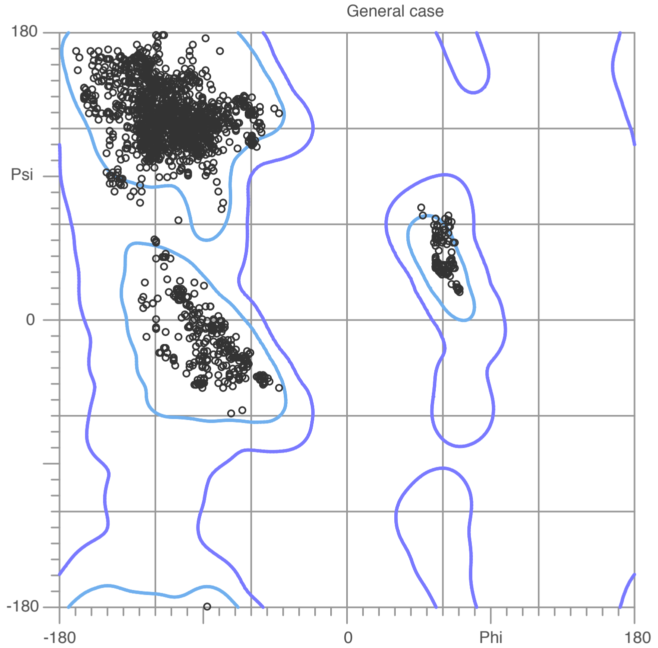
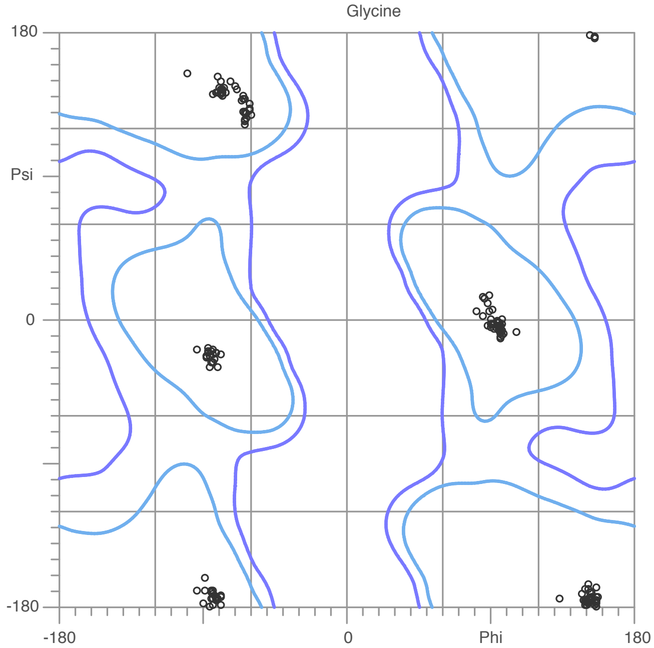
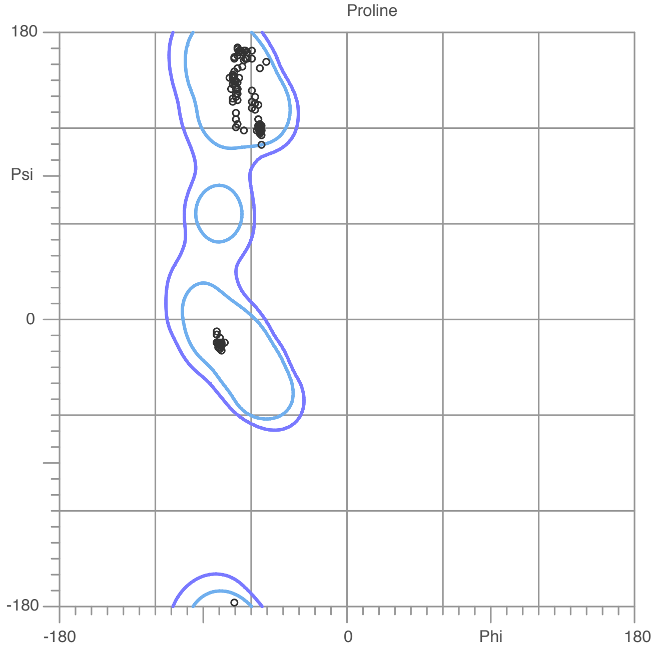
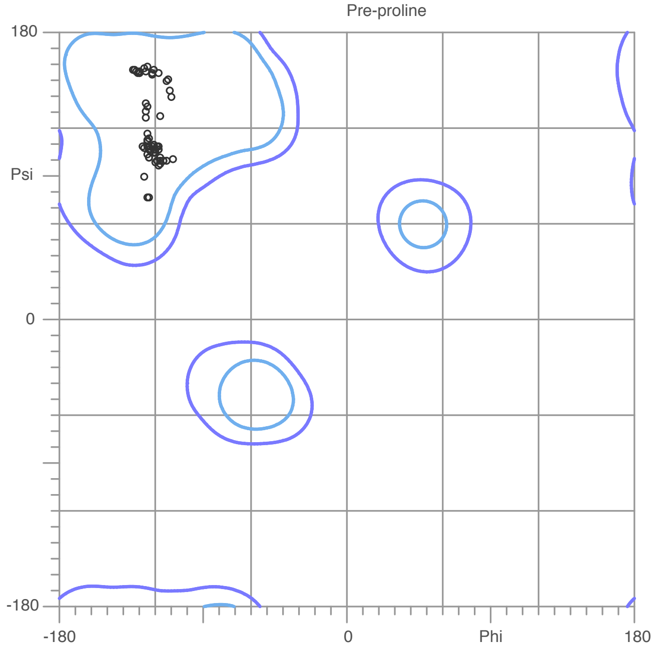
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, all models









98.3% (2084/2120) of all residues were in favored (98%) regions.
100.0% (2120/2120) of all residues were in allowed (>99.8%) regions.

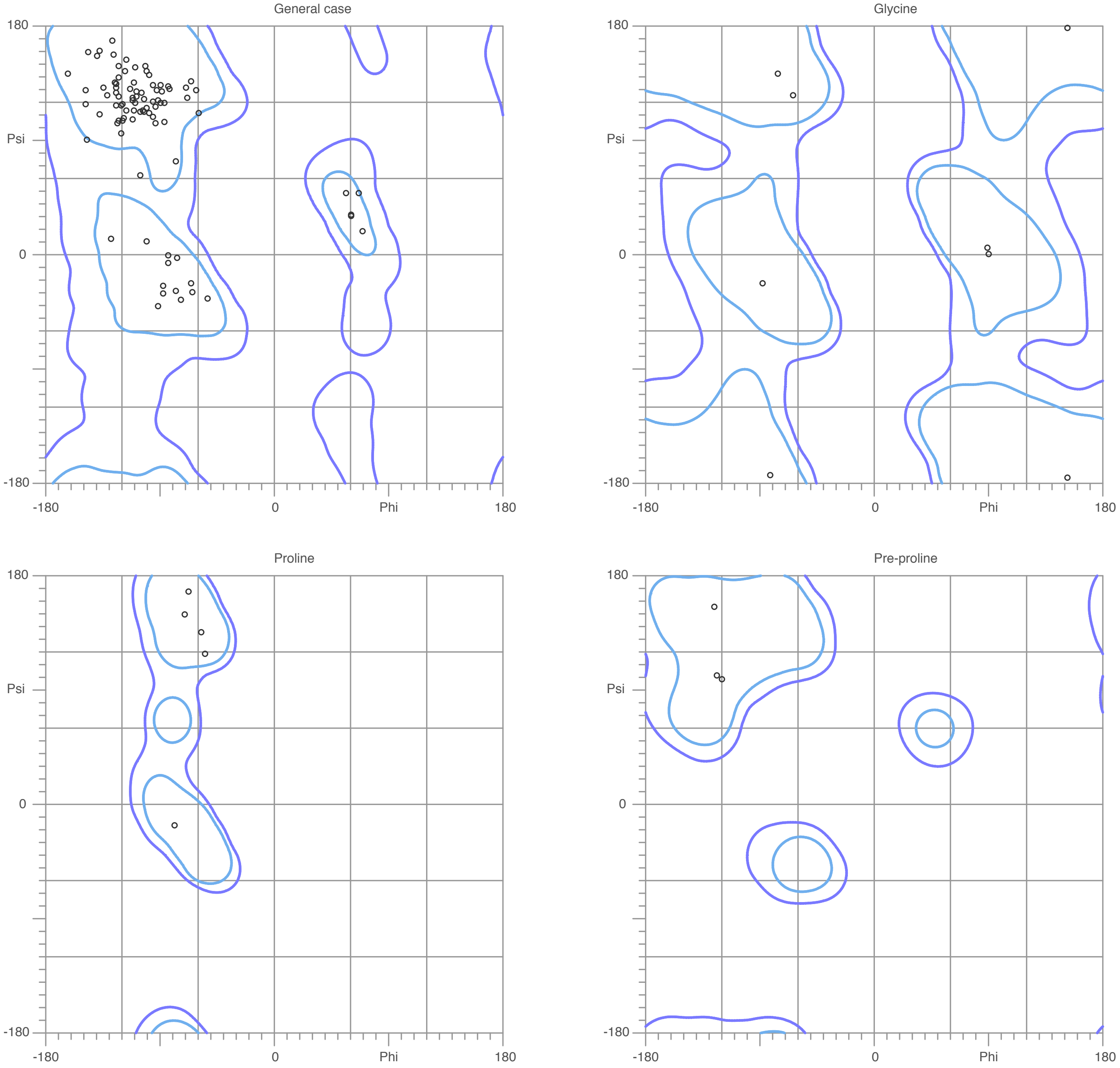
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 1



98.1% (104/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

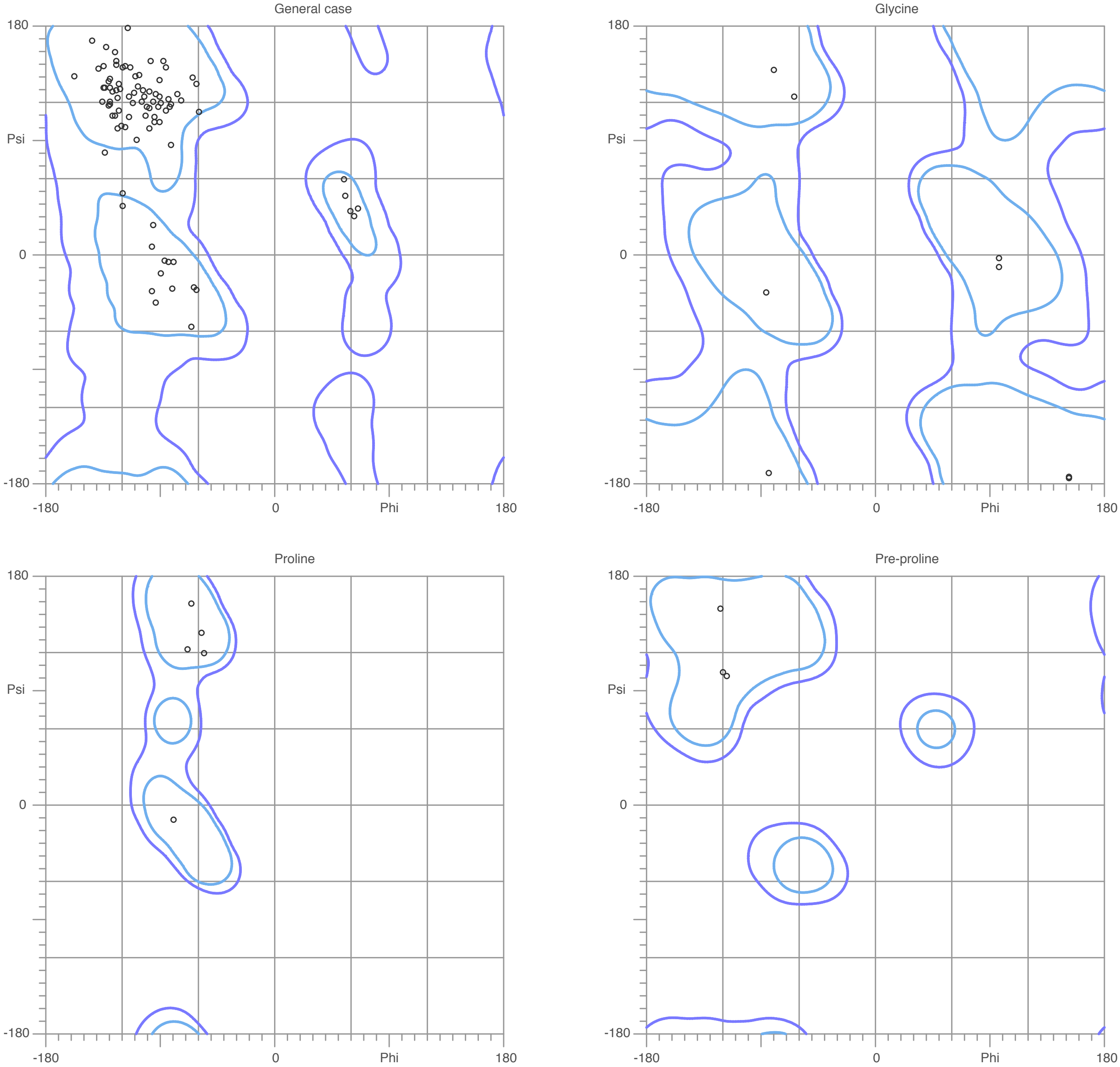
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 2



