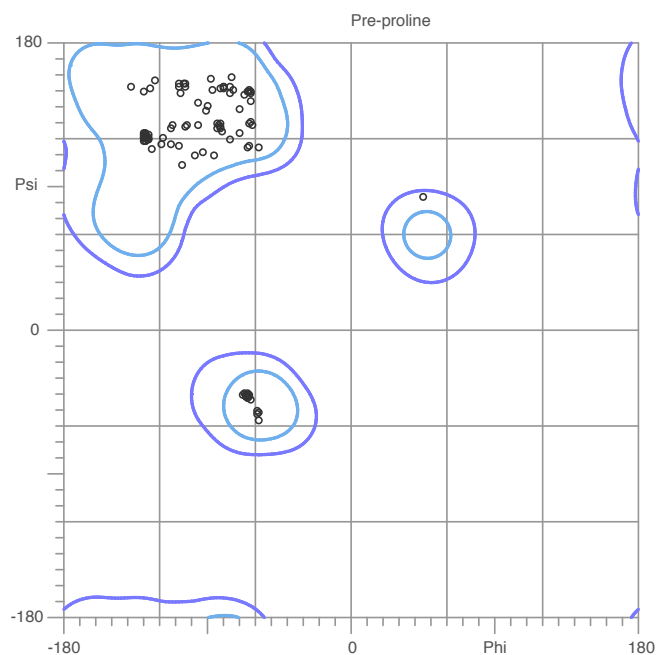
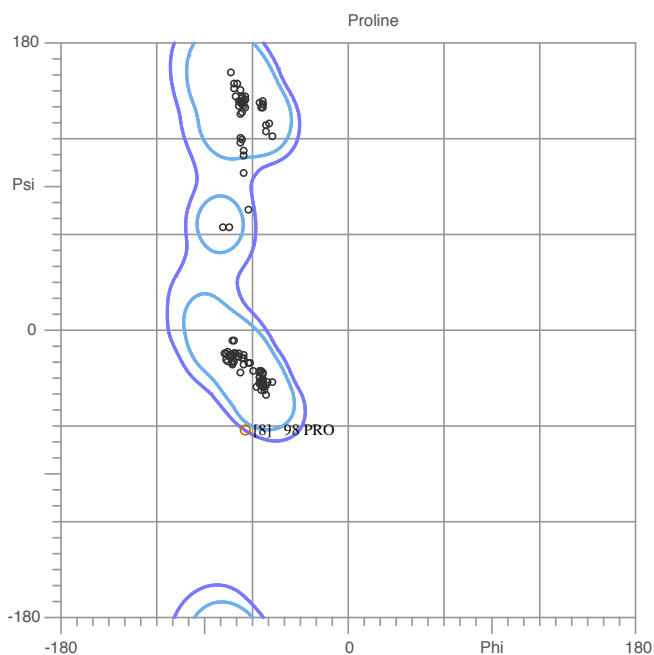
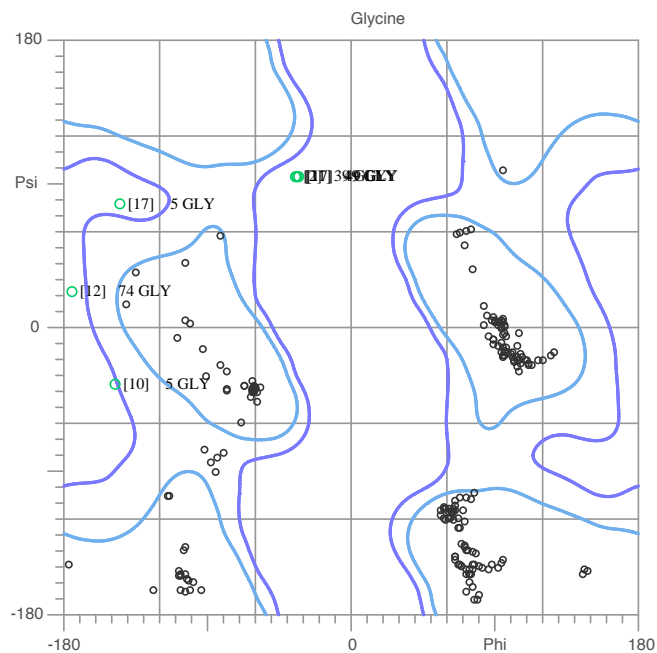
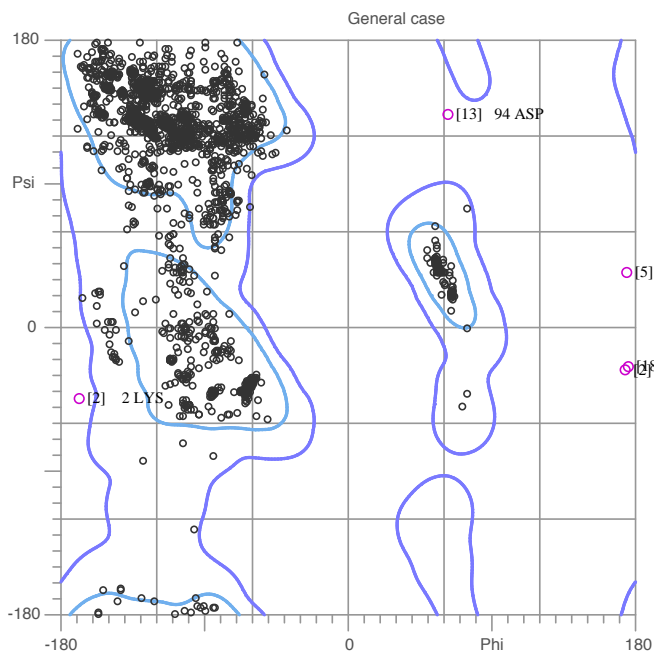


MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, all models



95.3% (2134/2240) of all residues were in favored (98%) regions.
99.5% (2228/2240) of all residues were in allowed (>99.8%) regions.

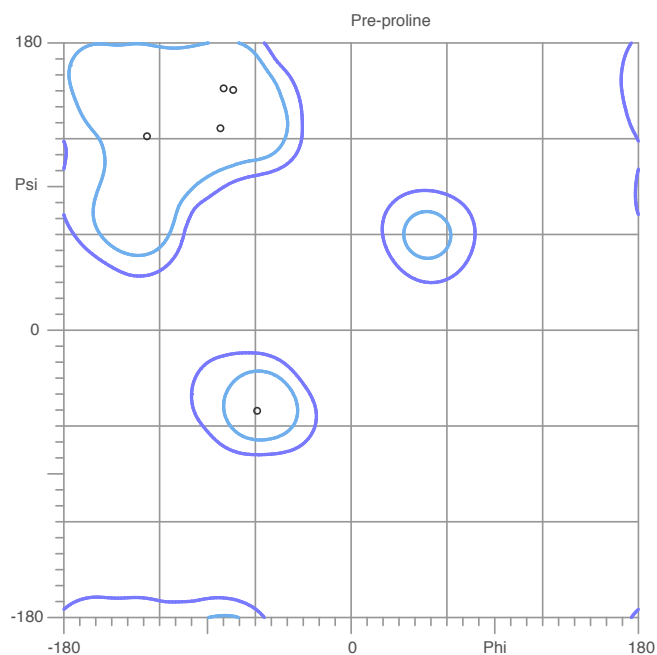
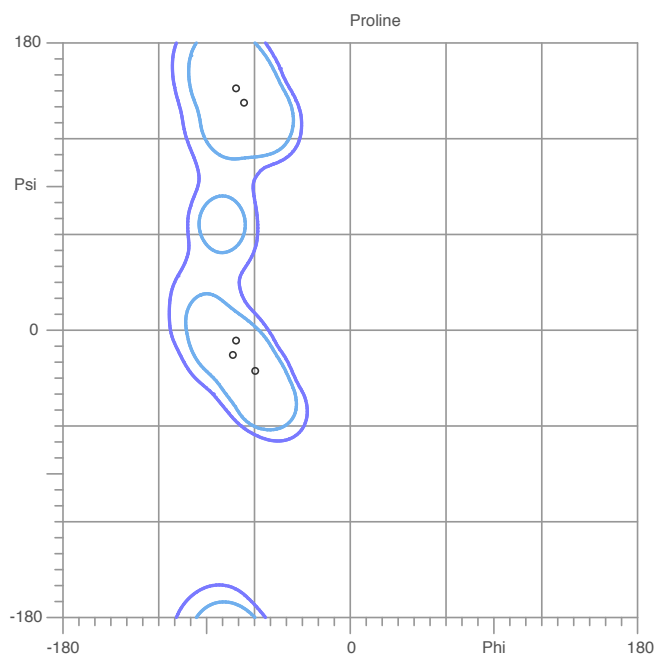
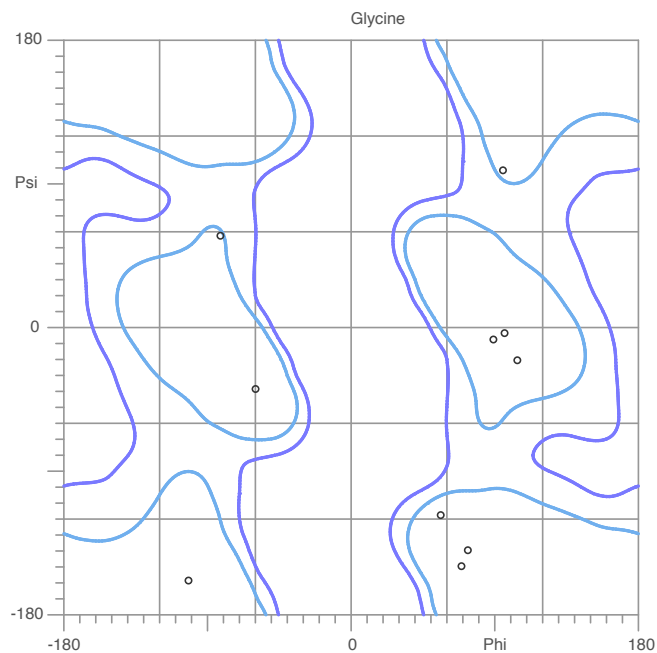
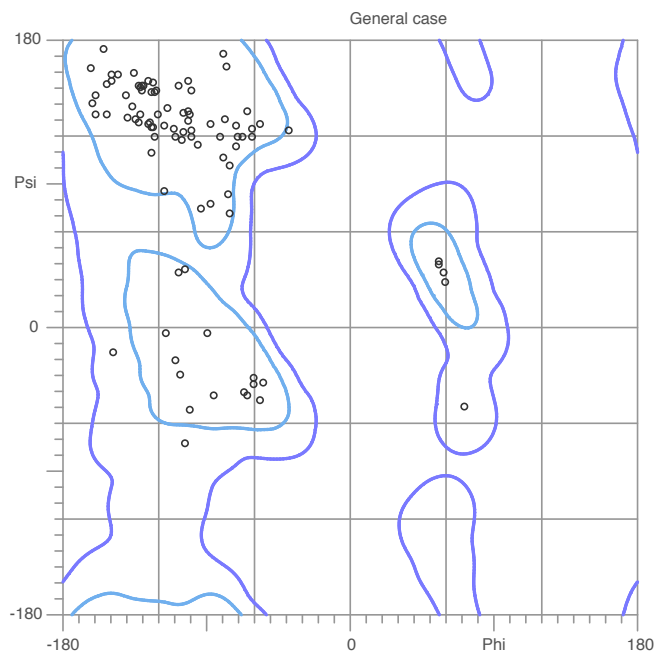
There were 12 outliers (phi, psi):

- [2] 2 LYS (-169.8, -44.9)
- [2] 39 GLY (-35.1, 95.4)
- [2] 112 HIS (173.8, -26.1)
- [5] 71 SER (175.0, 35.1)

- [8] 98 PRO (-65.8, -62.7)
- [10] 5 GLY (-148.4, -35.0)
- [11] 49 GLY (-34.9, 95.0)
- [12] 74 GLY (-175.2, 23.7)
- [13] 94 ASP (62.2, 134.7)
- [17] 5 GLY (-145.2, 78.7)
- [17] 49 GLY (-33.7, 95.1)
- [18] 100 THR (175.1, -25.0)

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 1



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.

