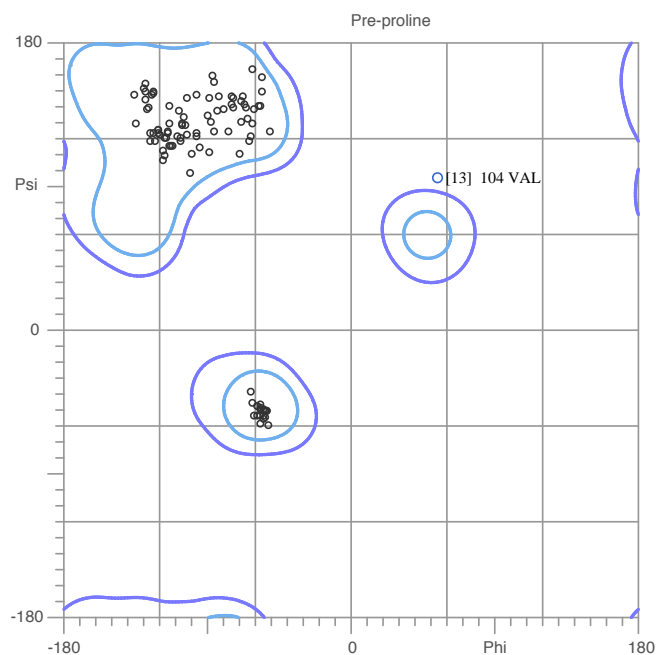
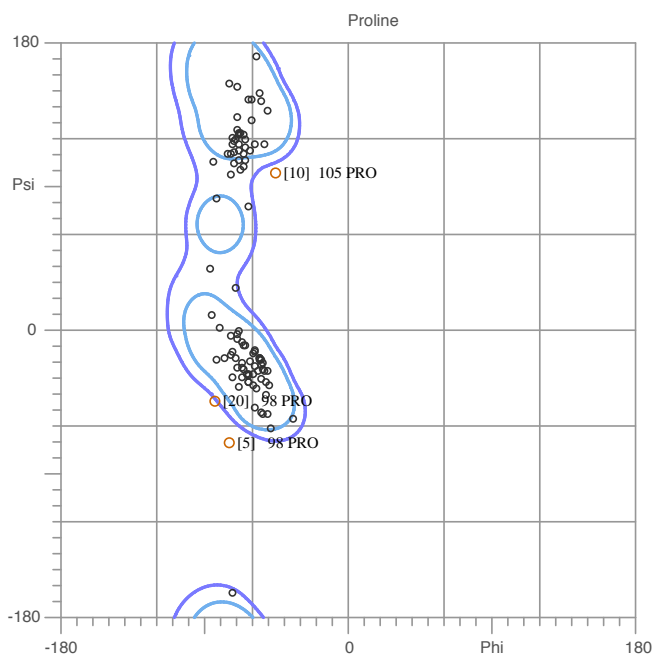
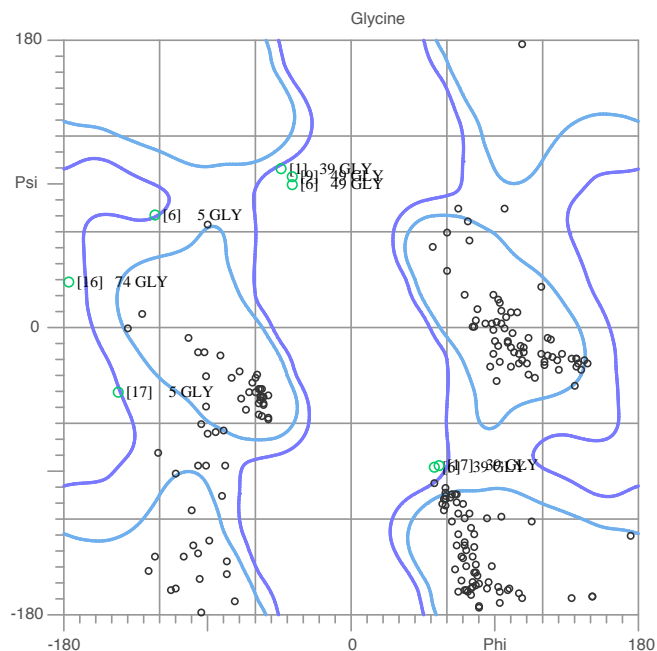
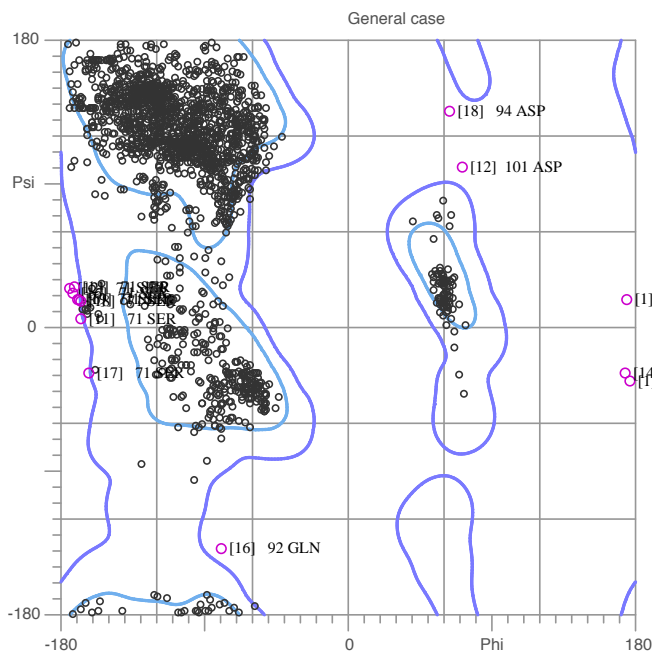


MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, all models



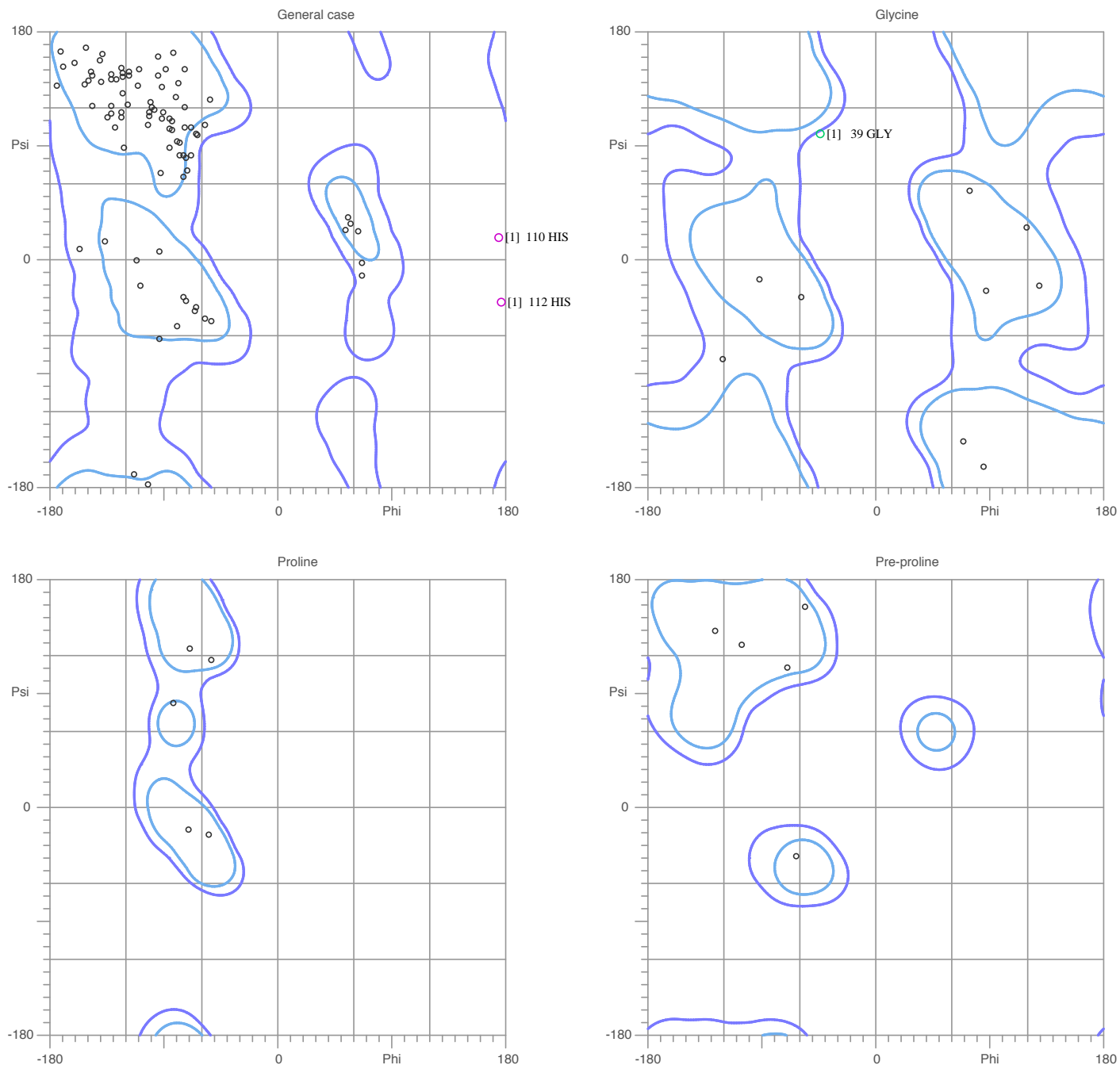
91.4% (2048/2240) of all residues were in favored (98%) regions.
98.8% (2214/2240) of all residues were in allowed (>99.8%) regions.

There were 26 outliers (phi, psi):

- | | |
|----------------------------|-----------------------------|
| [1] 39 GLY (-44.7, 100.0) | [12] 71 SER (-175.3, 25.4) |
| [1] 110 HIS (174.2, 18.1) | [12] 101 ASP (71.0, 101.8) |
| [1] 112 HIS (176.2, -33.1) | [13] 104 VAL (54.2, 96.2) |
| [5] 98 PRO (-75.8, -70.0) | [14] 71 SER (-172.2, 26.4) |
| [6] 5 GLY (-123.9, 71.2) | [14] 100 THR (173.0, -28.7) |
| [6] 39 GLY (52.7, -87.2) | [16] 71 SER (-173.7, 22.9) |
| [6] 49 GLY (-37.3, 90.4) | [16] 74 GLY (-177.2, 29.4) |
| [6] 71 SER (-169.2, 18.8) | [16] 92 GLN (-80.5, -138.8) |
| [9] 49 GLY (-37.5, 95.3) | [17] 5 GLY (-146.5, -40.4) |
| [10] 105 PRO (-46.8, 99.8) | [17] 39 GLY (55.4, -86.8) |
| [11] 71 SER (-168.6, 6.5) | [17] 71 SER (-163.8, -28.7) |
| | [18] 71 SER (-168.4, 17.5) |
| | [18] 94 ASP (63.6, 136.4) |
| | [19] 71 SER (-170.7, 19.0) |
| | [20] 98 PRO (-84.9, -44.0) |

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 1



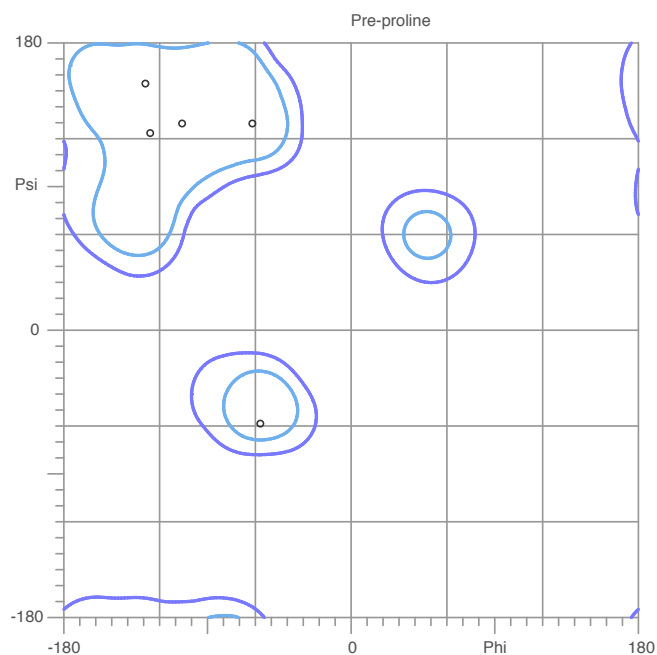
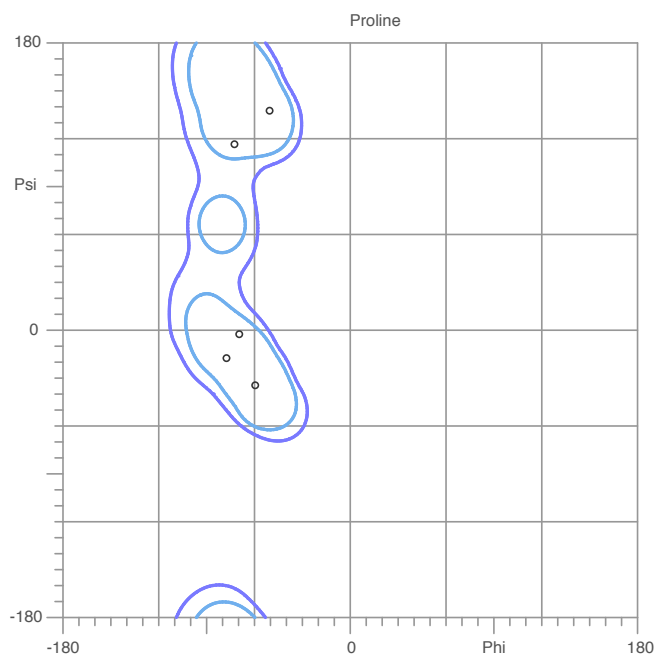
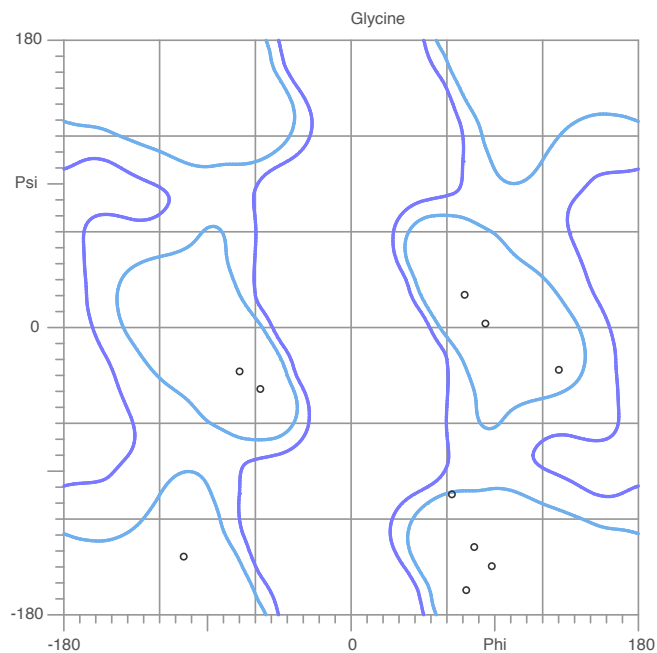
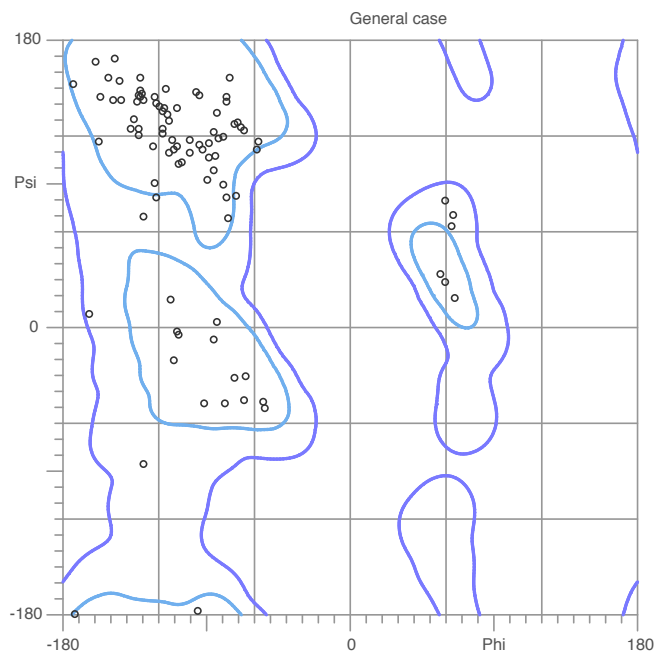
84.8% (95/112) of all residues were in favored (98%) regions.
97.3% (109/112) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 39 GLY (-44.7, 100.0)
- [1] 110 HIS (174.2, 18.1)
- [1] 112 HIS (176.2, -33.1)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 2



