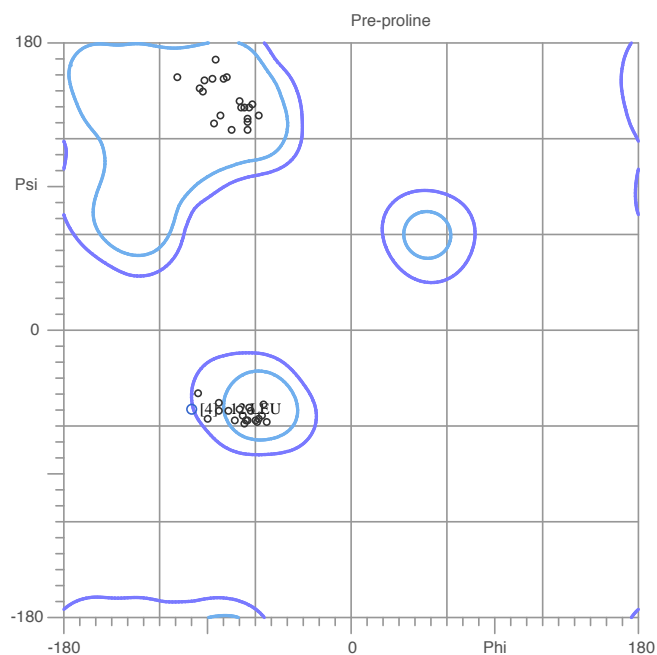
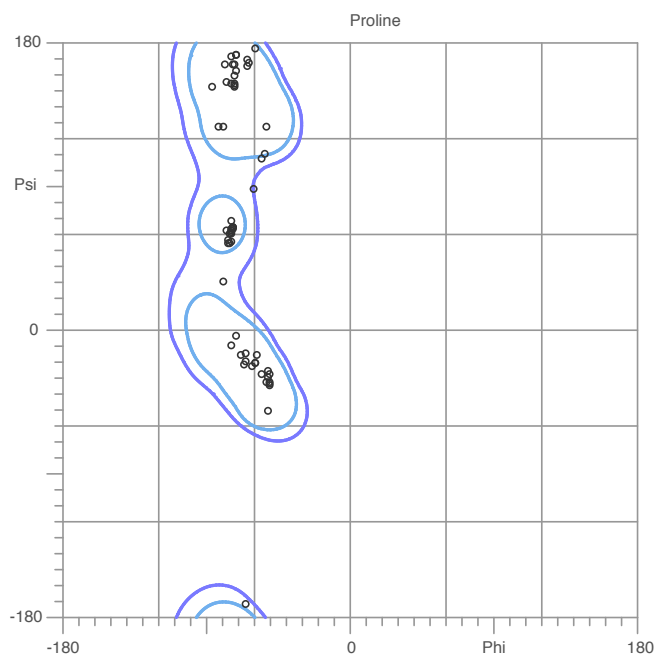
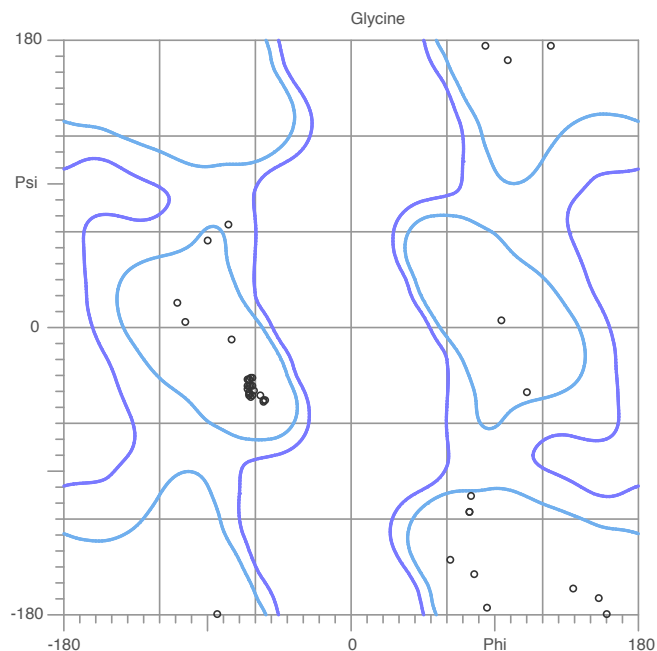
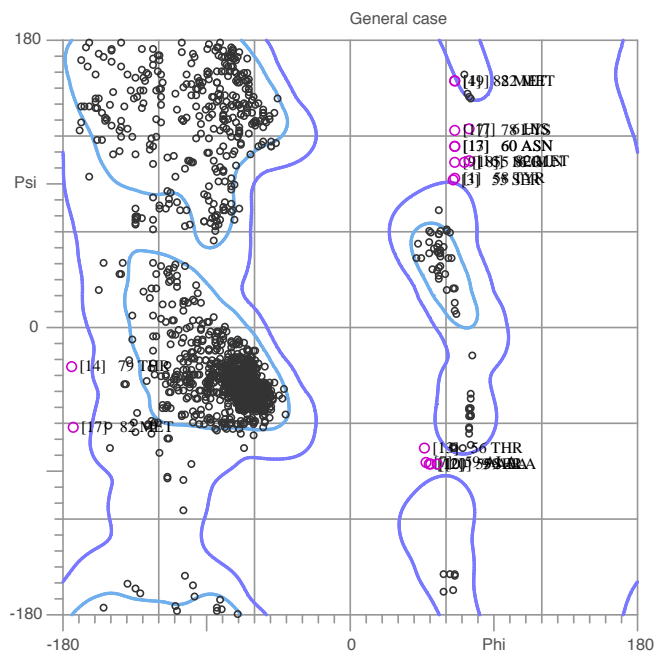


MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, all models



91.8% (1487/1620) of all residues were in favored (98%) regions.
98.8% (1601/1620) of all residues were in allowed (>99.8%) regions.

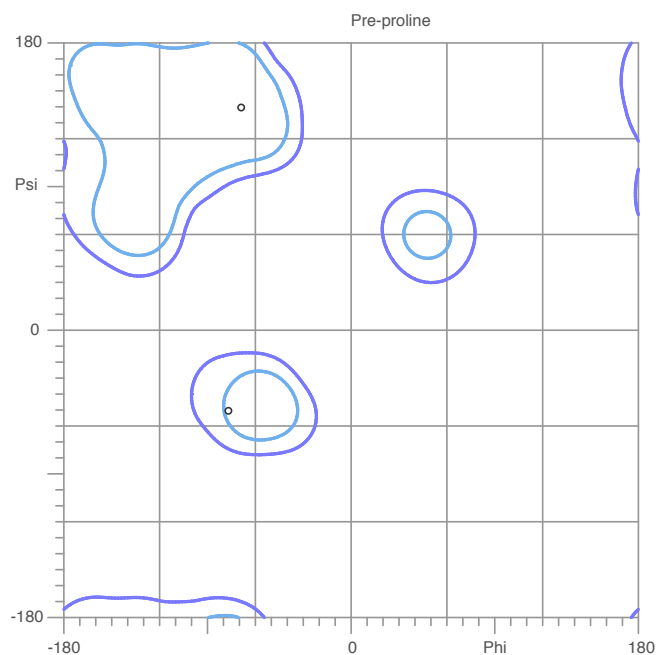
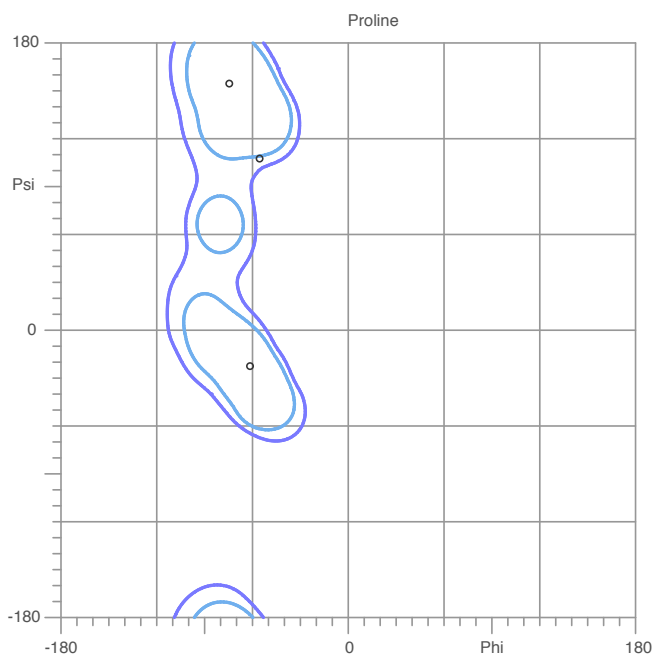
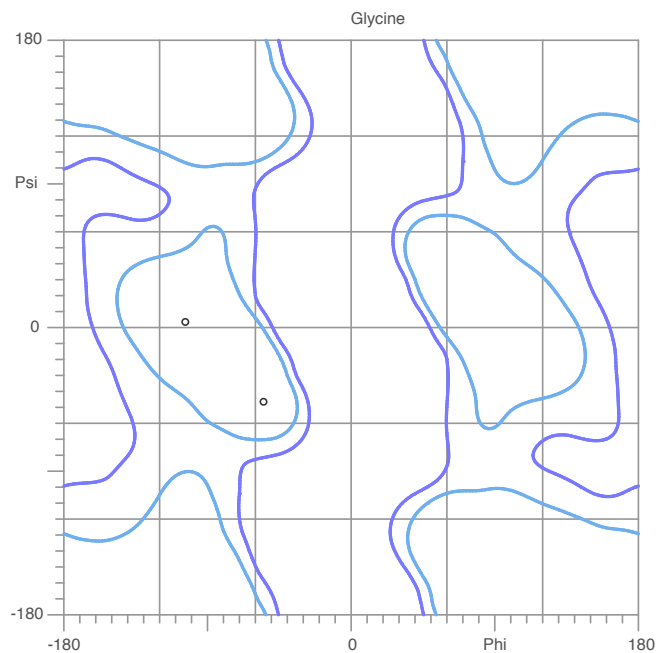
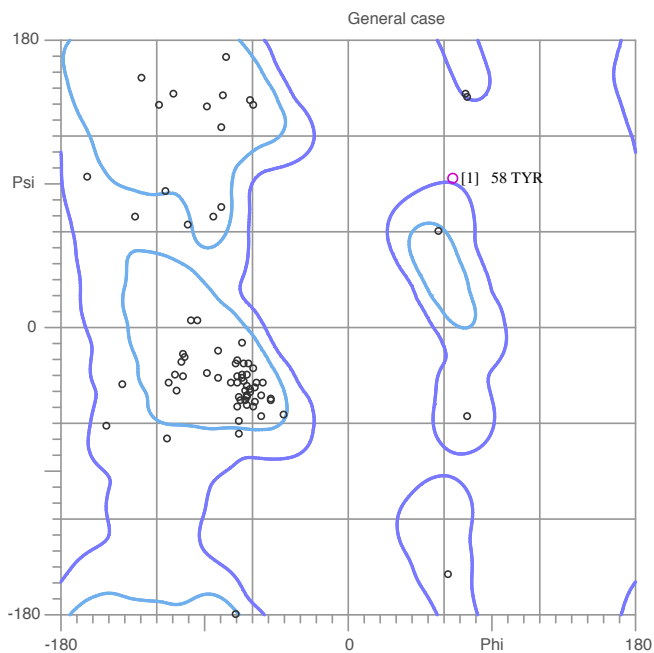
There were 19 outliers (phi, psi):

- [1] 58 TYR (65.1, 95.0)
- [3] 55 SER (64.6, 93.6)
- [4] 12 LEU (-100.4, -49.1)
- [4] 82 MET (65.0, 155.0)
- [7] 6 HIS (75.0, 125.1)
- [7] 59 ALA (47.3, -84.9)
- [9] 55 SER (65.0, 104.2)

- [10] 9 SER (50.6, -85.3)
- [12] 59 ALA (49.4, -85.0)
- [13] 56 THR (47.0, -75.0)
- [13] 60 ASN (65.1, 115.0)
- [14] 79 THR (75.0, 105.2)
- [16] 82 MET (75.0, 105.2)
- [17] 60 ASN (65.0, 114.9)
- [17] 78 LYS (65.0, 125.0)
- [17] 82 MET (-174.9, -62.7)
- [18] 16 GLN (71.8, 104.6)
- [19] 82 MET (65.1, 155.2)
- [20] 59 ALA (54.8, -85.0)

MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 1



84.0% (68/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

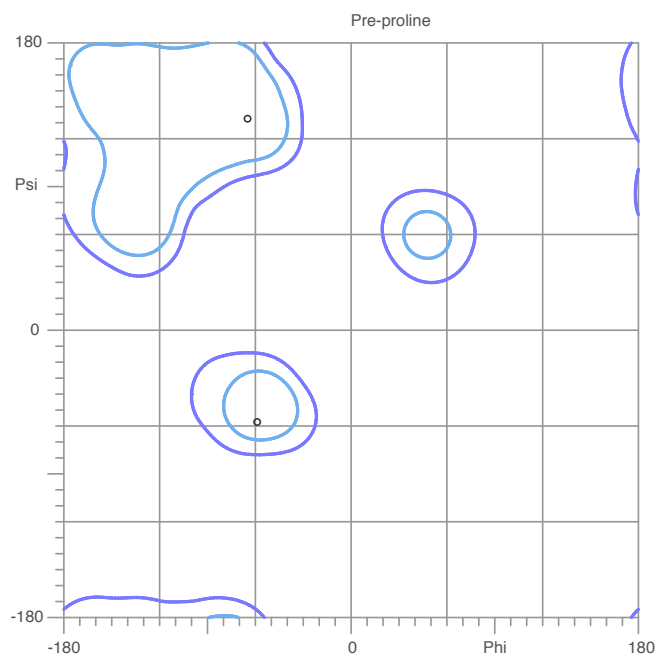
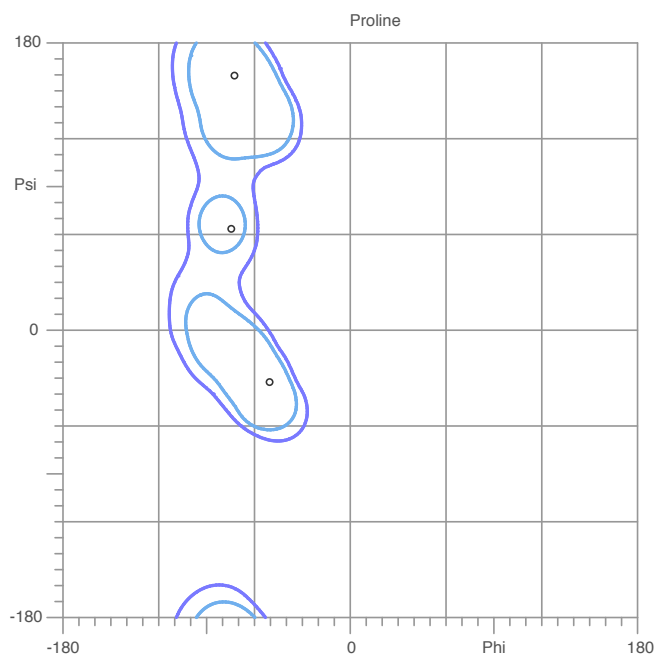
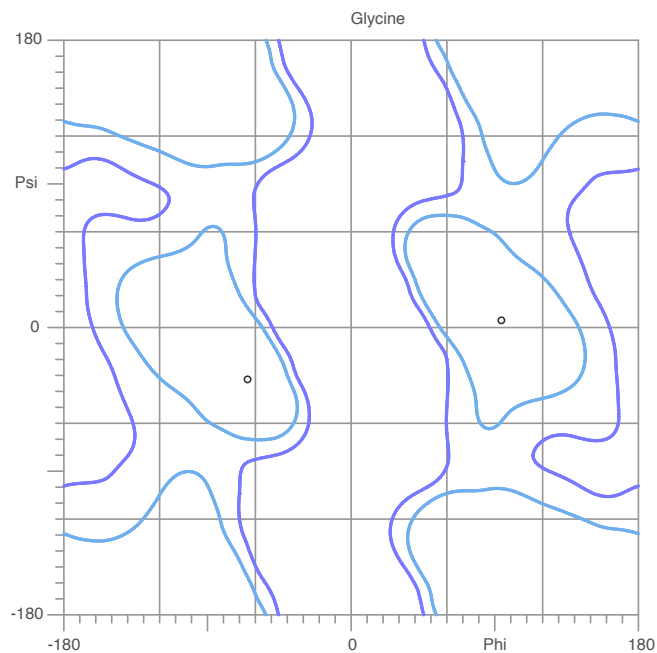
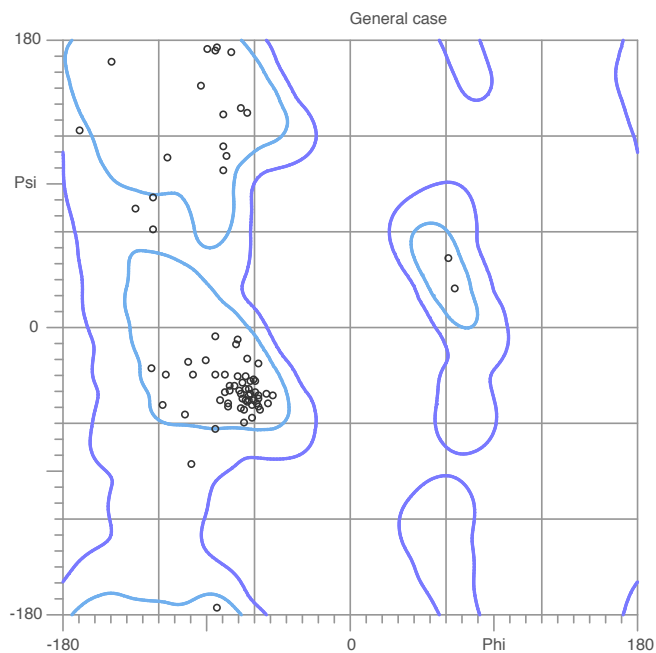
There were 1 outliers (phi, psi):
[1] 58 TYR (65.1, 95.0)

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 2



92.6% (75/81) of all residues were in favored (98%) regions.
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

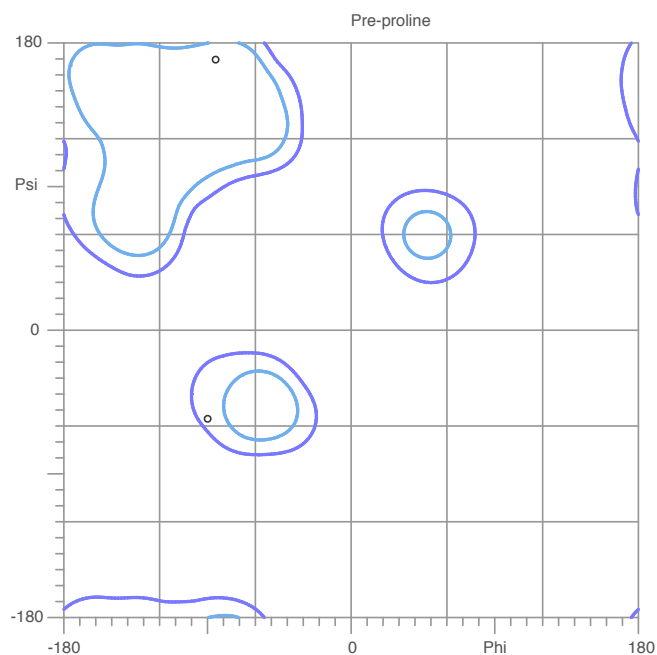
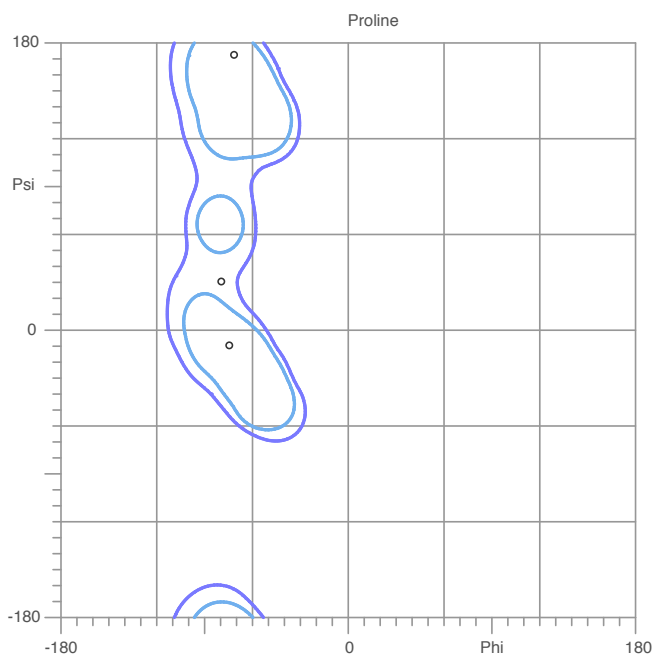
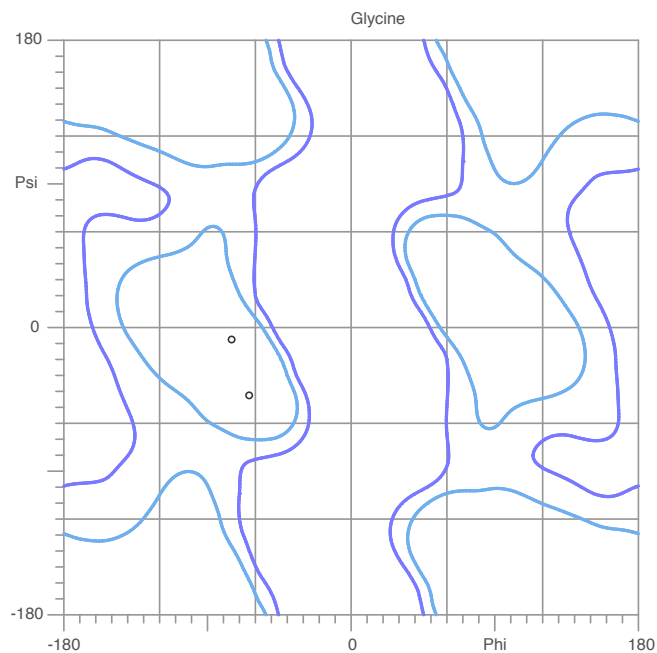
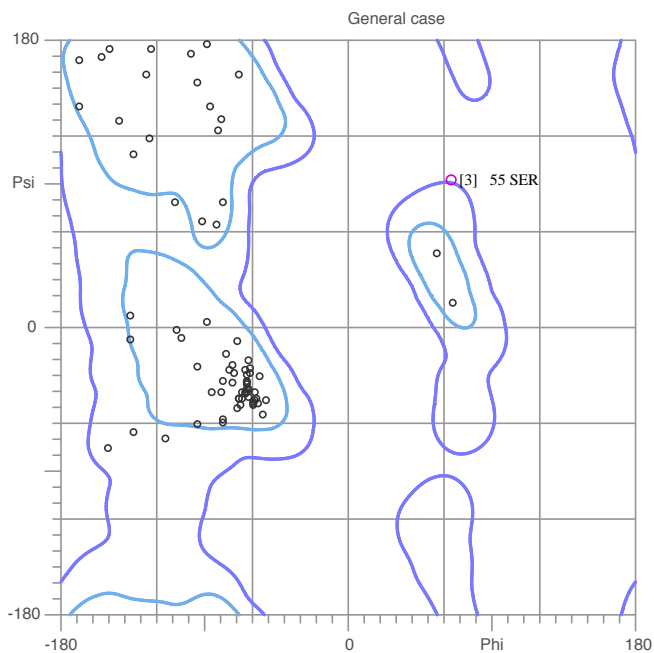
There were no outliers.

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

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

MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 3

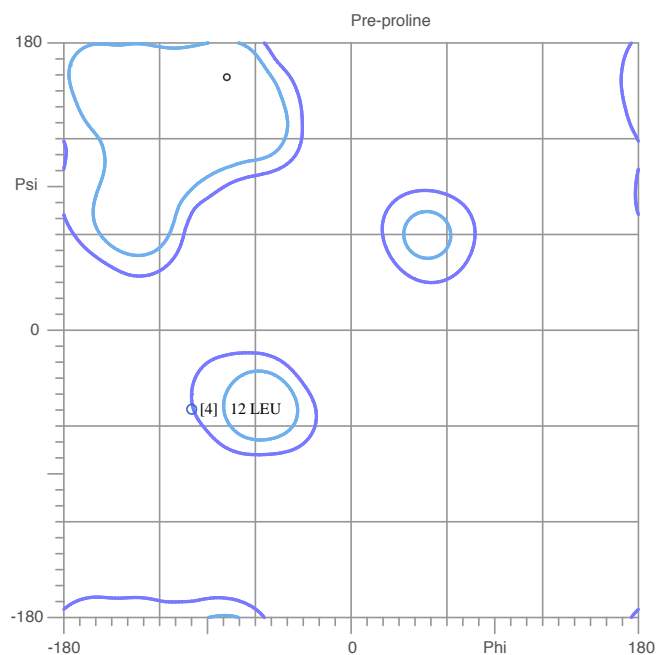
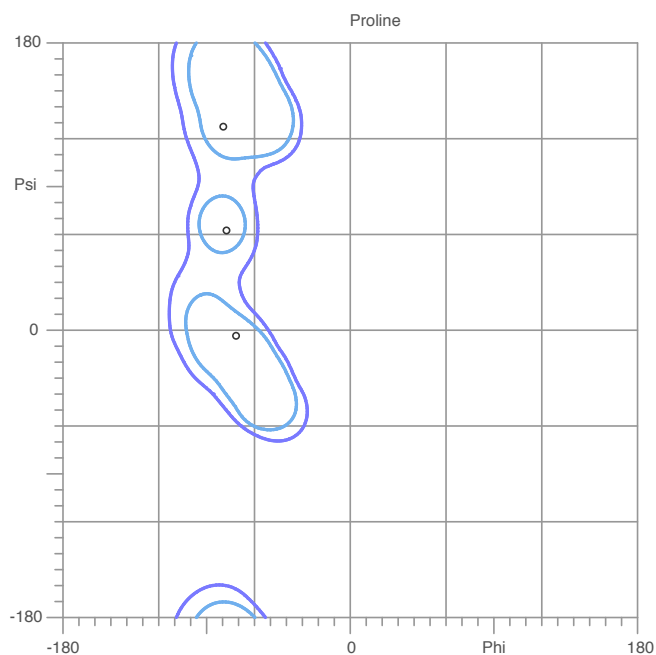
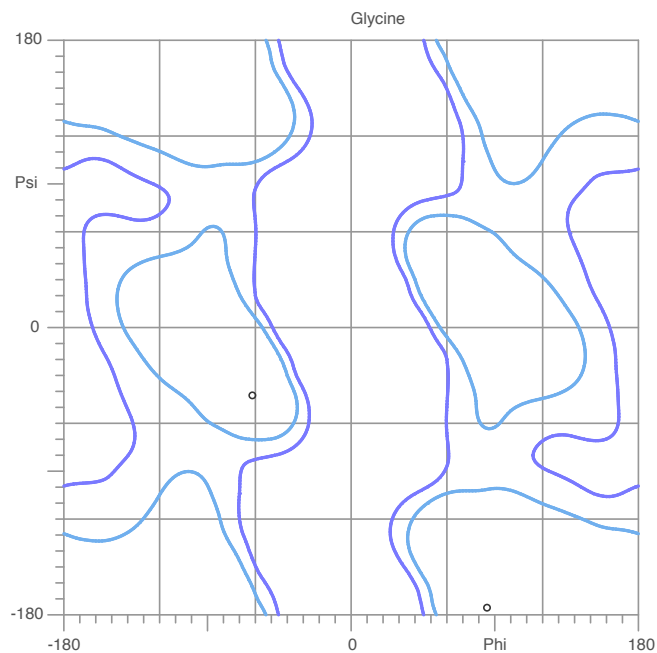
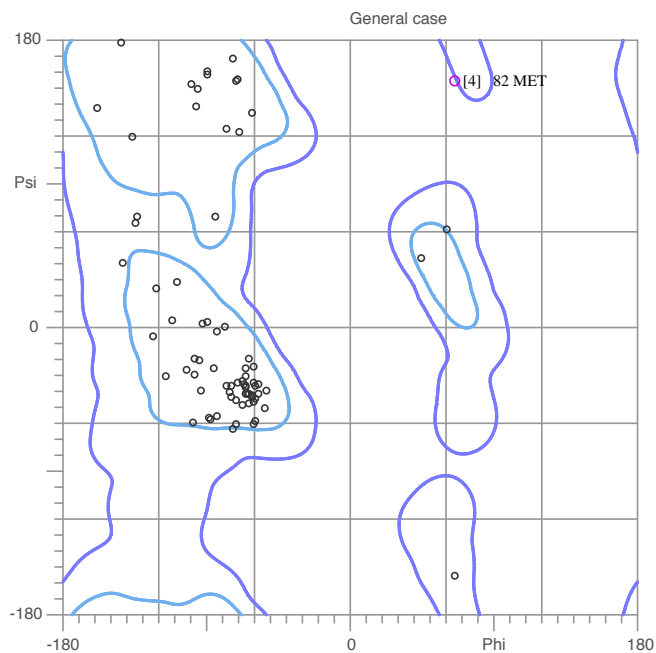


90.1% (73/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 55 SER (64.6, 93.6)

MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 4



90.1% (73/81) of all residues were in favored (98%) regions.
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

