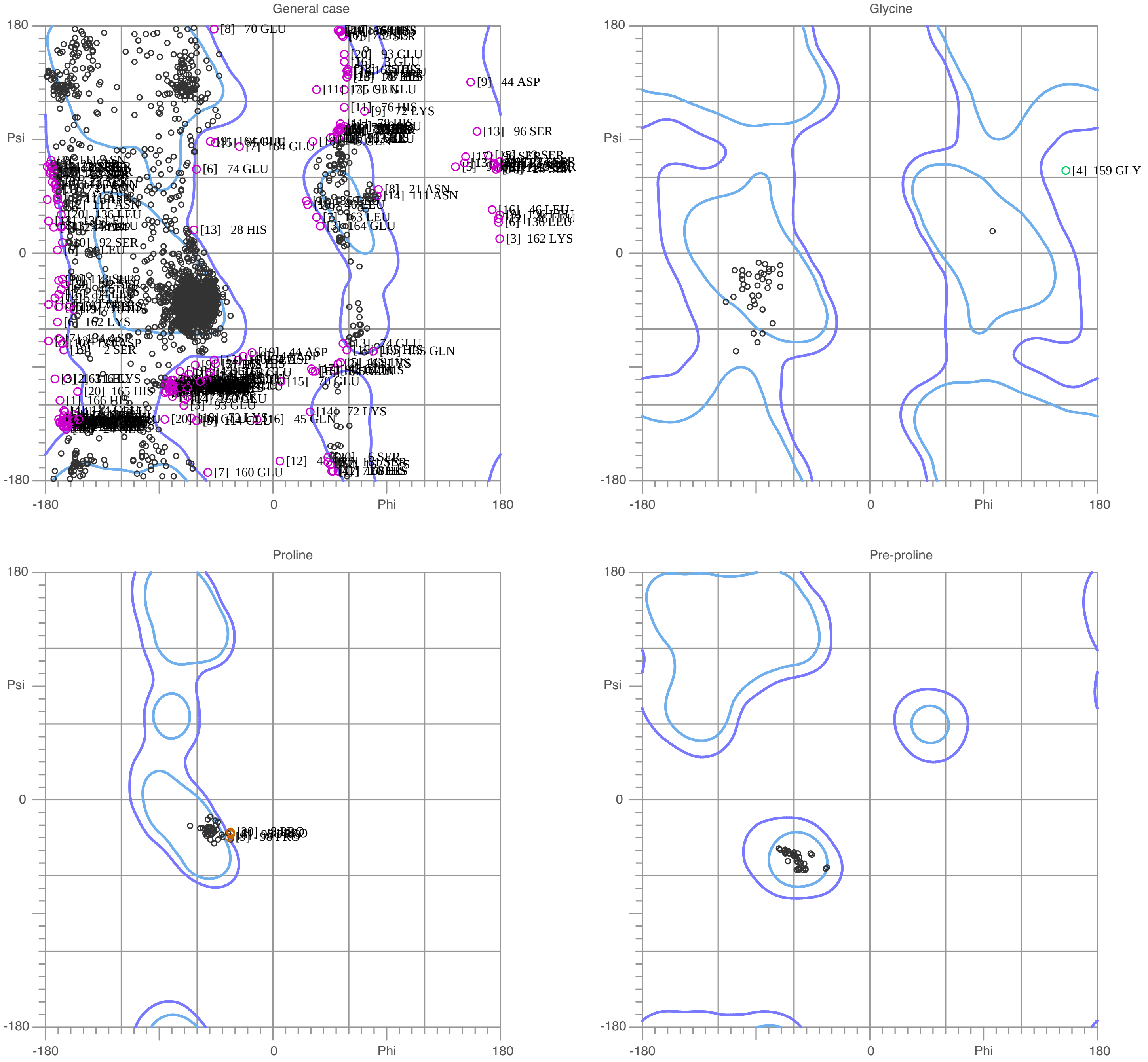
MolProbity Ramachandran analysis

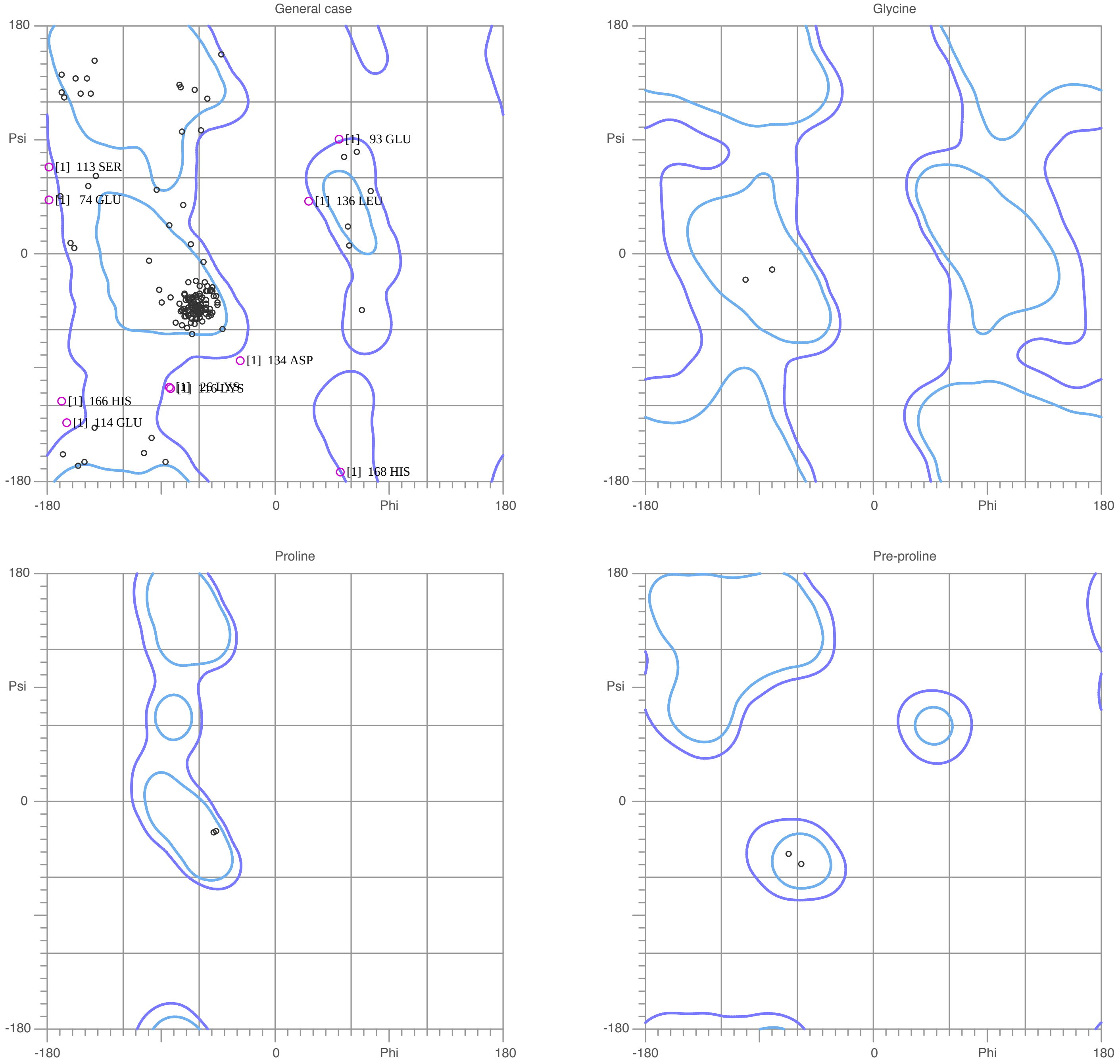
SR478_NMR_em_bcr3.pdb, all models



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

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 1



76.3% (119/156) of all residues were in favored (98%) regions.
93.6% (146/156) of all residues were in allowed (>99.8%) regions.

There were 10 outliers (phi, psi):
[1] 26 LYS (-84.2, -105.4)
[1] 74 GLU (-179.1, 43.1)
[1] 93 GLU (50.8, 91.4)
[1] 113 SER (-180.0, 69.4)
[1] 114 GLU (-165.1, -134.0)
[1] 116 LYS (-83.2, -106.1)
[1] 134 ASP (-28.5, -84.2)
[1] 136 LEU (26.0, 42.0)
[1] 166 HIS (-169.8, -116.9)
[1] 168 HIS (51.6, -172.9)

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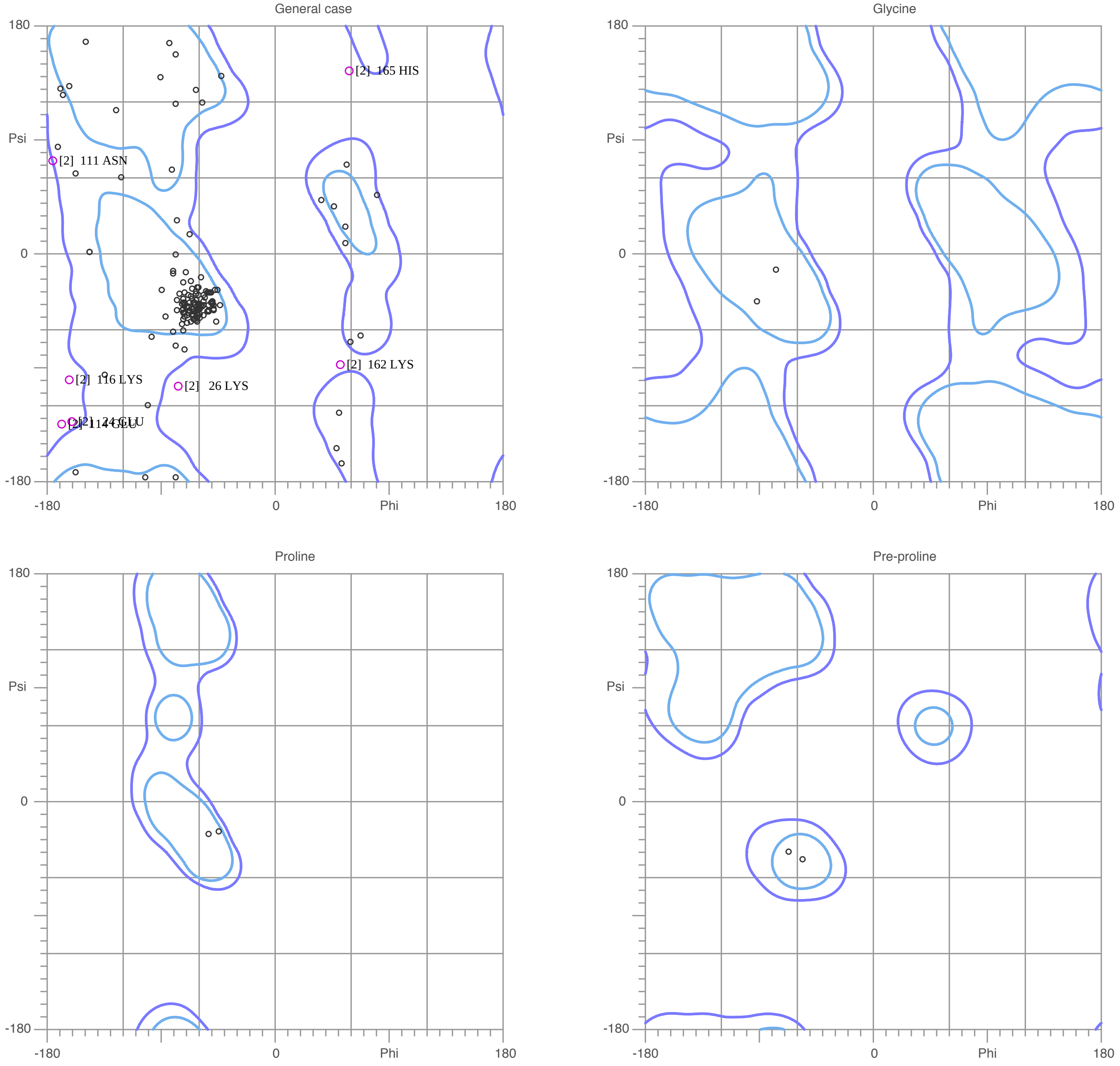
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 2



80.1% (125/156) of all residues were in favored (98%) regions.
95.5% (149/156) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[2] 24 GLU (-161.9, -132.1)
[2] 26 LYS (-77.7, -104.6)
[2] 111 ASN (-176.4, 74.3)
[2] 114 GLU (-169.7, -134.8)
[2] 116 LYS (-163.1, -99.5)
[2] 162 LYS (51.1, -87.4)
[2] 165 HIS (58.1, 145.7)

