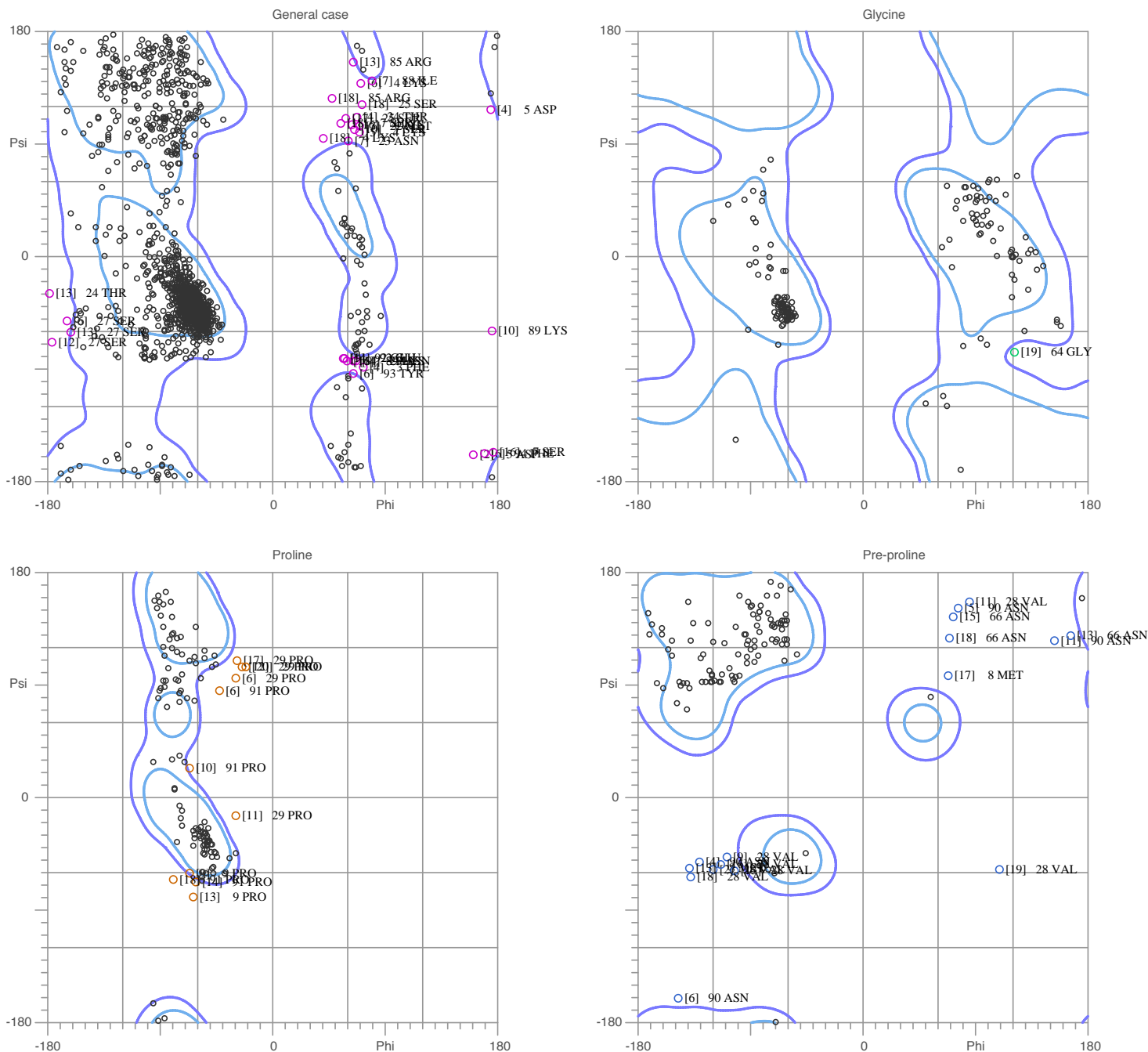


MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, all models



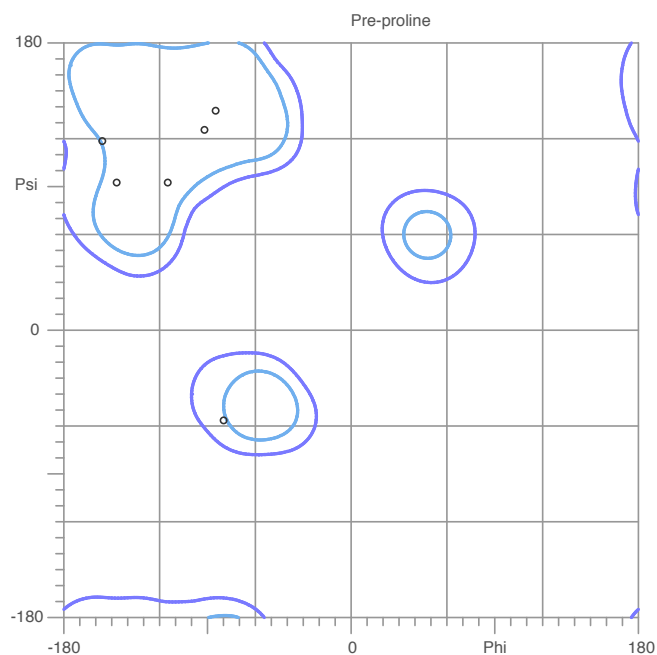
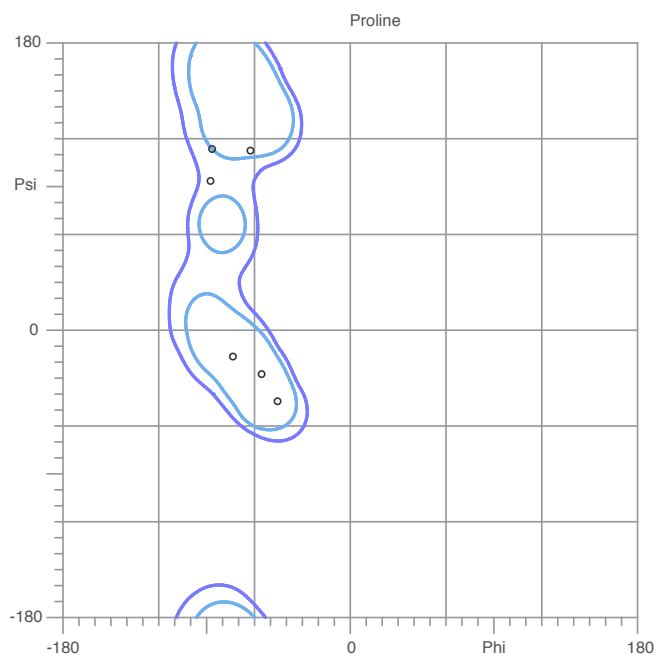
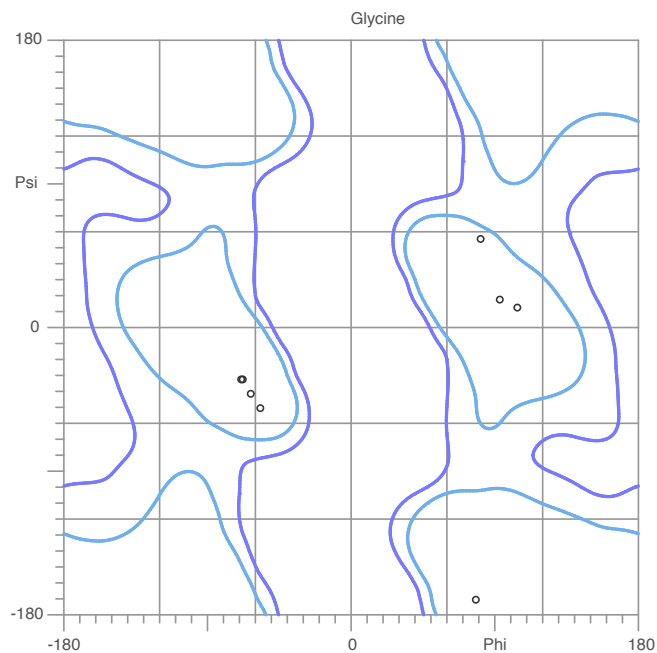
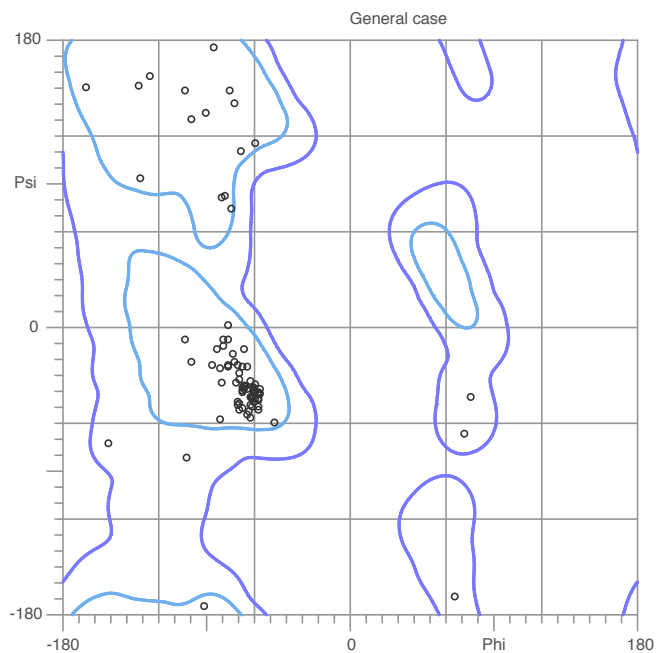
87.0% (1862/2140) of all residues were in favored (98%) regions.
97.3% (2082/2140) of all residues were in allowed (>99.8%) regions.

There were 58 outliers (phi, psi):

- | | | | |
|------|-------------------------|-------|------------------------|
| [12] | 5 ASP (160.0, -158.5) | [111] | 90 ASN (153.9, 126.4) |
| [13] | 28 VAL (-129.8, -58.0) | [112] | 27 SER (177.4, -68.5) |
| [14] | 22 MET (69.4, 105.1) | [121] | 29 PRO (-25.7, 105.4) |
| [15] | 3 PHE (72.4, 88.5) | [131] | 8 MET (-139.8, -56.7) |
| [16] | 5 ASP (174.6, 118.3) | [141] | 9 PRO (44.0, -79.4) |
| [17] | 24 THR (-179.1, -30.0) | [151] | 24 THR (-162.2, -60.9) |
| [18] | 23 ASN (67.3, 112.3) | [161] | 27 SER (-162.2, -60.9) |
| [19] | 90 ASN (-131.5, -51.3) | [171] | 66 ASN (166.2, 130.8) |
| [20] | 4 LYS (70.0, 100.2) | [181] | 85 ARG (64.5, 156.6) |
| [21] | 29 PRO (-30.2, 96.3) | [191] | 23 ASN (64.3, 83.2) |
| [22] | 90 ASN (-148.4, -160.3) | [201] | 91 PRO (-62.9, -67.9) |
| [23] | 91 PRO (-43.4, 86.7) | [211] | 92 GLU (56.4, -81.2) |
| [24] | 91 THR (64.6, -93.0) | [221] | 66 ASN (72.9, 145.1) |
| [25] | 94 PHE (169.9, -157.1) | [231] | 3 PHE (59.7, -83.3) |
| [26] | 23 ASN (60.5, 93.7) | [241] | 4 LYS (63.2, 106.2) |
| [27] | 88 ILE (79.3, 141.0) | [251] | 7 SER (176.4, -156.5) |
| [28] | 9 PRO (-67.8, -60.8) | [261] | 28 VAL (-114.6, -53.5) |
| [29] | 28 VAL (-109.2, -47.9) | [271] | 8 MET (86.6, 96.4) |
| [30] | 89 LYS (66.1, -83.5) | [281] | 25 SER (58.2, 111.8) |
| [31] | 29 PRO (-30.2, 96.3) | [291] | 29 PRO (-29.8, 110.3) |
| [32] | 92 GLU (57.2, -81.4) | [301] | 4 LYS (40.9, 95.3) |
| [33] | 7 SER (65.7, 102.5) | [311] | 7 SER (54.2, 107.6) |
| [34] | 89 LYS (175.7, -59.5) | [321] | 25 SER (71.2, 122.5) |
| [35] | 91 PRO (-67.8, -24.2) | [331] | 28 VAL (-138.6, -63.1) |
| [36] | 28 VAL (85.0, 157.9) | [341] | 66 ASN (69.6, 129.0) |
| [37] | 29 PRO (-30.5, -14.5) | [351] | 85 ARG (47.9, 127.7) |
| | | [361] | 91 PRO (-80.7, -65.1) |
| | | [371] | 28 VAL (-109.1, -57.1) |
| | | [381] | 64 GLY (121.8, -77.0) |
| | | [391] | 29 PRO (-22.3, 105.3) |

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 1



92.5% (99/107) of all residues were in favored (98%) regions.
100.0% (107/107) of all residues were in allowed (>99.8%) regions.

