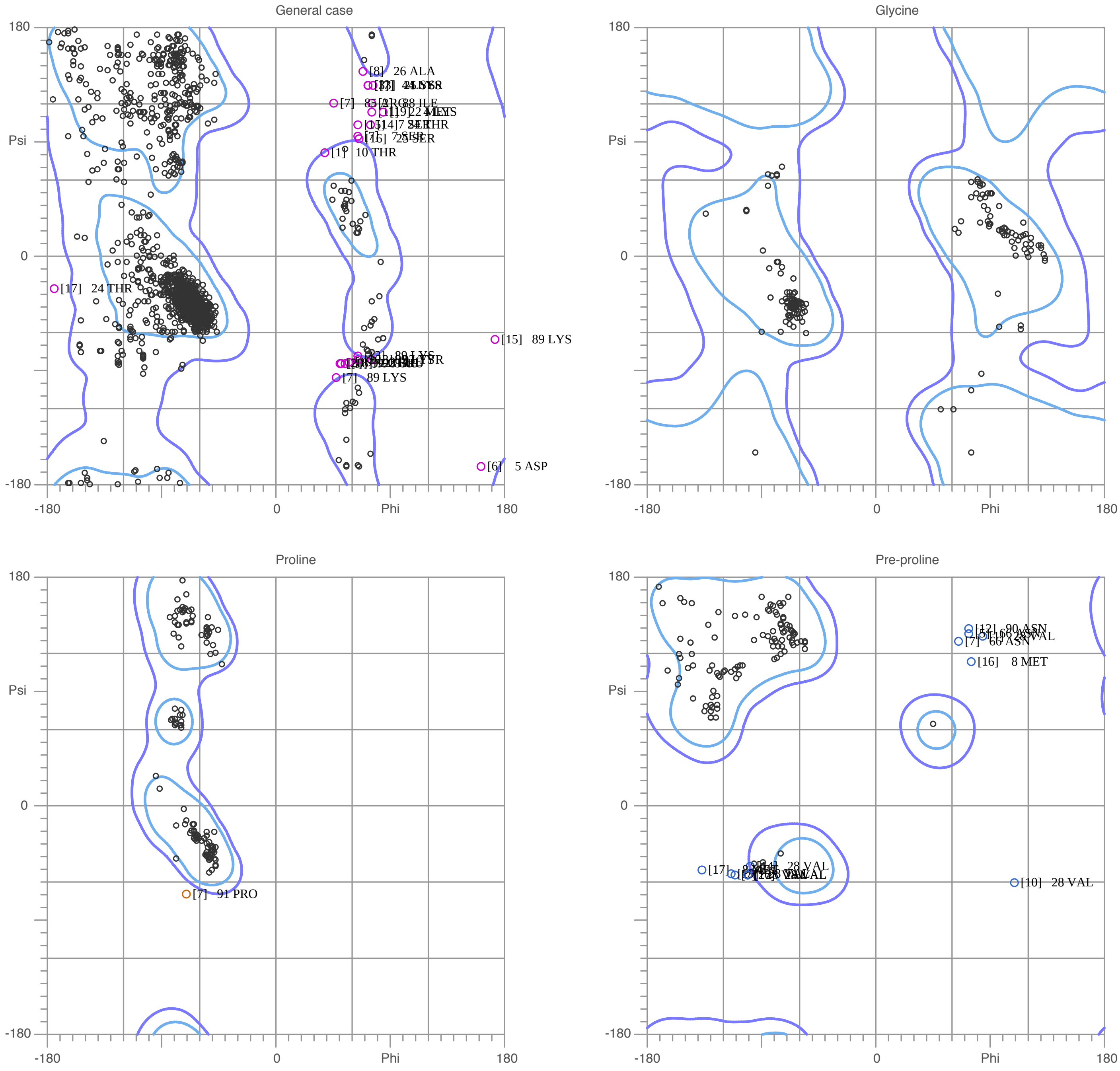
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, all models



92.5% (1980/2140) of all residues were in favored (98%) regions.
98.3% (2103/2140) of all residues were in allowed (>99.8%) regions.

There were 37 outliers (phi, psi):
[1] 10 THR (38.2, 82.7)
[1] 28 VAL (85.0, 135.0)
[2] 88 ILE (75.1, 121.6)
[3] 4 LYS (72.9, 135.4)
[3] 93 TYR (75.0, -81.4)
[5] 66 ASN (73.2, 137.0)
[6] 5 ASP (161.8, -165.0)
[7] 7 SER (64.9, 95.0)
[7] 25 SER (76.1, 135.0)
[7] 28 VAL (-112.0, -54.3)
[7] 66 ASN (65.0, 130.7)
[7] 85 ARG (45.1, 121.9)
[7] 89 LYS (47.7, -95.0)
[7] 91 PRO (-71.1, -69.9)
[8] 26 ALA (68.8, 146.2)
[8] 92 GLU (52.0, -85.0)
[10] 28 VAL (109.1, -60.9)
[11] 22 MET (75.2, 114.9)
[12] 90 ASN (73.4, 140.9)
[13] 4 LYS (72.2, 135.6)
[13] 89 LYS (64.9, -78.9)
[14] 24 THR (75.0, 104.7)
[14] 28 VAL (-99.6, -47.8)
[15] 7 SER (64.9, 104.9)
[15] 89 LYS (172.8, -65.0)
[16] 8 MET (75.0, 115.0)
[16] 25 SER (65.0, 93.3)
[17] 8 MET (-137.8, -50.0)
[17] 24 THR (-175.1, -25.1)
[17] 28 VAL (-101.7, -55.0)
[18] 92 GLU (54.4, -84.9)
[19] 3 PHE (57.5, -83.2)
[19] 4 LYS (84.9, 115.0)
[19] 28 VAL (-114.7, -53.2)
[20] 28 VAL (-101.5, -54.2)
[20] 89 LYS (64.9, -81.2)
[20] 92 GLU (50.3, -85.0)

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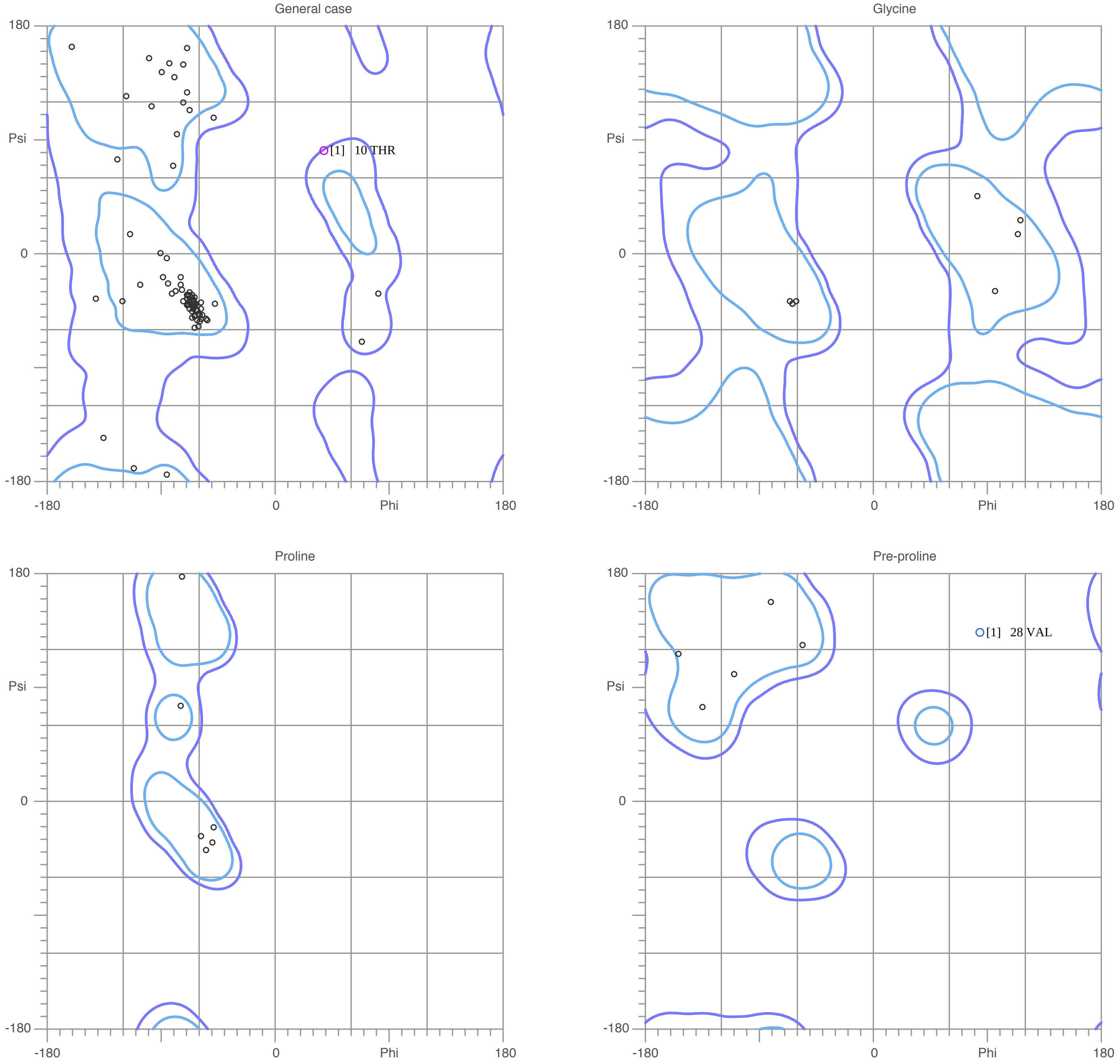
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 1

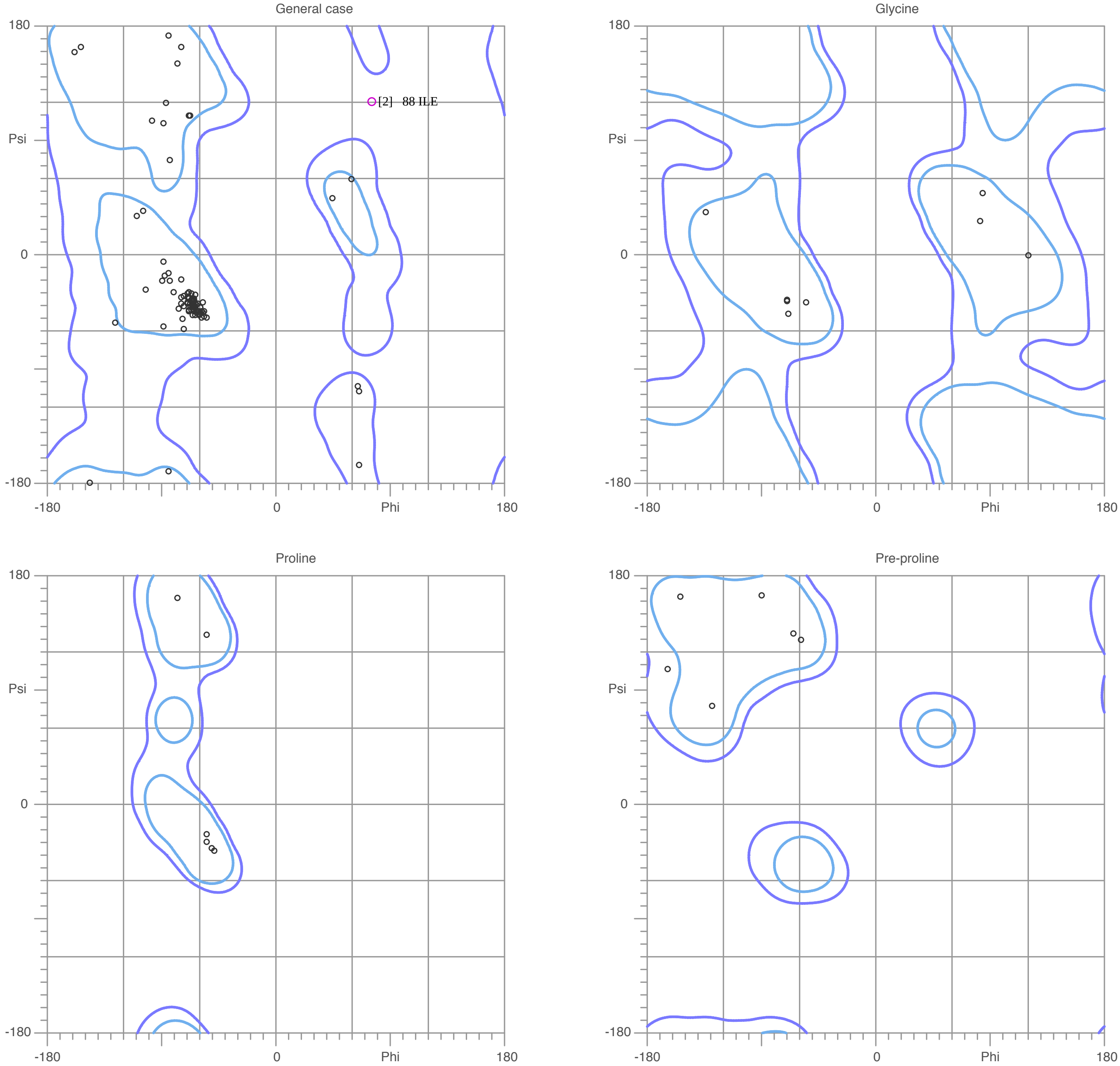


91.6% (98/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[1] 10 THR (38.2, 82.7)
[1] 28 VAL (85.0, 135.0)

MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 2



94.4% (101/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[2] 88 ILE (75.1, 121.6)

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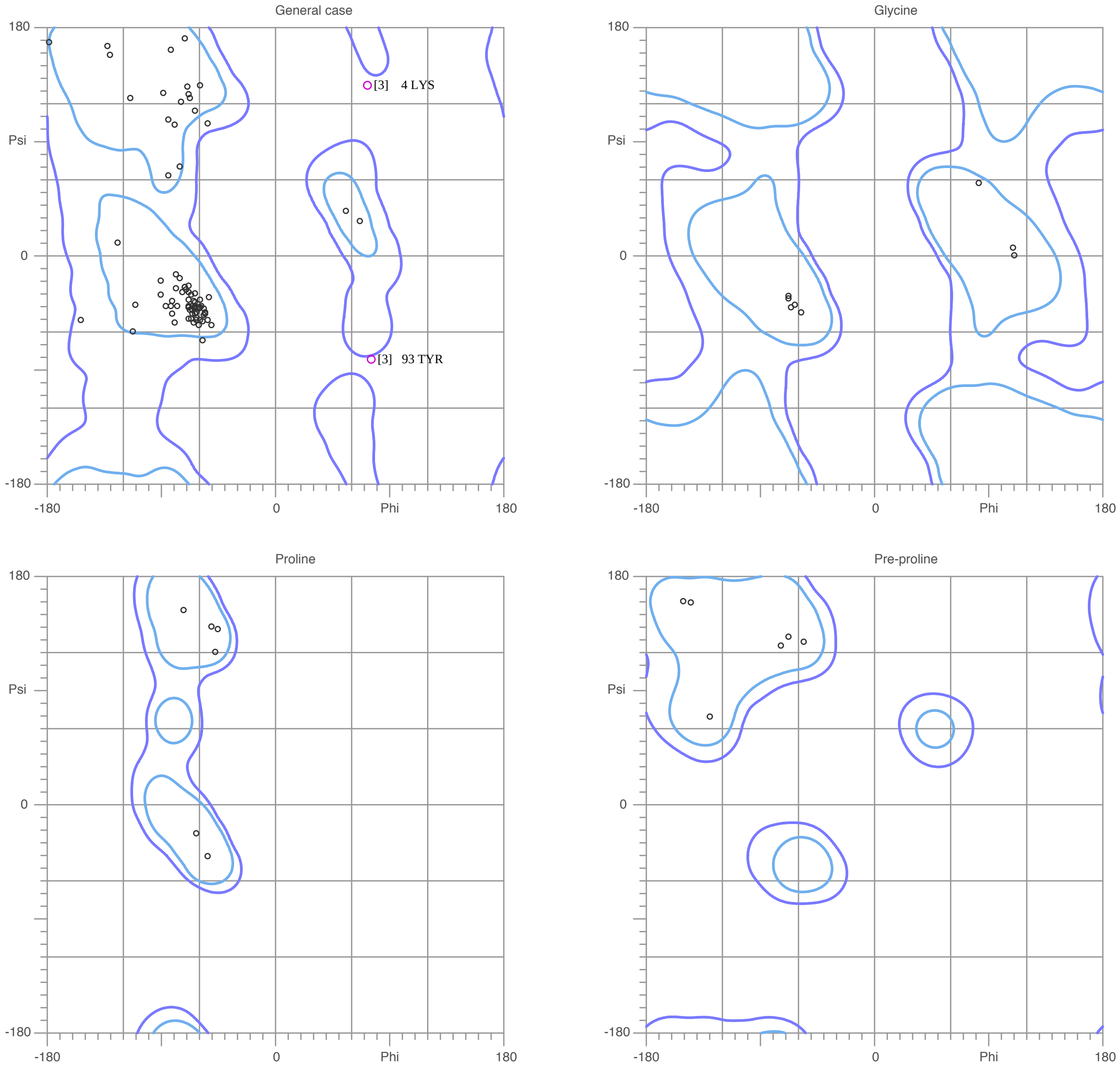
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 3



94.4% (101/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[3] 4 LYS (72.9, 135.4)
[3] 93 TYR (75.0, -81.4)

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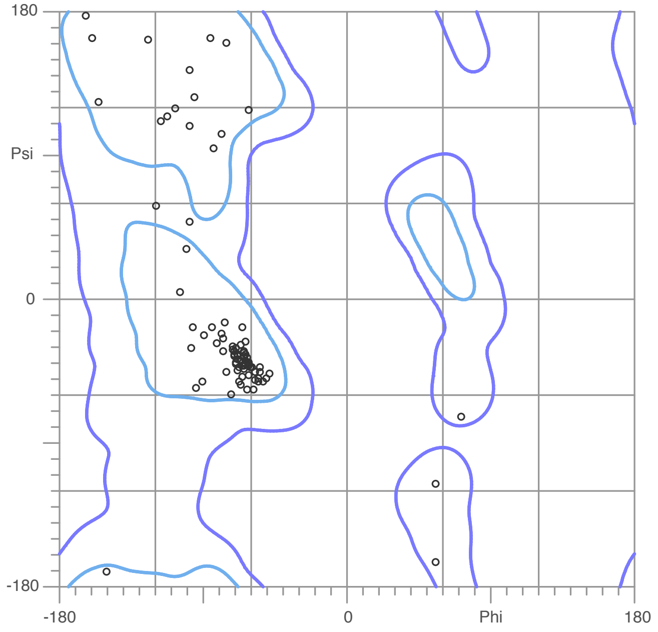
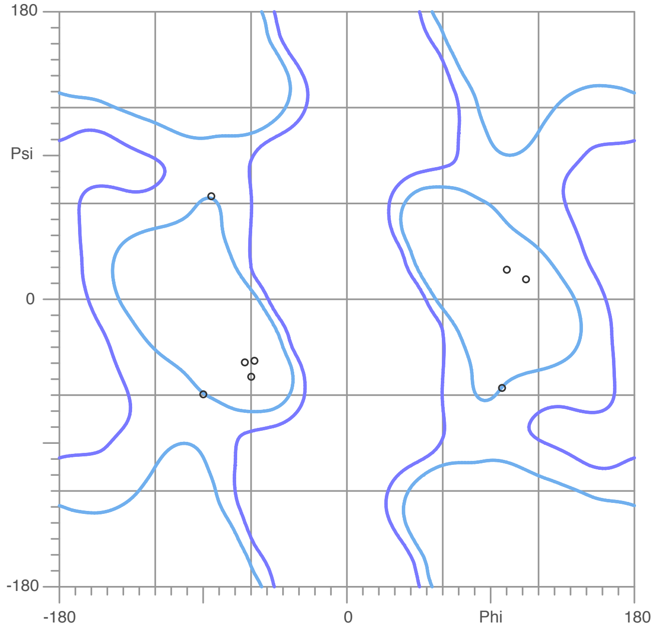
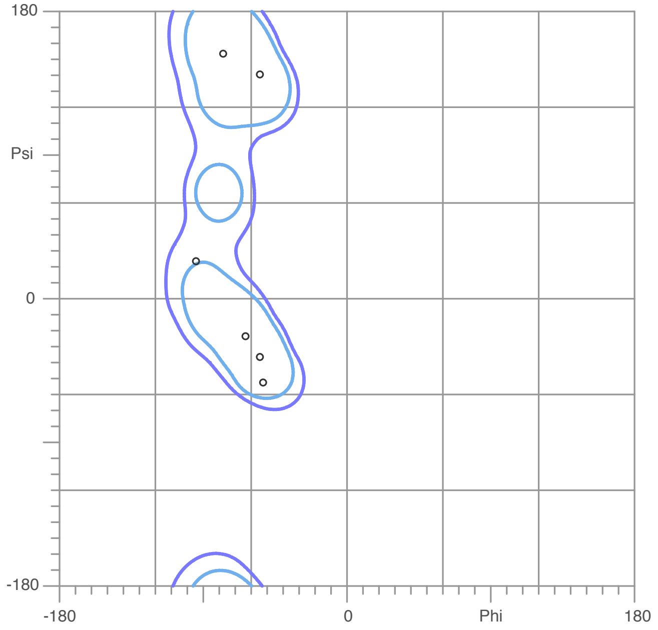
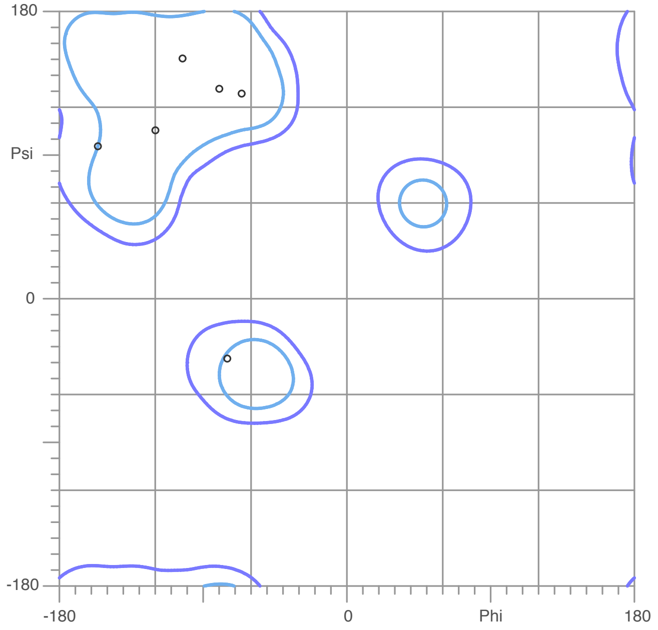
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 4


