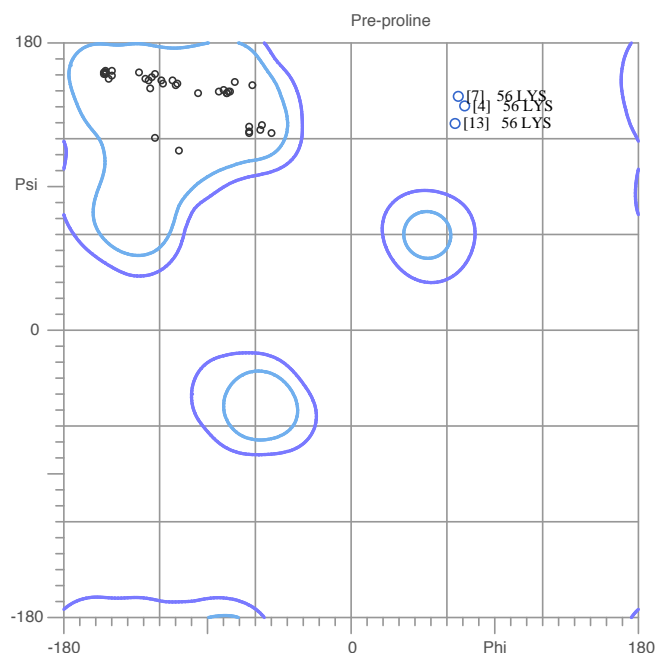
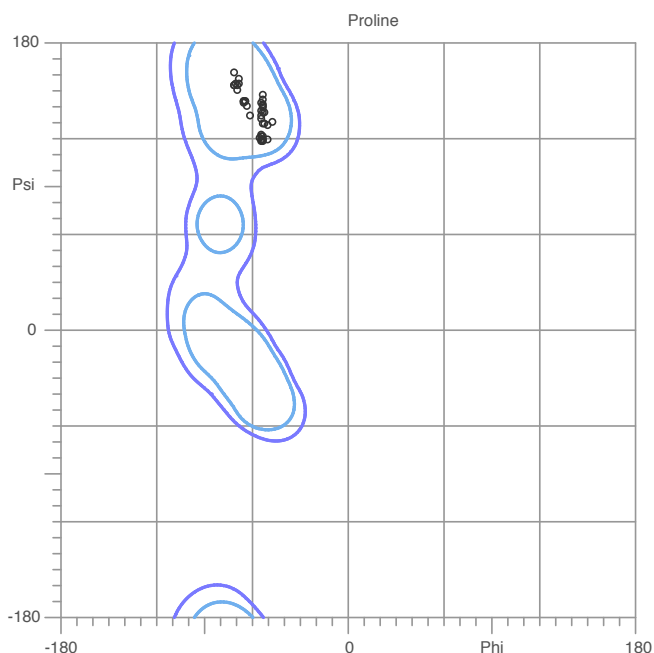
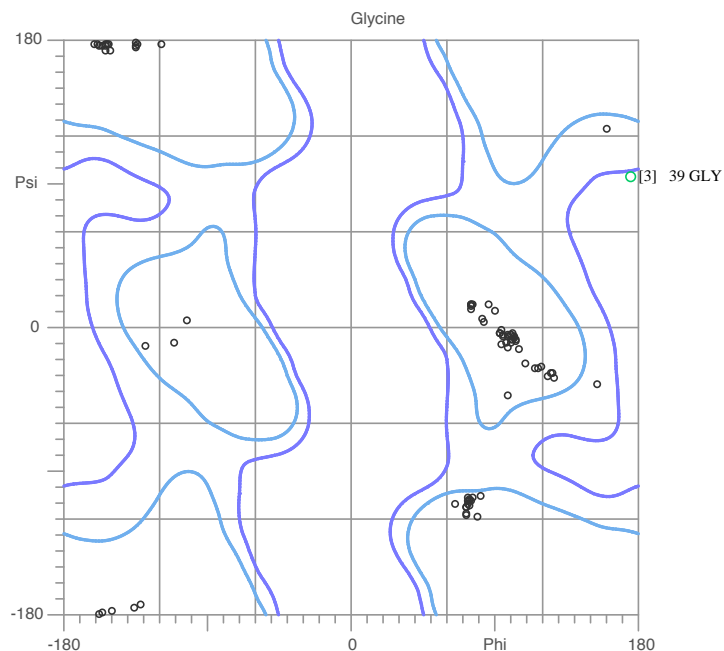
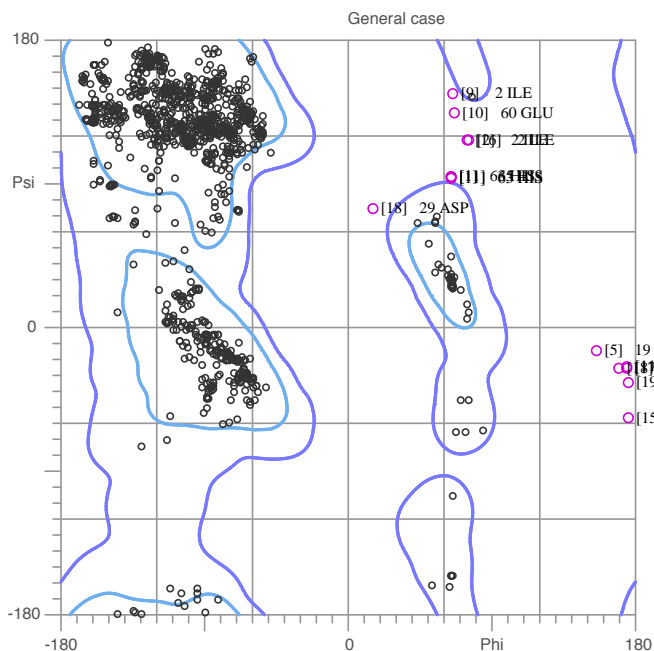


MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, all models



94.1% (1205/1280) of all residues were in favored (98%) regions.
98.6% (1262/1280) of all residues were in allowed (>99.8%) regions.

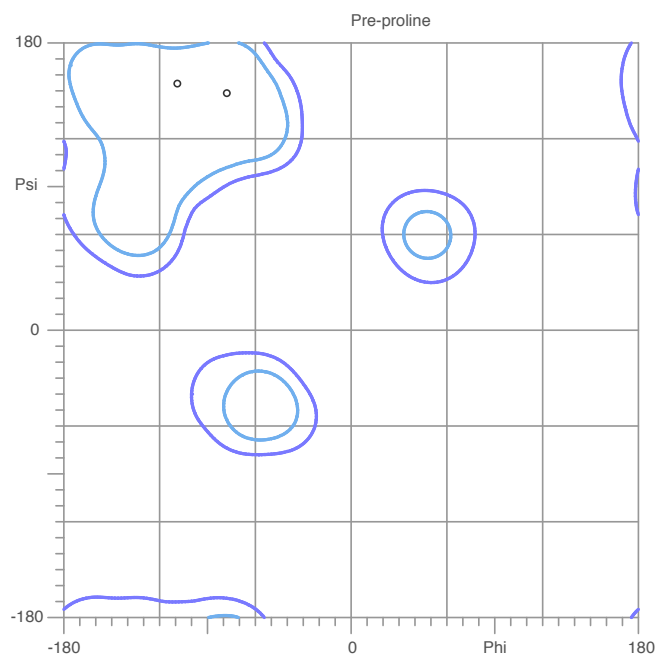
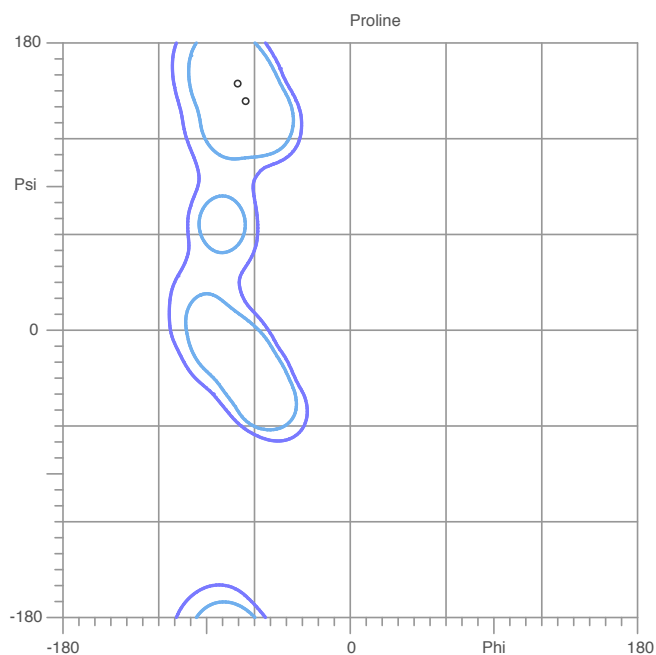
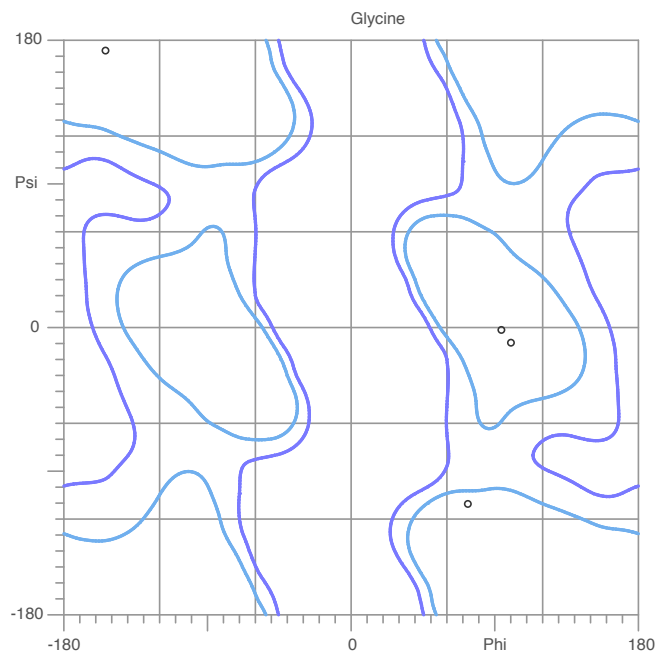
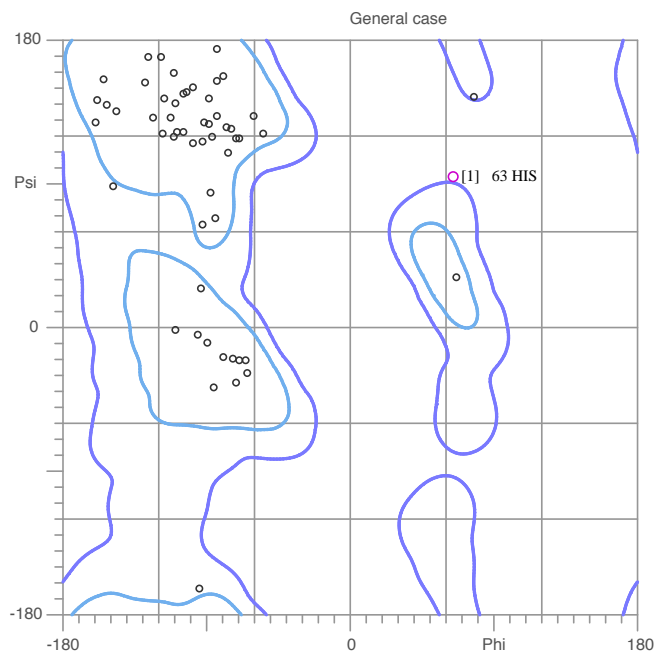
There were 18 outliers (phi, psi):

- [1] 63 HIS (65.0, 95.0)
- [2] 2 ILE (75.0, 118.8)
- [3] 39 GLY (175.0, 95.0)
- [4] 56 LYS (71.3, 141.0)
- [5] 19 ARG (155.4, -14.6)
- [7] 56 LYS (67.3, 147.7)
- [9] 2 ILE (65.0, 147.4)

- [10] 60 GLU (66.2, 135.0)
- [11] 19 ARG (174.9, -24.2)
- [11] 63 HIS (65.0, 95.0)
- [11] 65 HIS (65.0, 95.0)
- [13] 56 LYS (65.1, 130.2)
- [15] 40 ASN (175.1, -57.0)
- [16] 2 ILE (74.9, 118.9)
- [17] 19 ARG (174.9, -25.5)
- [18] 19 ARG (169.8, -25.6)
- [18] 29 ASP (15.1, 75.8)
- [19] 19 ARG (175.0, -35.0)

MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 1

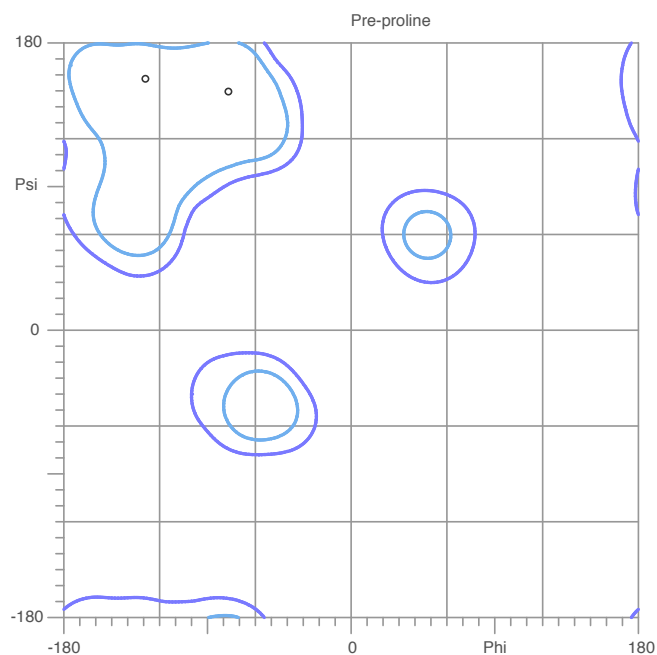
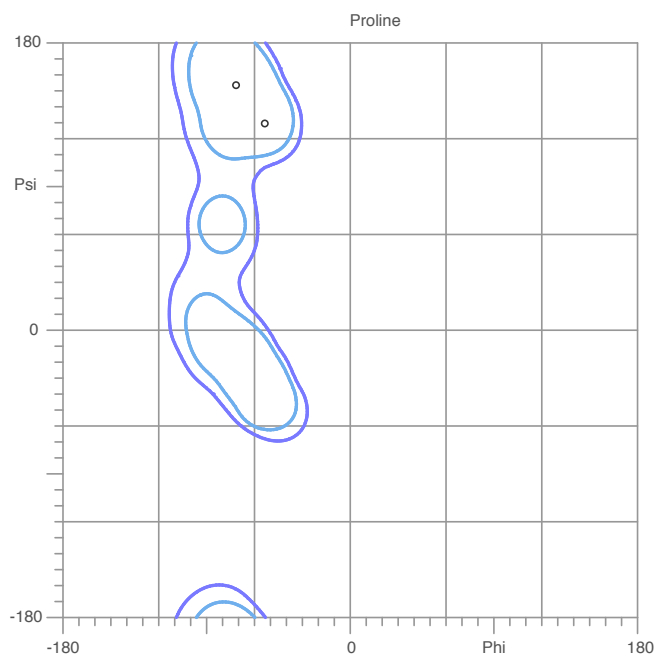
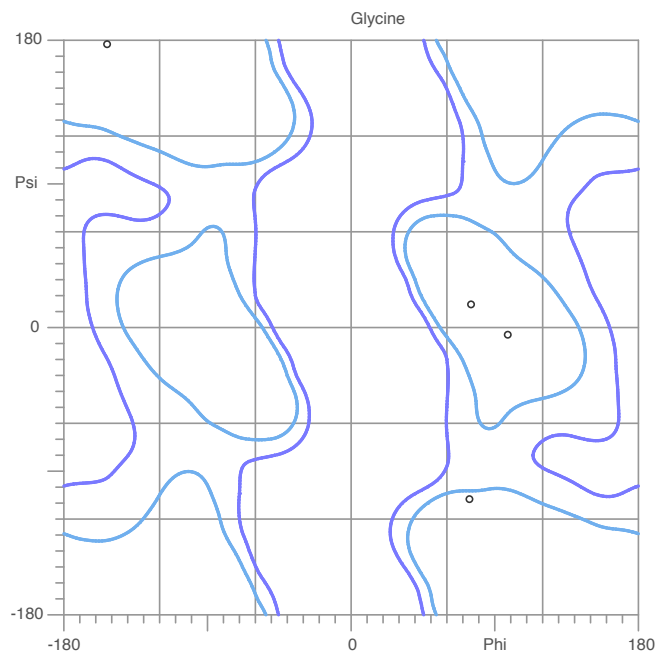
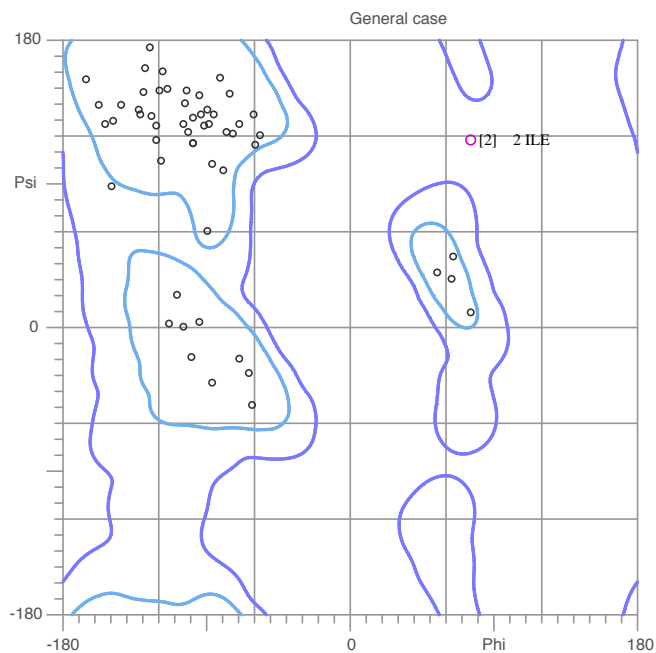


93.8% (60/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[1] 63 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 2



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.

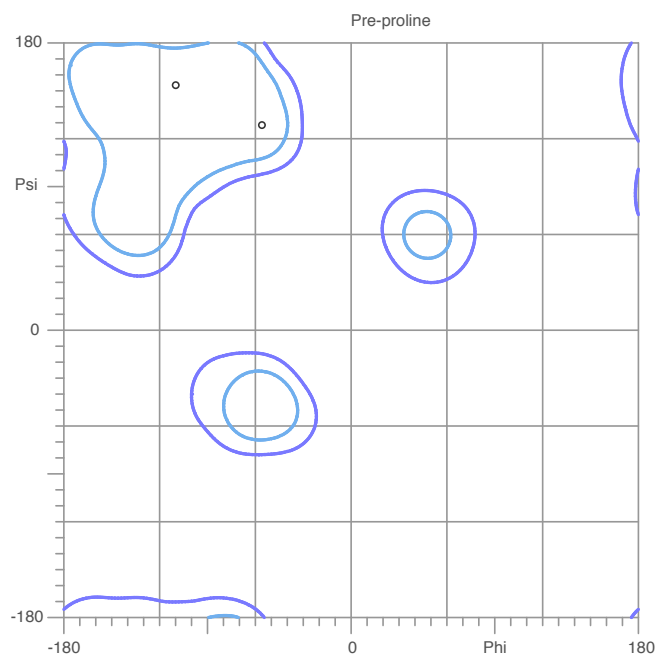
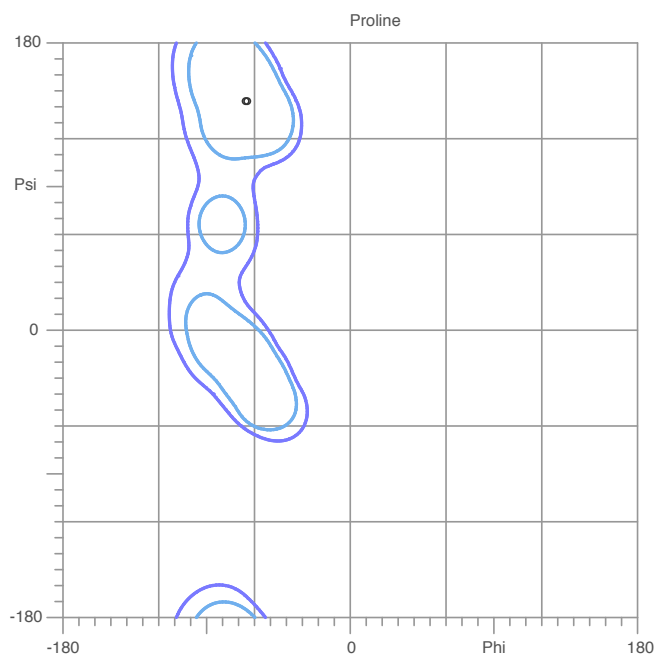
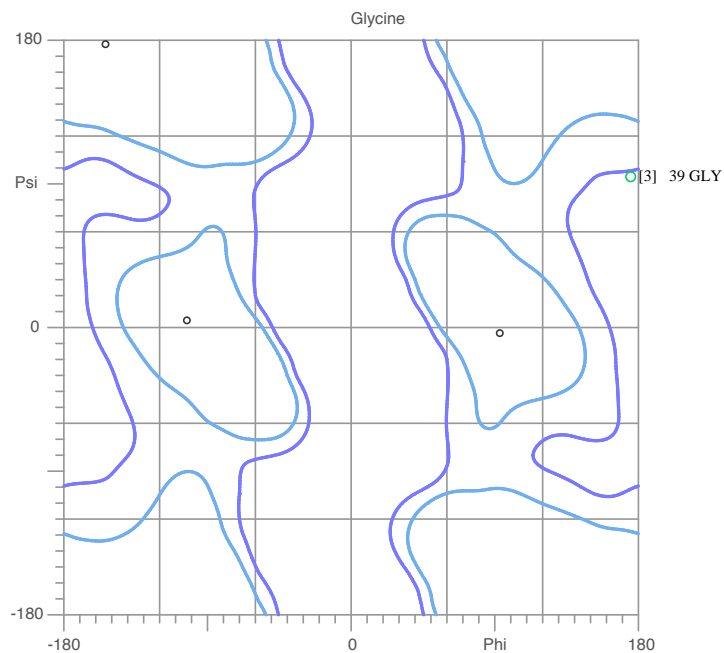
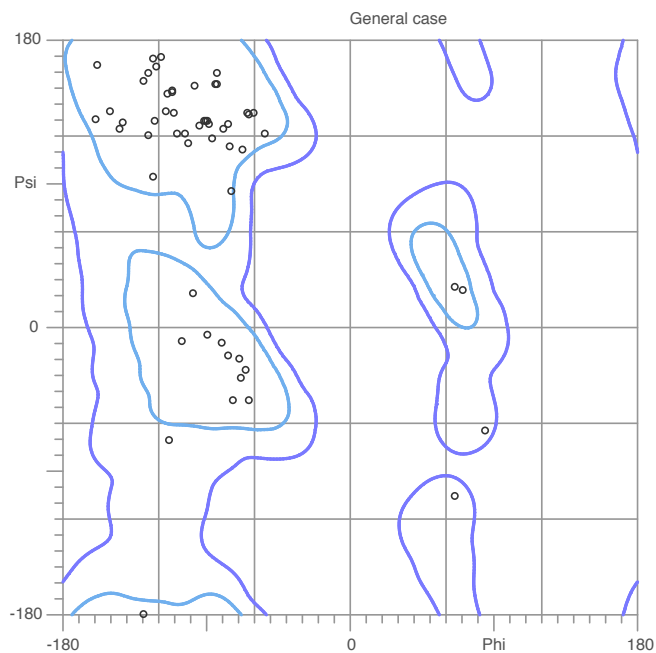
There were 1 outliers (phi, psi):
[2] 2 ILE (75.0, 118.8)

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 3

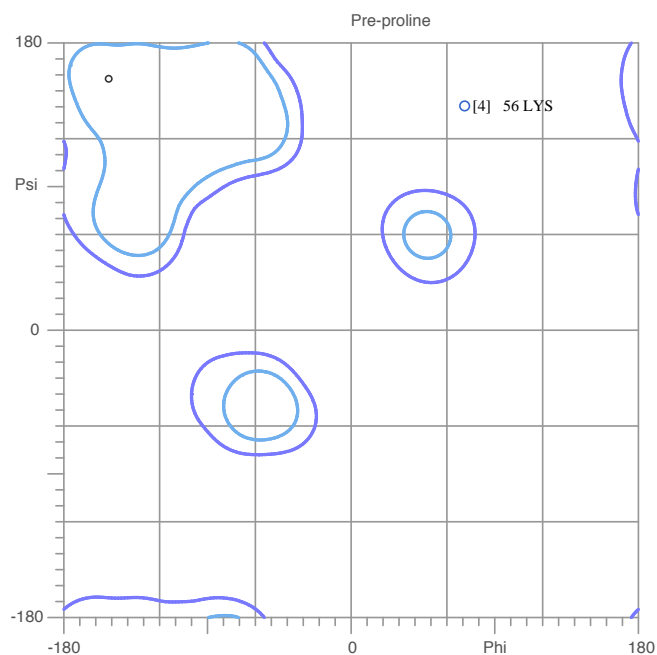
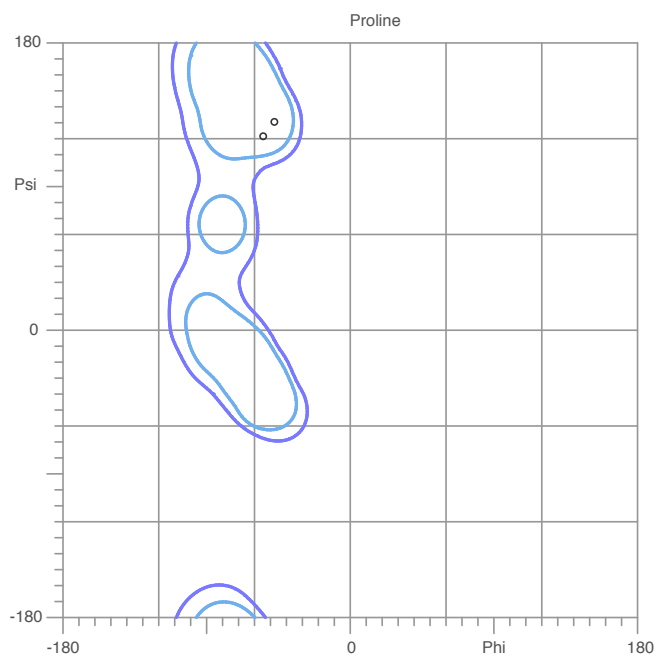
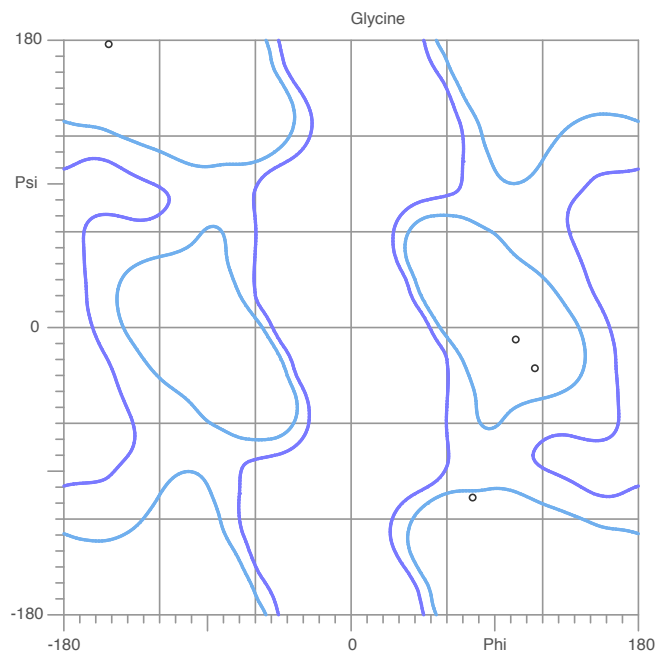
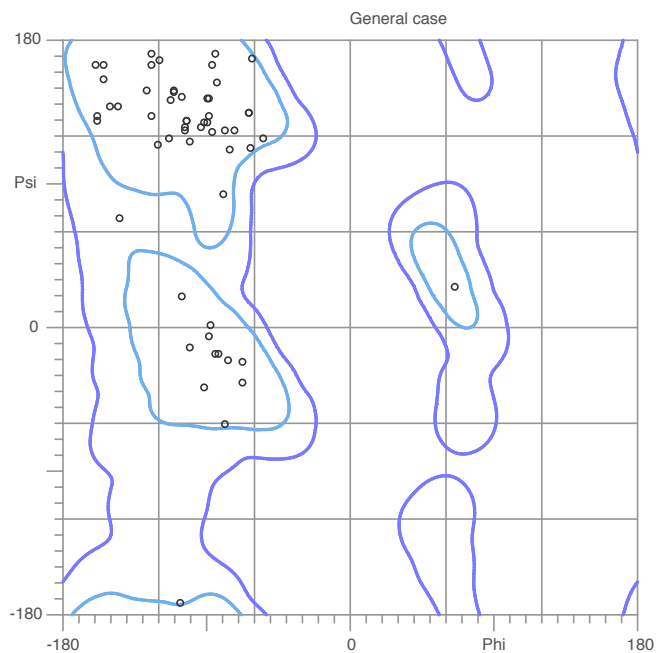


93.8% (60/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 39 GLY (175.0, 95.0)

MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 4



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.

