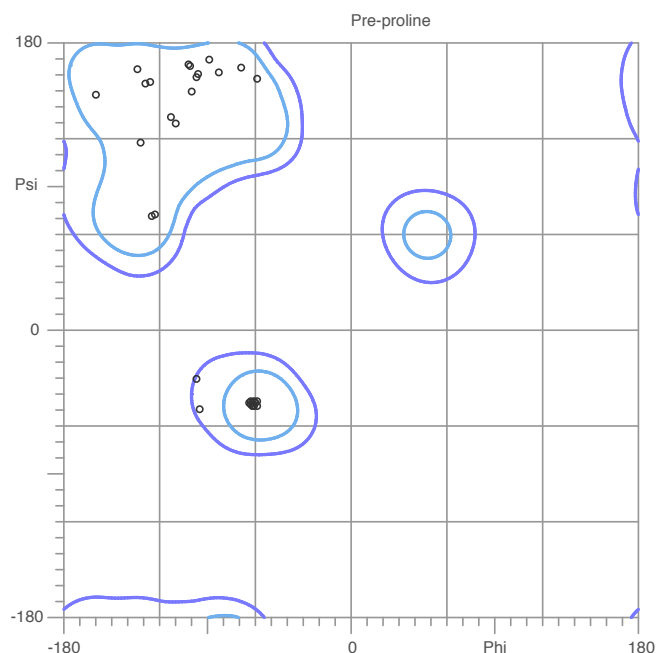
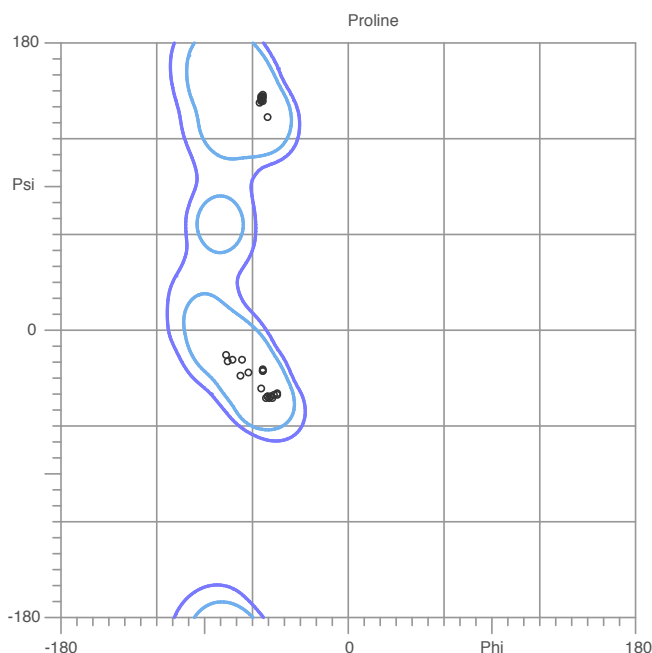
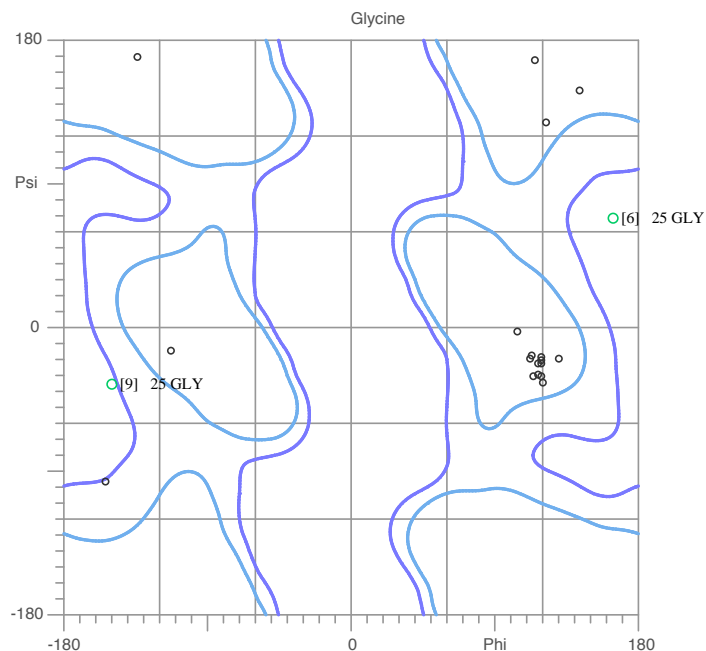
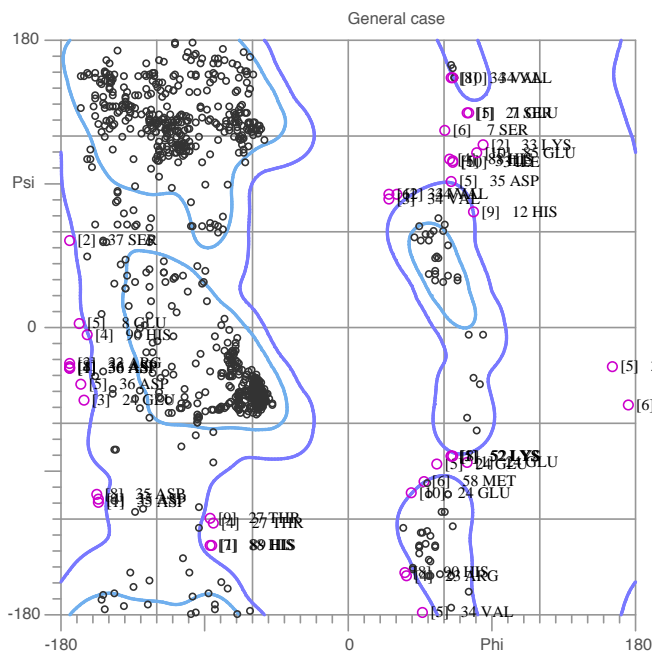


MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, all models



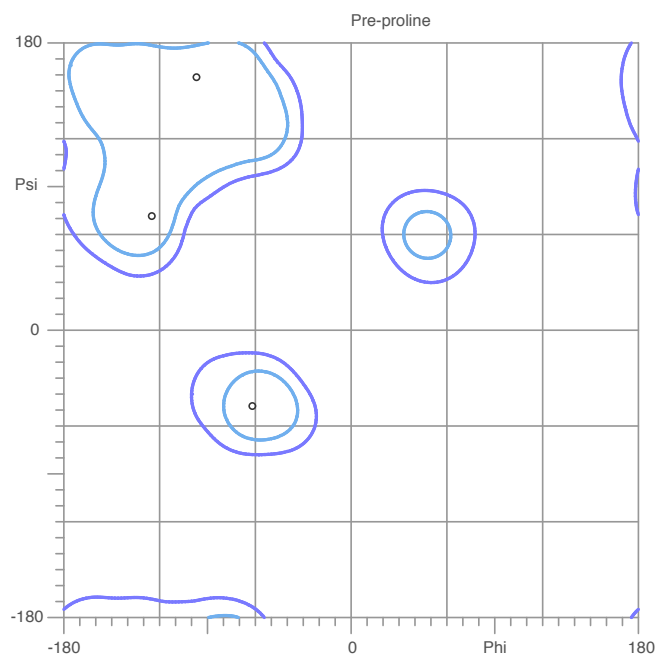
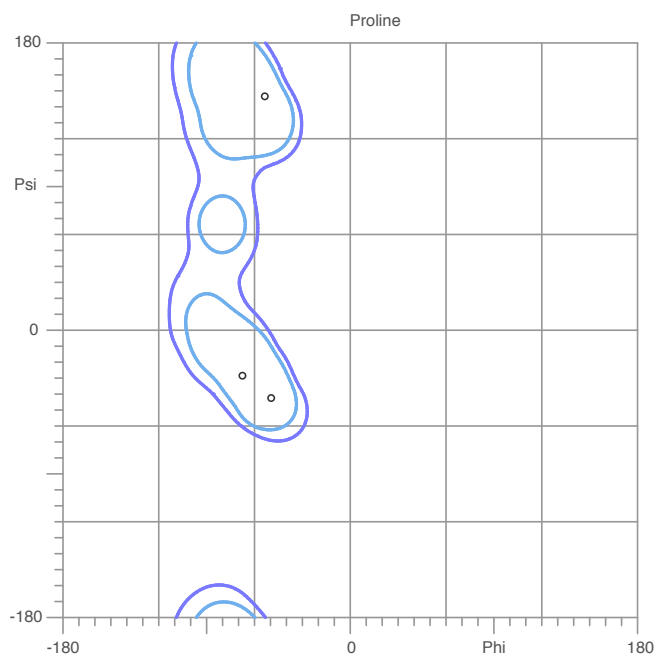
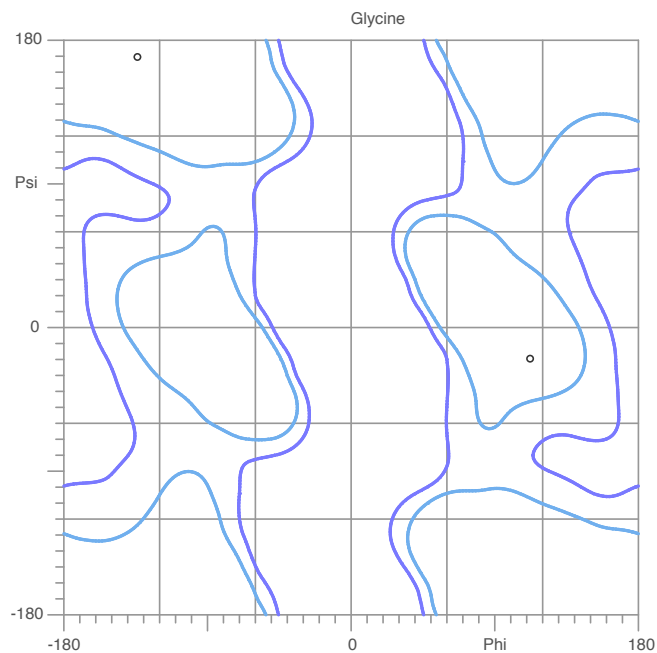
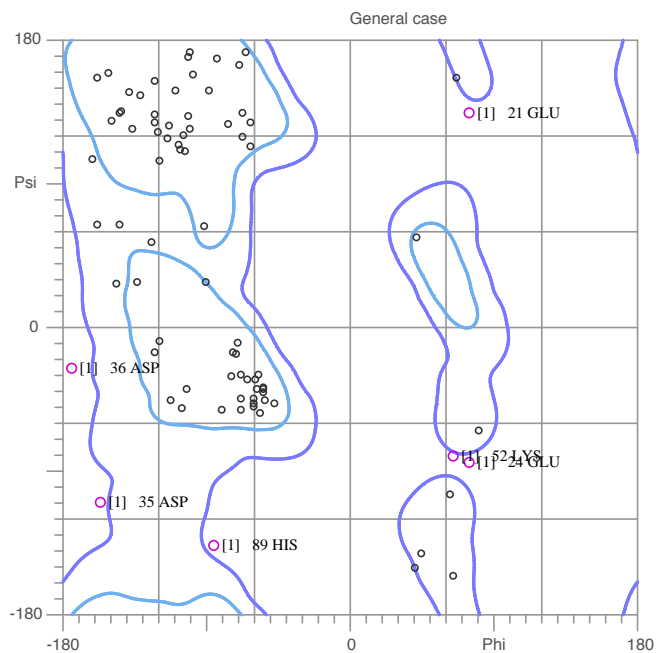
82.6% (735/890) of all residues were in favored (98%) regions.
94.9% (845/890) of all residues were in allowed (>99.8%) regions.

There were 45 outliers (phi, psi):

- [1] 21 GLU (75.0, 135.0)
- [1] 24 GLU (74.9, -85.0)
- [1] 35 ASP (-157.9, -109.0)
- [1] 36 ASP (-175.0, -25.2)
- [1] 52 LYS (65.0, -80.2)
- [1] 89 HIS (-86.4, -136.9)
- [2] 37 LYS (84.9, 115.1)
- [2] 34 VAL (30.6, 85.0)
- [2] 37 SER (-175.0, 55.0)
- [3] 23 ARG (-175.0, -22.0)
- [3] 24 GLU (-166.5, -45.0)
- [3] 34 VAL (25.0, 81.5)
- [4] 23 ARG (-36.8, -155.0)
- [4] 27 THR (85.2, -122.3)
- [4] 35 ASP (-157.7, -107.5)
- [4] 36 ASP (-175.1, -25.1)
- [4] 88 HIS (63.5, 106.7)
- [4] 90 HIS (-165.0, -5.0)
- [5] 3 ILE (65.1, 105.0)
- [5] 7 SER (75.9, 135.0)
- [5] 8 GLU (-169.6, 3.4)
- [5] 24 GLU (55.5, -85.1)
- [5] 34 VAL (66.2, -178.8)
- [5] 35 ASP (64.9, 92.5)
- [5] 36 ASP (-168.5, -35.0)
- [5] 37 SER (165.1, -25.0)
- [5] 52 LYS (65.0, -80.8)
- [6] 7 SER (61.0, 125.0)
- [6] 25 GLY (165.0, 69.1)
- [6] 34 VAL (25.0, 84.9)
- [6] 37 SER (175.0, -48.3)
- [6] 58 MET (47.1, -96.7)
- [7] 88 HIS (-87.2, -136.8)
- [8] 34 VAL (65.0, 157.7)
- [8] 35 ASP (-159.0, -105.0)
- [8] 36 ASP (-175.0, -25.0)
- [8] 52 LYS (65.0, -80.5)
- [8] 90 HIS (35.0, -153.8)
- [9] 12 HIS (78.2, 73.2)
- [9] 25 GLY (-150.3, -35.0)
- [9] 27 THR (-88.0, -119.7)
- [10] 3 ILE (65.0, 105.0)
- [10] 24 GLU (39.5, -103.9)
- [10] 34 VAL (65.0, 157.3)
- [10] 85 VAL (80.9, 111.0)

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 1



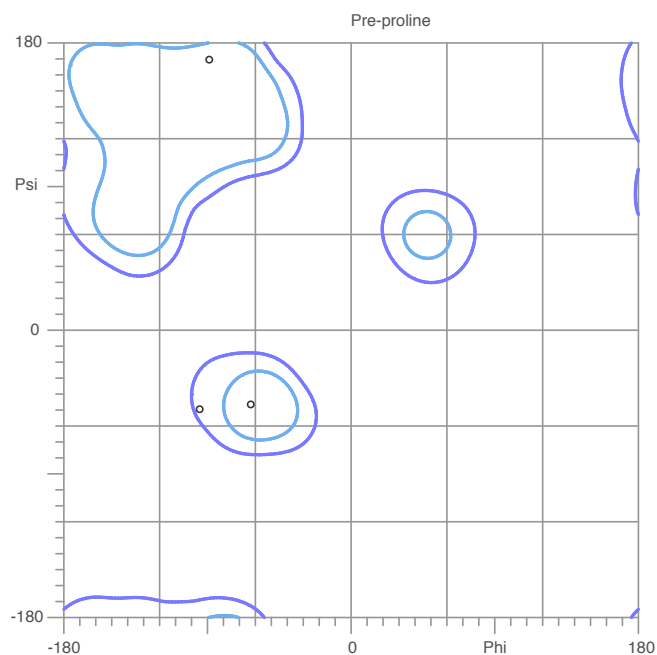
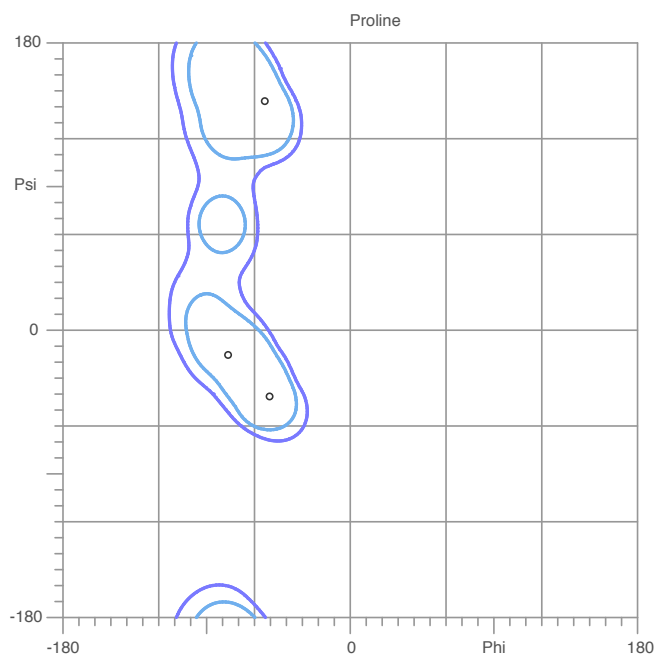
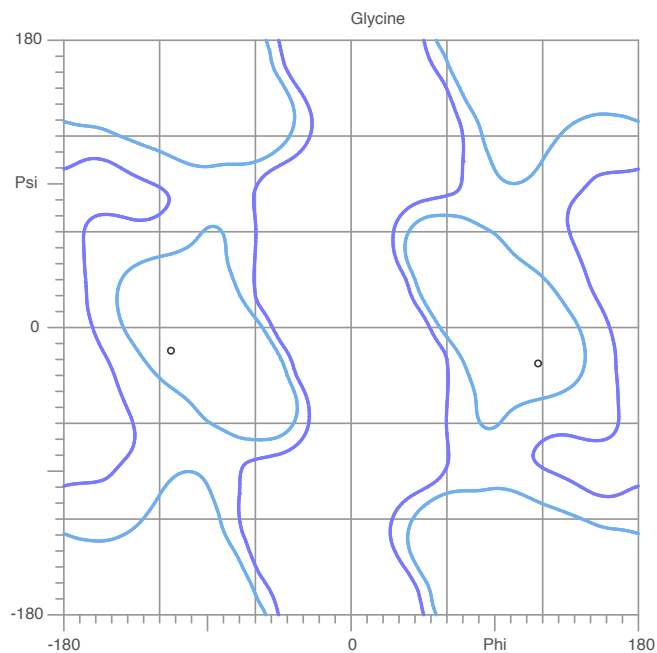
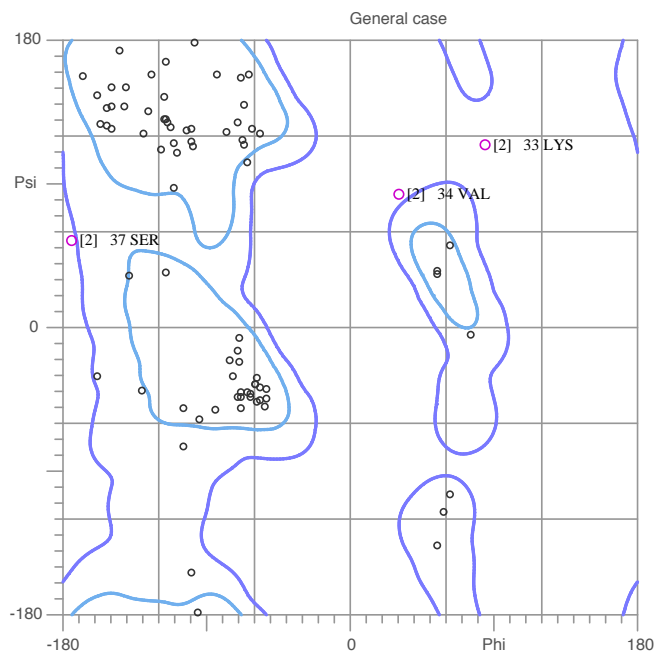
79.8% (71/89) of all residues were in favored (98%) regions.
93.3% (83/89) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[1] 21 GLU (75.0, 135.0)

