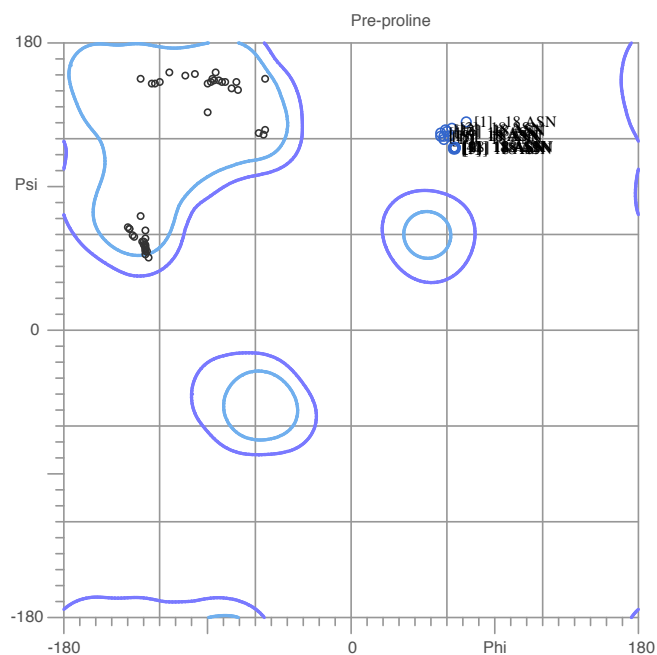
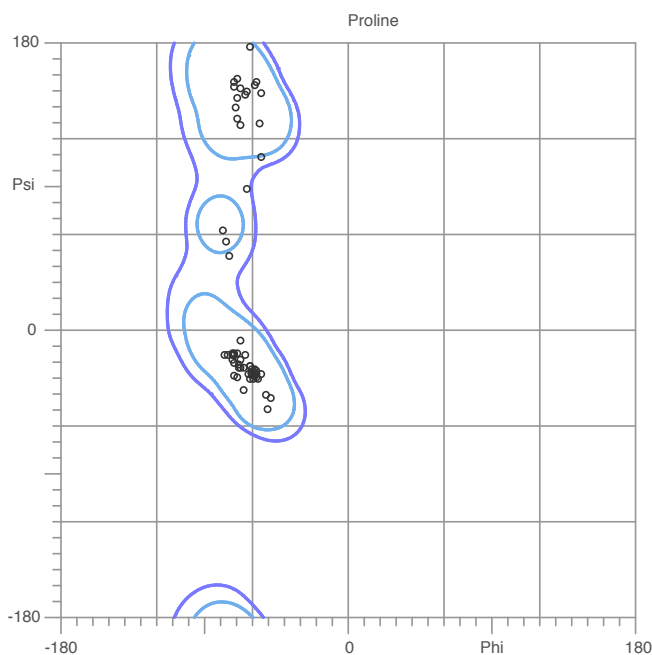
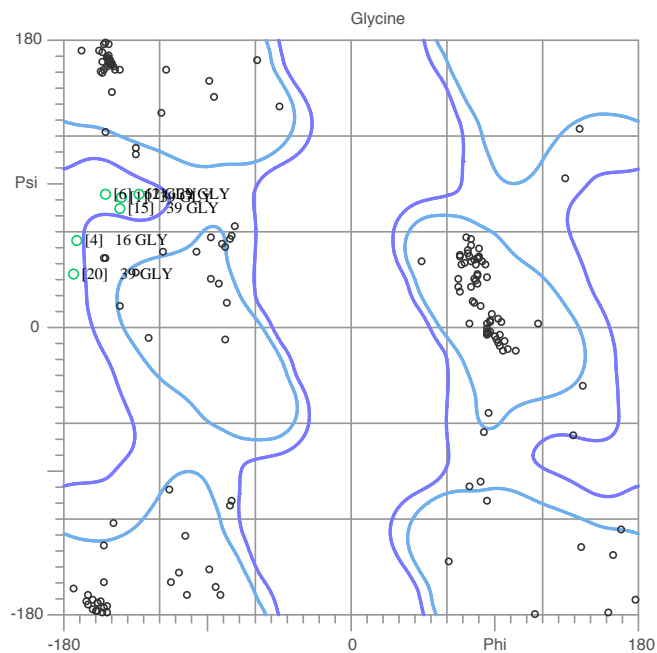
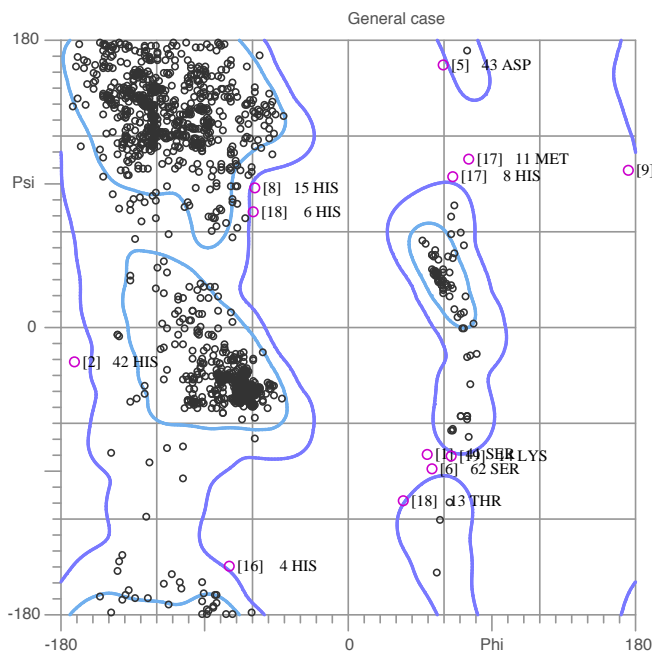


MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, all models



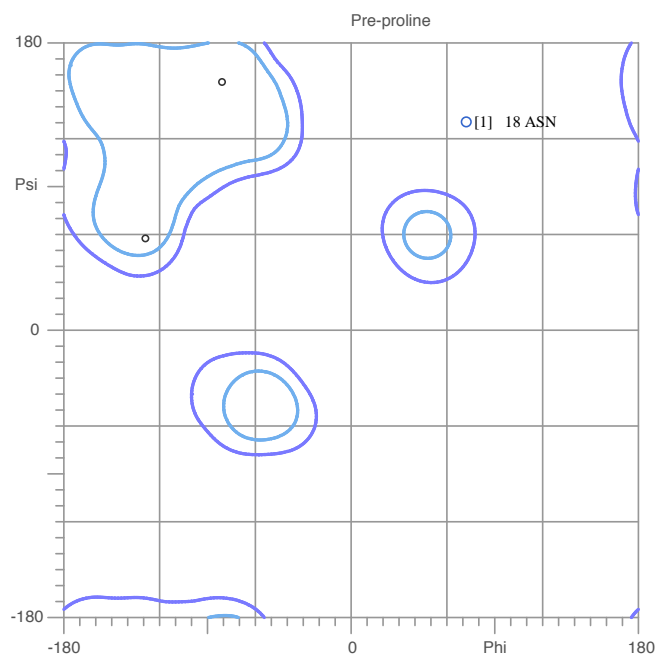
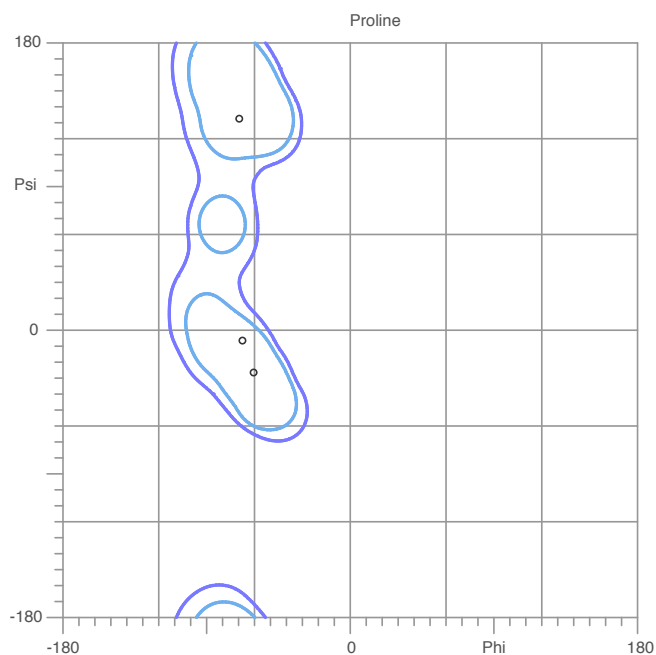
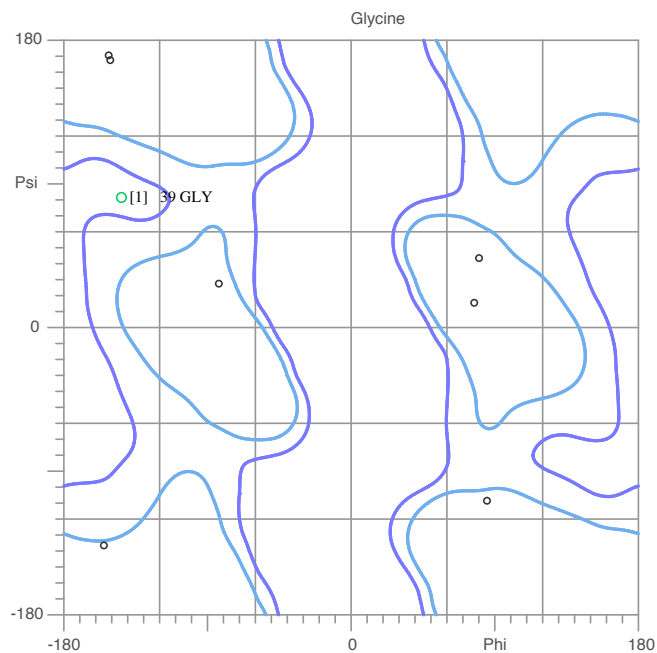
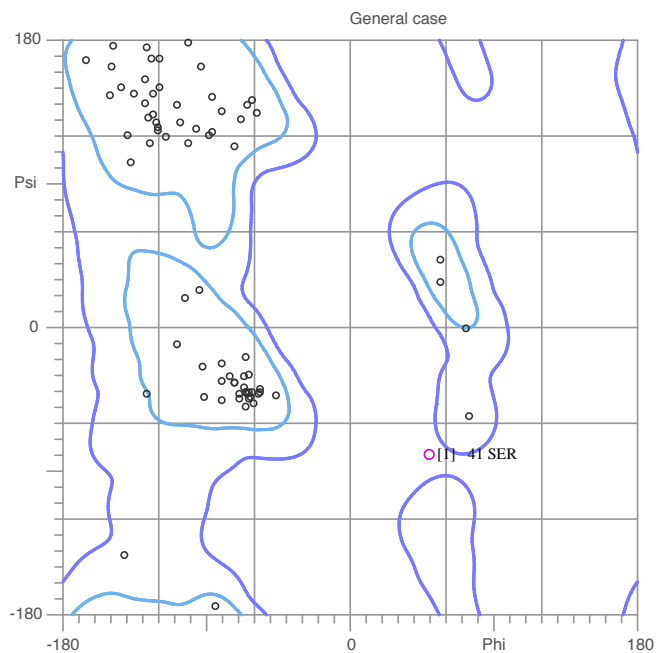
92.0% (1638/1780) of all residues were in favored (98%) regions.
98.0% (1745/1780) of all residues were in allowed (>99.8%) regions.

There were 35 outliers (phi, psi):

- | | |
|----------------------------|----------------------------|
| [1] 18 ASN (73.0, 131.4) | [8] 18 ASN (61.4, 122.3) |
| [1] 39 GLY (-144.9, 82.1) | [9] 4 HIS (175.1, 99.2) |
| [1] 41 SER (49.3, -79.2) | [9] 18 ASN (65.1, 115.1) |
| [2] 18 ASN (65.1, 115.4) | [10] 18 ASN (58.9, 120.7) |
| [2] 39 GLY (-133.3, 84.9) | [11] 18 ASN (64.9, 115.9) |
| [2] 42 HIS (-172.5, -21.7) | [12] 18 ASN (60.0, 126.1) |
| [3] 18 ASN (63.1, 127.5) | [14] 18 ASN (65.0, 115.0) |
| [4] 16 GLY (-172.2, 55.1) | [15] 18 ASN (58.1, 122.5) |
| [4] 18 ASN (65.0, 115.2) | [15] 39 GLY (-145.1, 75.7) |
| [5] 18 ASN (65.1, 115.0) | [16] 4 HIS (-75.9, -149.7) |
| [5] 43 ASP (59.7, 165.5) | [16] 18 ASN (60.5, 125.4) |
| [6] 18 ASN (65.3, 115.3) | [17] 8 HIS (65.8, 95.6) |
| [6] 61 GLY (-155.0, 84.9) | [17] 11 MET (75.3, 106.6) |
| [6] 62 SER (52.0, -88.1) | [17] 18 ASN (56.7, 124.6) |
| [8] 15 HIS (-59.1, 88.9) | [18] 6 HIS (-60.2, 73.7) |
| | [18] 13 THR (34.1, -108.5) |
| | [18] 18 ASN (65.2, 115.5) |
| | [19] 14 LYS (64.9, -80.2) |
| | [19] 18 ASN (56.7, 122.0) |
| | [20] 39 GLY (-174.9, 34.1) |

