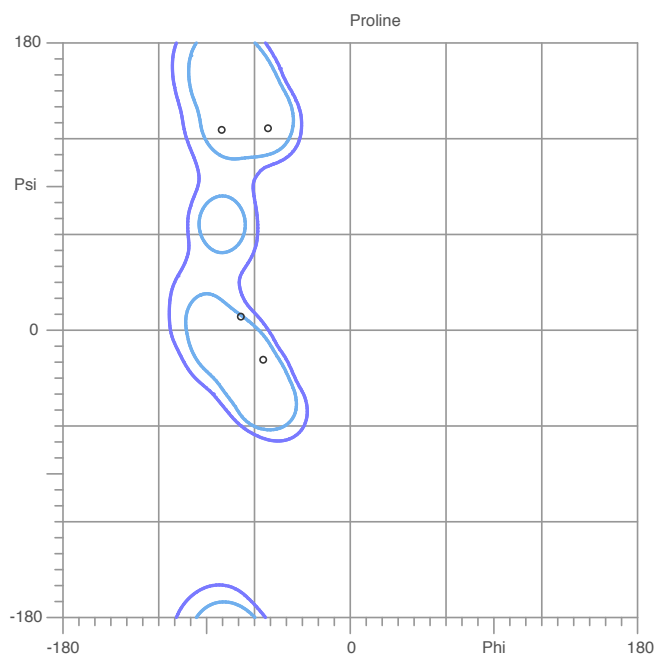
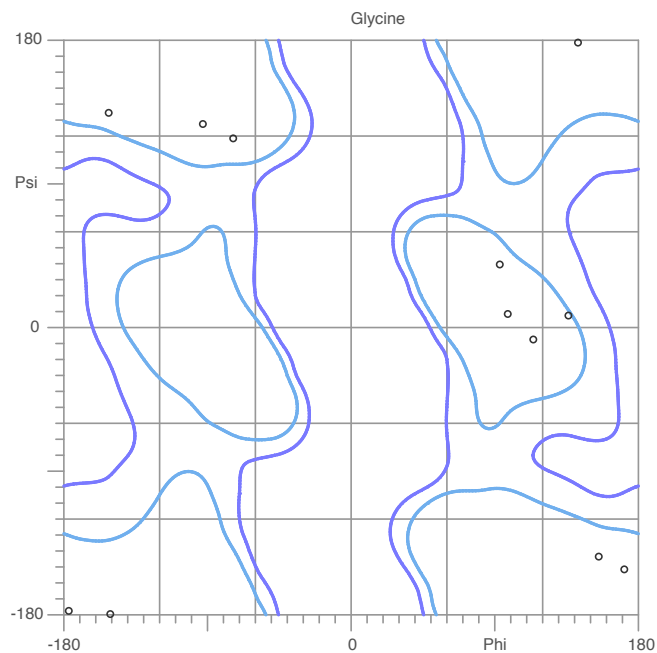
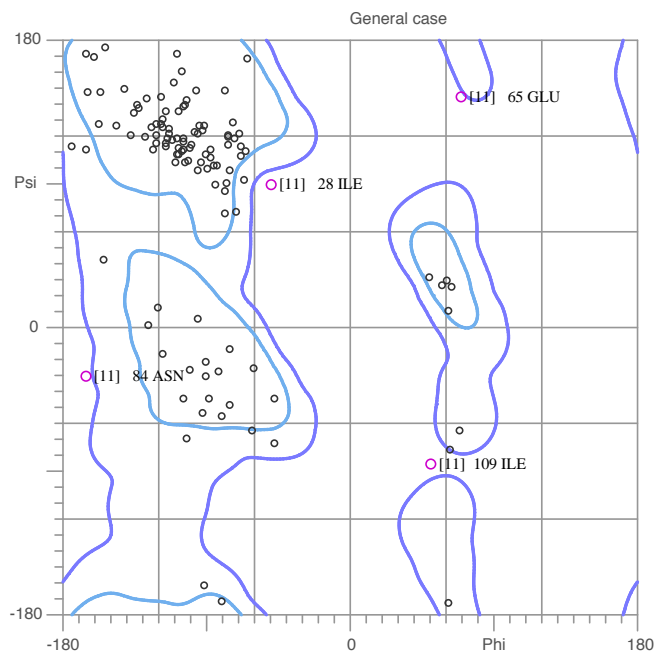
81.9% (113/138) of all residues were in favored (98%) regions.
96.4% (133/138) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[10] 28 ILE (-41.8, 92.1)
[10] 44 LEU (-163.1, -54.2)
[10] 63 PRO (-51.7, 100.2)
[10] 68 HIS (179.1, -75.5)
[10] 149 HIS (64.1, -88.9)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 11



