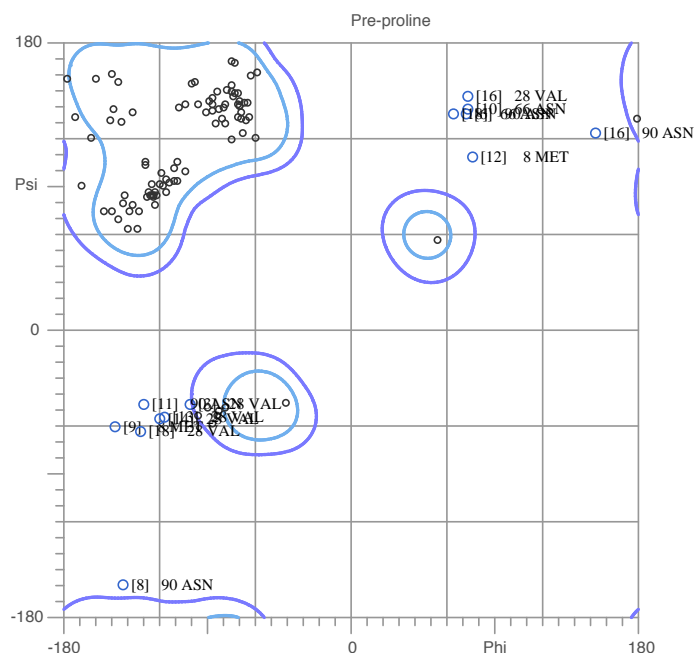
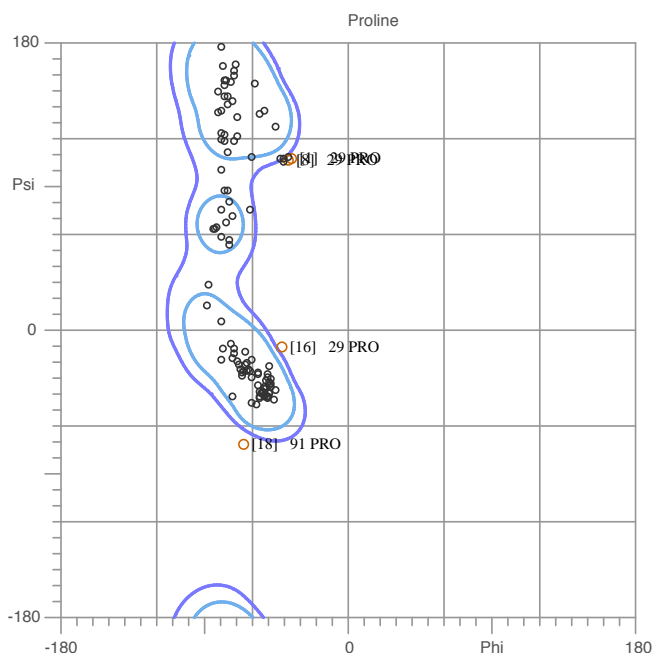
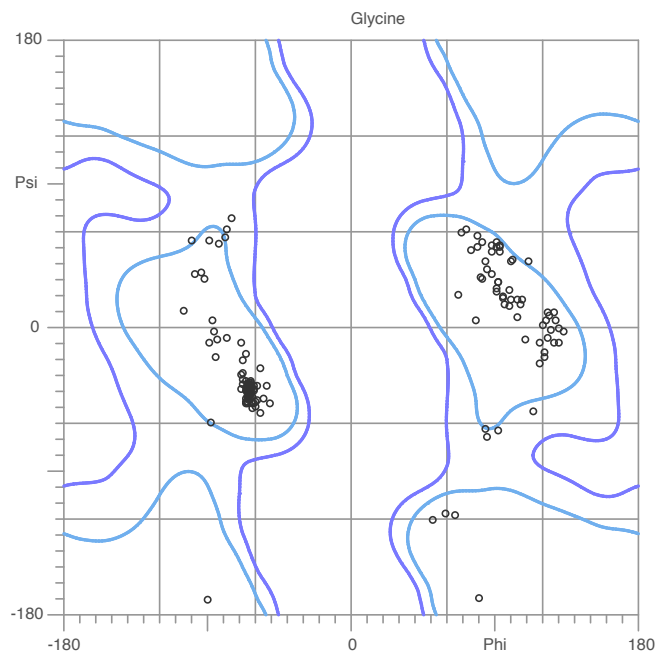
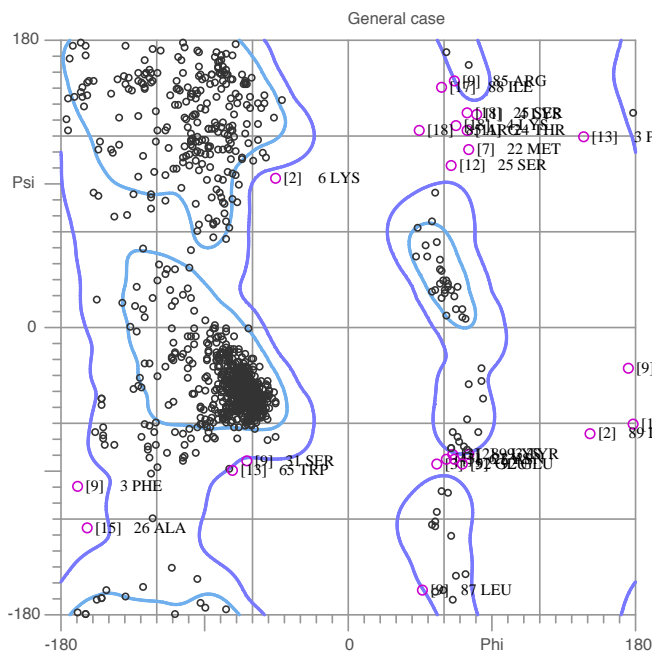


MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, all models



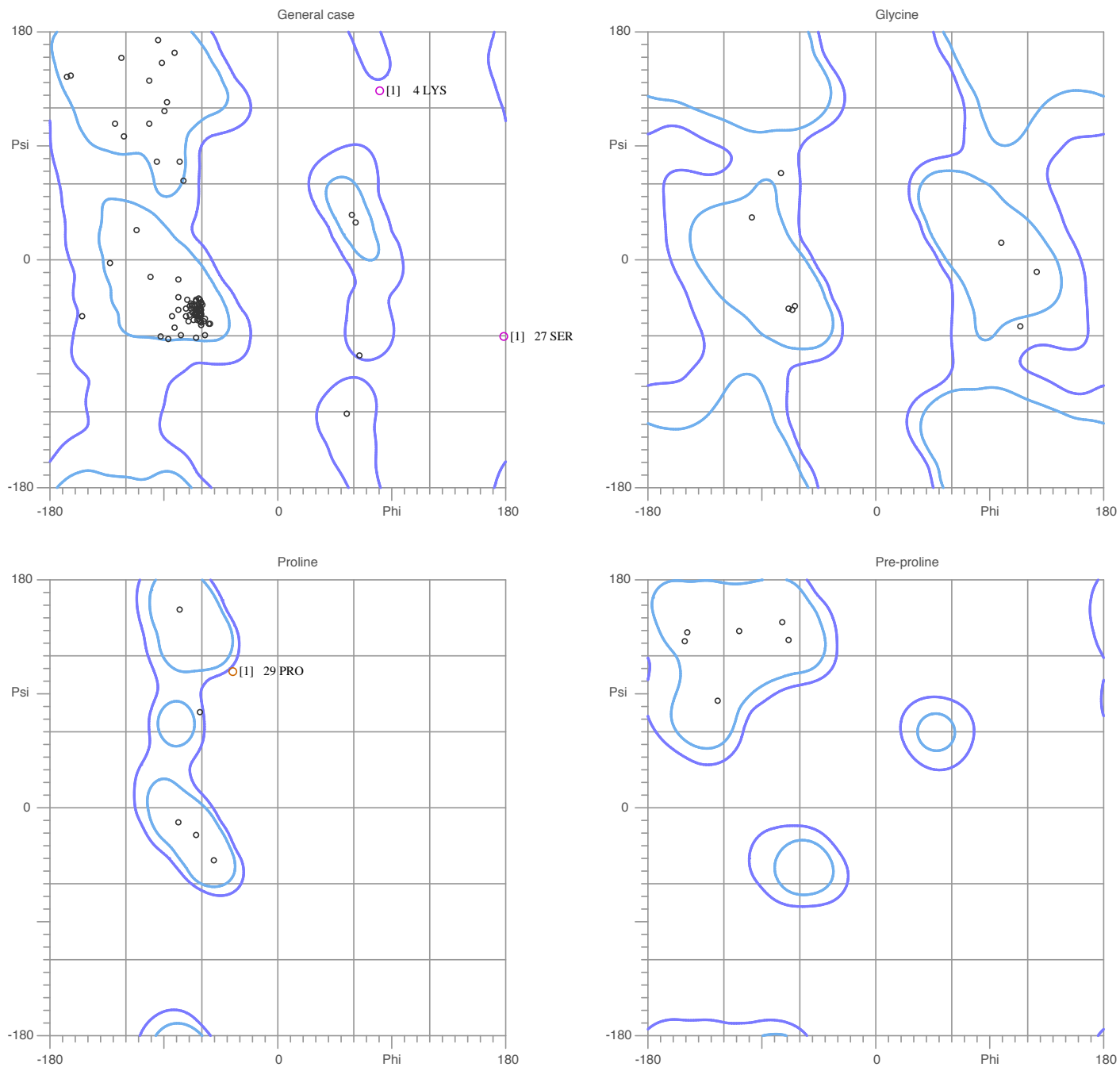
91.0% (1752/1926) of all residues were in favored (98%) regions.
97.8% (1884/1926) of all residues were in allowed (>99.8%) regions.

