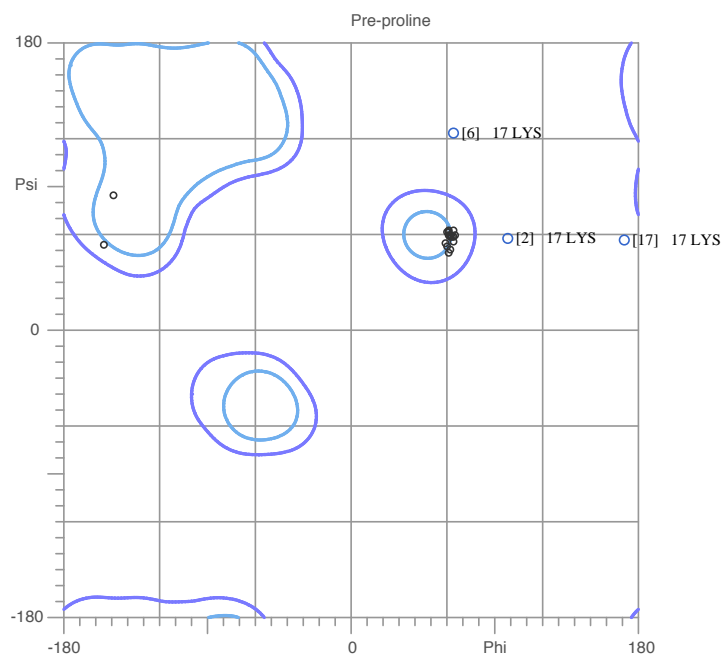
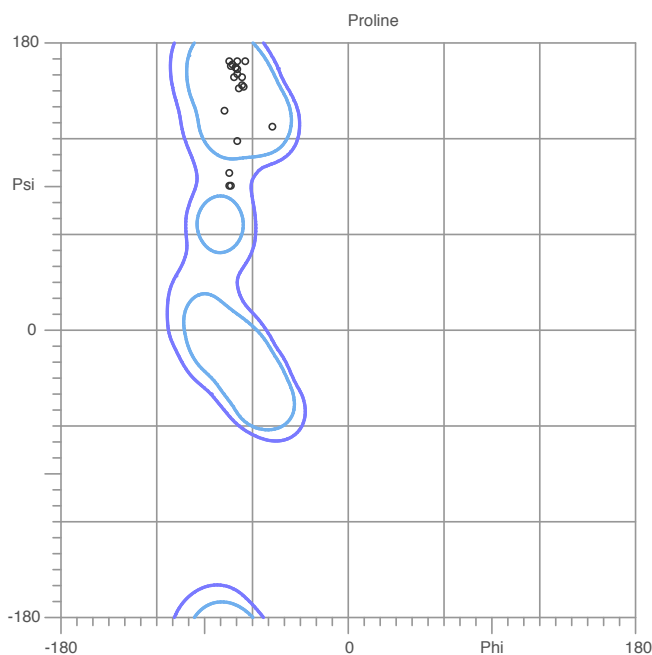
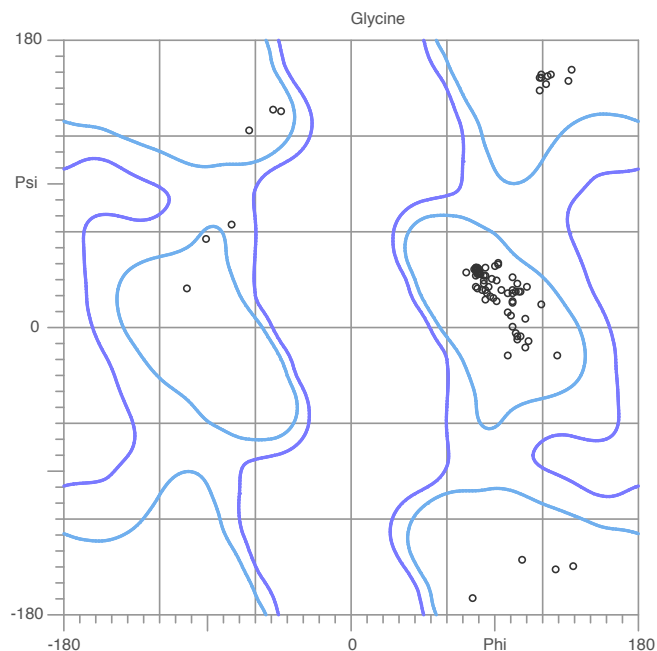
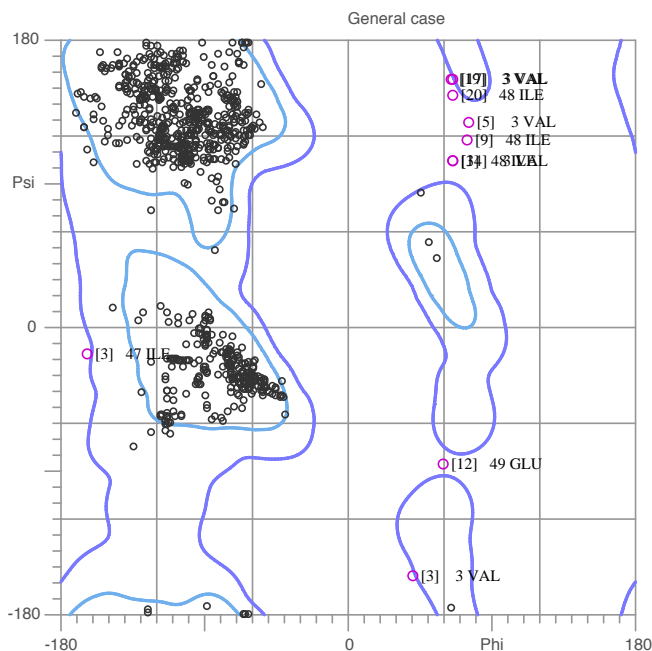


MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, all models



94.4% (906/960) of all residues were in favored (98%) regions.
98.6% (947/960) of all residues were in allowed (>99.8%) regions.

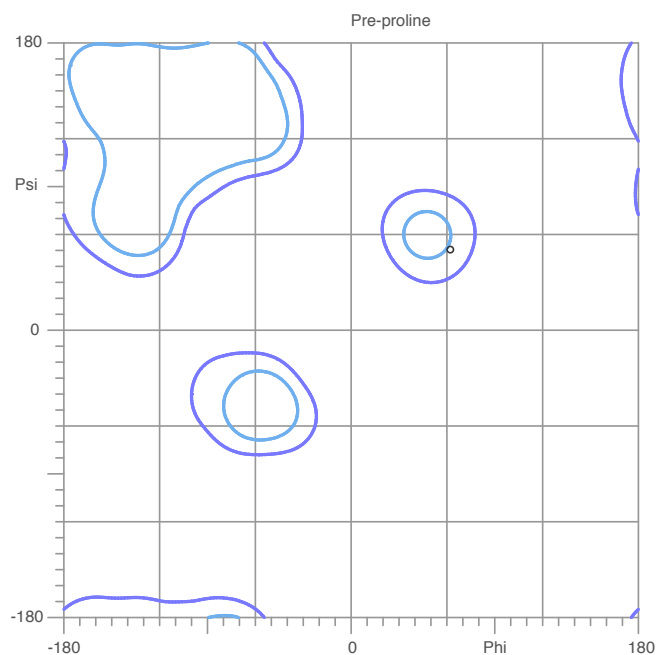
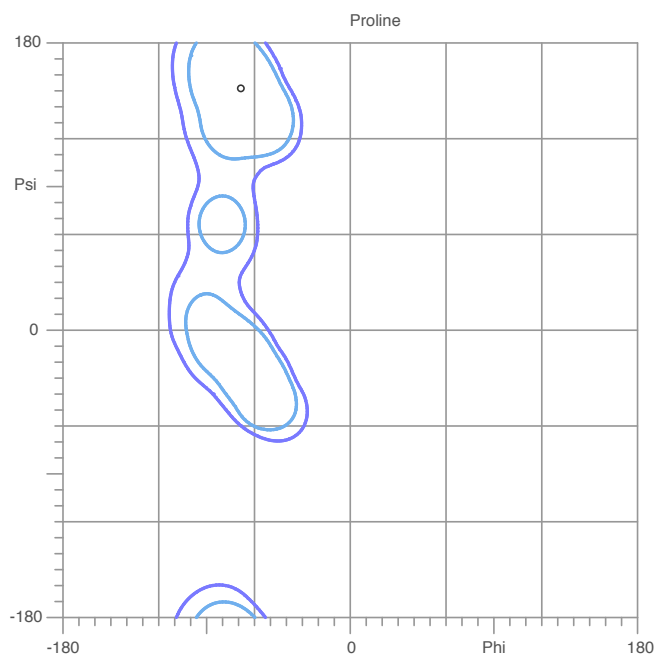
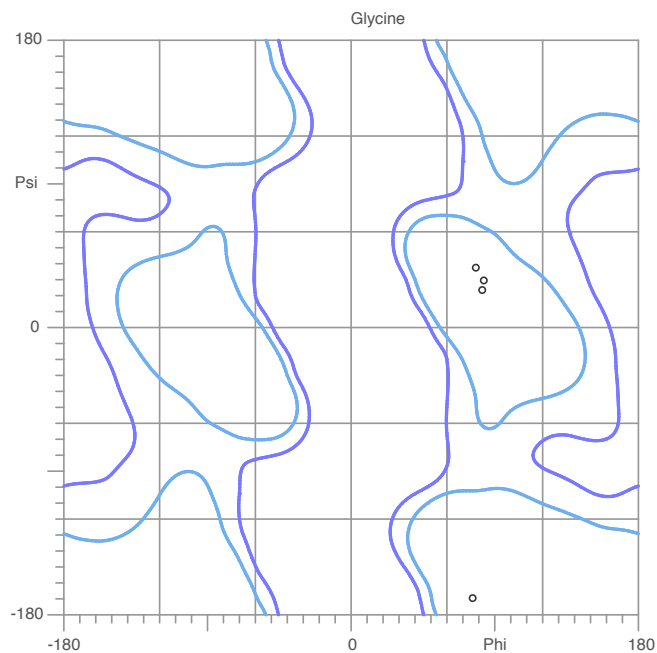
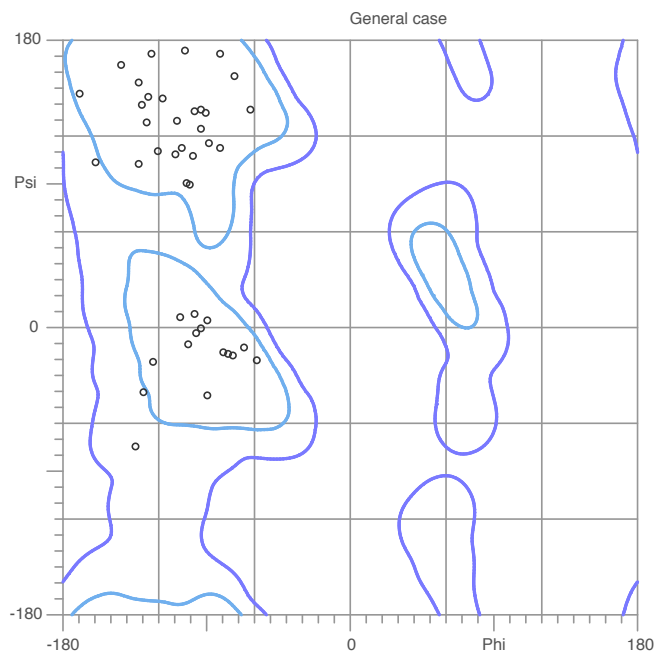
There were 13 outliers (phi, psi):

- [2] 17 LYS (98.9, 58.5)
- [3] 3 VAL (40.5, -155.0)
- [3] 47 ILE (-165.0, -16.5)
- [3] 48 ILE (65.1, 105.0)

- [5] 3 VAL (75.0, 129.5)
- [6] 17 LYS (65.0, 125.0)
- [9] 48 ILE (74.9, 118.3)
- [12] 49 GLU (59.5, -85.1)
- [14] 3 VAL (65.0, 105.1)
- [17] 3 VAL (65.0, 156.3)
- [17] 17 LYS (171.3, 57.0)
- [19] 3 VAL (64.1, 156.8)
- [20] 48 ILE (65.0, 146.9)

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 1



91.7% (44/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

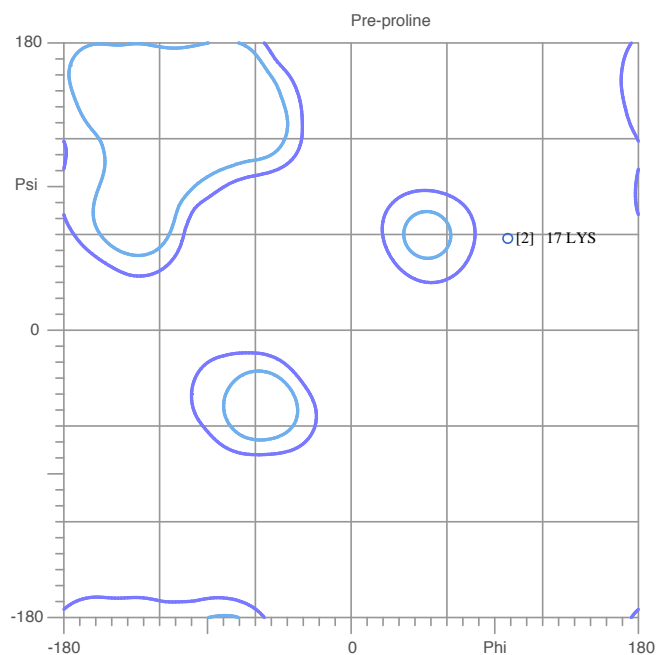
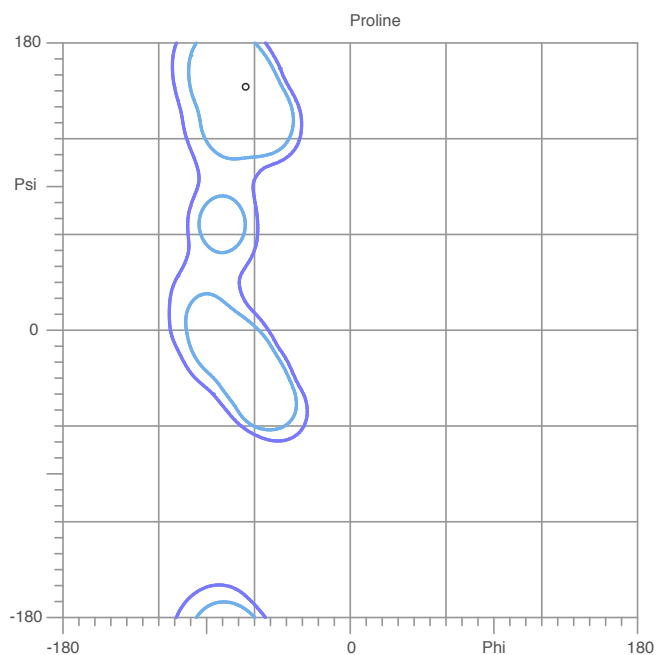
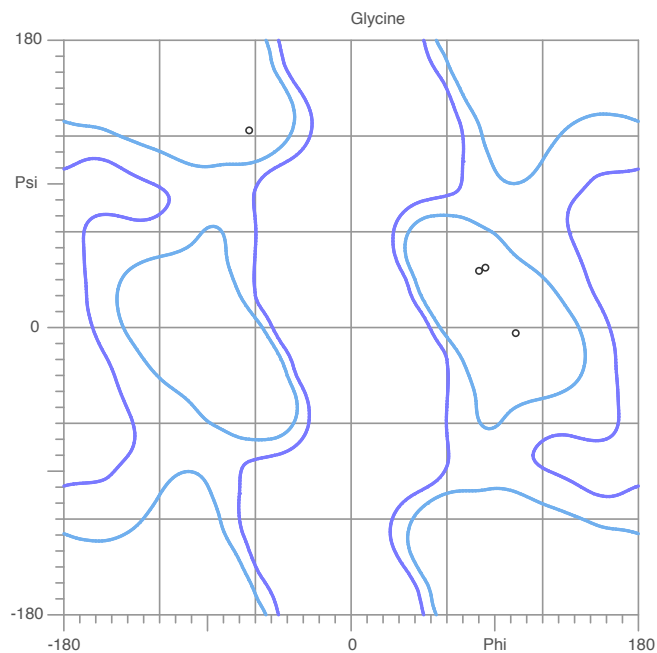
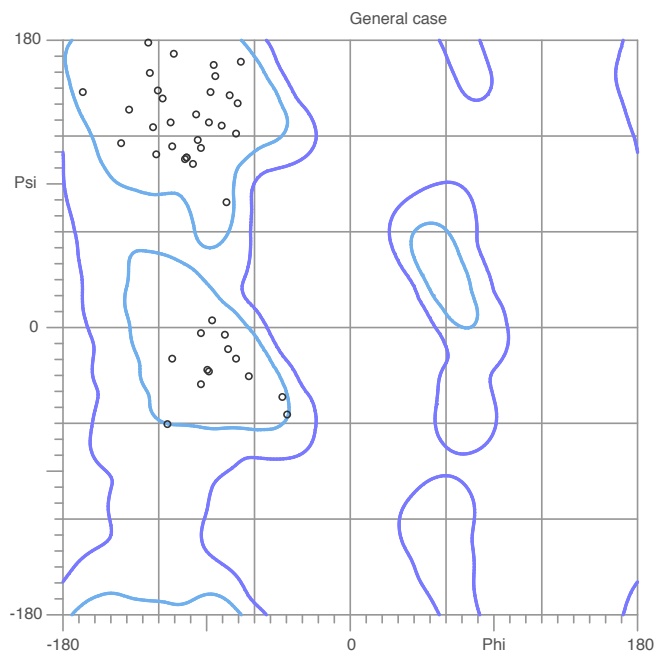
There were no outliers.