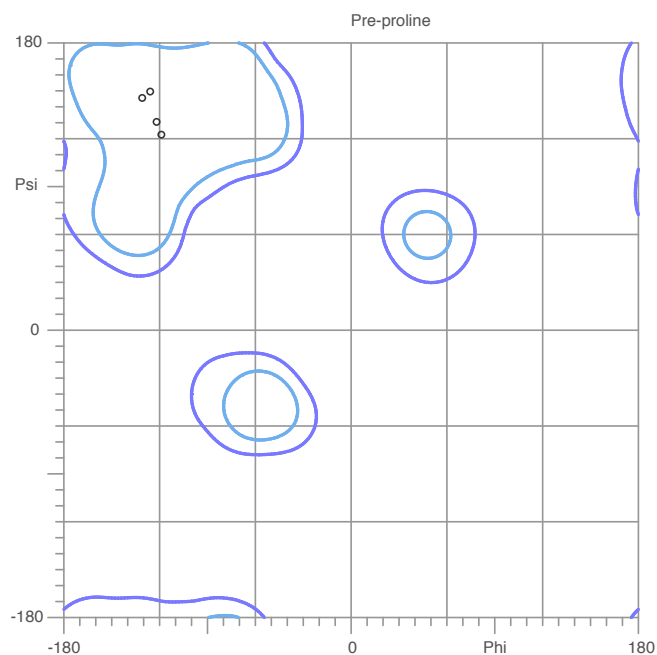
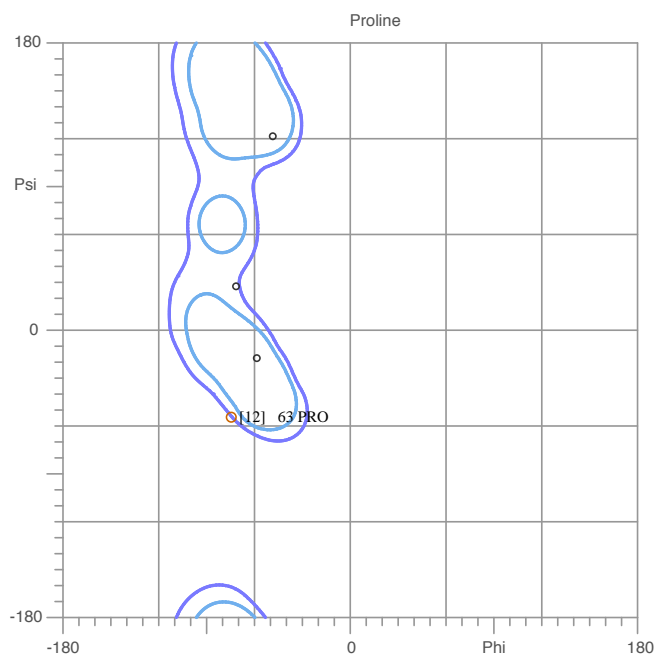
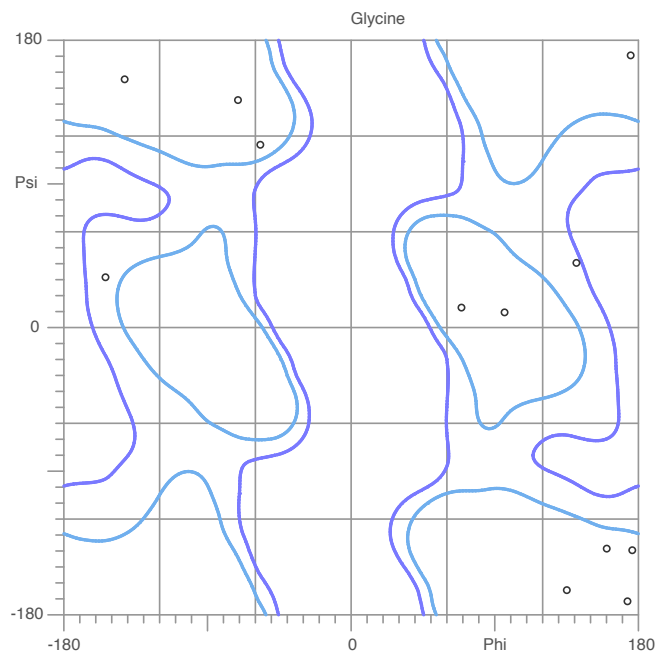
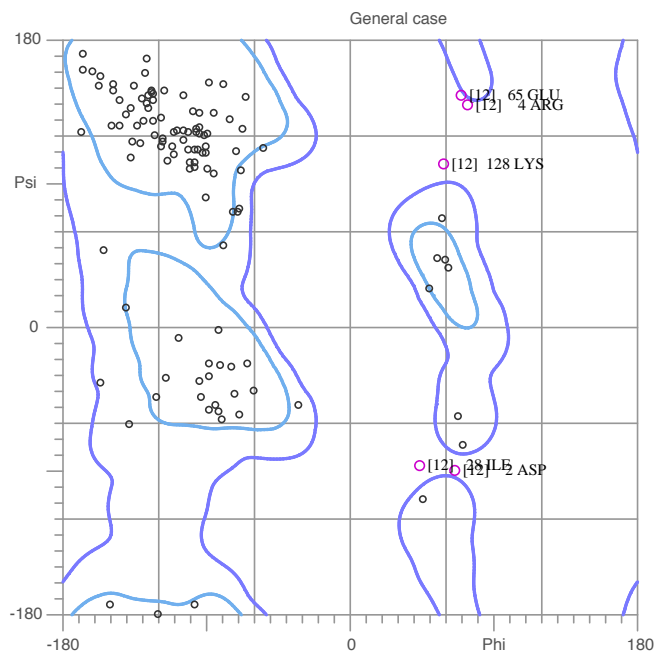
88.4% (122/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [11] 28 ILE (-51.0, 90.1)
- [11] 65 GLU (69.1, 145.9)
- [11] 84 ASN (-166.4, -30.9)
- [11] 109 ILE (51.0, -85.8)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 12



83.3% (115/138) 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):

[12] 2 ASP (65.6, -90.0)

[12] 4 ARG (74.0, 140.5)

[12] 28 ILE (43.3, -86.6)

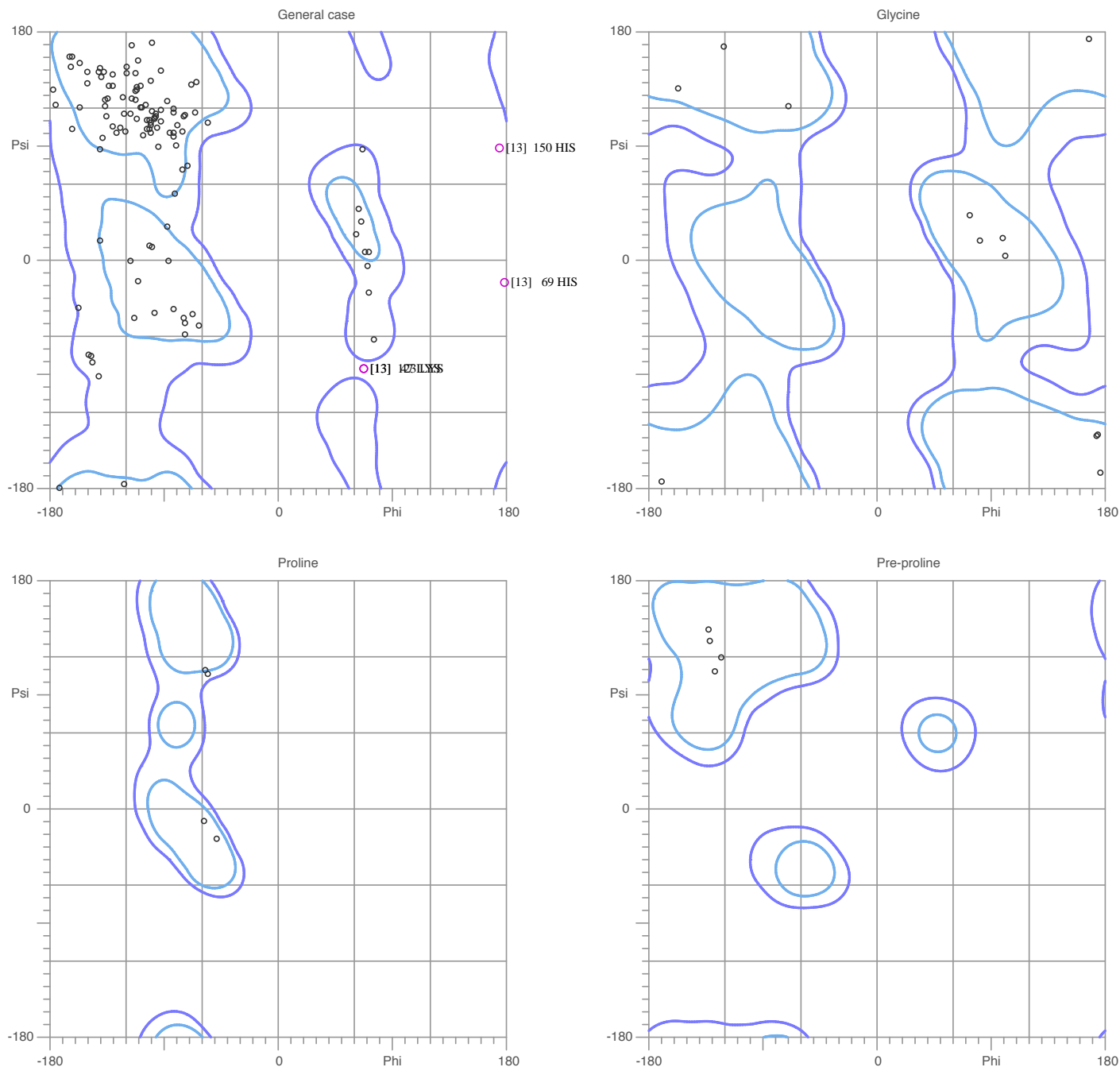
[12] 63 PRO (-75.9, -55.0)