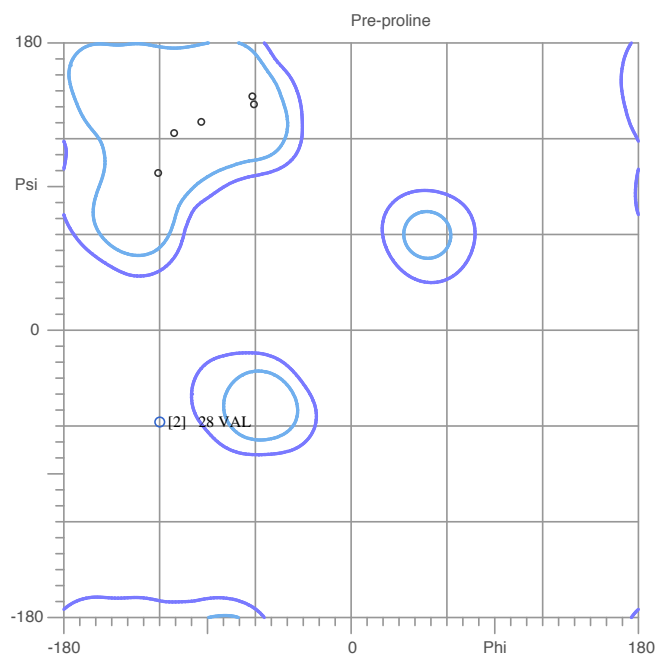
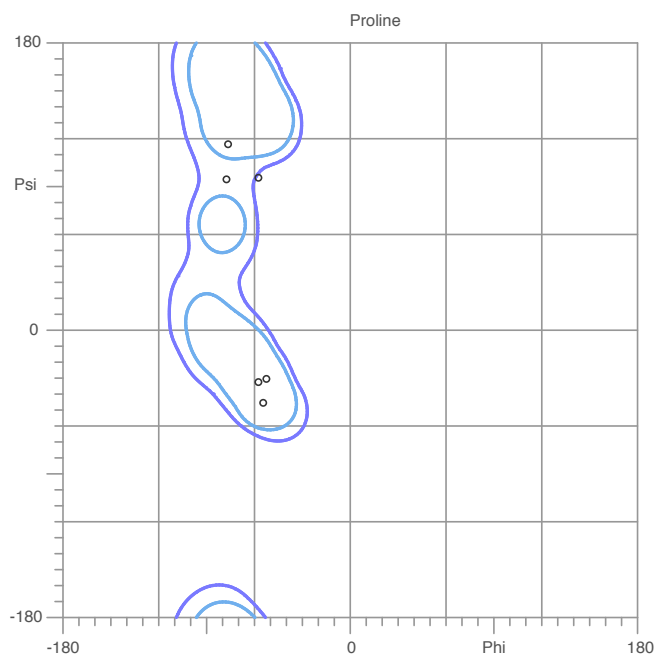
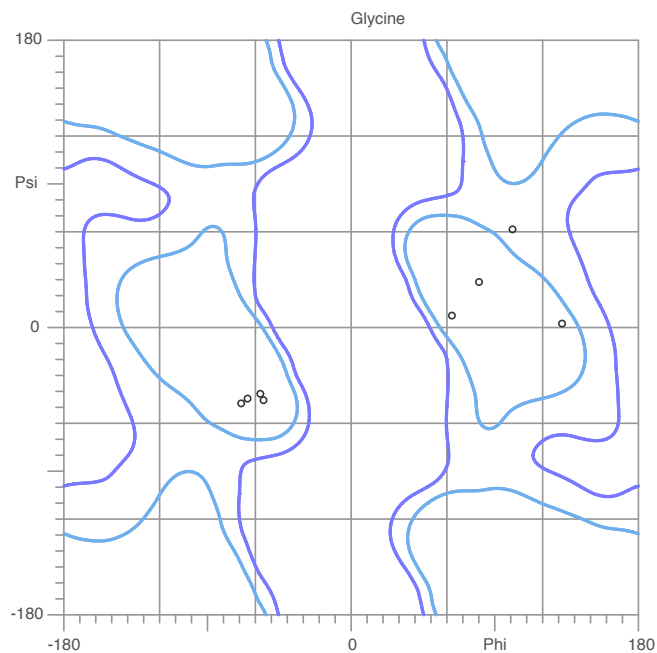
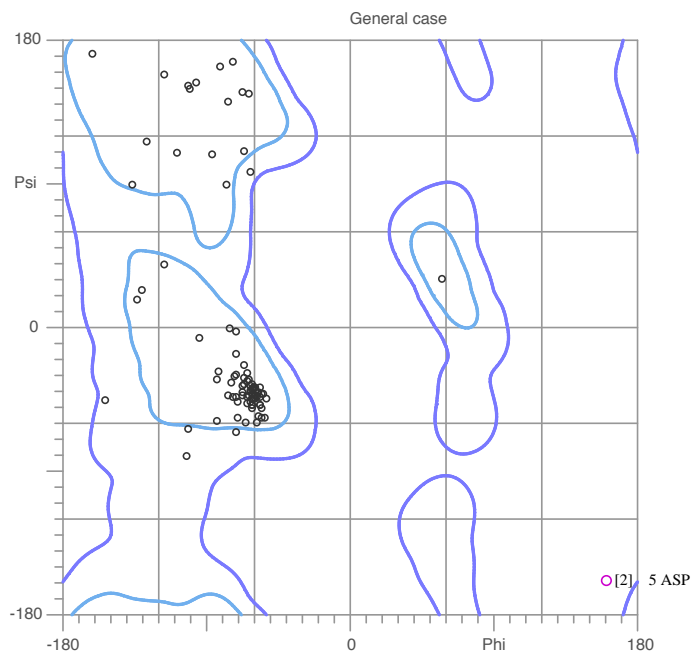
There were no outliers.

<http://kinemage.biochem.duke.edu>

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MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 2



90.7% (97/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

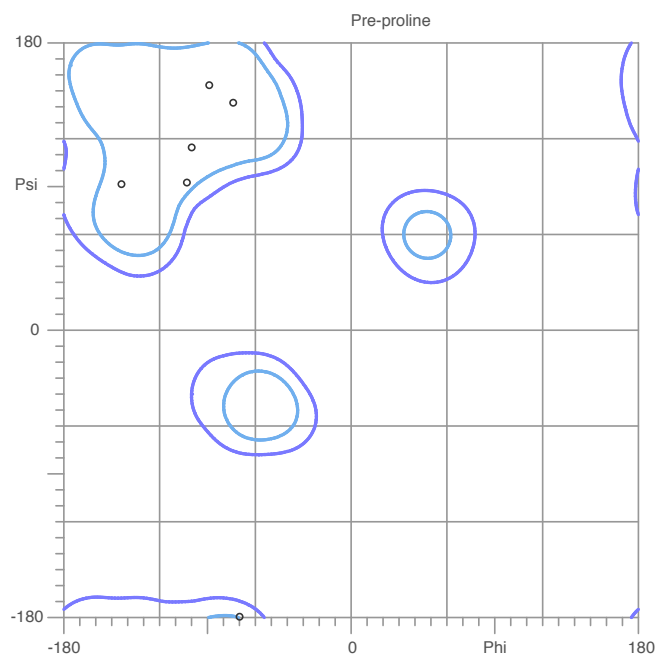
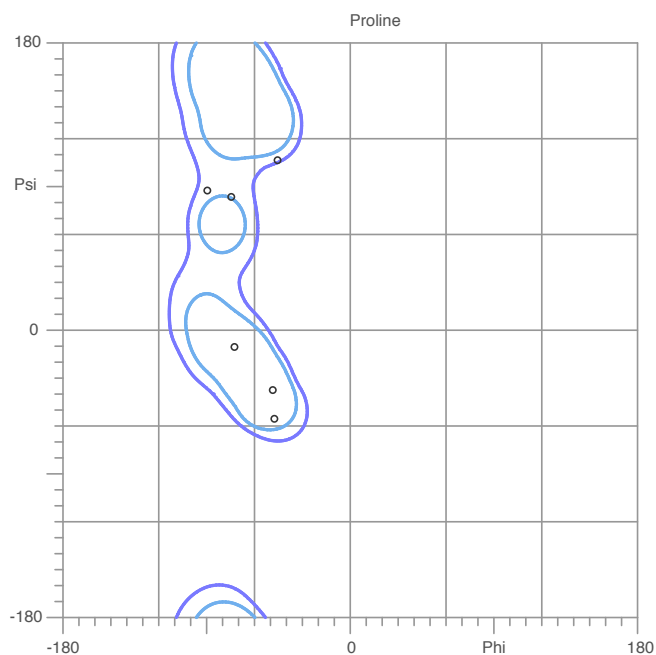
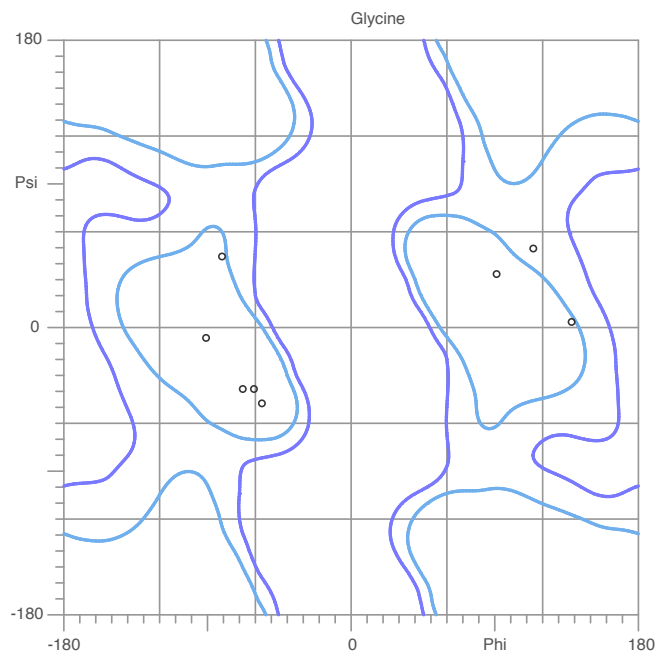
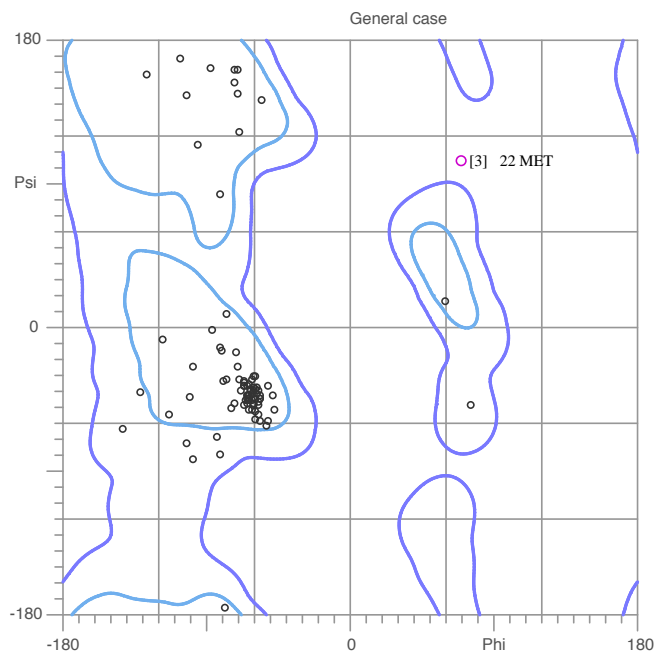
There were 2 outliers (phi, psi):

[2] 5 ASP (160.0, -158.5)

[2] 28 VAL (-120.8, -58.0)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 3



87.9% (94/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

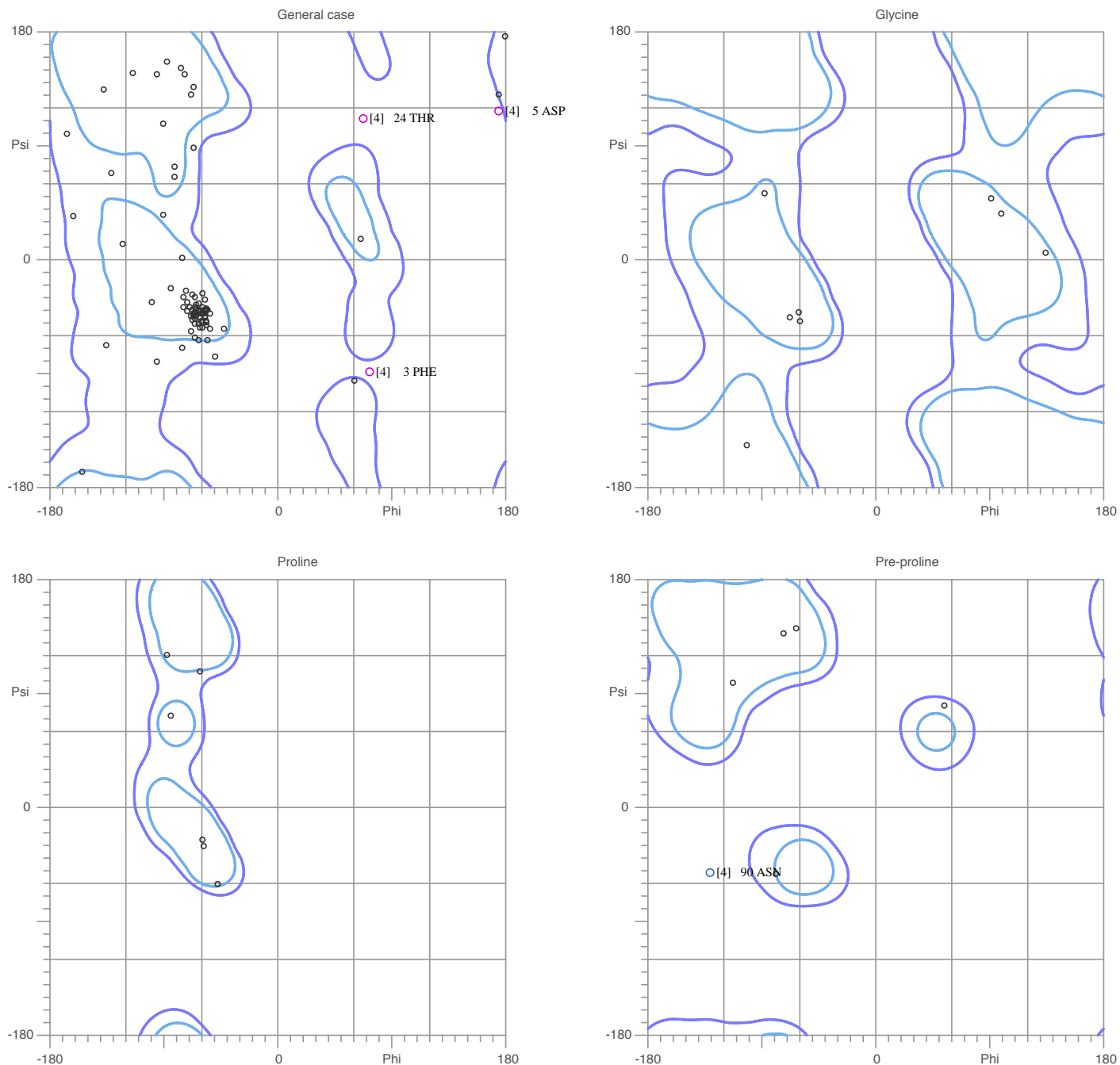
There were 1 outliers (phi, psi):
[3] 22 MET (69.4, 105.1)

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MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 4