General case


Glycine


Proline


Pre-proline

90.7% (97/107) of all residues were in favored (98%) regions.
100.0% (107/107) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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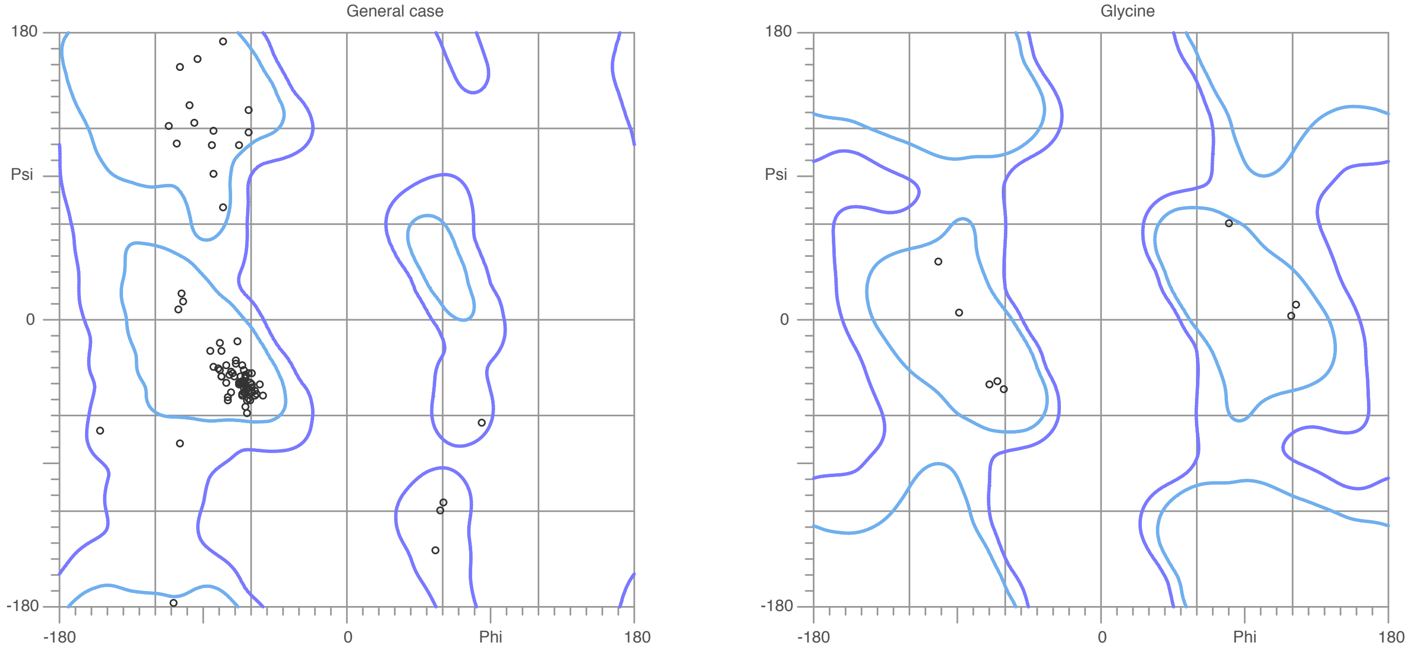
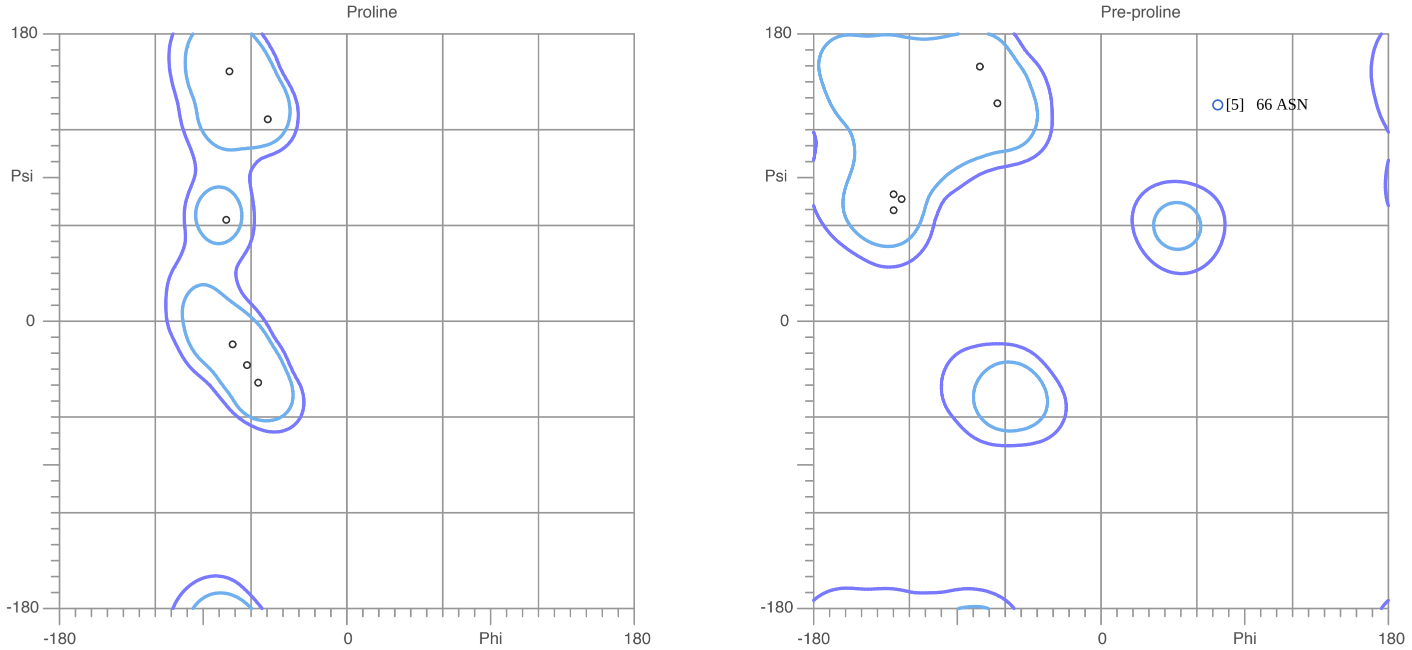
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 5





93.5% (100/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 66 ASN (73.2, 137.0)

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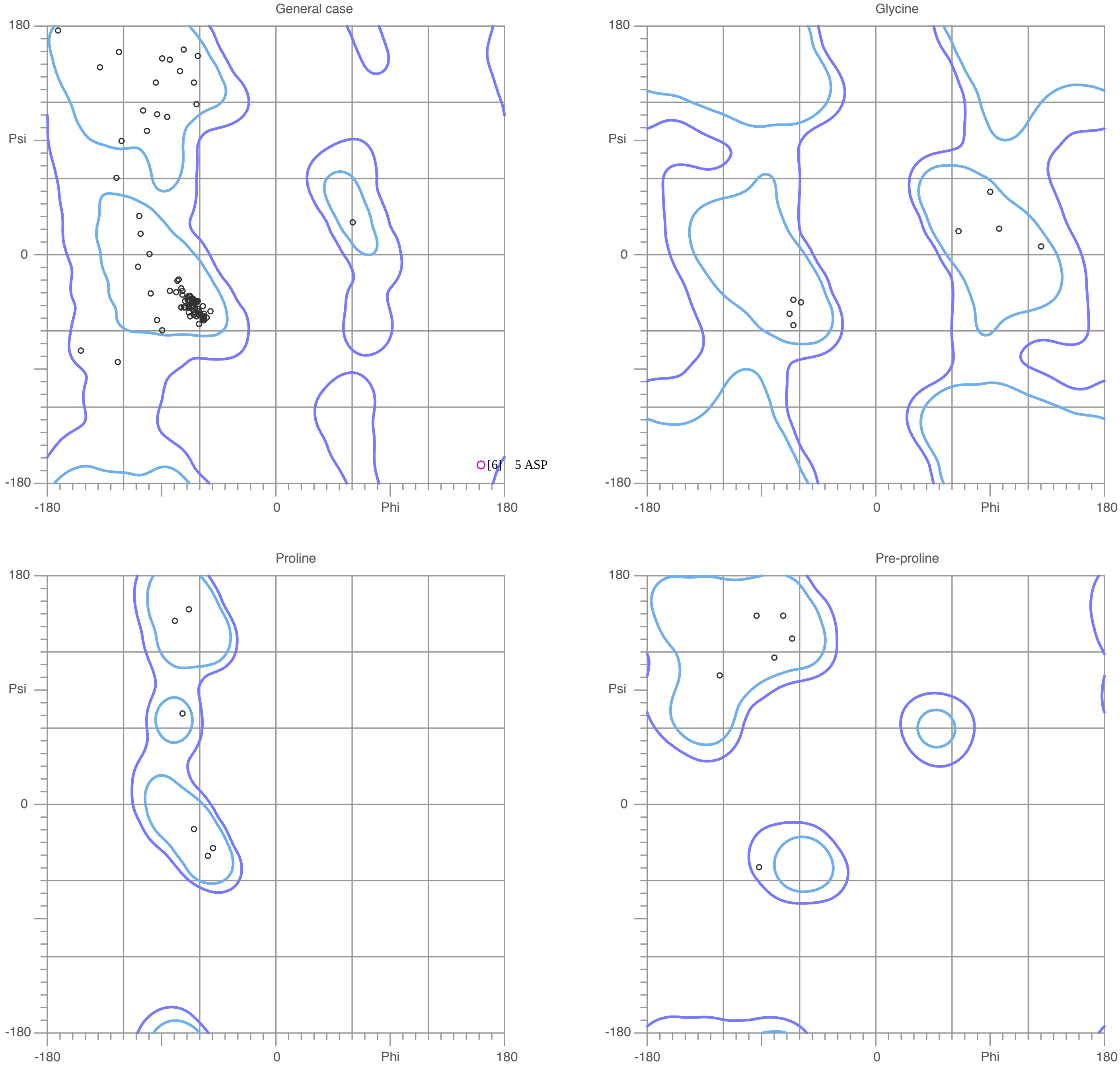
STR65_R3_em_bcr3.pdb, model 6



95.3% (102/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[6] 5 ASP (161.8, -165.0)

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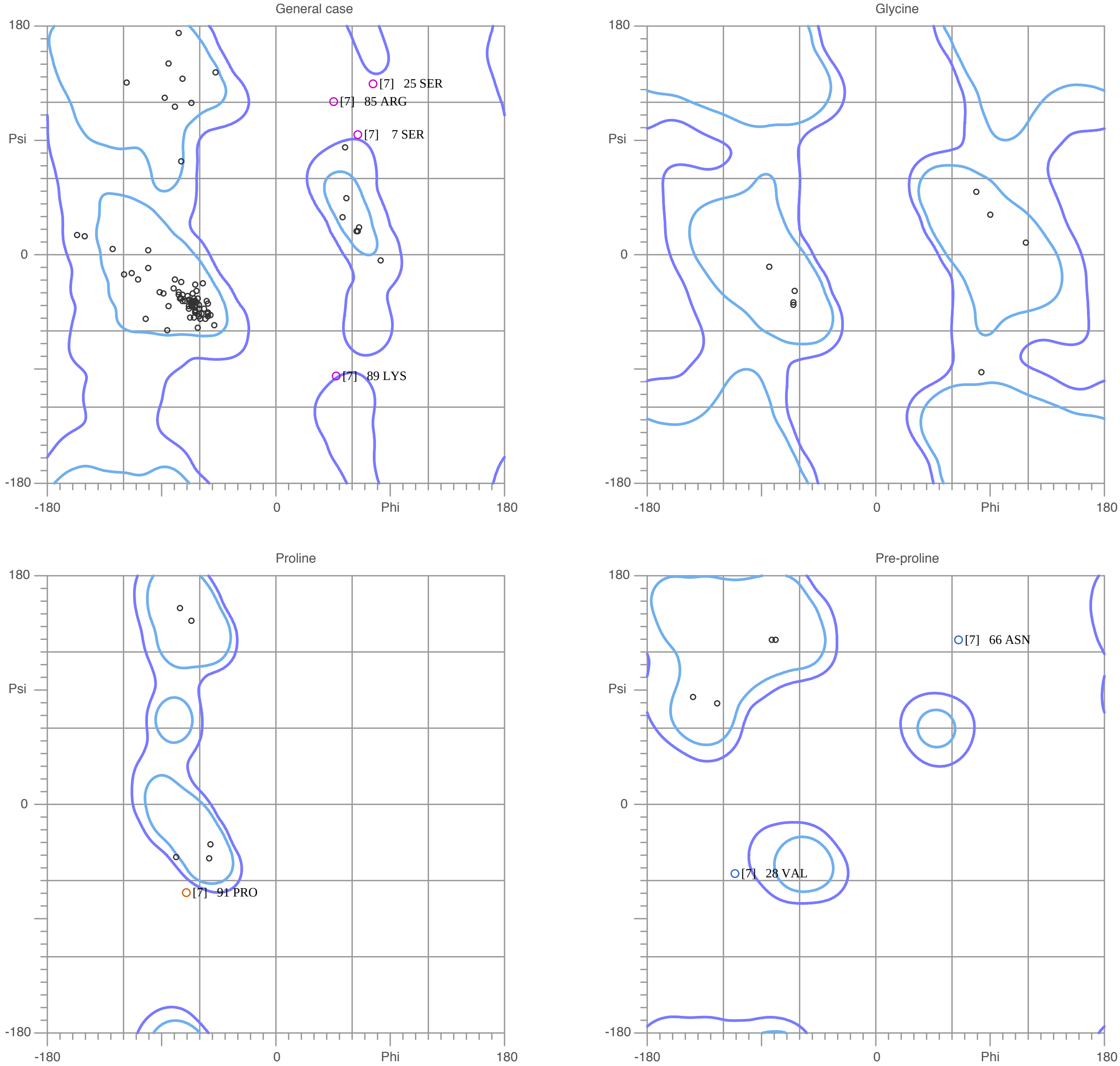
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 7