[1] 24 GLU (74.9, -85.0)
[1] 35 ASP (-157.9, -109.0)
[1] 36 ASP (-175.0, -25.2)
[1] 52 LYS (65.0, -80.2)
[1] 89 HIS (-86.4, -136.9)

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 2



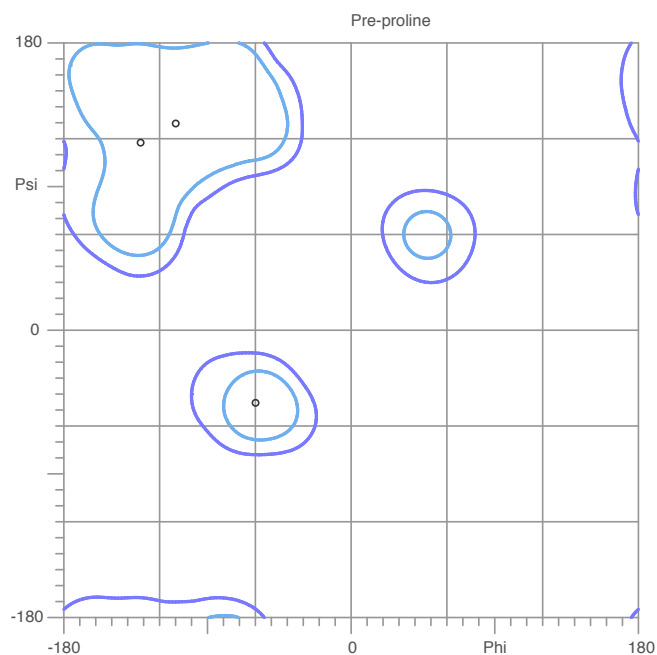
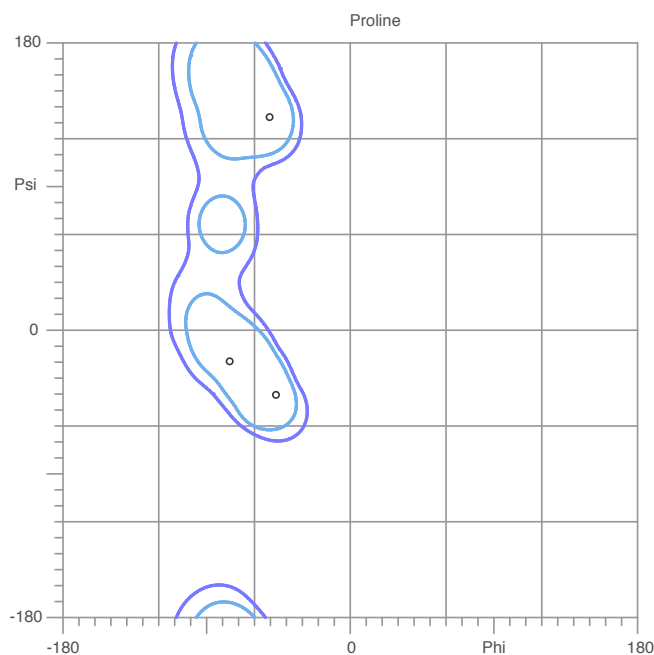
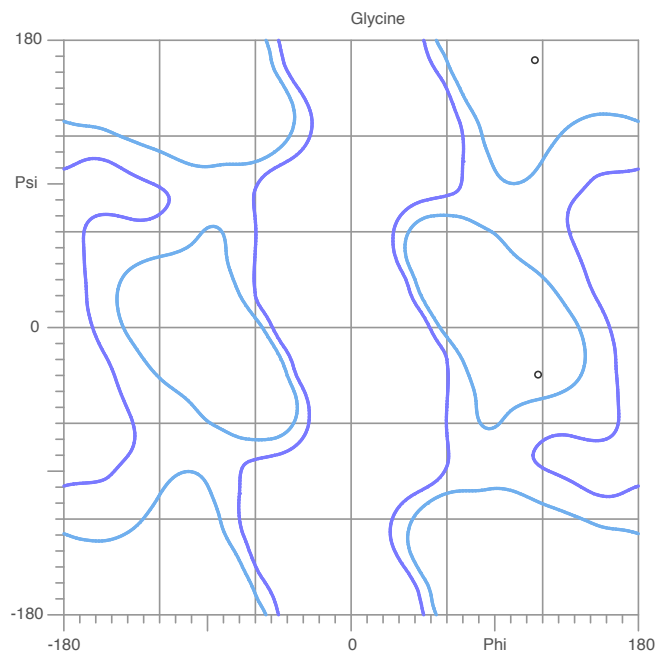
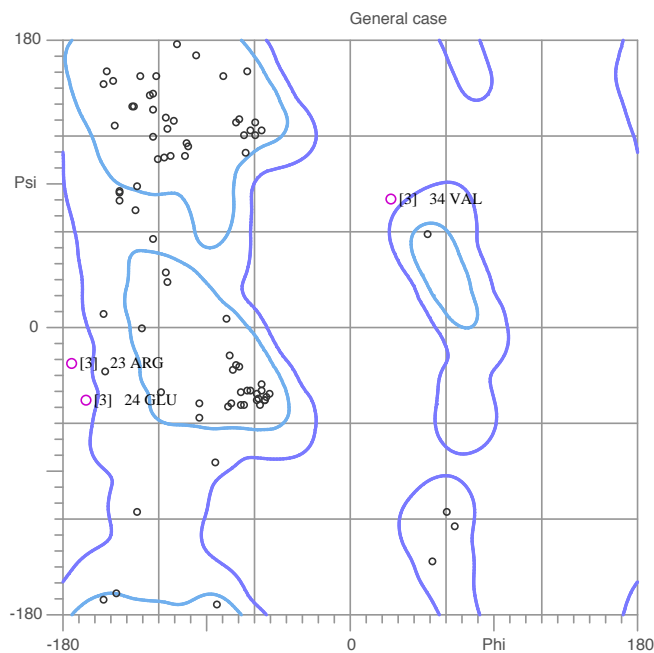
84.3% (75/89) of all residues were in favored (98%) regions.
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 33 LYS (84.9, 115.1)
- [2] 34 VAL (30.6, 85.0)
- [2] 37 SER (-175.0, 55.0)