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

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 2



97.9% (47/48) of all residues were in favored (98%) regions.
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

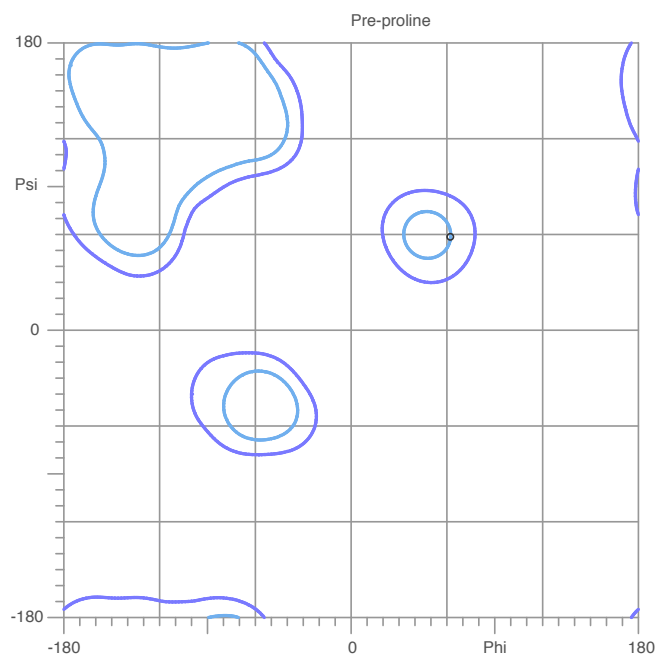
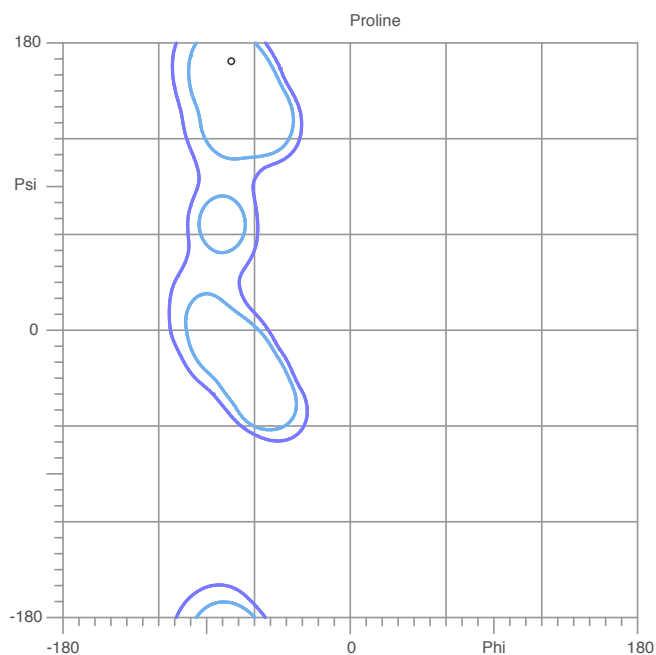
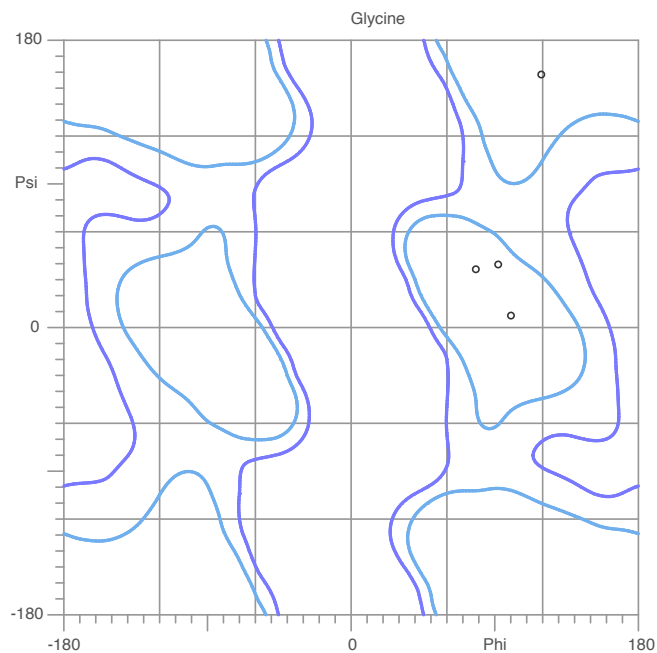
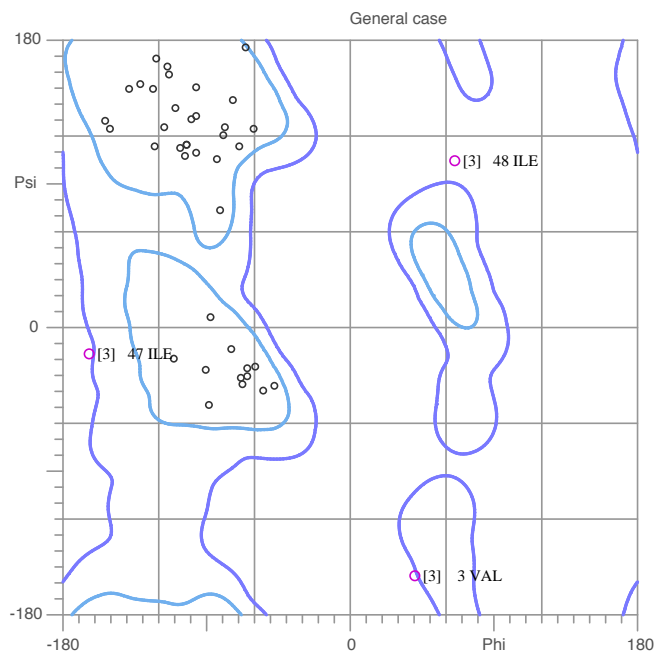
There were 1 outliers (phi, psi):
[2] 17 LYS (98.9, 58.5)

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

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 3



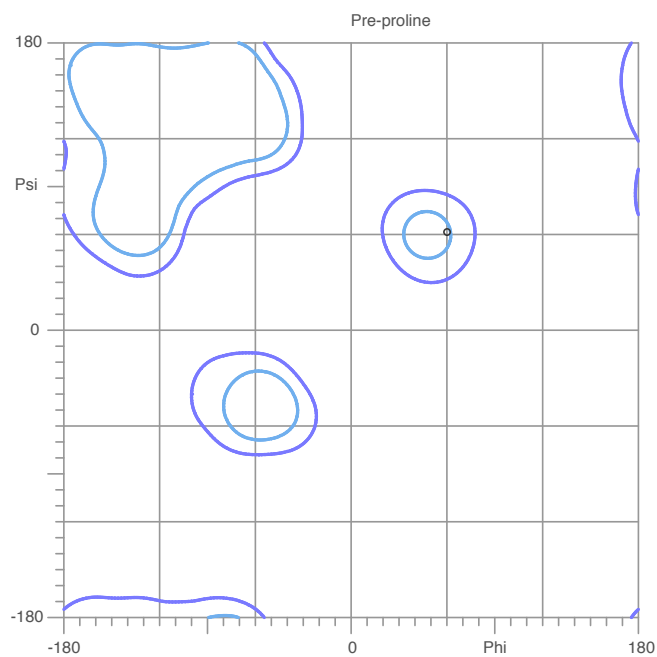
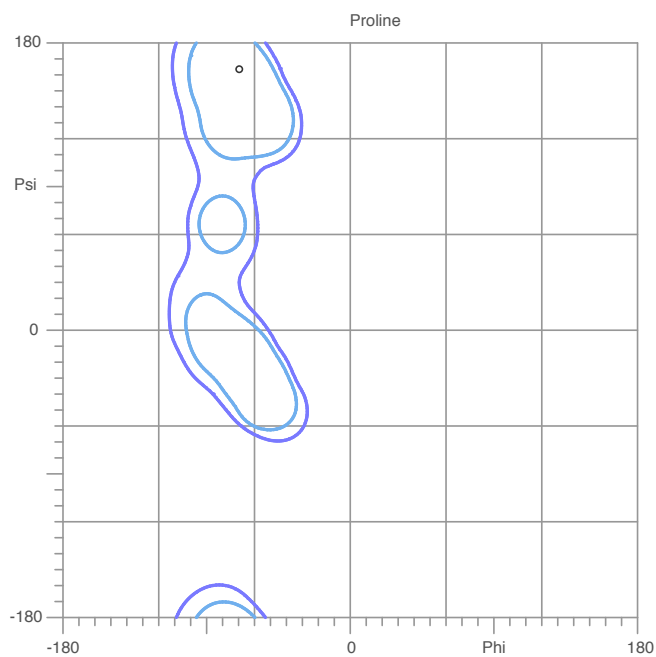
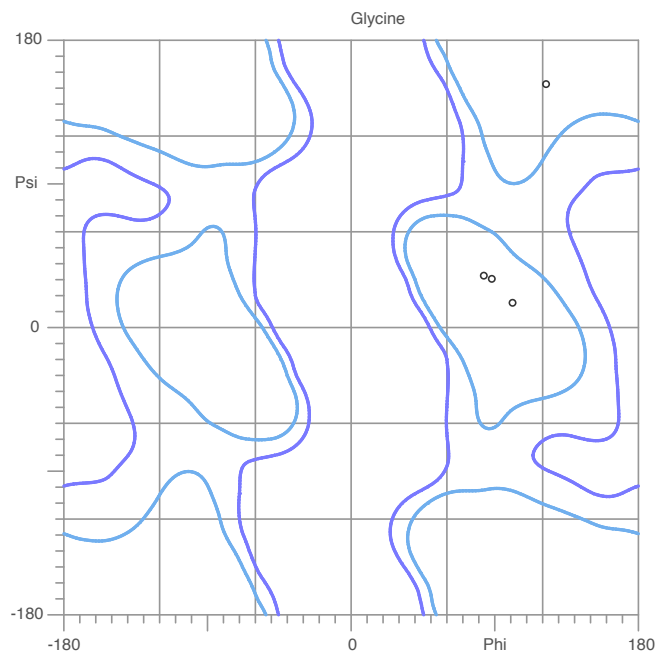
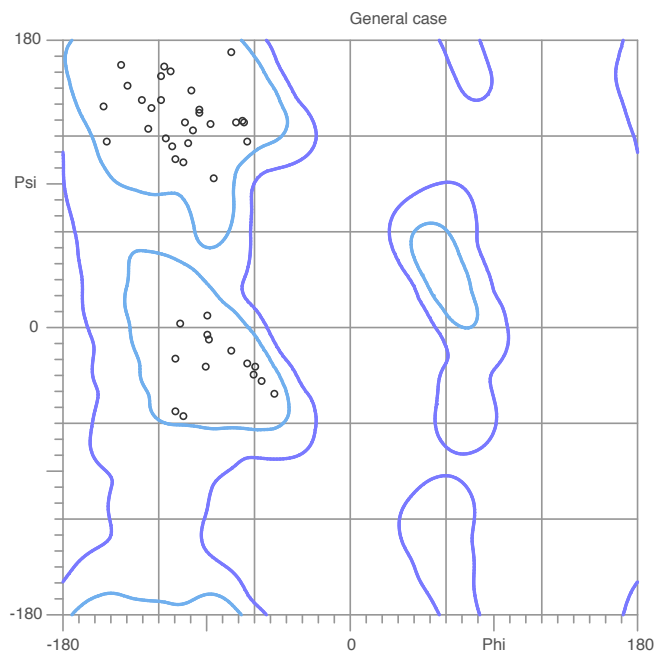
91.7% (44/48) of all residues were in favored (98%) regions.
93.8% (45/48) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 3 VAL (40.5, -155.0)
- [3] 47 ILE (-165.0, -16.5)
- [3] 48 ILE (65.1, 105.0)

