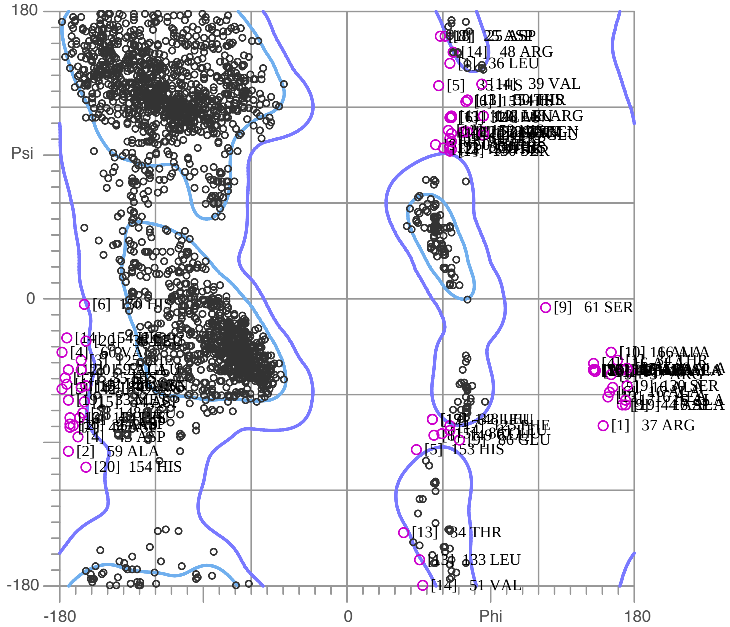
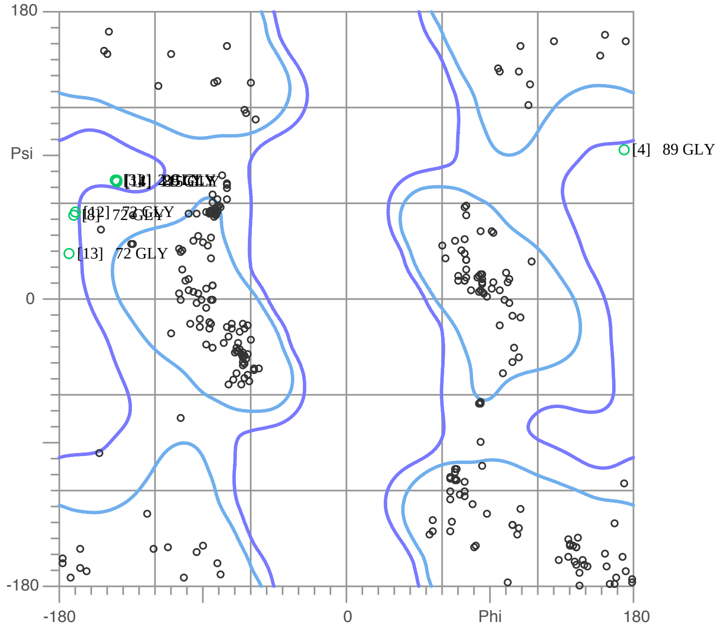
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, all models

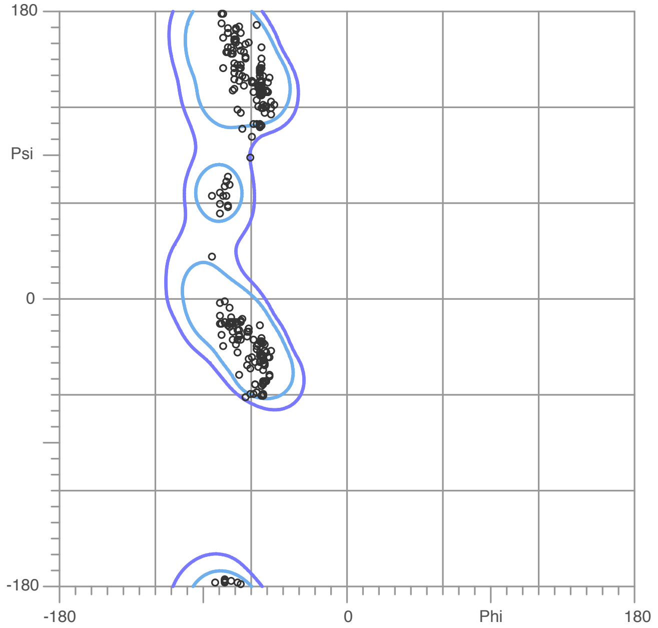
General case



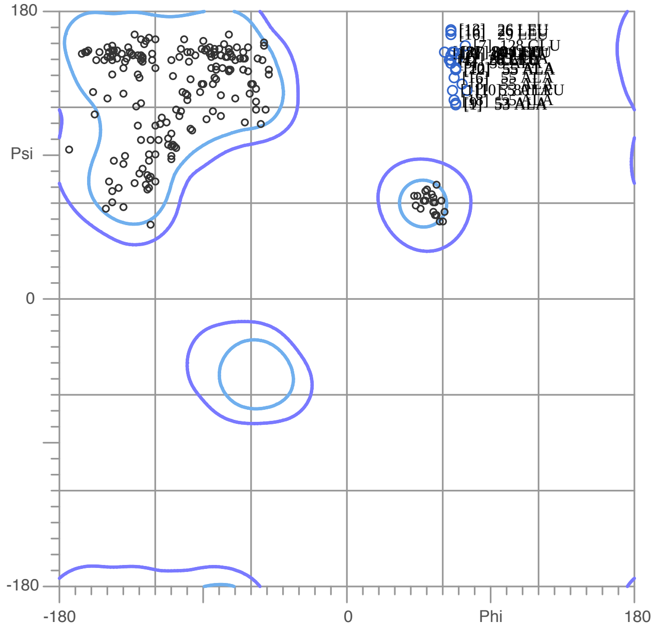
Glycine



Proline



Pre-proline



86.2% (2638/3060) of all residues were in favored (98%) regions.
96.0% (2938/3060) of all residues were in allowed (>99.8%) regions.

There were 122 outliers (phi, psi):
[1] 16 ALA (165.0, -33.5)
[1] 34 THR (169.9, -38.3)
[1] 36 LEU (64.9, 148.0)
[1] 37 ARG (160.7, -79.4)
[1] 42 LEU (-176.5, -53.3)
[1] 53 ALA (68.3, 122.2)
[1] 80 LEU (65.1, 150.2)
[2] 16 ALA (177.8, -45.1)
[2] 35 HIS (-172.2, -79.1)
[2] 42 LEU (-168.2, -75.0)
[2] 55 ALA (69.5, 151.0)
[2] 59 ALA (-175.0, -95.0)
[2] 80 LEU (67.4, 155.0)
[2] 132 GLN (73.4, 105.0)
[2] 153 HIS (65.1, 94.9)
[3] 2 GLY (-145.1, 75.2)
[3] 16 ALA (154.7, -45.0)
[3] 29 LEU (70.0, 154.9)
[3] 125 PHE (-167.9, -38.7)
[3] 127 GLN (85.0, 105.0)
[4] 16 ALA (154.9, -41.0)
[4] 26 LEU (65.0, 150.5)
[4] 43 ASP (-169.7, -86.9)
[4] 44 ASP (172.9, -45.0)
[4] 52 GLU (72.8, 105.2)
[4] 60 VAL (-179.9, -33.2)
[4] 89 GLY (174.9, 95.0)
[5] 16 ALA (166.3, -55.0)
[5] 35 HIS (57.5, 135.0)
[5] 42 LEU (-180.0, -56.4)
[5] 55 ALA (65.3, 148.7)
[5] 153 HIS (43.5, -95.0)
[6] 16 ALA (165.0, -58.6)
[6] 32 LEU (65.0, 114.9)
[6] 61 SER (64.0, 101.1)
[6] 149 GLU (85.1, 103.2)
[6] 150 HIS (-165.1, -3.9)
[6] 151 HIS (75.0, 124.9)
[7] 16 ALA (155.0, -44.5)
[7] 29 LEU (65.1, 153.2)
[7] 44 ASP (-175.0, -81.0)
[7] 128 GLU (74.7, 159.9)
[7] 148 LEU (-166.3, -71.5)
[8] 16 ALA (154.9, -45.0)
[8] 25 ASP (61.7, 165.0)
[8] 55 ALA (72.6, 135.3)
[8] 72 GLY (-171.3, 53.9)
[8] 80 LEU (66.9, 155.0)
[8] 149 GLU (54.4, -85.0)
[9] 16 ALA (155.0, -44.9)
[9] 35 HIS (65.0, 96.9)
[9] 37 ARG (165.0, -47.8)
[9] 44 ASP (172.4, -66.0)
[9] 50 THR (55.1, 97.1)
[9] 53 ALA (68.3, 124.0)
[9] 61 SER (124.4, -5.1)
[9] 86 GLU (70.0, -88.7)
[9] 130 SER (175.1, -55.0)
[10] 16 ALA (165.1, -33.6)
[10] 55 ALA (68.8, 144.9)
[10] 80 LEU (75.1, 131.9)
[11] 16 ALA (155.0, -44.9)
[11] 50 THR (75.1, 125.0)
[11] 55 ALA (66.2, 131.4)
[11] 89 GLY (-145.0, 75.0)
[11] 130 SER (65.1, 105.0)
[11] 148 LEU (65.0, 115.0)
[12] 16 ALA (173.9, -45.0)
[12] 28 GLY (-144.9, 75.1)
[12] 48 ARG (85.0, 115.0)
[12] 55 ALA (68.1, 144.9)
[12] 59 ALA (-175.1, -45.0)
[12] 72 GLY (-170.7, 55.0)
[12] 80 LEU (61.2, 155.1)
[12] 84 ARG (75.1, 105.0)
[12] 153 HIS (63.4, 106.5)
[13] 16 ALA (163.0, -61.7)
[13] 26 LEU (65.1, 169.2)
[13] 34 THR (35.1, -146.8)
[13] 72 GLY (-175.0, 29.3)
[13] 126 ASN (65.0, 114.9)
[13] 133 LEU (45.1, -163.1)
[13] 150 HIS (64.9, 95.0)
[13] 154 HIS (75.0, 125.1)
[14] 16 ALA (155.0, -45.0)
[14] 31 LEU (64.6, -82.7)
[14] 39 VAL (84.9, 135.0)
[14] 48 ARG (66.0, 155.1)
[14] 51 VAL (47.4, -179.7)
[14] 115 GLY (-144.9, 75.0)
[14] 130 SER (65.0, 94.0)
[14] 154 HIS (-177.0, -25.0)
[15] 16 ALA (175.1, -43.9)
[15] 44 ASP (-165.0, -65.0)
[15] 48 ARG (-164.9, -54.9)
[15] 86 GLU (59.6, -84.8)
[15] 126 ASN (-165.0, -55.0)
[16] 16 ALA (155.0, -44.9)
[16] 26 LEU (65.0, 168.8)
[16] 29 LEU (65.1, 166.6)
[16] 55 ALA (67.5, 139.9)
[16] 84 ARG (-167.7, -55.1)
[16] 154 HIS (-174.6, -74.0)
[17] 16 ALA (175.0, -63.4)
[17] 26 LEU (67.2, 155.0)
[17] 35 HIS (-177.8, -49.6)
[17] 50 THR (60.8, 95.1)
[17] 125 PHE (65.0, -79.4)
[17] 148 LEU (53.5, -75.1)
[18] 16 ALA (154.9, -44.9)
[18] 25 ASP (58.6, 165.0)
[18] 44 ASP (-175.0, -78.8)
[18] 47 SER (65.0, 99.9)
[18] 55 ALA (67.7, 125.0)
[19] 16 ALA (174.9, -66.7)
[19] 32 LEU (53.7, -75.1)
[19] 33 MET (-175.0, -63.2)
[20] 16 ALA (155.0, -45.1)
[20] 36 LEU (-165.0, -26.2)
[20] 52 GLU (-167.1, -45.0)
[20] 55 ALA (68.6, 145.0)
[20] 154 HIS (-165.0, -105.0)

