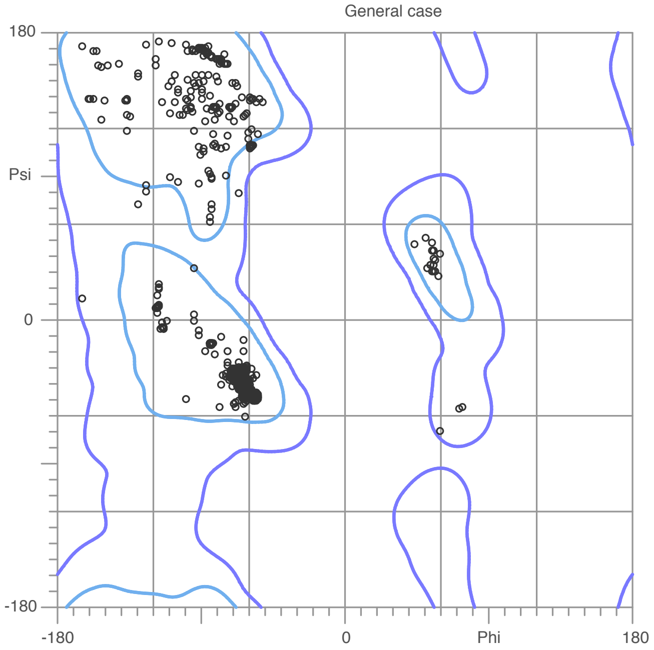
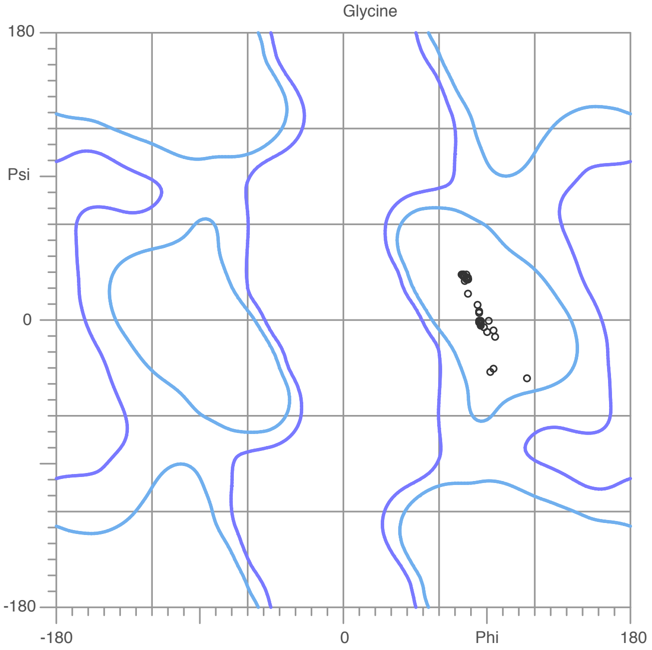
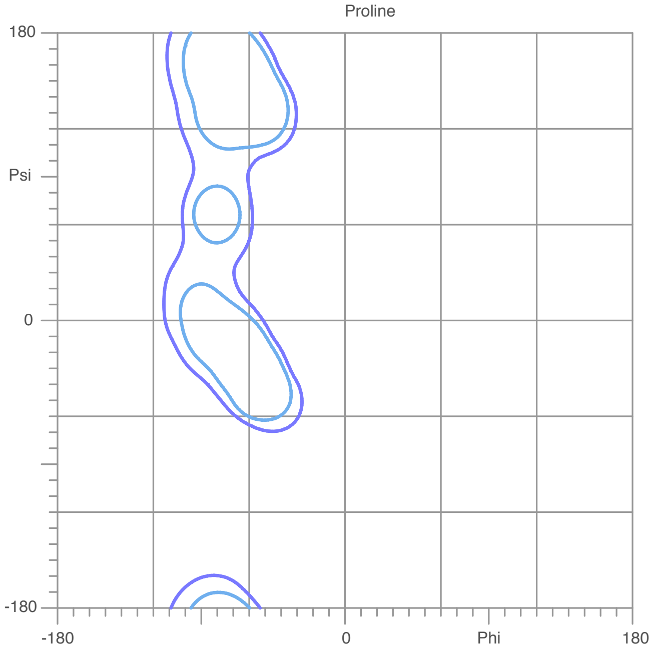
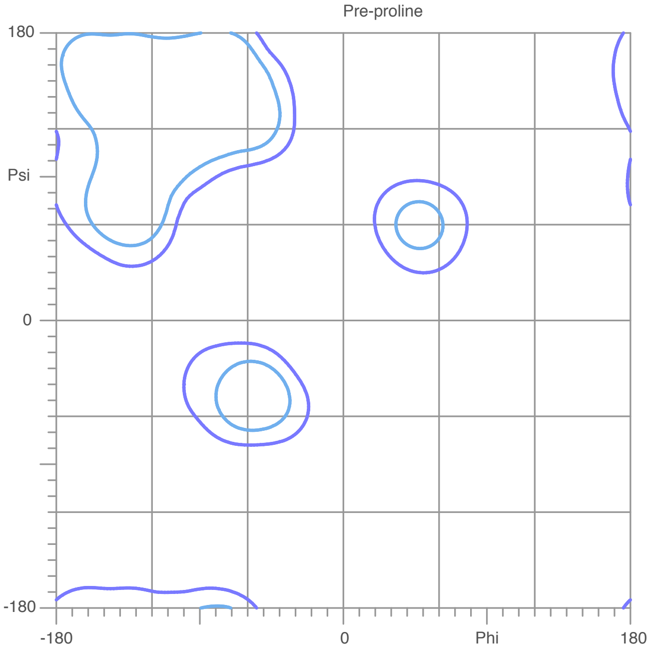
MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, all models









97.7% (809/828) of all residues were in favored (98%) regions.
100.0% (828/828) of all residues were in allowed (>99.8%) regions.

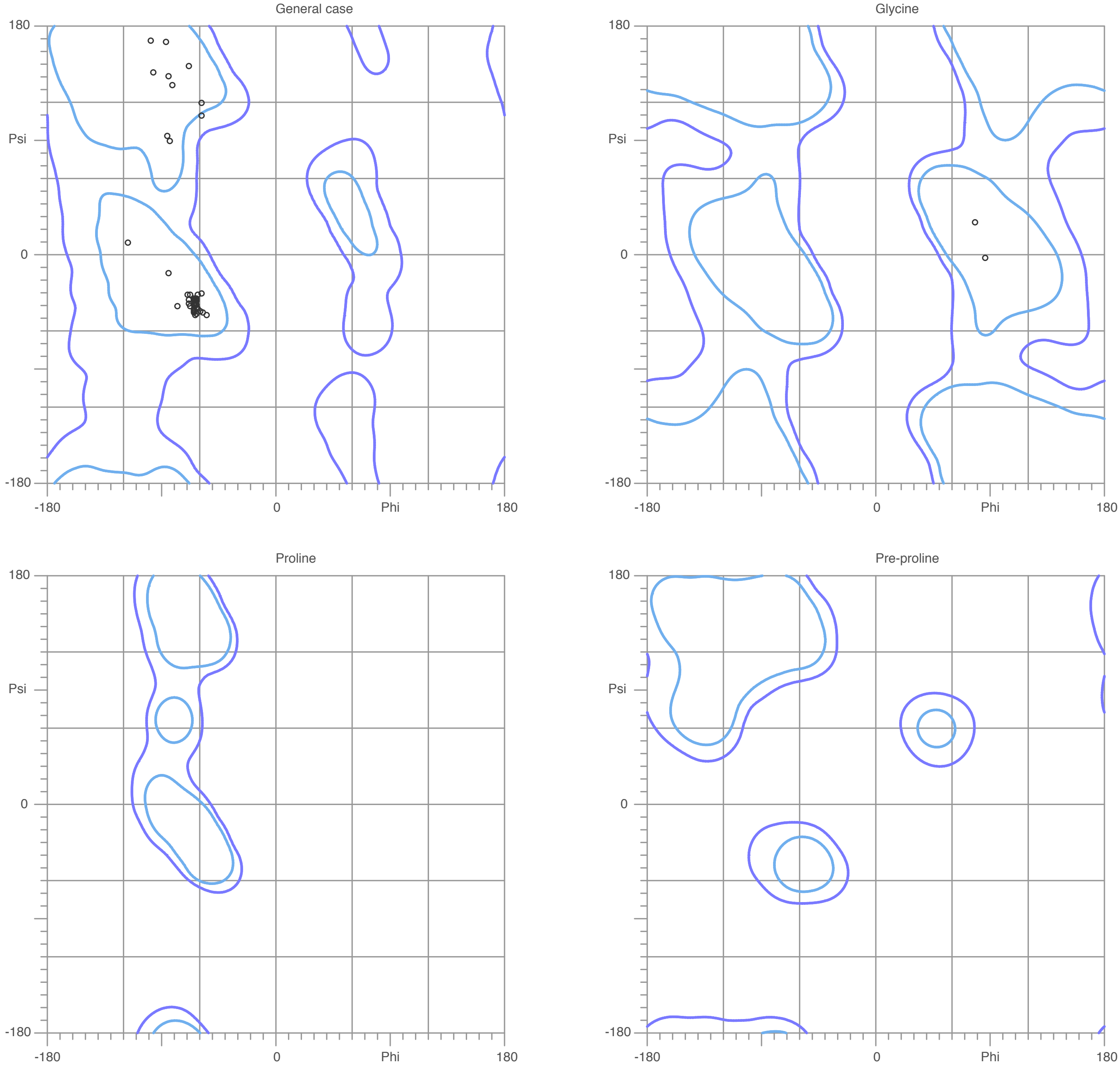
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 1