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 1



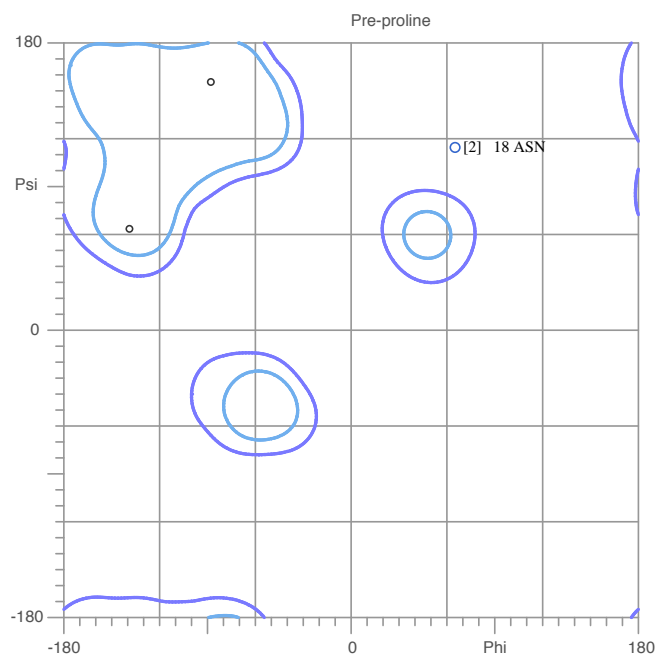
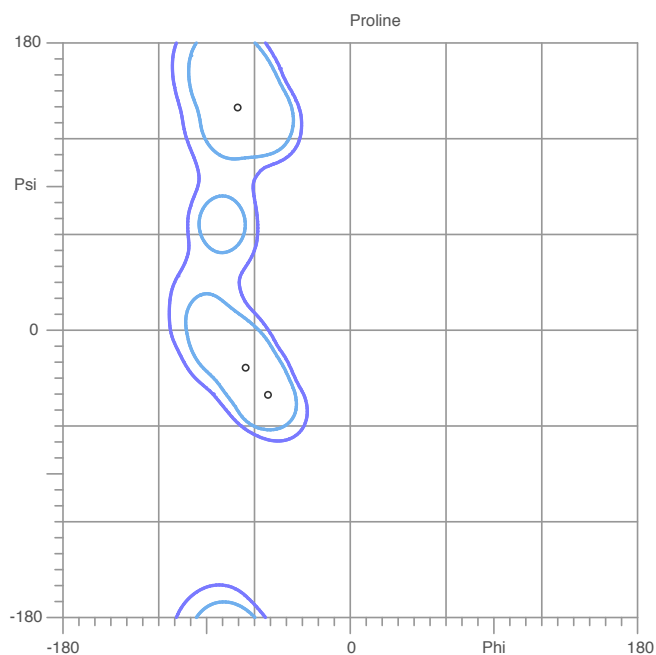
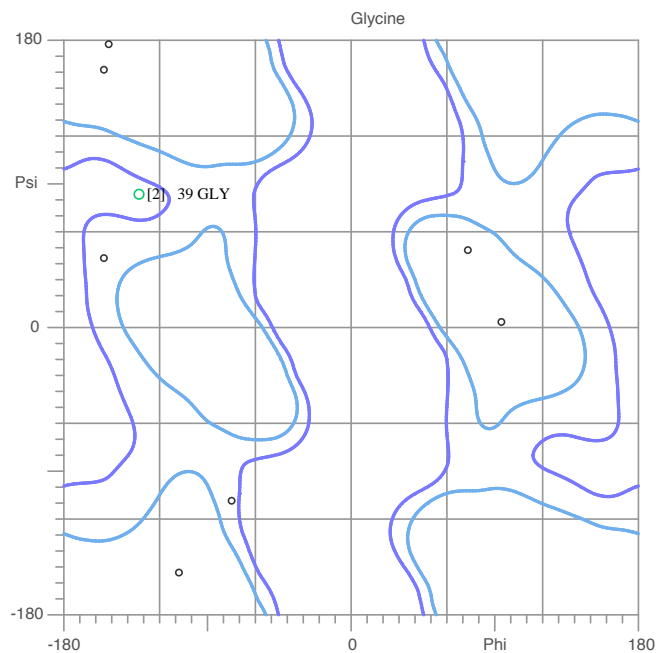
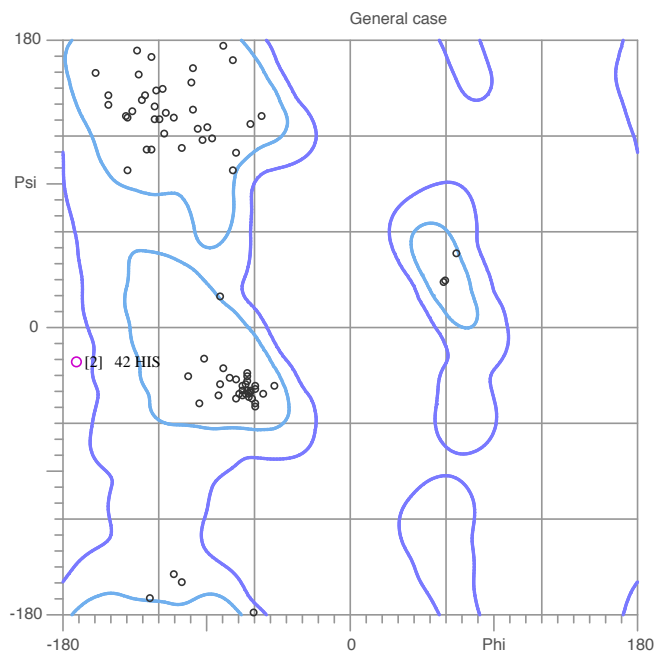
92.1% (82/89) of all residues were in favored (98%) regions.
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 18 ASN (73.0, 131.4)
- [1] 39 GLY (-144.9, 82.1)
- [1] 41 SER (49.3, -79.2)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 2



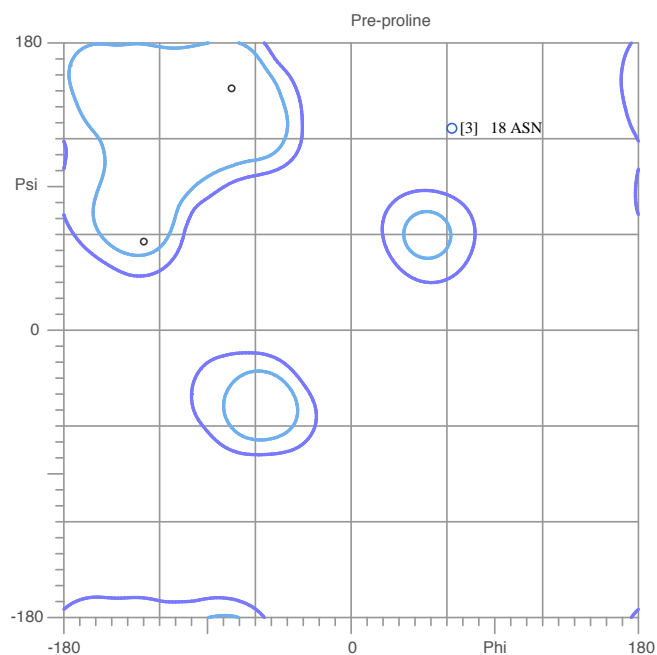
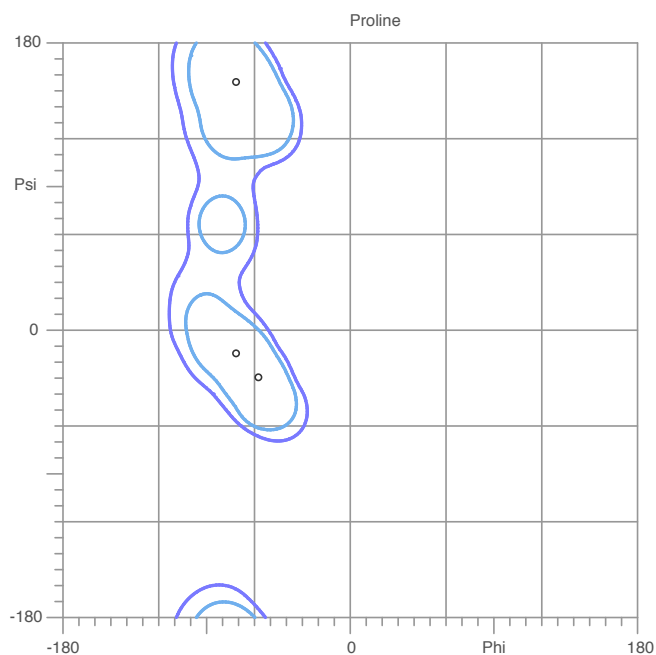
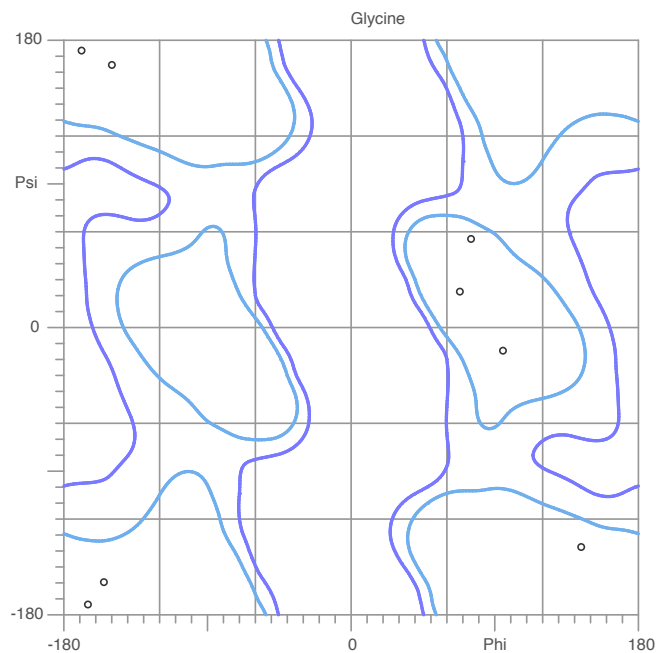
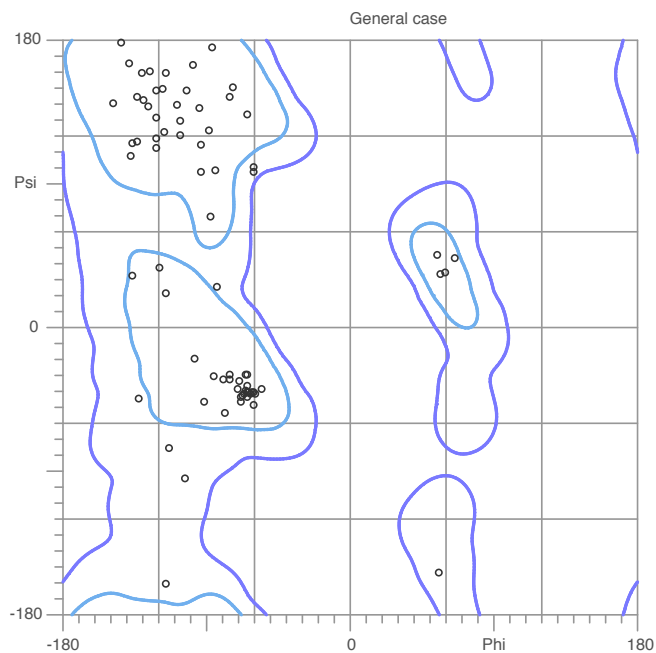
88.8% (79/89) of all residues were in favored (98%) regions.
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 18 ASN (65.1, 115.4)
- [2] 39 GLY (-133.3, 84.9)
- [2] 42 HIS (-172.5, -21.7)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 3

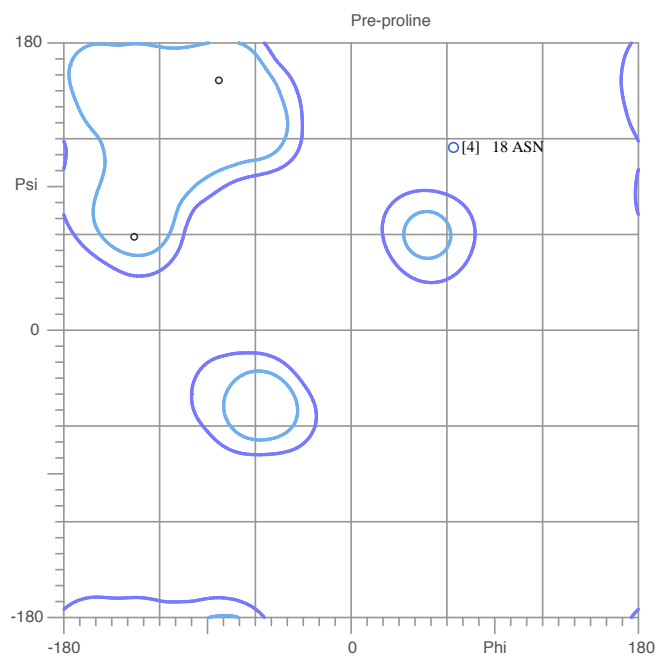
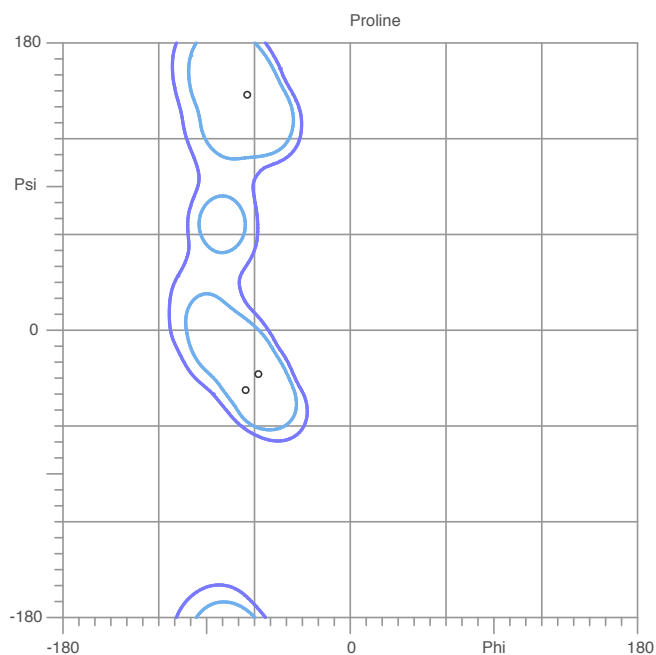
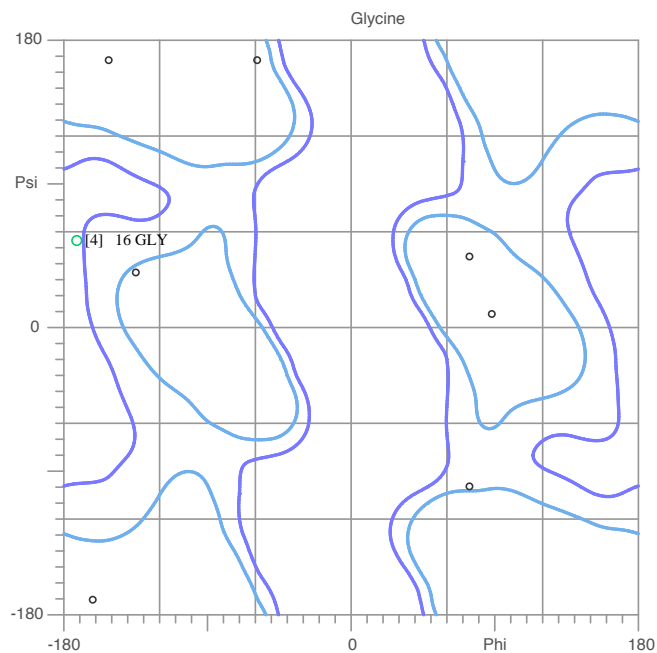
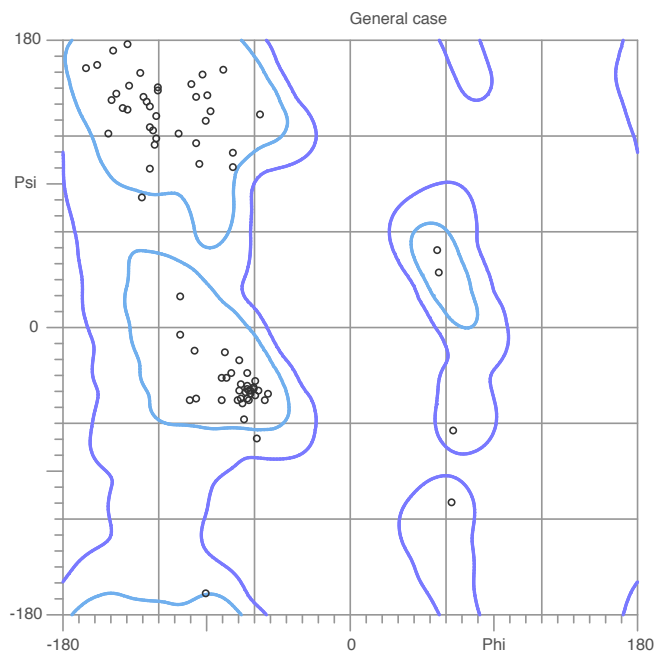