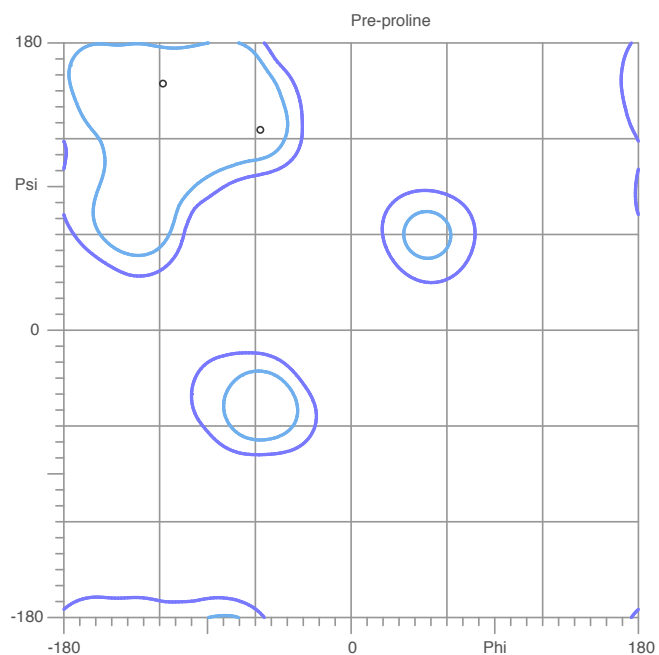
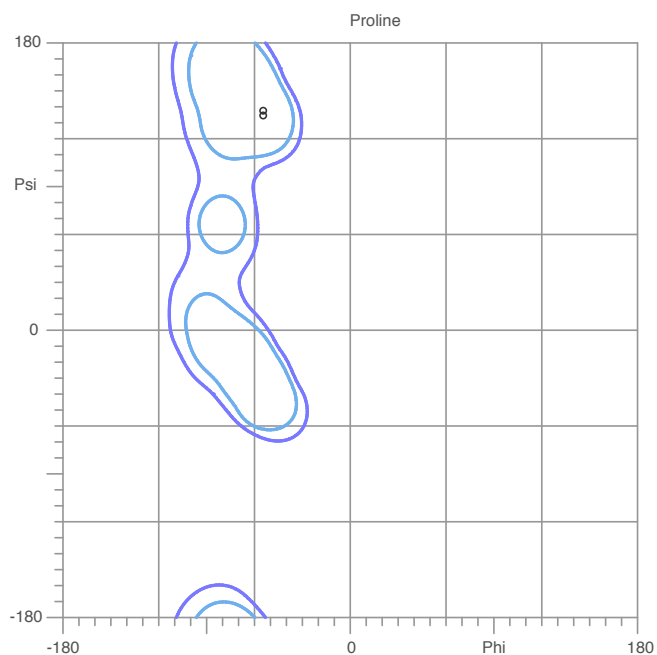
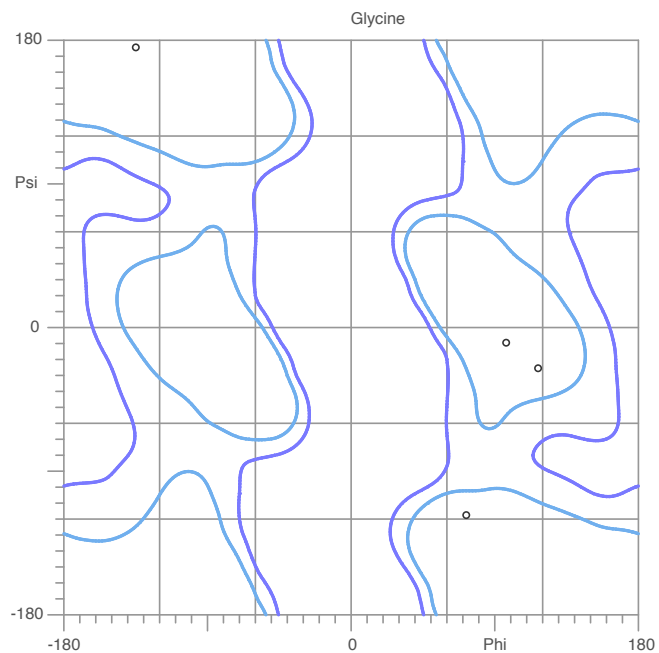
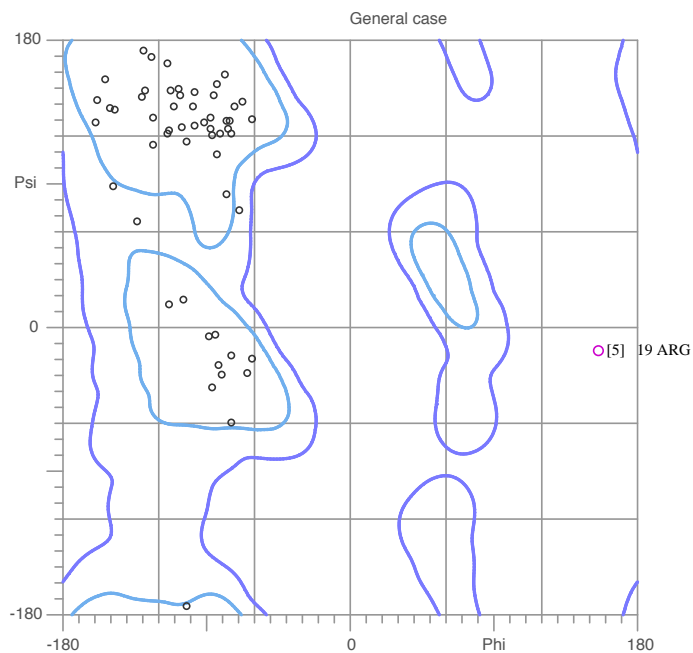
There were 1 outliers (phi, psi):
[4] 56 LYS (71.3, 141.0)

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 5



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.

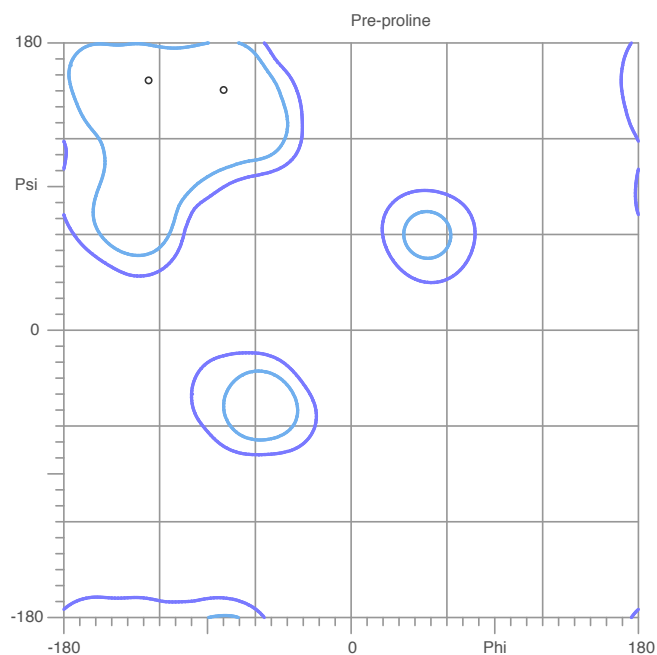
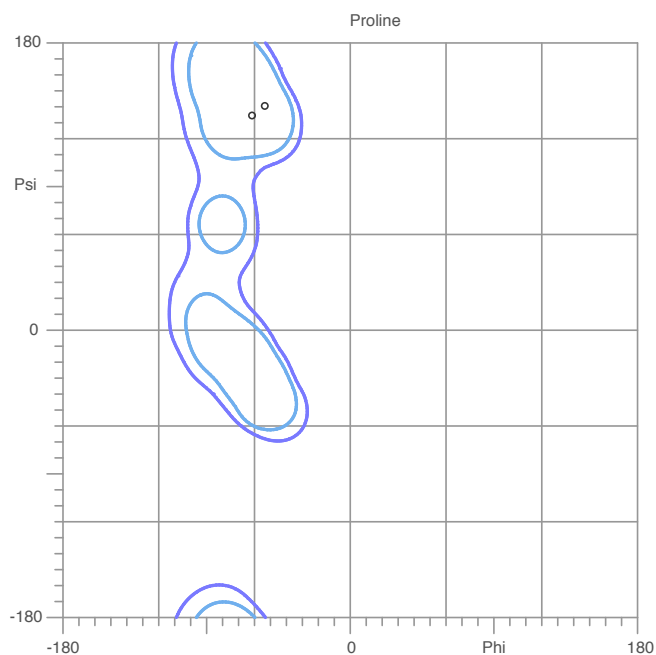
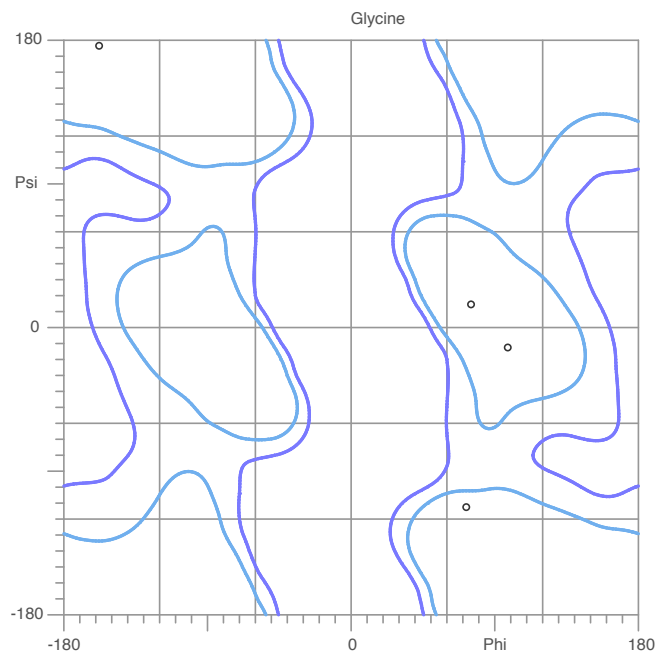
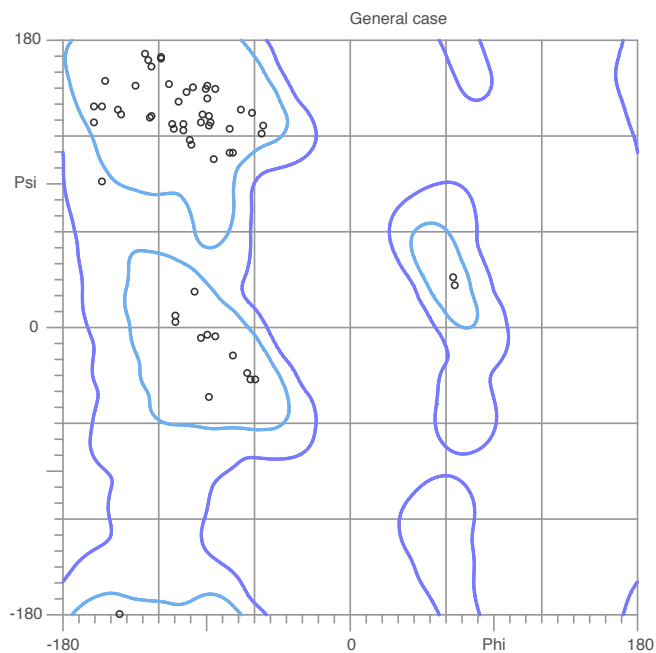
There were 1 outliers (phi, psi):
[5] 19 ARG (155.4, -14.6)

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 6



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.