98.1% (104/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

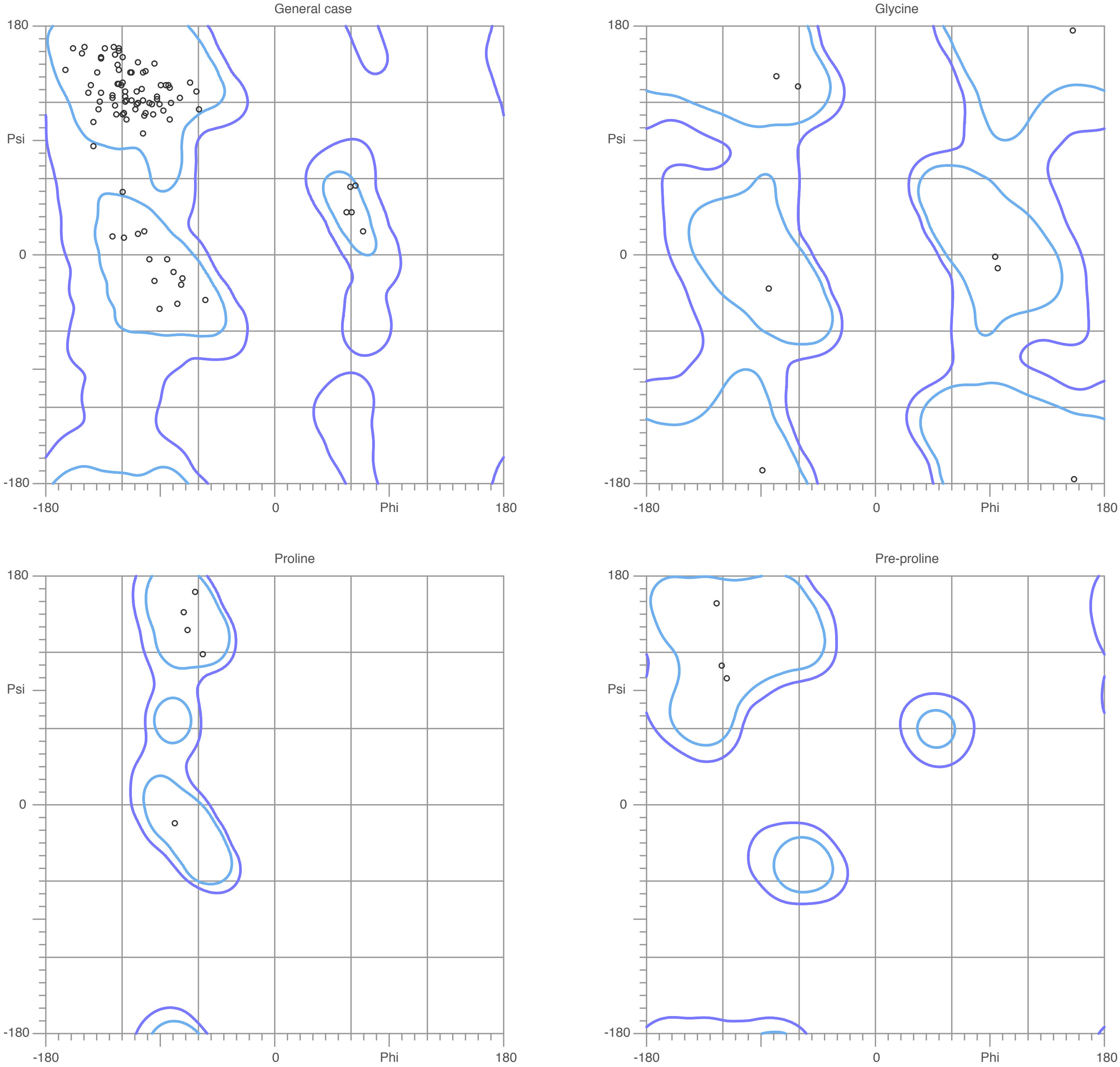
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 3

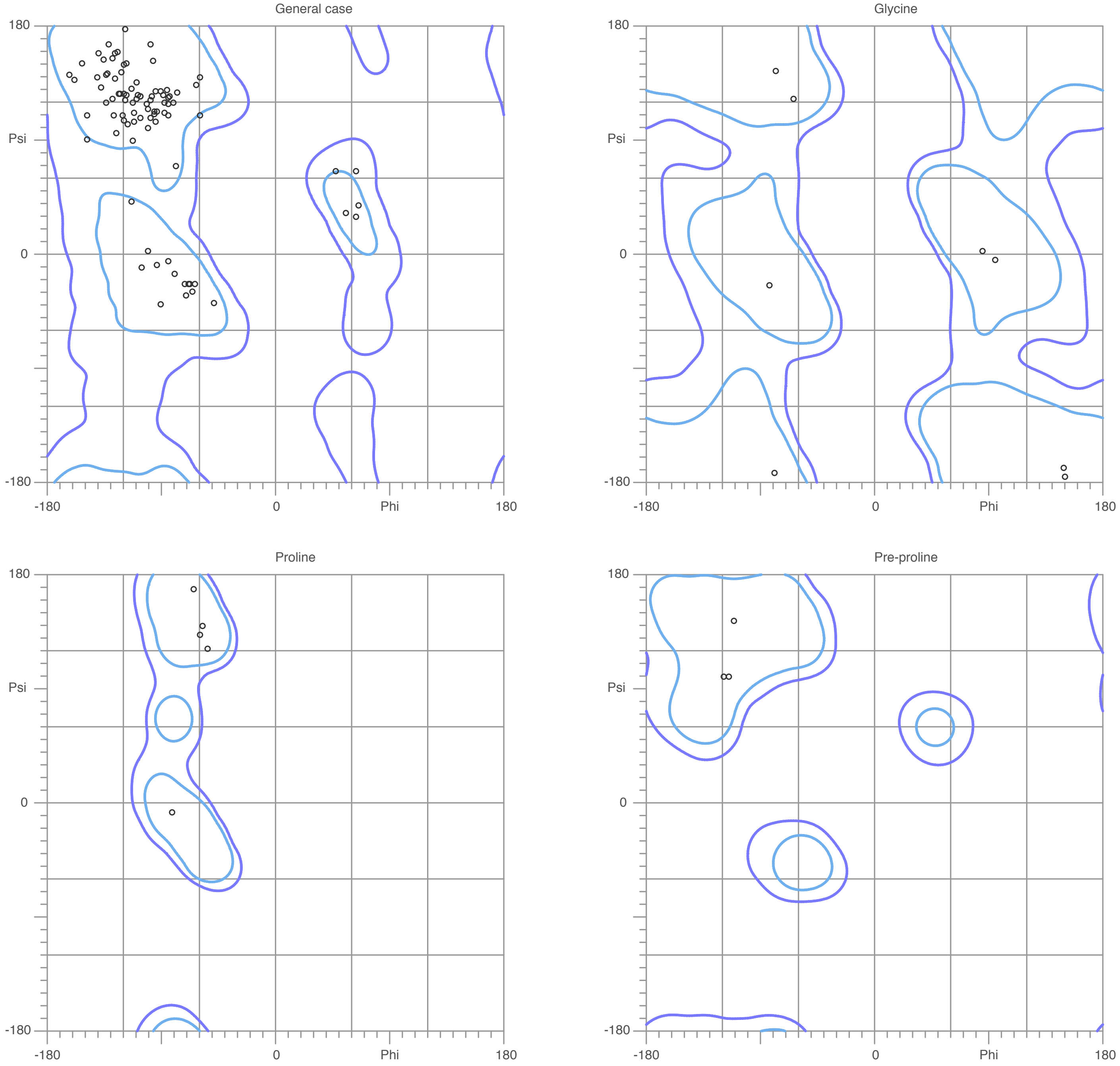


97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 4



96.2% (102/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

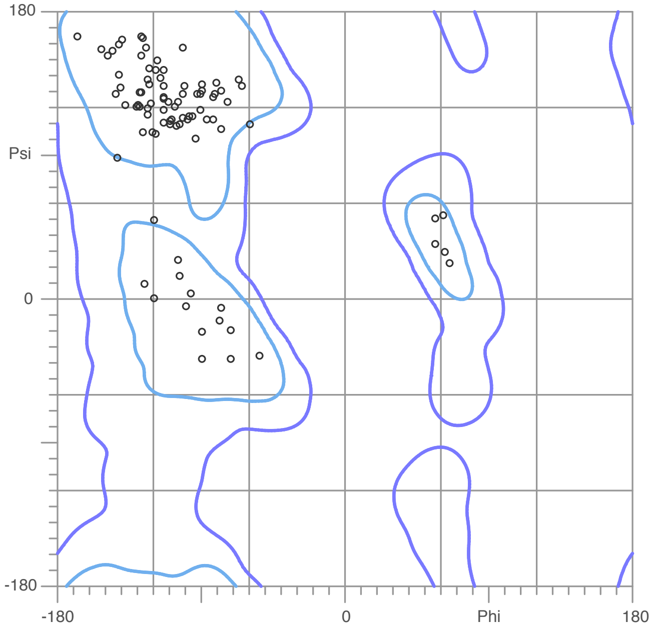
http://kinemage.biochem.duke.edu

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

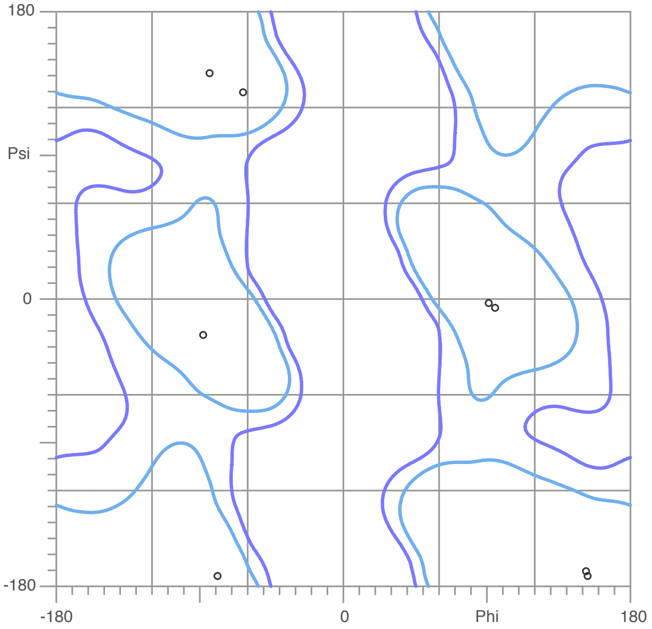
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 5

