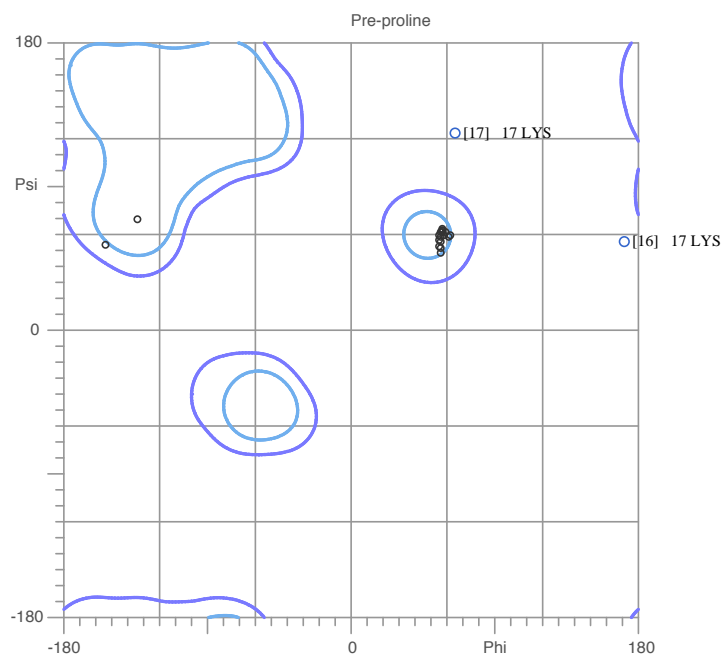
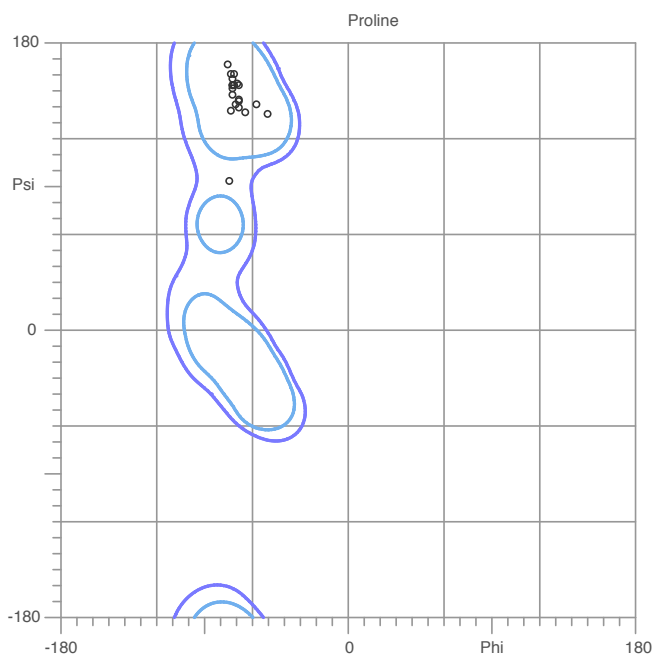
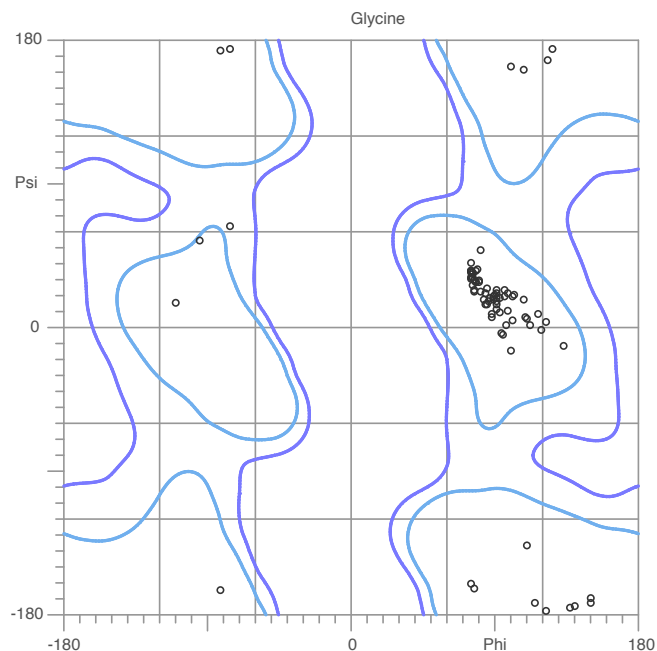
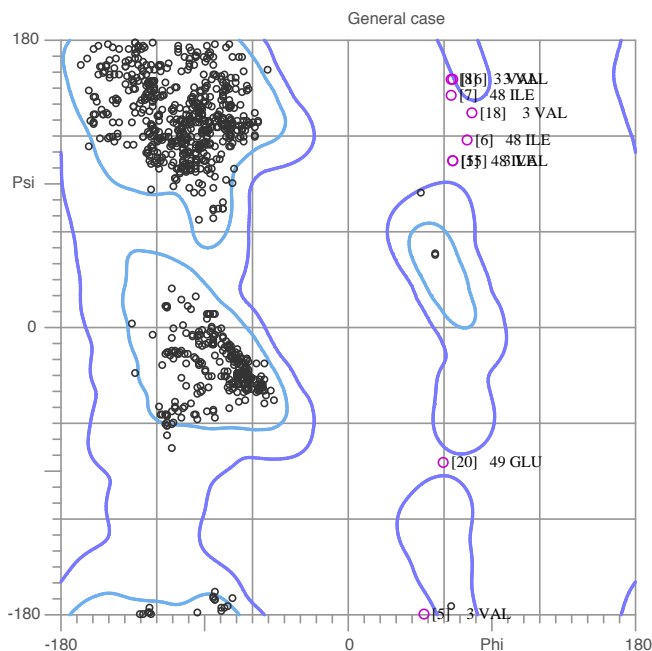


MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, all models



97.3% (934/960) of all residues were in favored (98%) regions.
98.9% (949/960) of all residues were in allowed (>99.8%) regions.

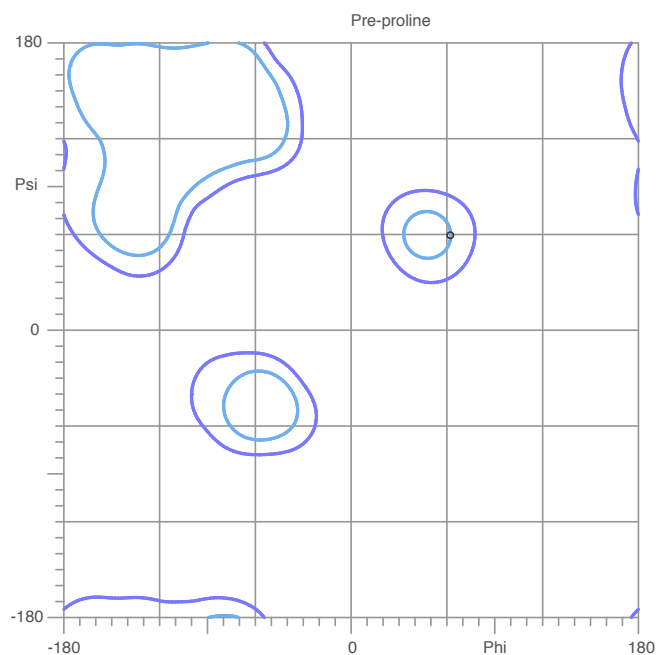
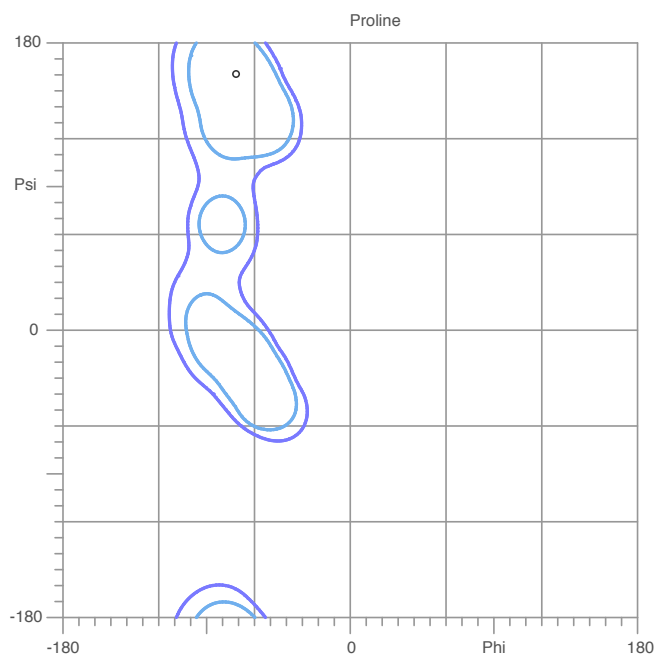
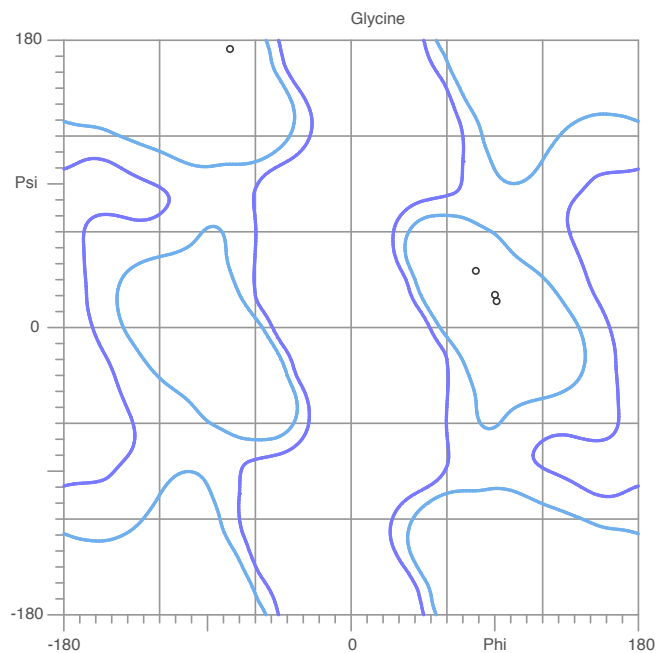
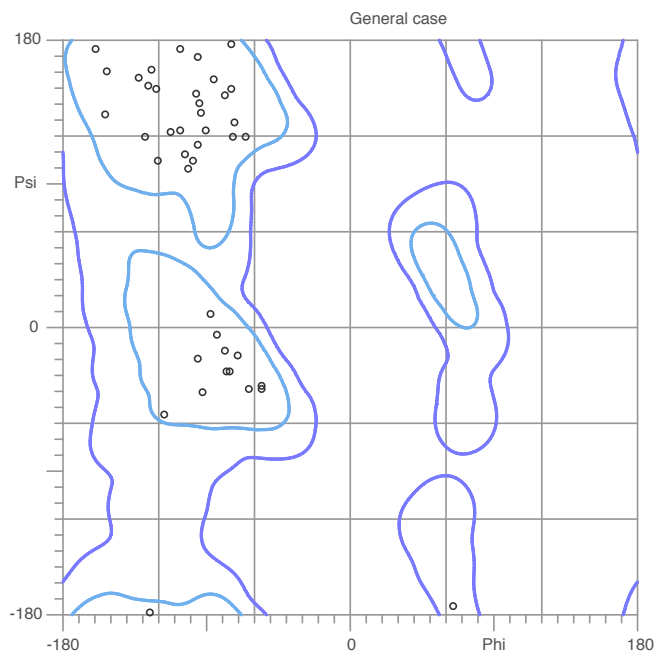
There were 11 outliers (phi, psi):

- [5] 3 VAL (47.3, -179.6)
- [5] 48 ILE (65.1, 105.0)
- [6] 48 ILE (75.0, 118.2)

- [7] 48 ILE (65.0, 146.9)
- [8] 3 VAL (64.9, 156.6)
- [15] 3 VAL (65.0, 105.0)
- [16] 3 VAL (65.1, 156.3)
- [16] 17 LYS (171.8, 56.8)
- [17] 17 LYS (65.1, 125.0)
- [18] 3 VAL (77.3, 135.0)
- [20] 49 GLU (60.0, -85.0)

MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 1



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.

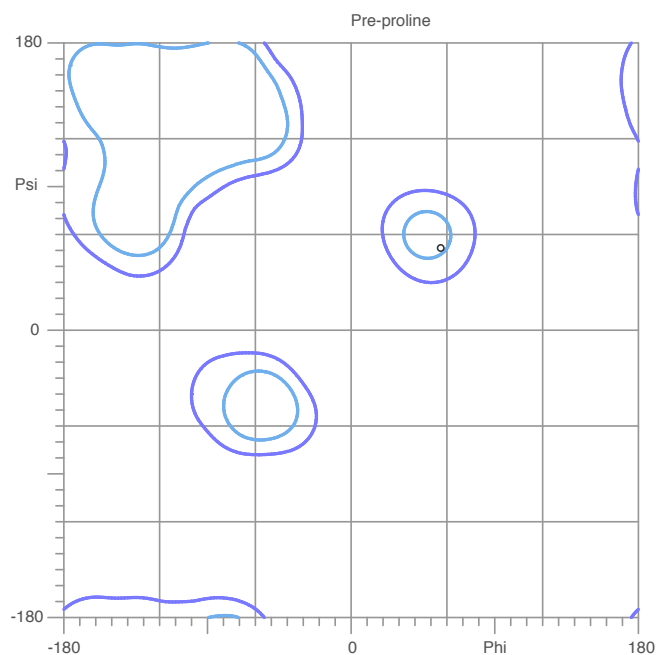
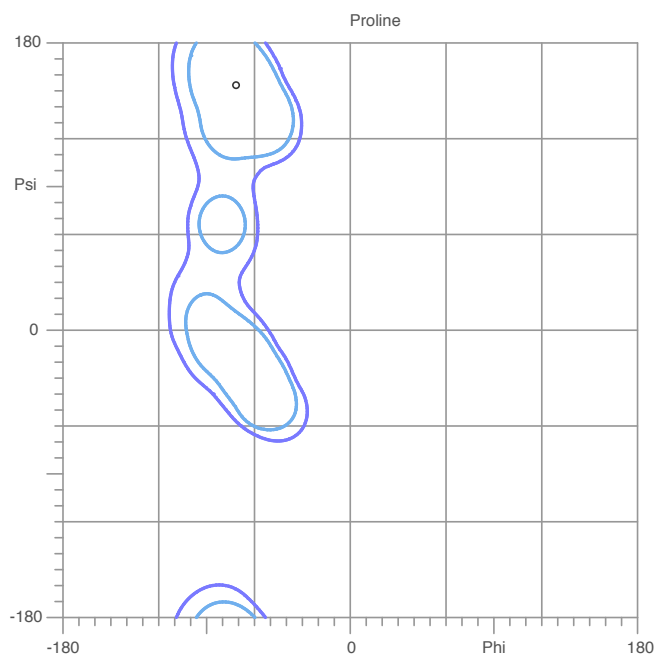
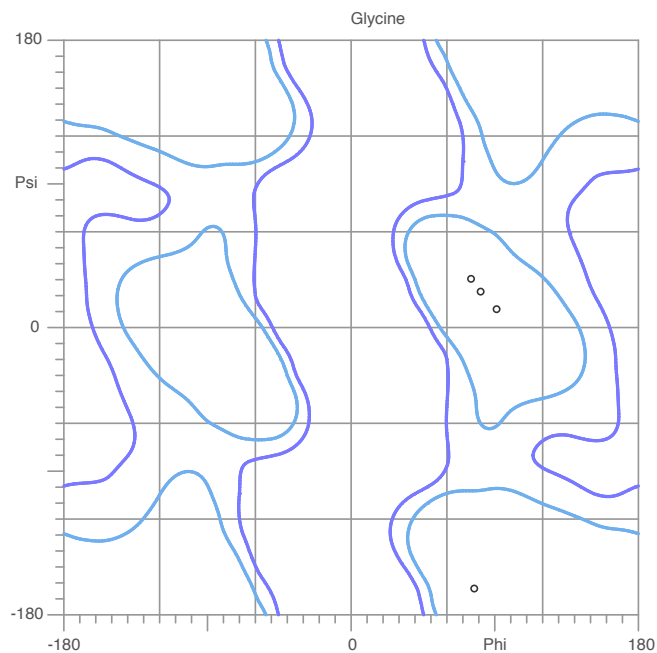
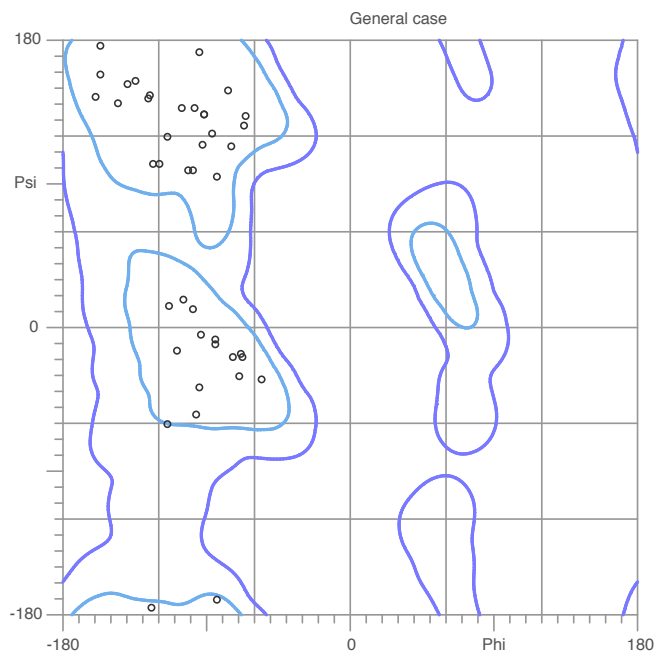
There were no outliers.

