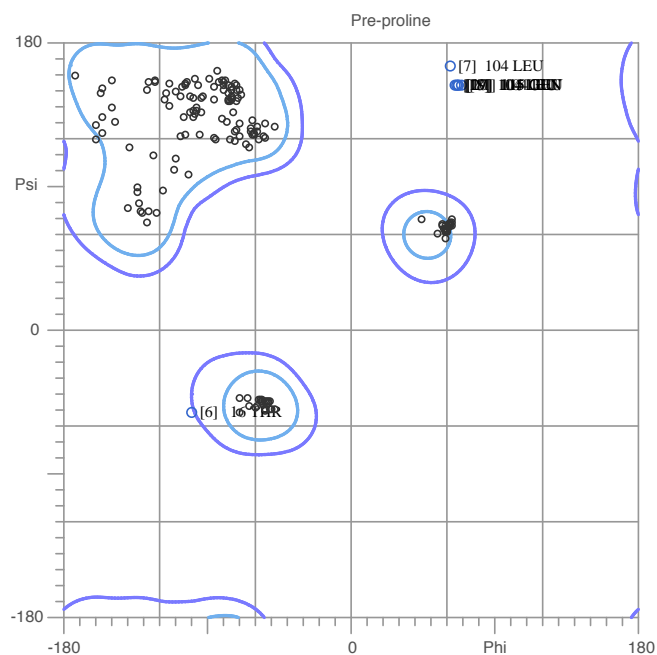
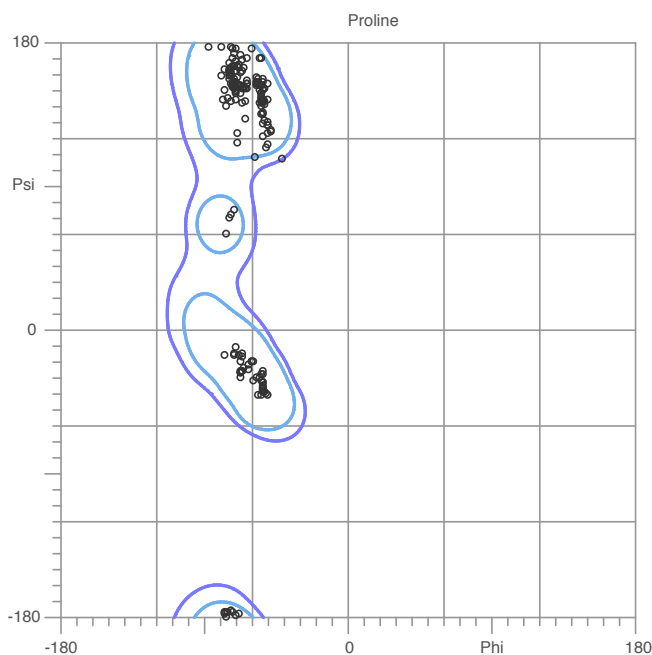
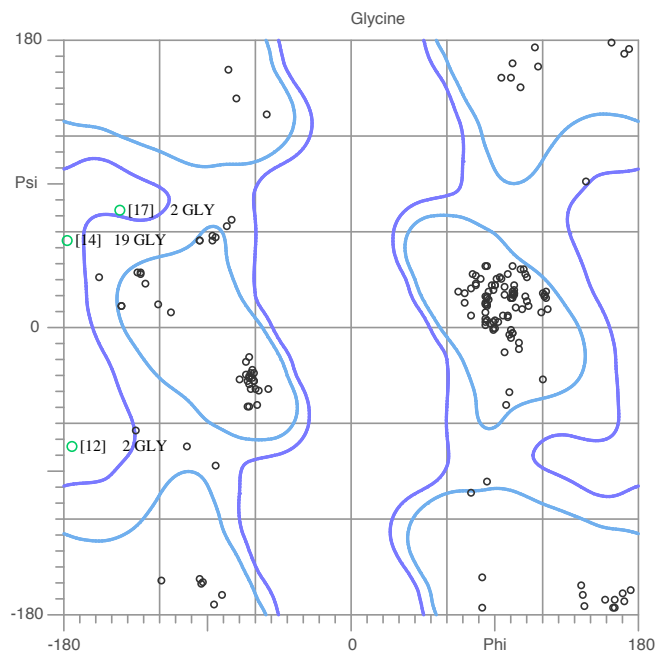
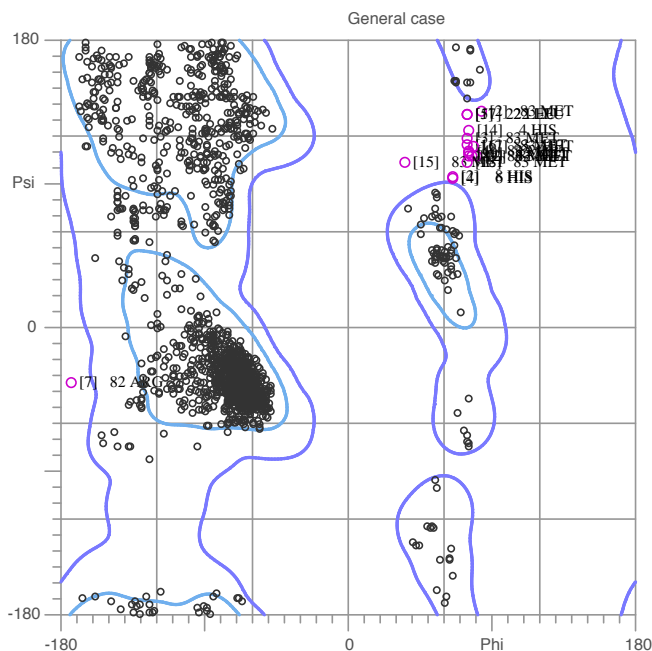


MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, all models



92.4% (2199/2380) of all residues were in favored (98%) regions.
98.9% (2353/2380) of all residues were in allowed (>99.8%) regions.

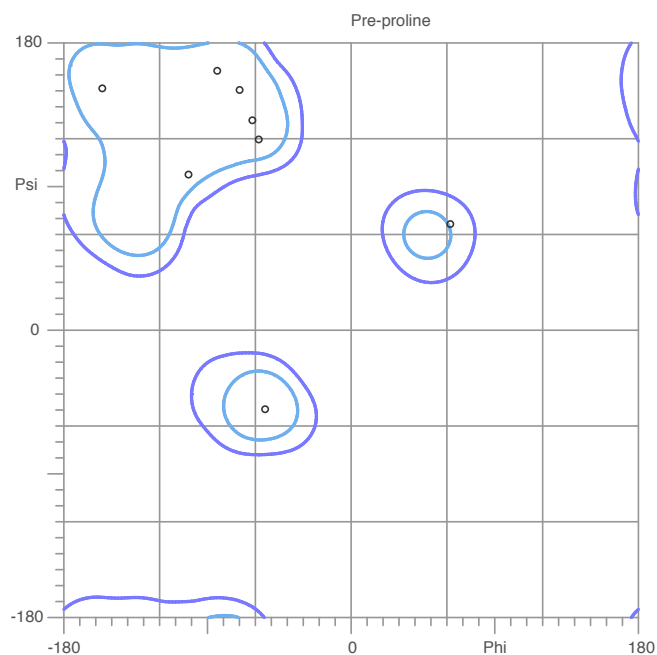
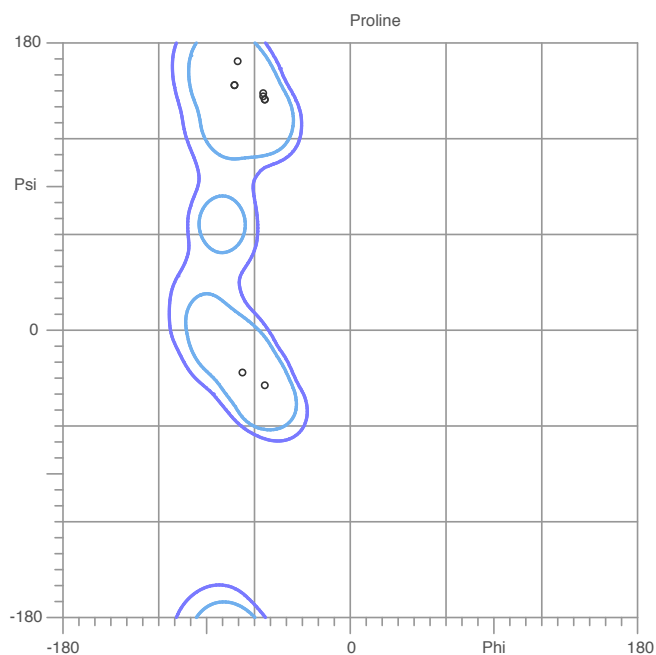
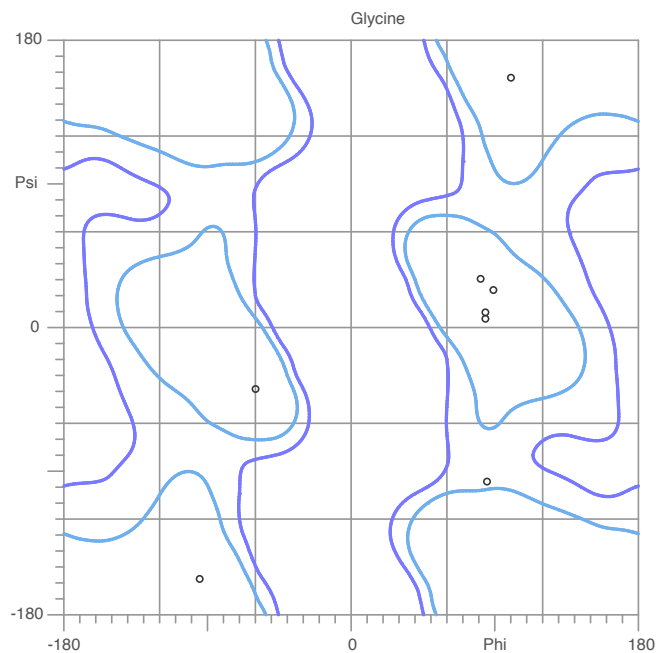
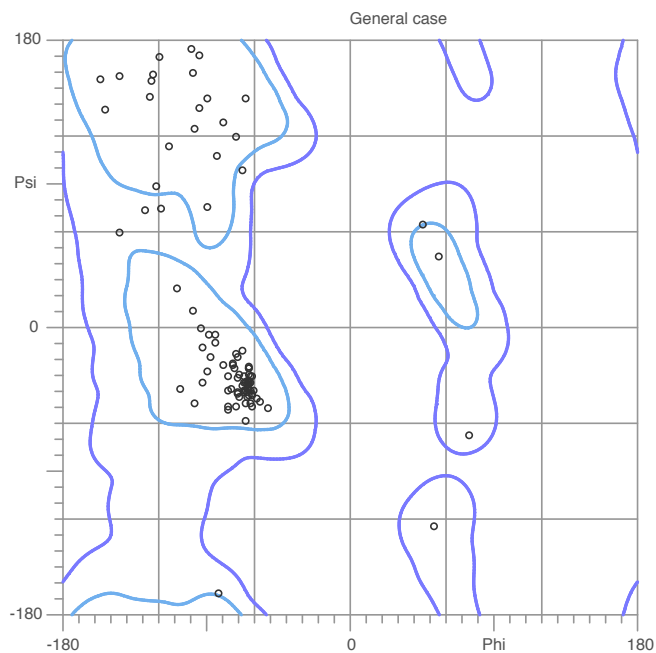
There were 27 outliers (phi, psi):

- [2] 8 HIS (65.0, 95.0)
- [2] 83 MET (83.7, 136.5)
- [3] 83 MET (74.9, 119.9)
- [4] 6 HIS (65.1, 94.9)
- [4] 83 MET (75.1, 111.7)
- [5] 22 LEU (74.9, 135.0)
- [6] 16 THR (-100.8, -51.1)
- [7] 82 ARG (-174.3, -35.0)
- [7] 104 LEU (62.7, 166.8)
- [8] 83 MET (75.0, 108.4)
- [9] 83 MET (80.1, 109.0)

- [11] 104 LEU (69.9, 155.0)
- [12] 2 GLY (-175.1, -74.9)
- [12] 83 MET (77.3, 108.5)
- [14] 4 HIS (75.1, 125.0)
- [14] 19 GLY (-178.2, 55.1)
- [15] 83 MET (35.2, 105.0)
- [16] 83 MET (74.9, 115.0)
- [17] 2 GLY (-145.0, 75.0)
- [17] 22 LEU (74.8, 134.5)
- [17] 83 MET (78.1, 114.8)
- [17] 115 GLN (67.6, 155.0)
- [18] 83 MET (74.9, 104.9)
- [18] 104 LEU (65.8, 155.0)
- [19] 83 MET (75.1, 110.9)
- [19] 104 LEU (66.2, 154.7)
- [20] 115 GLN (67.8, 155.0)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 1

