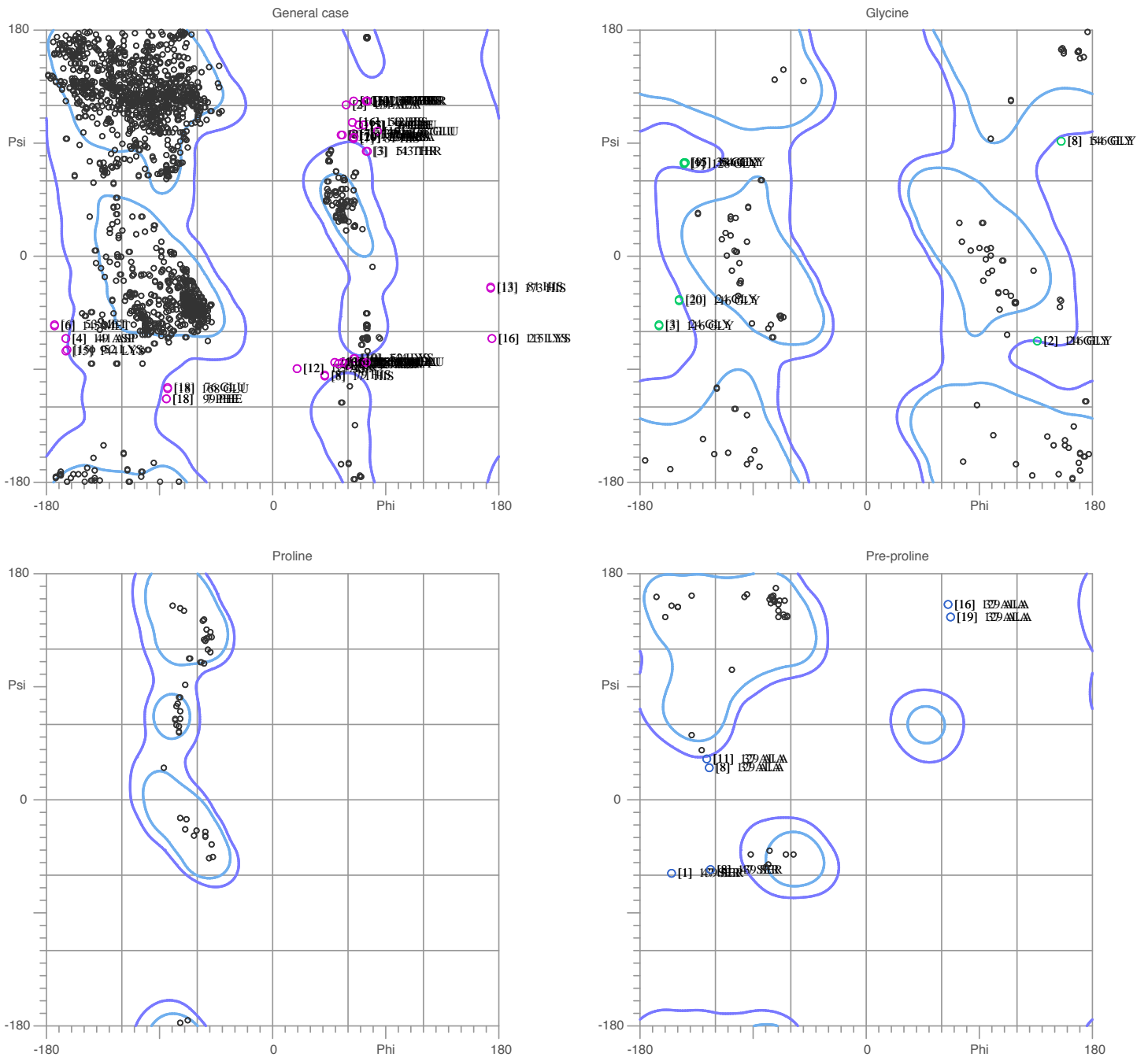


MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, all models



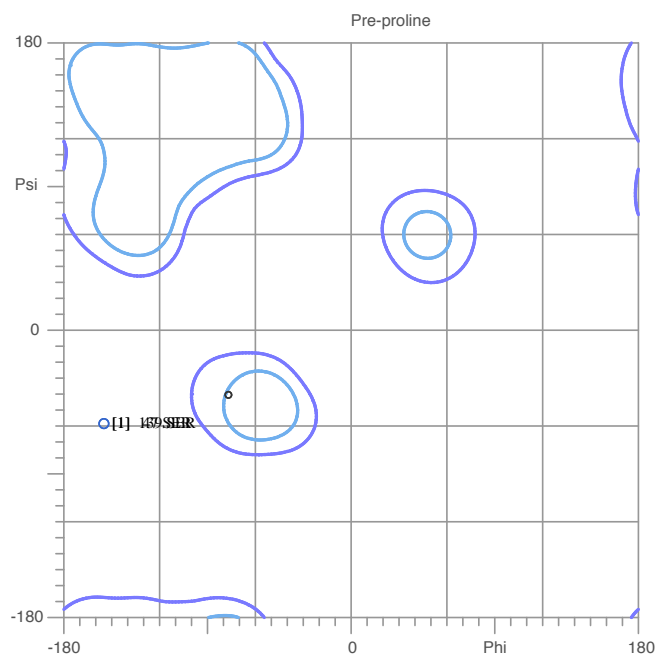
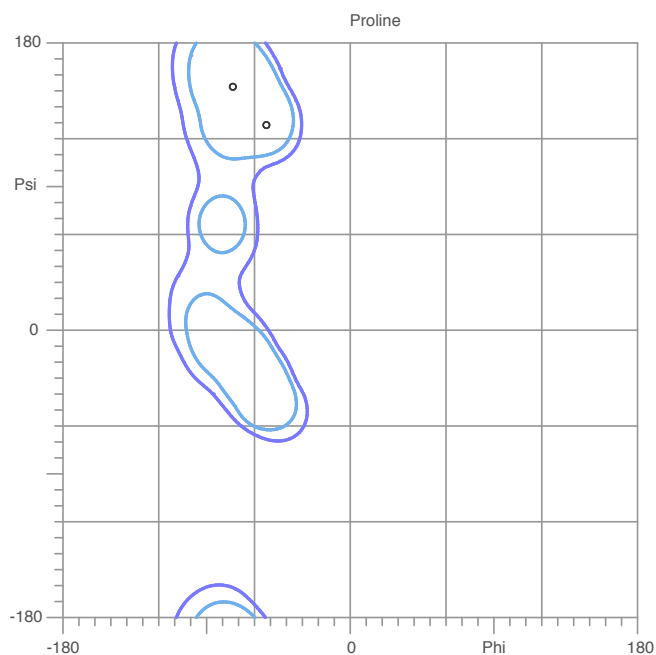
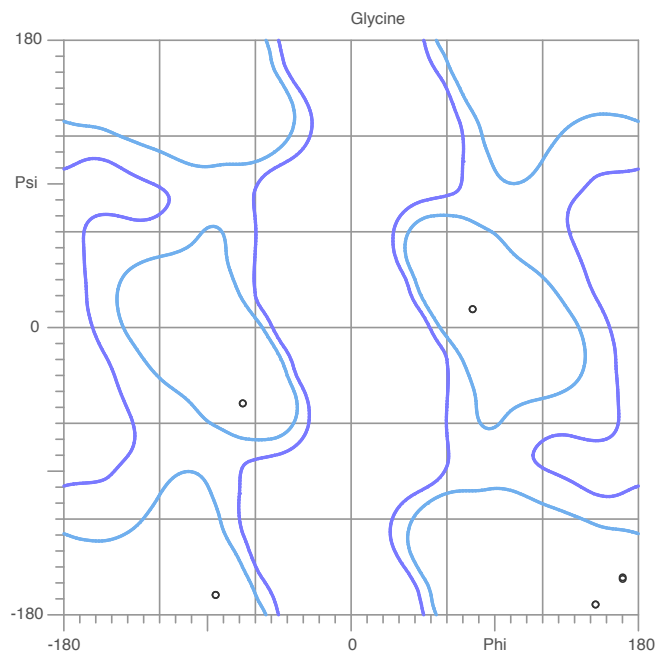
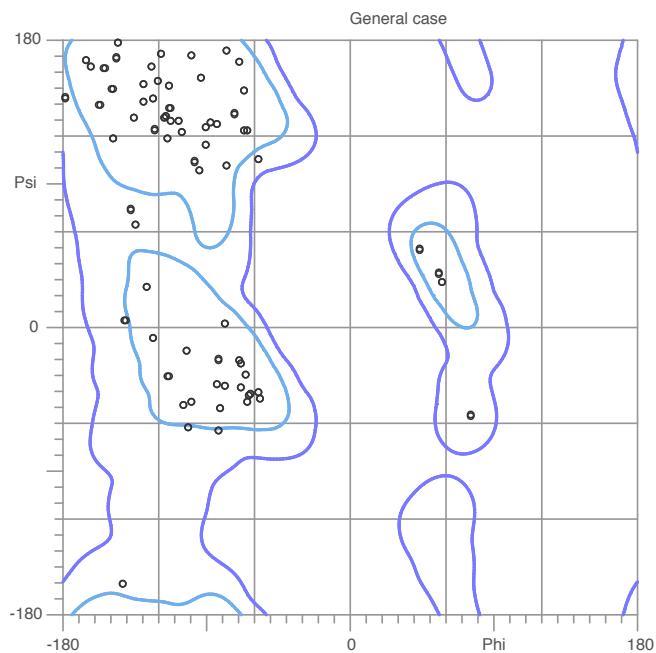
88.0% (220/250) of all residues were in favored (98%) regions.
 97.2% (219/220) of all residues were in allowed (100%) regions.

There were 30 outliers (12%):

(1) 97 THR (159.0, 98.2)	(17) 114 ALA (151.0, 84.9)
(2) 139 SER (151.6, -98.3)	(18) 114 ALA (151.0, 84.9)
(3) 243 VAL (148.8, 97.9)	(19) 114 ALA (151.0, 84.9)
(4) 39 ALA (131.0, 121.0)	(20) 114 ALA (151.0, 84.9)
(5) 116 LEU (126.7, 97.8)	(21) 114 ALA (151.0, 84.9)
(6) 113 ALA (91.7, 121.1)	(22) 114 ALA (151.0, 84.9)
(7) 8 ALA (71.0, 85.0)	(23) 114 ALA (151.0, 84.9)
(8) 134 LEU (64.3, 94.9)	(24) 114 ALA (151.0, 84.9)
(9) 97 ALA (51.0, 84.9)	(25) 114 ALA (151.0, 84.9)
(10) 116 LEU (41.0, 95.1)	(26) 114 ALA (151.0, 84.9)
(11) 101 ASP (30.0, 96.0)	(27) 114 ALA (151.0, 84.9)
(12) 7 THR (21.0, 105.0)	(28) 114 ALA (151.0, 84.9)
(13) 99 THR (21.2, 105.1)	(29) 114 ALA (151.0, 84.9)
(14) 102 MET (21.0, 120.0)	(30) 114 ALA (151.0, 84.9)
(15) 53 MET (17.0, 94.9)	(31) 114 ALA (151.0, 84.9)
(16) 103 MET (17.0, 94.9)	(32) 114 ALA (151.0, 84.9)
(17) 121 GLY (17.4, 87.1)	(33) 114 ALA (151.0, 84.9)
(18) 93 THR (16.0, 97.0)	(34) 114 ALA (151.0, 84.9)
(19) 40 ASP (16.0, 97.0)	(35) 114 ALA (151.0, 84.9)
(20) 114 ALA (151.0, 84.9)	(36) 114 ALA (151.0, 84.9)
(21) 114 ALA (151.0, 84.9)	(37) 114 ALA (151.0, 84.9)
(22) 114 ALA (151.0, 84.9)	(38) 114 ALA (151.0, 84.9)
(23) 114 ALA (151.0, 84.9)	(39) 114 ALA (151.0, 84.9)
(24) 114 ALA (151.0, 84.9)	(40) 114 ALA (151.0, 84.9)
(25) 114 ALA (151.0, 84.9)	(41) 114 ALA (151.0, 84.9)
(26) 114 ALA (151.0, 84.9)	(42) 114 ALA (151.0, 84.9)
(27) 114 ALA (151.0, 84.9)	(43) 114 ALA (151.0, 84.9)
(28) 114 ALA (151.0, 84.9)	(44) 114 ALA (151.0, 84.9)
(29) 114 ALA (151.0, 84.9)	(45) 114 ALA (151.0, 84.9)
(30) 114 ALA (151.0, 84.9)	(46) 114 ALA (151.0, 84.9)
(31) 114 ALA (151.0, 84.9)	(47) 114 ALA (151.0, 84.9)
(32) 114 ALA (151.0, 84.9)	(48) 114 ALA (151.0, 84.9)
(33) 114 ALA (151.0, 84.9)	(49) 114 ALA (151.0, 84.9)
(34) 114 ALA (151.0, 84.9)	(50) 114 ALA (151.0, 84.9)
(35) 114 ALA (151.0, 84.9)	(51) 114 ALA (151.0, 84.9)
(36) 114 ALA (151.0, 84.9)	(52) 114 ALA (151.0, 84.9)
(37) 114 ALA (151.0, 84.9)	(53) 114 ALA (151.0, 84.9)
(38) 114 ALA (151.0, 84.9)	(54) 114 ALA (151.0, 84.9)
(39) 114 ALA (151.0, 84.9)	(55) 114 ALA (151.0, 84.9)
(40) 114 ALA (151.0, 84.9)	(56) 114 ALA (151.0, 84.9)
(41) 114 ALA (151.0, 84.9)	(57) 114 ALA (151.0, 84.9)
(42) 114 ALA (151.0, 84.9)	(58) 114 ALA (151.0, 84.9)
(43) 114 ALA (151.0, 84.9)	(59) 114 ALA (151.0, 84.9)
(44) 114 ALA (151.0, 84.9)	(60) 114 ALA (151.0, 84.9)
(45) 114 ALA (151.0, 84.9)	(61) 114 ALA (151.0, 84.9)
(46) 114 ALA (151.0, 84.9)	(62) 114 ALA (151.0, 84.9)
(47) 114 ALA (151.0, 84.9)	(63) 114 ALA (151.0, 84.9)
(48) 114 ALA (151.0, 84.9)	(64) 114 ALA (151.0, 84.9)
(49) 114 ALA (151.0, 84.9)	(65) 114 ALA (151.0, 84.9)
(50) 114 ALA (151.0, 84.9)	(66) 114 ALA (151.0, 84.9)
(51) 114 ALA (151.0, 84.9)	(67) 114 ALA (151.0, 84.9)
(52) 114 ALA (151.0, 84.9)	(68) 114 ALA (151.0, 84.9)
(53) 114 ALA (151.0, 84.9)	(69) 114 ALA (151.0, 84.9)
(54) 114 ALA (151.0, 84.9)	(70) 114 ALA (151.0, 84.9)
(55) 114 ALA (151.0, 84.9)	(71) 114 ALA (151.0, 84.9)
(56) 114 ALA (151.0, 84.9)	(72) 114 ALA (151.0, 84.9)
(57) 114 ALA (151.0, 84.9)	(73) 114 ALA (151.0, 84.9)
(58) 114 ALA (151.0, 84.9)	(74) 114 ALA (151.0, 84.9)
(59) 114 ALA (151.0, 84.9)	(75) 114 ALA (151.0, 84.9)
(60) 114 ALA (151.0, 84.9)	(76) 114 ALA (151.0, 84.9)
(61) 114 ALA (151.0, 84.9)	(77) 114 ALA (151.0, 84.9)
(62) 114 ALA (151.0, 84.9)	(78) 114 ALA (151.0, 84.9)
(63) 114 ALA (151.0, 84.9)	(79) 114 ALA (151.0, 84.9)
(64) 114 ALA (151.0, 84.9)	(80) 114 ALA (151.0, 84.9)
(65) 114 ALA (151.0, 84.9)	(81) 114 ALA (151.0, 84.9)
(66) 114 ALA (151.0, 84.9)	(82) 114 ALA (151.0, 84.9)
(67) 114 ALA (151.0, 84.9)	(83) 114 ALA (151.0, 84.9)
(68) 114 ALA (151.0, 84.9)	(84) 114 ALA (151.0, 84.9)
(69) 114 ALA (151.0, 84.9)	(85) 114 ALA (151.0, 84.9)
(70) 114 ALA (151.0, 84.9)	(86) 114 ALA (151.0, 84.9)
(71) 114 ALA (151.0, 84.9)	(87) 114 ALA (151.0, 84.9)
(72) 114 ALA (151.0, 84.9)	(88) 114 ALA (151.0, 84.9)
(73) 114 ALA (151.0, 84.9)	(89) 114 ALA (151.0, 84.9)
(74) 114 ALA (151.0, 84.9)	(90) 114 ALA (151.0, 84.9)
(75) 114 ALA (151.0, 84.9)	(91) 114 ALA (151.0, 84.9)
(76) 114 ALA (151.0, 84.9)	(92) 114 ALA (151.0, 84.9)
(77) 114 ALA (151.0, 84.9)	(93) 114 ALA (151.0, 84.9)
(78) 114 ALA (151.0, 84.9)	(94) 114 ALA (151.0, 84.9)
(79) 114 ALA (151.0, 84.9)	(95) 114 ALA (151.0, 84.9)
(80) 114 ALA (151.0, 84.9)	(96) 114 ALA (151.0, 84.9)
(81) 114 ALA (151.0, 84.9)	(97) 114 ALA (151.0, 84.9)
(82) 114 ALA (151.0, 84.9)	(98) 114 ALA (151.0, 84.9)
(83) 114 ALA (151.0, 84.9)	(99) 114 ALA (151.0, 84.9)
(84) 114 ALA (151.0, 84.9)	(100) 114 ALA (151.0, 84.9)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 1



87.5% (140/160) of all residues were in favored (98%) regions.
98.8% (158/160) of all residues were in allowed (>99.8%) regions.

