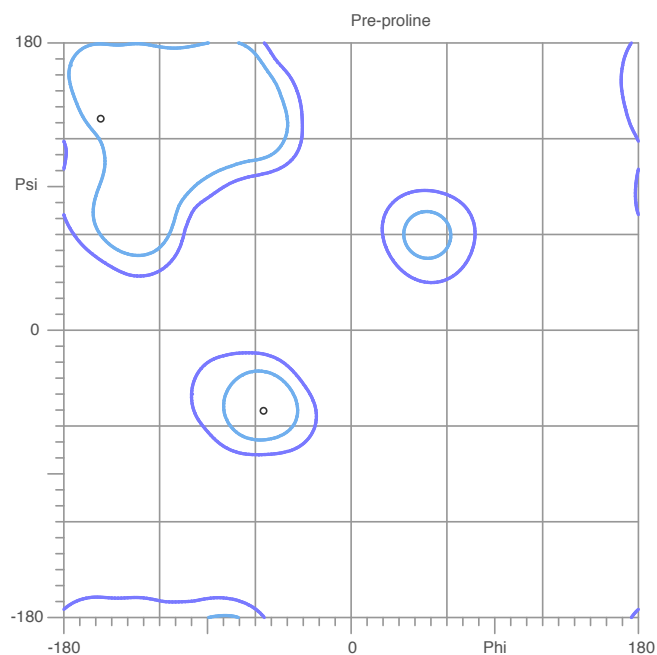
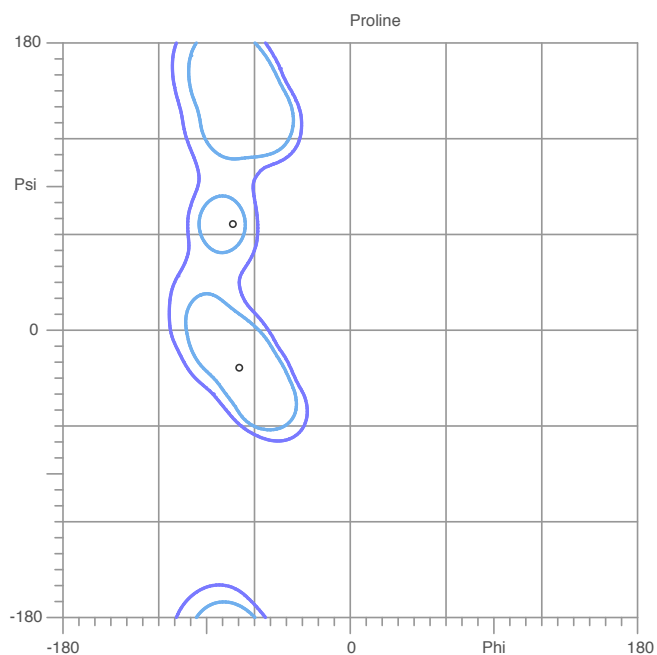
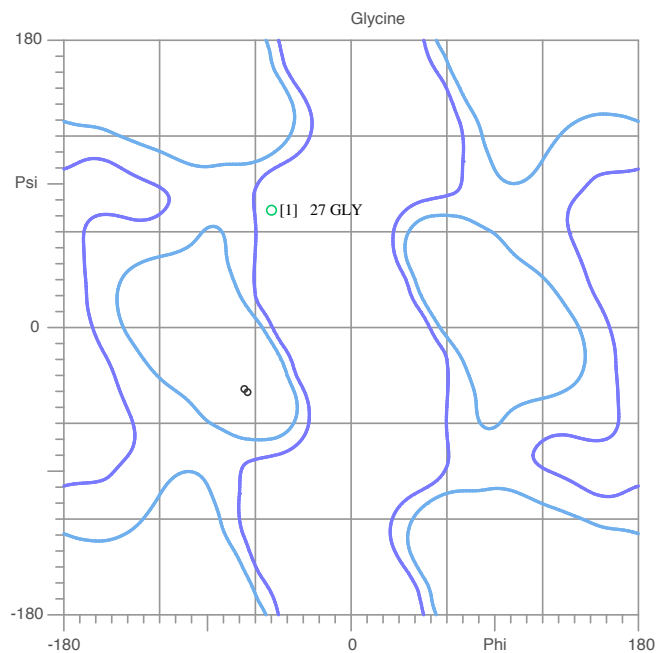
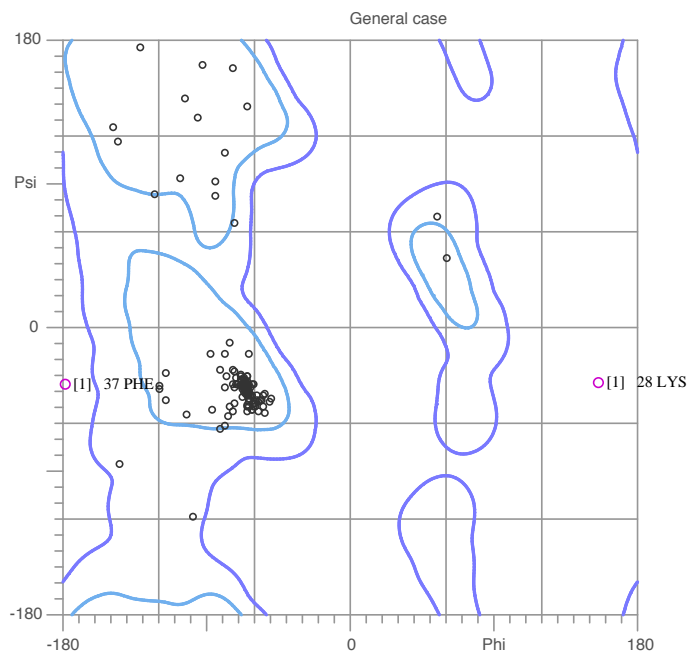


MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 1



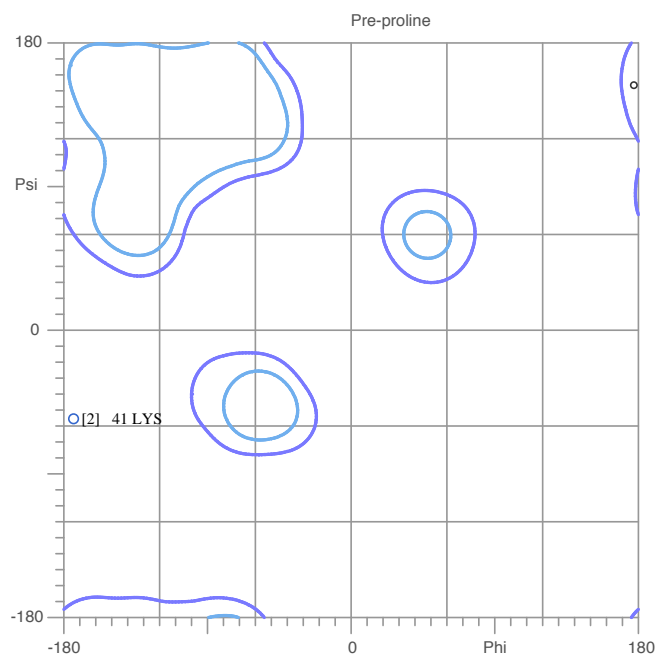
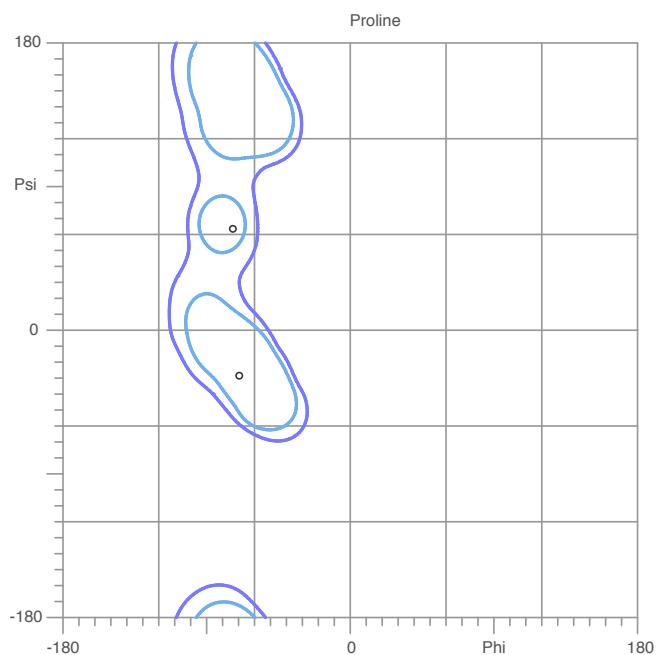
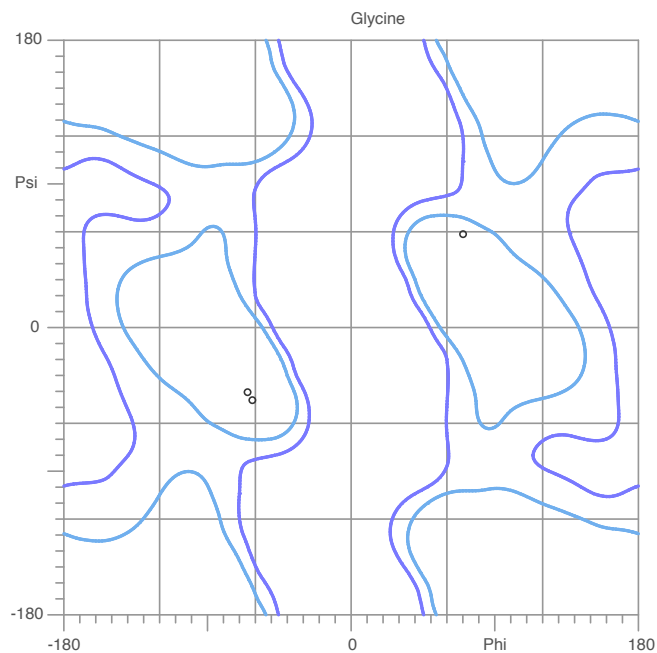
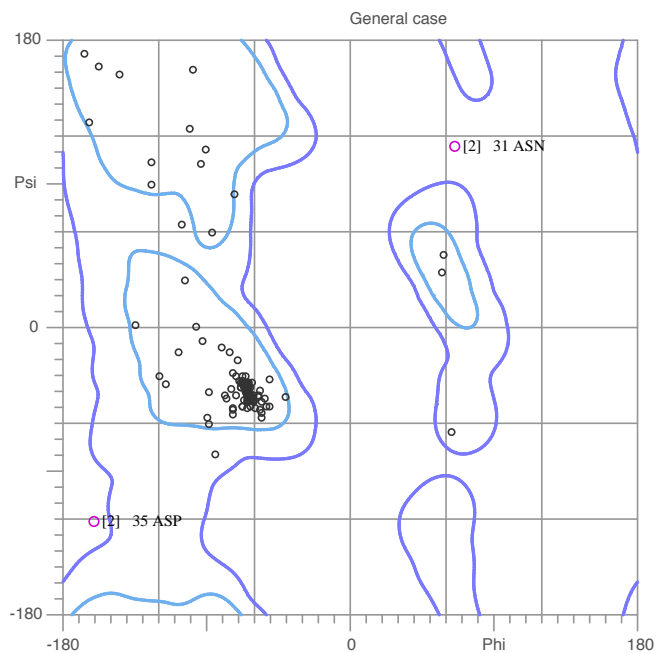
94.2% (114/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 27 GLY (-50.9, 75.0)
- [1] 28 LYS (155.0, -34.9)
- [1] 37 PHE (-179.2, -35.0)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 2



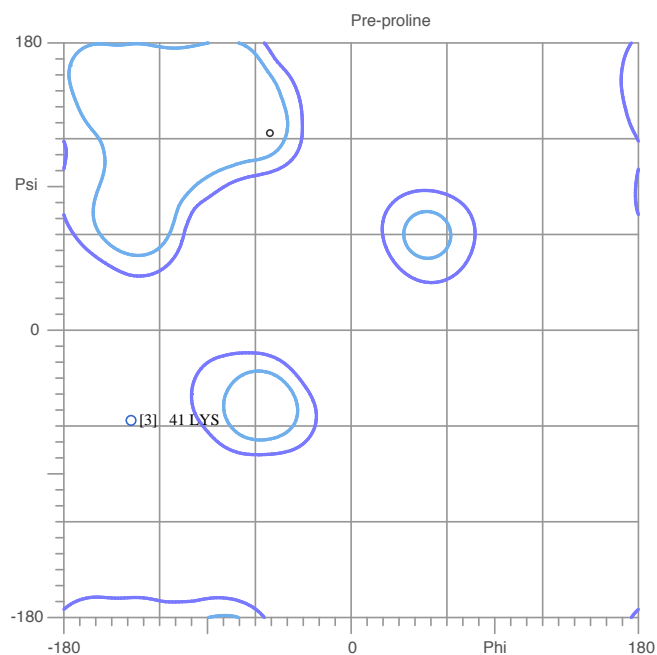
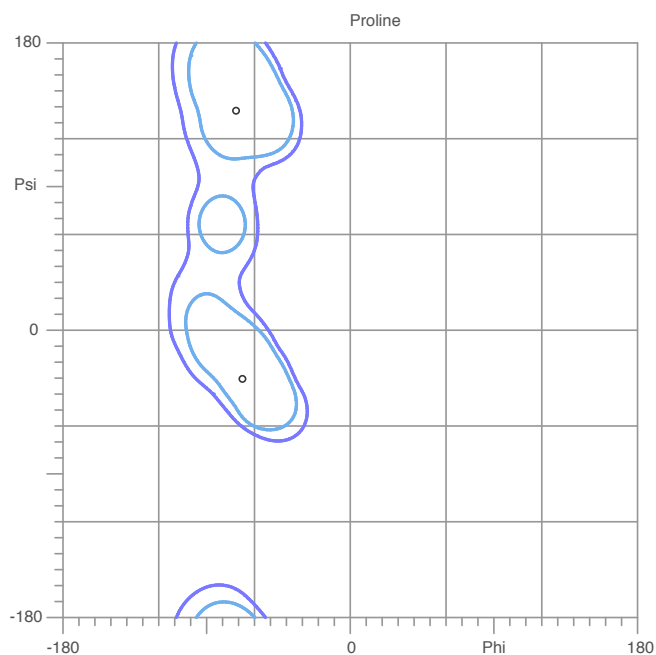
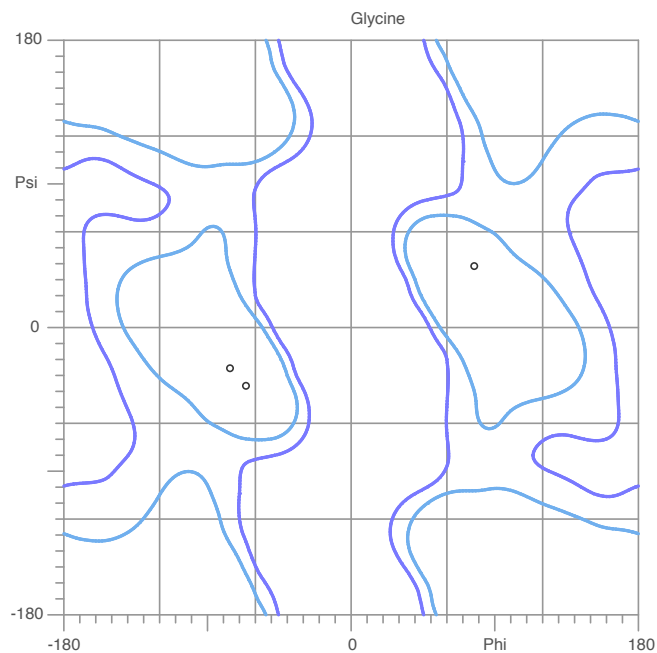
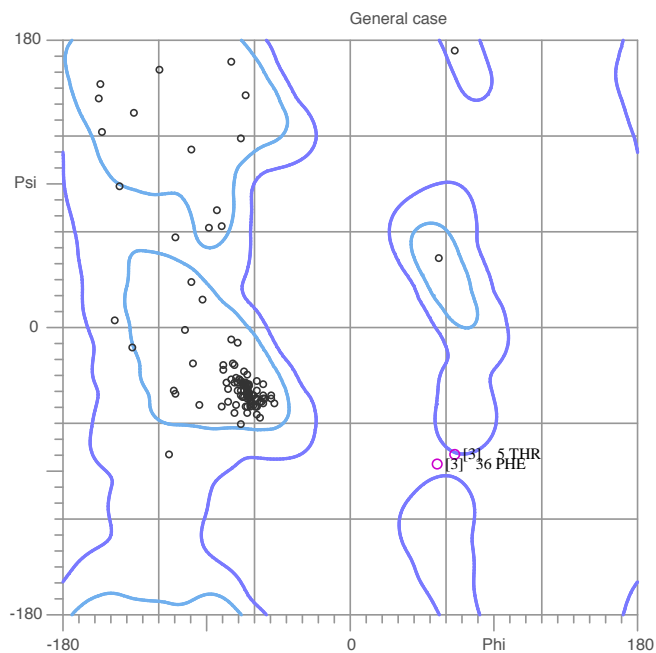
93.4% (113/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 31 ASN (65.0, 115.0)
- [2] 35 ASP (-161.3, -121.0)
- [2] 41 LYS (-174.1, -55.1)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 3