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

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

MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 2



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.

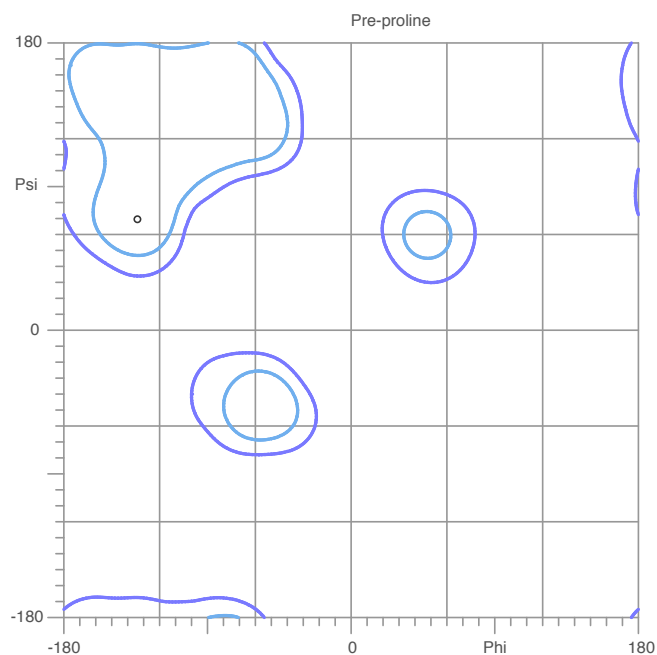
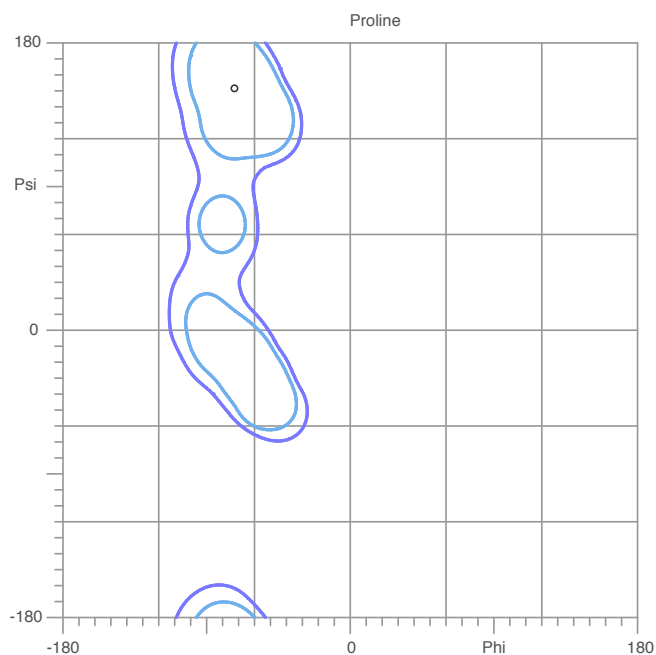
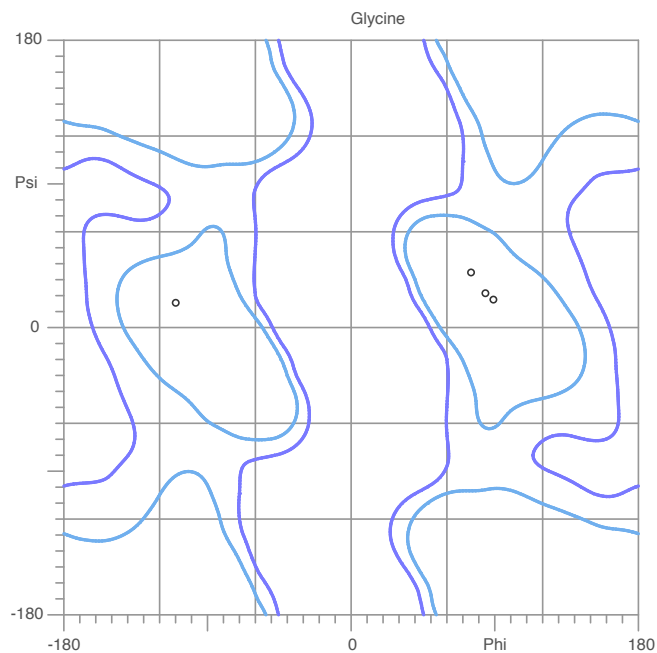
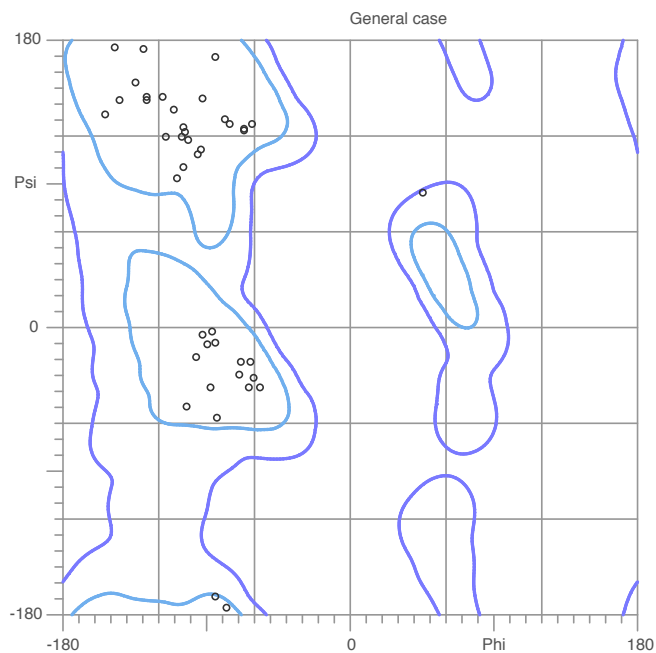
There were no outliers.

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

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

MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 3



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.

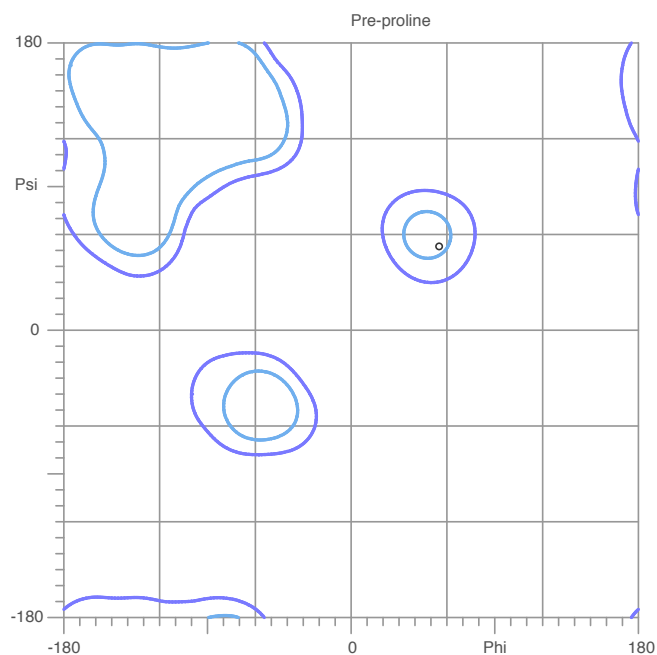
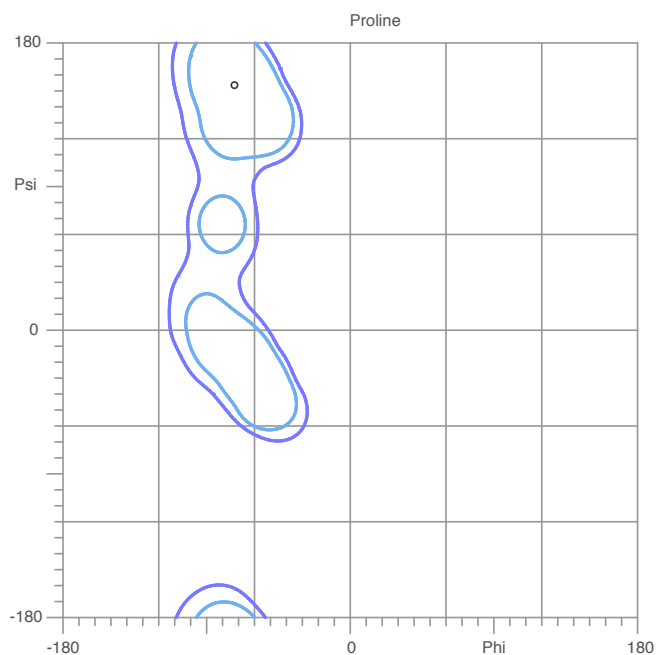
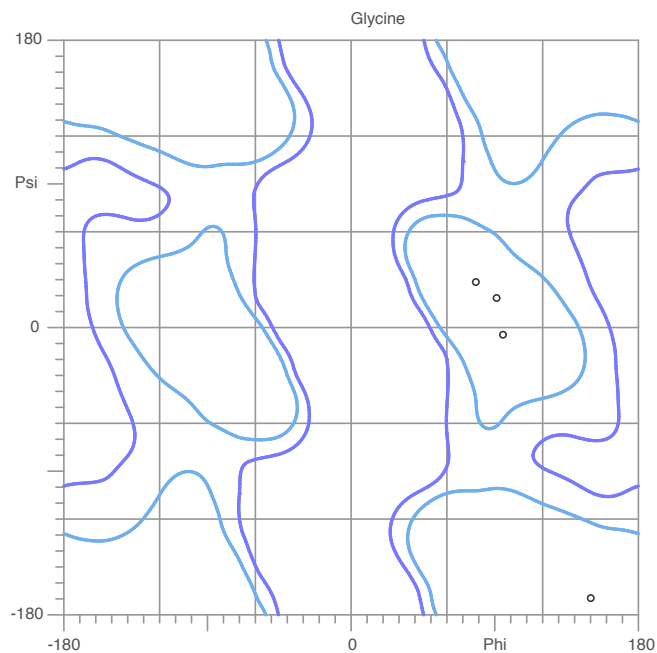
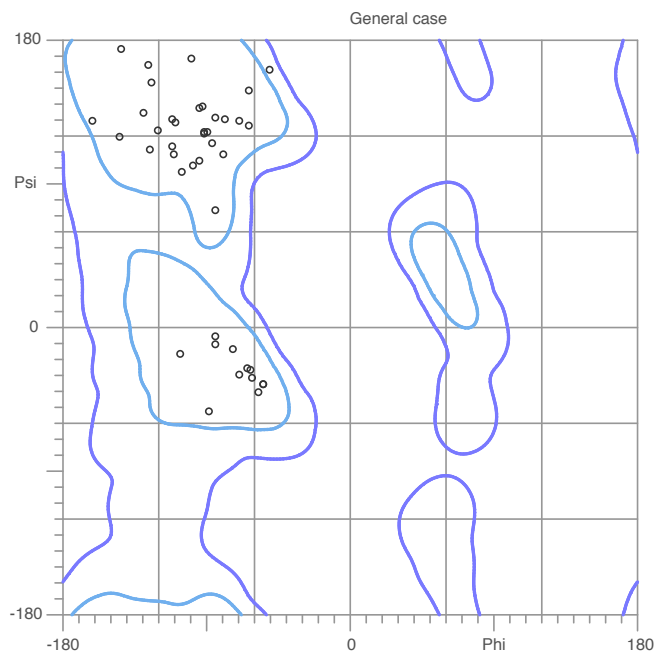
There were no outliers.

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

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 4



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.