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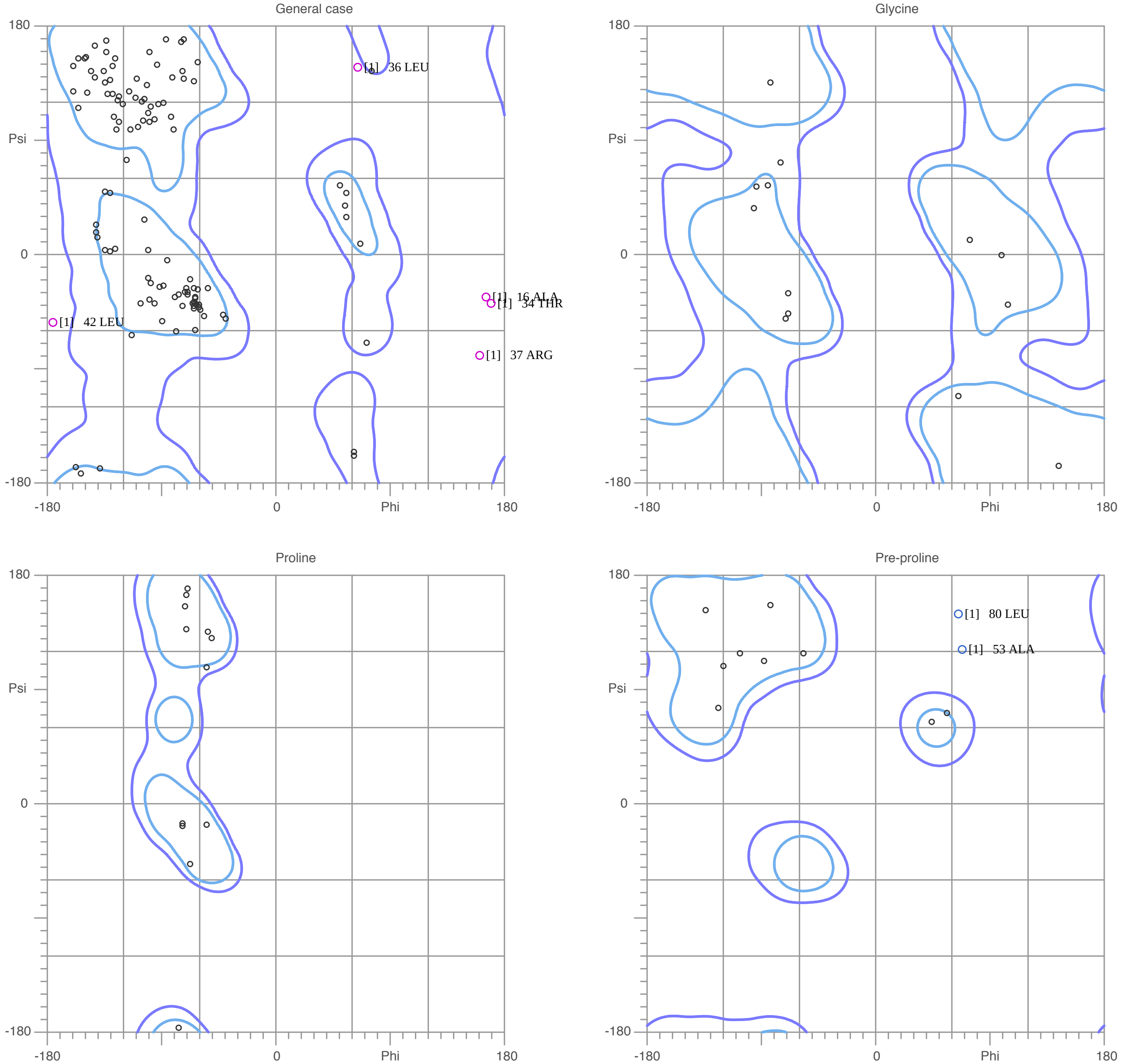
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 1



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):

[1] 16 ALA (165.0, -33.5)
[1] 34 THR (169.9, -38.3)
[1] 36 LEU (64.9, 148.0)
[1] 37 ARG (160.7, -79.4)
[1] 42 LEU (-176.5, -53.3)
[1] 53 ALA (68.3, 122.2)
[1] 80 LEU (65.1, 150.2)

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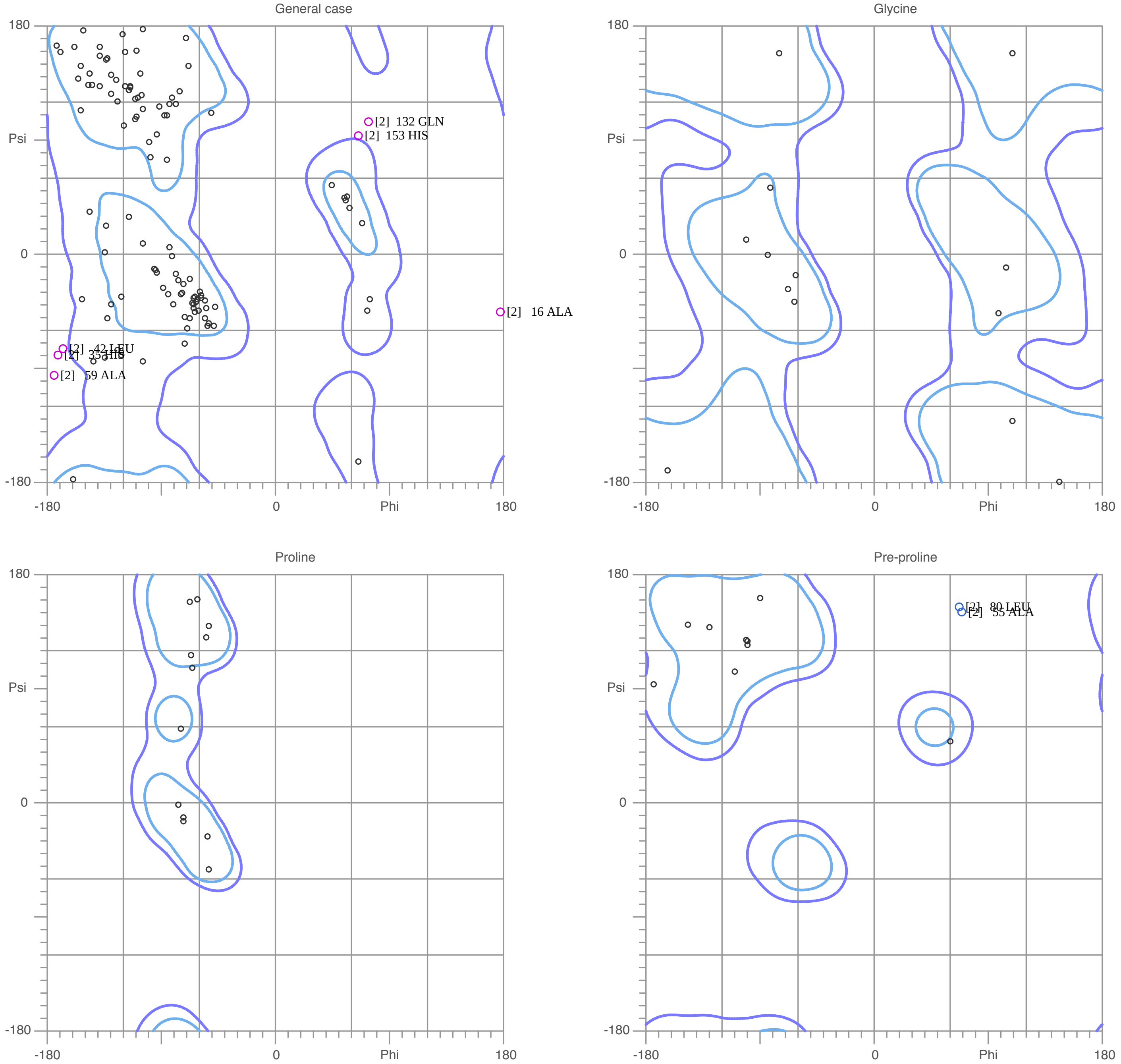
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 2

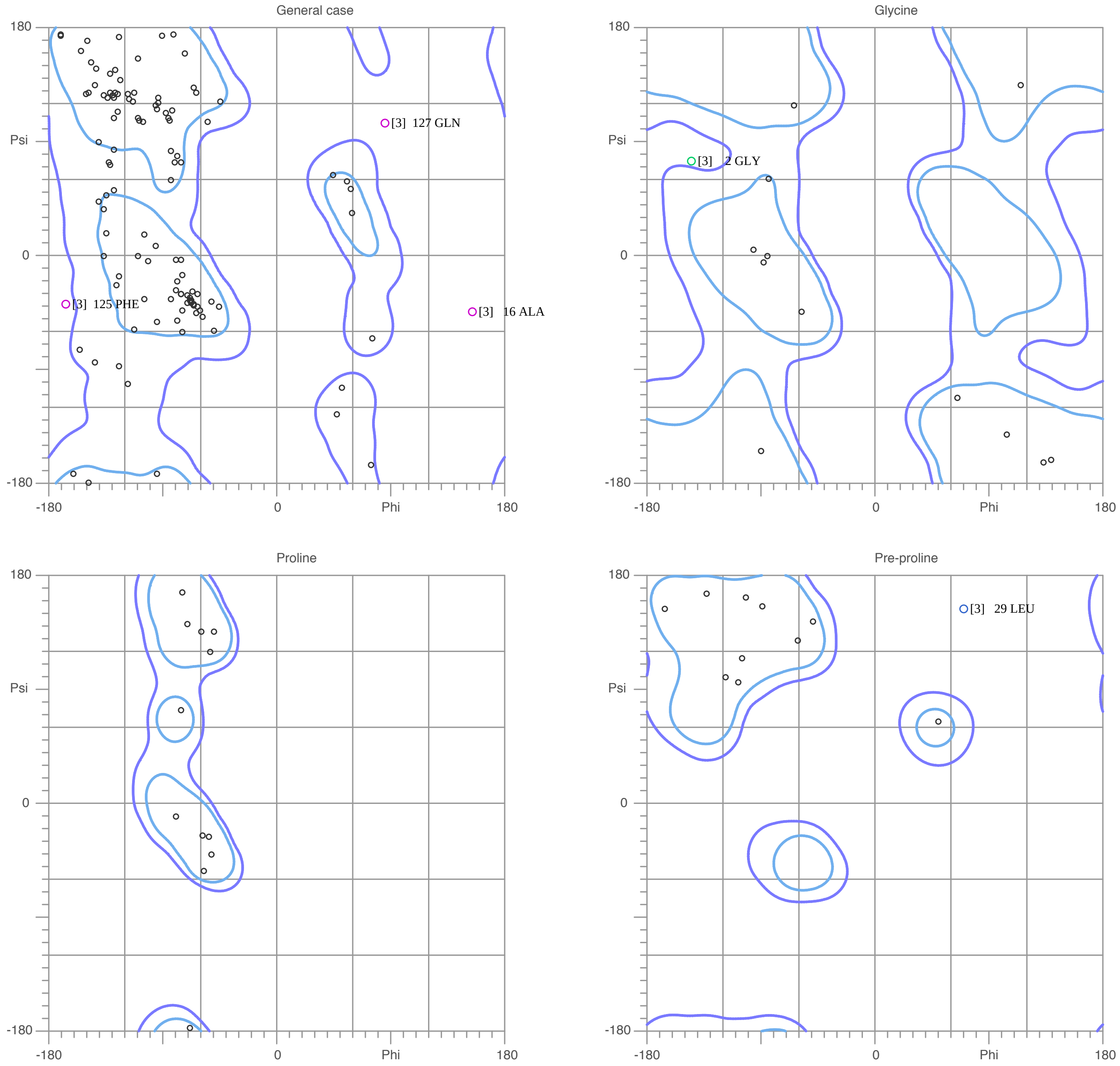


83.7% (128/153) of all residues were in favored (98%) regions.
94.8% (145/153) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):
- [2] 16 ALA (177.8, -45.1)
- [2] 35 HIS (-172.2, -79.1)
- [2] 42 LEU (-168.2, -75.0)
- [2] 55 ALA (69.5, 151.0)
- [2] 59 ALA (-175.0, -95.0)
- [2] 80 LEU (67.4, 155.0)
- [2] 132 GLN (73.4, 105.0)
- [2] 153 HIS (65.1, 94.9)

MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 3



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):

[3] 2 GLY (-145.1, 75.2)
[3] 16 ALA (154.7, -45.0)
[3] 29 LEU (70.0, 154.9)
[3] 125 PHE (-167.9, -38.7)
[3] 127 GLN (85.0, 105.0)

