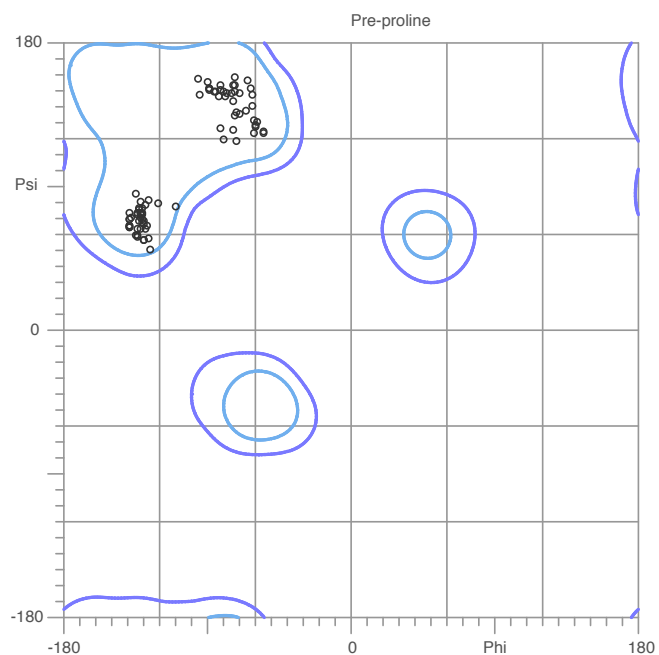
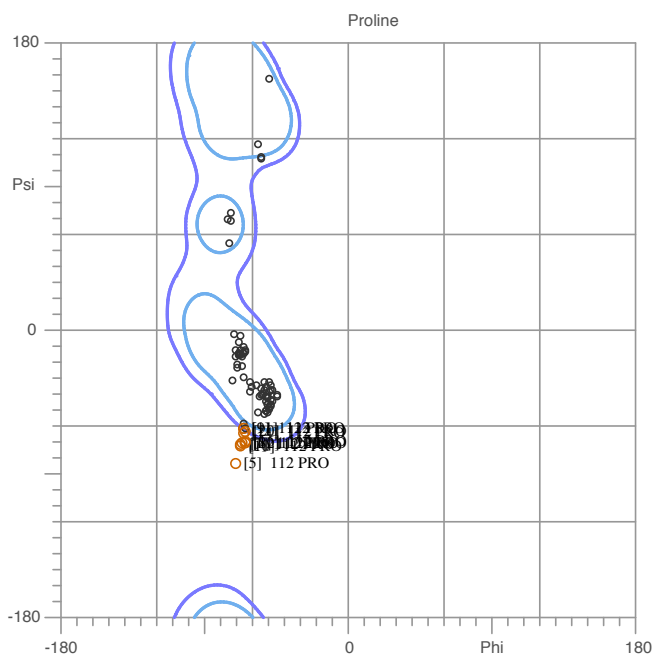
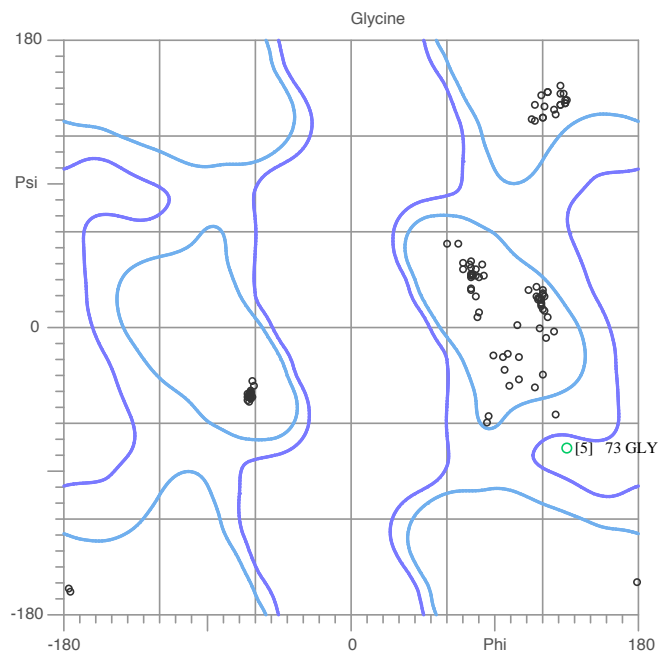
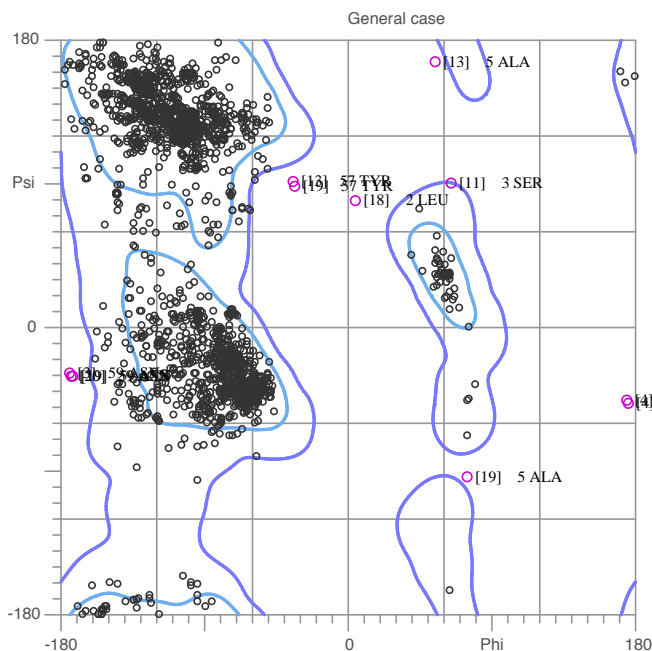


MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, all models



93.5% (2226/2380) of all residues were in favored (98%) regions.
99.0% (2357/2380) of all residues were in allowed (>99.8%) regions.

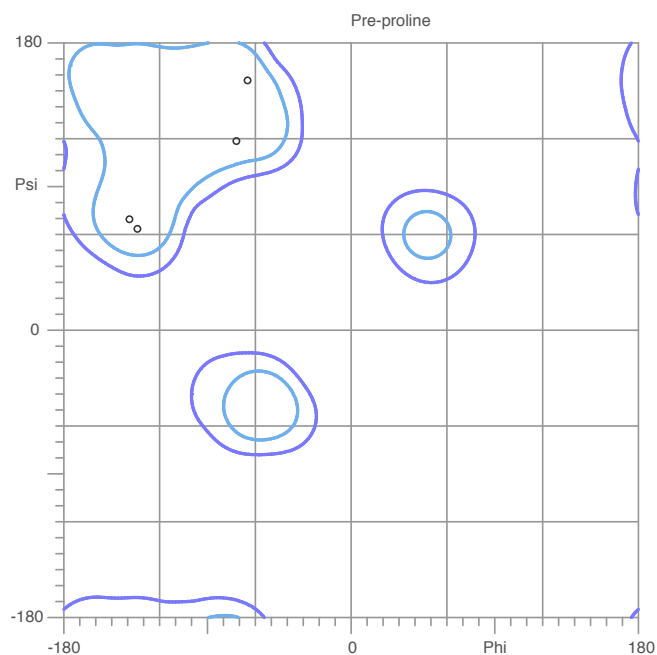
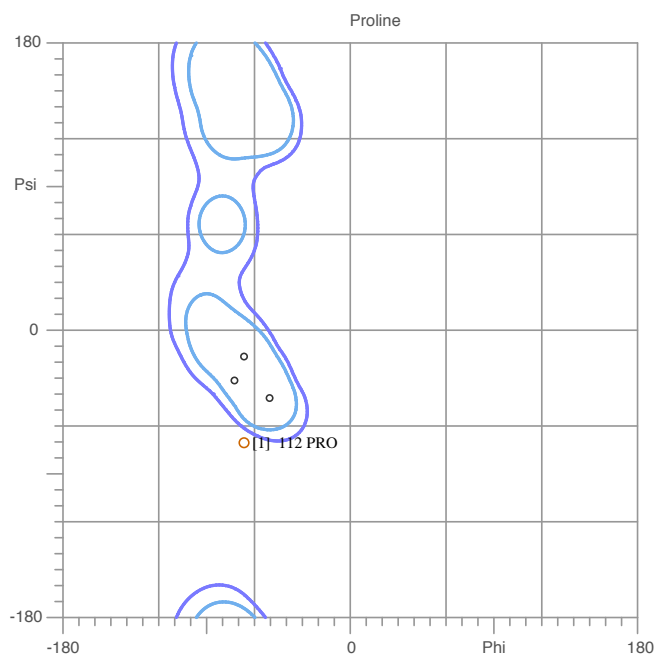
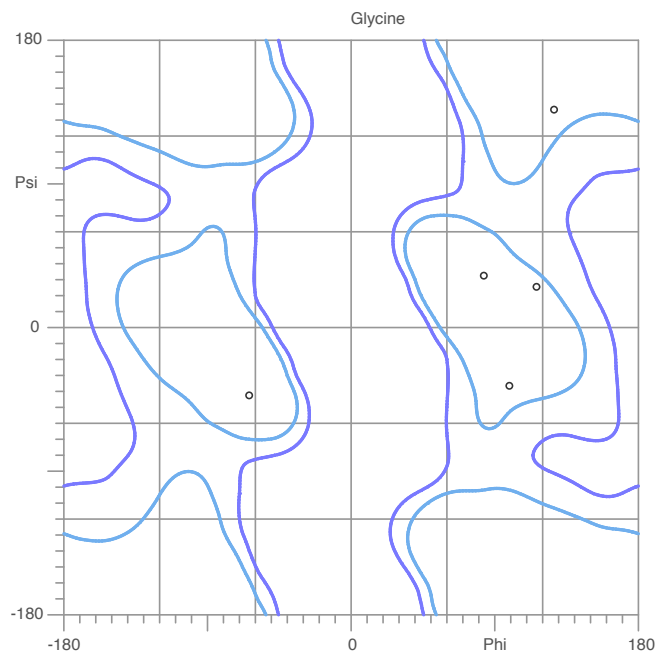
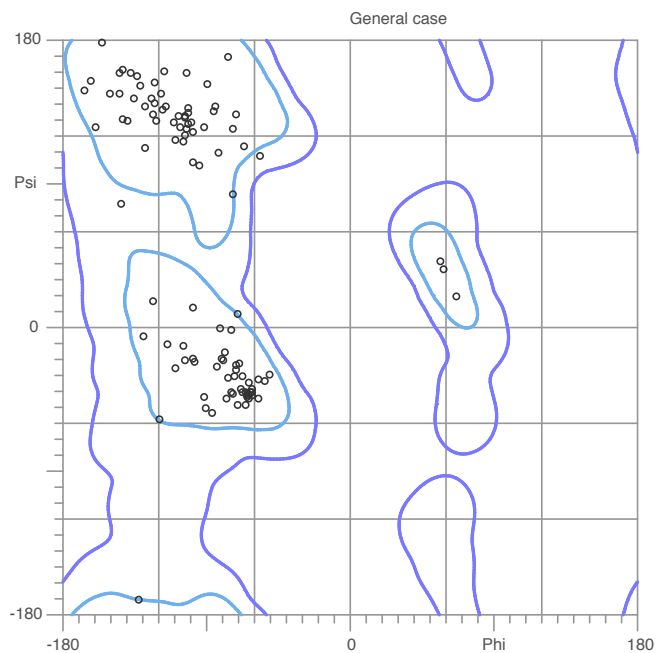
There were 23 outliers (phi, psi):

- [1] 112 PRO (-67.6, -70.2)
- [3] 59 ASN (-175.0, -28.7)
- [4] 4 GLN (175.3, -47.5)
- [4] 72 ASP (175.0, -45.0)
- [5] 73 GLY (135.2, -75.2)
- [5] 112 PRO (-71.9, -83.8)
- [7] 112 PRO (-68.3, -71.8)
- [8] 112 PRO (-65.7, -70.0)
- [9] 112 PRO (-66.7, -61.7)

- [10] 112 PRO (-68.8, -72.1)
- [11] 3 SER (65.0, 91.6)
- [11] 112 PRO (-67.0, -61.6)
- [12] 112 PRO (-65.2, -70.4)
- [13] 5 ALA (55.0, 167.9)
- [13] 57 TYR (-35.1, 92.5)
- [14] 112 PRO (-66.2, -64.2)
- [16] 112 PRO (-65.1, -69.9)
- [18] 2 LEU (4.7, 80.8)
- [19] 5 ALA (75.0, -93.3)
- [19] 57 TYR (-35.0, 89.3)
- [19] 59 ASN (-173.5, -31.0)
- [20] 59 ASN (-175.0, -30.4)
- [20] 112 PRO (-65.2, -63.5)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 1