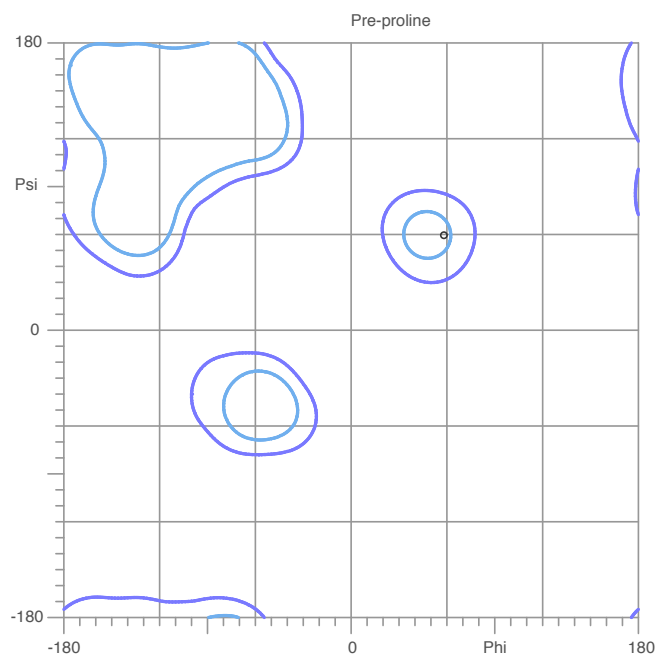
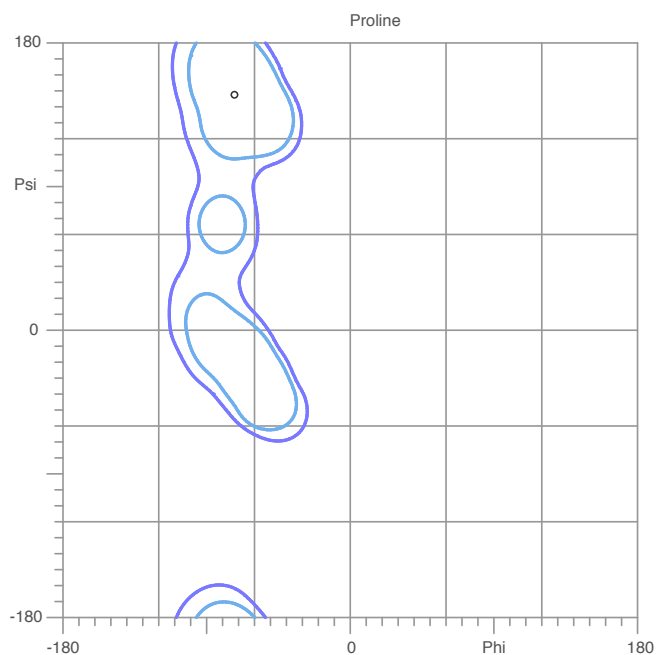
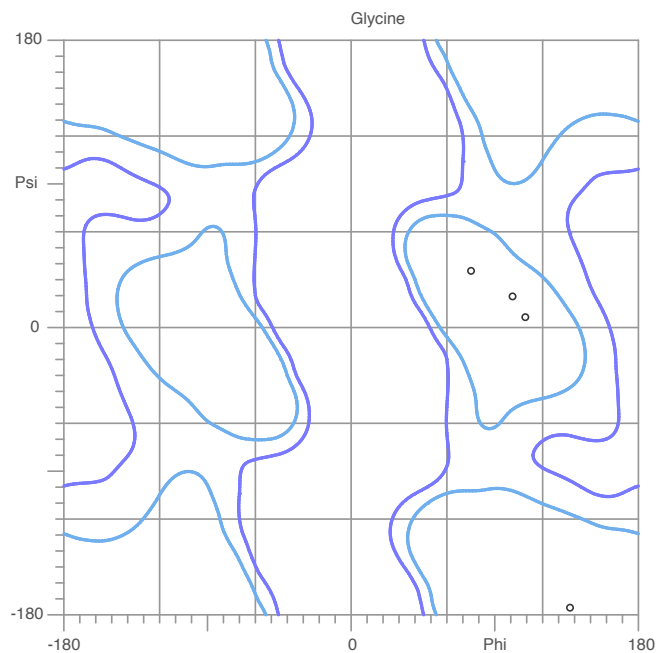
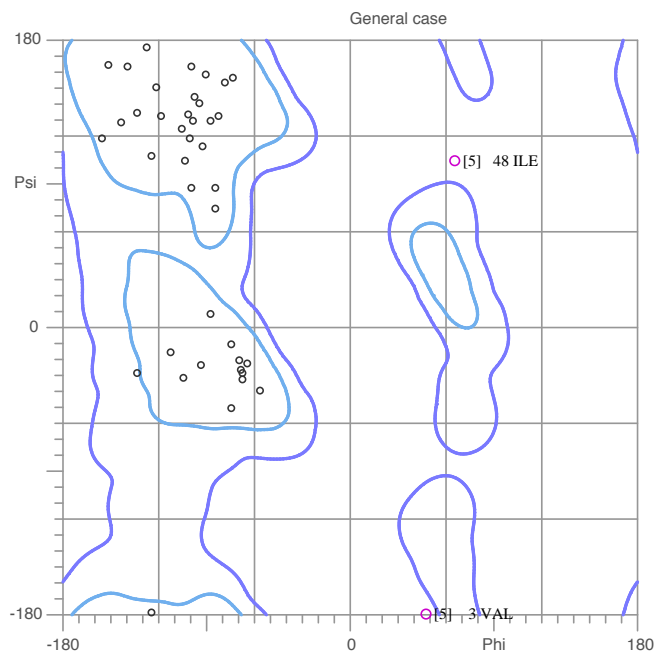
There were no outliers.

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

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 5



93.8% (45/48) of all residues were in favored (98%) regions.
95.8% (46/48) of all residues were in allowed (>99.8%) regions.

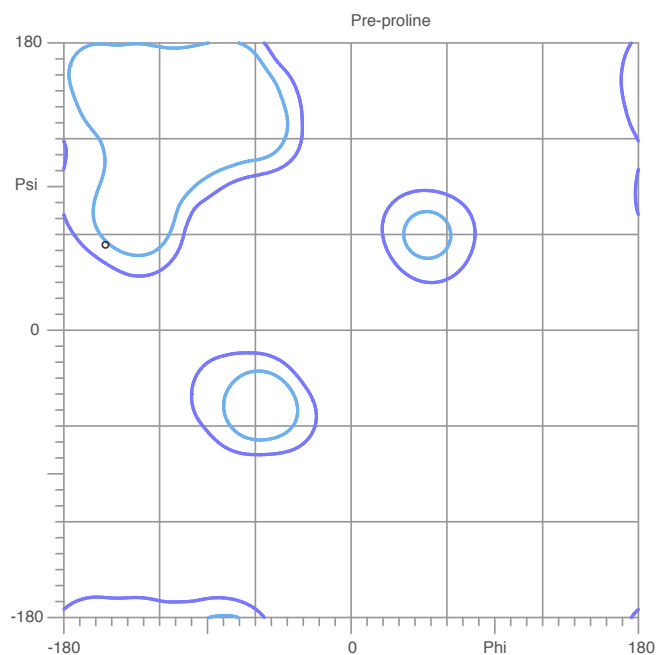
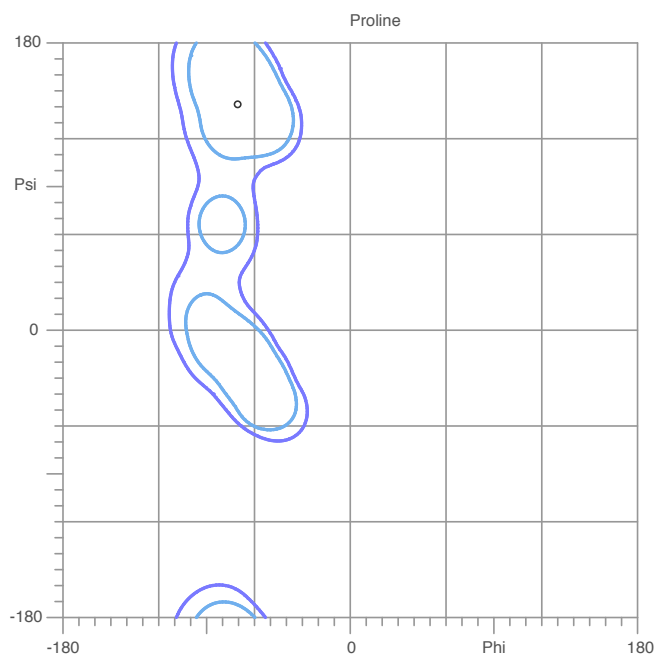
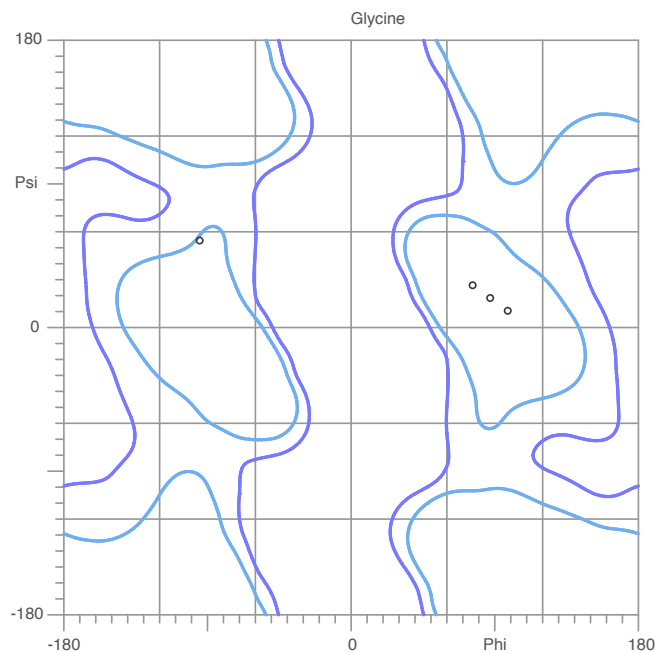
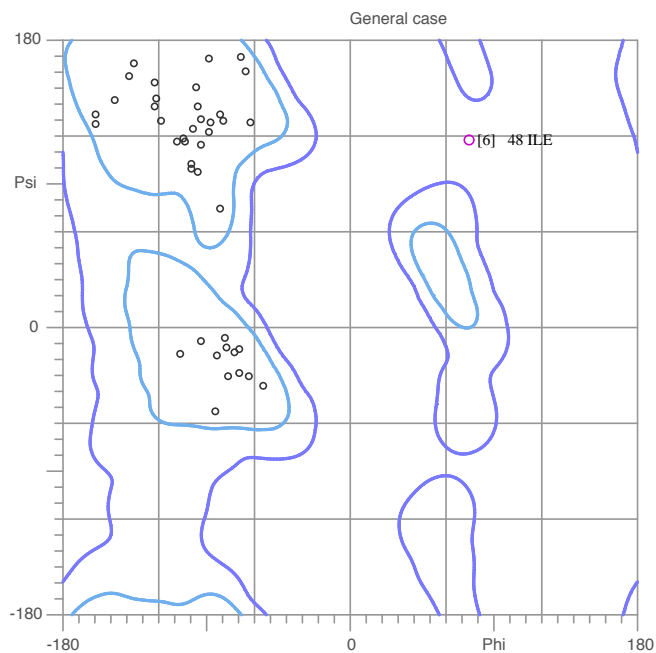
There were 2 outliers (phi, psi):

[5] 3 VAL (47.3, -179.6)

[5] 48 ILE (65.1, 105.0)

MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 6

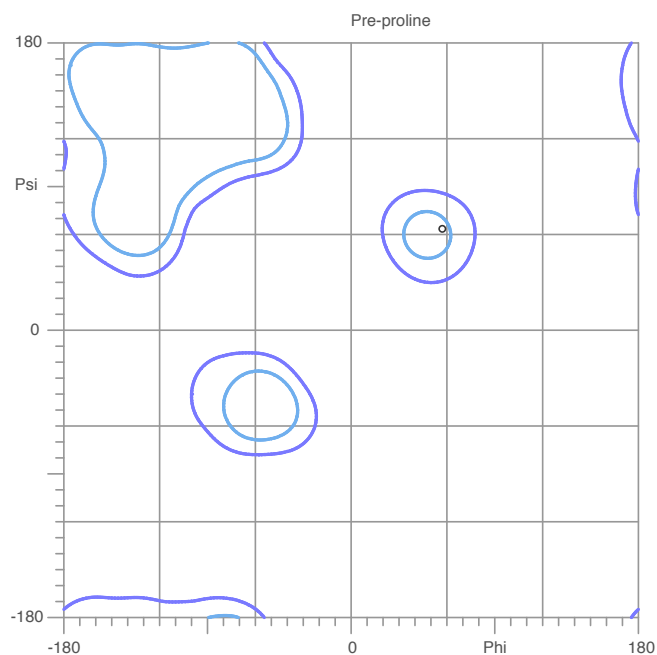
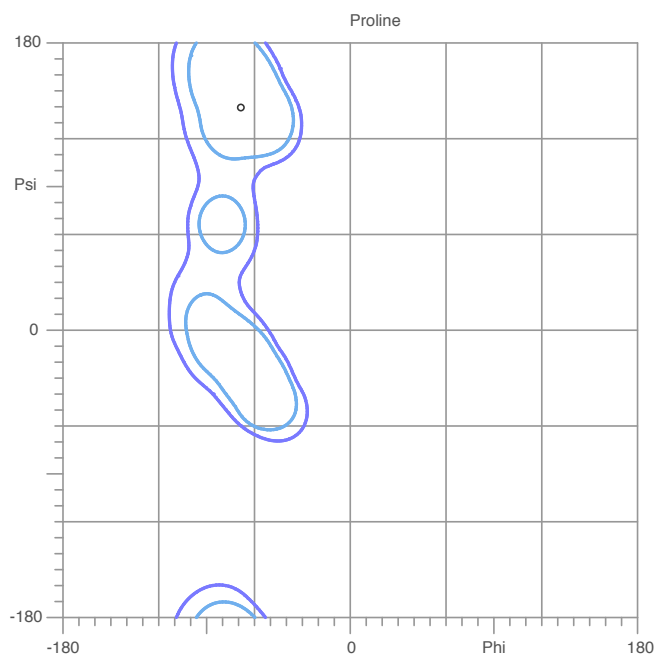
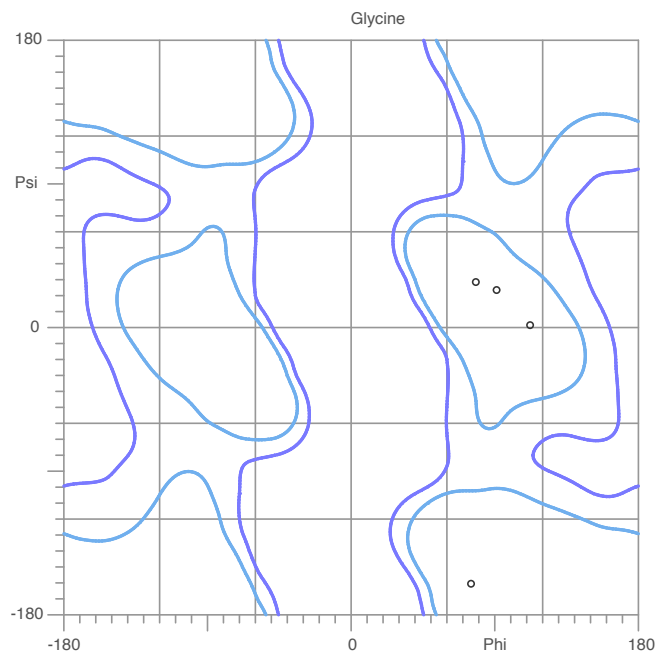
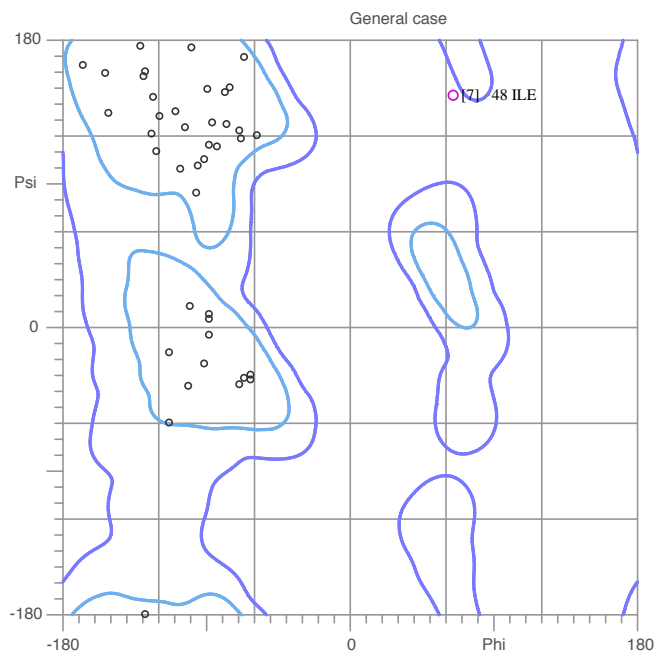


95.8% (46/48) of all residues were in favored (98%) regions.
97.9% (47/48) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[6] 48 ILE (75.0, 118.2)

MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 7



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.