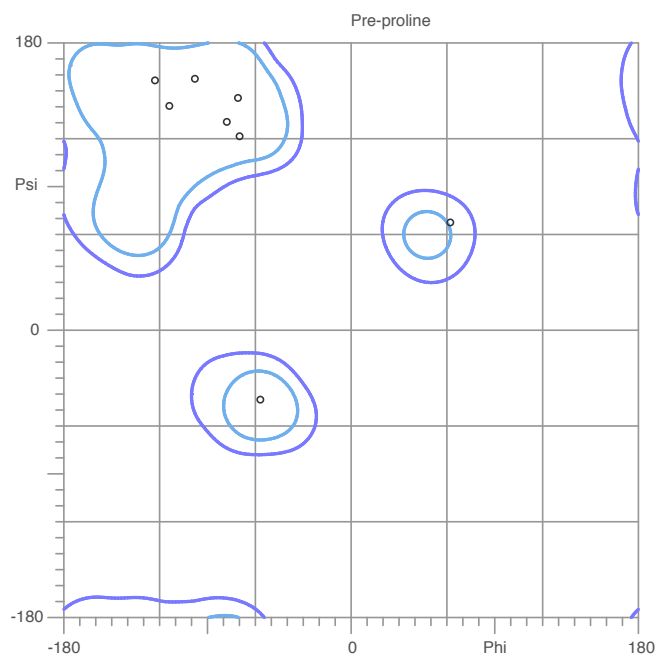
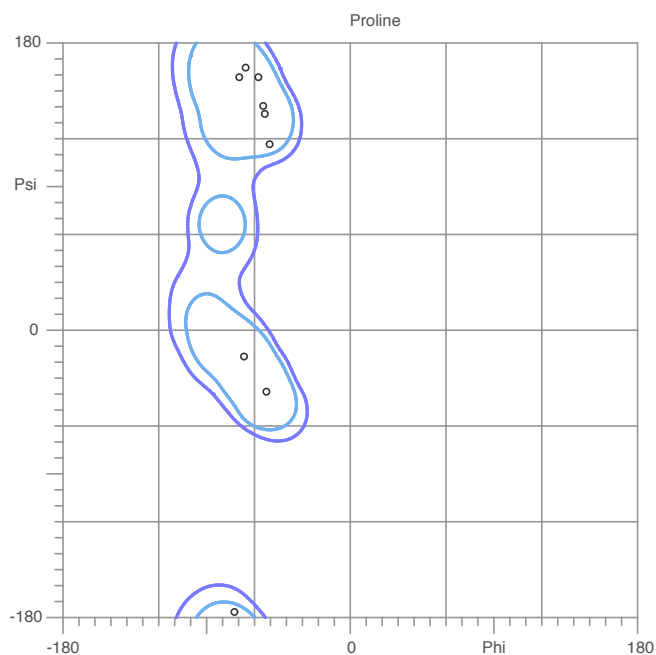
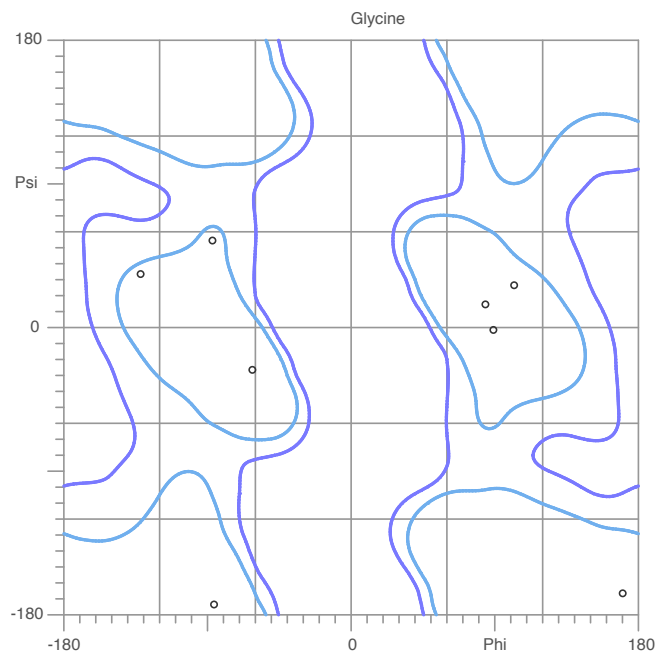
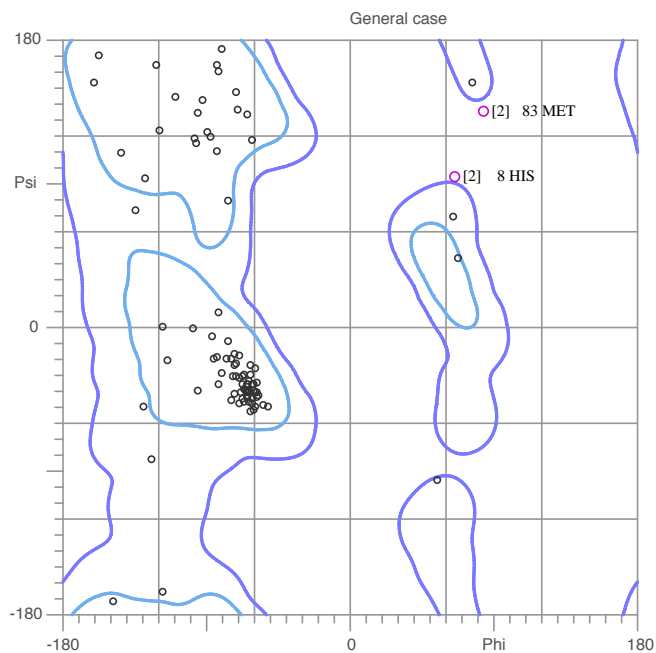


91.6% (109/119) of all residues were in favored (98%) regions.
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 2



91.6% (109/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

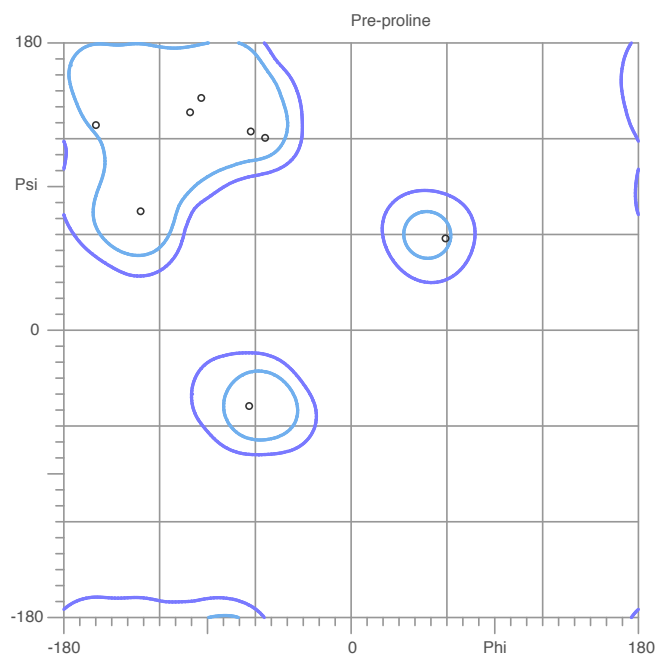
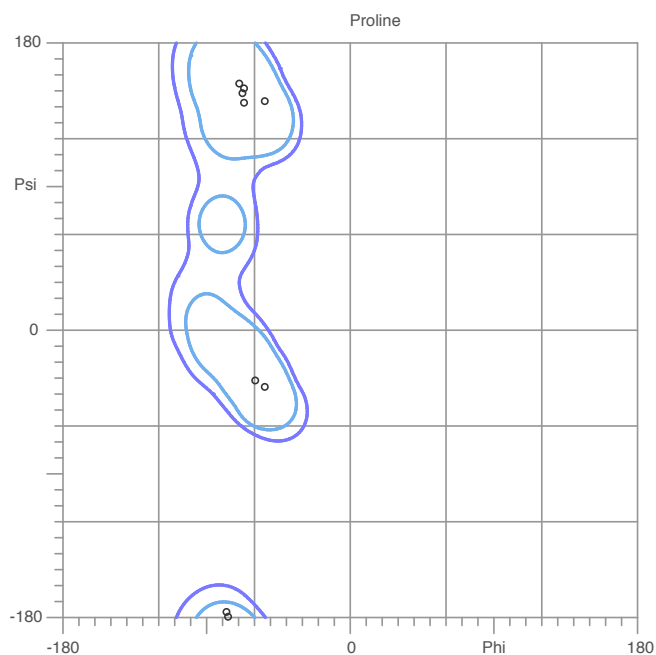
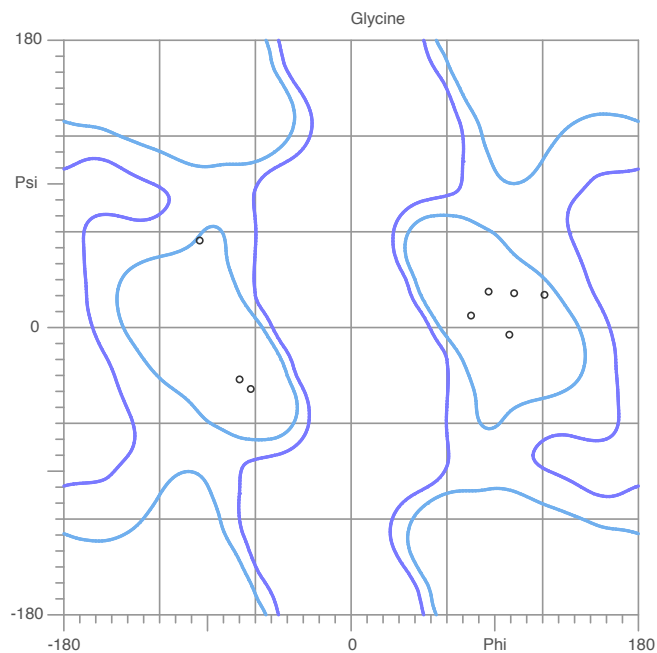
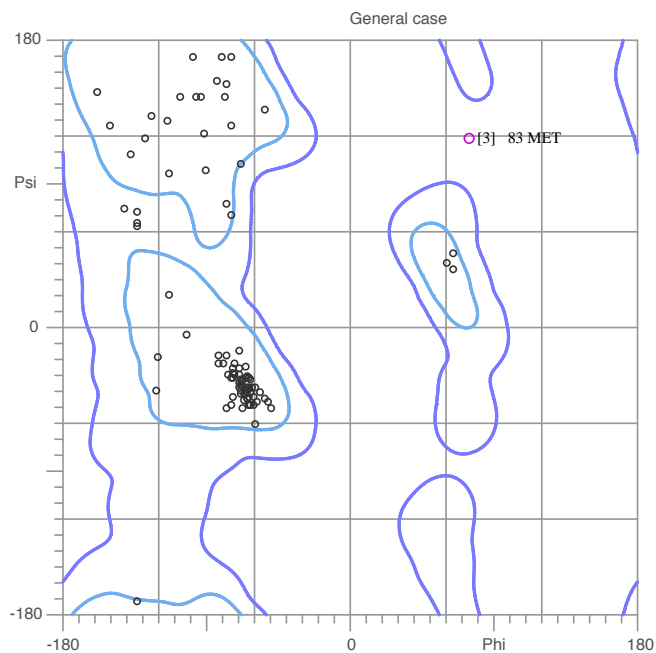
There were 2 outliers (phi, psi):

[2] 8 HIS (65.0, 95.0)

[2] 83 MET (83.7, 136.5)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 3

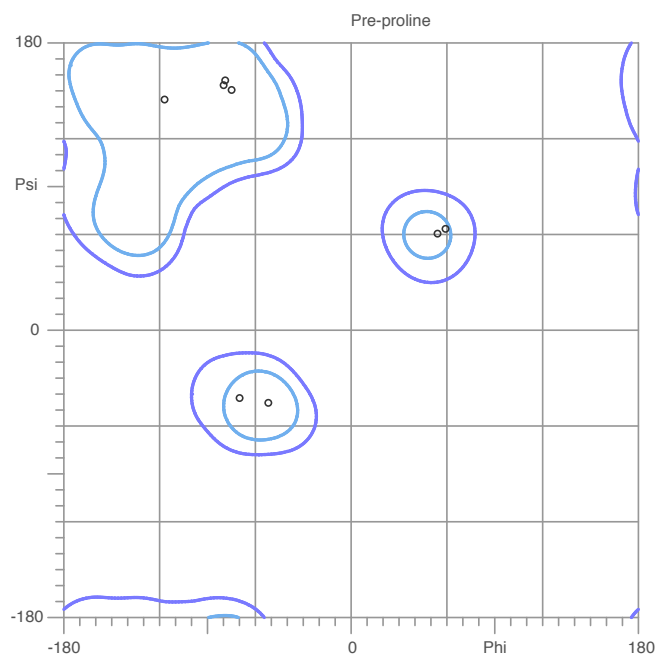
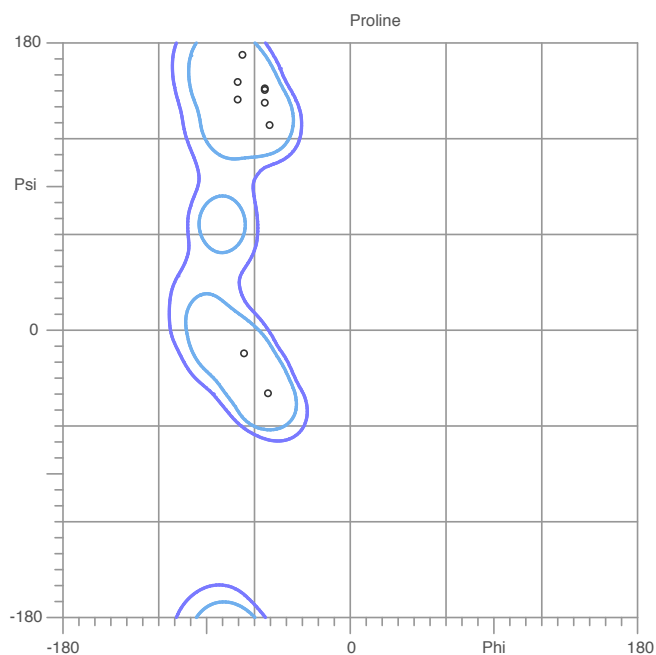
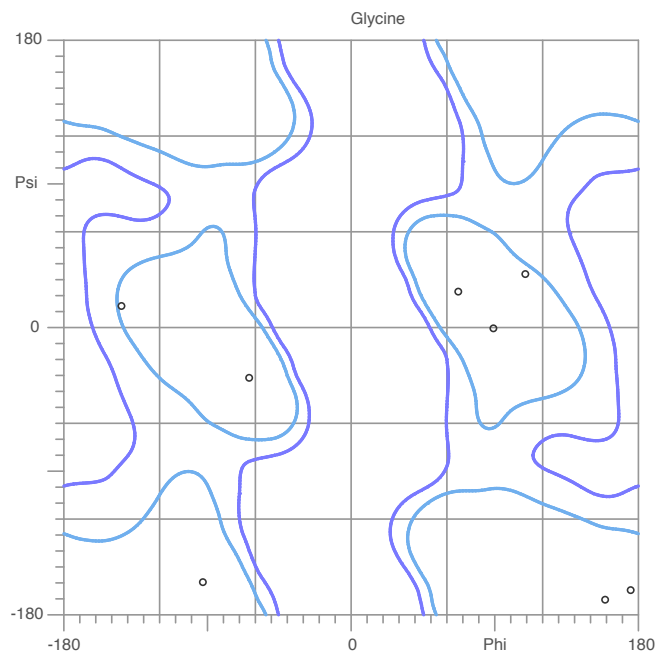
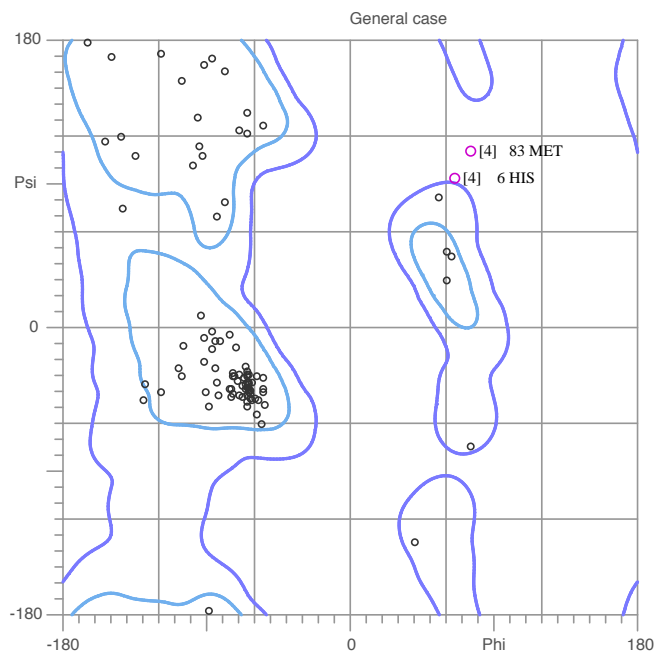


95.8% (114/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 83 MET (74.9, 119.9)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 4



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.

