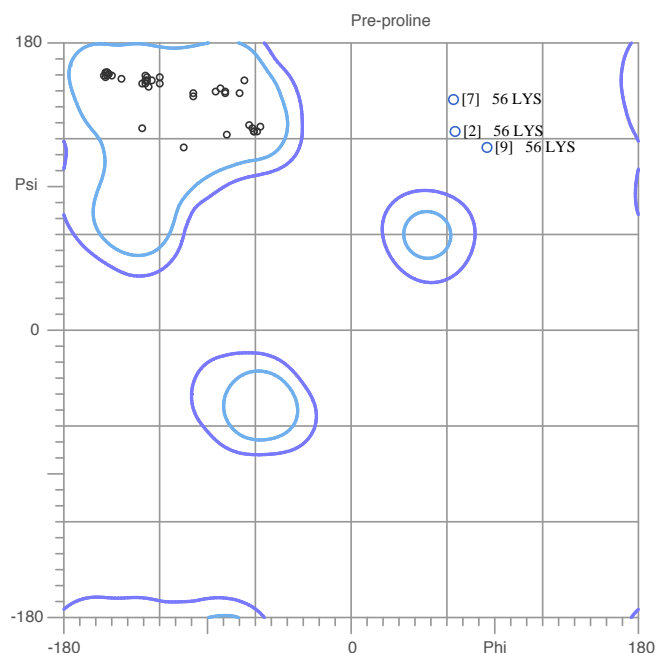
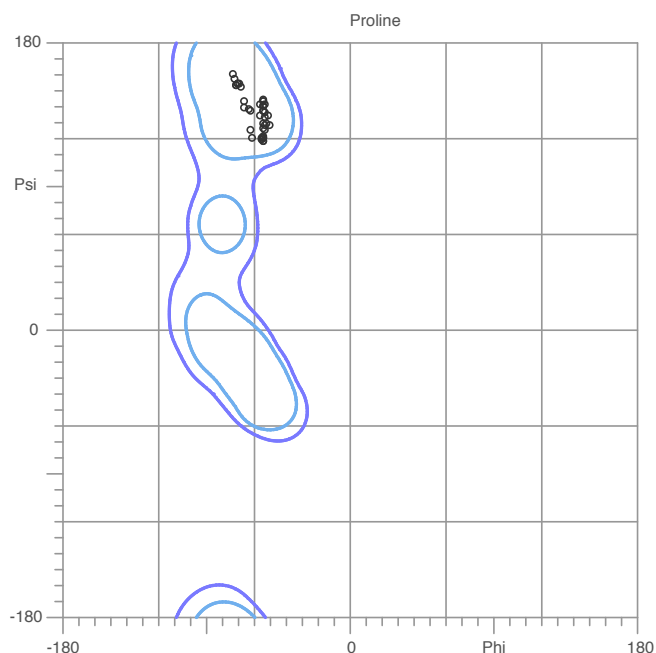
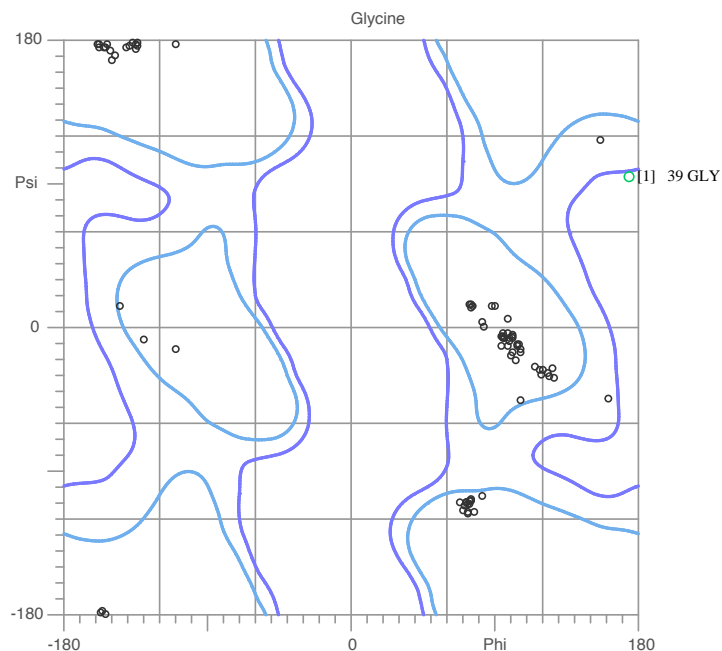
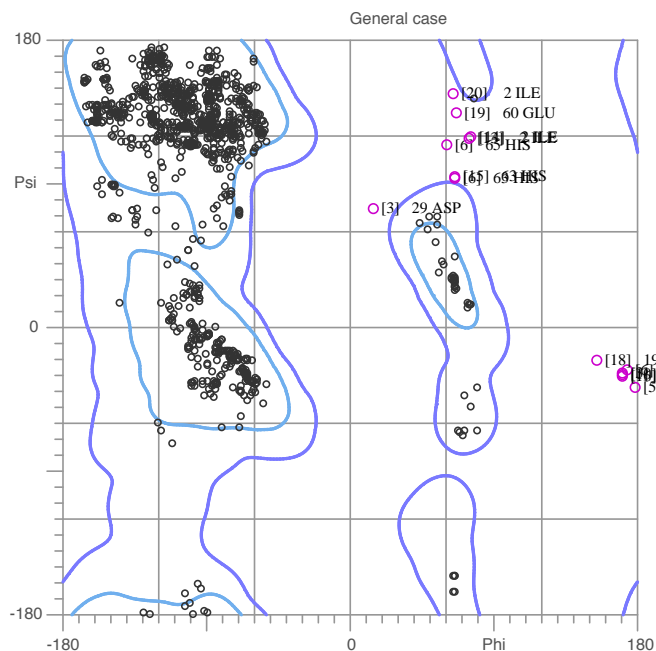


MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, all models



93.8% (1201/1280) of all residues were in favored (98%) regions.
98.6% (1262/1280) of all residues were in allowed (>99.8%) regions.

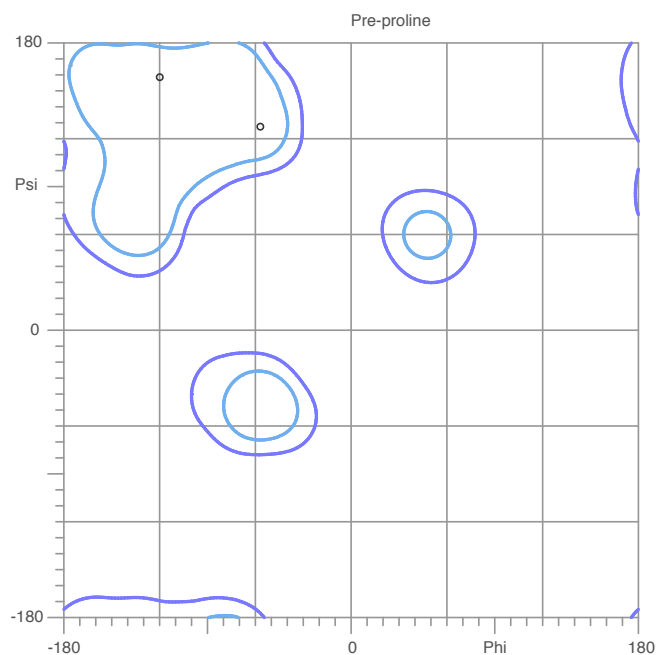
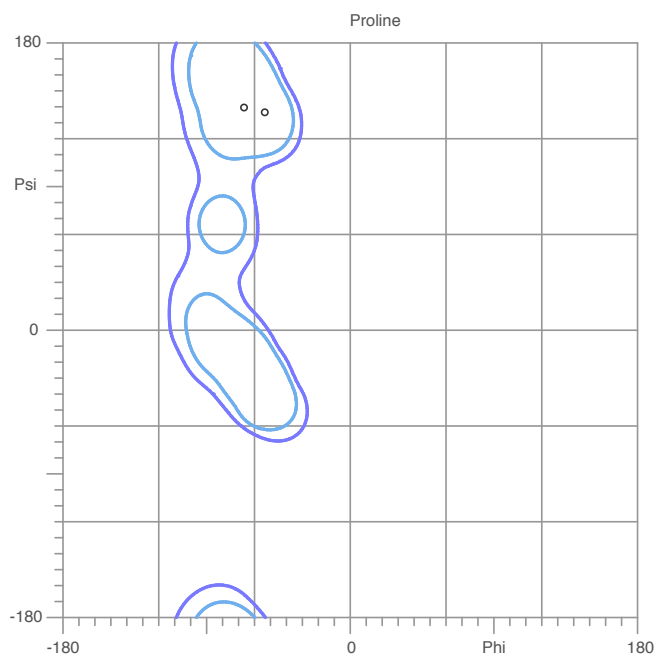
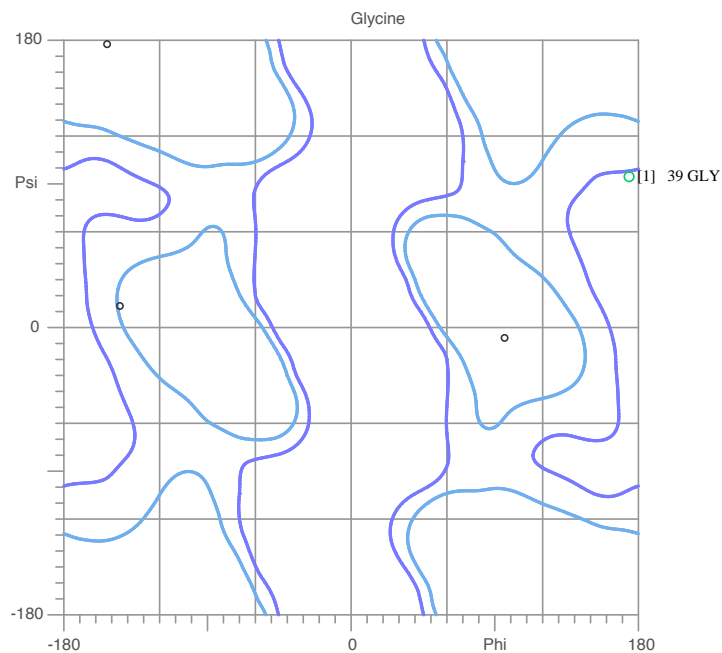
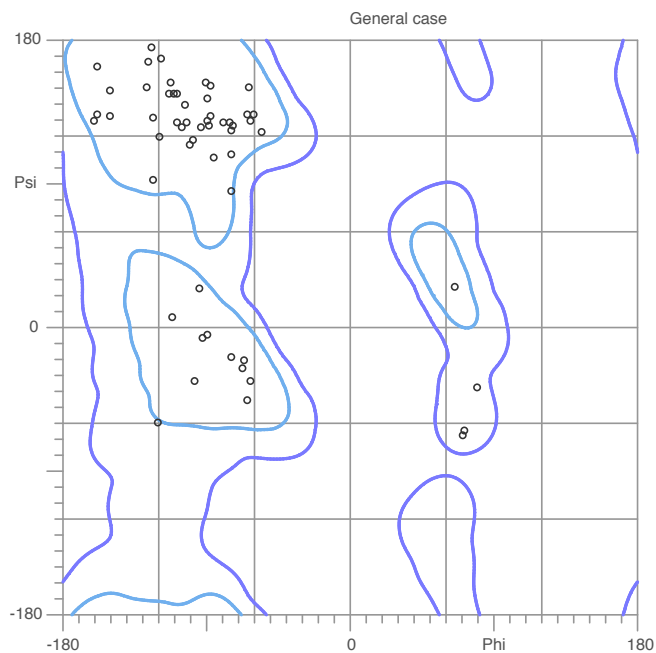
There were 18 outliers (phi, psi):

- [1] 39 GLY (175.0, 95.0)
- [2] 56 LYS (65.0, 125.0)
- [3] 19 ARG (170.2, -28.9)
- [3] 29 ASP (15.0, 75.6)
- [5] 40 ASN (178.6, -37.5)
- [6] 19 ARG (173.1, -26.3)
- [6] 63 HIS (65.0, 95.0)

- [6] 65 HIS (60.5, 115.1)
- [7] 56 LYS (64.9, 145.0)
- [9] 56 LYS (85.0, 115.1)
- [10] 19 ARG (170.2, -29.5)
- [13] 2 ILE (75.0, 119.1)
- [14] 2 ILE (75.0, 120.4)
- [15] 63 HIS (65.0, 95.1)
- [16] 19 ARG (170.6, -30.3)
- [18] 19 ARG (154.3, -20.6)
- [19] 60 GLU (66.3, 135.0)
- [20] 2 ILE (65.0, 147.3)