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 3



83.1% (74/89) of all residues were in favored (98%) regions.
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

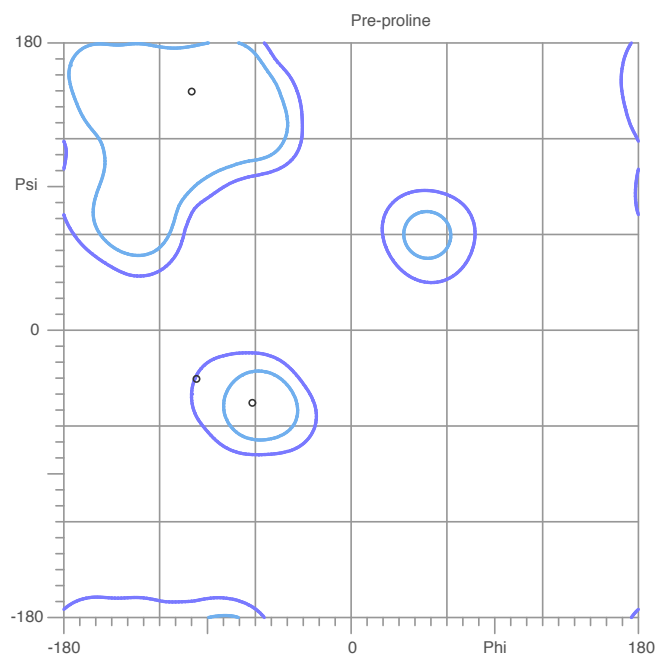
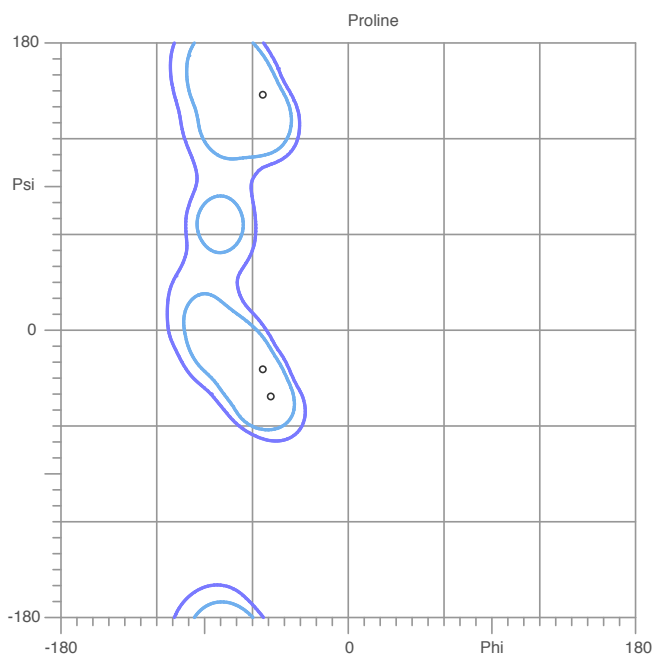
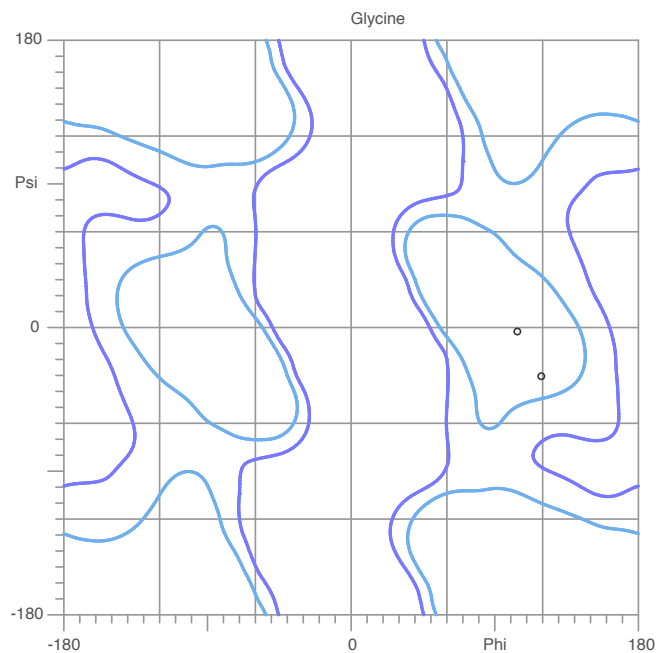
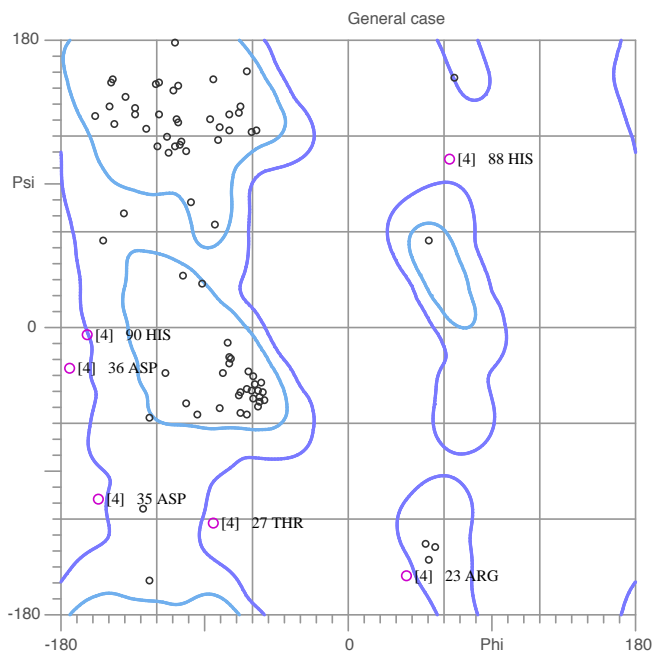
[3] 23 ARG (-175.0, -22.0)

[3] 24 GLU (-166.5, -45.0)

[3] 34 VAL (25.0, 81.5)

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 4



82.0% (73/89) of all residues were in favored (98%) regions.
93.3% (83/89) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[4] 23 ARG (36.8, -155.0)

[4] 27 THR (-85.2, -122.3)

[4] 35 ASP (-157.7, -107.5)