[12] 65 GLU (70.0, 146.0)

[12] 128 LYS (58.7, 103.6)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 13



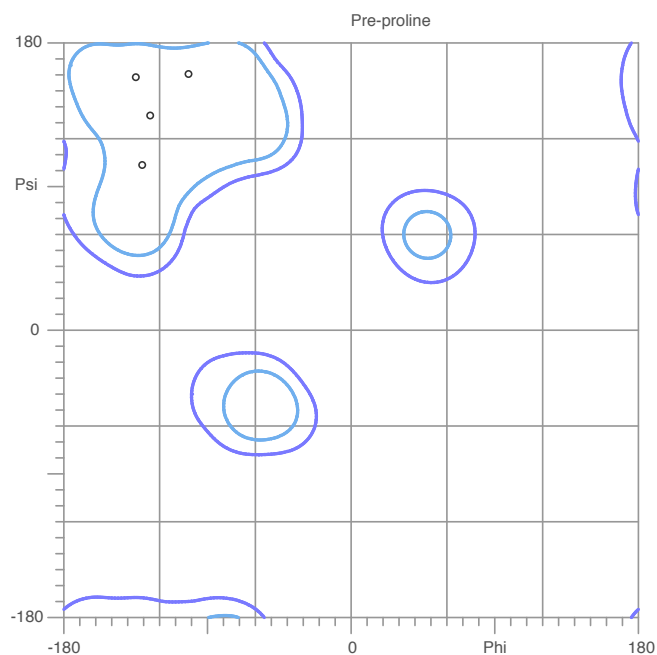
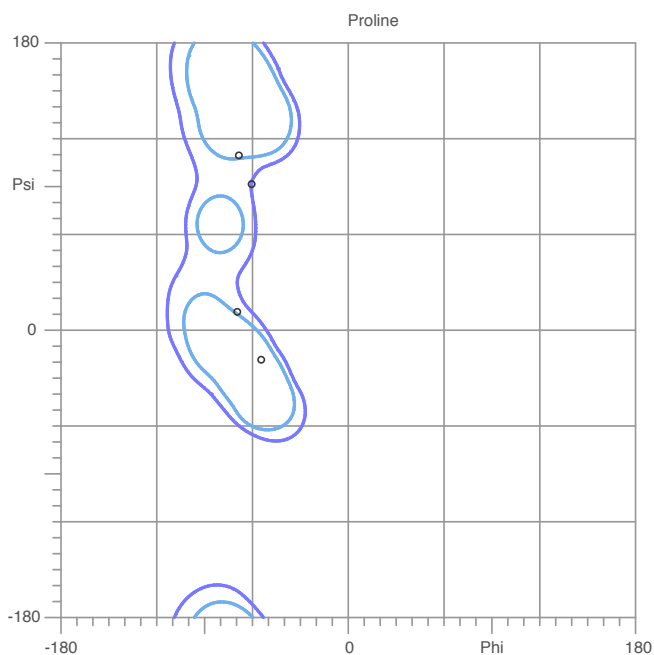
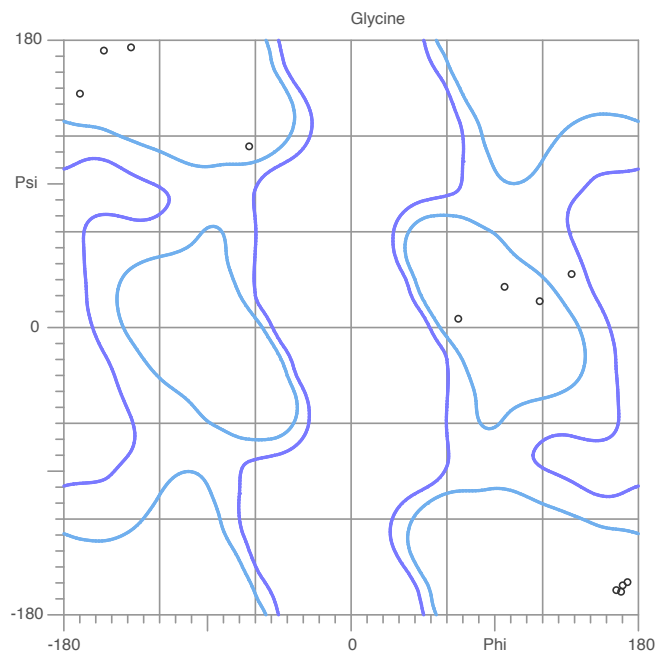
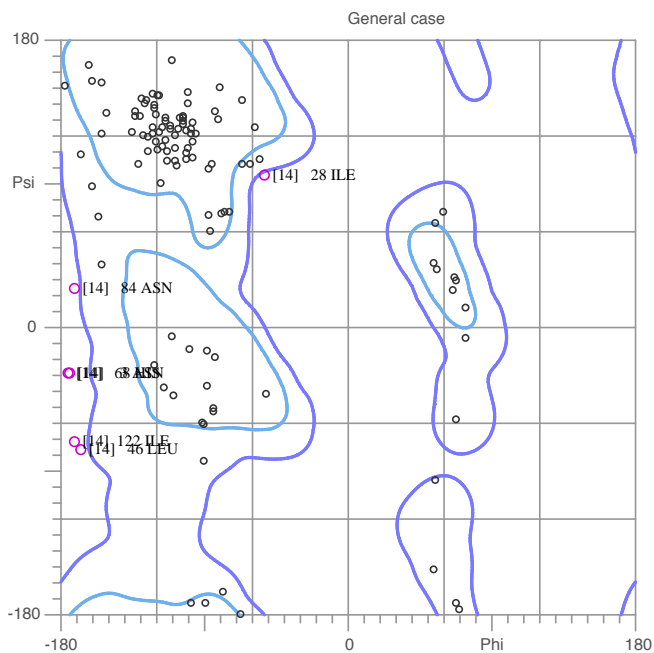
85.5% (118/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [13] 47 LYS (67.6, -85.2)
- [13] 69 HIS (178.4, -17.4)
- [13] 123 LYS (67.3, -85.7)
- [13] 150 HIS (174.2, 89.5)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 14



