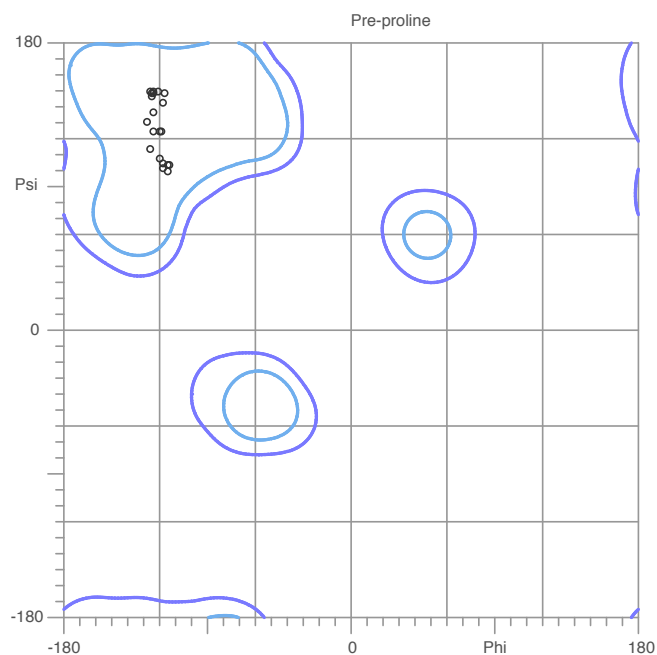
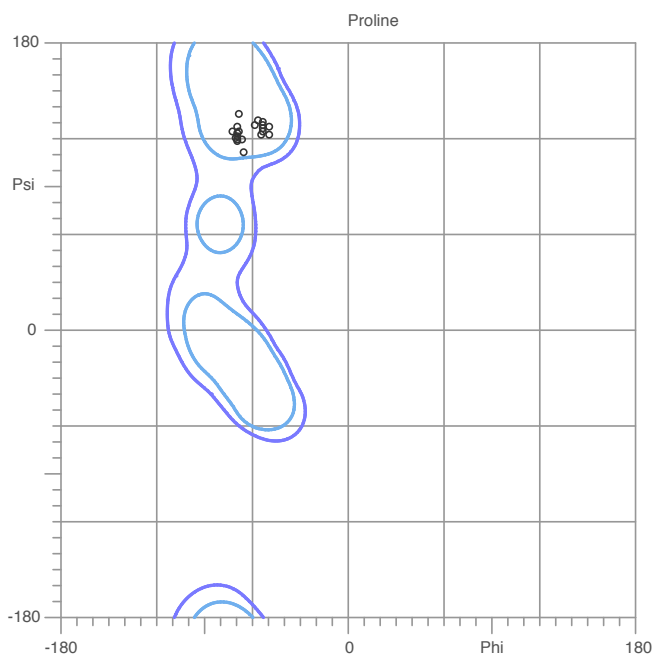
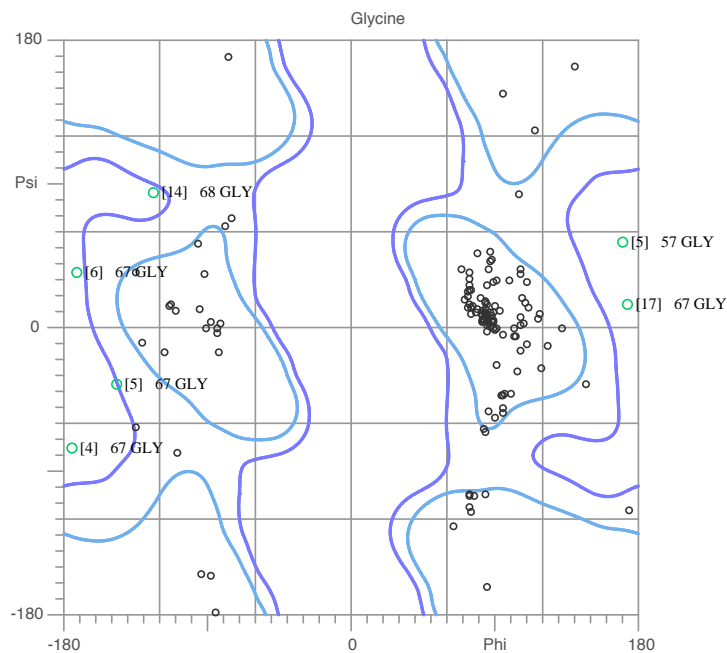
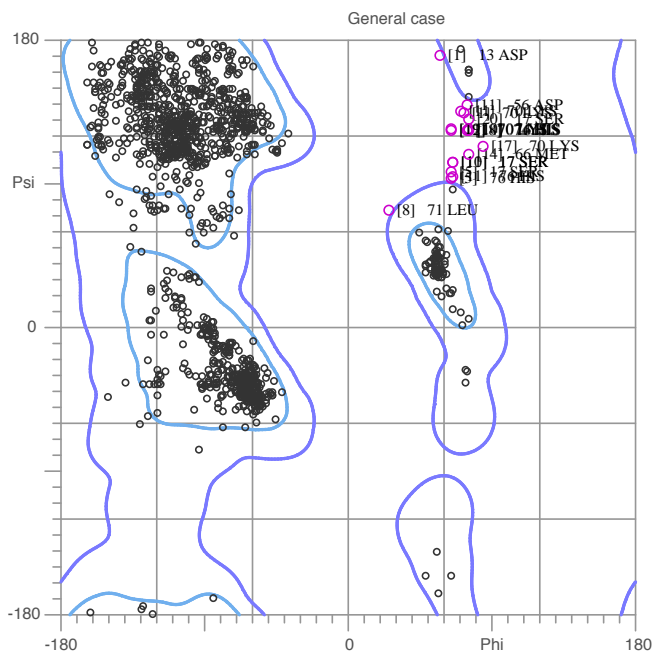


MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, all models



94.4% (1435/1520) of all residues were in favored (98%) regions.
98.4% (1496/1520) of all residues were in allowed (>99.8%) regions.

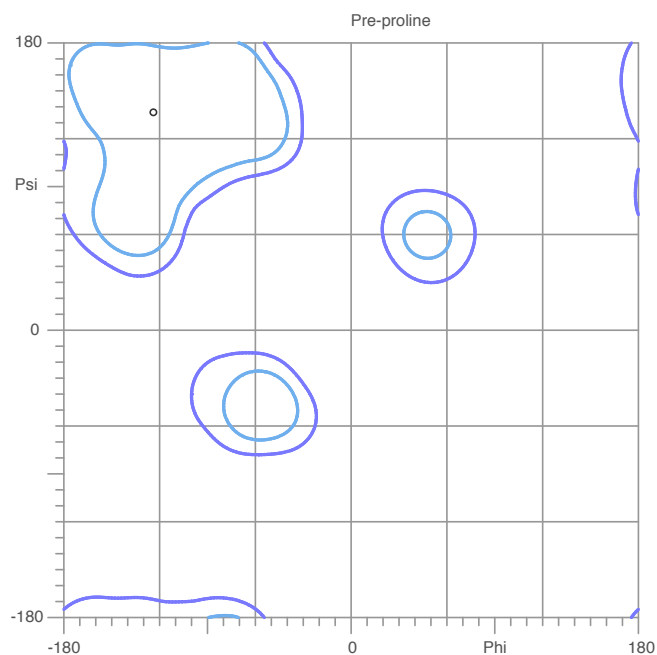
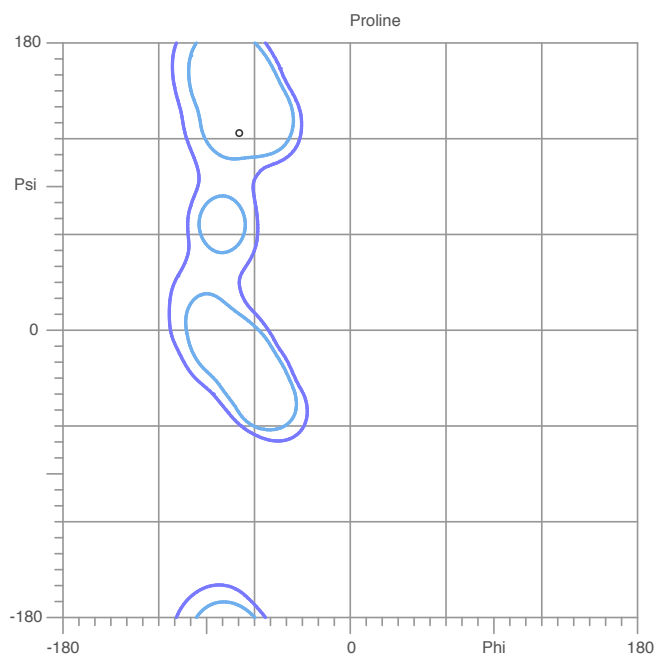
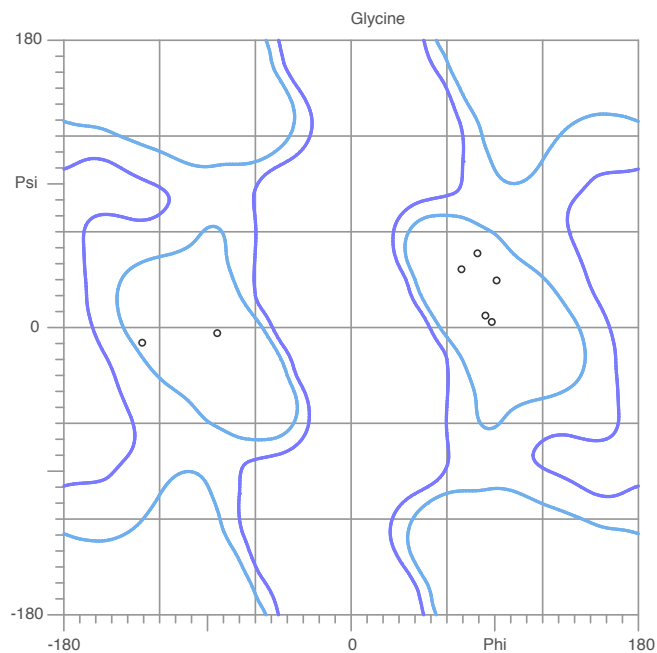
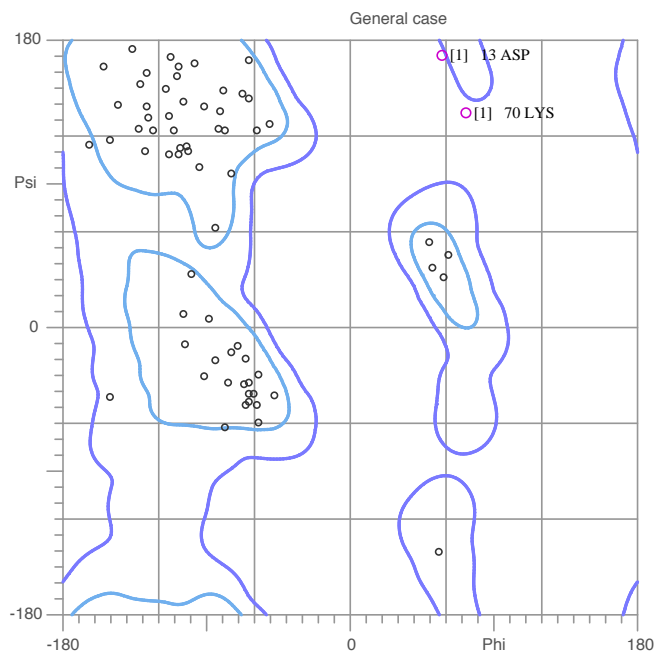
There were 24 outliers (phi, psi):

- [1] 13 ASP (57.4, 171.9)
- [1] 70 LYS (72.4, 135.4)
- [4] 67 GLY (-175.0, -75.0)
- [5] 17 SER (65.0, 98.0)
- [5] 57 GLY (170.2, 55.0)
- [5] 67 GLY (-147.2, -35.0)
- [5] 76 HIS (65.0, 94.9)
- [6] 67 GLY (-172.4, 35.1)
- [8] 71 LEU (25.0, 74.9)
- [10] 17 SER (65.0, 104.9)

- [10] 74 HIS (75.0, 125.0)
- [11] 17 SER (65.0, 105.0)
- [11] 56 ASP (75.0, 140.4)
- [11] 70 LYS (70.1, 136.5)
- [11] 76 HIS (65.0, 95.0)
- [12] 70 LYS (65.0, 125.0)
- [14] 66 MET (75.0, 110.0)
- [14] 68 GLY (-125.0, 85.1)
- [14] 76 HIS (75.1, 125.0)
- [17] 67 GLY (173.1, 15.1)
- [17] 70 LYS (85.0, 115.0)
- [18] 74 HIS (74.9, 125.0)
- [19] 70 LYS (65.0, 125.0)
- [20] 17 SER (75.3, 131.2)

MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 1



93.4% (71/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

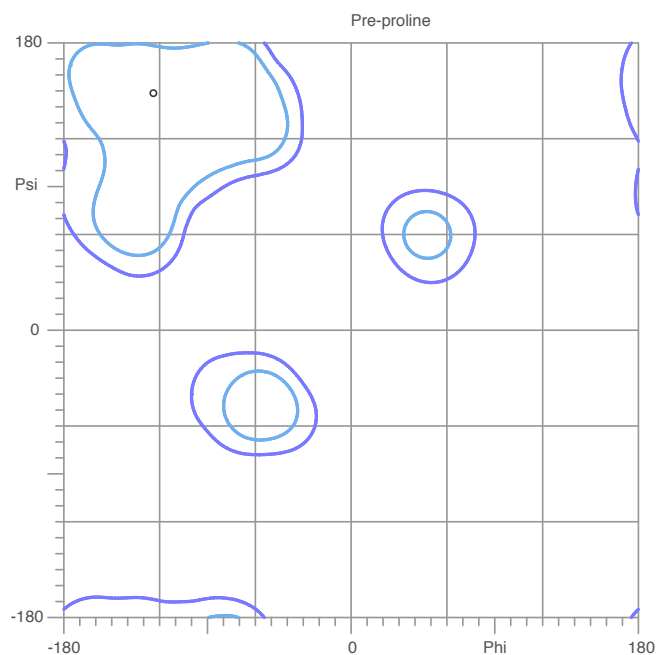
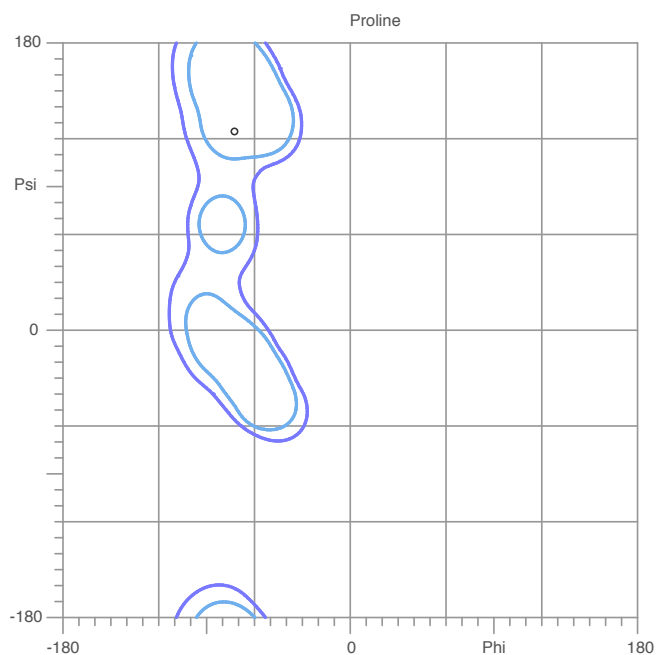
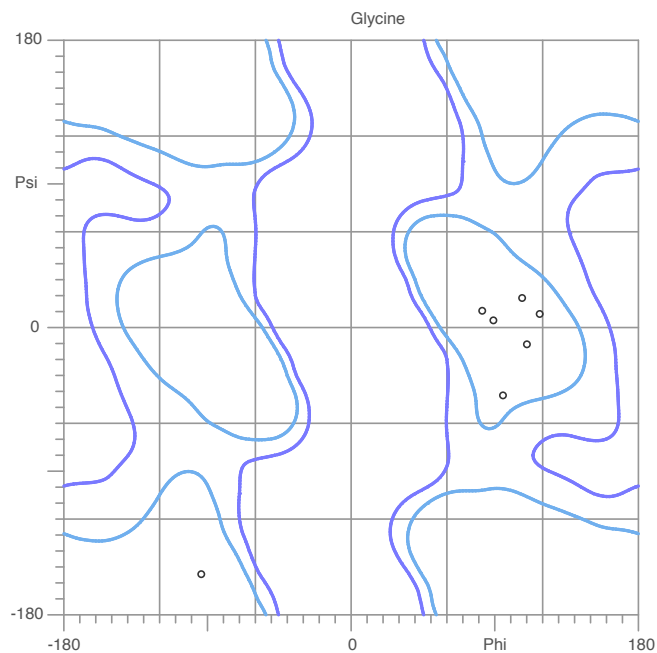
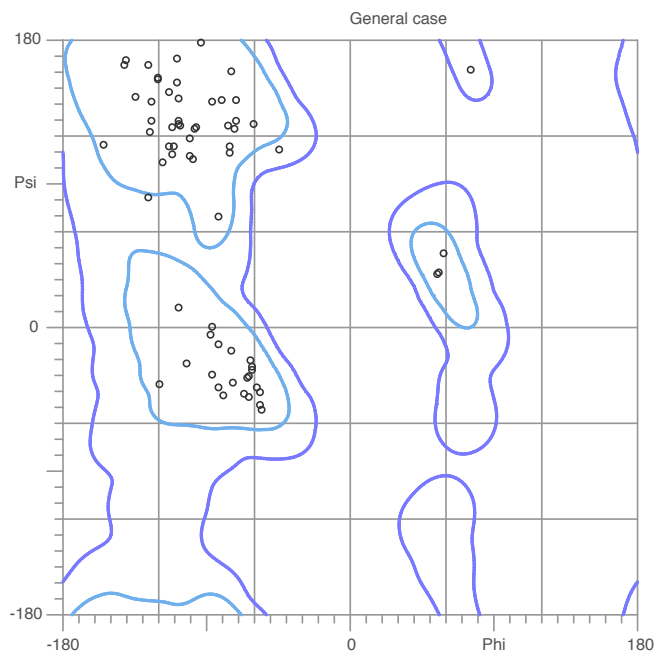
There were 2 outliers (phi, psi):

[1] 13 ASP (57.4, 171.9)

[1] 70 LYS (72.4, 135.4)

MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 2



96.1% (73/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

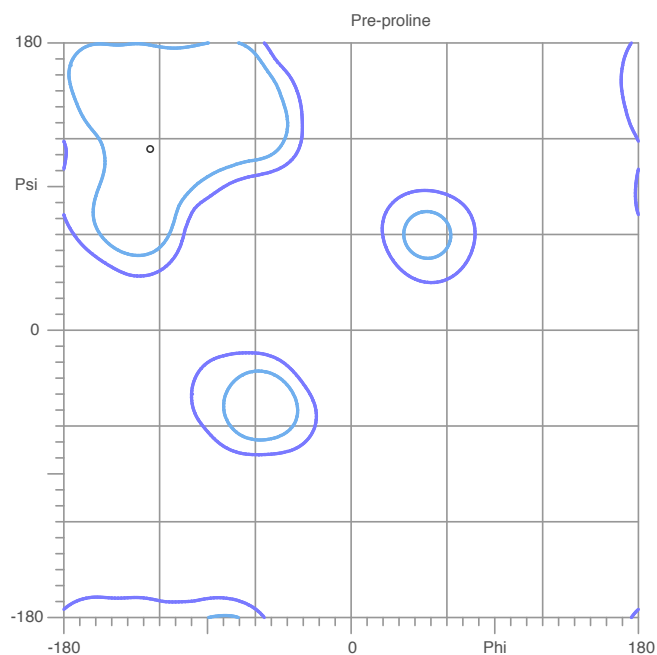
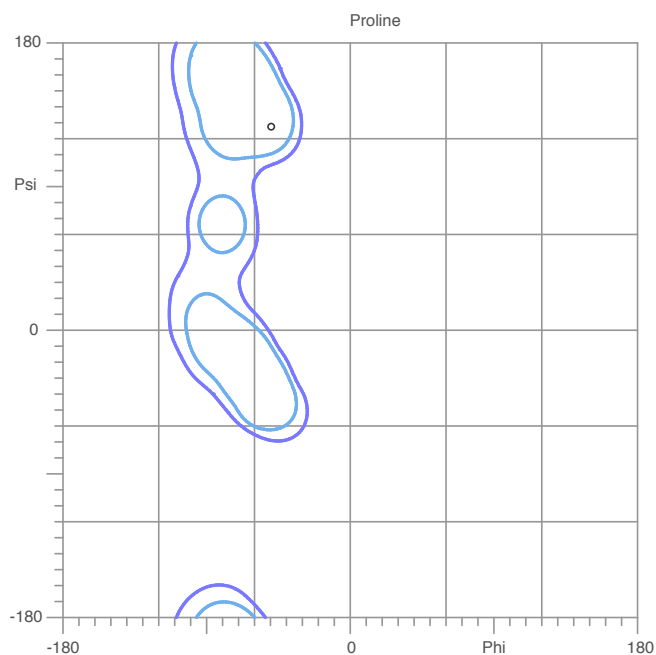
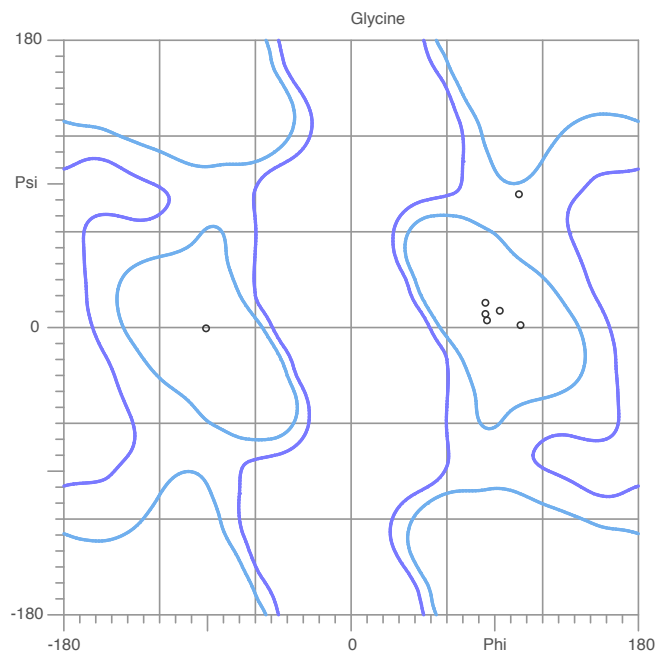
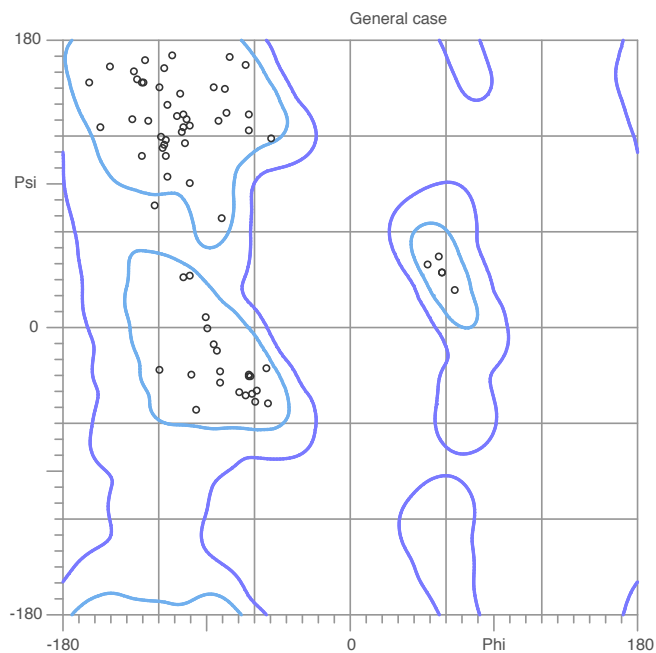
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 3



97.4% (74/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

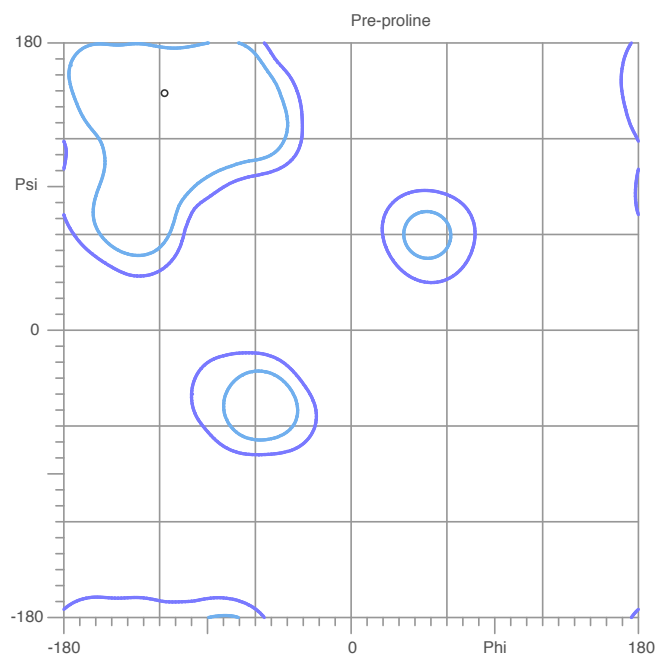
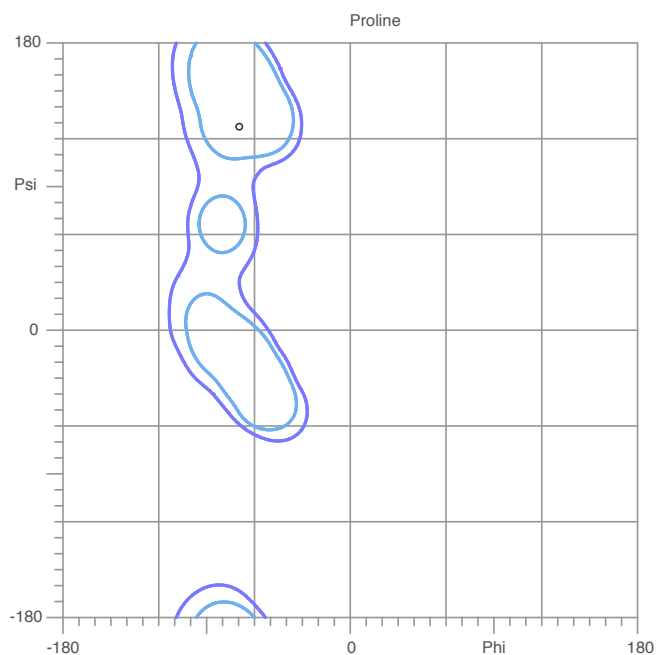
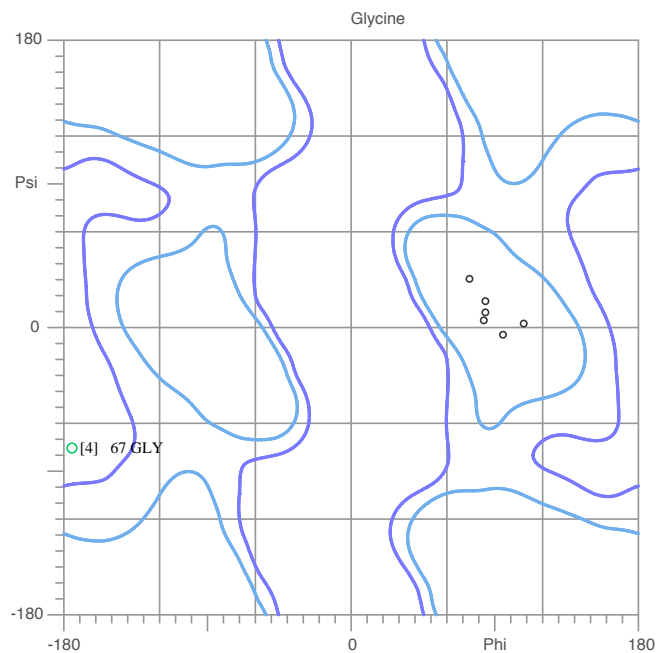
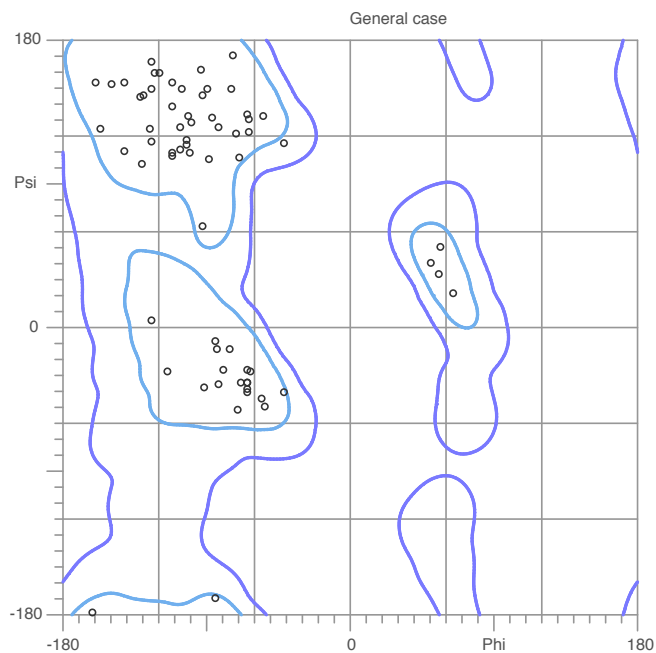
There were no outliers.