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 4



100.0% (48/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

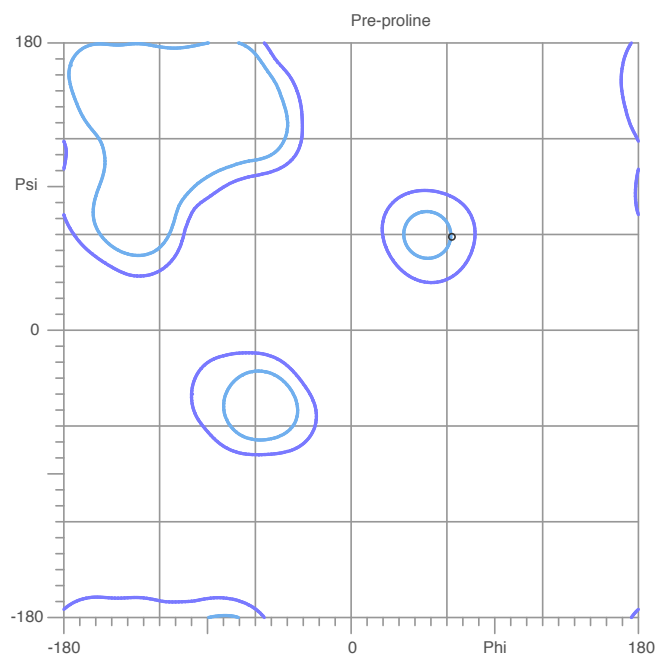
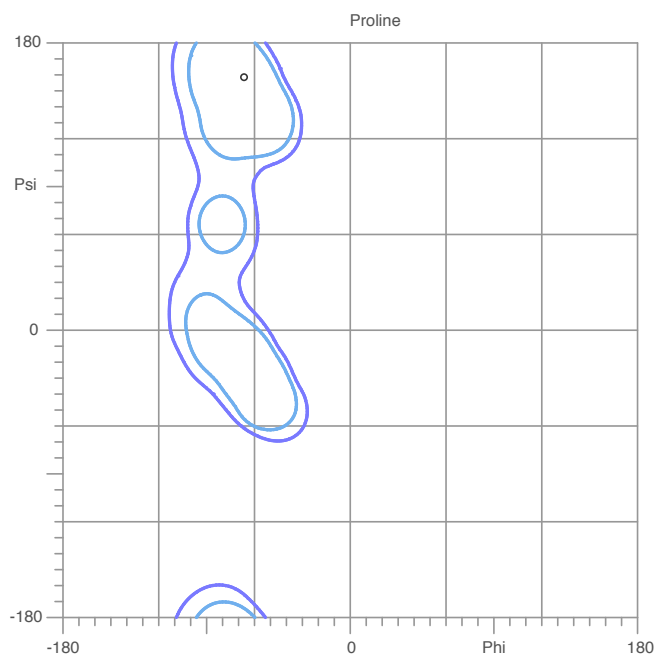
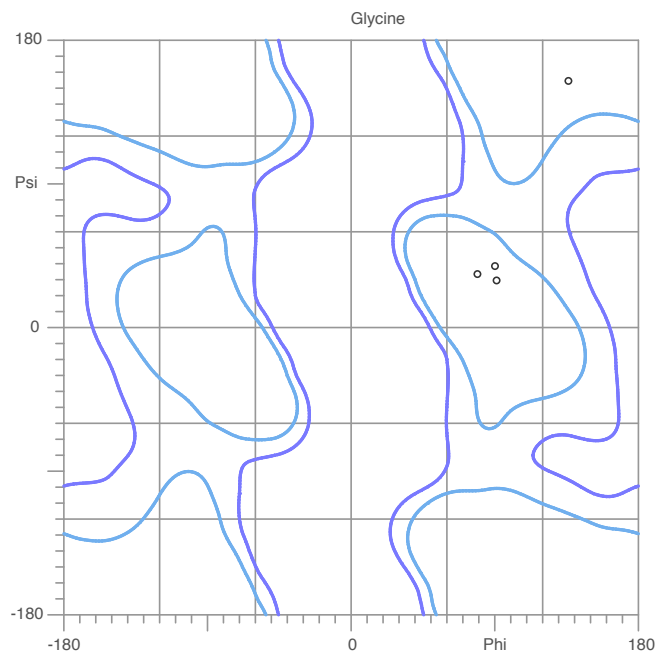
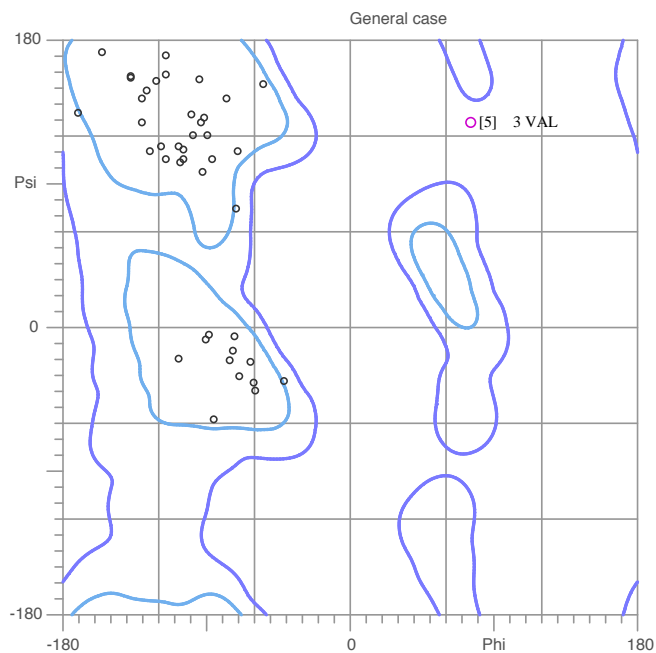
There were no outliers.

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 5

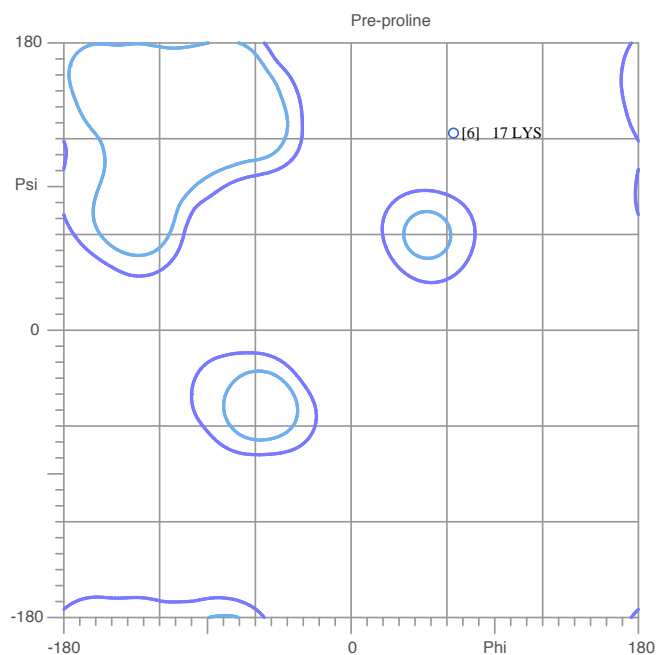
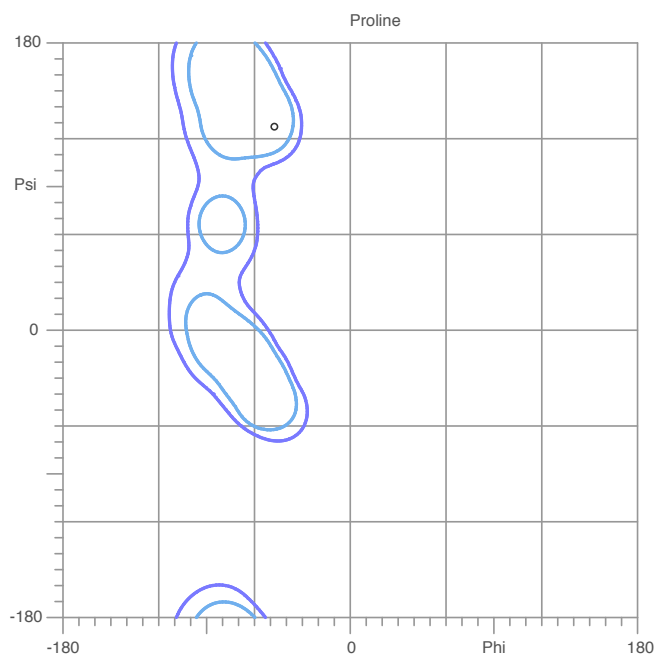
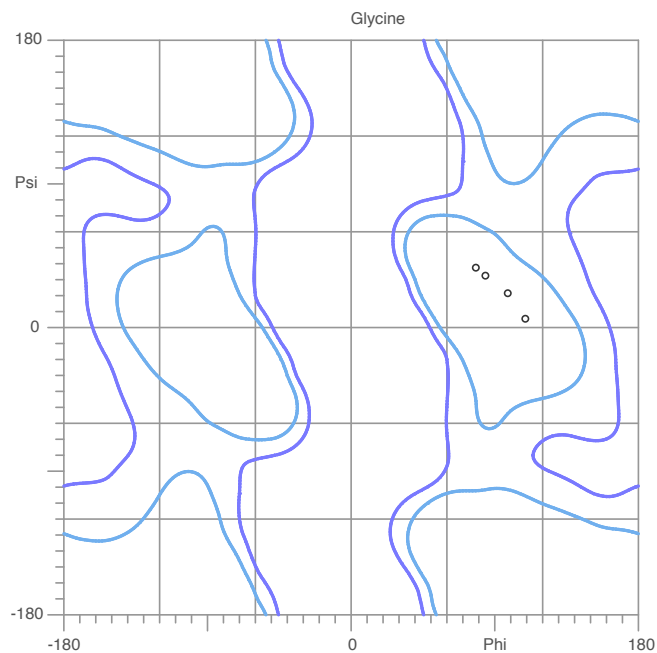
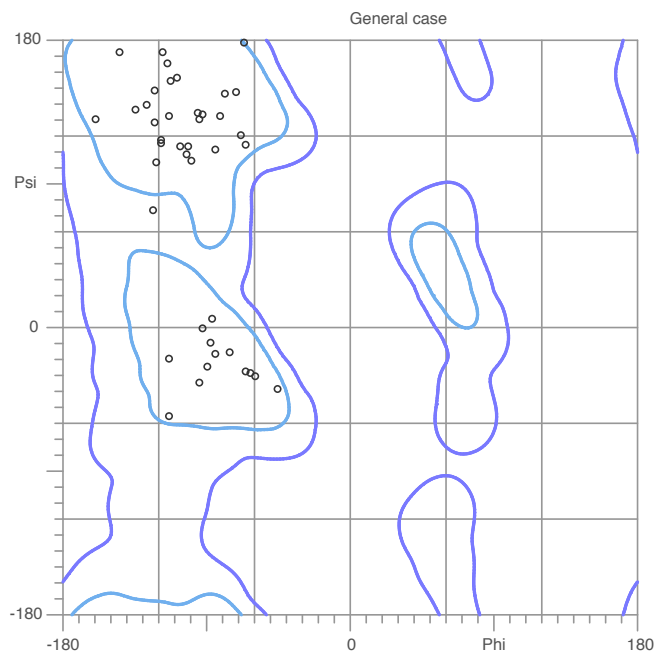


89.6% (43/48) of all residues were in favored (98%) regions.
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 3 VAL (75.0, 129.5)

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 6



93.8% (45/48) of all residues were in favored (98%) regions.
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

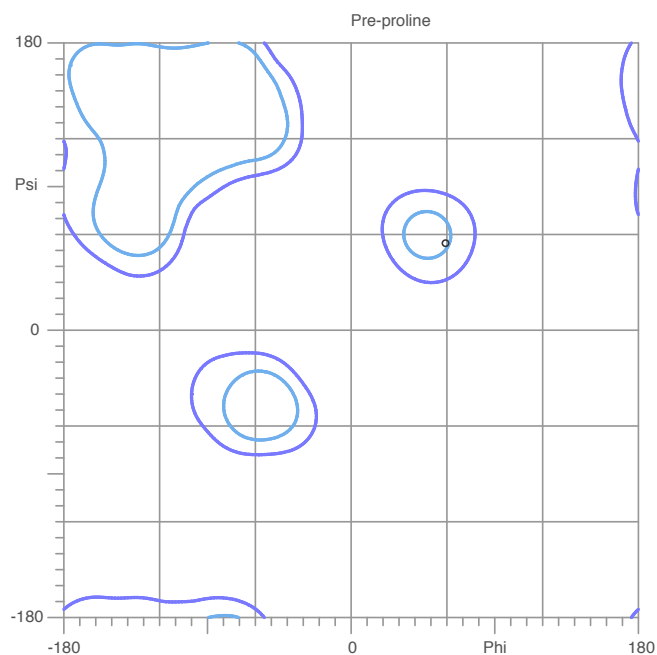
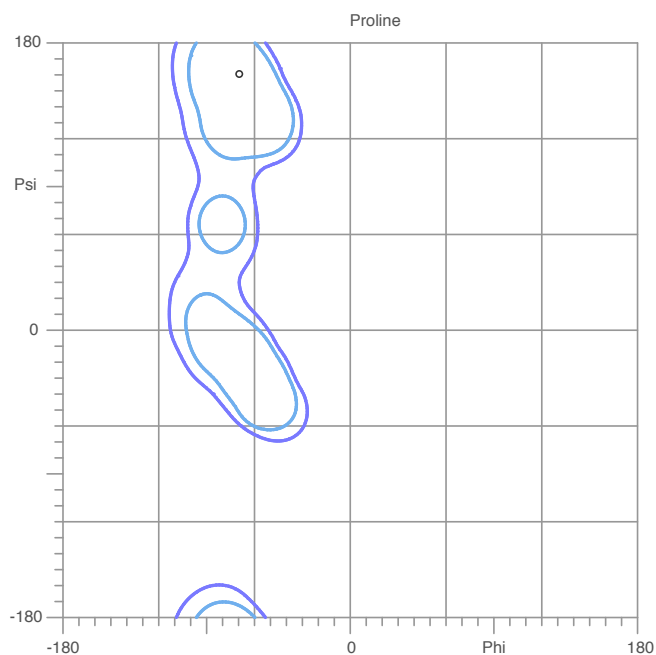
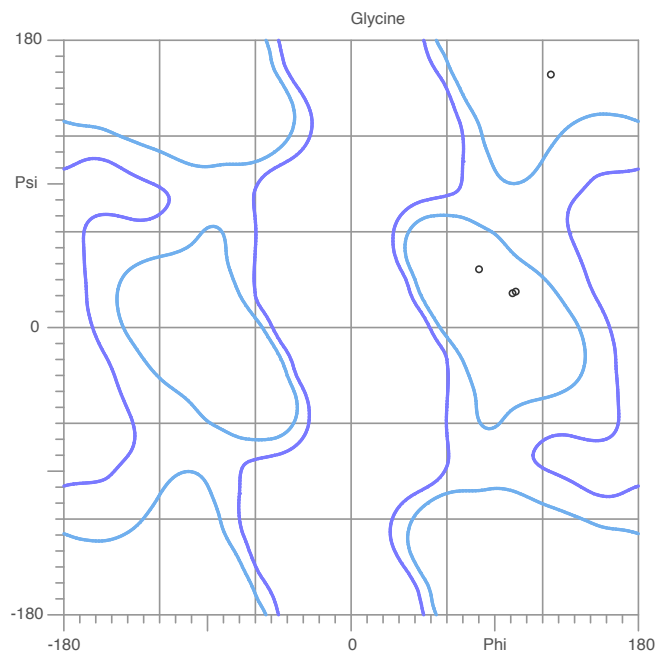
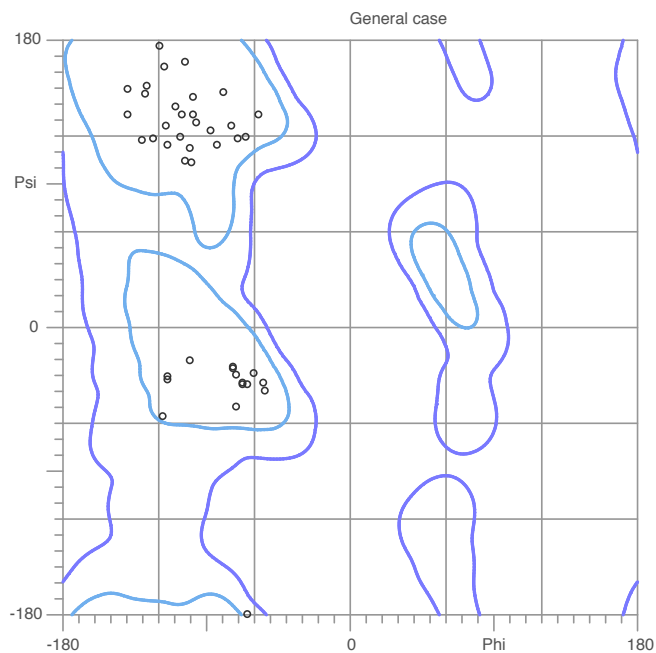
There were 1 outliers (phi, psi):
[6] 17 LYS (65.0, 125.0)

