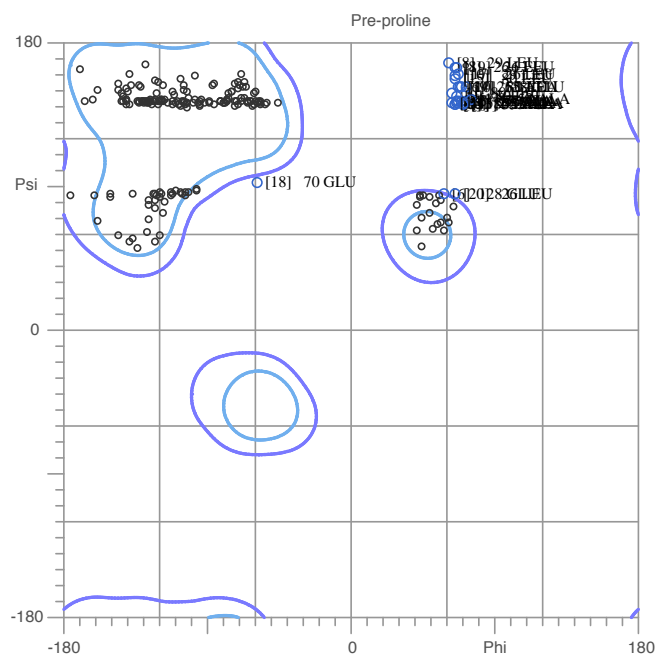
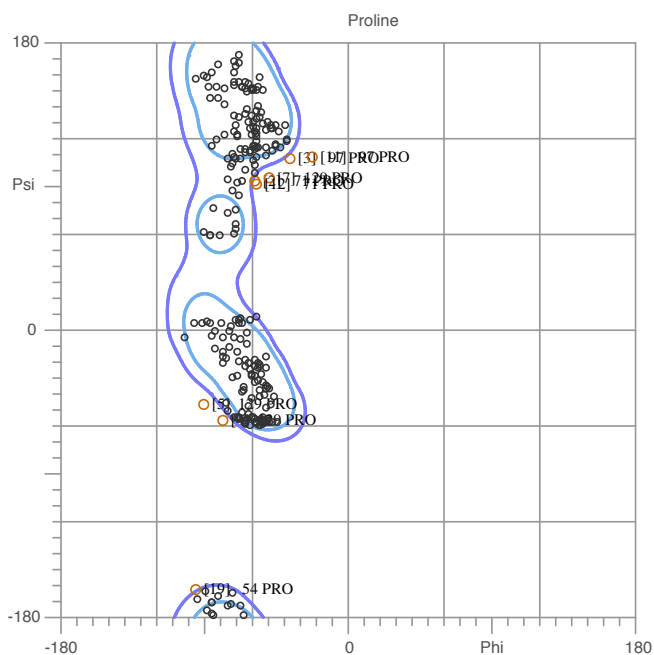
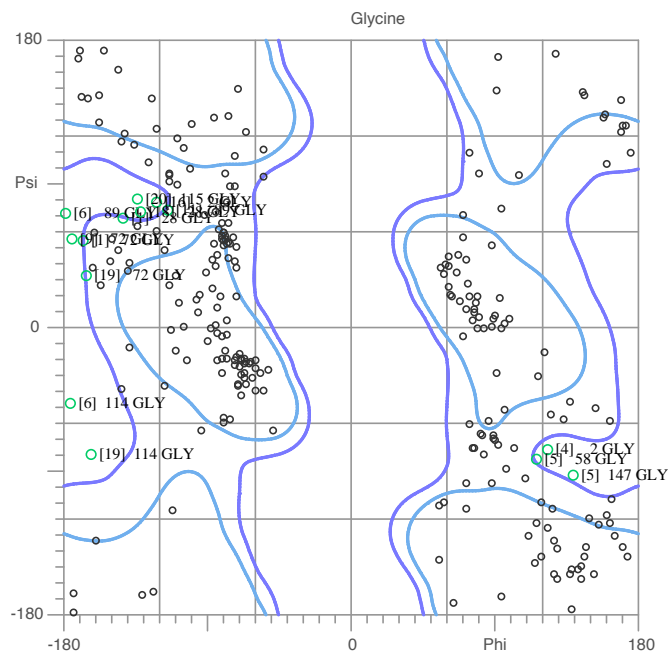
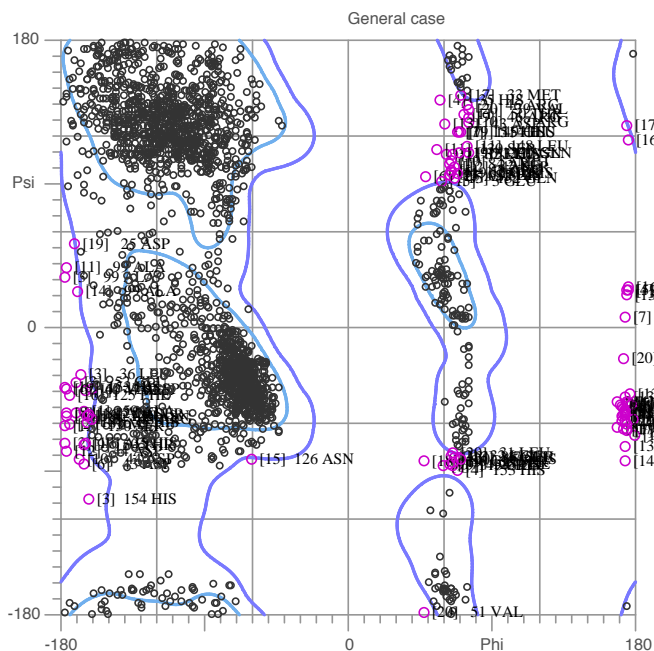


MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, all models

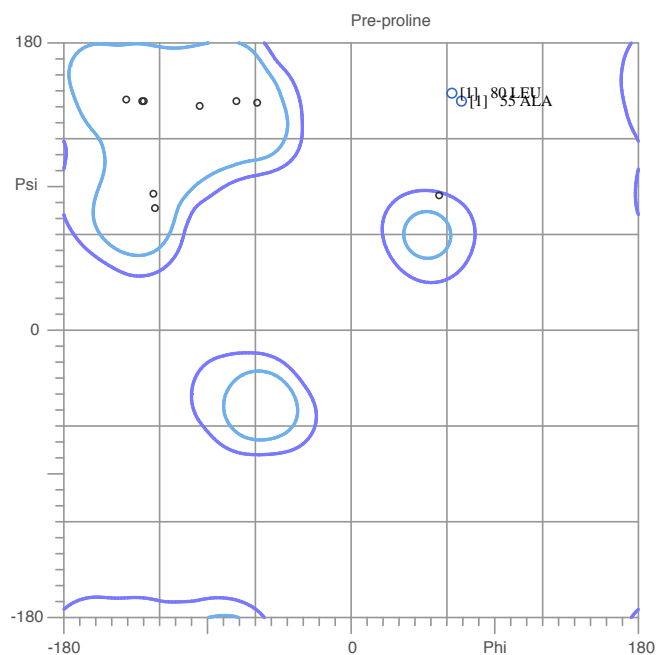
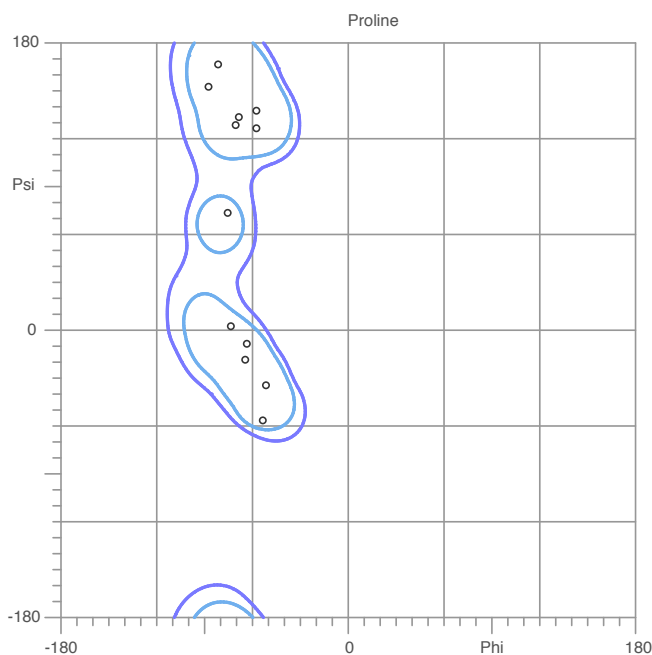
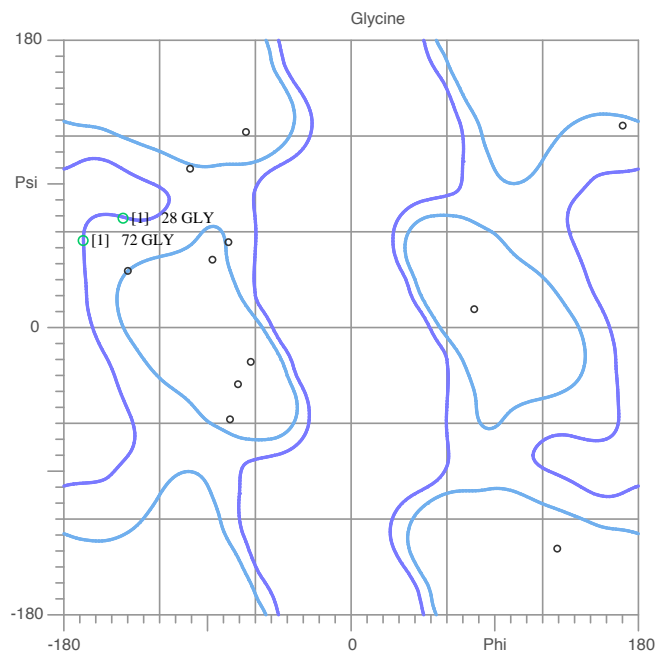
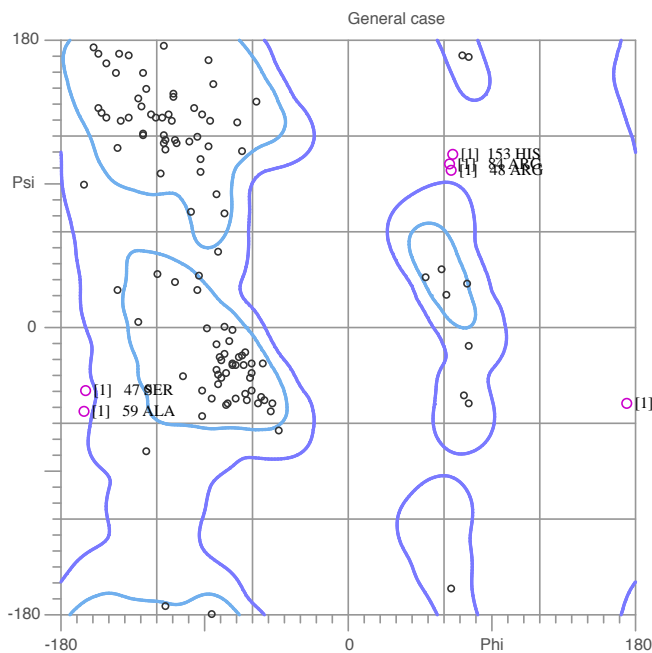


DRR147D_NMR_em_bcr3.pdb, all models

Residue	Phi (deg)	Psi (deg)
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2	100	100
3	100	100
4	100	100
5	100	100
6	100	100
7	100	100
8	100	100
9	100	100
10	100	100
11	100	100
12	100	100
13	100	100
14	100	100
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91	100	100
92	100	100
93	100	100
94	100	100
95	100	100
96	100	100
97	100	100
98	100	100
99	100	100
100	100	100

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 1



82.4% (126/153) of all residues were in favored (98%) regions.
 93.5% (143/153) of all residues were in allowed (>99.8%) regions.

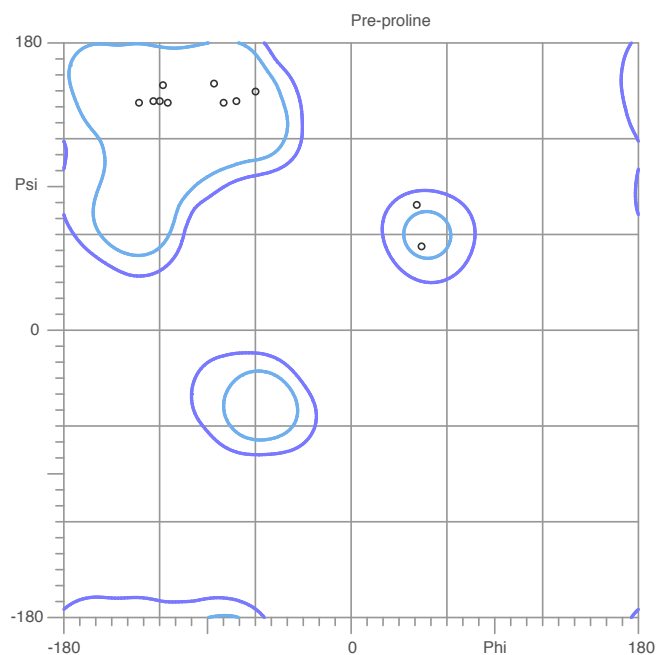
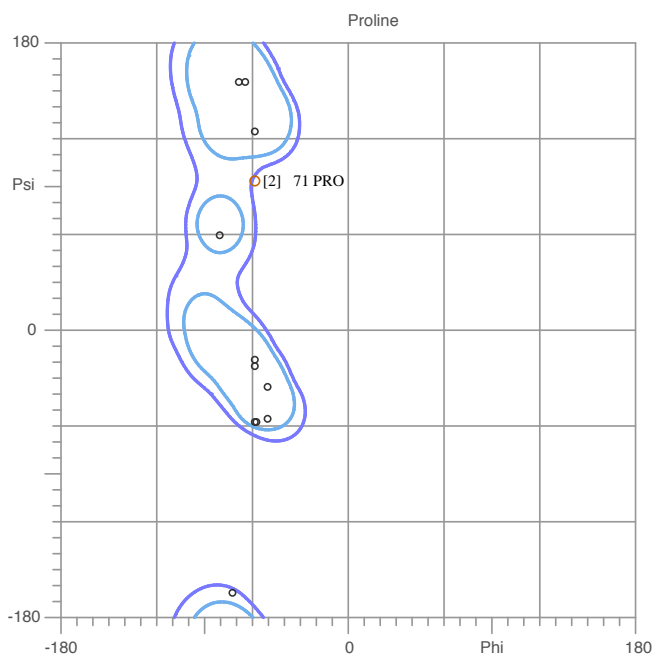
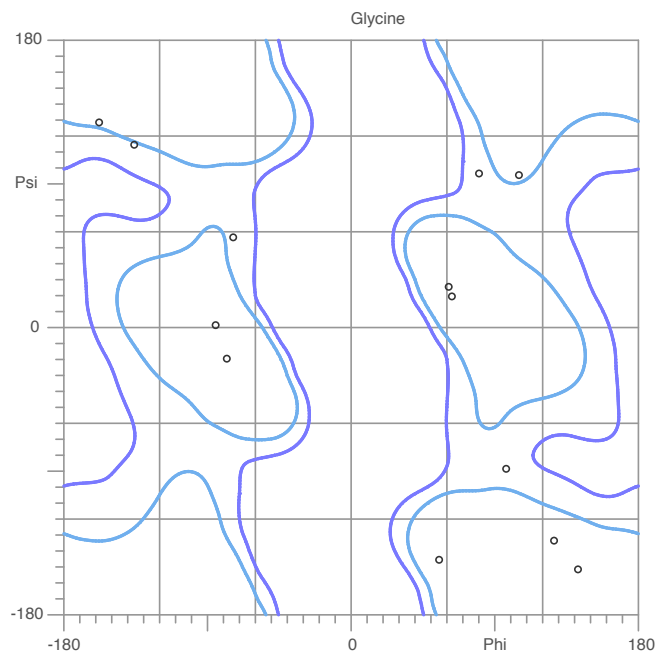
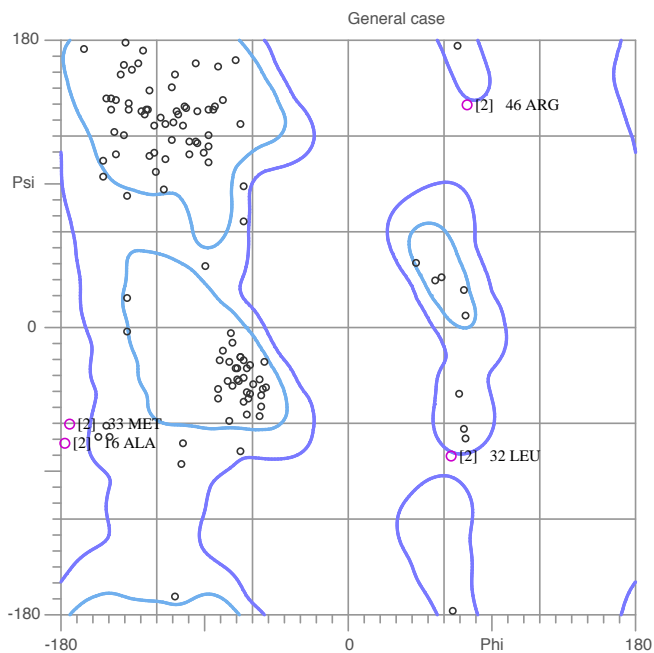
There were 10 outliers (phi, psi):