87.9% (94/107) of all residues were in favored (98%) regions.
93.5% (100/107) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):

[7] 7 SER (64.9, 95.0)
[7] 25 SER (76.1, 135.0)
[7] 28 VAL (-112.0, -54.3)
[7] 66 ASN (65.0, 130.7)
[7] 85 ARG (45.1, 121.9)
[7] 89 LYS (47.7, -95.0)
[7] 91 PRO (-71.1, -69.9)

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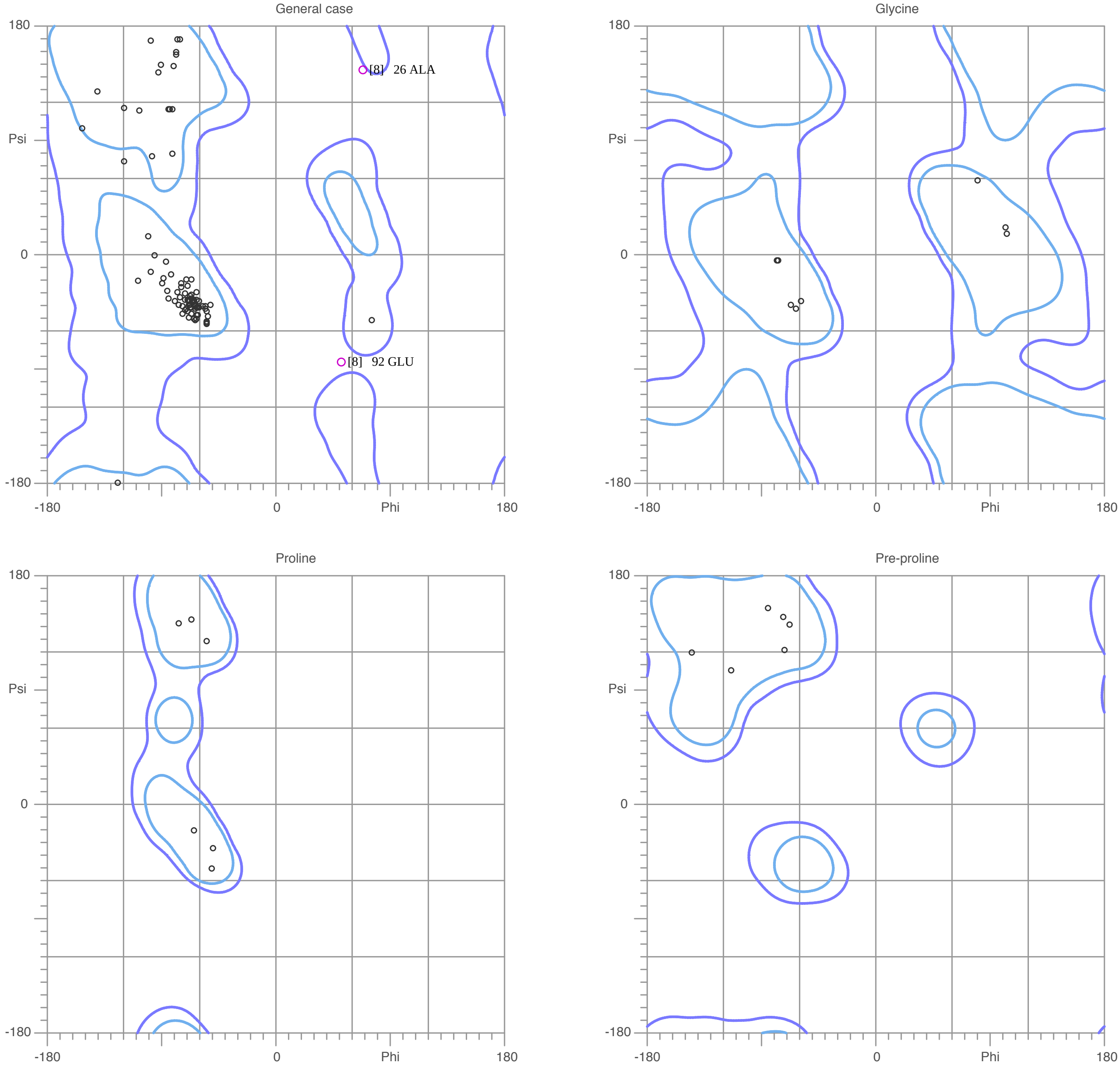
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 8

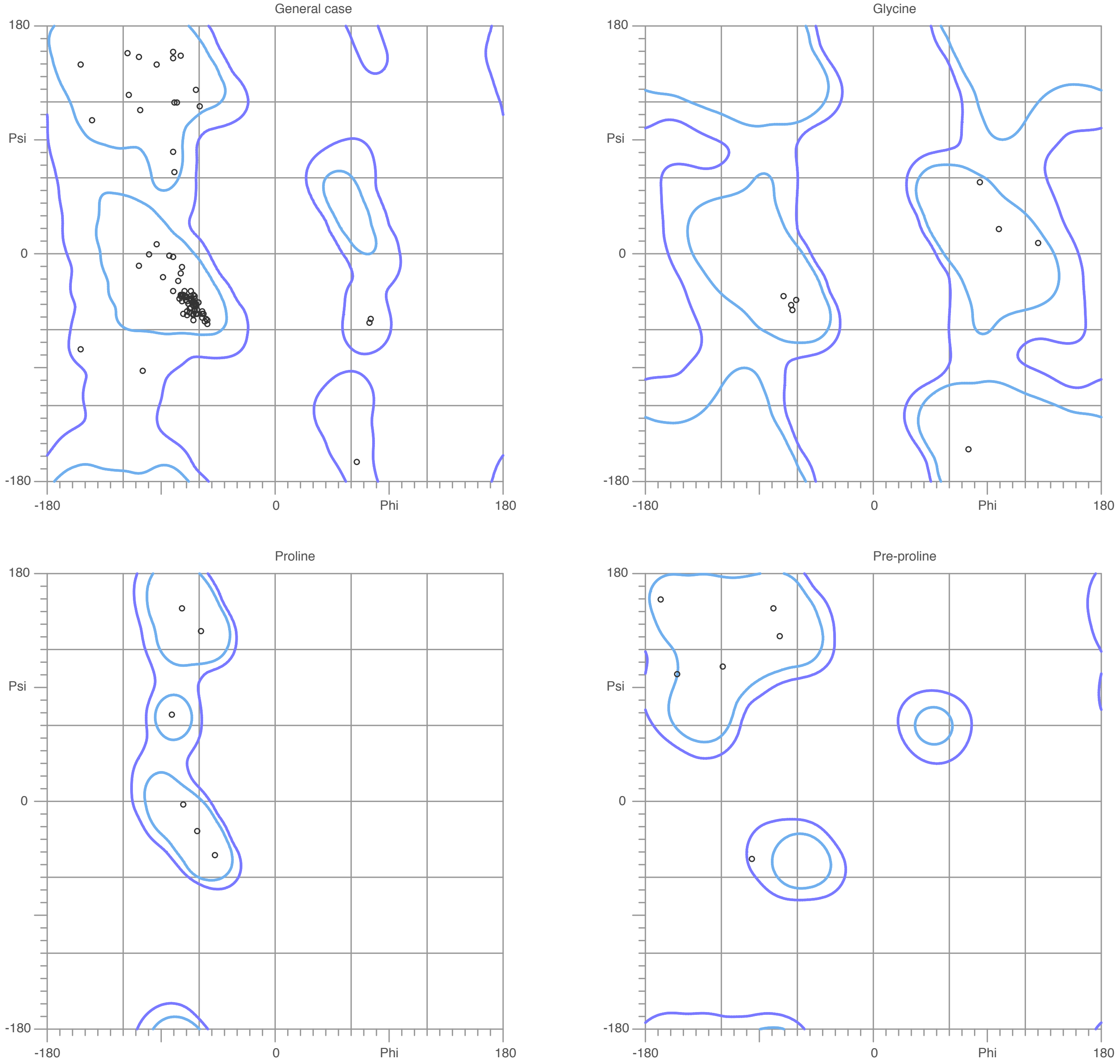


96.3% (103/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[8] 26 ALA (68.8, 146.2)
[8] 92 GLU (52.0, -85.0)

MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 9



93.5% (100/107) of all residues were in favored (98%) regions.
100.0% (107/107) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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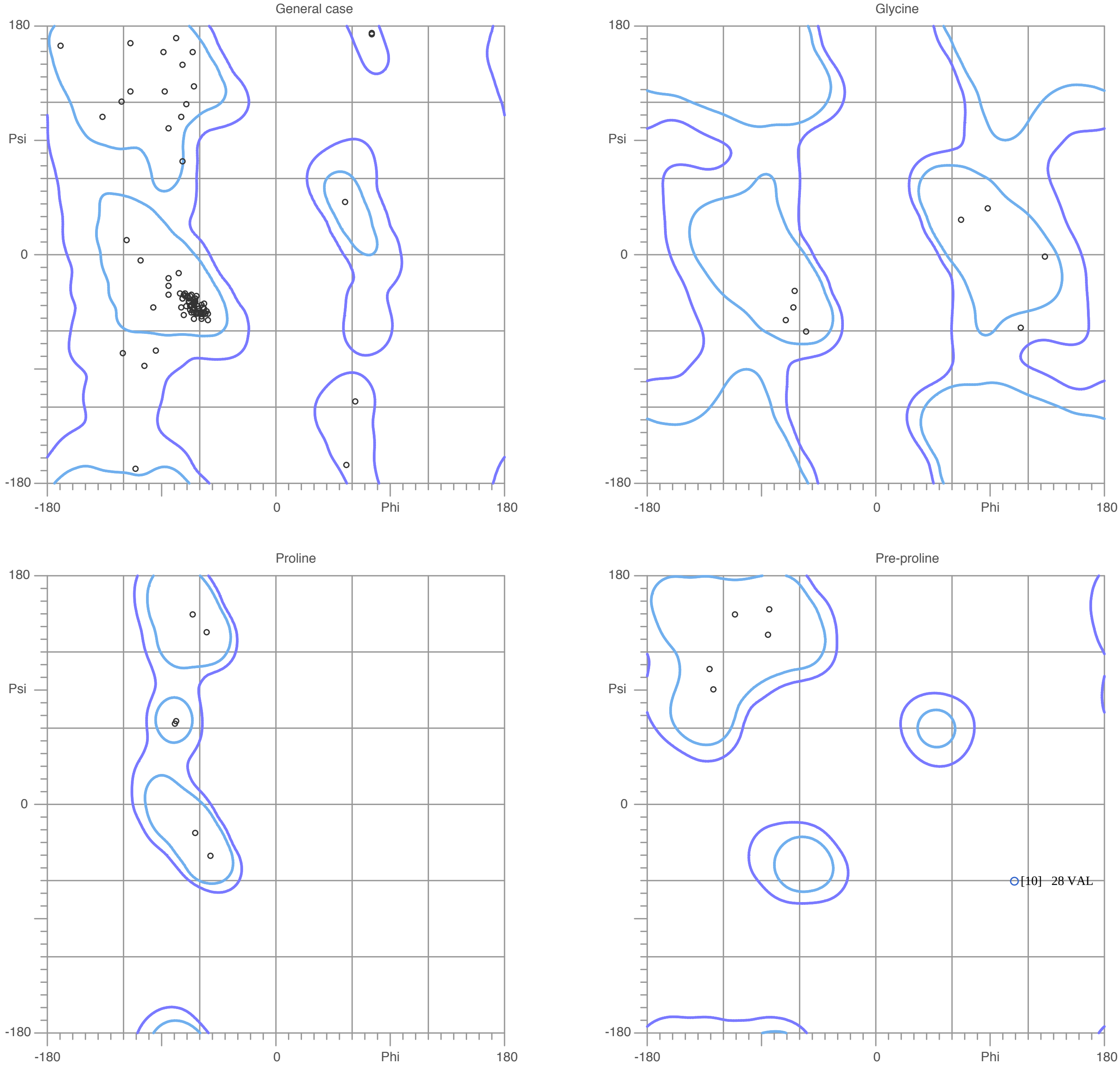
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 10