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

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 4

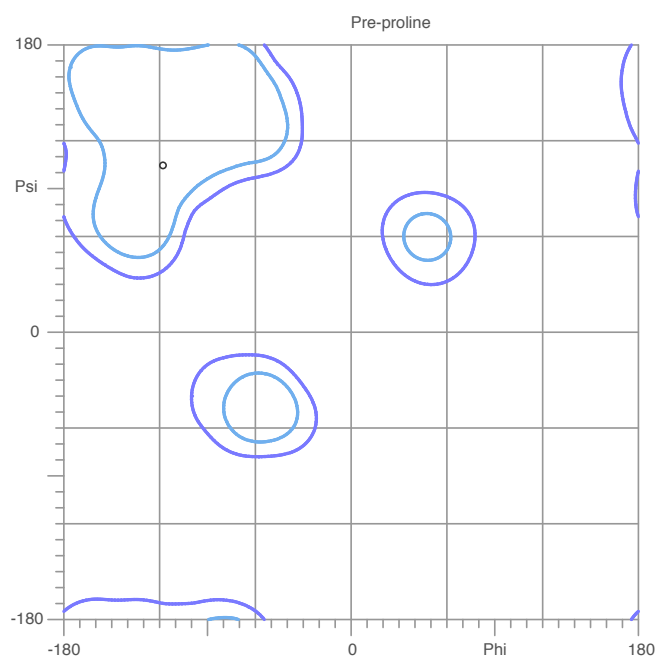
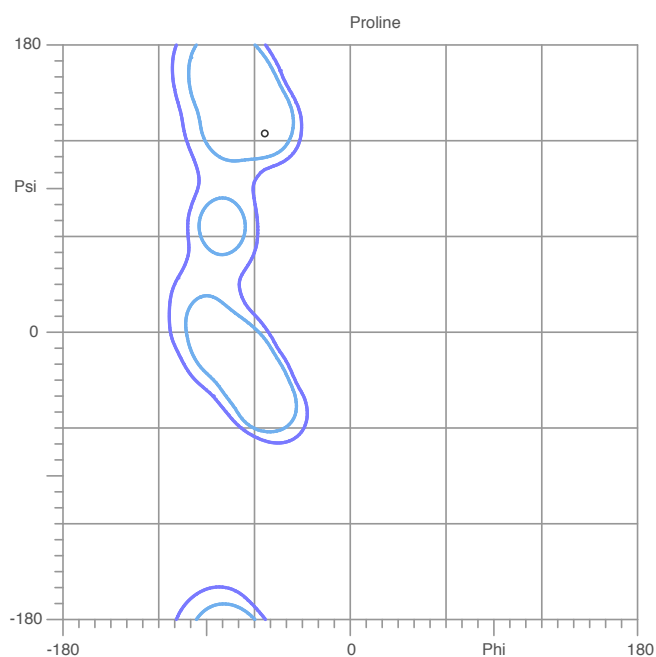
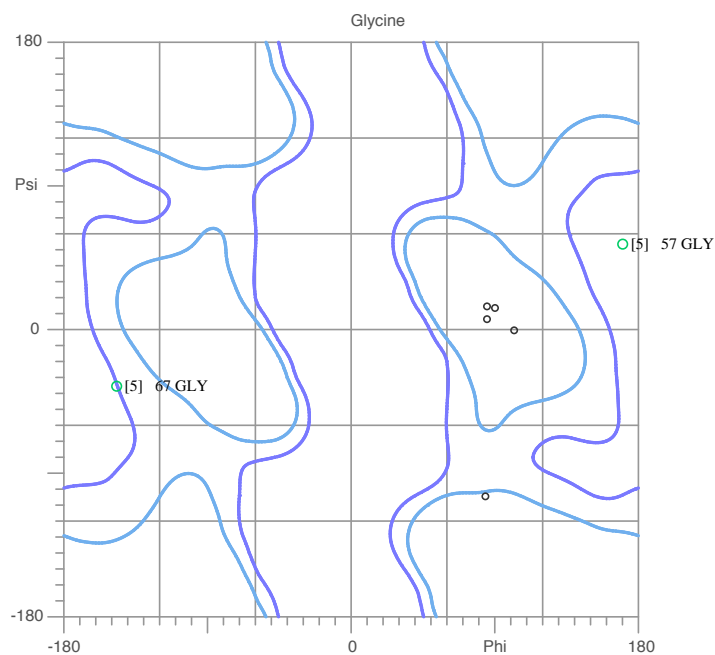
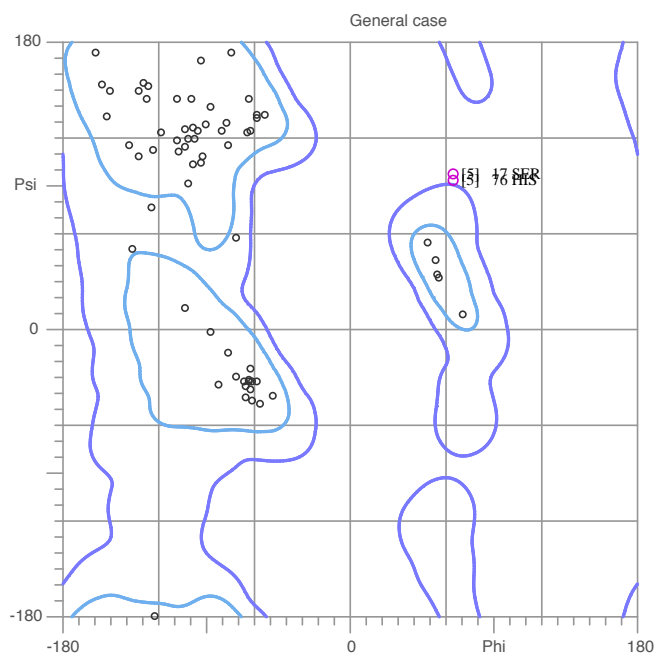


97.4% (74/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[4] 67 GLY (-175.0, -75.0)

MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 5



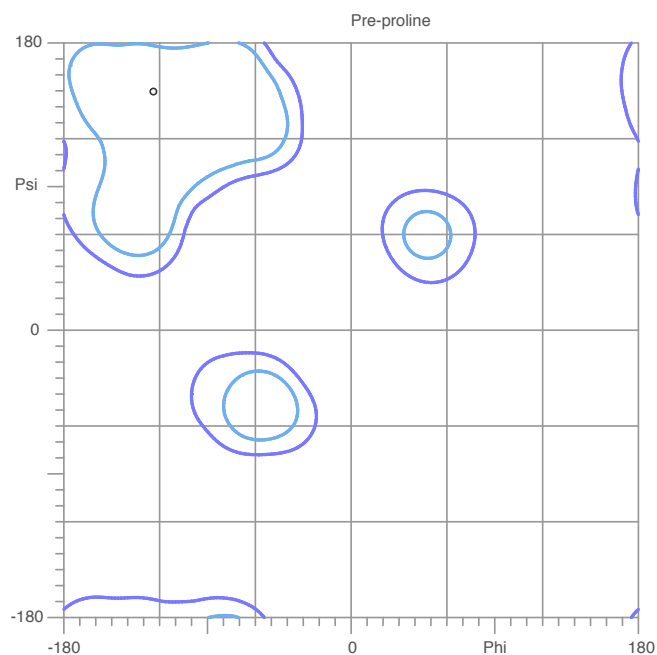
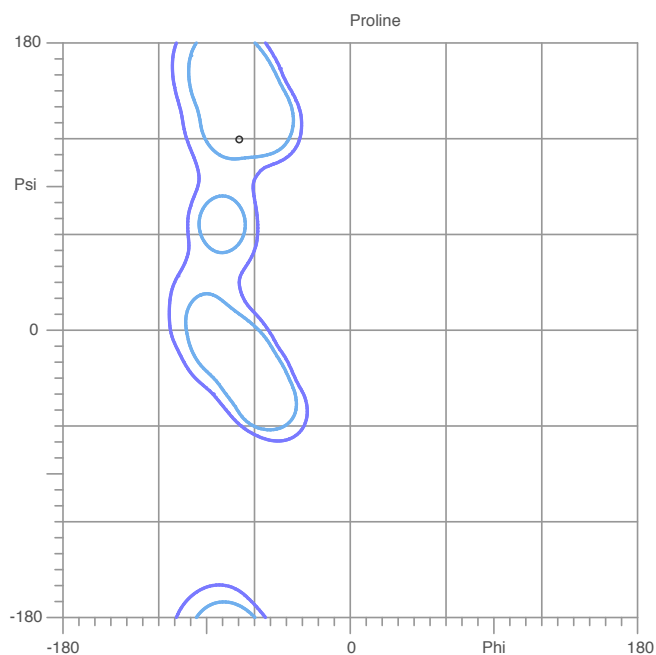
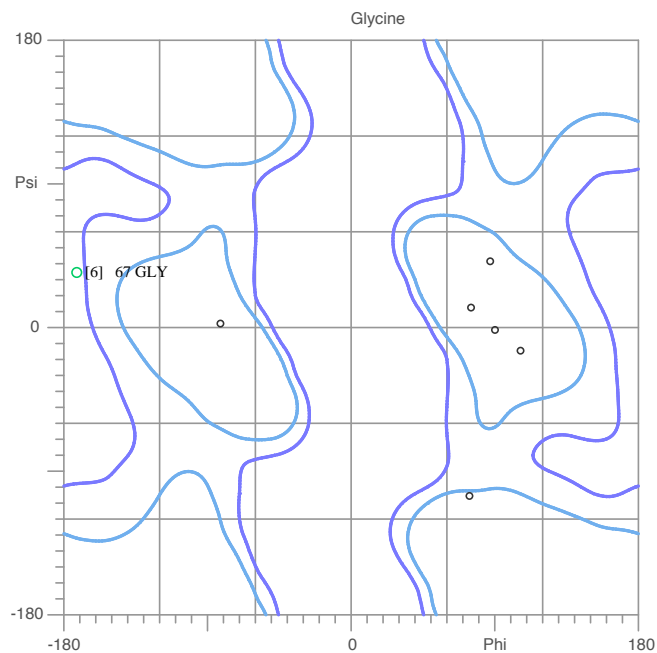
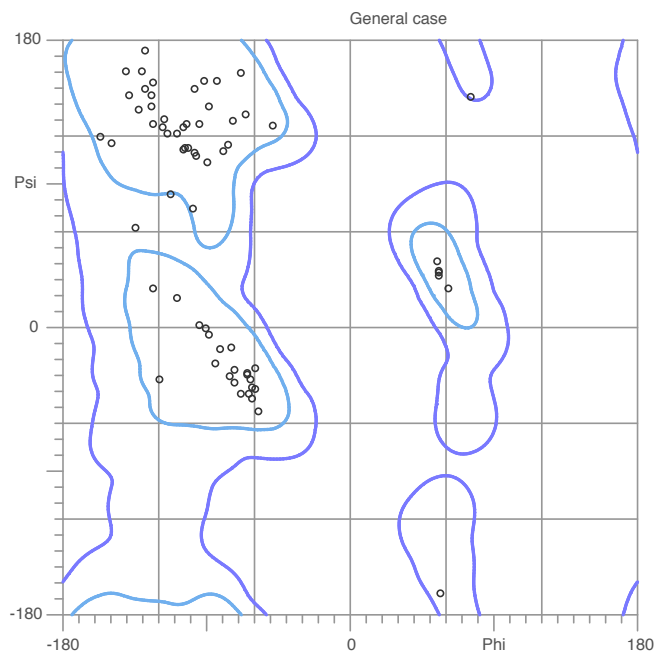
90.8% (69/76) of all residues were in favored (98%) regions.
94.7% (72/76) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [5] 17 SER (65.0, 98.0)
- [5] 57 GLY (170.2, 55.0)
- [5] 67 GLY (-147.2, -35.0)
- [5] 76 HIS (65.0, 94.9)

MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 6



94.7% (72/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

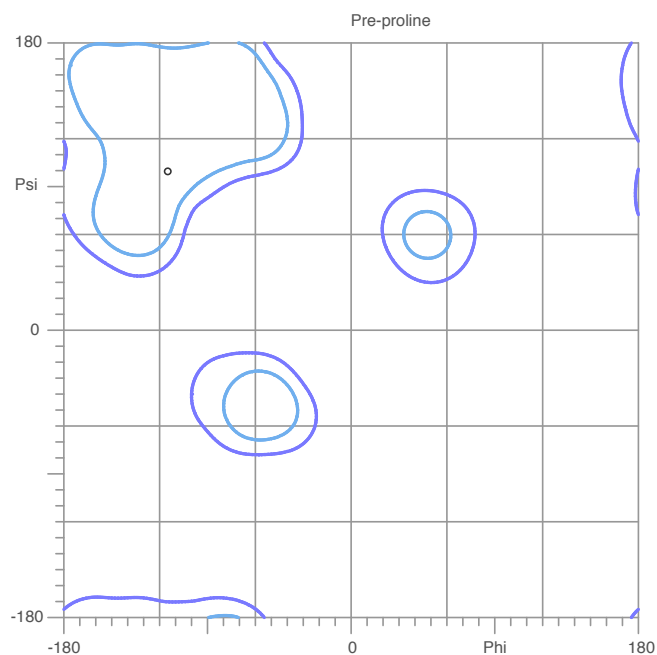
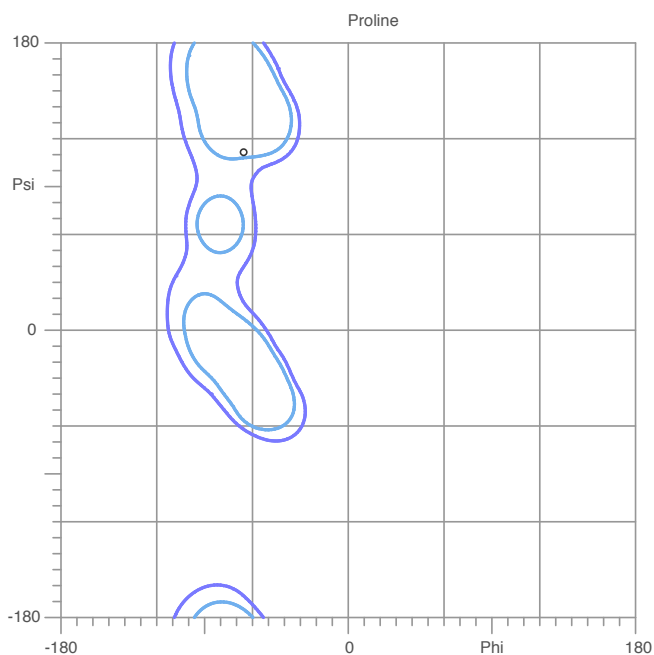
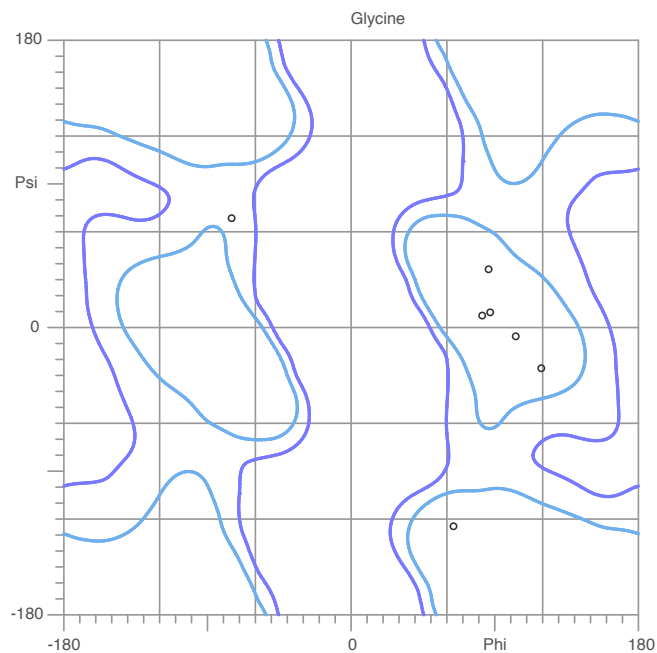
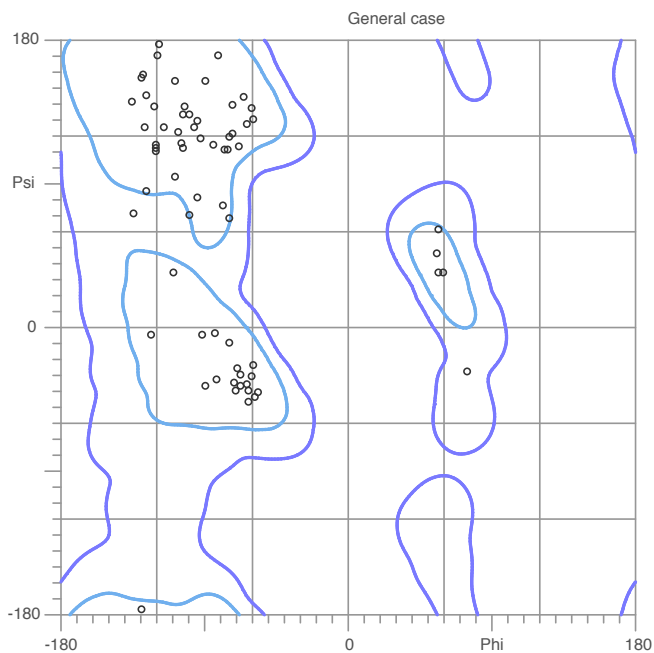
There were 1 outliers (phi, psi):
[6] 67 GLY (-172.4, 35.1)

