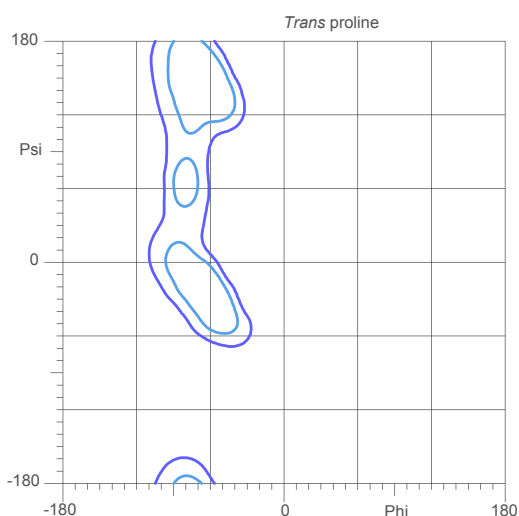
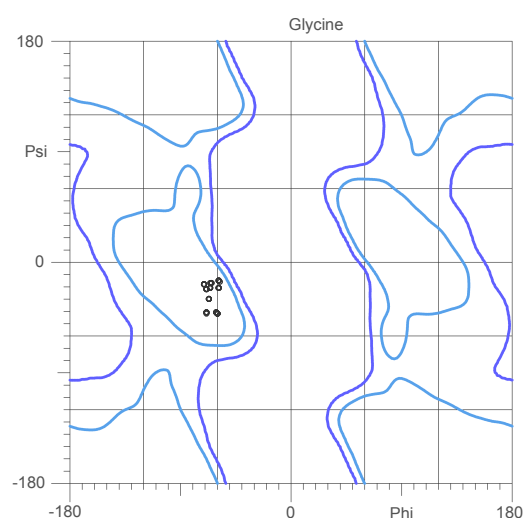
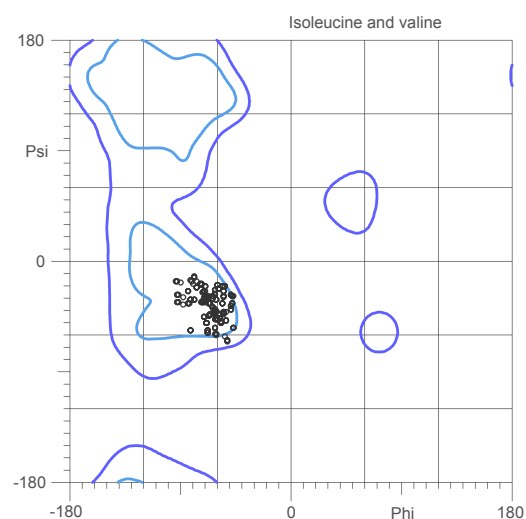
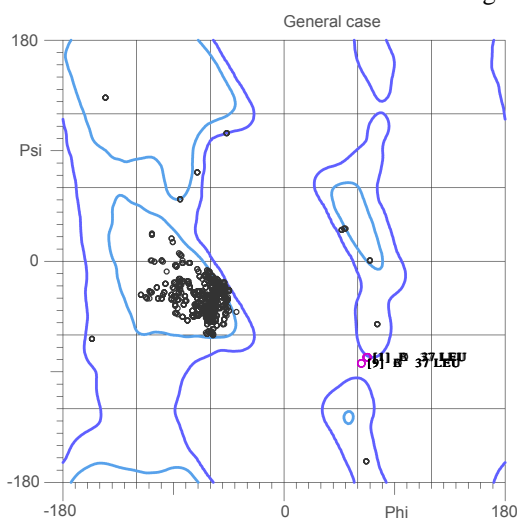


# MolProbity Ramachandran analysis

7k3g.H.pdb, all models



94.1% (1364/1450) of all residues were in favored (98%) regions.  
99.3% (1440/1450) of all residues were in allowed (>99.8%) regions.