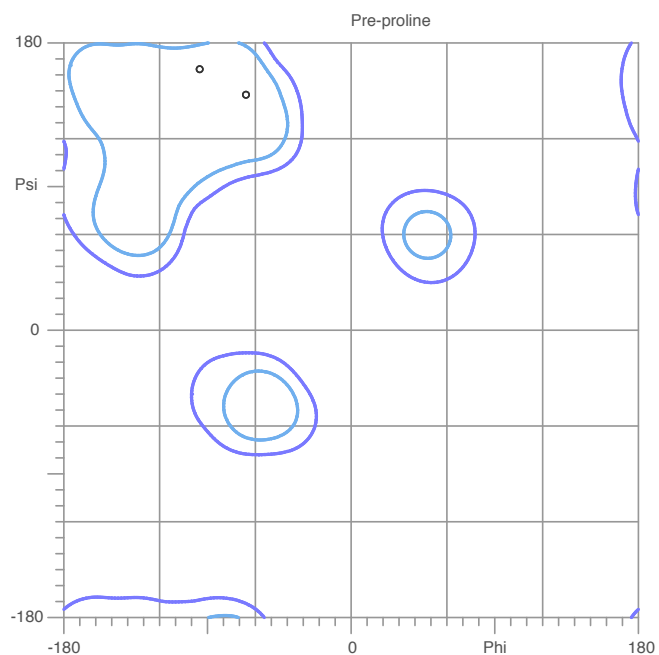
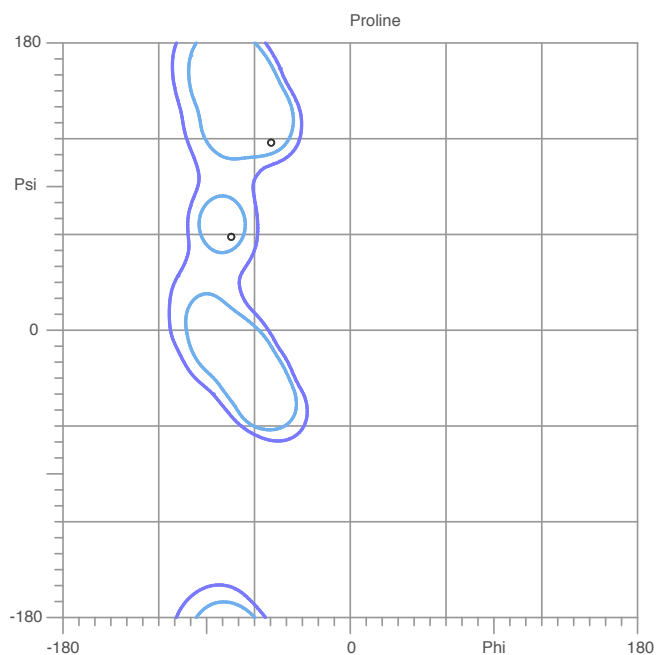
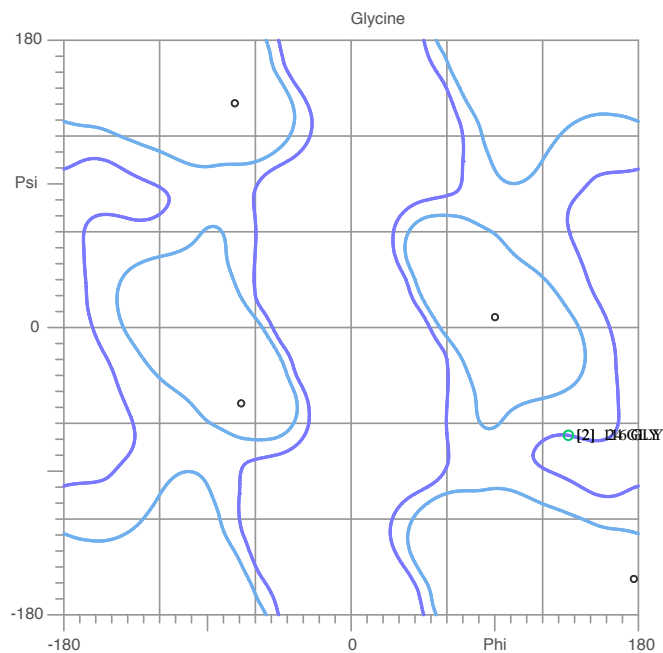
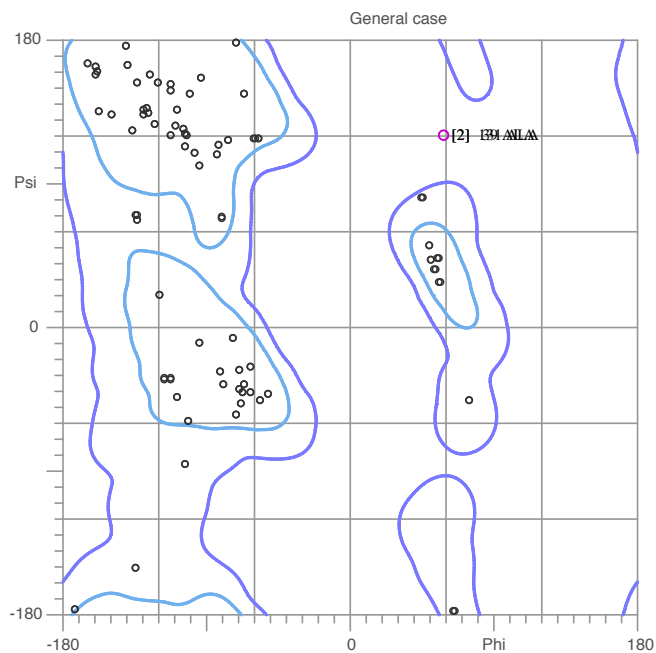
There were 2 outliers (phi, psi):

[1] 47 SER (-155.0, -58.2)

[1] 139 SER (-155.0, -58.3)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 2



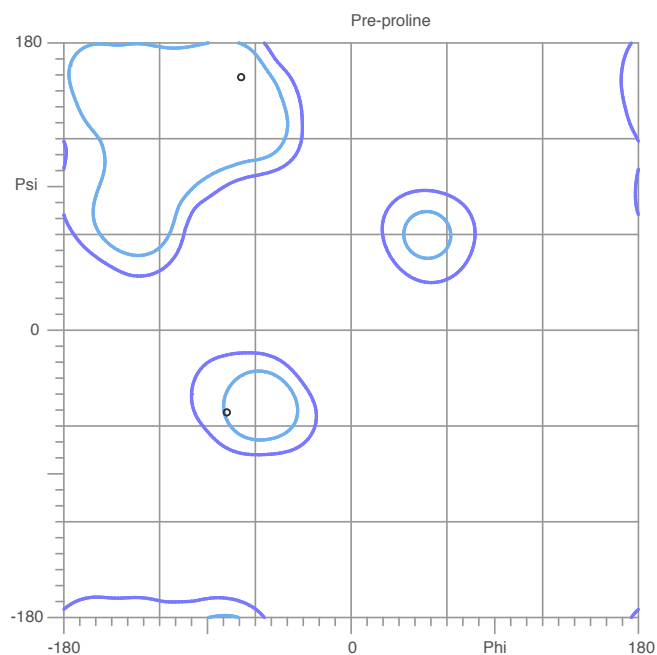
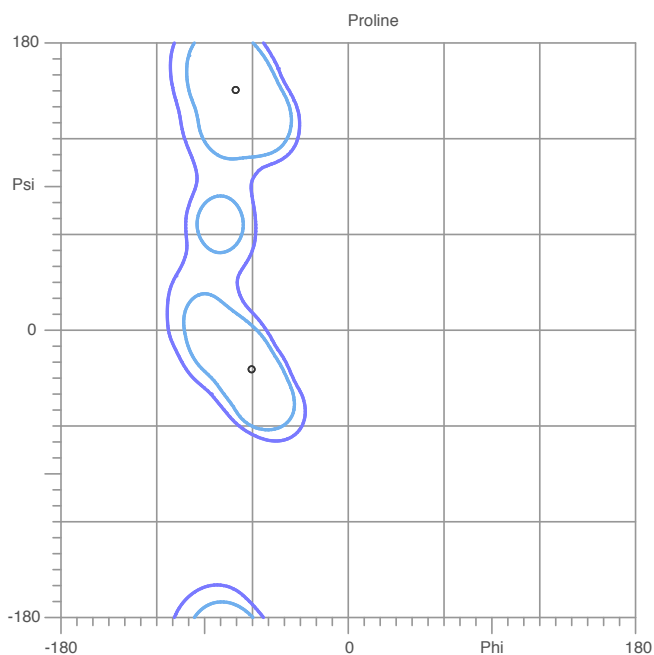
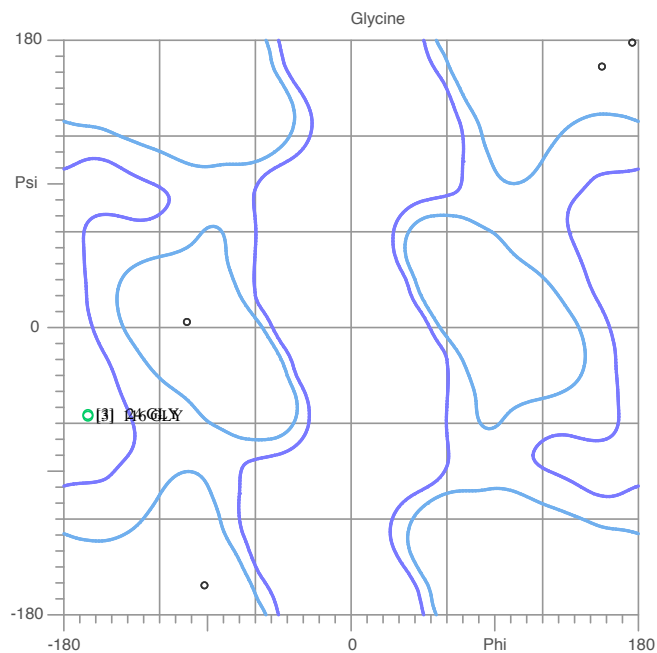
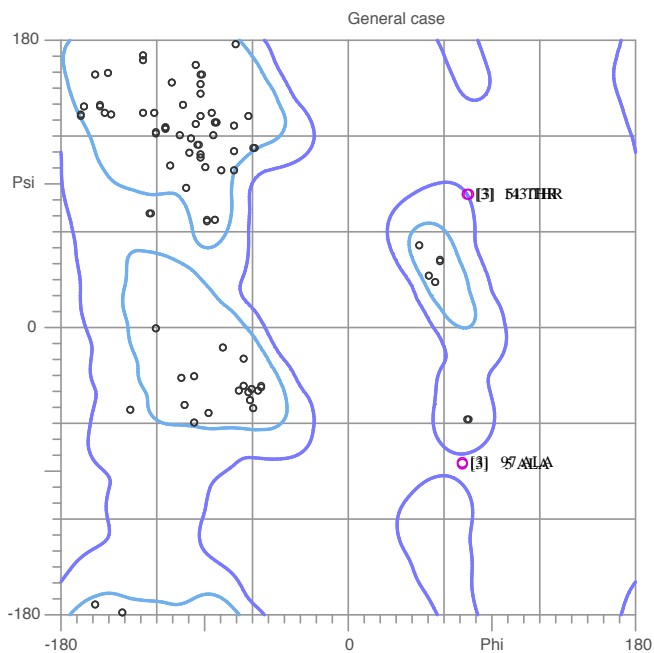
87.5% (140/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [2] 24 GLY (136.8, -67.9)
- [2] 39 ALA (58.8, 121.0)
- [2] 116 GLY (136.7, -67.8)
- [2] 131 ALA (58.7, 121.1)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 3



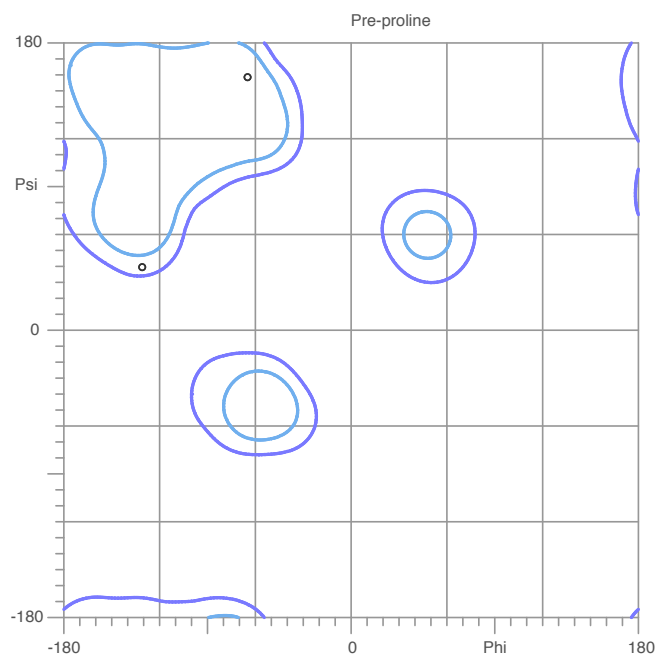
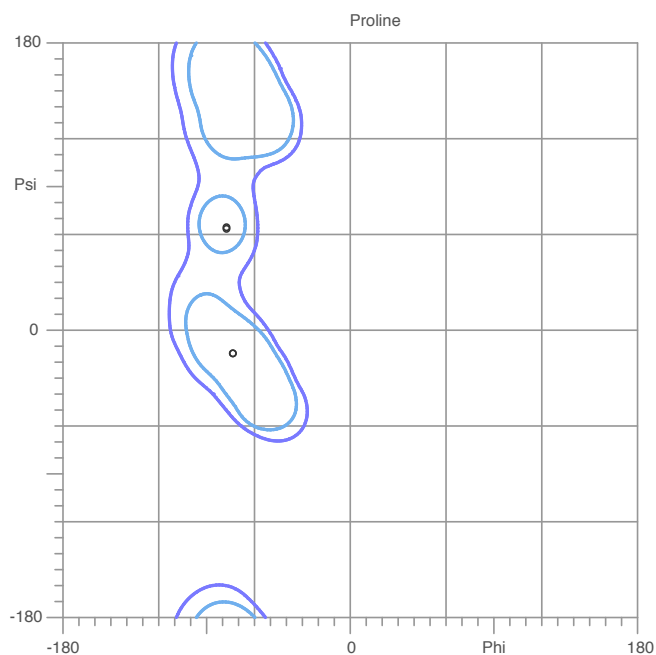
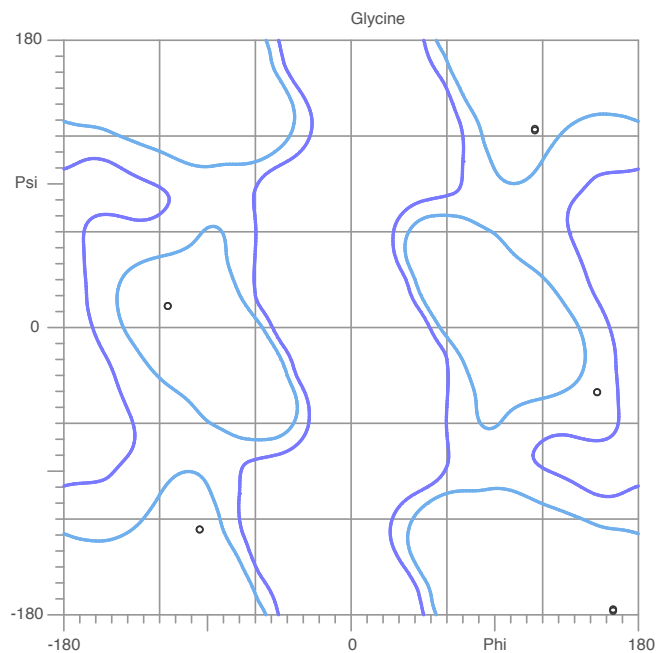
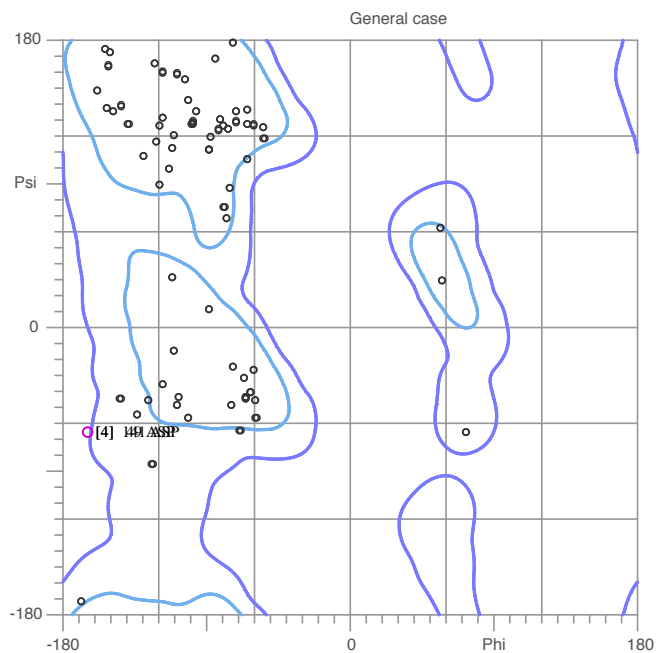
92.5% (148/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[3] 5 ALA (71.5, -85.0)

