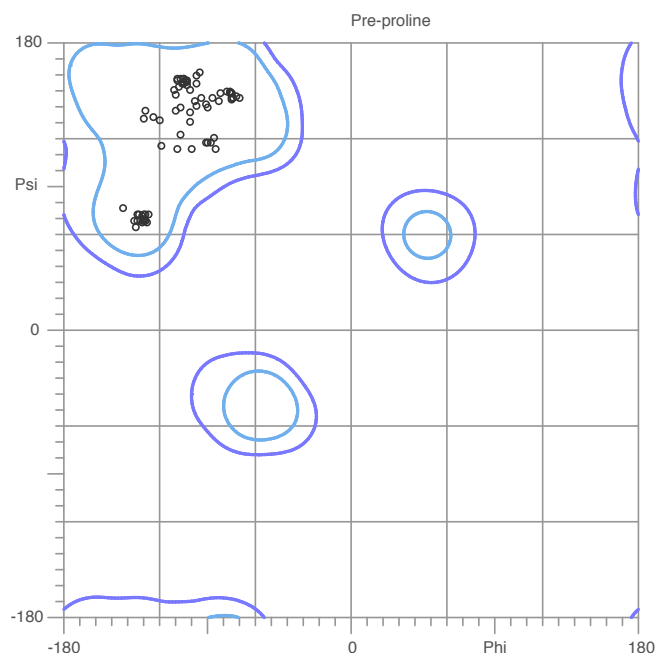
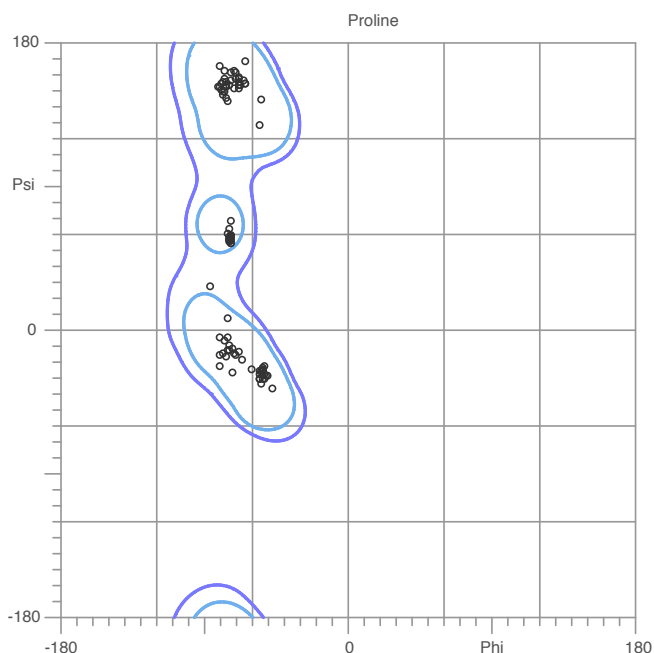
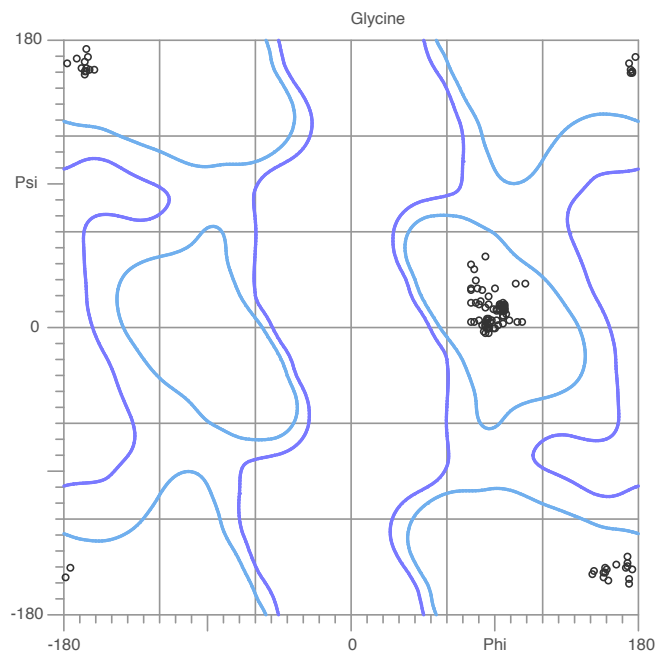
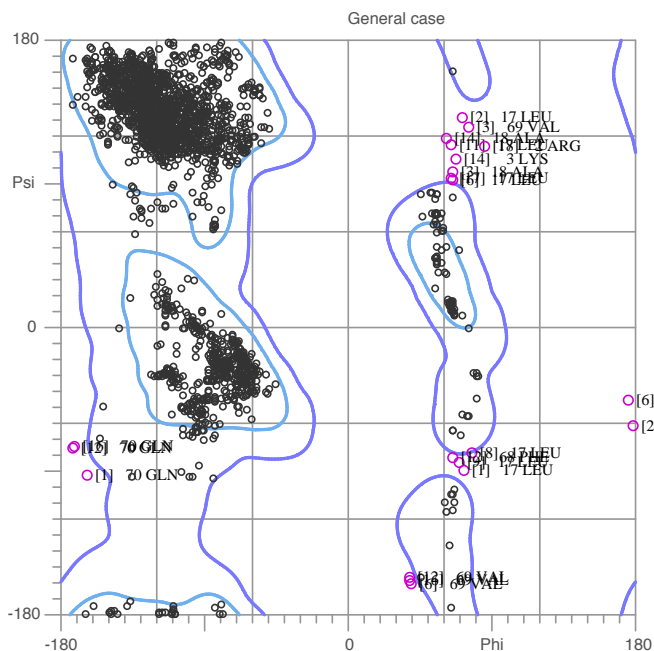


MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, all models



95.5% (2425/2538) of all residues were in favored (98%) regions.
99.2% (2517/2538) of all residues were in allowed (>99.8%) regions.

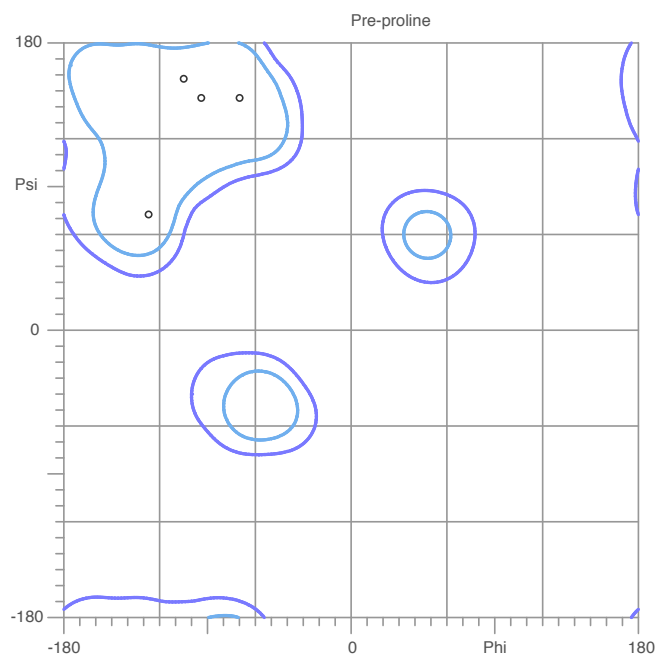
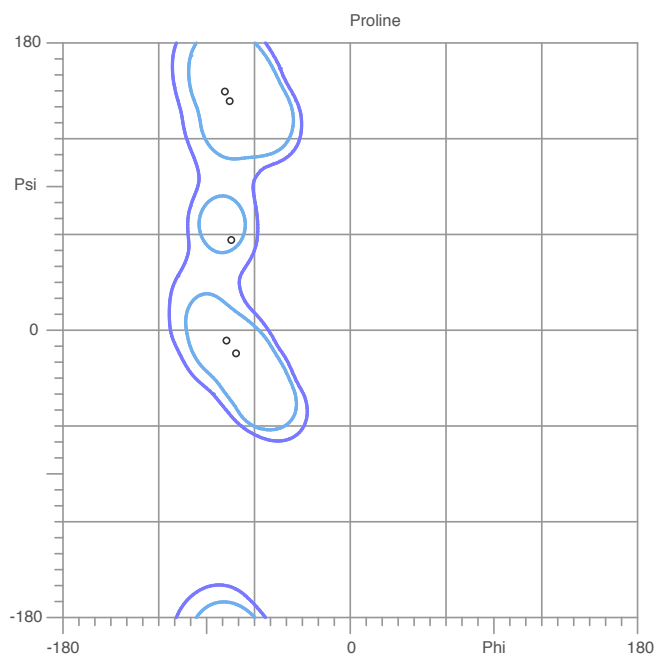
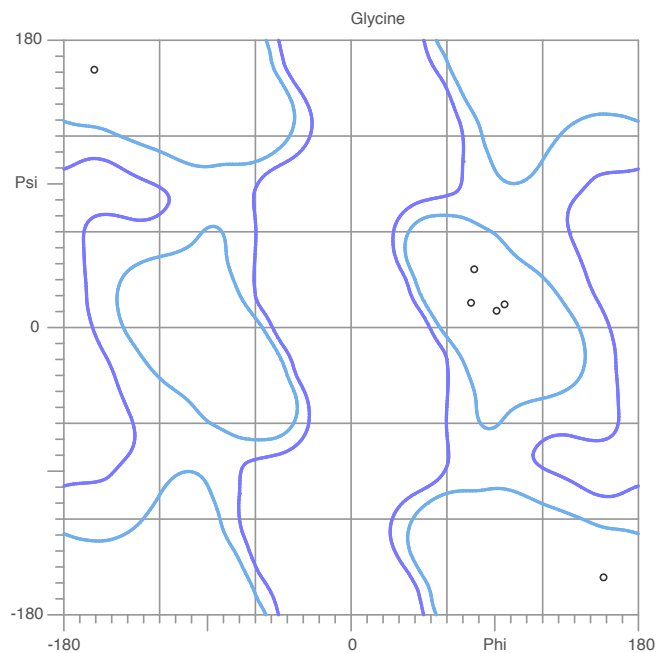
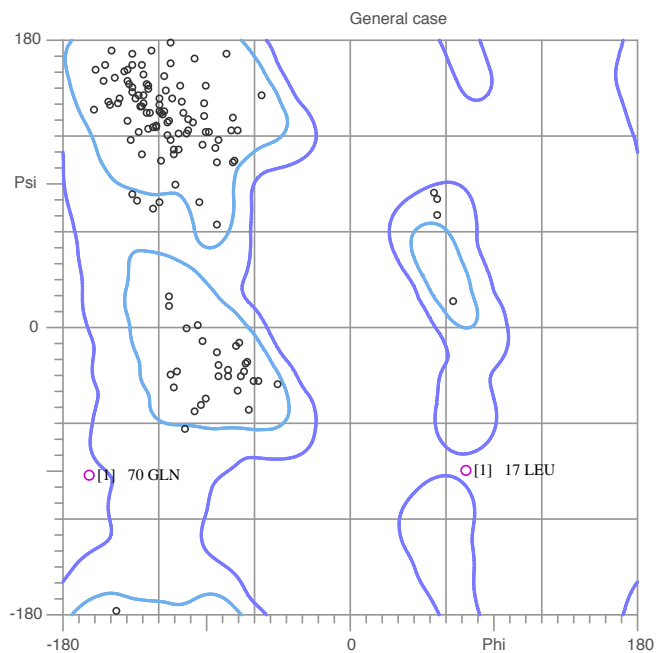
There were 21 outliers (phi, psi):

- [1] 17 LEU (72.7, -89.6)
- [1] 70 GLN (-164.3, -92.7)
- [2] 17 LEU (71.2, 132.8)
- [2] 70 GLN (178.6, -61.6)
- [3] 18 ALA (65.0, 98.4)
- [3] 69 VAL (75.0, 126.9)
- [6] 17 LEU (65.0, 93.6)
- [6] 69 VAL (39.3, -160.4)

- [6] 70 GLN (175.0, -45.0)
- [8] 17 LEU (77.0, -78.1)
- [9] 17 LEU (69.6, -84.6)
- [11] 17 LEU (64.9, 115.0)
- [12] 68 PHE (65.0, -81.2)
- [12] 69 VAL (38.4, -156.5)
- [12] 70 GLN (-173.3, -75.0)
- [14] 3 LYS (67.6, 106.9)
- [14] 18 ALA (61.1, 119.4)
- [16] 69 VAL (38.9, -158.2)
- [16] 70 GLN (-172.8, -75.0)
- [17] 17 LEU (65.0, 94.6)
- [18] 2 ARG (85.0, 115.0)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 1



92.9% (131/141) of all residues were in favored (98%) regions.
98.6% (139/141) of all residues were in allowed (>99.8%) regions.