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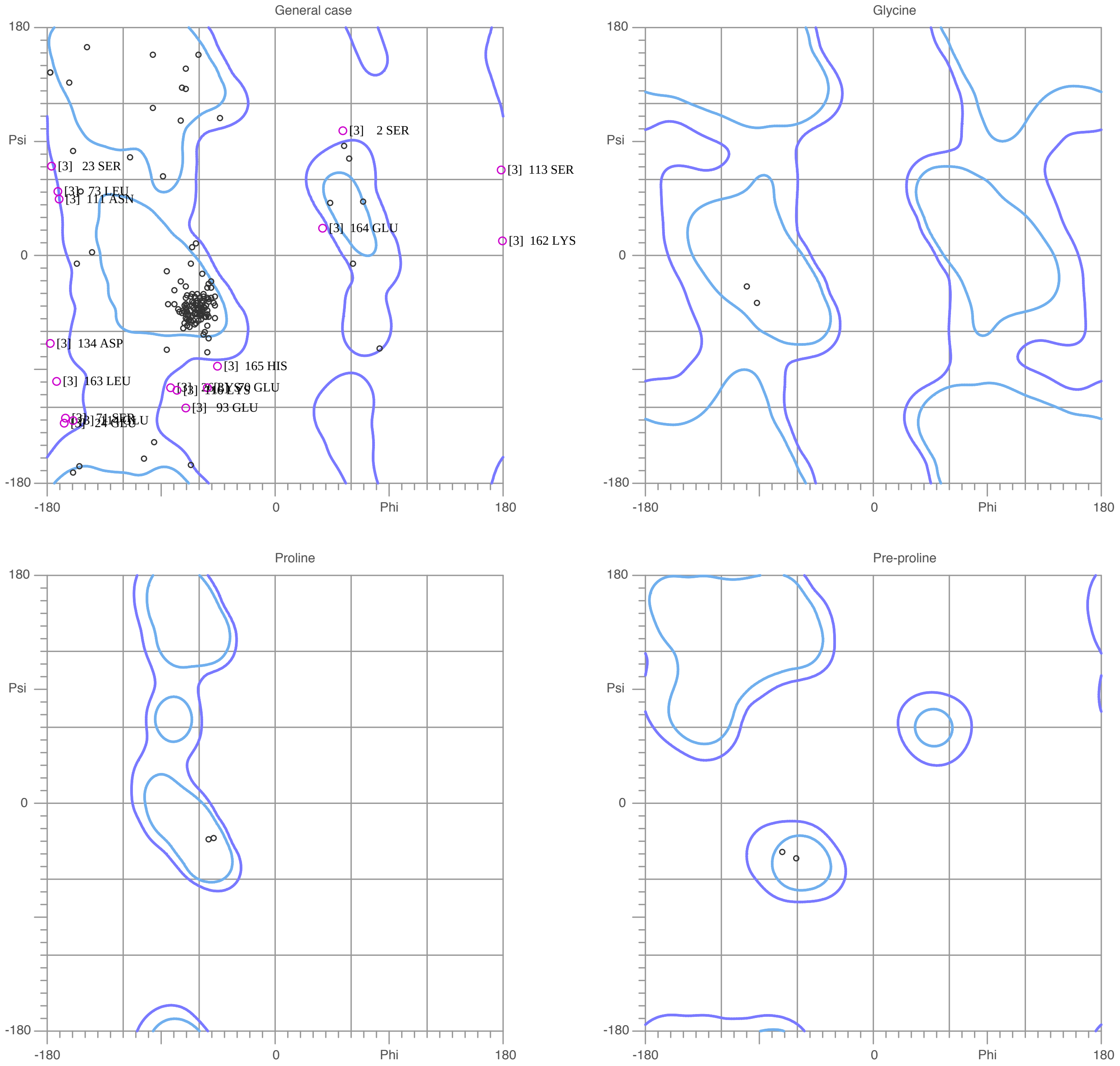
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 3



75.0% (117/156) of all residues were in favored (98%) regions.
89.1% (139/156) of all residues were in allowed (>99.8%) regions.

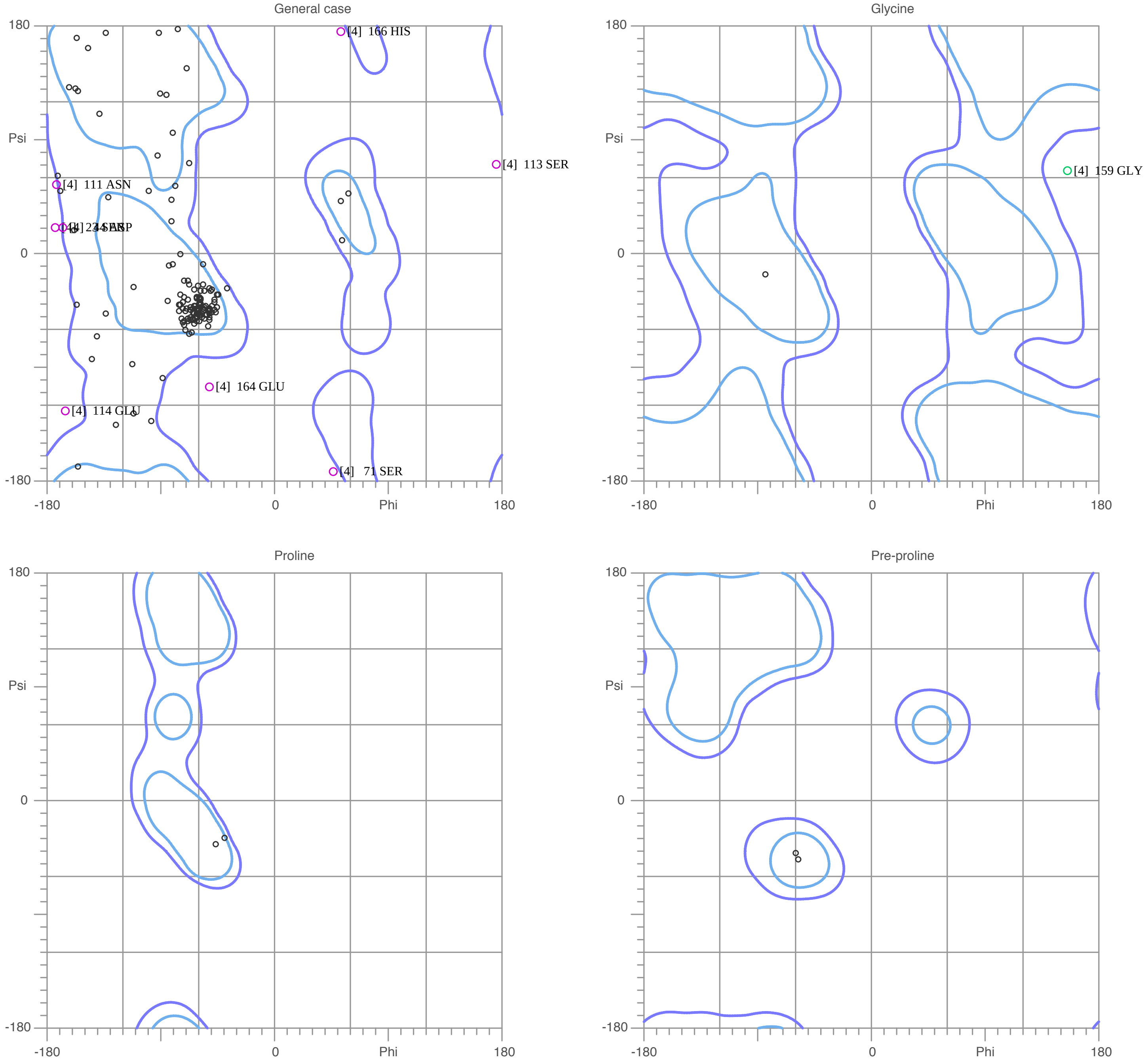
There were 17 outliers (phi, psi):

[3] 2 SER (53.3, 99.4)
[3] 23 SER (-177.2, 71.7)
[3] 24 GLU (-167.9, -132.6)
[3] 26 LYS (-83.9, -104.3)
[3] 70 GLU (-54.4, -104.2)
[3] 71 SER (-166.8, -128.2)
[3] 73 LEU (-172.6, 51.3)
[3] 93 GLU (-71.5, -120.9)
[3] 111 ASN (-171.2, 45.1)
[3] 113 SER (178.5, 68.5)
[3] 114 GLU (-160.9, -131.0)
[3] 116 LYS (-78.4, -106.4)
[3] 134 ASP (-178.4, -69.5)
[3] 162 LYS (179.6, 12.1)
[3] 163 LEU (-173.8, -99.0)
[3] 164 GLU (37.3, 22.8)
[3] 165 HIS (-46.1, -87.7)

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

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 4



81.4% (127/156) of all residues were in favored (98%) regions.
94.2% (147/156) of all residues were in allowed (>99.8%) regions.

There were 9 outliers (phi, psi):

[4] 23 SER (-174.2, 21.3)
[4] 44 ASP (-168.8, 21.5)
[4] 71 SER (46.5, -172.3)
[4] 111 ASN (-173.3, 55.9)
[4] 113 SER (175.3, 71.9)
[4] 114 GLU (-166.2, -124.8)
[4] 159 GLY (155.3, 66.7)
[4] 164 GLU (-52.0, -105.3)
[4] 166 HIS (52.6, 176.2)

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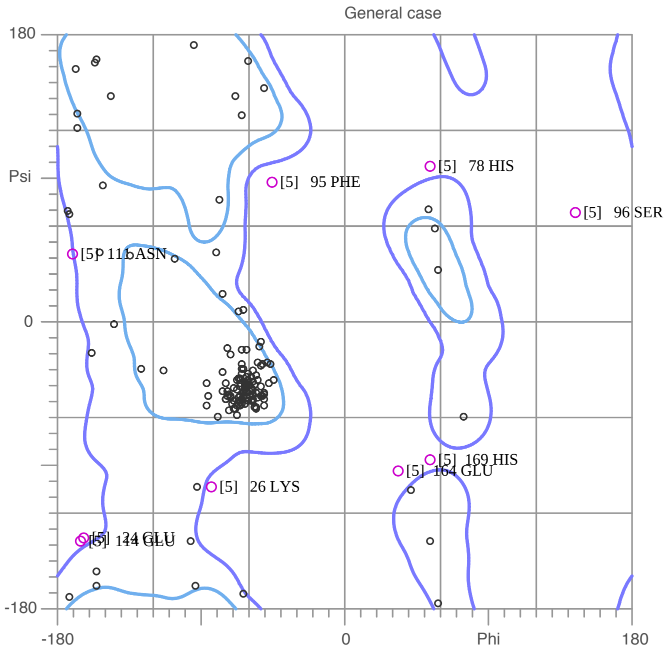
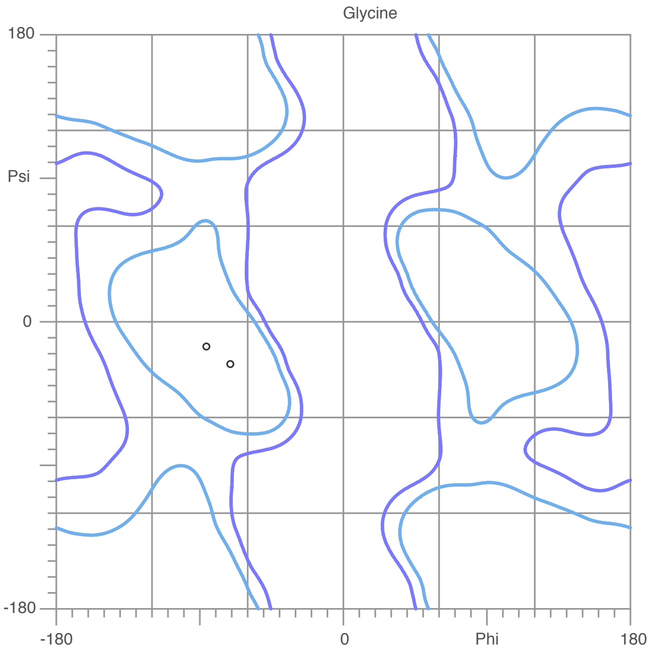
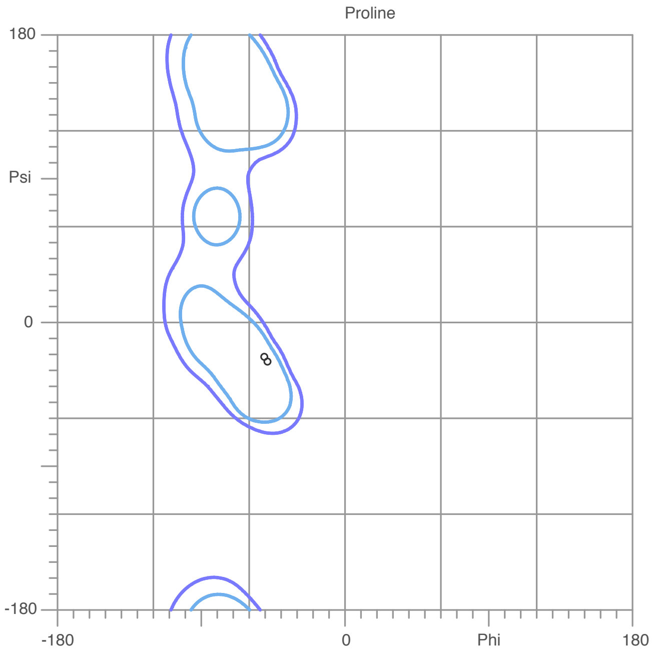
Lovell, Davis, et al. Proteins 50:437 (2003)

