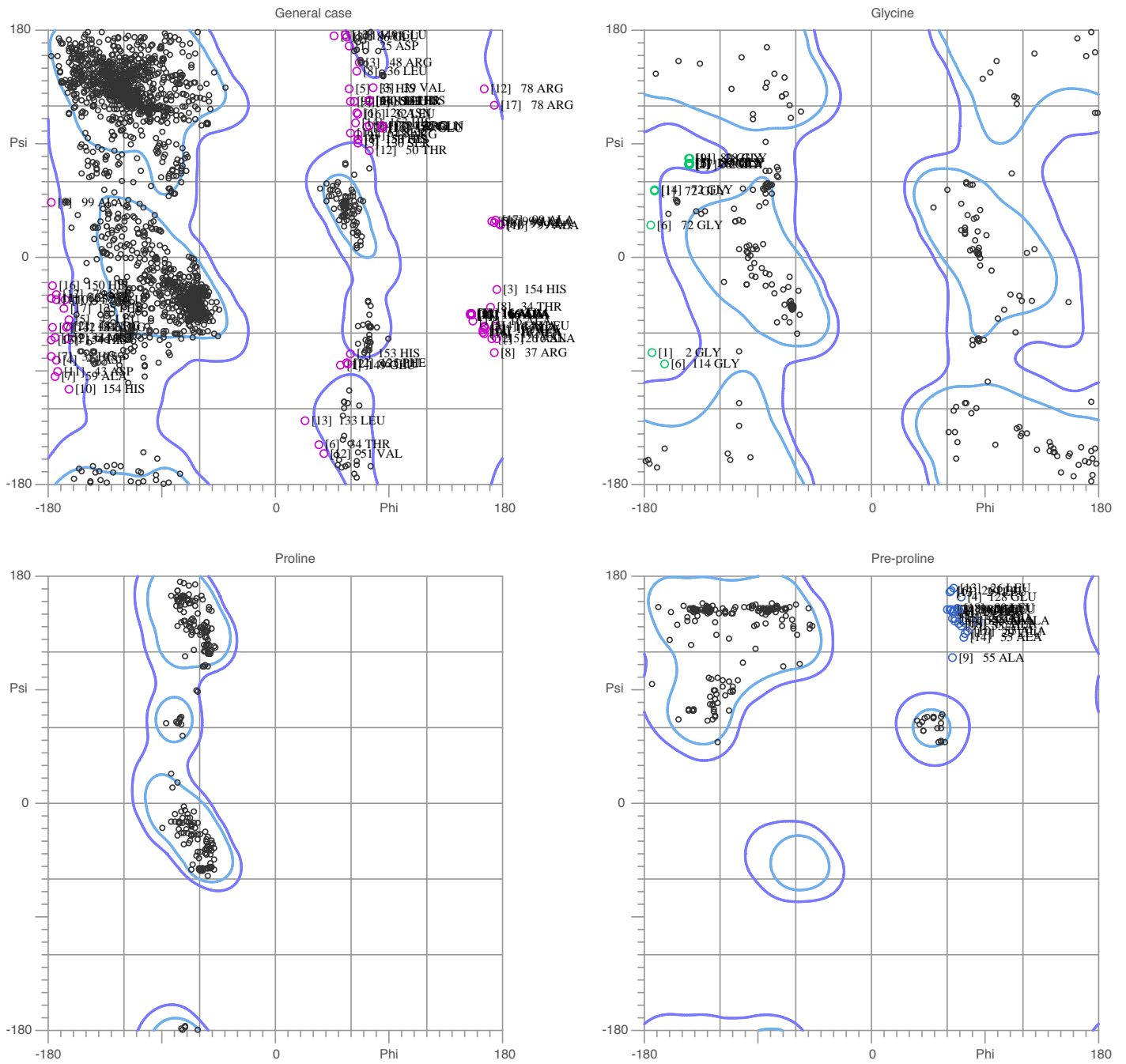


MolProbity Ramachandran analysis

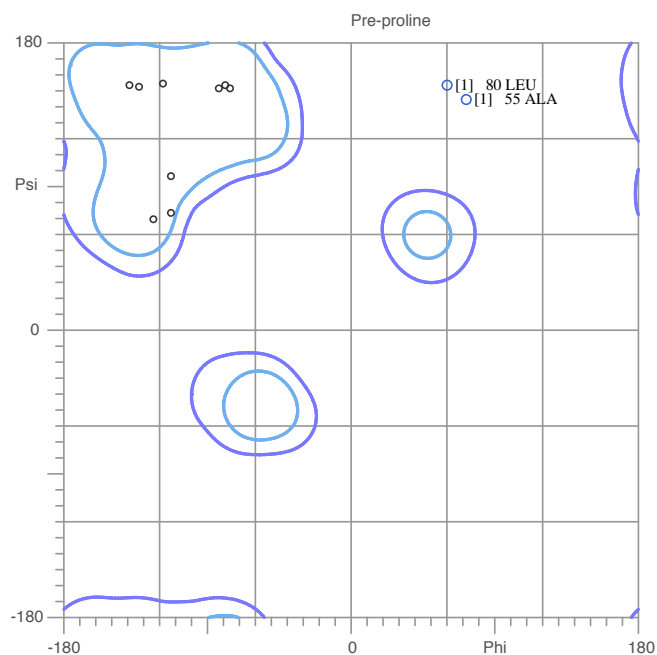
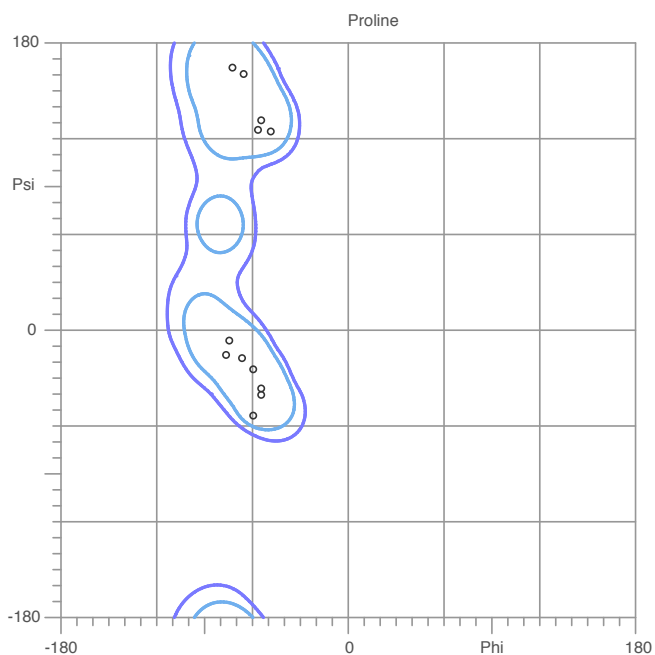
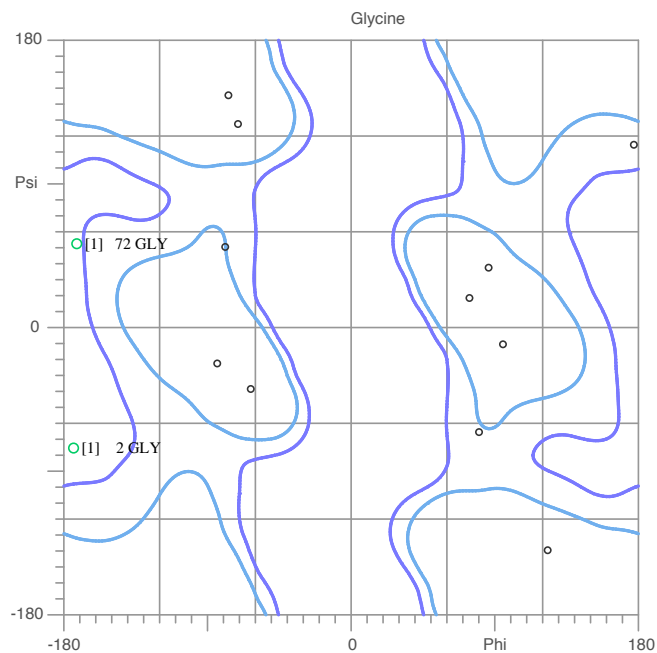
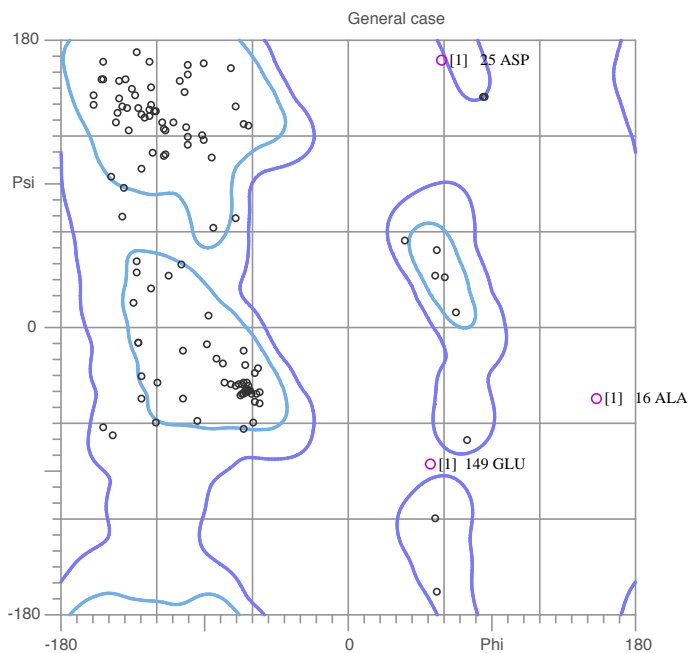
DRR147D_R3Cons_em_bcr3.pdb, all models



Residue	Phi	Psi
[1] 2 GLY	-100	100
[6] 72 GLY	-100	100
[11] 72 GLY	-100	100
[14] 72 GLY	-100	100
[9] 55 ALA	100	100
[13] 20 LEU	100	100
[14] 20 LEU	100	100
[15] 20 LEU	100	100
[16] 20 LEU	100	100
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[94] 20 LEU	100	100
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[96] 20 LEU	100	100
[97] 20 LEU	100	100
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[99] 20 LEU	100	100
[100] 20 LEU	100	100