- [1] 16 ALA (174.0, -47.5)
- [1] 28 GLY (-143.7, 70.0)
- [1] 47 SER (-165.1, -39.1)

- [1] 48 ARG (64.3, 99.8)
- [1] 55 ALA (69.2, 144.6)
- [1] 59 ALA (-166.7, -52.9)
- [1] 72 GLY (-168.7, 55.7)
- [1] 80 LEU (64.0, 149.6)
- [1] 84 ARG (63.3, 103.9)
- [1] 153 HIS (65.9, 109.0)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 2



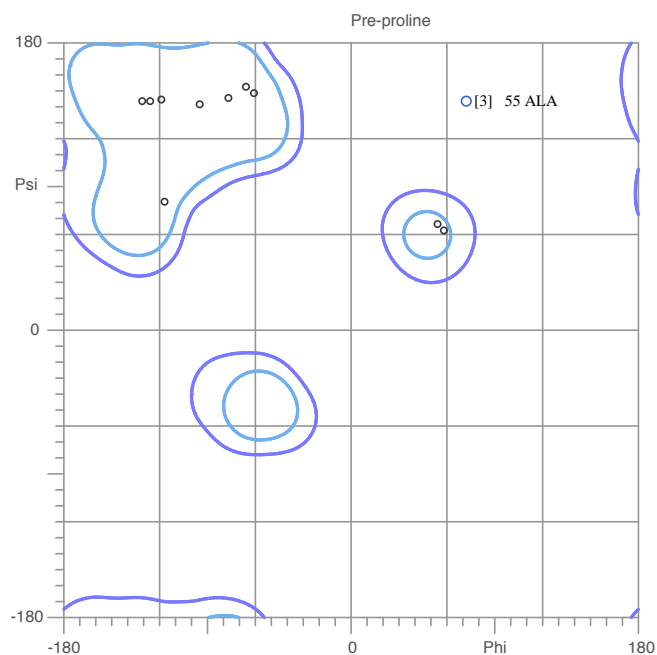
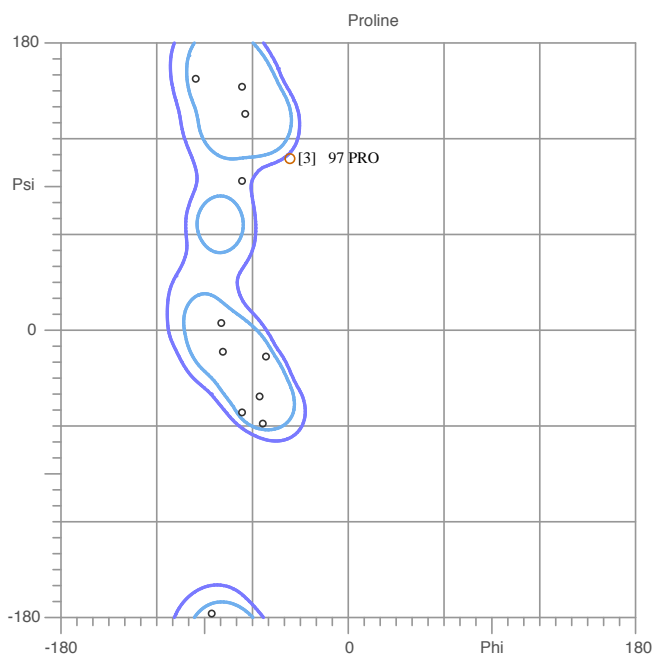
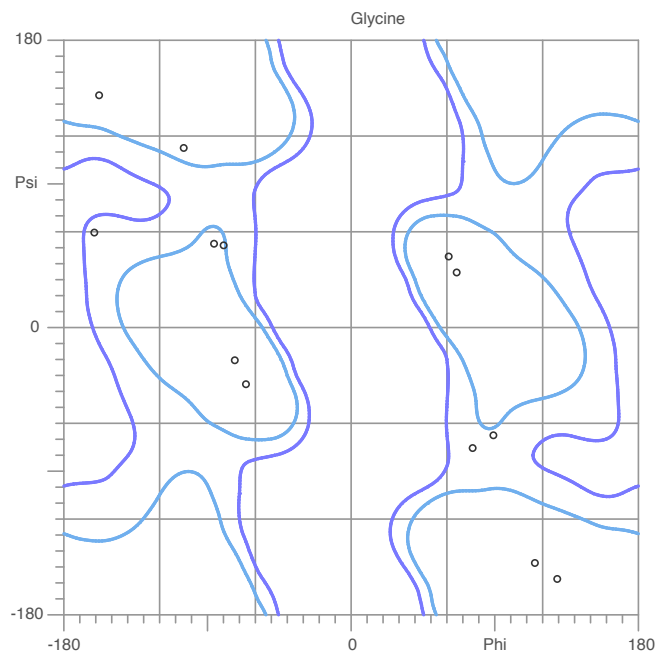
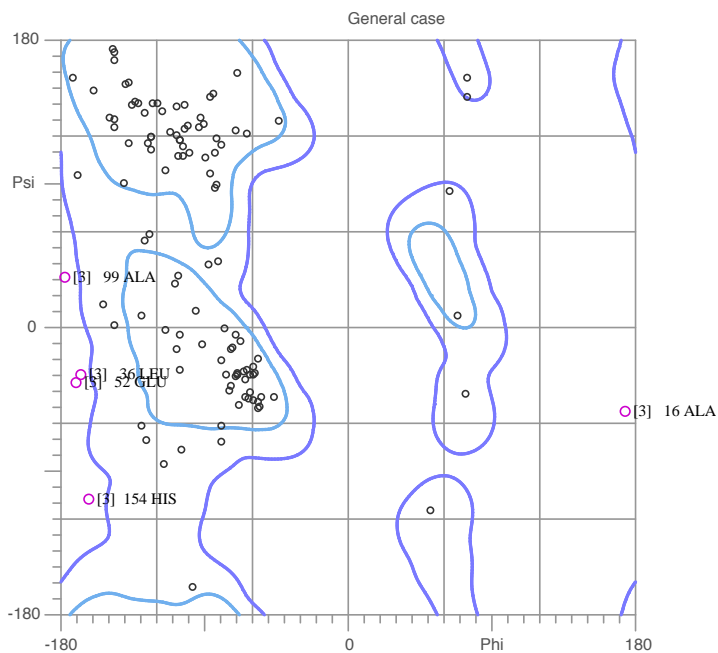
81.0% (124/153) of all residues were in favored (98%) regions.
96.7% (148/153) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[2] 16 ALA (-178.3, -72.9)
[2] 32 LEU (64.5, -80.1)
[2] 33 MET (-175.4, -60.9)
[2] 46 ARG (74.5, 140.2)
[2] 71 PRO (-59.8, 94.4)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 3



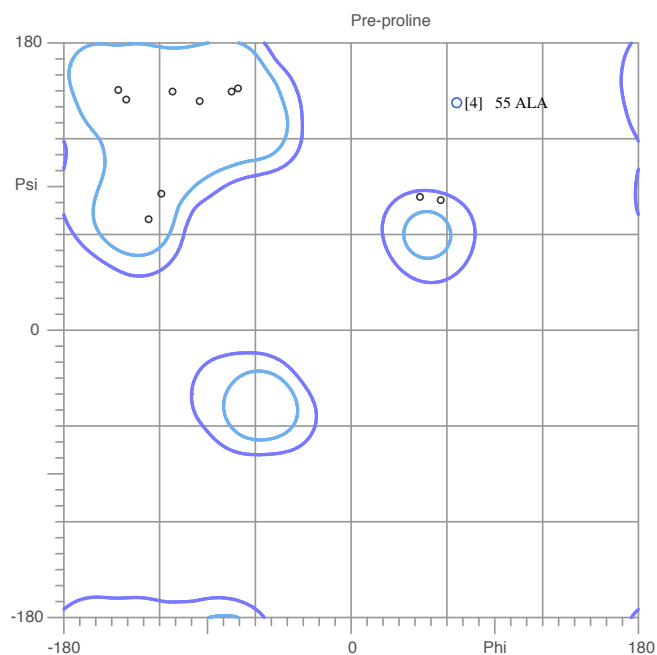
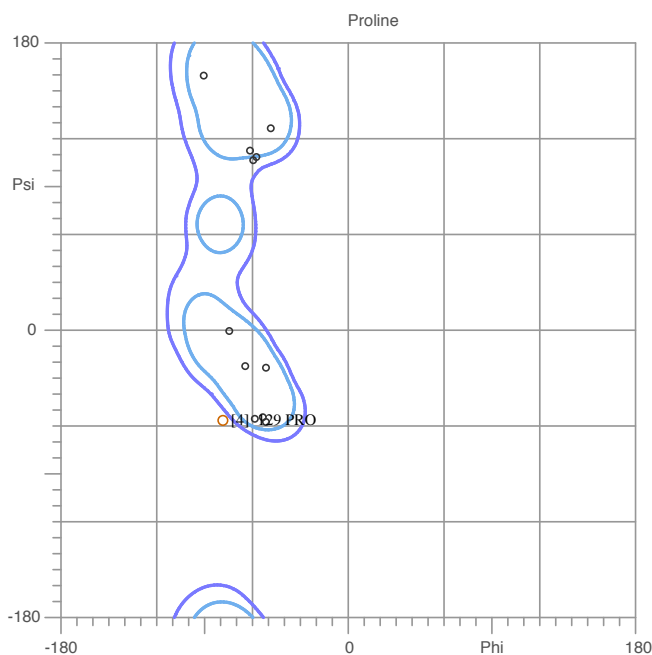
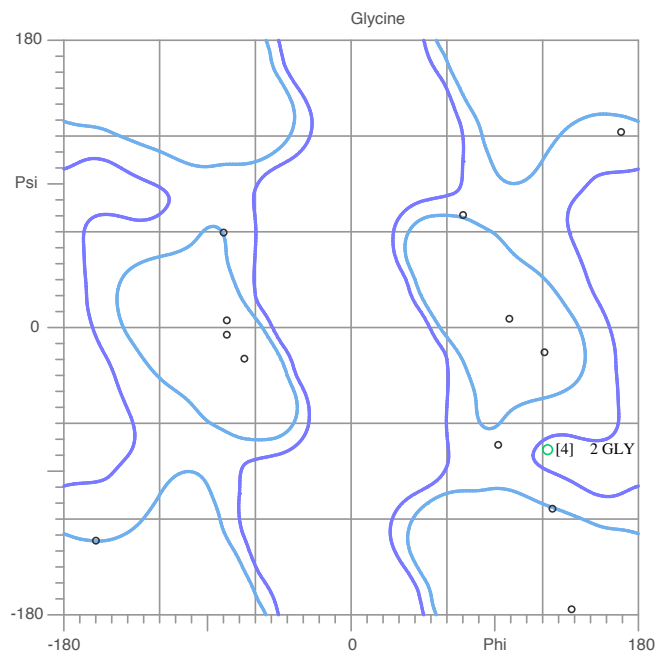
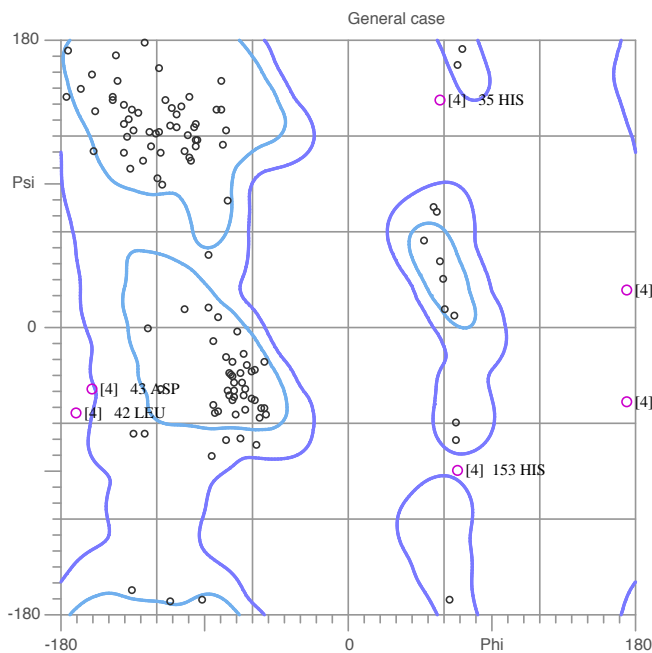
81.0% (124/153) of all residues were in favored (98%) regions.
 95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
 [3] 16 ALA (173.6, -52.9)

[3] 36 LEU (-168.0, -29.5)
 [3] 52 GLU (-171.3, -34.1)
 [3] 55 ALA (72.2, 144.1)
 [3] 97 PRO (-37.8, 108.9)
 [3] 99 ALA (-178.3, 32.1)
 [3] 154 HIS (-163.7, -107.9)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 4



77.1% (118/153) of all residues were in favored (98%) regions.
94.1% (144/153) of all residues were in allowed (>99.8%) regions.