92.9% (104/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

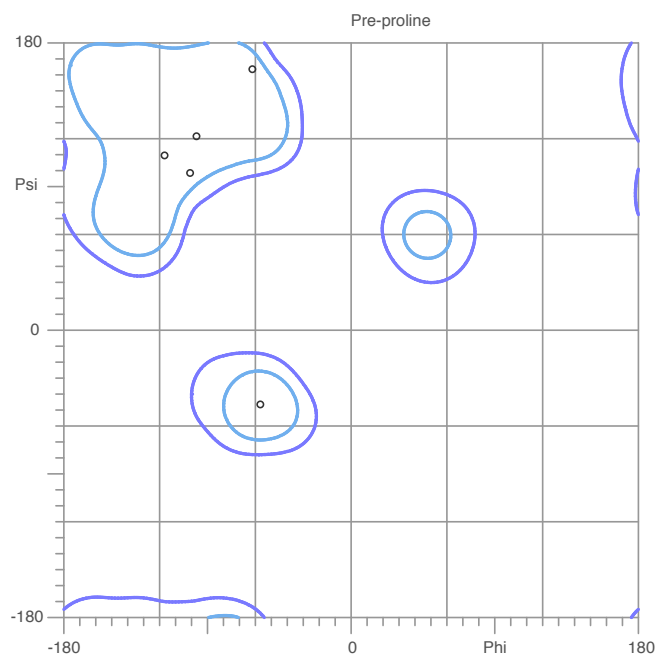
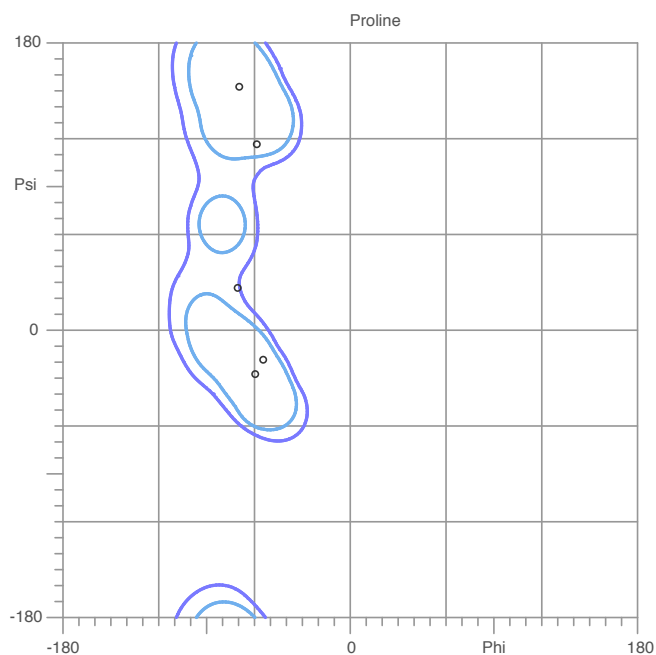
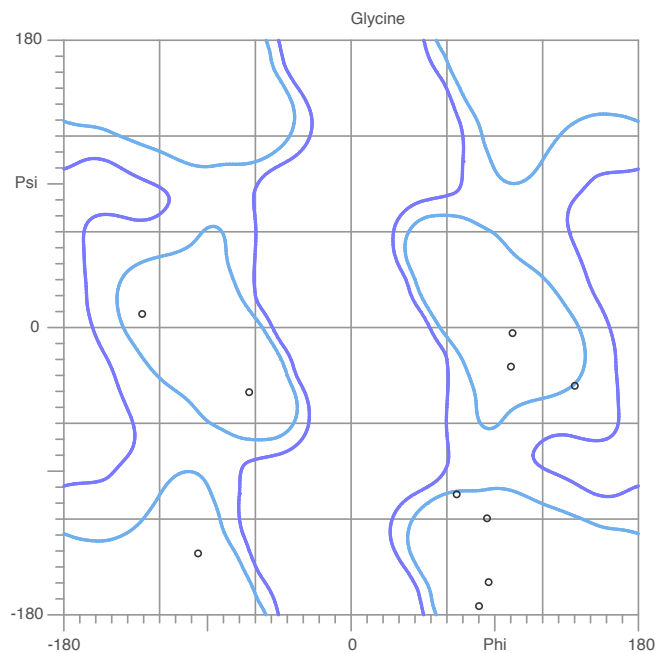
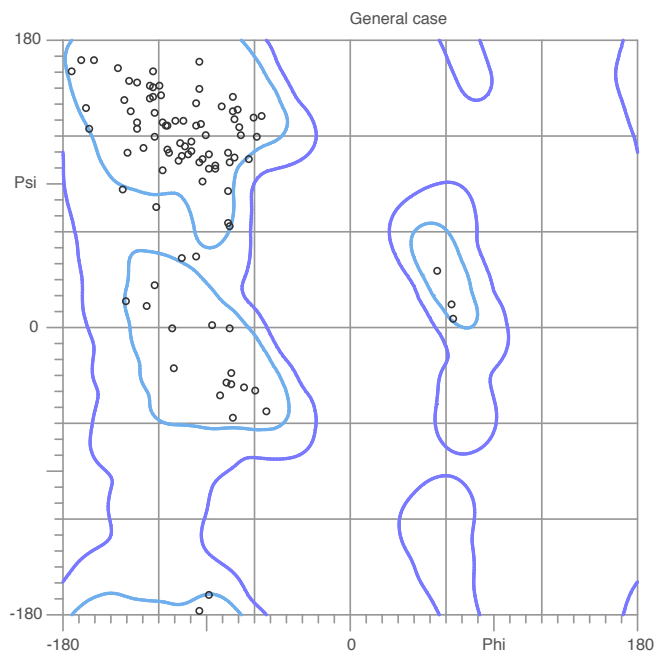
There were no outliers.

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

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 3

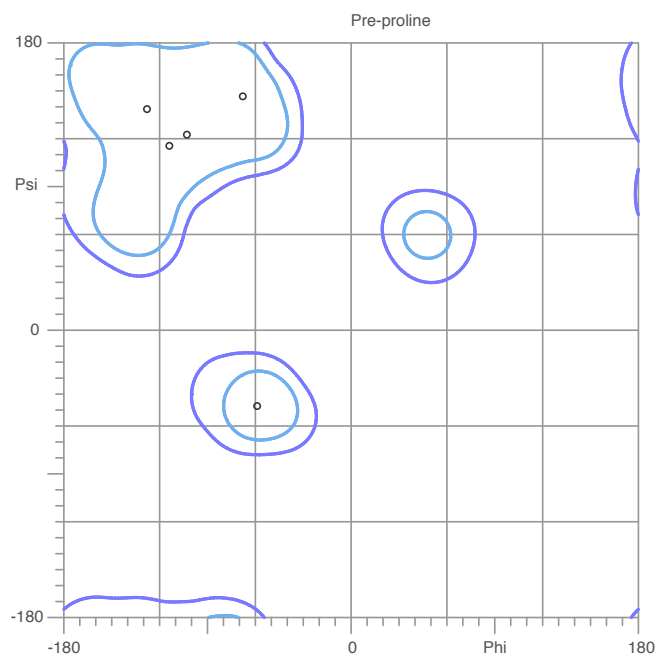
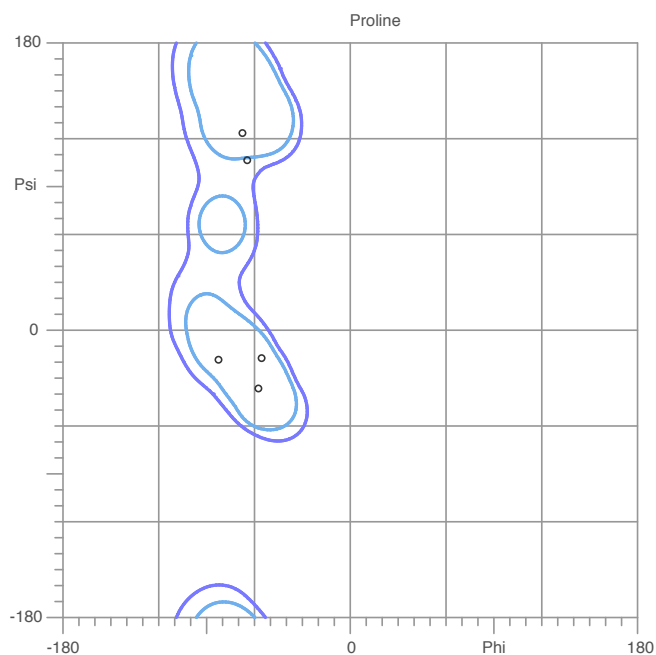
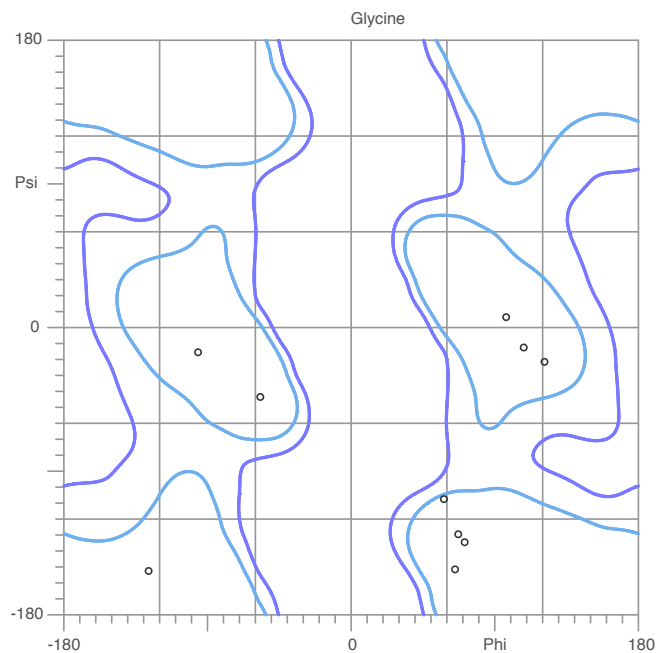
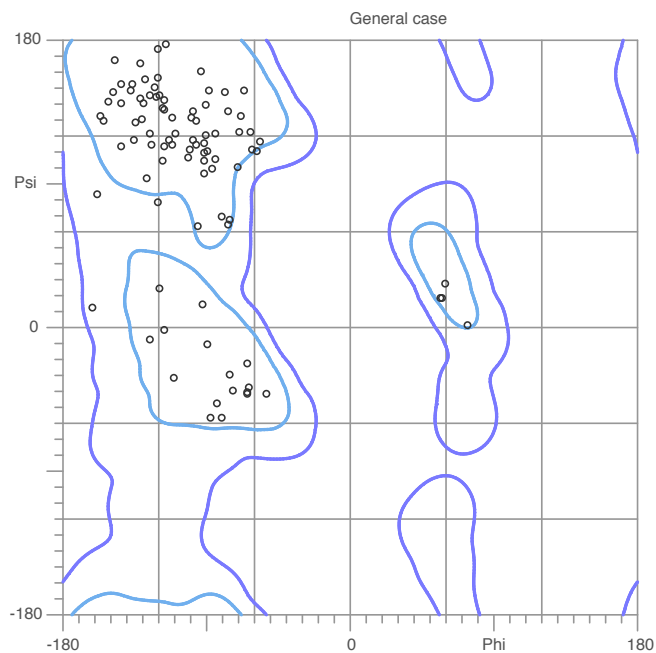


