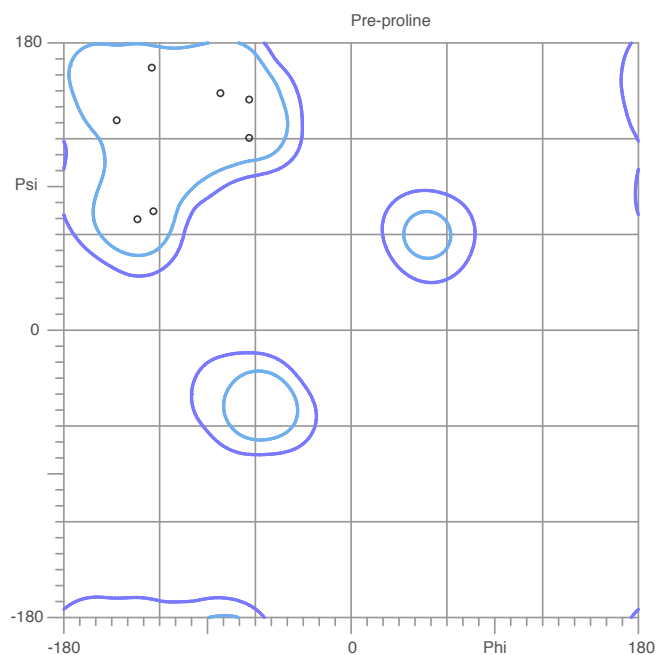
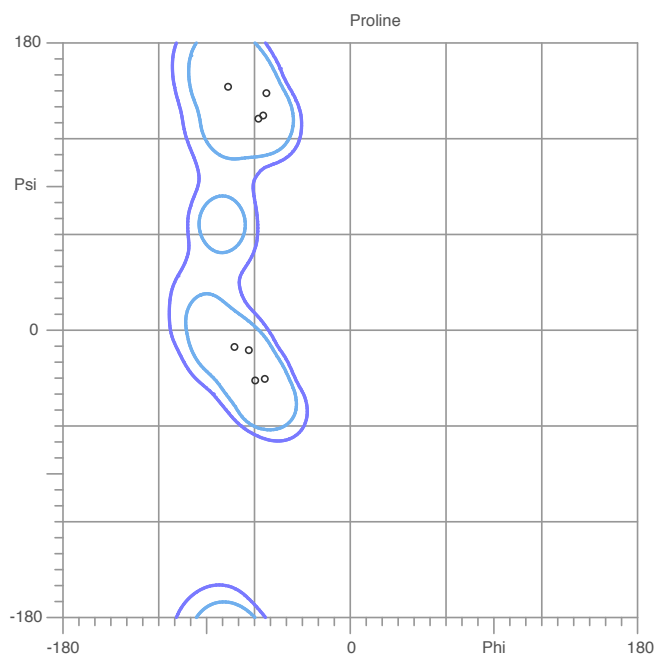
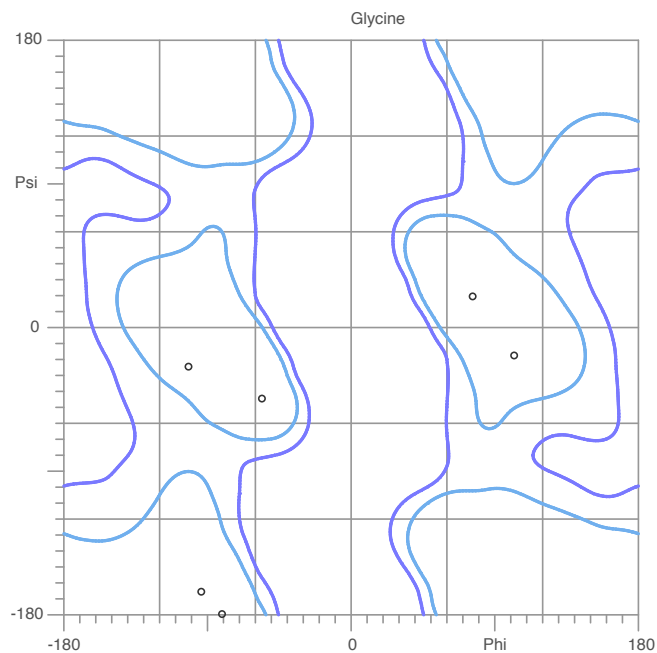
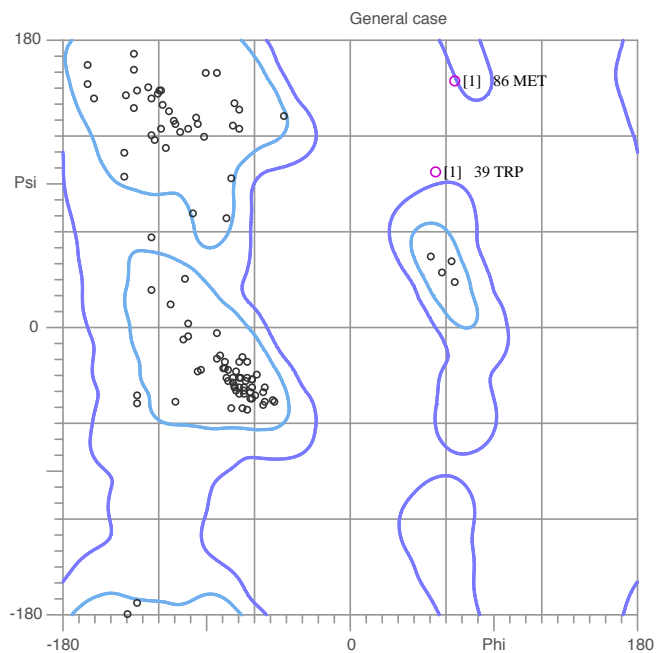


MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 1



95.9% (118/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

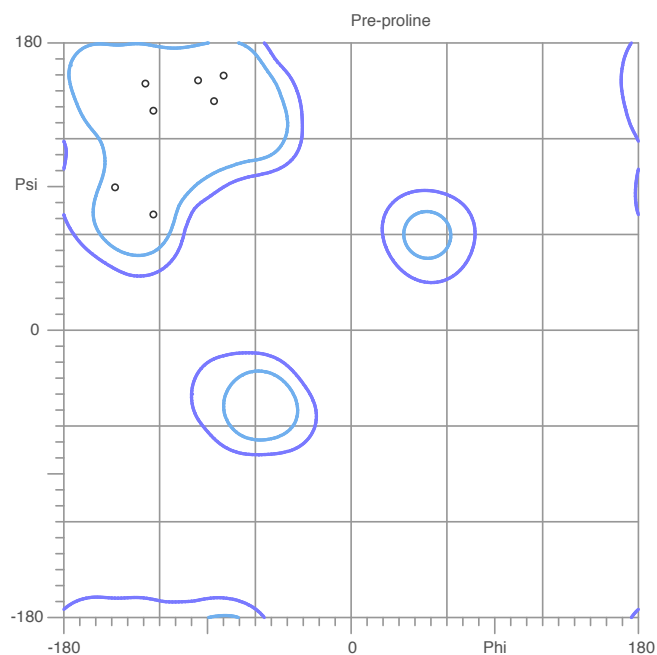
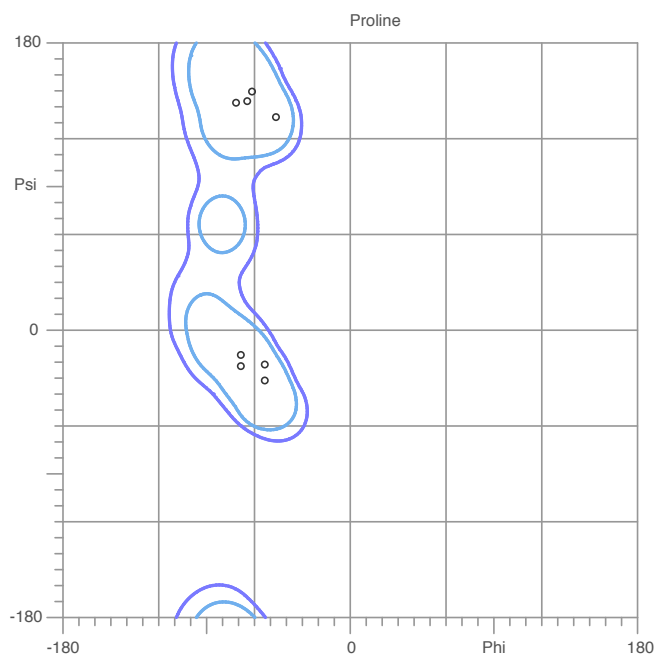
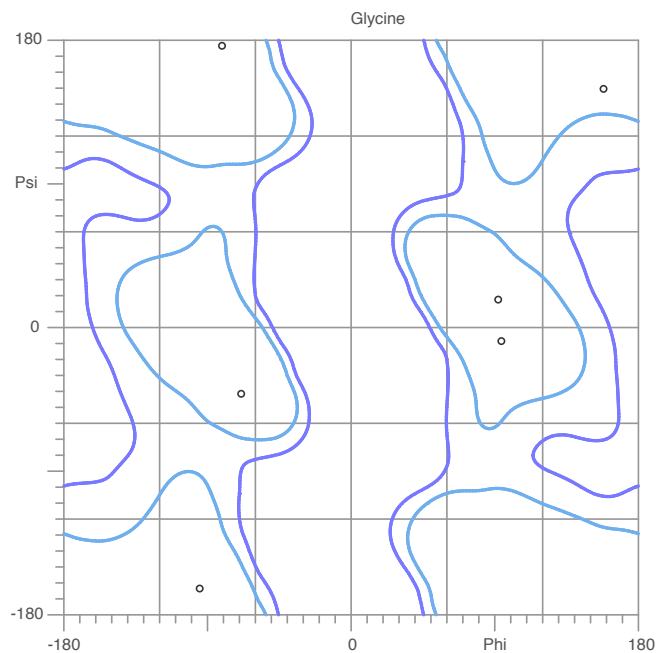
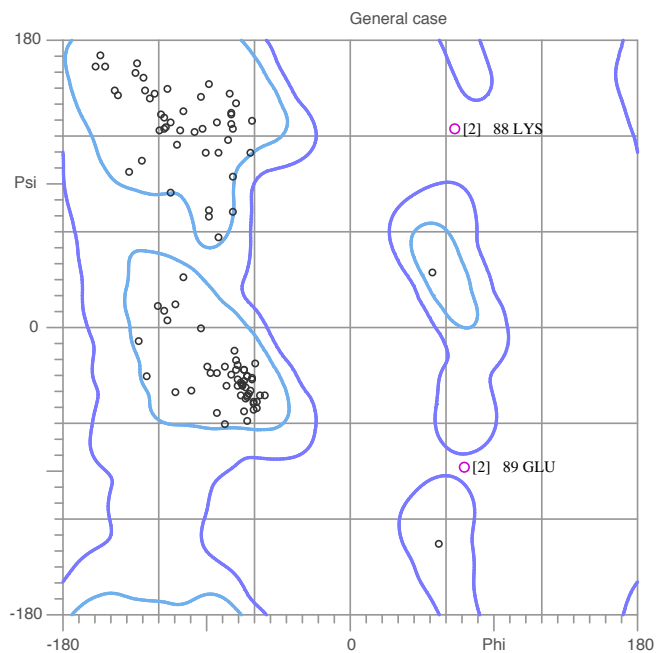
There were 2 outliers (phi, psi):

[1] 39 TRP (53.8, 98.4)

[1] 86 MET (65.1, 155.5)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 2



97.6% (120/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

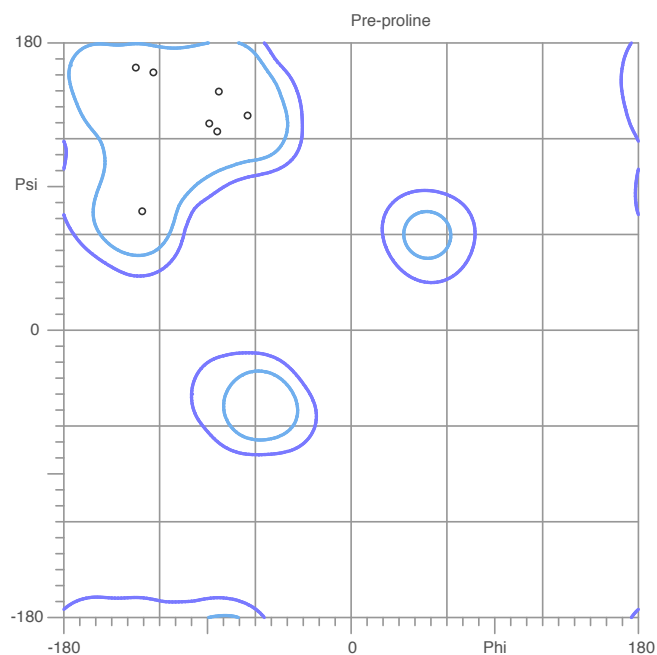
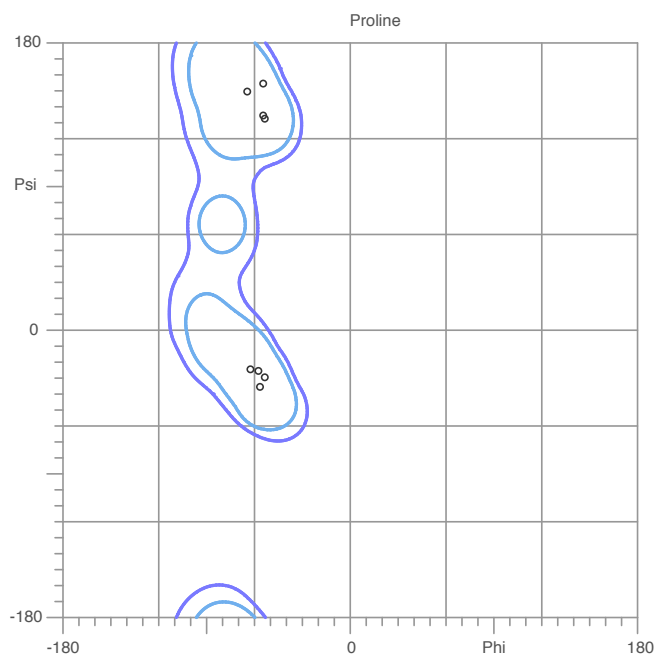
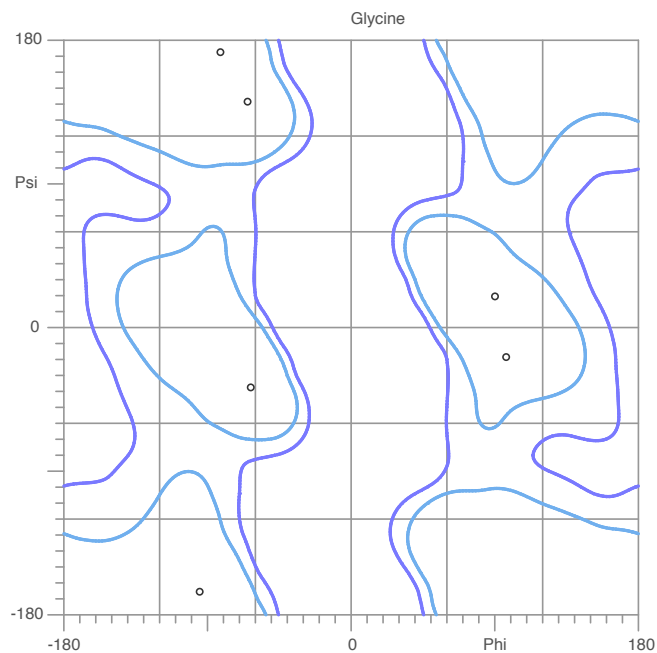
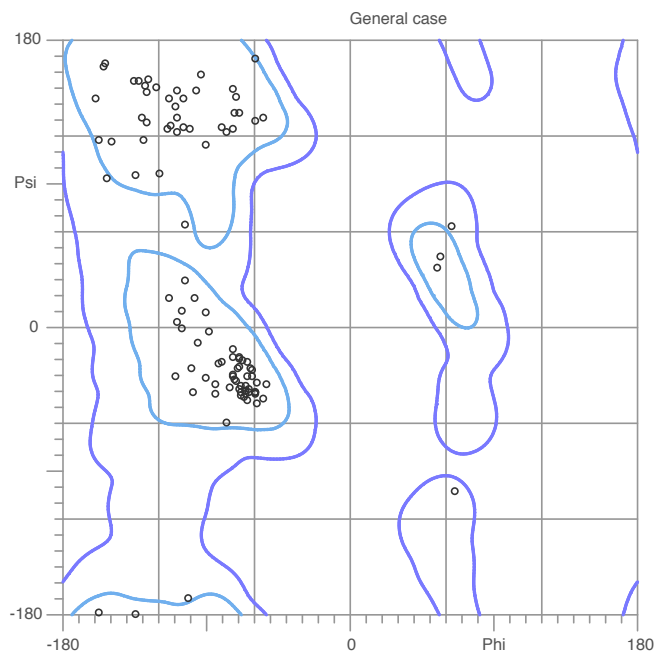
There were 2 outliers (phi, psi):