[3] 24 GLY (-165.1, -54.9)
[3] 51 THR (74.9, 85.0)
[3] 97 ALA (71.5, -85.0)
[3] 116 GLY (-165.1, -55.1)
[3] 143 THR (75.1, 85.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 4



87.5% (140/160) of all residues were in favored (98%) regions.
98.8% (158/160) of all residues were in allowed (>99.8%) regions.

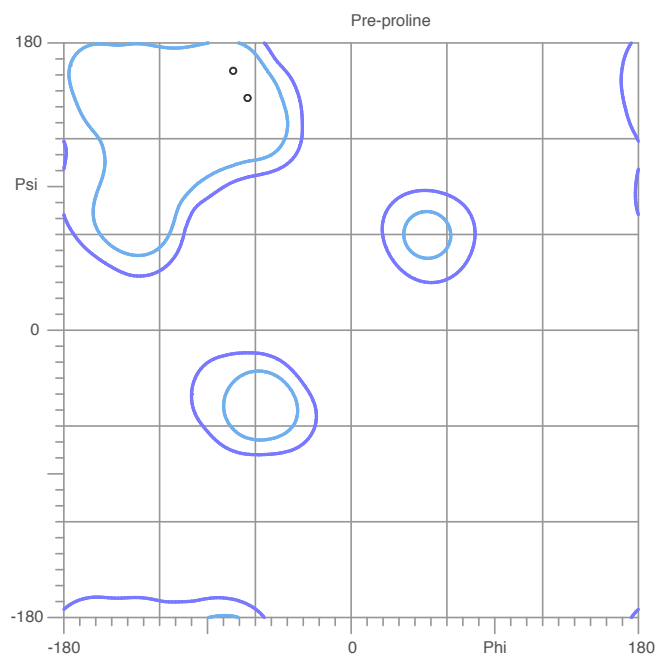
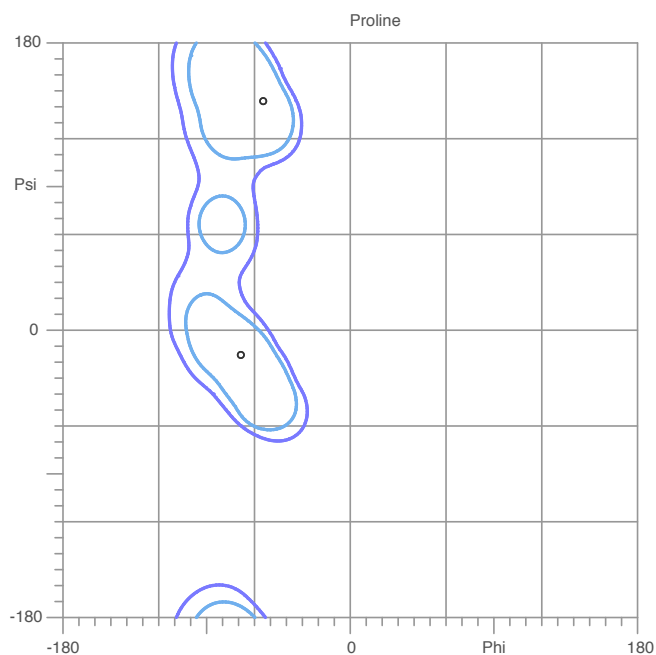
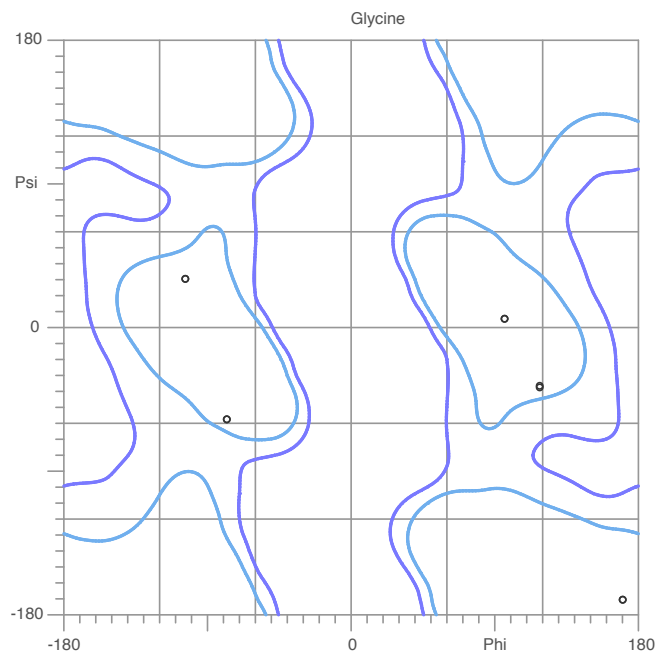
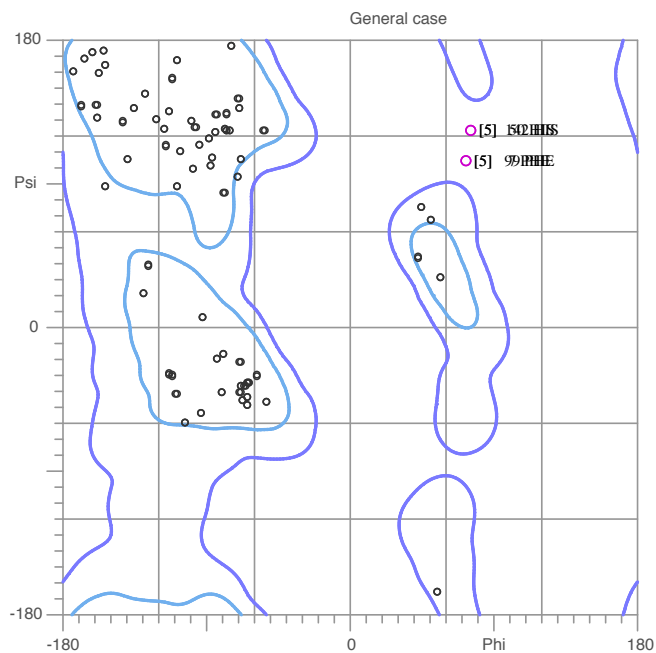
There were 2 outliers (phi, psi):

[4] 49 ASP (-165.0, -65.1)

[4] 141 ASP (-165.0, -65.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 5



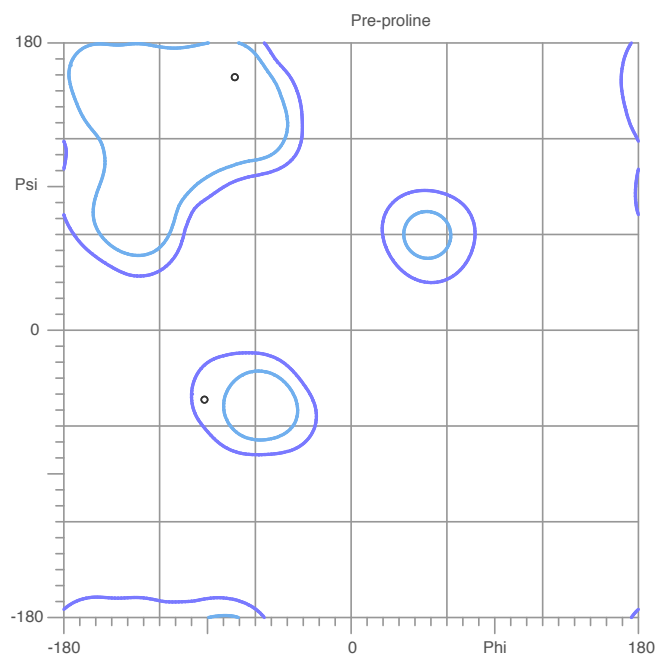
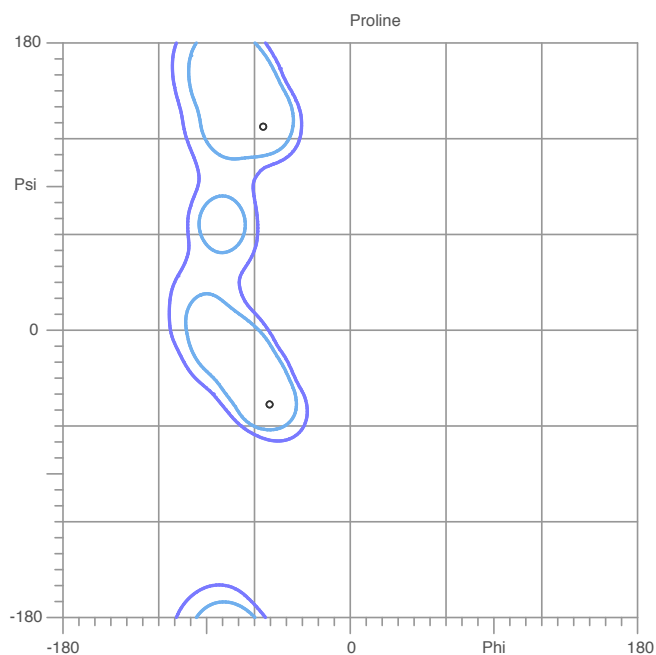
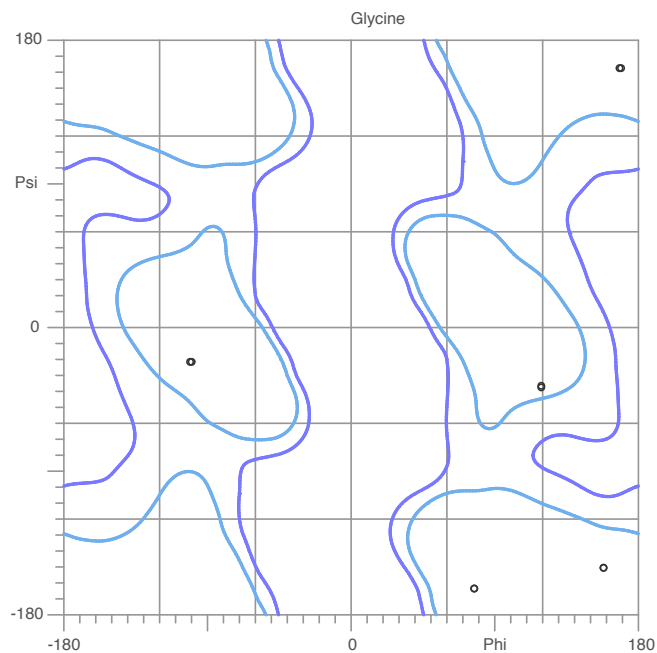
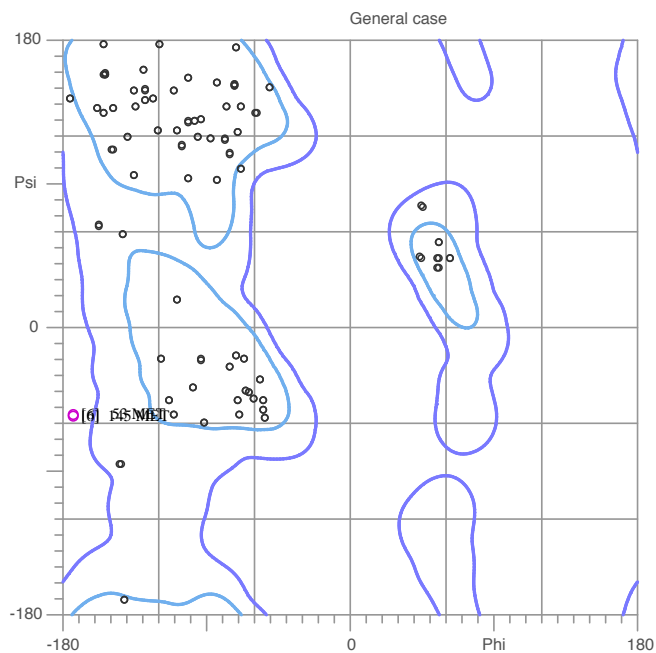
91.2% (146/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [5] 7 PHE (72.1, 105.0)
- [5] 50 HIS (75.1, 124.9)
- [5] 99 PHE (72.2, 105.1)
- [5] 142 HIS (75.0, 125.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 6



90.0% (144/160) of all residues were in favored (98%) regions.
98.8% (158/160) of all residues were in allowed (>99.8%) regions.