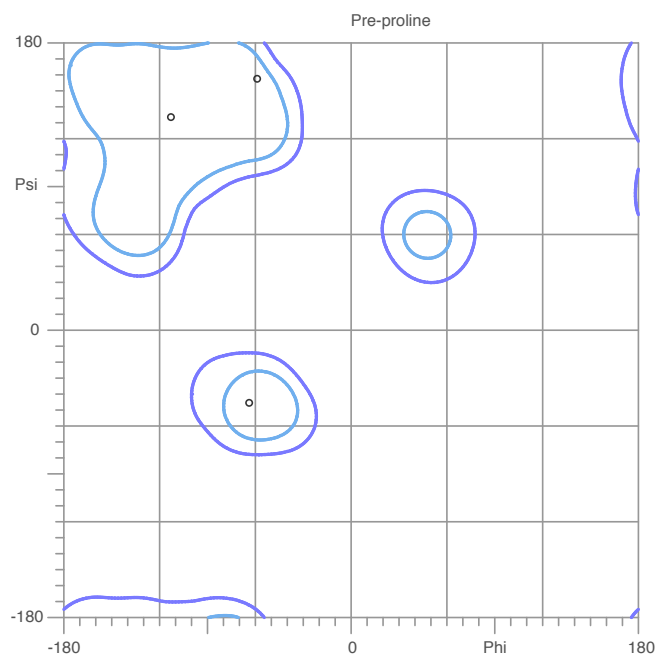
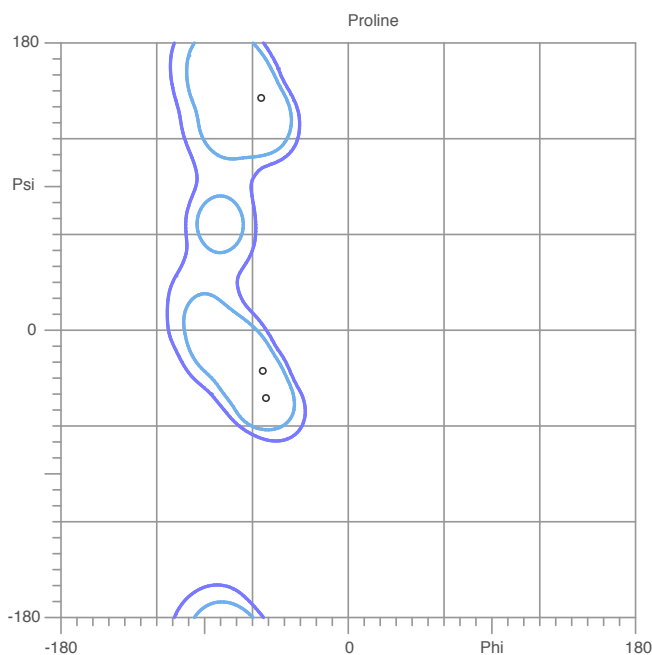
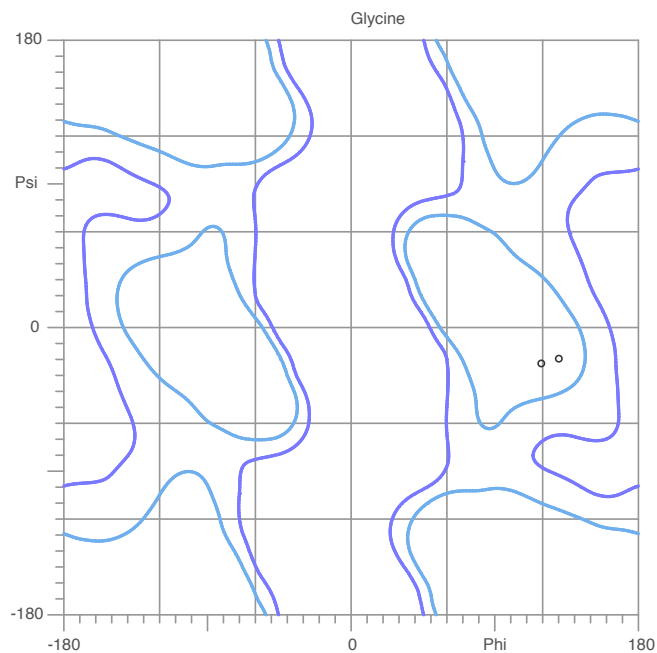
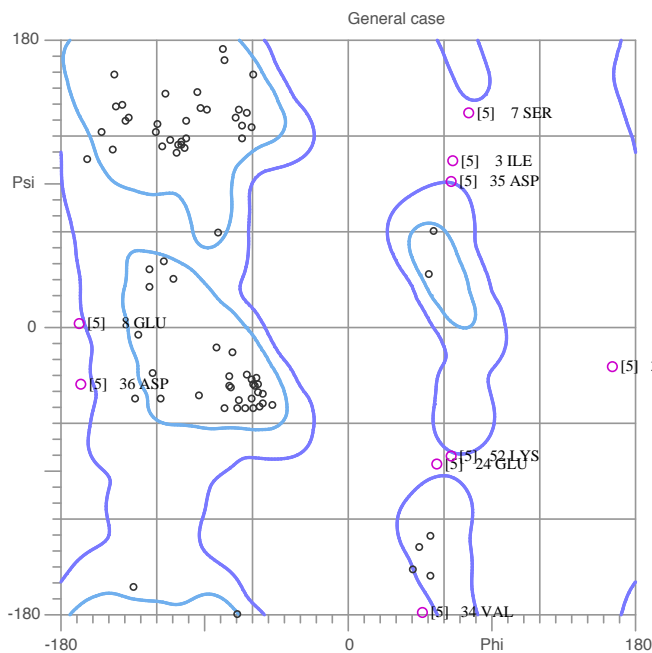
[4] 36 ASP (-175.1, -25.1)

[4] 88 HIS (63.5, 106.7)

[4] 90 HIS (-165.0, -5.0)

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 5



82.0% (73/89) of all residues were in favored (98%) regions.
89.9% (80/89) of all residues were in allowed (>99.8%) regions.

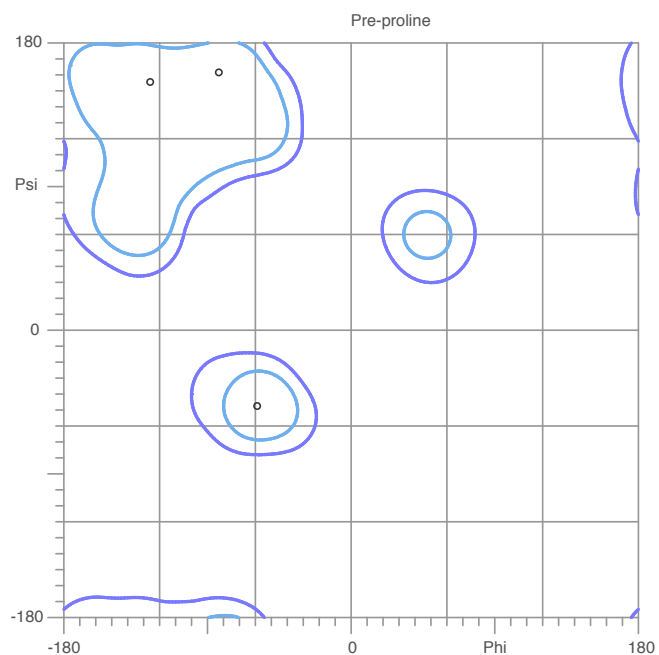
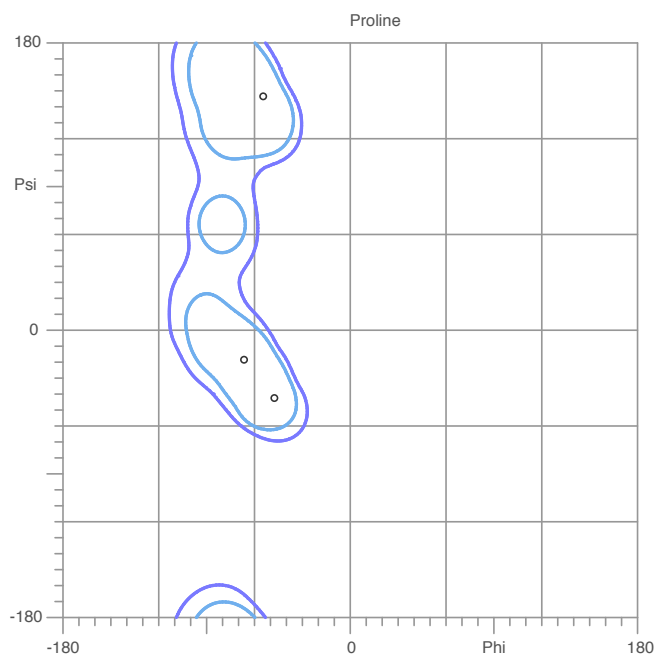
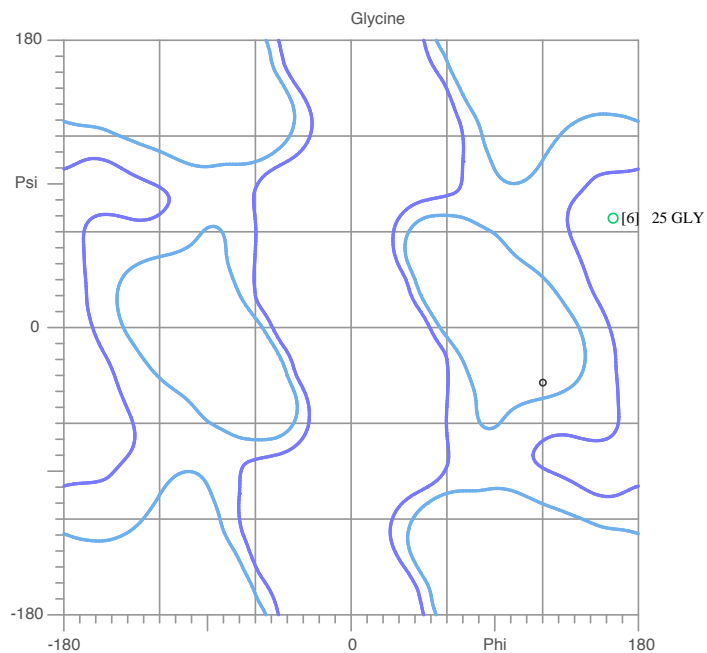
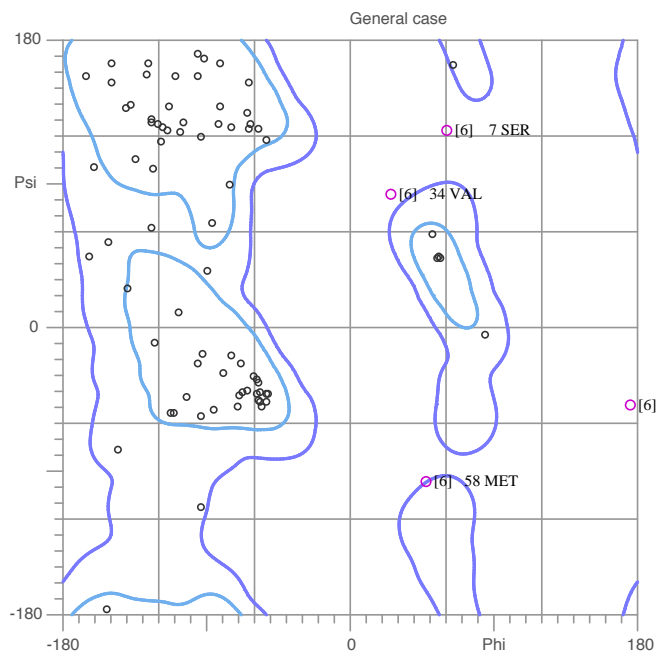
There were 9 outliers (phi, psi):