92.9% (104/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 4



96.4% (108/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

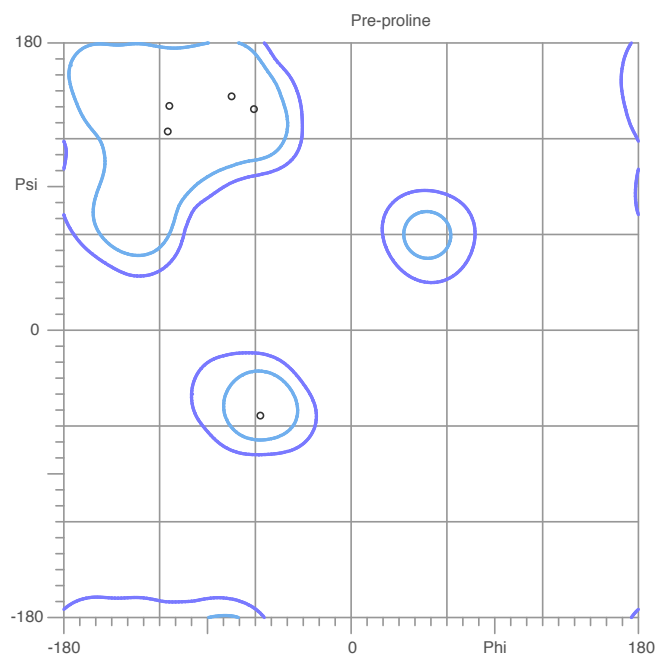
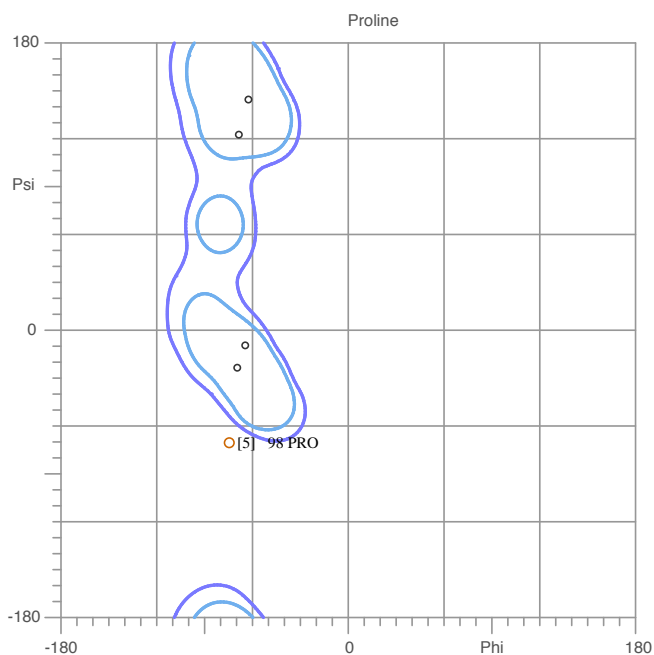
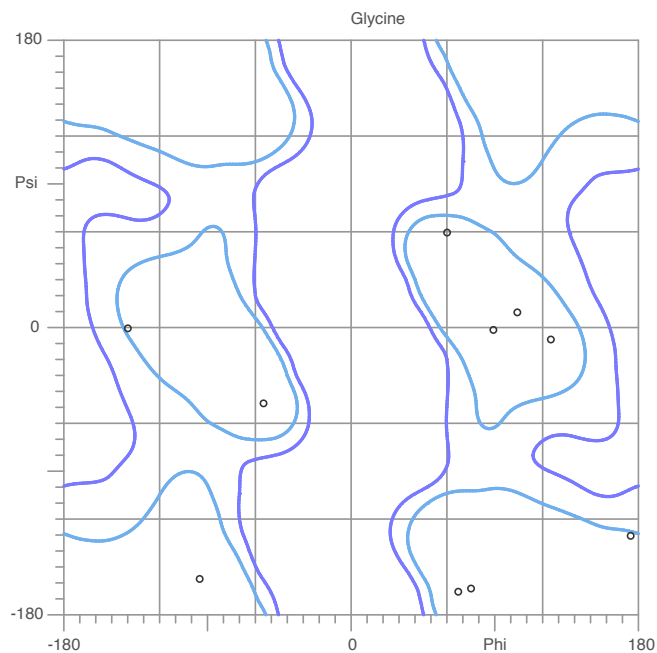
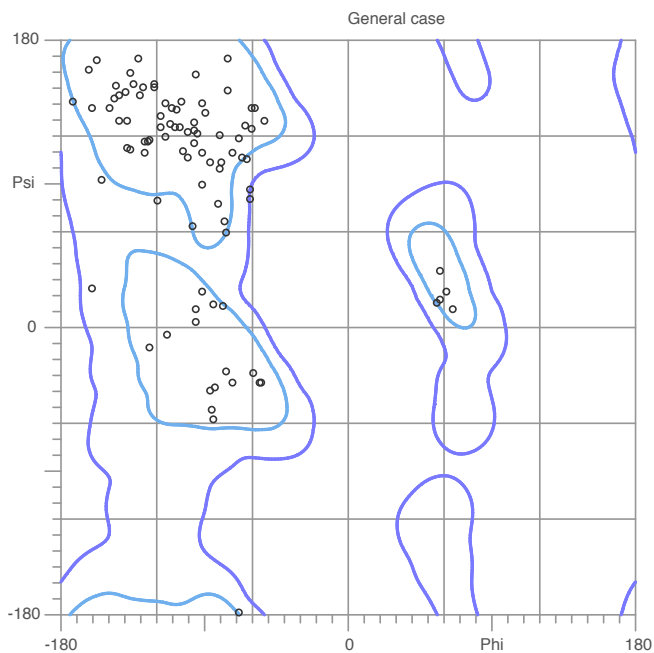
There were no outliers.

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

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 5

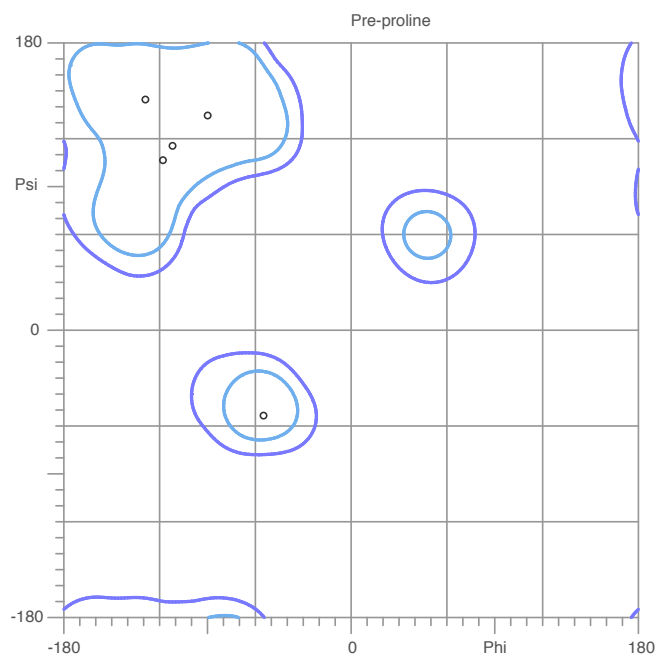
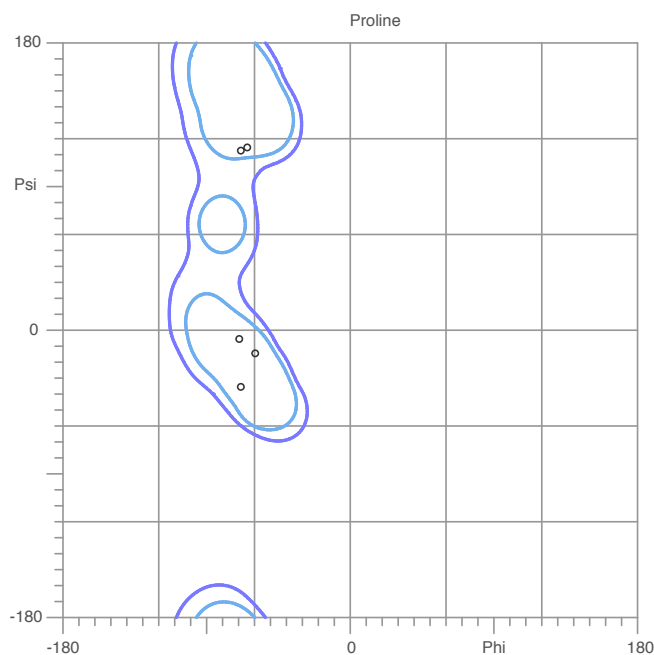
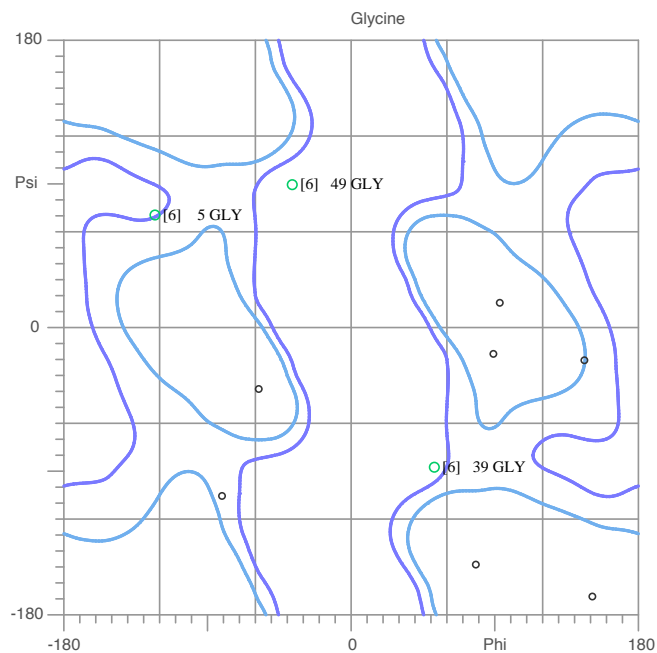
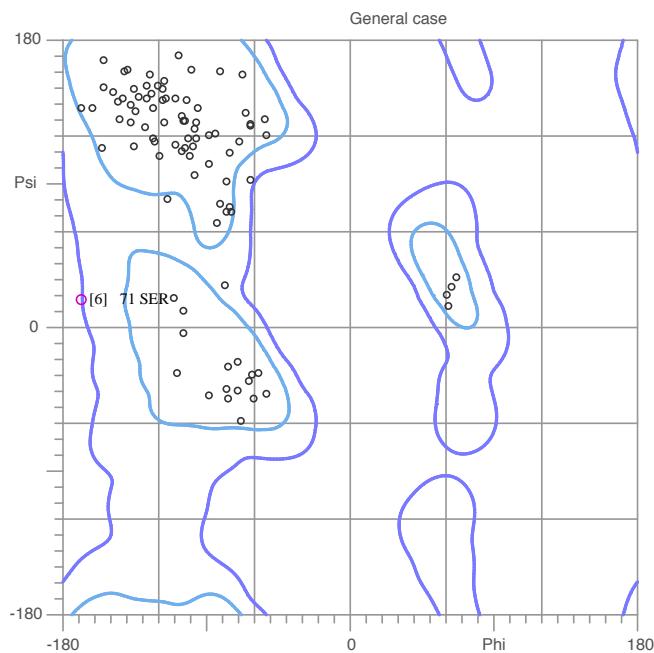


92.0% (103/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[5] 98 PRO (-75.8, -70.0)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 6



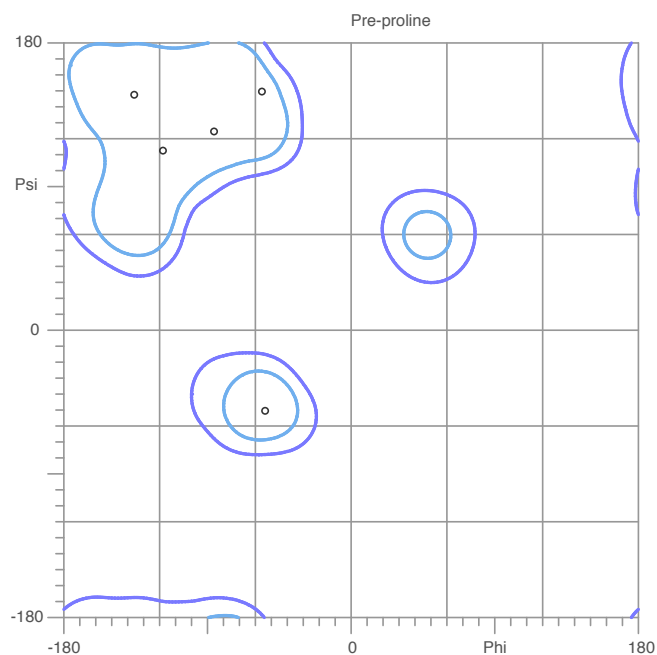
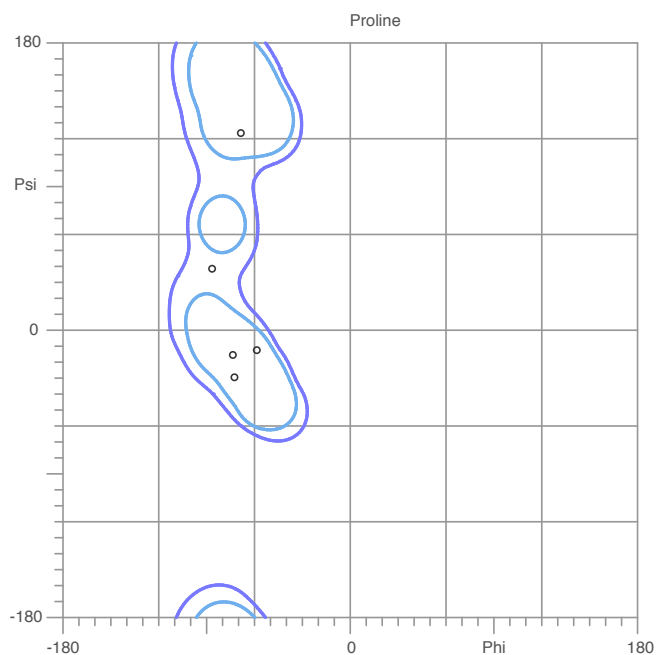
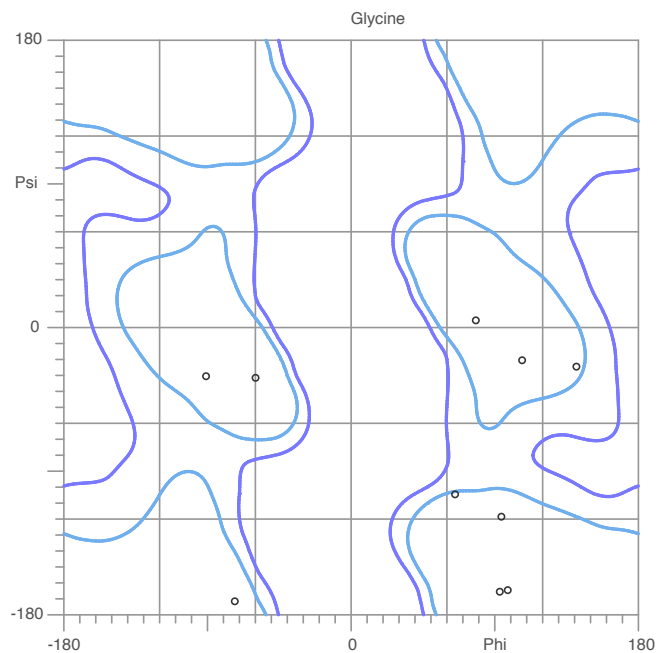
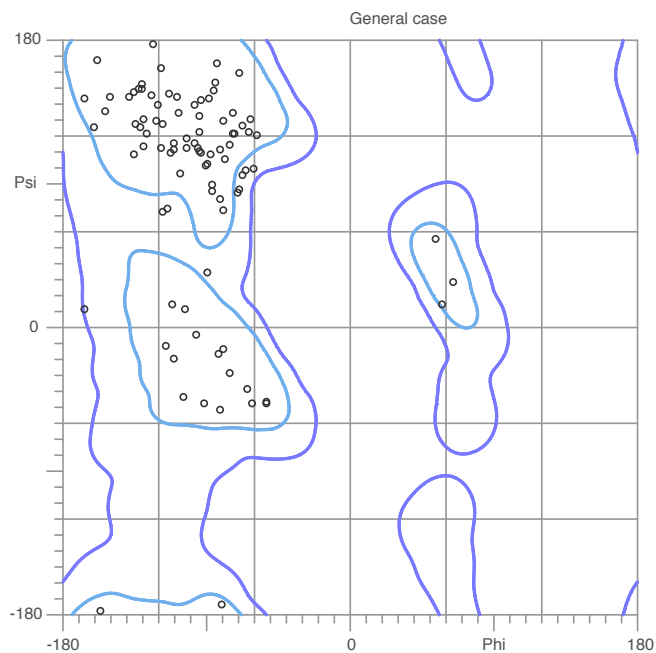
92.9% (104/112) of all residues were in favored (98%) regions.
96.4% (108/112) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [6] 5 GLY (-123.9, 71.2)
- [6] 39 GLY (52.7, -87.2)
- [6] 49 GLY (-37.3, 90.4)
- [6] 71 SER (-169.2, 18.8)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 7



