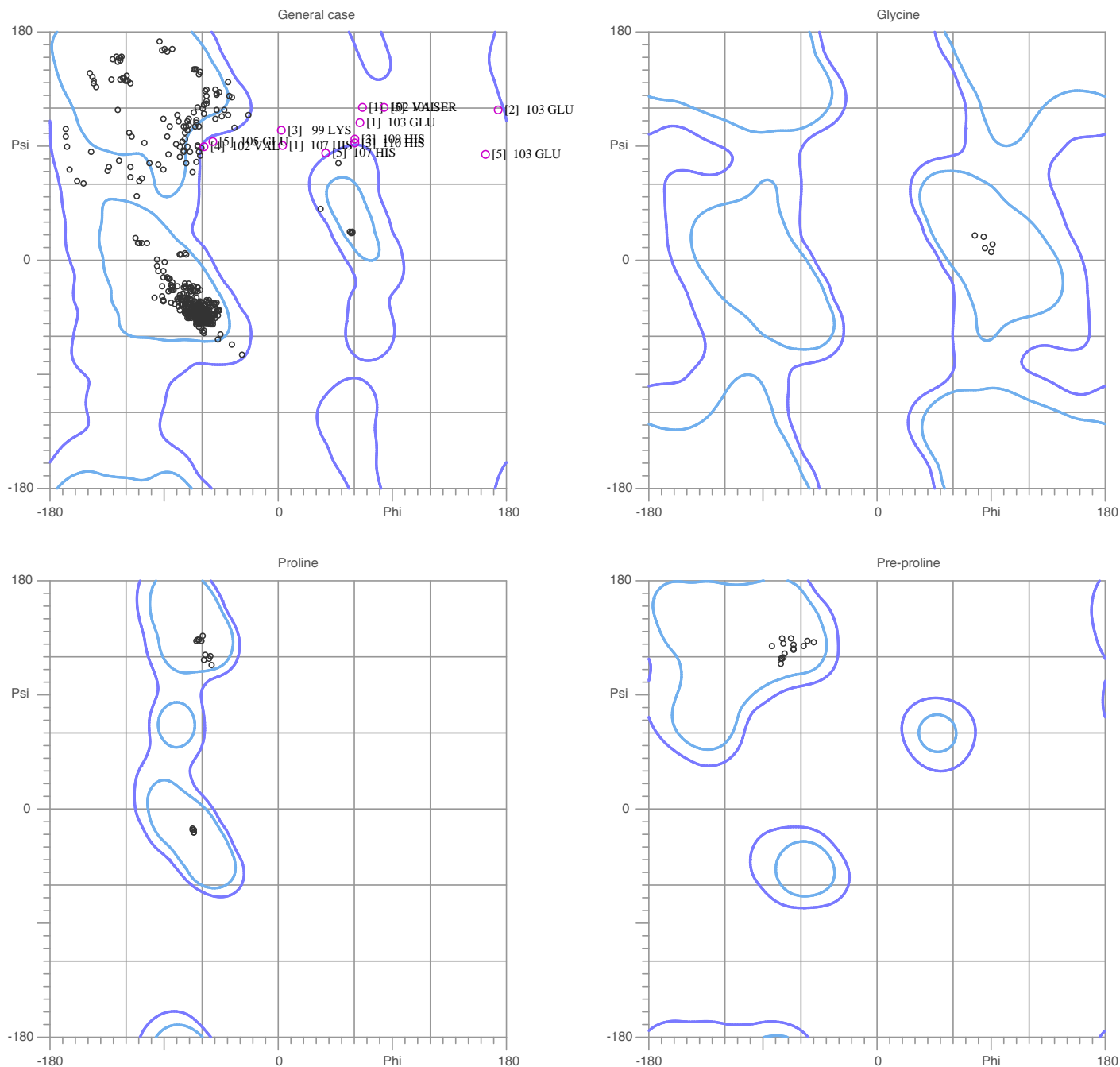


MolProbity Ramachandran analysis

2KIW_AF.pdb, all models



91.0% (496/545) of all residues were in favored (98%) regions.
97.8% (533/545) of all residues were in allowed (>99.8%) regions.