There were 42 outliers (phi, psi):

[1] 4 LYS (80.2, 134.9)	[9] 31 SER (-64.2, -83.1)
[1] 27 SER (178.8, -60.2)	[9] 85 ARG (66.0, 155.0)
[1] 29 PRO (-36.4, 108.8)	[9] 87 LEU (46.3, -164.9)
[1] 6 LYS (-46.9, 94.2)	[10] 66 ASN (73.8, 139.5)
[2] 6 LYS (-46.9, 94.2)	[11] 24 THR (75.0, 124.9)
[2] 89 LYS (151.7, -66.6)	[11] 90 ASN (-130.2, -46.5)
[3] 28 VAL (-101.4, -46.8)	[12] 8 MET (77.0, 109.4)
[3] 89 LYS (65.1, -79.1)	[12] 25 SER (64.6, 102.8)
[3] 92 GLU (55.5, -85.0)	[13] 3 PHE (147.4, 121.0)
[4] 6 LYS (61.4, -82.2)	[13] 28 VAL (-117.2, -54.8)
[5] 23 ASN (66.1, -82.4)	[13] 65 TRP (-73.1, -89.7)
[5] 92 GLU (71.0, -85.5)	[14] 28 VAL (-120.1, -55.3)
[6] 90 ASN (73.0, 136.2)	[15] 26 ALA (-164.6, -125.3)
[7] 22 MET (75.0, 112.6)	[16] 28 VAL (73.7, 147.5)
[8] 29 PRO (-38.3, 107.0)	[16] 29 PRO (-42.3, -10.0)
[8] 90 ASN (-143.7, -159.8)	[16] 90 ASN (153.1, 124.5)
[9] 3 PHE (-170.6, -99.6)	[17] 88 ILE (58.4, 151.2)
[9] 8 MET (-148.4, -60.9)	[18] 4 LYS (67.2, 127.9)
[9] 24 THR (175.0, -25.1)	[18] 25 SER (74.4, 135.3)
	[18] 28 VAL (-132.2, -63.9)
	[18] 66 ASN (64.8, 136.1)
	[18] 85 ARG (44.1, 124.1)
	[18] 91 PRO (-66.9, -71.4)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 1



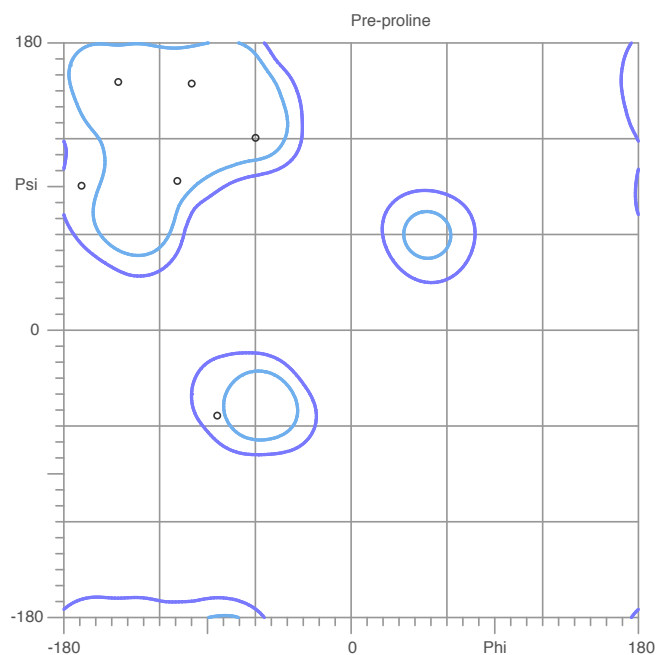
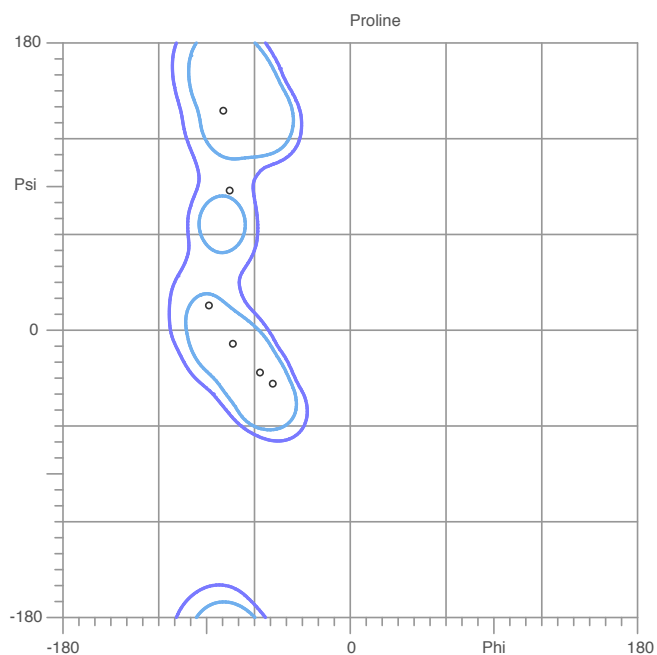
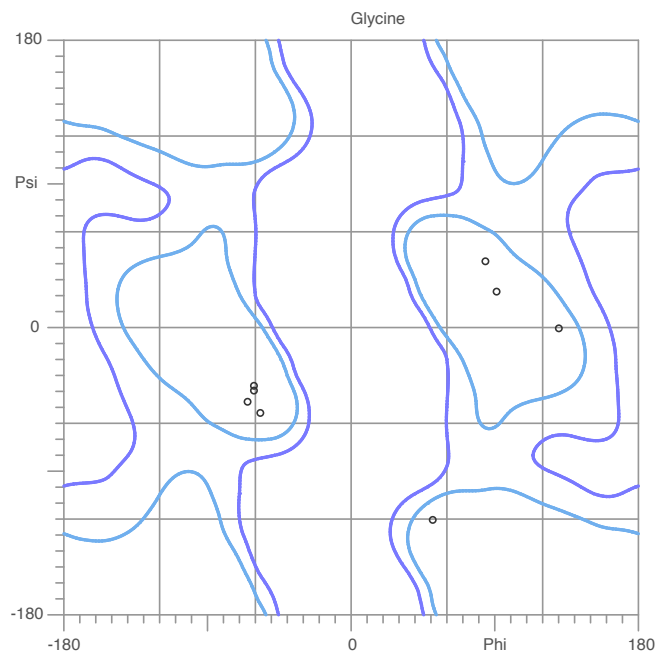
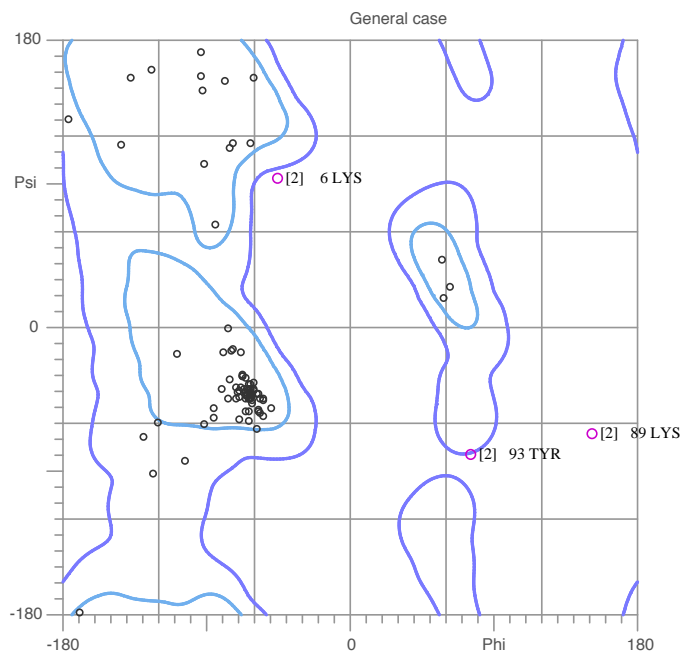
91.6% (98/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [1] 4 LYS (80.2, 134.9)
- [1] 27 SER (178.8, -60.2)
- [1] 29 PRO (-36.4, 108.8)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 2