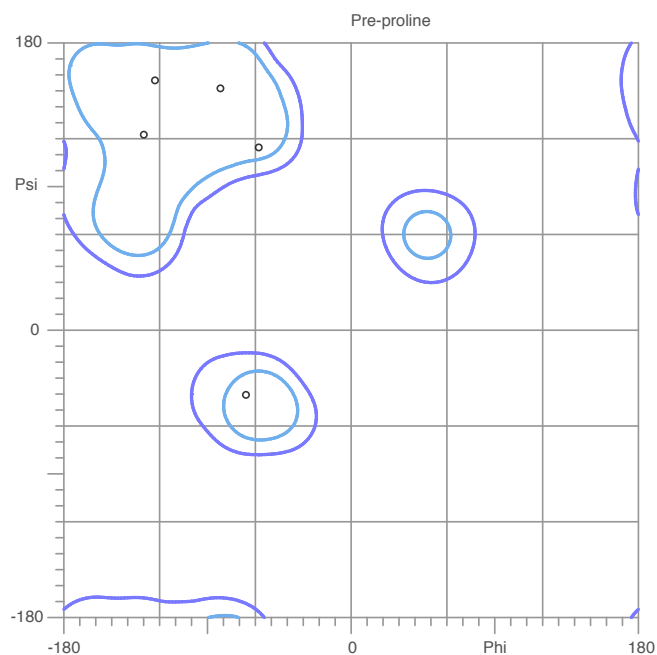
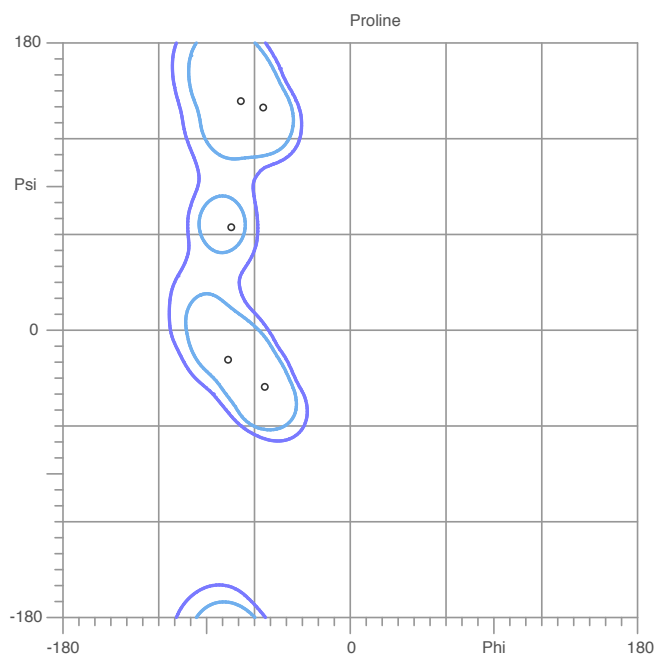
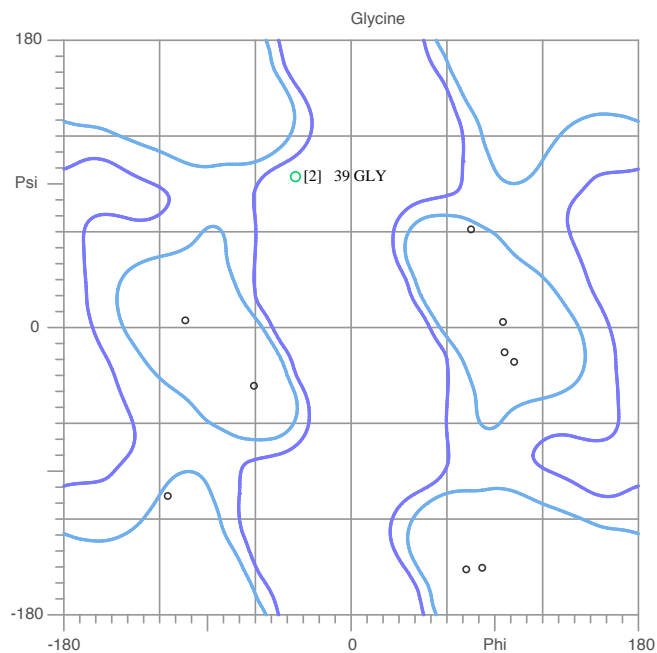
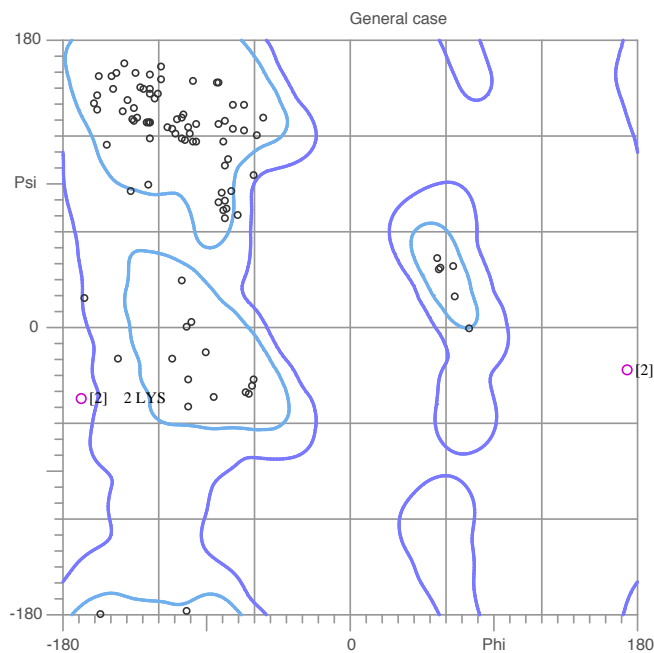
There were no outliers.

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MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 2



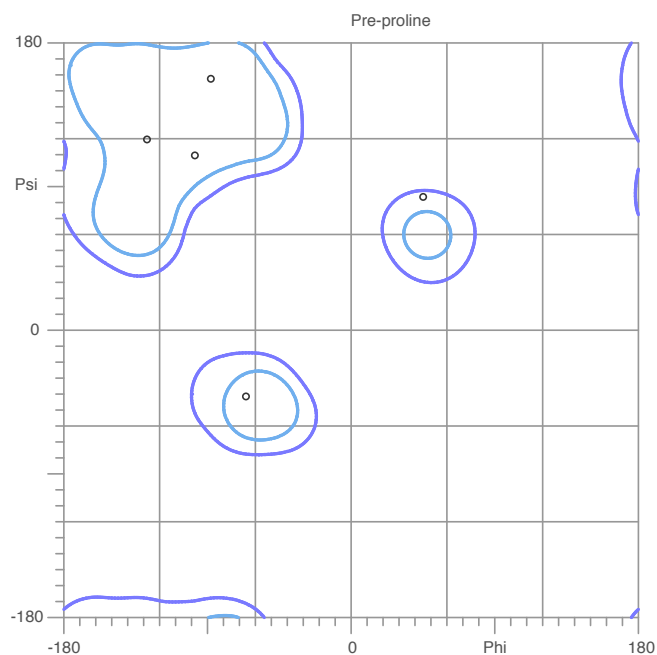
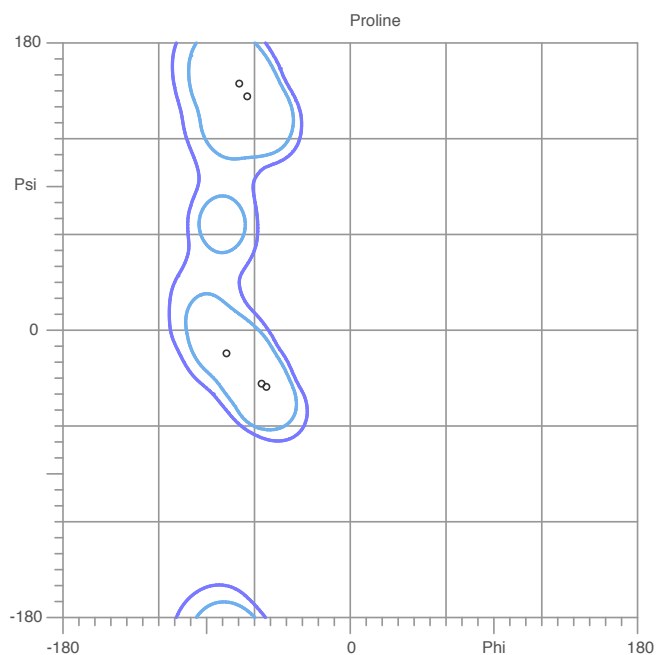
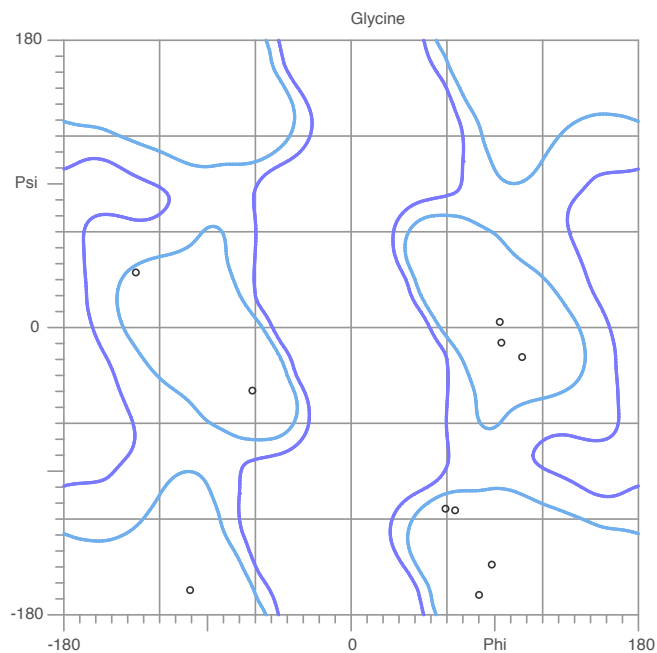
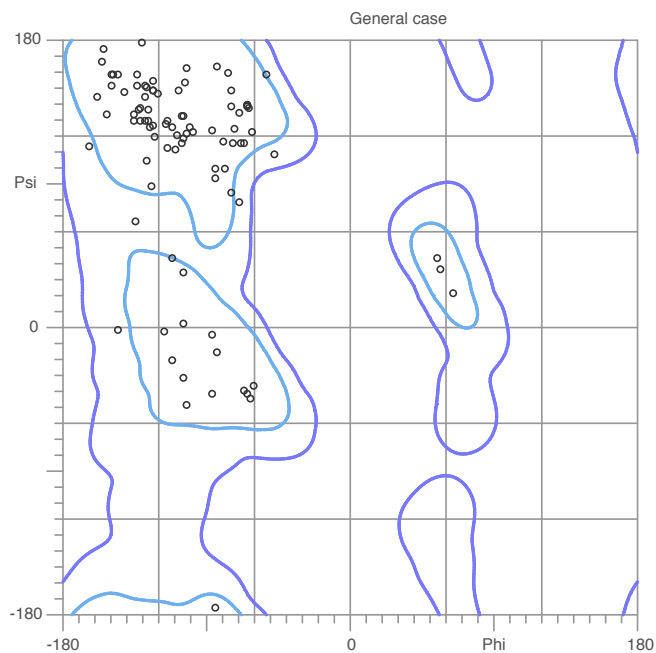
92.9% (104/112) of all residues were in favored (98%) regions.
97.3% (109/112) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 2 LYS (-169.8, -44.9)
- [2] 39 GLY (-35.1, 95.4)
- [2] 112 HIS (173.8, -26.1)

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 3

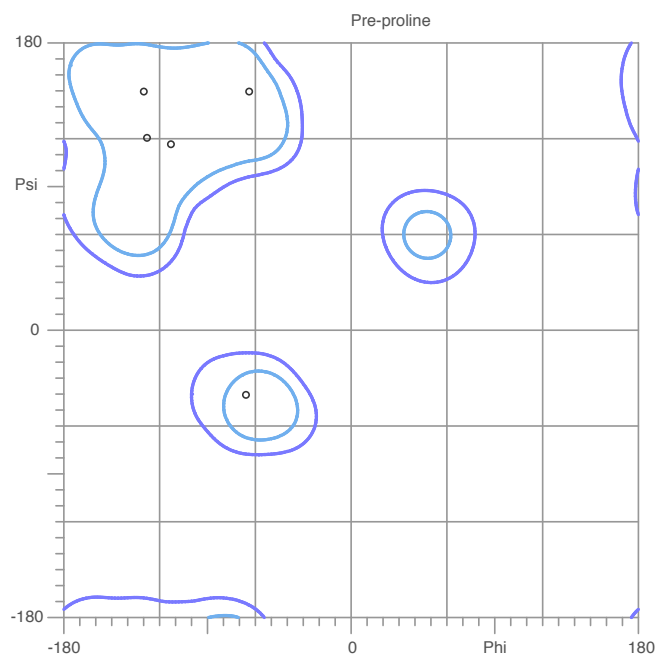
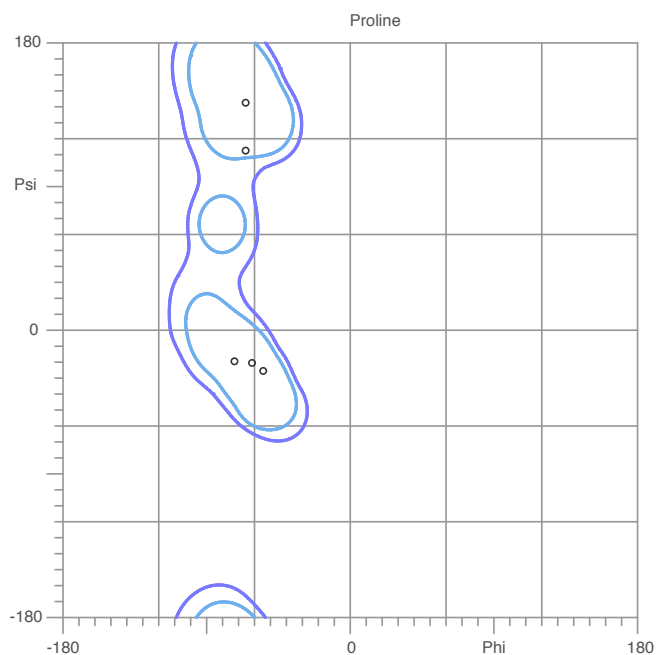
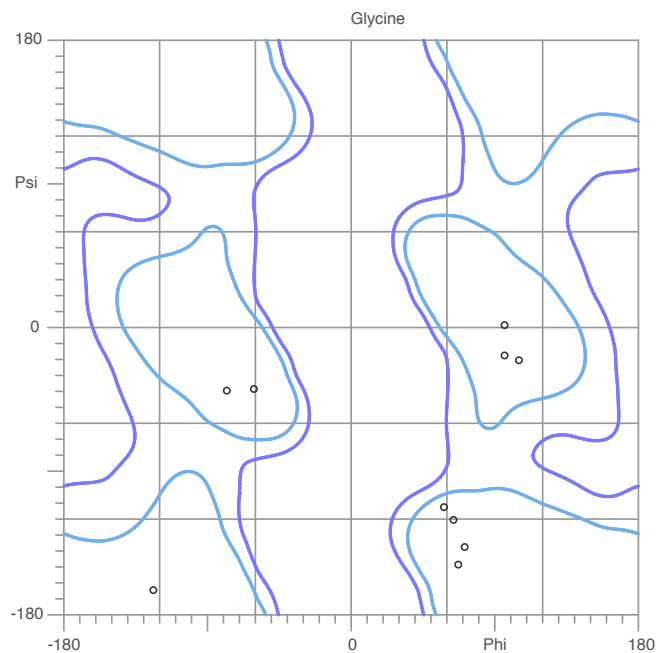
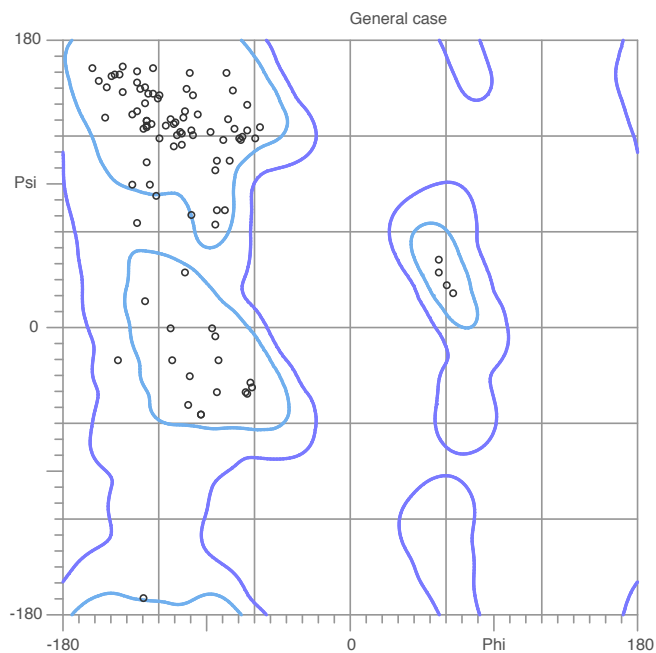


92.9% (104/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

LKR112_R3Cons_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.