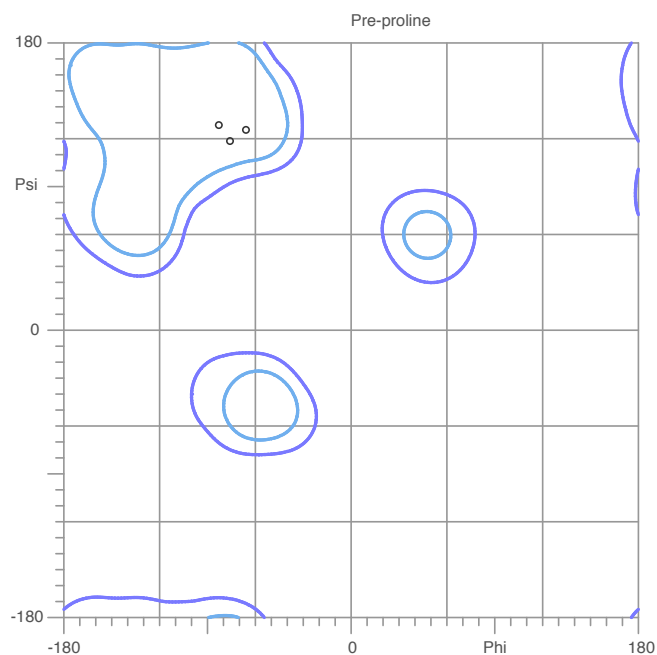
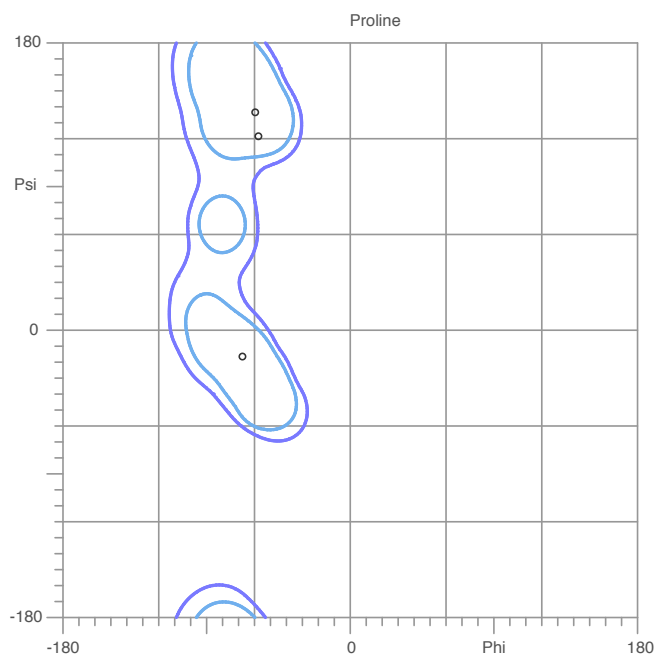
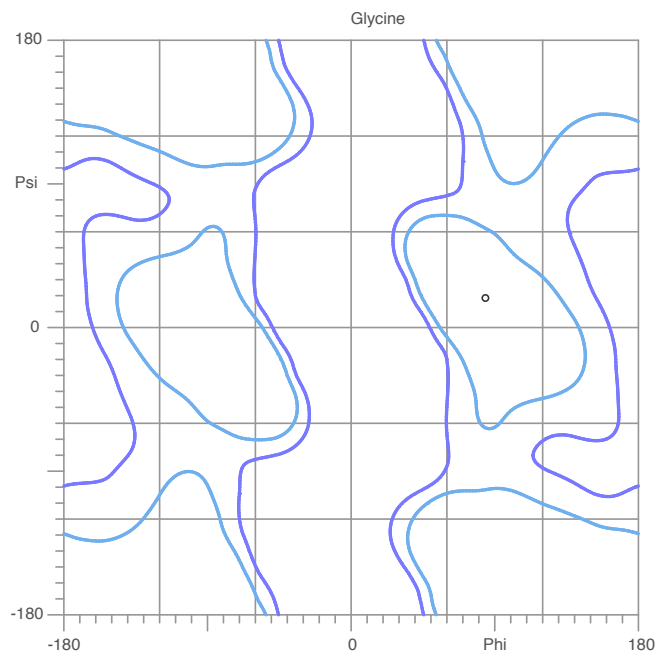
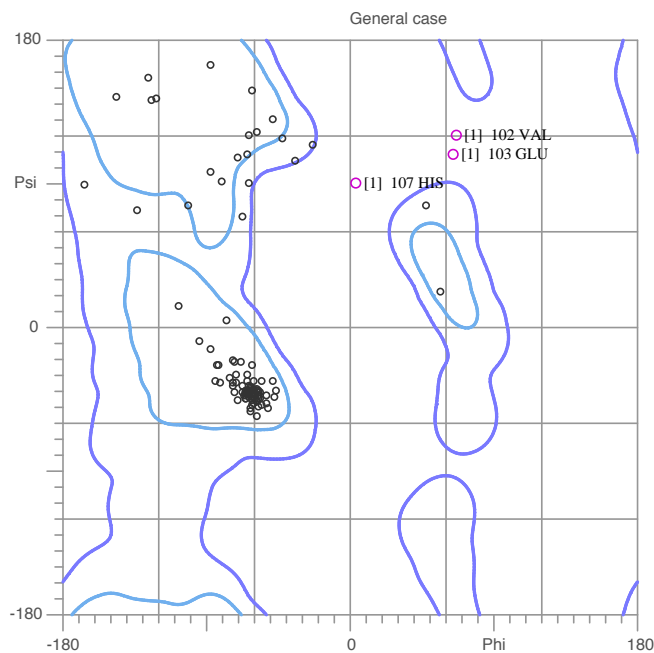
There were 12 outliers (phi, psi):