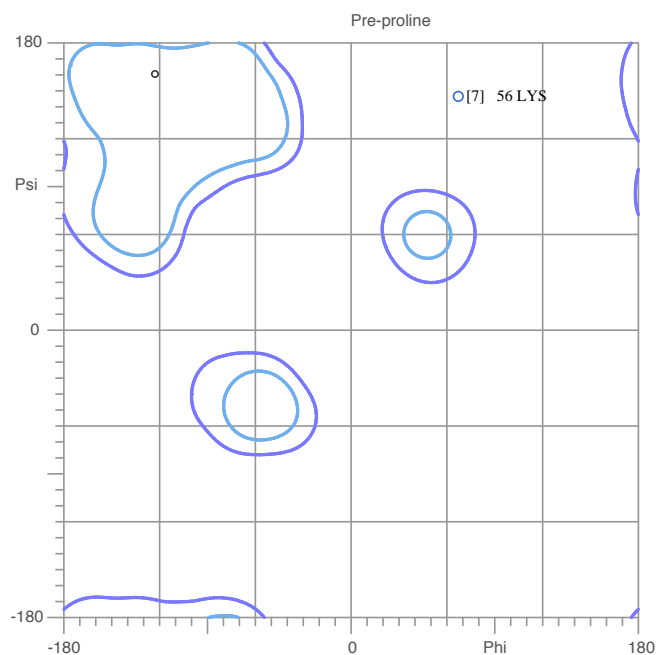
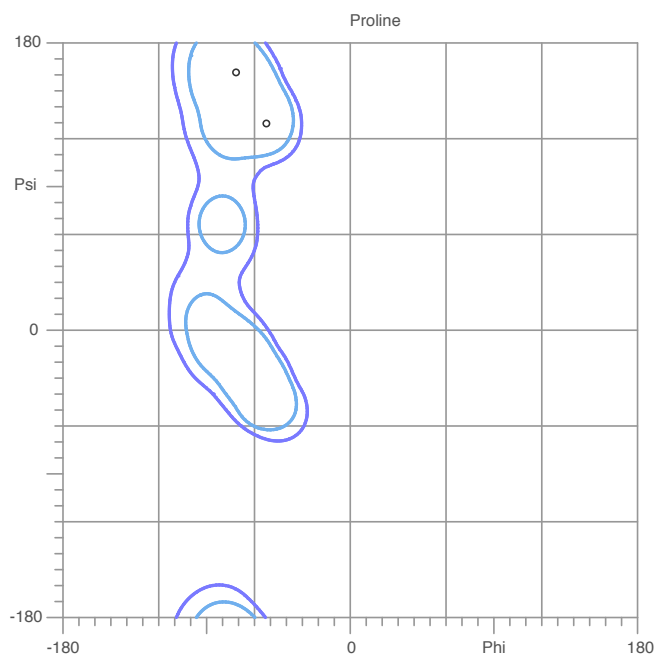
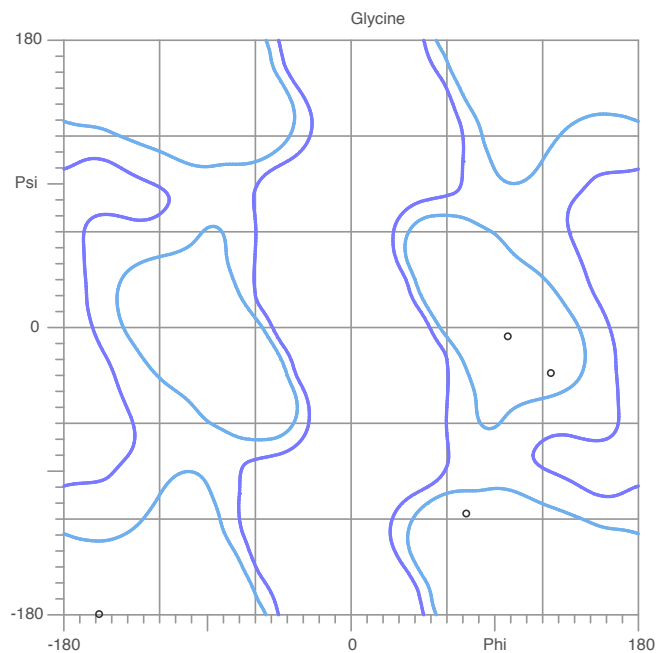
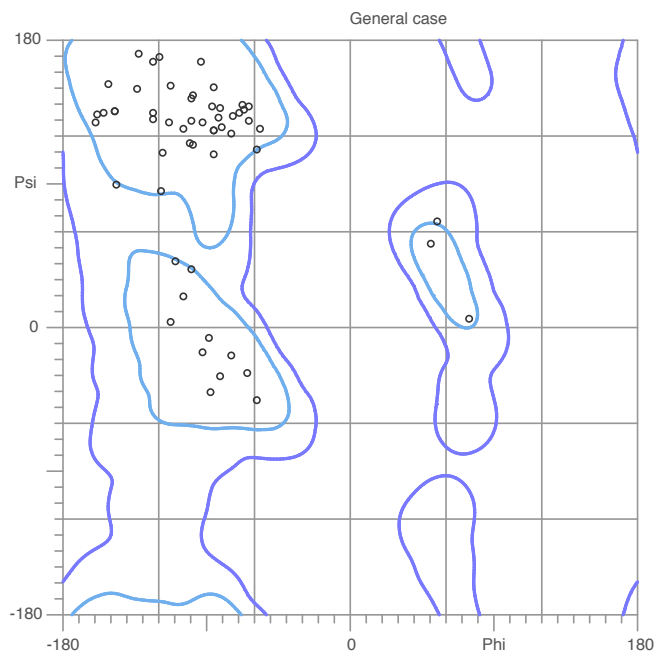
There were no outliers.

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 7



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.

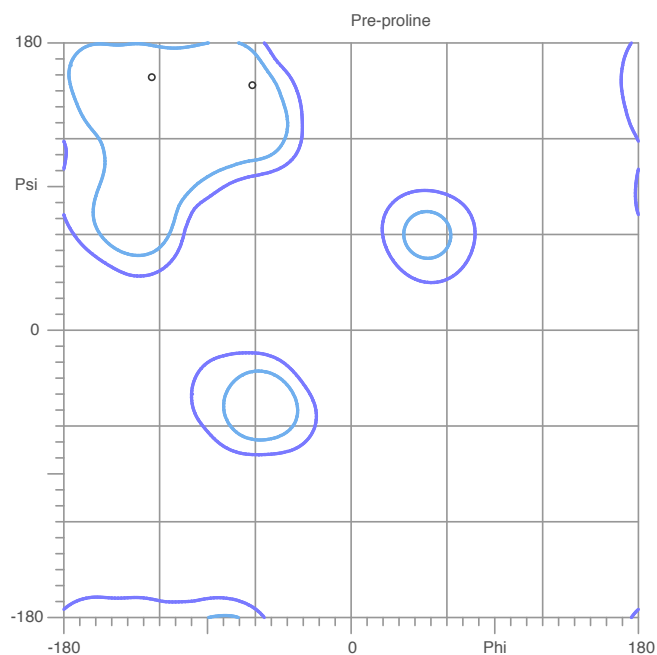
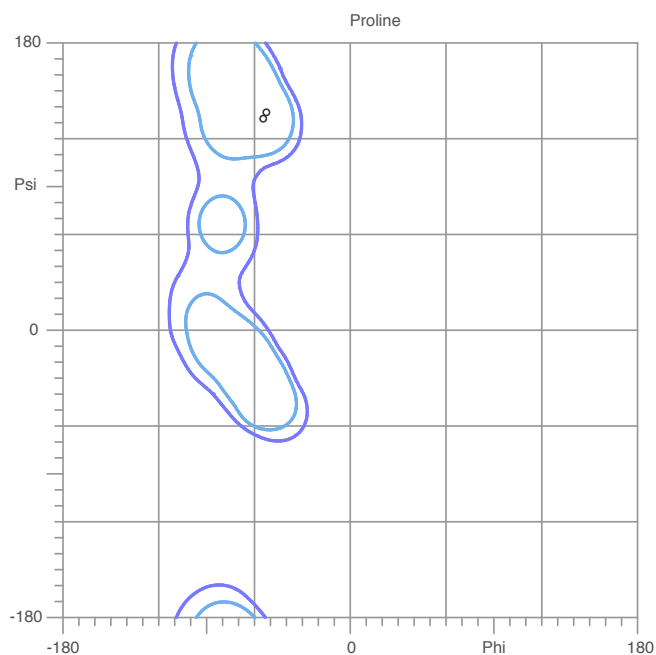
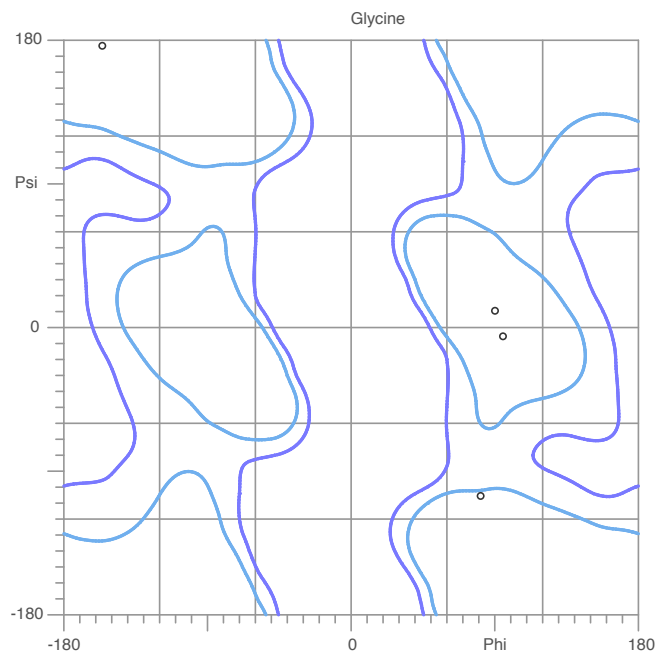
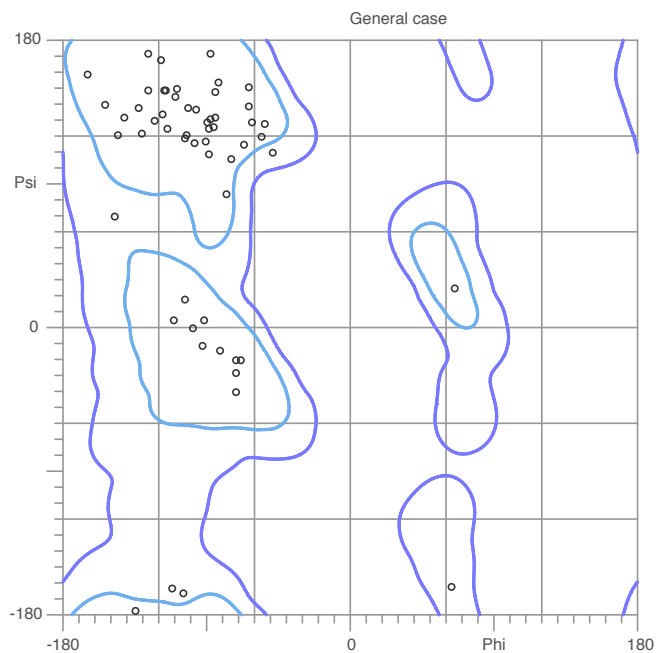
There were 1 outliers (phi, psi):
[7] 56 LYS (67.3, 147.7)

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 8



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.

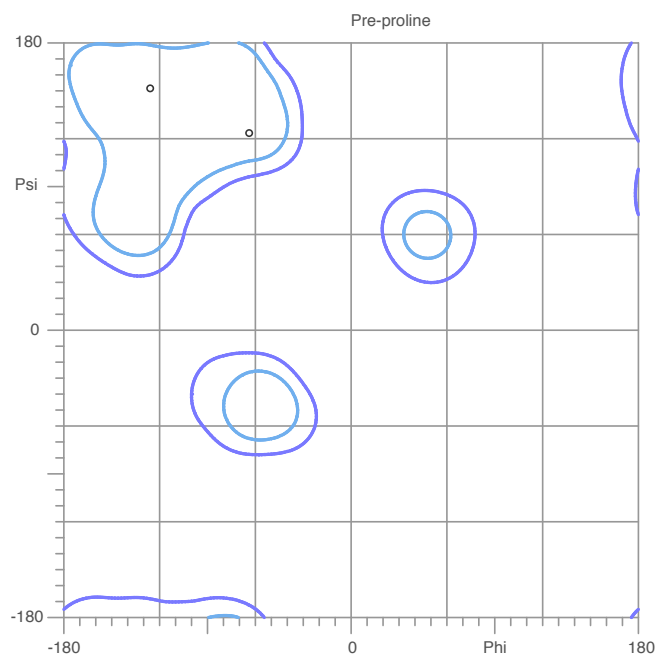
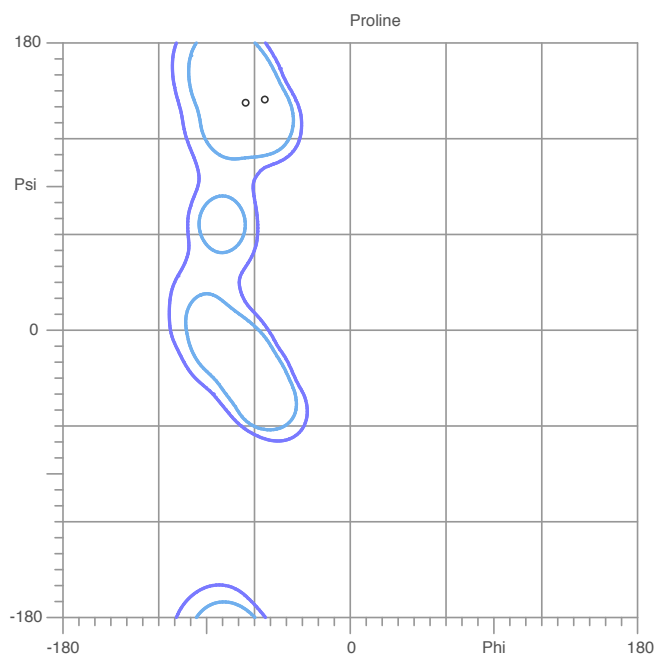
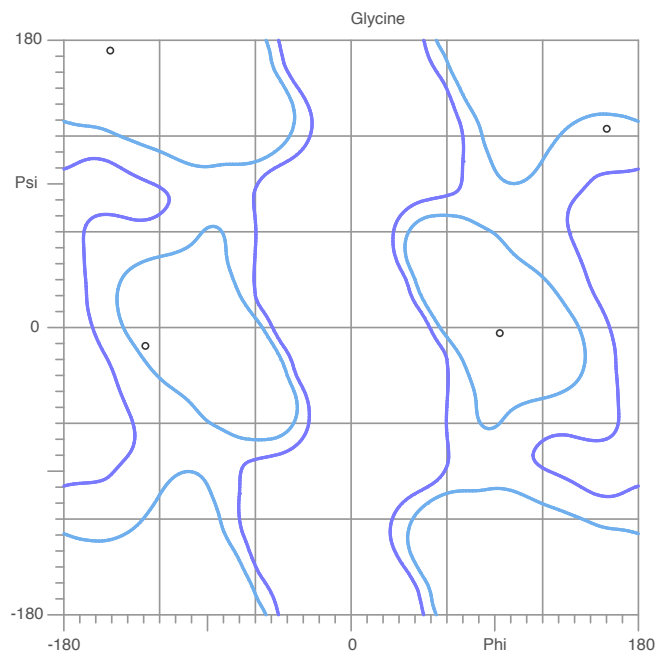
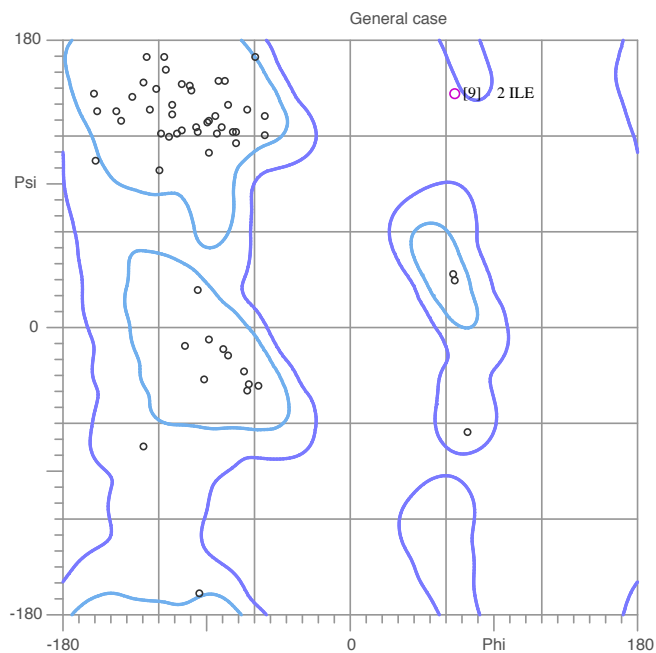
There were no outliers.