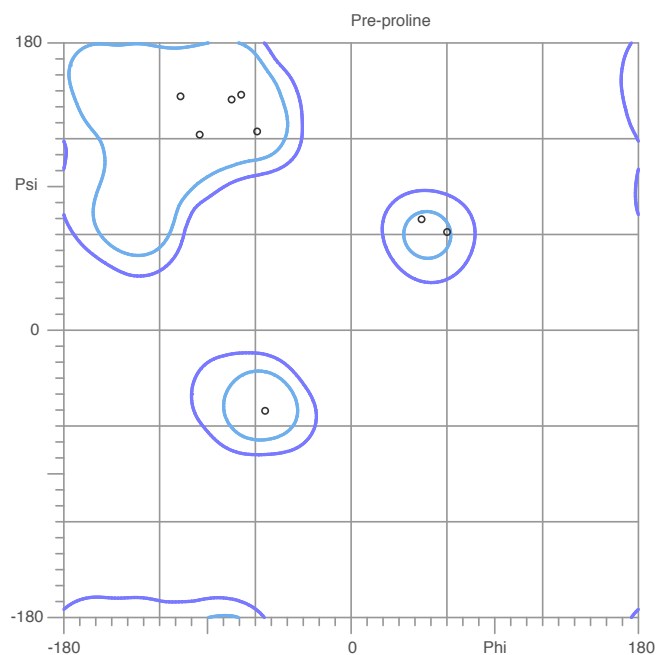
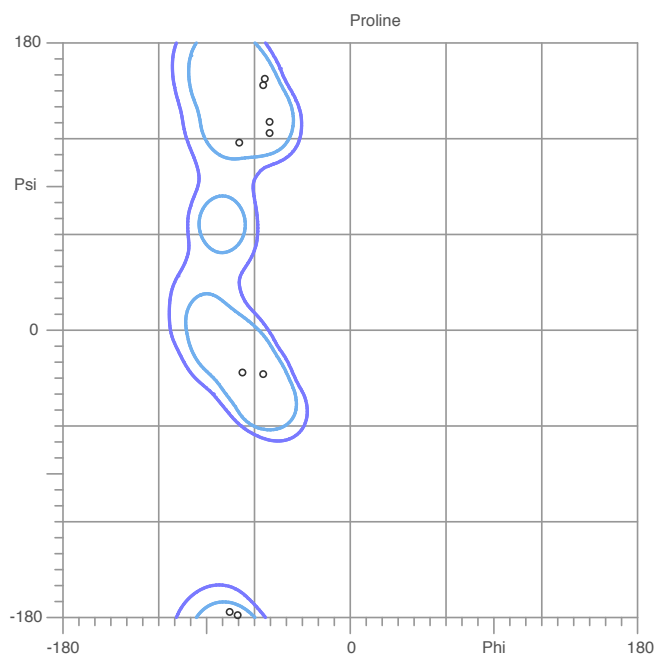
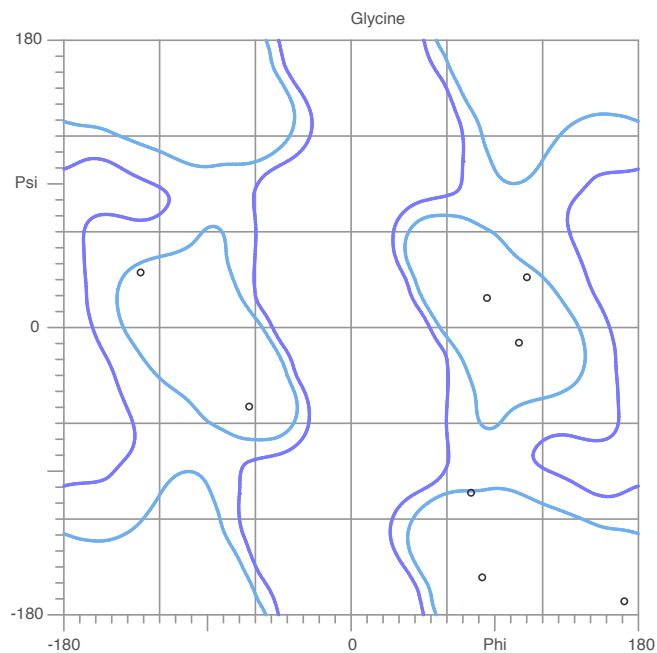
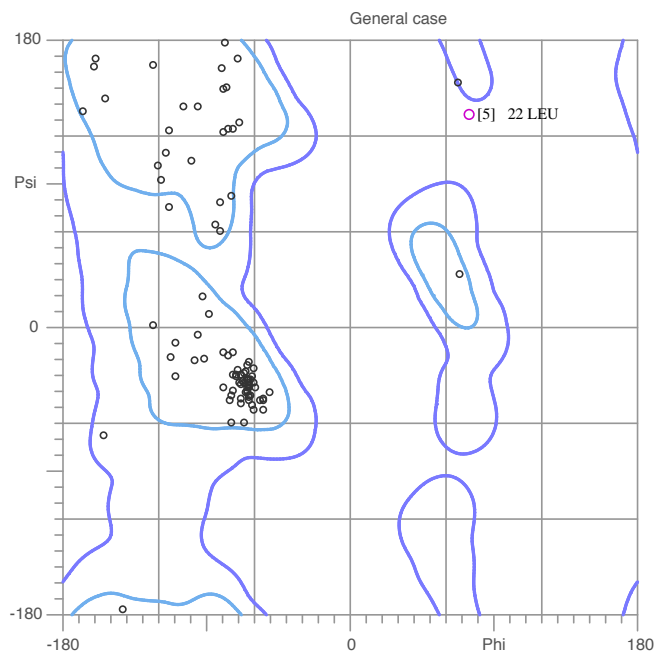
There were 2 outliers (phi, psi):

[4] 6 HIS (65.1, 94.9)

[4] 83 MET (75.1, 111.7)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 5



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.

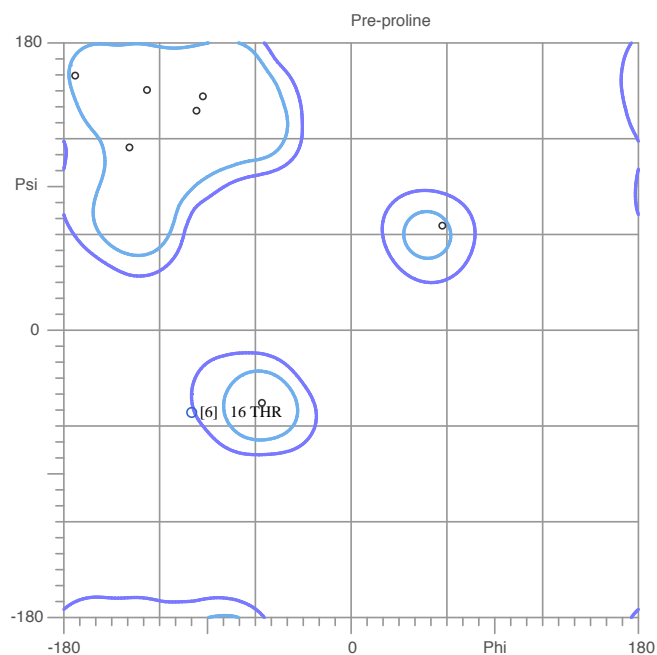
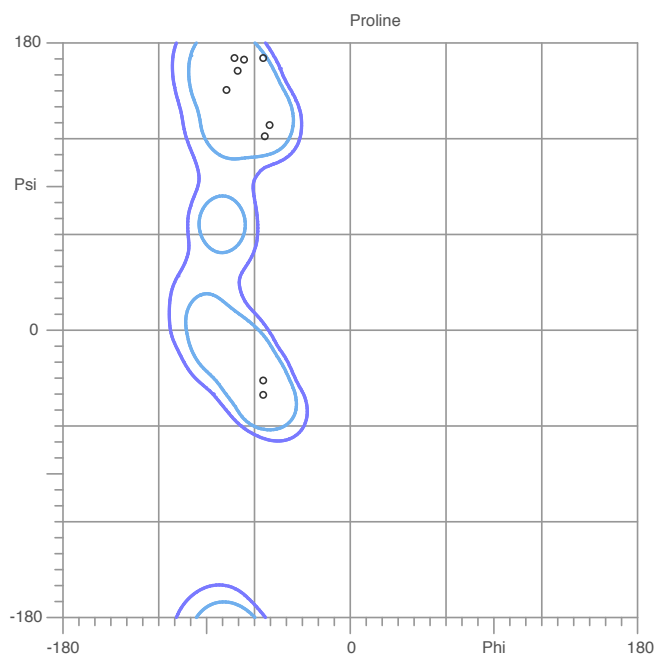
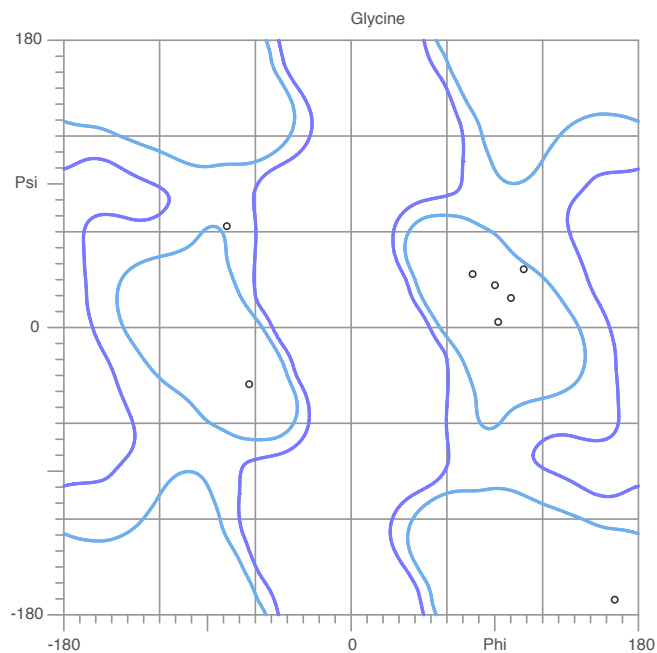
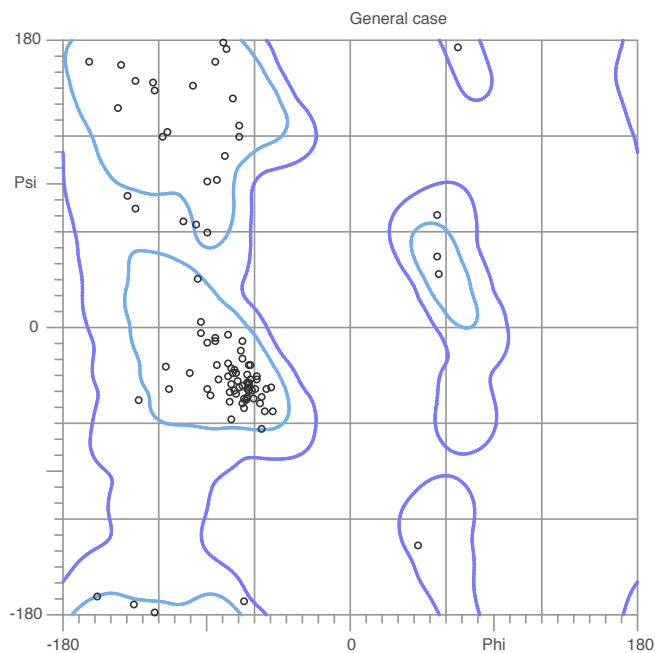
There were 1 outliers (phi, psi):
[5] 22 LEU (74.9, 135.0)

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

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 6

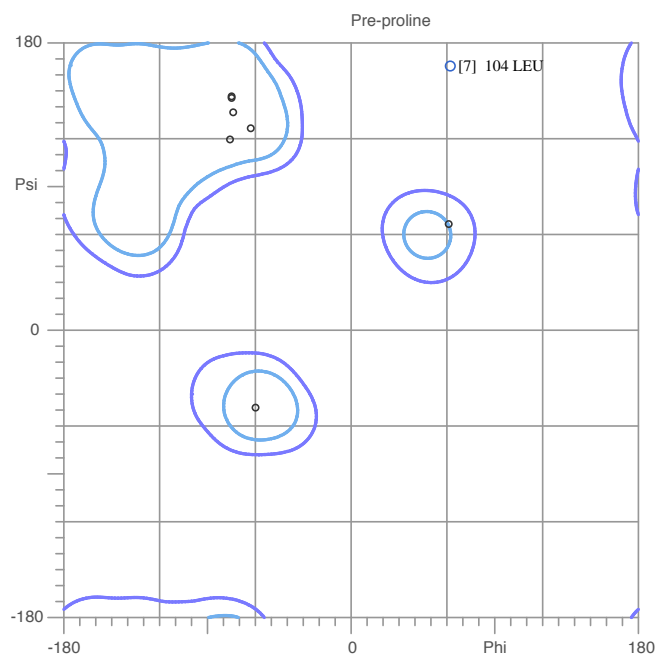
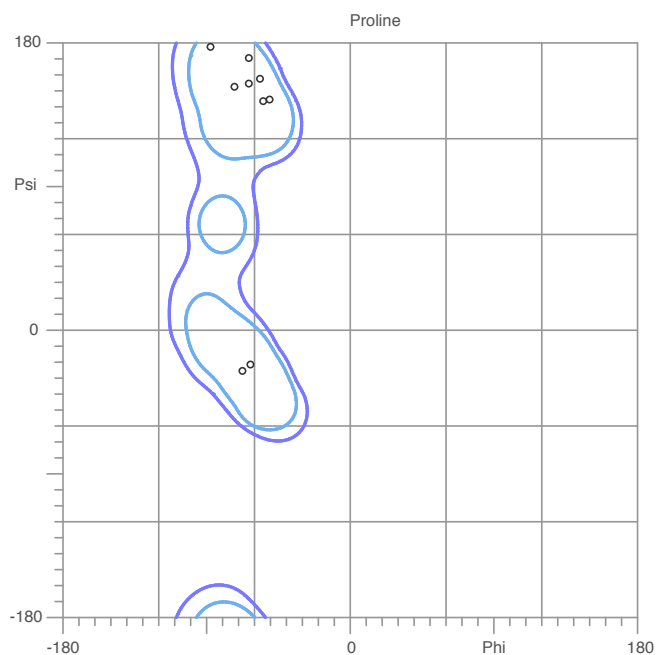
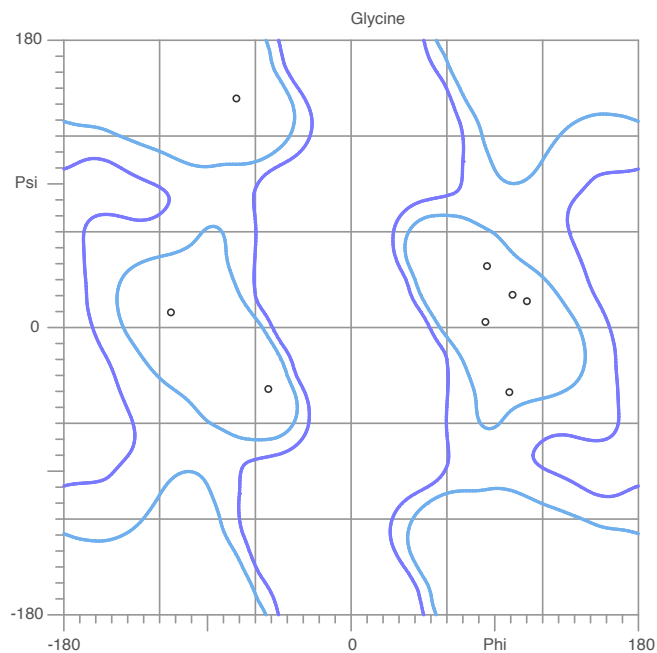
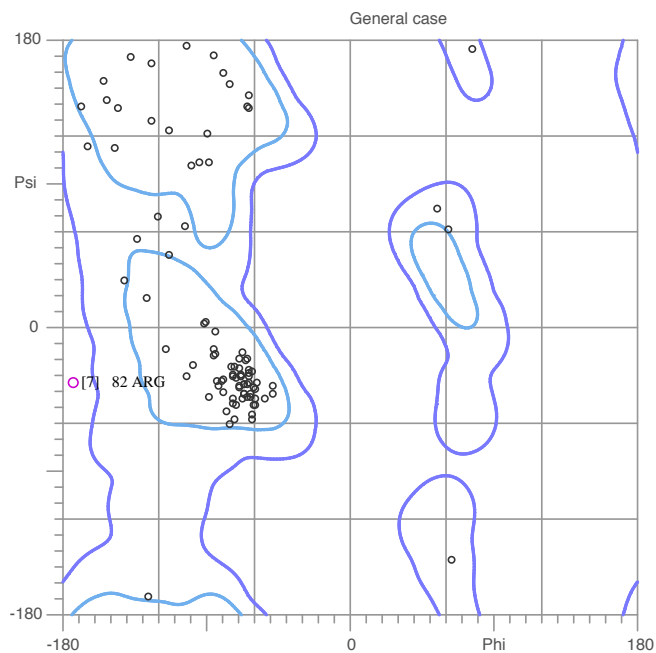