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 1



92.2% (59/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

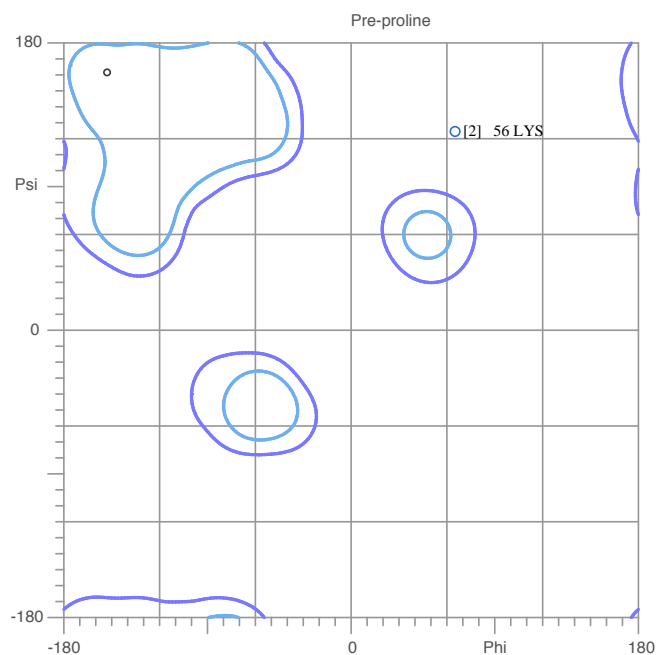
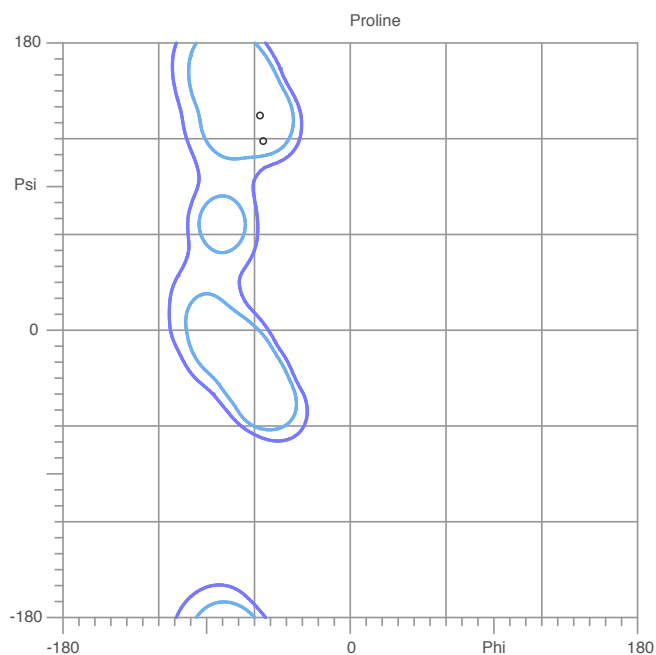
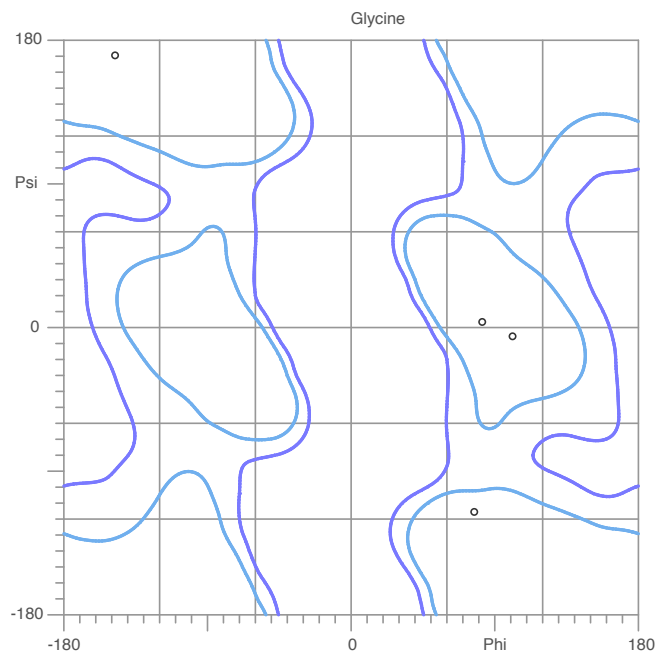
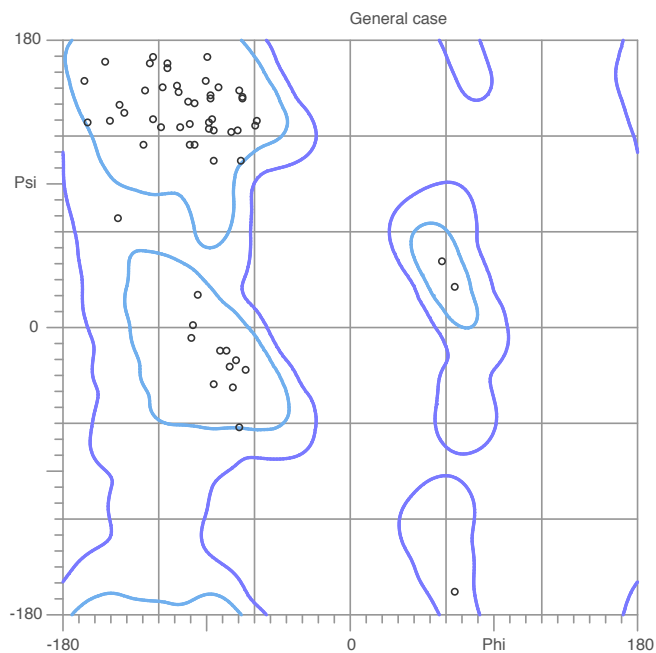
There were 1 outliers (phi, psi):
[1] 39 GLY (175.0, 95.0)

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MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 2



93.8% (60/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

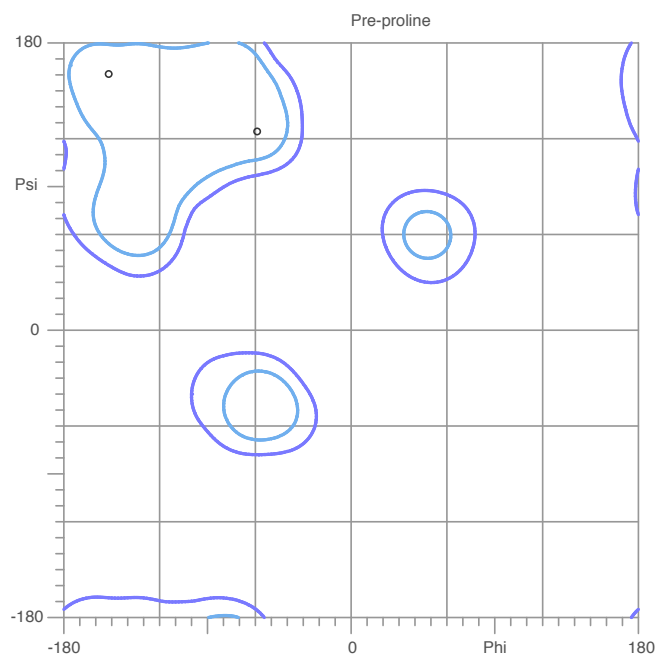
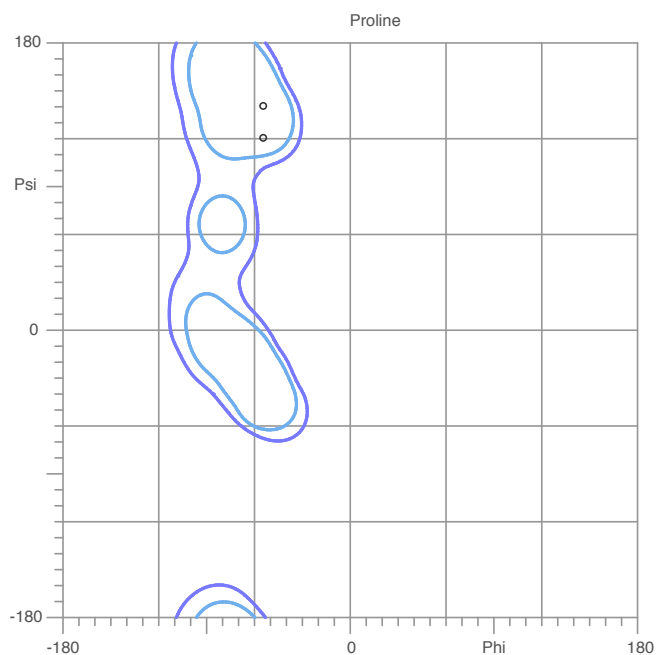
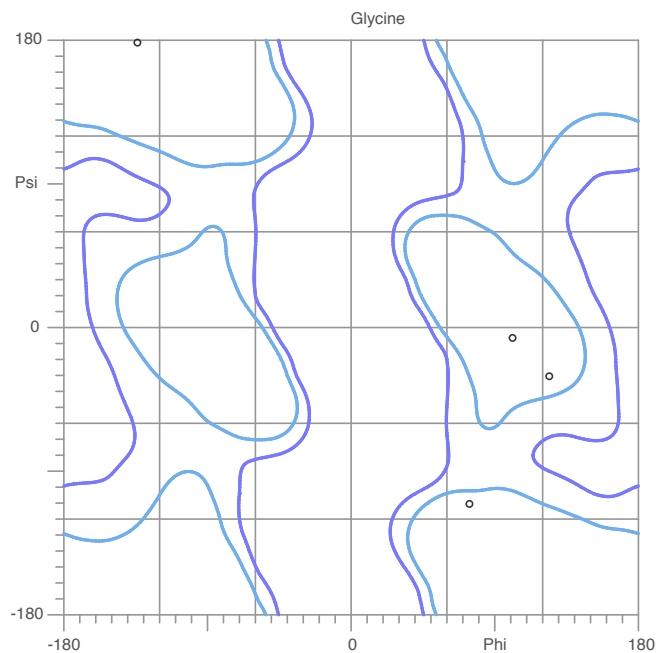
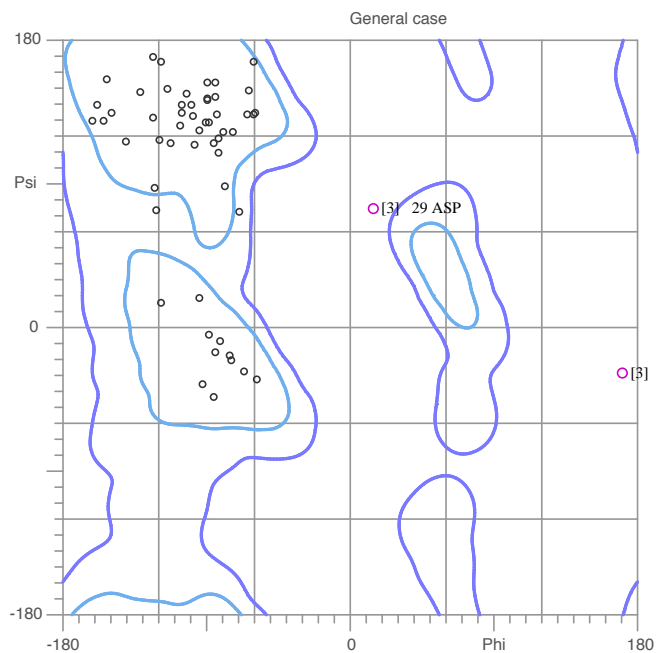
There were 1 outliers (phi, psi):
[2] 56 LYS (65.0, 125.0)

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

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

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 3



93.8% (60/64) of all residues were in favored (98%) regions.
96.9% (62/64) of all residues were in allowed (>99.8%) regions.

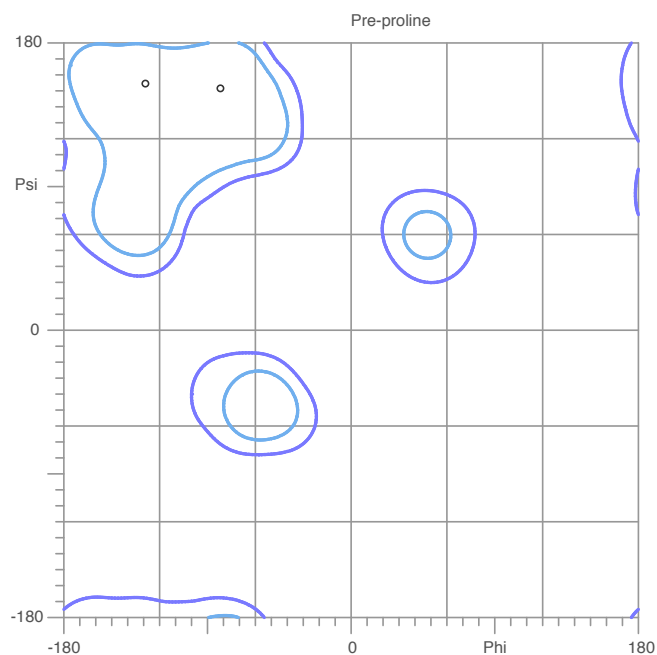
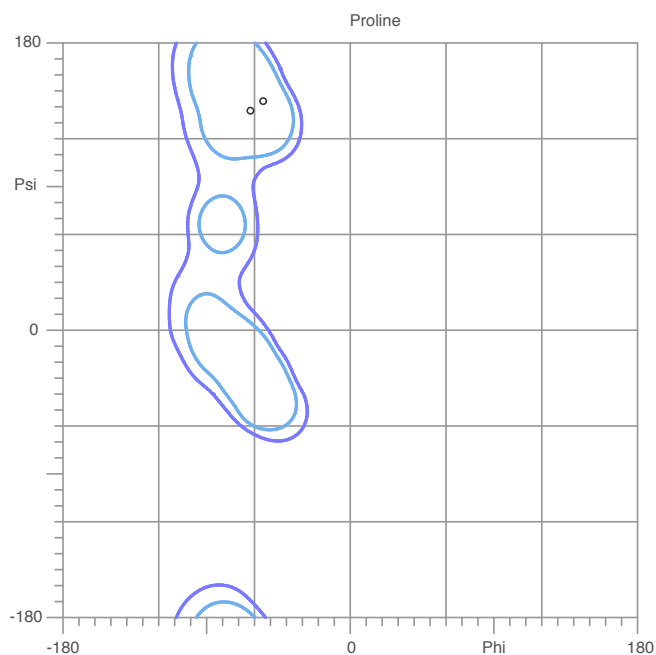
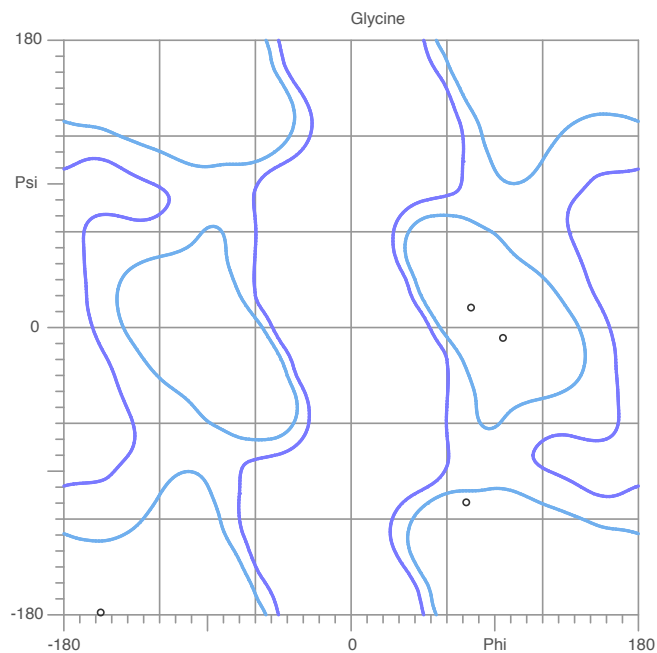
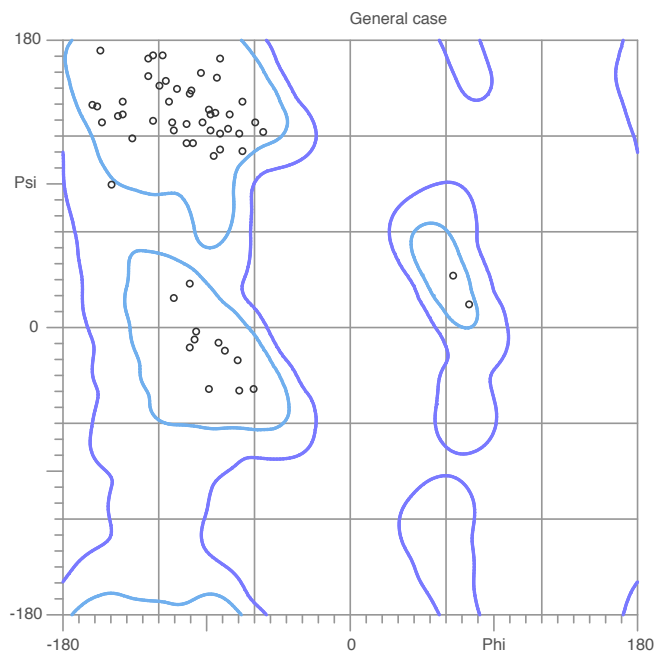
There were 2 outliers (phi, psi):