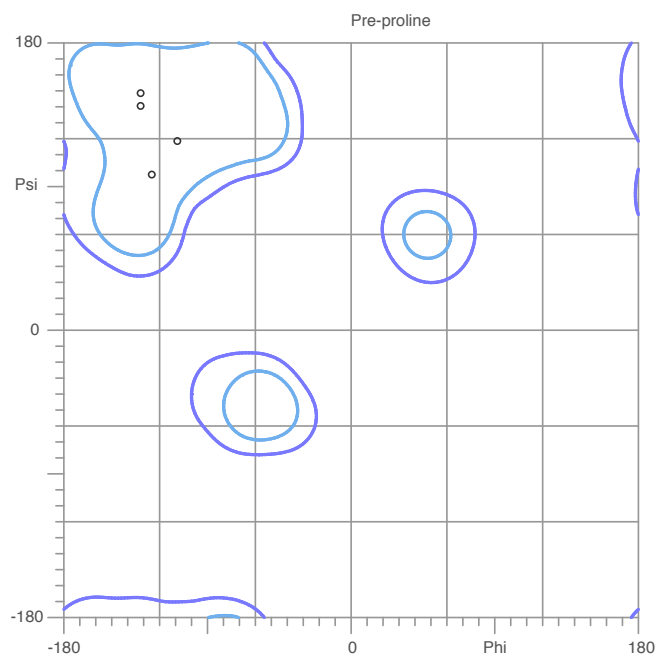
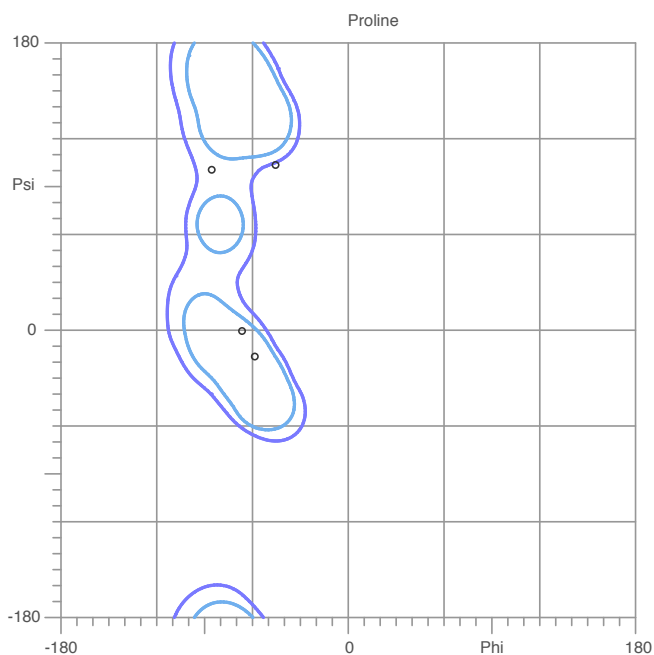
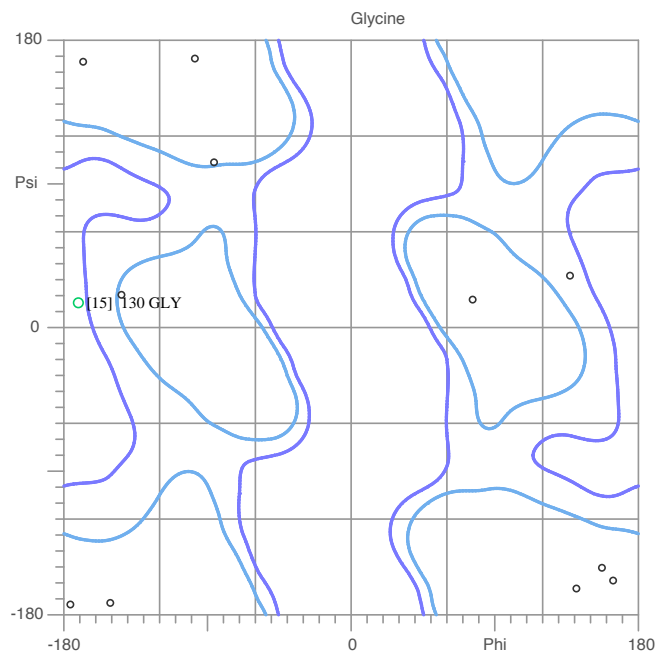
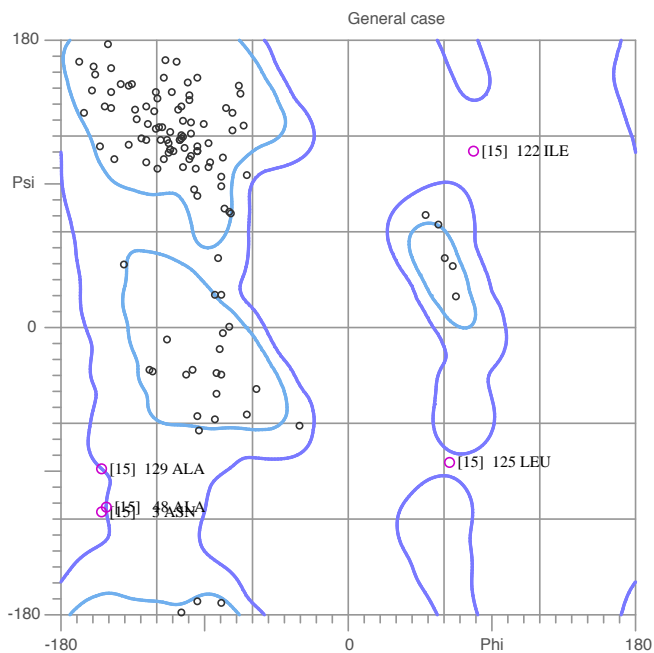
80.4% (111/138) of all residues were in favored (98%) regions.
95.7% (132/138) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[14] 3 ASN (-175.6, -28.5)

[14] 28 ILE (-53.0, 96.2)
[14] 46 LEU (-168.7, -76.1)
[14] 68 HIS (-176.2, -28.5)
[14] 84 ASN (-172.7, 25.5)
[14] 122 ILE (-172.0, -71.5)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 15



