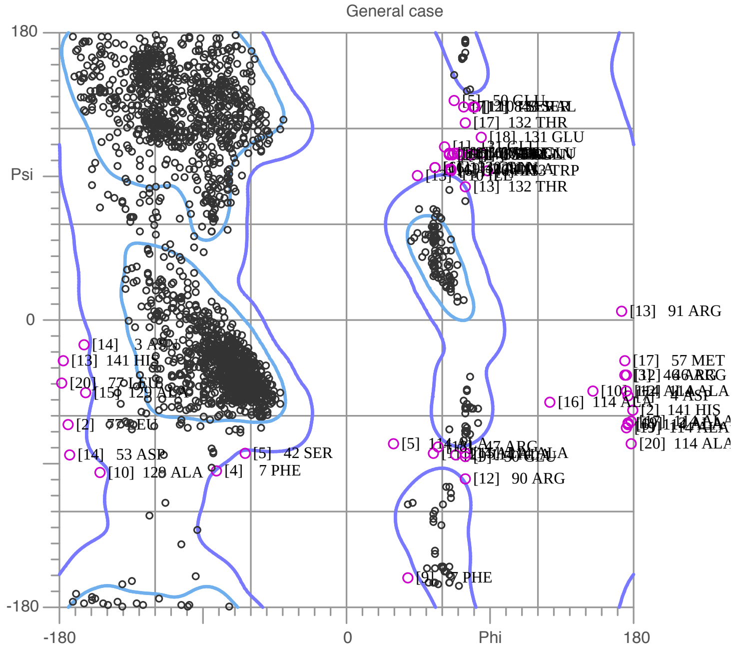
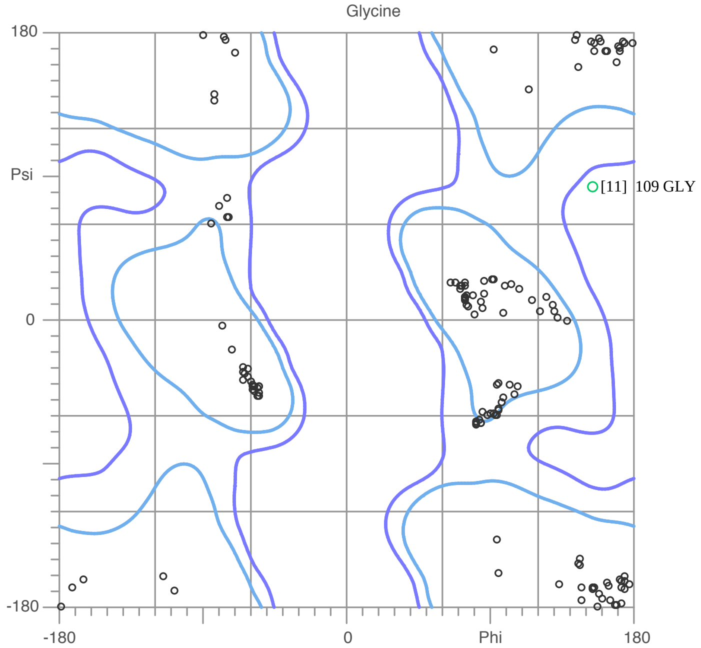
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, all models

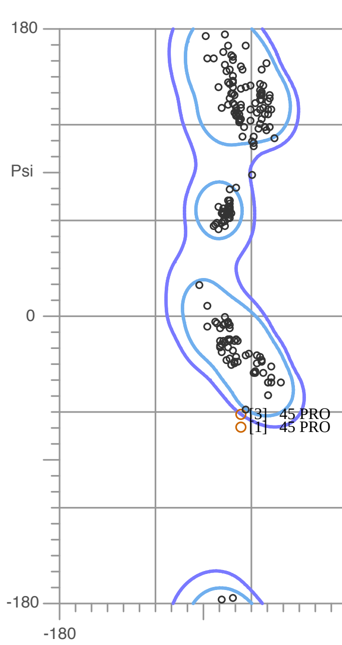
General case



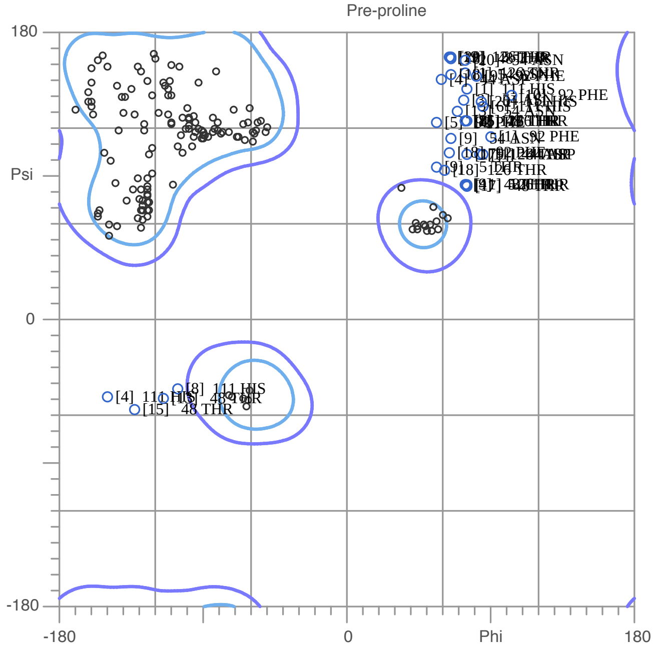
Glycine



Proline



Pre-proline



90.1% (2524/2800) of all residues were in favored (98%) regions.
96.7% (2707/2800) of all residues were in allowed (>99.8%) regions.

There were 93 outliers (phi, psi):
[1] 45 PRO (-67.9, -69.1)
[1] 92 PHE (90.9, 115.0)
[1] 111 HIS (75.0, 145.0)
[1] 114 ALA (54.5, -84.0)
[1] 126 THR (74.9, 155.0)
[1] 131 GLU (61.9, 109.2)
[2] 77 LEU (-175.0, -65.3)
[2] 114 ALA (68.4, -84.9)
[2] 126 THR (75.0, 125.0)
[2] 141 HIS (180.0, -56.1)
[3] 45 PRO (-67.7, -61.1)
[3] 46 ARG (174.9, -35.0)
[3] 54 ASN (73.5, 138.1)
[4] 2 ALA (65.0, 95.0)
[4] 5 THR (75.0, 85.1)
[4] 7 PHE (-83.0, -95.0)
[4] 44 ASP (59.8, 152.0)
[4] 48 THR (75.0, 125.0)
[4] 111 HIS (-150.9, -48.8)
[5] 42 SER (-64.9, -83.3)
[5] 50 GLU (67.4, 138.5)
[5] 92 PHE (56.0, 125.0)
[5] 114 ALA (29.6, -77.7)
[6] 51 VAL (65.0, 105.0)
[6] 111 HIS (85.1, 135.0)
[6] 113 TRP (88.3, 94.4)
[6] 114 ALA (176.7, -65.1)
[6] 134 GLN (55.0, 96.4)
[6] 136 GLU (84.1, 105.0)
[6] 140 HIS (65.1, 94.9)
[7] 4 ASP (177.0, -47.5)
[7] 108 SER (74.0, 134.9)
[8] 111 HIS (-106.5, -43.0)
[8] 126 THR (74.9, 125.0)
[9] 5 THR (56.2, 96.1)
[9] 7 PHE (38.7, -161.6)
[9] 44 ASP (85.0, 105.0)
[9] 48 THR (74.8, 85.3)
[9] 50 GLU (74.9, -85.1)
[9] 54 ASN (65.0, 114.9)
[9] 92 PHE (81.6, 153.5)
[10] 92 PHE (103.7, 141.1)
[10] 114 ALA (155.0, -44.3)
[10] 129 ALA (-155.5, -95.0)
[11] 43 SER (80.1, 135.0)
[11] 44 ASP (83.5, 105.0)
[11] 109 GLY (154.9, 84.9)
[11] 126 THR (75.0, 85.0)
[11] 134 GLN (71.5, 105.0)
[12] 46 ARG (175.0, -35.0)
[12] 90 ARG (75.0, -99.5)
[12] 114 ALA (175.1, -45.0)
[12] 133 VAL (79.6, 135.0)
[13] 48 THR (-115.8, -50.0)
[13] 54 ASN (69.6, 131.3)
[13] 91 ARG (172.2, 6.8)
[13] 110 ILE (44.9, 91.2)
[13] 132 THR (75.0, 85.0)
[13] 141 HIS (-178.4, -25.3)
[14] 3 ASN (-165.1, -15.0)
[14] 8 SER (66.6, 104.9)
[14] 53 ASP (-174.6, -84.9)
[14] 130 GLN (77.1, 104.9)
[15] 5 THR (74.9, 125.1)
[15] 7 PHE (69.4, 105.0)
[15] 48 THR (-133.3, -56.3)
[15] 114 ALA (75.0, -83.1)
[15] 129 ALA (-165.0, -45.0)
[16] 114 ALA (127.1, -51.8)
[16] 126 THR (75.0, 125.0)
[16] 130 GLN (55.1, 96.9)
[17] 48 THR (75.1, 85.0)
[17] 57 MET (175.0, -25.1)
[17] 114 ALA (179.0, -63.4)
[17] 126 THR (75.0, 105.0)
[17] 132 THR (75.0, 125.0)
[18] 47 ARG (57.6, -79.6)
[18] 48 THR (65.1, 164.8)
[18] 50 GLU (67.7, 105.0)
[18] 54 ASN (65.0, 155.0)
[18] 92 PHE (64.1, 105.0)
[18] 126 THR (61.9, 95.0)
[18] 131 GLU (84.1, 115.0)
[19] 2 ALA (176.8, -65.0)
[19] 8 SER (64.9, 104.9)
[19] 114 ALA (175.1, -67.1)
[19] 126 THR (64.9, 165.0)
[19] 128 ALA (65.2, 95.0)
[20] 5 THR (65.0, 165.0)
[20] 54 ASN (75.0, 163.7)
[20] 77 LEU (-179.3, -39.8)
[20] 111 HIS (85.0, 137.2)
[20] 114 ALA (178.5, -77.8)

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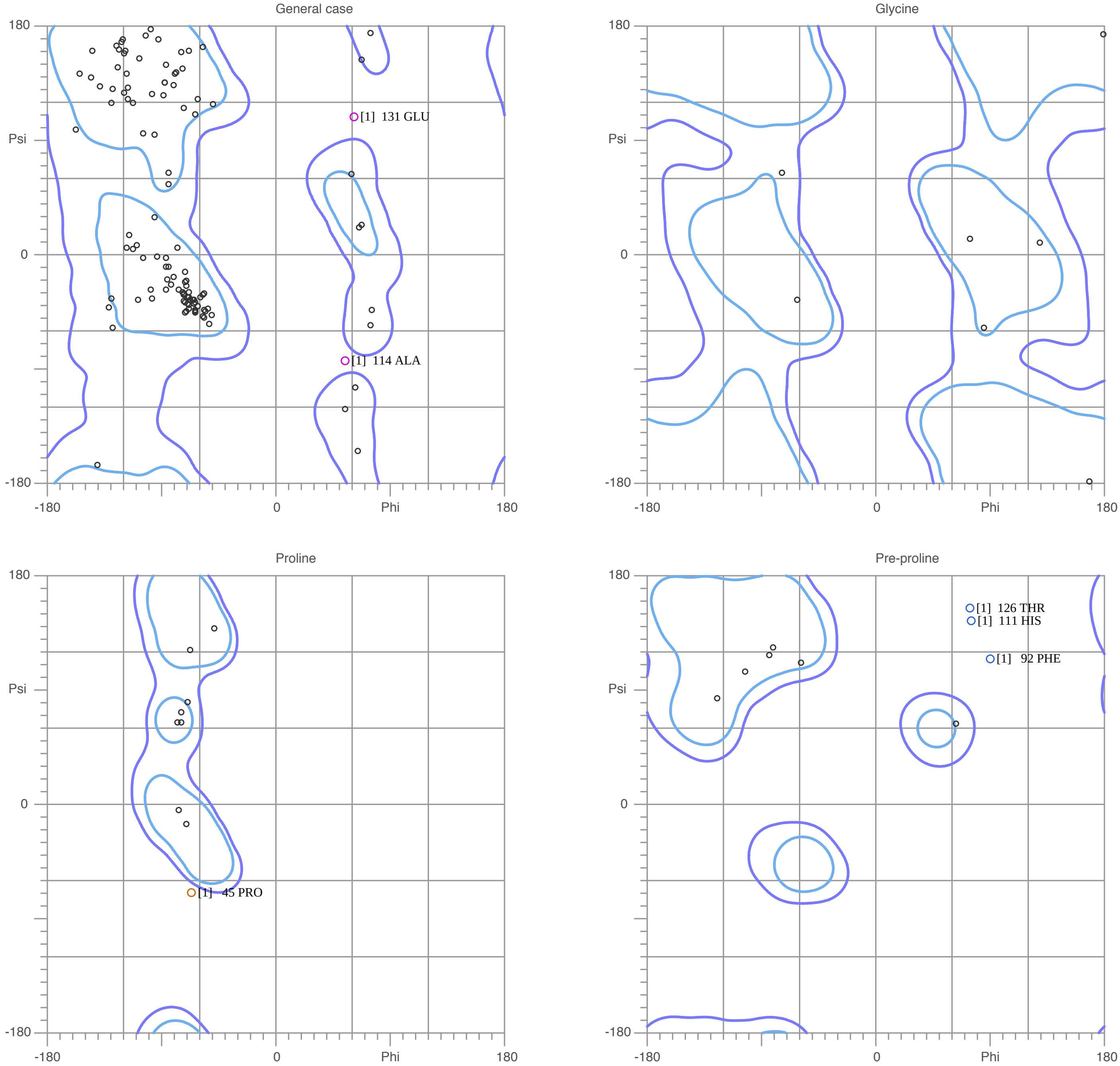
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 1