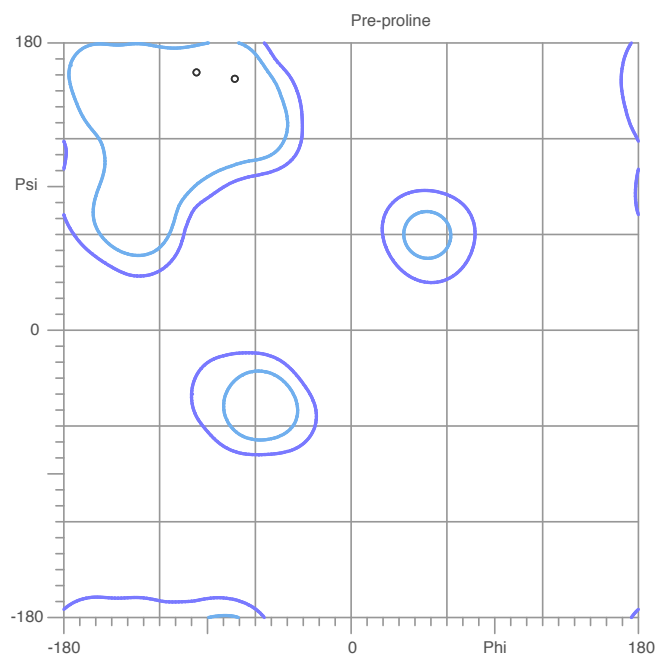
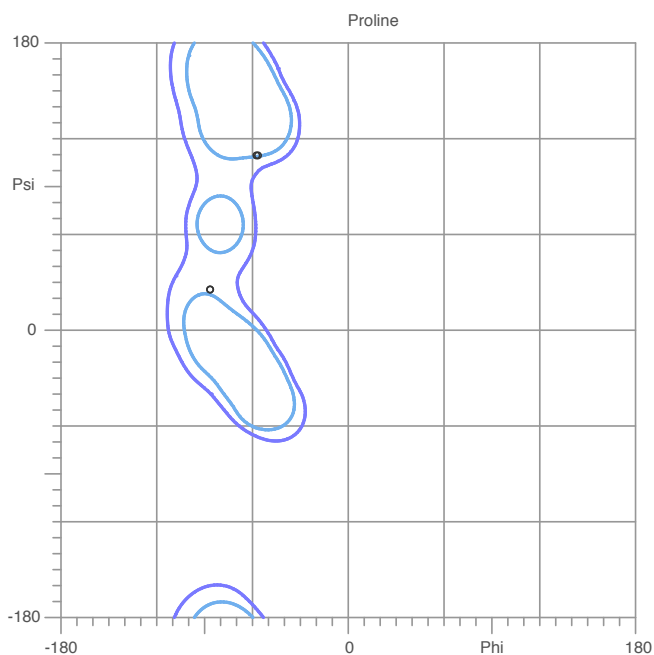
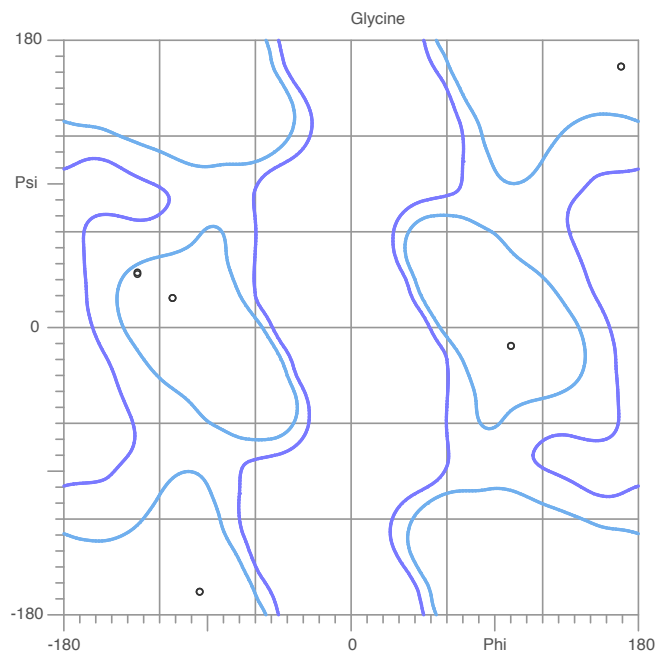
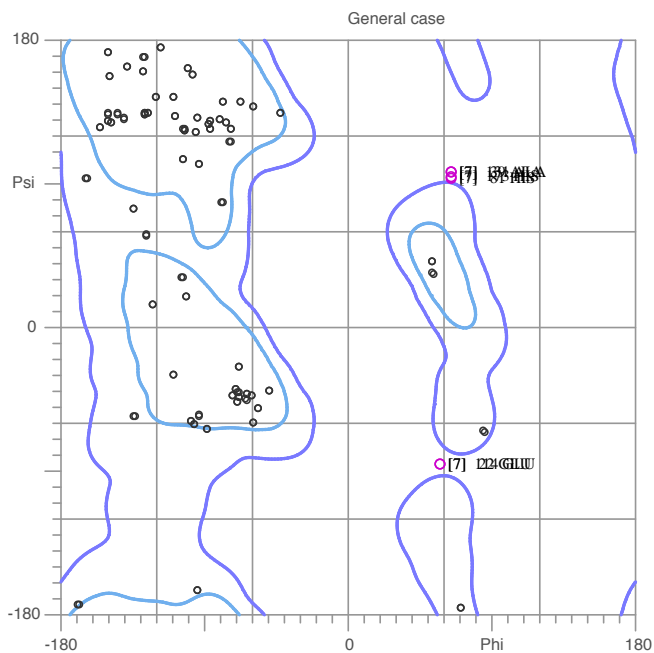
There were 2 outliers (phi, psi):

[6] 53 MET (-175.0, -54.9)

[6] 145 MET (-175.0, -55.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 7



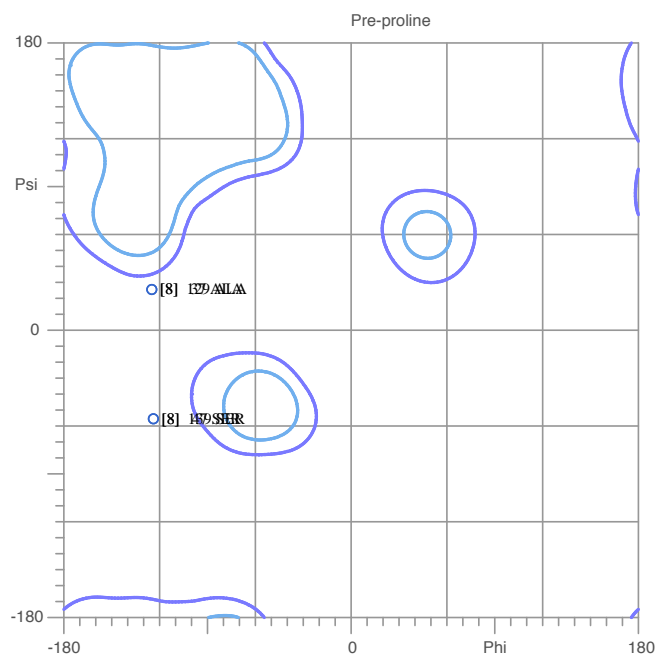
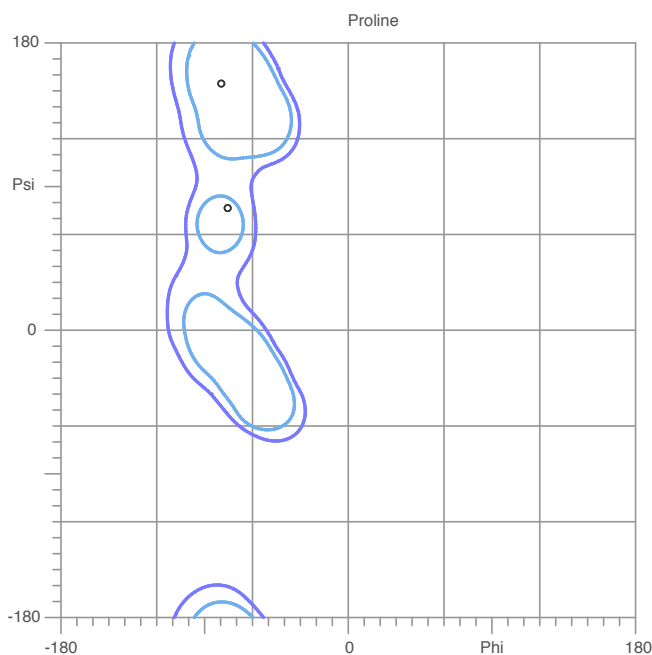
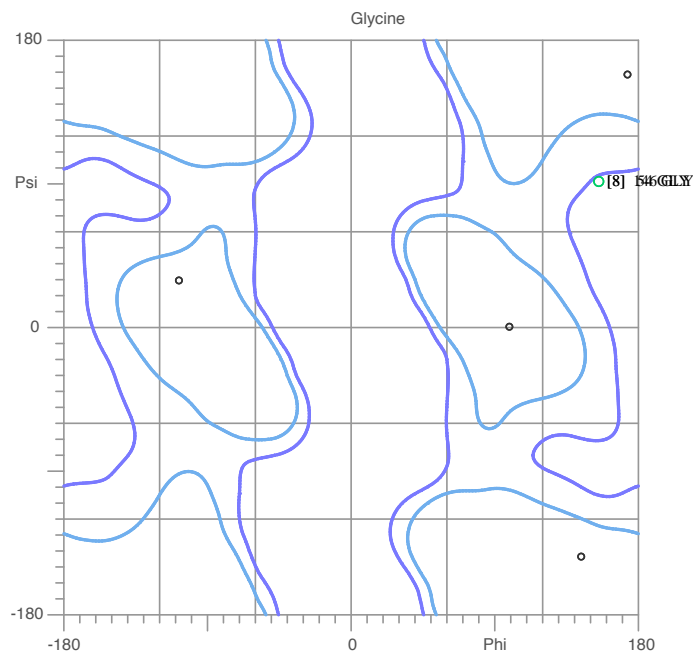
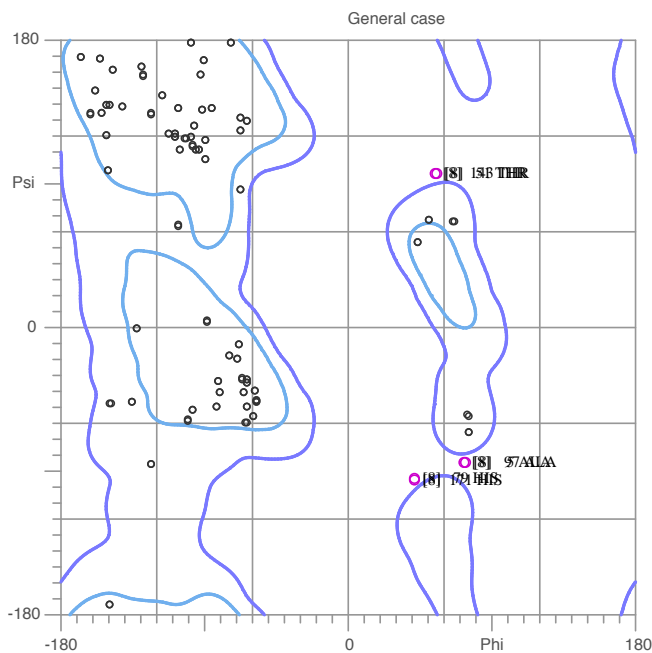
83.8% (134/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[7] 22 GLU (57.5, -85.3)

[7] 39 ALA (64.9, 98.3)
[7] 81 HIS (65.0, 94.9)
[7] 114 GLU (57.4, -85.2)
[7] 131 ALA (65.0, 98.3)
[7] 173 HIS (65.0, 95.1)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 8



81.2% (130/160) of all residues were in favored (98%) regions.
92.5% (148/160) of all residues were in allowed (>99.8%) regions.

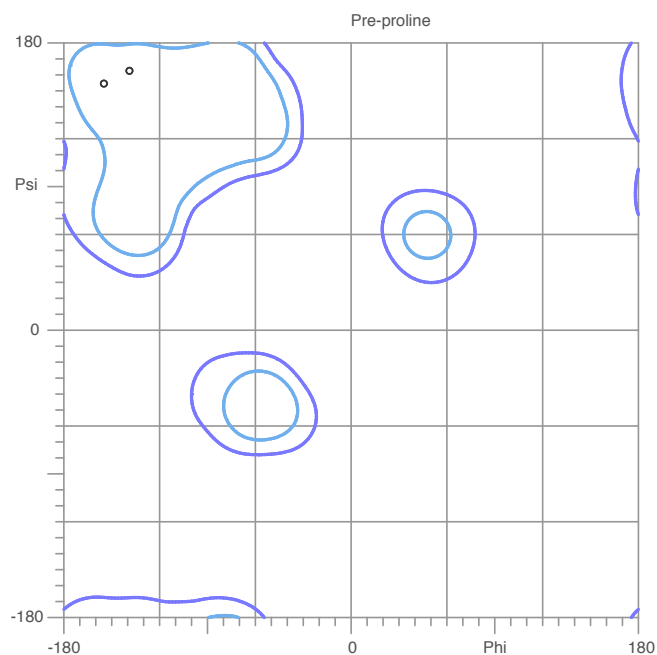
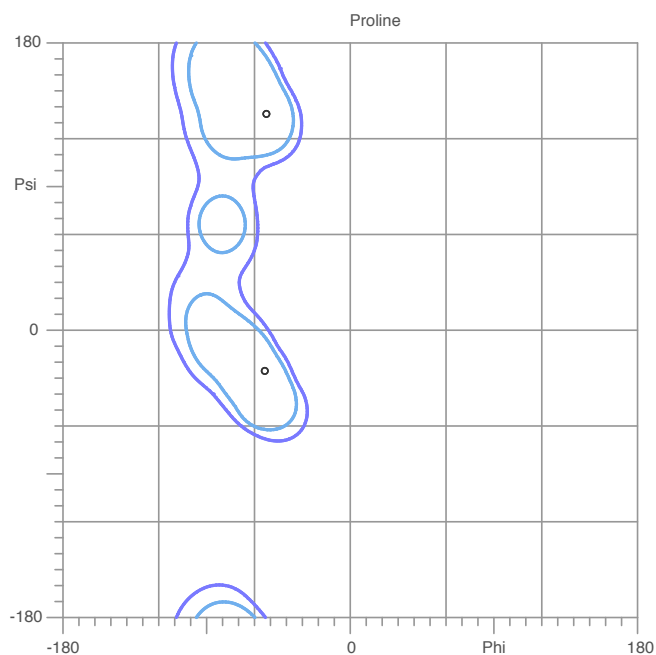
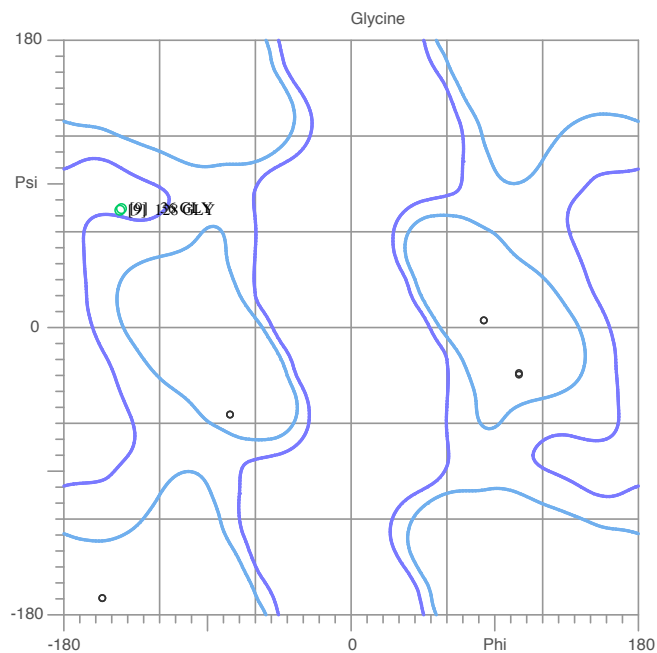
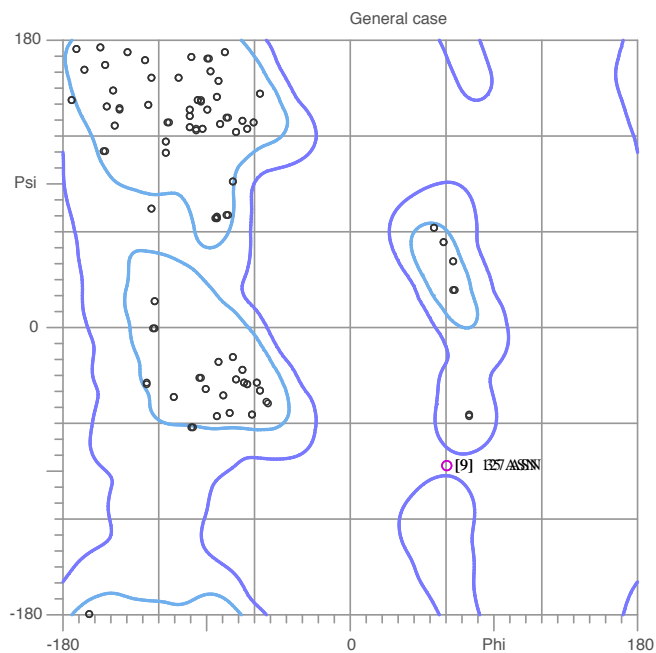
There were 12 outliers (phi, psi):

- [8] 5 ALA (73.0, -84.9)
- [8] 37 ALA (-125.1, 26.4)
- [8] 47 SER (-124.8, -55.5)
- [8] 51 THR (55.0, 97.7)

- [8] 54 GLY (155.0, 92.3)
- [8] 79 HIS (41.7, -94.9)
- [8] 97 ALA (73.1, -85.0)
- [8] 129 ALA (-125.1, 26.4)
- [8] 139 SER (-124.9, -55.5)
- [8] 143 THR (55.0, 97.6)
- [8] 146 GLY (155.0, 92.2)
- [8] 171 HIS (41.8, -95.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 9