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 7



94.7% (72/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

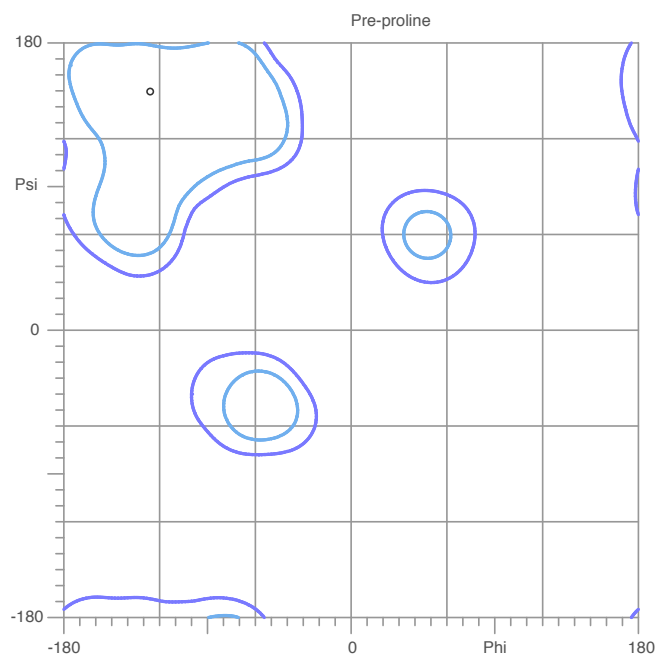
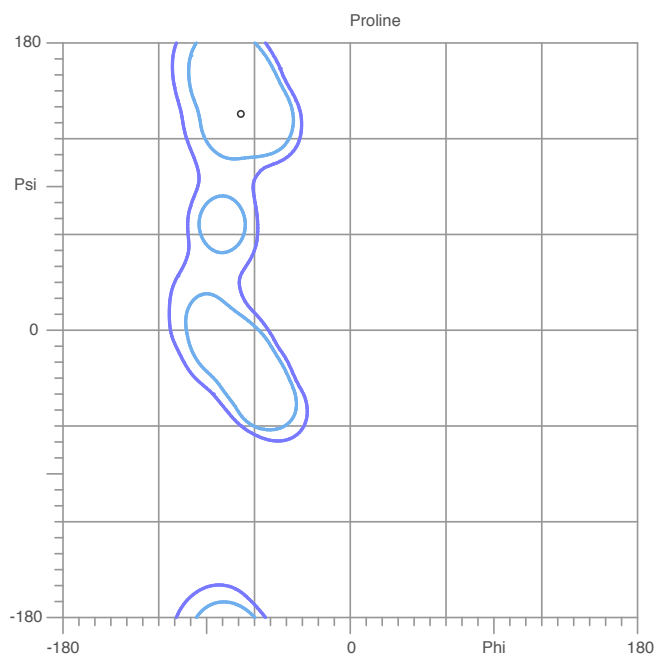
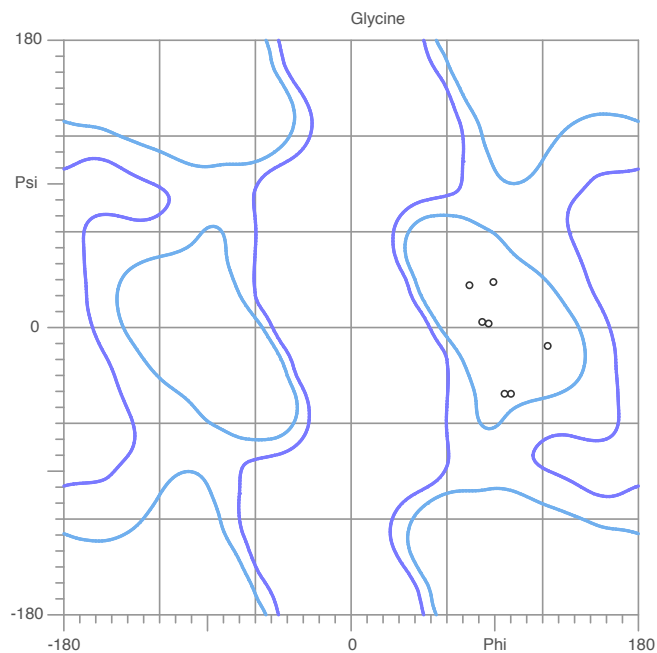
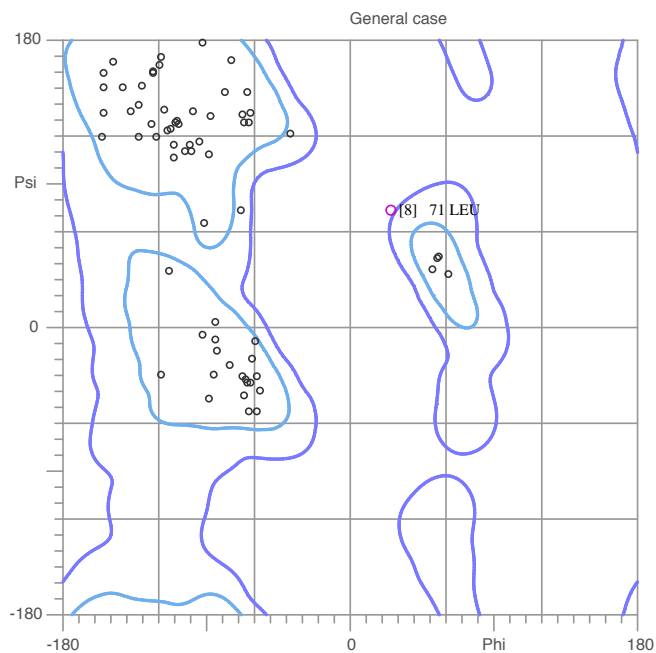
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 8



96.1% (73/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

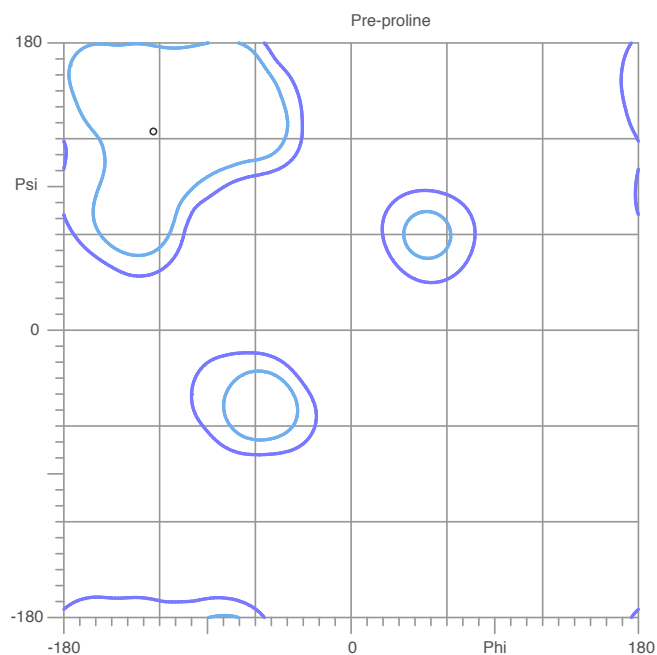
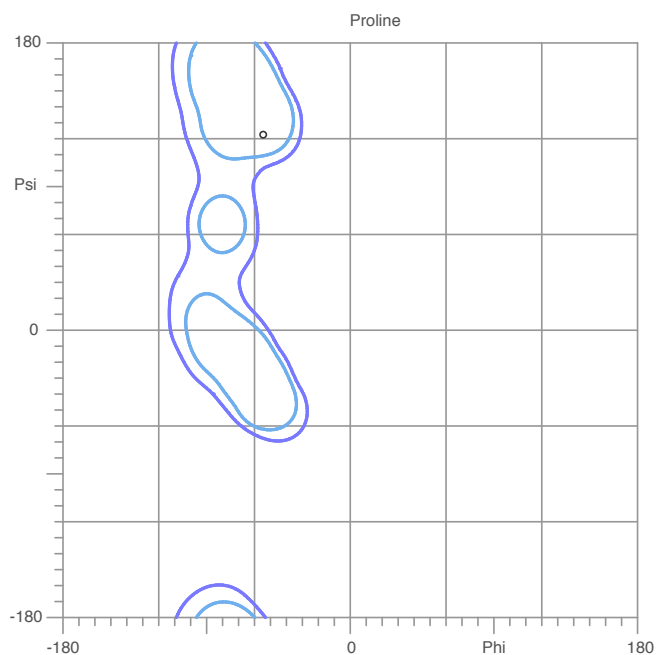
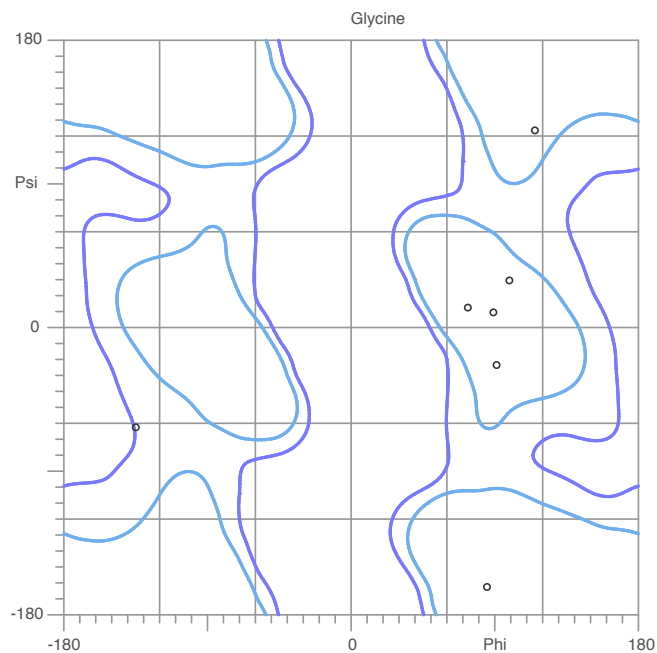
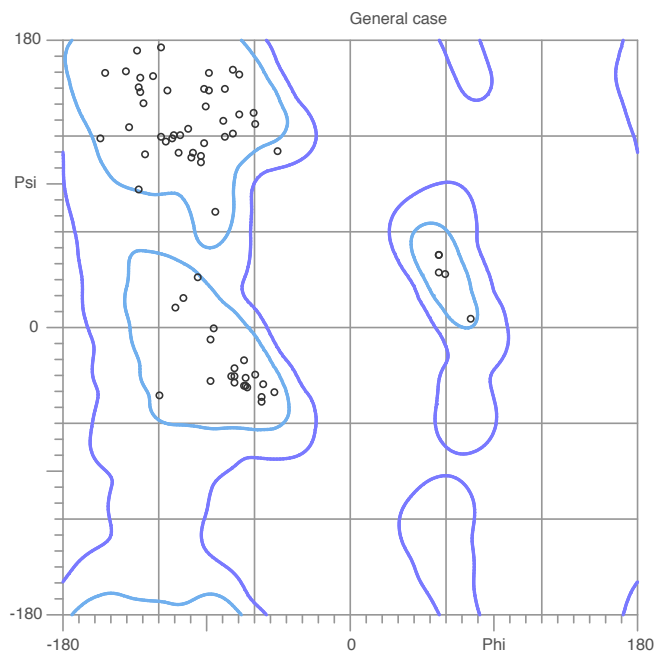
There were 1 outliers (phi, psi):
[8] 71 LEU (25.0, 74.9)