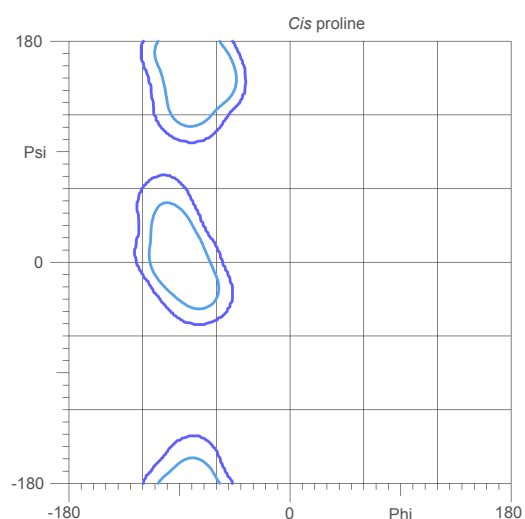
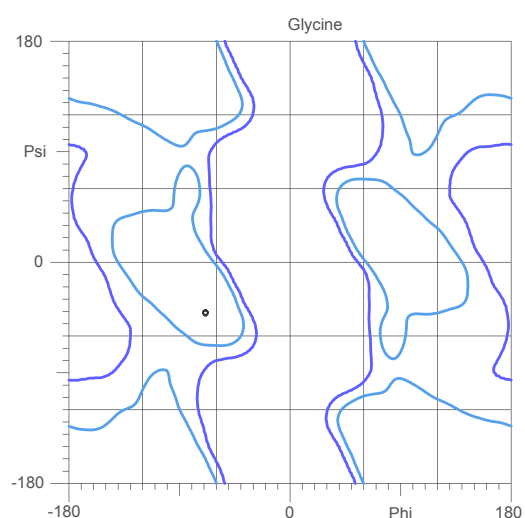
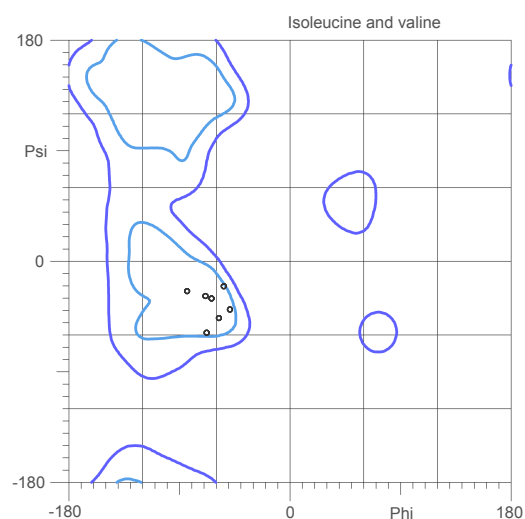
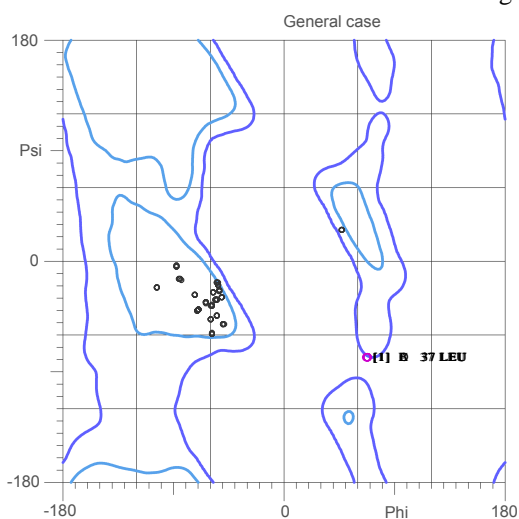
There were 10 outliers (phi, psi):

- [1] A 37 LEU (68.0, -78.1)
- [1] B 37 LEU (68.0, -78.0)
- [1] C 37 LEU (68.1, -78.1)

- [1] D 37 LEU (68.0, -78.1)
- [1] E 37 LEU (68.0, -78.1)
- [9] A 37 LEU (63.4, -83.8)
- [9] B 37 LEU (63.4, -83.8)
- [9] C 37 LEU (63.5, -83.9)
- [9] D 37 LEU (63.3, -83.9)
- [9] E 37 LEU (63.3, -83.9)

# MolProbity Ramachandran analysis

7k3g.H.pdb, model 1



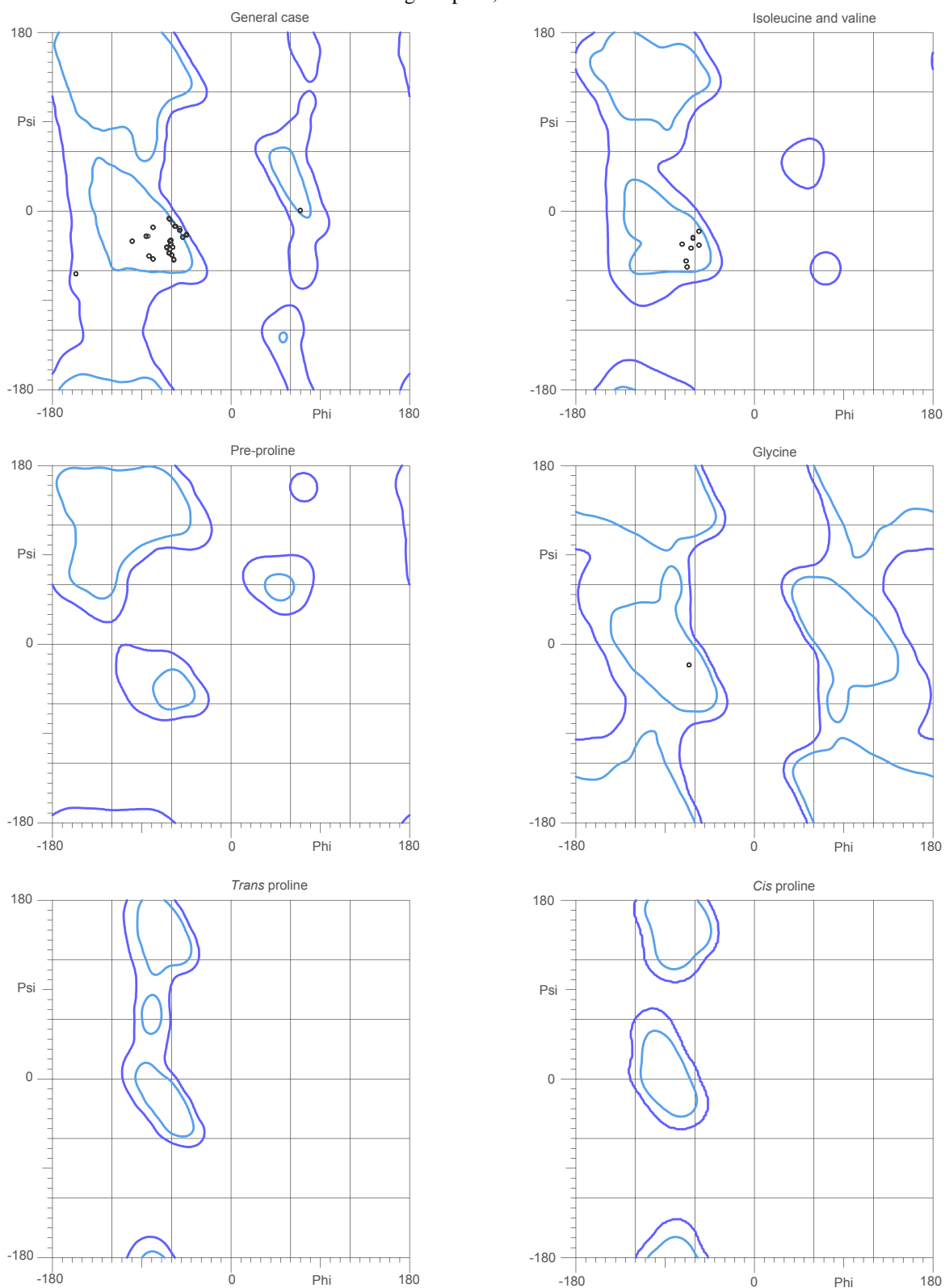
93.1% (135/145) of all residues were in favored (98%) regions.  
96.6% (140/145) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [1] A 37 LEU (68.0, -78.1)
- [1] B 37 LEU (68.0, -78.0)
- [1] C 37 LEU (68.1, -78.1)
- [1] D 37 LEU (68.0, -78.1)
- [1] E 37 LEU (68.0, -78.1)