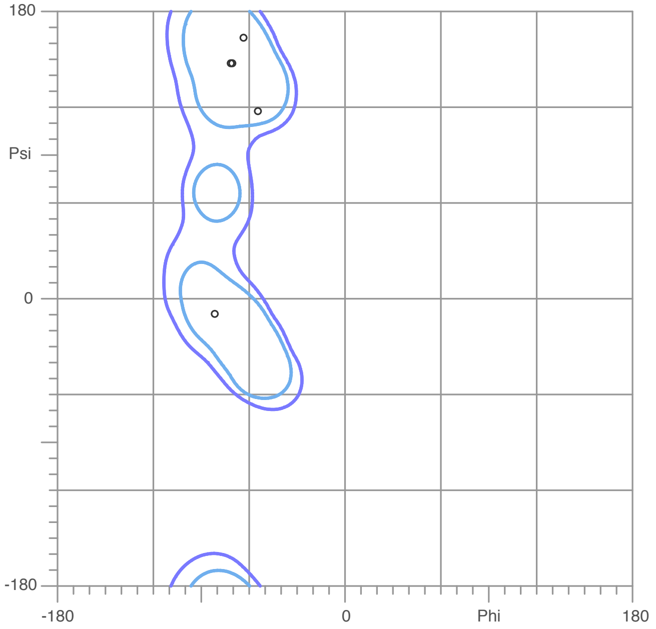
General case



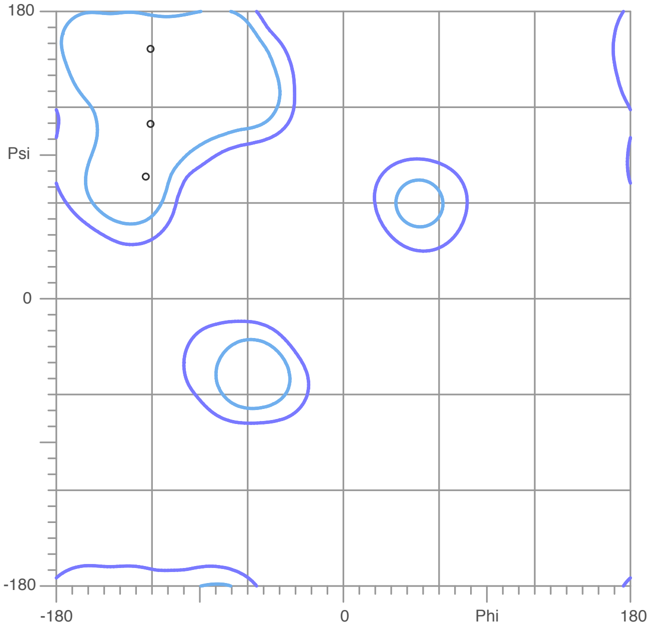
Glycine



Proline



Pre-proline



98.1% (104/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

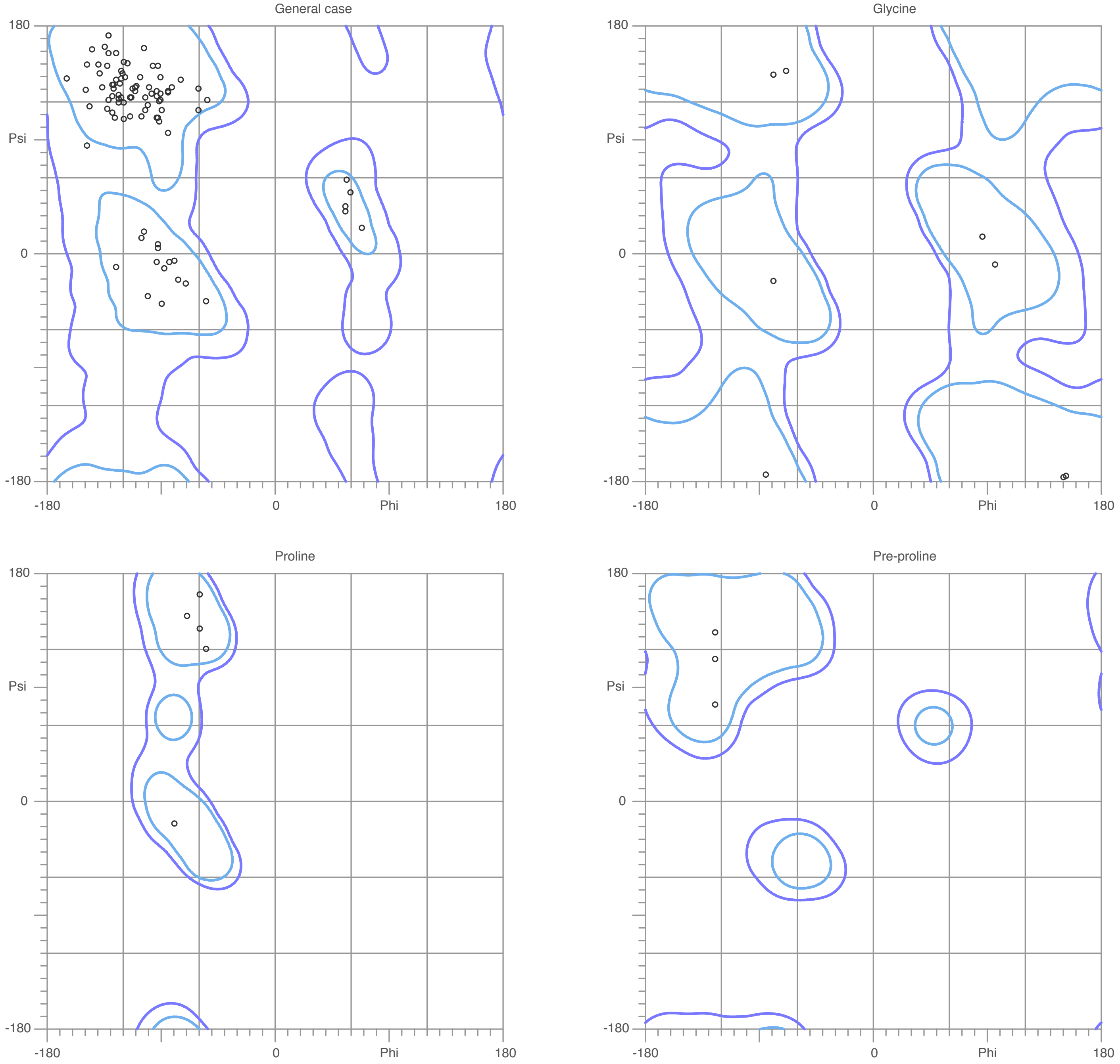
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 6

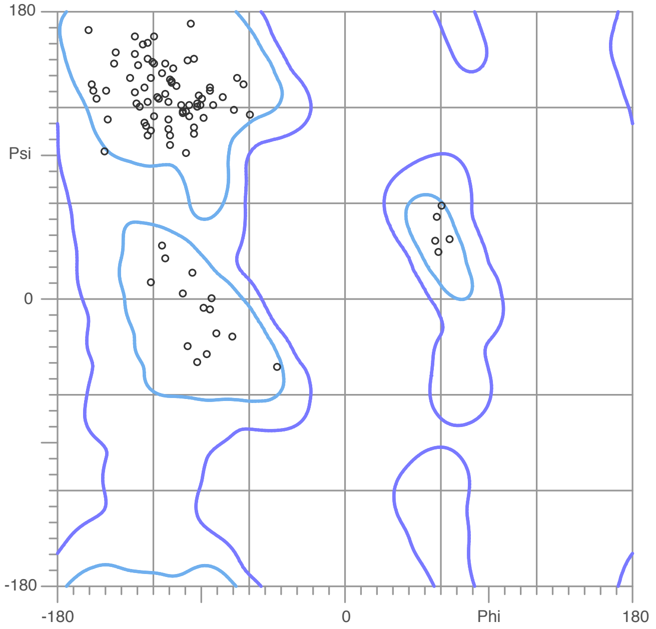


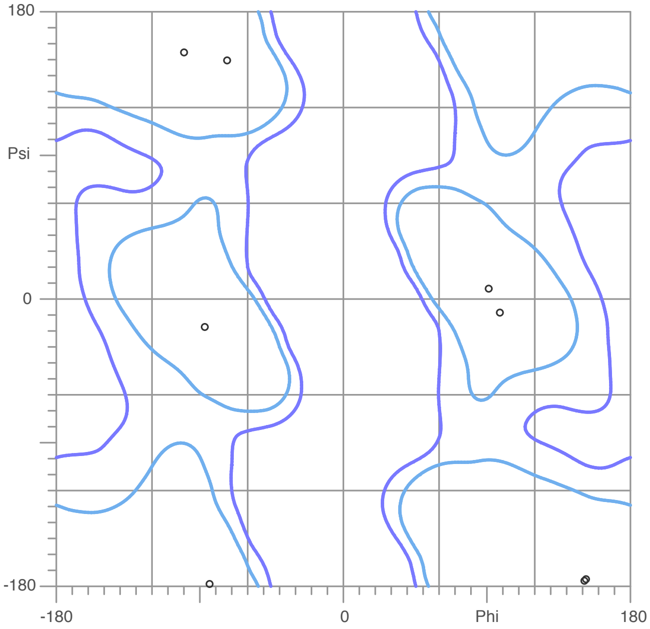
99.1% (105/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

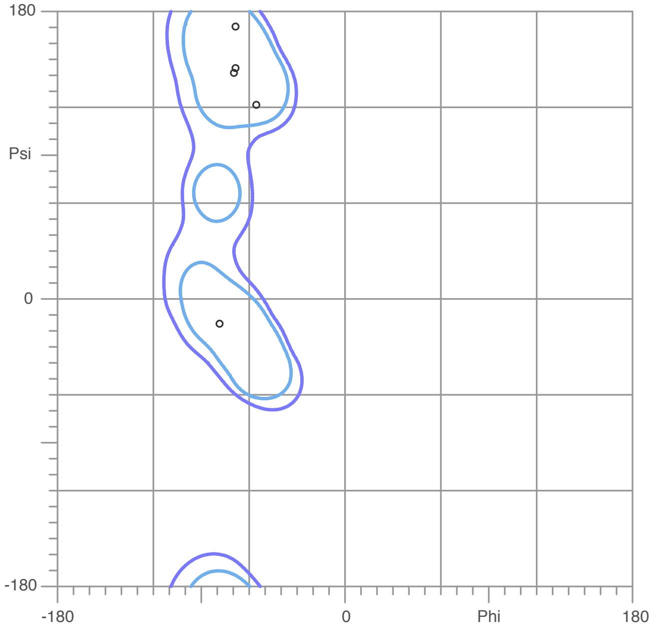
There were no outliers.

