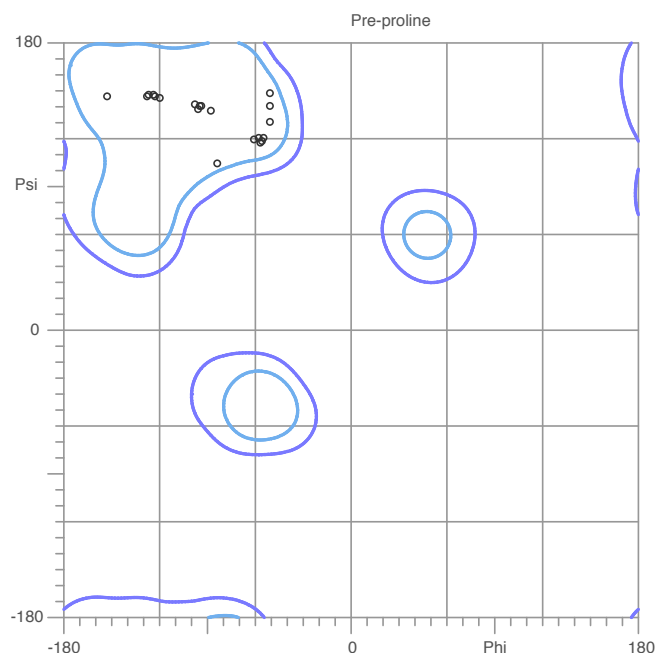
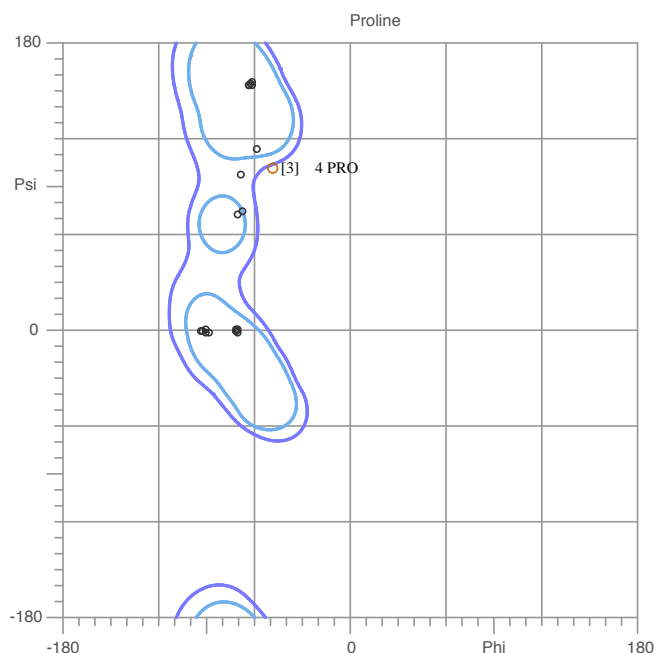
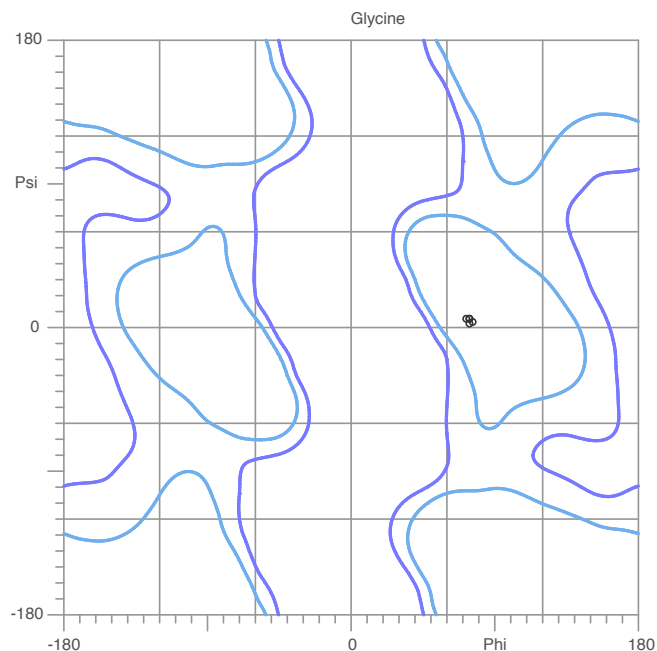
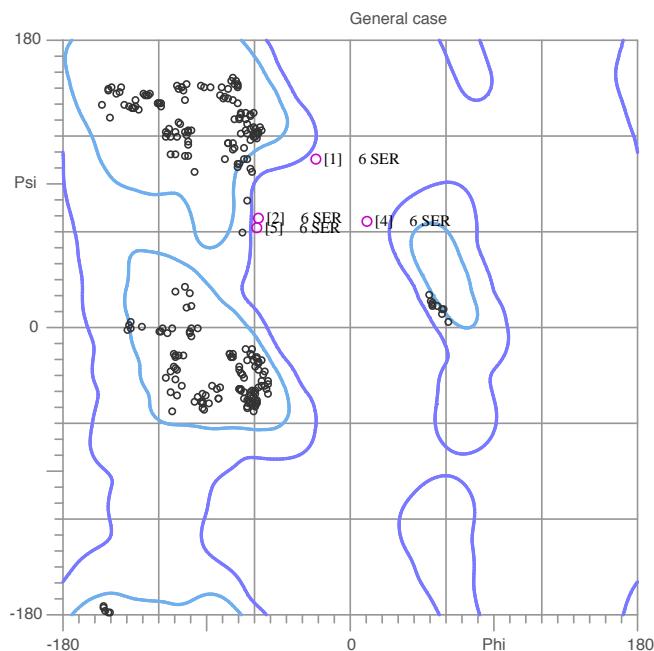


