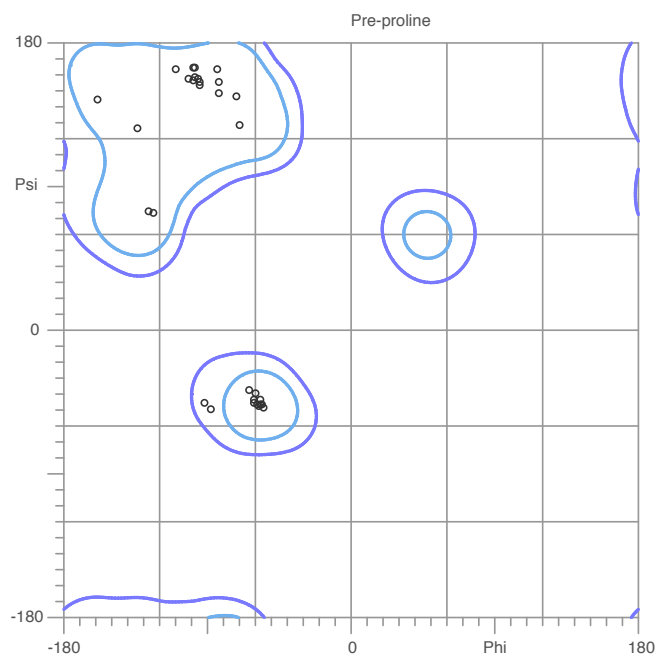
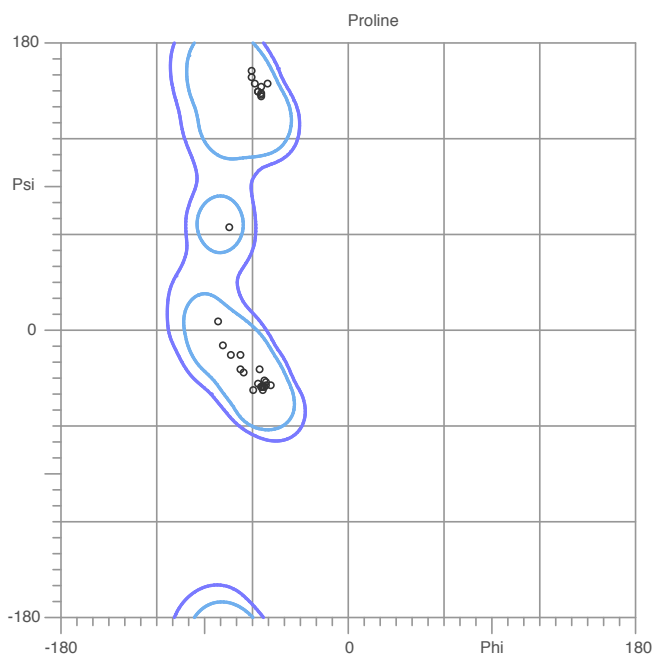
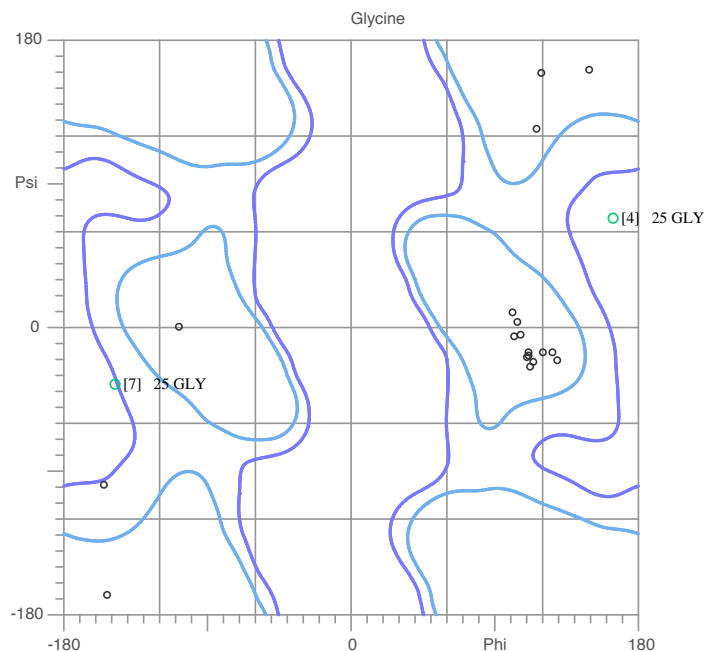
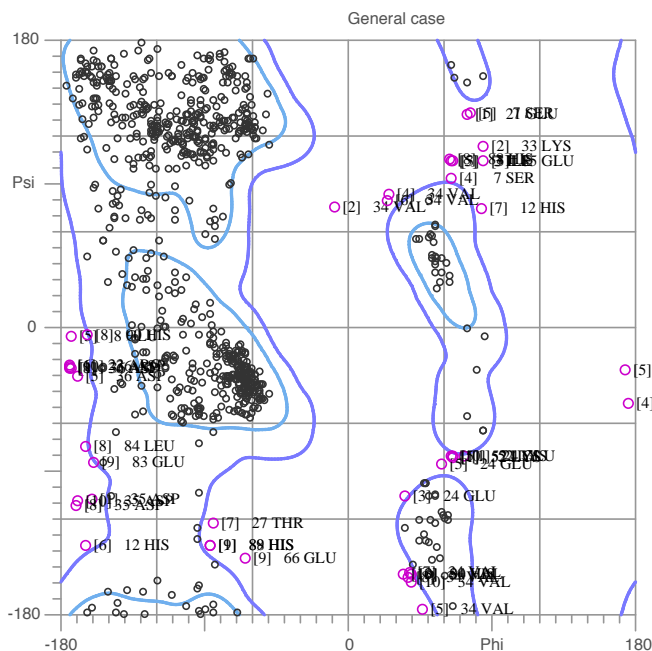


MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, all models



83.0% (739/890) of all residues were in favored (98%) regions.
94.9% (845/890) of all residues were in allowed (>99.8%) regions.