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 7



97.9% (47/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

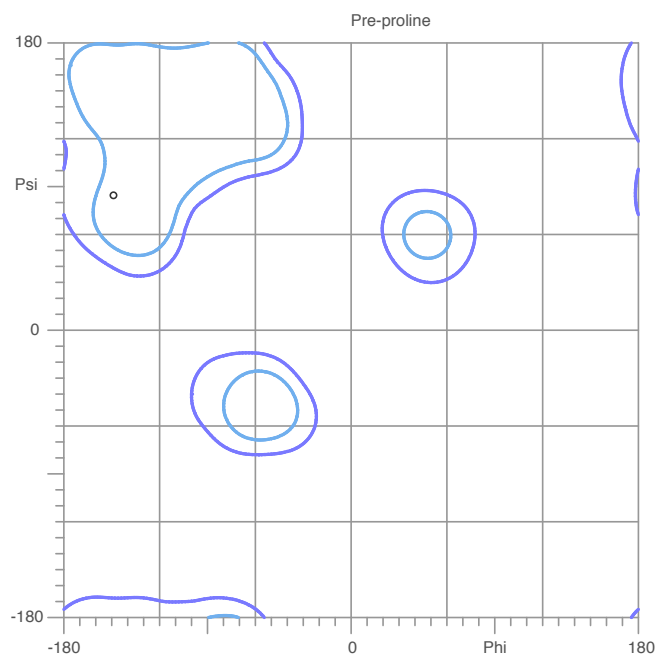
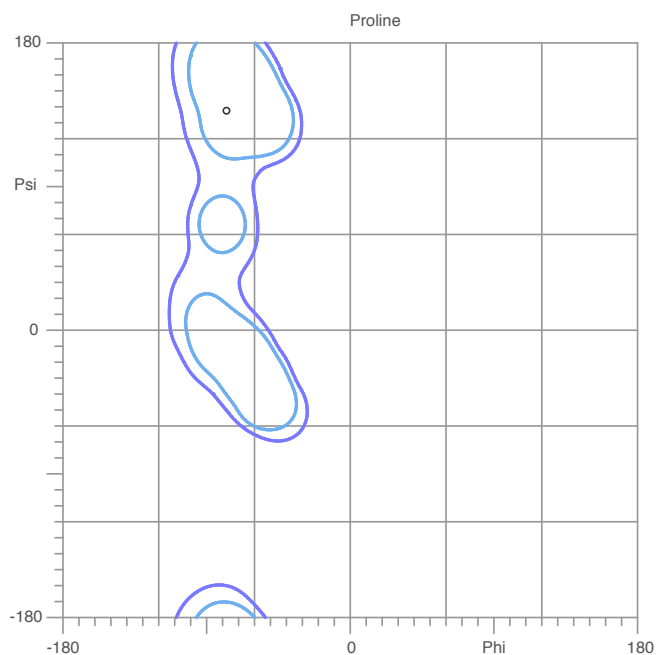
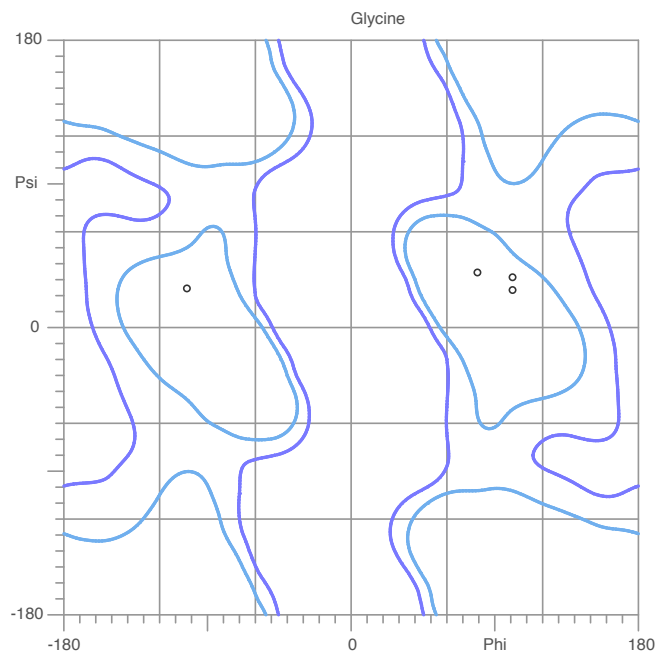
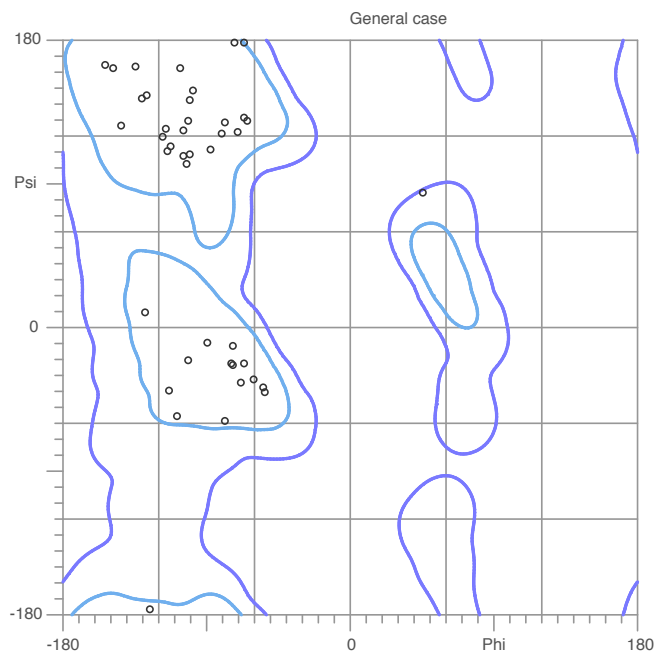
There were no outliers.

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

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 8



95.8% (46/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

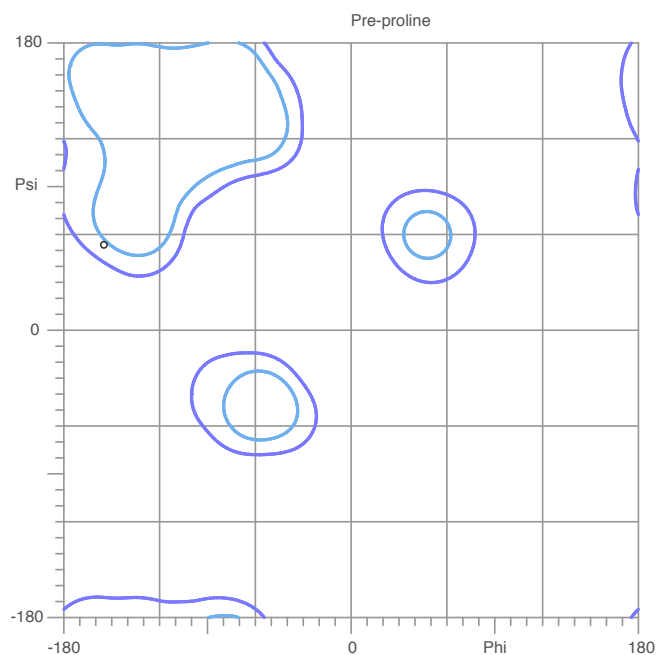
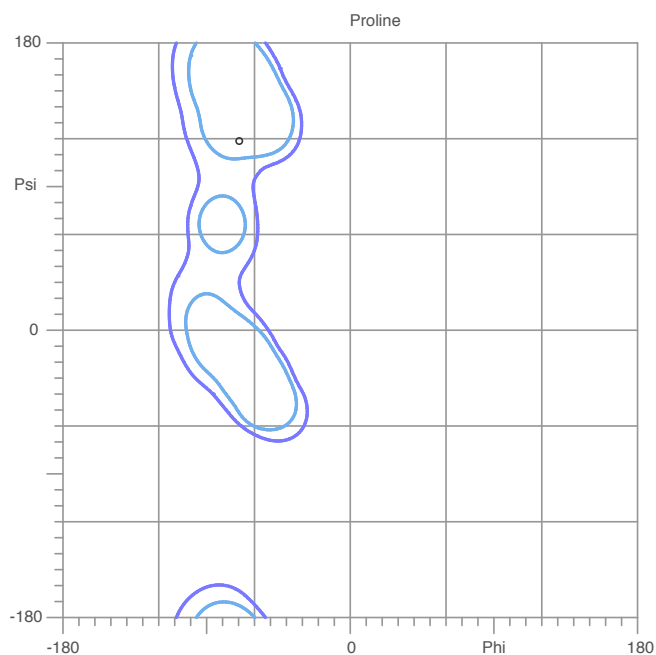
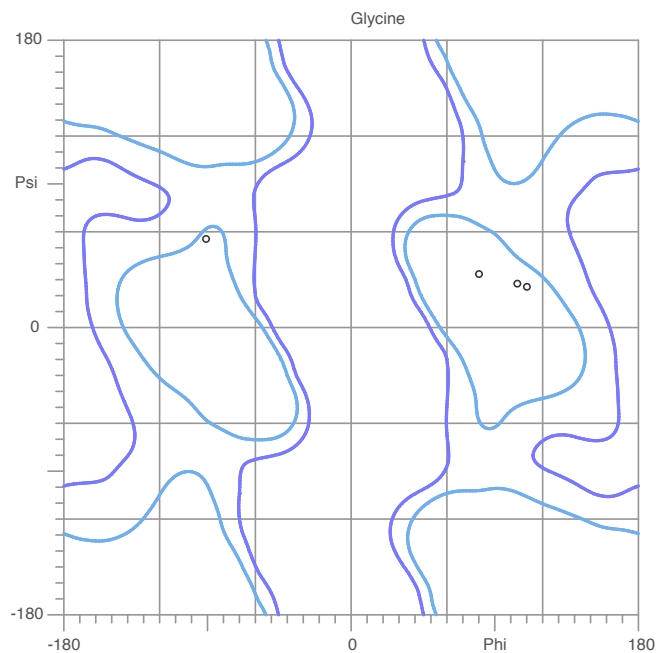
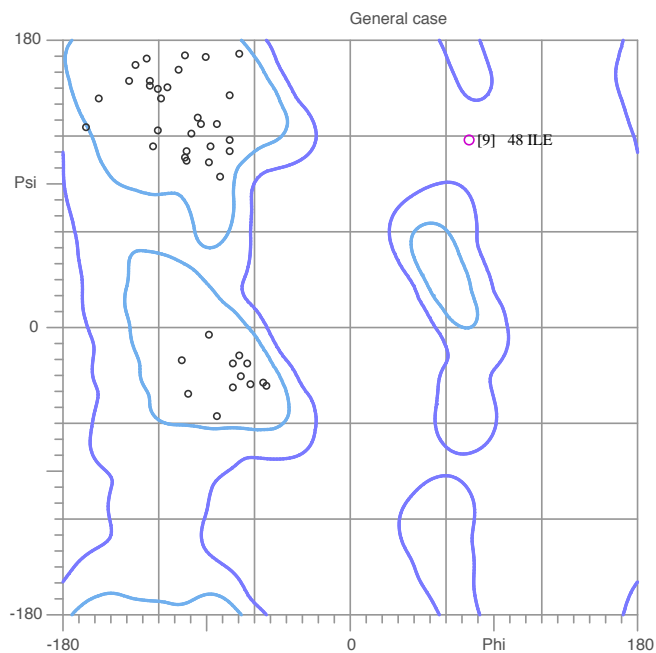
There were no outliers.