# MolProbity Ramachandran analysis

7k3g.H.pdb, model 2



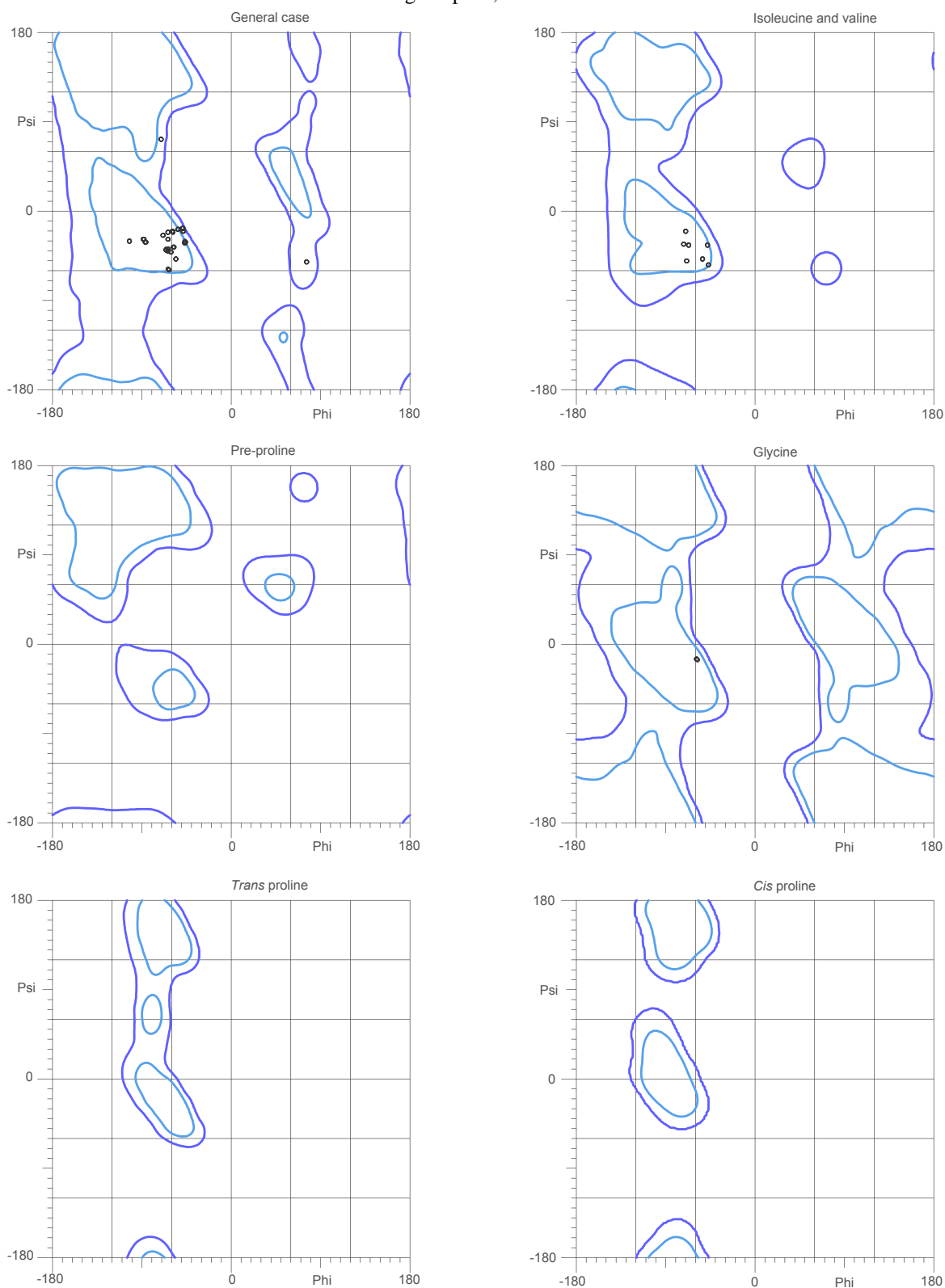
92.4% (134/145) of all residues were in favored (98%) regions.

