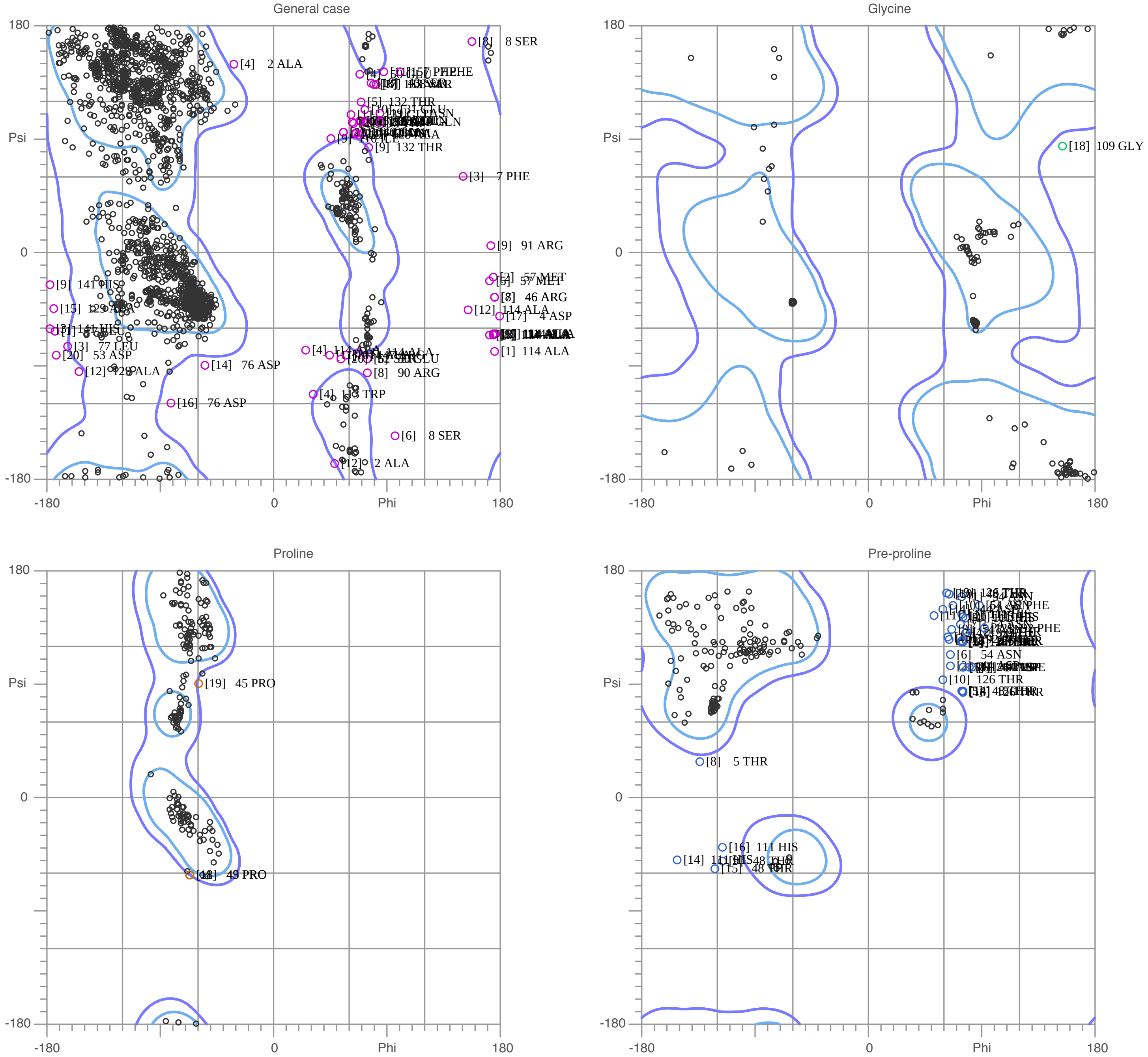
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, all models



89.5% (2505/2800) of all residues were in favored (98%) regions.
96.4% (2699/2800) of all residues were in allowed (>99.8%) regions.

There were 101 outliers (phi, psi):
[1] 54 ASN (74.7, 160.4)
[1] 77 LEU (-174.6, -62.9)
[1] 111 HIS (77.4, 143.5)
[1] 114 ALA (175.7, -78.6)
[2] 44 ASP (65.1, 105.0)
[2] 51 VAL (70.2, 95.2)
[2] 57 MET (175.0, -19.1)
[2] 111 HIS (75.0, 146.3)
[2] 113 TRP (63.4, 103.8)
[2] 114 ALA (176.7, -64.7)
[2] 134 GLN (55.1, 96.7)
[2] 136 GLU (70.0, 105.2)
[2] 140 HIS (64.9, 95.1)
[3] 7 PHE (150.1, 61.2)
[3] 77 LEU (-164.3, -74.7)
[3] 114 ALA (67.9, -79.5)
[3] 126 THR (74.9, 125.0)
[3] 141 HIS (-178.3, -60.8)
[4] 2 ALA (-32.9, 150.6)
[4] 50 GLU (68.1, 142.0)
[4] 92 PHE (77.3, 131.2)
[4] 113 TRP (31.8, -112.9)
[4] 114 ALA (25.7, -77.1)
[5] 48 THR (74.8, 85.0)
[5] 57 MET (171.1, -22.8)
[5] 114 ALA (175.0, -64.6)
[5] 126 THR (75.0, 104.9)
[5] 132 THR (69.6, 120.3)
[6] 5 THR (75.0, 124.8)
[6] 8 SER (97.0, -145.3)
[6] 44 ASP (82.7, 104.9)
[6] 50 GLU (74.6, -84.6)
[6] 53 ASP (71.2, 105.0)
[6] 54 ASN (65.2, 114.9)
[6] 92 PHE (88.4, 153.1)
[7] 46 ARG (175.0, -35.1)
[7] 54 ASN (73.7, 138.9)
[8] 5 THR (-134.1, 29.6)
[8] 8 SER (157.6, 168.4)
[8] 46 ARG (175.1, -35.0)
[8] 90 ARG (74.9, -95.0)
[8] 114 ALA (175.0, -65.2)
[8] 133 VAL (81.9, 135.0)
[9] 48 THR (-116.8, -50.6)
[9] 54 ASN (66.5, 134.9)
[9] 91 ARG (172.2, 6.0)
[9] 110 ILE (45.1, 91.0)
[9] 132 THR (75.0, 85.0)
[9] 141 HIS (-178.2, -25.4)
[10] 47 ARG (57.8, -81.2)
[10] 48 THR (65.0, 162.9)
[10] 50 GLU (68.2, 105.8)
[10] 54 ASN (67.1, 153.5)
[10] 92 PHE (64.8, 126.1)
[10] 126 THR (59.8, 95.0)
[10] 131 GLU (72.5, 114.9)
[11] 7 PHE (87.3, 145.0)
[11] 45 PRO (-67.6, -62.0)
[11] 92 PHE (80.7, 104.7)
[11] 111 HIS (75.2, 144.9)
[11] 114 ALA (44.8, -81.4)
[11] 126 THR (52.3, 145.2)
[11] 131 GLU (61.2, 110.6)
[12] 2 ALA (48.2, -167.2)
[12] 5 THR (78.1, 132.3)
[12] 92 PHE (92.5, 135.5)
[12] 114 ALA (154.8, -45.2)
[12] 129 ALA (-155.1, -94.7)
[13] 114 ALA (172.0, -65.5)
[13] 126 THR (74.9, 125.1)
[13] 130 GLN (55.1, 96.9)
[14] 2 ALA (65.0, 95.0)
[14] 5 THR (75.0, 85.2)
[14] 44 ASP (59.0, 151.0)
[14] 48 THR (74.9, 125.0)
[14] 76 ASP (-55.0, -89.3)
[14] 111 HIS (-152.5, -49.0)
[15] 5 THR (63.6, 128.4)
[15] 7 PHE (100.3, 145.0)
[15] 48 THR (-122.9, -56.1)
[15] 129 ALA (-175.0, -45.0)
[16] 76 ASP (-82.4, -119.3)
[16] 111 HIS (-116.8, -39.9)
[16] 126 THR (74.9, 125.2)
[17] 4 ASP (179.5, -50.7)
[17] 108 SER (79.8, 134.8)
[18] 43 SER (77.8, 135.0)
[18] 44 ASP (75.1, 105.0)
[18] 49 PRO (-67.0, -61.4)
[18] 109 GLY (155.0, 85.0)
[18] 126 THR (75.1, 85.0)
[18] 134 GLN (73.1, 105.1)
[19] 3 ASN (84.7, 111.0)
[19] 45 PRO (-60.1, 91.8)
[19] 114 ALA (174.7, -64.9)
[19] 126 THR (62.7, 163.2)
[19] 128 ALA (67.7, 94.9)
[20] 8 SER (62.6, 104.6)
[20] 52 SER (53.1, -84.9)
[20] 53 ASP (-173.5, -81.4)
[20] 130 GLN (84.5, 105.0)

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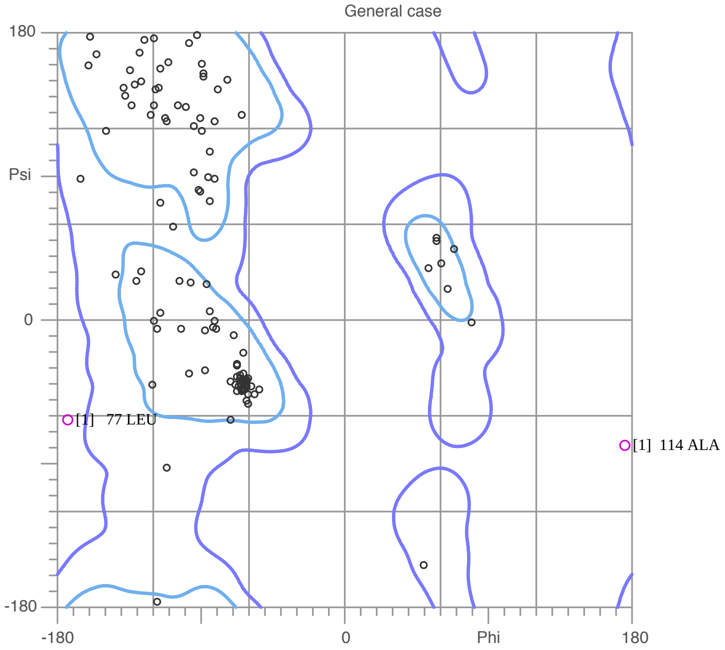
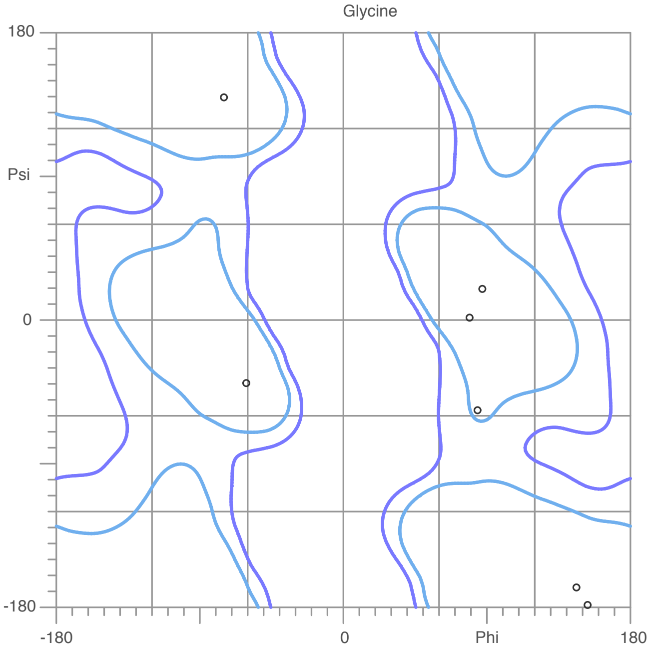
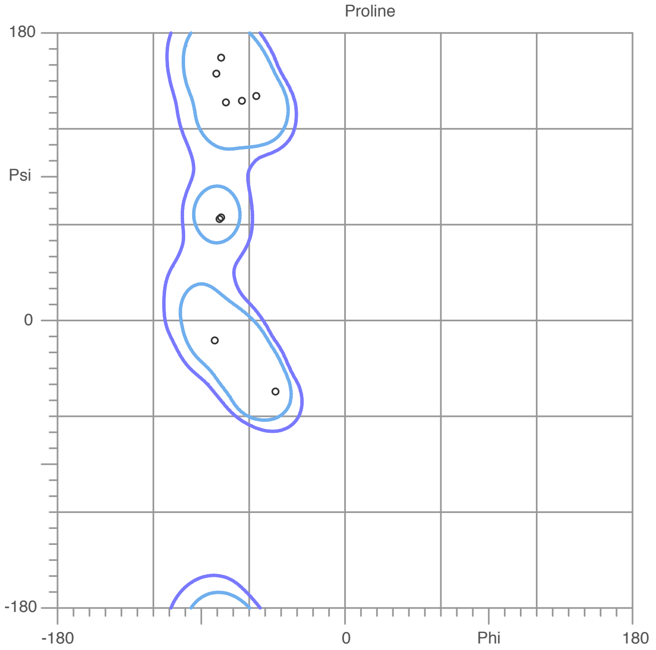
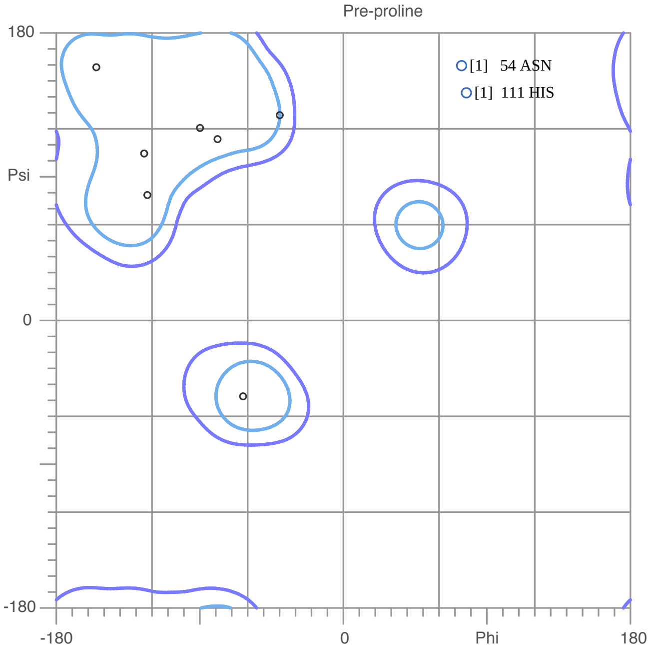
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 1