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

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 9

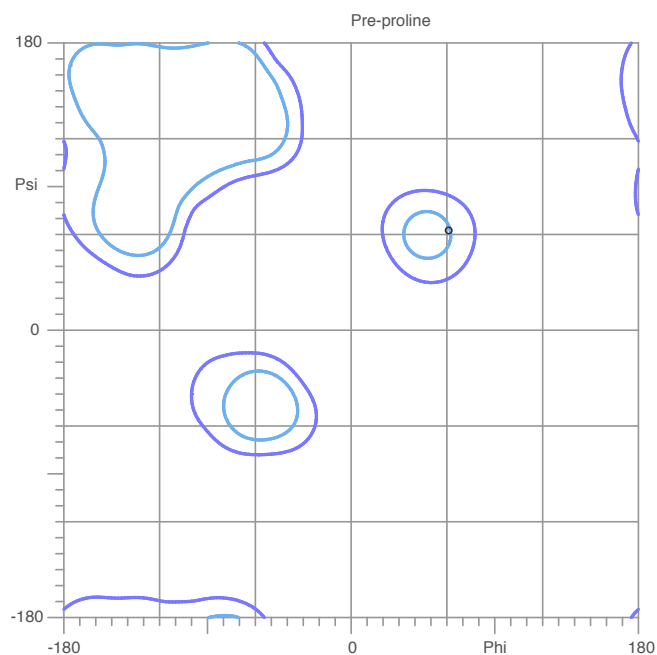
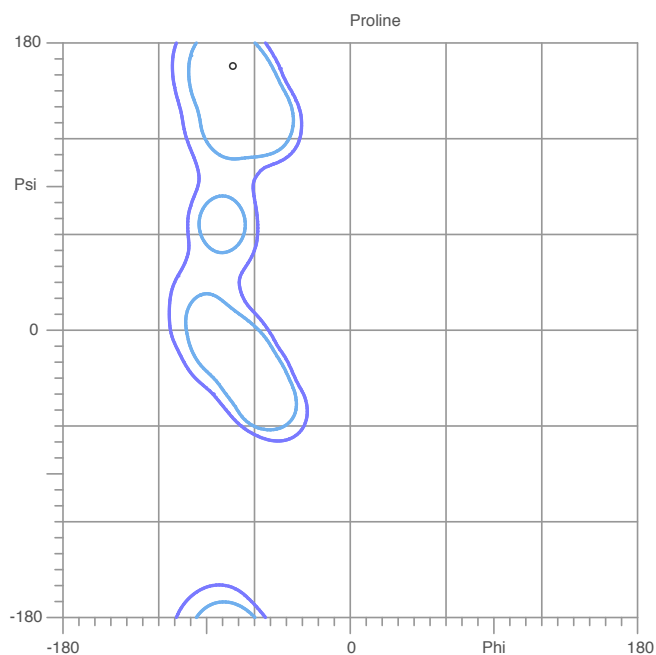
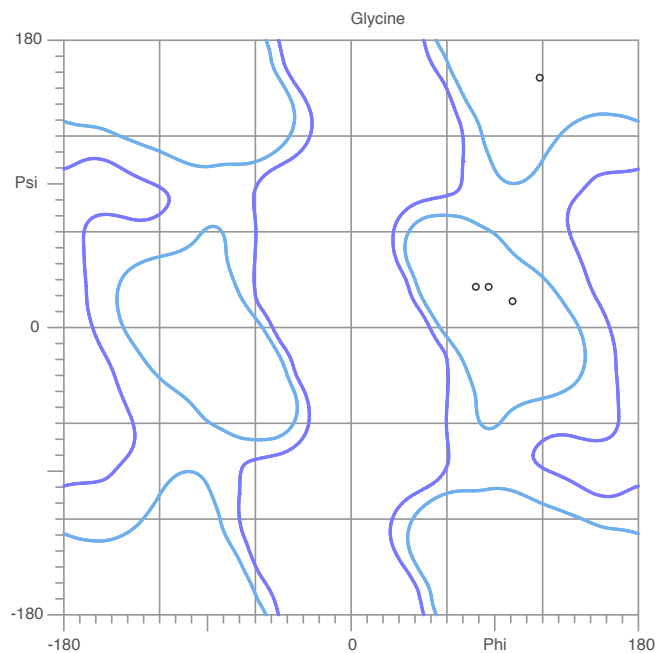
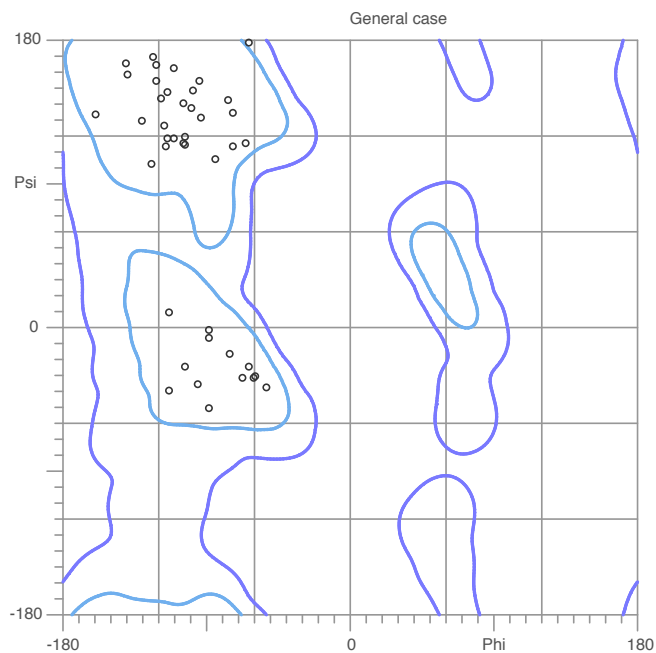


93.8% (45/48) of all residues were in favored (98%) regions.
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 48 ILE (74.9, 118.3)

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 10



97.9% (47/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

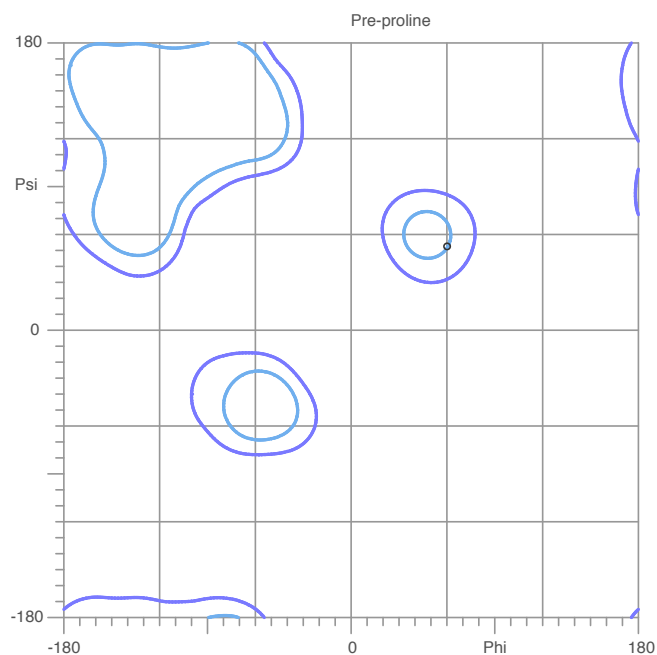
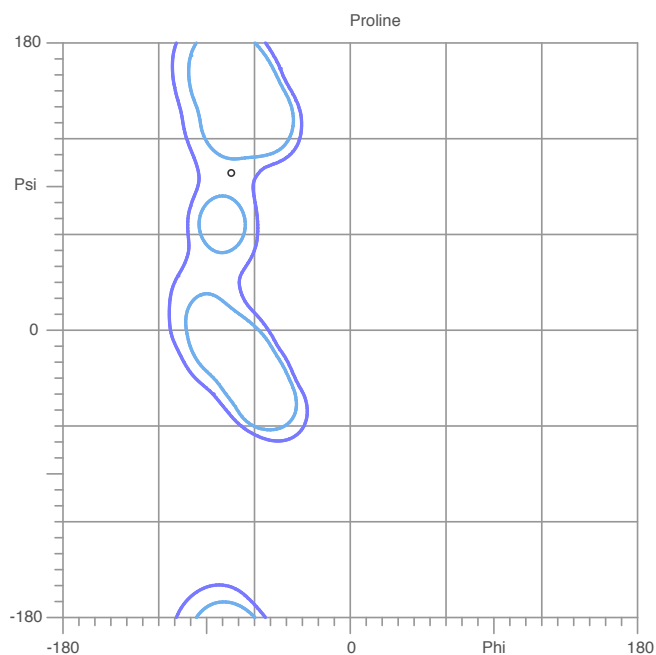
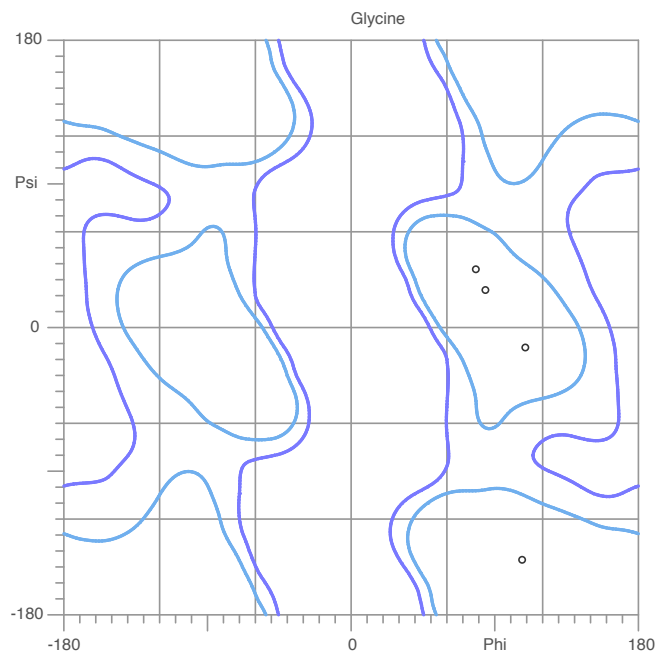
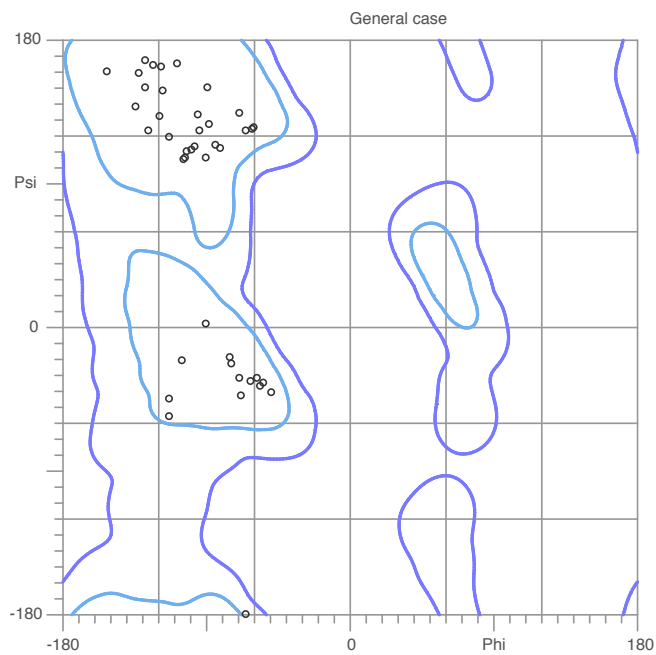
There were no outliers.

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 11



95.8% (46/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

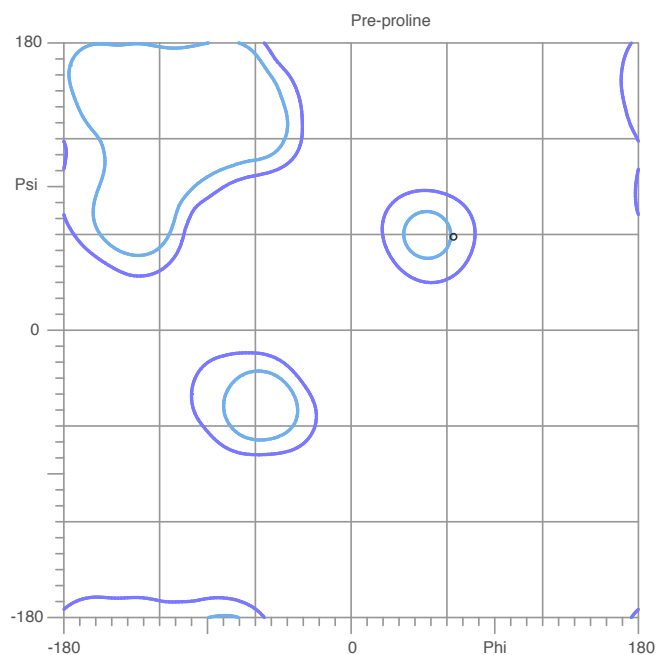
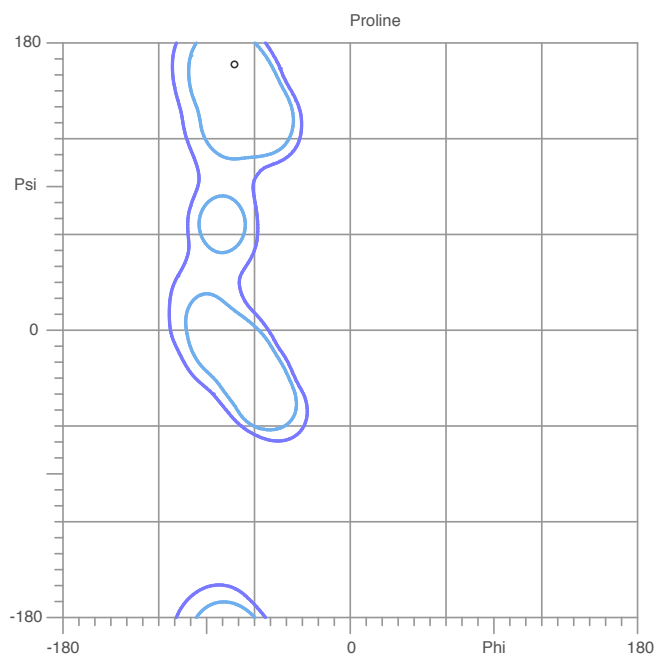
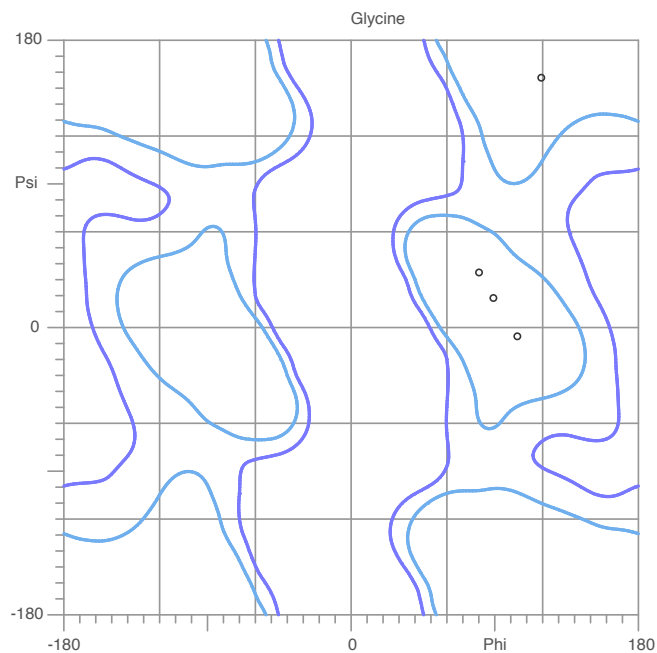
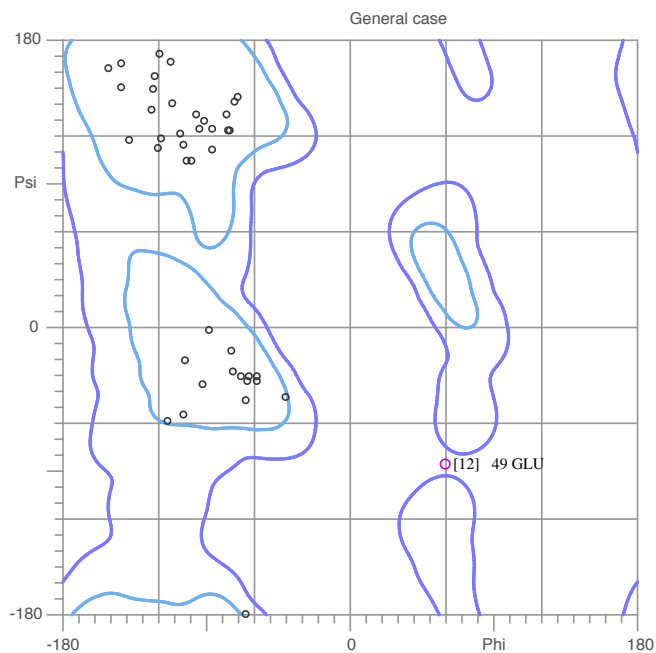
There were no outliers.