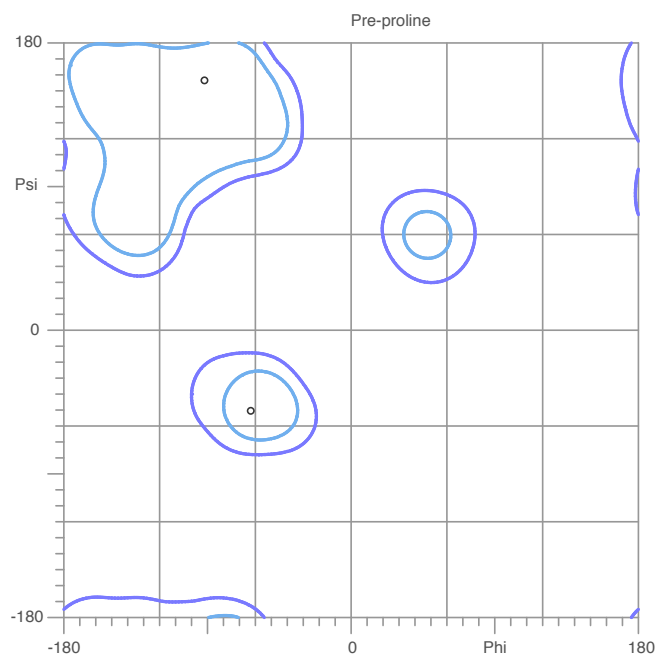
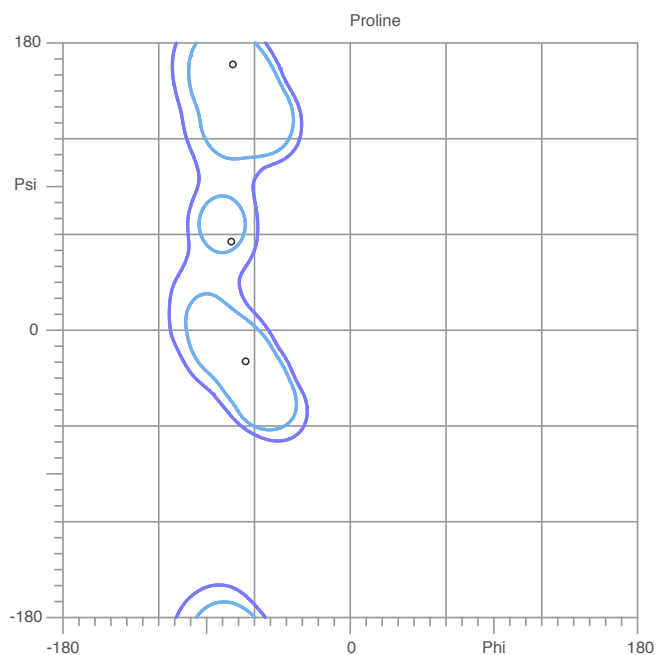
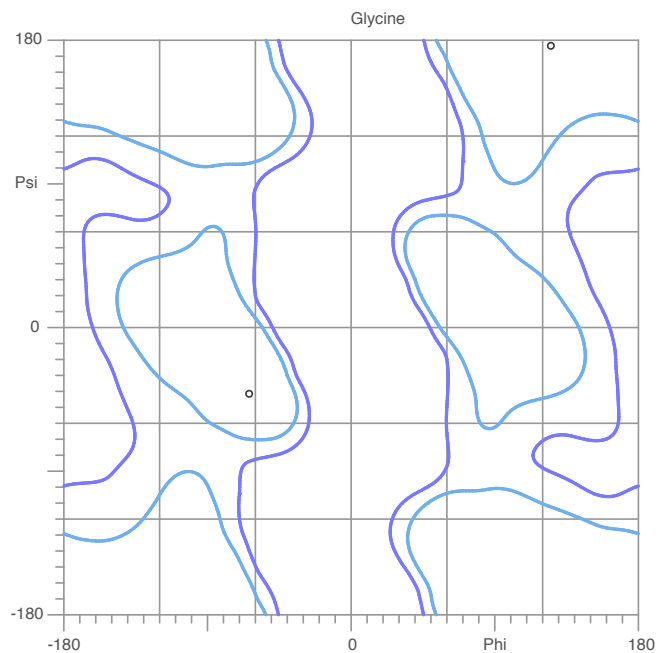
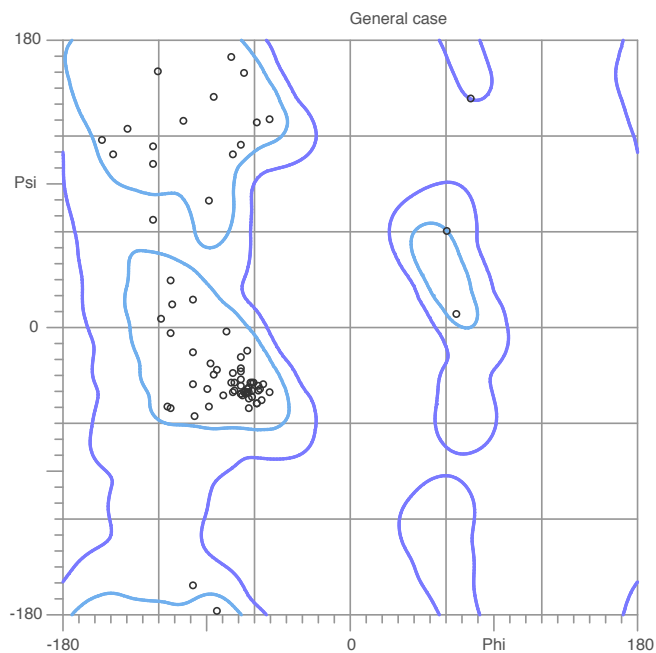
There were 2 outliers (phi, psi):

[4] 12 LEU (-100.4, -49.1)

[4] 82 MET (65.0, 155.0)

MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 5



95.1% (77/81) of all residues were in favored (98%) regions.
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

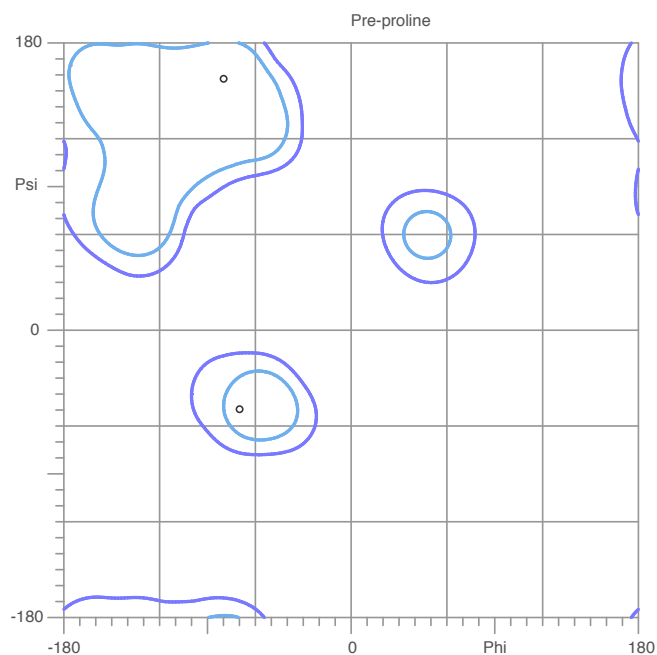
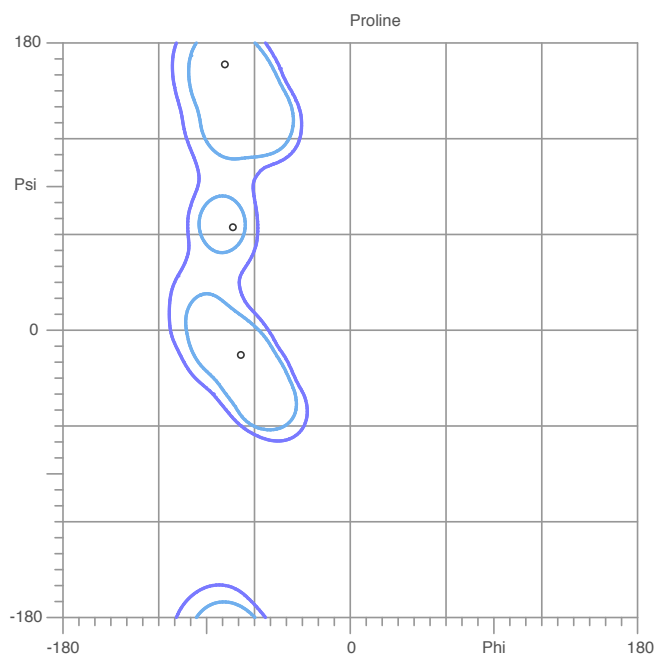
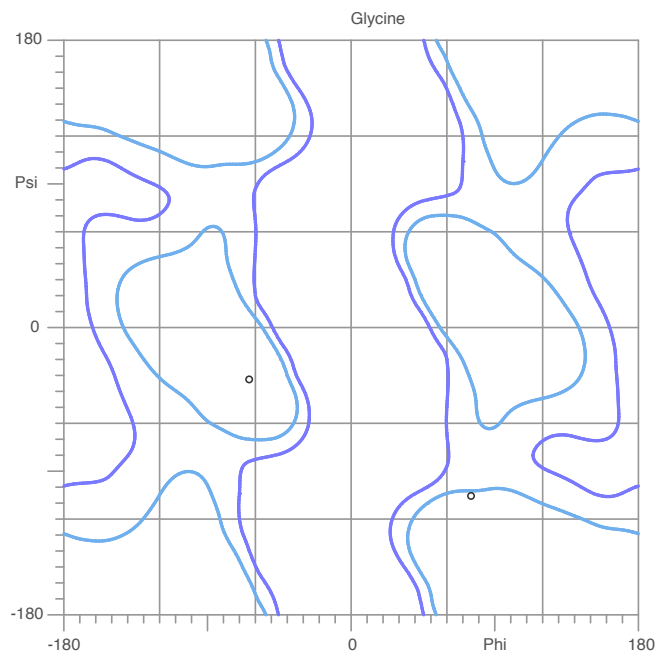
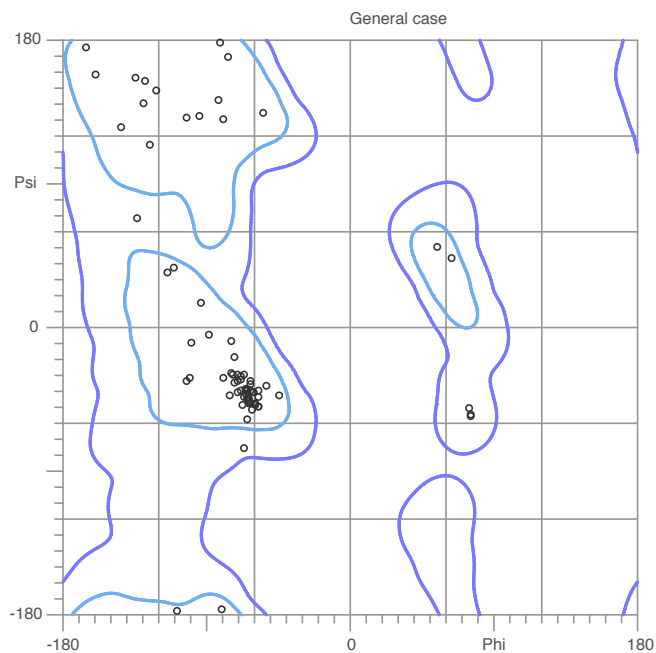
There were no outliers.

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

MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 6



93.8% (76/81) of all residues were in favored (98%) regions.
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

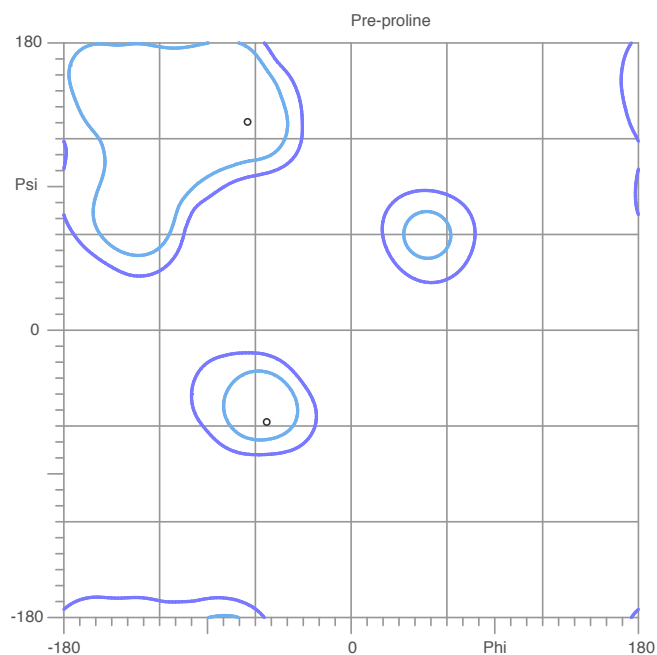
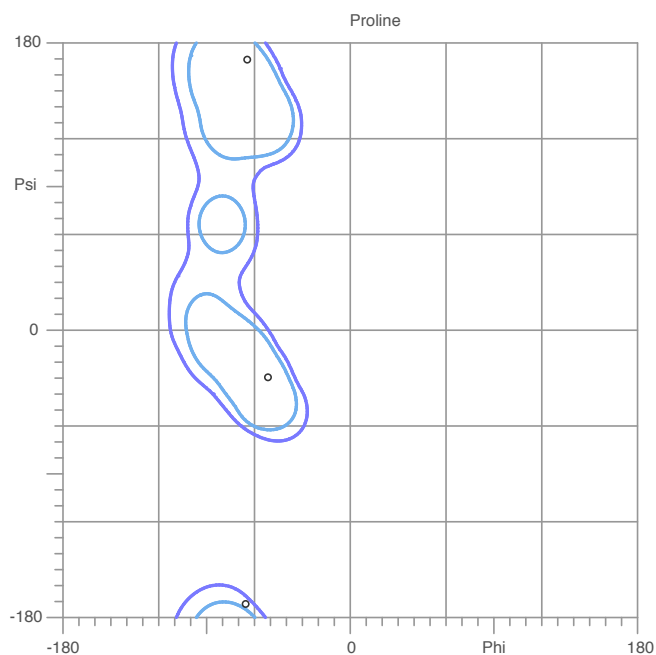
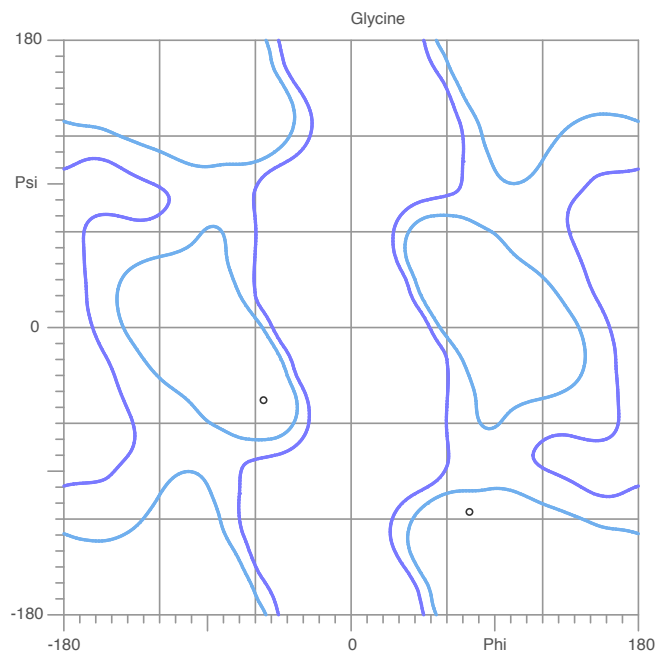
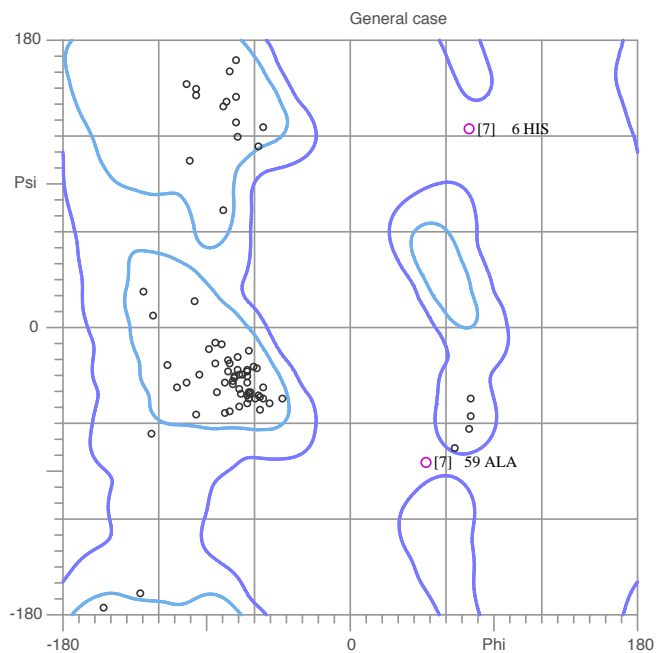
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 7