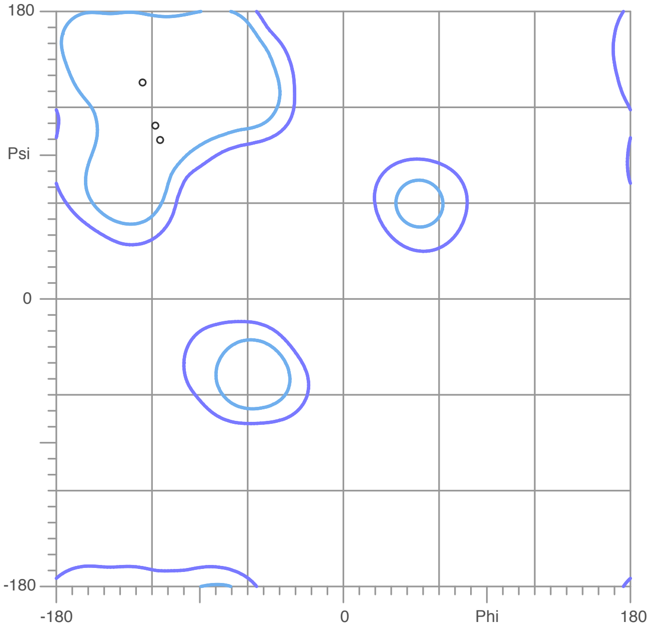
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 7


General case


Glycine


Proline


Pre-proline

99.1% (105/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

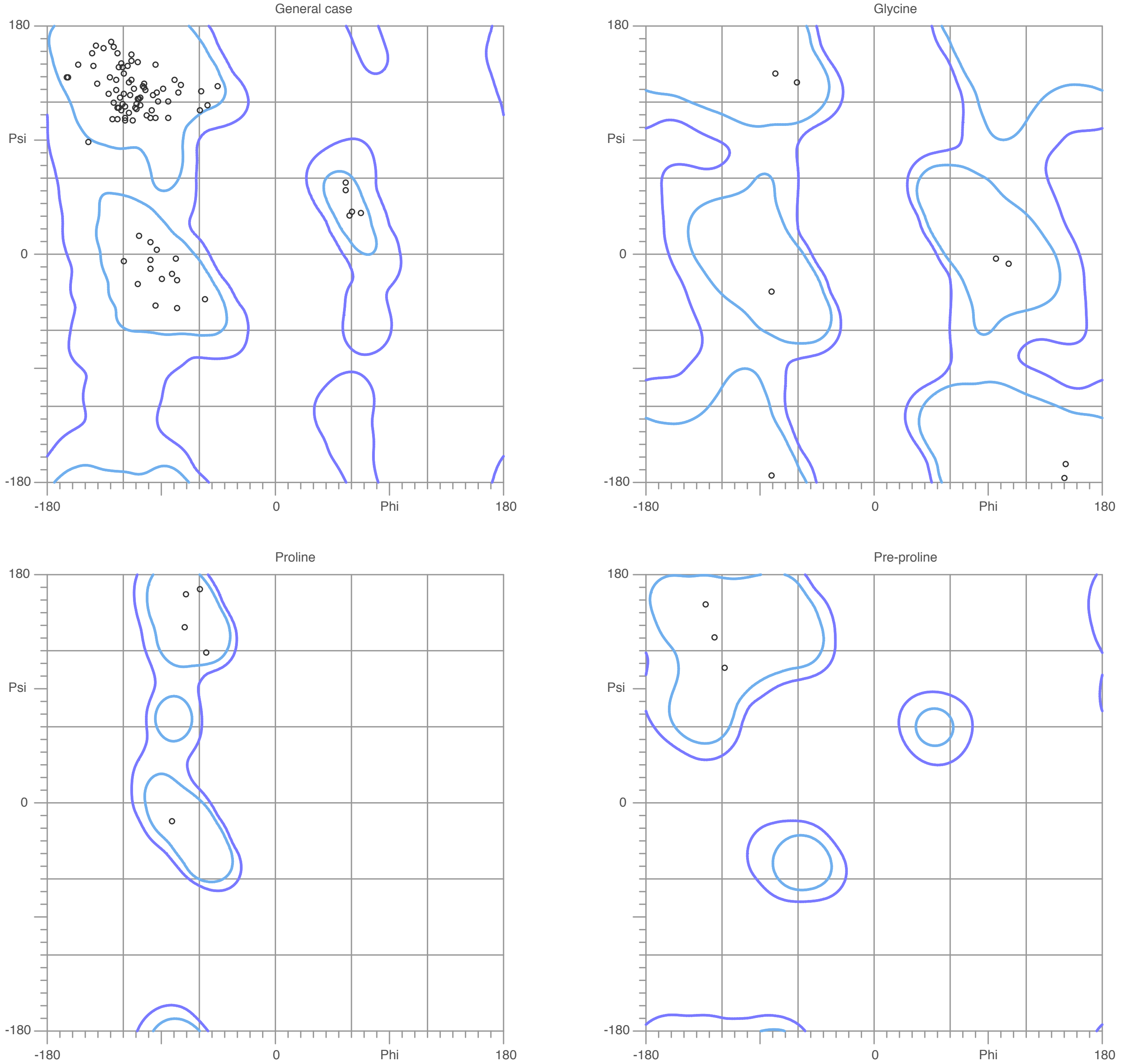
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 8



99.1% (105/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

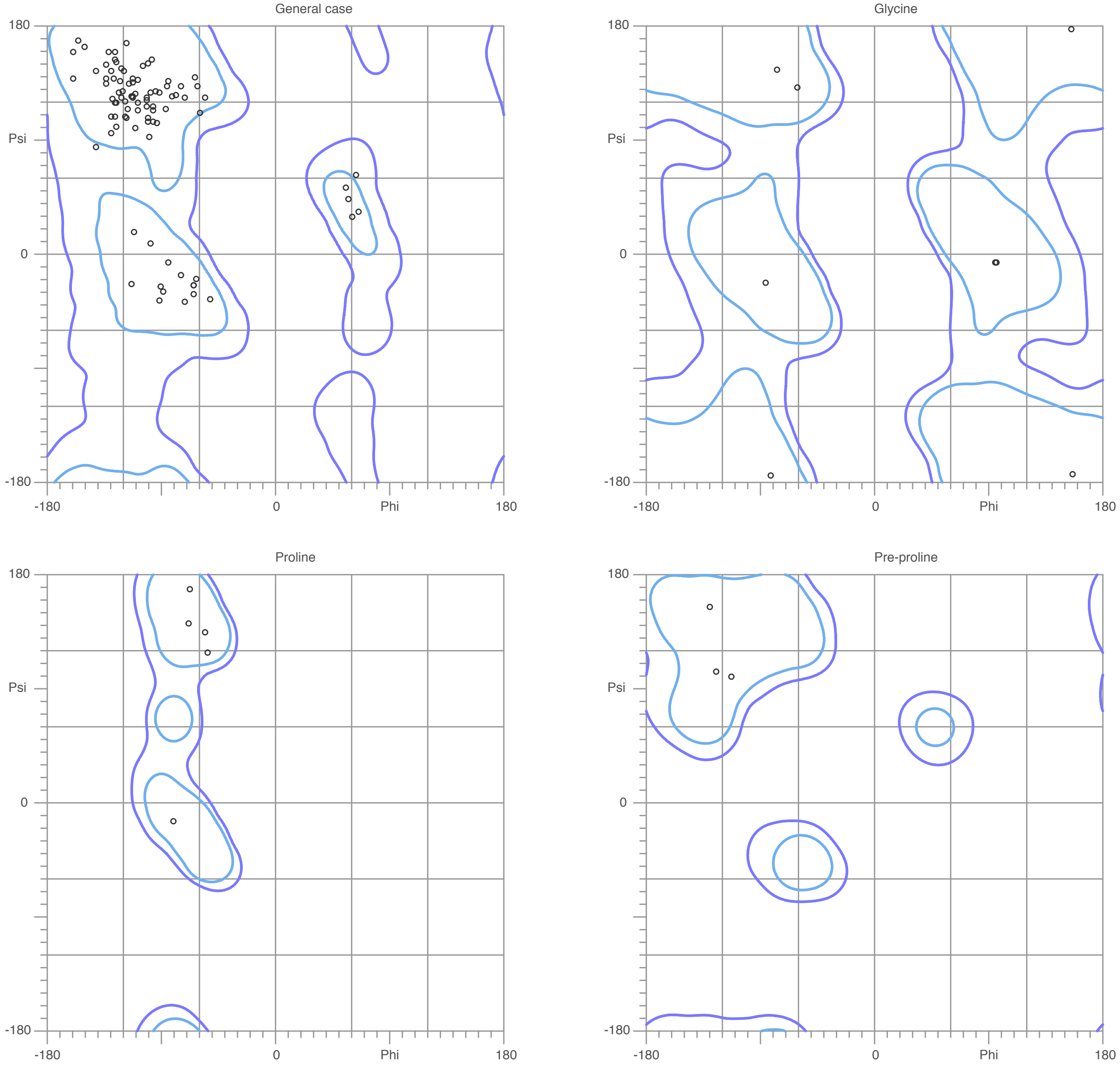
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 9



98.1% (104/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

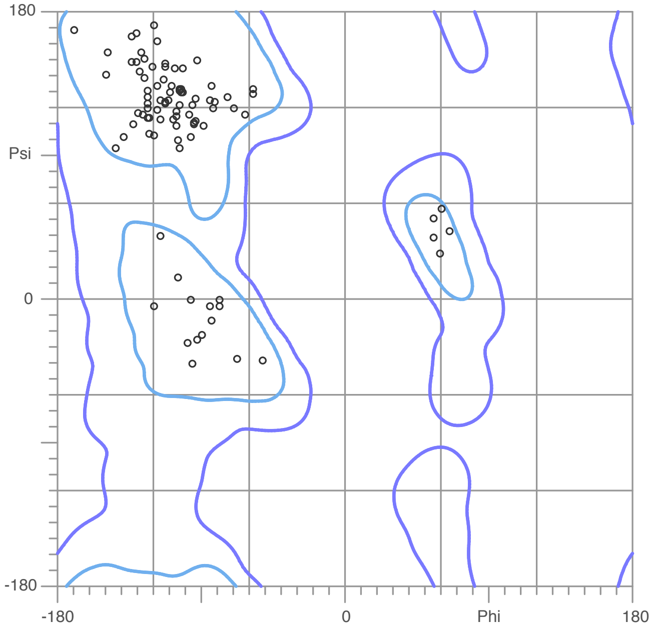
There were no outliers.

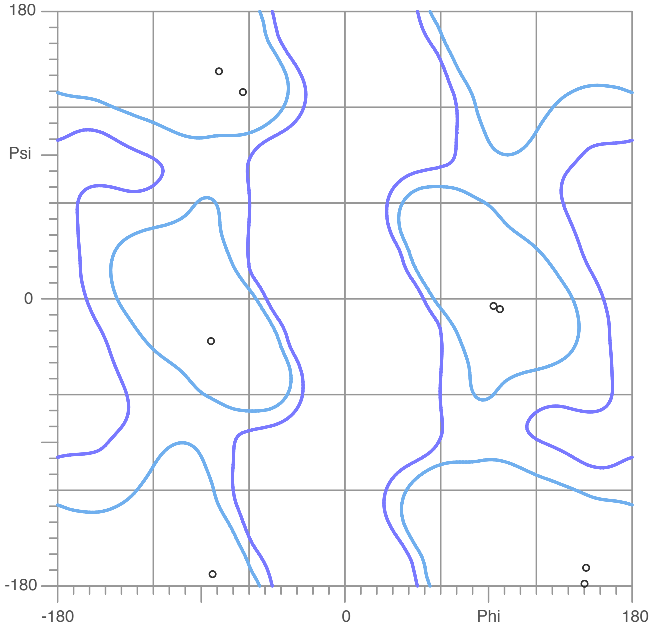
http://kinemage.biochem.duke.edu

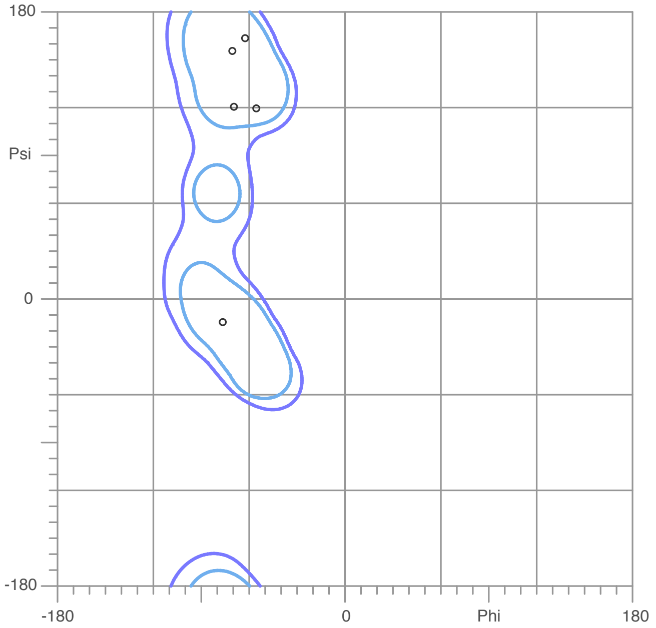
Lovell, Davis, et al. Proteins 50:437 (2003)