[2] 88 LYS (65.9, 125.0)

[2] 89 GLU (71.7, -87.6)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 3



95.9% (118/123) of all residues were in favored (98%) regions.
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

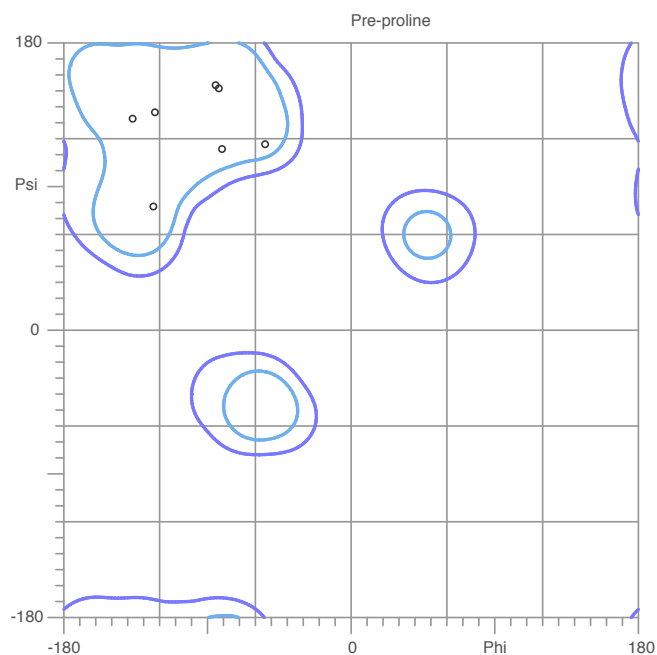
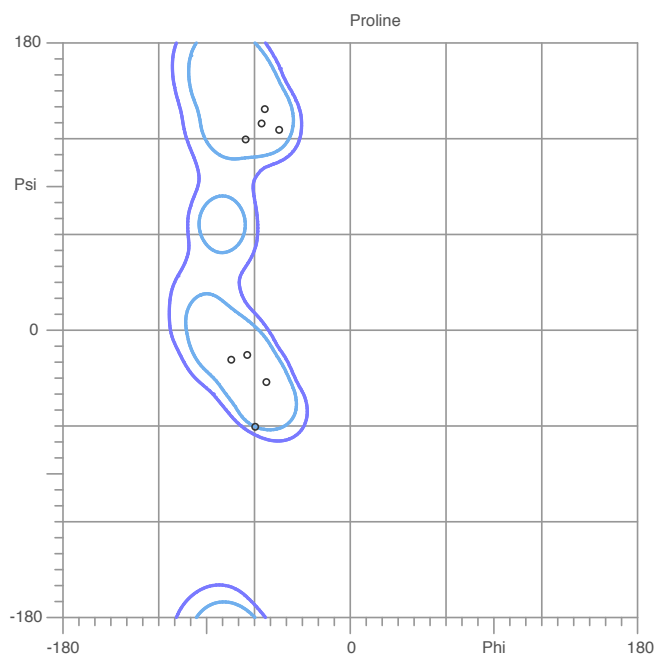
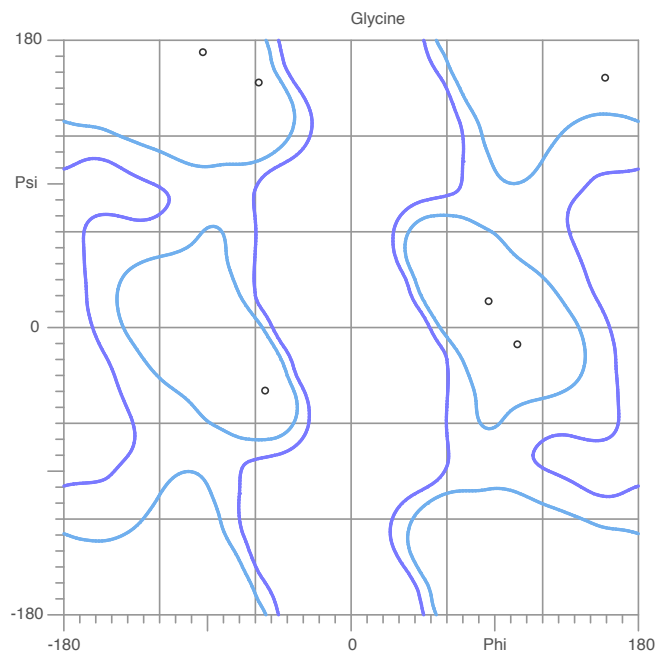
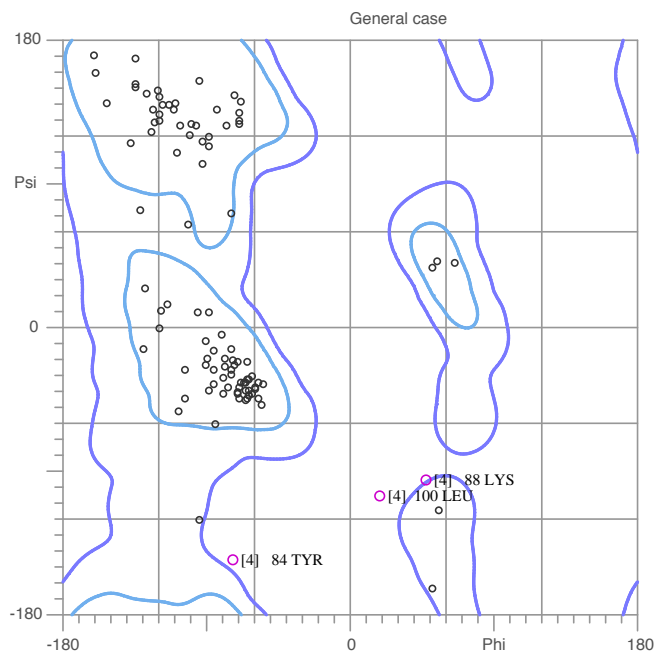
There were no outliers.

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MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 4



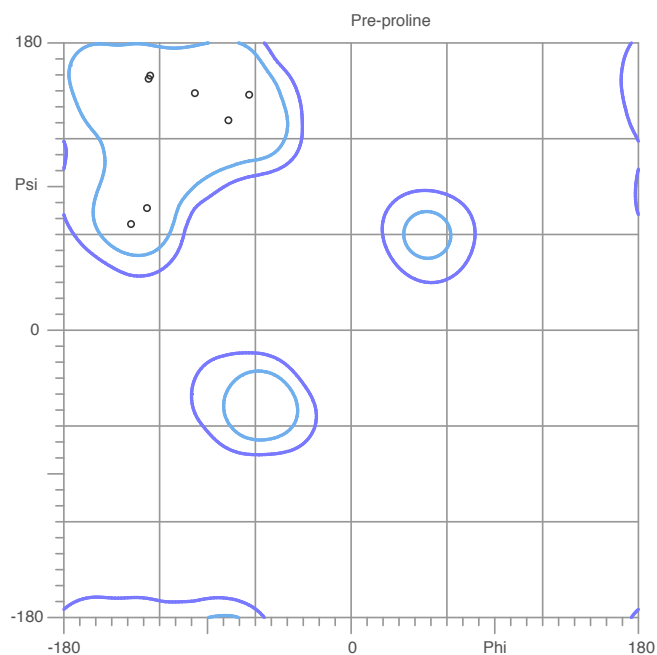
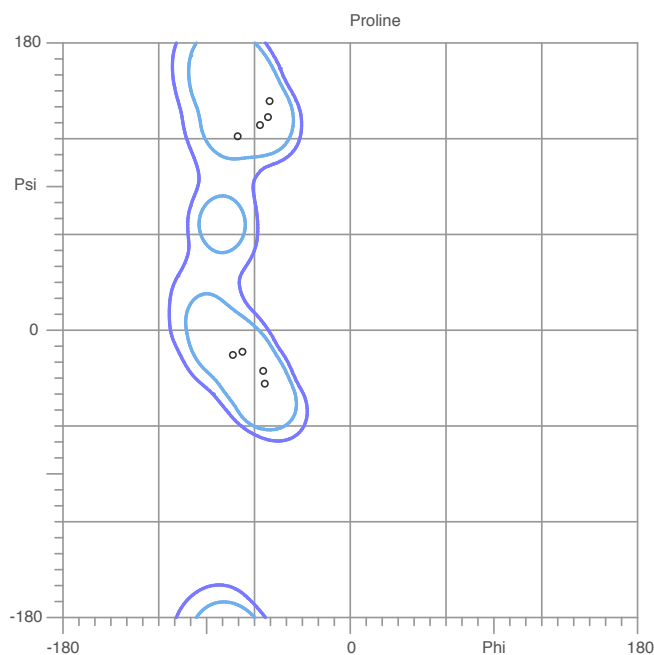
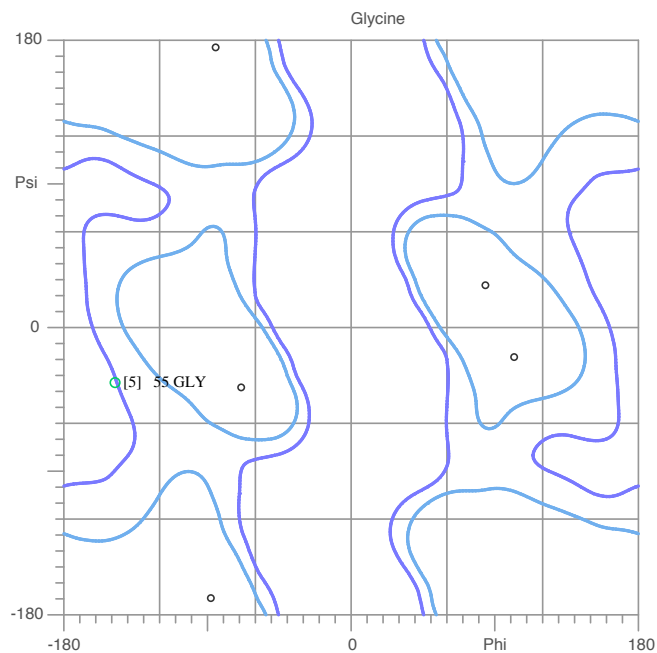
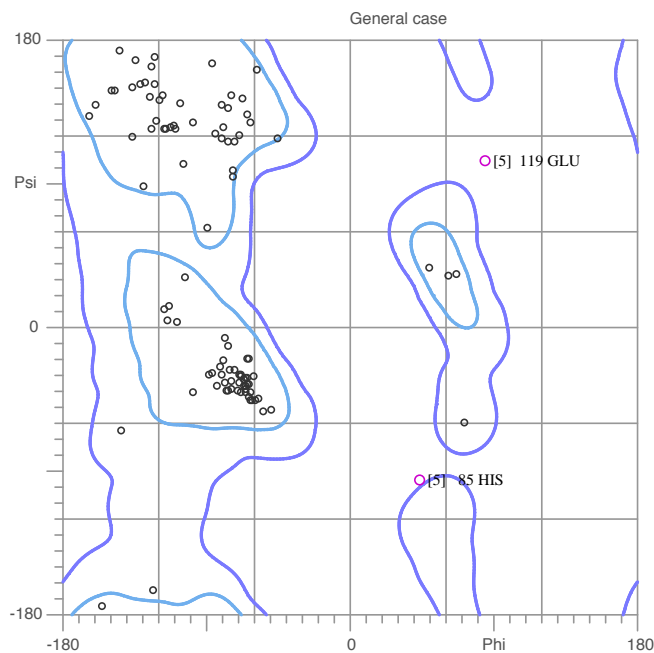
93.5% (115/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [4] 84 TYR (-75.0, -145.0)
- [4] 88 LYS (47.1, -95.0)
- [4] 100 LEU (18.8, -105.1)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 5