88.9% (72/81) of all residues were in favored (98%) regions.
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

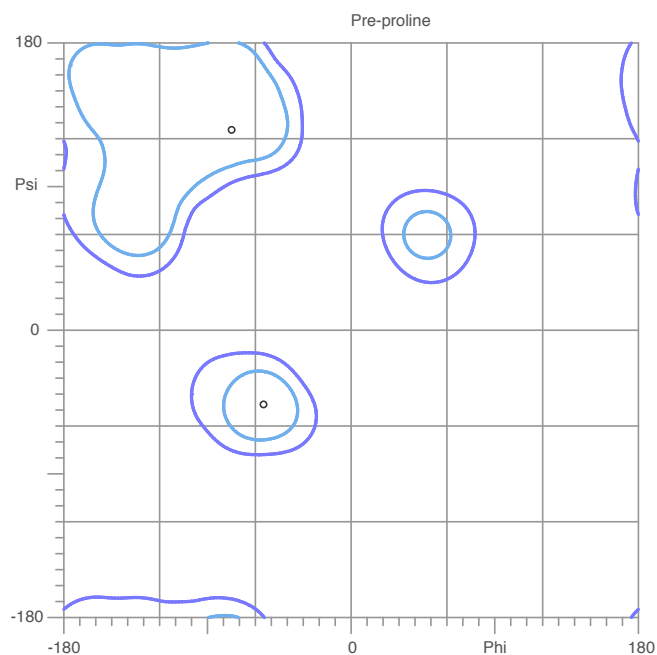
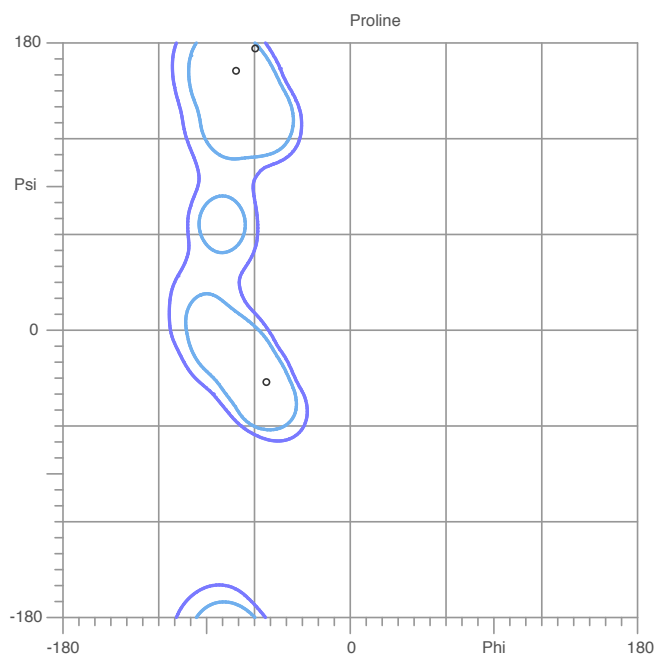
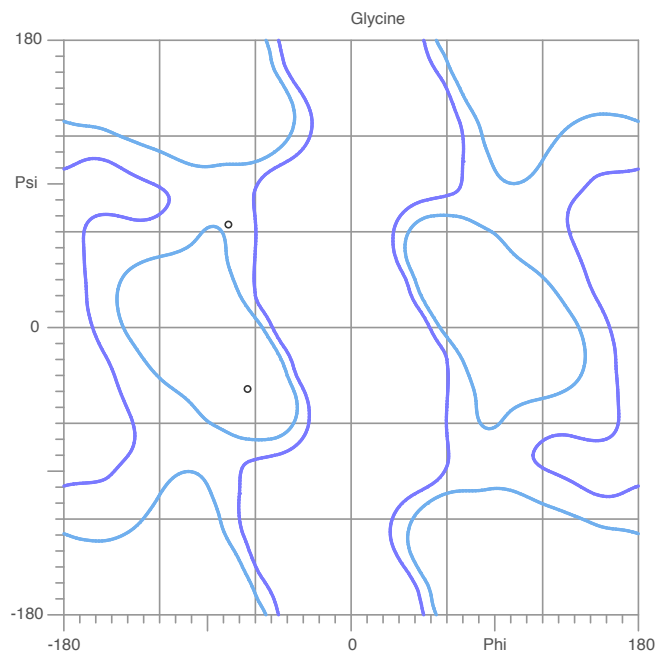
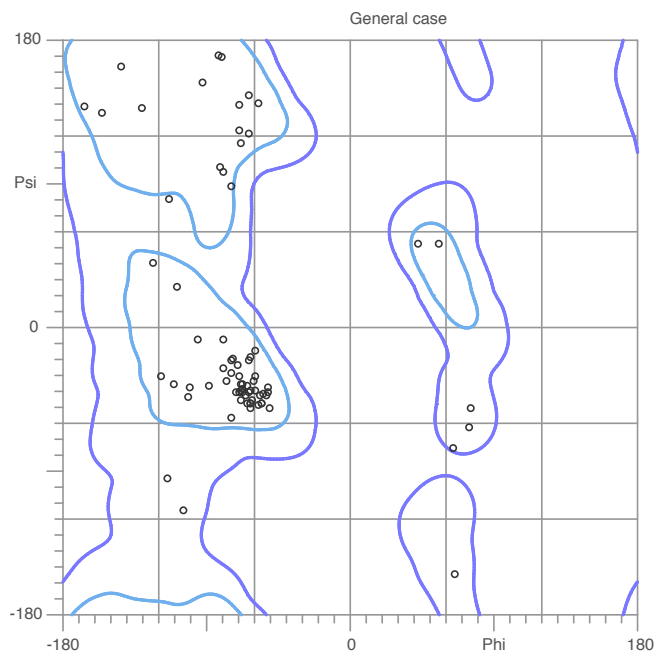
There were 2 outliers (phi, psi):

[7] 6 HIS (75.0, 125.1)

[7] 59 ALA (47.3, -84.9)

MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 8



90.1% (73/81) of all residues were in favored (98%) regions.
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

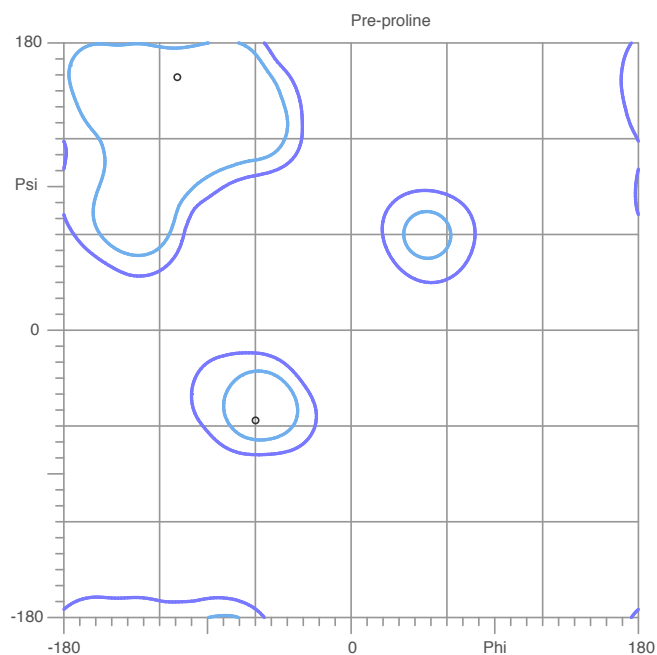
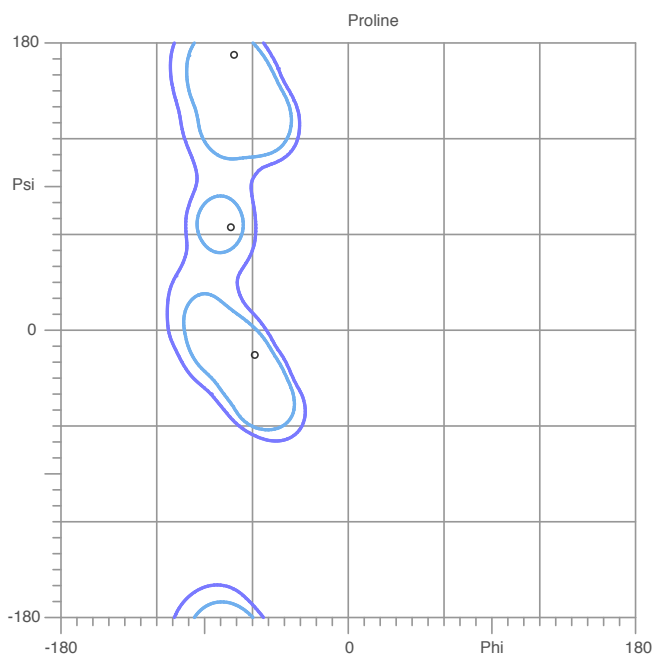
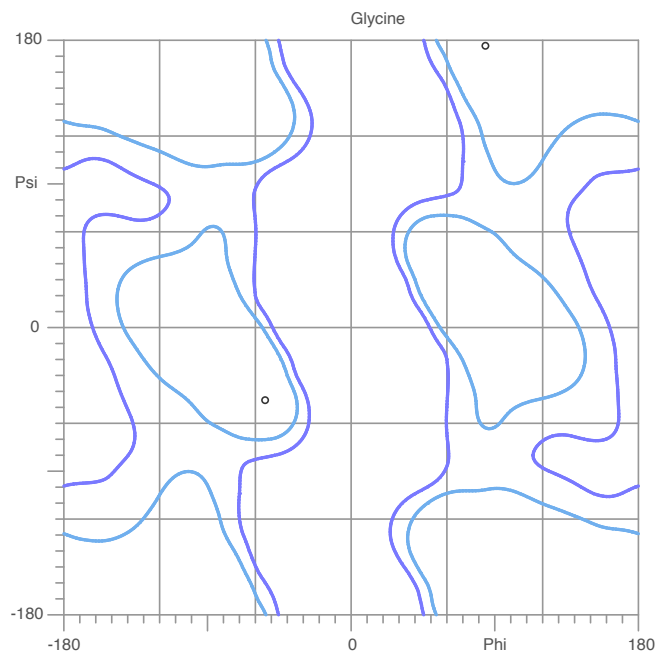
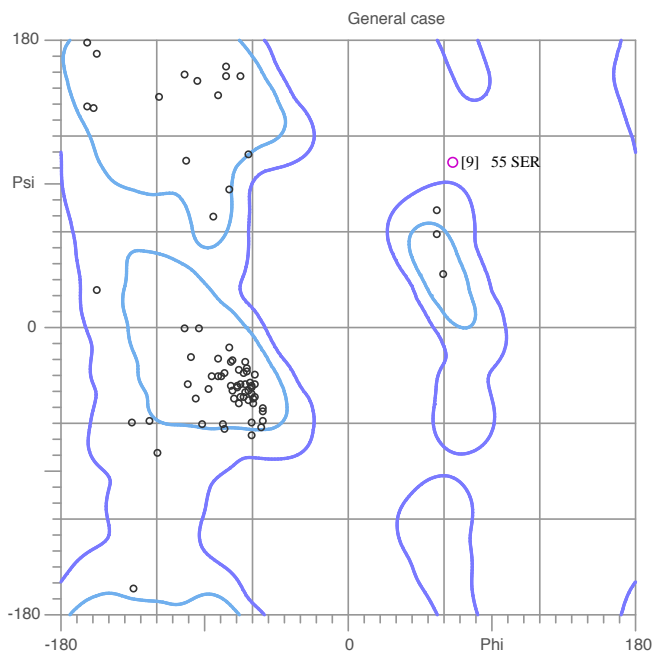
There were no outliers.