[3] 19 ARG (170.2, -28.9)

[3] 29 ASP (15.0, 75.6)

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 4



98.4% (63/64) of all residues were in favored (98%) regions.
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

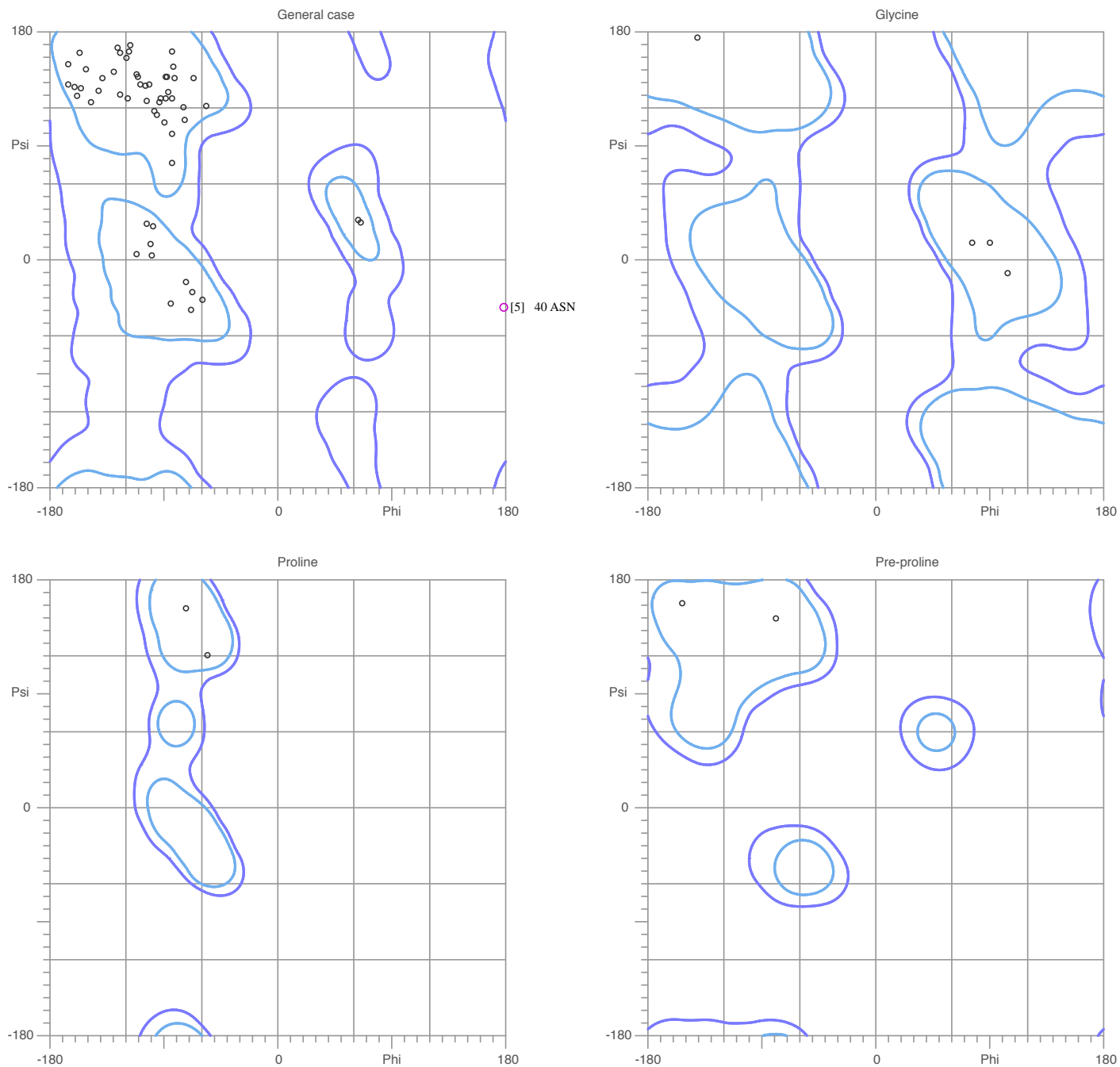
There were no outliers.

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

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 5



98.4% (63/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

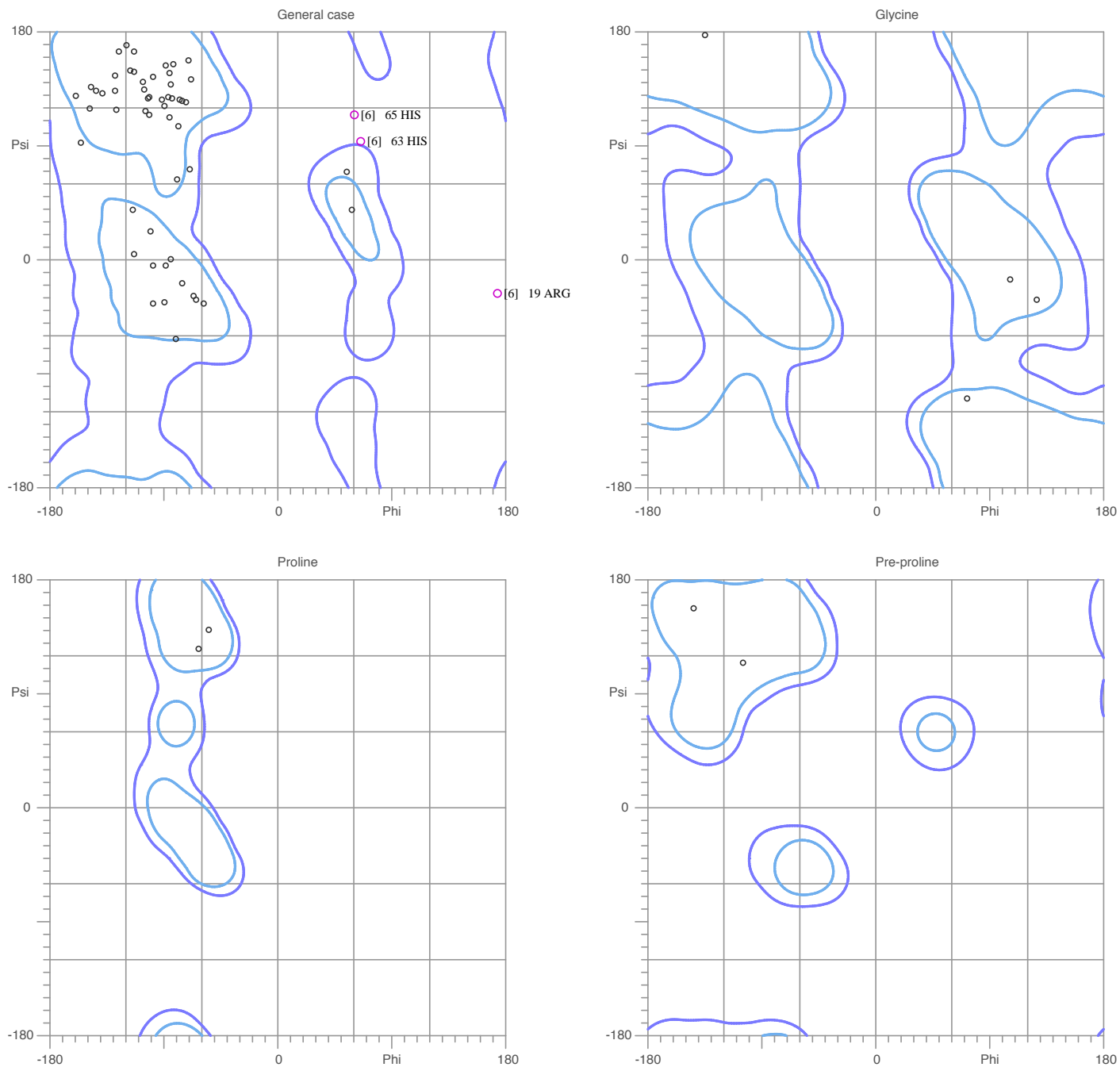
There were 1 outliers (phi, psi):
[5] 40 ASN (178.6, -37.5)

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

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MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 6



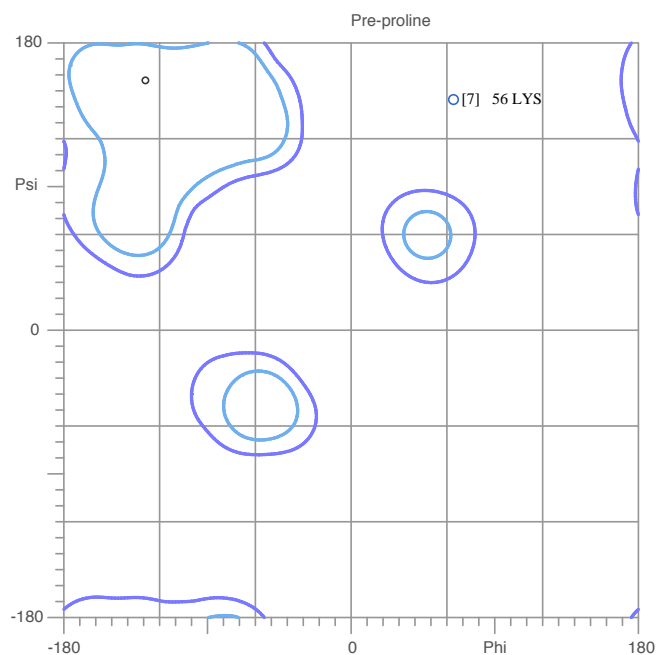
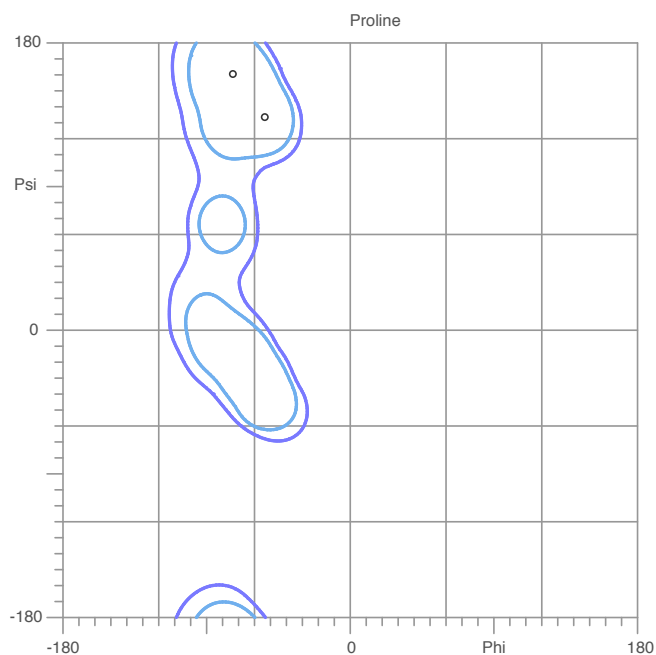
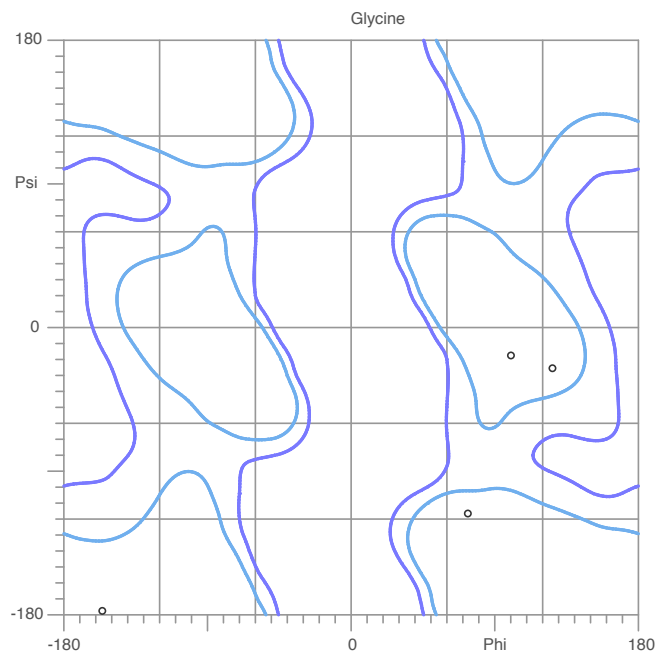
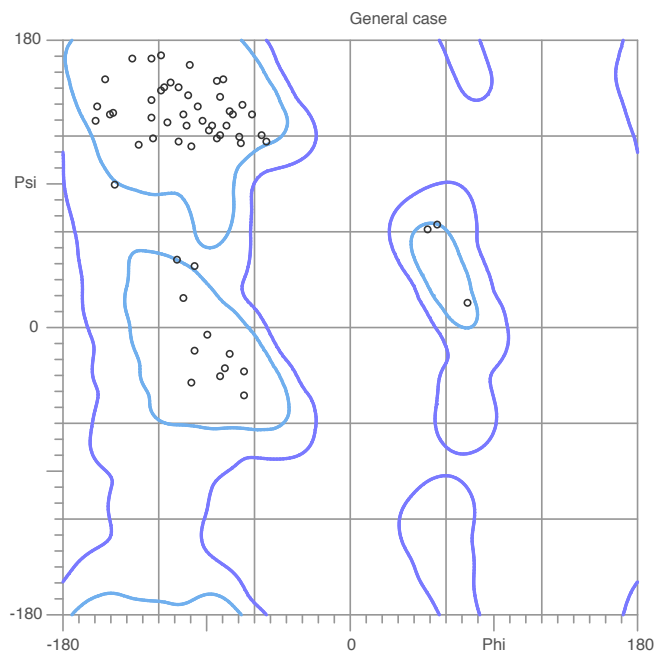
90.6% (58/64) of all residues were in favored (98%) regions.
95.3% (61/64) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 19 ARG (173.1, -26.3)
- [6] 63 HIS (65.0, 95.0)
- [6] 65 HIS (60.5, 115.1)

