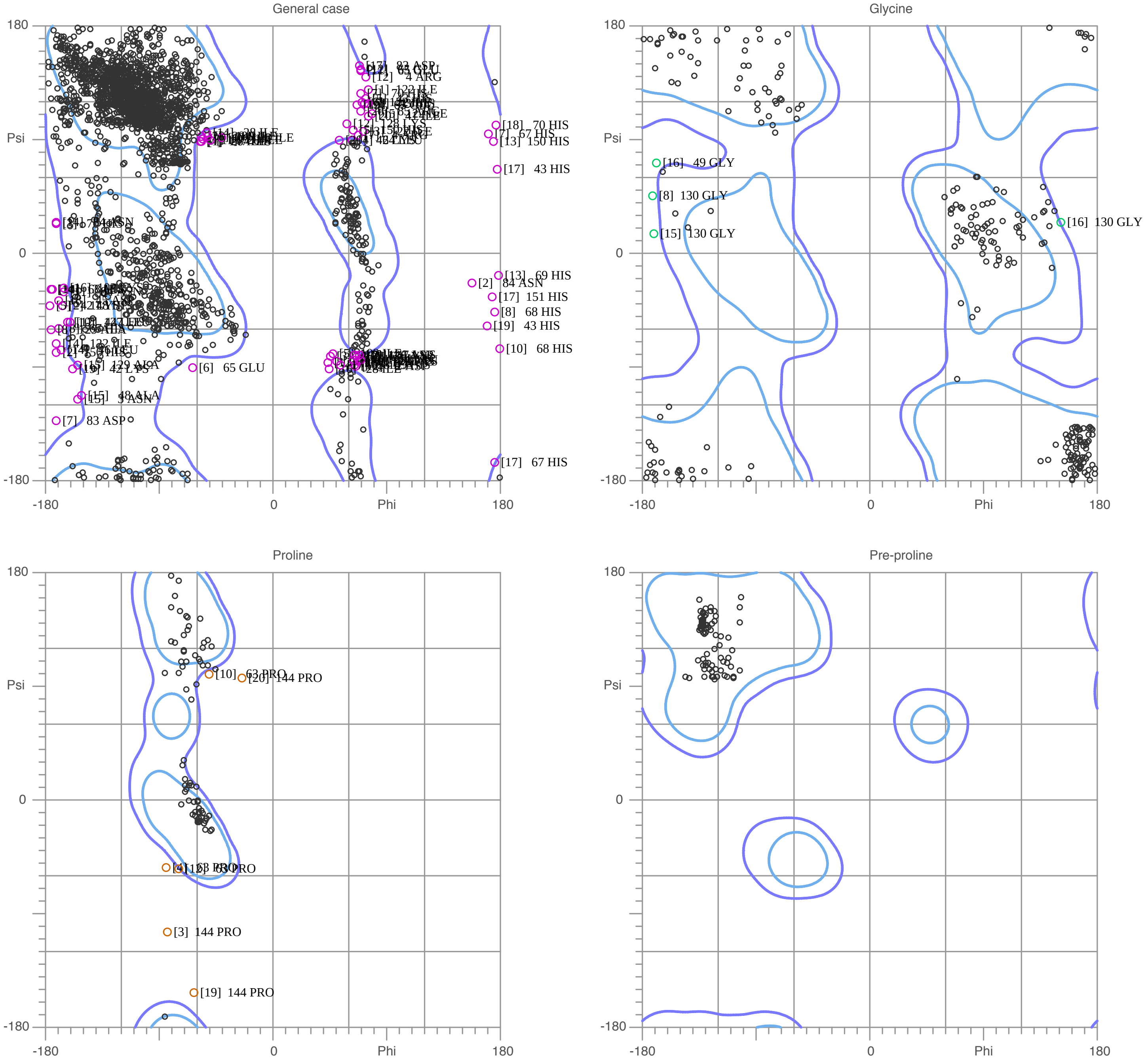
MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, all models



84.6% (2336/2760) of all residues were in favored (98%) regions.
96.8% (2673/2760) of all residues were in allowed (>99.8%) regions.

There were 87 outliers (phi, psi):
[1] 122 ILE (75.5, 130.9)
[1] 147 HIS (-57.3, 89.5)
[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)
[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)
[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)
[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)
[6] 47 LYS (66.9, -81.1)
[6] 65 GLU (-64.4, -90.3)
[6] 122 ILE (70.7, 120.1)
[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)
[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)
[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)
[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)
[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)
[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)
[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)
[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)
[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)
[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)
[18] 45 ASP (-170.0, -37.5)
[18] 70 HIS (176.4, 102.6)
[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)
[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)

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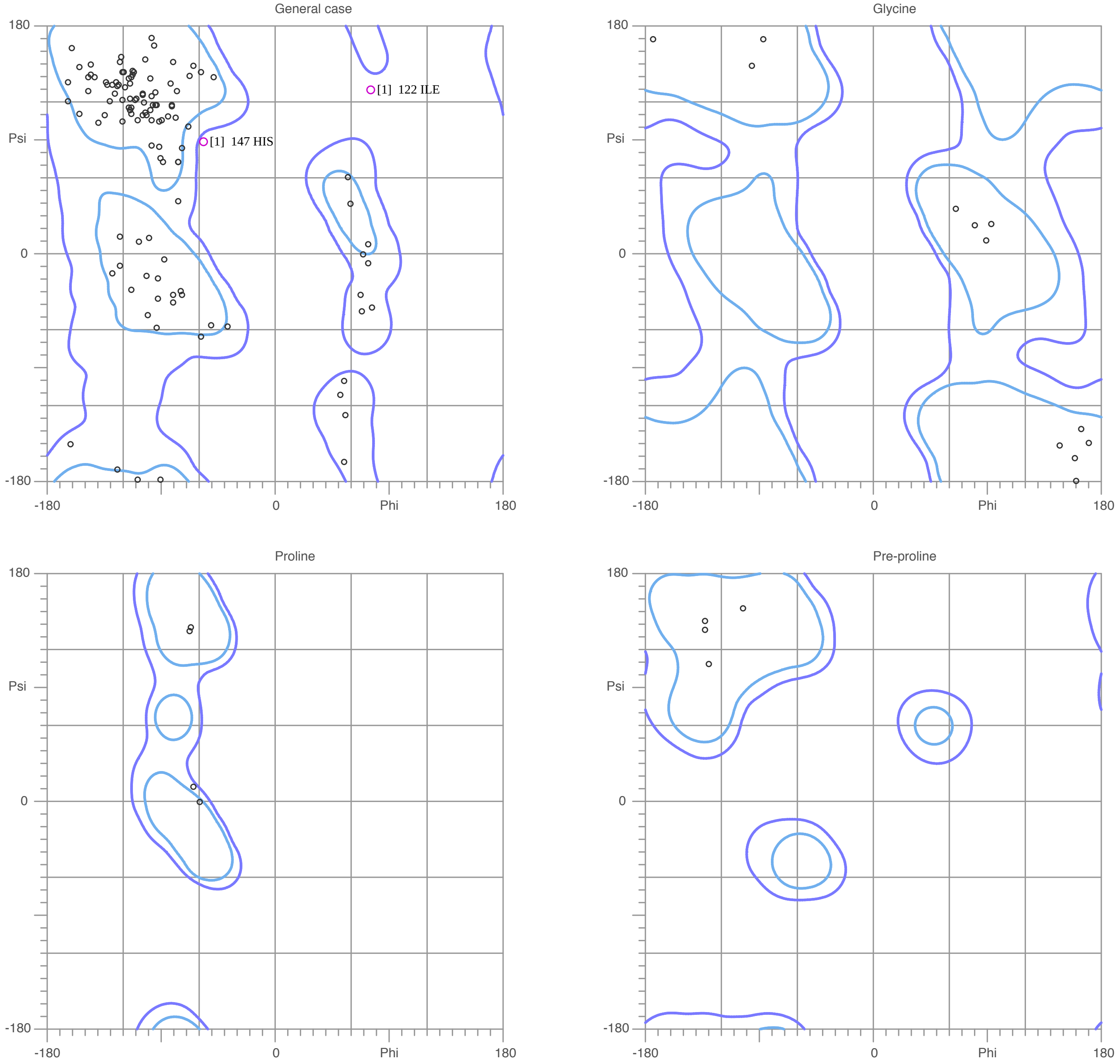
MolProbity Ramachandran analysis

DHR8C_NMR_em_bcr3.pdb, model 1



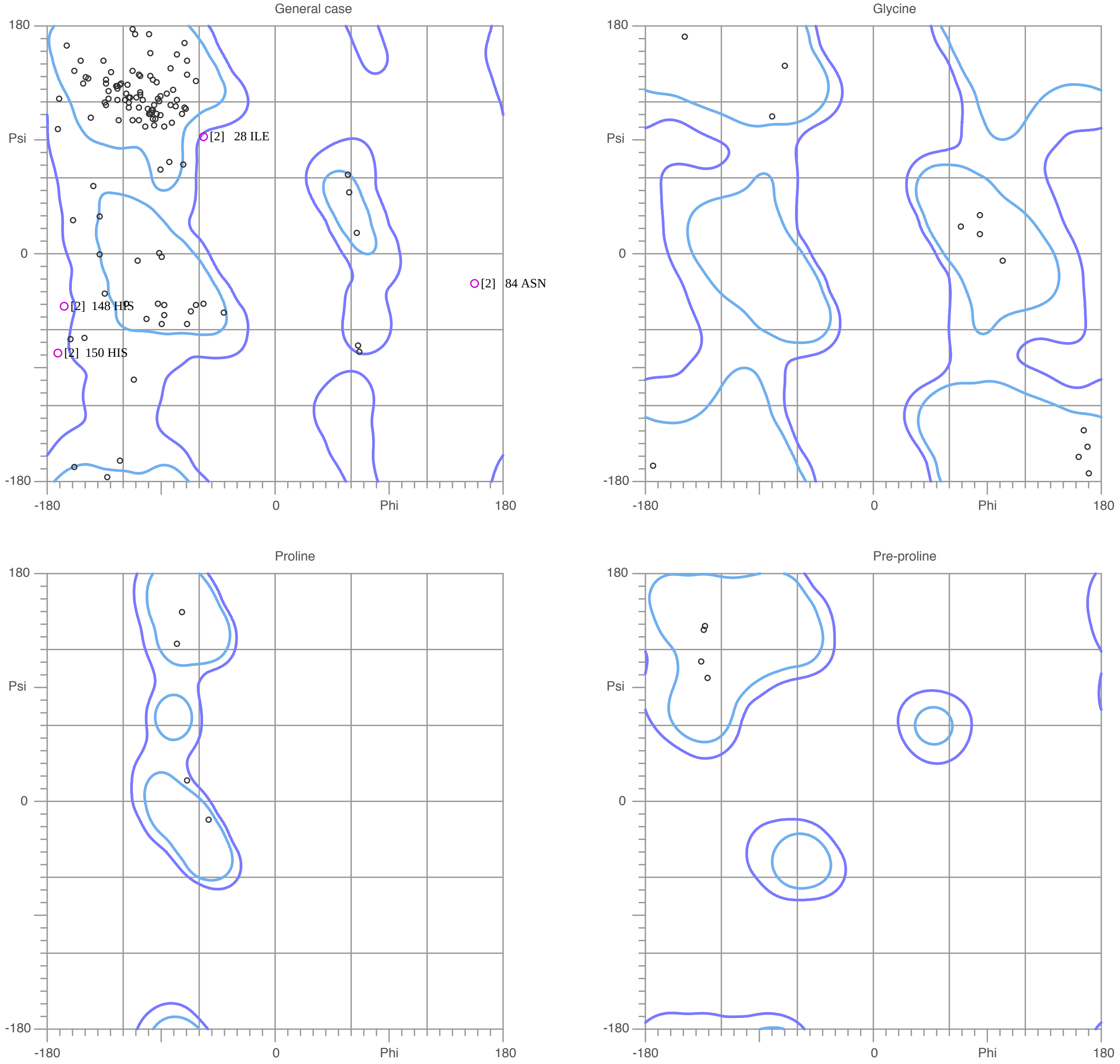
86.2% (119/138) of all residues were in favored (98%) regions.
98.6% (136/138) of all residues were in allowed (>99.8%) regions.

