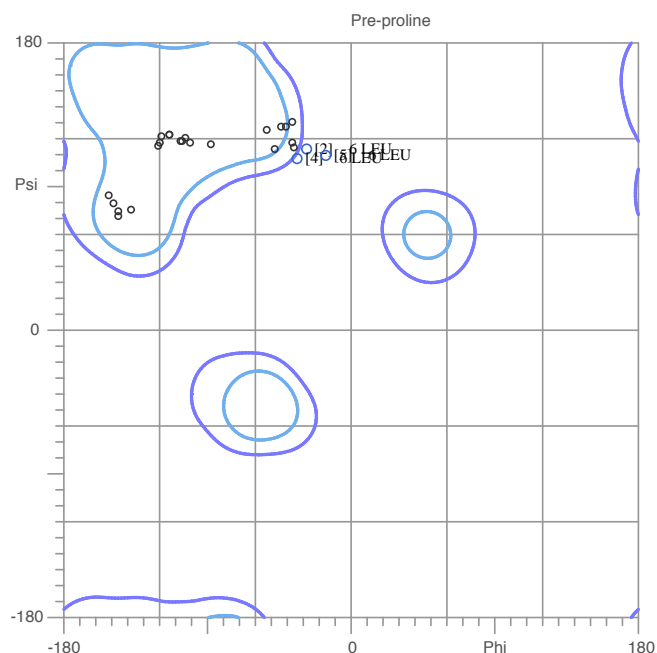
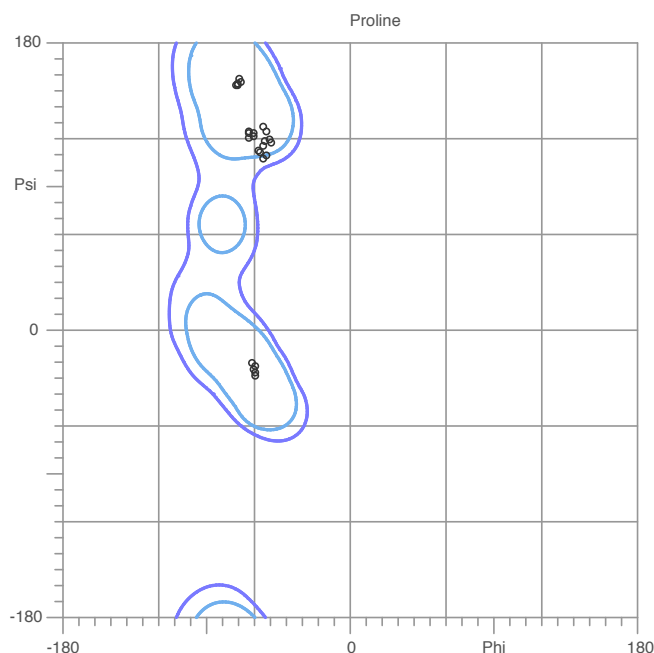
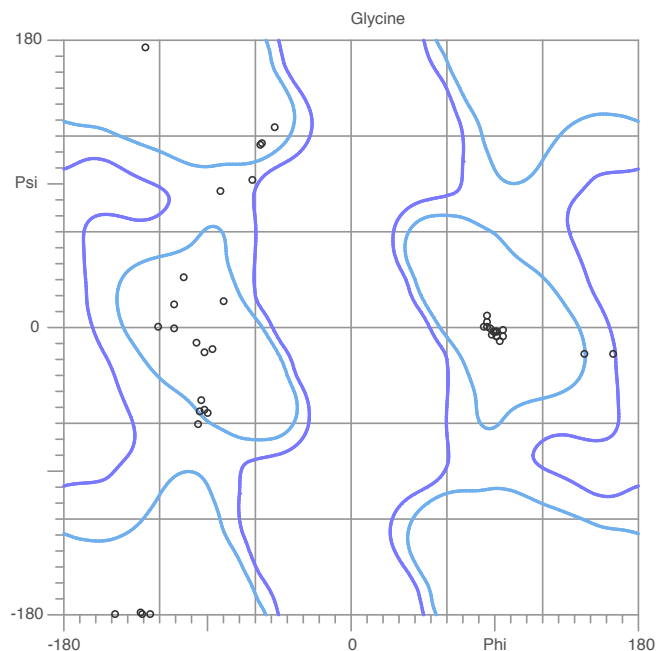
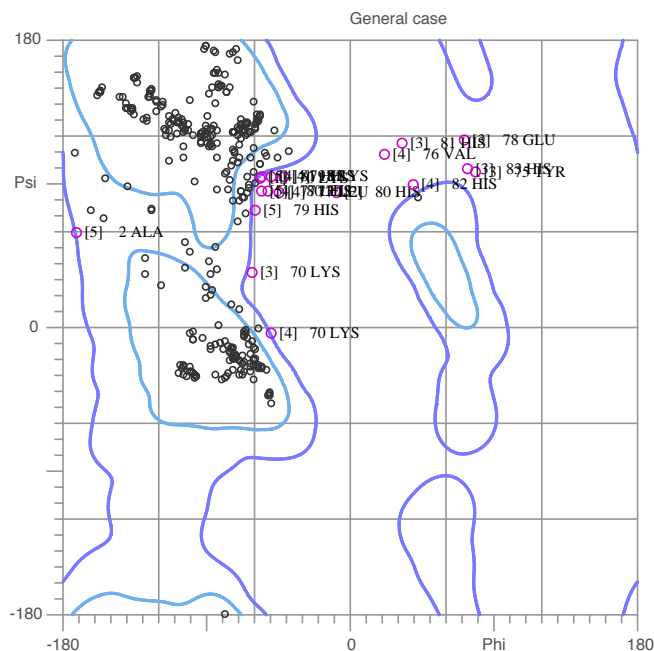