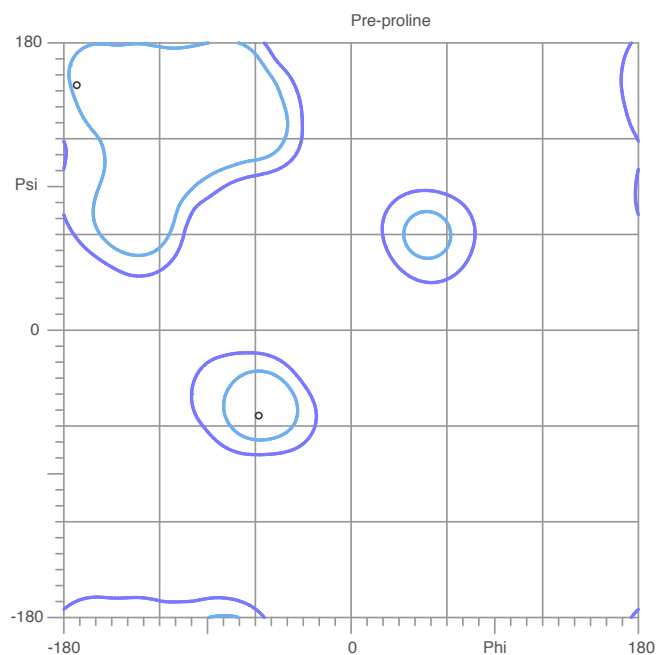
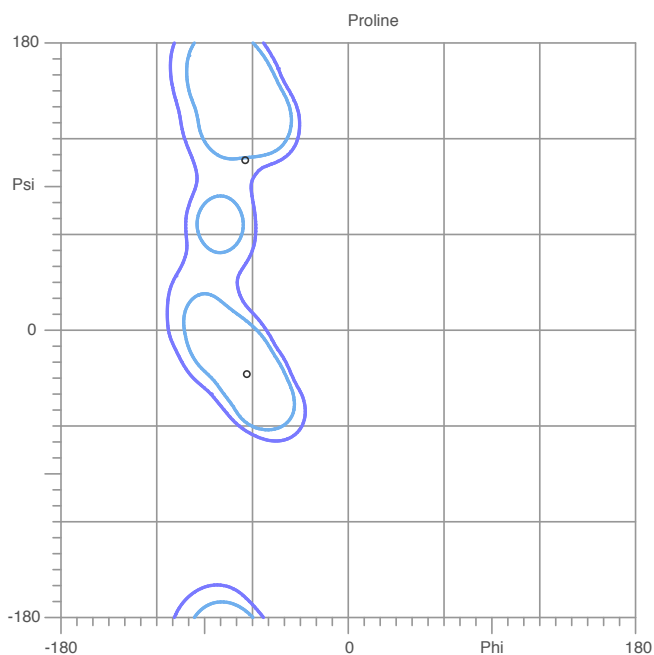
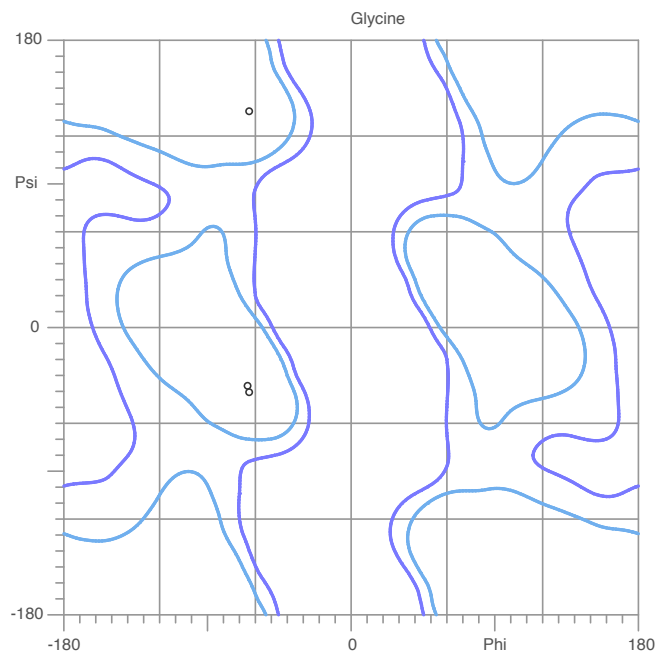
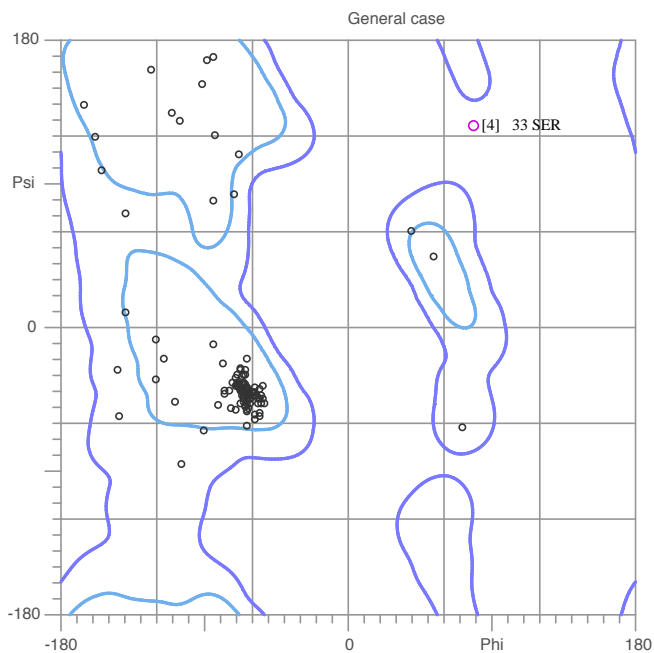
92.6% (112/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 5 THR (65.7, -79.8)
- [3] 36 PHE (55.0, -85.0)
- [3] 41 LYS (-138.6, -56.9)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 4



90.9% (110/121) of all residues were in favored (98%) regions.
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

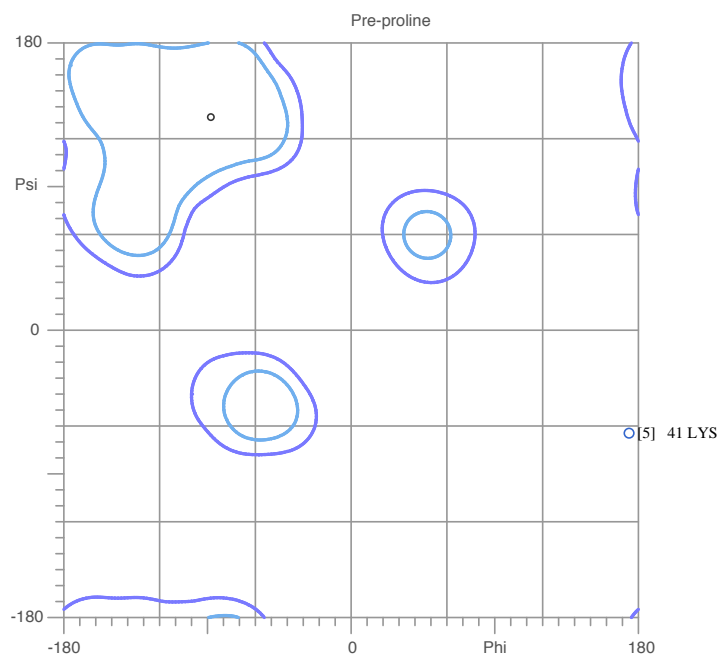
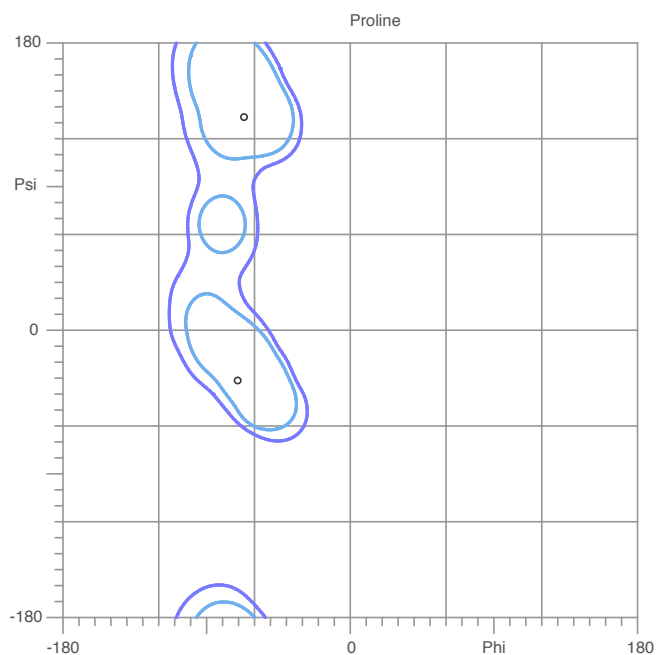
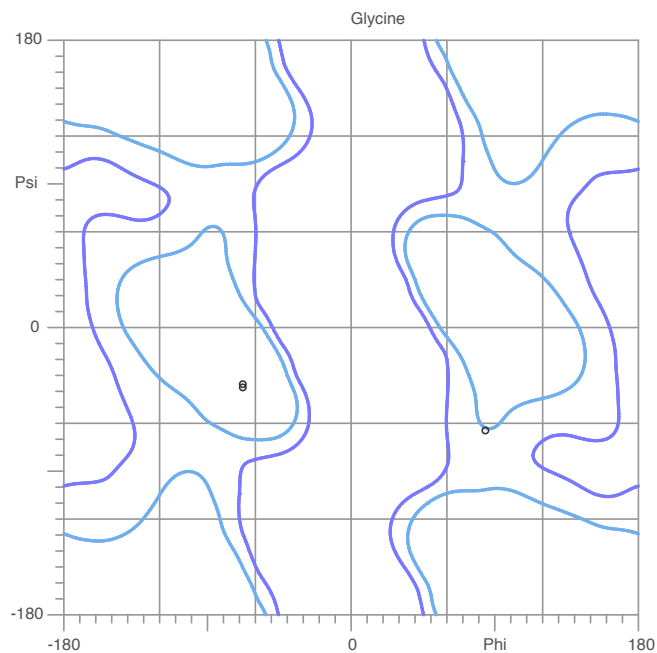
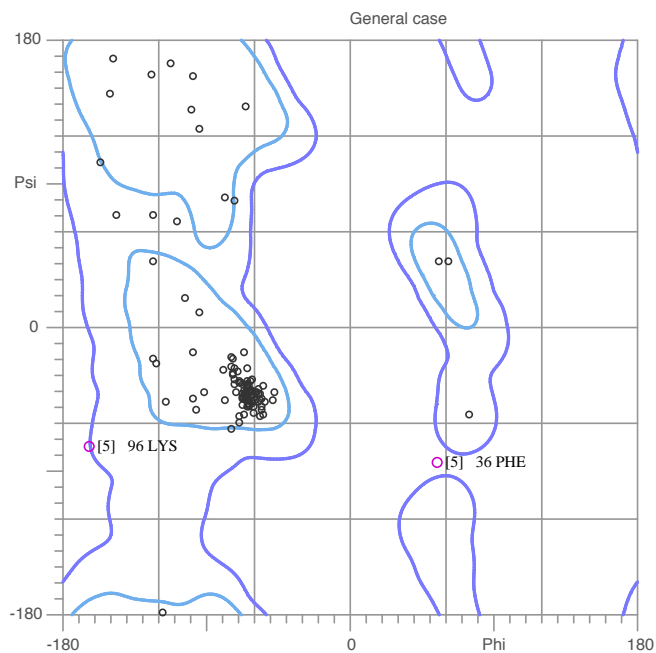
There were 1 outliers (phi, psi):
[4] 33 SER (78.6, 127.8)

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MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 5