- [1] 102 VAL (66.2, 121.0)
- [1] 103 GLU (64.5, 109.8)
- [1] 107 HIS (3.9, 91.9)
- [2] 103 GLU (173.4, 119.4)

- [3] 99 LYS (2.3, 103.4)
- [3] 109 HIS (60.4, 96.7)
- [3] 110 HIS (60.6, 93.8)
- [4] 102 VAL (-59.7, 90.0)
- [5] 101 SER (83.2, 121.9)
- [5] 103 GLU (163.2, 84.4)
- [5] 105 GLU (-52.6, 94.3)
- [5] 107 HIS (37.9, 85.7)

MolProbity Ramachandran analysis

2KIW_AF.pdb, model 1



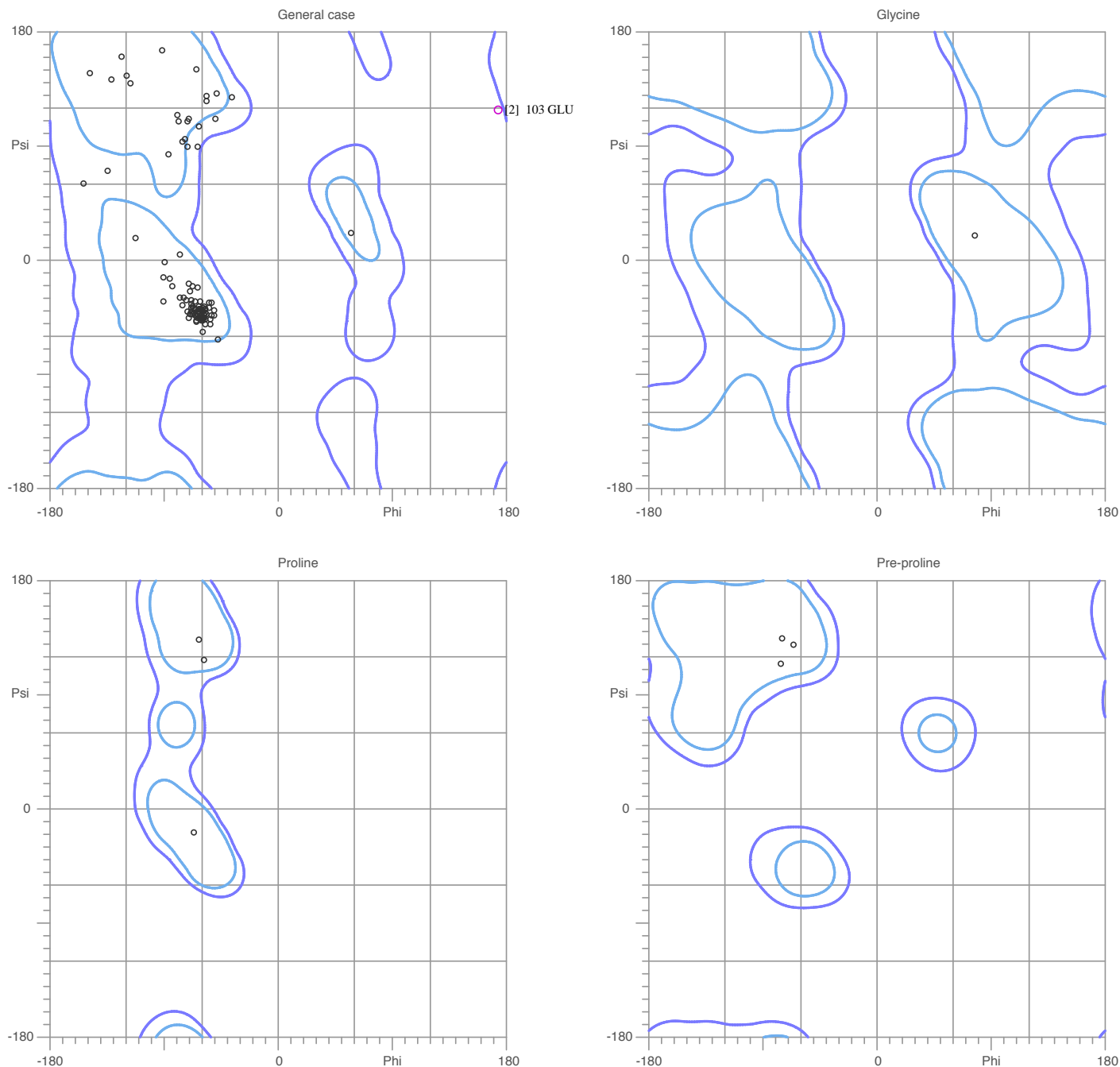
89.9% (98/109) of all residues were in favored (98%) regions.
97.2% (106/109) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 102 VAL (66.2, 121.0)
- [1] 103 GLU (64.5, 109.8)
- [1] 107 HIS (3.9, 91.9)

MolProbity Ramachandran analysis

2KIW_AF.pdb, model 2



92.7% (101/109) of all residues were in favored (98%) regions.
99.1% (108/109) of all residues were in allowed (>99.8%) regions.