91.4% (128/140) of all residues were in favored (98%) regions.
97.1% (136/140) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[1] 54 ASN (74.7, 160.4)
[1] 77 LEU (-174.6, -62.9)
[1] 111 HIS (77.4, 143.5)
[1] 114 ALA (175.7, -78.6)

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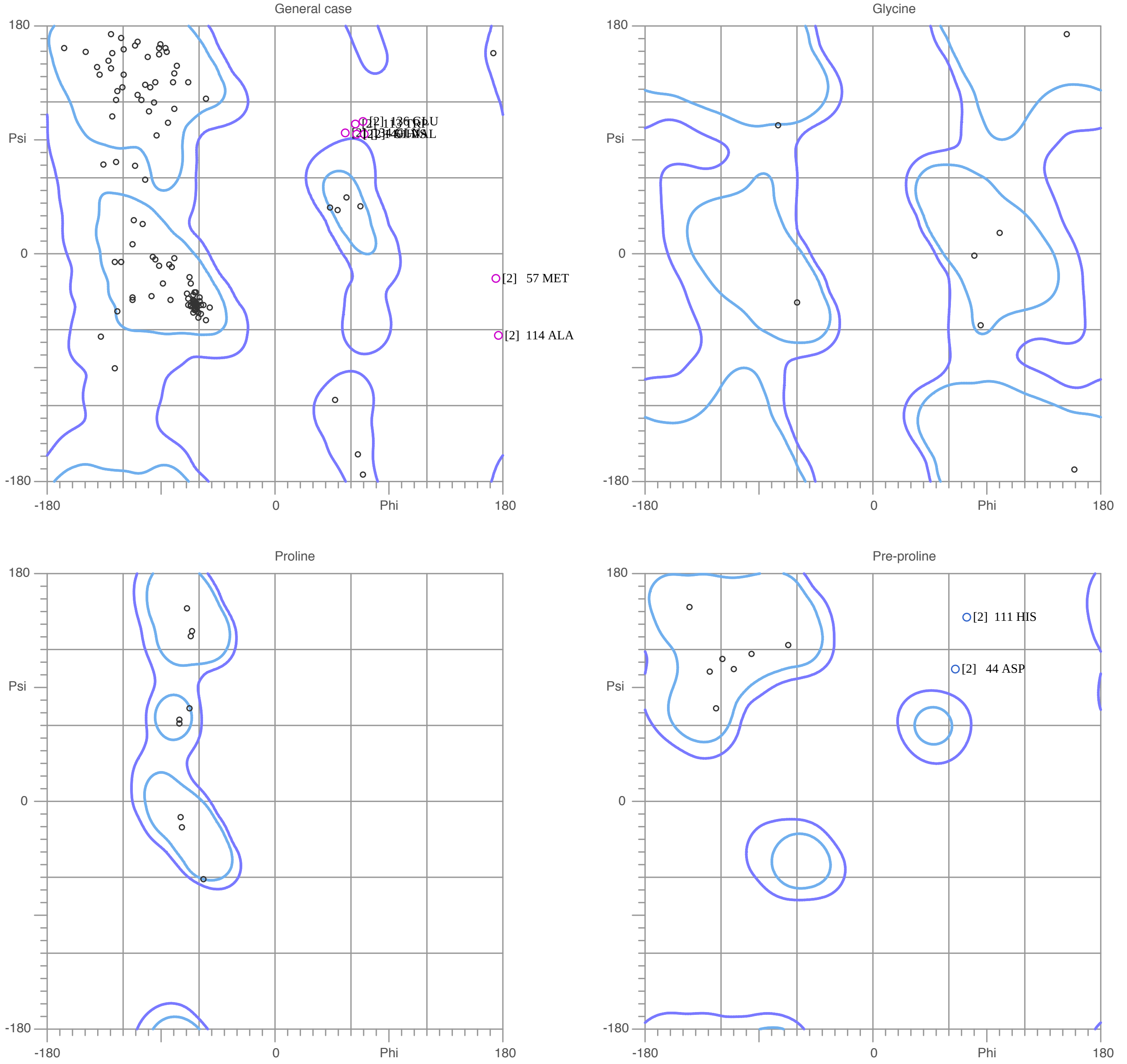
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 2



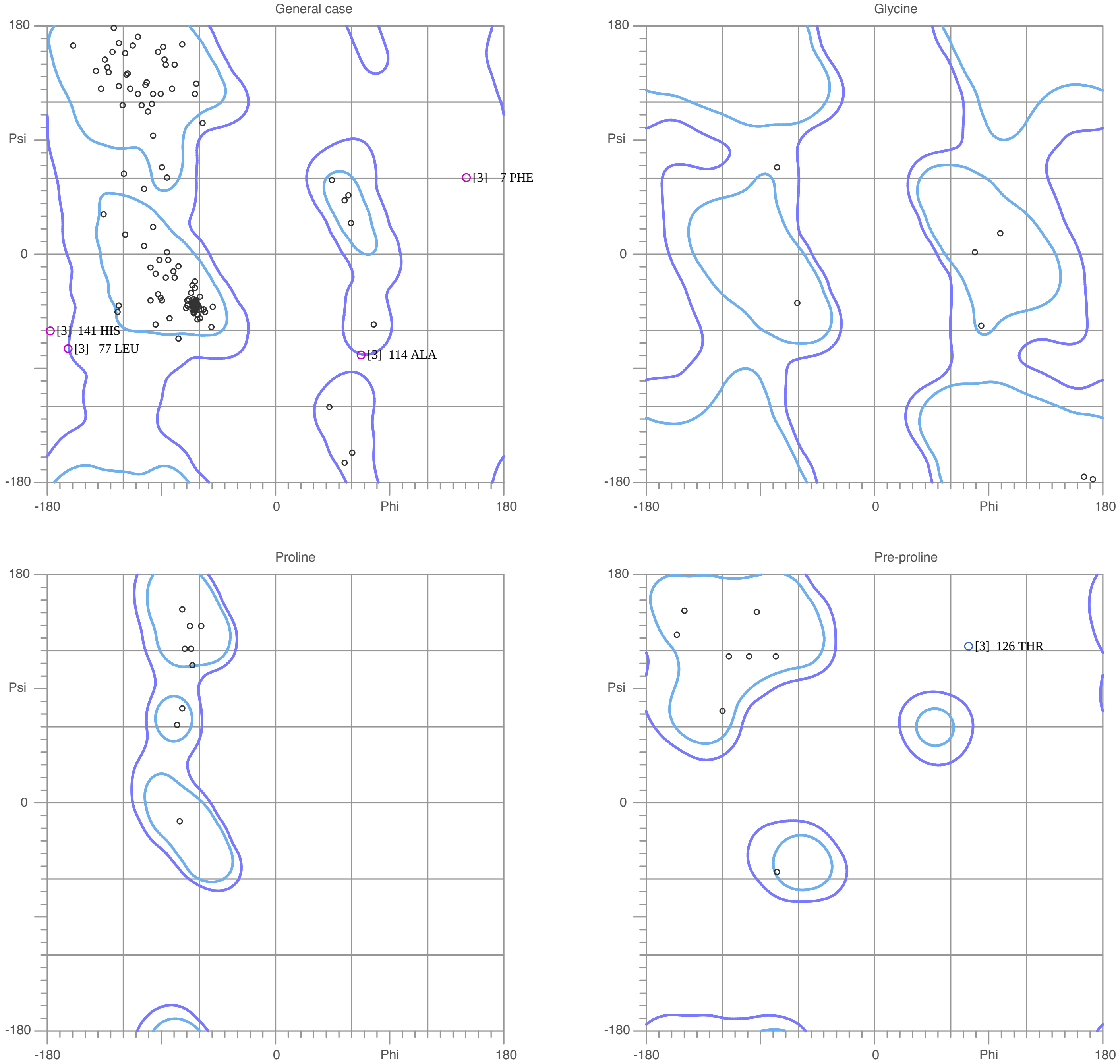
85.7% (120/140) of all residues were in favored (98%) regions.
93.6% (131/140) of all residues were in allowed (>99.8%) regions.

There were 9 outliers (phi, psi):

- [2] 44 ASP (65.1, 105.0)
- [2] 51 VAL (70.2, 95.2)
- [2] 57 MET (175.0, -19.1)
- [2] 111 HIS (75.0, 146.3)
- [2] 113 TRP (63.4, 103.8)
- [2] 114 ALA (176.7, -64.7)
- [2] 134 GLN (55.1, 96.7)
- [2] 136 GLU (70.0, 105.2)
- [2] 140 HIS (64.9, 95.1)

MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 3



89.3% (125/140) of all residues were in favored (98%) regions.
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[3] 7 PHE (150.1, 61.2)
[3] 77 LEU (-164.3, -74.7)
[3] 114 ALA (67.9, -79.5)
[3] 126 THR (74.9, 125.0)
[3] 141 HIS (-178.3, -60.8)

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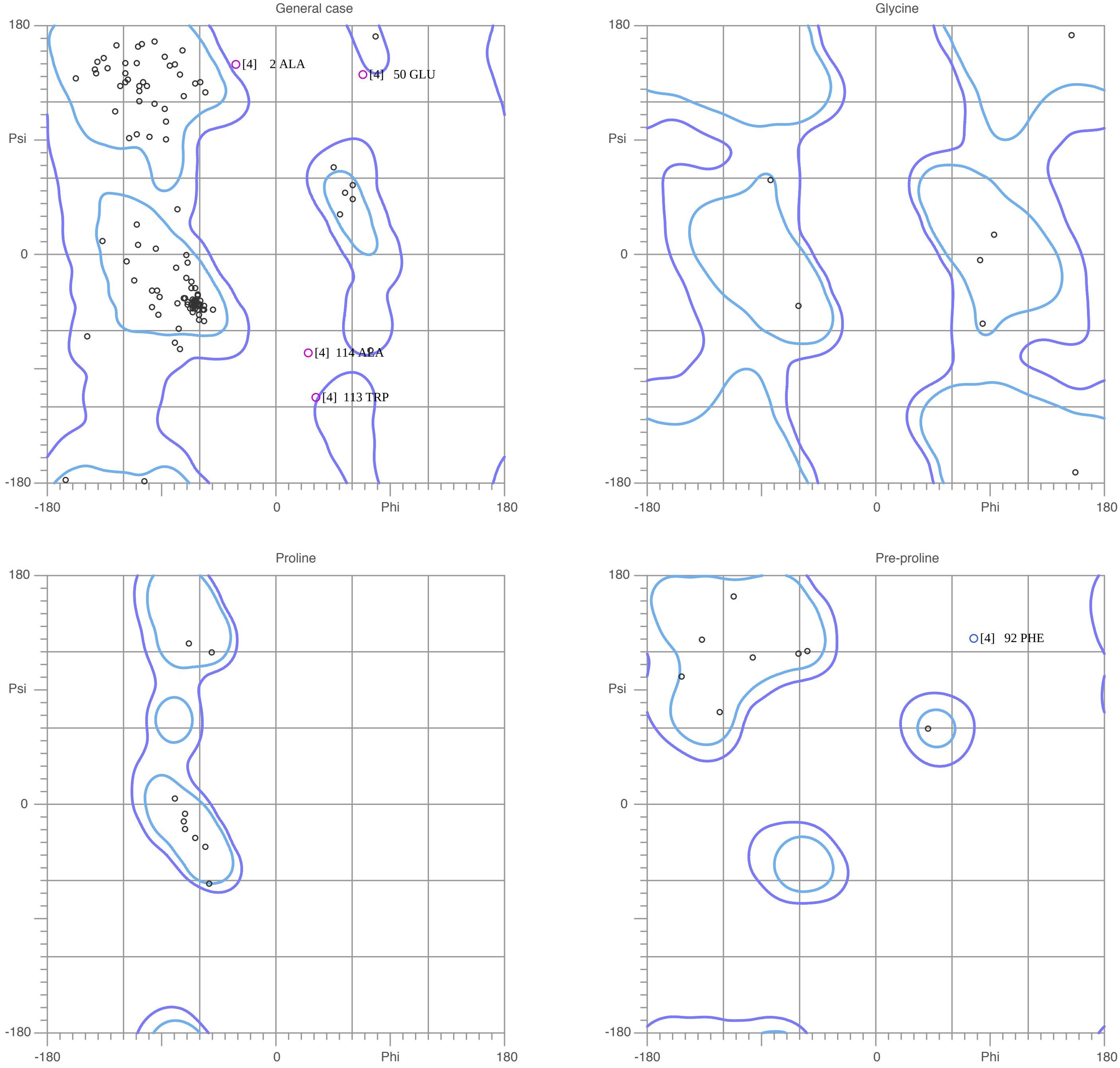
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 4