91.1% (102/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

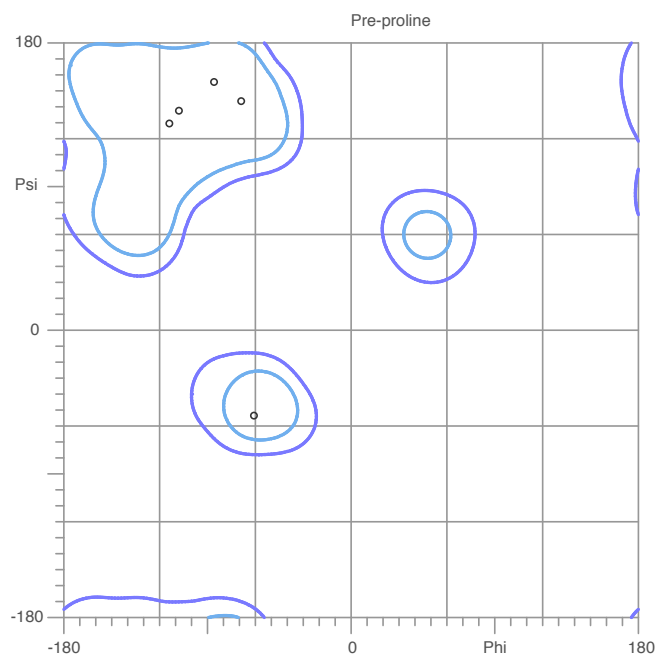
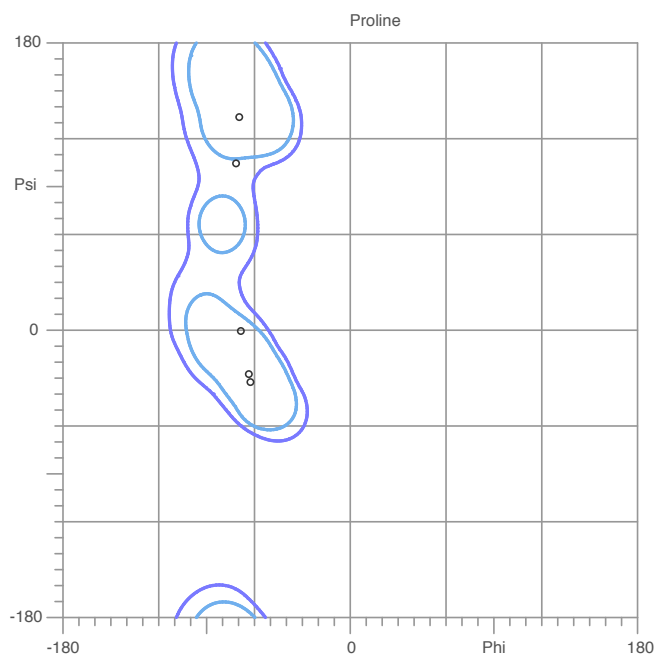
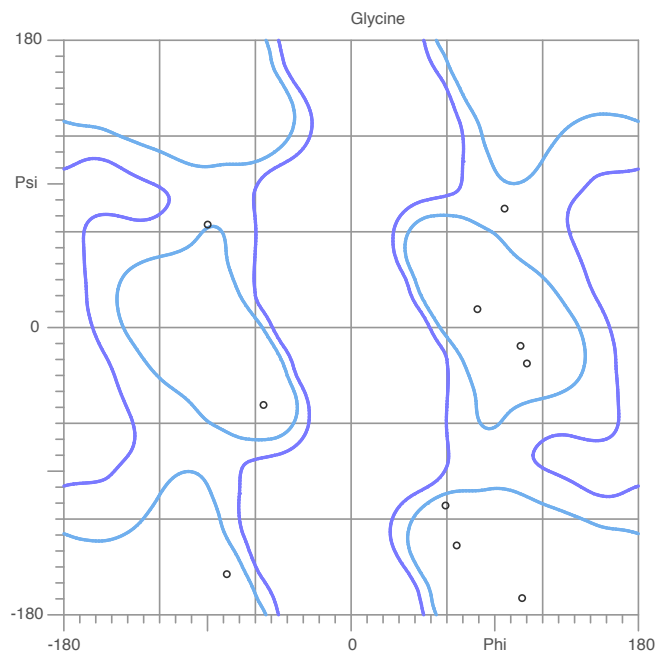
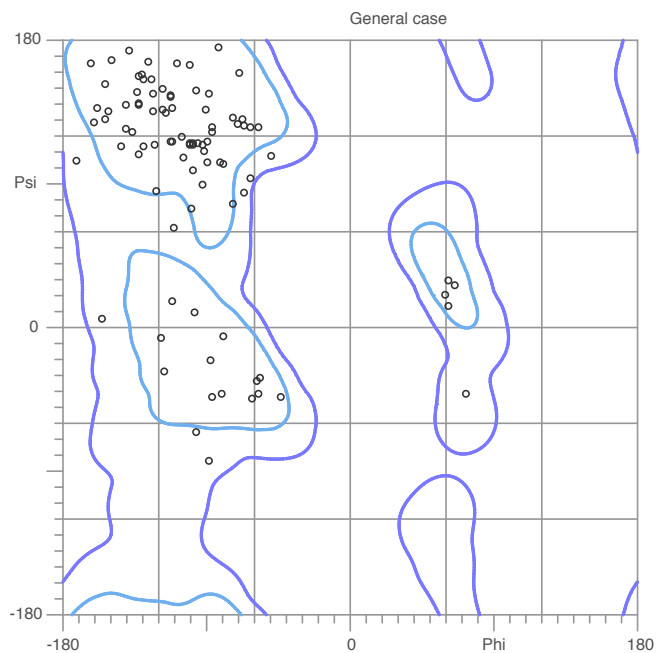
There were no outliers.

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

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

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 8



89.3% (100/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

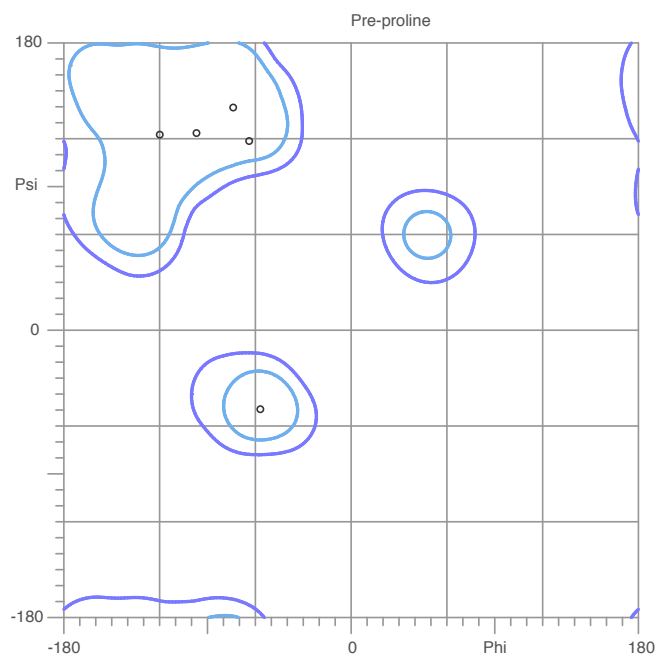
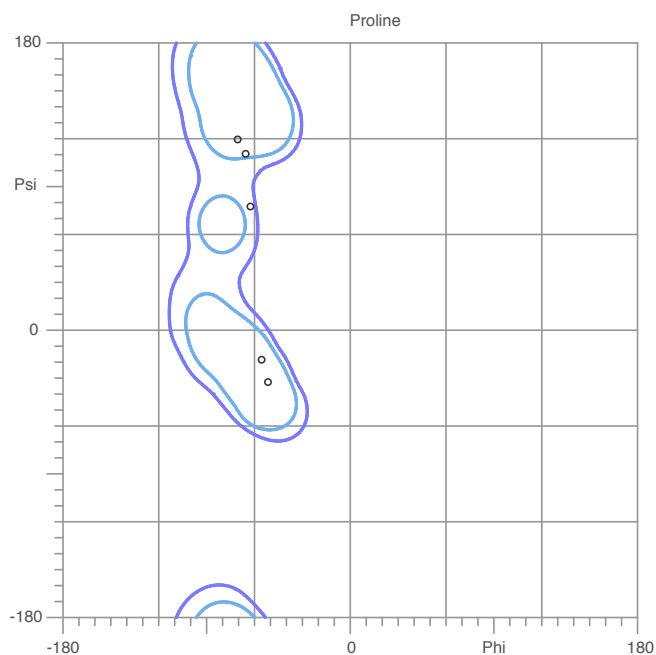
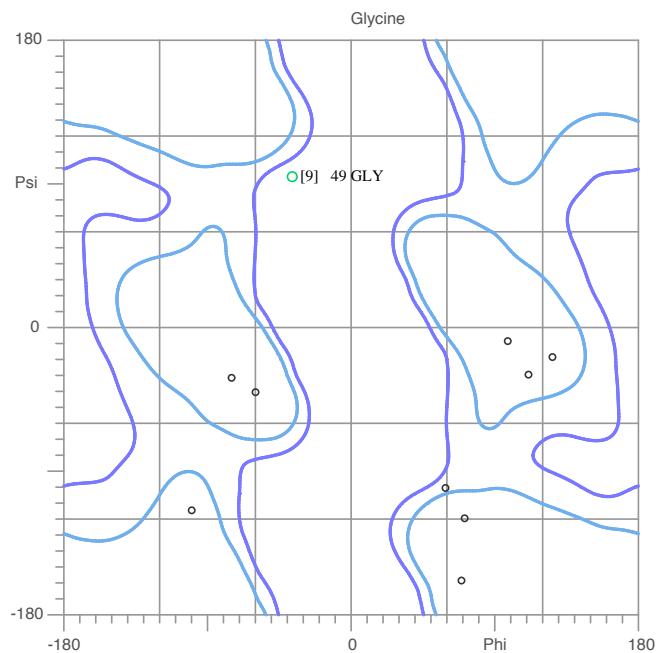
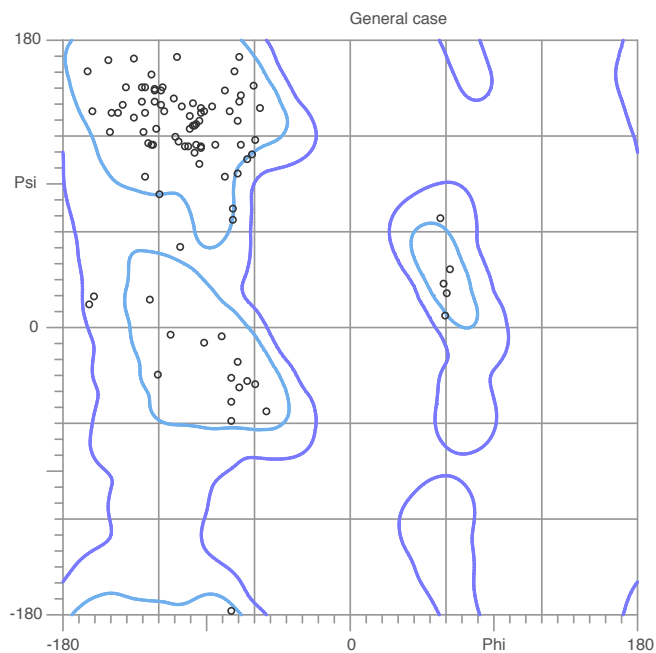
There were no outliers.

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

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 9

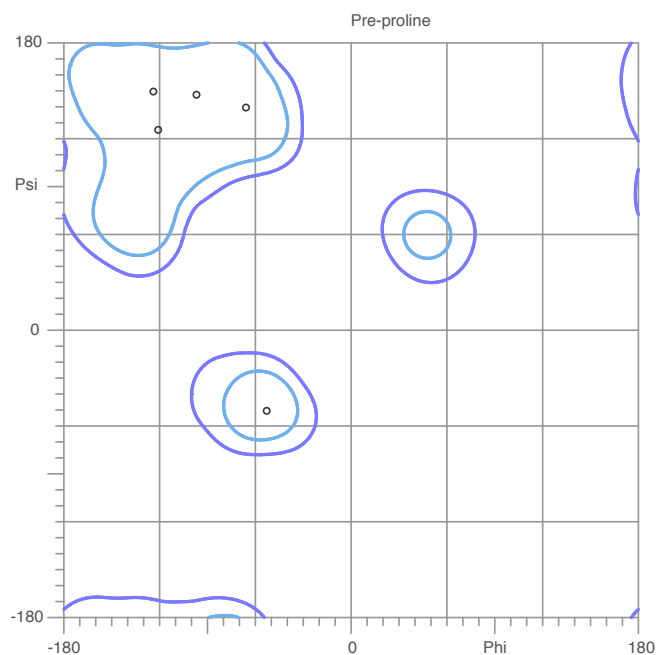
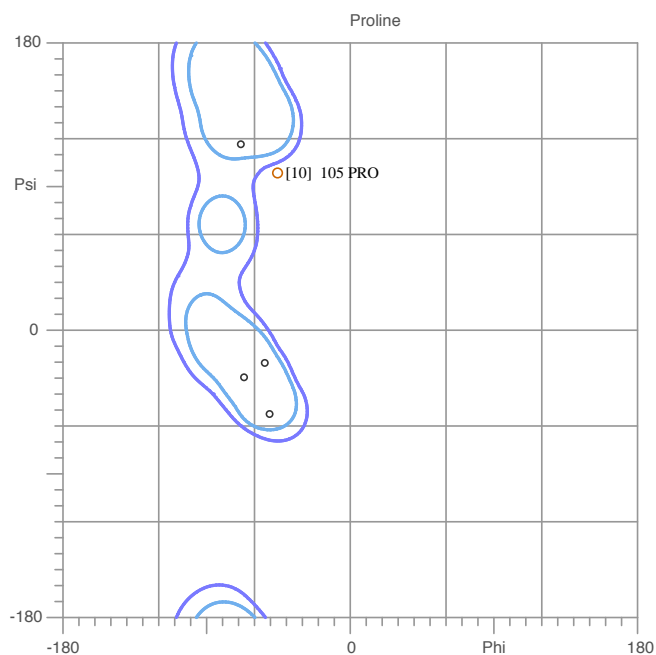
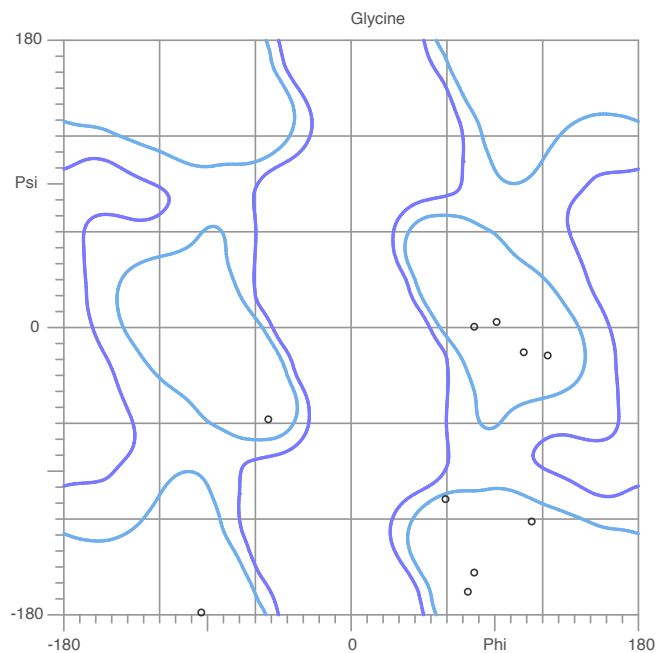
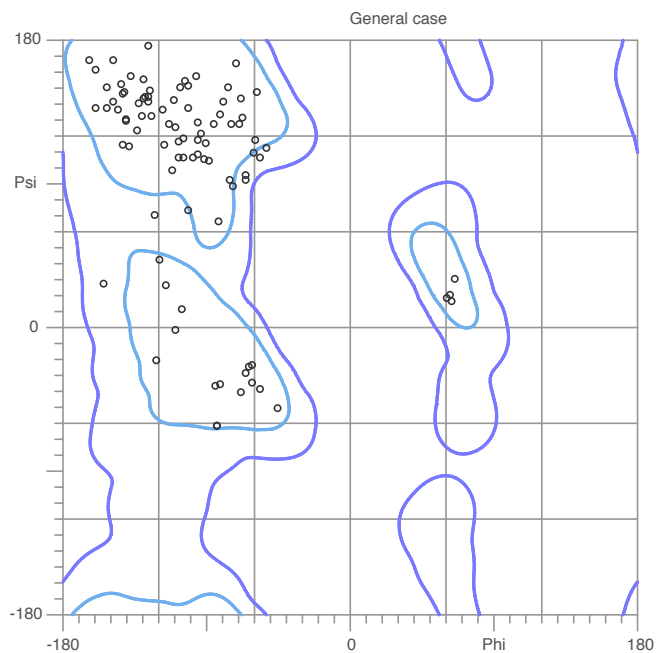