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

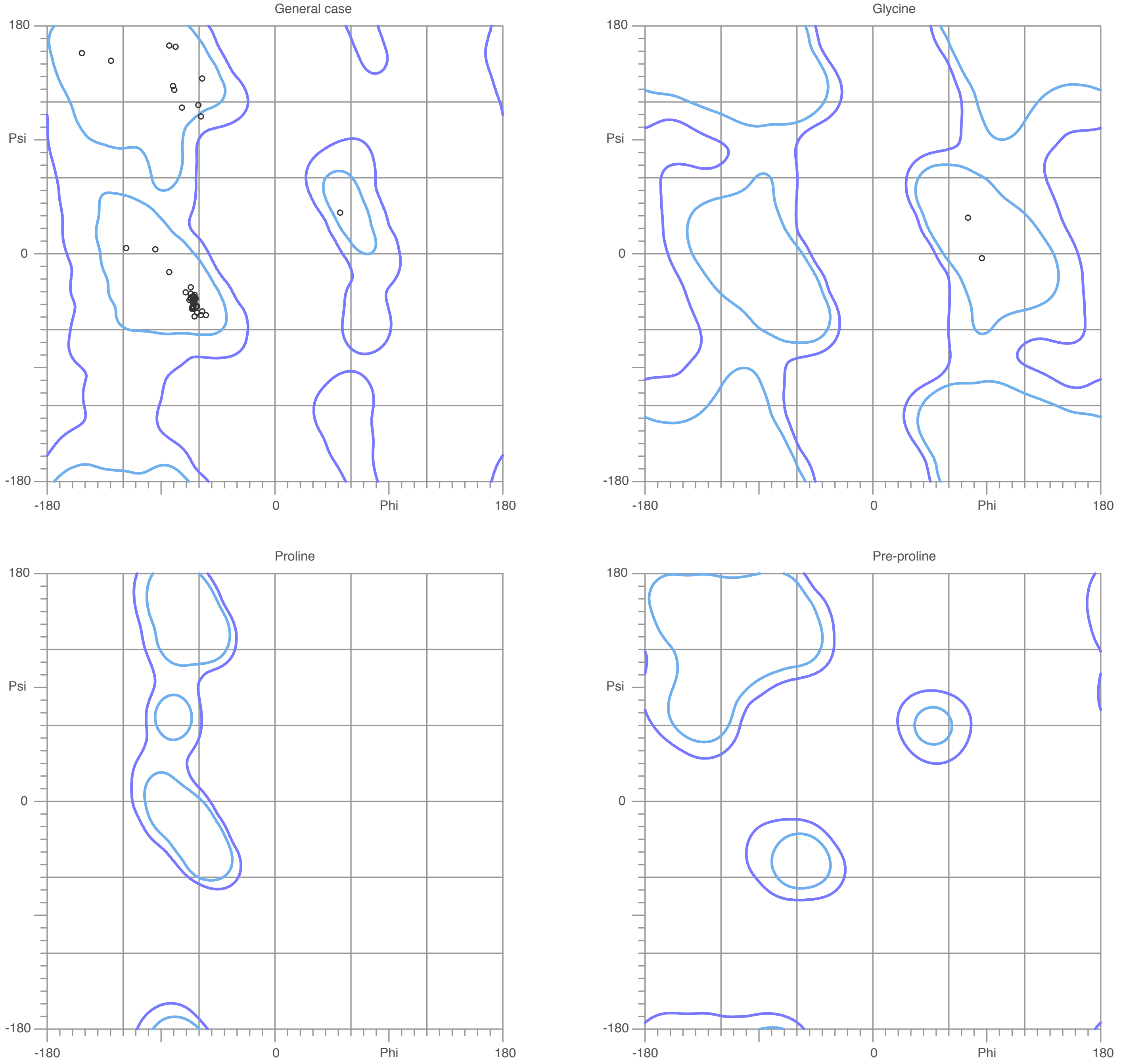
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 2



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

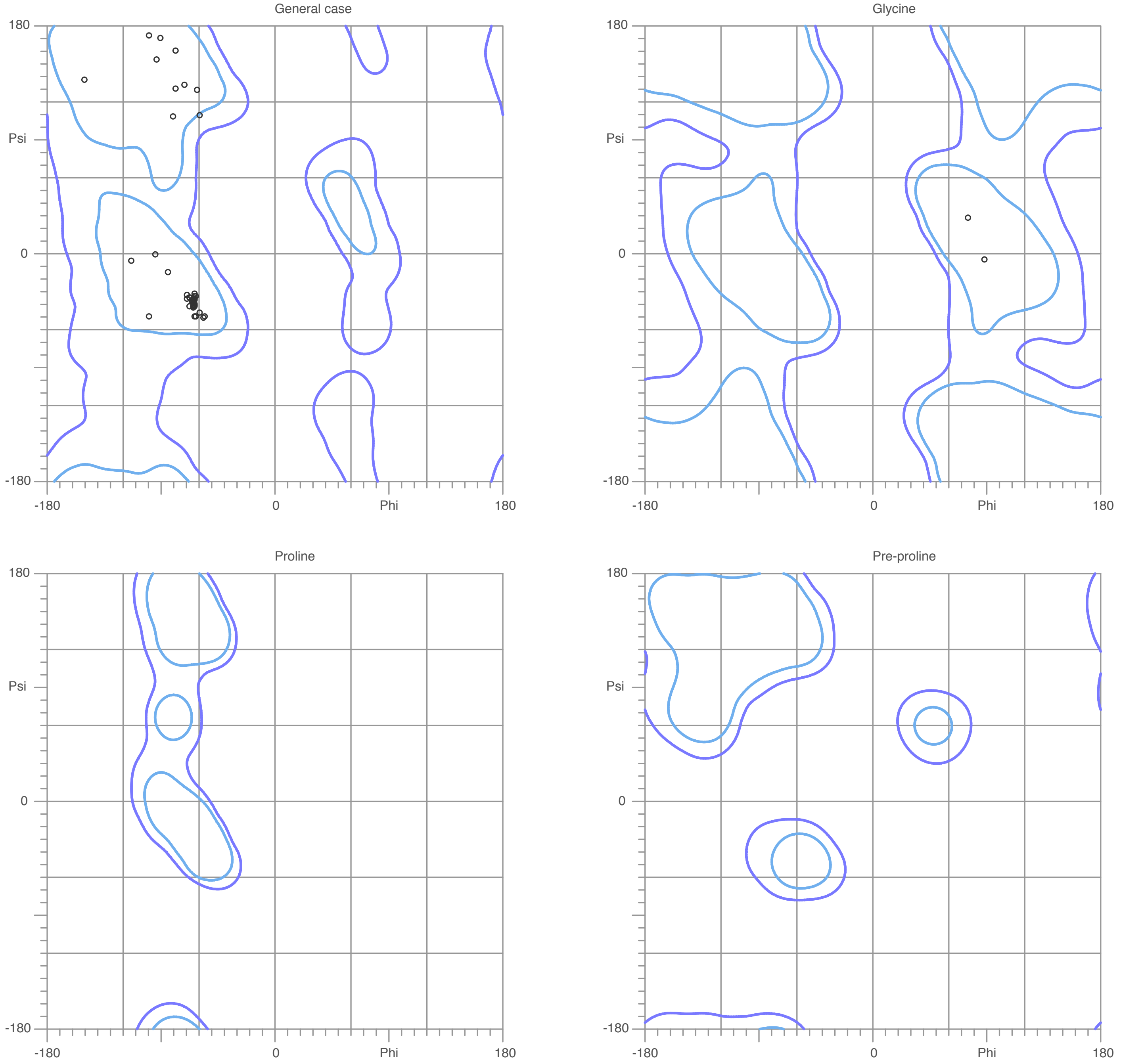
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 3



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

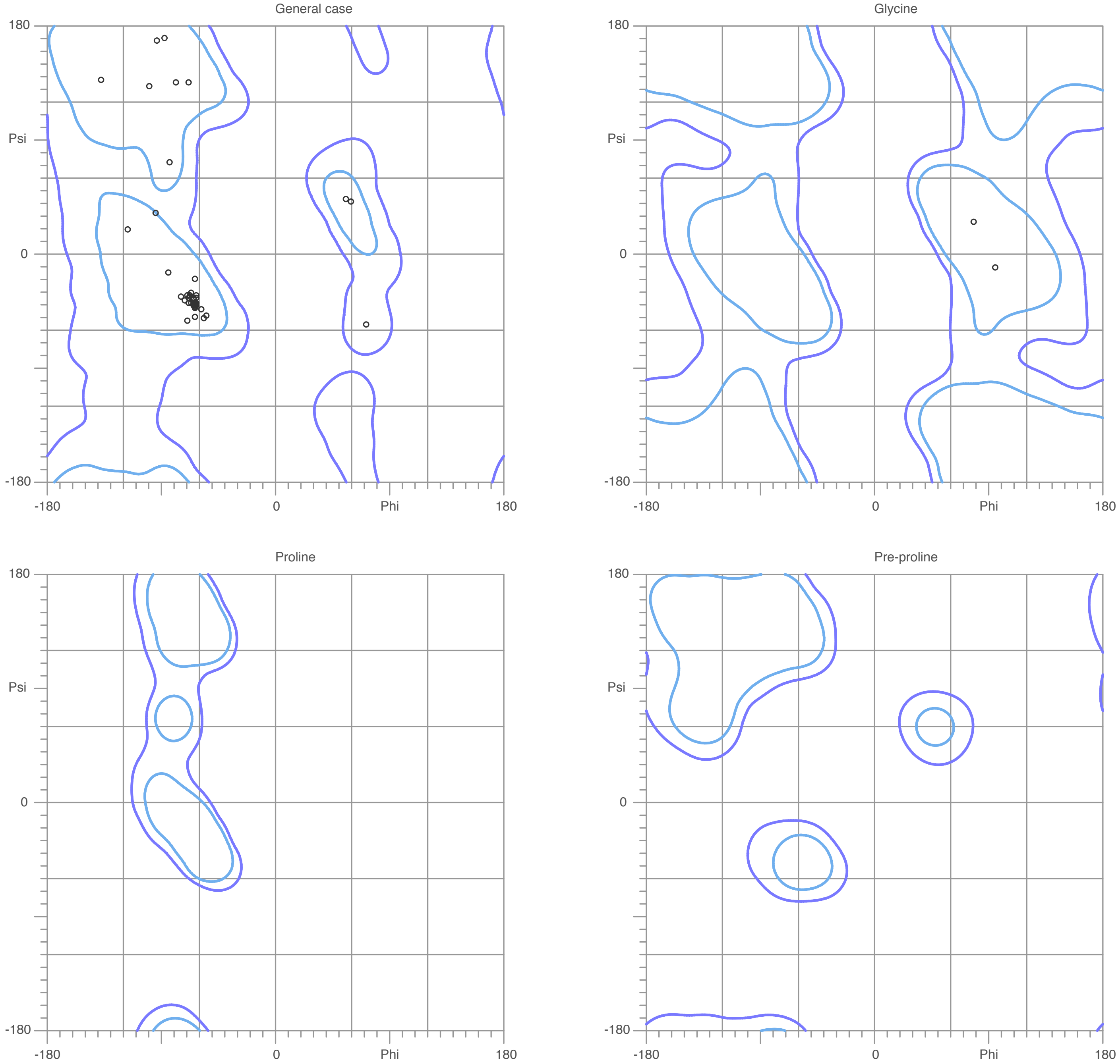
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 4