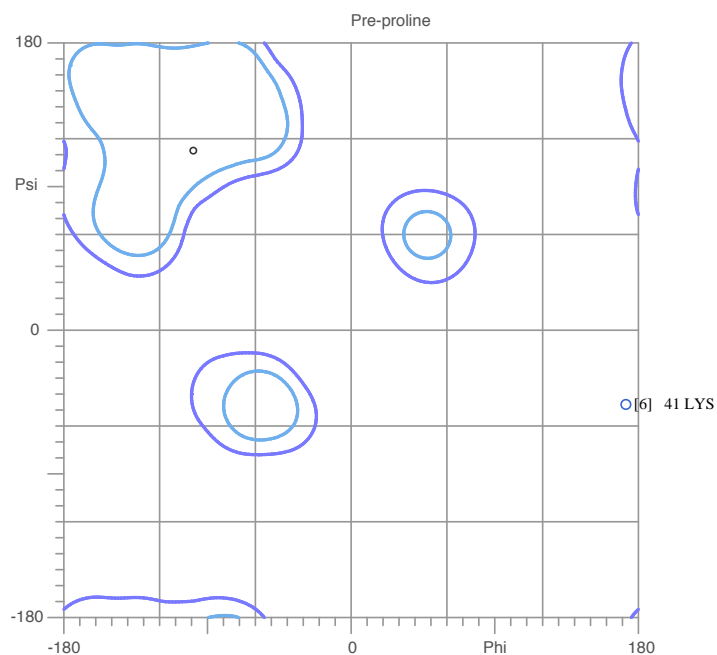
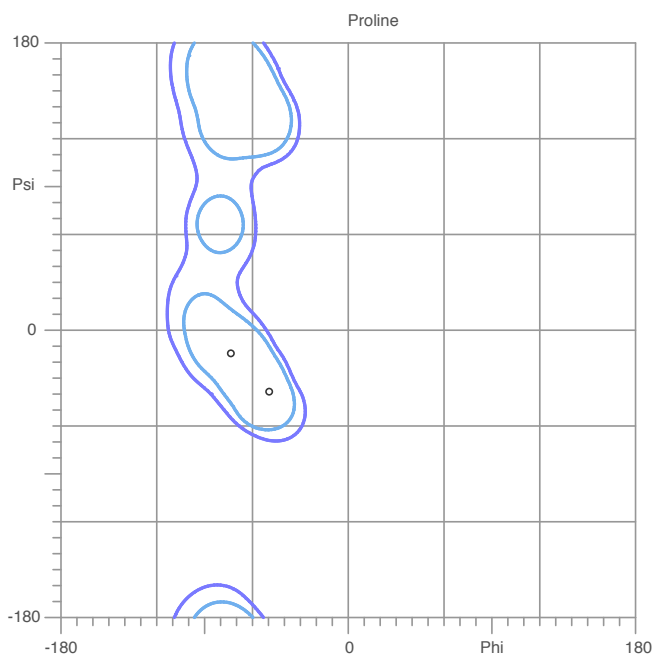
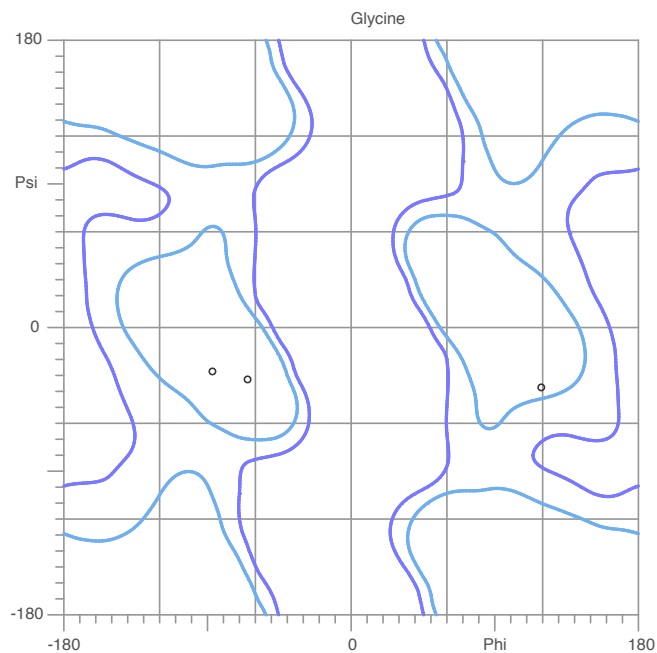
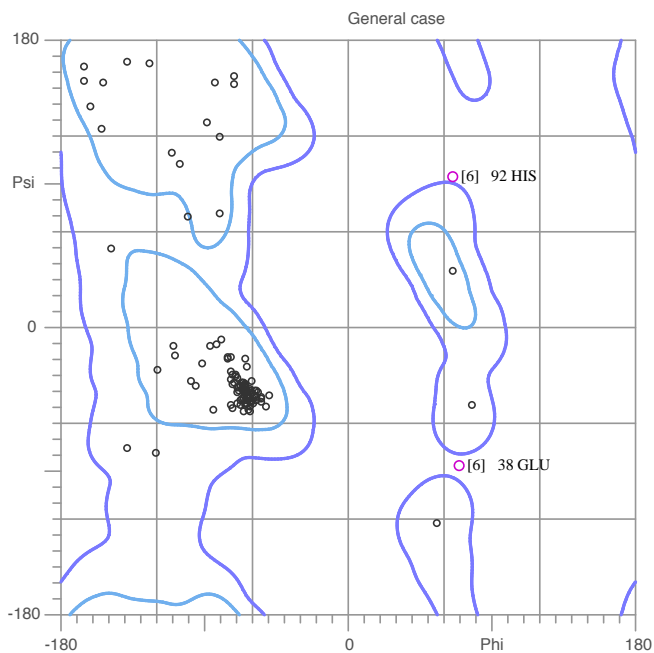
91.7% (111/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [5] 36 PHE (54.9, -84.9)
- [5] 41 LYS (174.9, -64.9)
- [5] 96 LYS (-164.9, -74.8)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 6



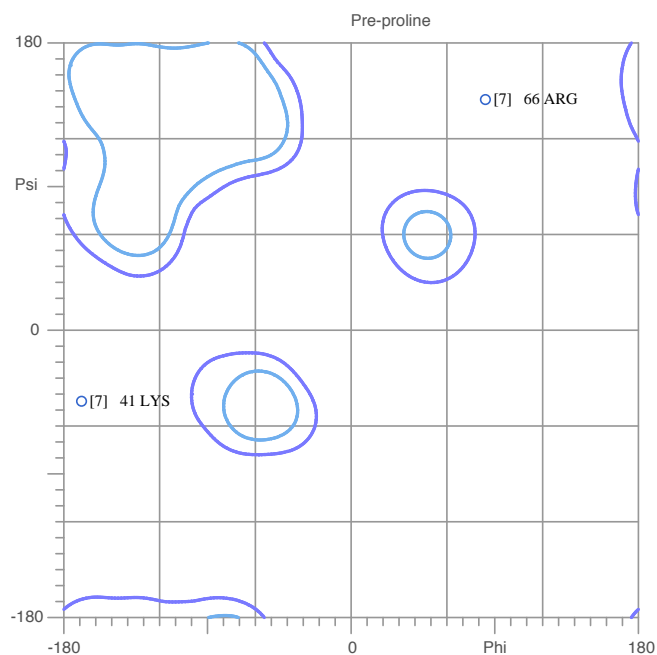
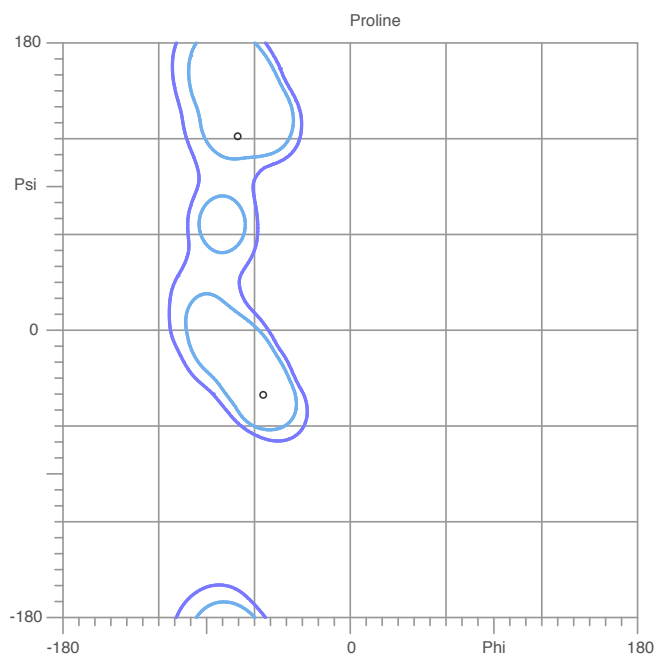
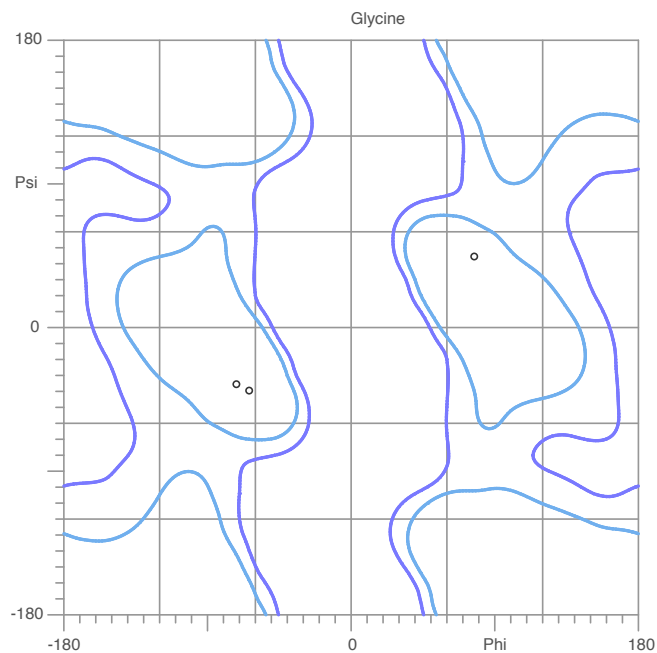
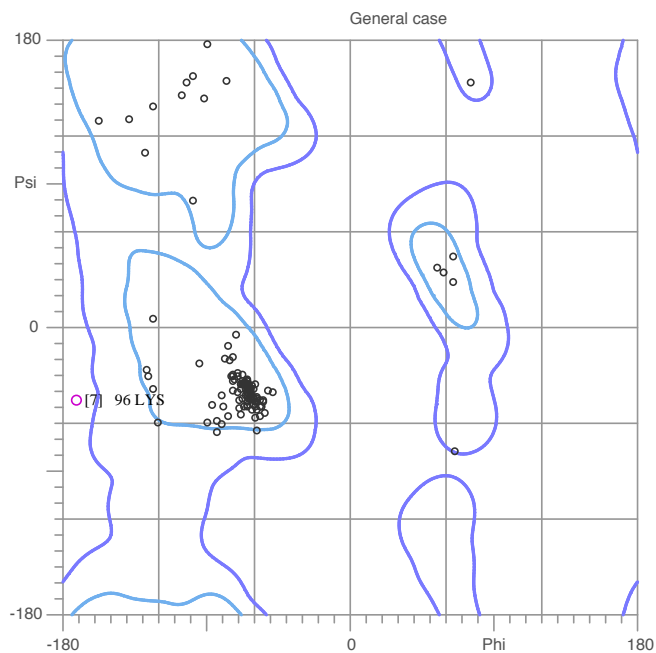
92.6% (112/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 38 GLU (69.1, -86.2)
- [6] 41 LYS (172.1, -46.1)
- [6] 92 HIS (65.0, 95.1)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 7



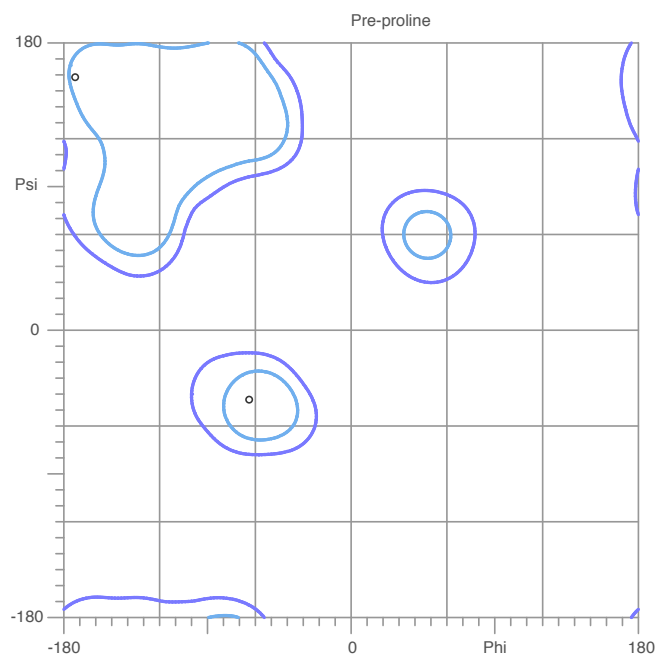
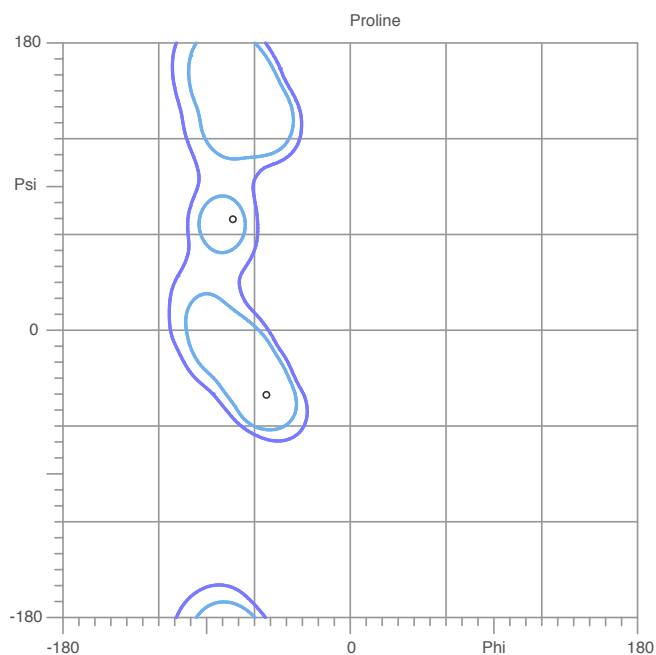
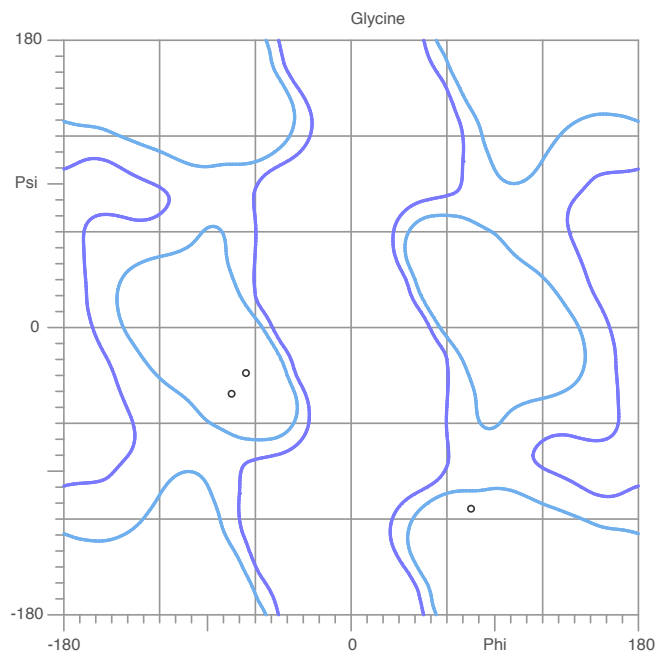
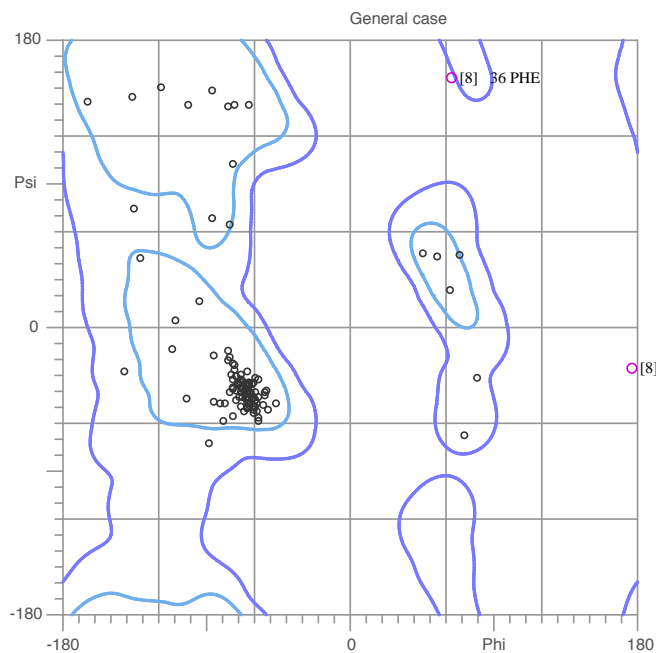
93.4% (113/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [7] 41 LYS (-169.6, -44.9)
- [7] 66 ARG (85.0, 145.6)
- [7] 96 LYS (-172.7, -45.1)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 8