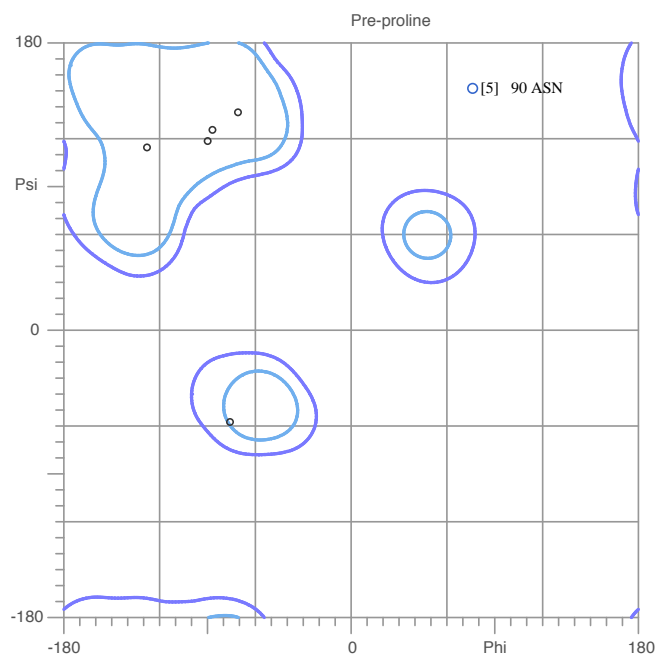
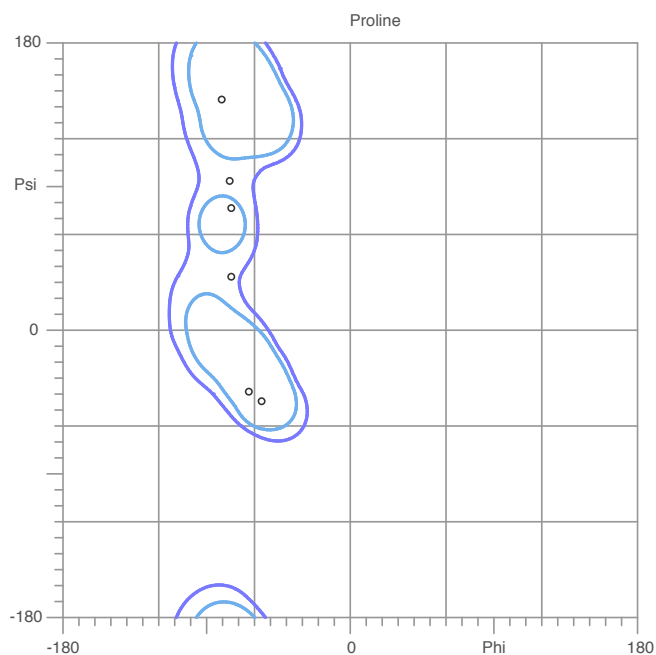
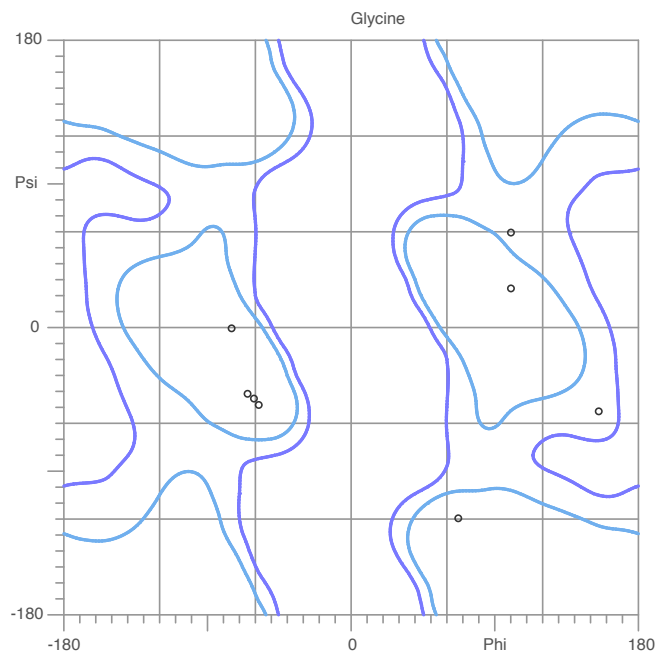
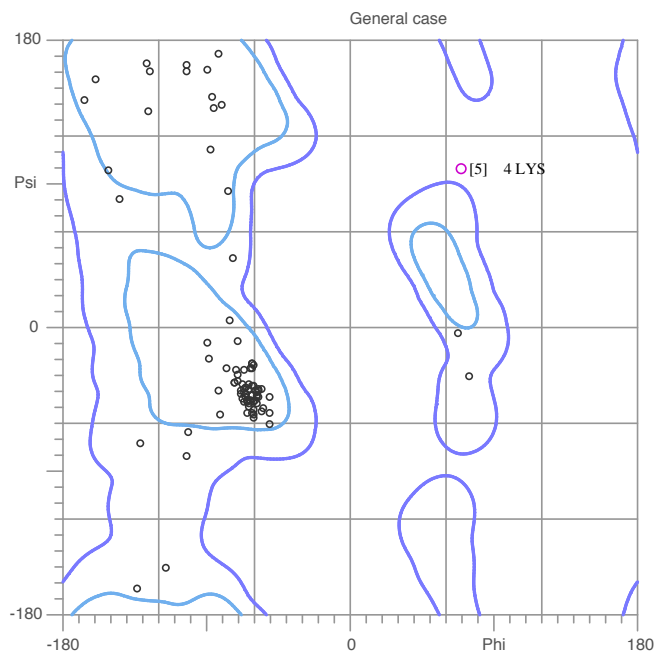
83.2% (89/107) of all residues were in favored (98%) regions.
96.3% (103/107) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [4] 3 PHE (72.4, -88.5)
- [4] 5 ASP (174.6, 118.3)
- [4] 24 THR (67.3, 112.3)
- [4] 90 ASN (-131.5, -51.3)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 5



86.0% (92/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

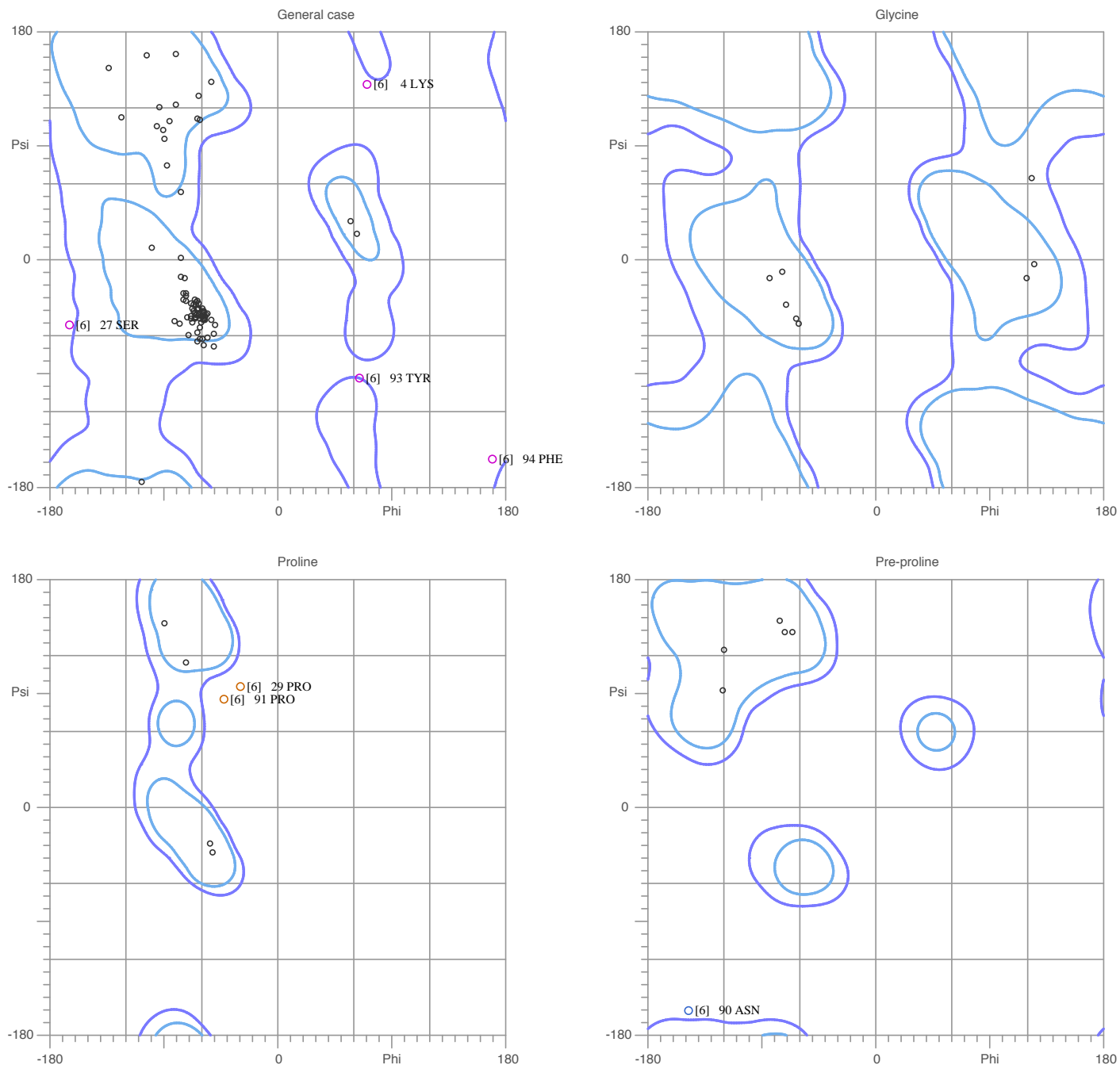
There were 2 outliers (phi, psi):

[5] 4 LYS (70.0, 100.2)

[5] 90 ASN (76.2, 152.2)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 6



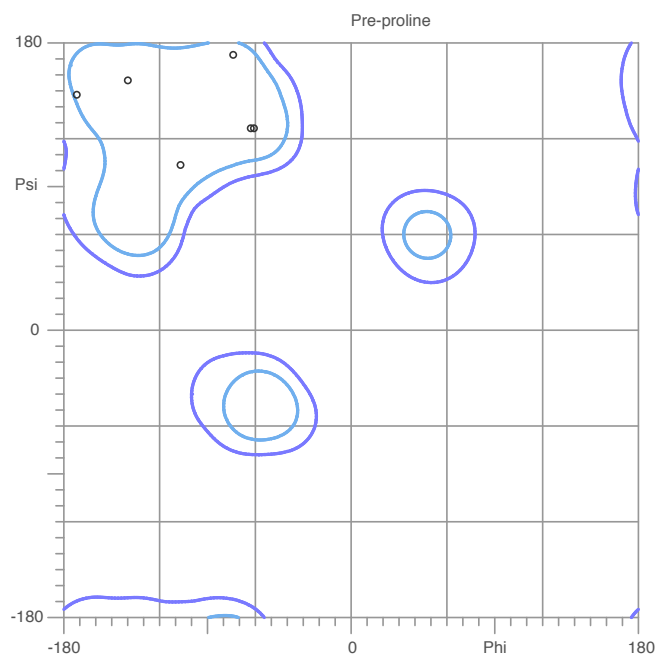
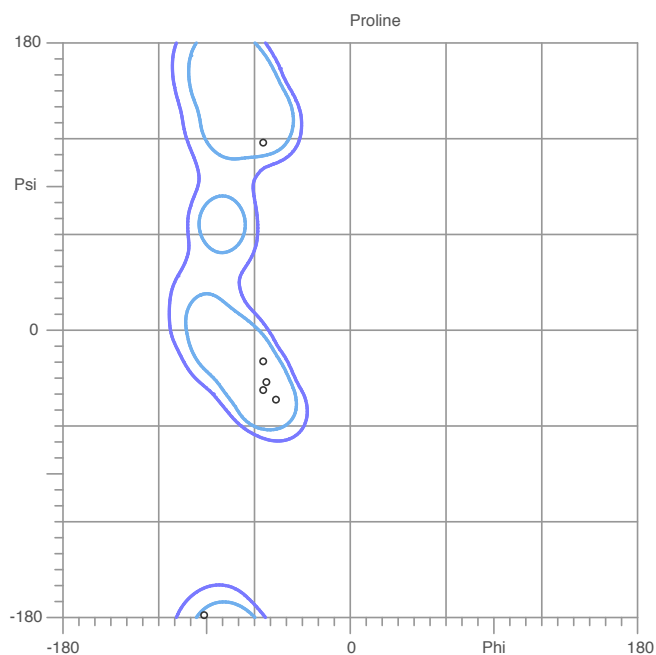
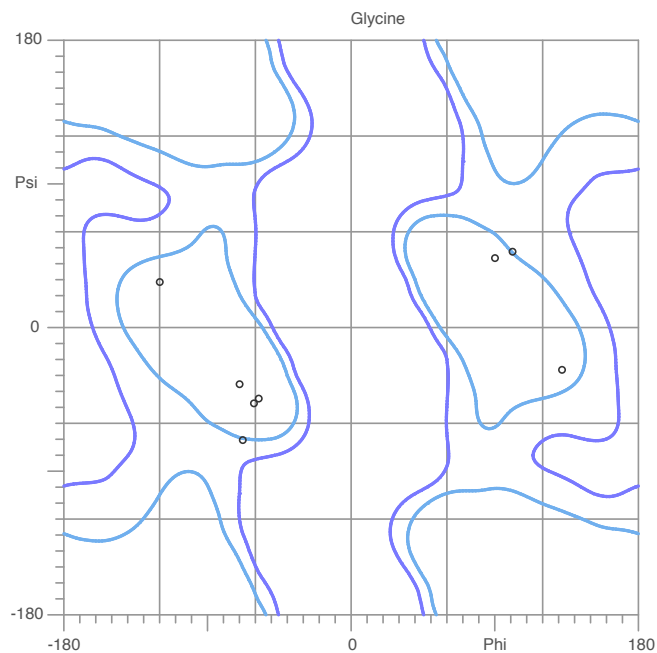
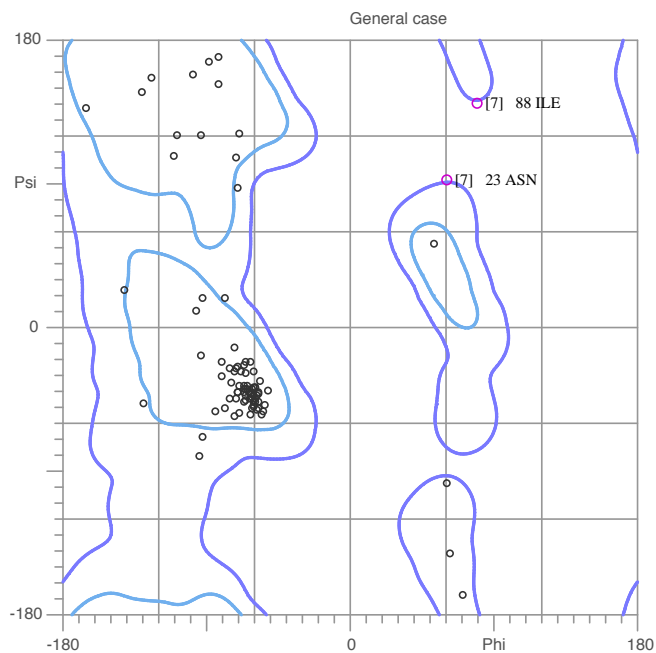
88.8% (95/107) of all residues were in favored (98%) regions.
 93.5% (100/107) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
 [6] 4 LYS (70.2, 139.6)