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

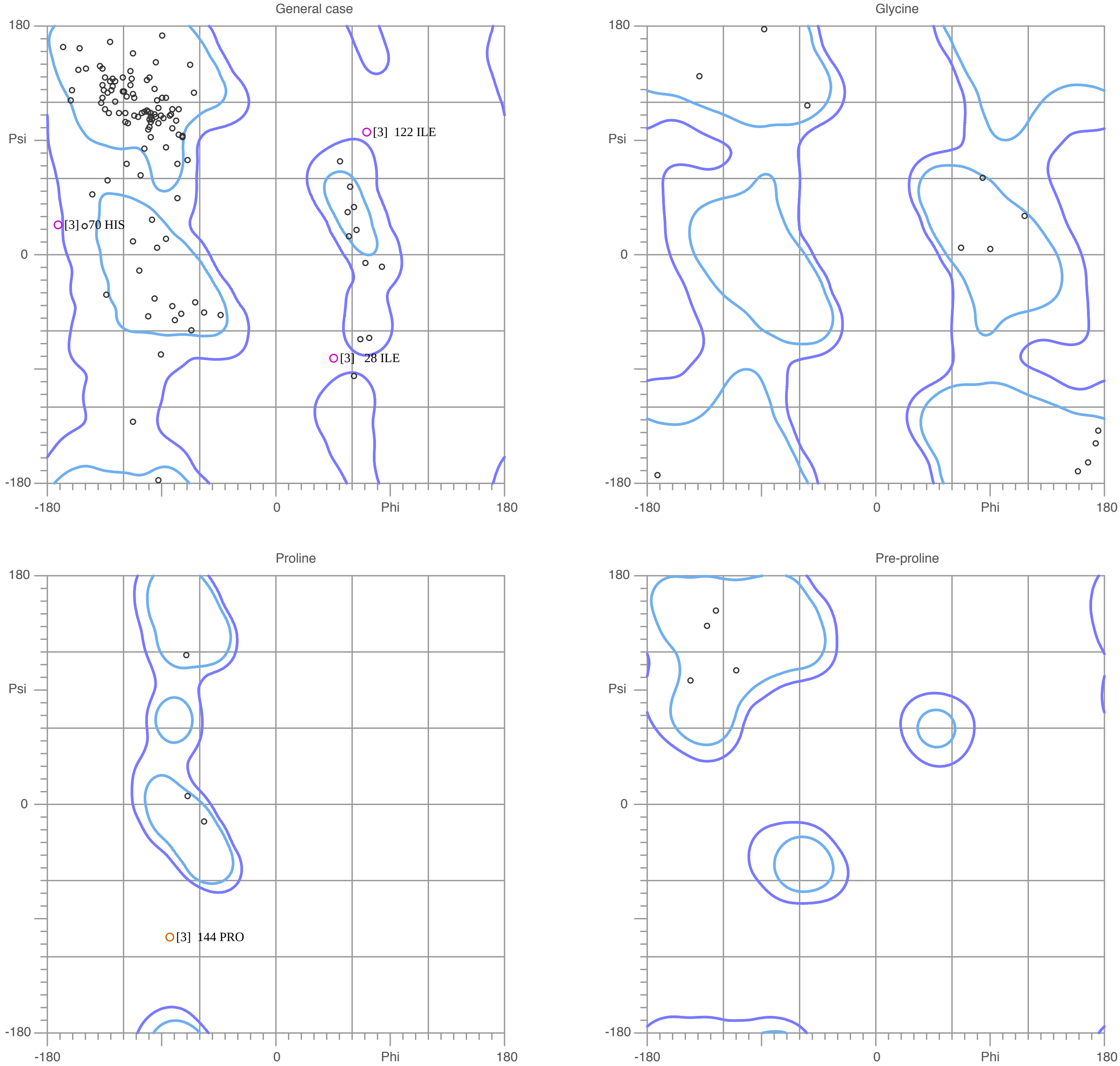


84.8% (117/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

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)

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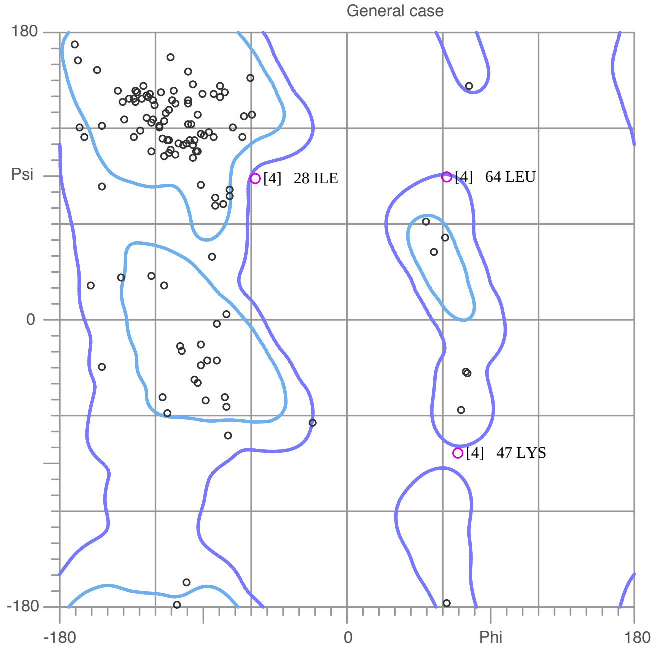
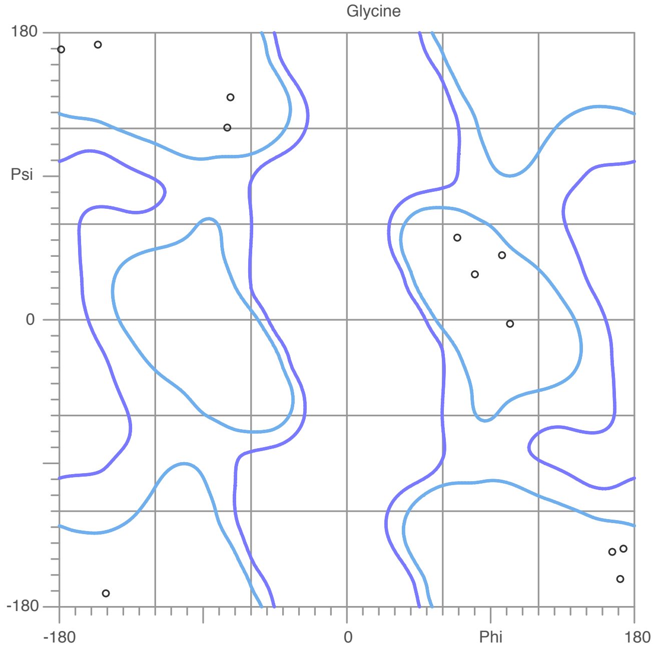
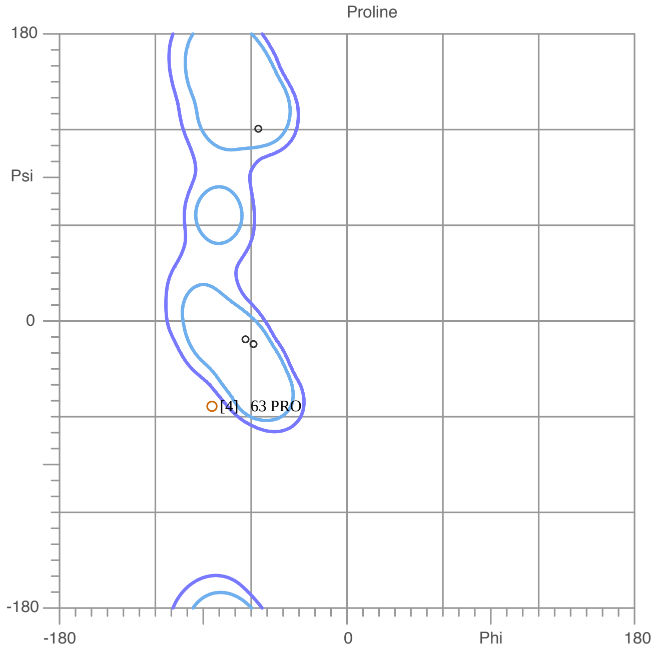
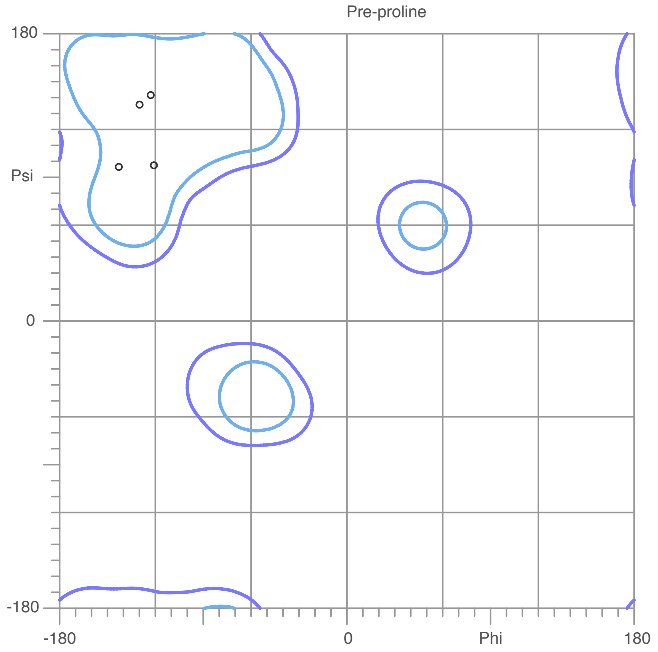
MolProbity Ramachandran analysis

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)