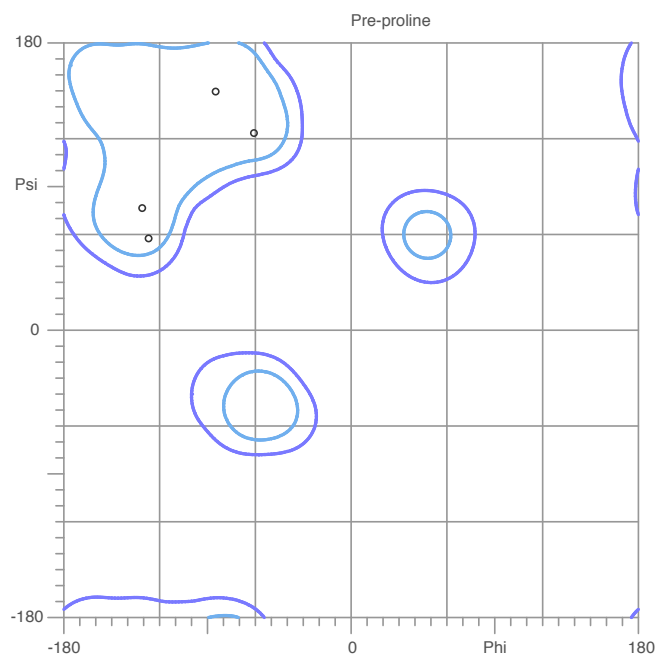
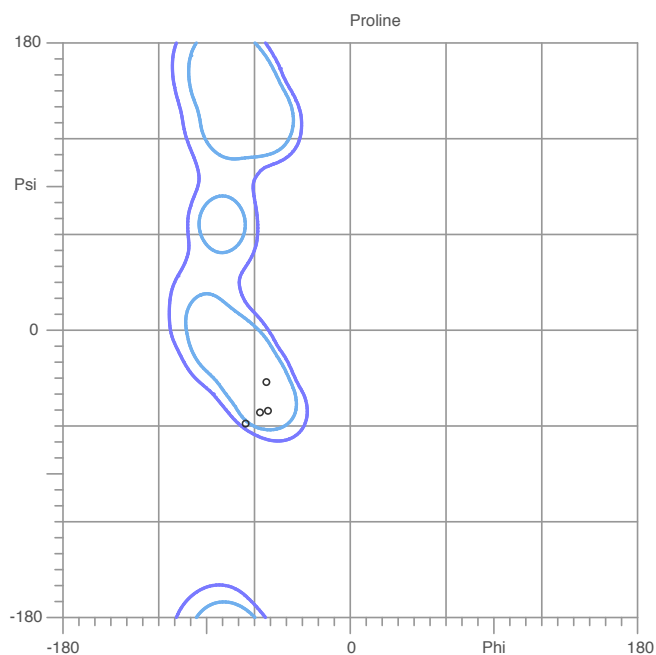
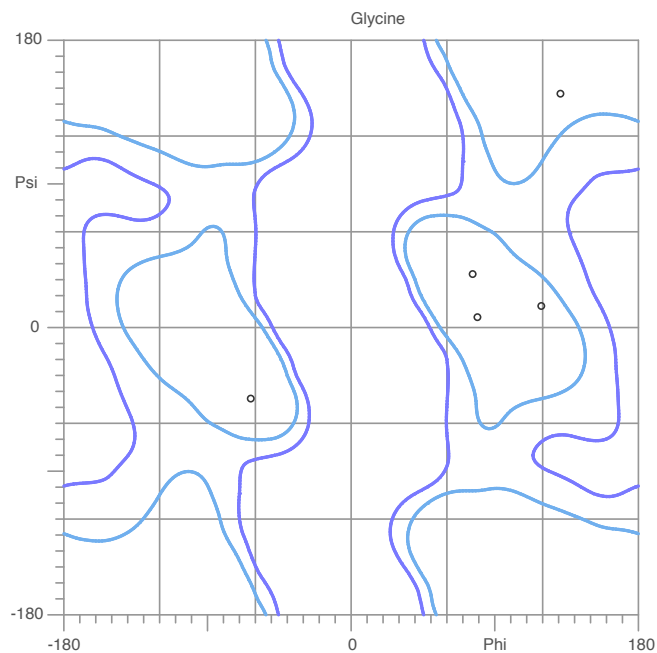
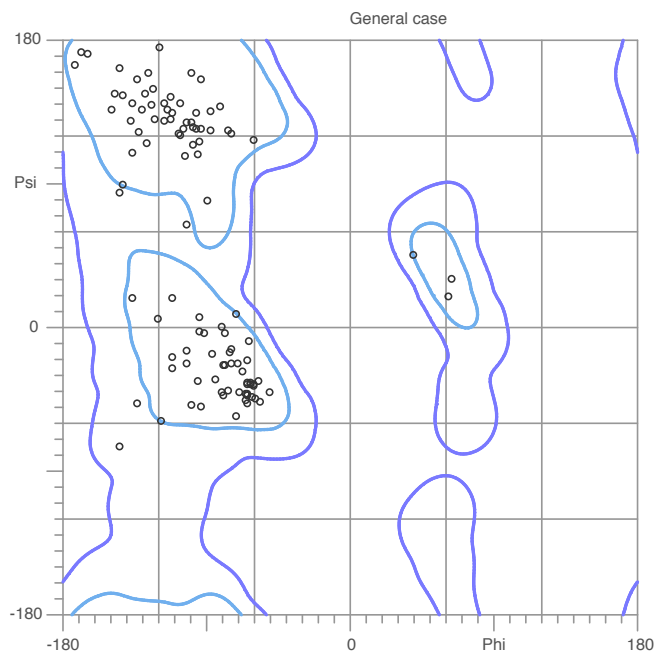


96.6% (115/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[1] 112 PRO (-67.6, -70.2)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 2



95.8% (114/119) of all residues were in favored (98%) regions.
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

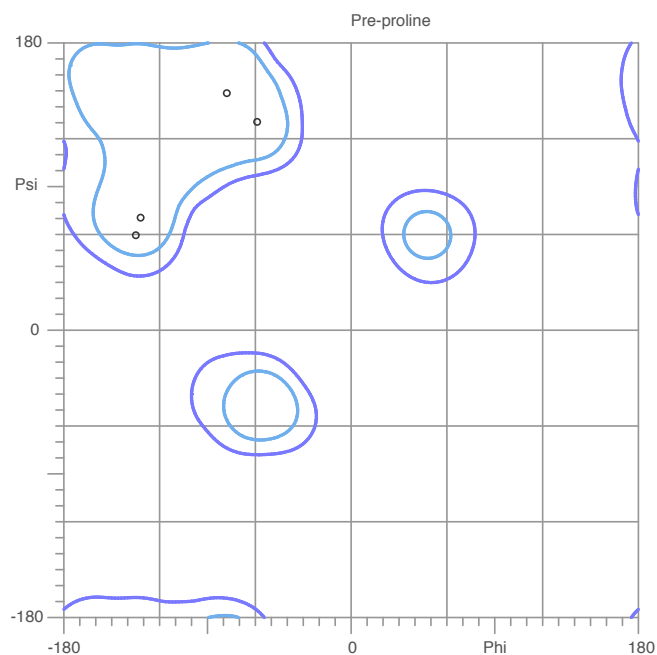
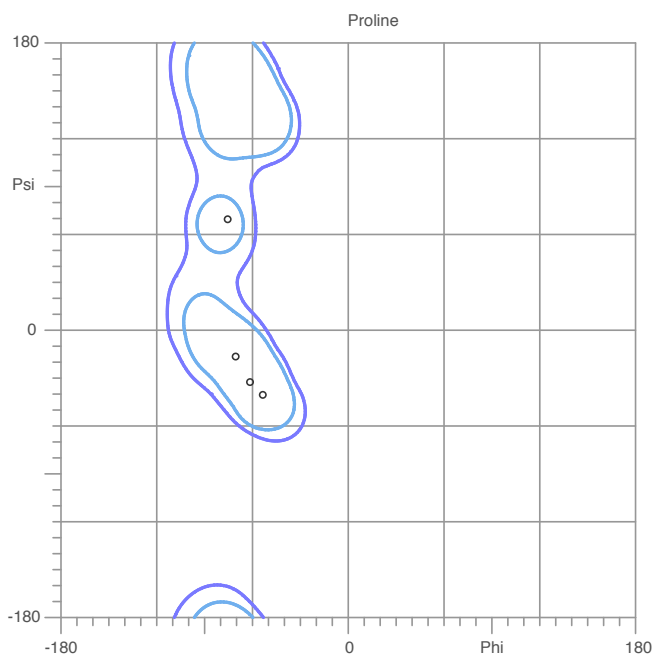
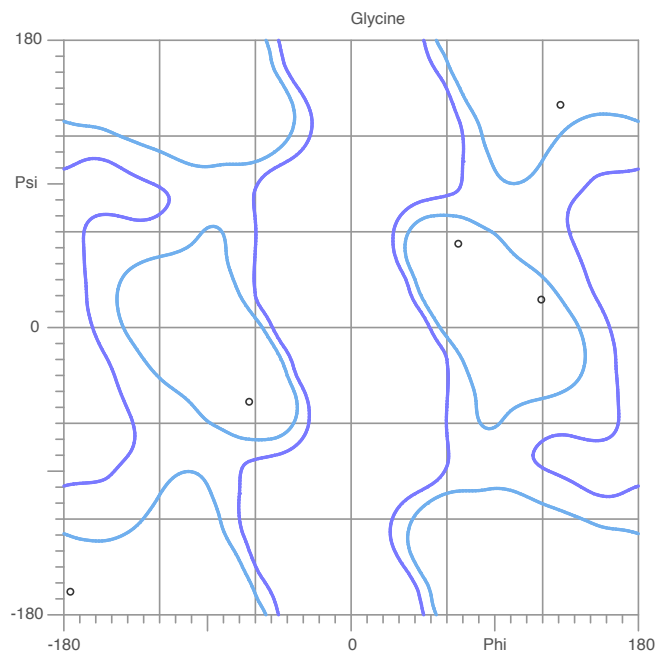
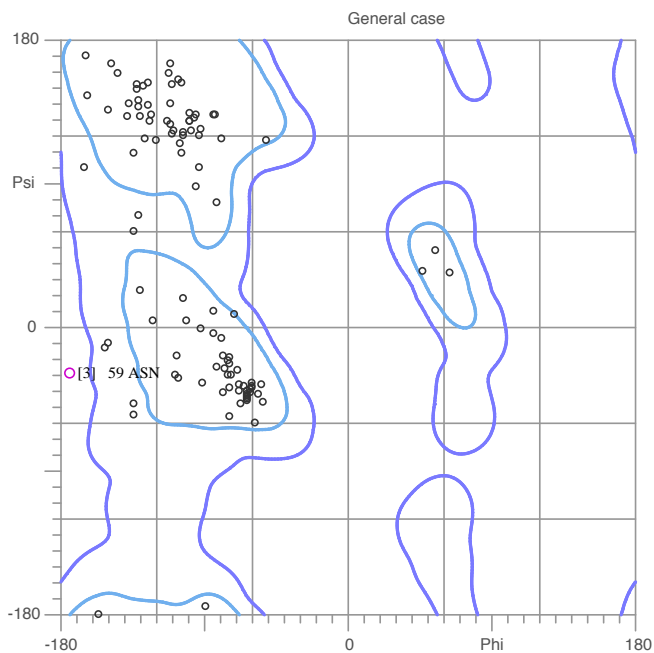
There were no outliers.

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MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 3

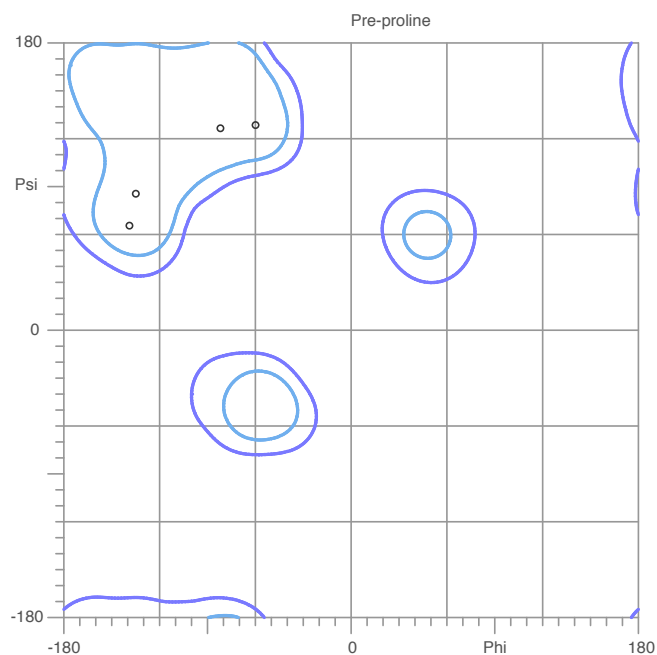
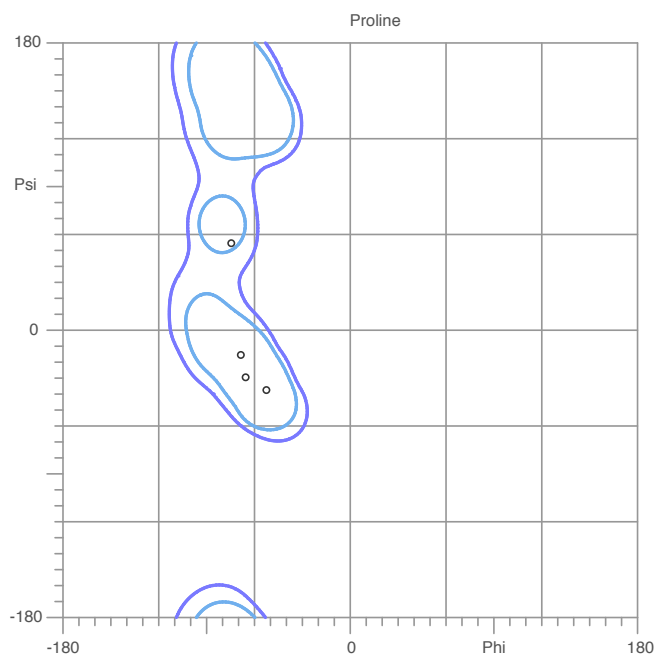
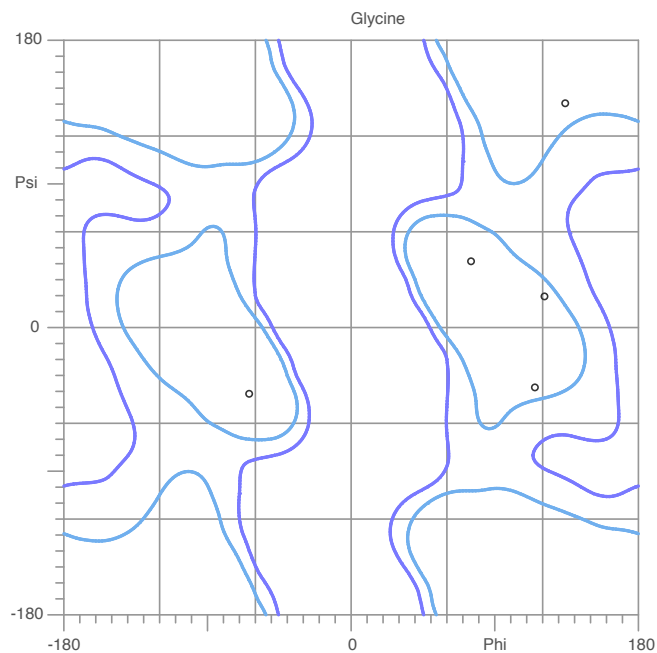
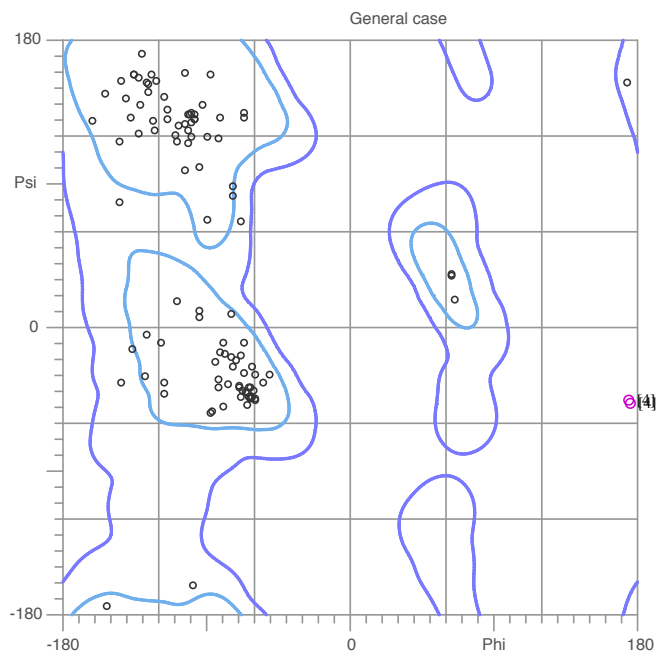


92.4% (110/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 59 ASN (-175.0, -28.7)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 4