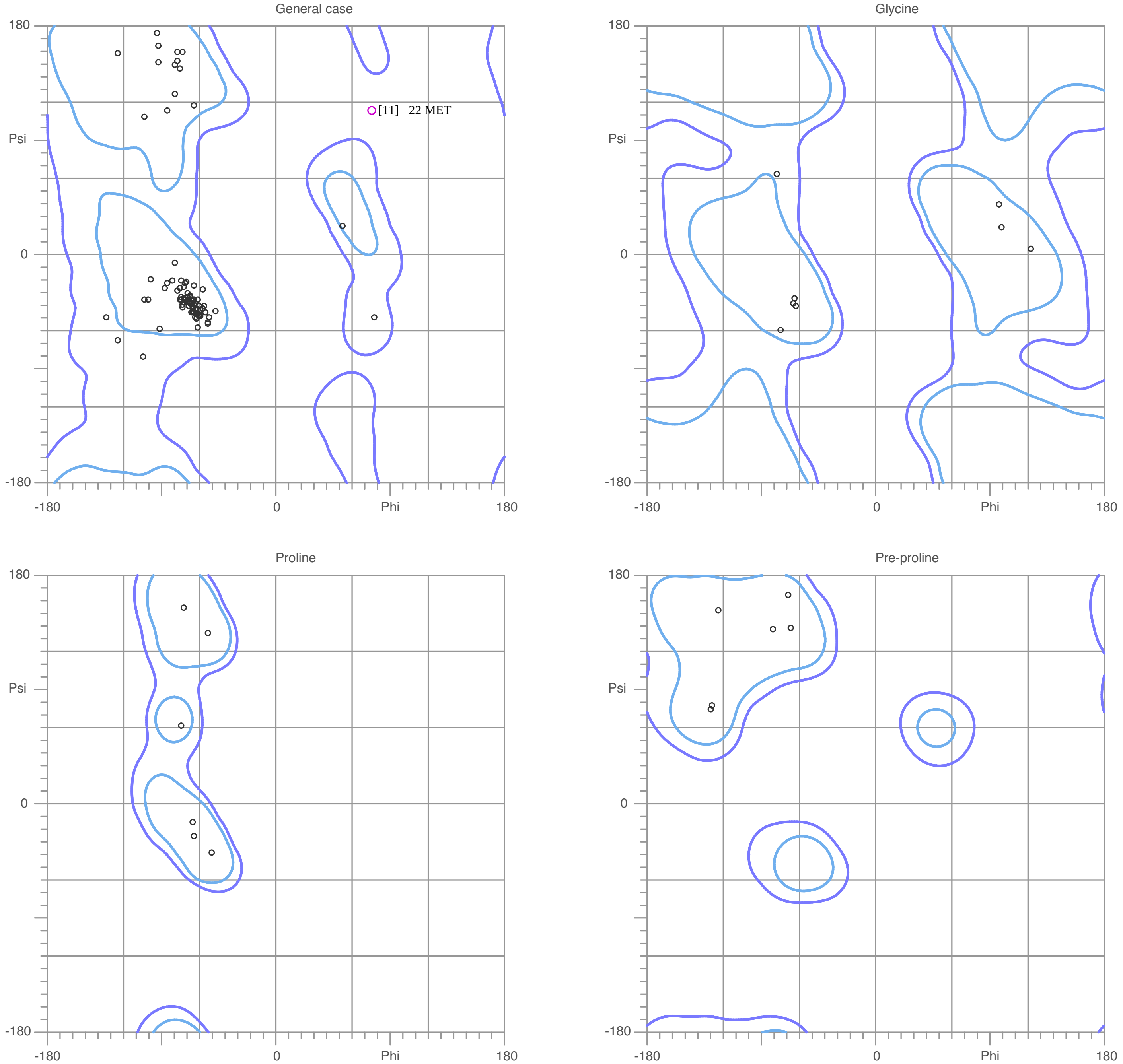


90.7% (97/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[10] 28 VAL (109.1, -60.9)

MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 11



94.4% (101/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[11] 22 MET (75.2, 114.9)

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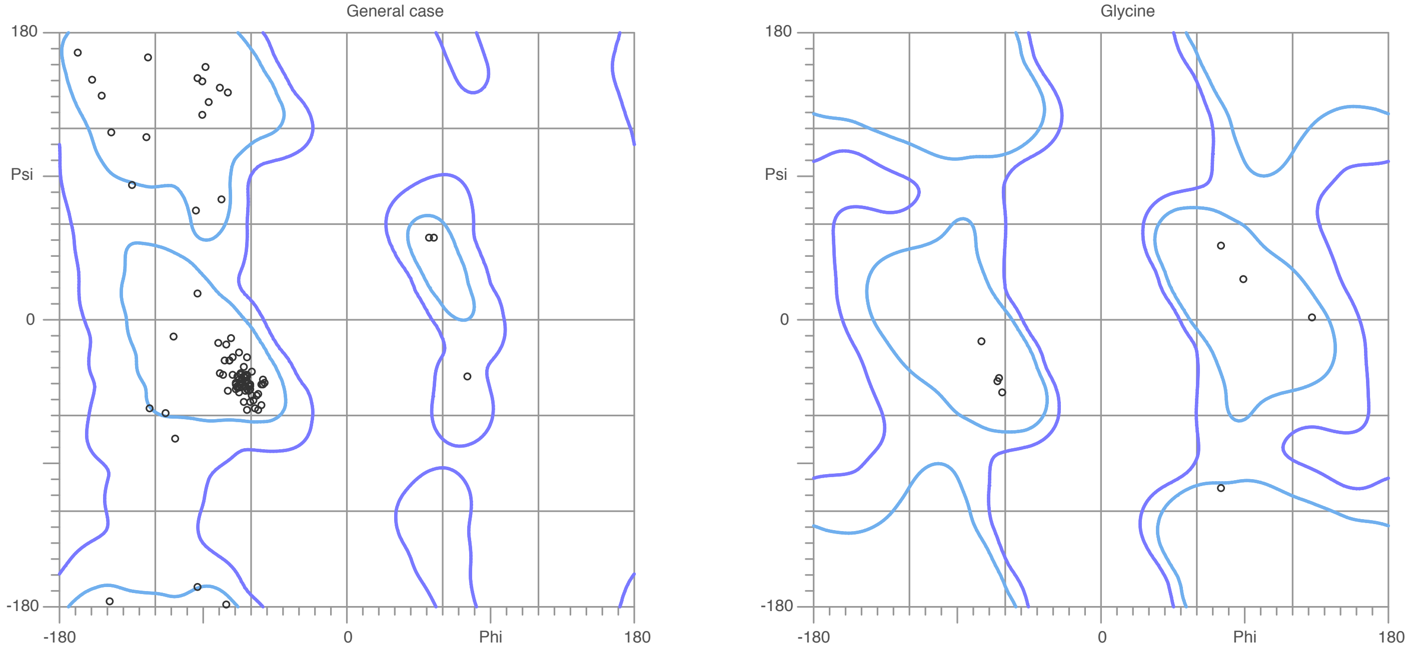
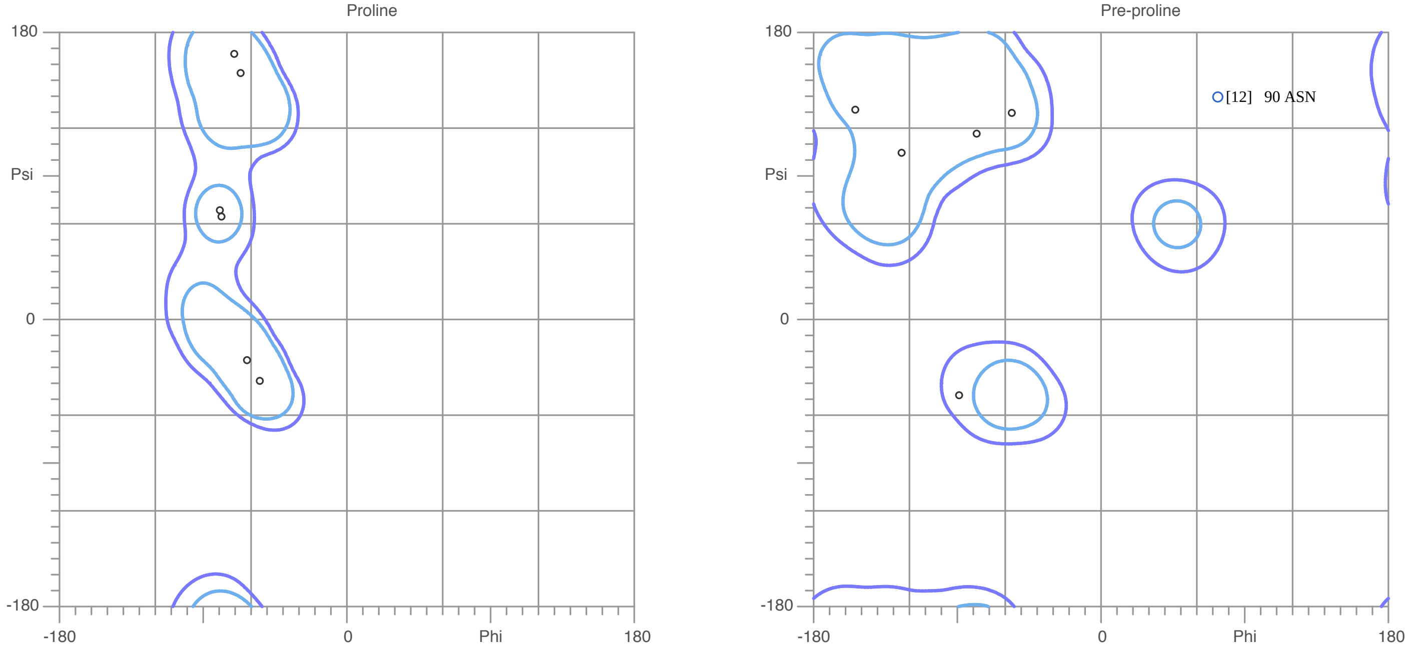
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 12





93.5% (100/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[12]   90 ASN (73.4, 140.9)