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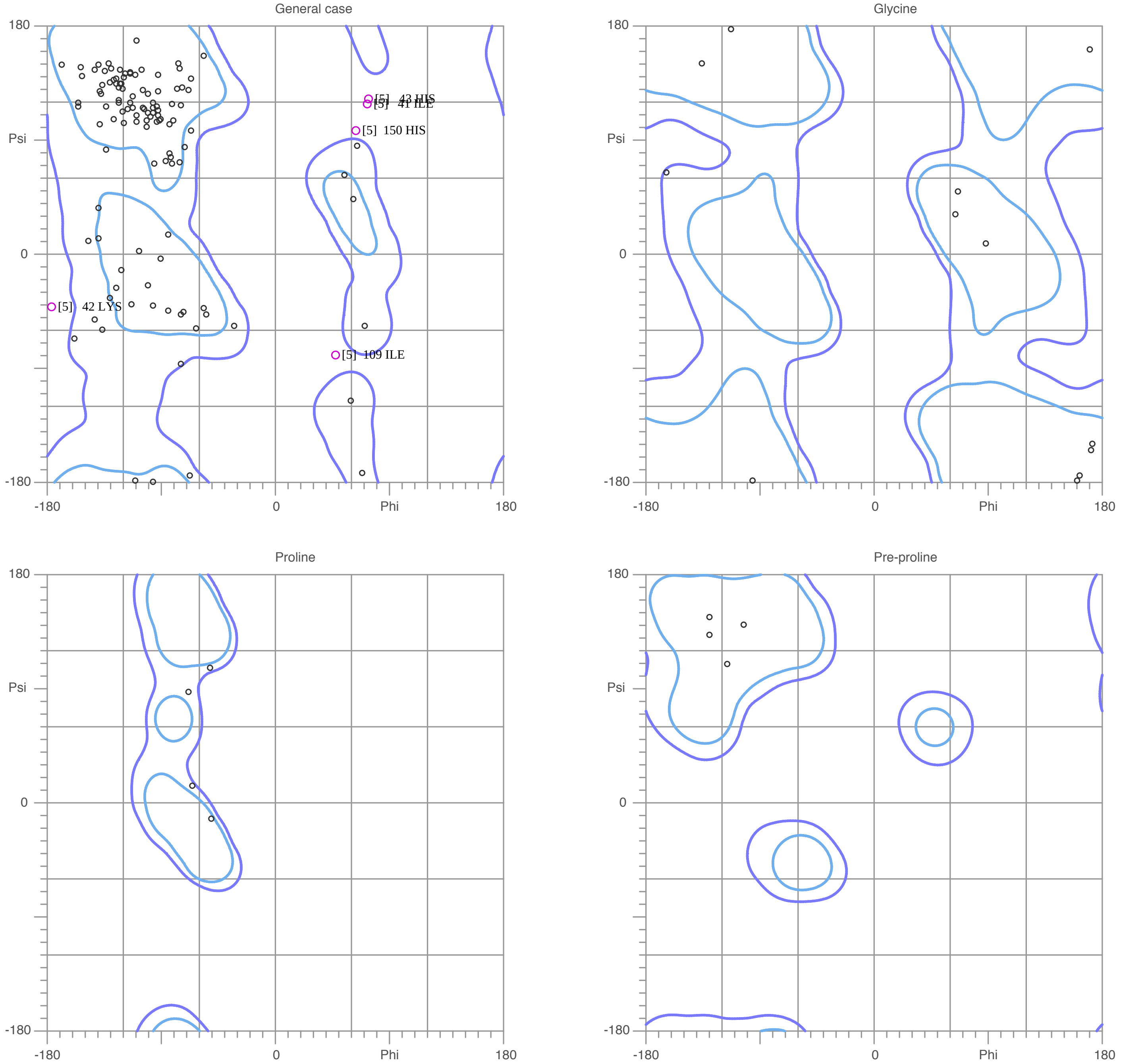
MolProbity Ramachandran analysis

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)

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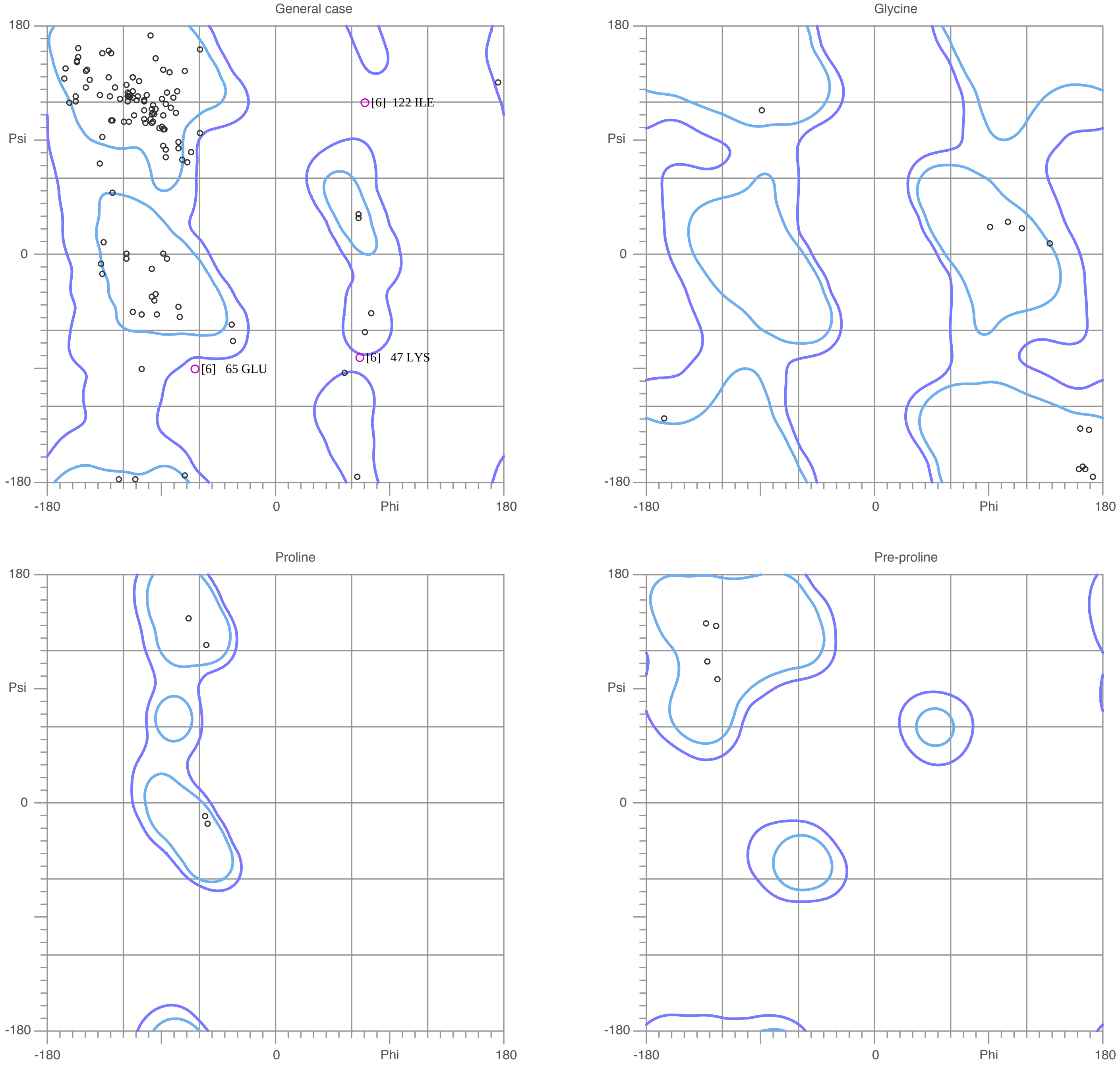
MolProbity Ramachandran analysis

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)

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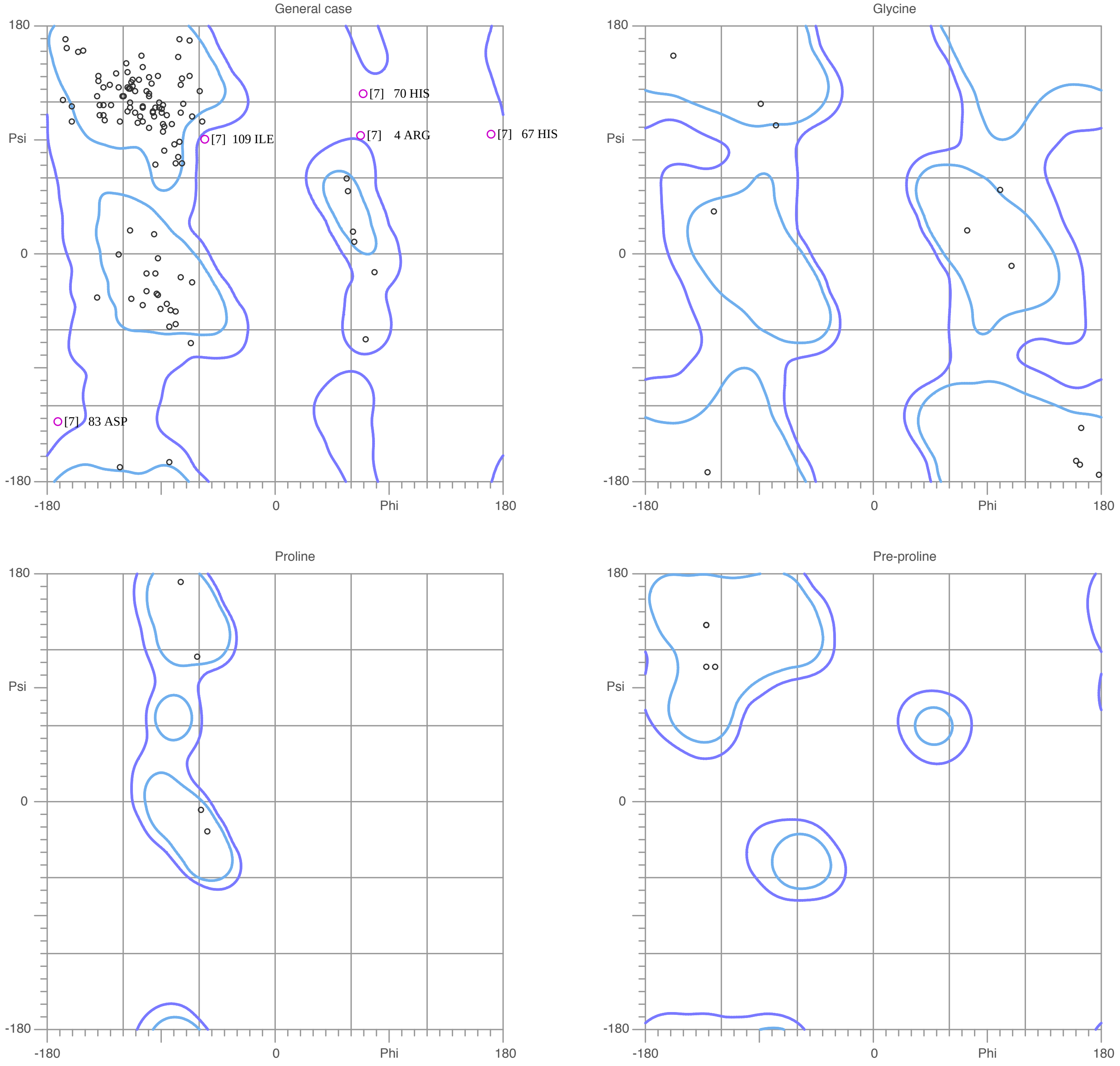
MolProbity Ramachandran analysis