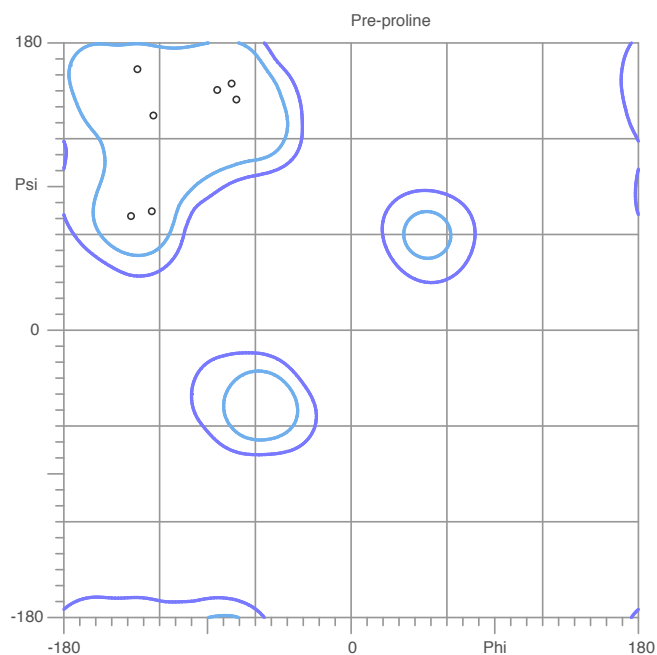
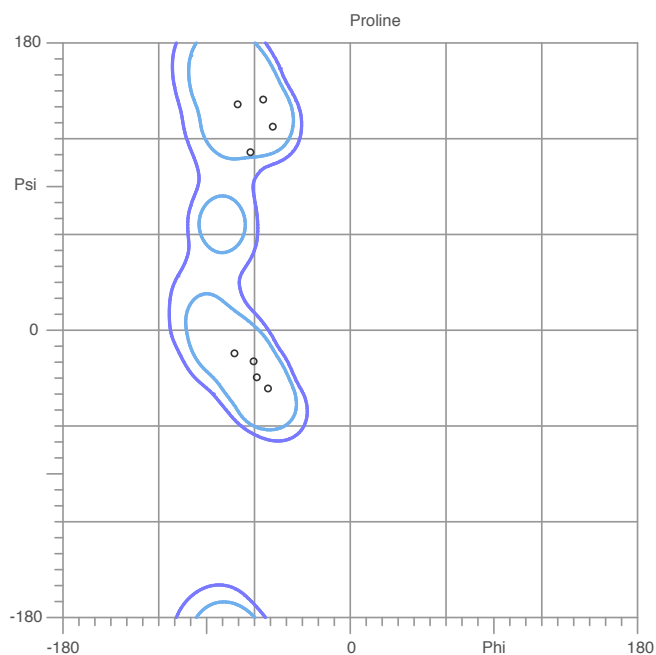
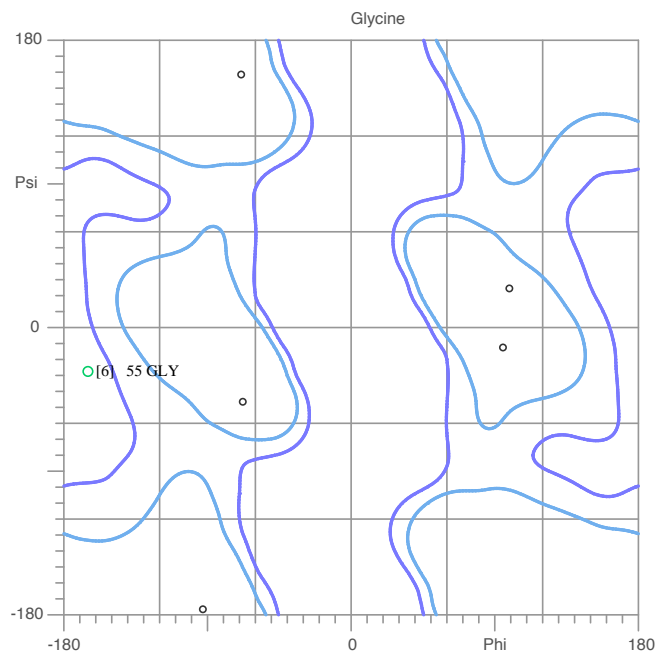
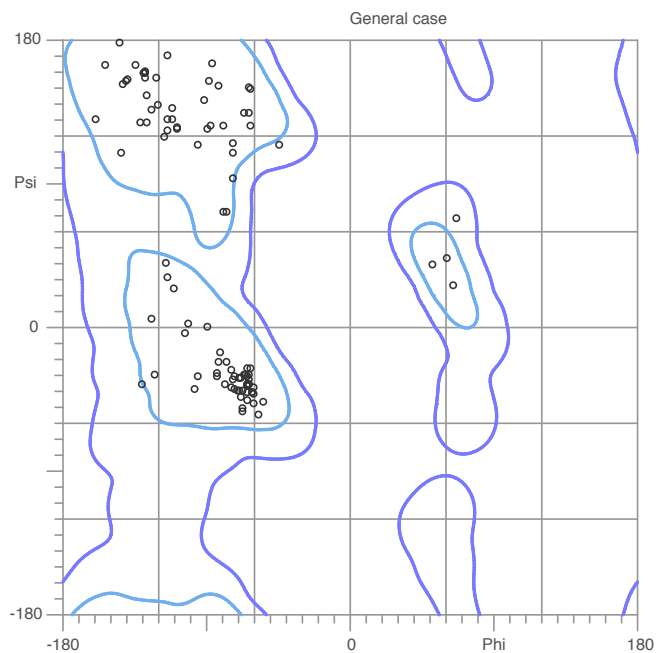
95.1% (117/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [5] 55 GLY (-148.6, -35.0)
- [5] 85 HIS (43.9, -95.2)
- [5] 119 GLU (85.0, 105.2)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 6

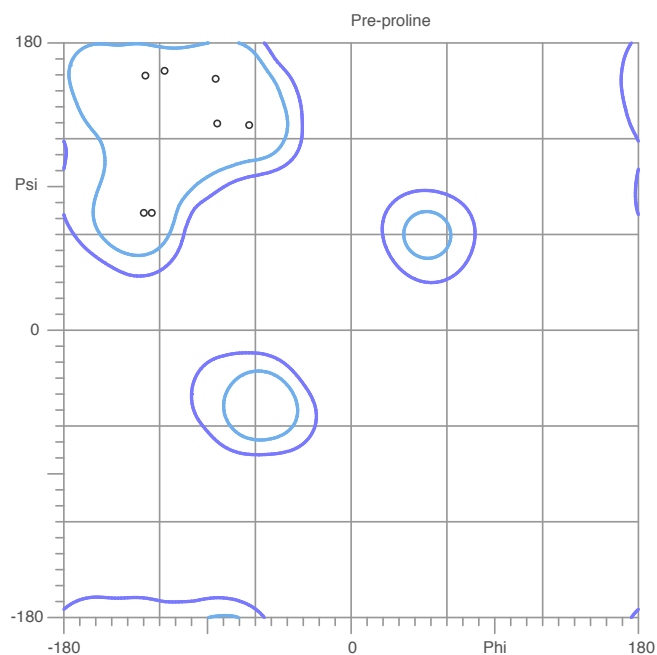
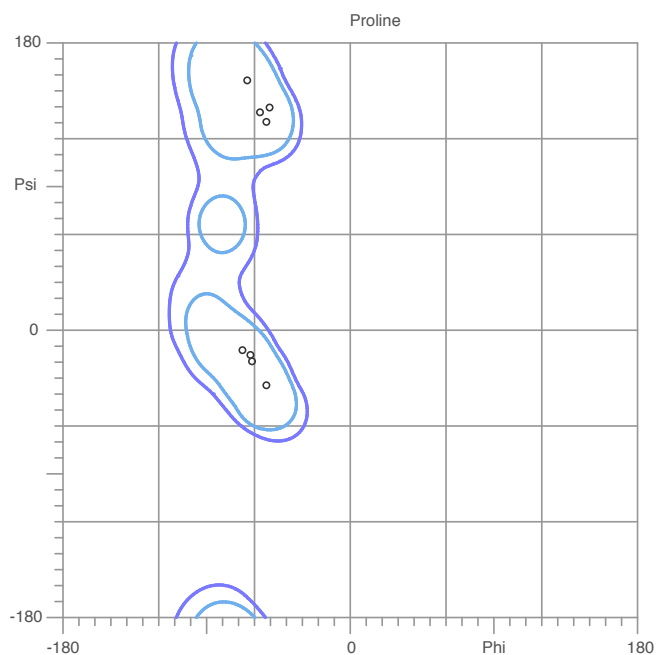
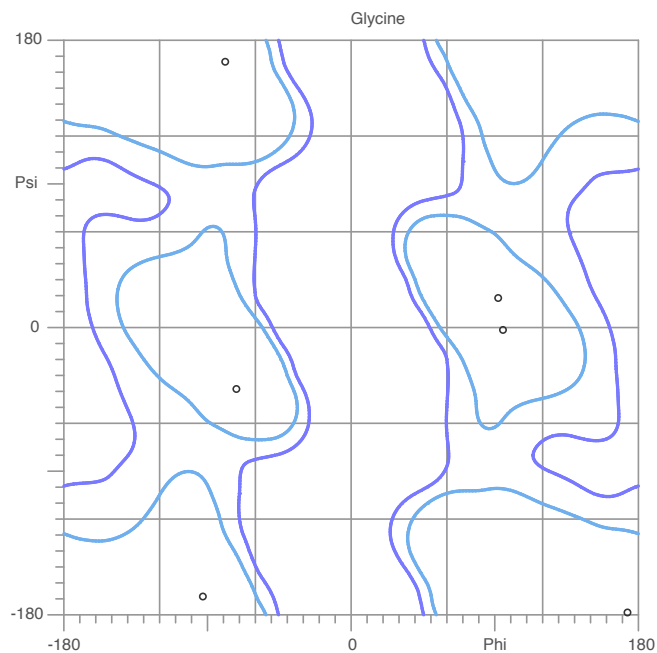
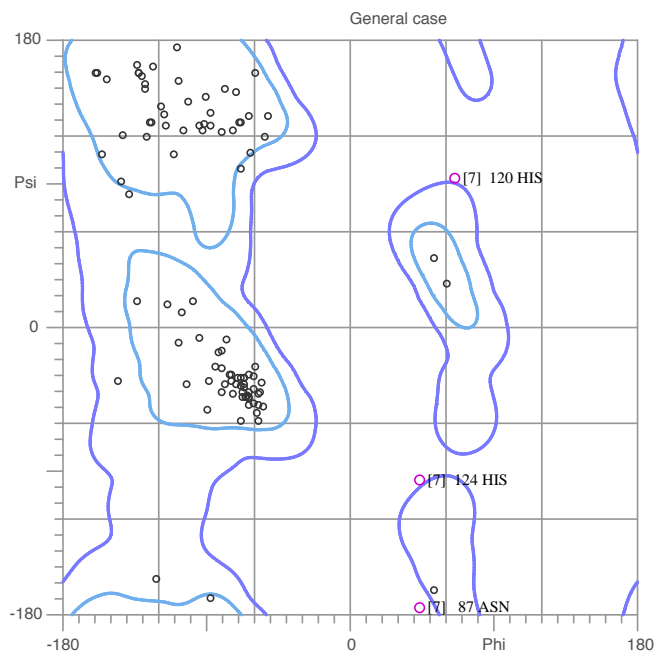


96.7% (119/123) of all residues were in favored (98%) regions.
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[6] 55 GLY (-165.0, -27.4)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 7



93.5% (115/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

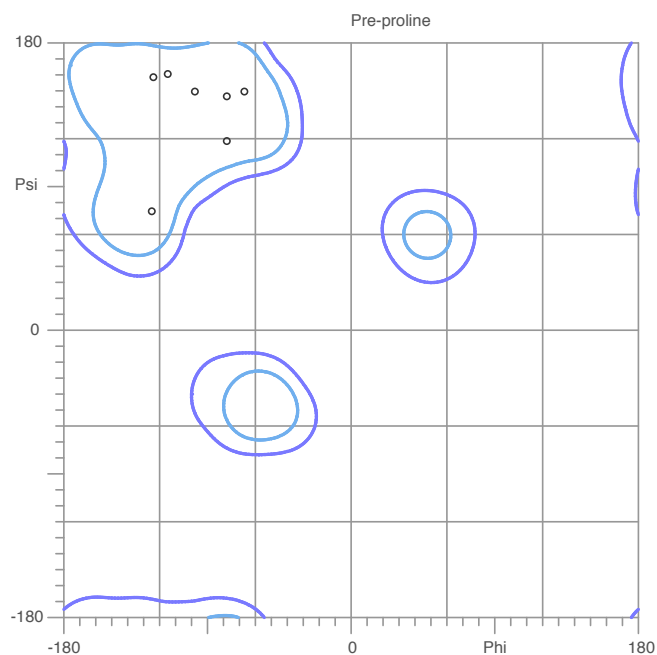
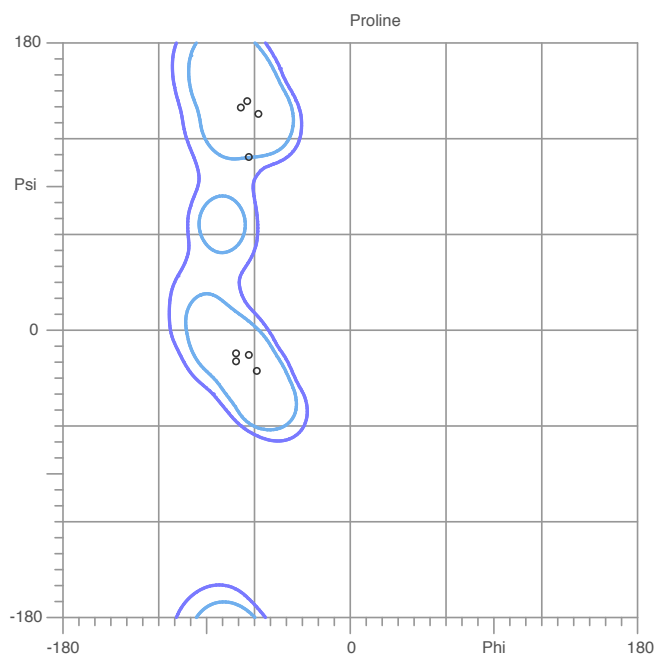
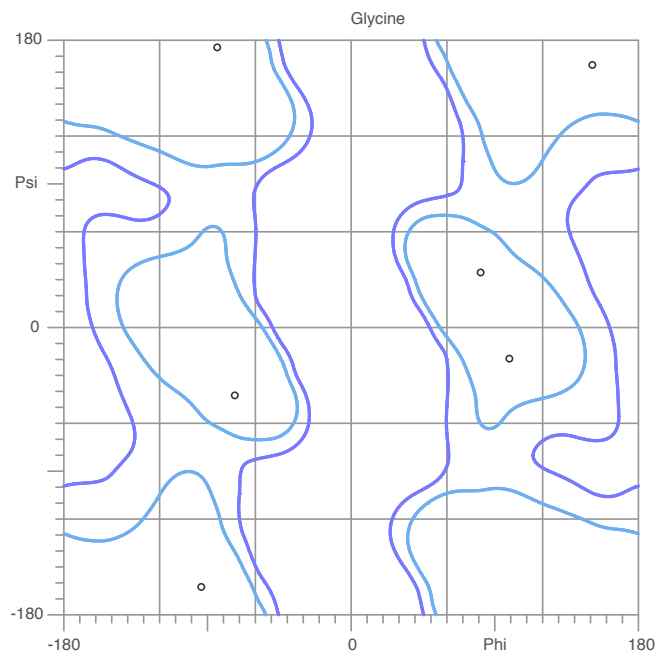
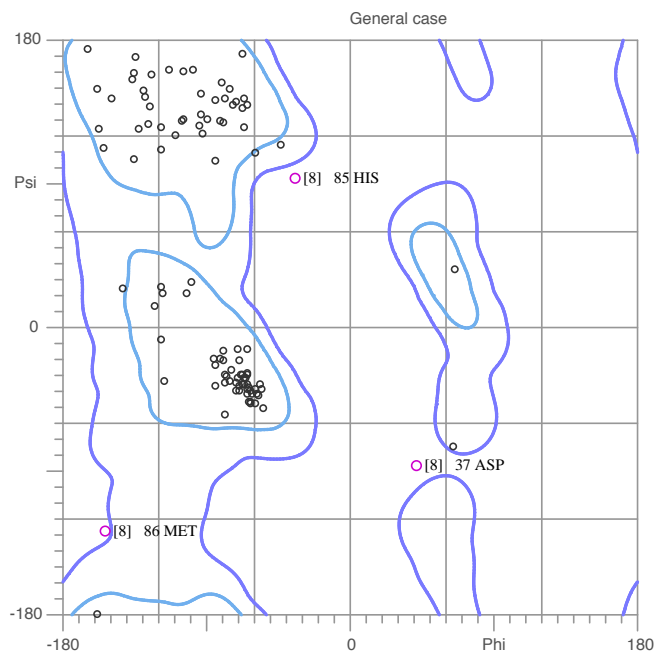
[7] 87 ASN (43.7, -175.1)

