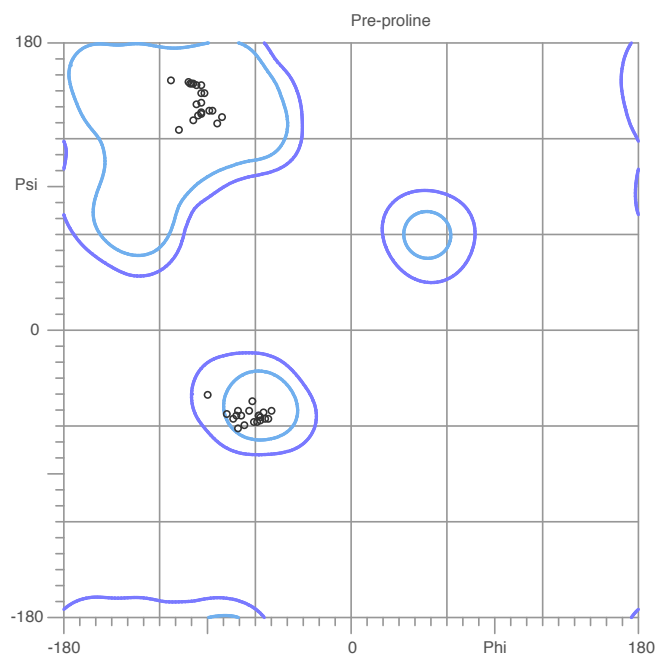
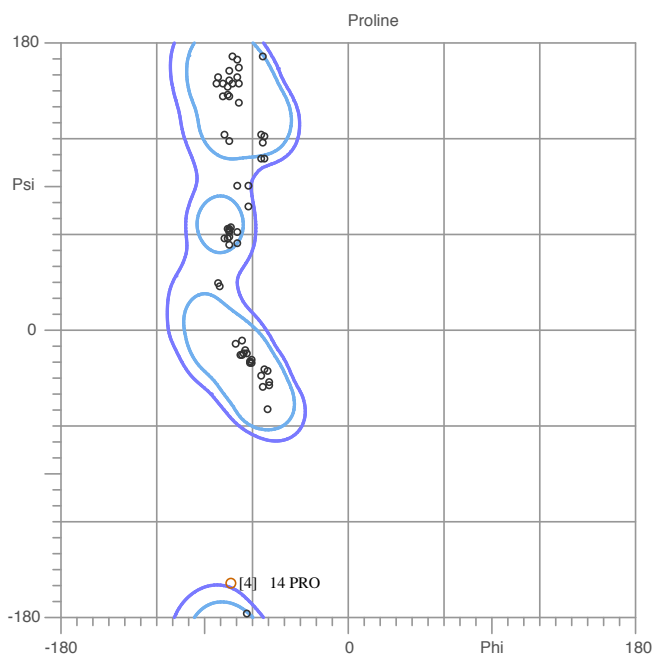
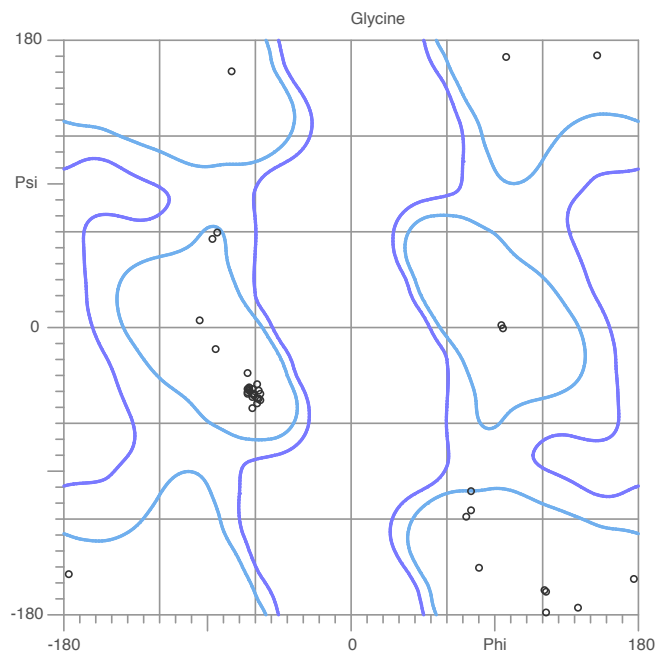
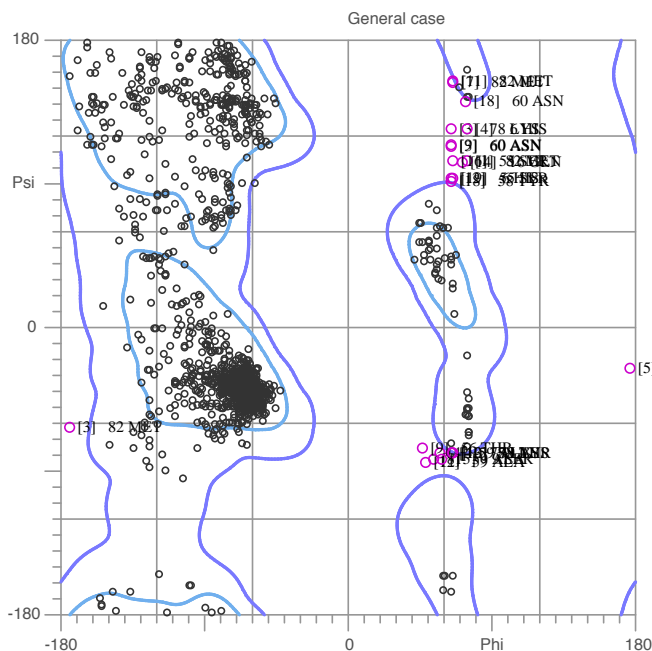


MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, all models



91.5% (1483/1620) of all residues were in favored (98%) regions.
98.5% (1596/1620) of all residues were in allowed (>99.8%) regions.

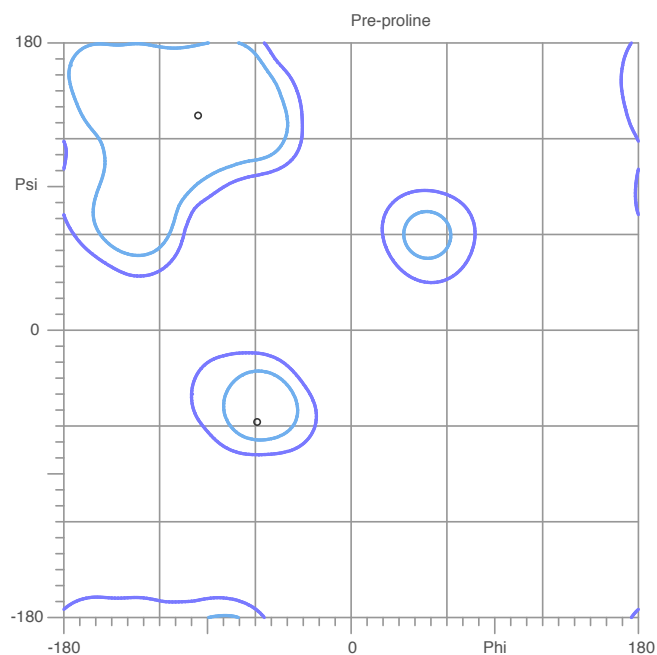
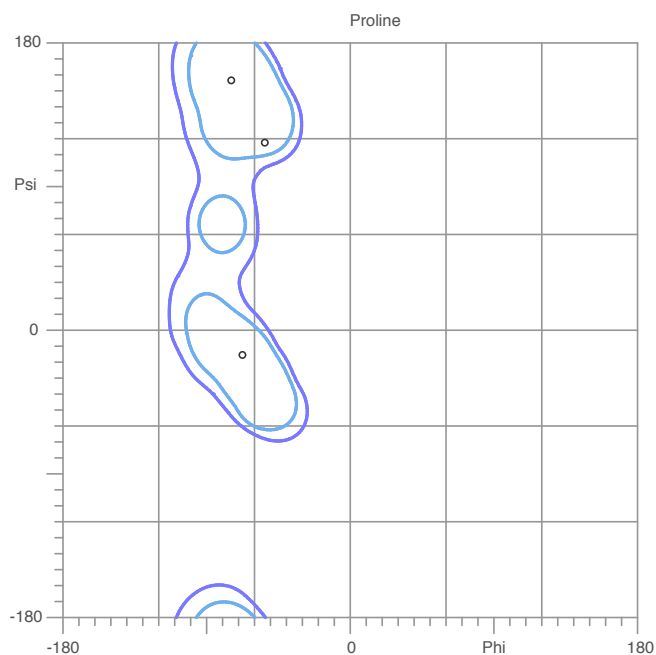
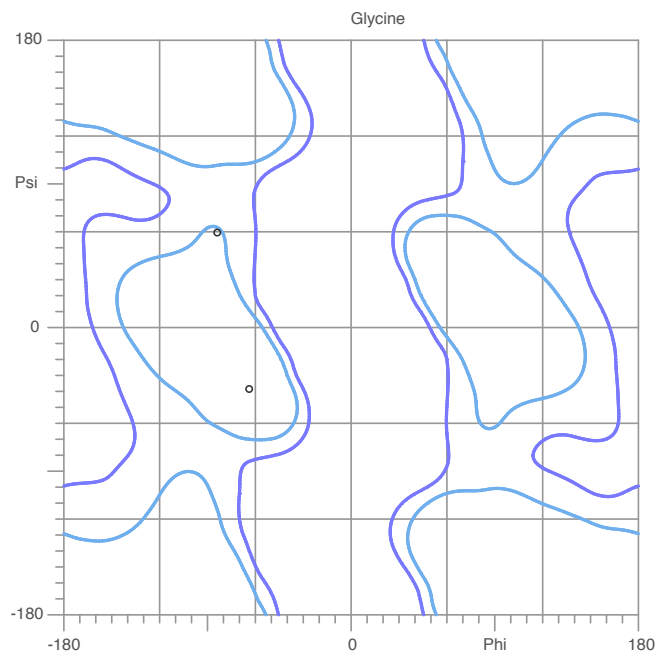
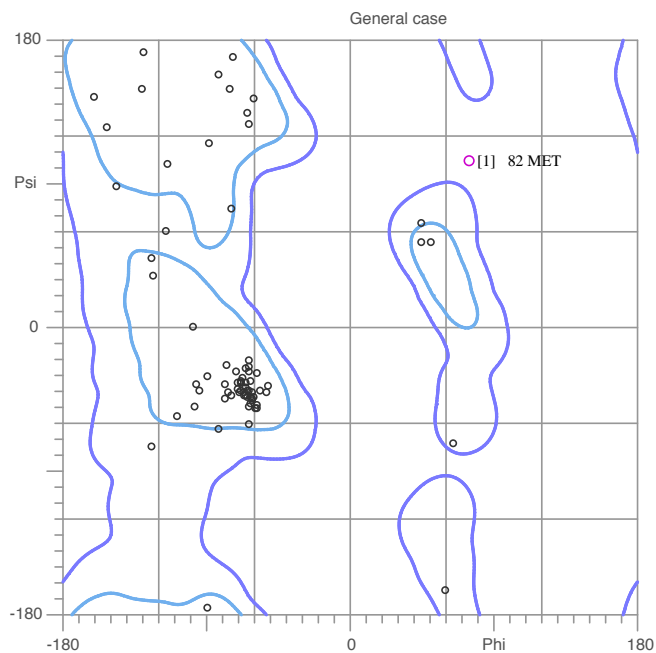
There were 24 outliers (phi, psi):

- [1] 82 MET (75.0, 105.0)
- [3] 60 ASN (65.0, 115.0)
- [3] 78 LYS (65.0, 125.0)
- [3] 82 MET (-175.0, -62.4)
- [4] 6 HIS (74.9, 125.1)
- [4] 14 PRO (-74.8, -158.4)
- [4] 59 ALA (57.1, -79.0)
- [4] 78 LYS (65.0, -78.8)
- [5] 79 THR (176.7, -25.1)
- [7] 82 MET (65.0, 155.0)

- [8] 59 ALA (53.1, -82.8)
- [9] 56 THR (46.5, -75.0)
- [9] 60 ASN (65.0, 115.0)
- [10] 79 THR (65.1, -78.5)
- [11] 82 MET (65.0, 155.0)
- [12] 6 HIS (65.0, 95.0)
- [12] 59 ALA (48.8, -84.9)
- [13] 78 LYS (65.0, -78.2)
- [14] 16 GLN (71.9, 104.9)
- [15] 9 SER (58.1, -82.3)
- [16] 55 SER (65.0, 105.0)
- [18] 58 TYR (64.7, 92.5)
- [18] 60 ASN (73.5, 142.0)
- [19] 55 SER (65.1, 95.0)

MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 1

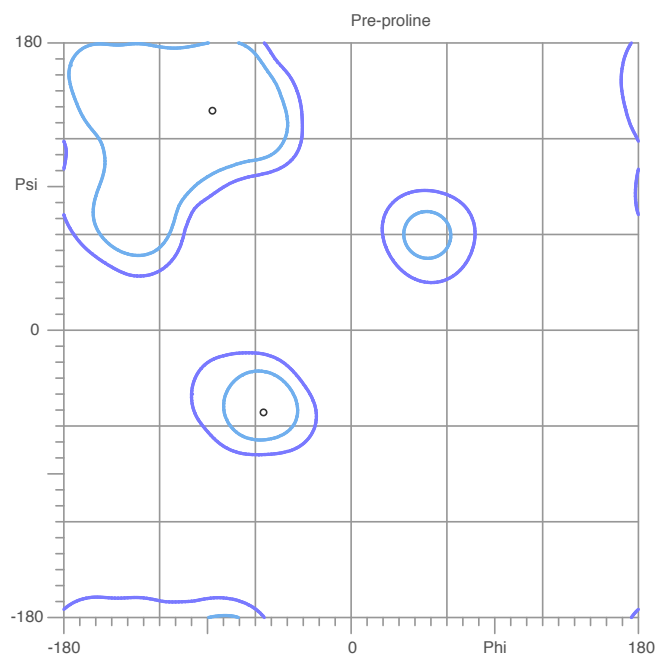
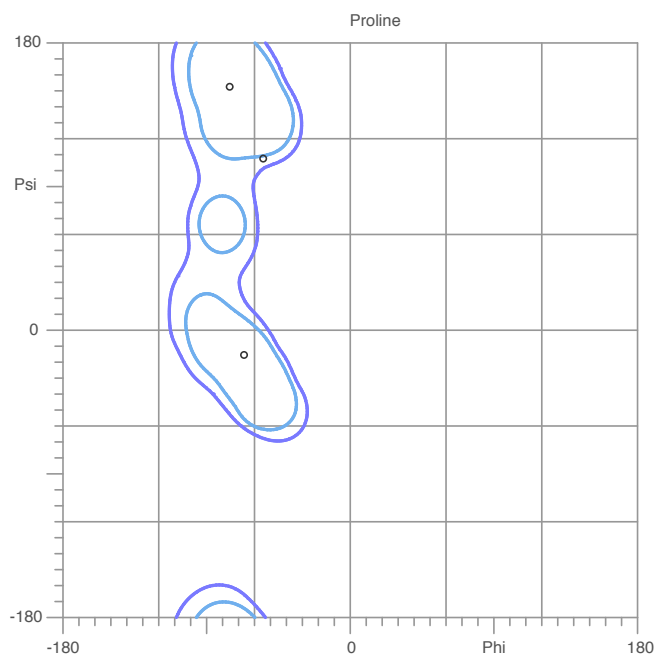
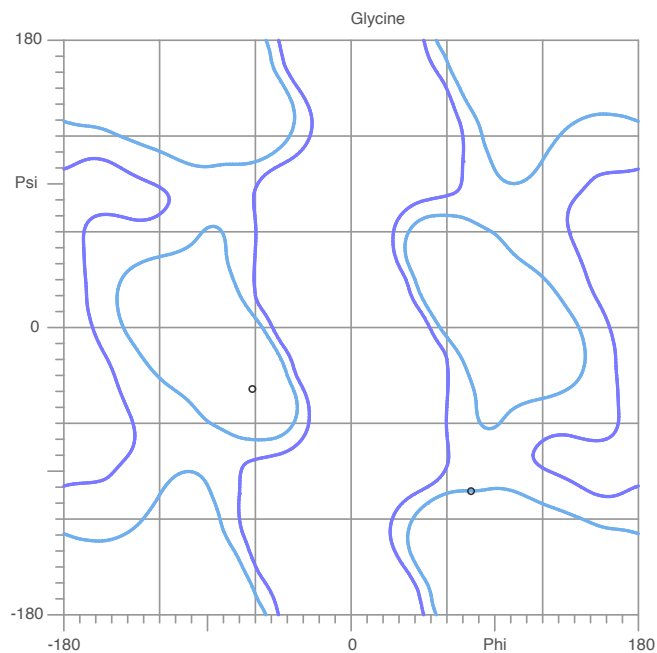
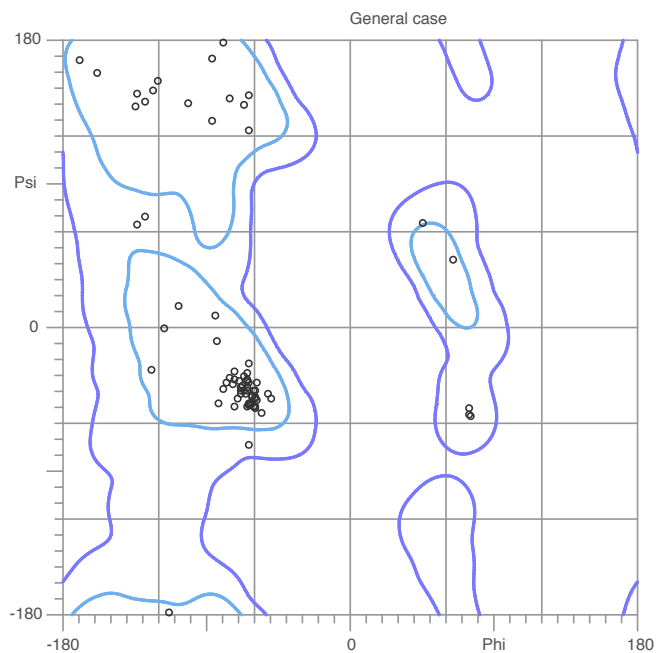


90.1% (73/81) of all residues were in favored (98%) regions.
98.8% (80/81) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[1] 82 MET (75.0, 105.0)

MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 2



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.

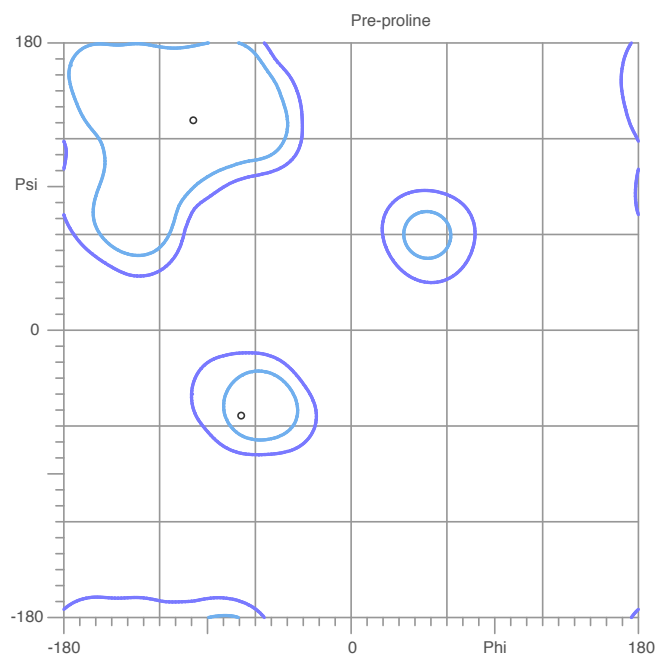
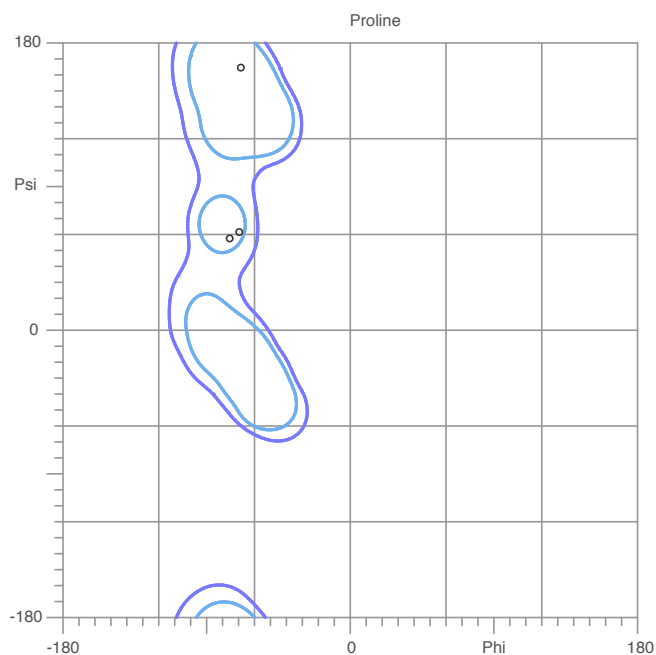
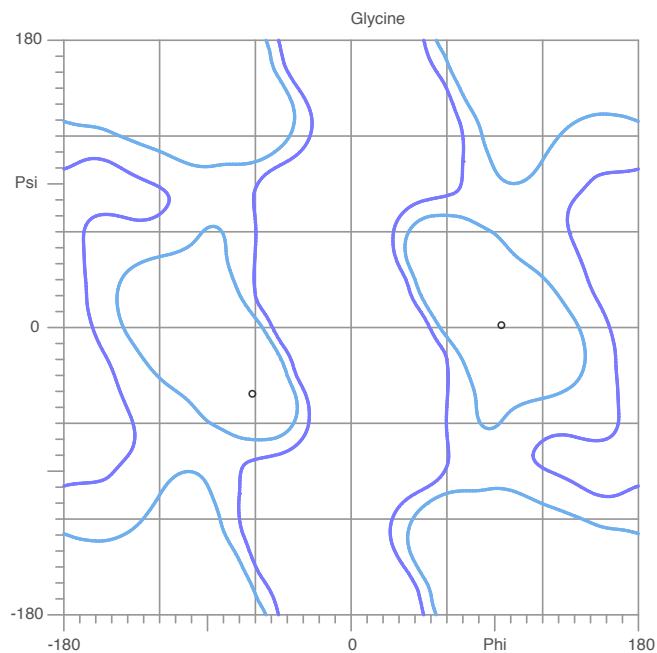
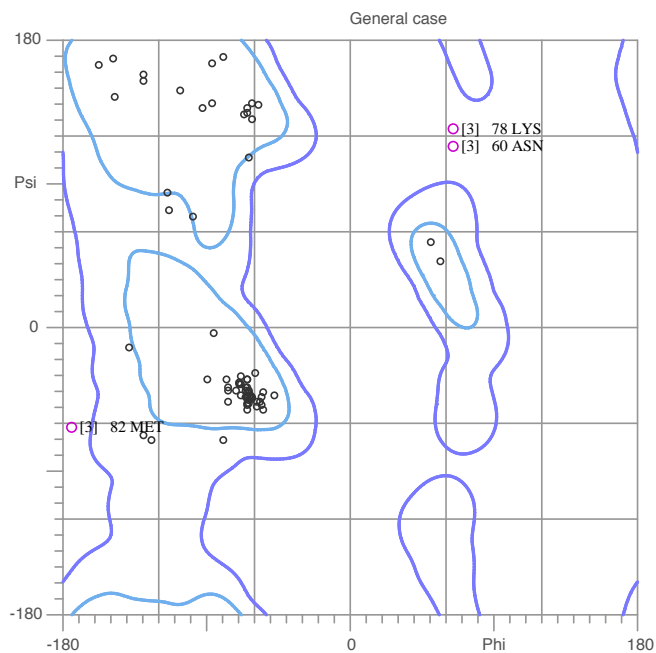
There were no outliers.

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

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 3



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):

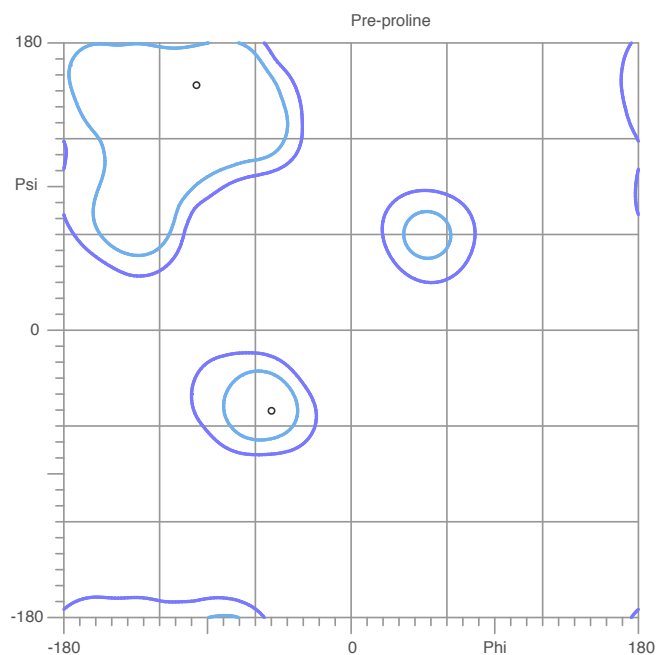
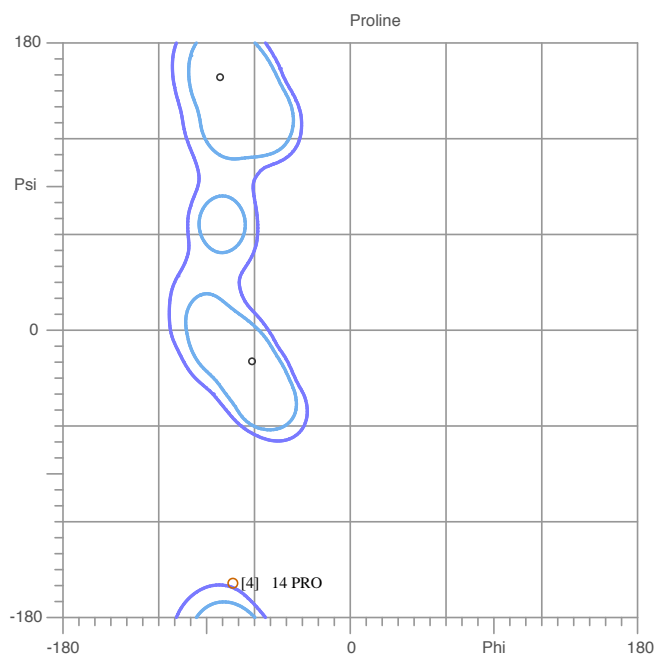
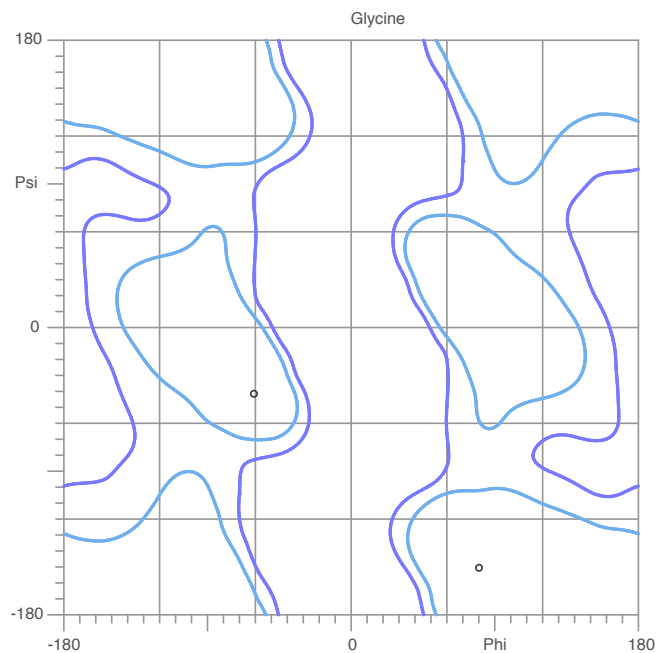
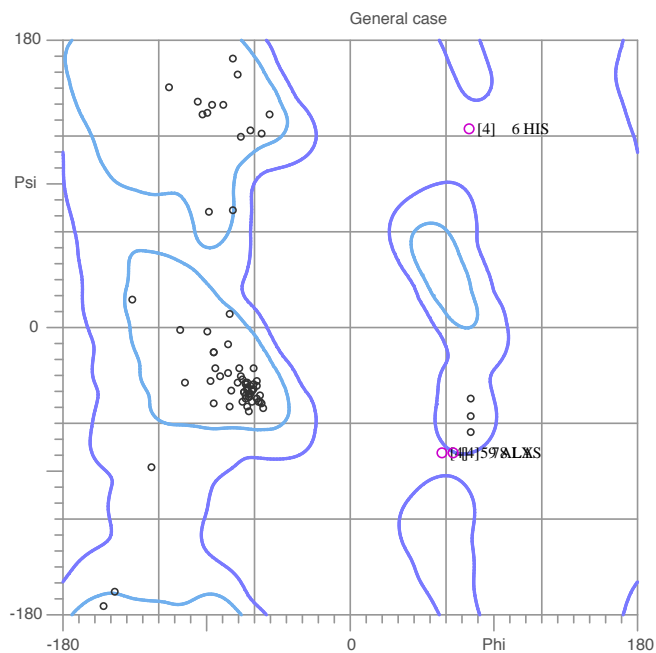
[3] 60 ASN (65.0, 115.0)

[3] 78 LYS (65.0, 125.0)

[3] 82 MET (-175.0, -62.4)

MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 4



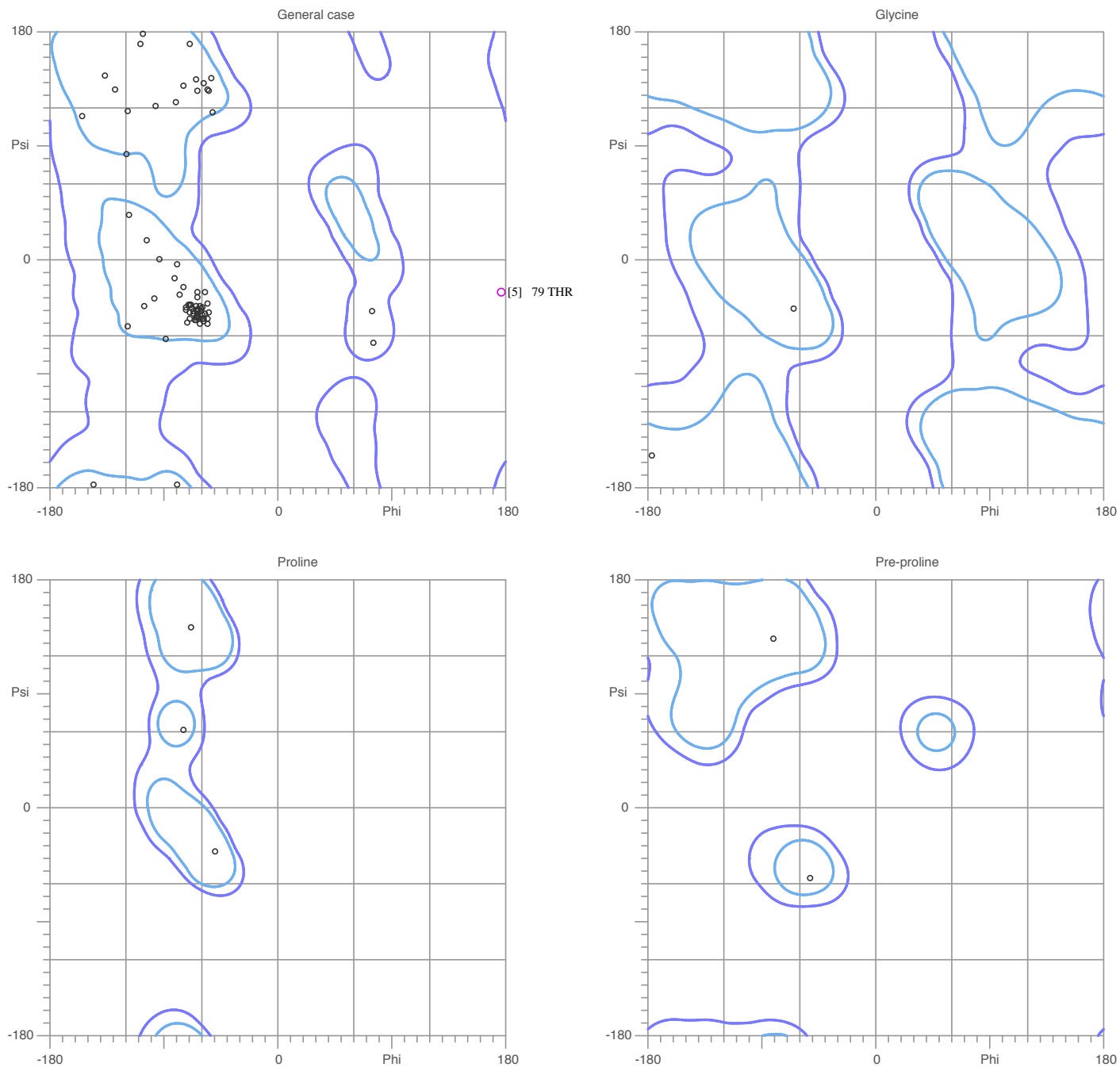
88.9% (72/81) of all residues were in favored (98%) regions.
95.1% (77/81) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [4] 6 HIS (74.9, 125.1)
- [4] 14 PRO (-74.8, -158.4)
- [4] 59 ALA (57.1, -79.0)
- [4] 78 LYS (65.0, -78.8)

MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 5



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.

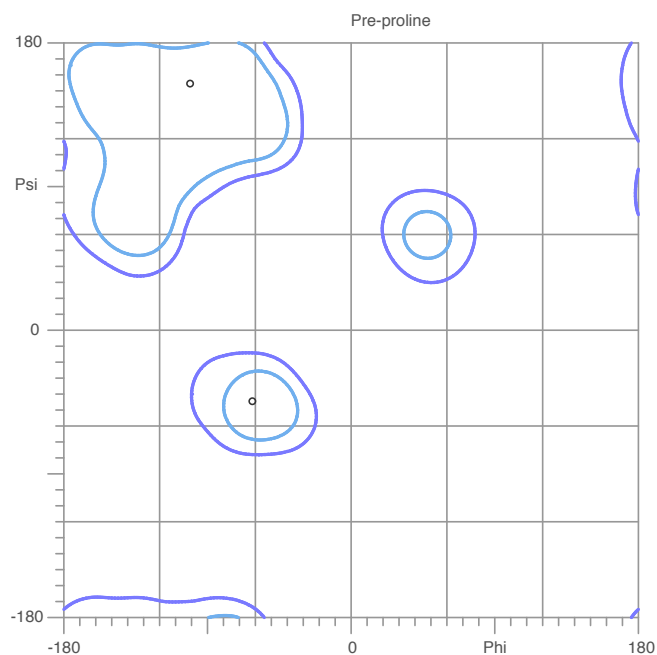
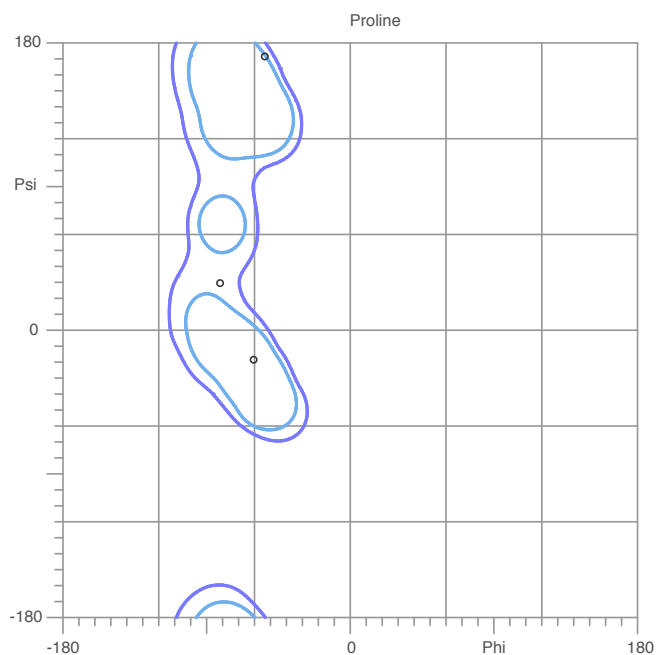
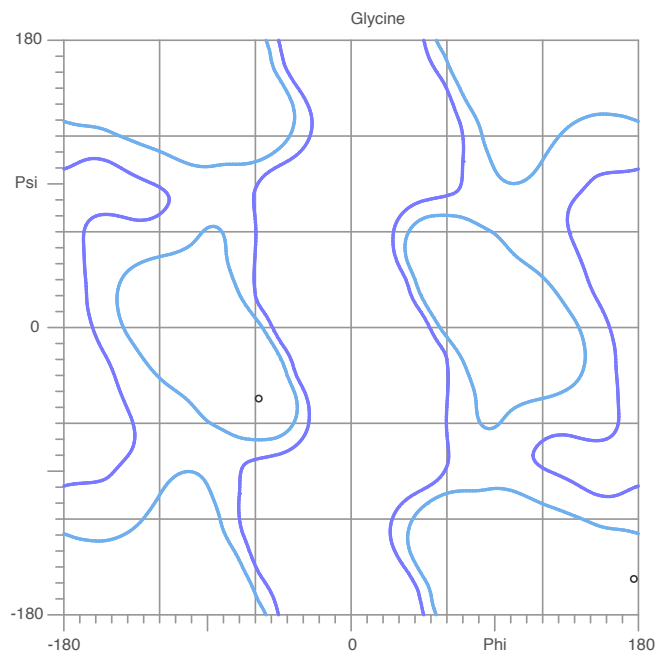
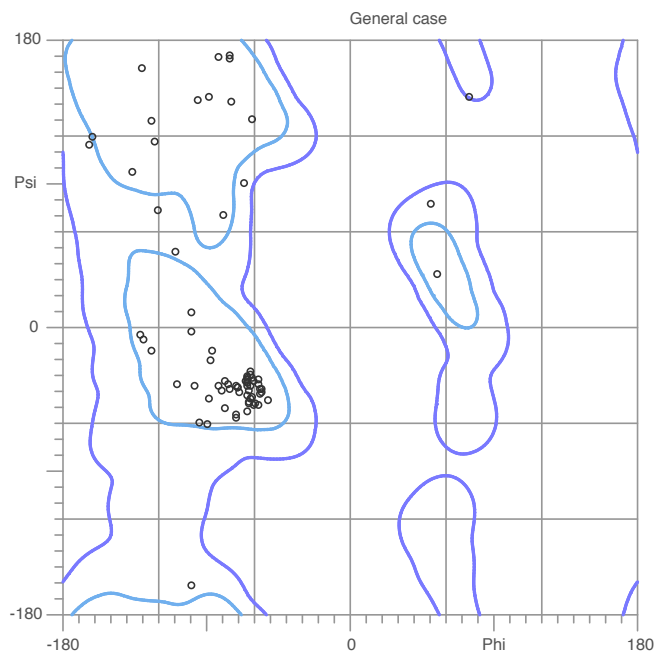
There were 1 outliers (phi, psi):
[5] 79 THR (176.7, -25.1)

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 6



88.9% (72/81) of all residues were in favored (98%) regions.
100.0% (81/81) of all residues were in allowed (>99.8%) regions.

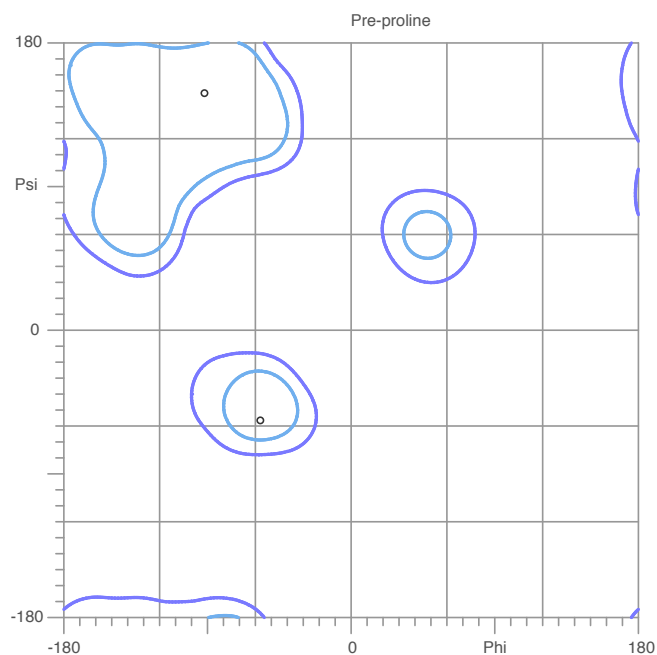
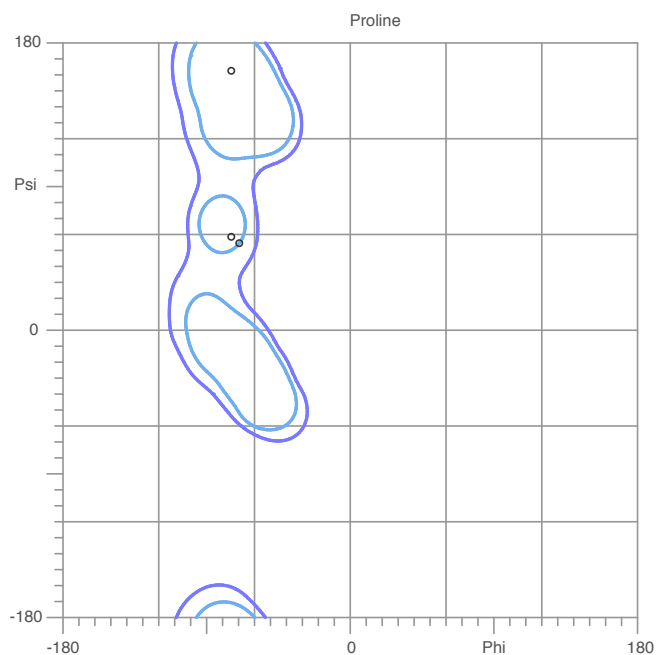
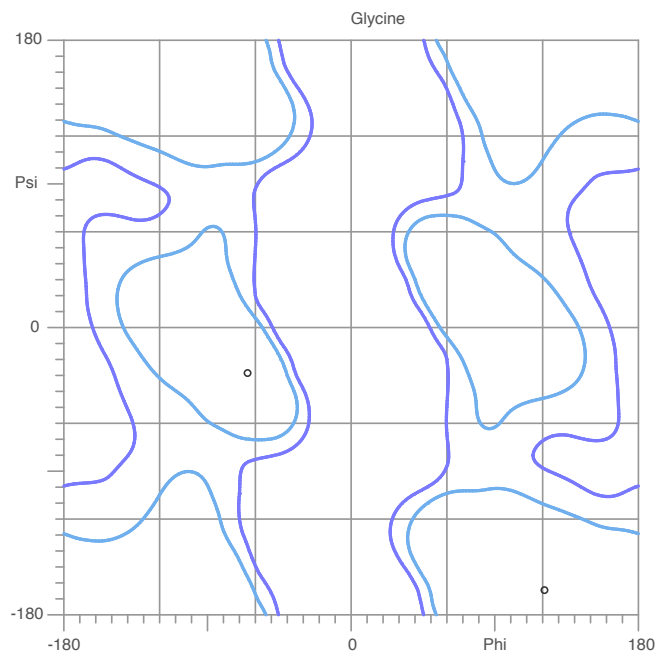
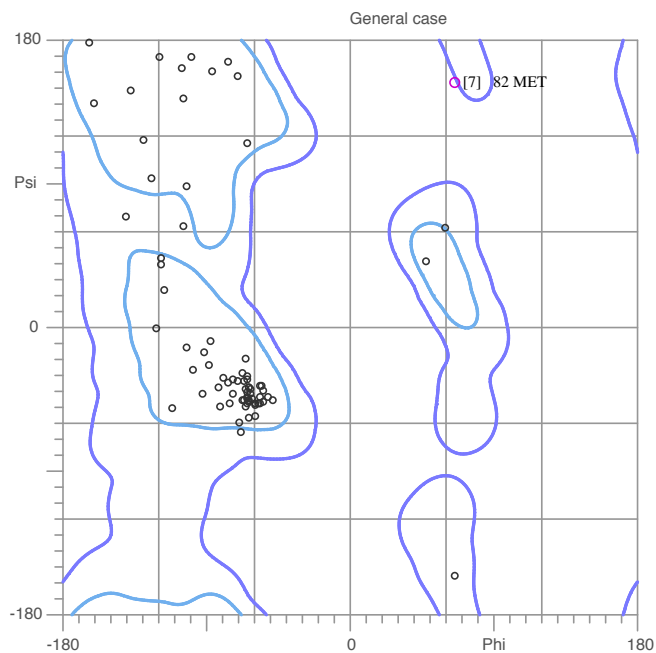
There were no outliers.