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 9



97.4% (74/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

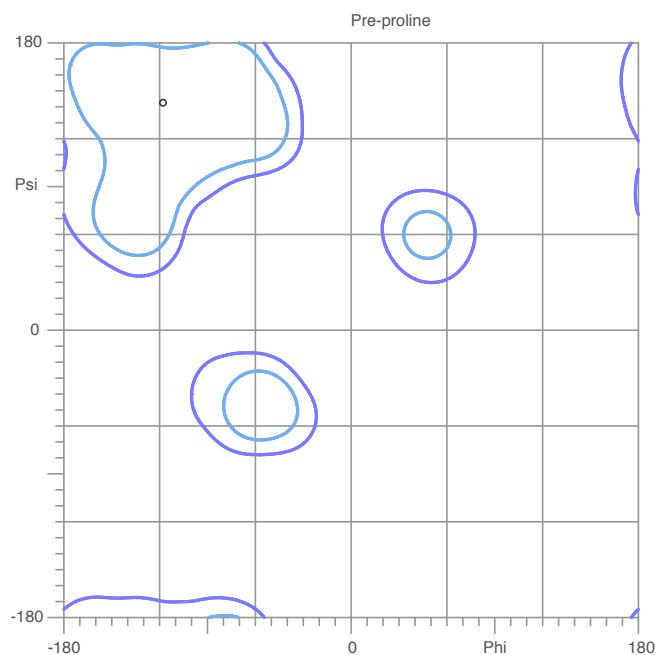
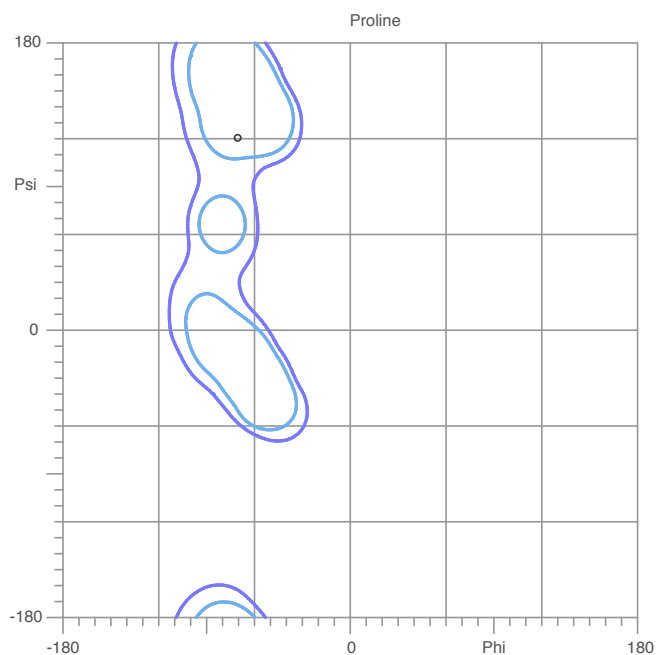
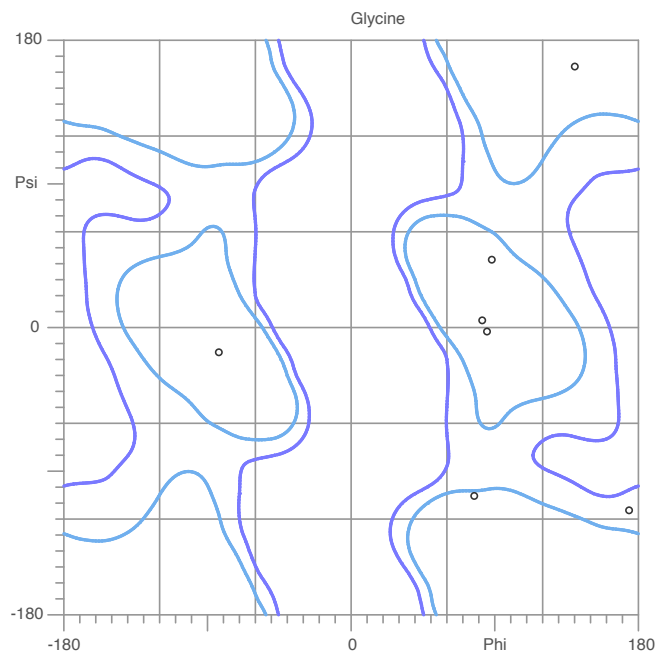
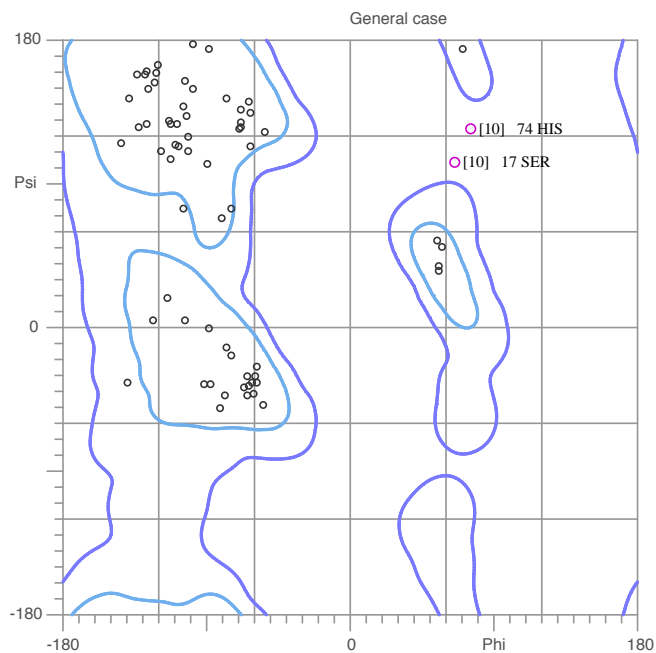
There were no outliers.

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

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 10



92.1% (70/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

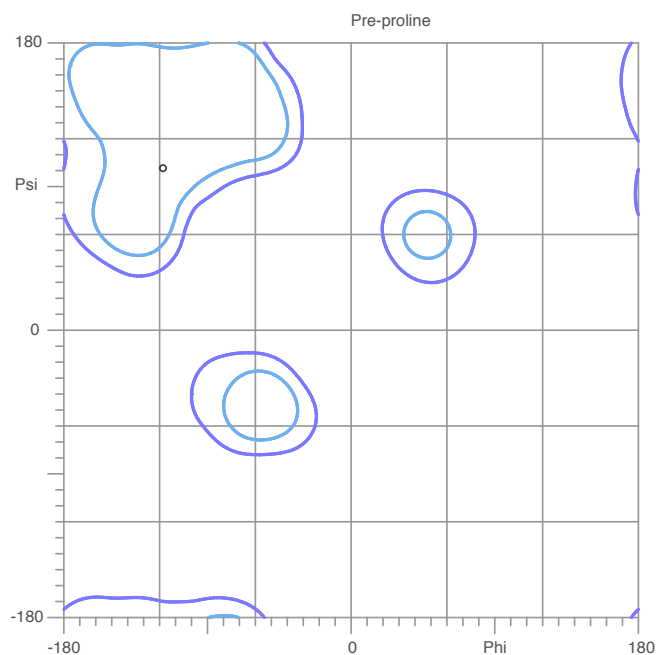
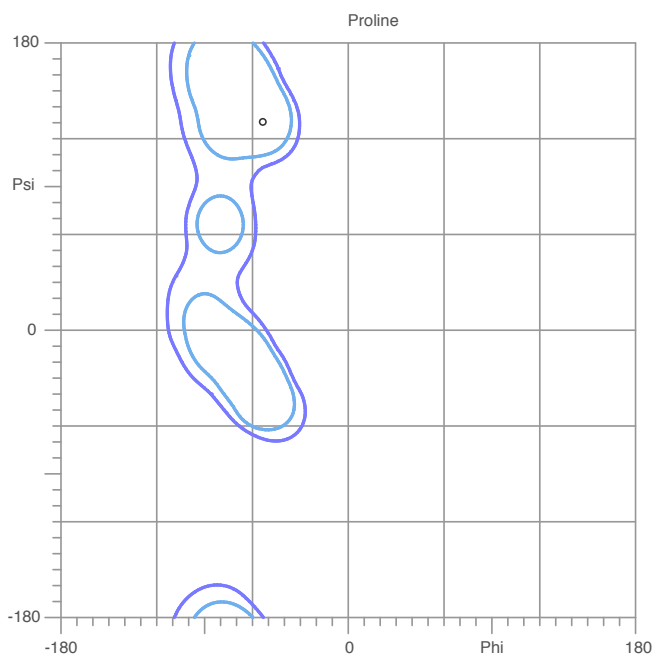
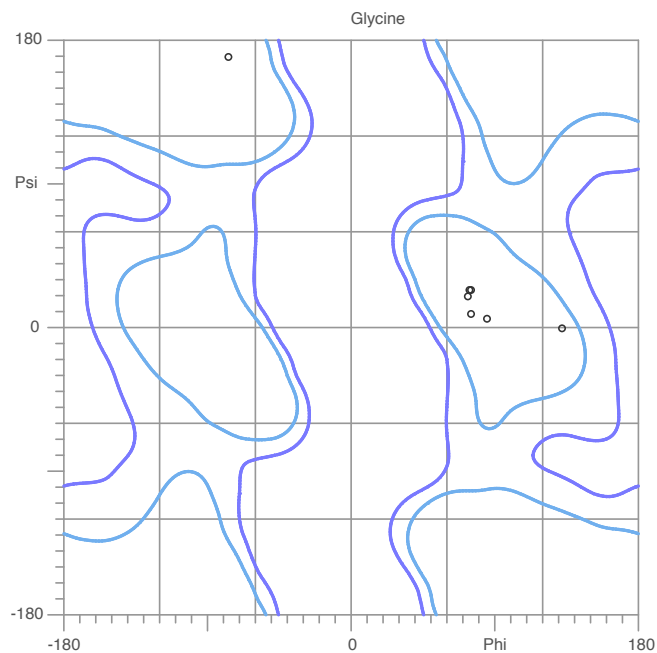
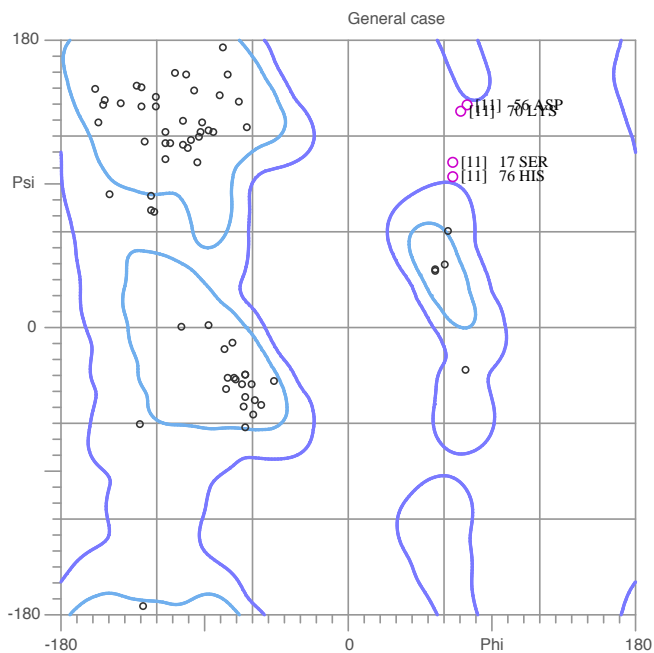
There were 2 outliers (phi, psi):

[10] 17 SER (65.0, 104.9)

[10] 74 HIS (75.0, 125.0)

MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 11



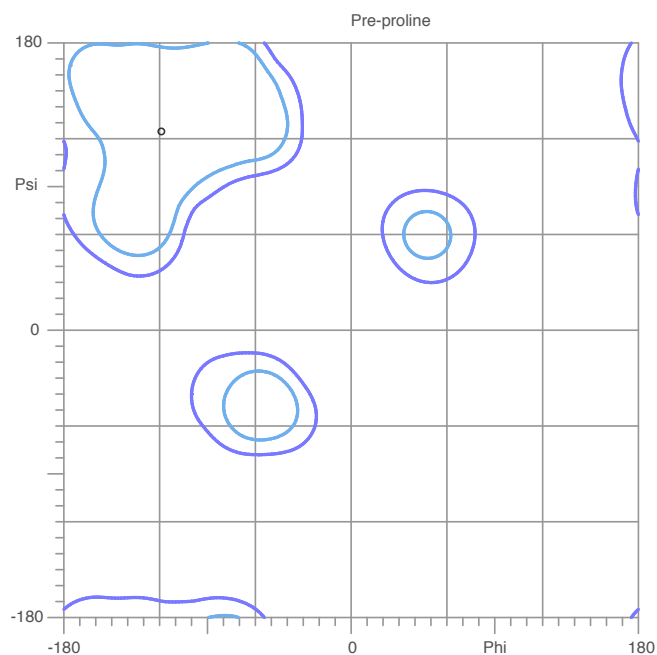
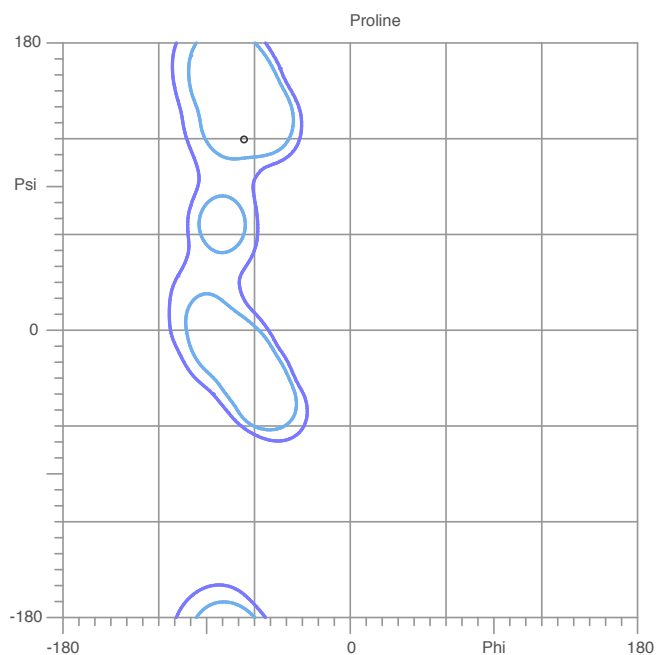
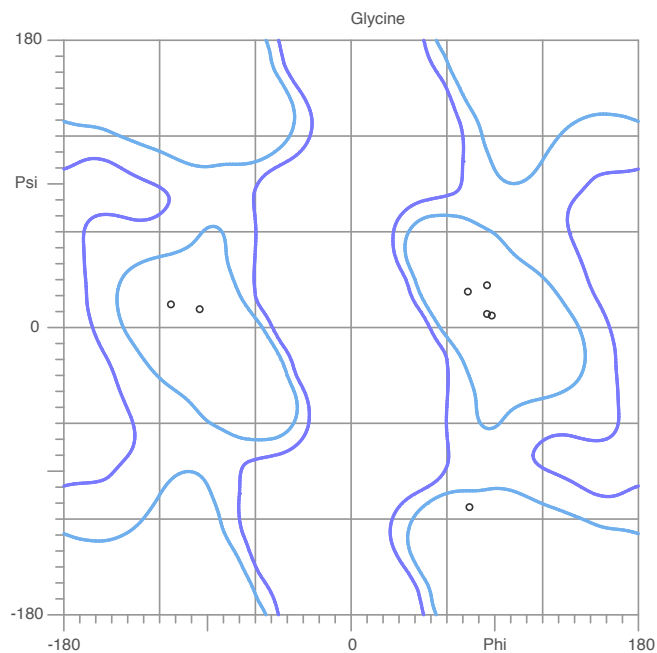
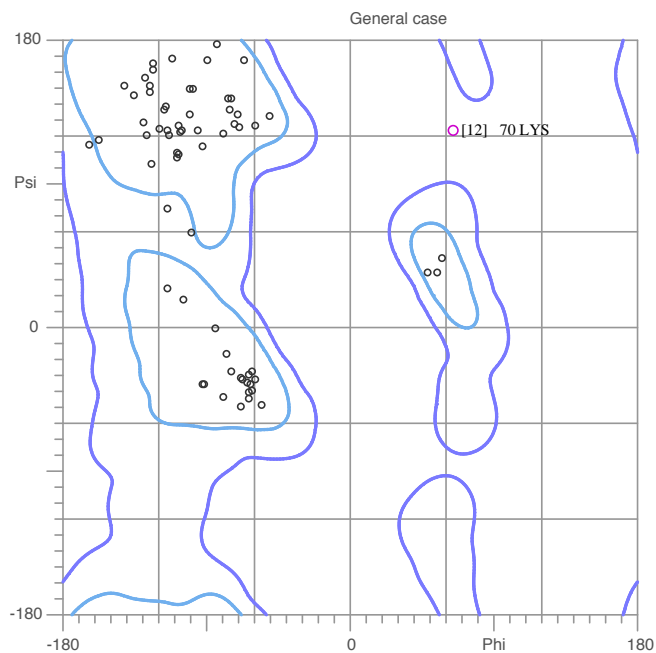
86.8% (66/76) of all residues were in favored (98%) regions.
94.7% (72/76) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [11] 17 SER (65.0, 105.0)
- [11] 56 ASP (75.0, 140.4)
- [11] 70 LYS (70.1, 136.5)
- [11] 76 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 12