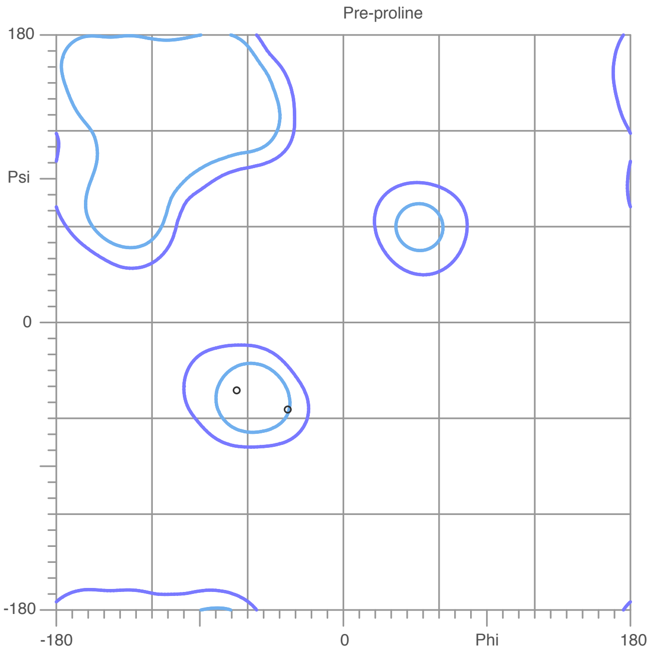
MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 5









78.2% (122/156) of all residues were in favored (98%) regions.
94.2% (147/156) of all residues were in allowed (>99.8%) regions.

There were 9 outliers (phi, psi):

[5] 24 GLU (-164.7, -135.4)
[5] 26 LYS (-85.0, -103.2)
[5] 78 HIS (53.6, 98.2)
[5] 95 PHE (-46.6, 88.7)
[5] 96 SER (144.6, 69.2)
[5] 111 ASN (-171.4, 43.5)
[5] 114 GLU (-166.9, -137.3)
[5] 164 GLU (33.3, -93.1)
[5] 169 HIS (53.9, -86.6)

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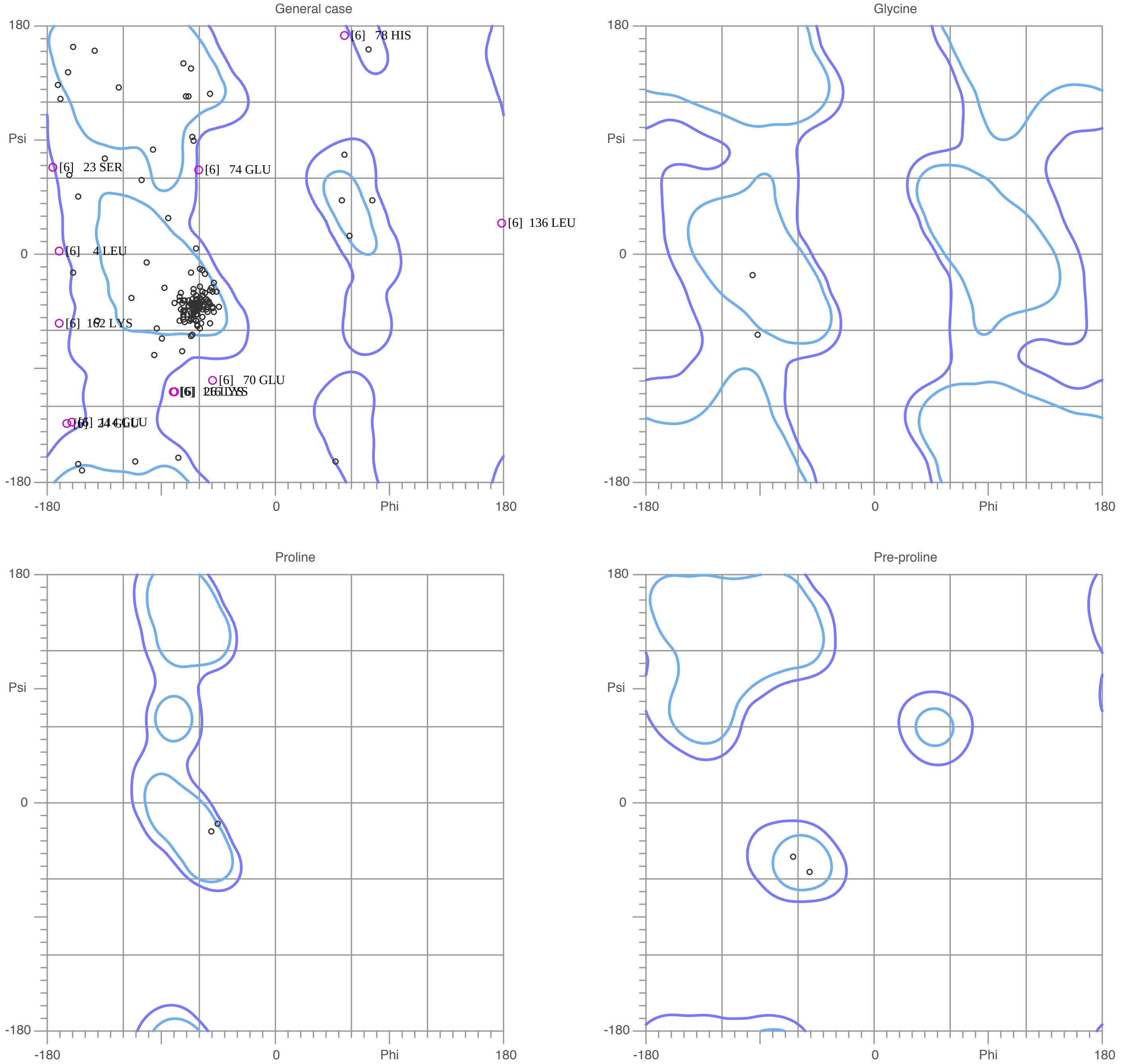
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 6



76.9% (120/156) of all residues were in favored (98%) regions.
92.9% (145/156) of all residues were in allowed (>99.8%) regions.

There were 11 outliers (phi, psi):

[6] 4 LEU (-171.4, 3.1)
[6] 23 SER (-176.2, 69.4)
[6] 24 GLU (-165.5, -133.7)
[6] 26 LYS (-81.4, -108.6)
[6] 70 GLU (-50.2, -99.7)
[6] 74 GLU (-61.6, 67.4)
[6] 78 HIS (54.8, 173.5)
[6] 114 GLU (-161.2, -132.8)
[6] 116 LYS (-81.0, -108.1)
[6] 136 LEU (178.3, 25.0)
[6] 162 LYS (-171.1, -54.8)

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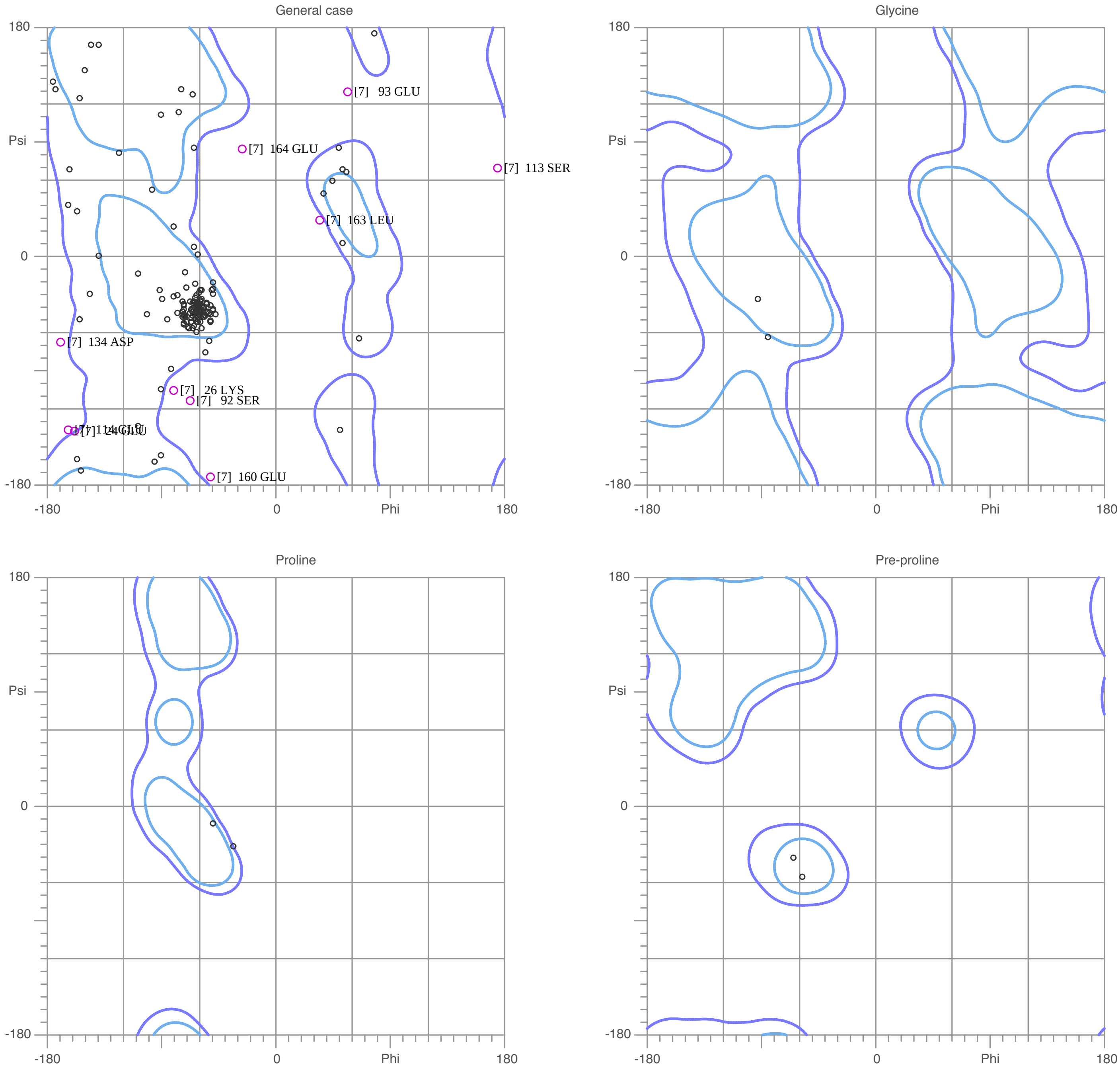
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 7



73.1% (114/156) of all residues were in favored (98%) regions.
93.6% (146/156) of all residues were in allowed (>99.8%) regions.