87.0% (120/138) 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):

[15] 3 ASN (-155.3, -115.3)

[15] 48 ALA (-152.5, -112.6)

[15] 122 ILE (78.3, 111.5)

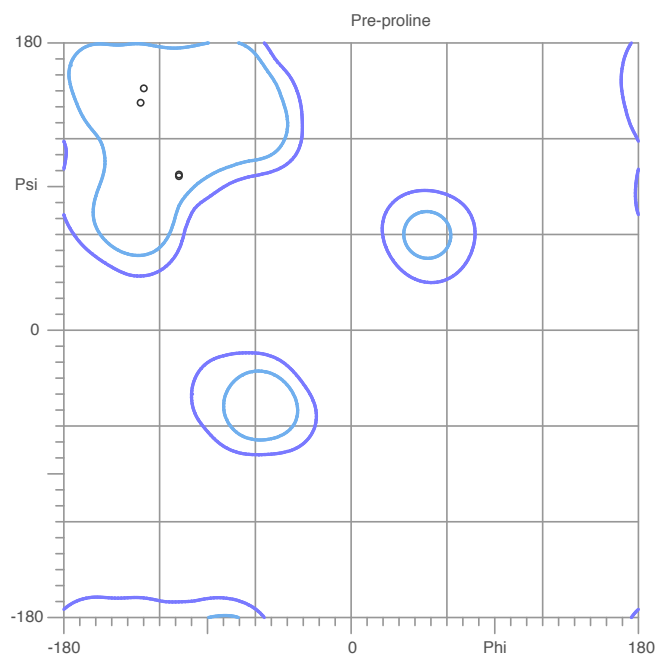
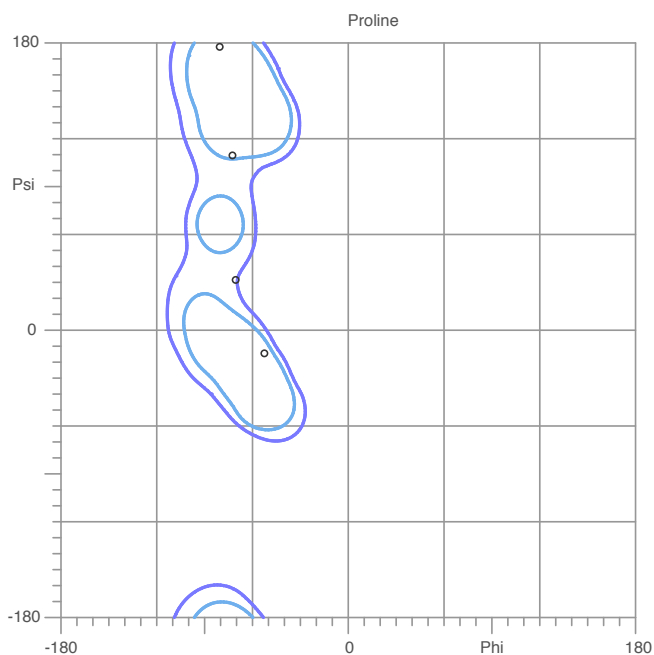
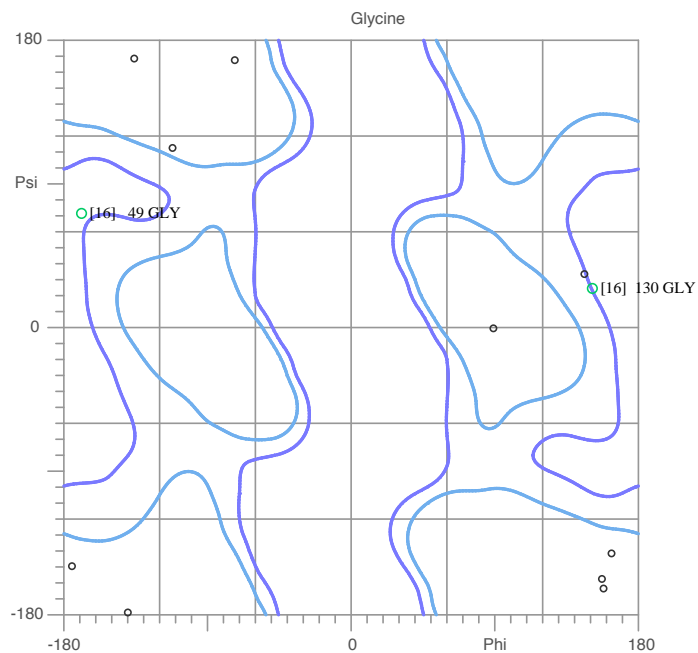
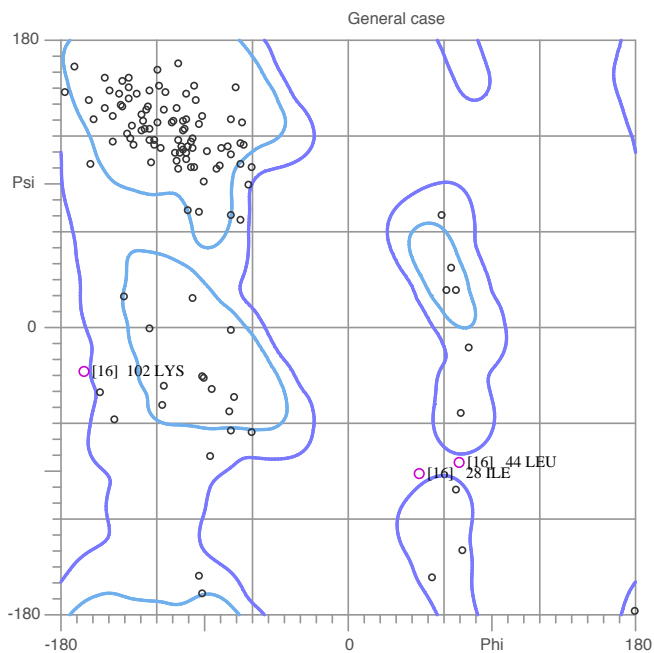
[15] 125 LEU (63.2, -85.0)

[15] 129 ALA (-155.1, -88.8)

[15] 130 GLY (-171.2, 16.2)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 16