MolProbity Ramachandran analysis

2HEQ_AF.pdb, all models



84.4% (346/410) of all residues were in favored (98%) regions.
94.9% (389/410) of all residues were in allowed (>99.8%) regions.

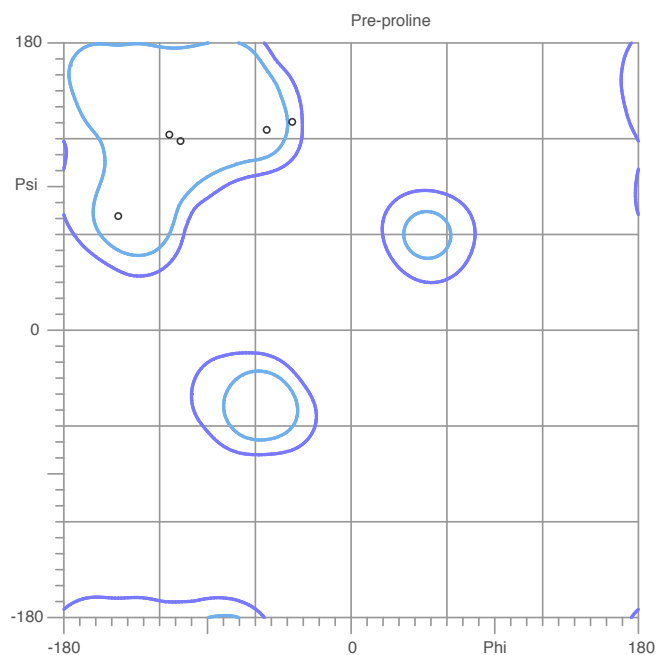
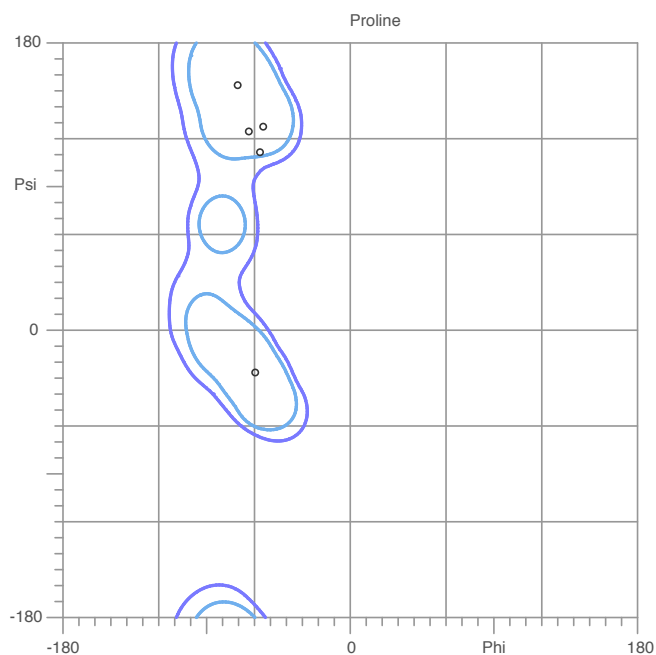
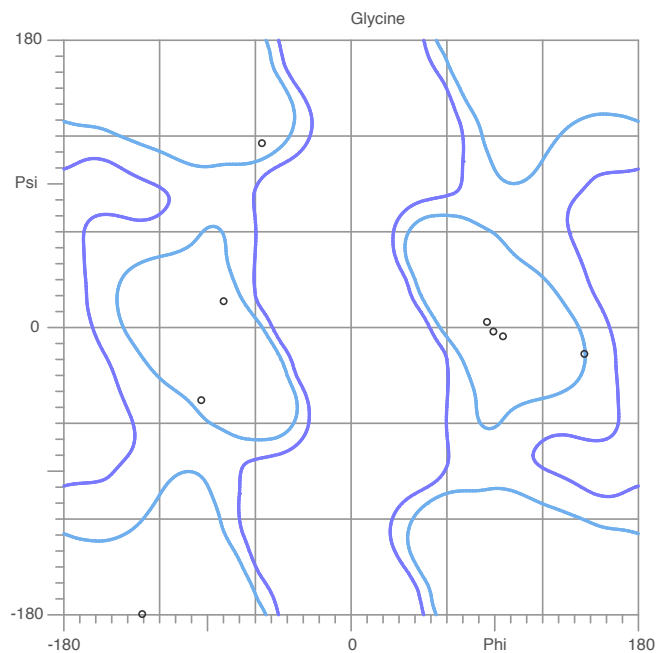
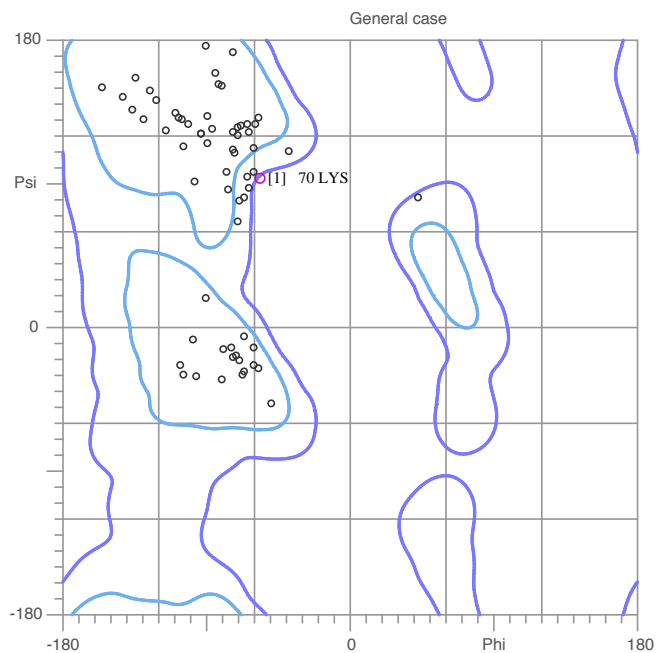
There were 21 outliers (phi, psi):