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 1



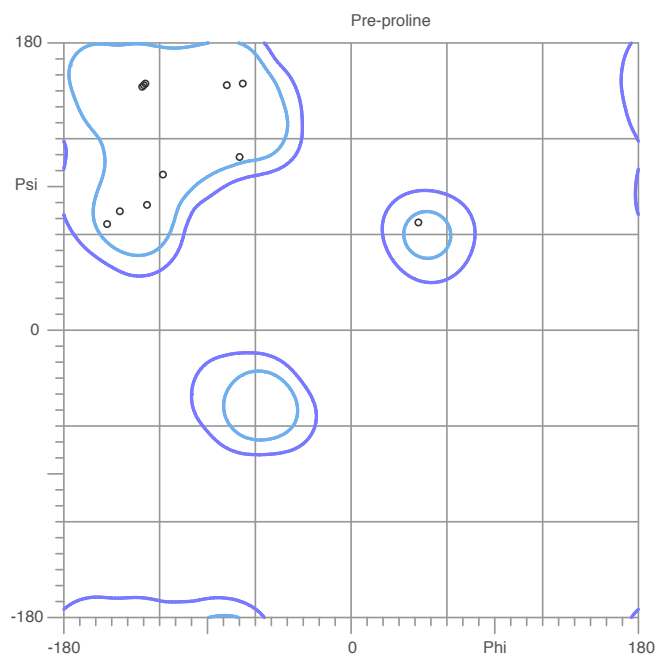
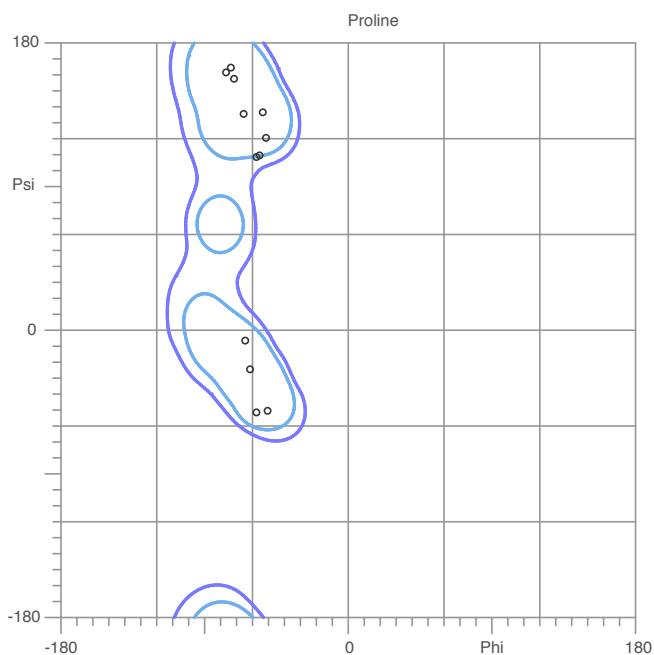
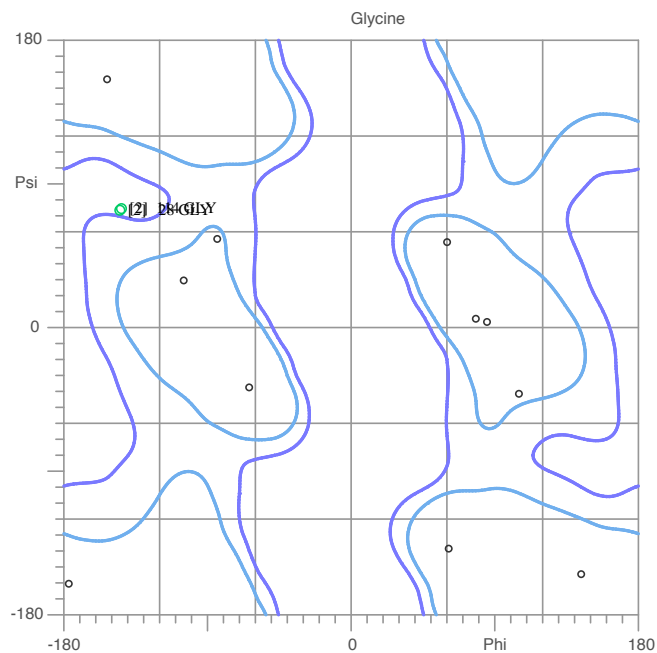
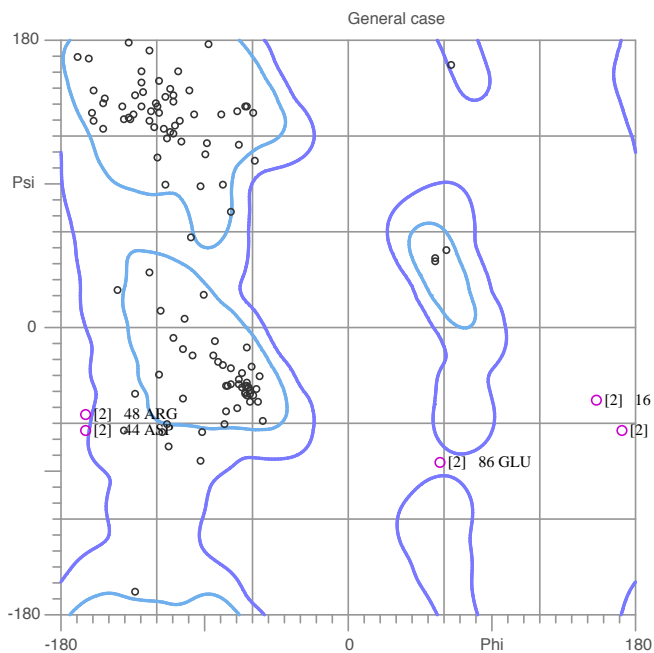
85.6% (131/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[1] 2 GLY (-175.0, -75.0)

[1] 16 ALA (155.0, -44.9)
[1] 25 ASP (58.9, 168.0)
[1] 55 ALA (72.4, 145.0)
[1] 72 GLY (-172.3, 53.4)
[1] 80 LEU (60.3, 155.0)
[1] 149 GLU (52.0, -85.0)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 2



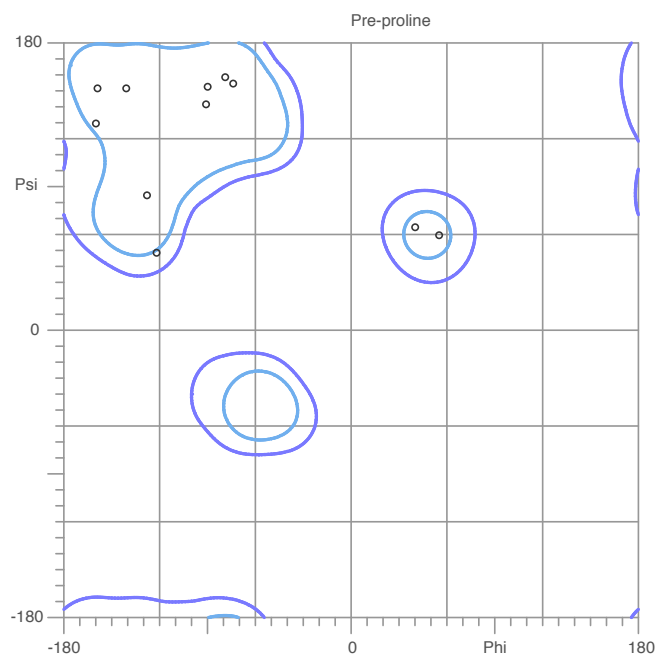
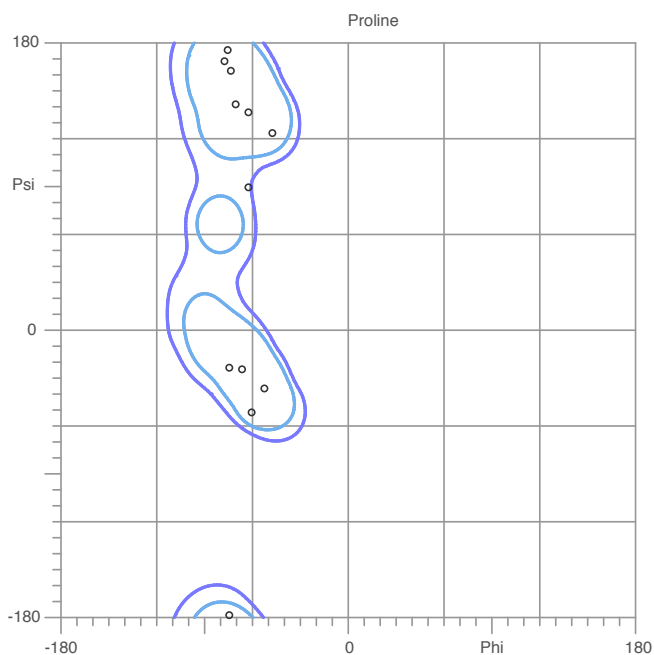
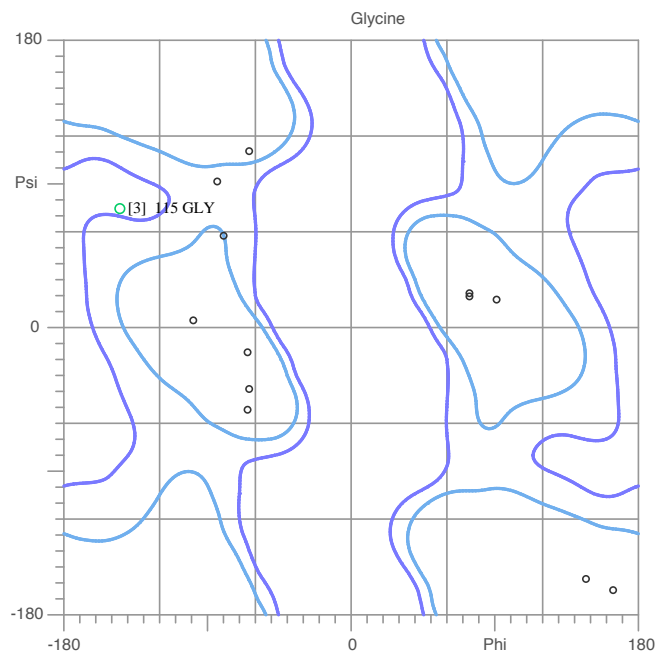
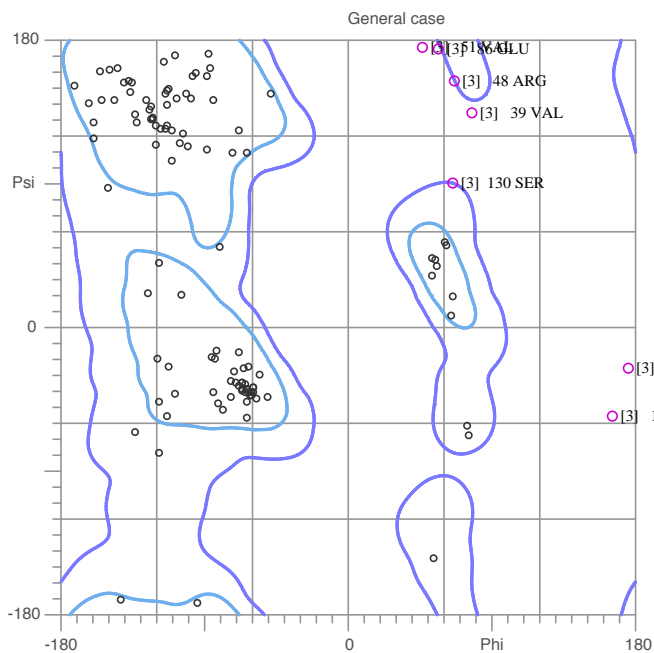
87.6% (134/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[2] 16 ALA (155.0, -45.1)

[2] 28 GLY (-145.0, 74.1)
[2] 44 ASP (-165.3, -64.8)
[2] 48 ARG (-165.0, -54.9)
[2] 86 GLU (57.7, -84.8)
[2] 114 GLY (-145.0, 75.3)
[2] 126 ASN (171.8, -64.9)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 3



88.2% (135/153) of all residues were in favored (98%) regions.
94.8% (145/153) of all residues were in allowed (>99.8%) regions.

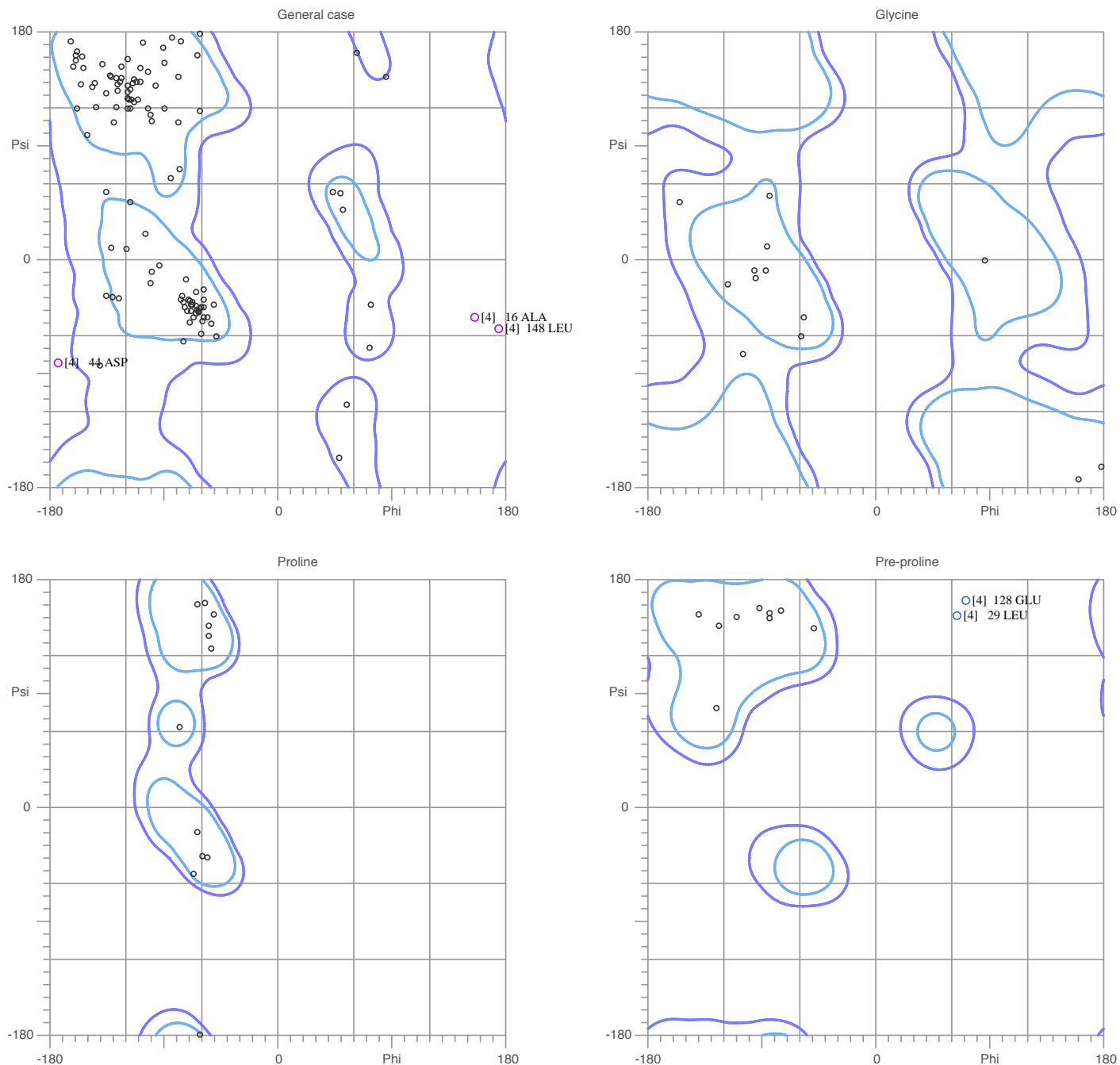
There were 8 outliers (phi, psi):