100.0% (145/145) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

7k3g.H.pdb, model 3



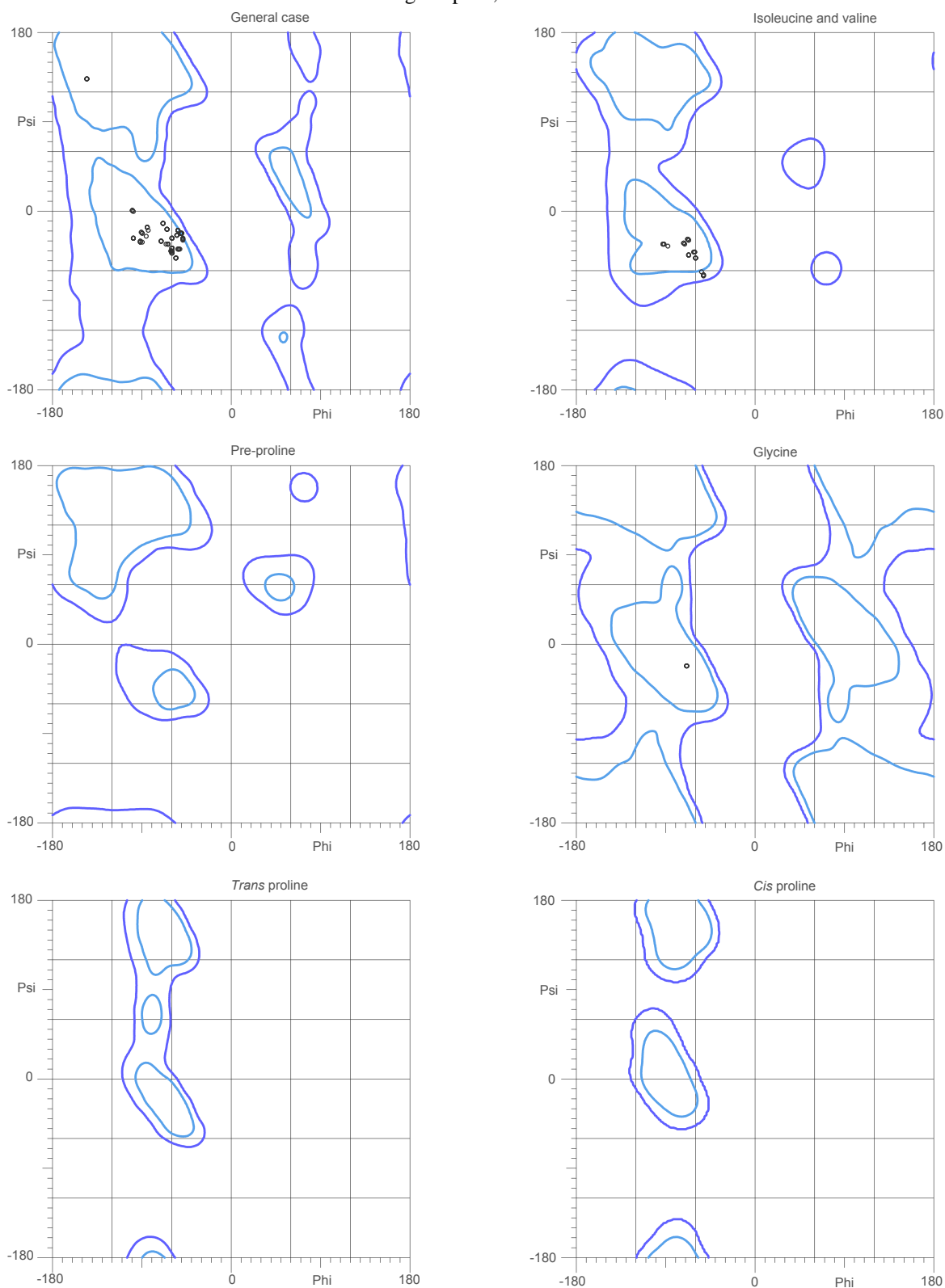
86.2% (125/145) of all residues were in favored (98%) regions.

100.0% (145/145) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

7k3g.H.pdb, model 4



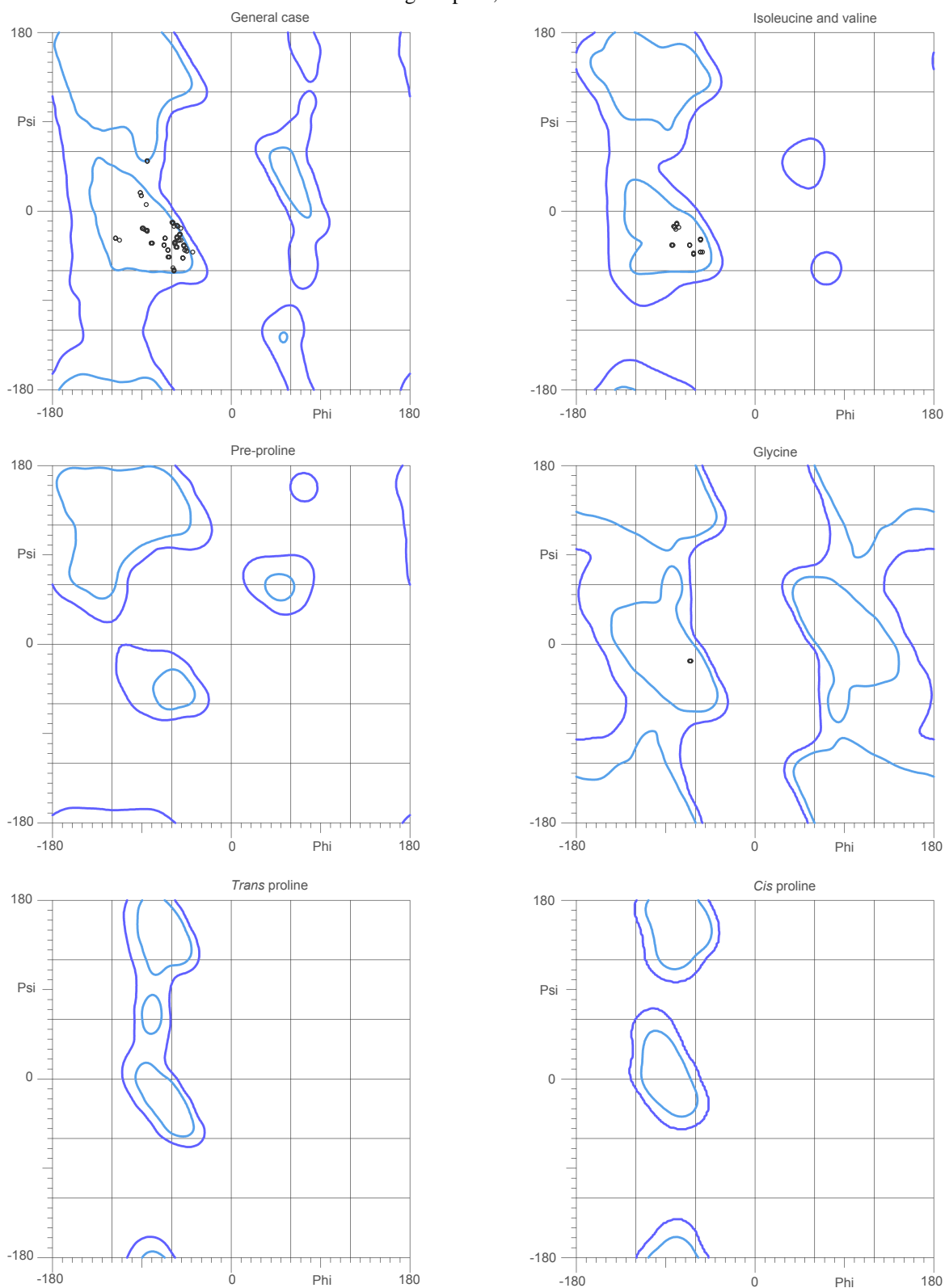
96.6% (140/145) of all residues were in favored (98%) regions.