93.3% (111/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

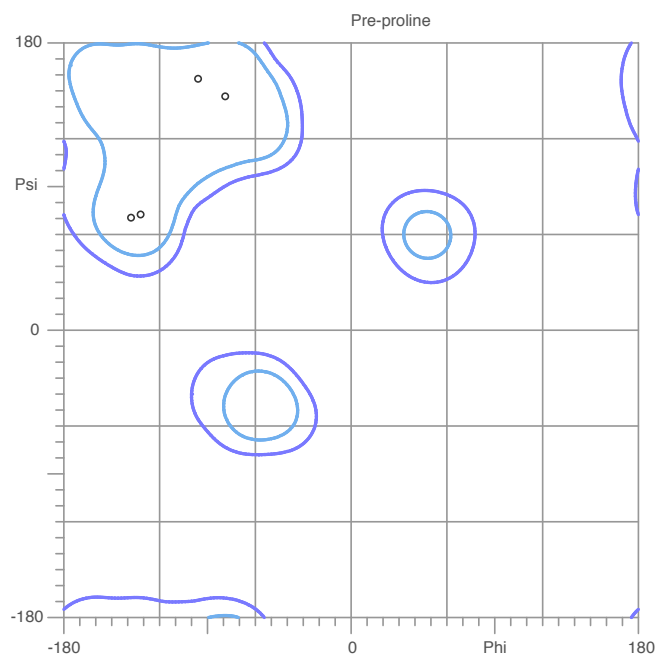
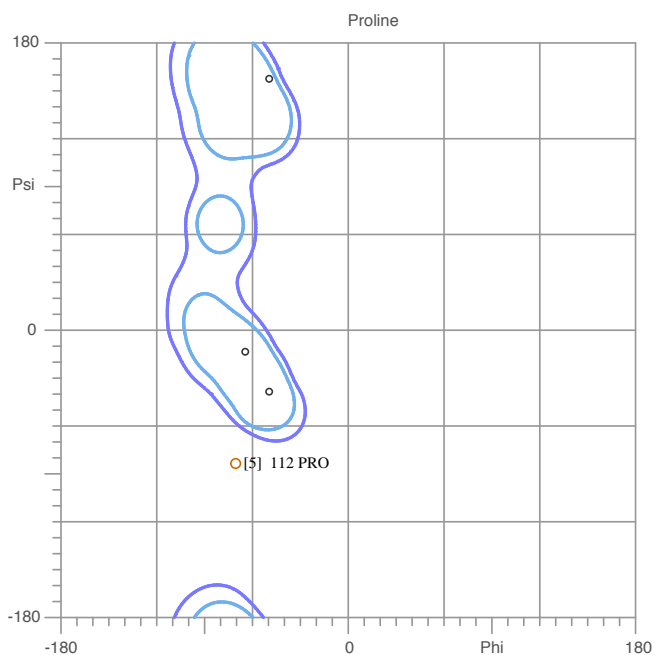
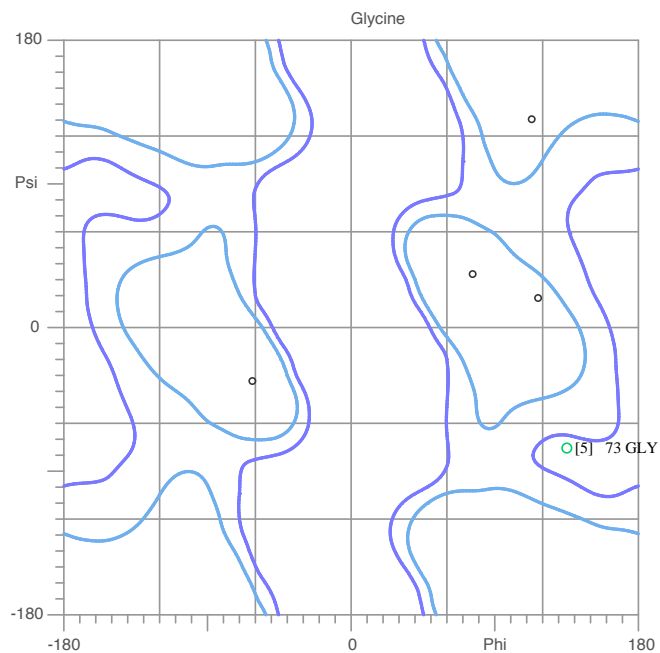
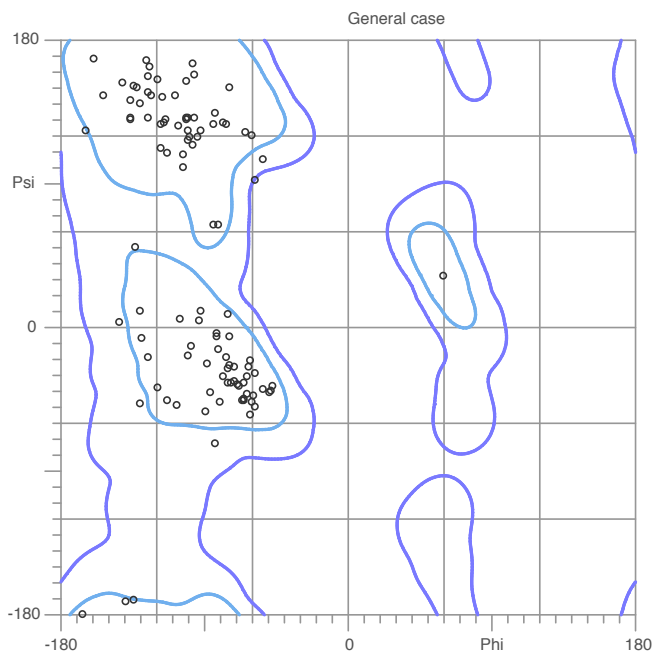
There were 2 outliers (phi, psi):

[4] 4 GLN (175.3, -47.5)

[4] 72 ASP (175.0, -45.0)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 5



92.4% (110/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

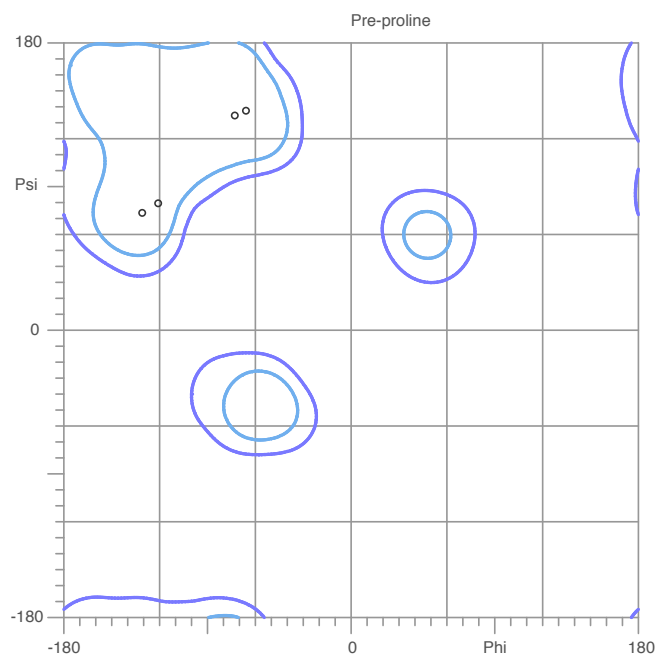
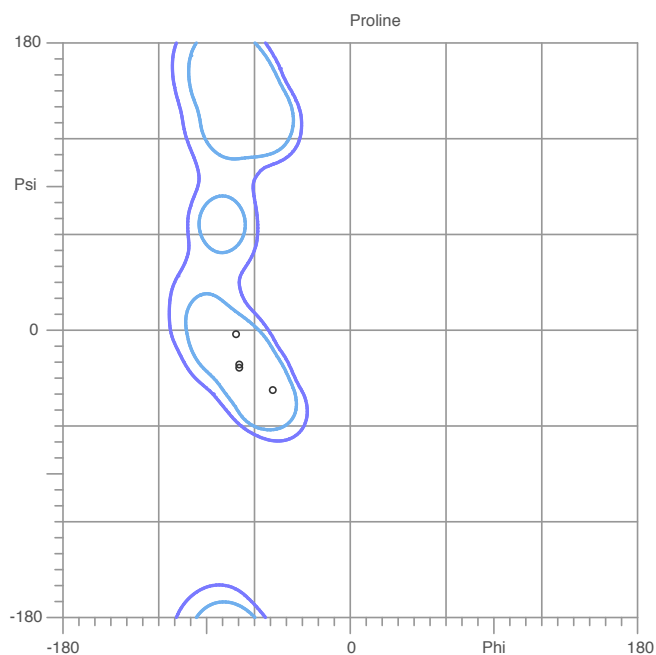
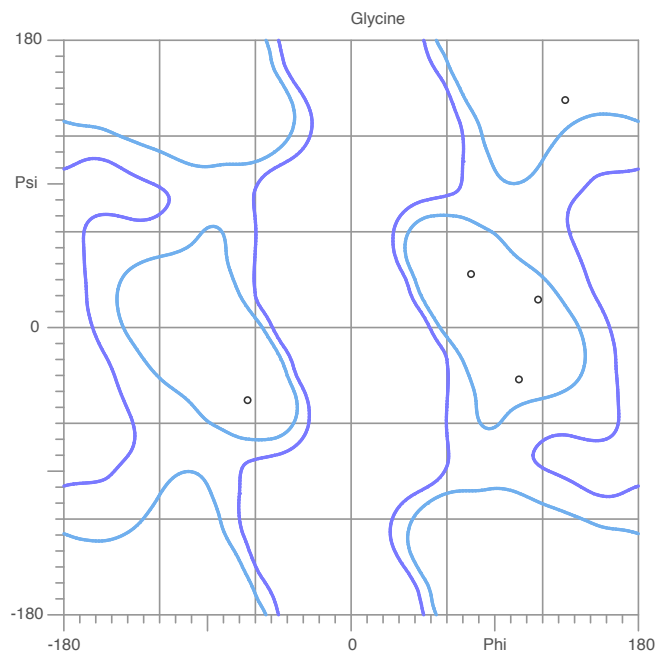
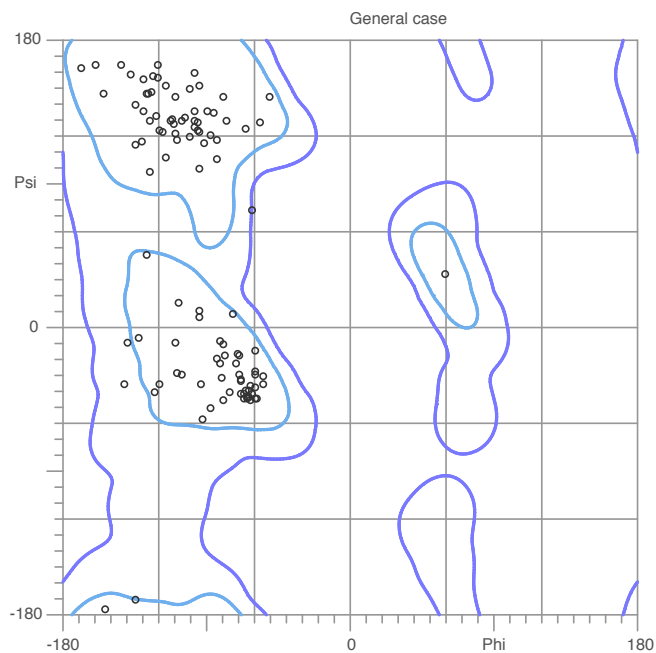
There were 2 outliers (phi, psi):

[5] 73 GLY (135.2, -75.2)

[5] 112 PRO (-71.9, -83.8)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 6



97.5% (116/119) of all residues were in favored (98%) regions.
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

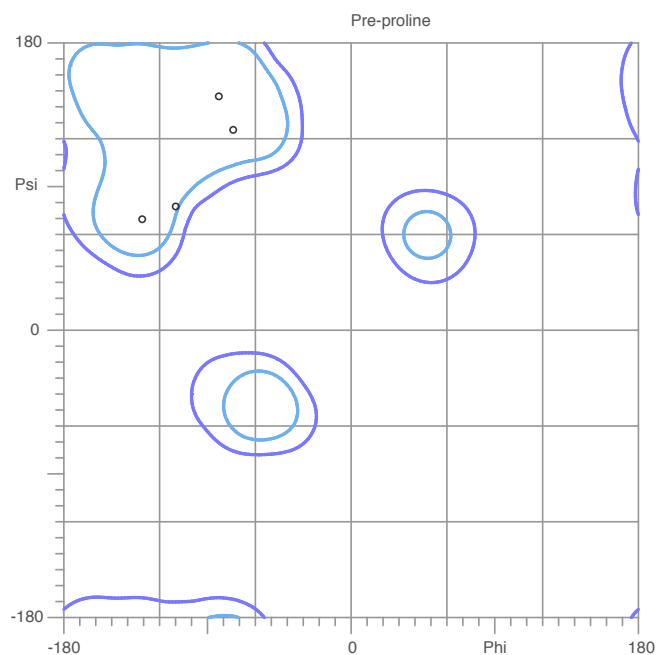
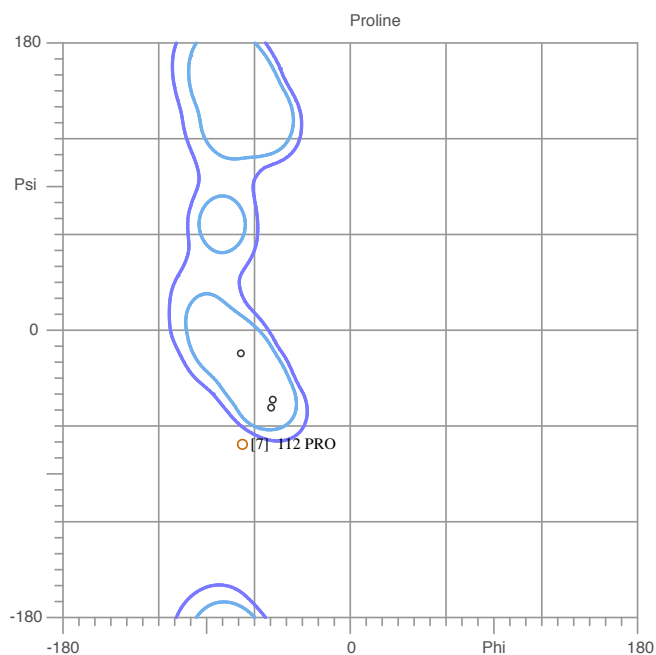
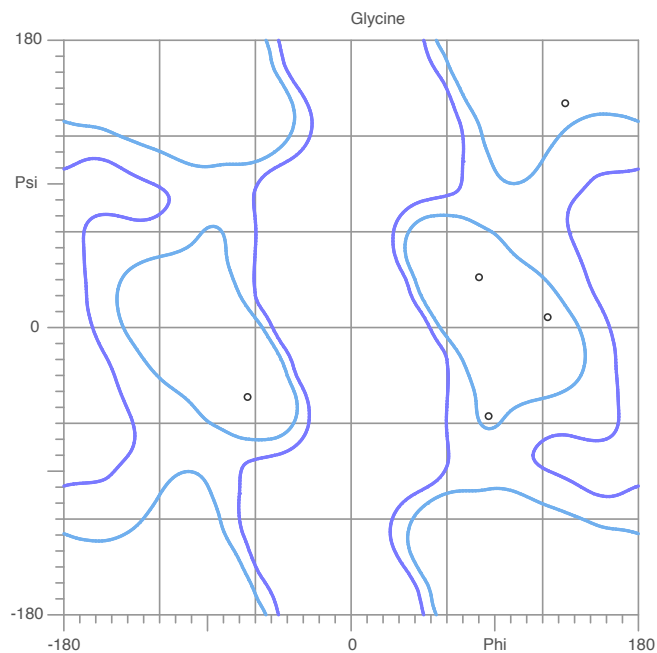
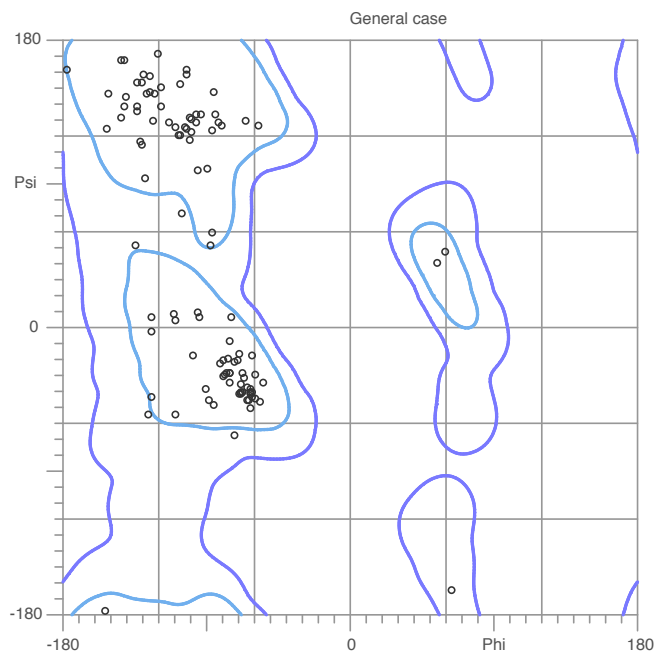
There were no outliers.