[3] 16 ALA (165.4, -55.0)
[3] 39 VAL (77.1, 135.0)

[3] 48 ARG (66.1, 155.0)
[3] 51 VAL (46.0, 176.7)
[3] 86 GLU (56.9, 175.0)
[3] 115 GLY (-145.0, 75.1)
[3] 130 SER (65.0, 91.2)
[3] 154 HIS (175.0, -25.0)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 4



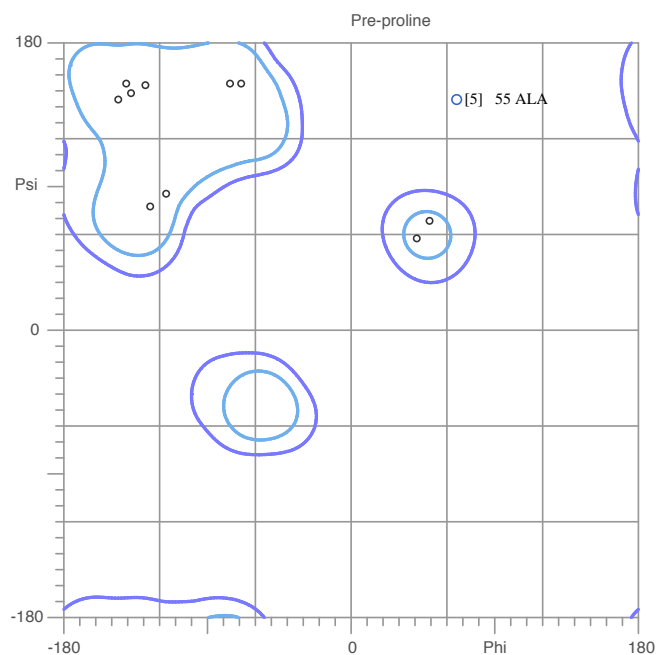
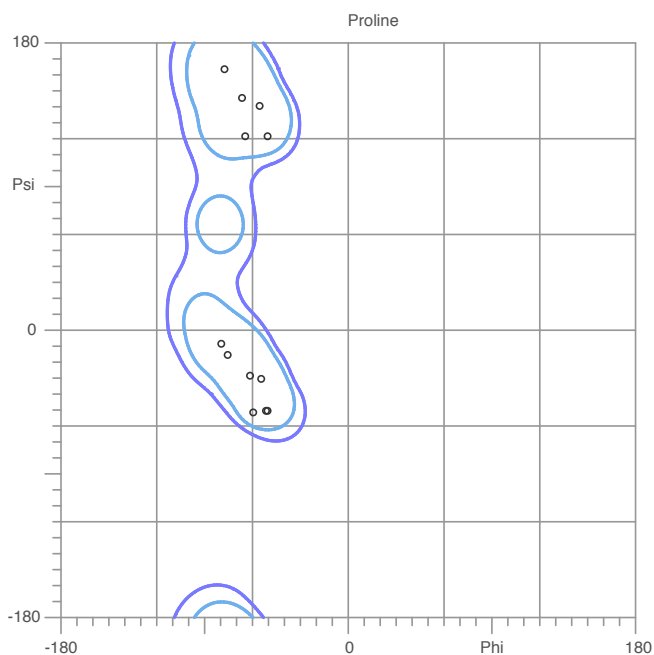
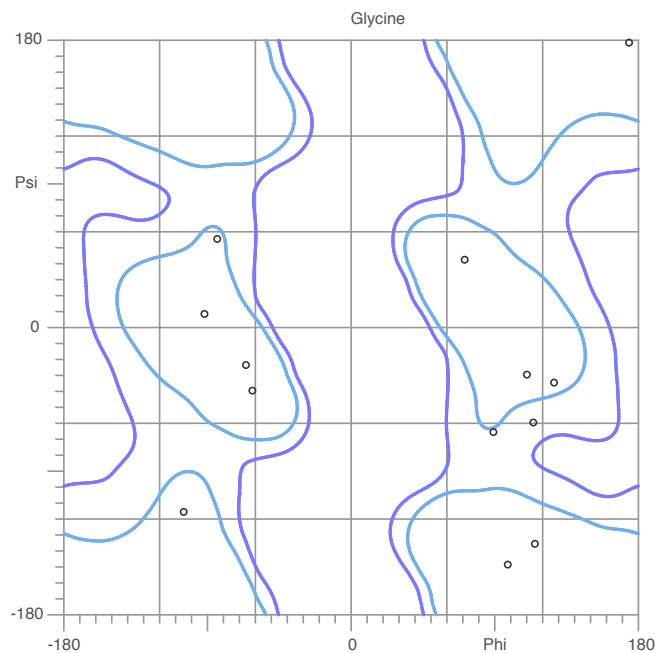
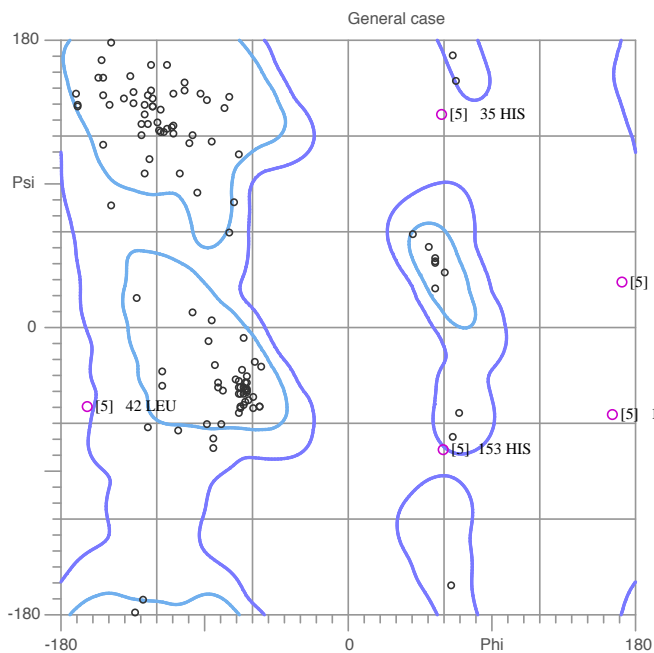
86.9% (133/153) of all residues were in favored (98%) regions.
96.7% (148/153) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[4] 16 ALA (155.0, -45.0)
[4] 29 LEU (64.9, 152.4)
[4] 44 ASP (-174.9, -81.0)
[4] 128 GLU (71.6, 165.0)
[4] 148 LEU (174.3, -55.0)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 5



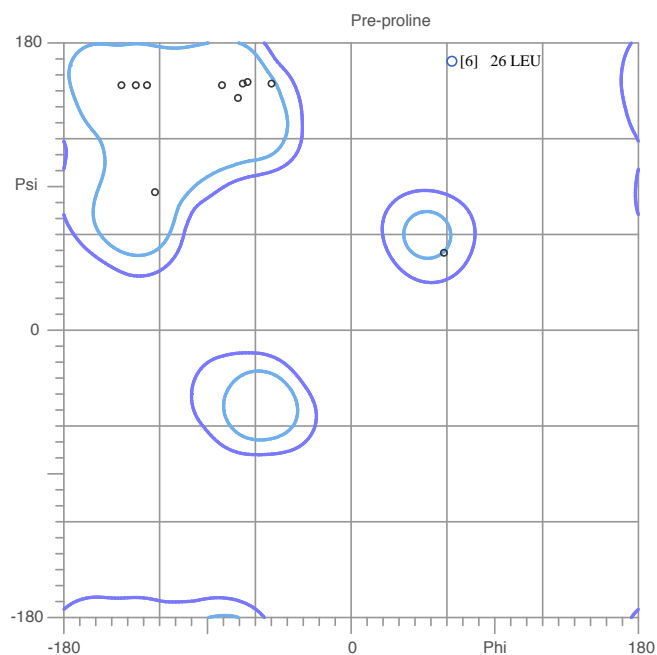
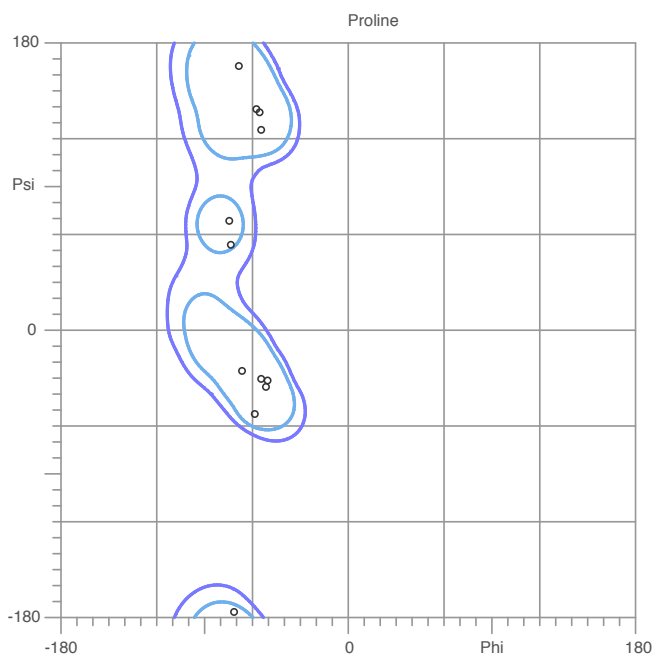
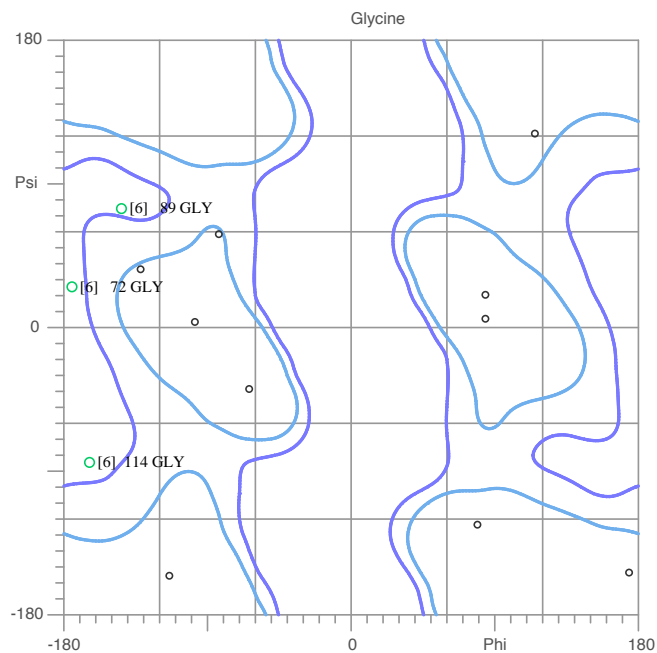
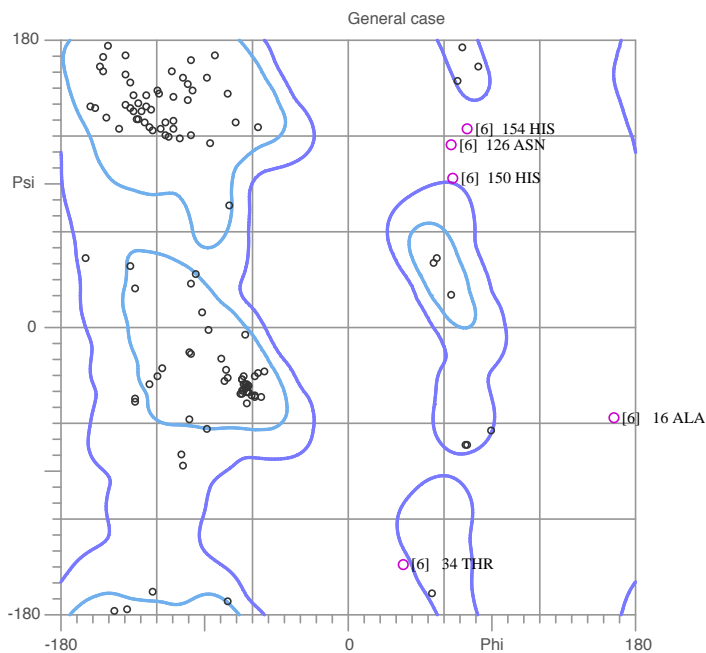
86.3% (132/153) of all residues were in favored (98%) regions.
96.1% (147/153) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[5] 16 ALA (165.2, -55.0)

[5] 35 HIS (58.8, 134.9)
[5] 42 LEU (-164.8, -49.6)
[5] 55 ALA (66.9, 145.3)
[5] 99 ALA (171.6, 29.5)
[5] 153 HIS (59.7, -76.7)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 6



84.3% (129/153) of all residues were in favored (98%) regions.
94.1% (144/153) of all residues were in allowed (>99.8%) regions.