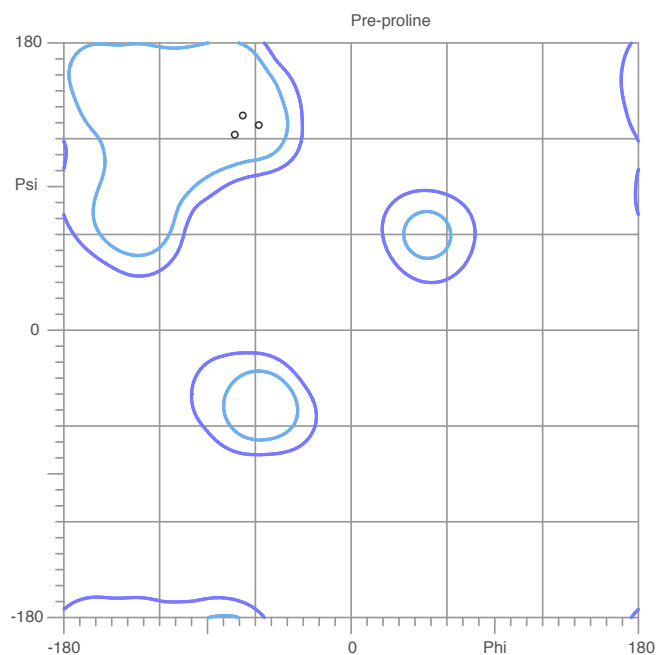
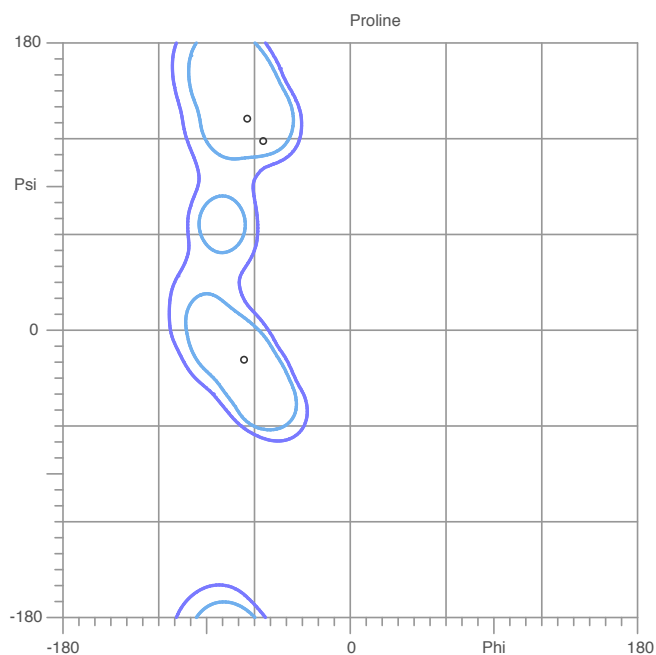
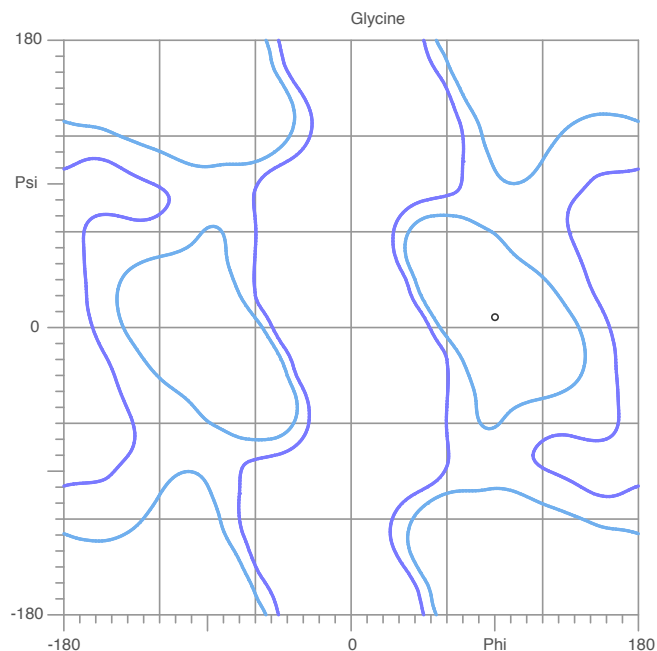
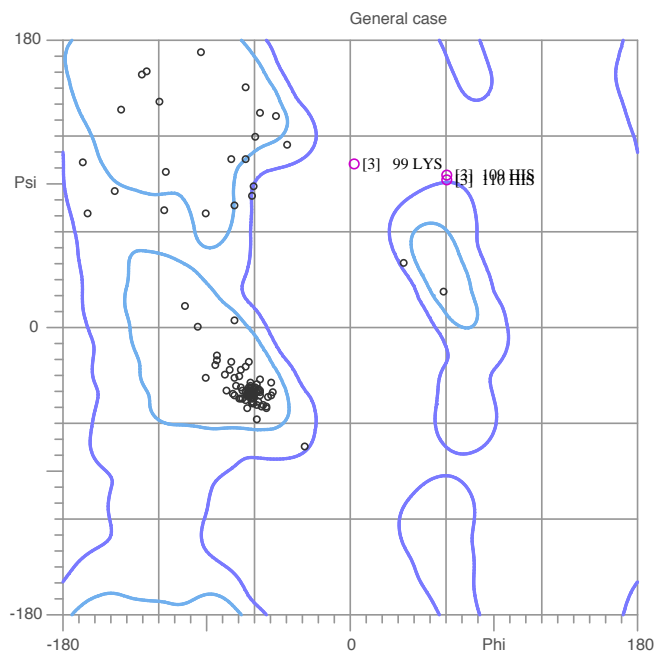
There were 1 outliers (phi, psi):
[2] 103 GLU (173.4, 119.4)