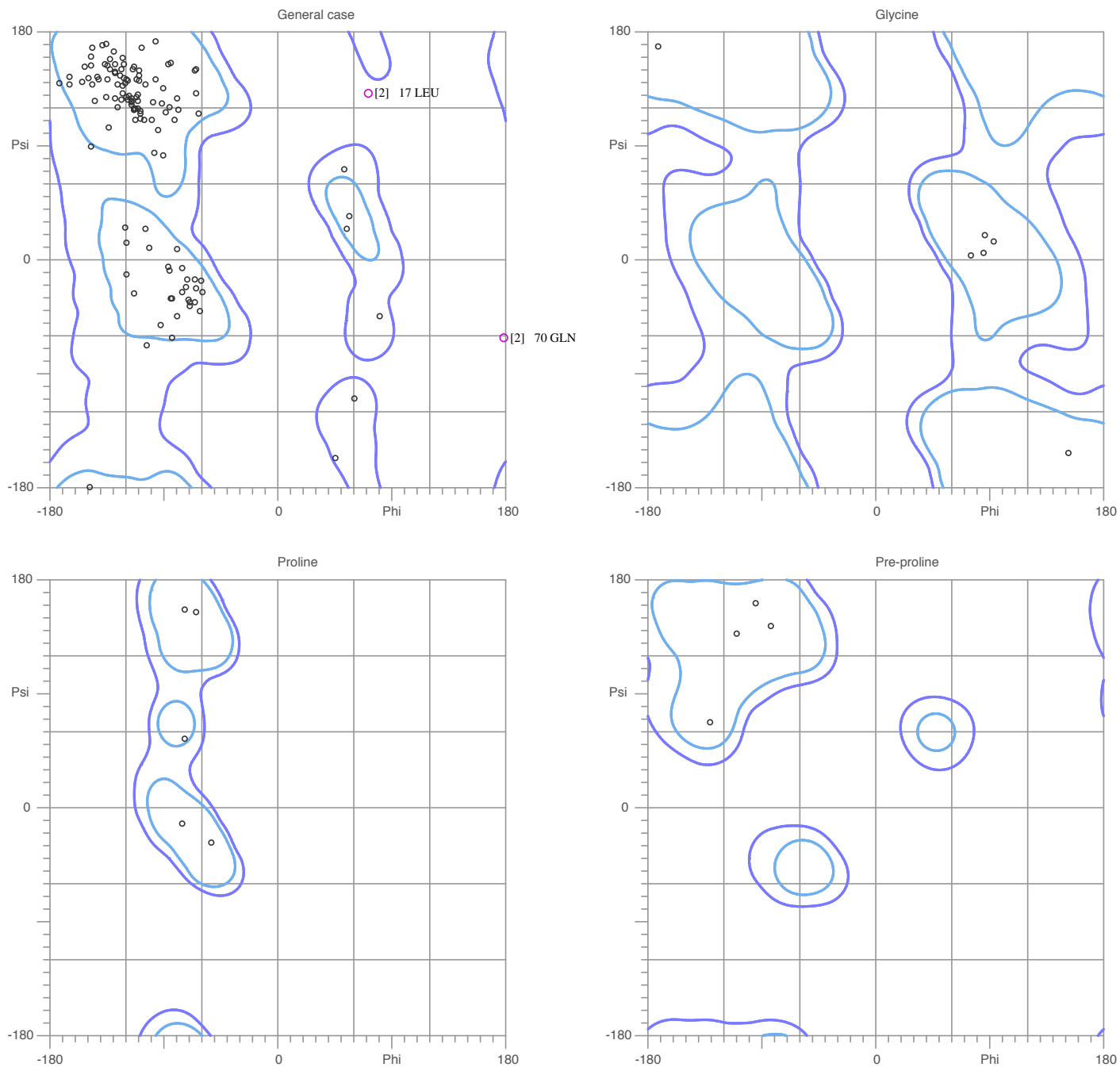
There were 2 outliers (phi, psi):

[1] 17 LEU (72.7, -89.6)

[1] 70 GLN (-164.3, -92.7)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 2



93.6% (132/141) of all residues were in favored (98%) regions.
98.6% (139/141) of all residues were in allowed (>99.8%) regions.

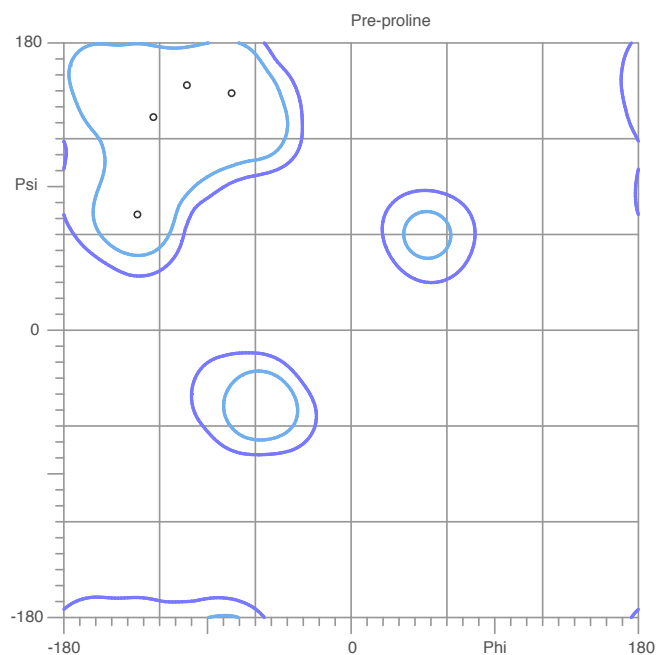
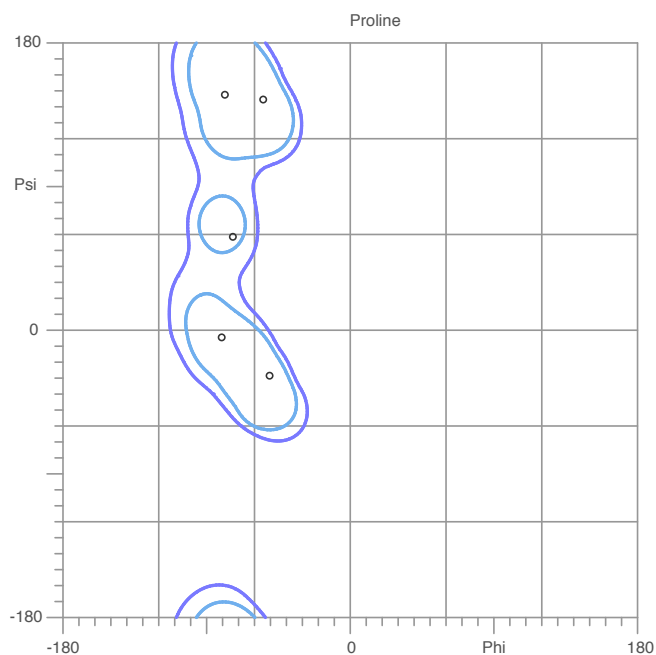
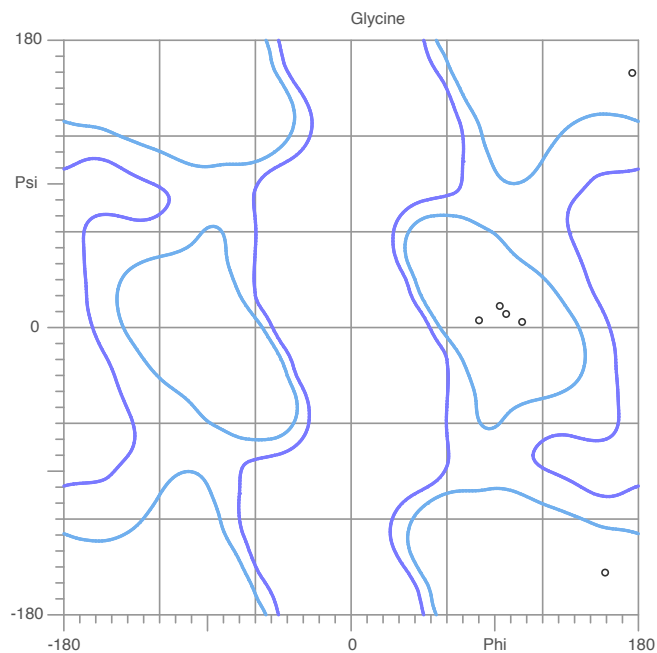
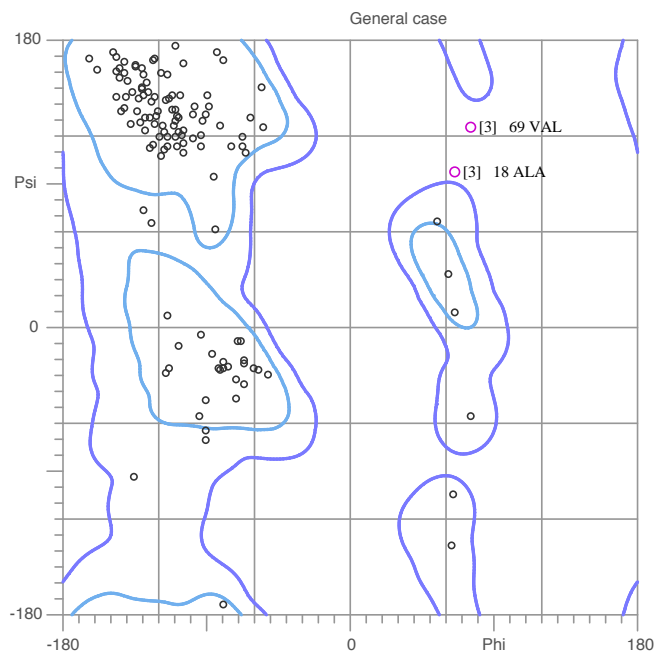
There were 2 outliers (phi, psi):

[2] 17 LEU (71.2, 132.8)

[2] 70 GLN (178.6, -61.6)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 3



92.2% (130/141) of all residues were in favored (98%) regions.
98.6% (139/141) of all residues were in allowed (>99.8%) regions.

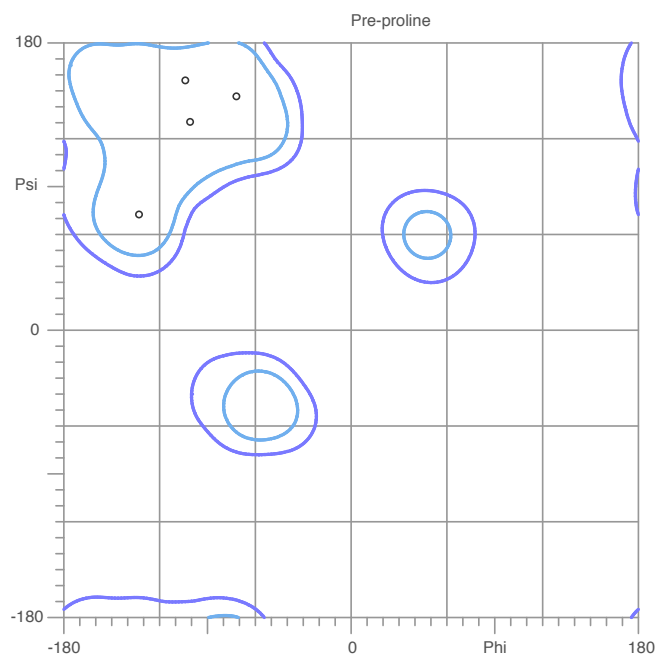
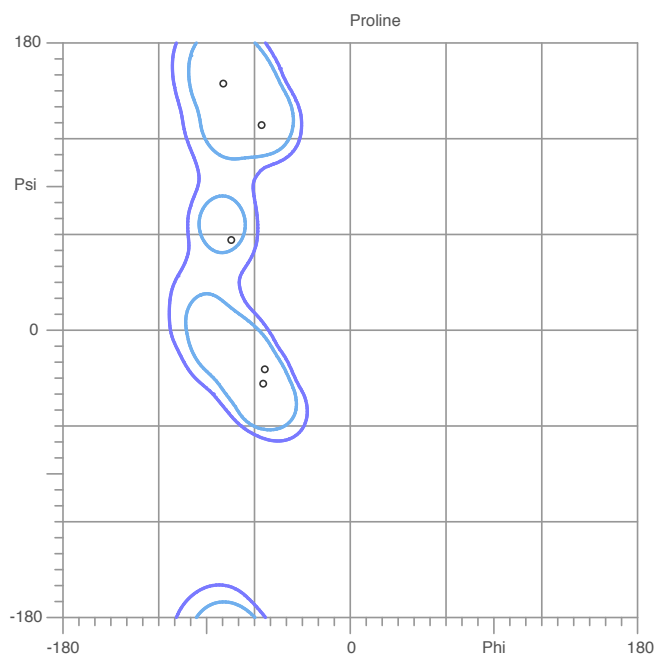
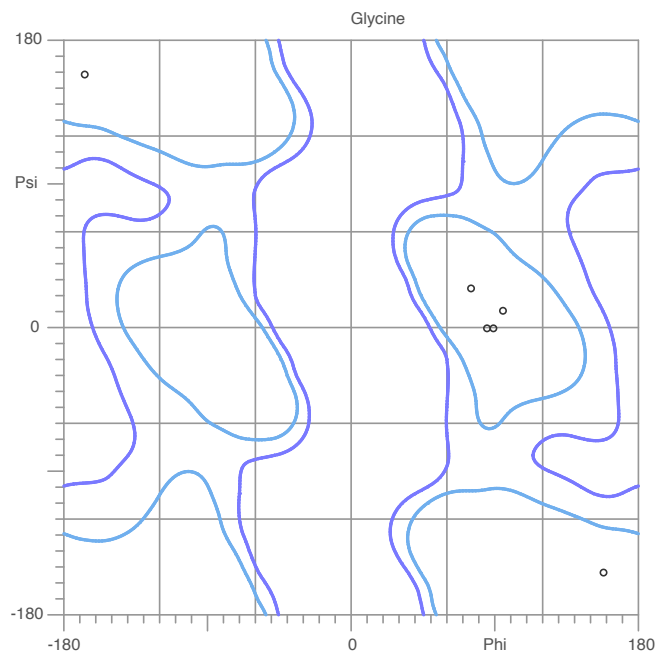
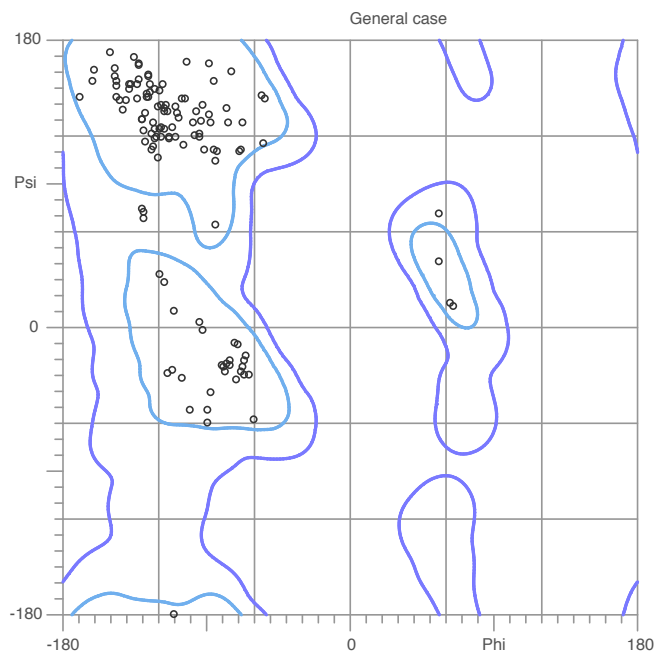
There were 2 outliers (phi, psi):

[3] 18 ALA (65.0, 98.4)

[3] 69 VAL (75.0, 126.9)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 4



97.2% (137/141) of all residues were in favored (98%) regions.
100.0% (141/141) of all residues were in allowed (>99.8%) regions.