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 7



92.2% (59/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

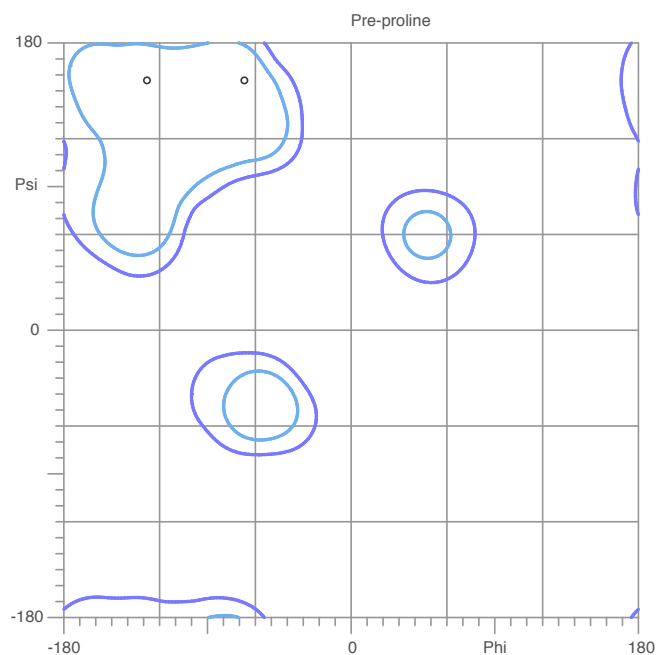
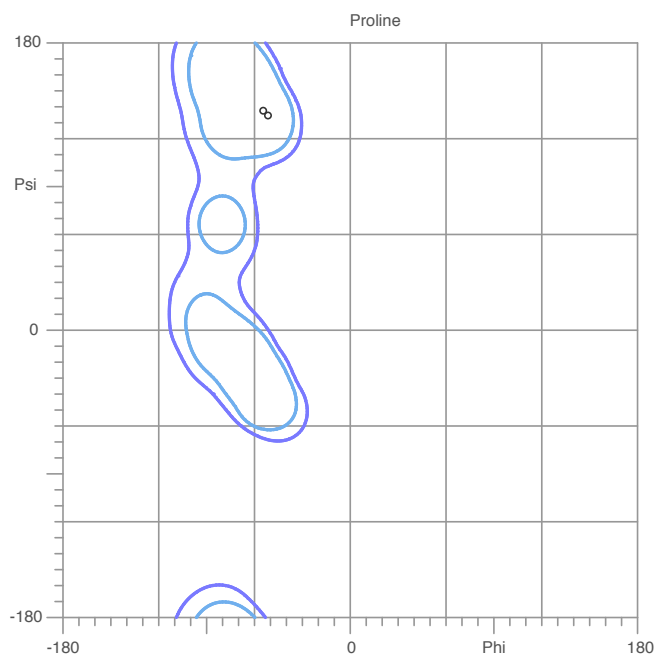
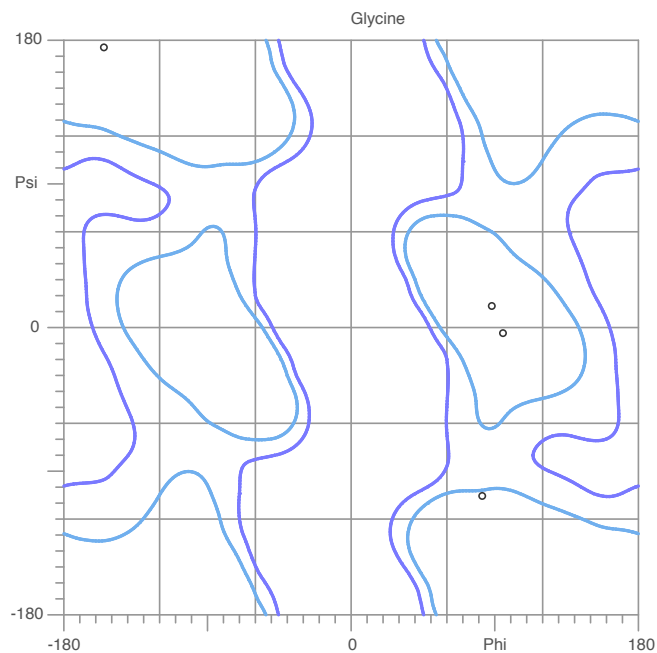
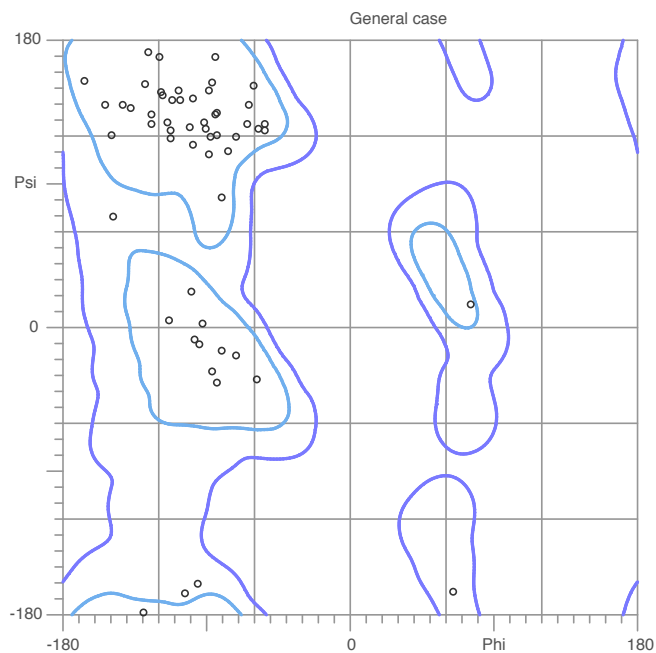
There were 1 outliers (phi, psi):
[7] 56 LYS (64.9, 145.0)

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MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 8



93.8% (60/64) of all residues were in favored (98%) regions.
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

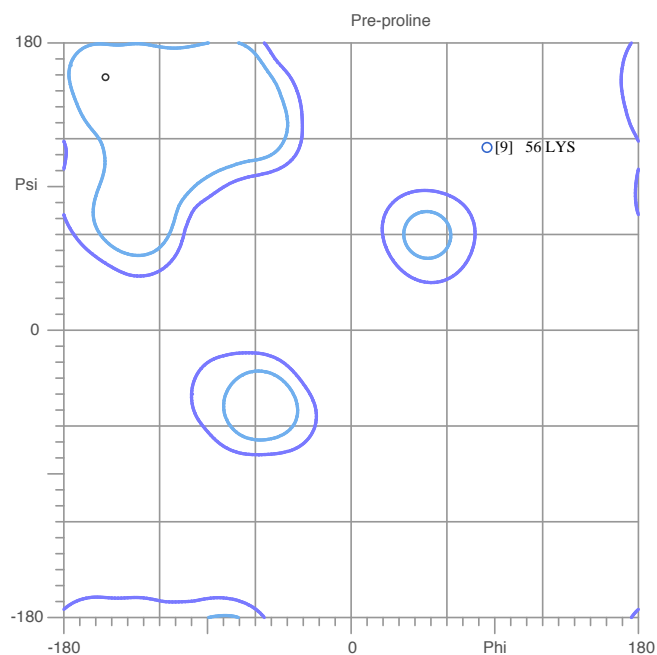
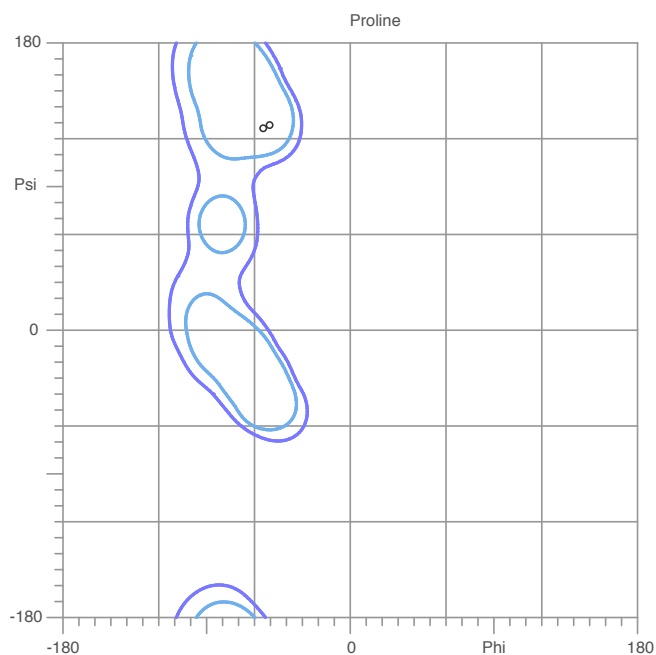
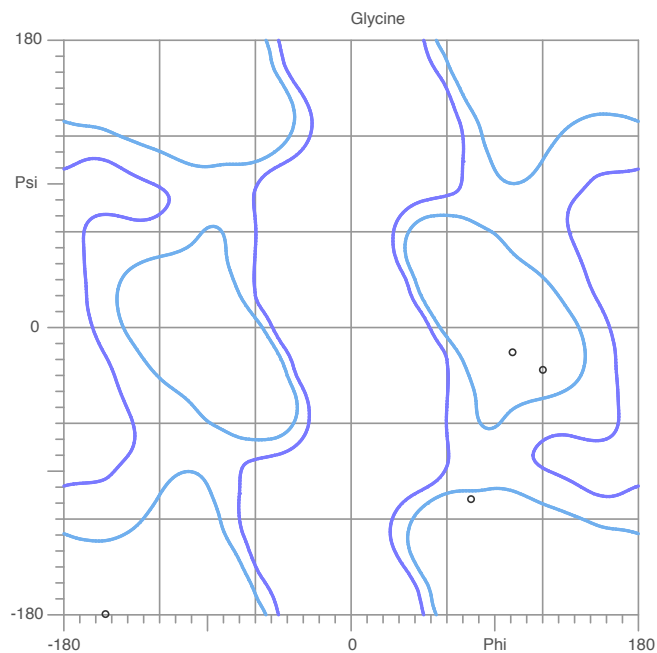
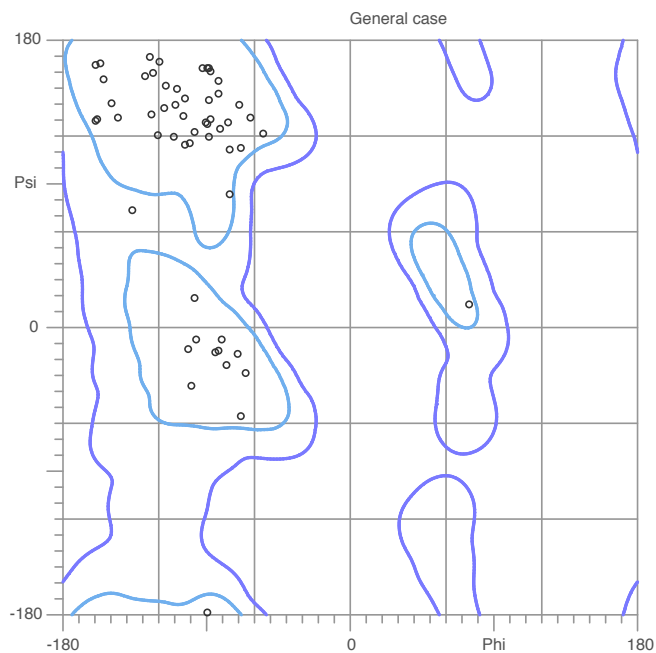
There were no outliers.

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MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 9



96.9% (62/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

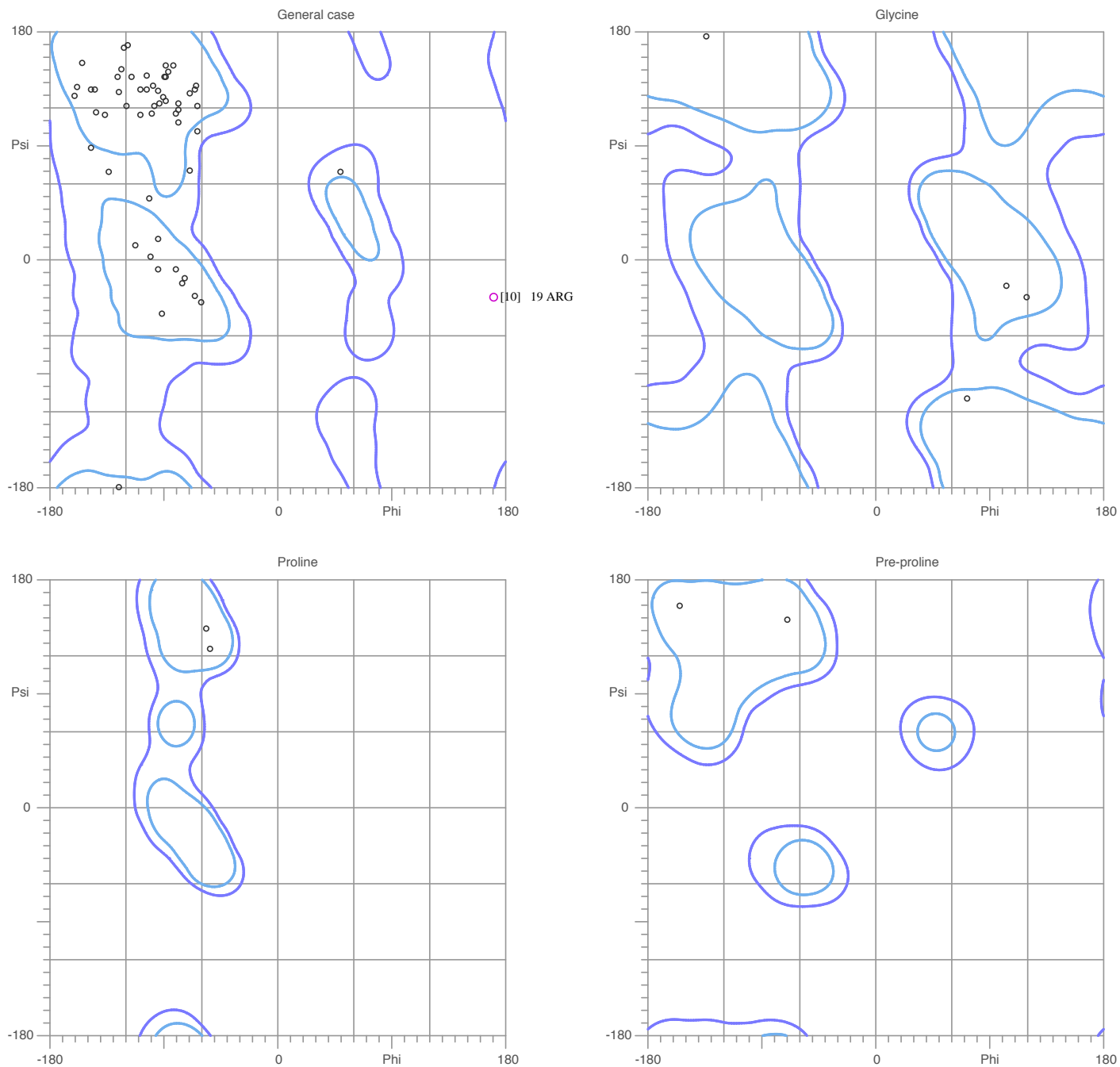
There were 1 outliers (phi, psi):
[9] 56 LYS (85.0, 115.1)