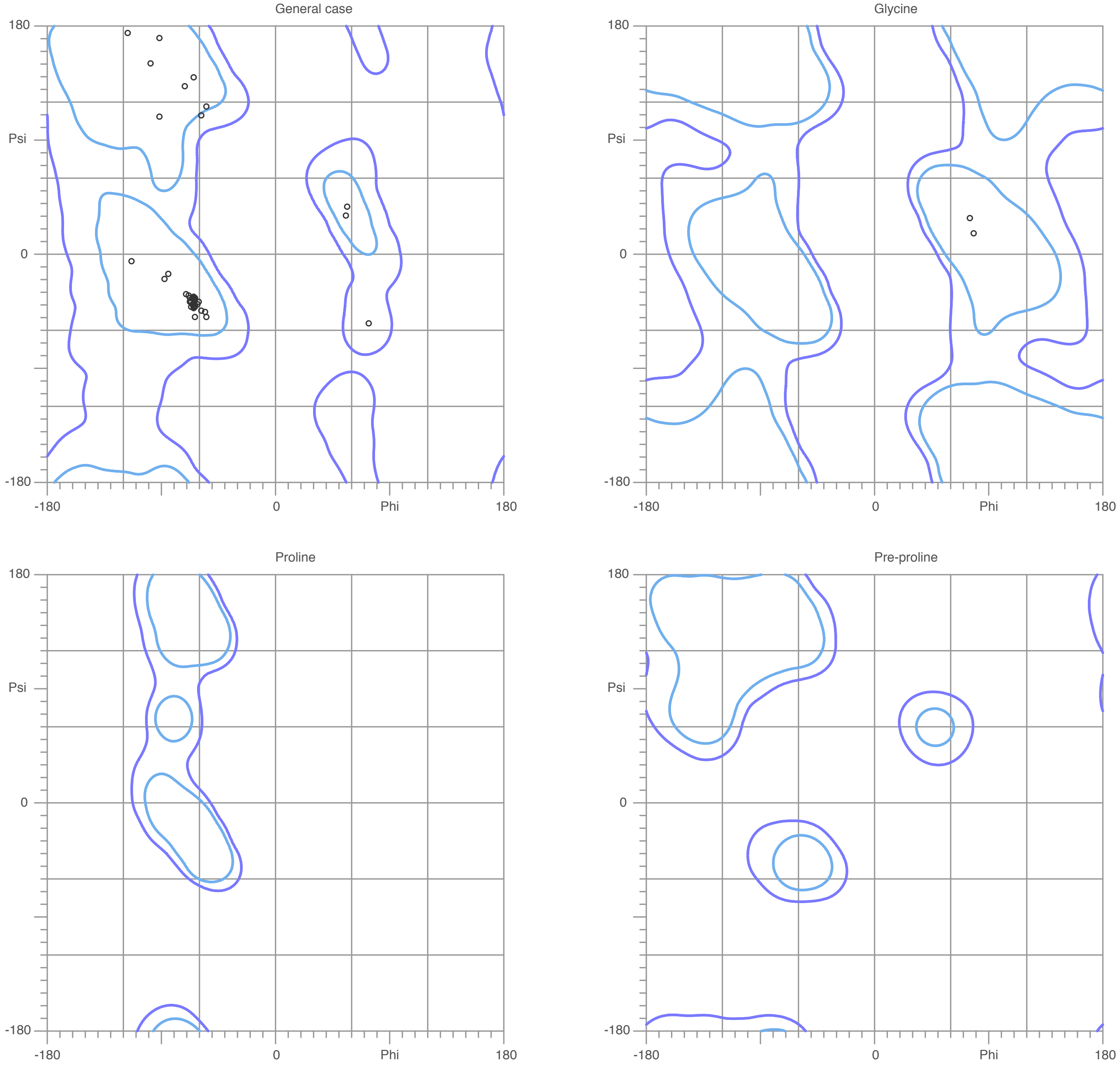


97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 5



95.7% (44/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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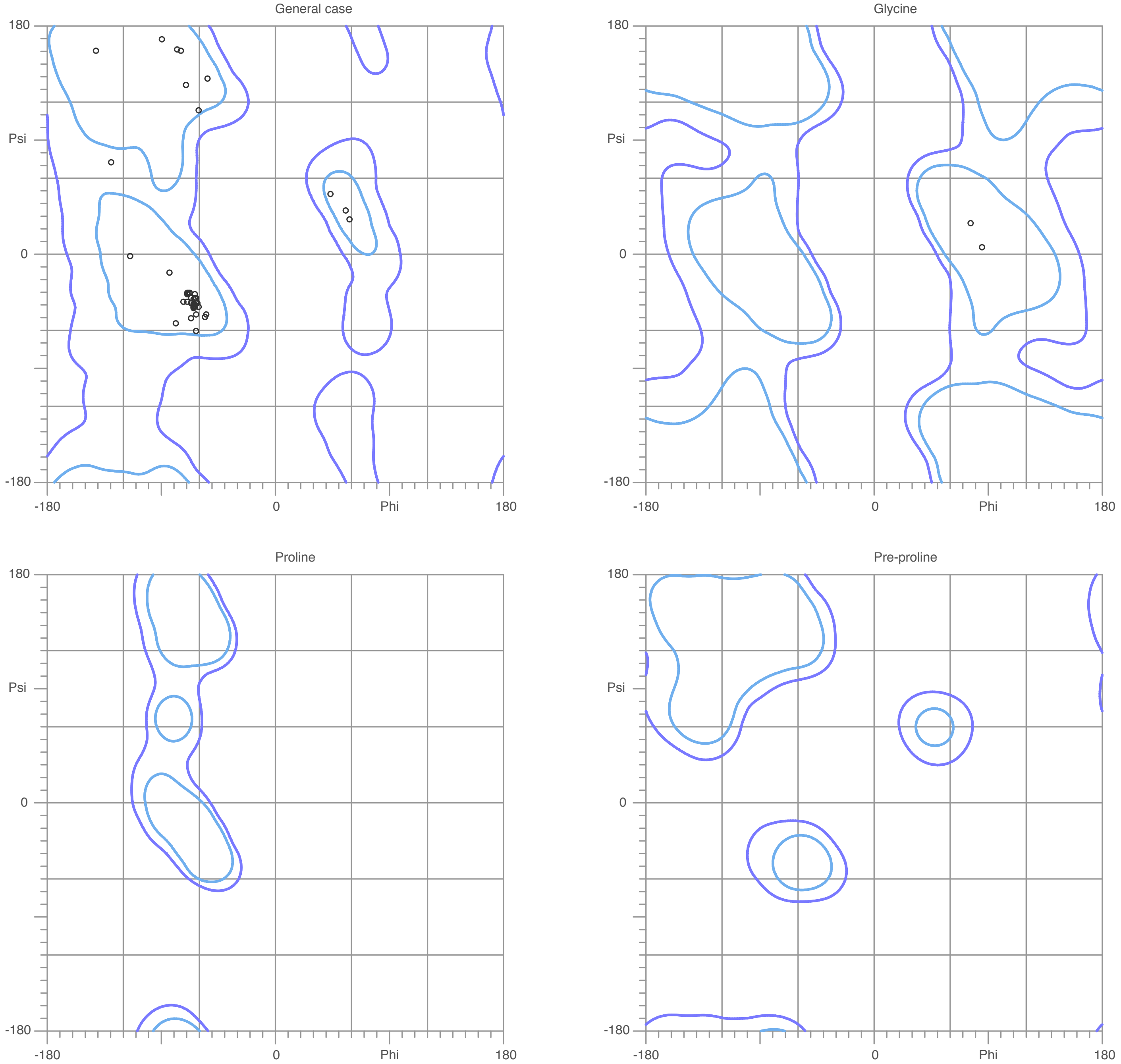
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 6