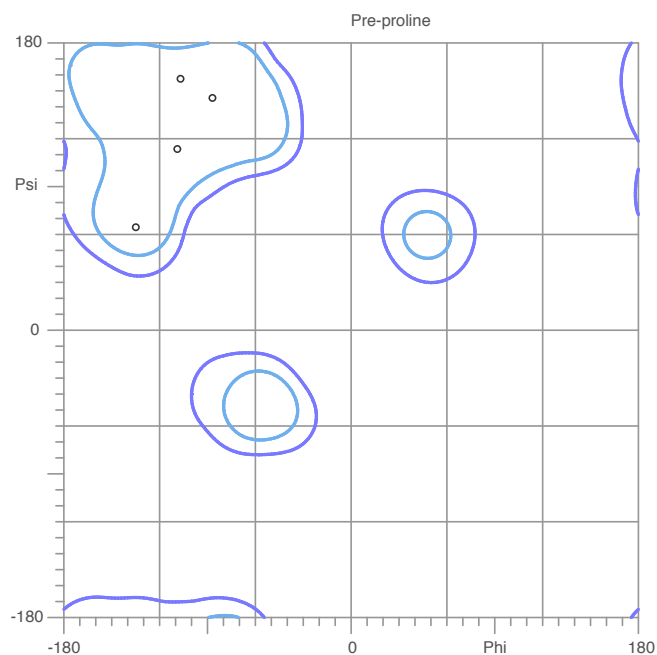
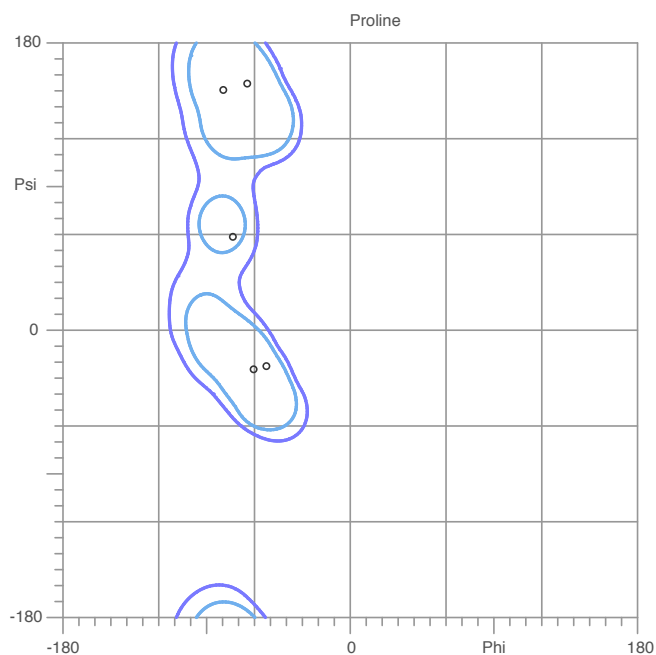
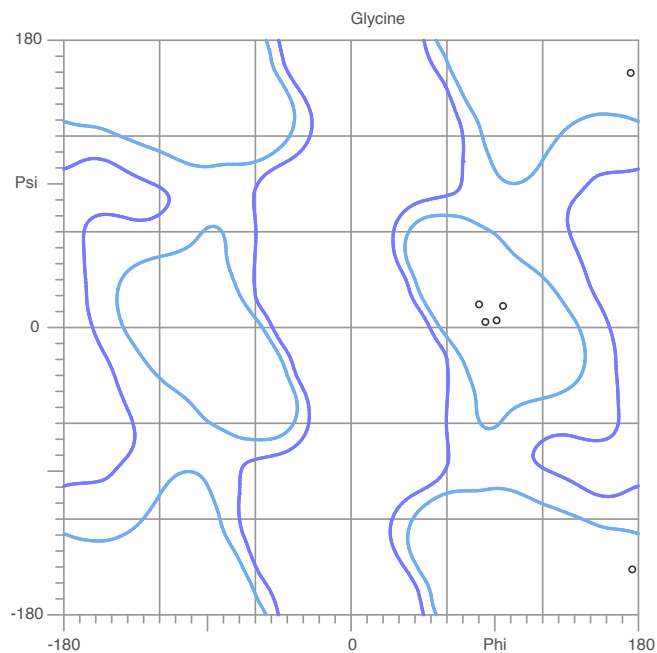
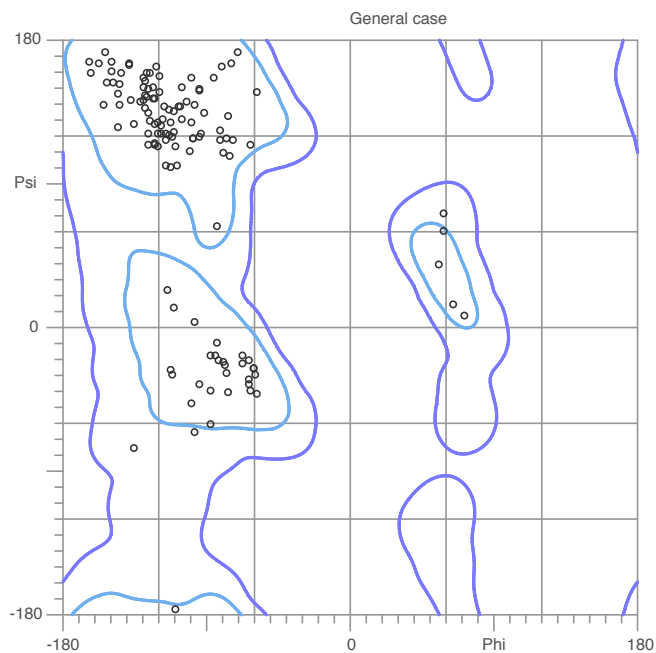
There were no outliers.

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

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MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 5



97.9% (138/141) of all residues were in favored (98%) regions.
100.0% (141/141) of all residues were in allowed (>99.8%) regions.

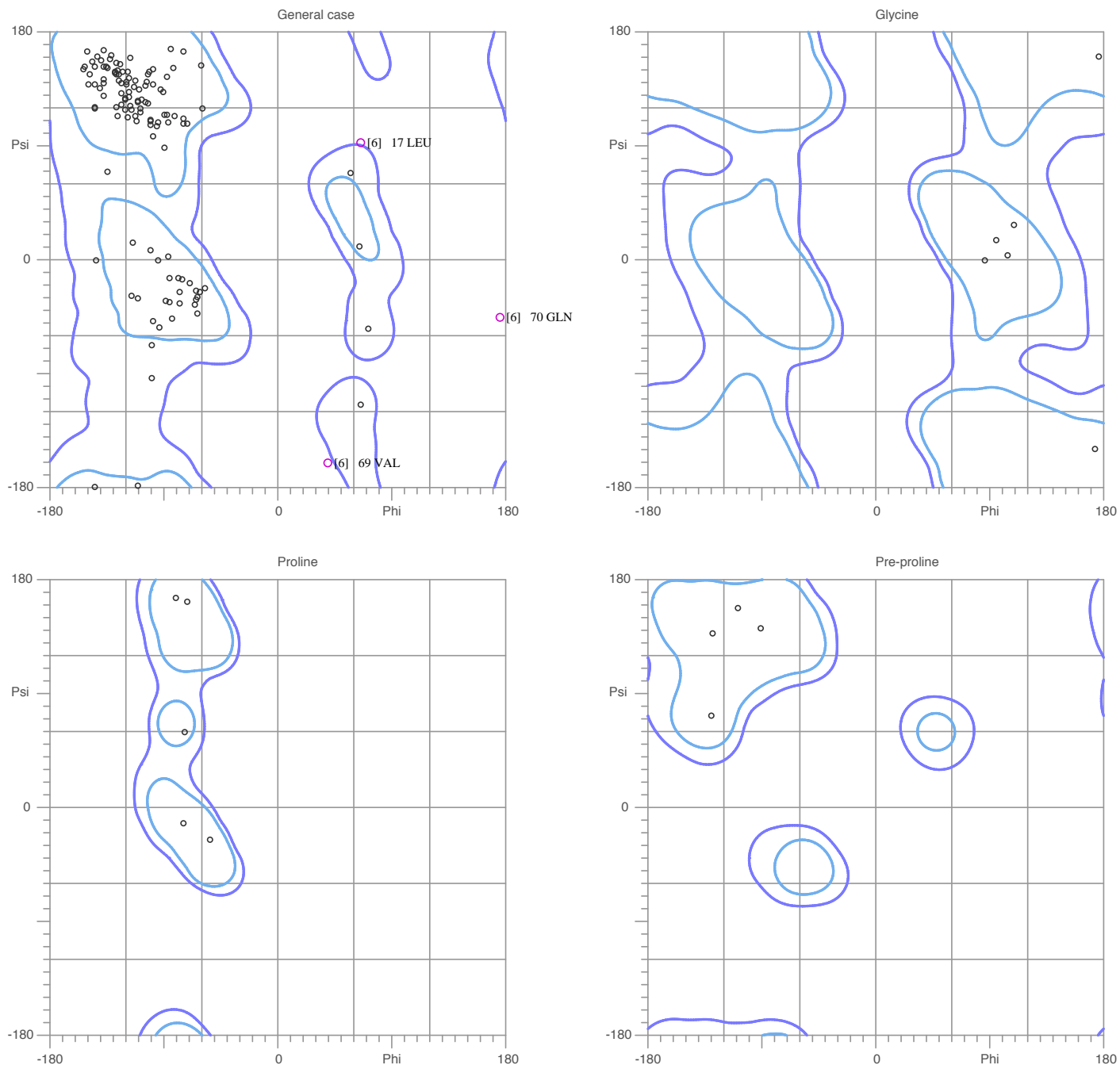
There were no outliers.

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

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MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 6