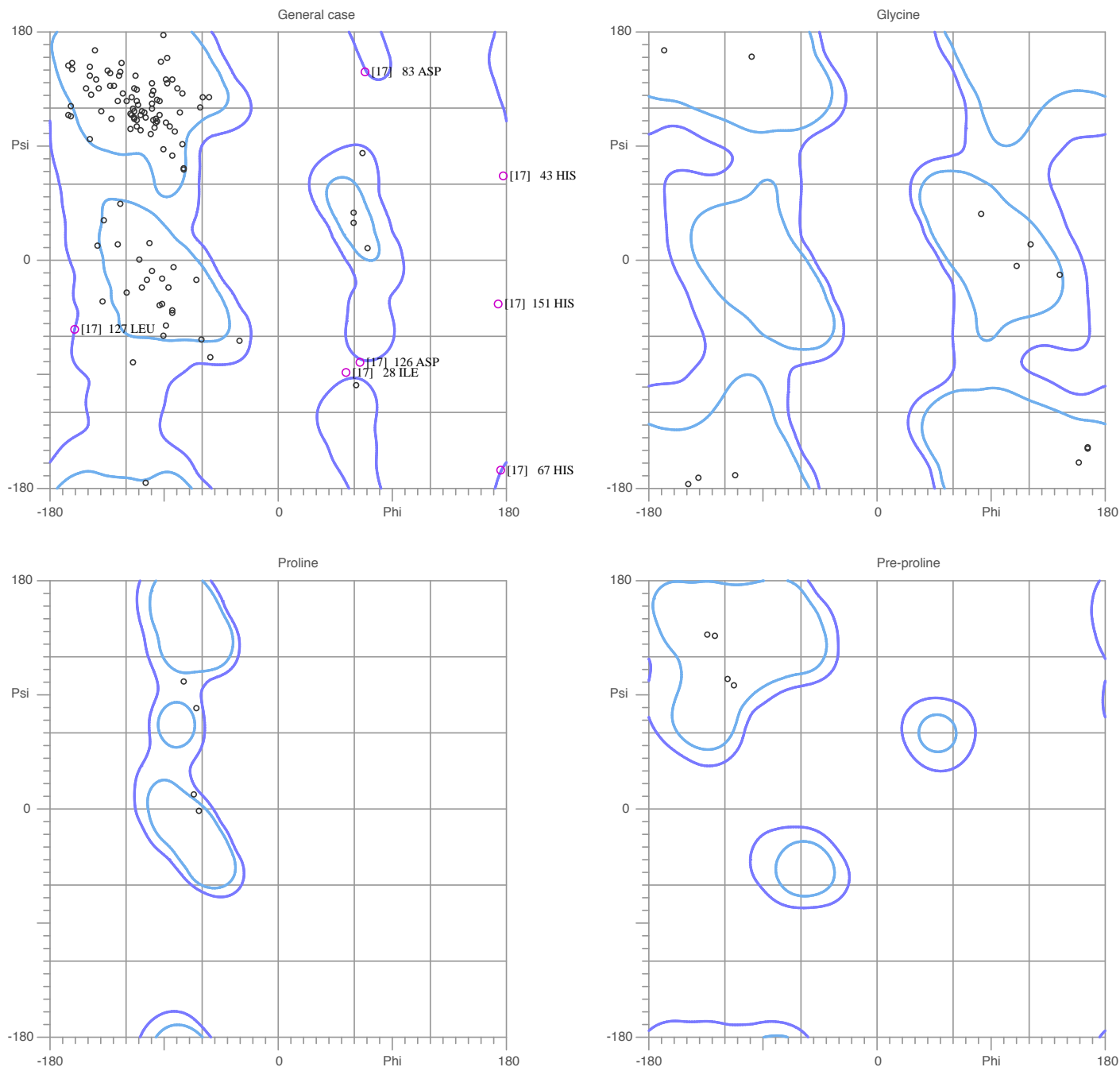
79.7% (110/138) of all residues were in favored (98%) regions.
96.4% (133/138) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[16] 28 ILE (44.3, -91.7)
[16] 44 LEU (69.8, -84.6)
[16] 49 GLY (-169.8, 72.1)
[16] 102 LYS (-166.1, -27.6)
[16] 130 GLY (151.8, 26.0)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 17



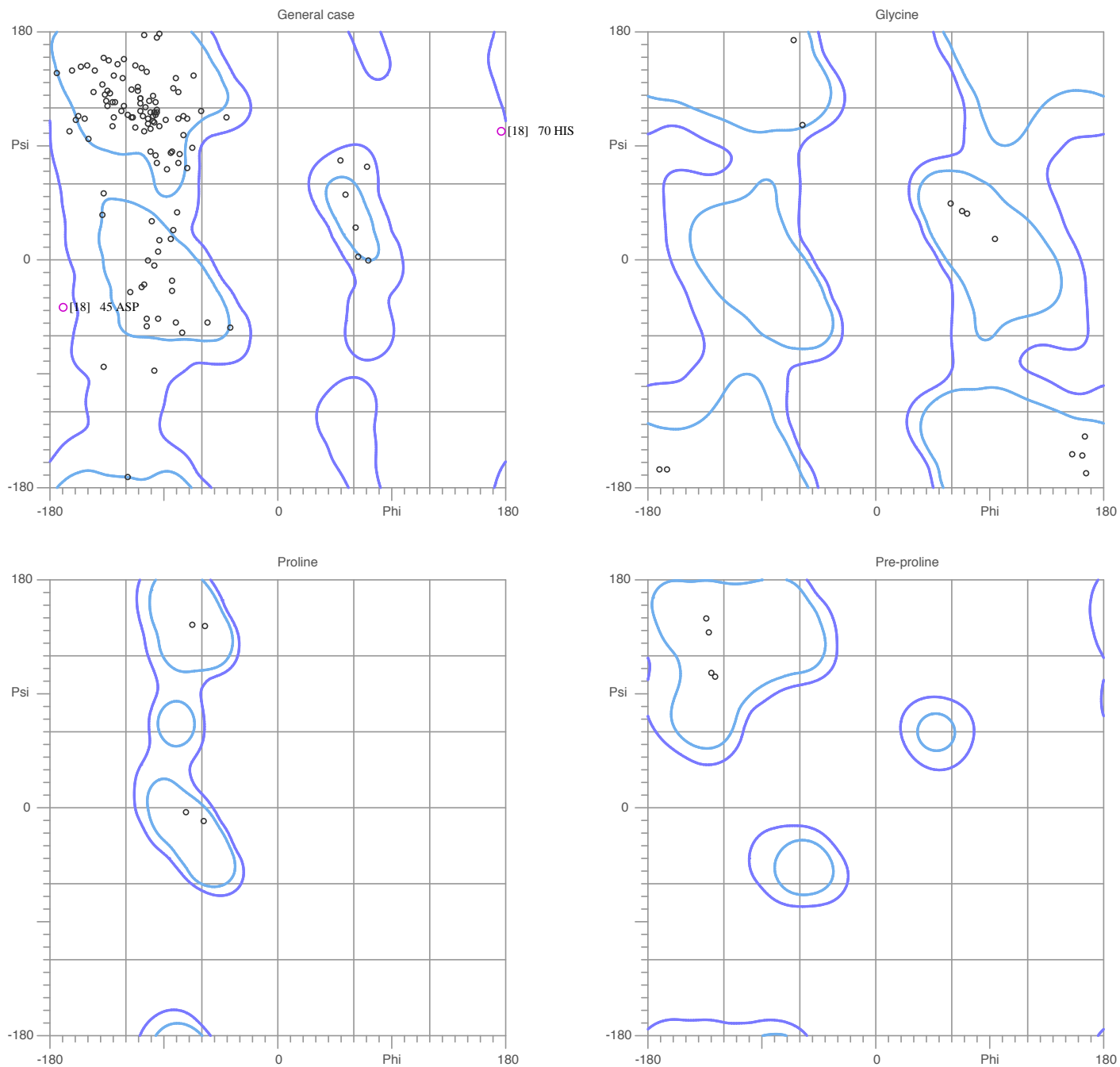
85.5% (118/138) of all residues were in favored (98%) regions.
94.9% (131/138) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[17] 28 ILE (53.4, -88.6)