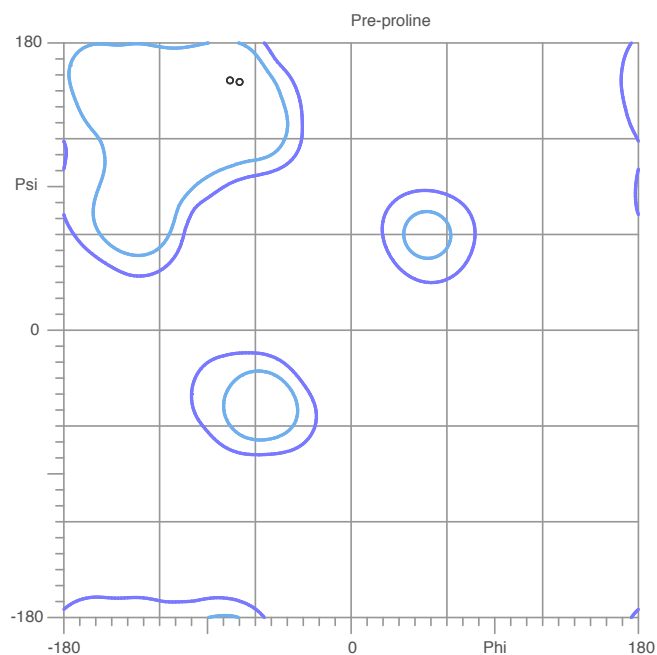
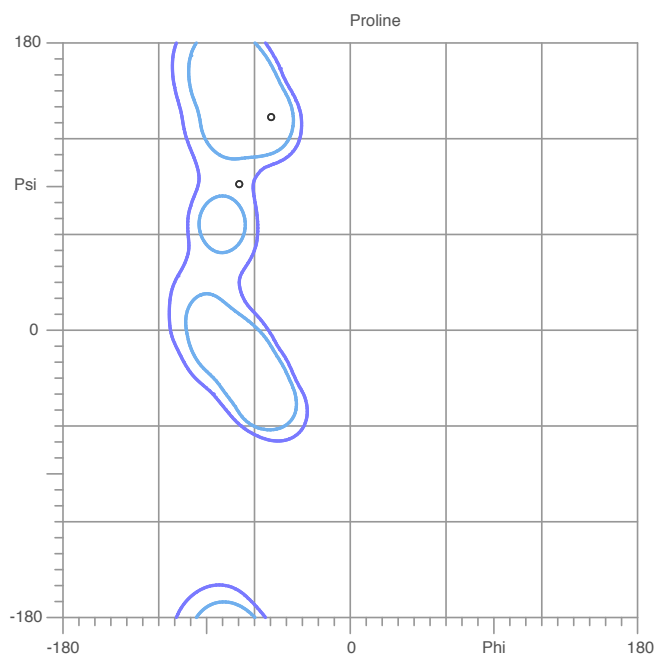
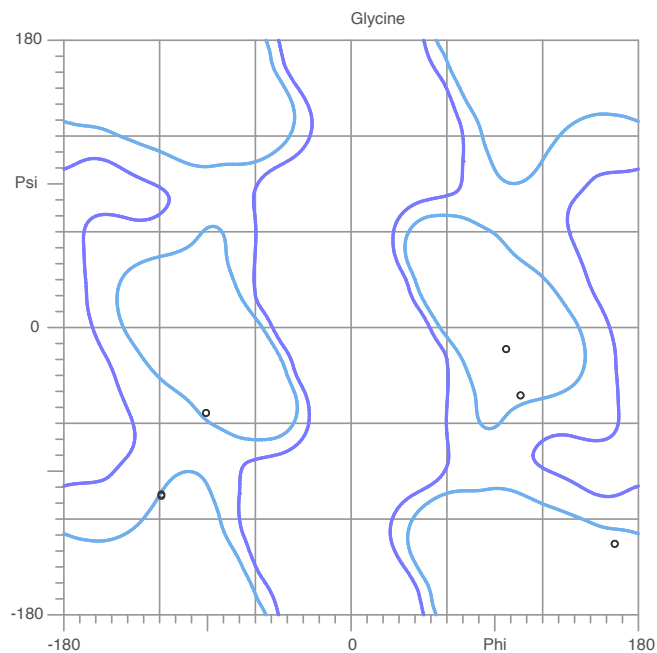
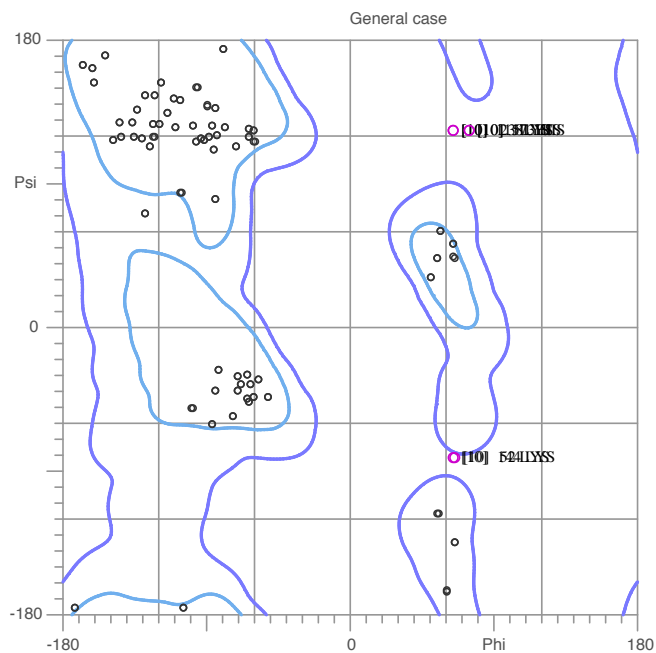
92.5% (148/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [9] 35 ASN (60.9, -86.5)
- [9] 36 GLY (-145.0, 75.0)
- [9] 127 ASN (60.9, -86.4)
- [9] 128 GLY (-145.0, 75.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 10



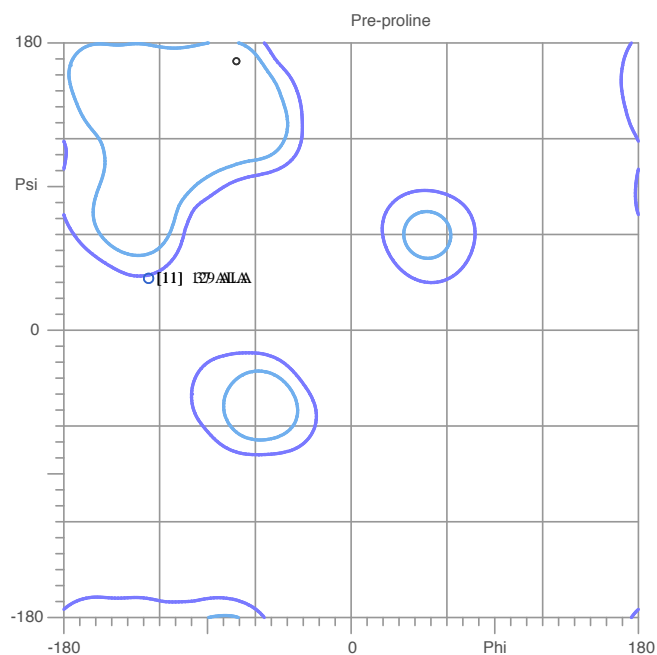
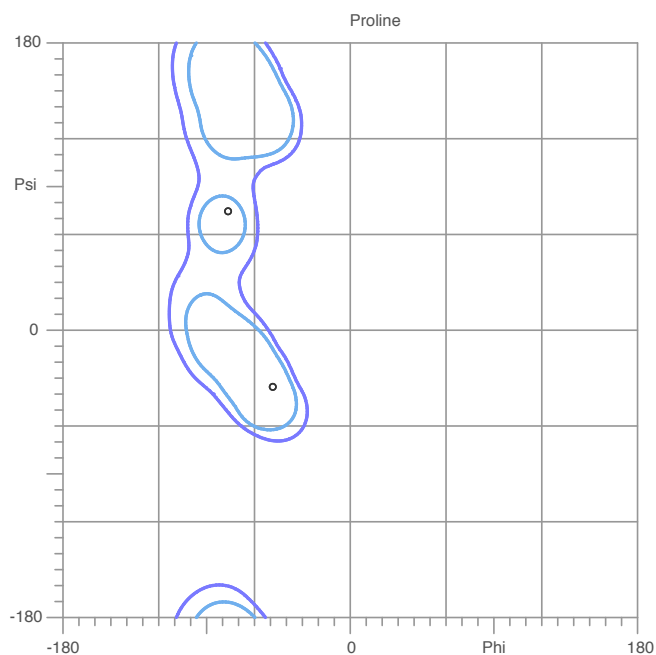
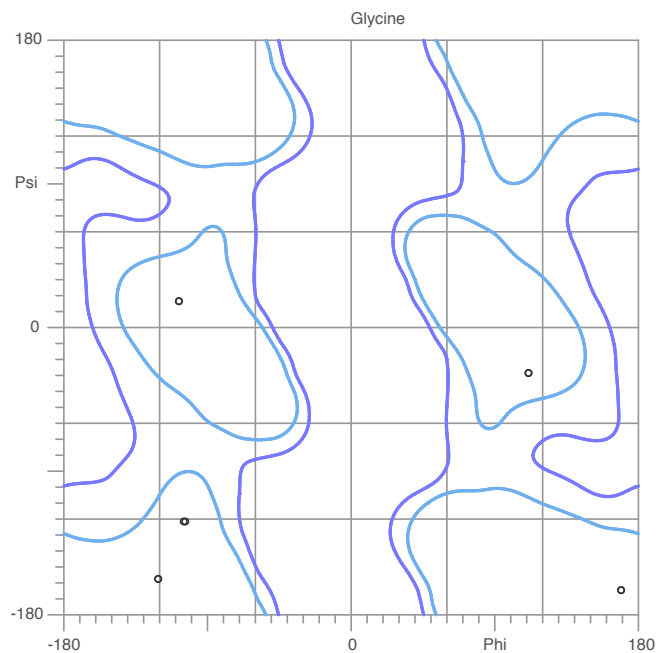
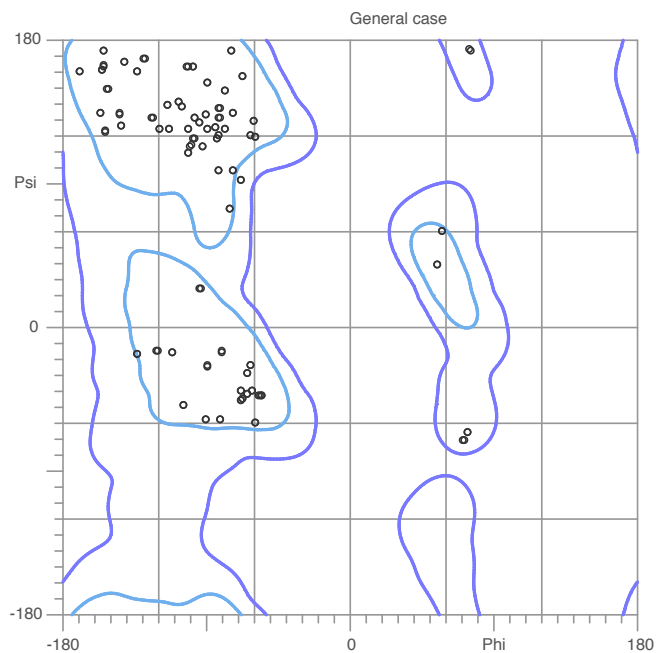
88.8% (142/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[10] 23 LYS (65.0, 125.0)

[10] 52 LYS (64.9, -81.3)
[10] 81 HIS (74.8, 125.0)
[10] 115 LYS (64.9, 125.0)
[10] 144 LYS (65.0, -81.3)
[10] 173 HIS (74.8, 125.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 11



92.5% (148/160) of all residues were in favored (98%) regions.
98.8% (158/160) of all residues were in allowed (>99.8%) regions.

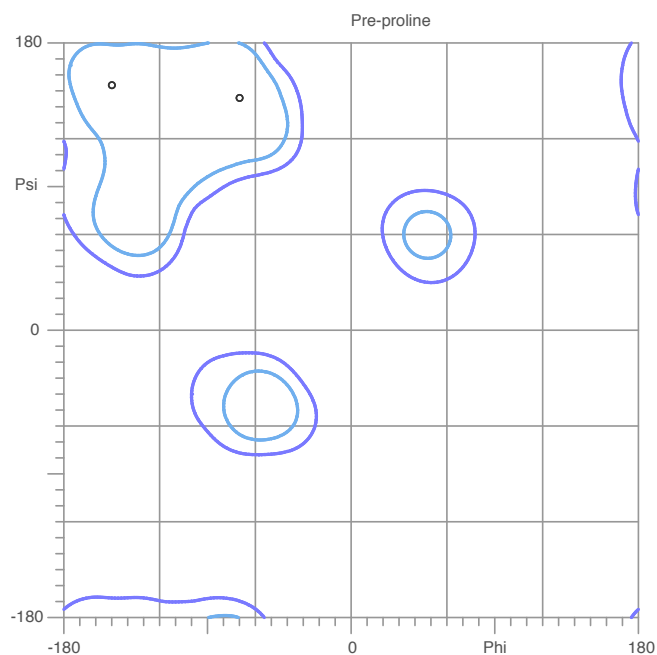
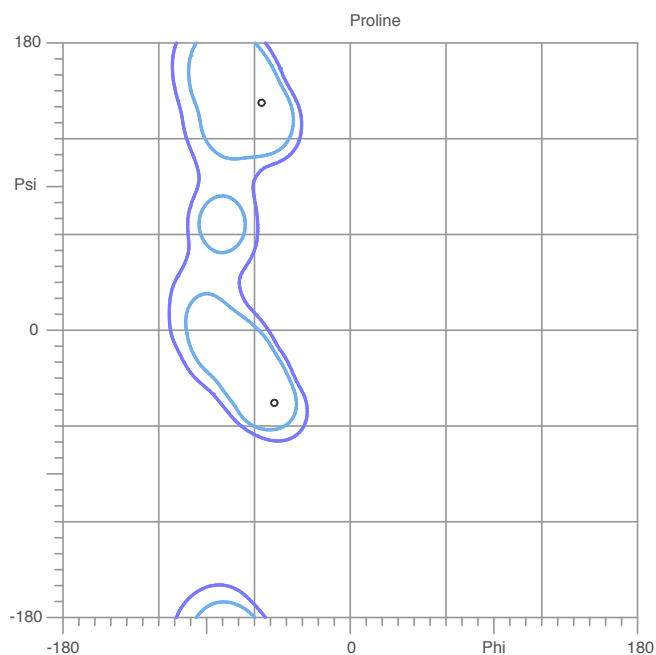
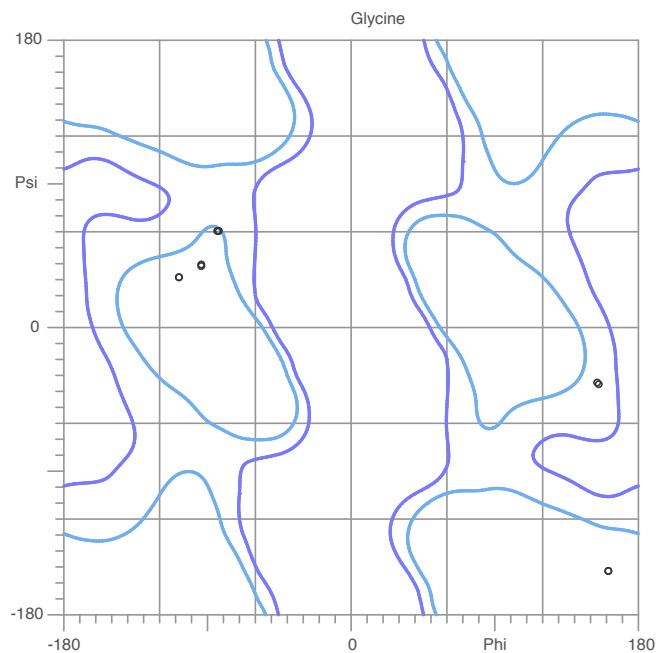
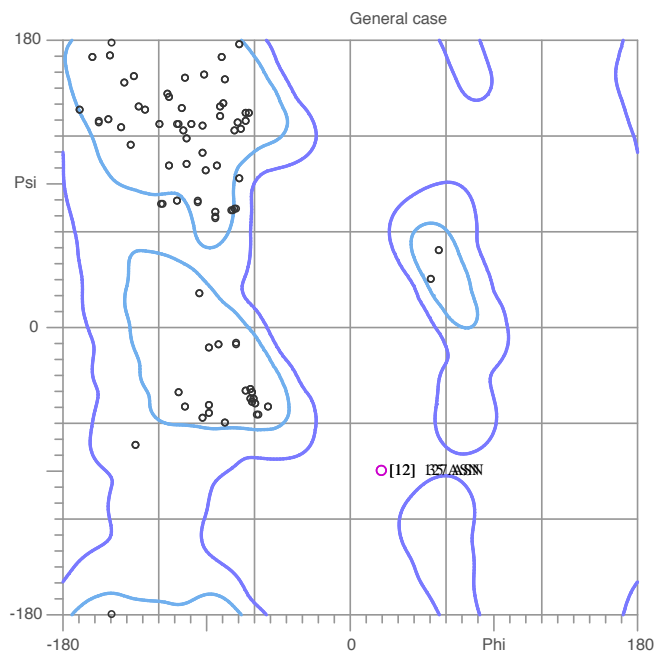
There were 2 outliers (phi, psi):

[11] 37 ALA (-127.6, 33.6)

[11] 129 ALA (-127.7, 33.6)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 12



90.6% (145/160) of all residues were in favored (98%) regions.
98.8% (158/160) of all residues were in allowed (>99.8%) regions.