90.8% (108/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[6] 16 THR (-100.8, -51.1)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 7



88.2% (105/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

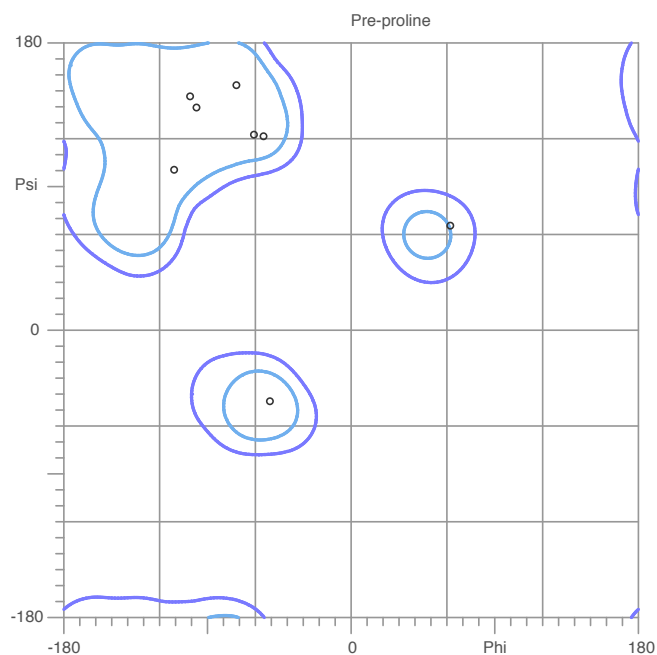
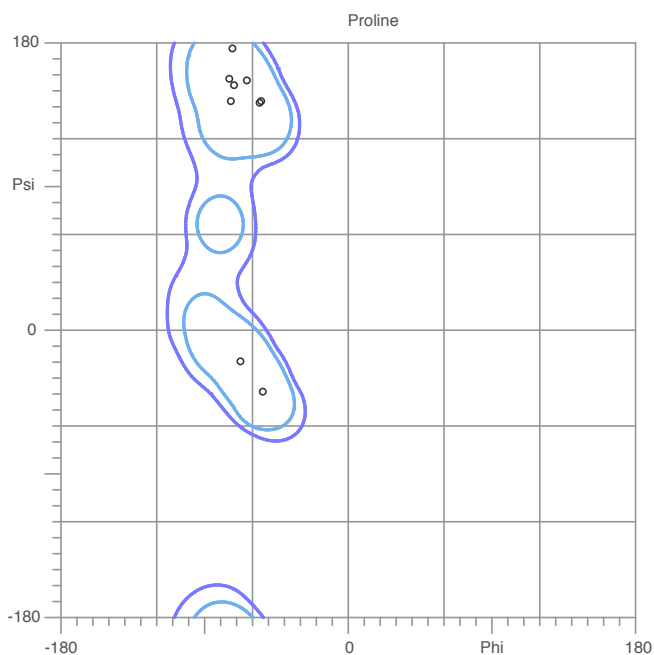
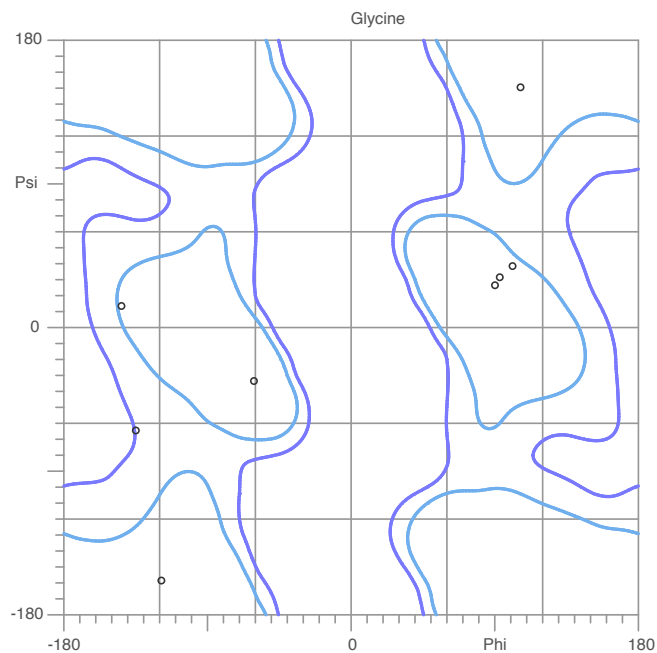
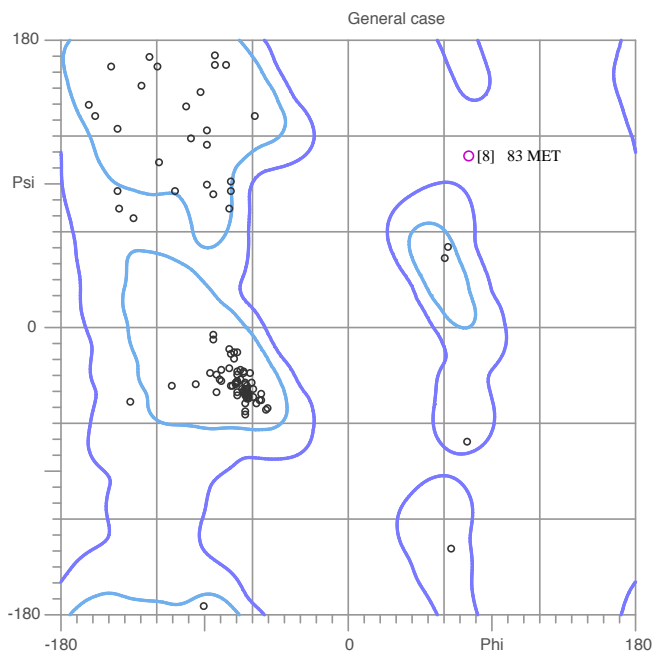
There were 2 outliers (phi, psi):

[7] 82 ARG (-174.3, -35.0)

[7] 104 LEU (62.7, 166.8)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 8



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.

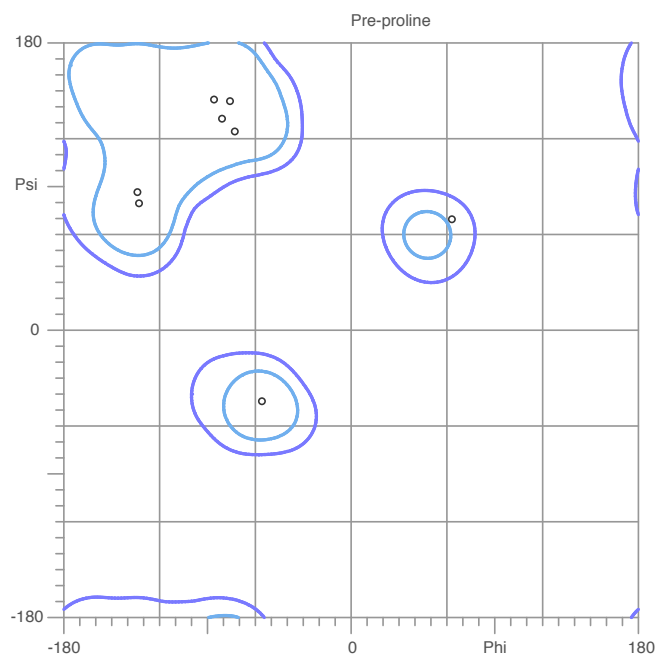
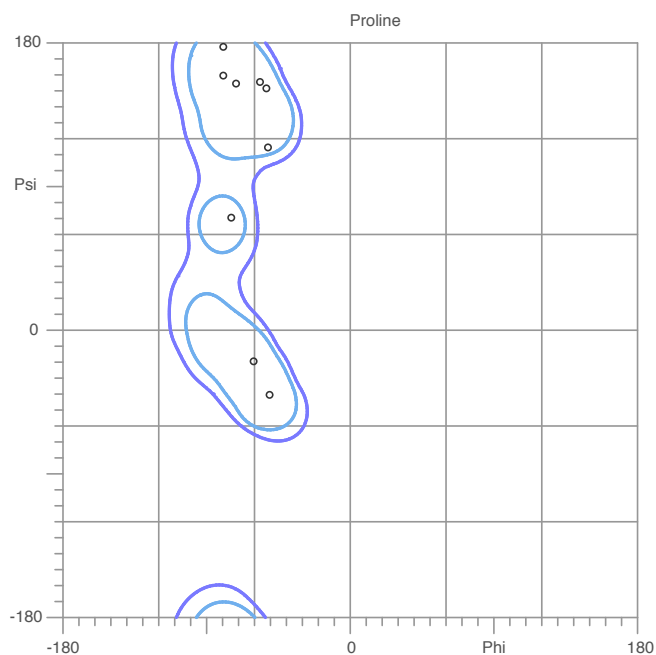
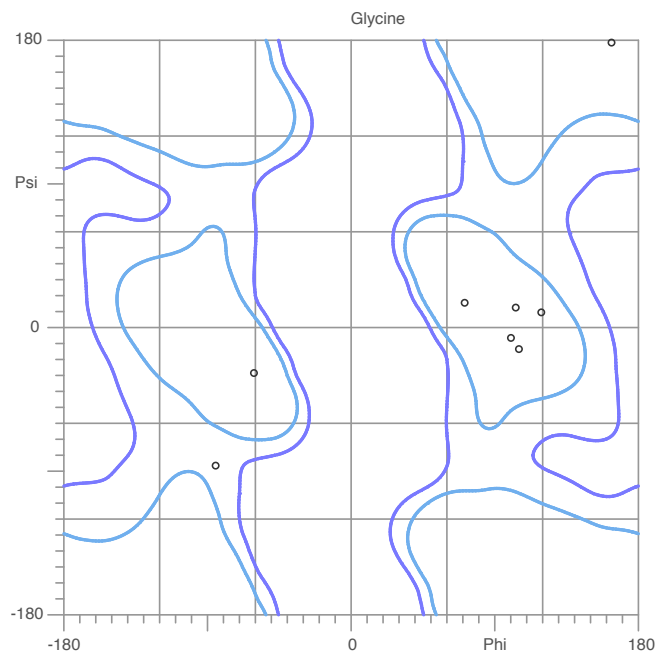
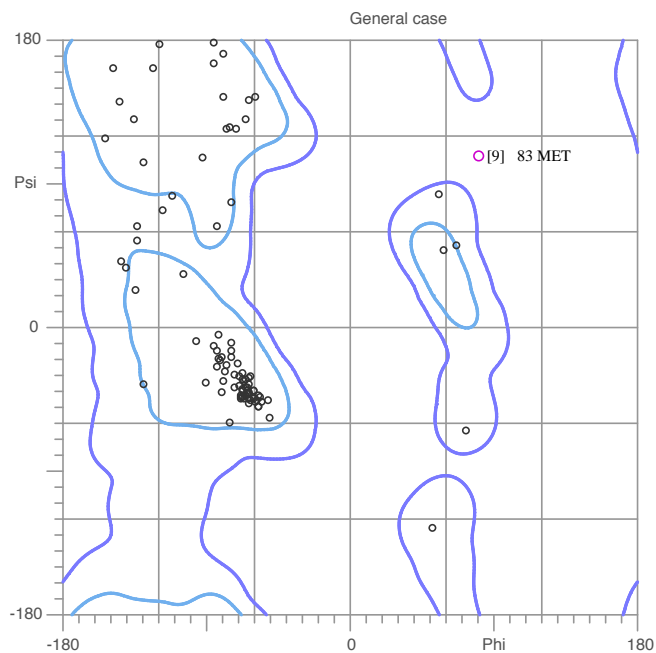
There were 1 outliers (phi, psi):
[8] 83 MET (75.0, 108.4)

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MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 9

