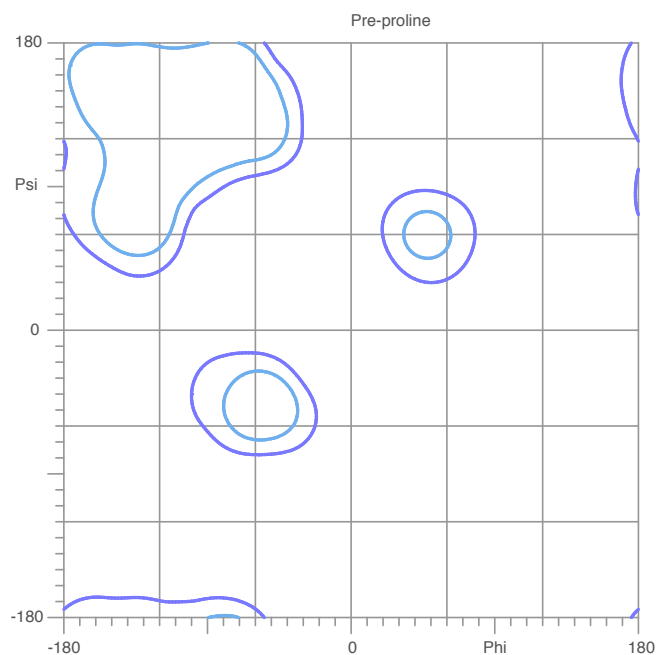
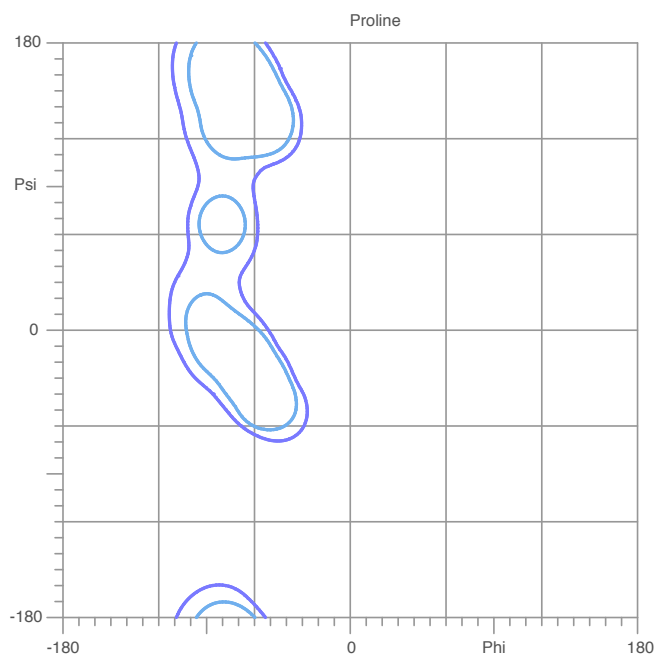
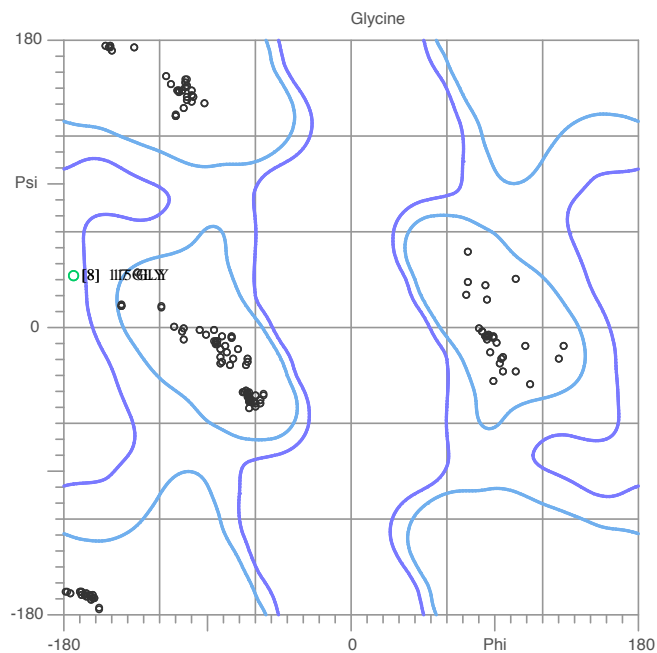
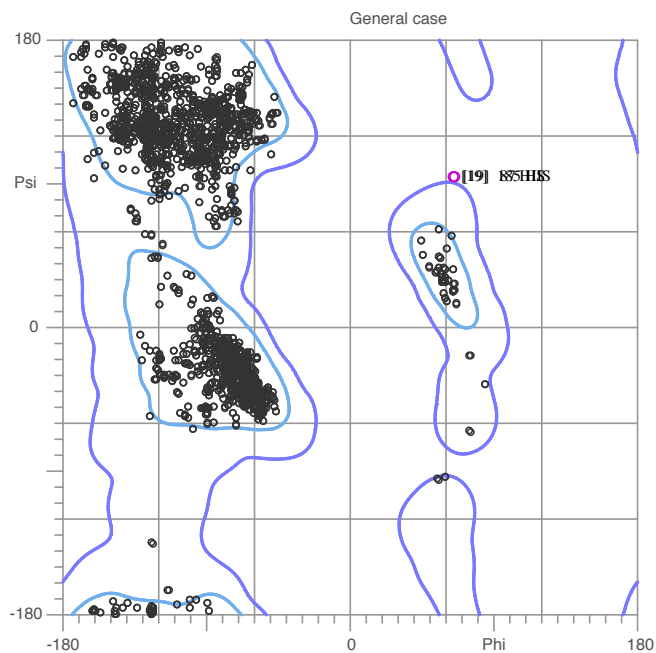


MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, all models



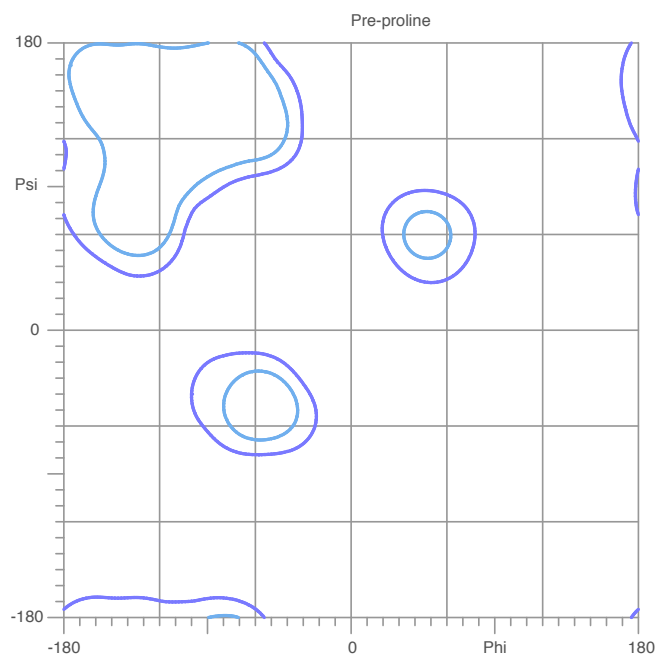
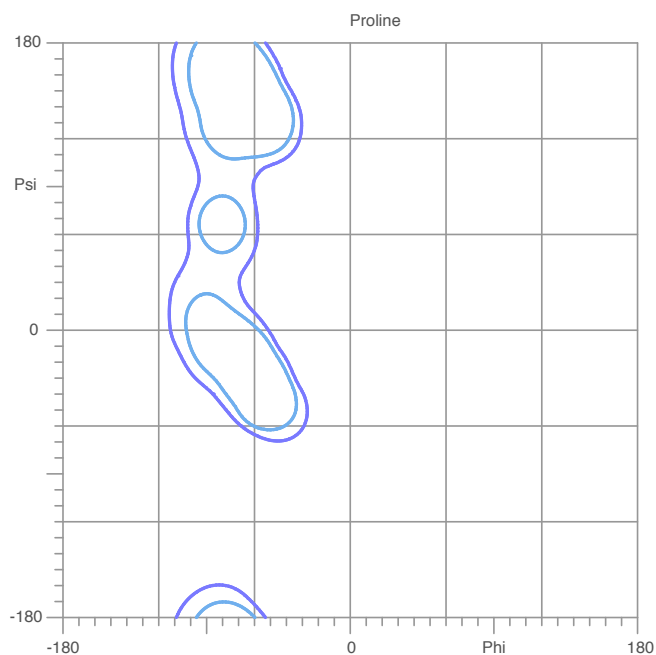
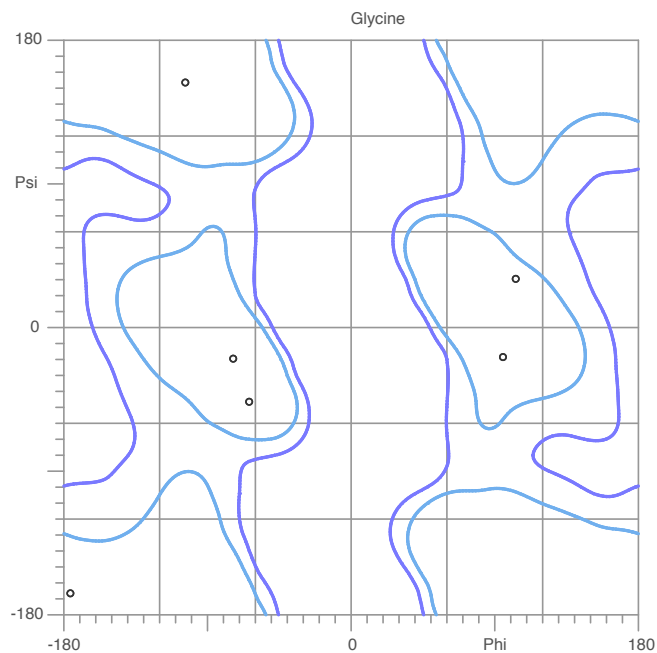
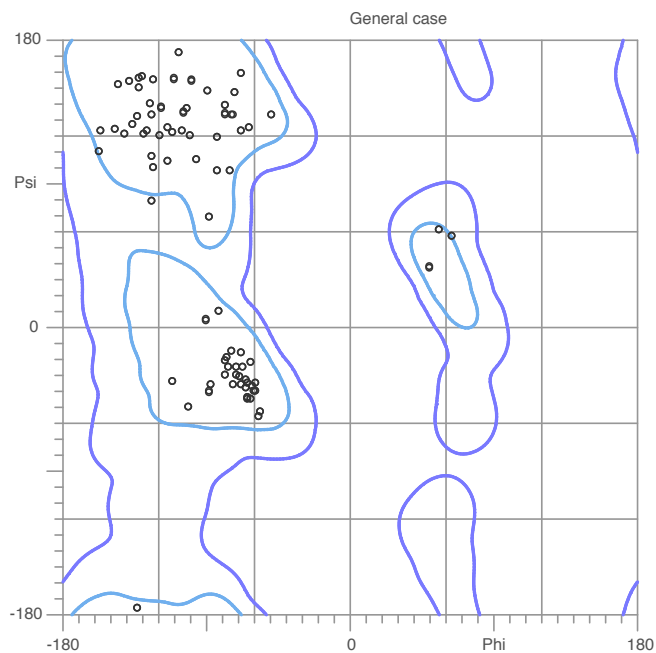
98.0% (3372/3440) of all residues were in favored (98%) regions.
99.9% (3436/3440) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [8] 17 GLY (-175.0, 34.0)
- [8] 115 GLY (-175.0, 33.8)
- [19] 87 HIS (65.0, 95.0)
- [19] 185 HIS (65.1, 95.0)

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 1

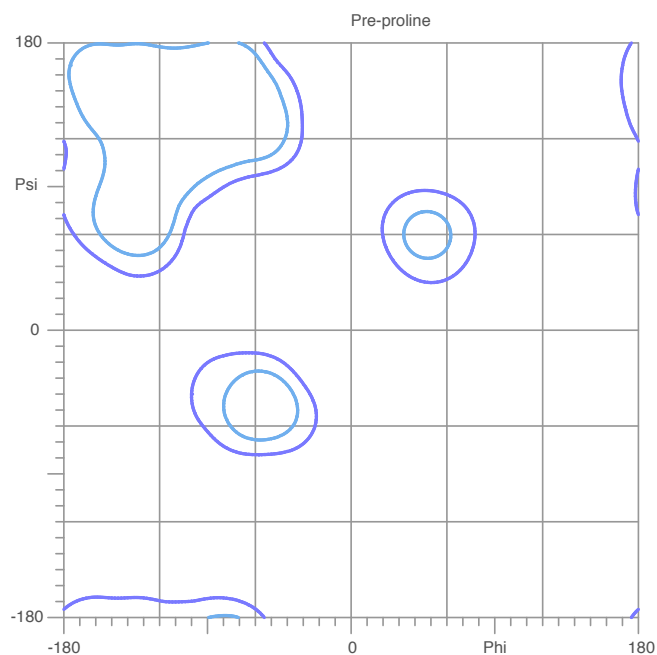
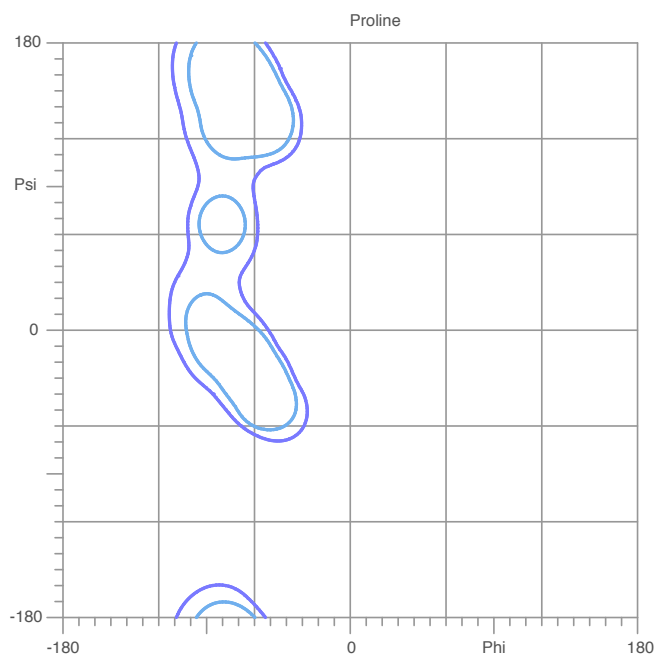
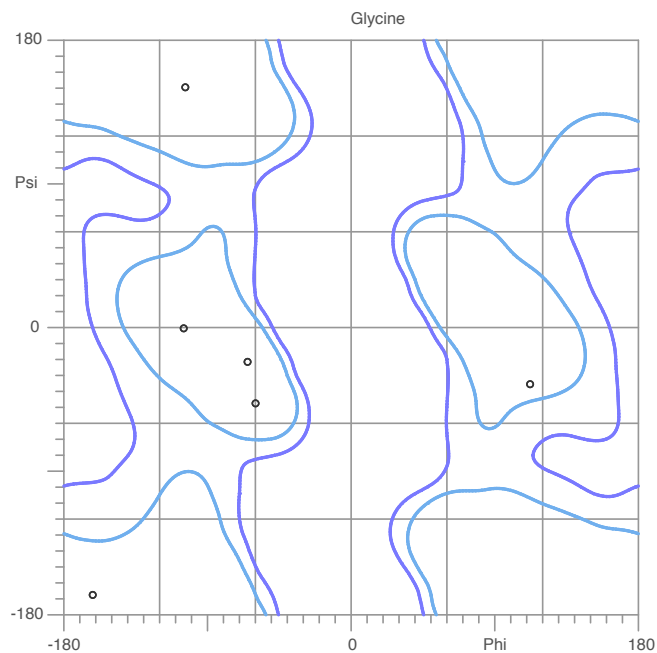
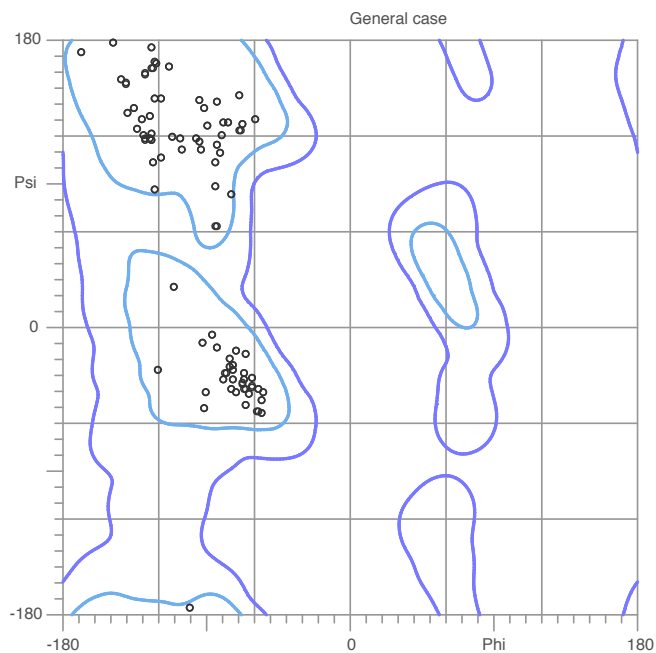