There were 10 outliers (phi, psi):

[7] 24 GLU (-159.9, -137.4)
[7] 26 LYS (-81.2, -106.0)
[7] 92 SER (-68.6, -113.7)
[7] 93 GLU (56.7, 130.6)
[7] 113 SER (174.4, 70.1)
[7] 114 GLU (-164.5, -136.9)
[7] 134 ASP (-170.9, -67.0)
[7] 160 GLU (-52.9, -173.7)
[7] 163 LEU (34.6, 29.6)
[7] 164 GLU (-27.9, 85.3)

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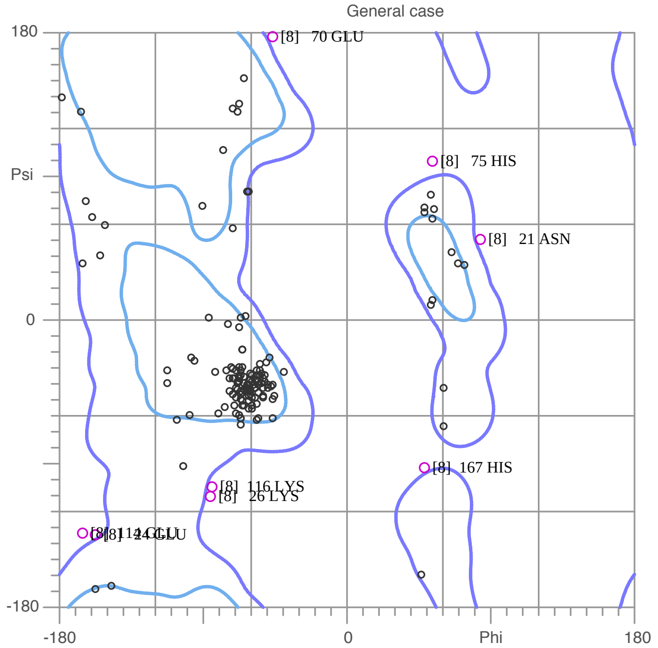
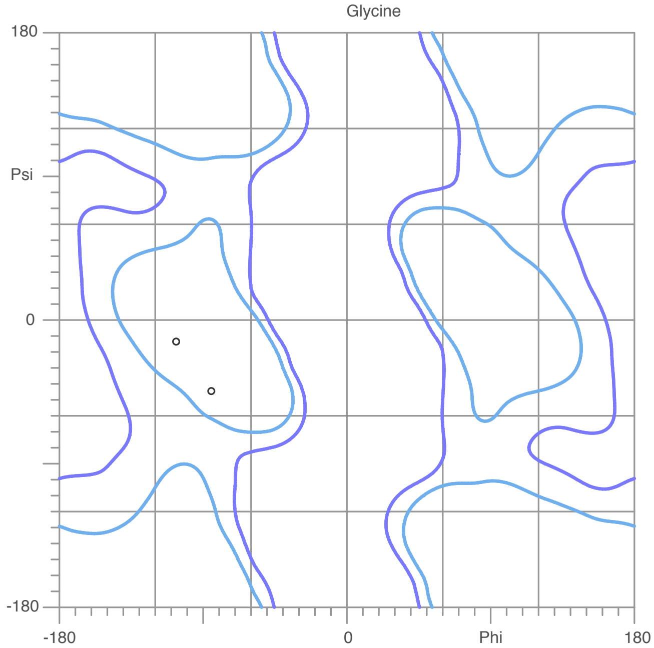
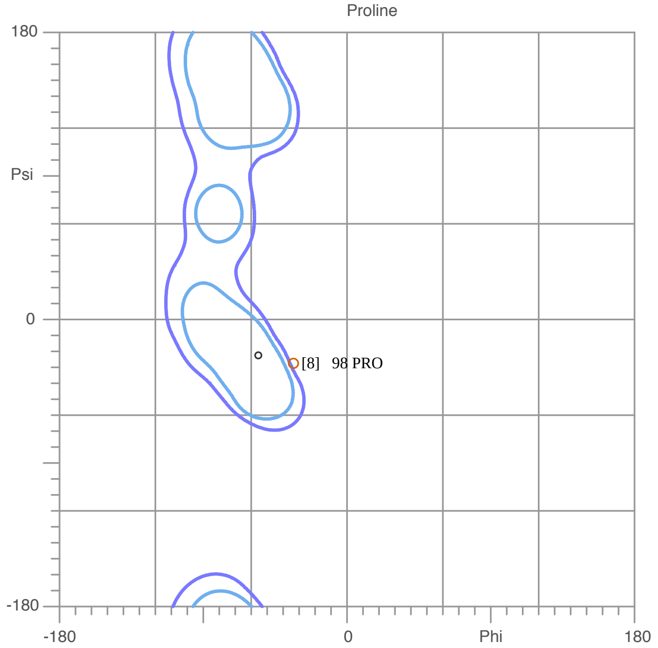
Lovell, Davis, et al. Proteins 50:437 (2003)

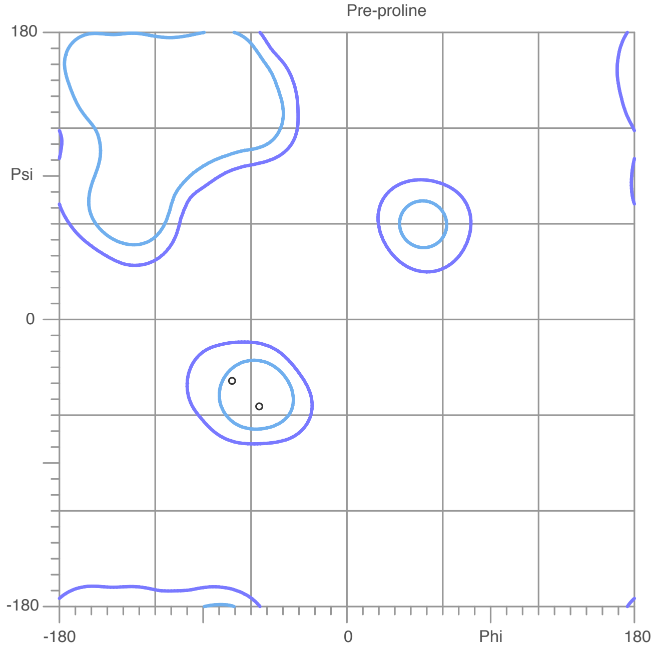
MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 8









78.2% (122/156) of all residues were in favored (98%) regions.
94.2% (147/156) of all residues were in allowed (>99.8%) regions.

There were 9 outliers (phi, psi):
[8] 21 ASN (83.6, 51.6)
[8] 24 GLU (-158.7, -134.7)
[8] 26 LYS (-86.1, -110.0)
[8] 70 GLU (-47.9, 178.2)
[8] 75 HIS (54.0, 100.8)
[8] 98 PRO (-34.3, -27.5)
[8] 114 GLU (-166.7, -134.0)
[8] 116 LYS (-85.8, -104.2)
[8] 167 HIS (48.1, -92.7)

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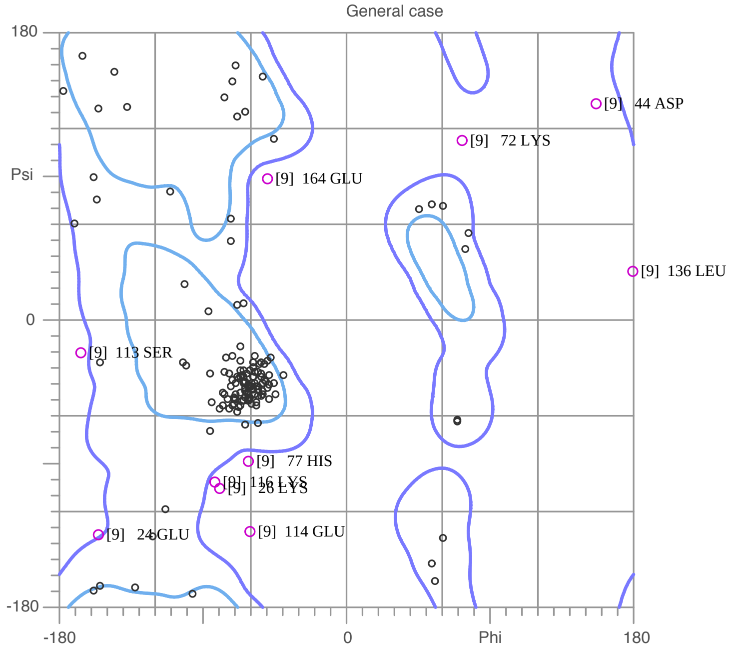
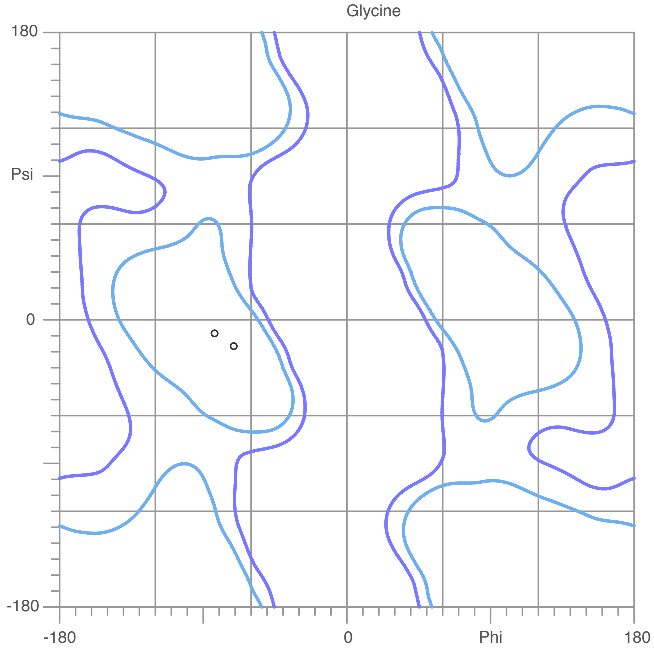
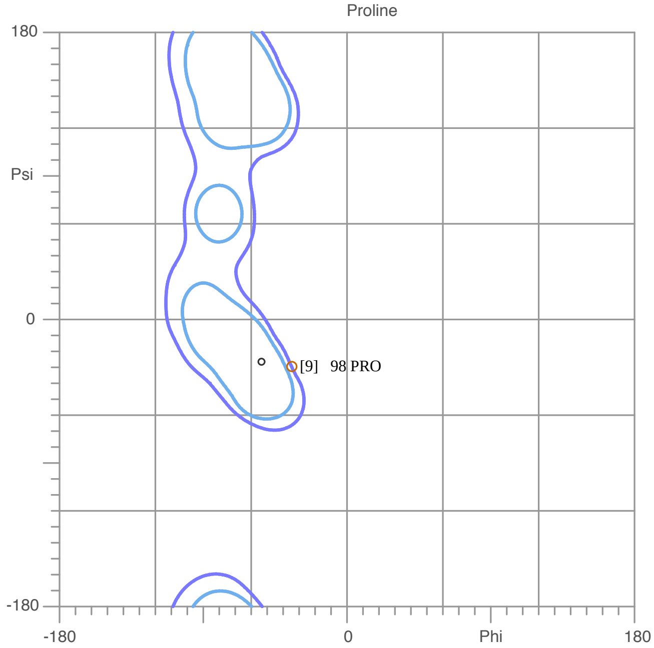
Lovell, Davis, et al. Proteins 50:437 (2003)

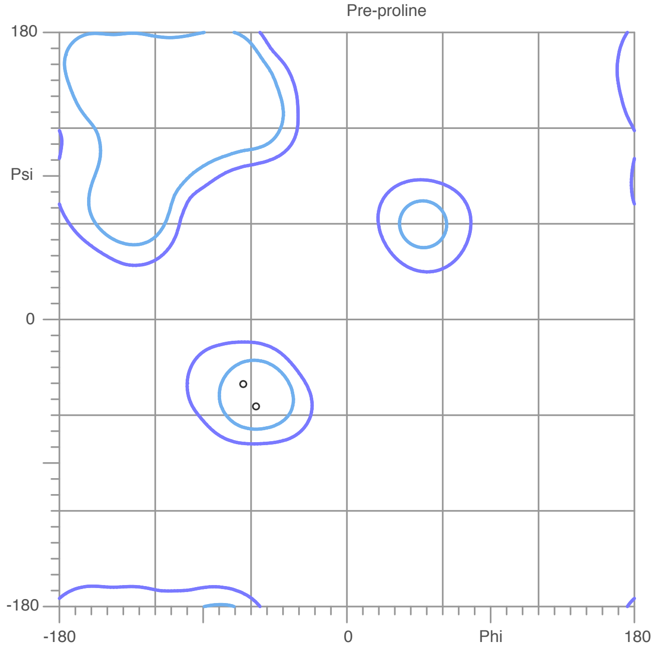
MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 9









74.4% (116/156) of all residues were in favored (98%) regions.
92.9% (145/156) of all residues were in allowed (>99.8%) regions.