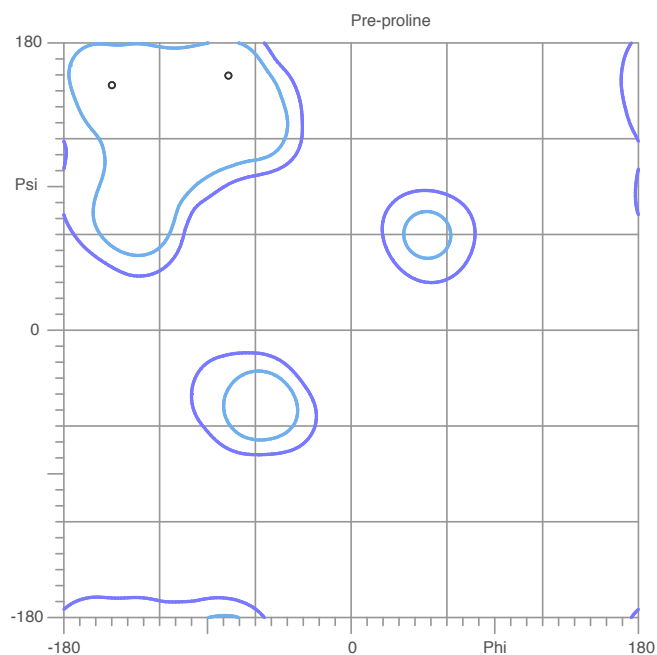
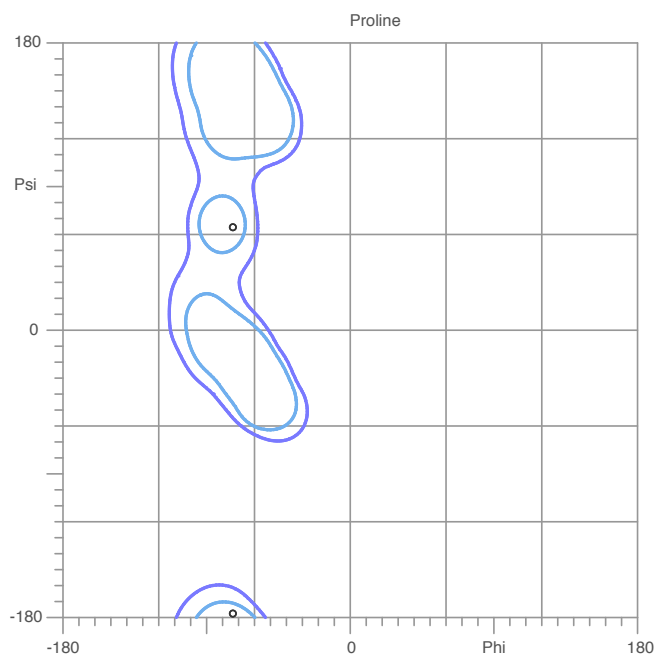
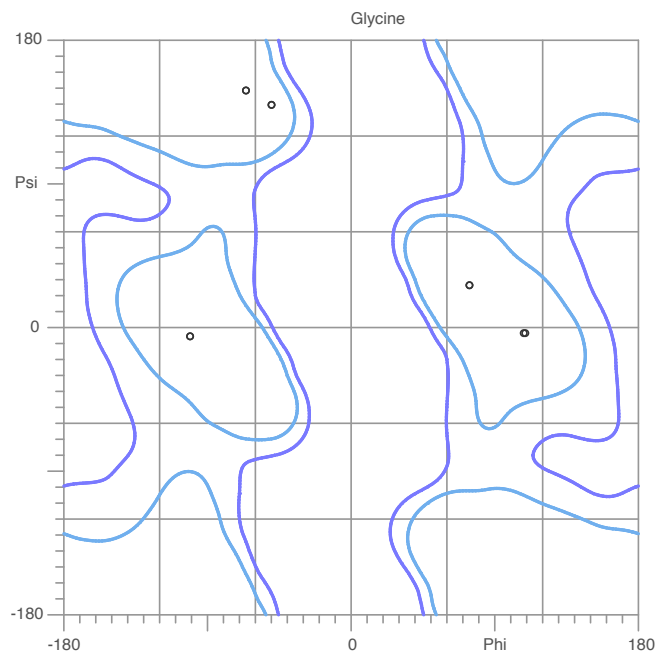
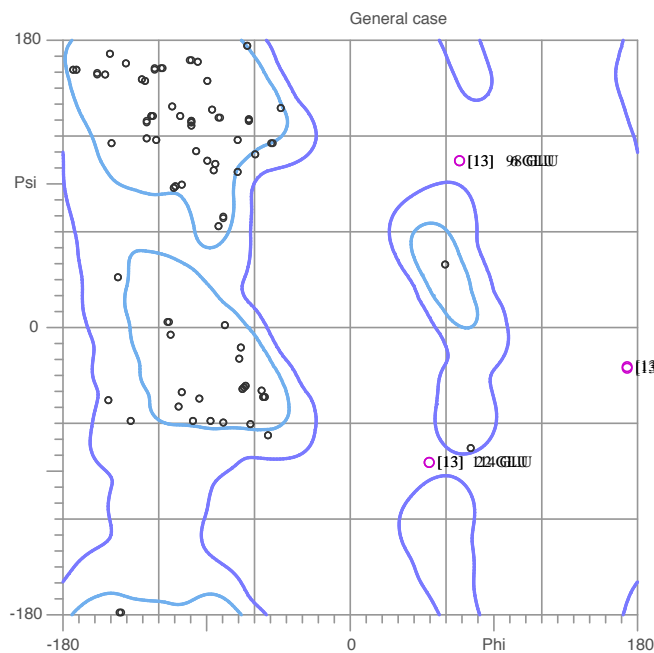
There were 2 outliers (phi, psi):

[12] 35 ASN (19.9, -89.6)

[12] 127 ASN (20.0, -89.6)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 13



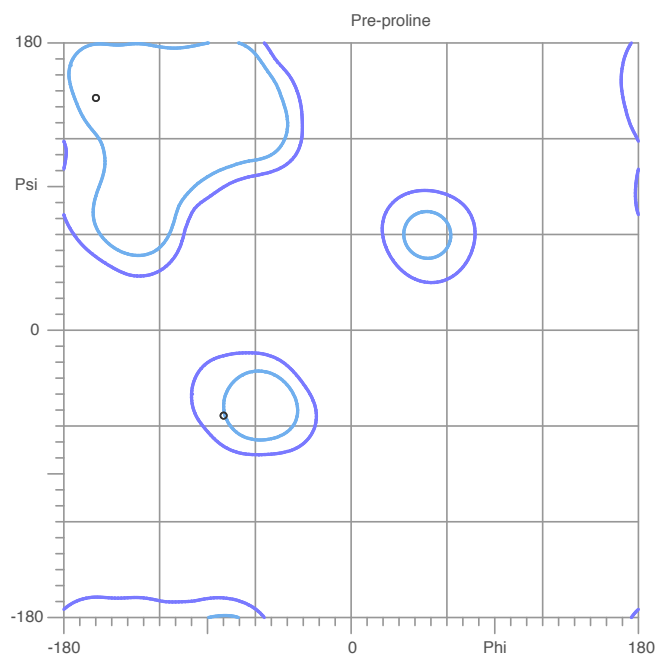
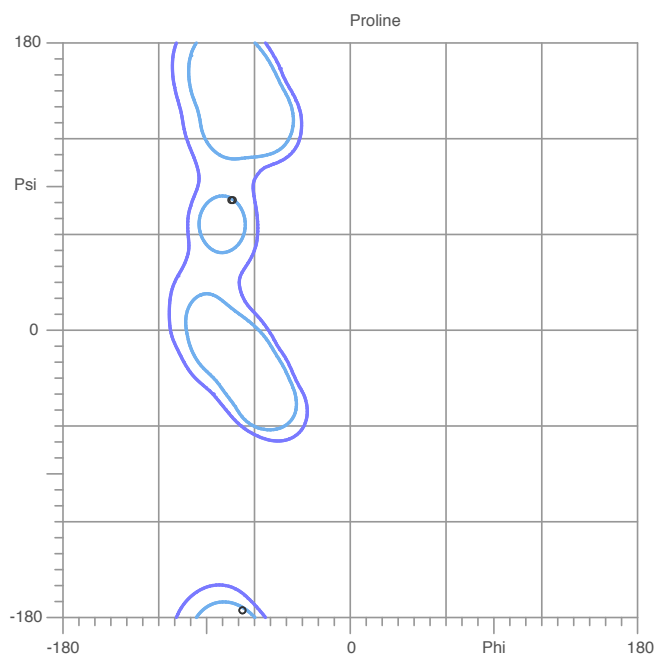
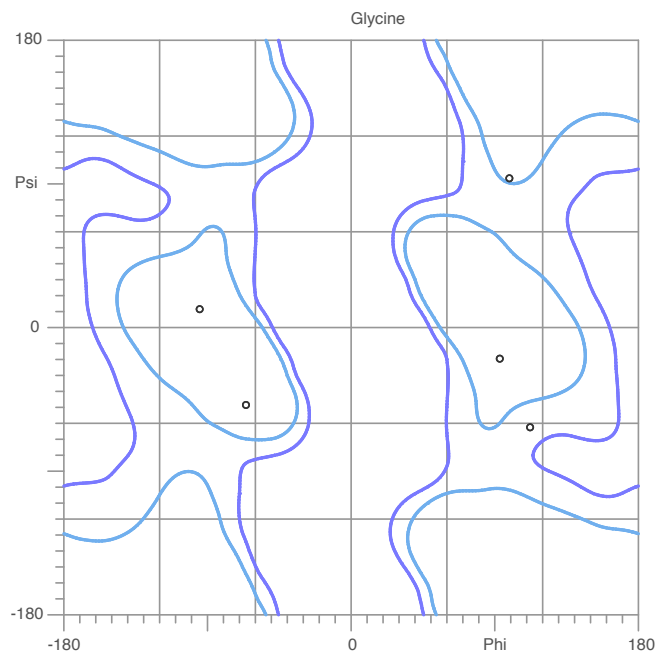
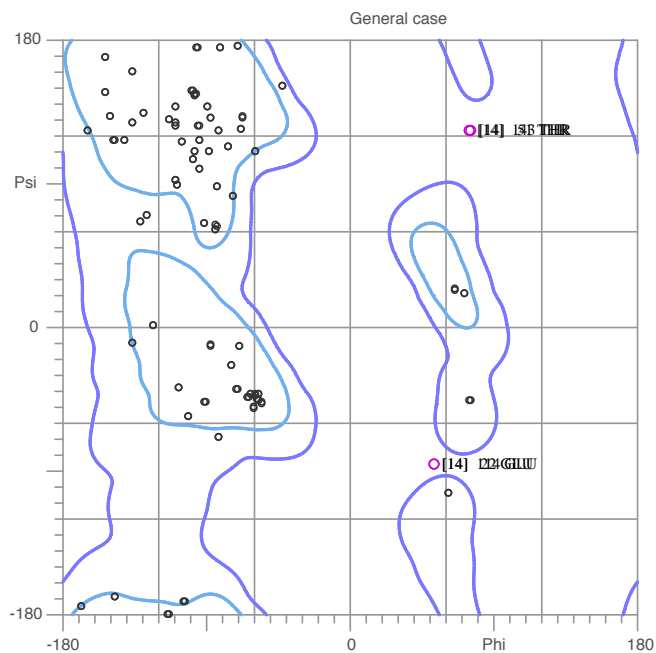
88.8% (142/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[13] 6 GLU (68.5, 105.1)

[13] 22 GLU (49.2, -84.9)
[13] 81 HIS (173.6, -25.0)
[13] 98 GLU (68.6, 105.0)
[13] 114 GLU (49.2, -84.9)
[13] 173 HIS (173.6, -25.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 14



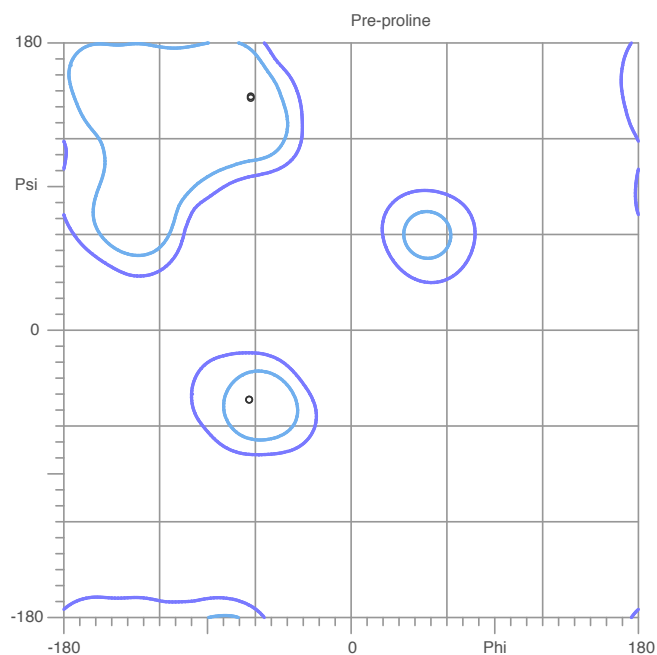
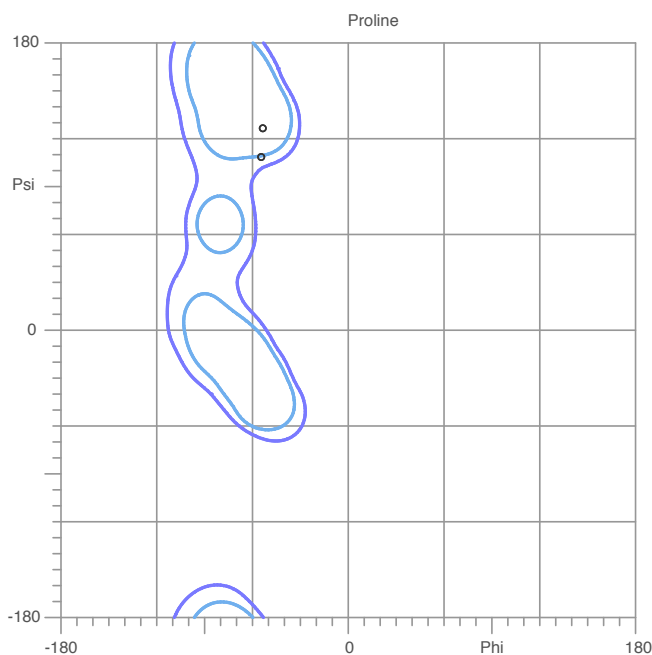
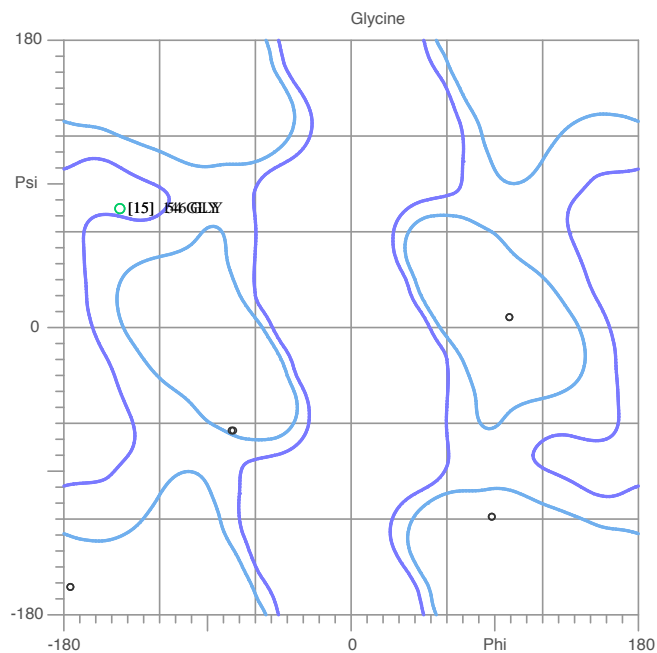
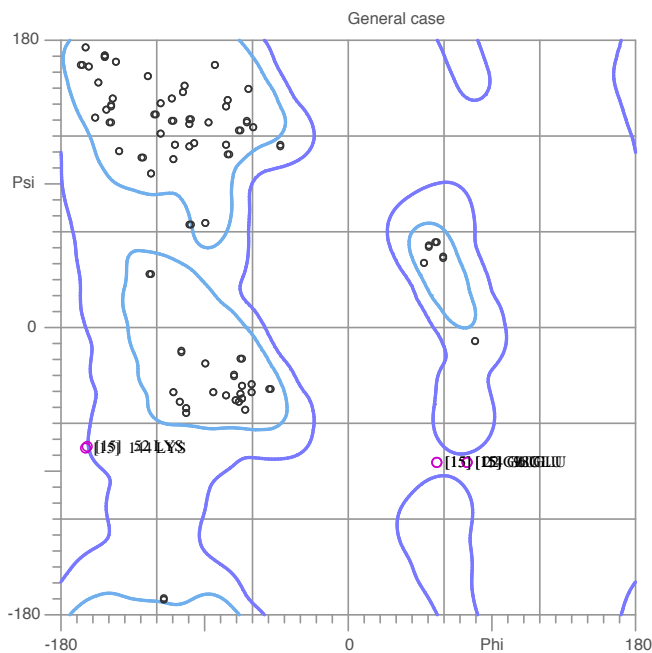
82.5% (132/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [14] 22 GLU (52.4, -85.0)
- [14] 51 THR (75.1, 125.0)
- [14] 114 GLU (52.4, -85.0)
- [14] 143 THR (75.0, 125.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 15