85.0% (119/140) 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):

[1] 45 PRO (-67.9, -69.1)
[1] 92 PHE (90.9, 115.0)
[1] 111 HIS (75.0, 145.0)
[1] 114 ALA (54.5, -84.0)
[1] 126 THR (74.9, 155.0)
[1] 131 GLU (61.9, 109.2)

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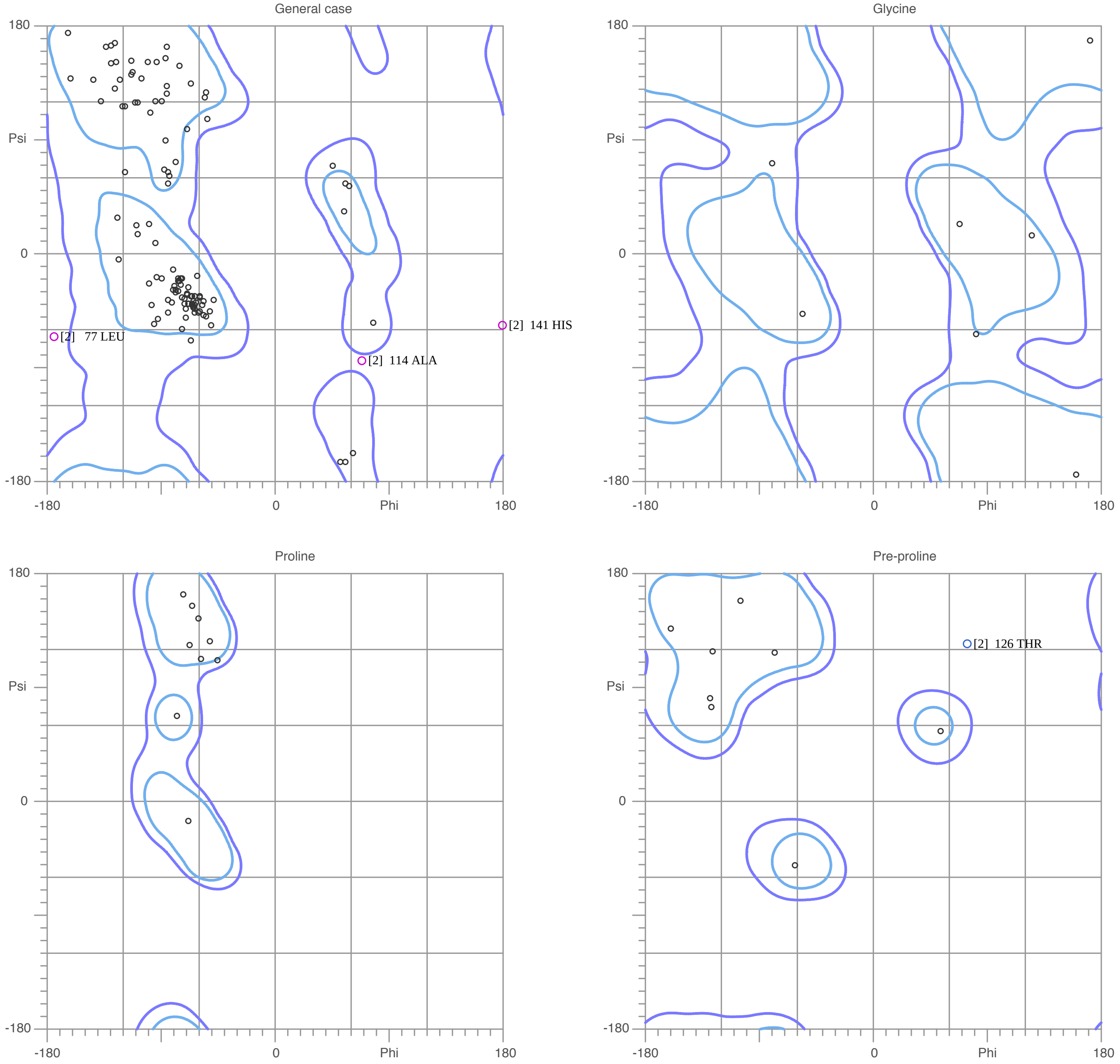
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 2



89.3% (125/140) 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):
- [2] 77 LEU (-175.0, -65.3)
- [2] 114 ALA (68.4, -84.9)
- [2] 126 THR (75.0, 125.0)
- [2] 141 HIS (180.0, -56.1)

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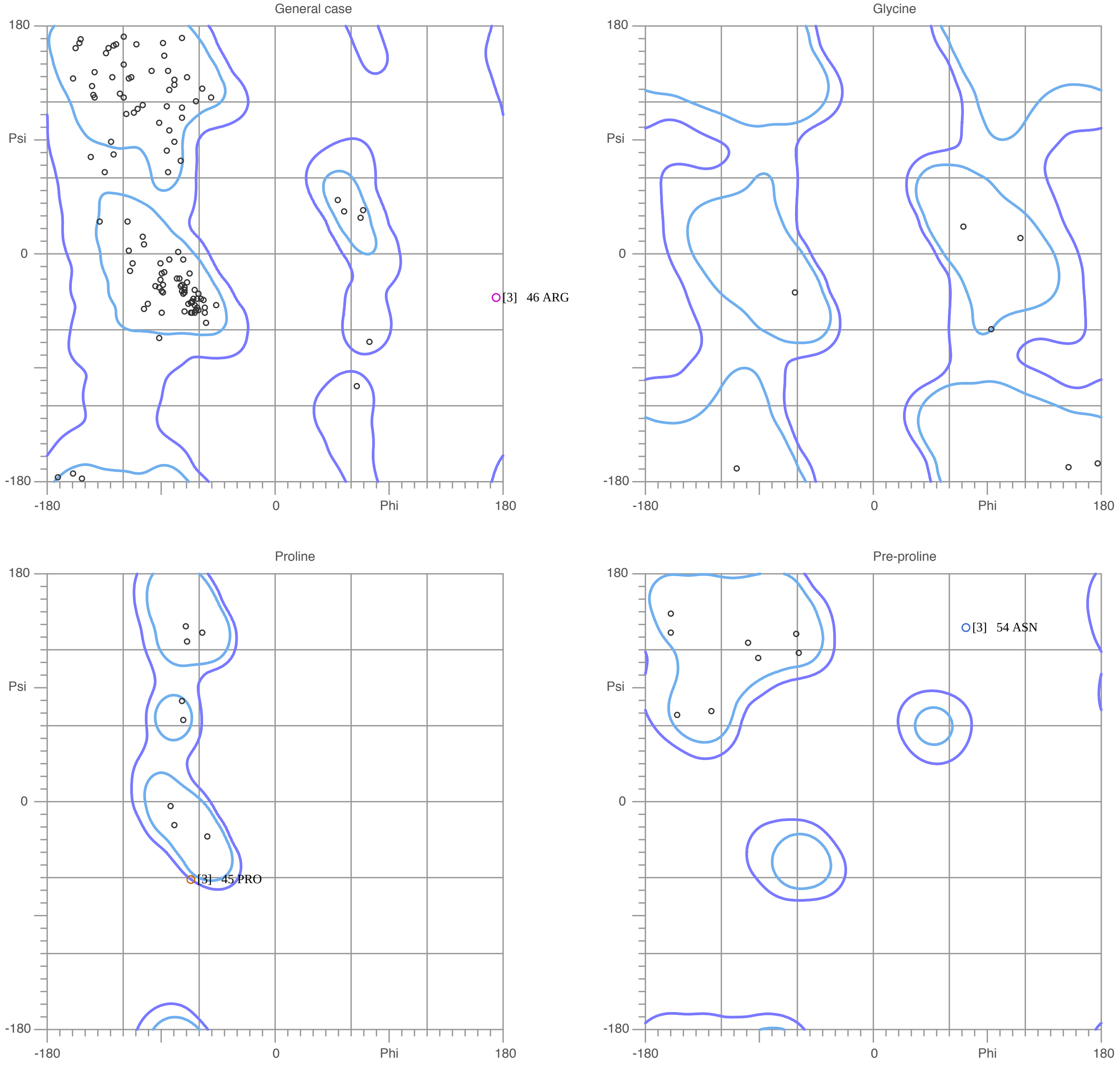
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 3



92.9% (130/140) 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):
- [3] 45 PRO (-67.7, -61.1)
- [3] 46 ARG (174.9, -35.0)
- [3] 54 ASN (73.5, 138.1)

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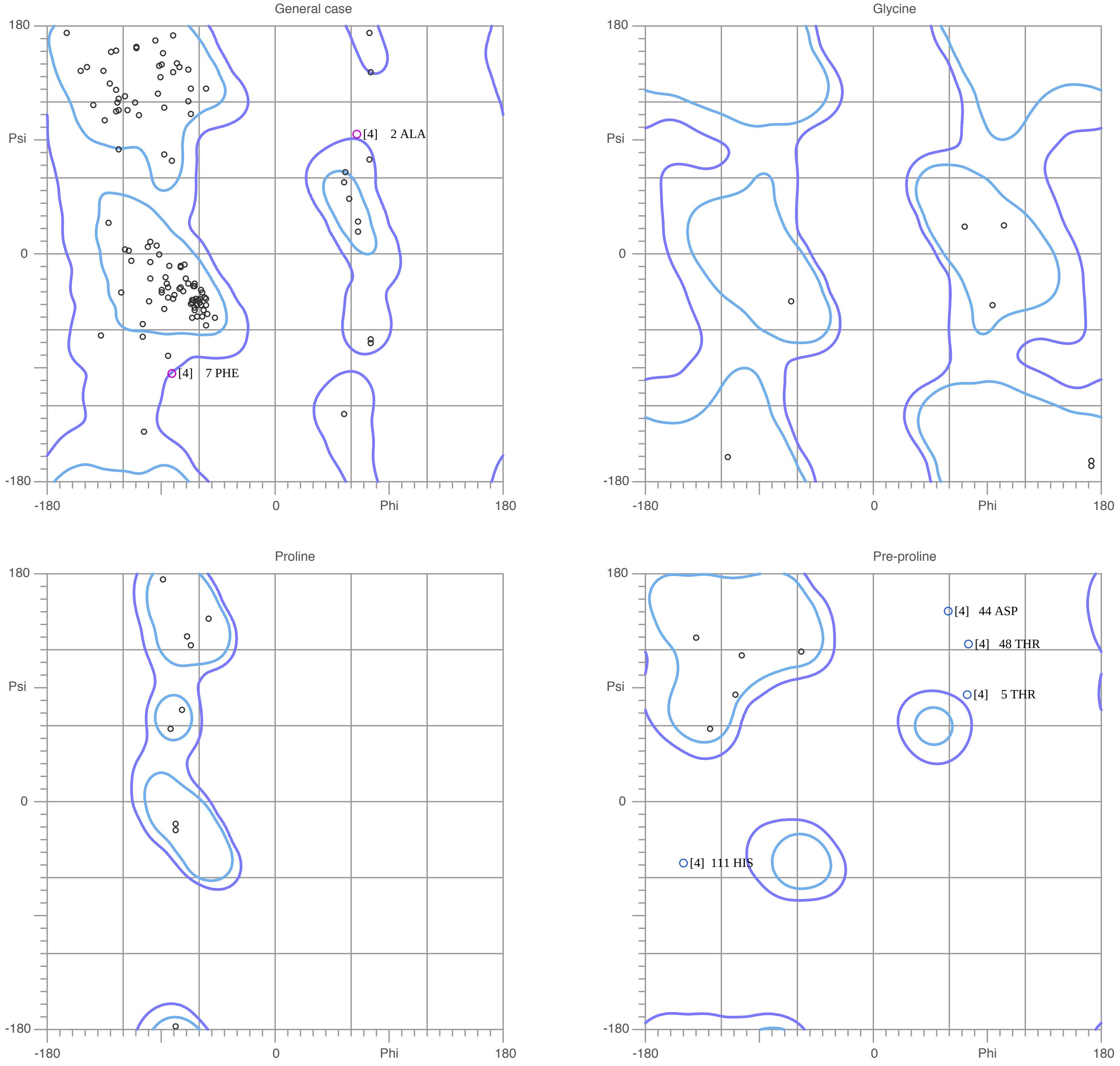
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 4