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MolProbity Ramachandran analysis

2KIW_AF.pdb, model 3



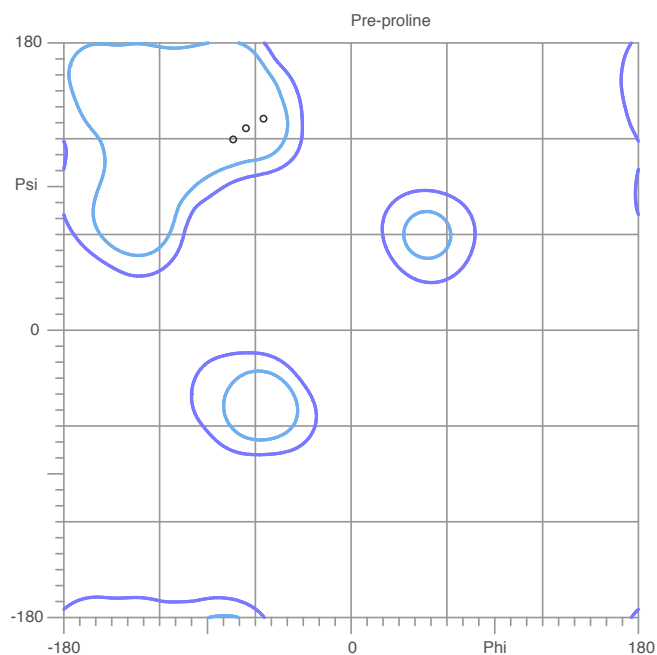
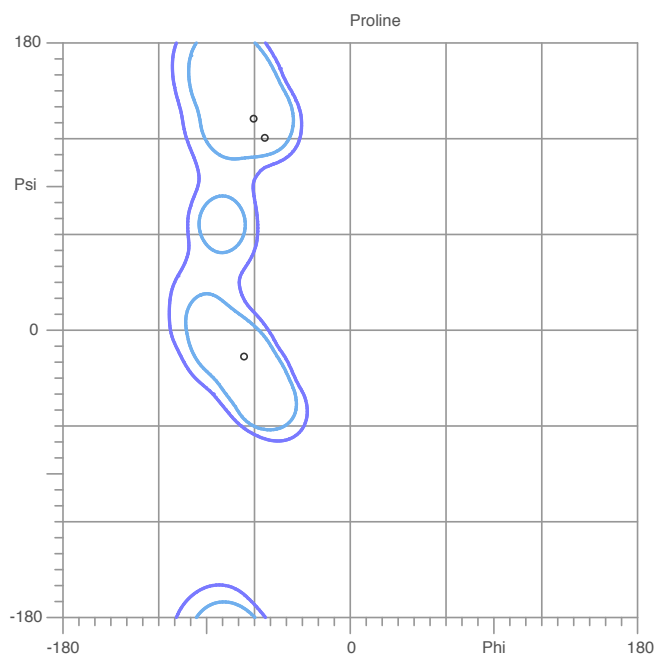
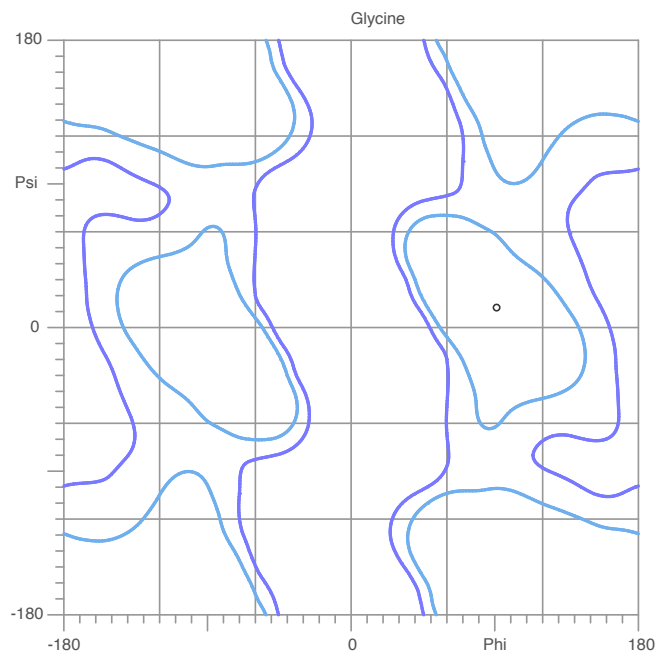