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 9

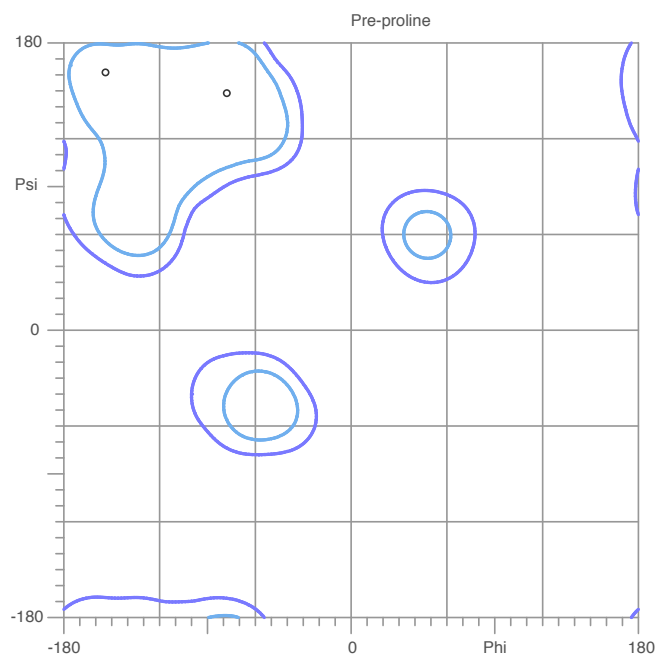
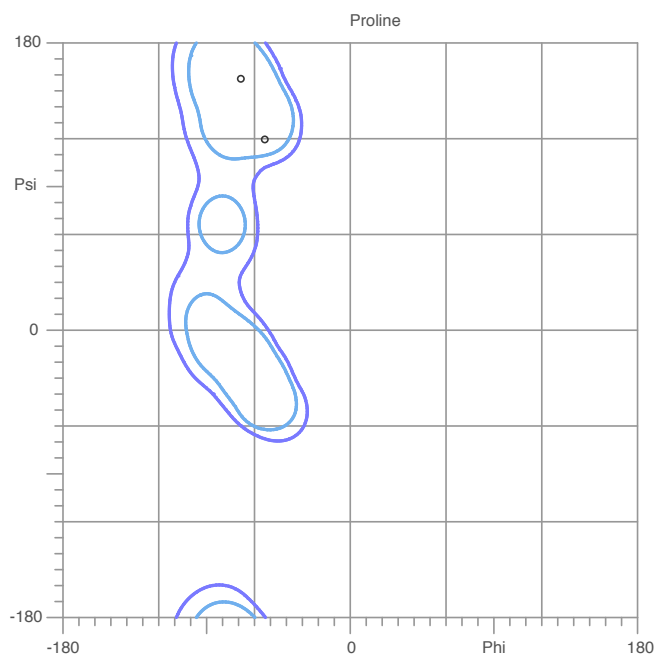
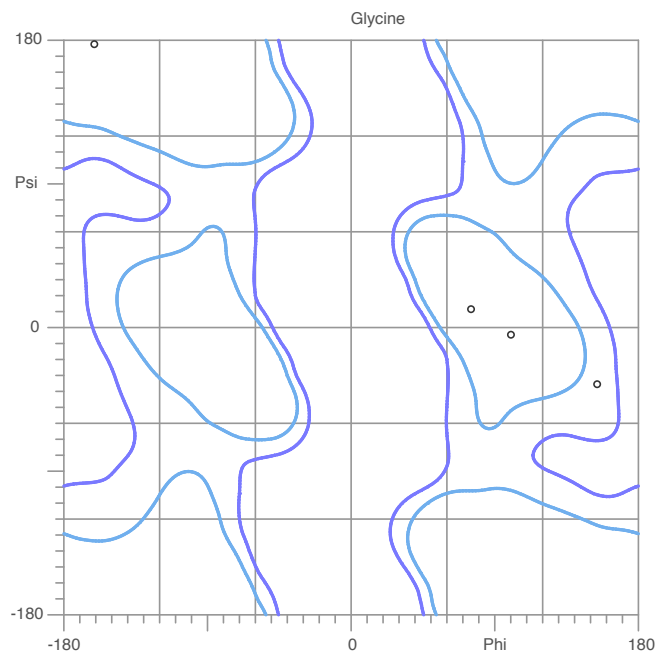
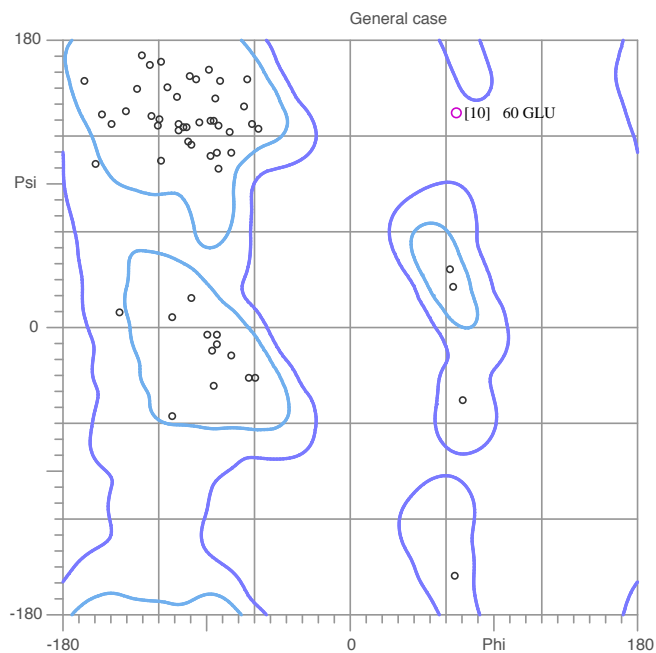


90.6% (58/64) of all residues were in favored (98%) regions.
98.4% (63/64) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 2 ILE (65.0, 147.4)

MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 10



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.

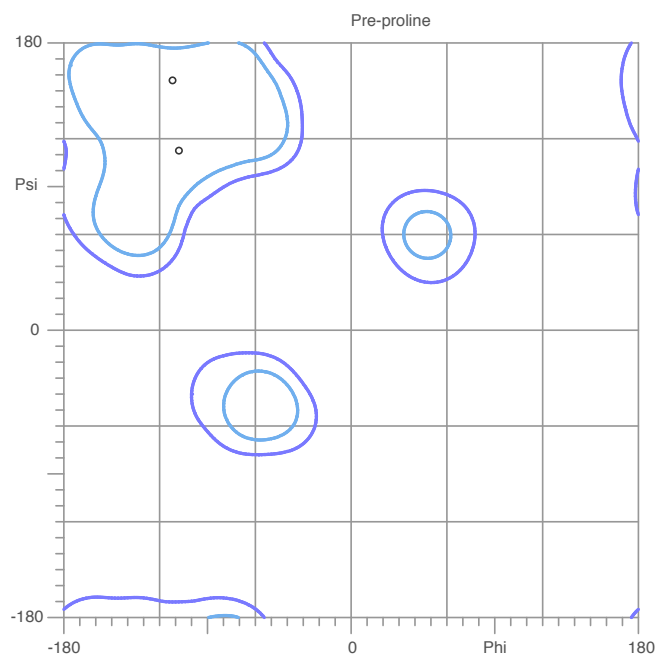
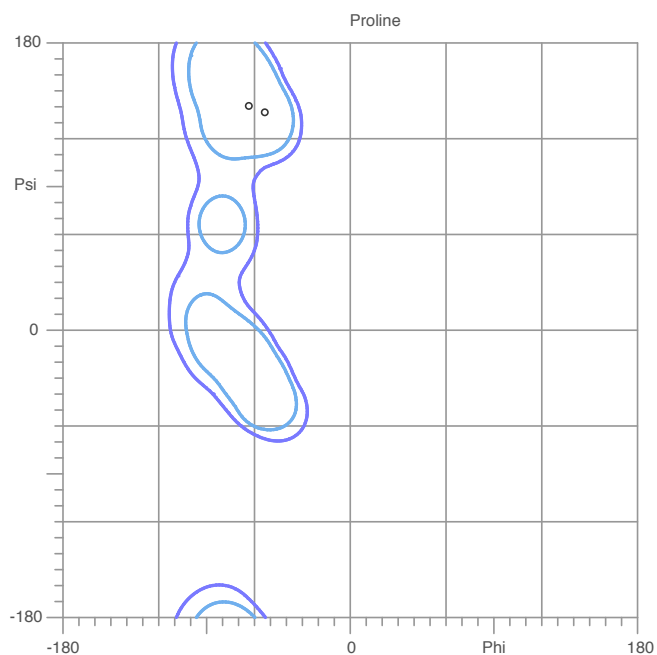
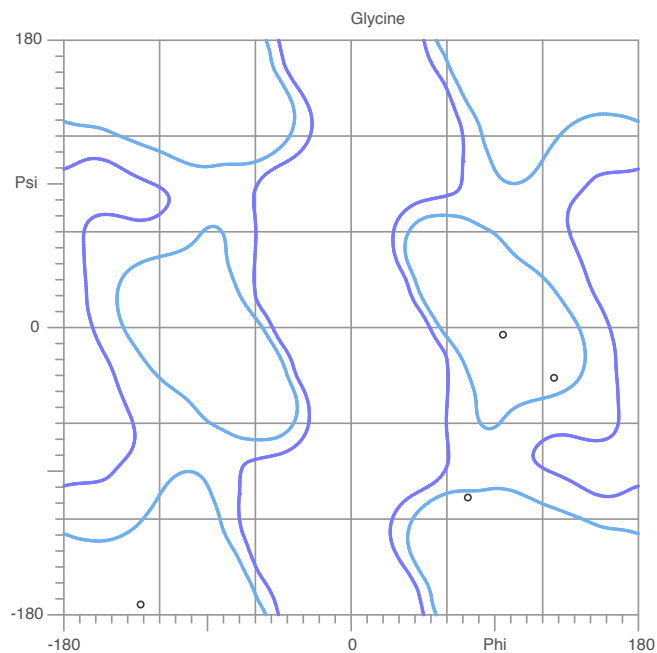
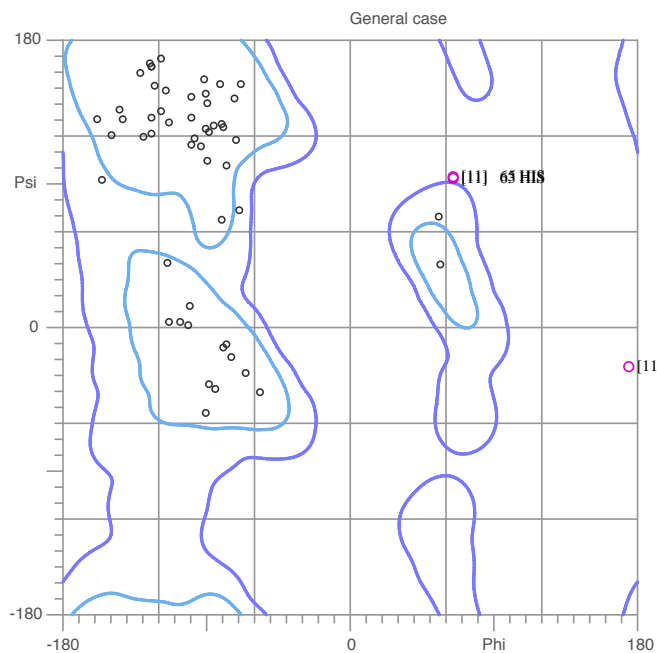
There were 1 outliers (phi, psi):
[10] 60 GLU (66.2, 135.0)

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 11



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):