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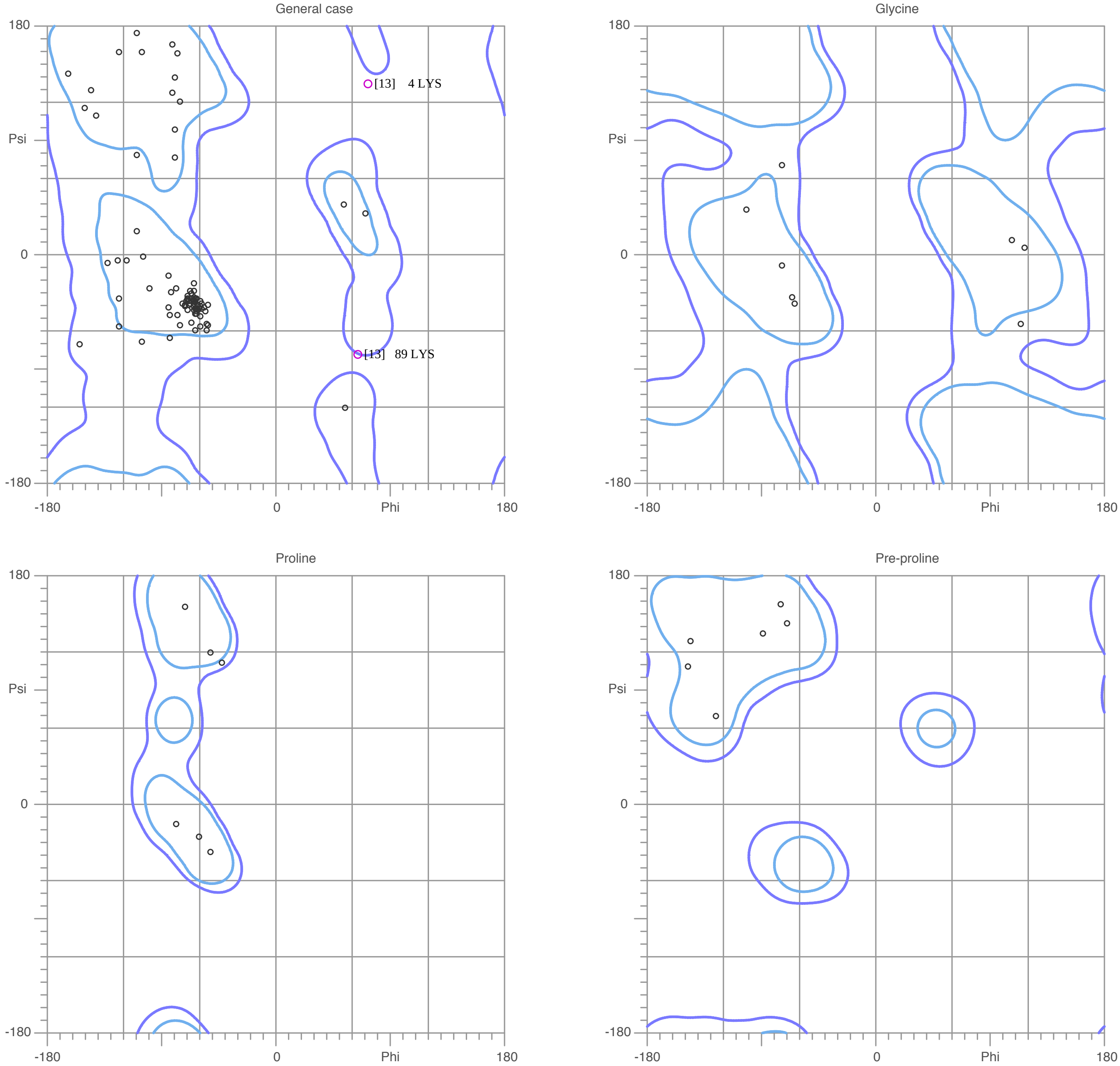
STR65_R3_em_bcr3.pdb, model 13



89.7% (96/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[13] 4 LYS (72.2, 135.6)
[13] 89 LYS (64.9, -78.9)

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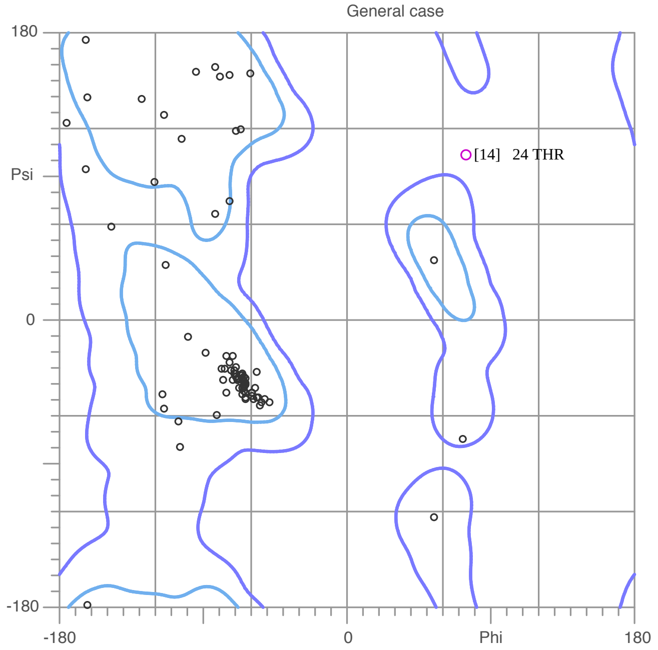
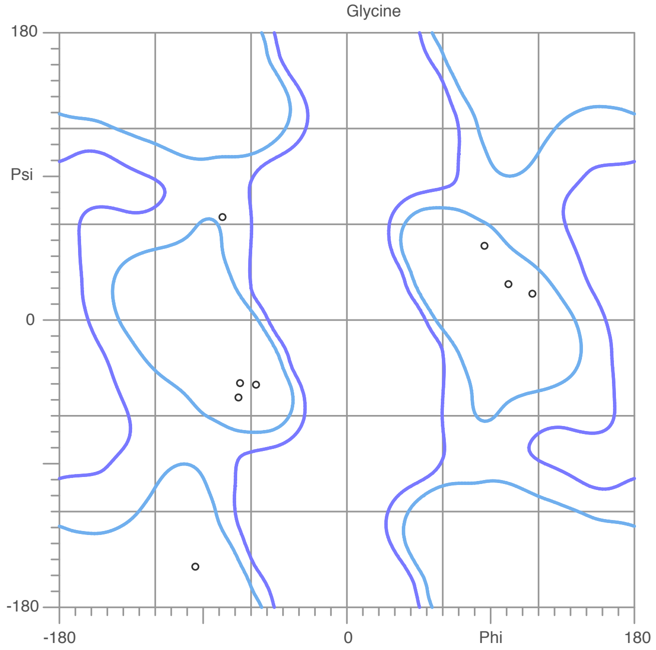
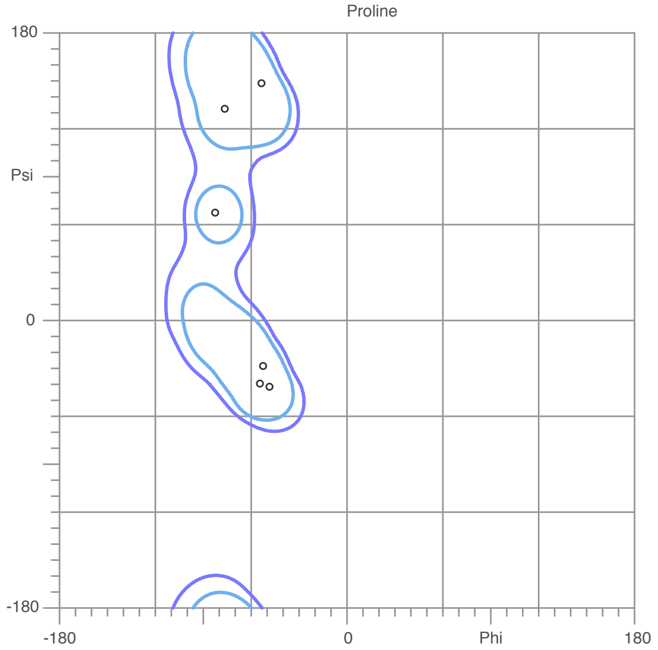
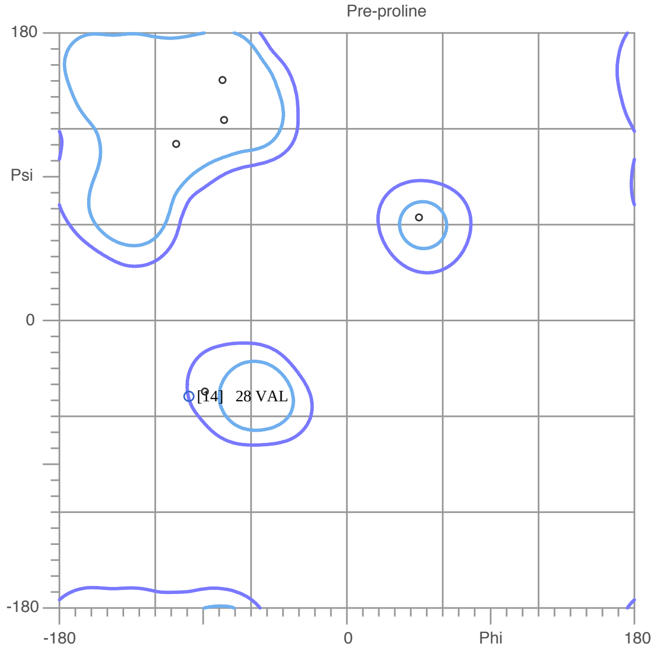
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 14







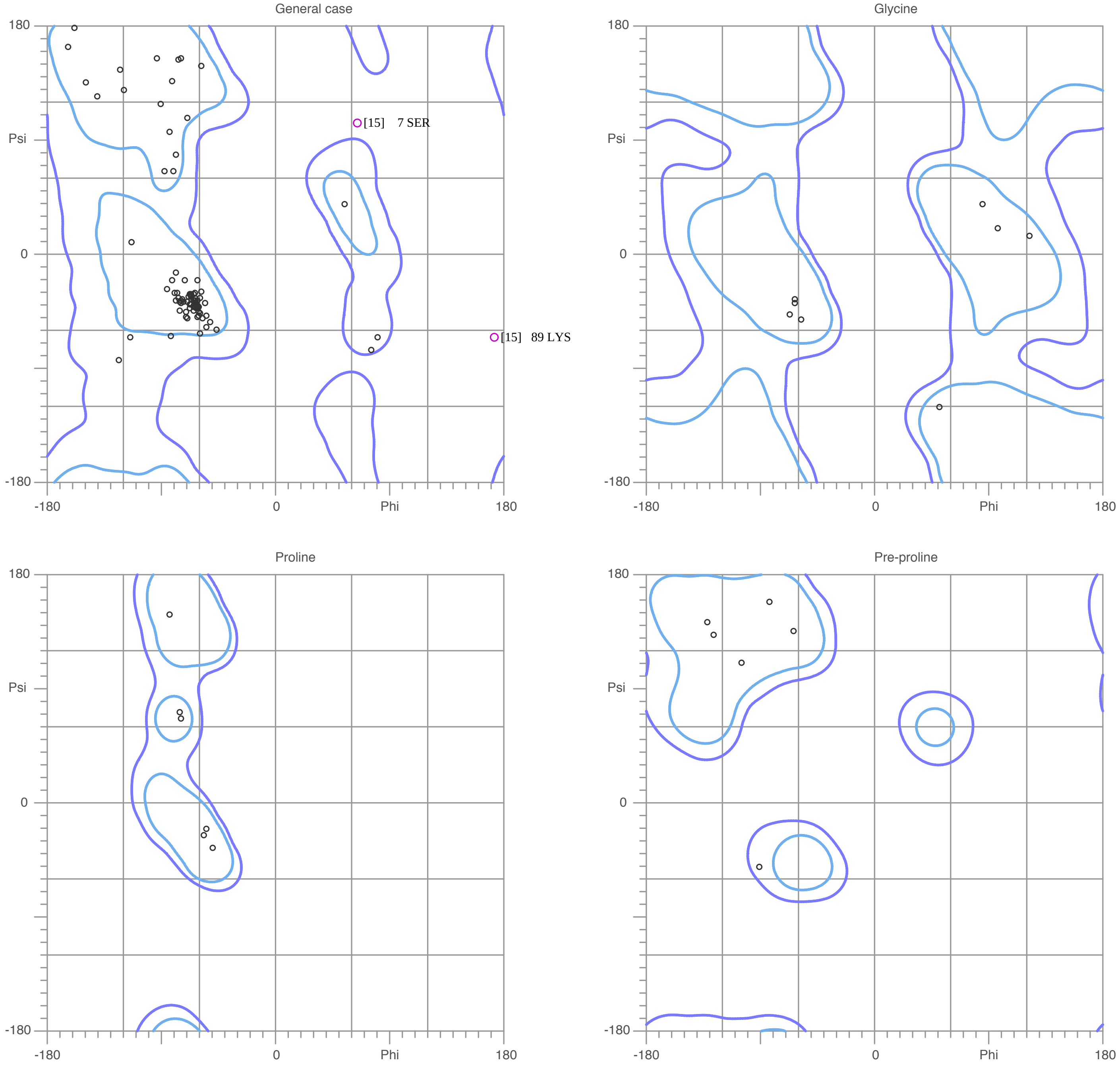


89.7% (96/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[14] 24 THR (75.0, 104.7)
[14] 28 VAL (-99.6, -47.8)

MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 15



92.5% (99/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[15] 7 SER (64.9, 104.9)
[15] 89 LYS (172.8, -65.0)

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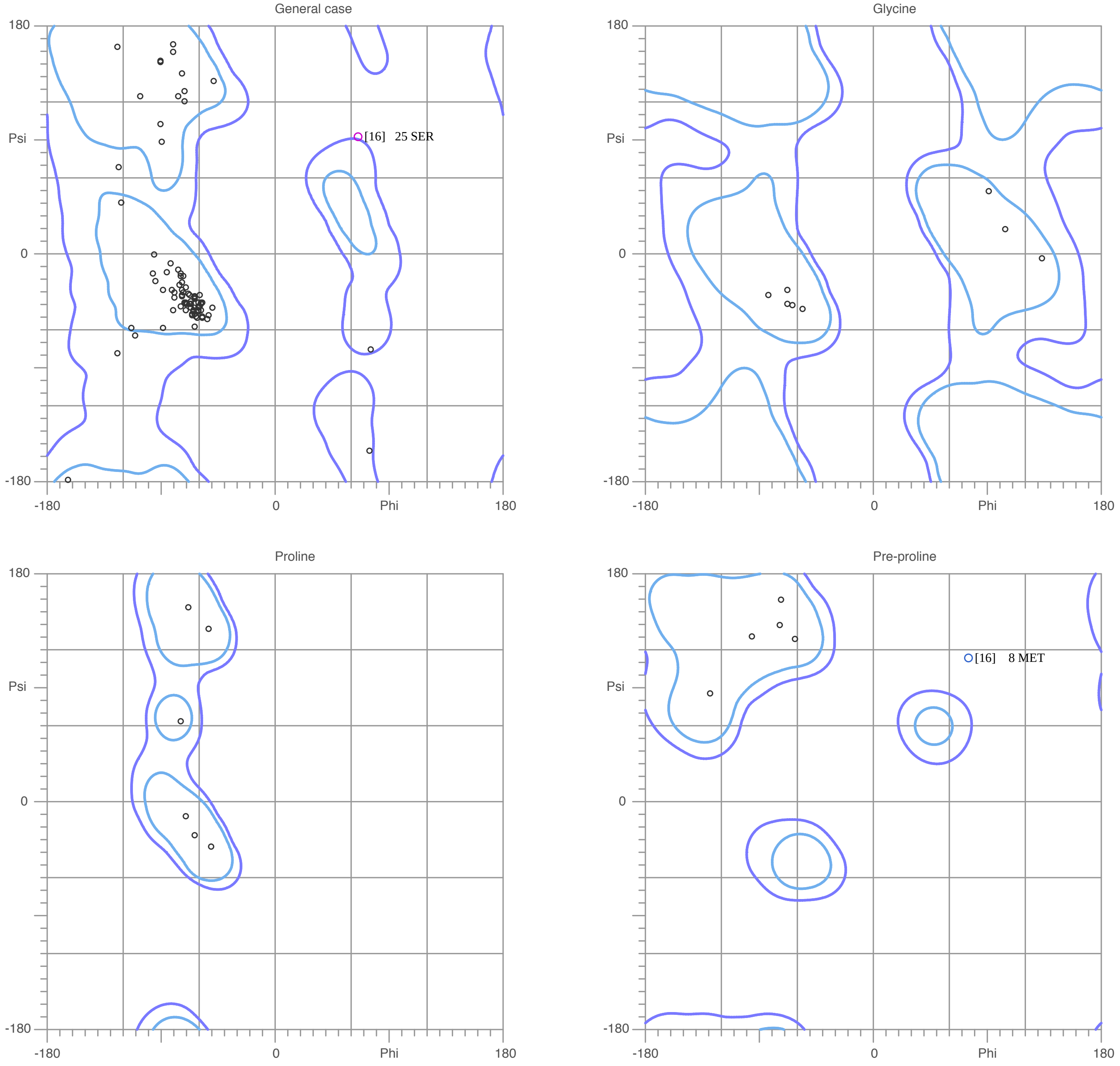
STR65_R3_em_bcr3.pdb, model 16


General case

Glycine

Proline

Pre-proline

93.5% (100/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[16] 8 MET (75.0, 115.0)
[16] 25 SER (65.0, 93.3)

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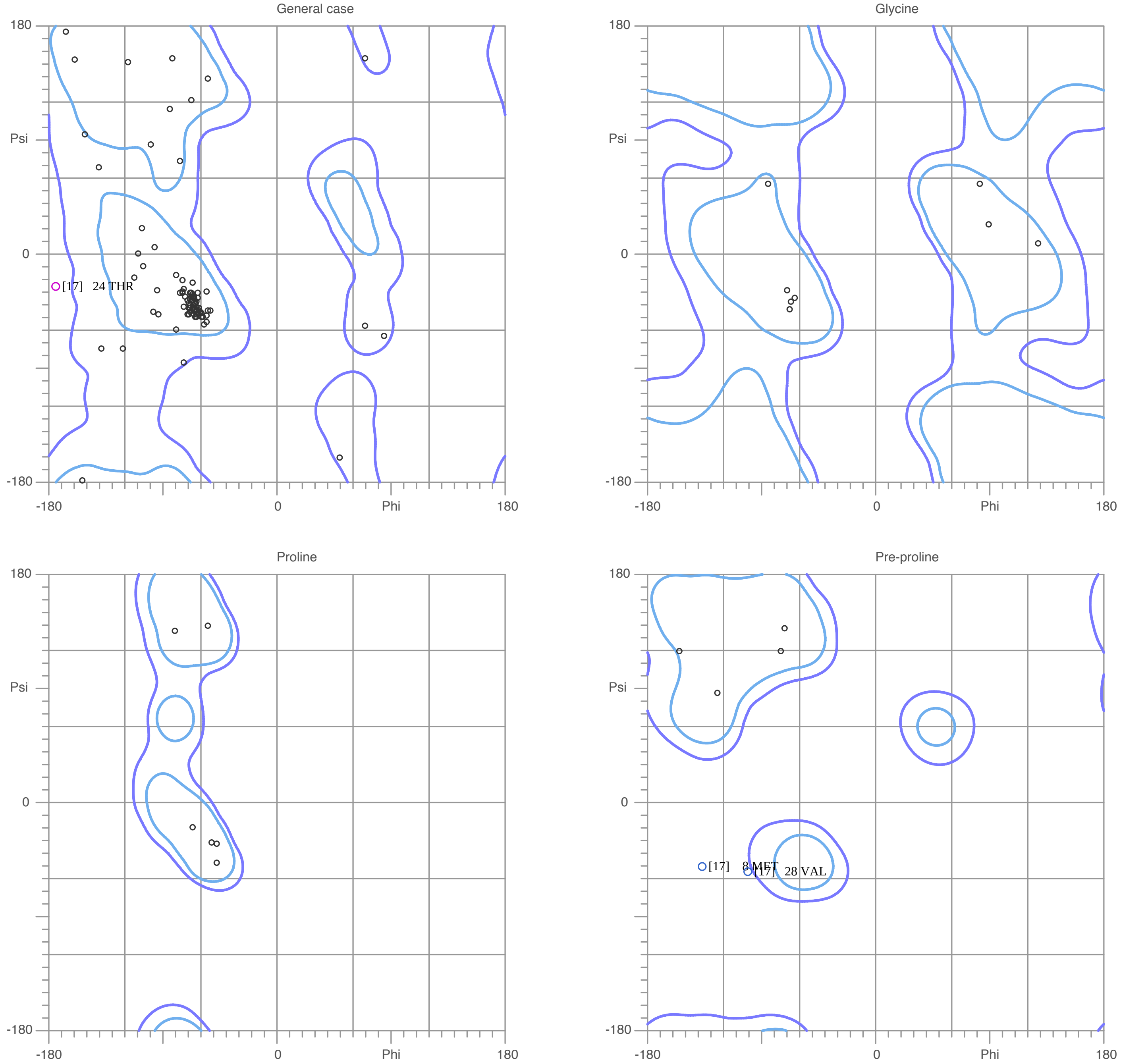
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 17



88.8% (95/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[17] 8 MET (-137.8, -50.0)
[17] 24 THR (-175.1, -25.1)
[17] 28 VAL (-101.7, -55.0)

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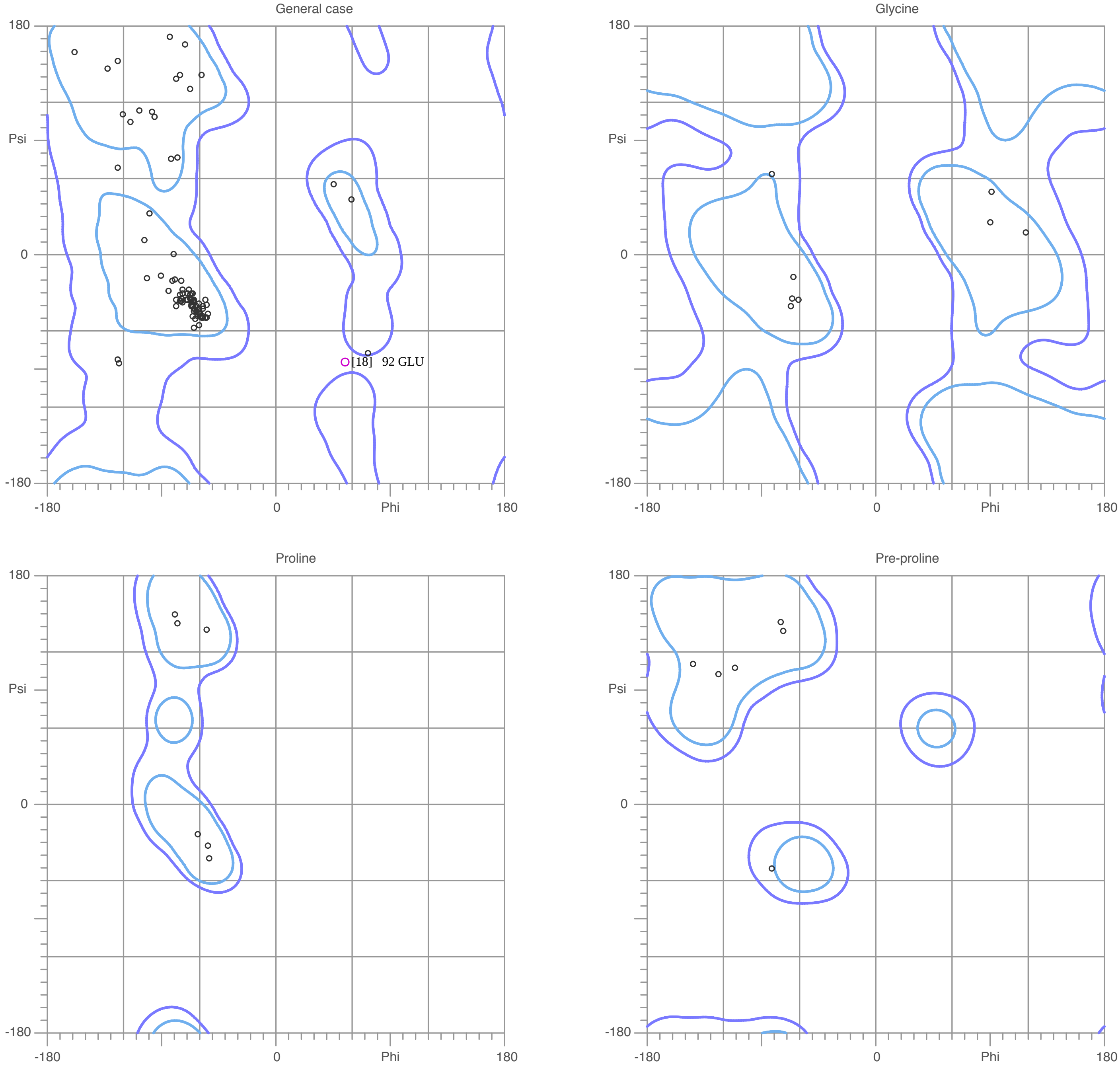
STR65_R3_em_bcr3.pdb, model 18