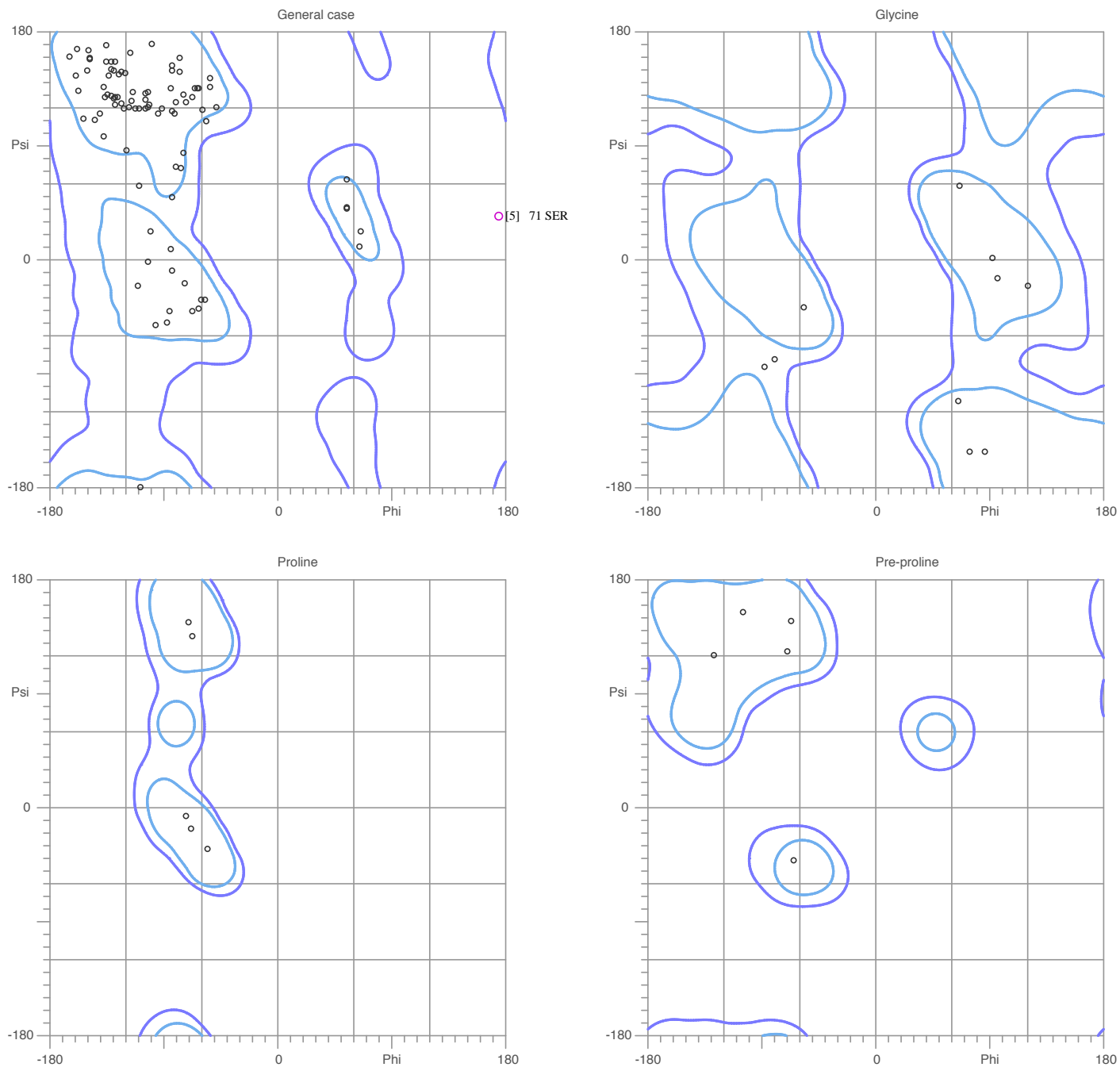
There were no outliers.

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MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 5



93.8% (105/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

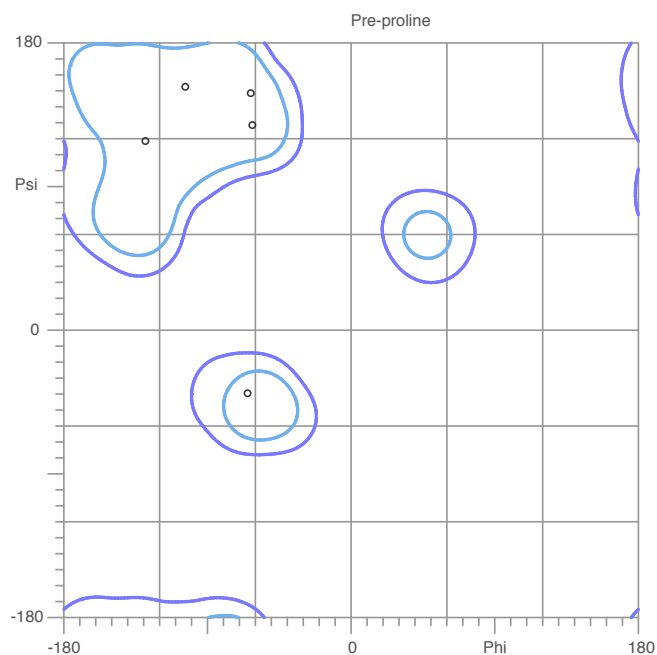
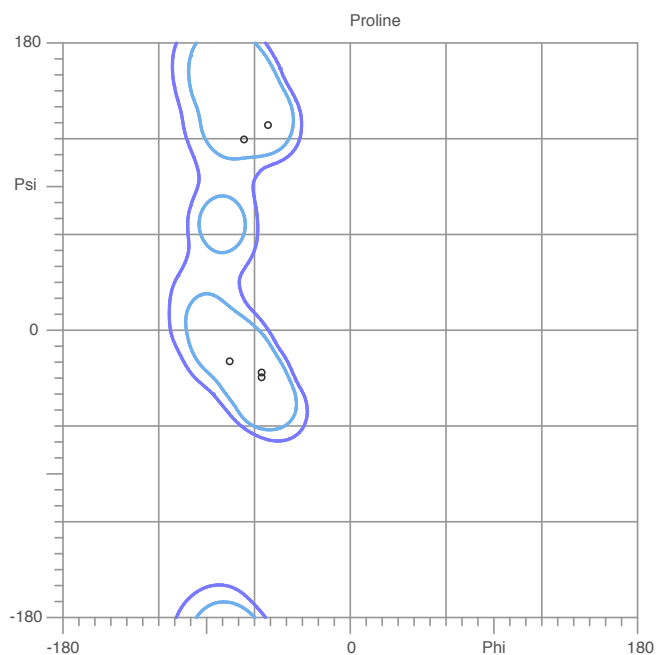
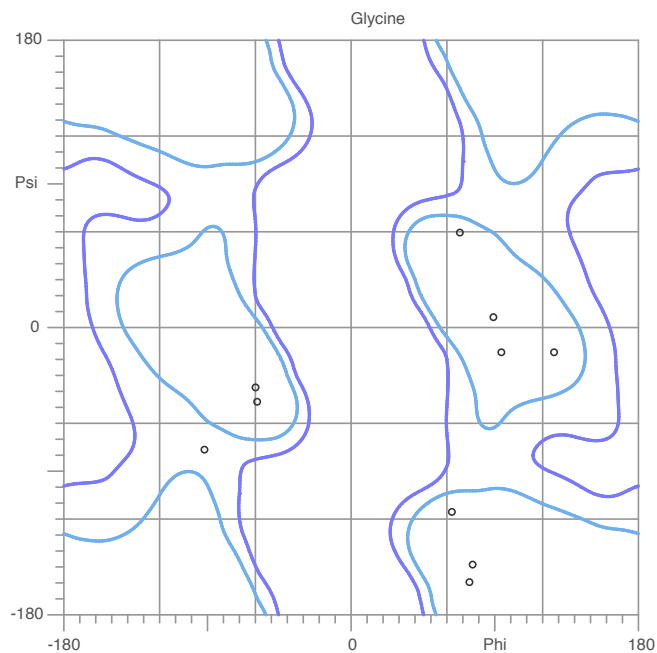
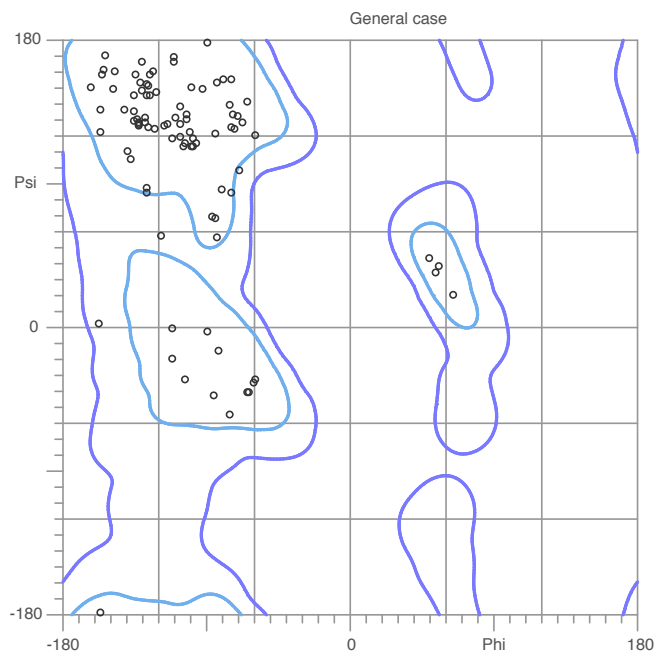
There were 1 outliers (phi, psi):
[5] 71 SER (175.0, 35.1)

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MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 6



97.3% (109/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

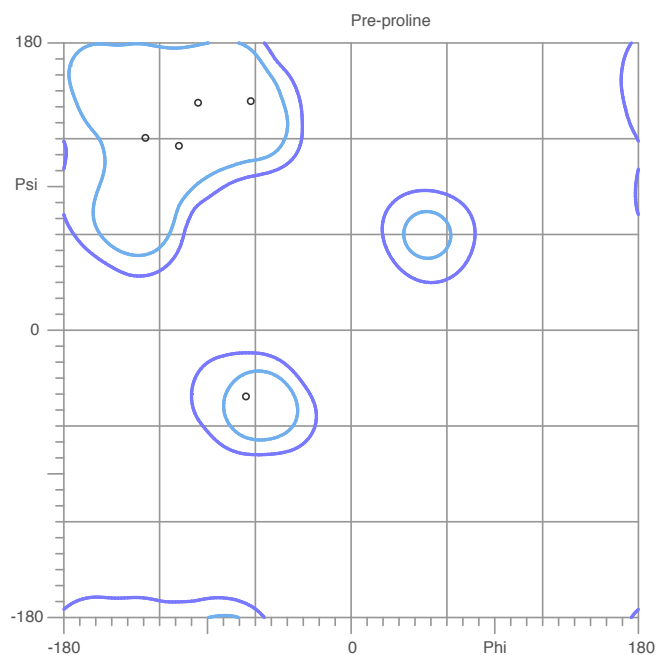
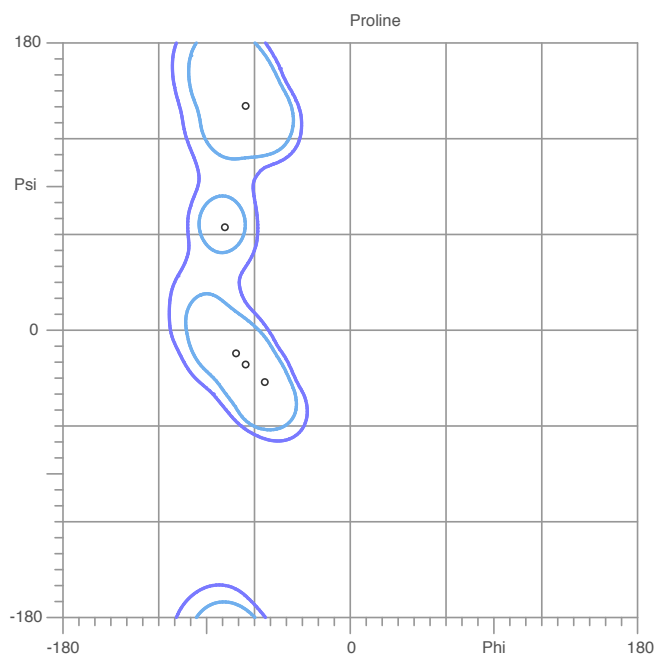
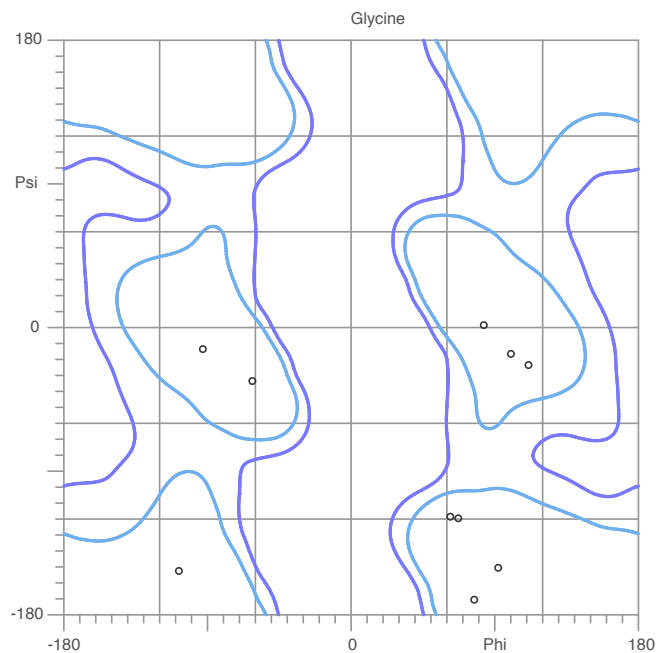
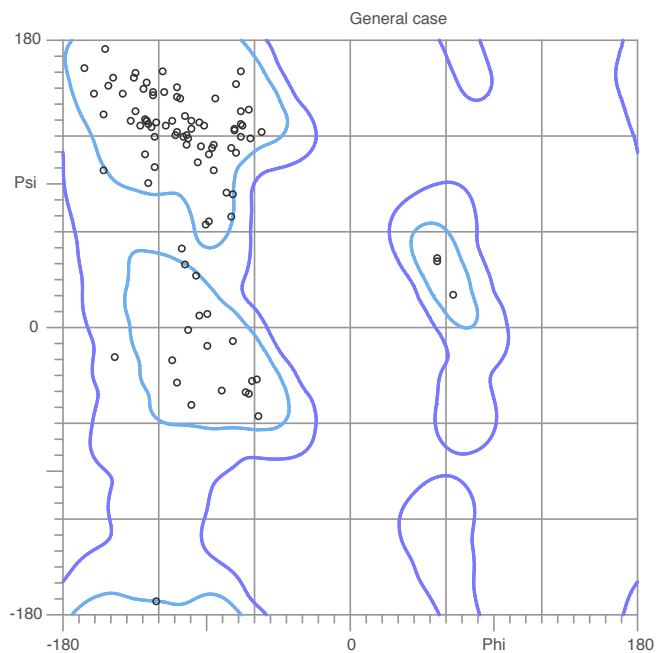
There were no outliers.