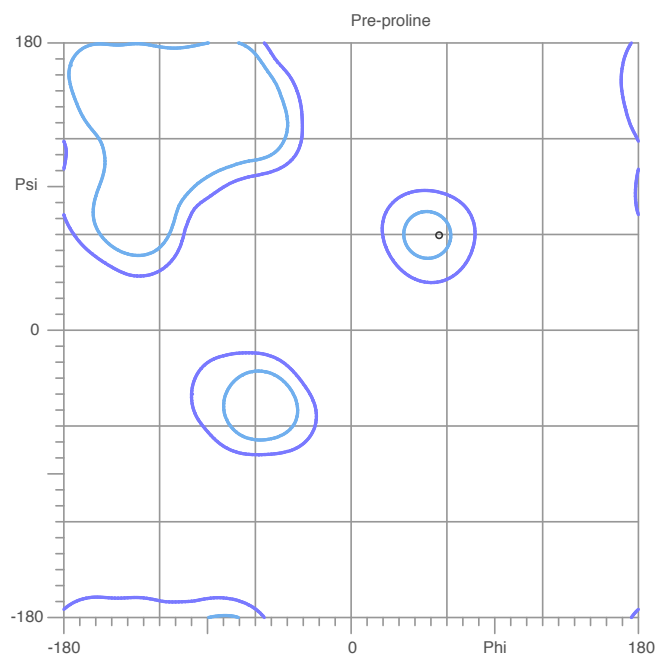
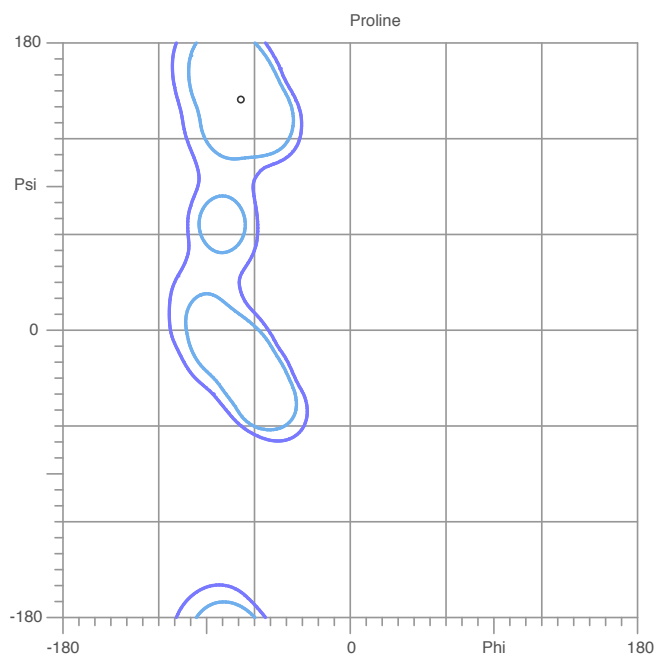
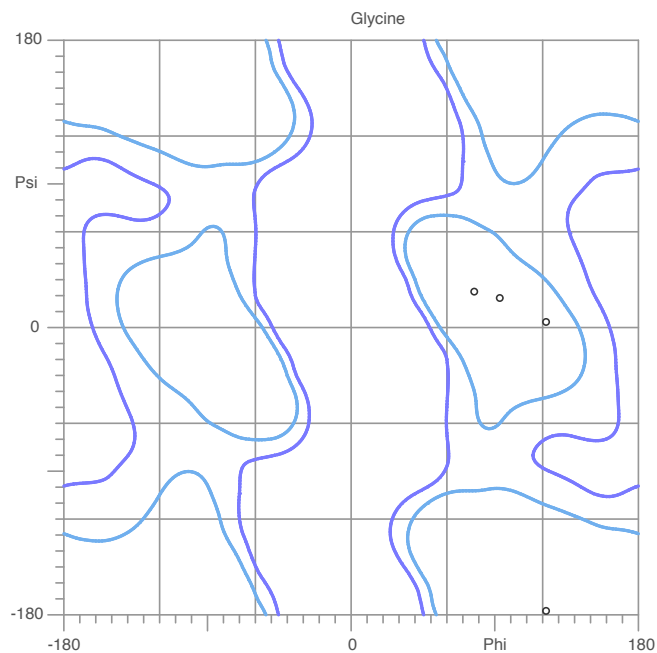
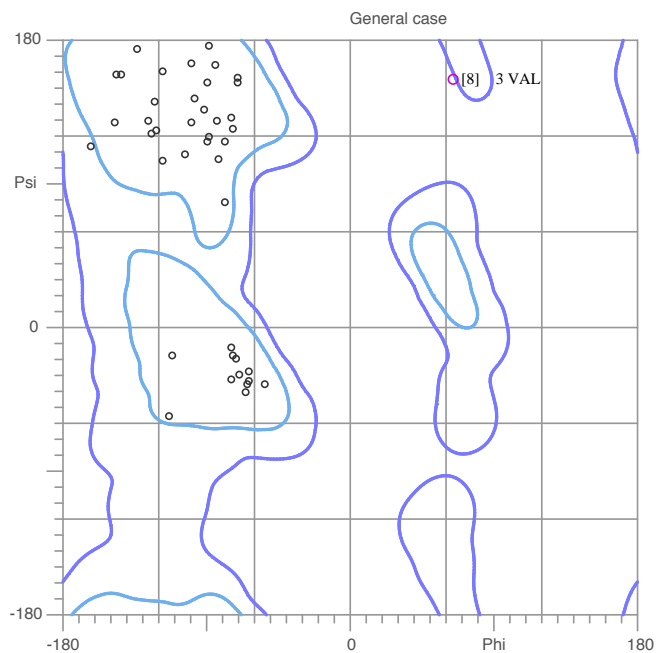
There were 1 outliers (phi, psi):
[7] 48 ILE (65.0, 146.9)

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 8



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.

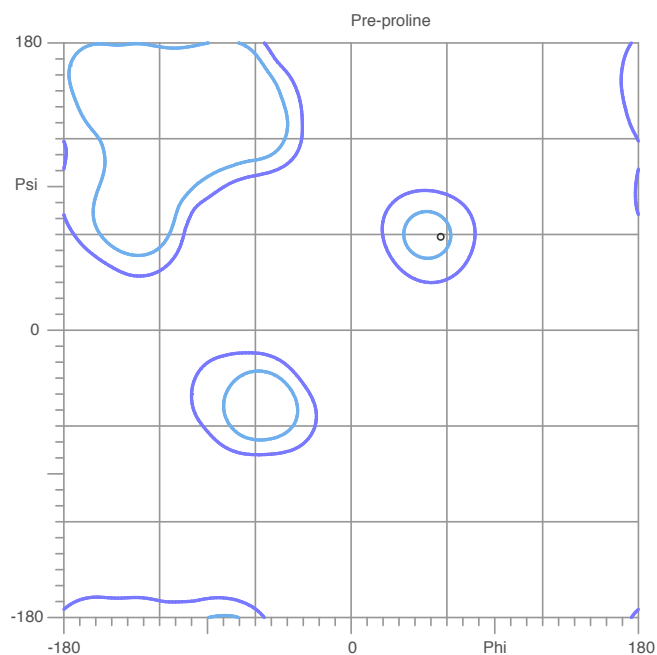
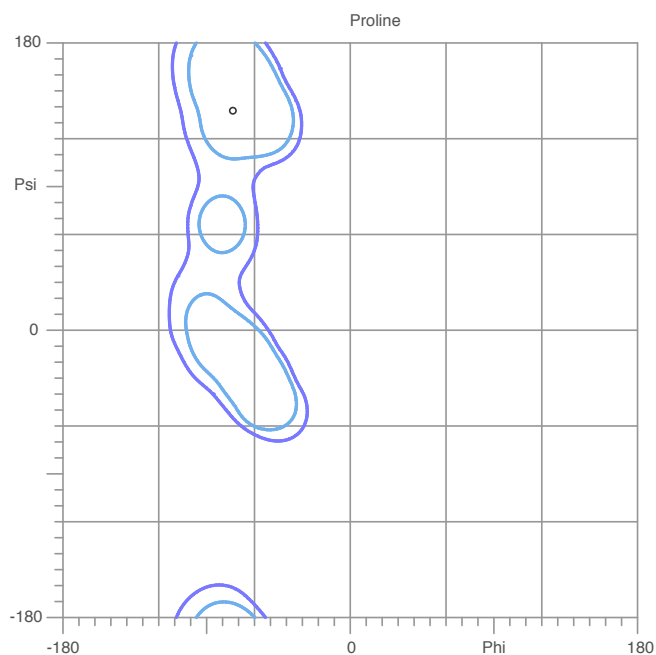
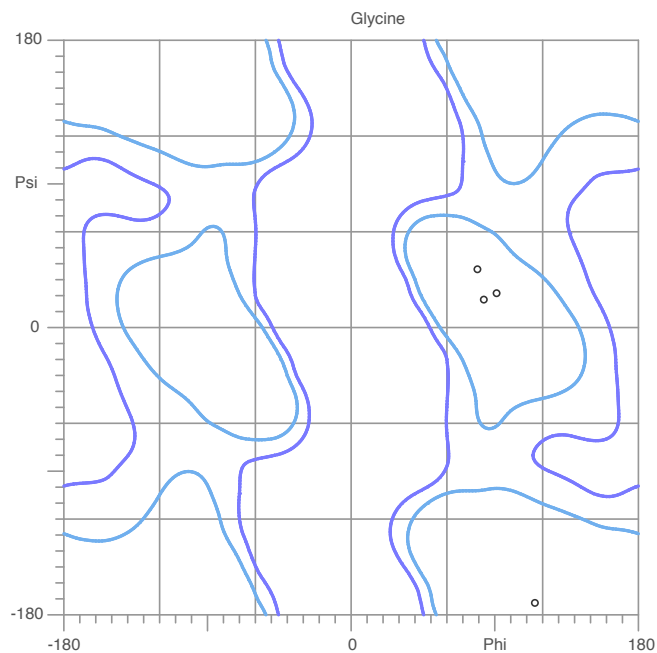
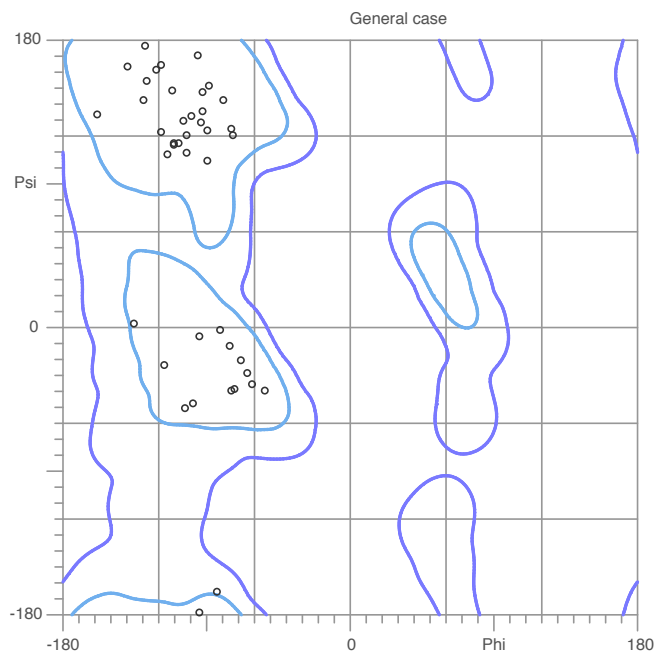
There were 1 outliers (phi, psi):
[8] 3 VAL (64.9, 156.6)

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 9



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.