[6] 27 SER (-165.1, -51.4)
 [6] 29 PRO (-30.2, 96.3)
 [6] 90 ASN (-148.4, -160.3)
 [6] 91 PRO (-43.4, 86.7)
 [6] 93 TYR (64.6, -93.0)
 [6] 94 PHE (169.9, -157.1)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 7



87.9% (94/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

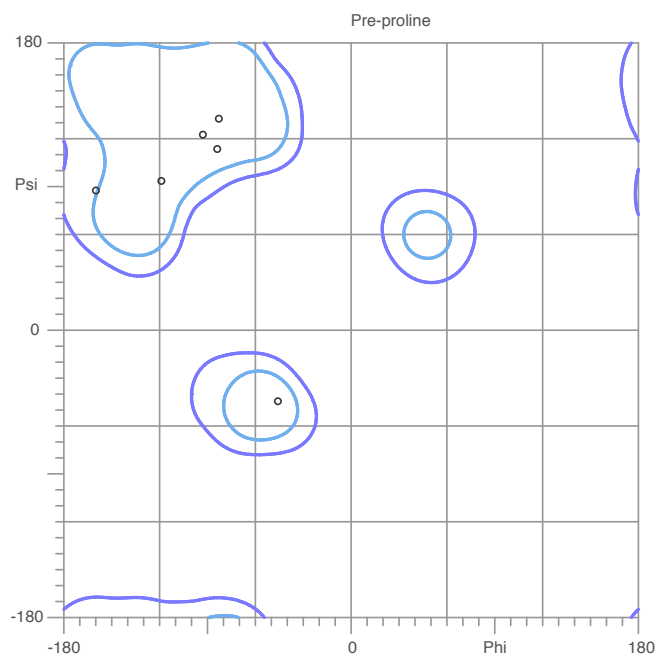
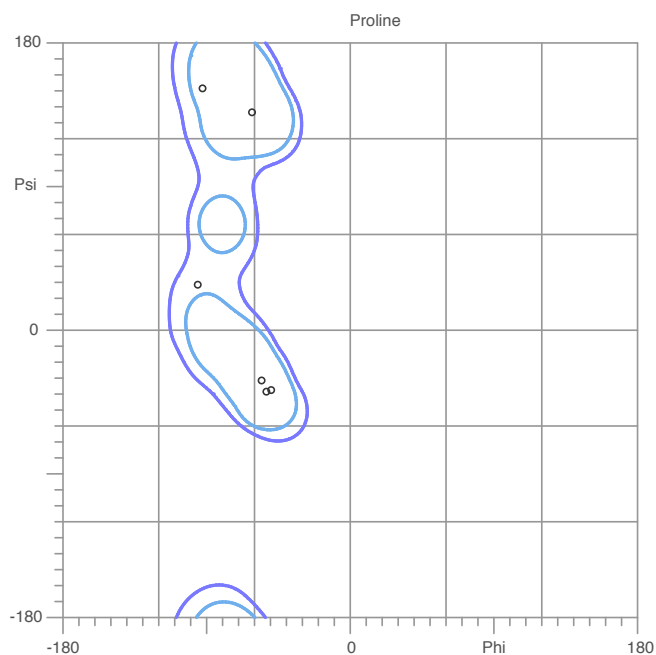
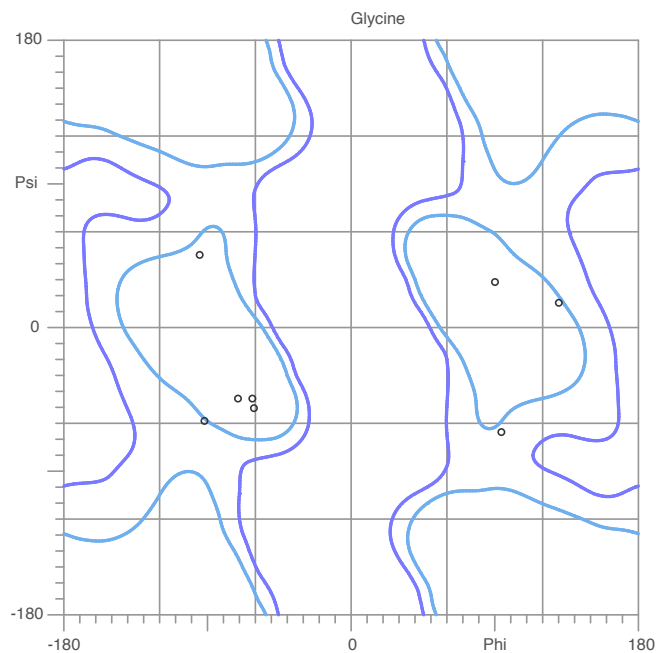
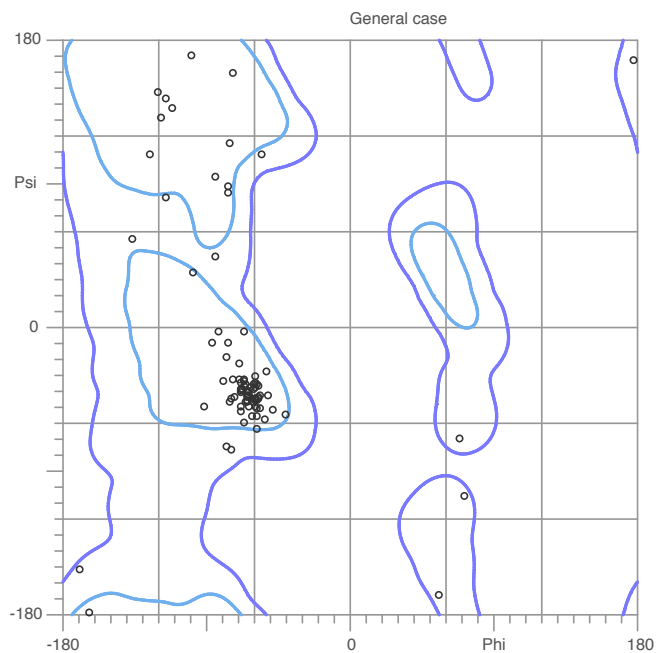
There were 2 outliers (phi, psi):

[7] 23 ASN (60.5, 93.7)

[7] 88 ILE (79.3, 141.0)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 8



86.0% (92/107) of all residues were in favored (98%) regions.
100.0% (107/107) of all residues were in allowed (>99.8%) regions.

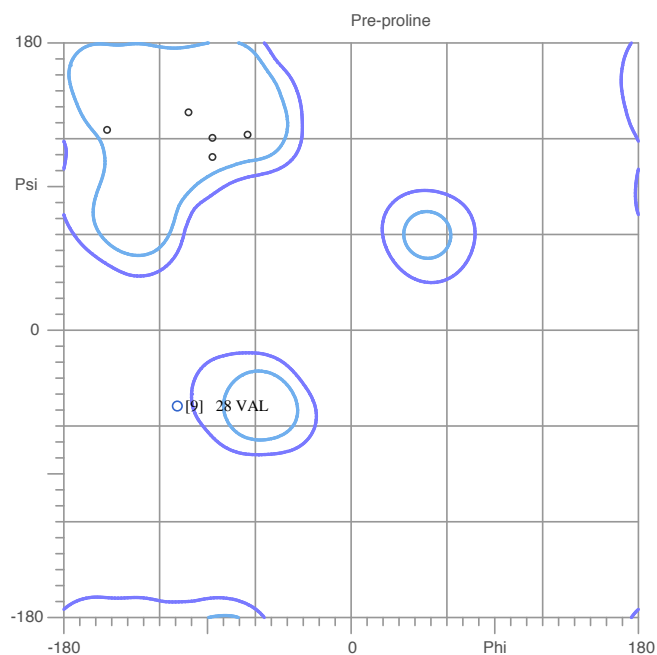
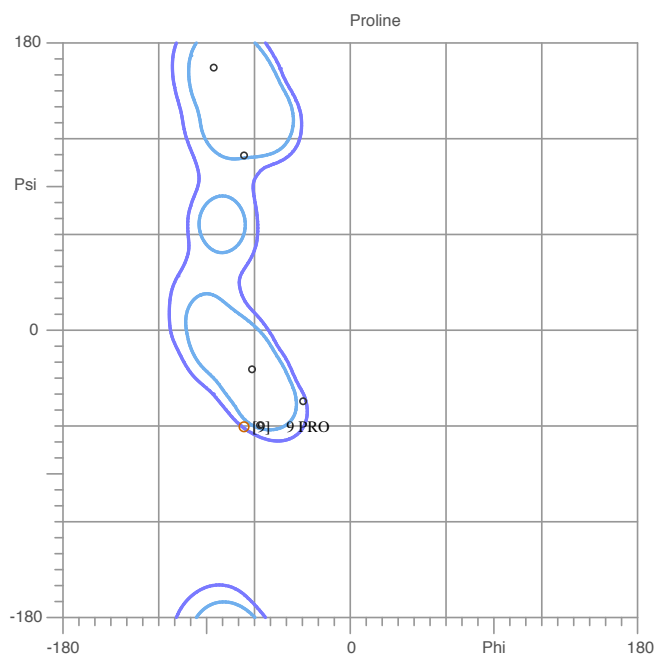
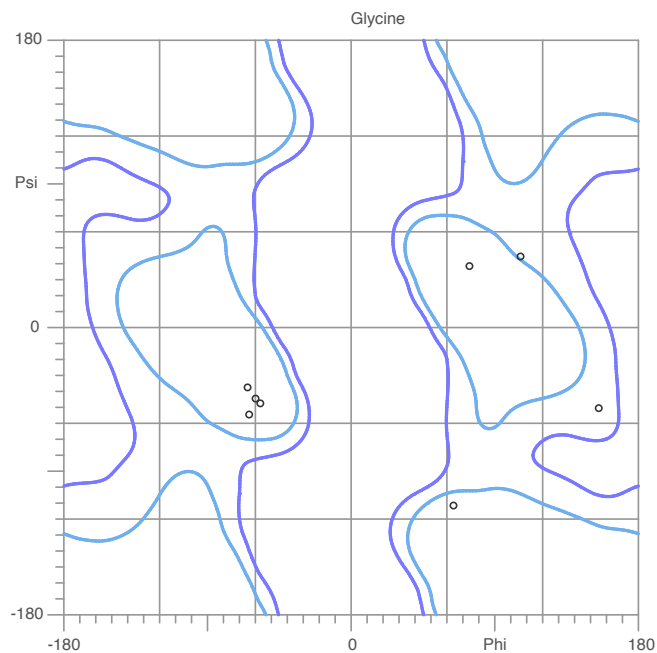
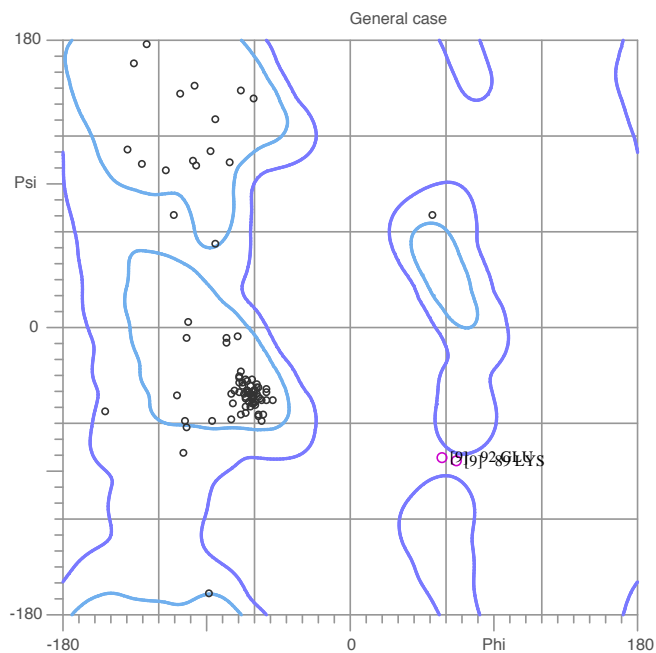
There were no outliers.

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MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 9



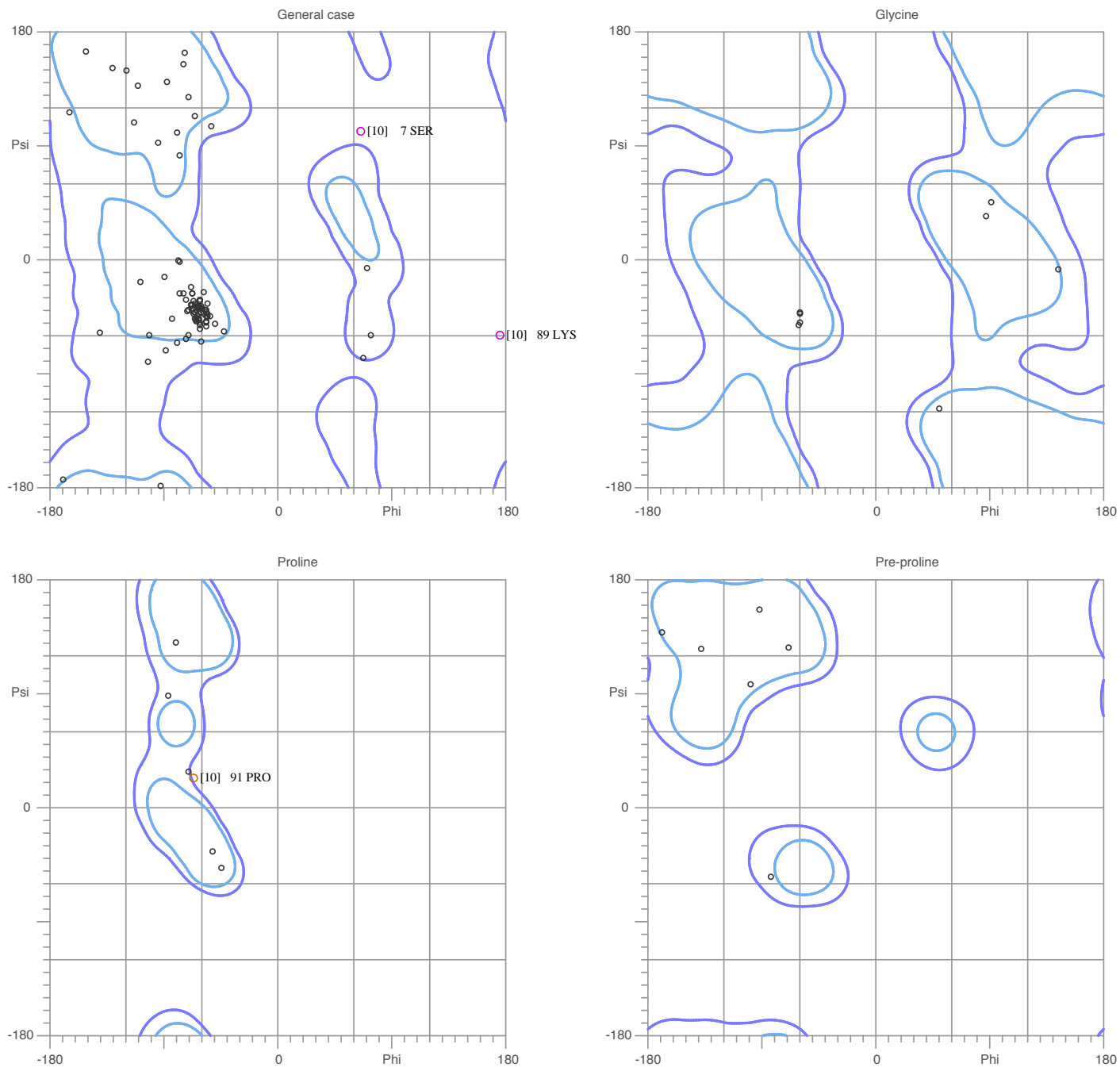
87.9% (94/107) of all residues were in favored (98%) regions.
96.3% (103/107) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [9] 9 PRO (-67.8, -60.8)
- [9] 28 VAL (-109.2, -47.9)
- [9] 89 LYS (66.1, -83.5)
- [9] 92 GLU (57.2, -81.4)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 10