[5] 3 ILE (65.1, 105.0)
[5] 7 SER (75.9, 135.0)

[5] 8 GLU (-169.6, 3.4)
[5] 24 GLU (55.5, -85.1)
[5] 34 VAL (46.2, -178.8)
[5] 35 ASP (64.9, 92.5)
[5] 36 ASP (-168.5, -35.0)
[5] 37 SER (165.1, -25.0)
[5] 52 LYS (65.0, -80.8)

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 6



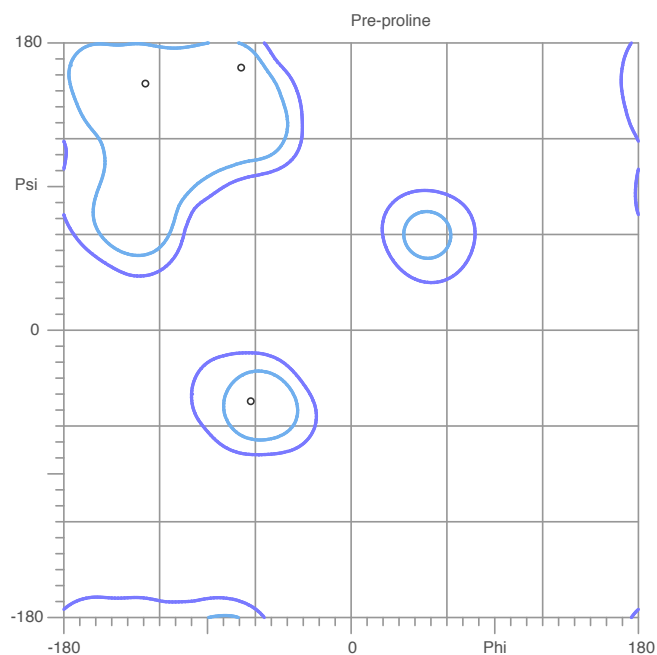
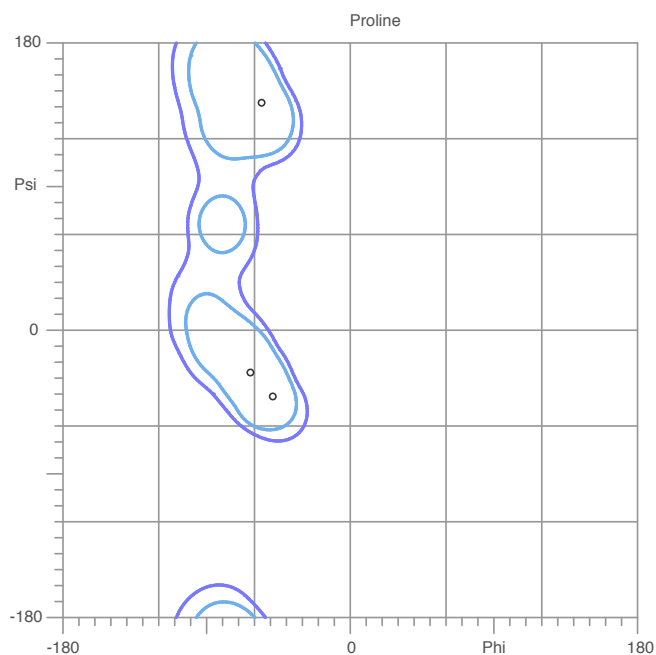
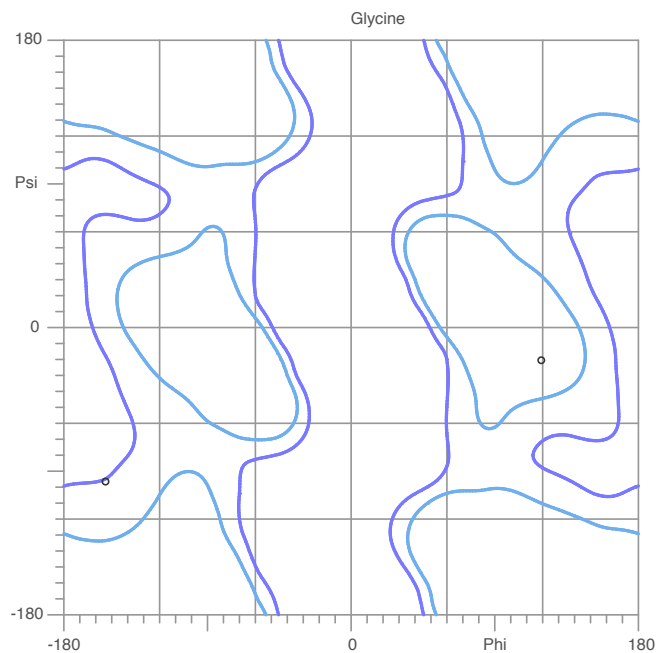
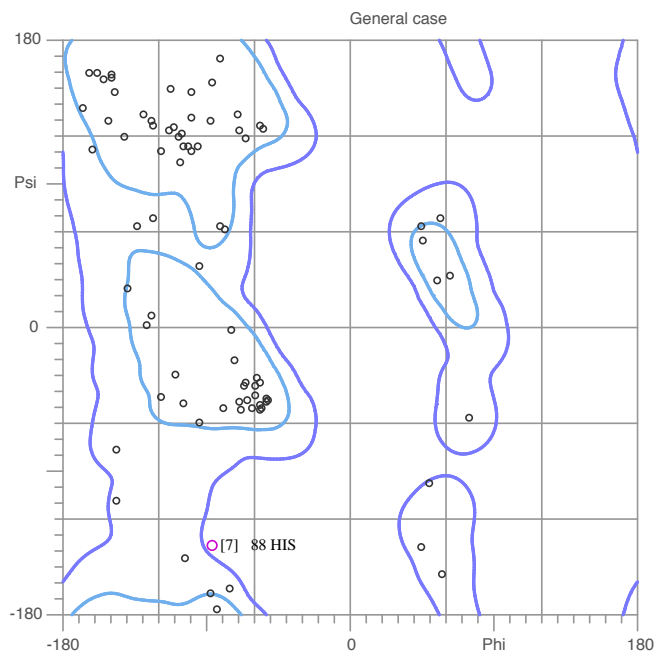
83.1% (74/89) of all residues were in favored (98%) regions.
94.4% (84/89) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[6] 7 SER (61.0, 125.0)
[6] 25 GLY (165.0, 69.1)
[6] 34 VAL (25.0, 84.9)
[6] 37 SER (175.0, -48.3)
[6] 58 MET (47.1, -96.7)

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 7



79.8% (71/89) of all residues were in favored (98%) regions.
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

