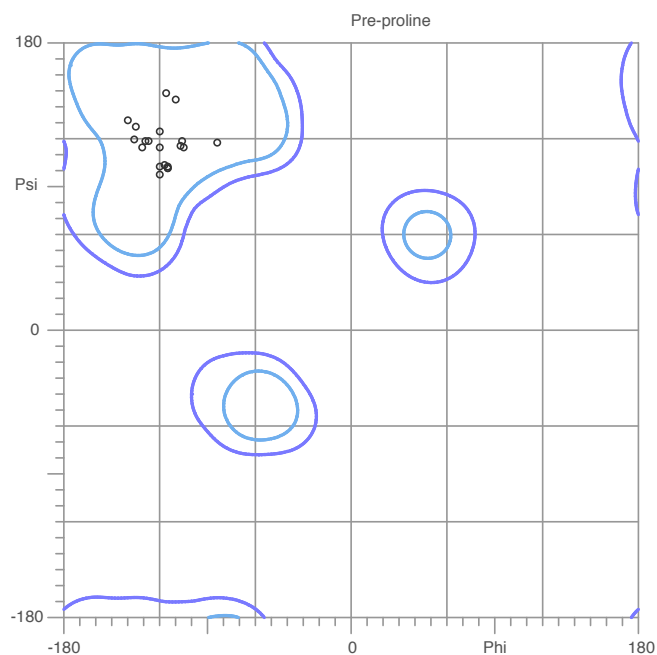
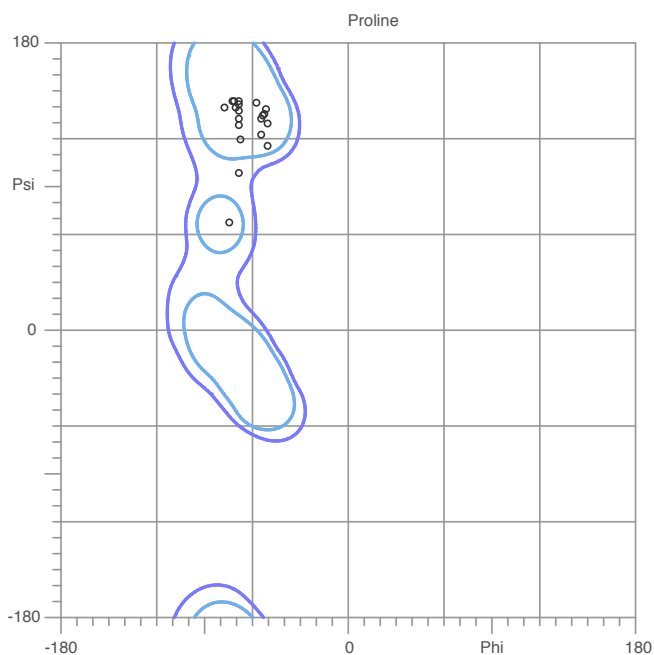
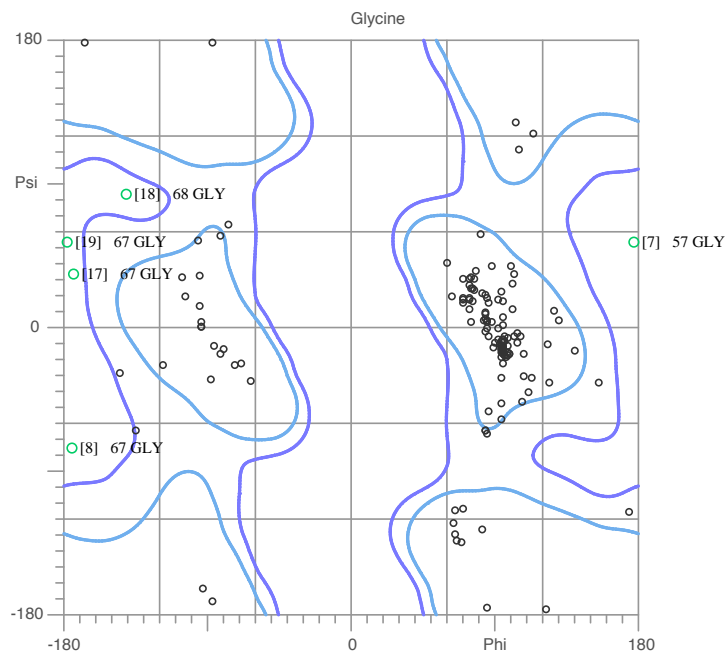
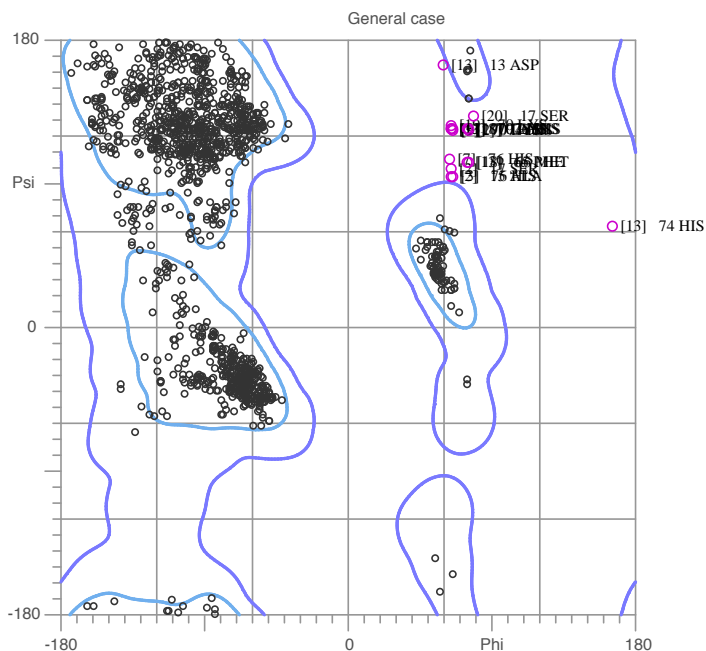


MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, all models



94.1% (1431/1520) of all residues were in favored (98%) regions.
98.6% (1498/1520) of all residues were in allowed (>99.8%) regions.

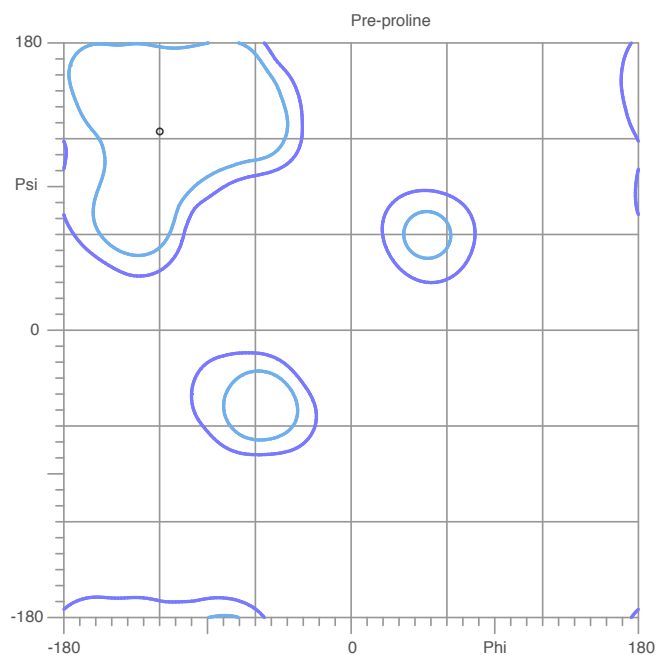
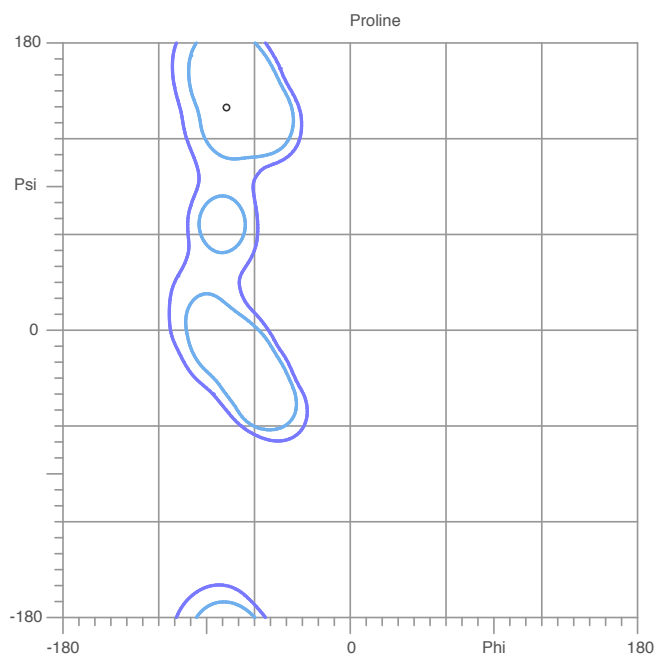
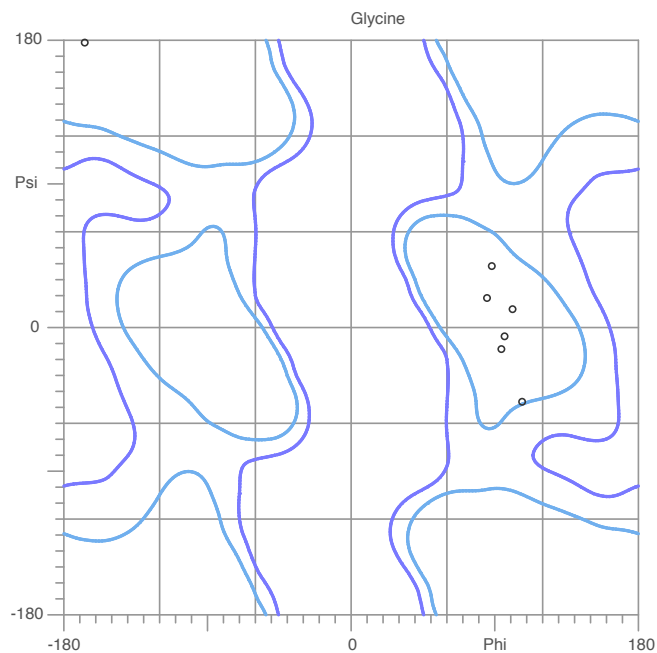
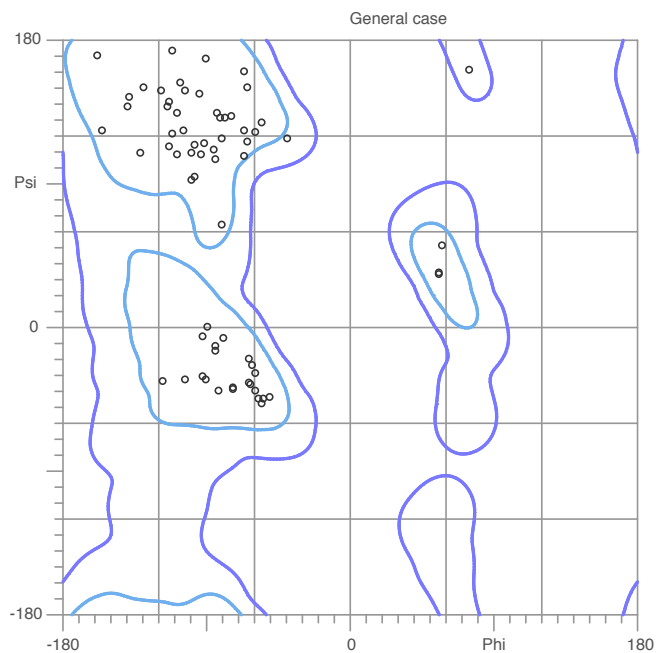
There were 22 outliers (phi, psi):

- [2] 15 ALA (64.9, 95.1)
- [2] 17 SER (64.8, 100.0)
- [2] 74 HIS (75.0, 125.0)
- [3] 70 LYS (65.0, 125.1)
- [3] 76 HIS (65.1, 95.0)
- [7] 57 GLY (177.8, 54.7)
- [7] 76 HIS (63.4, 106.3)
- [8] 67 GLY (-175.1, -75.0)
- [9] 70 LYS (65.2, 124.9)

- [10] 74 HIS (75.0, 125.1)
- [11] 70 LYS (65.0, 125.0)
- [13] 13 ASP (59.5, 165.0)
- [13] 65 PHE (74.9, 105.0)
- [13] 70 LYS (65.0, 125.1)
- [13] 74 HIS (165.0, 64.9)
- [17] 67 GLY (-174.9, 34.9)
- [18] 66 MET (75.0, 104.9)
- [18] 68 GLY (-141.1, 84.7)
- [18] 76 HIS (75.0, 125.0)
- [19] 67 GLY (-178.5, 55.0)
- [19] 70 LYS (65.0, 127.3)
- [20] 17 SER (78.4, 133.4)

MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 1



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.