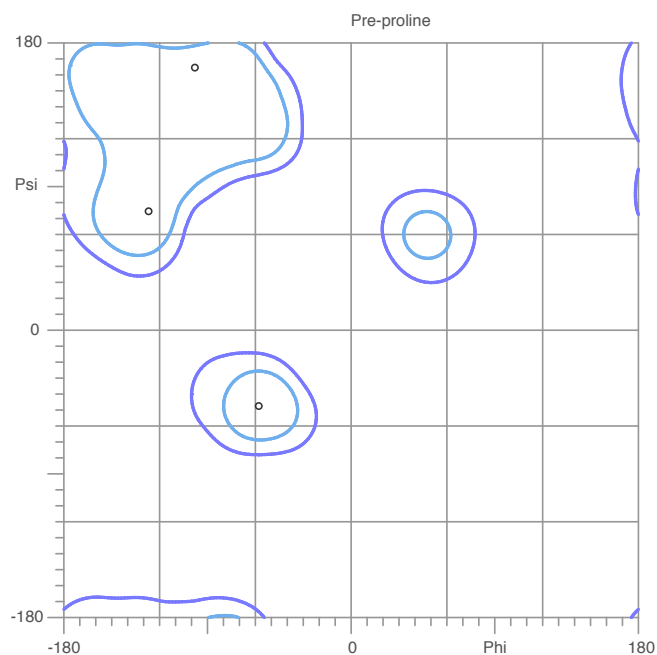
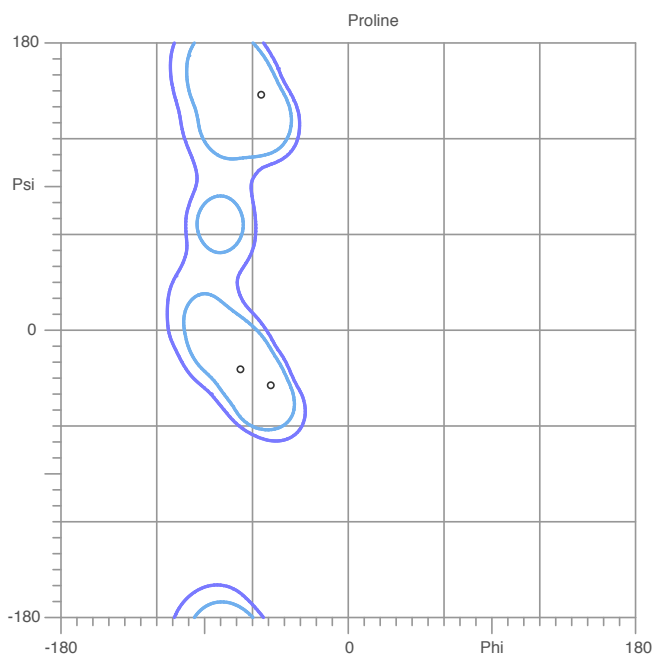
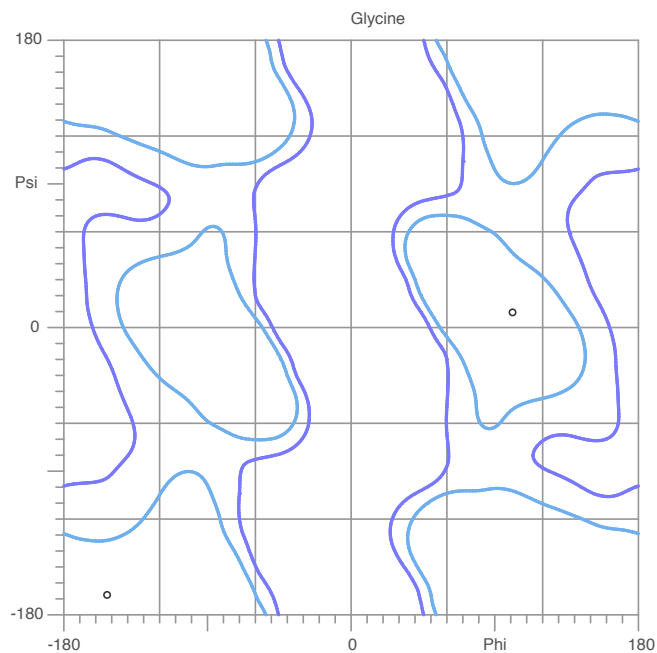
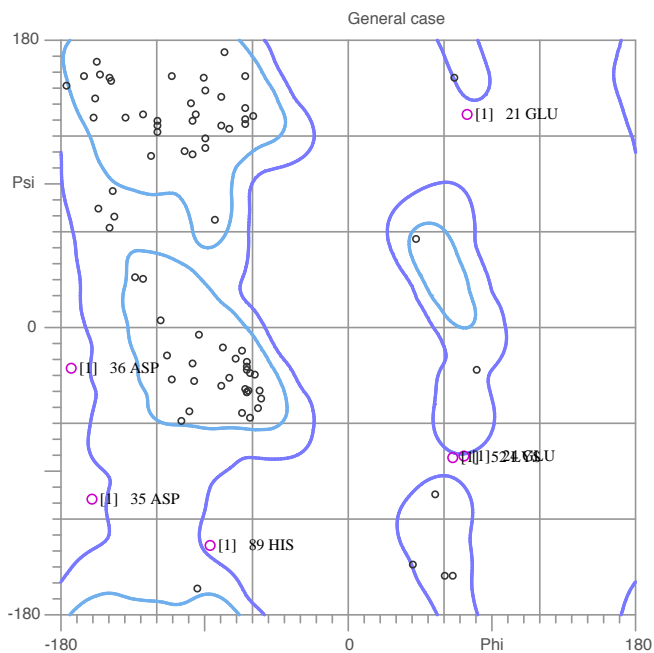
There were 45 outliers (phi, psi):

- [1] 21 GLU (74.9, 135.0)
- [1] 24 GLU (72.9, -80.0)
- [1] 35 ASP (-161.3, -107.8)
- [1] 36 ASP (-175.0, -25.7)
- [1] 52 LYS (65.0, -81.2)
- [1] 89 HIS (-87.6, -136.9)
- [2] 33 LYS (84.4, 115.0)
- [2] 34 VAL (-9.9, 76.6)
- [3] 3 ILE (65.0, 105.0)
- [3] 24 GLU (35.1, -105.1)
- [3] 34 VAL (39.4, -154.6)
- [3] 85 GLU (85.0, 105.1)
- [4] 7 SER (64.2, 95.0)
- [4] 25 GLY (164.9, 69.2)
- [4] 34 VAL (25.0, 84.9)
- [4] 37 SER (175.3, -47.6)
- [5] 3 ILE (65.0, 105.0)
- [5] 7 SER (76.3, 135.0)
- [5] 8 GLU (-174.9, -5.1)
- [5] 24 GLU (58.2, -85.0)

- [5] 34 VAL (46.9, -176.6)
- [5] 36 ASP (-170.3, -30.7)
- [5] 37 SER (173.6, -26.3)
- [5] 52 LYS (65.1, 80.1)
- [6] 12 HIS (-165.1, -136.5)
- [6] 23 ARG (-175.0, -23.4)
- [6] 34 VAL (24.9, 80.9)
- [7] 12 HIS (83.7, 75.4)
- [7] 25 GLY (-148.8, -35.1)
- [7] 27 THR (-85.2, -122.7)
- [7] 34 VAL (38.5, -153.7)
- [8] 34 VAL (37.4, -156.9)
- [8] 35 ASP (-171.7, -111.5)
- [8] 36 ASP (-175.2, -25.2)
- [8] 84 LEU (-165.1, -75.0)
- [8] 88 HIS (63.5, 106.9)
- [8] 90 HIS (-165.0, -5.0)
- [9] 66 GLU (65.6, -144.9)
- [9] 83 GLU (-160.1, -84.9)
- [9] 88 HIS (-87.9, -136.6)
- [10] 34 VAL (39.1, -159.4)
- [10] 35 ASP (-170.3, -109.0)
- [10] 36 ASP (-175.1, -25.0)
- [10] 52 LYS (64.9, -80.9)
- [10] 90 HIS (35.0, -155.0)

MolProbity Ramachandran analysis

ZR18_R3_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 (74.9, 135.0)

[1] 24 GLU (72.9, -80.0)

[1] 35 ASP (-161.3, -107.8)