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MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 7



94.1% (112/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

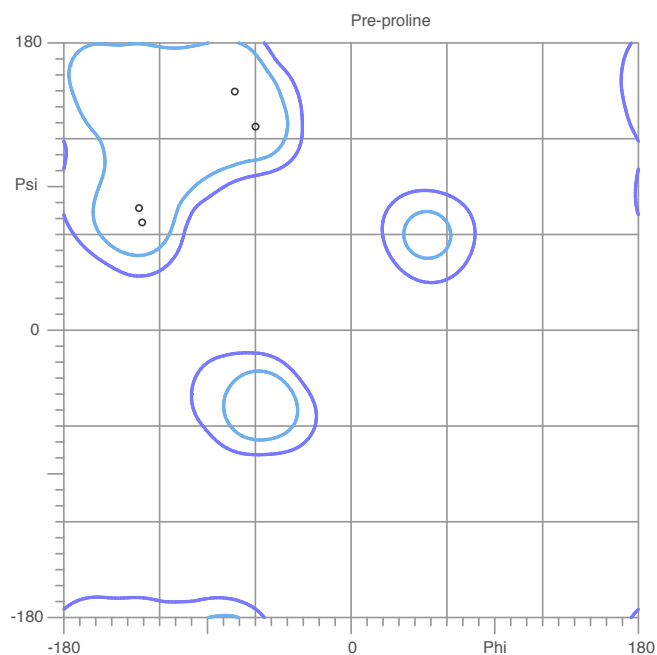
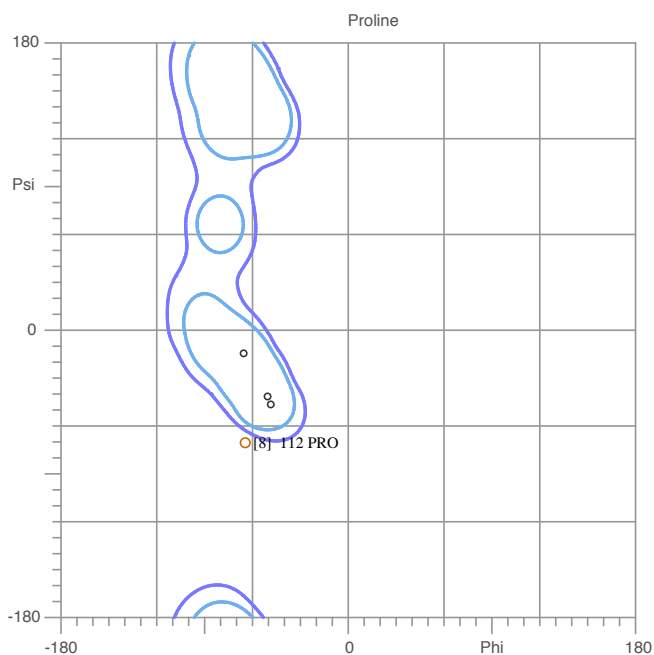
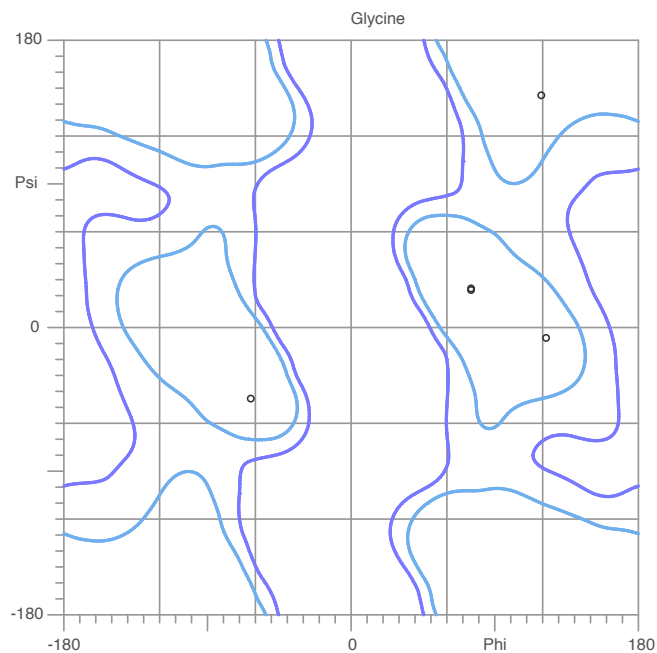
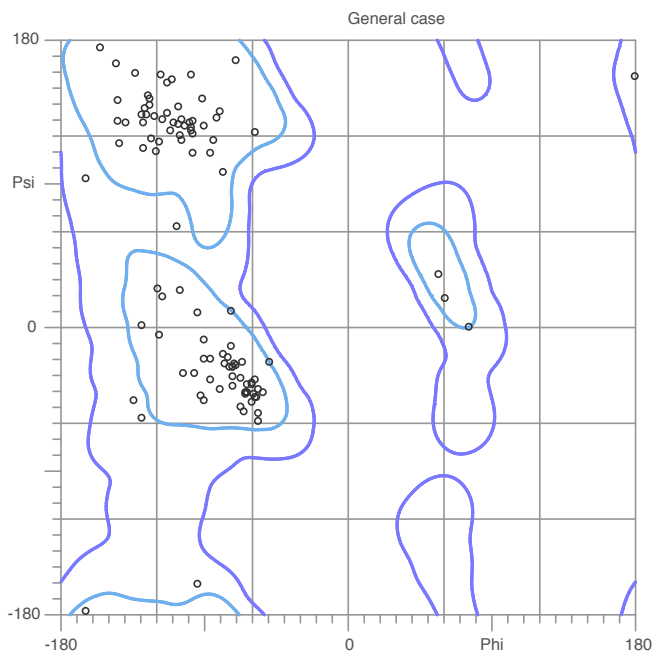
There were 1 outliers (phi, psi):
[7] 112 PRO (-68.3, -71.8)

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MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 8

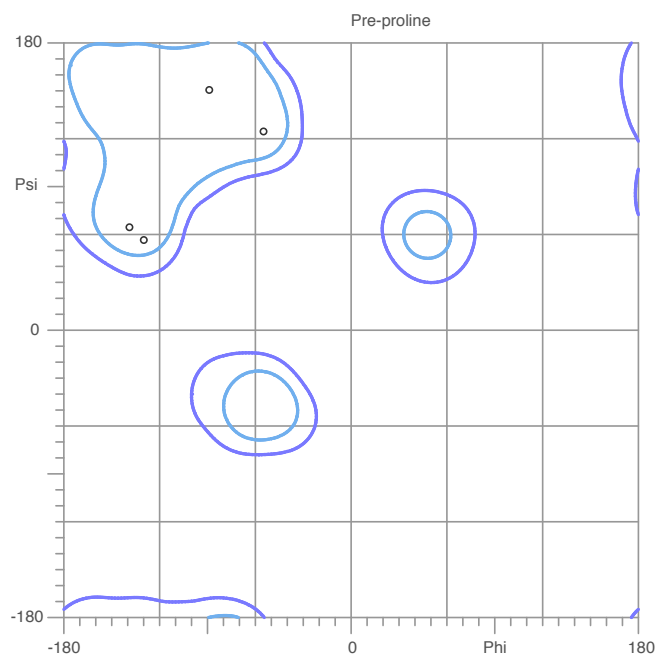
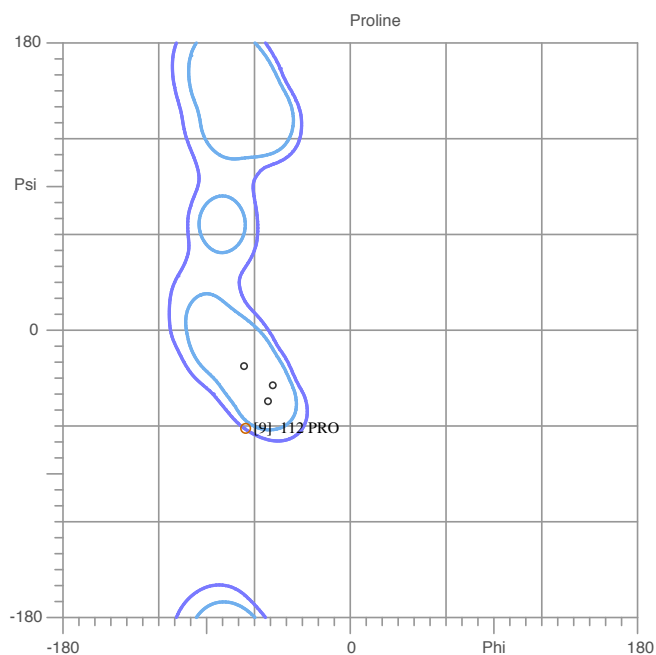
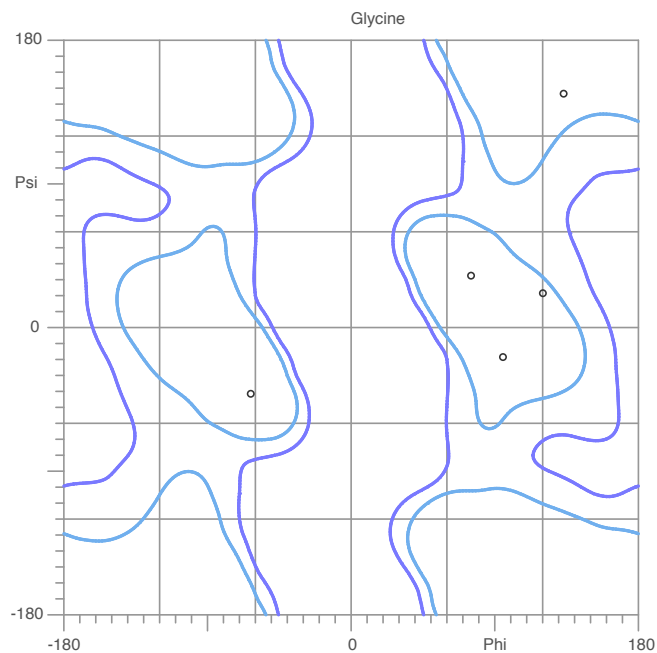
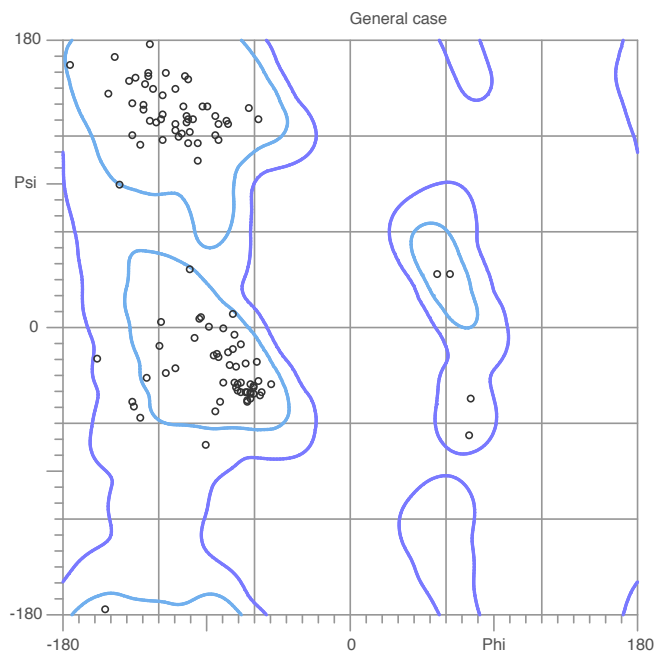


94.1% (112/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 112 PRO (-65.7, -70.0)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 9