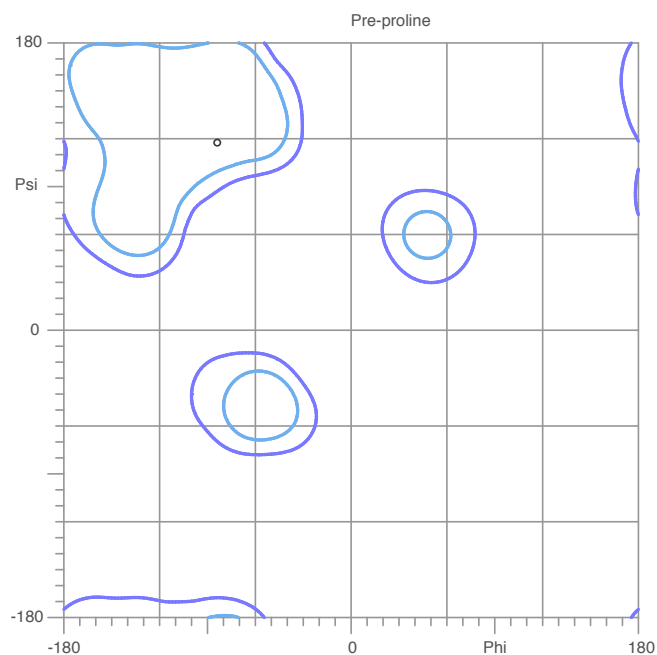
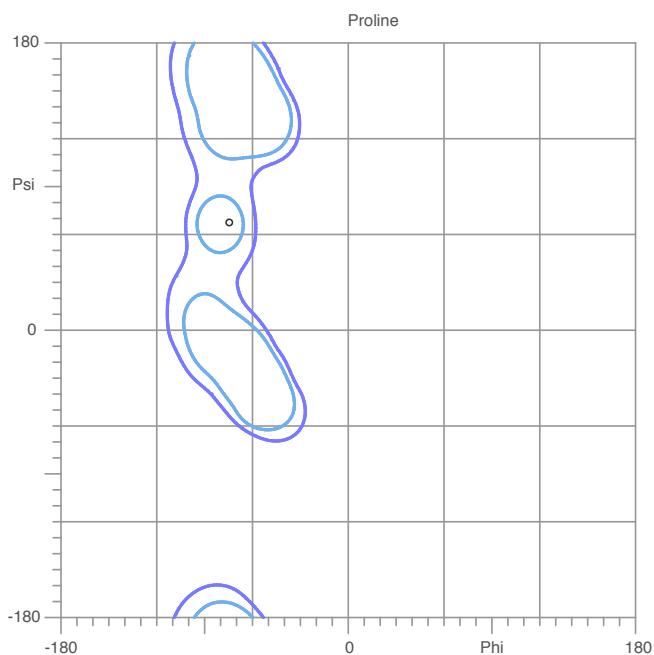
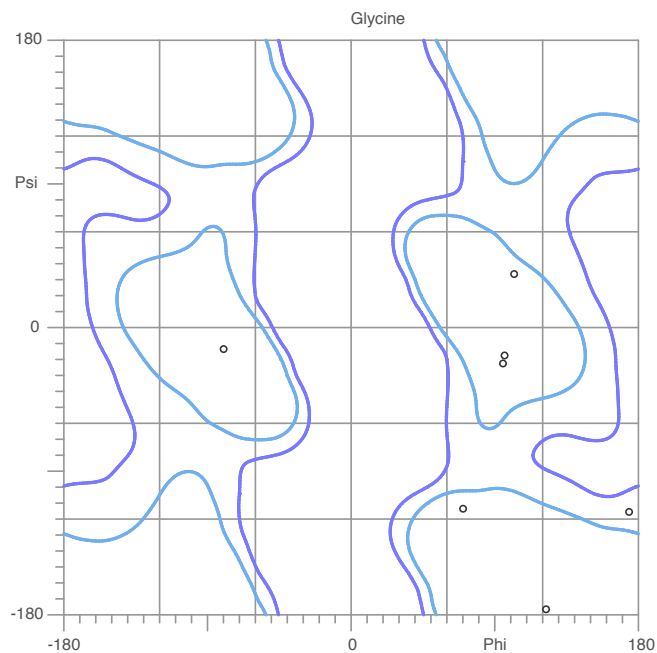
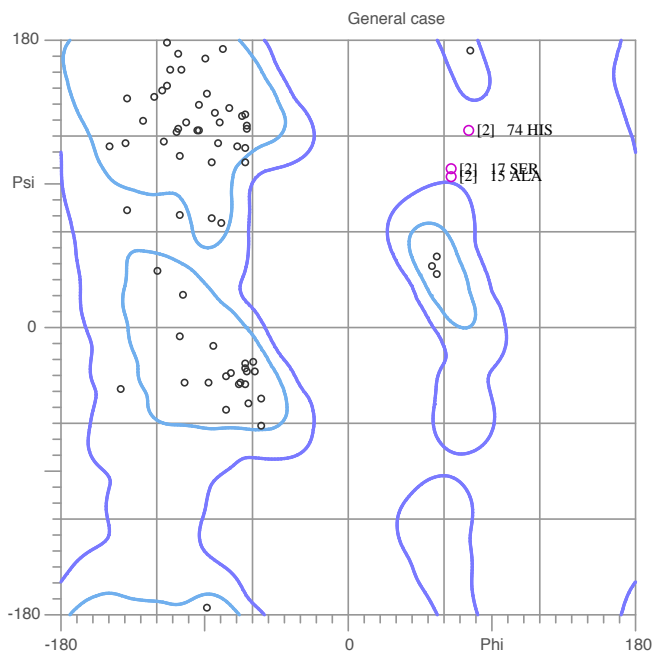
There were no outliers.

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

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 2



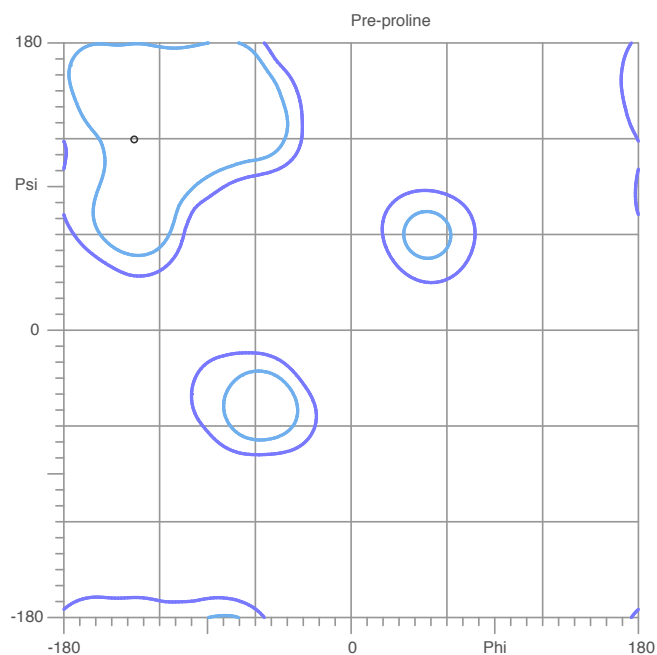
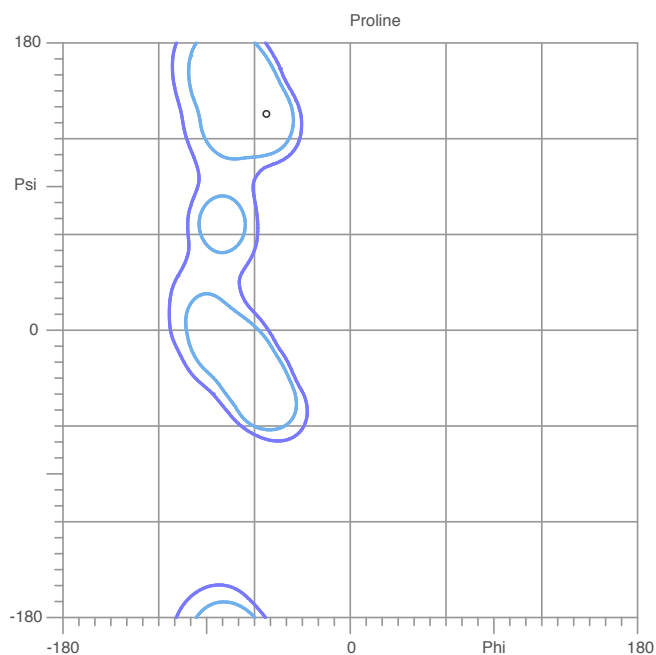
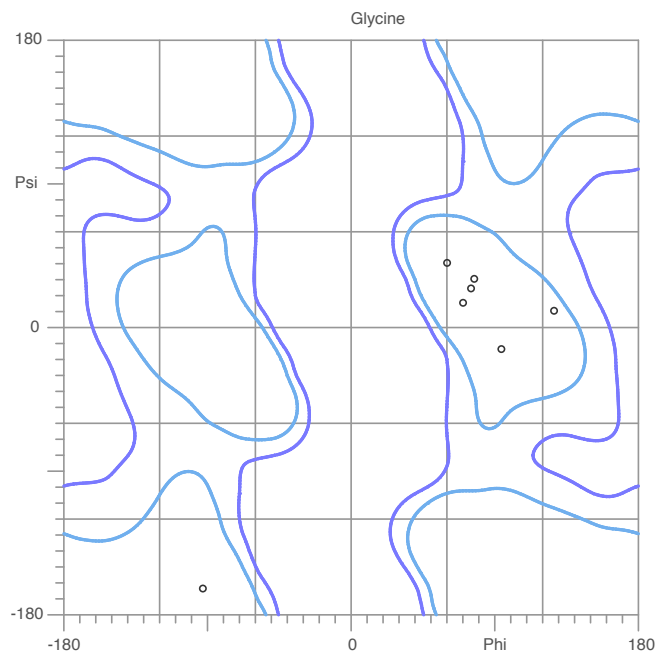
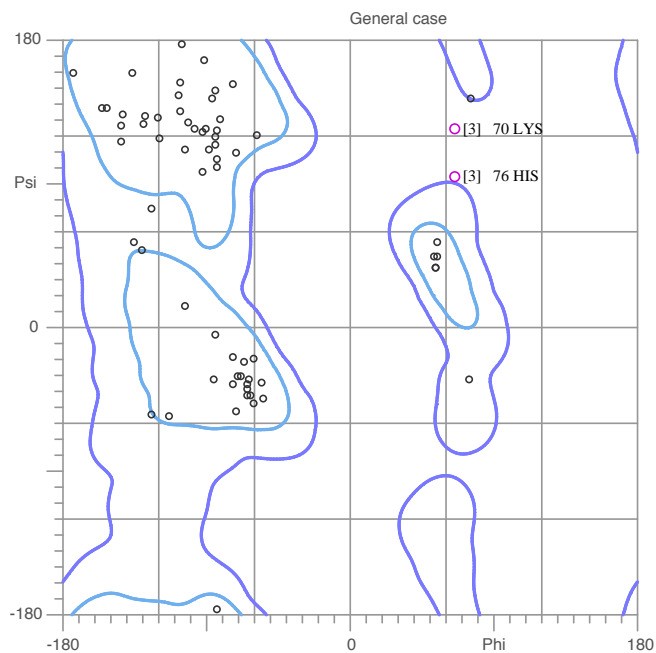
88.2% (67/76) of all residues were in favored (98%) regions.
96.1% (73/76) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 15 ALA (64.9, 95.1)
- [2] 17 SER (64.8, 100.0)
- [2] 74 HIS (75.0, 125.0)

MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 3



89.5% (68/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

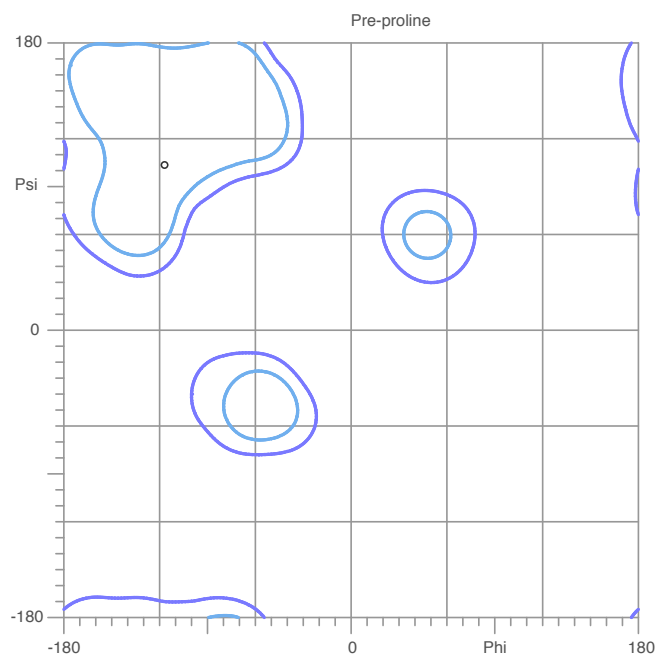
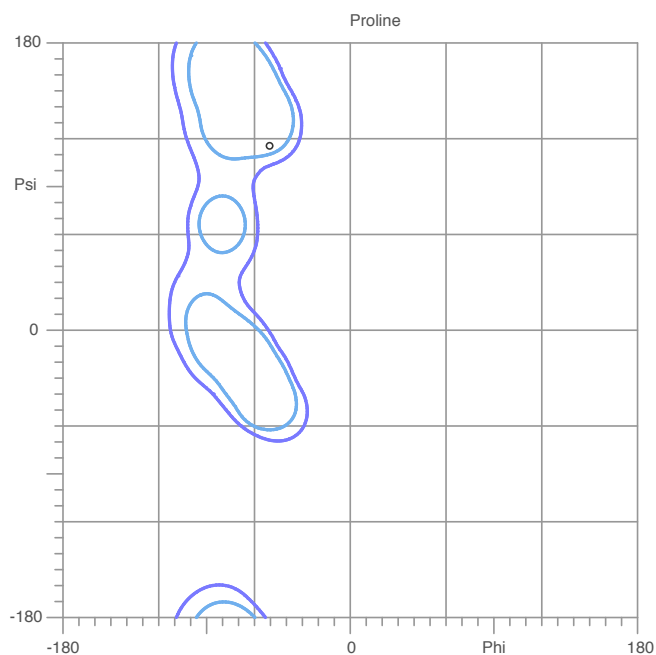
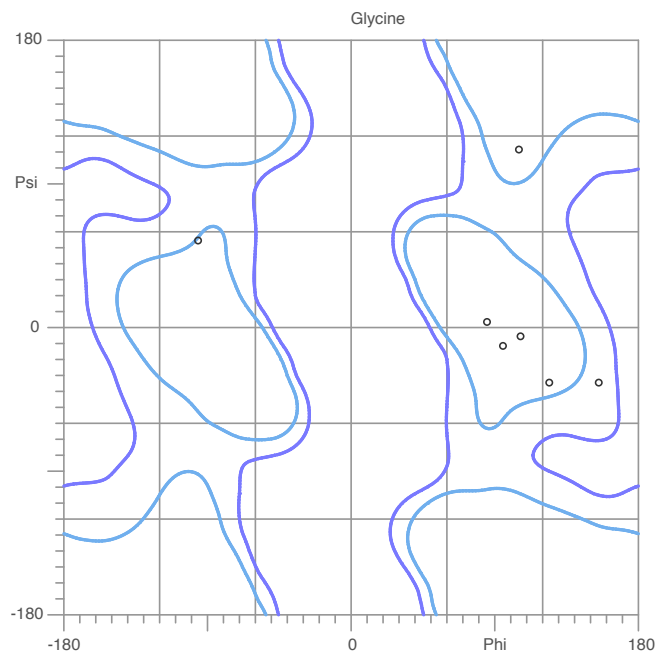
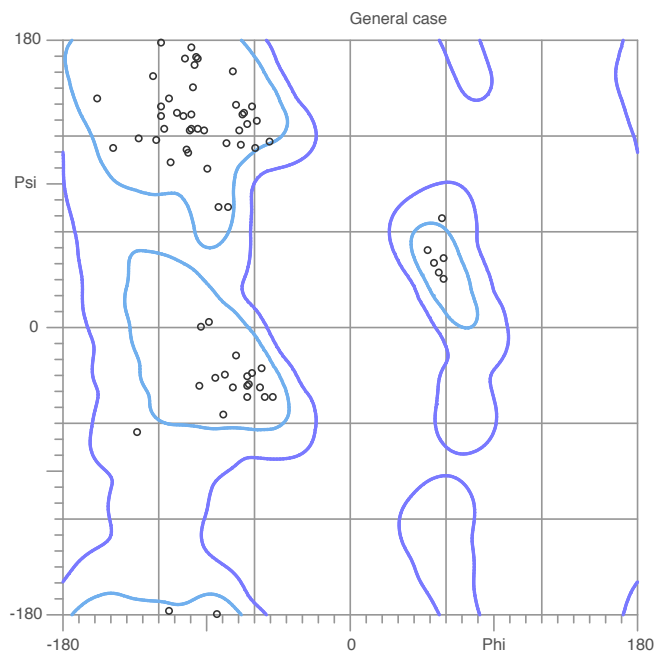
There were 2 outliers (phi, psi):

[3] 70 LYS (65.0, 125.1)

[3] 76 HIS (65.1, 95.0)

MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 4



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.