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

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MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 7

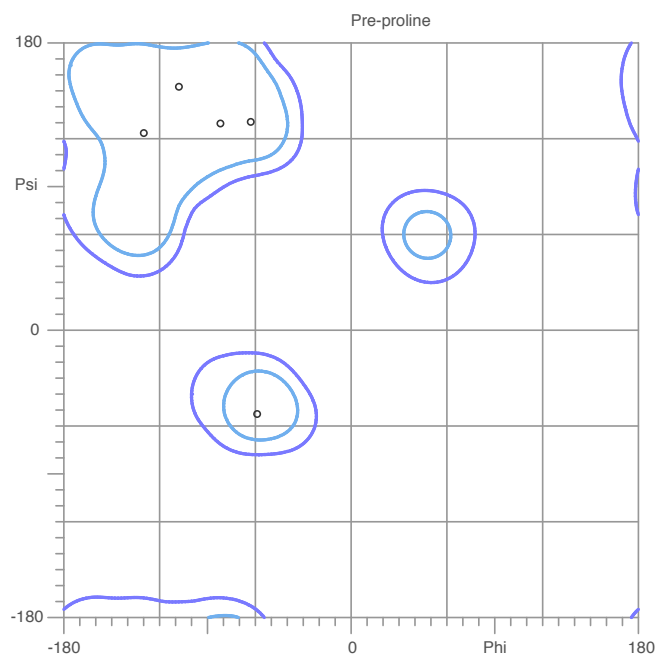
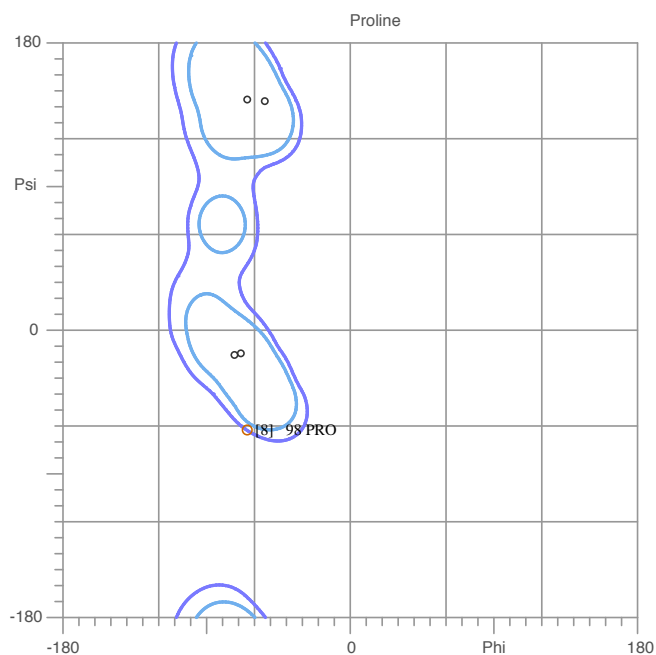
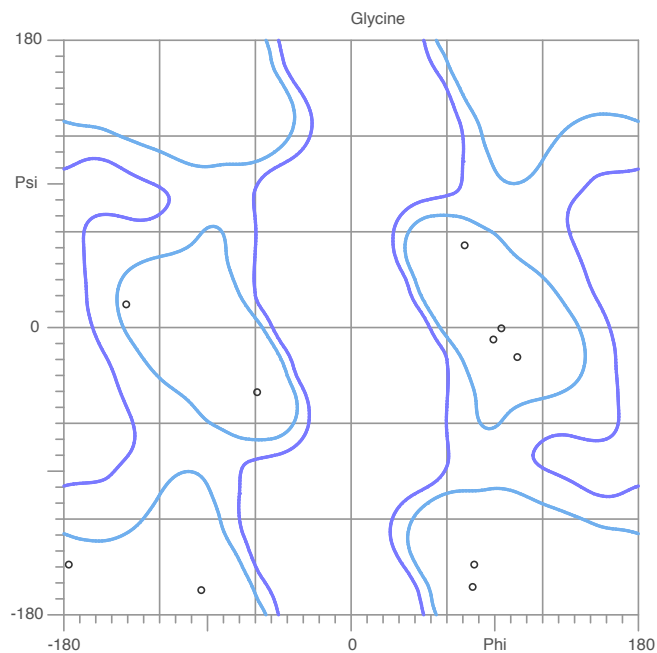
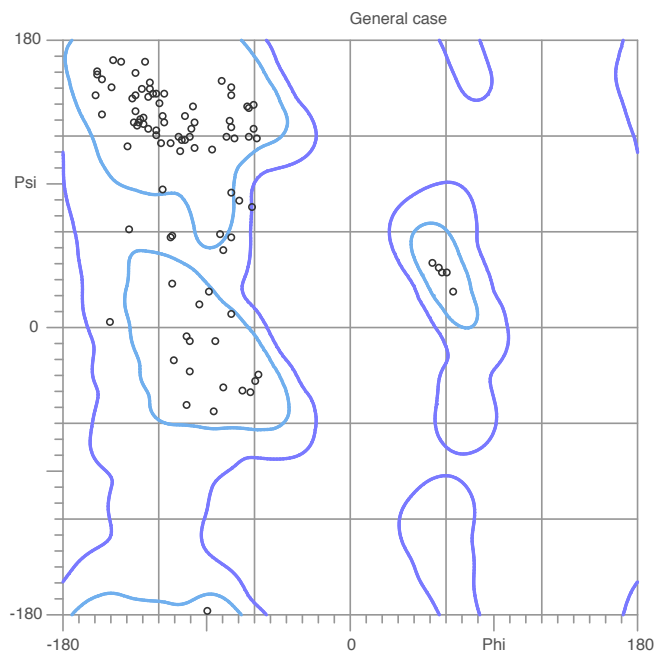


96.4% (108/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 8

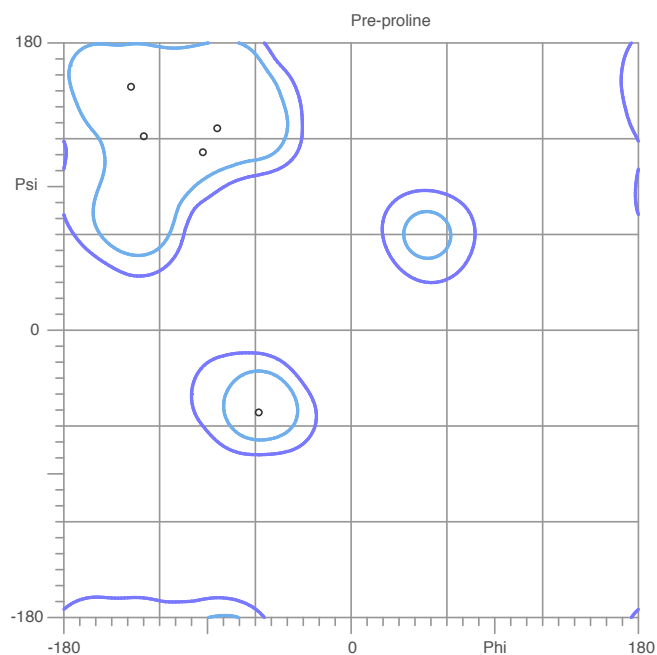
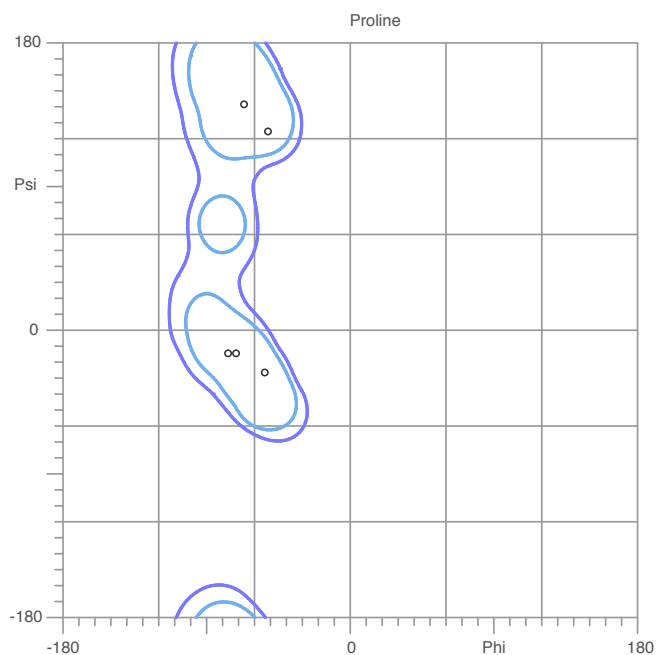
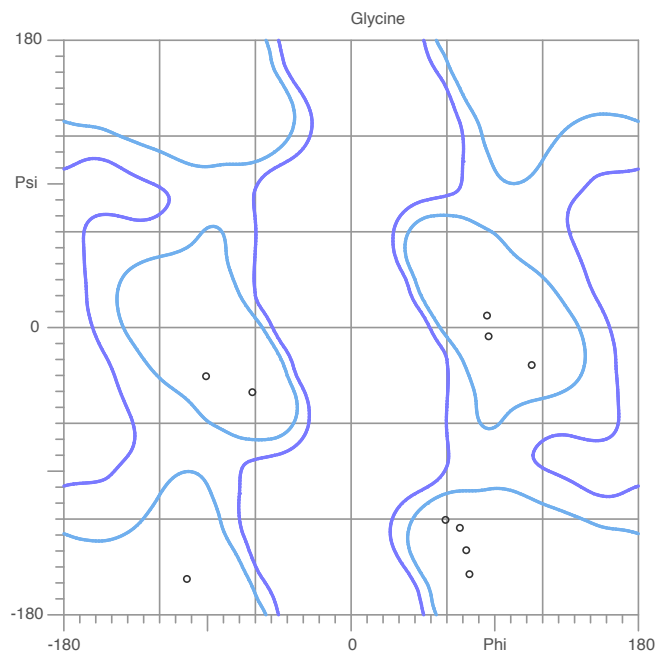
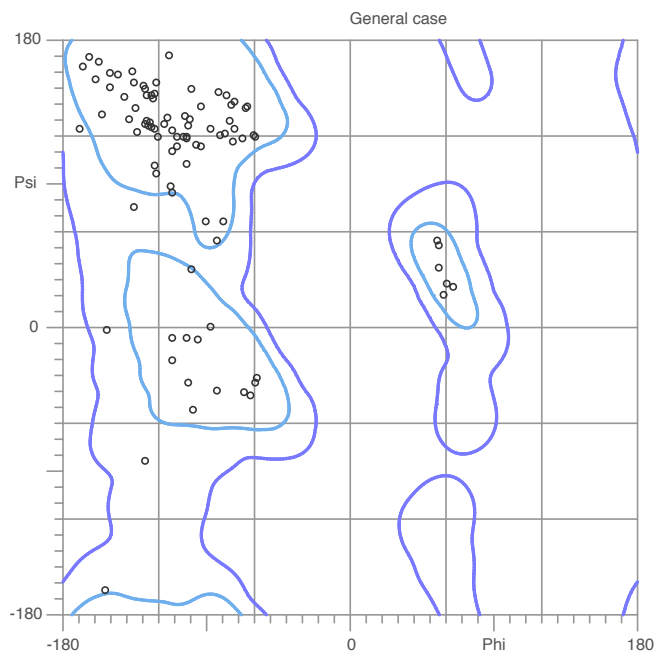


92.0% (103/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 98 PRO (-65.8, -62.7)