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

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MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 10



89.1% (57/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

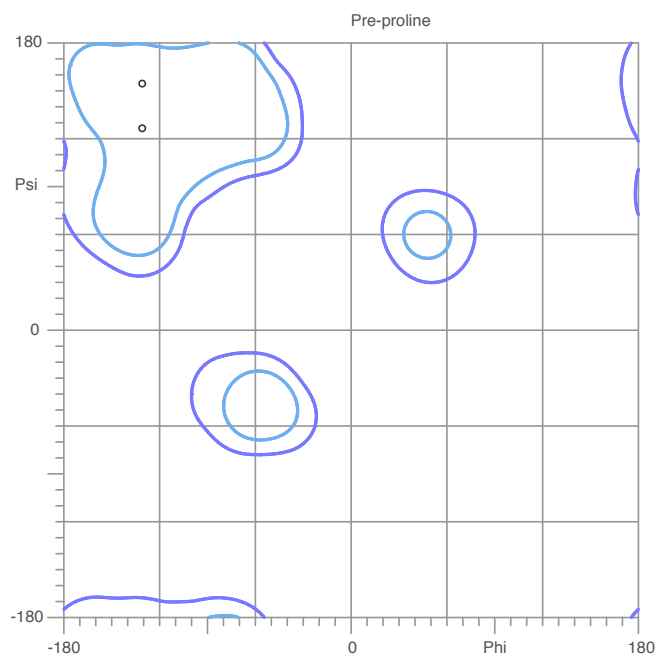
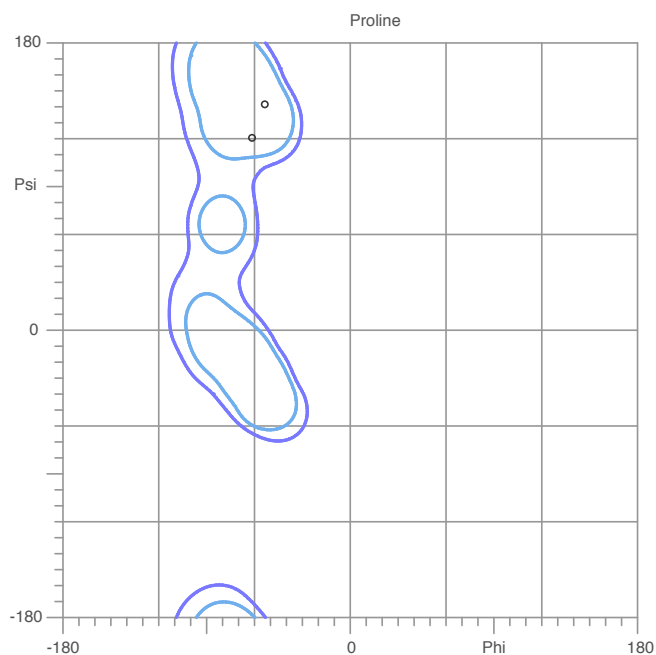
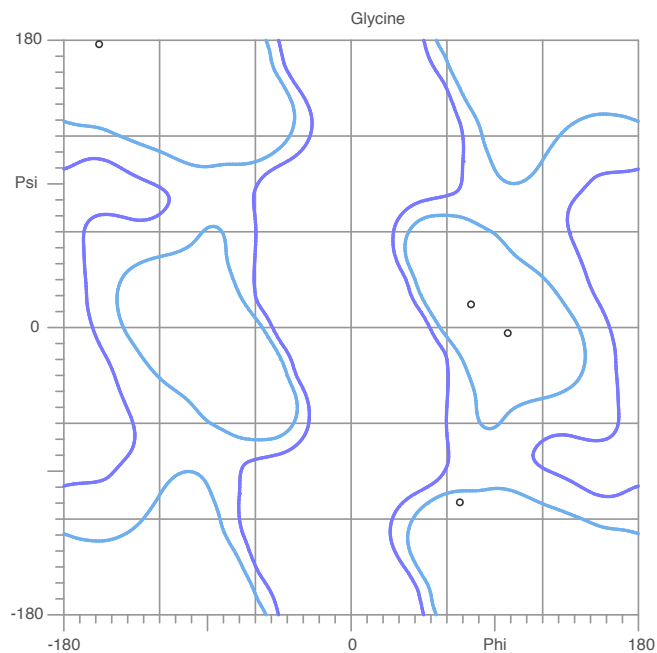
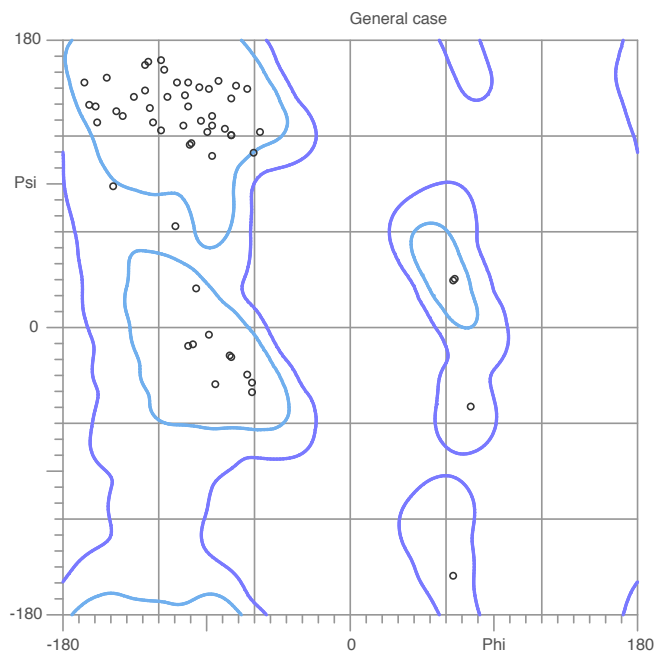
There were 1 outliers (phi, psi):
[10] 19 ARG (170.2, -29.5)

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MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 11



93.8% (60/64) of all residues were in favored (98%) regions.
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

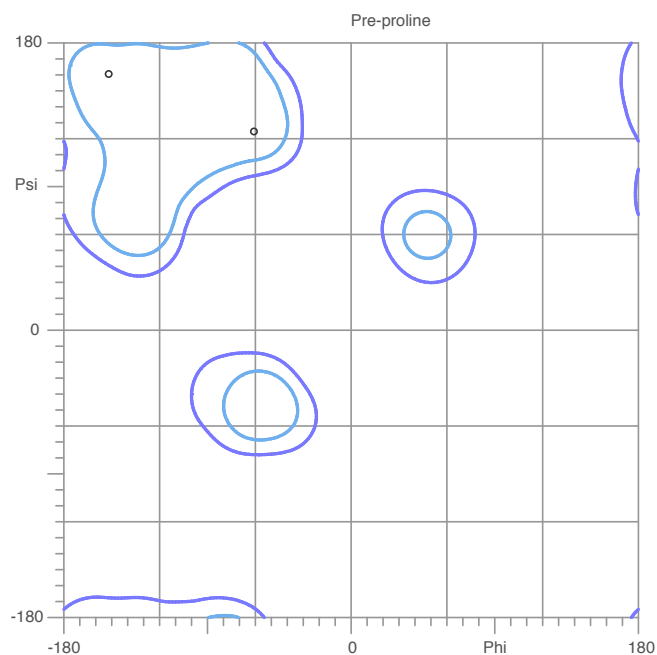
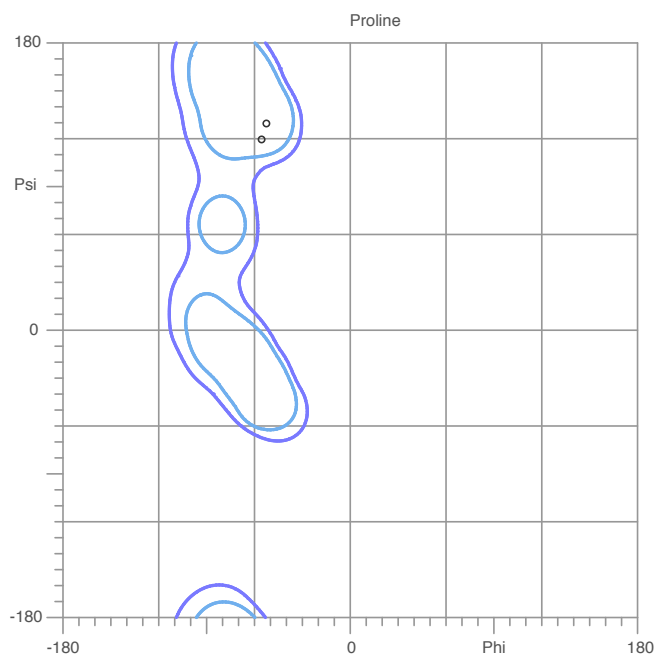
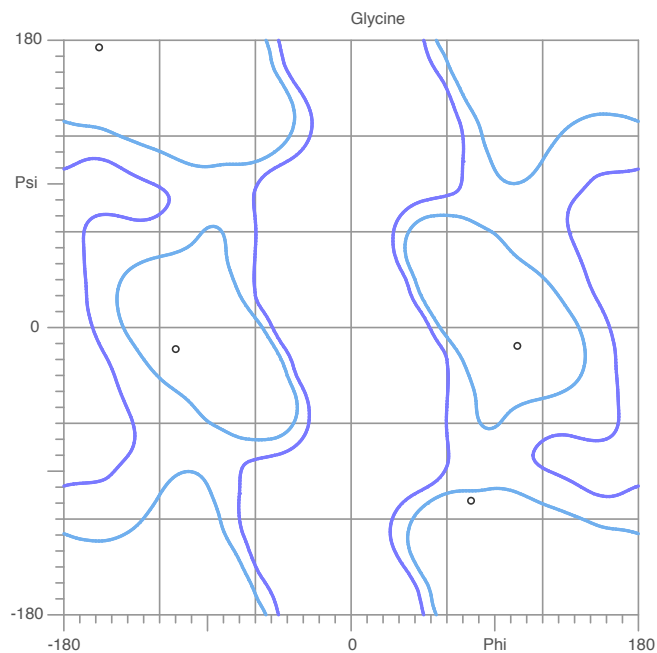
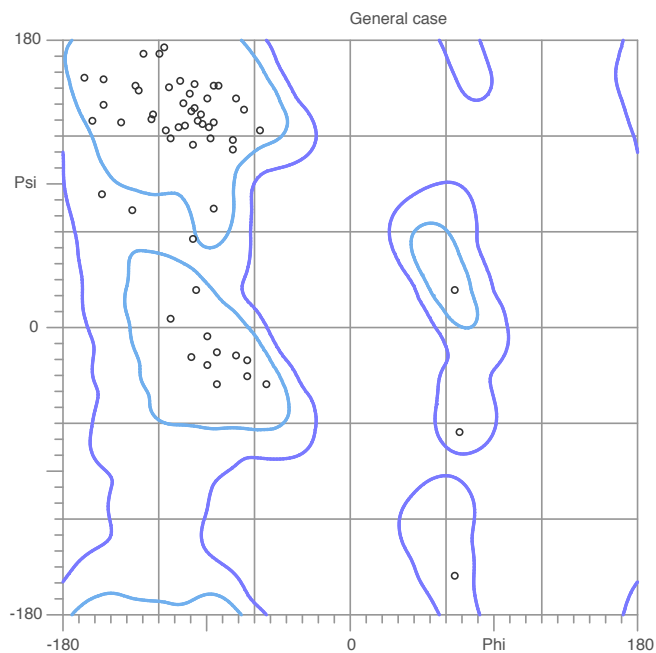
There were no outliers.