[7] 120 HIS (65.0, 94.9)

[7] 124 HIS (43.0, -95.0)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 8



95.1% (117/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

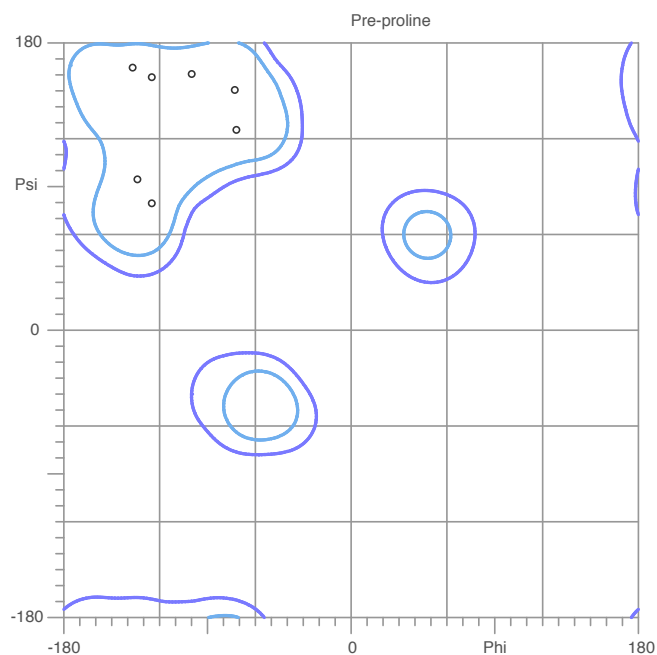
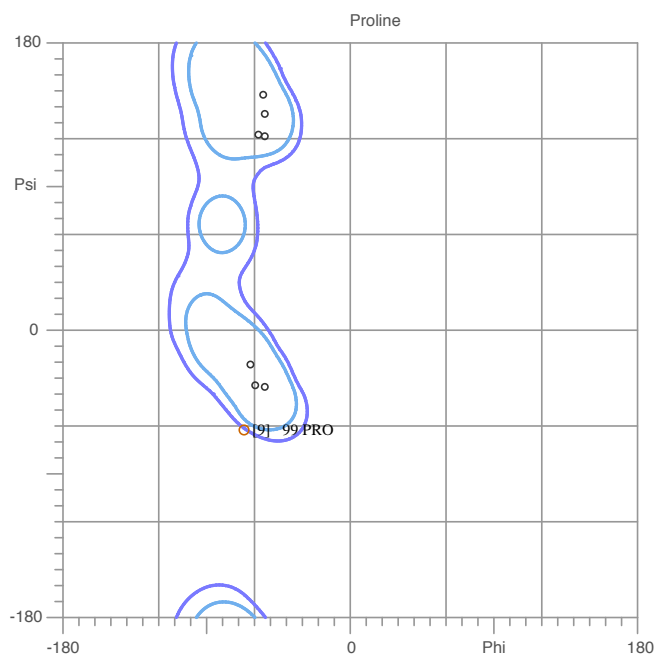
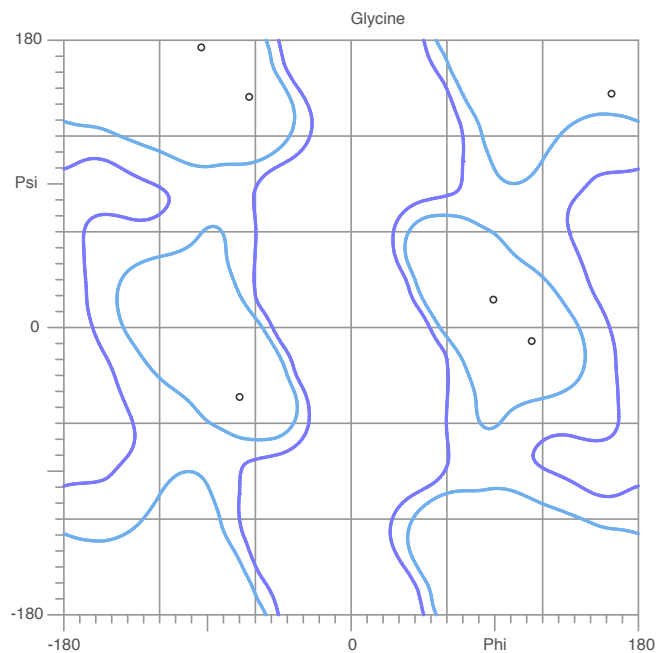
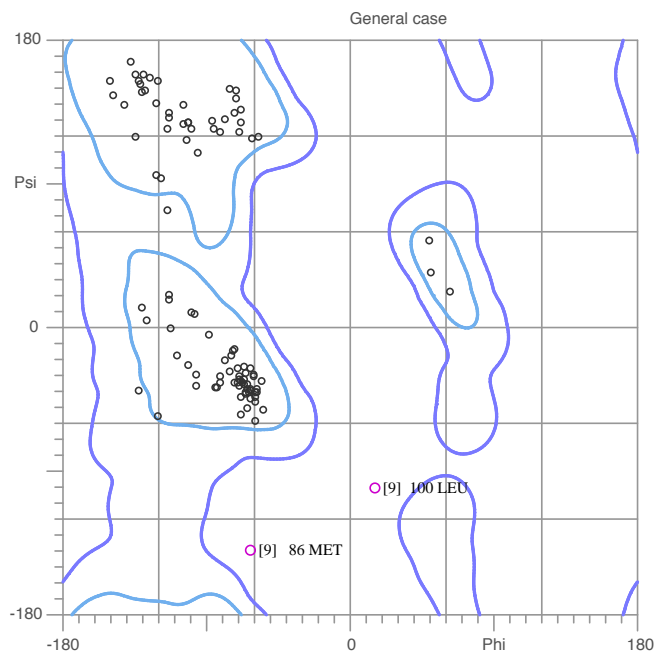
[8] 37 ASP (41.4, -86.3)

[8] 85 HIS (-35.0, 95.0)

[8] 86 MET (-155.0, -127.3)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 9



95.9% (118/123) of all residues were in favored (98%) regions.
97.6% (120/123) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

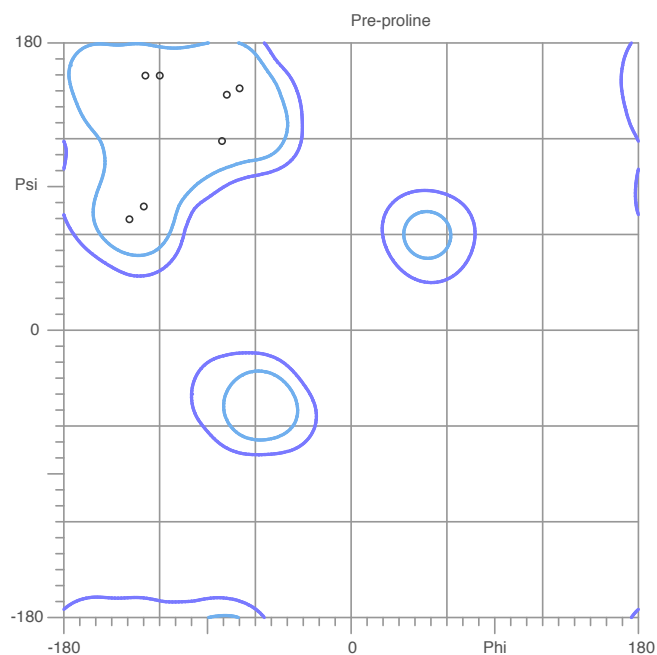
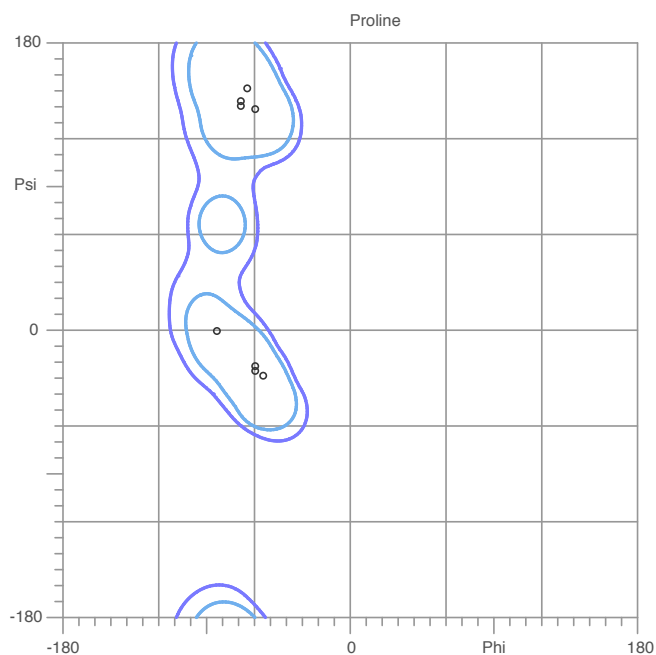
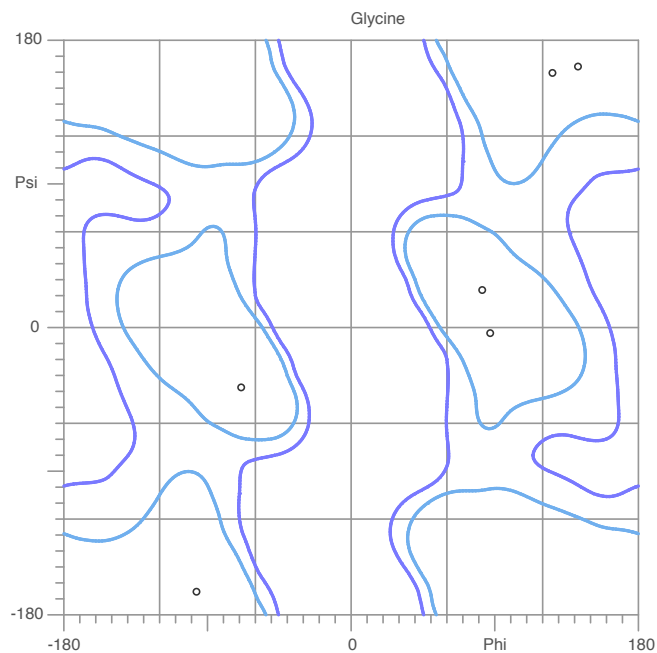
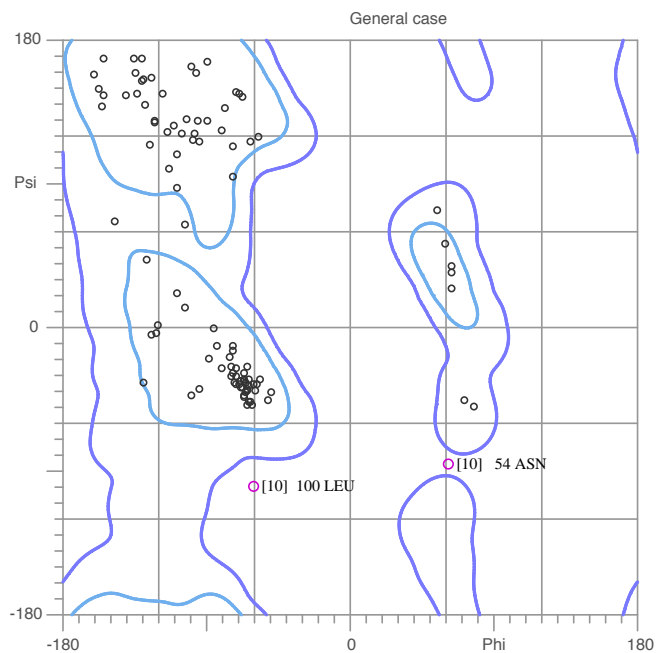
[9] 86 MET (-63.4, -139.5)

[9] 99 PRO (-67.6, -62.2)

[9] 100 LEU (15.0, -100.7)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 10