89.9% (80/89) of all residues were in favored (98%) regions.
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[3] 18 ASN (63.1, 127.5)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 4



91.0% (81/89) of all residues were in favored (98%) regions.
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

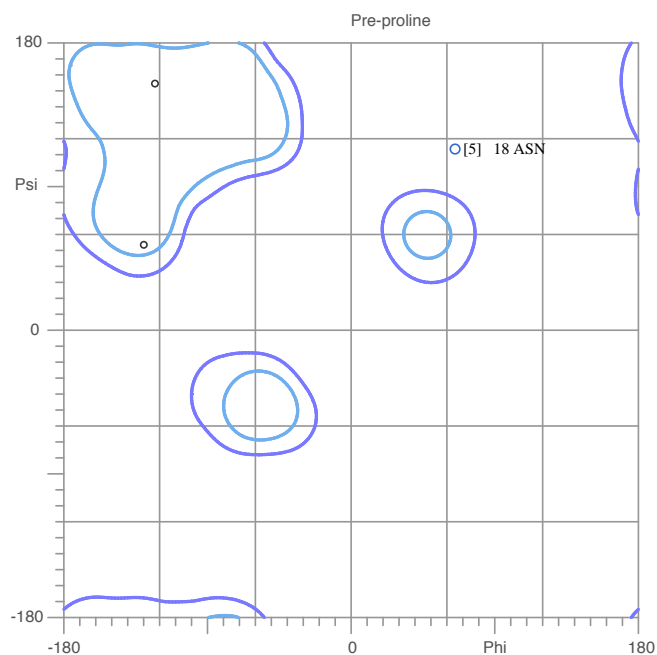
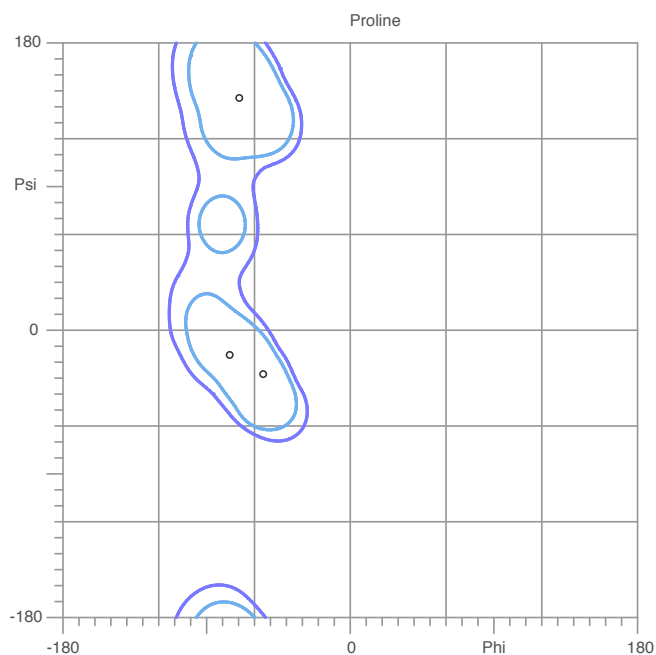
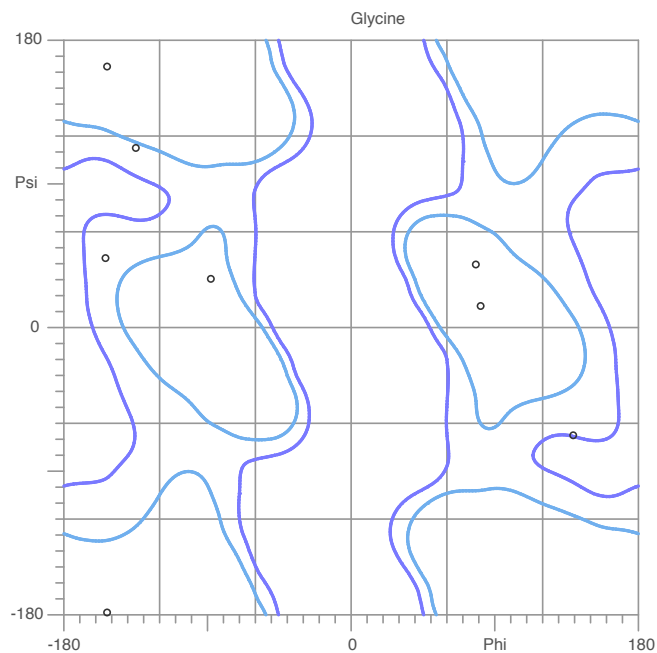
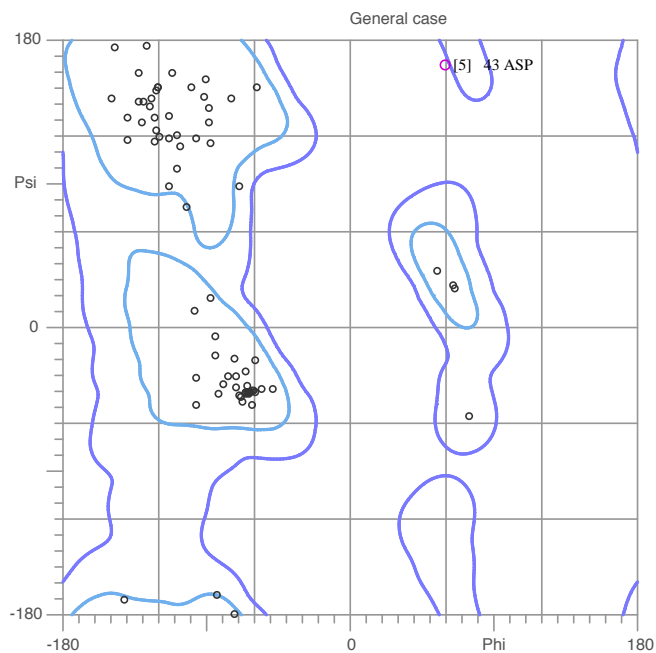
There were 2 outliers (phi, psi):

[4] 16 GLY (-172.2, 55.1)

[4] 18 ASN (65.0, 115.2)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 5



91.0% (81/89) of all residues were in favored (98%) regions.
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

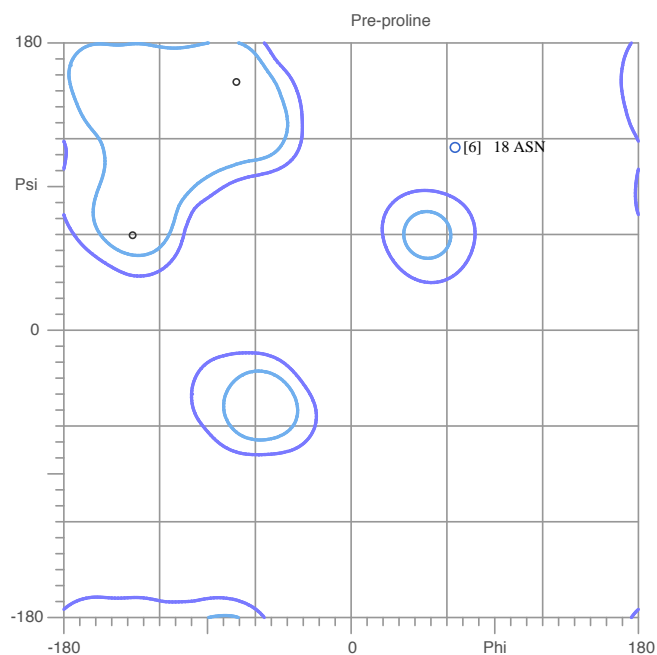
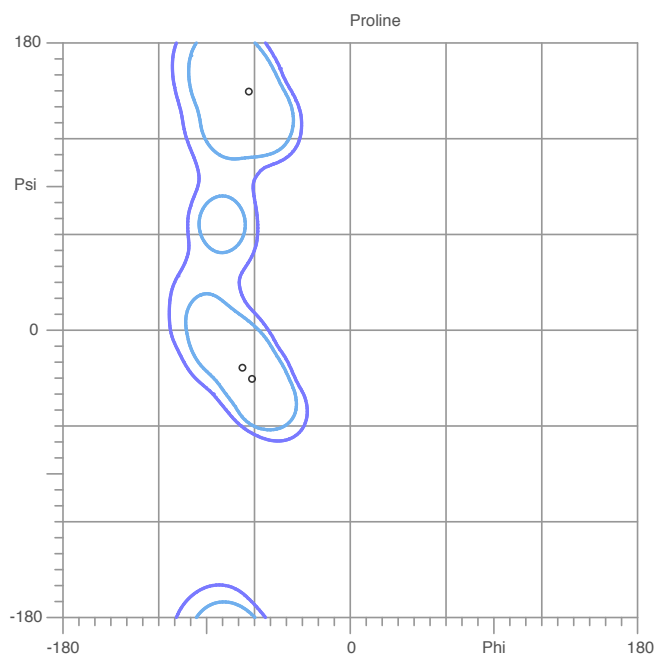
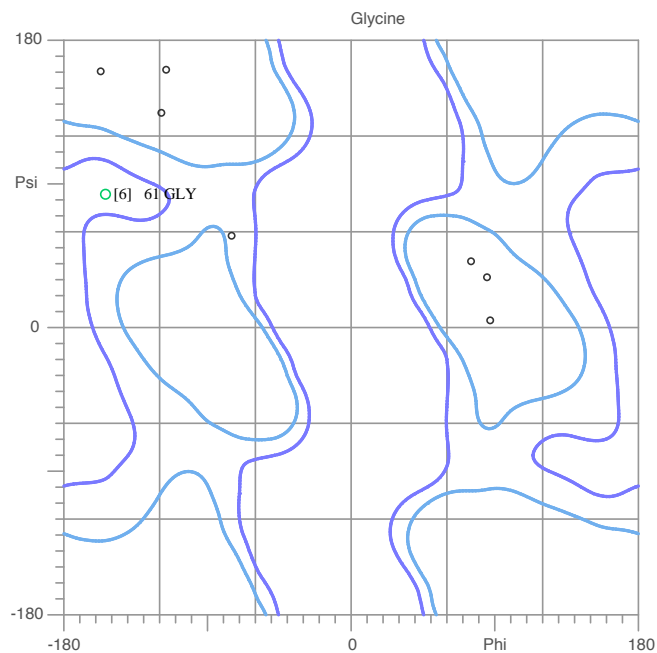
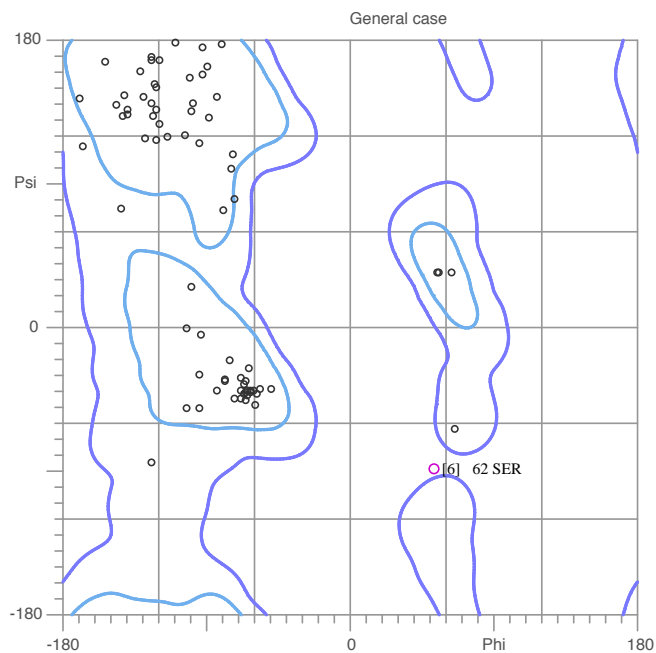
There were 2 outliers (phi, psi):

[5] 18 ASN (65.1, 115.0)

[5] 43 ASP (59.7, 165.5)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 6



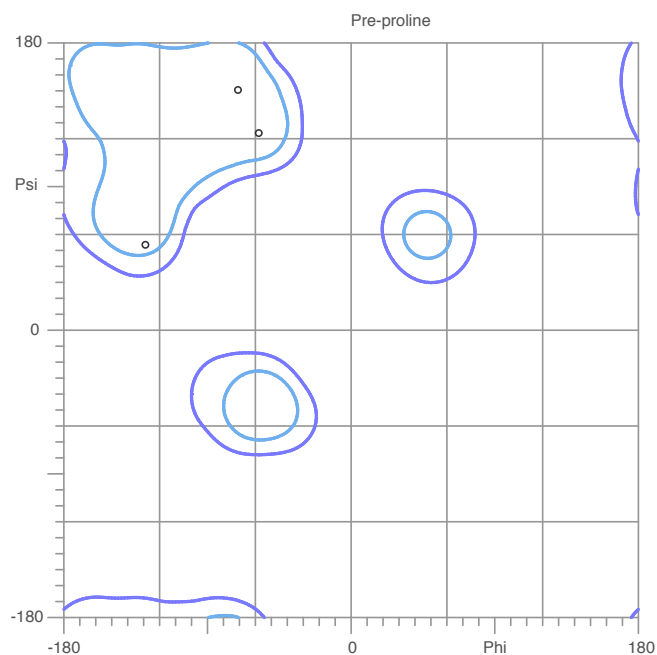
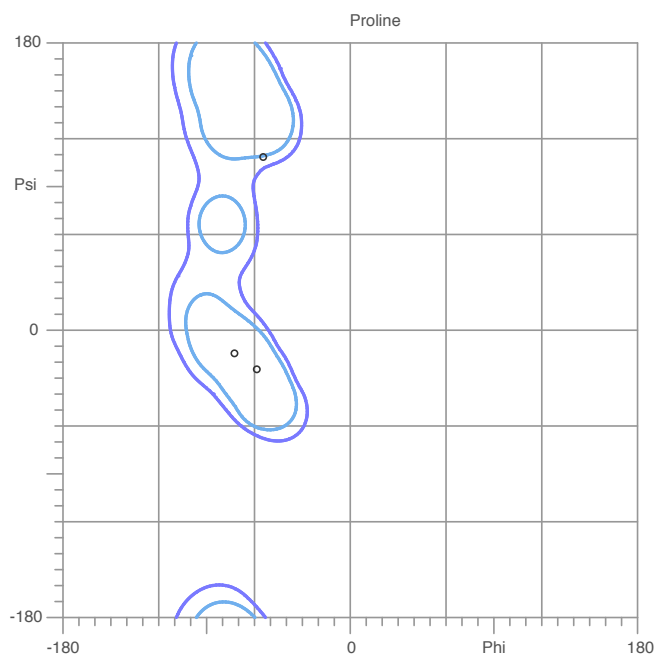
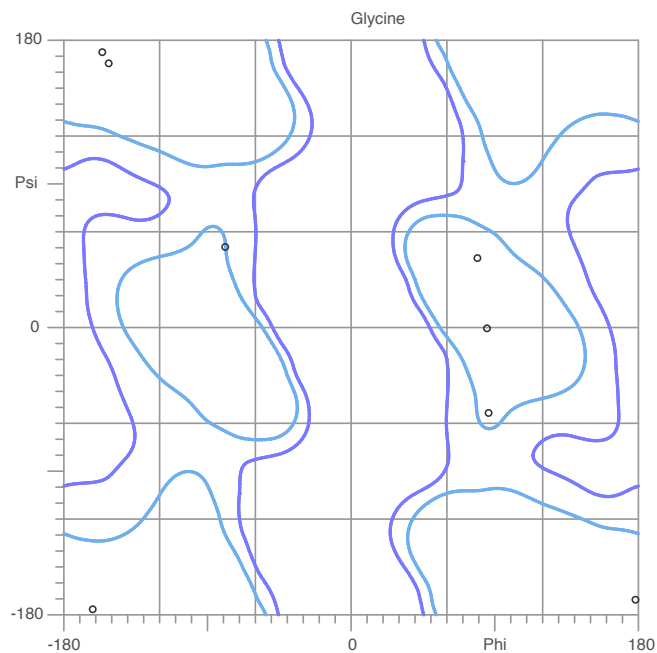
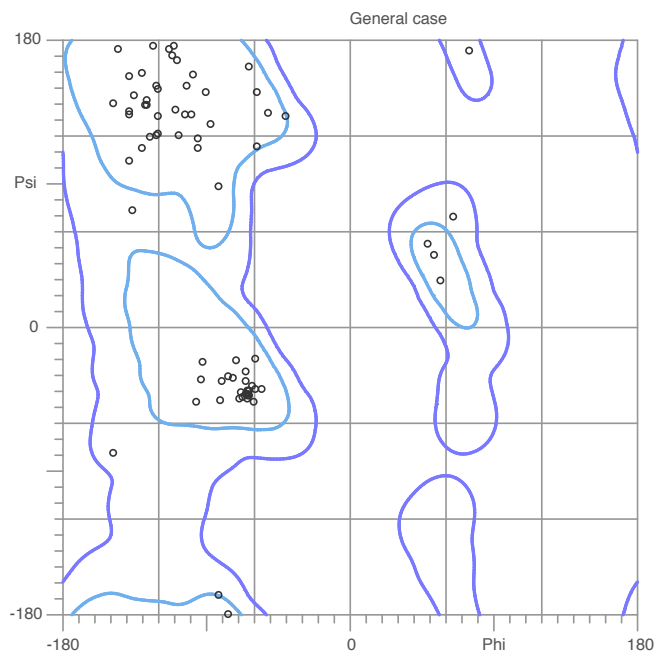
91.0% (81/89) of all residues were in favored (98%) regions.
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [6] 18 ASN (65.3, 115.3)
- [6] 61 GLY (-155.0, 84.9)
- [6] 62 SER (52.0, -88.1)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 7