91.4% (128/140) of all residues were in favored (98%) regions.
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[4] 2 ALA (-32.9, 150.6)
[4] 50 GLU (68.1, 142.0)
[4] 92 PHE (77.3, 131.2)
[4] 113 TRP (31.8, -112.9)
[4] 114 ALA (25.7, -77.1)

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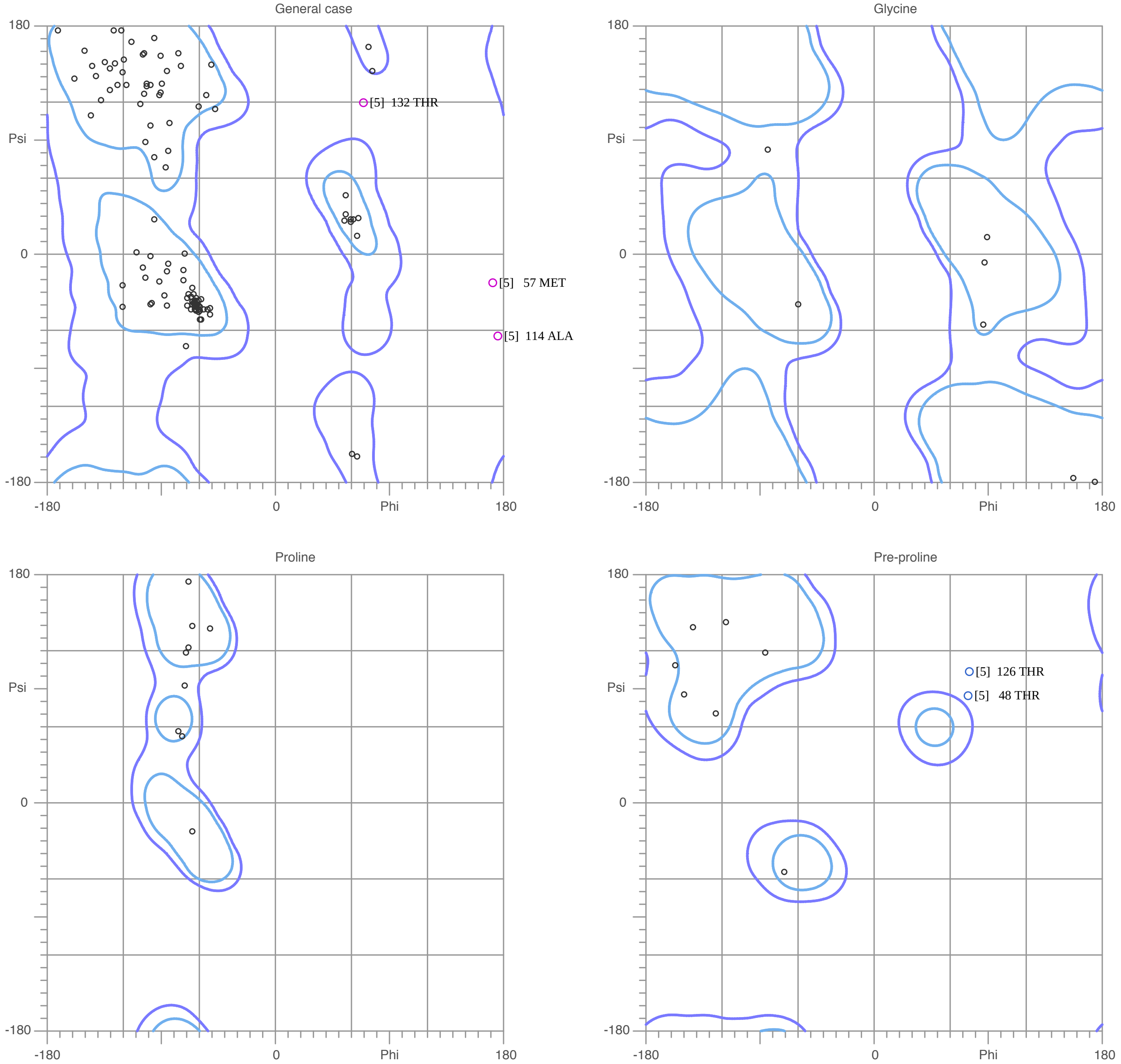
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 5



90.0% (126/140) of all residues were in favored (98%) regions.
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[5] 48 THR (74.8, 85.0)
[5] 57 MET (171.1, -22.8)
[5] 114 ALA (175.0, -64.6)
[5] 126 THR (75.0, 104.9)
[5] 132 THR (69.6, 120.3)

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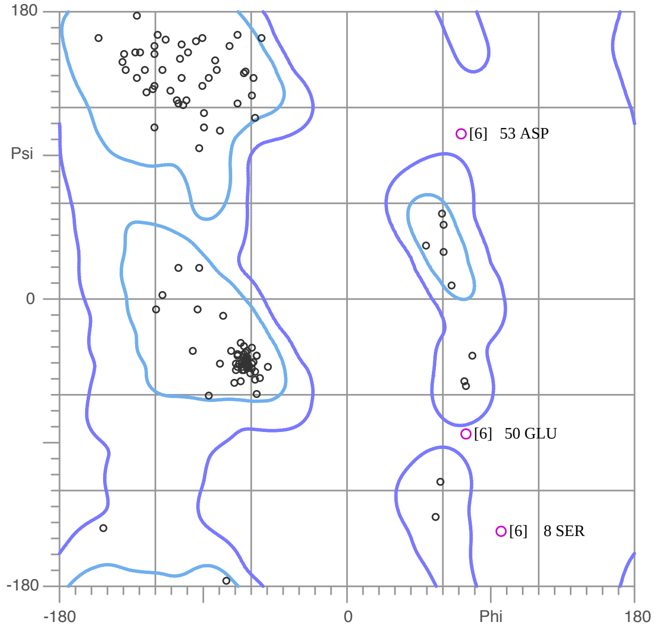
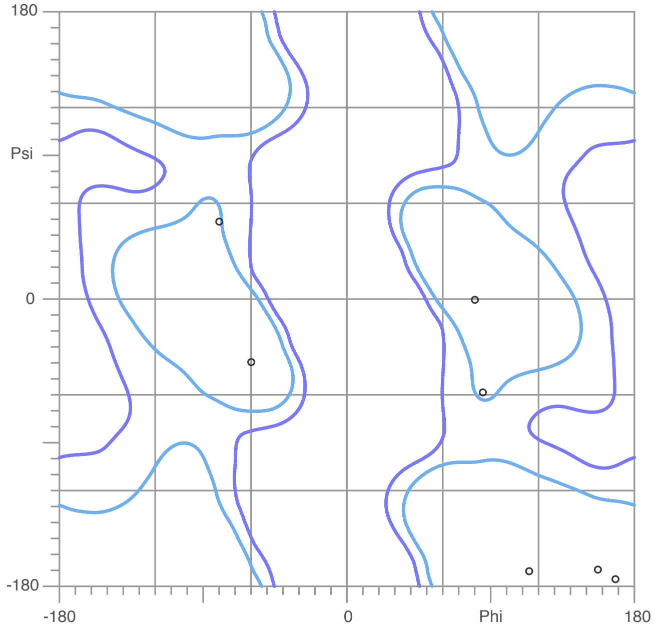
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 6

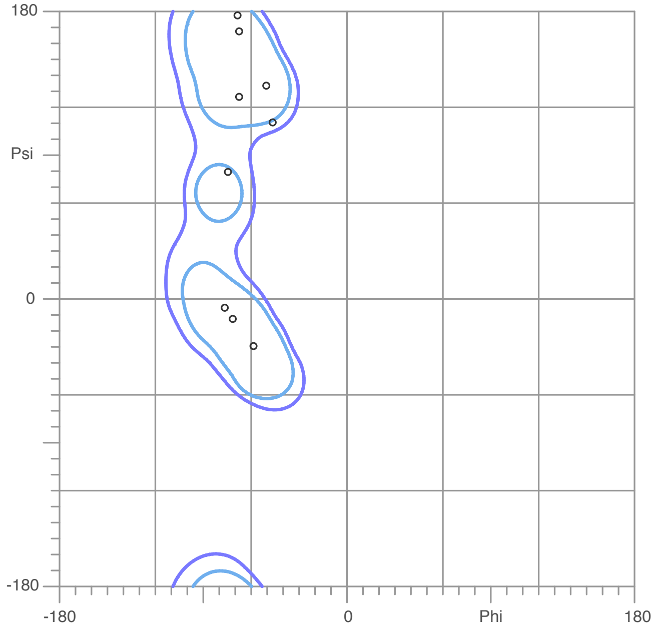
General case



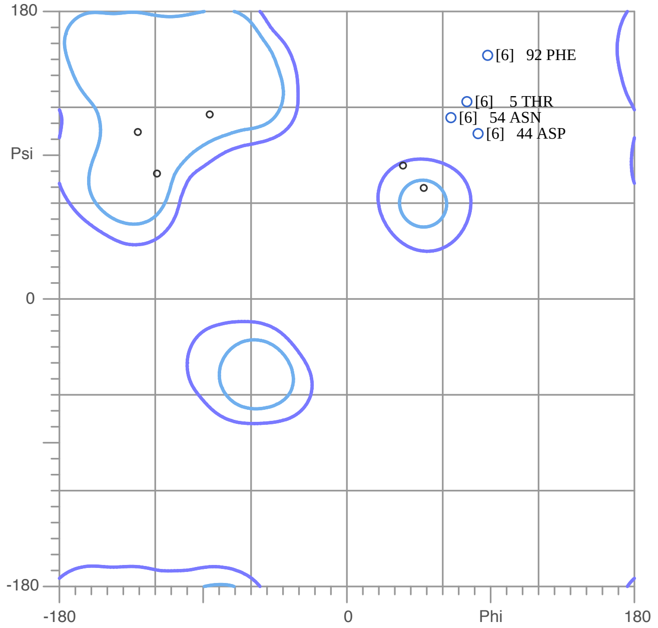
Glycine



Proline



Pre-proline



88.6% (124/140) of all residues were in favored (98%) regions.
95.0% (133/140) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[6] 5 THR (75.0, 124.8)
[6] 8 SER (97.0, -145.3)
[6] 44 ASP (82.7, 104.9)
[6] 50 GLU (74.6, -84.6)
[6] 53 ASP (71.2, 105.0)
[6] 54 ASN (65.2, 114.9)
[6] 92 PHE (88.4, 153.1)