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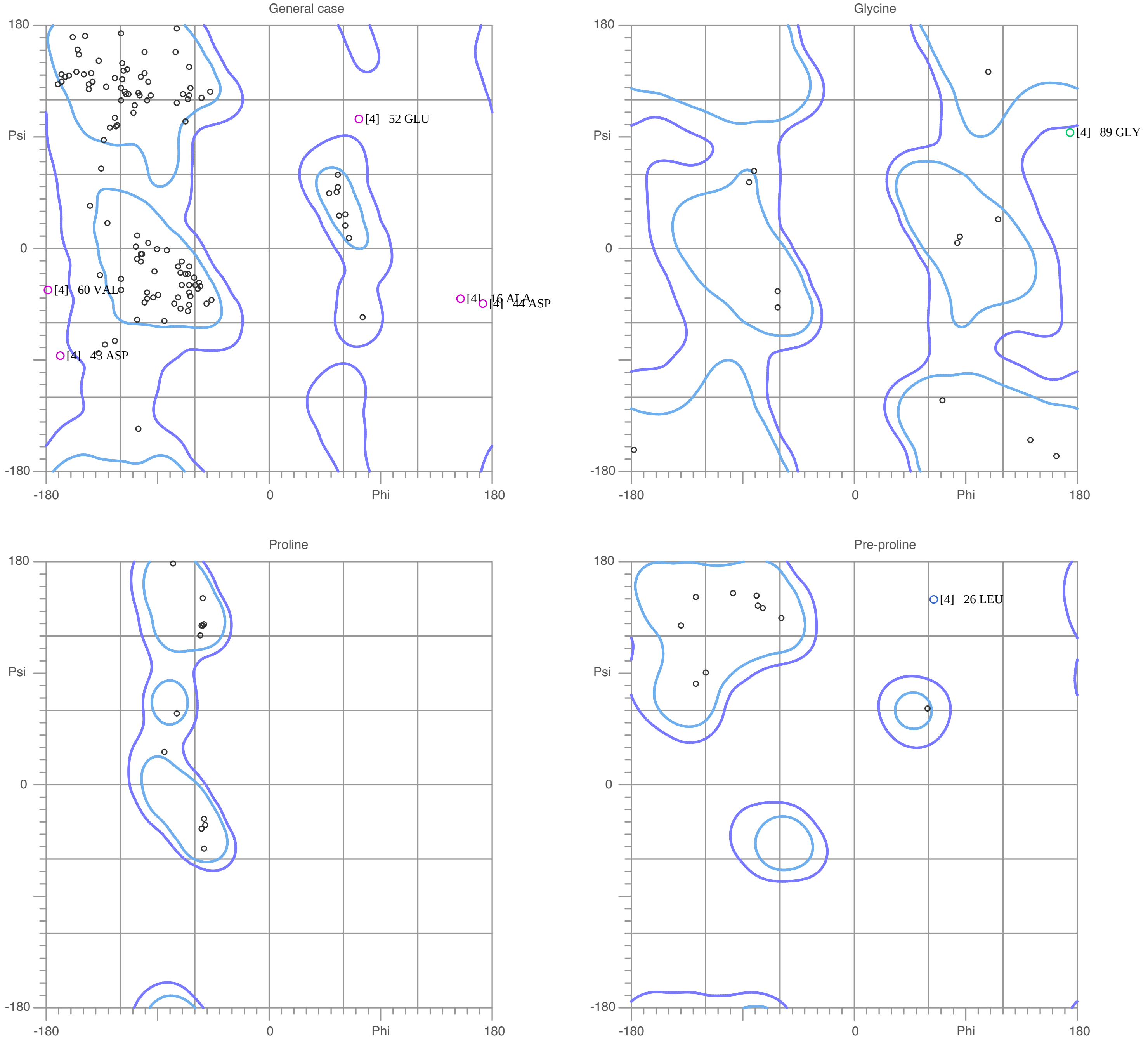
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 4



88.2% (135/153) 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):
[4] 16 ALA (154.9, -41.0)
[4] 26 LEU (65.0, 150.5)
[4] 43 ASP (-169.7, -86.9)
[4] 44 ASP (172.9, -45.0)
[4] 52 GLU (72.8, 105.2)
[4] 60 VAL (-179.9, -33.2)
[4] 89 GLY (174.9, 95.0)

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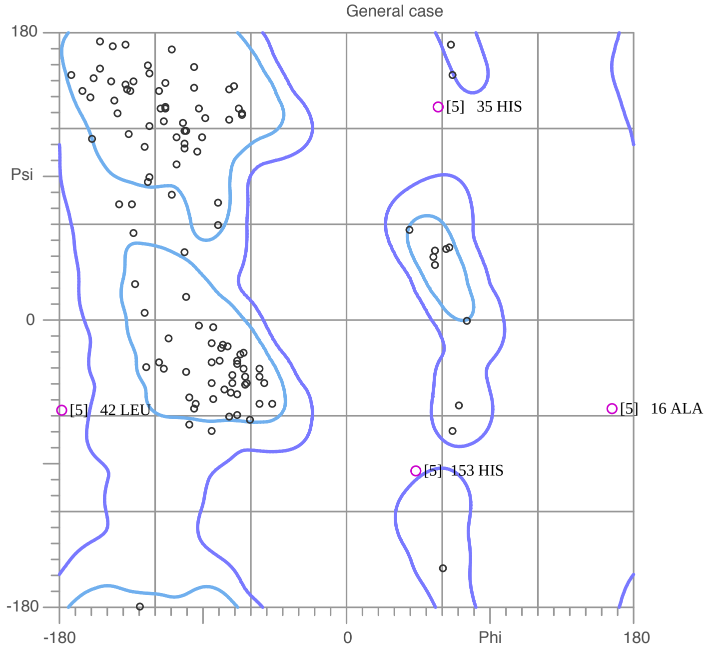
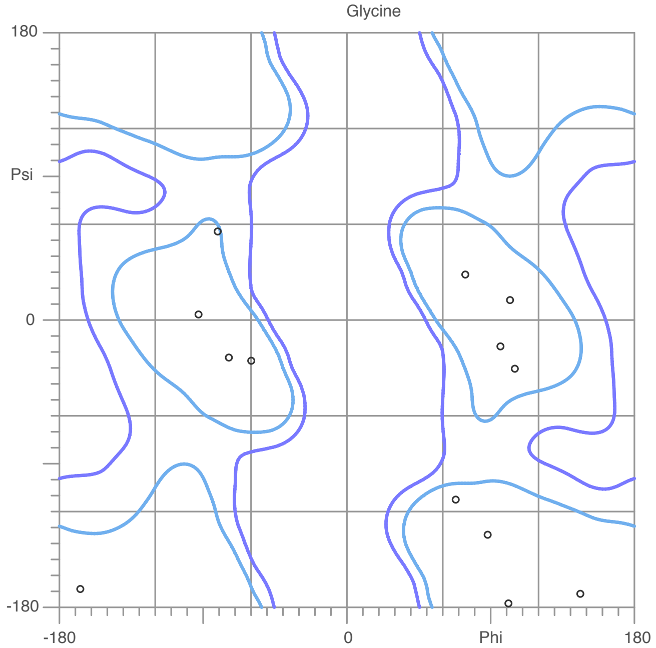
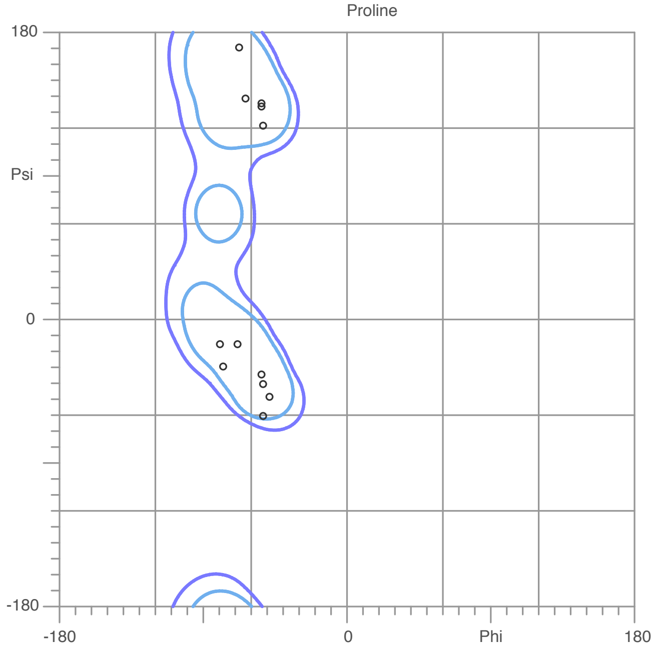
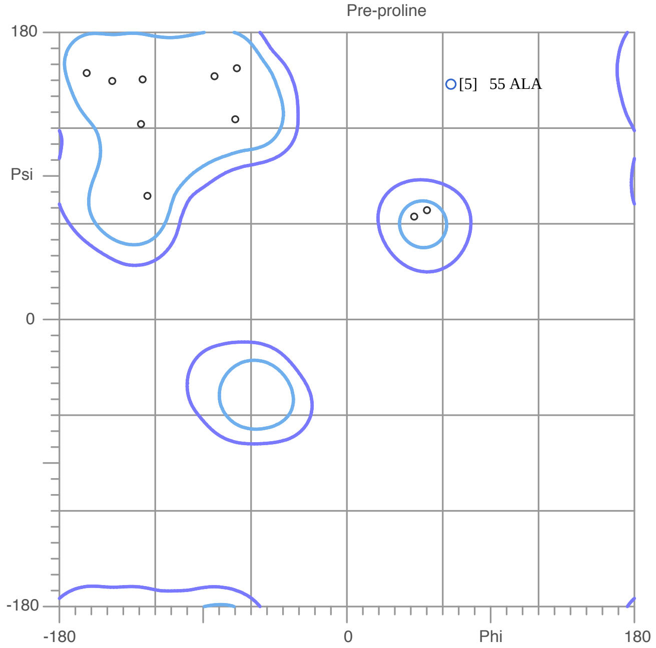
DRR147D_R3_em_bcr3.pdb, model 5









87.6% (134/153) 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):

[5] 16 ALA (166.3, -55.0)
[5] 35 HIS (57.5, 135.0)
[5] 42 LEU (-180.0, -56.4)
[5] 55 ALA (65.3, 148.7)
[5] 153 HIS (43.5, -95.0)

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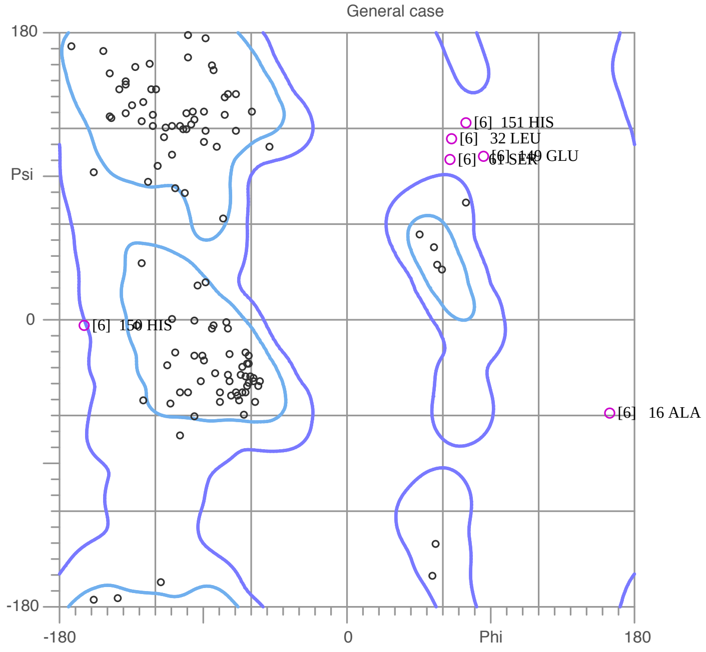
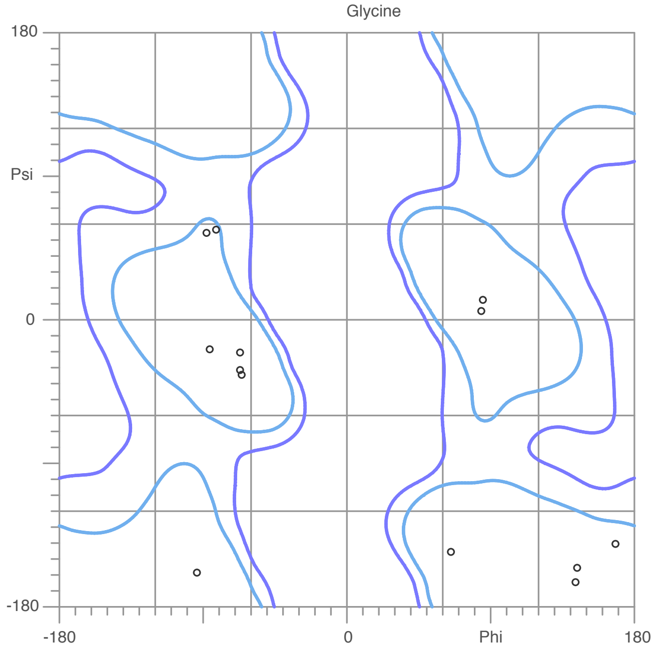
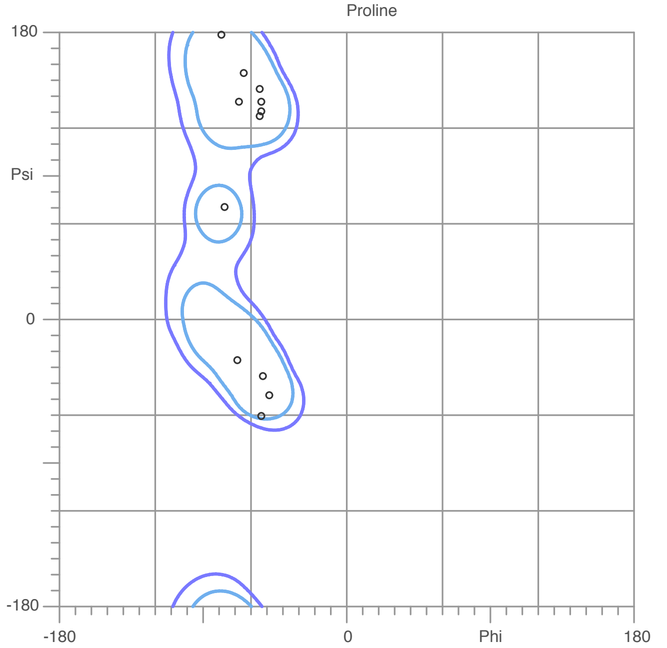
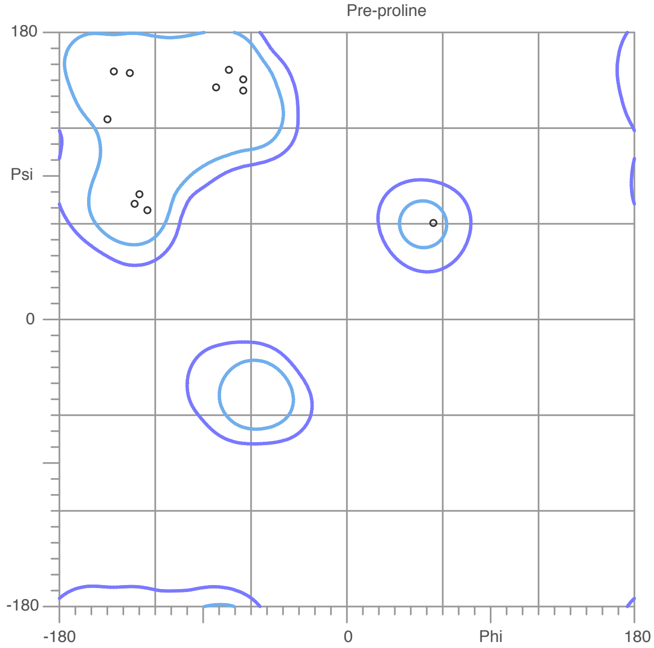
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 6