- [1] 70 LYS (-57.0, 94.1)
- [2] 6 LEU (-28.6, 114.9)
- [2] 80 HIS (-9.4, 85.7)
- [3] 70 LYS (-62.0, 35.1)
- [3] 75 TYR (78.5, 98.6)
- [3] 78 GLU (71.4, 118.9)
- [3] 81 HIS (32.9, 116.6)
- [3] 83 HIS (73.8, 100.3)

- [4] 6 LEU (-34.9, 108.3)
- [4] 8 LYS (-42.2, 95.4)
- [4] 70 LYS (-50.1, -3.6)
- [4] 76 VAL (21.5, 109.7)
- [4] 77 LEU (-45.9, 85.2)
- [4] 79 HIS (-51.0, 95.5)
- [4] 80 HIS (-52.2, 86.8)
- [4] 82 HIS (39.7, 90.6)
- [5] 2 ALA (-172.9, 60.4)
- [5] 6 LEU (-16.6, 110.2)
- [5] 77 LEU (-56.1, 87.0)
- [5] 79 HIS (-60.9, 74.2)
- [5] 81 HIS (-56.0, 95.2)

MolProbity Ramachandran analysis

2HEQ_AF.pdb, model 1



87.8% (72/82) of all residues were in favored (98%) regions.
98.8% (81/82) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