100.0% (145/145) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

7k3g.H.pdb, model 5



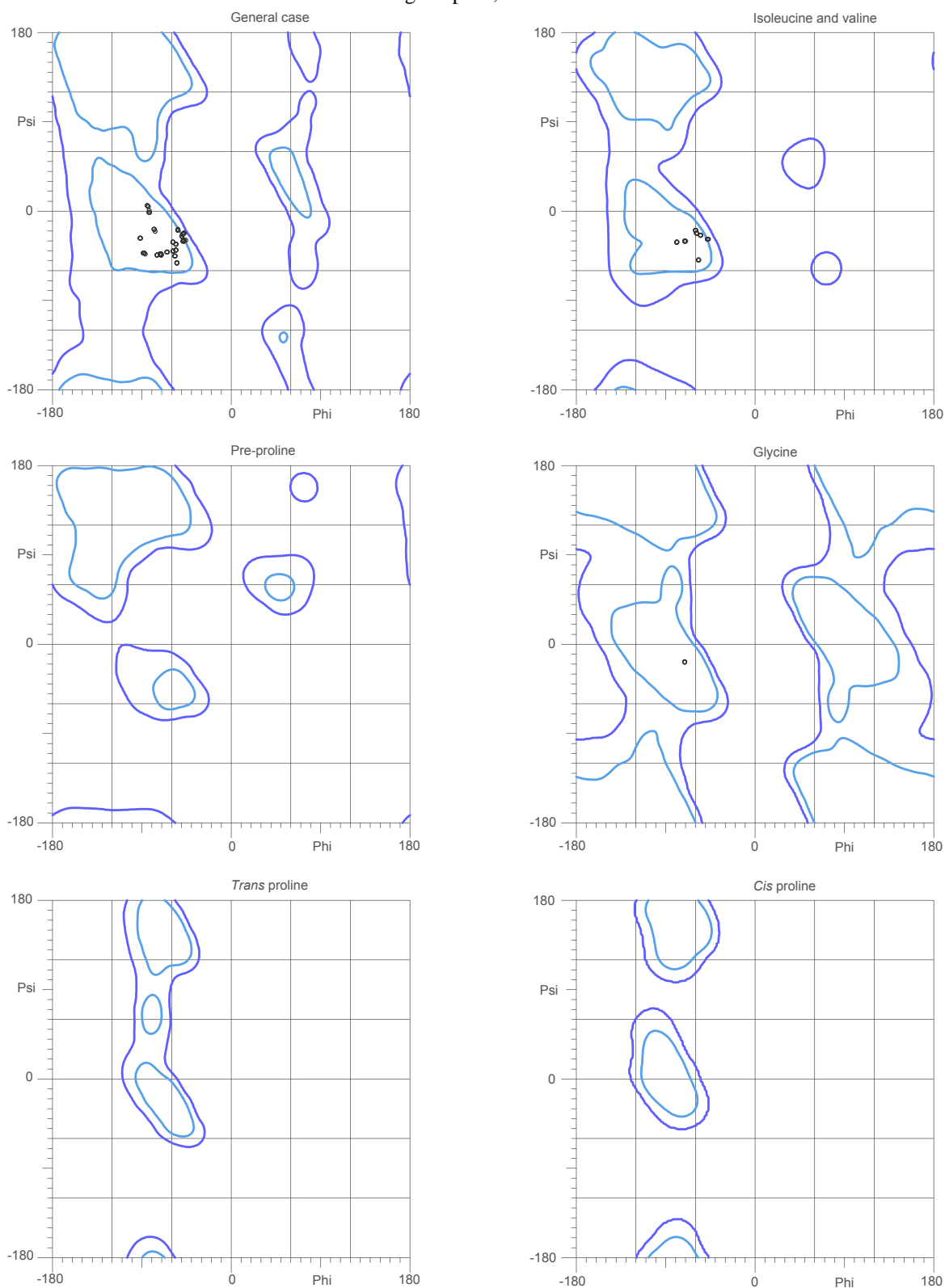
97.2% (141/145) of all residues were in favored (98%) regions.