90.2% (138/153) 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):
[6] 16 ALA (165.0, -58.6)
[6] 32 LEU (65.0, 114.9)
[6] 61 SER (64.0, 101.1)
[6] 149 GLU (85.1, 103.2)
[6] 150 HIS (-165.1, -3.9)
[6] 151 HIS (75.0, 124.9)

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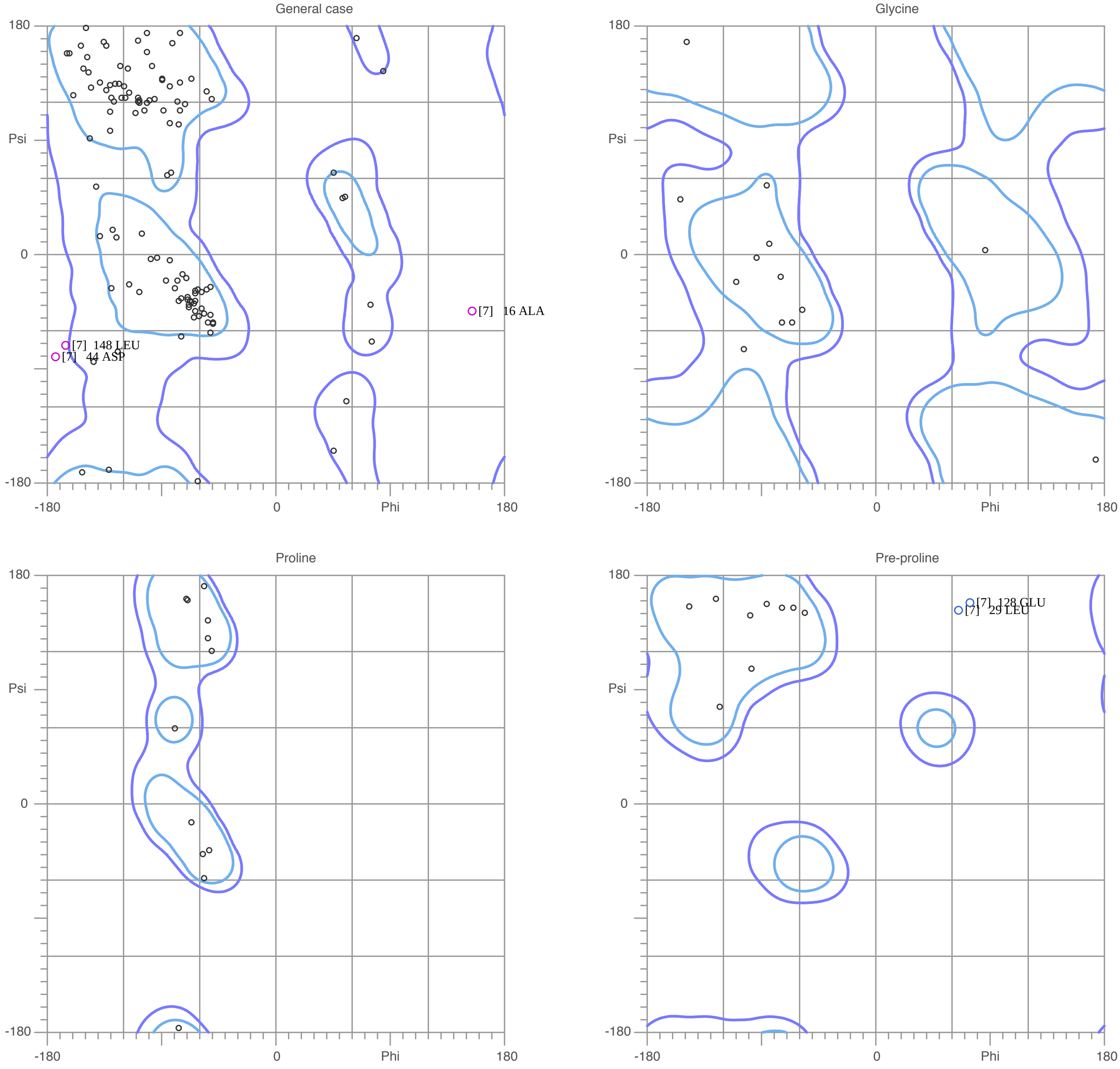
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 7



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):

[7] 16 ALA (155.0, -44.5)
[7] 29 LEU (65.1, 153.2)
[7] 44 ASP (-175.0, -81.0)
[7] 128 GLU (74.7, 159.9)
[7] 148 LEU (-166.3, -71.5)

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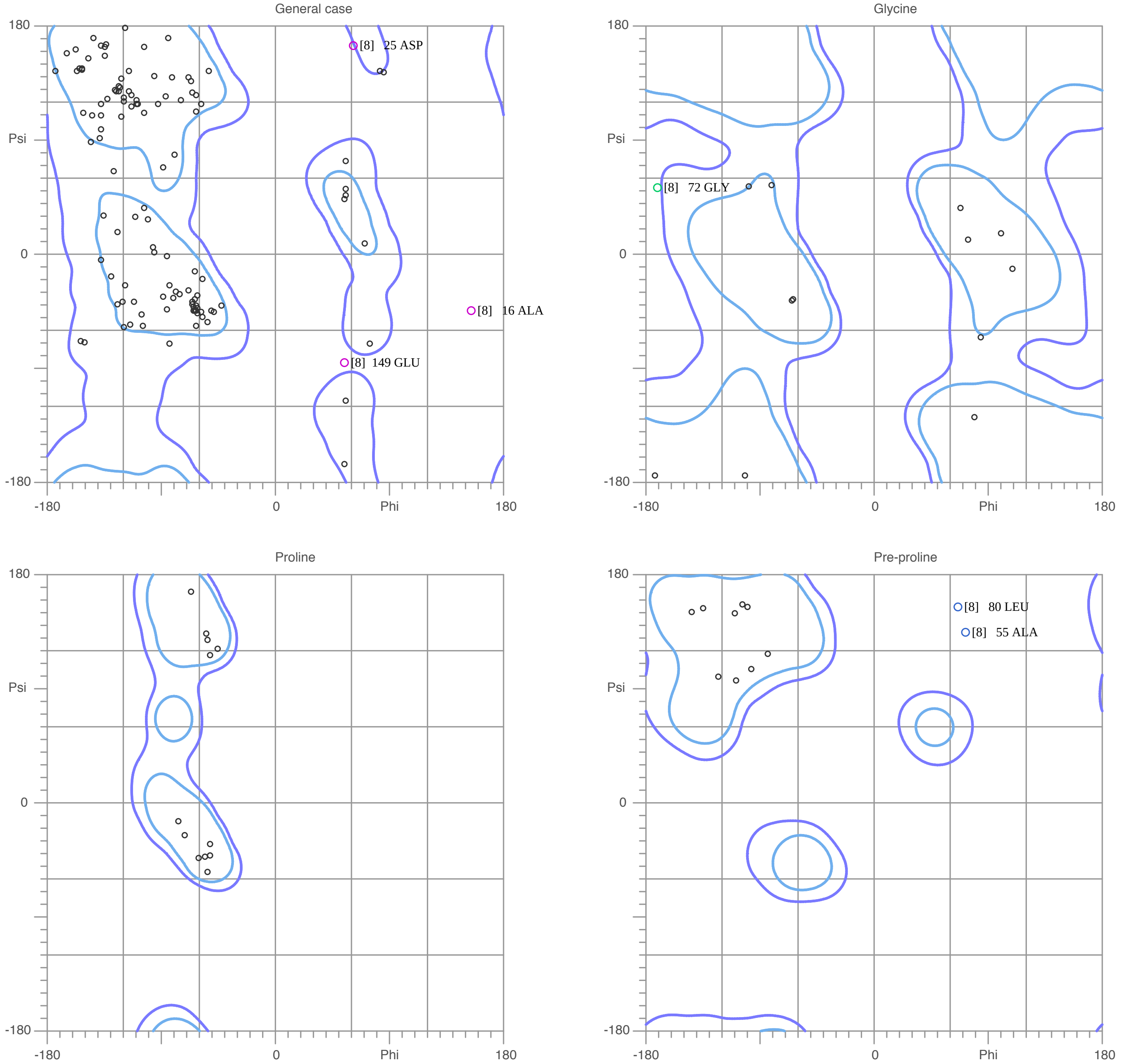
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 8



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):

[8] 16 ALA (154.9, -45.0)

[8] 25 ASP (61.7, 165.0)

[8] 55 ALA (72.6, 135.3)

[8] 72 GLY (-171.3, 53.9)

[8] 80 LEU (66.9, 155.0)

[8] 149 GLU (54.4, -85.0)