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):
[4] 2 ALA (65.0, 95.0)
[4] 5 THR (75.0, 85.1)
[4] 7 PHE (-83.0, -95.0)
[4] 44 ASP (59.8, 152.0)
[4] 48 THR (75.0, 125.0)
[4] 111 HIS (-150.9, -48.8)

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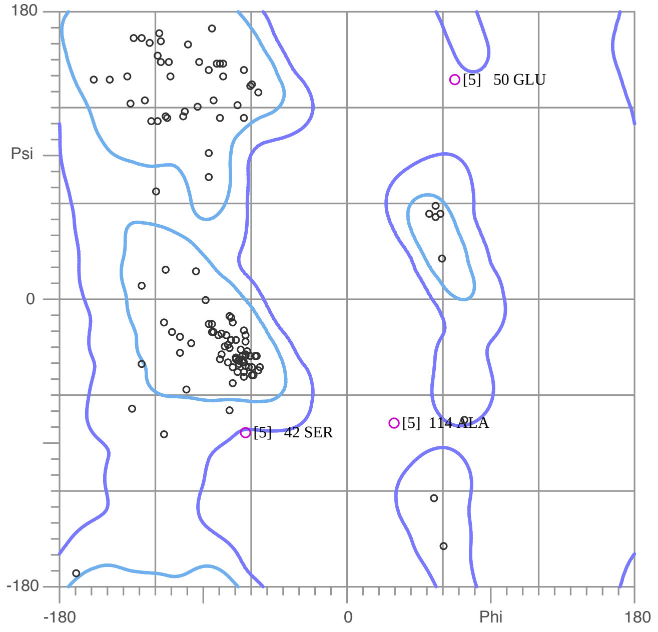
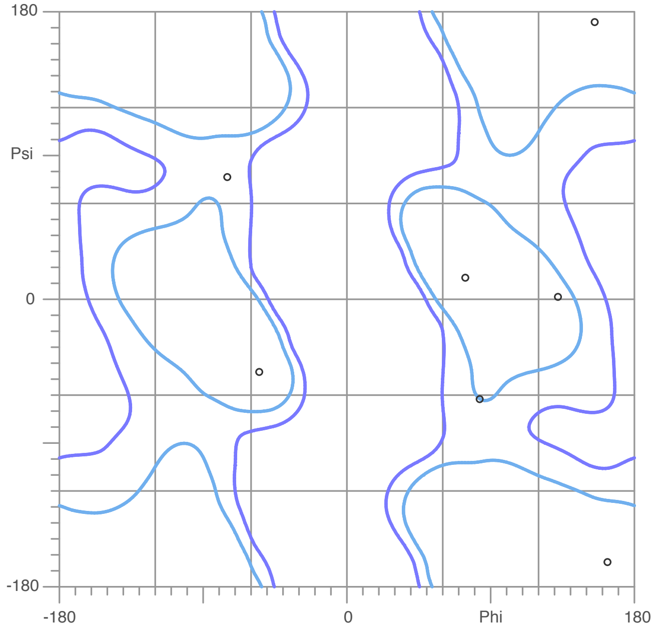
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 5

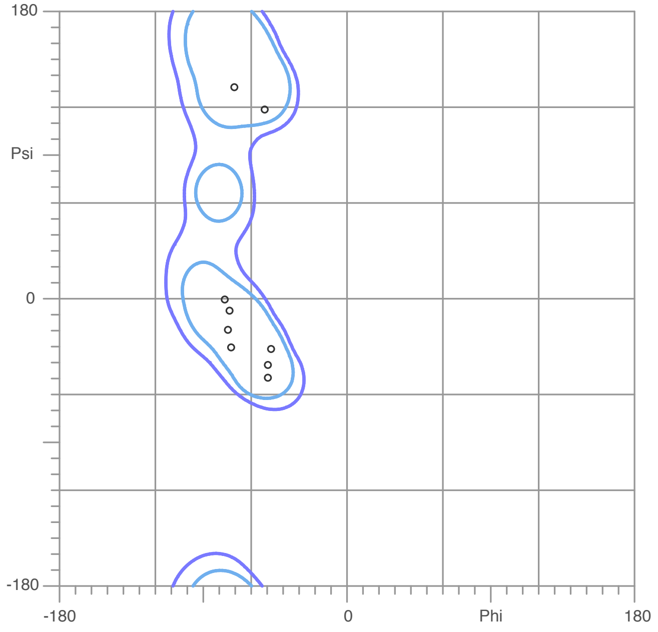
General case



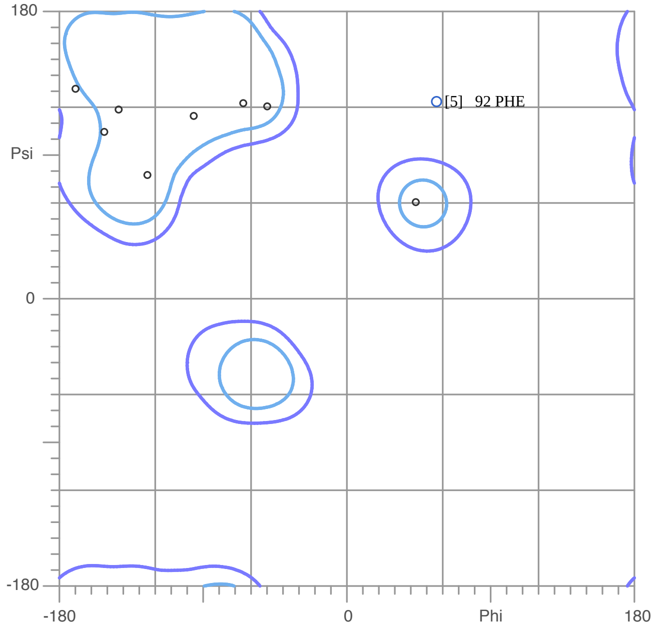
Glycine



Proline



Pre-proline



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):

[5] 42 SER (-64.9, -83.3)
[5] 50 GLU (67.4, 138.5)
[5] 92 PHE (56.0, 125.0)
[5] 114 ALA (29.6, -77.7)

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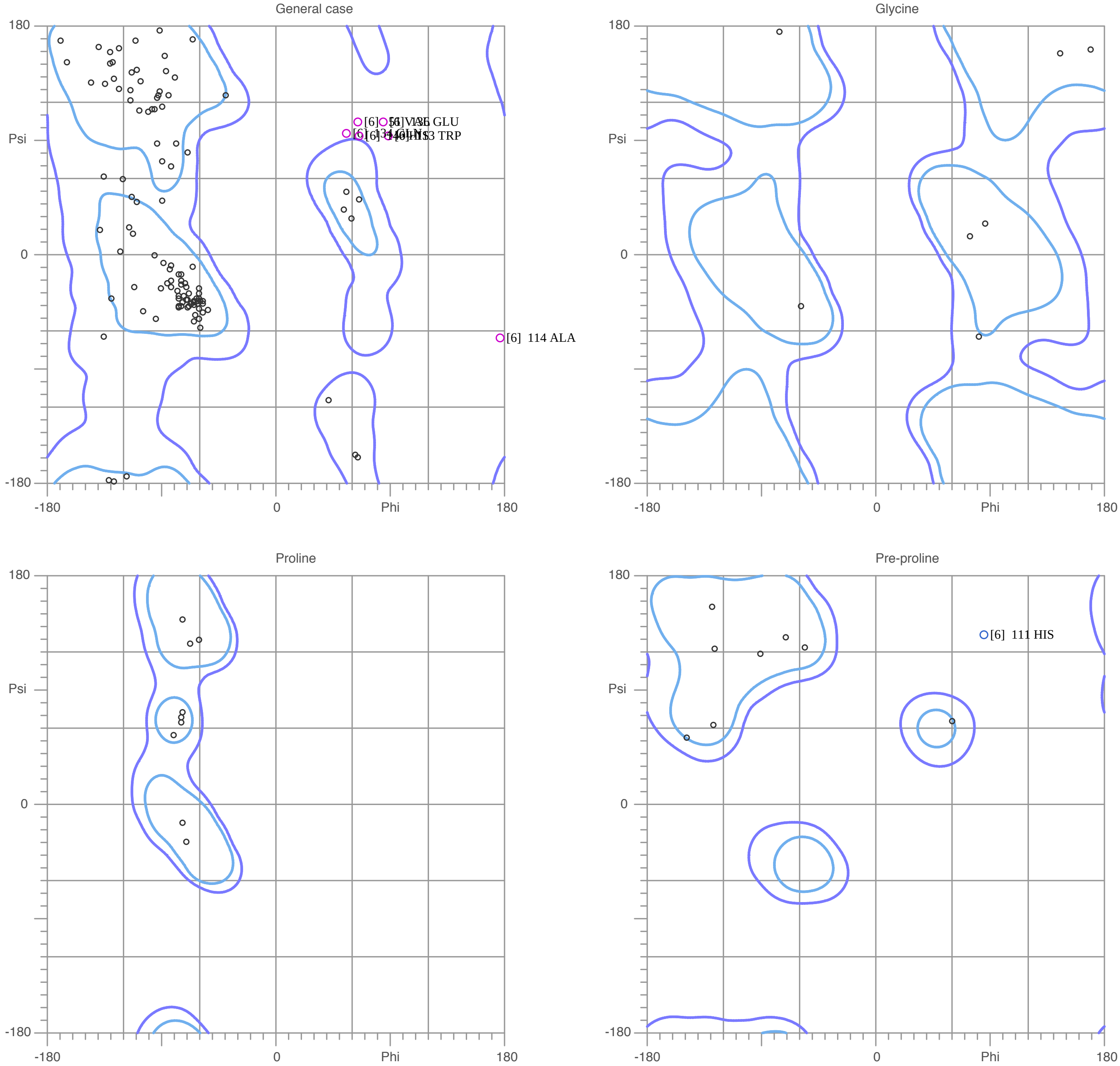
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 6



87.9% (123/140) 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] 51 VAL (65.0, 105.0)
[6] 111 HIS (85.1, 135.0)
[6] 113 TRP (88.3, 94.4)
[6] 114 ALA (176.7, -65.1)
[6] 134 GLN (55.0, 96.4)
[6] 136 GLU (84.1, 105.0)
[6] 140 HIS (65.1, 94.9)