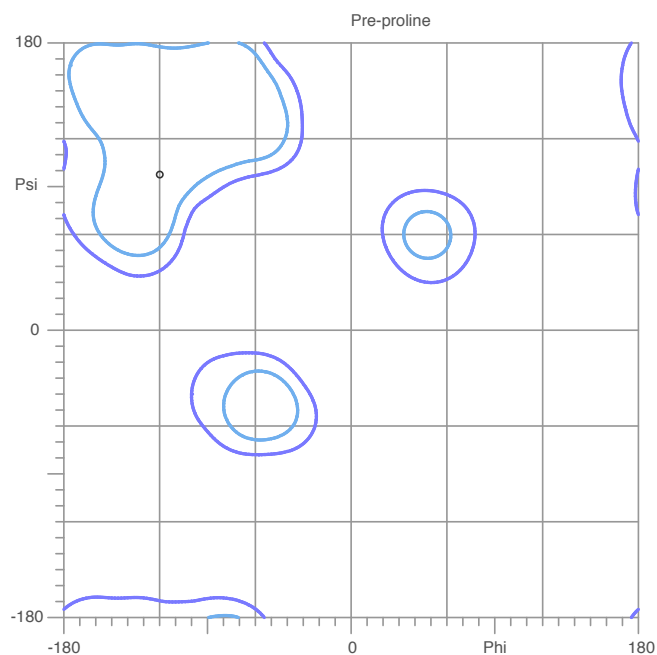
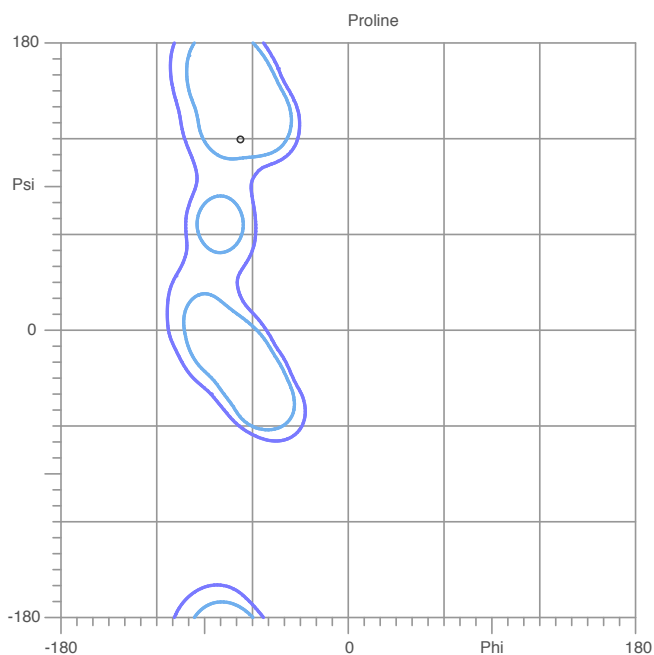
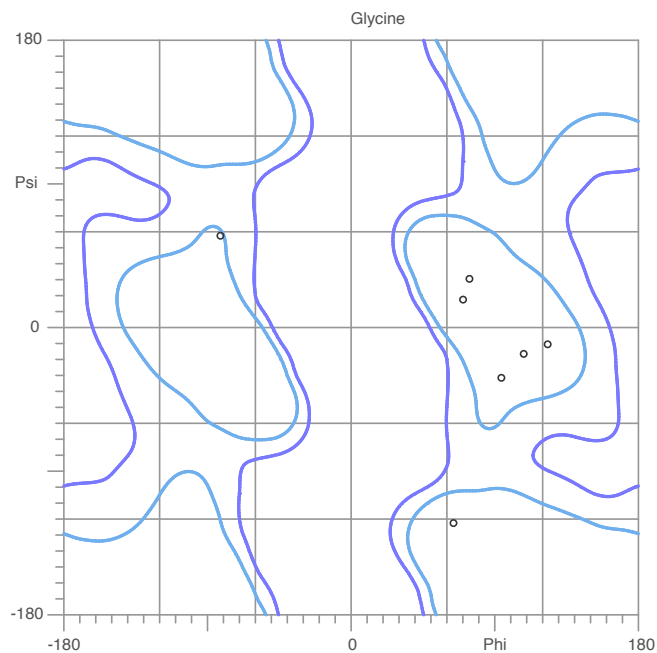
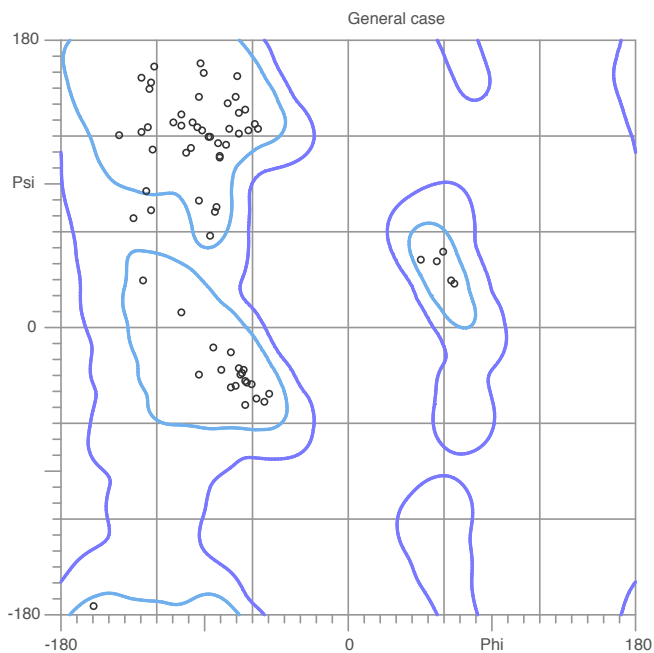
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 5



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.

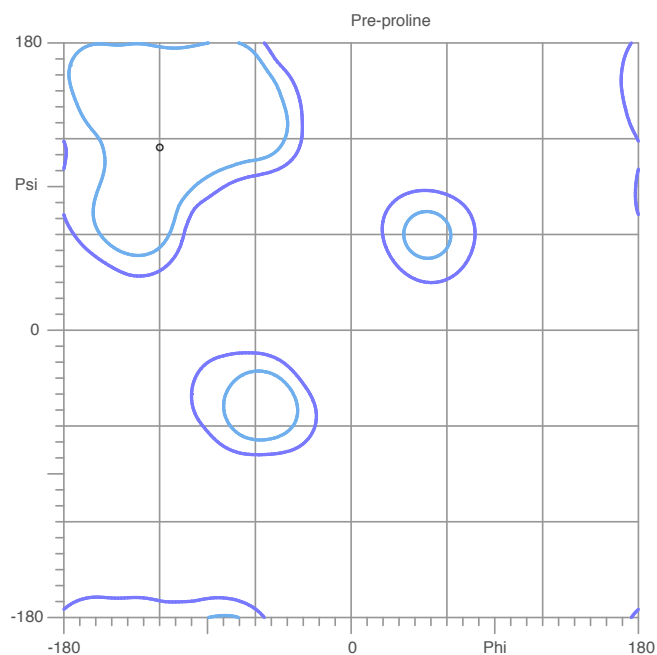
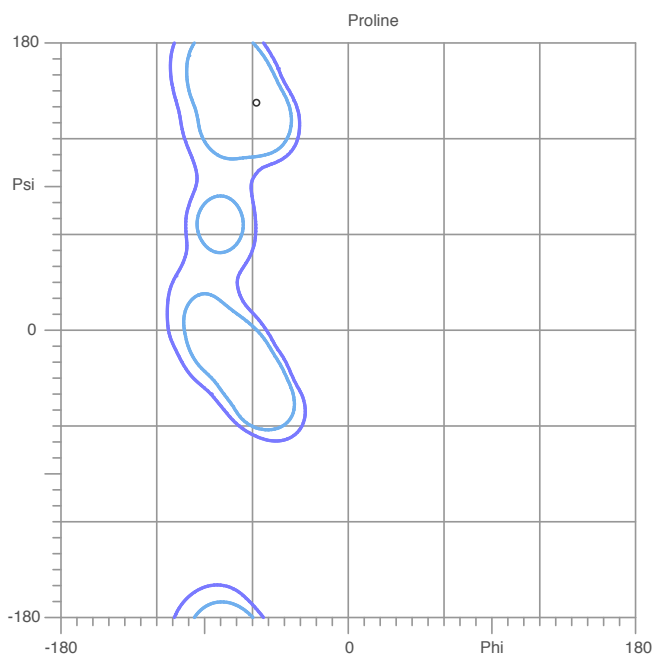
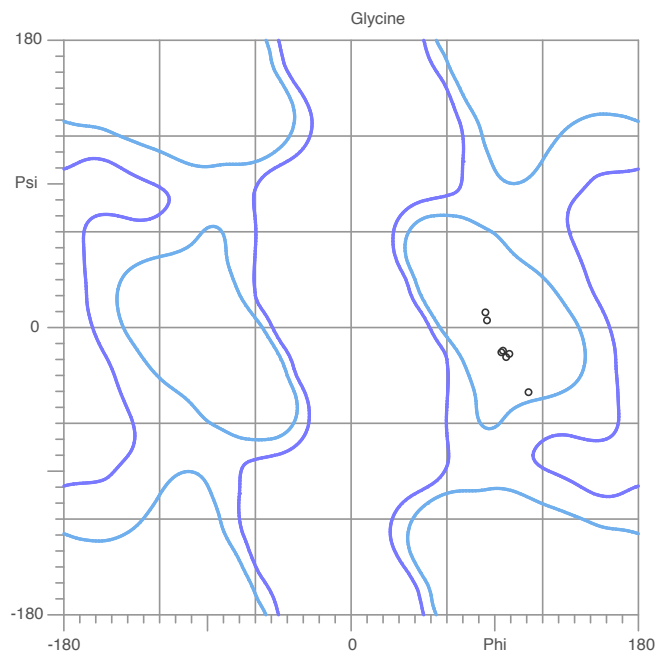
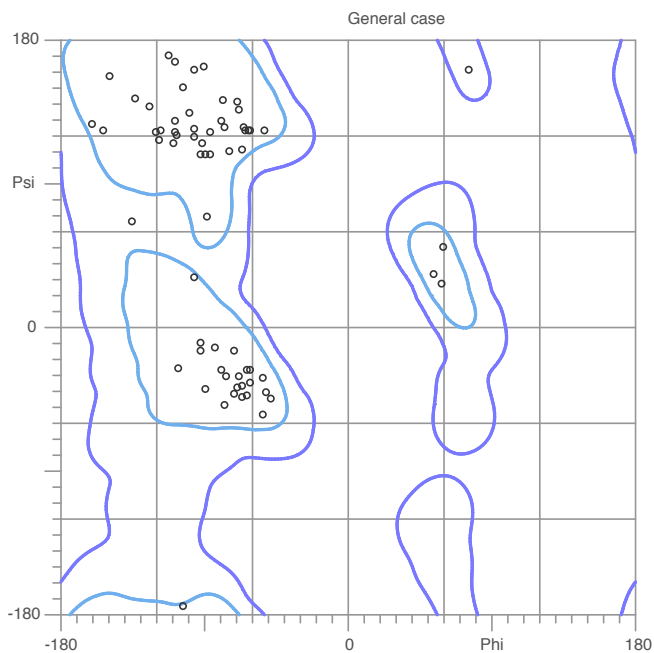
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 6



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.

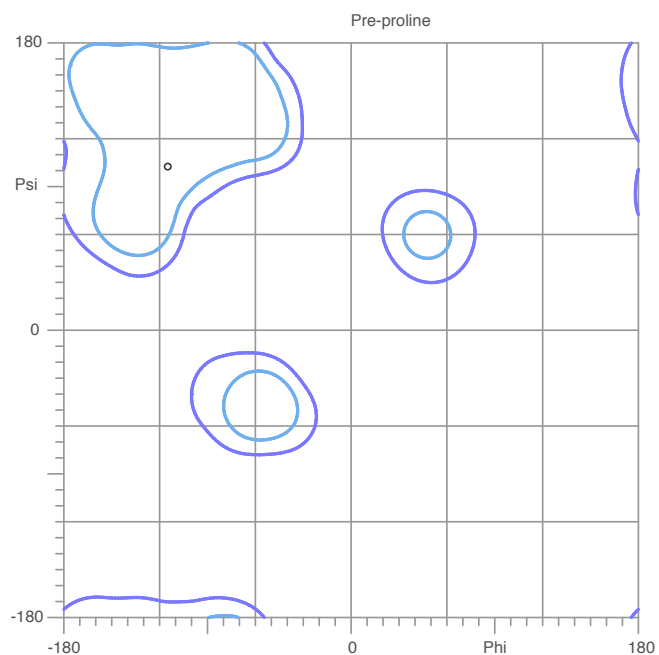
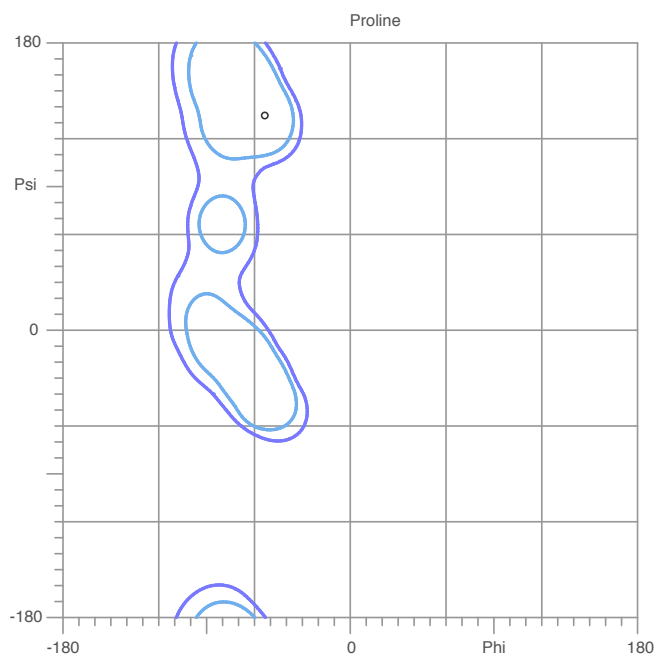
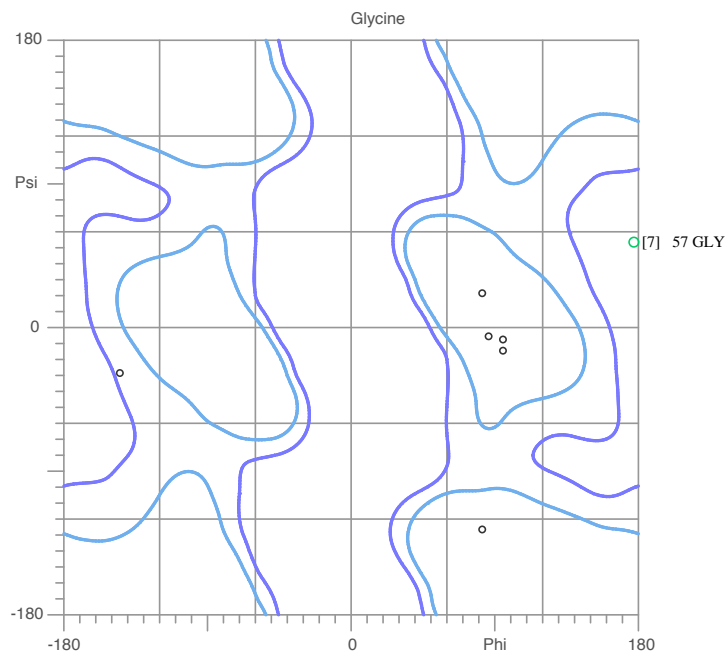
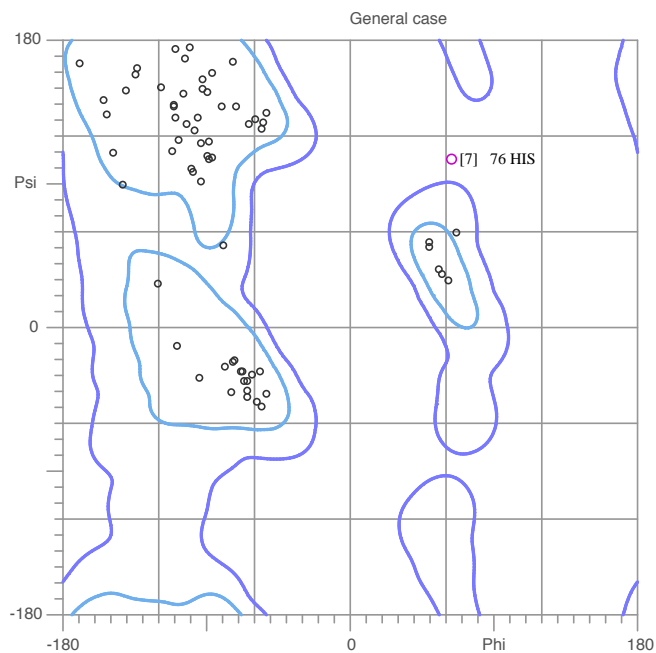
There were no outliers.