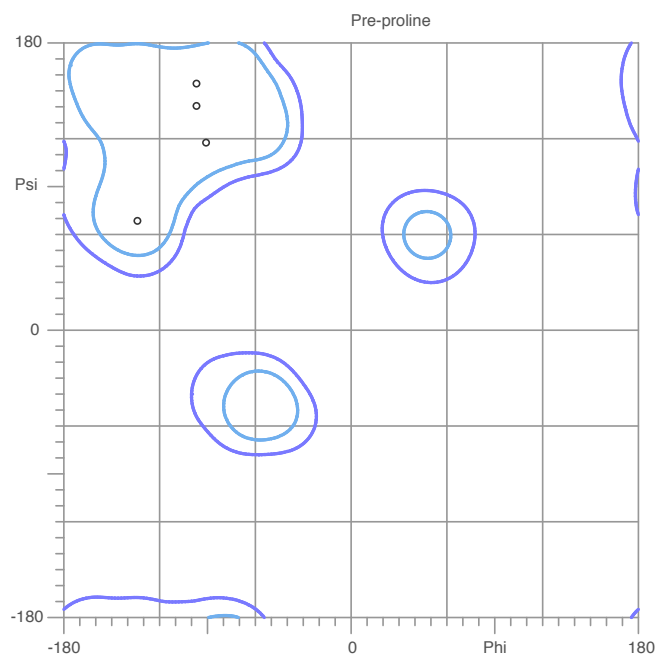
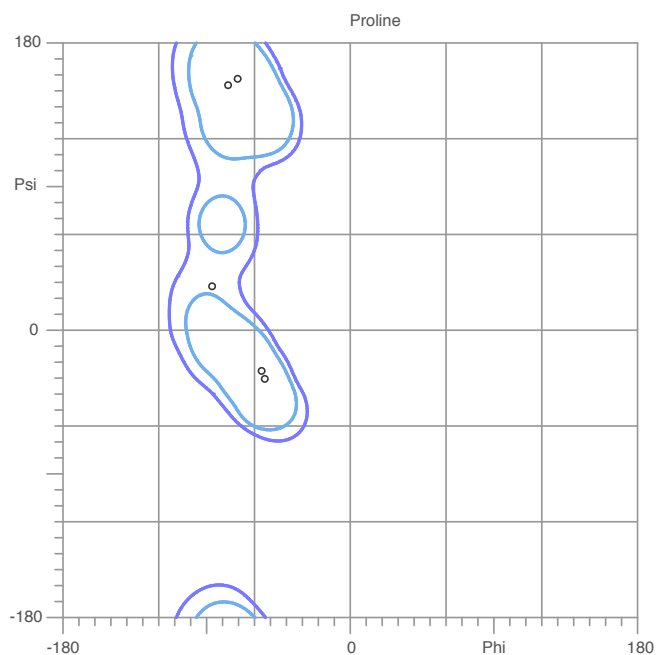
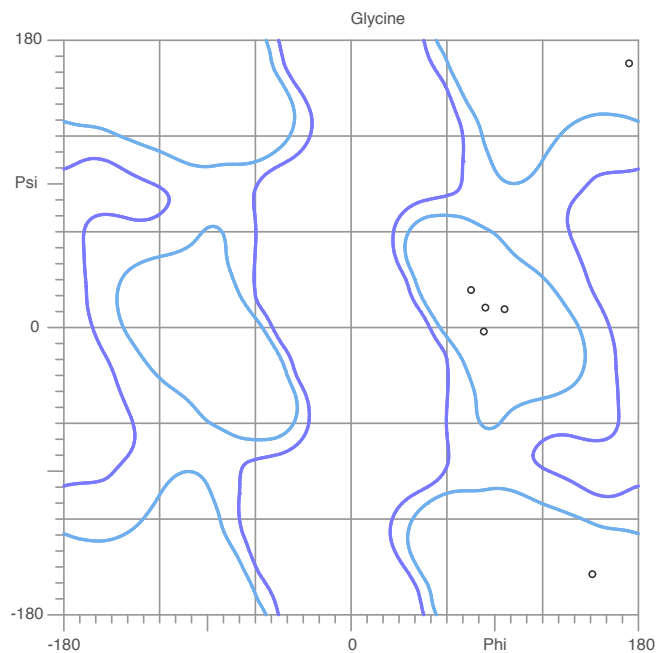
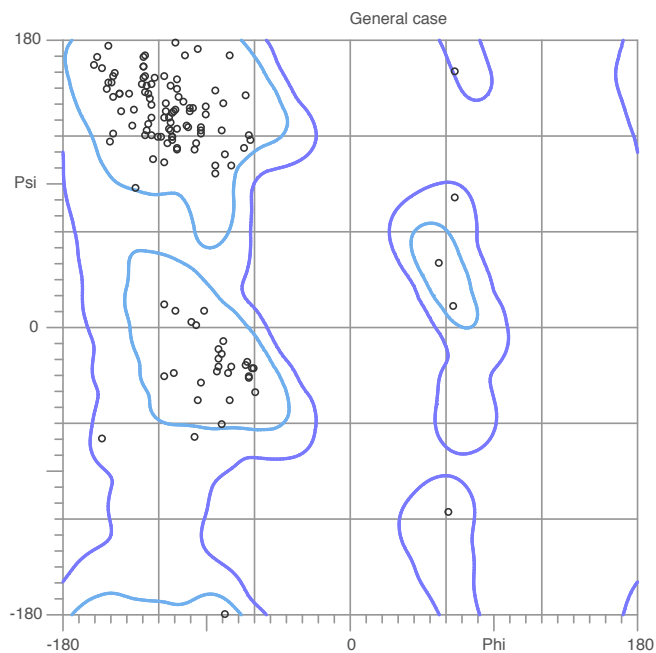
92.9% (131/141) of all residues were in favored (98%) regions.
97.9% (138/141) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 17 LEU (65.0, 93.6)
- [6] 69 VAL (39.3, -160.4)
- [6] 70 GLN (175.0, -45.0)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 7



95.7% (135/141) of all residues were in favored (98%) regions.
100.0% (141/141) of all residues were in allowed (>99.8%) regions.

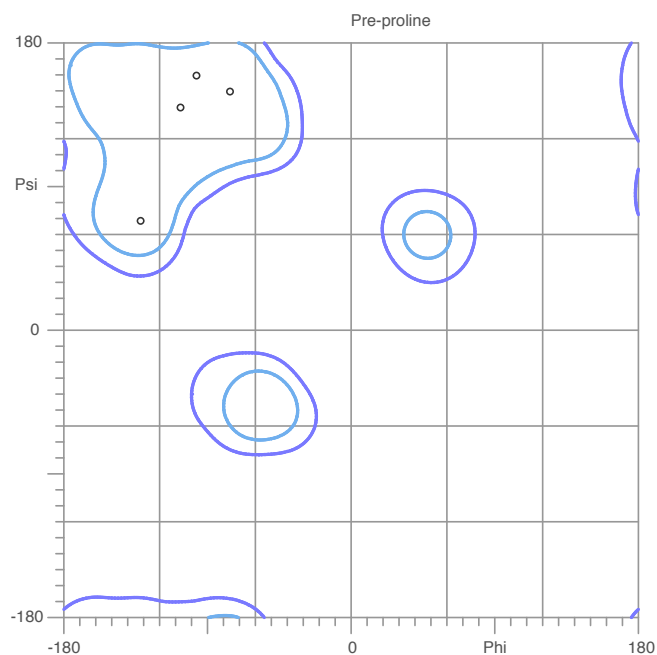
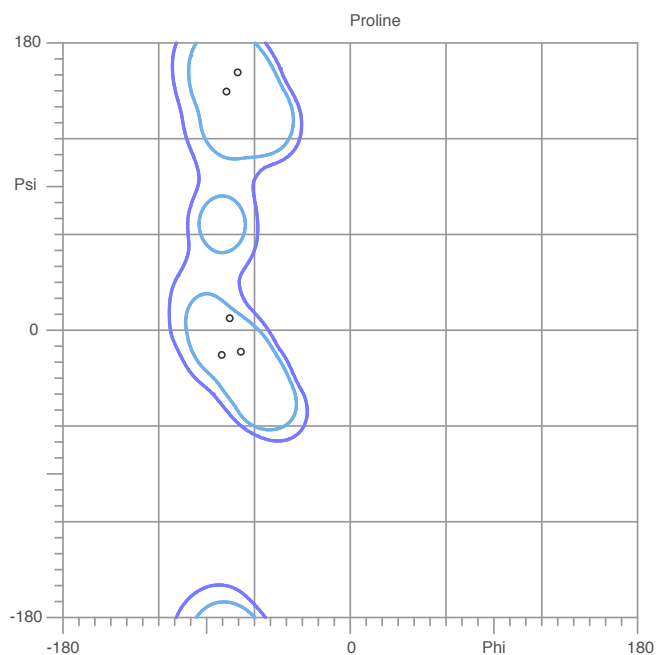
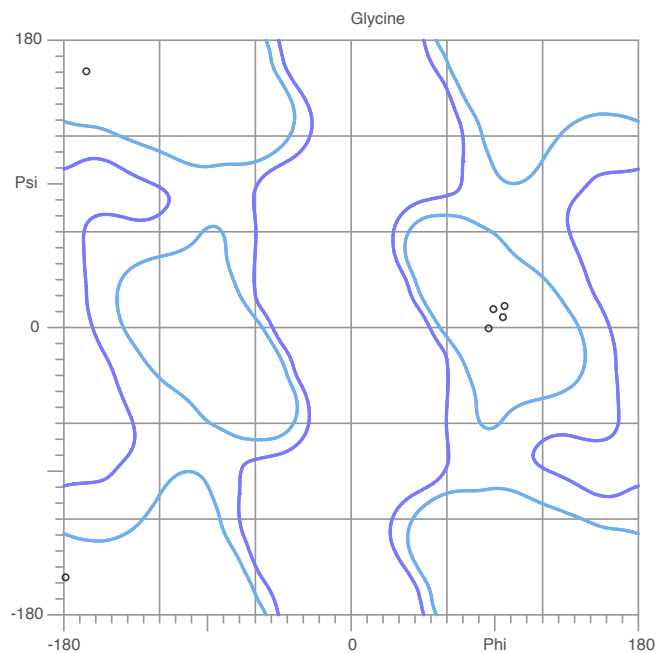
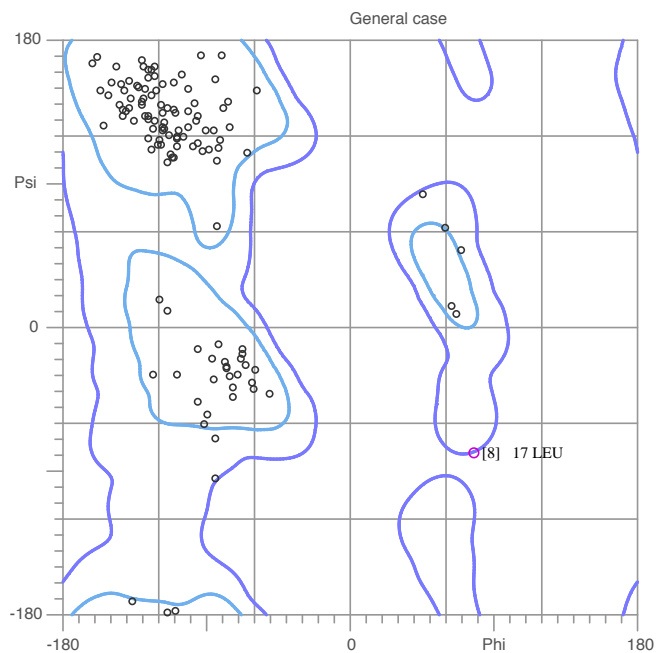
There were no outliers.

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MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 8

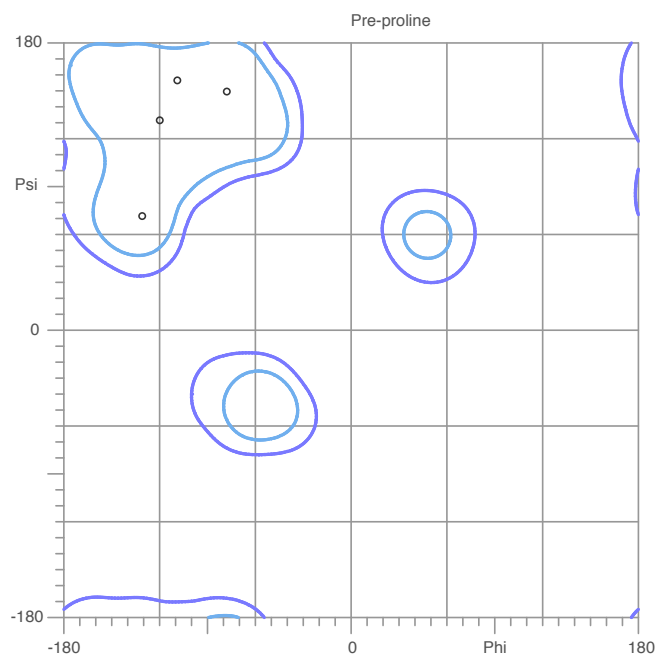
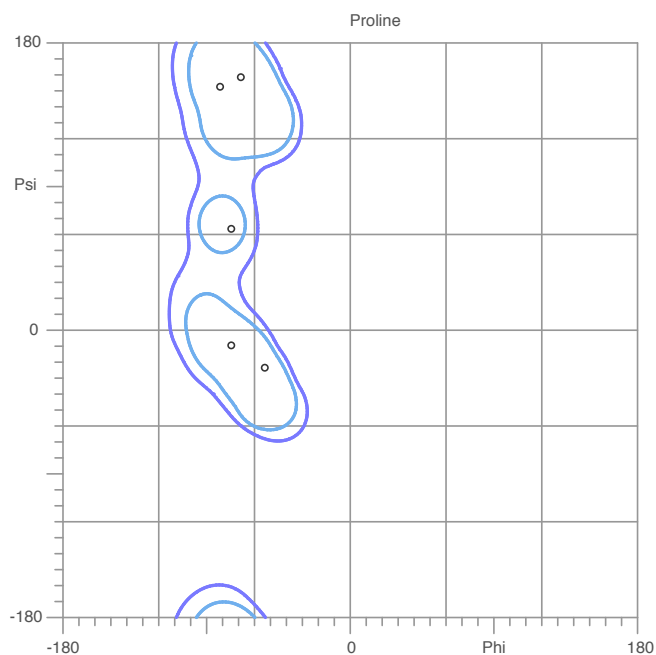
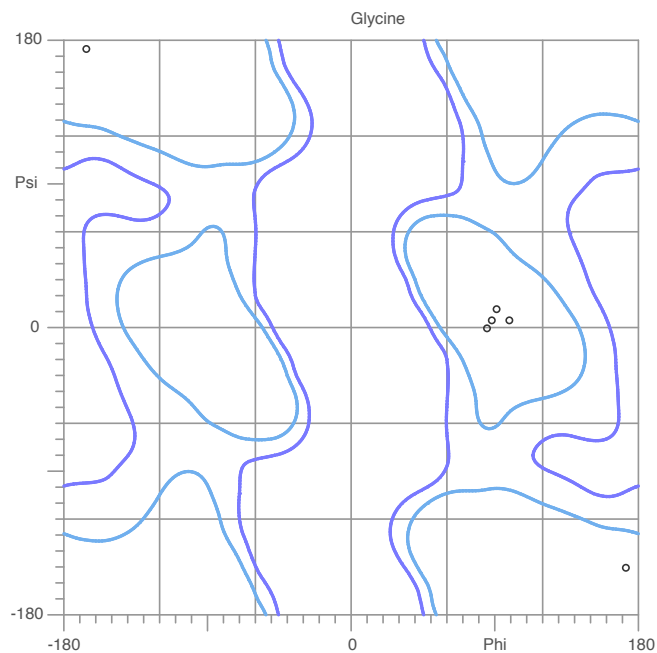
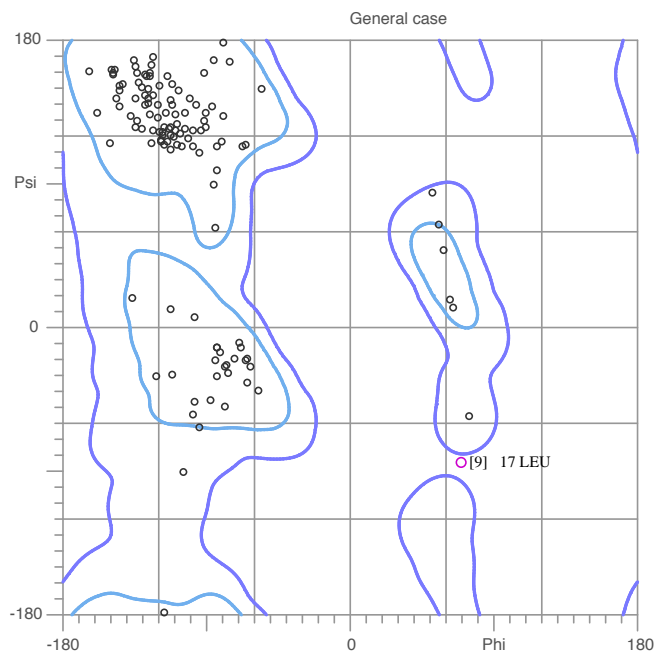