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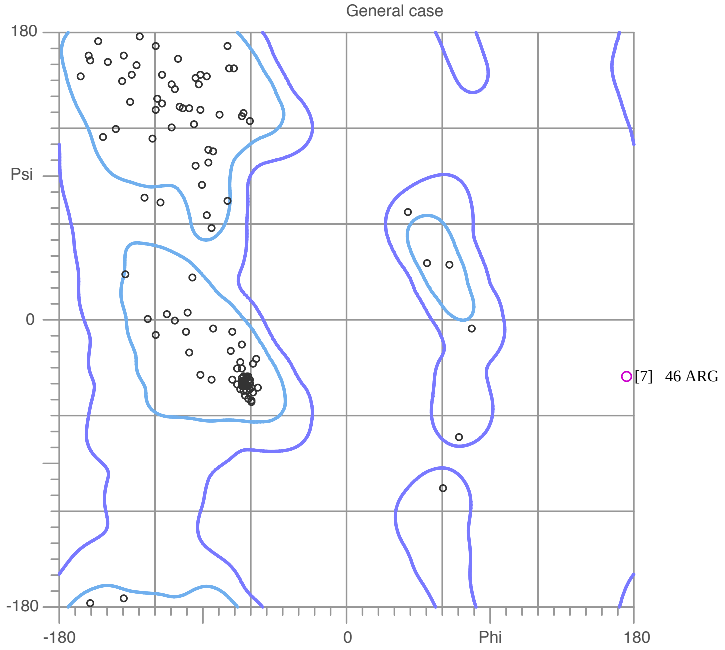
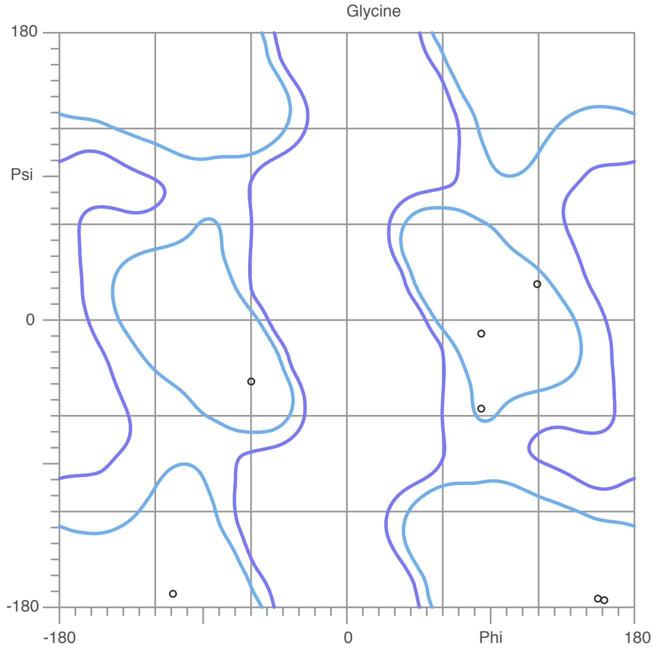
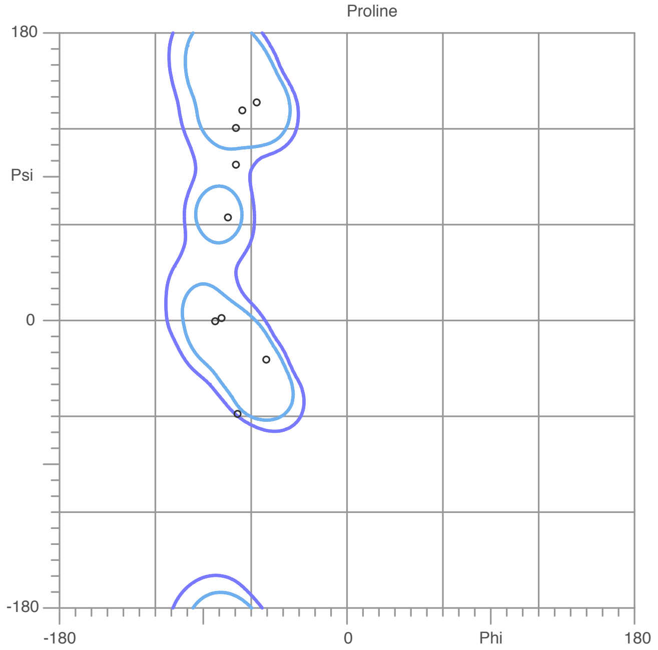
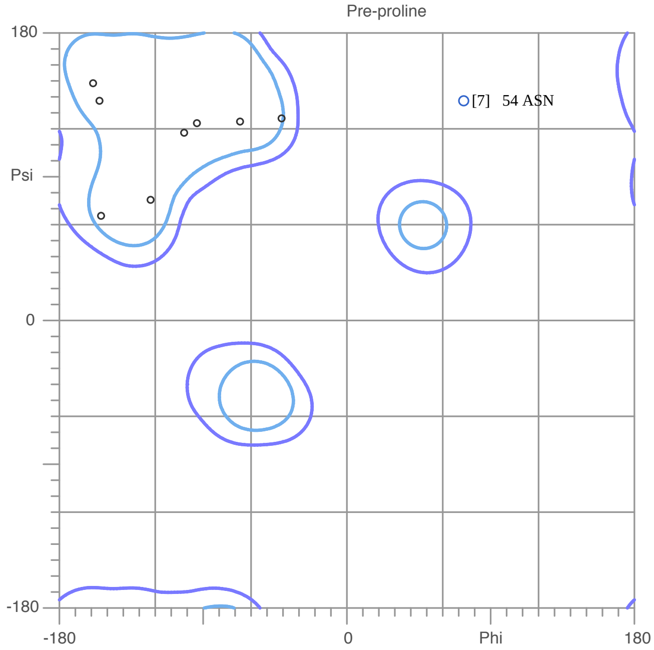
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 7









92.1% (129/140) of all residues were in favored (98%) regions.
98.6% (138/140) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[7] 46 ARG (175.0, -35.1)
[7] 54 ASN (73.7, 138.9)

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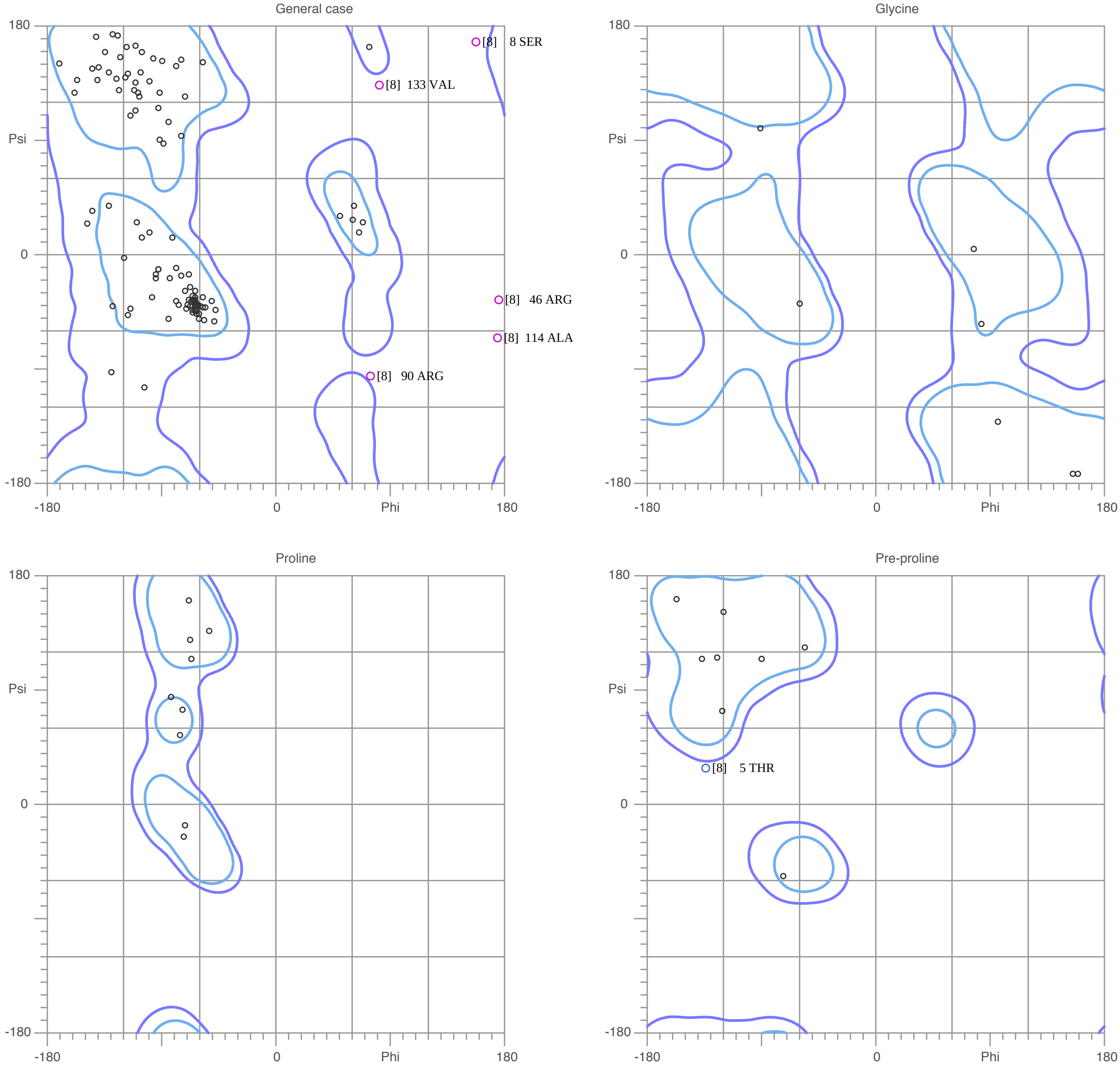
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 8

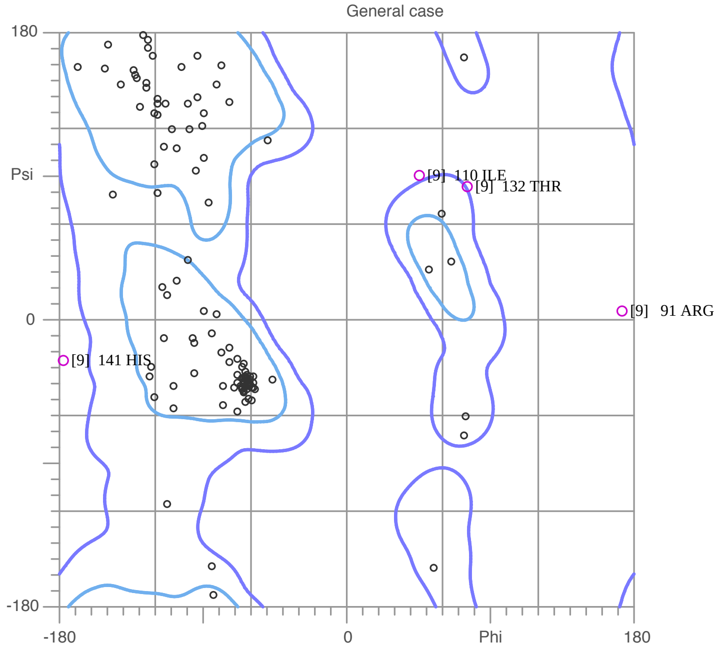


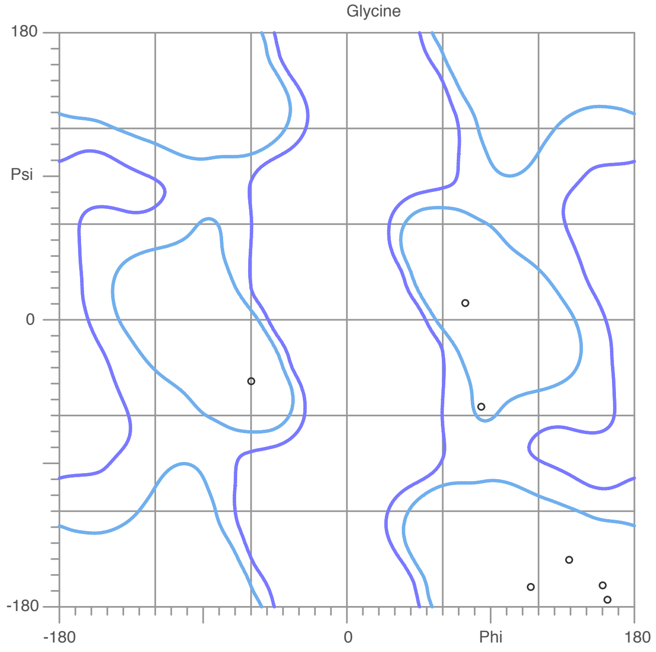
90.7% (127/140) of all residues were in favored (98%) regions.
95.7% (134/140) of all residues were in allowed (>99.8%) regions.