[17] 43 HIS (177.6, 67.1)
[17] 67 HIS (175.4, -165.7)
[17] 83 ASP (68.7, 149.6)
[17] 126 ASP (64.0, -80.3)
[17] 127 LEU (-161.9, -54.6)
[17] 151 HIS (173.9, -34.3)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 18

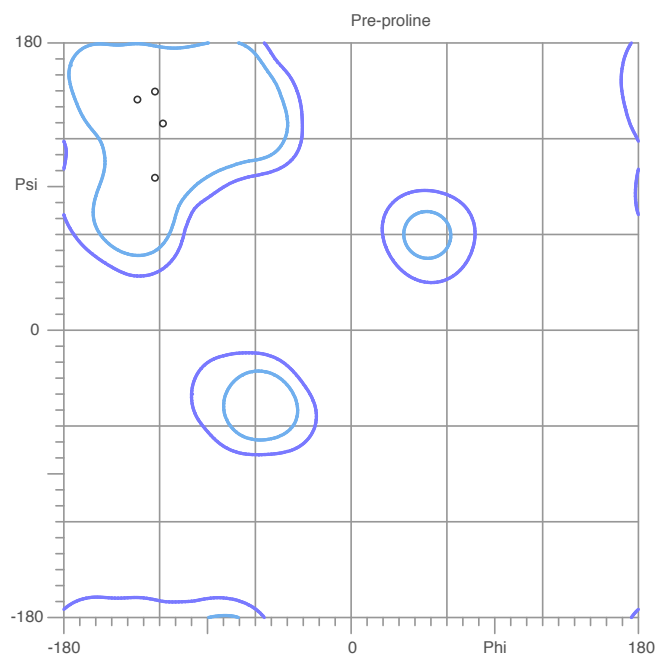
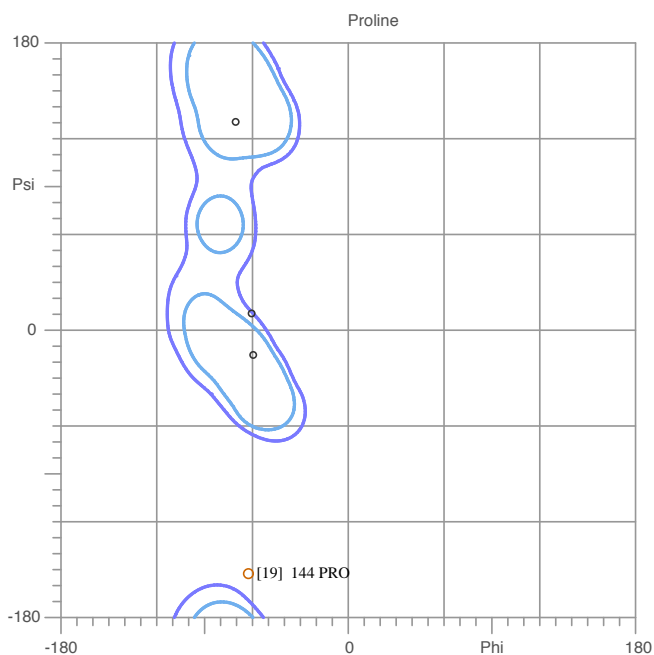
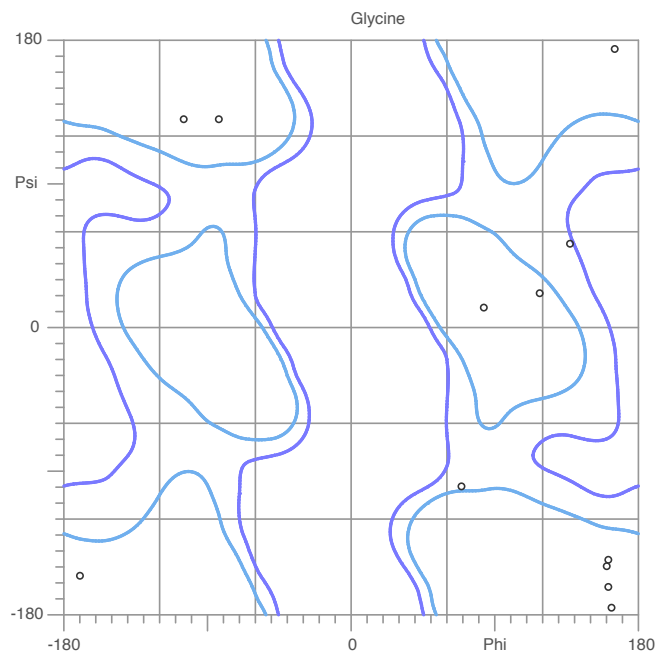
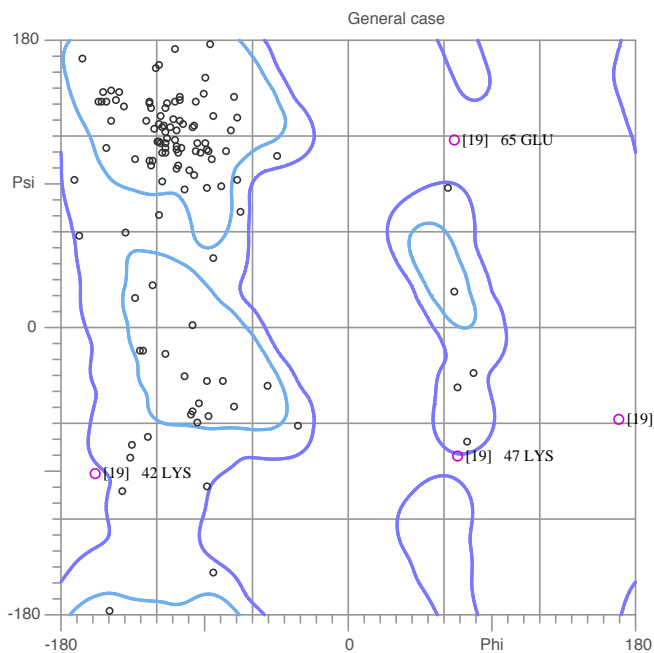