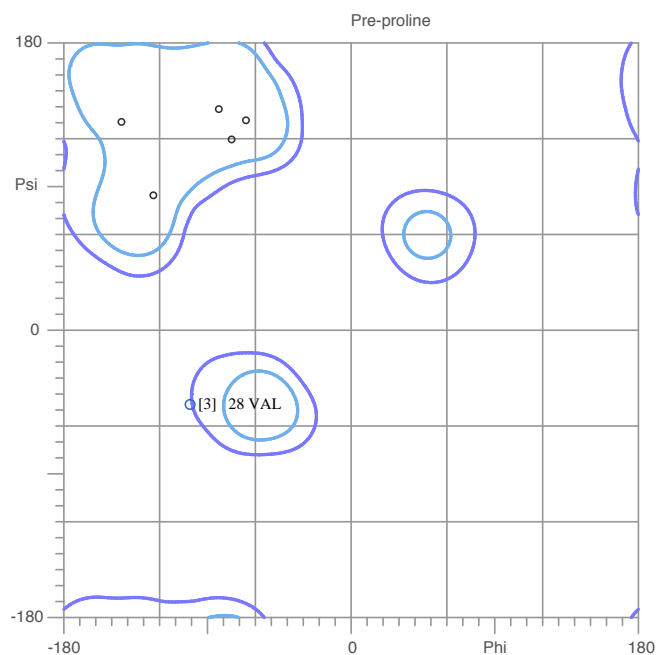
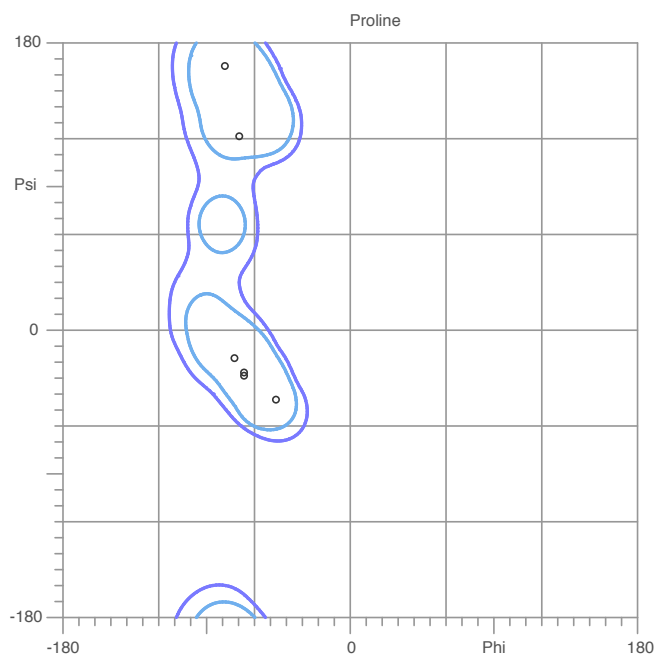
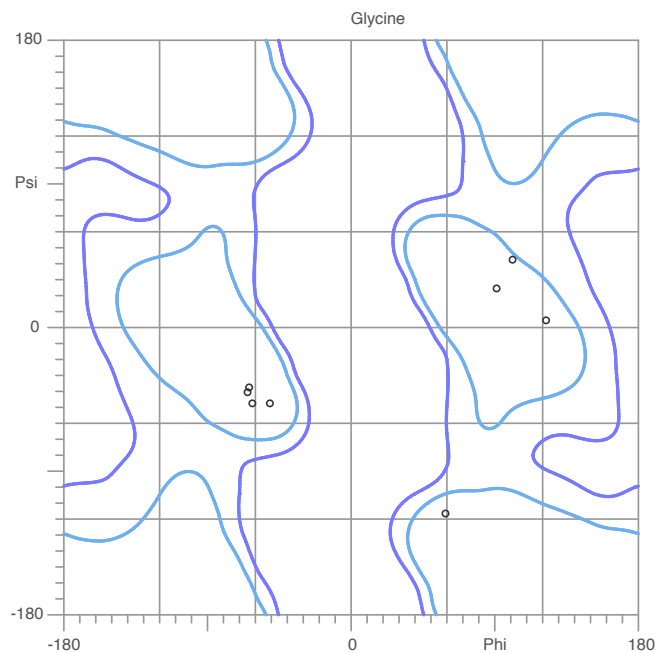
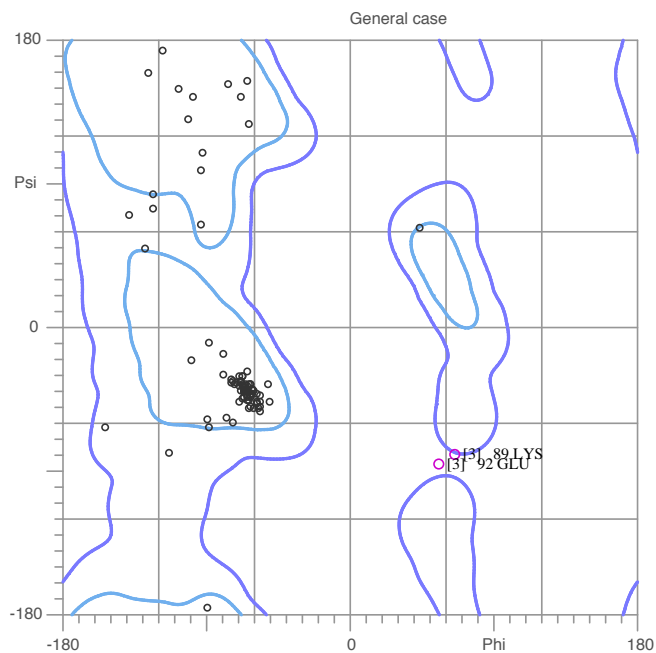
89.7% (96/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [2] 6 LYS (-46.9, 94.2)
- [2] 89 LYS (151.7, -66.6)
- [2] 93 TYR (75.5, -80.0)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 3



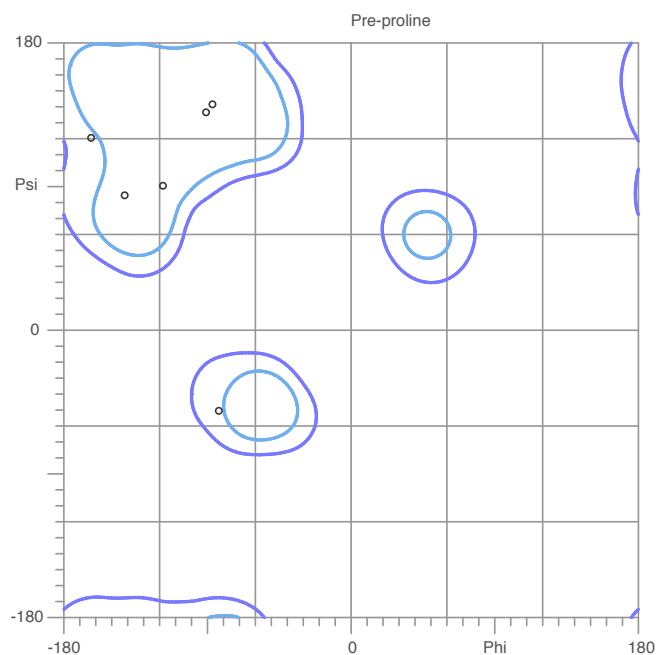
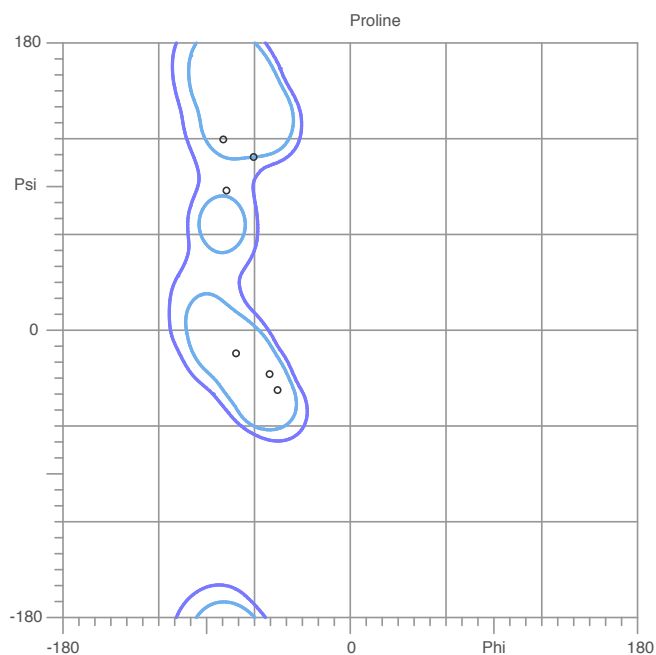
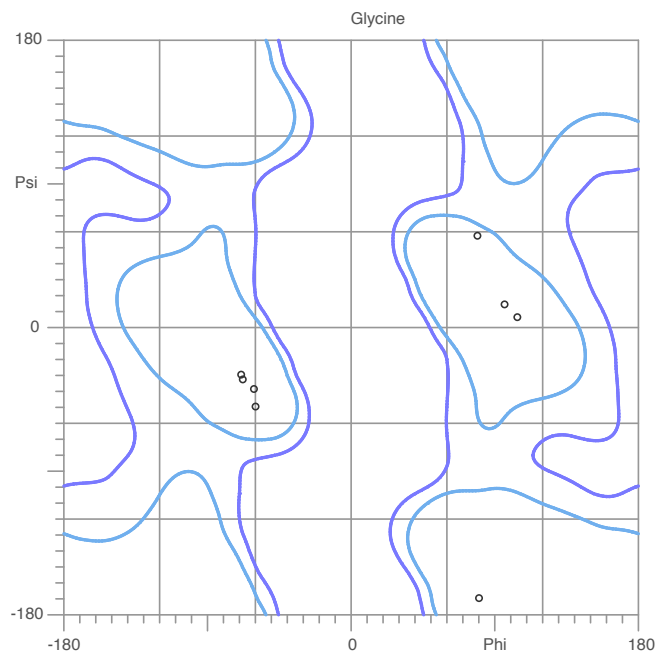
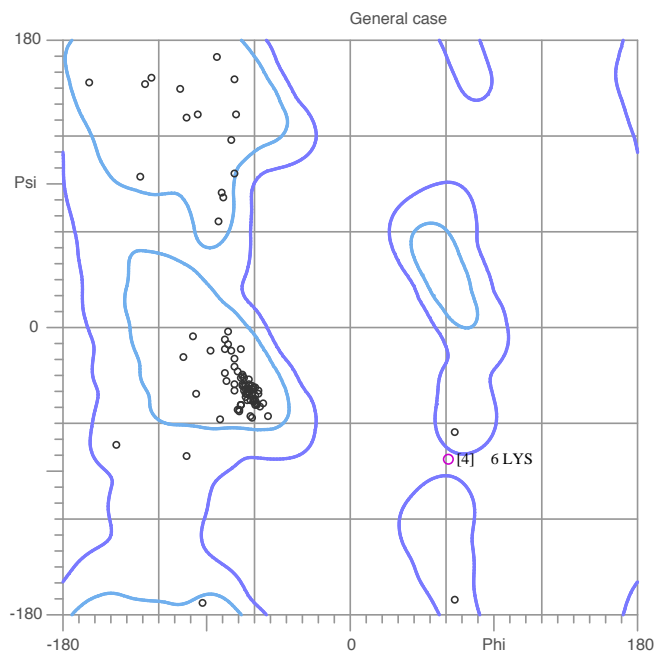
91.6% (98/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 28 VAL (-101.4, -46.8)
- [3] 89 LYS (65.1, -79.1)
- [3] 92 GLU (55.5, -85.0)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 4