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

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 12



93.8% (45/48) of all residues were in favored (98%) regions.
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

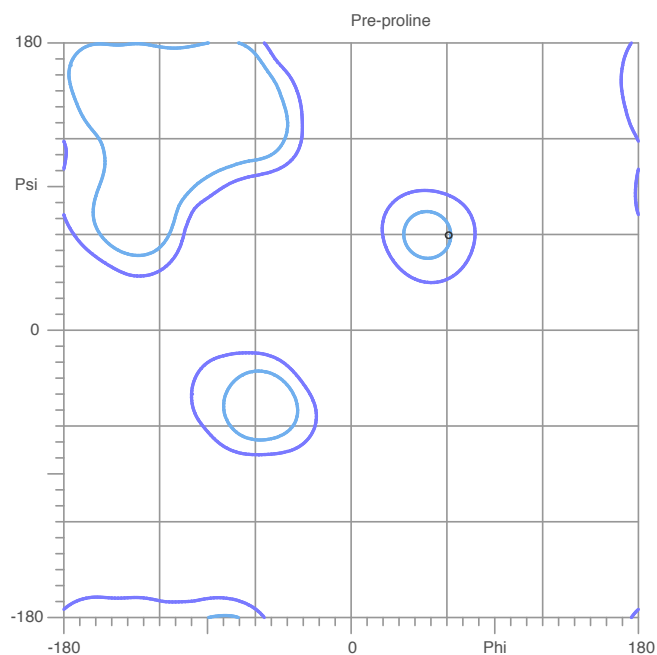
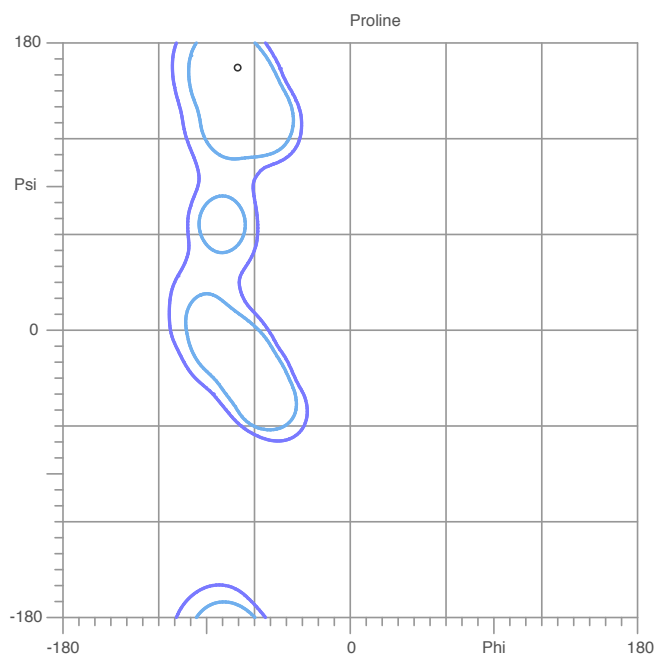
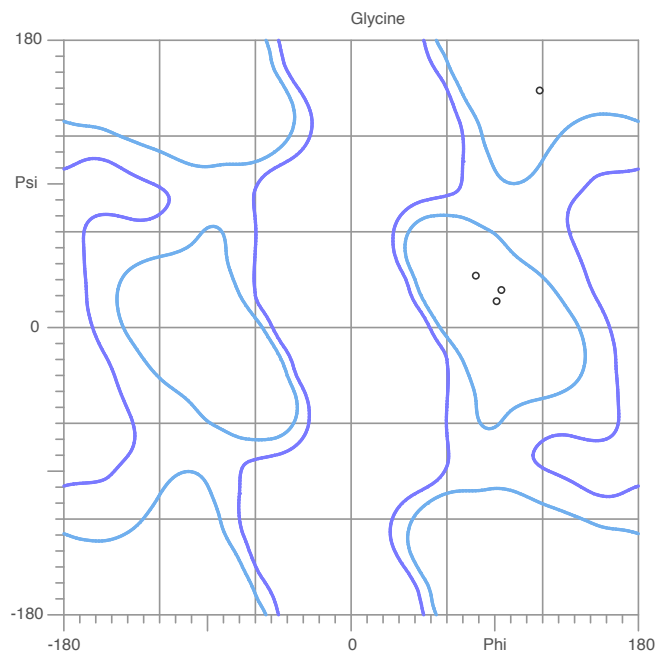
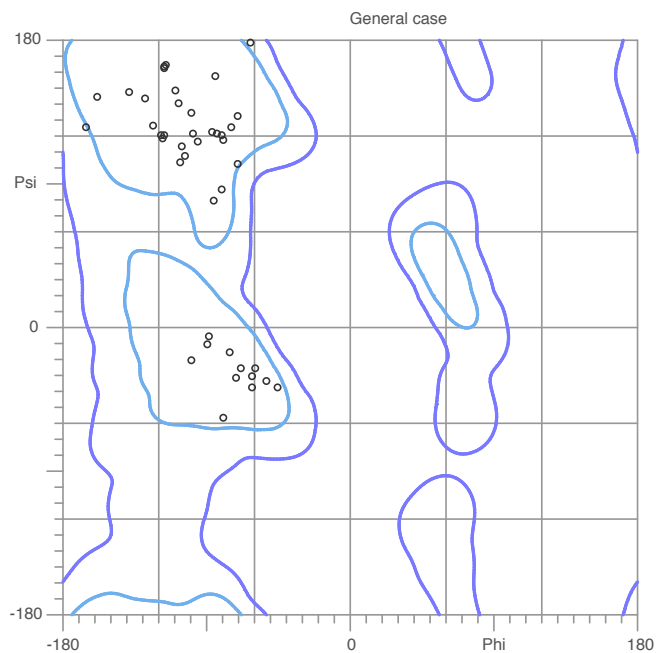
There were 1 outliers (phi, psi):
[12] 49 GLU (59.5, -85.1)

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 13

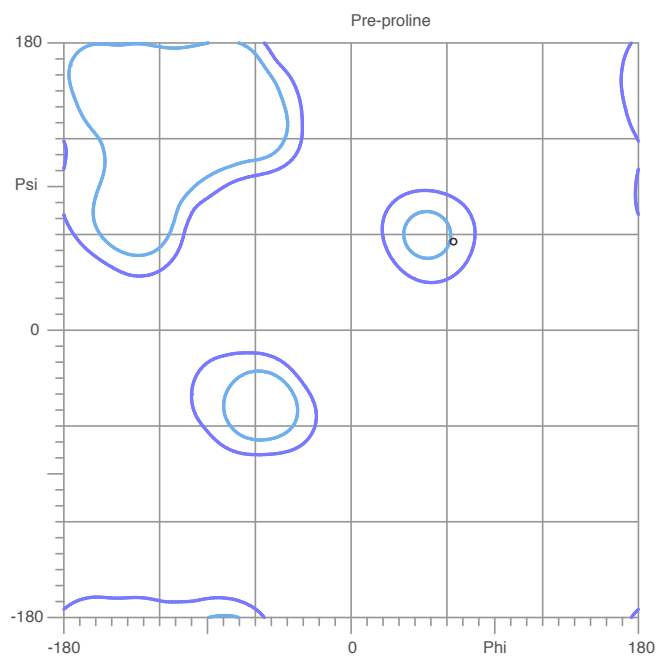
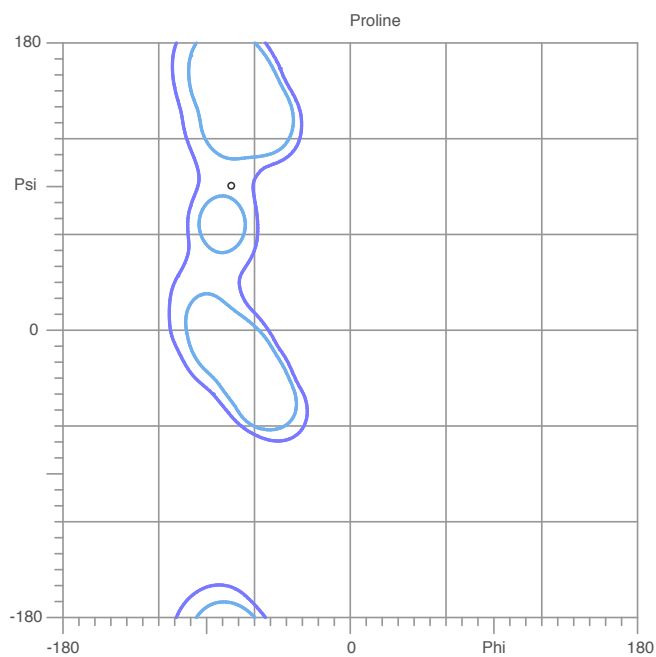
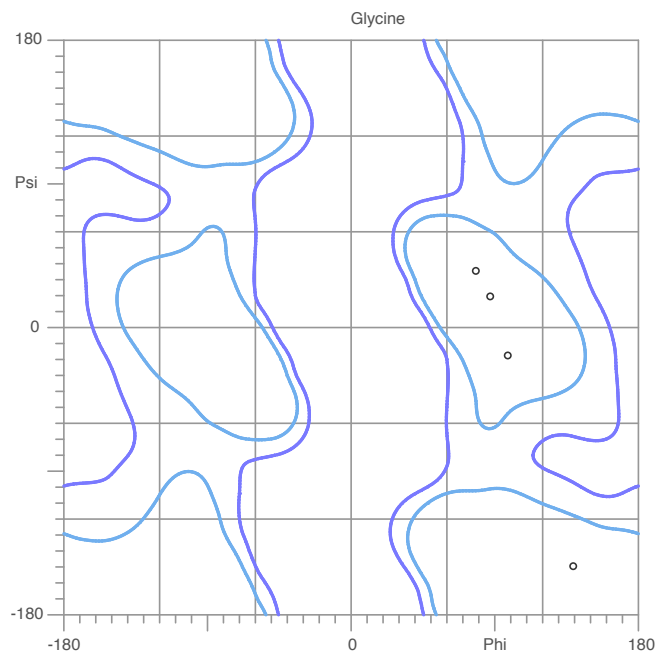
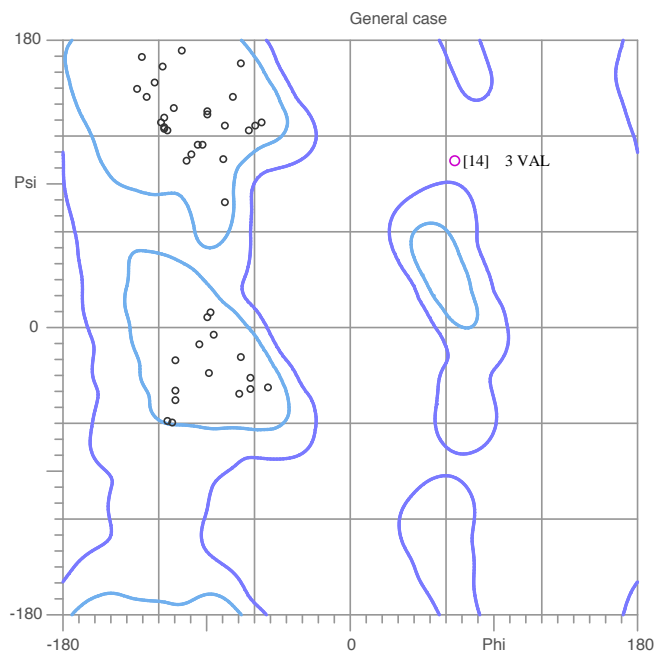


95.8% (46/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 14

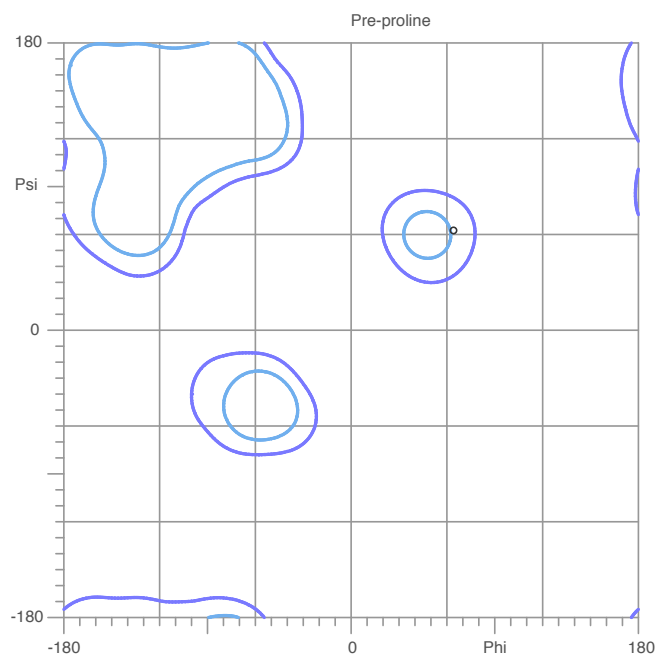
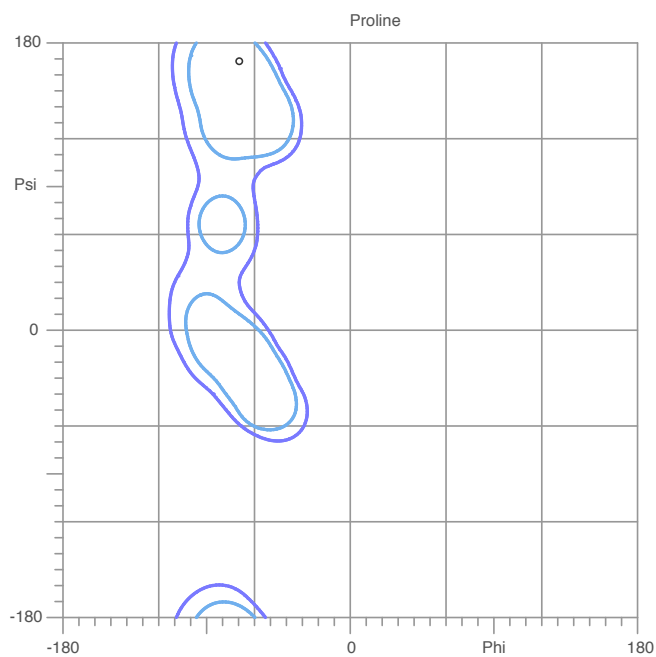
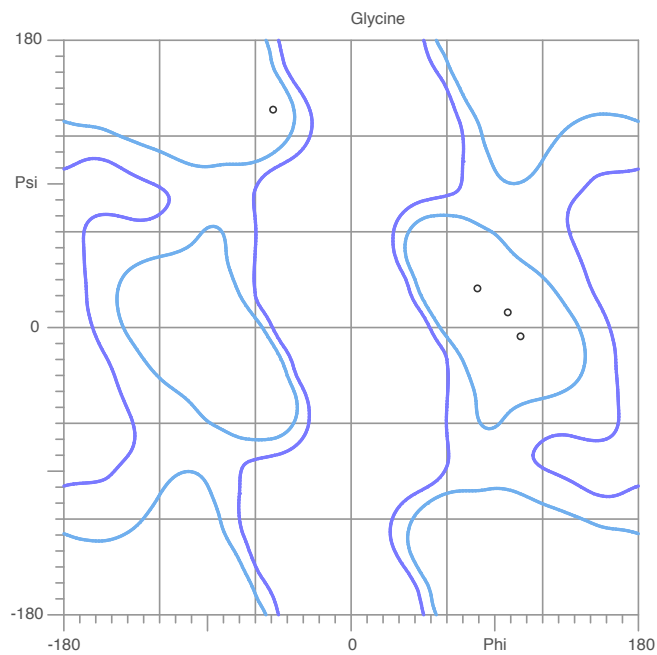
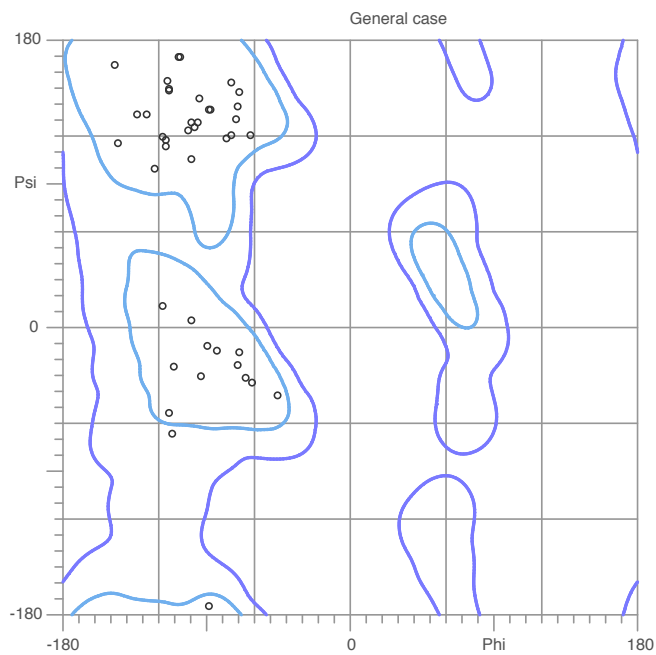