94.4% (84/89) of all residues were in favored (98%) regions.
100.0% (89/89) of all residues were in allowed (>99.8%) regions.

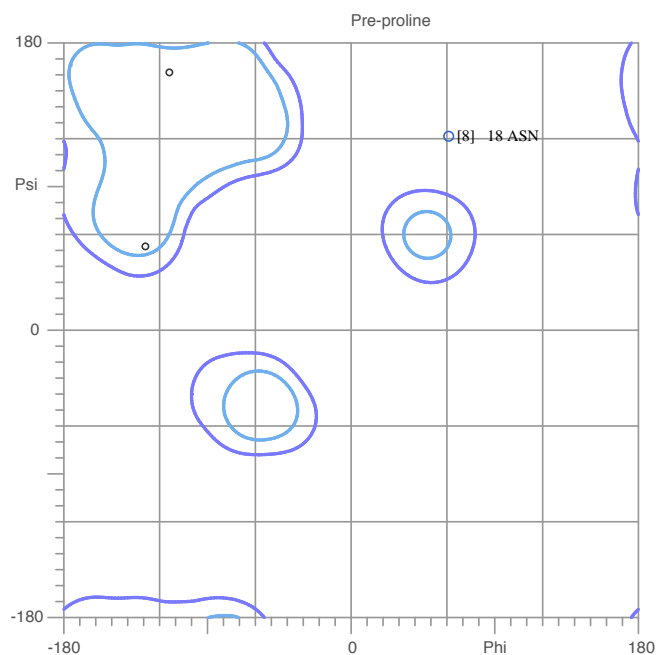
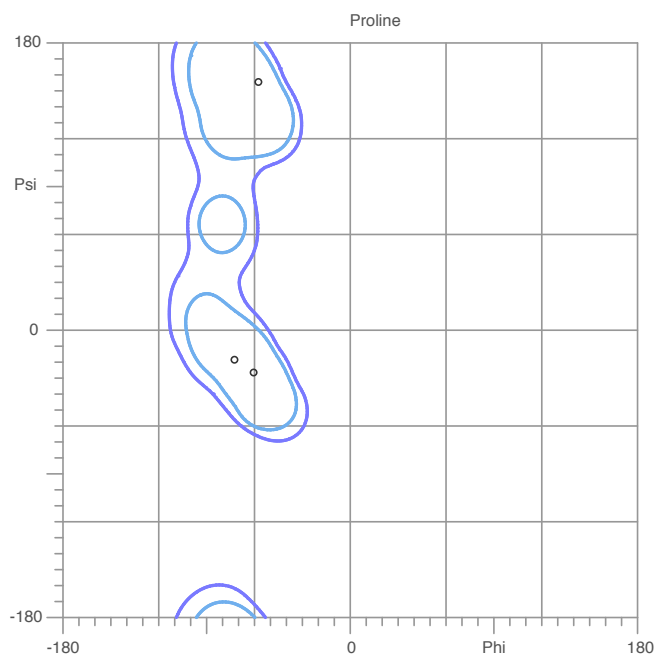
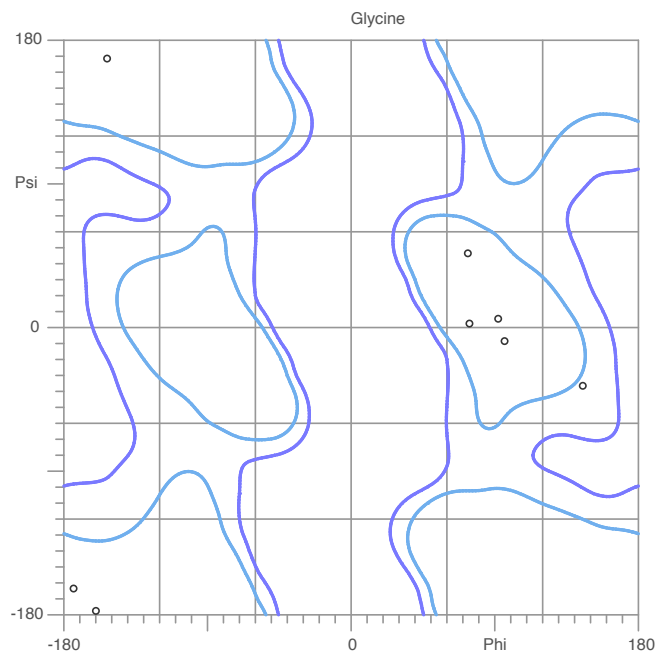
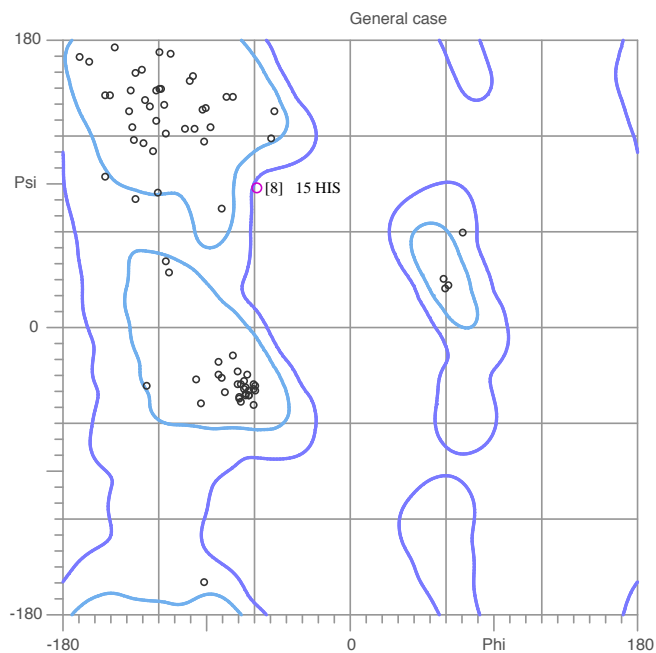
There were no outliers.

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MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 8



92.1% (82/89) of all residues were in favored (98%) regions.
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

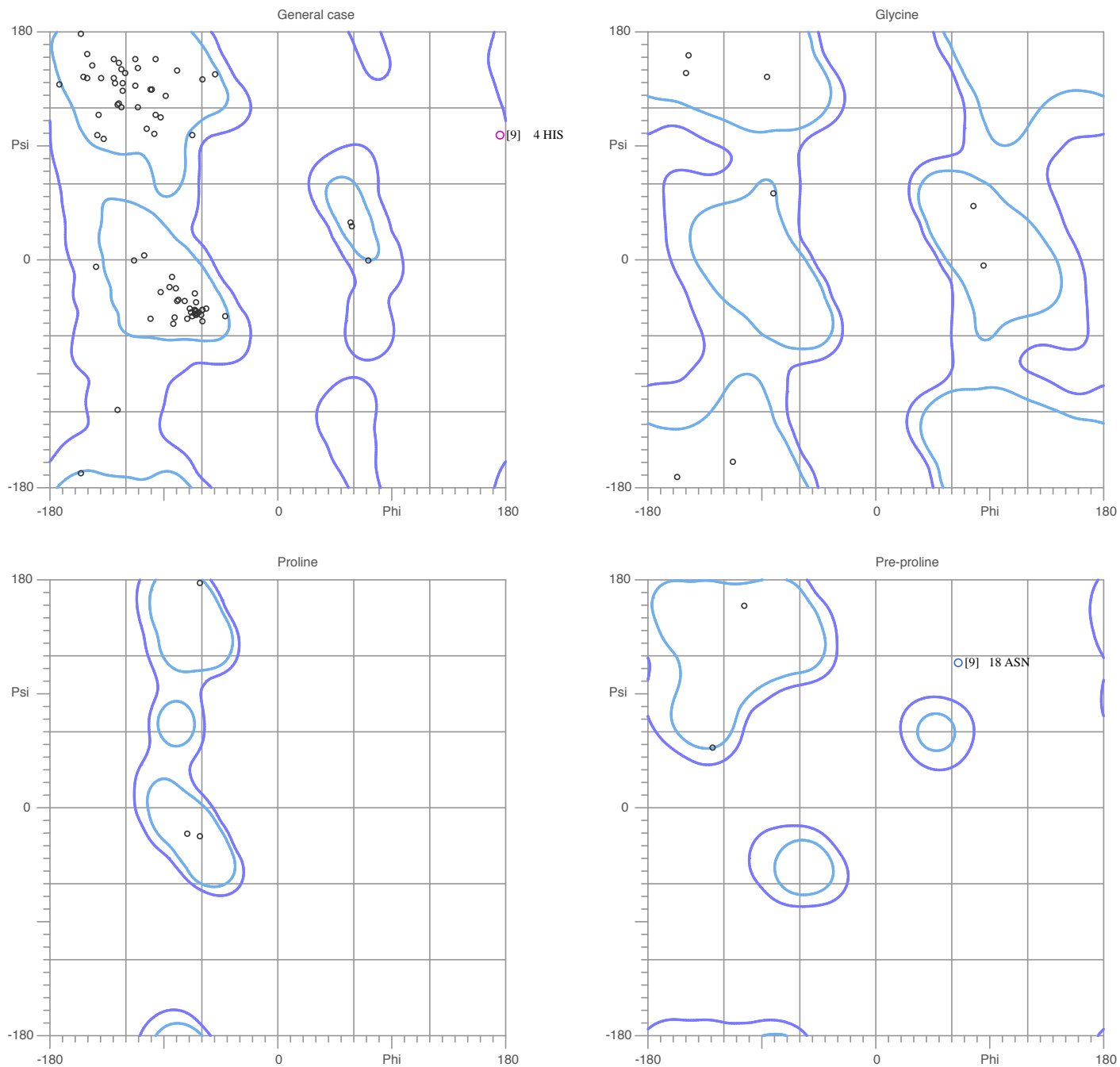
There were 2 outliers (phi, psi):

[8] 15 HIS (-59.1, 88.9)

[8] 18 ASN (61.4, 122.3)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 9



93.3% (83/89) of all residues were in favored (98%) regions.
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

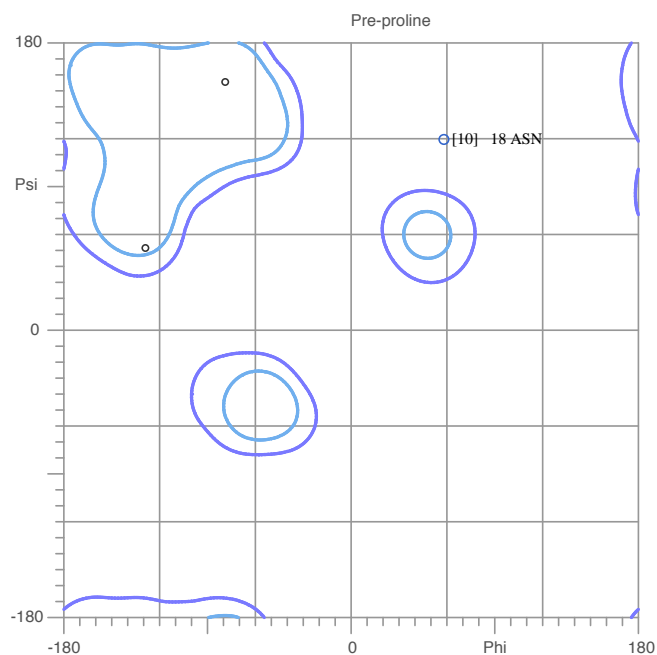
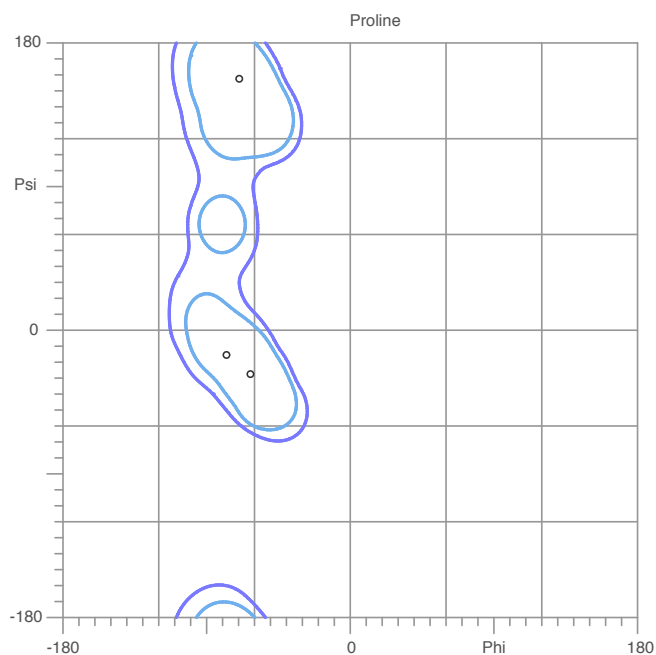
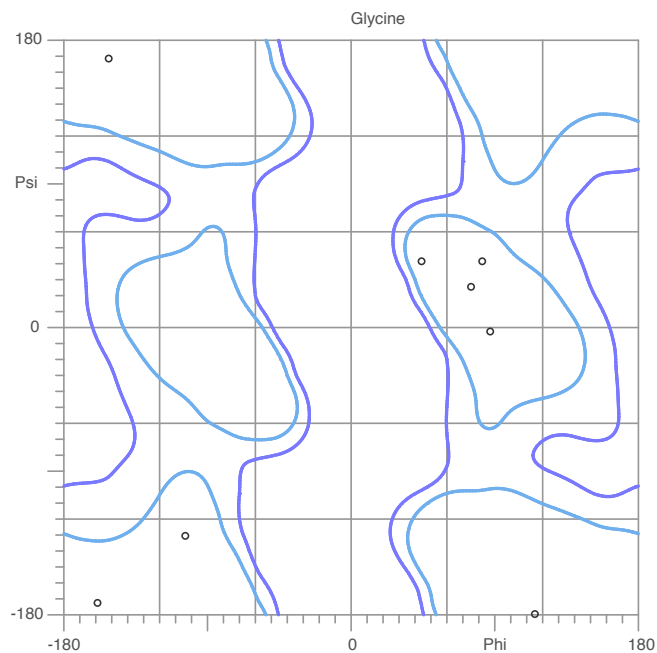
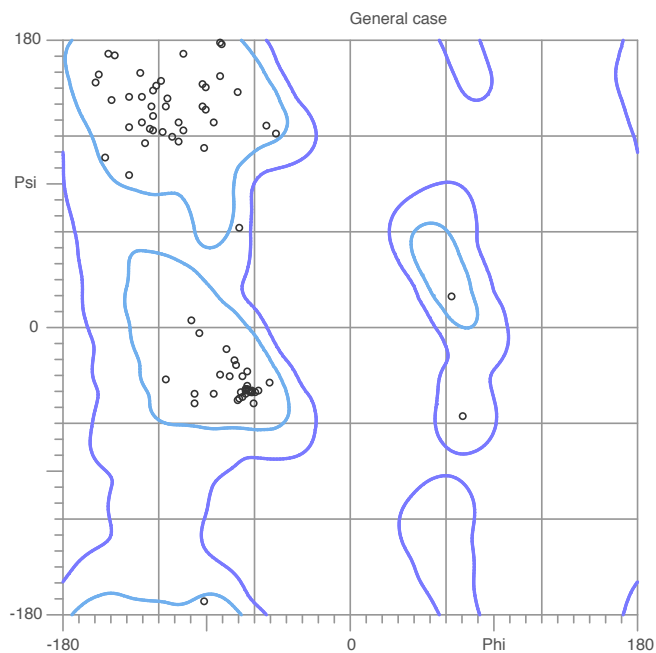
There were 2 outliers (phi, psi):