100.0% (145/145) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

7k3g.H.pdb, model 6



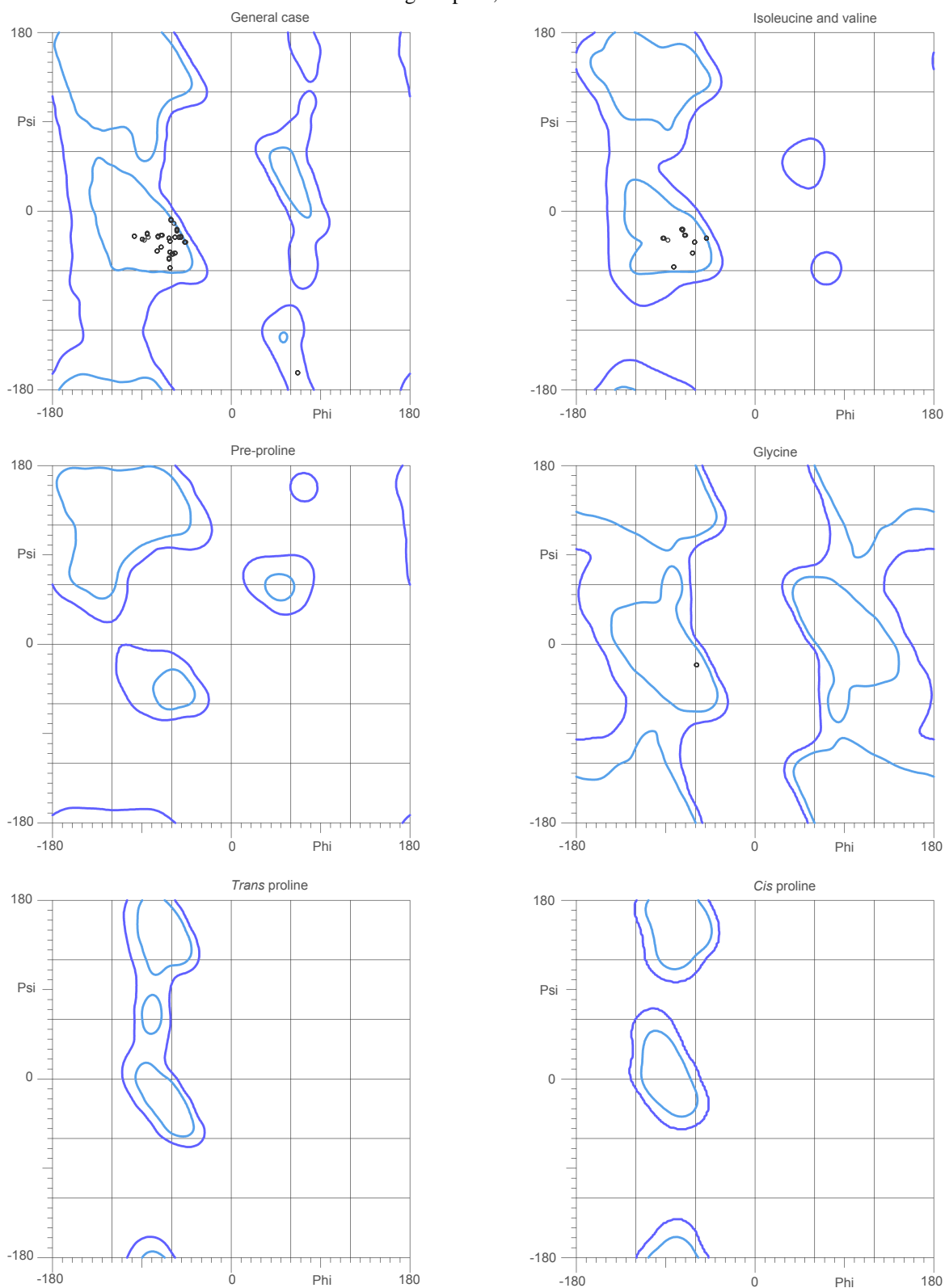
89.7% (130/145) of all residues were in favored (98%) regions.

100.0% (145/145) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

7k3g.H.pdb, model 7



96.6% (140/145) of all residues were in favored (98%) regions.