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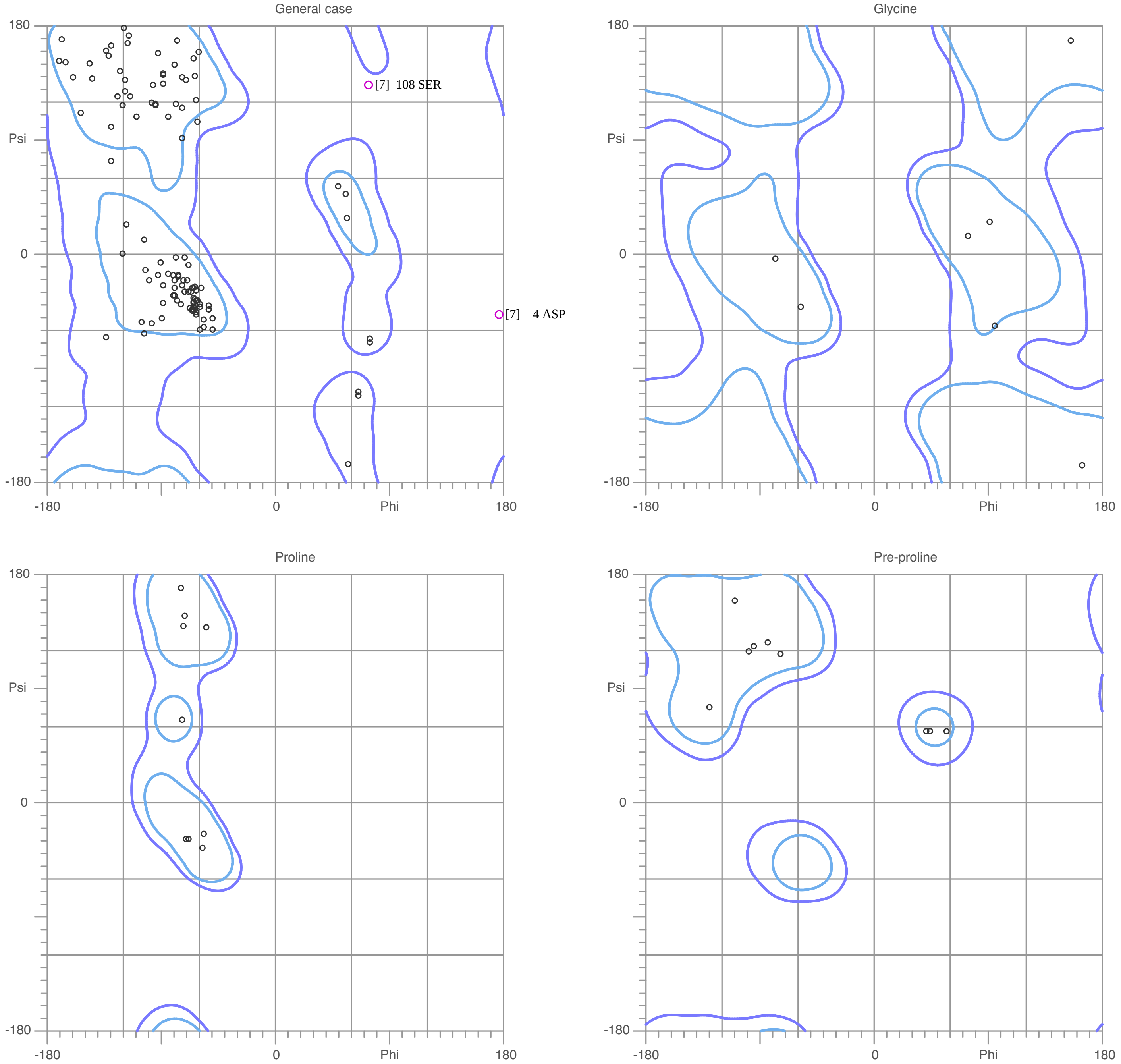
MolProbity Ramachandran analysis

STR70_R3_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] 4 ASP (177.0, -47.5)
[7] 108 SER (74.0, 134.9)

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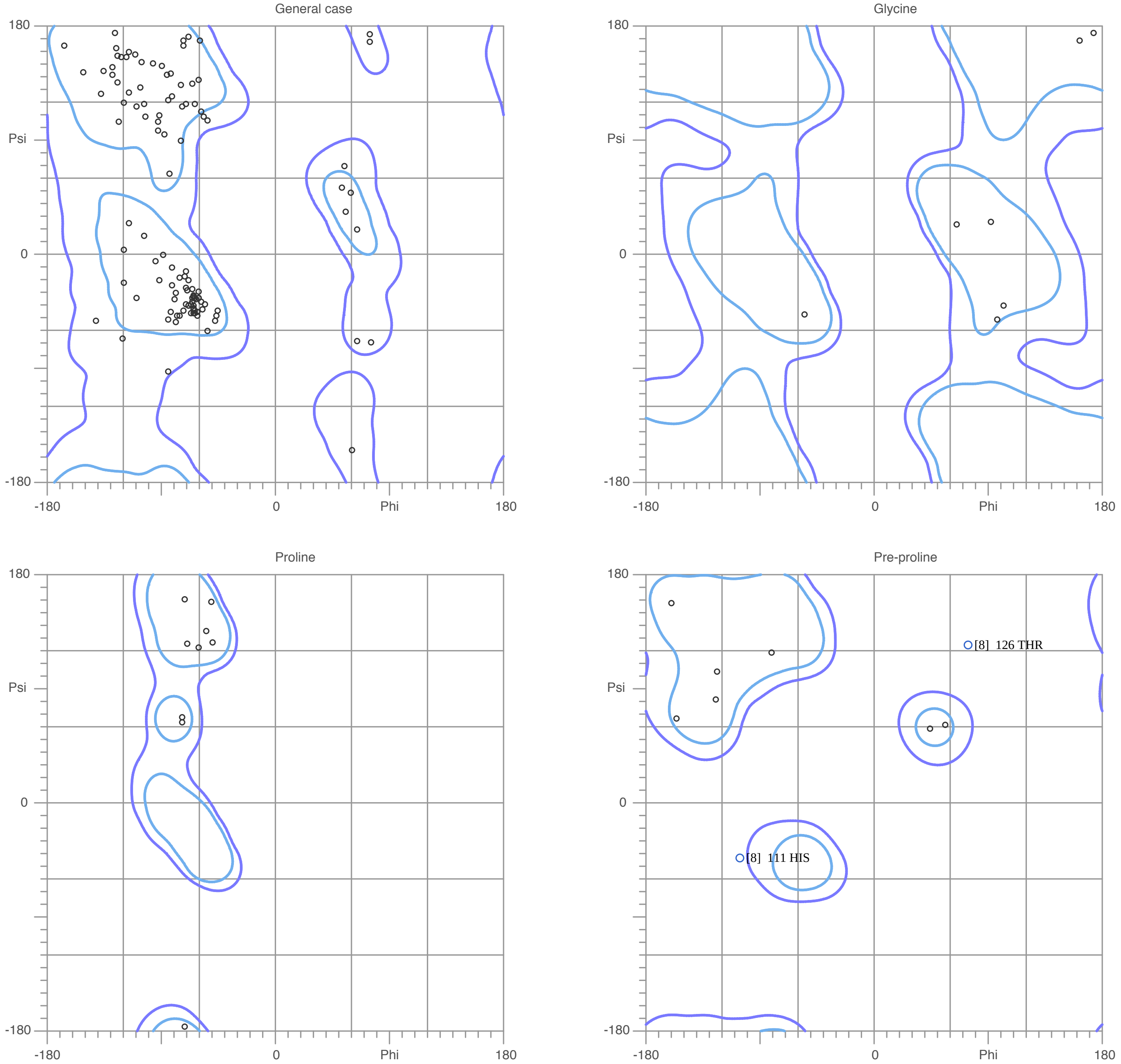
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 8



90.7% (127/140) 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):
[8] 111 HIS (-106.5, -43.0)
[8] 126 THR (74.9, 125.0)

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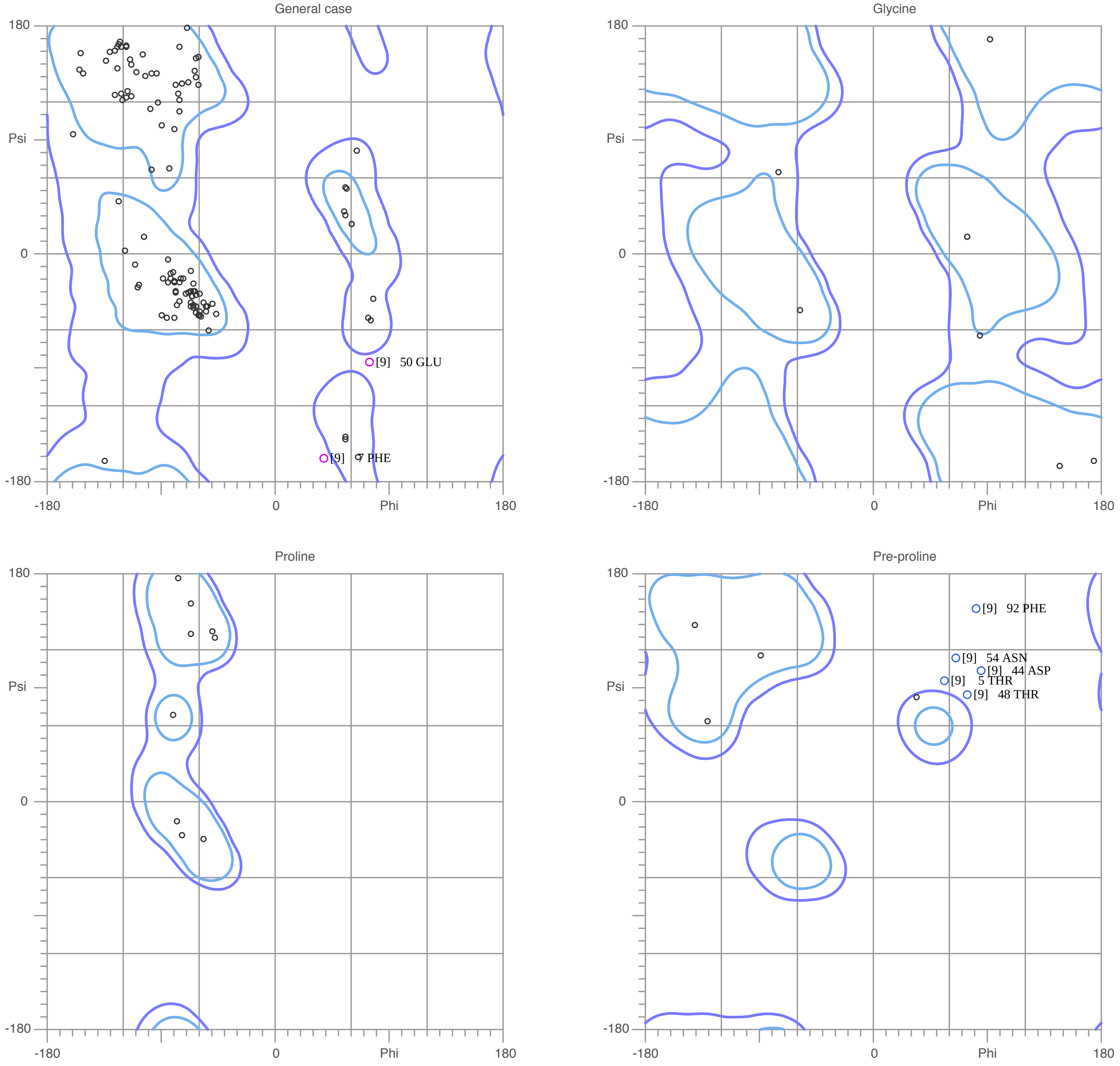
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 9



86.4% (121/140) 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):

[9] 5 THR (56.2, 96.1)
[9] 7 PHE (38.7, -161.6)
[9] 44 ASP (85.0, 105.0)
[9] 48 THR (74.8, 85.3)
[9] 50 GLU (74.9, -85.1)
[9] 54 ASN (65.0, 114.9)
[9] 92 PHE (81.6, 153.5)