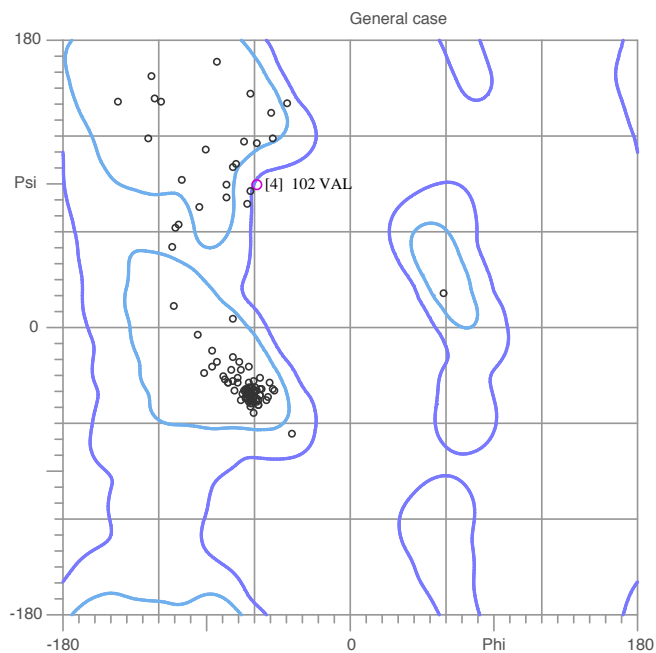
89.0% (97/109) of all residues were in favored (98%) regions.
97.2% (106/109) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 99 LYS (2.3, 103.4)
- [3] 109 HIS (60.4, 96.7)
- [3] 110 HIS (60.6, 93.8)