There were 11 outliers (phi, psi):

[9] 24 GLU (-156.5, -134.7)
[9] 26 LYS (-80.7, -105.2)
[9] 44 ASP (156.9, 136.4)
[9] 72 LYS (72.4, 113.9)
[9] 77 HIS (-62.9, -88.0)
[9] 98 PRO (-35.1, -29.1)
[9] 113 SER (-167.1, -20.9)
[9] 114 GLU (-61.4, -132.5)
[9] 116 LYS (-83.4, -101.8)
[9] 136 LEU (179.1, 31.9)
[9] 164 GLU (-50.4, 89.2)

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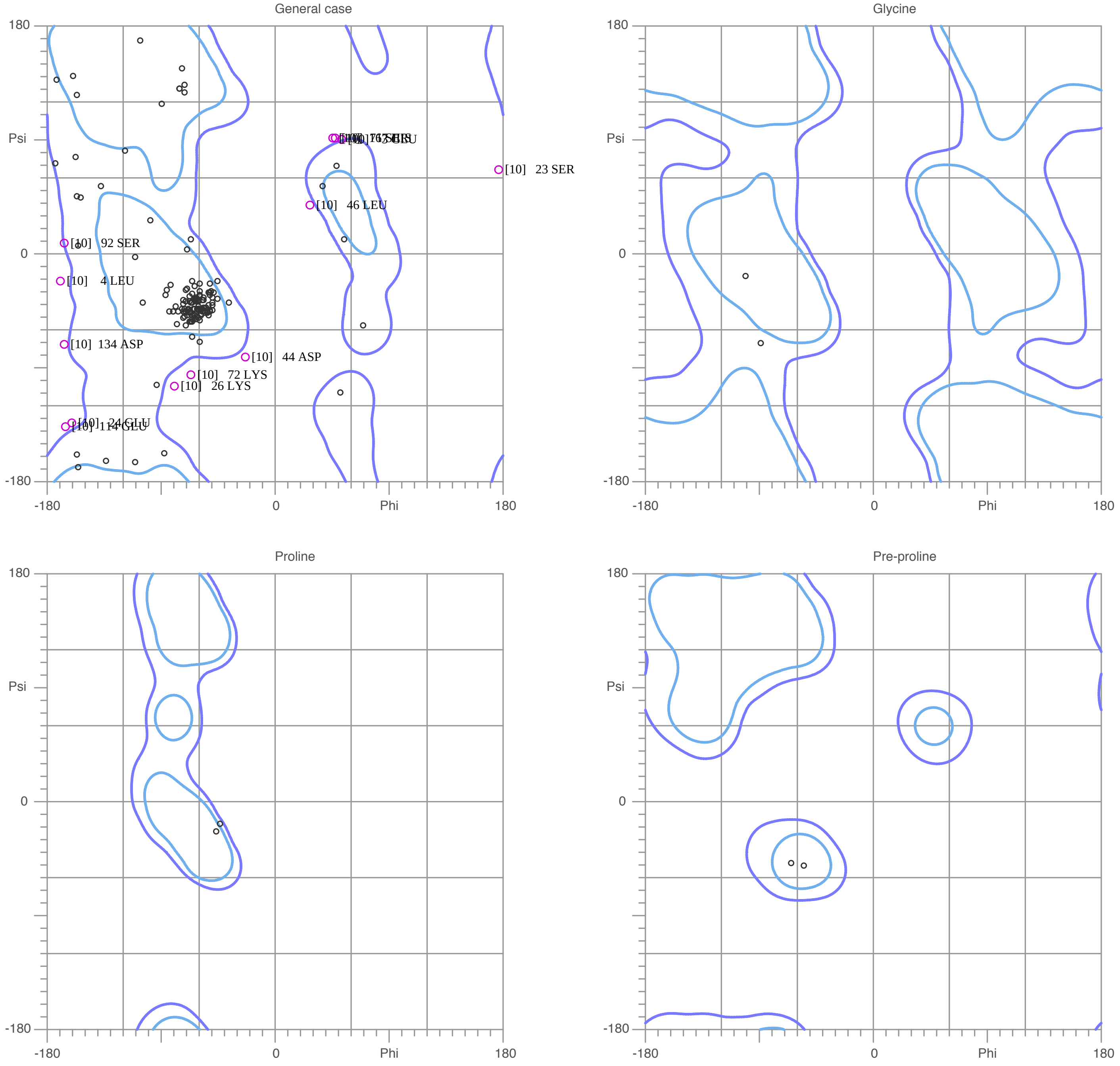
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 10



75.6% (118/156) of all residues were in favored (98%) regions.
91.7% (143/156) of all residues were in allowed (>99.8%) regions.

There were 13 outliers (phi, psi):

[10] 3 GLU (52.9, 91.0)
[10] 4 LEU (-170.7, -21.4)
[10] 23 SER (176.8, 67.7)
[10] 24 GLU (-161.4, -133.7)
[10] 26 LYS (-80.3, -104.9)
[10] 44 ASP (-25.0, -81.8)
[10] 46 LEU (27.9, 39.8)
[10] 71 SER (45.5, 92.3)
[10] 72 LYS (-67.9, -95.3)
[10] 92 SER (-167.6, 9.5)
[10] 114 GLU (-166.5, -136.2)
[10] 134 ASP (-167.6, -71.2)
[10] 167 HIS (48.0, 92.2)

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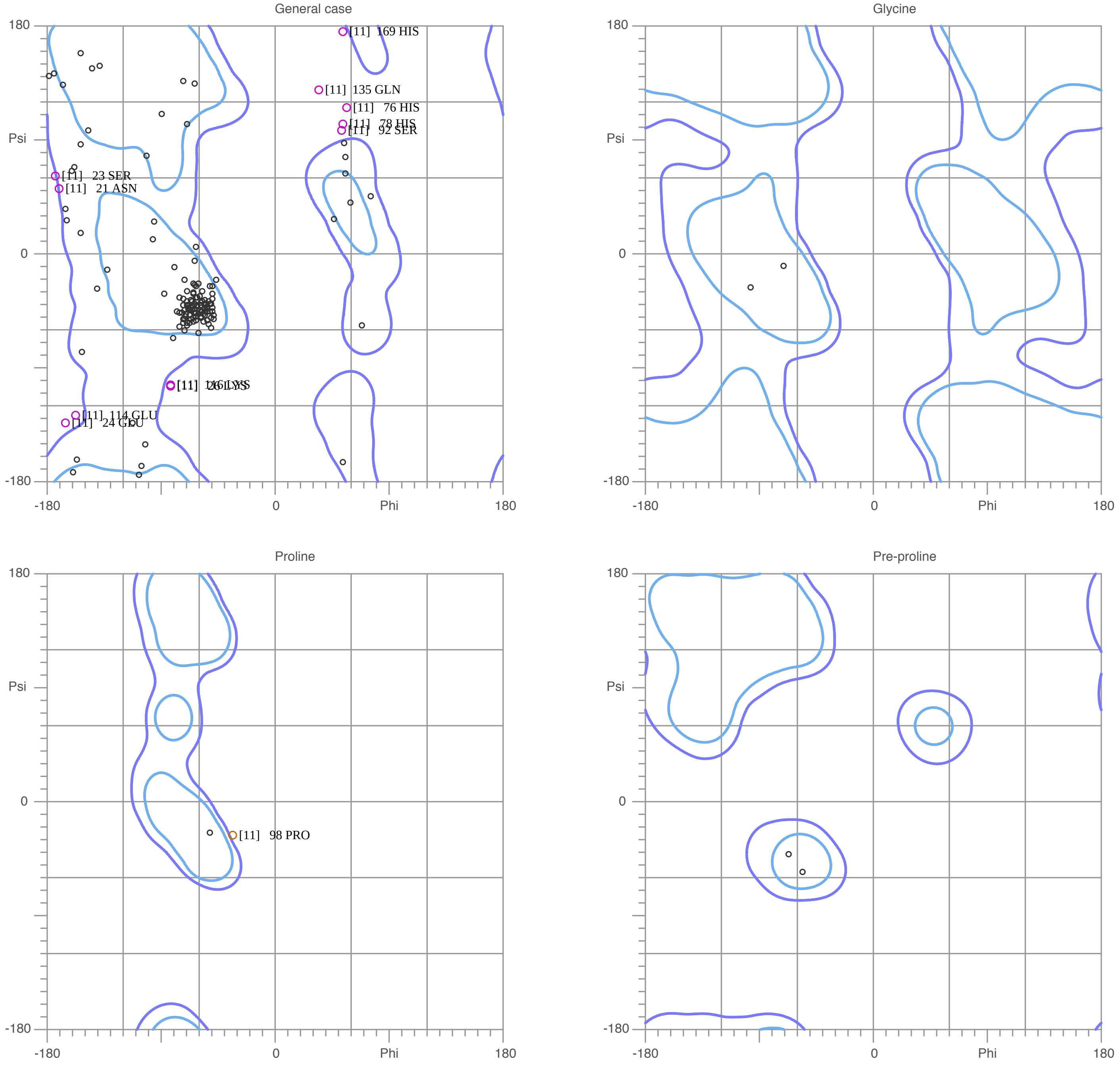
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 11



76.9% (120/156) of all residues were in favored (98%) regions.
92.3% (144/156) of all residues were in allowed (>99.8%) regions.

There were 12 outliers (phi, psi):
[11] 21 ASN (-171.5, 52.1)
[11] 23 SER (-174.6, 62.2)
[11] 24 GLU (-166.2, -133.9)
[11] 26 LYS (-83.4, -105.0)
[11] 76 HIS (56.2, 116.0)
[11] 78 HIS (53.4, 103.1)
[11] 92 SER (52.2, 98.2)
[11] 98 PRO (-34.8, -26.7)
[11] 114 GLU (-158.0, -127.1)
[11] 116 LYS (-83.4, -103.5)
[11] 135 GLN (34.1, 130.4)
[11] 169 HIS (53.0, 176.1)

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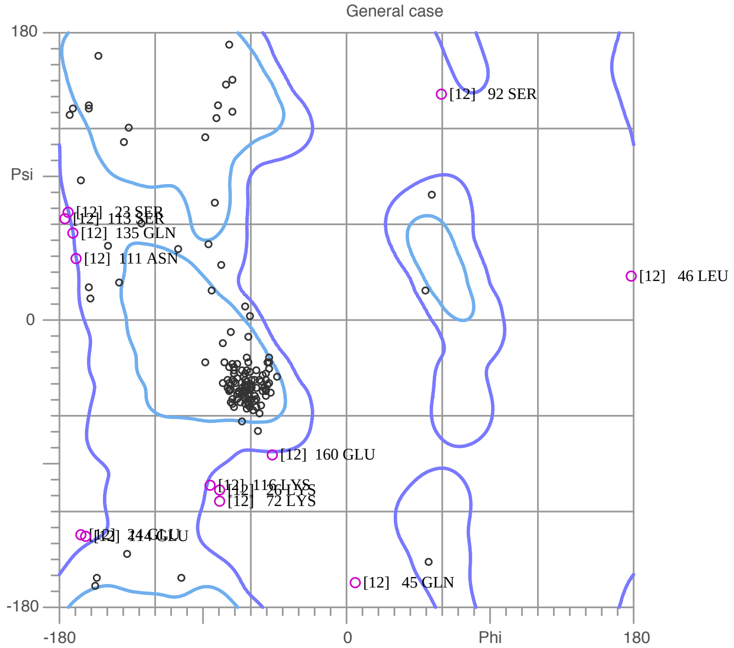
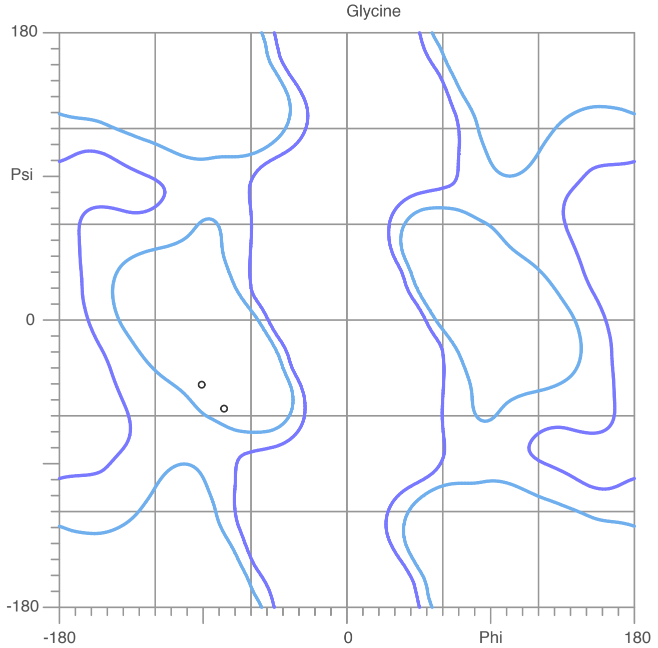
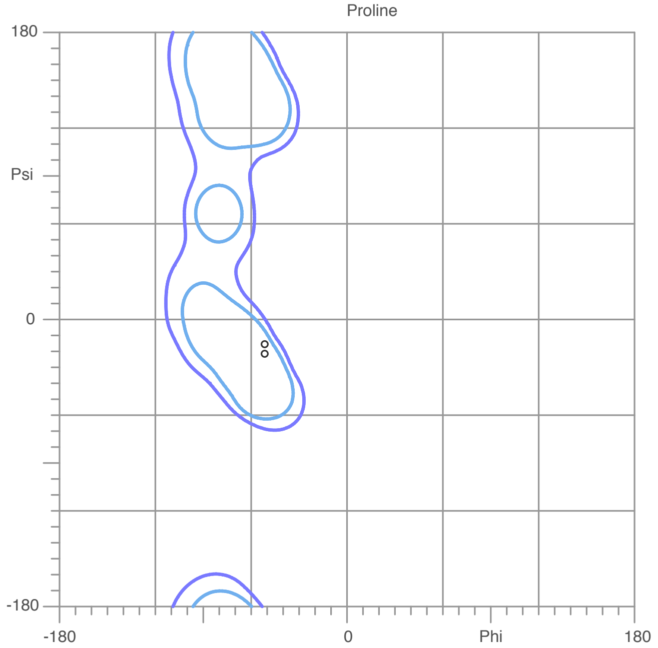
Lovell, Davis, et al. Proteins 50:437 (2003)

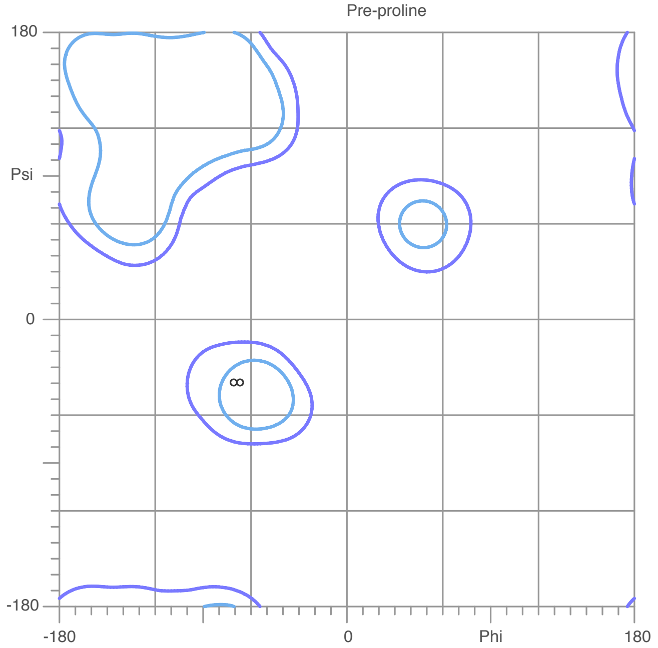
MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 12









77.6% (121/156) of all residues were in favored (98%) regions.
91.7% (143/156) of all residues were in allowed (>99.8%) regions.