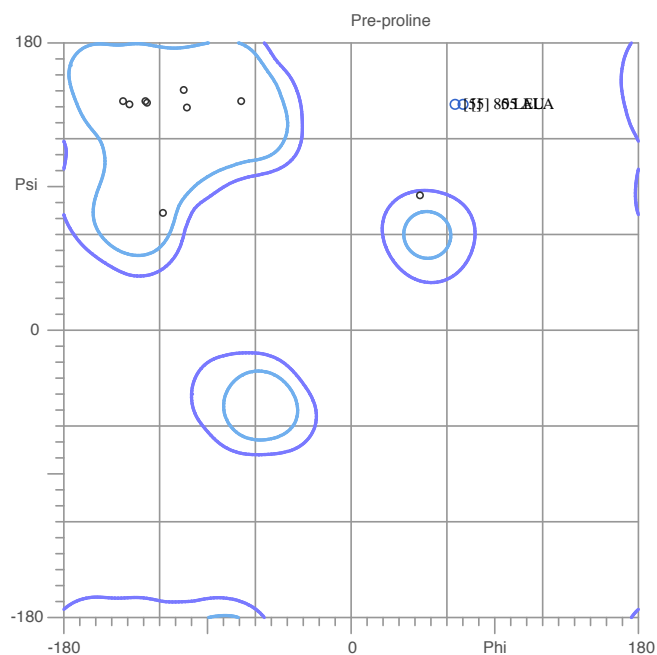
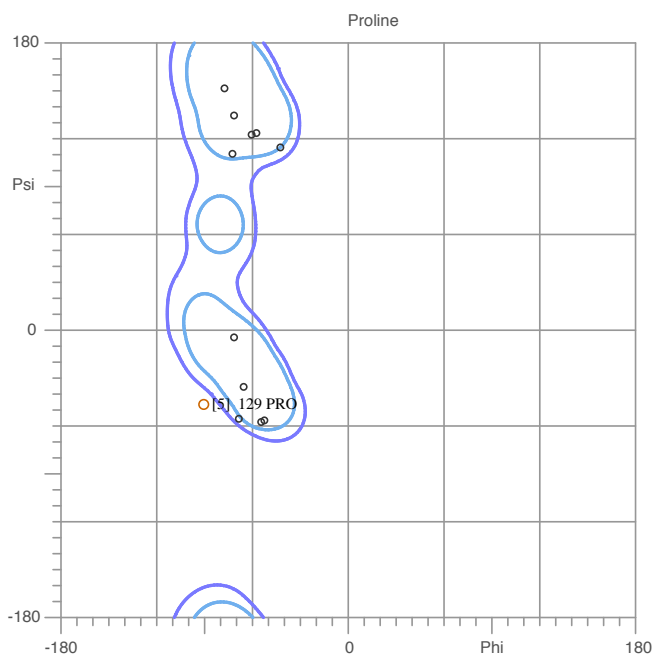
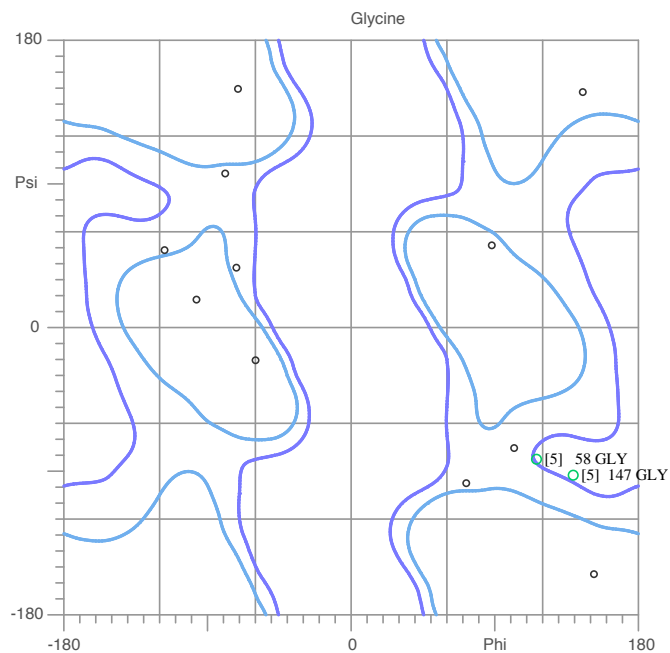
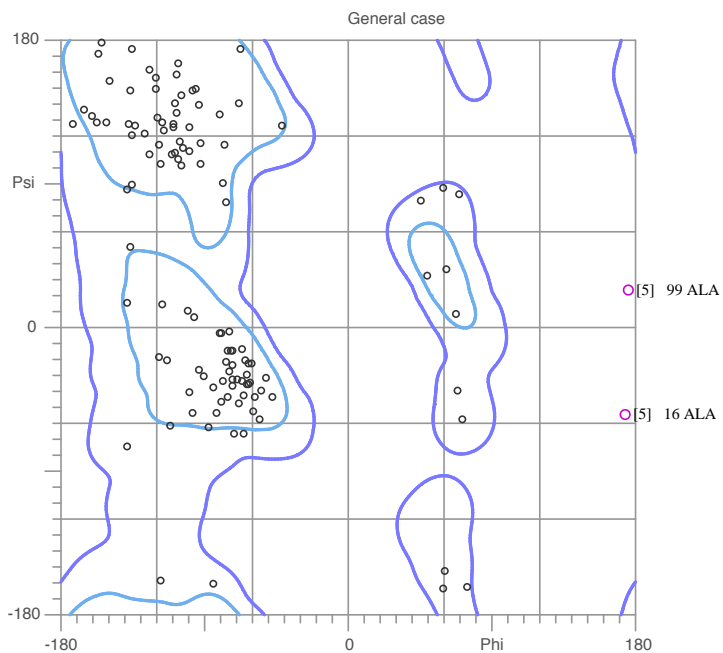
There were 9 outliers (phi, psi):

- [4] 2 GLY (123.0, -76.9)
- [4] 16 ALA (174.6, -46.7)

- [4] 35 HIS (57.6, 143.7)
- [4] 42 LEU (-171.8, -53.8)
- [4] 43 ASP (-161.1, -38.6)
- [4] 55 ALA (66.4, 143.3)
- [4] 99 ALA (174.3, 24.6)
- [4] 129 PRO (-79.0, -56.5)
- [4] 153 HIS (68.4, -89.3)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 5



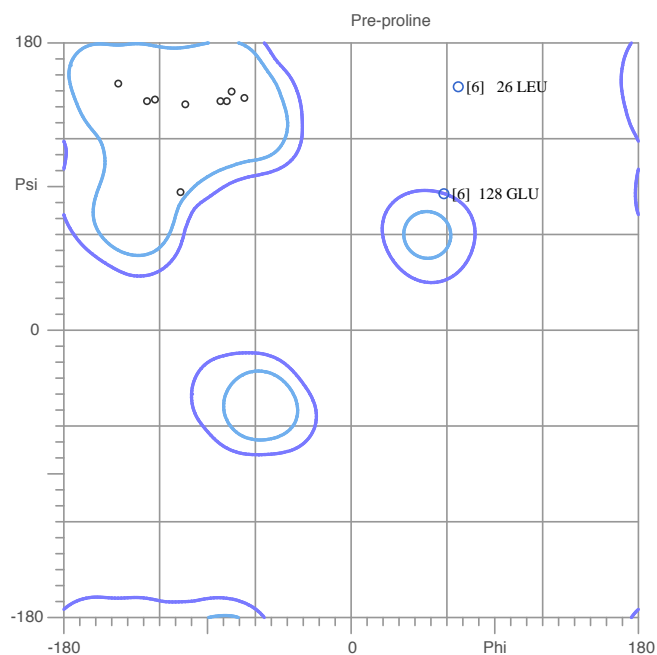
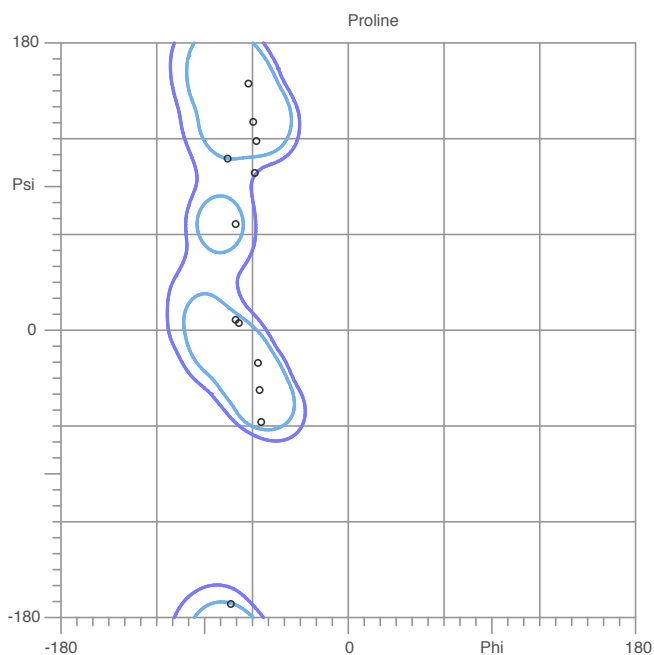
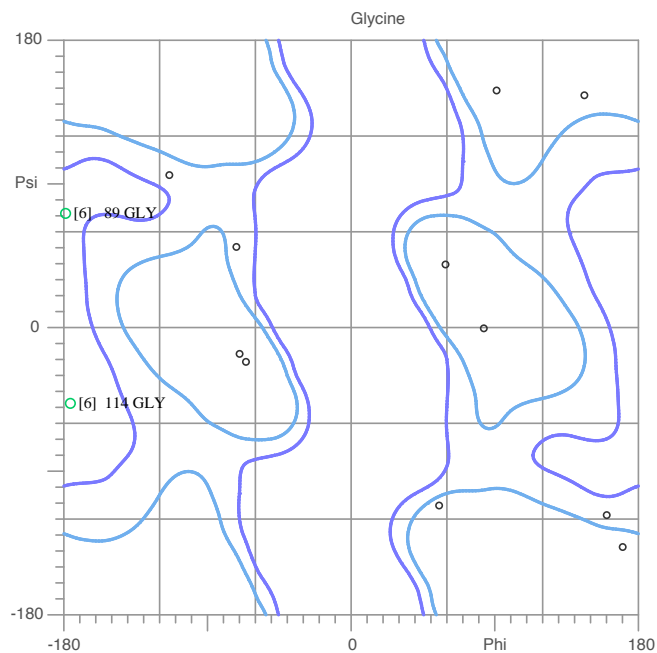
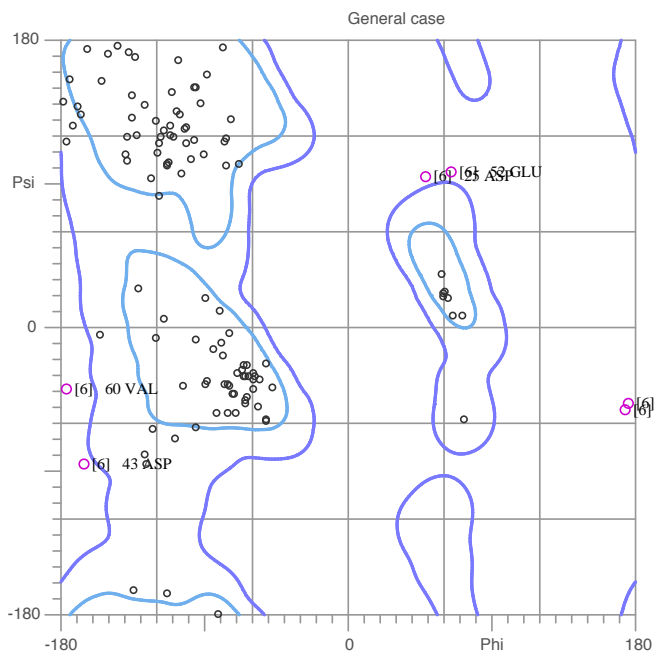
79.7% (122/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[5] 16 ALA (173.3, -54.1)

[5] 55 ALA (70.3, 142.4)
[5] 58 GLY (116.8, -82.7)
[5] 80 LEU (65.3, 142.2)
[5] 99 ALA (175.1, 24.2)
[5] 129 PRO (-91.7, -46.8)
[5] 147 GLY (139.5, -92.8)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 6



82.4% (126/153) of all residues were in favored (98%) regions.
93.5% (143/153) of all residues were in allowed (>99.8%) regions.

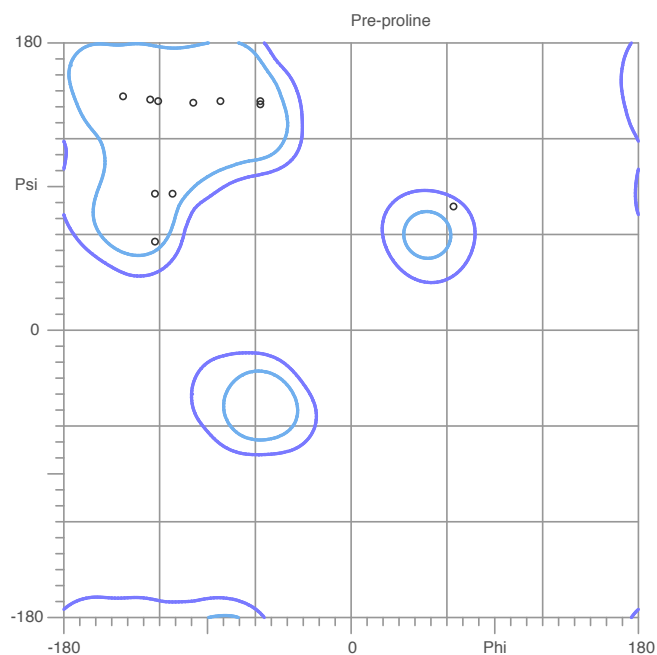
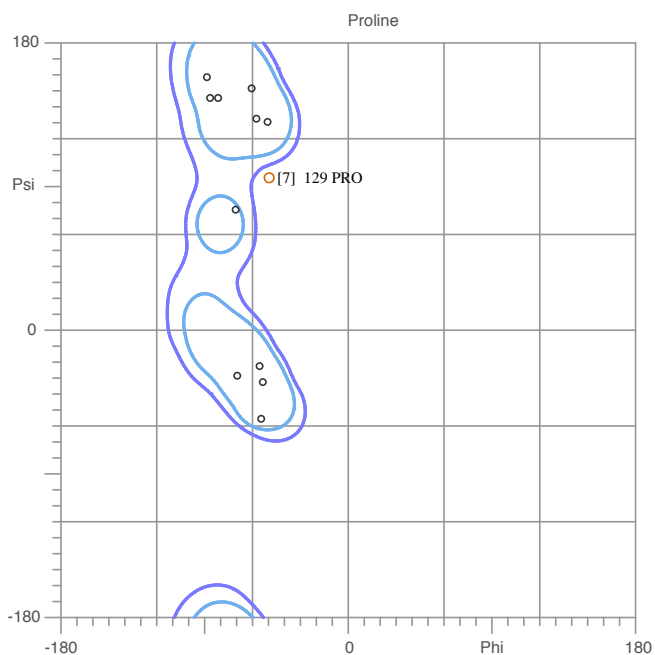
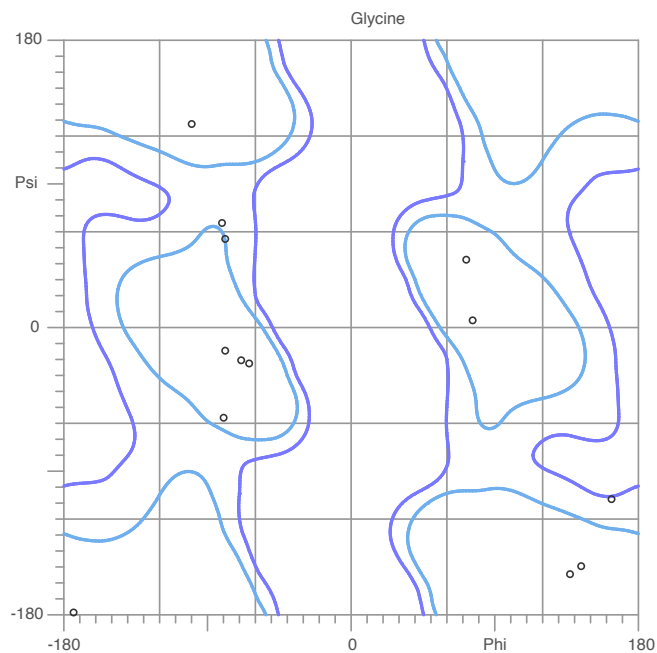
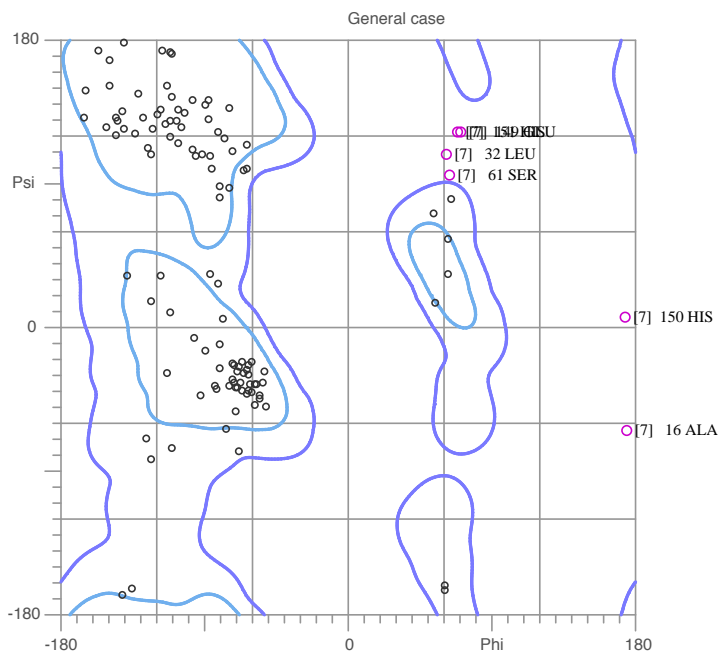
There were 10 outliers (phi, psi):