86.2% (119/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 45 ASP (-170.0, -37.5)
[18] 70 HIS (176.4, 102.6)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 19



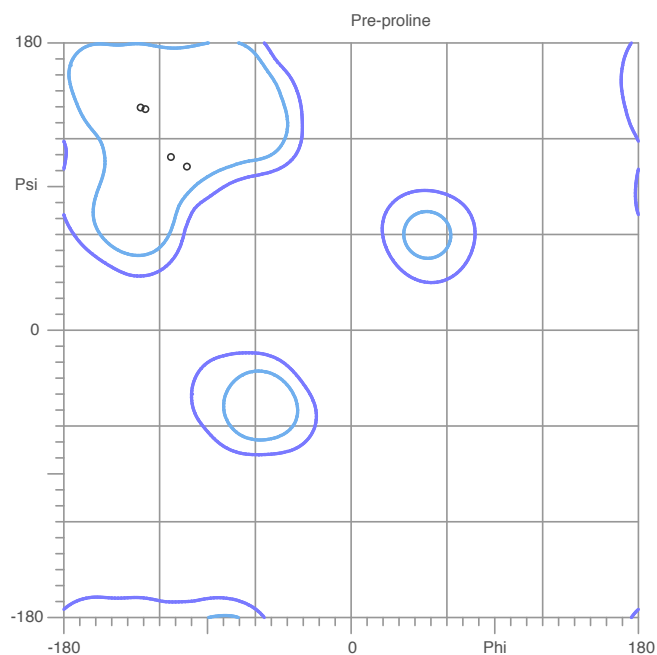
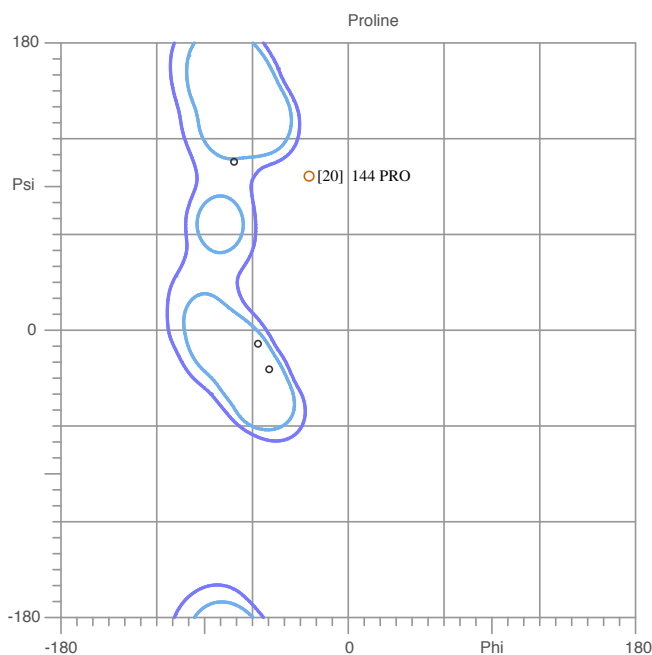
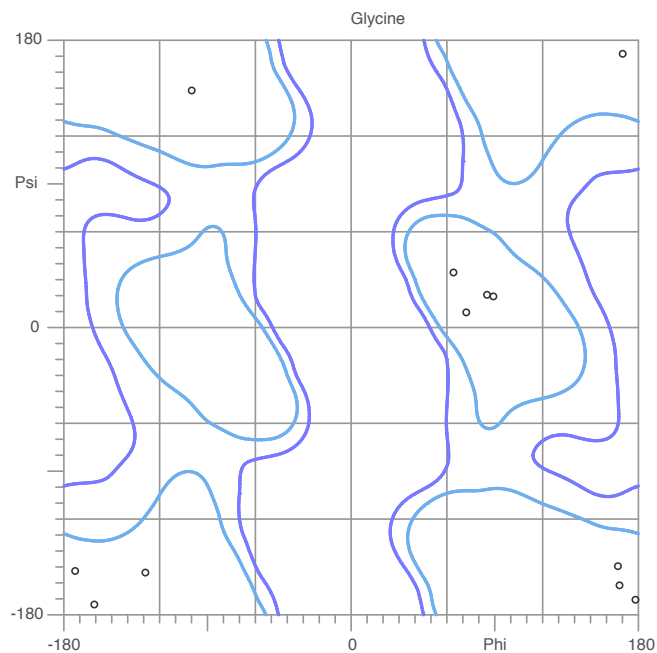
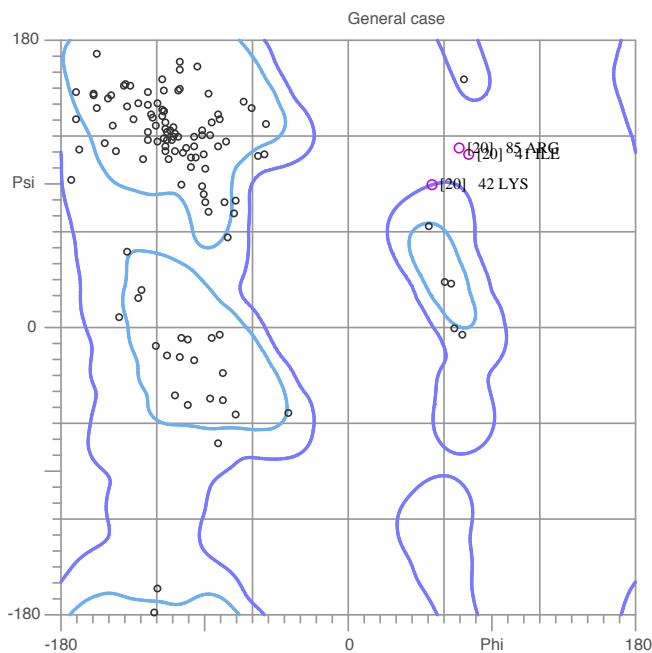
80.4% (111/138) of all residues were in favored (98%) regions.
96.4% (133/138) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[19] 42 LYS (-159.1, -92.0)
[19] 43 HIS (169.2, -57.2)
[19] 47 LYS (68.8, -80.5)
[19] 65 GLU (66.6, 118.0)
[19] 144 PRO (-63.6, -153.0)

MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 20



84.8% (117/138) 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):

- [20] 41 ILE (75.8, 109.5)
- [20] 42 LYS (53.0, 90.3)
- [20] 85 ARG (69.7, 113.3)
- [20] 144 PRO (-25.2, 97.9)