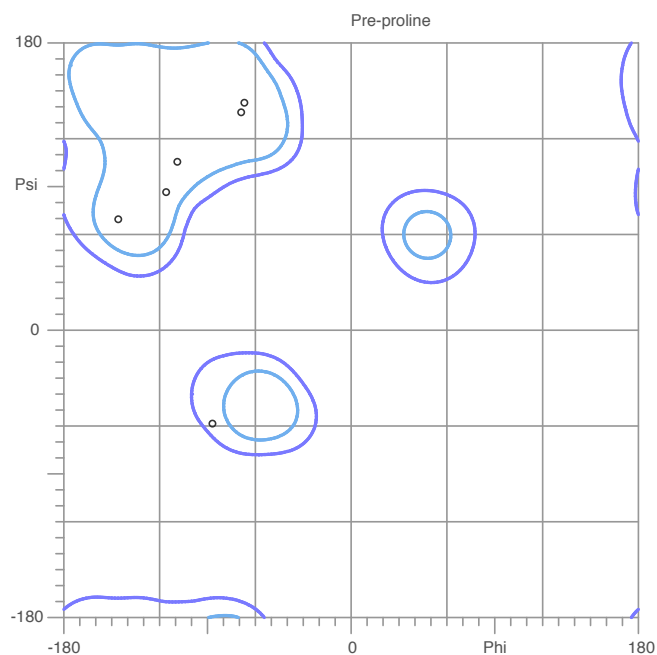
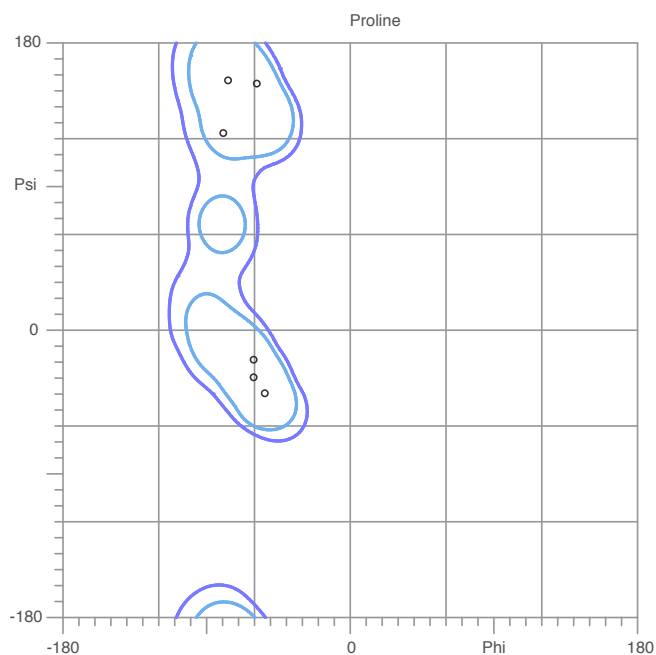
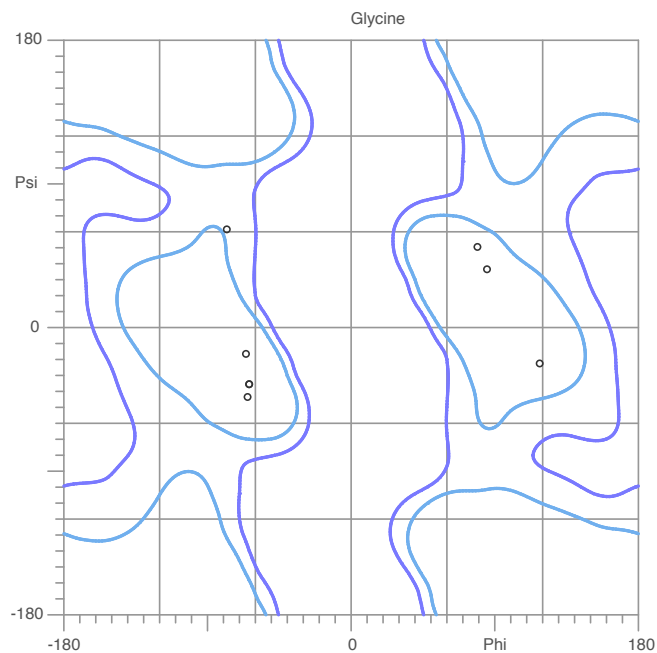
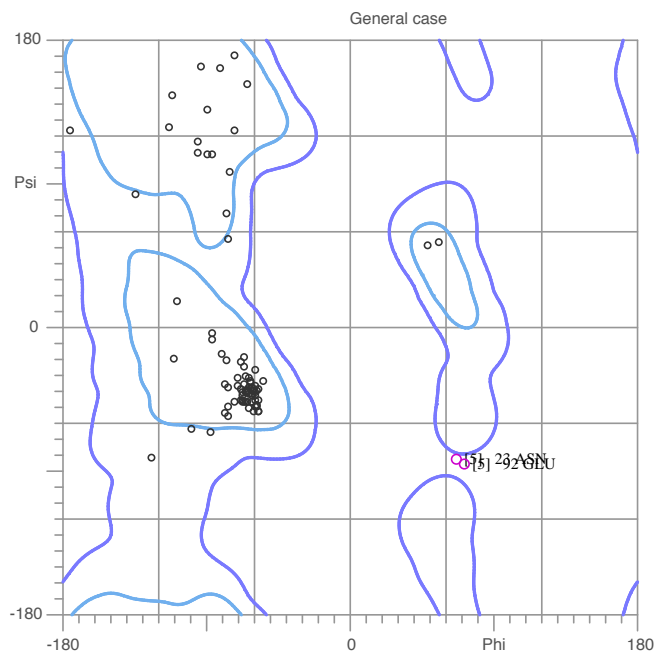


92.5% (99/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[4] 6 LYS (61.4, -82.2)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 5