- [6] 16 ALA (173.3, -51.4)
- [6] 25 ASP (48.6, 95.7)
- [6] 26 LEU (67.3, 153.8)

- [6] 43 ASP (-166.1, -85.4)
- [6] 44 ASP (175.4, -47.8)
- [6] 52 GLU (64.8, 98.9)
- [6] 60 VAL (-177.8, -38.5)
- [6] 89 GLY (-179.3, 72.3)
- [6] 114 GLY (-176.5, -47.4)
- [6] 128 GLU (58.5, 86.8)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 7



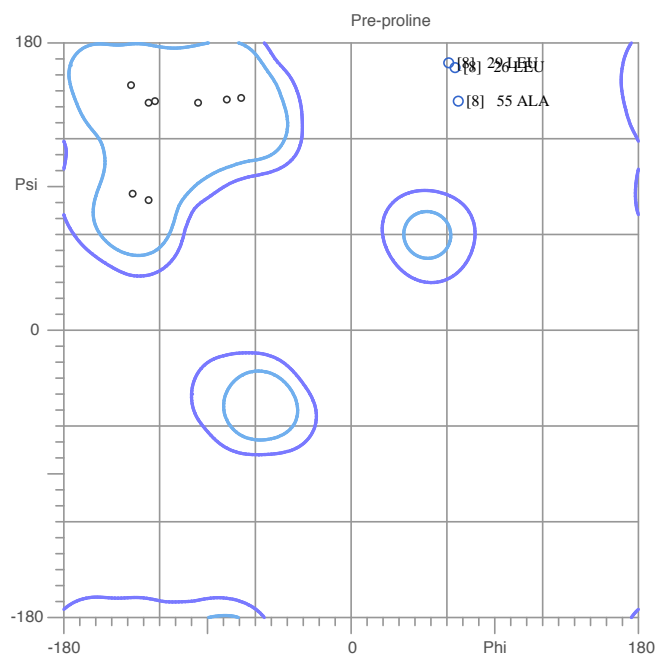
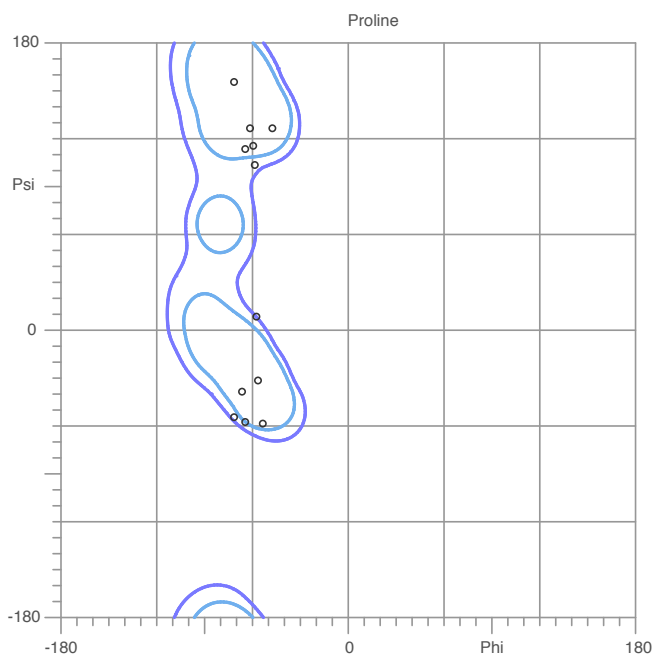
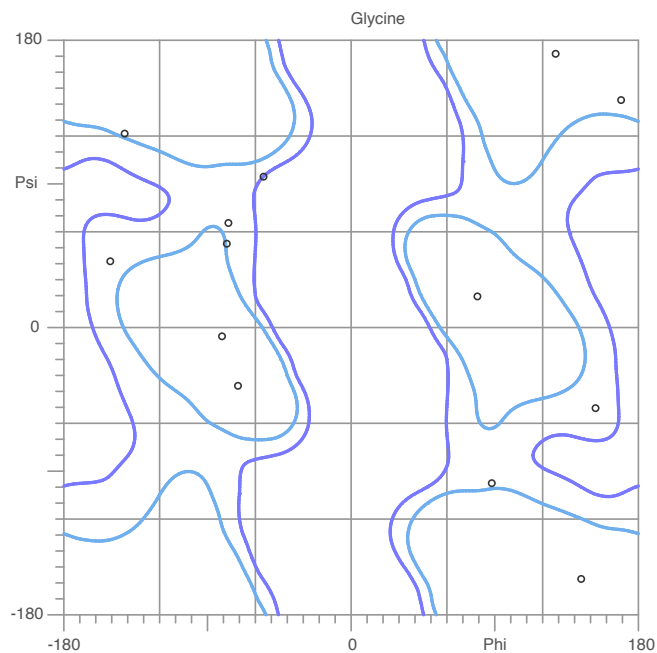
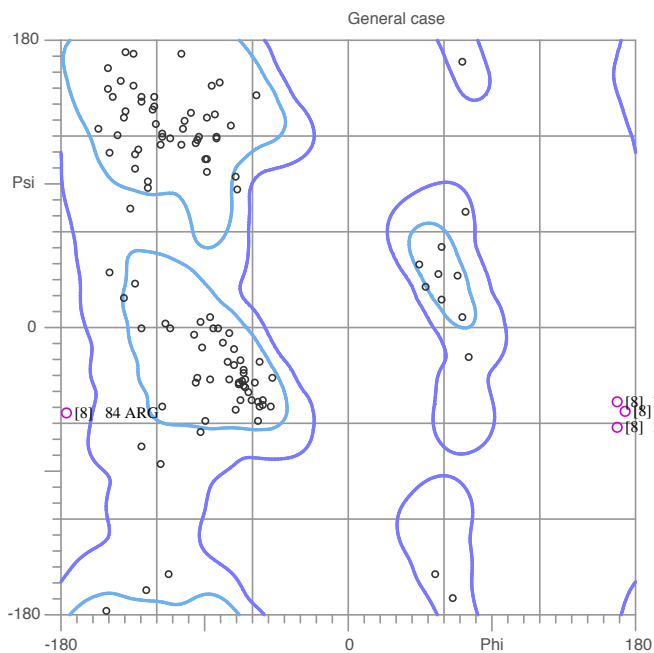
82.4% (126/153) of all residues were in favored (98%) regions.
 95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
 [7] 16 ALA (174.6, -64.0)

[7] 32 LEU (61.5, 109.8)
 [7] 61 SER (63.4, 96.7)
 [7] 129 PRO (-50.3, 96.1)
 [7] 149 GLU (70.3, 123.6)
 [7] 150 HIS (173.4, 7.5)
 [7] 151 HIS (68.7, 123.8)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 8



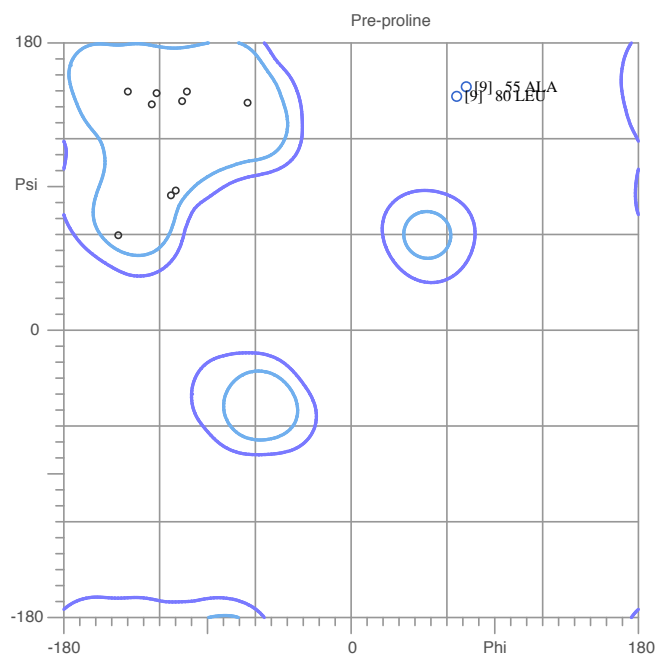
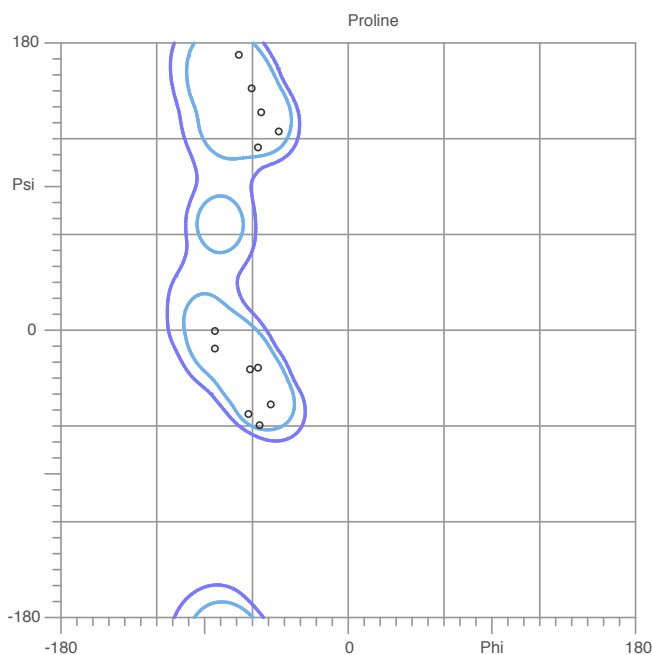
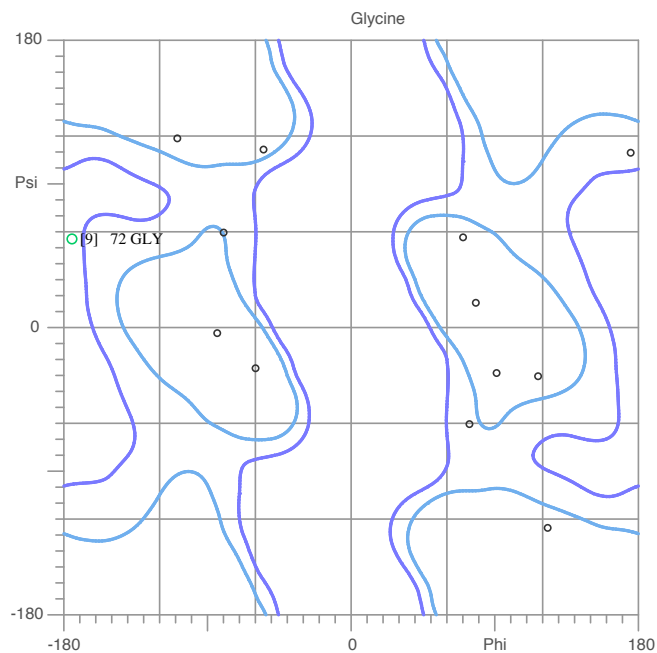
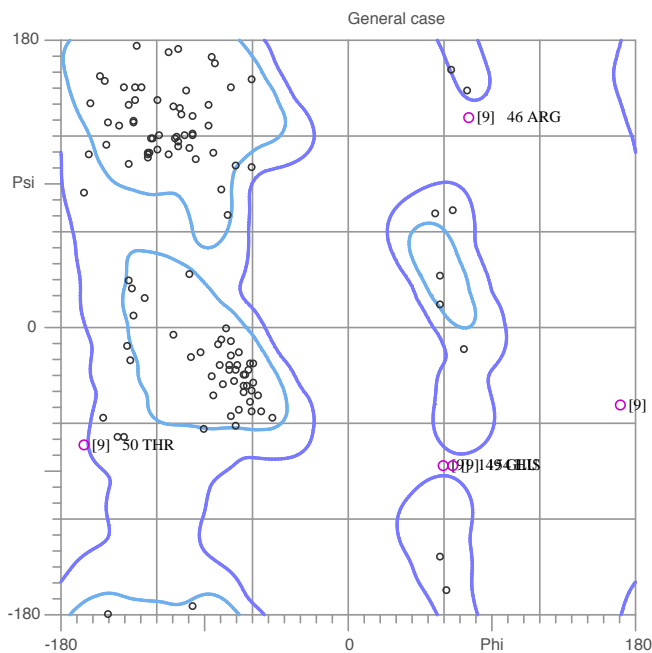
79.1% (121/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[8] 16 ALA (173.4, -53.0)

[8] 26 LEU (65.6, 165.4)
[8] 29 LEU (61.6, 168.1)
[8] 55 ALA (67.4, 144.1)
[8] 84 ARG (-177.5, -53.6)
[8] 153 HIS (168.9, -62.8)
[8] 154 HIS (168.3, -46.9)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 9



82.4% (126/153) of all residues were in favored (98%) regions.
94.8% (145/153) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[9] 16 ALA (170.7, -48.0)

[9] 46 ARG (75.5, 132.7)

[9] 50 THR (-166.3, -73.9)

[9] 55 ALA (72.5, 153.8)

[9] 72 GLY (-175.0, 56.9)

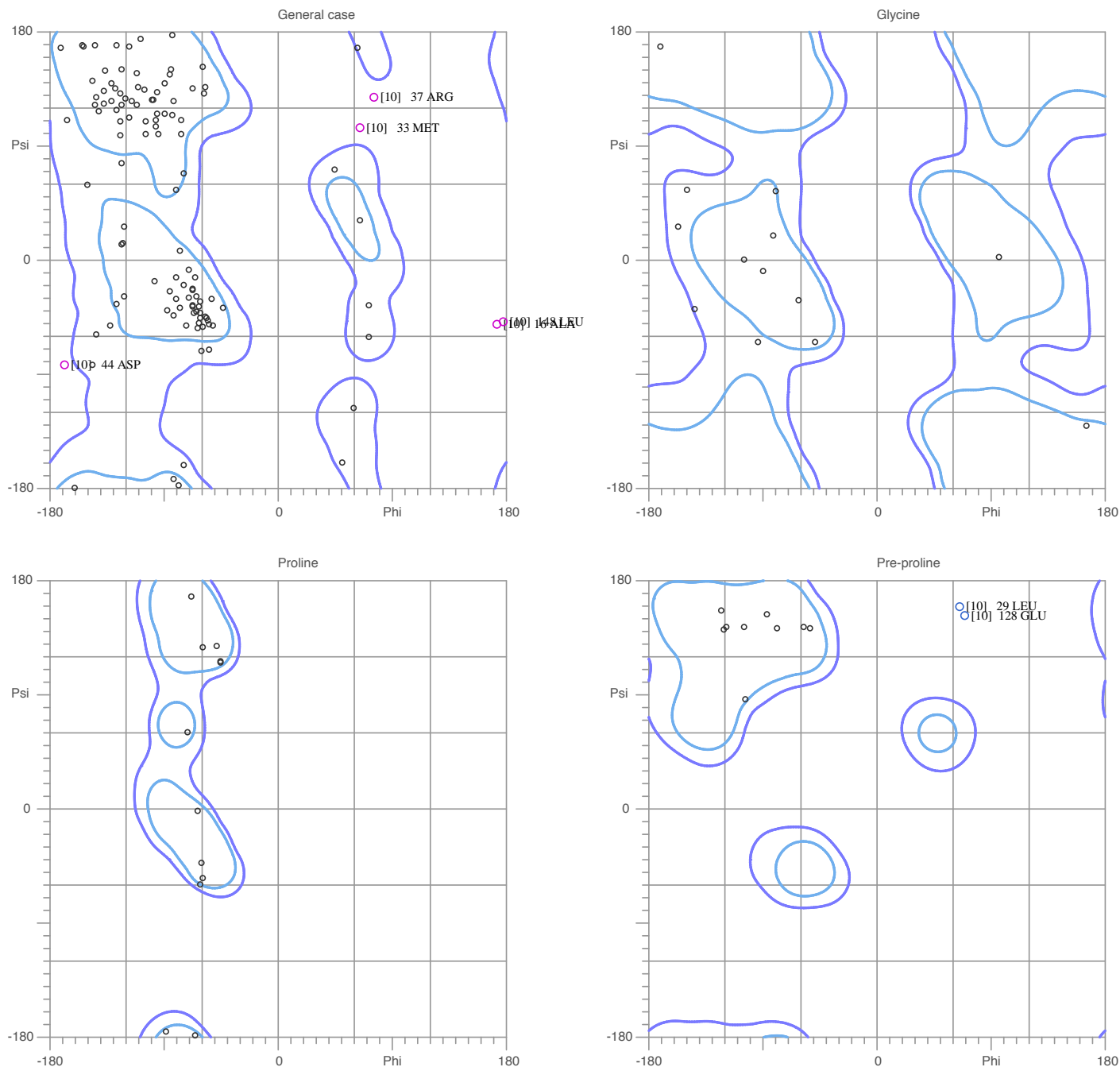
[9] 80 LEU (66.6, 147.0)