97.7% (168/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 2



100.0% (172/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

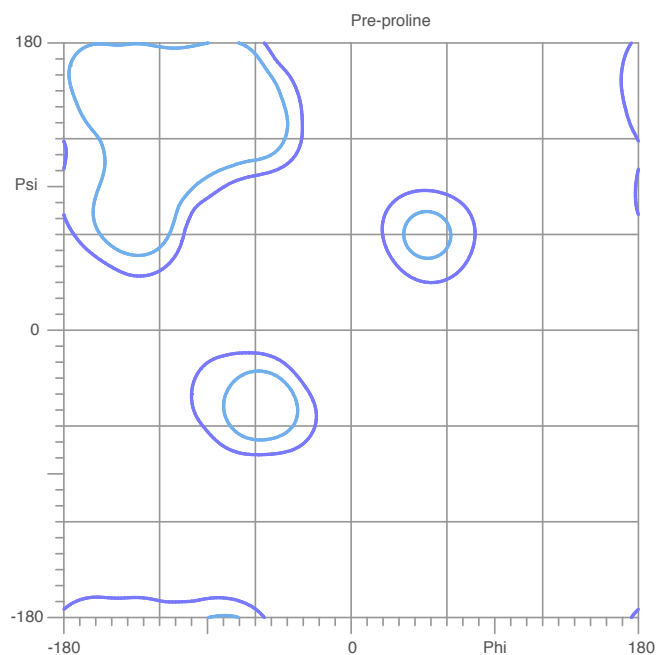
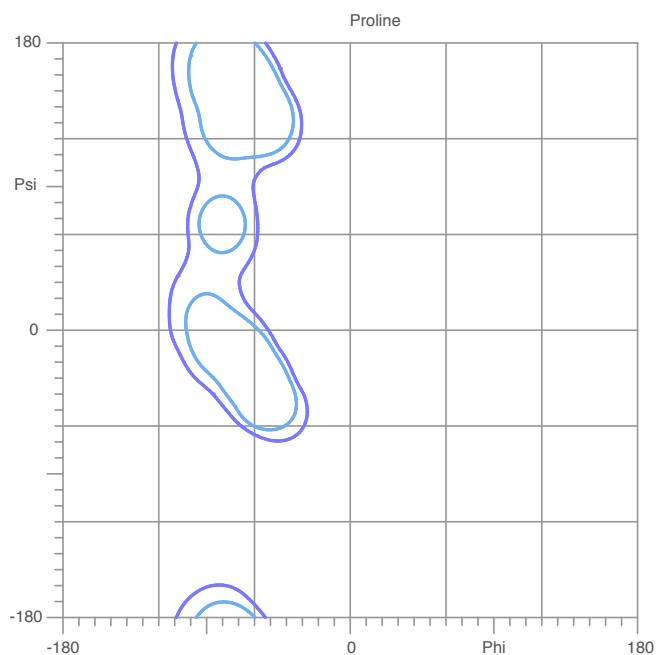
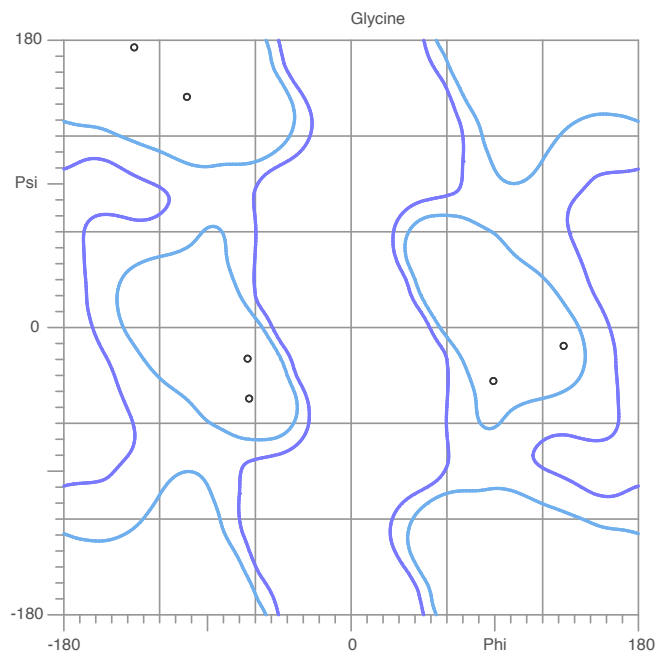
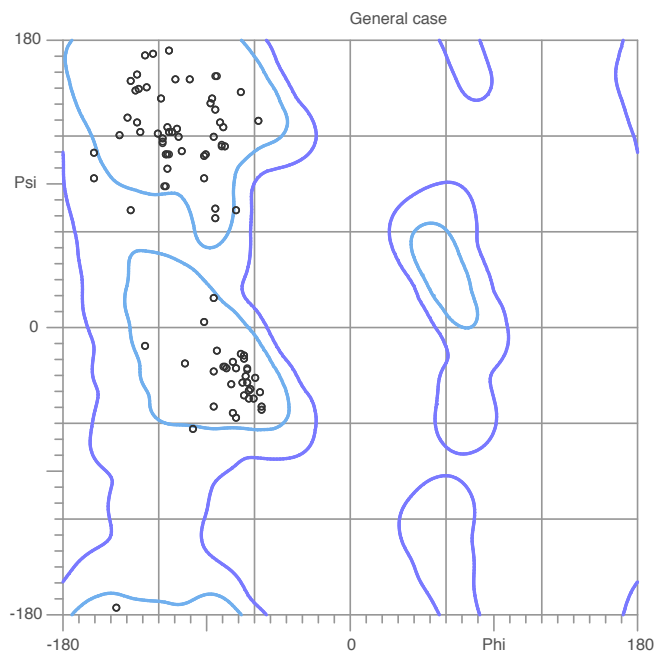
There were no outliers.

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

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MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 3



94.2% (162/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

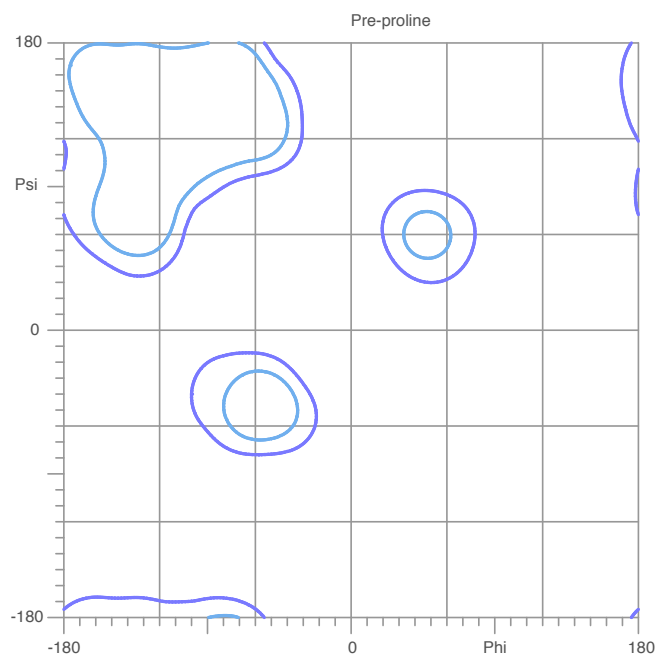
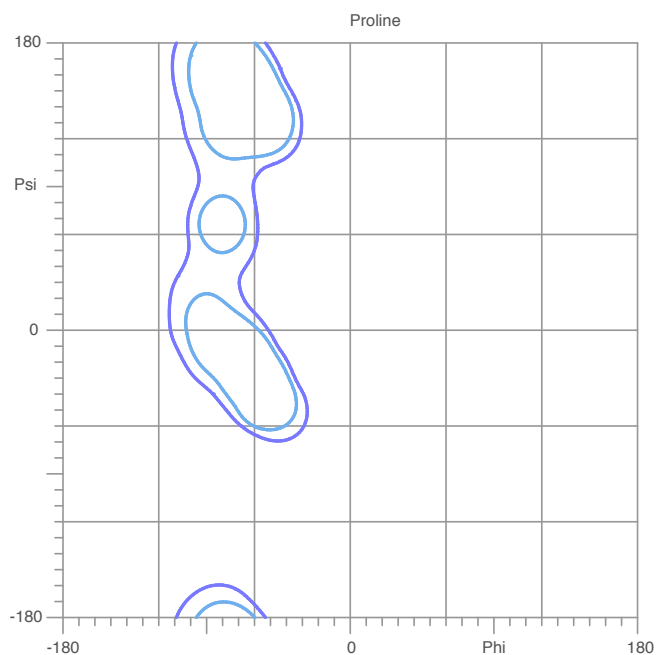
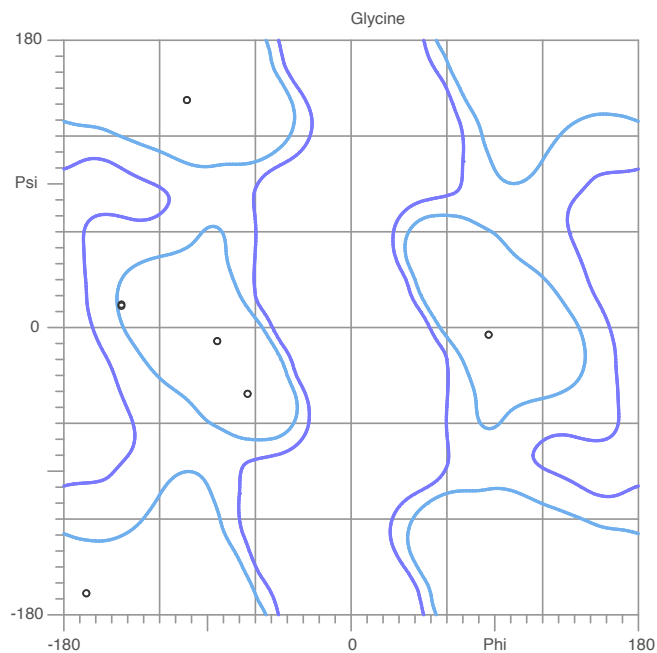
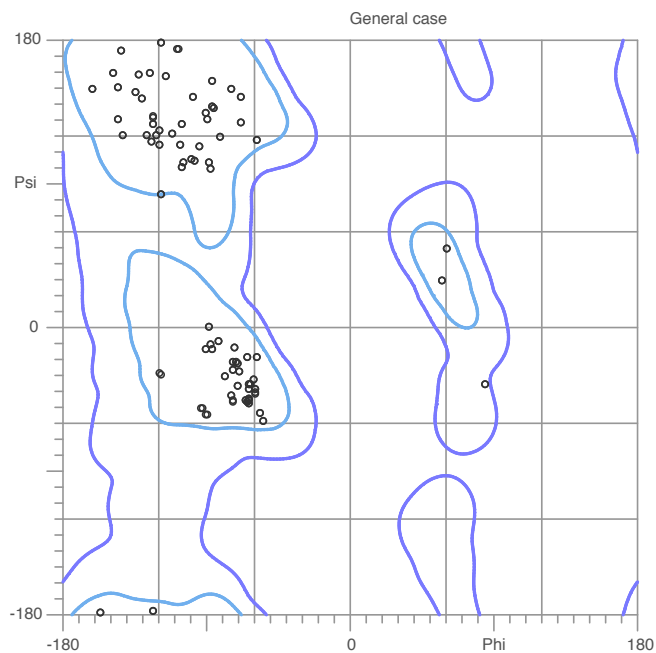
There were no outliers.