92.0% (103/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 49 GLY (-37.5, 95.3)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 10



92.9% (104/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

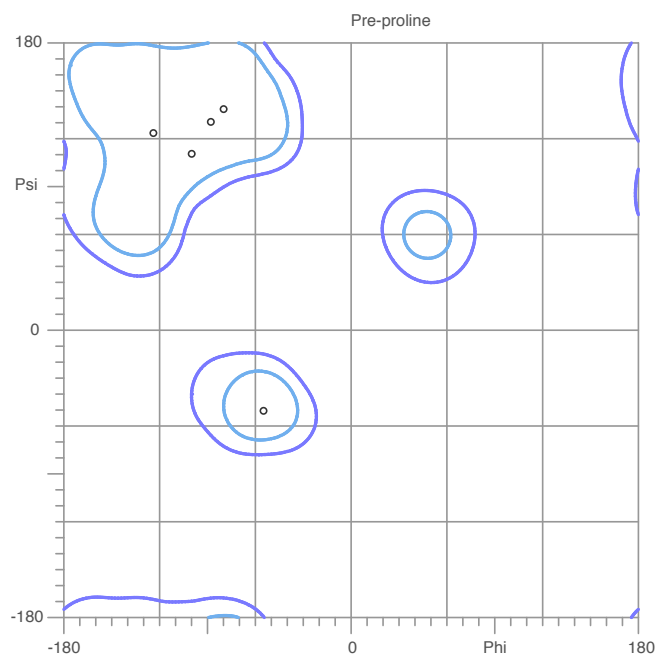
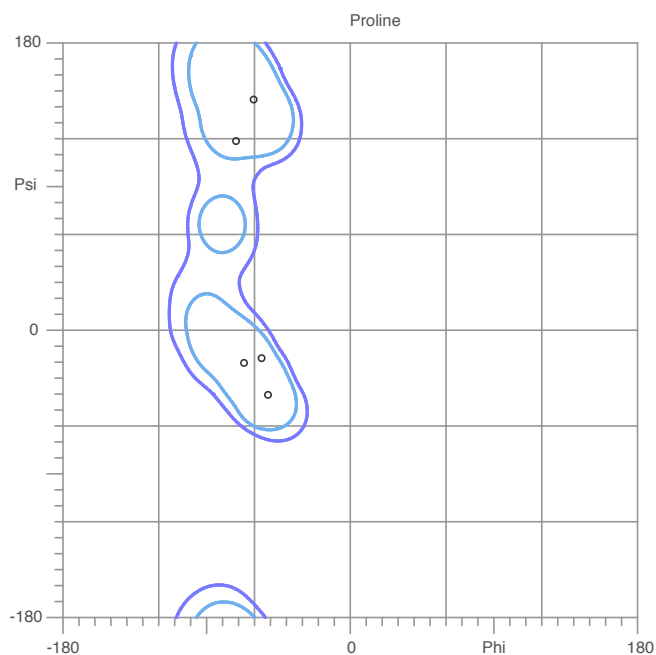
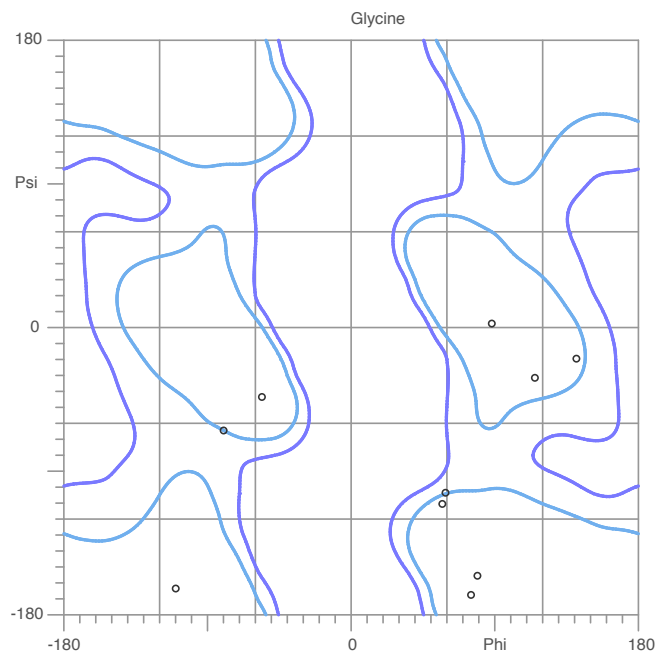
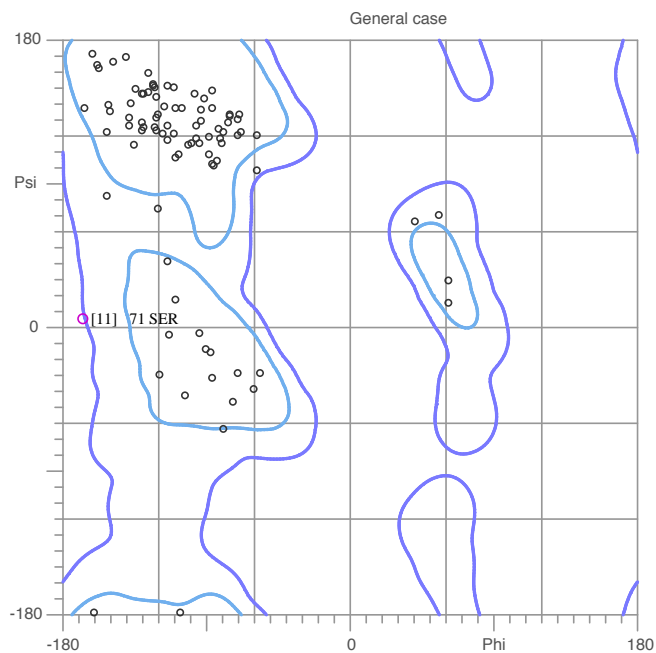
There were 1 outliers (phi, psi):
[10] 105 PRO (-46.8, 99.8)

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

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 11



92.9% (104/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

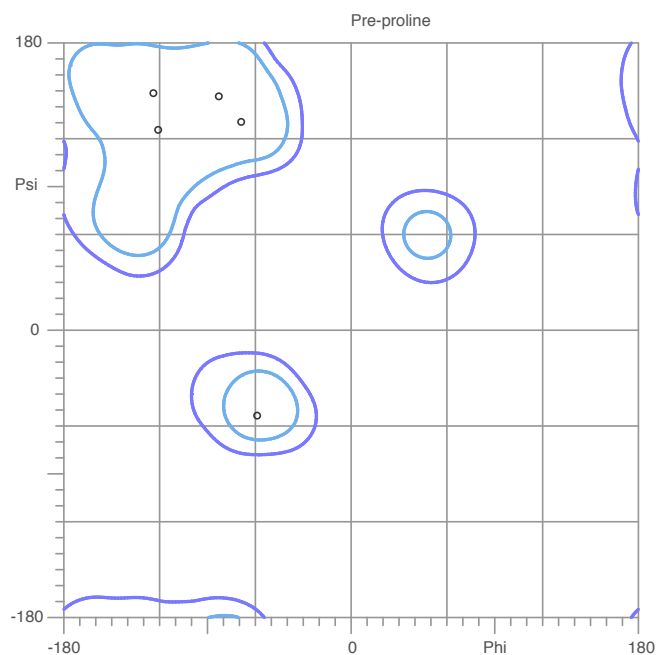
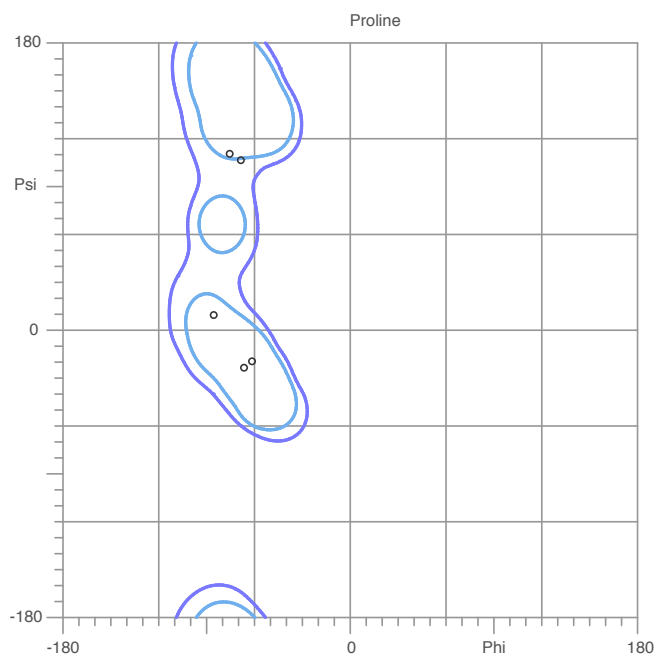
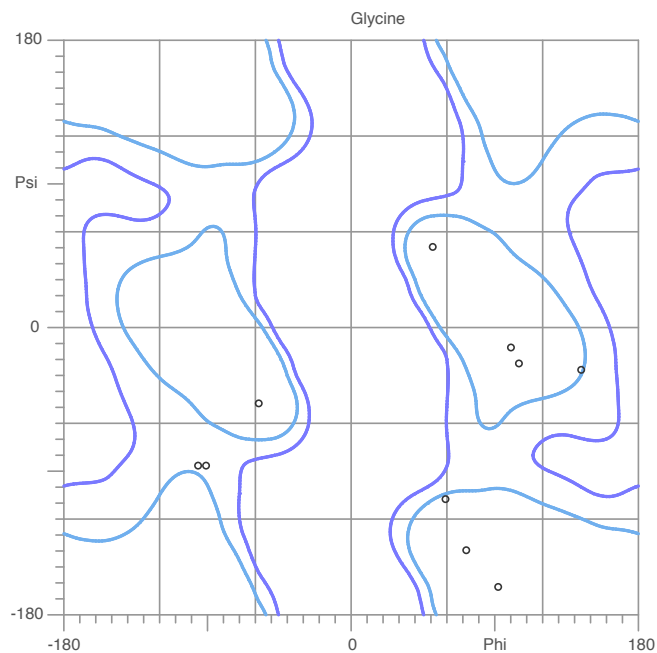
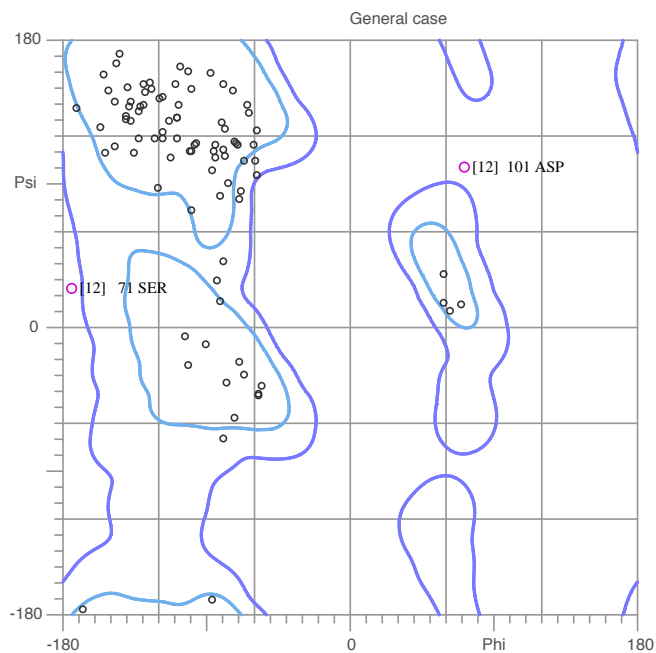
There were 1 outliers (phi, psi):
[11] 71 SER (-168.6, 6.5)

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

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 12



88.4% (99/112) of all residues were in favored (98%) regions.
98.2% (110/112) of all residues were in allowed (>99.8%) regions.