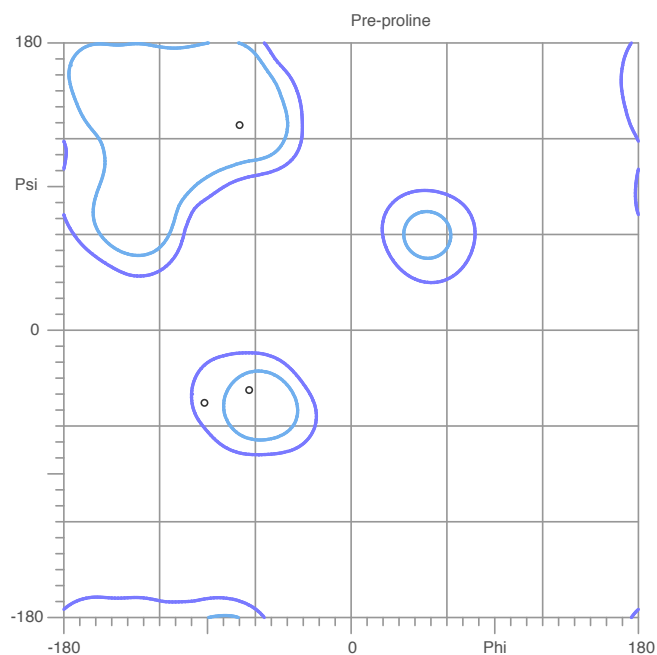
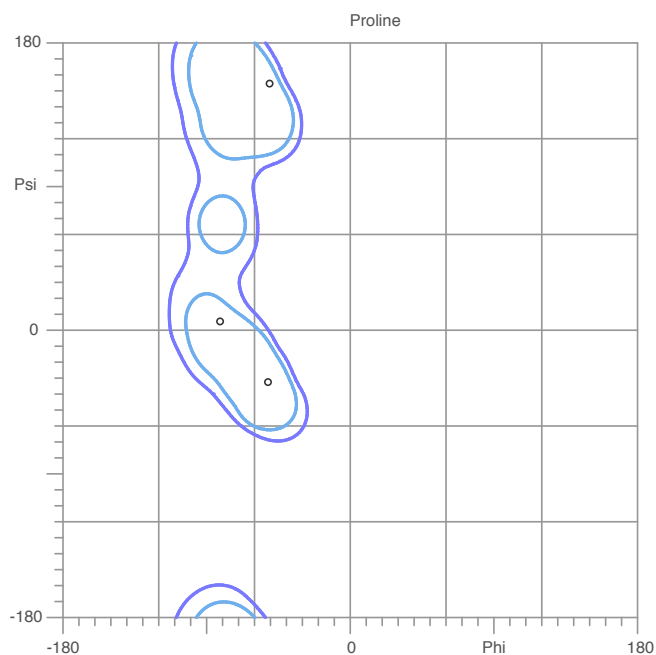
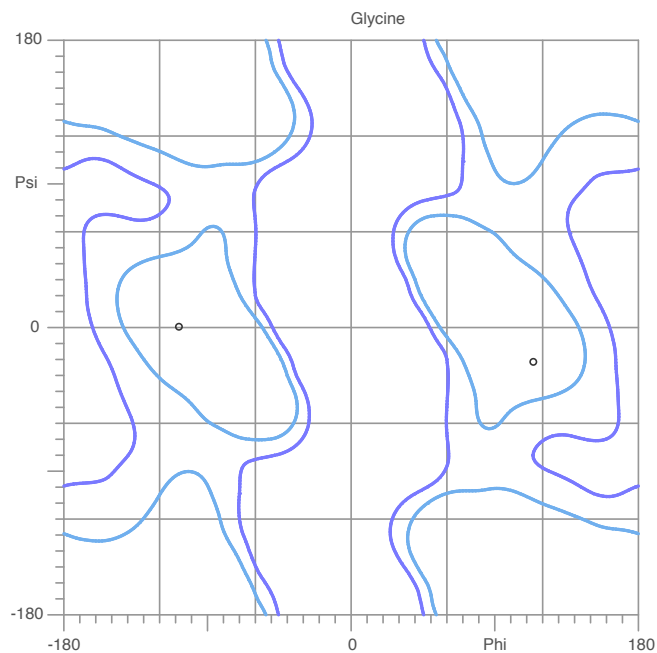
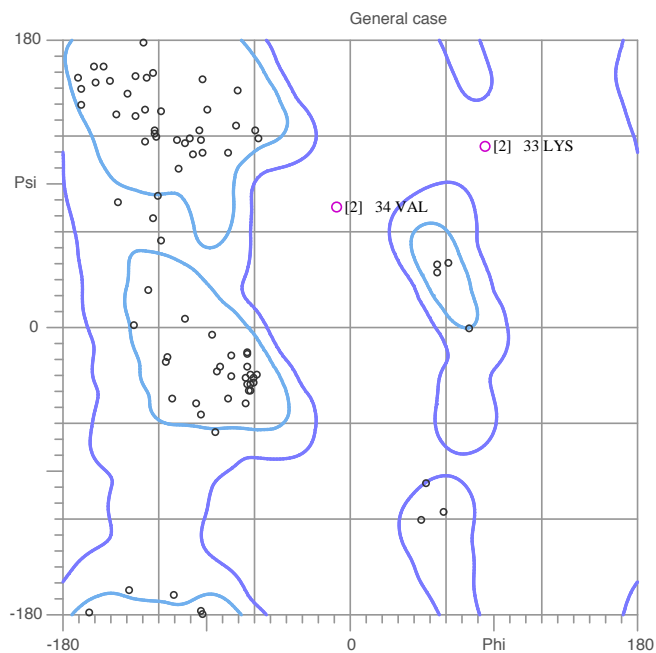
[1] 36 ASP (-175.0, -25.7)

[1] 52 LYS (65.0, -81.2)

[1] 89 HIS (-87.6, -136.9)

MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, model 2



85.4% (76/89) of all residues were in favored (98%) regions.
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

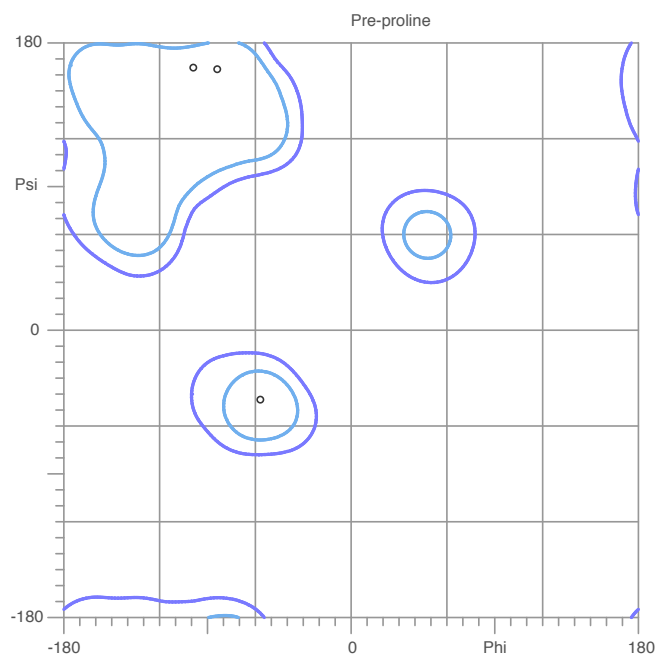
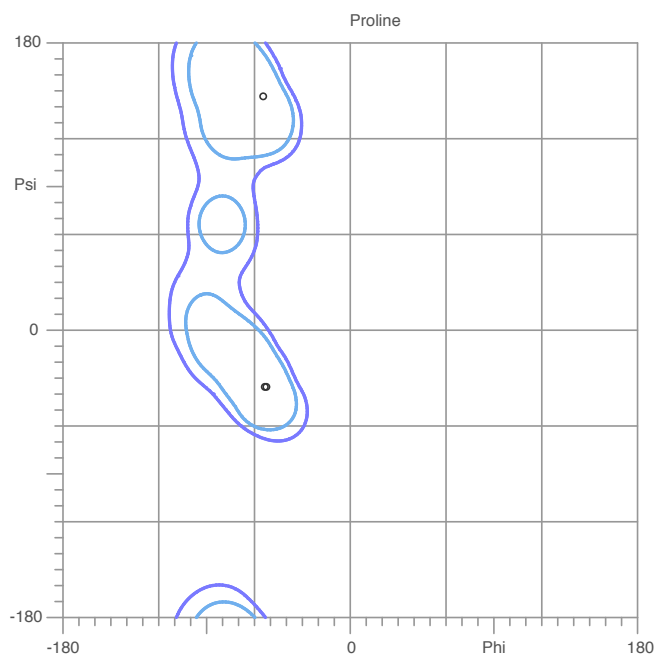
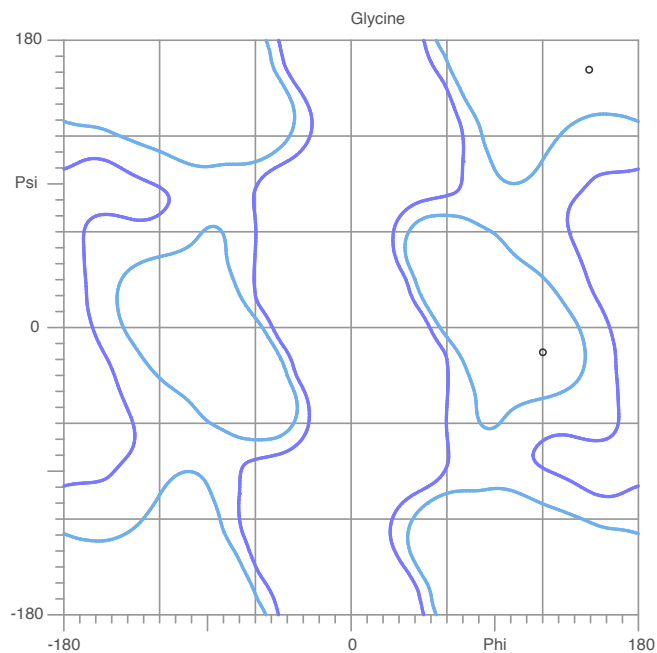
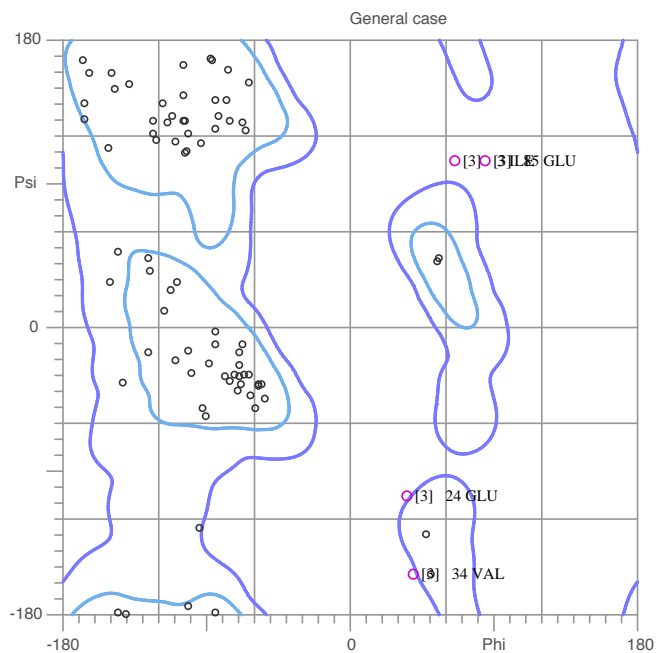
There were 2 outliers (phi, psi):