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 7

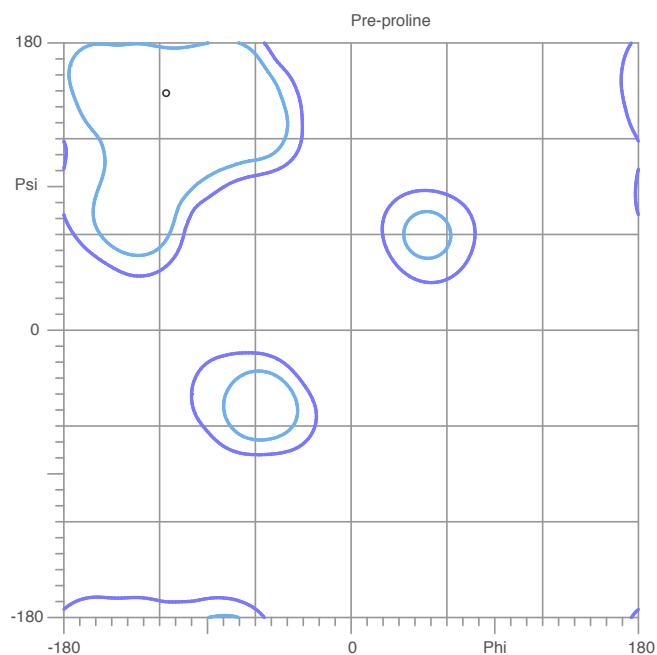
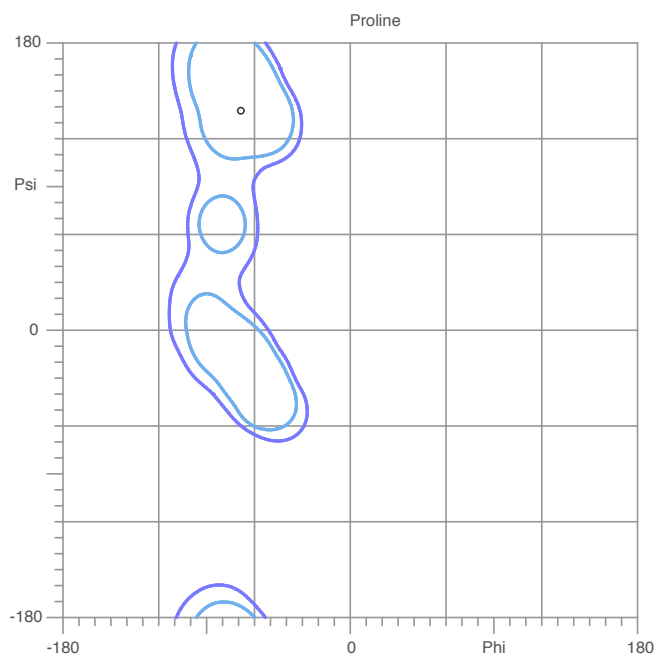
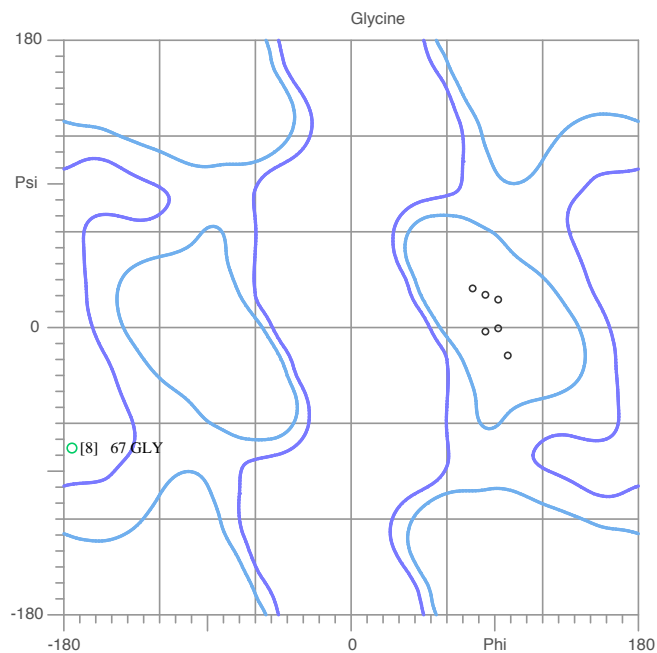
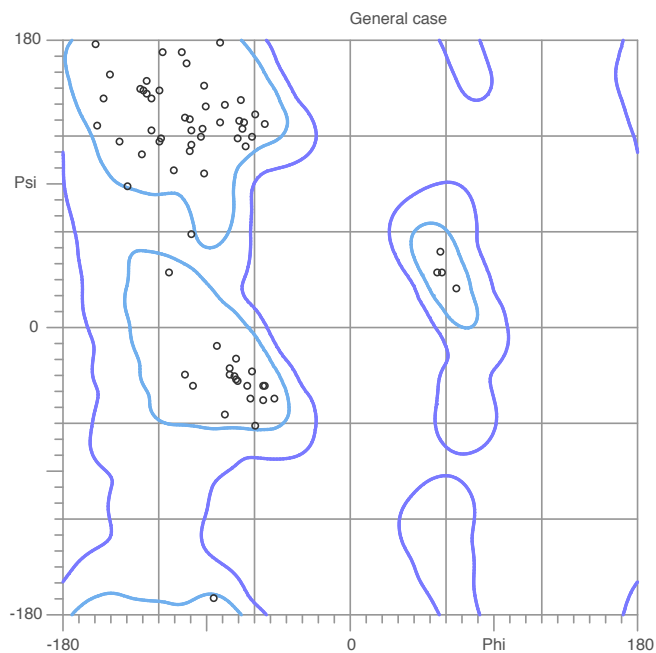


93.4% (71/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[7] 57 GLY (177.8, 54.7)
[7] 76 HIS (63.4, 106.3)

MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 8

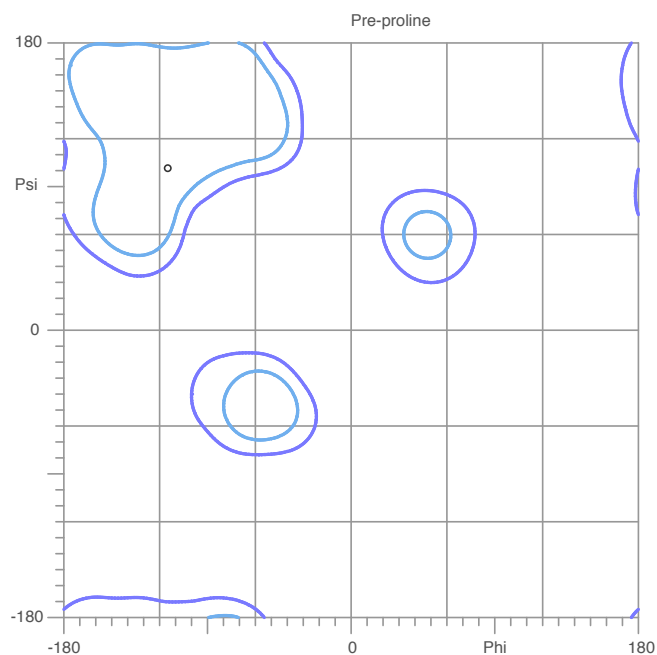
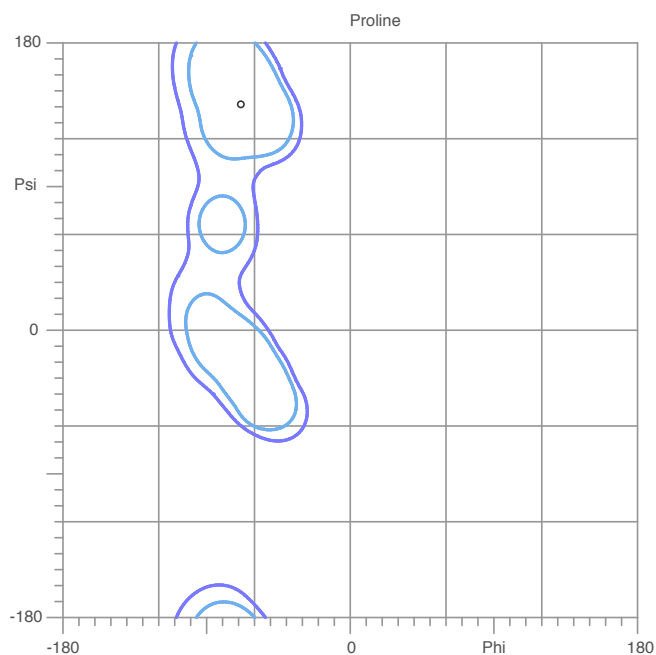
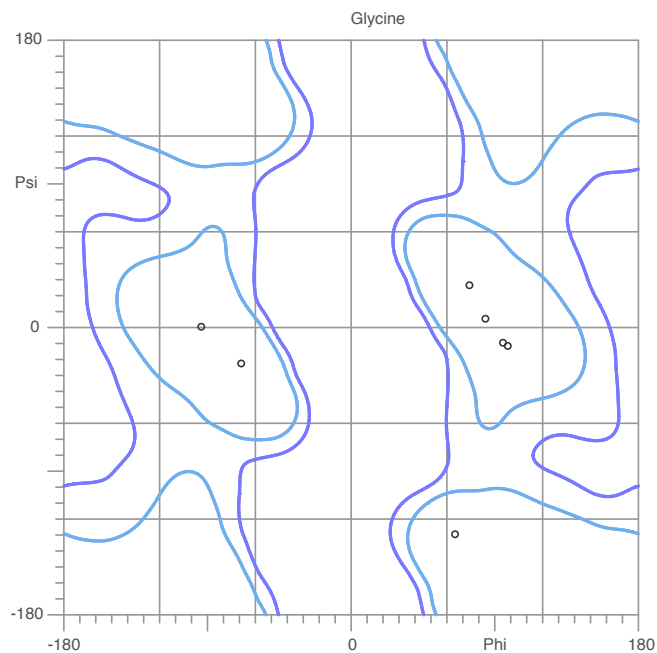
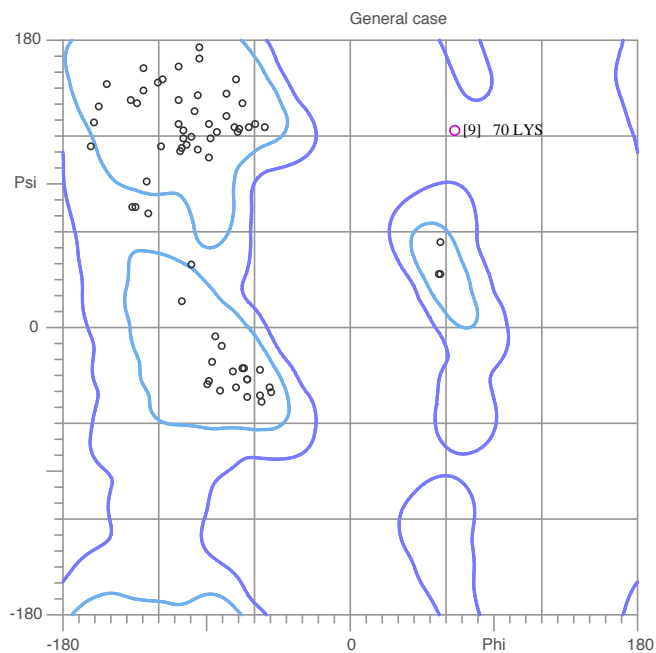


97.4% (74/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 67 GLY (-175.1, -75.0)

MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 9



92.1% (70/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

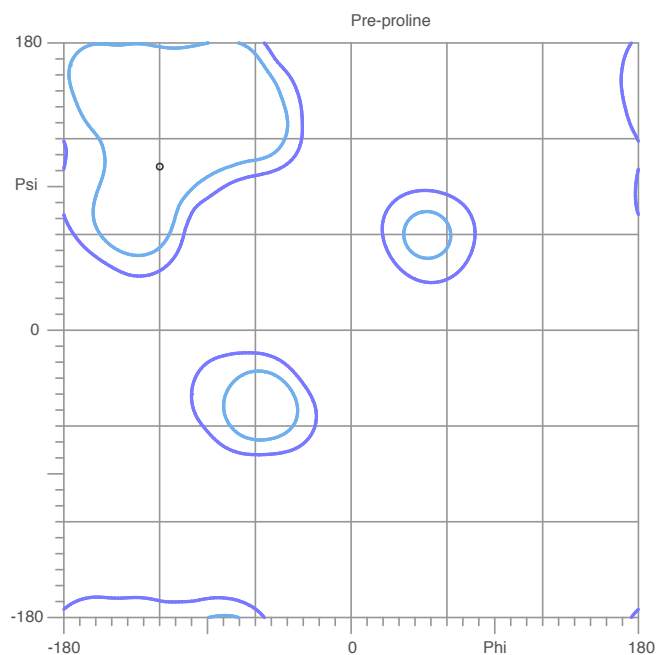
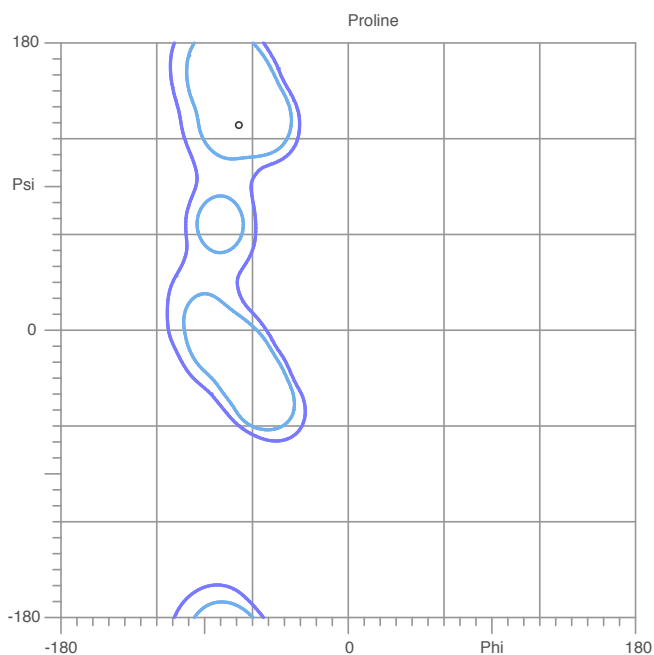
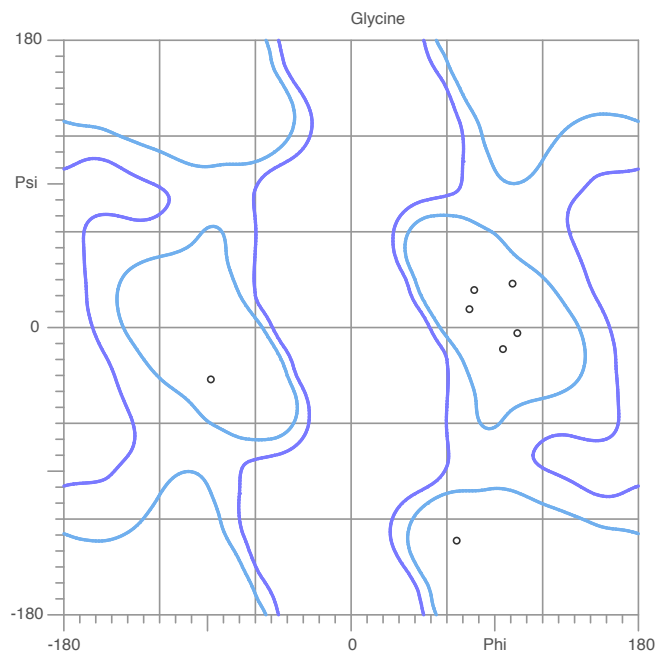
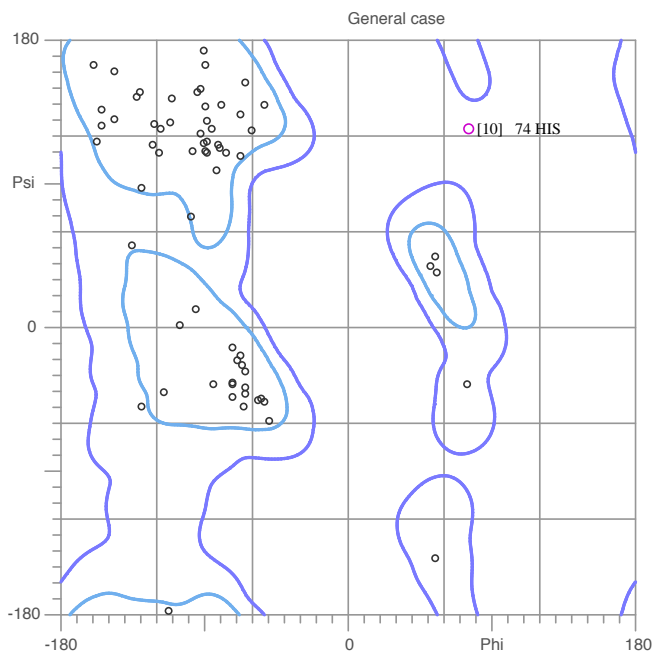
There were 1 outliers (phi, psi):
[9] 70 LYS (65.2, 124.9)

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 10



92.1% (70/76) of all residues were in favored (98%) regions.
98.7% (75/76) of all residues were in allowed (>99.8%) regions.

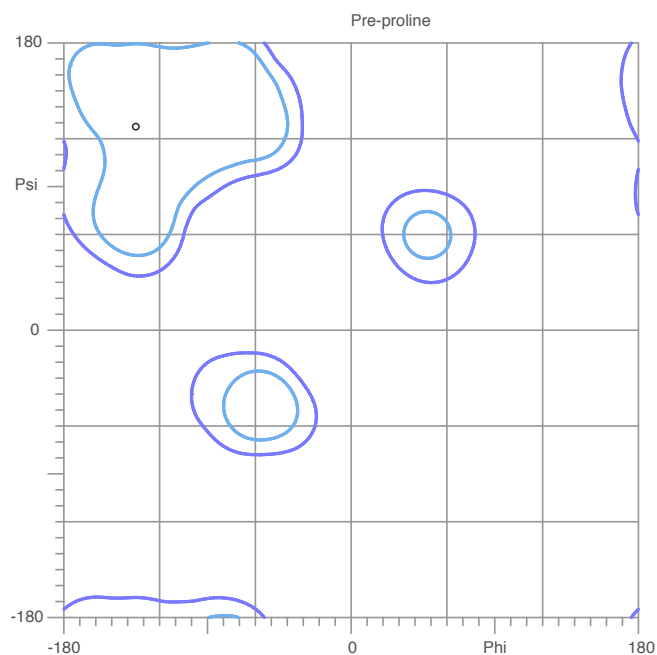
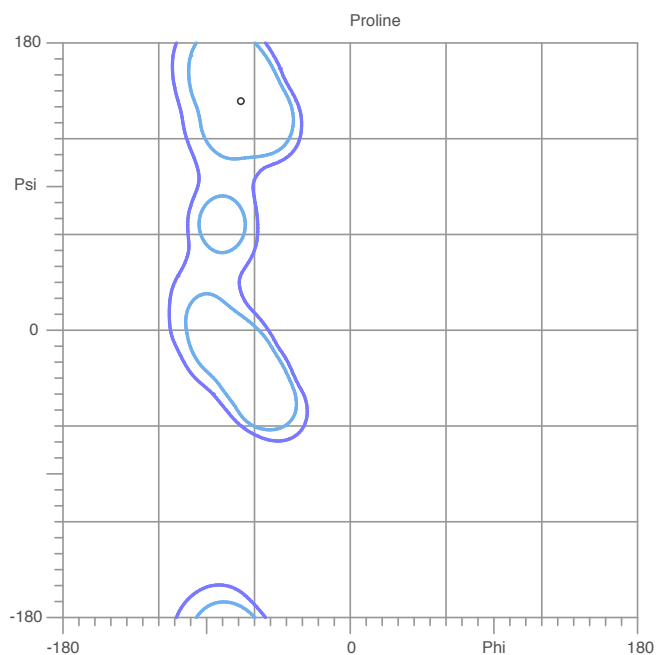
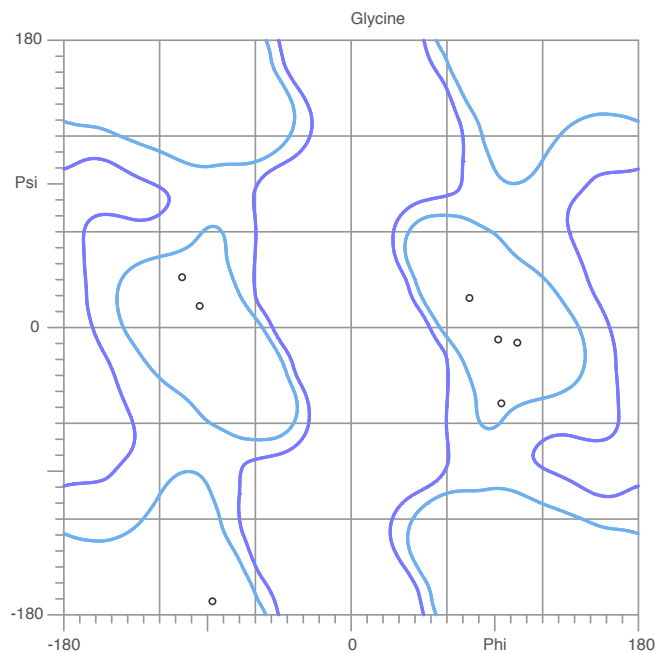
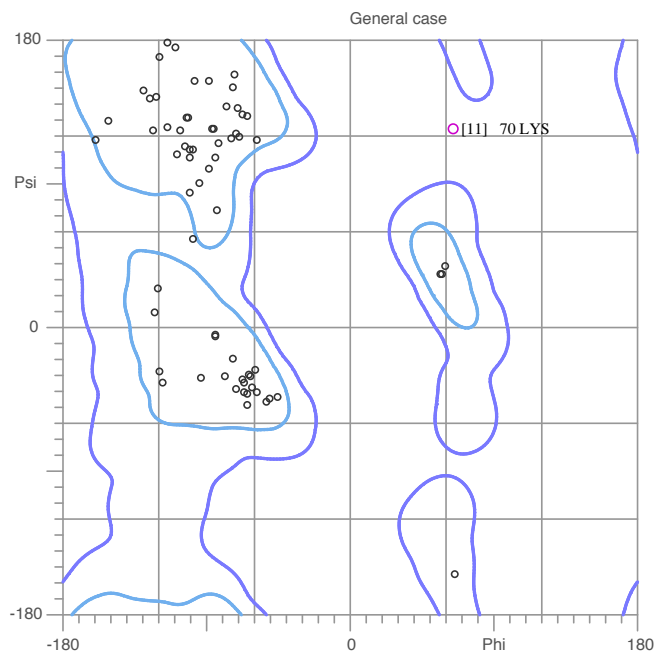
There were 1 outliers (phi, psi):
[10] 74 HIS (75.0, 125.1)

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 11



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.

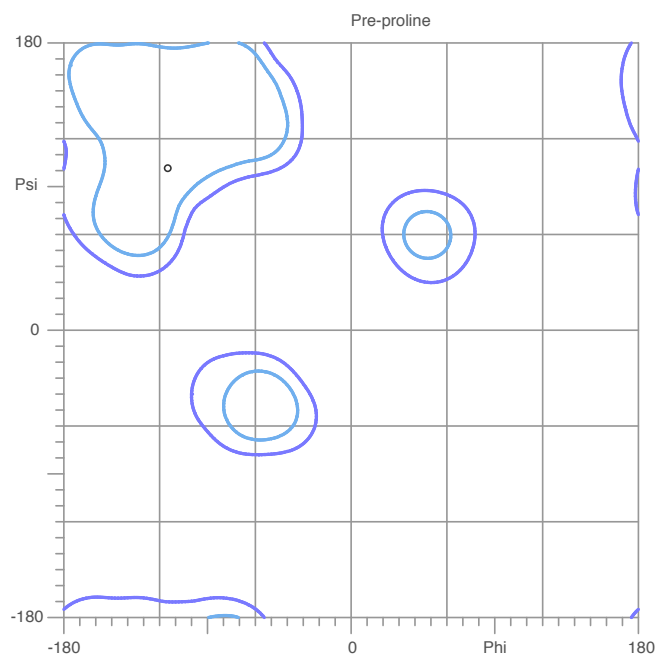
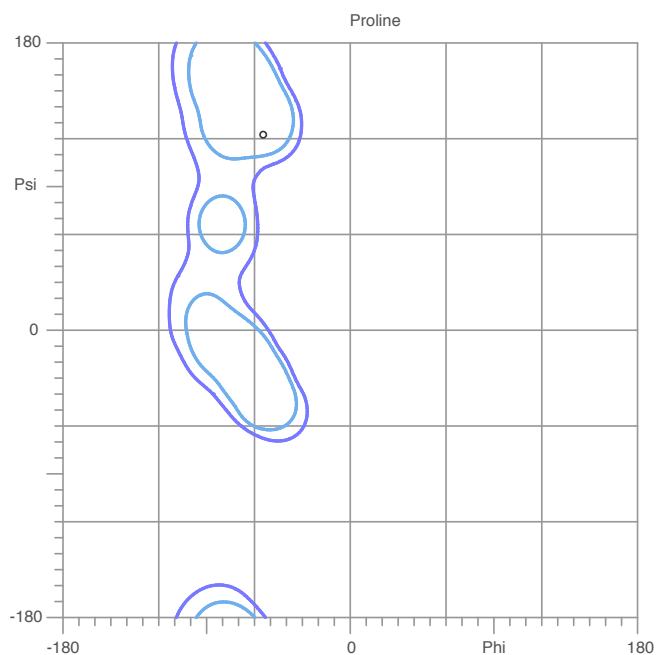
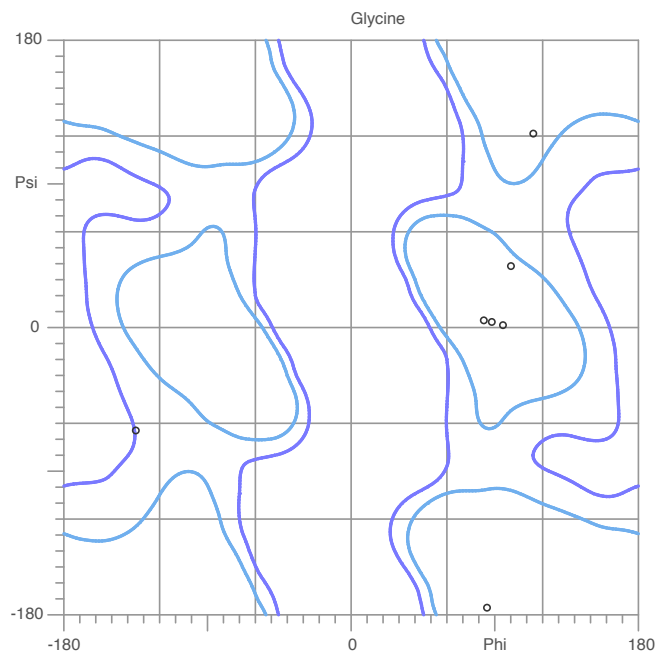
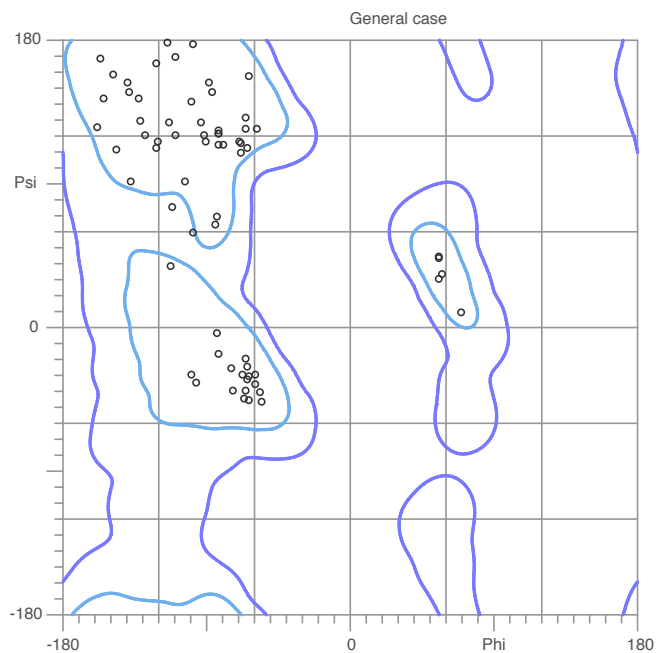
There were 1 outliers (phi, psi):
[11] 70 LYS (65.0, 125.0)

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 12



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.