[9] 4 HIS (175.1, 99.2)

[9] 18 ASN (65.1, 115.1)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 10



96.6% (86/89) of all residues were in favored (98%) regions.
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

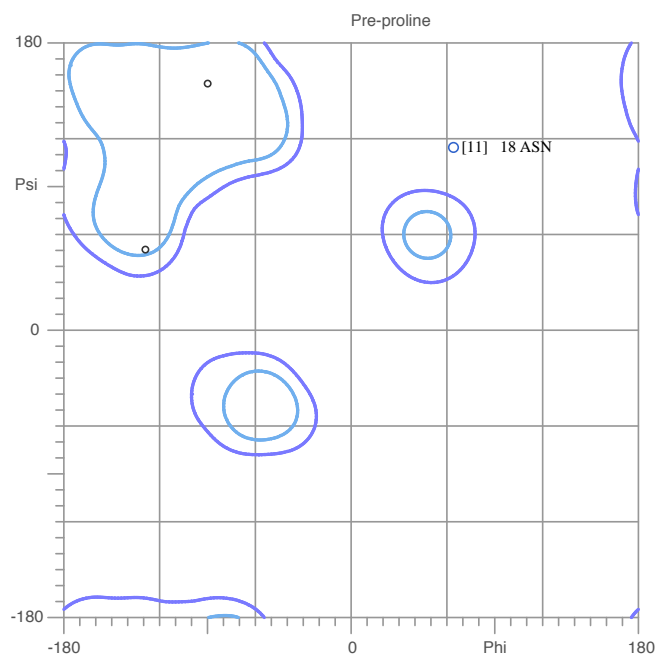
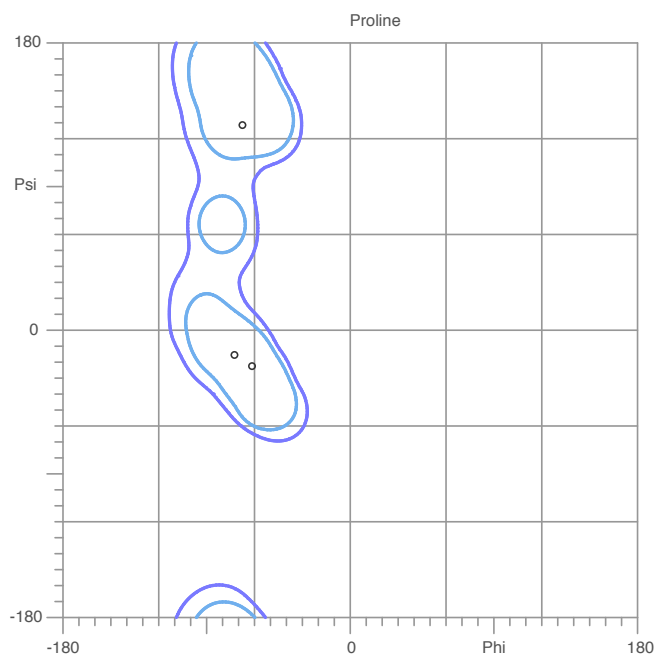
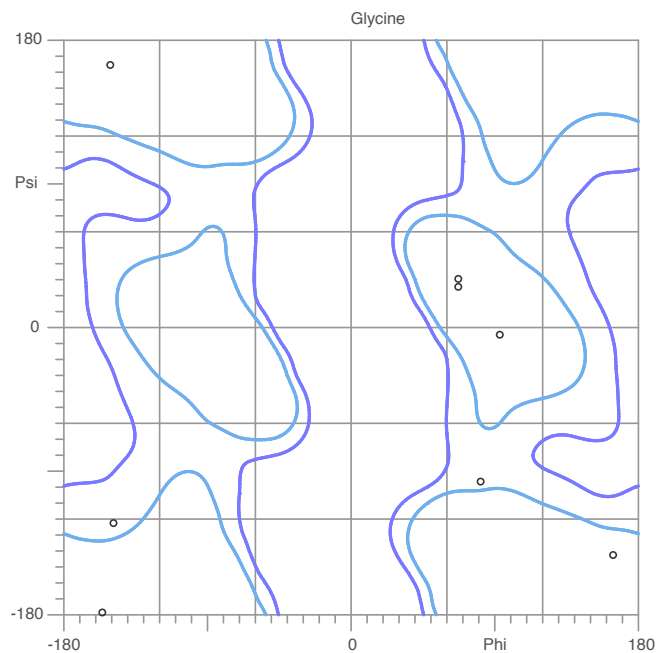
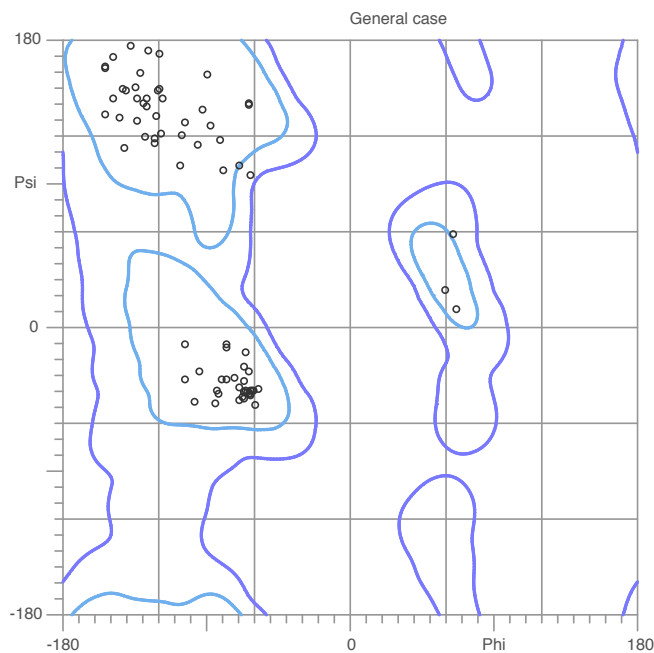
There were 1 outliers (phi, psi):
[10] 18 ASN (58.9, 120.7)

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MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 11



94.4% (84/89) of all residues were in favored (98%) regions.
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

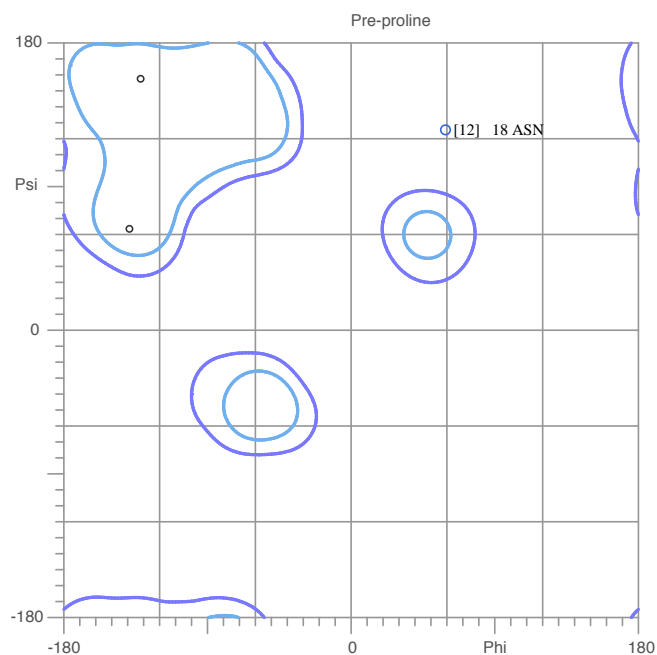
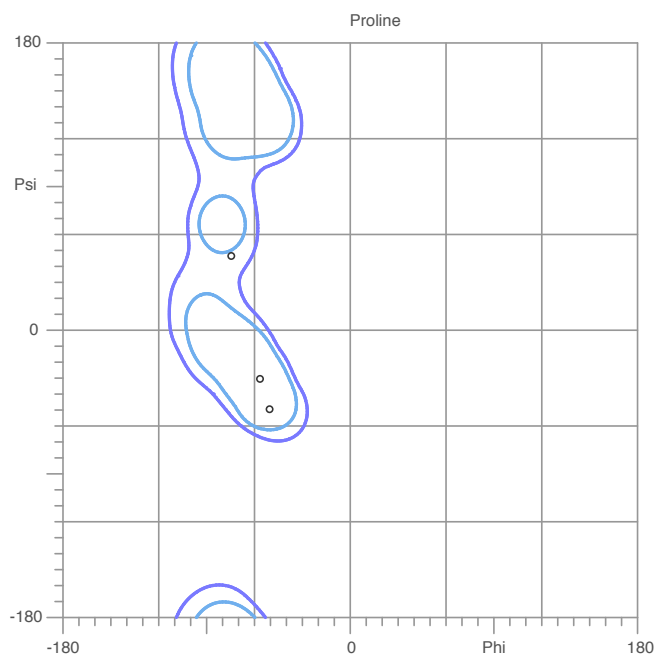
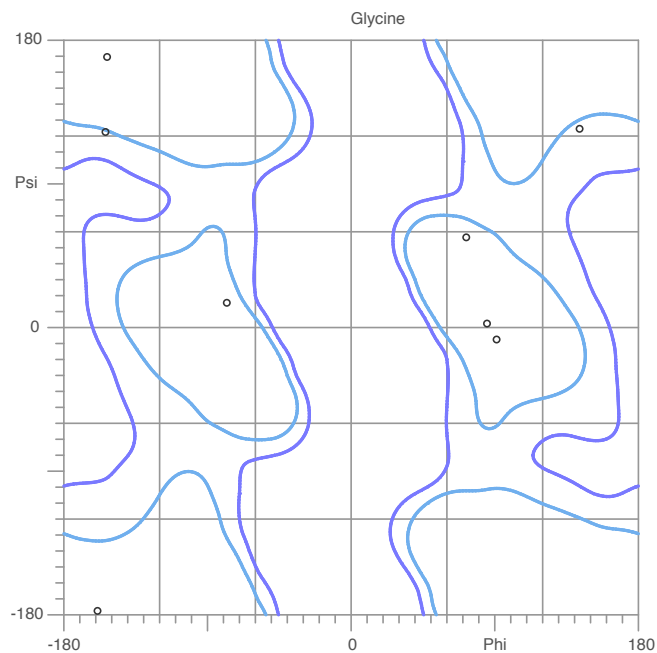
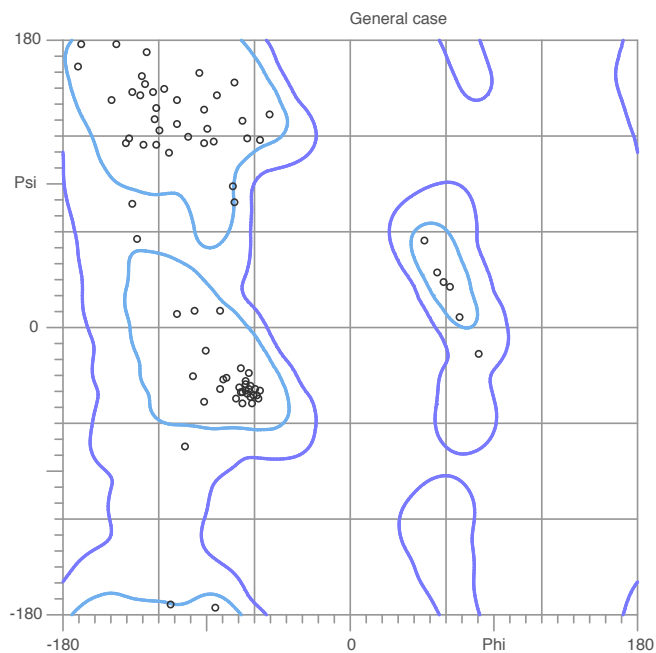
There were 1 outliers (phi, psi):
[11] 18 ASN (64.9, 115.9)

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MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 12



91.0% (81/89) of all residues were in favored (98%) regions.
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