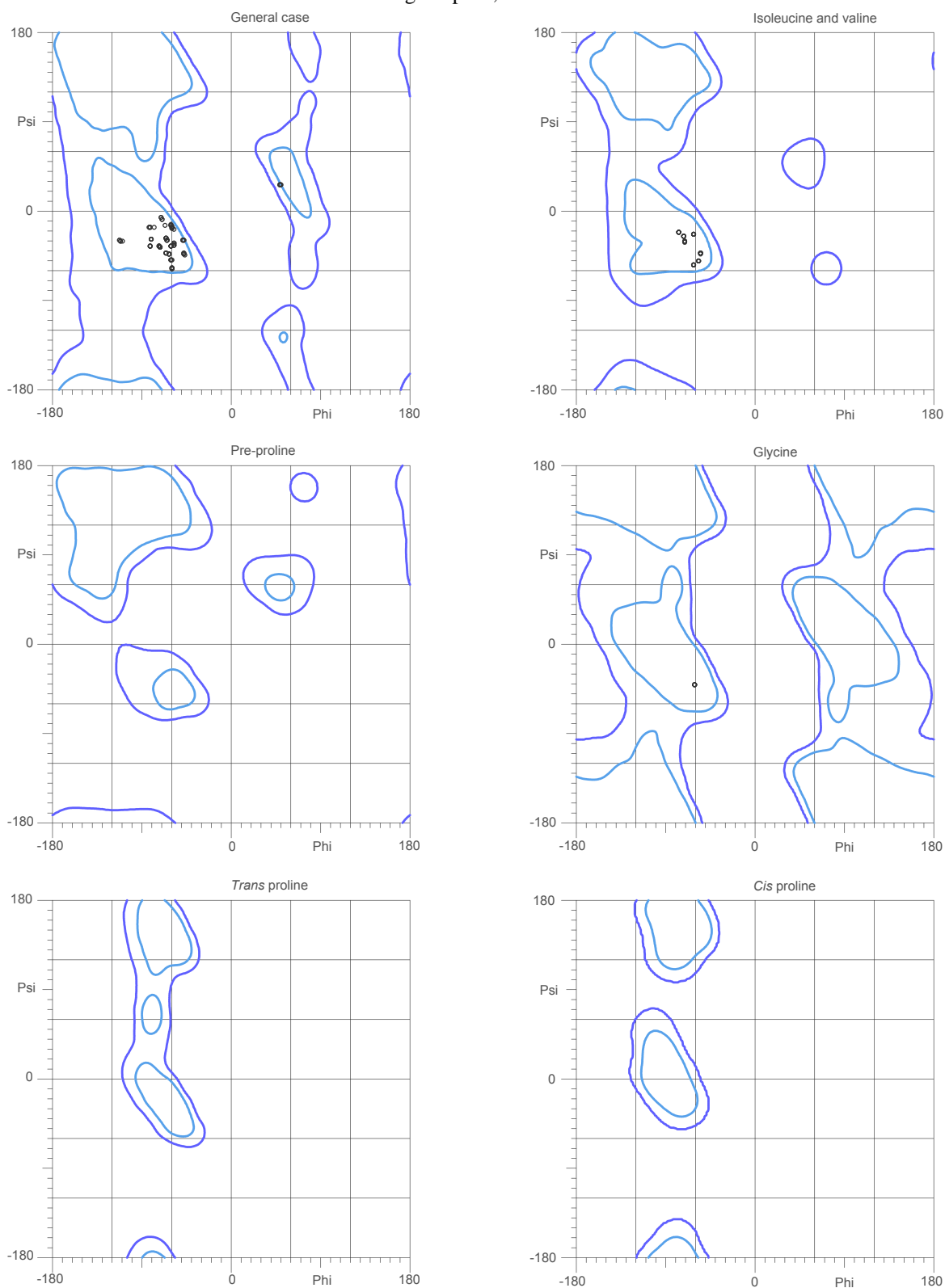
100.0% (145/145) of all residues were in allowed (>99.8%) regions.

There were no outliers.



# MolProbity Ramachandran analysis

7k3g.H.pdb, model 8



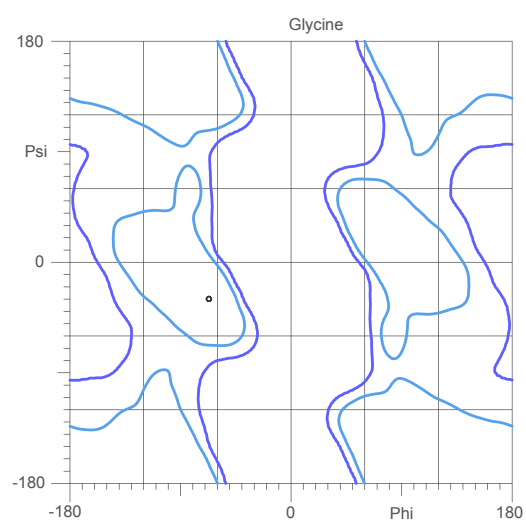
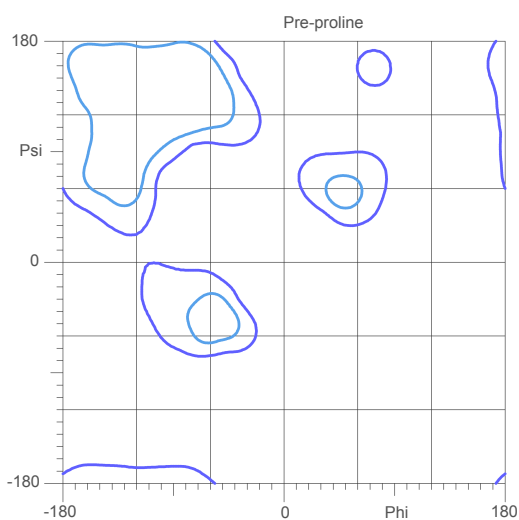
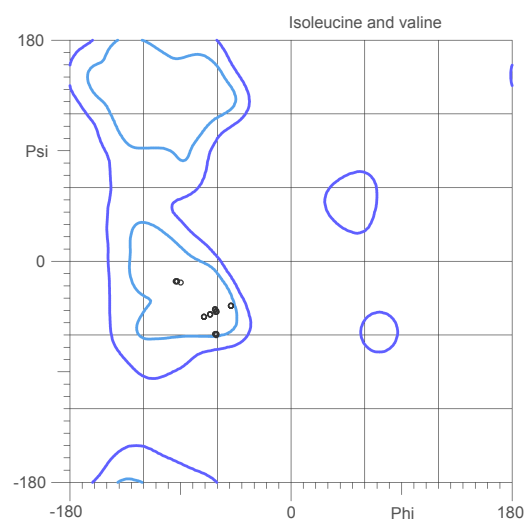
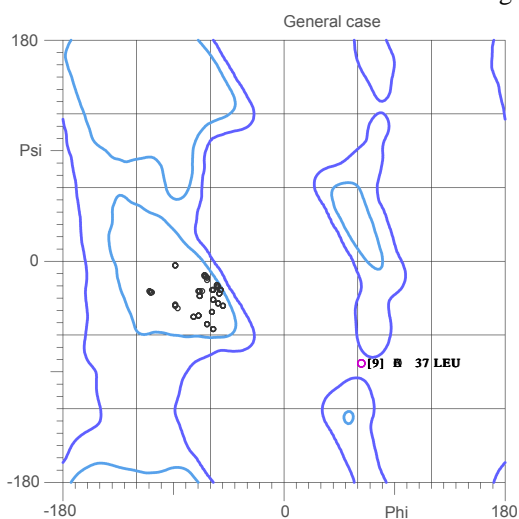
100.0% (145/145) of all residues were in favored (98%) regions.