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)

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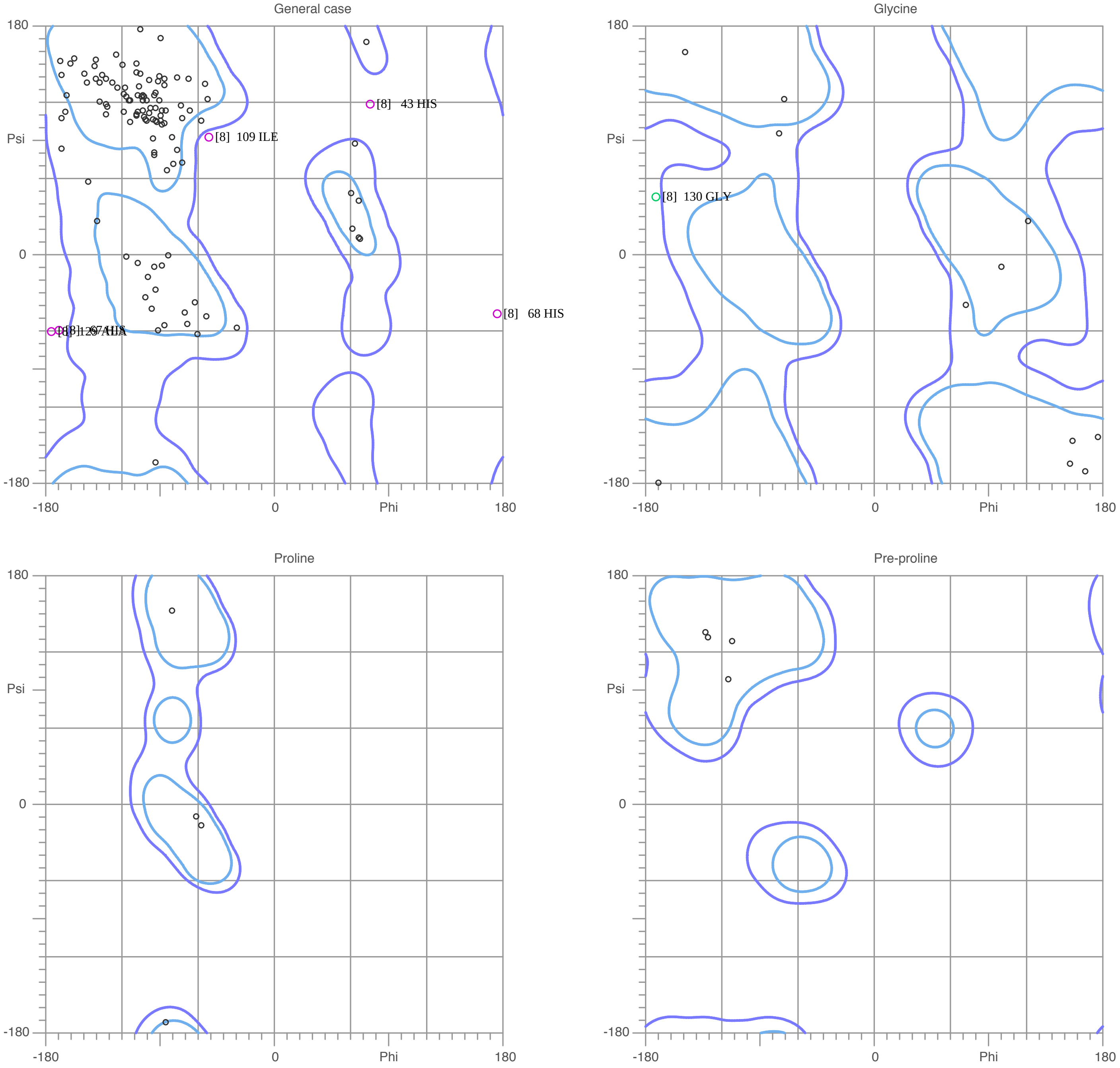
MolProbity Ramachandran analysis

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)

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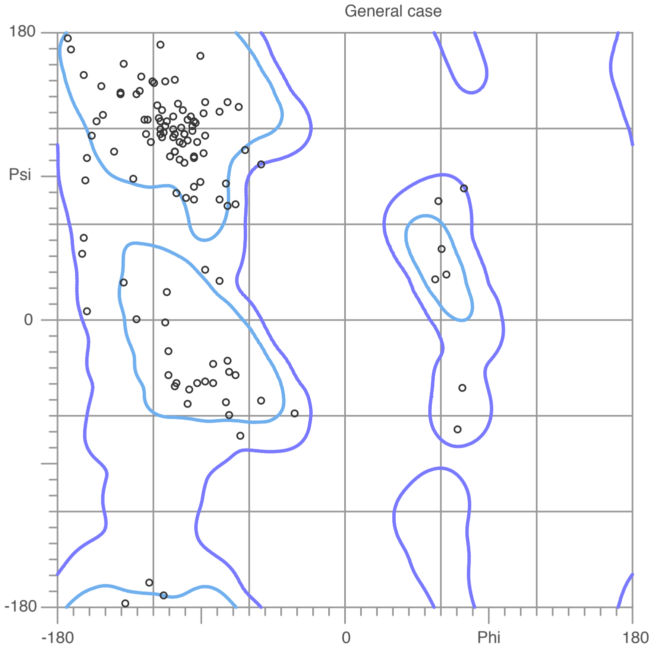
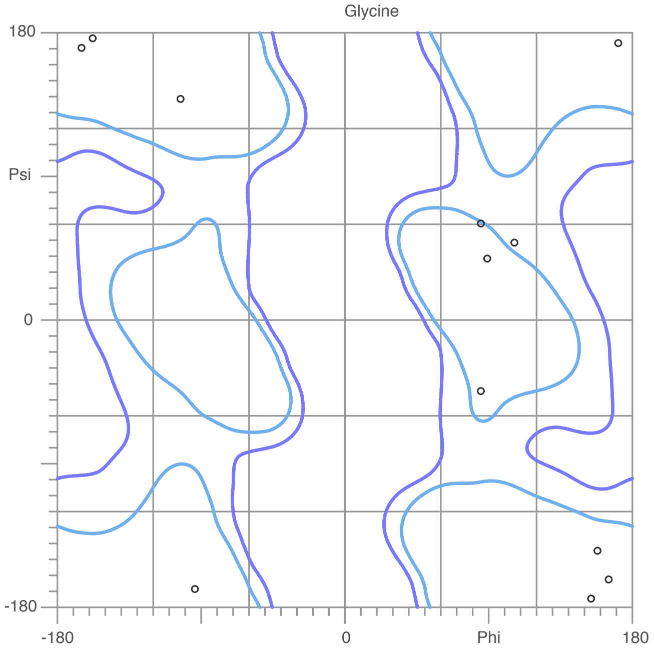
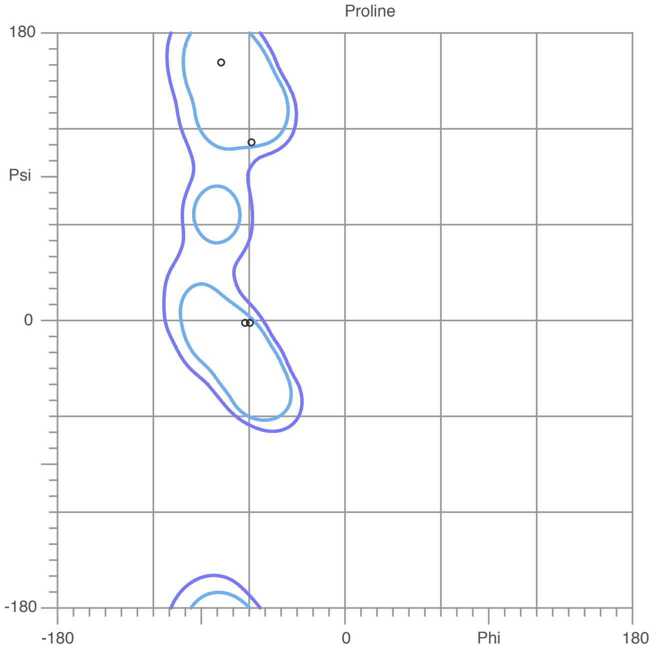
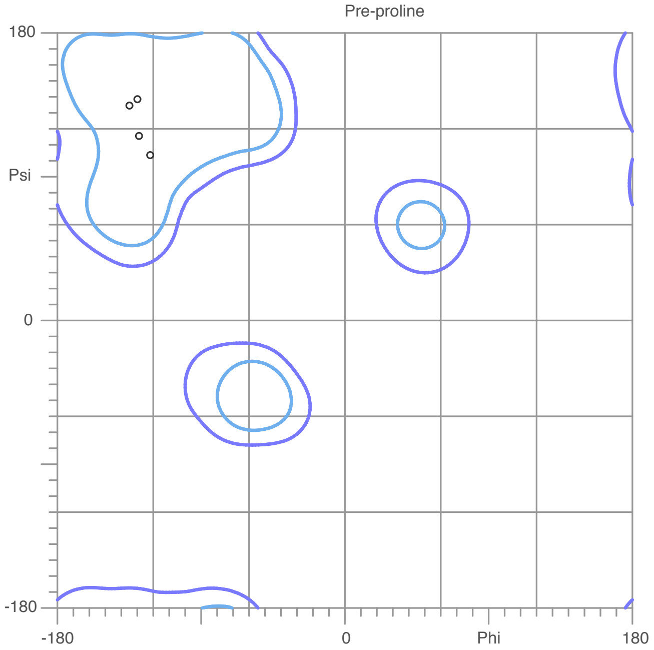
MolProbity Ramachandran analysis

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.