93.8% (45/48) of all residues were in favored (98%) regions.
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[14] 3 VAL (65.0, 105.1)

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 15



95.8% (46/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

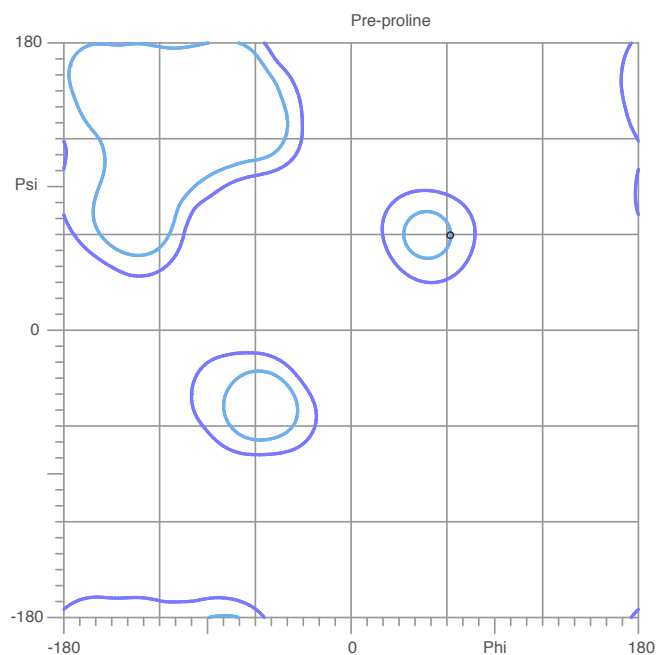
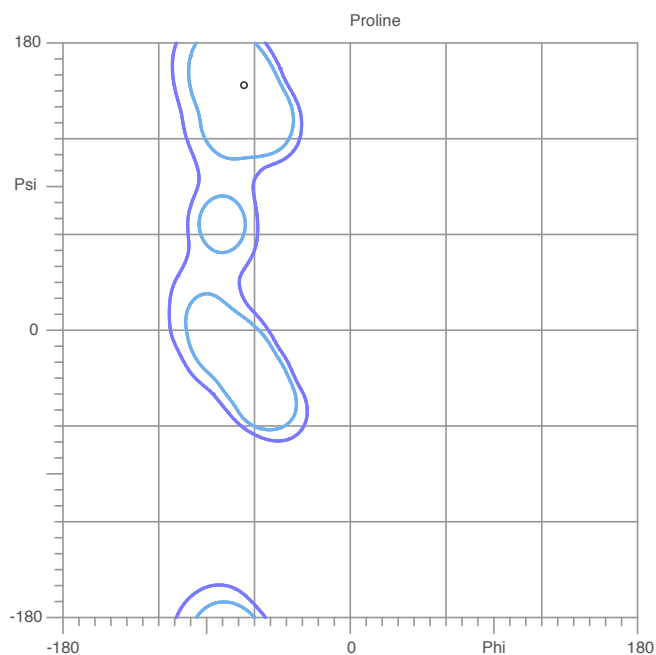
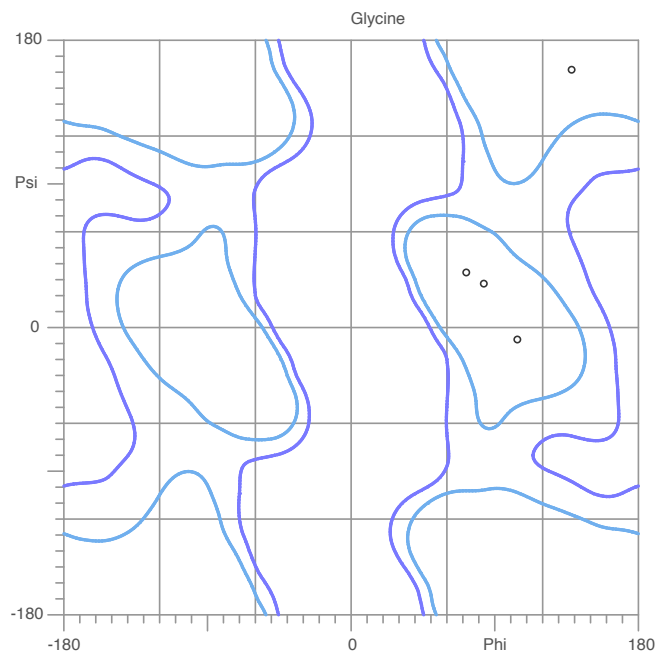
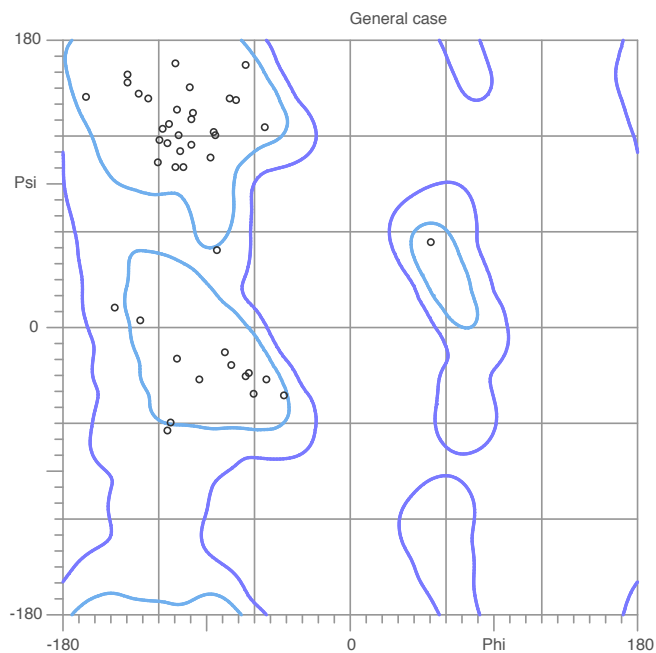
There were no outliers.

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

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 16

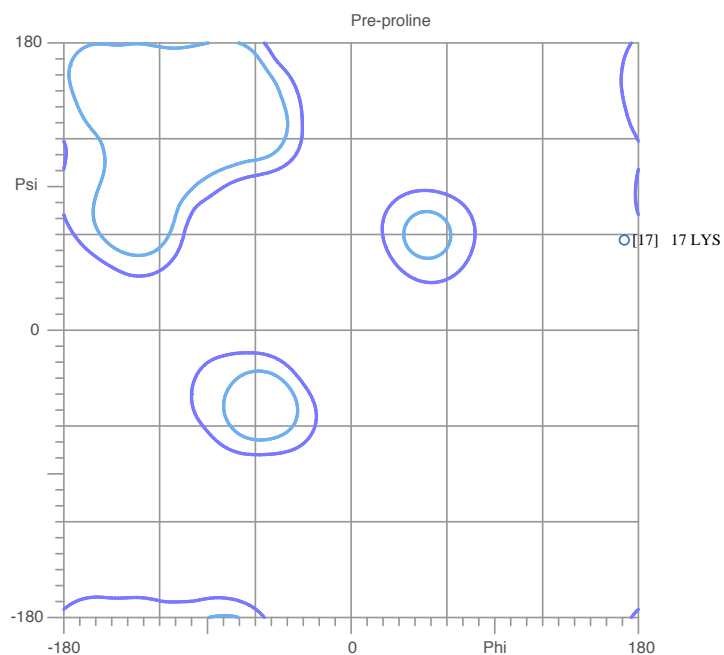
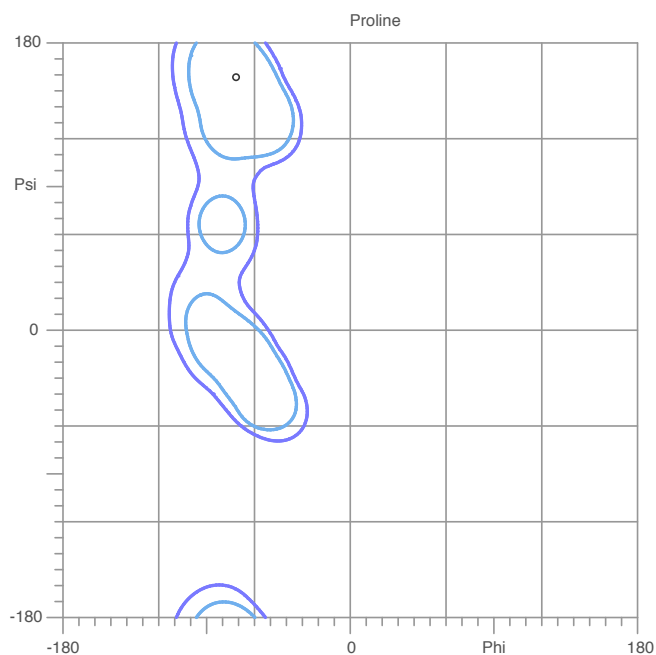
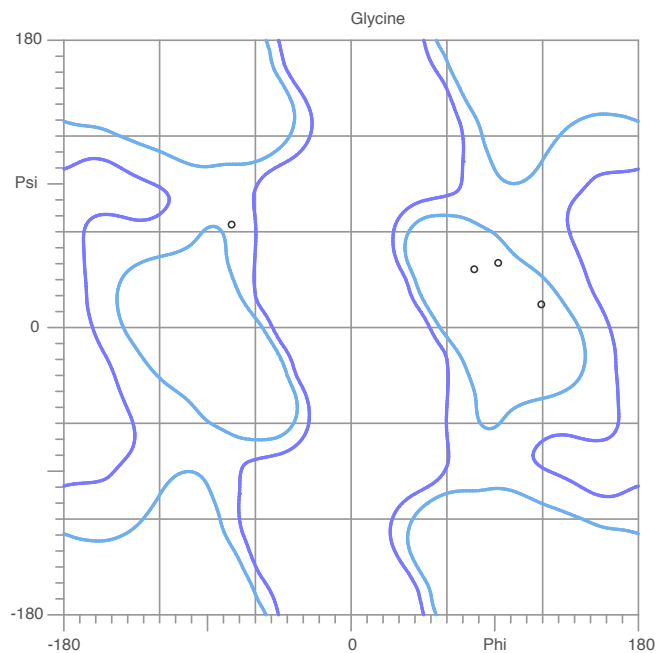
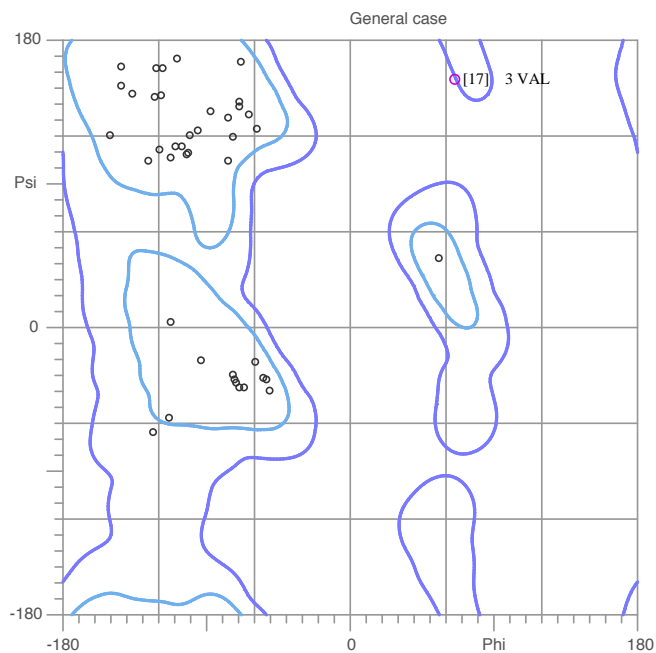