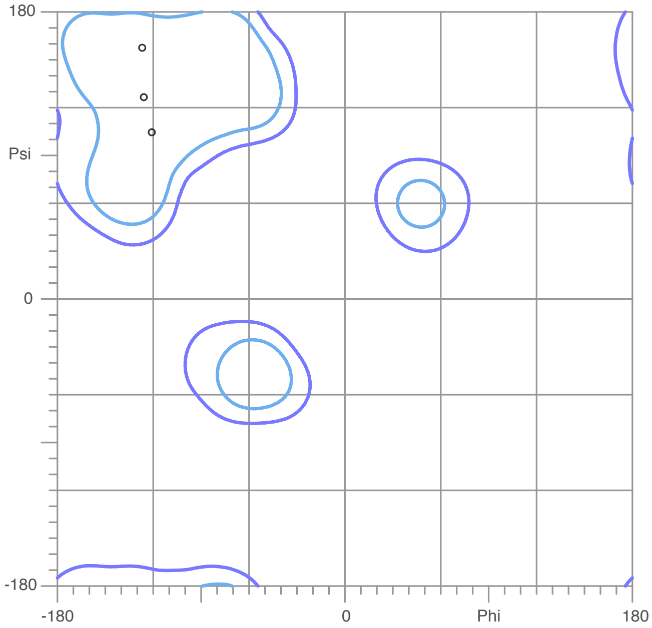
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 10


General case


Glycine


Proline


Pre-proline

100.0% (106/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

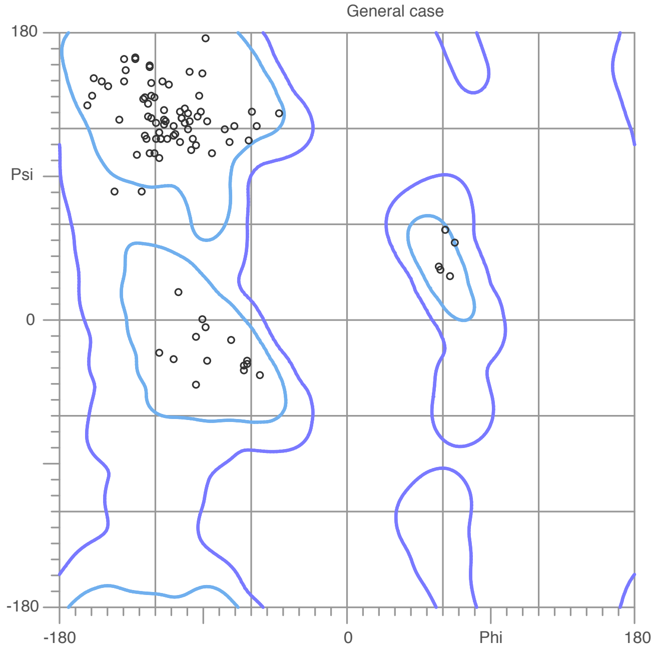
There were no outliers.

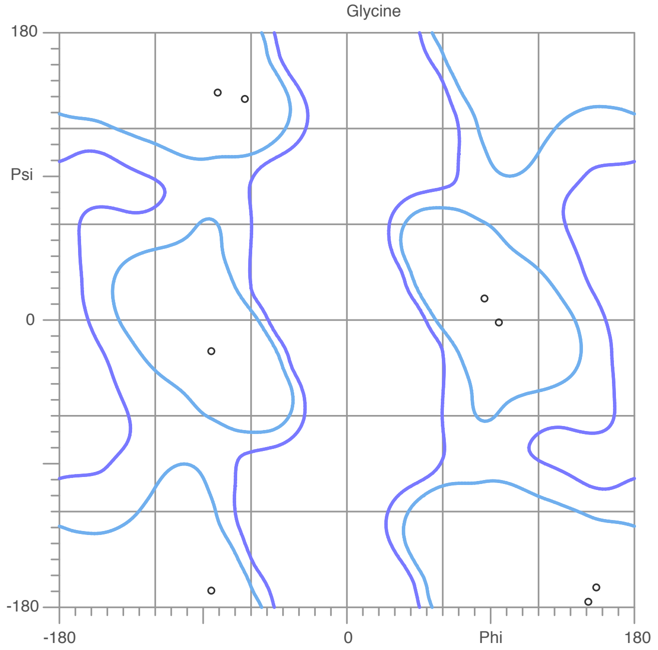
http://kinemage.biochem.duke.edu

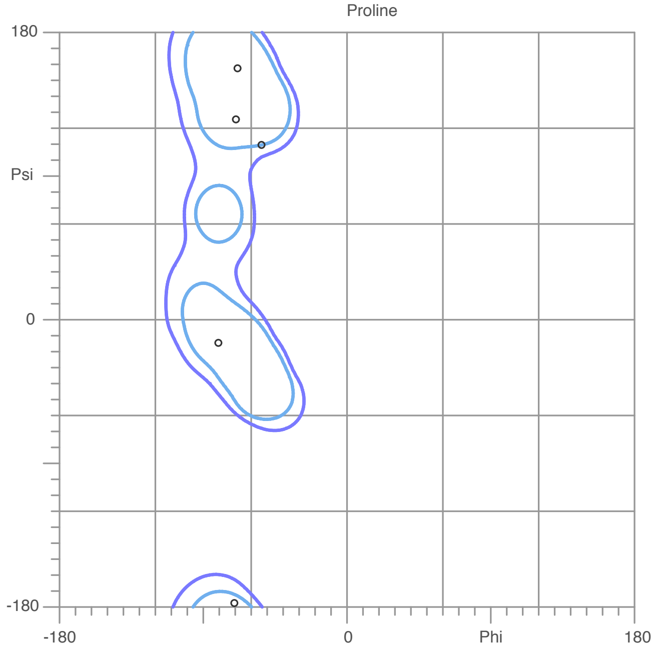
Lovell, Davis, et al. Proteins 50:437 (2003)

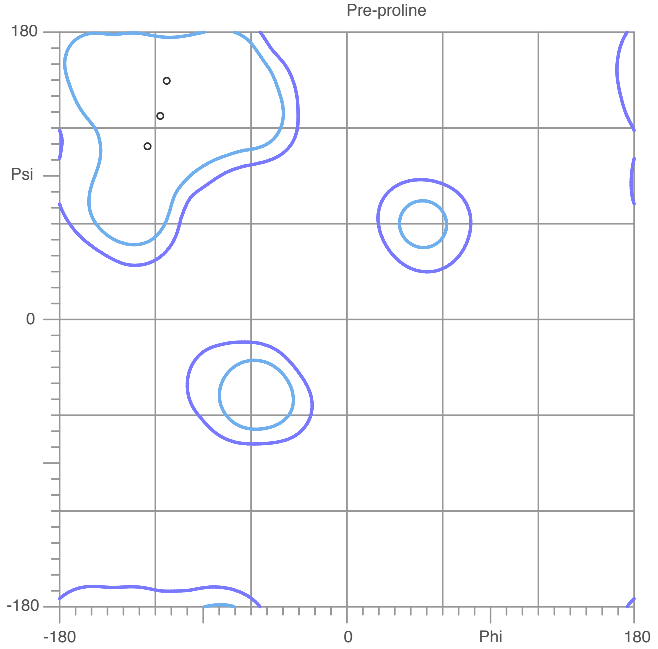
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 11


General case


Glycine


Proline

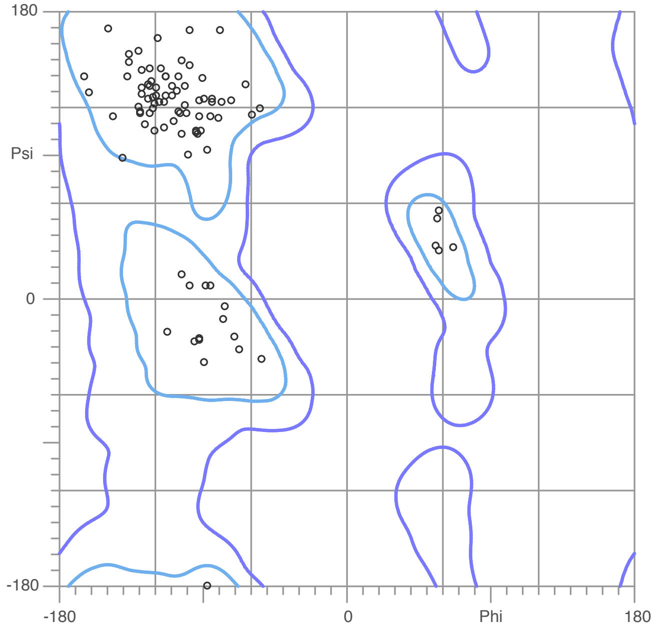

Pre-proline

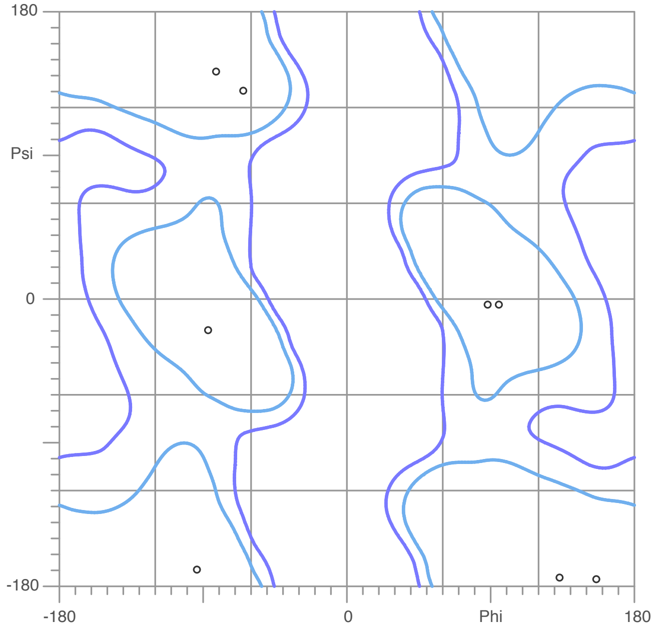
97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

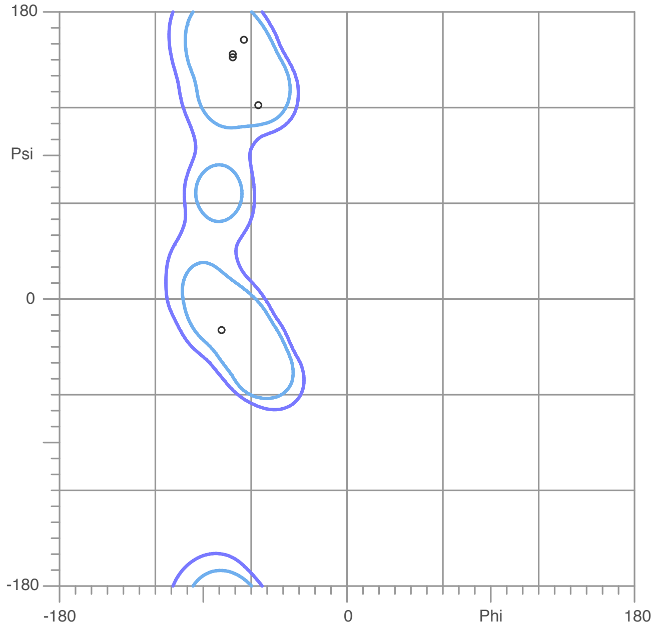
There were no outliers.