93.4% (113/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

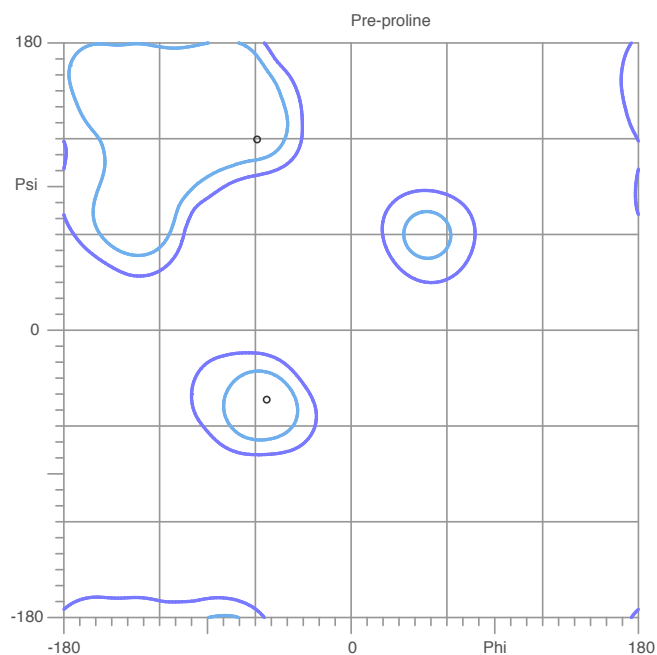
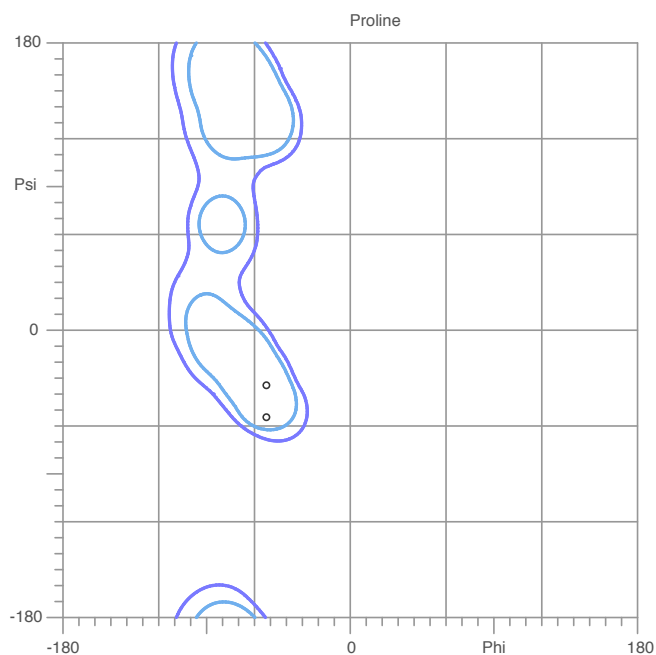
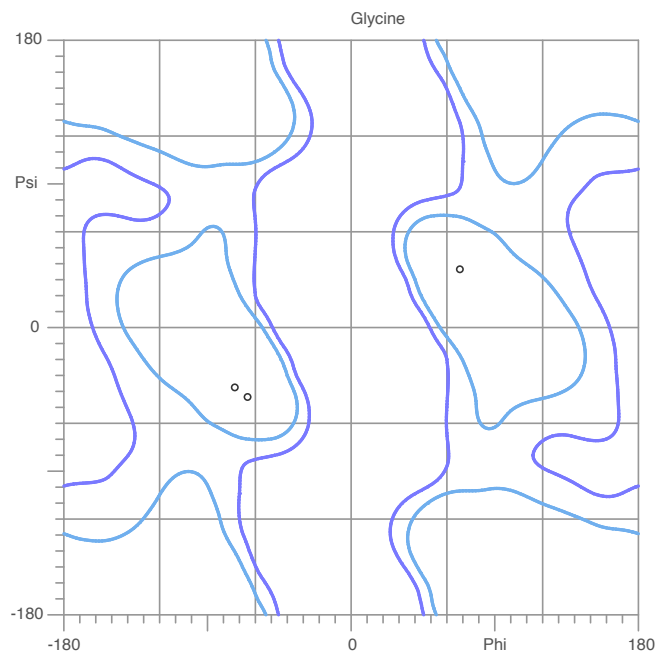
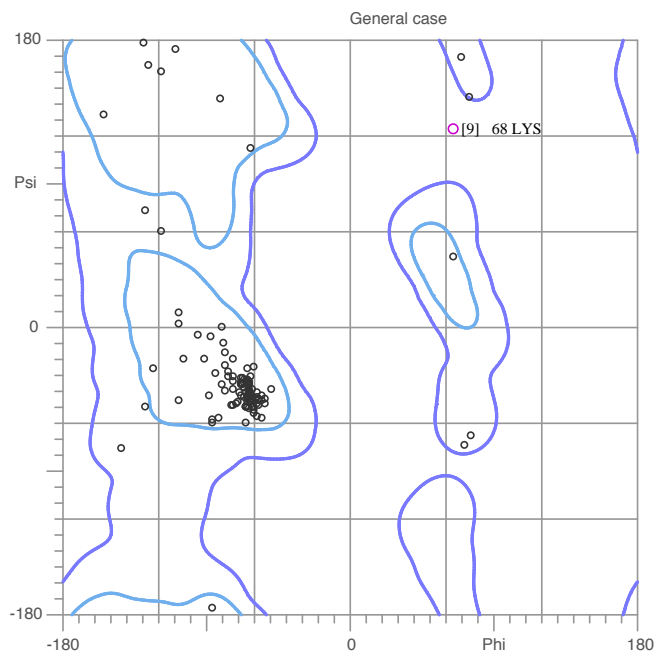
There were 2 outliers (phi, psi):

[8] 5 THR (176.8, -25.1)

[8] 36 PHE (63.5, 157.1)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 9



92.6% (112/121) of all residues were in favored (98%) regions.
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

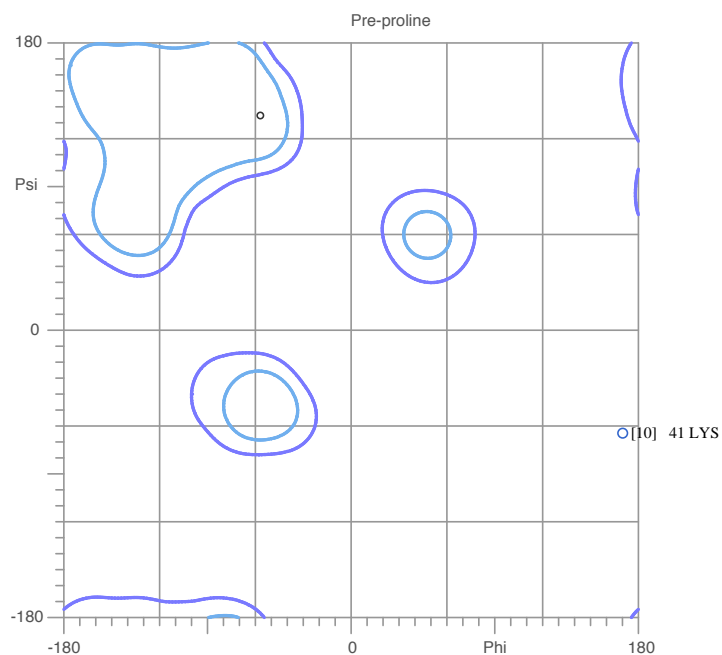
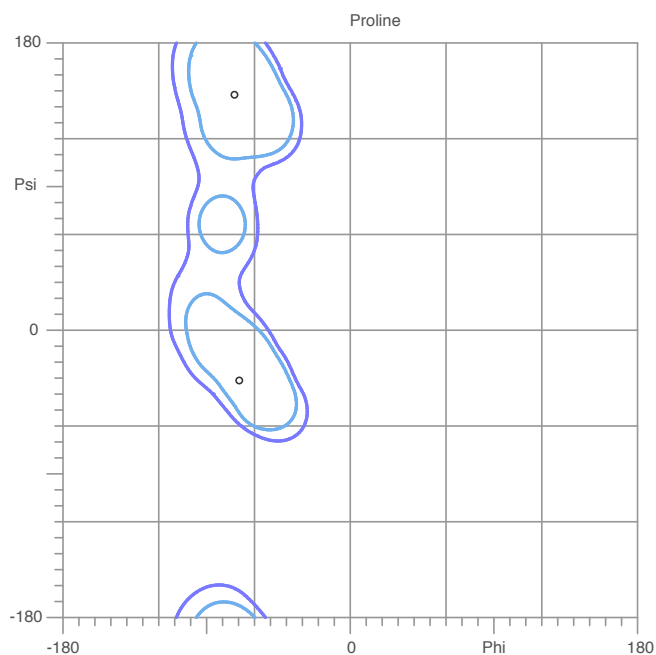
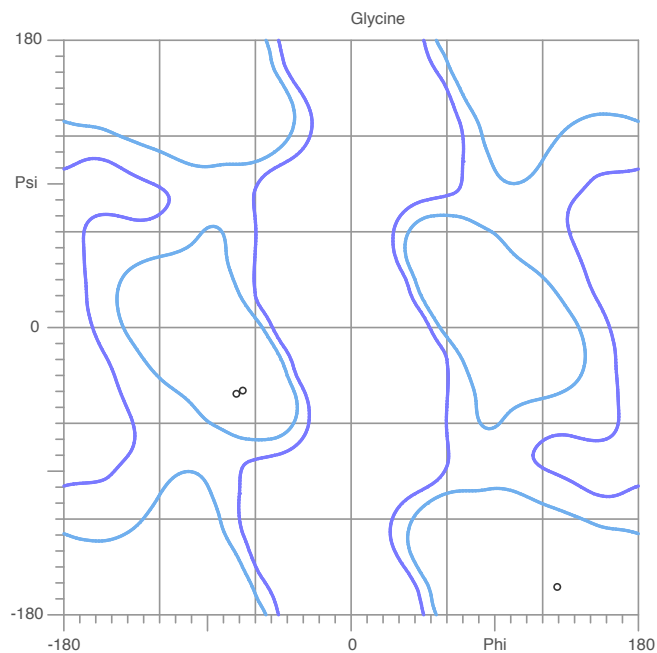
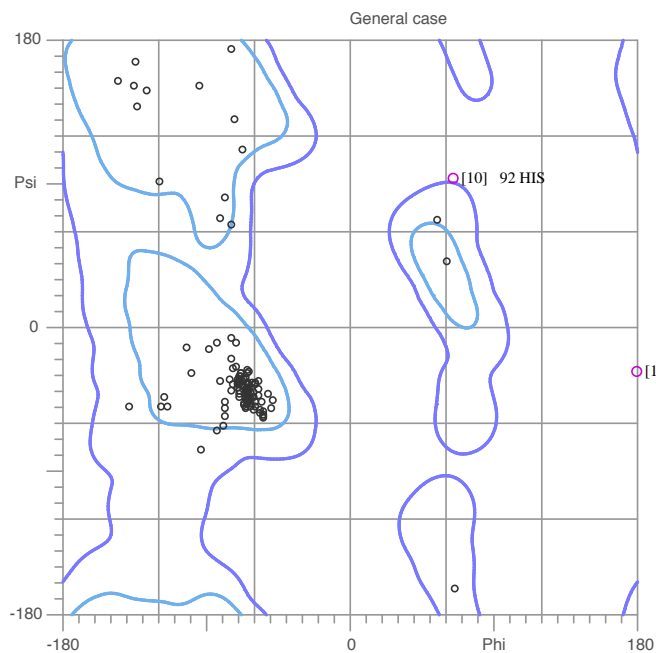
There were 1 outliers (phi, psi):
[9] 68 LYS (64.3, 125.9)

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MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 10