94.7% (72/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

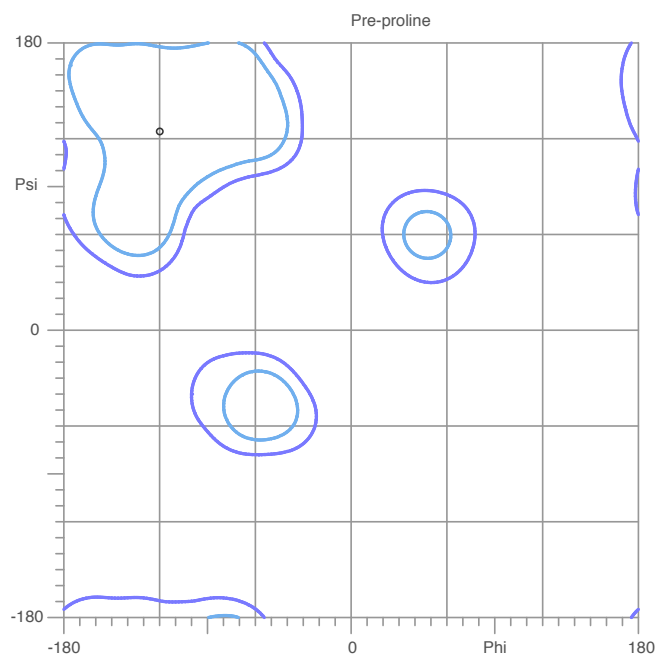
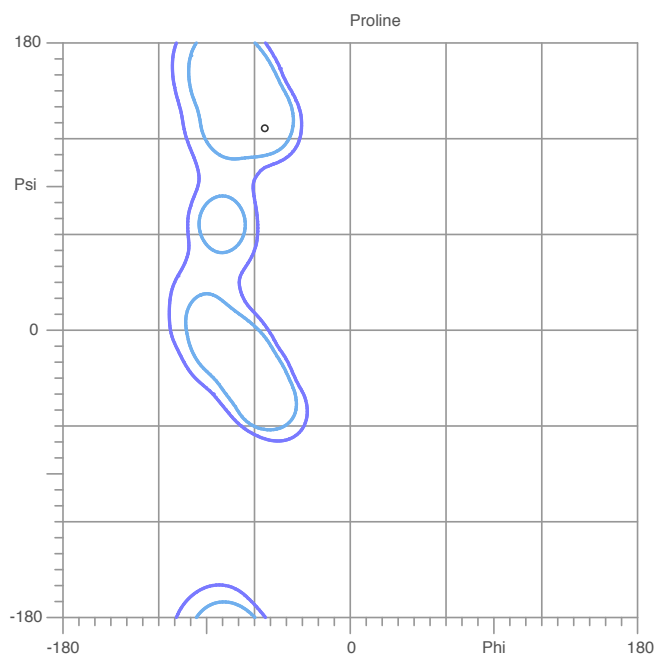
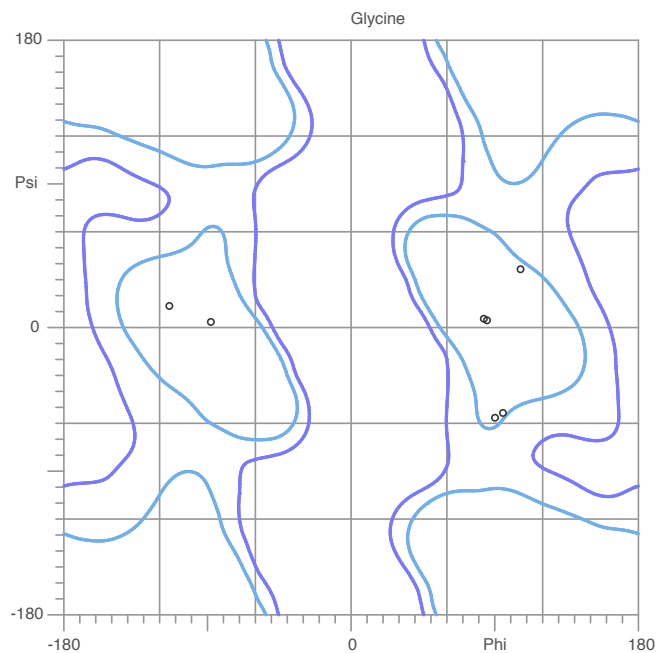
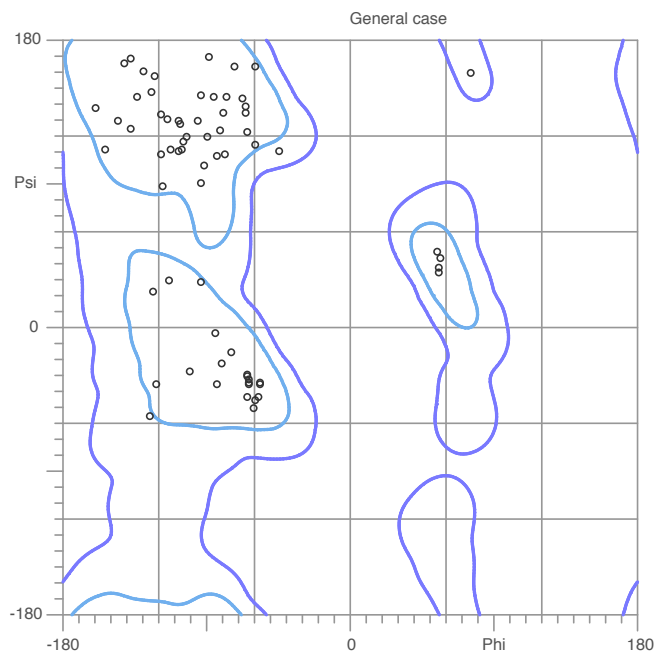
There were 1 outliers (phi, psi):
[12] 70 LYS (65.0, 125.0)

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 13



96.1% (73/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

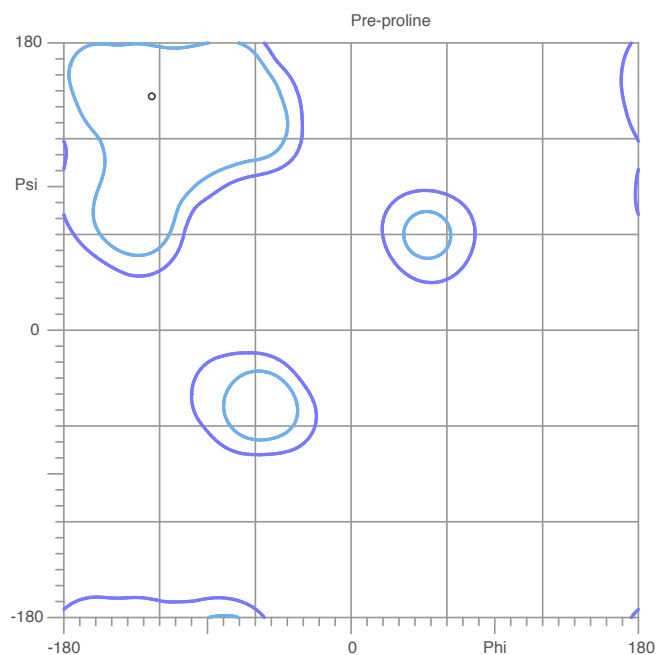
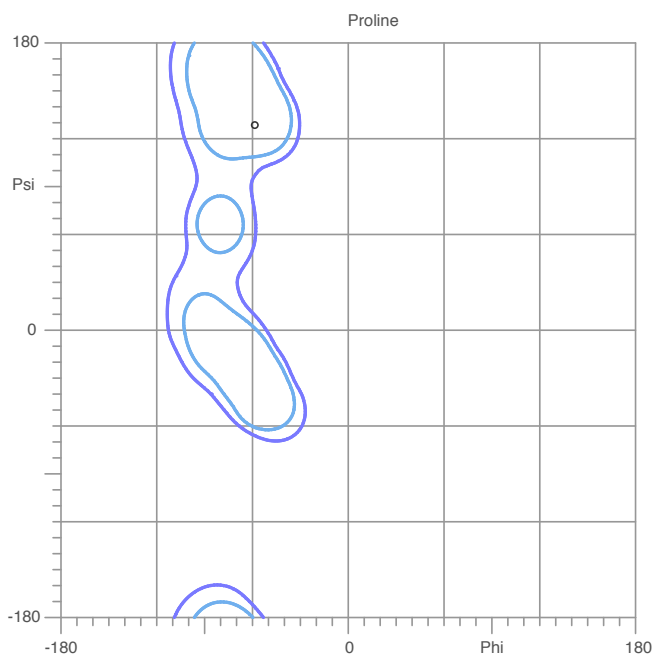
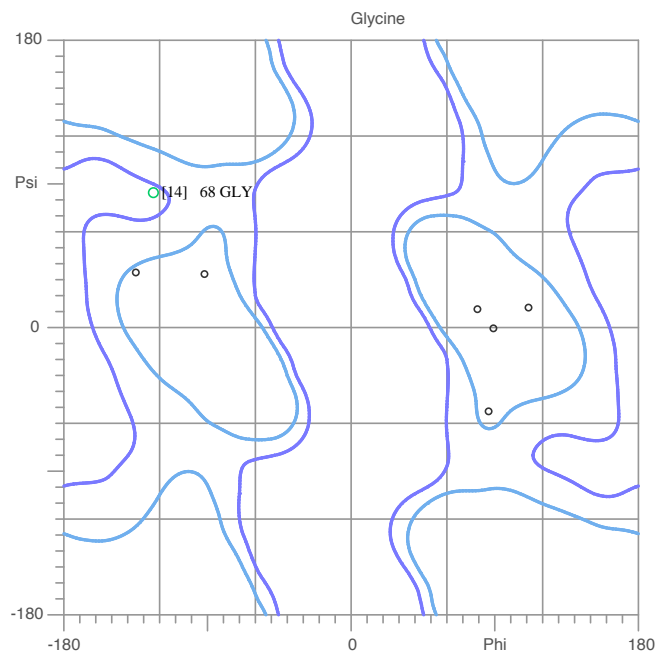
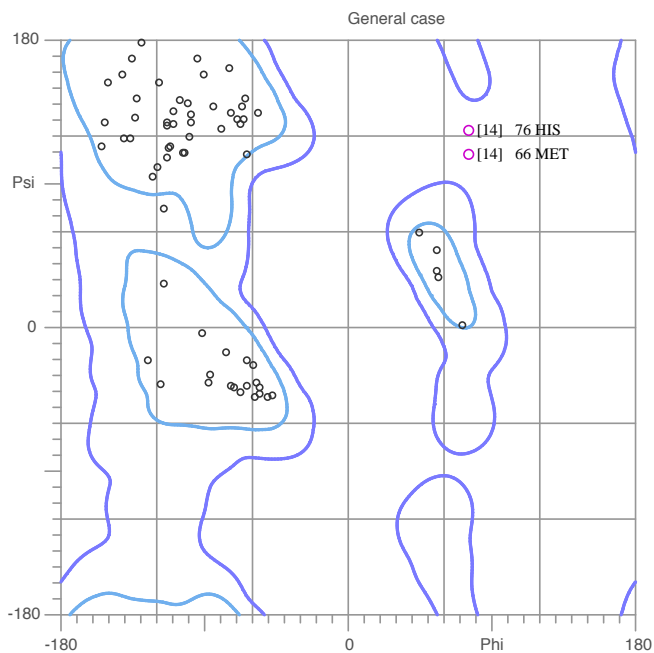
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 14



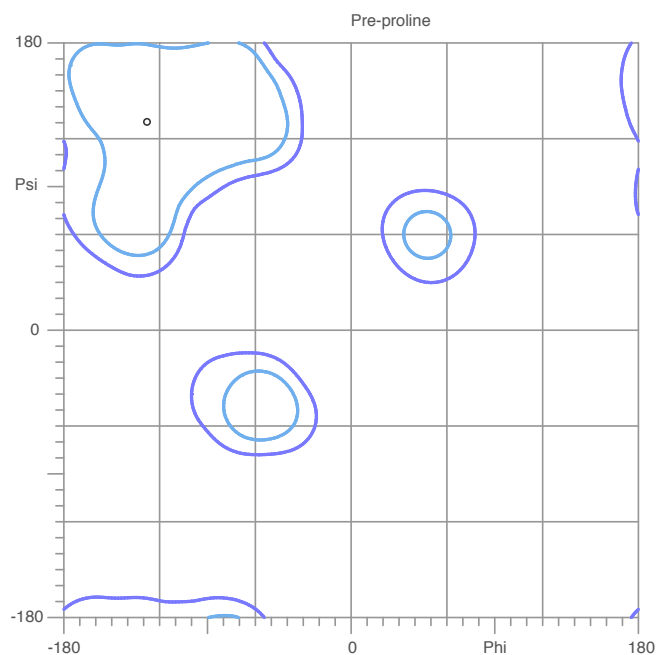
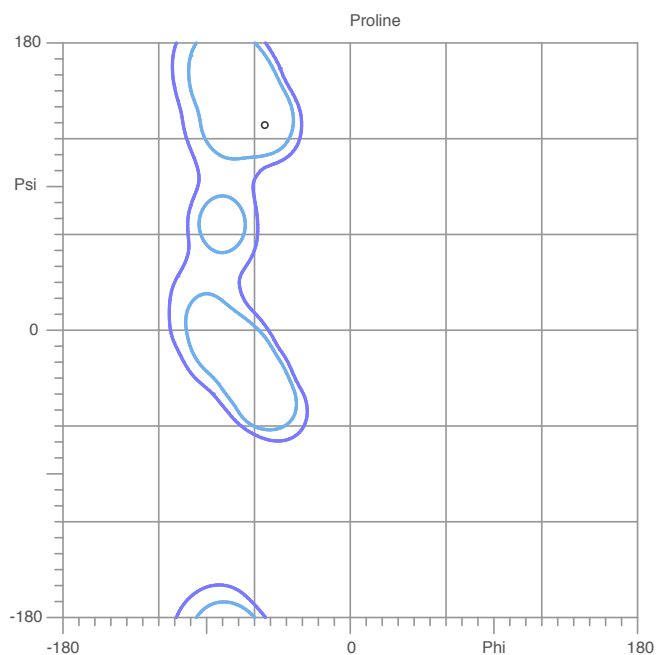
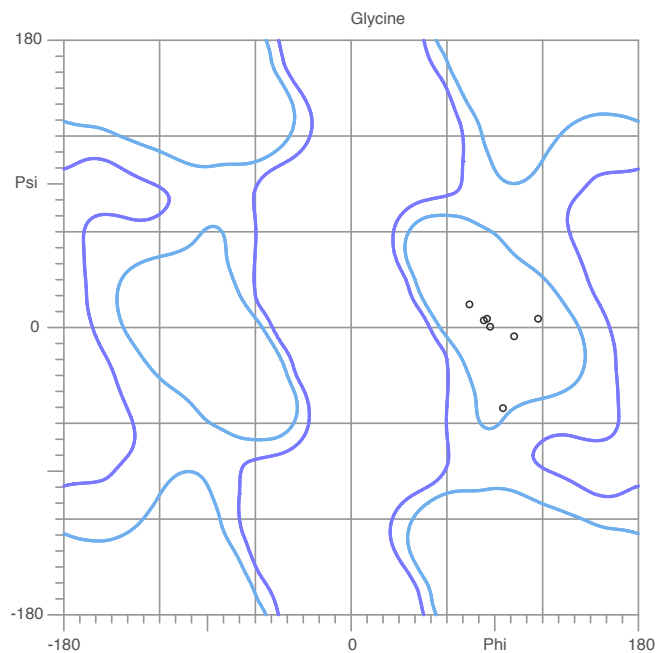
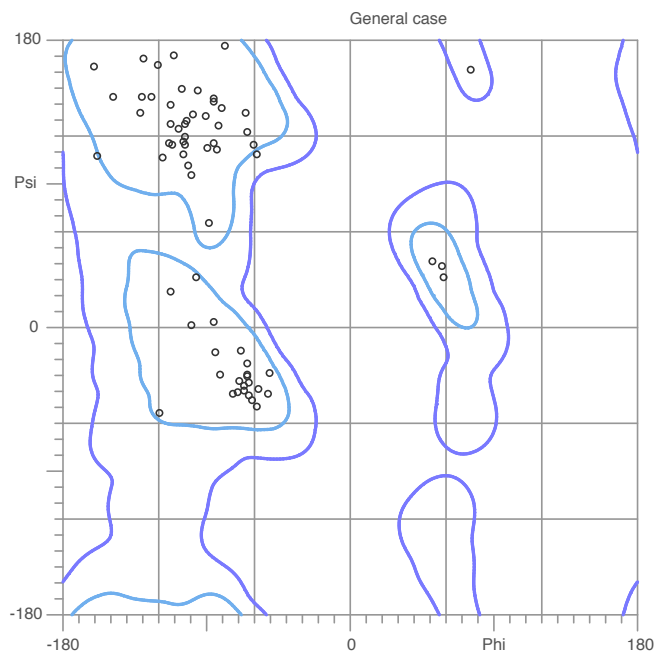
94.7% (72/76) of all residues were in favored (98%) regions.
96.1% (73/76) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [14] 66 MET (75.0, 110.0)
- [14] 68 GLY (-125.0, 85.1)
- [14] 76 HIS (75.1, 125.0)

MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 15



96.1% (73/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

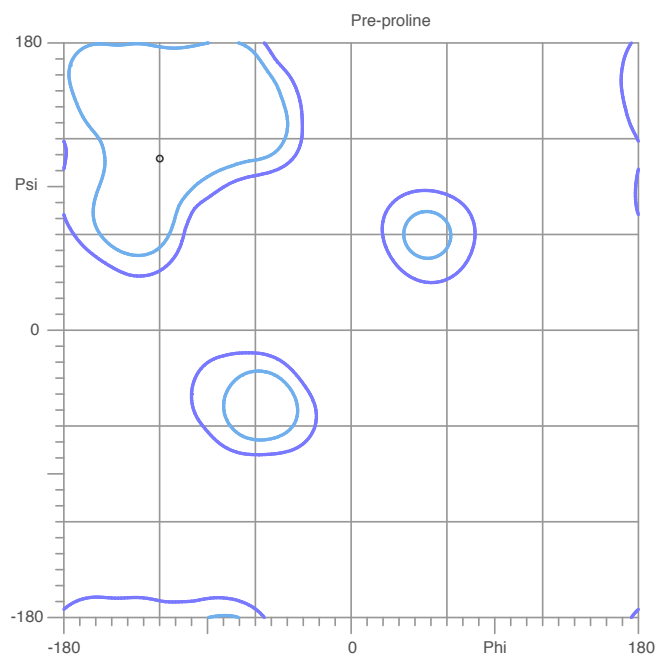
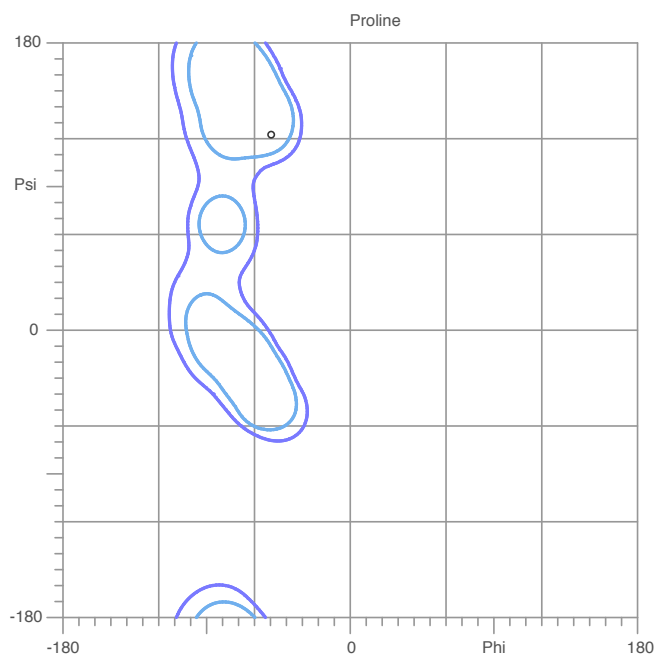
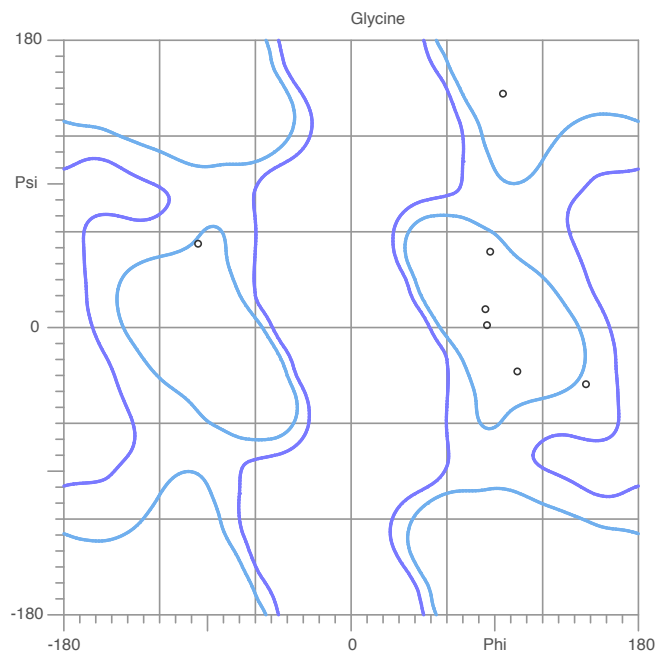
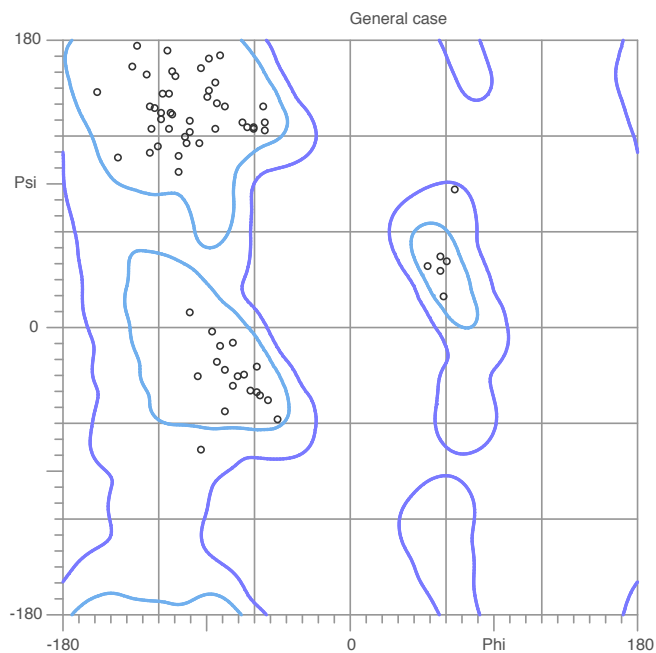
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 16



96.1% (73/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

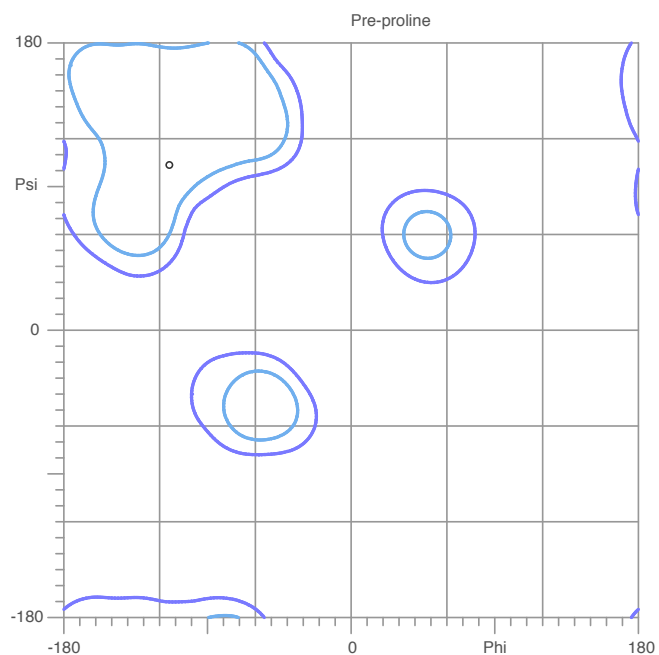
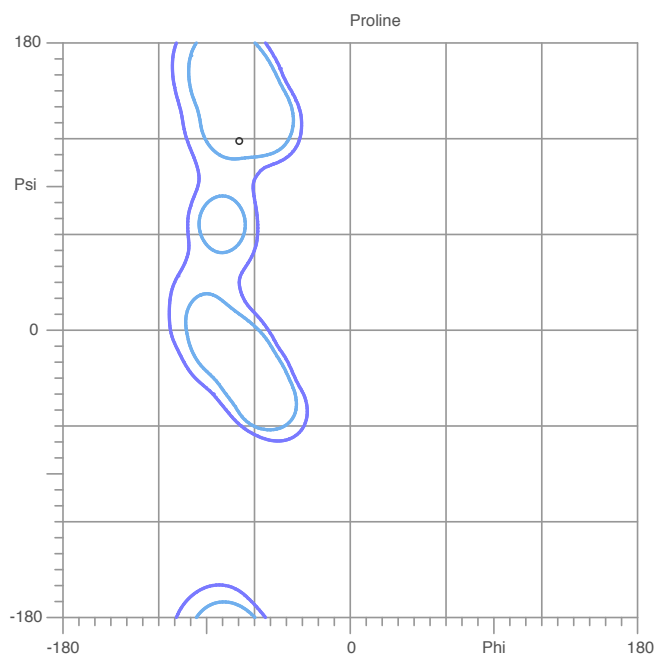
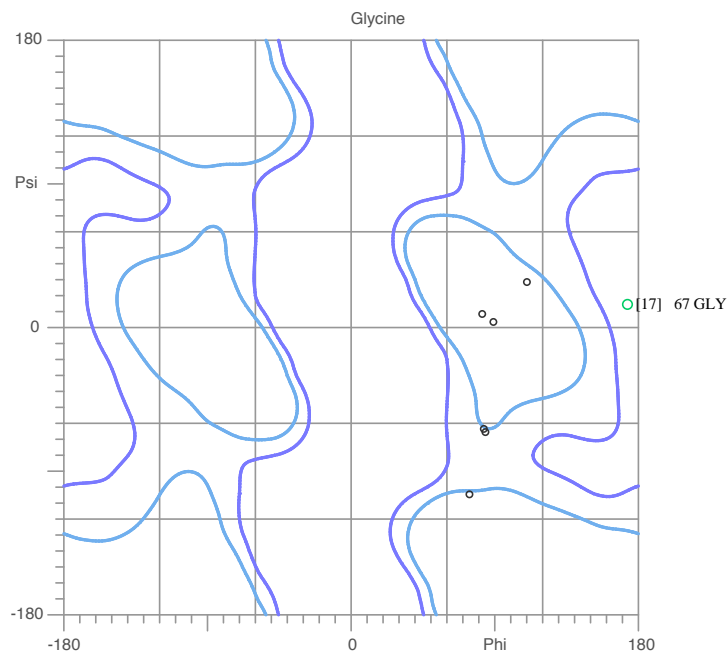
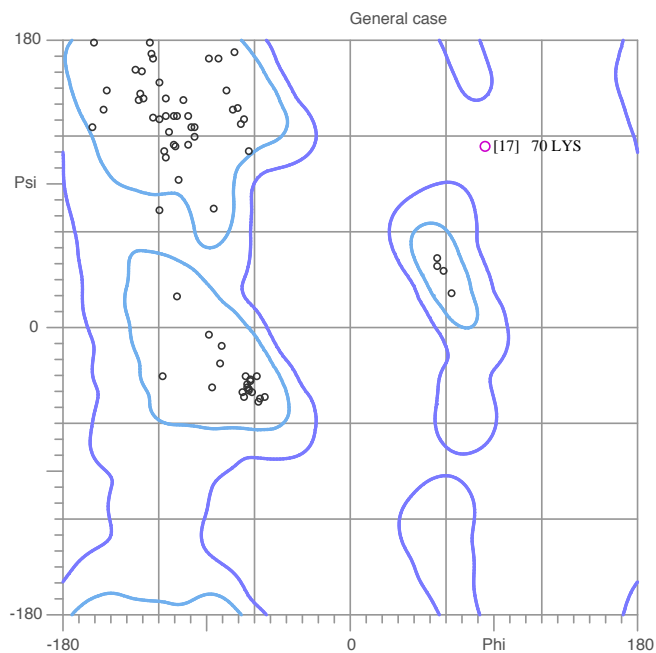
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 17