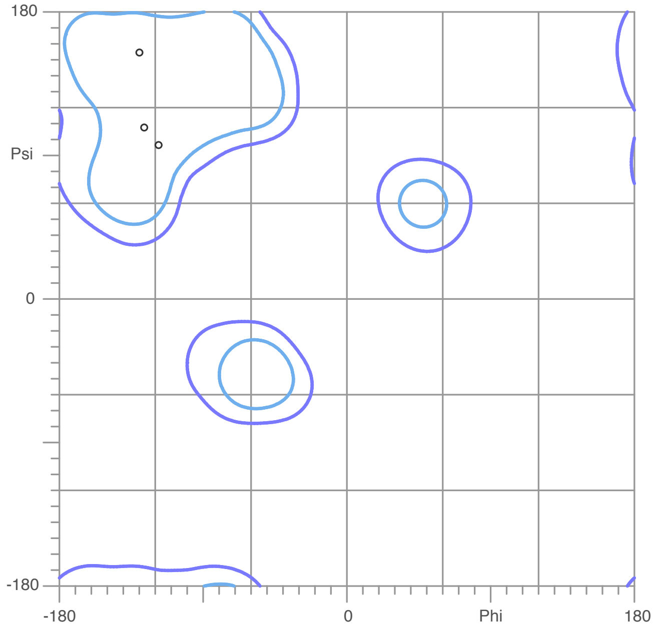
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 12


General case


Glycine


Proline


Pre-proline

100.0% (106/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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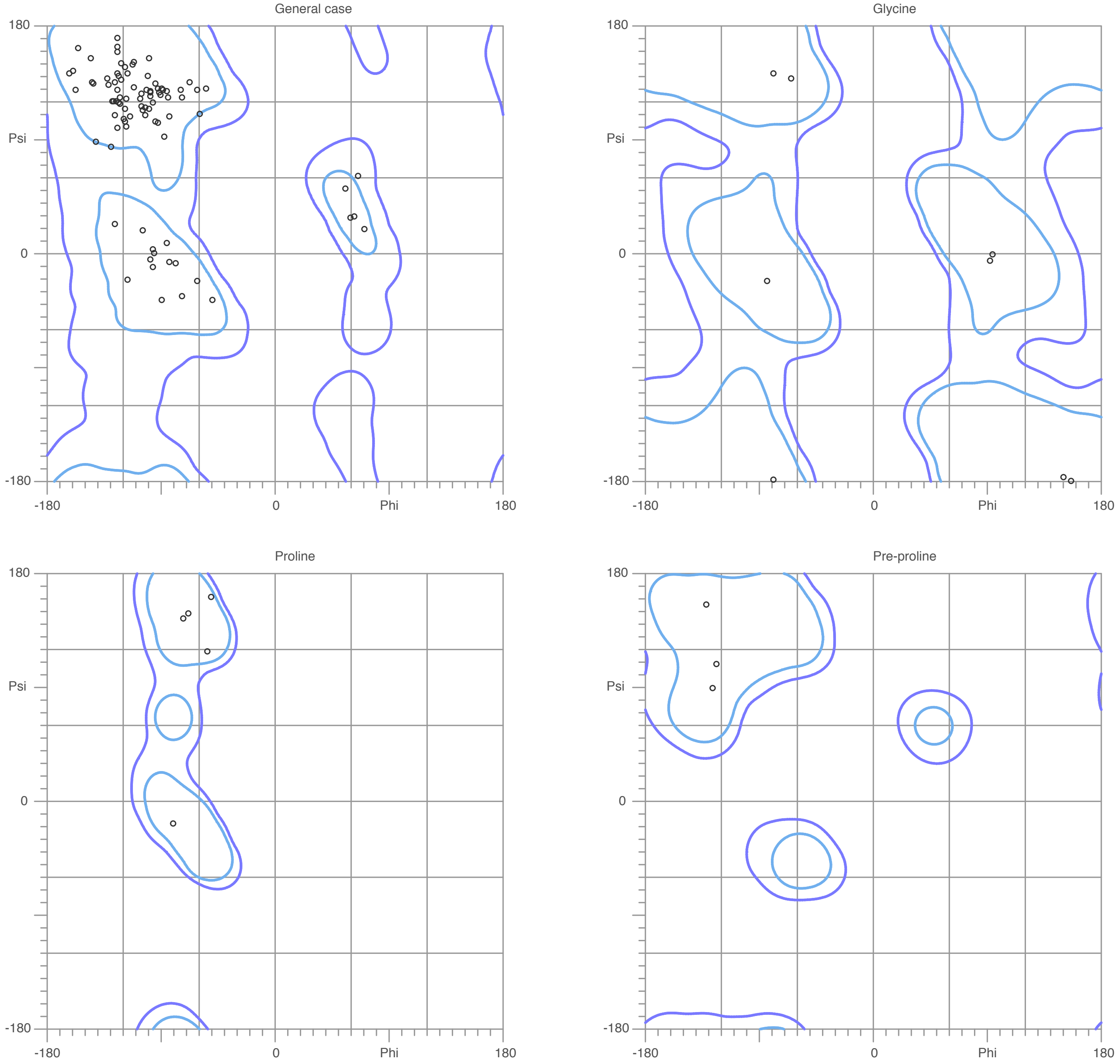
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 13

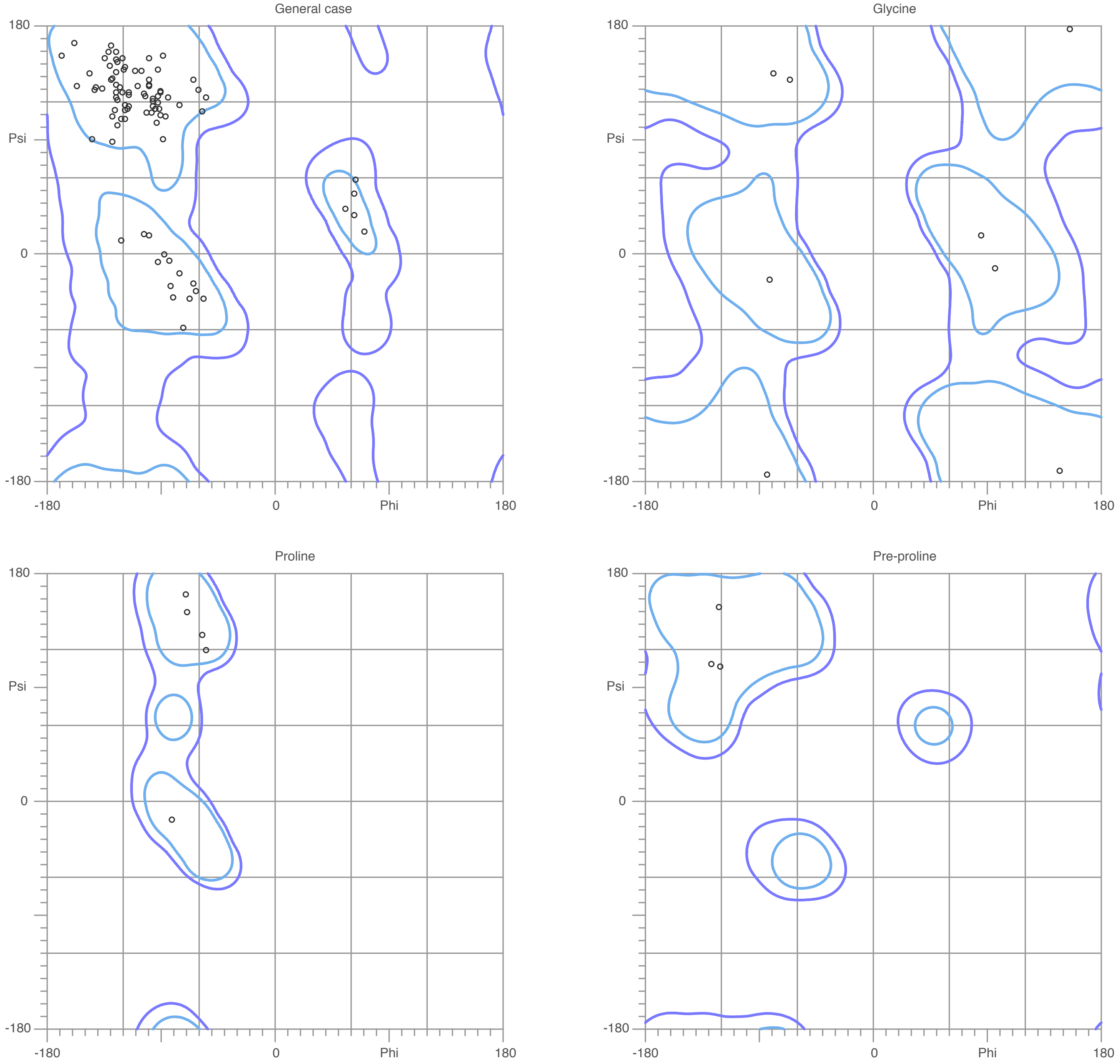


99.1% (105/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 14



99.1% (105/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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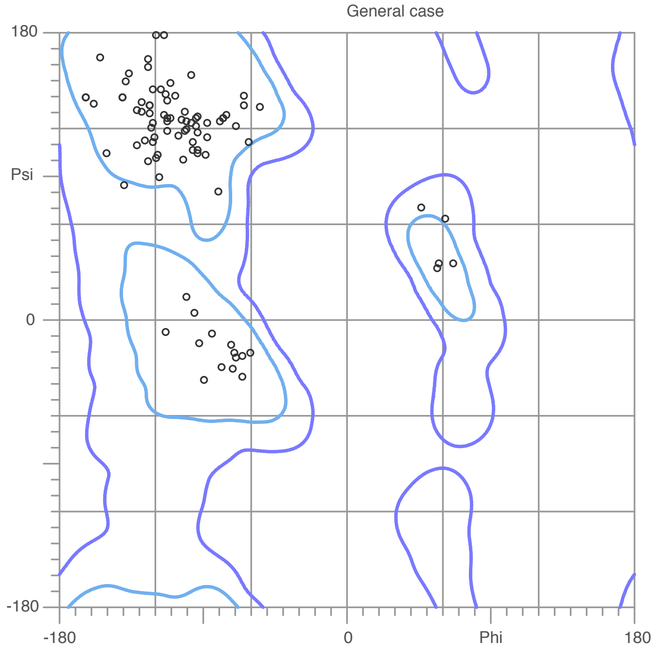
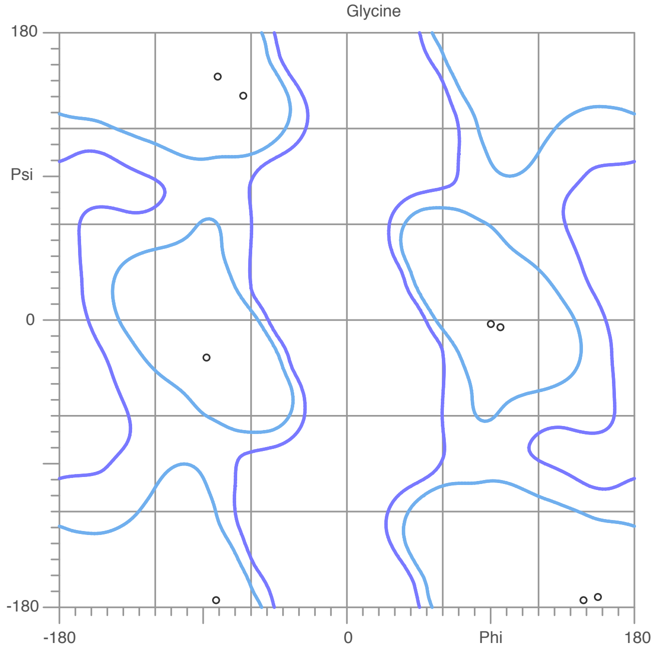
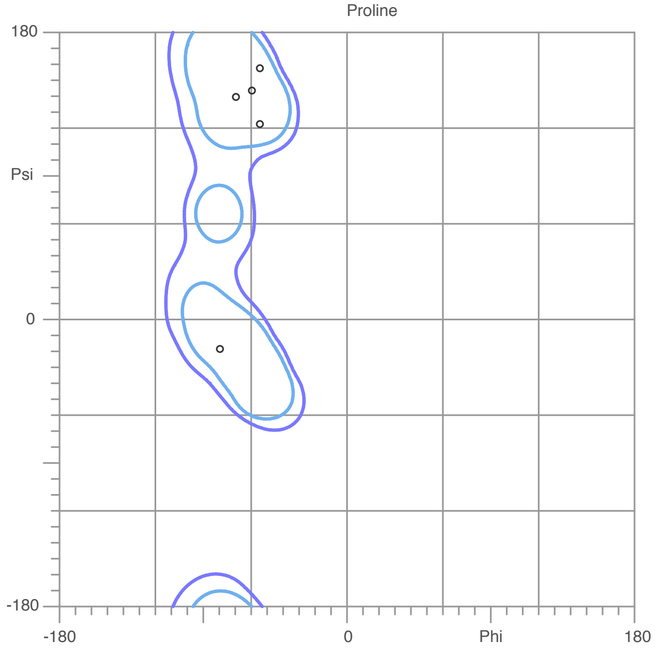
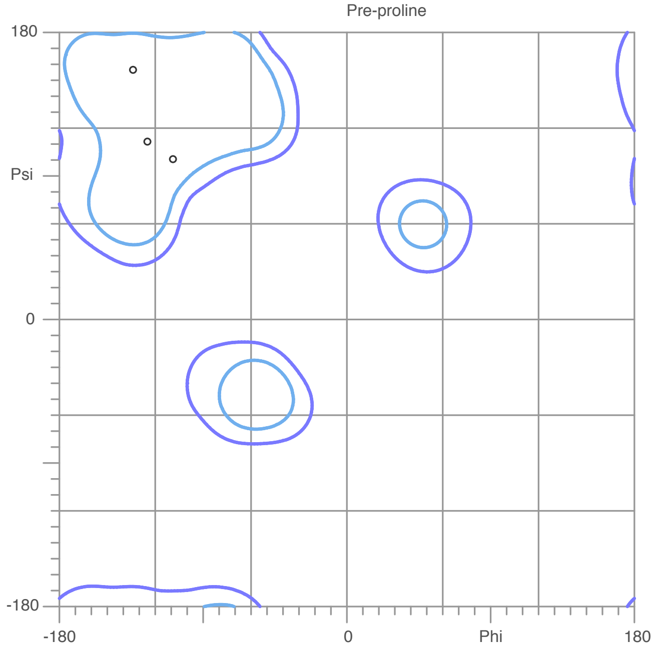
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 15