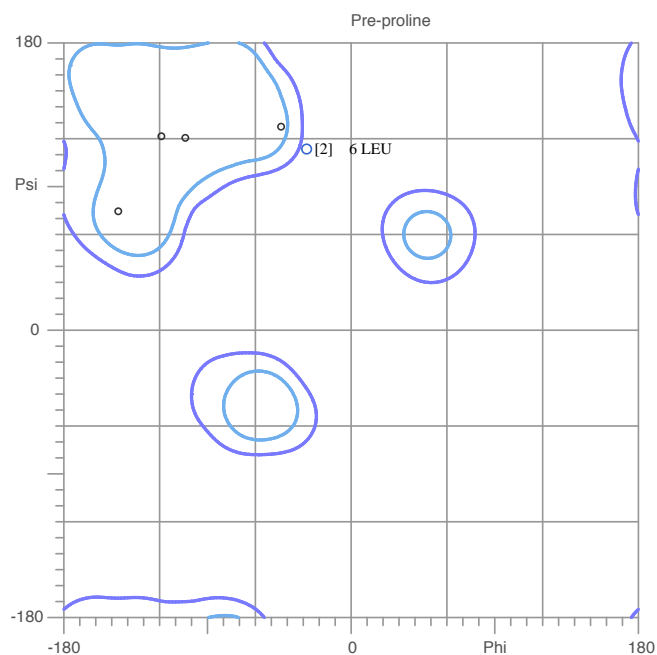
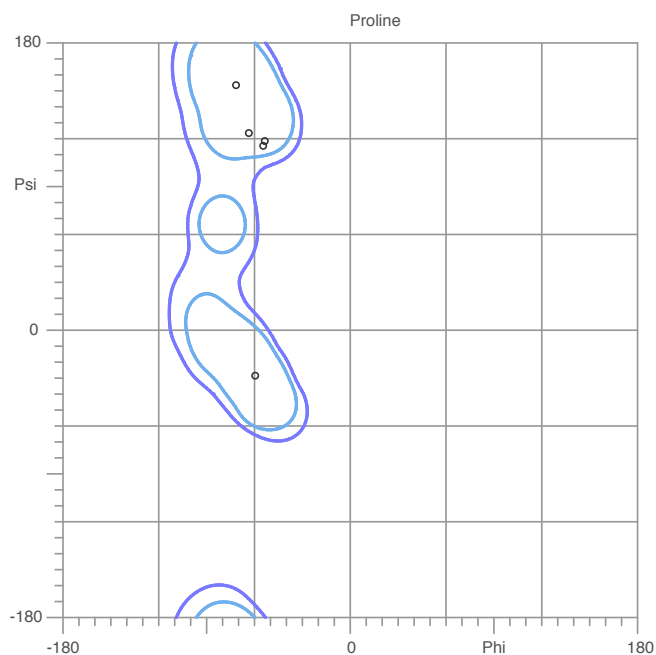
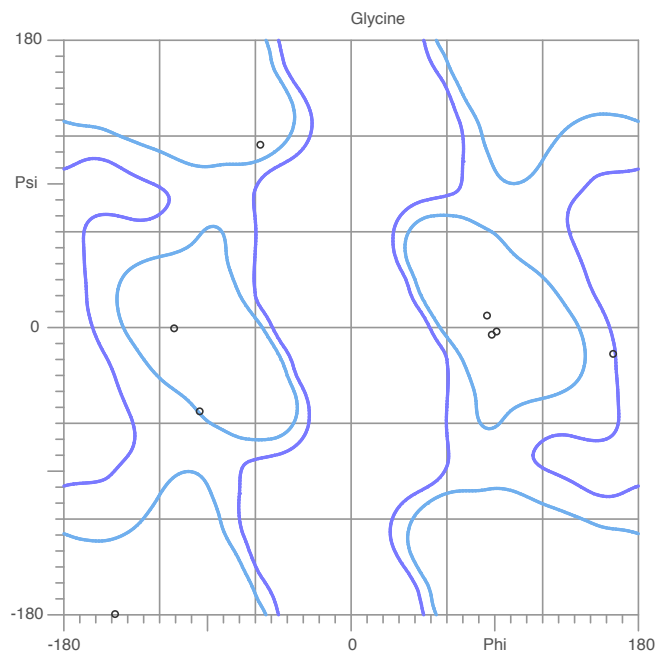
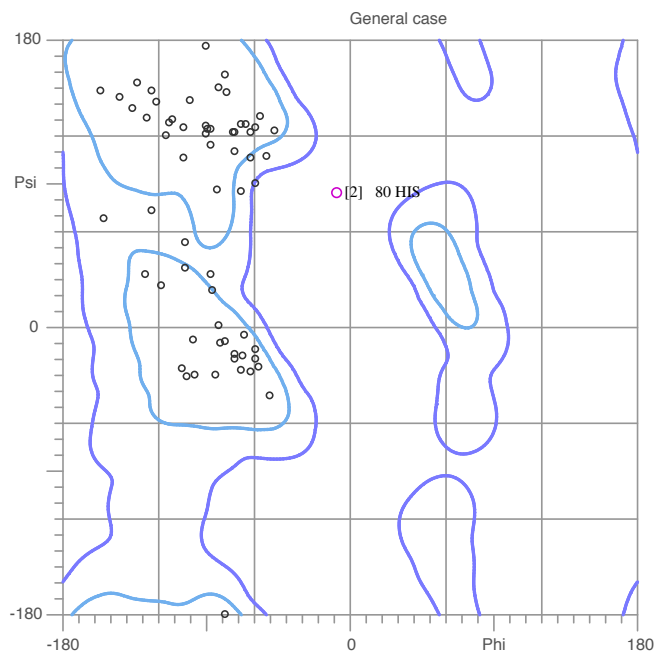
[1] 70 LYS (-57.0, 94.1)

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

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

MolProbity Ramachandran analysis

2HEQ_AF.pdb, model 2



86.6% (71/82) of all residues were in favored (98%) regions.
97.6% (80/82) of all residues were in allowed (>99.8%) regions.