[9] 149 GLU (59.7, -86.8)

[9] 154 HIS (66.0, -86.3)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 10



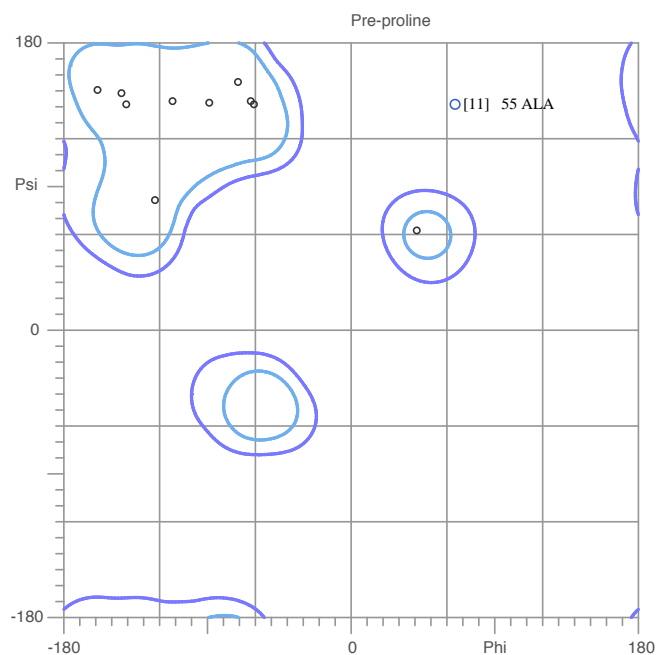
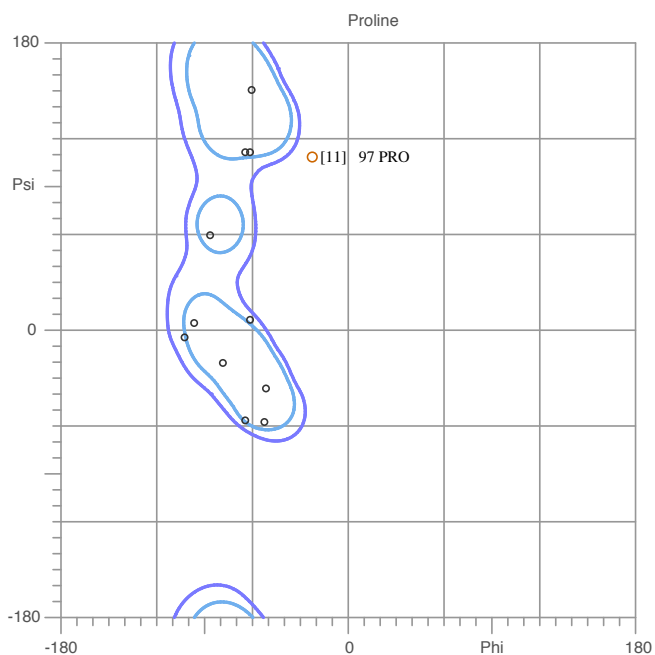
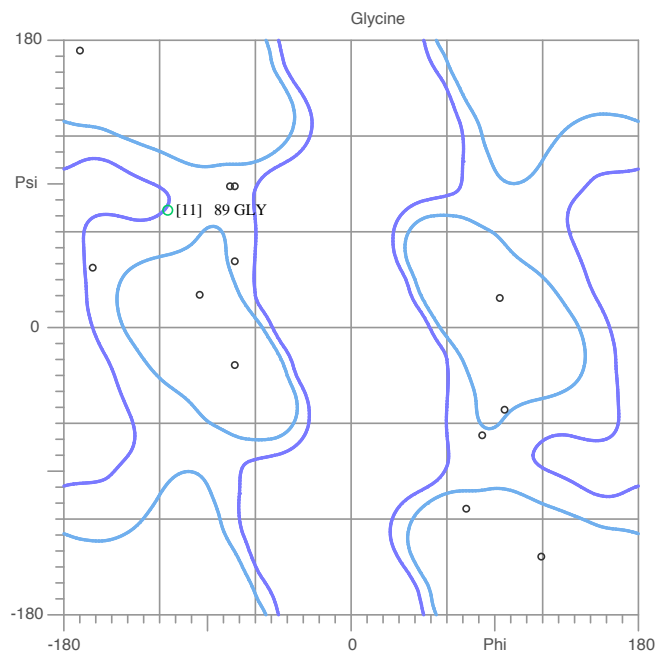
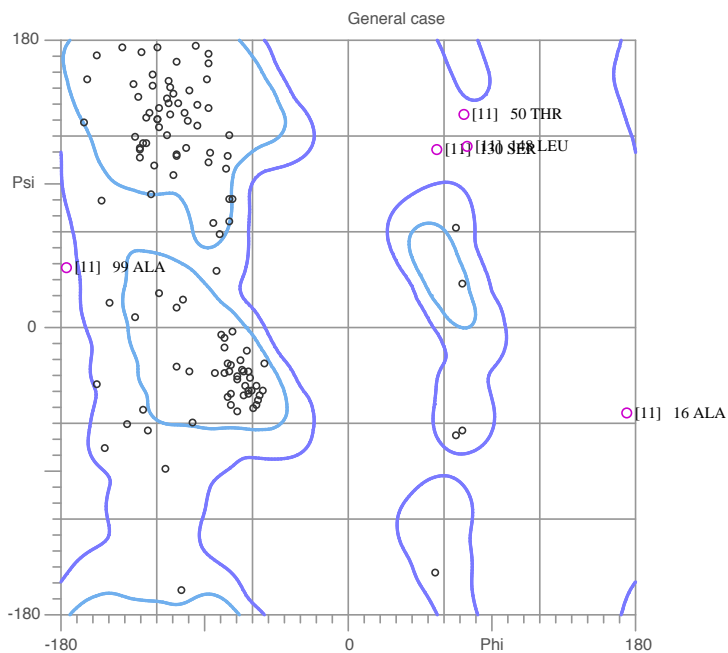
82.4% (126/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[10] 16 ALA (172.2, -50.8)

[10] 29 LEU (65.2, 160.9)
[10] 33 MET (64.6, 105.4)
[10] 37 ARG (75.4, 129.9)
[10] 44 ASP (-169.4, -82.7)
[10] 128 GLU (69.8, 153.2)
[10] 148 LEU (177.5, -48.2)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 11



81.0% (124/153) of all residues were in favored (98%) regions.
 94.8% (145/153) of all residues were in allowed (>99.8%) regions.

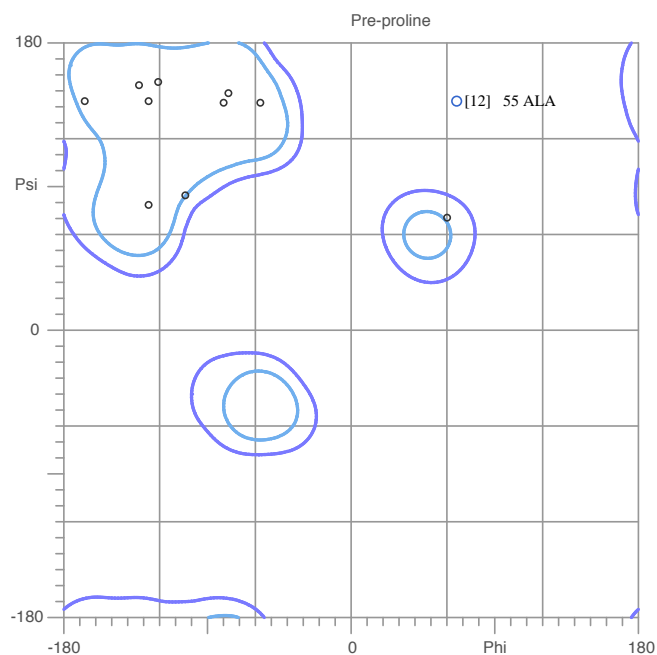
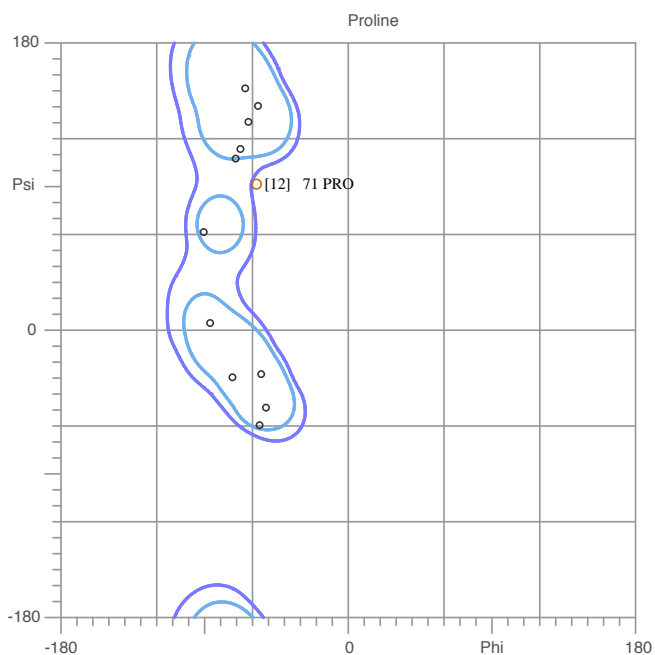
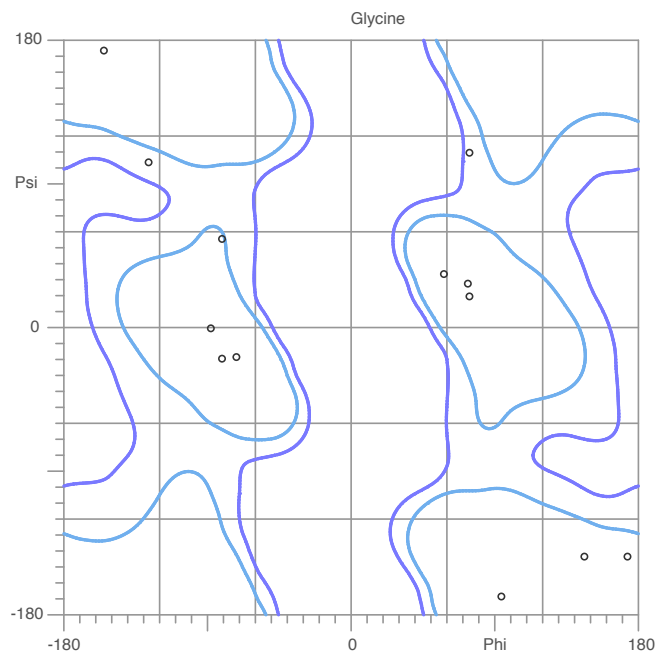
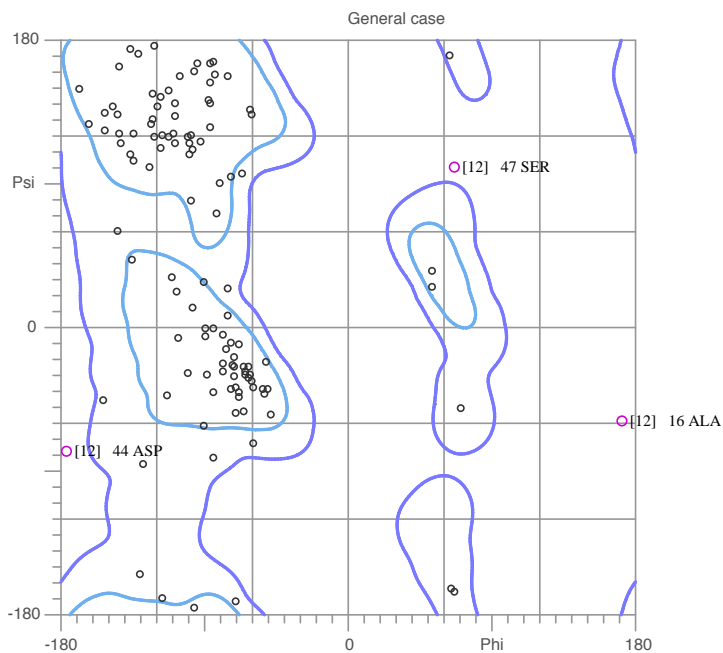
There were 8 outliers (phi, psi):

[11] 16 ALA (174.4, -53.4)
 [11] 50 THR (72.5, 134.1)

[11] 55 ALA (65.6, 142.2)
 [11] 89 GLY (-115.9, 74.9)
 [11] 97 PRO (-23.5, 109.2)
 [11] 99 ALA (-177.8, 38.5)
 [11] 130 SER (55.8, 112.0)
 [11] 148 LEU (74.0, 114.2)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 12