[2] 33 LYS (84.4, 115.0)

[2] 34 VAL (-9.9, 76.6)

MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, model 3



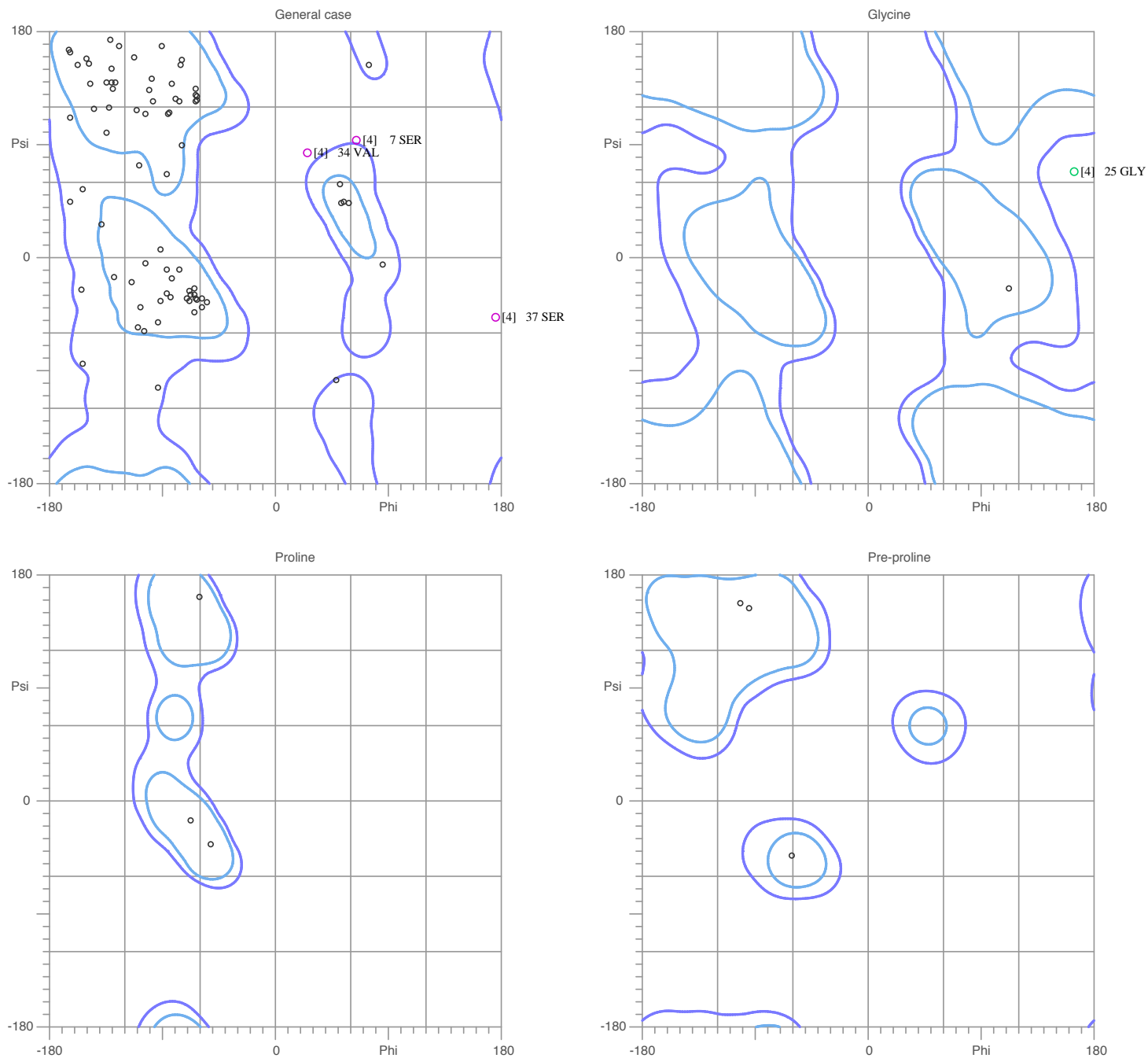
88.8% (79/89) of all residues were in favored (98%) regions.
95.5% (85/89) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [3] 3 ILE (65.0, 105.0)
- [3] 24 GLU (35.1, -105.1)
- [3] 34 VAL (39.4, -154.6)
- [3] 85 GLU (85.0, 105.1)

MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, model 4



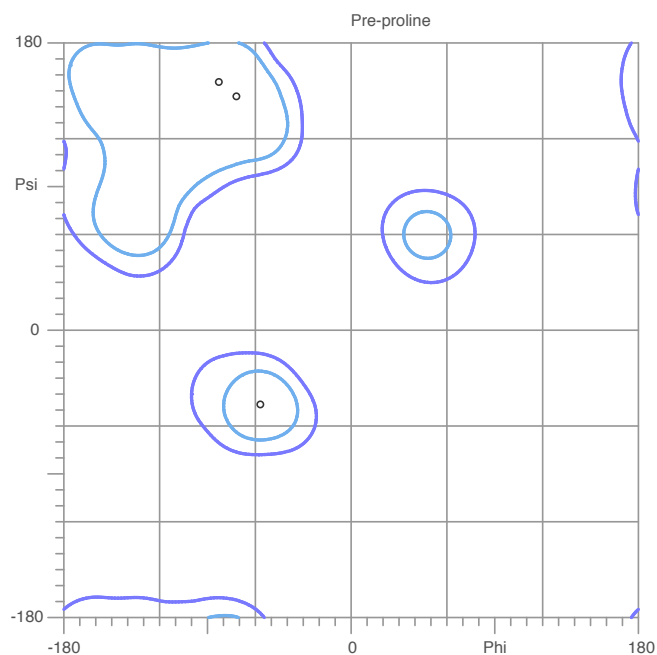
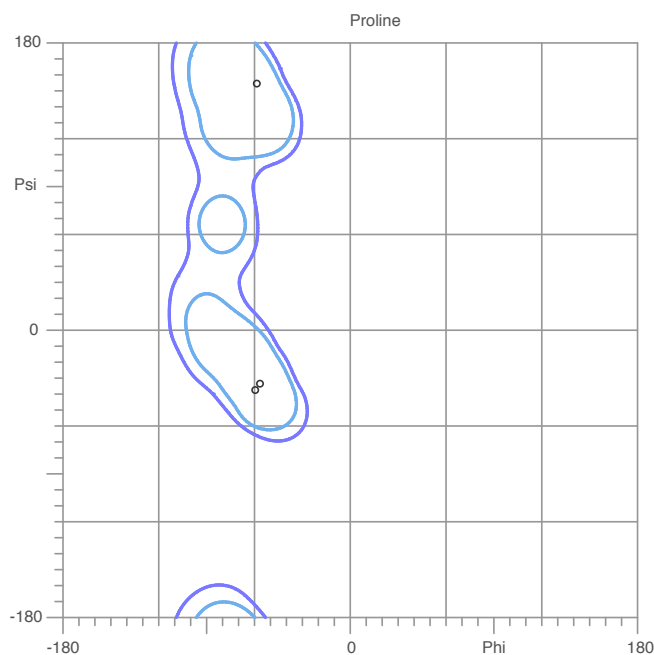
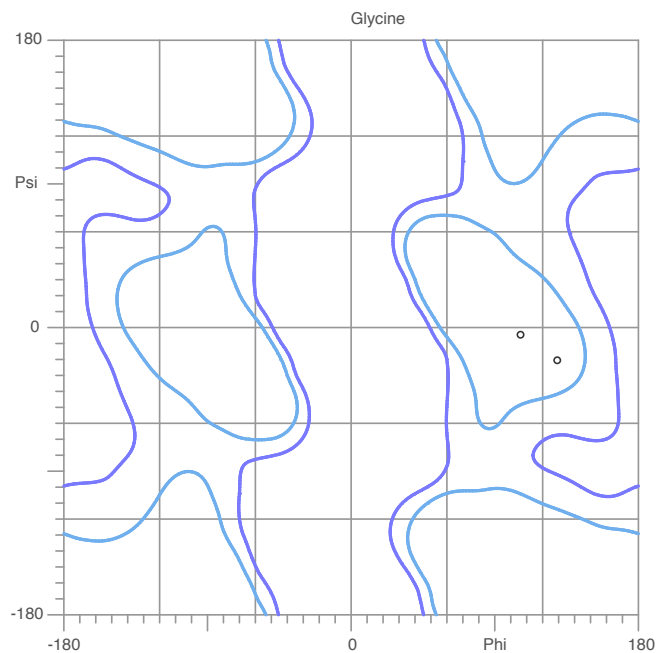
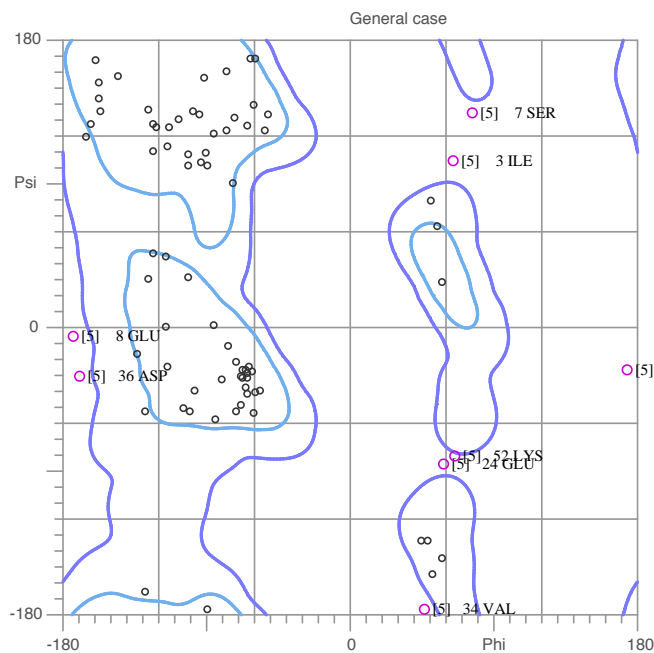
84.3% (75/89) of all residues were in favored (98%) regions.
95.5% (85/89) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [4] 7 SER (64.2, 95.0)
- [4] 25 GLY (164.9, 69.2)
- [4] 34 VAL (25.0, 84.9)
- [4] 37 SER (175.3, -47.6)

MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, model 5



78.7% (70/89) of all residues were in favored (98%) regions.
91.0% (81/89) of all residues were in allowed (>99.8%) regions.

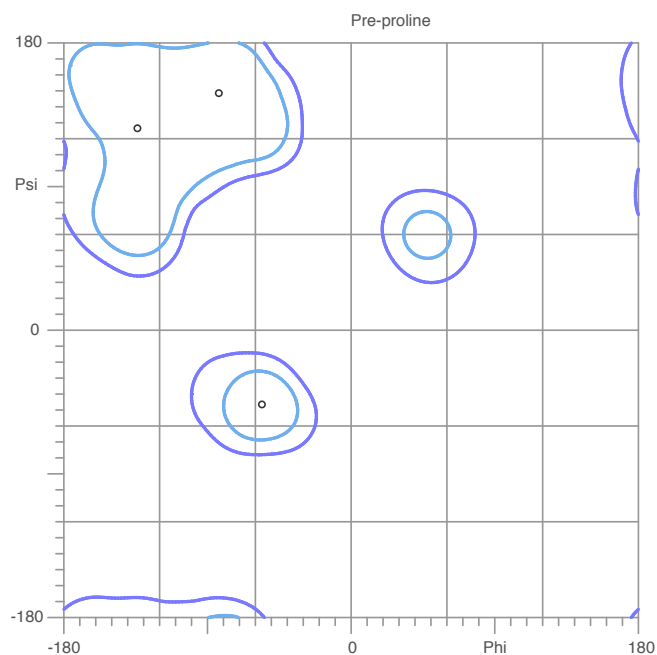
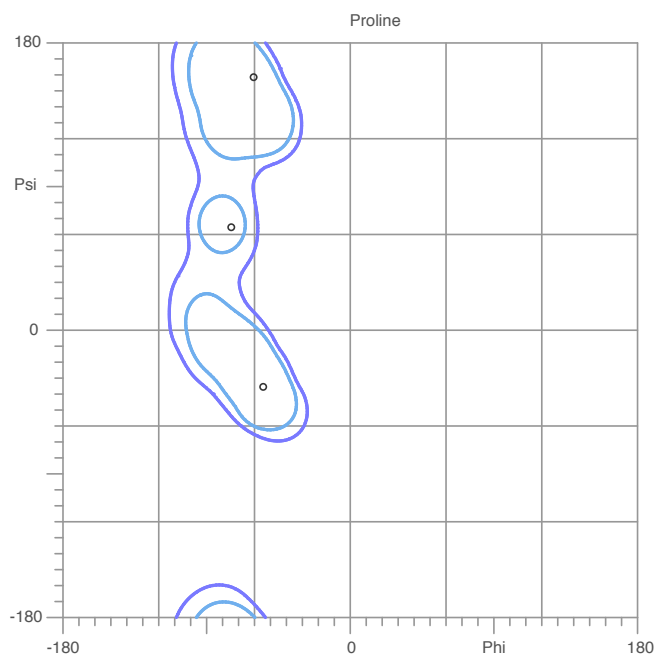
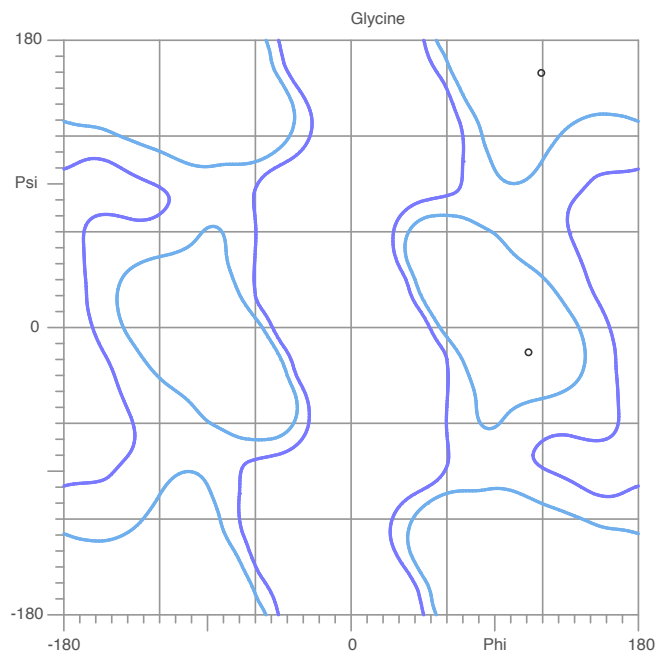
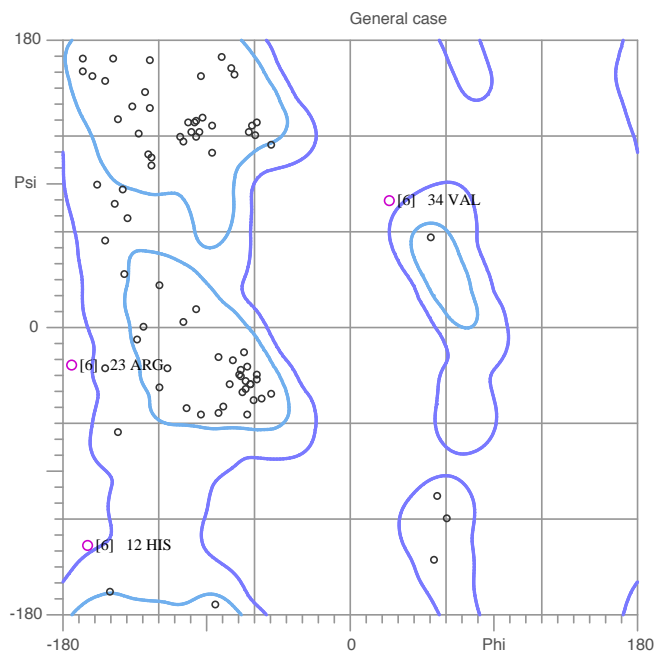
There were 8 outliers (phi, psi):