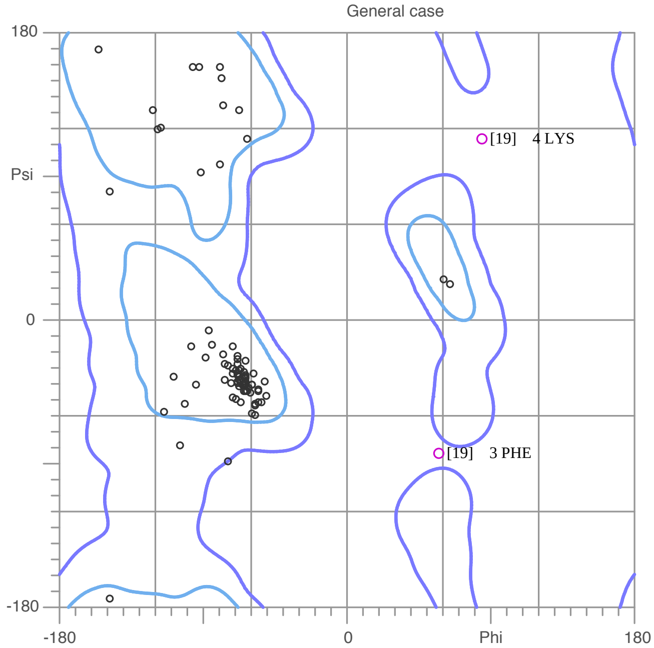


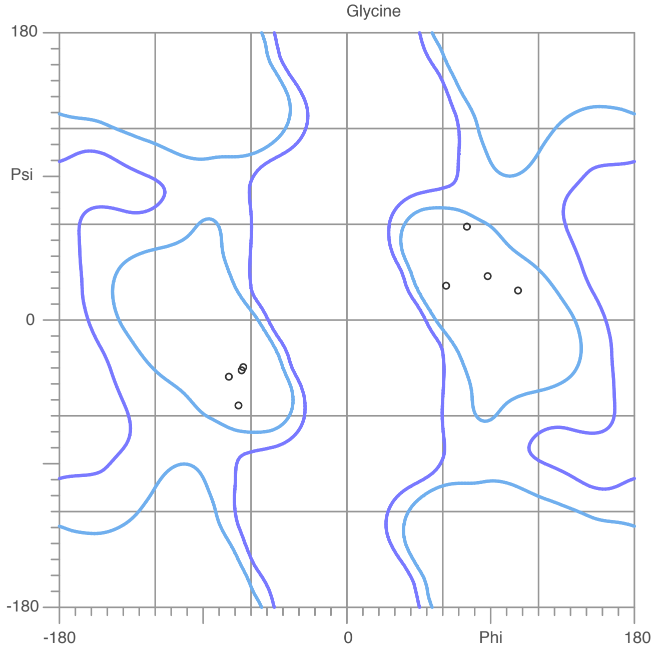
93.5% (100/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

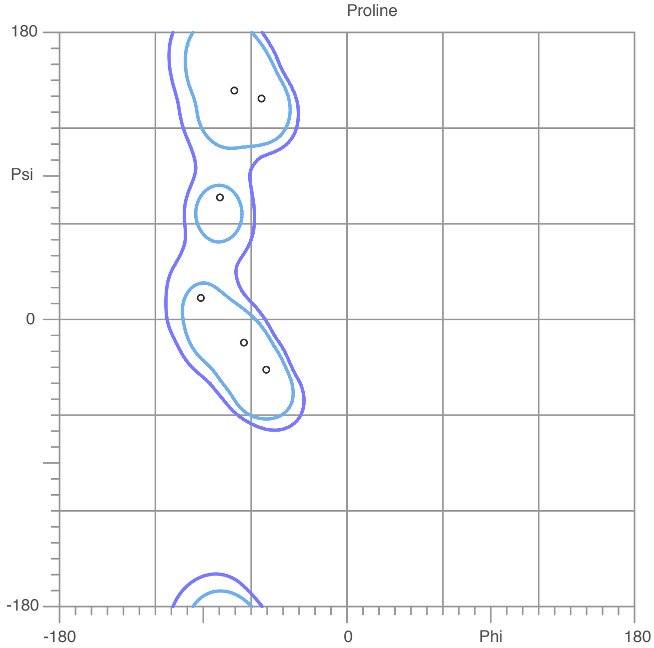
There were 1 outliers (phi, psi):
[18] 92 GLU (54.4, -84.9)

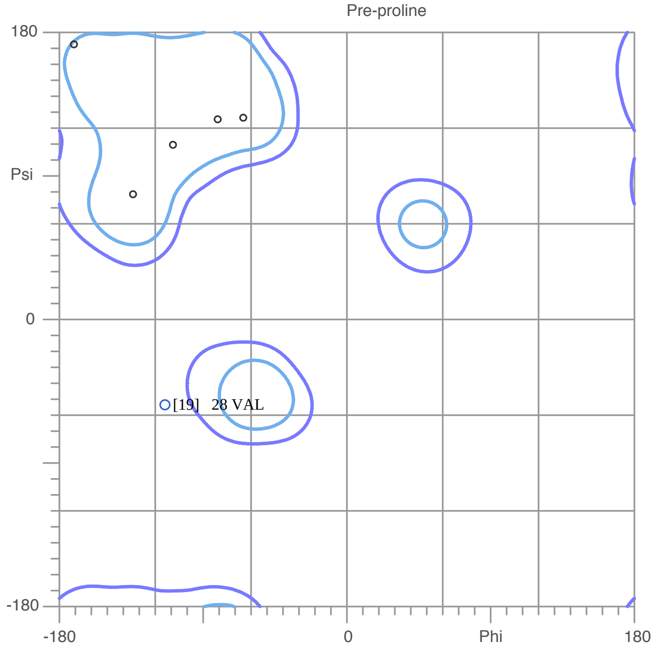
MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 19


General case


Glycine


Proline

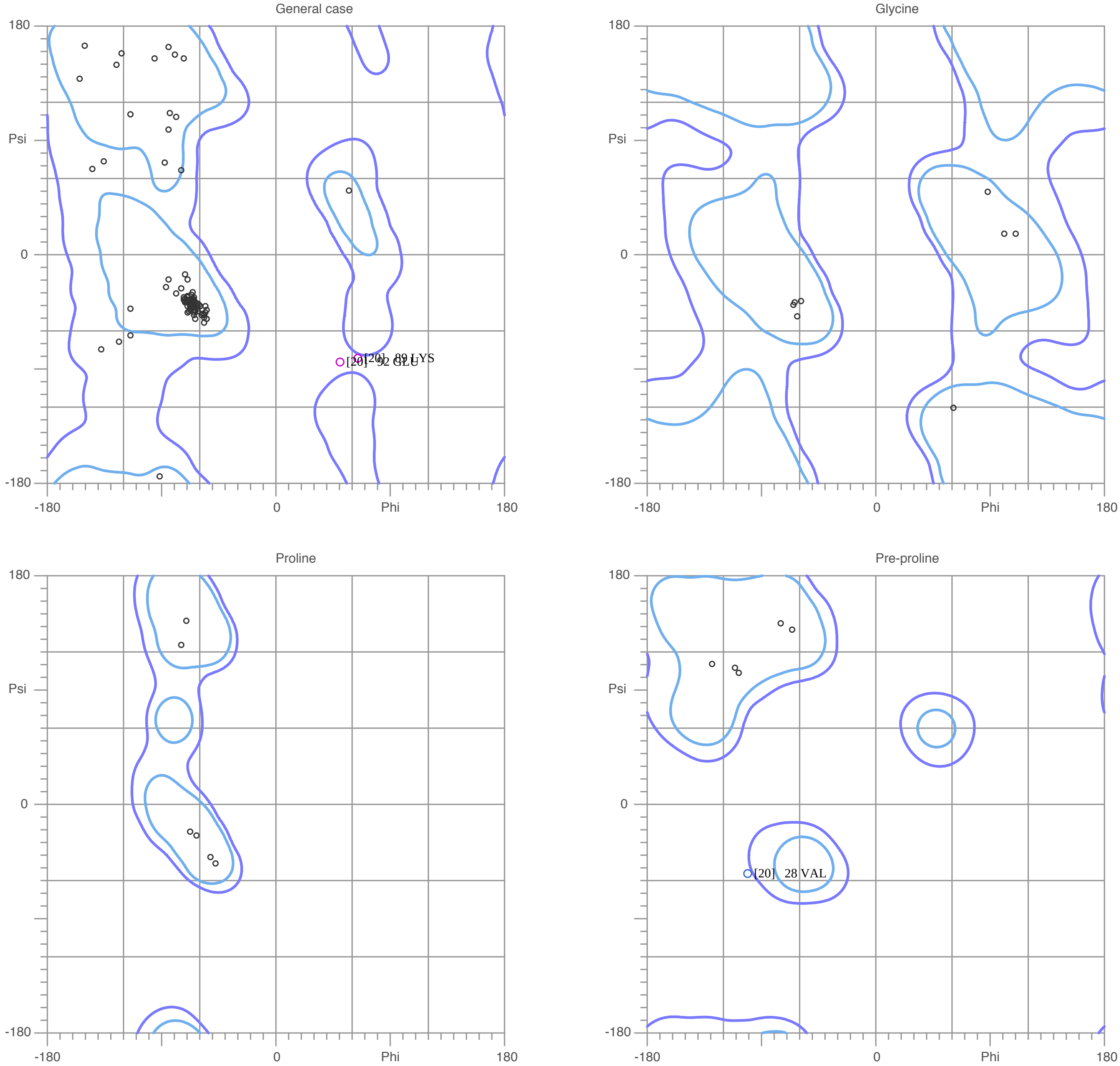

Pre-proline

94.4% (101/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[19] 3 PHE (57.5, -83.2)
[19] 4 LYS (84.9, 115.0)
[19] 28 VAL (-114.7, -53.2)

MolProbity Ramachandran analysis

STR65_R3_em_bcr3.pdb, model 20



92.5% (99/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):
[20] 28 VAL (-101.5, -54.2)
[20] 89 LYS (64.9, -81.2)
[20] 92 GLU (50.3, -85.0)

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