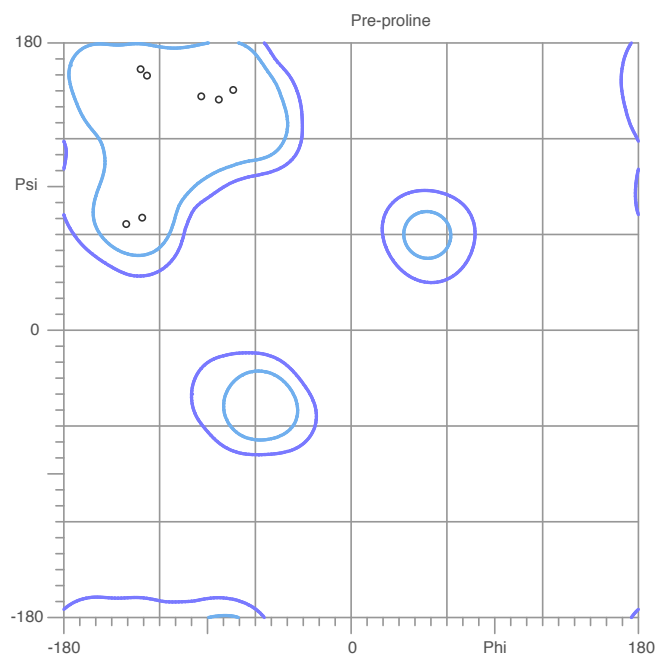
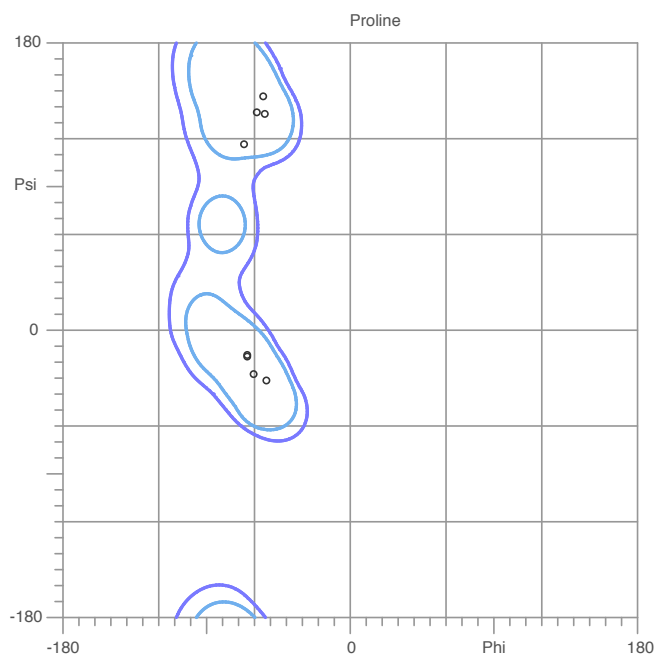
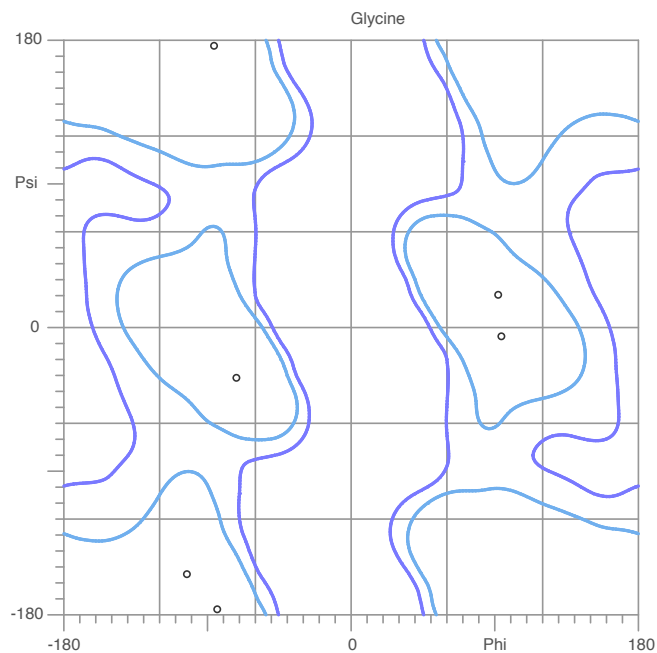
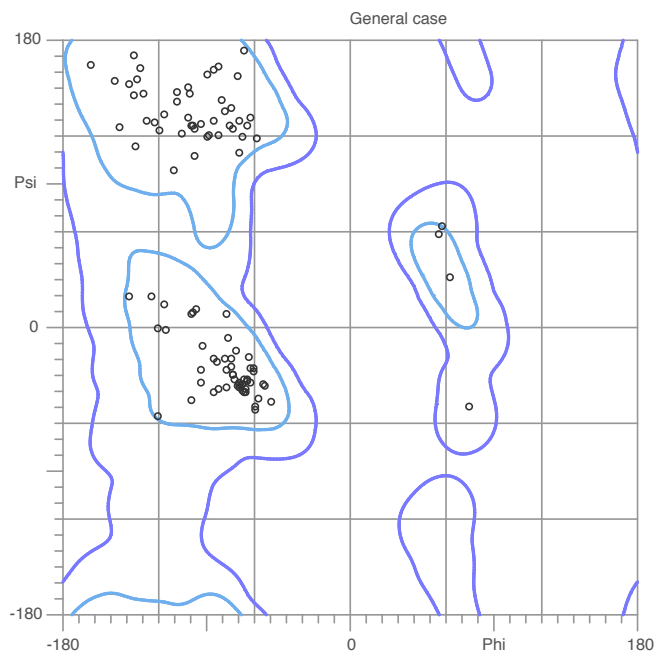


93.5% (115/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[10] 54 ASN (62.0, -85.1)
[10] 100 LEU (-61.7, -99.9)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 11



98.4% (121/123) of all residues were in favored (98%) regions.
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

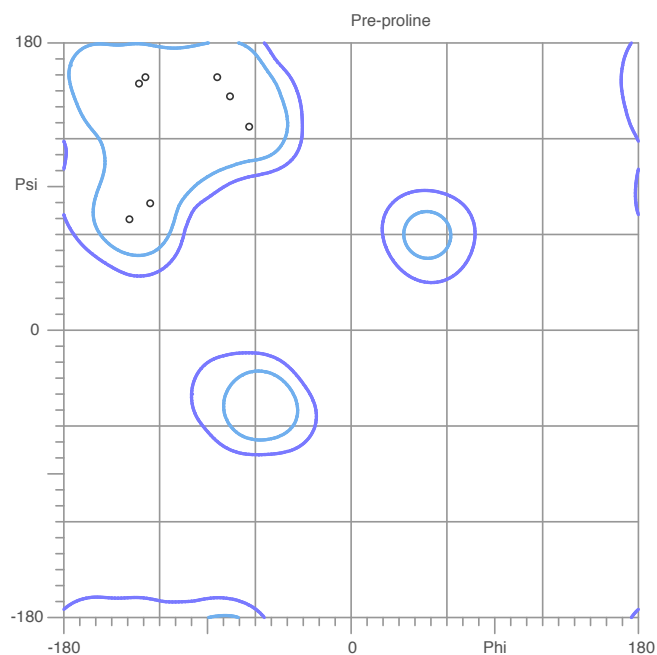
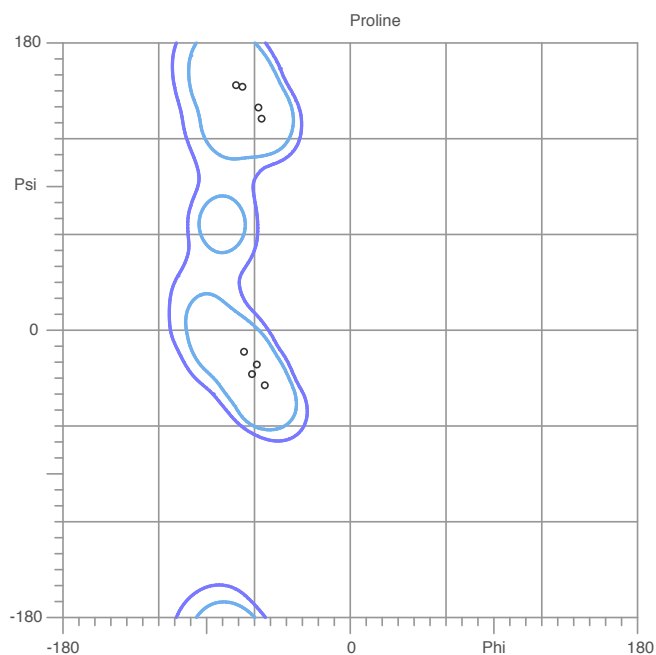
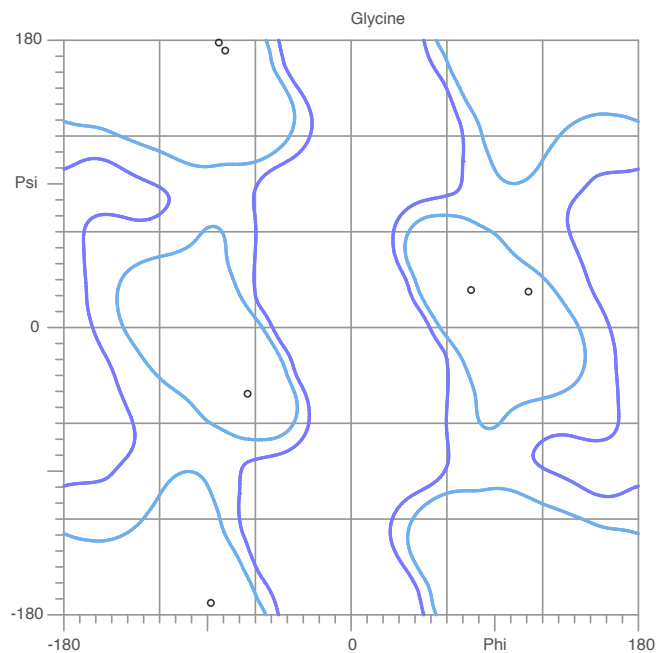
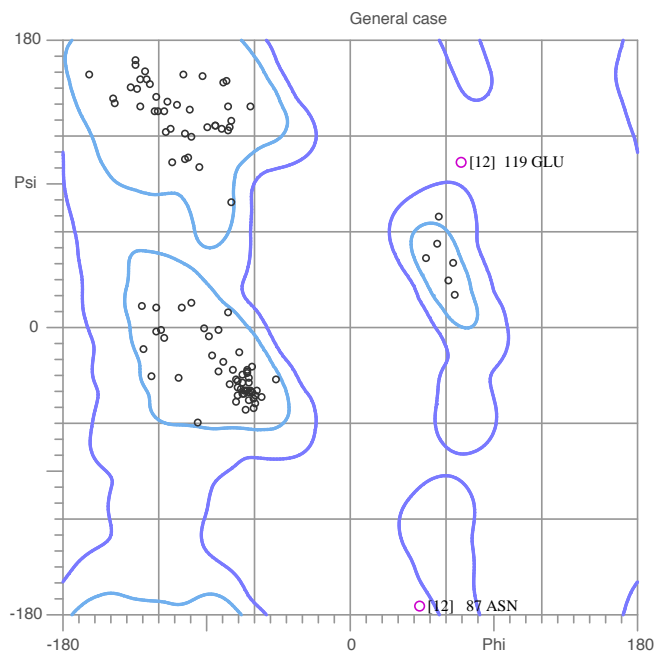
There were no outliers.

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MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 12

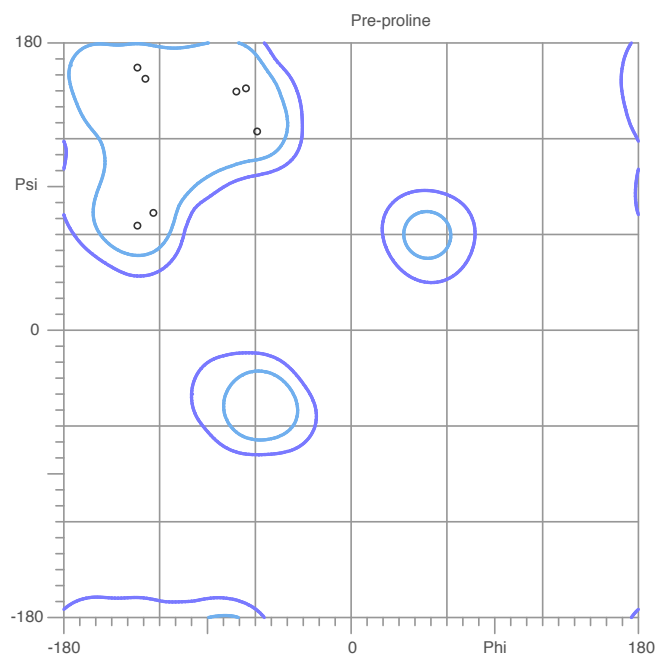
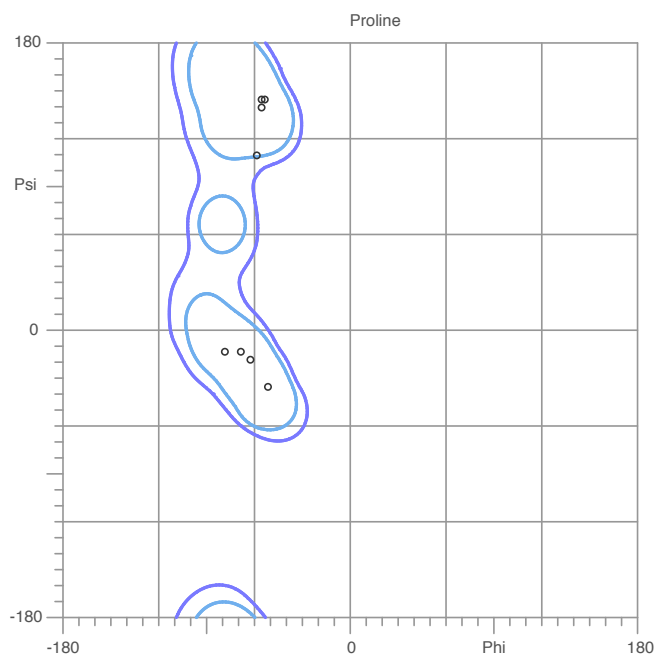
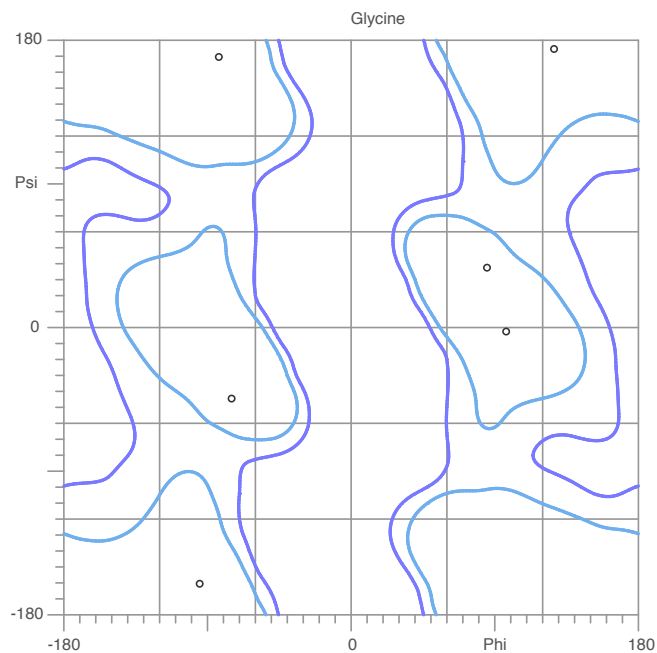
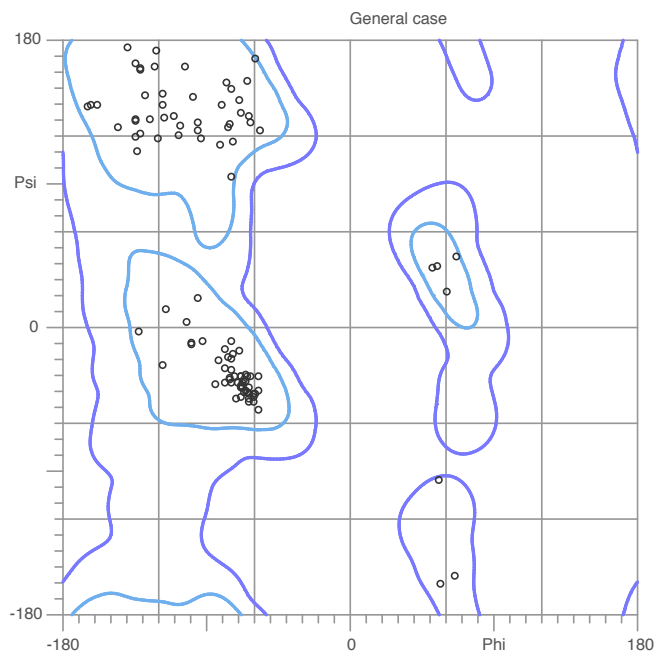