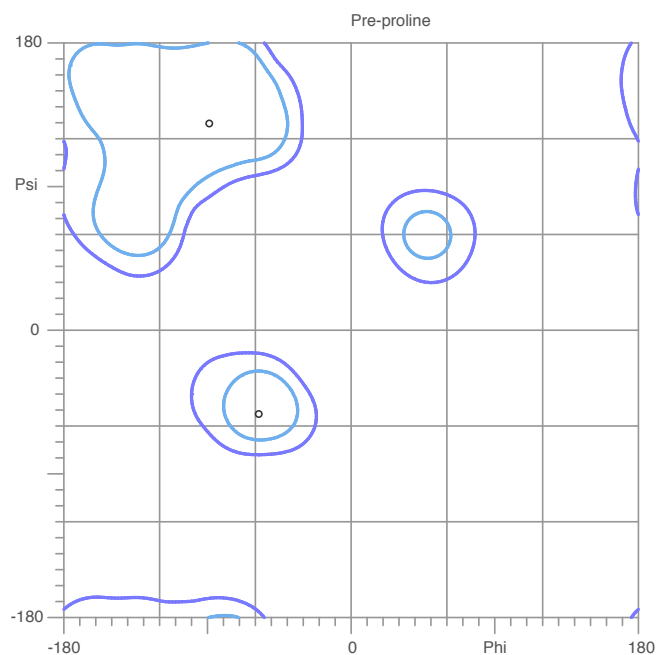
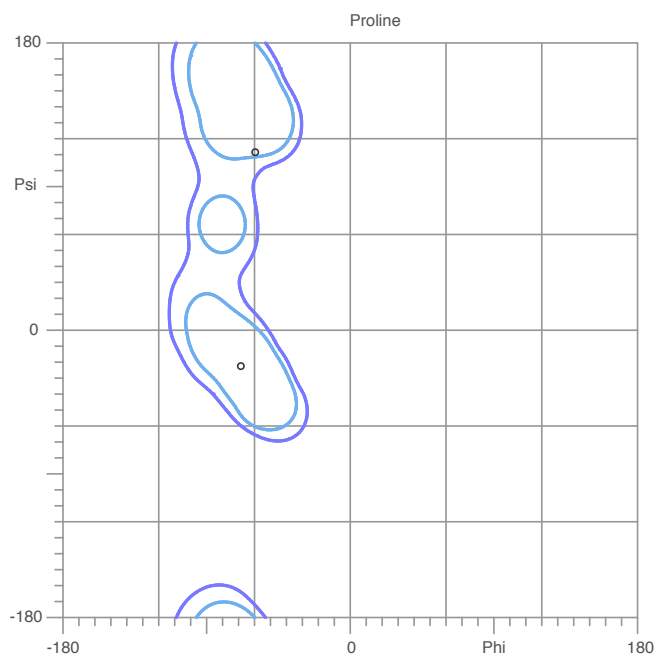
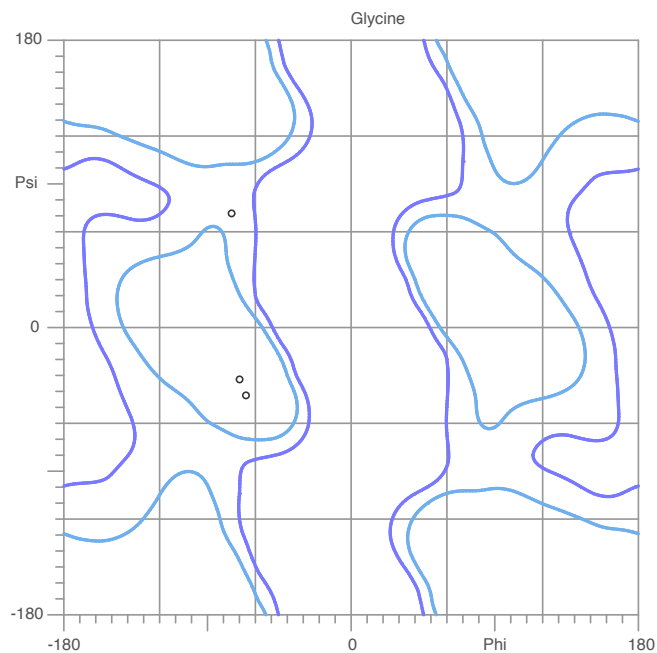
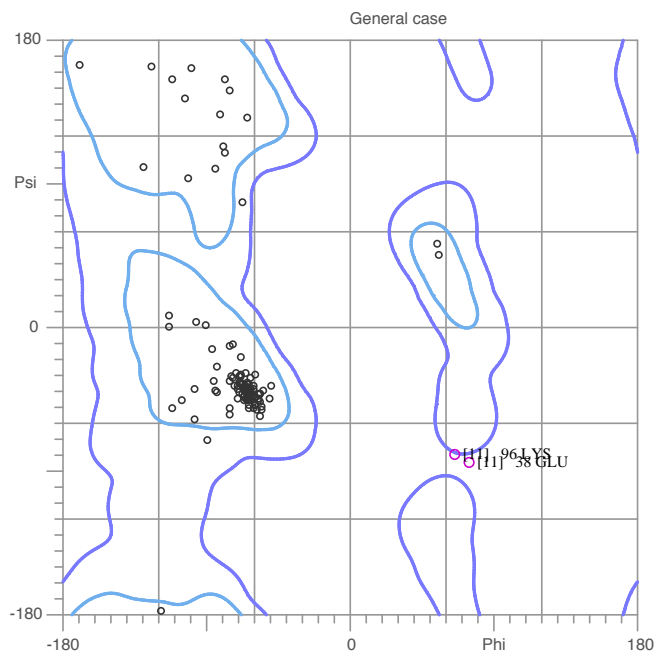
93.4% (113/121) of all residues were in favored (98%) regions.
97.5% (118/121) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [10] 6 LEU (179.5, -27.6)
- [10] 41 LYS (170.5, -64.1)
- [10] 92 HIS (65.0, 94.9)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 11



95.9% (116/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

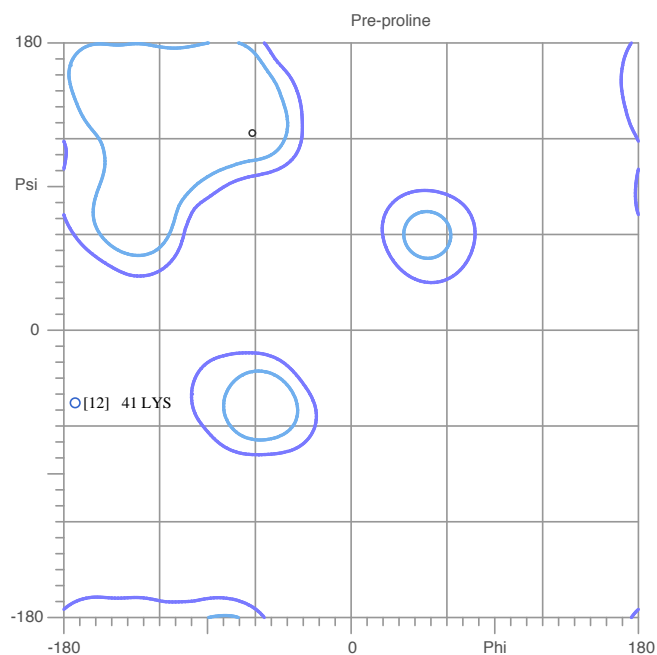
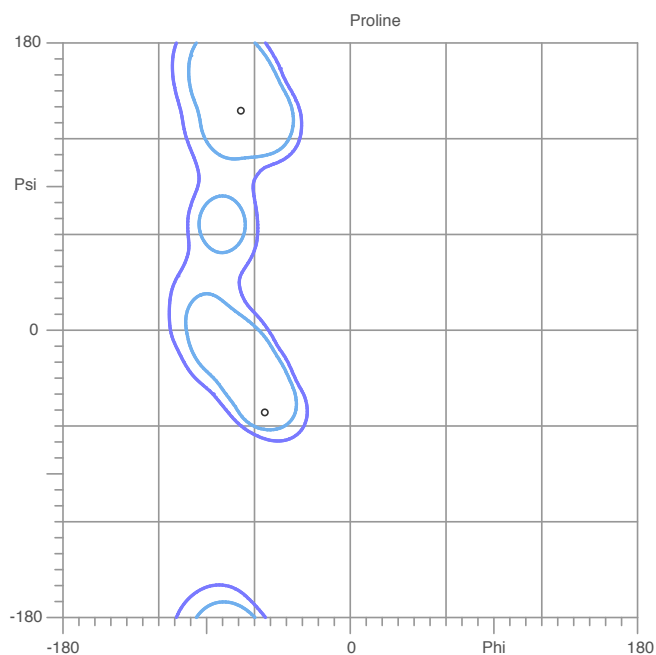
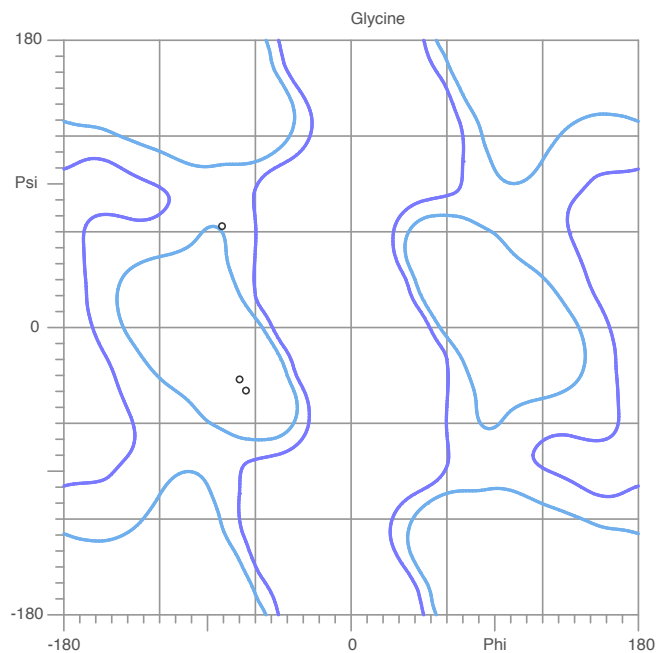
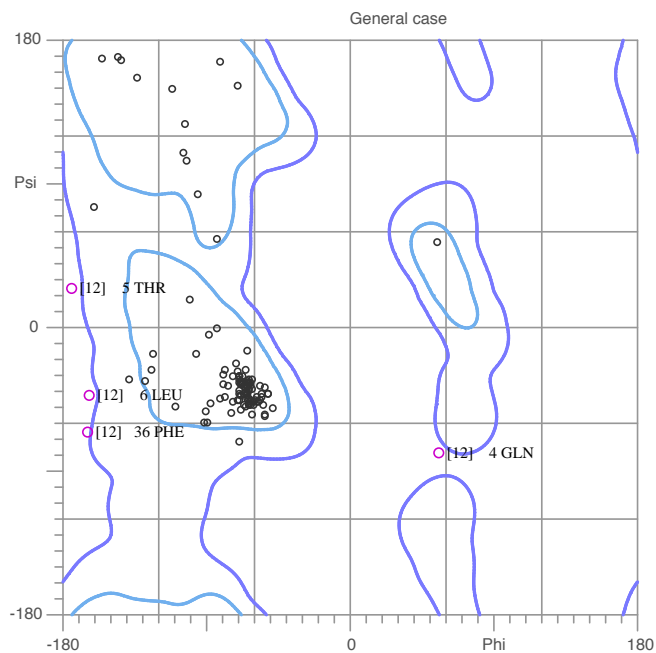
There were 2 outliers (phi, psi):

[11] 38 GLU (74.1, -85.0)

[11] 96 LYS (65.0, -79.4)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 12



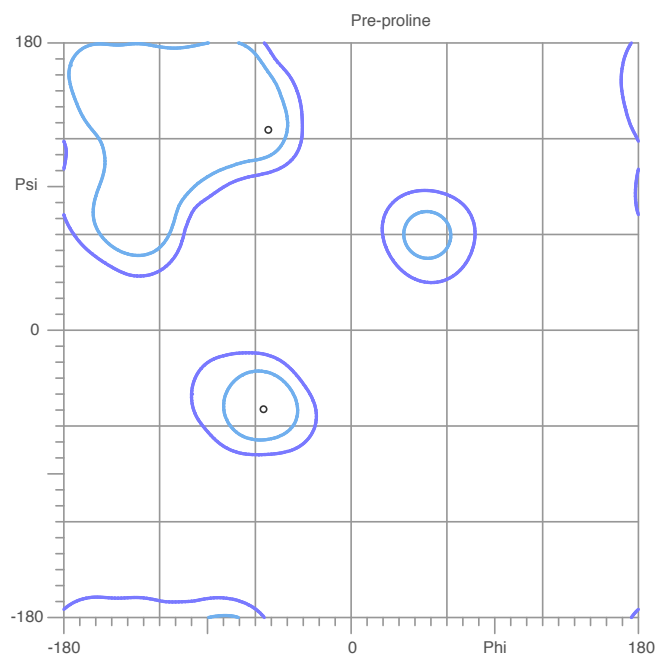
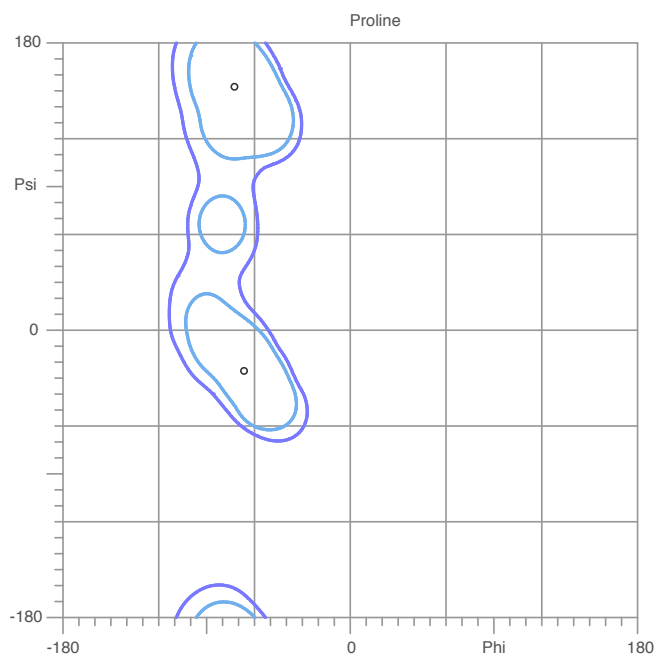
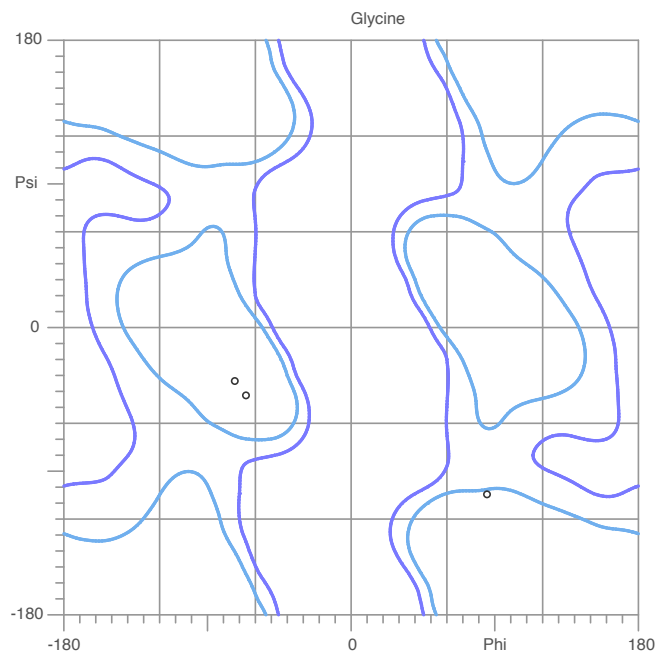
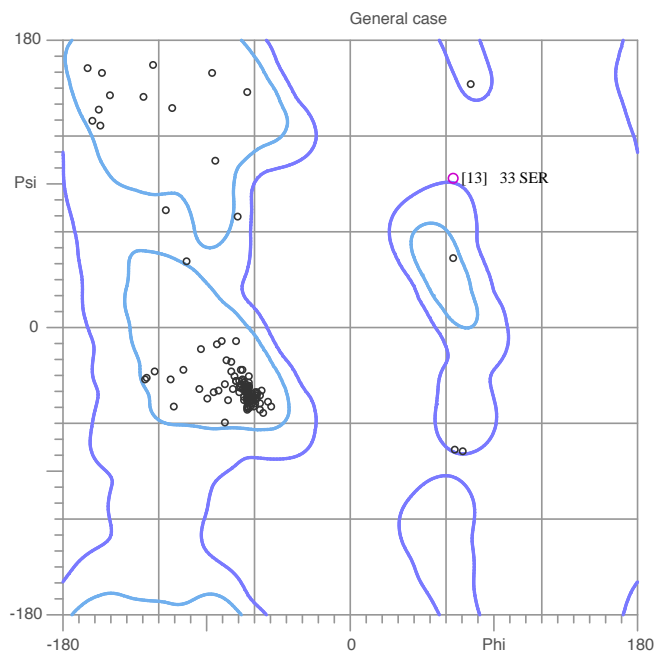
92.6% (112/121) of all residues were in favored (98%) regions.
95.9% (116/121) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[12] 4 GLN (55.1, -78.3)
[12] 5 THR (-175.0, 25.0)
[12] 6 LEU (-164.9, -42.7)
[12] 36 PHE (-165.1, -65.0)
[12] 41 LYS (-173.7, -45.1)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 13