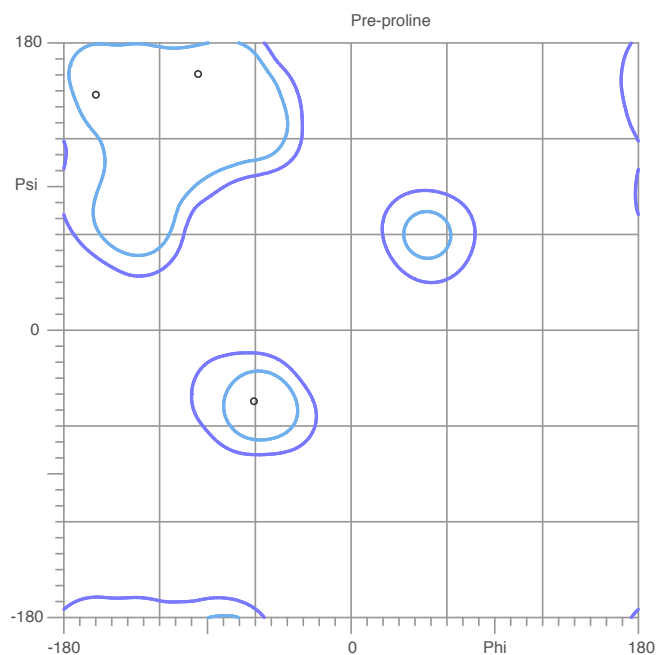
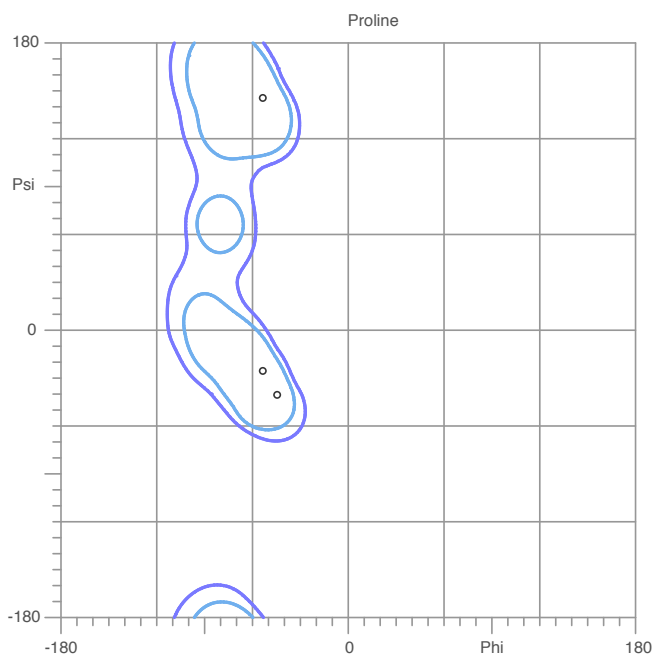
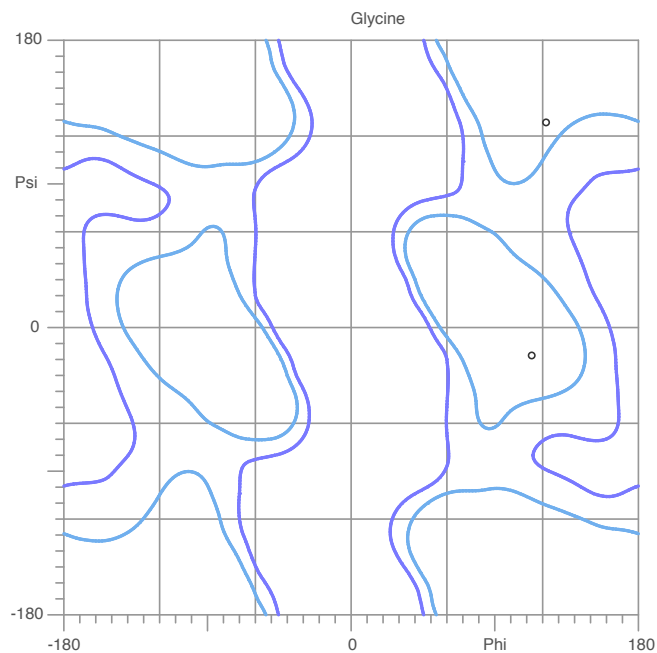
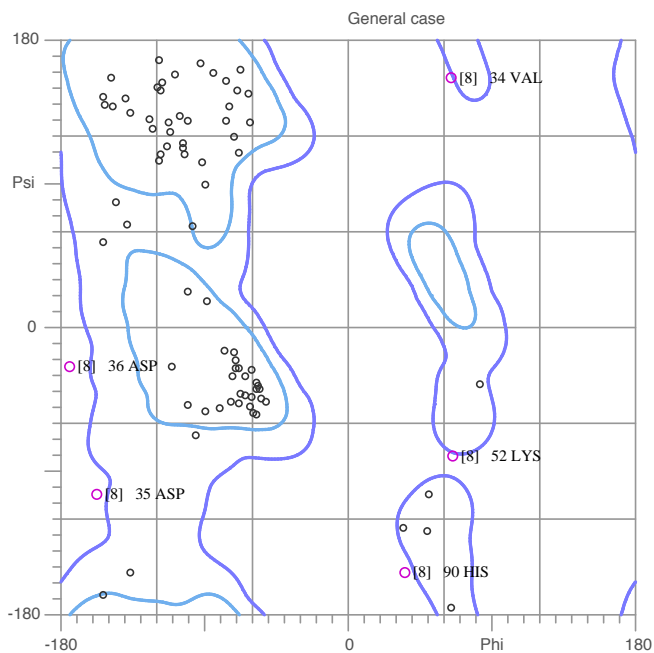
There were 1 outliers (phi, psi):
[7] 88 HIS (-87.2, -136.8)

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

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

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 8



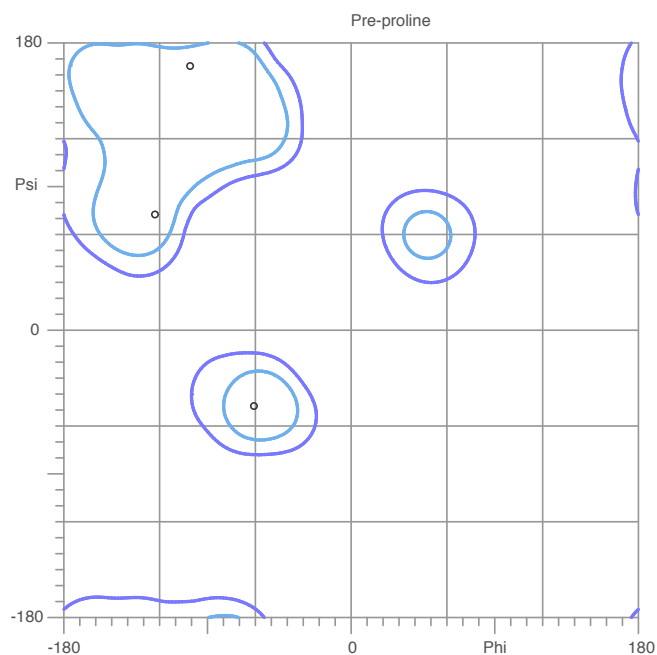
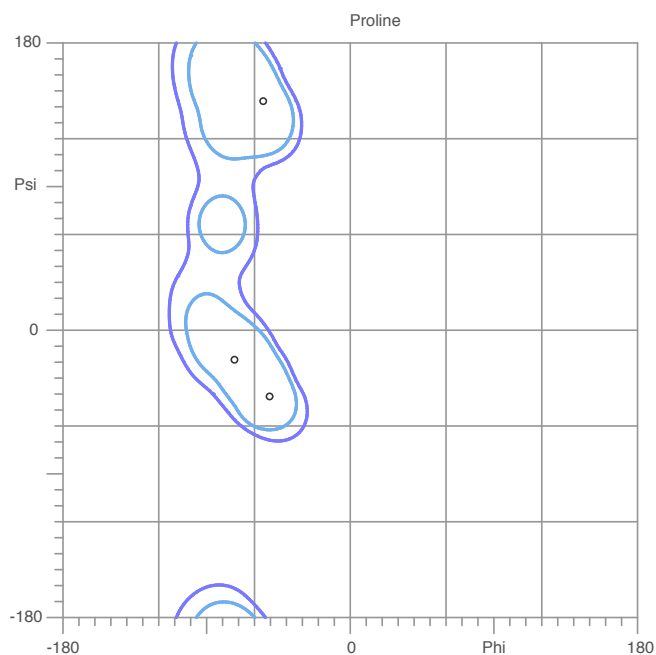
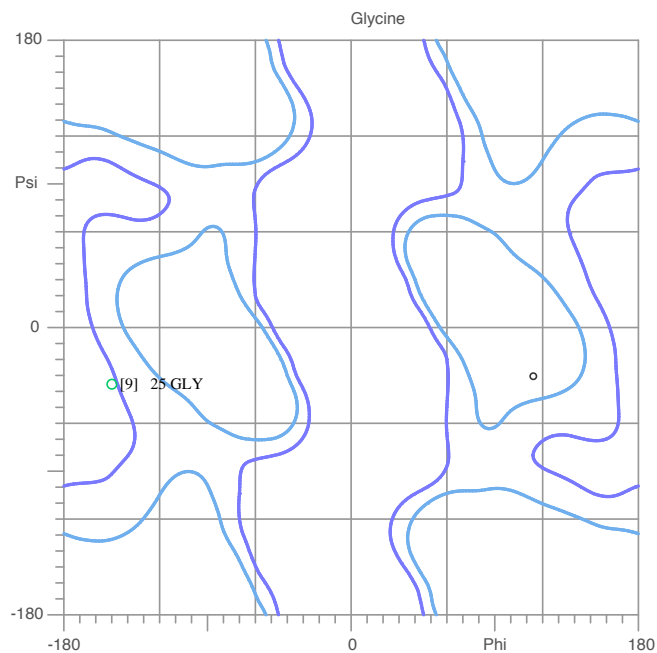
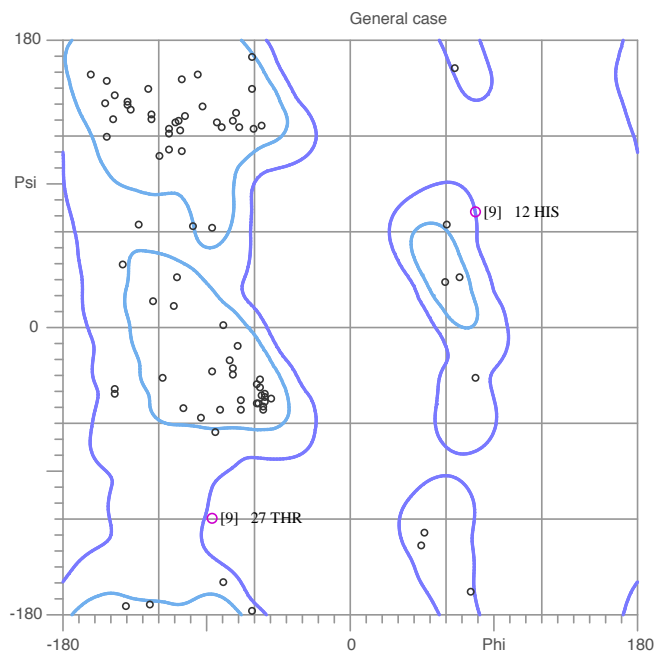
82.0% (73/89) of all residues were in favored (98%) regions.
94.4% (84/89) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [8] 34 VAL (65.0, 157.7)
- [8] 35 ASP (-159.0, -105.0)
- [8] 36 ASP (-175.0, -25.0)
- [8] 52 LYS (65.0, -80.5)
- [8] 90 HIS (35.0, -153.8)