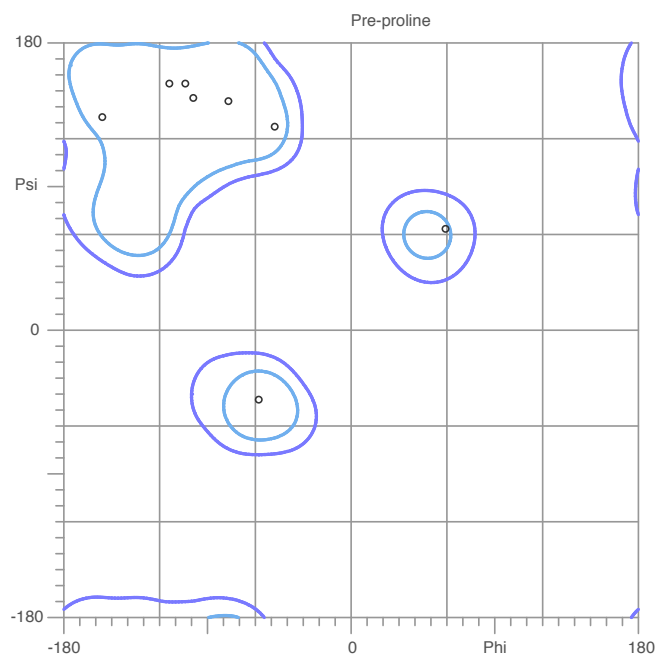
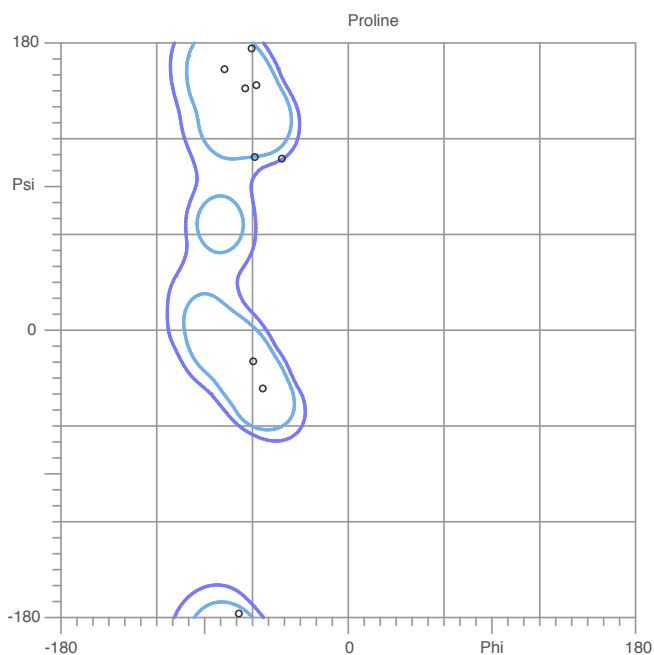
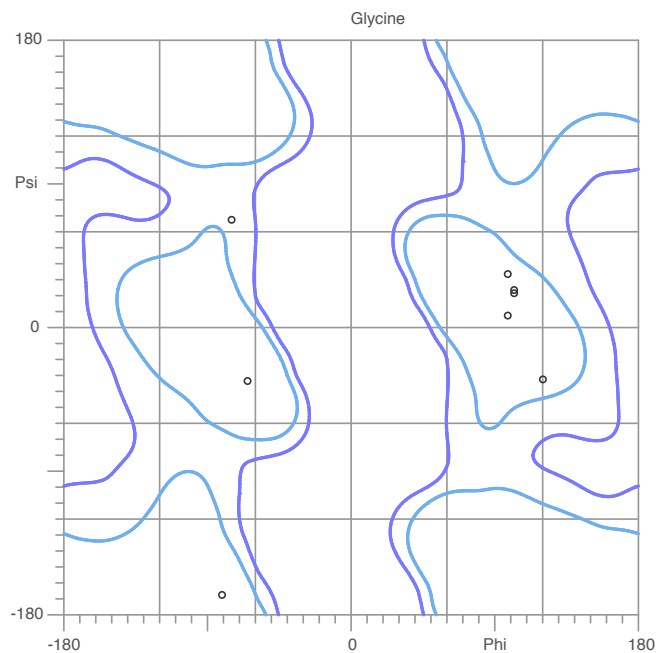
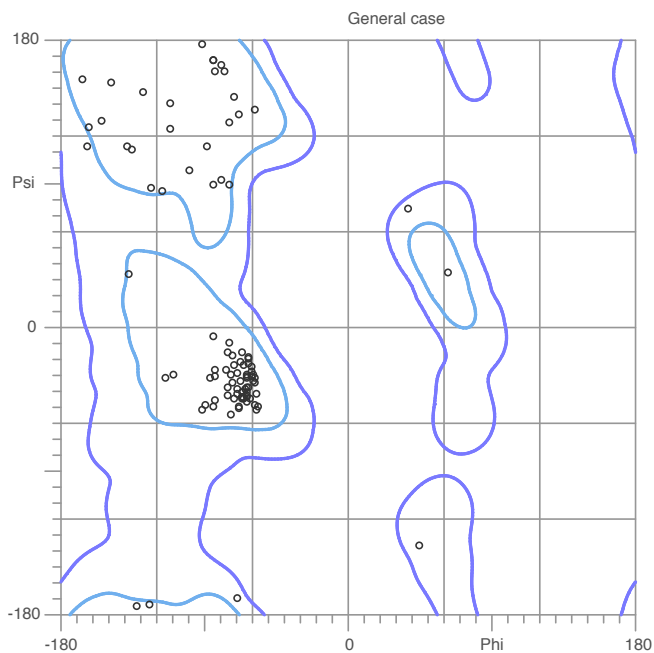


88.2% (105/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 83 MET (80.1, 109.0)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 10

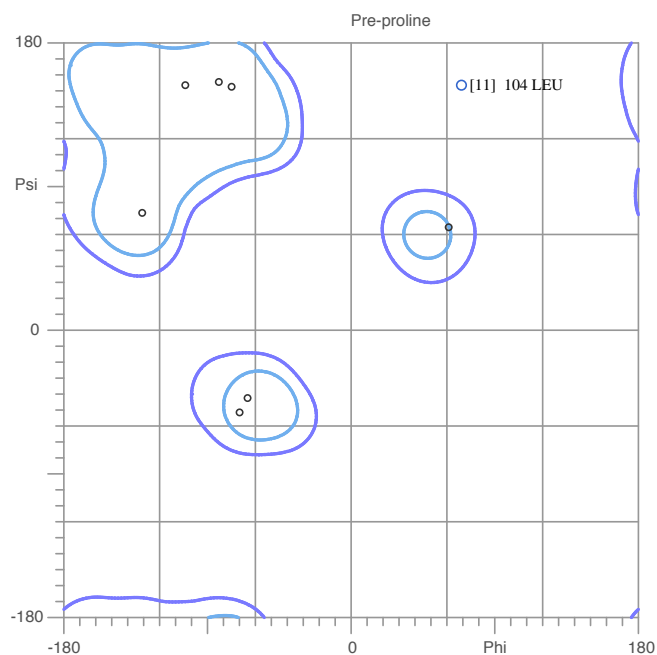
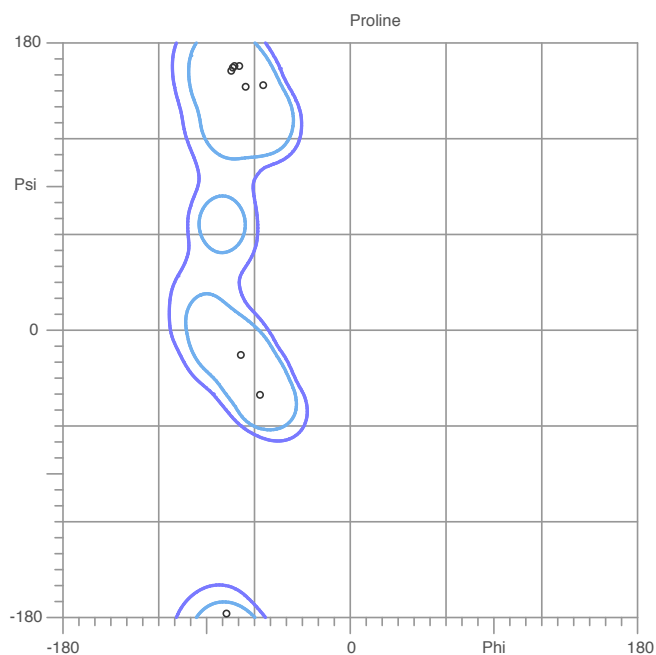
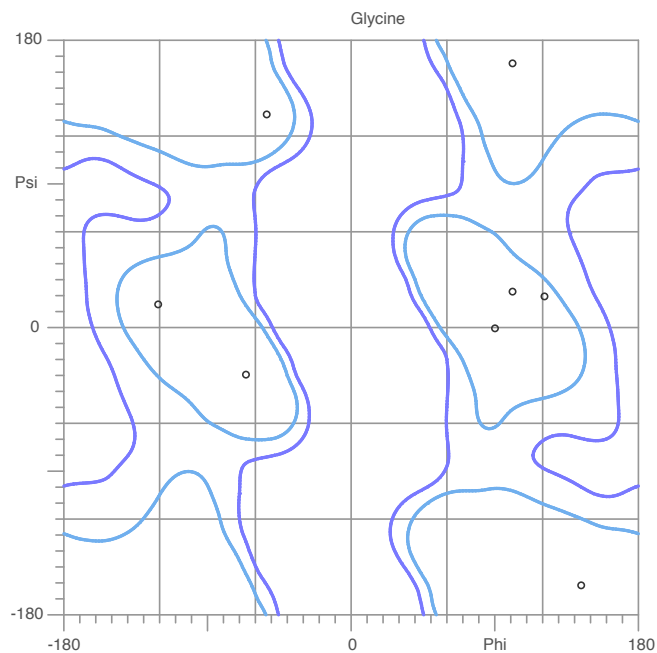
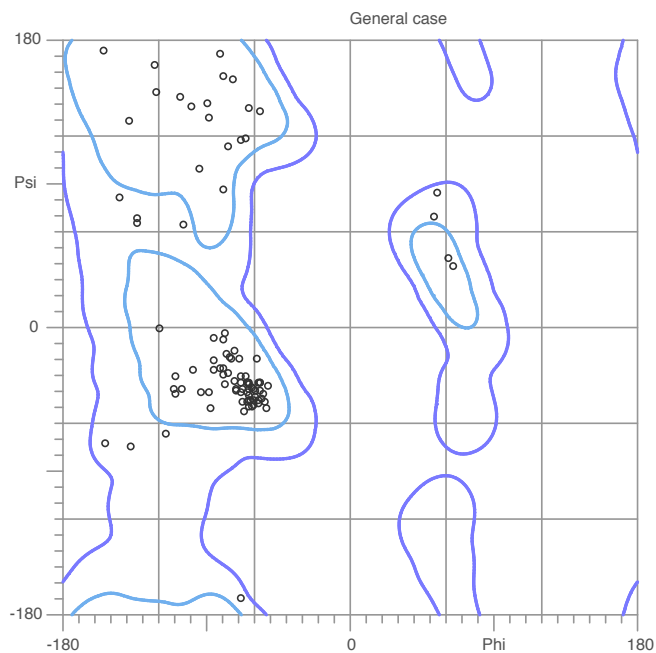


95.0% (113/119) of all residues were in favored (98%) regions.
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 11



89.9% (107/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

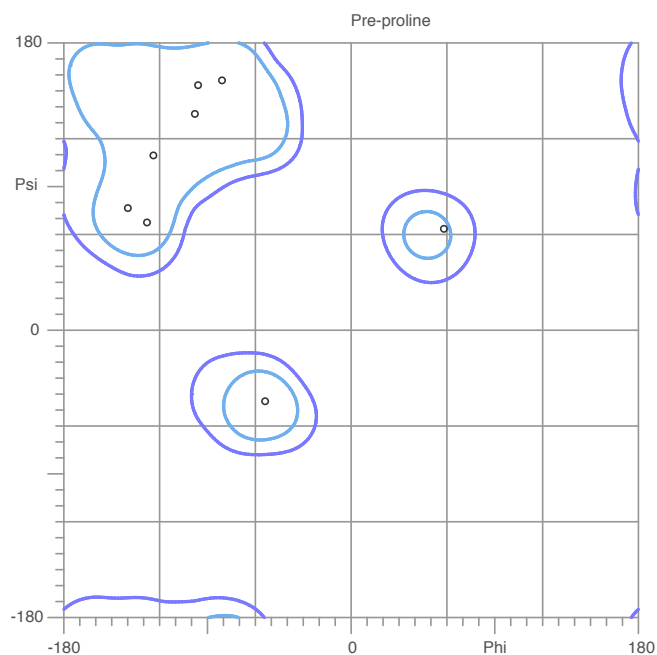
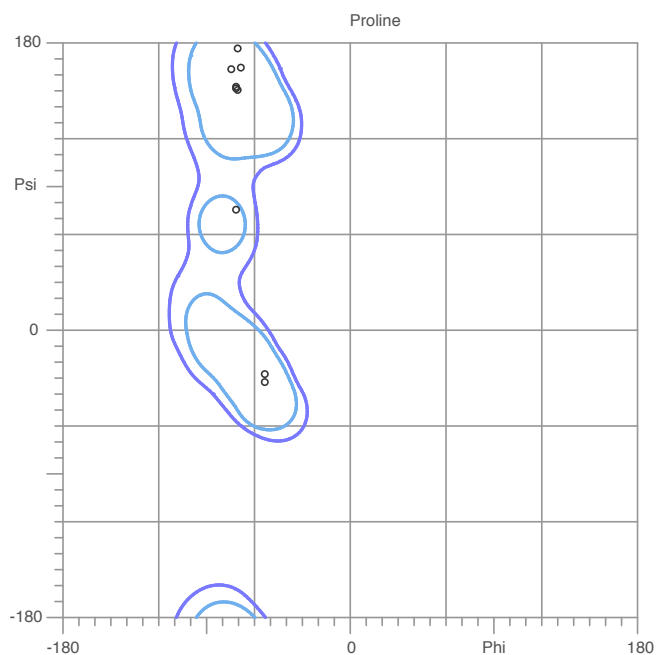
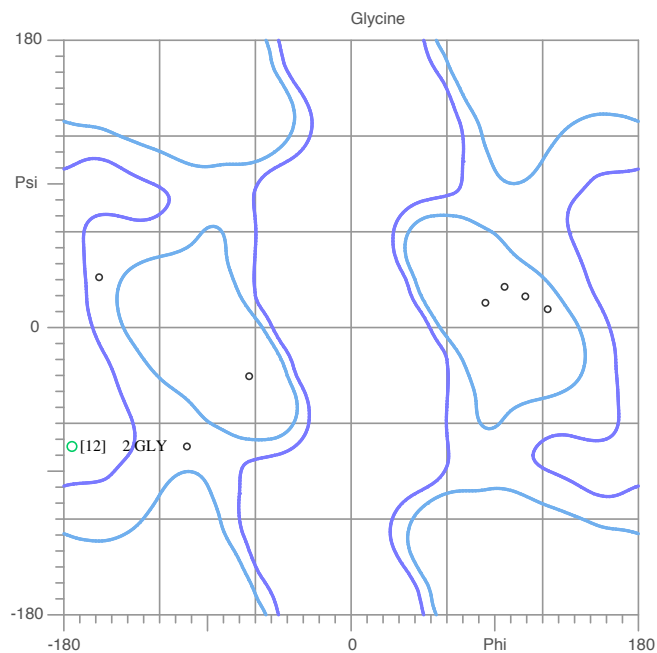
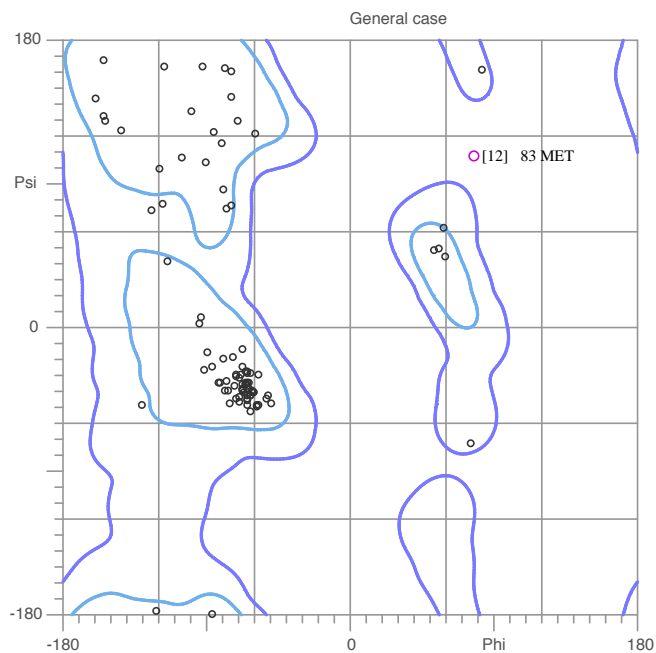
There were 1 outliers (phi, psi):
[11] 104 LEU (69.9, 155.0)

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MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 12