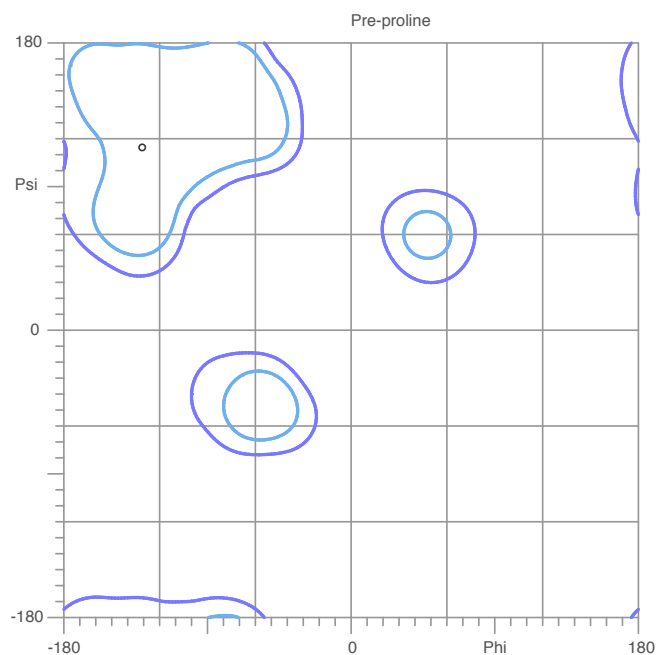
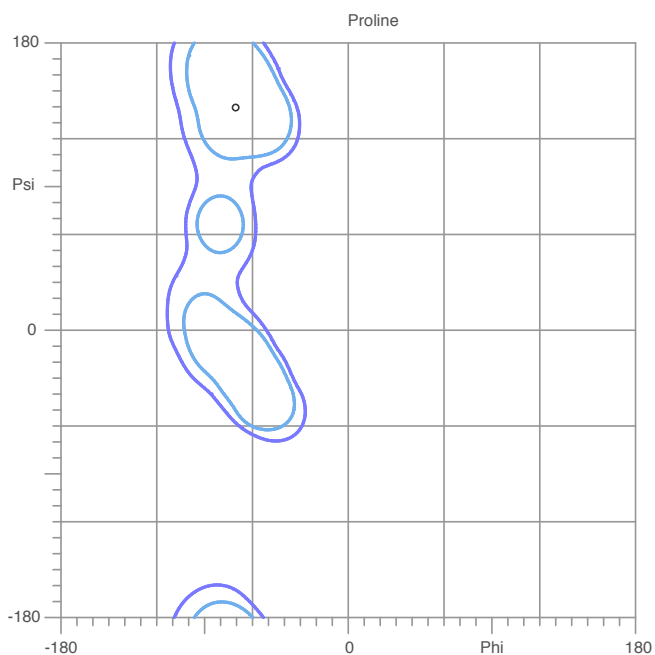
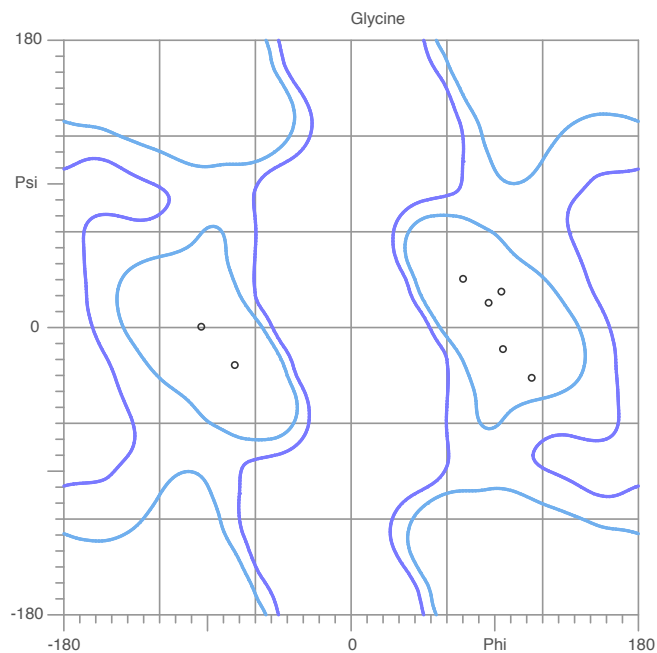
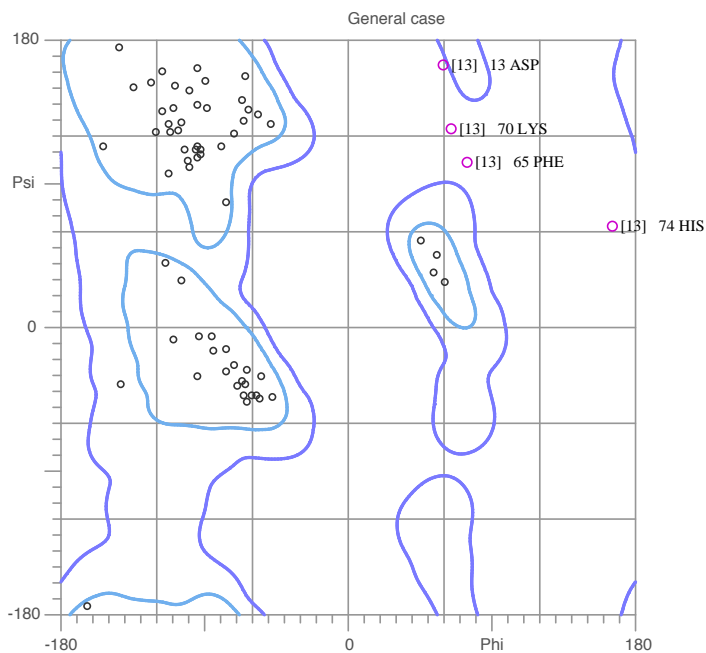
There were no outliers.

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

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 13



93.4% (71/76) 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):

[13] 13 ASP (59.5, 165.0)

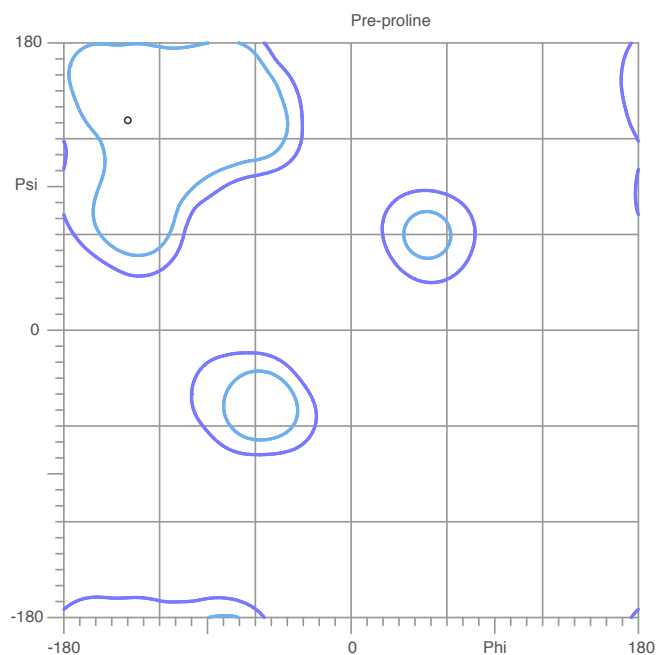
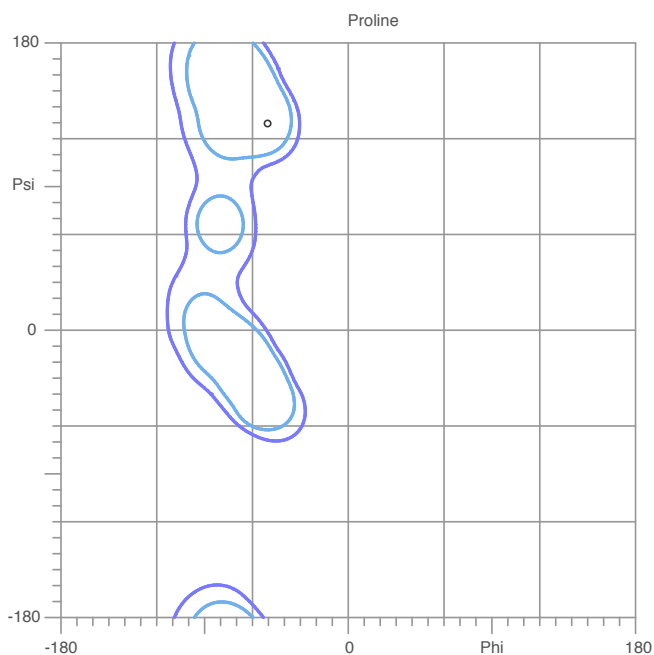
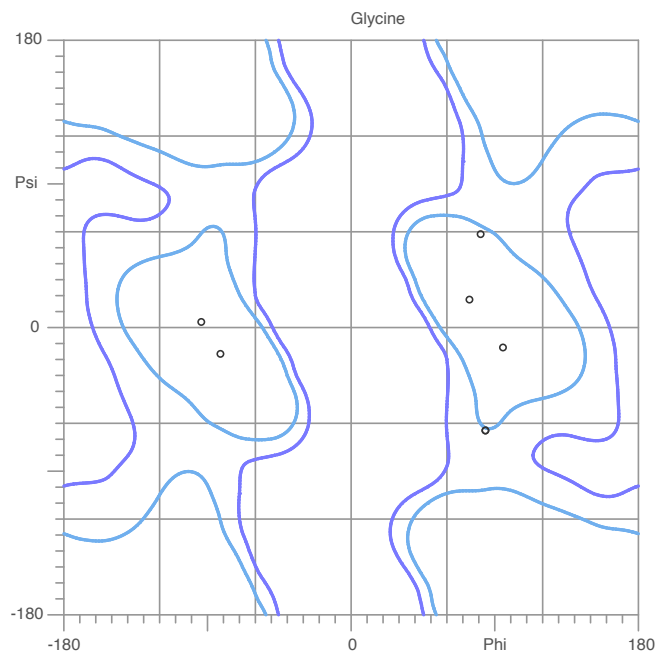
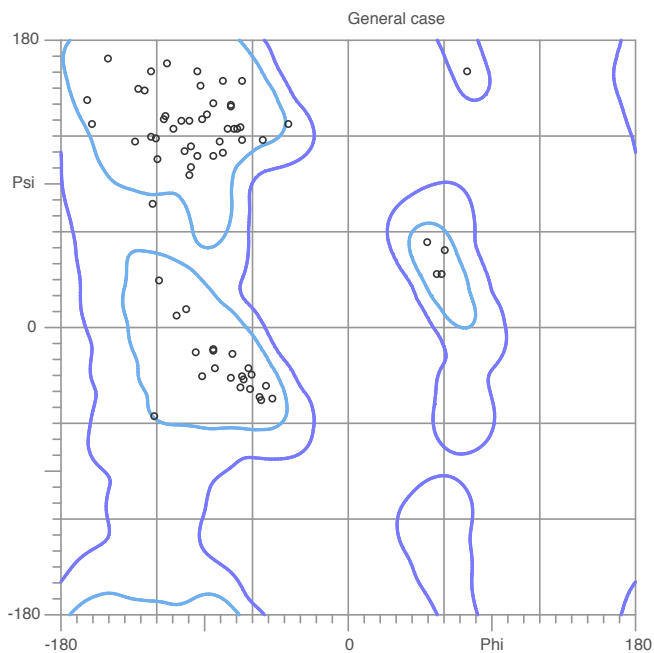
[13] 65 PHE (74.9, 105.0)

[13] 70 LYS (65.0, 125.1)

[13] 74 HIS (165.0, 64.9)

MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 14



93.4% (71/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

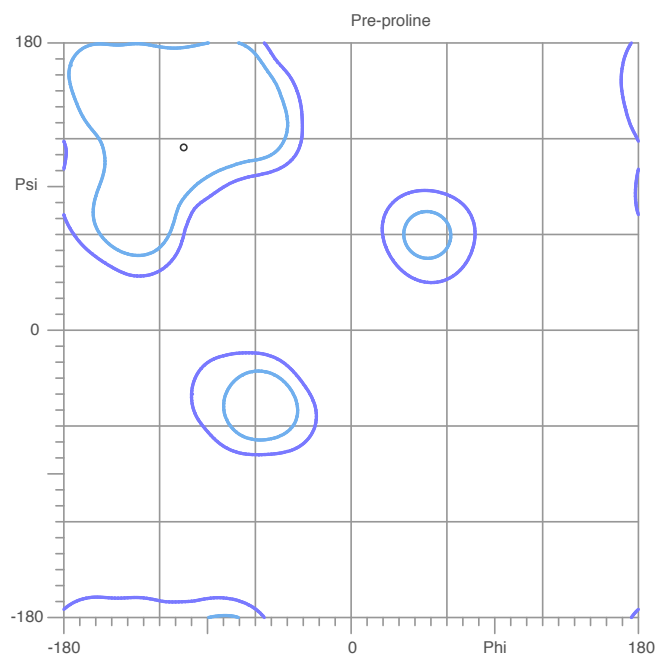
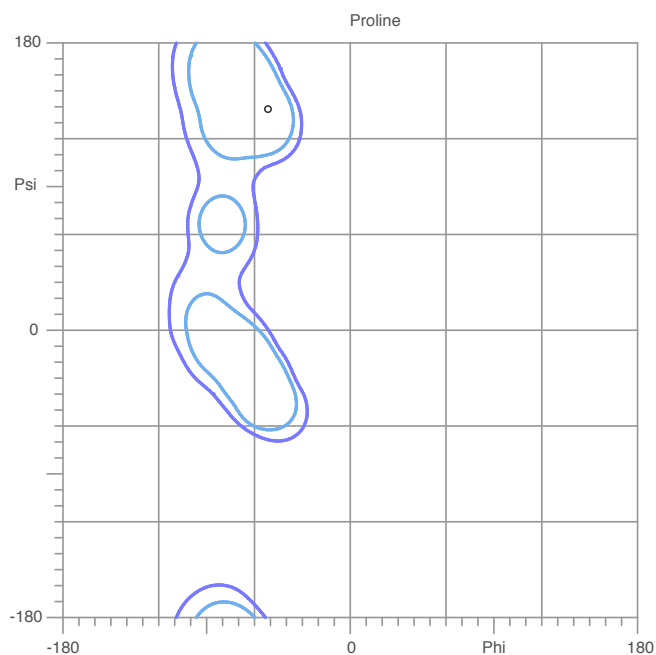
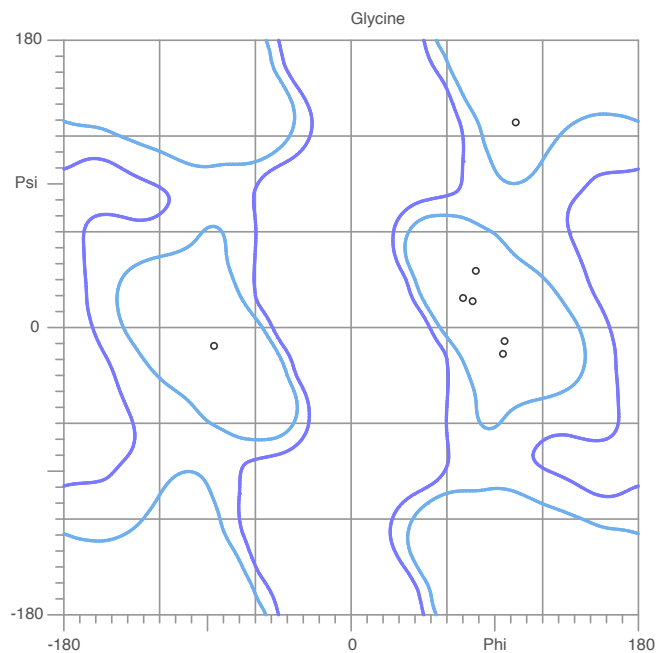
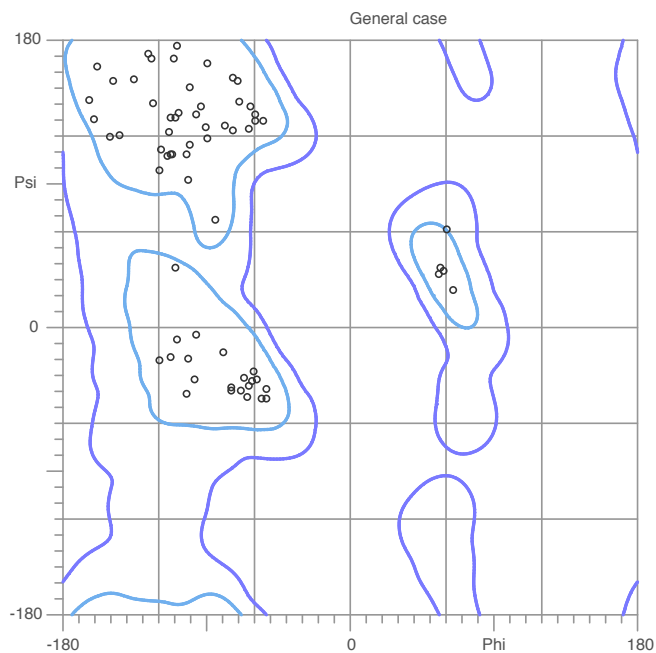
There were no outliers.