90.0% (144/160) of all residues were in favored (98%) regions.
95.0% (152/160) of all residues were in allowed (>99.8%) regions.

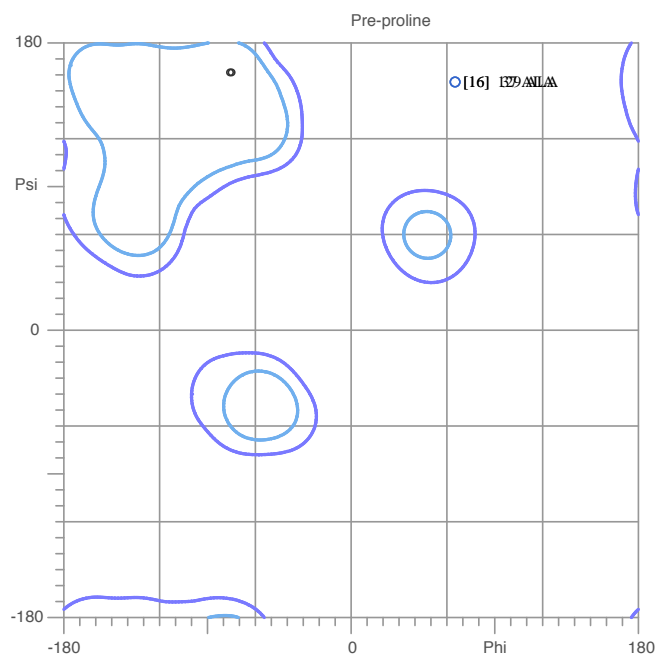
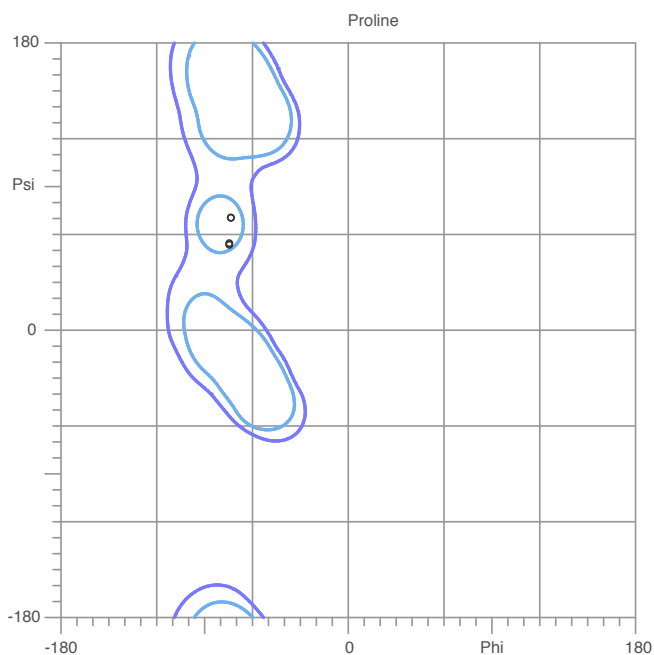
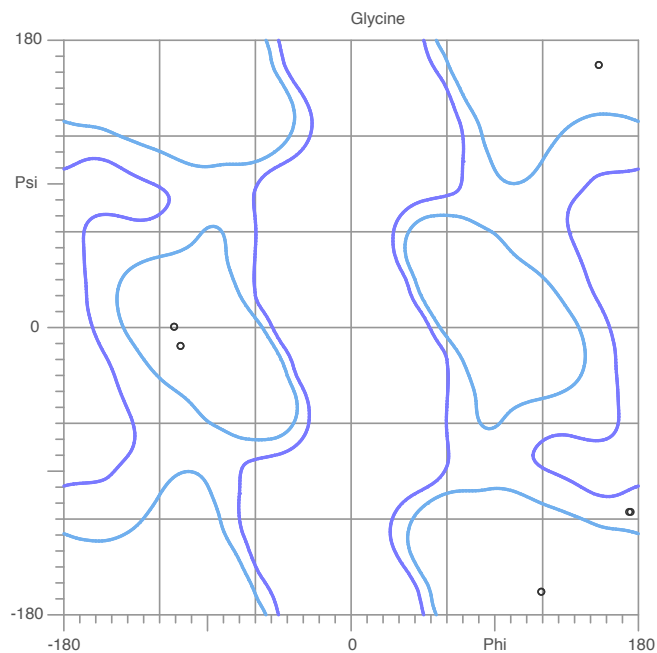
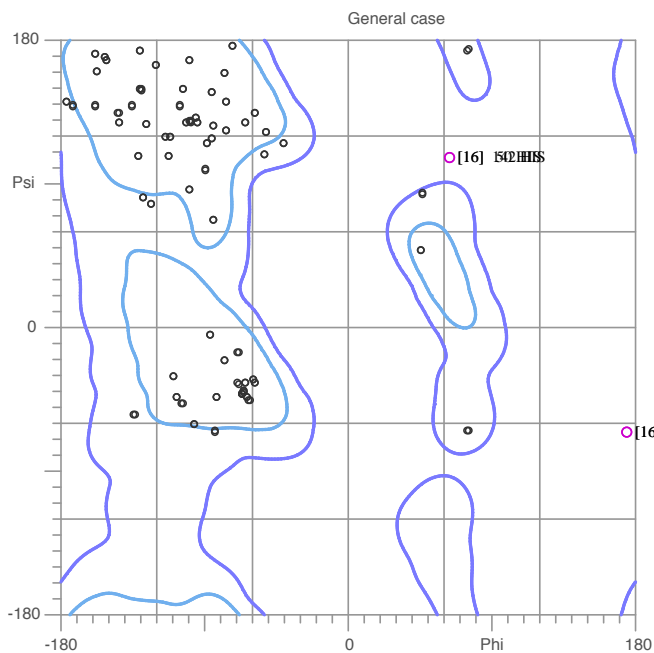
There were 8 outliers (phi, psi):

[15] 6 GLU (74.9, -84.9)
[15] 22 GLU (55.4, -85.0)

[15] 52 LYS (-165.0, -74.9)
[15] 54 GLY (-145.0, 75.0)
[15] 98 GLU (74.9, -85.0)
[15] 114 GLU (55.5, -85.0)
[15] 144 LYS (-165.1, -75.0)
[15] 146 GLY (-145.0, 75.1)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 16



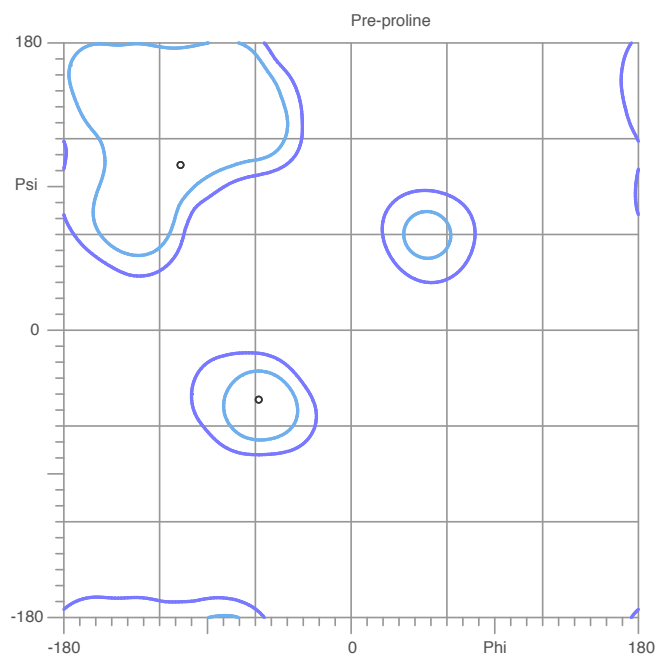
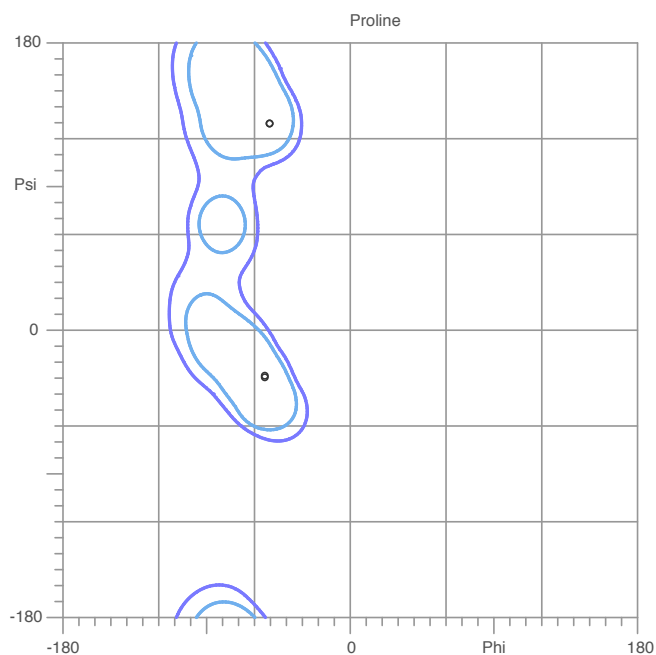
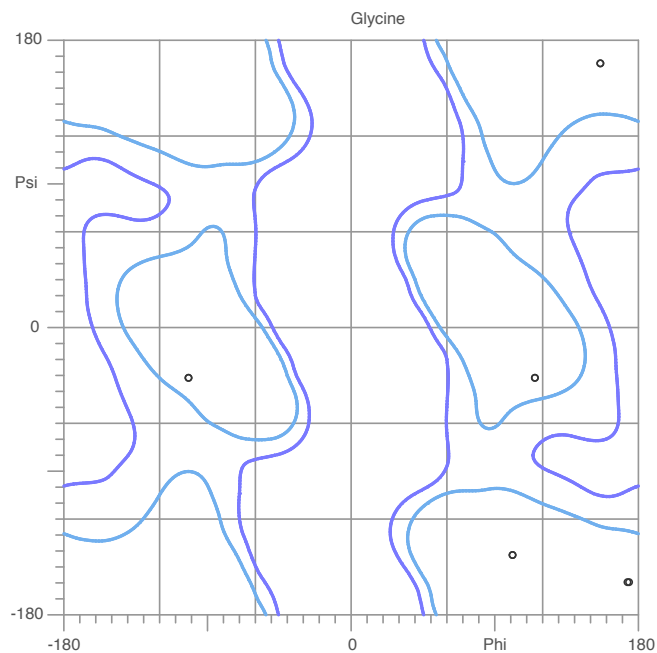
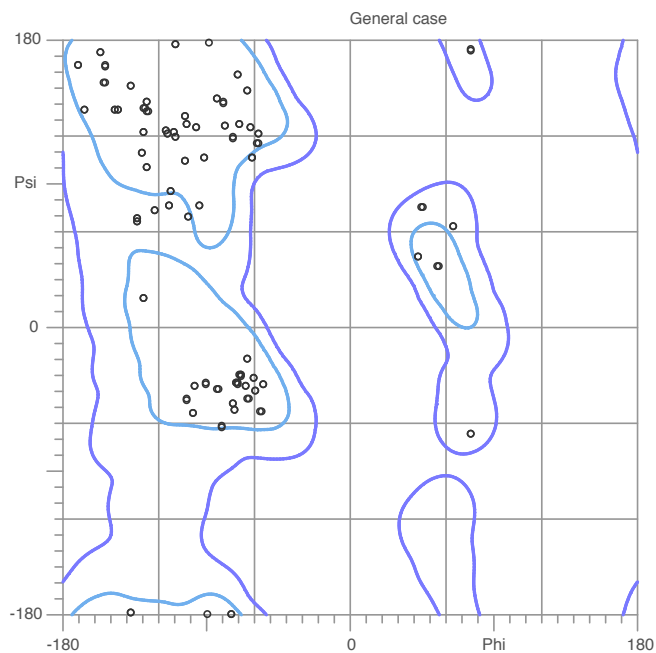
81.2% (130/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[16] 23 LYS (175.0, -65.1)

[16] 37 ALA (65.3, 156.1)
[16] 50 HIS (63.3, 107.3)
[16] 115 LYS (174.9, -65.0)
[16] 129 ALA (65.3, 156.2)
[16] 142 HIS (63.3, 107.1)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 17



87.5% (140/160) of all residues were in favored (98%) regions.
100.0% (160/160) of all residues were in allowed (>99.8%) regions.