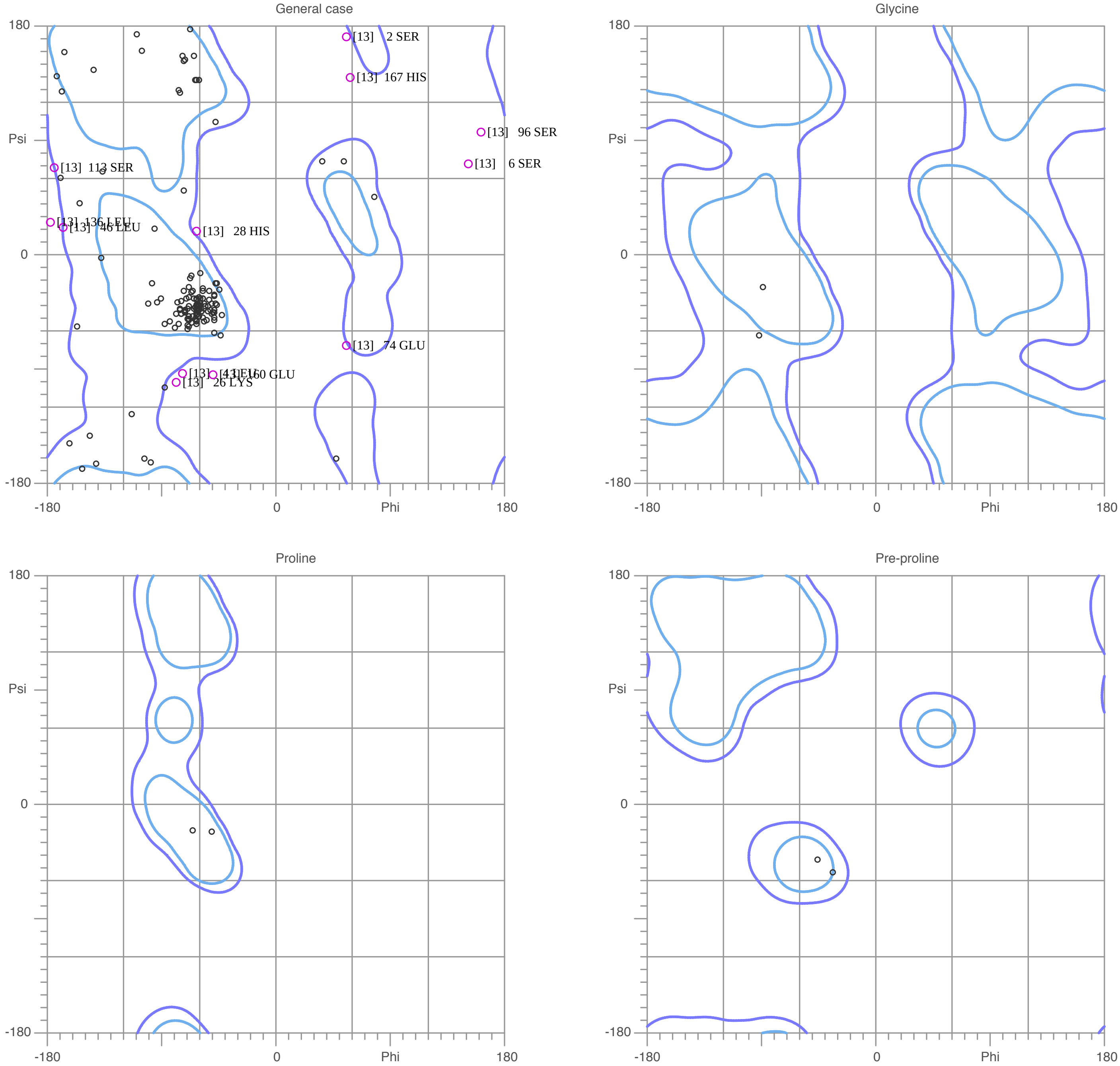
There were 13 outliers (phi, psi):

[12] 23 SER (-175.5, 68.6)
[12] 24 GLU (-167.1, -134.8)
[12] 26 LYS (-80.9, -106.1)
[12] 45 GLN (5.6, -164.0)
[12] 46 LEU (178.1, 28.8)
[12] 72 LYS (-80.1, -113.7)
[12] 92 SER (59.4, 142.3)
[12] 111 ASN (-170.1, 39.4)
[12] 113 SER (-177.5, 64.0)
[12] 114 GLU (-164.7, -135.4)
[12] 116 LYS (-86.5, -103.6)
[12] 135 GLN (-172.6, 55.6)
[12] 160 GLU (-47.0, -85.0)

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

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 13



76.3% (119/156) of all residues were in favored (98%) regions.
92.3% (144/156) of all residues were in allowed (>99.8%) regions.

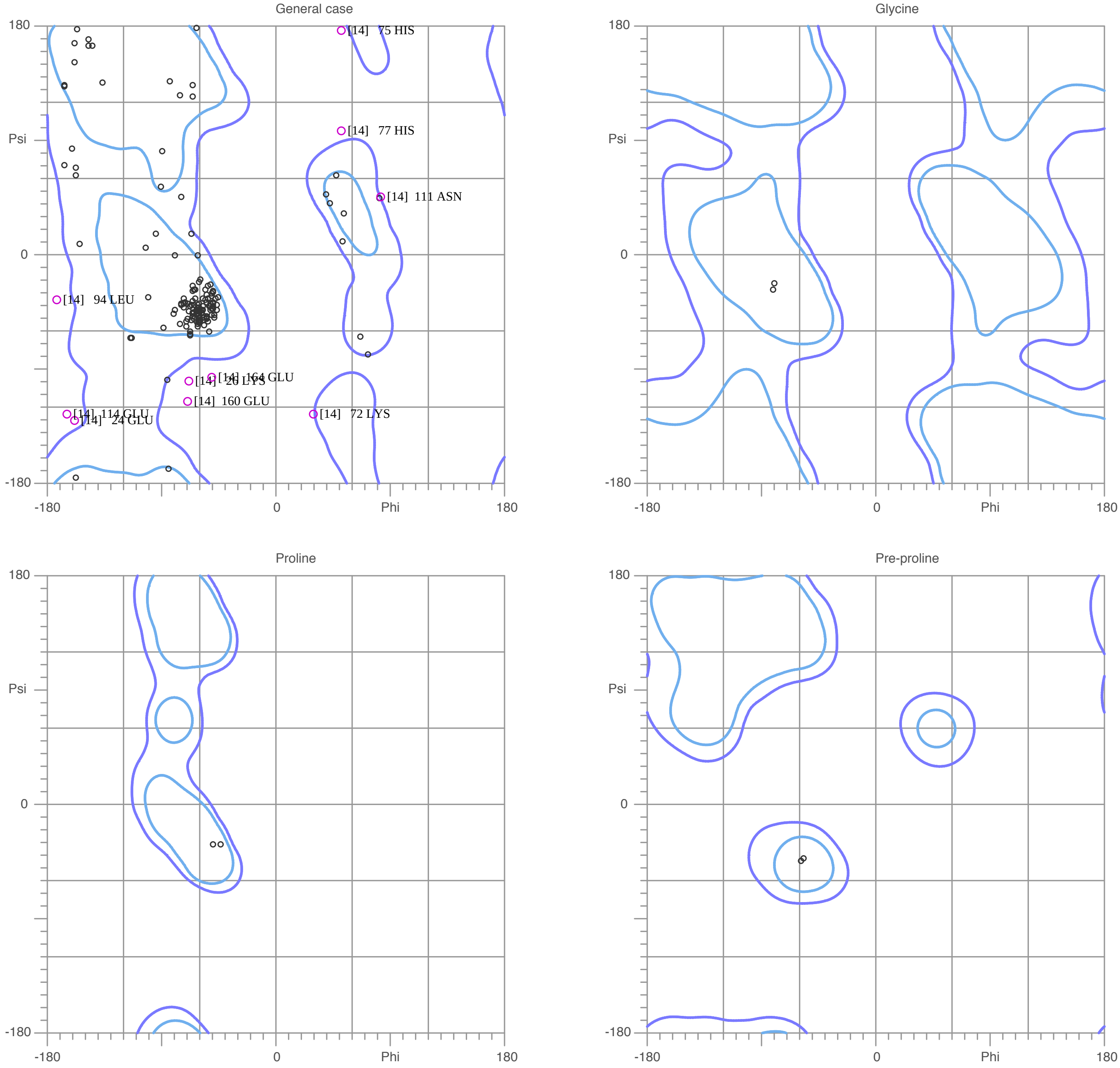
There were 12 outliers (phi, psi):

[13] 2 SER (55.3, 172.5)
[13] 4 LEU (-74.3, -93.9)
[13] 6 SER (151.2, 72.1)
[13] 26 LYS (-79.3, -100.8)
[13] 28 HIS (-63.8, 19.4)
[13] 46 LEU (-168.3, 23.0)
[13] 74 GLU (55.9, -71.1)
[13] 96 SER (161.3, 97.1)
[13] 113 SER (-175.5, 69.8)
[13] 136 LEU (-178.6, 26.3)
[13] 160 GLU (-50.4, -94.5)
[13] 167 HIS (58.6, 140.6)

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

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 14



82.7% (129/156) of all residues were in favored (98%) regions.
93.6% (146/156) of all residues were in allowed (>99.8%) regions.

There were 10 outliers (phi, psi):

[14] 24 GLU (-159.7, -130.9)
[14] 26 LYS (-69.9, -99.7)
[14] 72 LYS (29.4, -125.2)
[14] 75 HIS (52.0, 178.0)
[14] 77 HIS (51.1, 98.0)
[14] 94 LEU (-173.9, -35.3)
[14] 111 ASN (82.9, 46.8)
[14] 114 GLU (-165.2, -125.3)
[14] 160 GLU (-70.7, -115.7)
[14] 164 GLU (-51.1, -96.1)