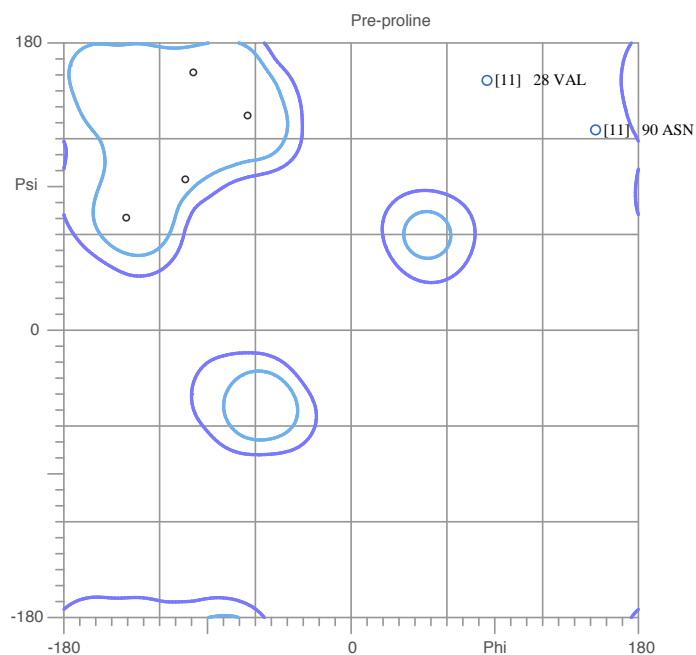
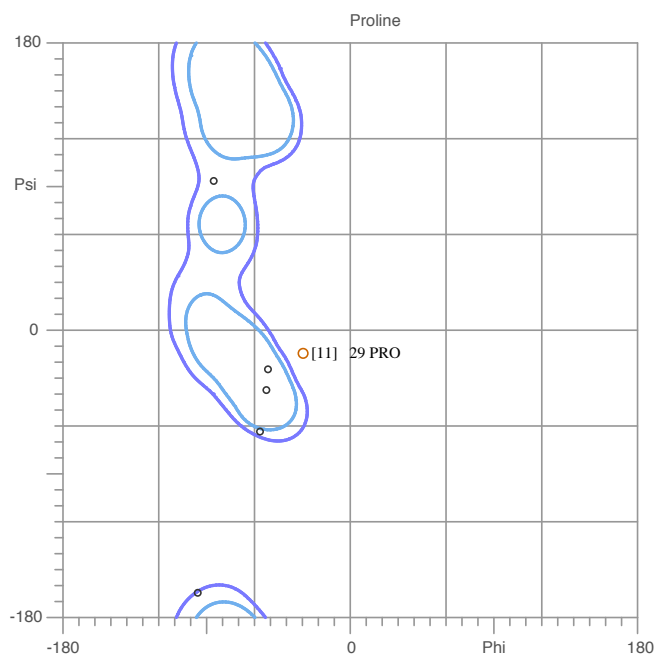
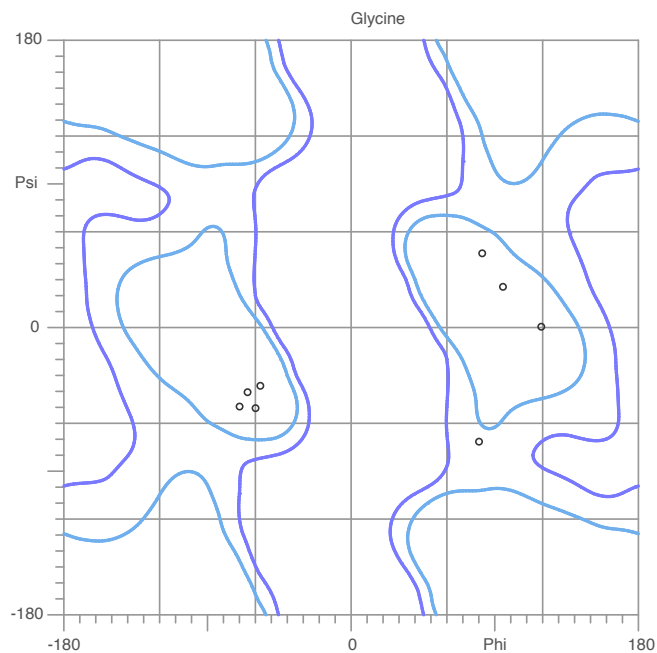
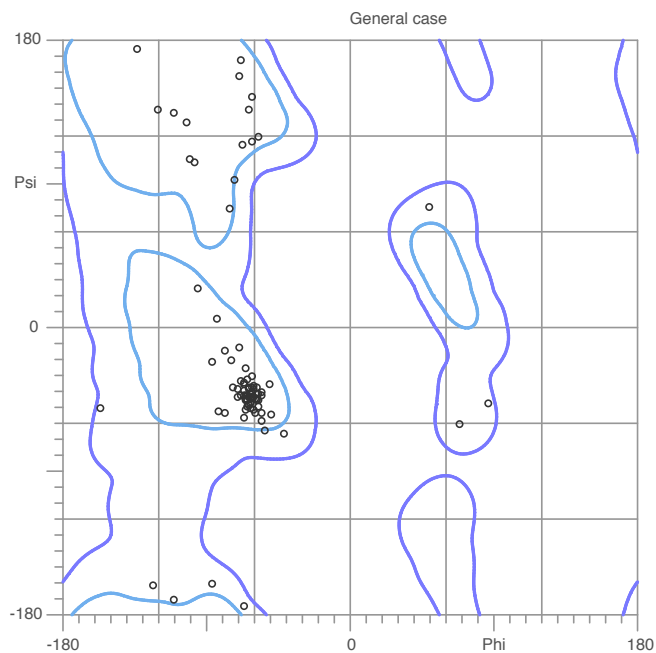
84.1% (90/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [10] 7 SER (65.7, 102.5)
- [10] 89 LYS (175.7, -59.5)
- [10] 91 PRO (-67.8, 24.2)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 11



84.1% (90/107) 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):

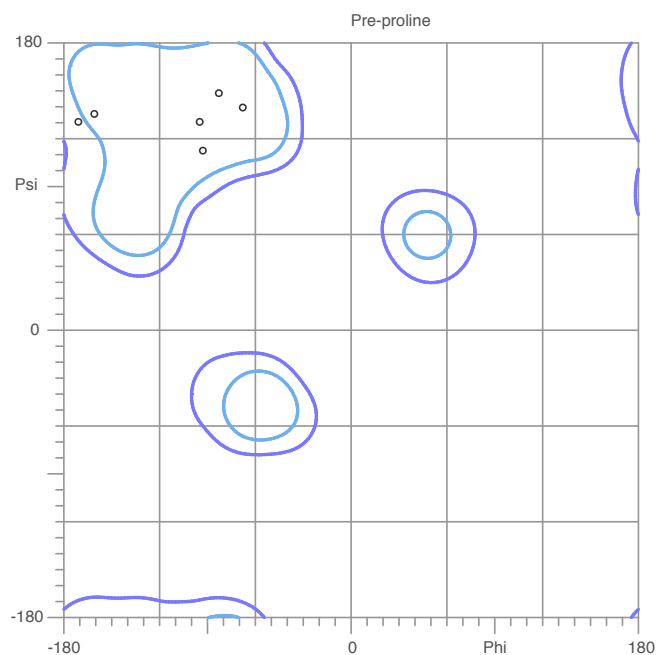
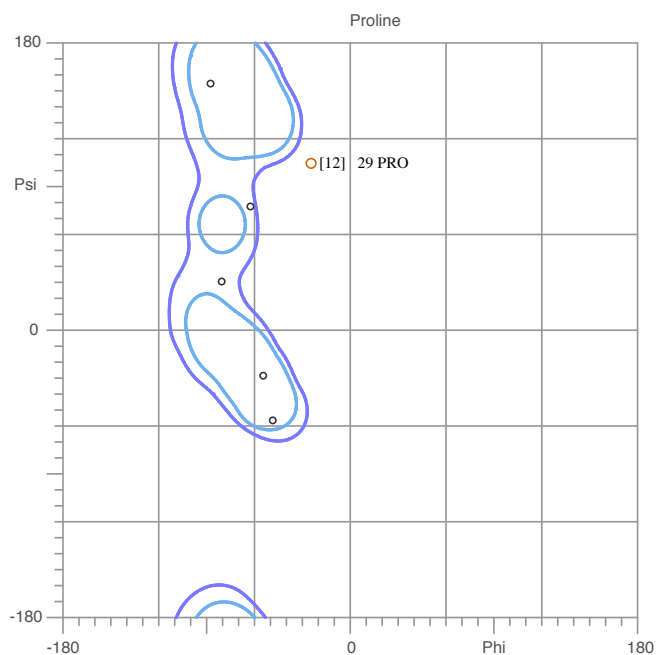
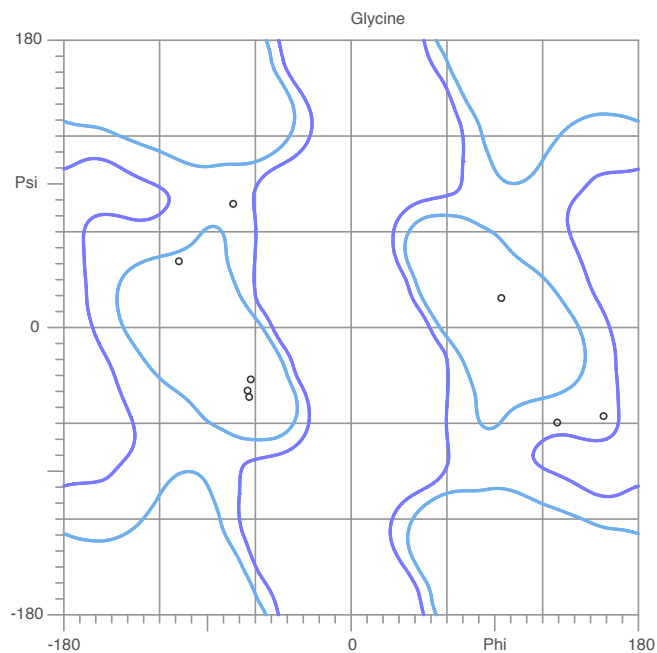
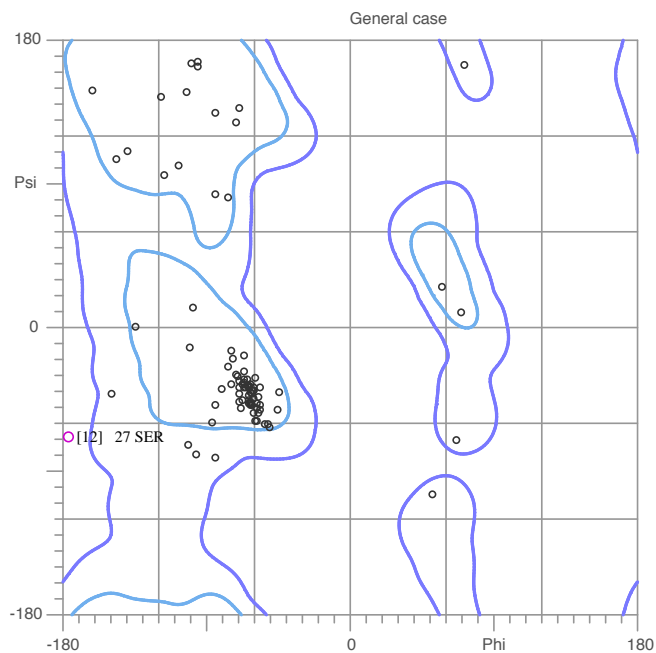
[11] 28 VAL (85.0, 157.9)

[11] 29 PRO (-30.5, -14.5)

[11] 90 ASN (153.9, 126.4)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 12