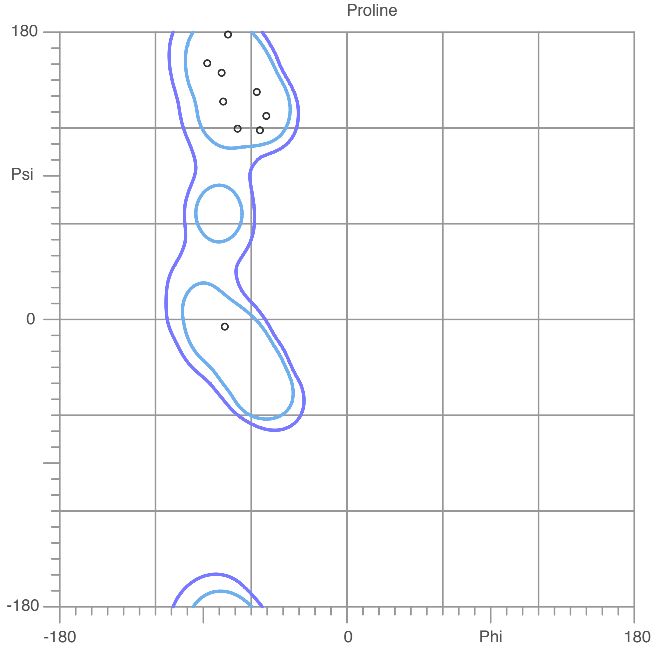
There were 6 outliers (phi, psi):
[8] 5 THR (-134.1, 29.6)
[8] 8 SER (157.6, 168.4)
[8] 46 ARG (175.1, -35.0)
[8] 90 ARG (74.9, -95.0)
[8] 114 ALA (175.0, -65.2)
[8] 133 VAL (81.9, 135.0)

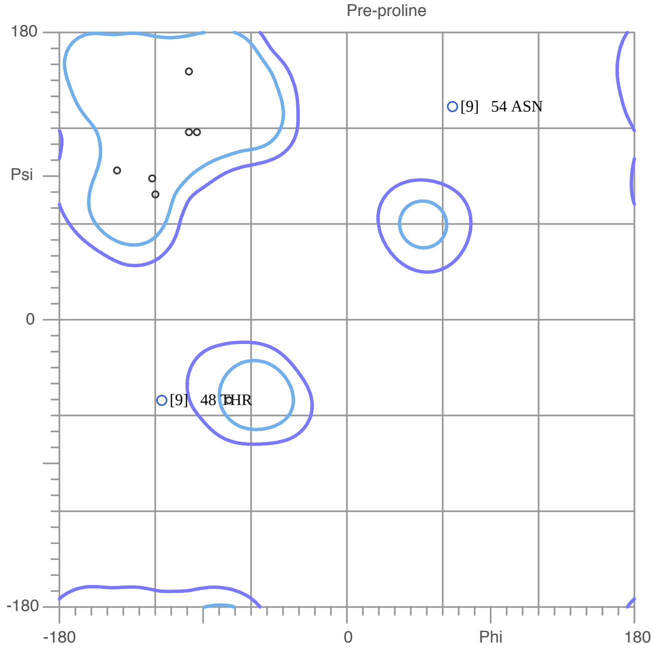
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 9









87.9% (123/140) of all residues were in favored (98%) regions.
95.7% (134/140) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[9] 48 THR (-116.8, -50.6)
[9] 54 ASN (66.5, 134.9)
[9] 91 ARG (172.2, 6.0)
[9] 110 ILE (45.1, 91.0)
[9] 132 THR (75.0, 85.0)
[9] 141 HIS (-178.2, -25.4)

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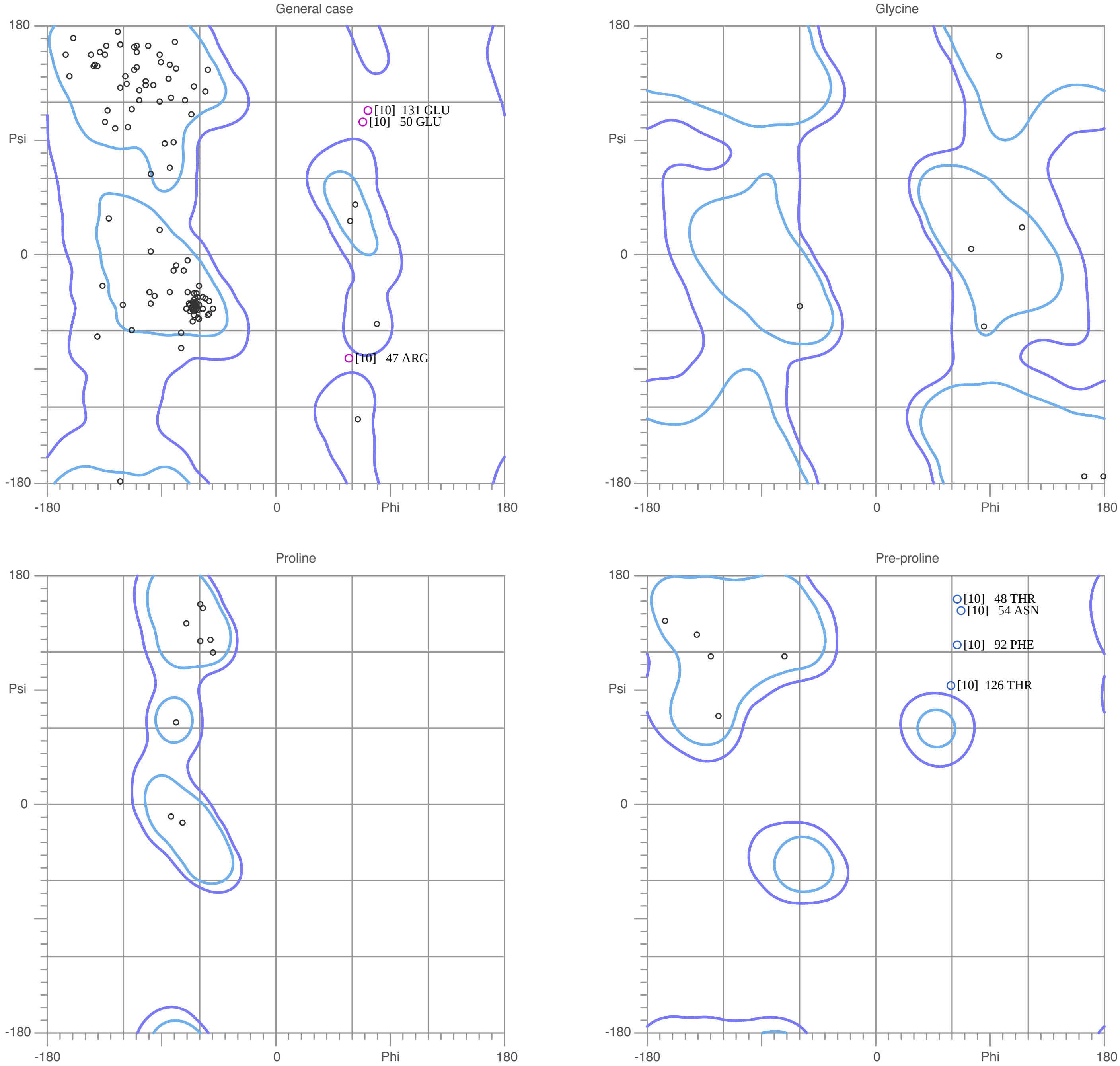
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 10

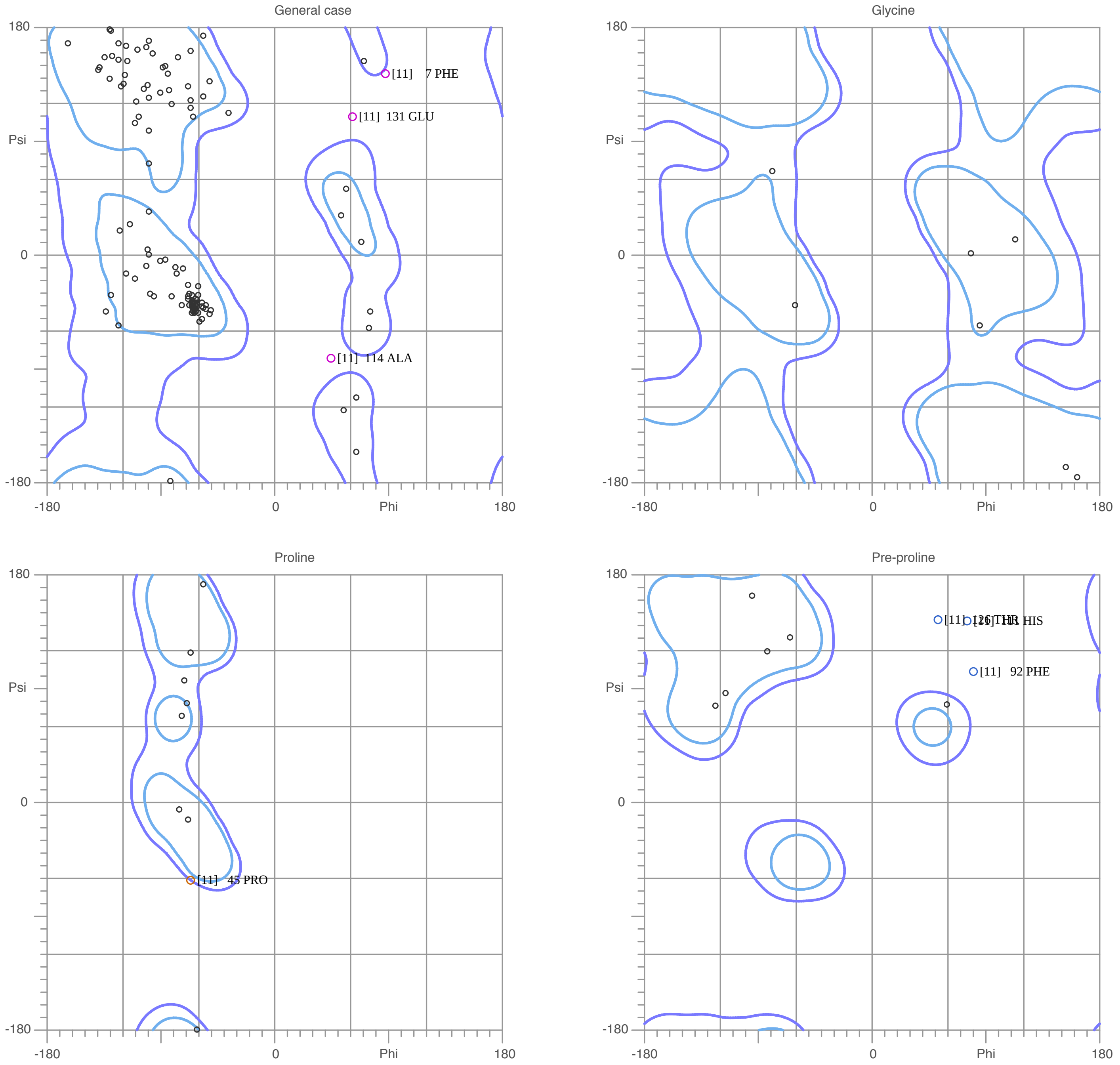


90.7% (127/140) of all residues were in favored (98%) regions.
95.0% (133/140) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[10] 47 ARG (57.8, -81.2)
[10] 48 THR (65.0, 162.9)
[10] 50 GLU (68.2, 105.8)
[10] 54 ASN (67.1, 153.5)
[10] 92 PHE (64.8, 126.1)
[10] 126 THR (59.8, 95.0)
[10] 131 GLU (72.5, 114.9)

MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 11



85.0% (119/140) of all residues were in favored (98%) regions.
95.0% (133/140) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):

[11]	7 PHE (87.3, 145.0)
[11]	45 PRO (-67.6, -62.0)
[11]	92 PHE (80.7, 104.7)
[11]	111 HIS (75.2, 144.9)
[11]	114 ALA (44.8, -81.4)
[11]	126 THR (52.3, 145.2)
[11]	131 GLU (61.2, 110.6)

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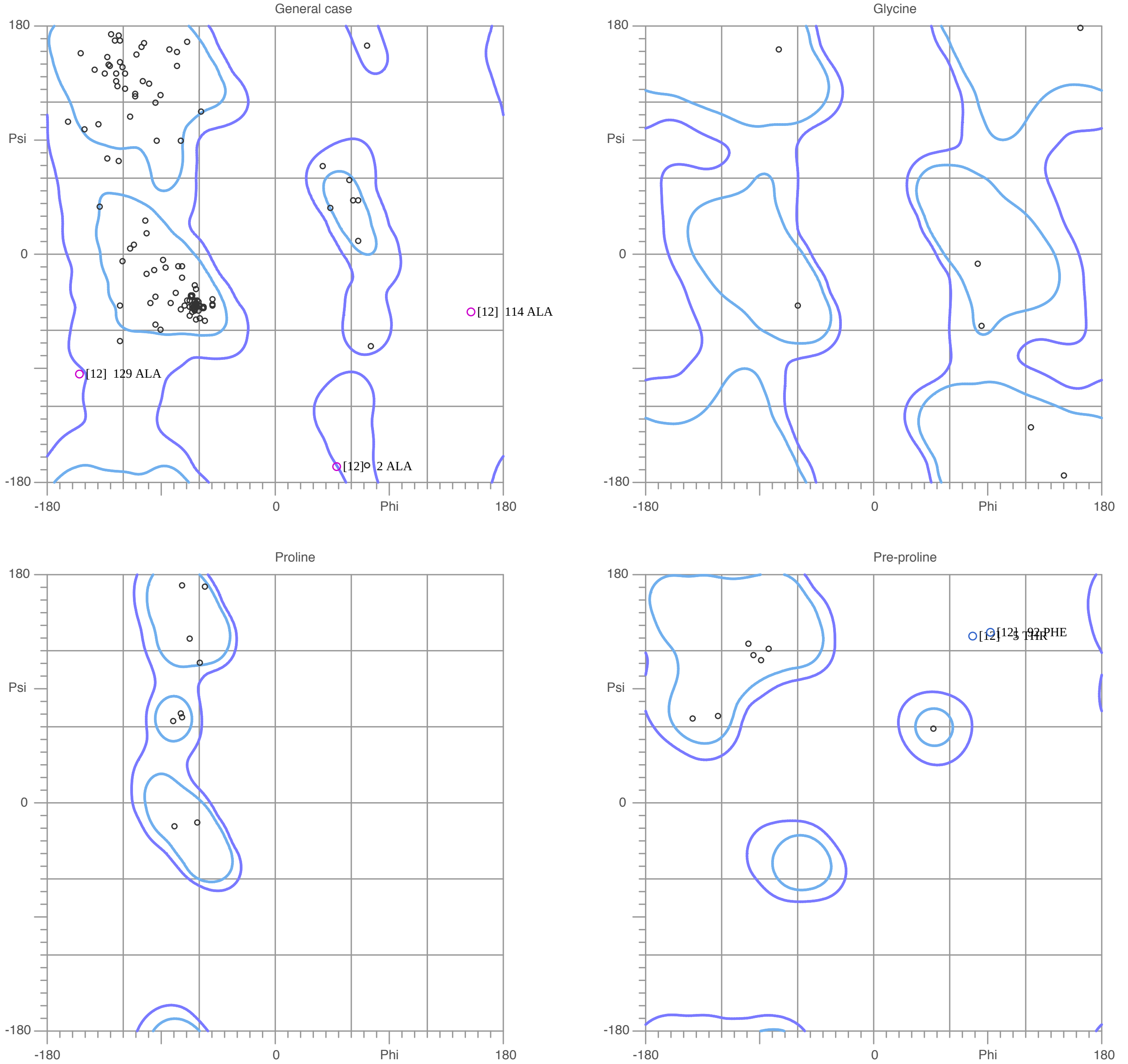
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 12