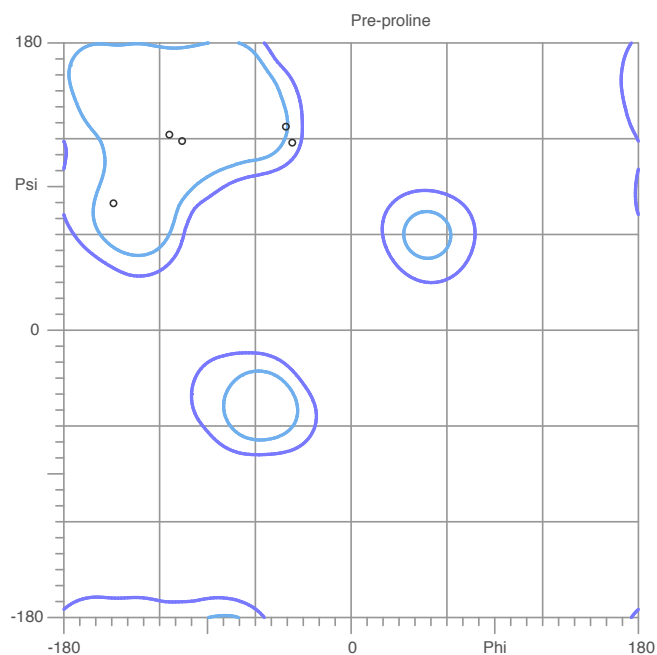
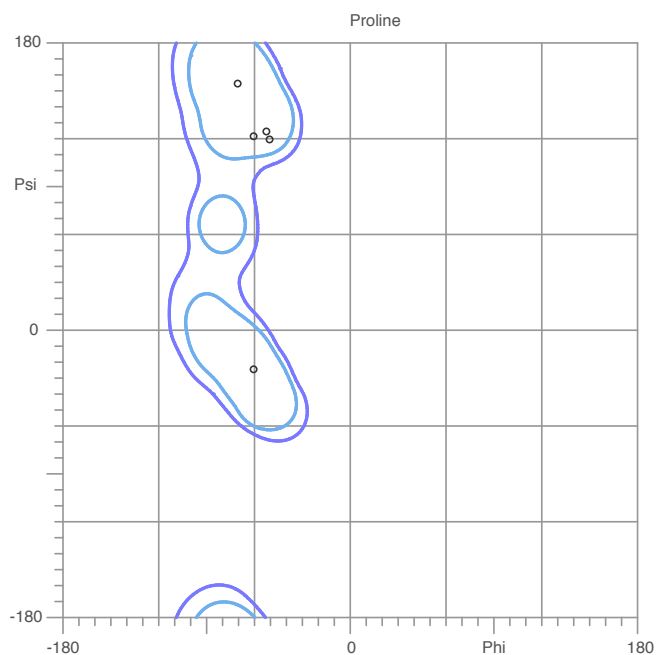
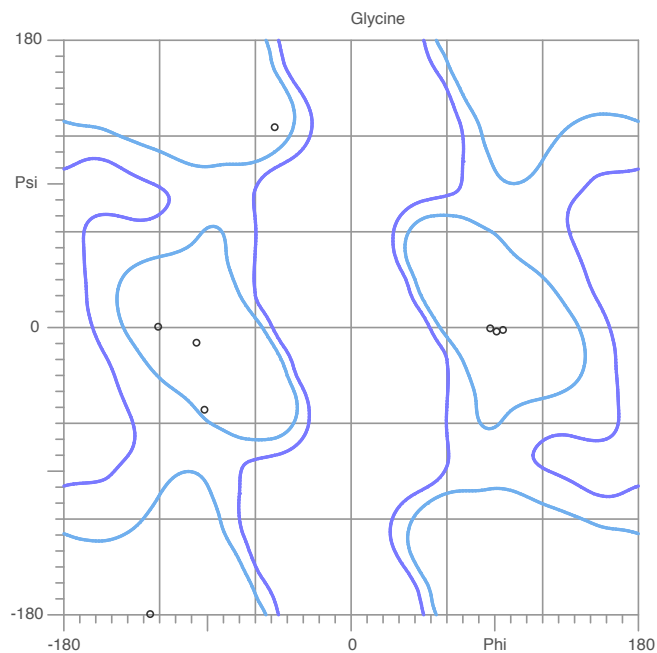
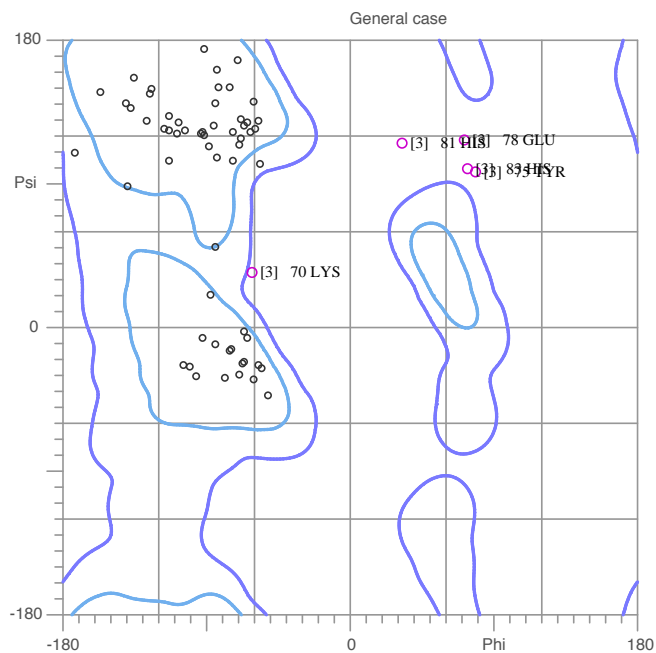
There were 2 outliers (phi, psi):