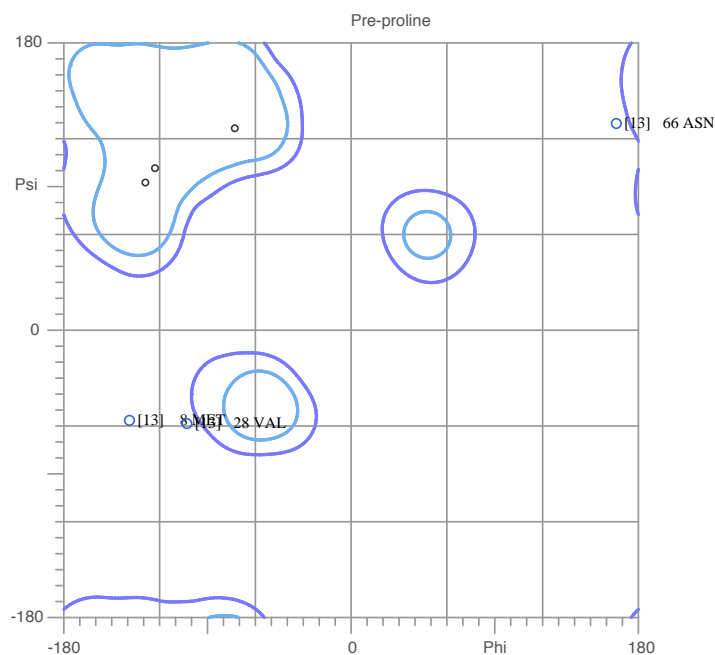
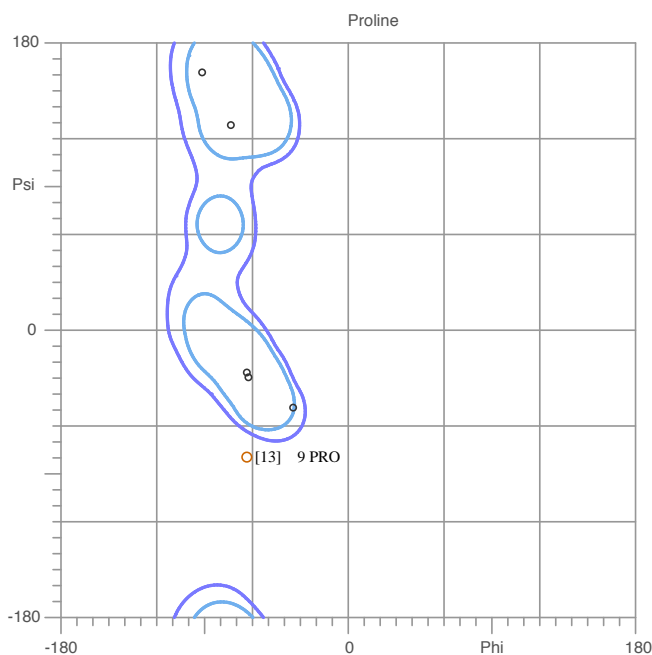
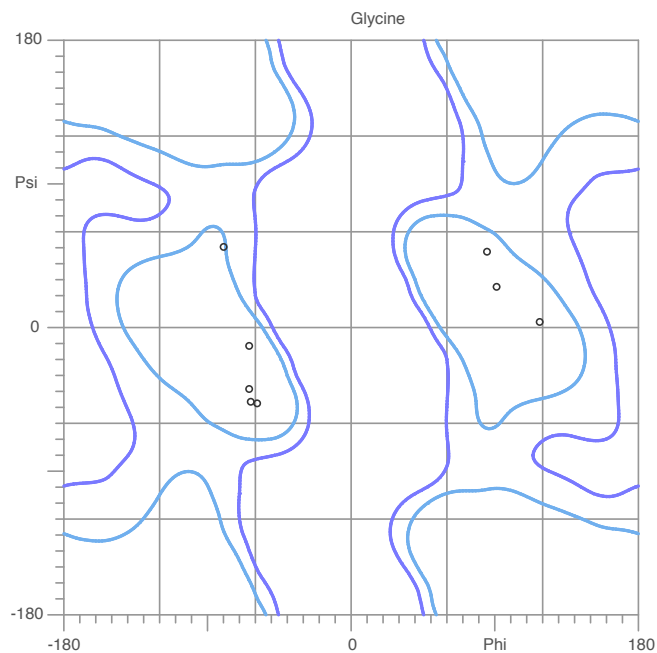
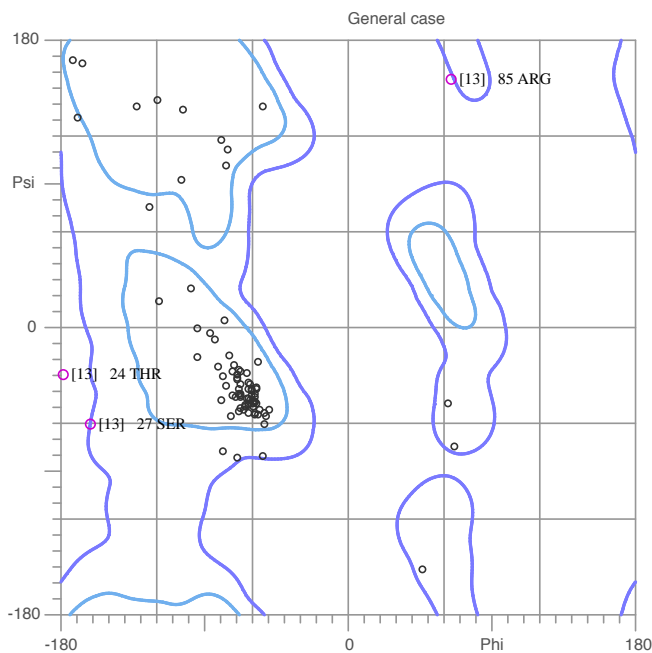


86.0% (92/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 27 SER (-177.4, -68.5)
[12] 29 PRO (-25.7, 105.4)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 13



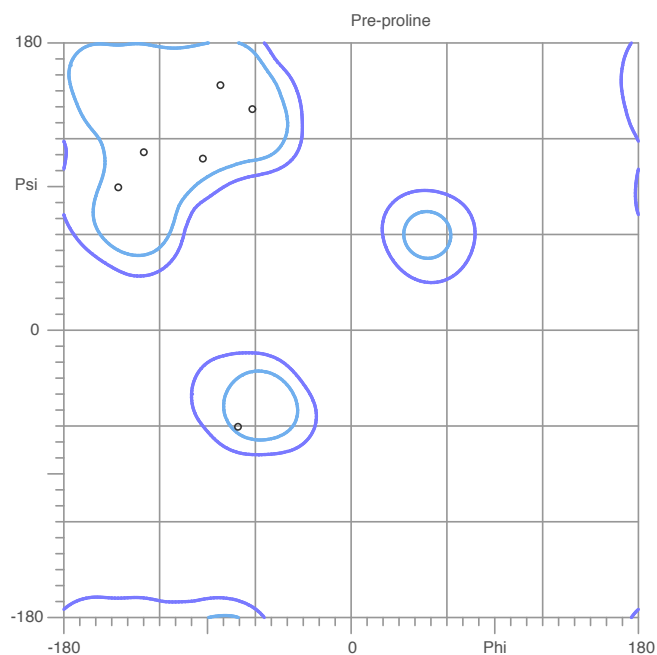
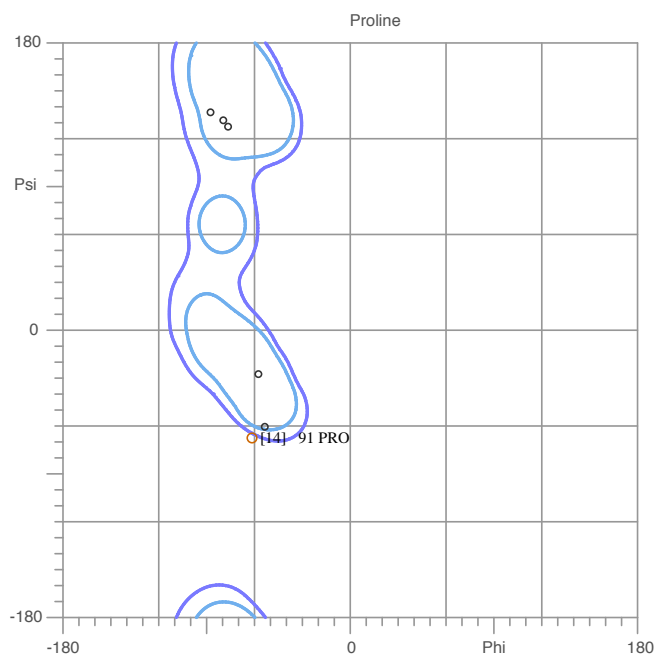
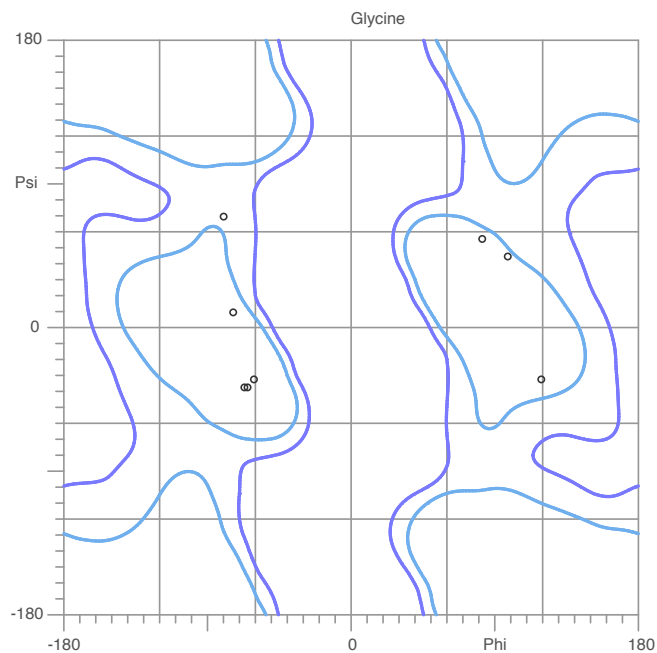
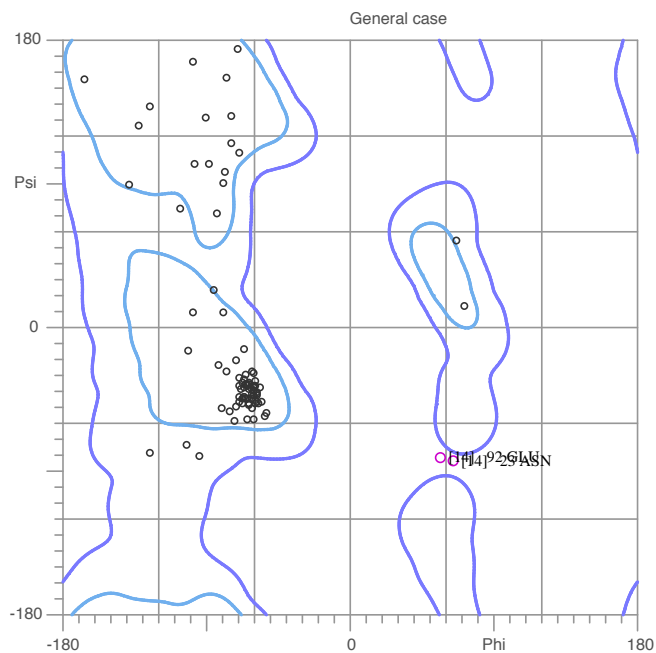
86.0% (92/107) of all residues were in favored (98%) regions.
93.5% (100/107) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[13] 8 MET (-139.8, -56.7)

[13] 9 PRO (-64.0, -79.4)
[13] 24 THR (-179.1, -30.0)
[13] 27 SER (-162.2, -60.9)
[13] 28 VAL (-103.2, -58.4)
[13] 66 ASN (166.2, 130.8)
[13] 85 ARG (64.5, 156.6)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 14



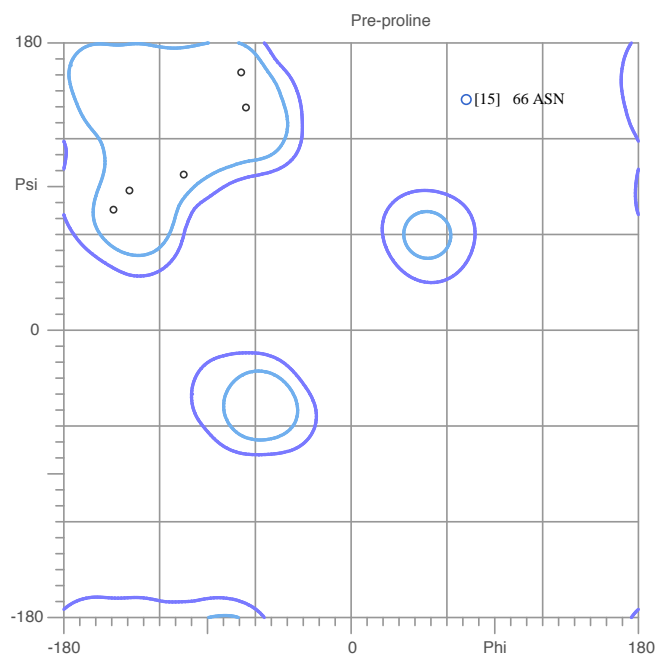
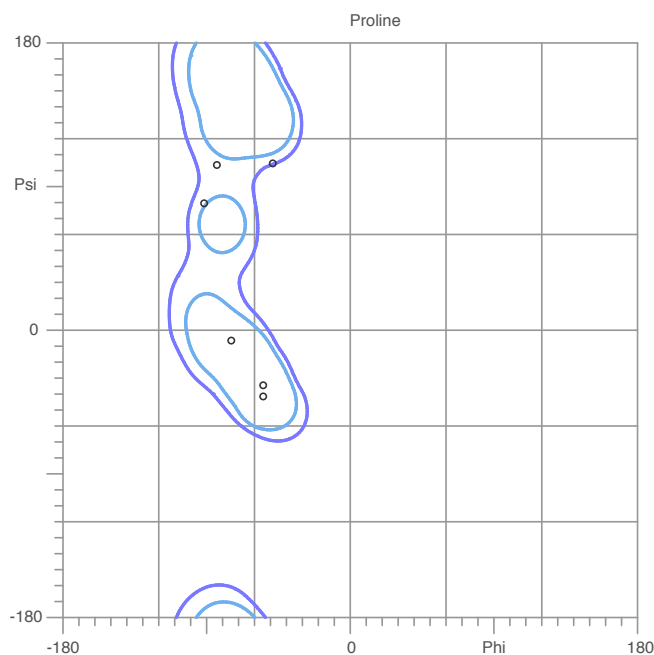
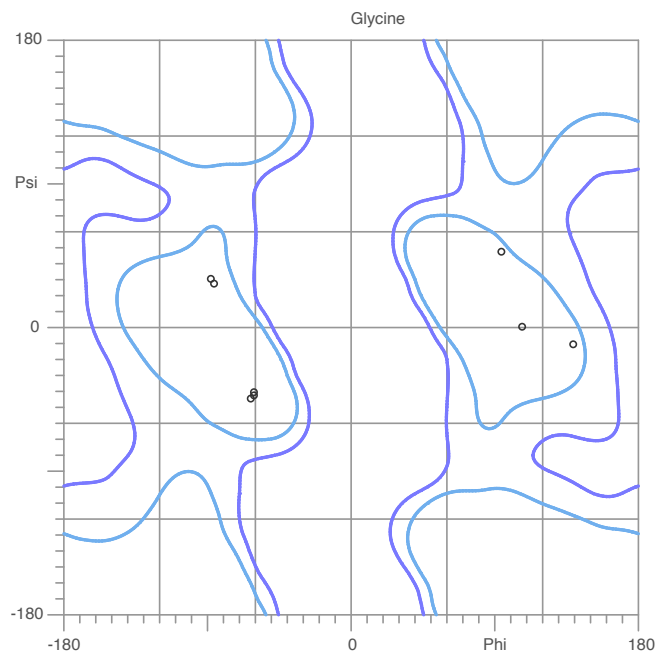
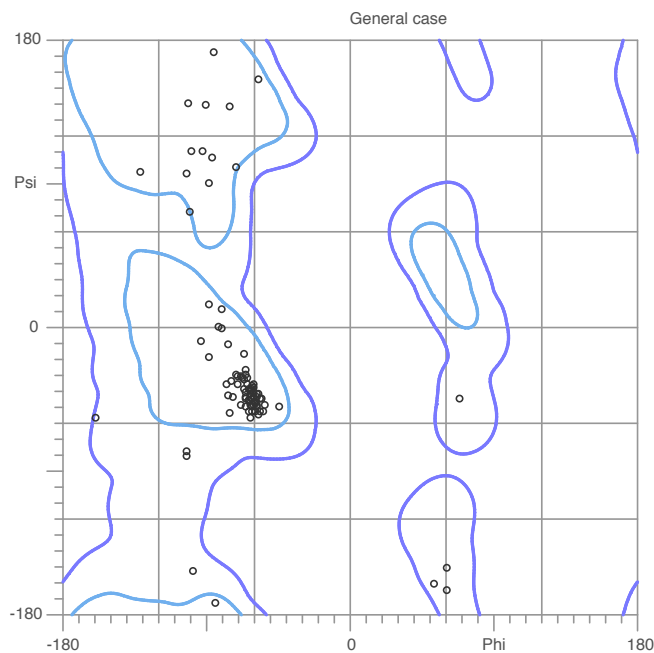
90.7% (97/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [14] 23 ASN (64.3, -83.2)
- [14] 91 PRO (-62.9, -67.9)
- [14] 92 GLU (56.4, -81.2)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 15