[5] 3 ILE (65.0, 105.0)
[5] 7 SER (76.3, 135.0)

[5] 8 GLU (-174.9, -5.1)
[5] 24 GLU (58.2, -85.0)
[5] 34 VAL (46.9, -176.6)
[5] 36 ASP (-170.3, -30.7)
[5] 37 SER (173.6, -26.3)
[5] 52 LYS (65.1, -80.1)

MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, model 6



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):

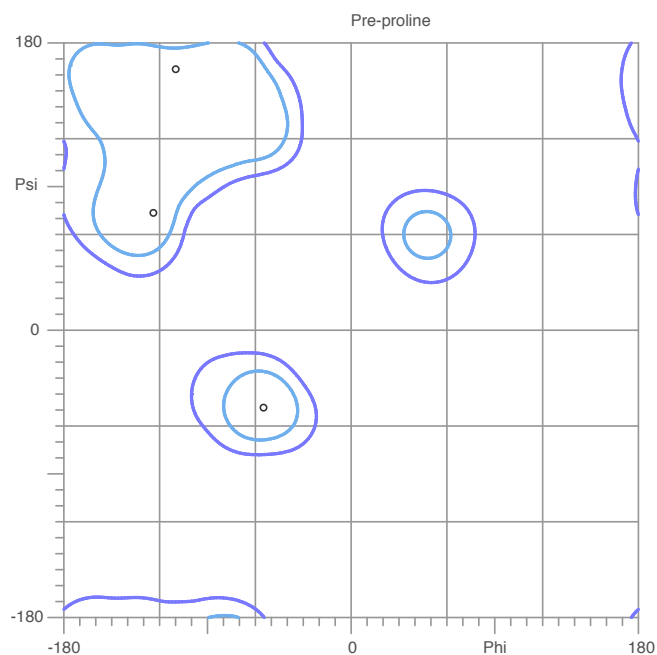
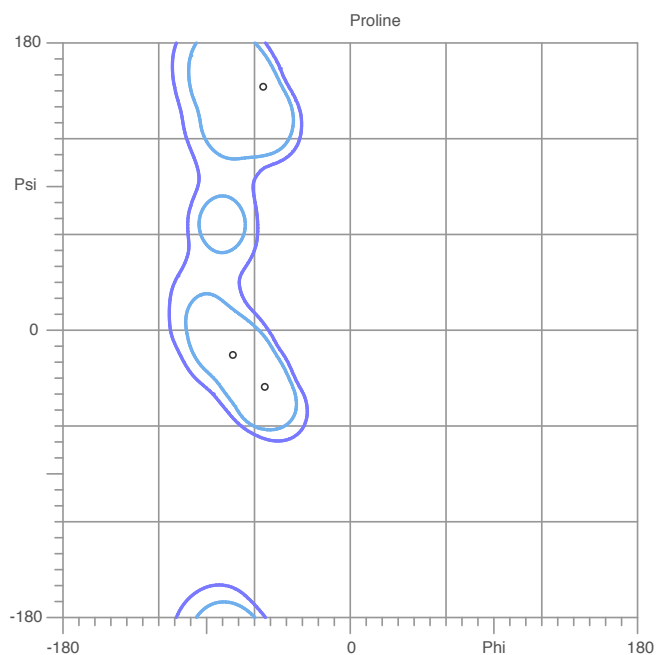
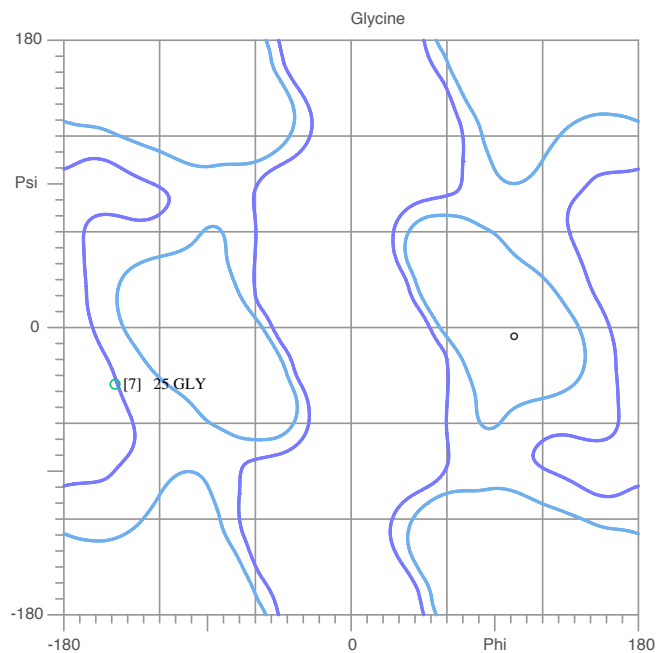
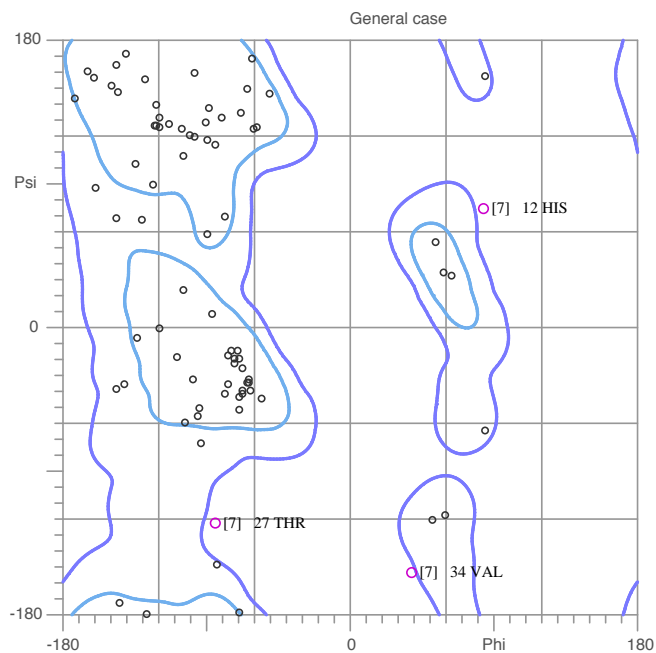
[6] 12 HIS (-165.1, -136.5)

[6] 23 ARG (-175.0, -23.4)

[6] 34 VAL (24.9, 80.9)

MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, model 7



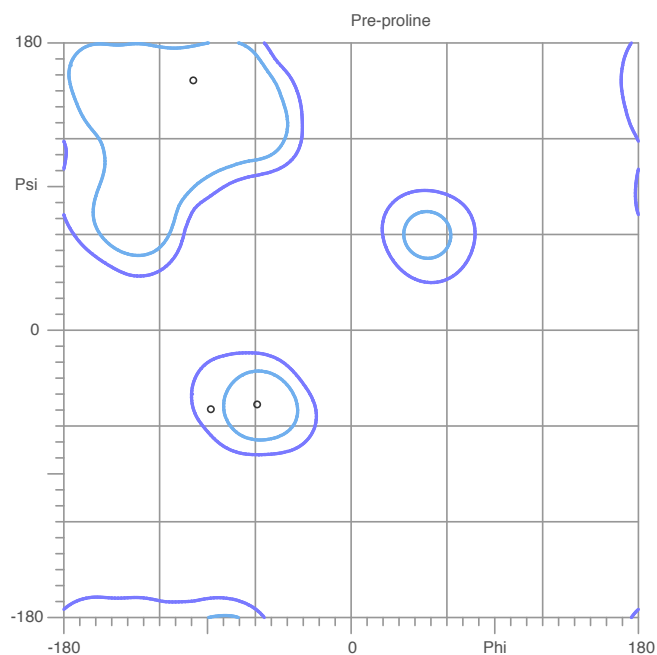
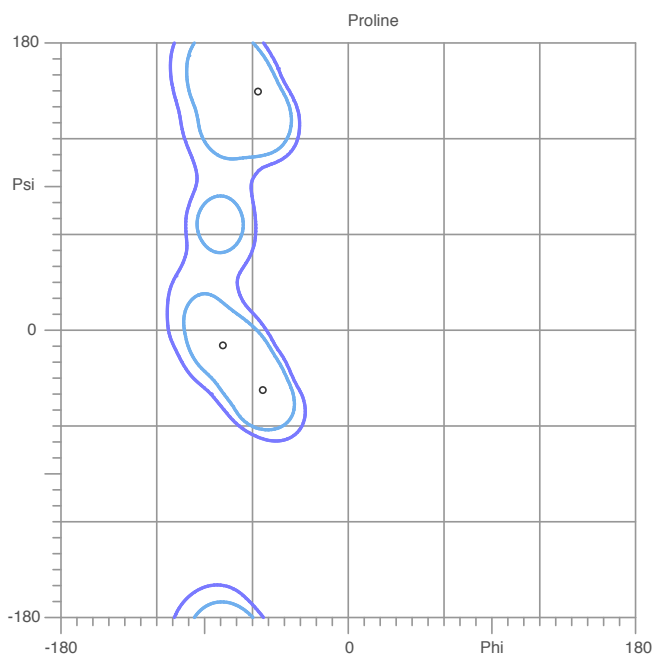
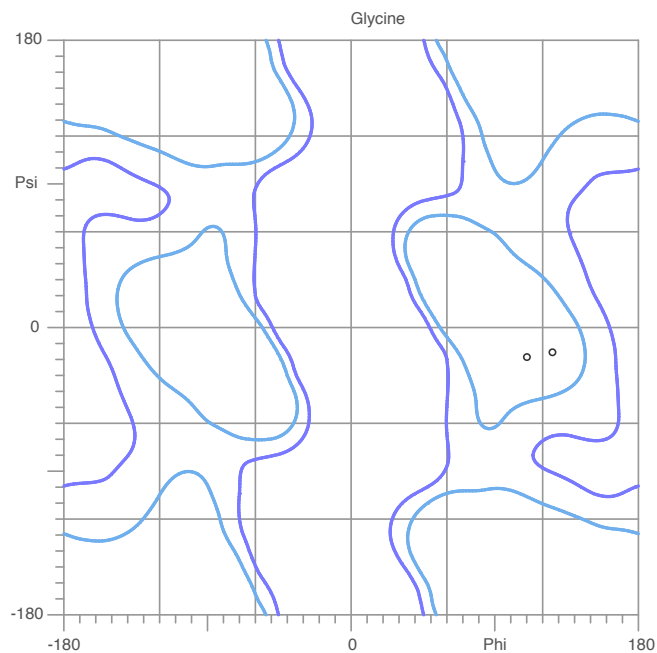
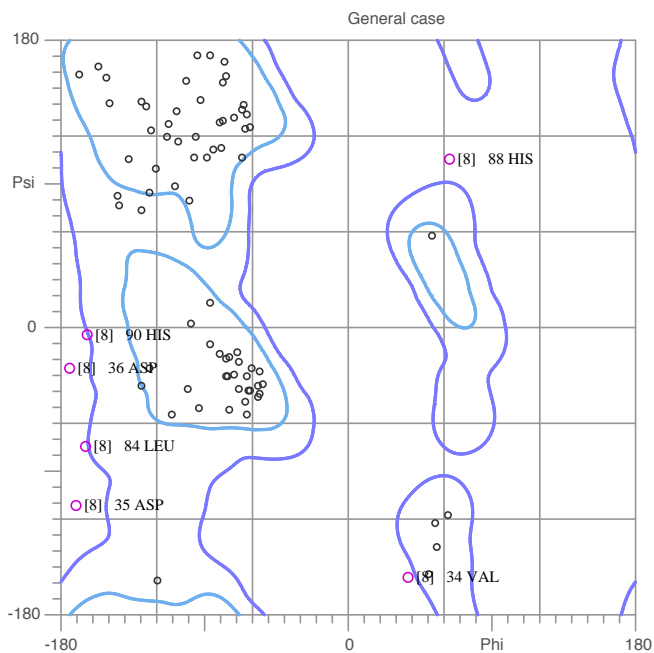
82.0% (73/89) of all residues were in favored (98%) regions.
95.5% (85/89) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [7] 12 HIS (83.7, 75.4)
- [7] 25 GLY (-148.8, -35.1)
- [7] 27 THR (-85.2, -122.7)
- [7] 34 VAL (38.3, -153.7)

MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, model 8



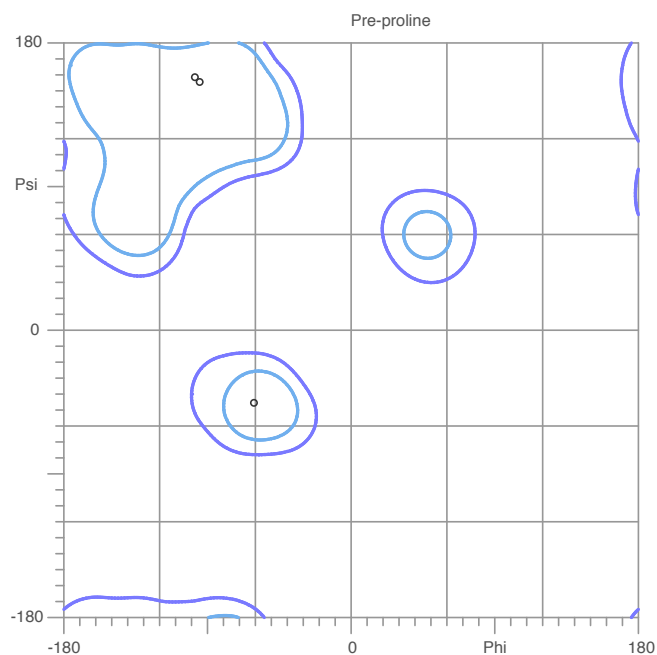
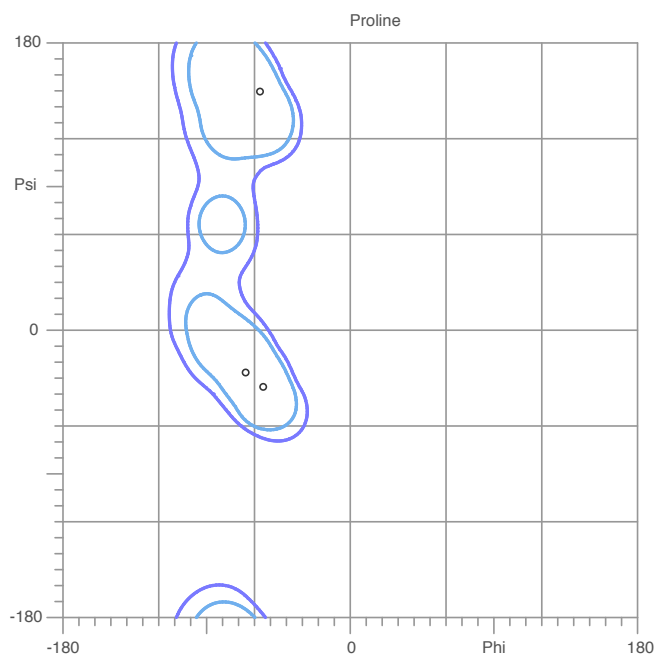
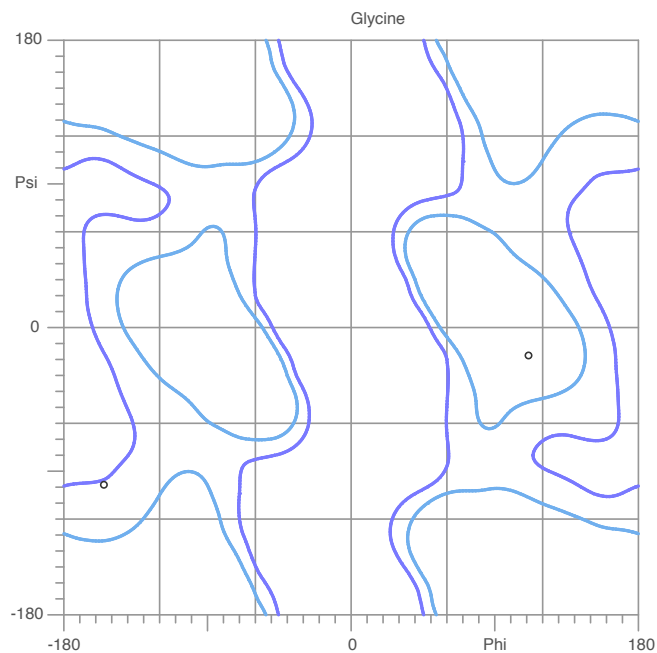
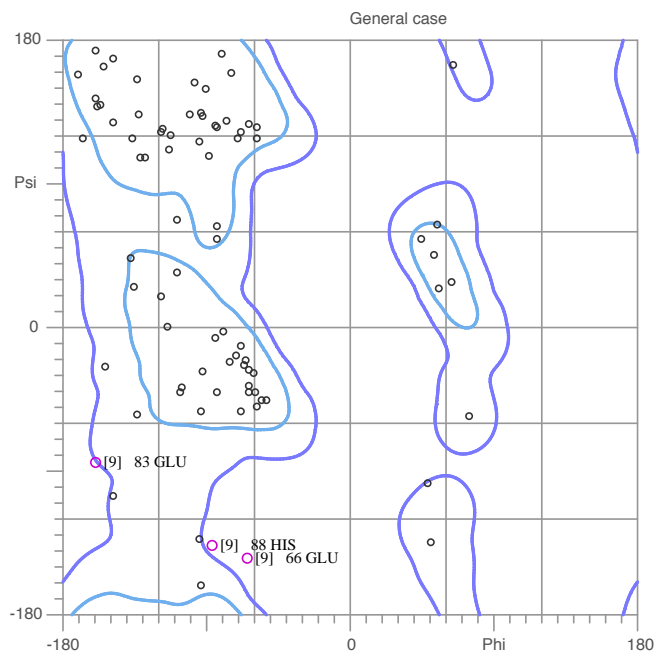
82.0% (73/89) of all residues were in favored (98%) regions.
93.3% (83/89) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[8] 34 VAL (37.4, -156.9)