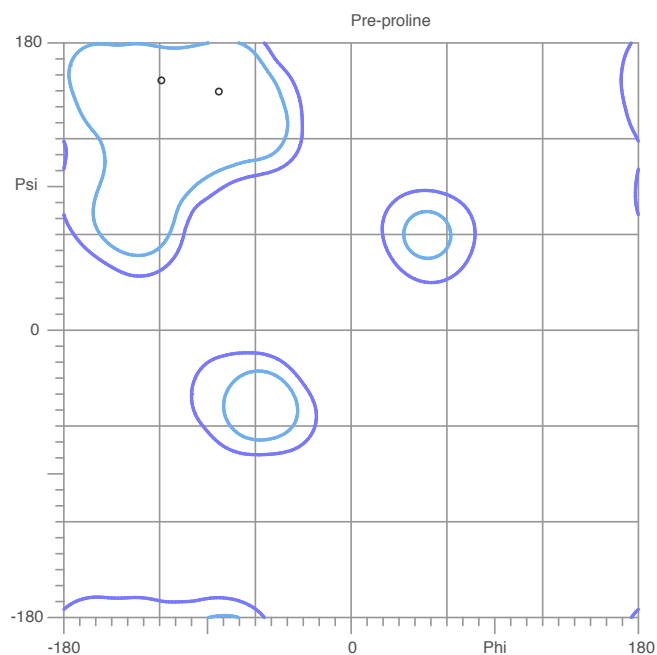
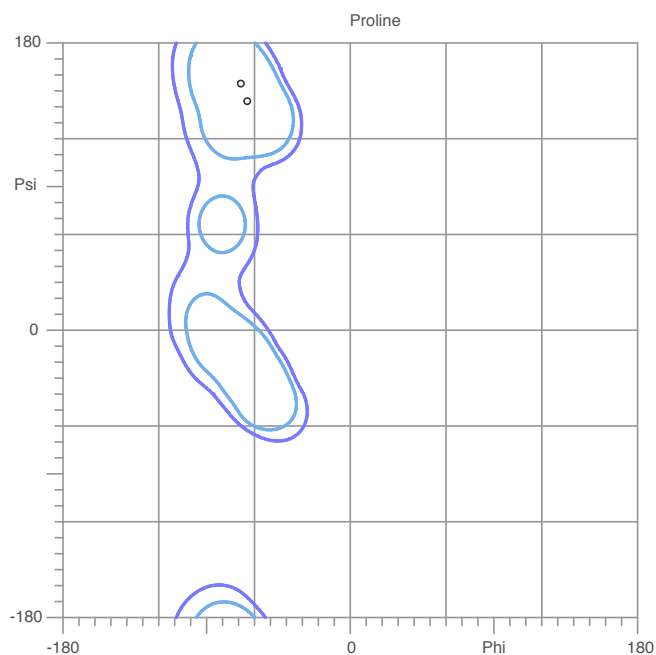
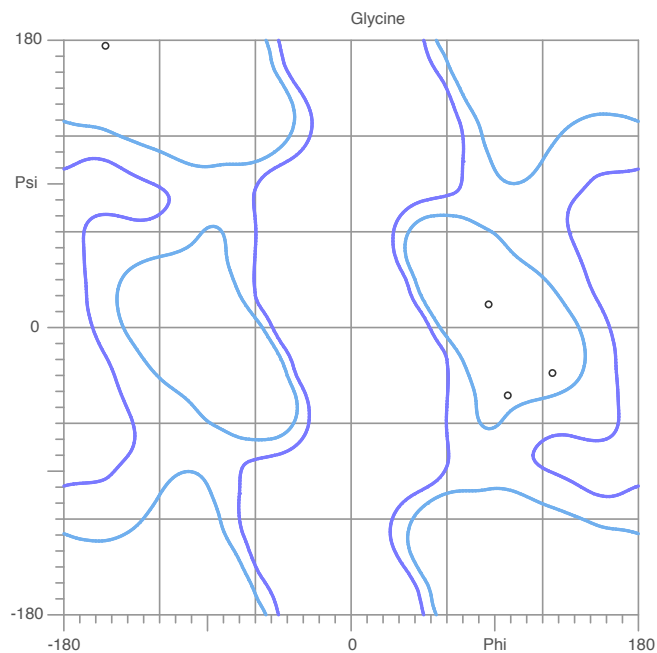
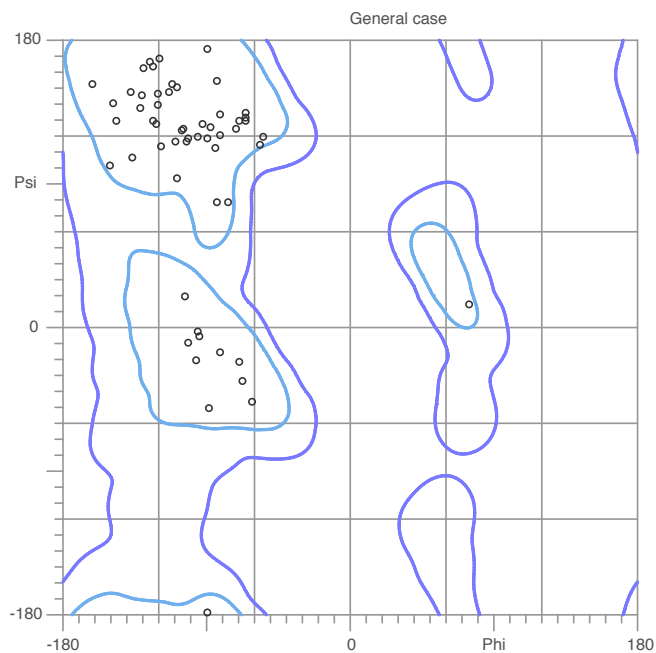
[11] 19 ARG (174.9, -24.2)

[11] 63 HIS (65.0, 95.0)

[11] 65 HIS (65.0, 95.0)

MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 12



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

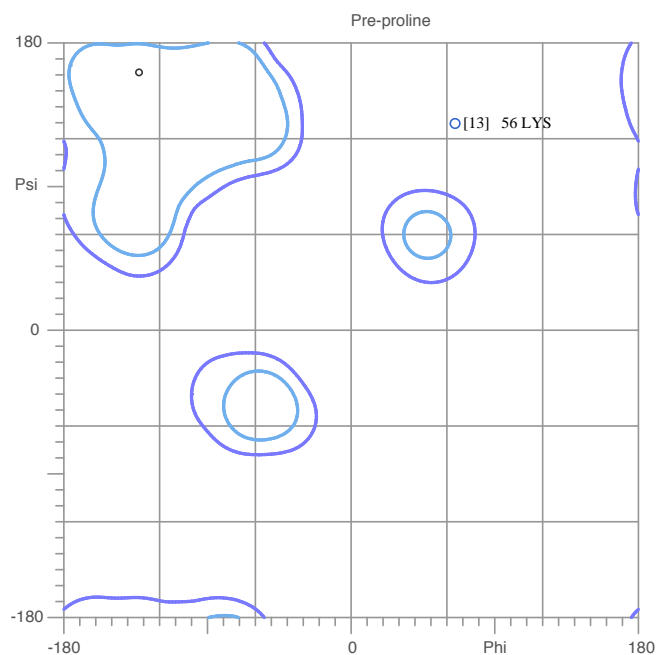
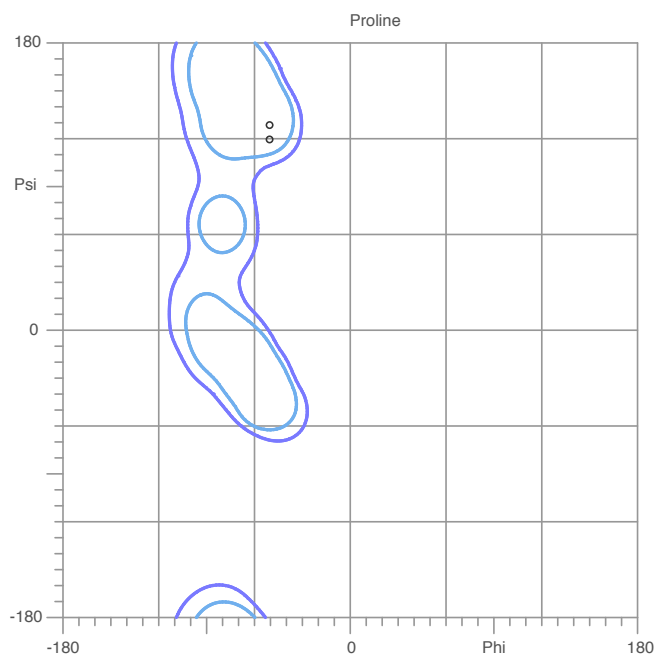
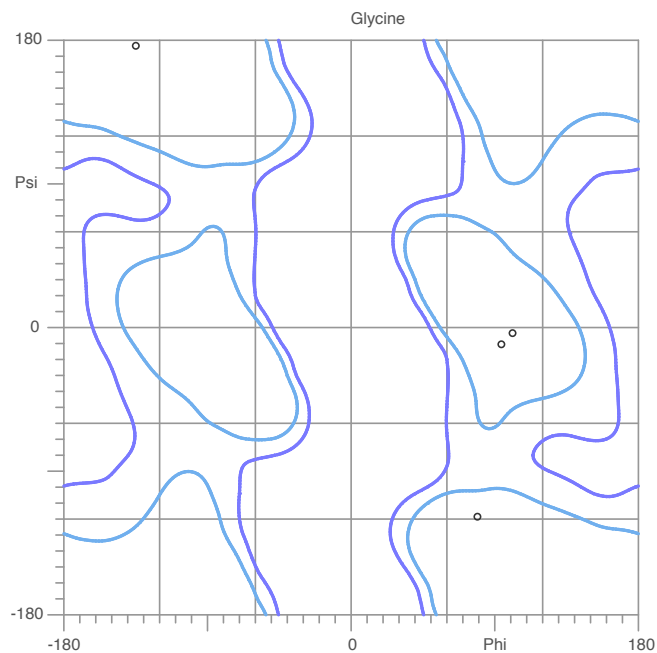
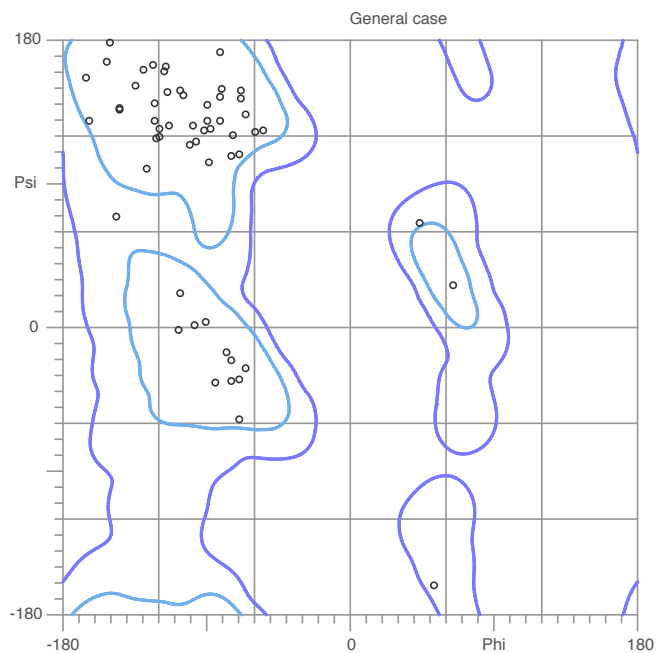
There were no outliers.

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 13



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.

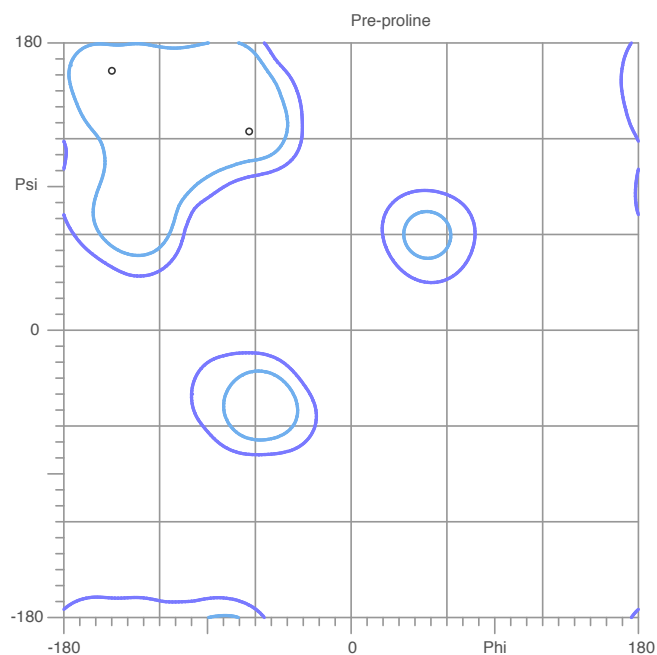
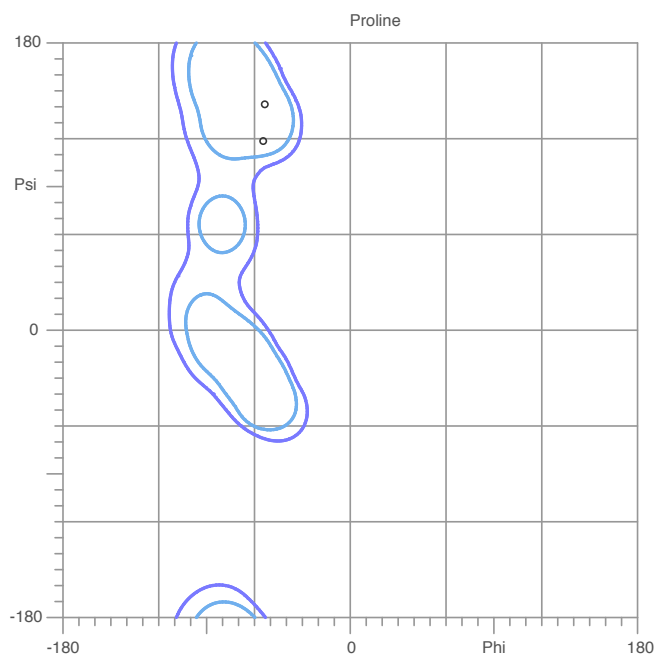
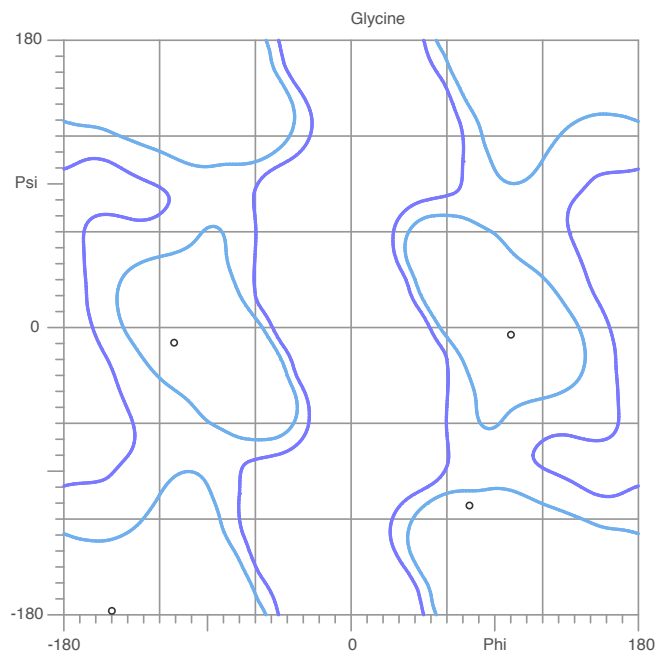
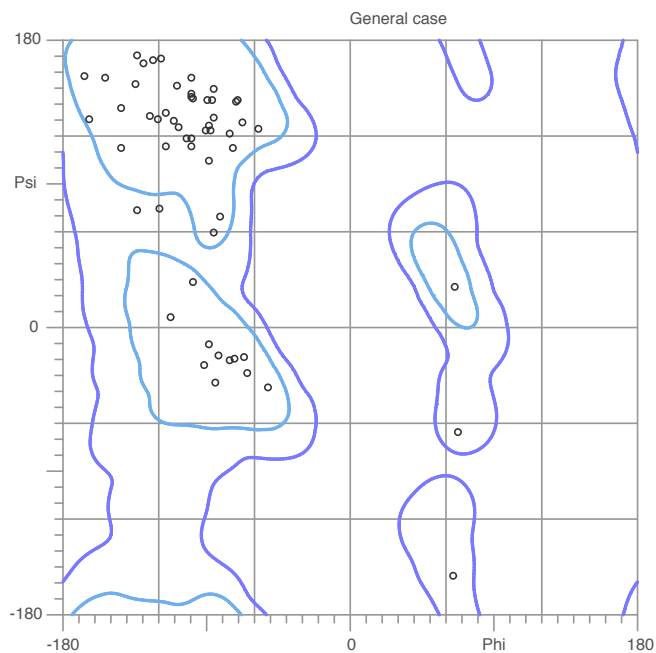
There were 1 outliers (phi, psi):
[13] 56 LYS (65.1, 130.2)

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 14



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.