[2] 6 LEU (-28.6, 114.9)

[2] 80 HIS (-9.4, 85.7)

MolProbity Ramachandran analysis

2HEQ_AF.pdb, model 3



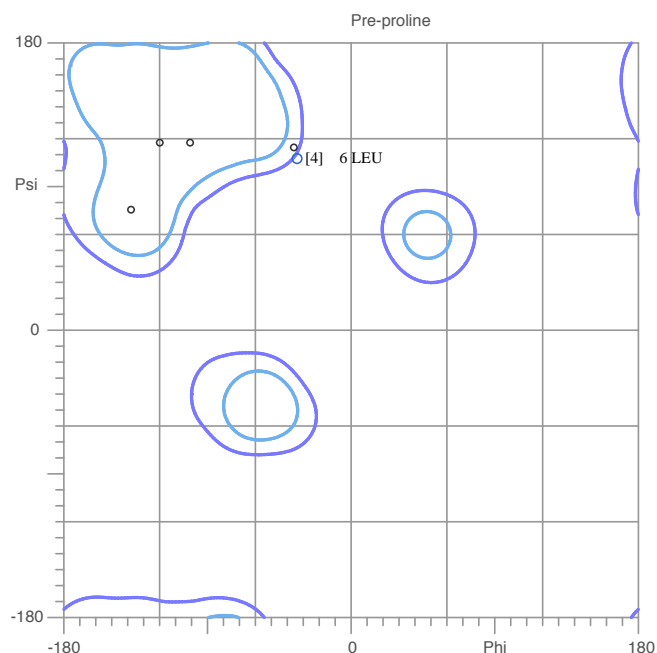
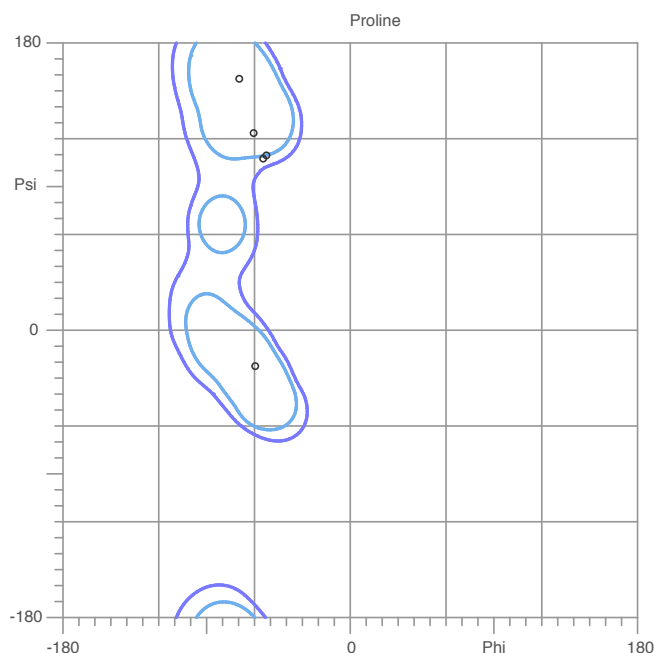
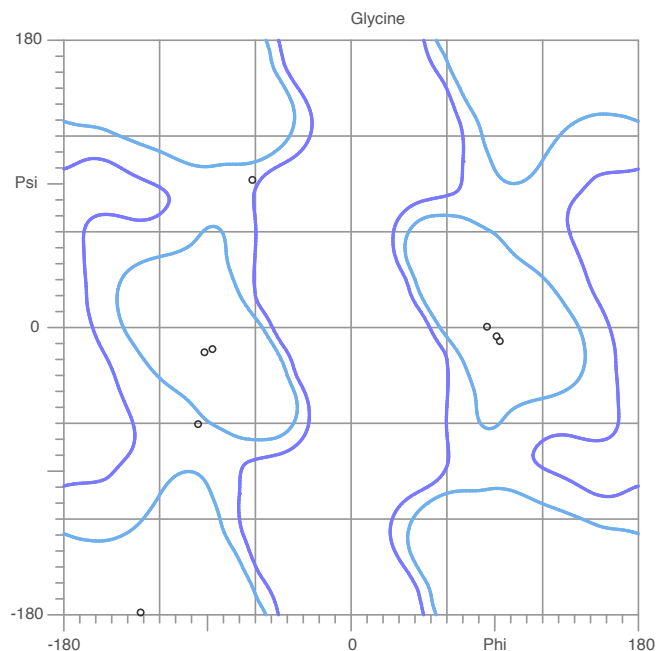
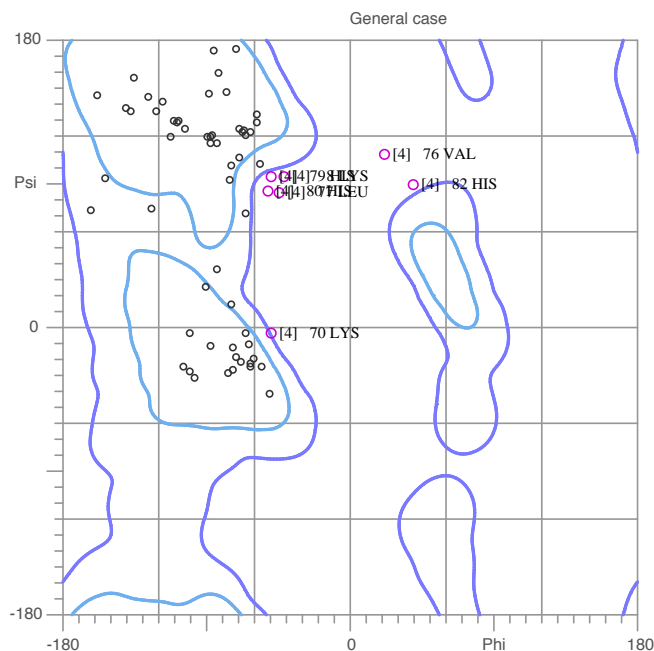
90.2% (74/82) of all residues were in favored (98%) regions.
93.9% (77/82) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[3] 70 LYS (-62.0, 35.1)
[3] 75 TYR (78.5, 98.6)
[3] 78 GLU (71.4, 118.9)
[3] 81 HIS (32.9, 116.6)
[3] 83 HIS (73.8, 100.3)