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 7



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.

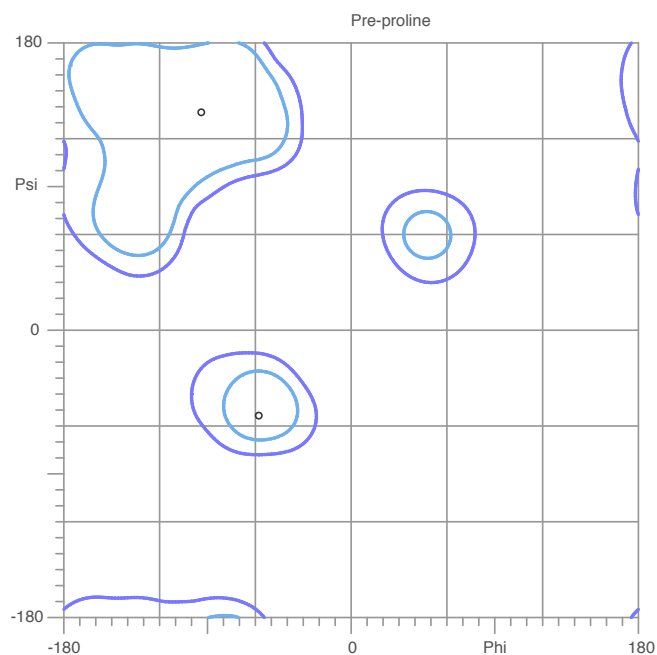
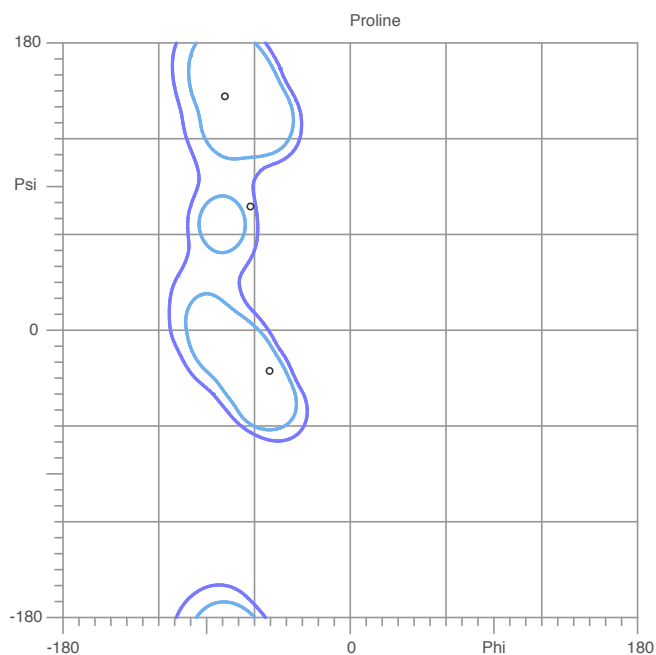
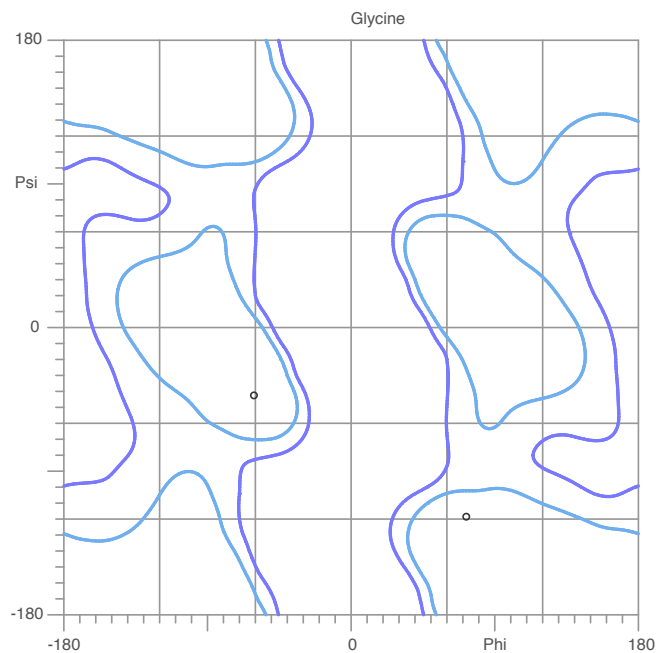
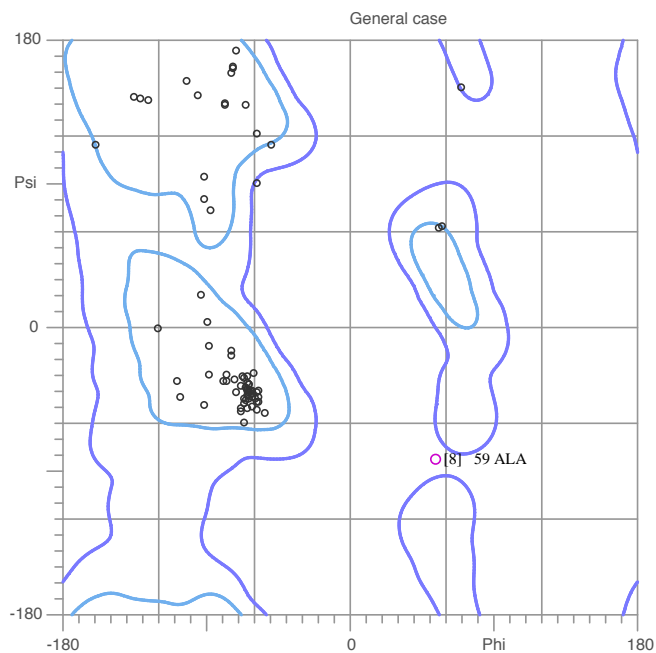
There were 1 outliers (phi, psi):
[7] 82 MET (65.0, 155.0)

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 8



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.

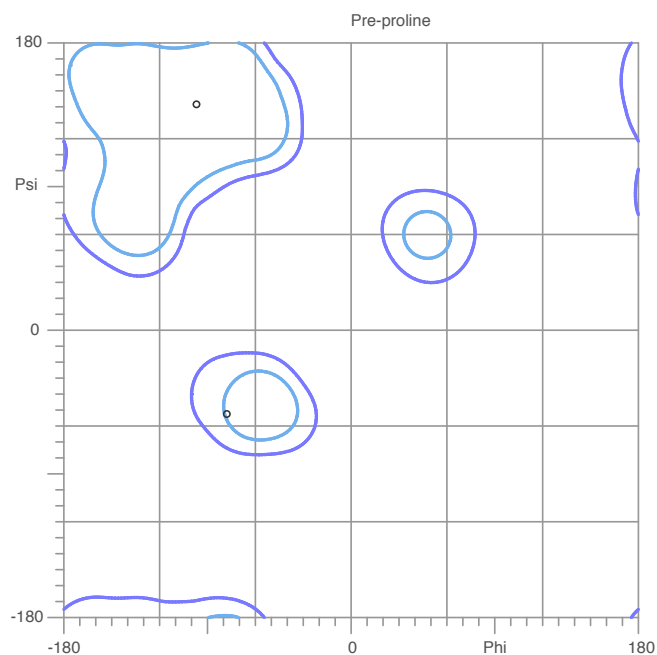
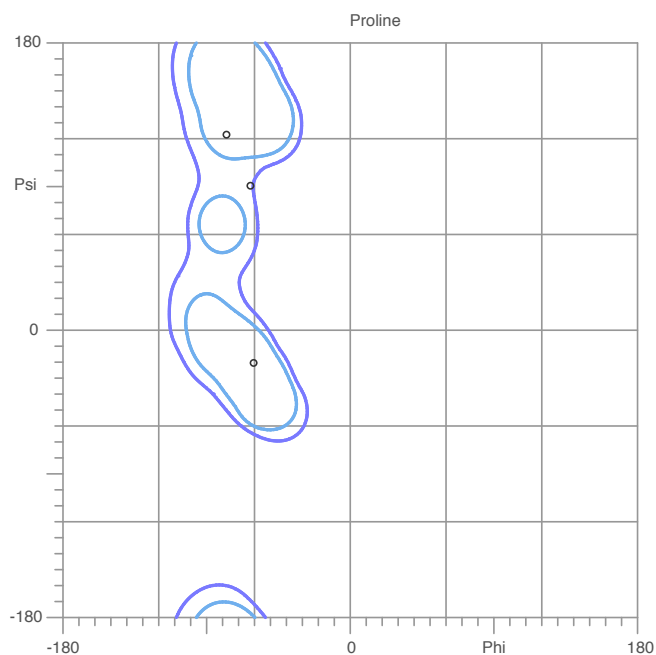
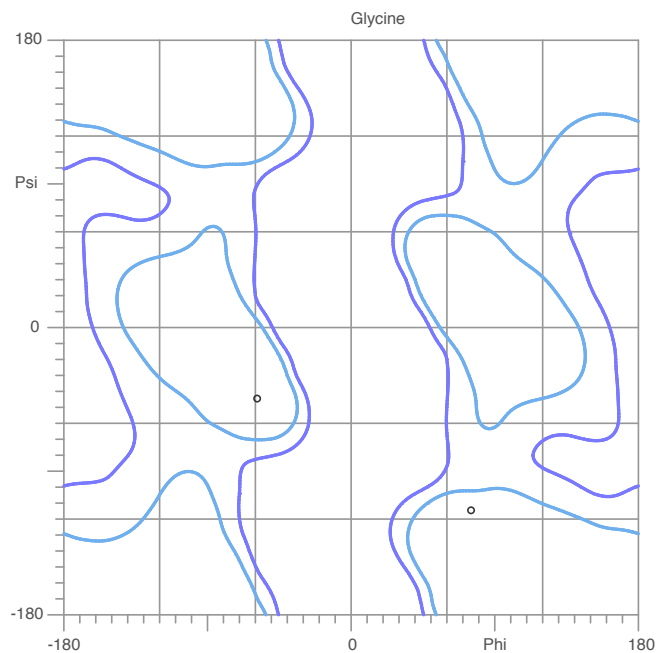
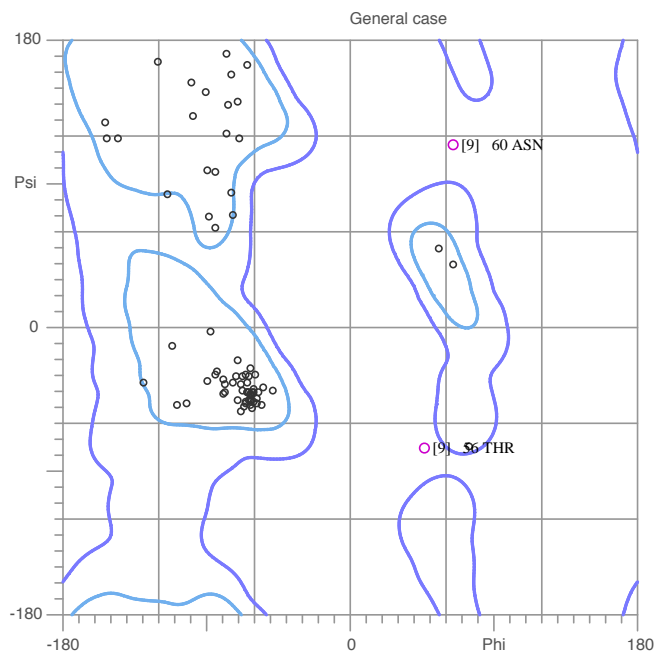
There were 1 outliers (phi, psi):
[8] 59 ALA (53.1, -82.8)

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 9



93.8% (76/81) of all residues were in favored (98%) regions.
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

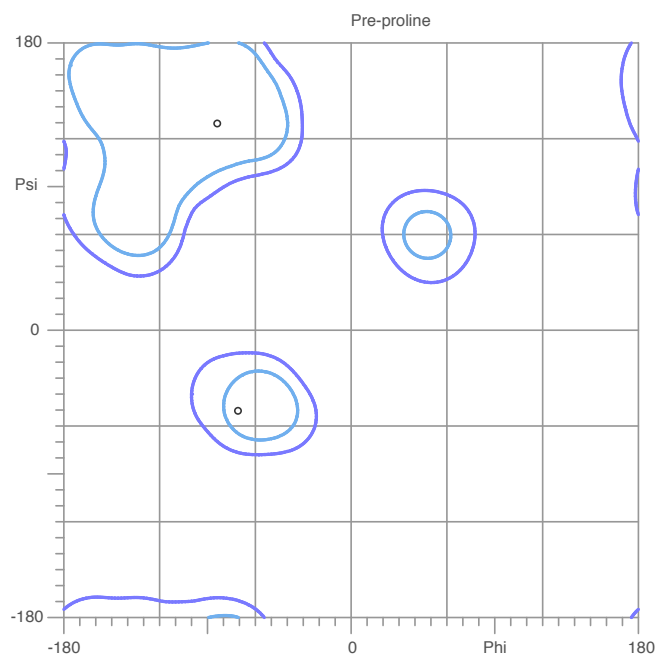
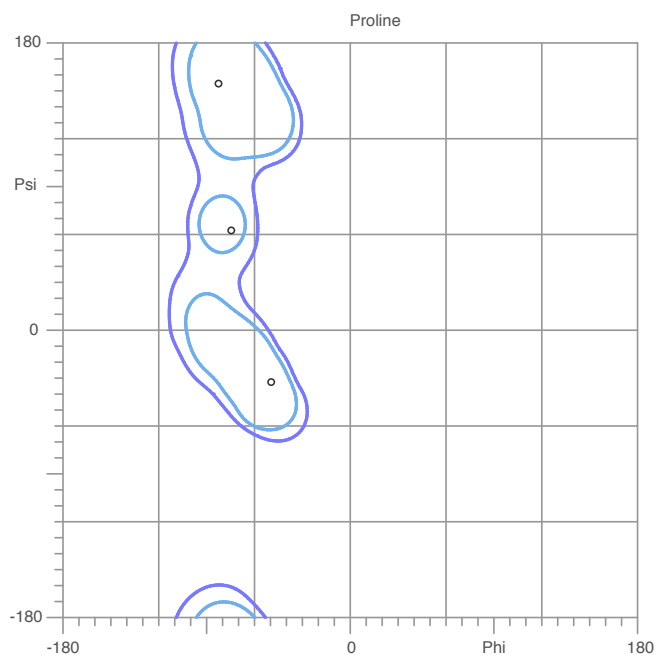
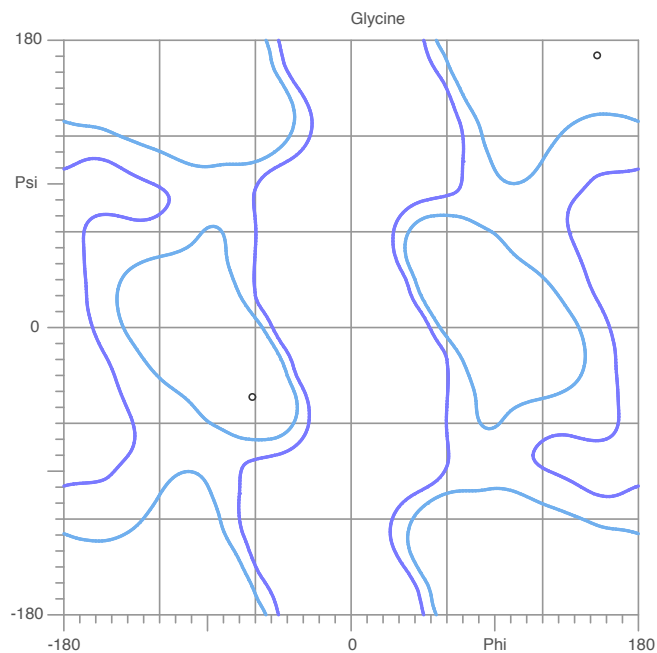
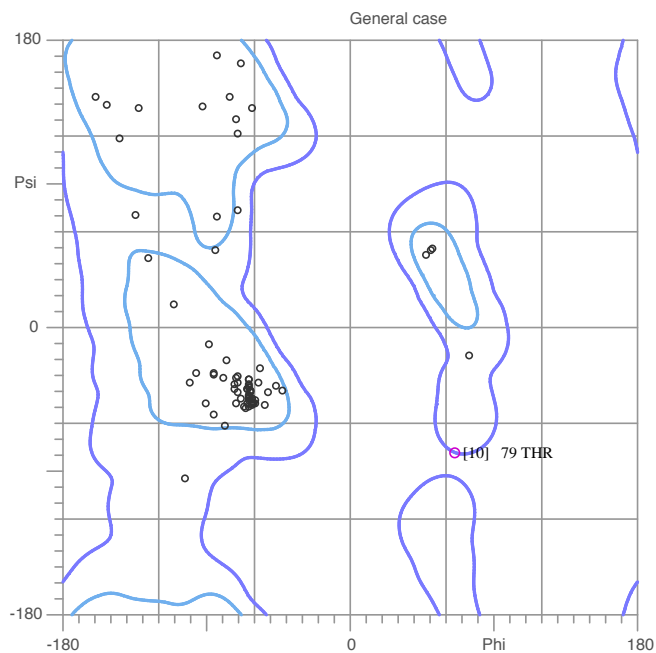
There were 2 outliers (phi, psi):