95.7% (135/141) of all residues were in favored (98%) regions.
99.3% (140/141) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[8] 17 LEU (77.0, -78.1)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 9

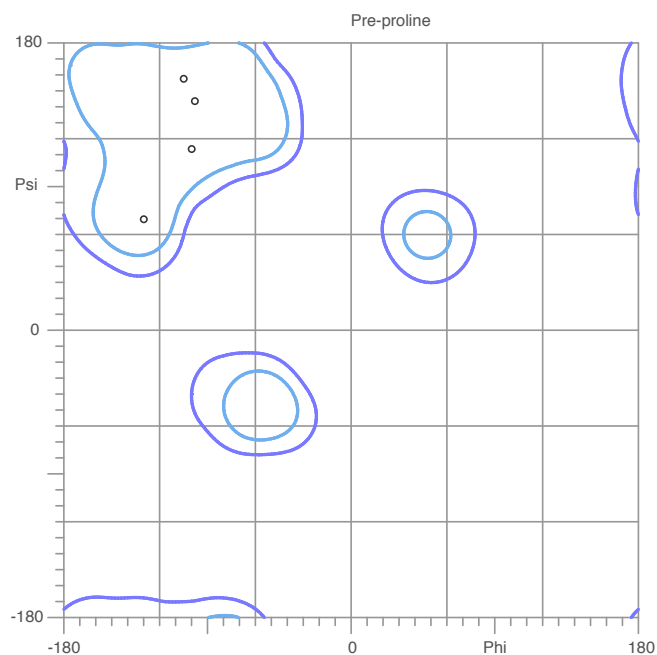
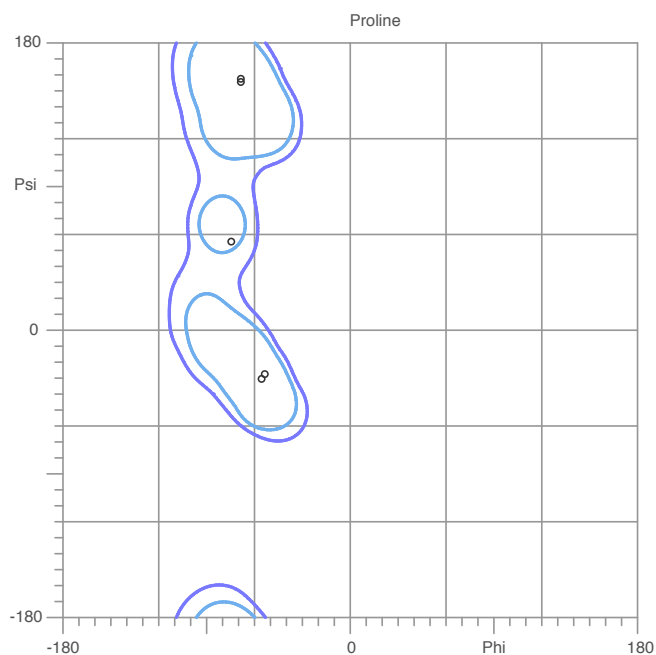
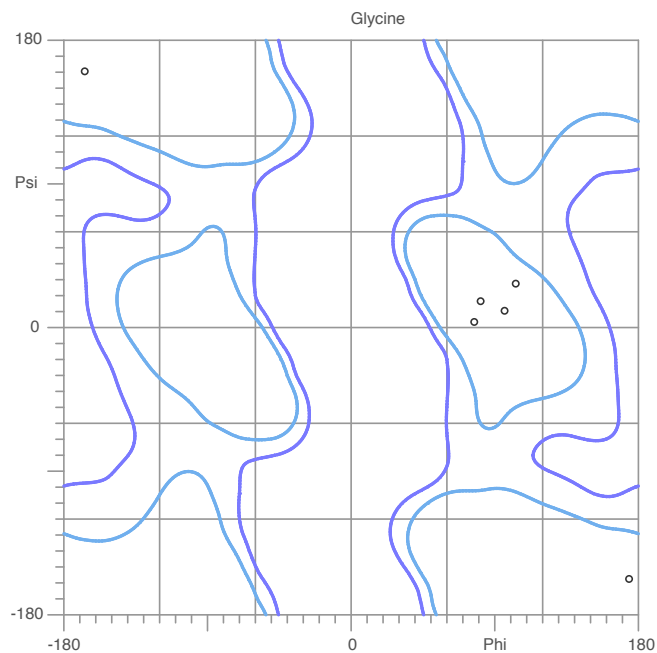
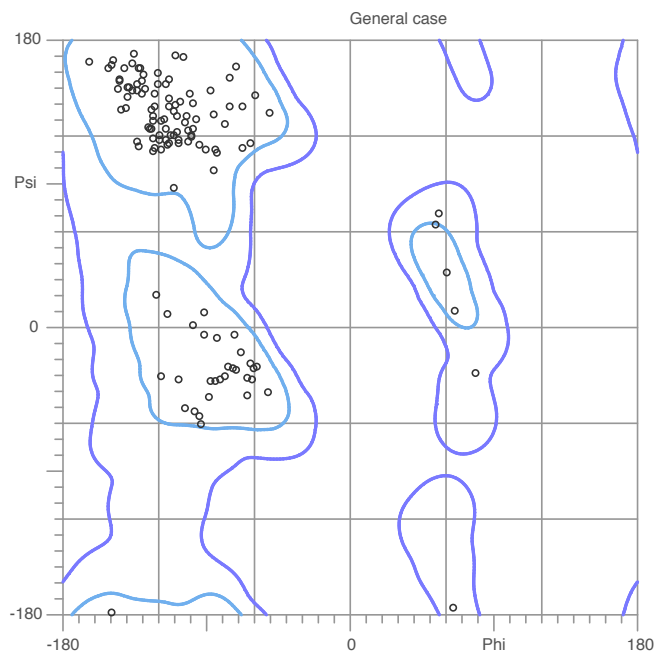


95.7% (135/141) of all residues were in favored (98%) regions.
99.3% (140/141) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[9] 17 LEU (69.6, -84.6)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 10



97.2% (137/141) of all residues were in favored (98%) regions.
100.0% (141/141) of all residues were in allowed (>99.8%) regions.

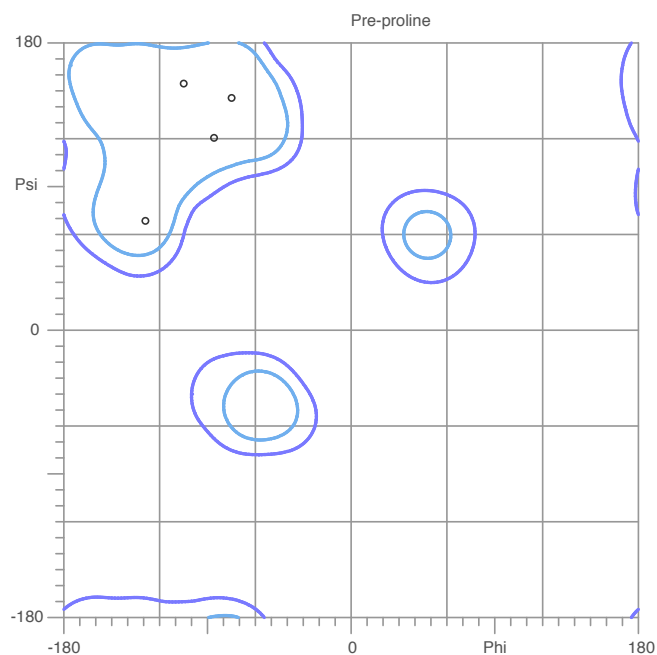
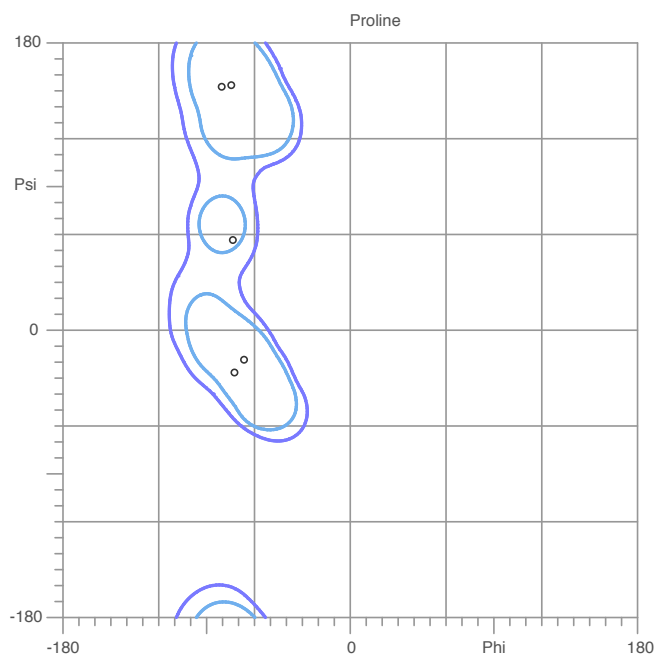
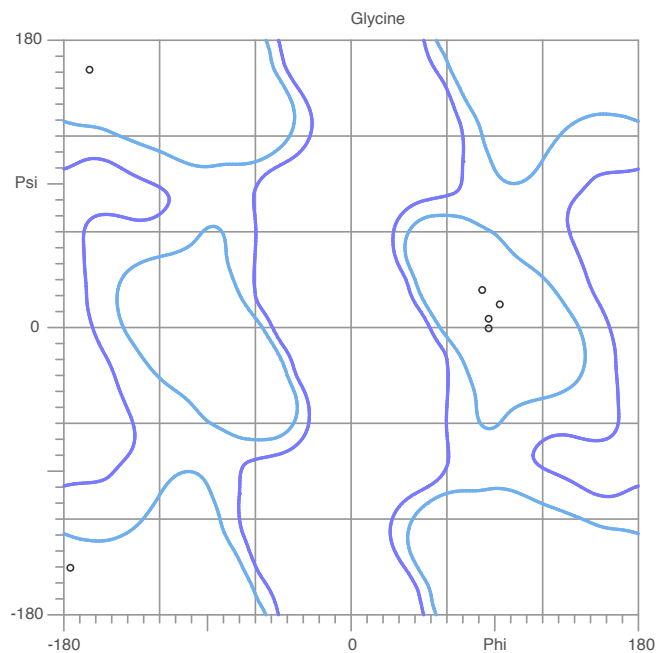
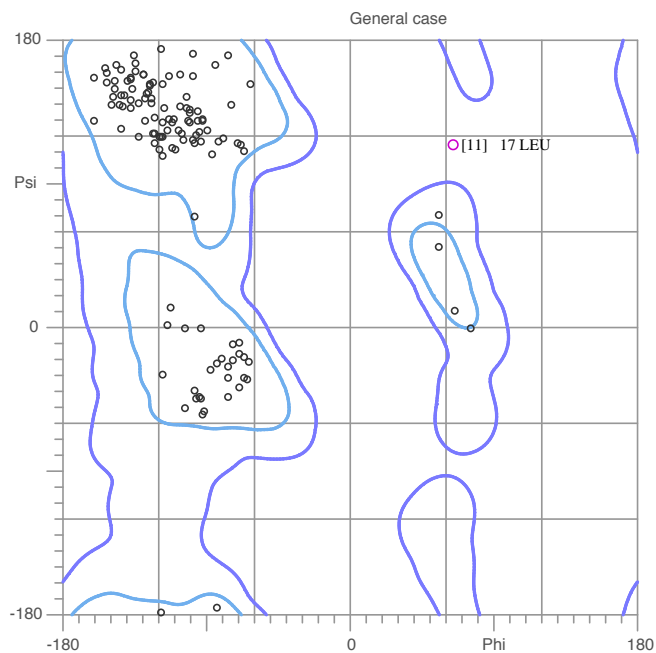
There were no outliers.

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MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 11



97.9% (138/141) of all residues were in favored (98%) regions.
99.3% (140/141) of all residues were in allowed (>99.8%) regions.