[8] 35 ASP (-171.7, -111.5)
[8] 36 ASP (-175.2, -25.2)
[8] 84 LEU (-165.1, -75.0)
[8] 88 HIS (63.5, 106.9)
[8] 90 HIS (-165.0, -5.0)

MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, model 9



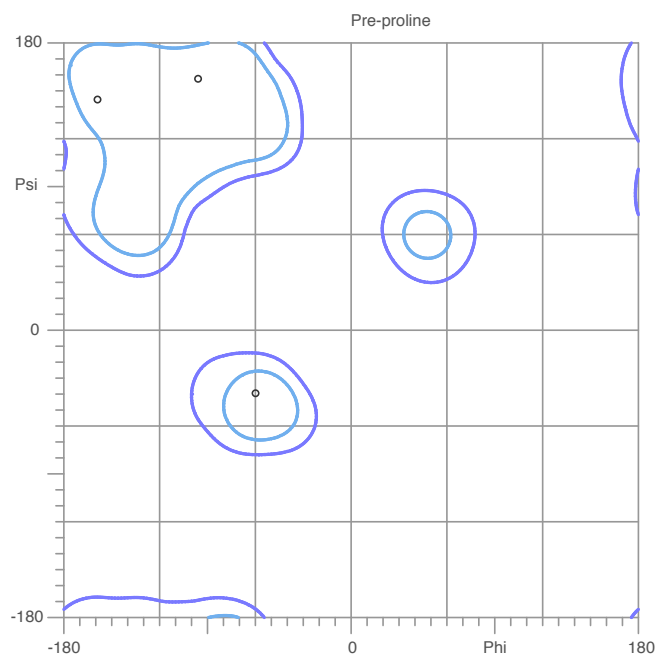
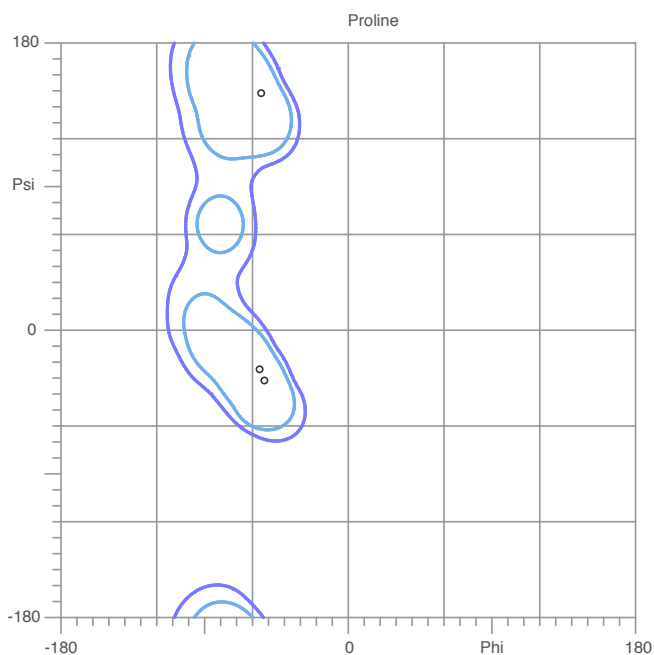
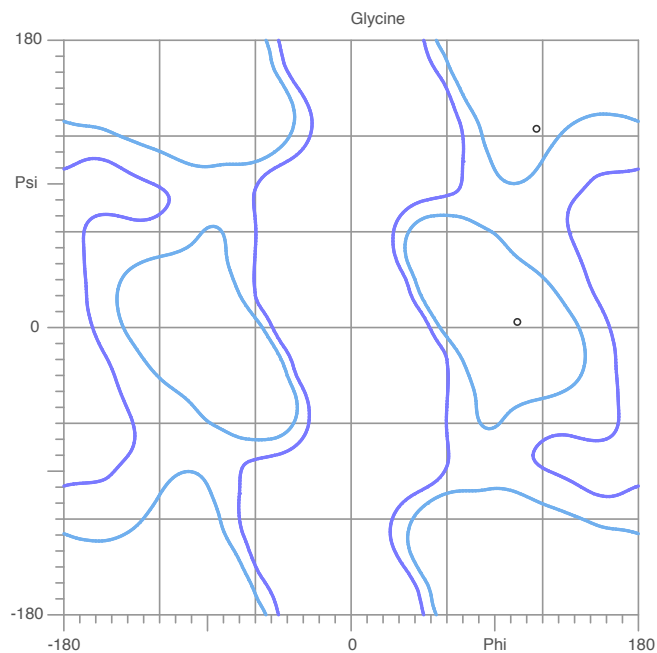
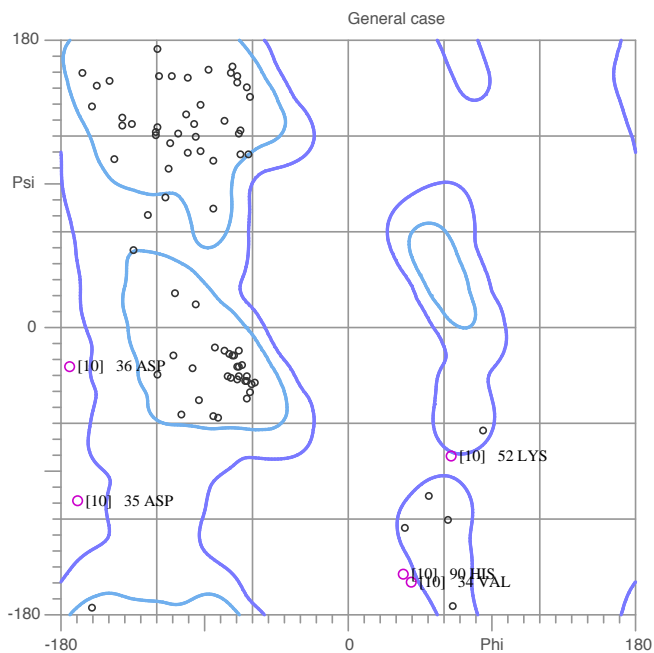
80.9% (72/89) of all residues were in favored (98%) regions.
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [9] 66 GLU (-65.6, -144.9)
- [9] 83 GLU (-160.1, -84.9)
- [9] 88 HIS (-87.9, -136.6)

MolProbity Ramachandran analysis

ZR18_R3_em_bcr3.pdb, model 10



85.4% (76/89) 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):

[10] 34 VAL (39.1, -159.4)
[10] 35 ASP (-170.3, -109.0)
[10] 36 ASP (-175.1, -25.0)
[10] 52 LYS (64.9, -80.9)
[10] 90 HIS (35.0, -155.0)