90.0% (126/140) of all residues were in favored (98%) regions.
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[12] 2 ALA (48.2, -167.2)
[12] 5 THR (78.1, 132.3)
[12] 92 PHE (92.5, 135.5)
[12] 114 ALA (154.8, -45.2)
[12] 129 ALA (-155.1, -94.7)

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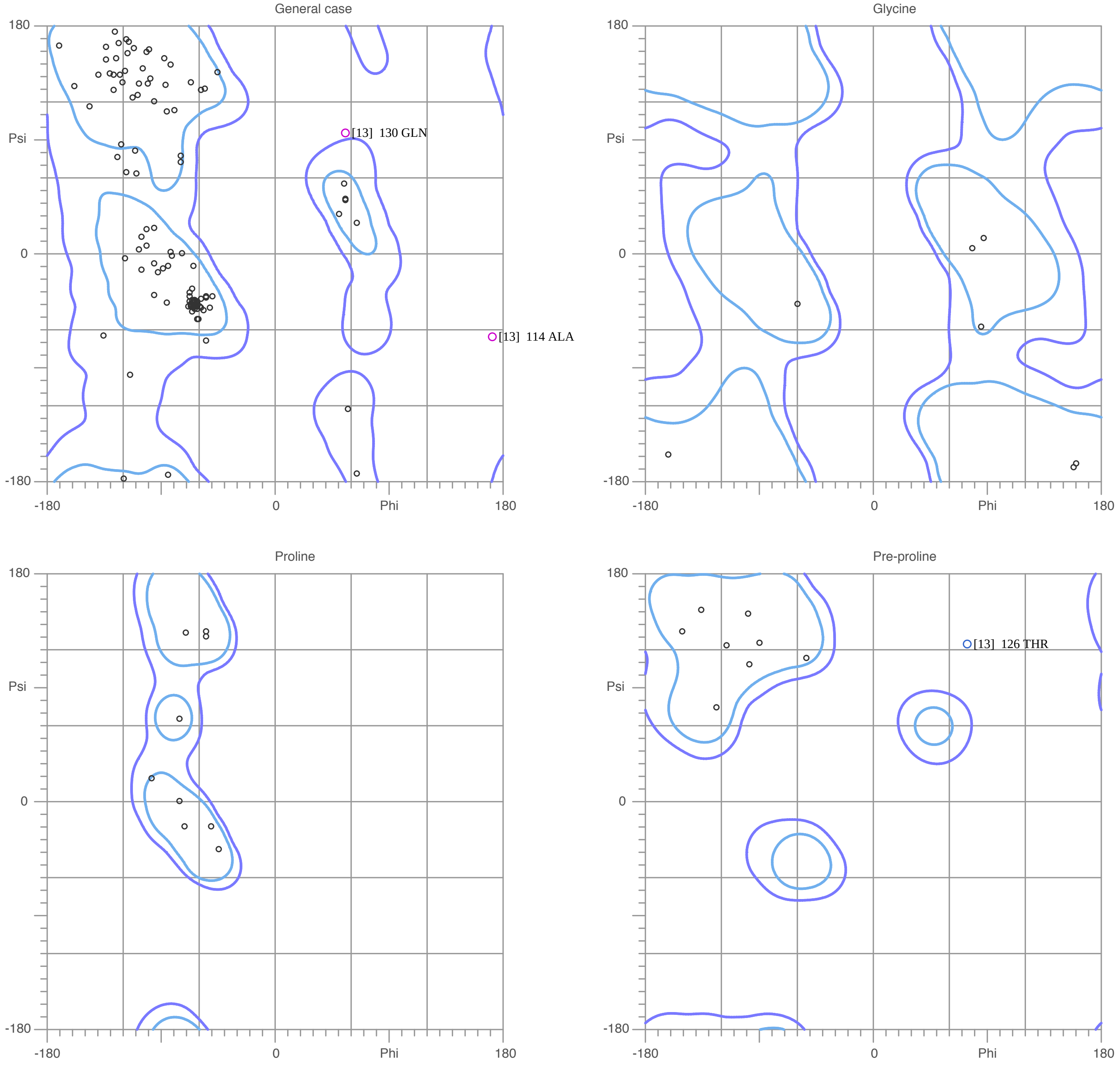
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 13



90.7% (127/140) of all residues were in favored (98%) regions.
97.9% (137/140) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[13] 114 ALA (172.0, -65.5)
[13] 126 THR (74.9, 125.1)
[13] 130 GLN (55.1, 96.9)

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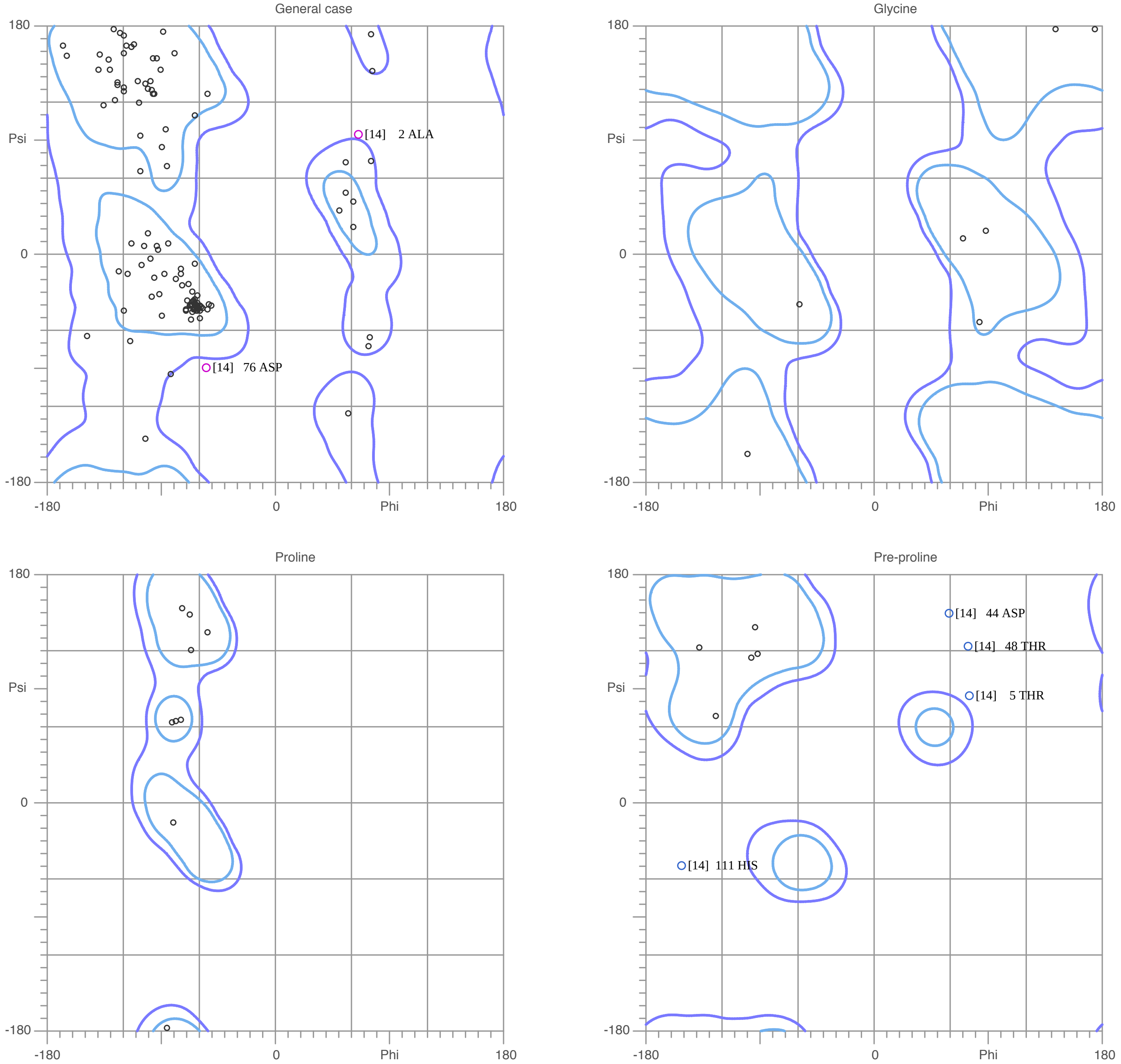
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 14



87.1% (122/140) of all residues were in favored (98%) regions.
95.7% (134/140) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[14] 2 ALA (65.0, 95.0)
[14] 5 THR (75.0, 85.2)
[14] 44 ASP (59.0, 151.0)
[14] 48 THR (74.9, 125.0)
[14] 76 ASP (-55.0, -89.3)
[14] 111 HIS (-152.5, -49.0)

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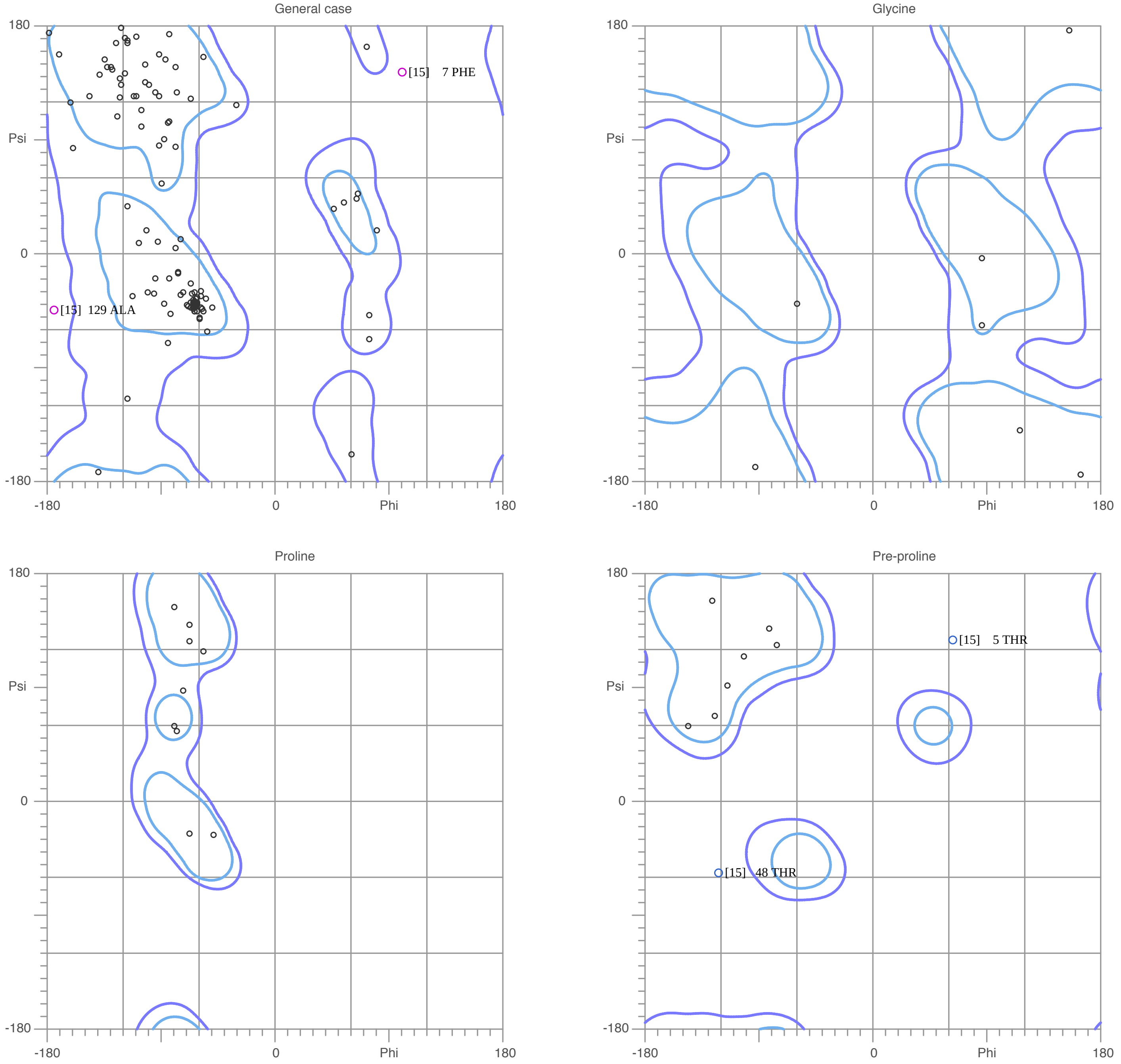
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 15