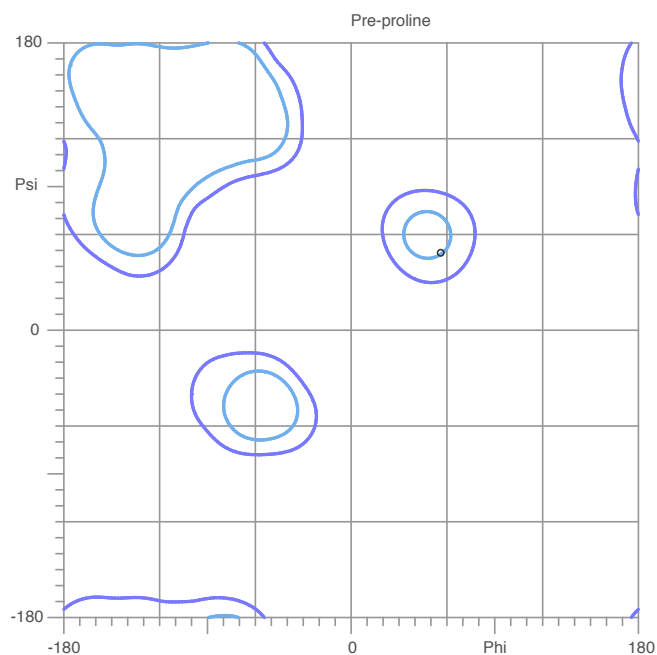
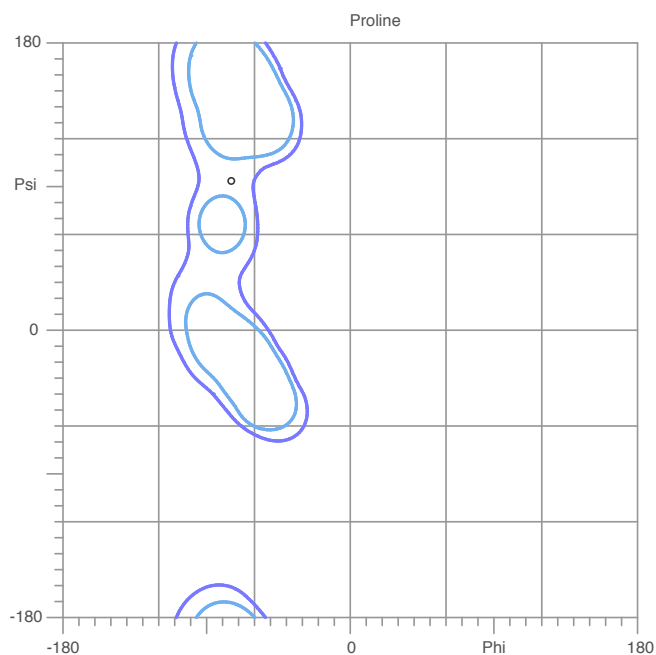
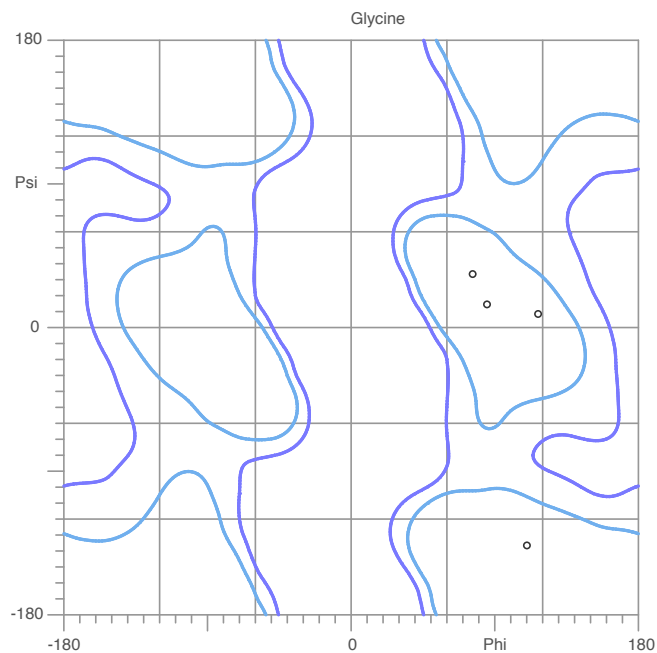
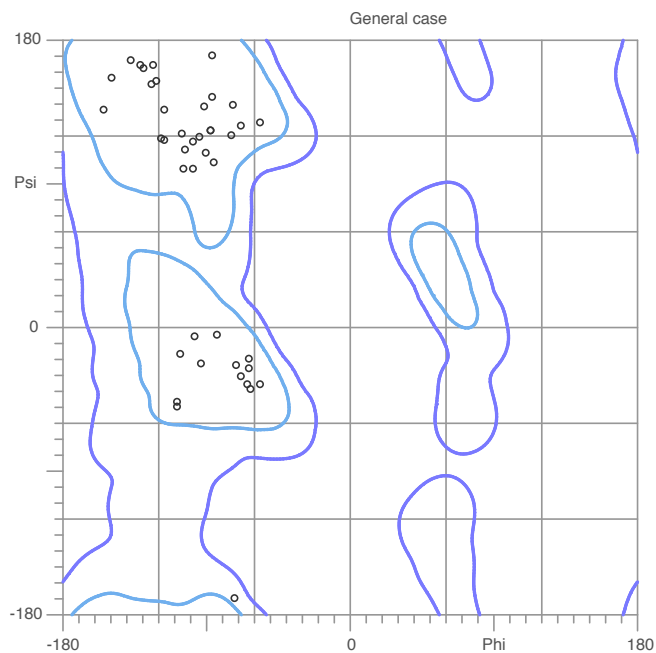
There were no outliers.

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

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 10



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.

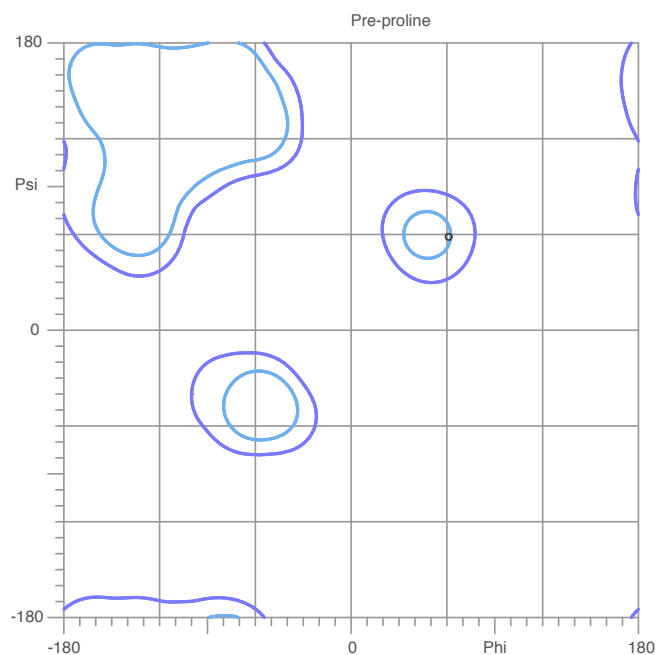
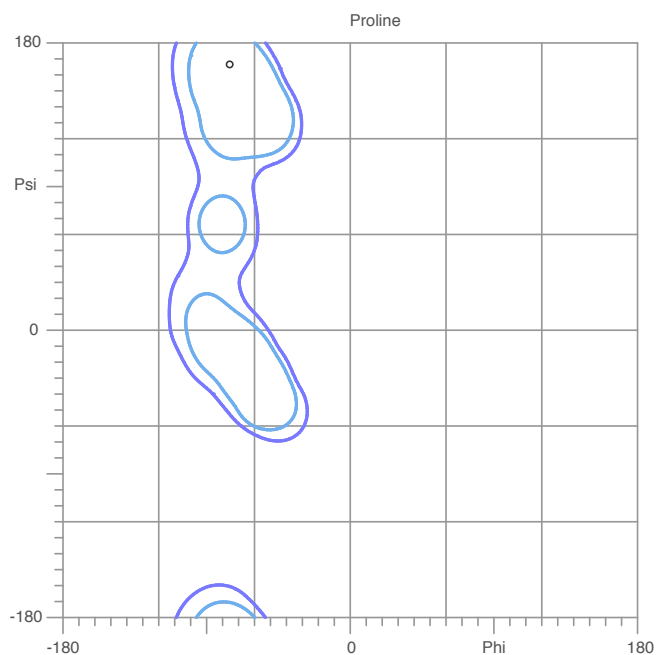
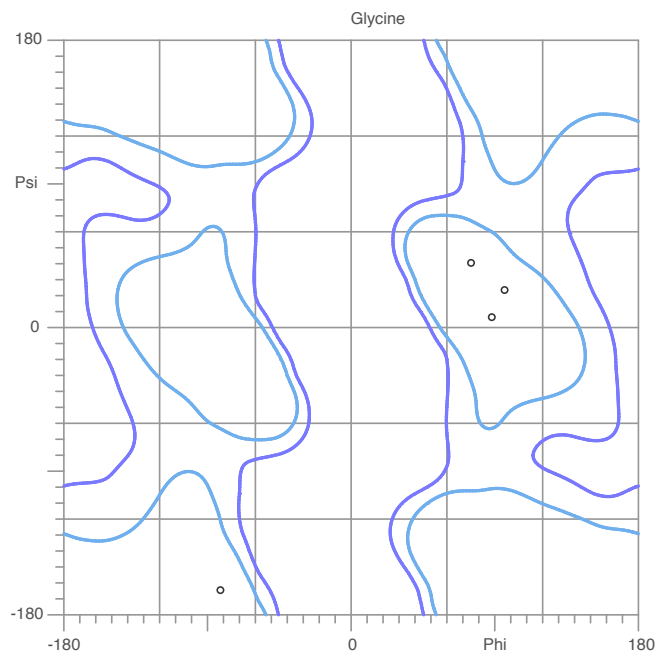
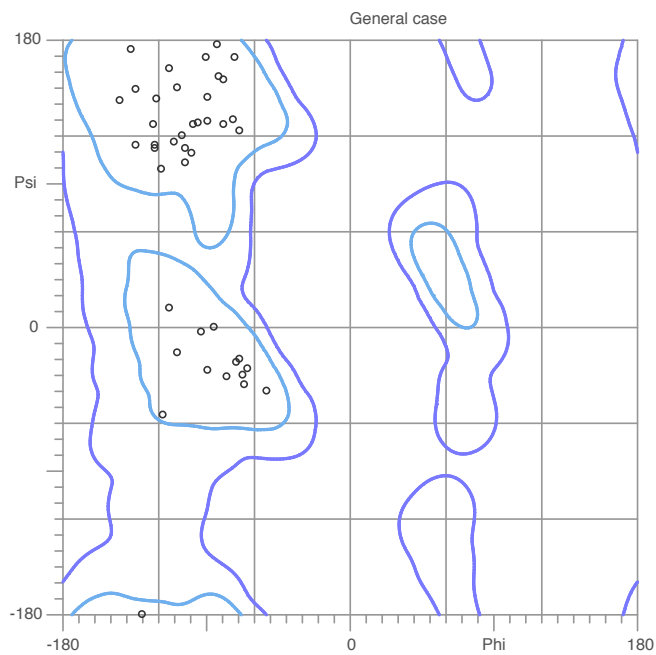
There were no outliers.

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

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 11



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.

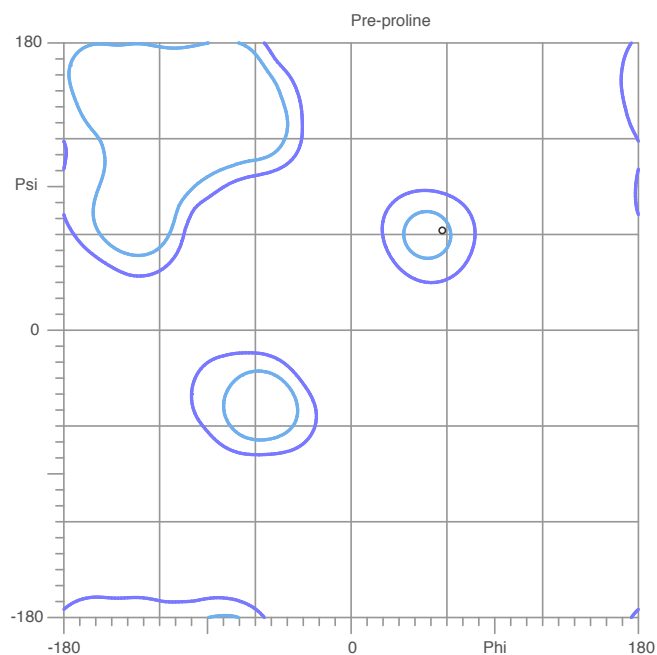
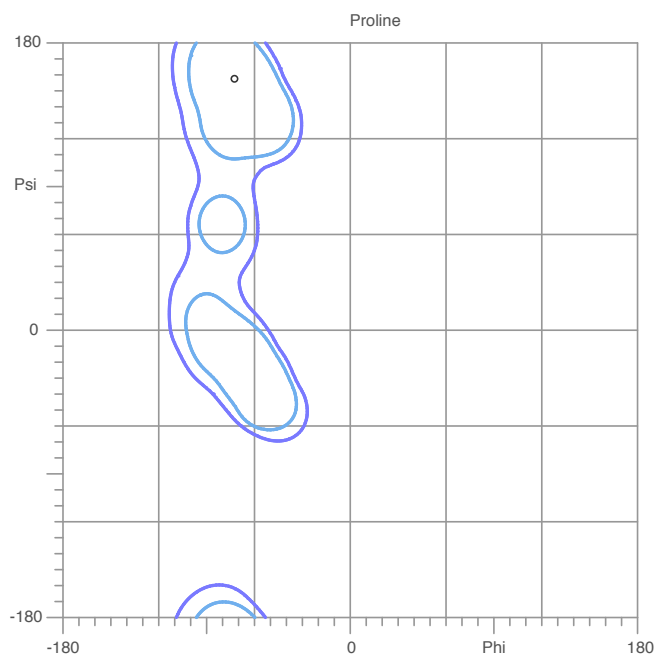
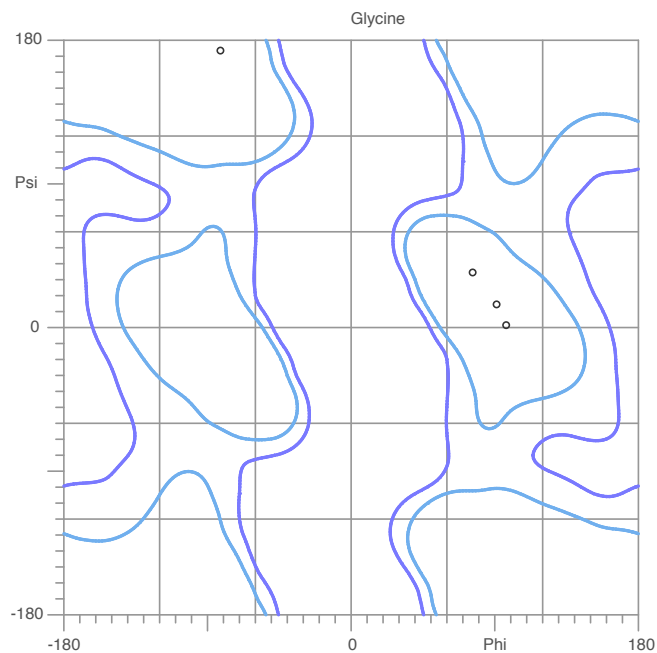
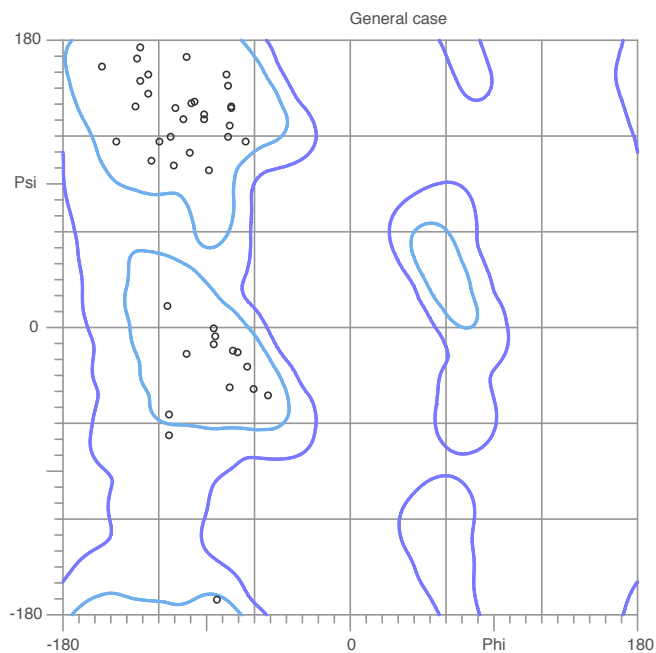
There were no outliers.

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 12



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.