90.7% (97/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

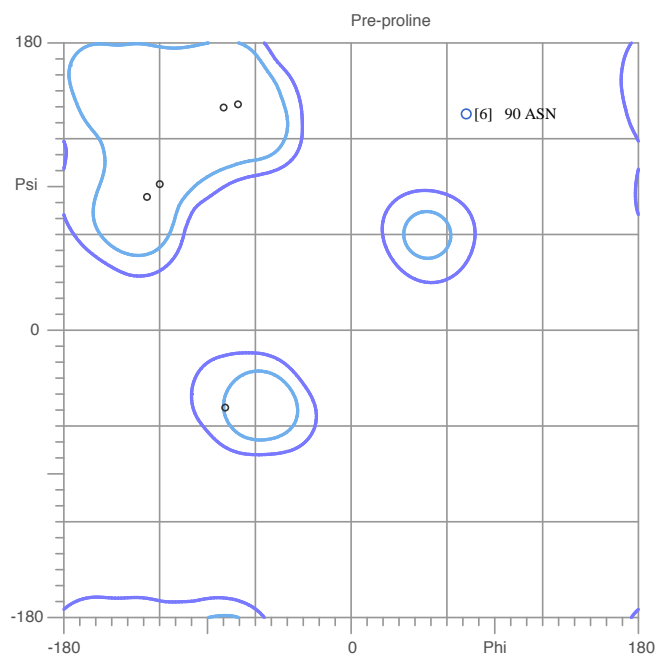
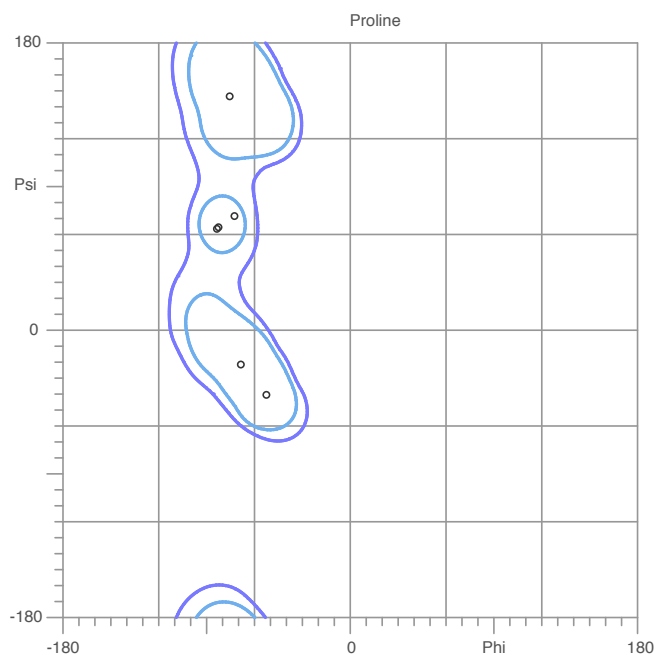
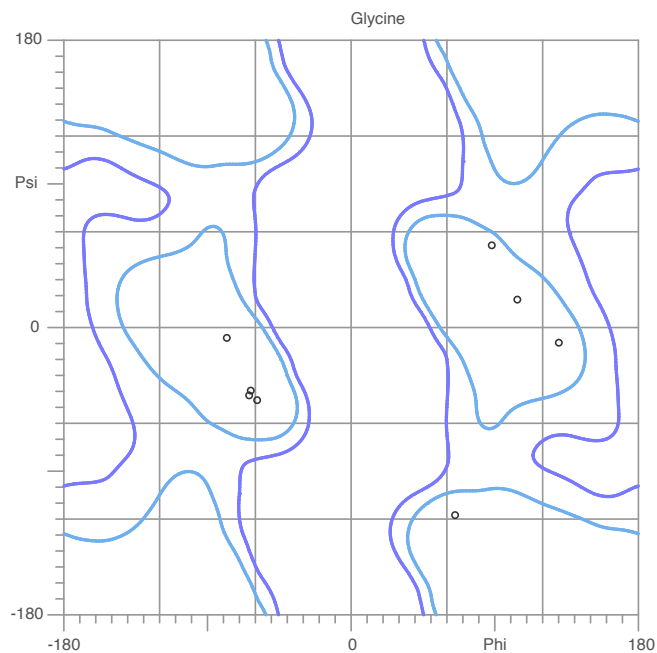
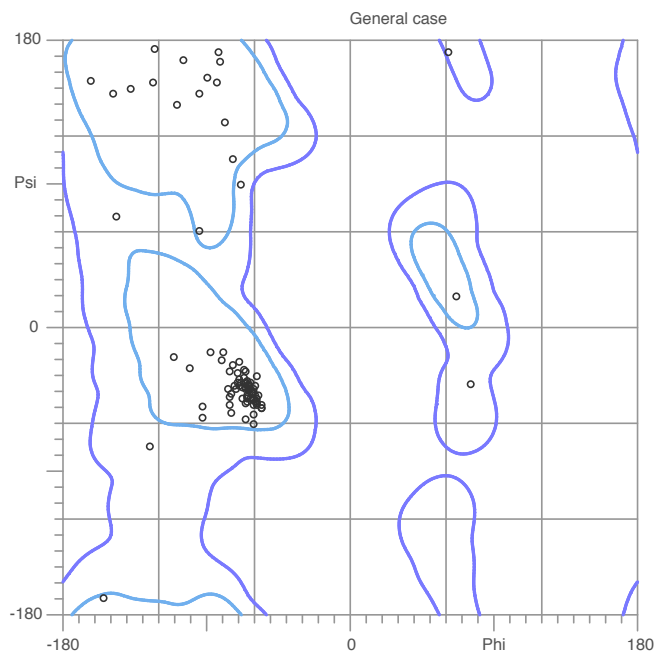
There were 2 outliers (phi, psi):

[5] 23 ASN (66.1, -82.4)

[5] 92 GLU (71.0, -85.5)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 6



94.4% (101/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

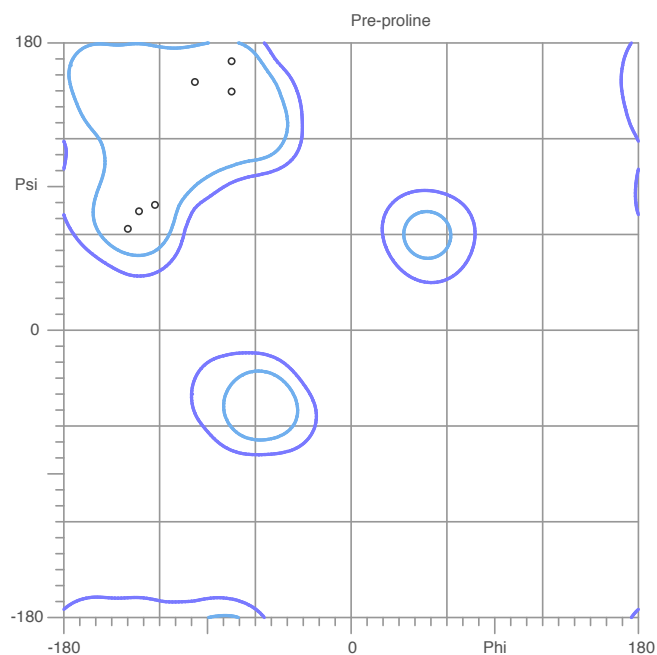
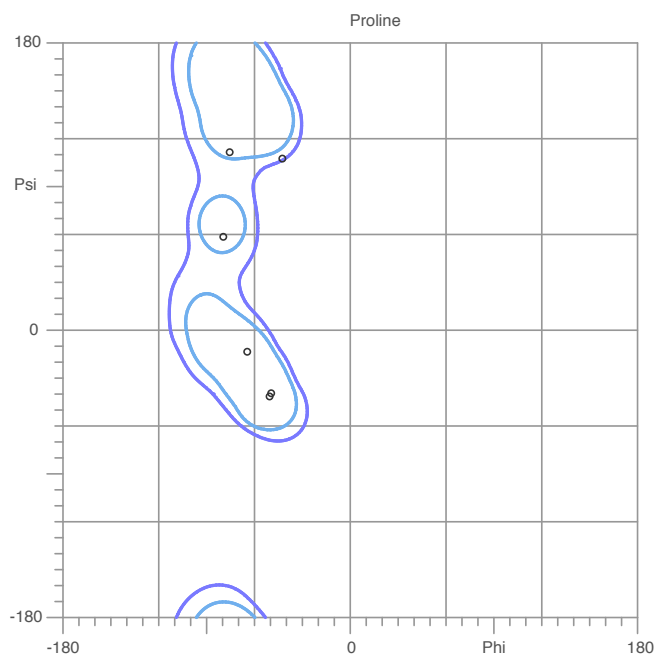
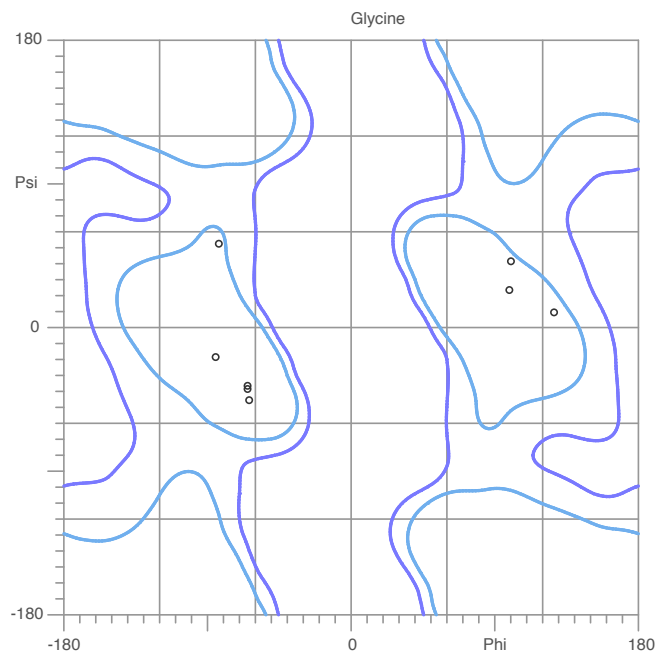
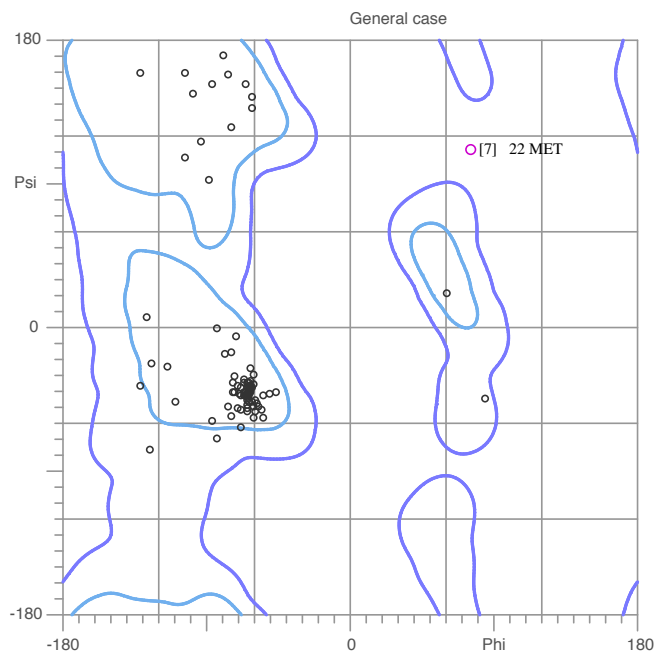
There were 1 outliers (phi, psi):
[6] 90 ASN (73.0, 136.2)