[9] 56 THR (46.5, -75.0)

[9] 60 ASN (65.0, 115.0)

MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 10



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.

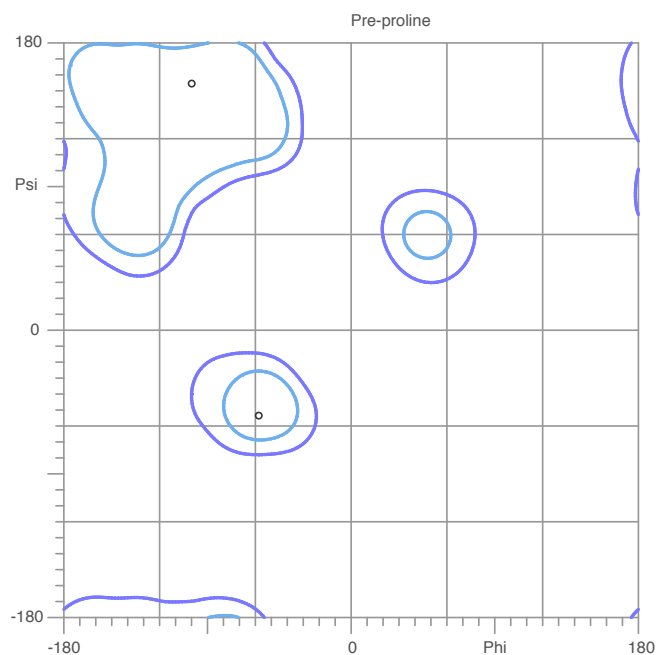
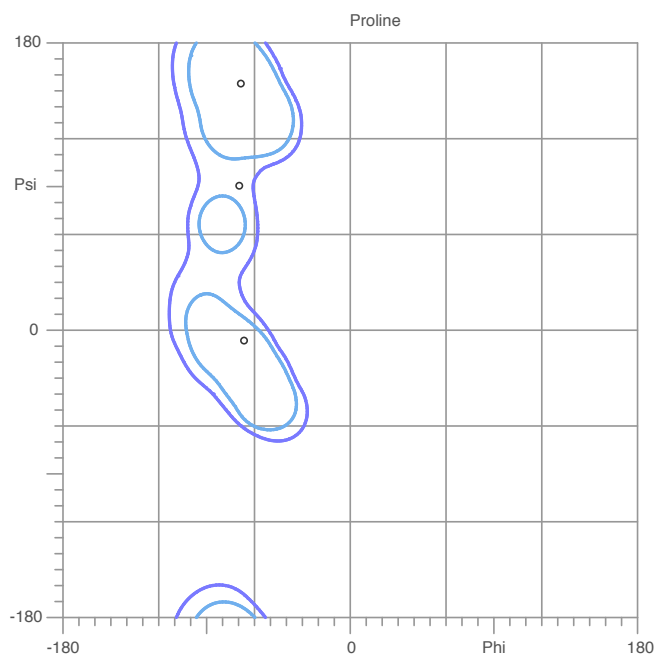
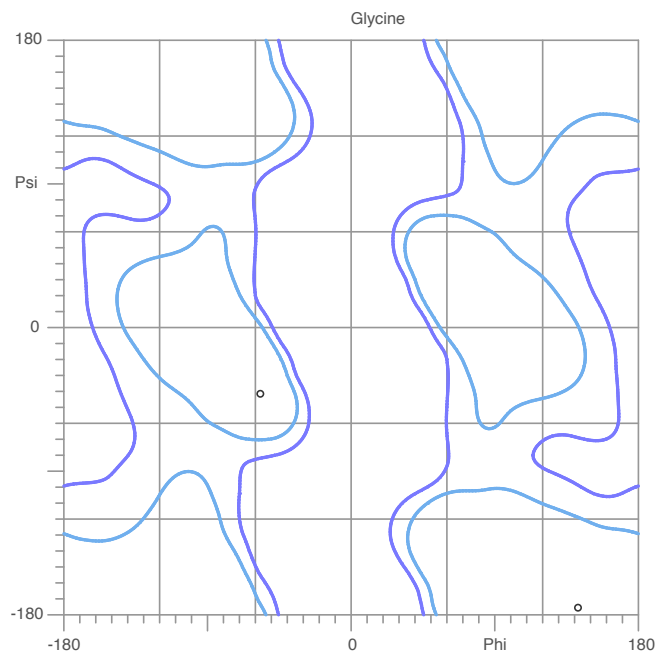
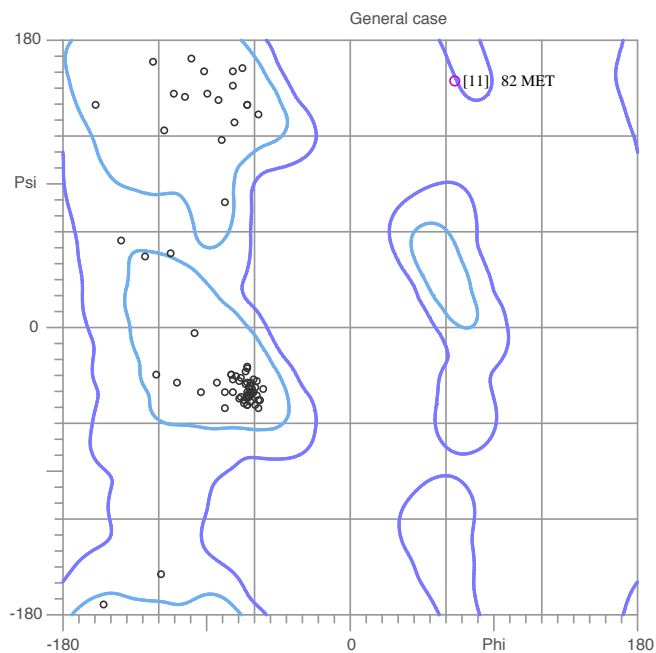
There were 1 outliers (phi, psi):
[10] 79 THR (65.1, -78.5)

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 11



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.

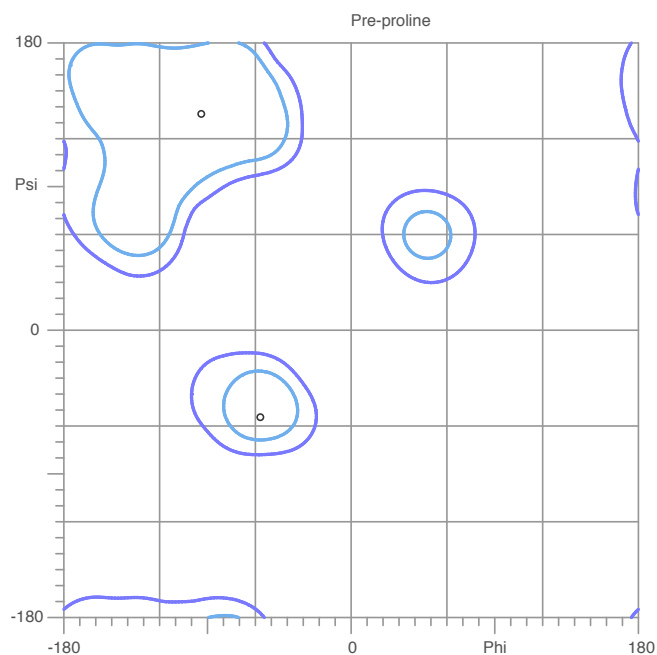
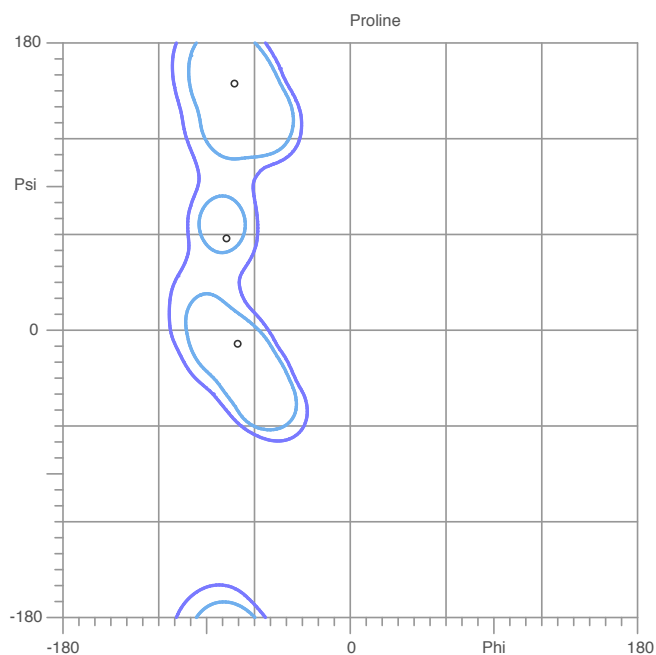
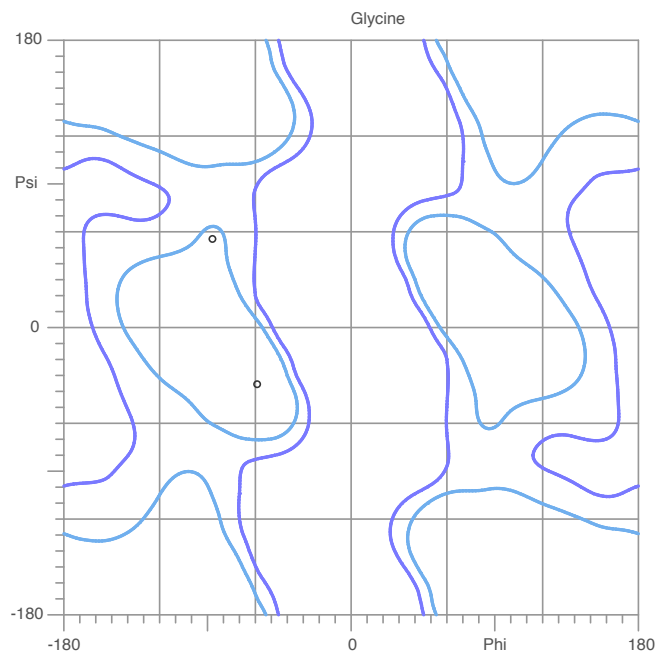
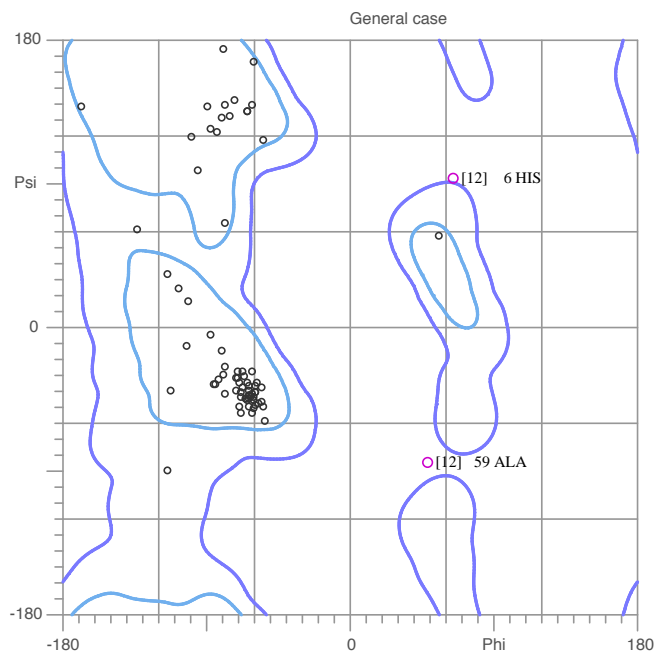
There were 1 outliers (phi, psi):
[11] 82 MET (65.0, 155.0)

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 12



95.1% (77/81) of all residues were in favored (98%) regions.
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