97.6% (120/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 87 ASN (43.7, -174.9)
[12] 119 GLU (69.5, 105.0)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 13



97.6% (120/123) of all residues were in favored (98%) regions.
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

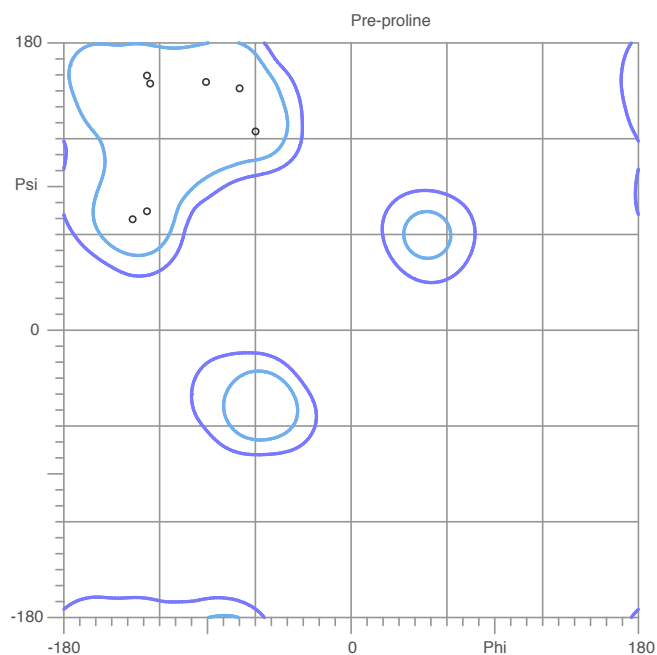
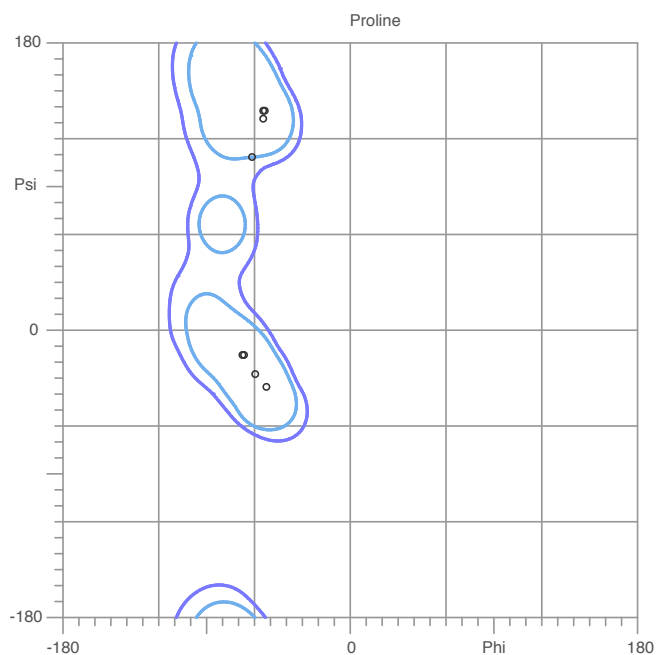
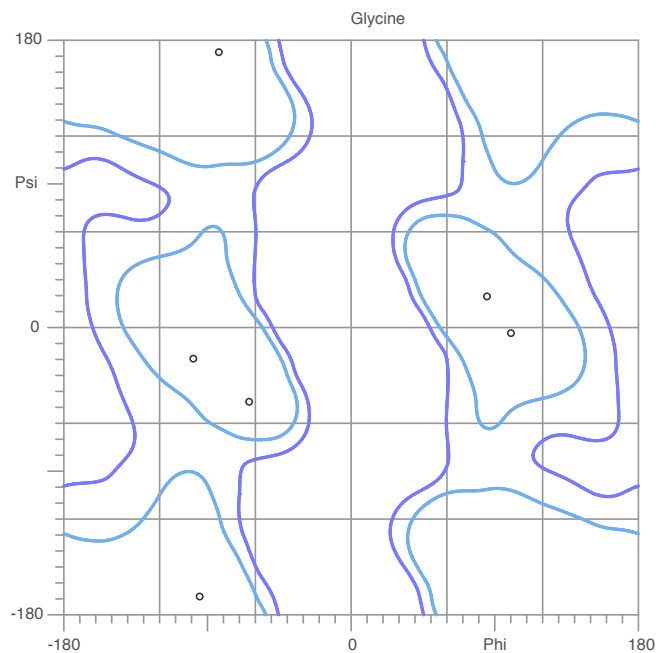
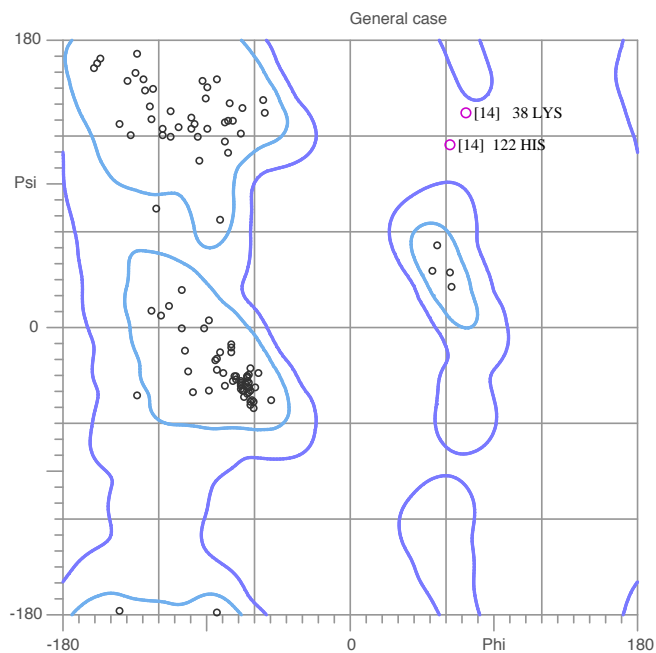
There were no outliers.

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MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 14

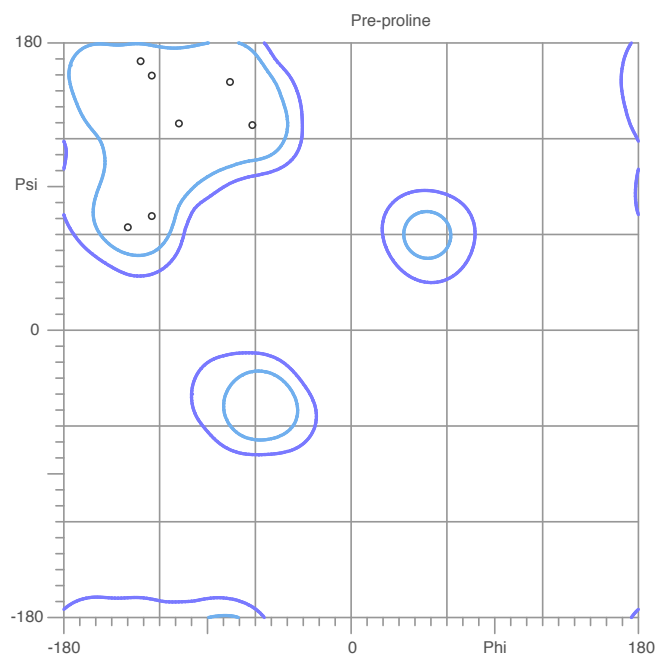
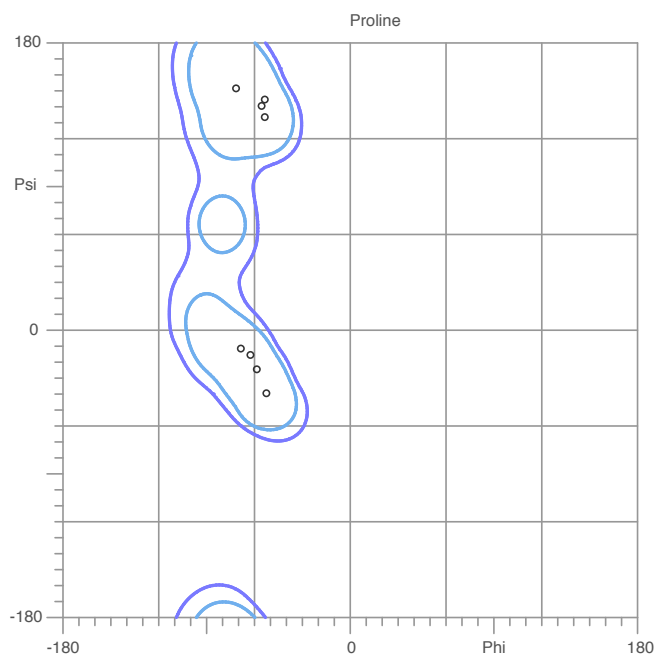
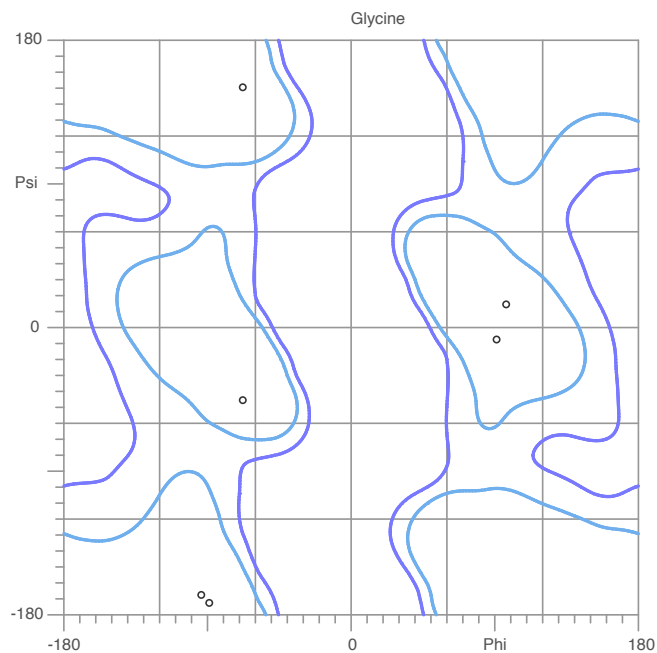
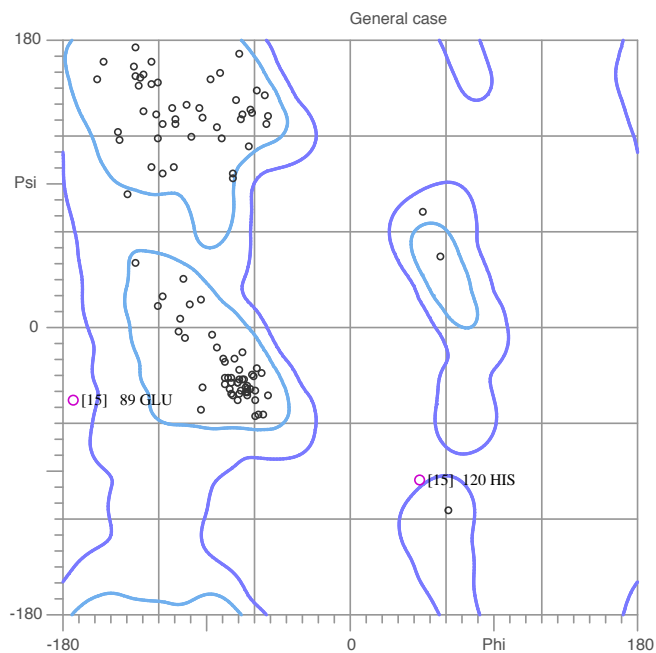


96.7% (119/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[14] 38 LYS (72.5, 135.9)
[14] 122 HIS (62.3, 115.1)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 15