94.2% (114/121) of all residues were in favored (98%) regions.
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

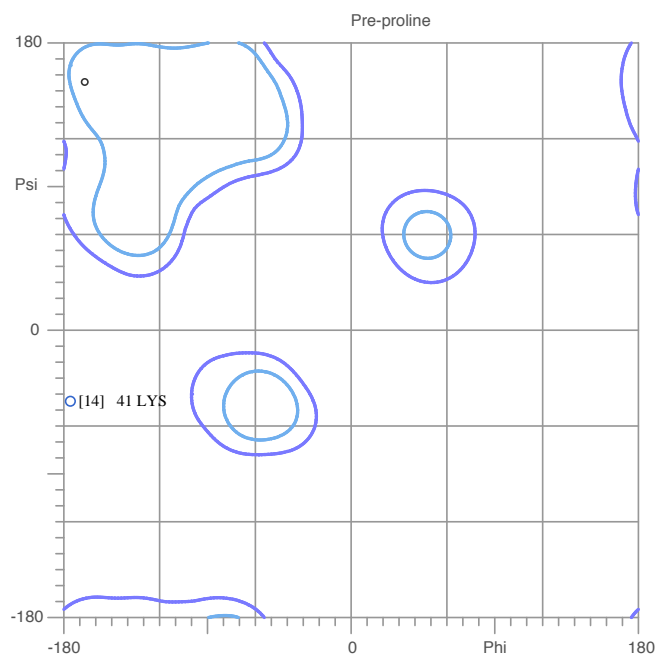
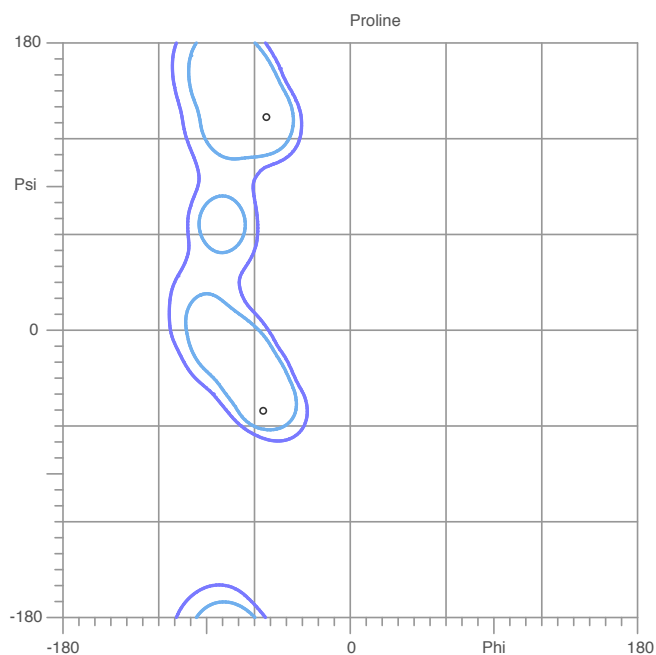
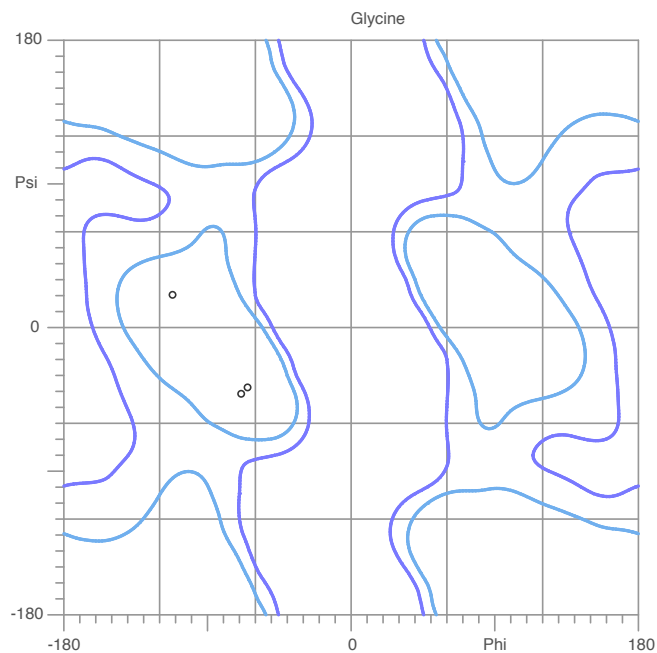
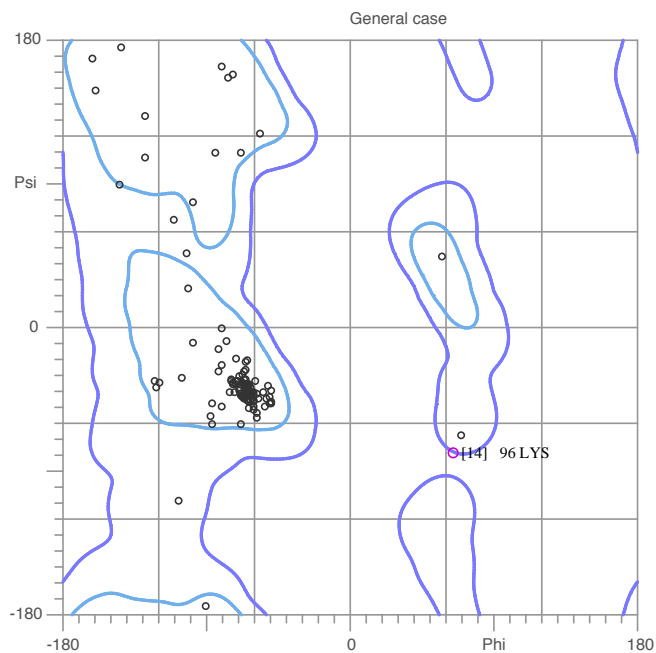
There were 1 outliers (phi, psi):
[13] 33 SER (65.0, 94.9)

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MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 14

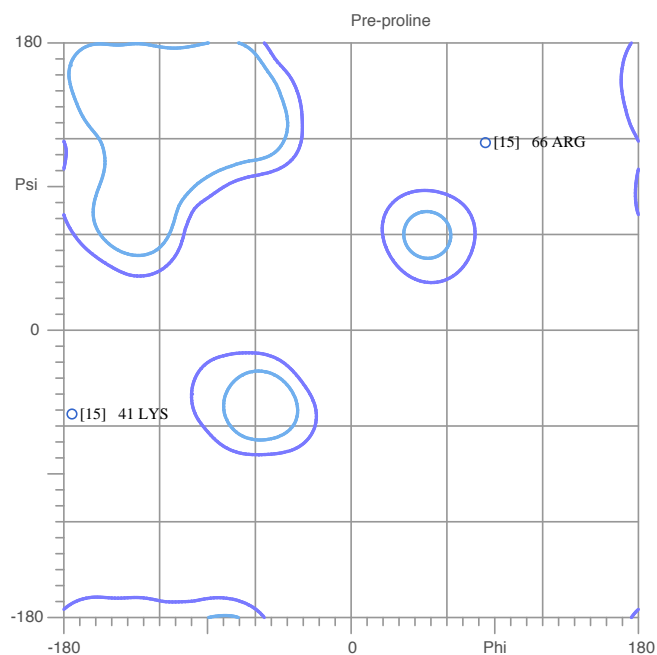
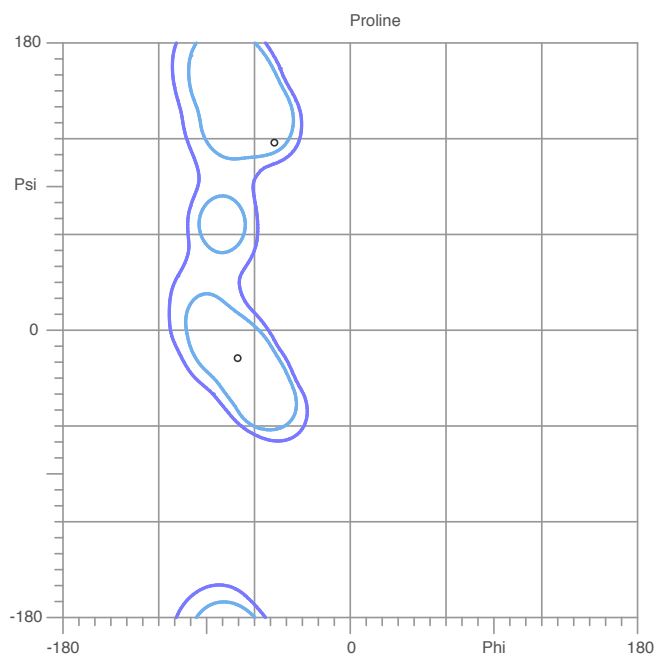
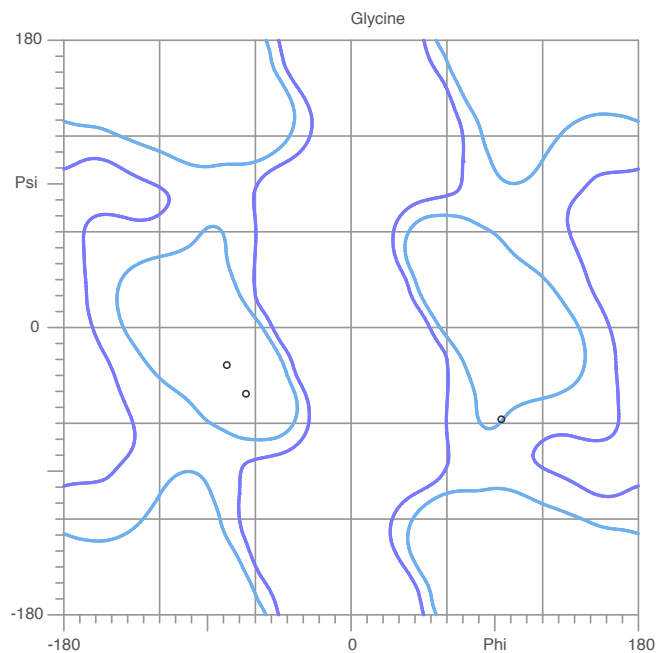
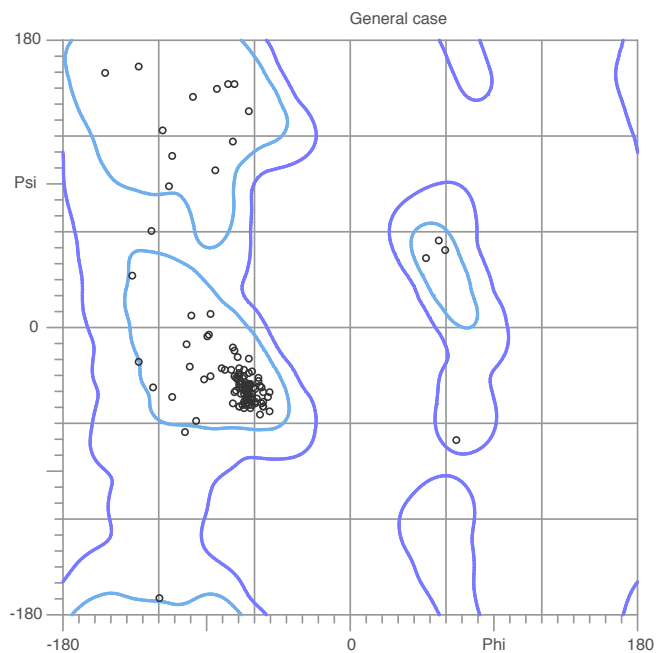


94.2% (114/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[14] 41 LYS (-176.0, -45.0)
[14] 96 LYS (65.0, -79.0)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 15