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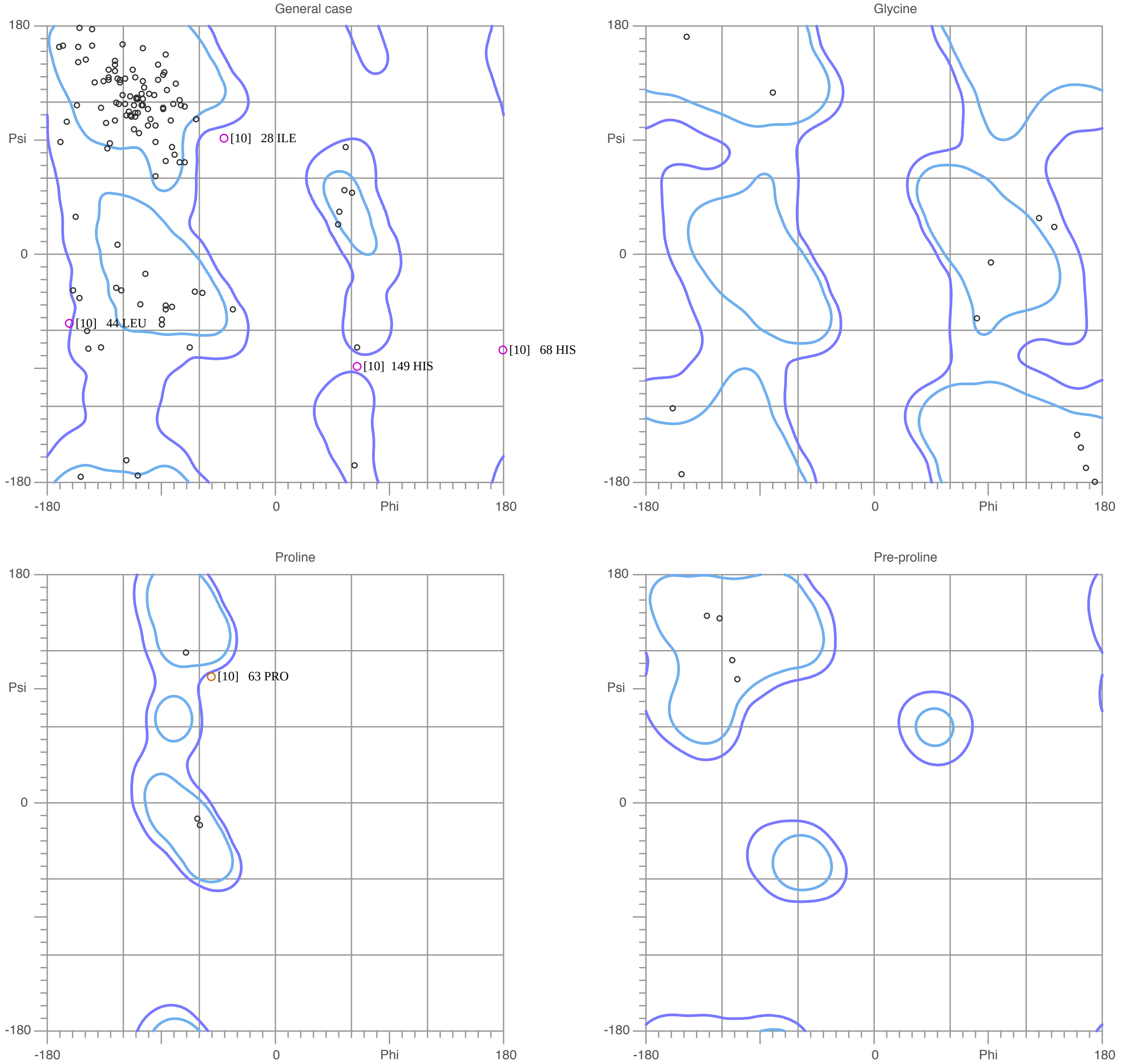
MolProbity Ramachandran analysis

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)

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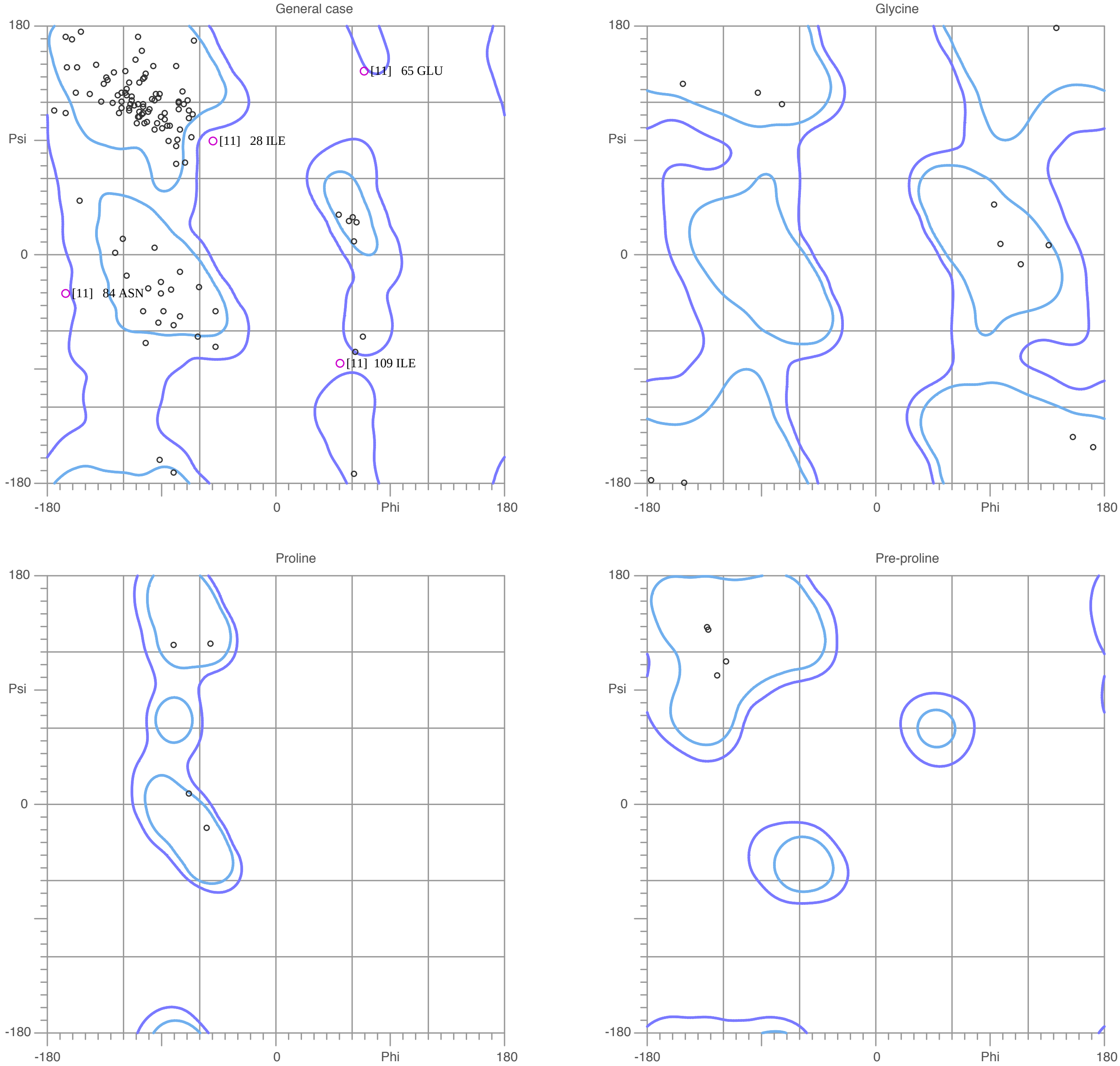
MolProbity Ramachandran analysis

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)

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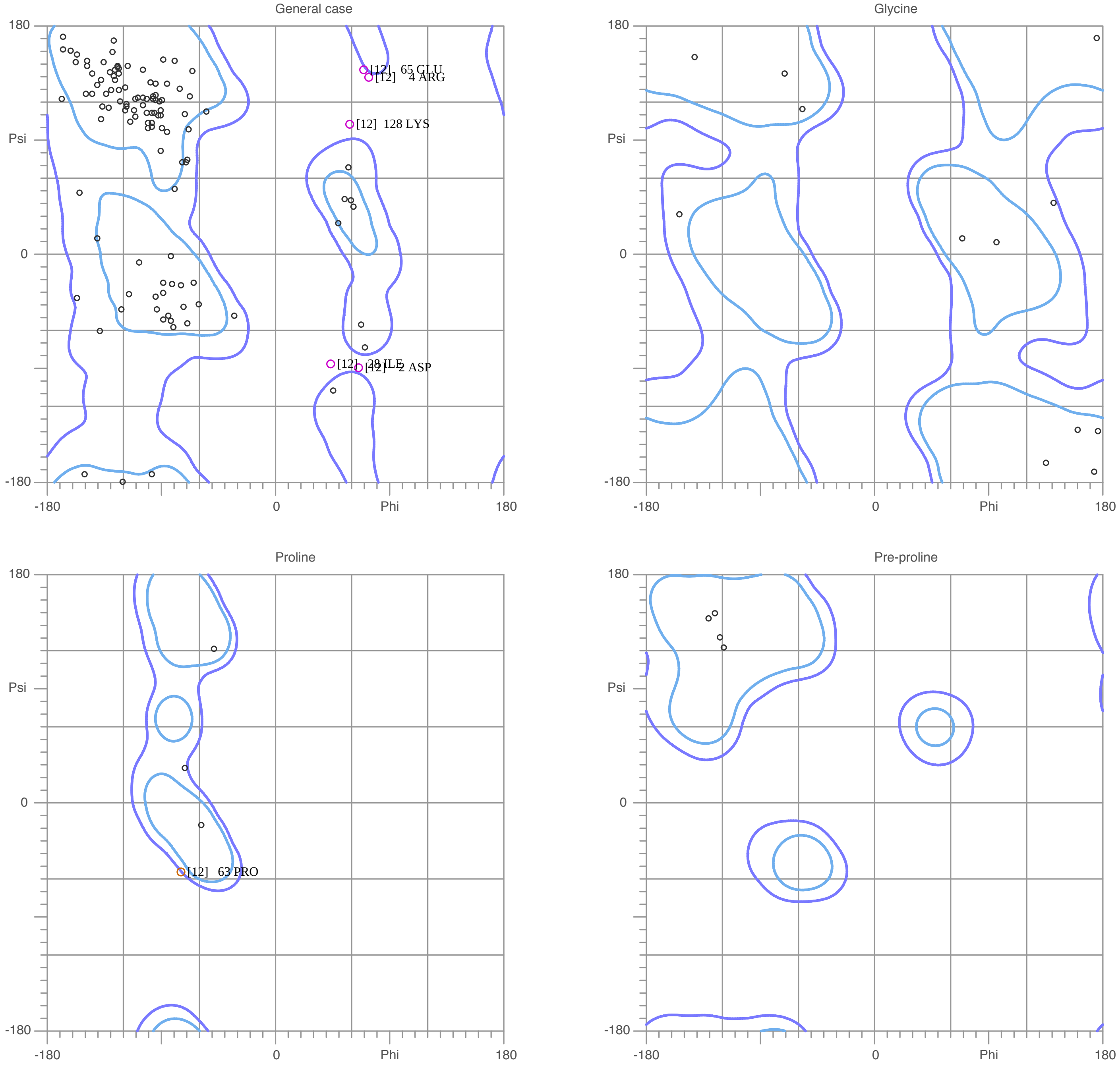
MolProbity Ramachandran analysis

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)