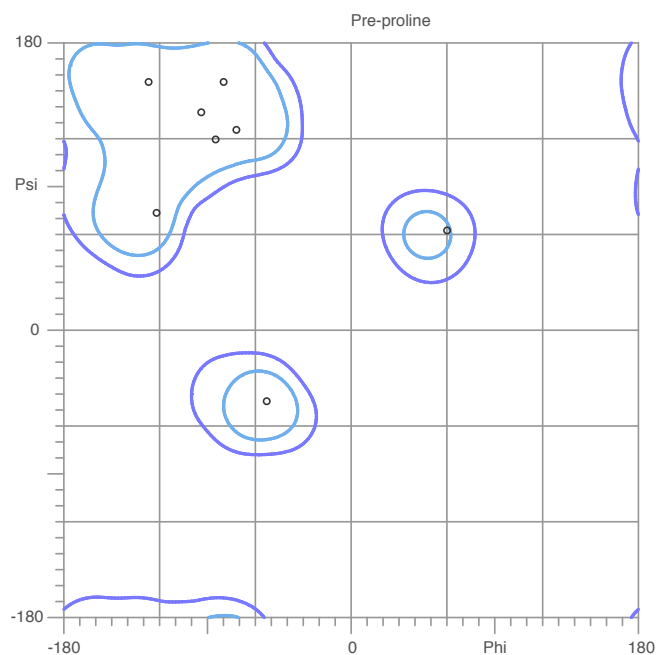
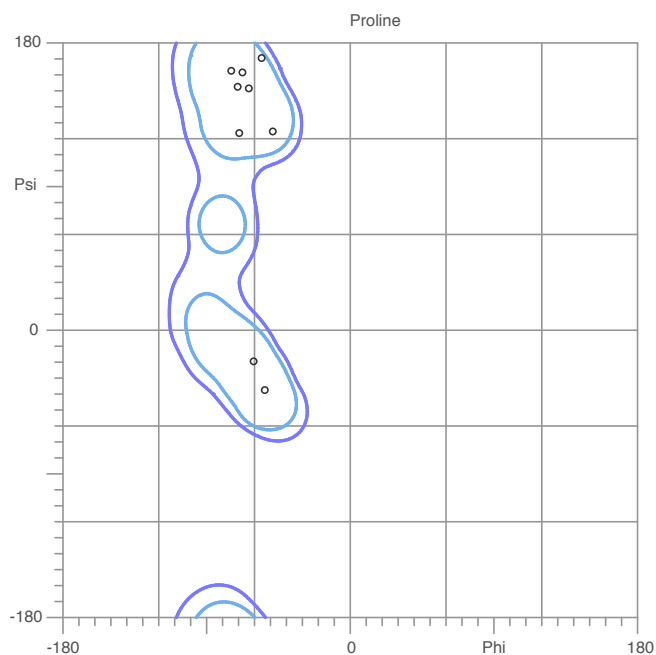
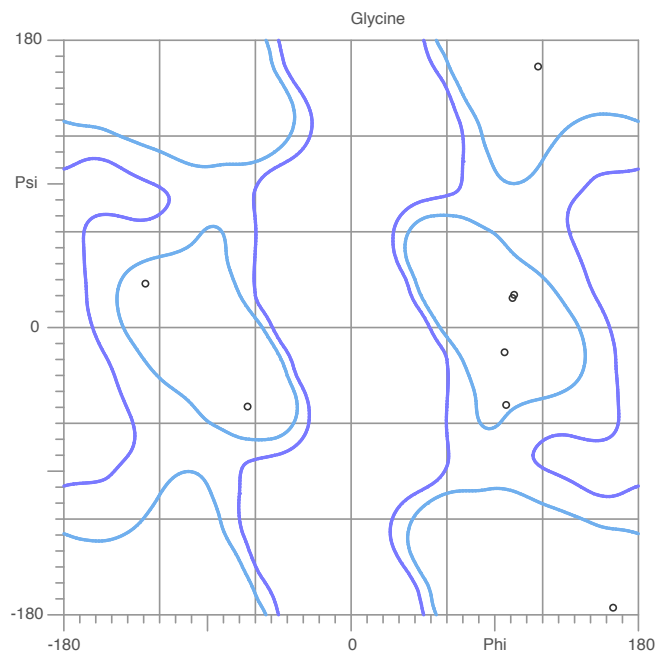
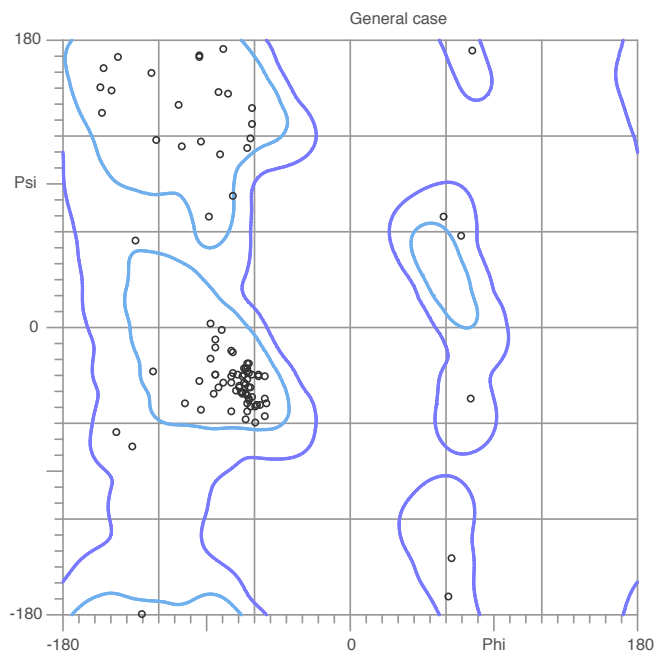


91.6% (109/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 2 GLY (-175.1, -74.9)
[12] 83 MET (77.3, 108.5)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 13

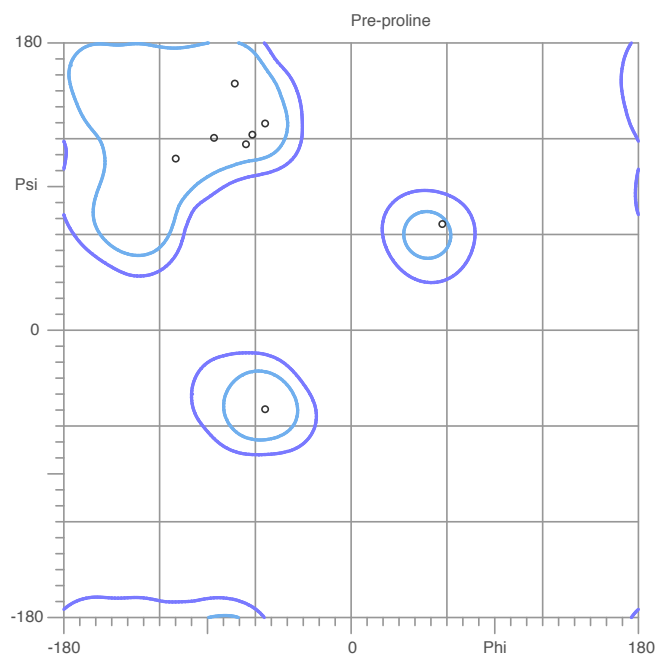
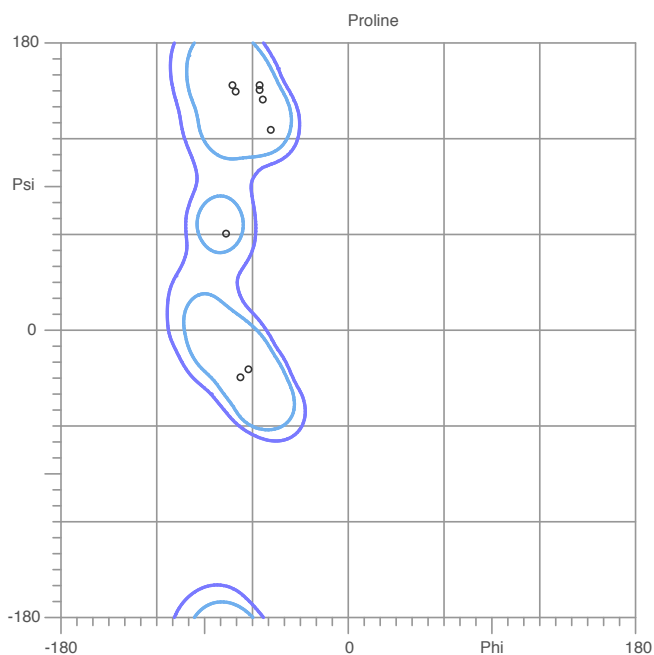
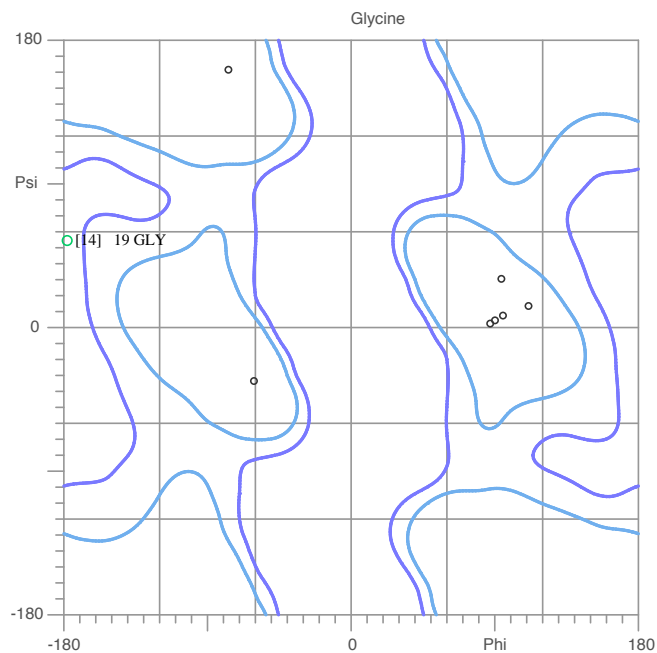
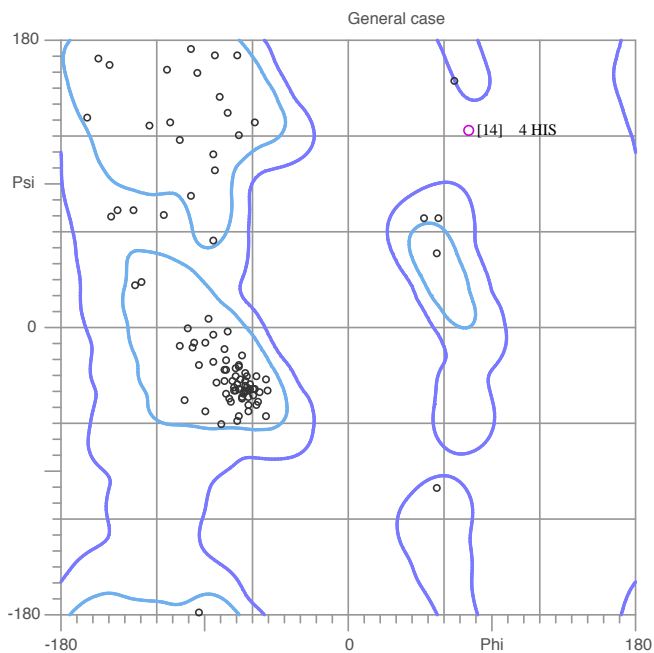


92.4% (110/119) of all residues were in favored (98%) regions.
100.0% (119/119) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 14

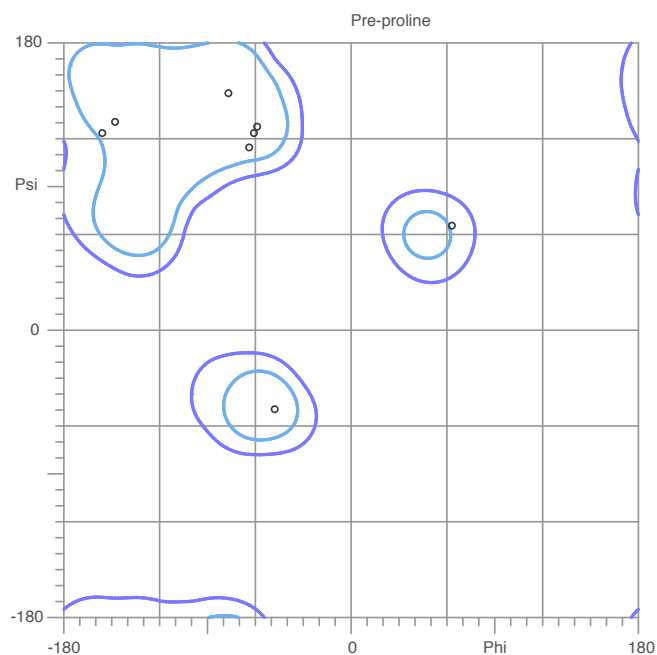
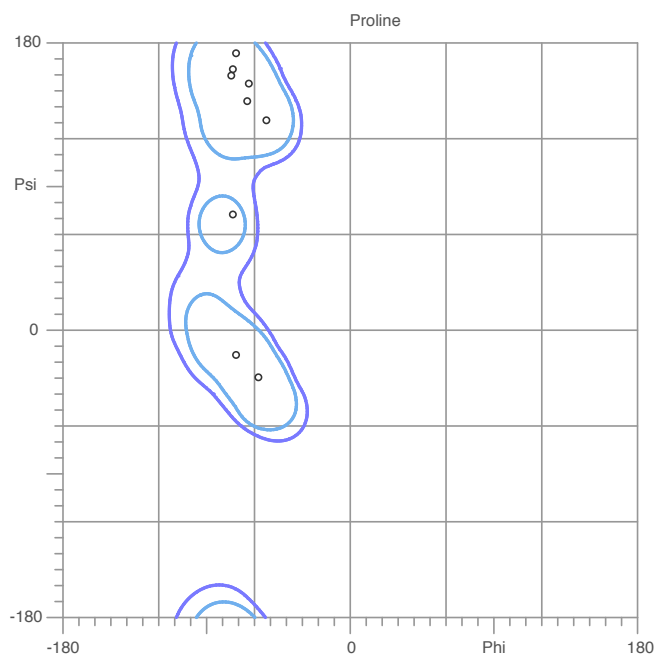
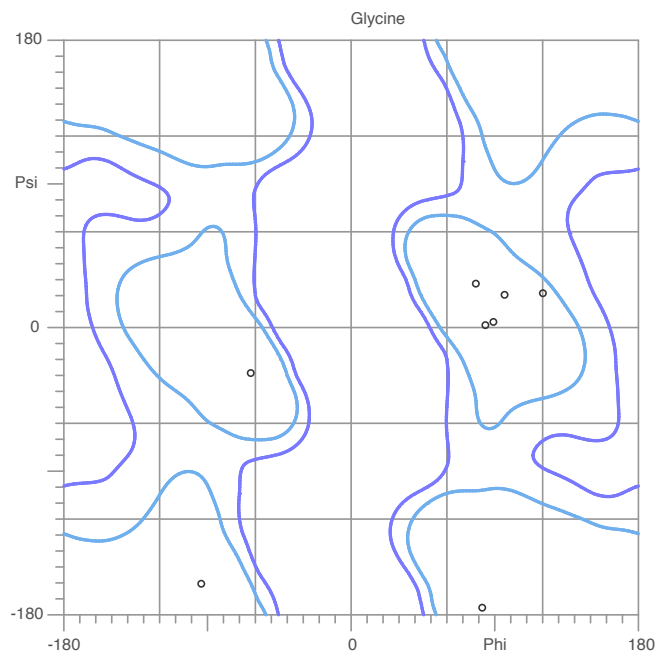
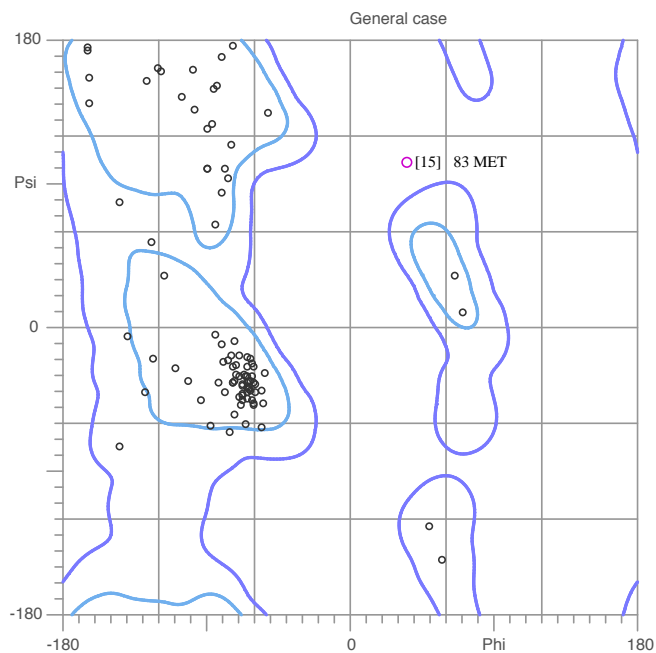


91.6% (109/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[14] 4 HIS (75.1, 125.0)
[14] 19 GLY (-178.2, 55.1)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 15



91.6% (109/119) of all residues were in favored (98%) regions.
99.2% (118/119) of all residues were in allowed (>99.8%) regions.