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MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 7



93.5% (100/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

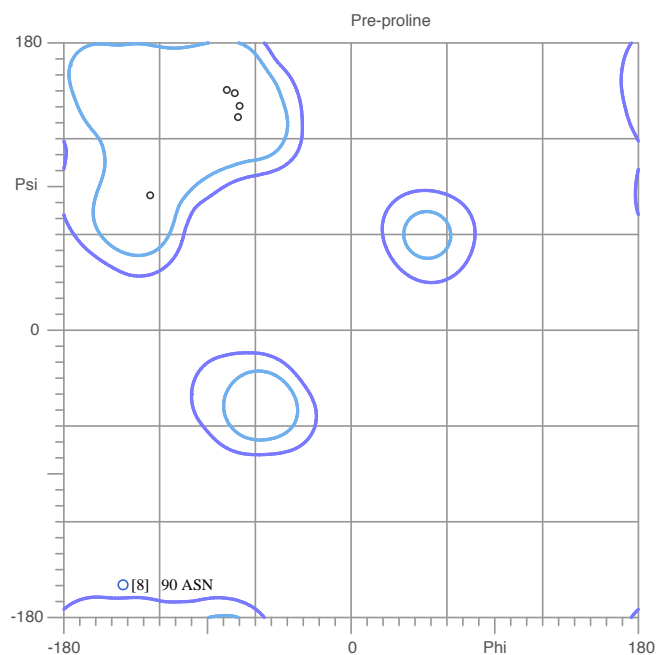
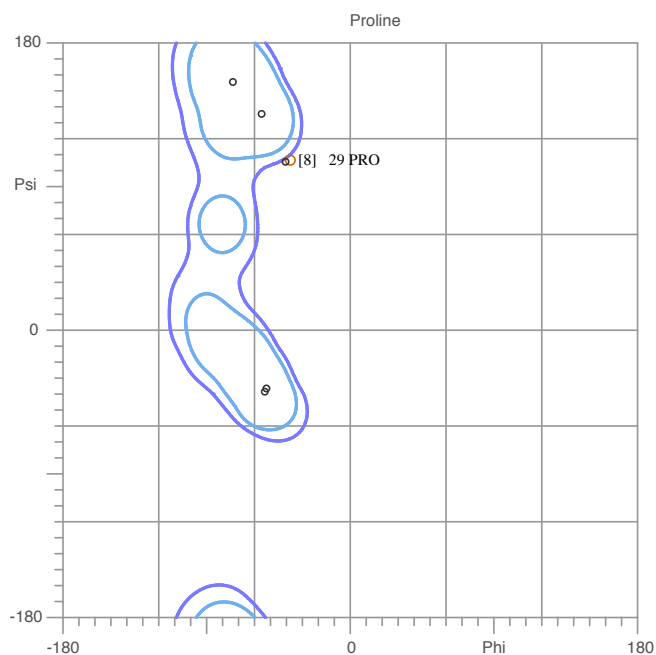
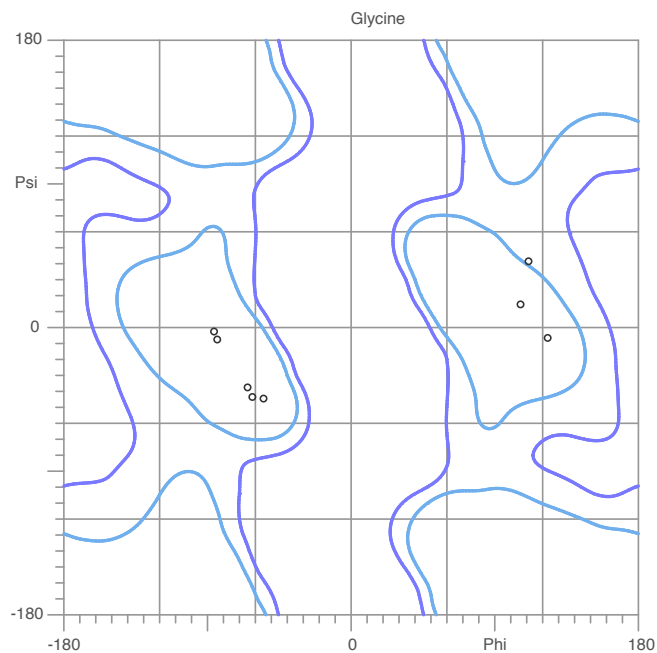
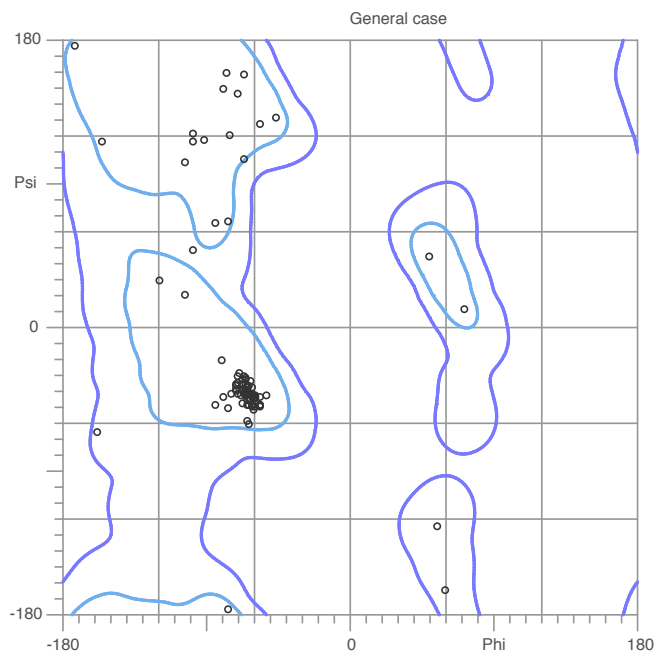
There were 1 outliers (phi, psi):
[7] 22 MET (75.0, 112.6)

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

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 8

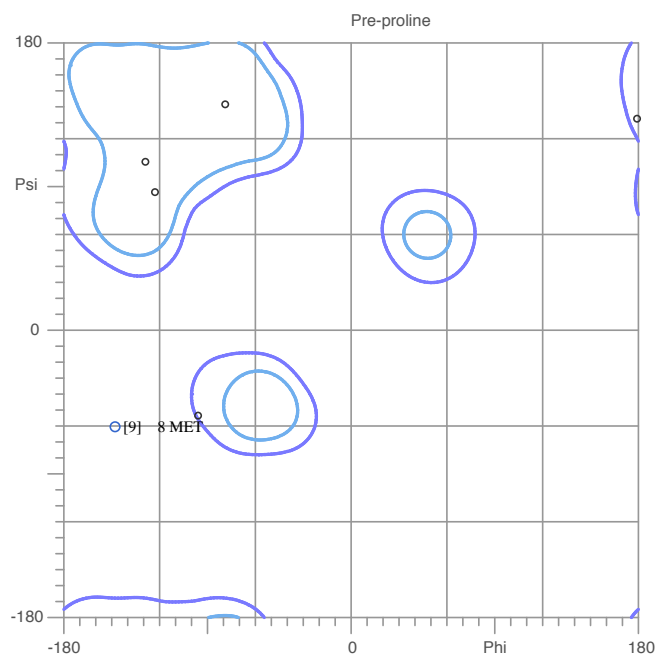
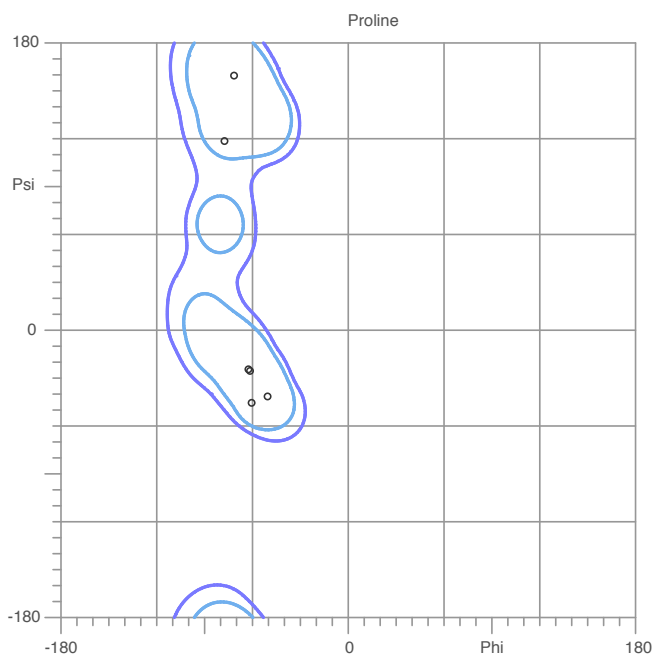
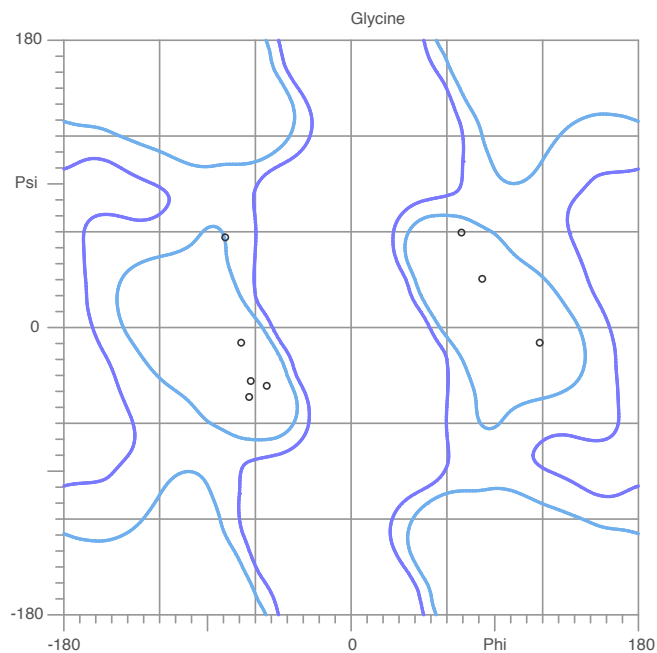
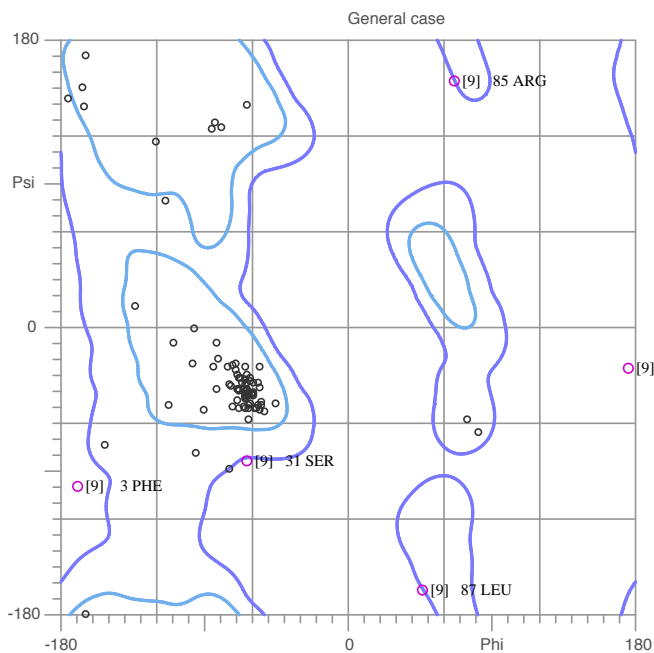