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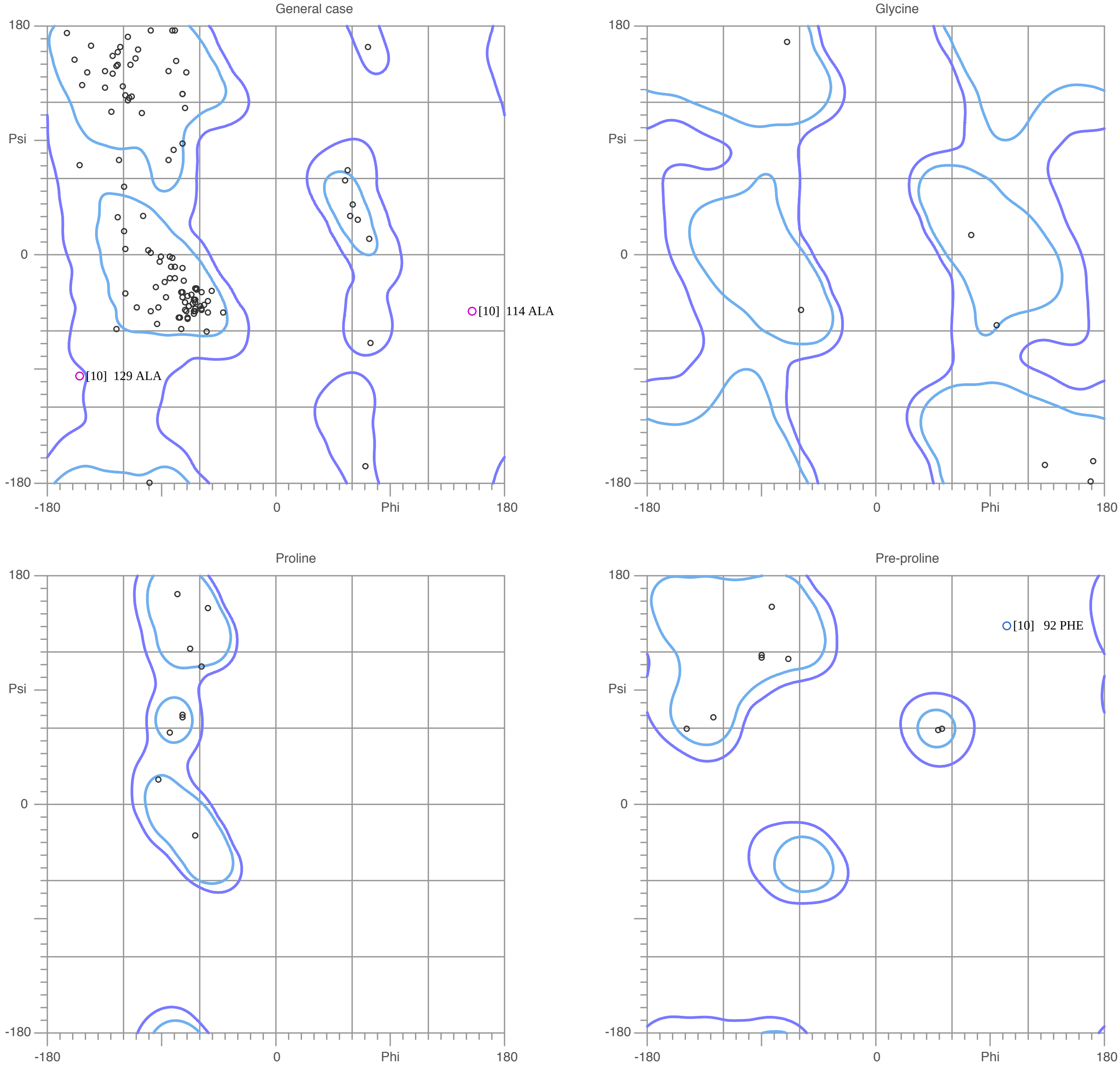
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 10



92.1% (129/140) 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):
[10] 92 PHE (103.7, 141.1)
[10] 114 ALA (155.0, -44.3)
[10] 129 ALA (-155.5, -95.0)

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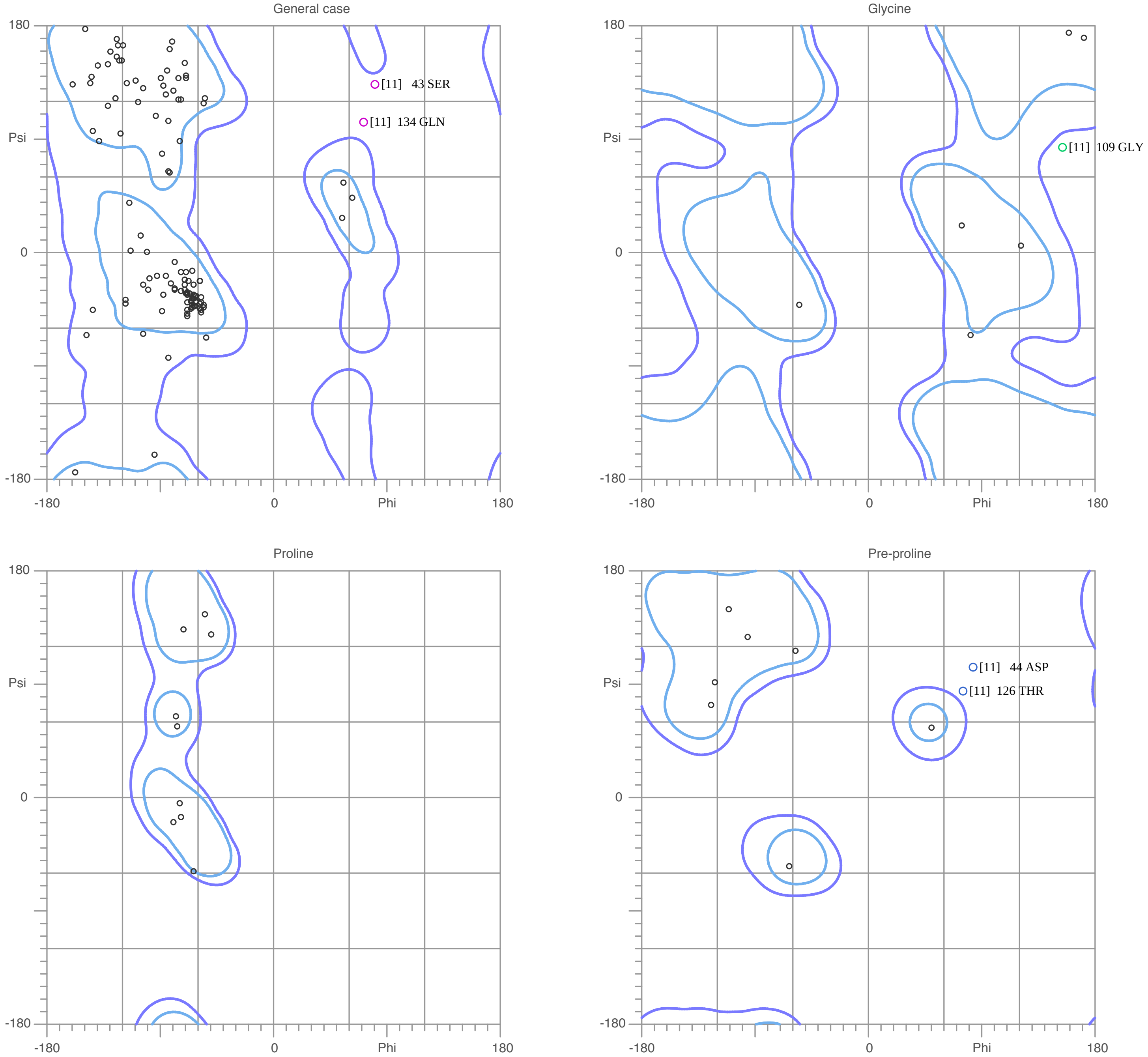
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 11



90.7% (127/140) 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):

[11] 43 SER (80.1, 135.0)
[11] 44 ASP (83.5, 105.0)
[11] 109 GLY (154.9, 84.9)
[11] 126 THR (75.0, 85.0)
[11] 134 GLN (71.5, 105.0)

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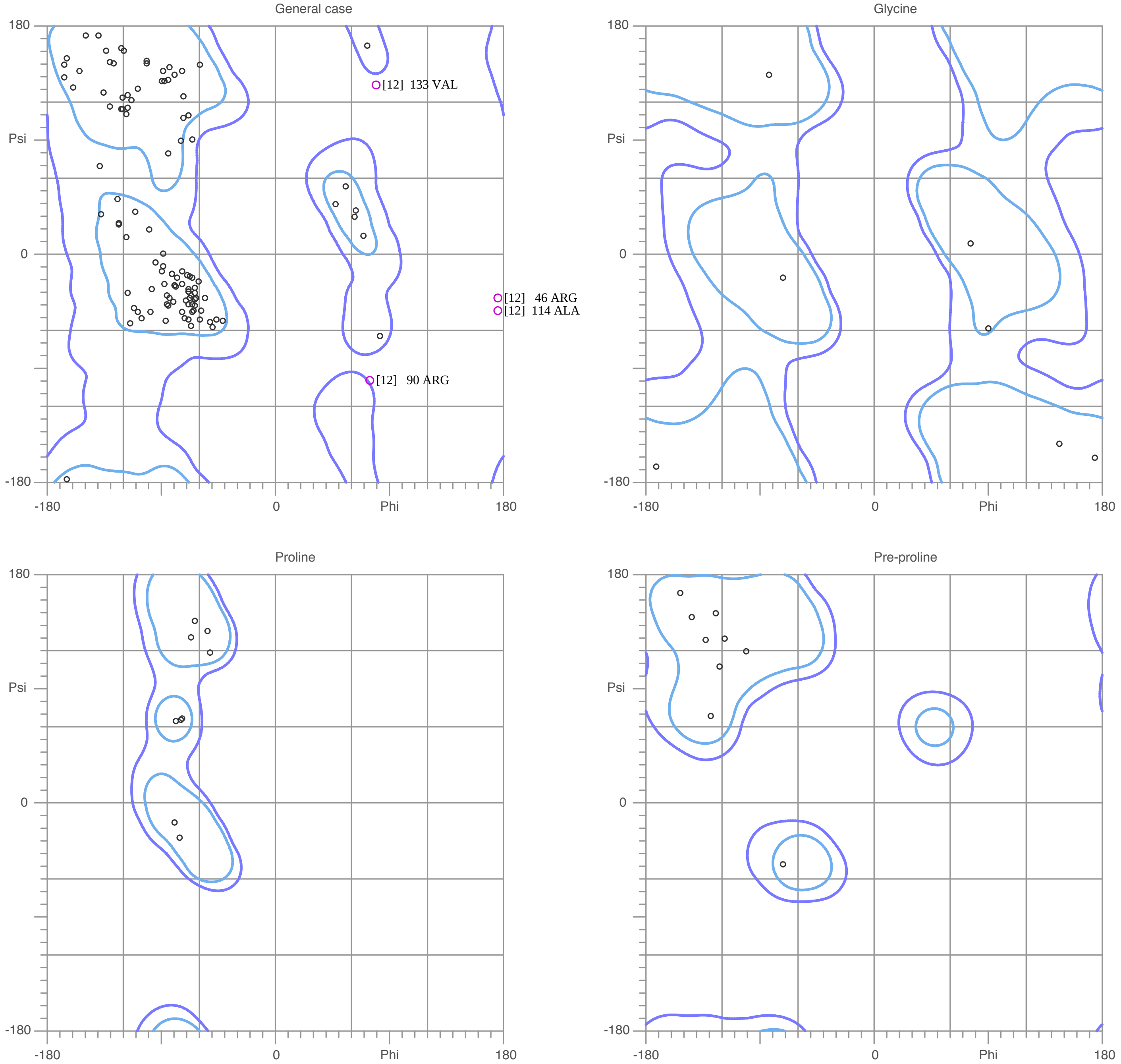
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 12



94.3% (132/140) 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):

[12] 46 ARG (175.0, -35.0)
[12] 90 ARG (75.0, -99.5)
[12] 114 ALA (175.1, -45.0)
[12] 133 VAL (79.6, 135.0)