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

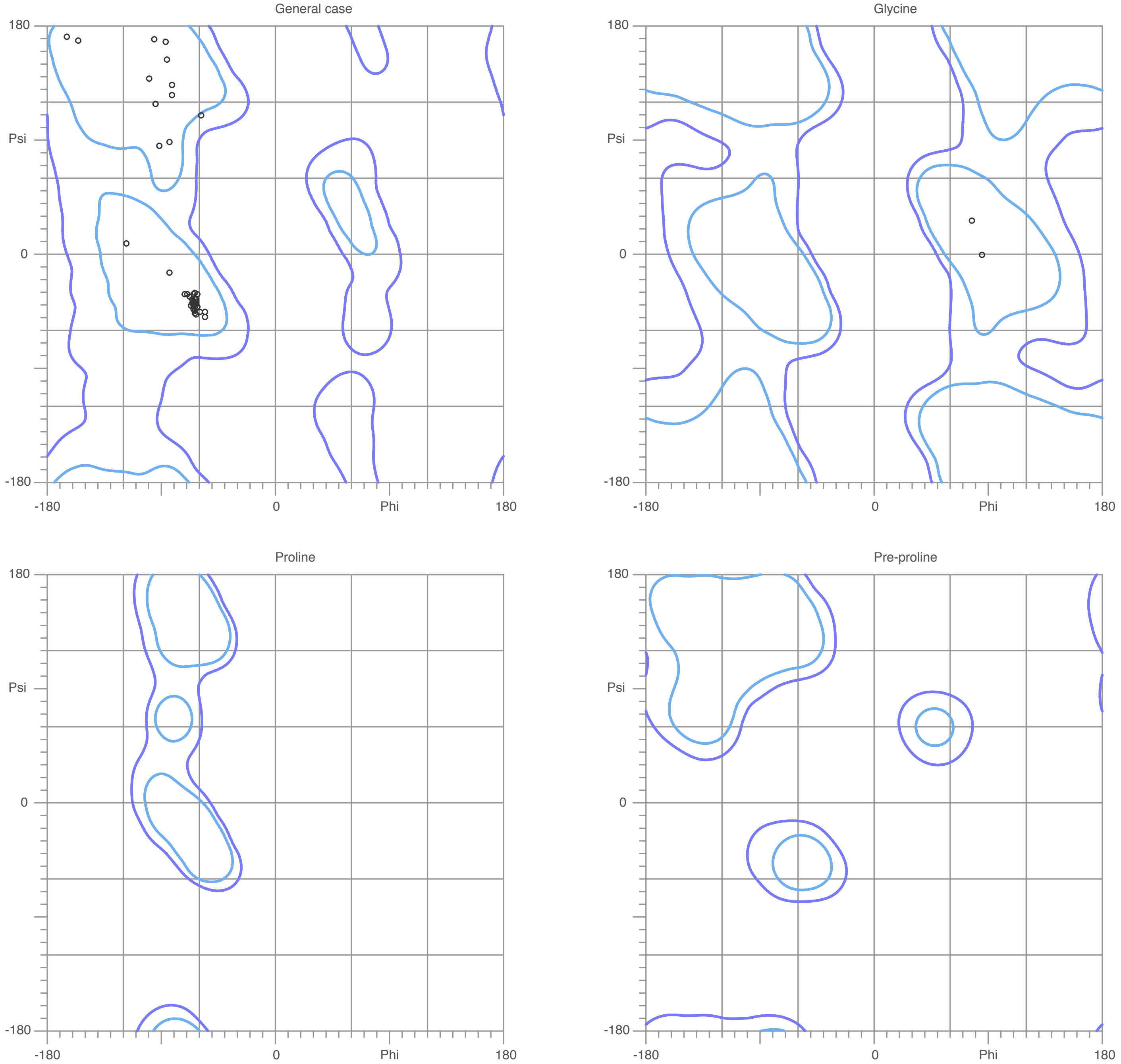
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 7



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

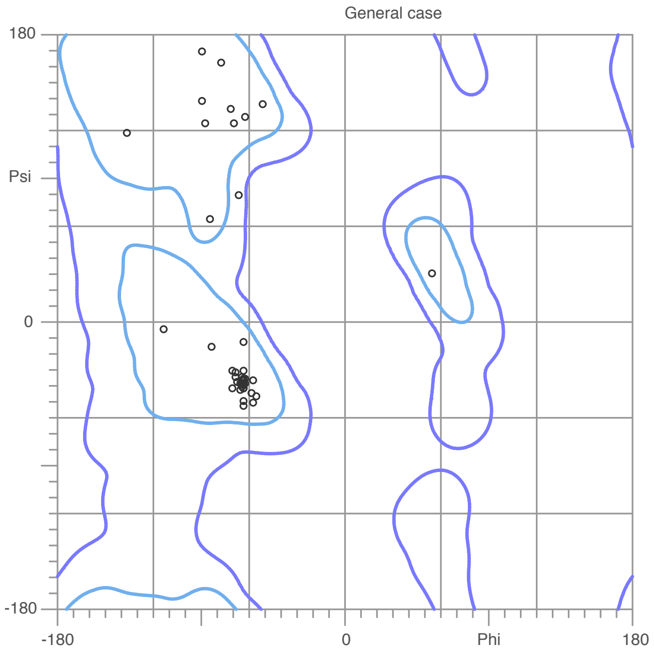
There were no outliers.

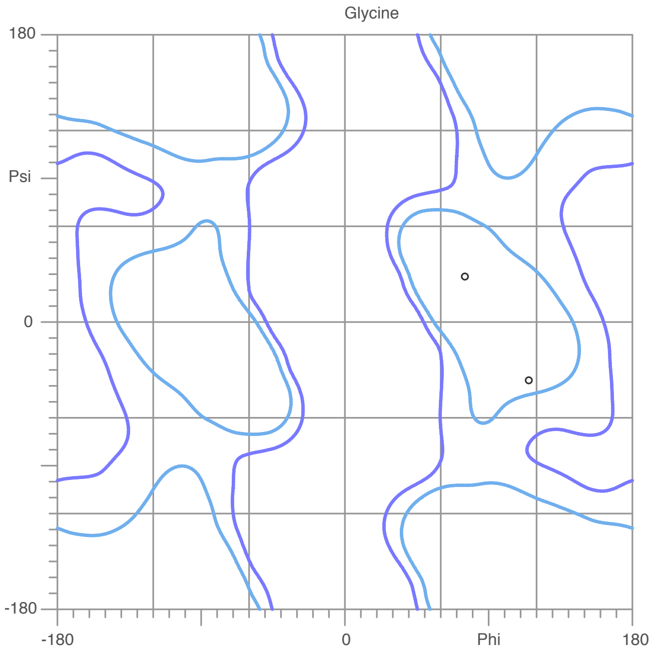
http://kinemage.biochem.duke.edu

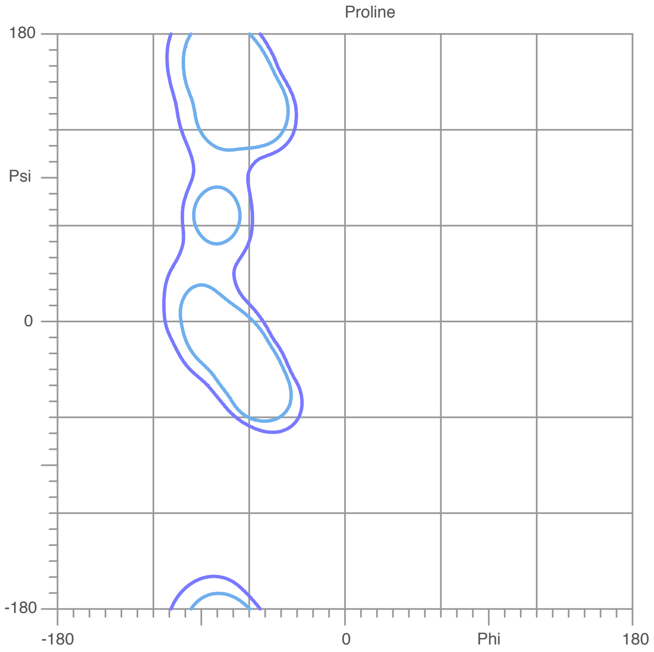
Lovell, Davis, et al. Proteins 50:437 (2003)

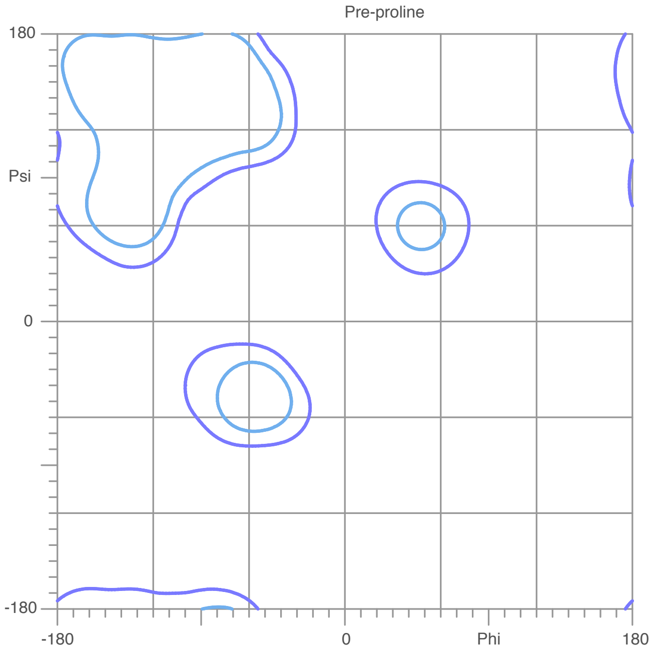
MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 8


General case


Glycine


Proline


Pre-proline

97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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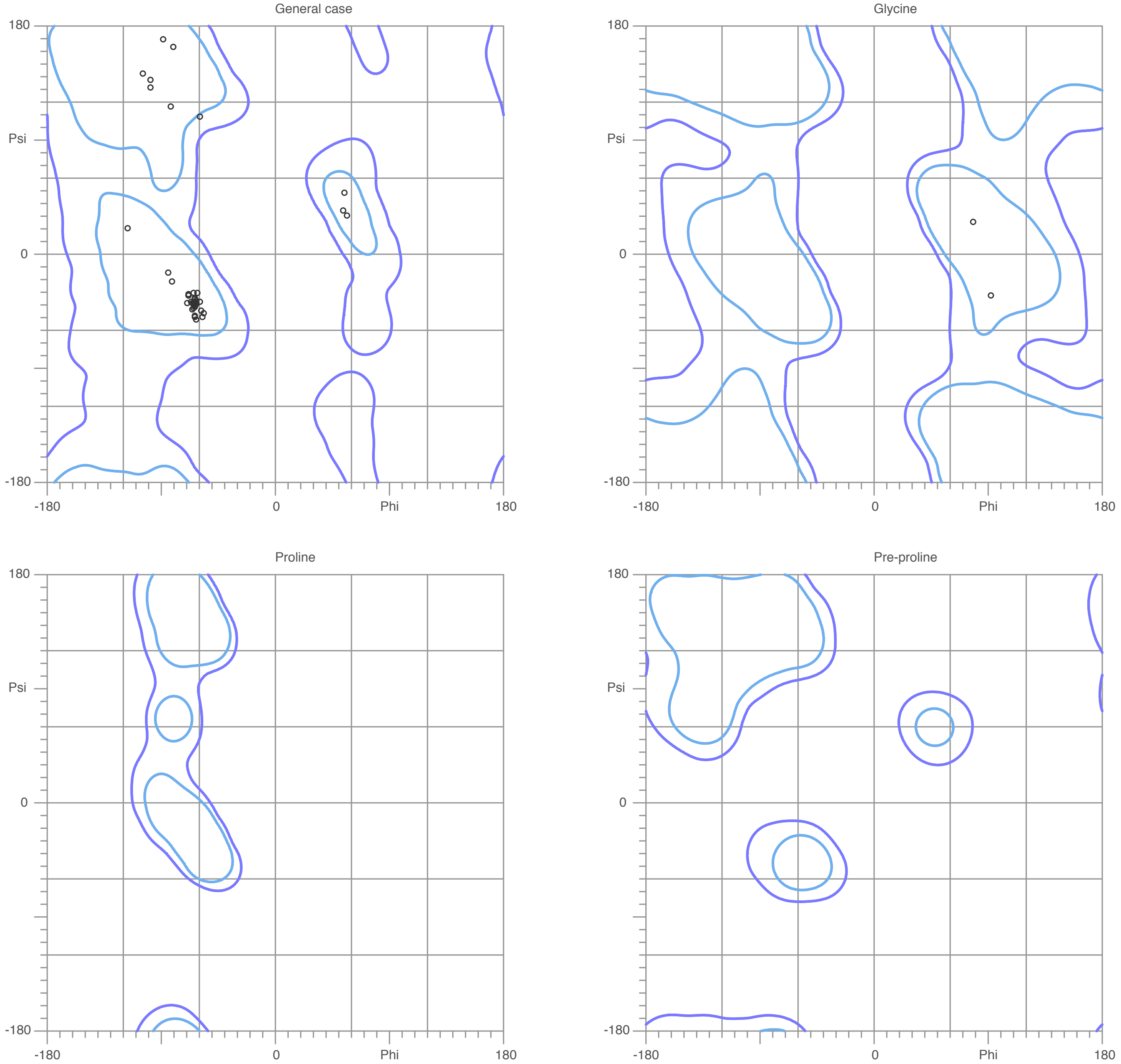
Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 9