92.5% (99/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[8] 29 PRO (-38.3, 107.0)
[8] 90 ASN (-143.7, -159.8)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 9



85.0% (91/107) of all residues were in favored (98%) regions.
94.4% (101/107) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

[9] 3 PHE (-170.6, -99.6)

[9] 8 MET (-148.4, -60.9)

[9] 24 THR (175.0, -25.1)

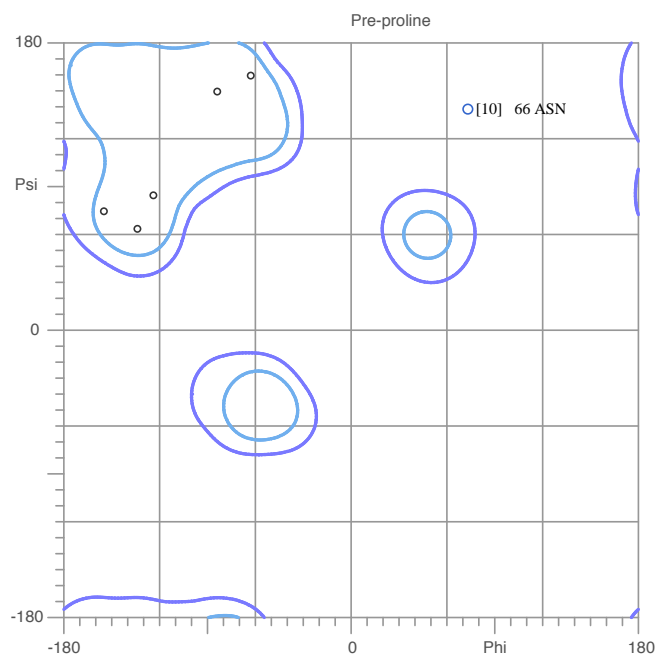
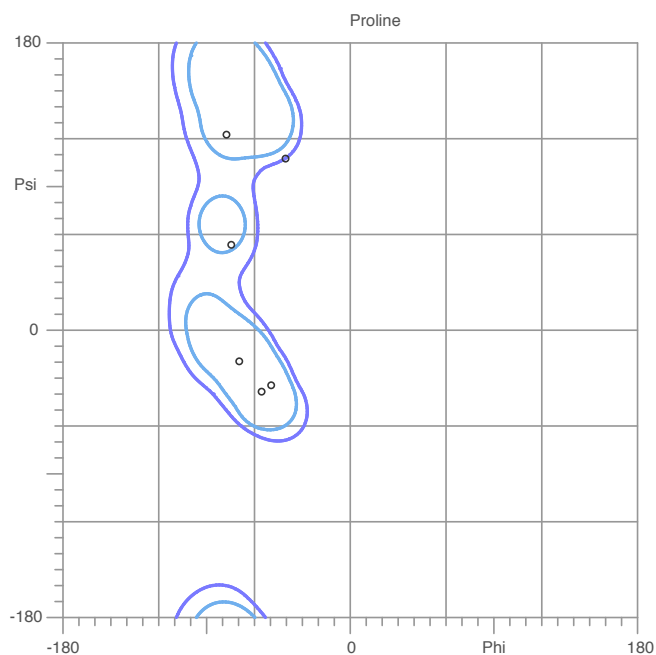
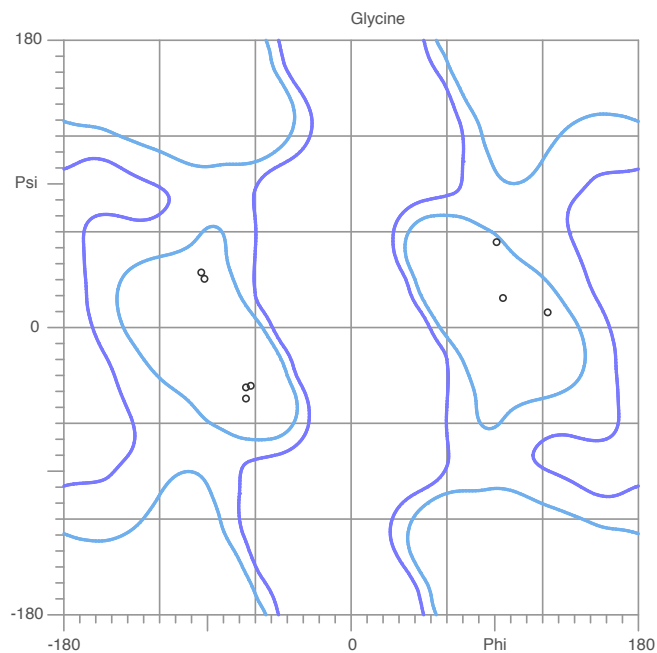
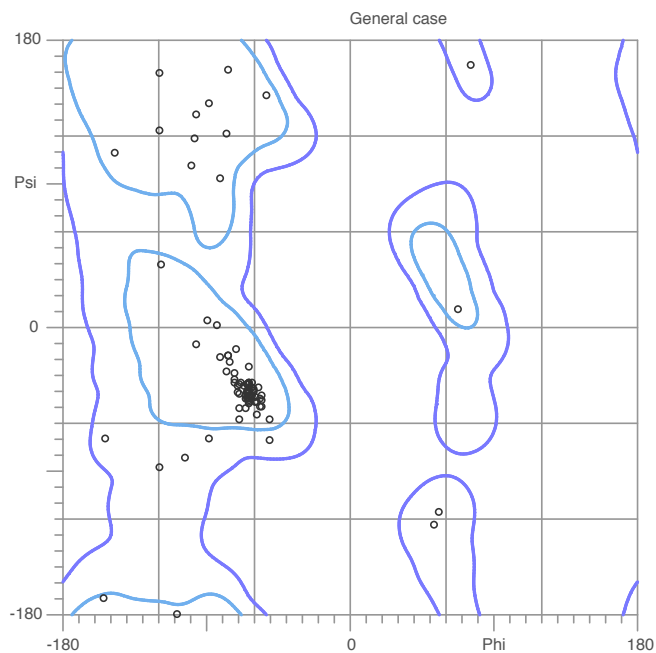
[9] 31 SER (-64.2, -83.1)

[9] 85 ARG (66.0, 155.0)

[9] 87 LEU (46.3, -164.9)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 10