MolProbity Ramachandran analysis

2KIW_AF.pdb, model 4



92.7% (101/109) of all residues were in favored (98%) regions.
99.1% (108/109) of all residues were in allowed (>99.8%) regions.

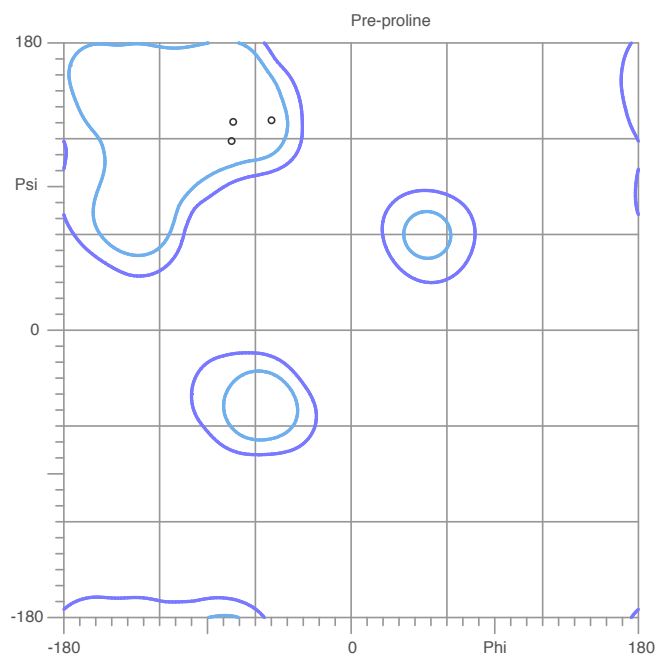
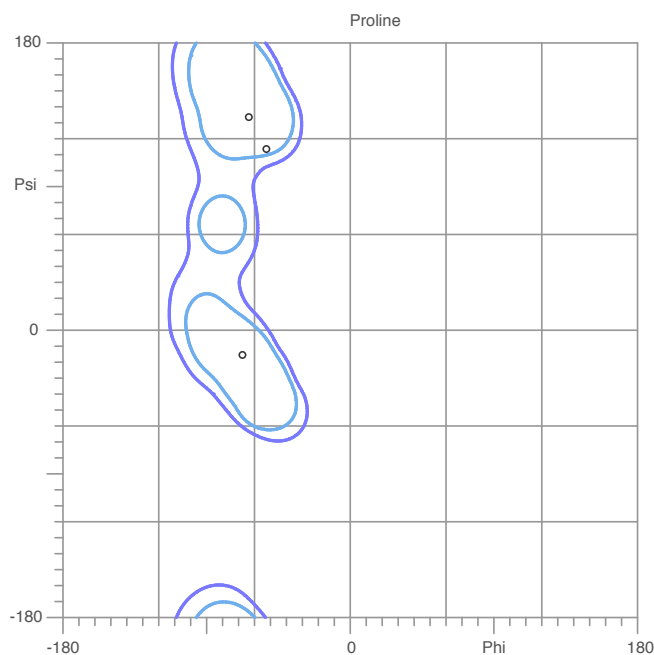
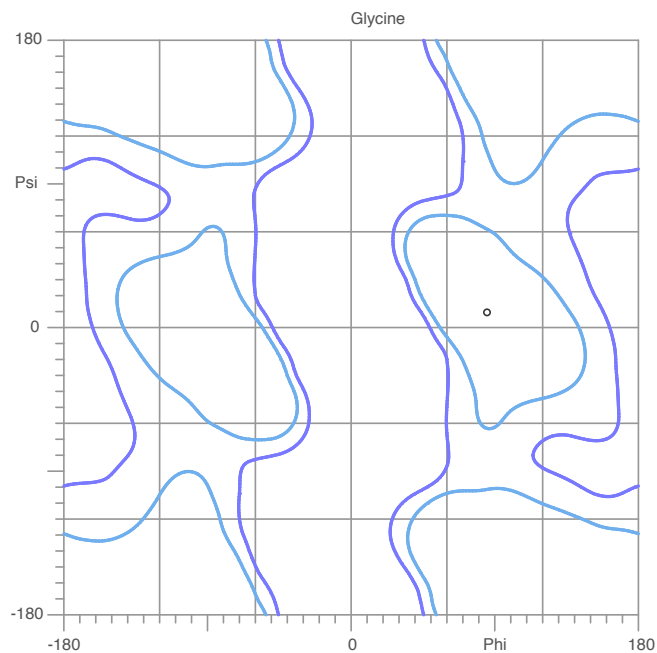
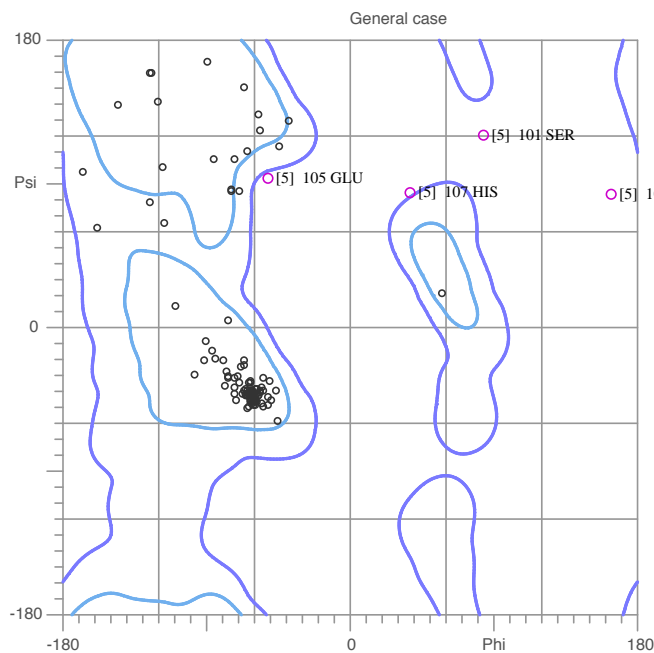
There were 1 outliers (phi, psi):
[4] 102 VAL (-59.7, 90.0)

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MolProbity Ramachandran analysis

2KIW_AF.pdb, model 5



90.8% (99/109) of all residues were in favored (98%) regions.
96.3% (105/109) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [5] 101 SER (83.2, 121.9)
- [5] 103 GLU (163.2, 84.4)
- [5] 105 GLU (-52.6, 94.3)
- [5] 107 HIS (37.9, 85.7)