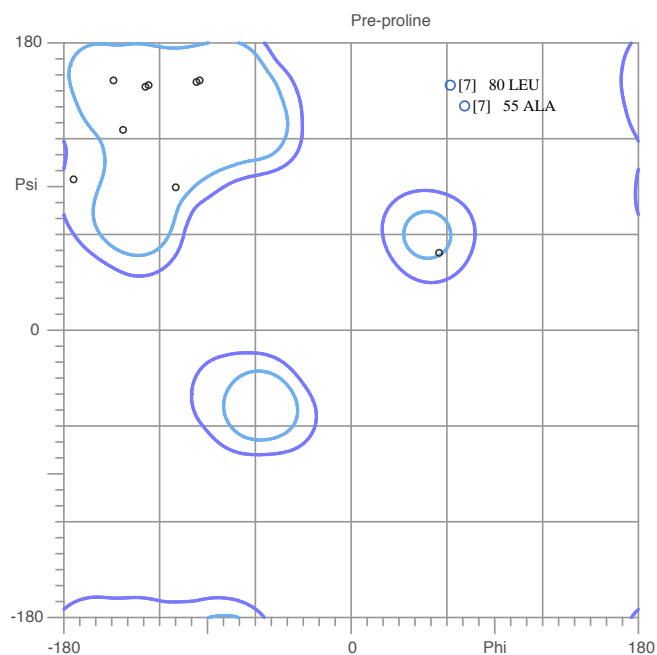
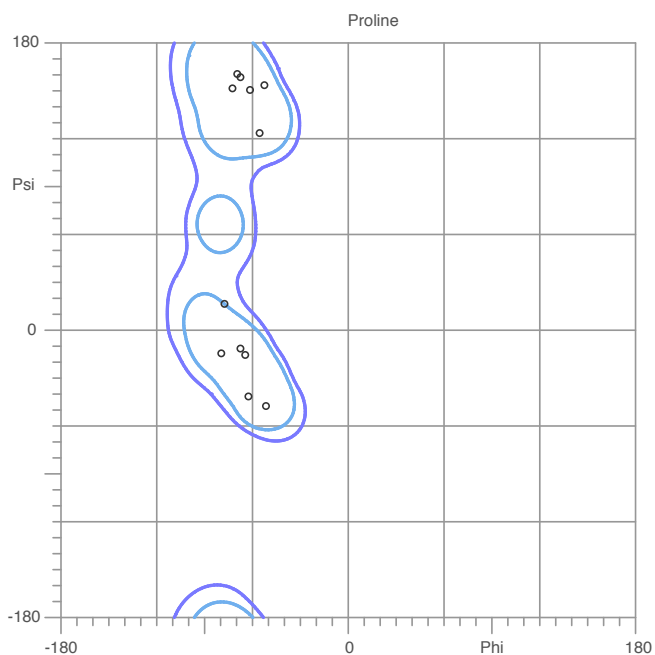
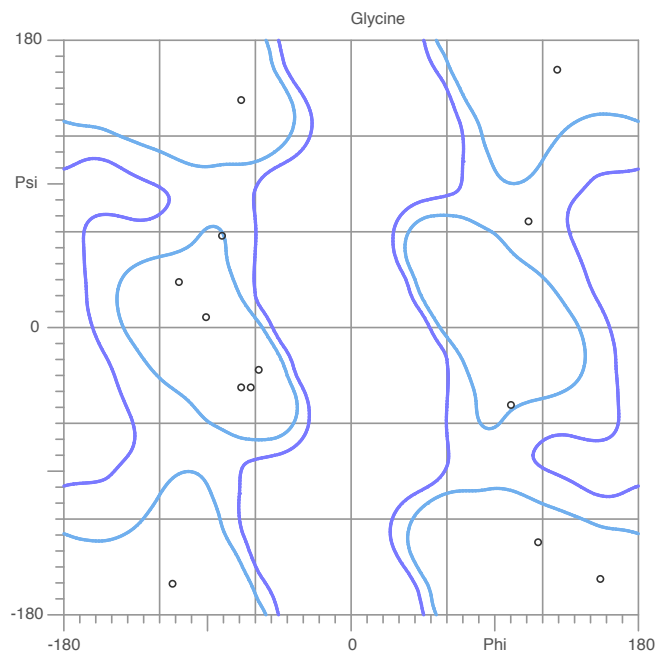
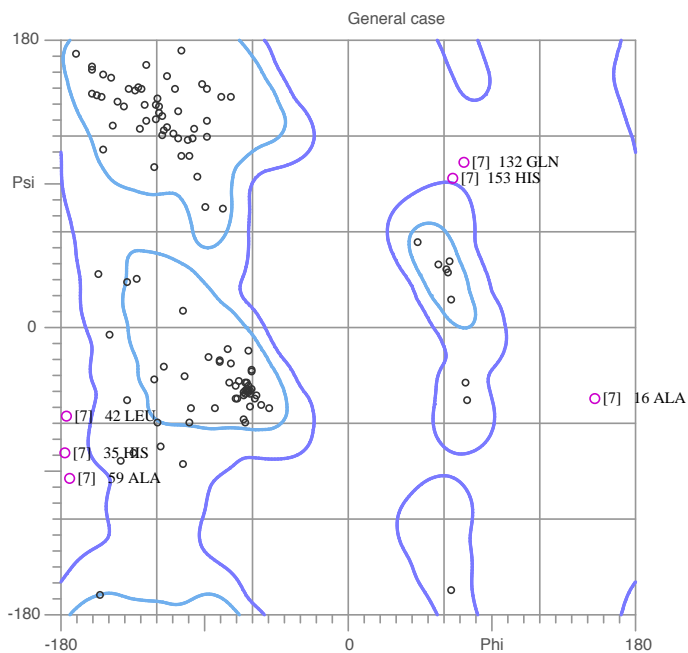
There were 9 outliers (phi, psi):

[6] 16 ALA (166.0, -56.1)
[6] 26 LEU (64.0, 169.6)

[6] 34 THR (34.5, -148.5)
[6] 72 GLY (-175.0, 26.6)
[6] 89 GLY (-144.9, 75.7)
[6] 114 GLY (-165.0, -85.0)
[6] 126 ASN (65.0, 115.0)
[6] 150 HIS (65.0, 94.9)
[6] 154 HIS (75.0, 125.0)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 7



85.6% (131/153) of all residues were in favored (98%) regions.
94.8% (145/153) of all residues were in allowed (>99.8%) regions.

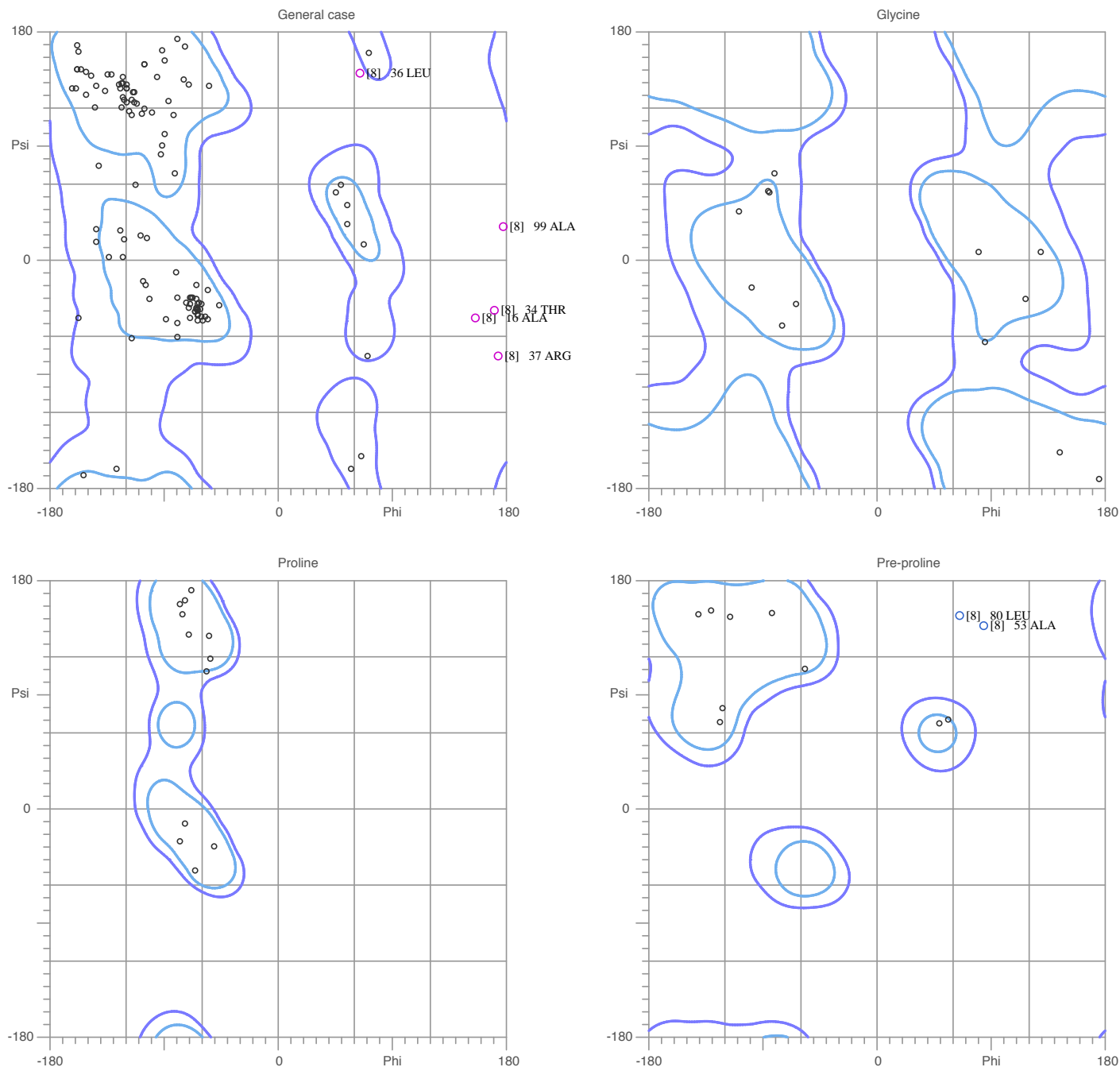
There were 8 outliers (phi, psi):

[7] 16 ALA (155.0, -45.0)
[7] 35 HIS (-179.0, -78.2)

[7] 42 LEU (-177.3, -55.4)
[7] 55 ALA (72.0, 141.9)
[7] 59 ALA (-175.0, -95.0)
[7] 80 LEU (62.5, 155.0)
[7] 132 GLN (72.4, 105.0)
[7] 153 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 8