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

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 15



98.7% (75/76) of all residues were in favored (98%) regions.
100.0% (76/76) of all residues were in allowed (>99.8%) regions.

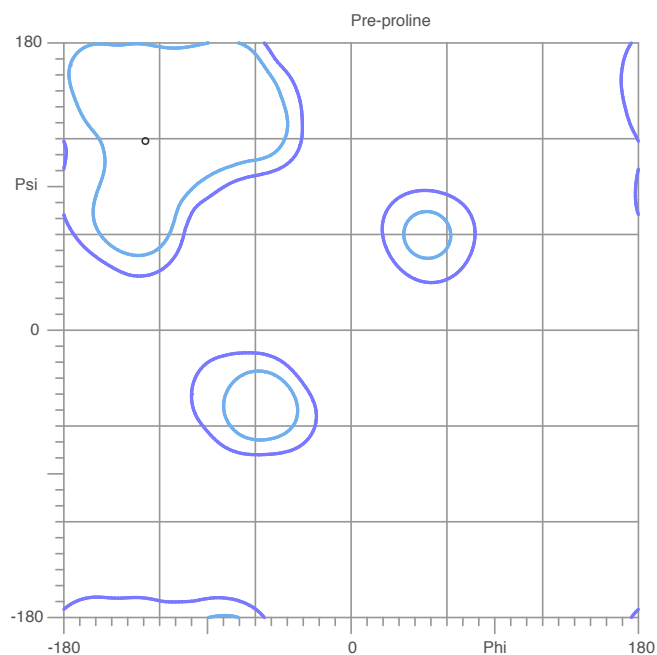
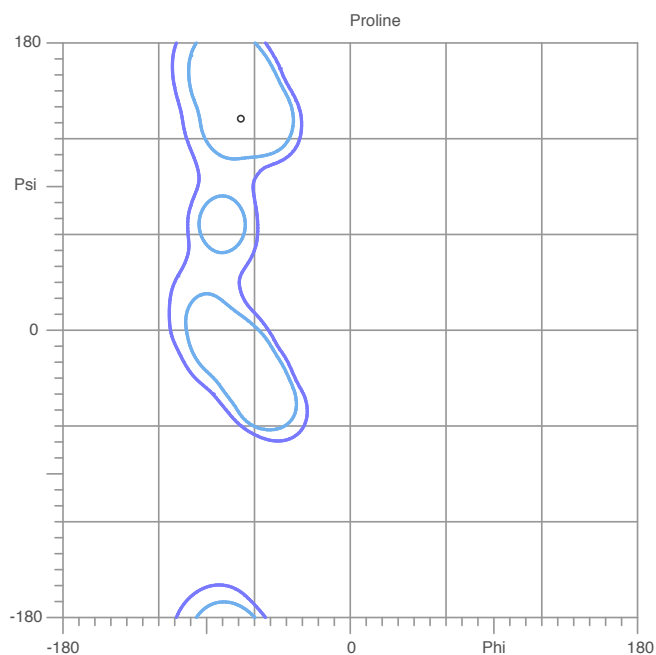
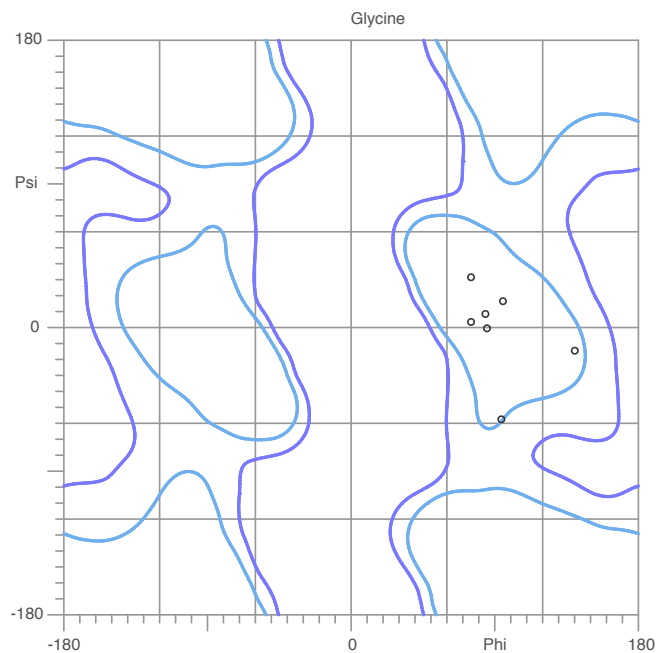
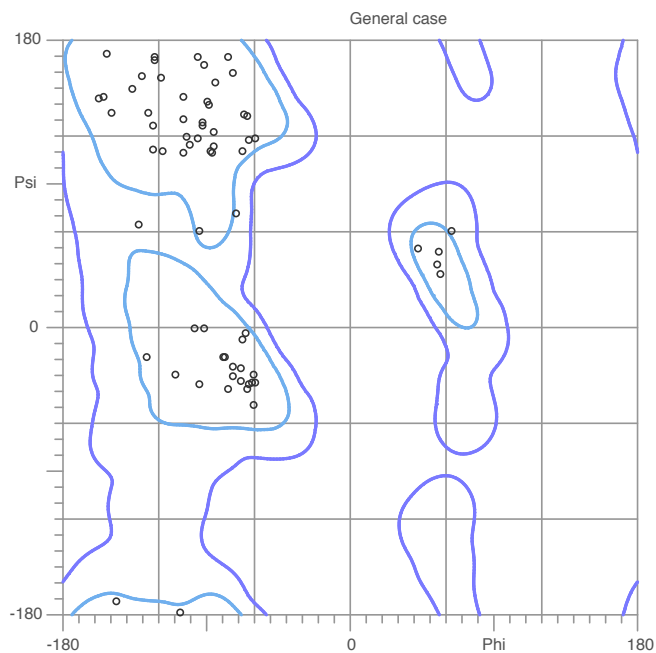
There were no outliers.

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

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

MolProbity Ramachandran analysis

GMR137_R3_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.

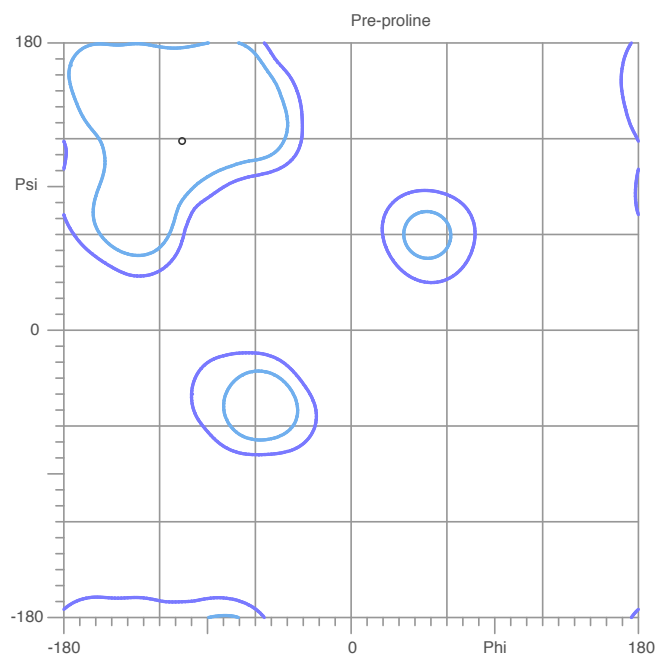
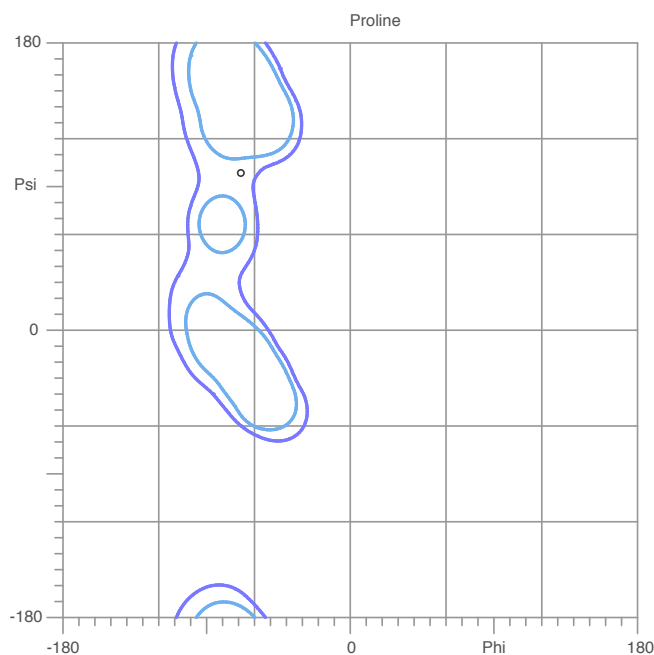
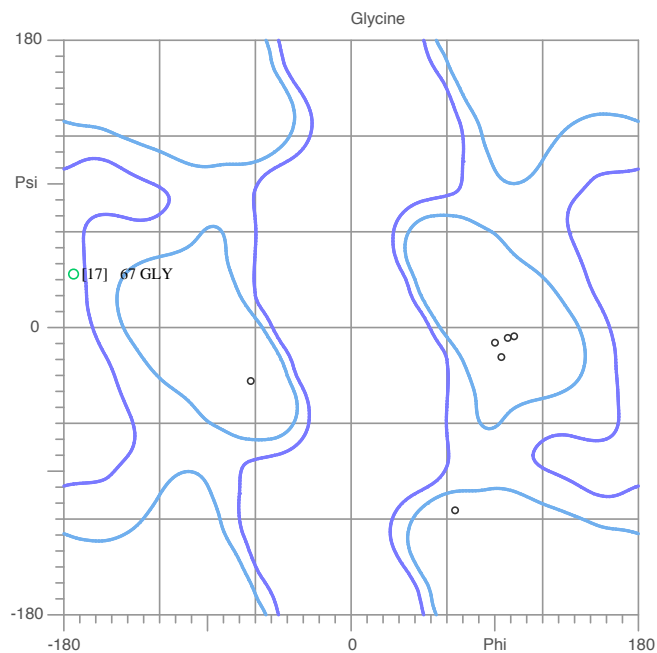
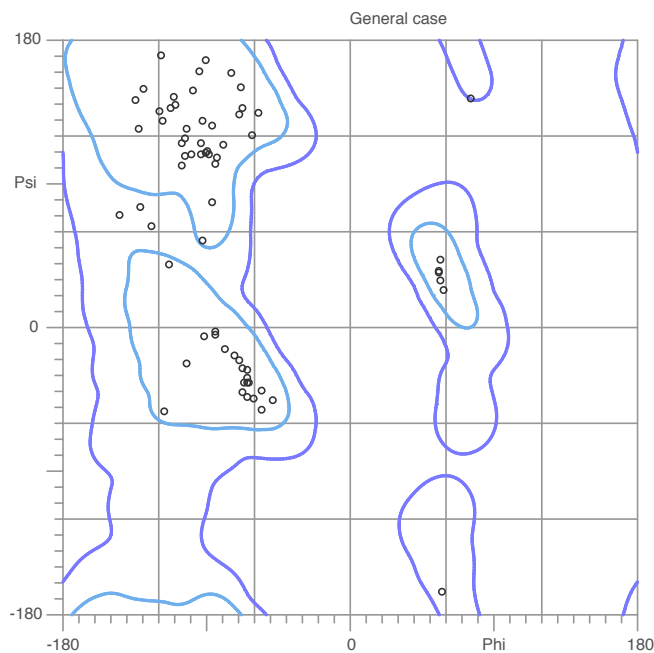
There were no outliers.

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

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 17



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.