100.0% (145/145) of all residues were in allowed (>99.8%) regions.

There were no outliers.

# MolProbity Ramachandran analysis

7k3g.H.pdb, model 9



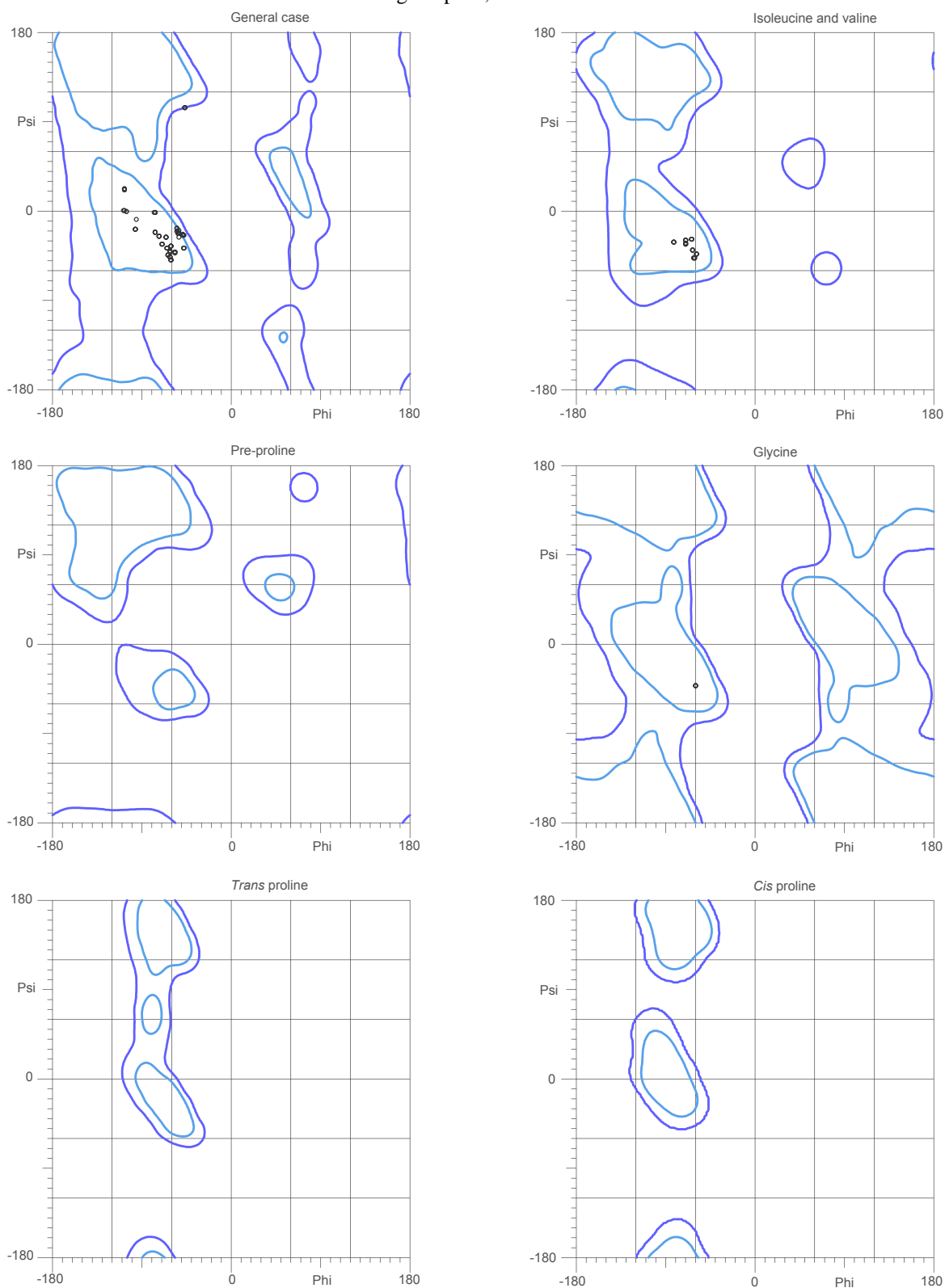
96.6% (140/145) of all residues were in favored (98%) regions.  
96.6% (140/145) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [9] A 37 LEU (63.4, -83.8)
- [9] B 37 LEU (63.4, -83.8)
- [9] C 37 LEU (63.5, -83.9)
- [9] D 37 LEU (63.3, -83.9)
- [9] E 37 LEU (63.3, -83.9)

# MolProbity Ramachandran analysis

7k3g.H.pdb, model 10



92.4% (134/145) of all residues were in favored (98%) regions.

100.0% (145/145) of all residues were in allowed (>99.8%) regions.

There were no outliers.