MolProbity Ramachandran analysis

2MA6_AF.pdb, all models



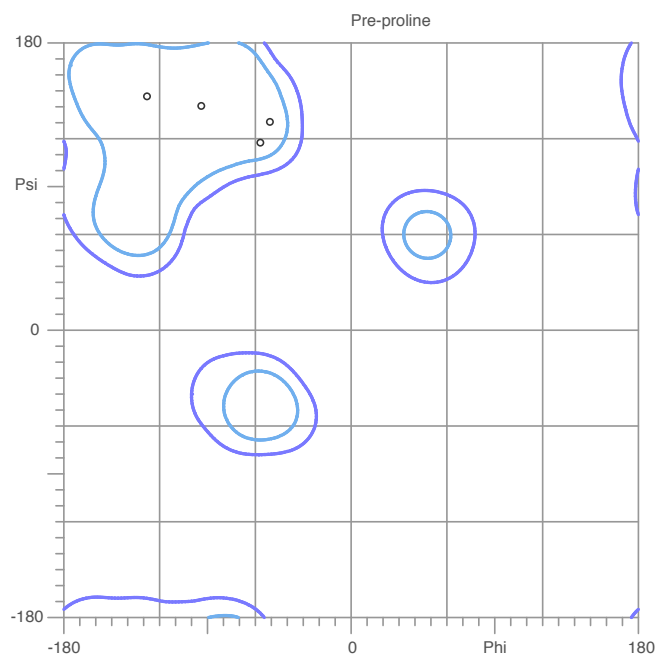
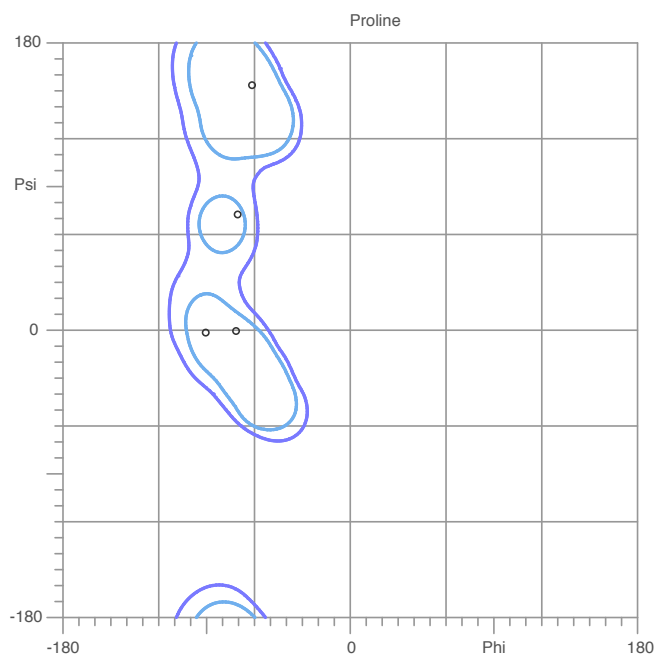
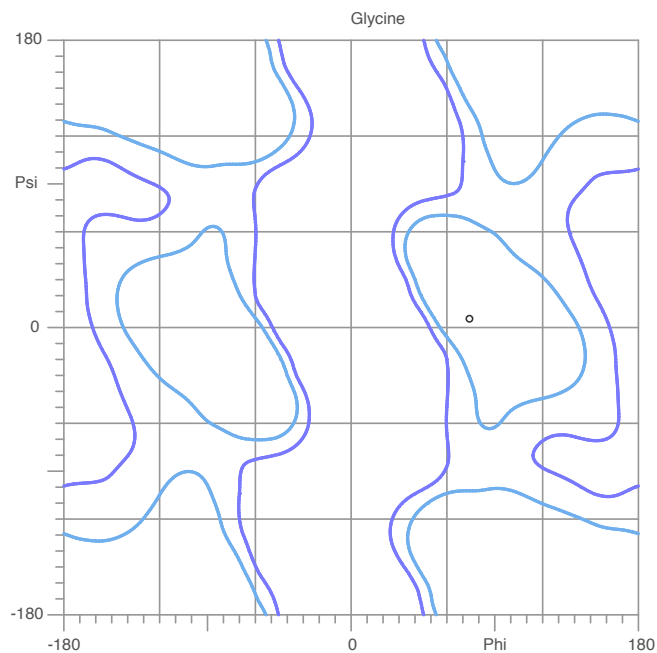
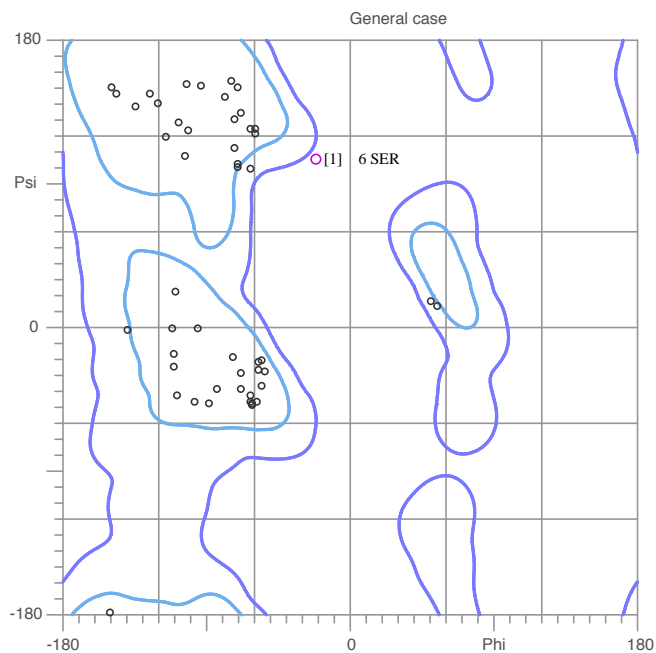
92.5% (273/295) of all residues were in favored (98%) regions.
98.3% (290/295) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [1] 6 SER (-22.7, 106.6)
- [2] 6 SER (-58.8, 69.4)
- [3] 4 PRO (-49.8, 102.7)
- [4] 6 SER (10.2, 67.8)
- [5] 6 SER (-59.4, 63.6)