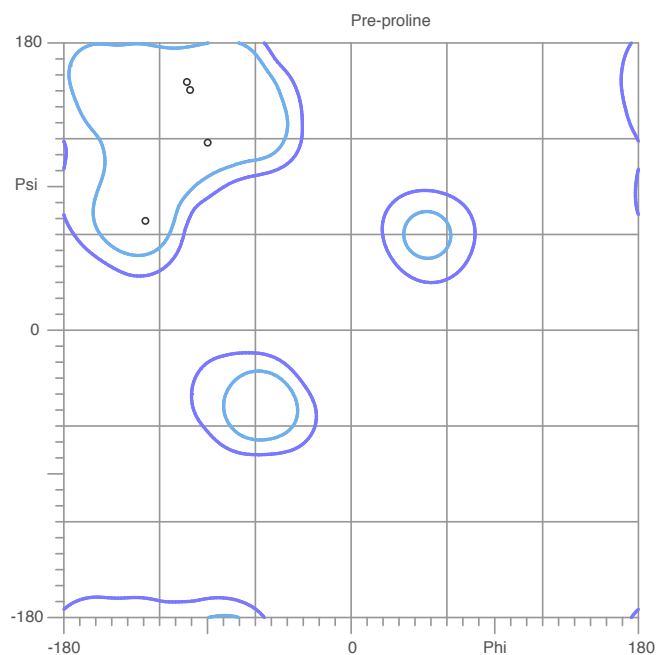
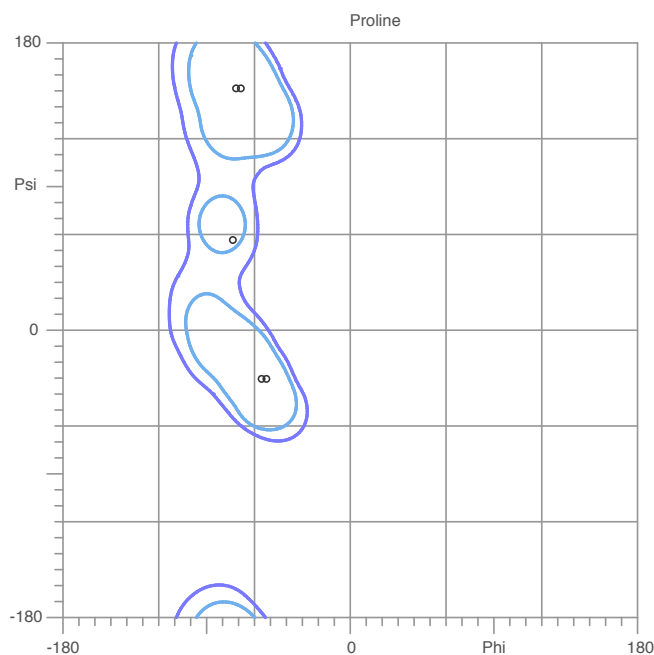
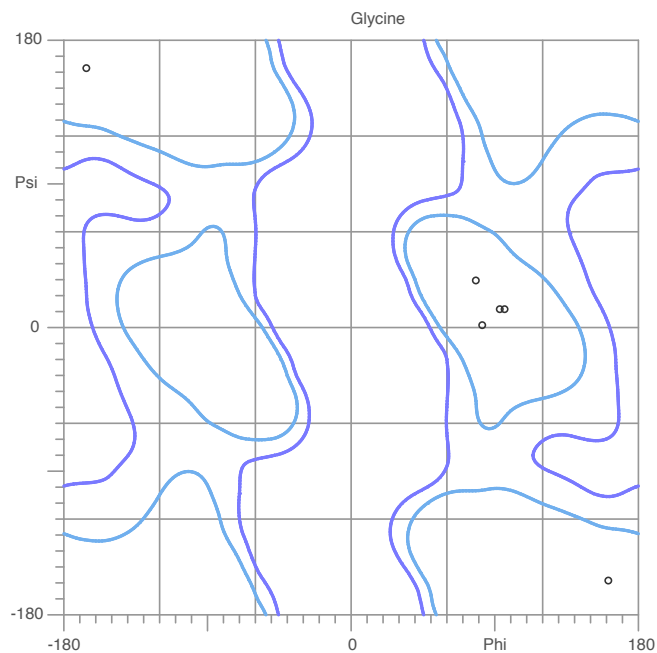
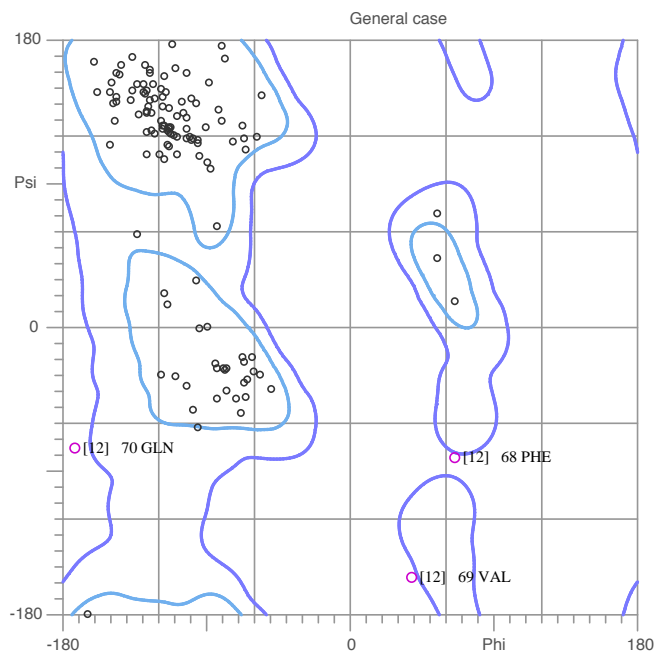
There were 1 outliers (phi, psi):
[11] 17 LEU (64.9, 115.0)

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MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 12



95.7% (135/141) of all residues were in favored (98%) regions.
97.9% (138/141) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

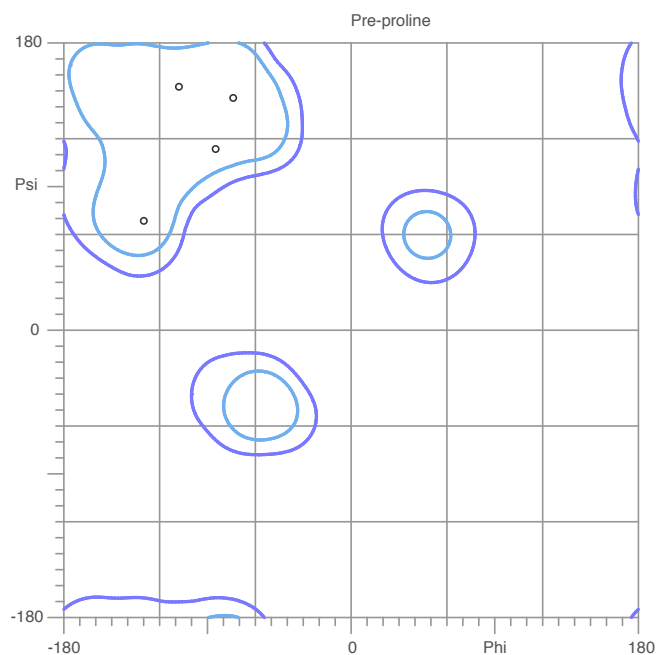
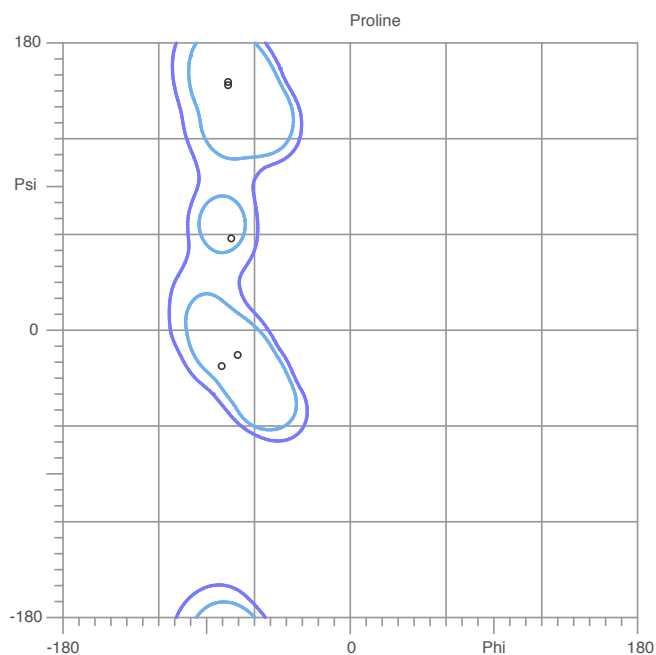
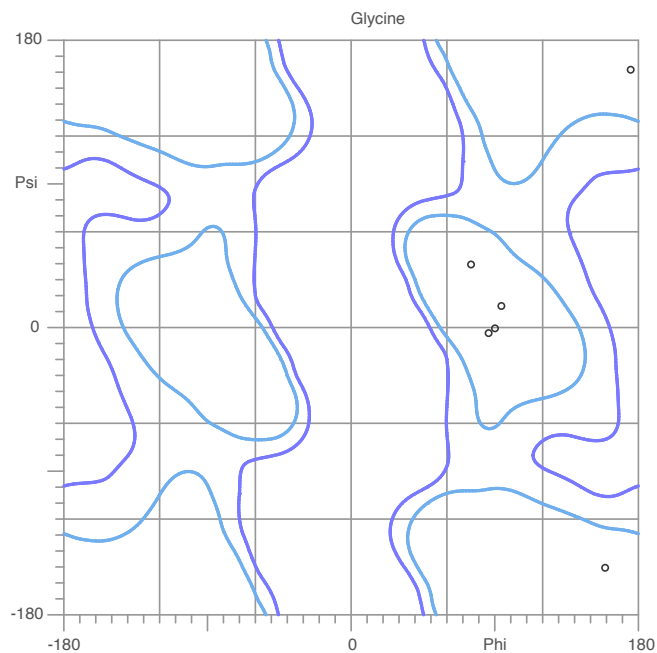
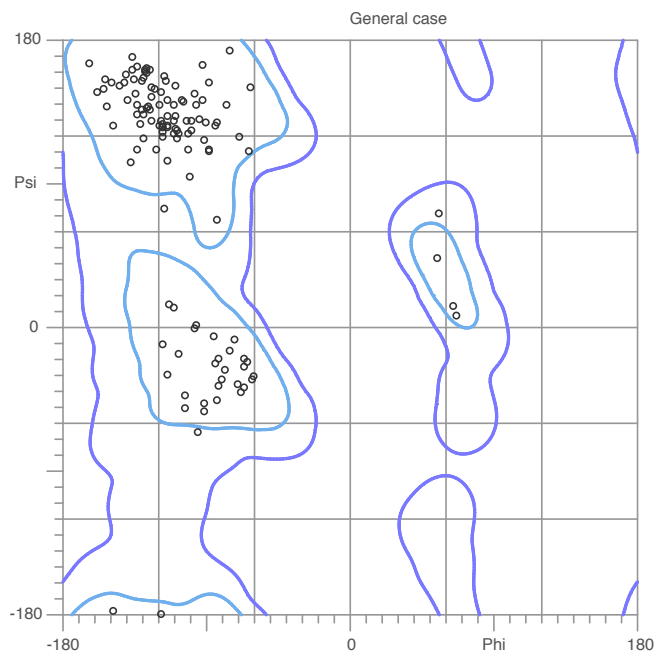
[12] 68 PHE (65.0, -81.2)

[12] 69 VAL (38.4, -156.5)

[12] 70 GLN (-173.3, -75.0)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 13



97.9% (138/141) of all residues were in favored (98%) regions.
100.0% (141/141) of all residues were in allowed (>99.8%) regions.