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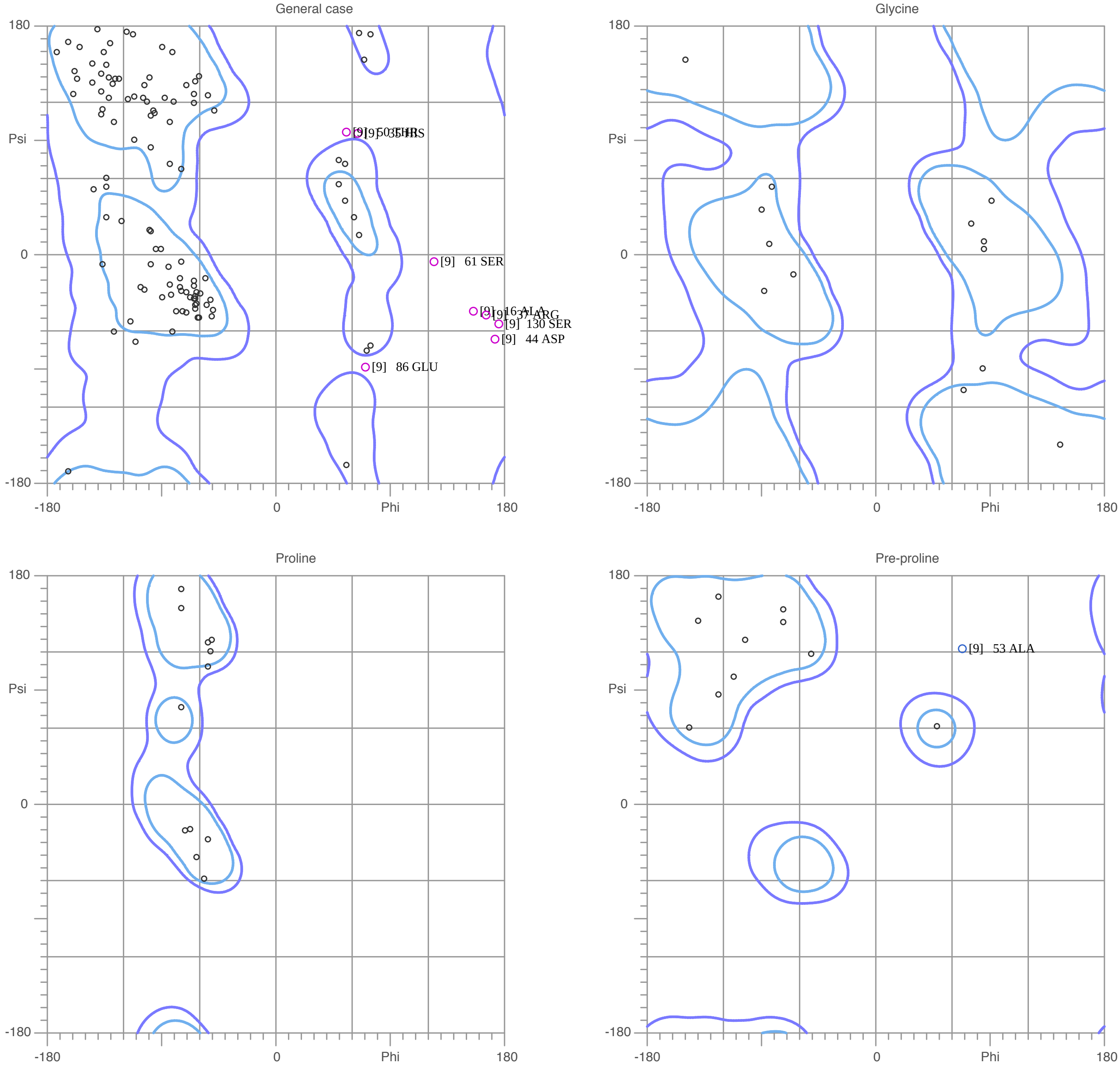
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 9



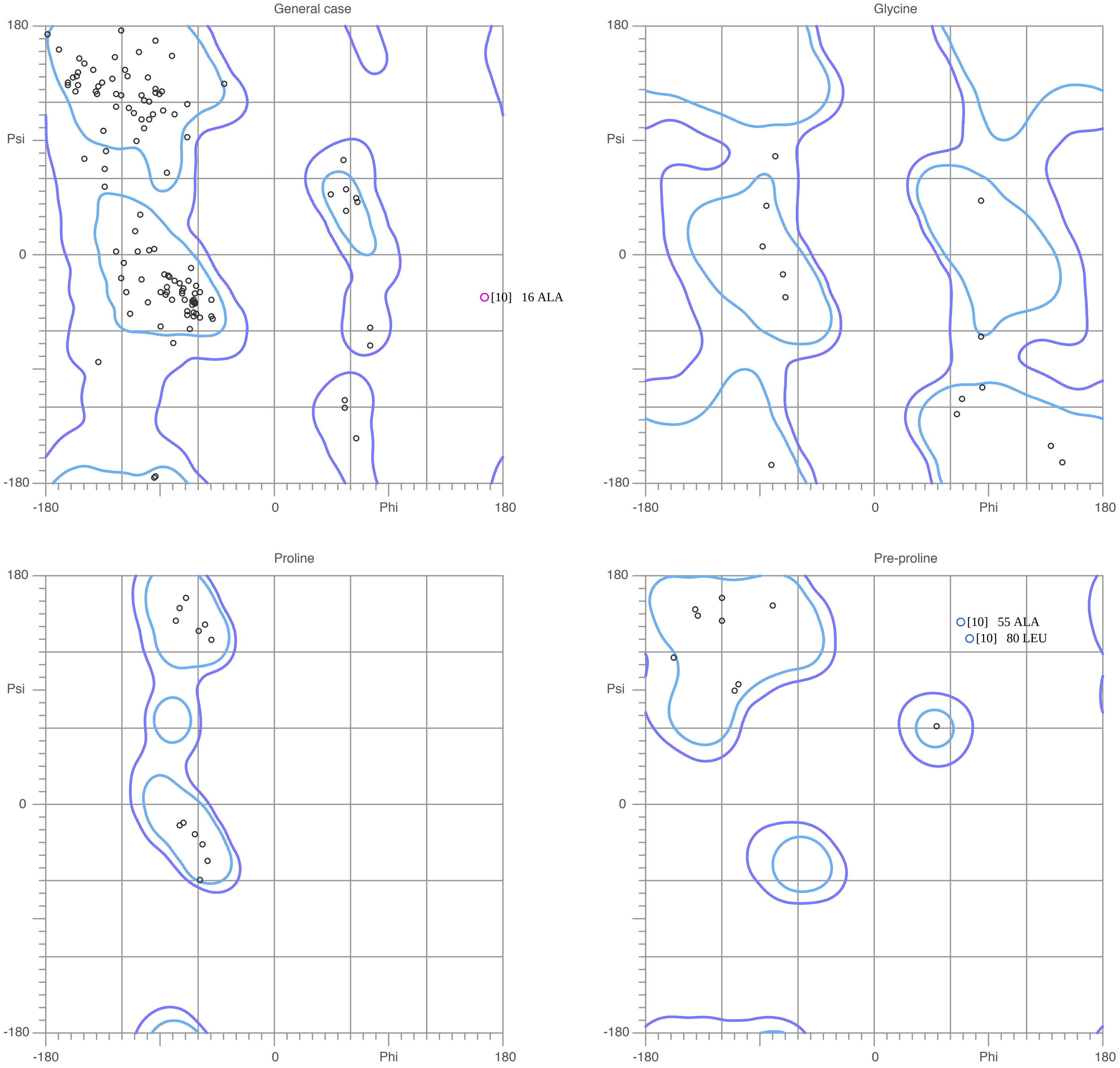
83.0% (127/153) of all residues were in favored (98%) regions.
94.1% (144/153) of all residues were in allowed (>99.8%) regions.

There were 9 outliers (phi, psi):

[9] 16 ALA (155.0, -44.9)
[9] 35 HIS (65.0, 96.9)
[9] 37 ARG (165.0, -47.8)
[9] 44 ASP (172.4, -66.0)
[9] 50 THR (55.1, 97.1)
[9] 53 ALA (68.3, 124.0)
[9] 61 SER (124.4, -5.1)
[9] 86 GLU (70.0, -88.7)
[9] 130 SER (175.1, -55.0)

MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 10



86.3% (132/153) of all residues were in favored (98%) regions.
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[10] 16 ALA (165.1, -33.6)
[10] 55 ALA (68.8, 144.9)
[10] 80 LEU (75.1, 131.9)

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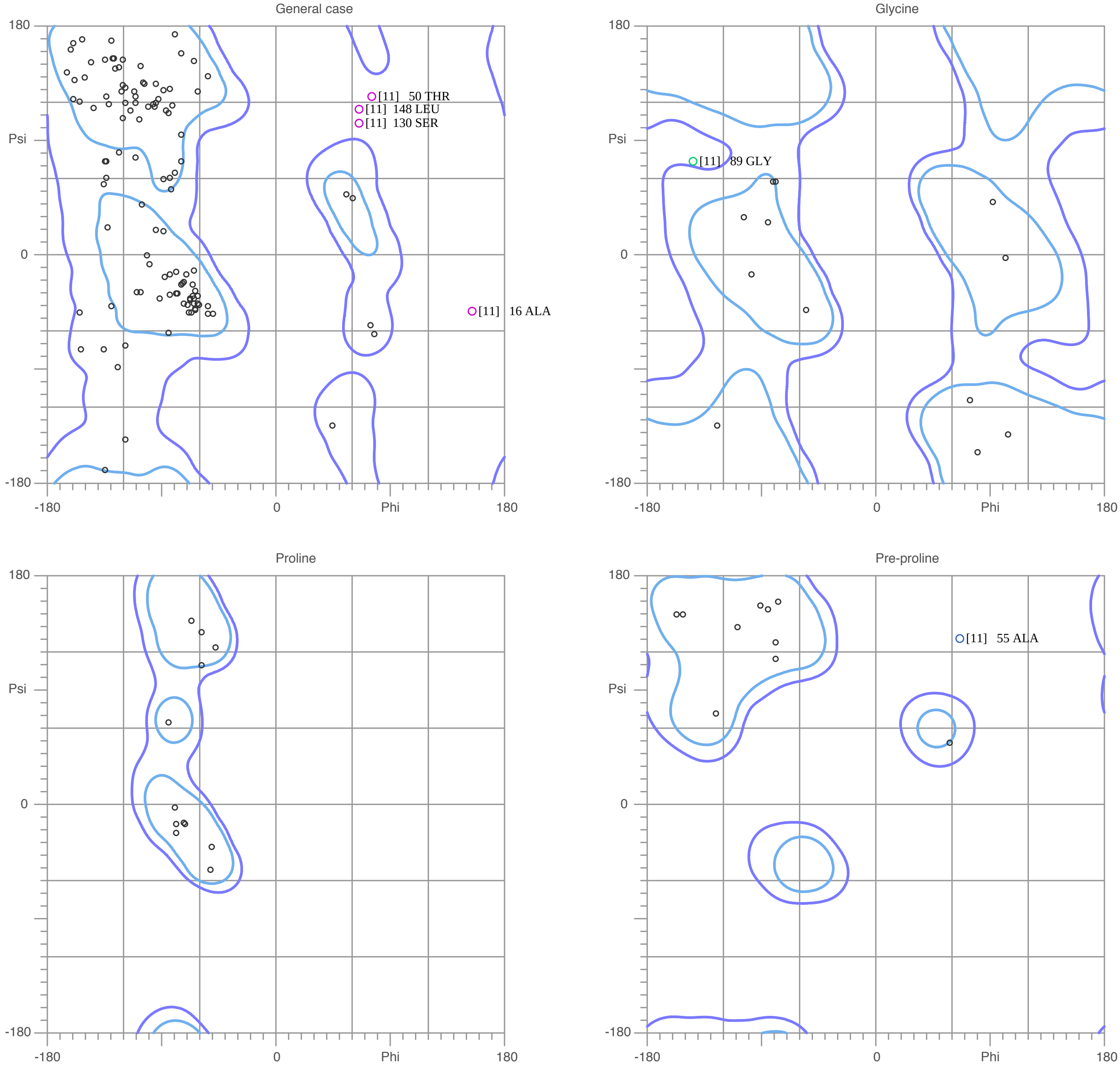
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 11



83.7% (128/153) 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, -44.9)
[11] 50 THR (75.1, 125.0)
[11] 55 ALA (66.2, 131.4)
[11] 89 GLY (-145.0, 75.0)
[11] 130 SER (65.1, 105.0)
[11] 148 LEU (65.0, 115.0)