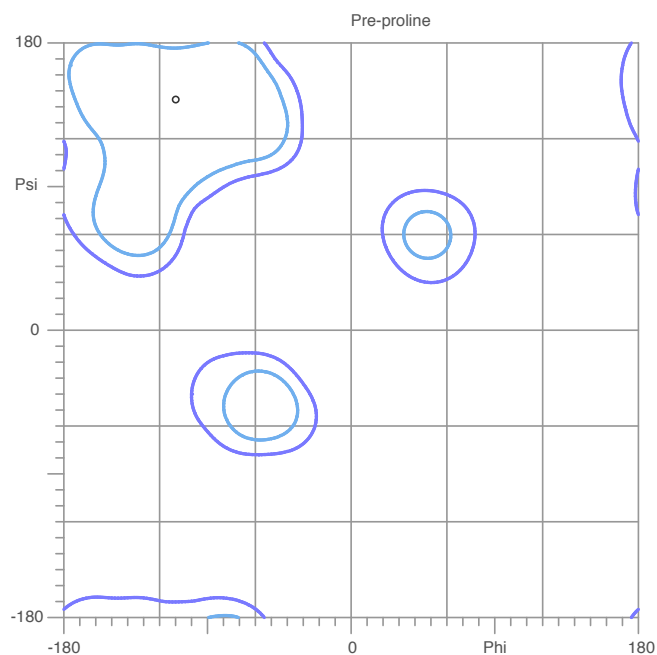
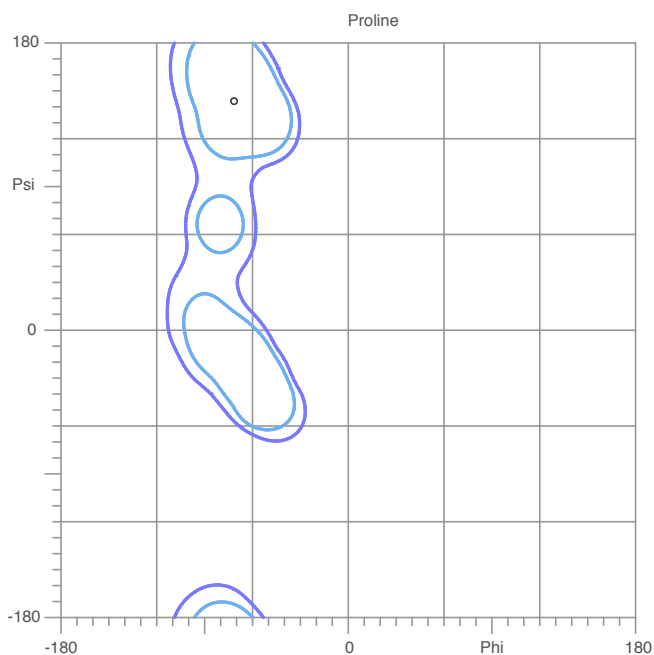
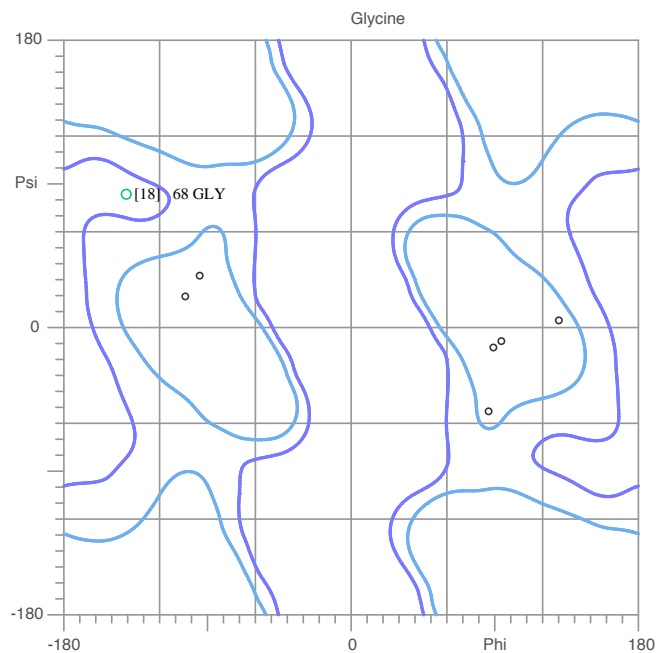
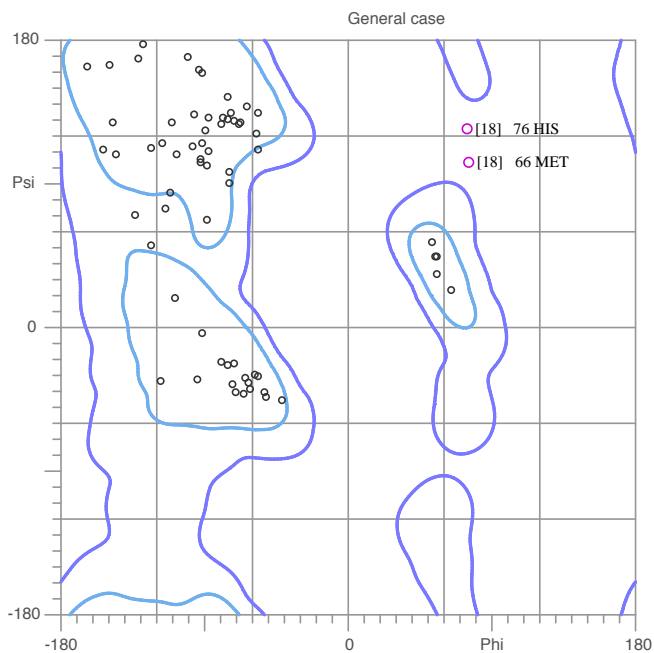
There were 1 outliers (phi, psi):
[17] 67 GLY (-174.9, 34.9)

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MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 18



92.1% (70/76) 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):

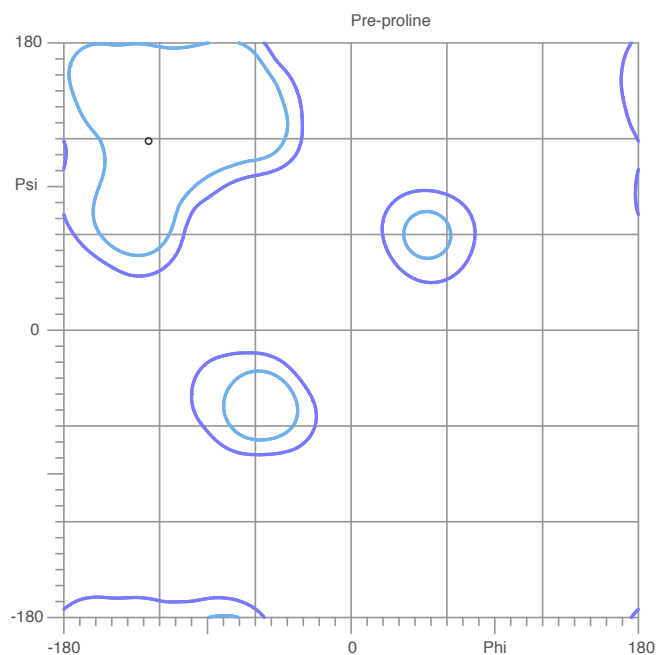
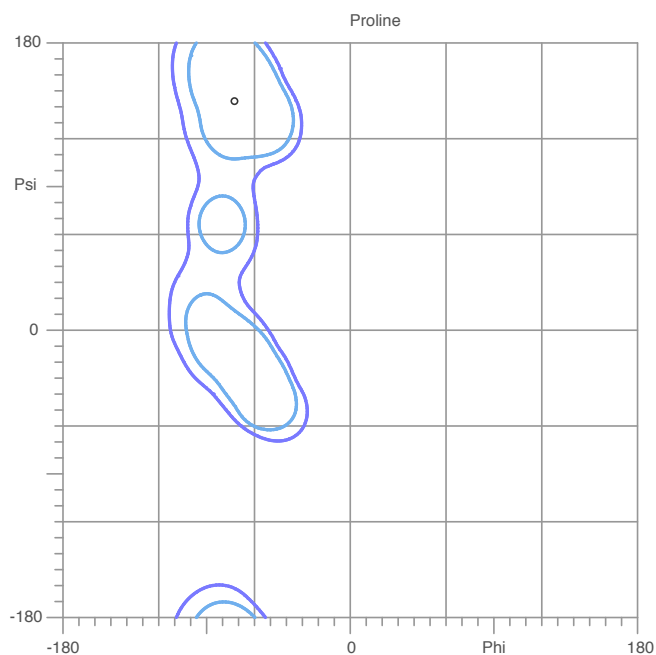
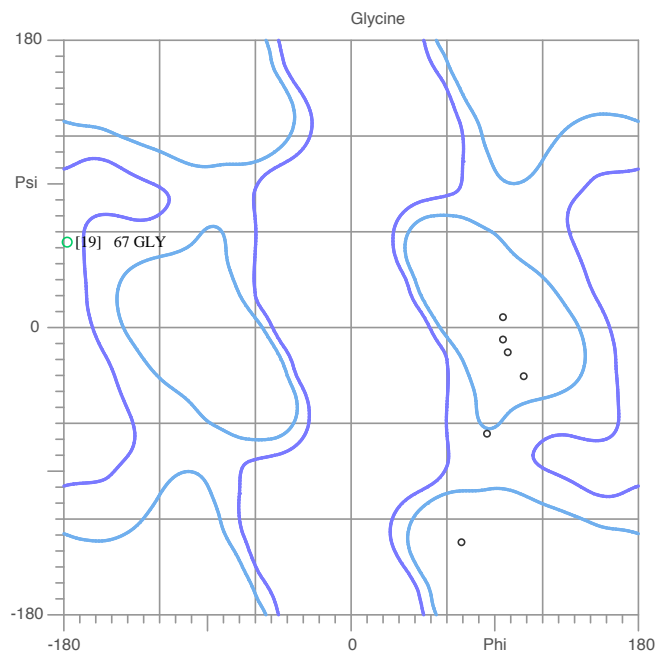
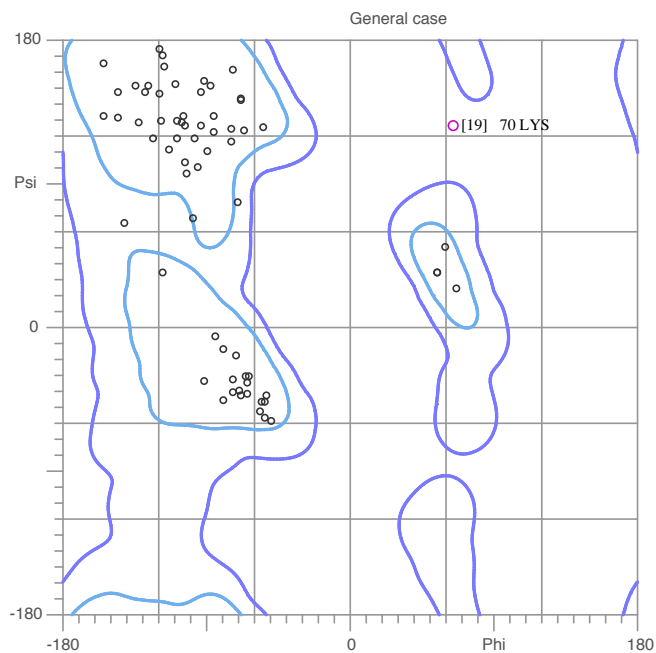
[18] 66 MET (75.0, 104.9)

[18] 68 GLY (-141.1, 84.7)

[18] 76 HIS (75.0, 125.0)

MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 19

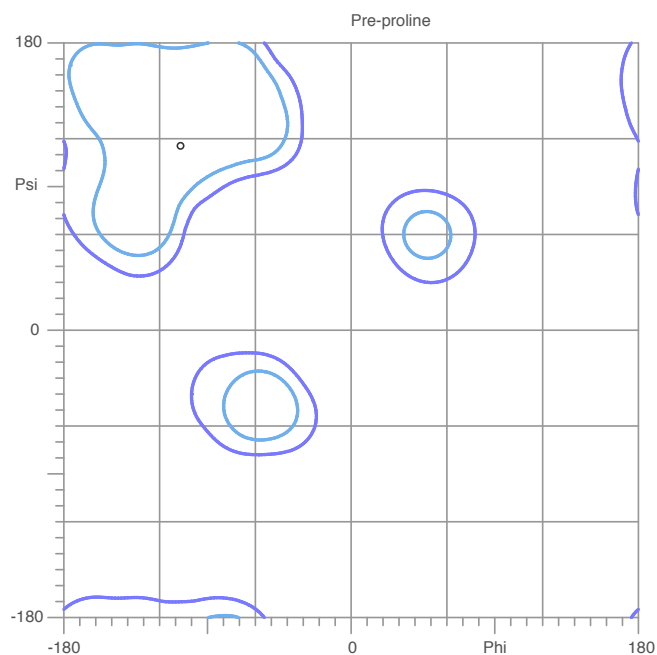
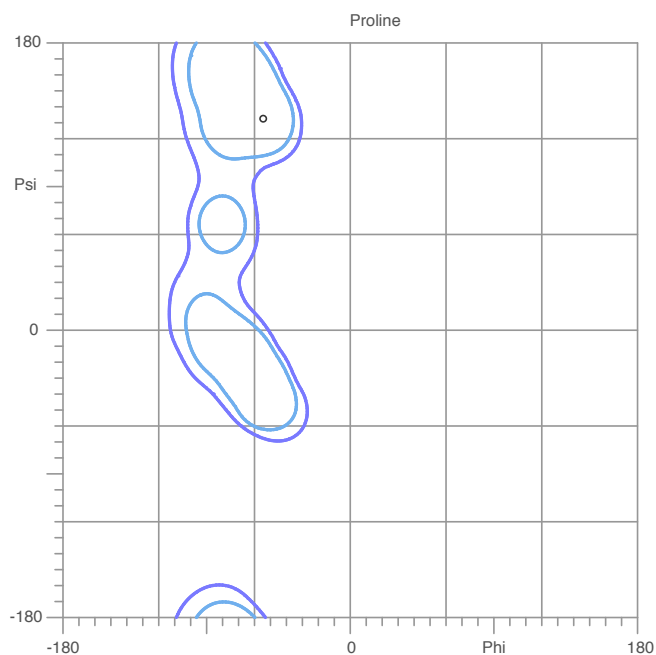
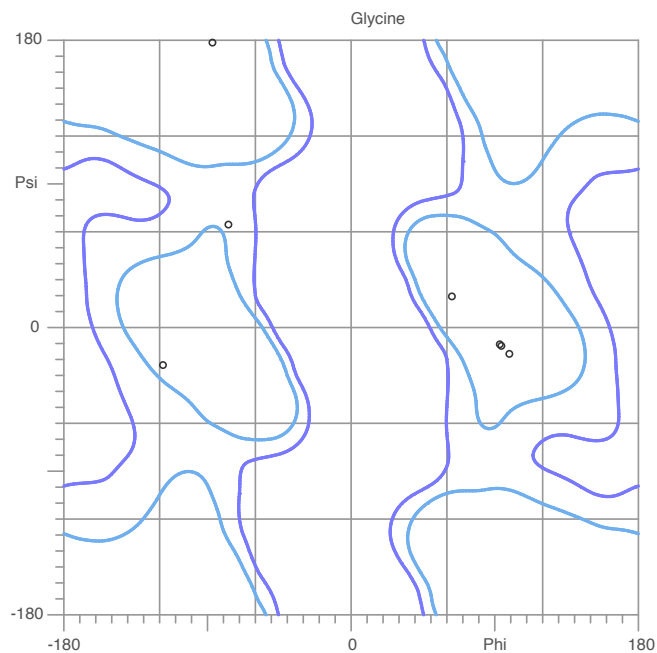
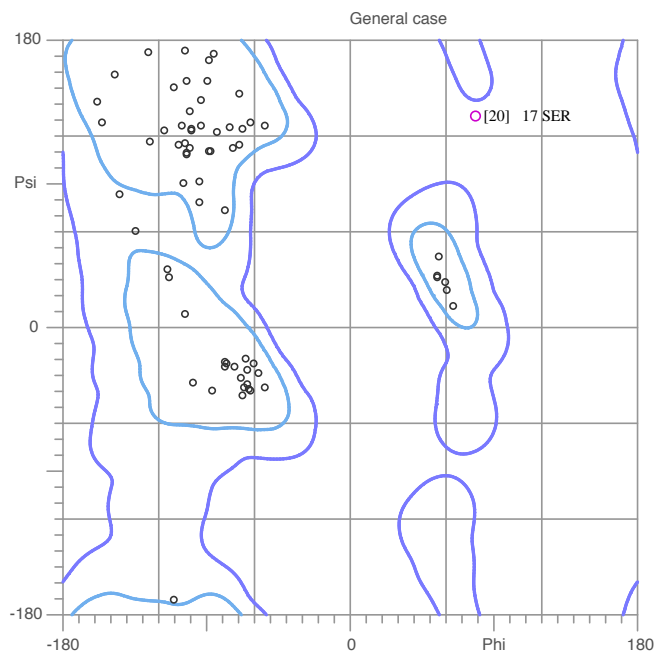


92.1% (70/76) of all residues were in favored (98%) regions.
97.4% (74/76) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[19] 67 GLY (-178.5, 55.0)
[19] 70 LYS (65.0, 127.3)

MolProbity Ramachandran analysis

GMR137_R3_em_bcr3.pdb, model 20



93.4% (71/76) 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 (78.4, 133.4)

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