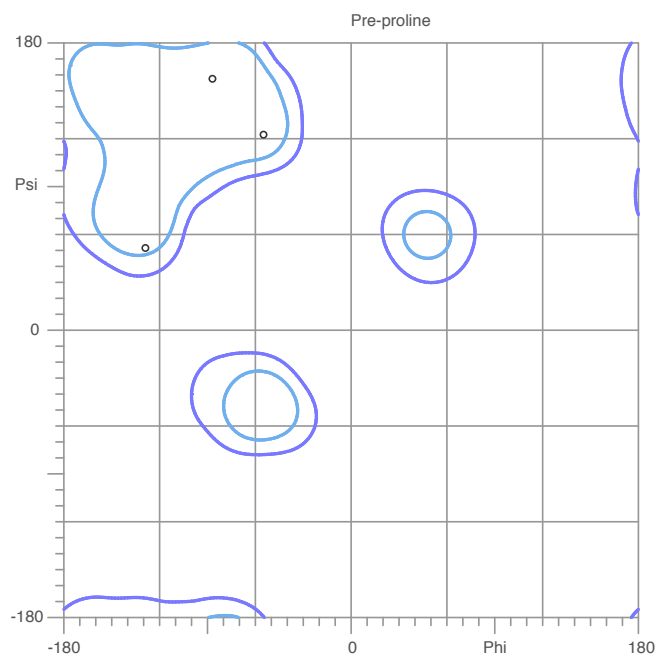
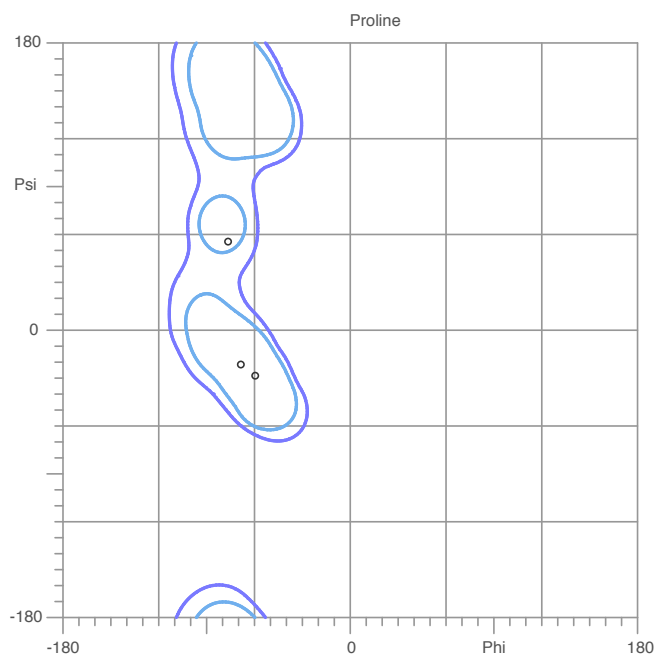
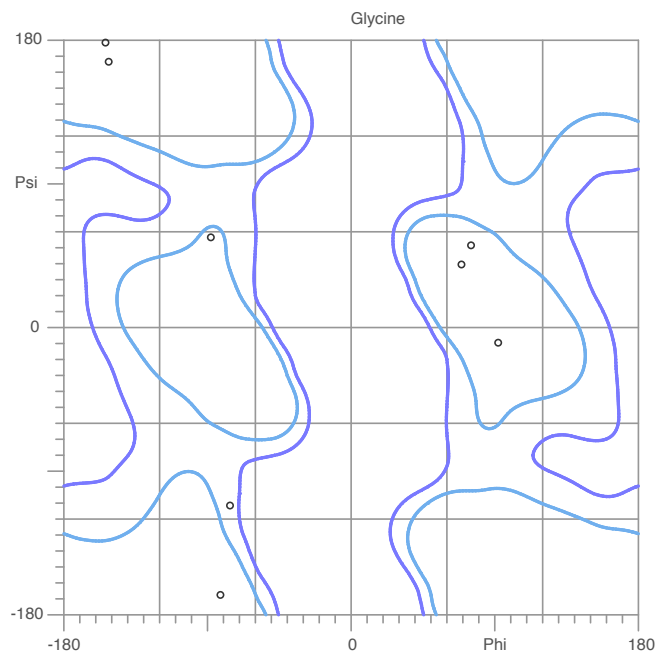
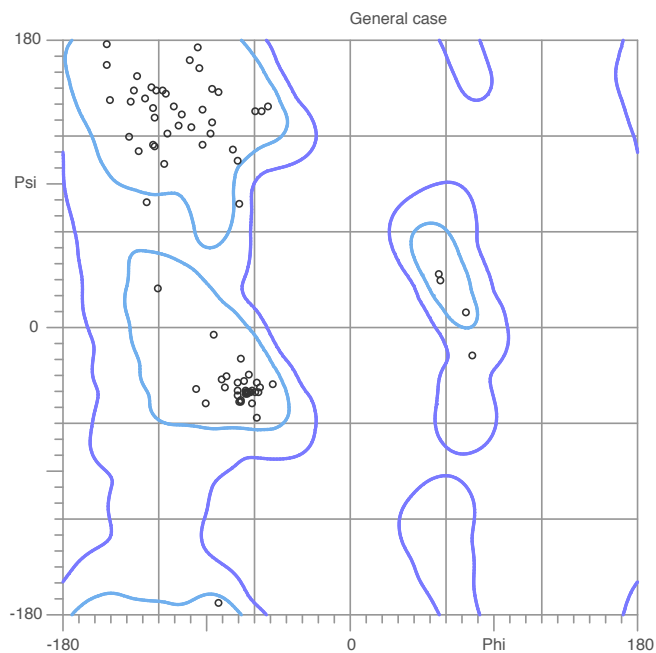
There were 1 outliers (phi, psi):
[12] 18 ASN (60.0, 126.1)

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

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MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 13



95.5% (85/89) of all residues were in favored (98%) regions.
100.0% (89/89) of all residues were in allowed (>99.8%) regions.

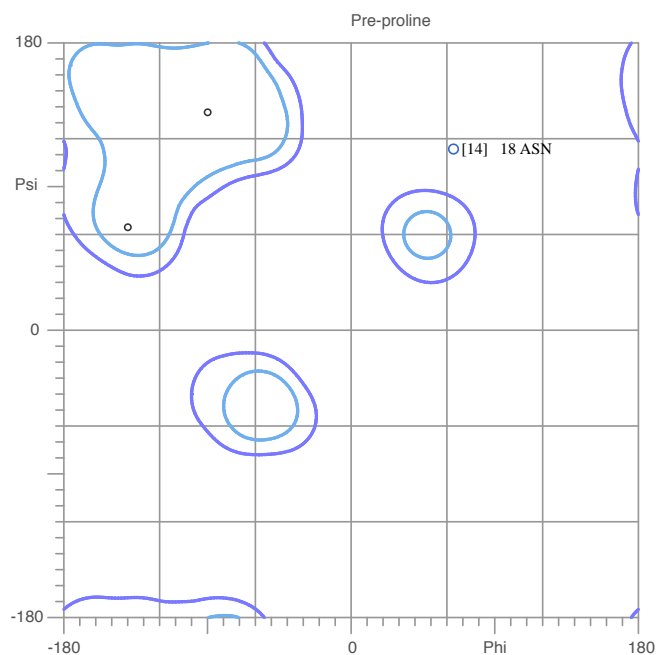
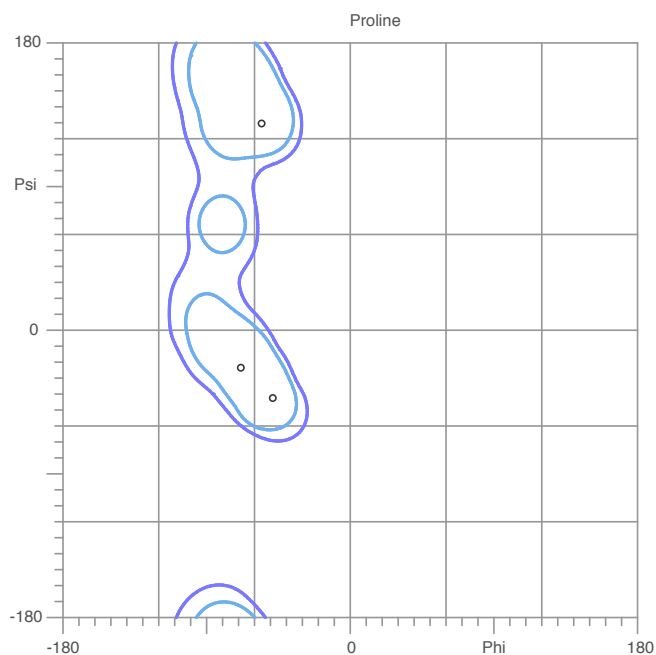
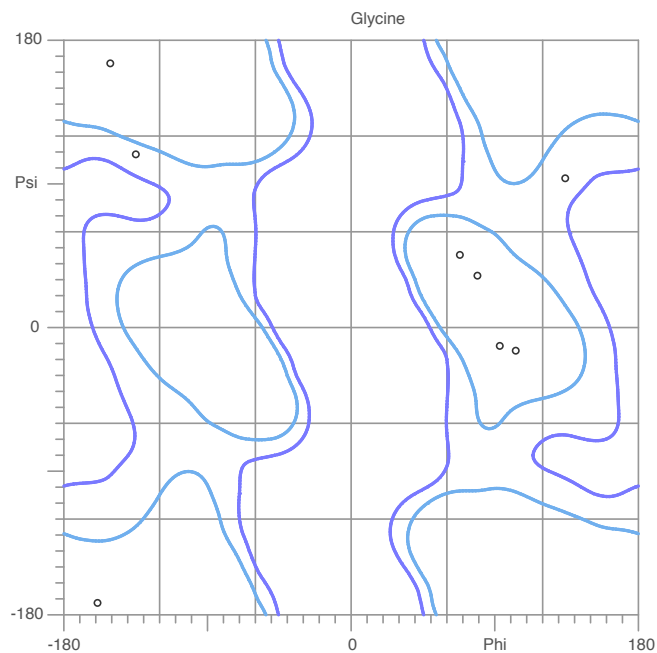
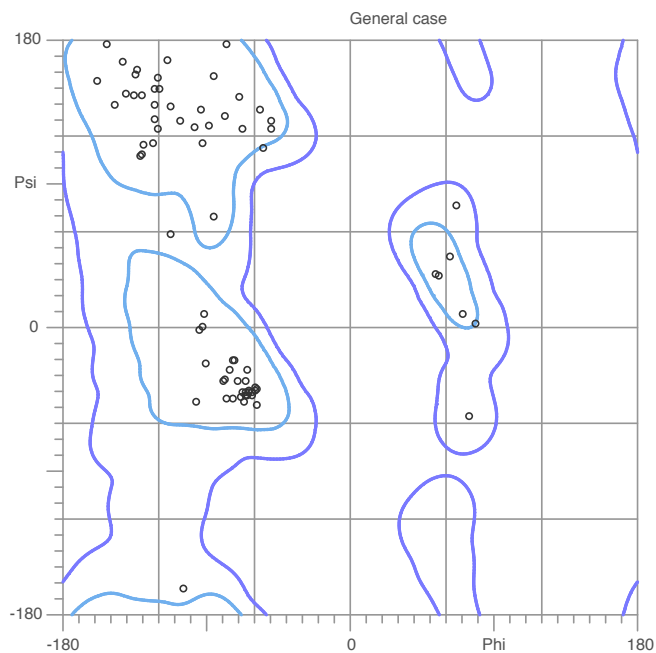
There were no outliers.

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MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 14



92.1% (82/89) of all residues were in favored (98%) regions.
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

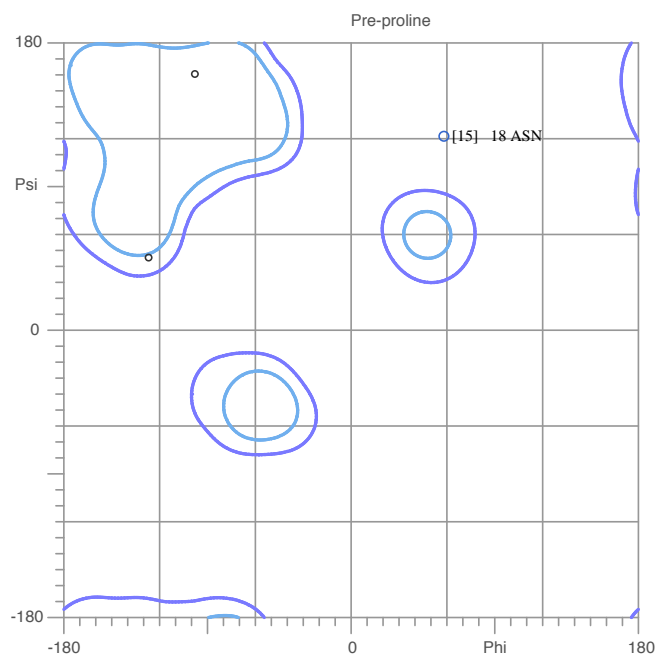
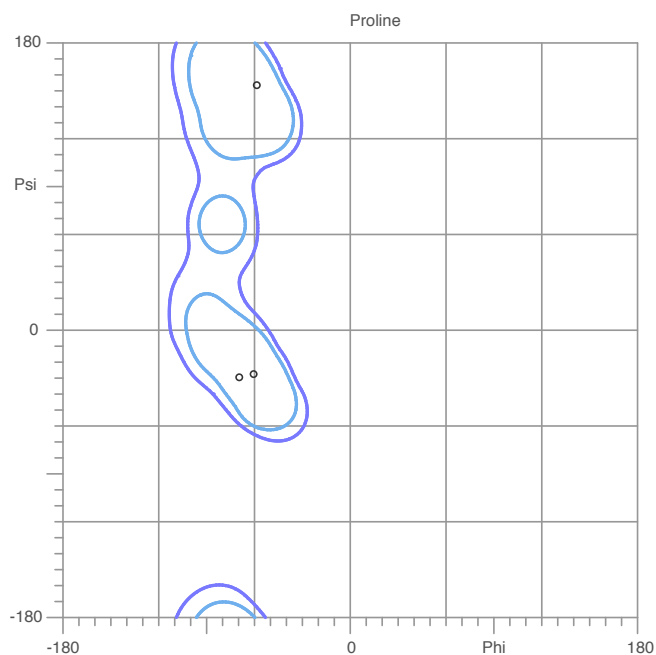
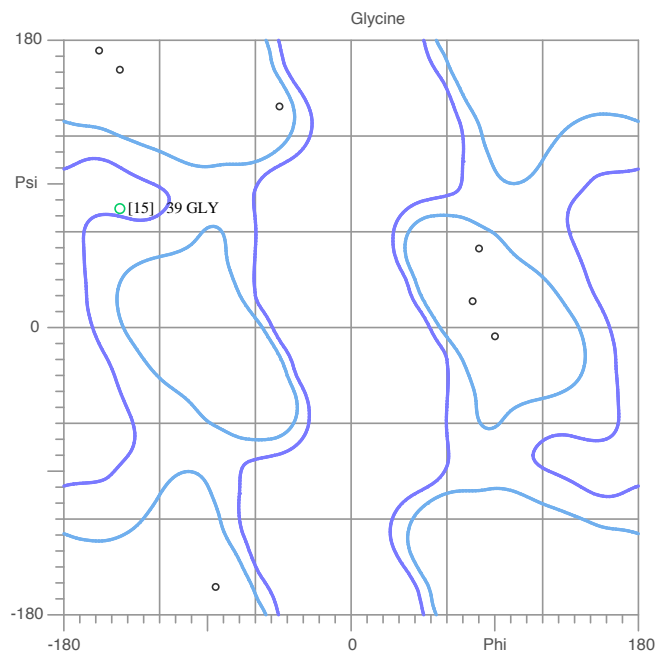
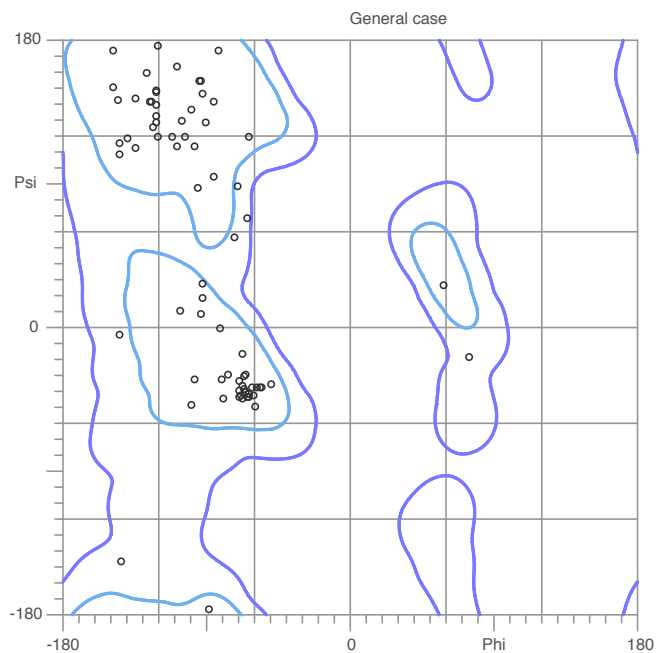
There were 1 outliers (phi, psi):
[14] 18 ASN (65.0, 115.0)