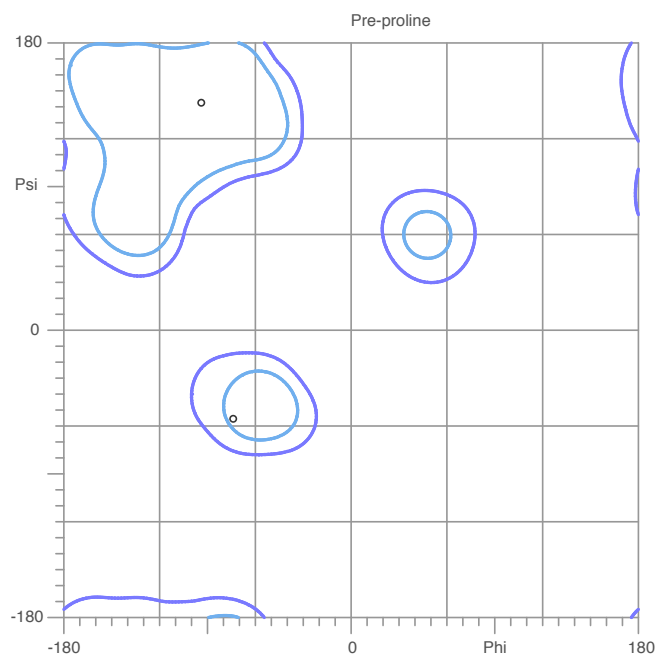
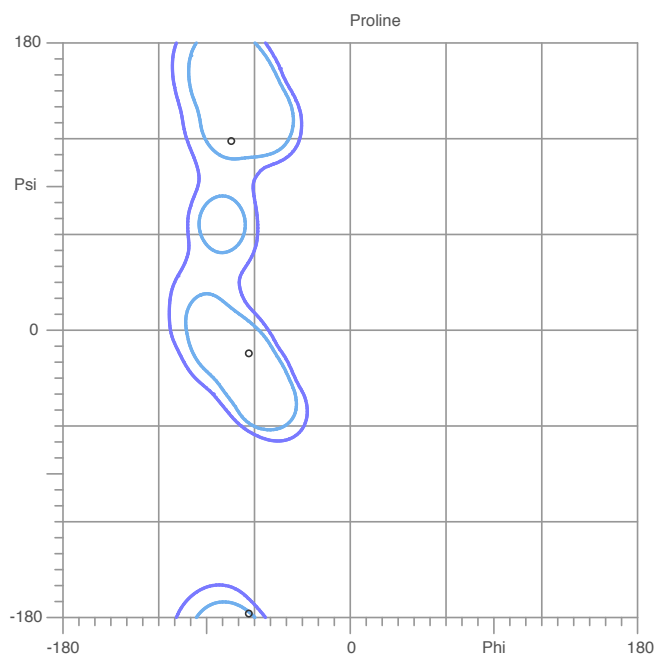
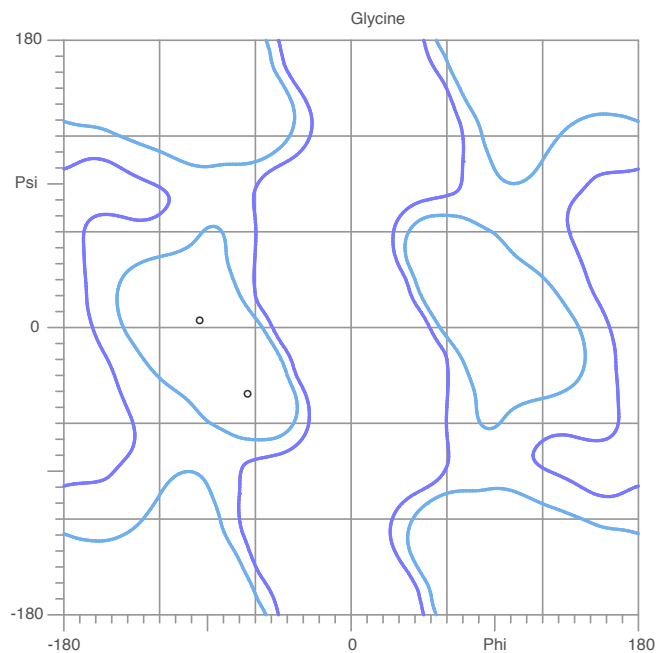
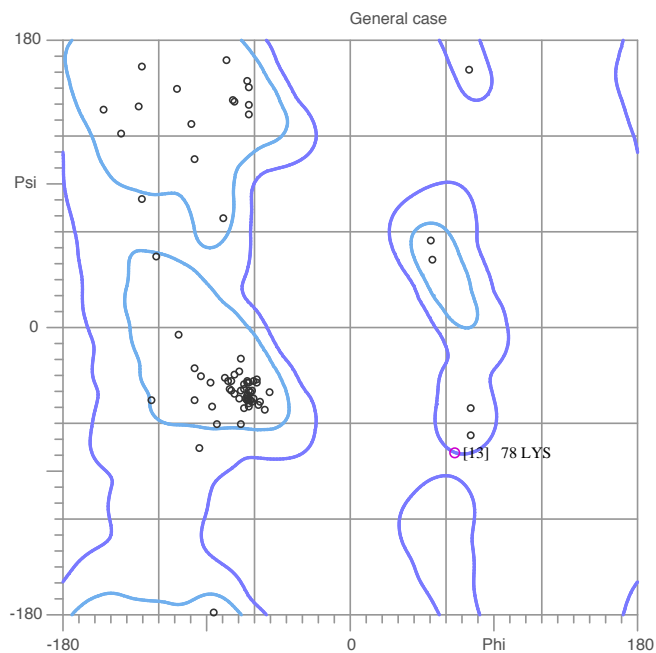
There were 2 outliers (phi, psi):

[12] 6 HIS (65.0, 95.0)

[12] 59 ALA (48.8, -84.9)

MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 13



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.

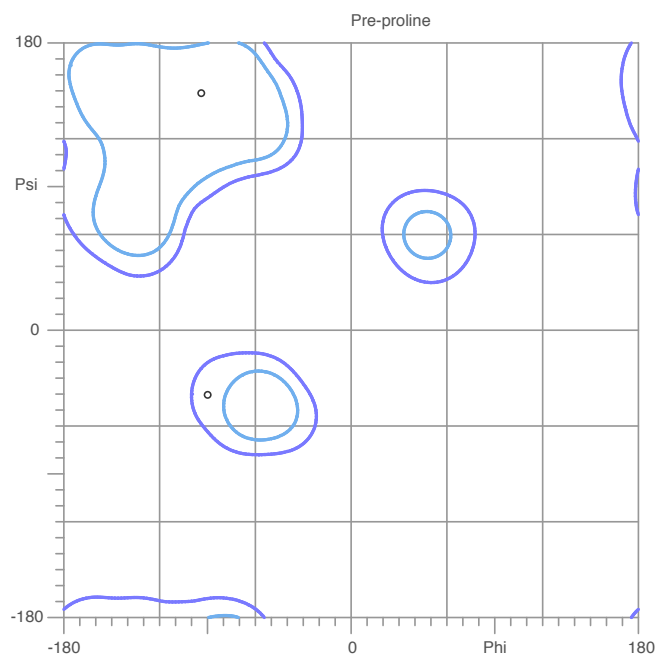
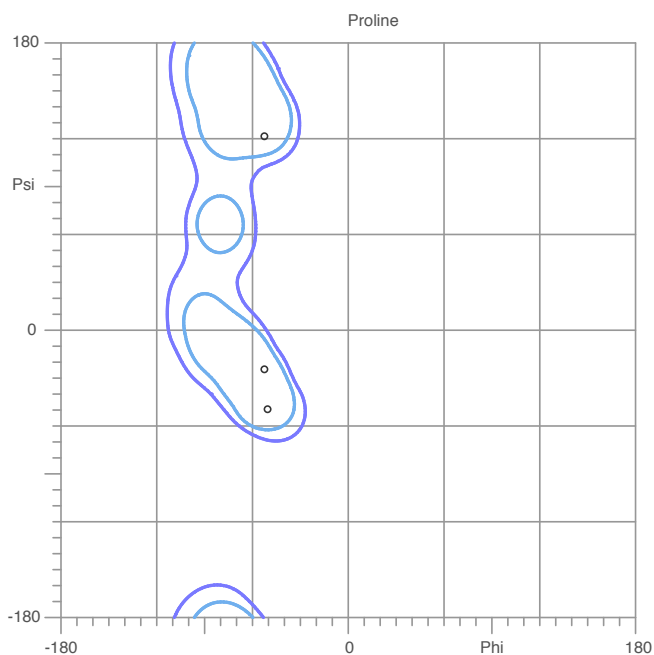
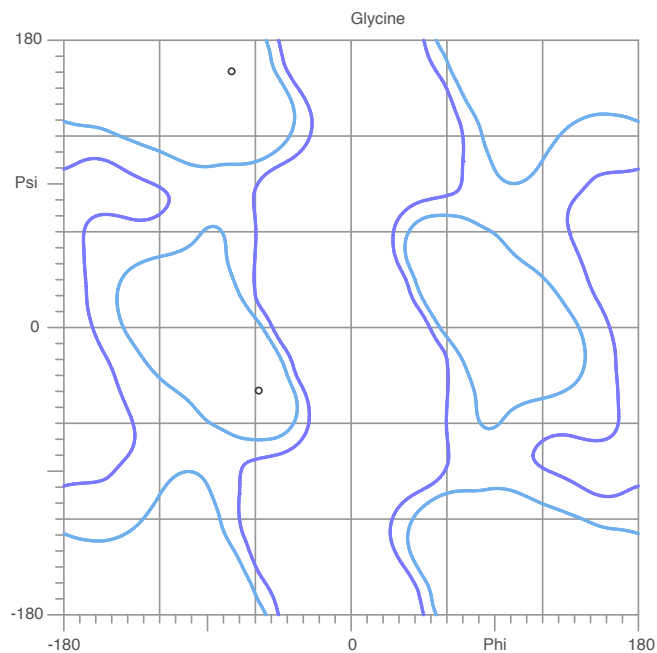
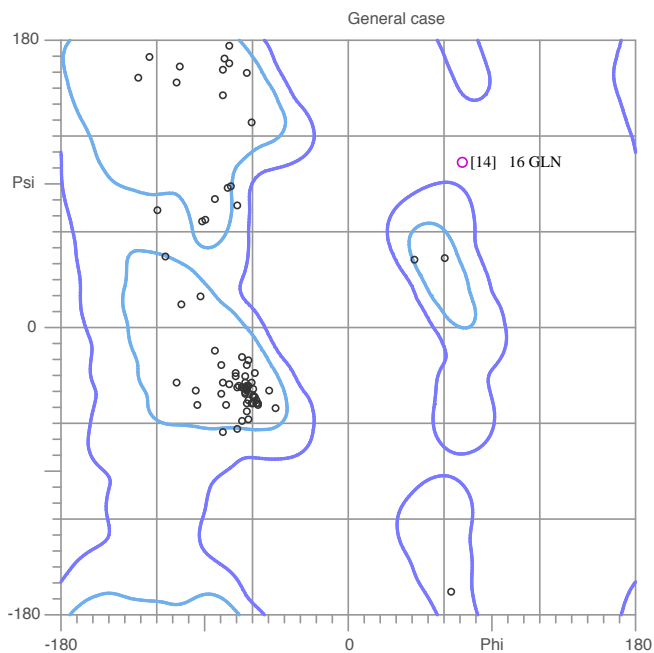
There were 1 outliers (phi, psi):
[13] 78 LYS (65.0, -78.2)

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 14



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.

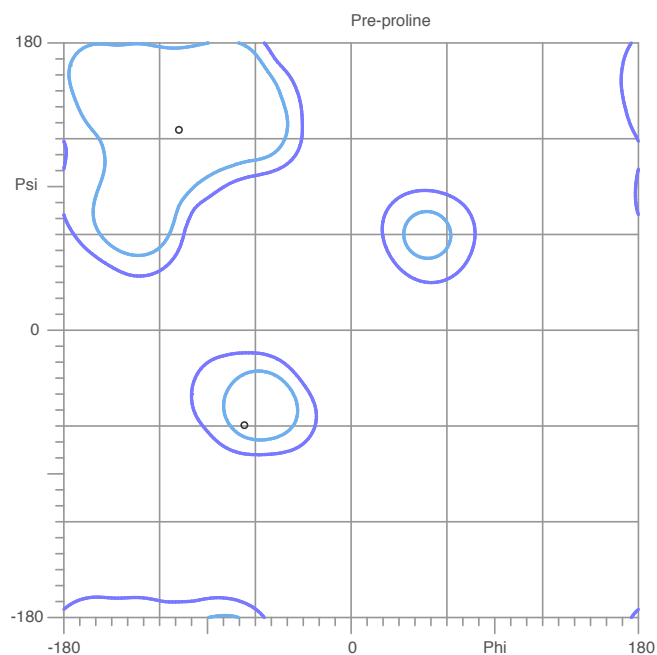
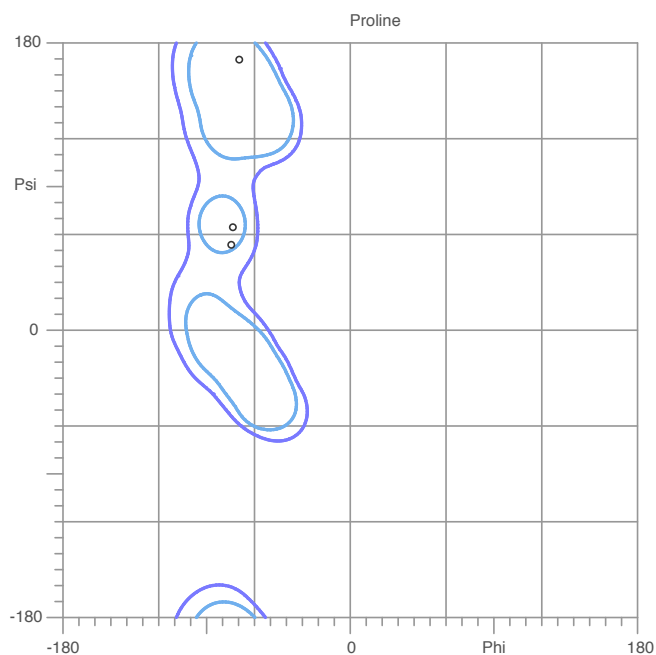
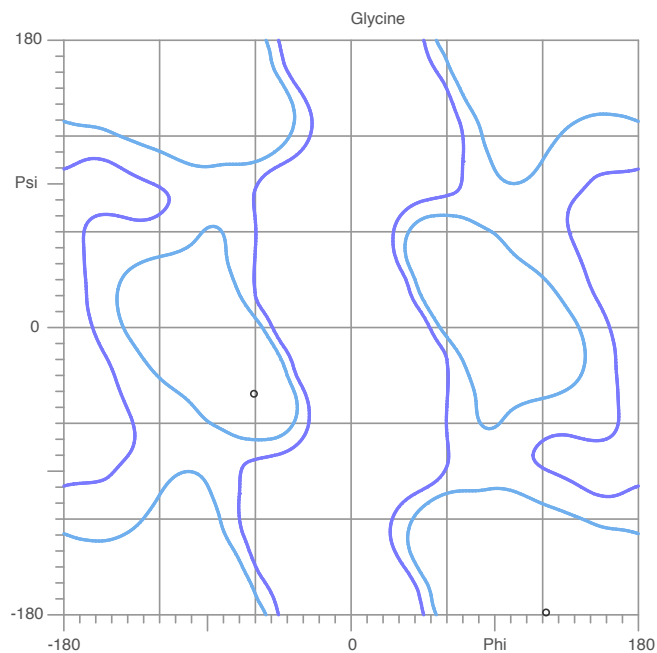
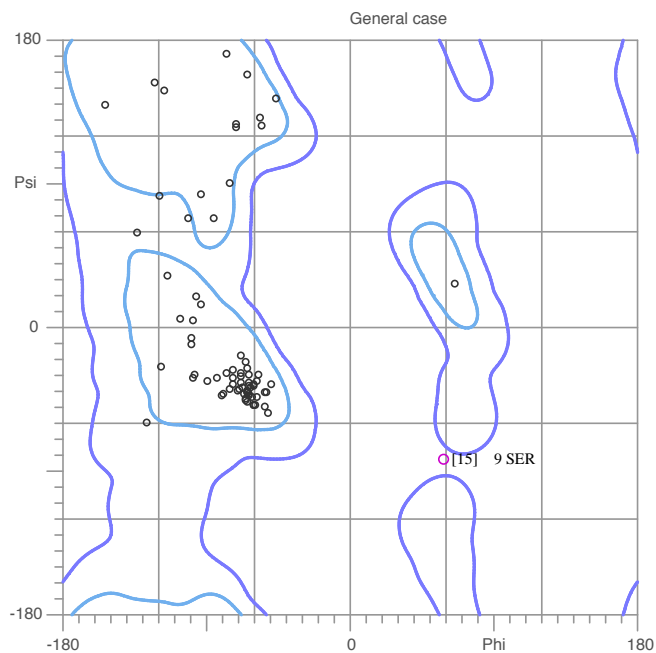
There were 1 outliers (phi, psi):
[14] 16 GLN (71.9, 104.9)

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

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 15



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.