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

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

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 12

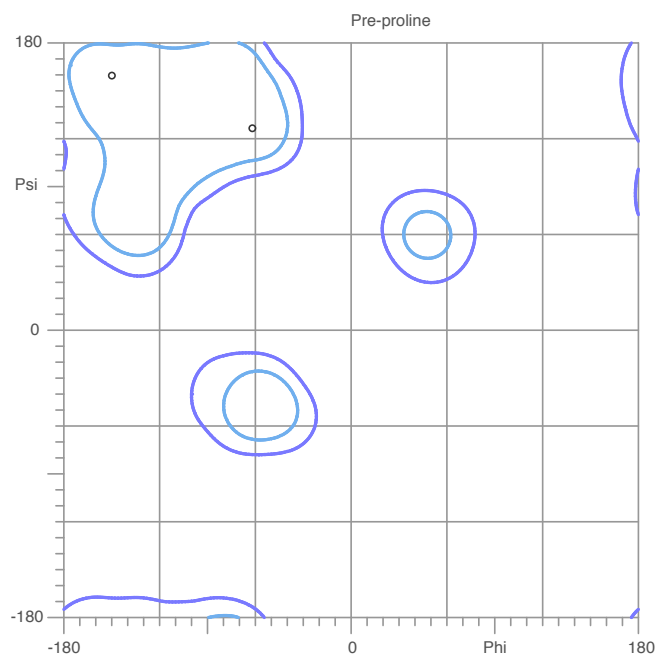
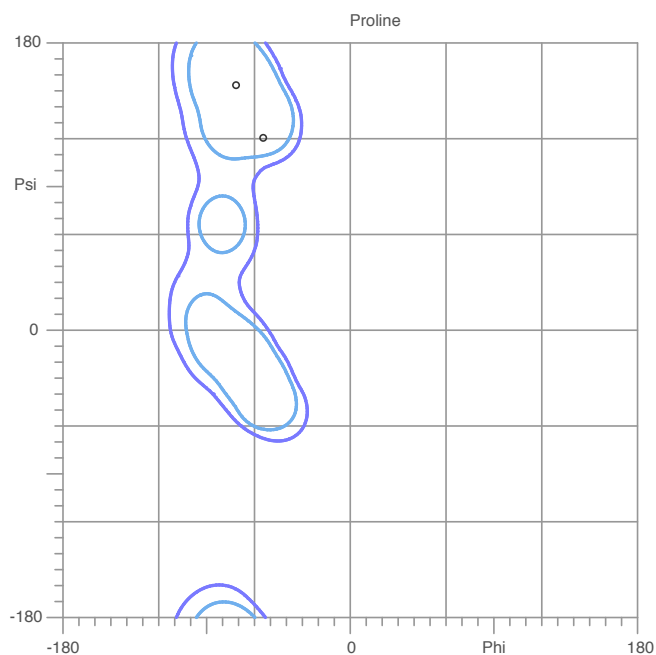
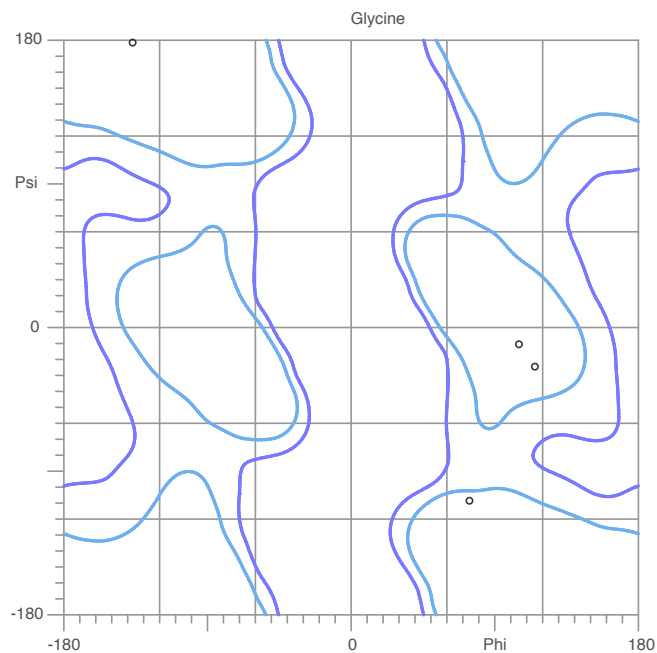
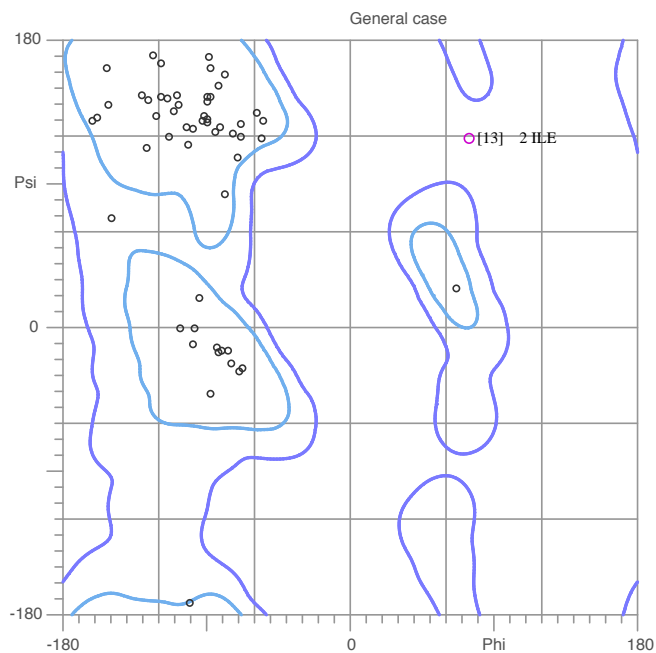


92.2% (59/64) of all residues were in favored (98%) regions.
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 13



96.9% (62/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

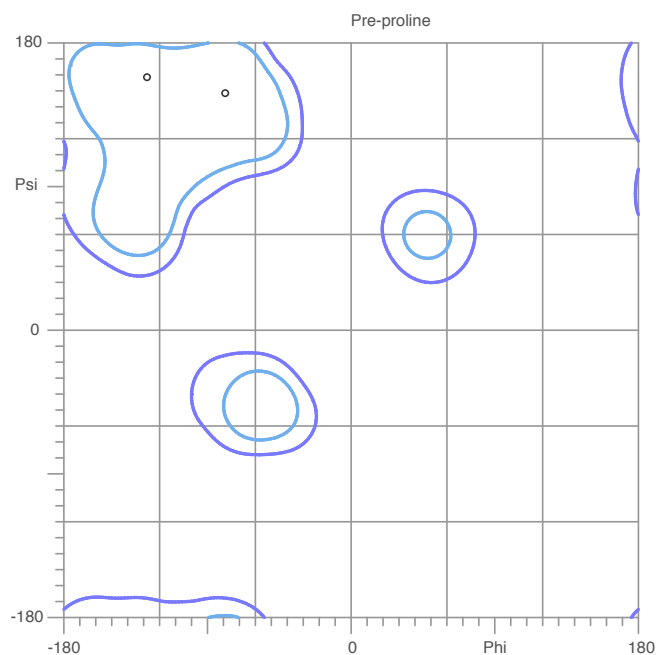
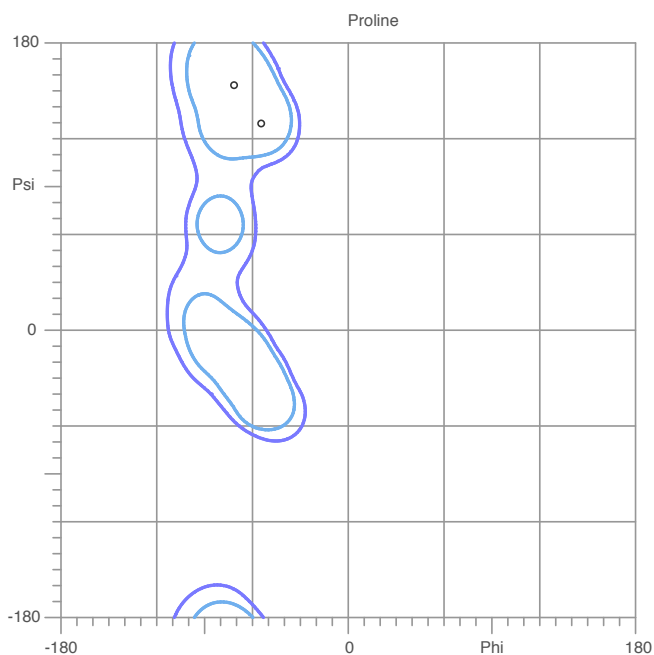
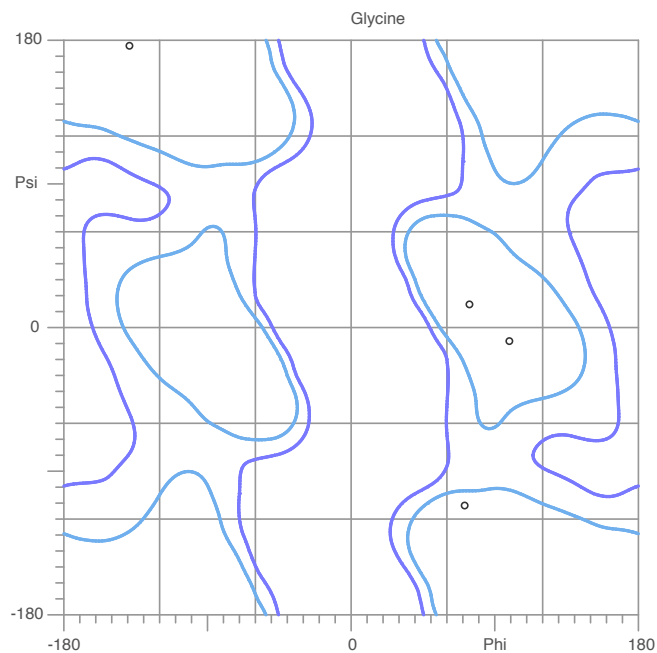
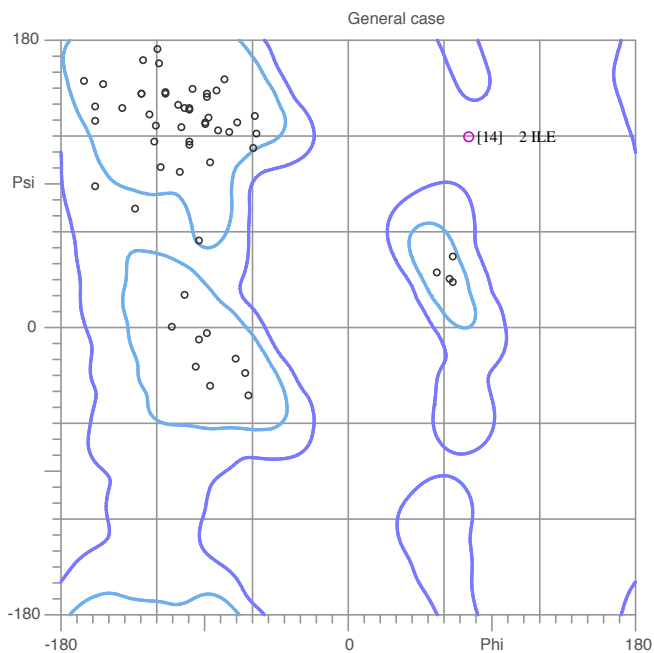
There were 1 outliers (phi, psi):
[13] 2 ILE (75.0, 119.1)

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MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 14



95.3% (61/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

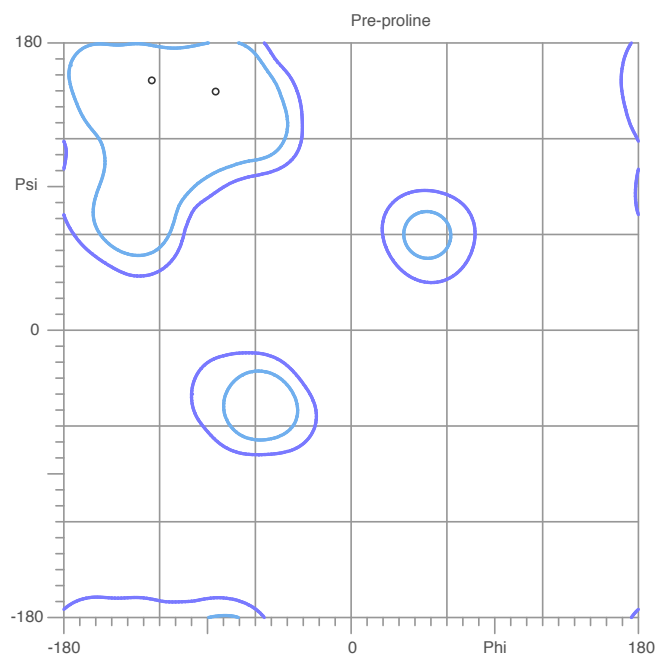
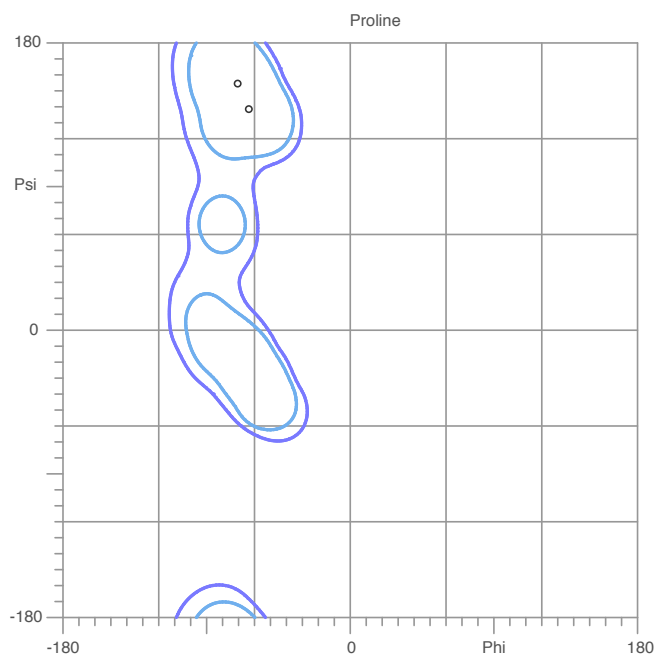
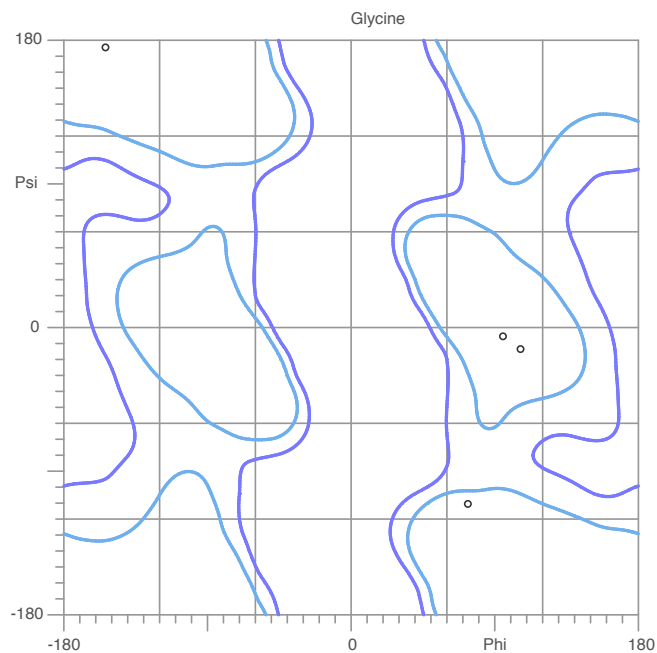
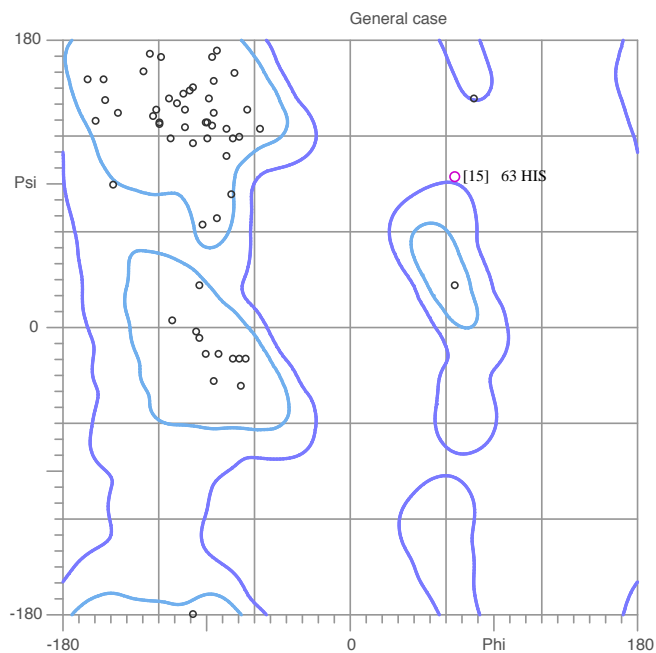
There were 1 outliers (phi, psi):
[14] 2 ILE (75.0, 120.4)