88.6% (124/140) of all residues were in favored (98%) regions.
97.1% (136/140) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):
[15] 5 THR (63.6, 128.4)
[15] 7 PHE (100.3, 145.0)
[15] 48 THR (-122.9, -56.1)
[15] 129 ALA (-175.0, -45.0)

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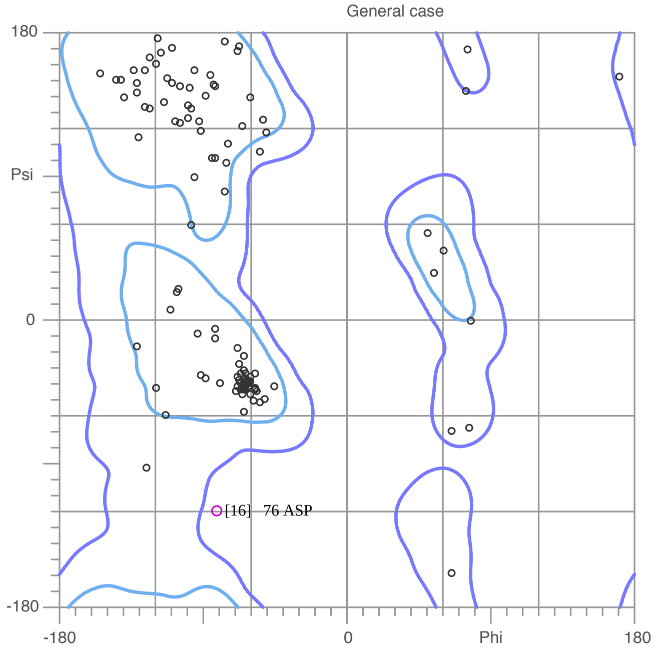
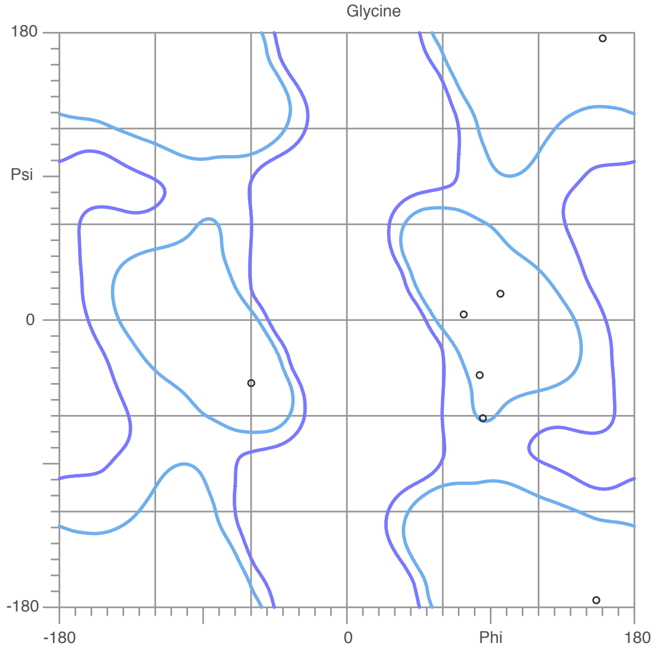
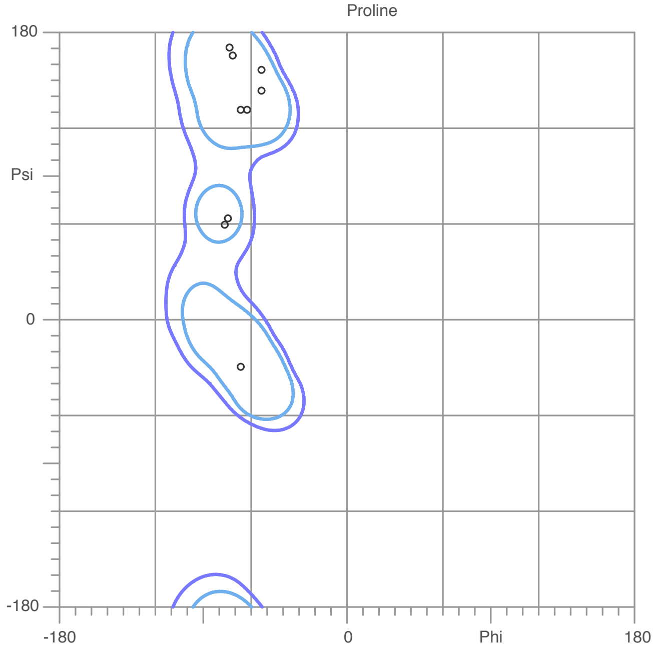
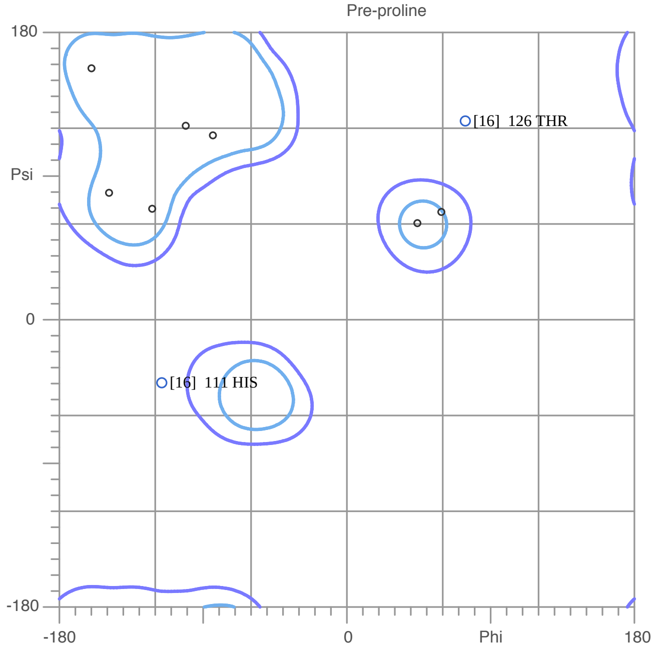
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 16


General case


Glycine


Proline


Pre-proline

90.7% (127/140) of all residues were in favored (98%) regions.
97.9% (137/140) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[16] 76 ASP (-82.4, -119.3)
[16] 111 HIS (-116.8, -39.9)
[16] 126 THR (74.9, 125.2)

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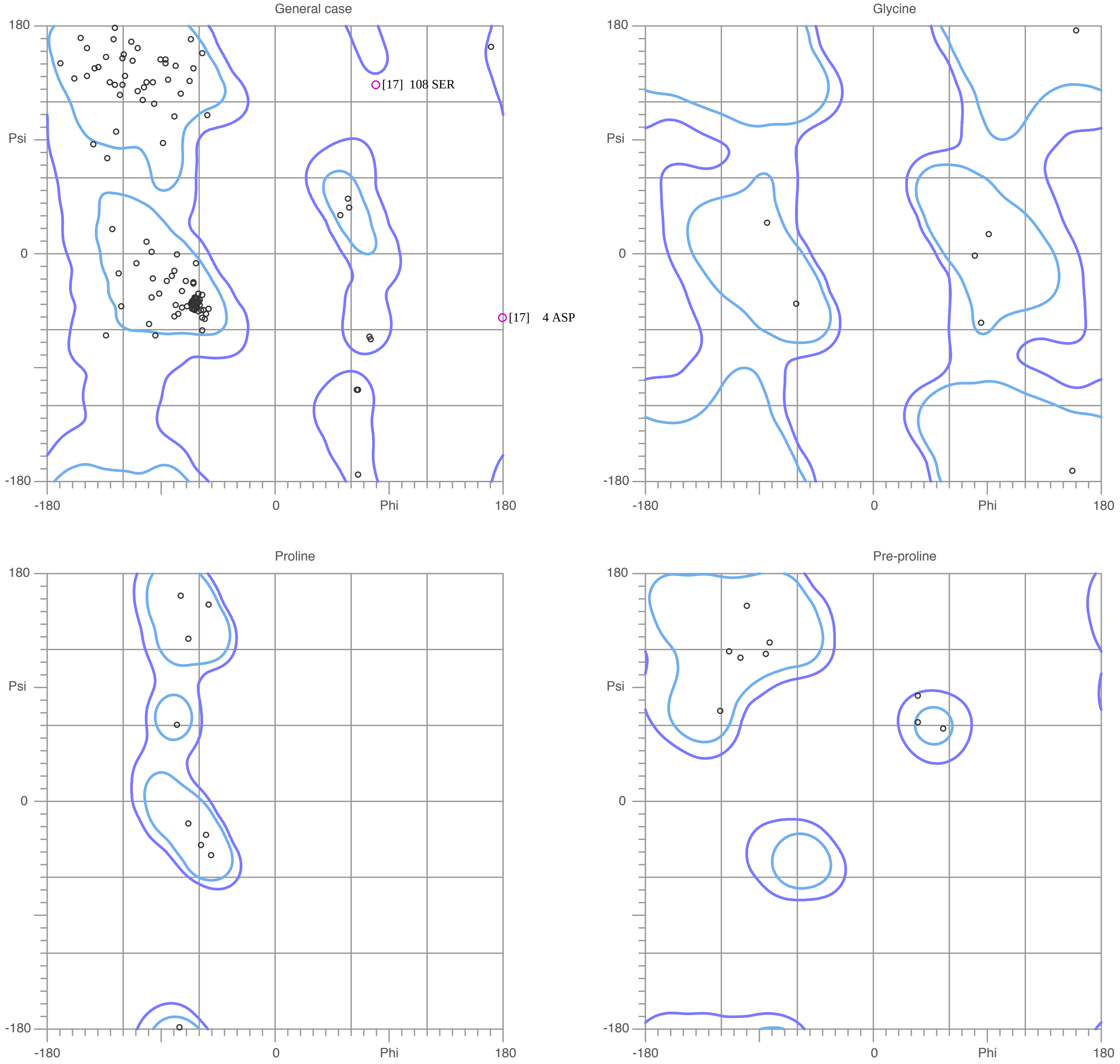
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 17



90.0% (126/140) of all residues were in favored (98%) regions.
98.6% (138/140) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[17] 4 ASP (179.5, -50.7)
[17] 108 SER (79.8, 134.8)