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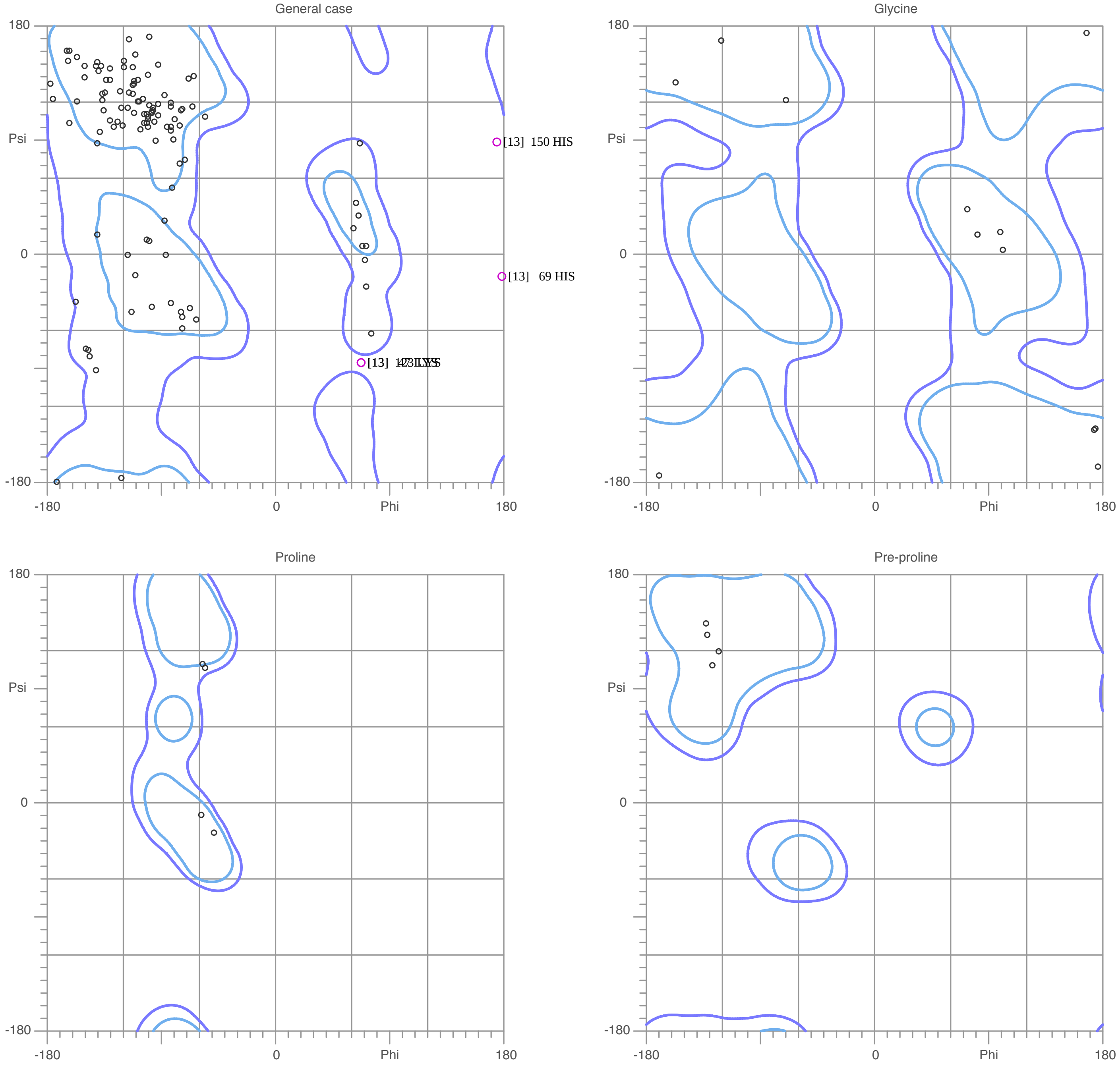
MolProbity Ramachandran analysis

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)

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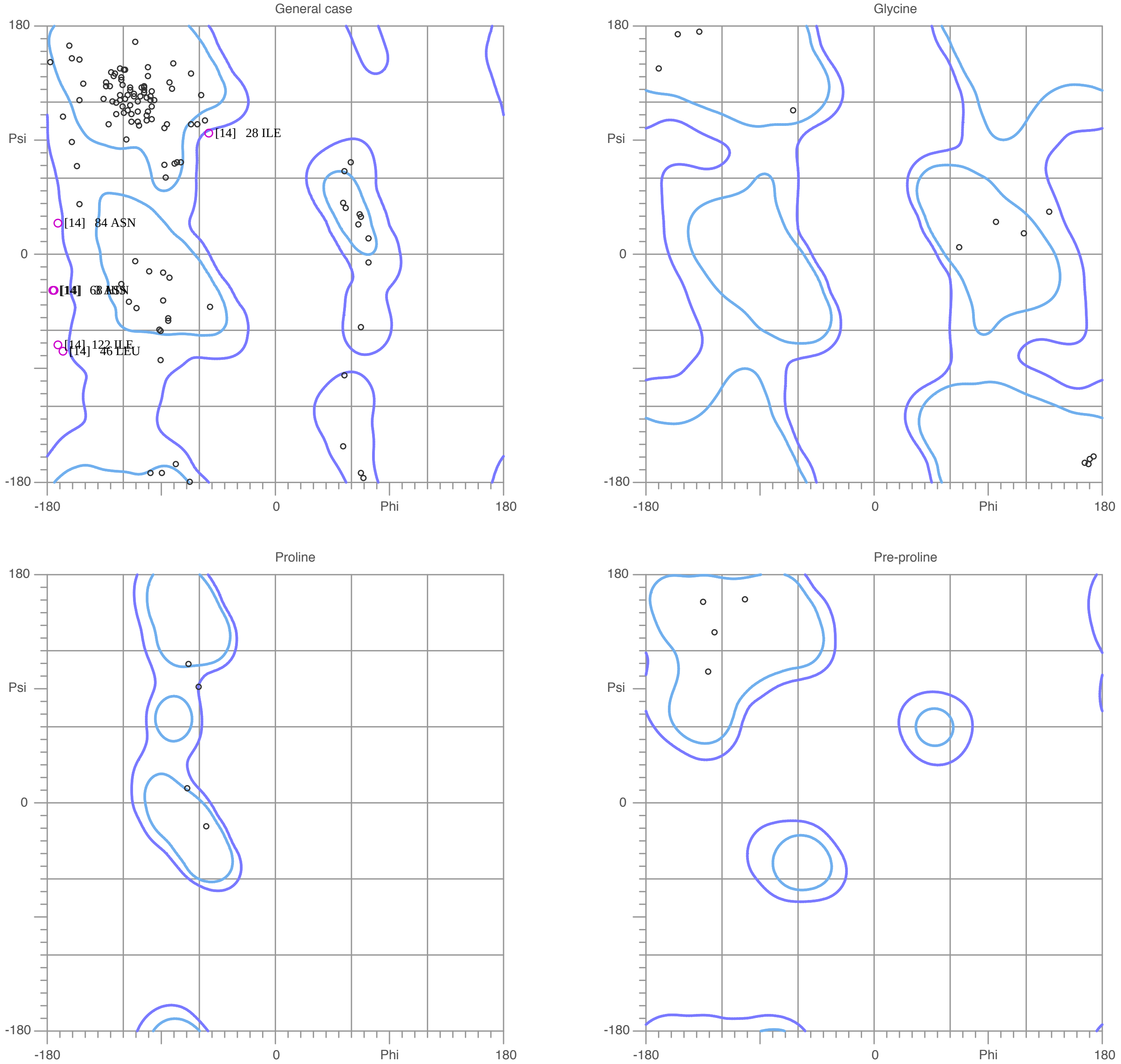
MolProbity Ramachandran analysis

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)

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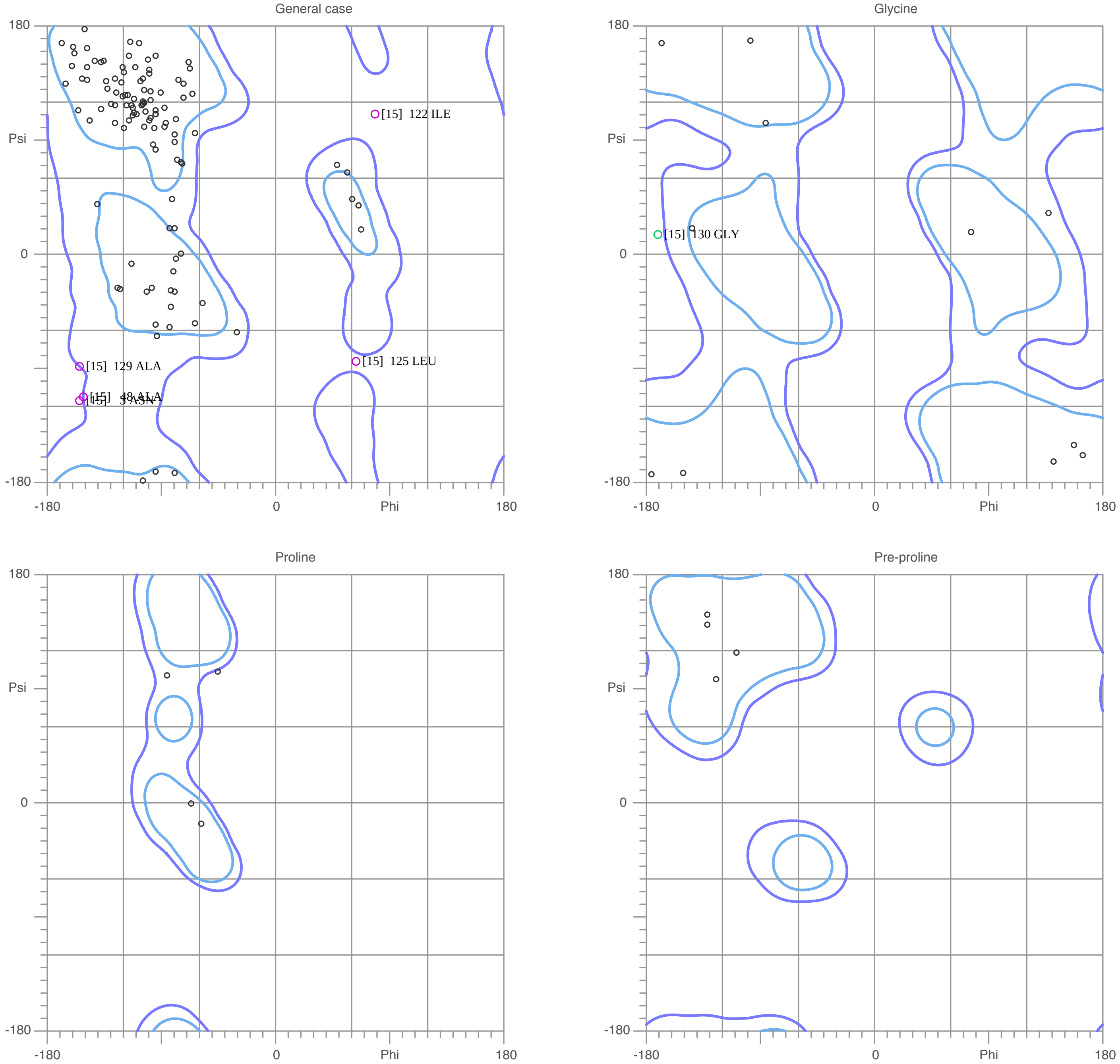
MolProbity Ramachandran analysis