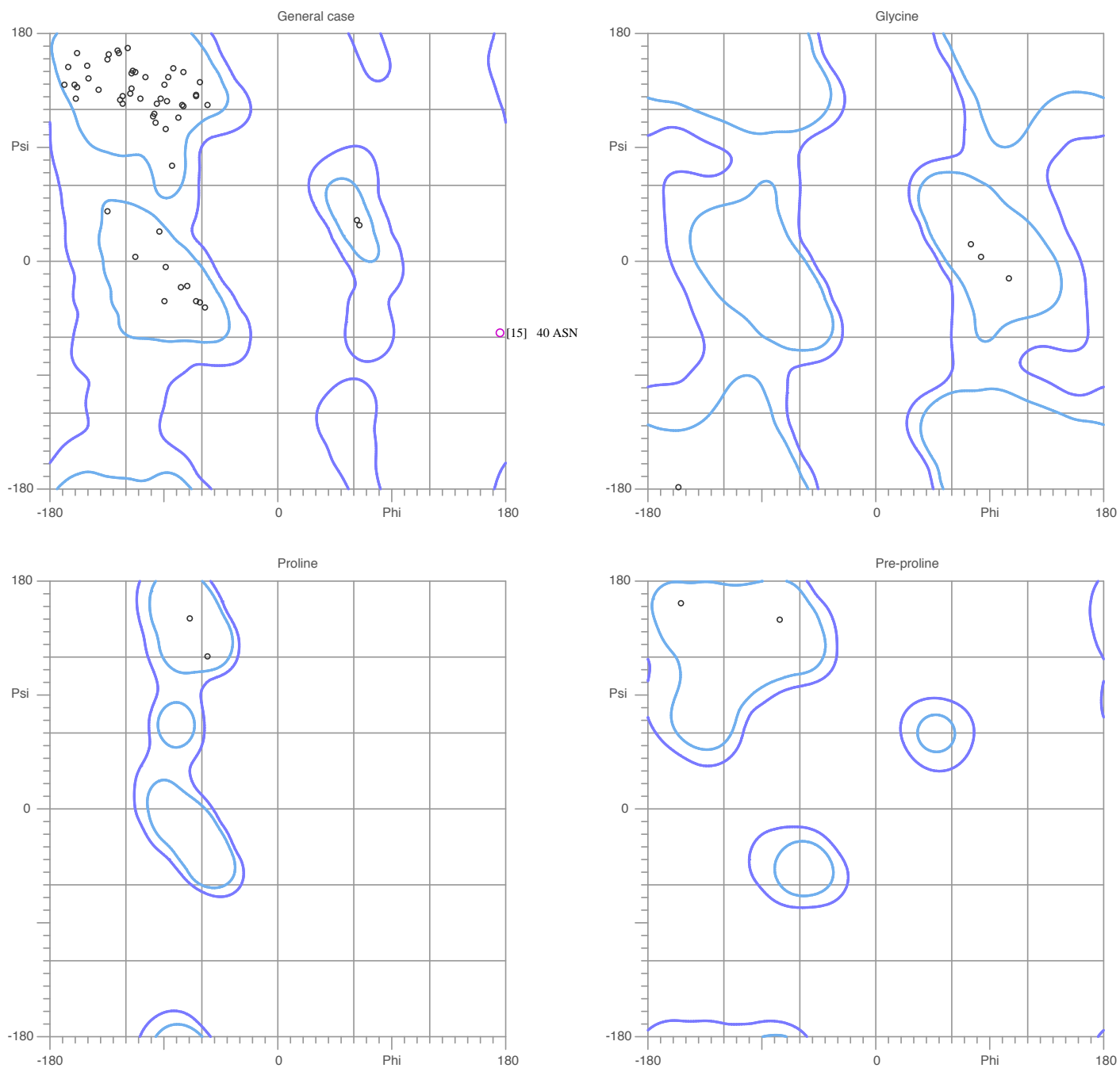
There were no outliers.

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

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 15



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.

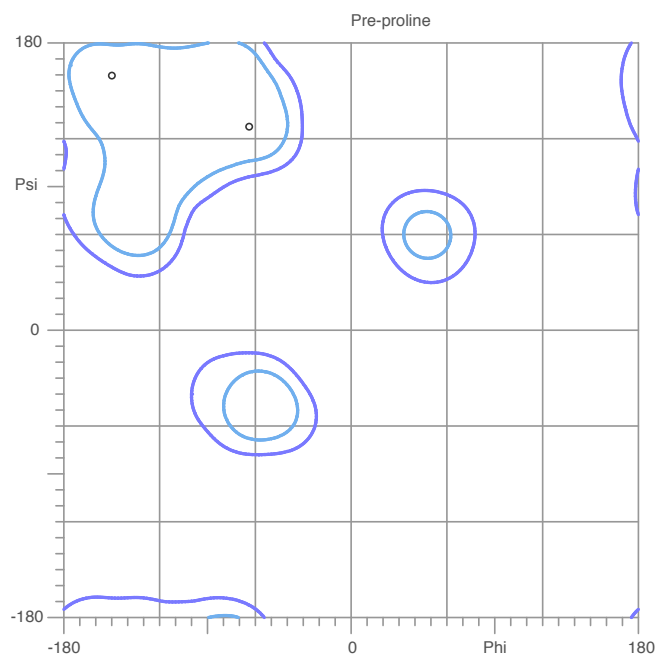
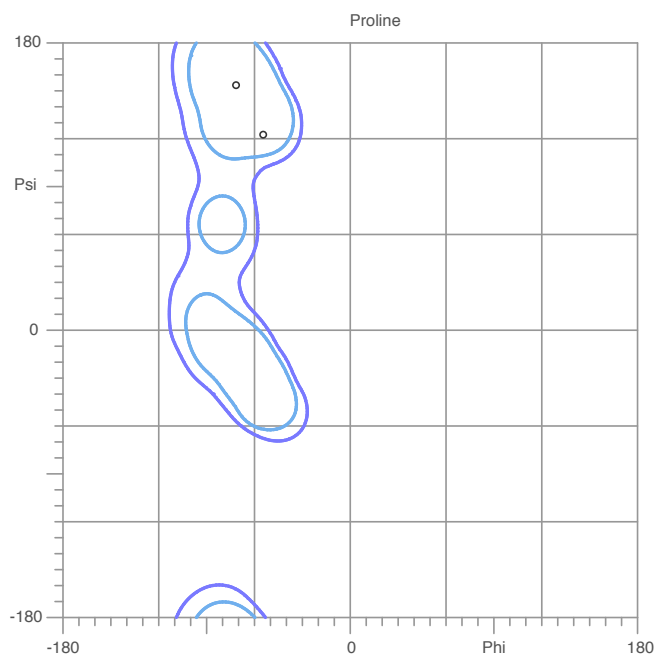
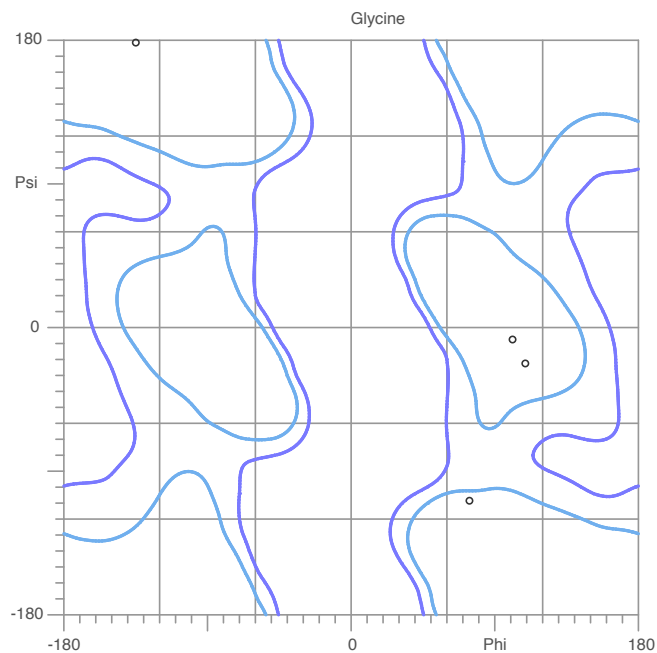
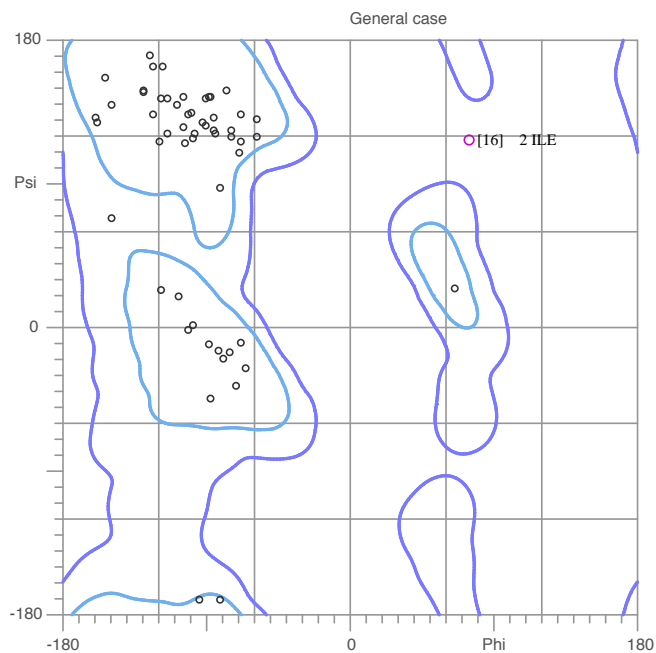
There were 1 outliers (phi, psi):
[15] 40 ASN (175.1, -57.0)

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

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 16



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.

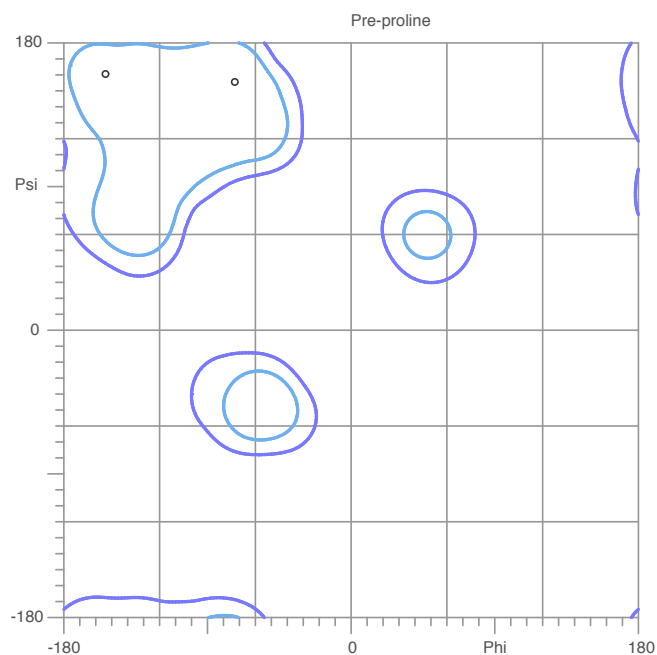
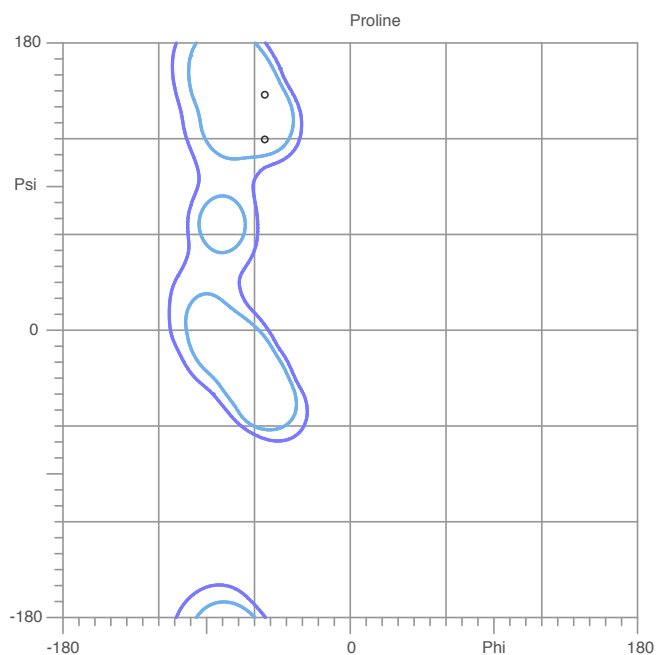
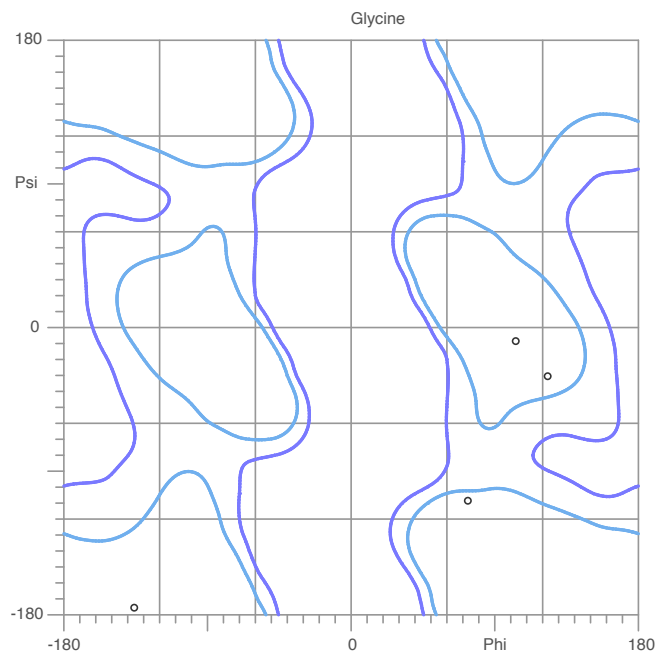
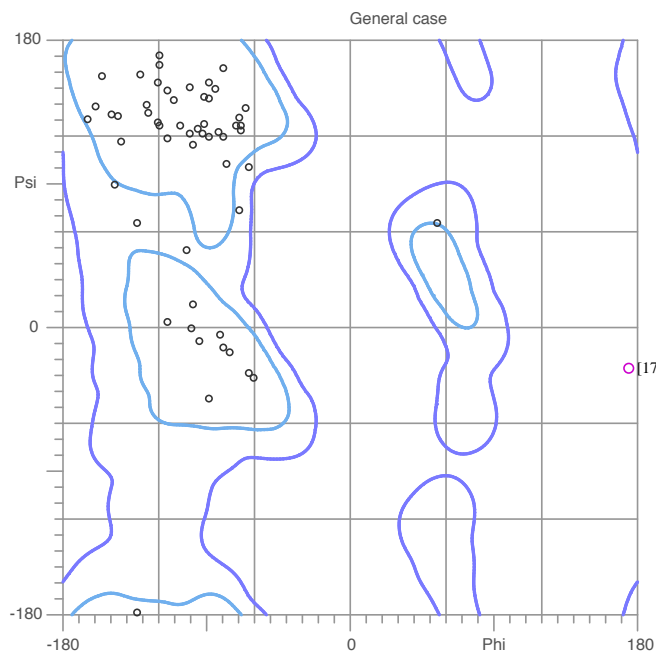
There were 1 outliers (phi, psi):
[16] 2 ILE (74.9, 118.9)

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 17



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.