93.3% (111/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

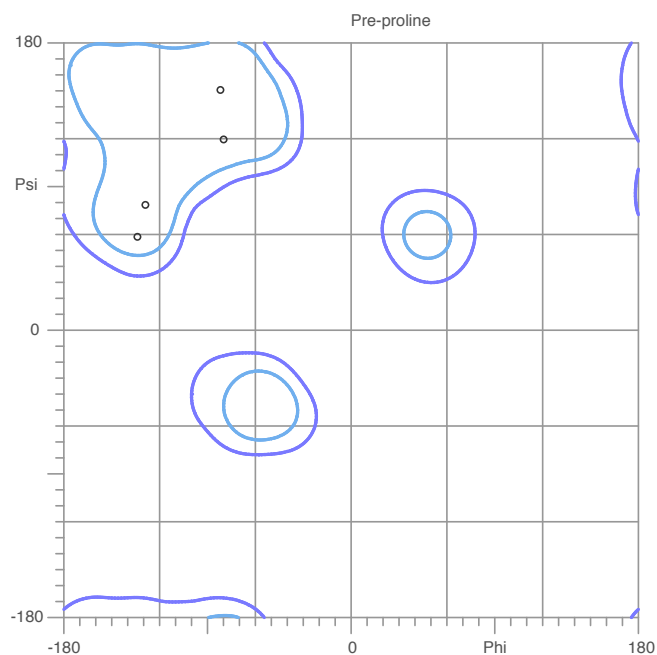
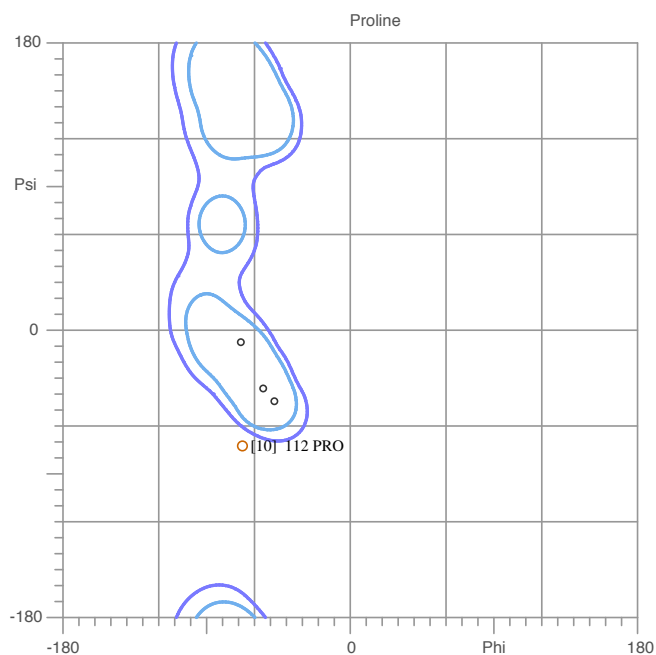
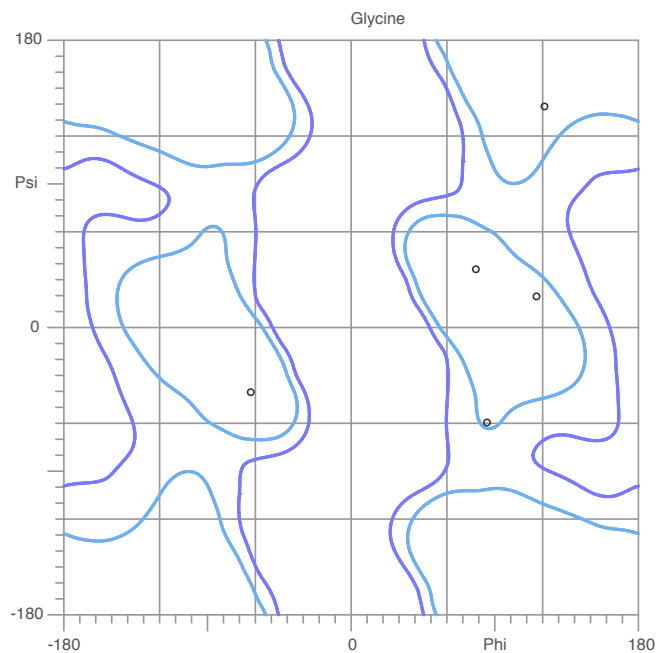
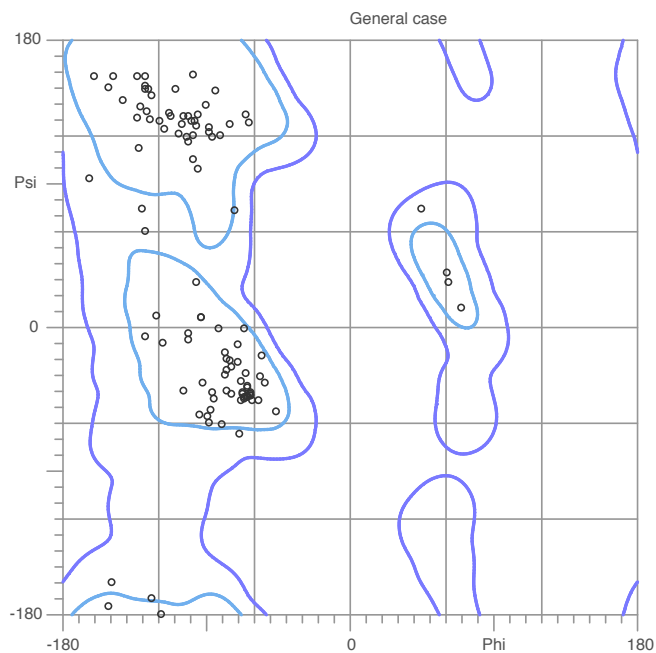
There were 1 outliers (phi, psi):
[9] 112 PRO (-66.7, -61.7)

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MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 10

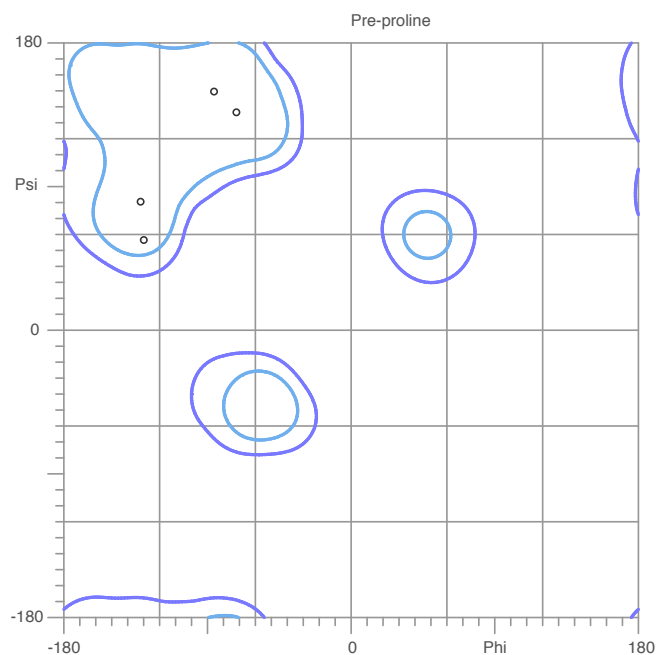
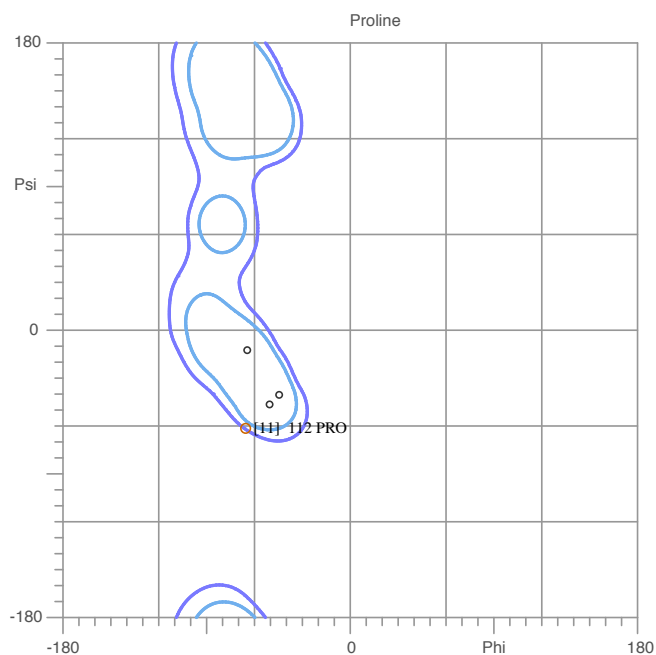
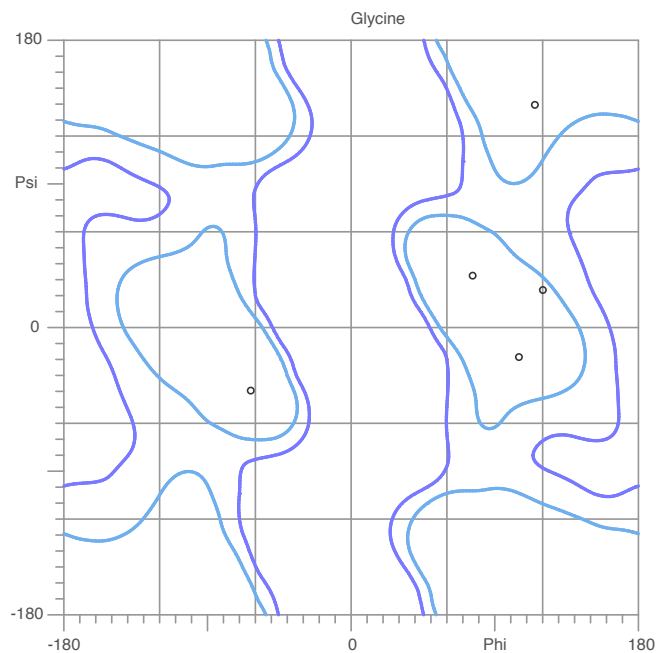
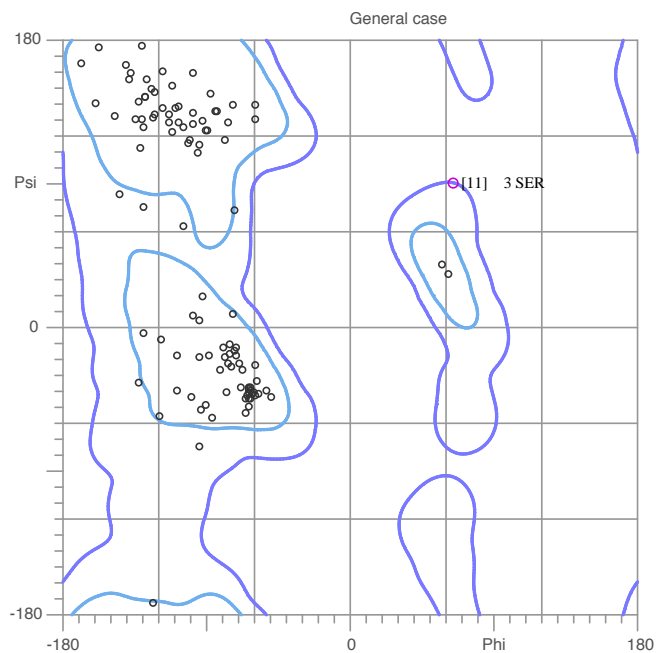


93.3% (111/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[10] 112 PRO (-68.8, -72.1)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 11

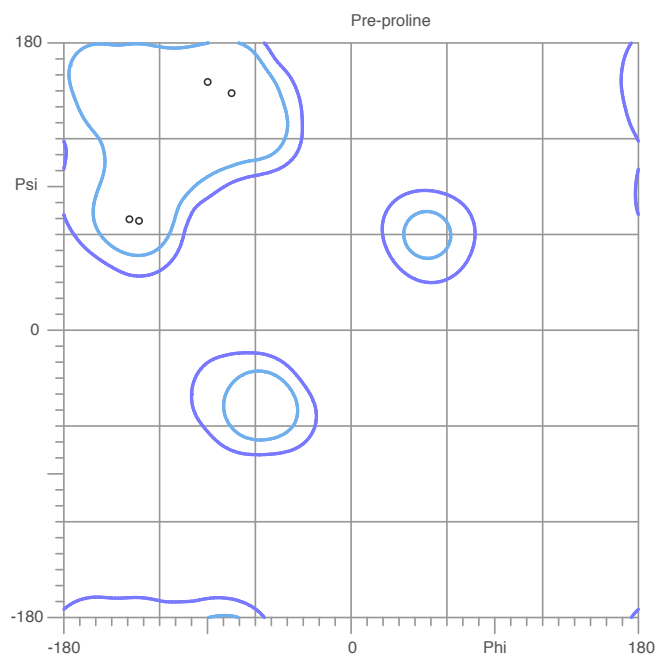
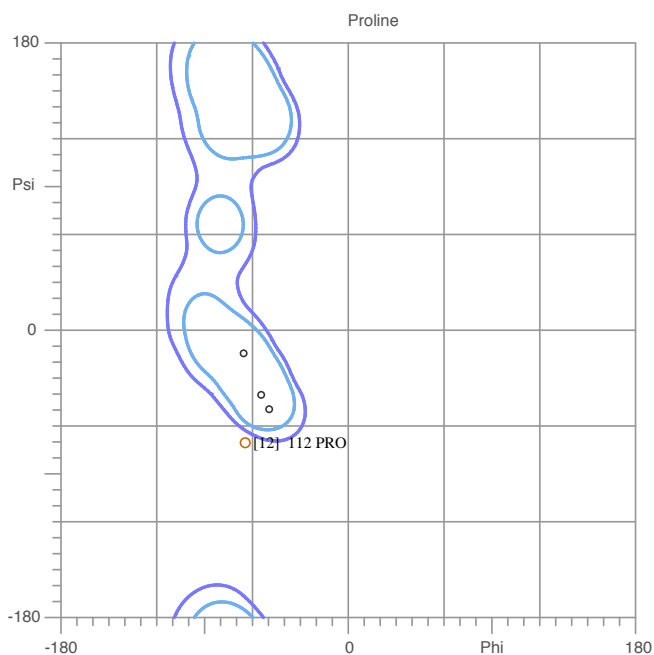
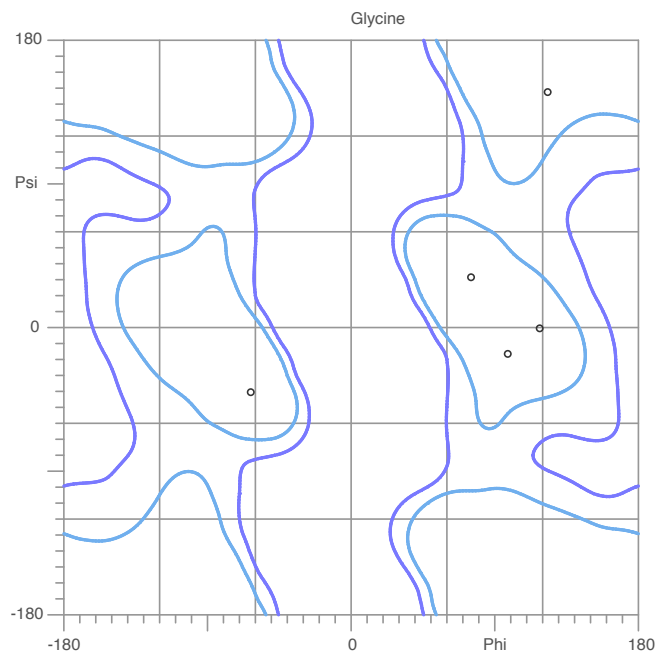
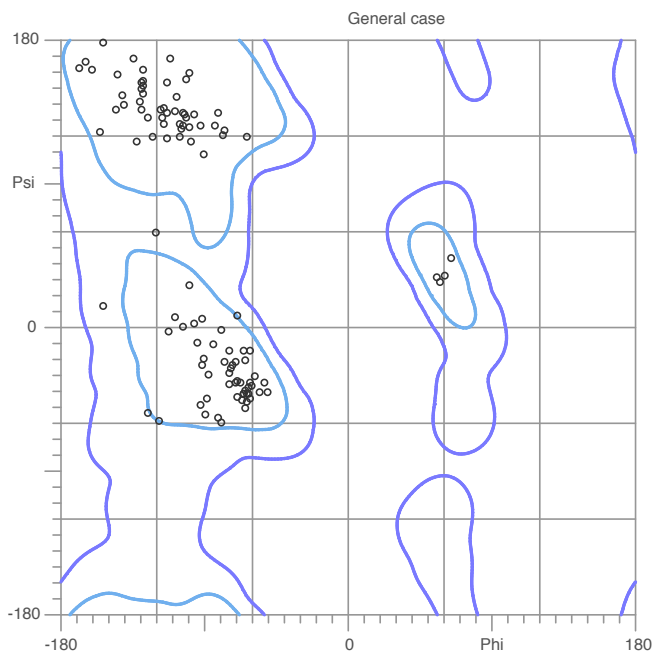


94.1% (112/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[11] 3 SER (65.0, 91.6)
[11] 112 PRO (-67.0, -61.6)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 12