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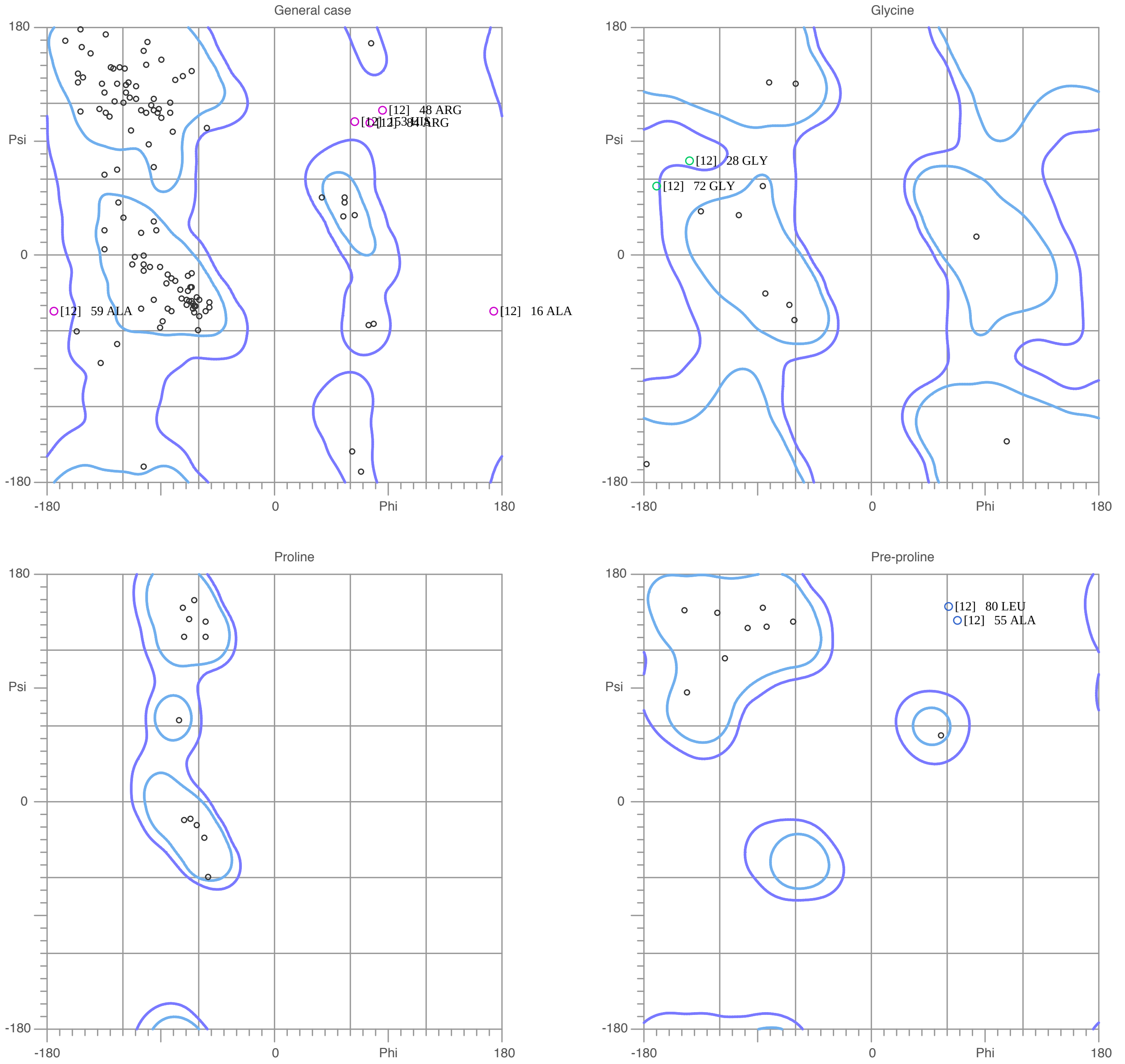
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 12



85.6% (131/153) 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):

[12] 16 ALA (173.9, -45.0)
[12] 28 GLY (-144.9, 75.1)
[12] 48 ARG (85.0, 115.0)
[12] 55 ALA (68.1, 144.9)
[12] 59 ALA (-175.1, -45.0)
[12] 72 GLY (-170.7, 55.0)
[12] 80 LEU (61.2, 155.1)
[12] 84 ARG (75.1, 105.0)
[12] 153 HIS (63.4, 106.5)

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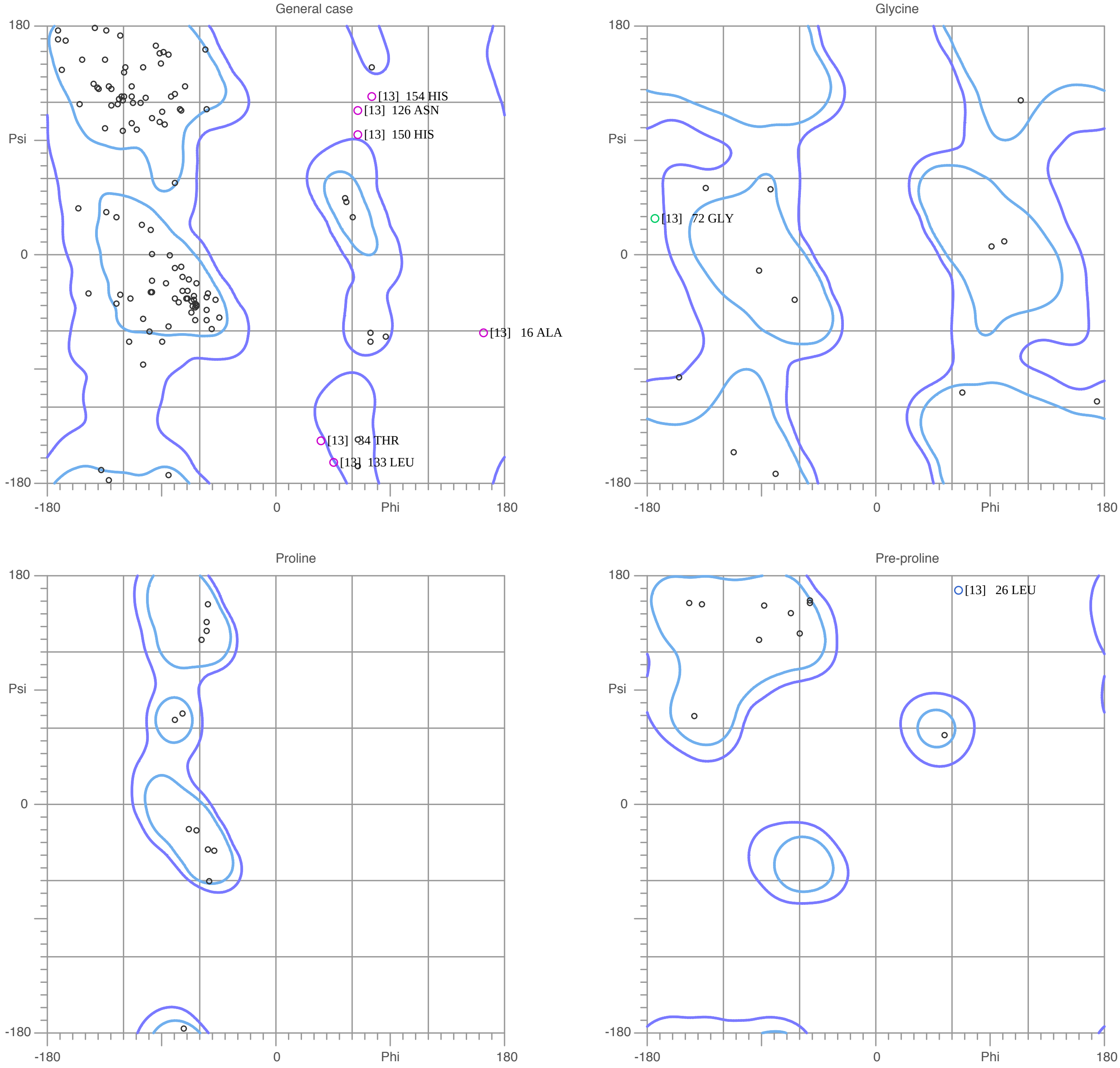
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 13



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):

[13] 16 ALA (163.0, -61.7)
[13] 26 LEU (65.1, 169.2)
[13] 34 THR (35.1, -146.8)
[13] 72 GLY (-175.0, 29.3)
[13] 126 ASN (65.0, 114.9)
[13] 133 LEU (45.1, -163.1)
[13] 150 HIS (64.9, 95.0)
[13] 154 HIS (75.0, 125.1)

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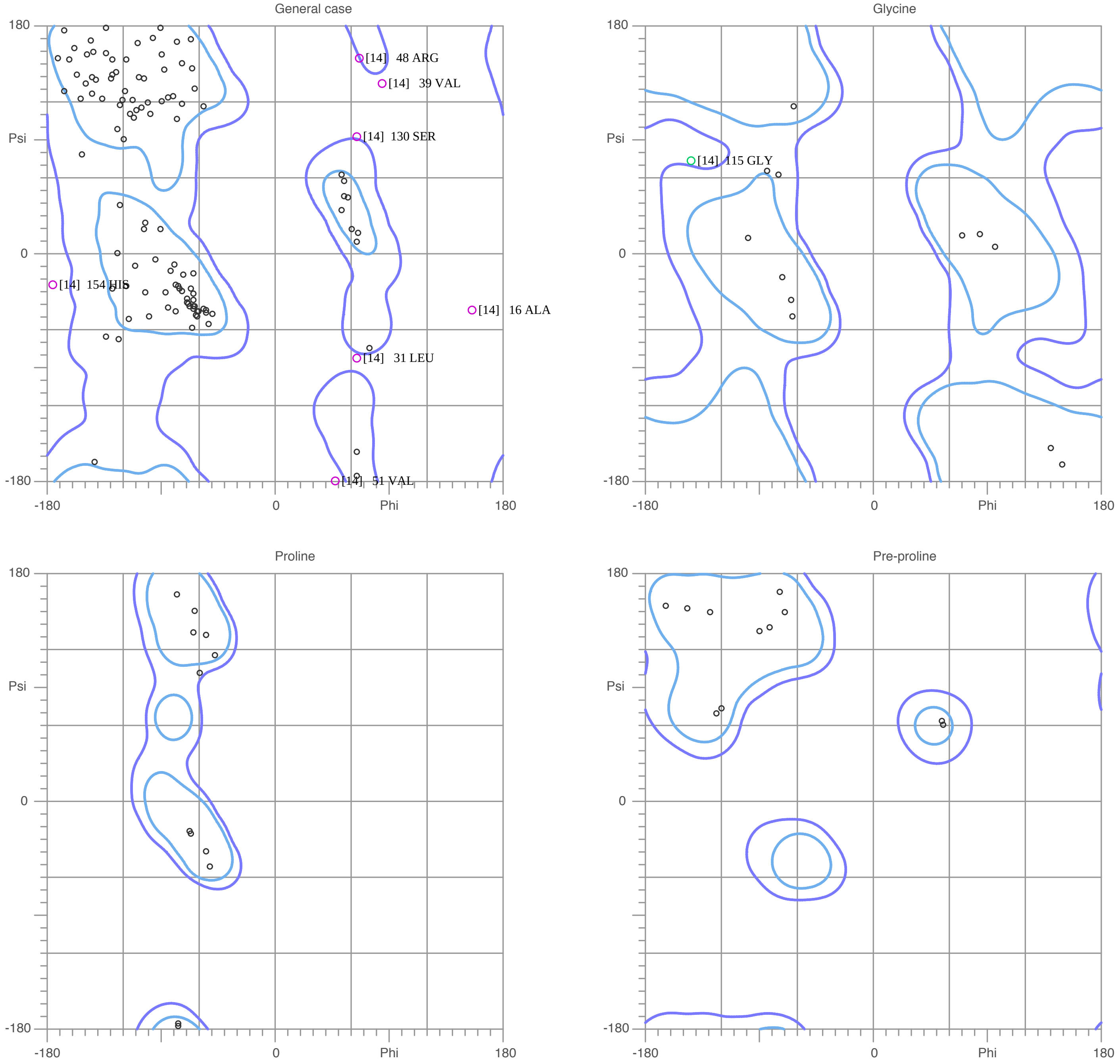
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 14