91.7% (44/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 17

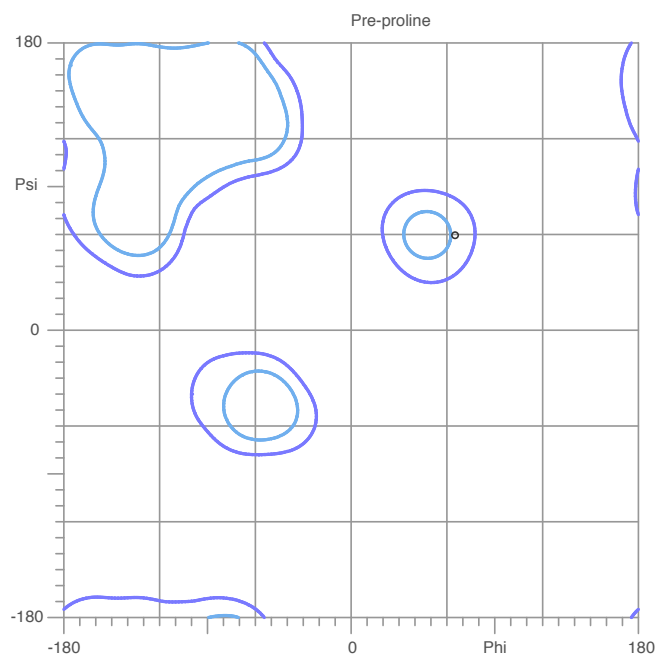
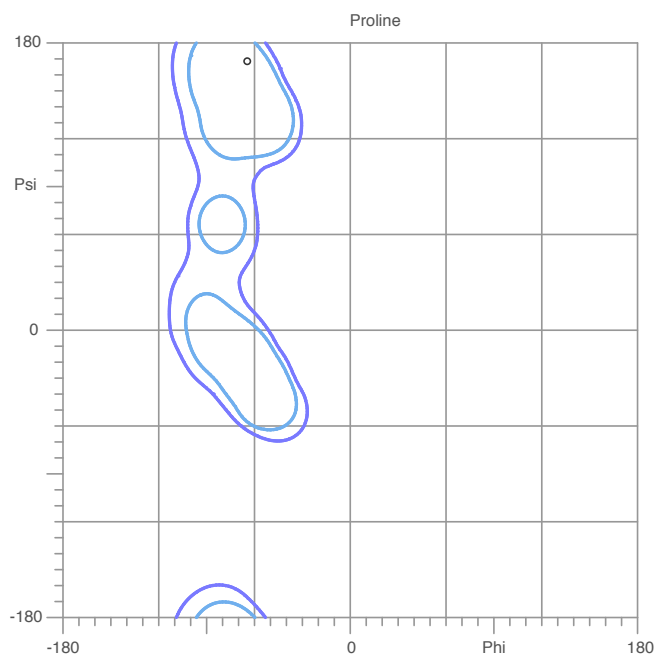
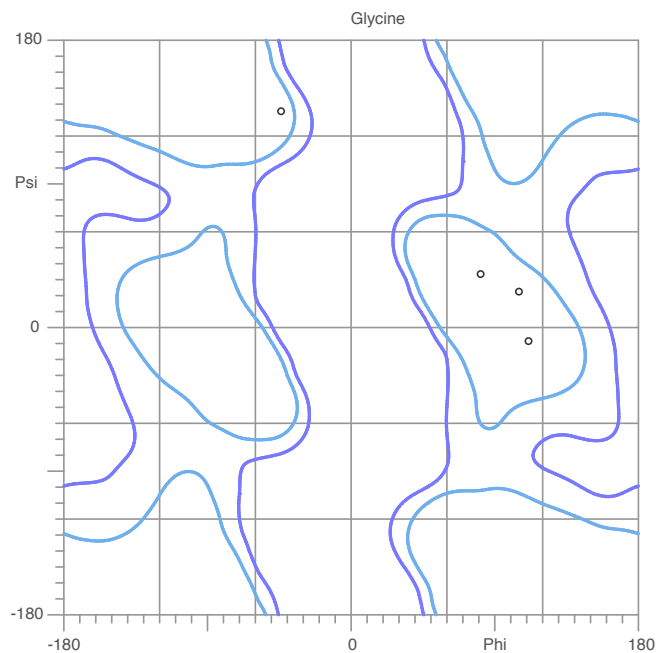
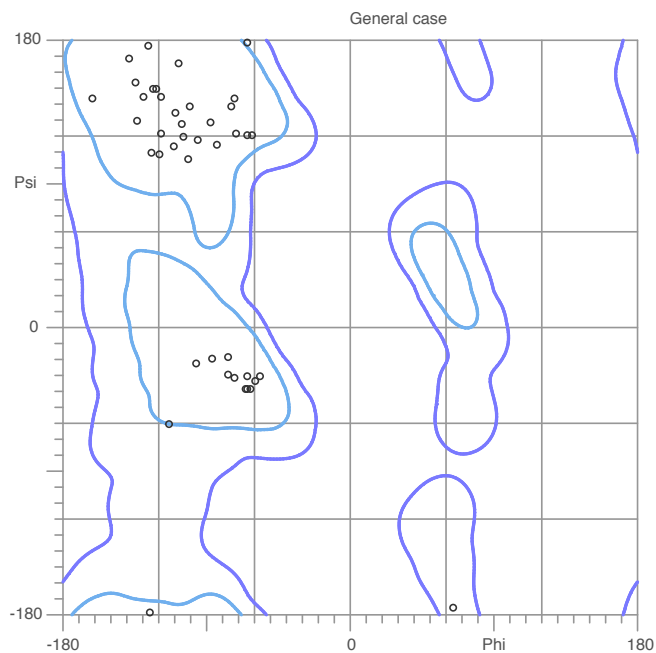


91.7% (44/48) of all residues were in favored (98%) regions.
95.8% (46/48) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[17] 3 VAL (65.0, 156.3)
[17] 17 LYS (171.3, 57.0)

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 18



91.7% (44/48) of all residues were in favored (98%) regions.
100.0% (48/48) of all residues were in allowed (>99.8%) regions.

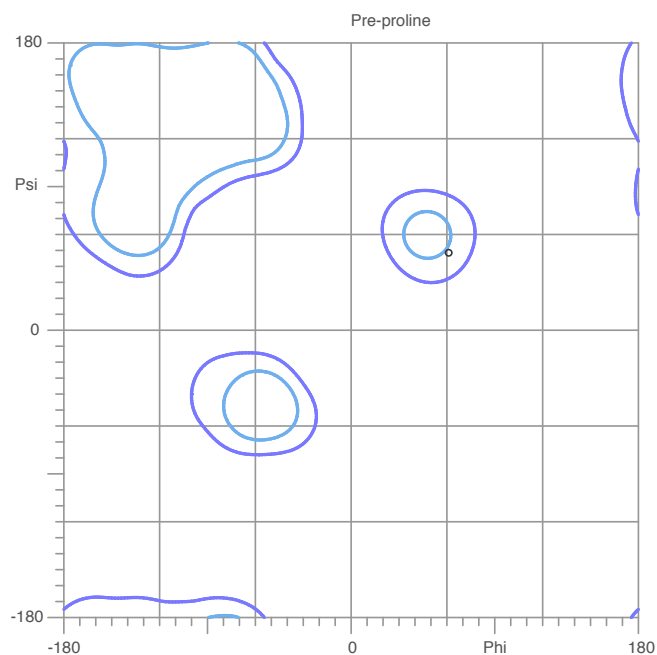
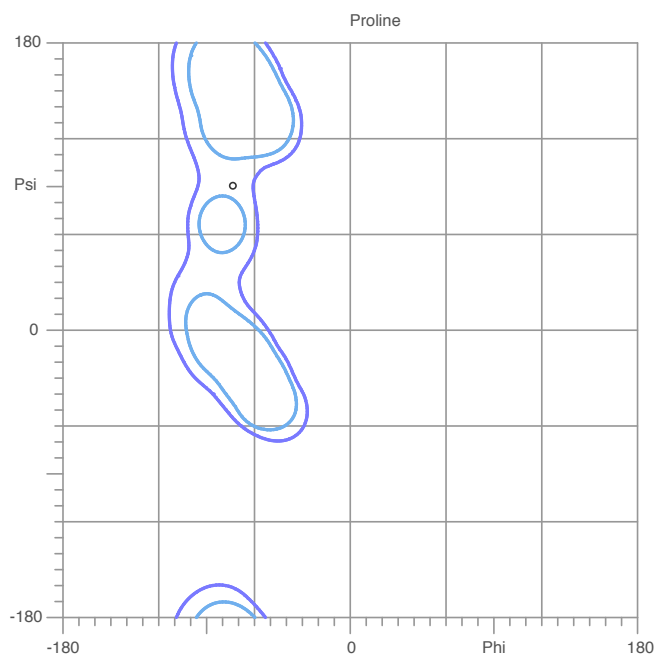
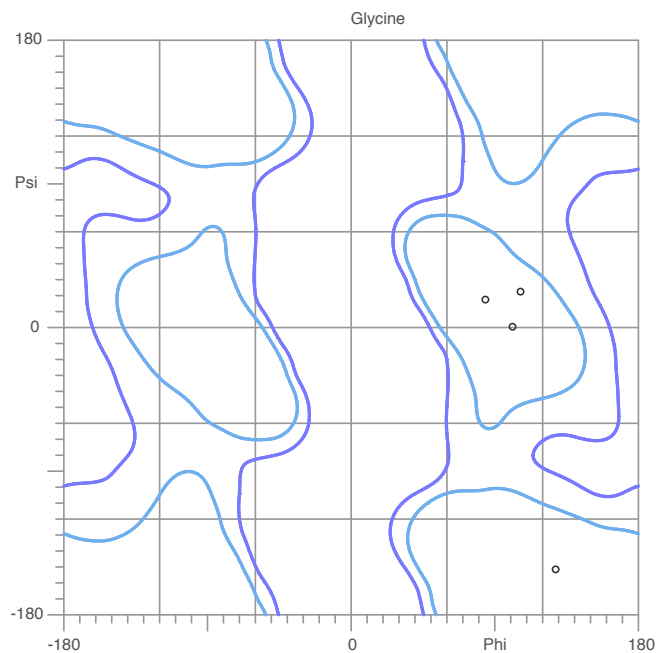
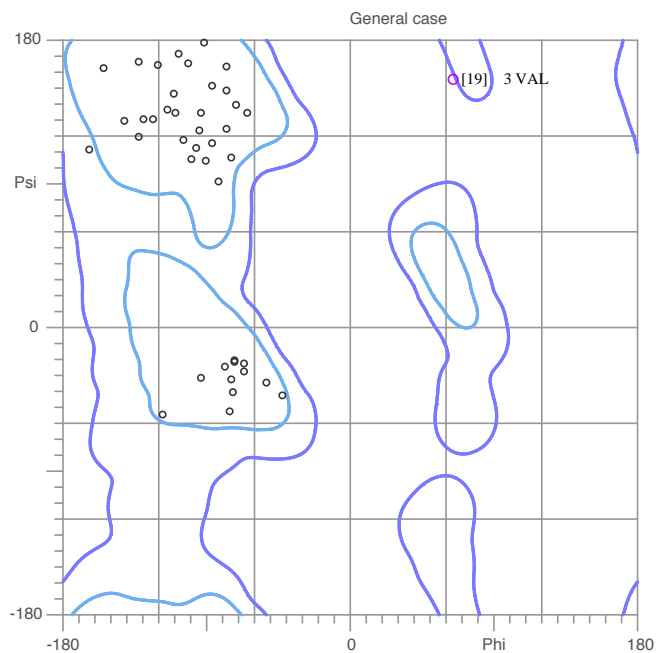
There were no outliers.

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

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 19

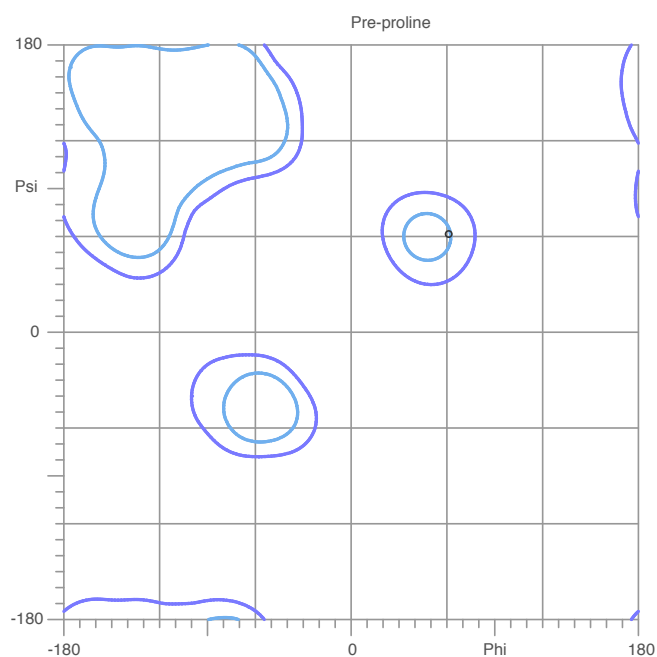
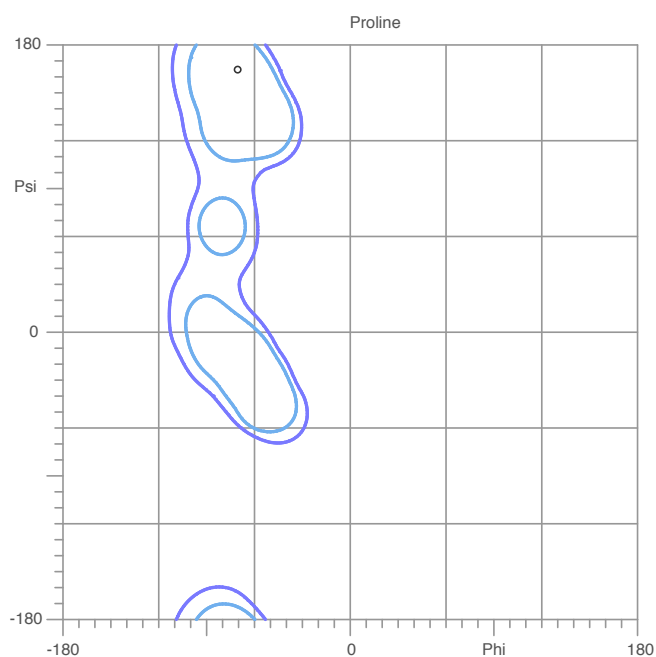
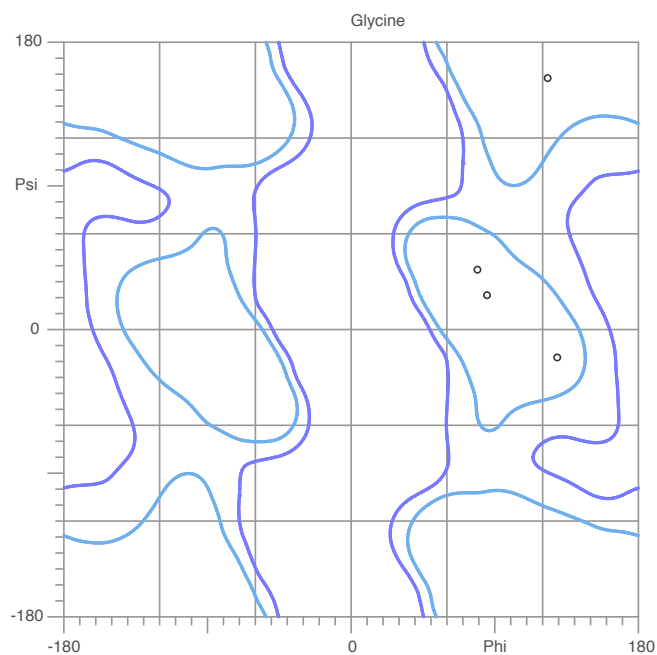
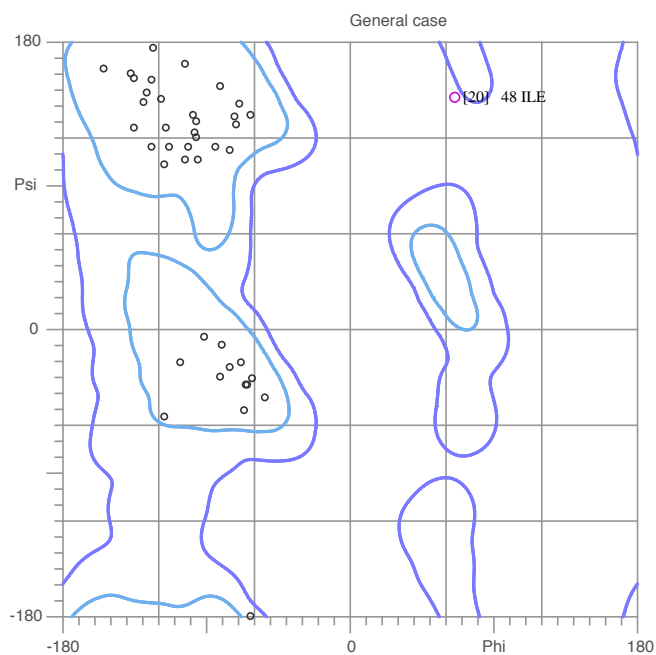


91.7% (44/48) of all residues were in favored (98%) regions.
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[19] 3 VAL (64.1, 156.8)

MolProbity Ramachandran analysis

ER382A_R3Cons_em_bcr3.pdb, model 20



95.8% (46/48) of all residues were in favored (98%) regions.
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 48 ILE (65.0, 146.9)

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

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