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

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MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 4

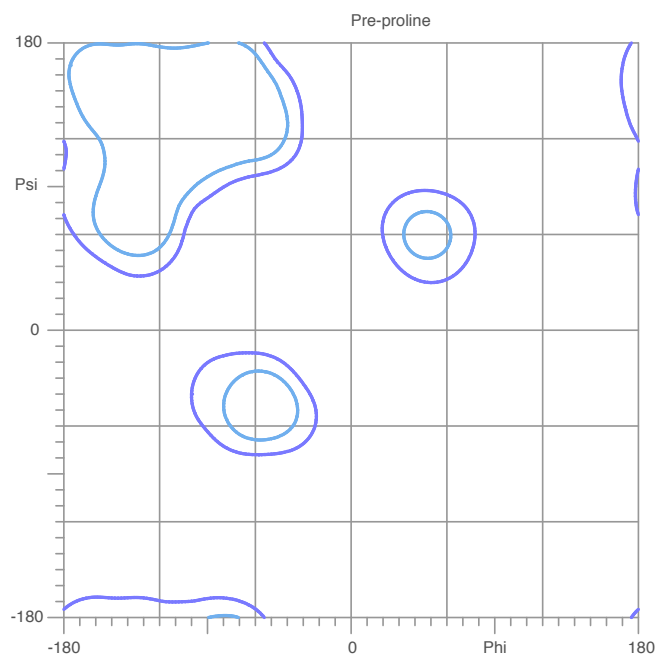
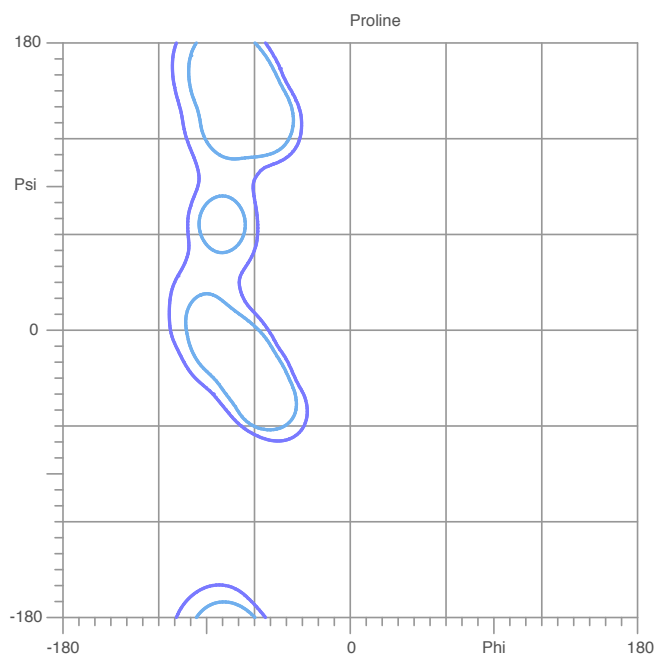
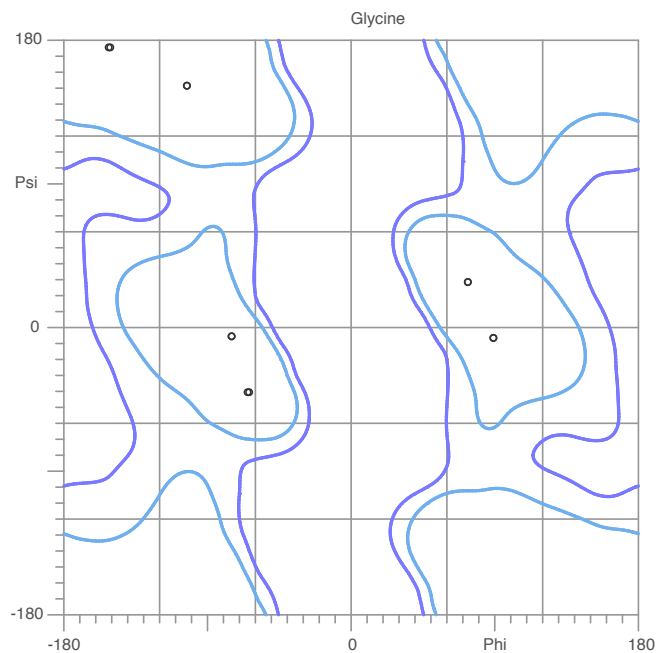
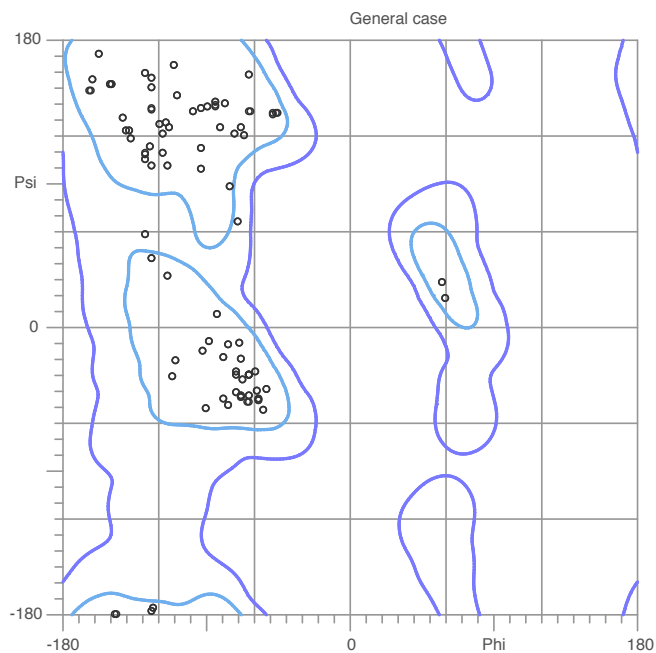


98.8% (170/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 5

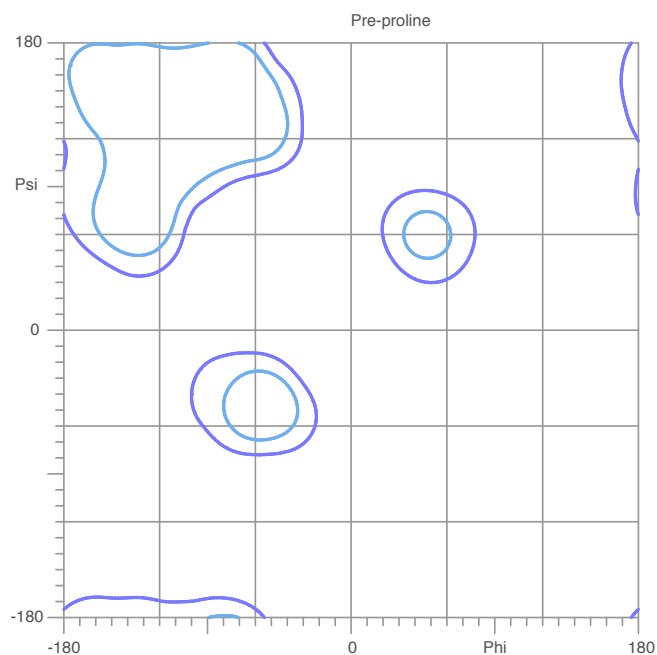
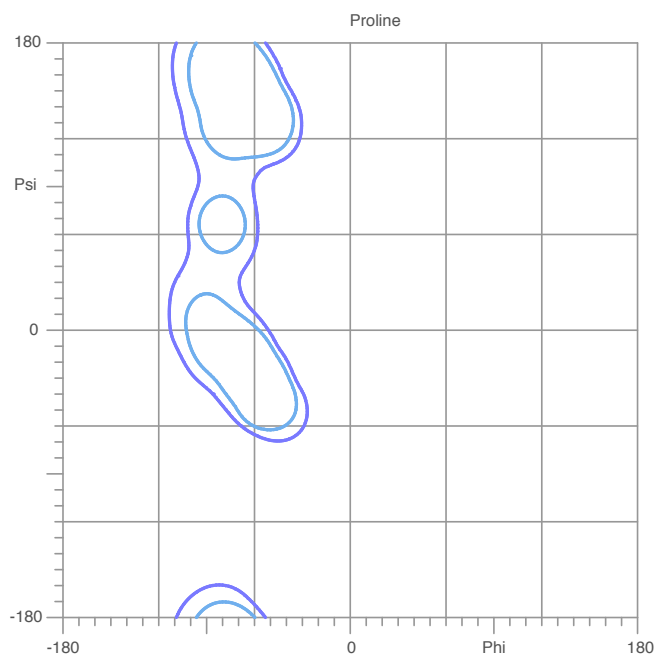
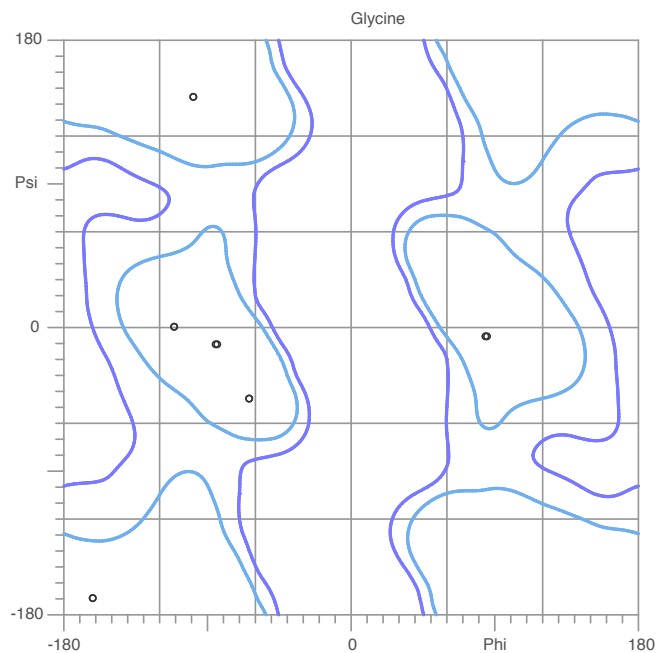
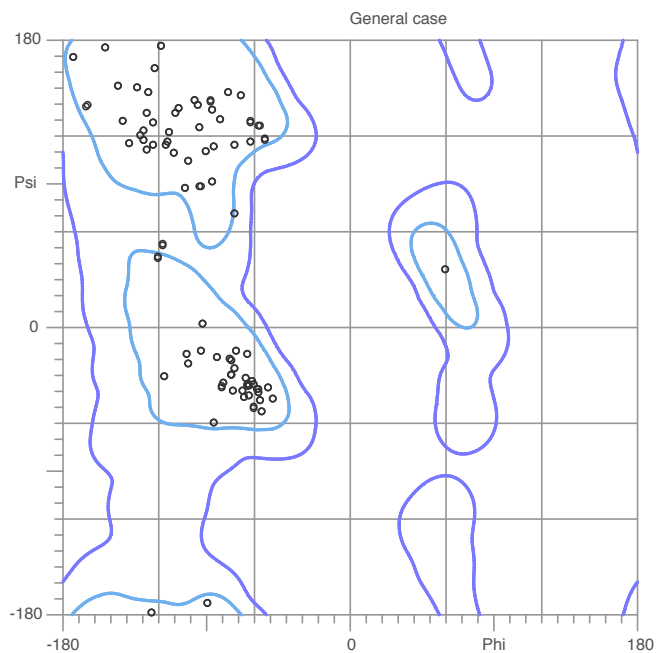


97.7% (168/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 6



98.8% (170/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

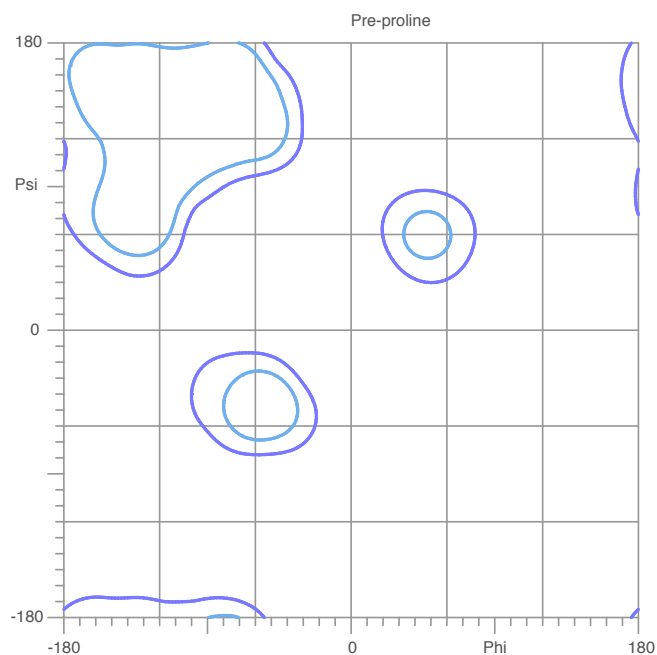
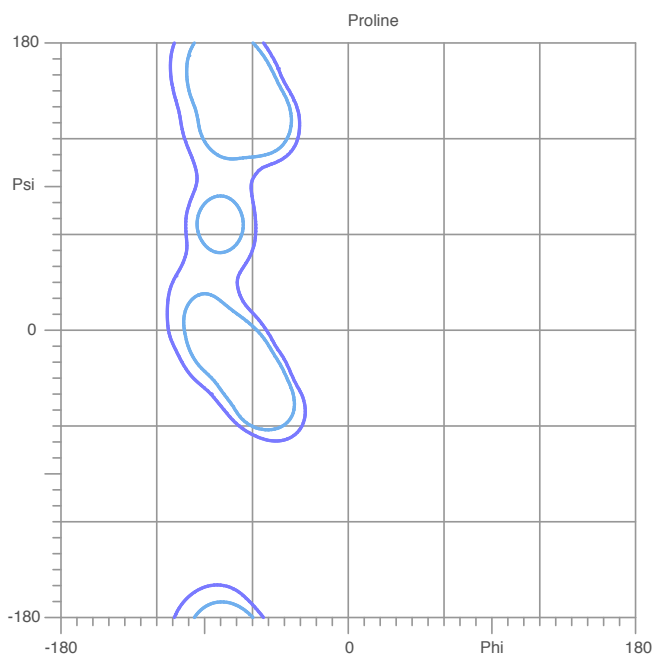
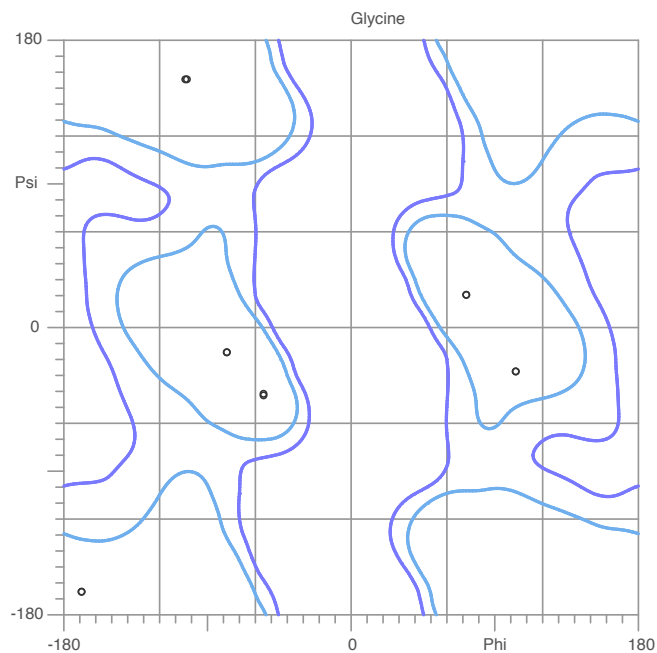
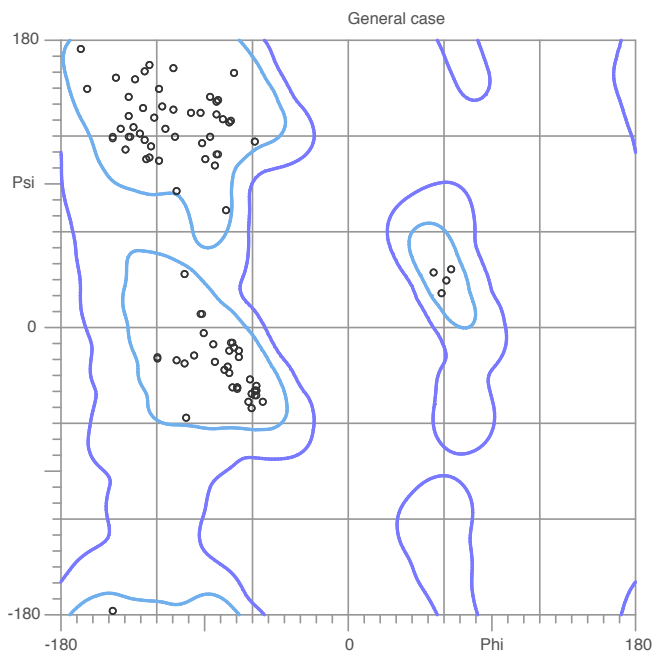
There were no outliers.