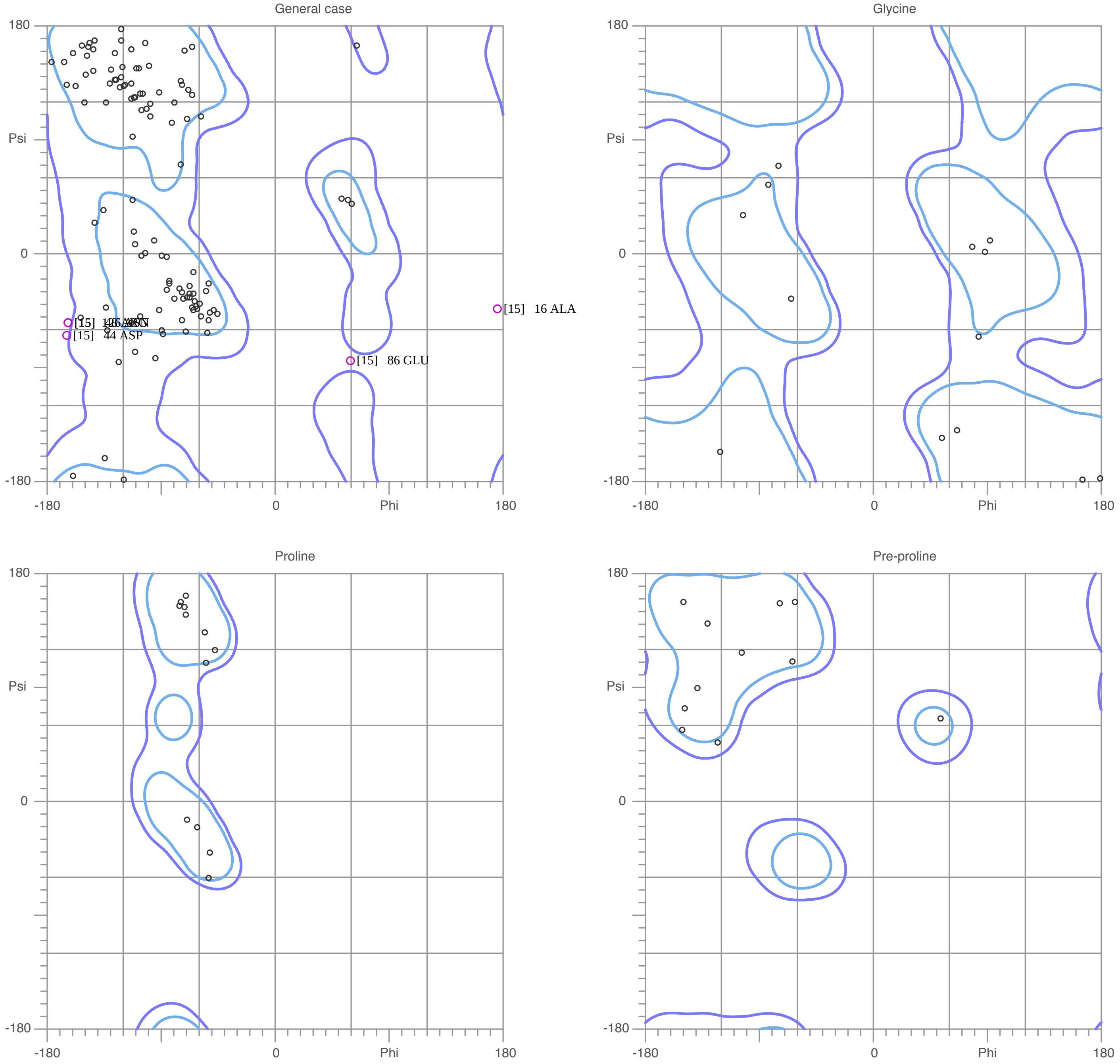


87.6% (134/153) of all residues were in favored (98%) regions.
94.8% (145/153) of all residues were in allowed (>99.8%) regions.

There were 8 outliers (phi, psi):
[14] 16 ALA (155.0, -45.0)
[14] 31 LEU (64.6, -82.7)
[14] 39 VAL (84.9, 135.0)
[14] 48 ARG (66.0, 155.1)
[14] 51 VAL (47.4, -179.7)
[14] 115 GLY (-144.9, 75.0)
[14] 130 SER (65.0, 94.0)
[14] 154 HIS (-177.0, -25.0)

MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 15



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):

[15] 16 ALA (175.1, -43.9)
[15] 44 ASP (-165.0, -65.0)
[15] 48 ARG (-164.9, -54.9)
[15] 86 GLU (59.6, -84.8)
[15] 126 ASN (-165.0, -55.0)

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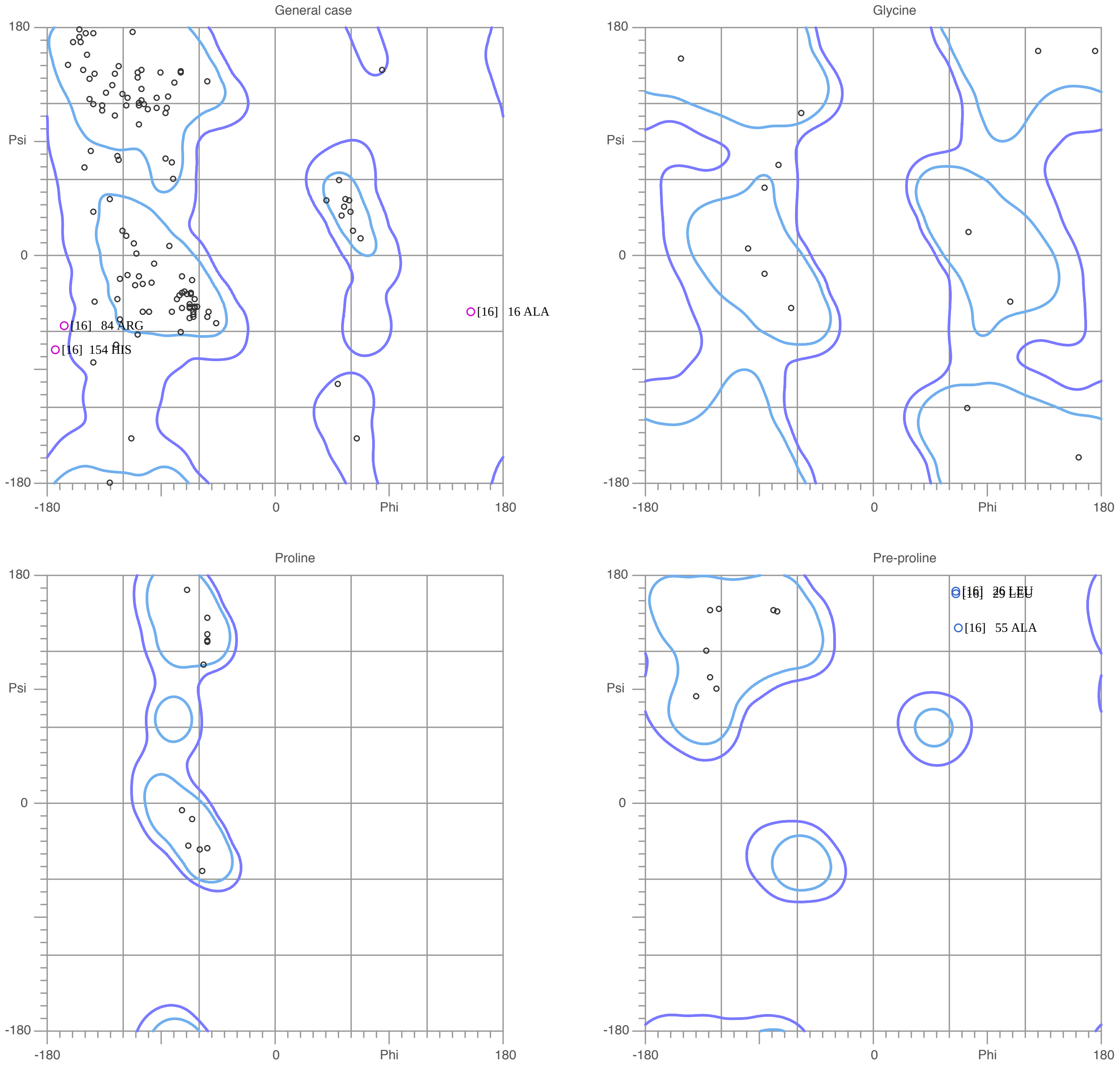
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 16



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):
[16] 16 ALA (155.0, -44.9)
[16] 26 LEU (65.0, 168.8)
[16] 29 LEU (65.1, 166.6)
[16] 55 ALA (67.5, 139.9)
[16] 84 ARG (-167.7, -55.1)
[16] 154 HIS (-174.6, -74.0)

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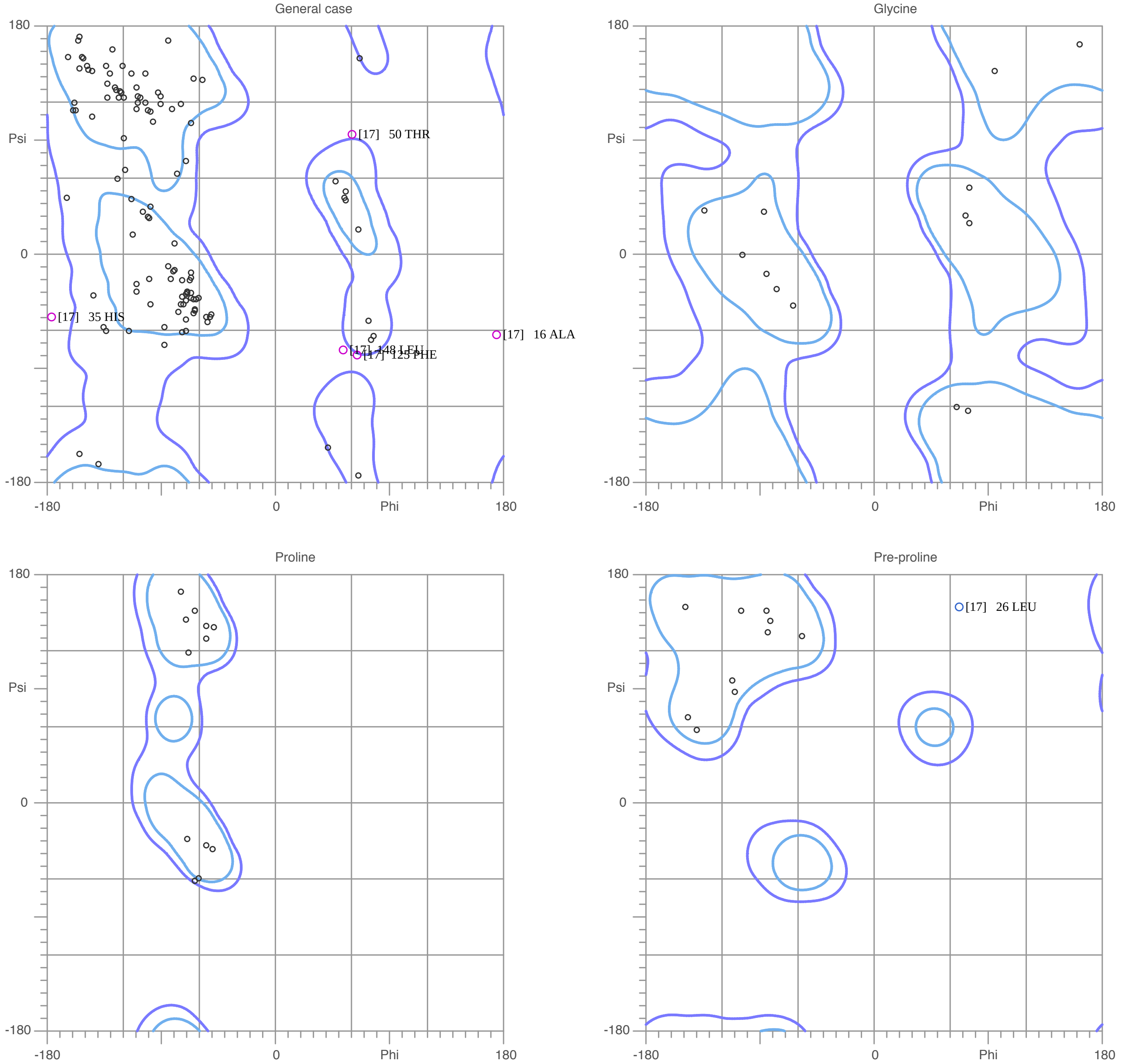
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 17



82.4% (126/153) 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 (175.0, -63.4)
[17] 26 LEU (67.2, 155.0)
[17] 35 HIS (-177.8, -49.6)
[17] 50 THR (60.8, 95.1)
[17] 125 PHE (65.0, -79.4)
[17] 148 LEU (53.5, -75.1)