MolProbity Ramachandran analysis

2MA6_AF.pdb, model 1



91.5% (54/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

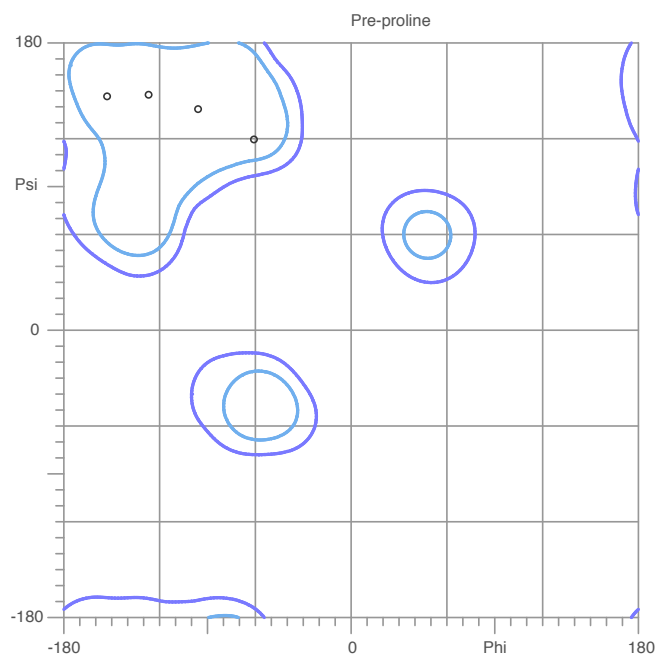
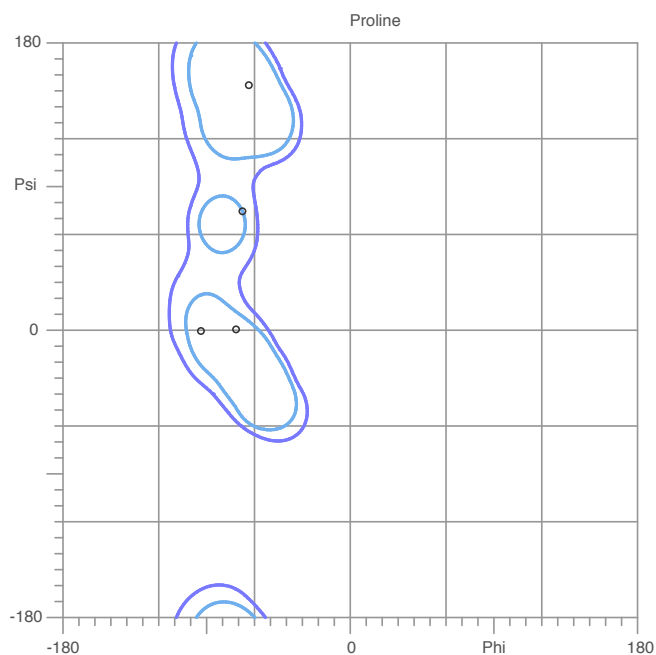
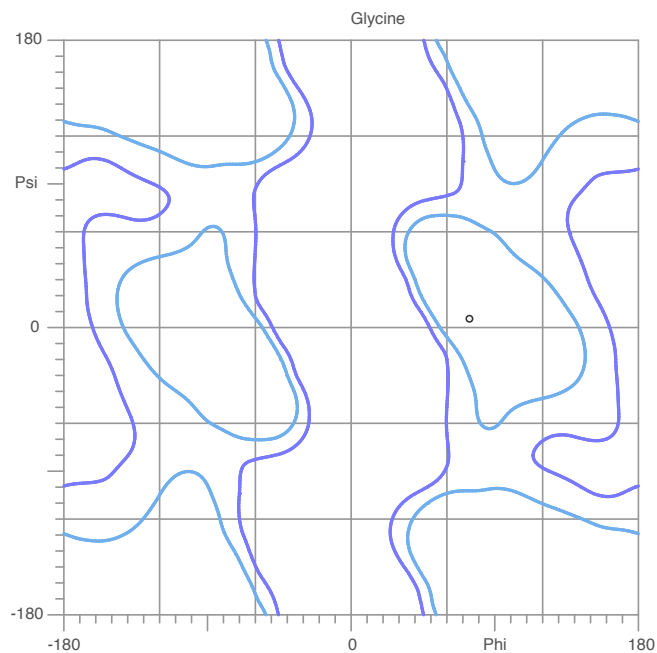
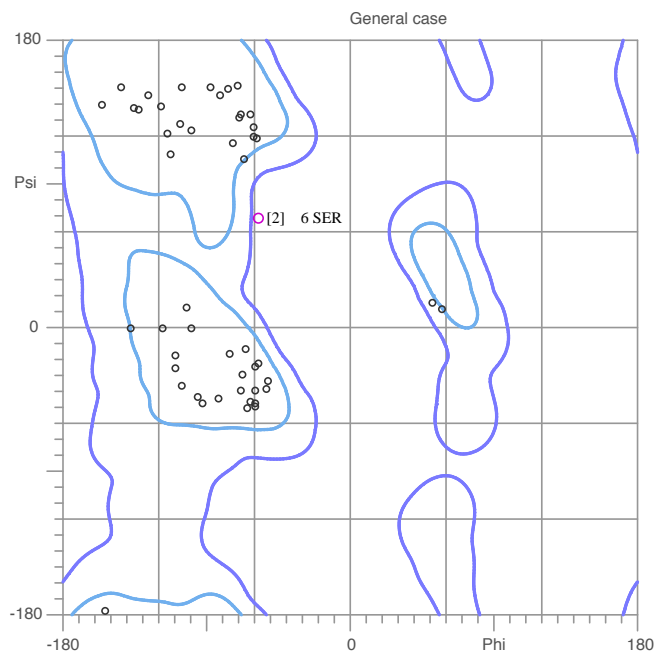
[1] 6 SER (-22.7, 106.6)

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MolProbity Ramachandran analysis

2MA6_AF.pdb, model 2



93.2% (55/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.