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MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 7

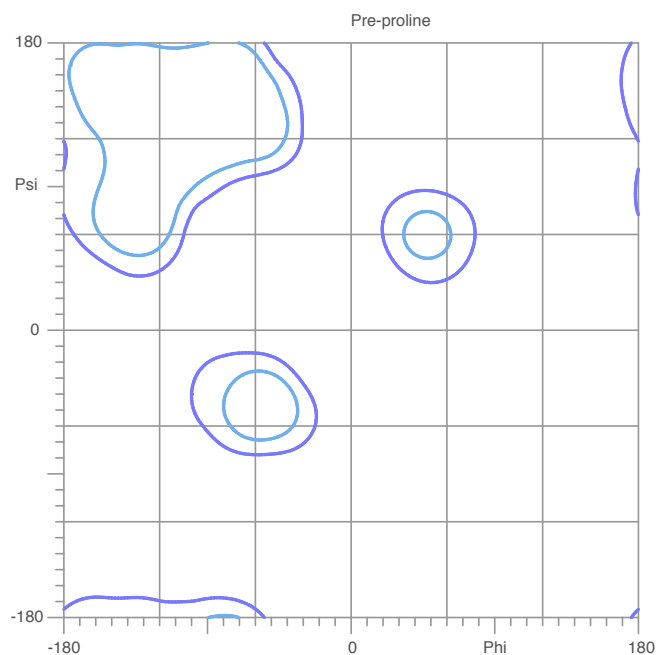
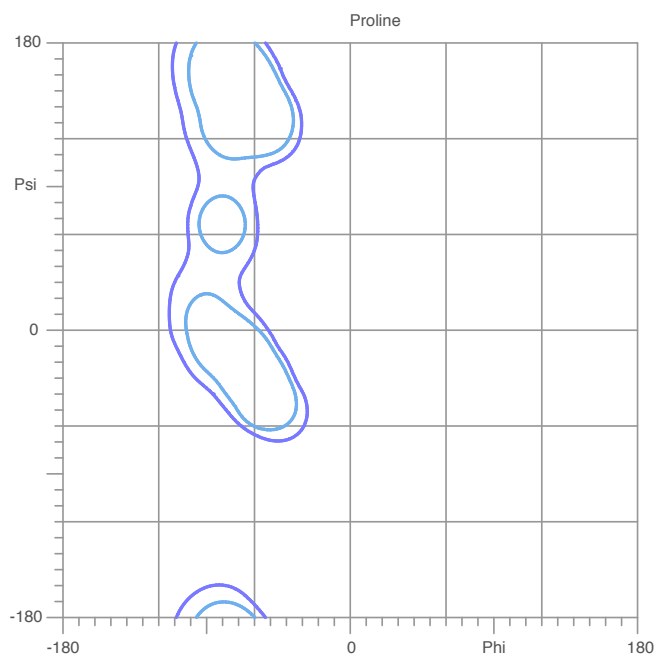
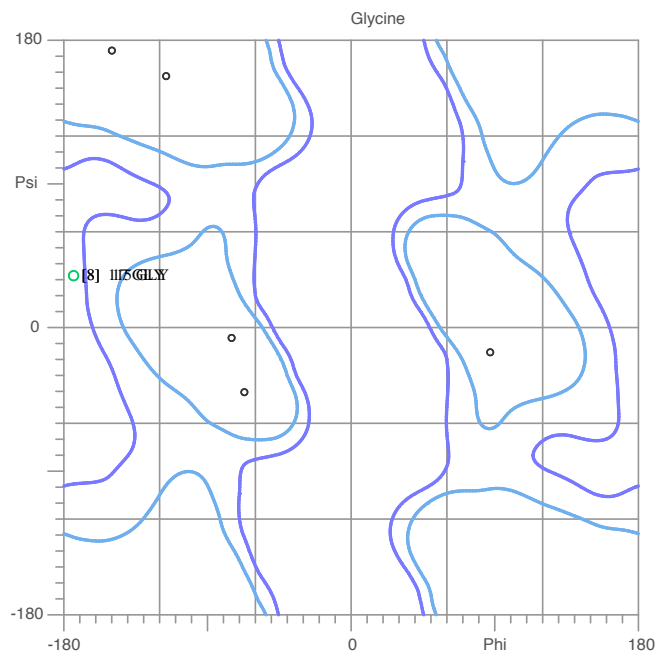
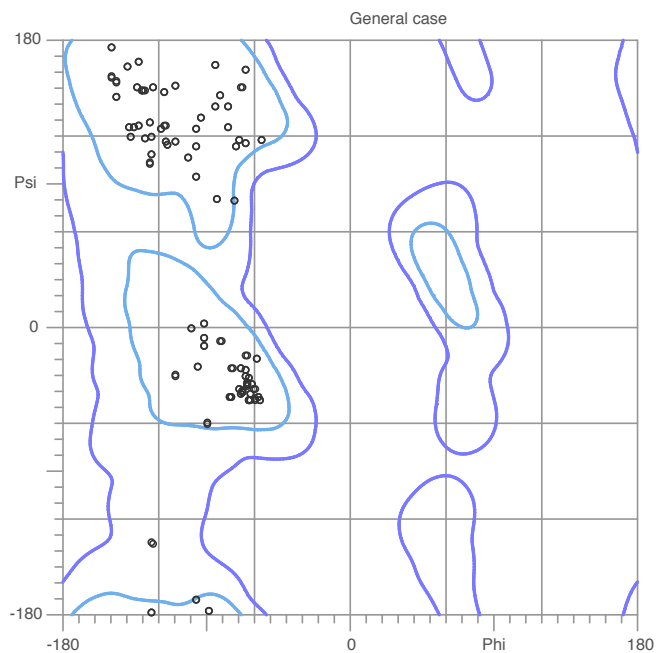


100.0% (172/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 8



97.7% (168/172) of all residues were in favored (98%) regions.
98.8% (170/172) of all residues were in allowed (>99.8%) regions.

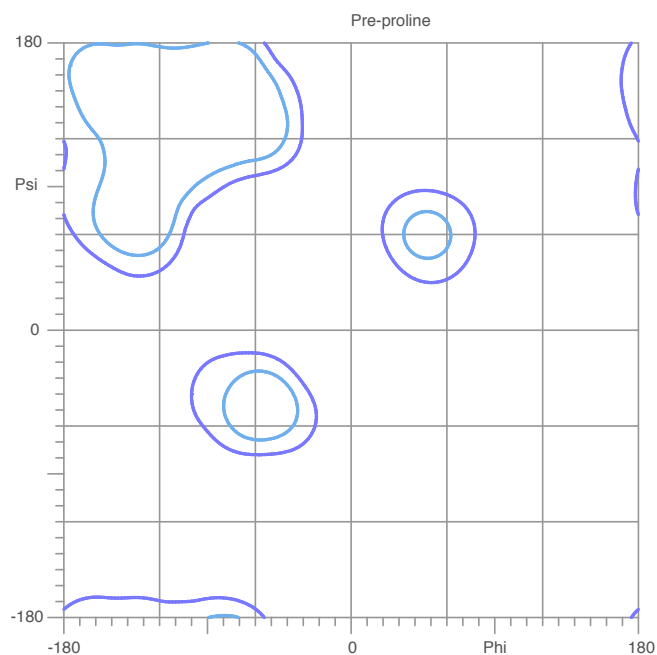
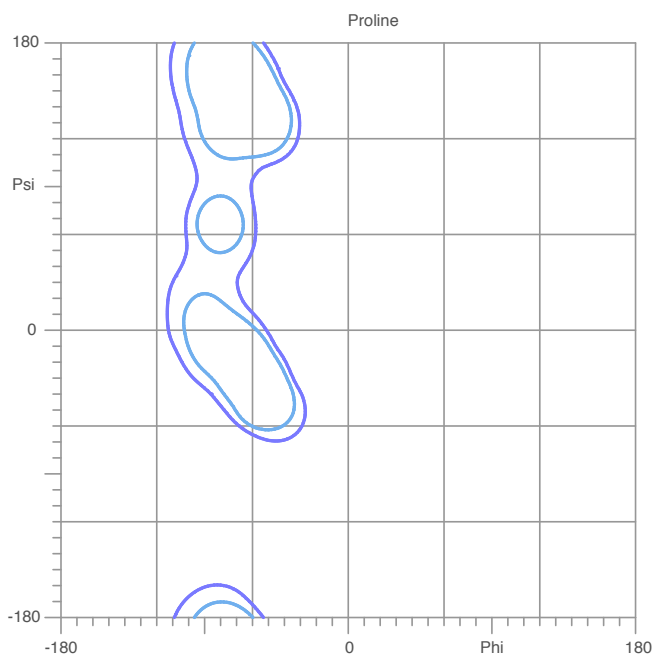
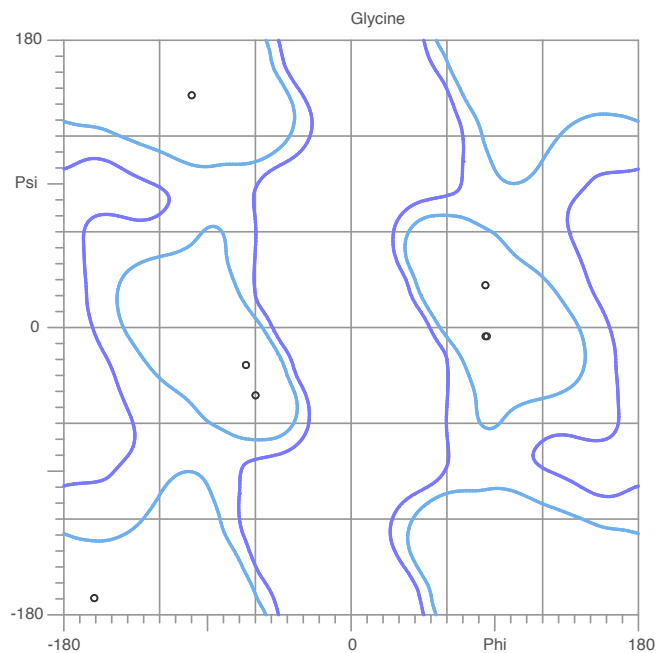
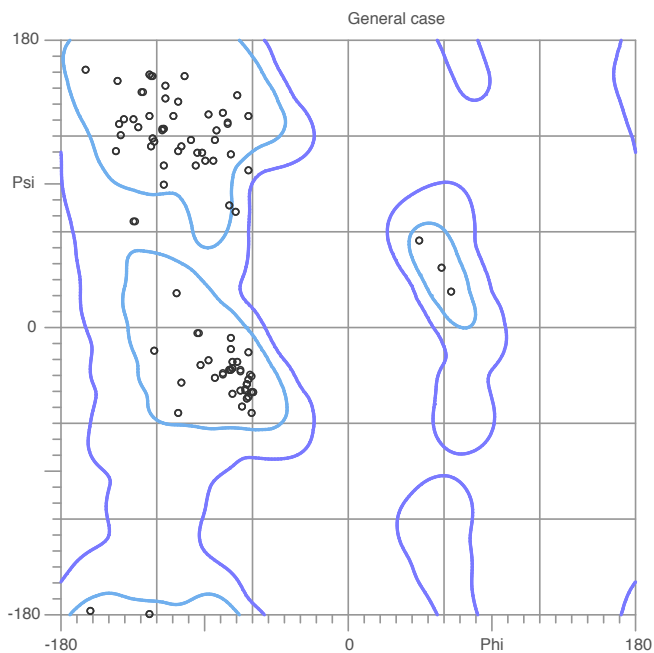
There were 2 outliers (phi, psi):

[8] 17 GLY (-175.0, 34.0)

[8] 115 GLY (-175.0, 33.8)

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 9



96.5% (166/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

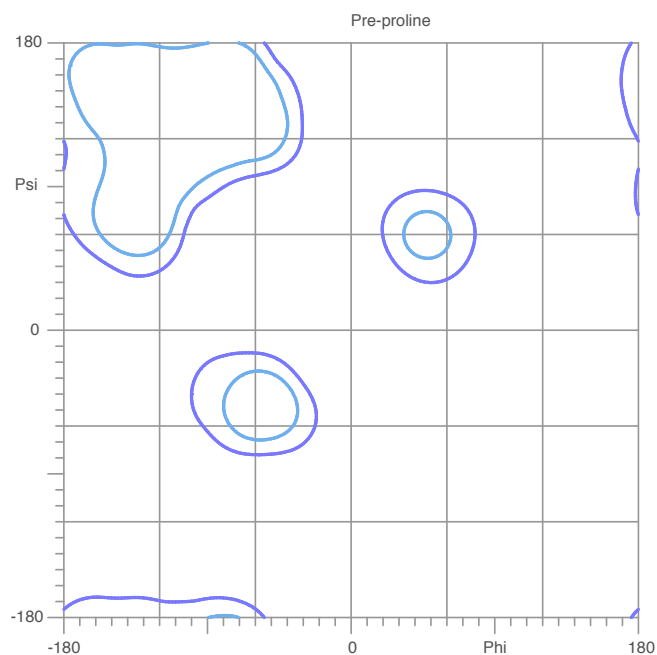
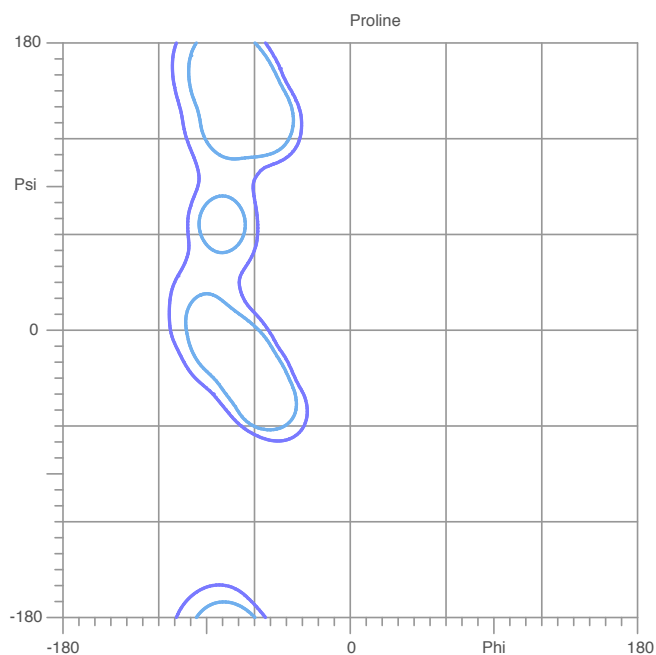
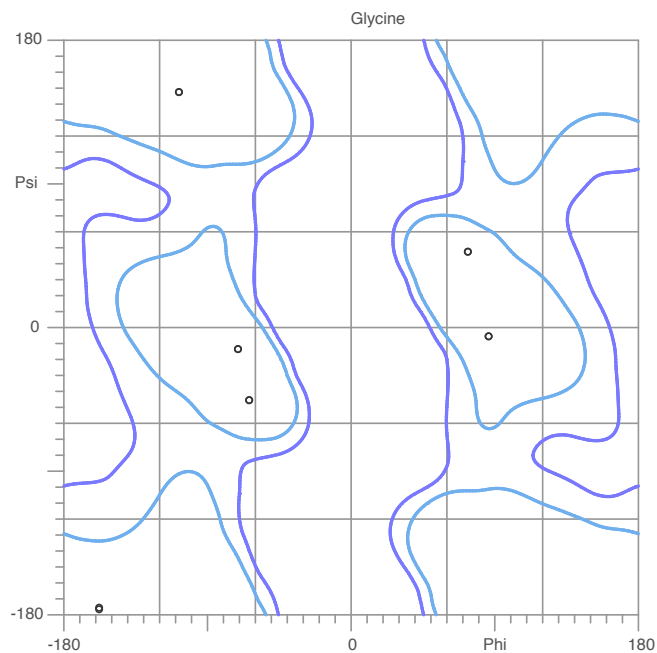
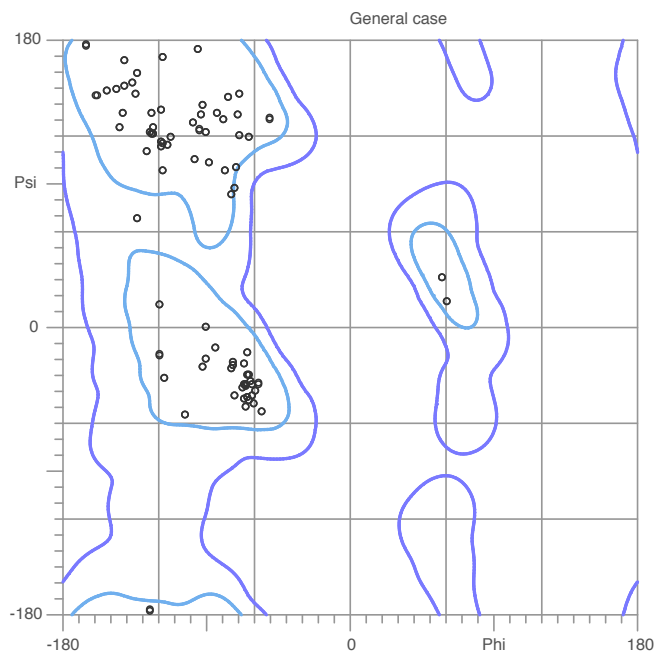
There were no outliers.