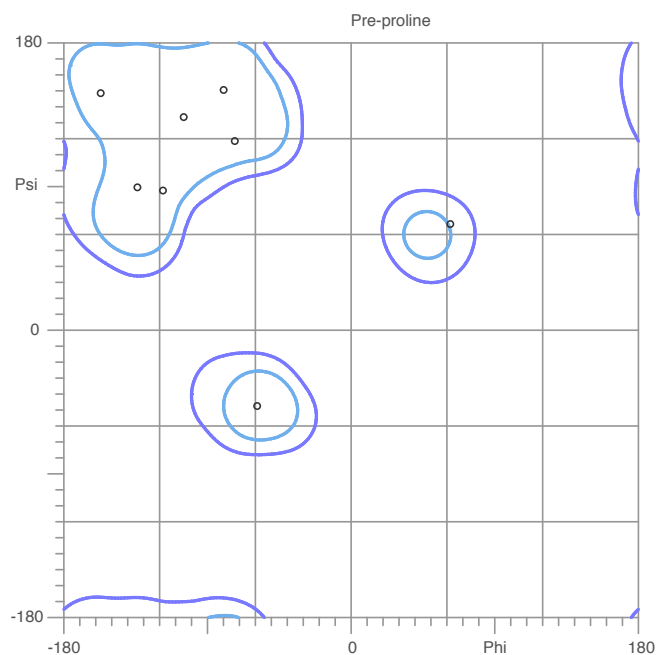
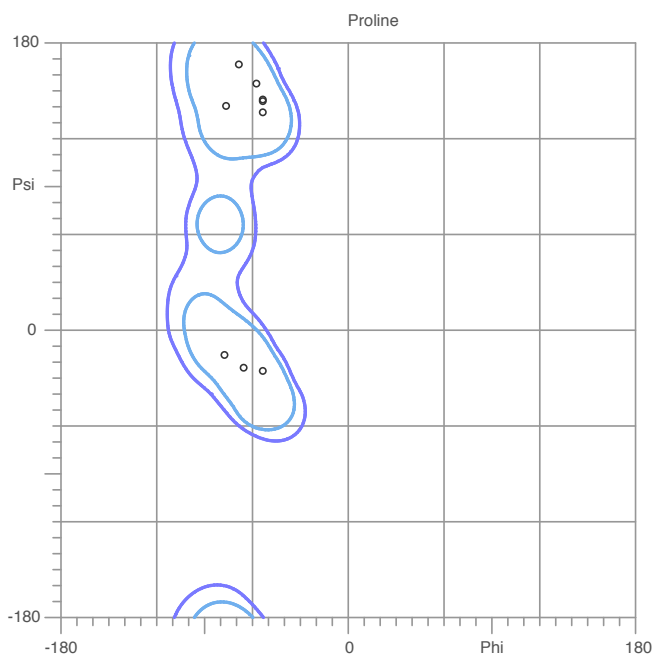
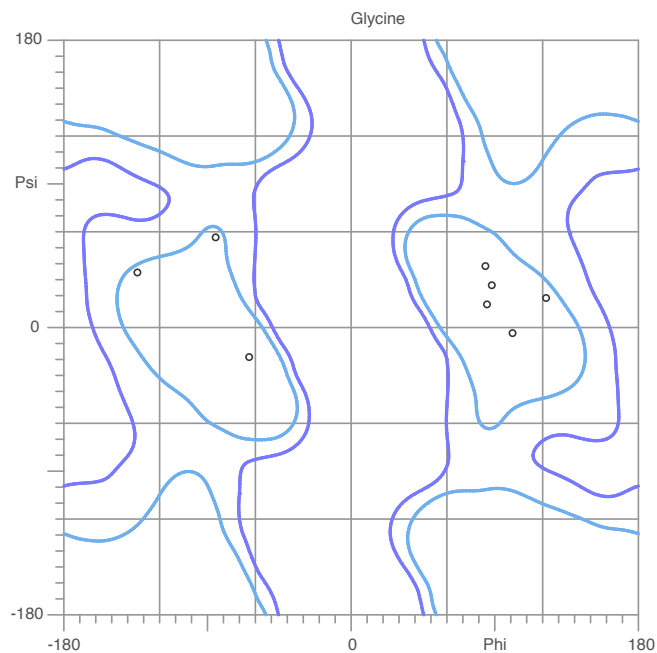
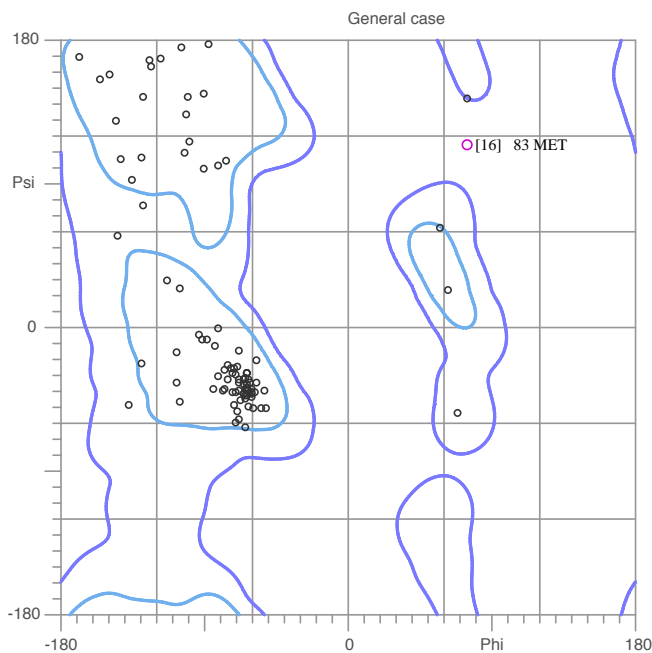
There were 1 outliers (phi, psi):
[15] 83 MET (35.2, 105.0)

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

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 16



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.

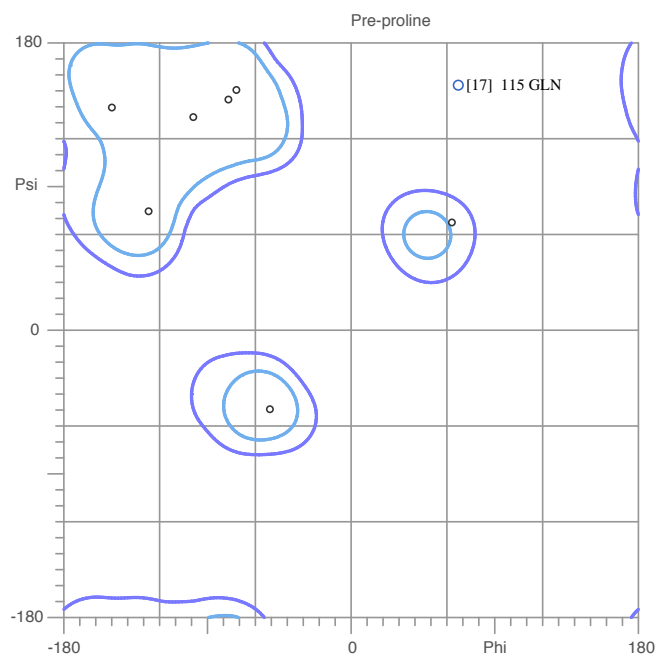
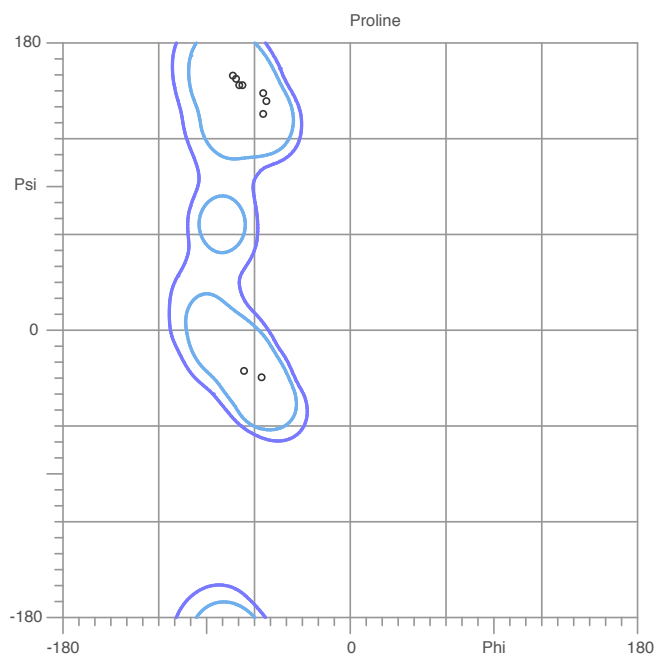
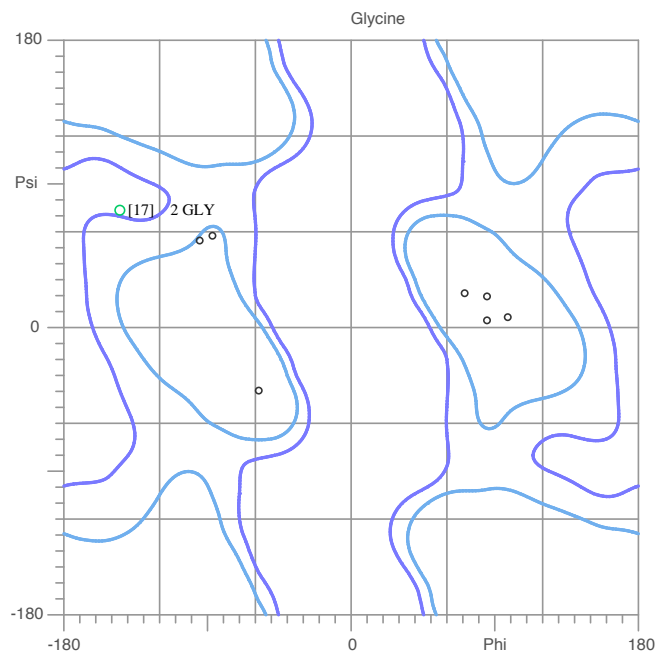
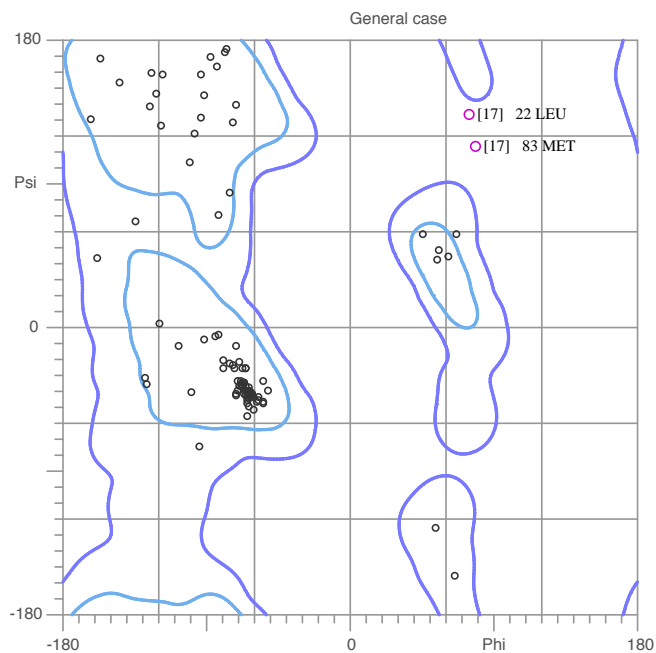
There were 1 outliers (phi, psi):
[16] 83 MET (74.9, 115.0)

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MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 17