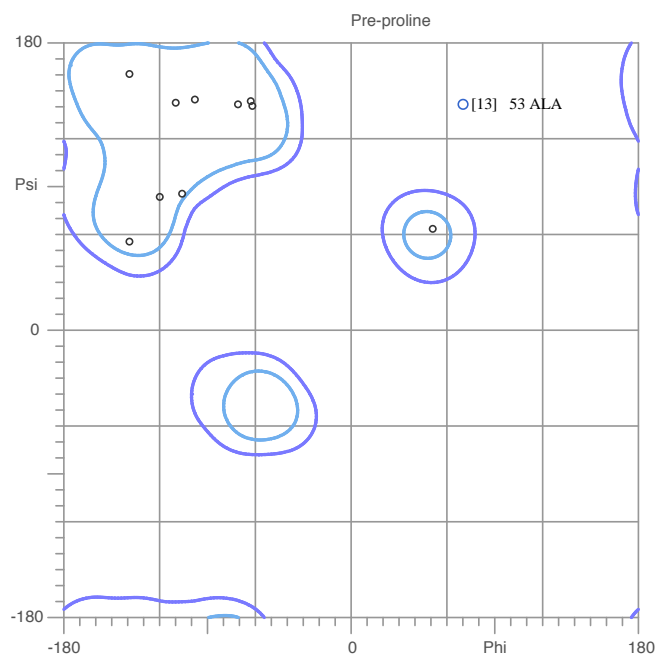
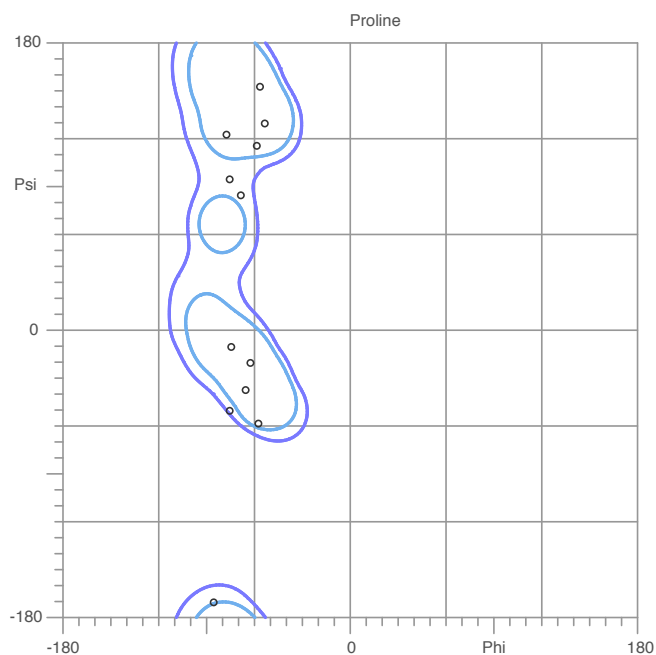
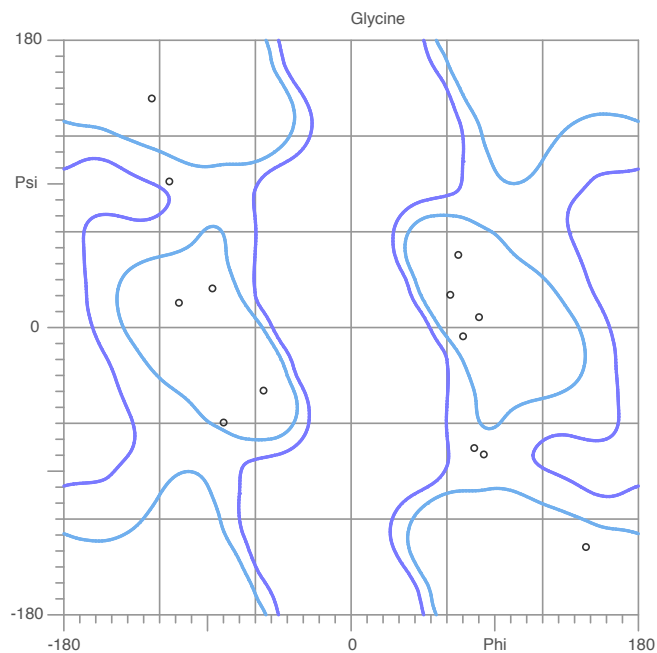
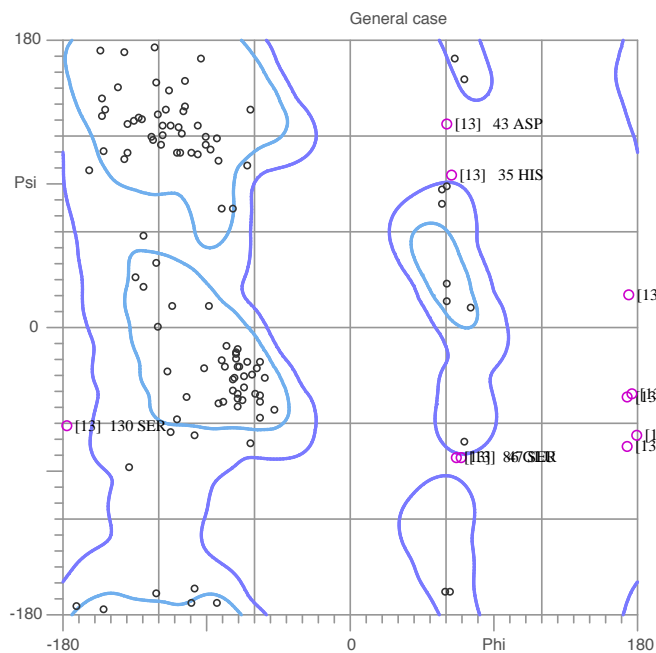
85.6% (131/153) of all residues were in favored (98%) regions.
96.7% (148/153) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[12] 16 ALA (171.1, -58.7)
[12] 44 ASP (-177.0, -77.3)
[12] 47 SER (66.5, 101.9)
[12] 55 ALA (67.0, 144.2)
[12] 71 PRO (-58.9, 92.9)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 13



76.5% (117/153) of all residues were in favored (98%) regions.
92.8% (142/153) of all residues were in allowed (>99.8%) regions.

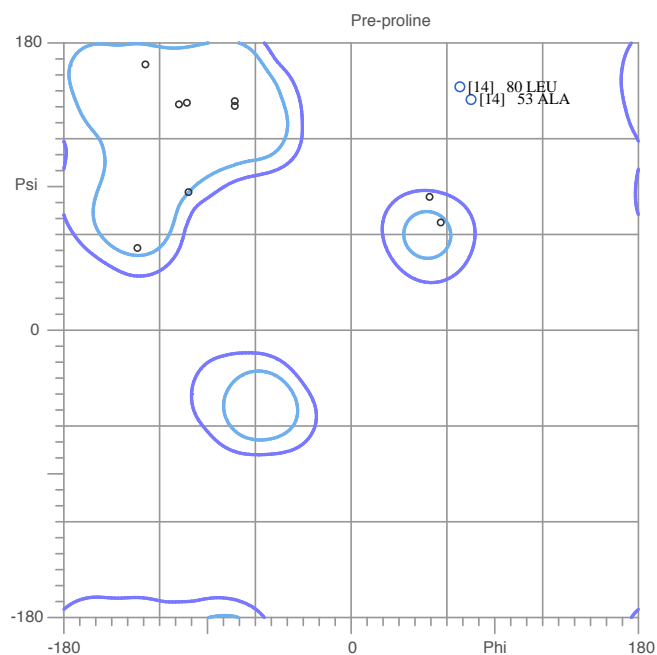
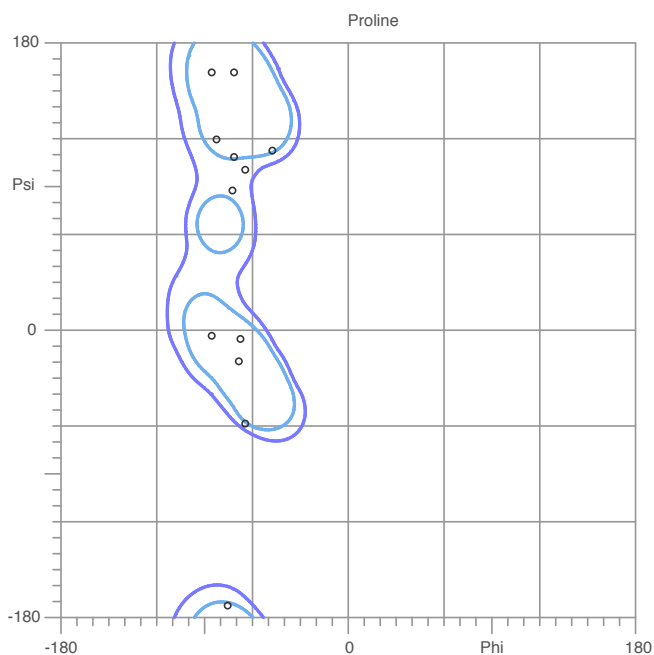
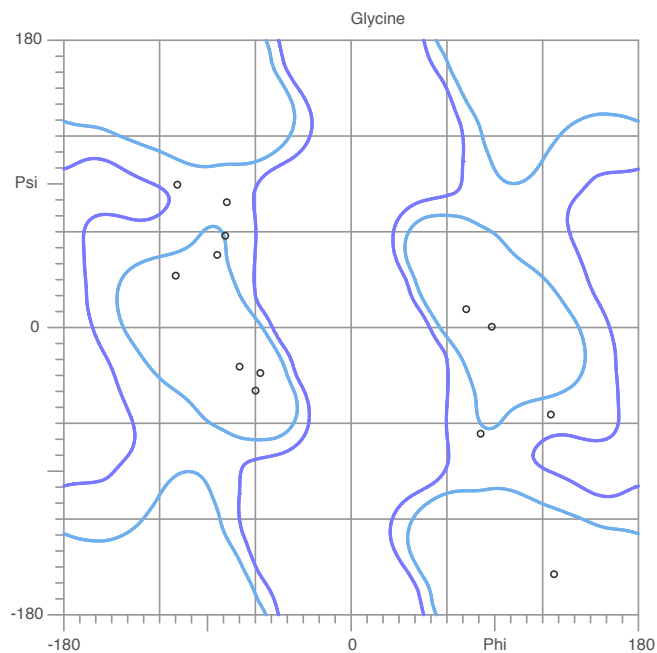
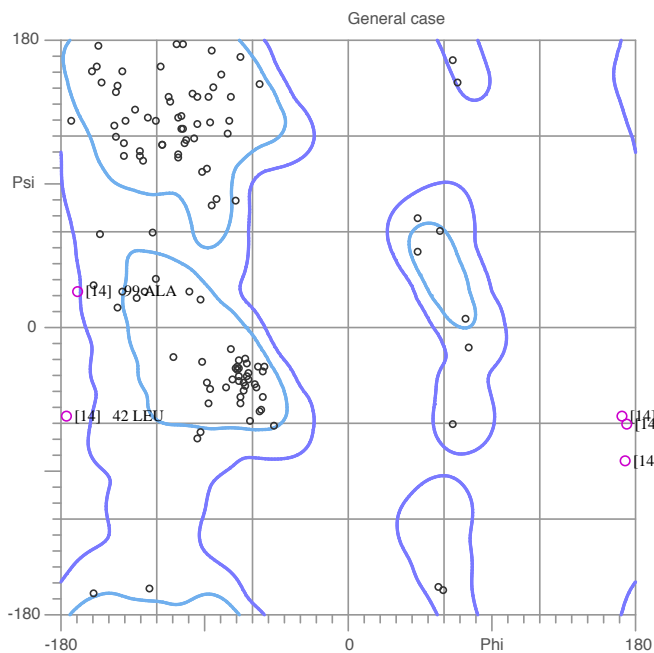
There were 11 outliers (phi, psi):

- [13] 16 ALA (173.5, -43.6)
- [13] 35 HIS (63.5, 96.1)
- [13] 37 ARG (176.8, -41.5)

- [13] 43 ASP (60.7, 129.0)
- [13] 44 ASP (173.4, -74.3)
- [13] 47 SER (69.4, -81.6)
- [13] 53 ALA (71.0, 142.9)
- [13] 61 SER (174.5, 21.3)
- [13] 86 GLU (66.4, -81.7)
- [13] 130 SER (-178.7, -61.7)
- [13] 154 HIS (179.1, -67.2)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 14



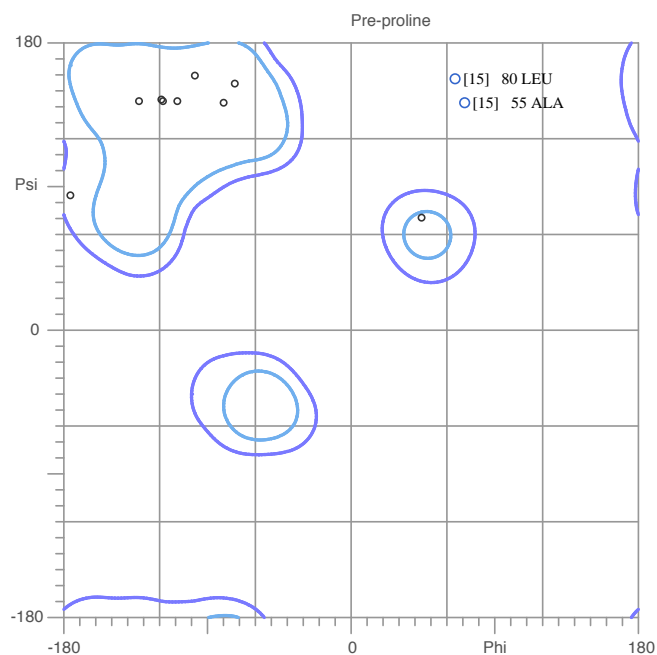
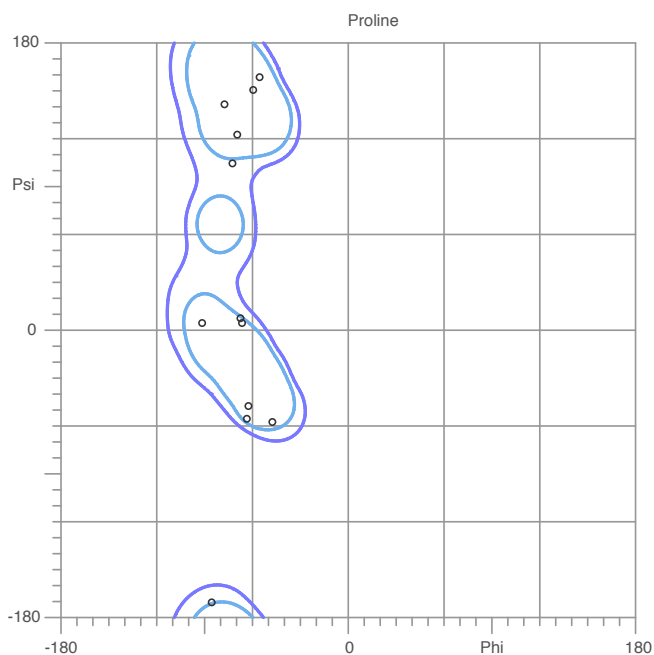
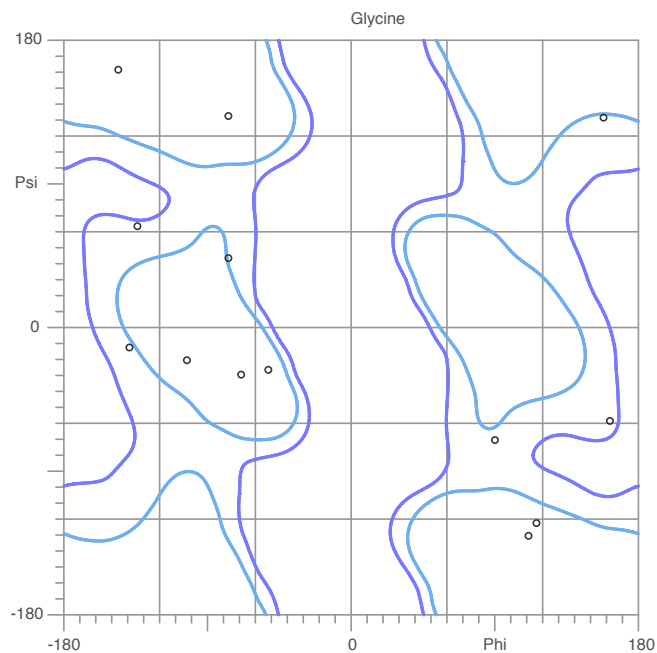
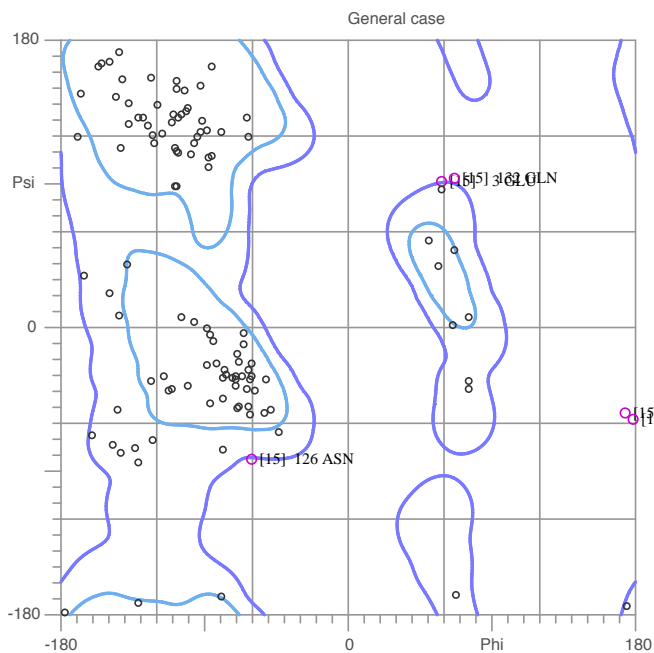
77.8% (119/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[14] 16 ALA (171.7, -55.8)