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

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MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 15

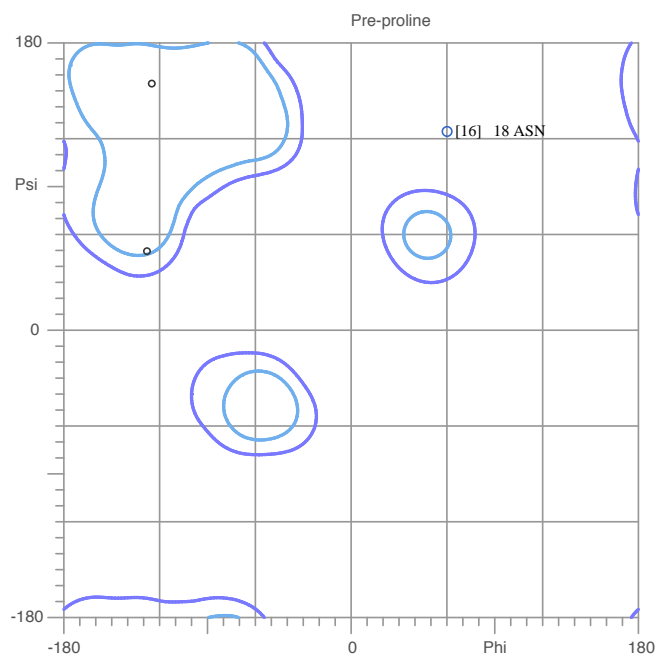
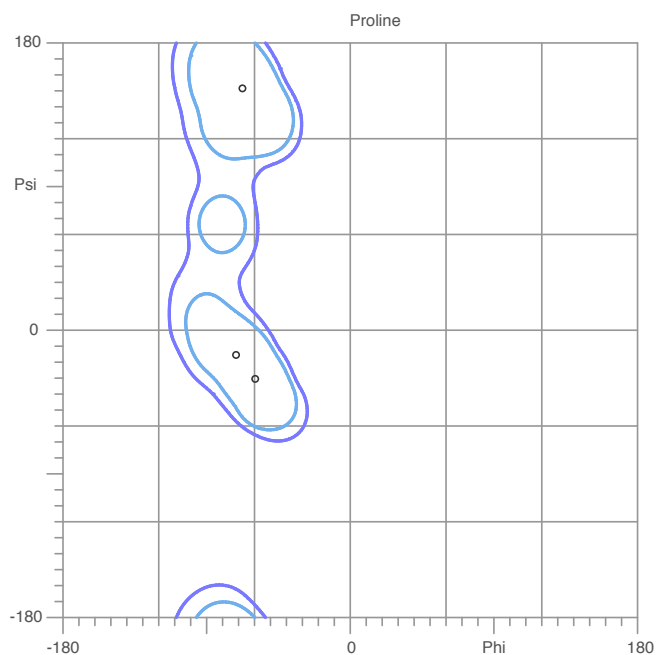
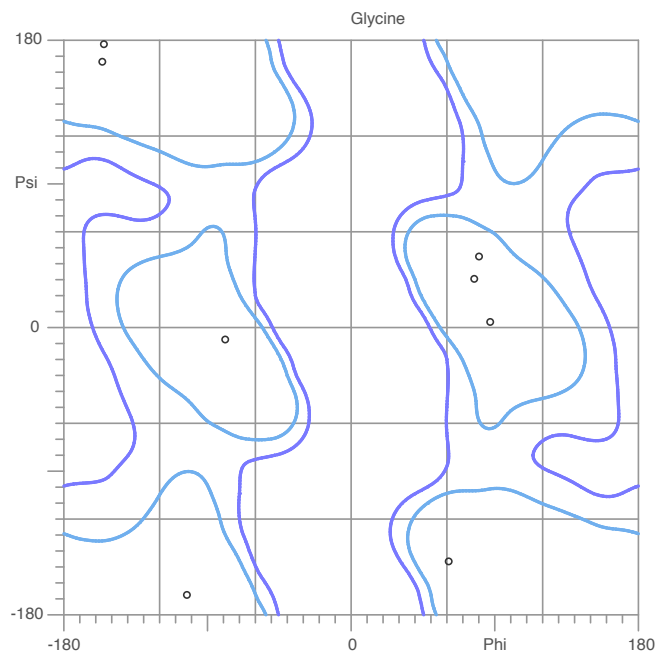
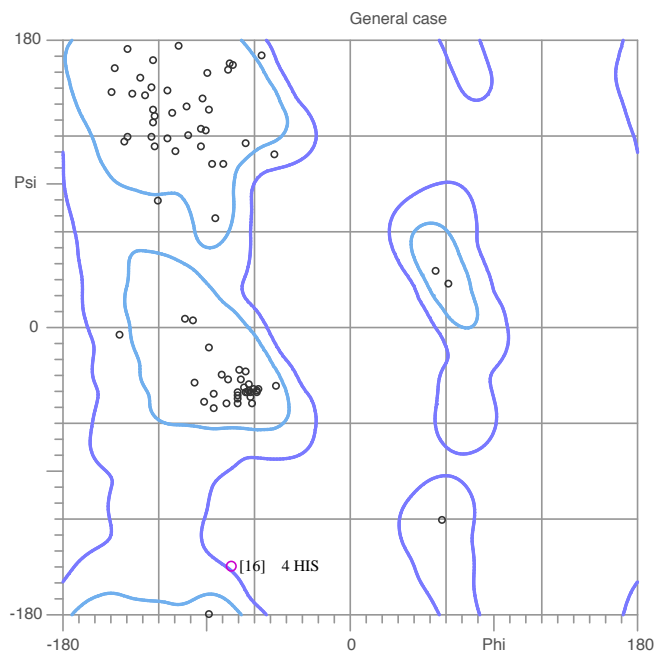


89.9% (80/89) of all residues were in favored (98%) regions.
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[15] 18 ASN (58.1, 122.5)
[15] 39 GLY (-145.1, 75.7)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 16



92.1% (82/89) of all residues were in favored (98%) regions.
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

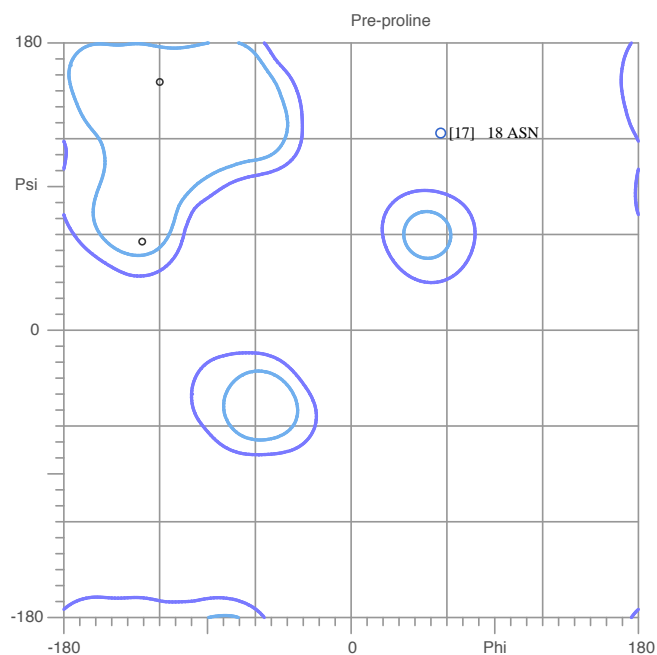
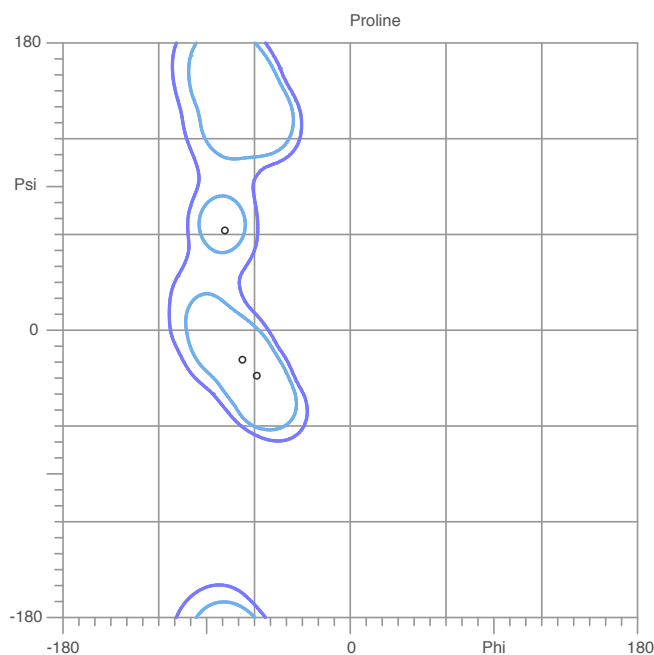
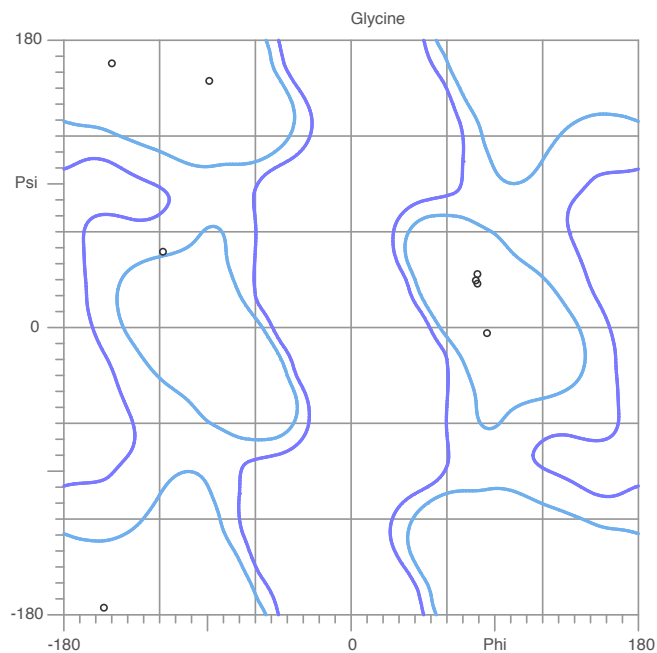
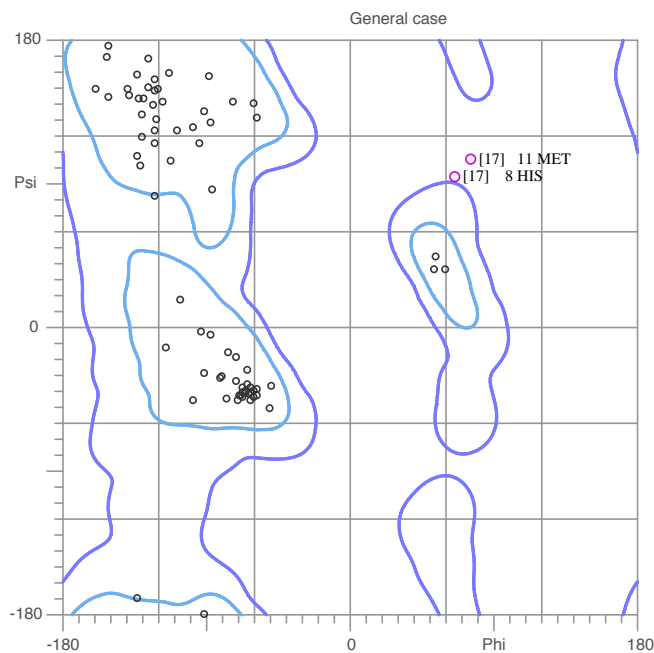
There were 2 outliers (phi, psi):

[16] 4 HIS (-75.9, -149.7)

[16] 18 ASN (60.5, 125.4)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 17