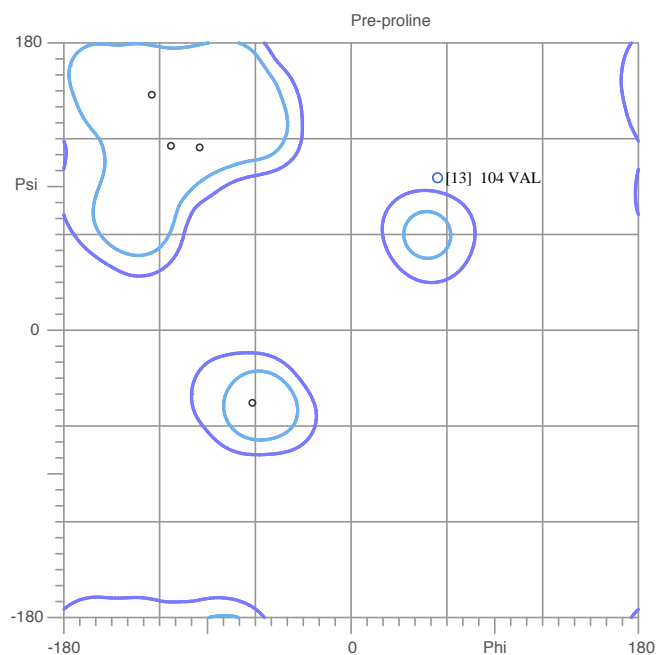
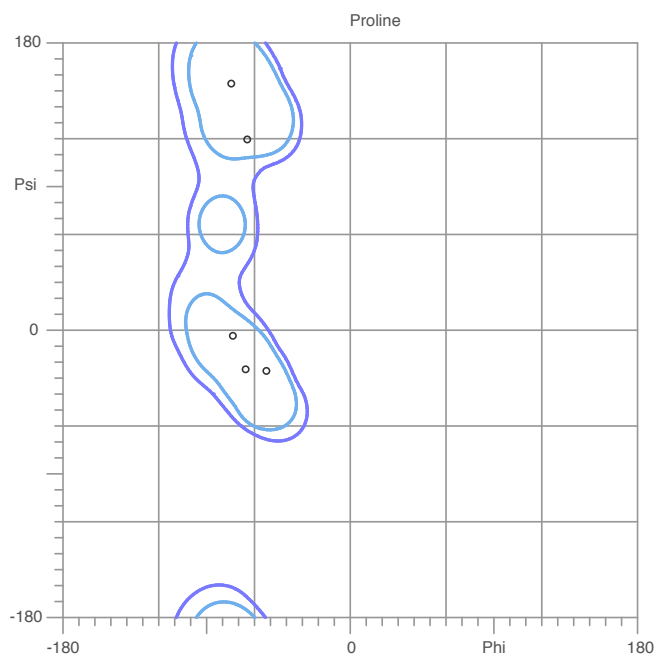
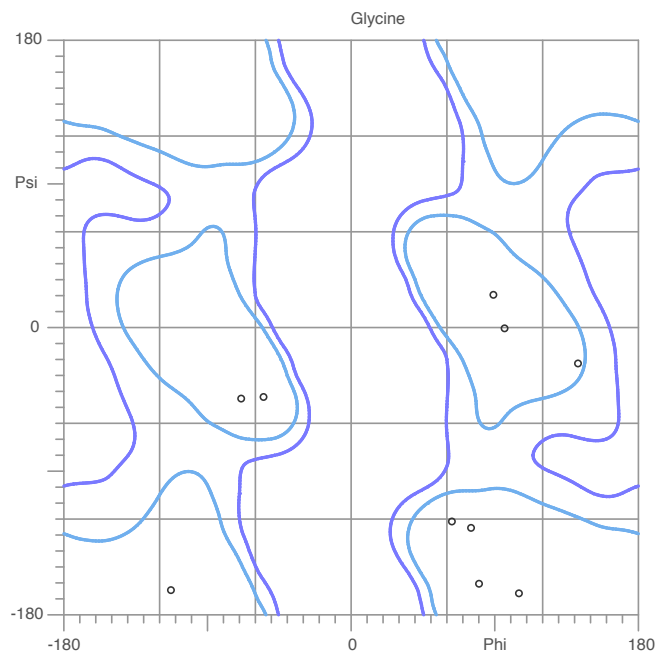
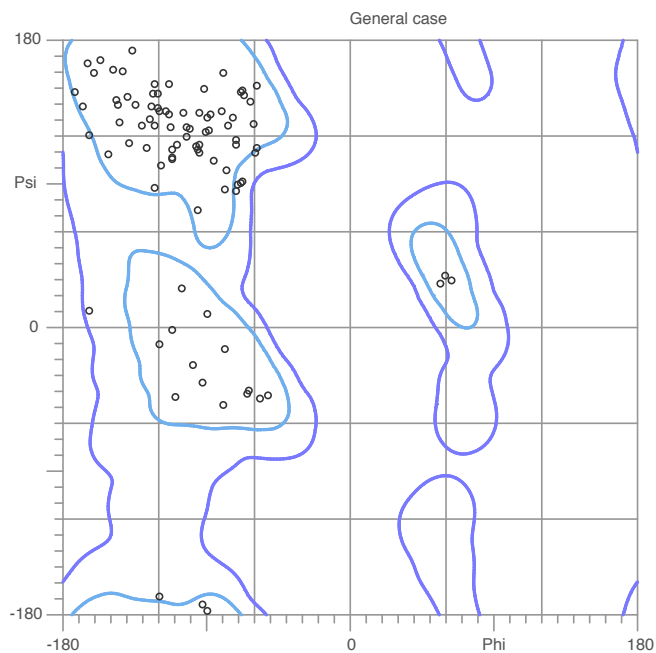
There were 2 outliers (phi, psi):

[12] 71 SER (-175.3, 25.4)

[12] 101 ASP (71.0, 101.8)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 13



92.9% (104/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

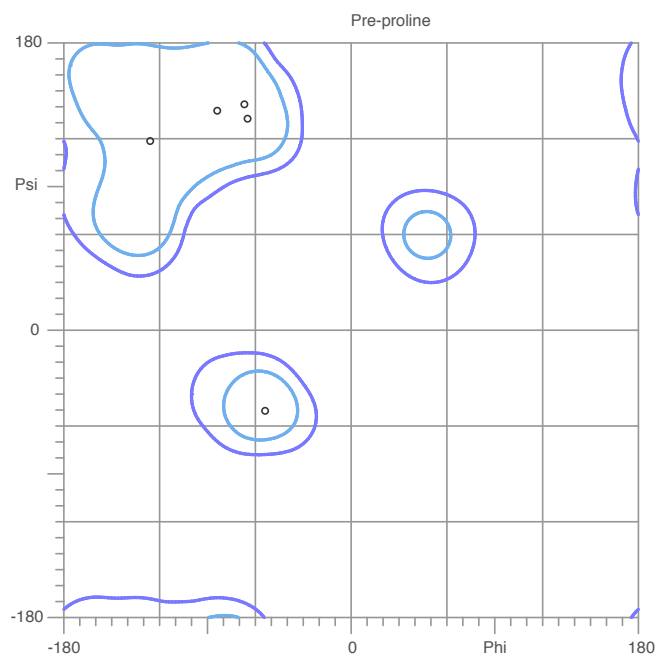
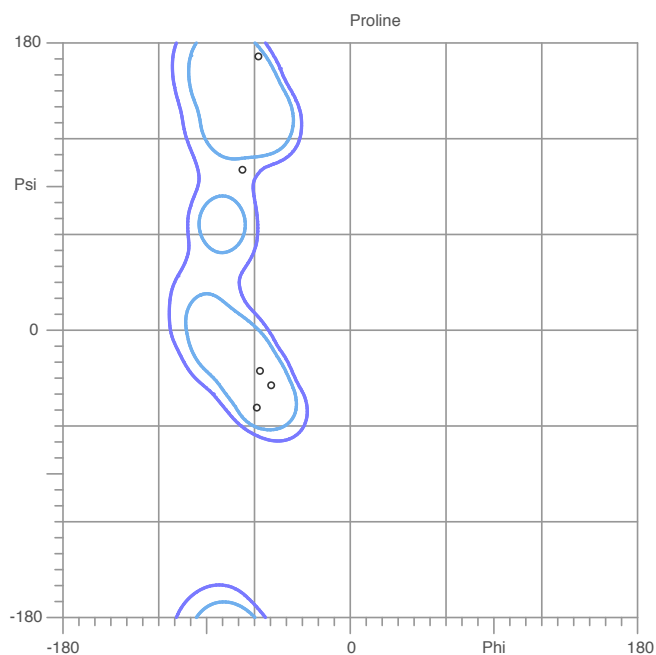
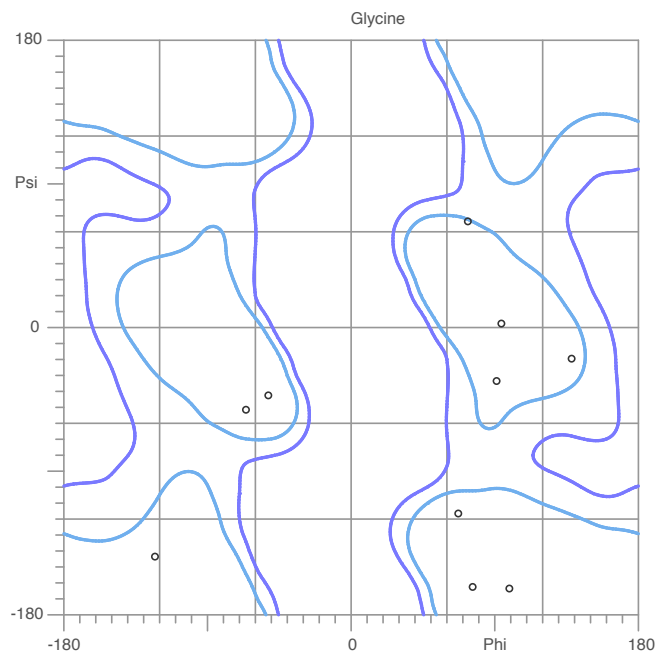
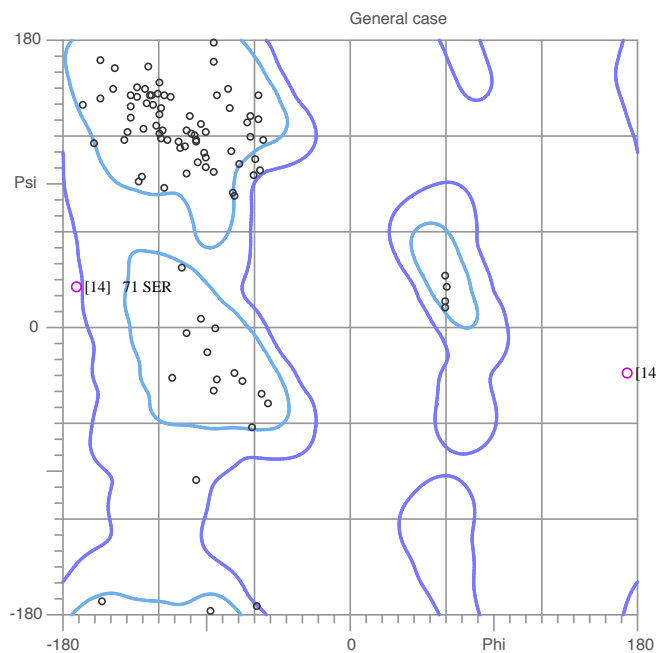
There were 1 outliers (phi, psi):
[13] 104 VAL (54.2, 96.2)

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

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 14

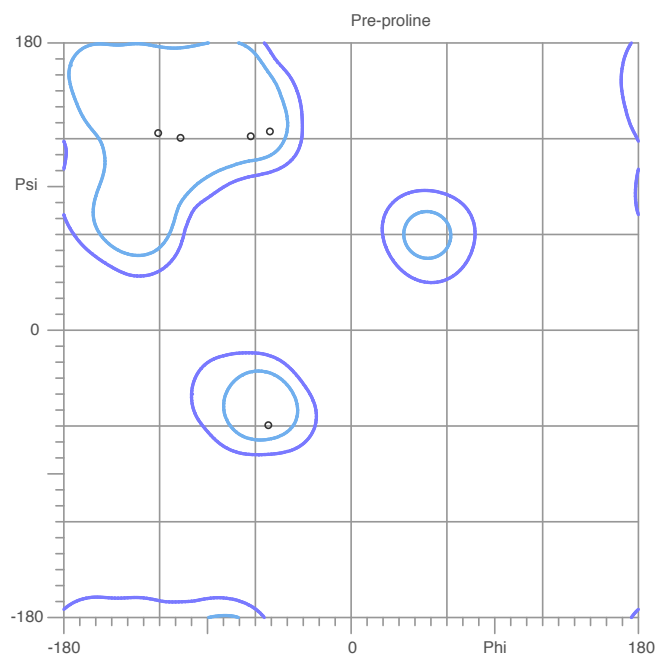
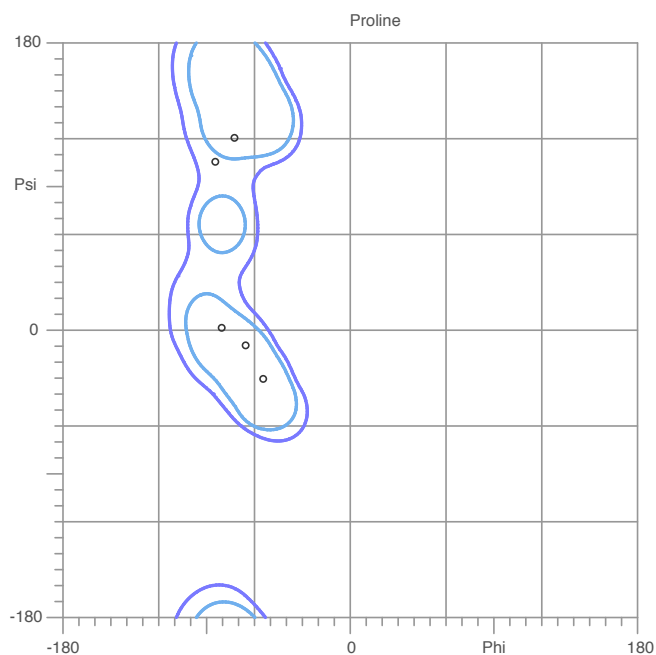
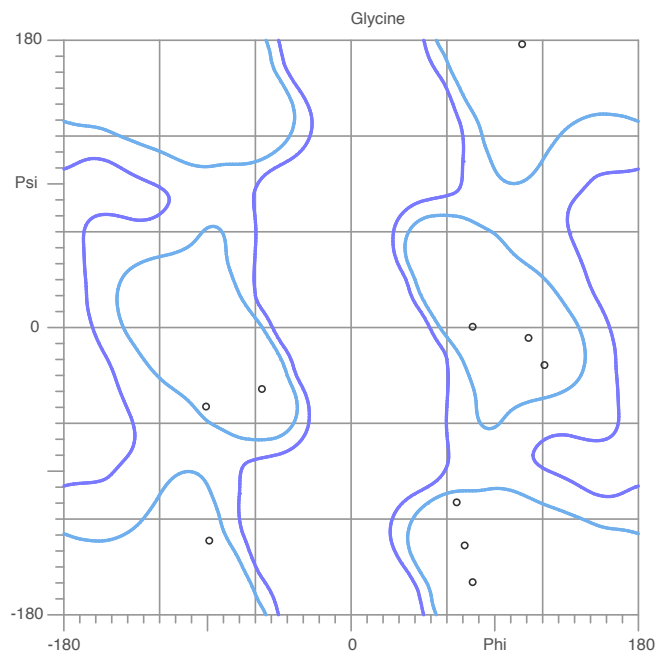
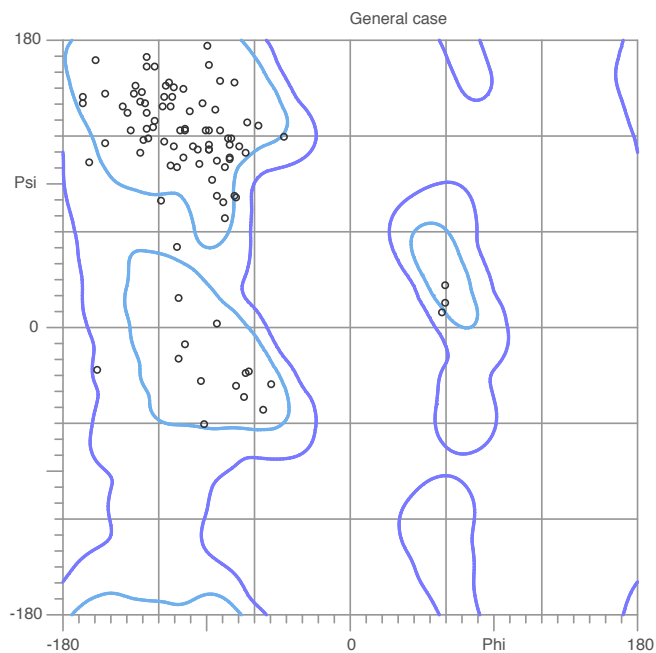