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 9

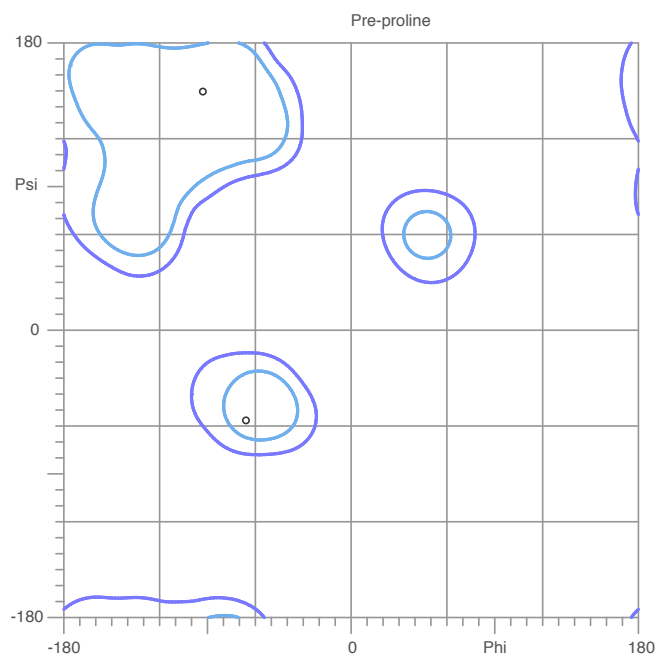
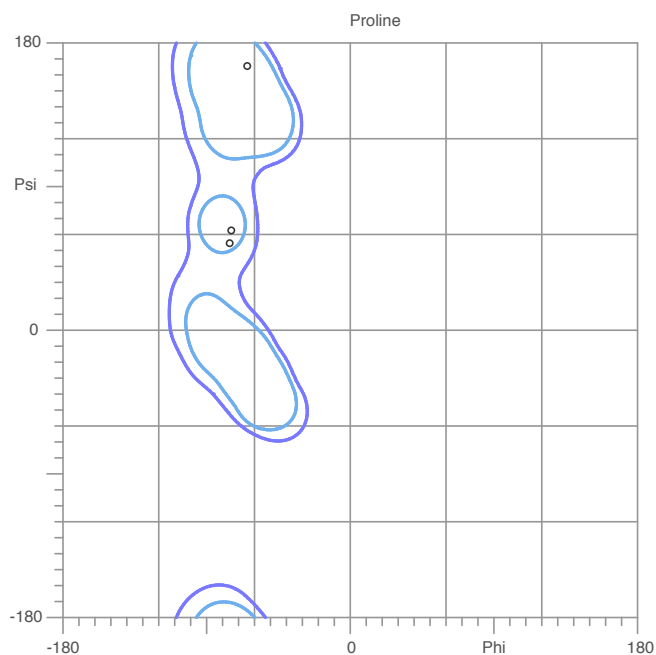
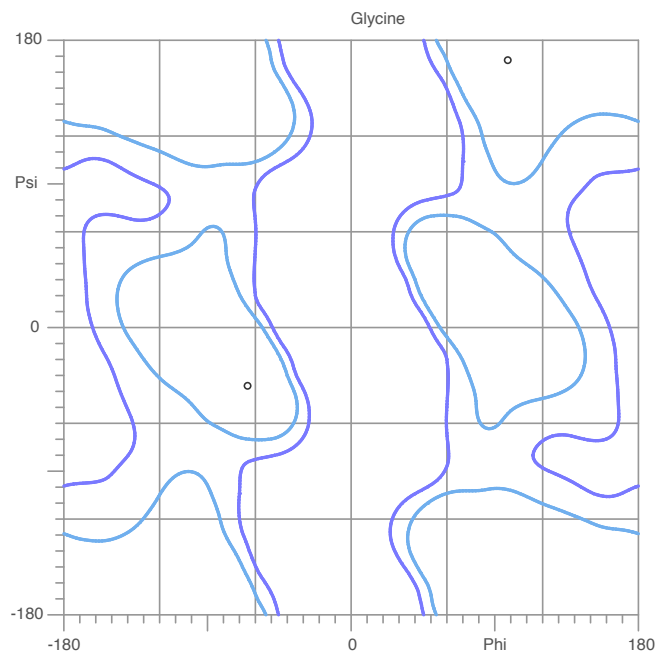
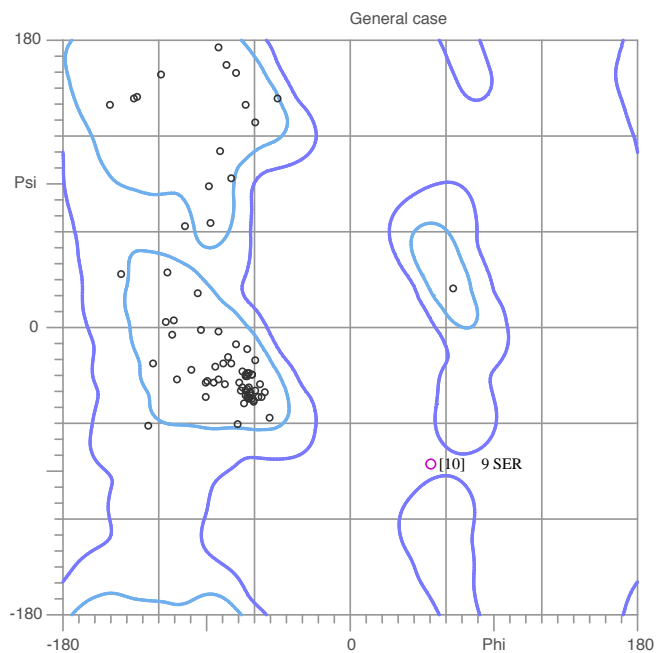


88.9% (72/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 55 SER (65.0, 104.2)

MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 10



95.1% (77/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

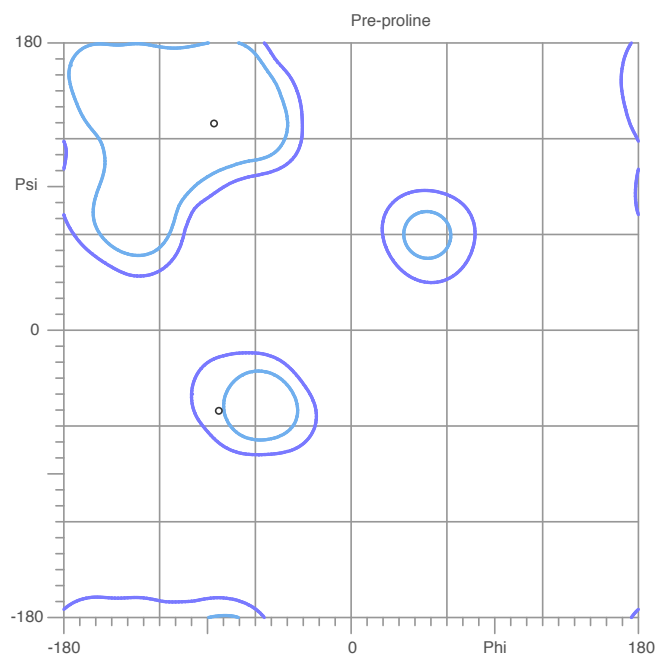
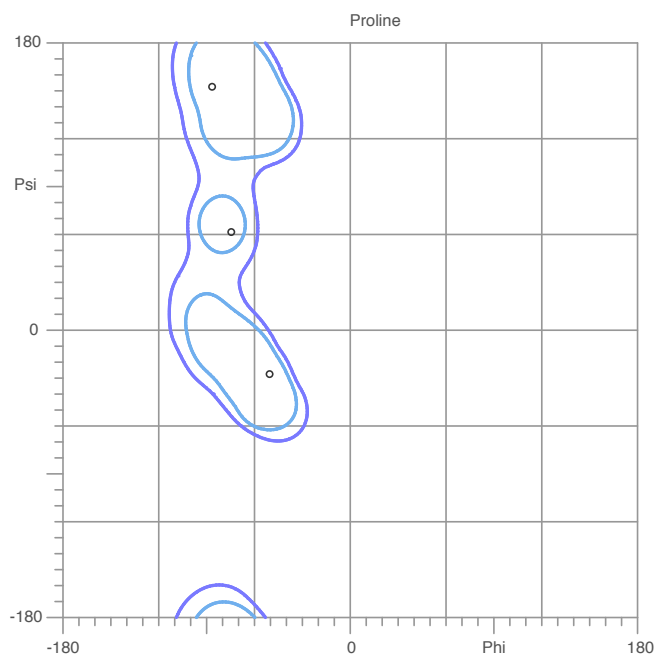
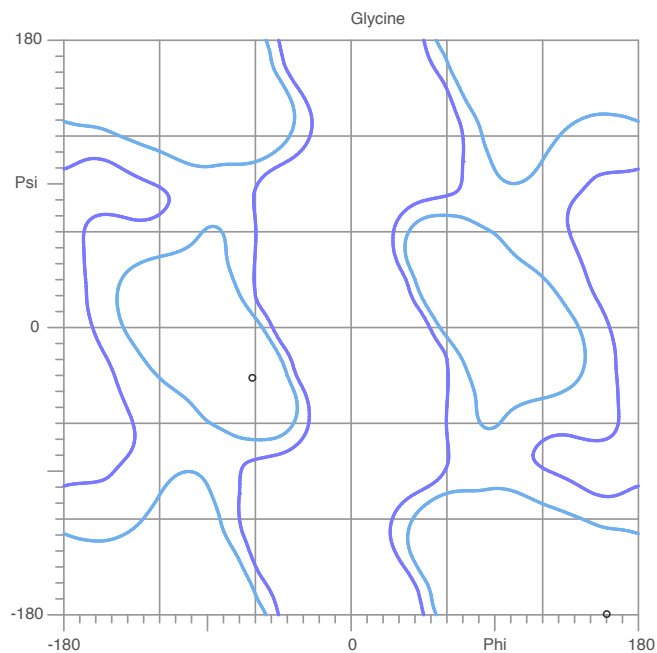
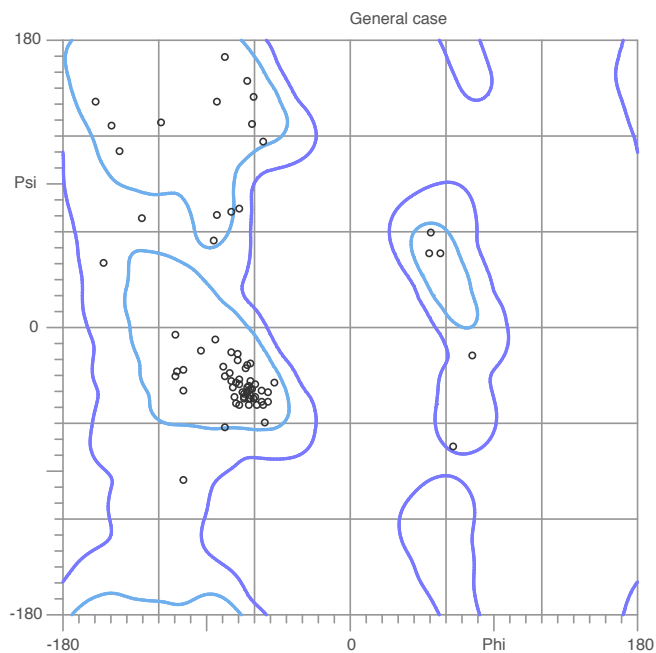
There were 1 outliers (phi, psi):
[10] 9 SER (50.6, -85.3)

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 11



91.4% (74/81) of all residues were in favored (98%) regions.
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

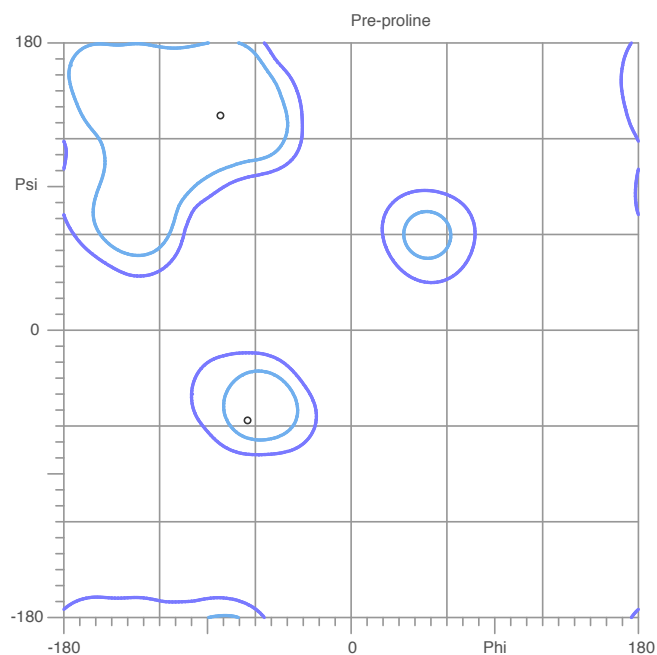
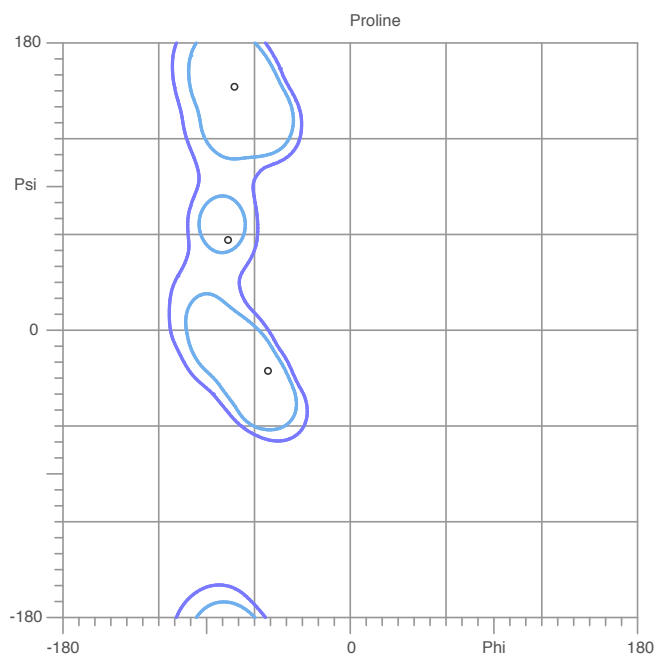
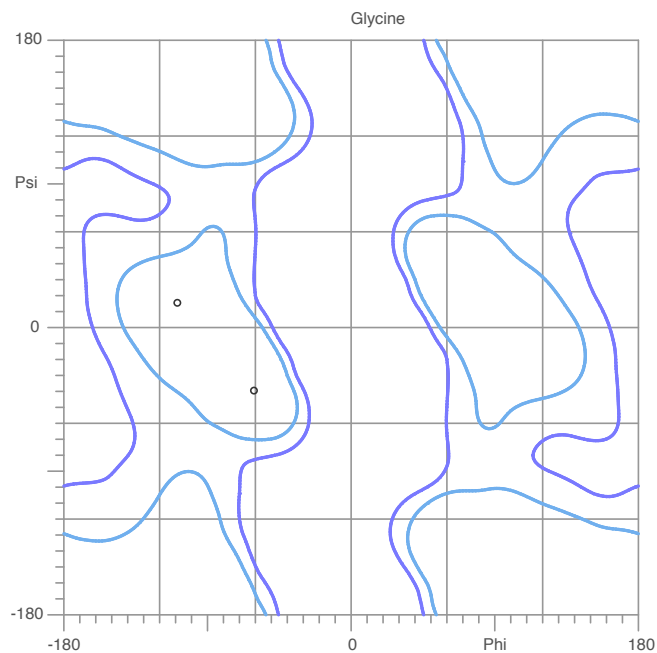
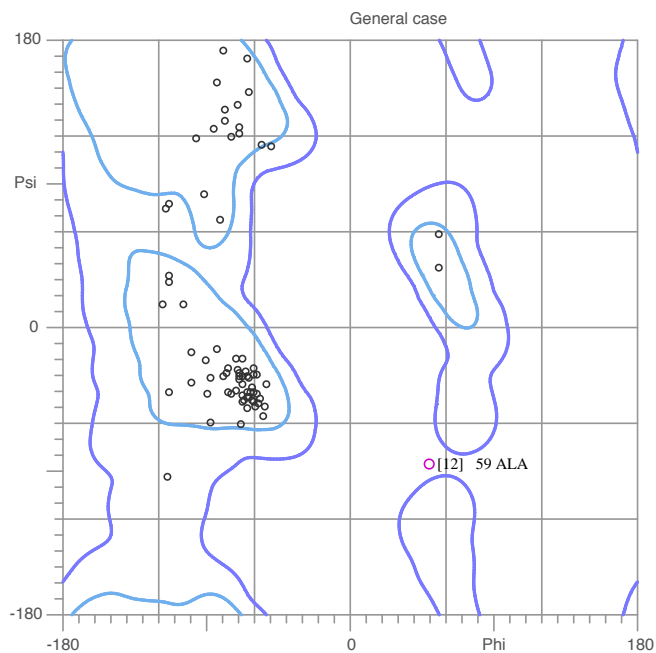
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 12