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MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 10

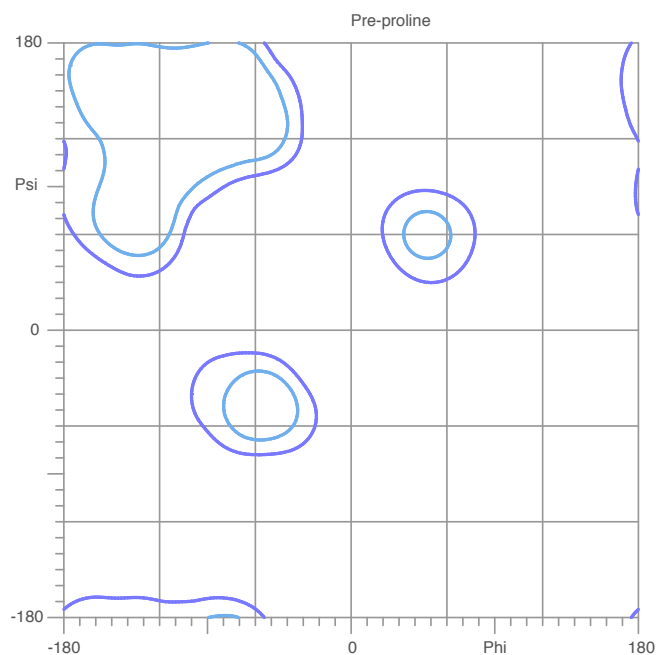
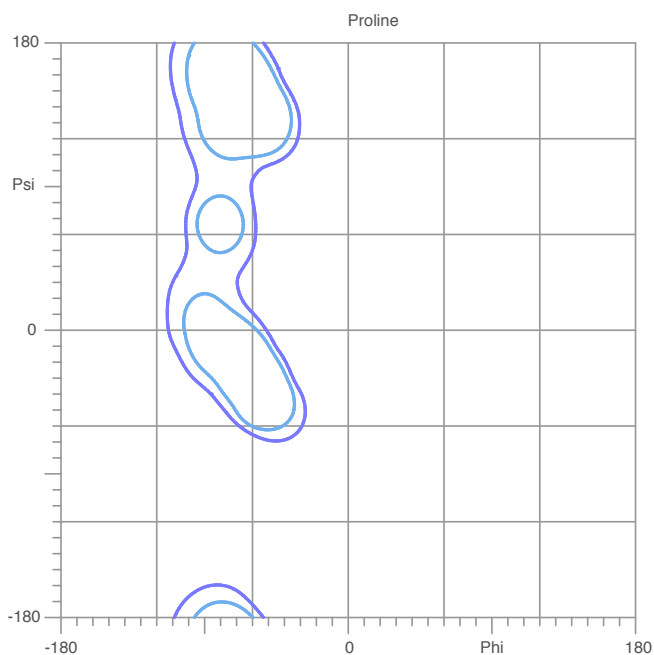
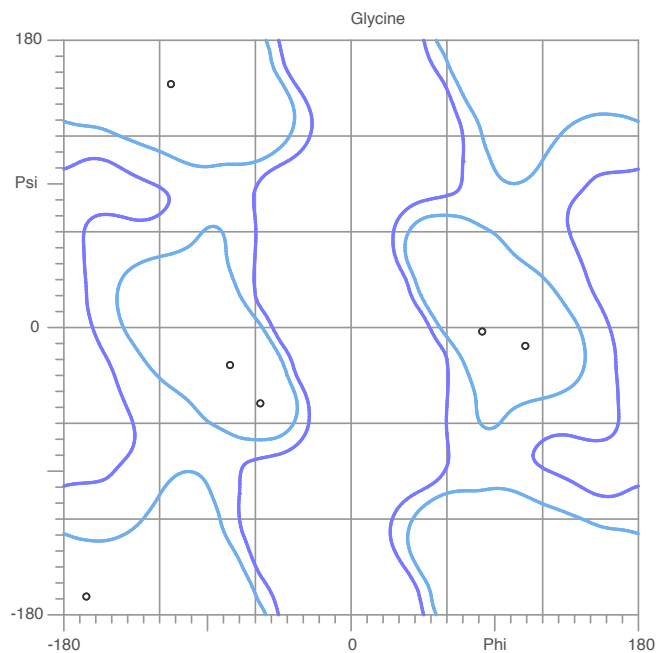
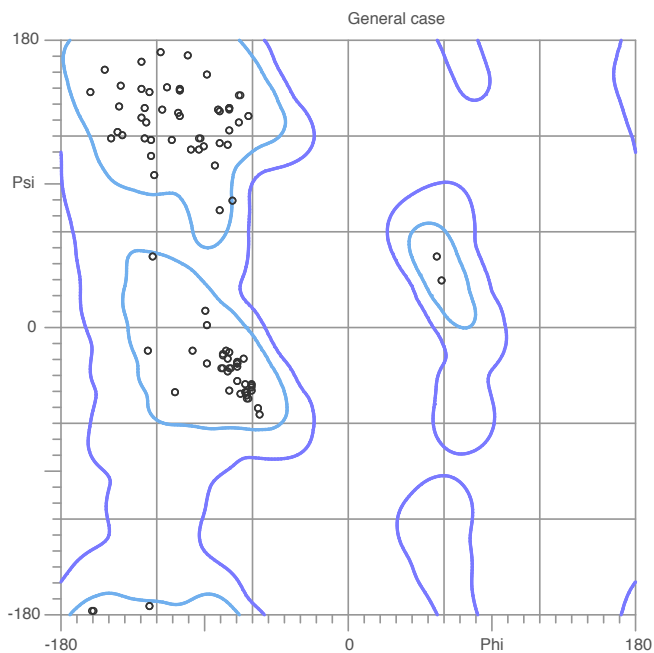


98.8% (170/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 11



100.0% (172/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

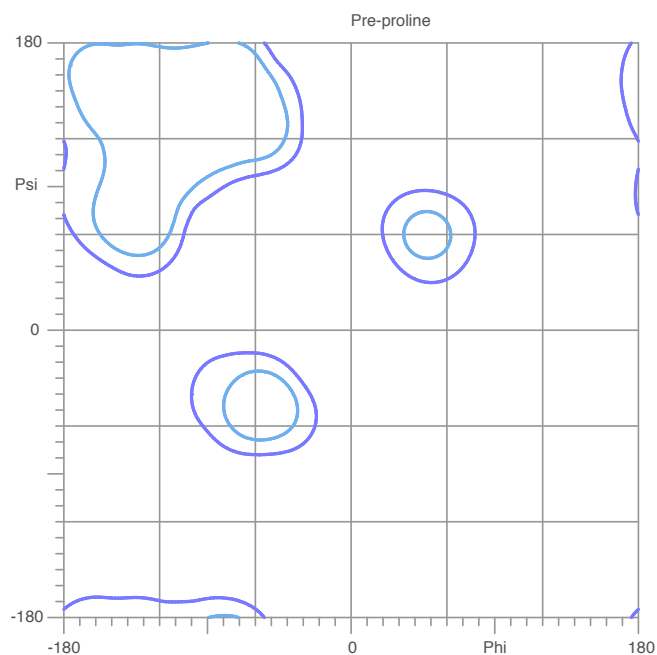
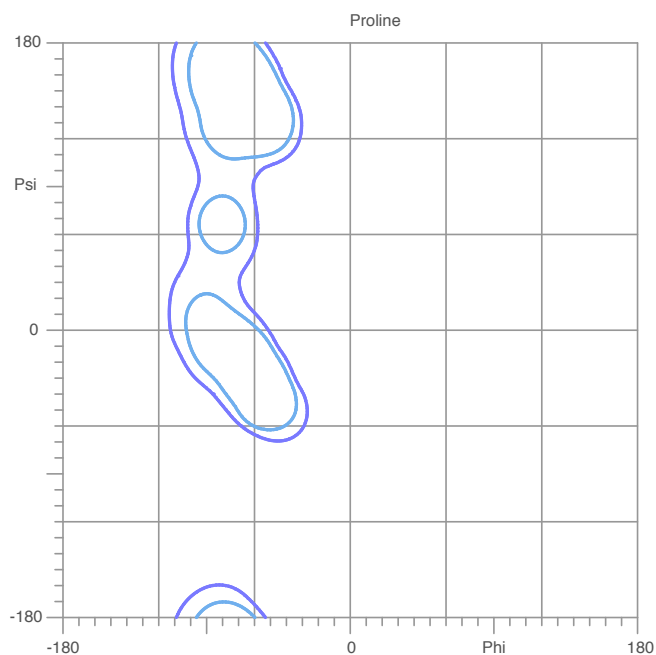
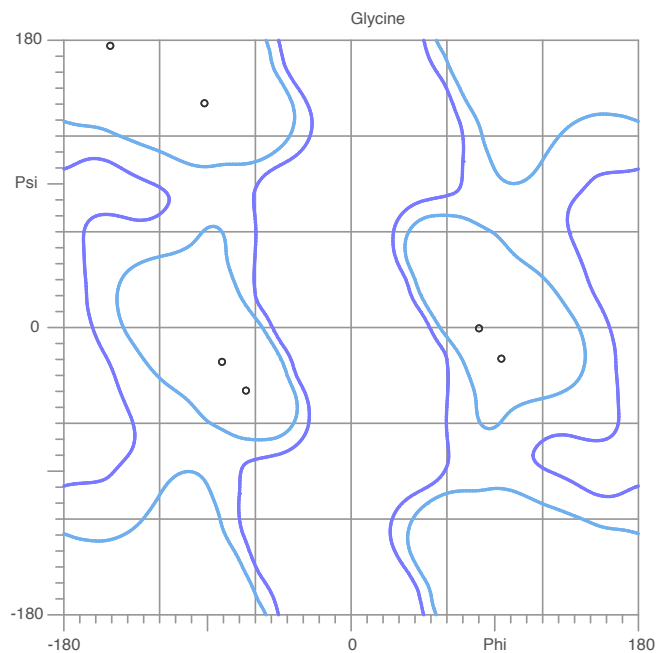
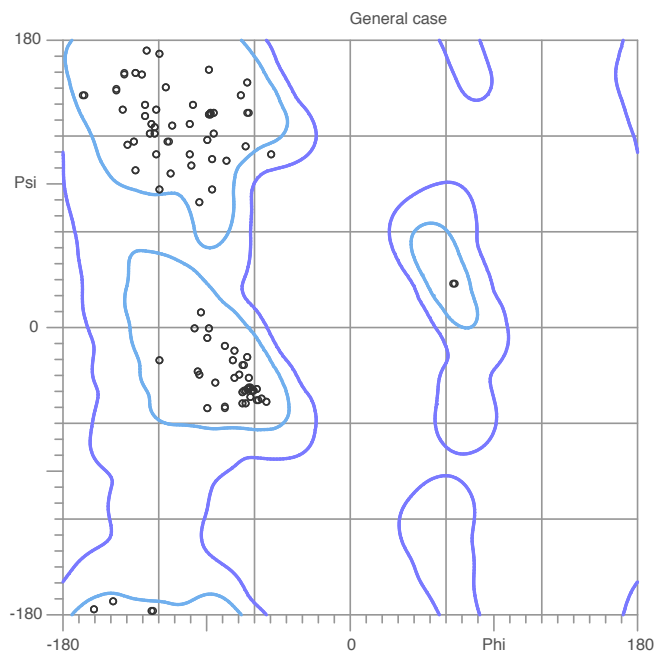
There were no outliers.