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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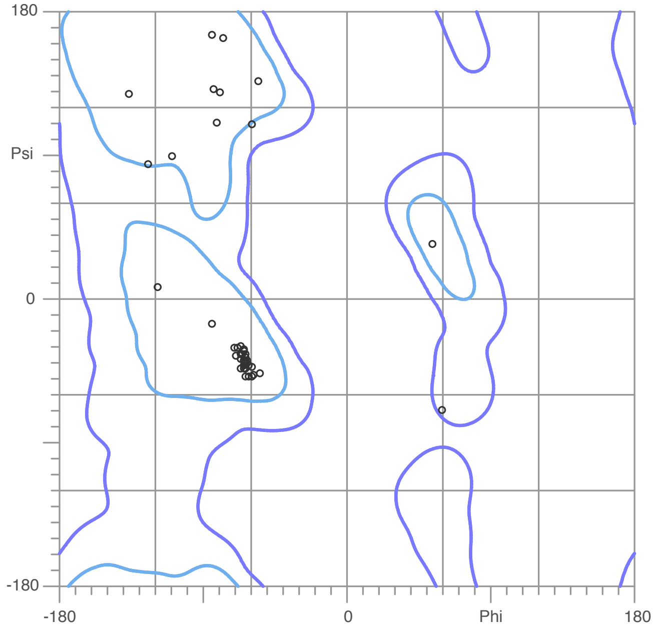
Lovell, Davis, et al. Proteins 50:437 (2003)

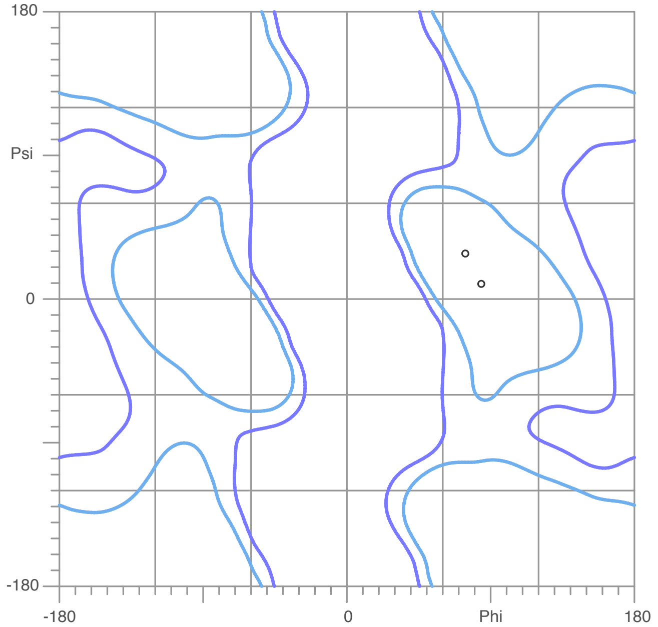
MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 10

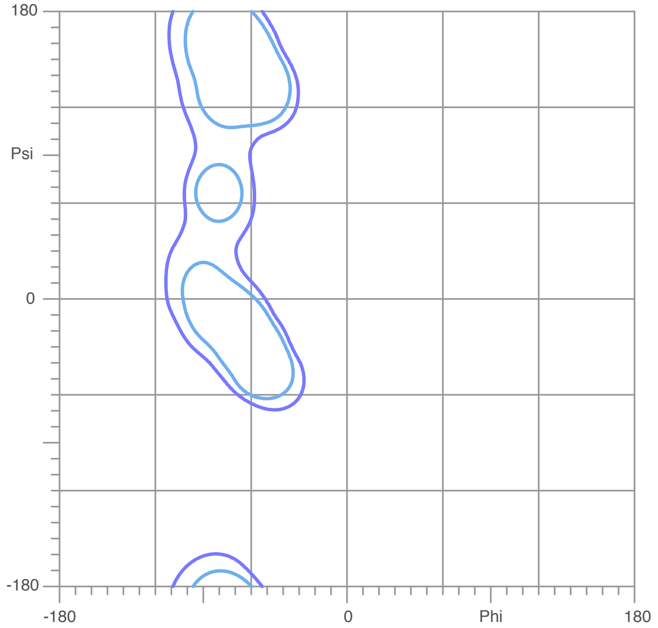
General case



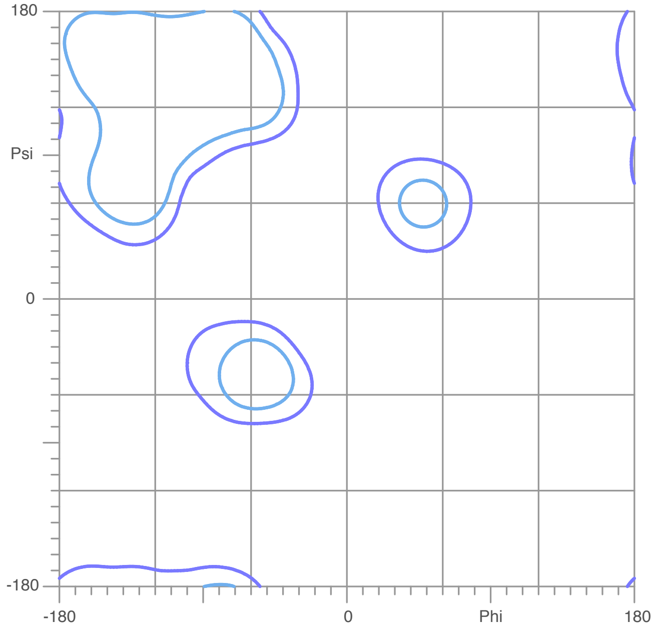
Glycine



Proline



Pre-proline



95.7% (44/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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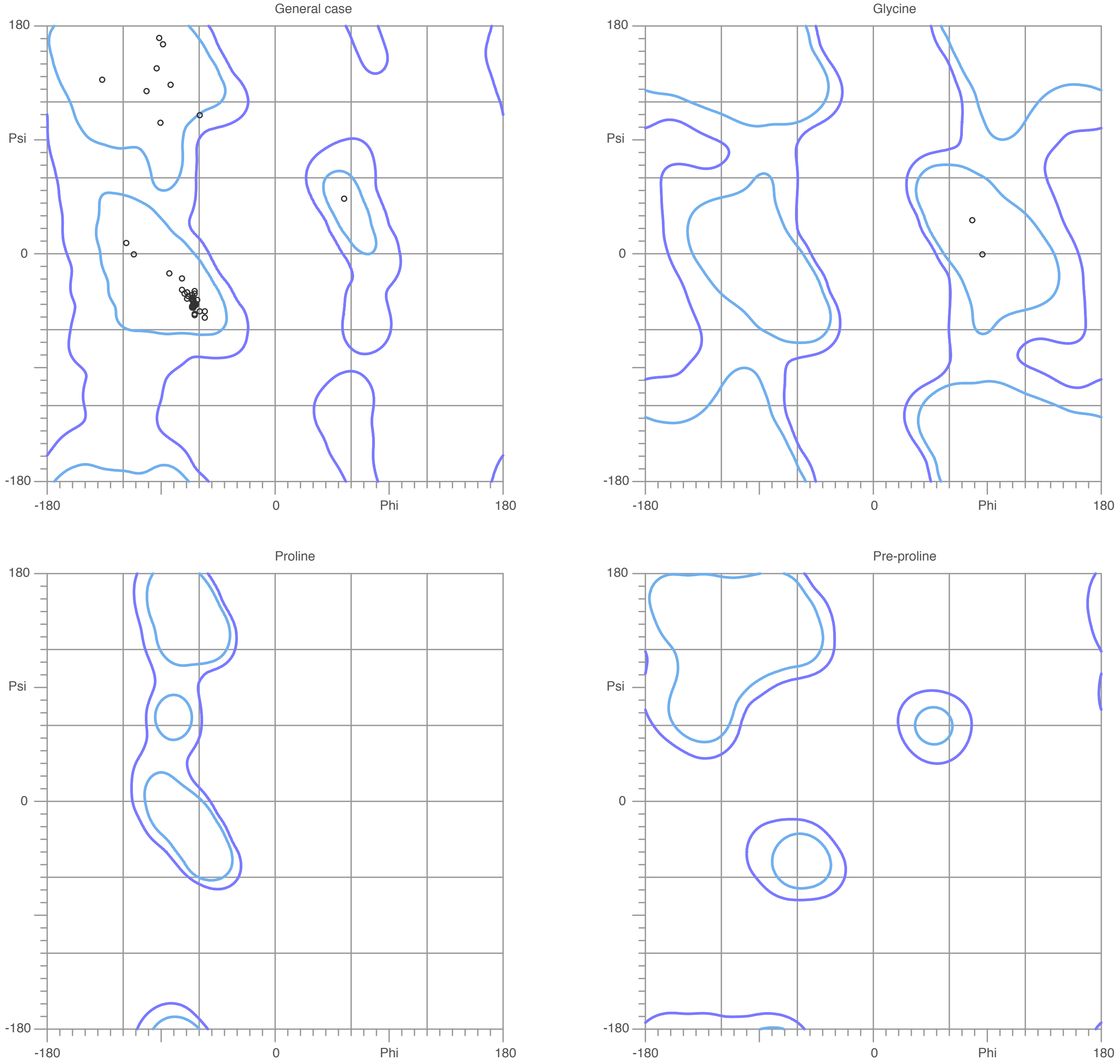
MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 11