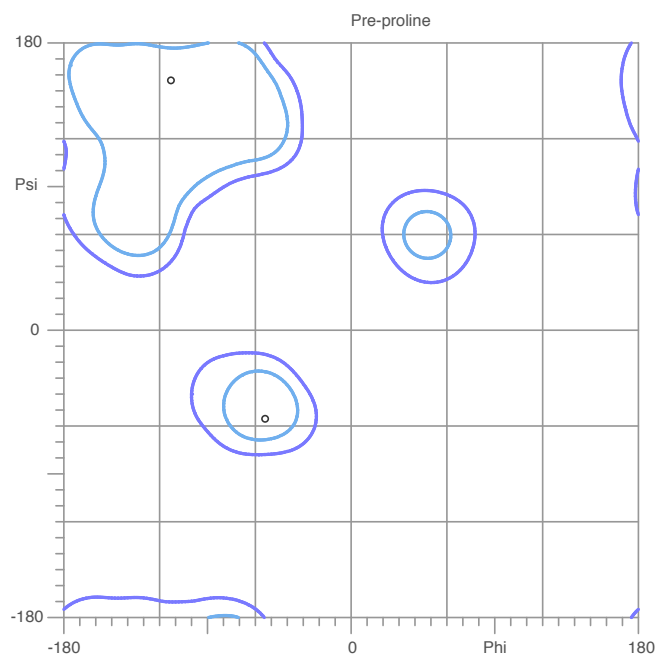
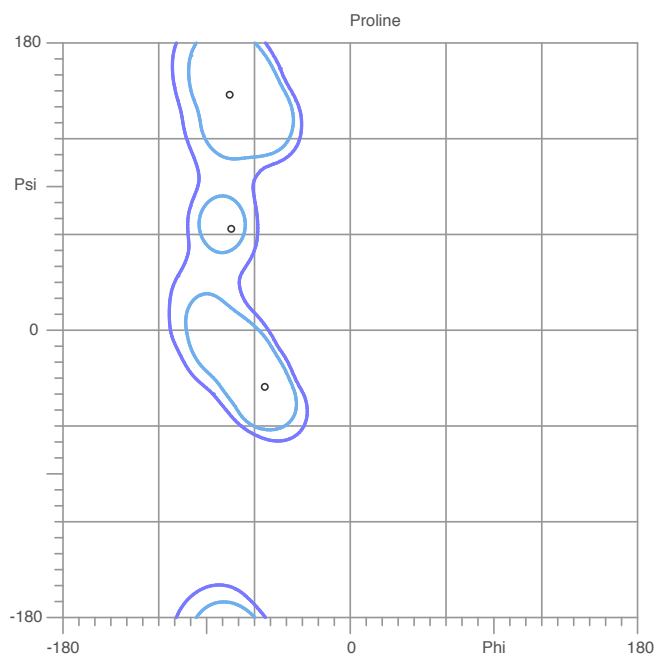
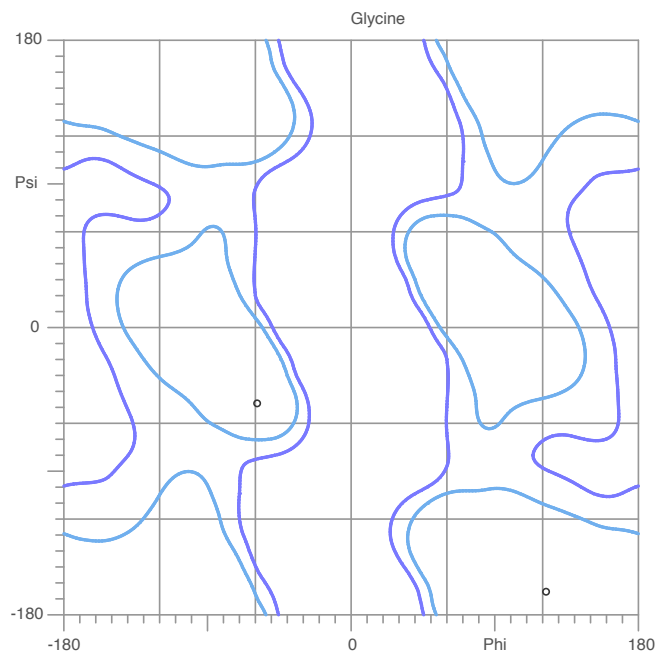
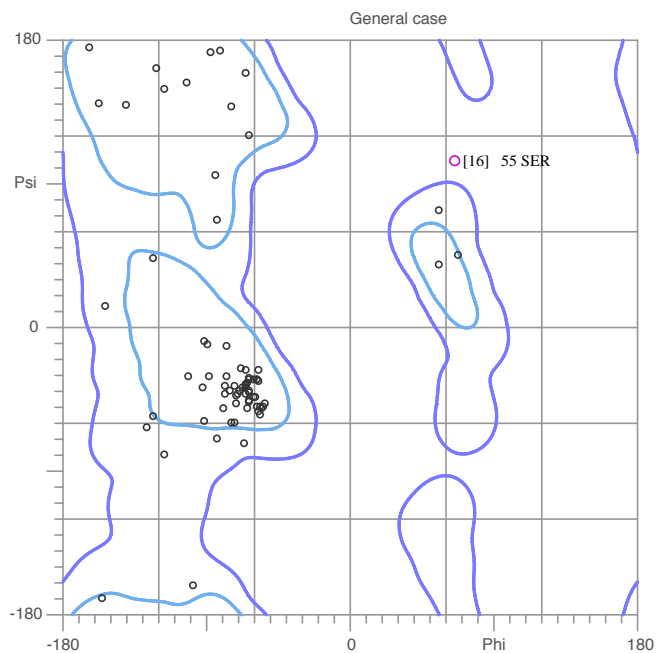
There were 1 outliers (phi, psi):
[15] 9 SER (58.1, -82.3)

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 16



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.

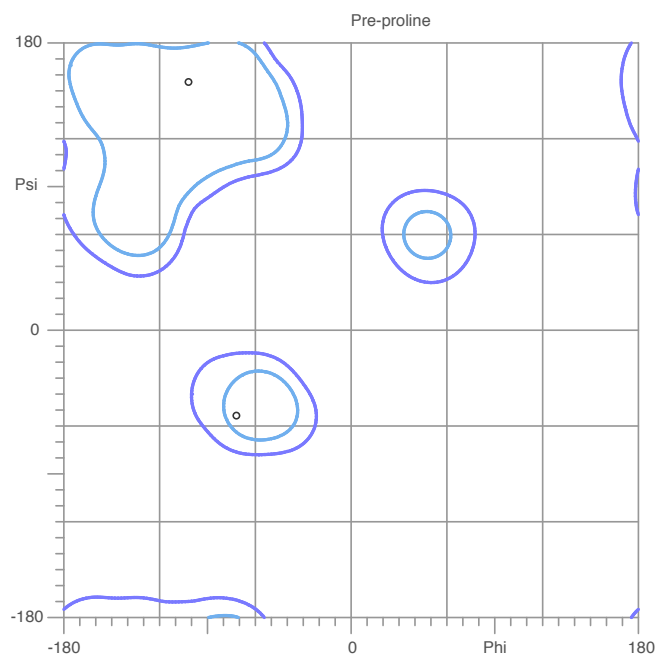
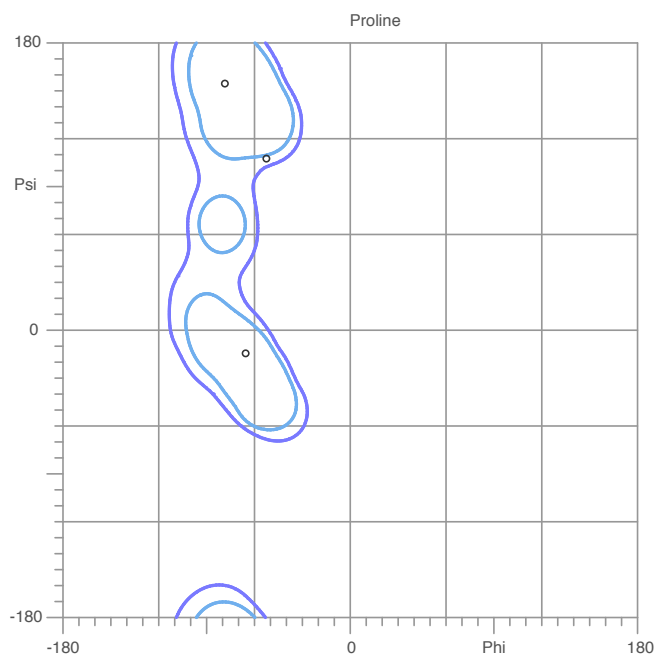
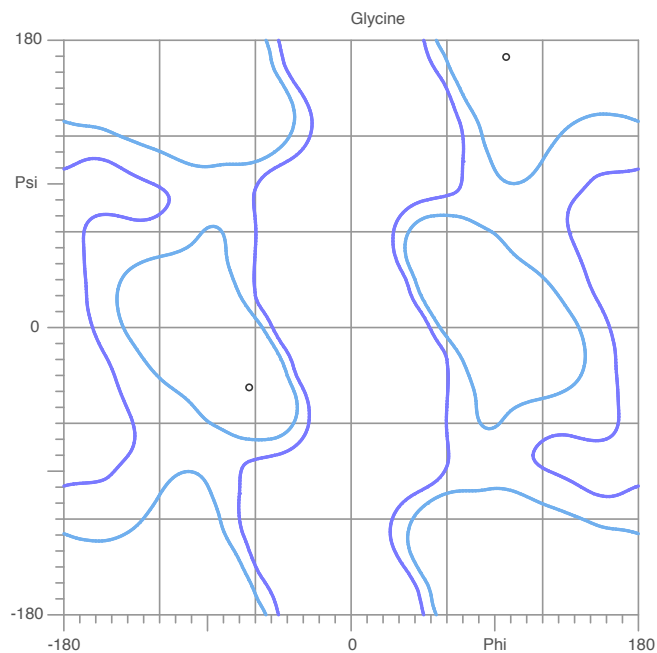
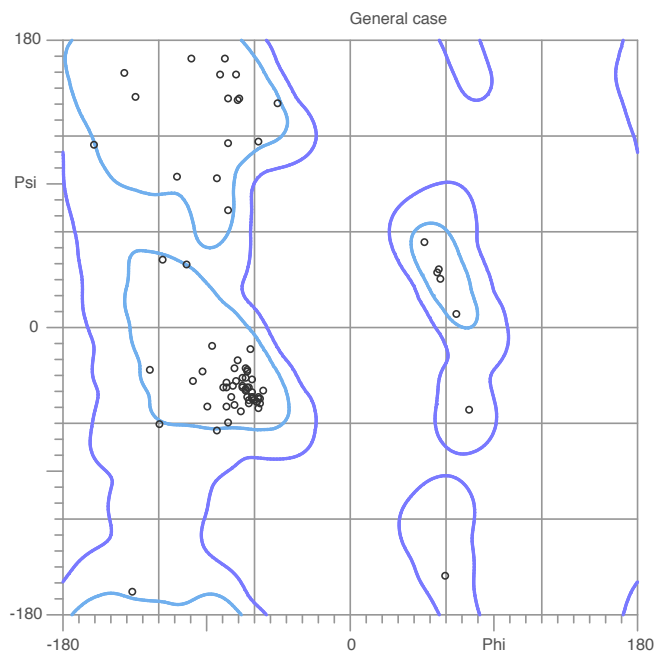
There were 1 outliers (phi, psi):
[16] 55 SER (65.0, 105.0)

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 17



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.