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 9



95.5% (107/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

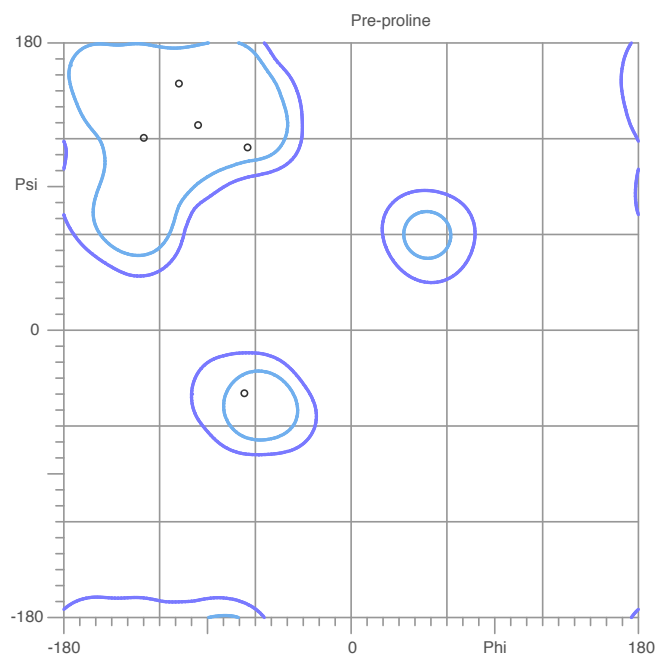
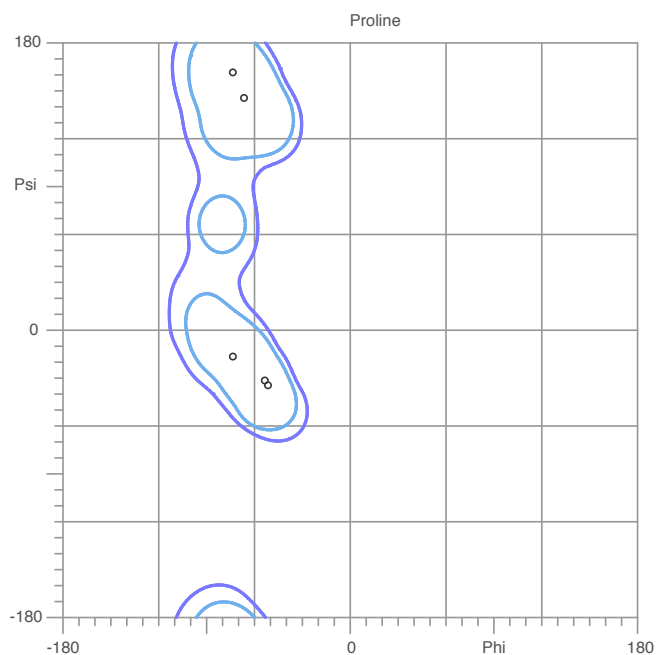
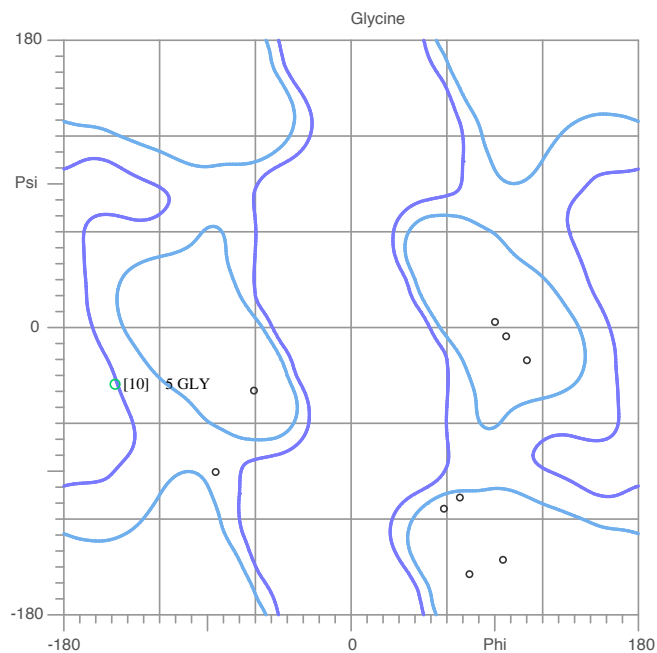
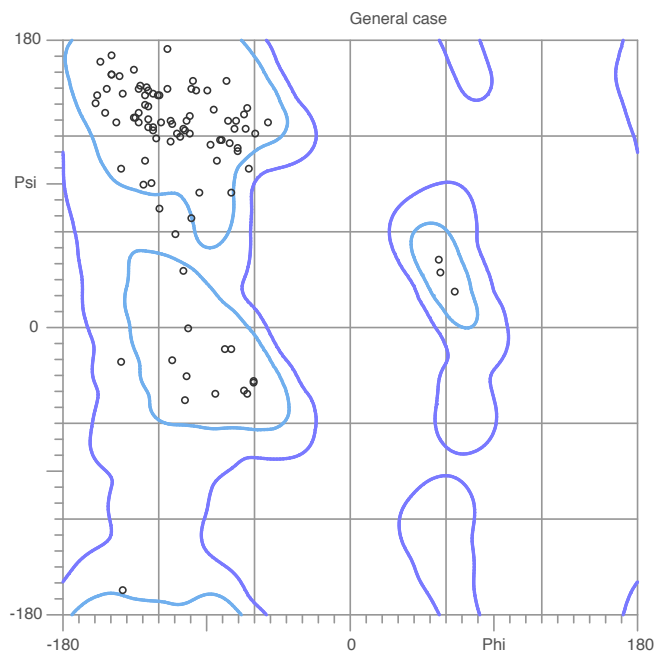
There were no outliers.

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MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 10

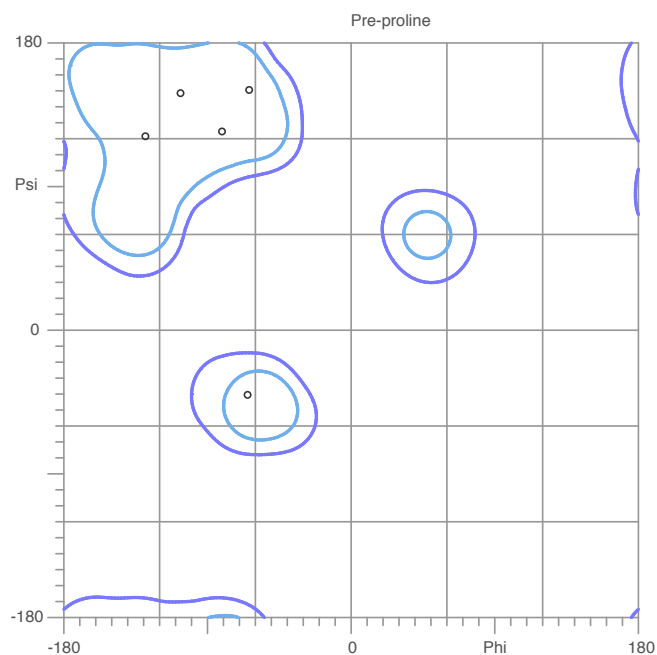
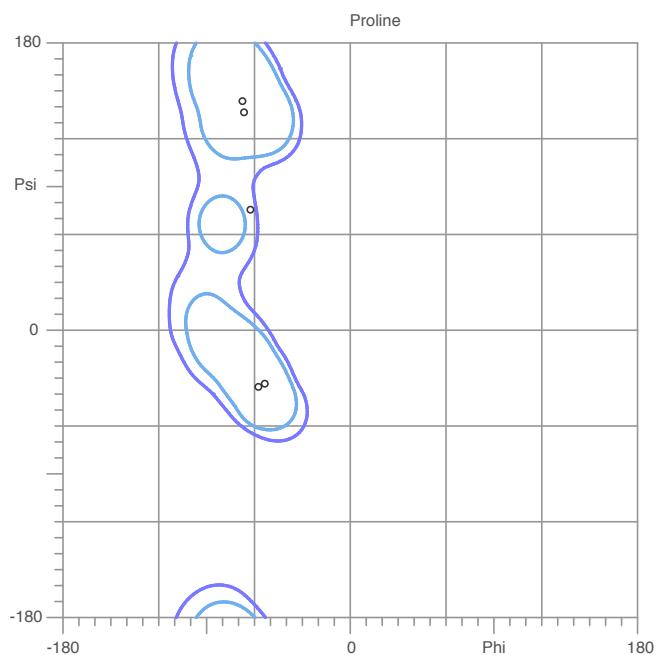
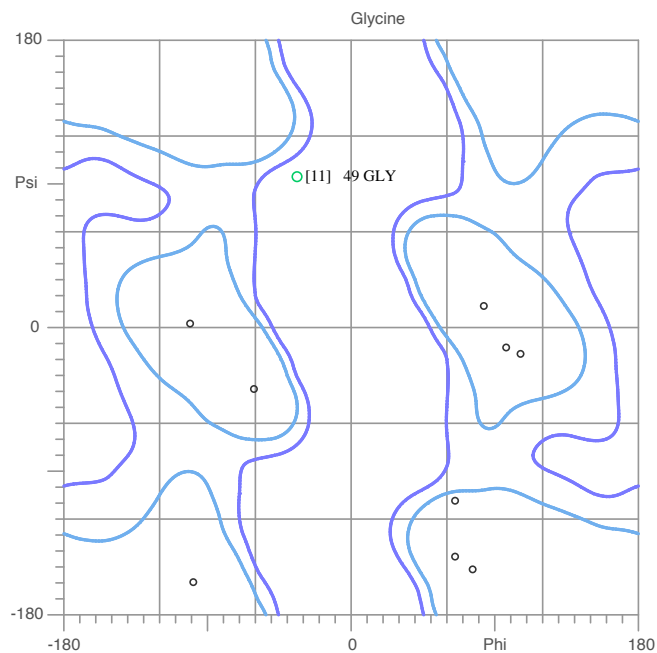
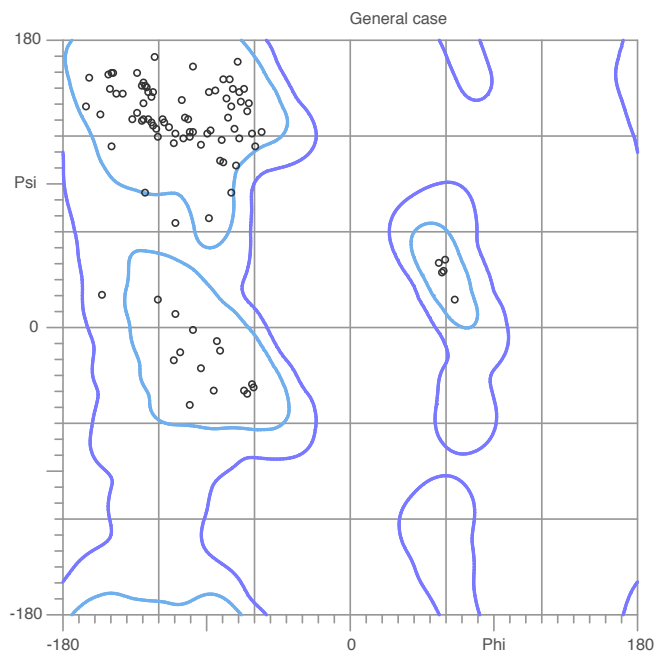


92.9% (104/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[10] 5 GLY (-148.4, -35.0)

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 11



96.4% (108/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

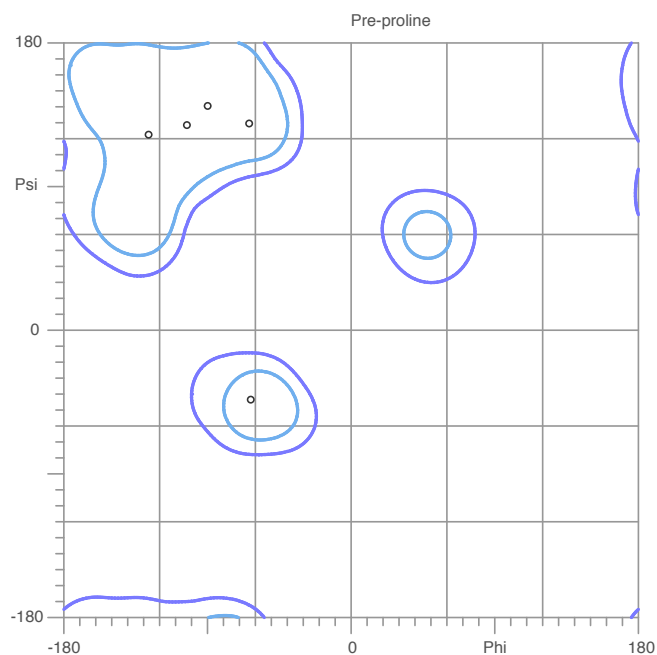
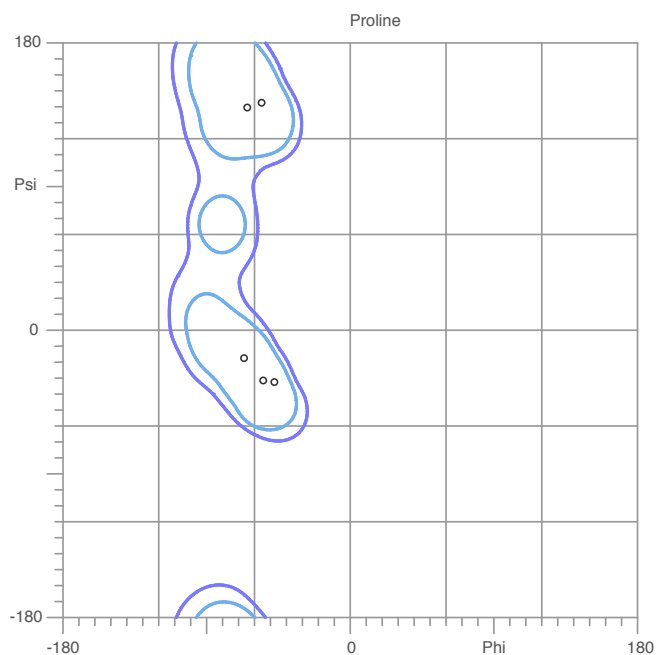
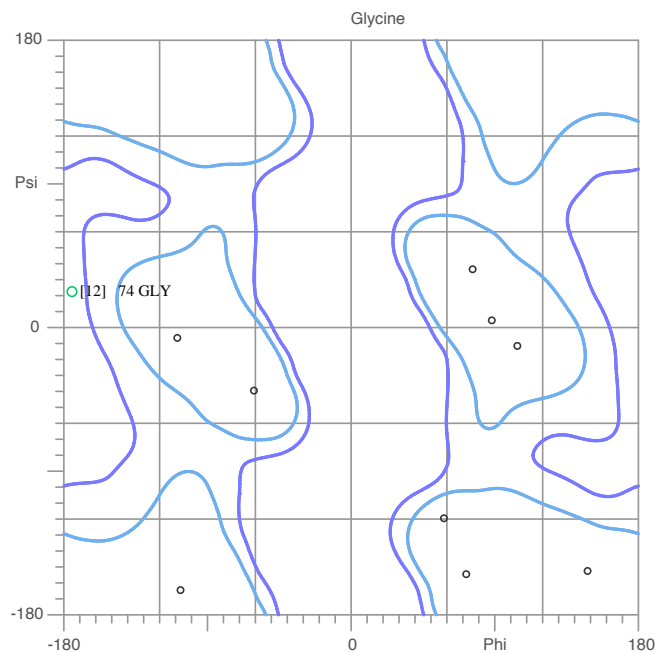
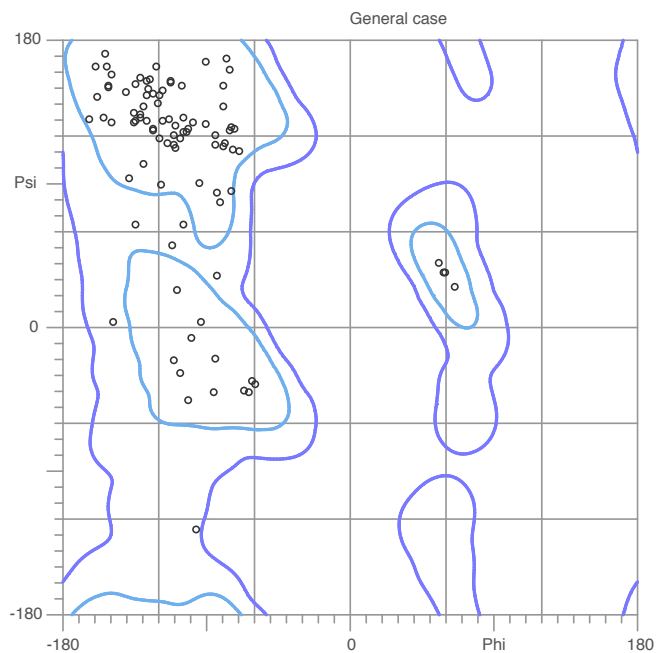
There were 1 outliers (phi, psi):
[11] 49 GLY (-34.9, 95.0)

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MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 12