[14] 34 THR (174.9, -60.1)
[14] 37 ARG (173.7, -83.3)
[14] 42 LEU (-177.8, -55.3)
[14] 53 ALA (75.2, 145.4)
[14] 80 LEU (68.1, 154.0)
[14] 99 ALA (-170.0, 24.0)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 15



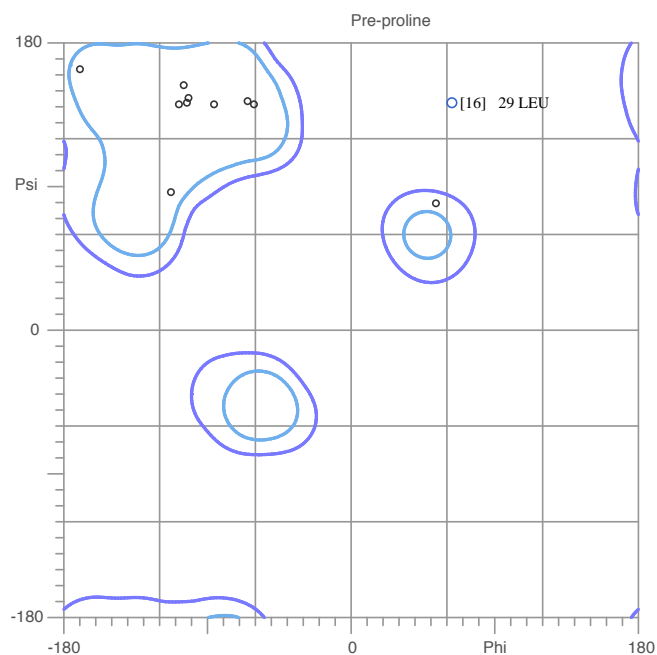
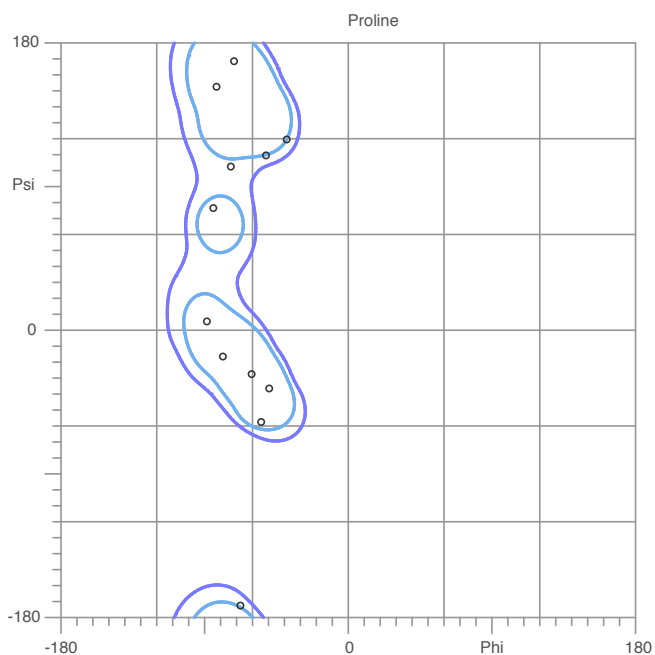
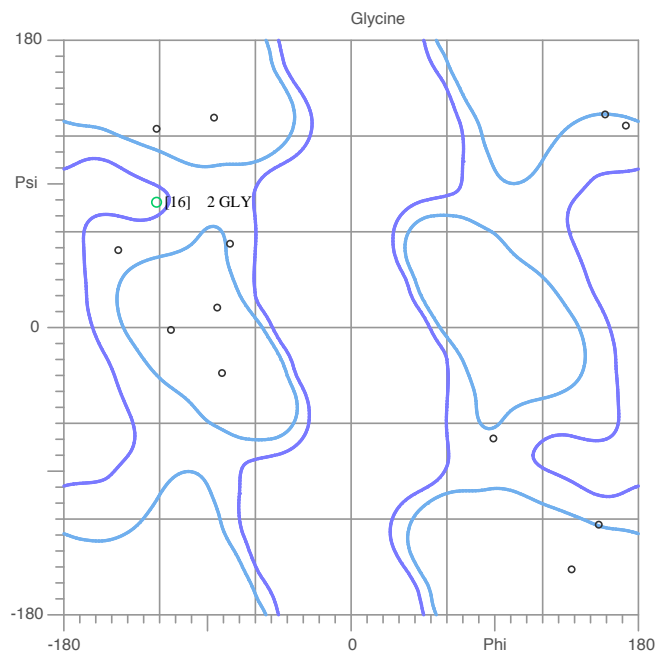
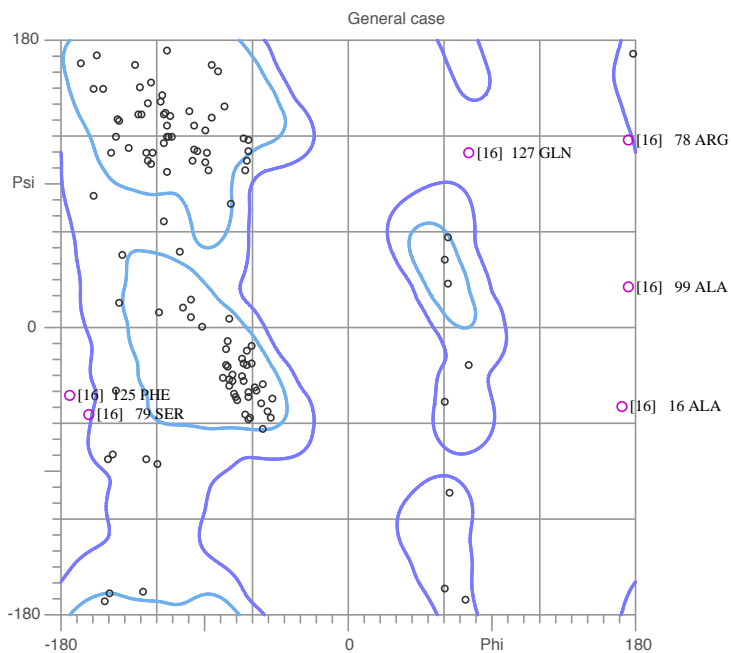
75.8% (116/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[15] 3 GLU (58.6, 92.7)

[15] 16 ALA (173.3, -53.3)
[15] 42 LEU (178.8, -57.2)
[15] 55 ALA (71.3, 143.9)
[15] 80 LEU (65.9, 158.4)
[15] 126 ASN (-61.5, -82.7)
[15] 132 GLN (67.0, 94.3)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 16



77.1% (118/153) of all residues were in favored (98%) regions.
94.8% (145/153) of all residues were in allowed (>99.8%) regions.

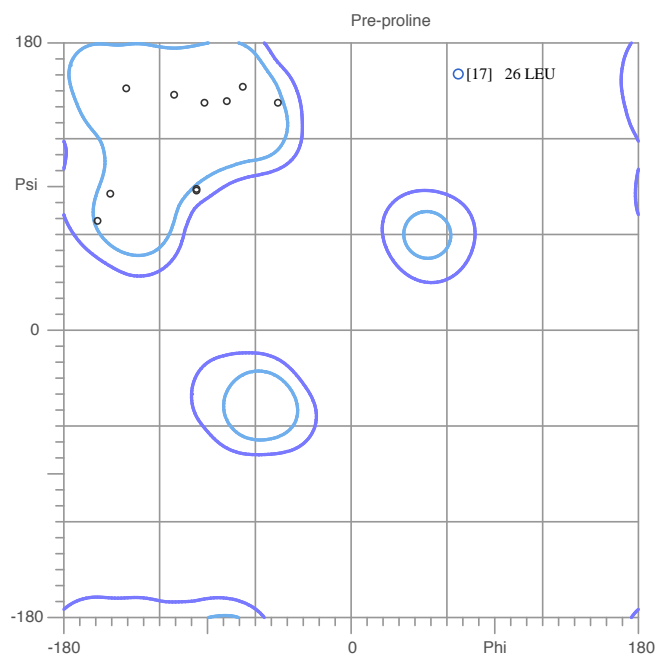
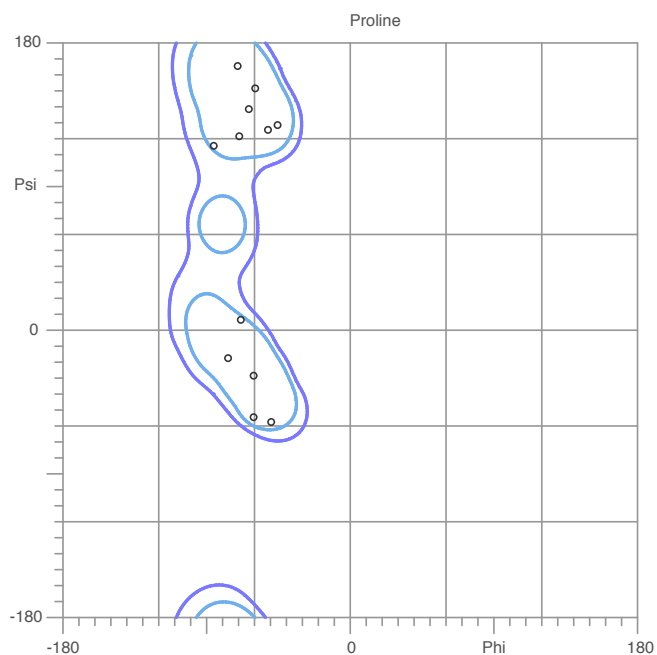
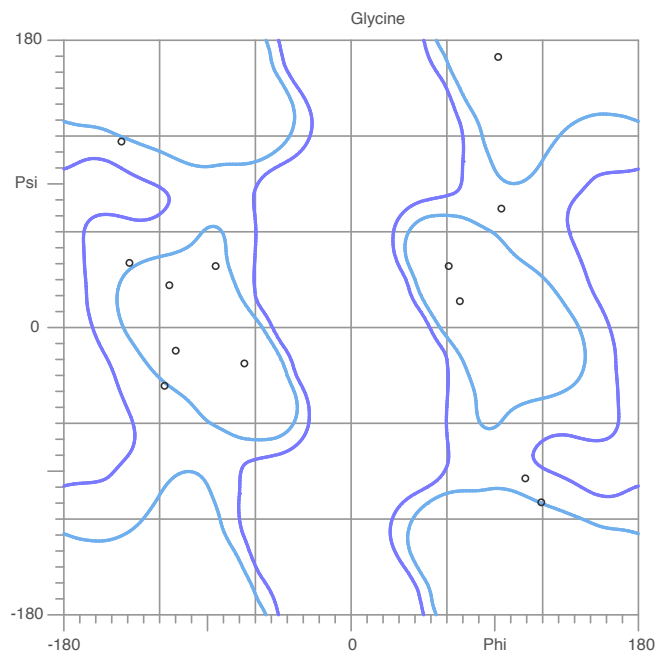
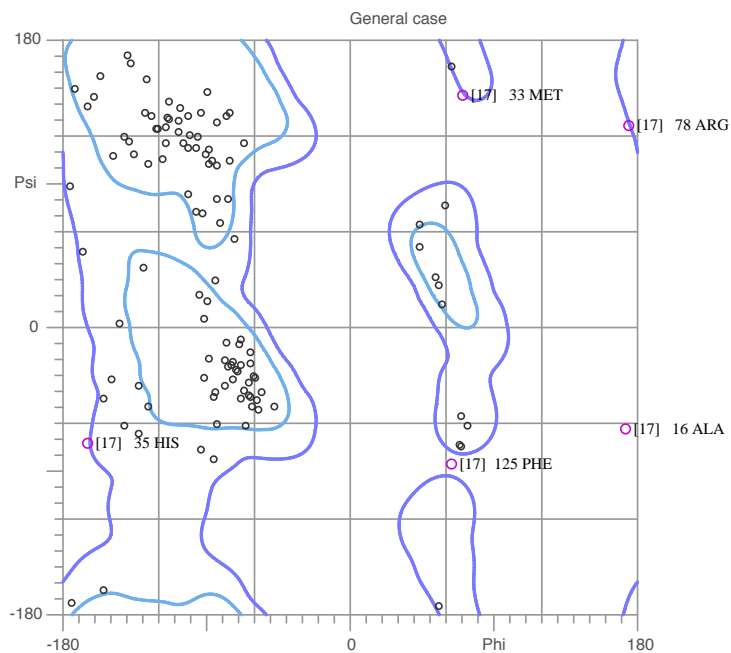
There were 8 outliers (phi, psi):

[16] 2 GLY (-122.3, 79.6)
[16] 16 ALA (171.4, -49.7)

[16] 29 LEU (64.0, 143.3)
[16] 78 ARG (175.6, 118.7)
[16] 79 SER (-163.2, -54.3)
[16] 99 ALA (175.7, 26.8)
[16] 125 PHE (-175.7, -42.7)
[16] 127 GLN (75.3, 110.4)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 17



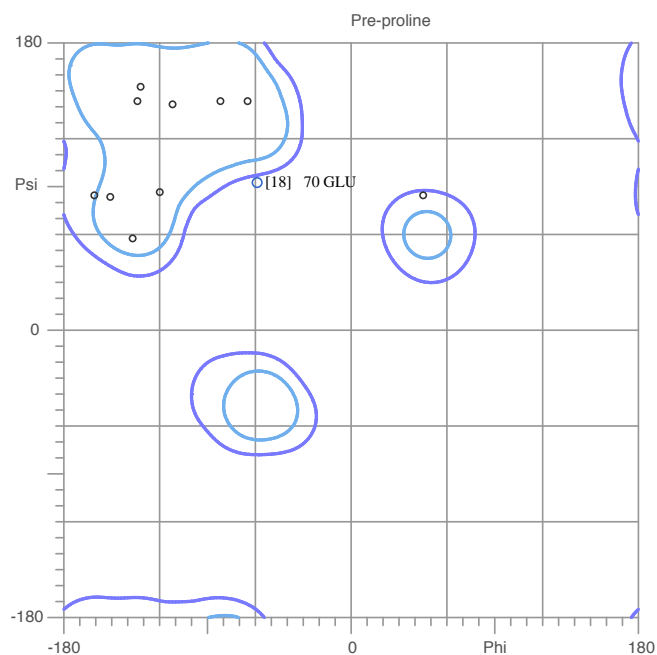
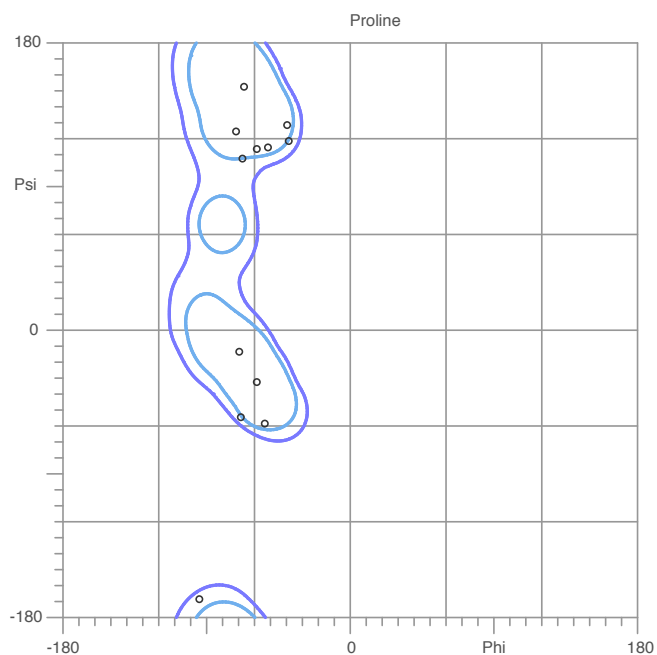
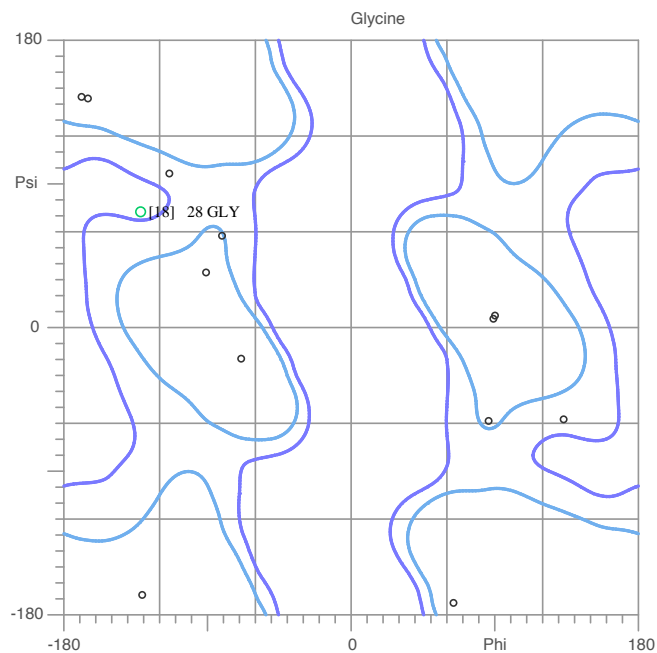
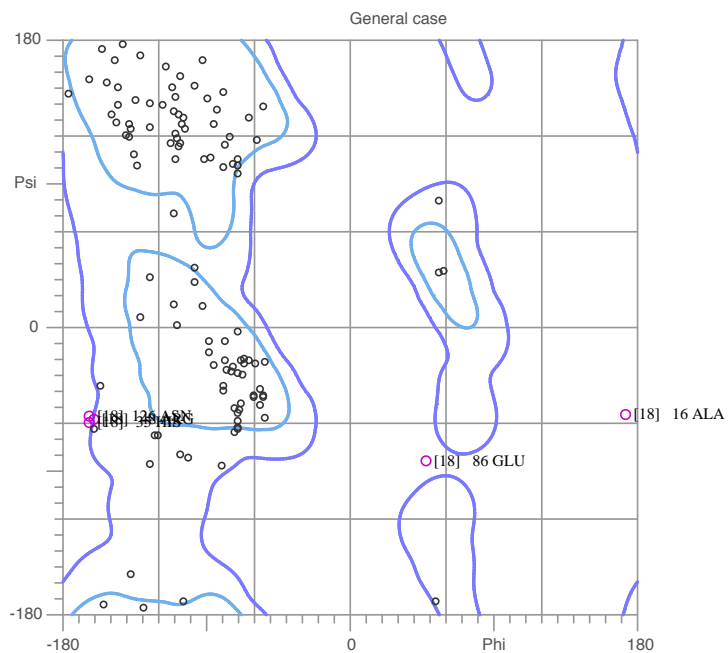
75.8% (116/153) of all residues were in favored (98%) regions.
96.1% (147/153) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[17] 16 ALA (172.9, -63.5)