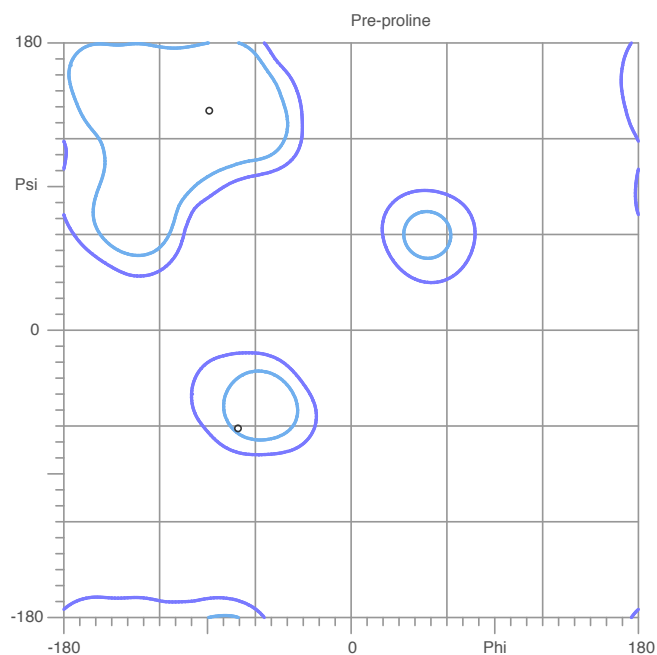
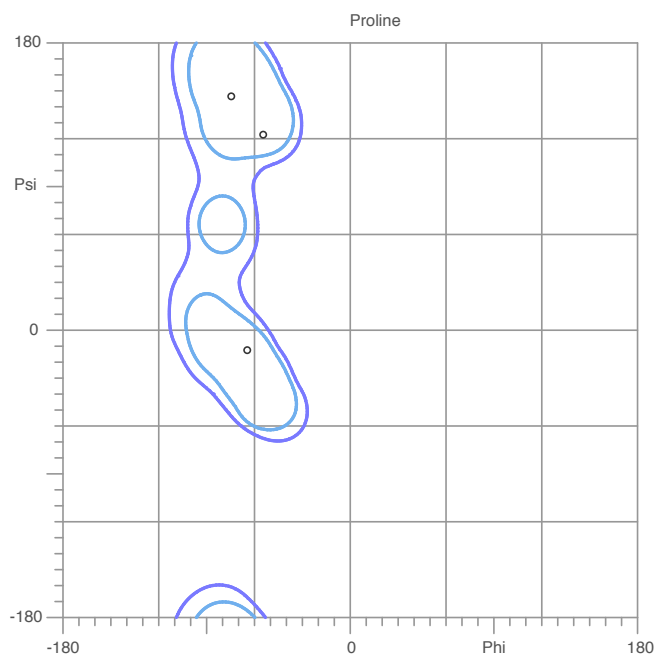
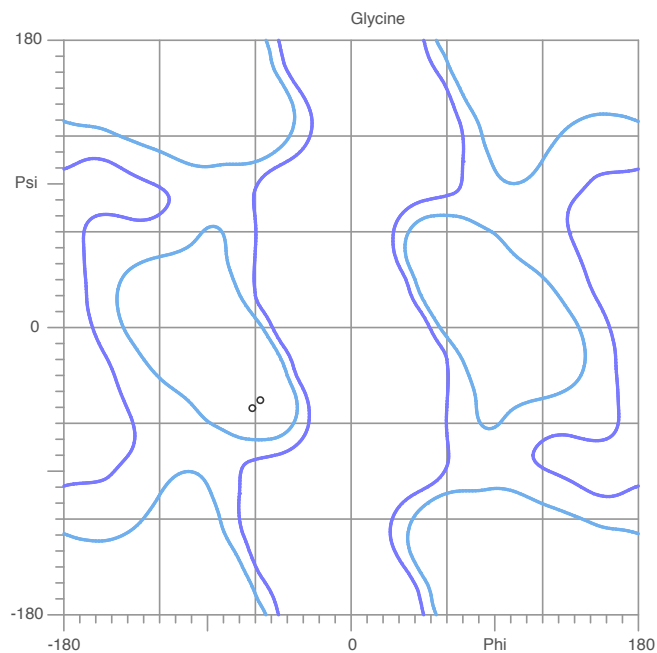
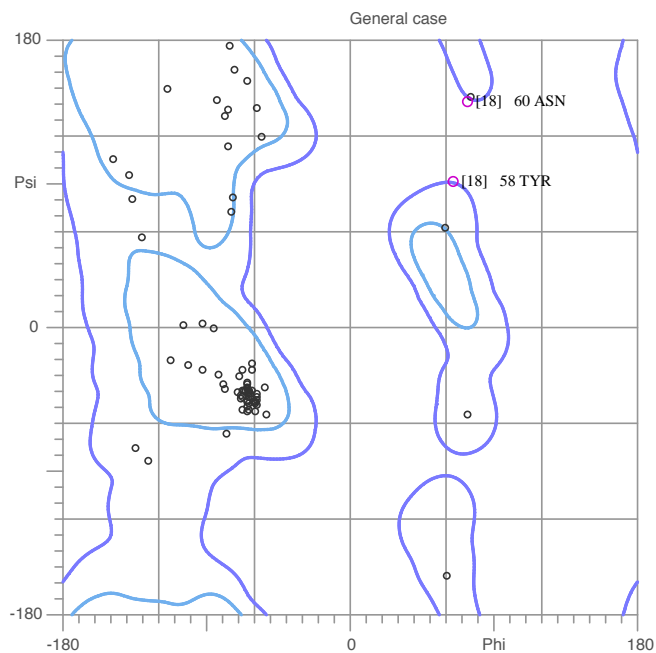
There were no outliers.

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 18



86.4% (70/81) of all residues were in favored (98%) regions.
97.5% (79/81) of all residues were in allowed (>99.8%) regions.

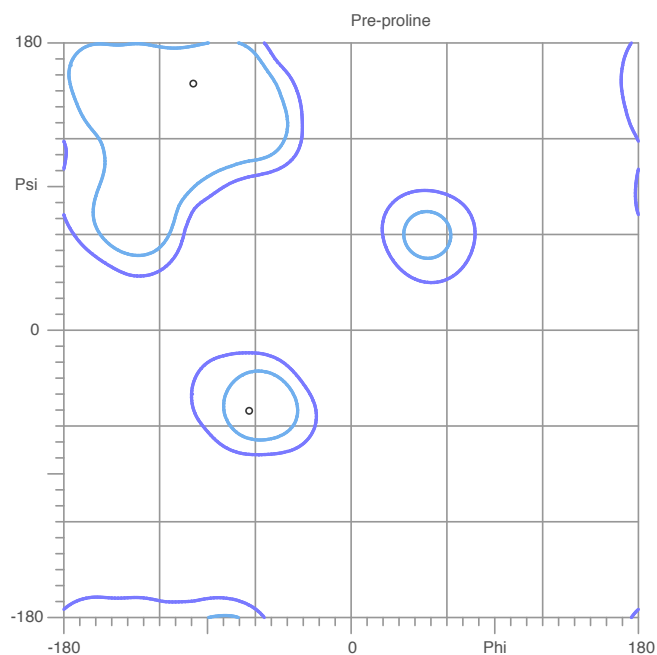
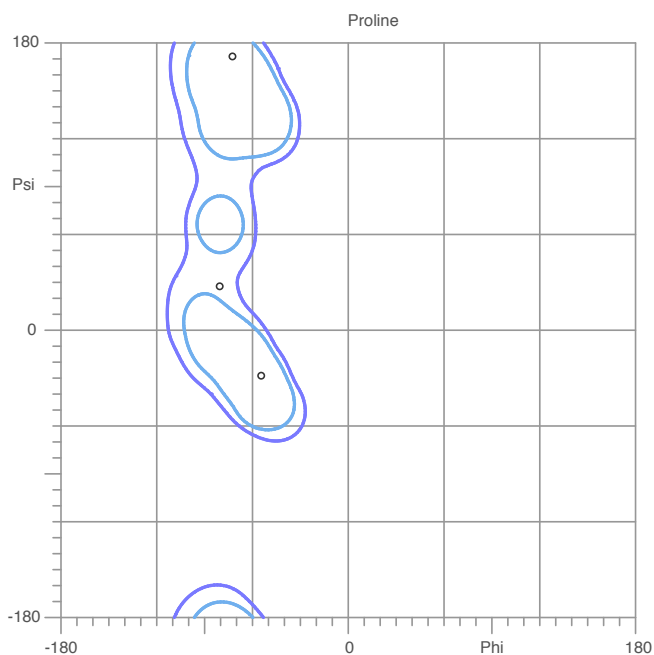
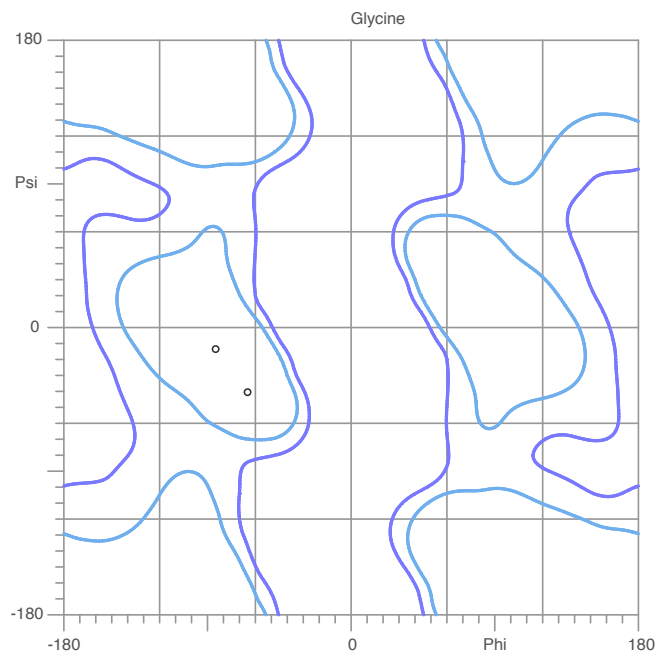
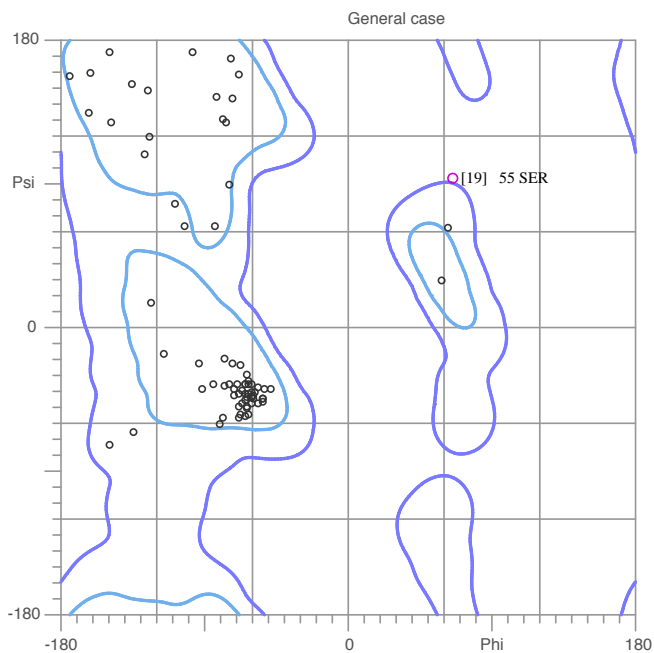
There were 2 outliers (phi, psi):

[18] 58 TYR (64.7, 92.5)

[18] 60 ASN (73.5, 142.0)

MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 19



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.

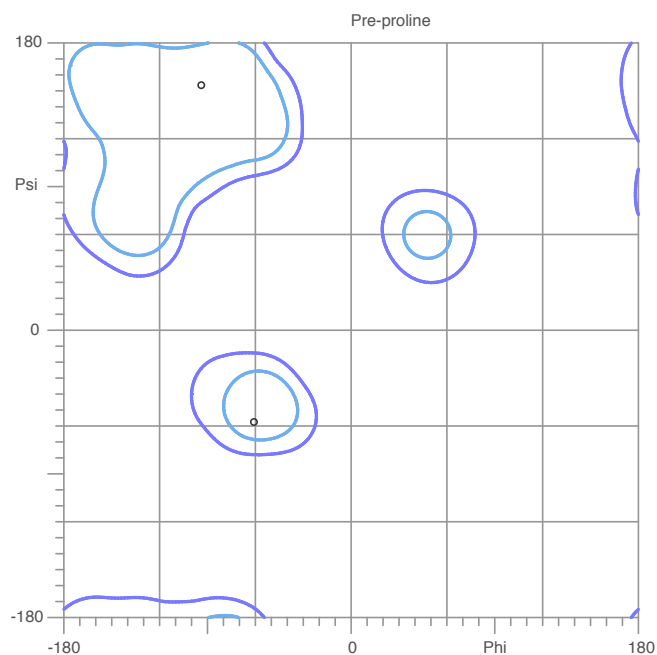
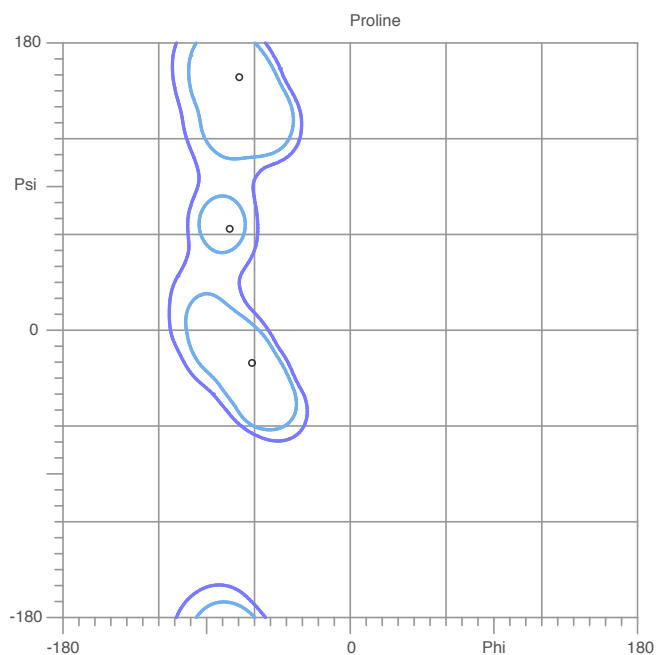
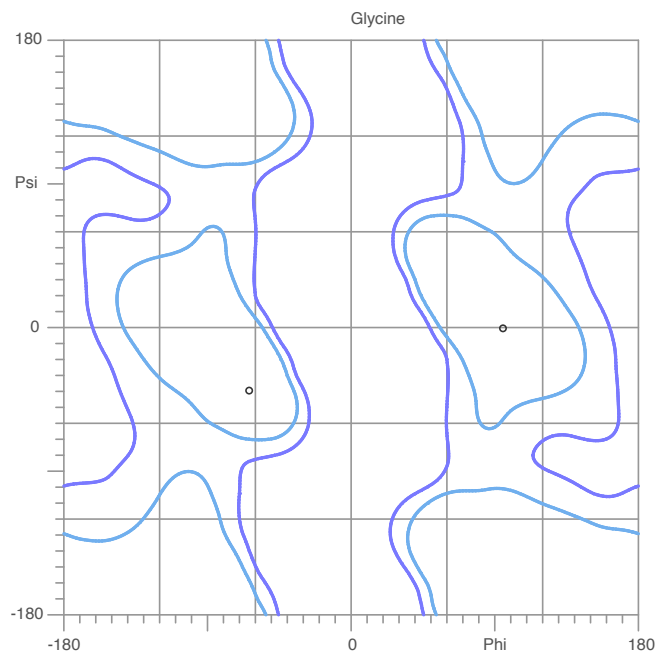
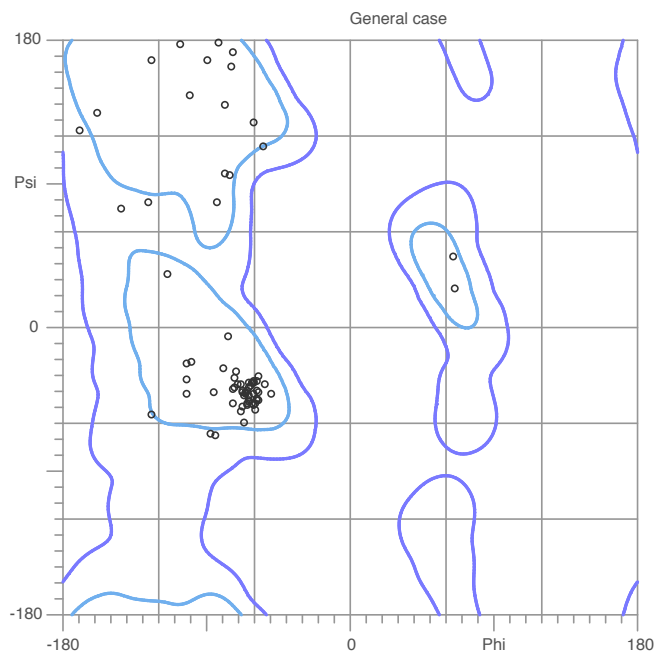
There were 1 outliers (phi, psi):
[19] 55 SER (65.1, 95.0)

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MolProbity Ramachandran analysis

HR4435B_R3Cons_em_bcr3.pdb, model 20



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.

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