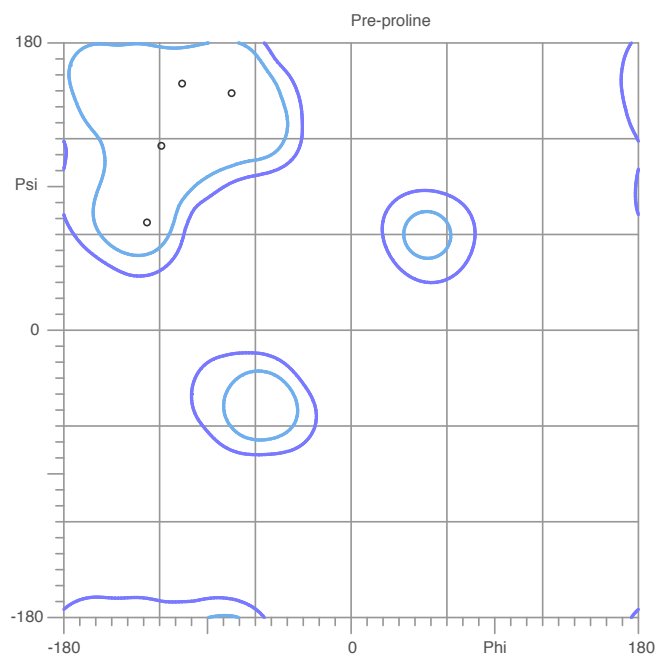
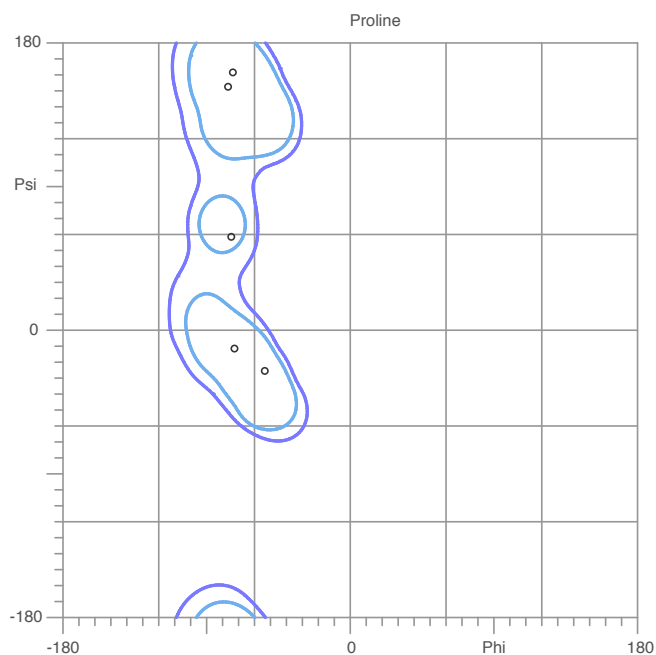
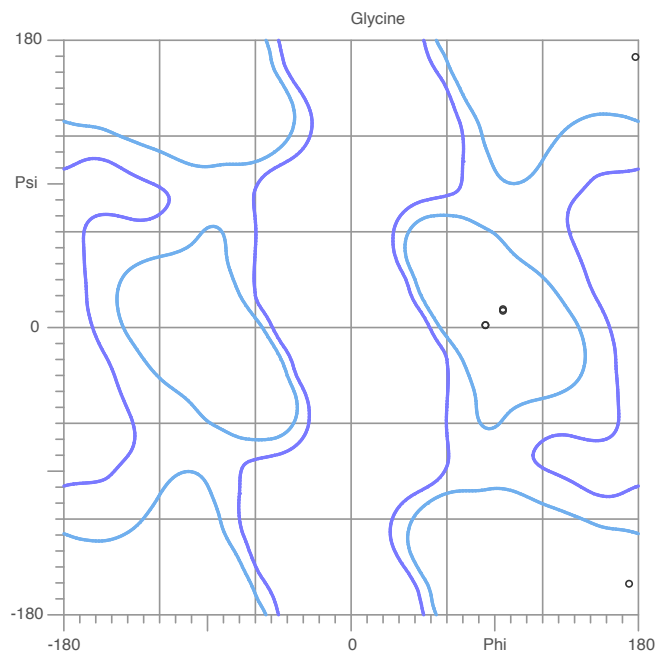
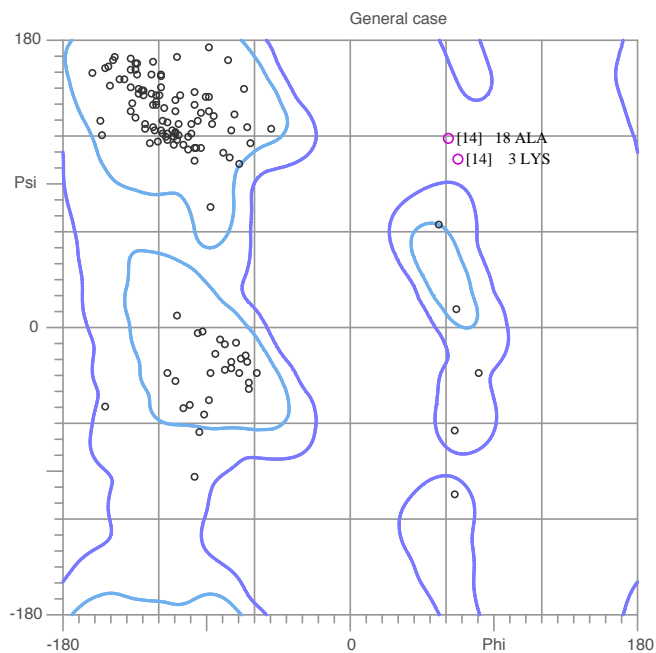
There were no outliers.

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MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 14

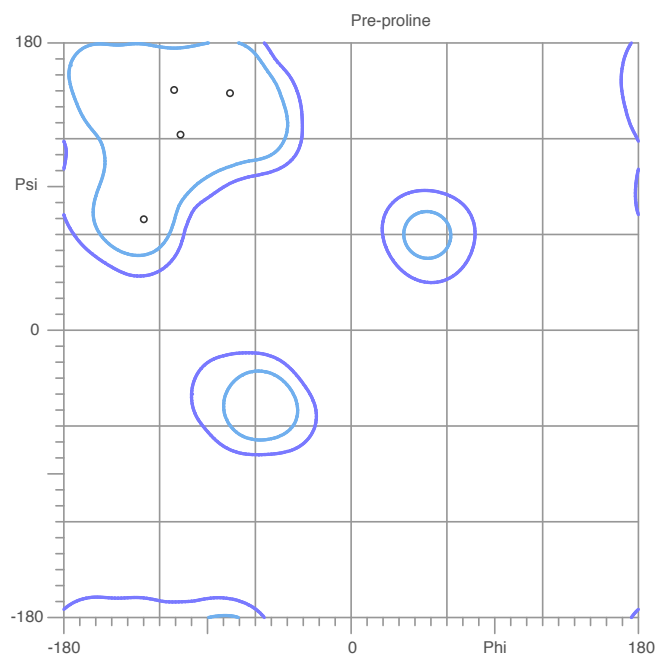
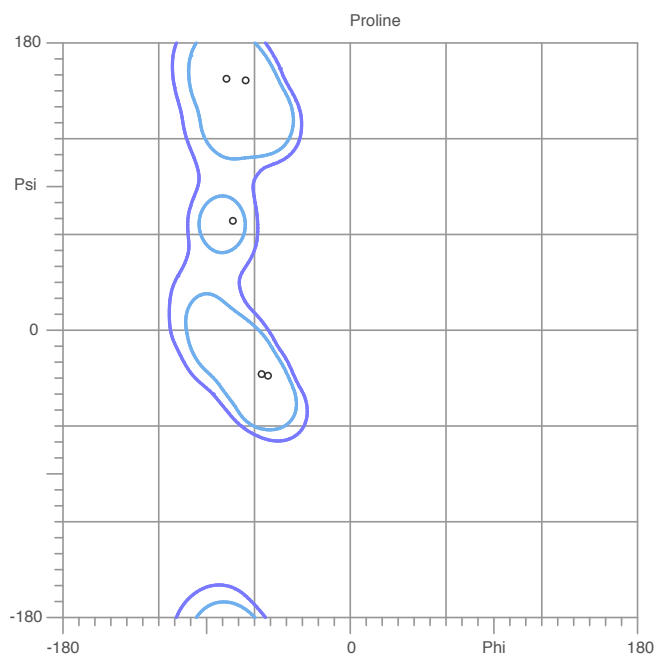
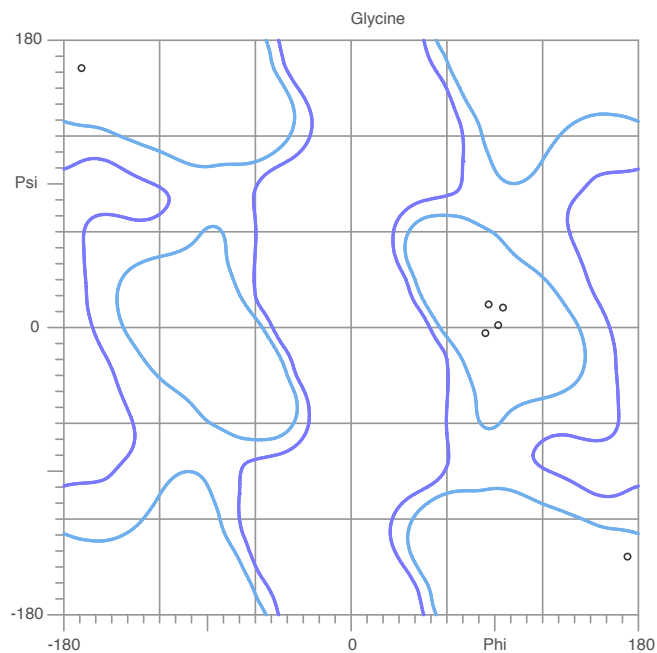
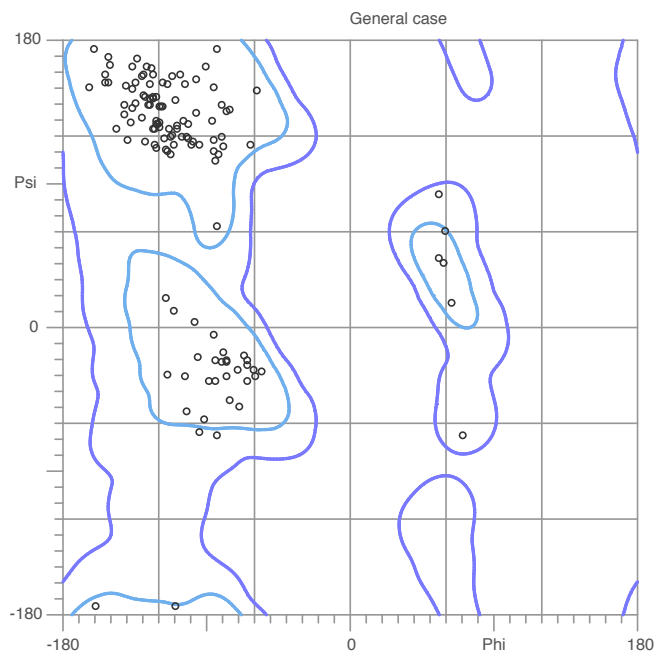


93.6% (132/141) of all residues were in favored (98%) regions.
98.6% (139/141) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[14] 3 LYS (67.6, 106.9)
[14] 18 ALA (61.1, 119.4)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 15



96.5% (136/141) of all residues were in favored (98%) regions.
100.0% (141/141) of all residues were in allowed (>99.8%) regions.

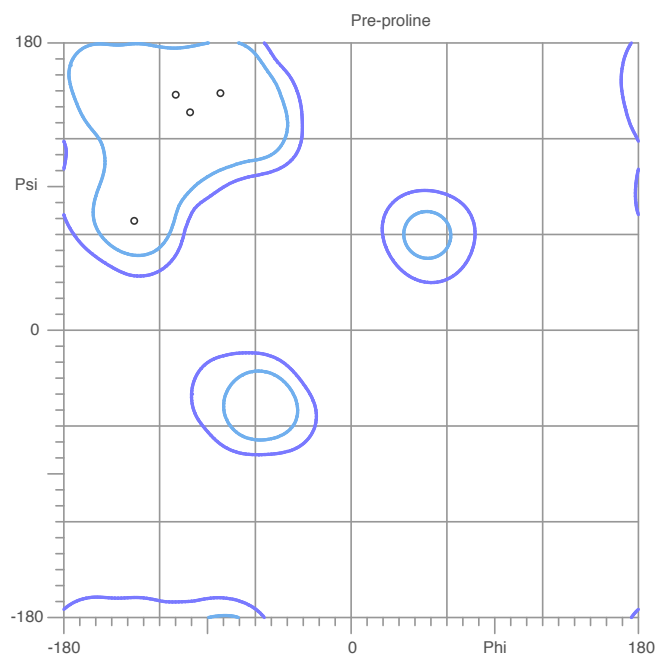
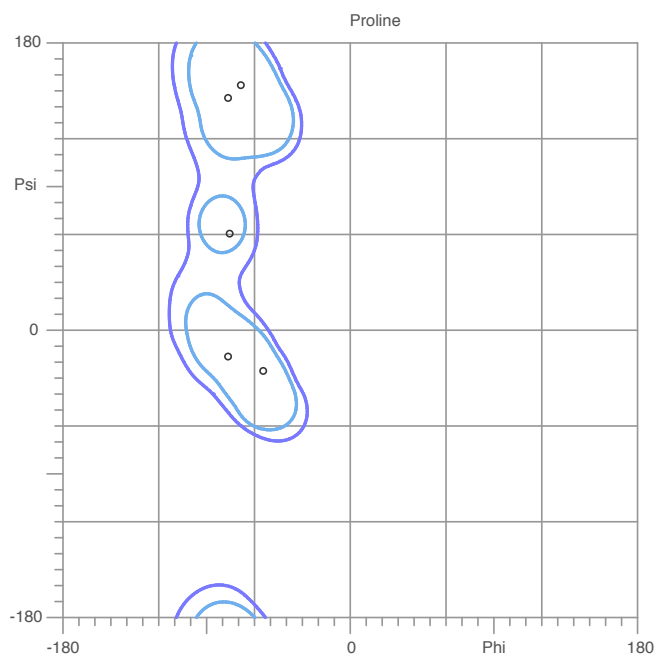
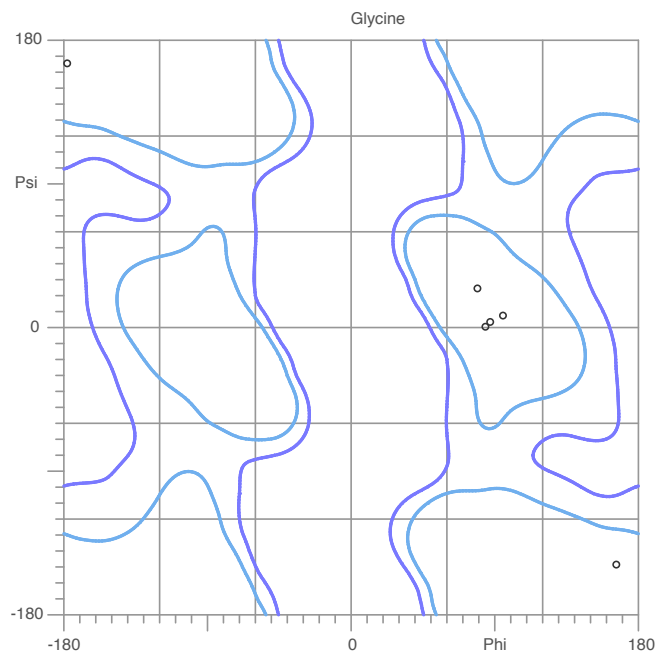
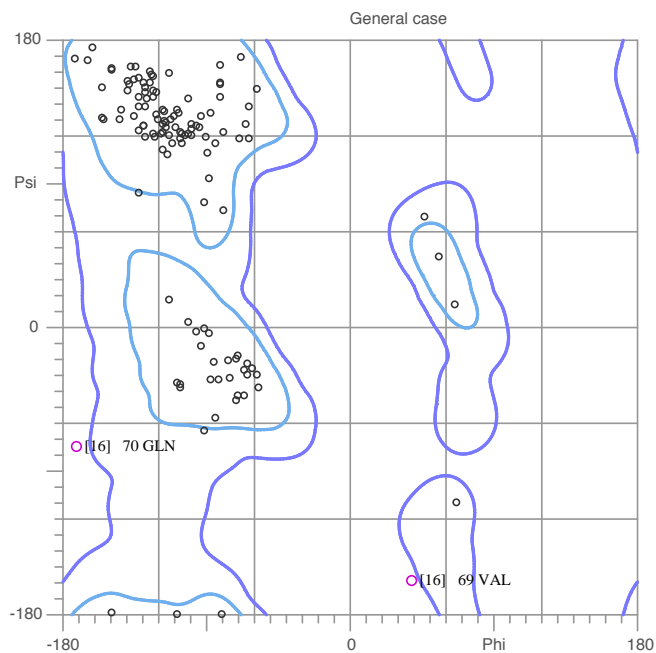
There were no outliers.