93.8% (76/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

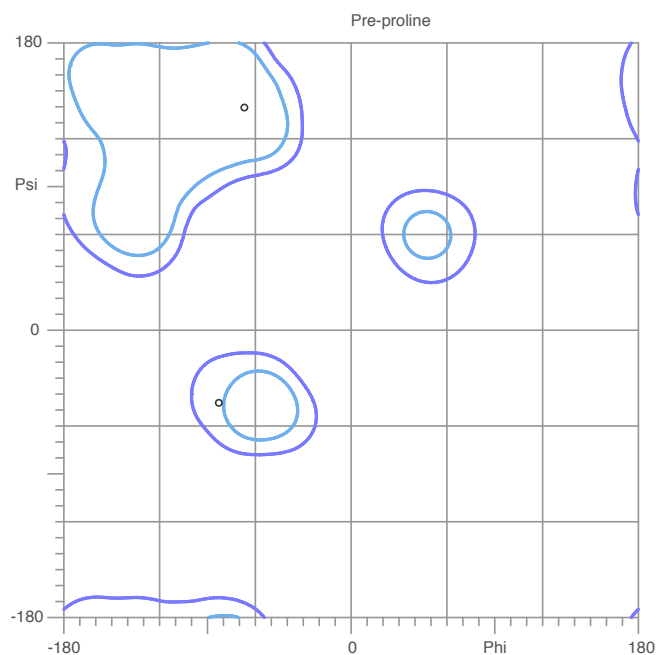
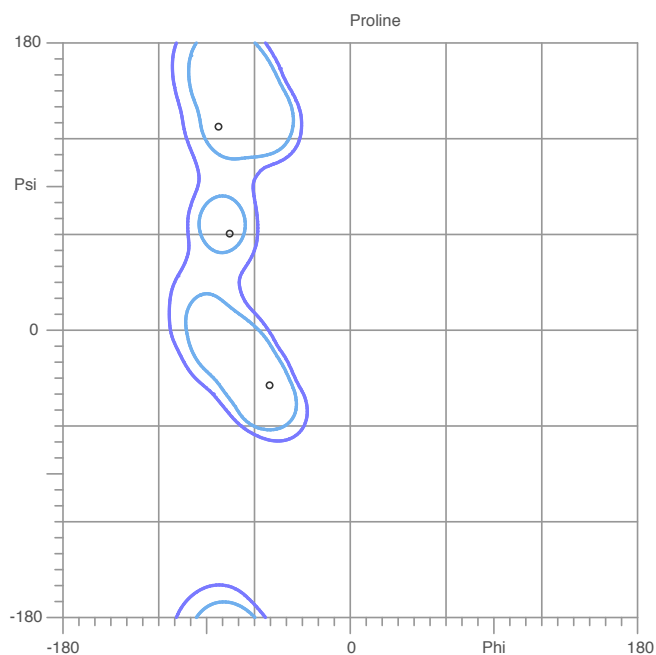
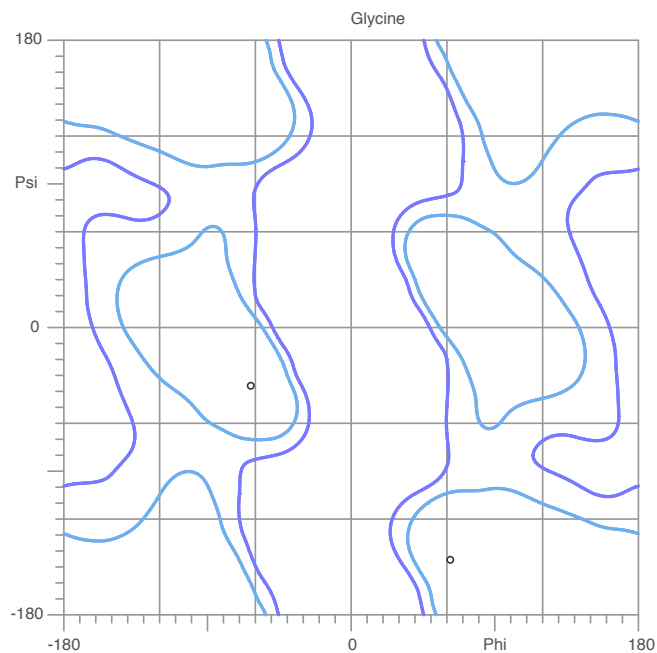
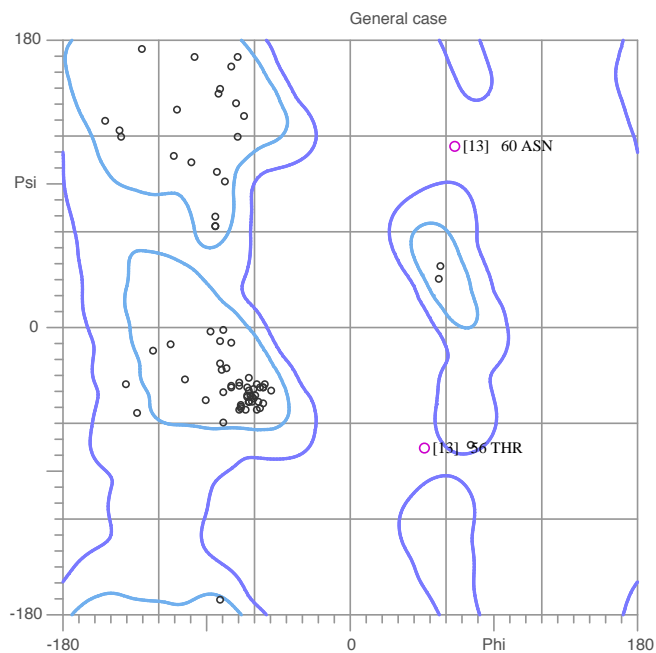
There were 1 outliers (phi, psi):
[12] 59 ALA (49.4, -85.0)

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 13



92.6% (75/81) of all residues were in favored (98%) regions.
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

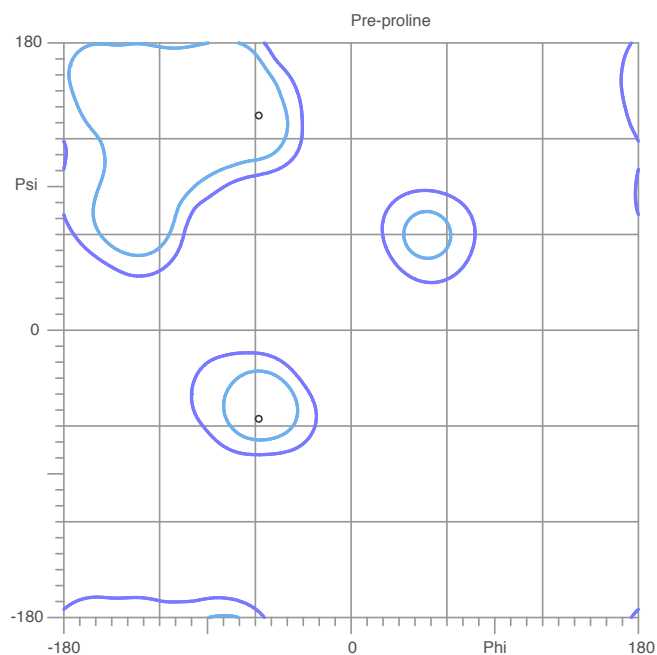
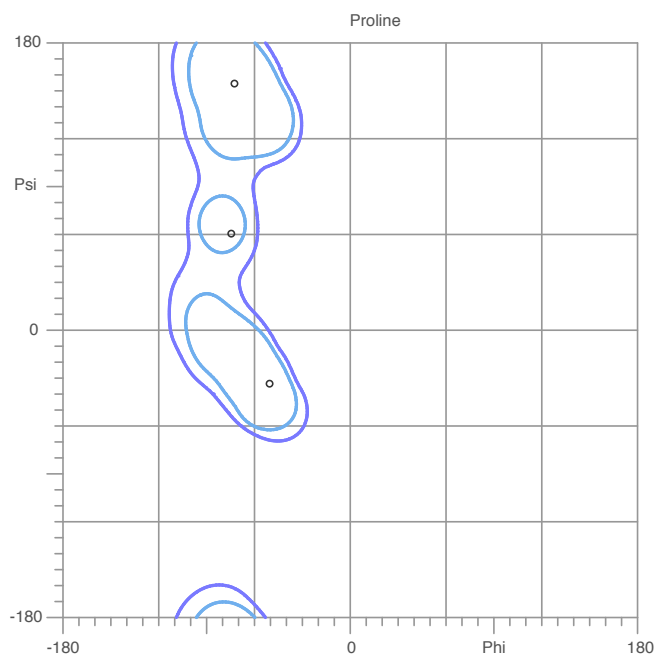
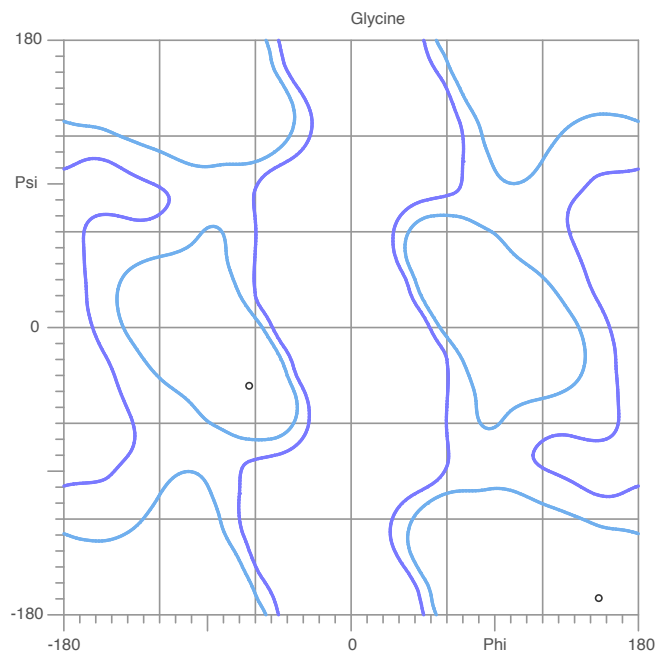
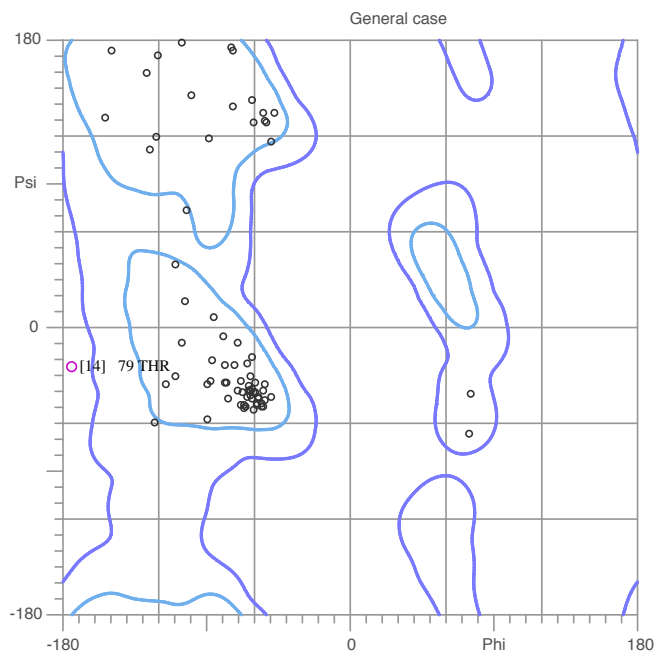
There were 2 outliers (phi, psi):

[13] 56 THR (47.0, -75.0)

[13] 60 ASN (65.1, 115.0)

MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 14



93.8% (76/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

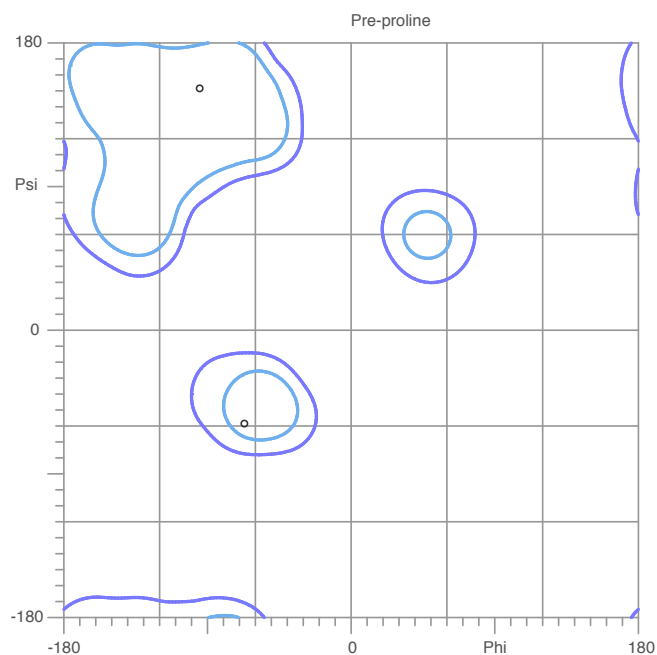
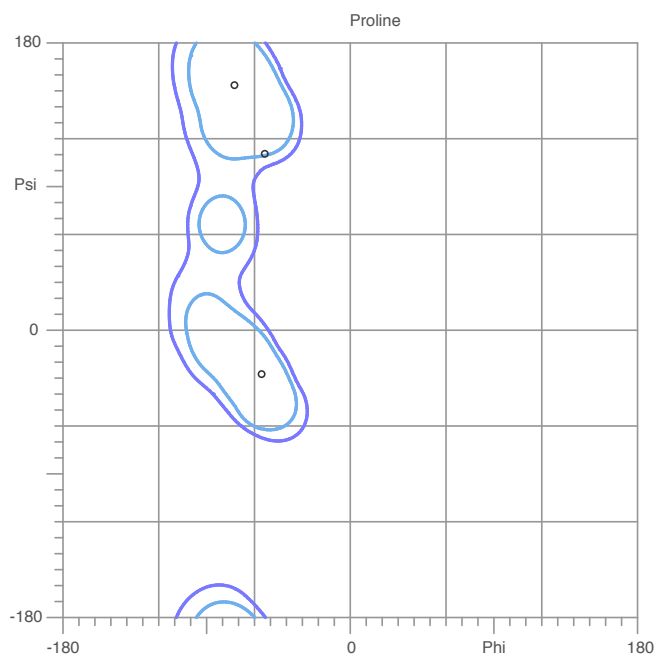
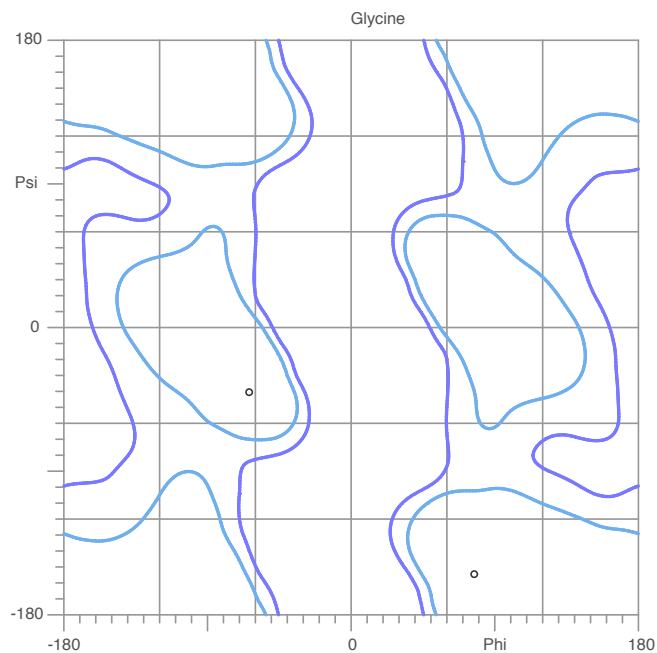
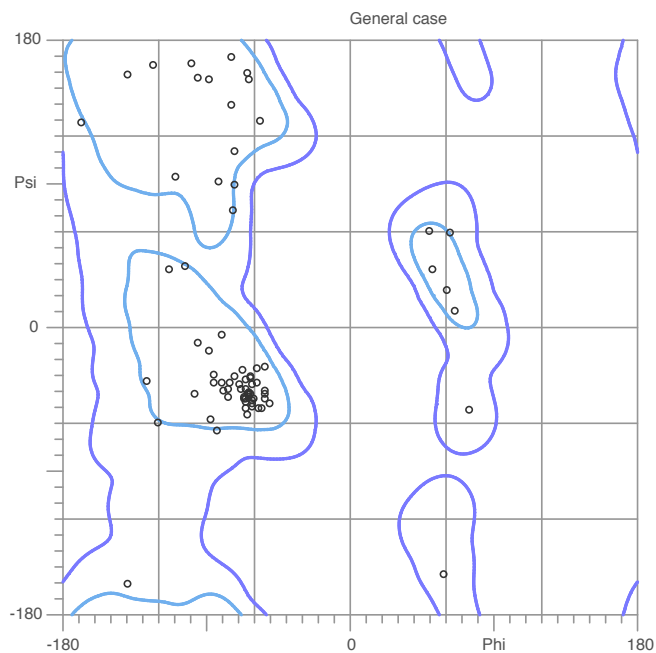
There were 1 outliers (phi, psi):
[14] 79 THR (-175.0, -25.0)