93.4% (71/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

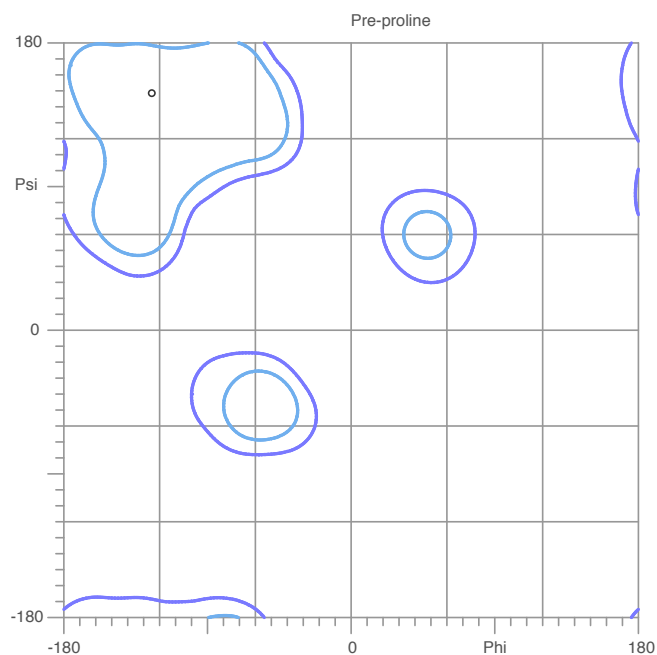
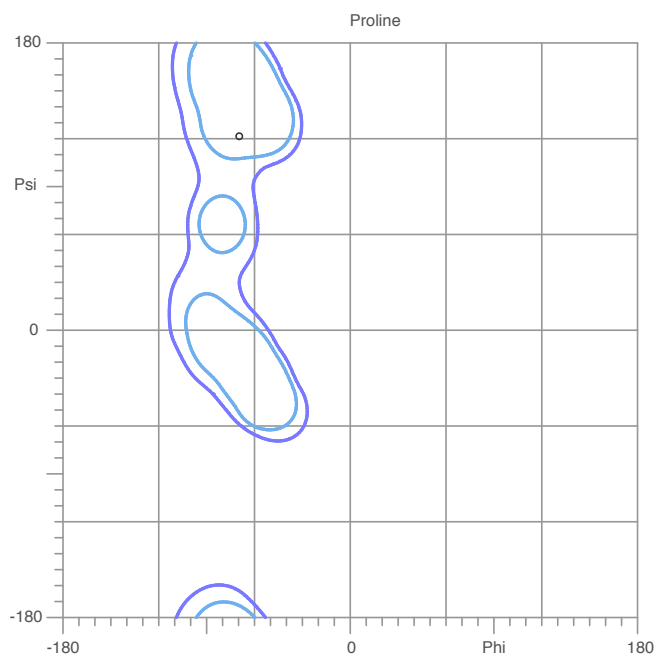
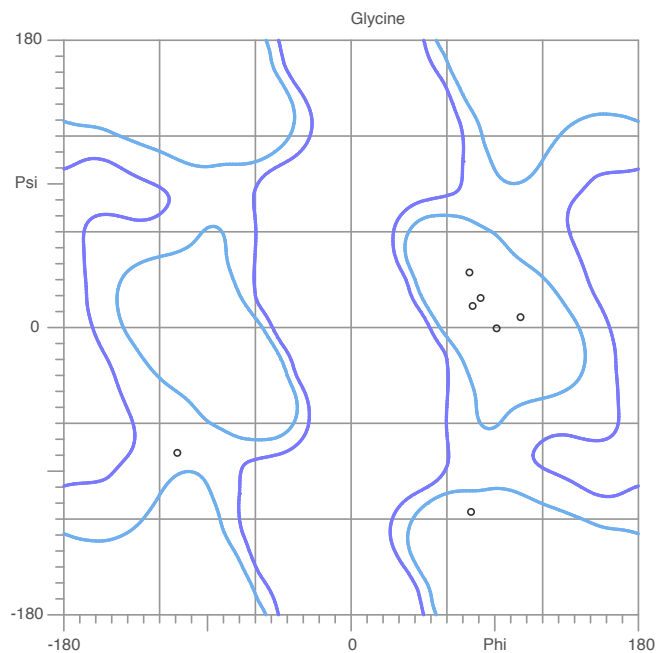
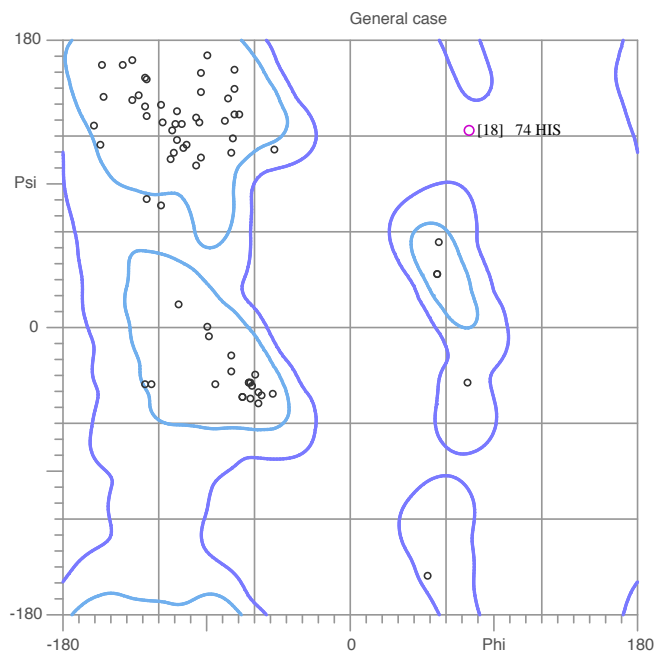
There were 2 outliers (phi, psi):

[17] 67 GLY (173.1, 15.1)

[17] 70 LYS (85.0, 115.0)

MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 18



90.8% (69/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

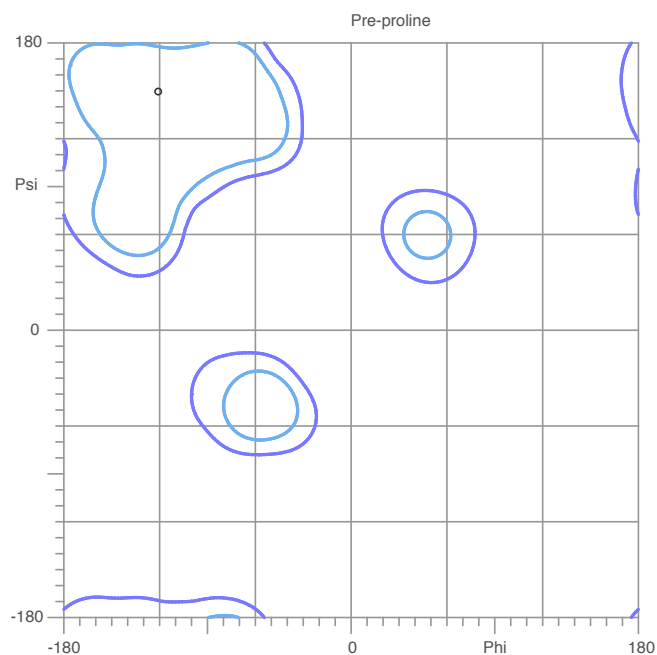
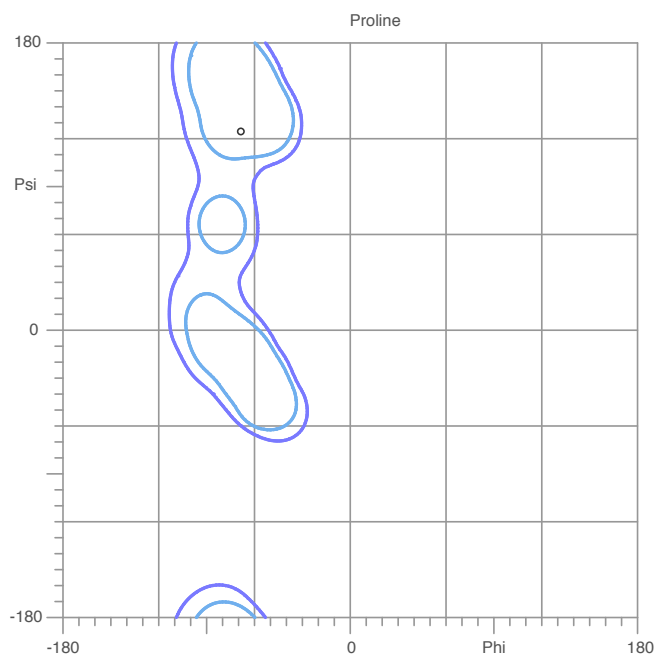
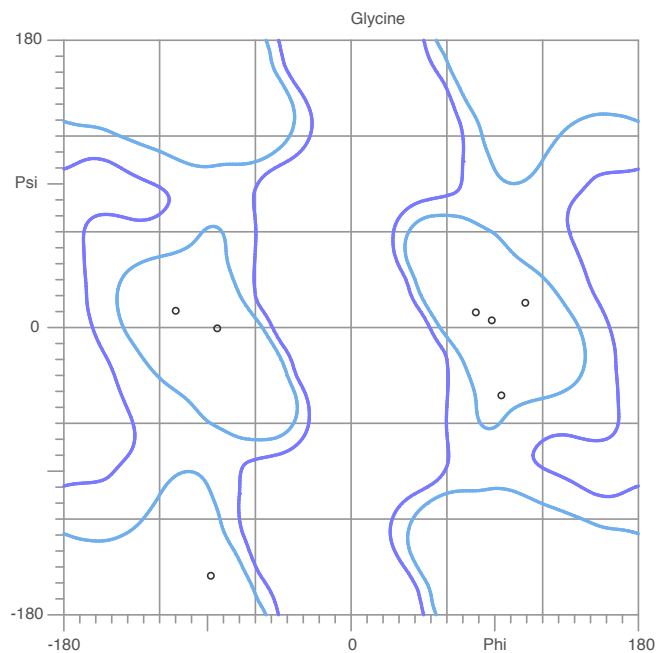
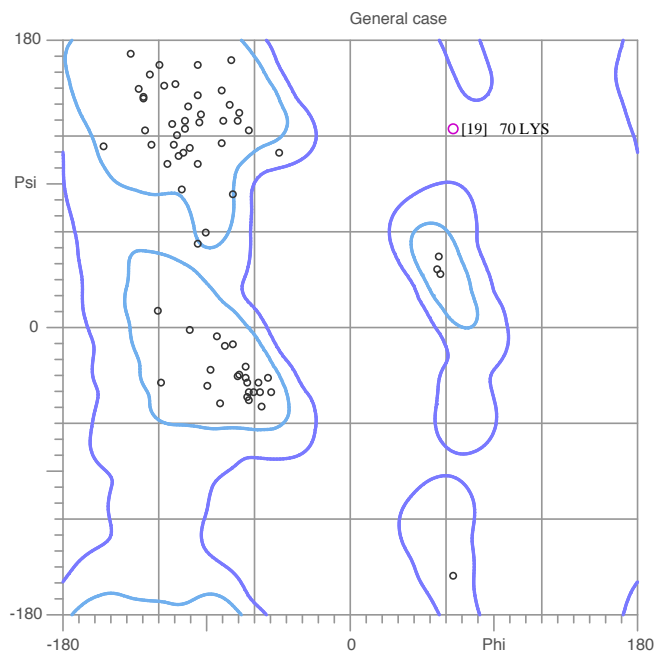
There were 1 outliers (phi, psi):
[18] 74 HIS (74.9, 125.0)

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 19



94.7% (72/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

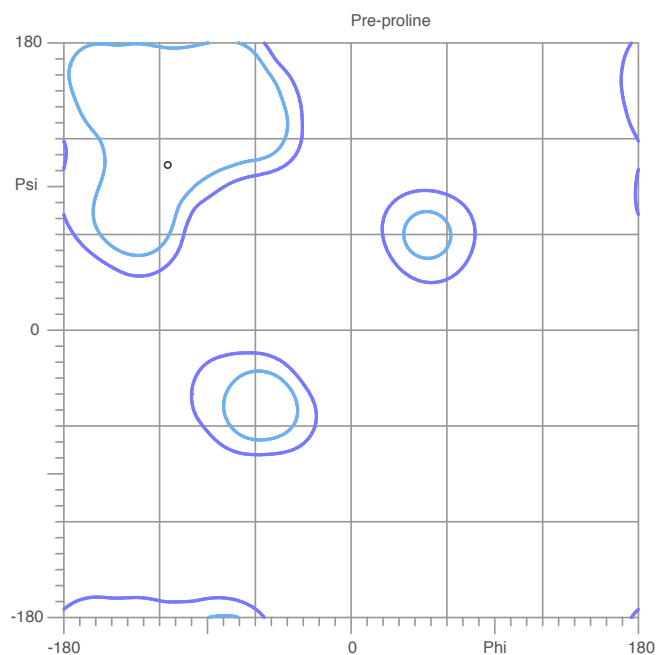
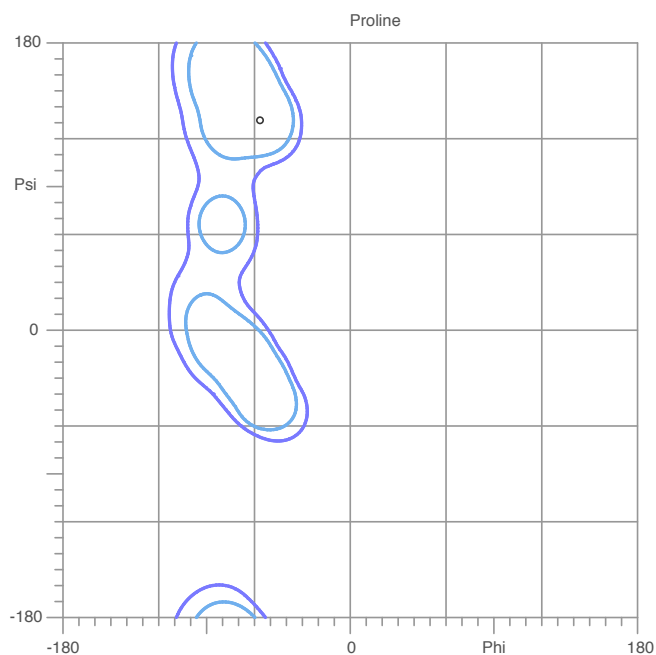
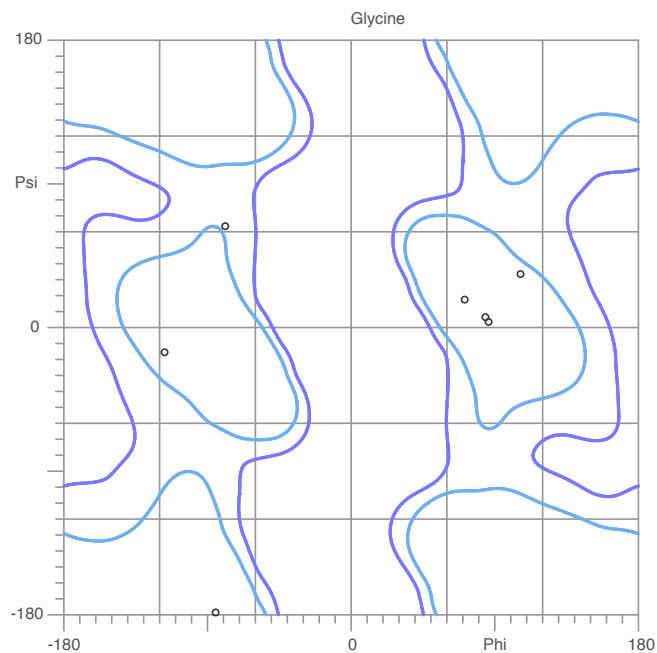
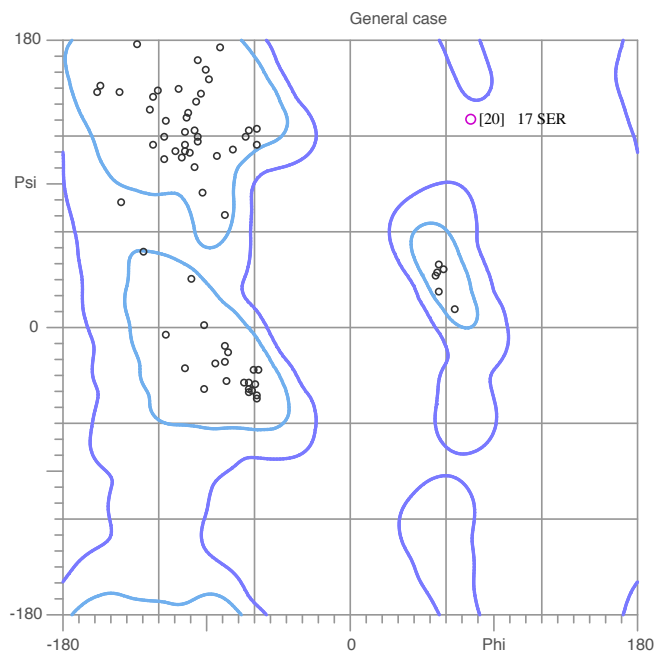
There were 1 outliers (phi, psi):
[19] 70 LYS (65.0, 125.0)

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MolProbity Ramachandran analysis

GMR137_R3Cons_em_bcr3.pdb, model 20



94.7% (72/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 17 SER (75.3, 131.2)

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