MolProbity Ramachandran analysis

2HEQ_AF.pdb, model 4



76.8% (63/82) of all residues were in favored (98%) regions.
90.2% (74/82) of all residues were in allowed (>99.8%) regions.

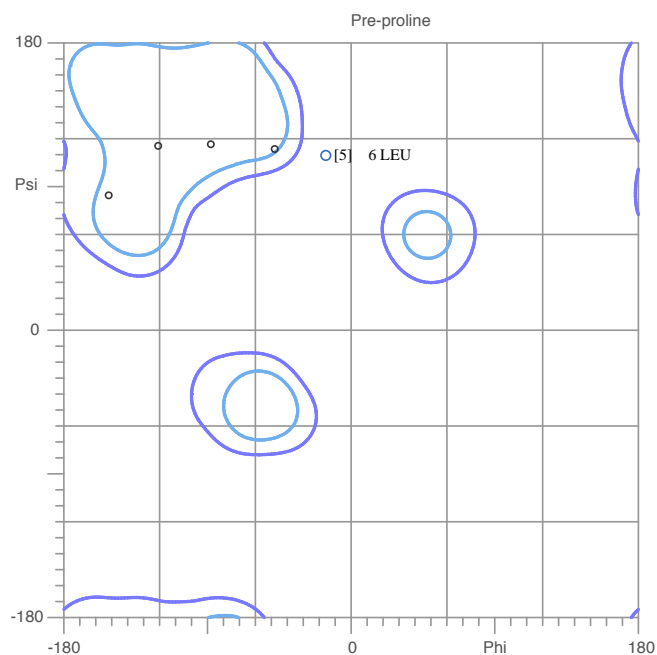
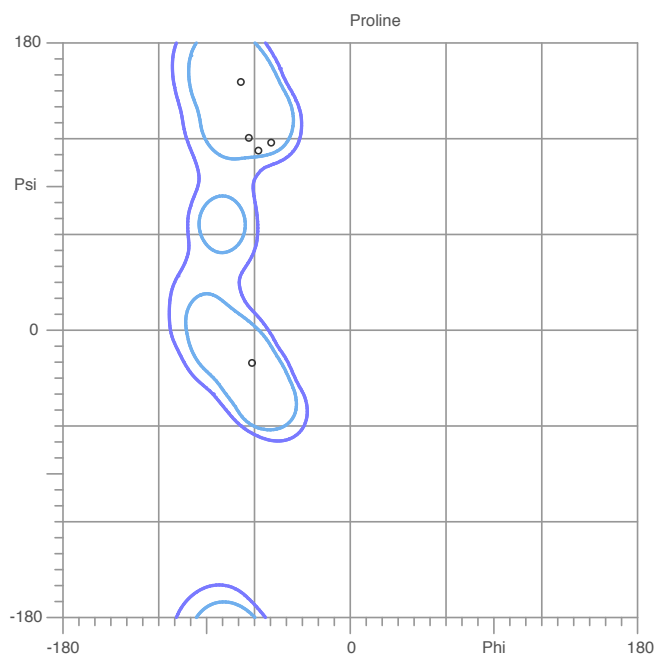
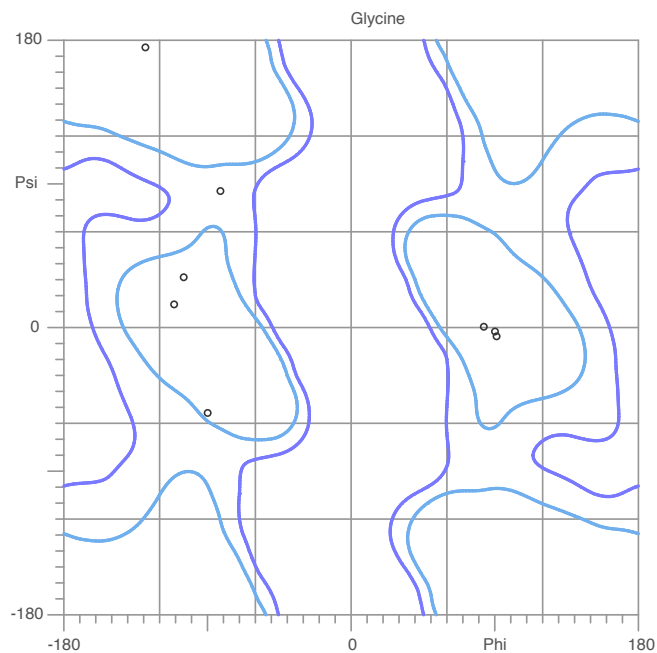
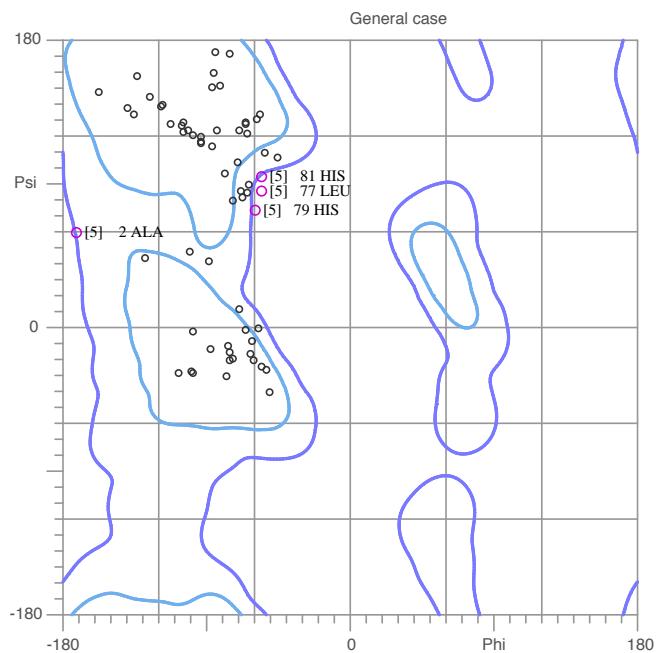
There were 8 outliers (phi, psi):

- [4] 6 LEU (-34.9, 108.3)
- [4] 8 LYS (-42.2, 95.4)

- [4] 70 LYS (-50.1, -3.6)
- [4] 76 VAL (21.5, 109.7)
- [4] 77 LEU (-45.9, 85.2)
- [4] 79 HIS (-51.0, 95.5)
- [4] 80 HIS (-52.2, 86.8)
- [4] 82 HIS (39.7, 90.6)

MolProbity Ramachandran analysis

2HEQ_AF.pdb, model 5



80.5% (66/82) of all residues were in favored (98%) regions.
93.9% (77/82) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

[5] 2 ALA (-172.9, 60.4)
[5] 6 LEU (-16.6, 110.2)
[5] 77 LEU (-56.1, 87.0)
[5] 79 HIS (-60.9, 74.2)
[5] 81 HIS (-56.0, 95.2)