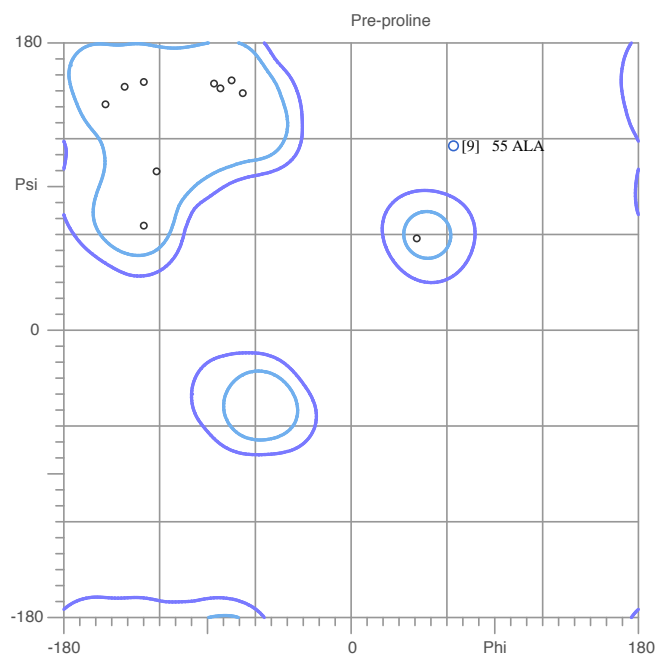
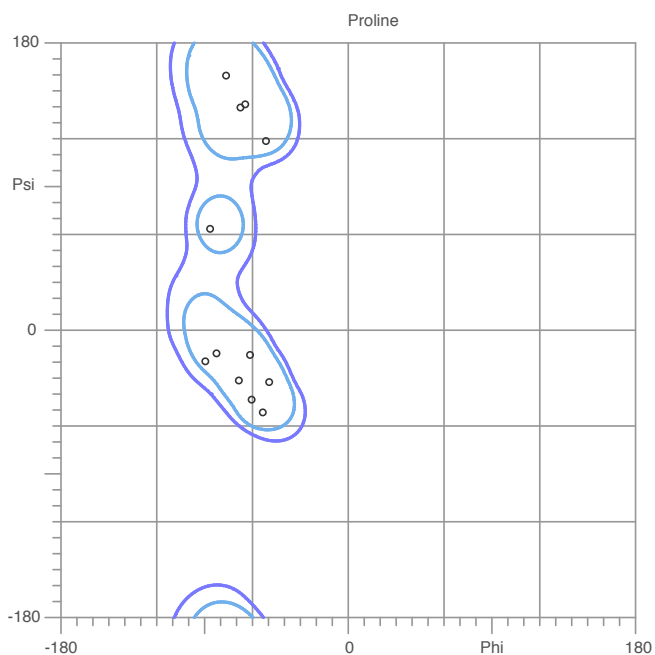
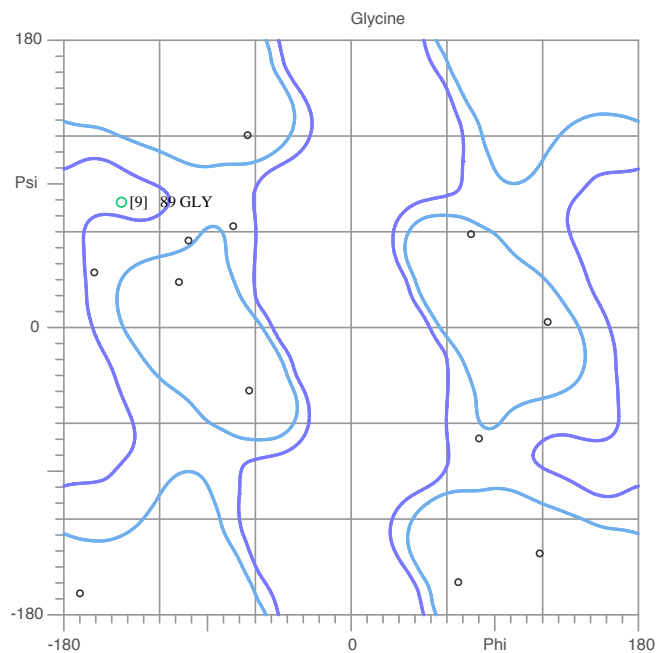
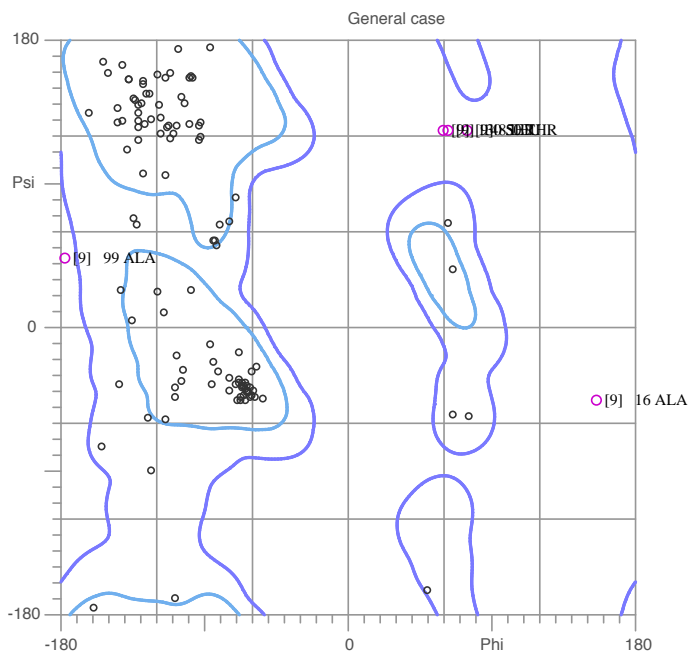
86.9% (133/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[8] 16 ALA (155.1, -45.0)

[8] 34 THR (170.0, -39.9)
[8] 36 LEU (64.9, 148.1)
[8] 37 ARG (173.7, -75.0)
[8] 53 ALA (85.0, 145.0)
[8] 80 LEU (65.2, 153.3)
[8] 99 ALA (177.3, 27.3)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 9



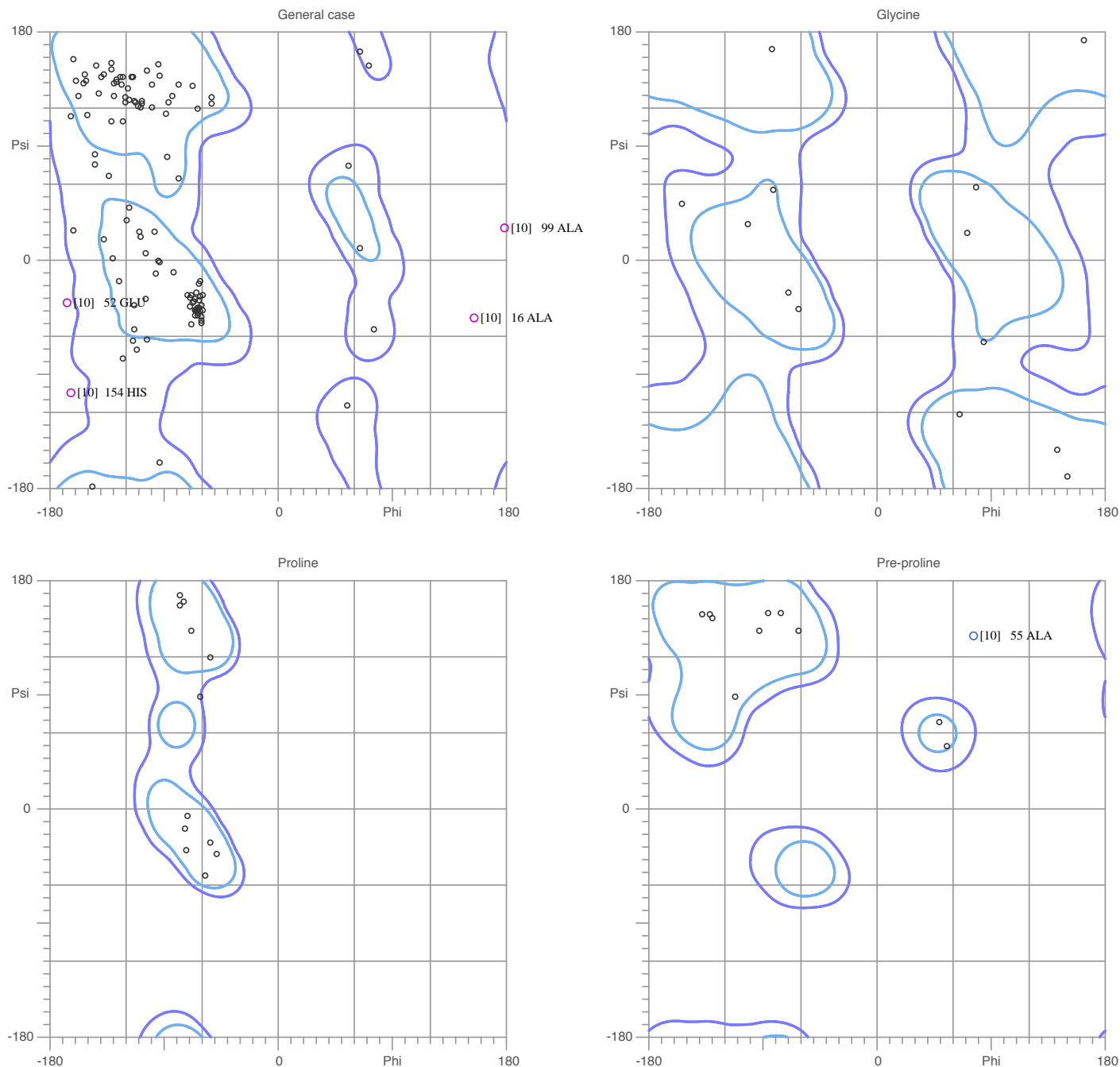
84.3% (129/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[9] 16 ALA (155.0, -45.0)

[9] 50 THR (75.0, 125.0)
[9] 55 ALA (65.0, 116.2)
[9] 89 GLY (-144.9, 79.9)
[9] 99 ALA (-178.6, 44.2)
[9] 130 SER (59.8, 125.0)
[9] 148 LEU (62.9, 125.0)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 10



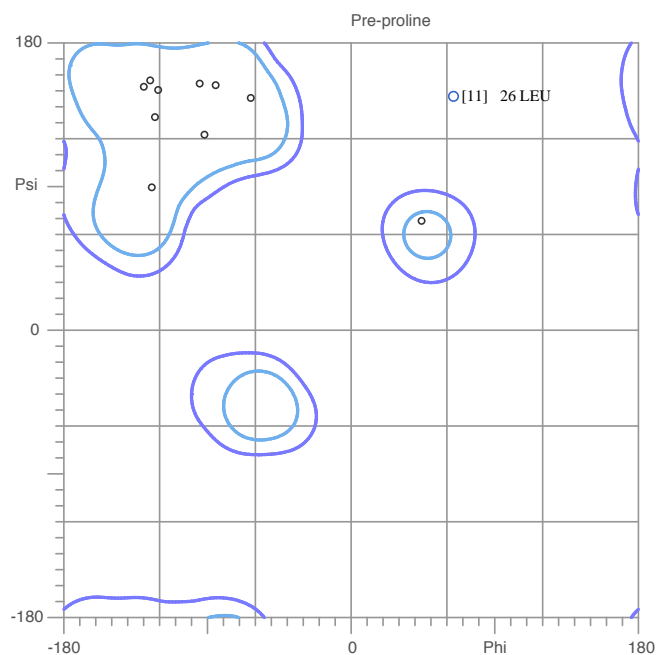
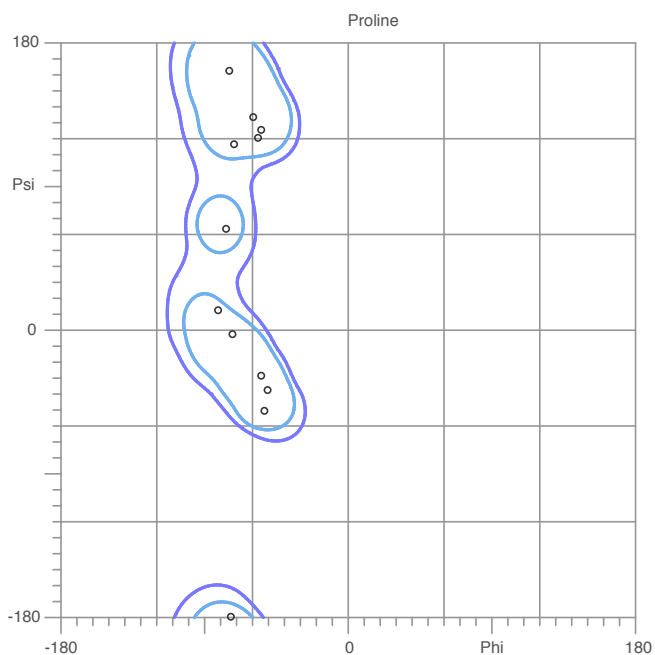
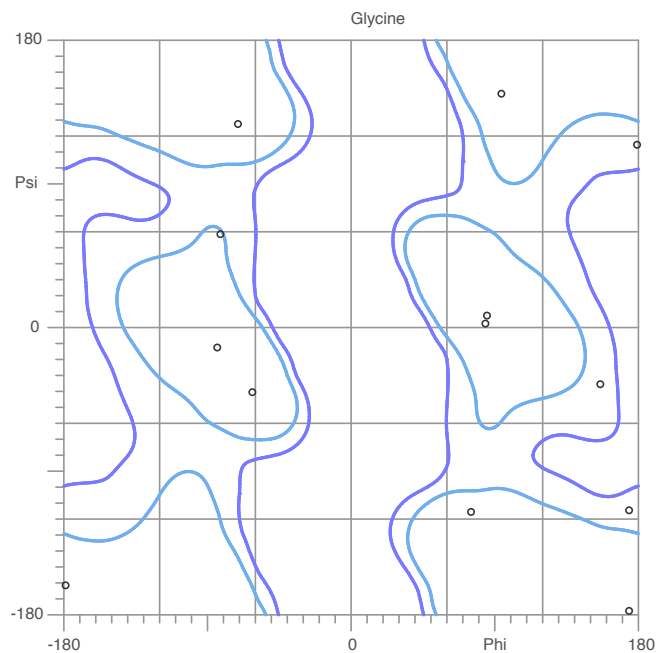
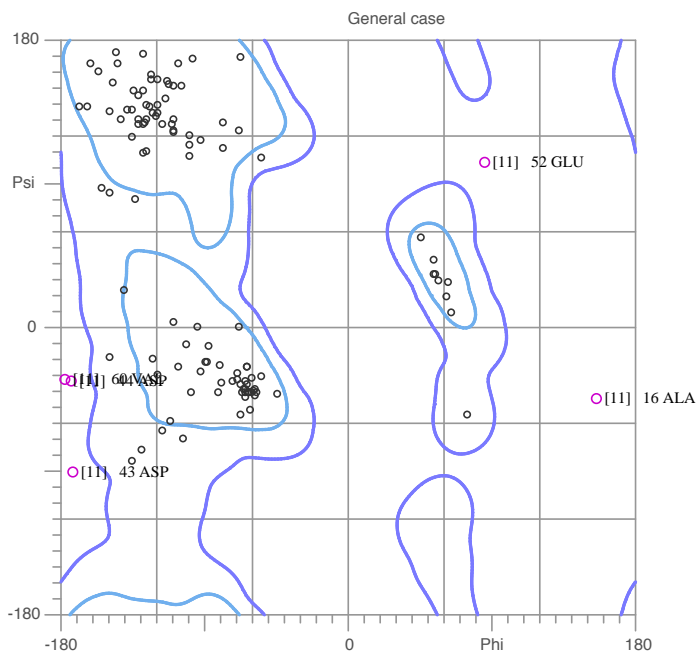
85.0% (130/153) of all residues were in favored (98%) regions.
96.7% (148/153) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[10] 16 ALA (155.0, -45.1)
[10] 52 GLU (-167.8, -33.8)
[10] 55 ALA (76.6, 137.4)
[10] 99 ALA (178.2, 26.3)
[10] 154 HIS (-164.9, -105.0)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 11