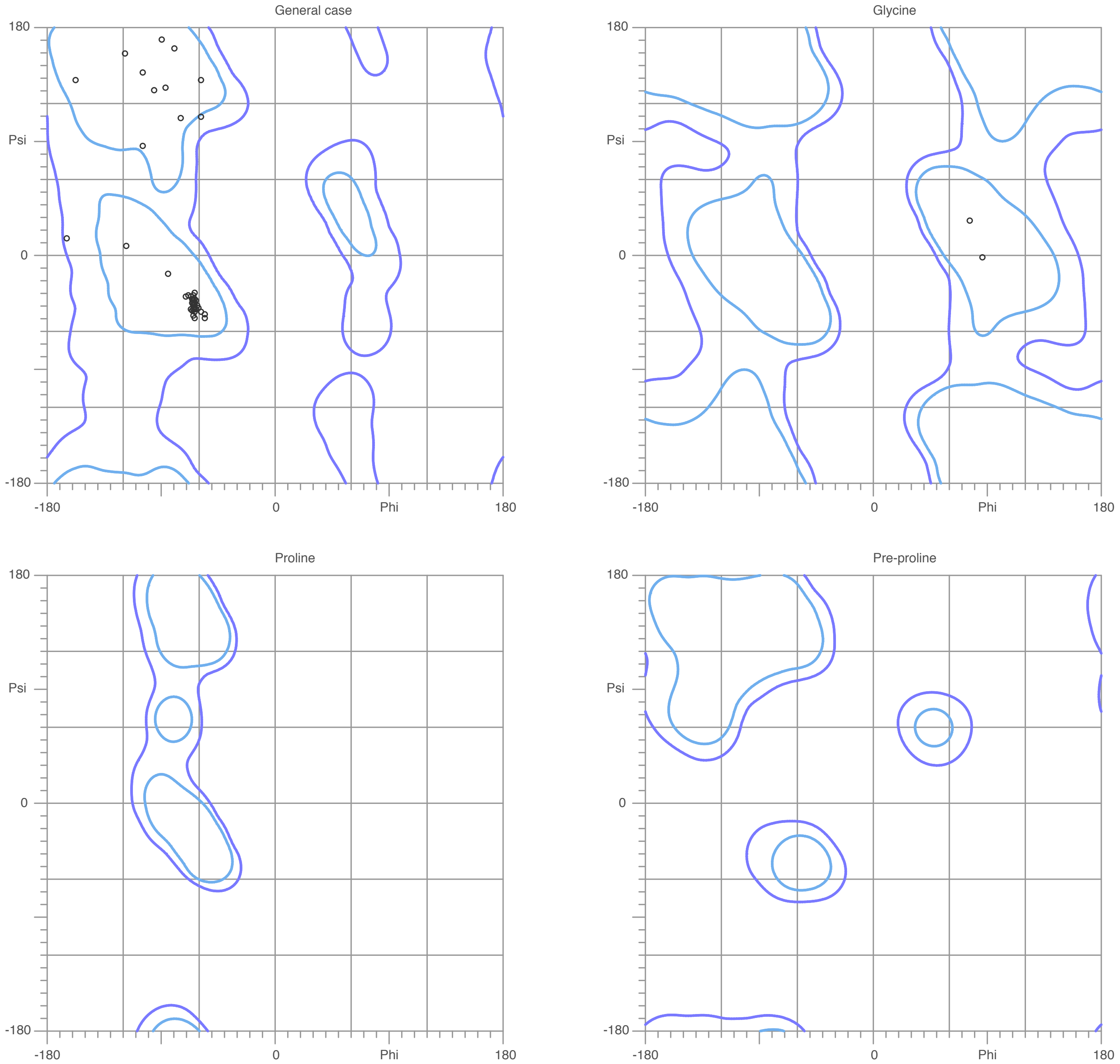
100.0% (46/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 12