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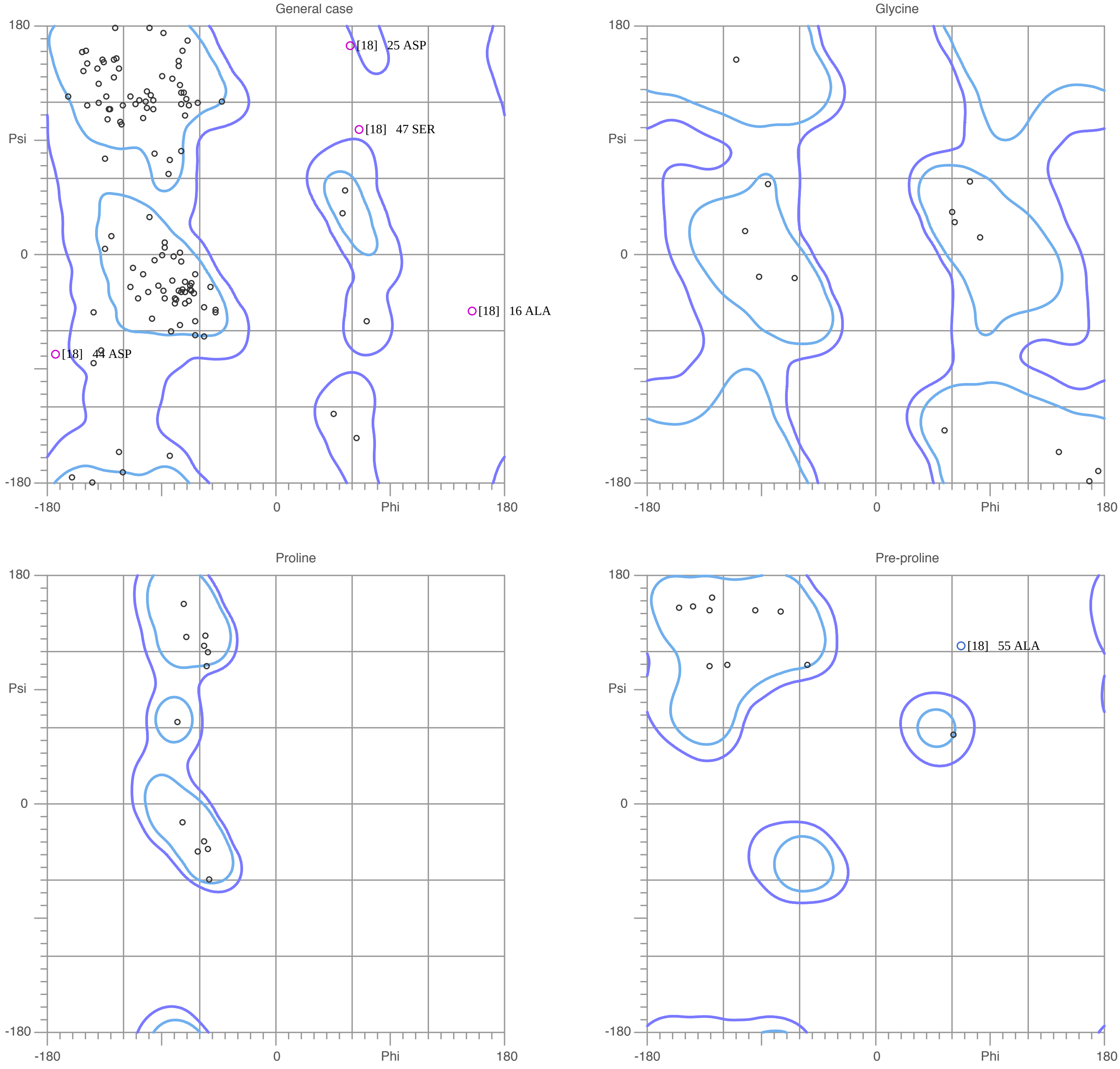
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 18



88.2% (135/153) 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):

[18] 16 ALA (154.9, -44.9)
[18] 25 ASP (58.6, 165.0)
[18] 44 ASP (-175.0, -78.8)
[18] 47 SER (65.0, 99.9)
[18] 55 ALA (67.7, 125.0)

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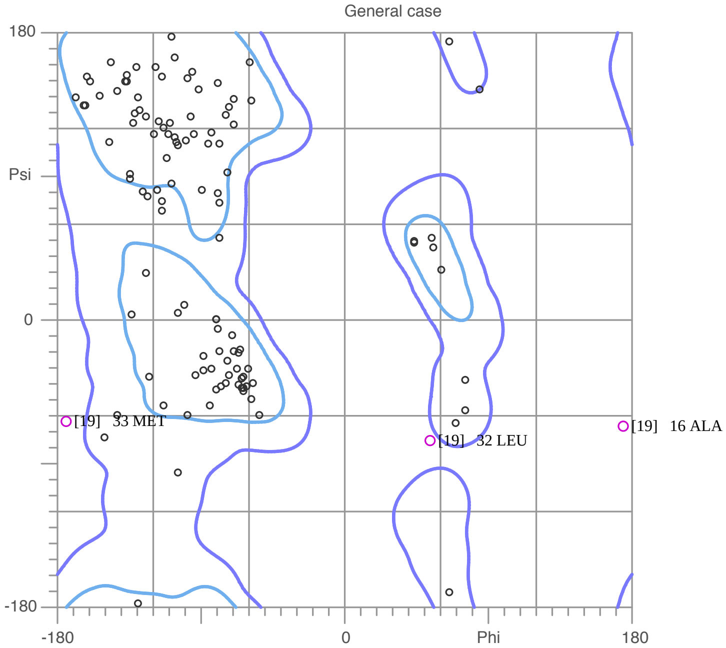
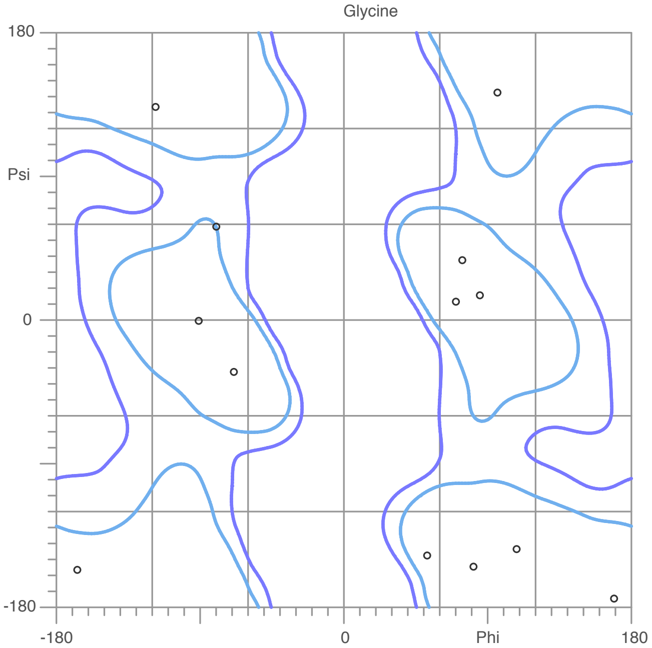
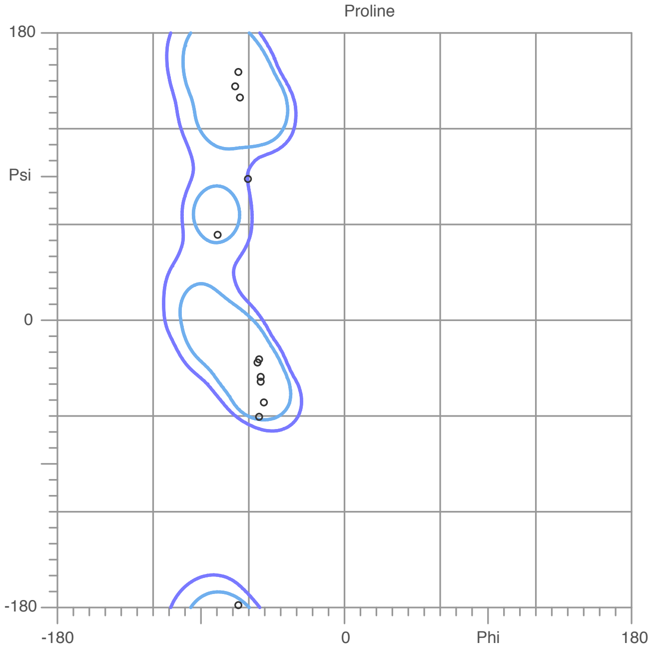
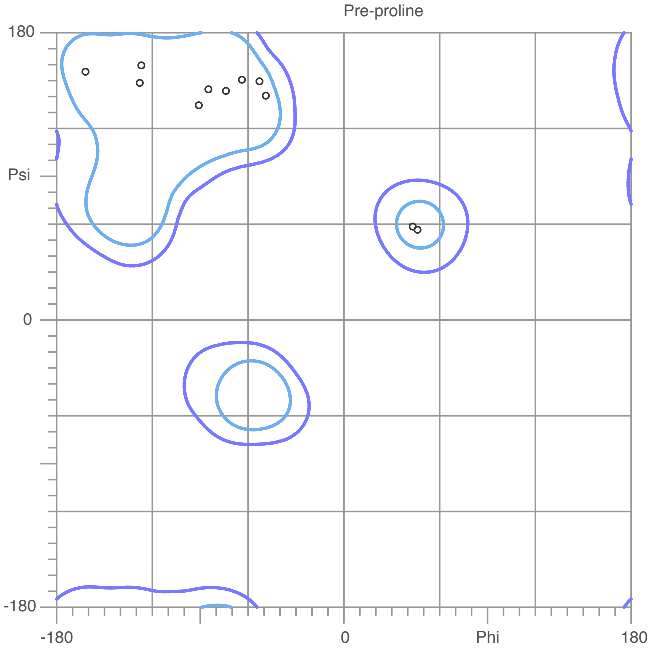
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 19









86.9% (133/153) of all residues were in favored (98%) regions.
98.0% (150/153) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[19] 16 ALA (174.9, -66.7)
[19] 32 LEU (53.7, -75.1)
[19] 33 MET (-175.0, -63.2)

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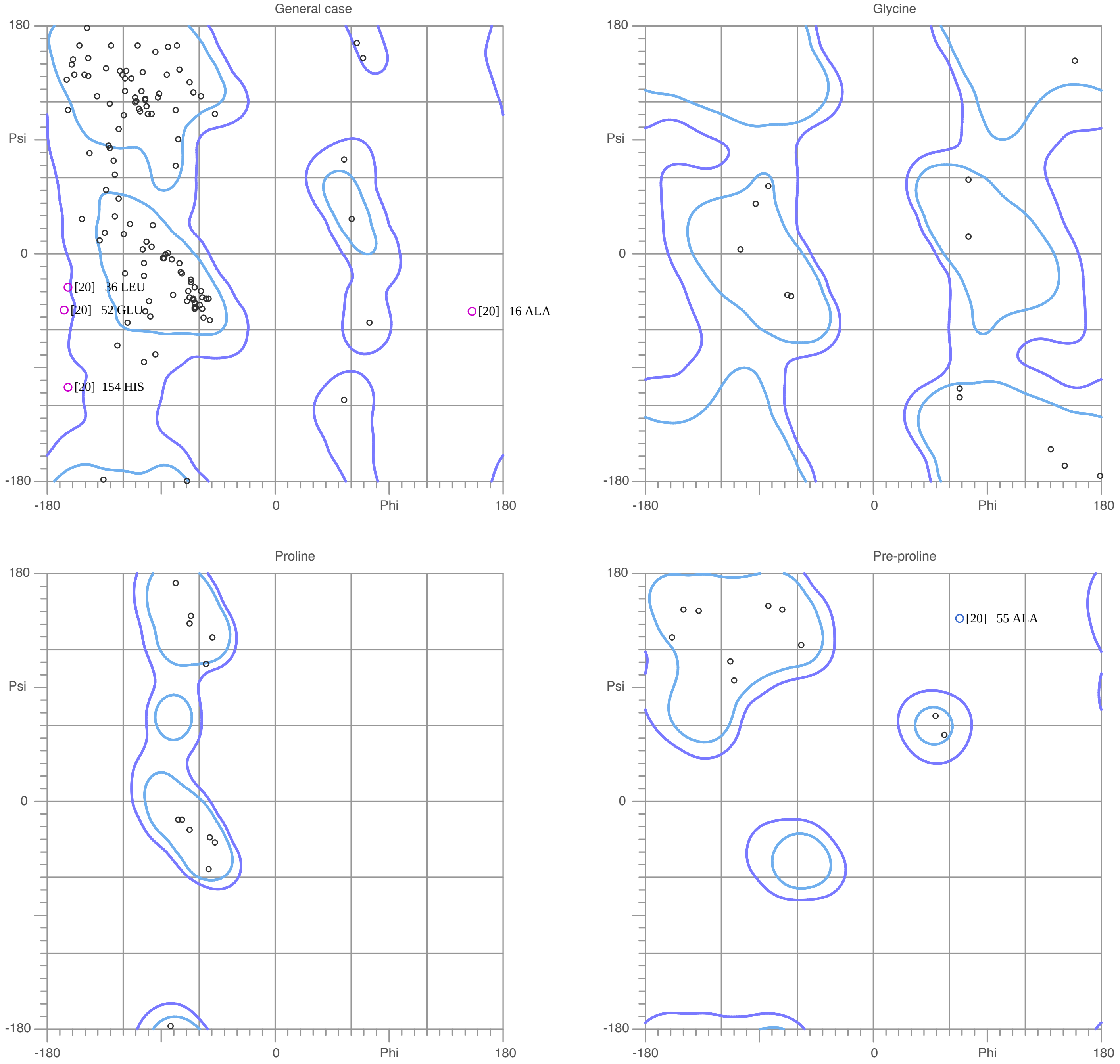
MolProbity Ramachandran analysis

DRR147D_R3_em_bcr3.pdb, model 20



86.3% (132/153) 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):

[20] 16 ALA (155.0, -45.1)
[20] 36 LEU (-165.0, -26.2)
[20] 52 GLU (-167.1, -45.0)
[20] 55 ALA (68.6, 145.0)
[20] 154 HIS (-165.0, -105.0)