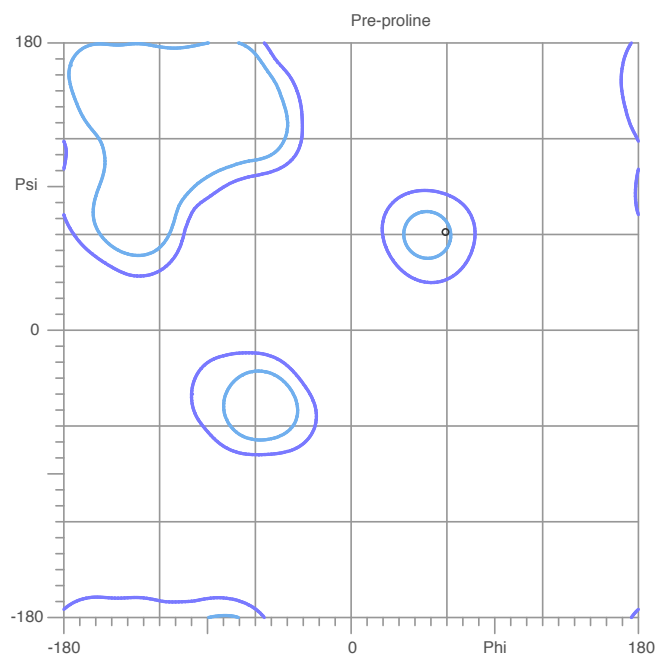
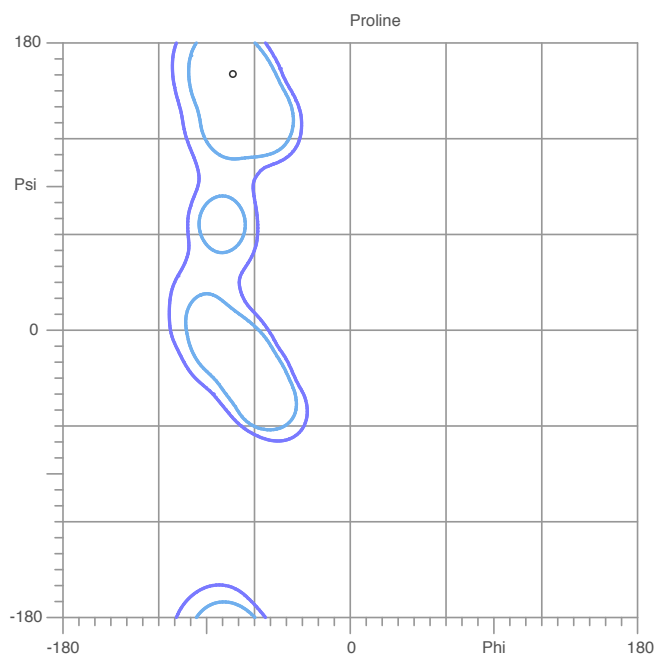
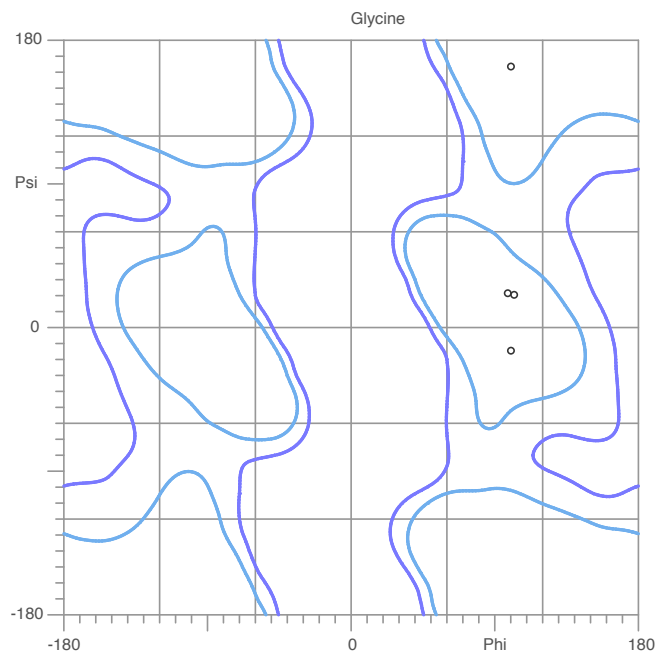
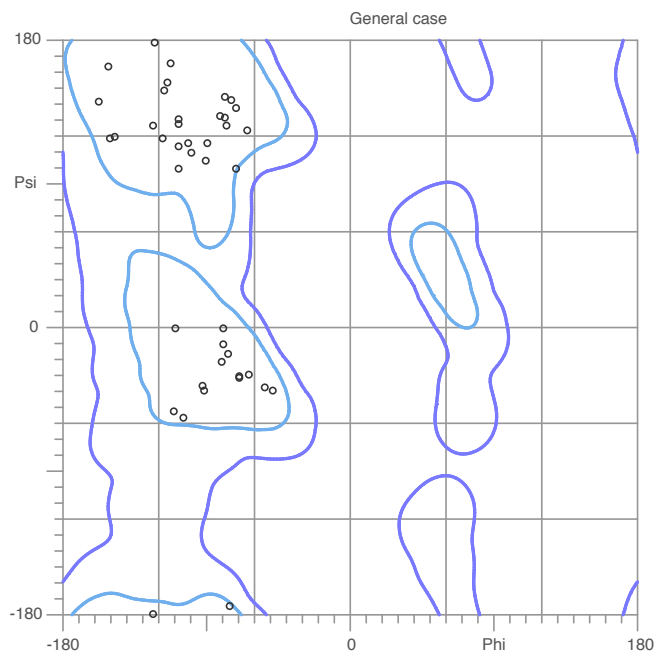
There were no outliers.

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 13



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.

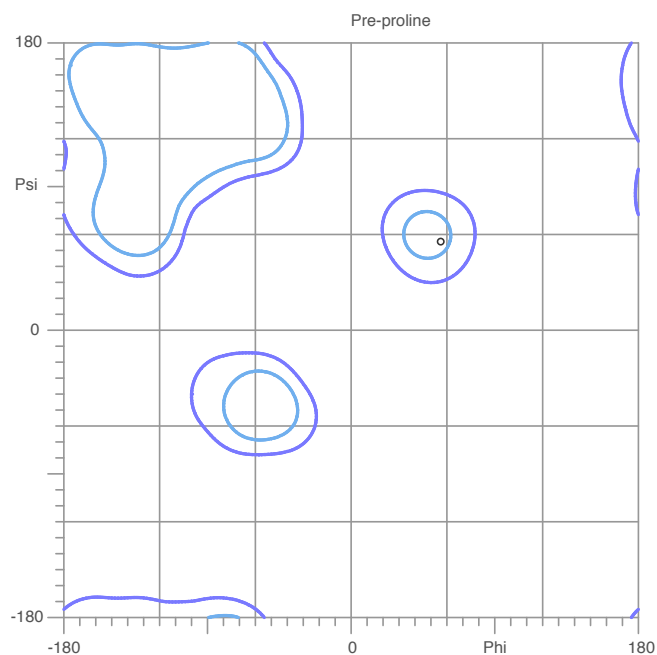
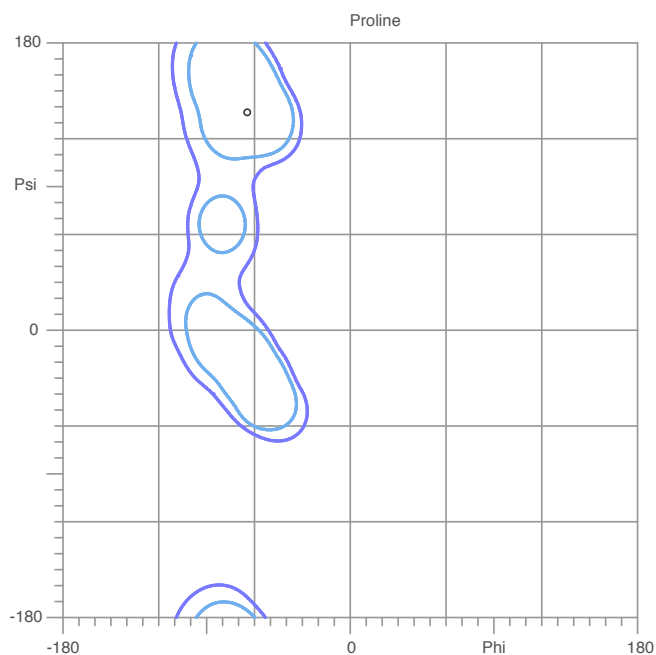
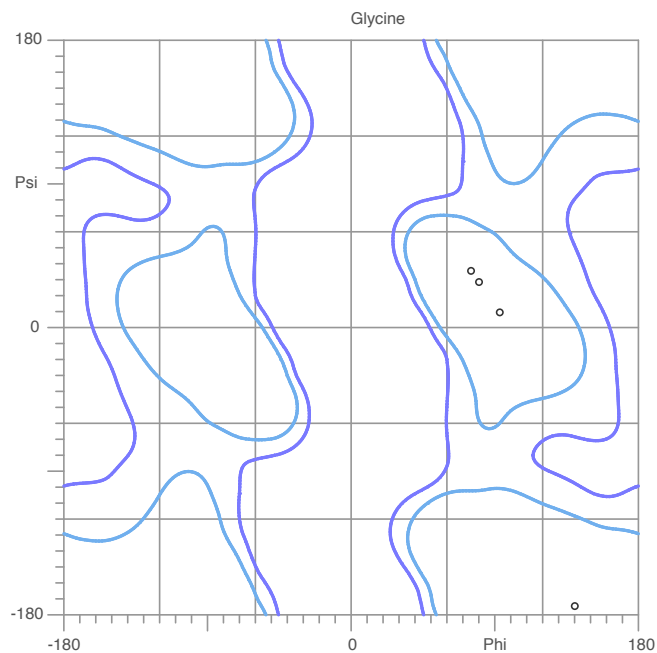
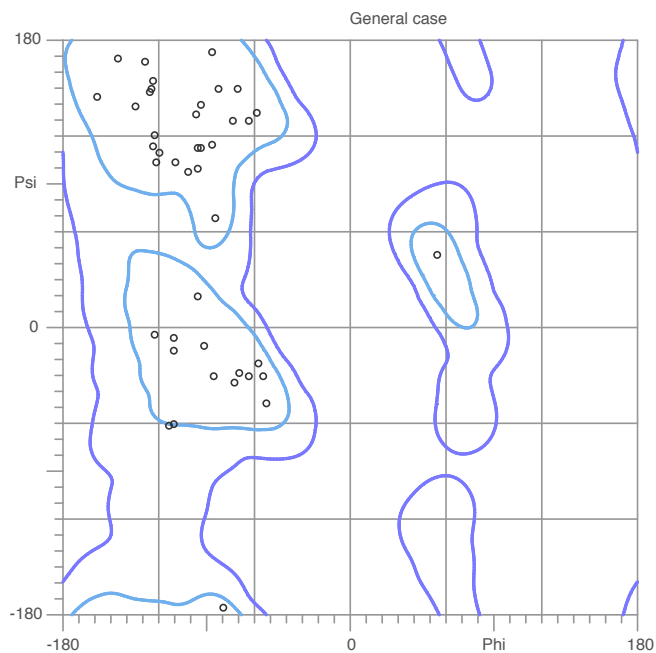
There were no outliers.

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

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 14



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.

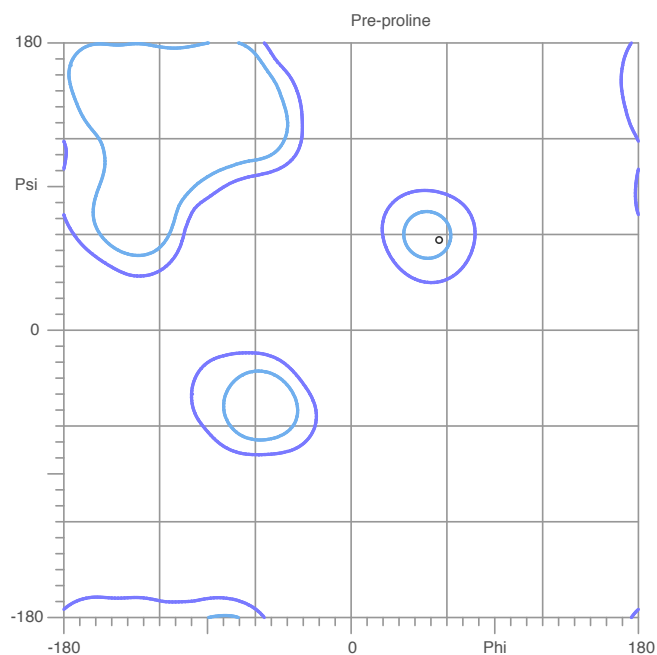
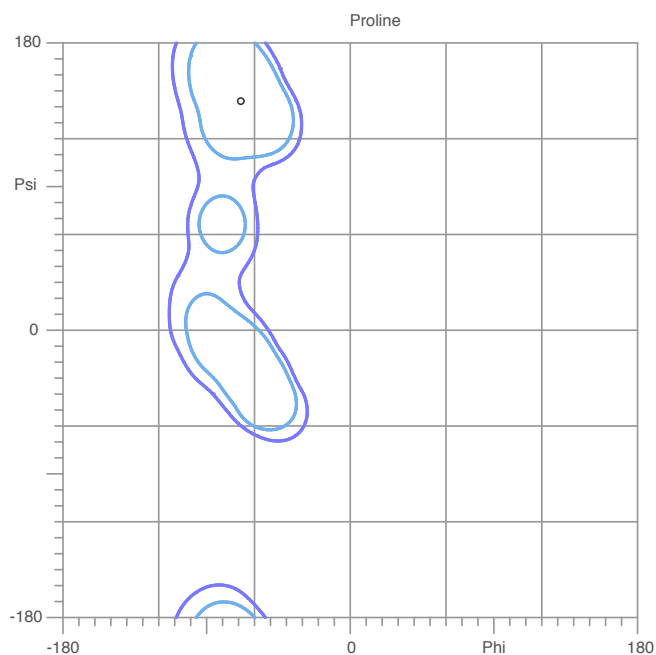
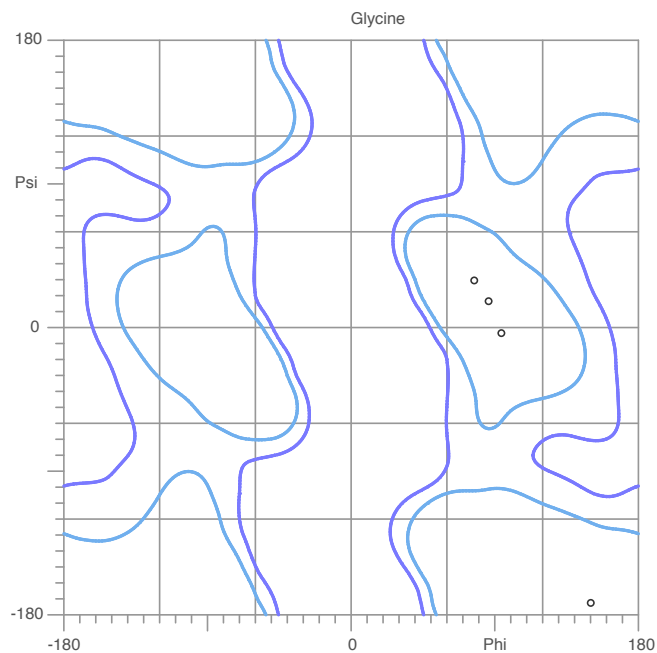
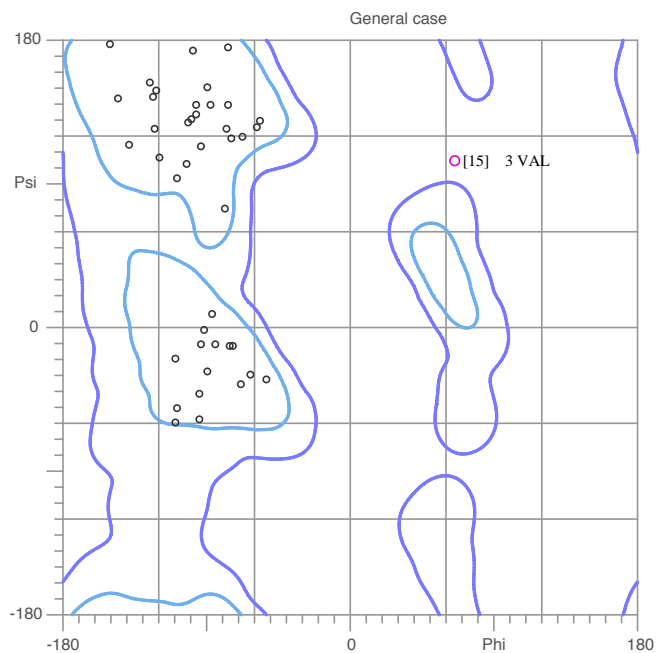
There were no outliers.