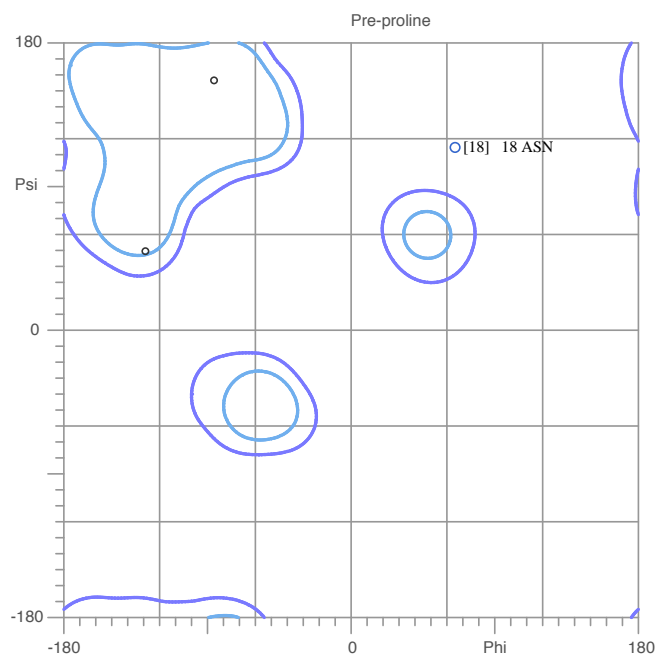
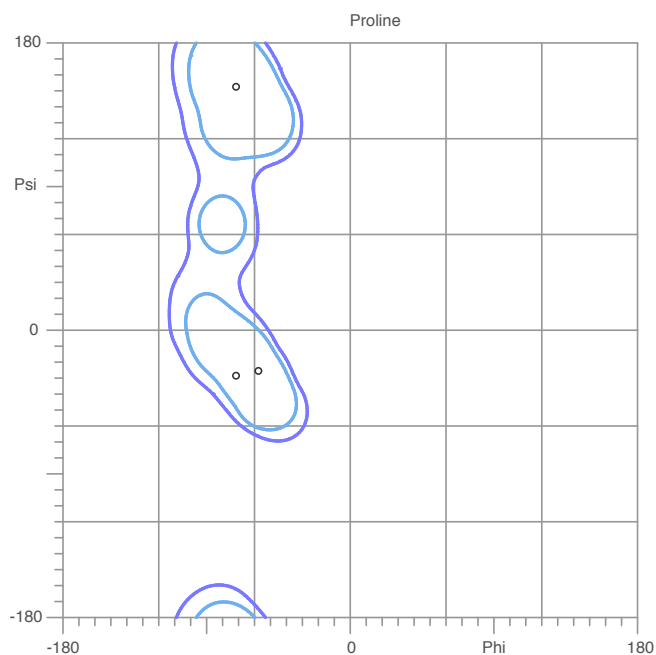
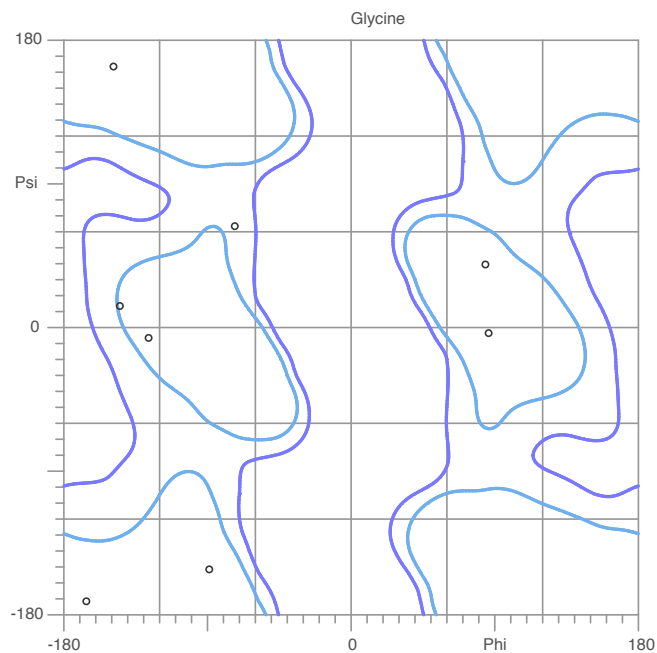
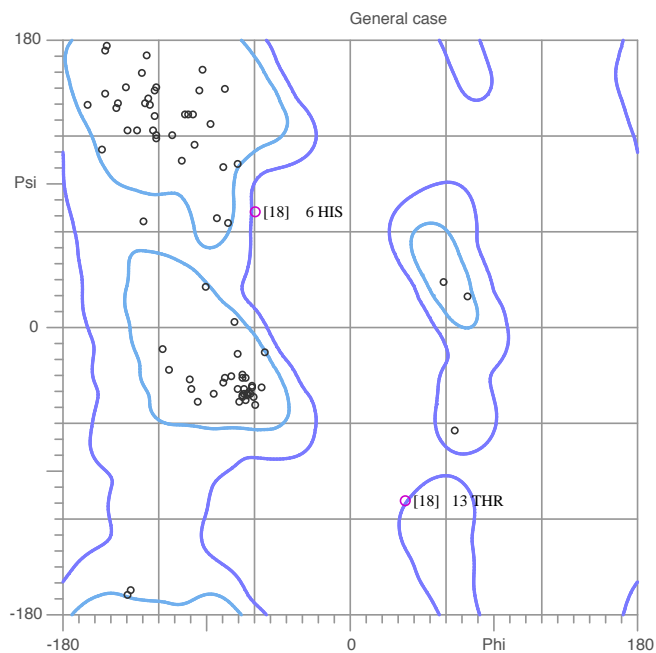
93.3% (83/89) of all residues were in favored (98%) regions.
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [17] 8 HIS (65.8, 95.6)
- [17] 11 MET (75.3, 106.6)
- [17] 18 ASN (56.7, 124.6)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 18



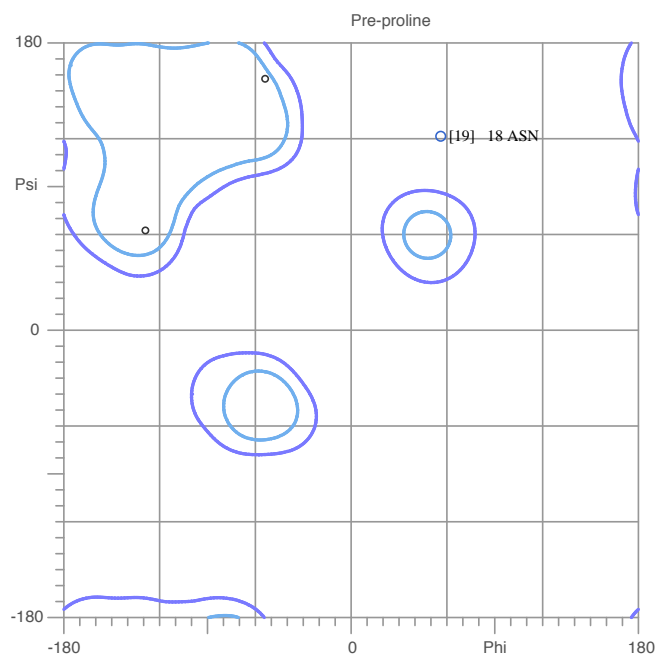
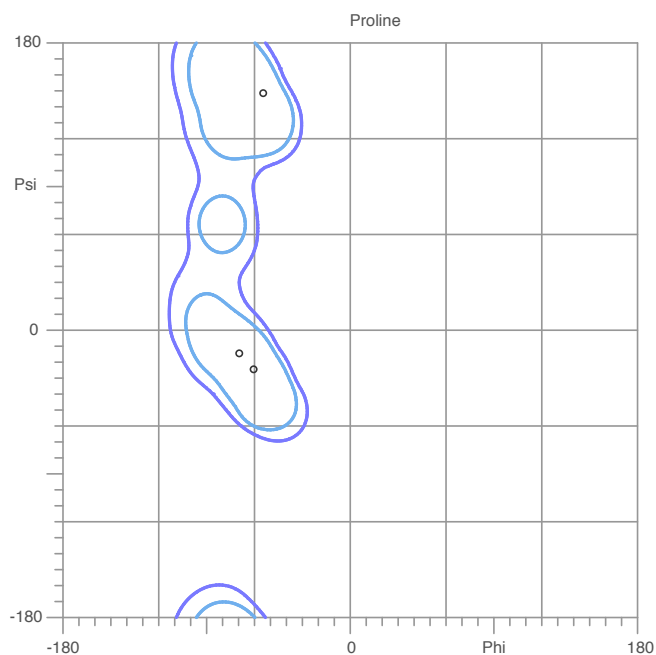
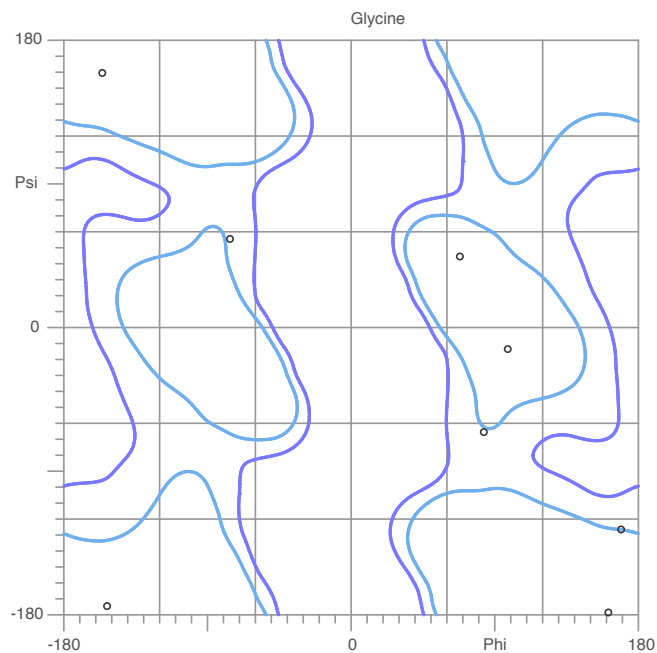
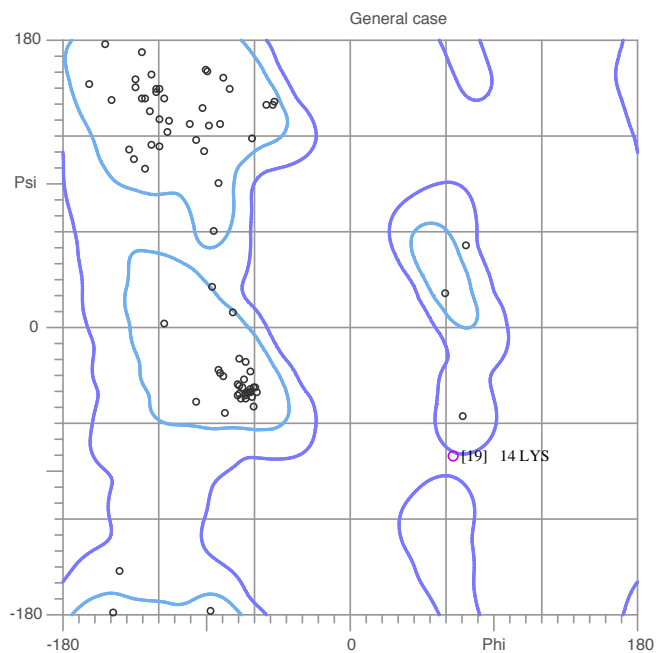
91.0% (81/89) of all residues were in favored (98%) regions.
96.6% (86/89) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [18] 6 HIS (-60.2, 73.7)
- [18] 13 THR (34.1, -108.5)
- [18] 18 ASN (65.2, 115.5)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 19



89.9% (80/89) of all residues were in favored (98%) regions.
97.8% (87/89) of all residues were in allowed (>99.8%) regions.

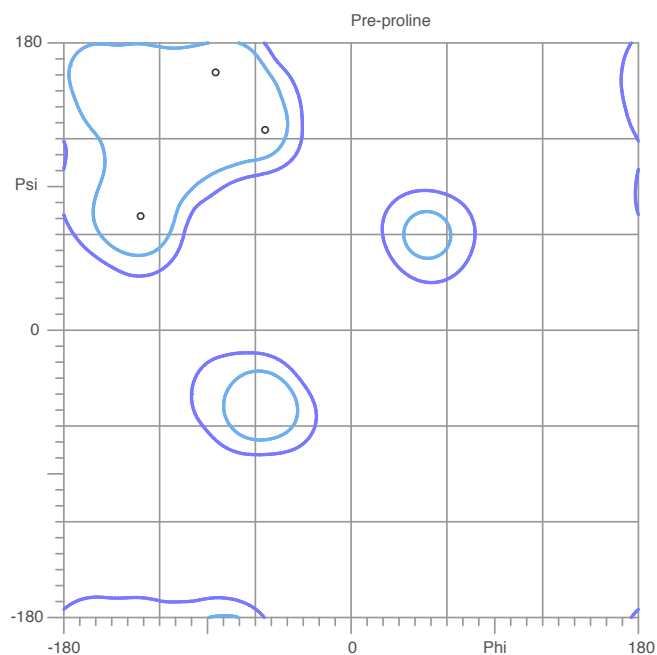
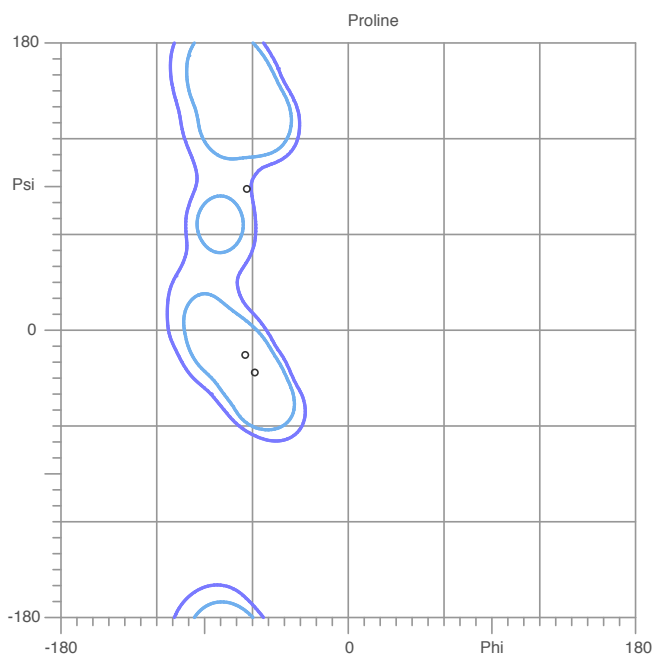
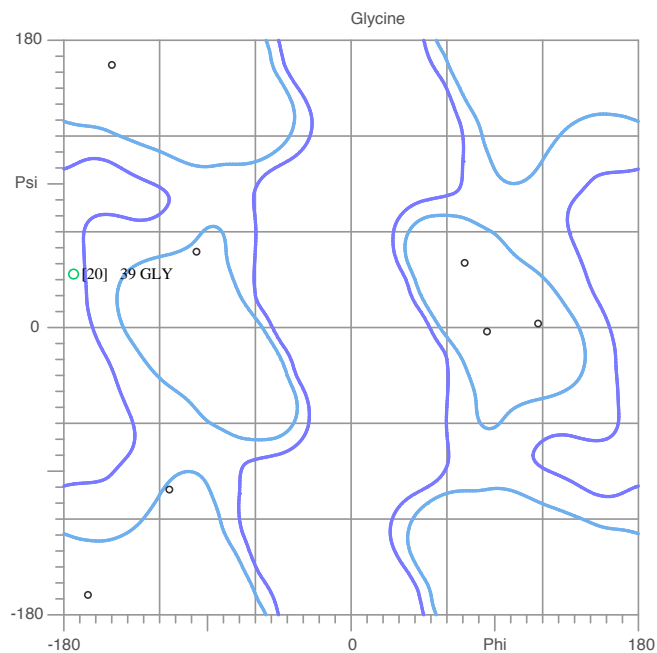
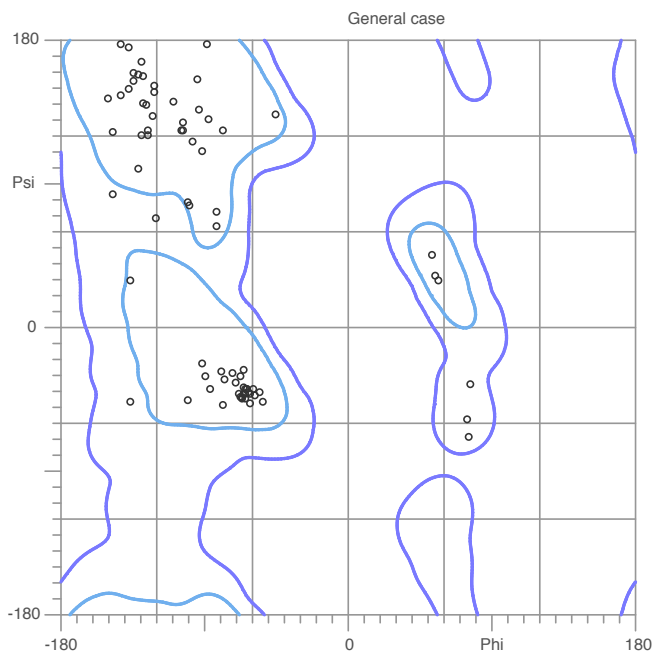
There were 2 outliers (phi, psi):

[19] 14 LYS (64.9, -80.2)

[19] 18 ASN (56.7, 122.0)

MolProbity Ramachandran analysis

HR4527E_R3Cons_em_bcr3.pdb, model 20



91.0% (81/89) of all residues were in favored (98%) regions.
98.9% (88/89) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[20] 39 GLY (-174.9, 34.1)

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

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