91.1% (102/112) of all residues were in favored (98%) regions.
98.2% (110/112) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[14] 71 SER (-172.2, 26.4)
[14] 100 THR (173.0, -28.7)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 15



92.9% (104/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

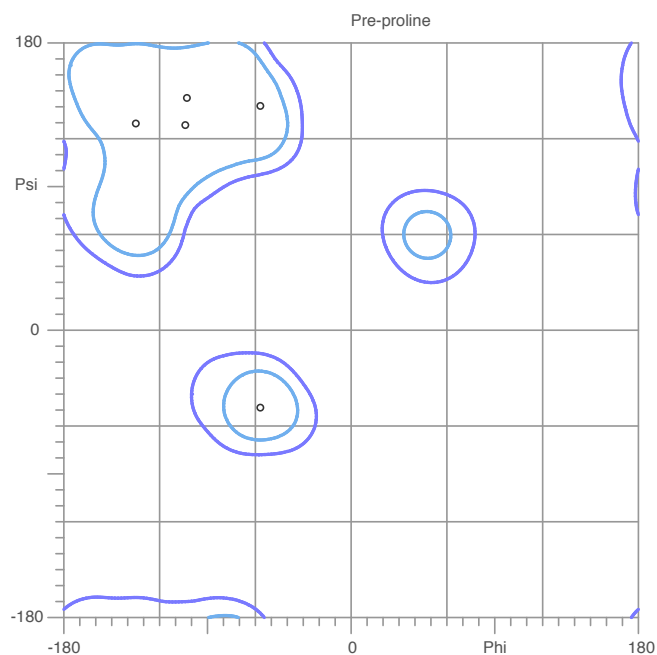
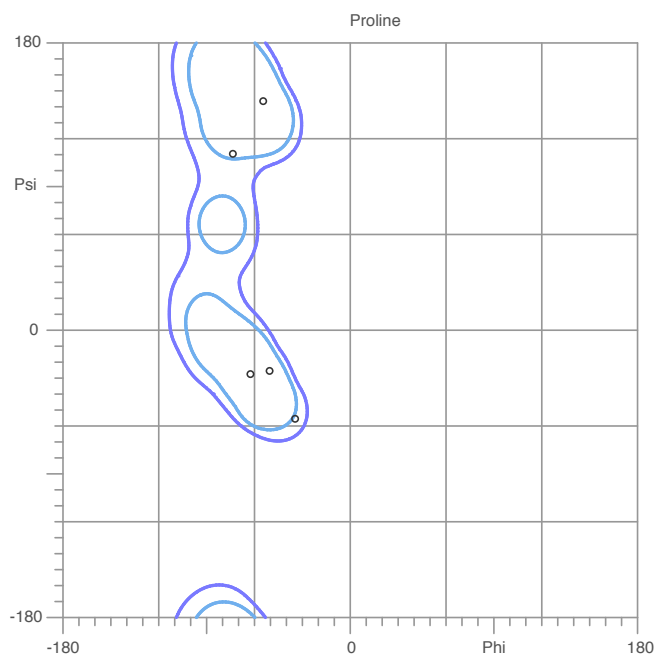
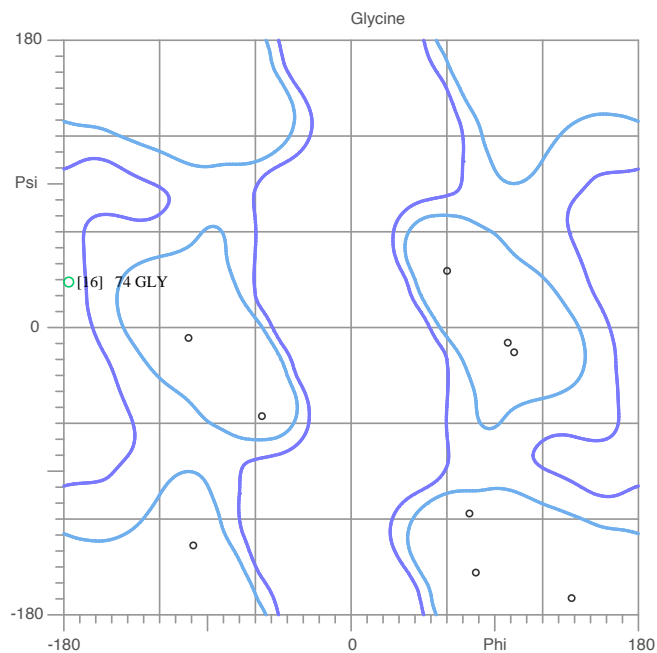
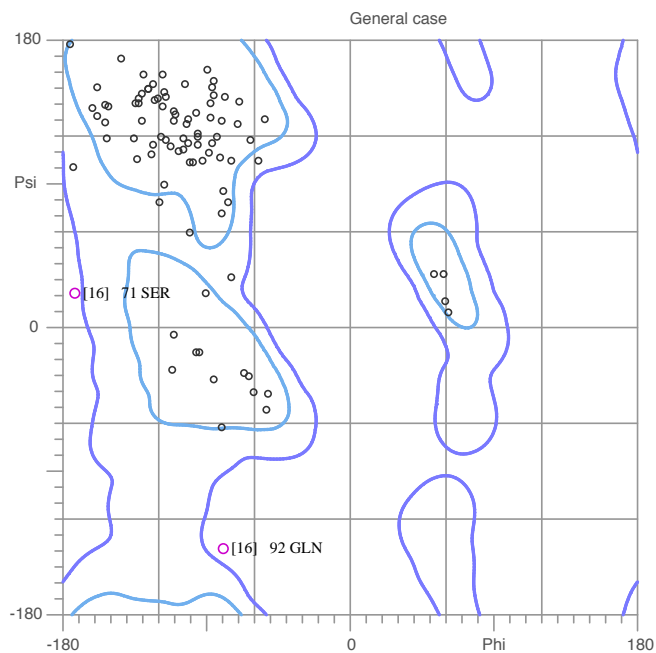
There were no outliers.

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

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 16



91.1% (102/112) of all residues were in favored (98%) regions.
97.3% (109/112) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

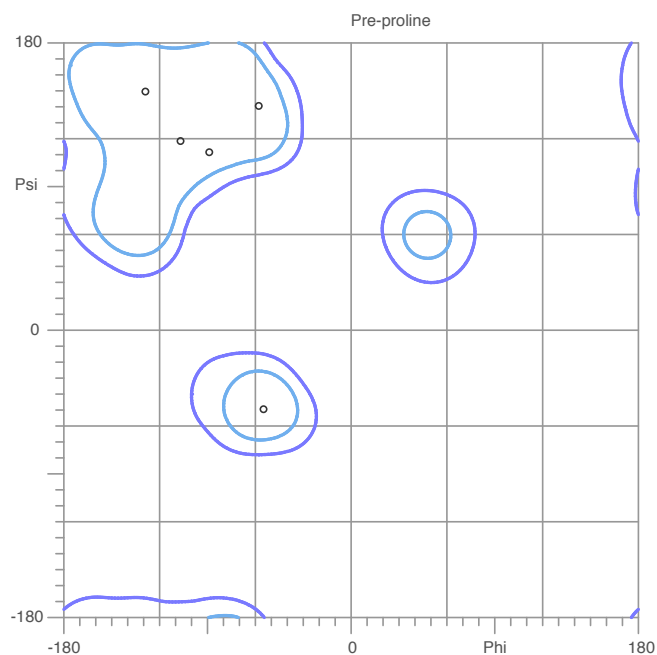
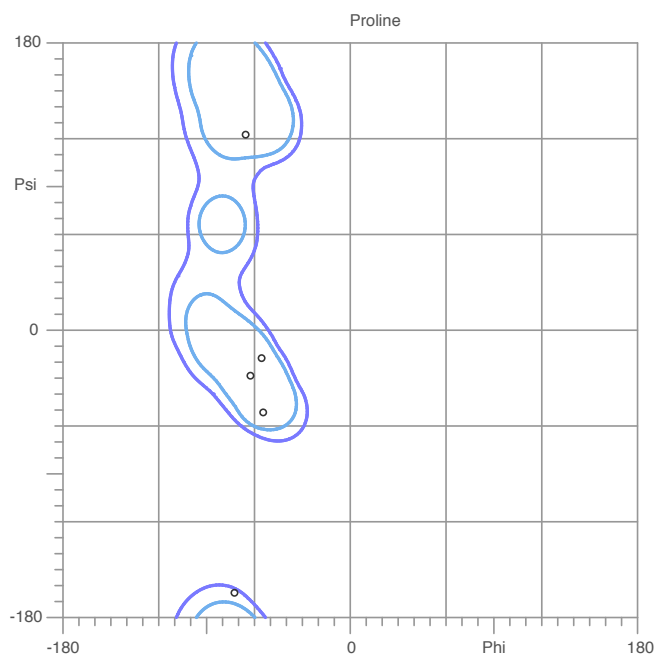
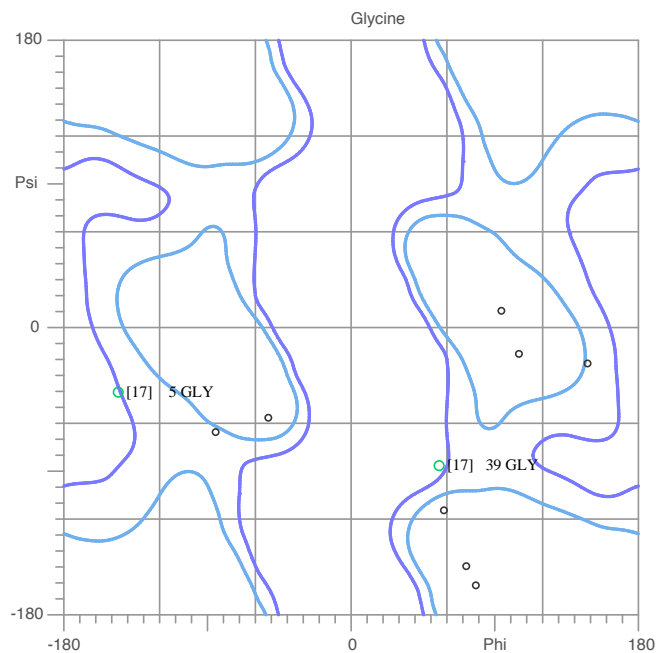
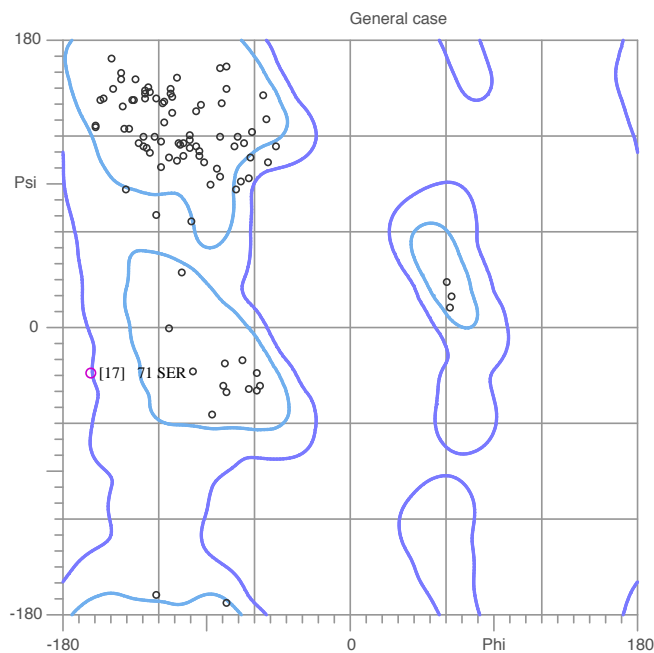
[16] 71 SER (-173.7, 22.9)

[16] 74 GLY (-177.2, 29.4)

[16] 92 GLN (-80.5, -138.8)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 17



85.7% (96/112) of all residues were in favored (98%) regions.
97.3% (109/112) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