[17] 26 LEU (67.5, 161.1)
[17] 33 MET (70.9, 146.4)
[17] 35 HIS (-165.6, -72.2)
[17] 78 ARG (174.3, 127.6)
[17] 125 PHE (63.6, -85.7)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 18



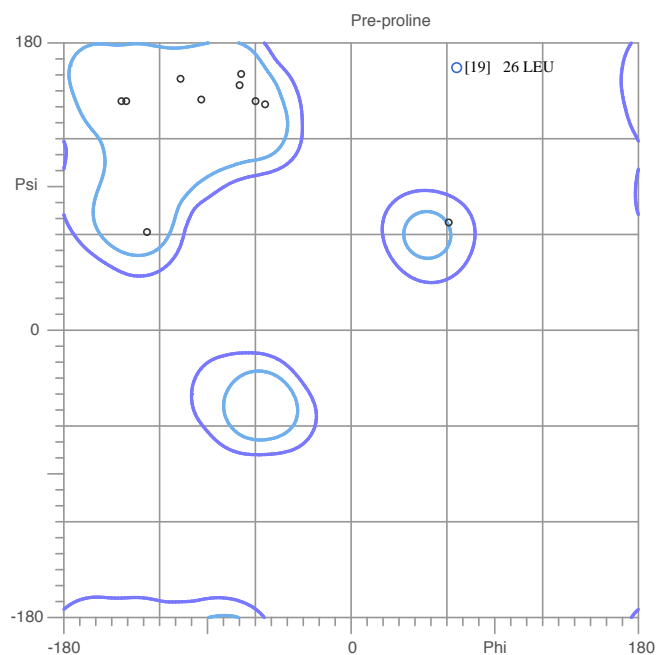
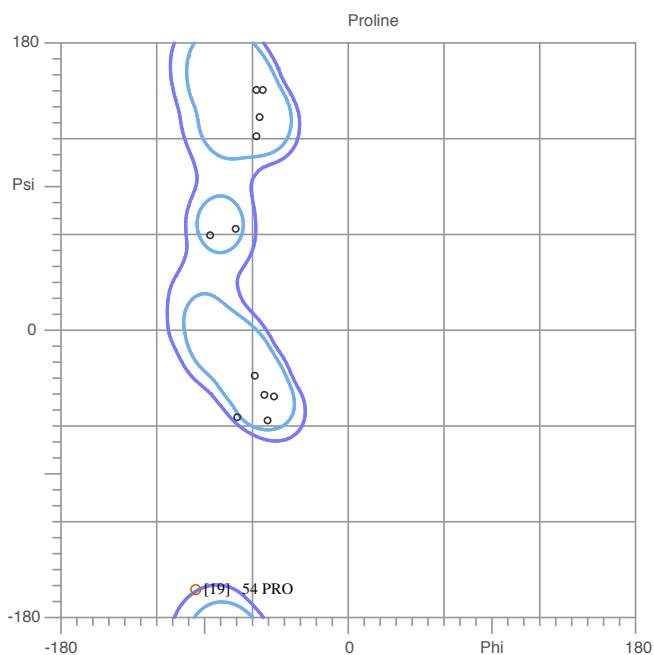
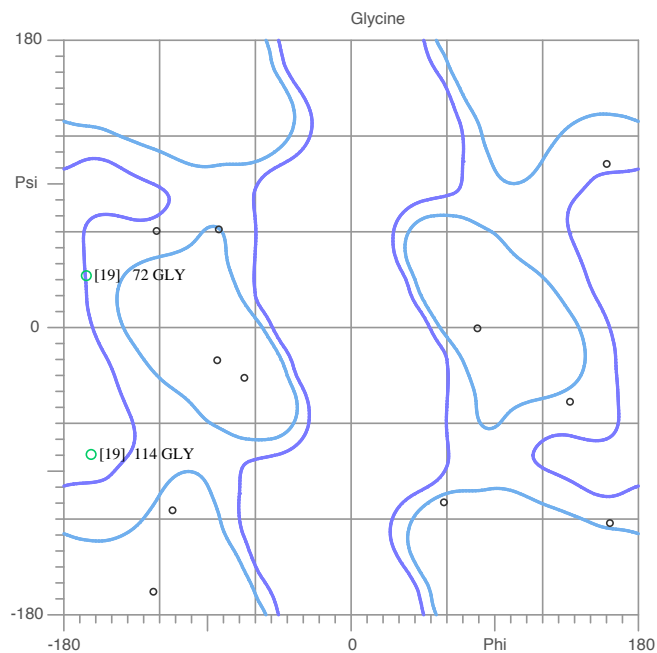
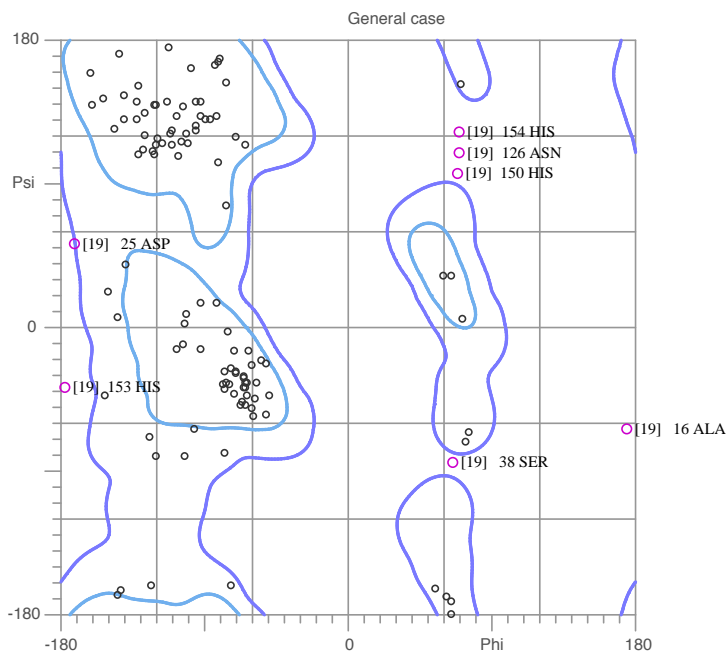
79.1% (121/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[18] 16 ALA (172.2, -54.1)

[18] 28 GLY (-132.2, 74.0)
[18] 35 HIS (-164.0, -59.8)
[18] 48 ARG (-161.6, -57.0)
[18] 70 GLU (-59.2, 93.4)
[18] 86 GLU (47.8, -83.2)
[18] 126 ASN (-164.6, -55.9)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 19



75.2% (115/153) of all residues were in favored (98%) regions.
 92.8% (142/153) of all residues were in allowed (>99.8%) regions.

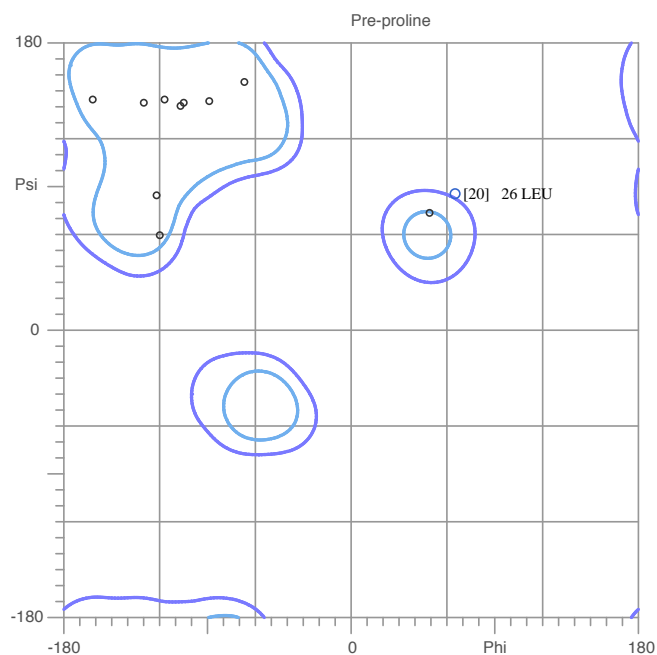
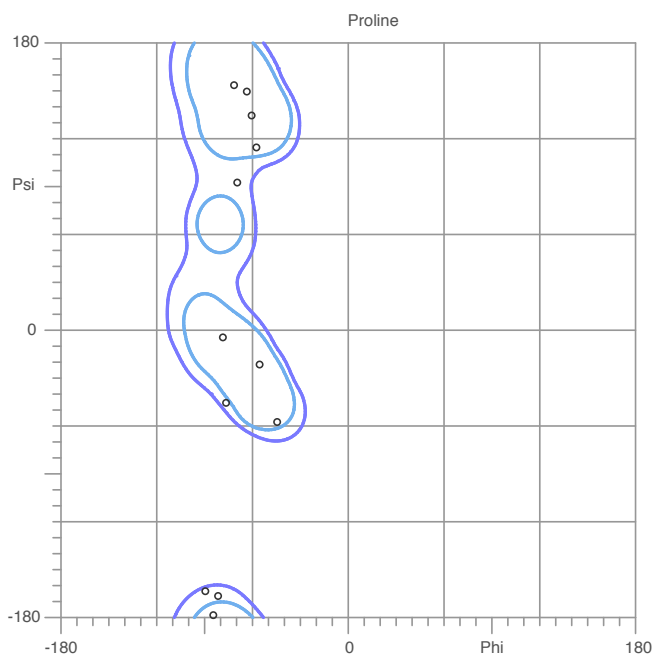
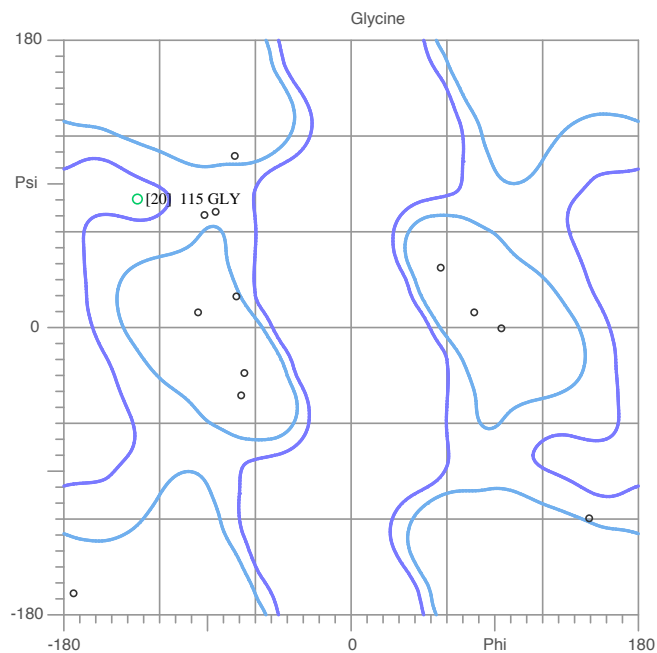
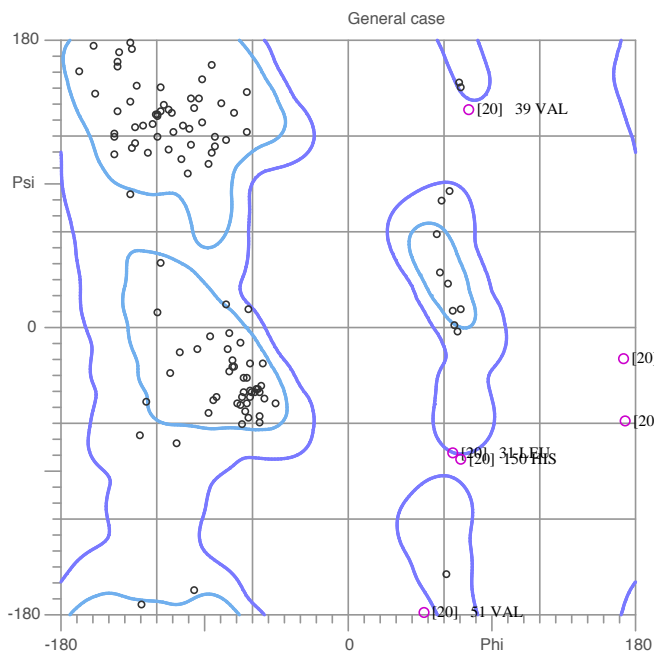
There were 11 outliers (phi, psi):

- [19] 16 ALA (174.5, -63.1)
- [19] 25 ASP (-172.2, 53.7)
- [19] 26 LEU (66.4, 165.9)

- [19] 38 SER (65.4, -84.9)
- [19] 54 PRO (-96.1, -162.4)
- [19] 72 GLY (-166.5, 33.3)
- [19] 114 GLY (-163.8, -79.5)
- [19] 126 ASN (69.6, 110.9)
- [19] 150 HIS (68.7, 97.9)
- [19] 153 HIS (-178.9, -37.5)
- [19] 154 HIS (69.2, 123.0)

MolProbity Ramachandran analysis

DRR147D_NMR_em_bcr3.pdb, model 20



80.4% (123/153) of all residues were in favored (98%) regions.
94.8% (145/153) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):

[20] 16 ALA (173.2, -58.2)
[20] 26 LEU (65.4, 86.1)

[20] 31 LEU (65.2, -79.0)
[20] 39 VAL (75.3, 137.4)
[20] 51 VAL (47.7, -178.9)
[20] 115 GLY (-135.0, 81.7)
[20] 150 HIS (70.7, -82.5)
[20] 154 HIS (172.3, -19.7)