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

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MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 15



95.3% (61/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

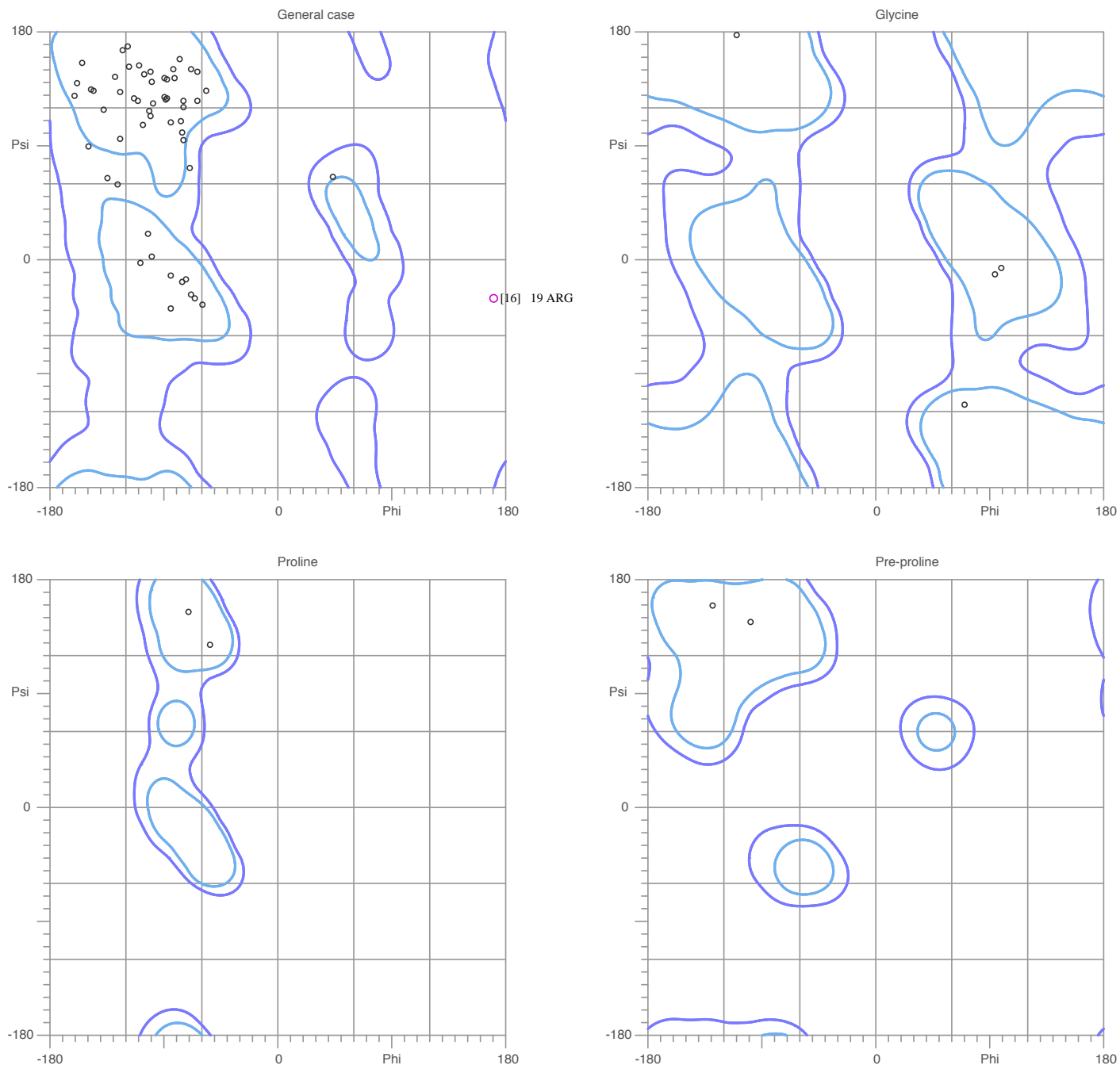
There were 1 outliers (phi, psi):
[15] 63 HIS (65.0, 95.1)

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

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

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 16



90.6% (58/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

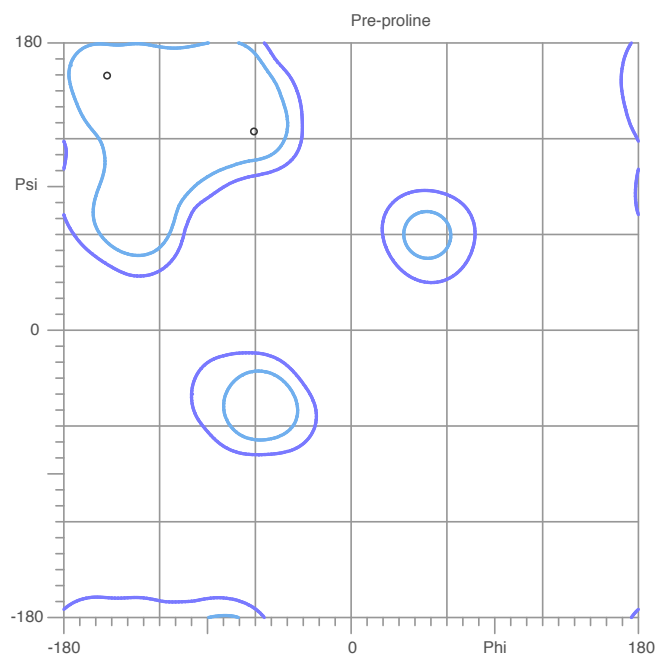
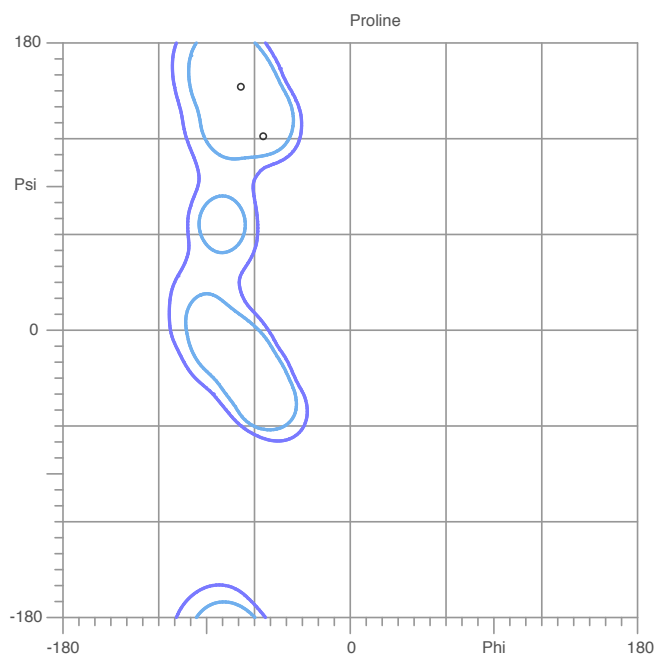
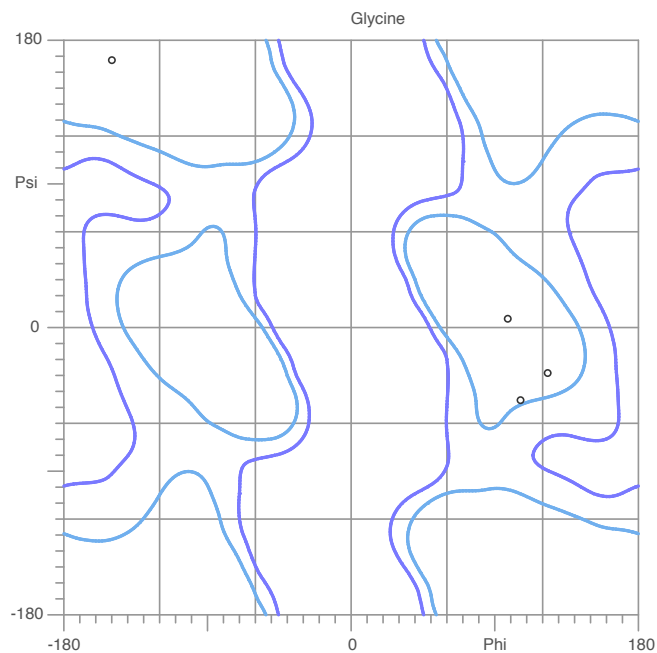
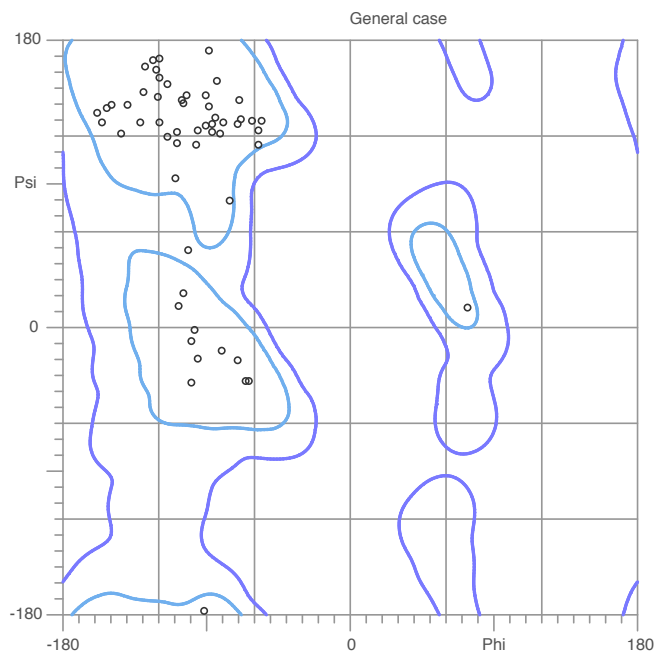
There were 1 outliers (phi, psi):
[16] 19 ARG (170.6, -30.3)

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

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

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 17



98.4% (63/64) of all residues were in favored (98%) regions.
100.0% (64/64) of all residues were in allowed (>99.8%) regions.

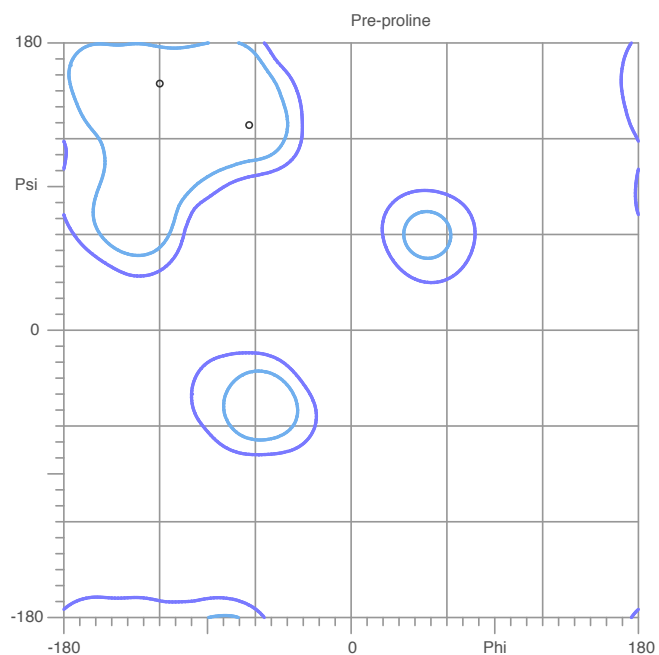
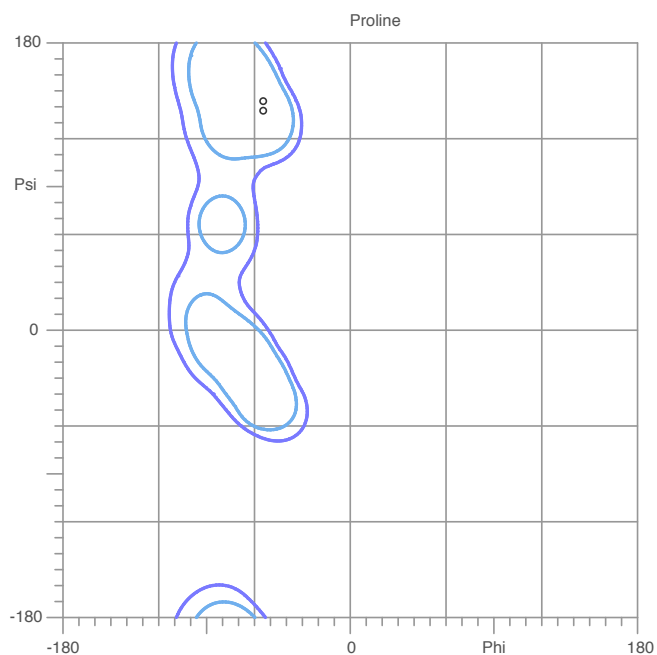
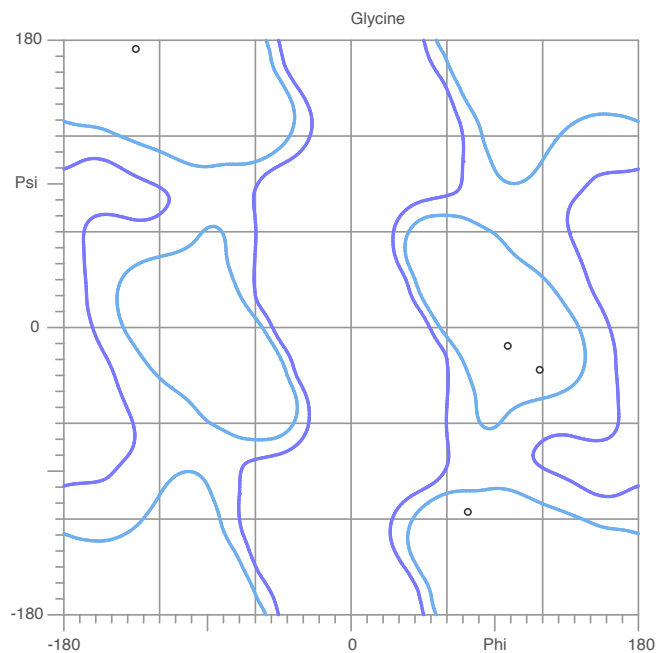
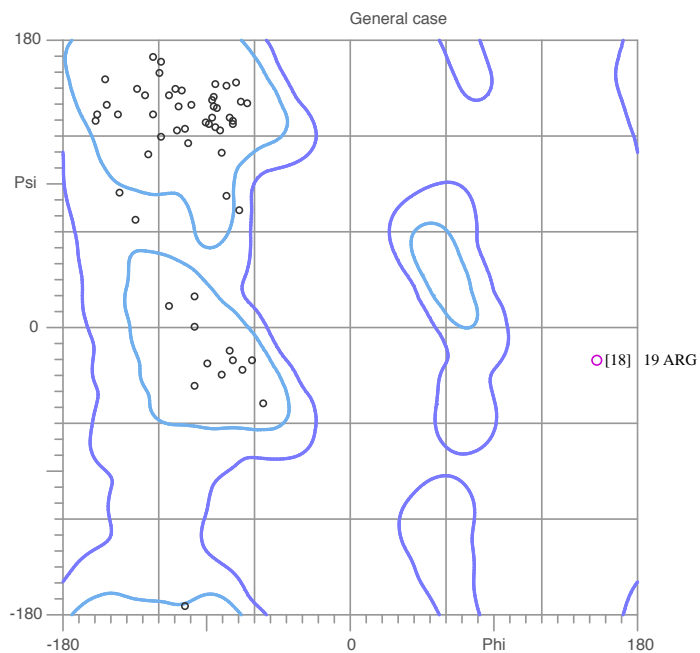
There were no outliers.