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MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 12



98.8% (170/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

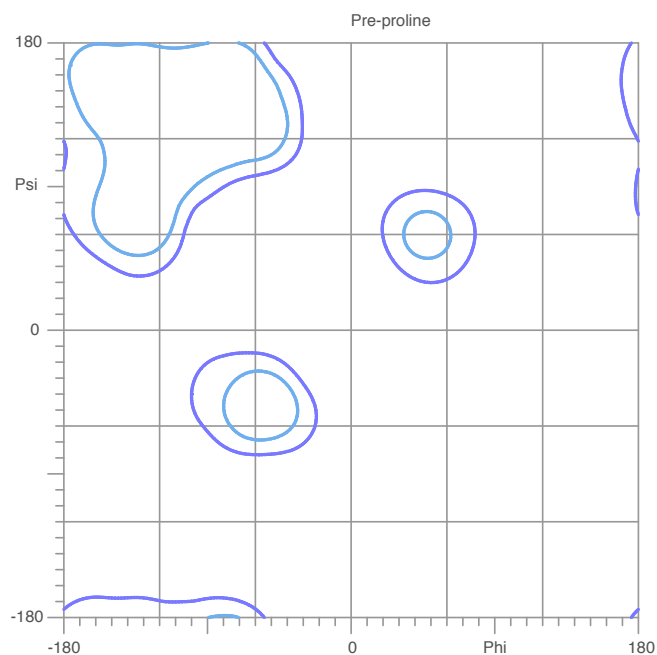
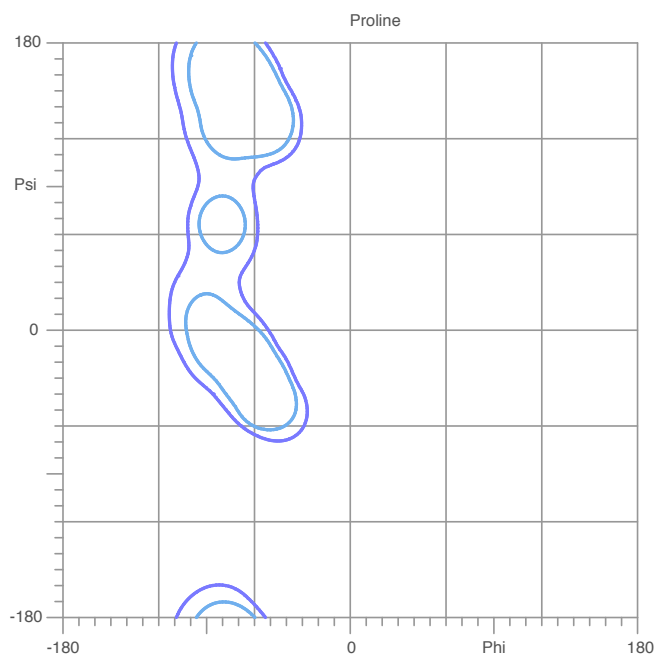
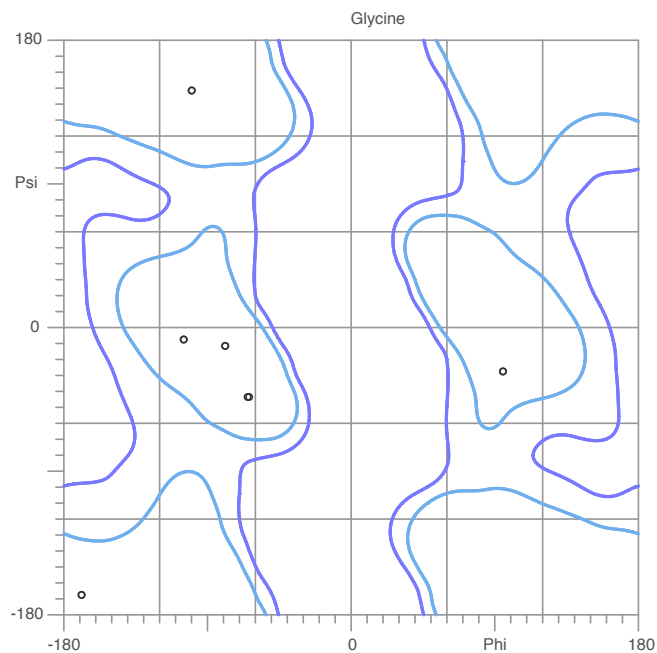
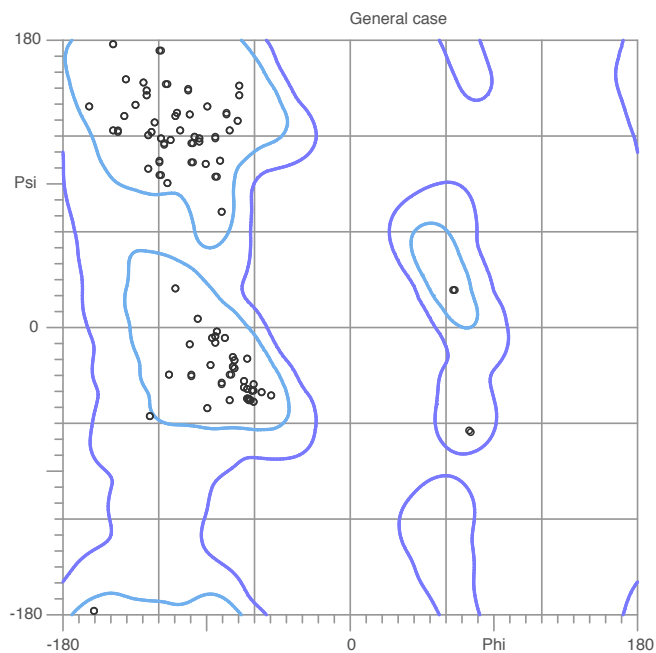
There were no outliers.

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

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MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 13

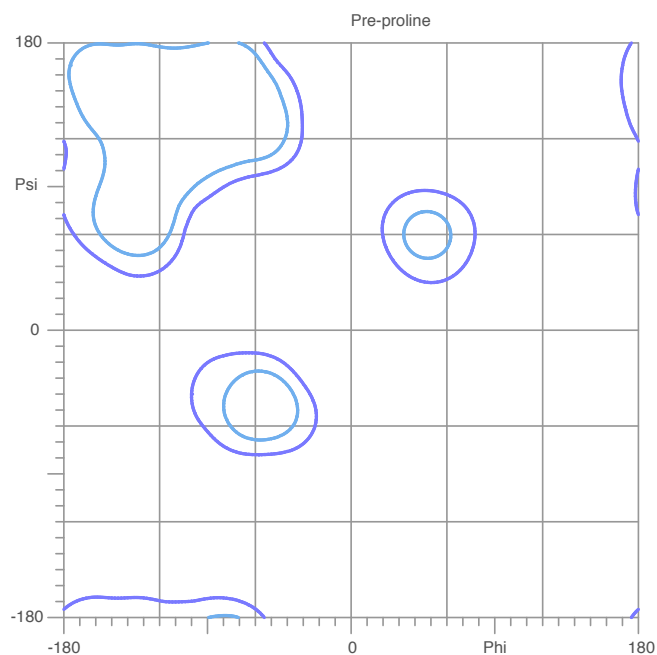
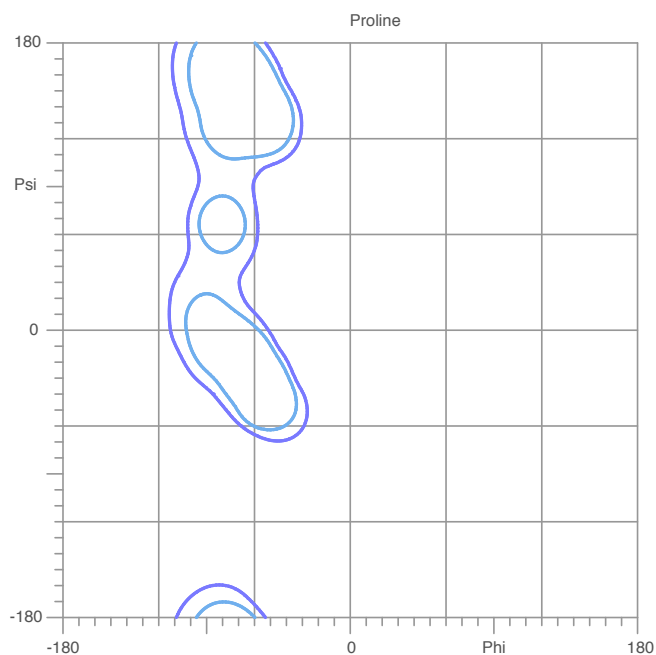
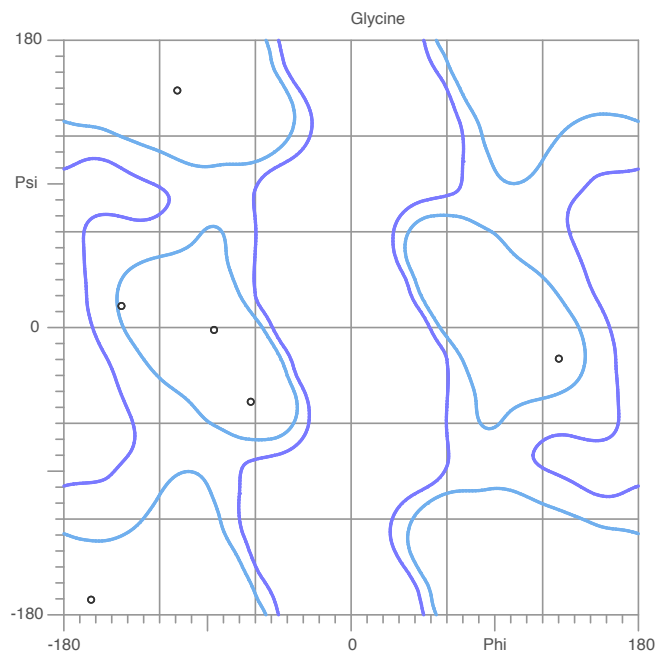
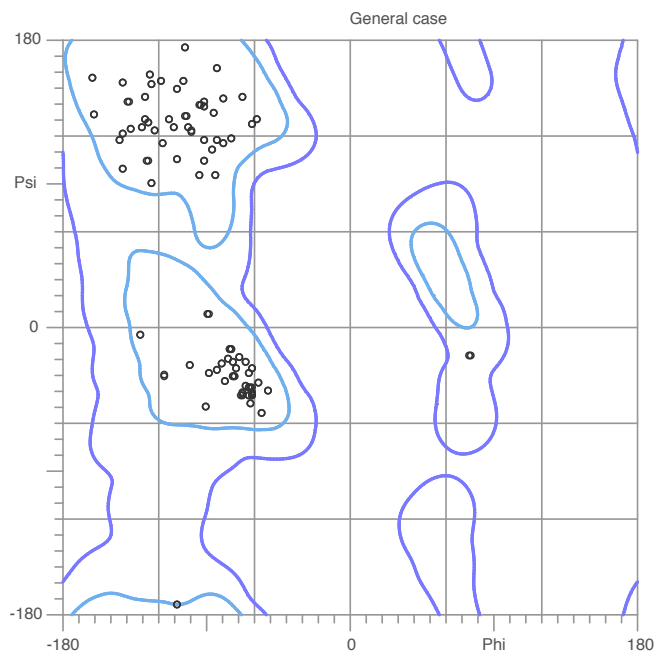


97.7% (168/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 14



97.7% (168/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

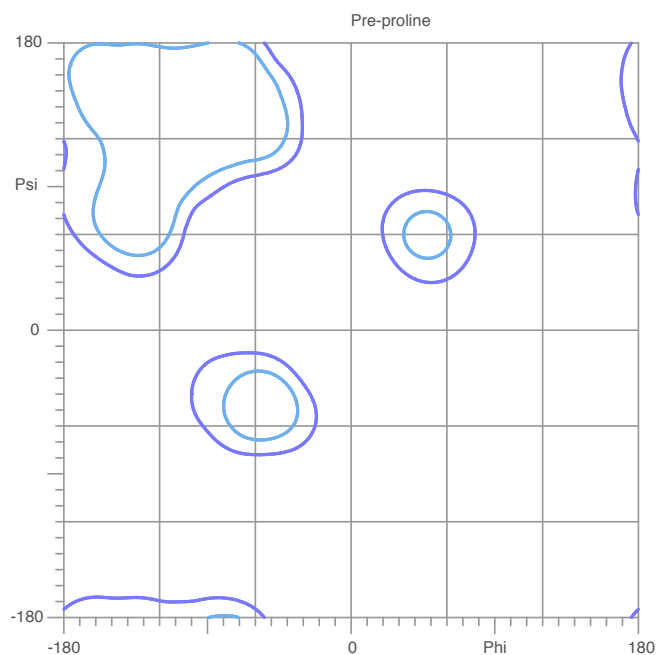
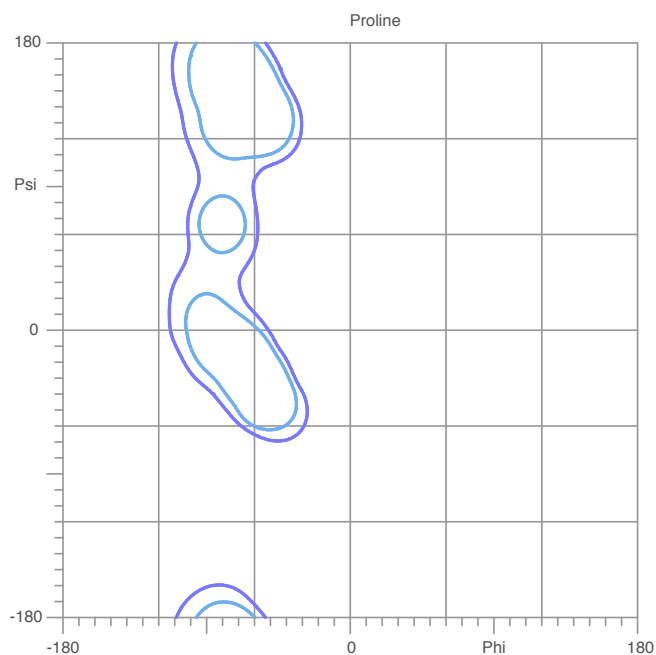
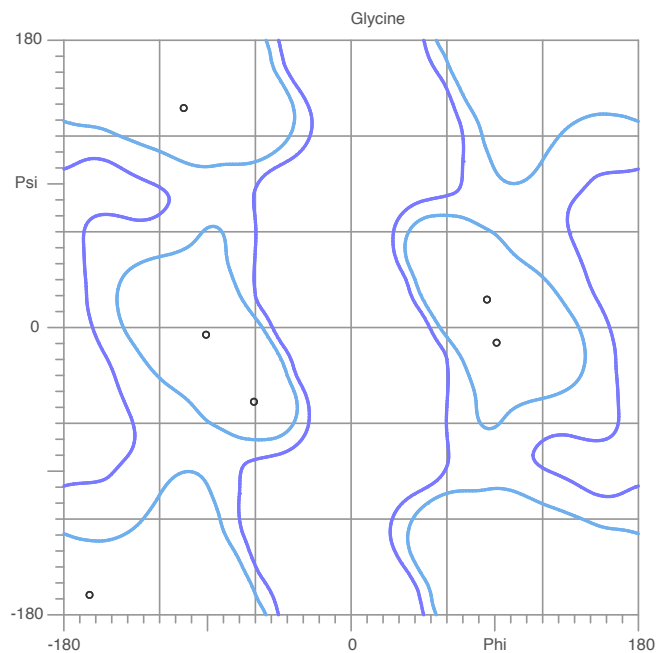
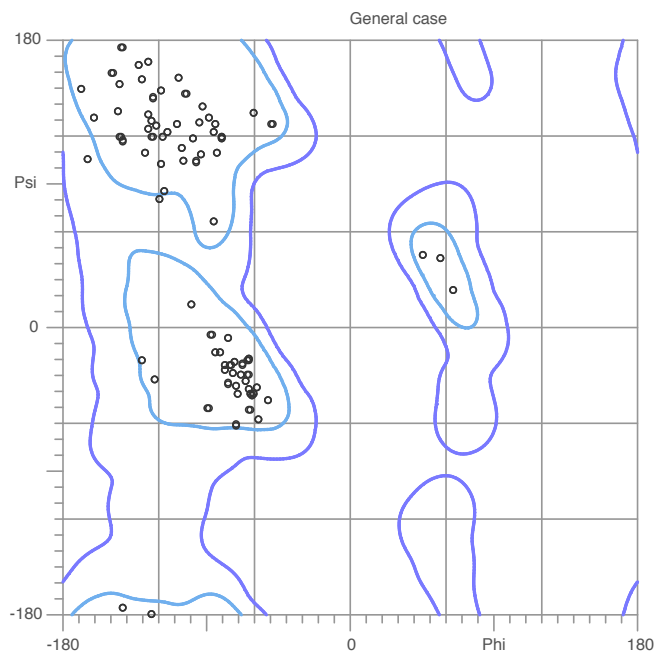
There were no outliers.