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

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MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 16

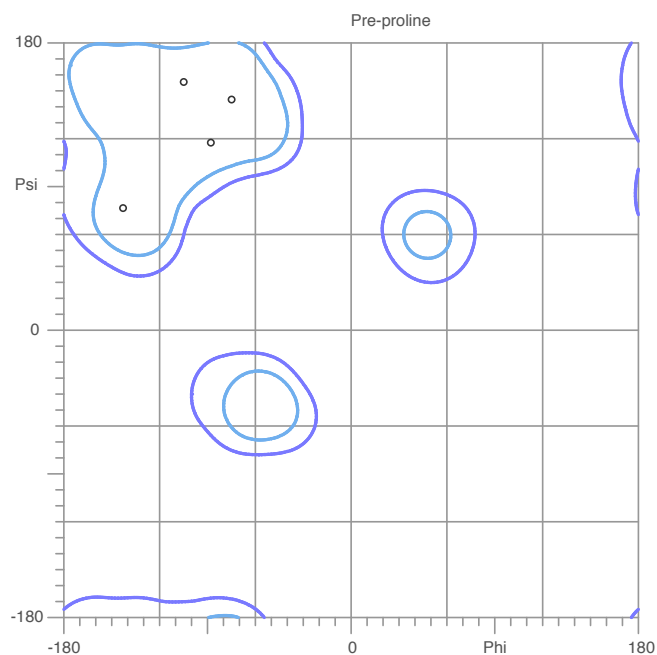
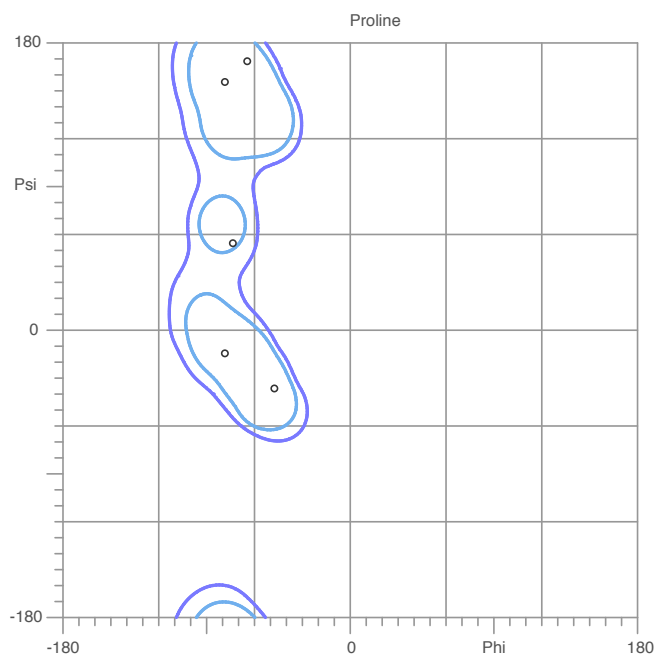
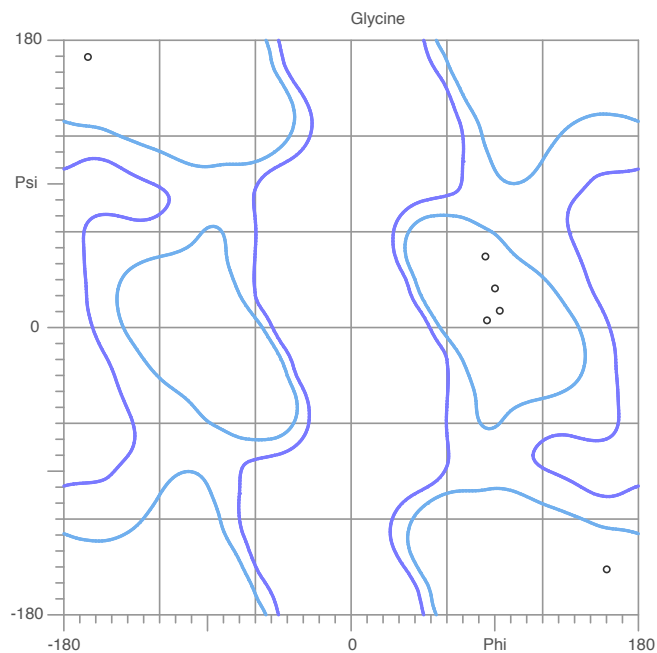
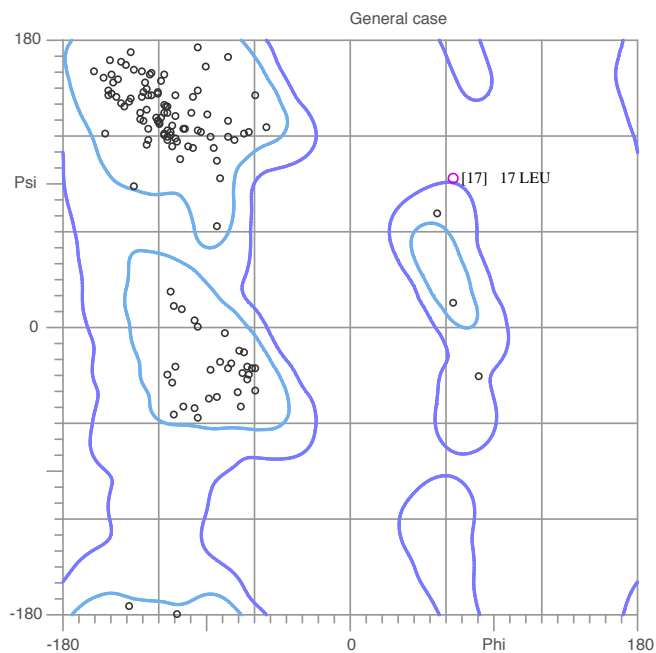


95.7% (135/141) of all residues were in favored (98%) regions.
98.6% (139/141) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[16] 69 VAL (38.9, -158.2)
[16] 70 GLN (-172.8, -75.0)

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 17



97.9% (138/141) of all residues were in favored (98%) regions.
99.3% (140/141) of all residues were in allowed (>99.8%) regions.

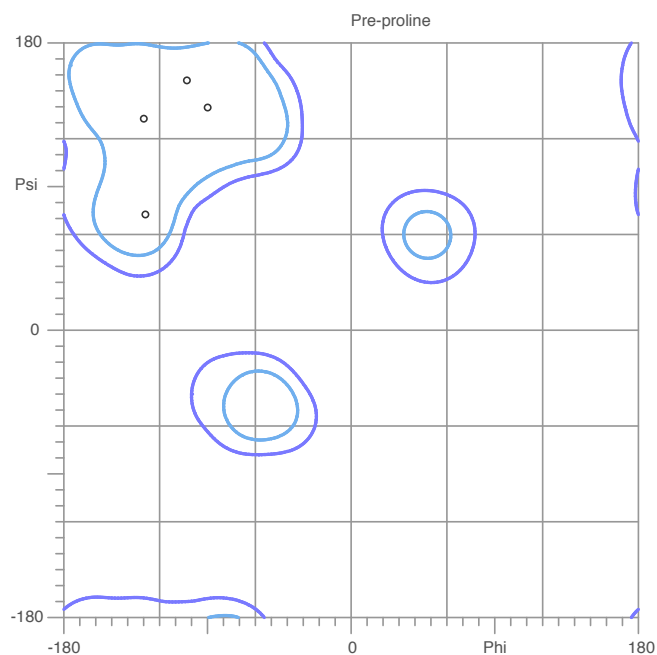
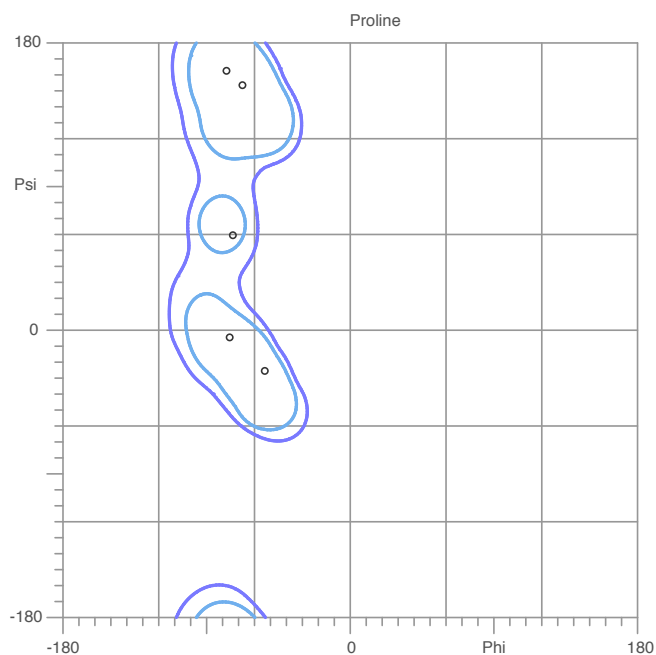
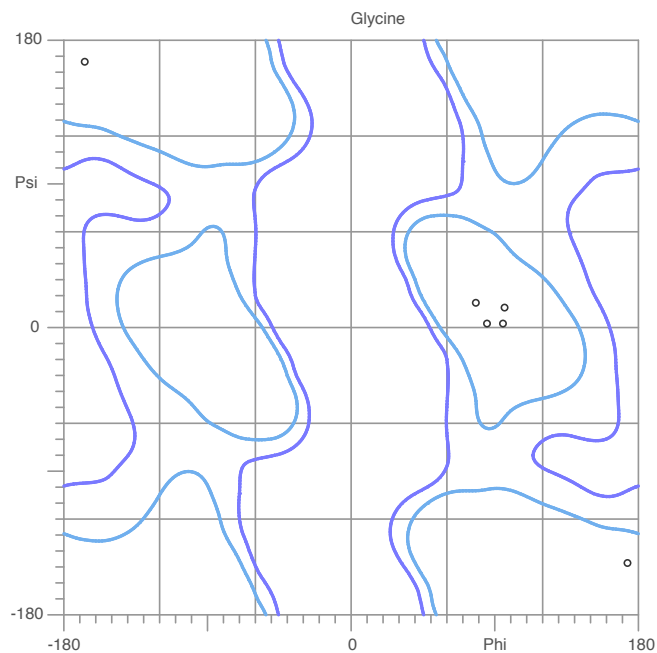
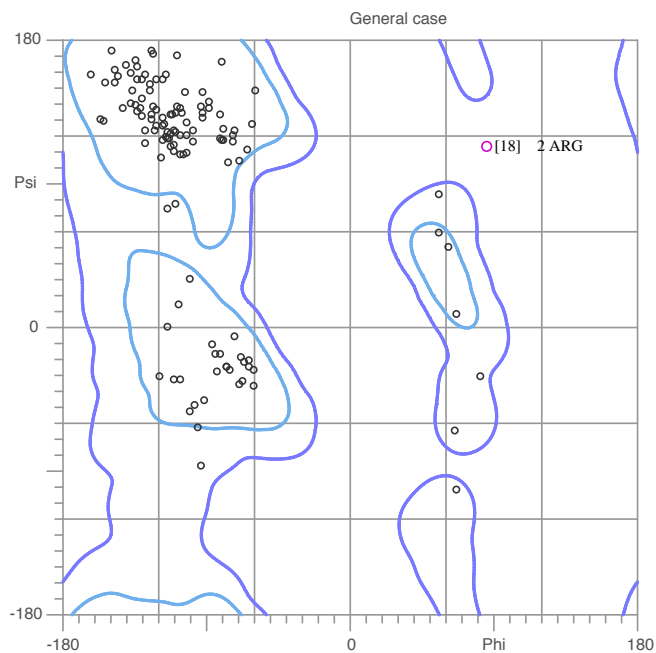
There were 1 outliers (phi, psi):
[17] 17 LEU (65.0, 94.6)

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

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

MolProbity Ramachandran analysis

HR1958_R3Cons_em_bcr3.pdb, model 18



93.6% (132/141) of all residues were in favored (98%) regions.
99.3% (140/141) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[18] 2 ARG (85.0, 115.0)

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

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