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

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

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 18



93.8% (60/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

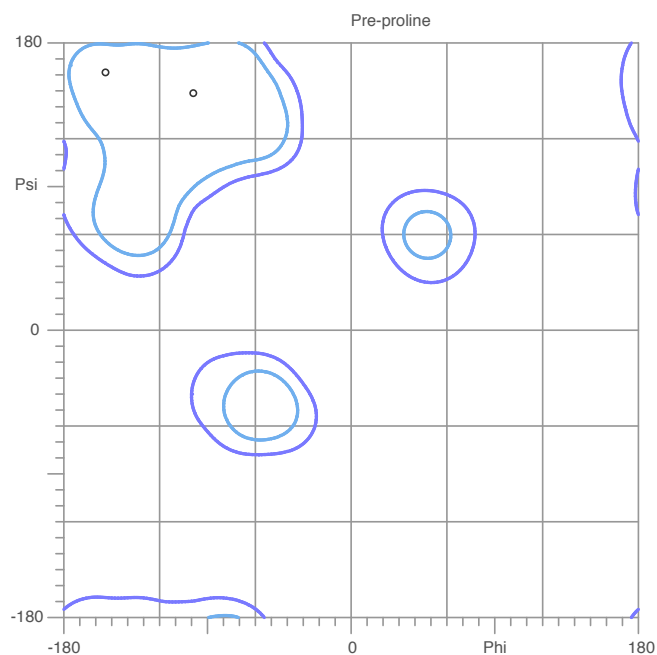
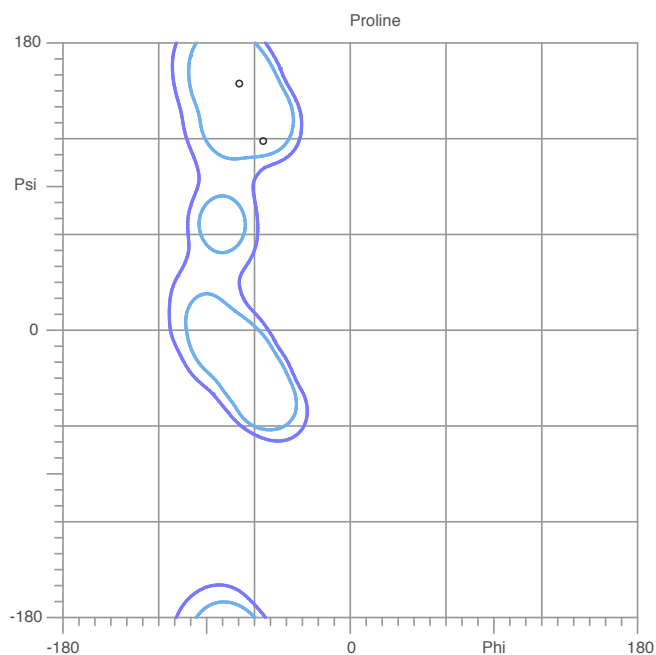
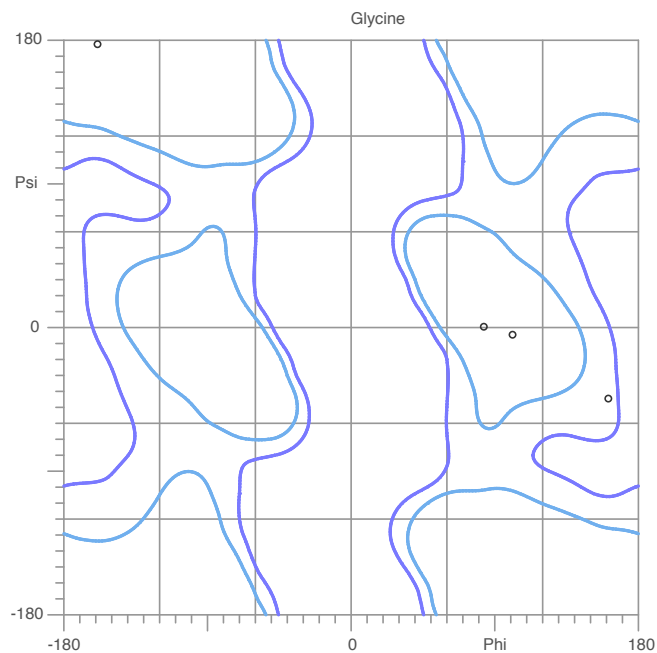
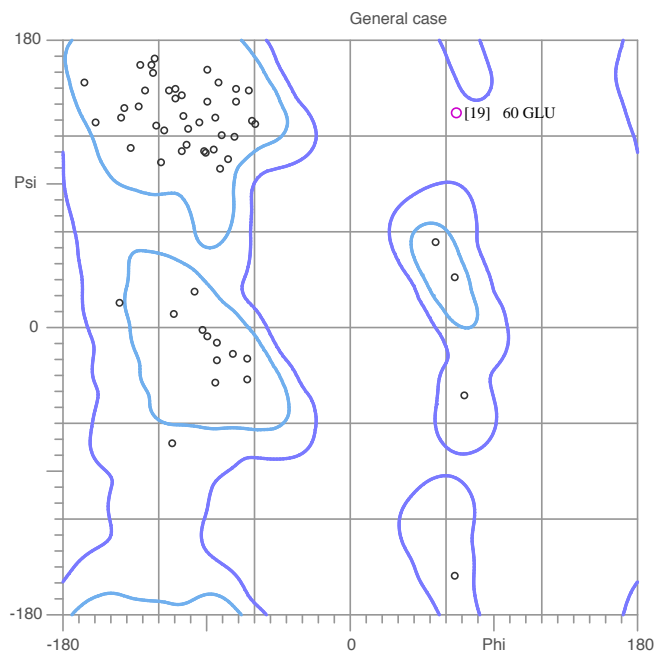
There were 1 outliers (phi, psi):
[18] 19 ARG (154.3, -20.6)

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

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

MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 19



90.6% (58/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

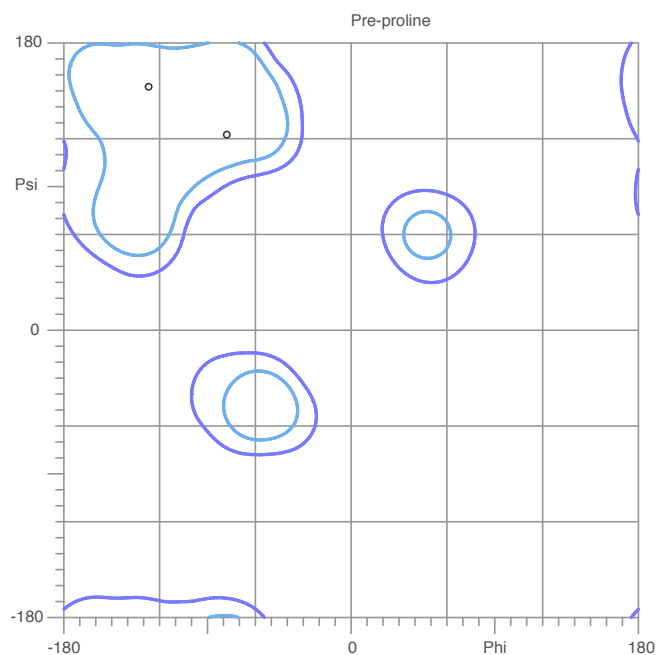
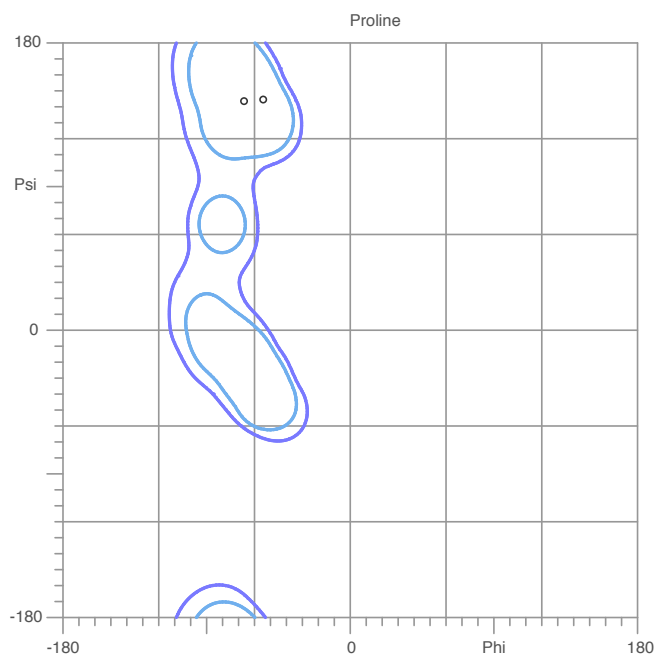
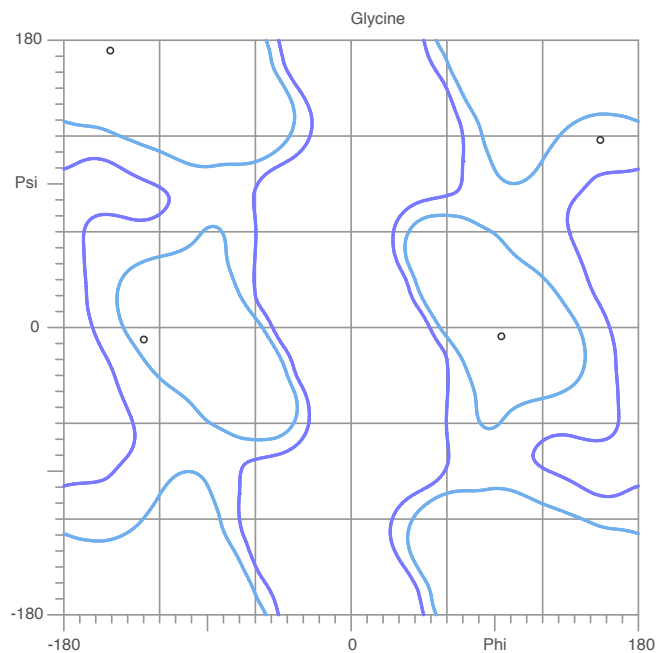
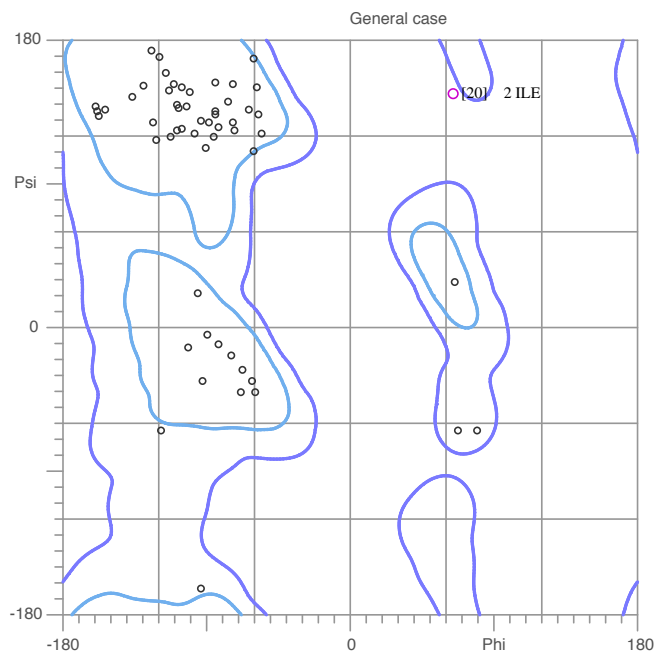
There were 1 outliers (phi, psi):
[19] 60 GLU (66.3, 135.0)

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MolProbity Ramachandran analysis

SGR42_R3Cons_em_bcr3.pdb, model 20



90.6% (58/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 2 ILE (65.0, 147.3)

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

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