97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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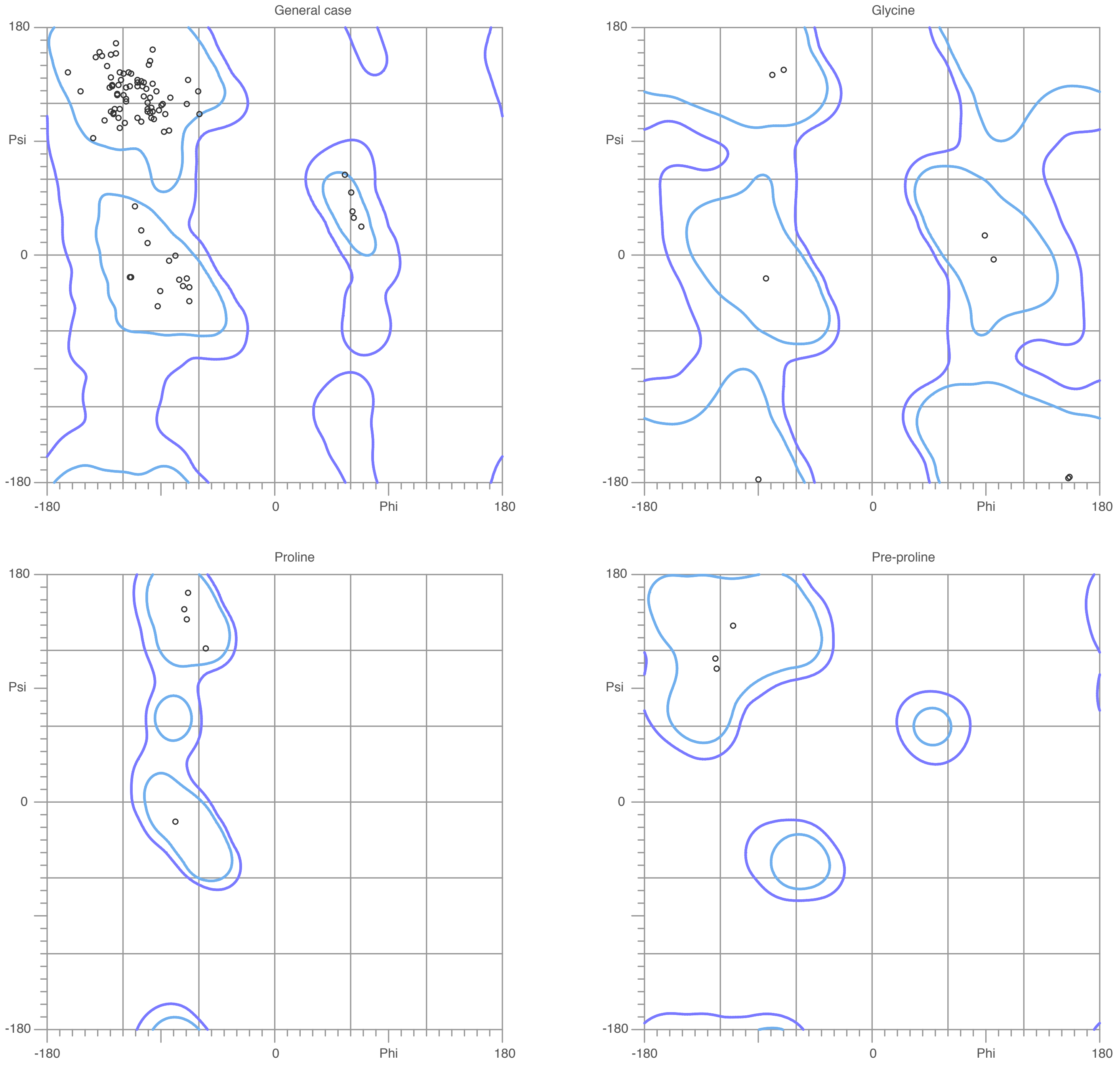
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 16



99.1% (105/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

http://kinemage.biochem.duke.edu

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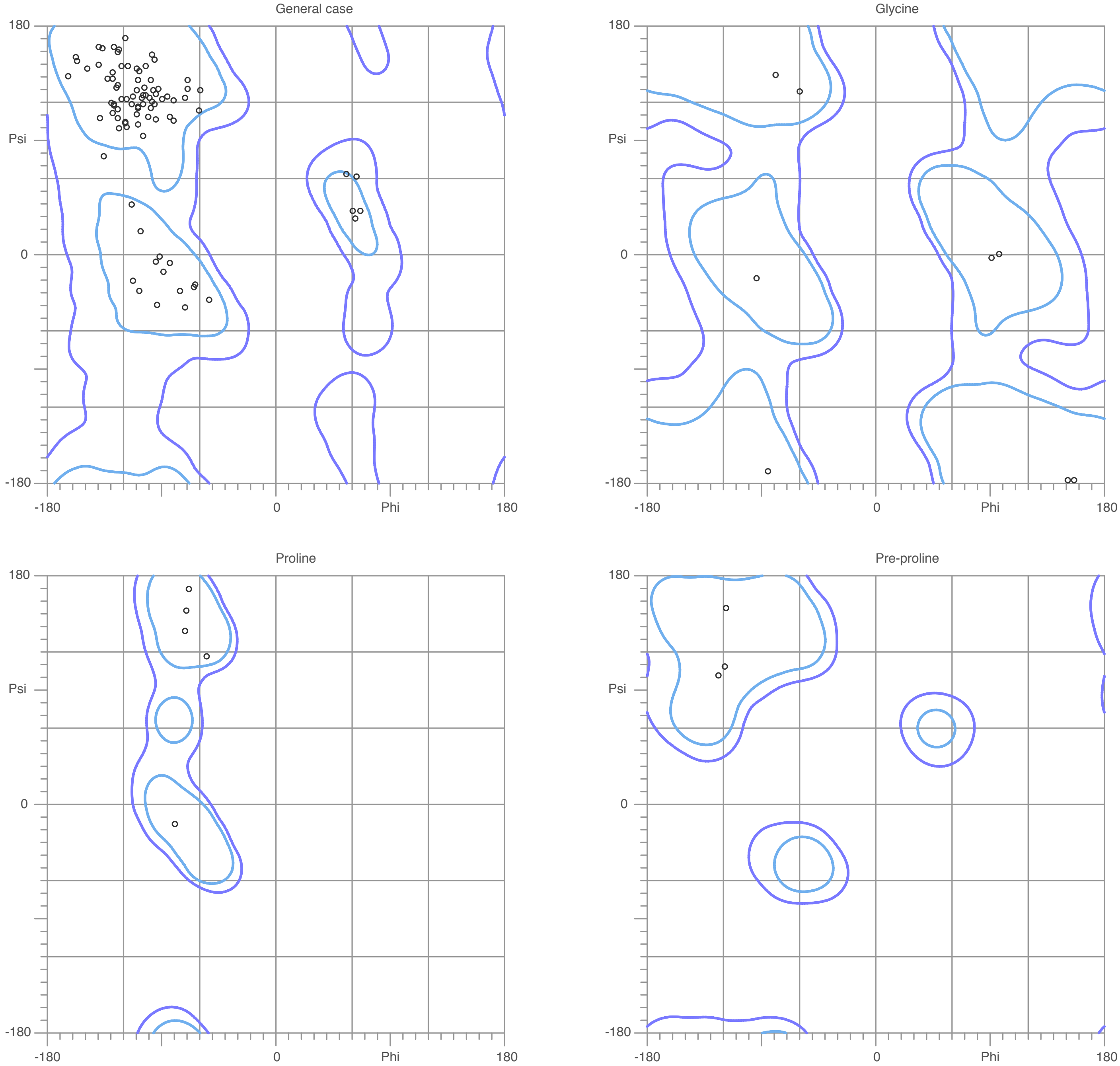
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 17