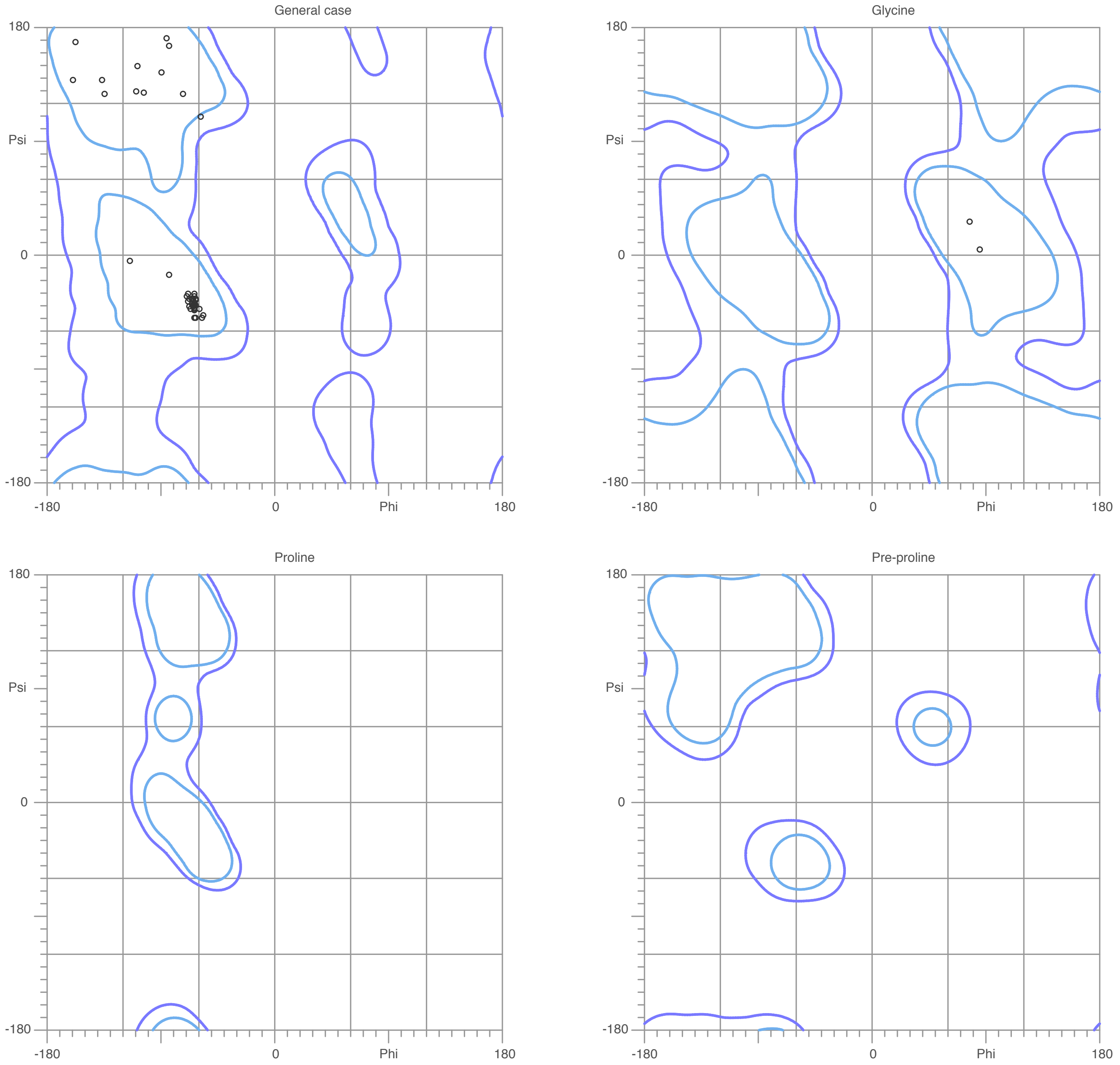


95.7% (44/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 13



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

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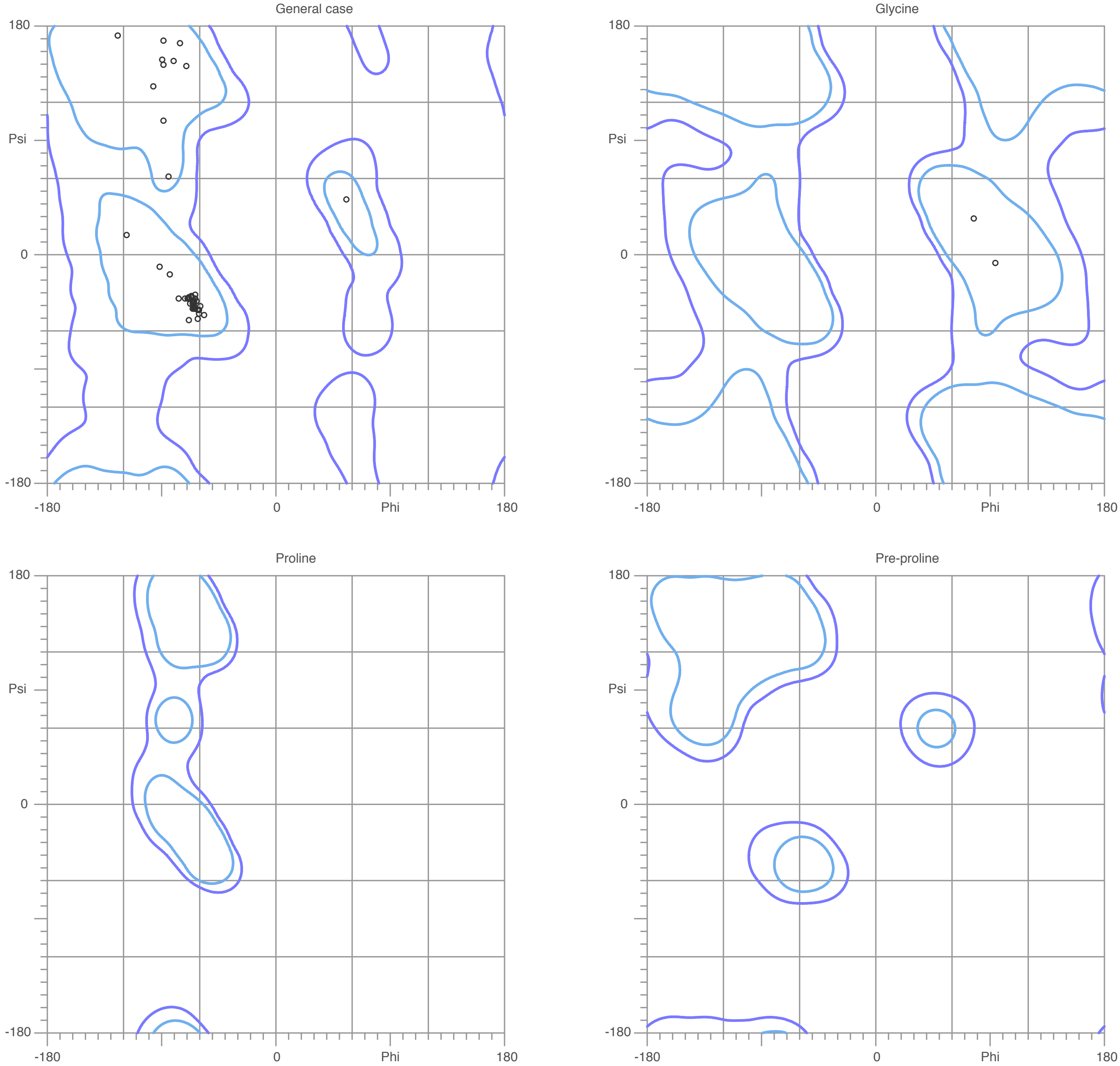
MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 14



100.0% (46/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

http://kinemage.biochem.duke.edu

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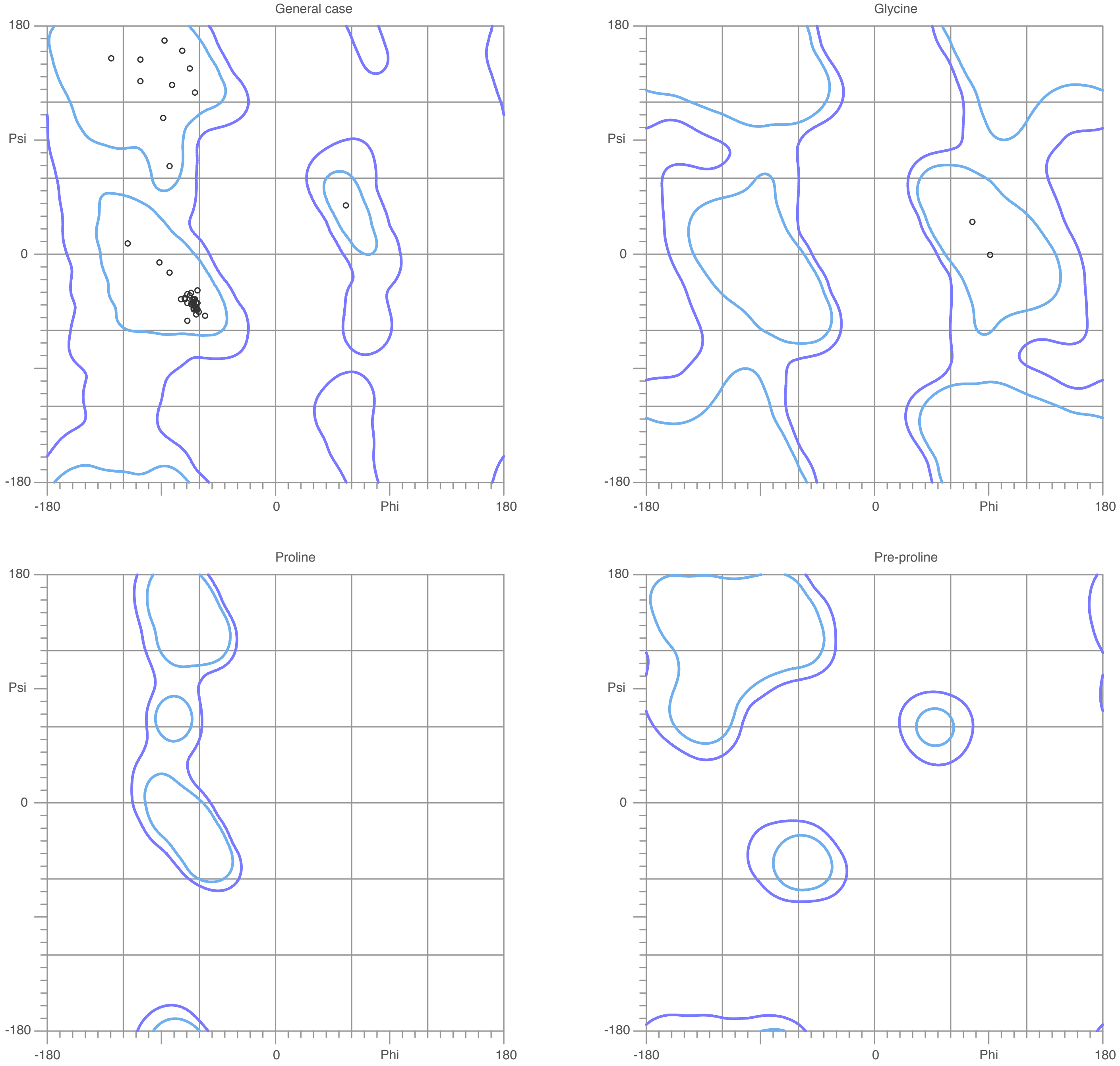
MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 15



100.0% (46/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

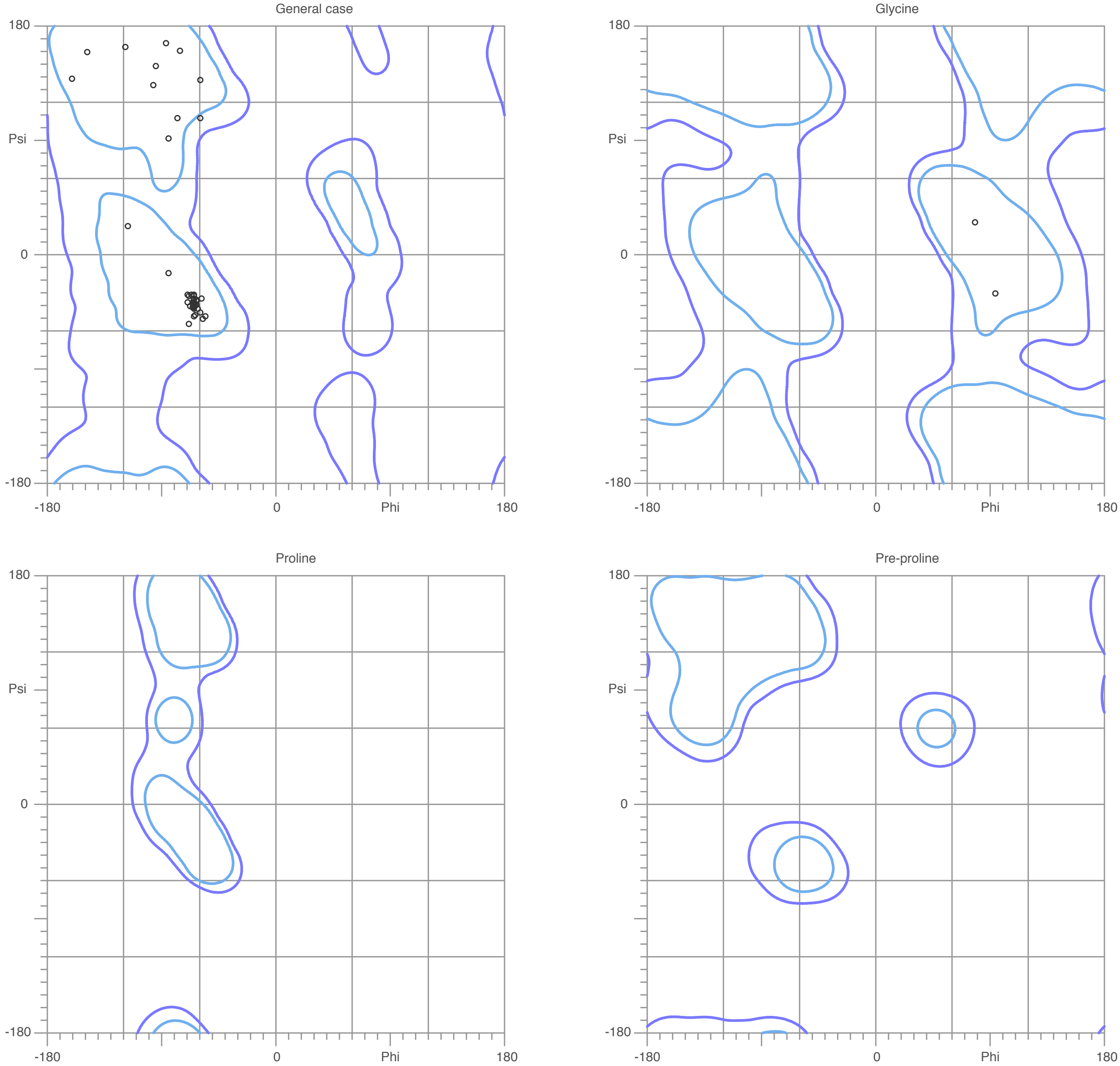
There were no outliers.