95.0% (113/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

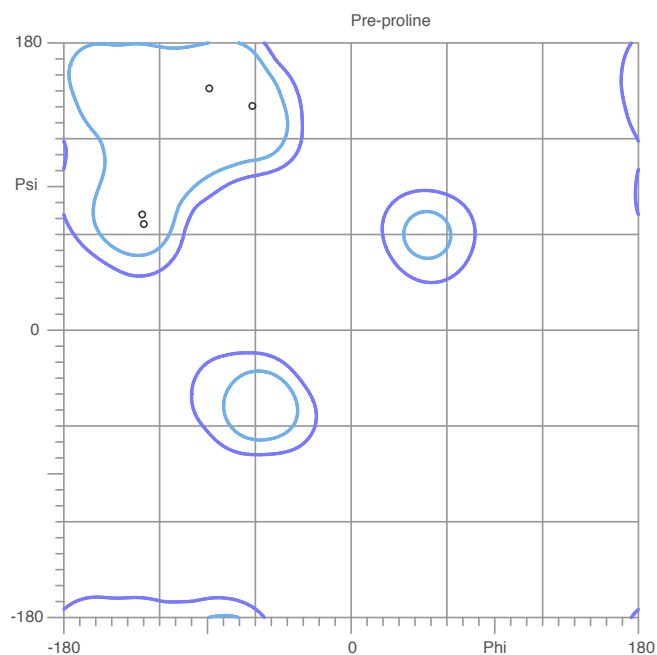
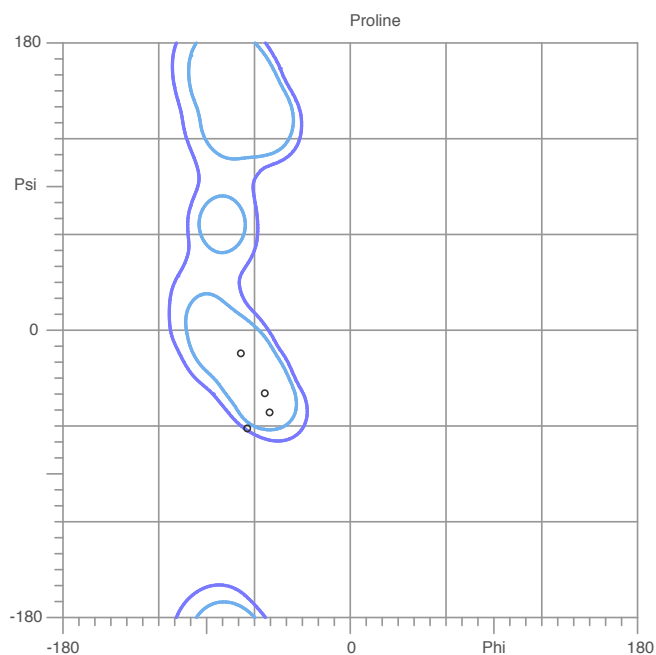
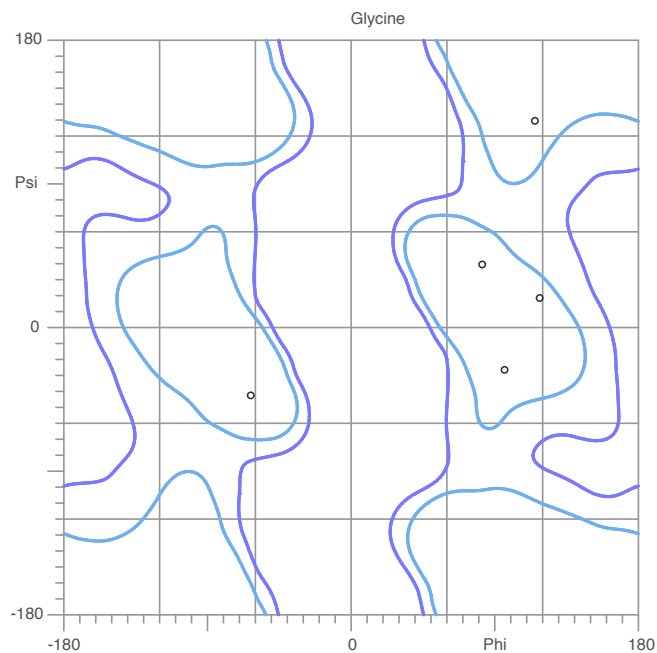
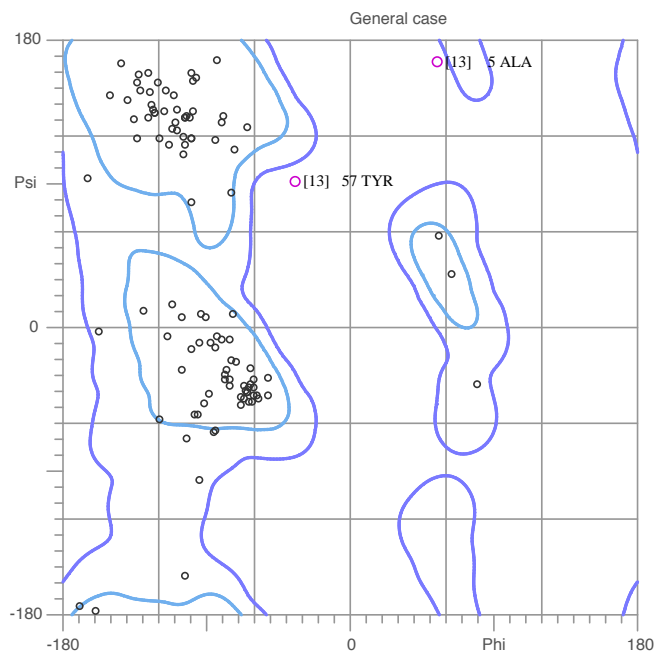
There were 1 outliers (phi, psi):
[12] 112 PRO (-65.2, -70.4)

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MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 13



89.9% (107/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

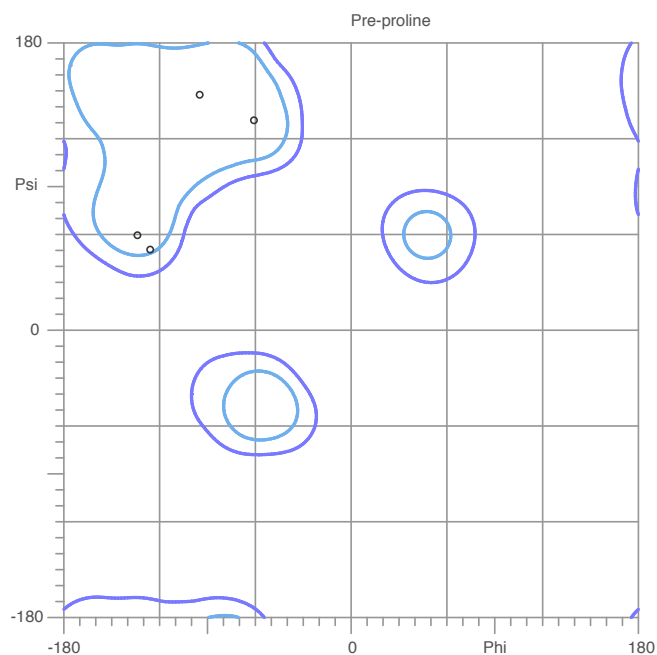
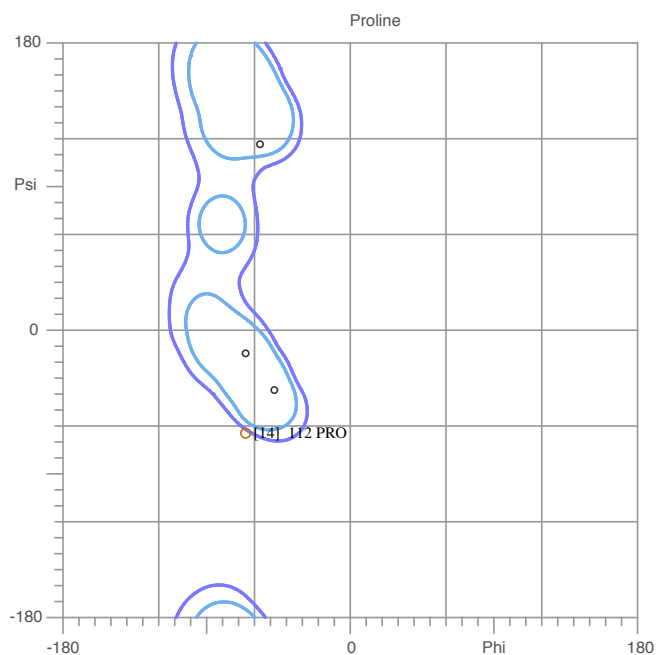
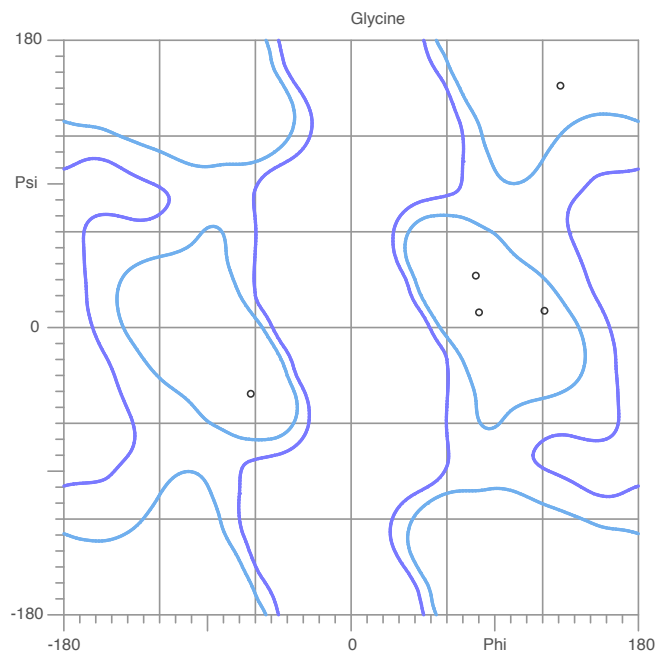
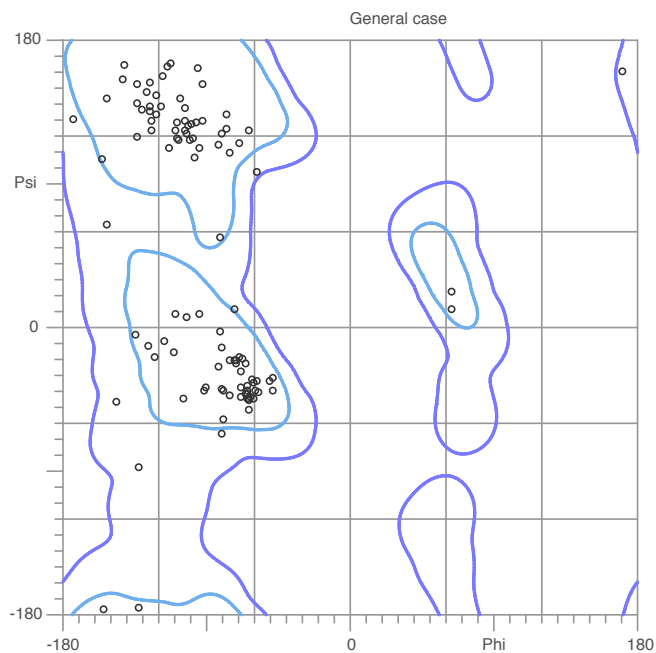
There were 2 outliers (phi, psi):

[13] 5 ALA (55.0, 167.9)

[13] 57 TYR (-35.1, 92.5)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 14



92.4% (110/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

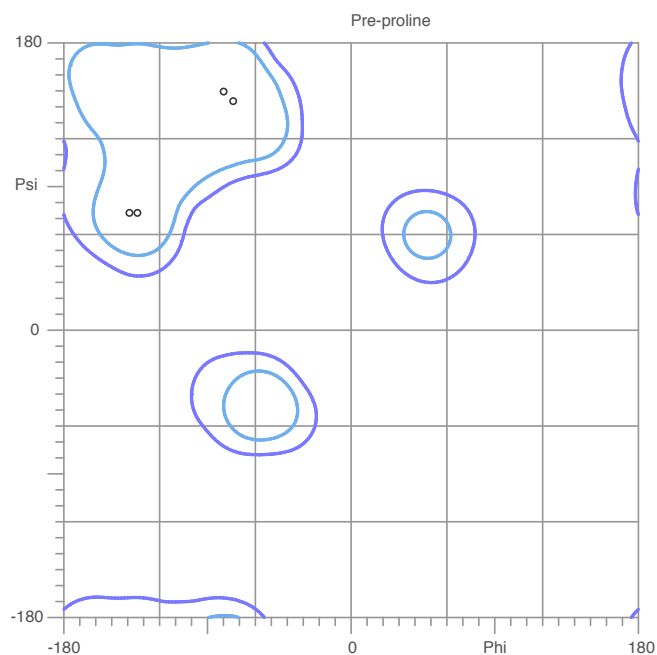
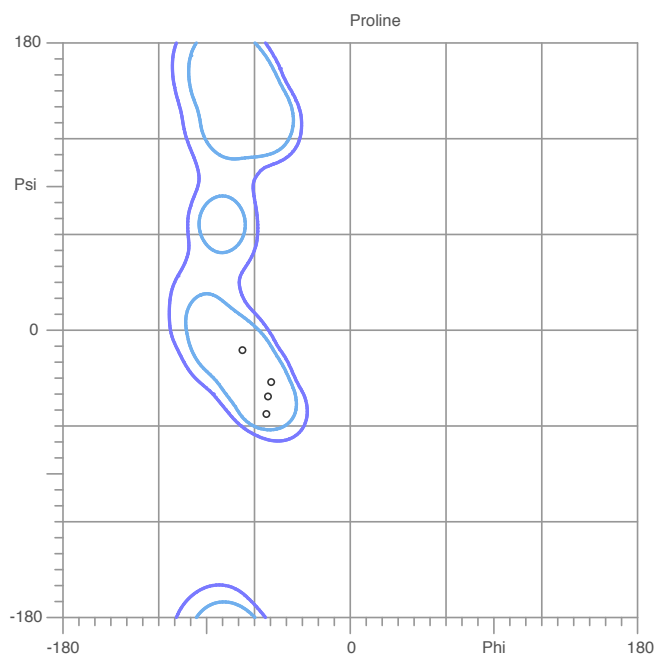
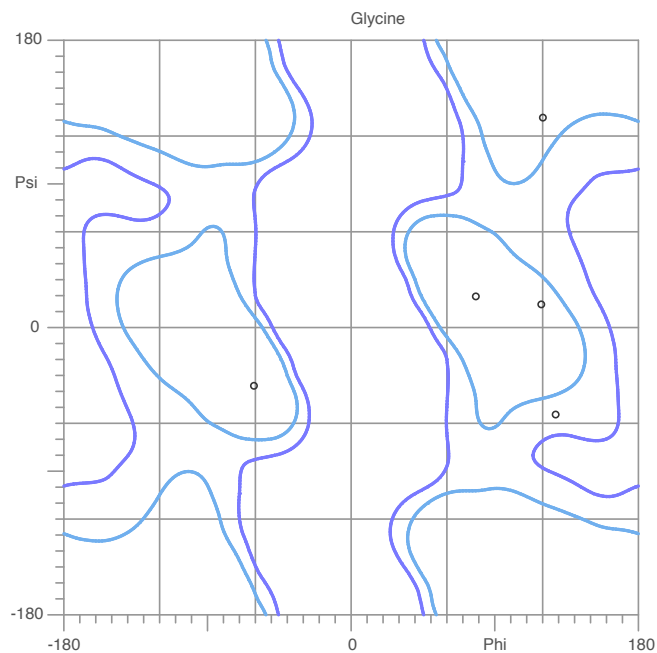
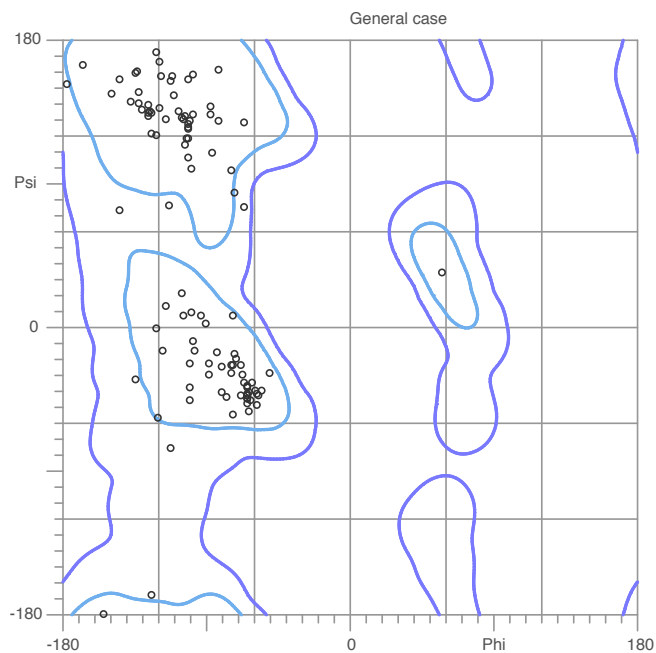
There were 1 outliers (phi, psi):
[14] 112 PRO (-66.2, -64.2)