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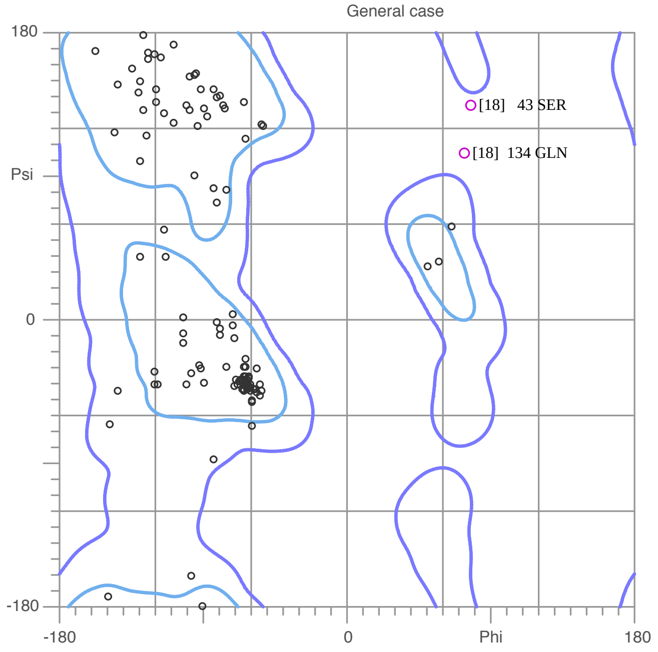
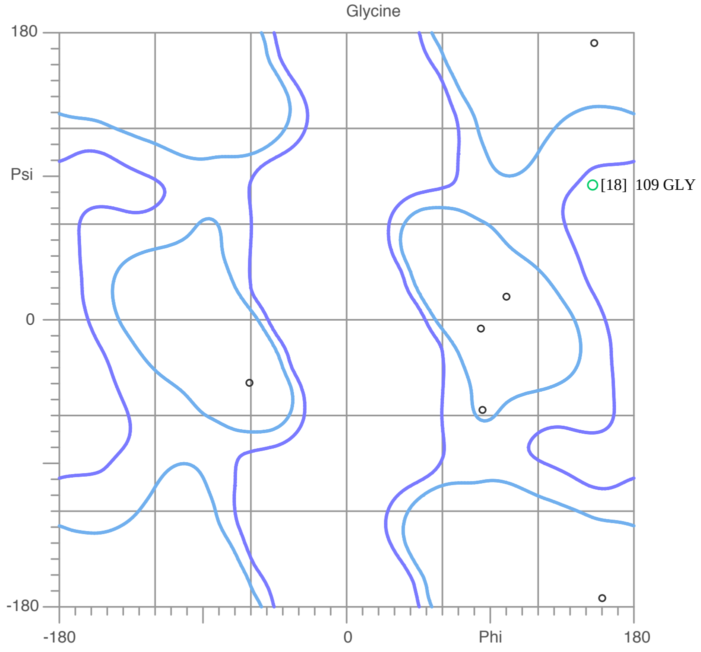
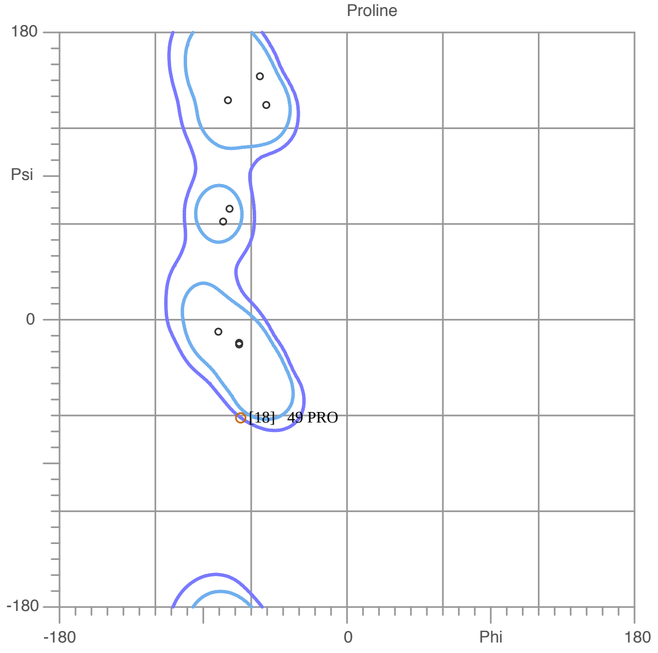
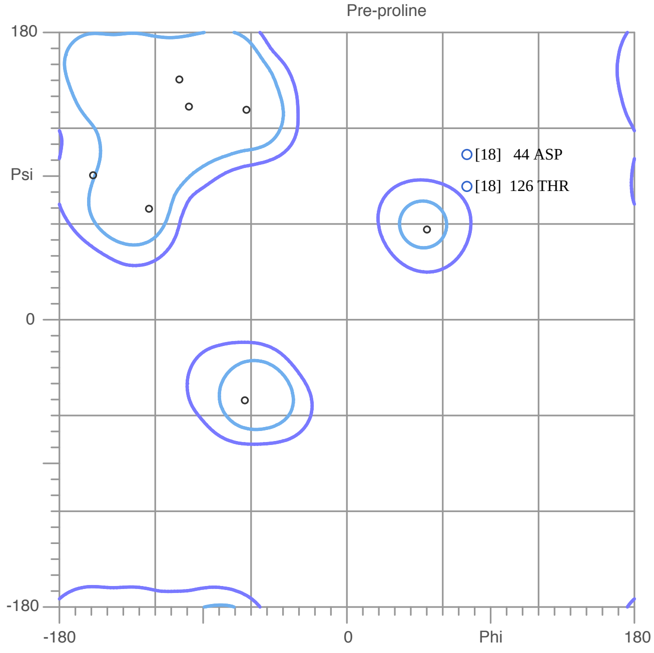
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 18







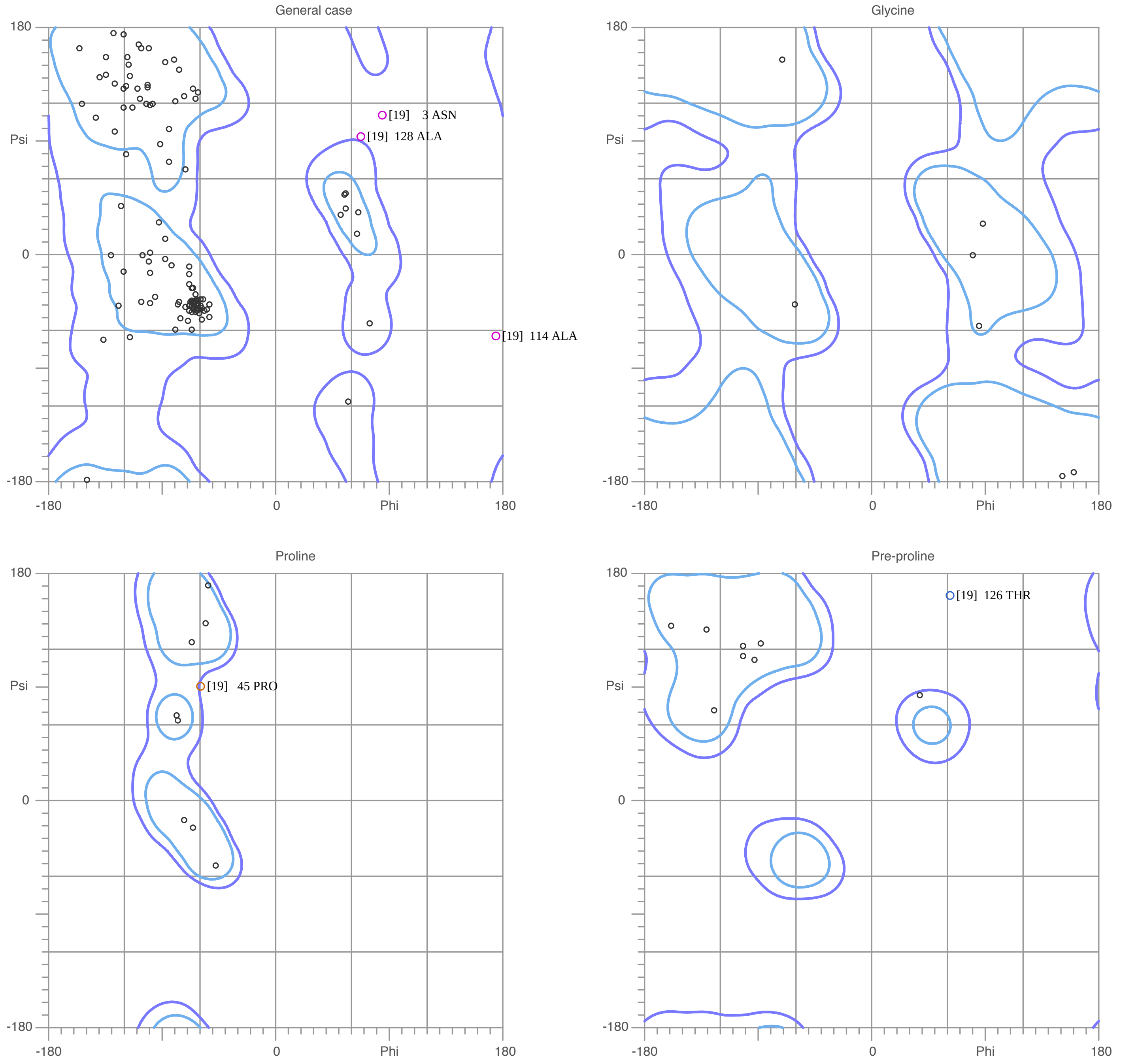


90.0% (126/140) of all residues were in favored (98%) regions.
95.7% (134/140) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[18] 43 SER (77.8, 135.0)
[18] 44 ASP (75.1, 105.0)
[18] 49 PRO (-67.0, -61.4)
[18] 109 GLY (155.0, 85.0)
[18] 126 THR (75.1, 85.0)
[18] 134 GLN (73.1, 105.1)

MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 19



91.4% (128/140) of all residues were in favored (98%) regions.
96.4% (135/140) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[19] 3 ASN (84.7, 111.0)
[19] 45 PRO (-60.1, 91.8)
[19] 114 ALA (174.7, -64.9)
[19] 126 THR (62.7, 163.2)
[19] 128 ALA (67.7, 94.9)

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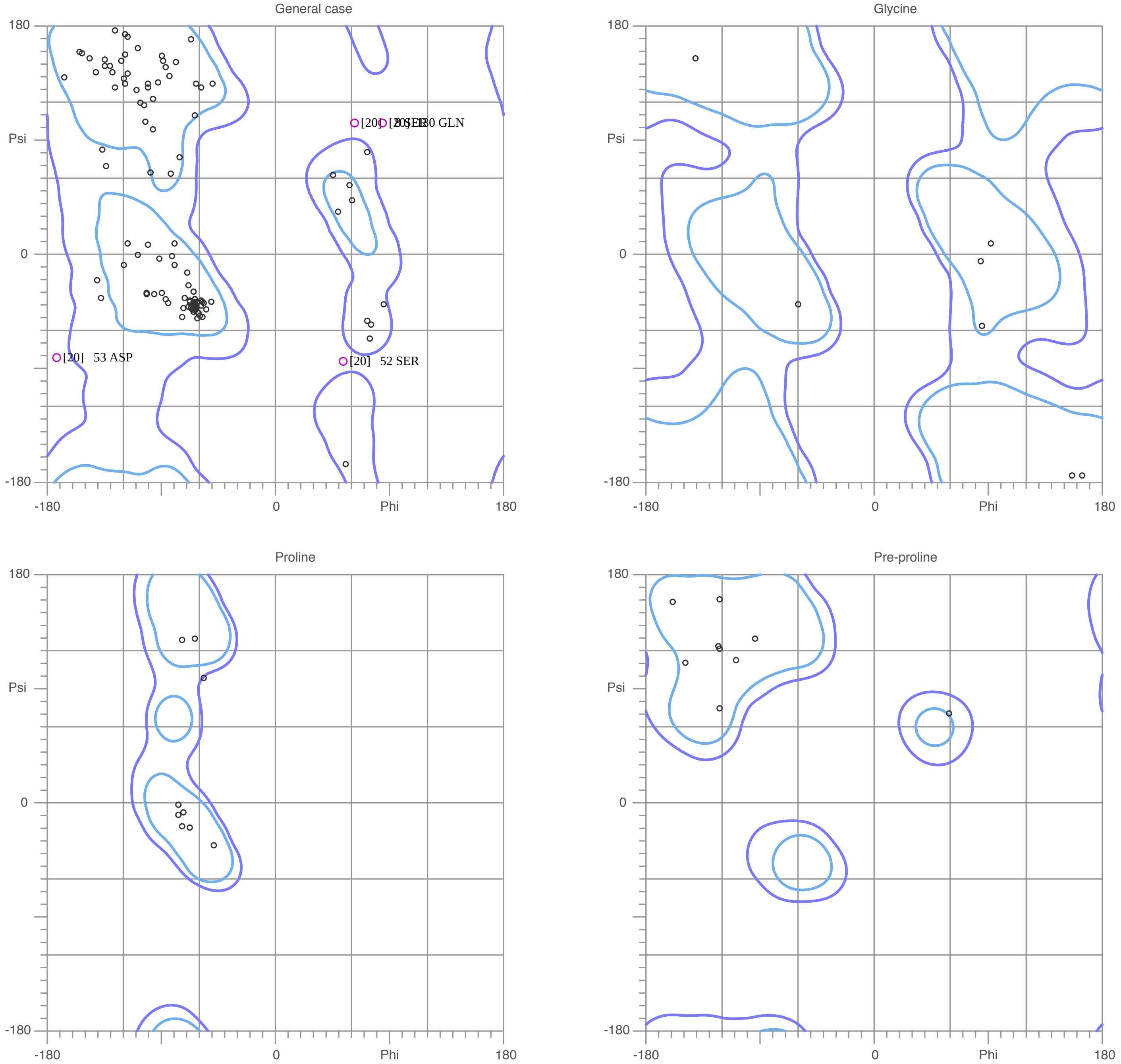
MolProbity Ramachandran analysis

STR70_R3Cons_em_bcr3.pdb, model 20



87.9% (123/140) of all residues were in favored (98%) regions.
97.1% (136/140) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[20]	8 SER (62.6, 104.6)
[20]	52 SER (53.1, -84.9)
[20]	53 ASP (-173.5, -81.4)
[20]	130 GLN (84.5, 105.0)