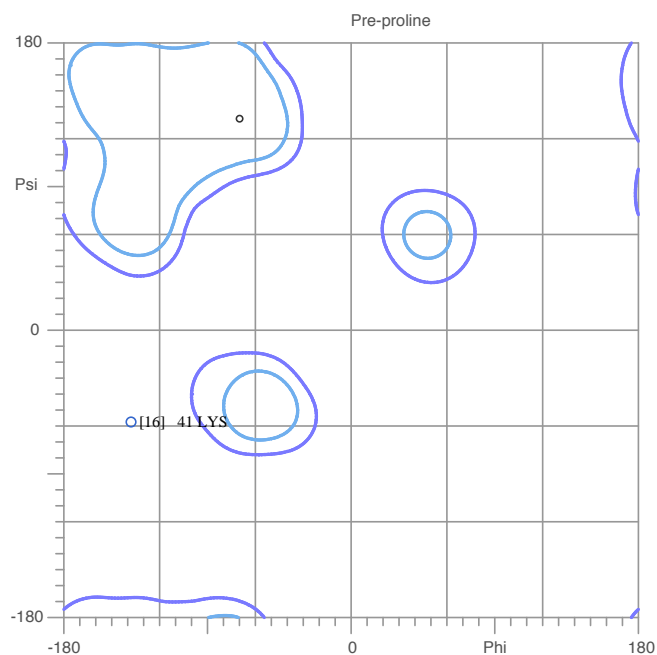
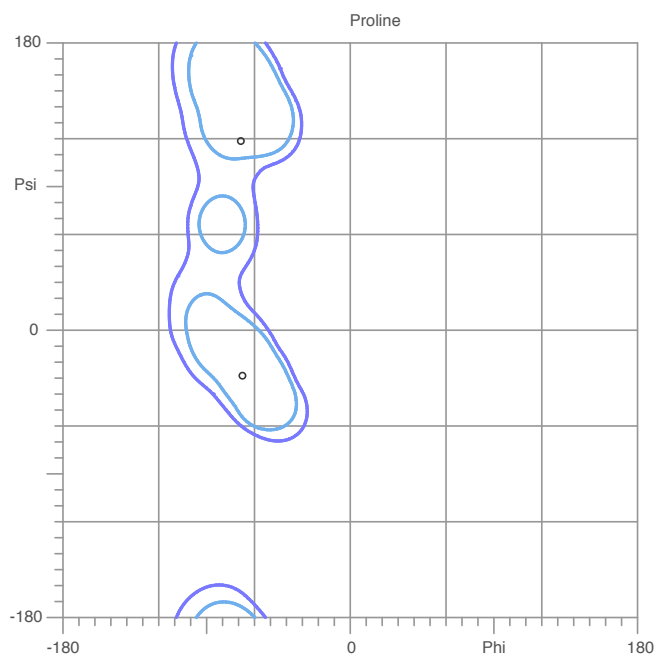
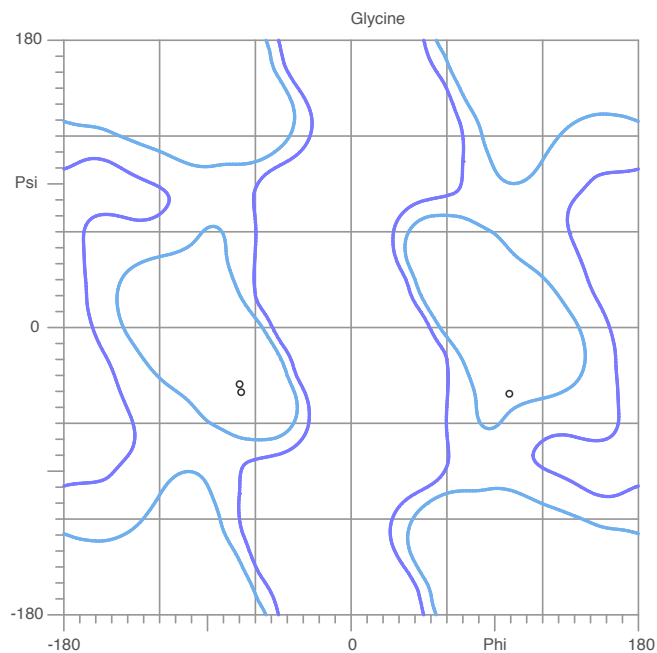
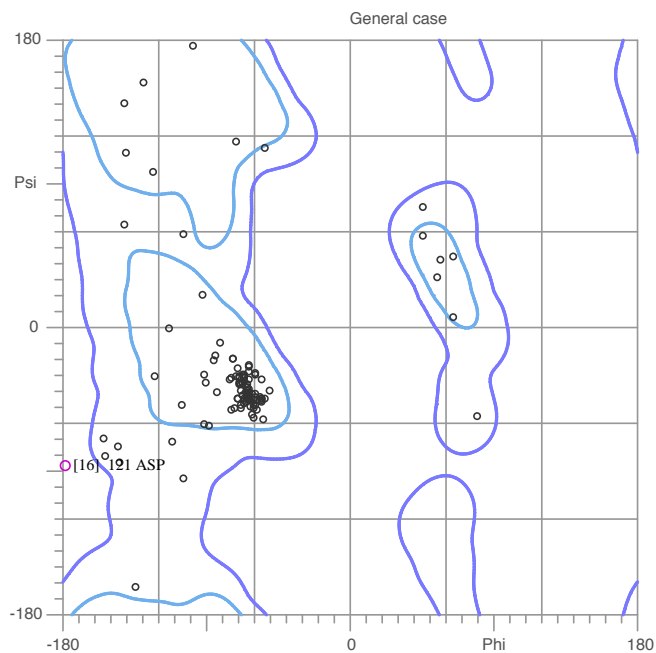


94.2% (114/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[15] 41 LYS (-175.0, -52.0)
[15] 66 ARG (85.0, 118.7)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 16

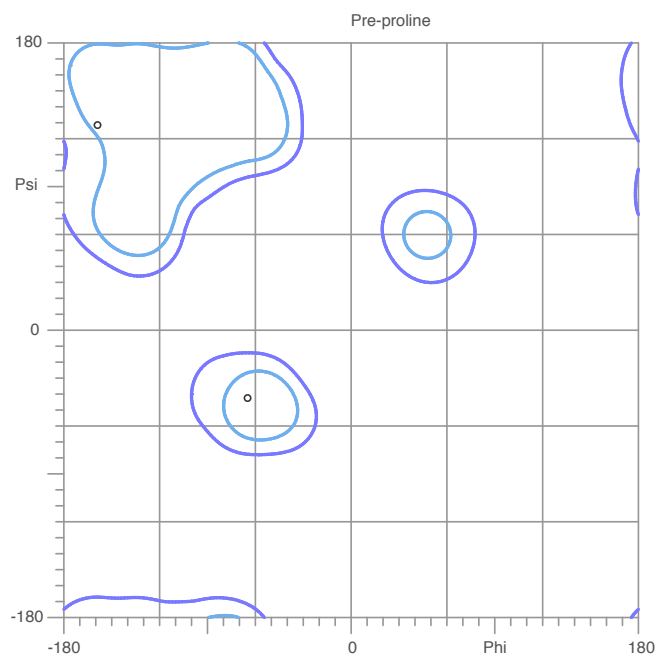
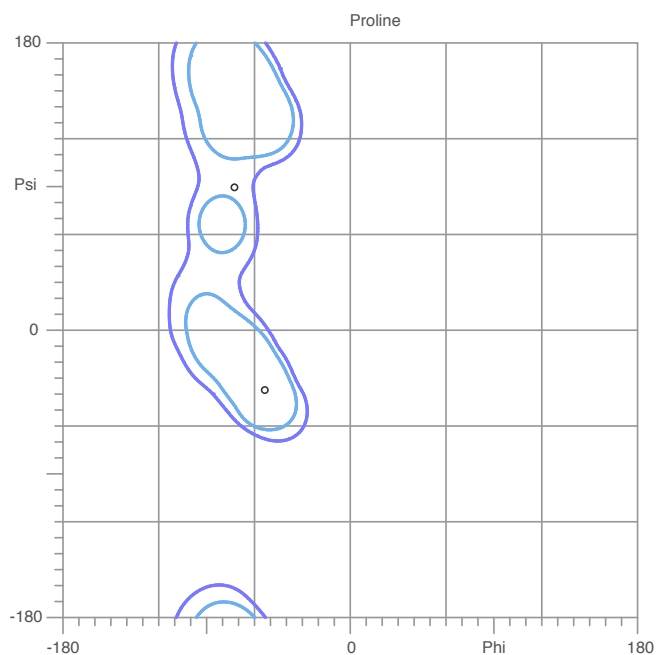
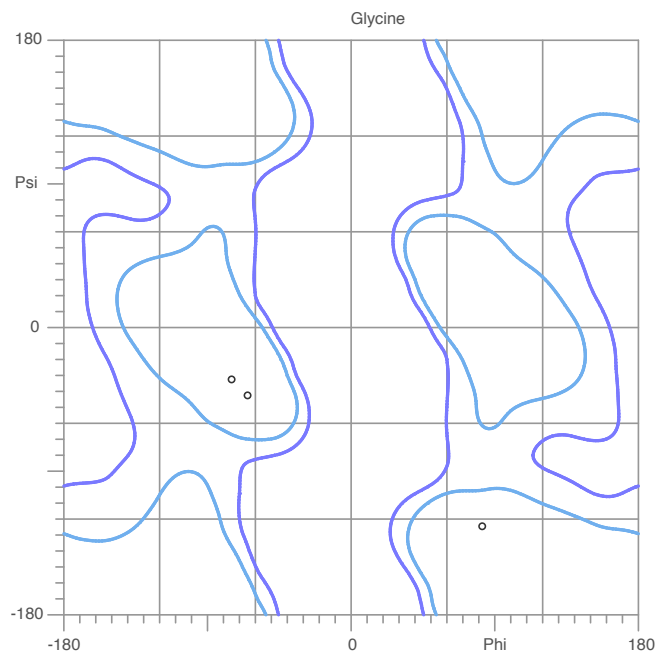
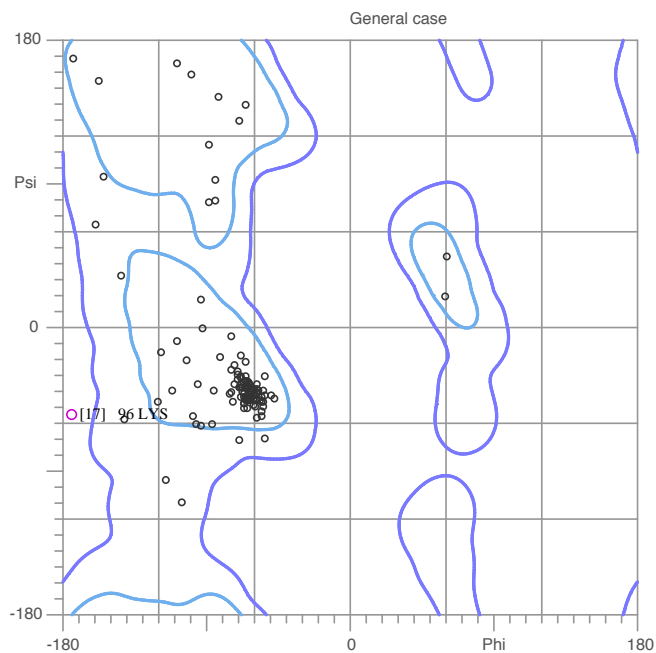


89.3% (108/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[16] 41 LYS (-138.7, -57.3)
[16] 121 ASP (-179.9, -86.2)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 17

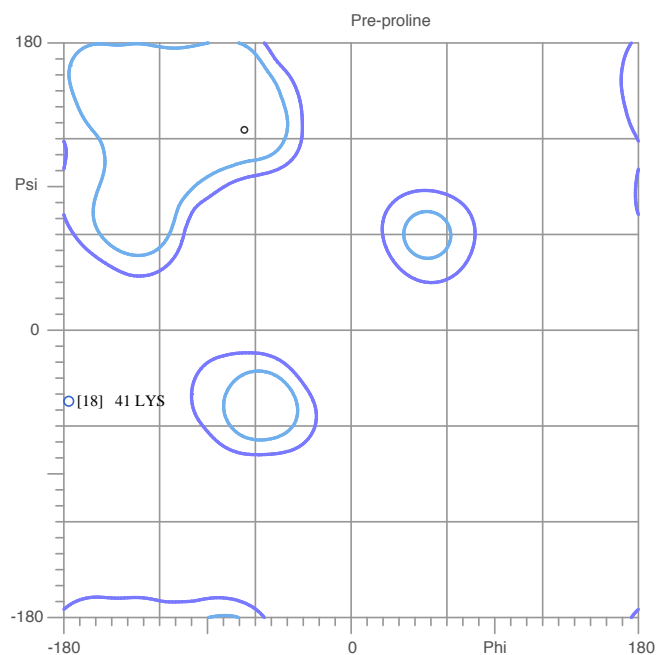
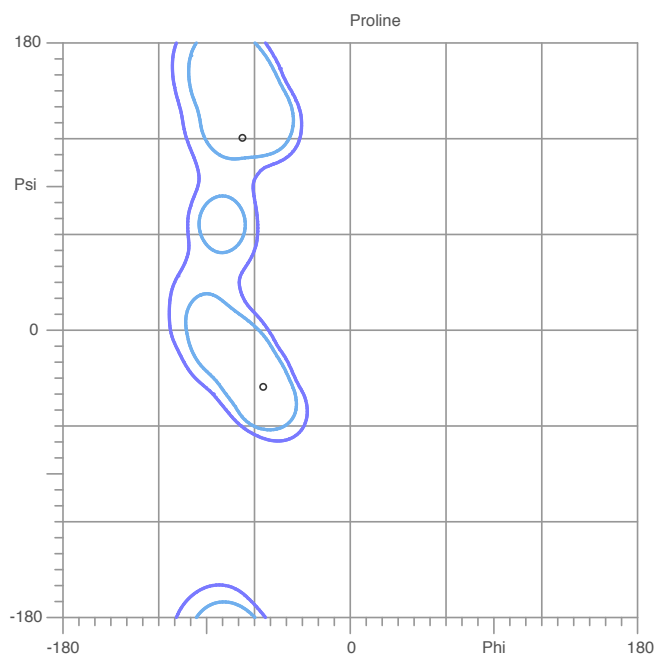
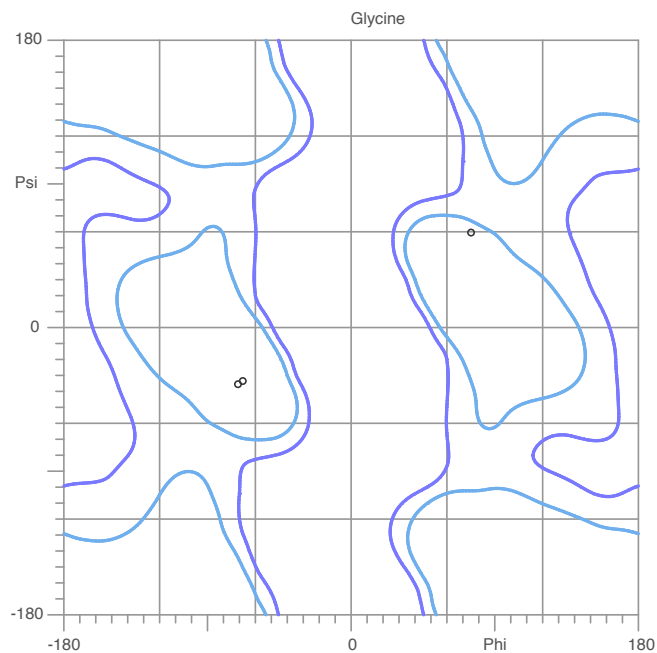
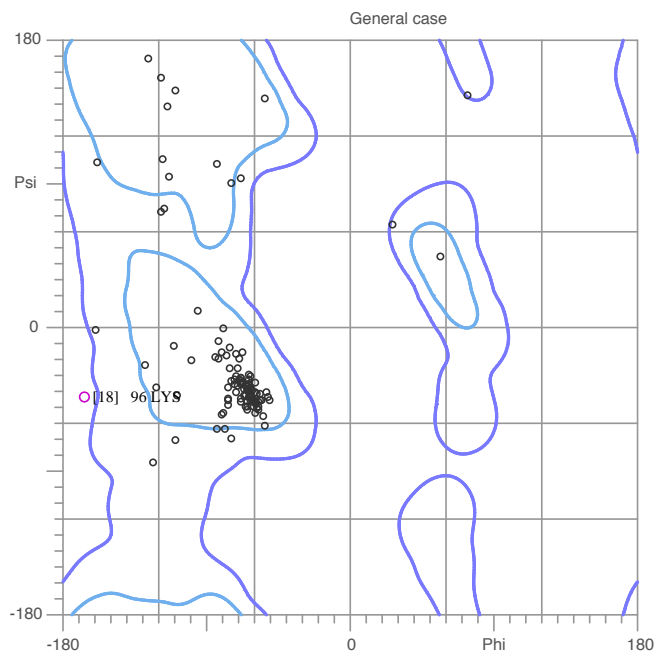