http://kinemage.biochem.duke.edu

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

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 16



97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

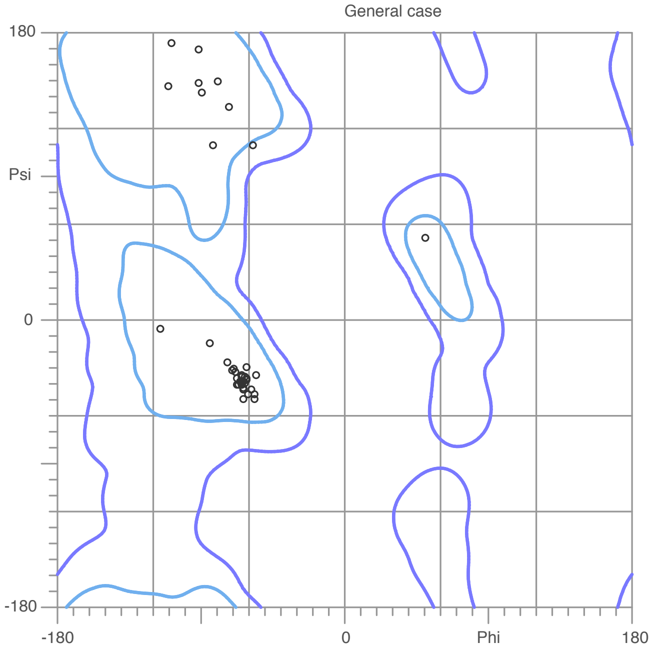
There were no outliers.

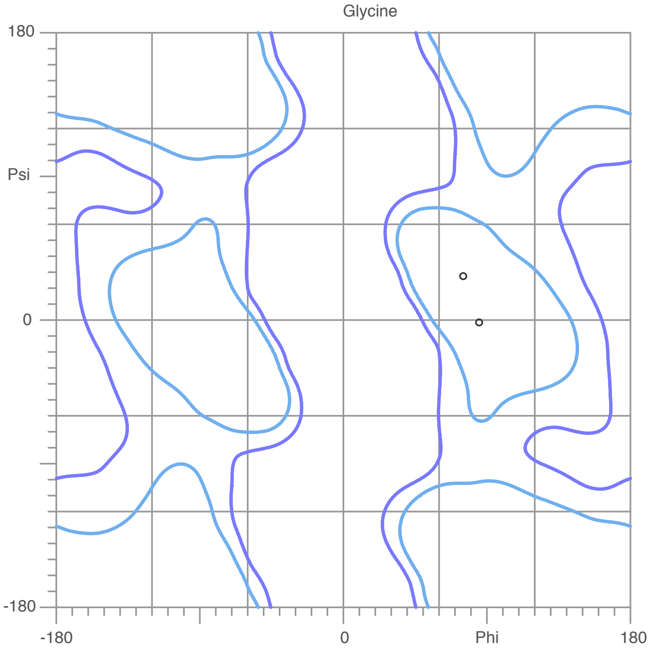
http://kinemage.biochem.duke.edu

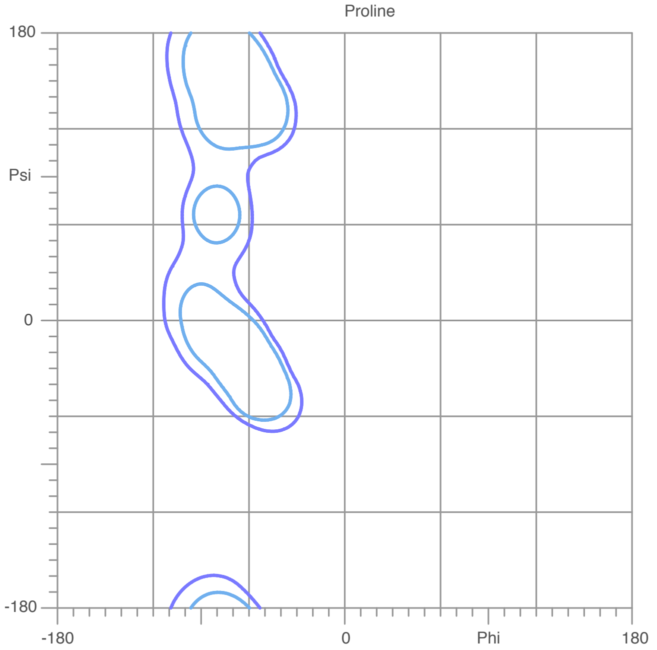
Lovell, Davis, et al. Proteins 50:437 (2003)

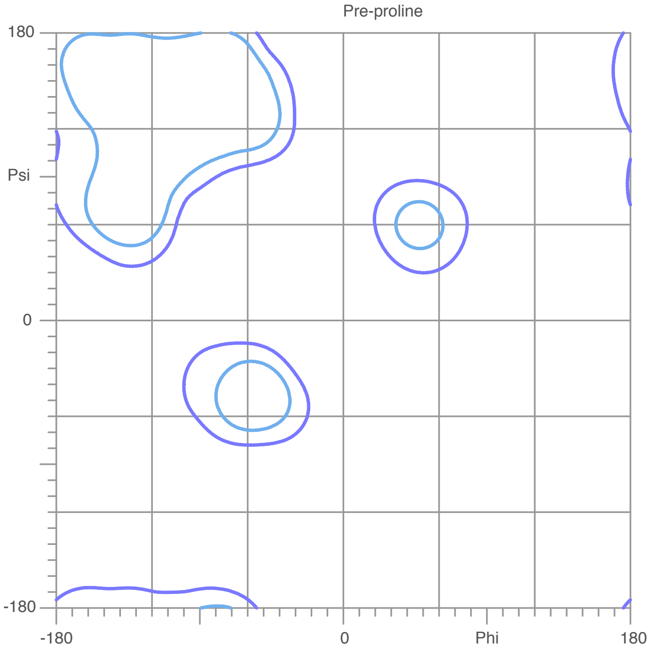
MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 17







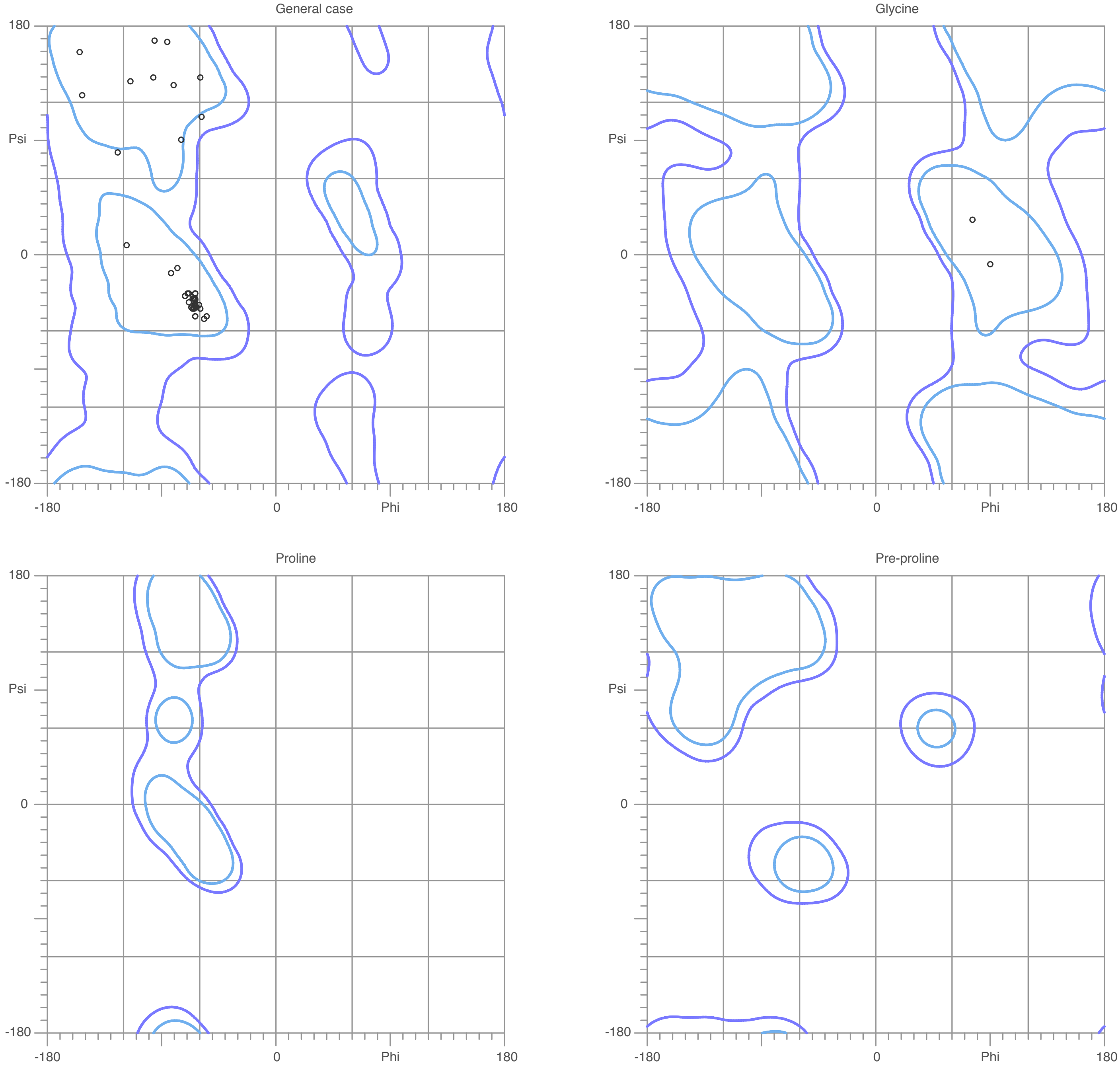


97.8% (45/46) of all residues were in favored (98%) regions.
100.0% (46/46) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

SR384_R3Cons_em_bcr3.pdb, model 18



95.7% (44/46) of all residues were in favored (98%) regions.
100.0% (46/46) 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)