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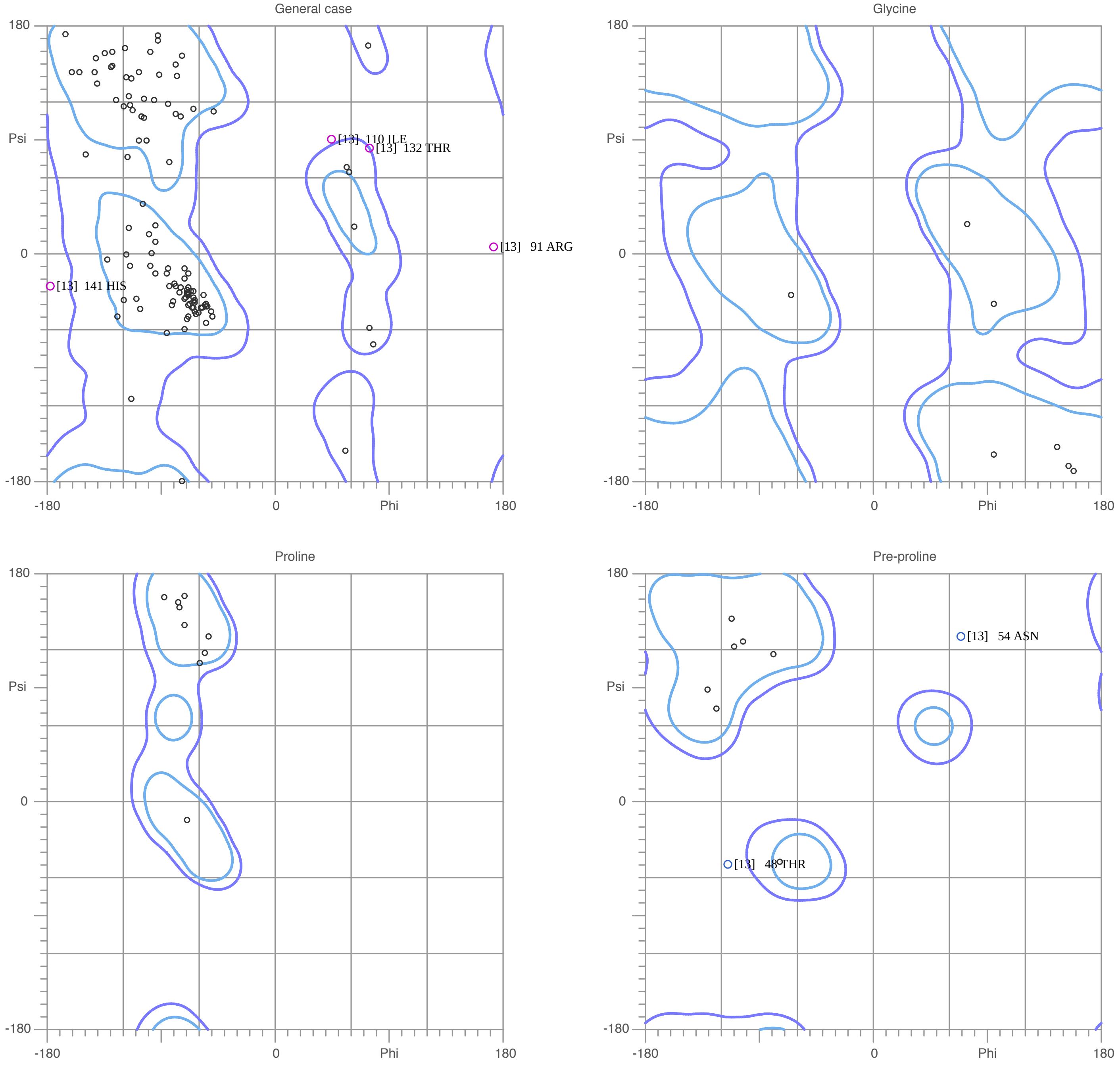
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 13



88.6% (124/140) 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):
- [13] 48 THR (-115.8, -50.0)
- [13] 54 ASN (69.6, 131.3)
- [13] 91 ARG (172.2, 6.8)
- [13] 110 ILE (44.9, 91.2)
- [13] 132 THR (75.0, 85.0)
- [13] 141 HIS (-178.4, -25.3)

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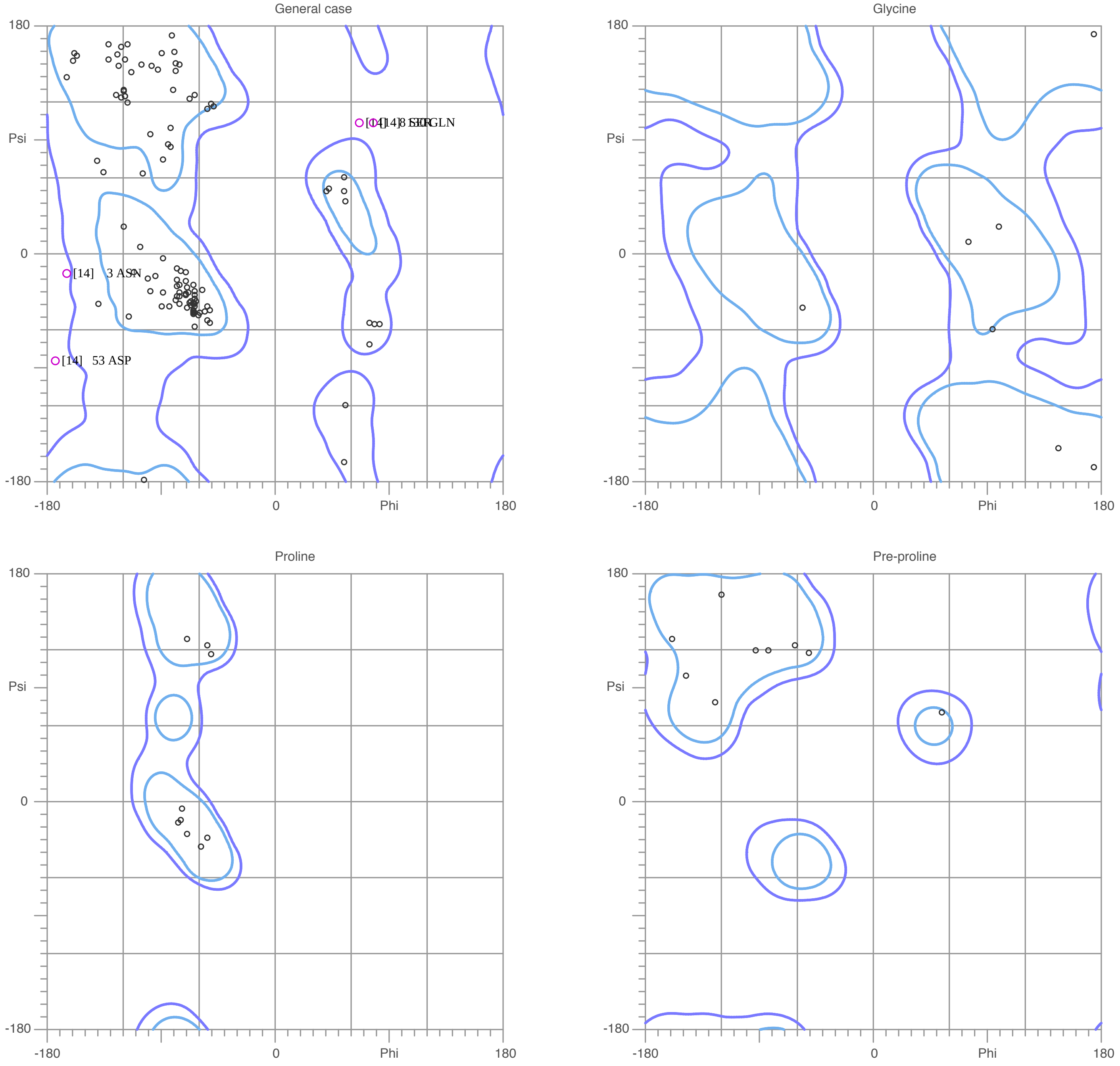
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 14



89.3% (125/140) 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):

[14] 3 ASN (-165.1, -15.0)
[14] 8 SER (66.6, 104.9)
[14] 53 ASP (-174.6, -84.9)
[14] 130 GLN (77.1, 104.9)

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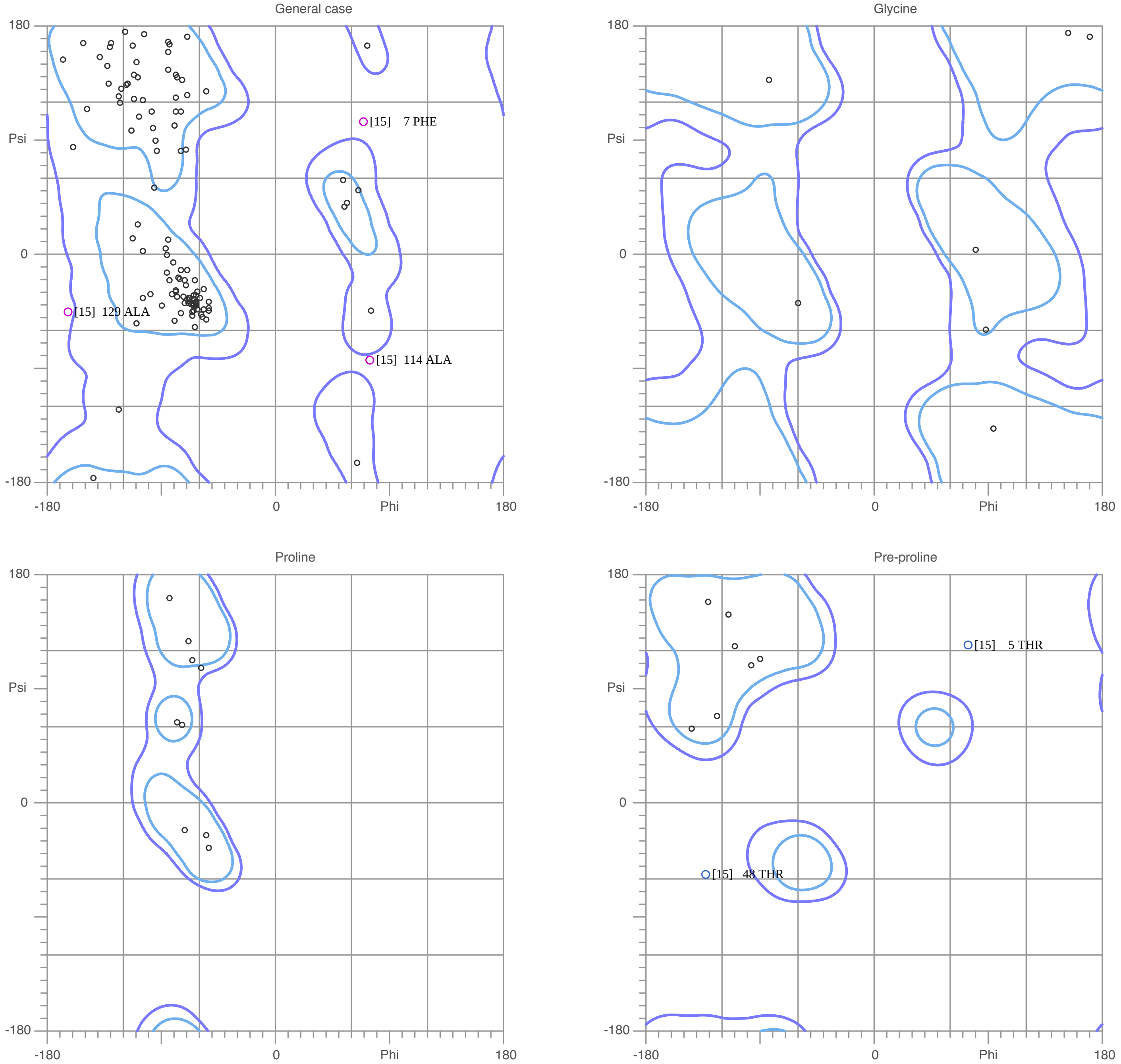
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 15



90.7% (127/140) 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):

[15] 5 THR (74.9, 125.1)
[15] 7 PHE (69.4, 105.0)
[15] 48 THR (-133.3, -56.3)
[15] 114 ALA (75.0, -83.1)
[15] 129 ALA (-165.0, -45.0)