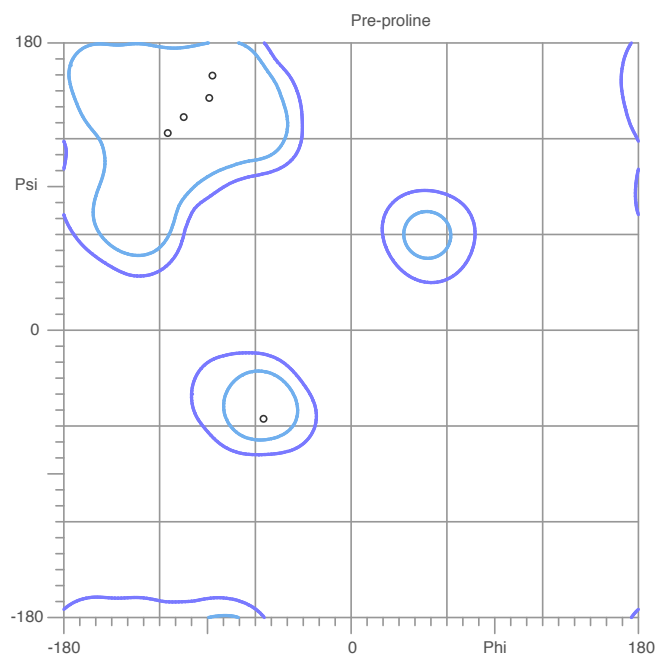
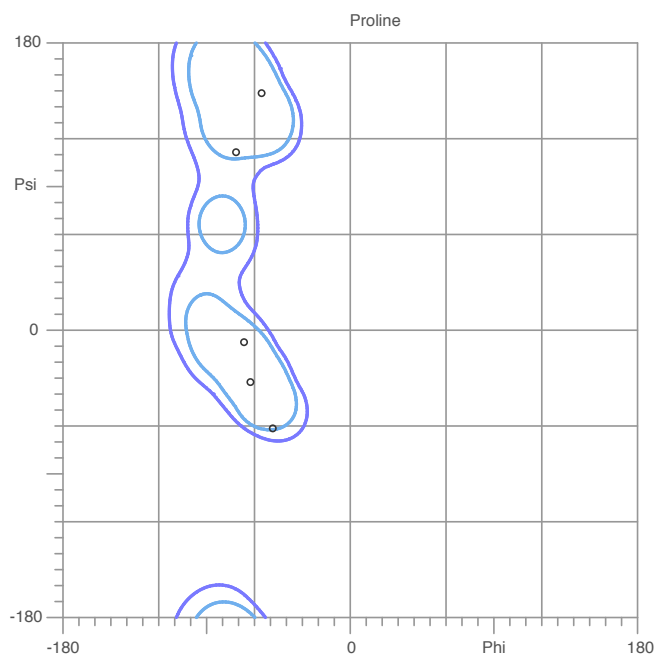
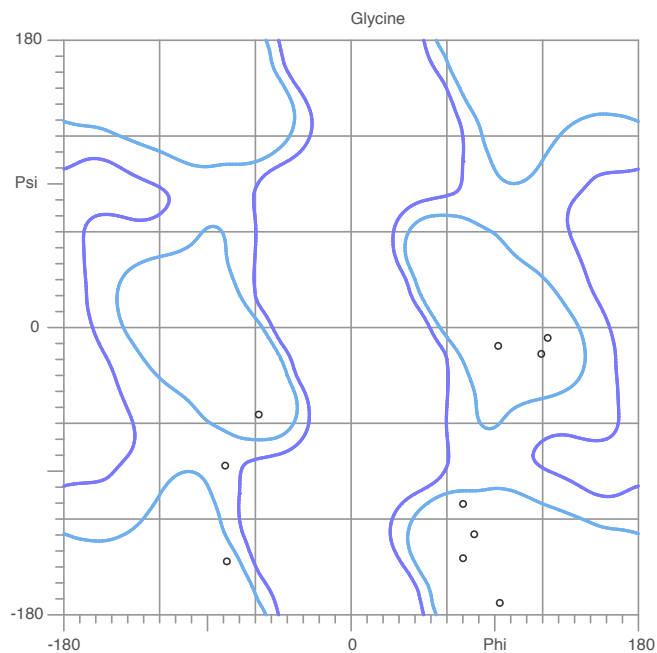
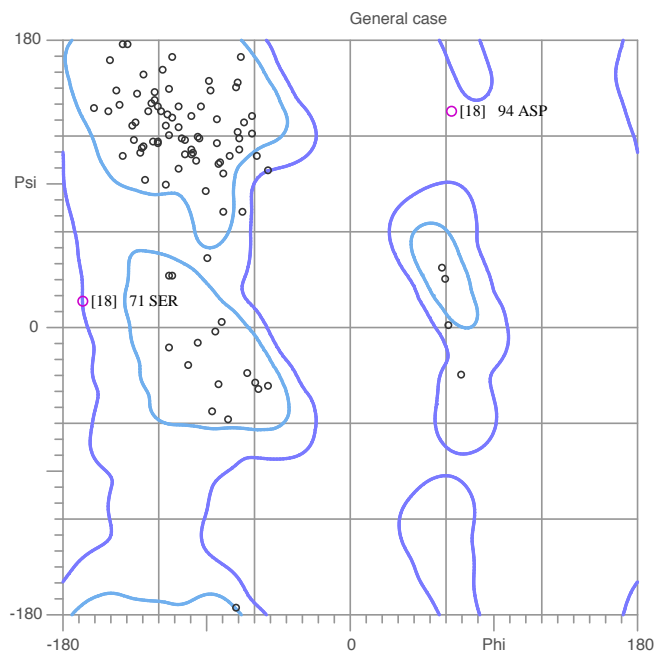
[17] 5 GLY (-146.5, -40.4)

[17] 39 GLY (55.4, -86.8)

[17] 71 SER (-163.8, -28.7)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 18

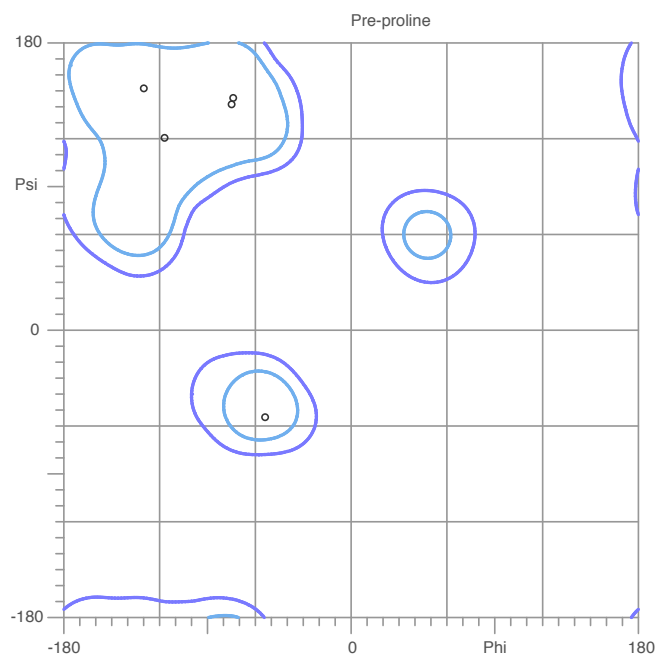
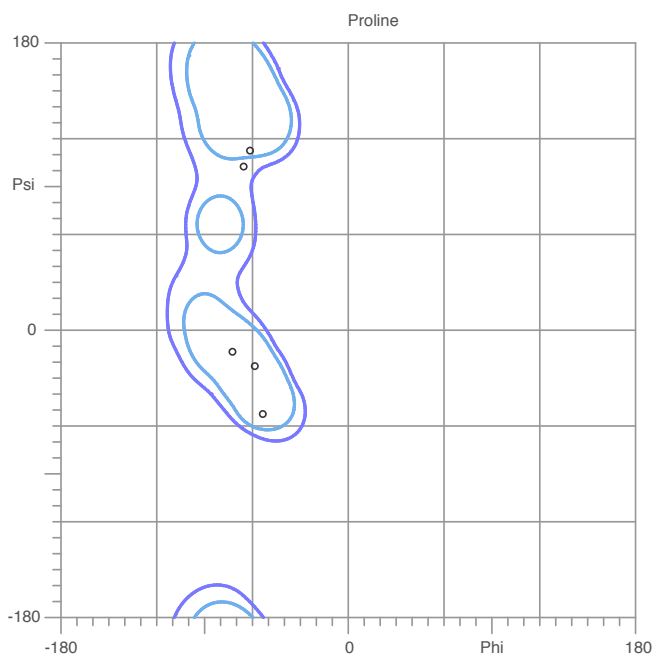
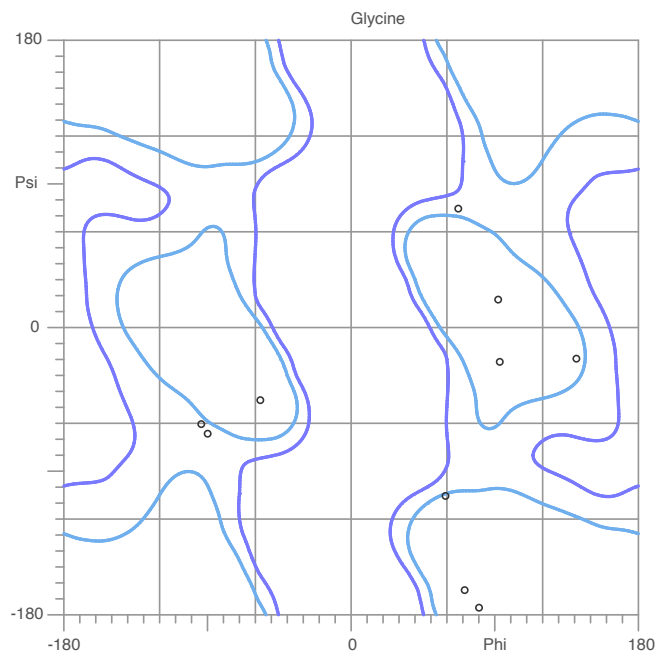
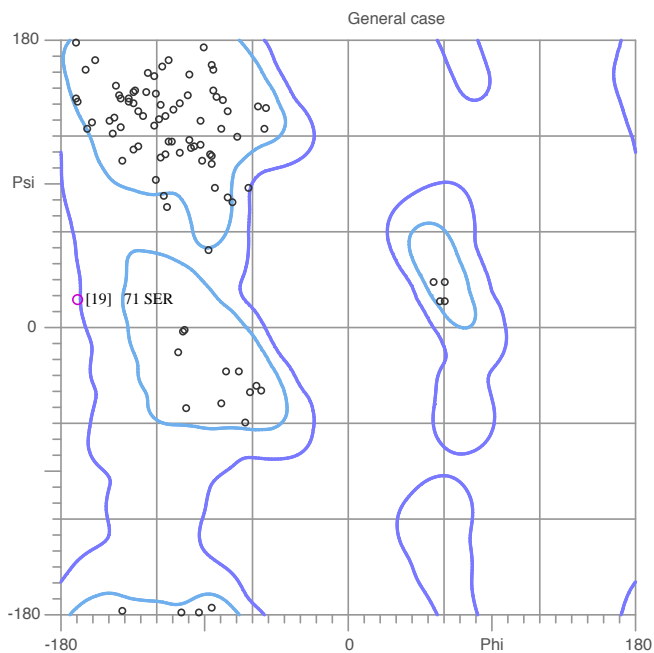


92.0% (103/112) of all residues were in favored (98%) regions.
98.2% (110/112) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[18] 71 SER (-168.4, 17.5)
[18] 94 ASP (63.6, 136.4)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 19

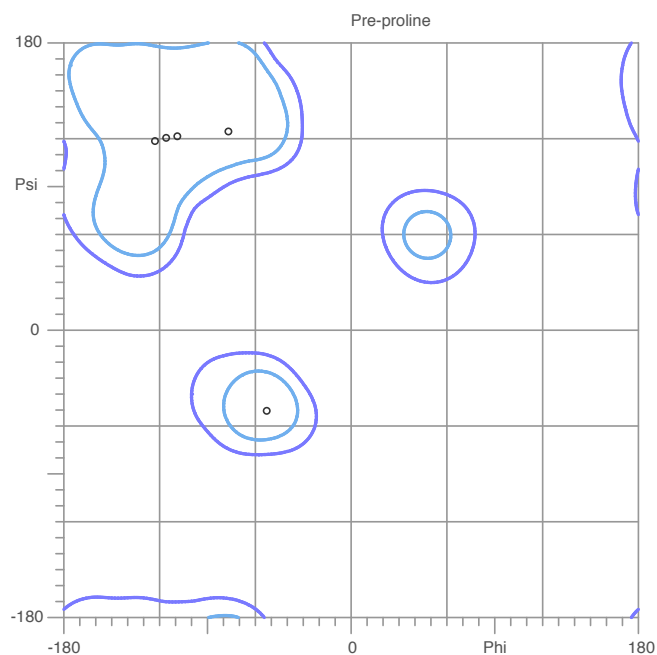
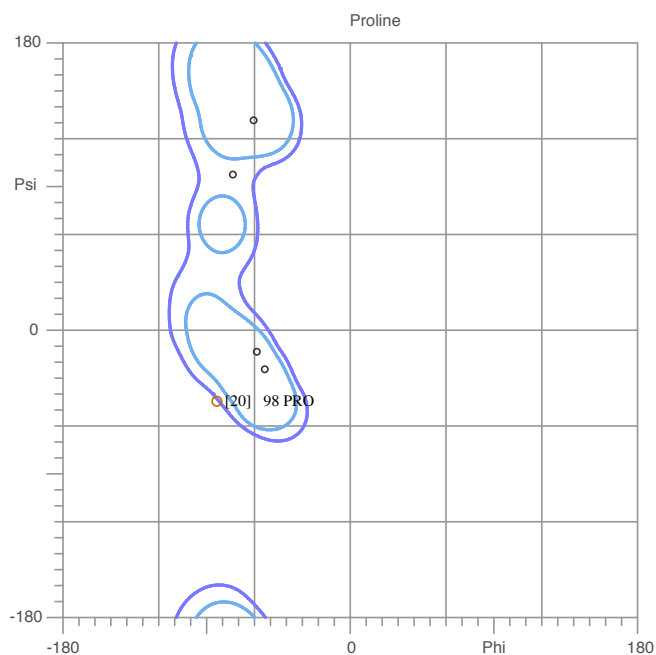
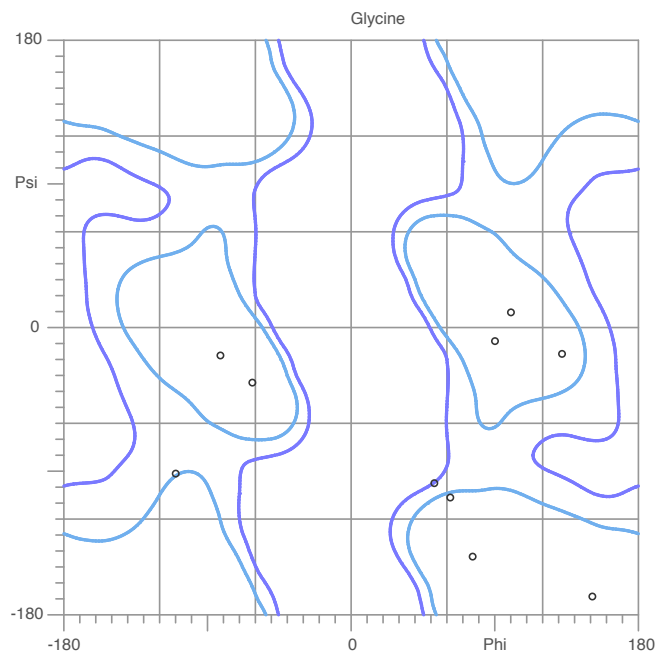
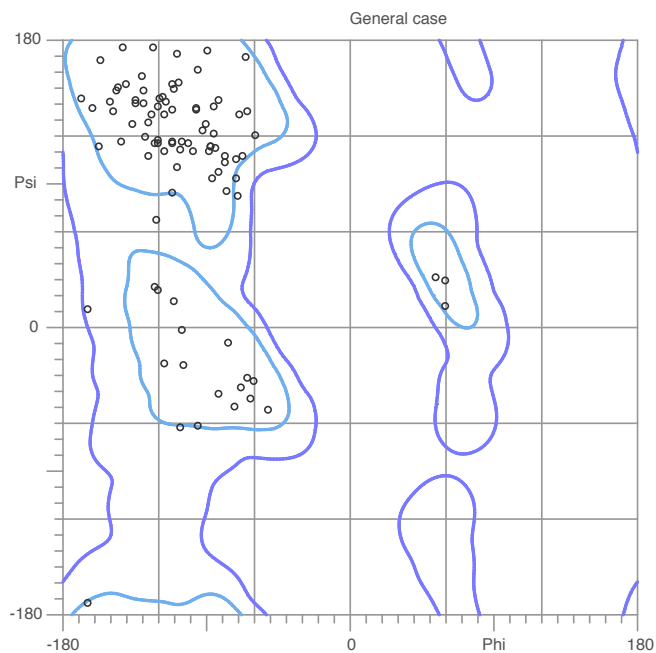


92.0% (103/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[19] 71 SER (-170.7, 19.0)

MolProbity Ramachandran analysis

LKR112_NMR_em_bcr3.pdb, model 20



92.9% (104/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 98 PRO (-84.9, -44.0)