87.9% (94/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

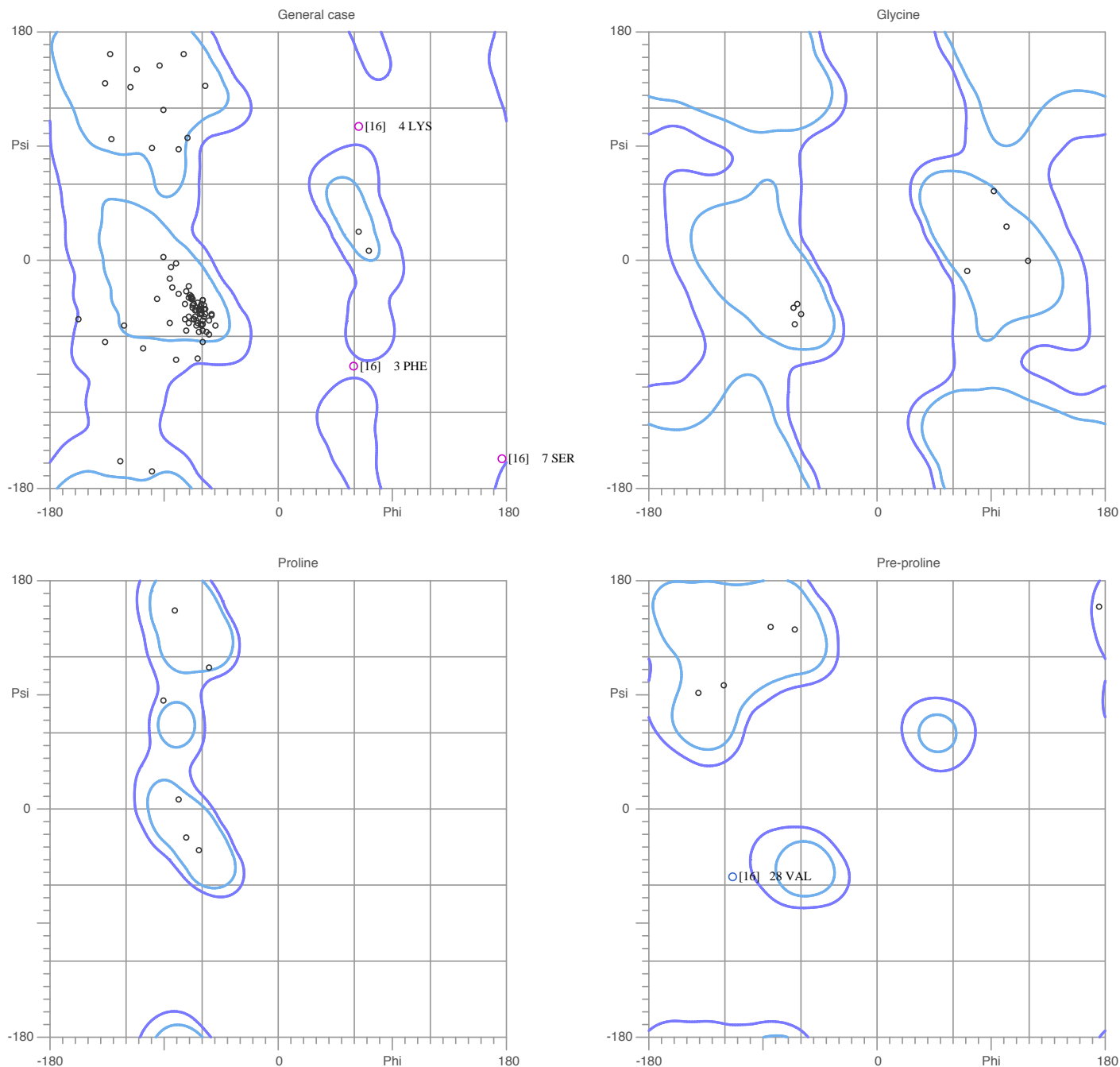
There were 1 outliers (phi, psi):
[15] 66 ASN (72.9, 145.1)

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MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 16



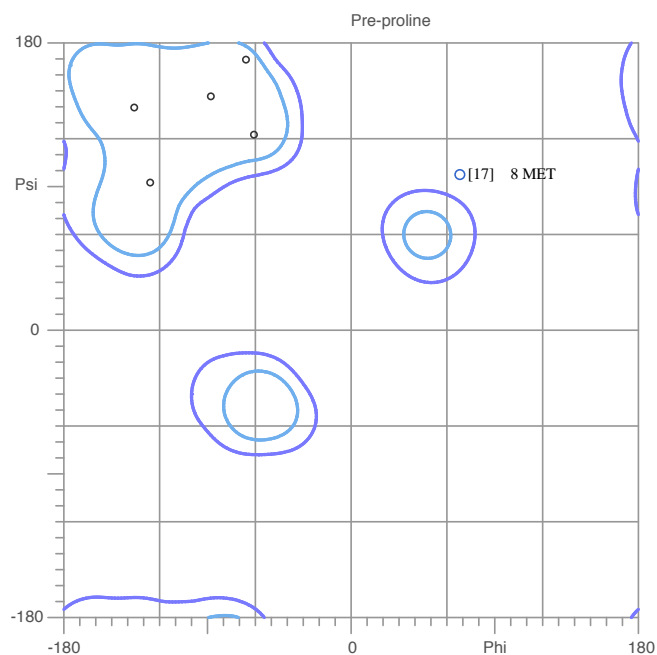
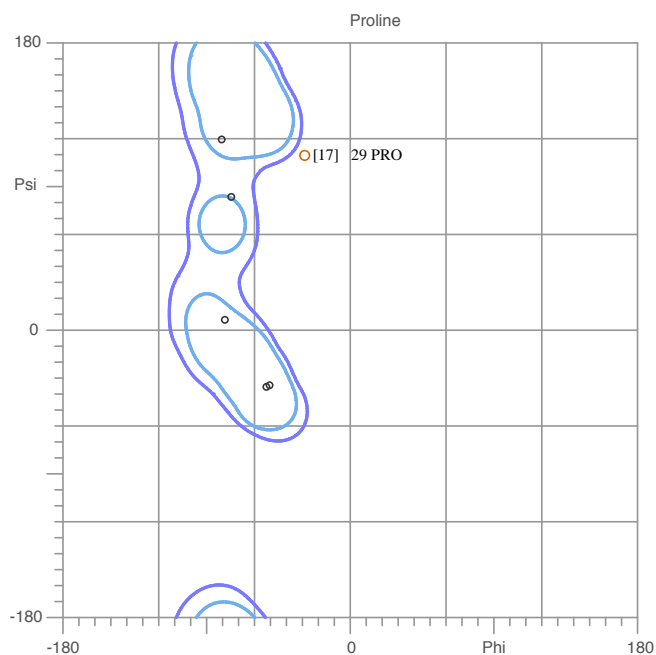
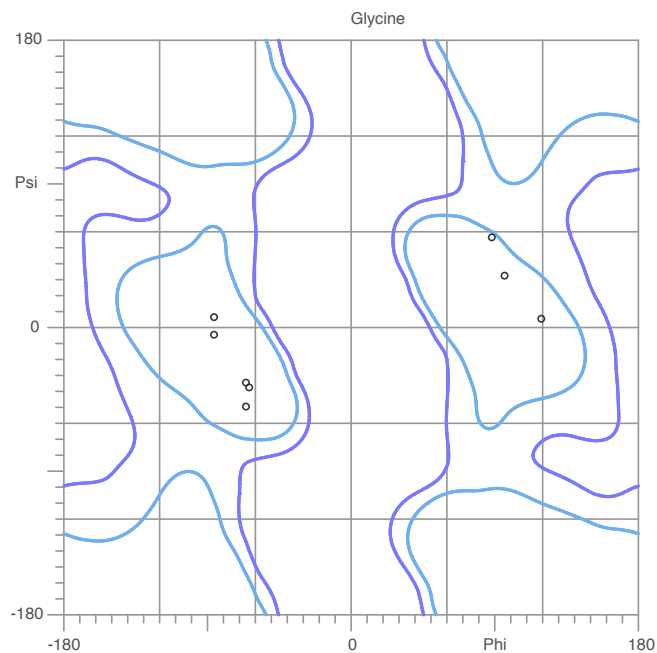
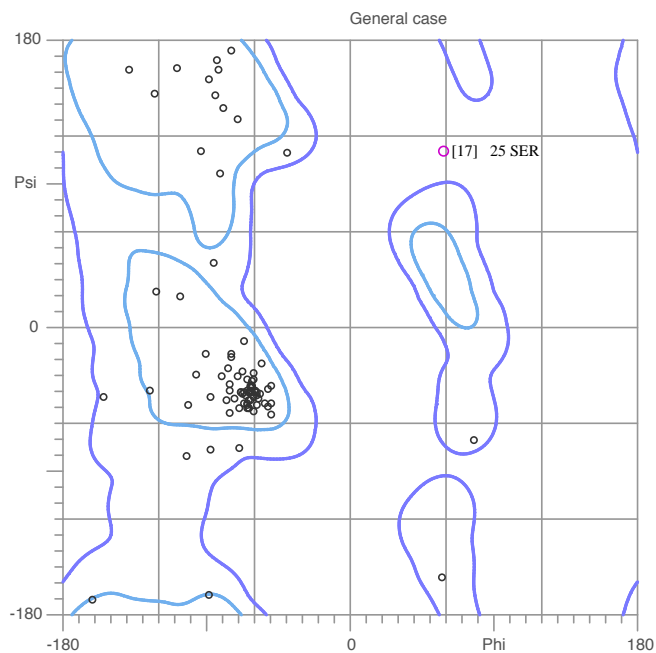
86.9% (93/107) of all residues were in favored (98%) regions.
96.3% (103/107) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [16] 3 PHE (59.7, -83.3)
- [16] 4 LYS (63.2, 106.2)
- [16] 7 SER (176.4, -156.5)
- [16] 28 VAL (-114.6, -53.5)

MolProbity Ramachandran analysis

STR65_NMR_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):

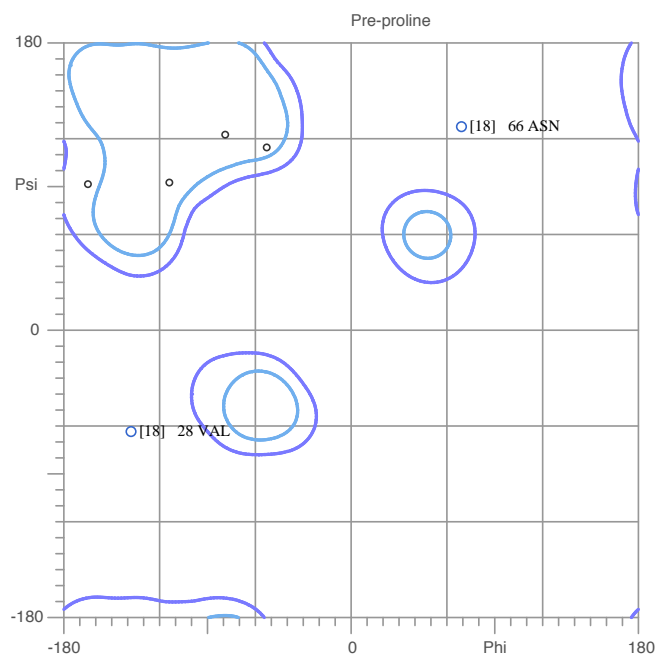
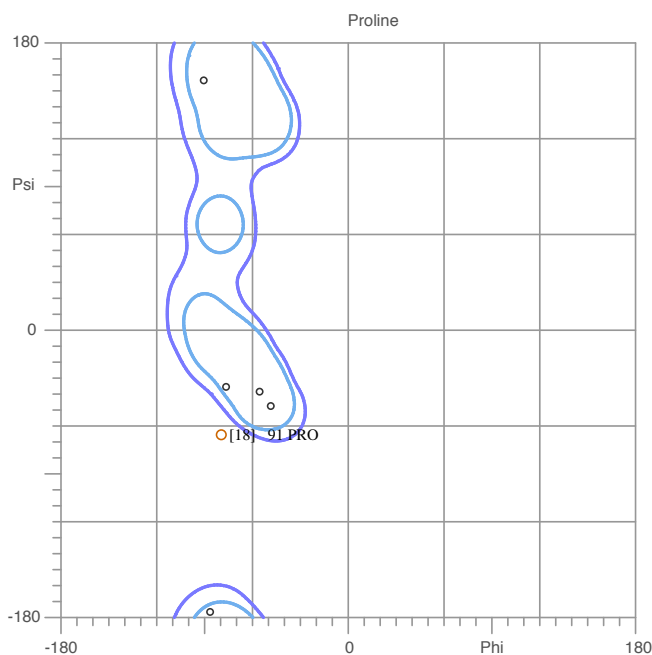
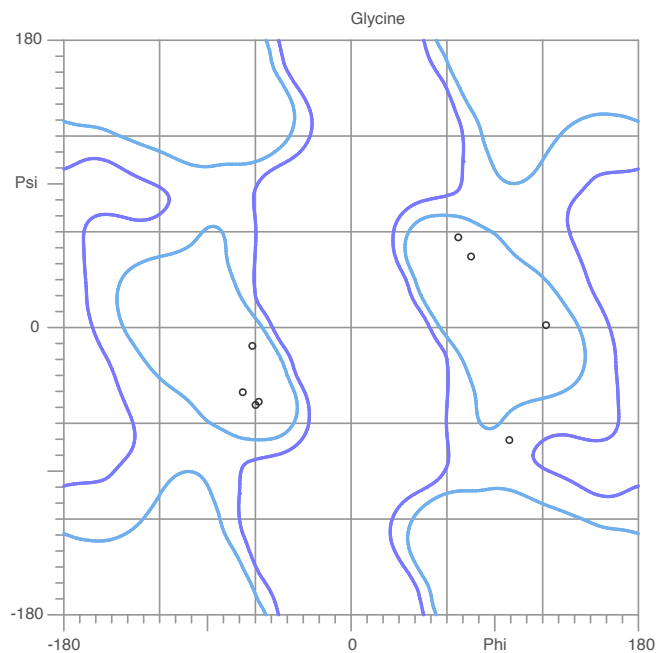
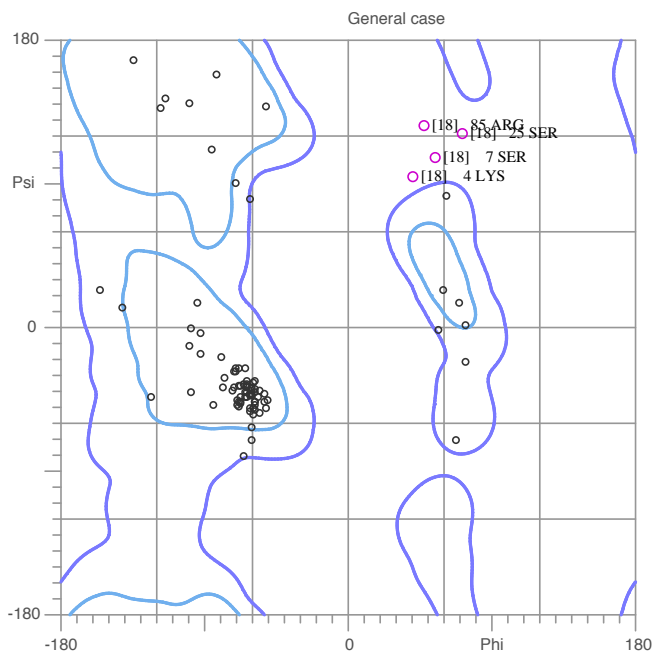
[17] 8 MET (68.6, 98.4)