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 15



91.4% (74/81) of all residues were in favored (98%) regions.
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

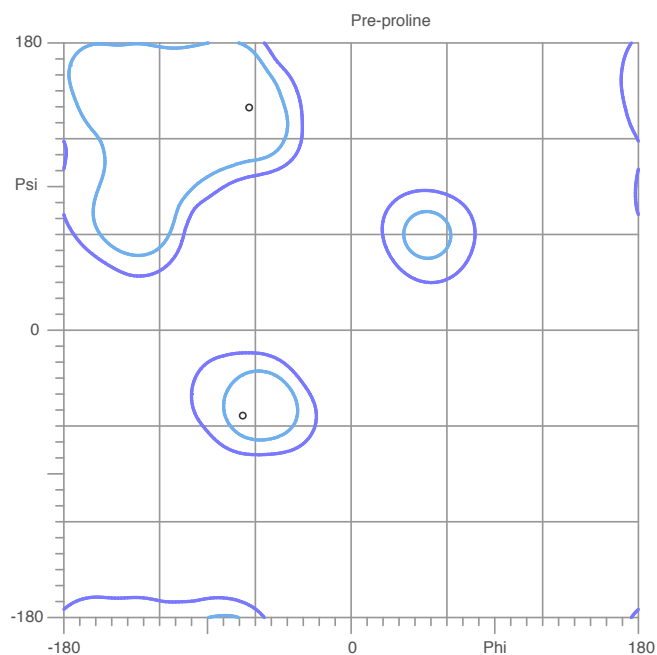
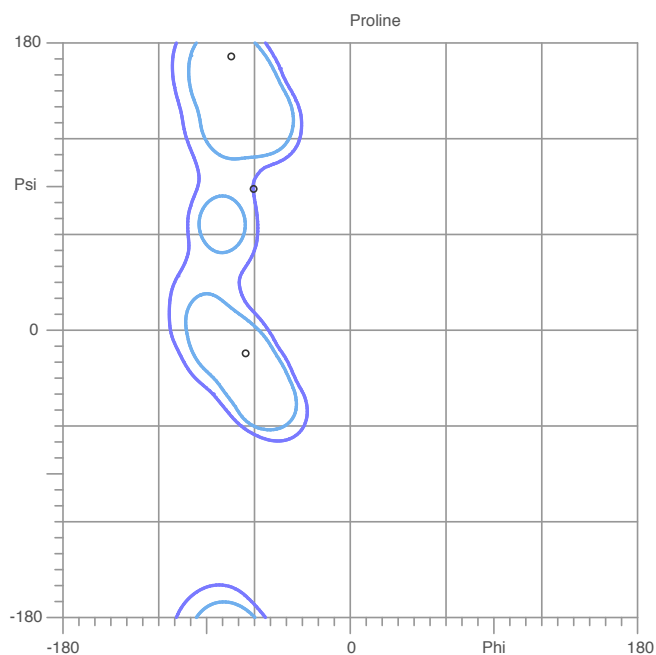
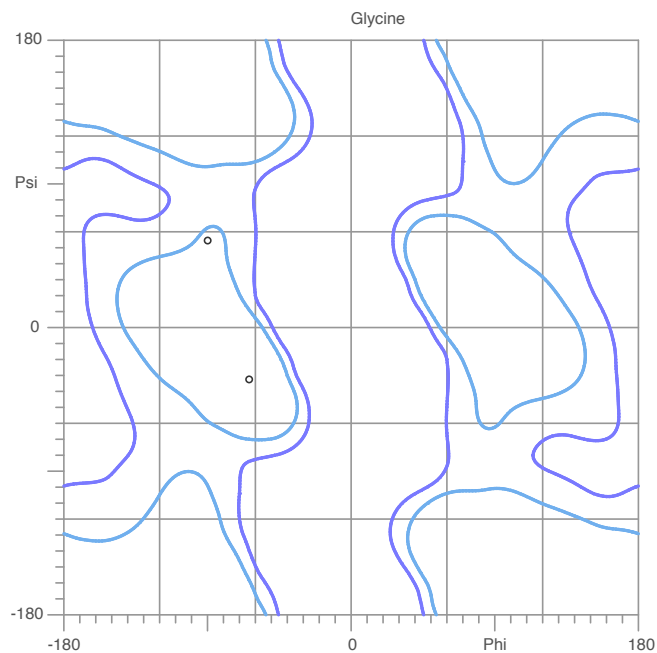
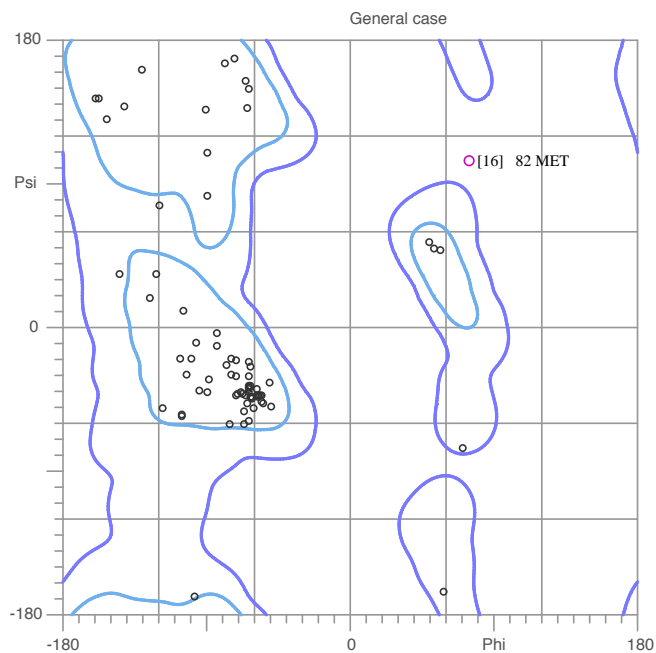
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 16



91.4% (74/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

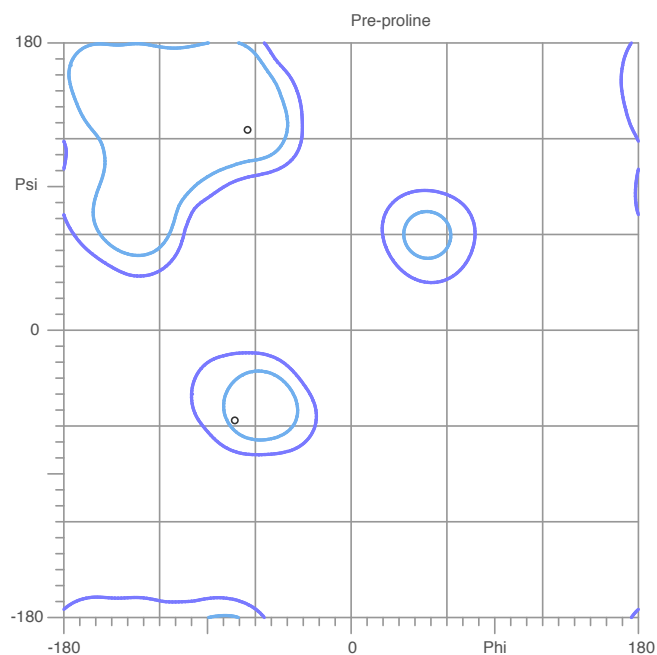
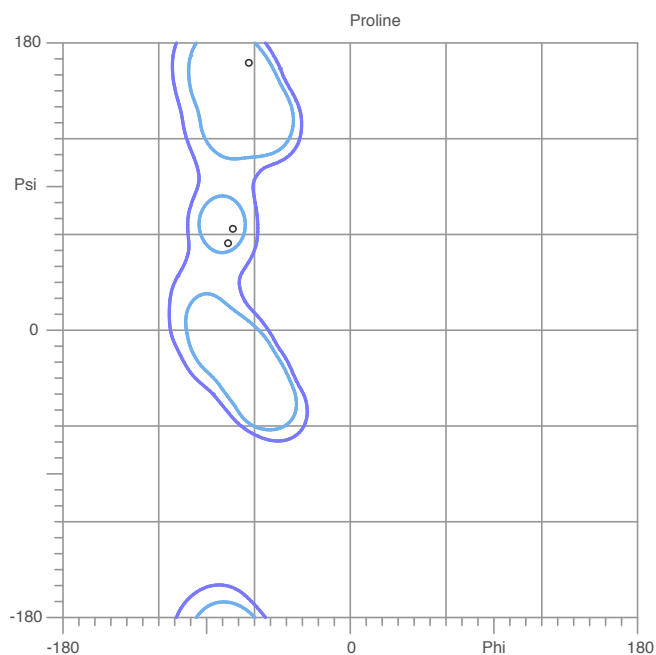
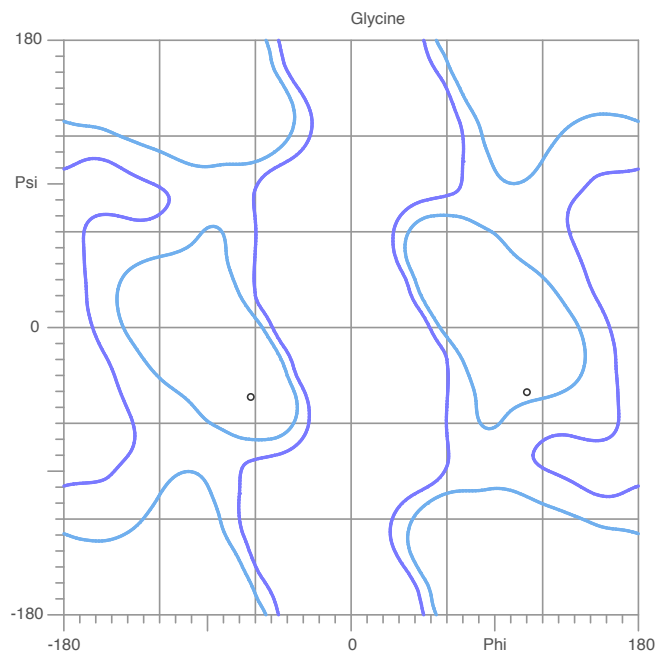
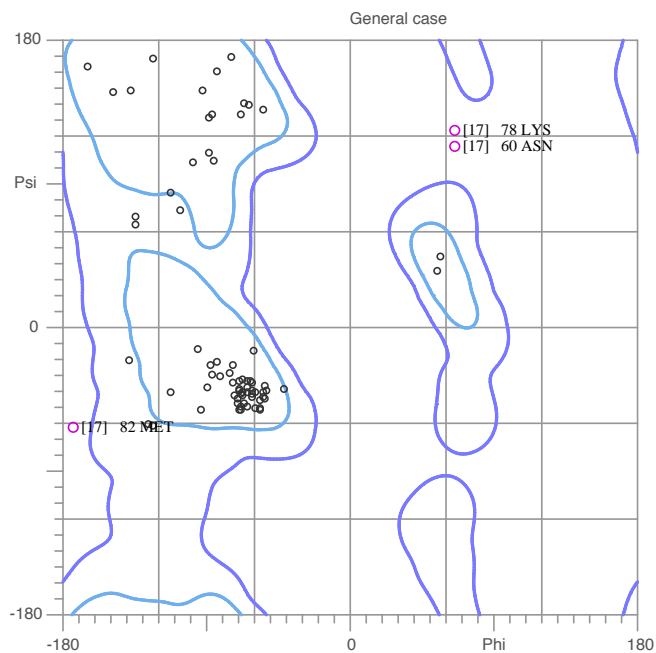
There were 1 outliers (phi, psi):
[16] 82 MET (75.0, 105.2)

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 17



88.9% (72/81) of all residues were in favored (98%) regions.
96.3% (78/81) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