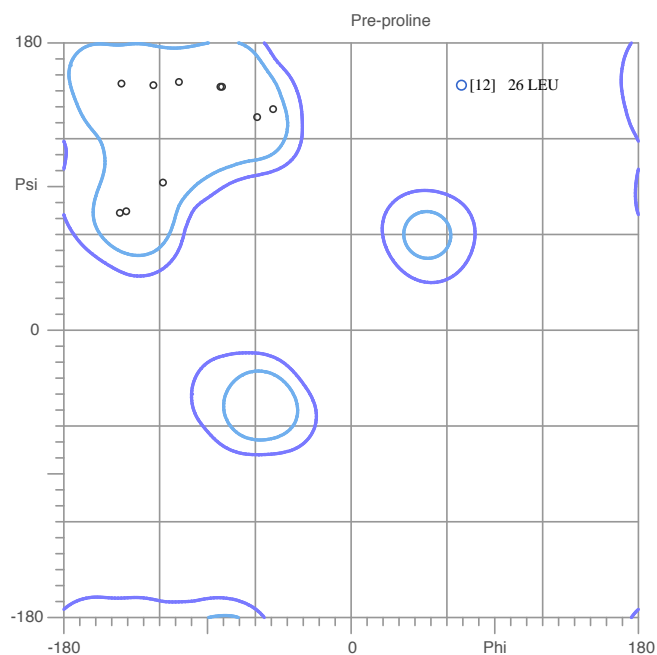
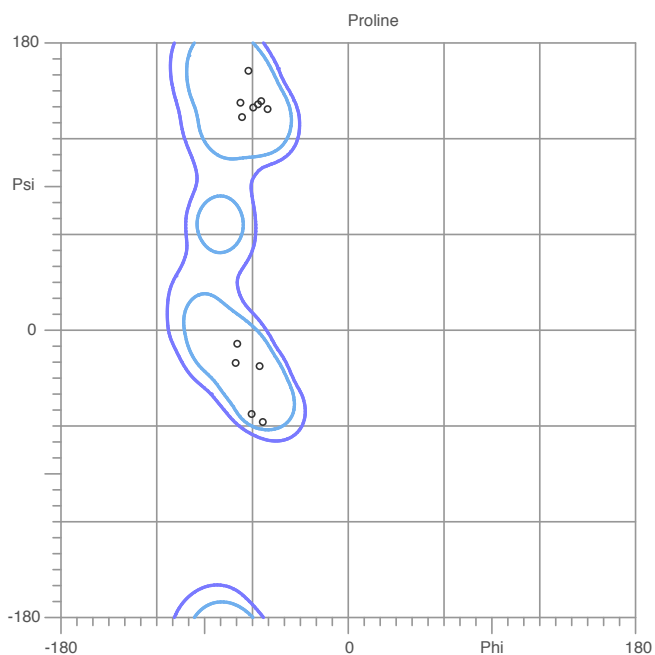
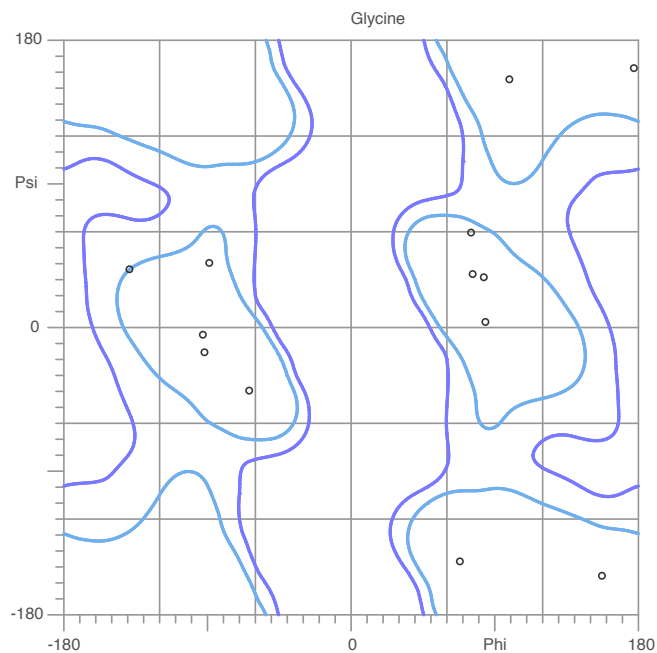
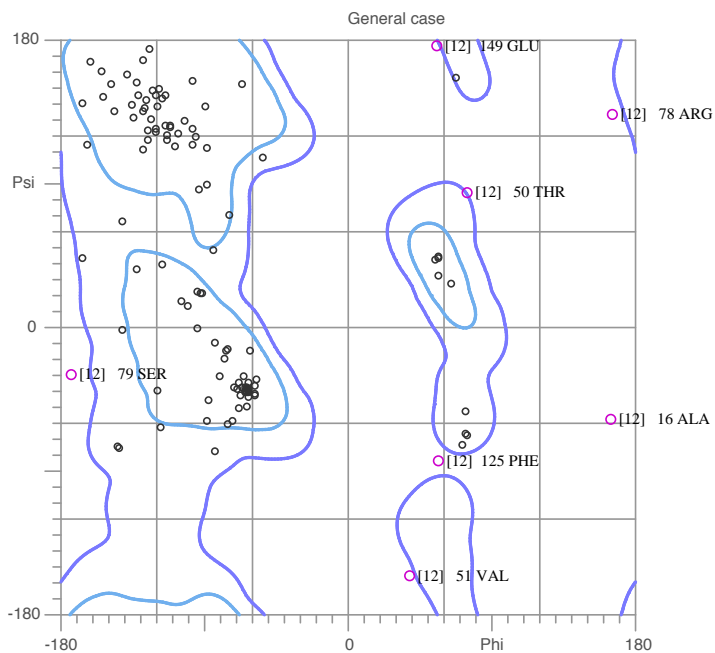
86.9% (133/153) of all residues were in favored (98%) regions.
96.1% (147/153) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[11] 16 ALA (155.0, -45.0)

[11] 26 LEU (64.9, 147.6)
[11] 43 ASP (-173.1, -90.4)
[11] 44 ASP (-175.0, -33.6)
[11] 52 GLU (85.0, 105.0)
[11] 60 VAL (-178.1, -32.9)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 12



84.3% (129/153) of all residues were in favored (98%) regions.
94.8% (145/153) of all residues were in allowed (>99.8%) regions.

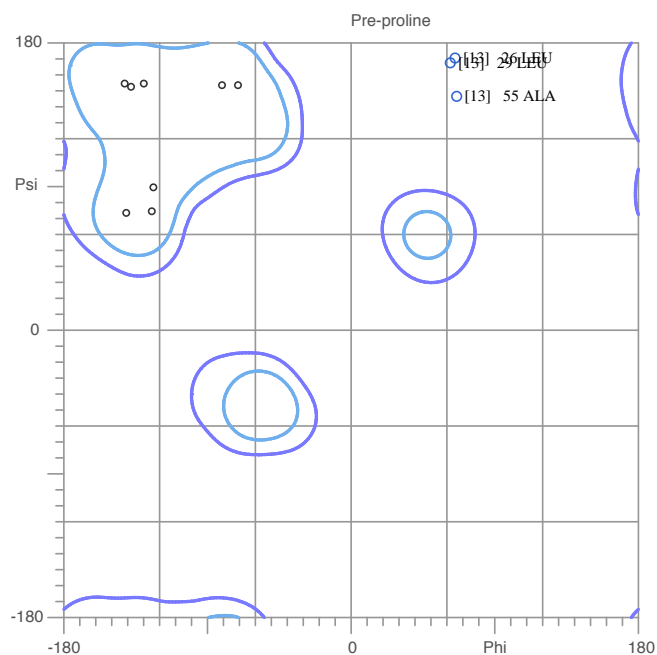
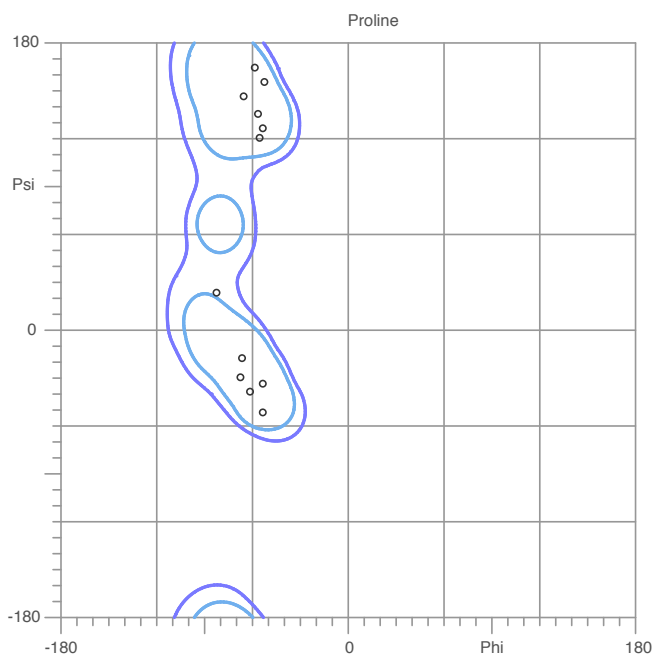
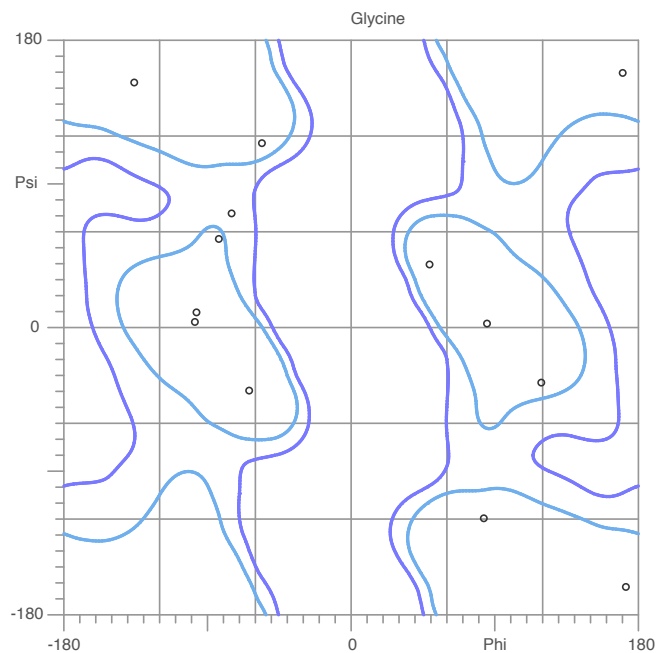
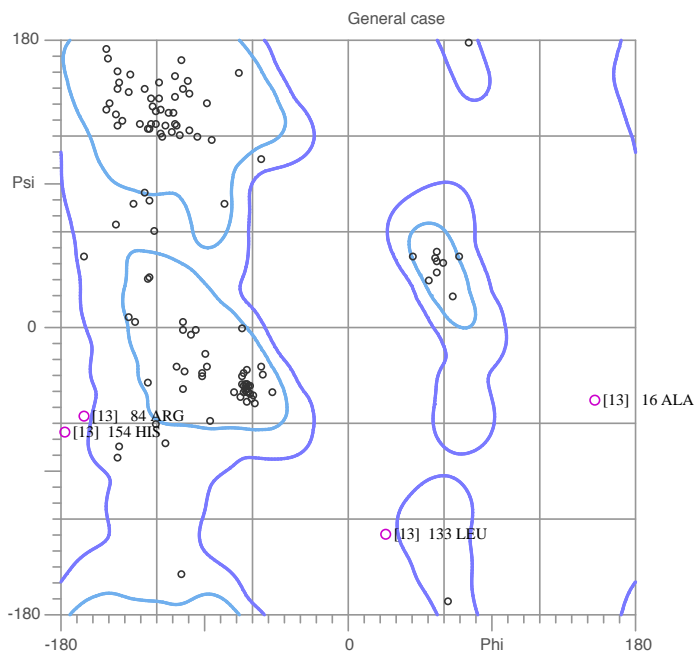
There were 8 outliers (phi, psi):