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

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MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 15

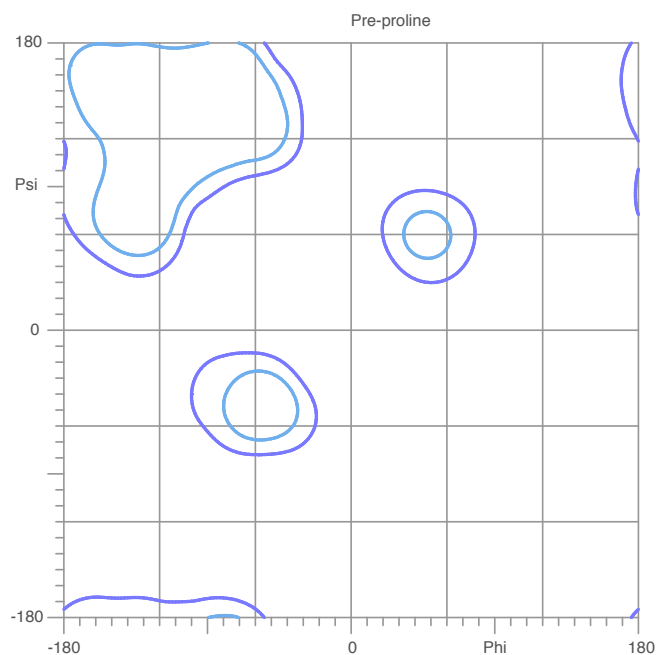
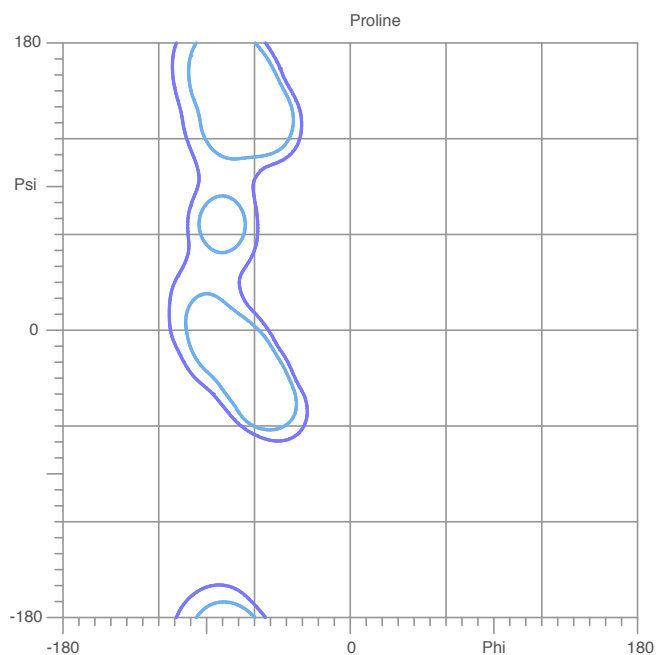
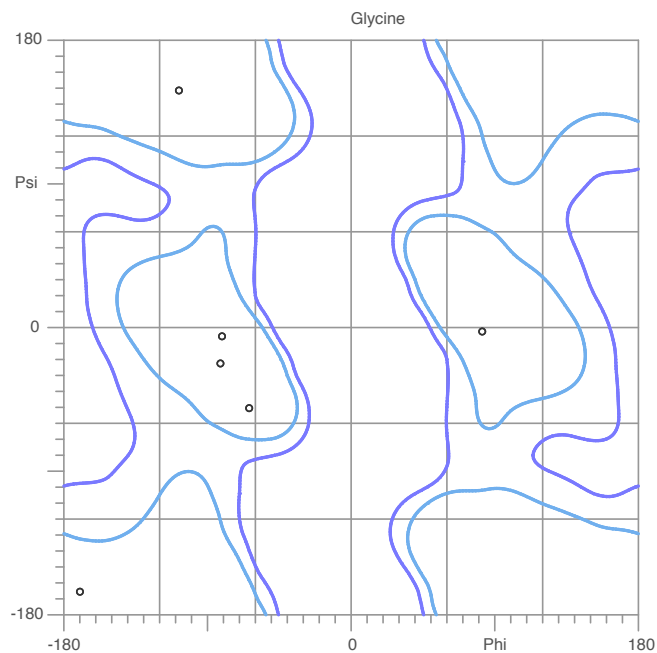
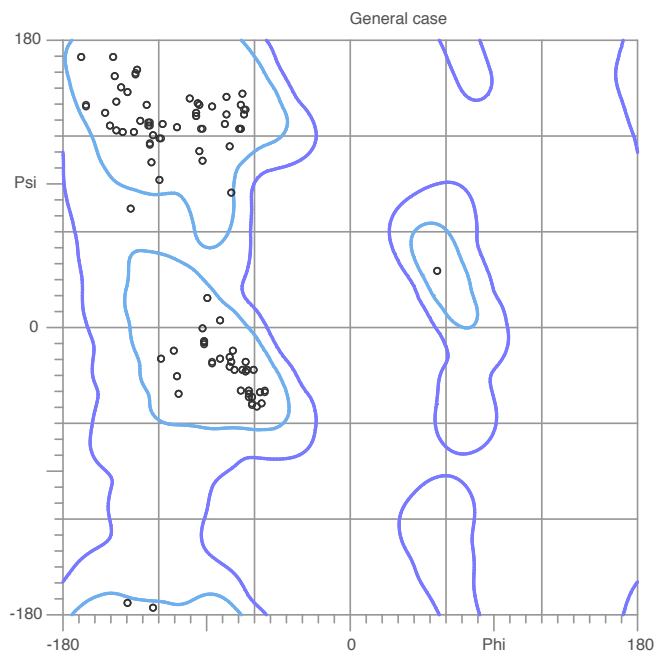


97.7% (168/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 16



98.8% (170/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

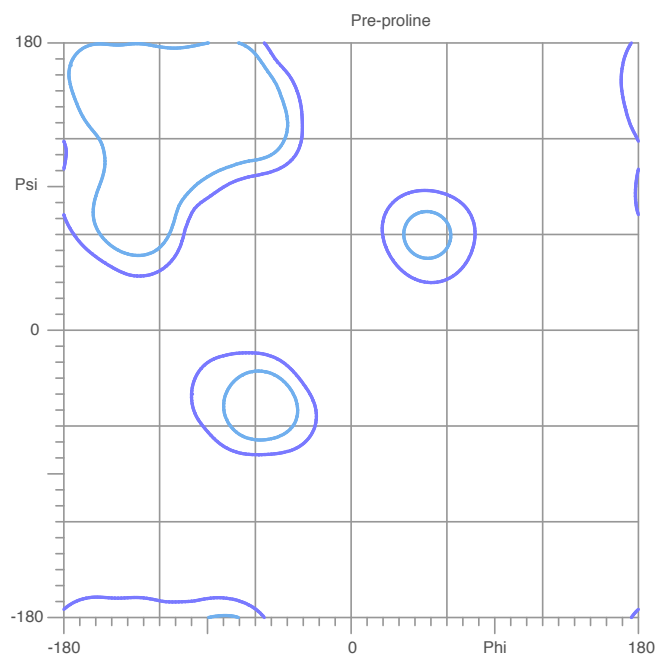
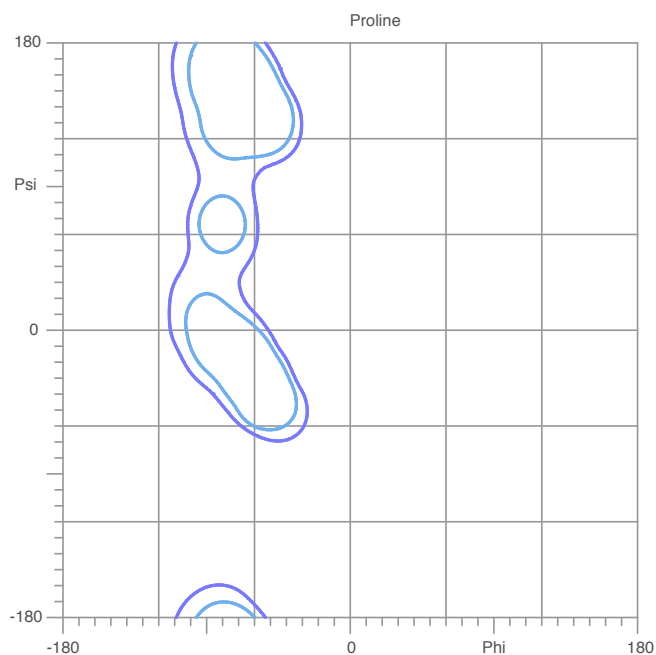
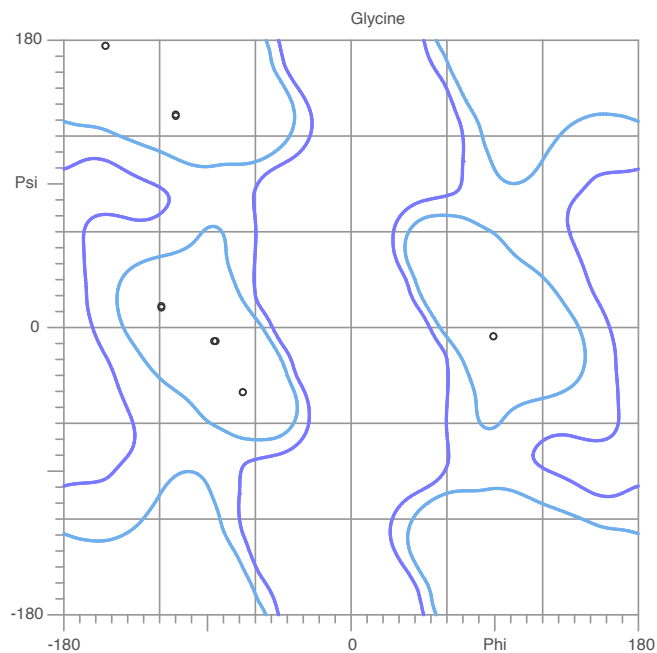
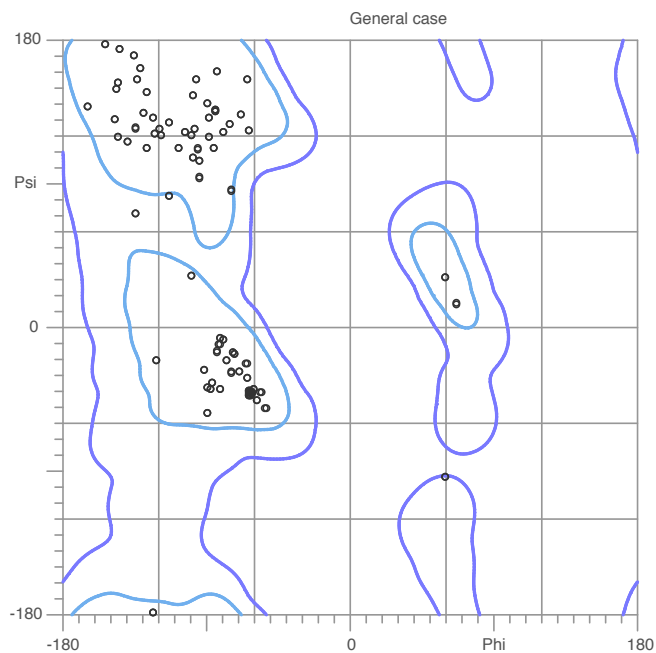
There were no outliers.

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

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MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 17