93.8% (105/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

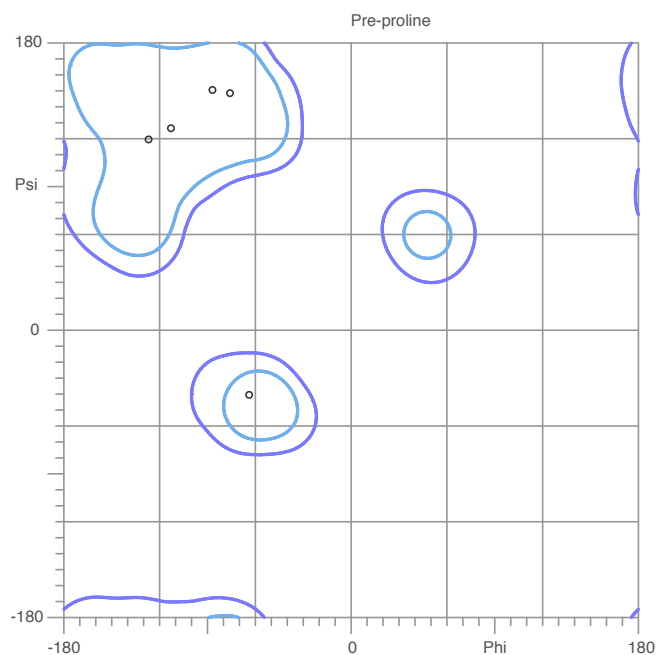
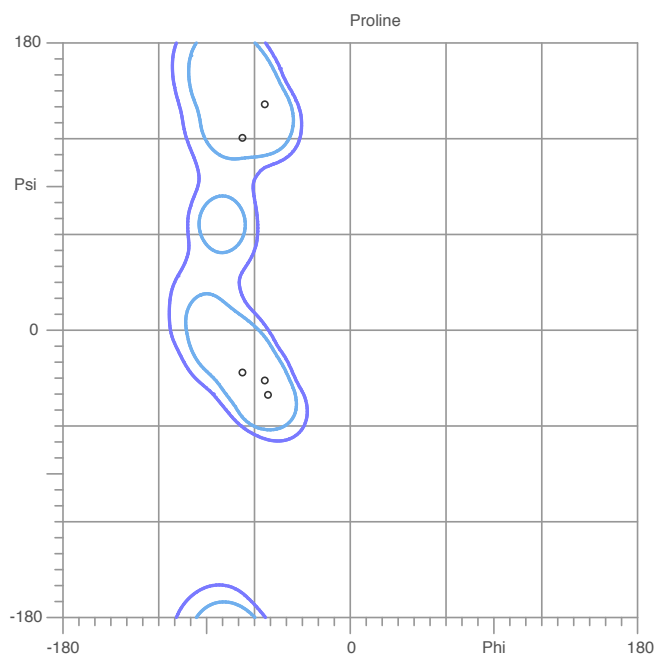
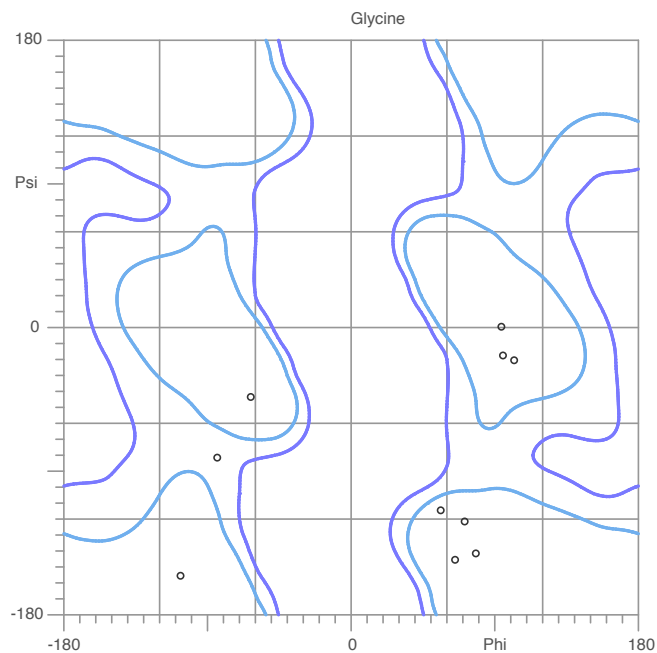
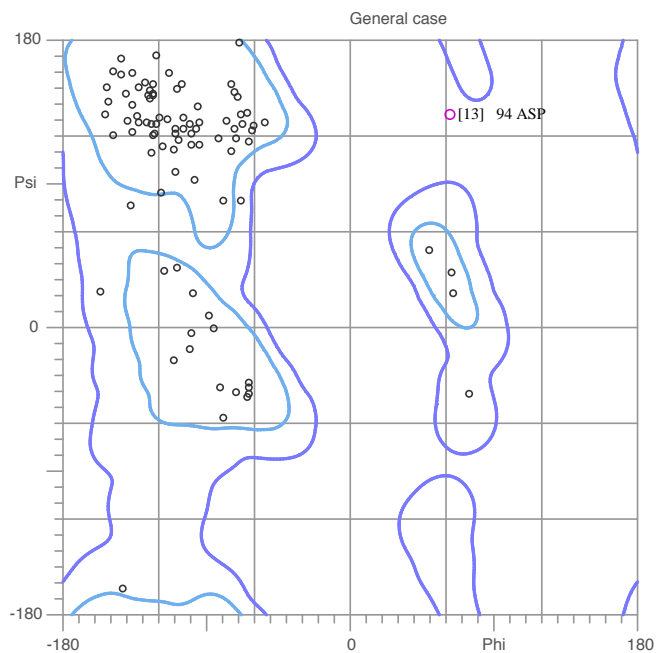
There were 1 outliers (phi, psi):
[12] 74 GLY (-175.2, 23.7)

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MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 13



93.8% (105/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

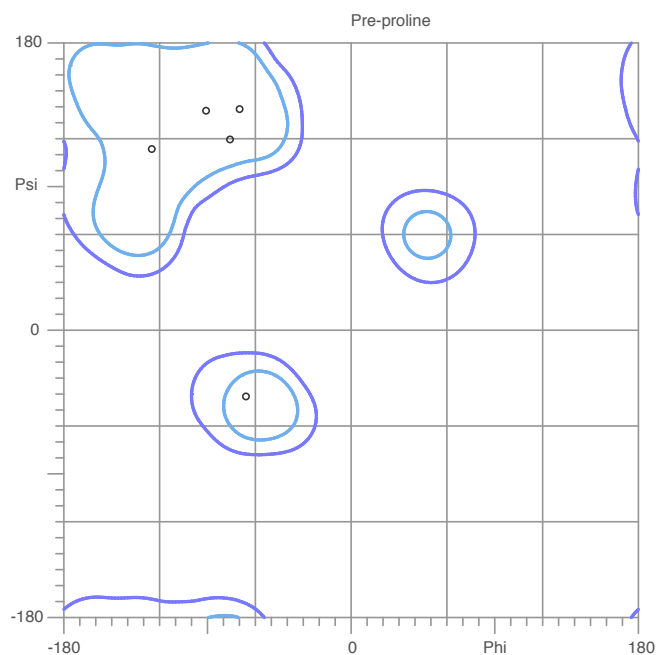
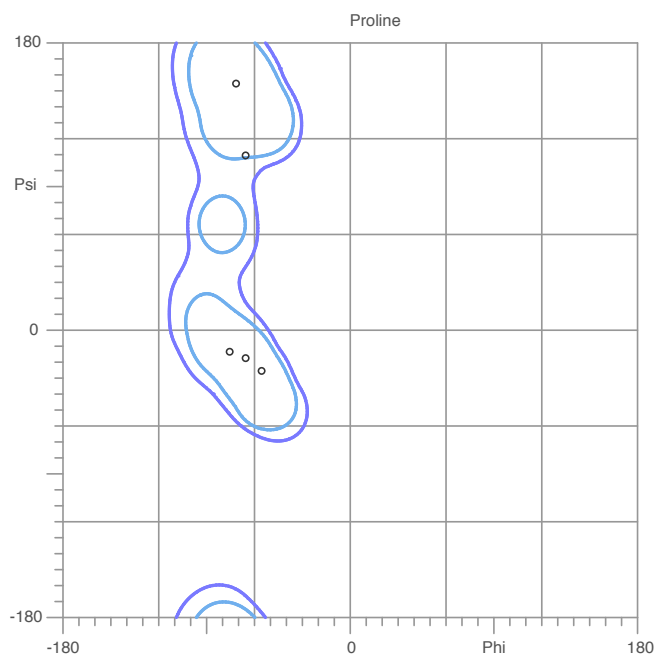
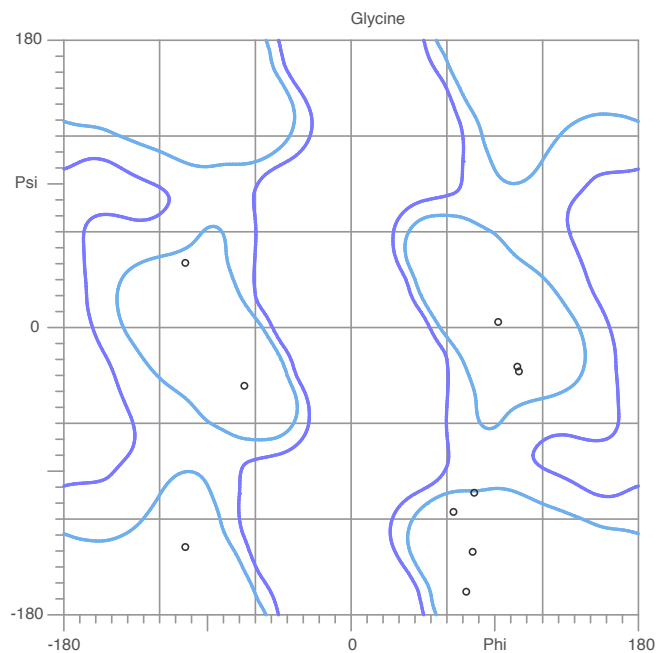
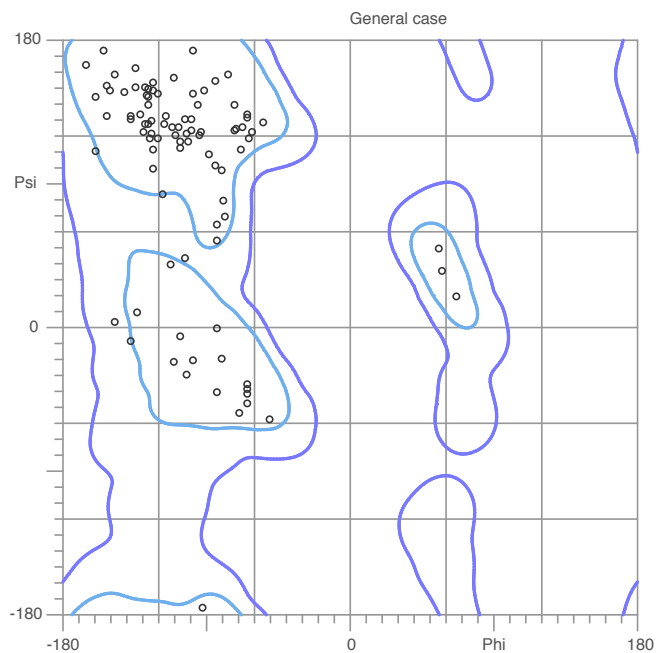
There were 1 outliers (phi, psi):
[13] 94 ASP (62.2, 134.7)

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MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 14

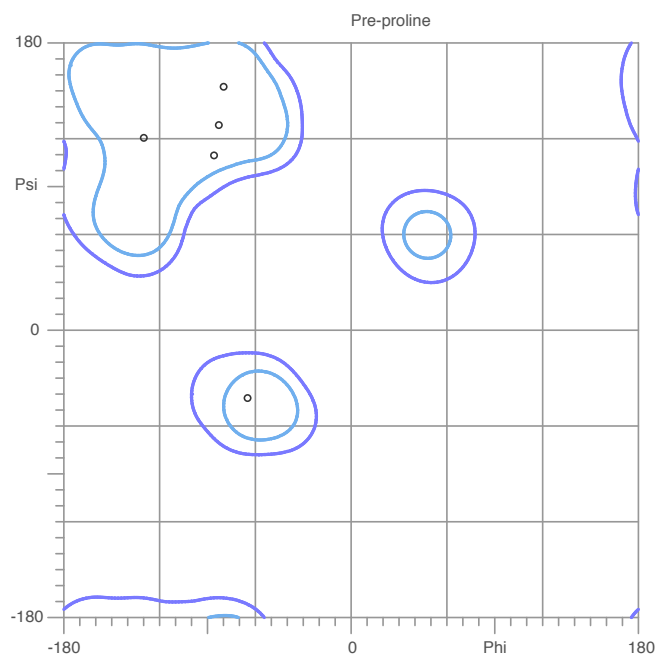
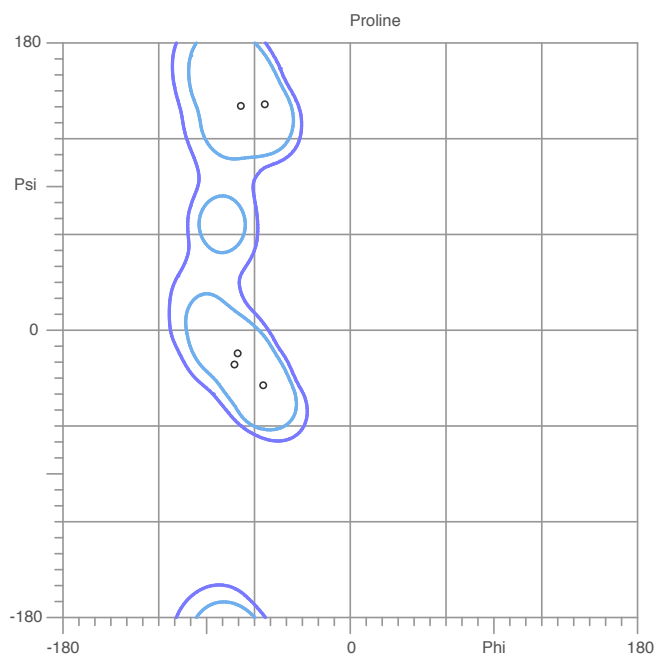
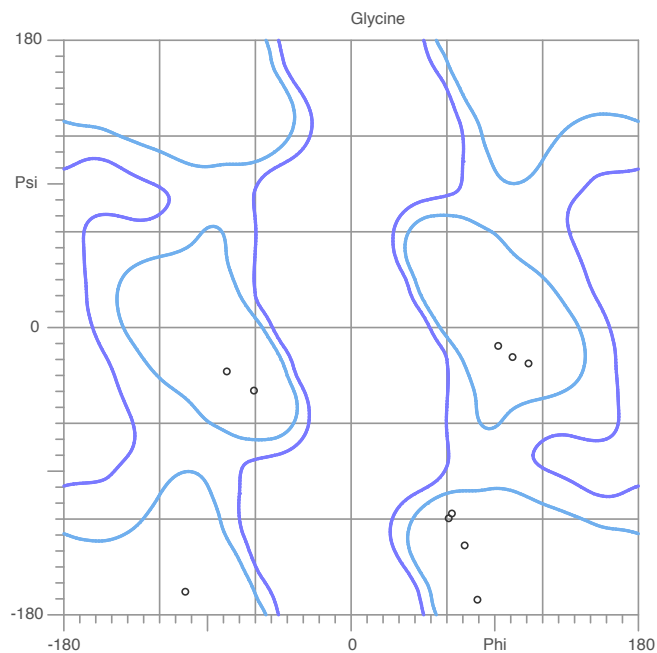
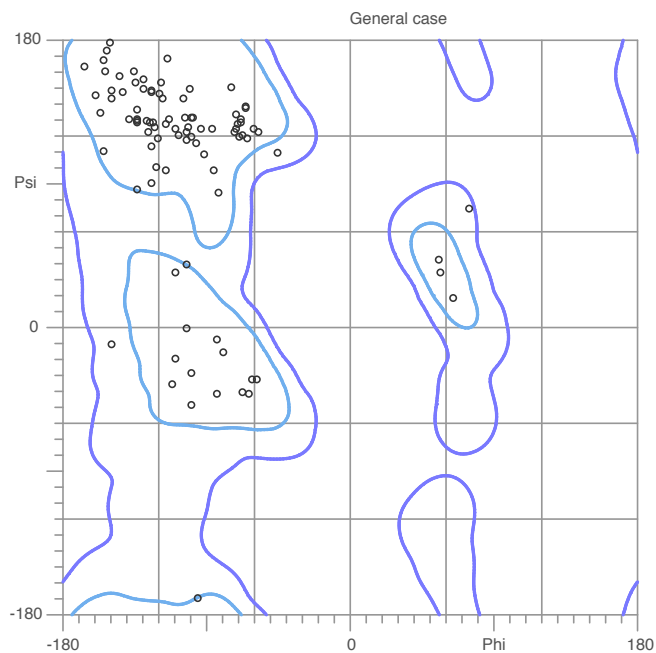