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)

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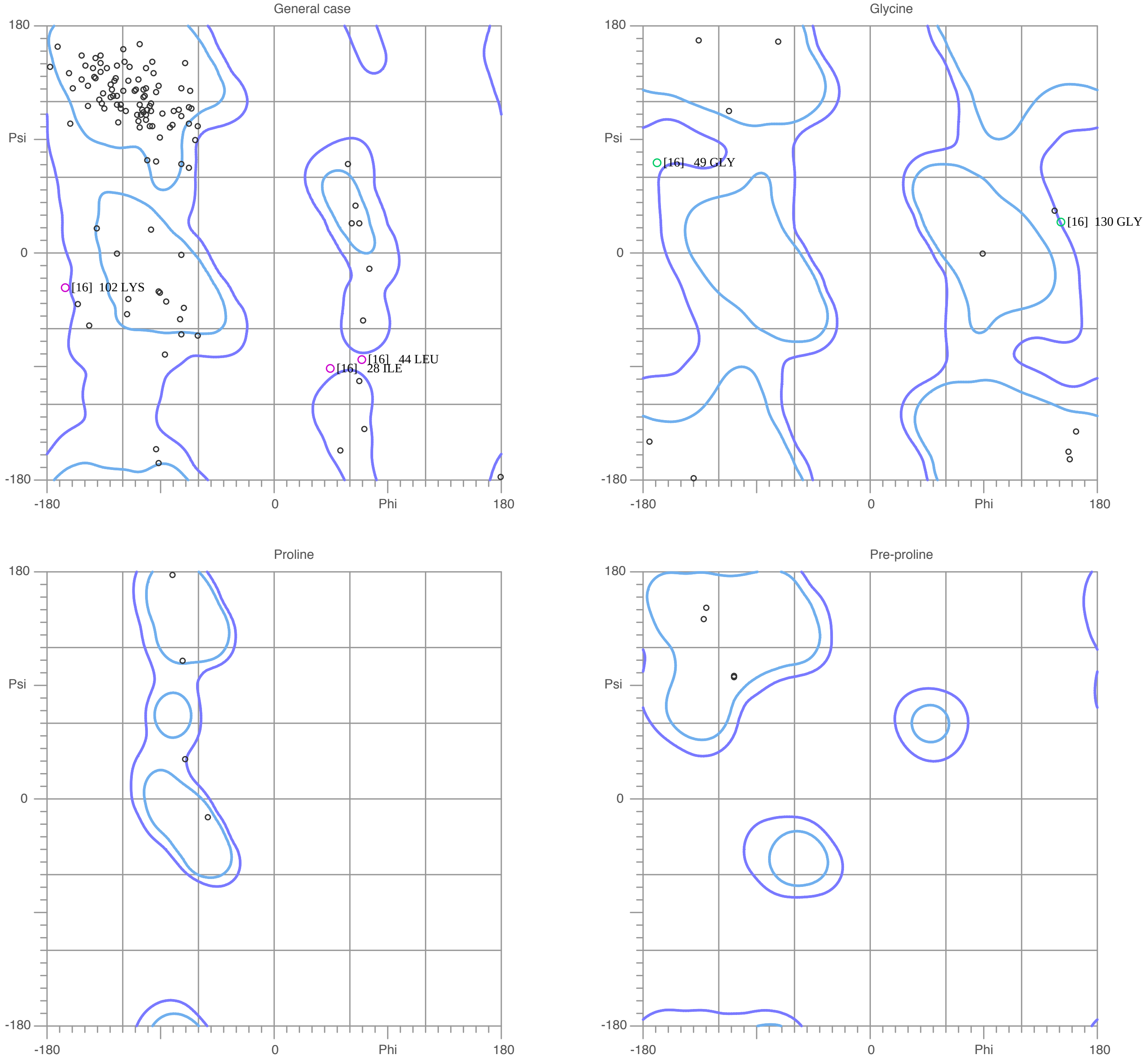
MolProbity Ramachandran analysis

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)

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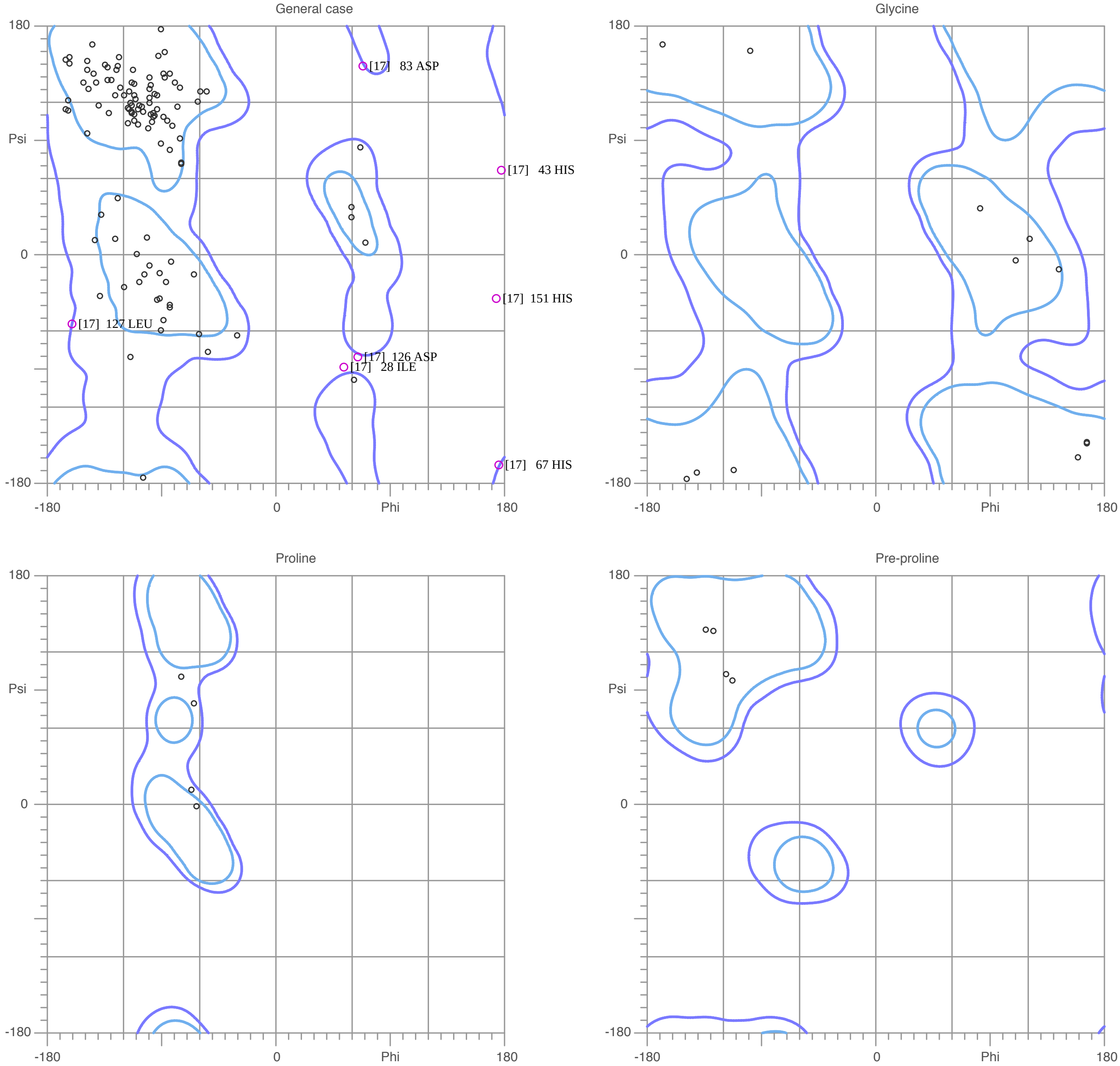
MolProbity Ramachandran analysis

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)

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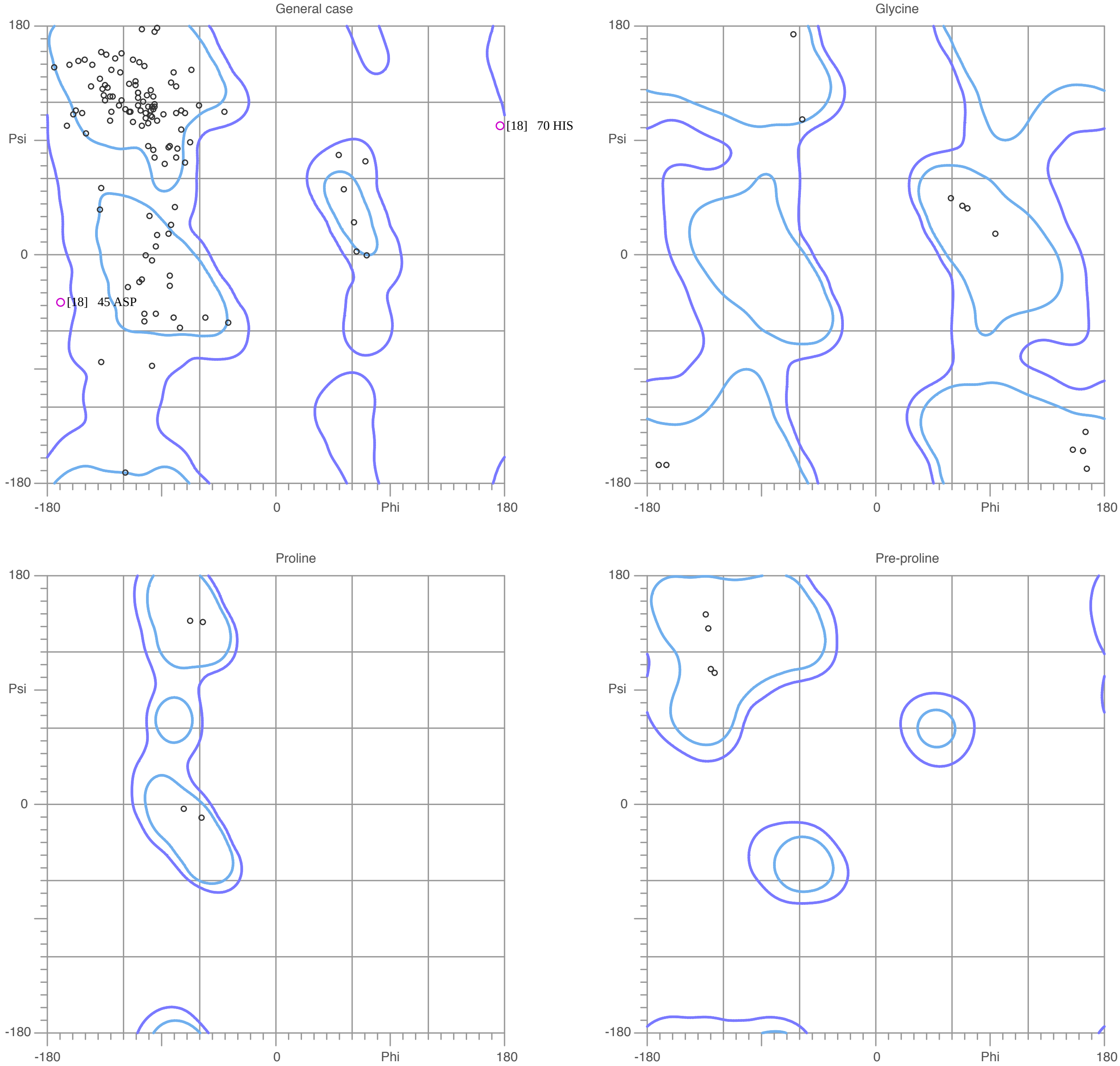
MolProbity Ramachandran analysis