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MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 15



93.3% (111/119) of all residues were in favored (98%) regions.
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

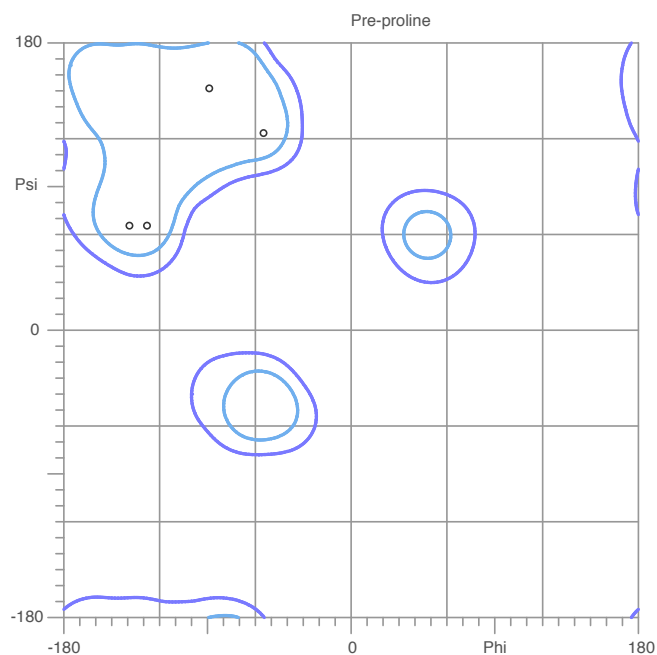
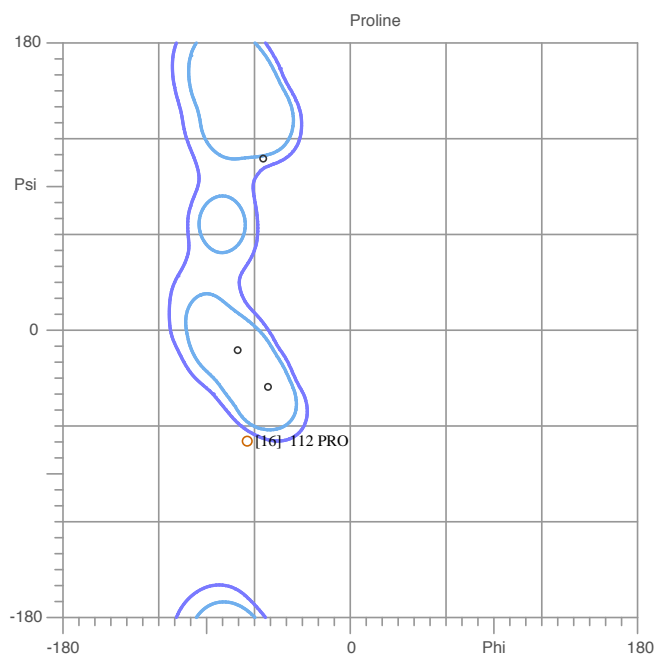
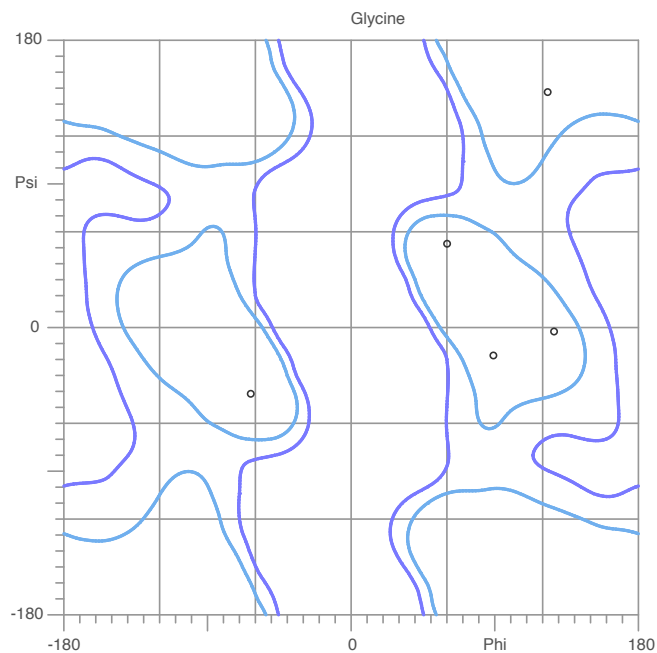
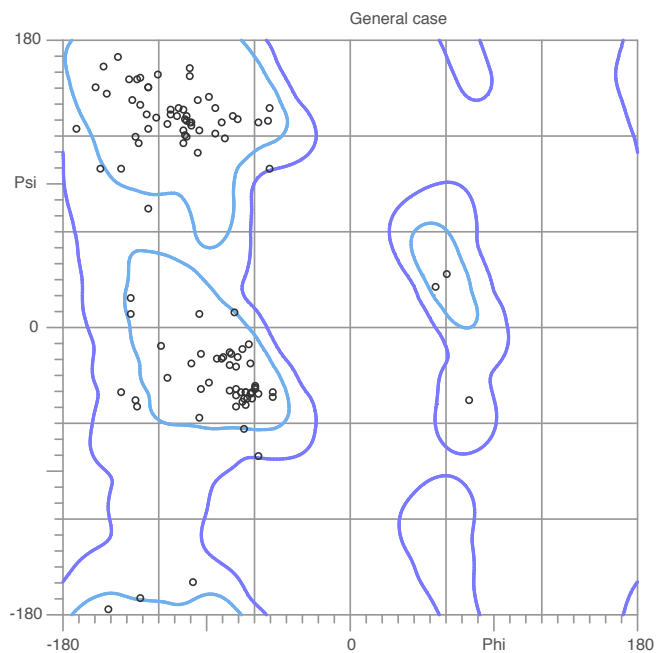
There were no outliers.

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

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

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 16



88.2% (105/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

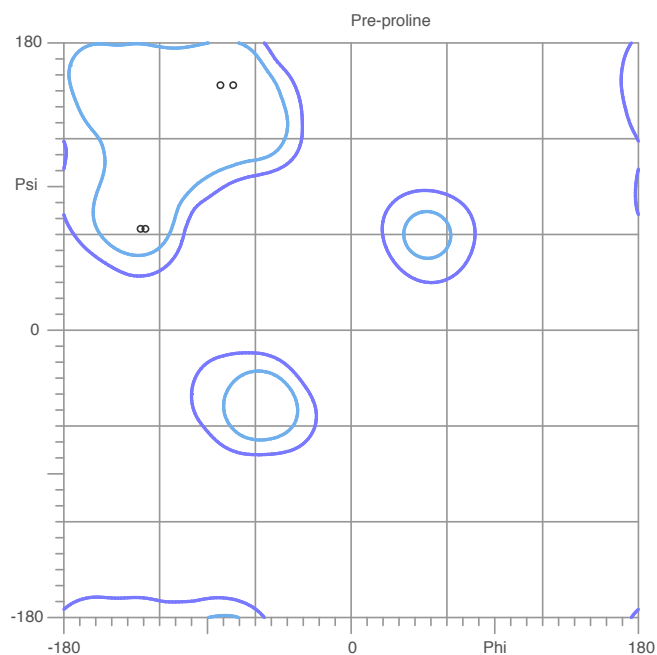
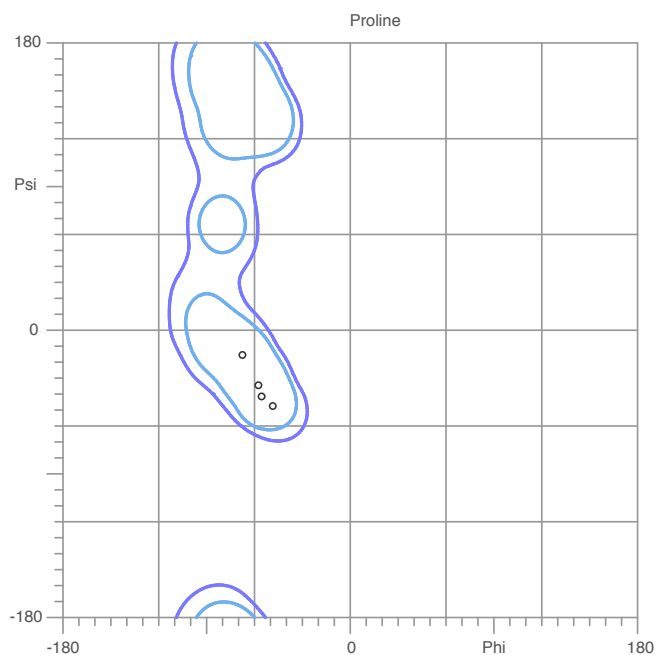
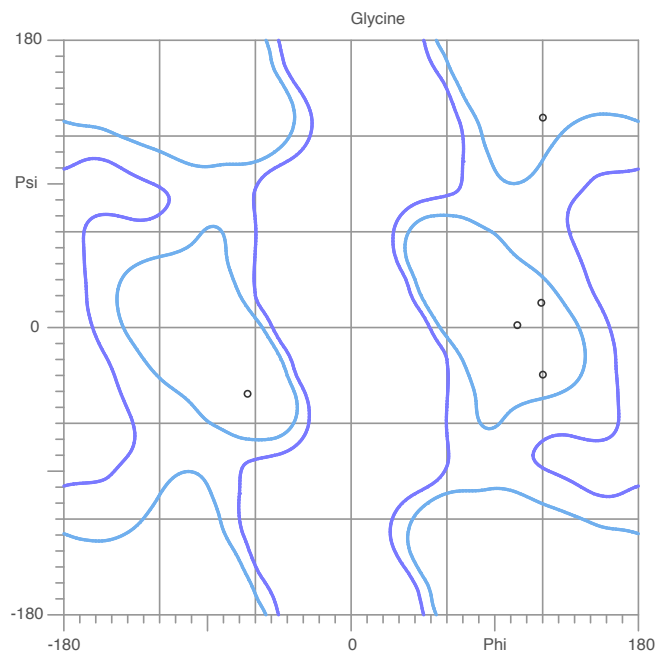
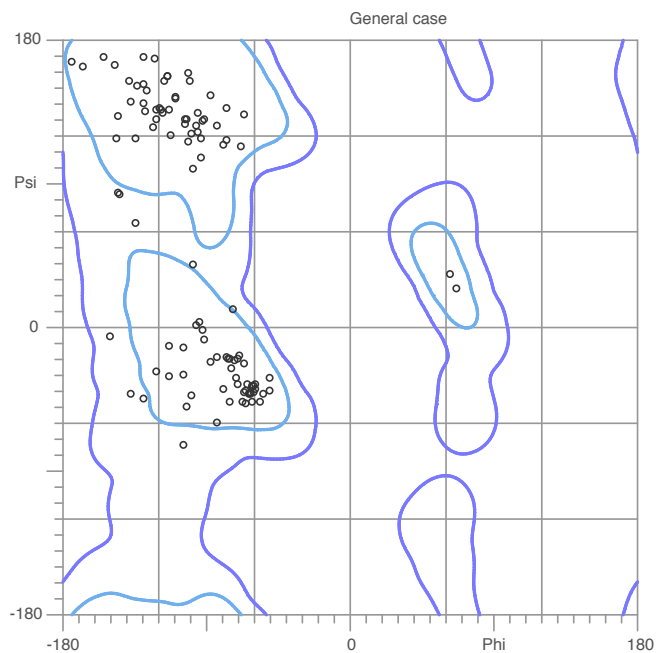
There were 1 outliers (phi, psi):
[16] 112 PRO (-65.1, -69.9)

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MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 17



92.4% (110/119) of all residues were in favored (98%) regions.
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