96.4% (108/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 15



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.

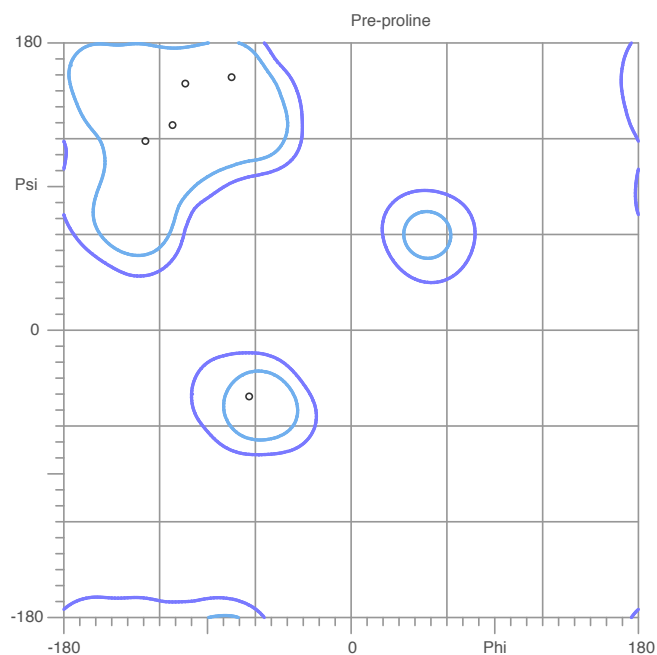
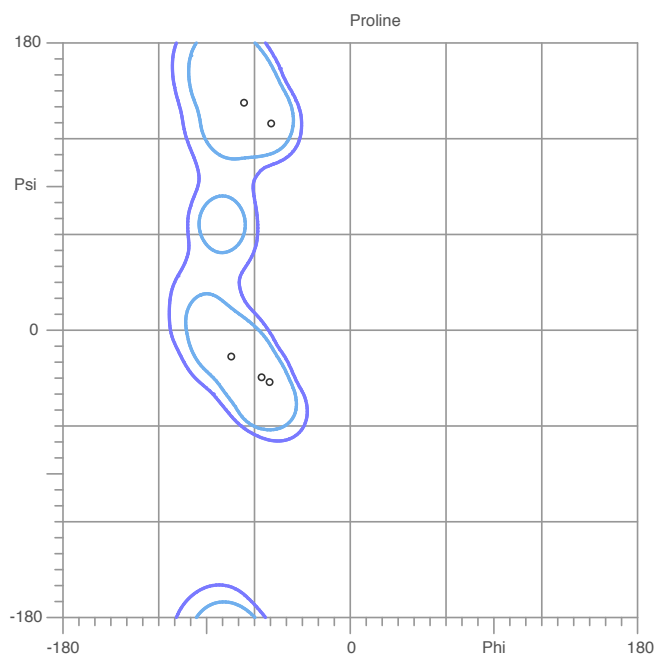
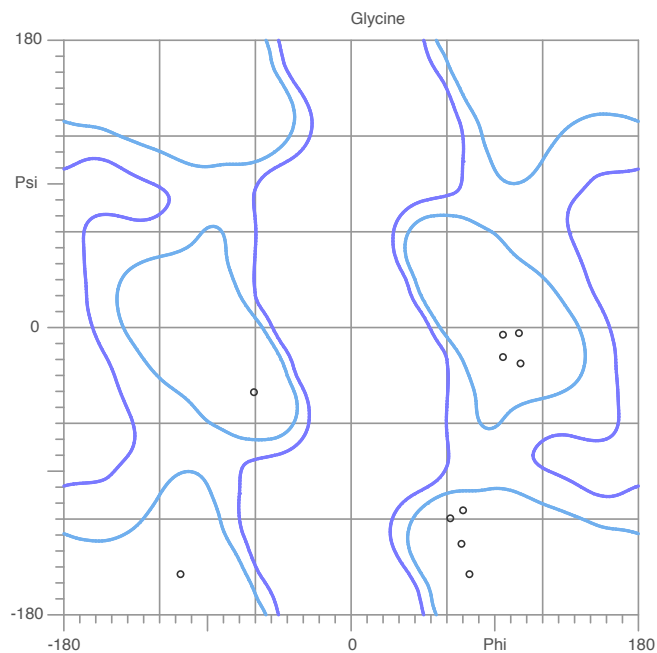
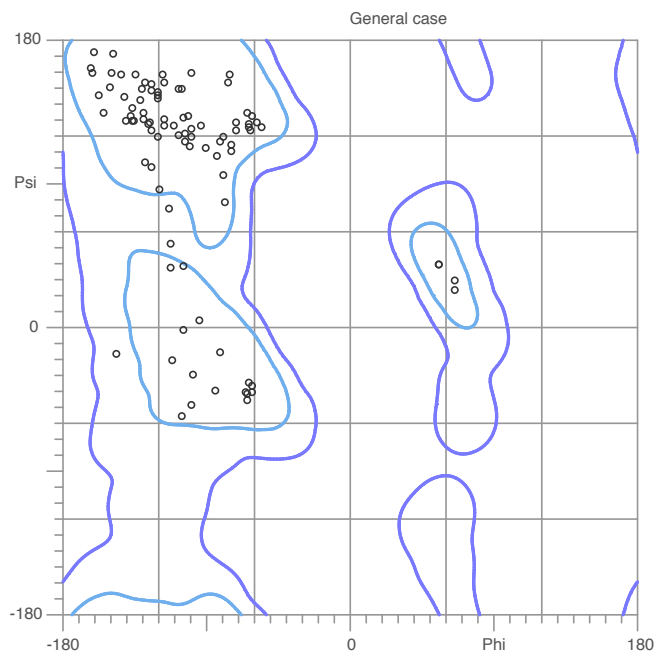
There were no outliers.

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

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MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 16

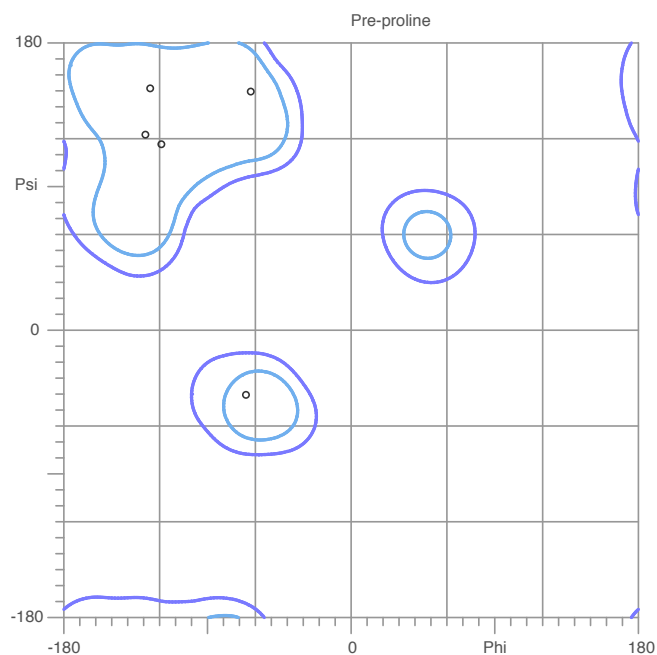
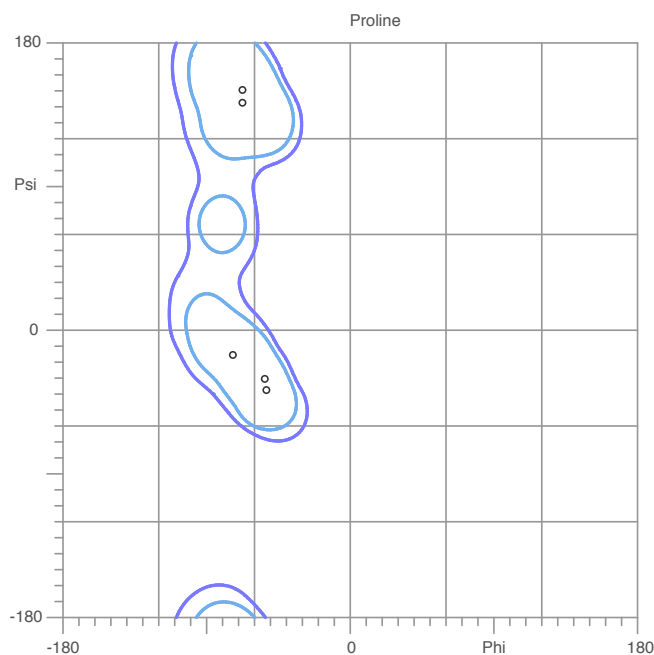
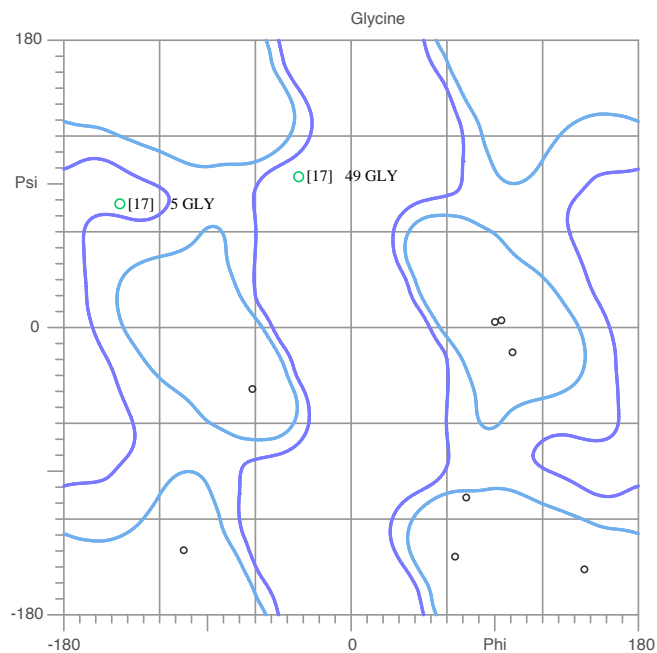
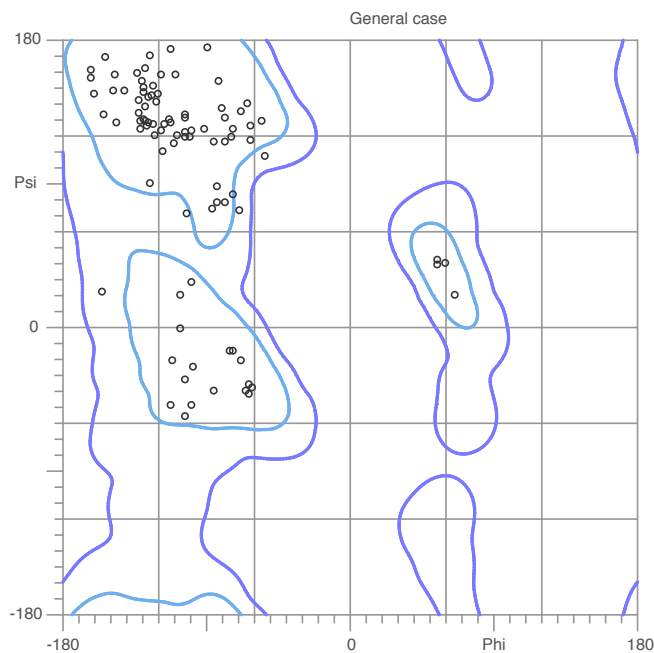