91.7% (111/121) of all residues were in favored (98%) regions.
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[17] 96 LYS (-175.1, -54.7)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 18

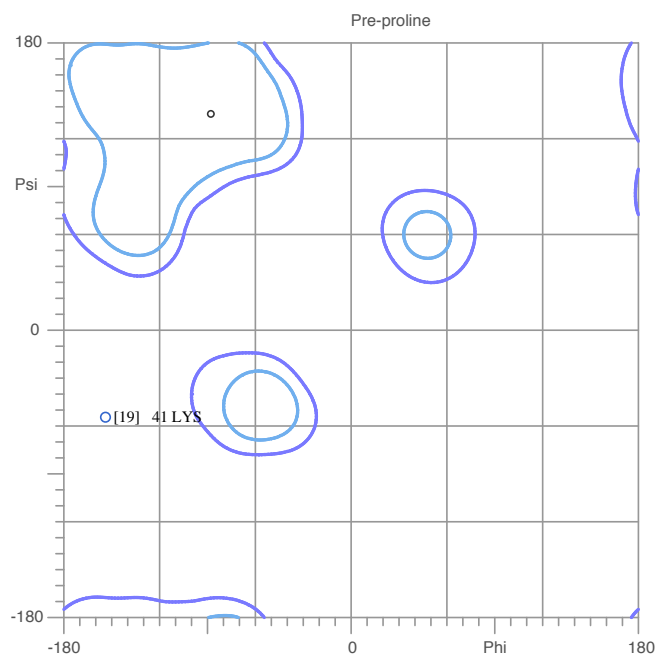
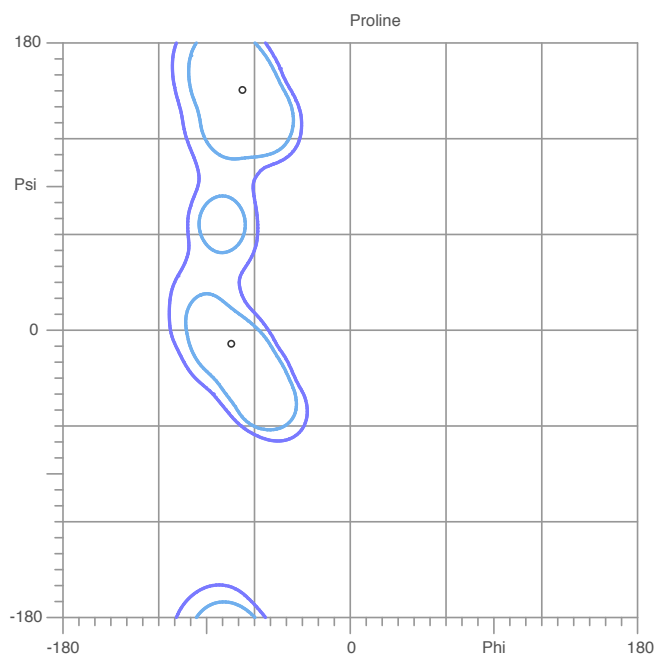
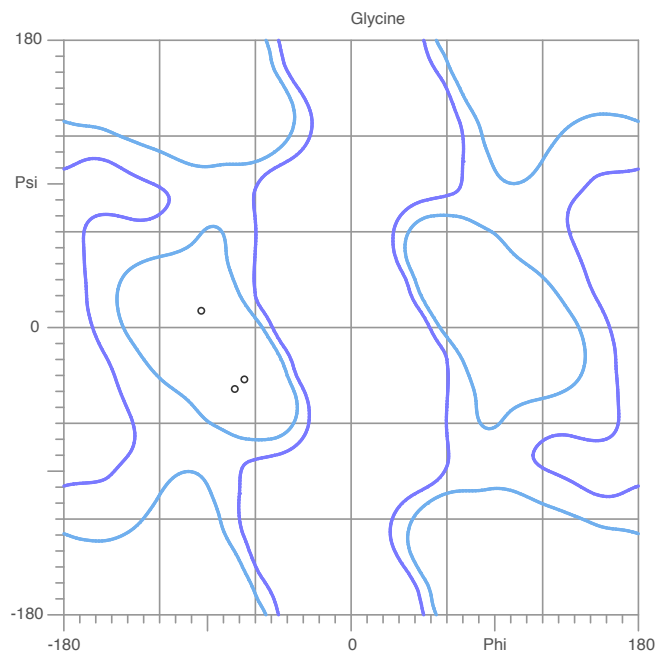
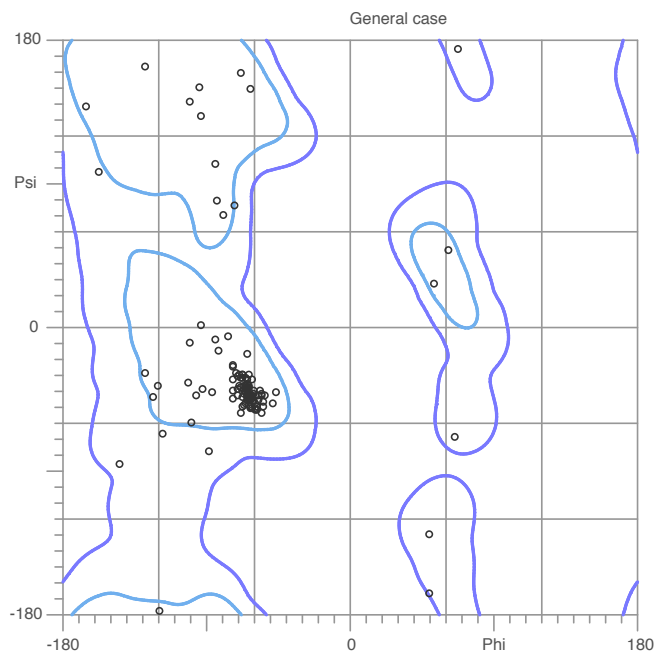


88.4% (107/121) of all residues were in favored (98%) regions.
98.3% (119/121) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 41 LYS (-177.5, -44.9)
[18] 96 LYS (-167.3, -43.3)

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 19



92.6% (112/121) of all residues were in favored (98%) regions.
99.2% (120/121) of all residues were in allowed (>99.8%) regions.

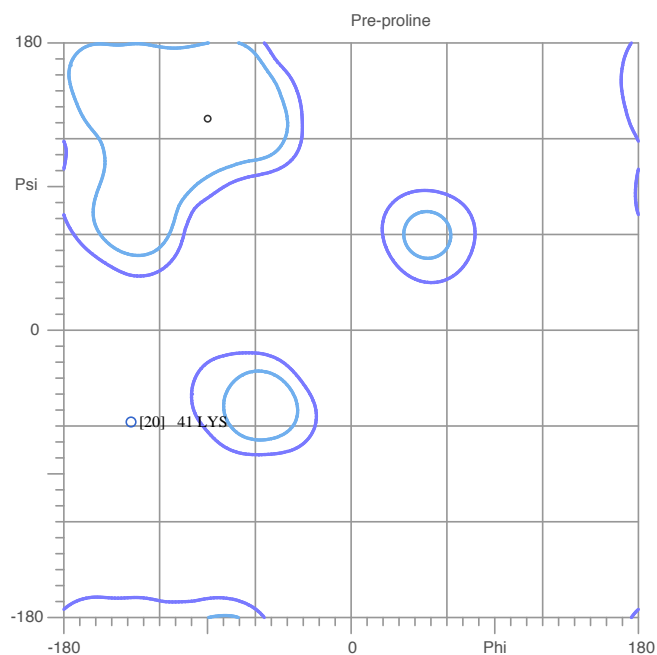
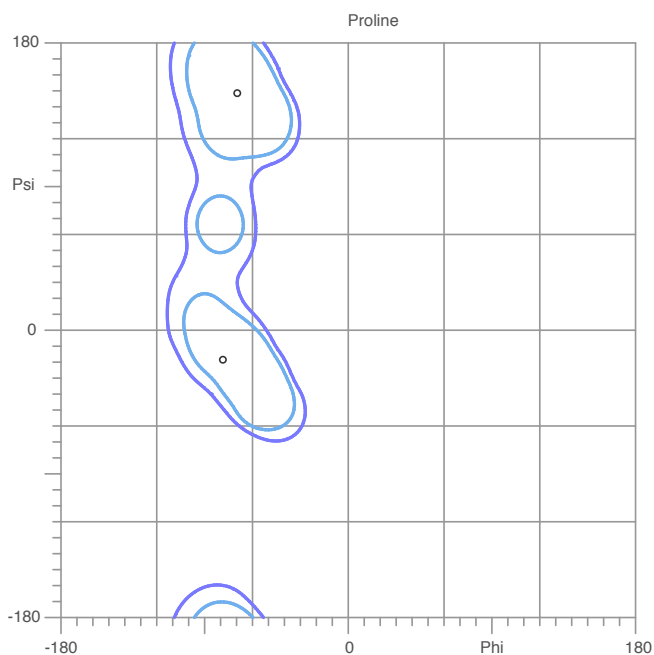
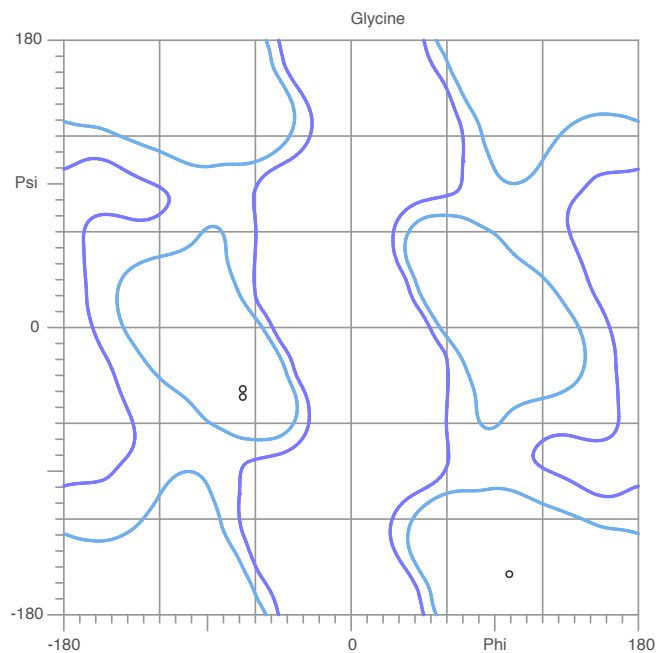
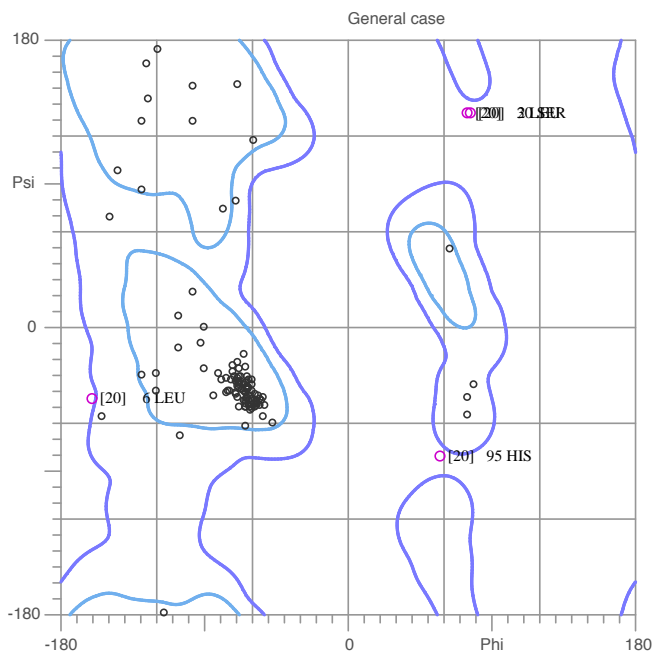
There were 1 outliers (phi, psi):
[19] 41 LYS (-154.9, -54.5)

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

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

MolProbity Ramachandran analysis

SR213_R3_em_bcr3.pdb, model 20



90.1% (109/121) of all residues were in favored (98%) regions.
95.9% (116/121) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[20] 2 LEU (75.0, 135.0)
[20] 6 LEU (-161.7, -45.0)
[20] 30 SER (76.7, 135.0)
[20] 41 LYS (-138.7, -57.1)
[20] 95 HIS (57.9, -80.7)