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)

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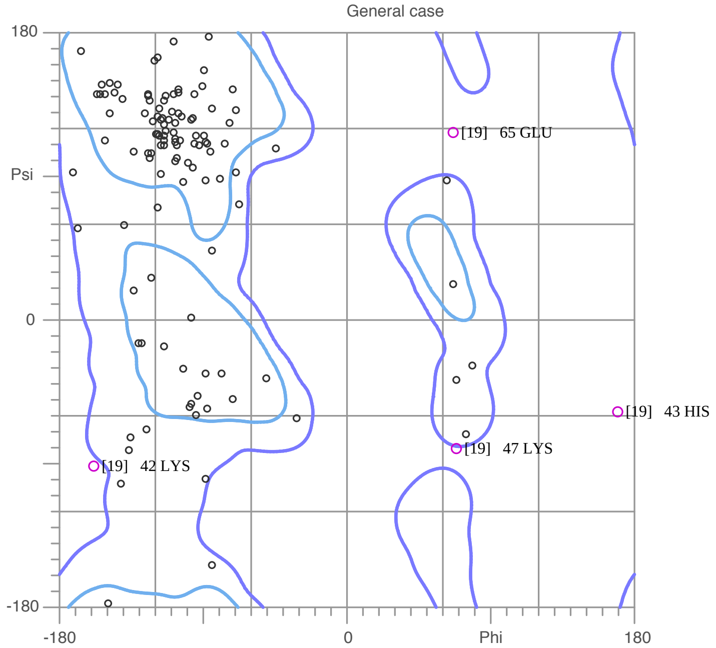
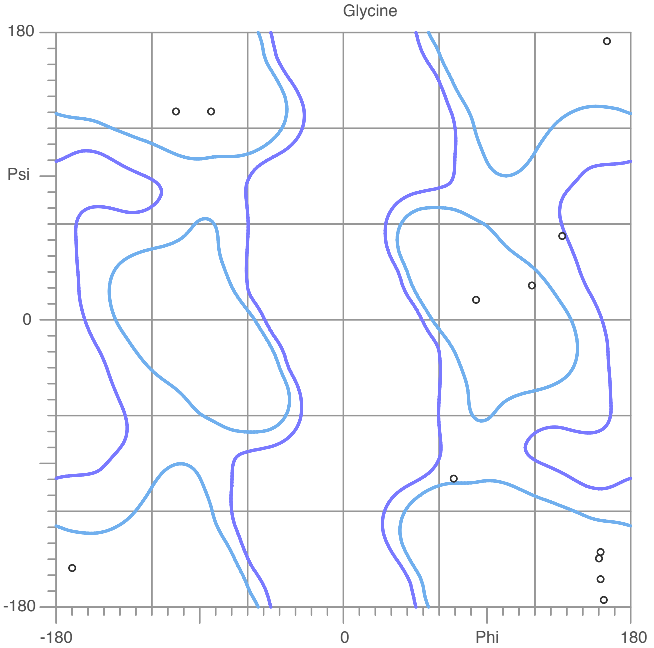
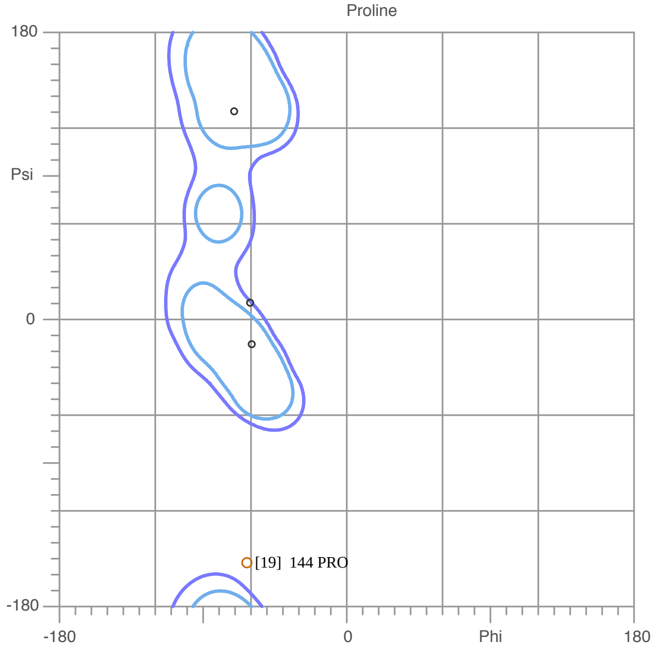
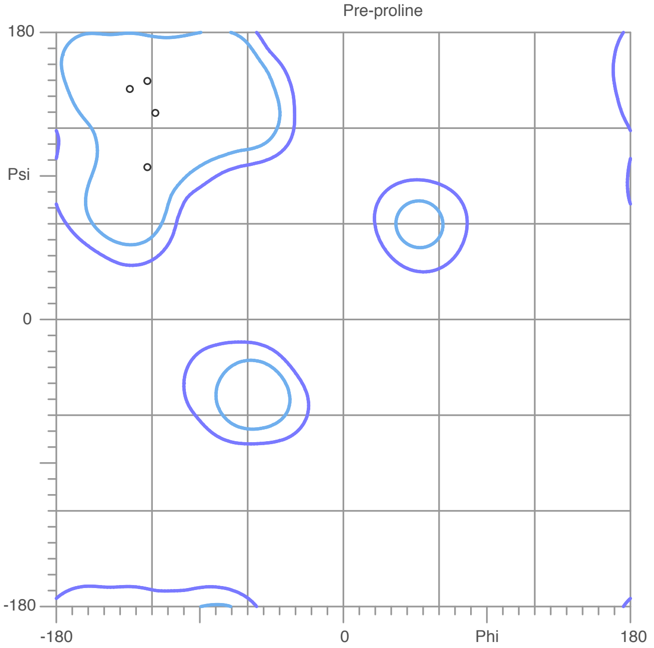
MolProbity Ramachandran analysis

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)

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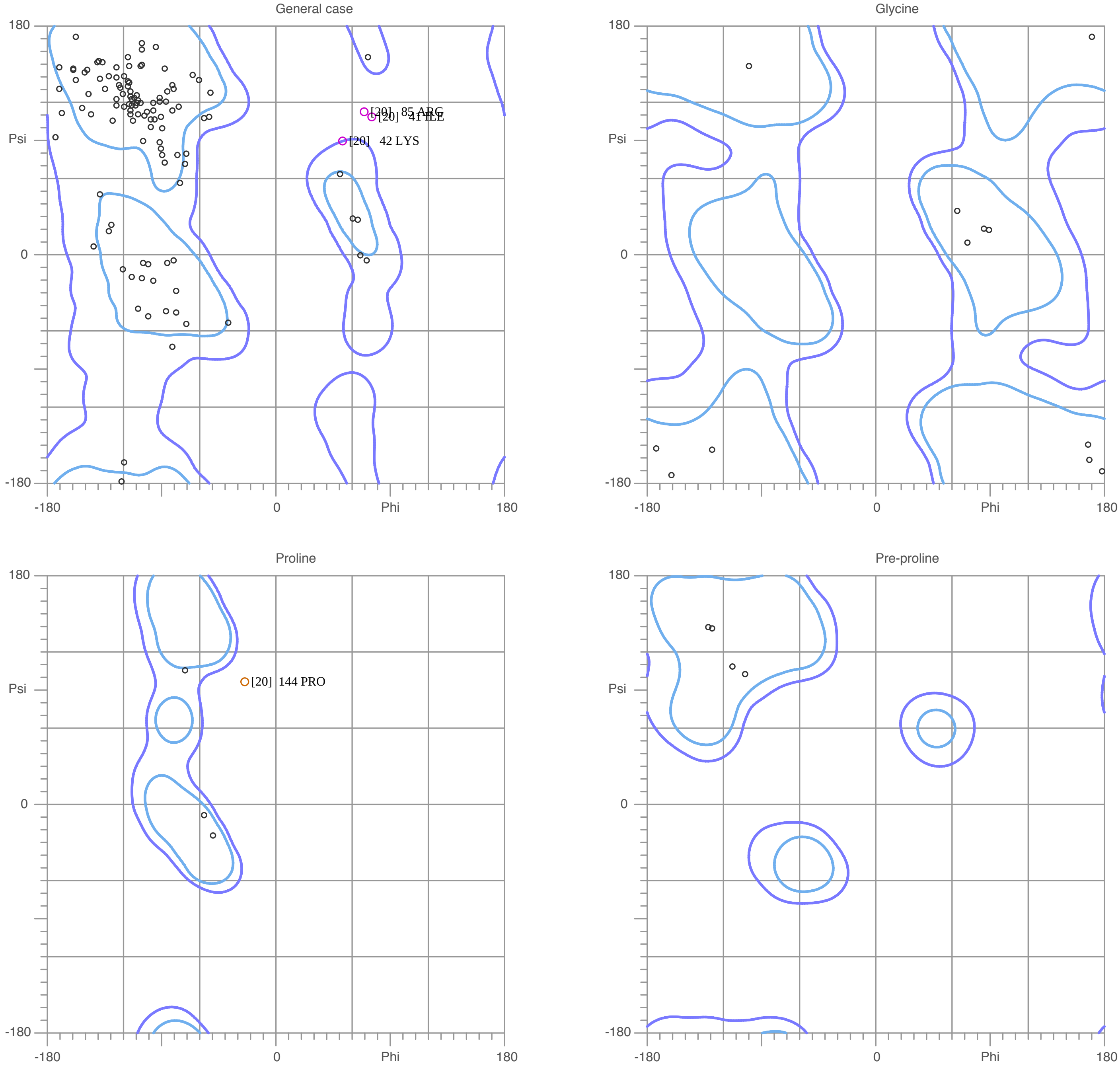
MolProbity Ramachandran analysis

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)

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