97.3% (109/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 17

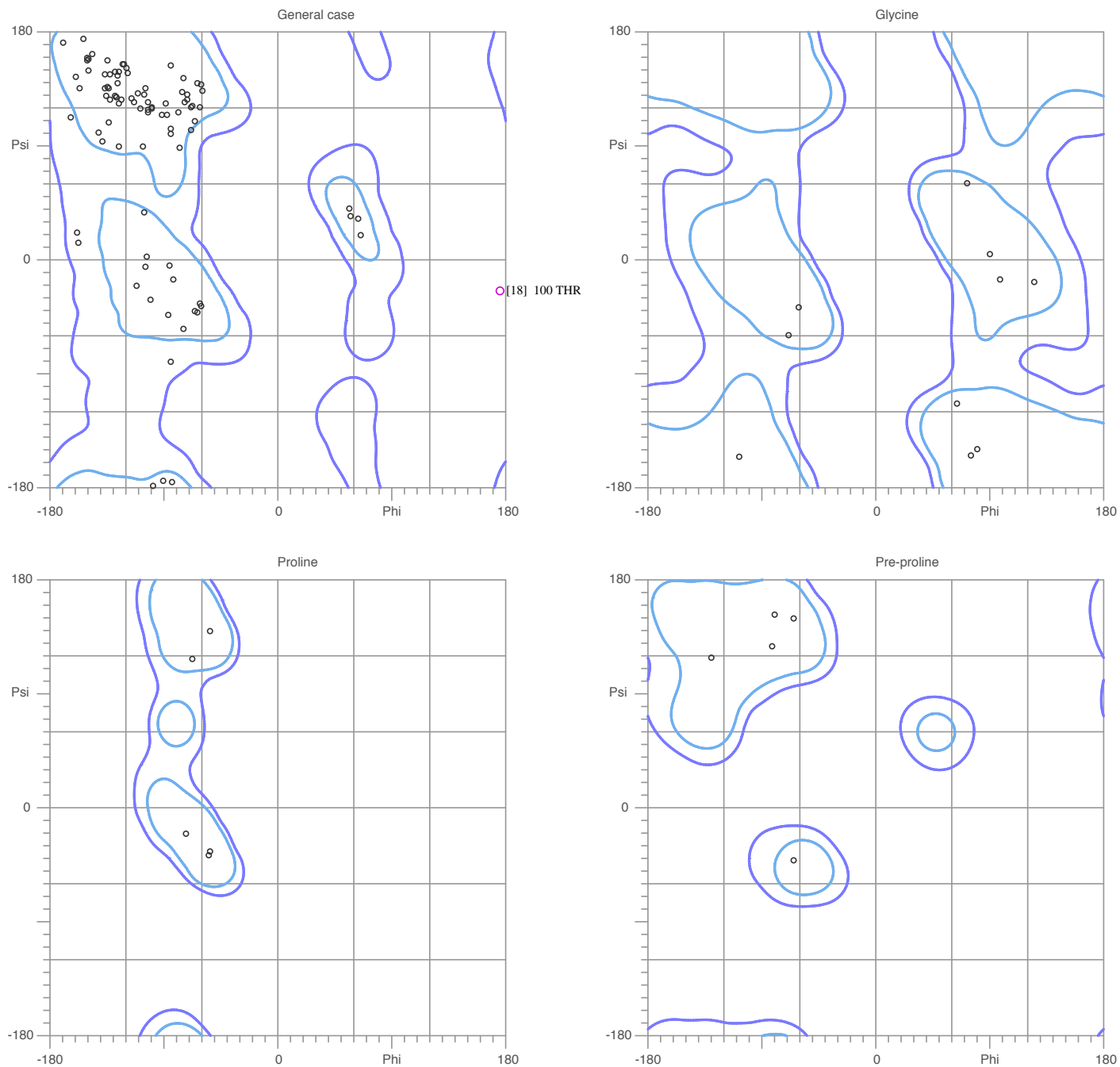


94.6% (106/112) of all residues were in favored (98%) regions.
98.2% (110/112) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[17] 5 GLY (-145.2, 78.7)
[17] 49 GLY (-33.7, 95.1)

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 18



95.5% (107/112) of all residues were in favored (98%) regions.
99.1% (111/112) of all residues were in allowed (>99.8%) regions.

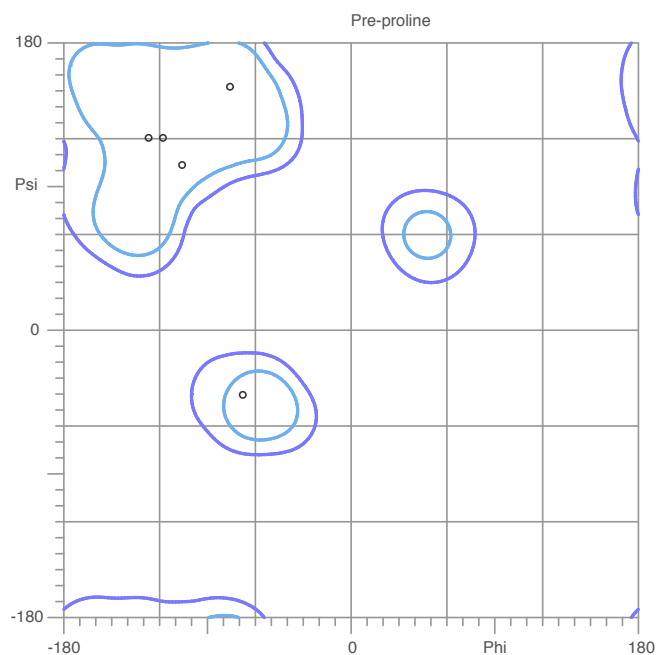
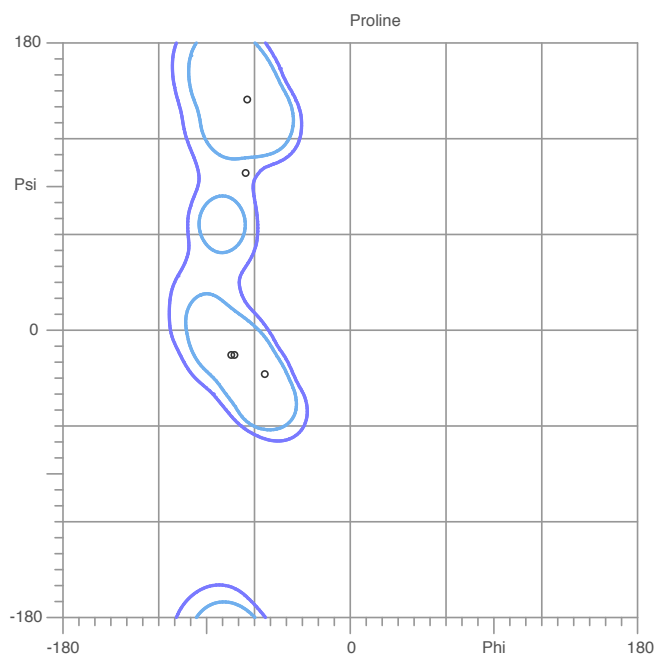
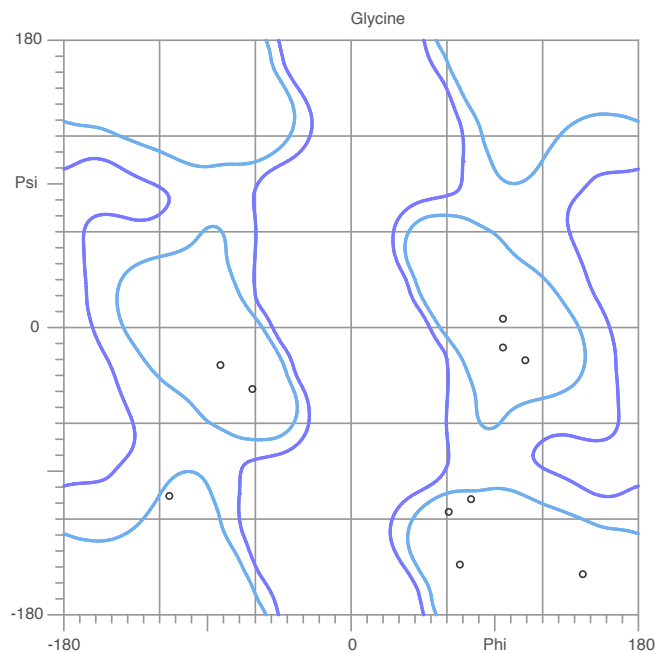
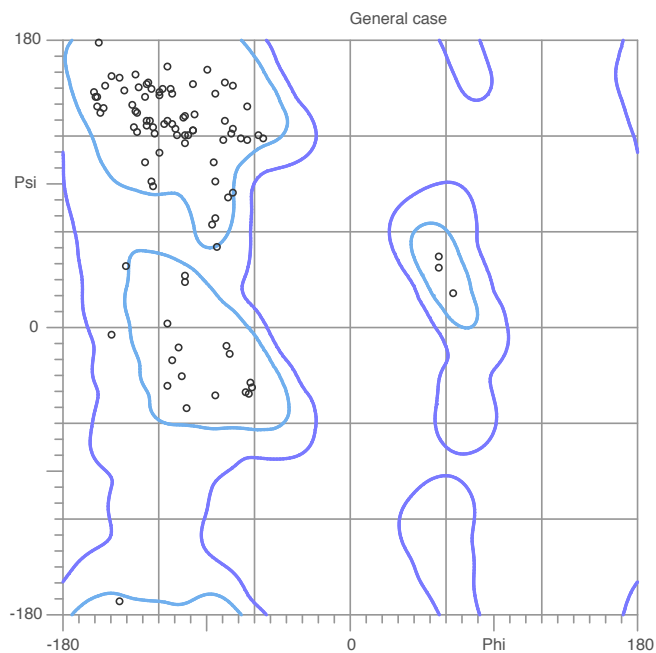
There were 1 outliers (phi, psi):
[18] 100 THR (175.1, -25.0)

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

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

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 19

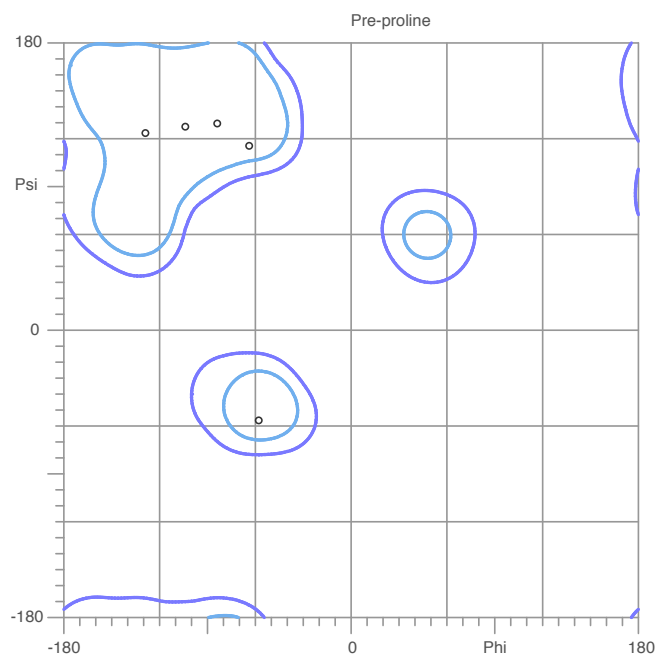
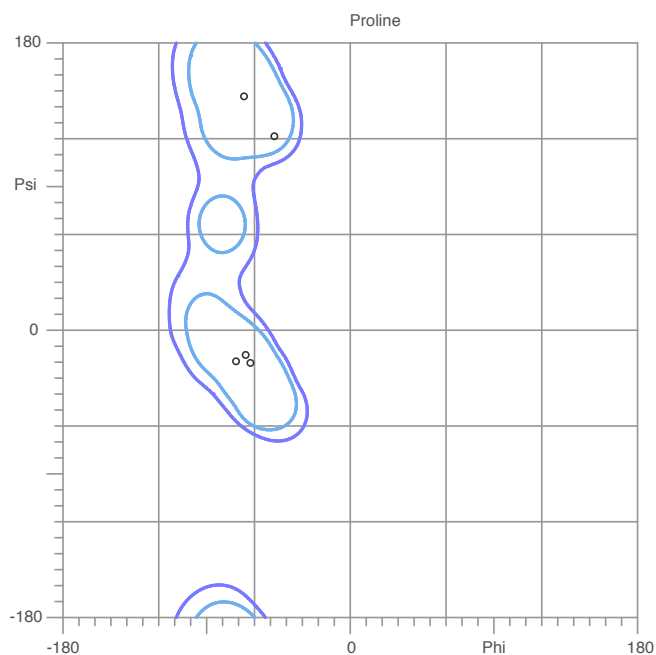
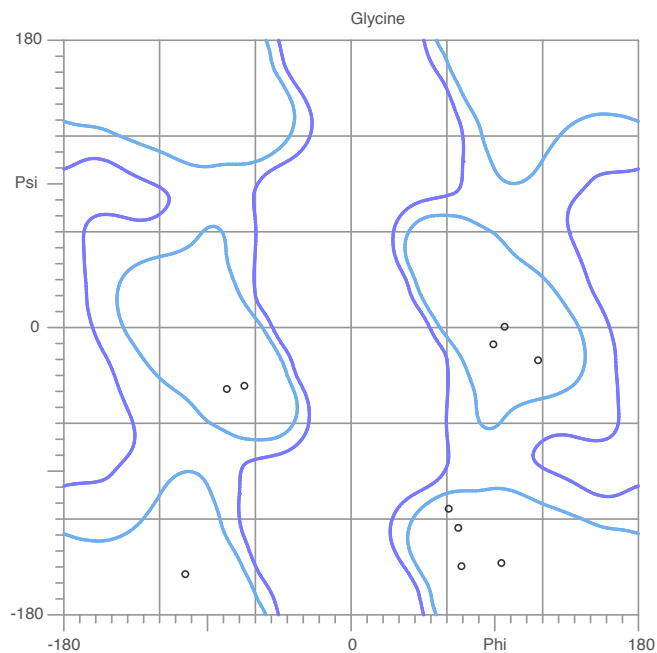
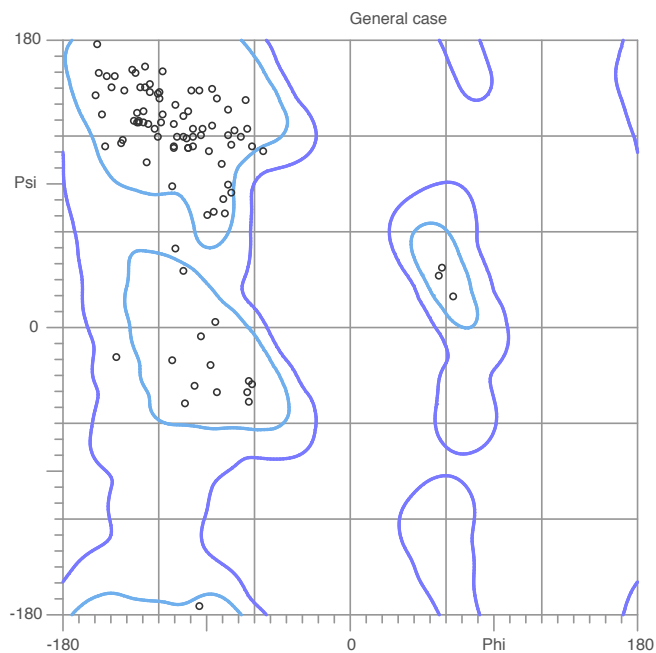


97.3% (109/112) of all residues were in favored (98%) regions.
100.0% (112/112) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

LKR112_R3Cons_em_bcr3.pdb, model 20



97.3% (109/112) 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)