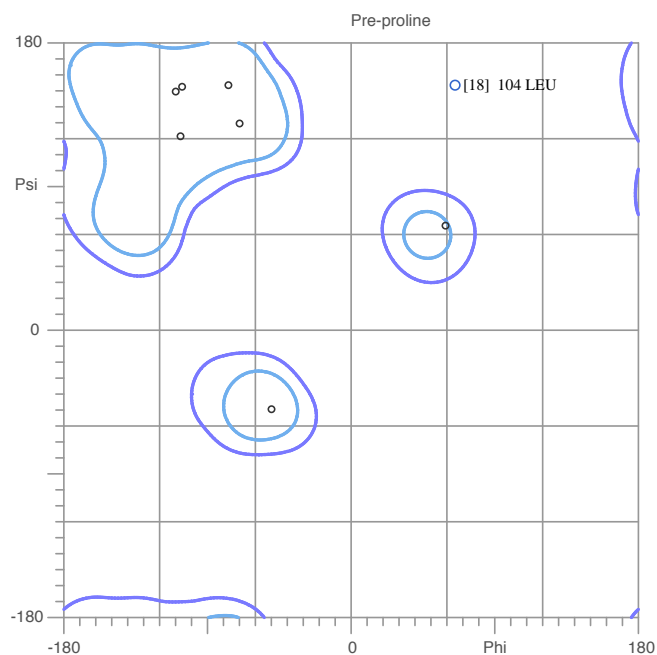
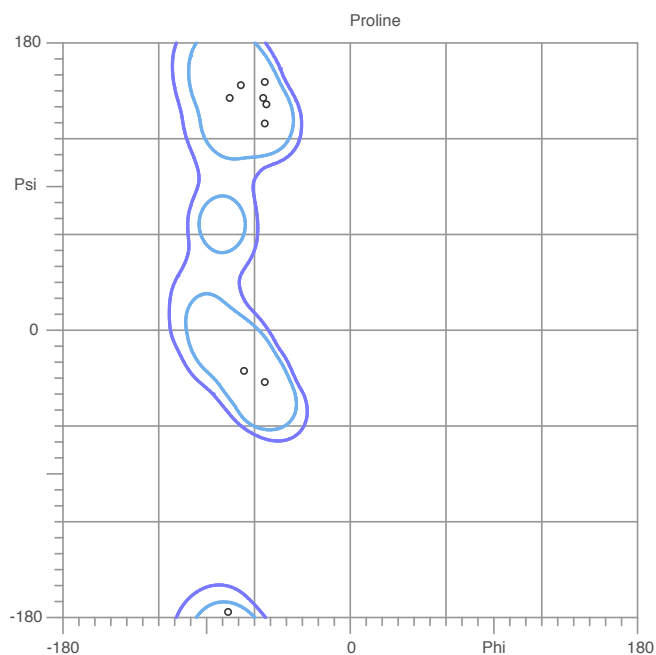
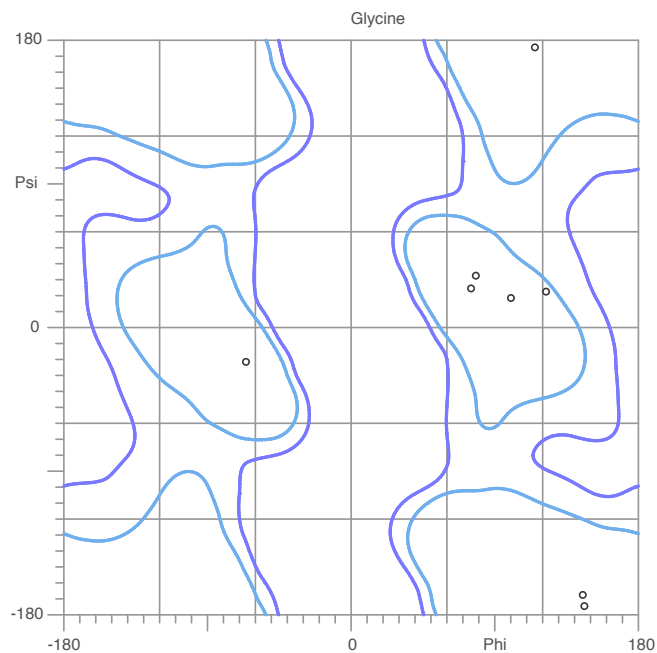
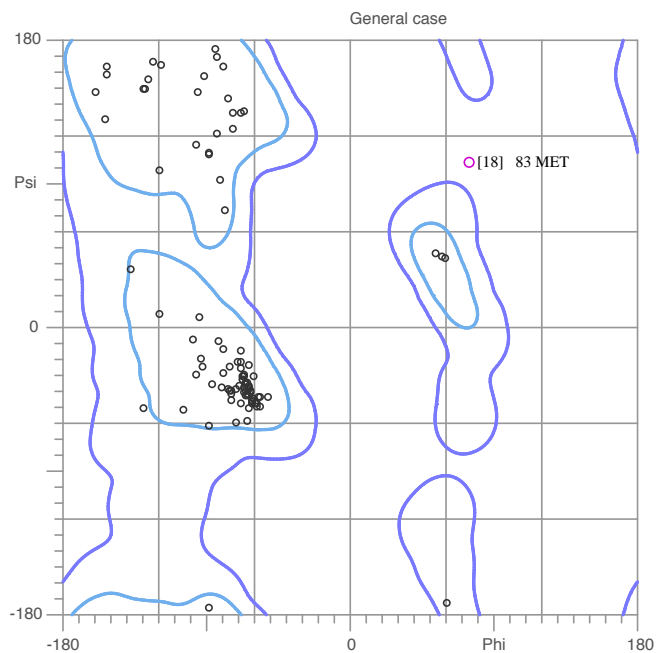
90.8% (108/119) of all residues were in favored (98%) regions.
96.6% (115/119) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [17] 2 GLY (-145.0, 75.0)
- [17] 22 LEU (74.8, 134.5)
- [17] 83 MET (78.1, 114.8)
- [17] 115 GLN (67.6, 155.0)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 18

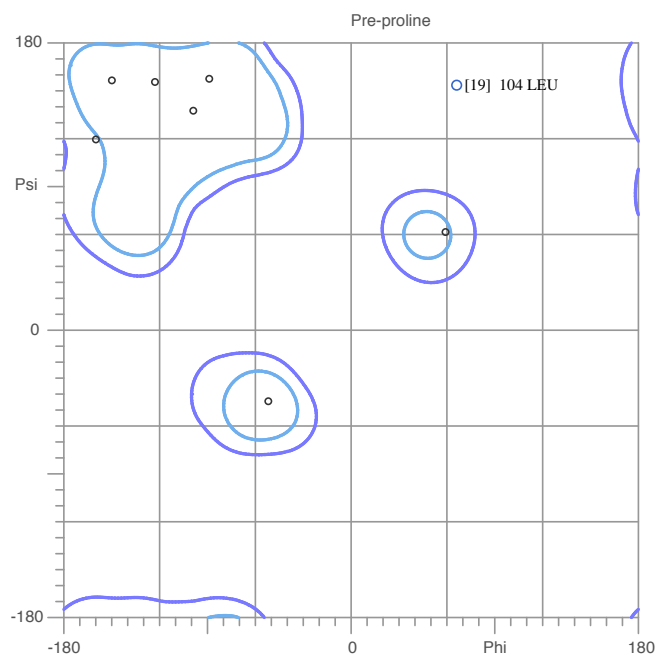
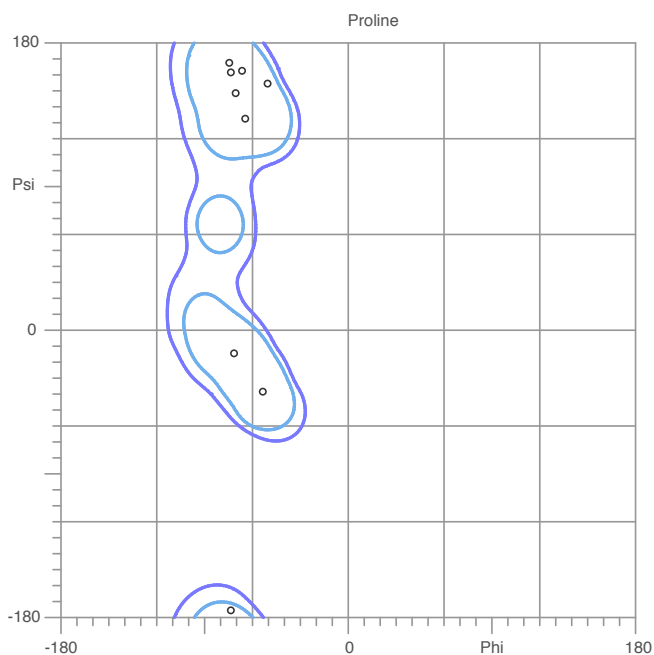
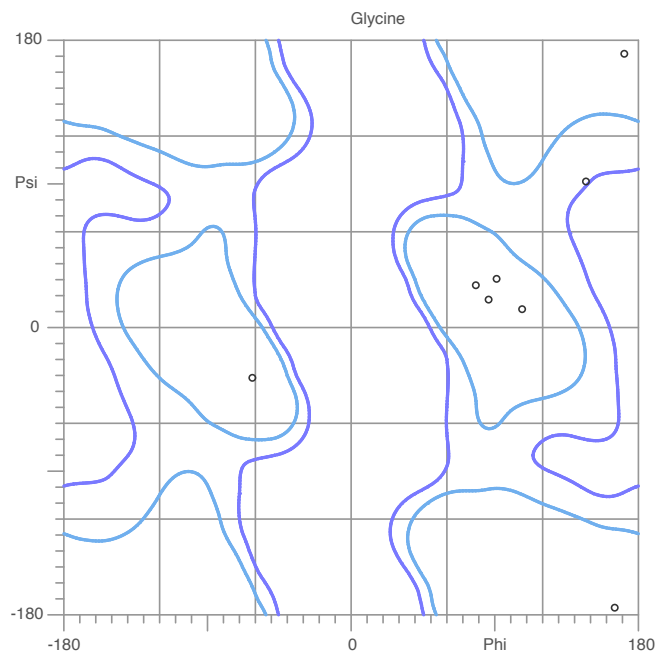
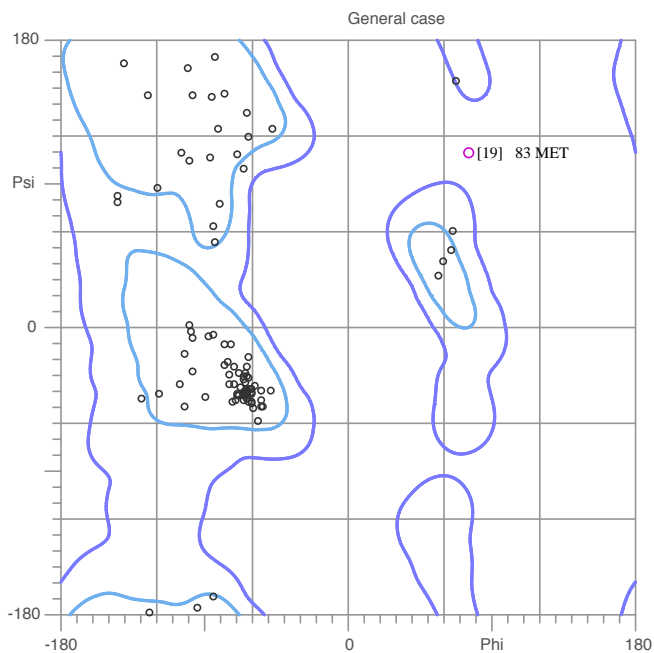


95.8% (114/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 83 MET (74.9, 104.9)
[18] 104 LEU (65.8, 155.0)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 19

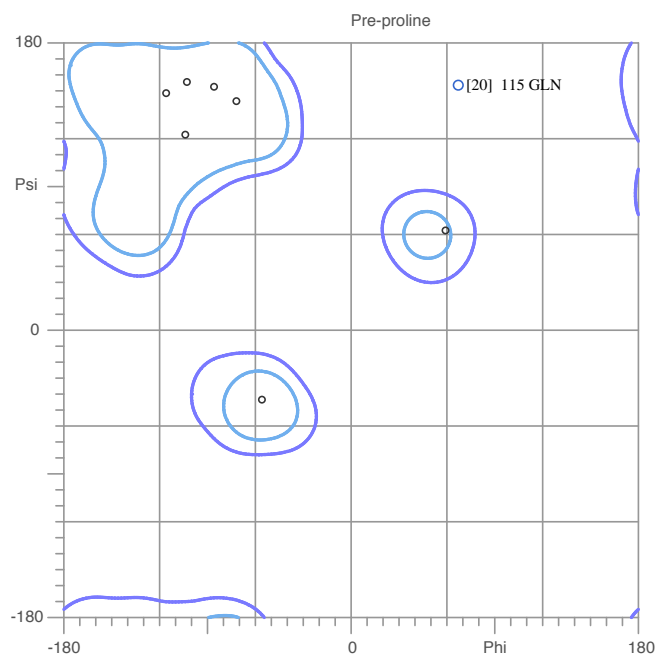
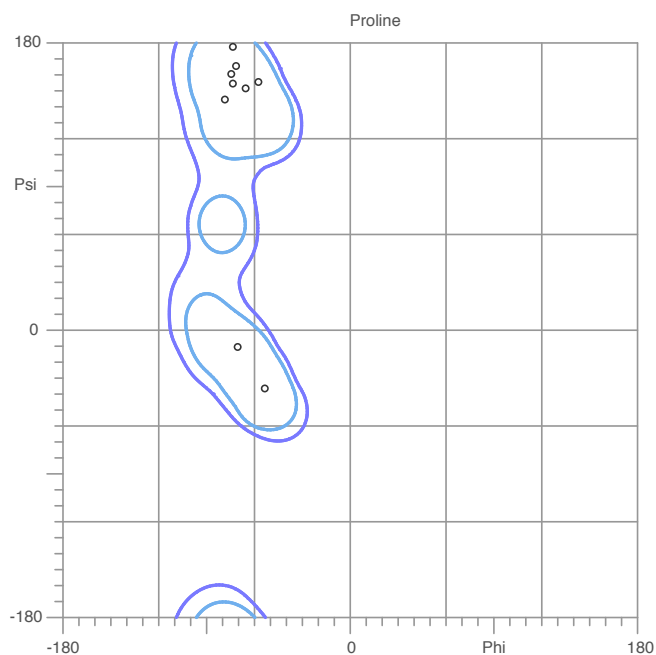
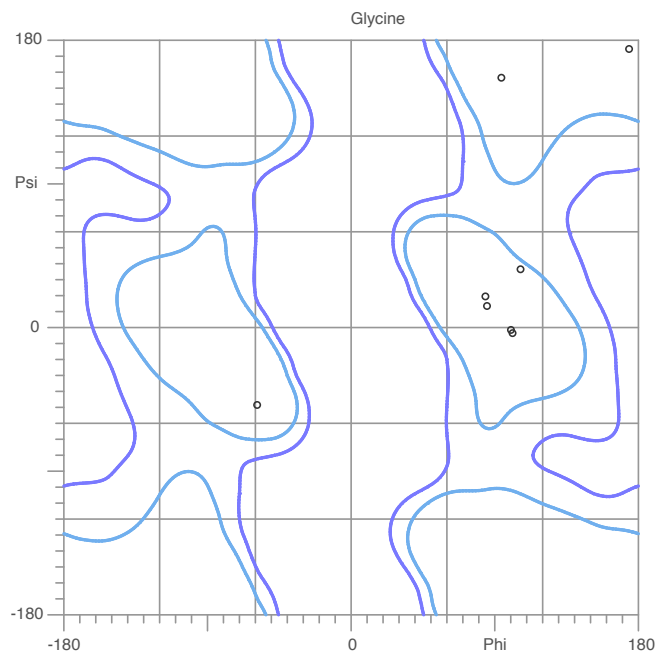
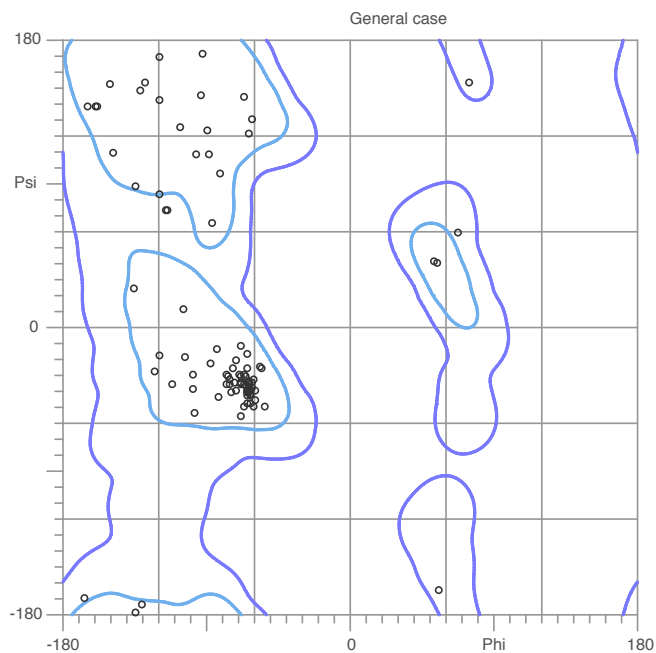


91.6% (109/119) of all residues were in favored (98%) regions.
98.3% (117/119) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 83 MET (75.1, 110.9)
[19] 104 LEU (66.2, 154.7)

MolProbity Ramachandran analysis

HR3646E_R3_em_bcr3.pdb, model 20



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):
[20] 115 GLN (67.8, 155.0)

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