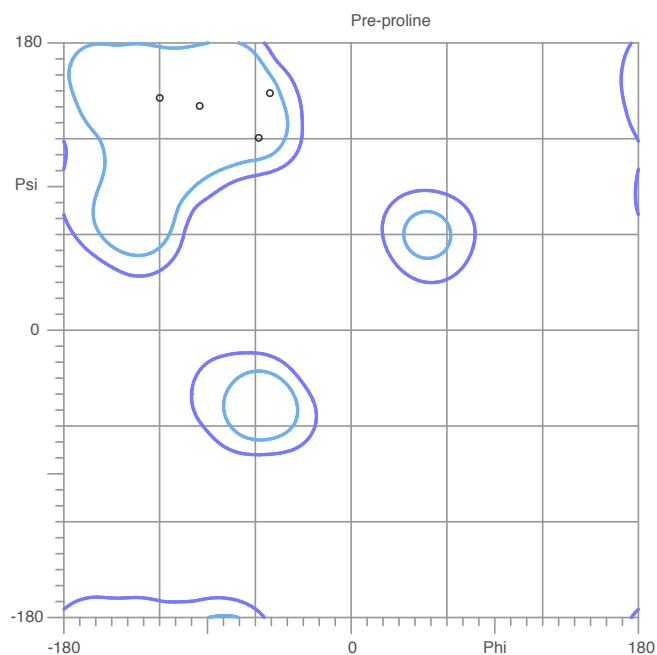
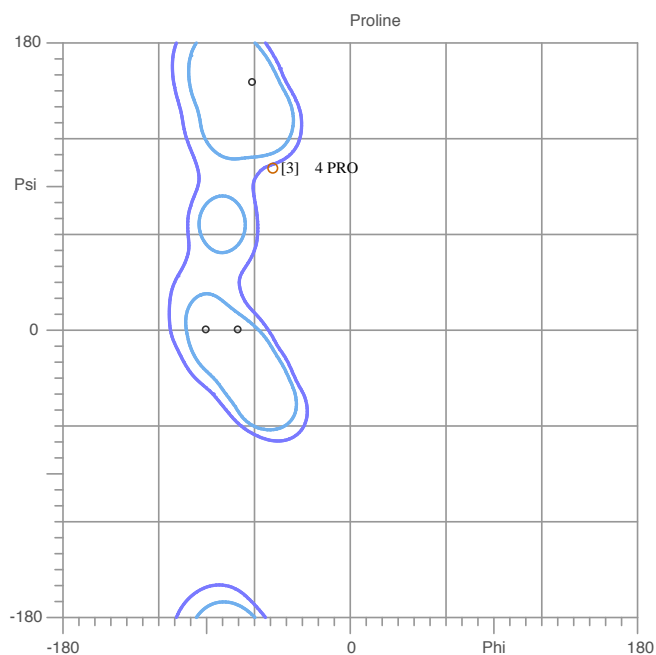
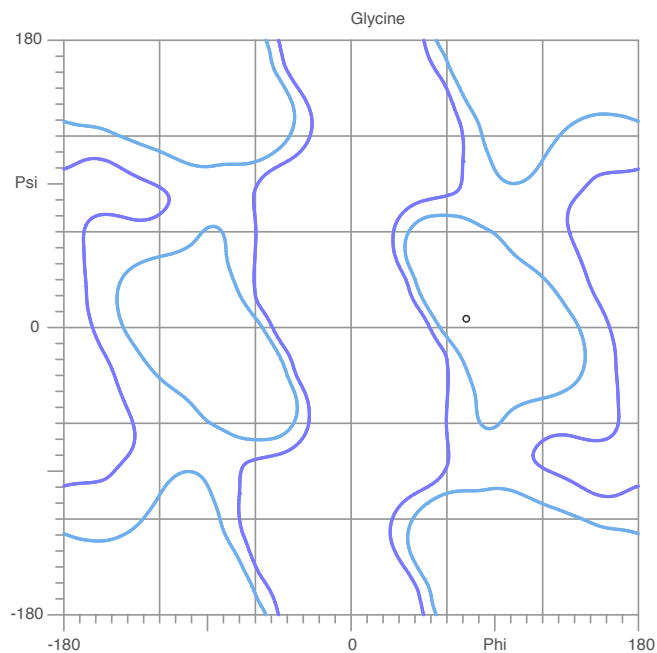
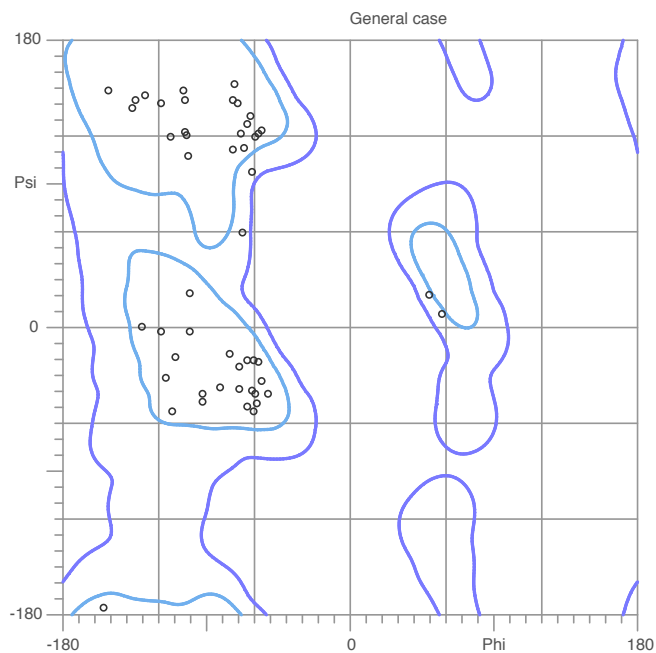
There were 1 outliers (phi, psi):
[2] 6 SER (-58.8, 69.4)