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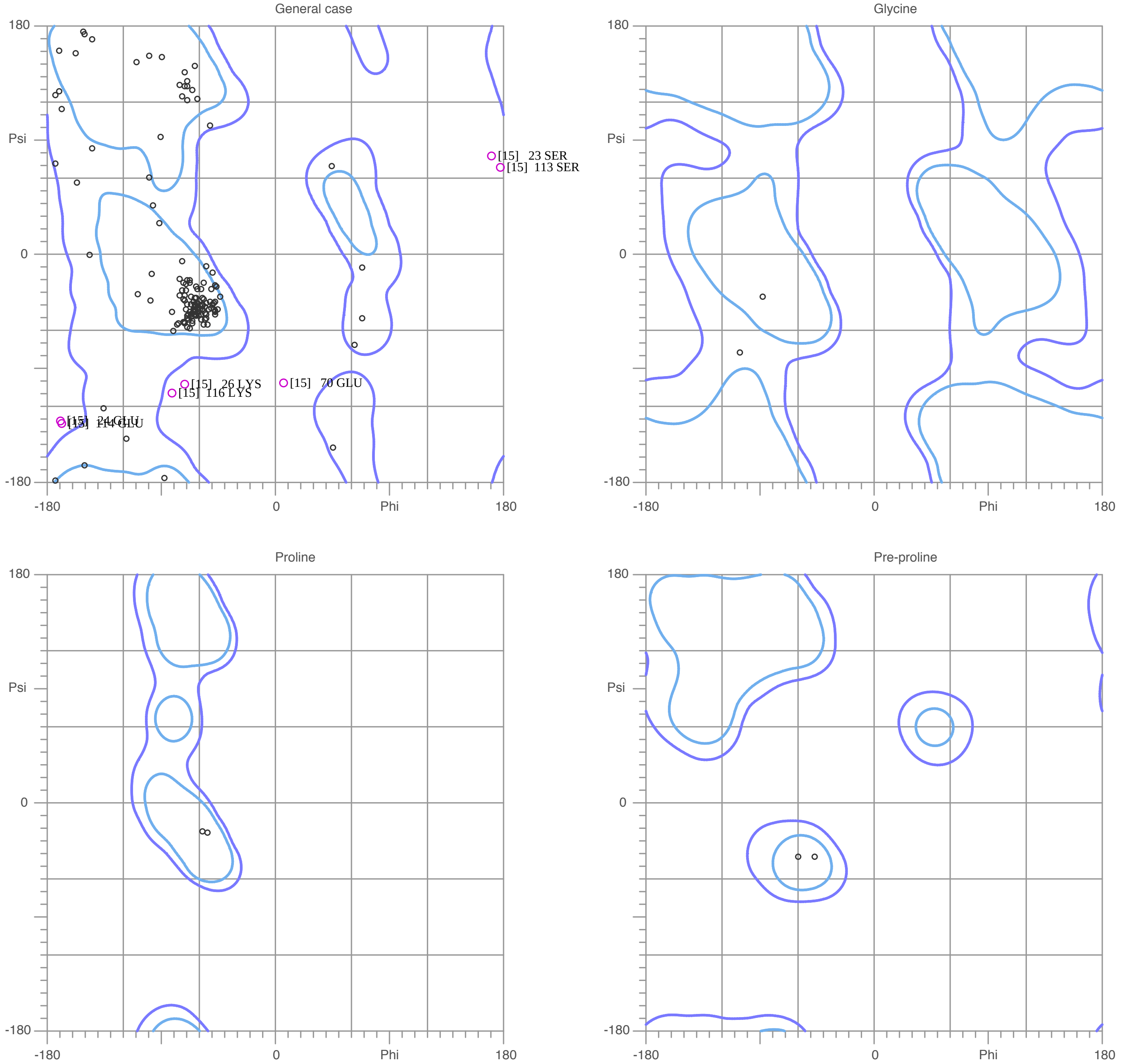
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 15



82.1% (128/156) of all residues were in favored (98%) regions.
95.5% (149/156) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):

[15] 23 SER (170.6, 78.3)
[15] 24 GLU (-170.7, -131.5)
[15] 26 LYS (-72.9, -102.5)
[15] 70 GLU (6.3, -101.6)
[15] 113 SER (177.6, 69.0)
[15] 114 GLU (-169.7, -133.2)
[15] 116 LYS (-82.2, -109.5)

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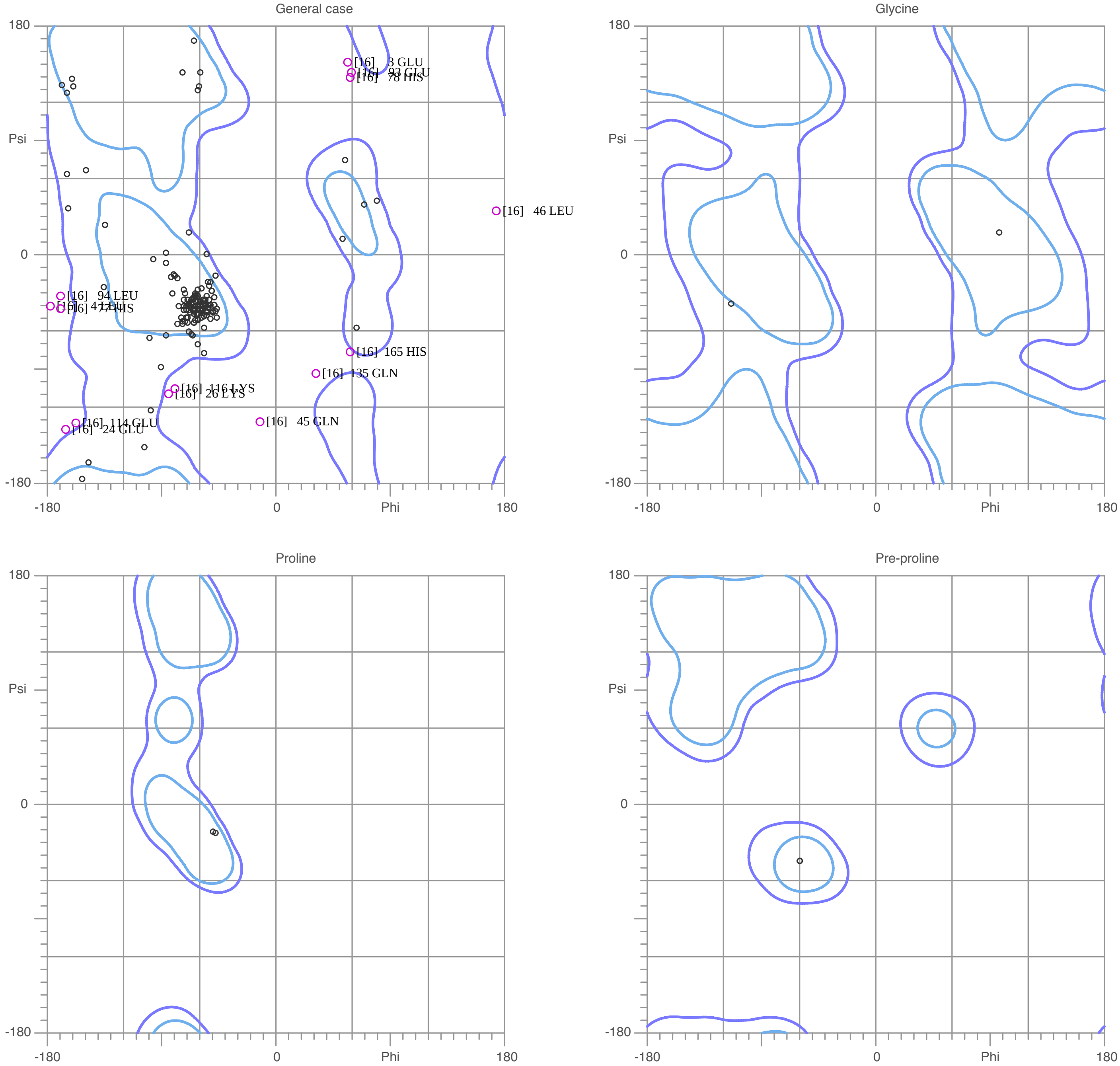
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 16



76.9% (120/156) of all residues were in favored (98%) regions.
91.0% (142/156) of all residues were in allowed (>99.8%) regions.

There were 14 outliers (phi, psi):
[16] 3 GLU (56.7, 152.5)
[16] 4 LEU (-178.4, -40.1)
[16] 24 GLU (-166.9, -137.1)
[16] 26 LYS (-85.9, -109.9)
[16] 45 GLN (-13.1, -131.6)
[16] 46 LEU (173.8, 35.3)
[16] 77 HIS (-170.3, -42.3)
[16] 78 HIS (58.8, 140.7)
[16] 93 GLU (59.4, 144.5)
[16] 94 LEU (-170.9, -32.7)
[16] 114 GLU (-158.6, -132.1)
[16] 116 LYS (-80.8, -105.6)
[16] 135 GLN (31.9, -94.0)
[16] 165 HIS (58.5, -77.0)

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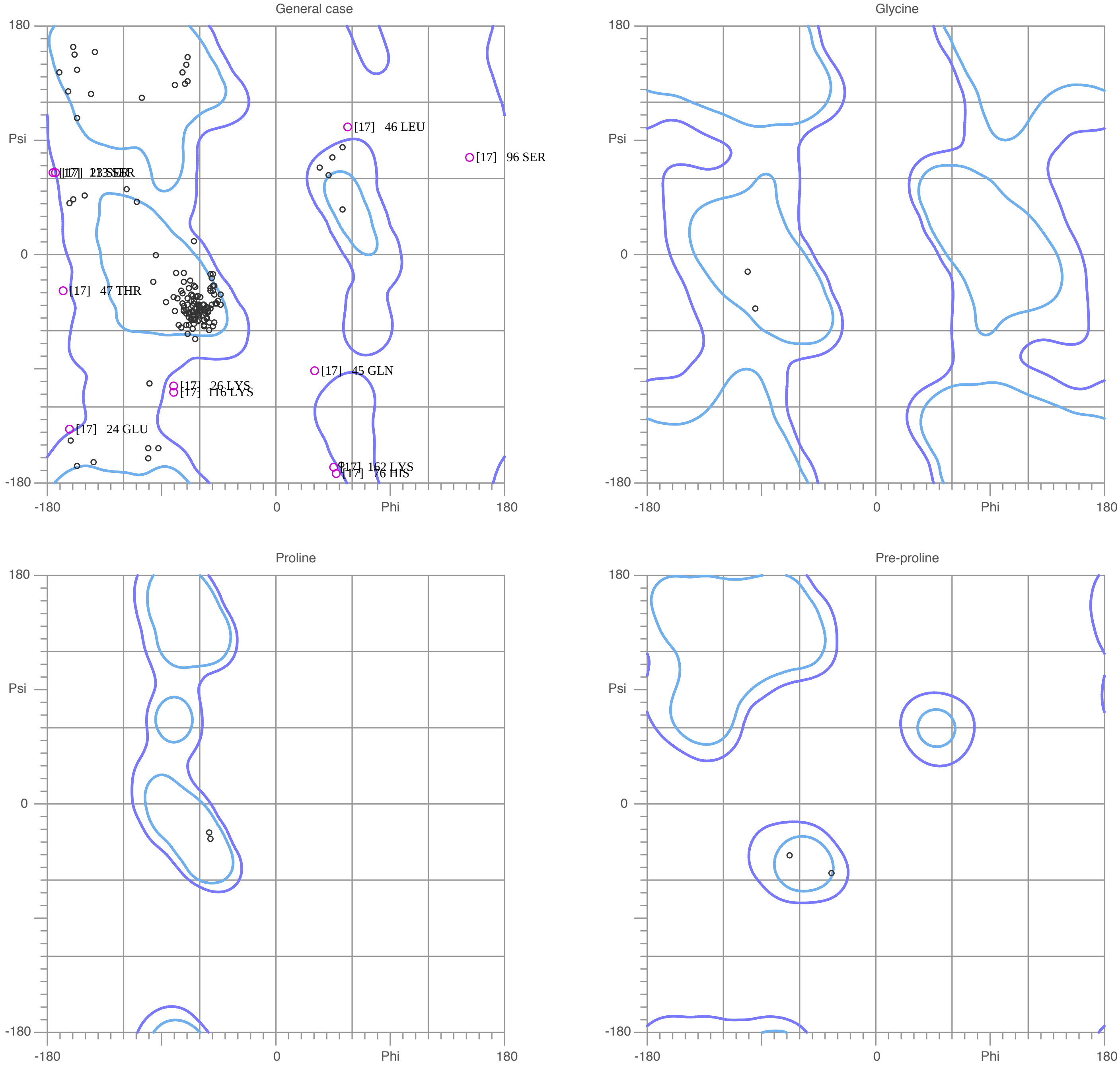
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 17



79.5% (124/156) of all residues were in favored (98%) regions.
92.9% (145/156) of all residues were in allowed (>99.8%) regions.