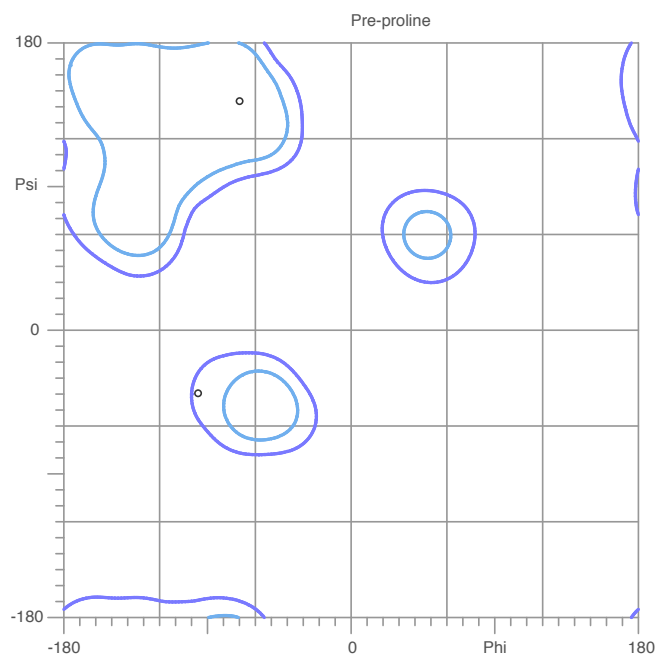
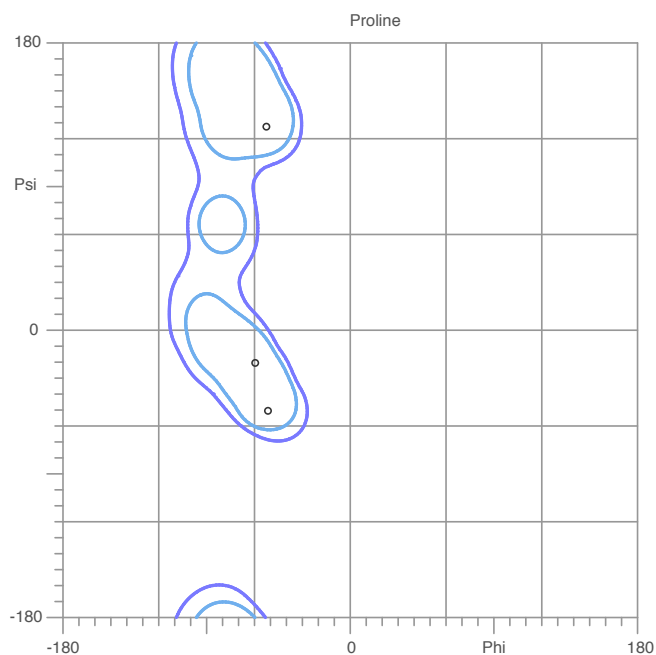
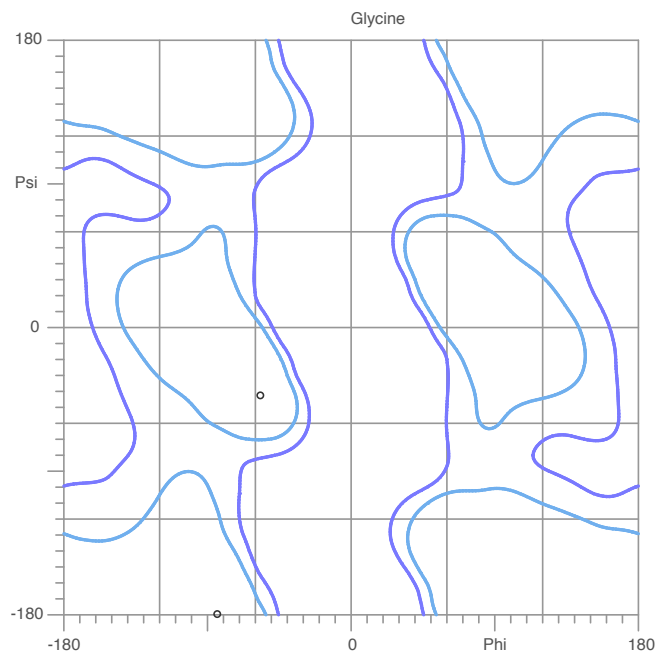
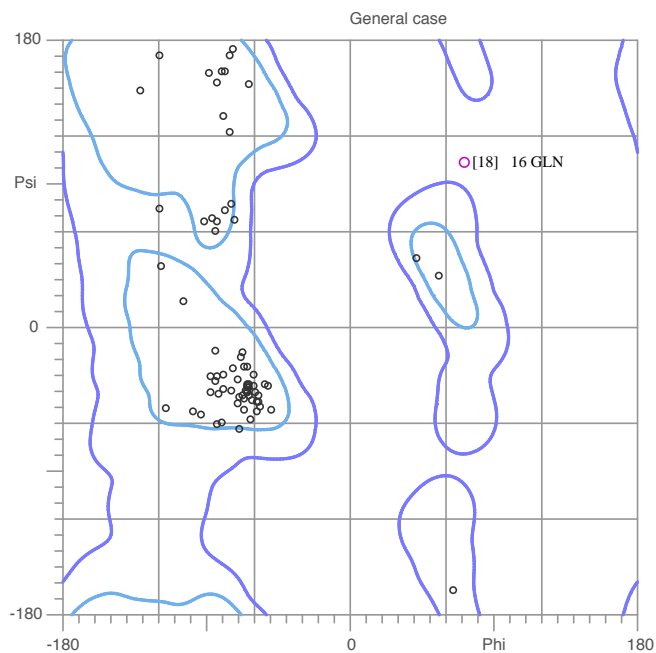
[17] 60 ASN (65.0, 114.9)

[17] 78 LYS (65.0, 125.0)

[17] 82 MET (-174.9, -62.7)

MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 18



92.6% (75/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

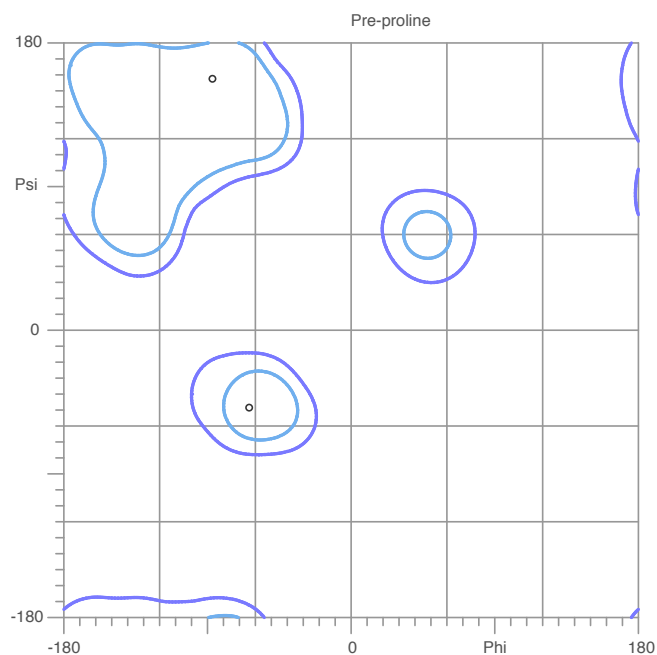
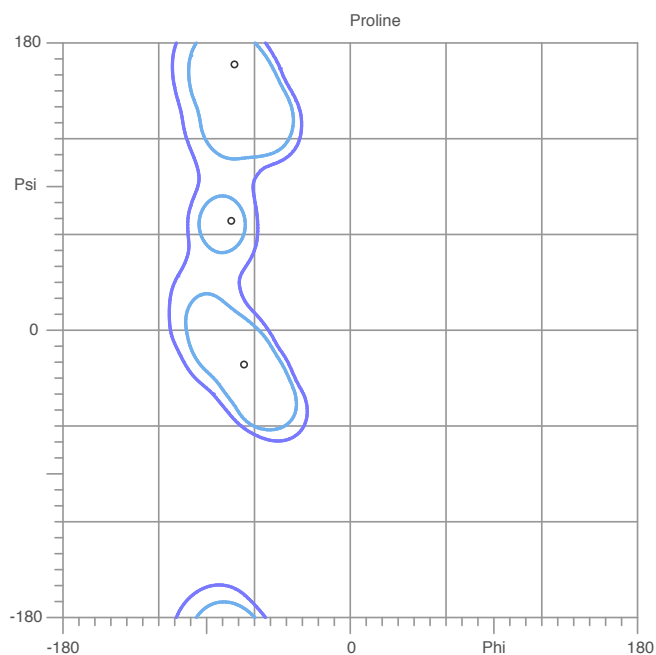
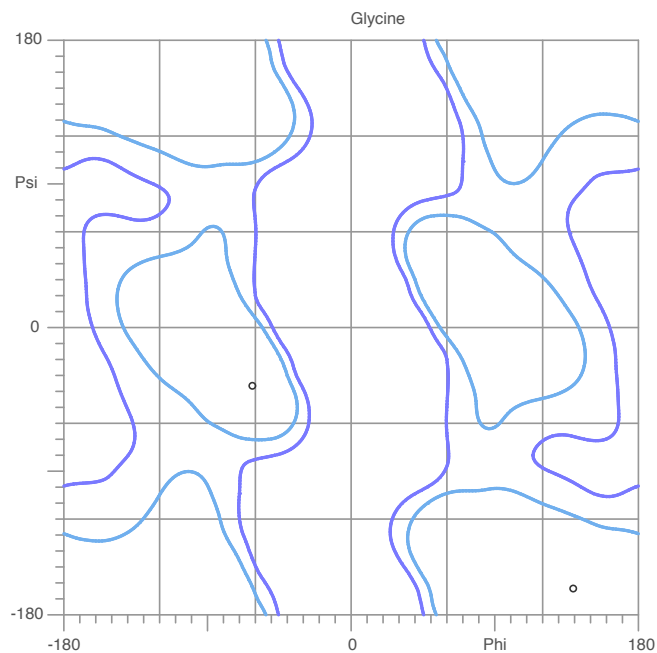
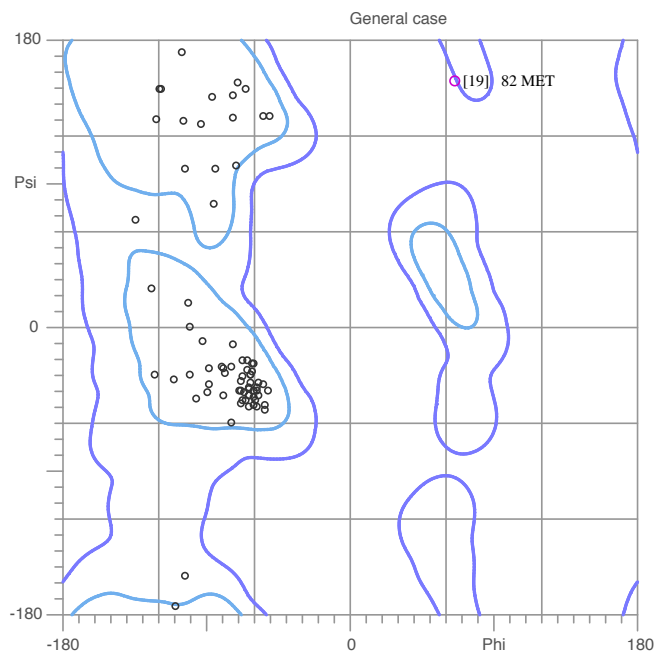
There were 1 outliers (phi, psi):
[18] 16 GLN (71.8, 104.6)

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 19



96.3% (78/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

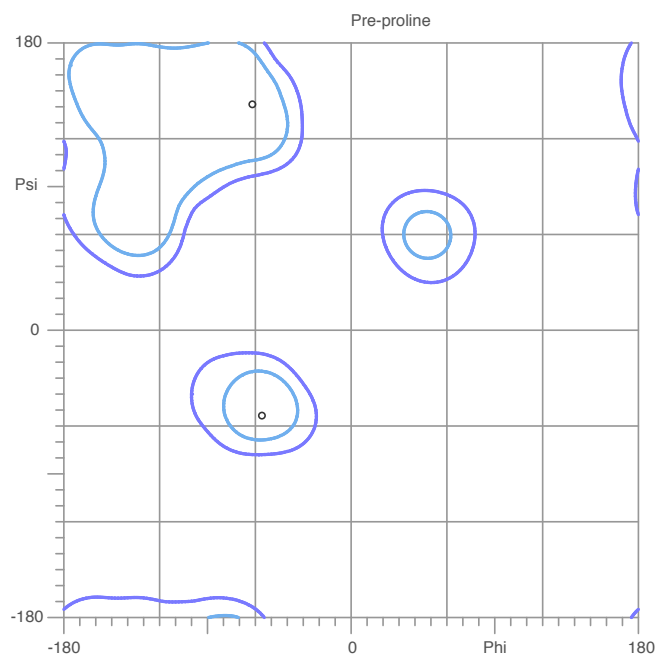
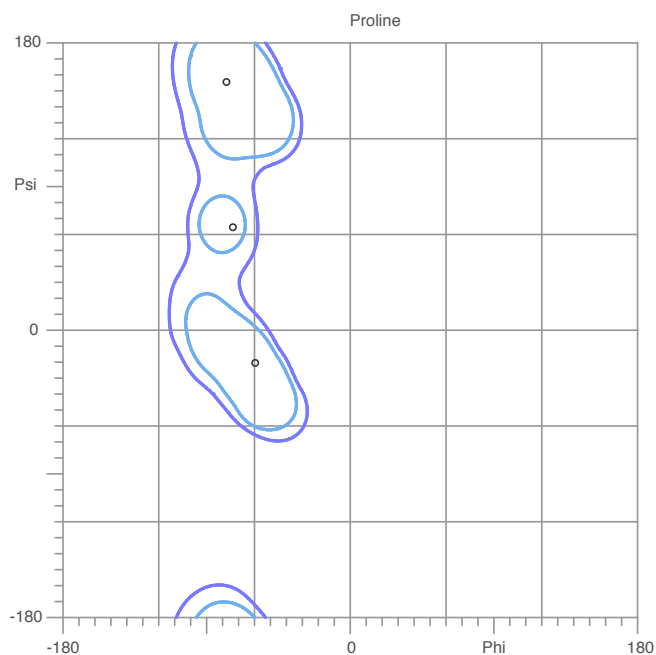
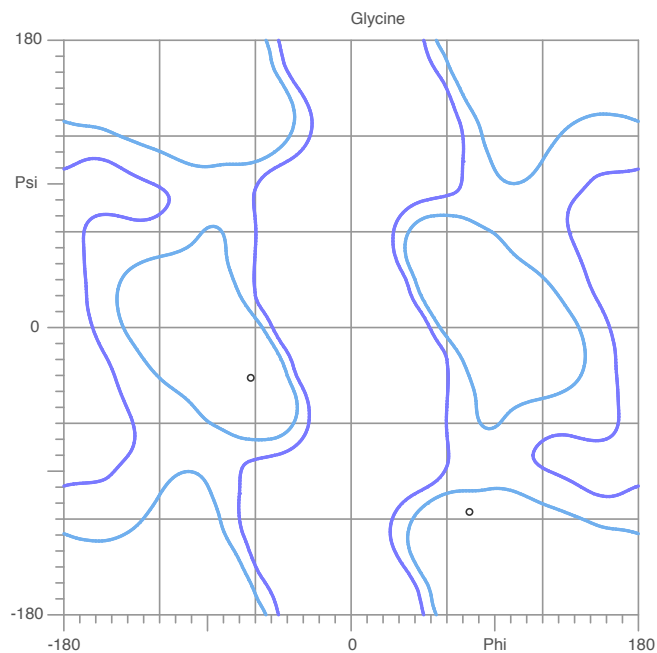
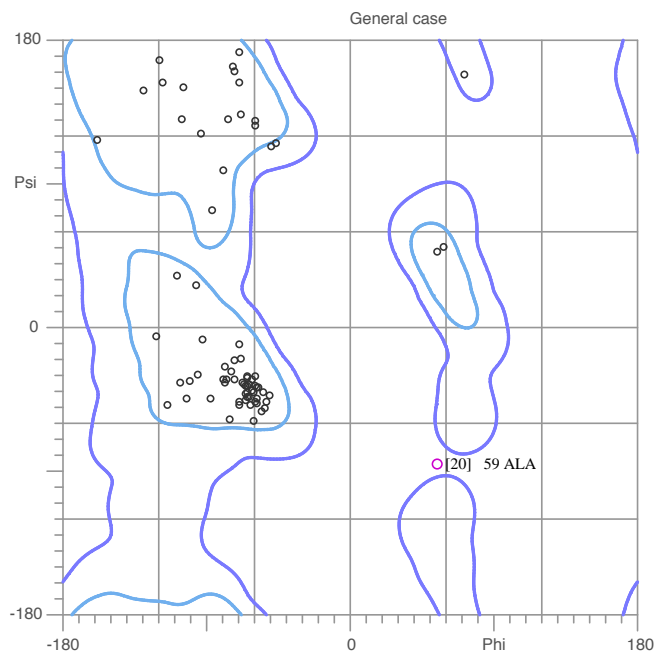
There were 1 outliers (phi, psi):
[19] 82 MET (65.1, 155.2)

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MolProbity Ramachandran analysis

HR4435B_R3_em_bcr3.pdb, model 20



95.1% (77/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 59 ALA (54.8, -85.0)

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