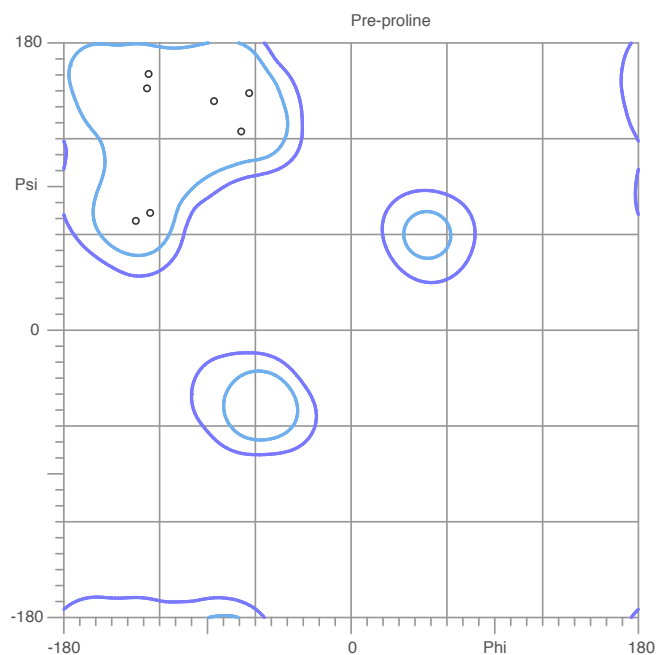
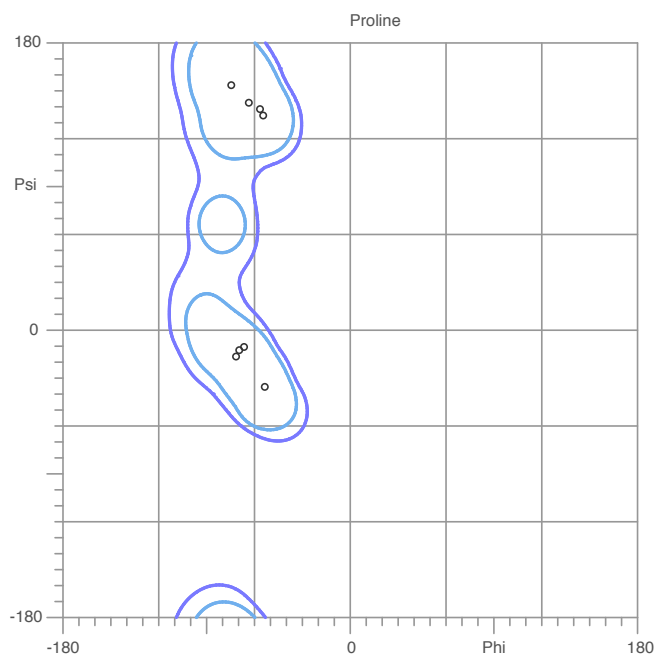
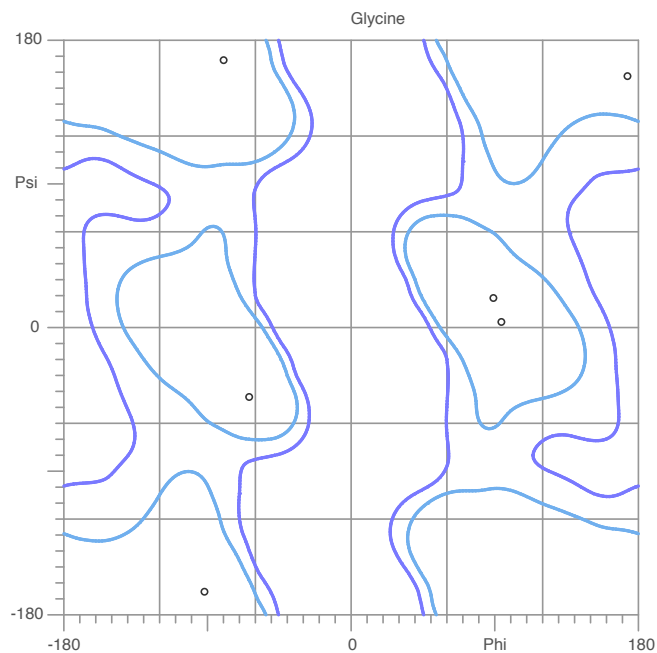
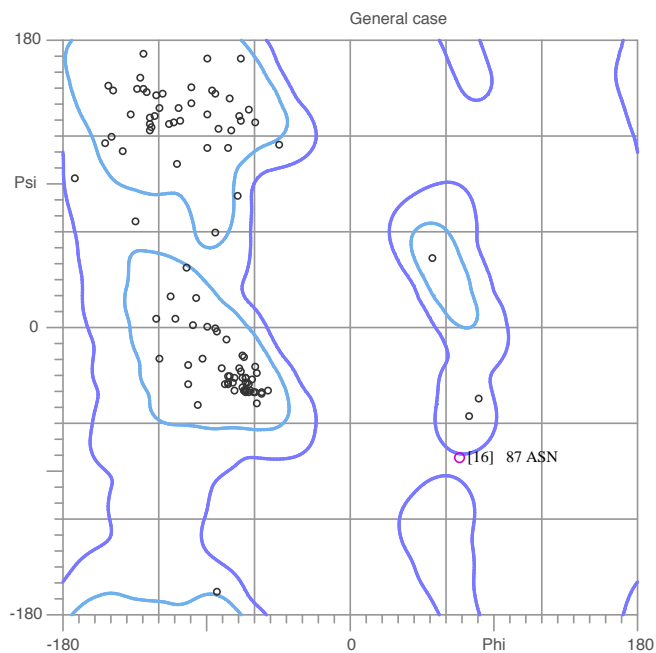


95.9% (118/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[15] 89 GLU (-174.3, -45.1)
[15] 120 HIS (43.5, -95.1)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 16



93.5% (115/123) of all residues were in favored (98%) regions.
99.2% (122/123) of all residues were in allowed (>99.8%) regions.

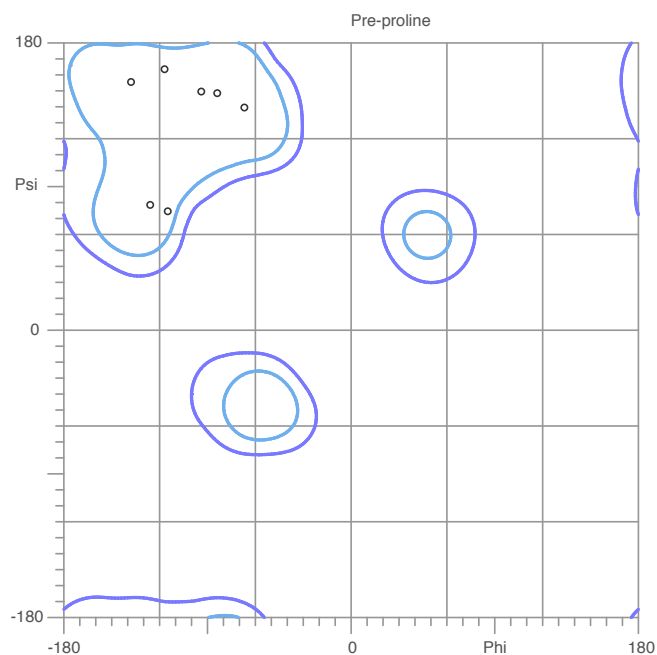
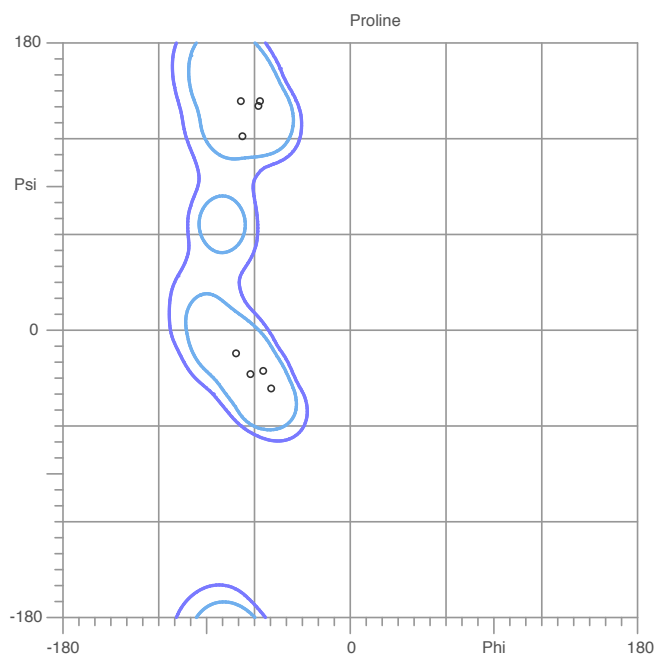
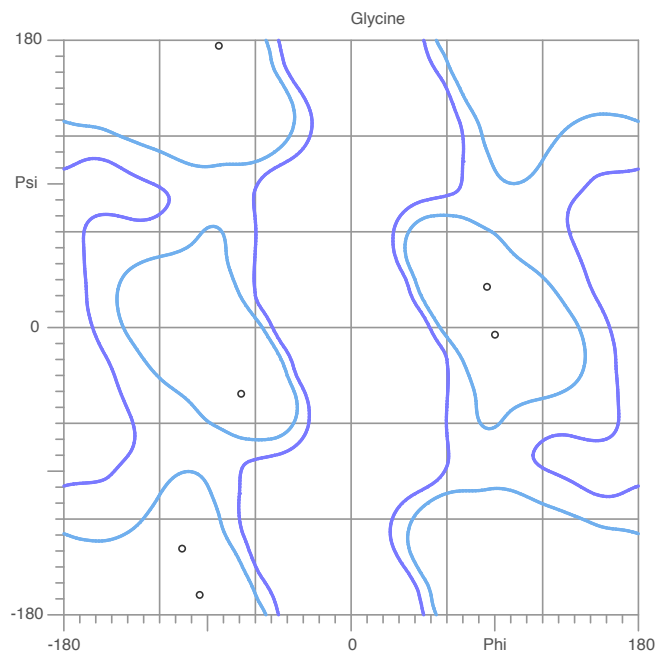
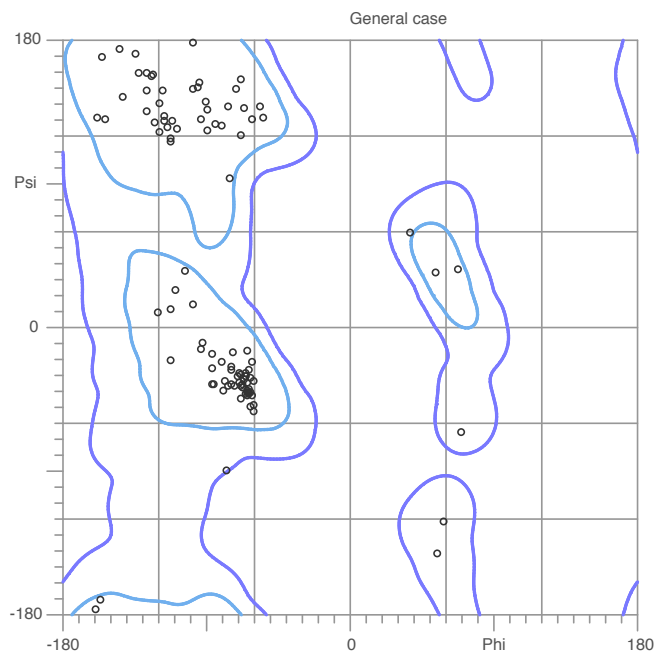
There were 1 outliers (phi, psi):
[16] 87 ASN (68.9, -81.7)

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MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 17



95.9% (118/123) of all residues were in favored (98%) regions.
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

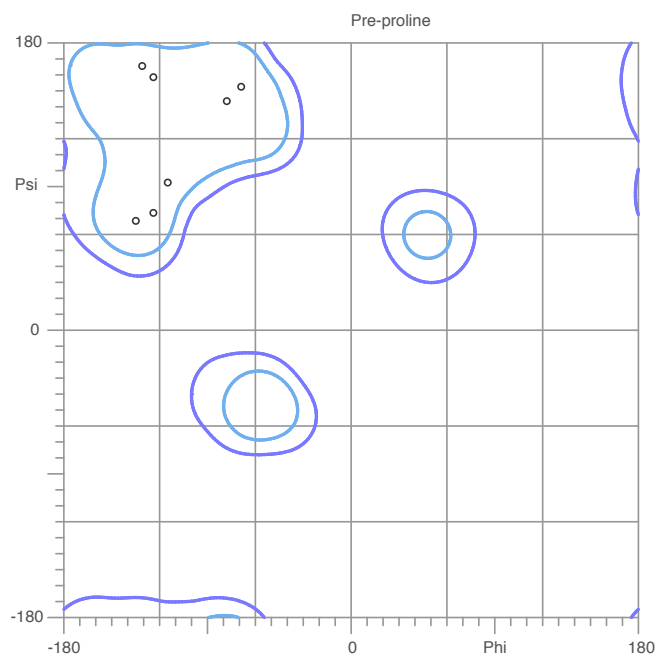
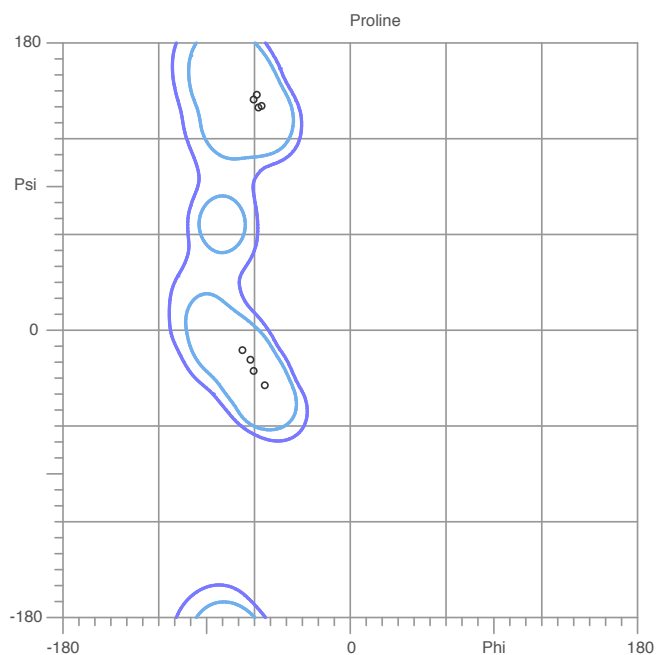
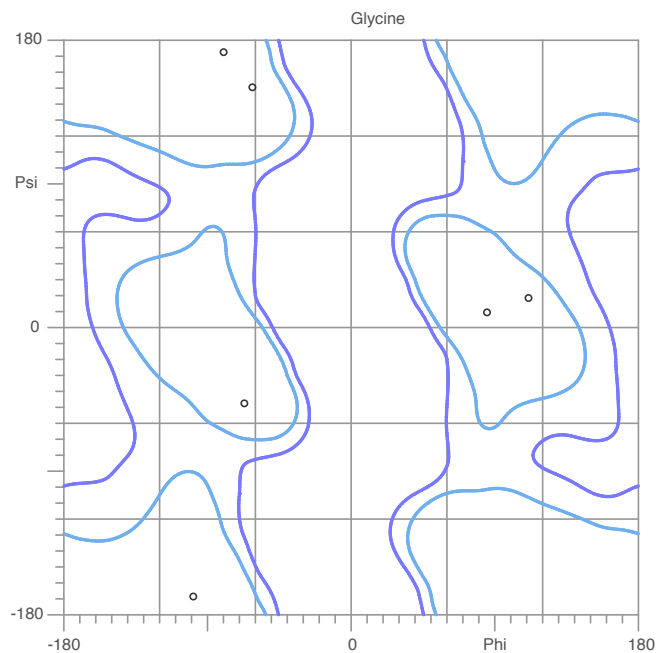
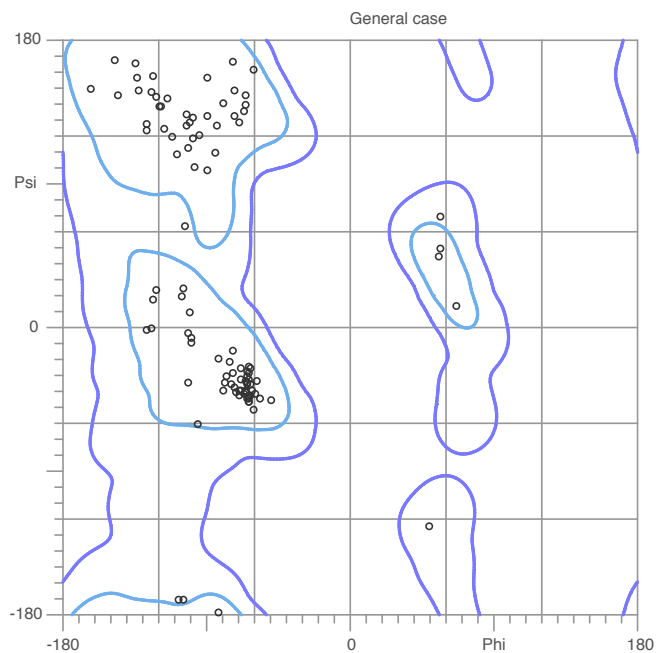
There were no outliers.