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

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 15



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.

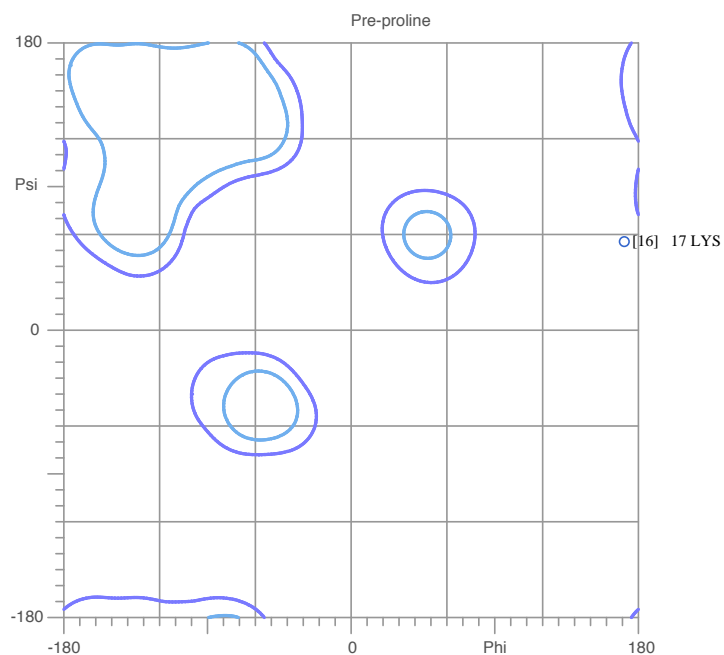
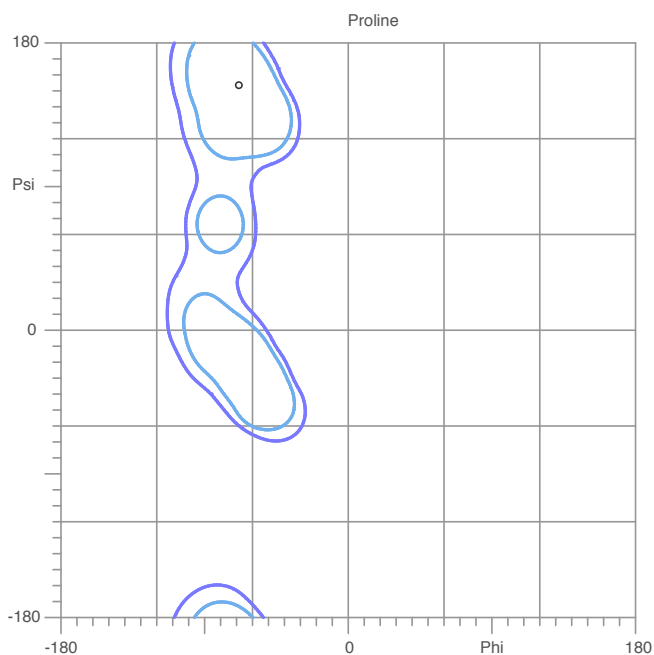
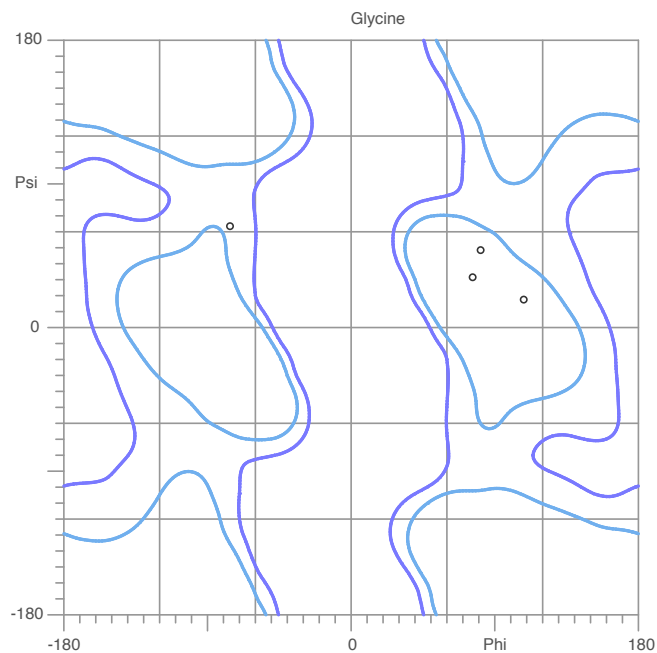
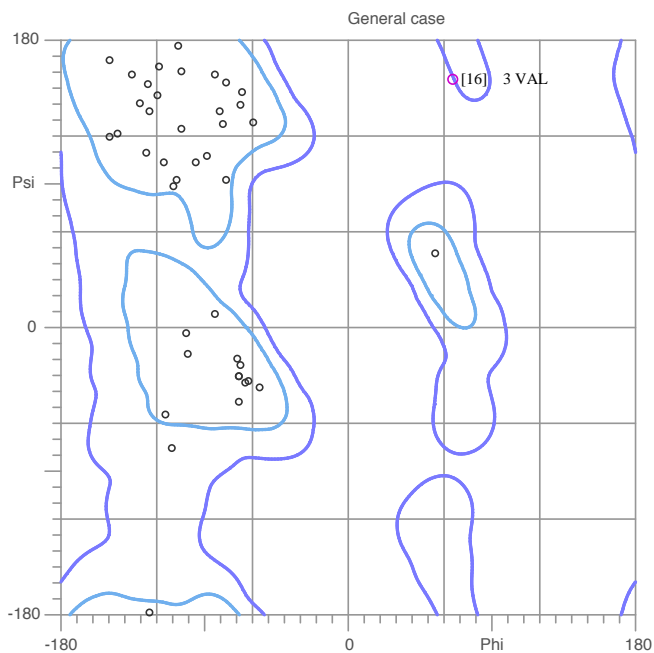
There were 1 outliers (phi, psi):
[15] 3 VAL (65.0, 105.0)

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

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 16

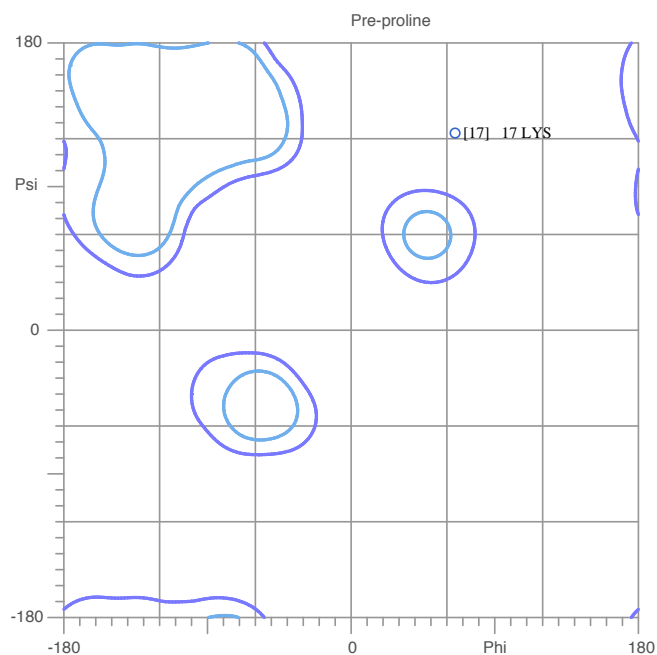
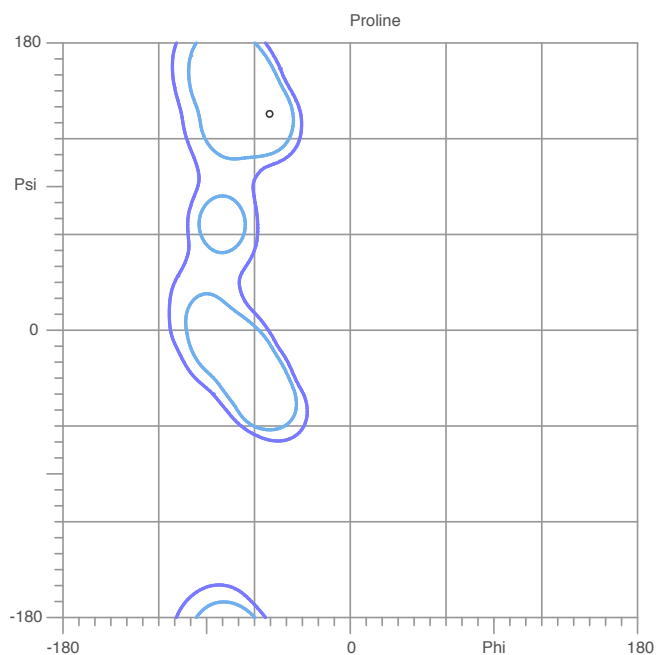
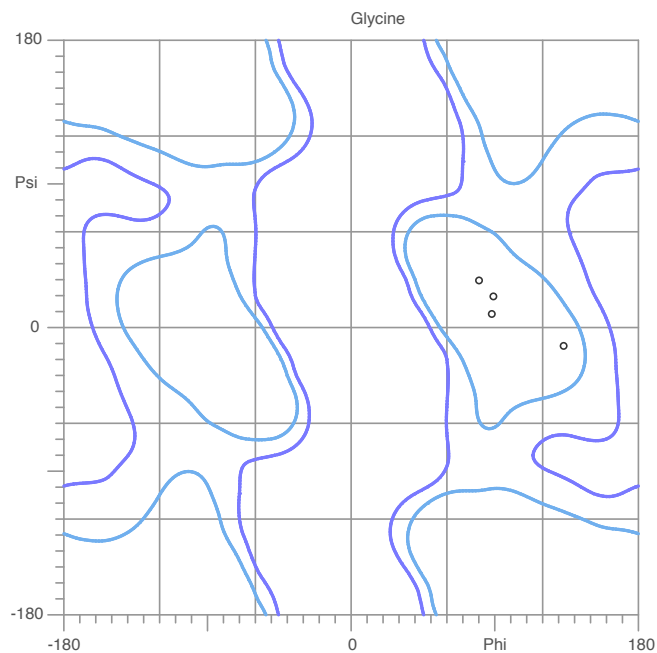
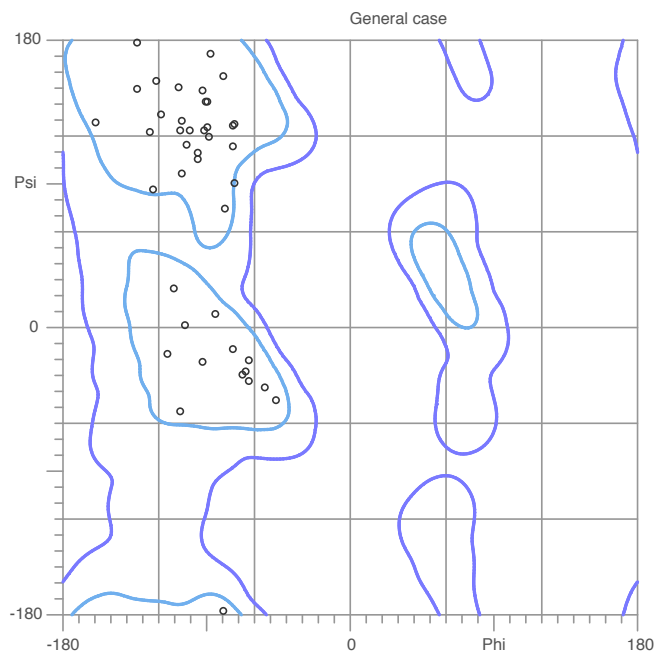


91.7% (44/48) of all residues were in favored (98%) regions.
95.8% (46/48) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[16] 3 VAL (65.1, 156.3)
[16] 17 LYS (171.8, 56.8)

MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 17



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.