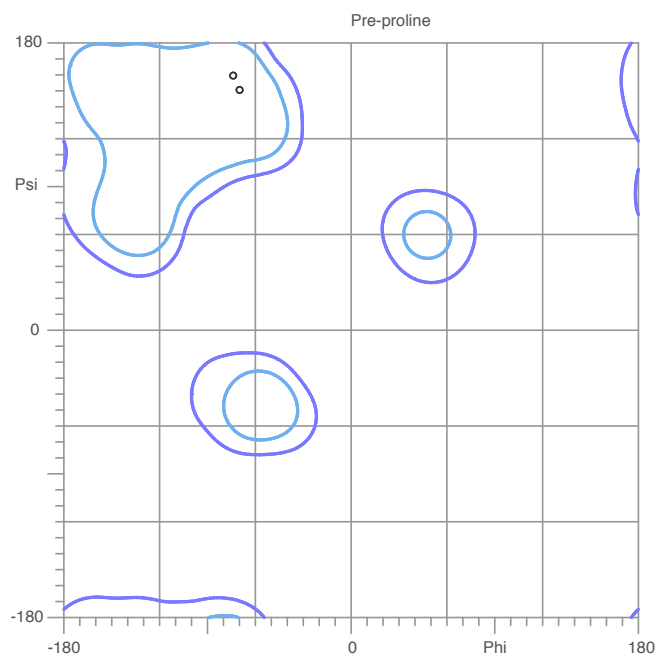
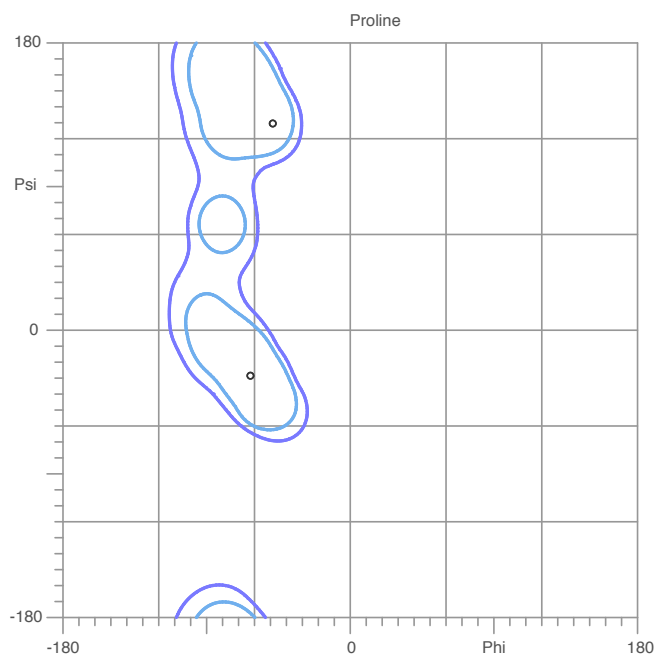
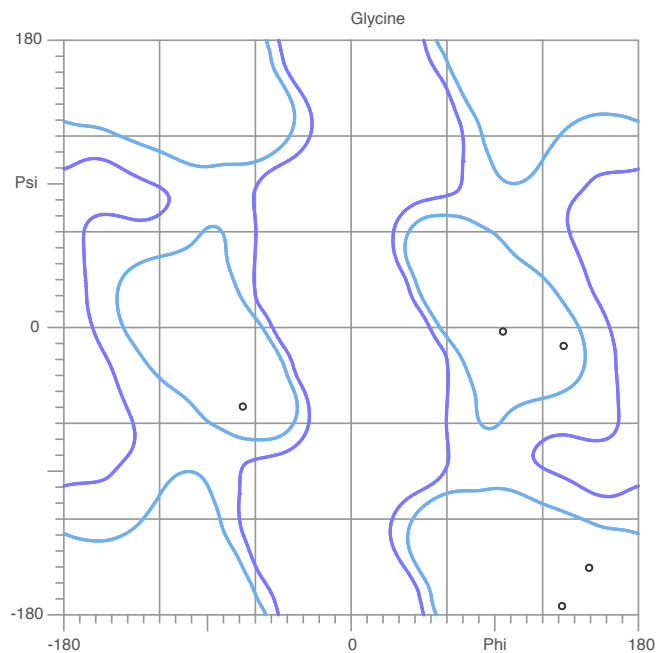
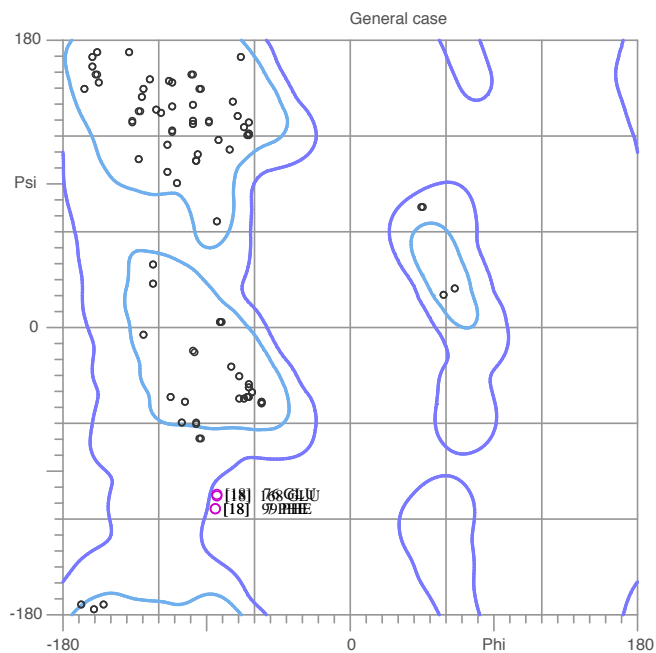
There were no outliers.

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

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

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 18



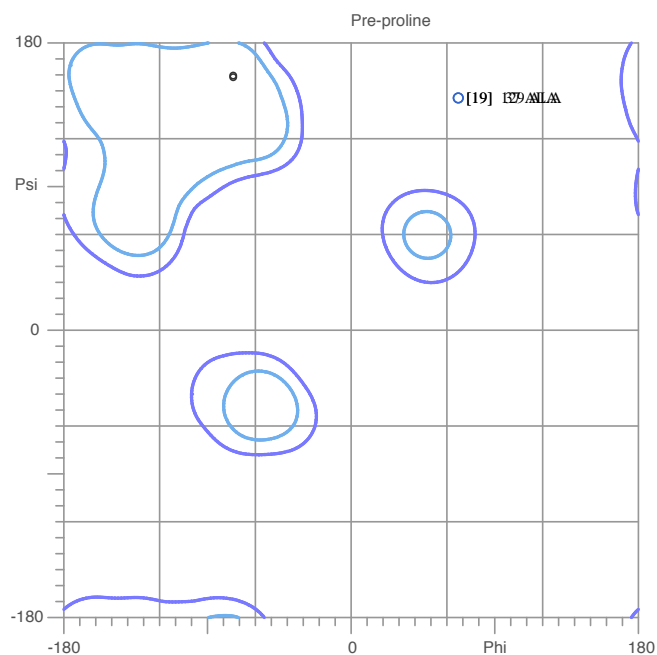
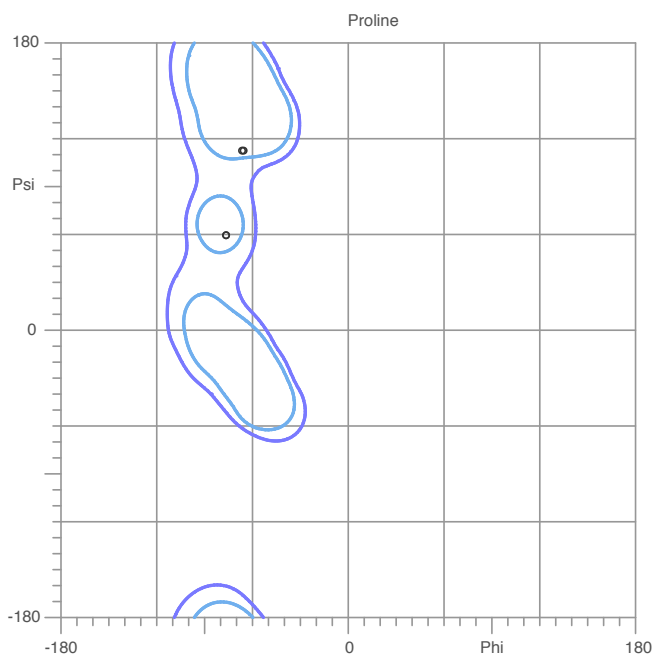
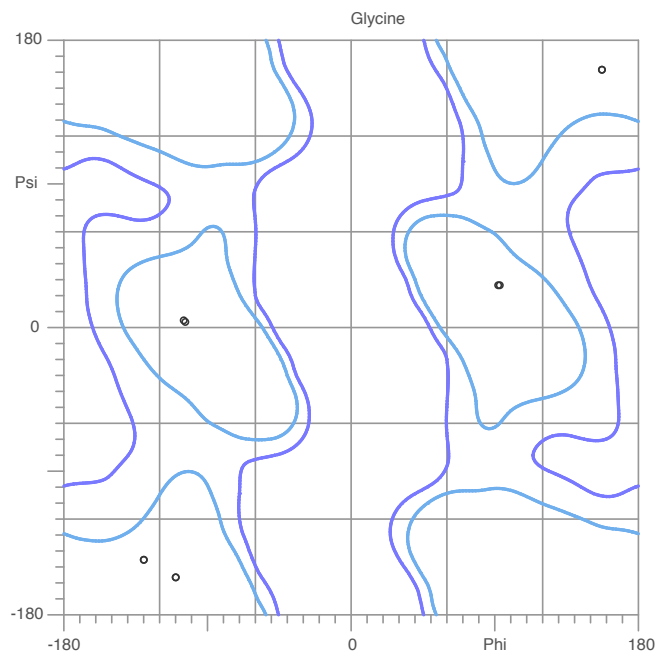
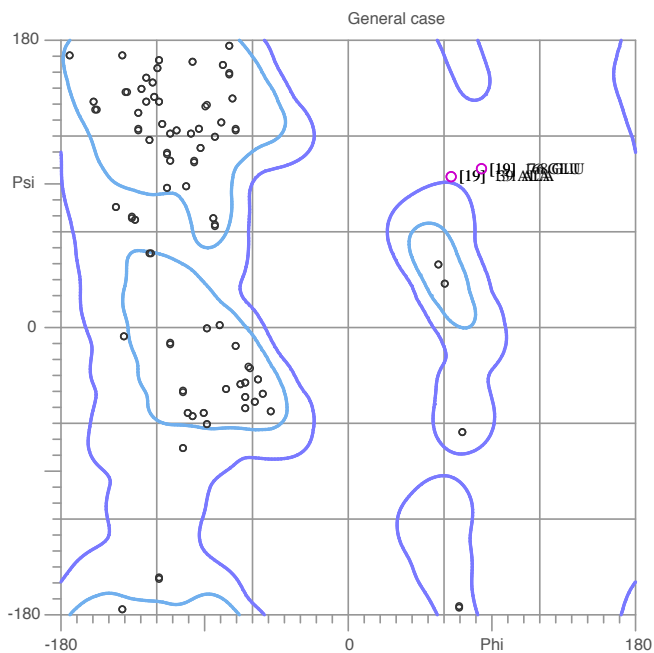
93.8% (150/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [18] 7 PHE (-85.0, -113.5)
- [18] 76 GLU (-85.0, -104.9)
- [18] 99 PHE (-85.0, -113.5)
- [18] 168 GLU (-85.0, -105.0)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 19



85.0% (136/160) of all residues were in favored (98%) regions.
96.2% (154/160) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[19] 37 ALA (67.8, 146.0)

[19] 39 ALA (64.9, 95.0)

[19] 76 GLU (83.5, 100.8)

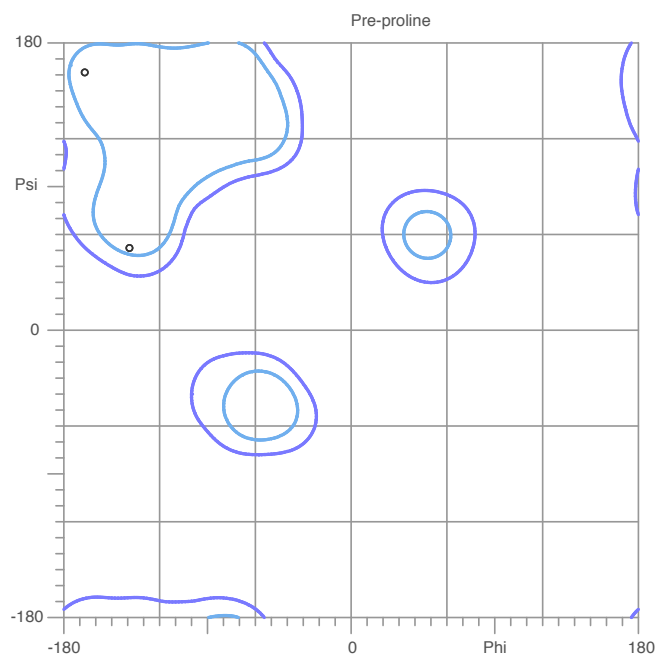
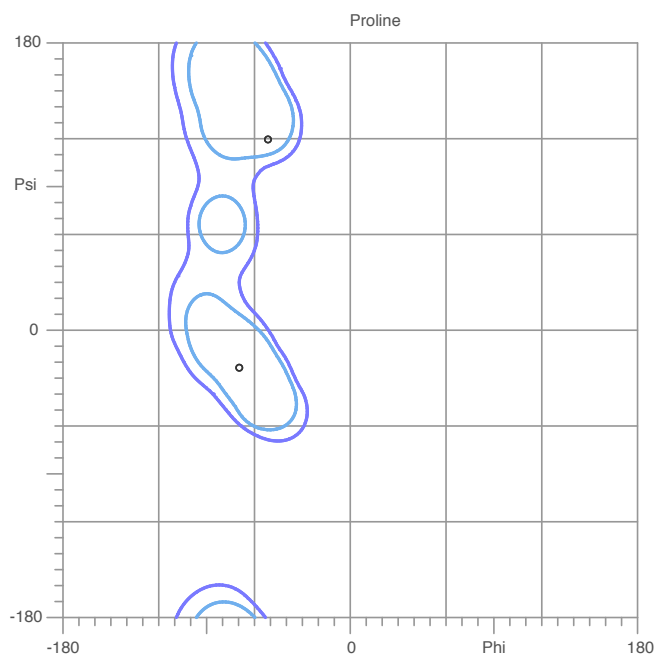
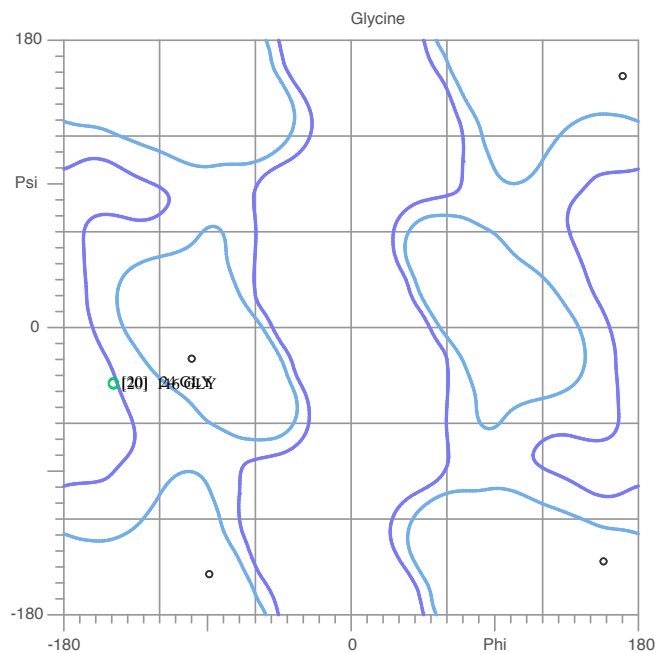
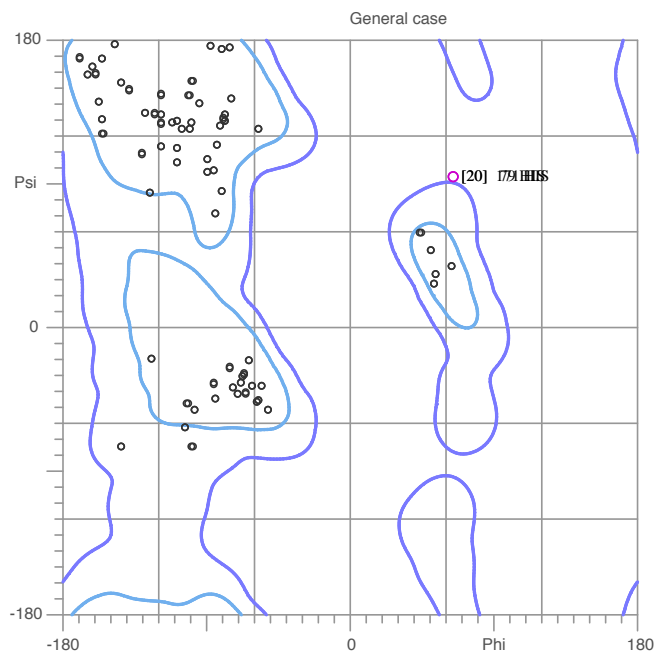
[19] 129 ALA (67.7, 146.0)

[19] 131 ALA (65.0, 95.1)

[19] 168 GLU (83.4, 100.8)

MolProbity Ramachandran analysis

SPR104_R3_em_bcr3.pdb, model 20



93.8% (150/160) of all residues were in favored (98%) regions.
97.5% (156/160) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[20] 24 GLY (-149.2, -35.0)

[20] 79 HIS (65.0, 95.1)

[20] 116 GLY (-149.2, -35.0)

[20] 171 HIS (65.0, 95.1)