[17] 25 SER (58.2, 111.8)

[17] 29 PRO (-29.8, 110.3)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 18



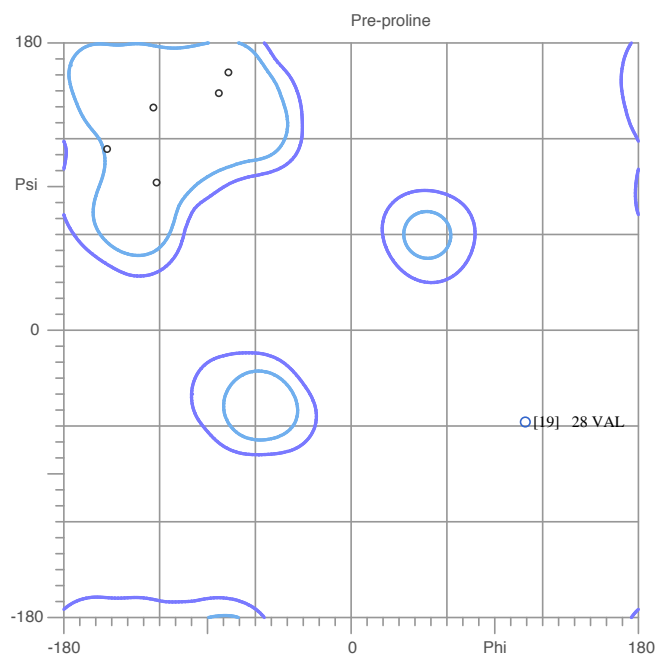
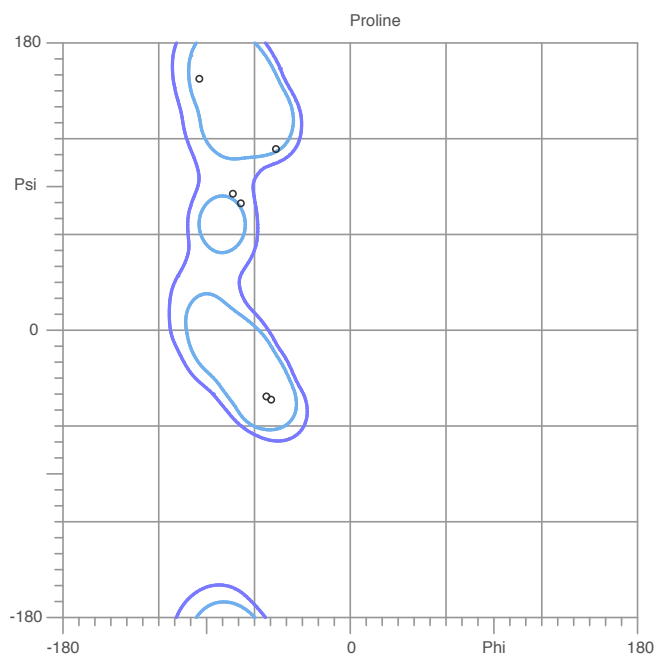
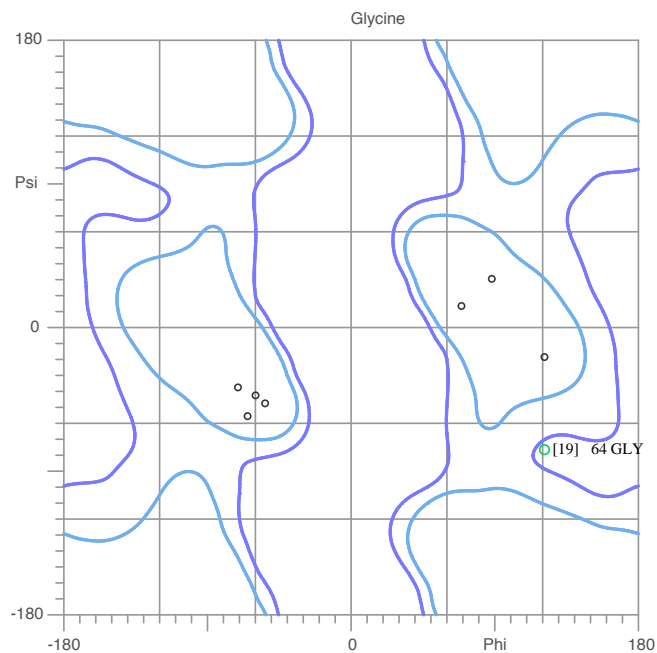
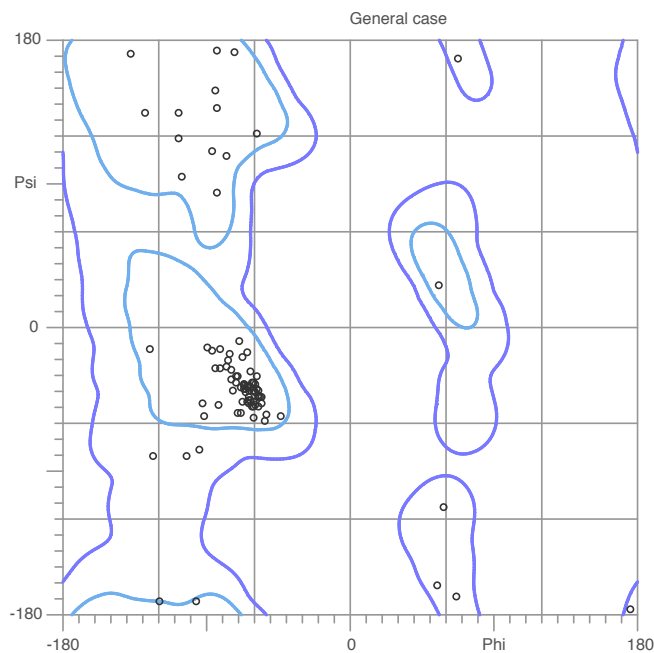
82.2% (88/107) of all residues were in favored (98%) regions.
93.5% (100/107) of all residues were in allowed (>99.8%) regions.

There were 7 outliers (phi, psi):
[18] 4 LYS (40.9, 95.3)

[18] 7 SER (54.2, 107.6)
[18] 25 SER (71.2, 122.5)
[18] 28 VAL (-138.6, -63.1)
[18] 66 ASN (69.6, 129.0)
[18] 85 ARG (47.9, 127.7)
[18] 91 PRO (-80.7, -65.1)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 19

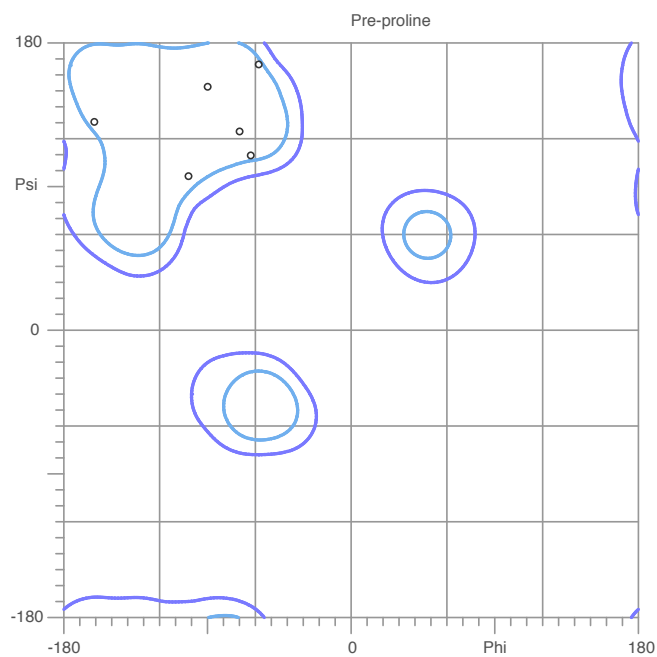
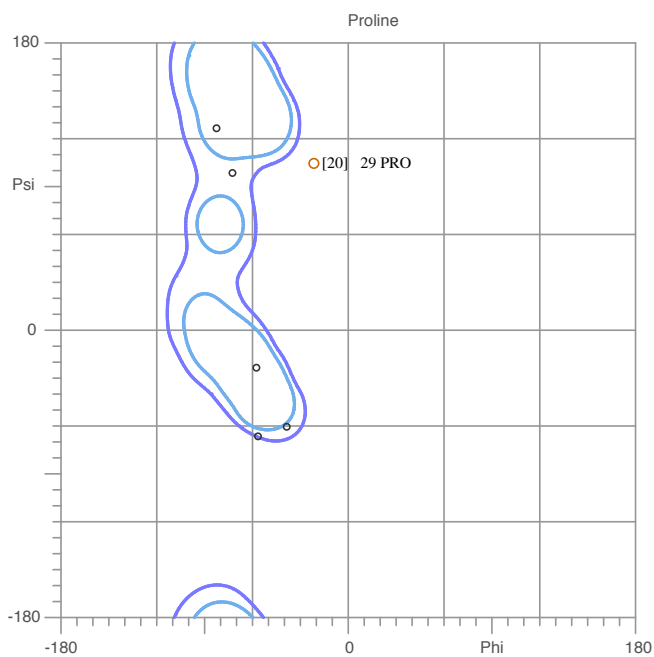
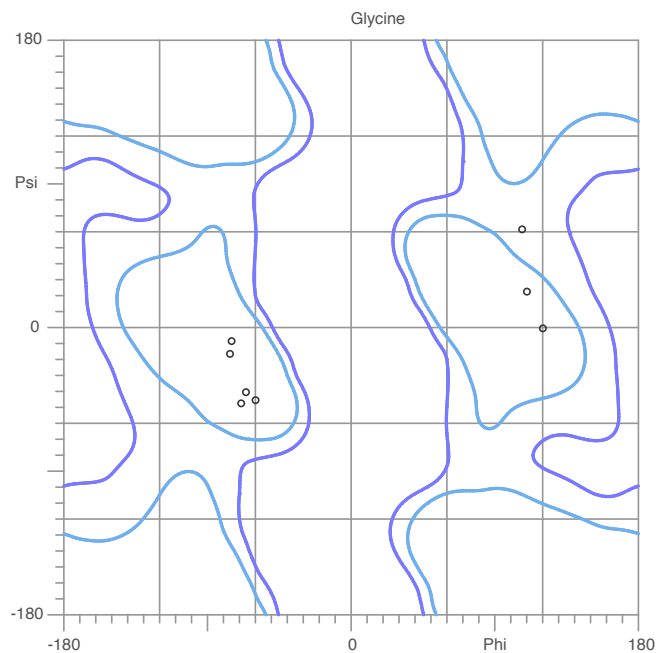
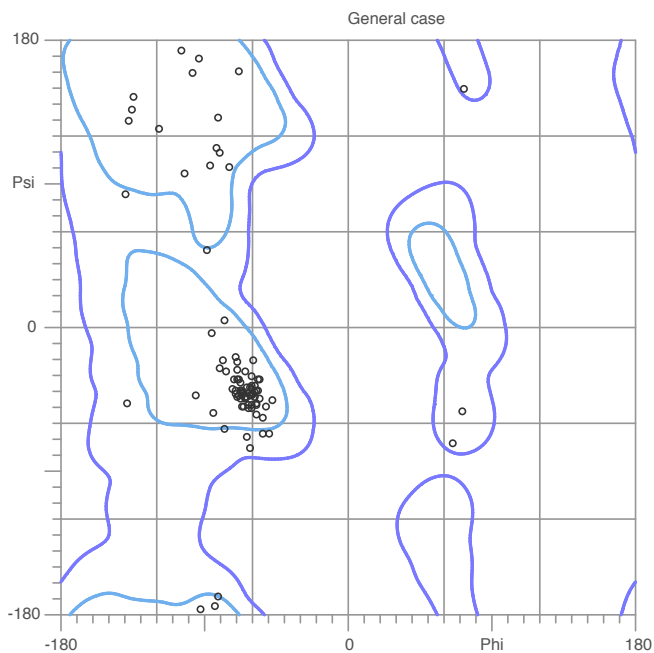


87.9% (94/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 28 VAL (109.1, -57.1)
[19] 64 GLY (121.8, -77.0)

MolProbity Ramachandran analysis

STR65_NMR_em_bcr3.pdb, model 20



85.0% (91/107) 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):
[20] 29 PRO (-22.3, 105.3)

<http://kinemage.biochem.duke.edu>

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