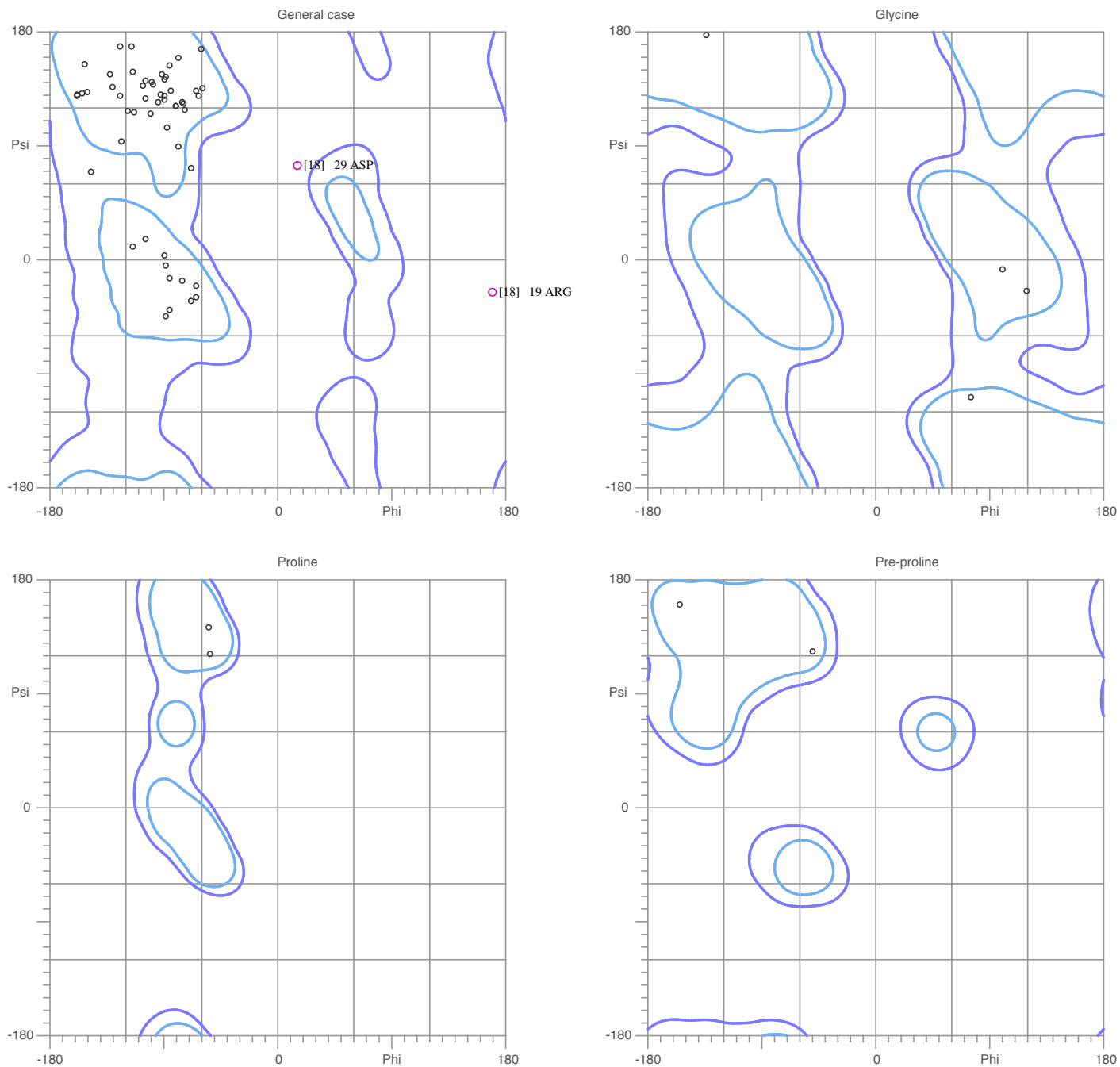
There were 1 outliers (phi, psi):
[17] 19 ARG (174.9, -25.5)

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 18

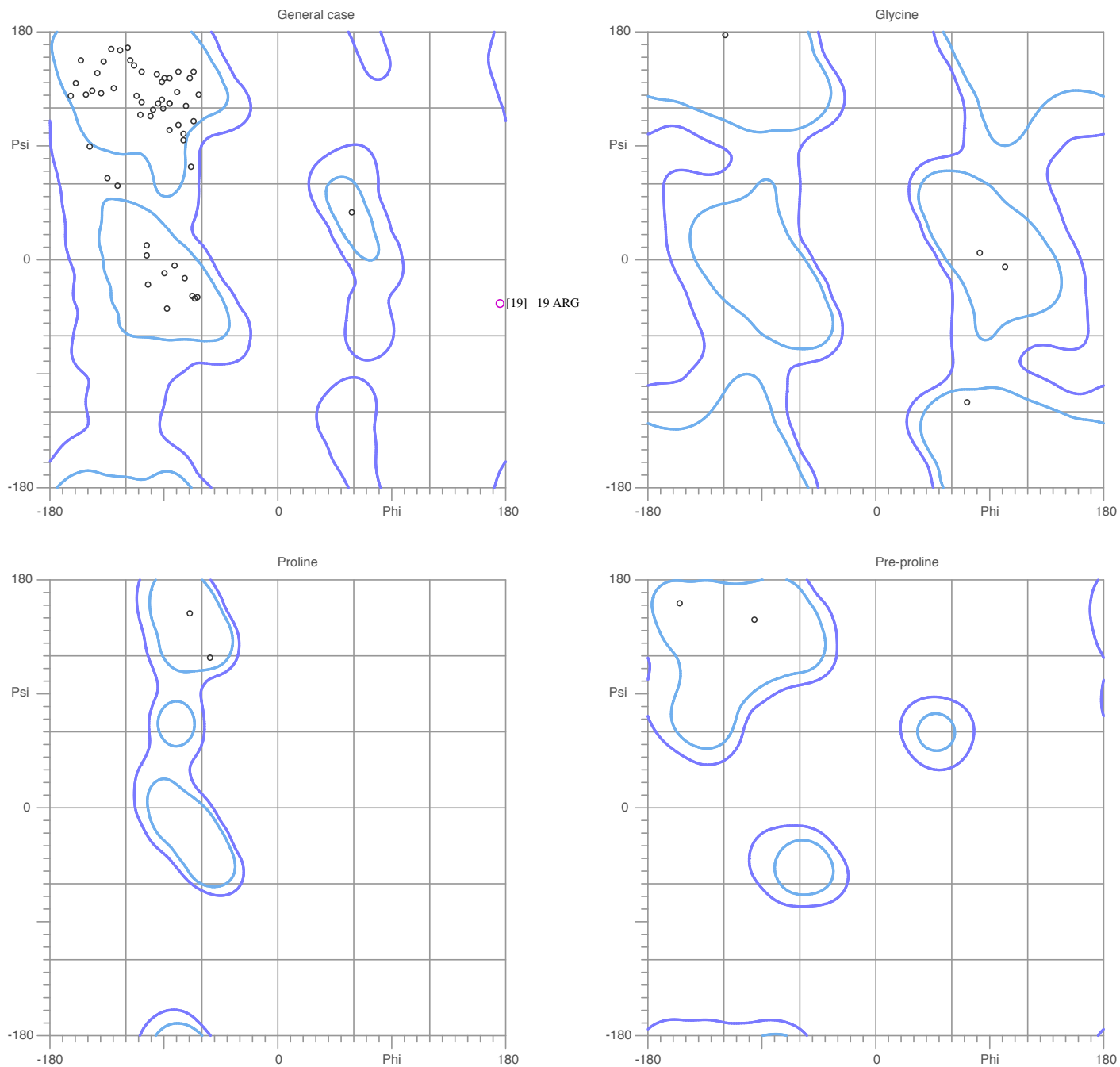


93.8% (60/64) of all residues were in favored (98%) regions.
96.9% (62/64) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 19 ARG (169.8, -25.6)
[18] 29 ASP (15.1, 75.8)

MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 19



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.

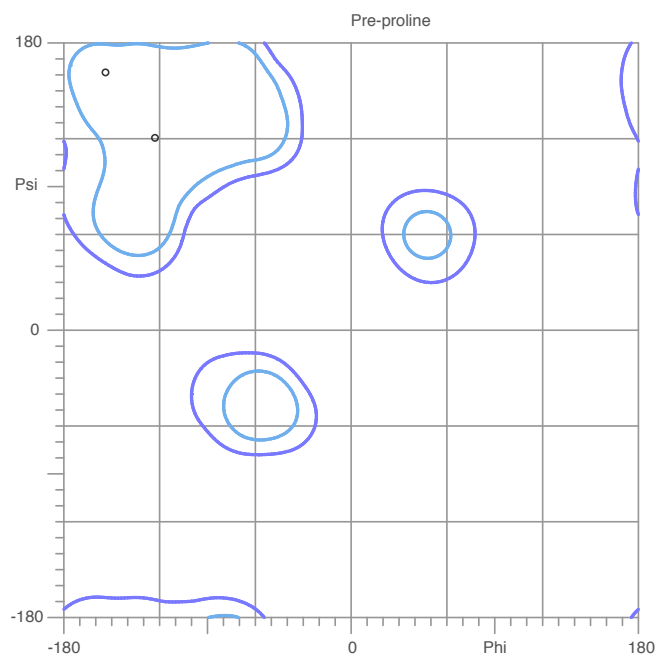
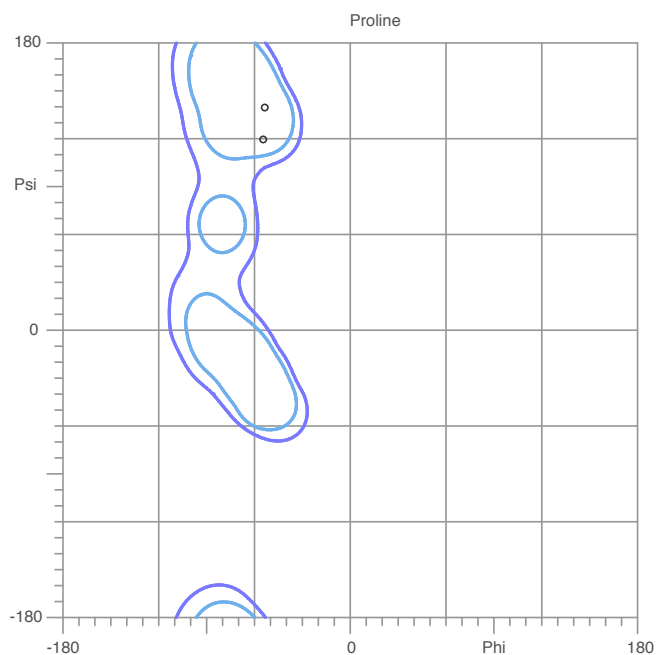
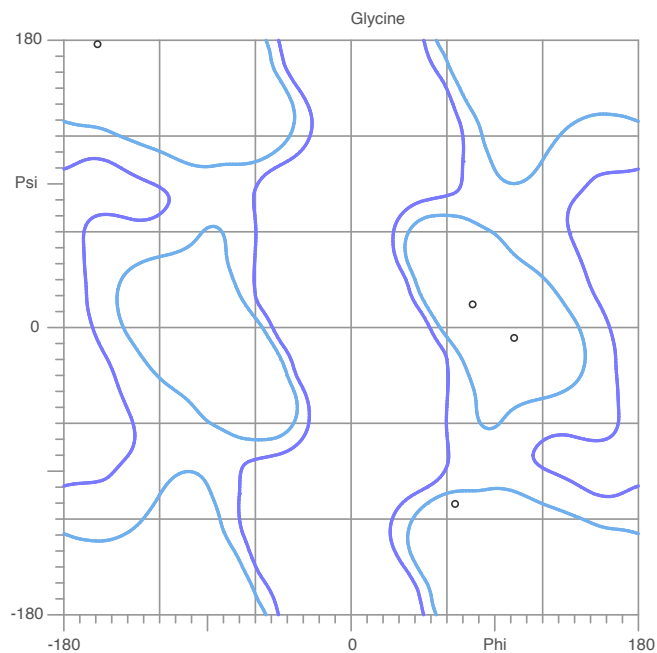
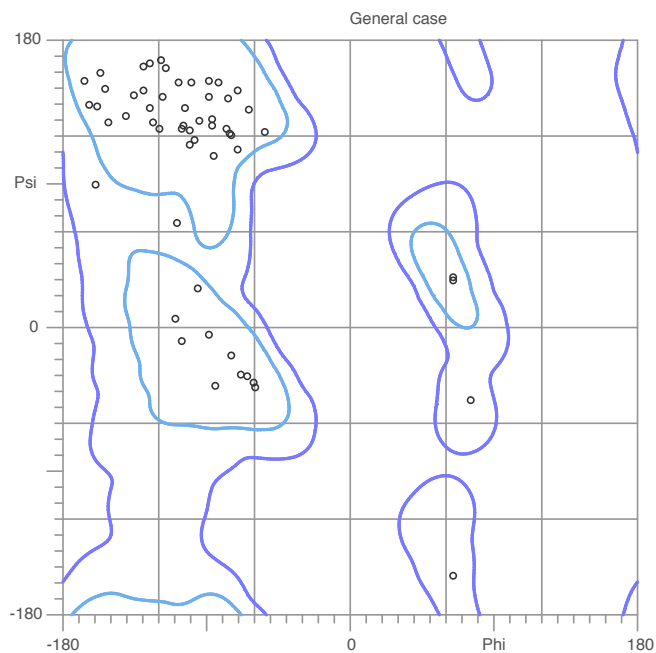
There were 1 outliers (phi, psi):
[19] 19 ARG (175.0, -35.0)

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MolProbity Ramachandran analysis

SGR42_R3_em_bcr3.pdb, model 20



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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