[12] 16 ALA (165.0, -57.8)
[12] 26 LEU (69.7, 155.0)

[12] 50 THR (75.0, 85.0)
[12] 51 VAL (39.0, -155.0)
[12] 78 ARG (165.0, 135.0)
[12] 79 SER (-175.0, -29.7)
[12] 125 PHE (56.5, -83.9)
[12] 149 GLU (55.3, 177.1)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 13



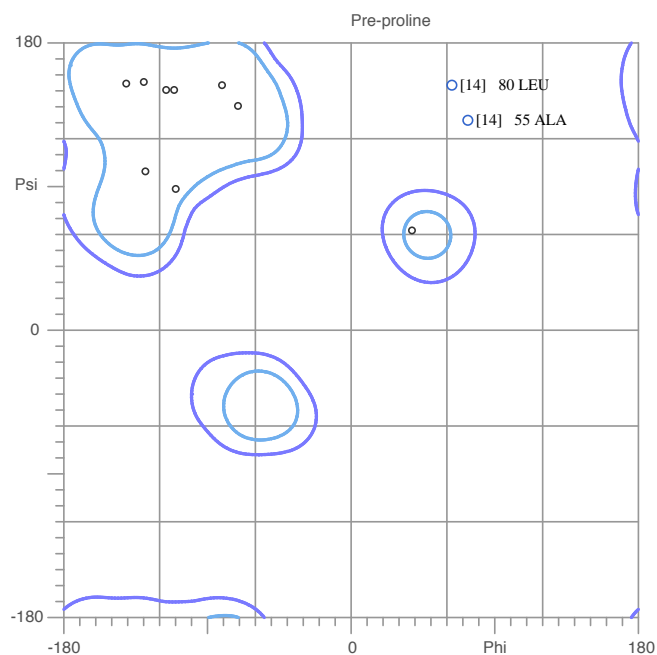
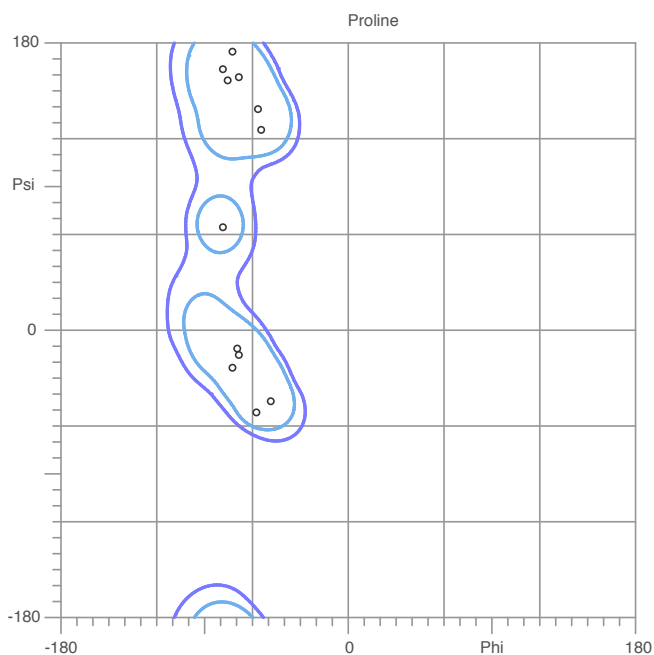
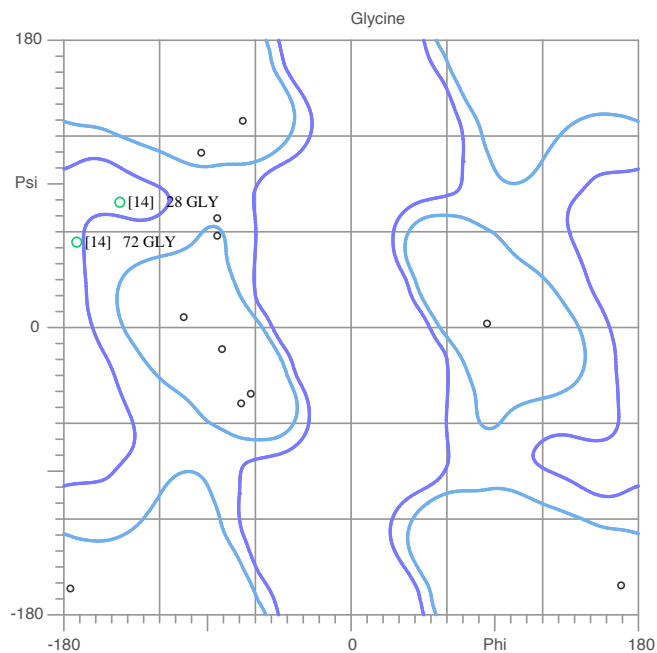
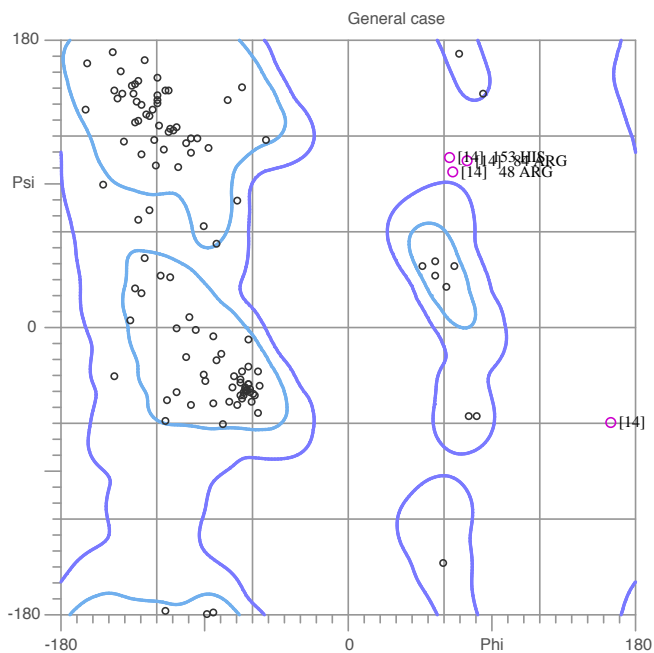
85.0% (130/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[13] 16 ALA (155.0, -45.0)

[13] 26 LEU (65.7, 171.7)
[13] 29 LEU (62.9, 168.9)
[13] 55 ALA (66.6, 147.9)
[13] 84 ARG (-166.3, -55.0)
[13] 133 LEU (23.1, -129.7)
[13] 154 HIS (-178.5, -65.2)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 14



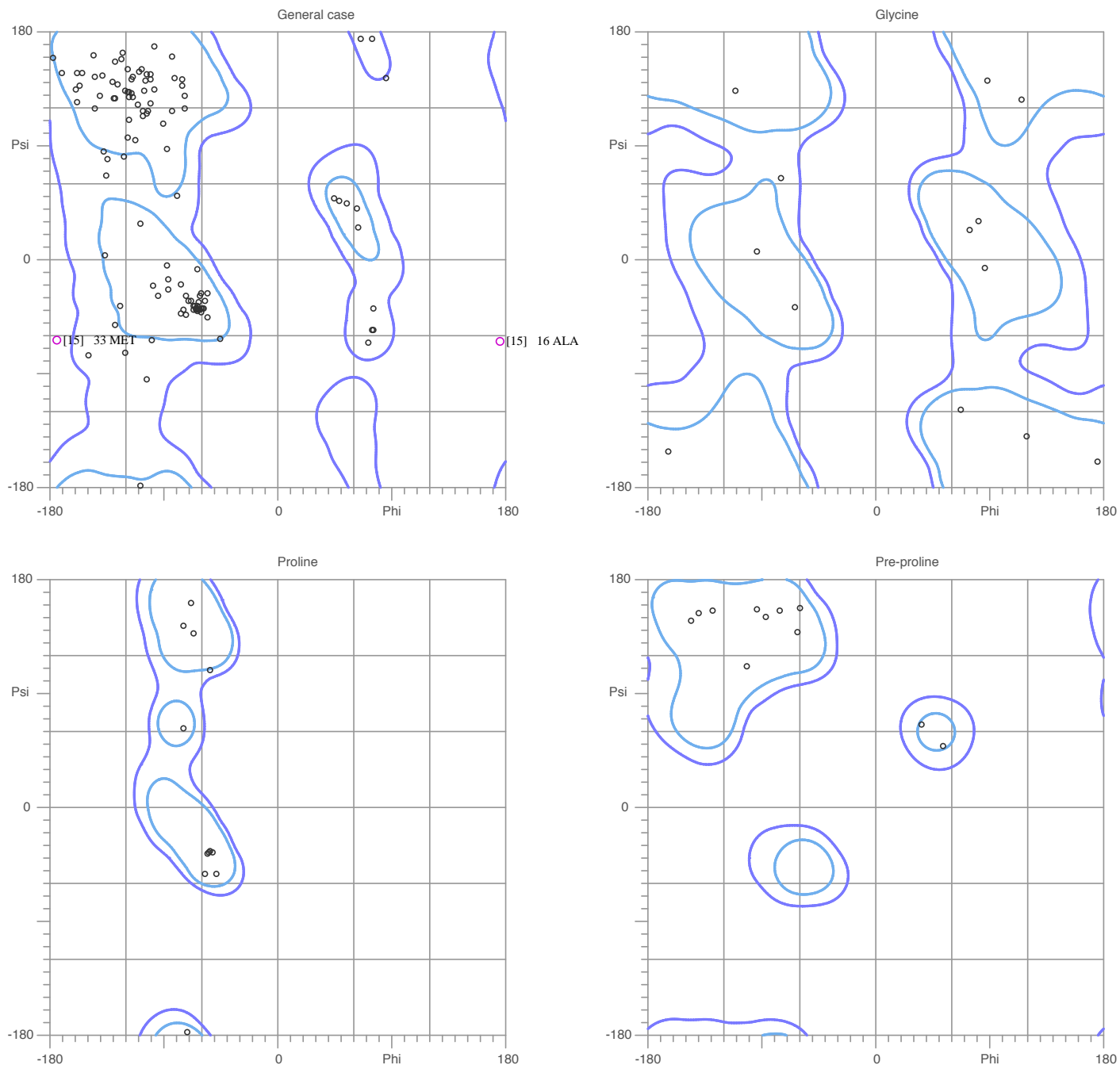
87.6% (134/153) of all residues were in favored (98%) regions.
 94.8% (145/153) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):
 [14] 16 ALA (165.0, -59.5)
 [14] 28 GLY (-145.0, 79.9)

[14] 48 ARG (65.8, 98.3)
 [14] 55 ALA (73.6, 132.6)
 [14] 72 GLY (-172.9, 54.9)
 [14] 80 LEU (63.1, 155.0)
 [14] 84 ARG (75.0, 105.0)
 [14] 153 HIS (63.4, 107.1)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 15