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 9



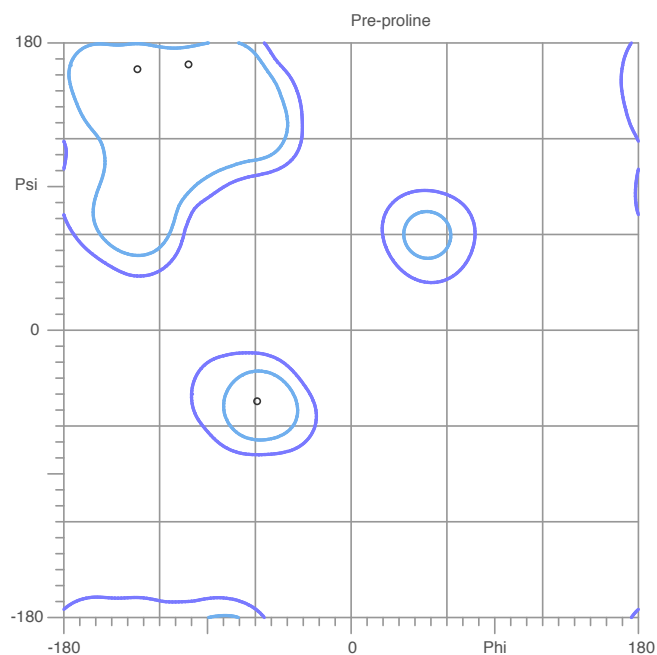
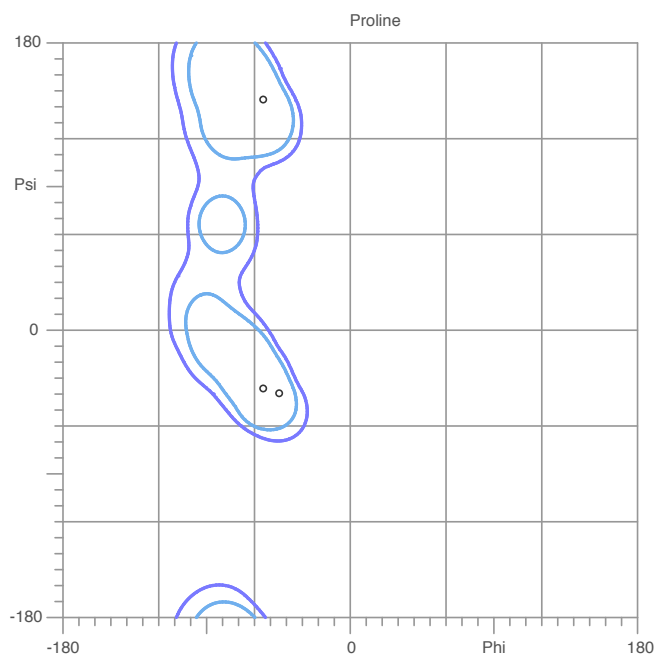
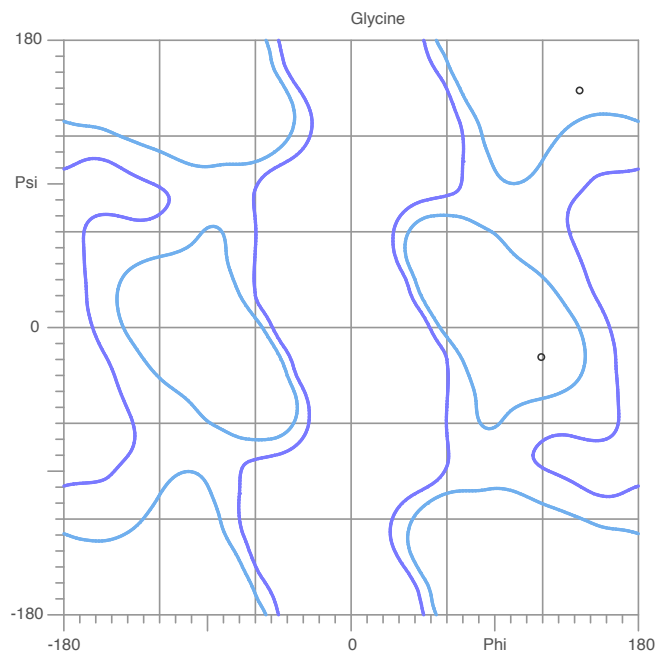
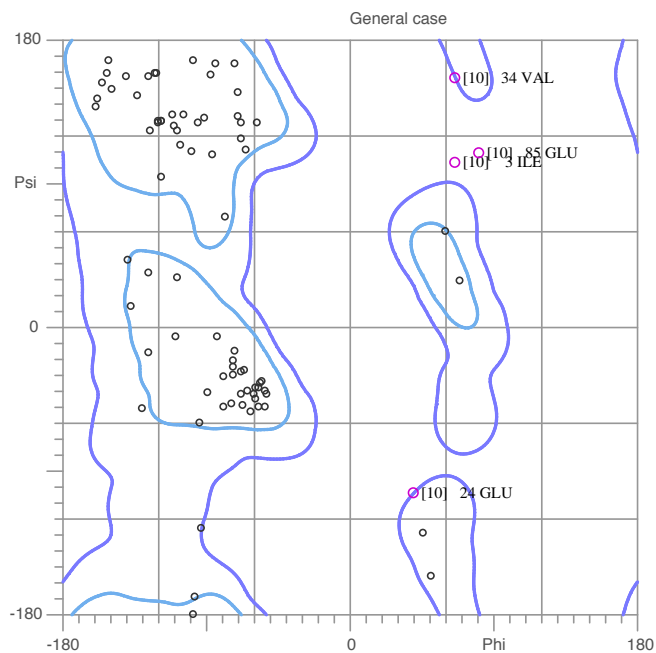
80.9% (72/89) of all residues were in favored (98%) regions.
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [9] 12 HIS (78.2, 73.2)
- [9] 25 GLY (-150.3, -35.0)
- [9] 27 THR (-88.0, -119.7)

MolProbity Ramachandran analysis

ZR18_R3Cons_em_bcr3.pdb, model 10



88.8% (79/89) of all residues were in favored (98%) regions.
95.5% (85/89) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [10] 3 ILE (65.0, 105.0)
- [10] 24 GLU (39.5, -103.9)
- [10] 34 VAL (65.0, 157.3)
- [10] 85 GLU (80.9, 111.0)