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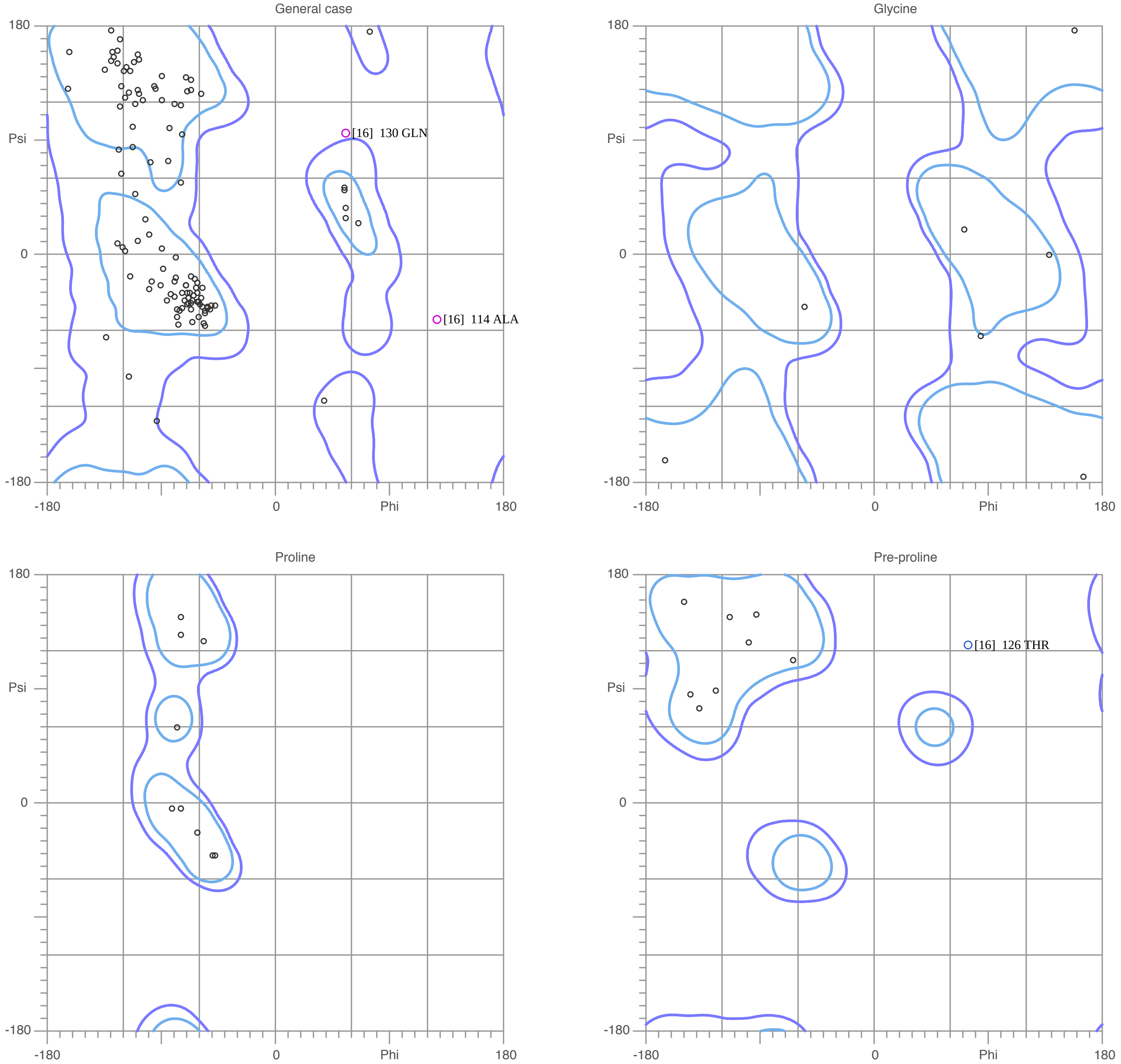
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 16



91.4% (128/140) 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] 114 ALA (127.1, -51.8)
[16] 126 THR (75.0, 125.0)
[16] 130 GLN (55.1, 96.9)

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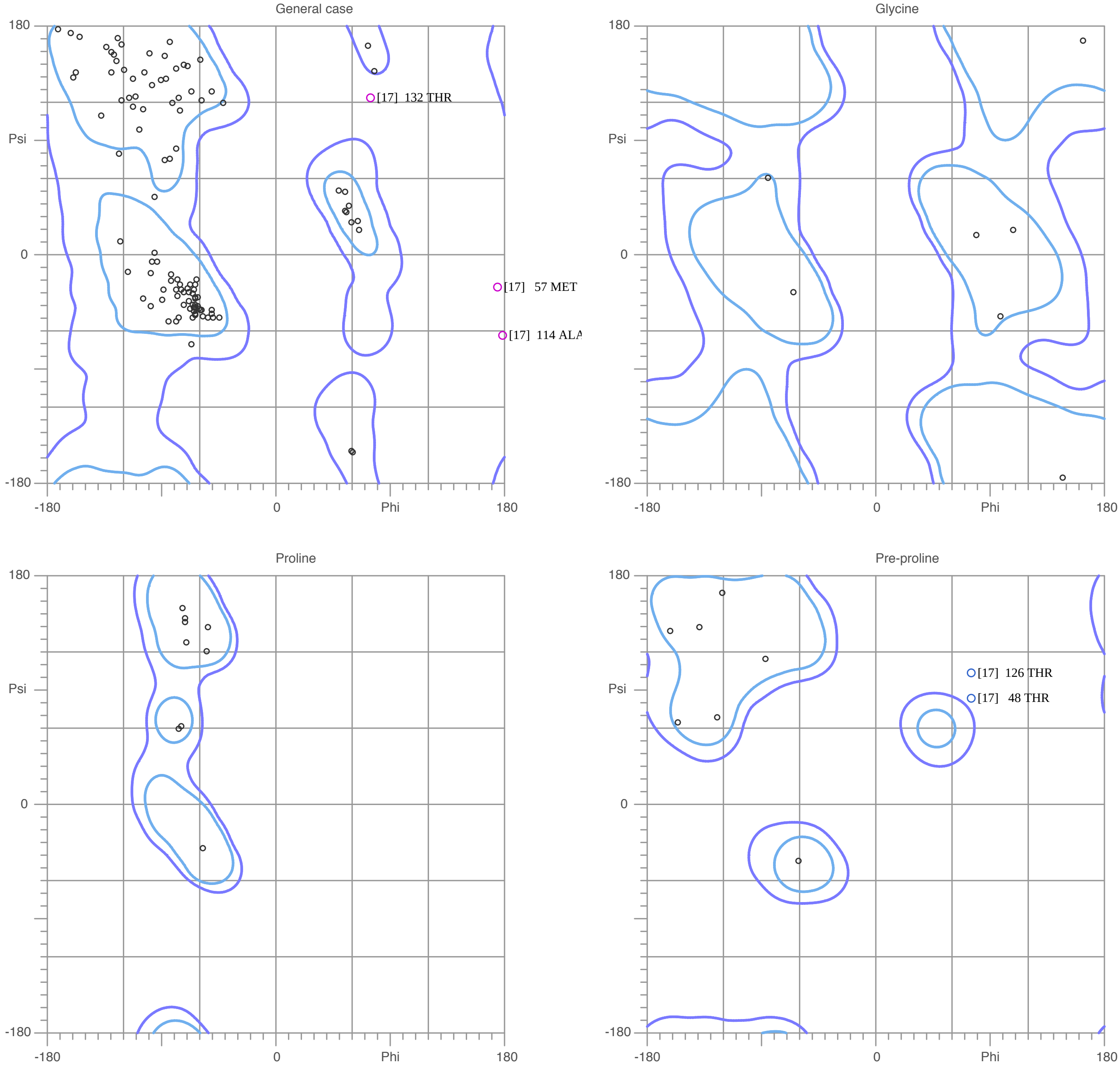
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 17



90.7% (127/140) 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):

[17] 48 THR (75.1, 85.0)
[17] 57 MET (175.0, -25.1)
[17] 114 ALA (179.0, -63.4)
[17] 126 THR (75.0, 105.0)
[17] 132 THR (75.0, 125.0)

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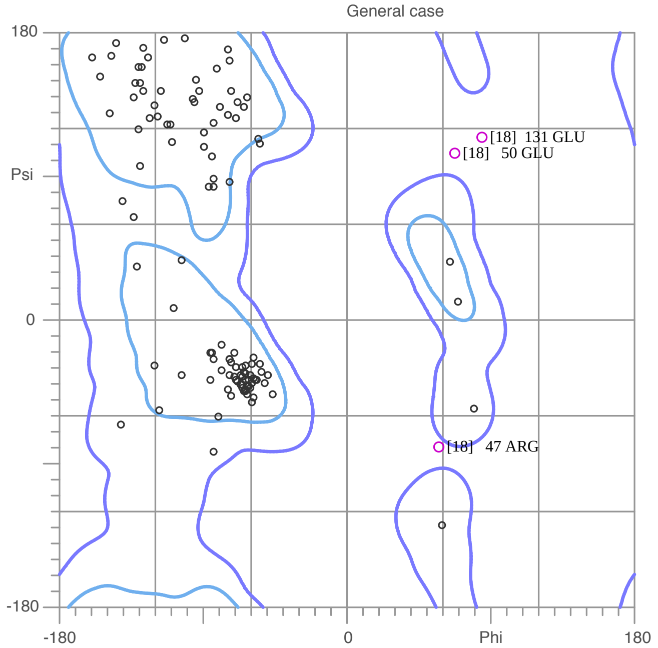
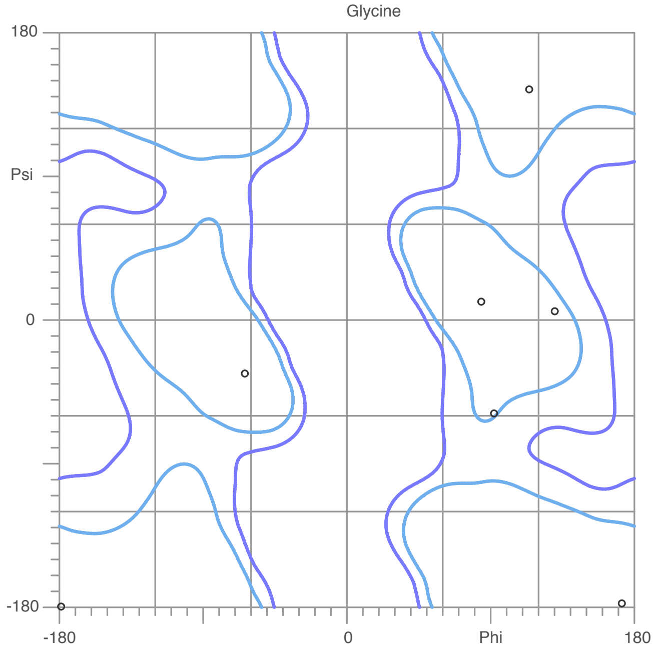
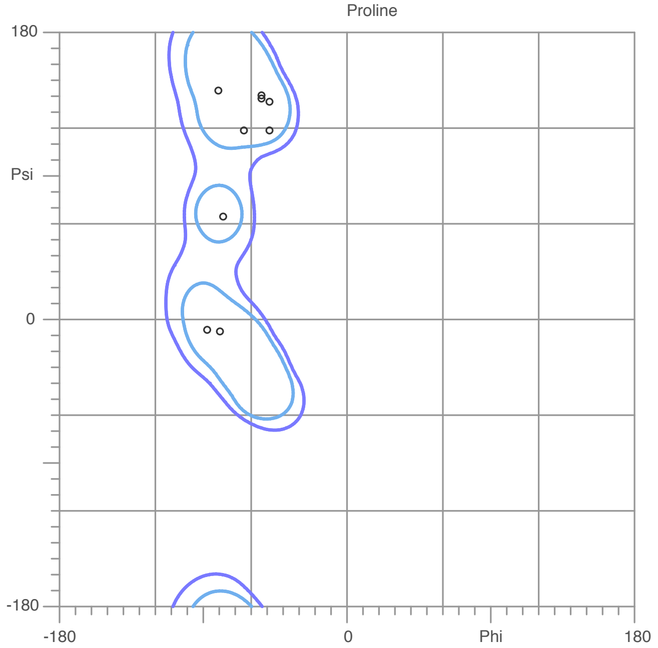
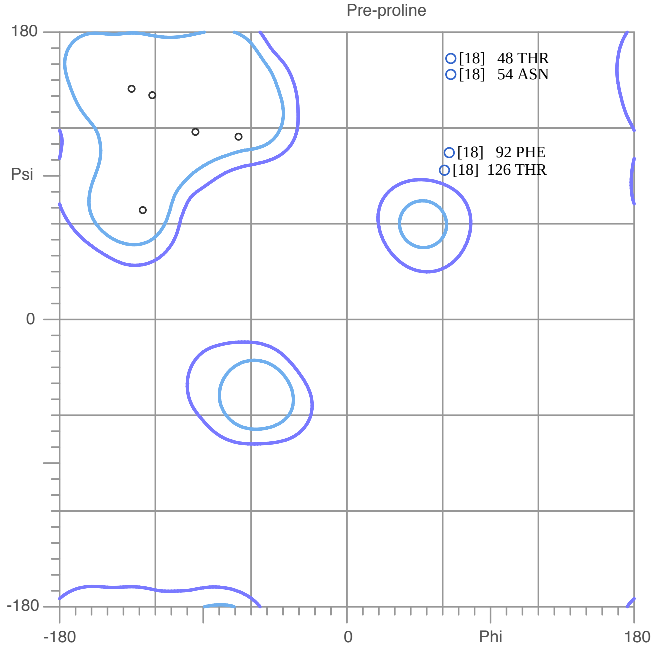
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 18