96.5% (166/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

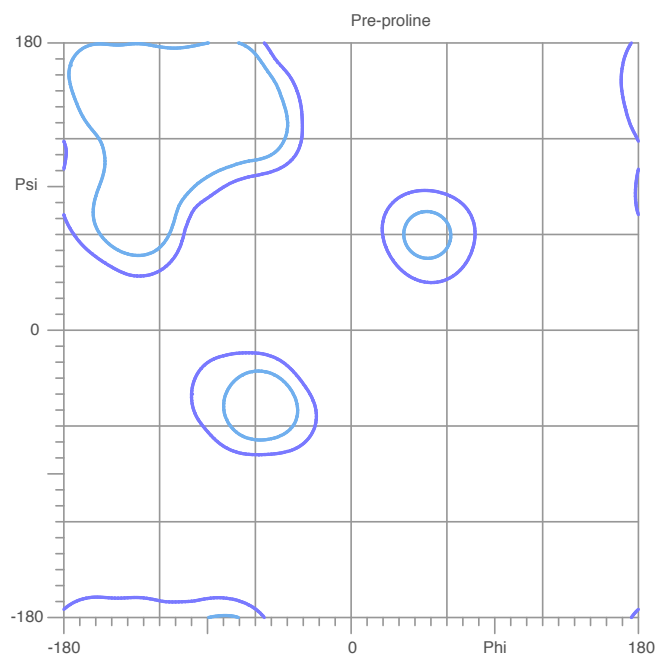
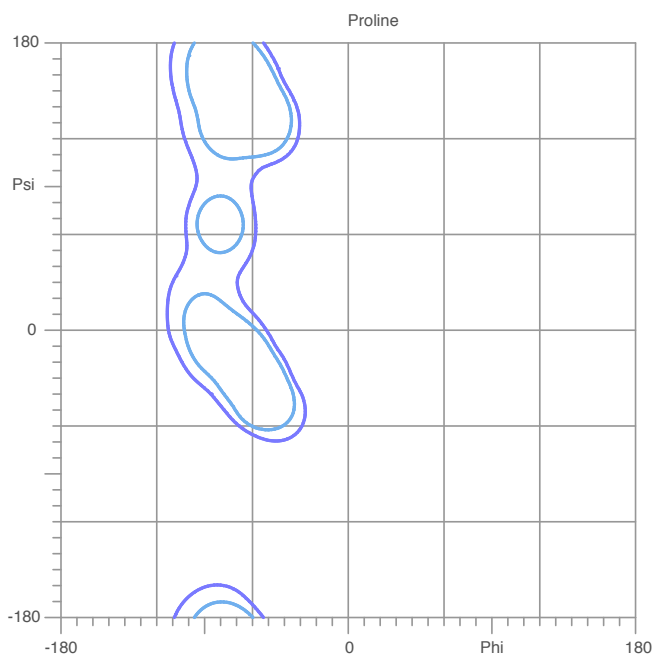
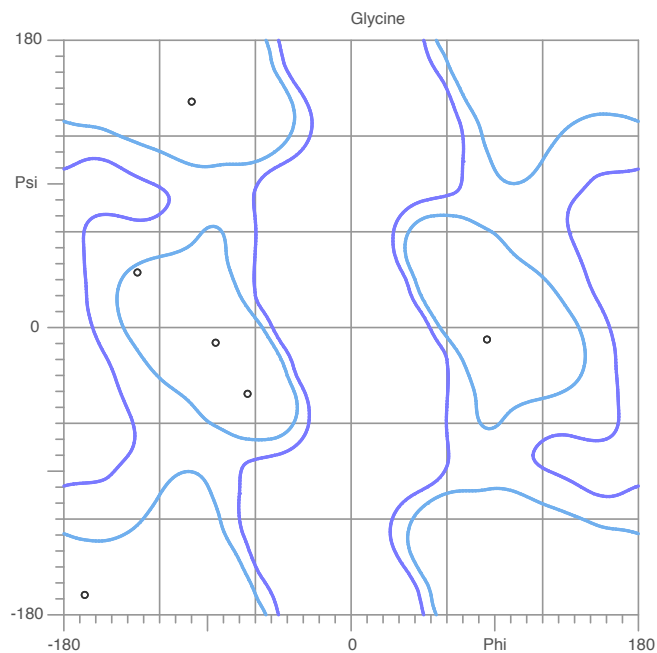
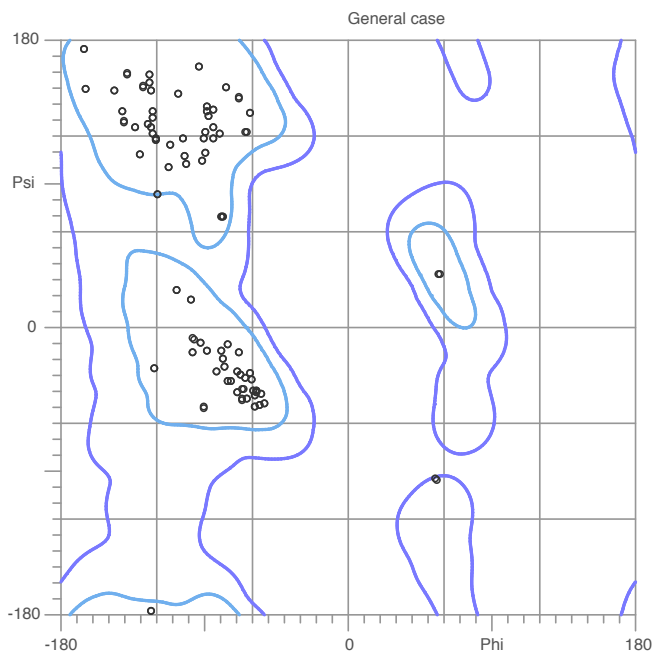
There were no outliers.

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

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

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 18



98.8% (170/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

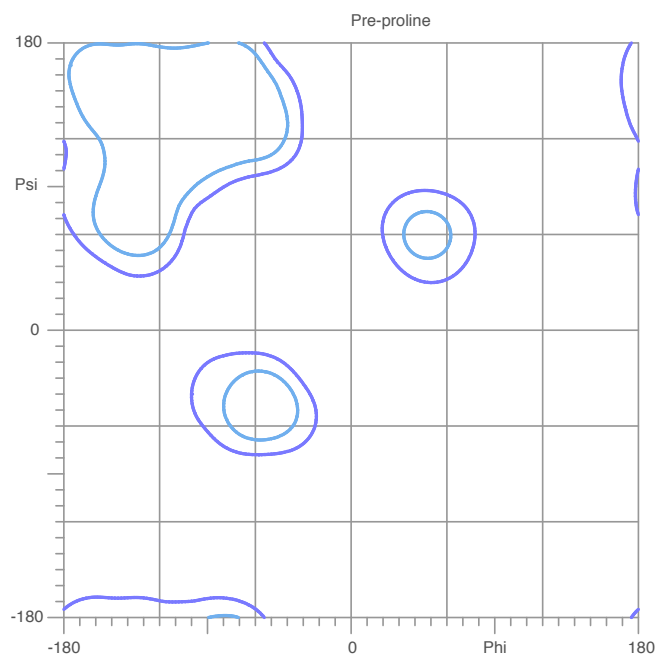
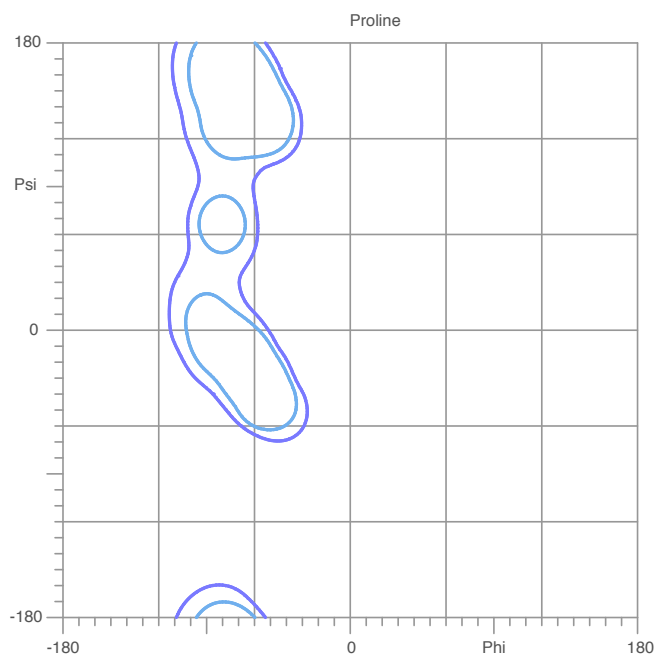
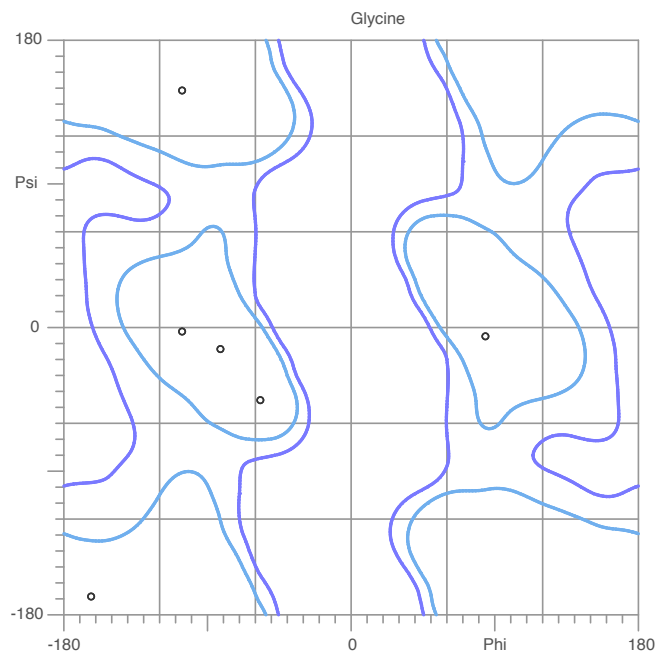
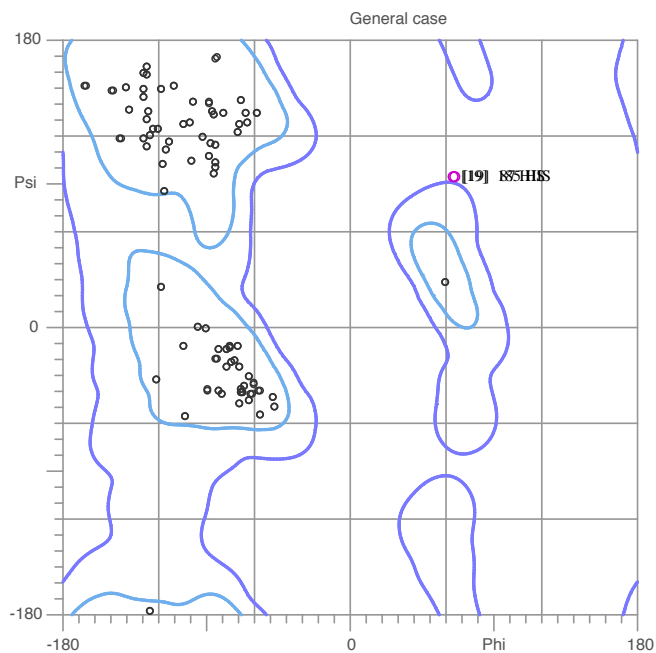
There were no outliers.

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

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

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 19



98.8% (170/172) of all residues were in favored (98%) regions.
98.8% (170/172) of all residues were in allowed (>99.8%) regions.

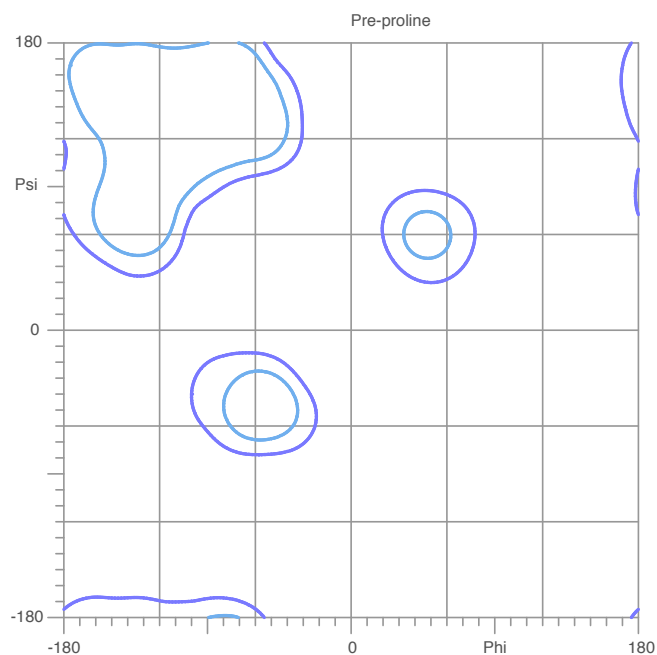
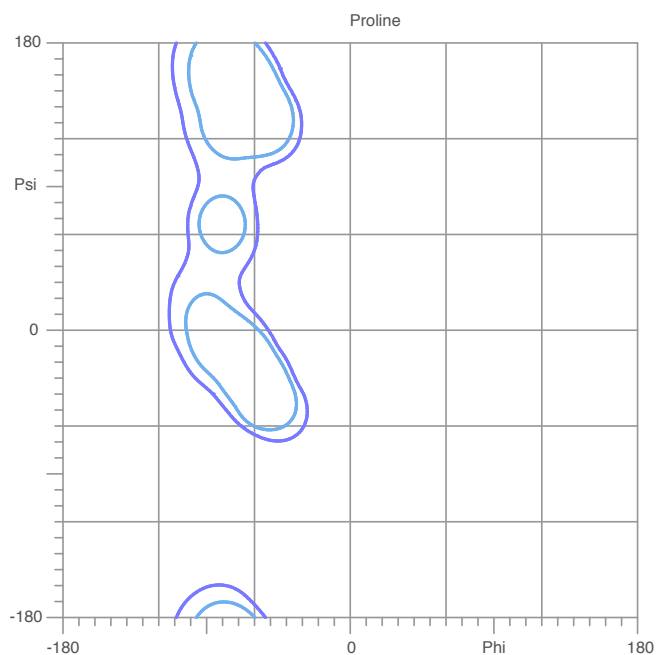
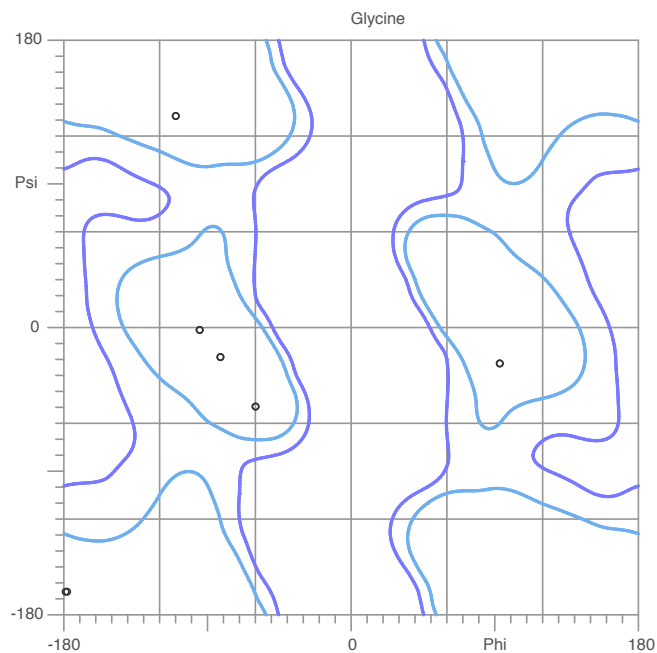
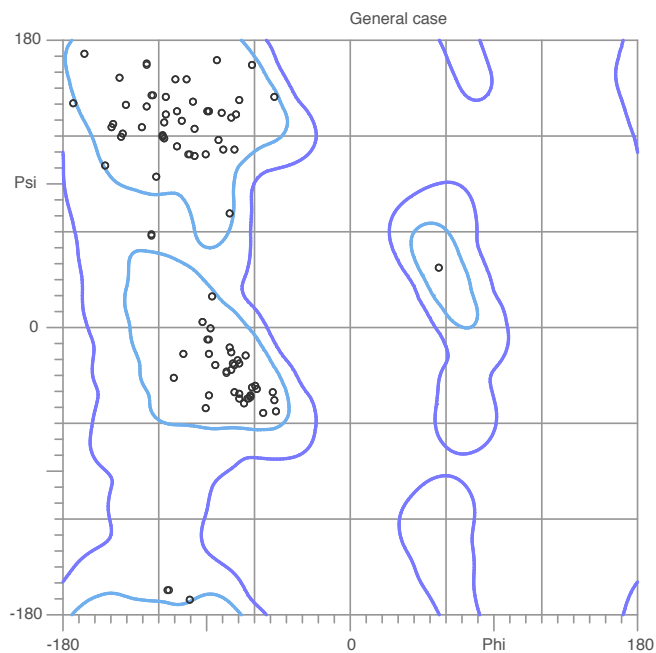
There were 2 outliers (phi, psi):

[19] 87 HIS (65.0, 95.0)

[19] 185 HIS (65.1, 95.0)

MolProbity Ramachandran analysis

CTR148A_R3_em_bcr3.pdb, model 20



95.3% (164/172) of all residues were in favored (98%) regions.
100.0% (172/172) of all residues were in allowed (>99.8%) regions.

There were no outliers.