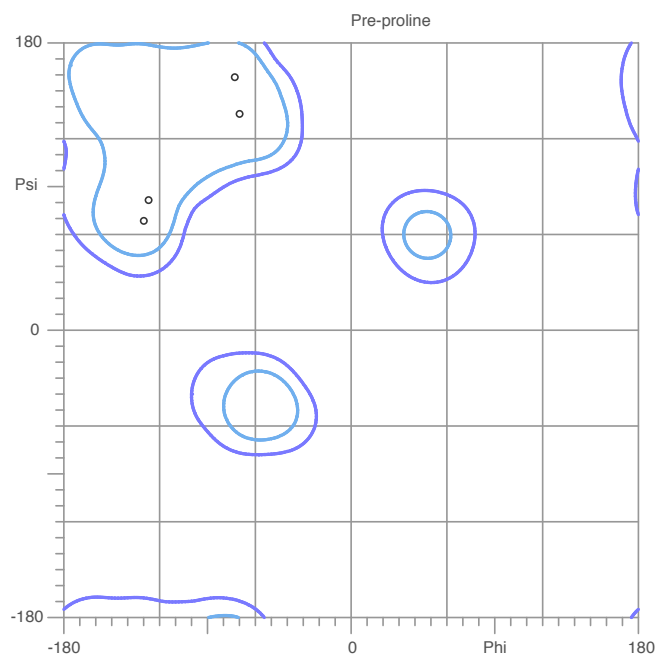
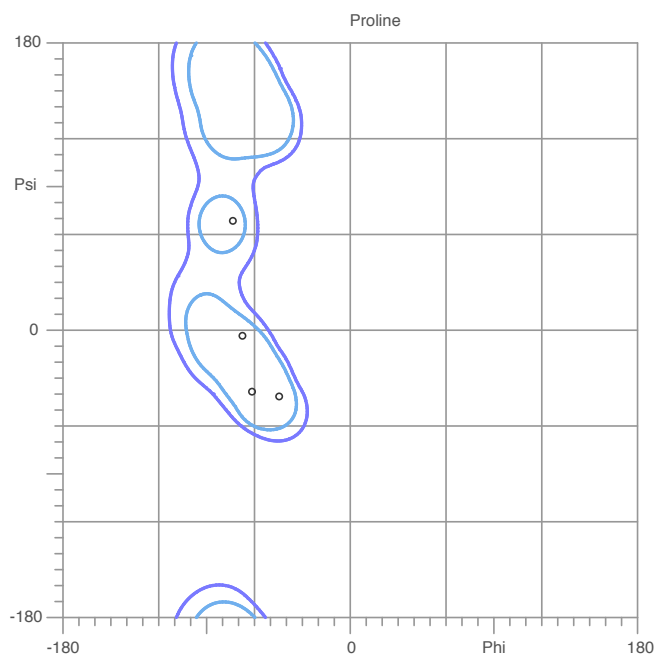
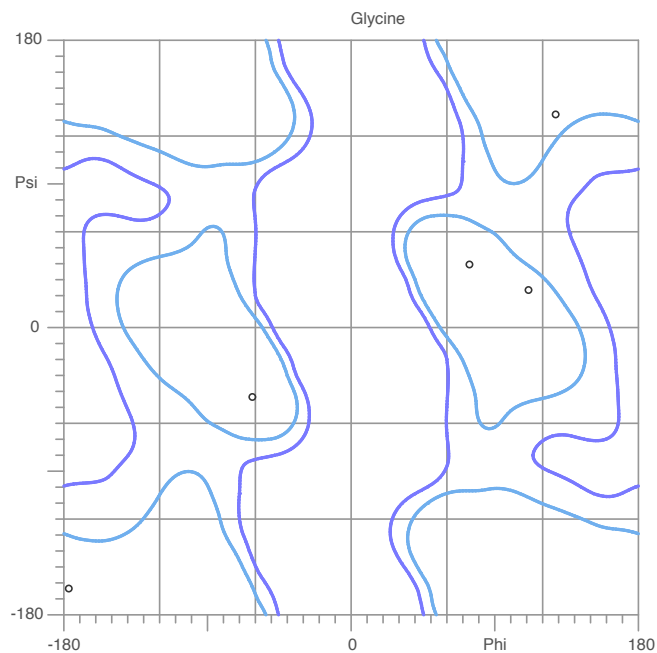
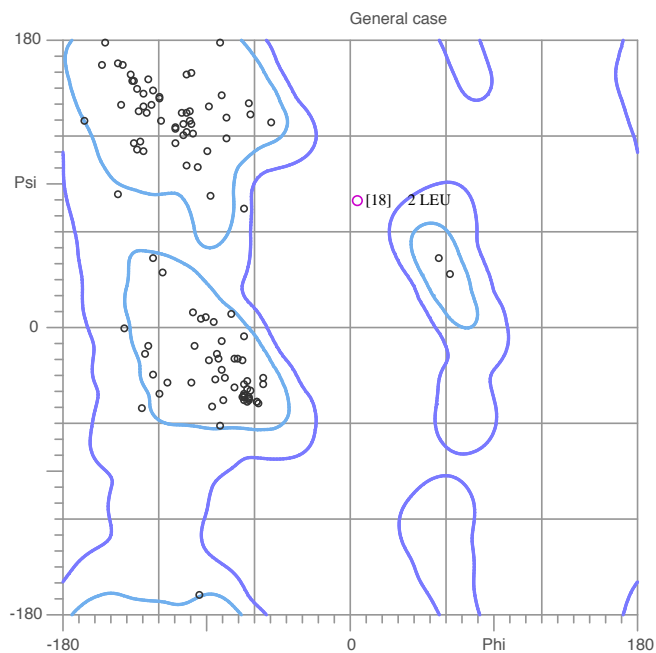
There were no outliers.

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

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

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 18



94.1% (112/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

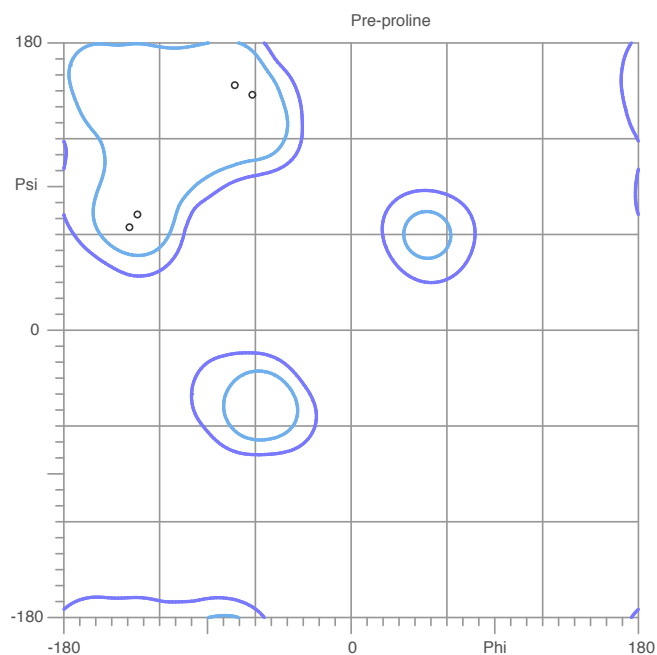
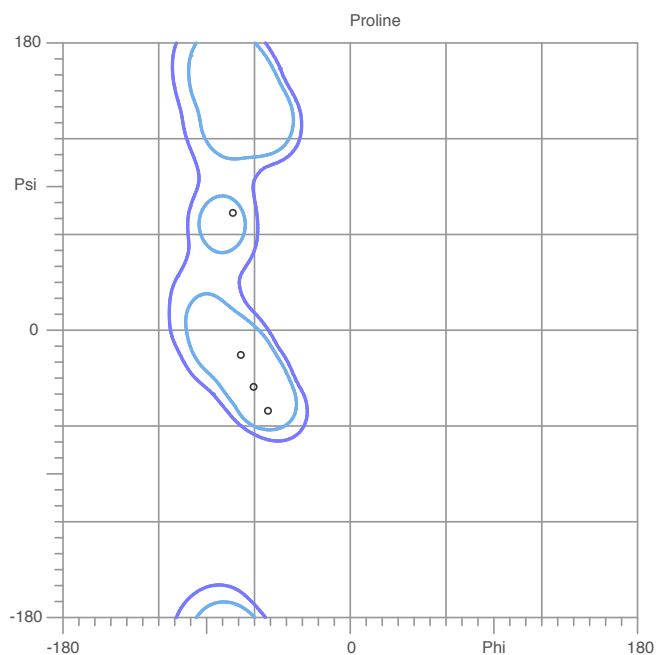
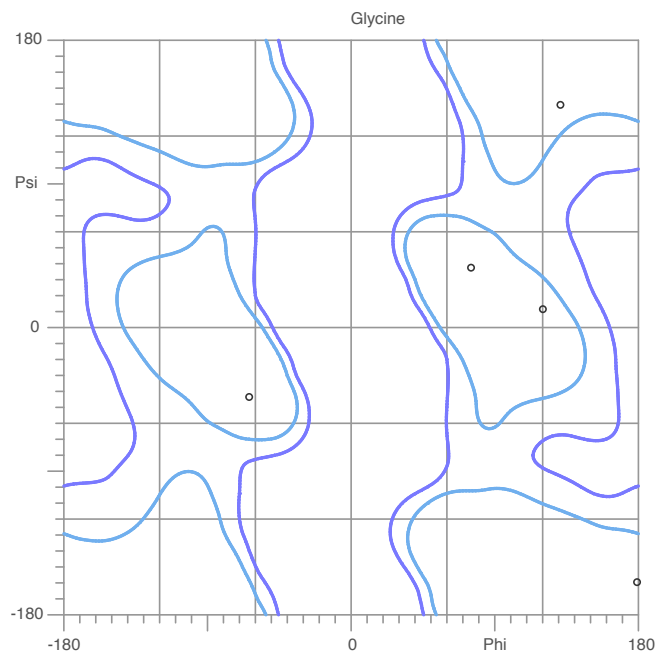
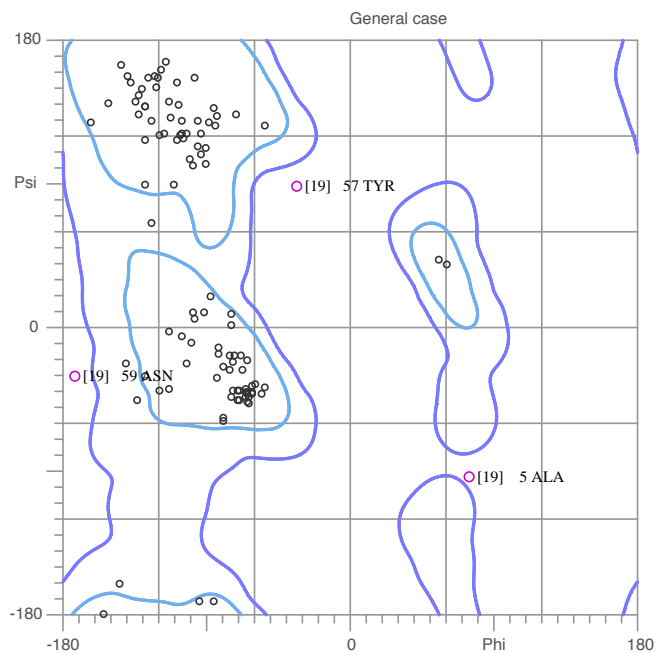
There were 1 outliers (phi, psi):
[18] 2 LEU (4.7, 80.8)

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

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

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 19



94.1% (112/119) of all residues were in favored (98%) regions.
97.5% (116/119) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

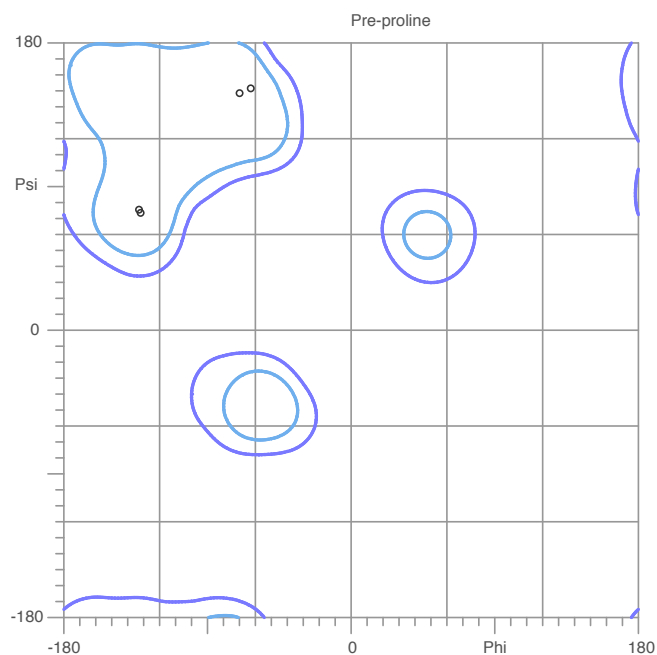
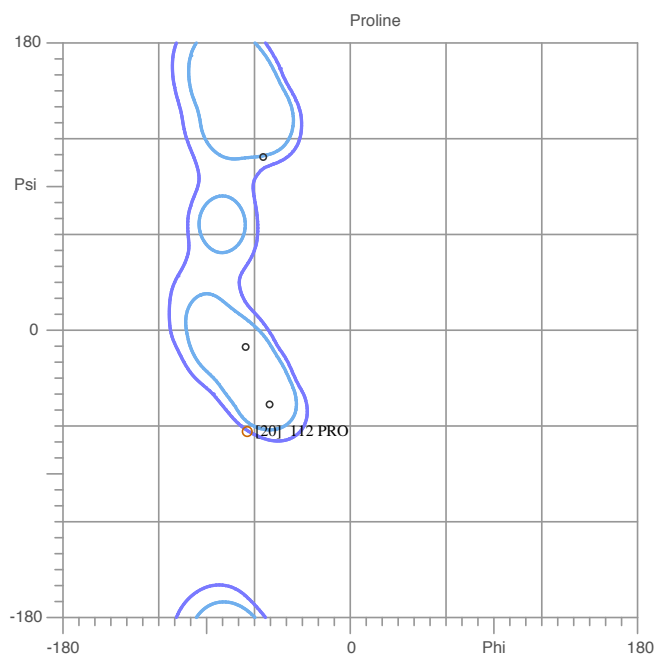
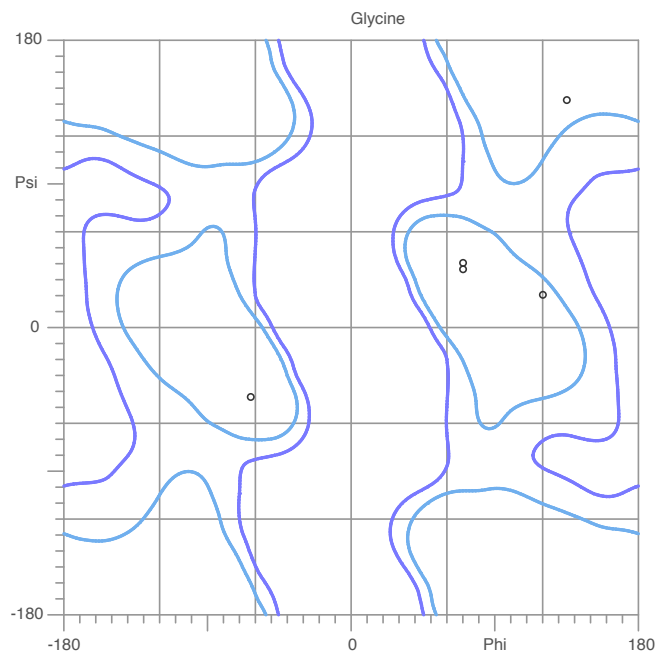
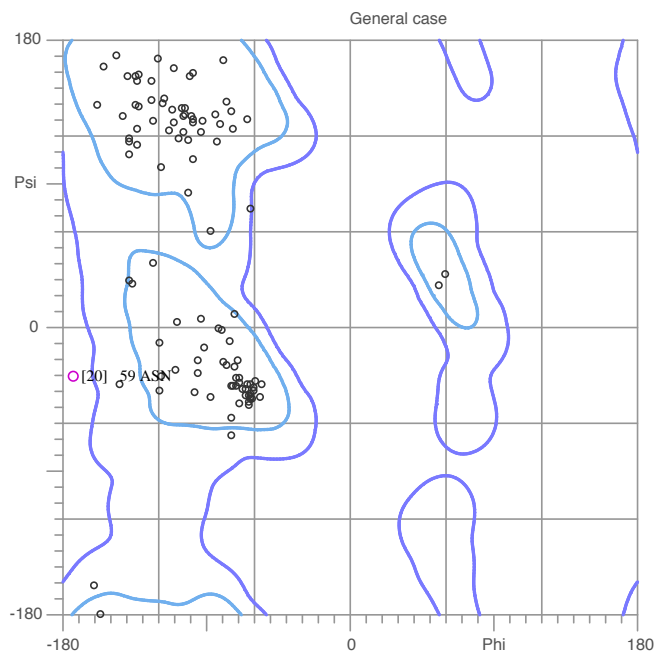
[19] 5 ALA (75.0, -93.3)

[19] 57 TYR (-35.0, 89.3)

[19] 59 ASN (-173.5, -31.0)

MolProbity Ramachandran analysis

UUR17A_R3Cons_em_bcr3.pdb, model 20



94.1% (112/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[20] 59 ASN (-175.0, -30.4)
[20] 112 PRO (-65.2, -63.5)