General case


Glycine


Proline


Pre-proline

90.0% (126/140) 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):
[18] 47 ARG (57.6, -79.6)
[18] 48 THR (65.1, 164.8)
[18] 50 GLU (67.7, 105.0)
[18] 54 ASN (65.0, 155.0)
[18] 92 PHE (64.1, 105.0)
[18] 126 THR (61.9, 95.0)
[18] 131 GLU (84.1, 115.0)

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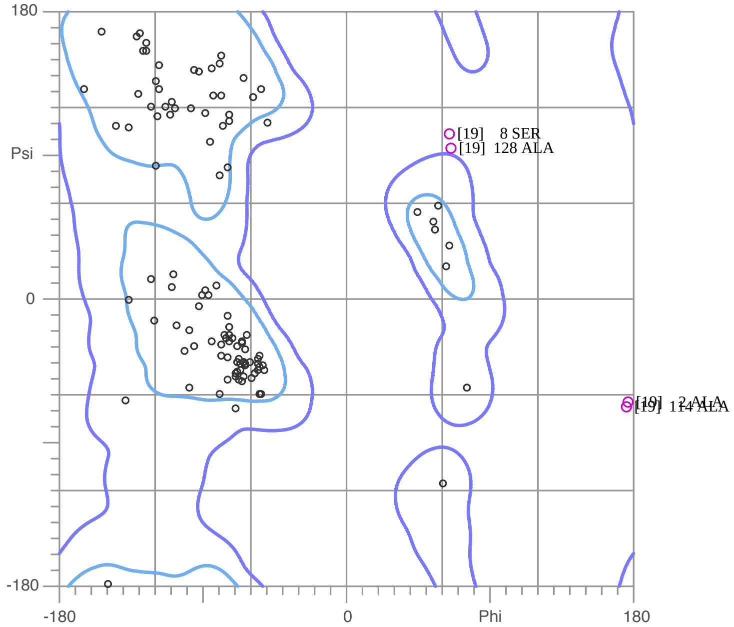
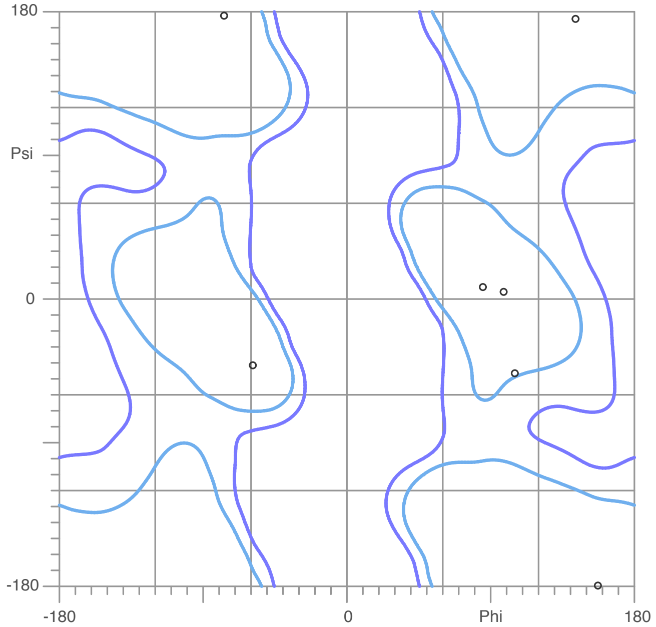
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 19

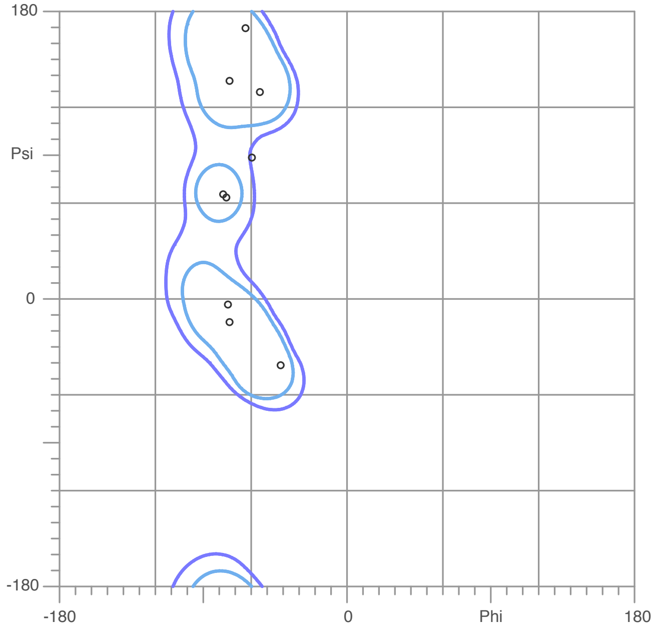
General case



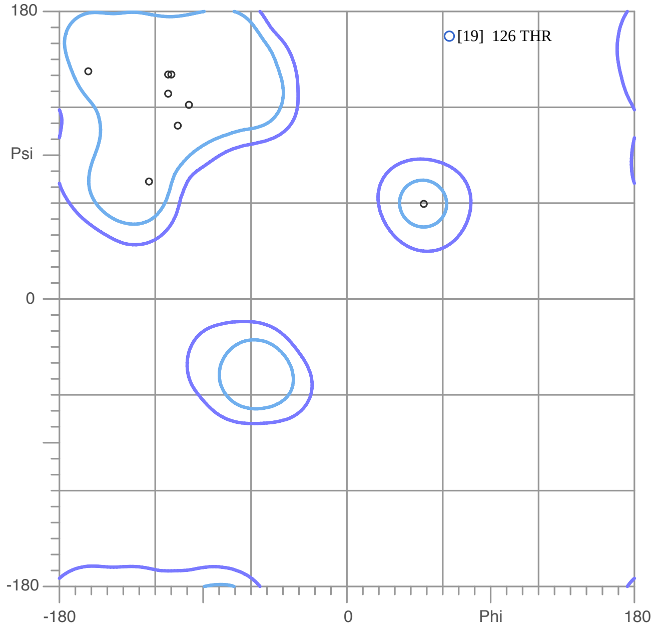
Glycine



Proline



Pre-proline



92.1% (129/140) 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] 2 ALA (176.8, -65.0)
[19] 8 SER (64.9, 104.9)
[19] 114 ALA (175.1, -67.1)
[19] 126 THR (64.9, 165.0)
[19] 128 ALA (65.2, 95.0)

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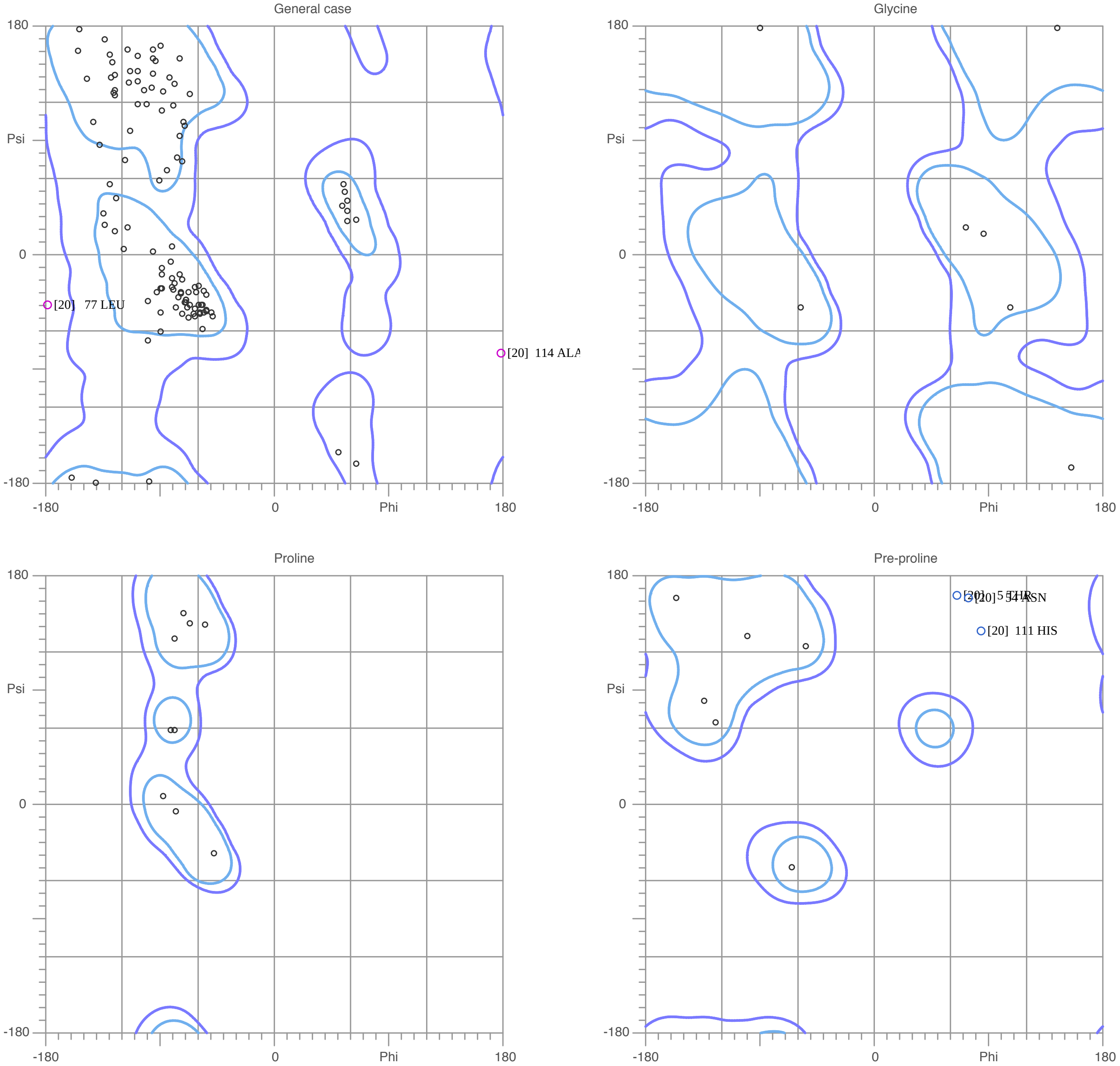
MolProbity Ramachandran analysis

STR70_R3_em_bcr3.pdb, model 20



92.1% (129/140) 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):

[20] 5 THR (65.0, 165.0)
[20] 54 ASN (75.0, 163.7)
[20] 77 LEU (-179.3, -39.8)
[20] 111 HIS (85.0, 137.2)
[20] 114 ALA (178.5, -77.8)

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