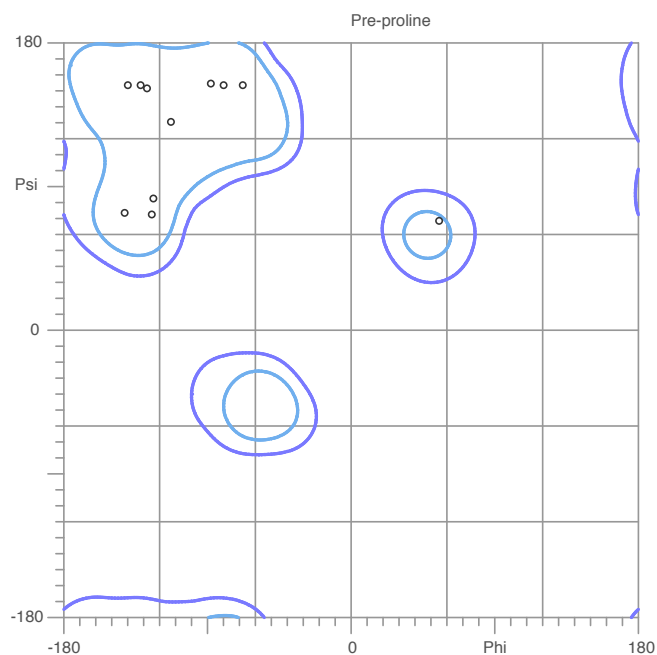
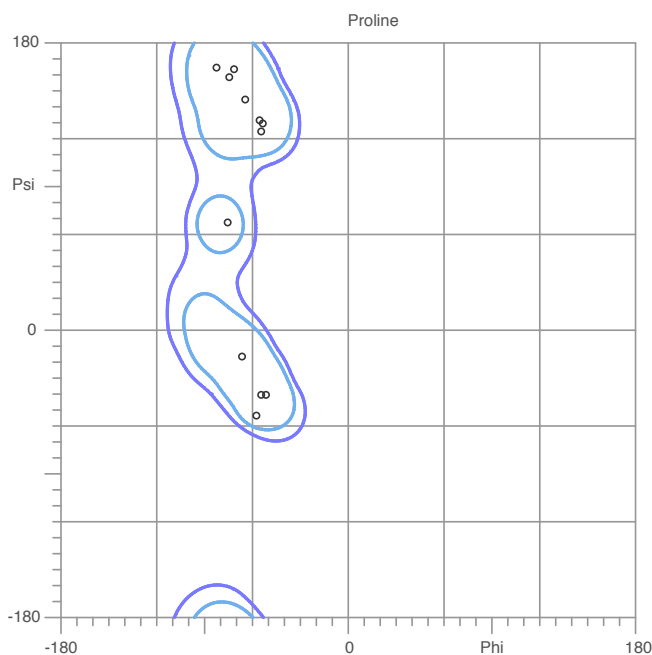
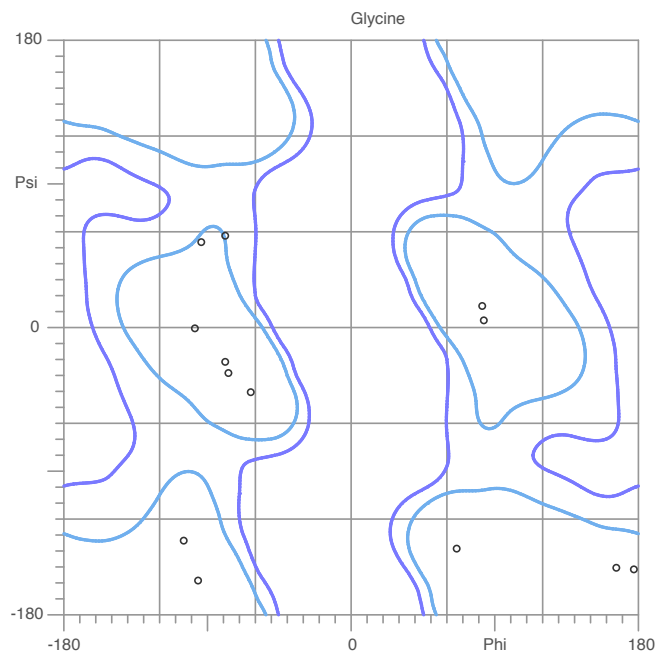
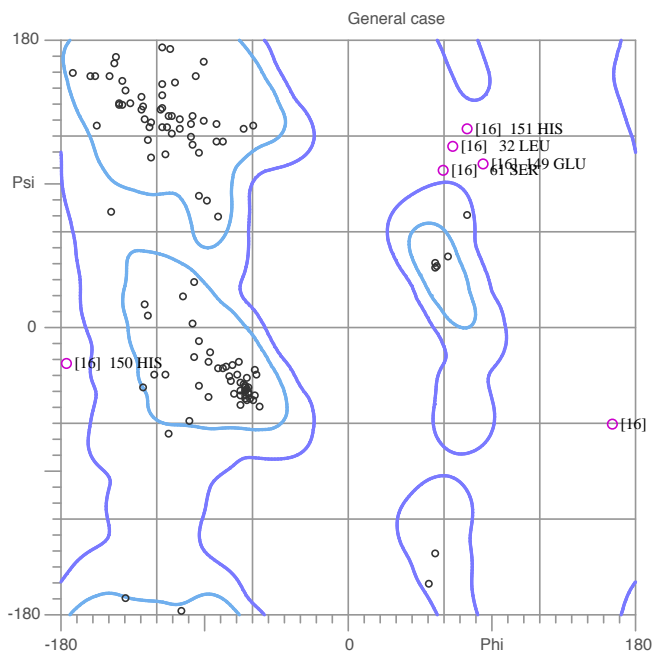


86.3% (132/153) of all residues were in favored (98%) regions.
98.7% (151/153) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[15] 16 ALA (175.0, -65.0)
[15] 33 MET (-175.0, -63.3)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 16



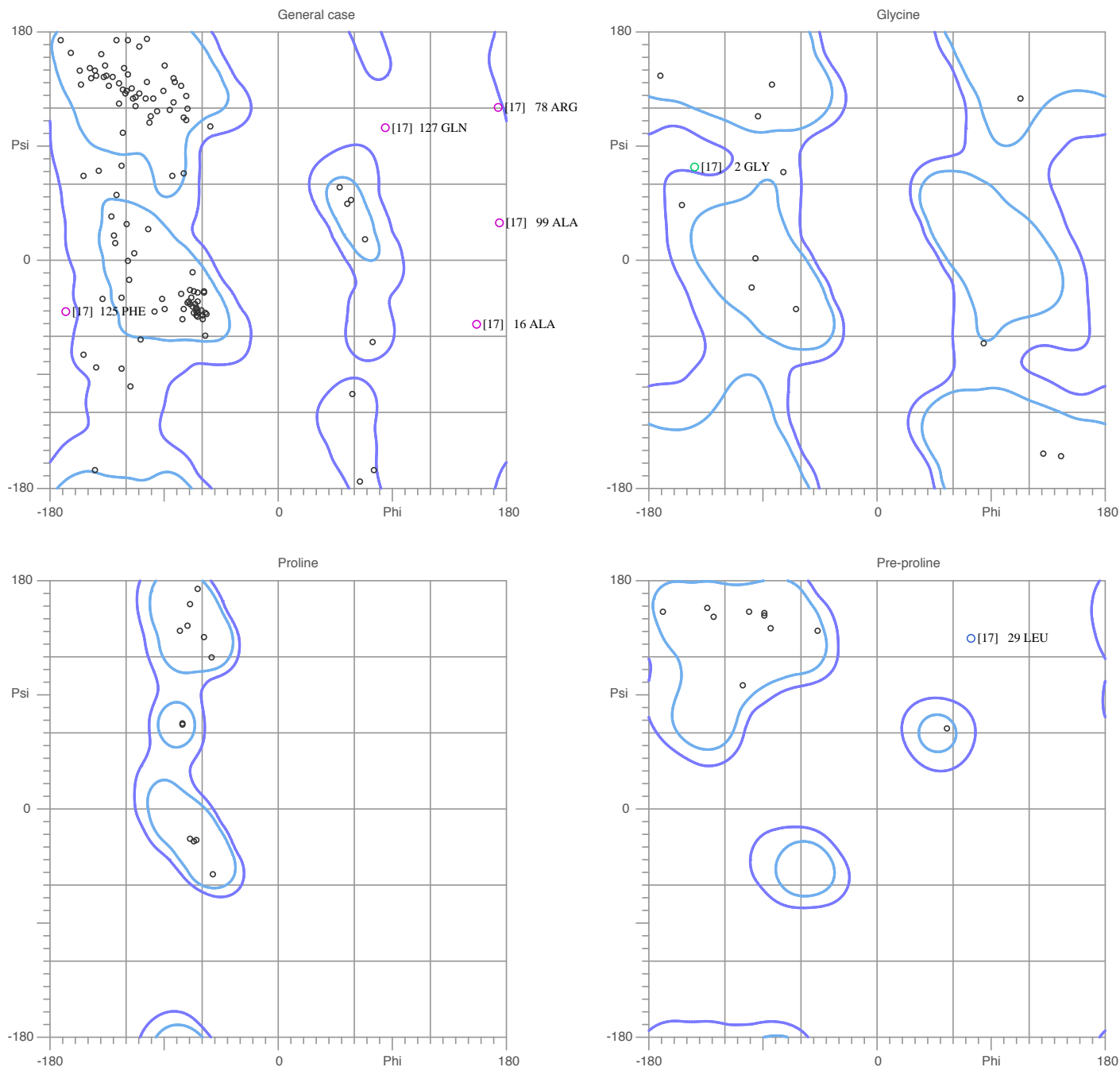
91.5% (140/153) of all residues were in favored (98%) regions.
96.1% (147/153) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[16] 16 ALA (165.0, -60.4)

[16] 32 LEU (65.0, 115.0)
[16] 61 SER (59.7, 99.9)
[16] 149 GLU (85.0, 103.7)
[16] 150 HIS (-177.4, -22.4)
[16] 151 HIS (74.9, 125.0)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 17



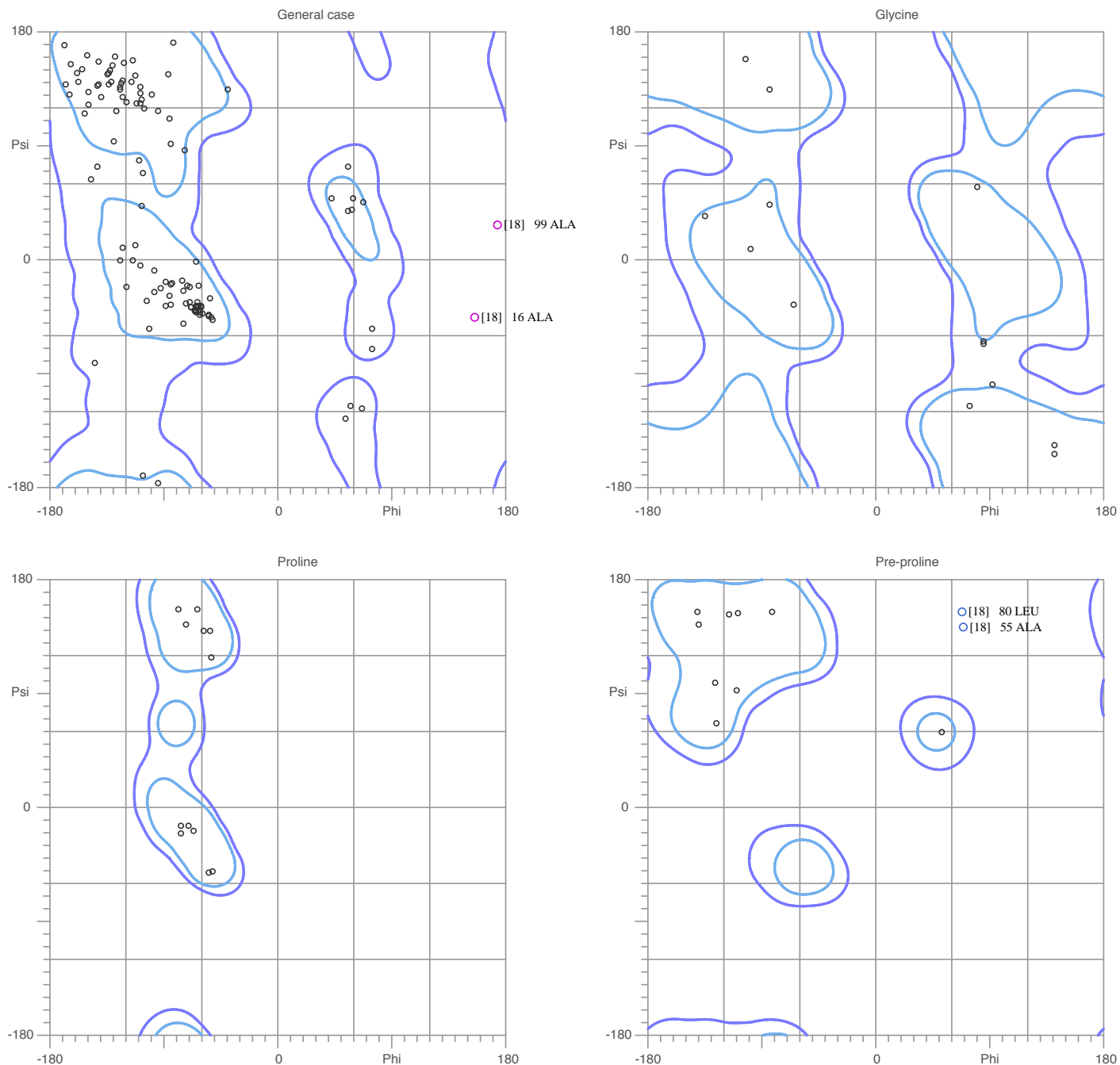
83.0% (127/153) of all residues were in favored (98%) regions.
95.4% (146/153) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[17] 2 GLY (-144.8, 75.0)

[17] 16 ALA (156.1, -50.4)
[17] 29 LEU (74.8, 135.0)
[17] 78 ARG (173.6, 121.8)
[17] 99 ALA (174.7, 30.8)
[17] 125 PHE (-168.1, -40.3)
[17] 127 GLN (84.7, 105.2)

MolProbity Ramachandran analysis

DRR147D_R3Cons_em_bcr3.pdb, model 18



86.3% (132/153) of all residues were in favored (98%) regions.
97.4% (149/153) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [18] 16 ALA (155.1, -45.0)
- [18] 55 ALA (69.3, 143.8)
- [18] 80 LEU (68.8, 155.0)
- [18] 99 ALA (173.4, 28.1)