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MolProbity Ramachandran analysis

2MA6_AF.pdb, model 3



91.5% (54/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.

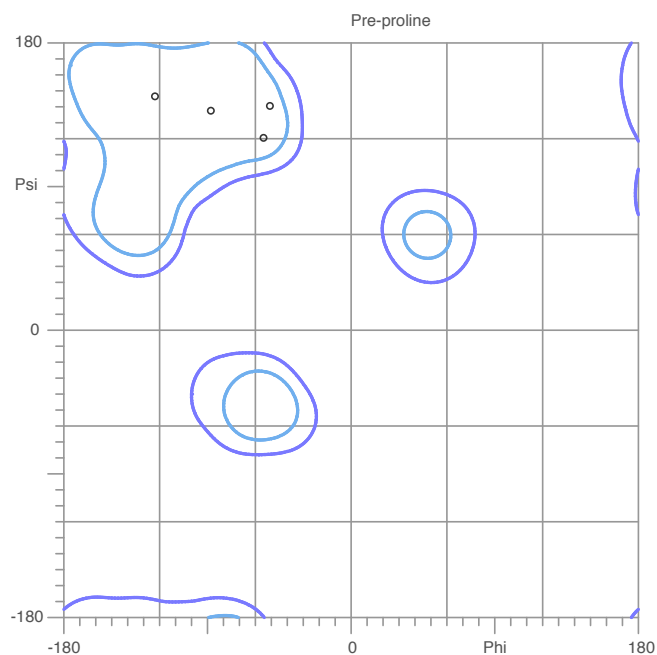
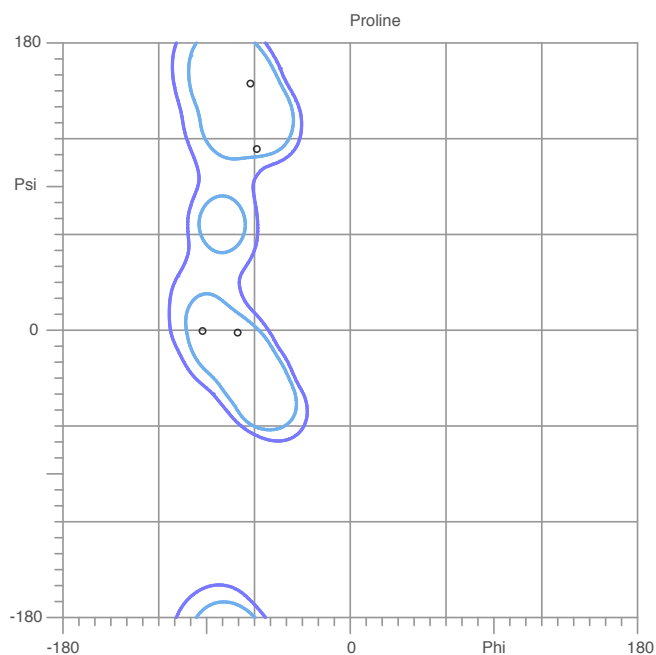
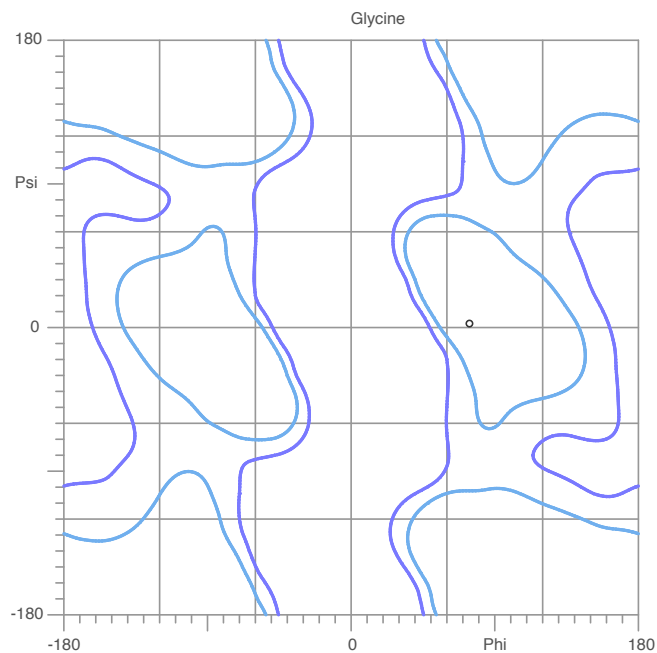
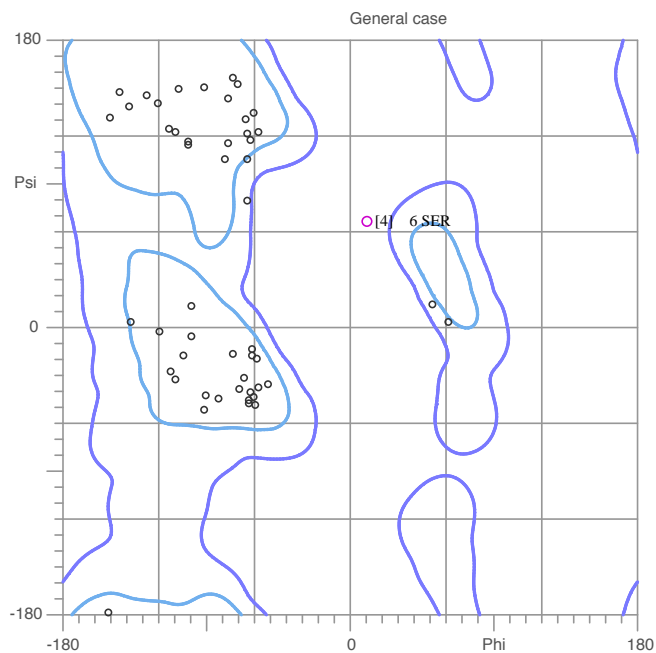
There were 1 outliers (phi, psi):
[3] 4 PRO (-49.8, 102.7)