There were 11 outliers (phi, psi):
[17] 23 SER (-176.2, 65.1)
[17] 24 GLU (-163.1, -137.0)
[17] 26 LYS (-81.8, -103.4)
[17] 45 GLN (30.4, -92.0)
[17] 46 LEU (56.7, 101.3)
[17] 47 THR (-168.3, -28.1)
[17] 76 HIS (47.2, -172.5)
[17] 96 SER (152.3, 77.9)
[17] 113 SER (-174.6, 65.9)
[17] 116 LYS (-81.5, -108.1)
[17] 162 LYS (45.0, -167.5)

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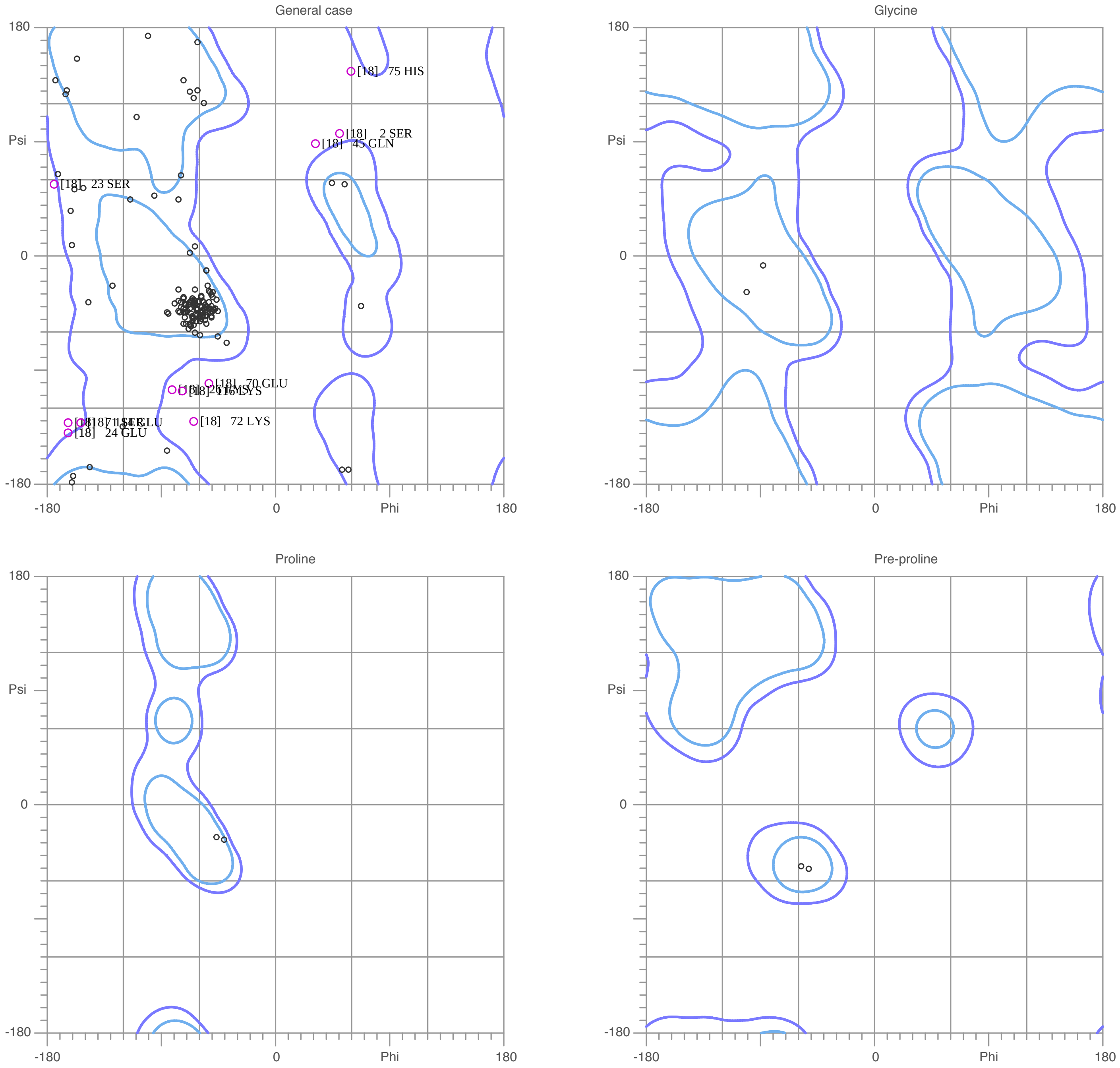
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 18



80.1% (125/156) of all residues were in favored (98%) regions.
92.9% (145/156) of all residues were in allowed (>99.8%) regions.

There were 11 outliers (phi, psi):

[18] 2 SER (50.7, 97.0)
[18] 23 SER (-175.4, 57.8)
[18] 24 GLU (-164.7, -139.3)
[18] 26 LYS (-82.5, -105.7)
[18] 45 GLN (31.6, 89.4)
[18] 70 GLU (-53.8, -100.5)
[18] 71 SER (-164.8, -131.4)
[18] 72 LYS (-65.8, -131.0)
[18] 75 HIS (59.6, 146.8)
[18] 114 GLU (-154.9, -131.3)
[18] 116 LYS (-74.3, -106.4)

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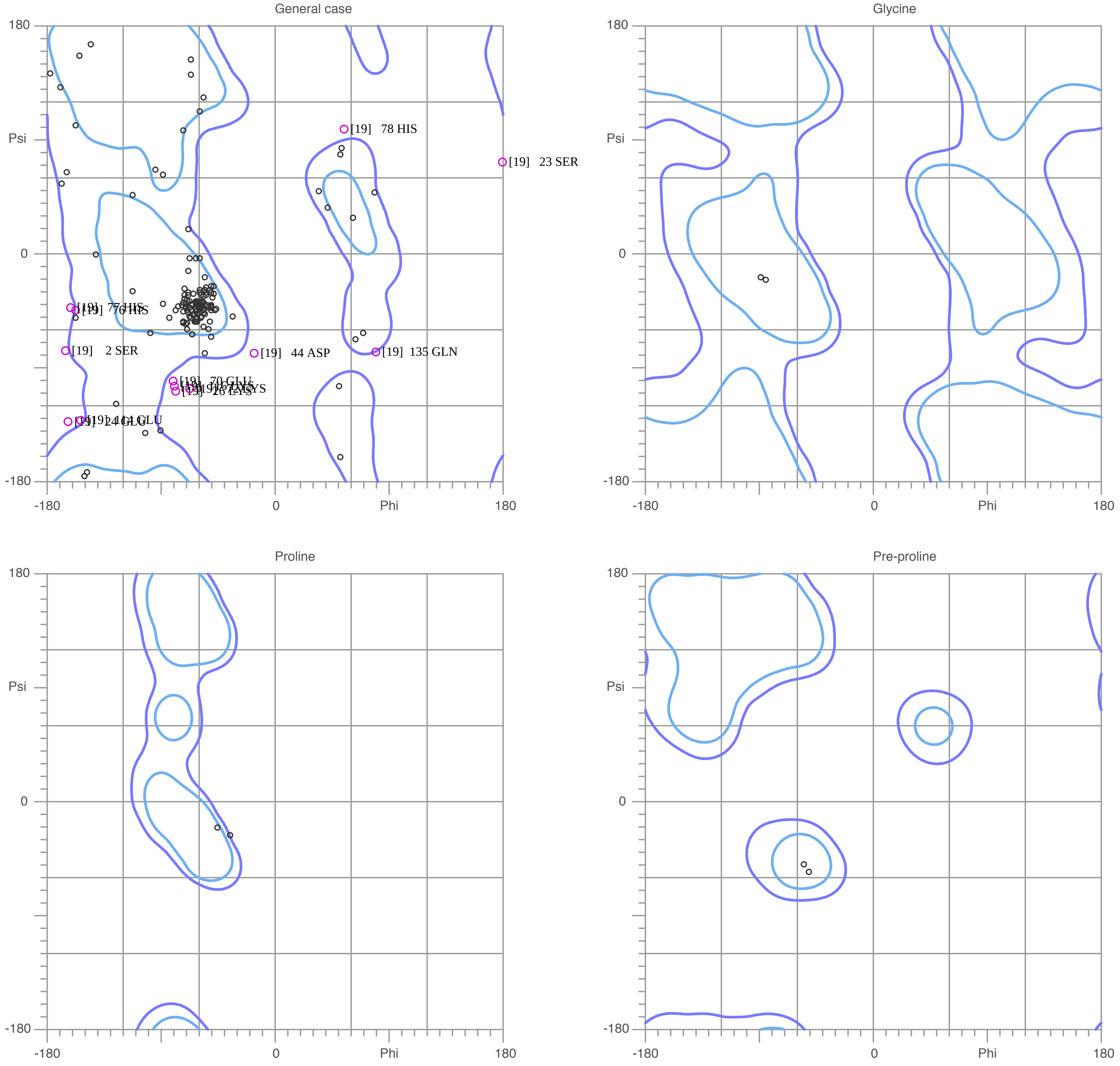
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 19



73.1% (114/156) of all residues were in favored (98%) regions.
91.7% (143/156) of all residues were in allowed (>99.8%) regions.

There were 13 outliers (phi, psi):

[19] 2 SER (-166.5, -76.7)
[19] 23 SER (179.4, 73.4)
[19] 24 GLU (-164.6, -132.3)
[19] 26 LYS (-79.7, -108.0)
[19] 44 ASP (-17.8, -78.9)
[19] 70 GLU (-81.1, -100.3)
[19] 72 LYS (-68.3, -106.1)
[19] 76 HIS (-158.9, -44.5)
[19] 77 HIS (-162.6, -42.8)
[19] 78 HIS (54.2, 99.8)
[19] 114 GLU (-154.4, -132.0)
[19] 116 LYS (-80.0, -104.7)
[19] 135 GLN (79.2, -78.0)

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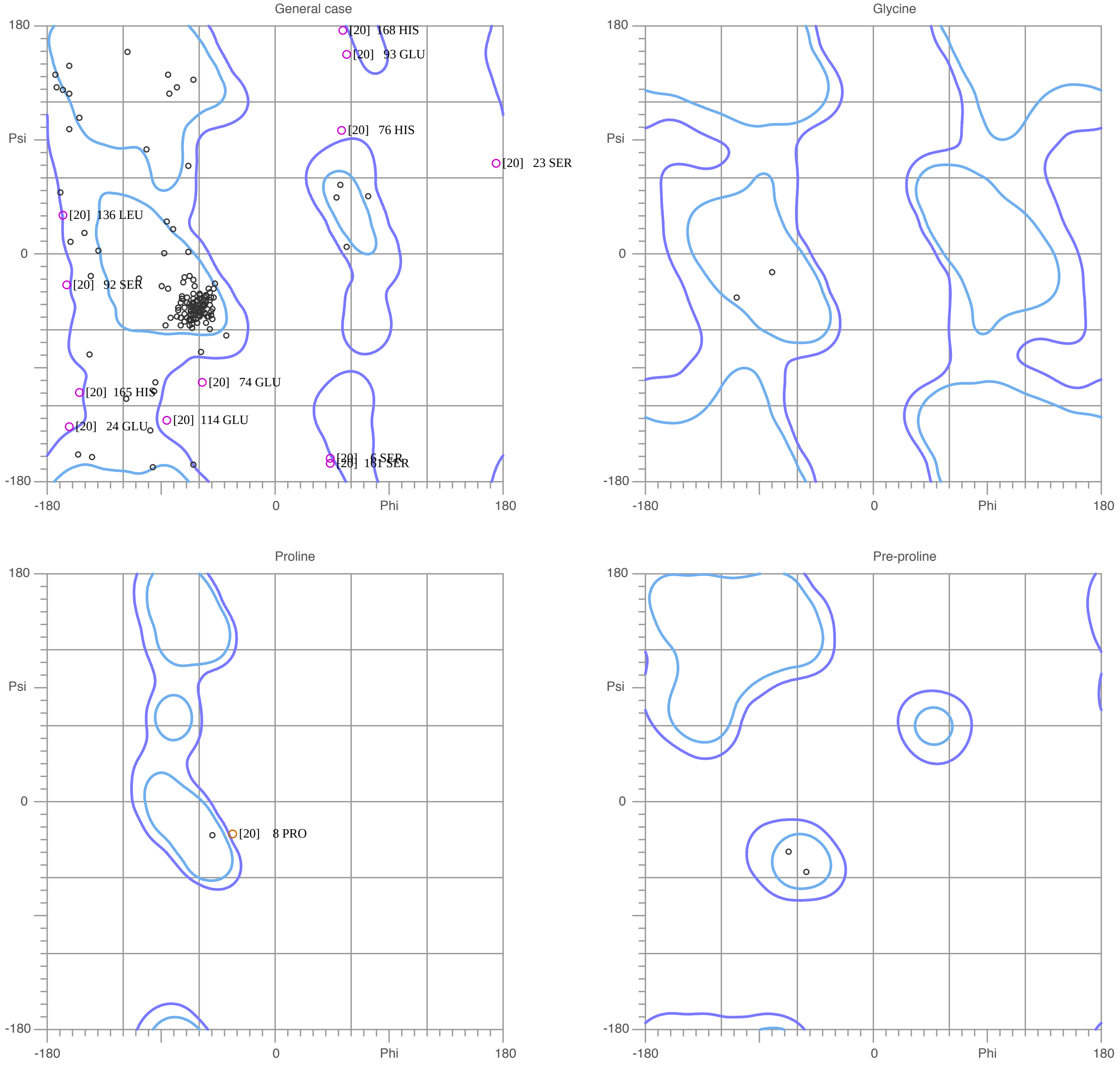
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR478_NMR_em_bcr3.pdb, model 20



75.6% (118/156) of all residues were in favored (98%) regions.
91.7% (143/156) of all residues were in allowed (>99.8%) regions.

There were 13 outliers (phi, psi):

[20] 6 SER (43.7, -161.4)
[20] 8 PRO (-34.9, -25.5)
[20] 23 SER (174.5, 72.1)
[20] 24 GLU (-163.8, -136.8)
[20] 74 GLU (-58.9, -101.0)
[20] 76 HIS (52.7, 98.6)
[20] 92 SER (-165.5, -24.8)
[20] 93 GLU (56.5, 158.0)
[20] 114 GLU (-87.0, -131.8)
[20] 136 LEU (-168.7, 31.3)
[20] 161 SER (43.1, -165.8)
[20] 165 HIS (-155.5, -109.3)
[20] 168 HIS (53.1, 177.9)

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