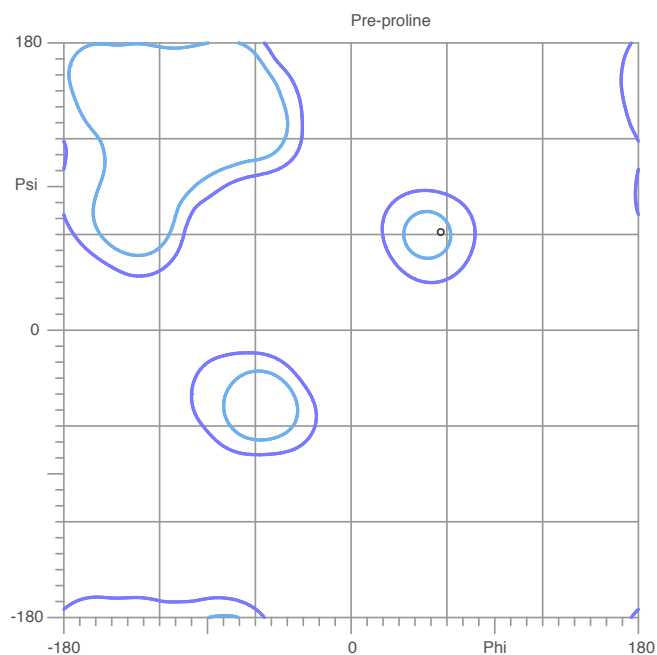
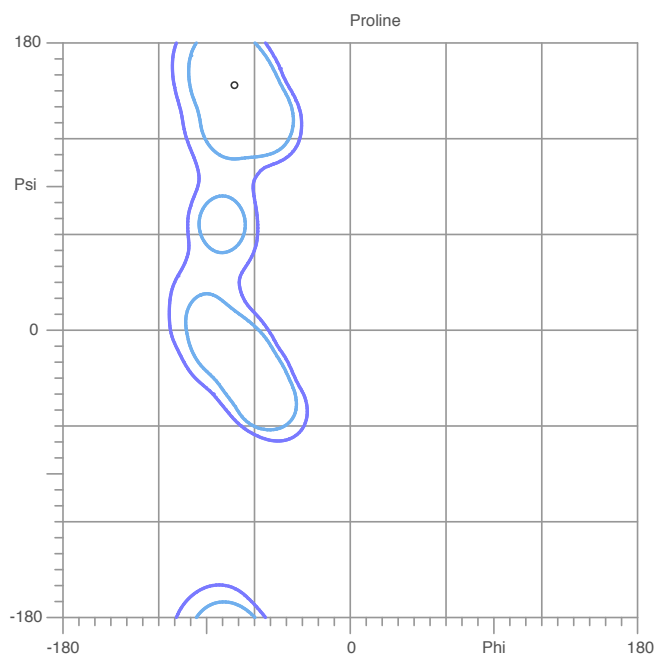
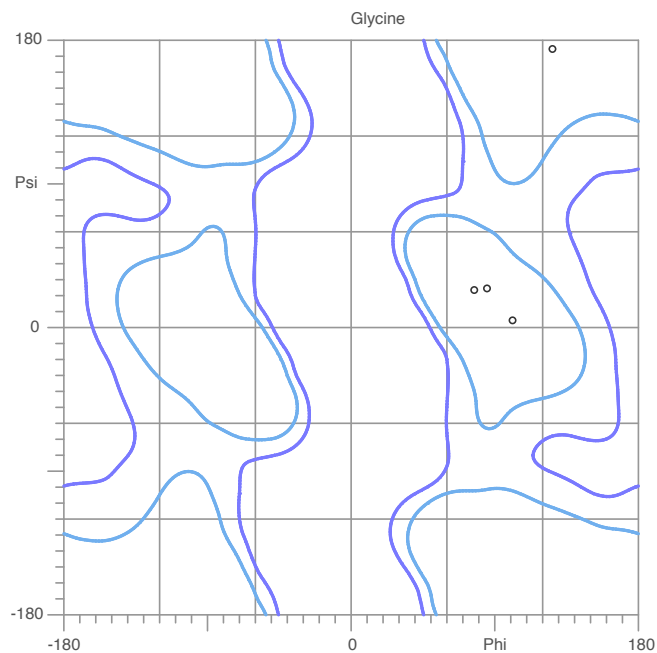
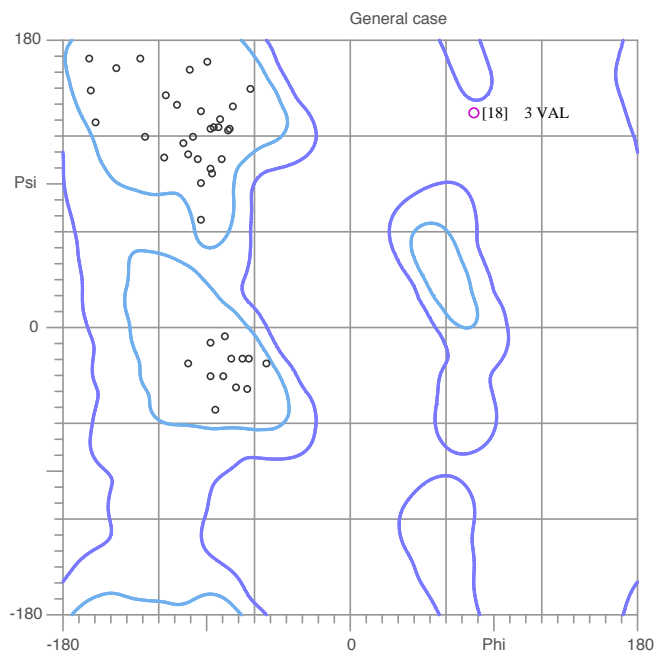
There were 1 outliers (phi, psi):
[17] 17 LYS (65.1, 125.0)

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 18



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.

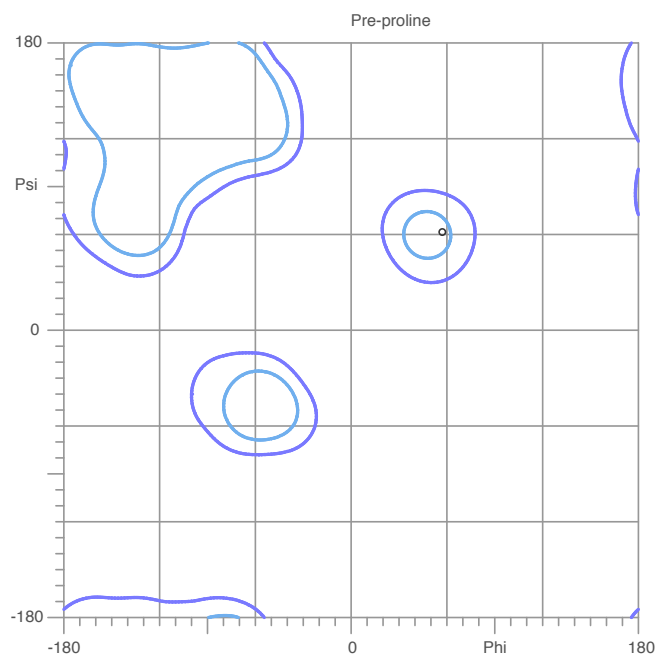
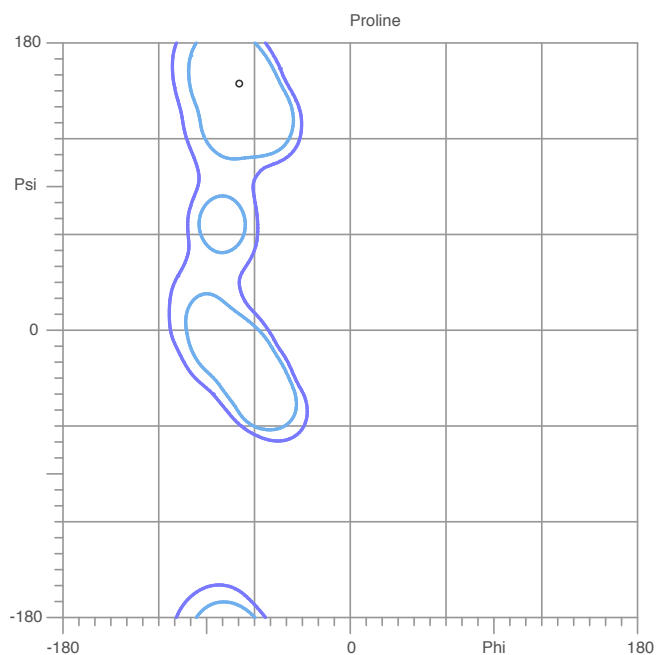
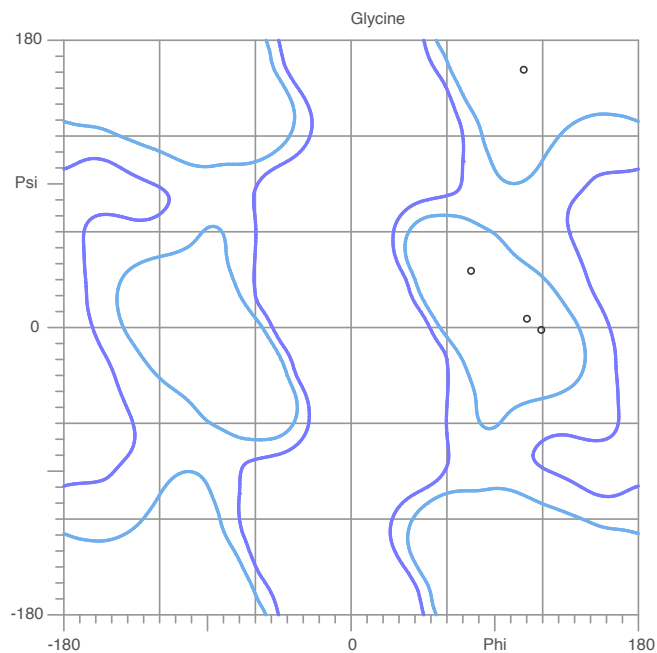
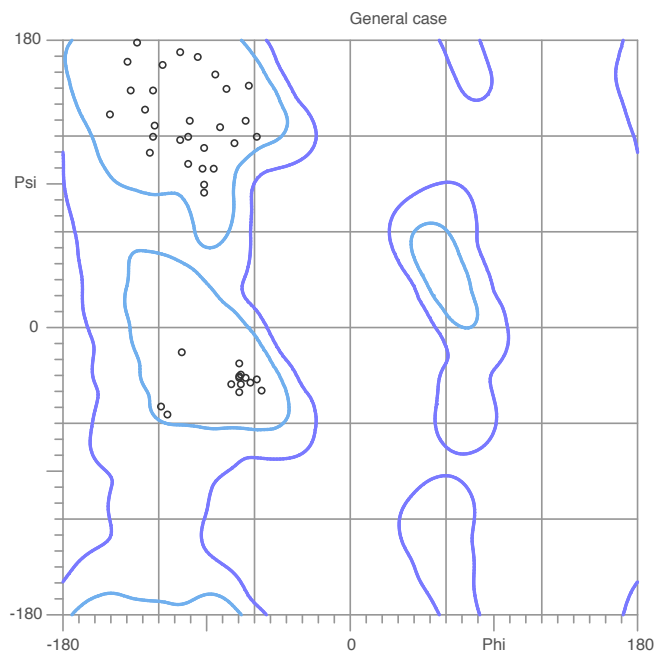
There were 1 outliers (phi, psi):
[18] 3 VAL (77.3, 135.0)

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MolProbity Ramachandran analysis

ER382A_R3_em_bcr3.pdb, model 19



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.

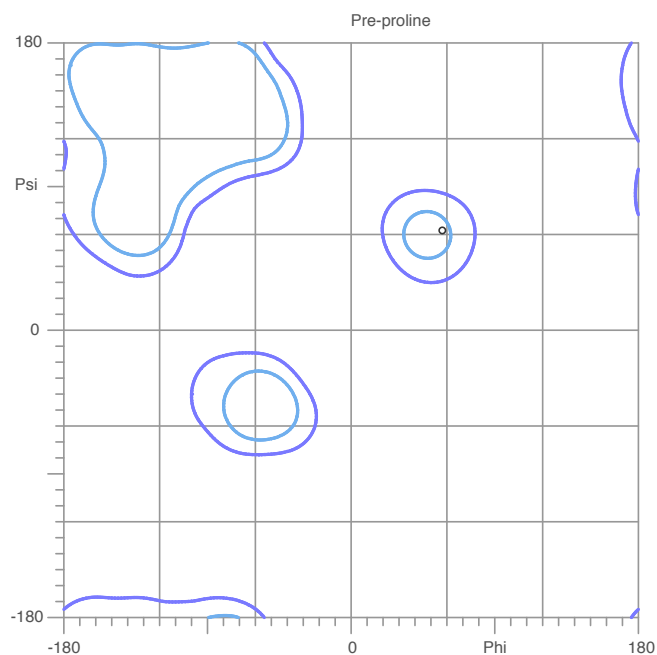
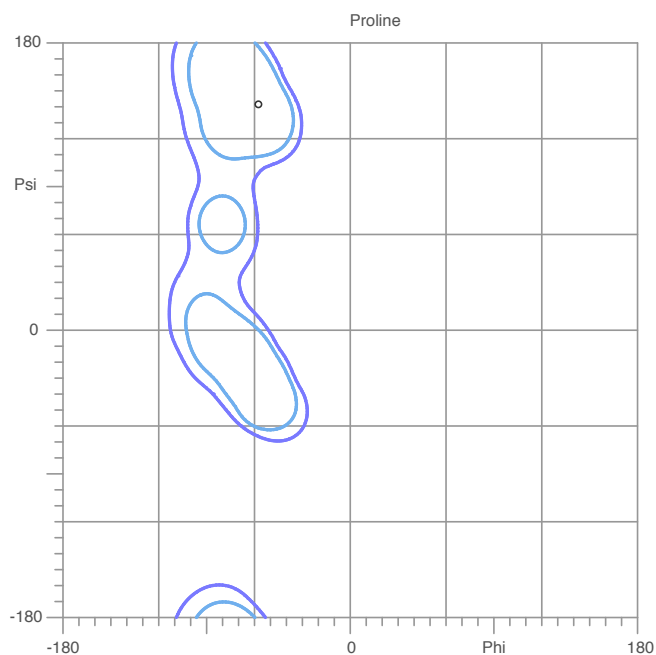
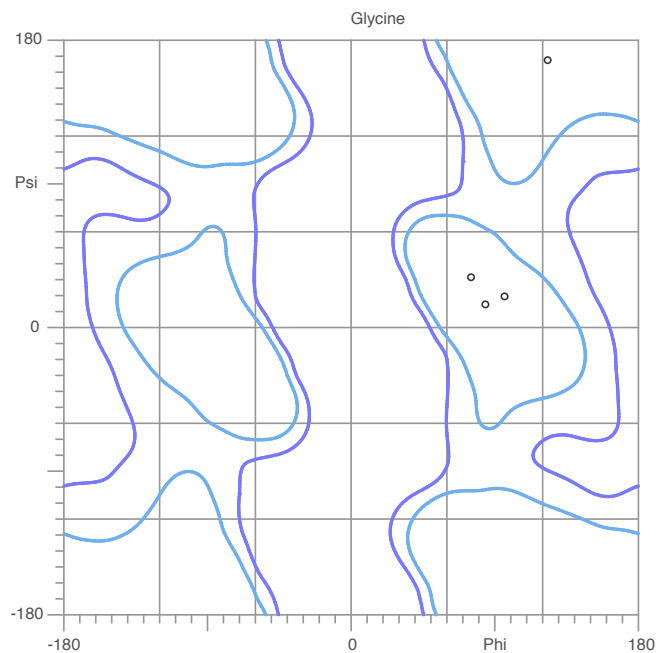
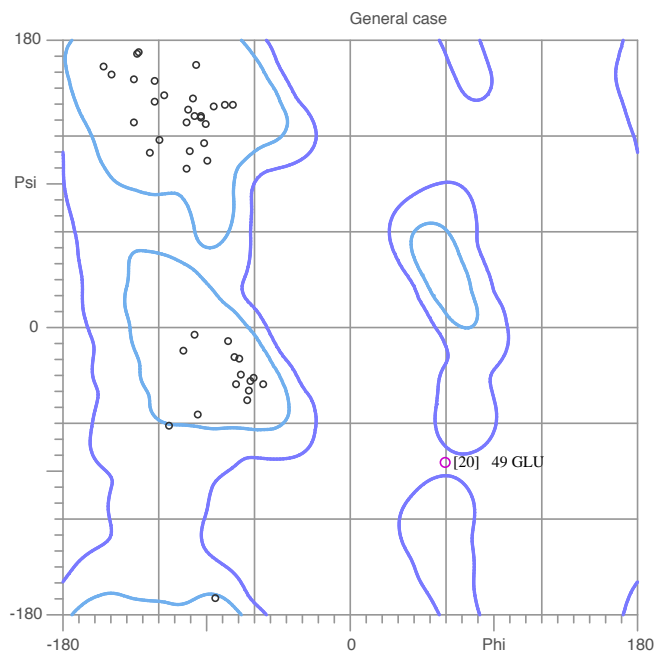
There were no outliers.

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MolProbity Ramachandran analysis

ER382A_R3_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] 49 GLU (60.0, -85.0)

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