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MolProbity Ramachandran analysis

2MA6_AF.pdb, model 4



93.2% (55/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.

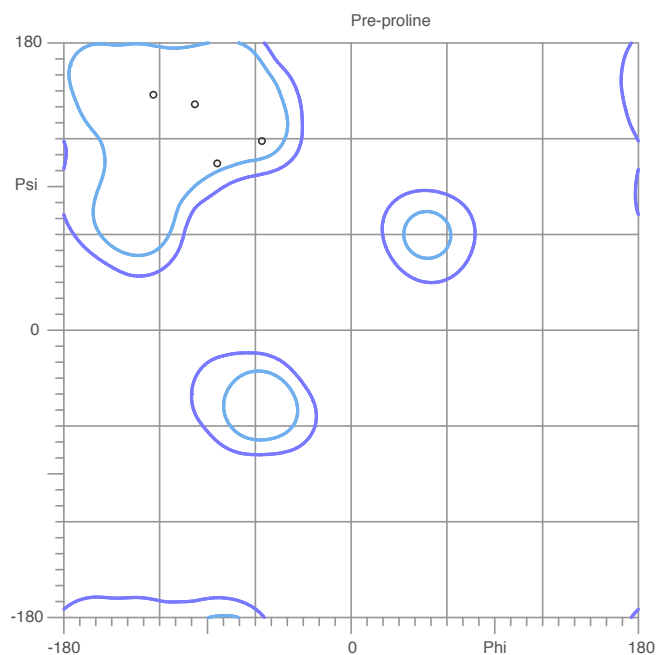
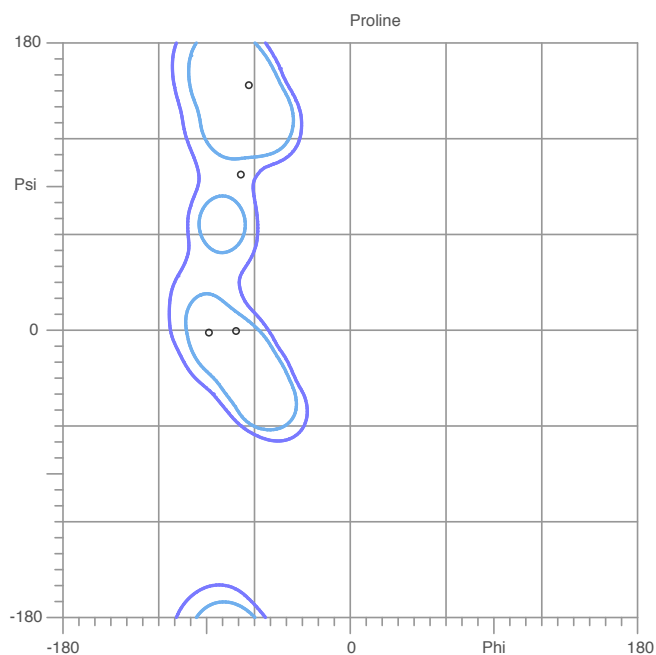
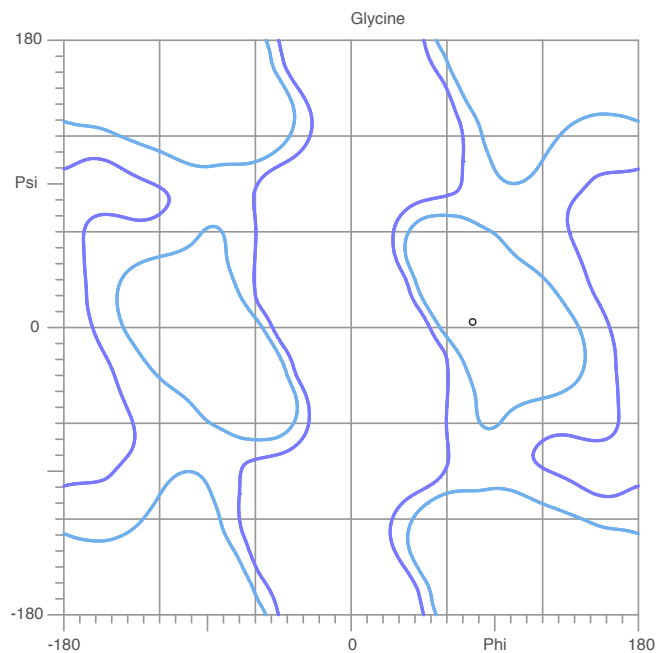
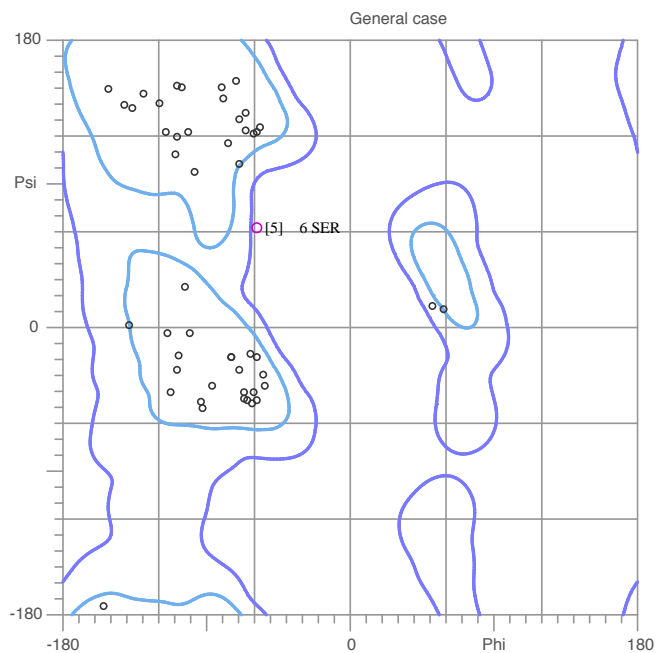
There were 1 outliers (phi, psi):
[4] 6 SER (10.2, 67.8)

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MolProbity Ramachandran analysis

2MA6_AF.pdb, model 5



93.2% (55/59) of all residues were in favored (98%) regions.
98.3% (58/59) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 6.SER (-59.4, 63.6)

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

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