97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

http://kinemage.biochem.duke.edu

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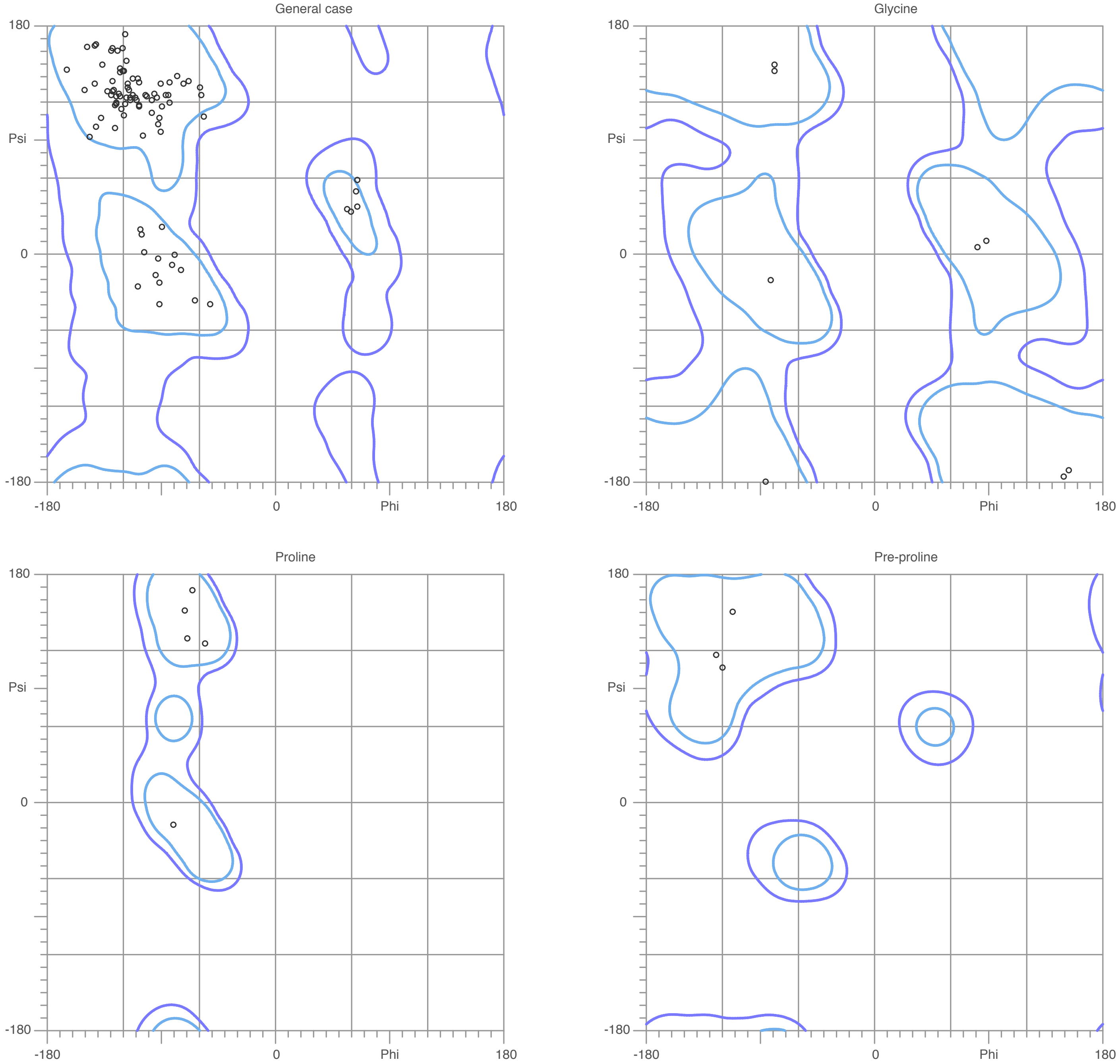
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 18



98.1% (104/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

http://kinemage.biochem.duke.edu

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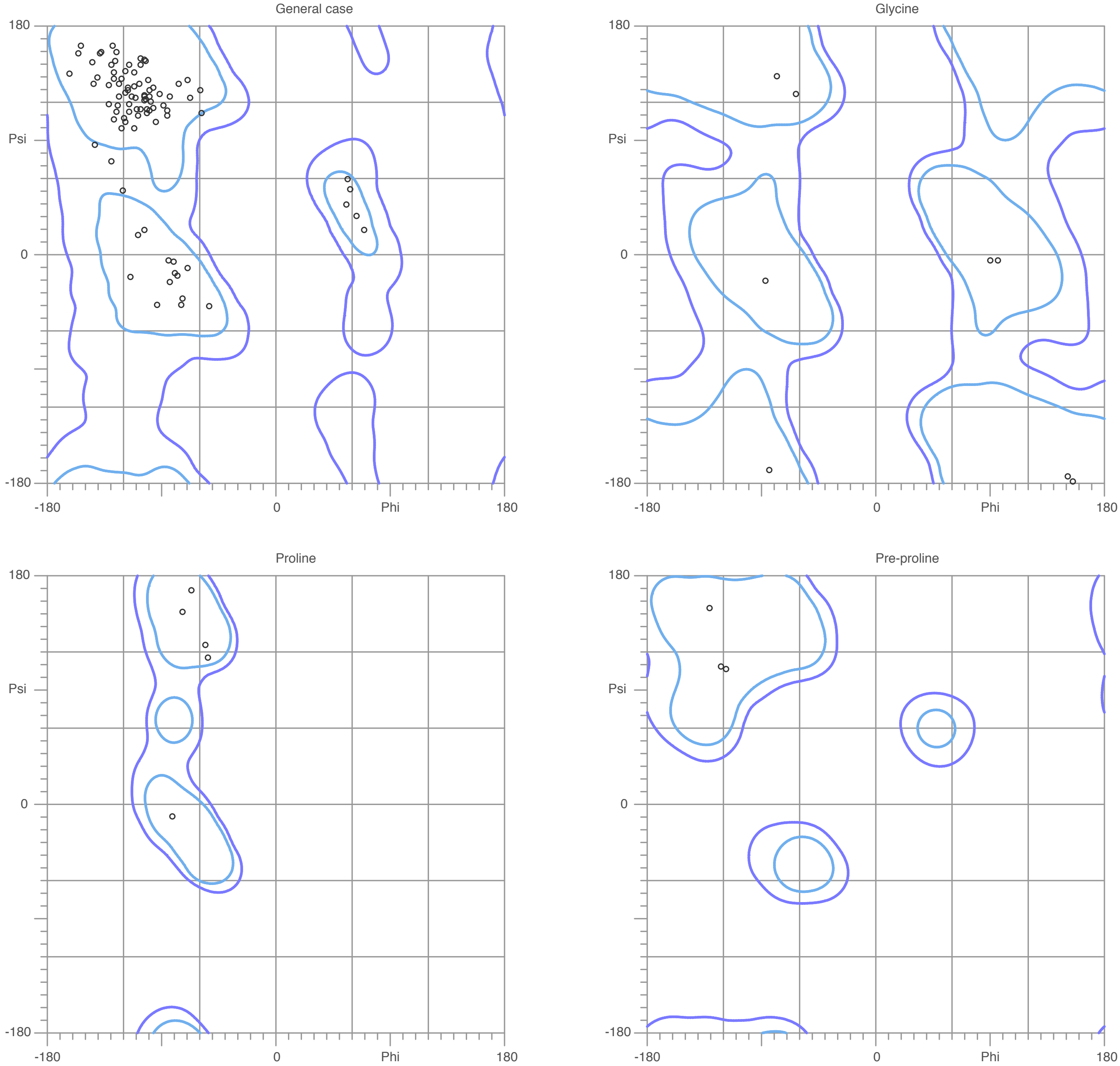
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 19



97.2% (103/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

http://kinemage.biochem.duke.edu

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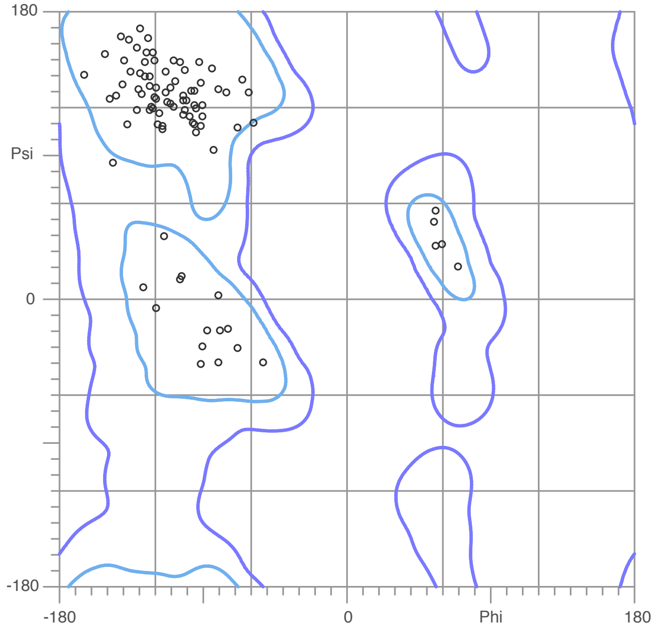
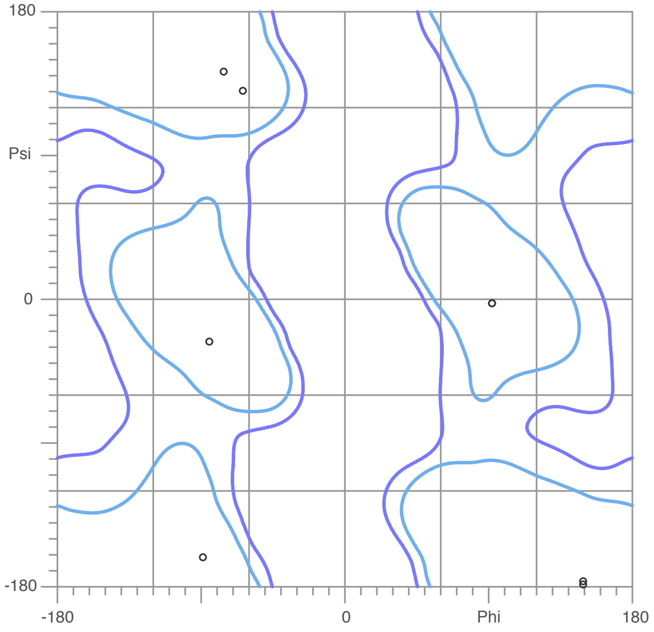
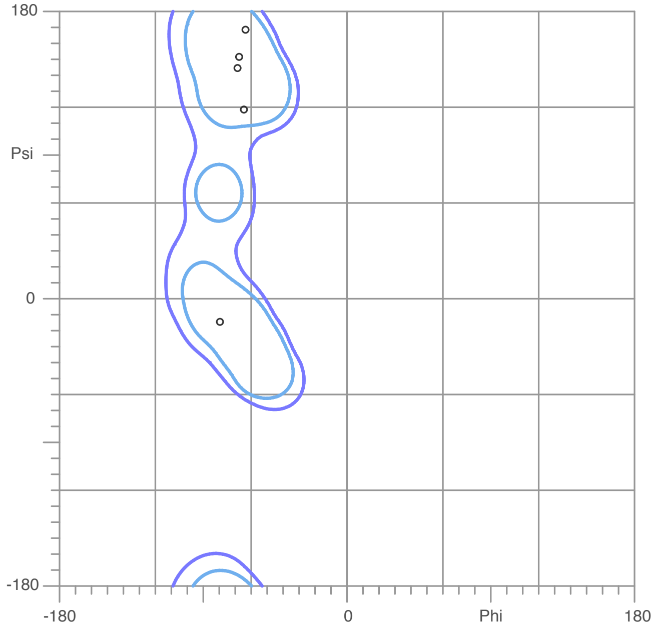
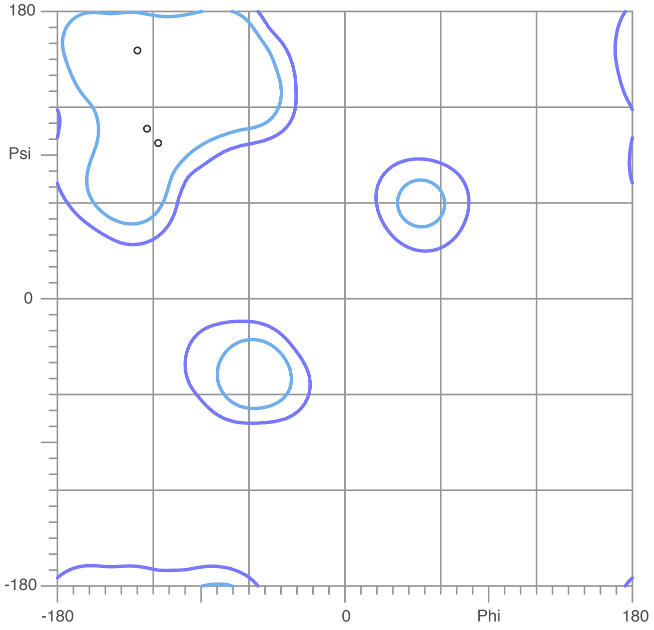
MolProbity Ramachandran analysis

PFR193A_R3_em_bcr3.pdb, model 20


General case


Glycine


Proline


Pre-proline

99.1% (105/106) of all residues were in favored (98%) regions.
100.0% (106/106) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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