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

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

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 18



95.9% (118/123) of all residues were in favored (98%) regions.
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

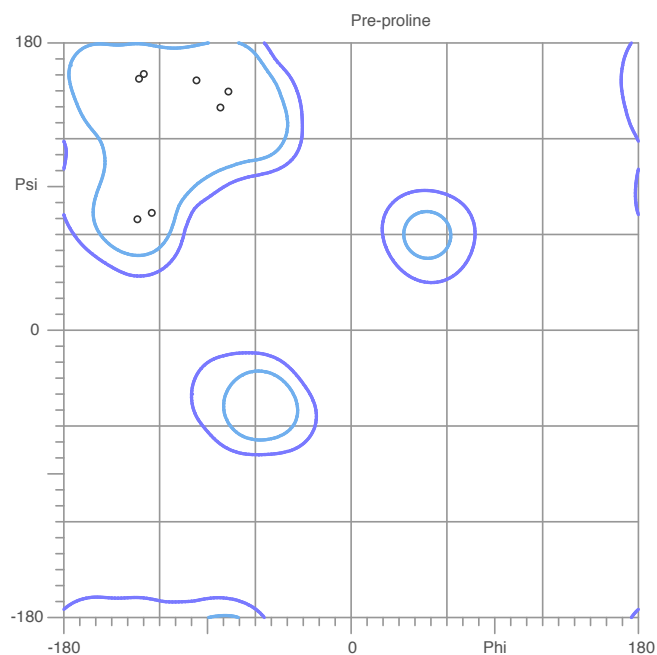
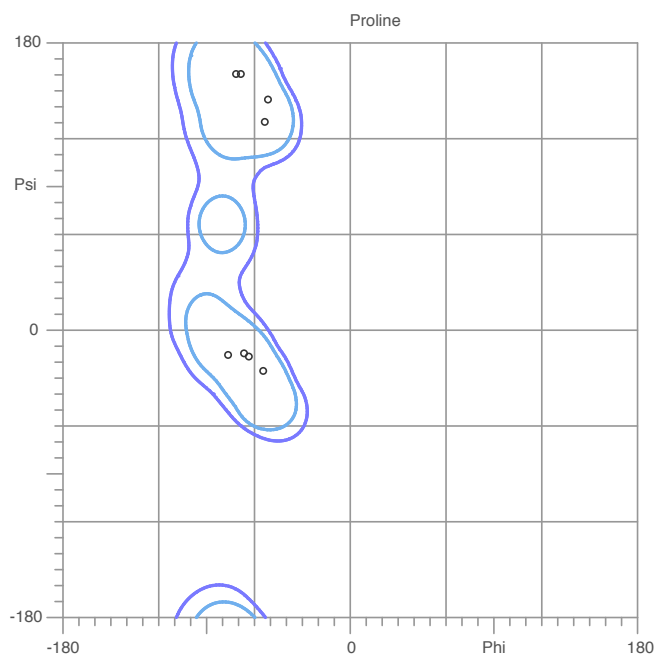
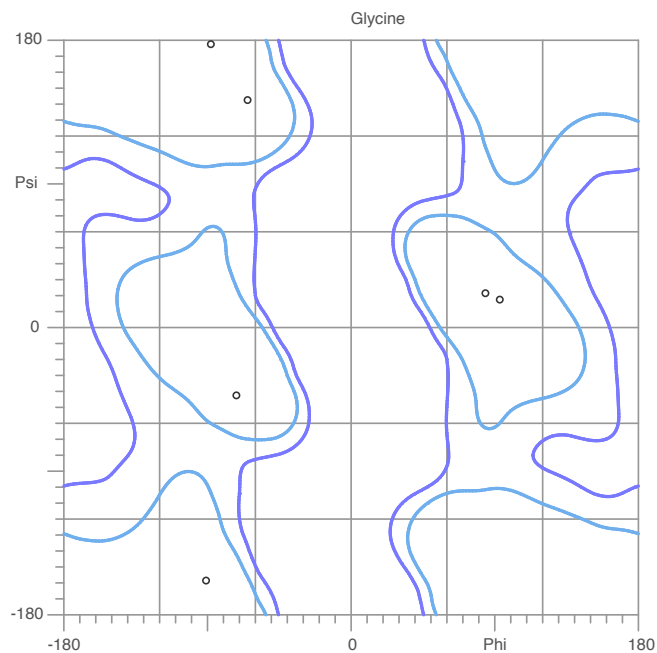
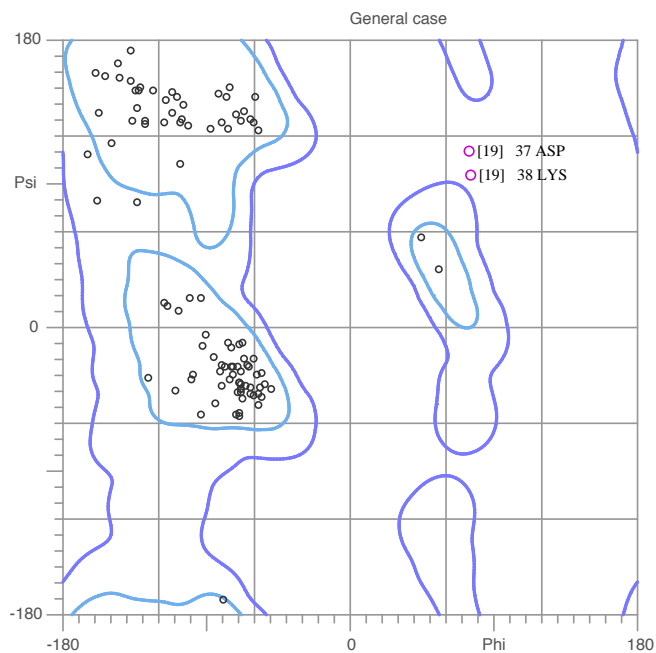
There were no outliers.

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

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

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 19

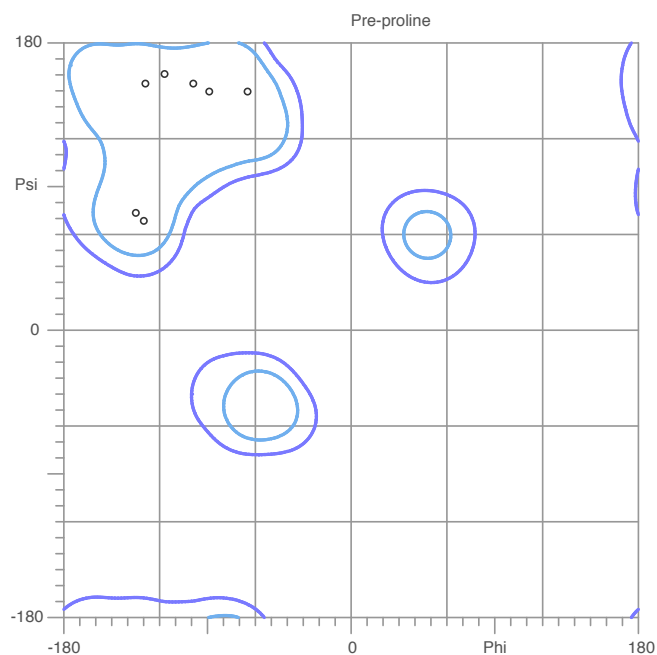
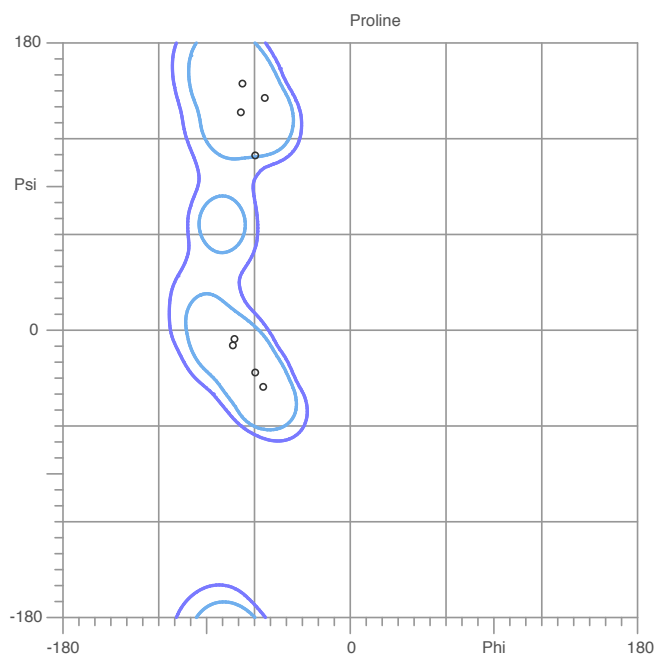
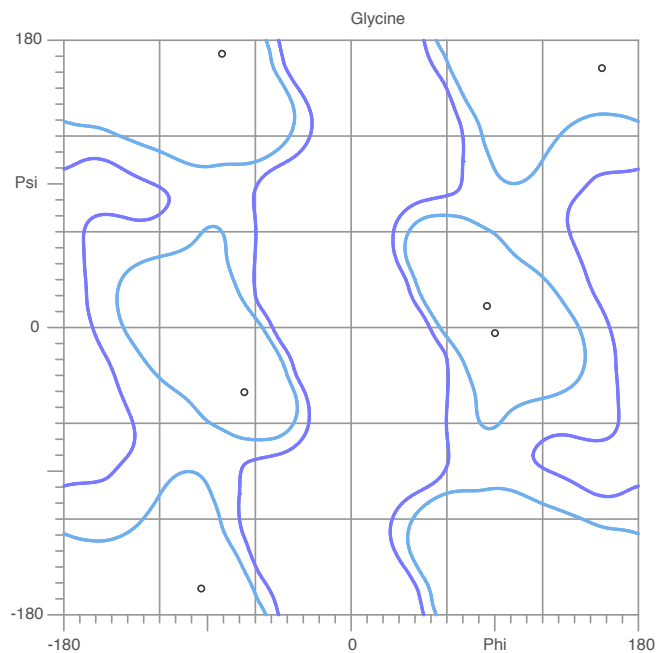
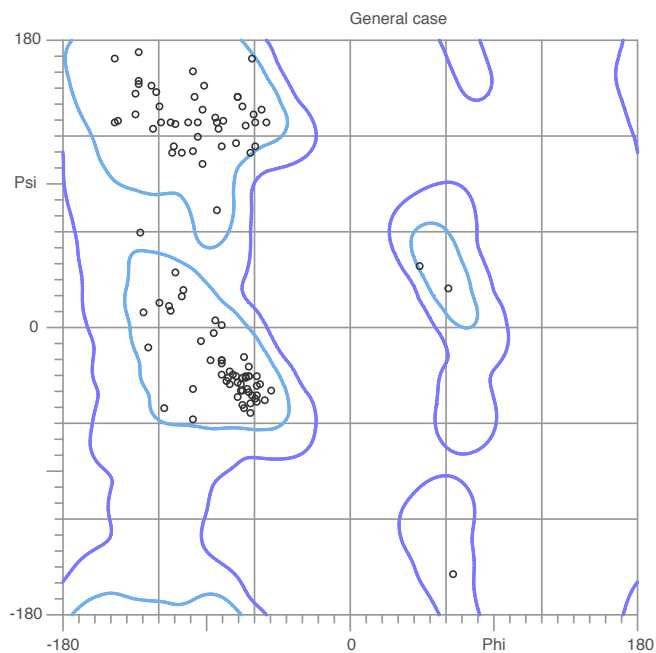


95.9% (118/123) of all residues were in favored (98%) regions.
98.4% (121/123) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 37 ASP (74.9, 111.0)
[19] 38 LYS (75.0, 96.7)

MolProbity Ramachandran analysis

PSR293_R3_em_bcr3.pdb, model 20



98.4% (121/123) of all residues were in favored (98%) regions.
100.0% (123/123) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

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