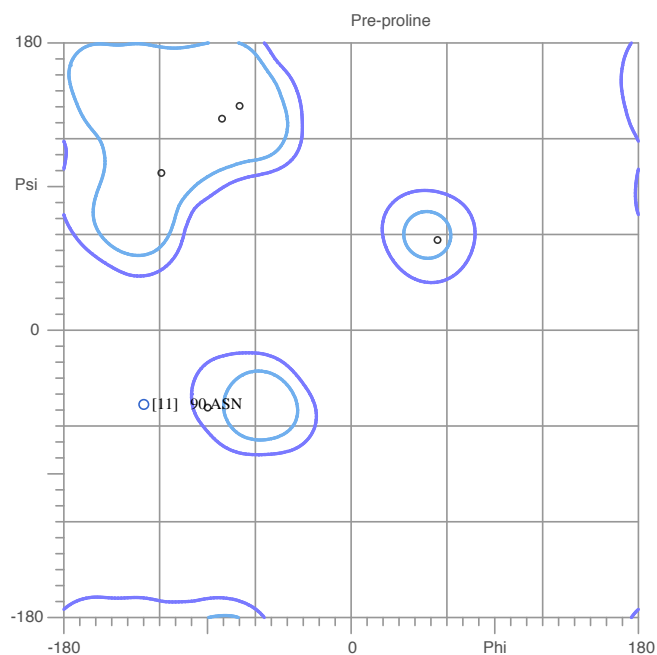
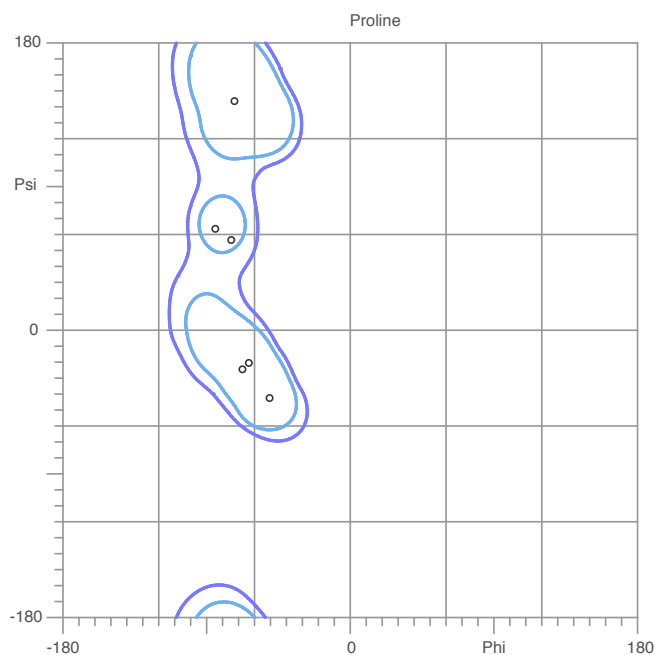
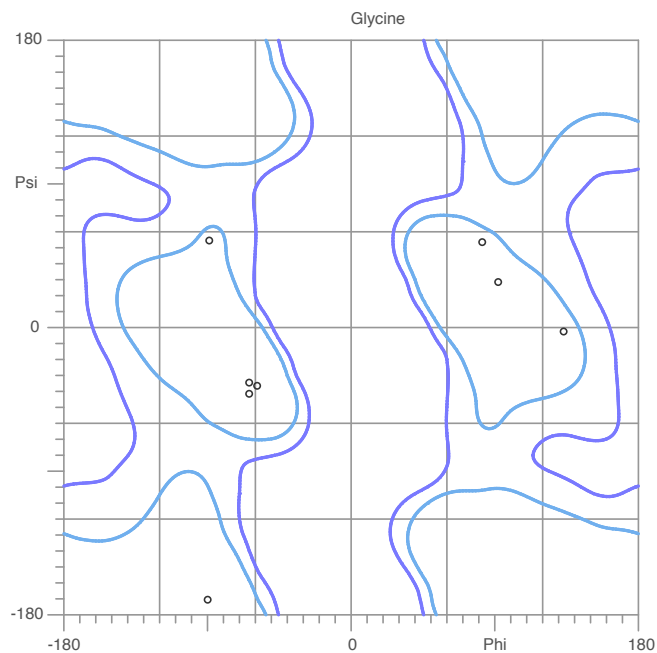
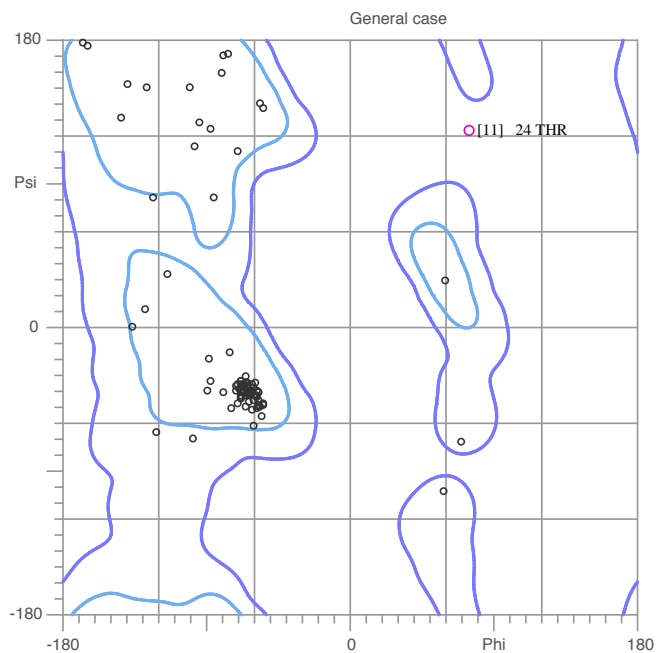


90.7% (97/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):
[10] 66 ASN (73.8, 139.5)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 11

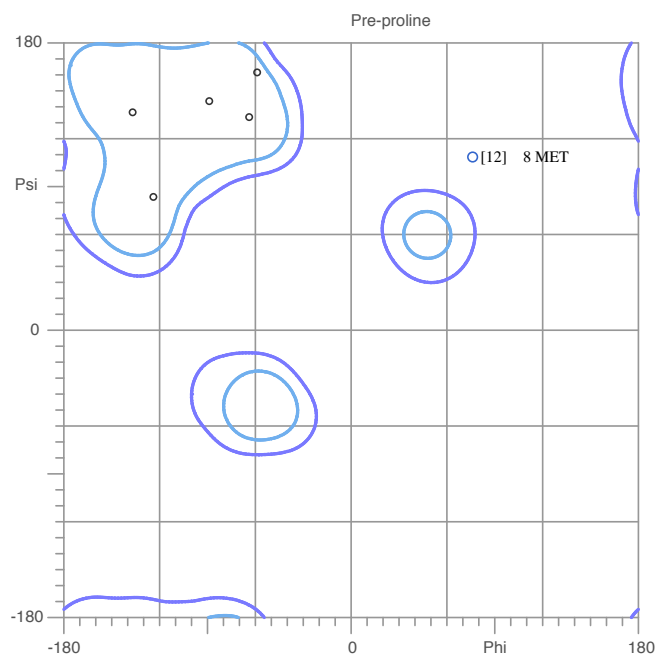
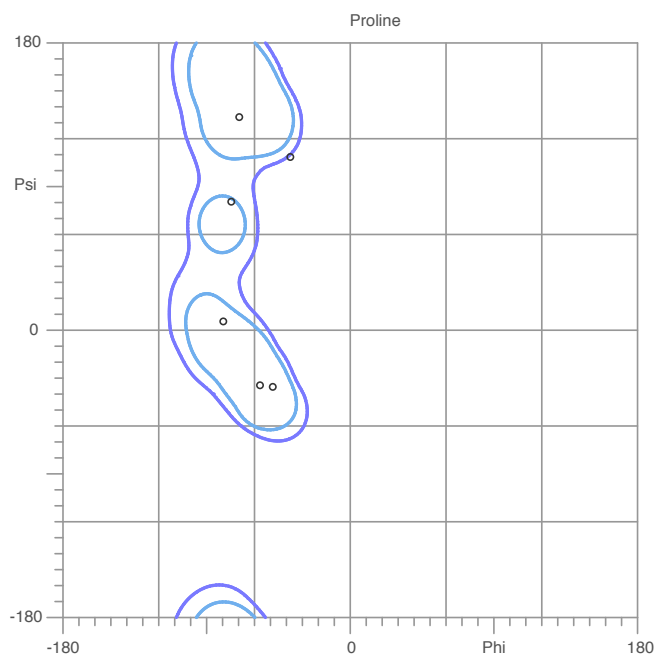
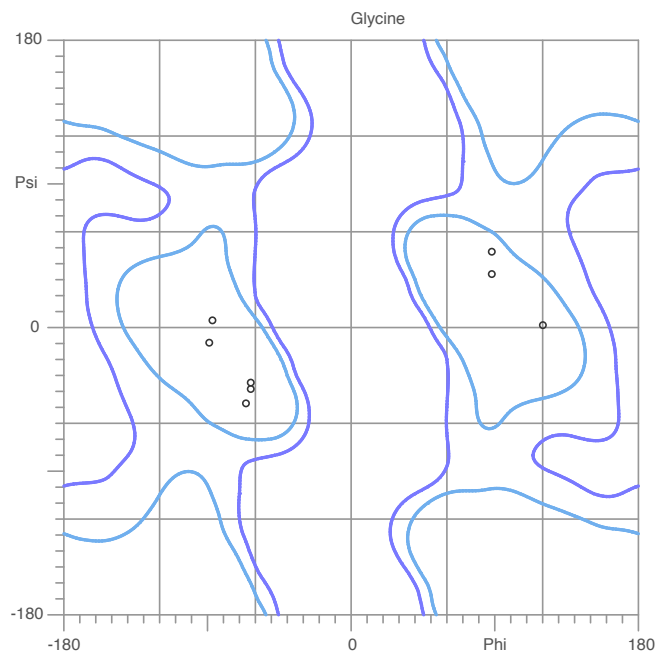
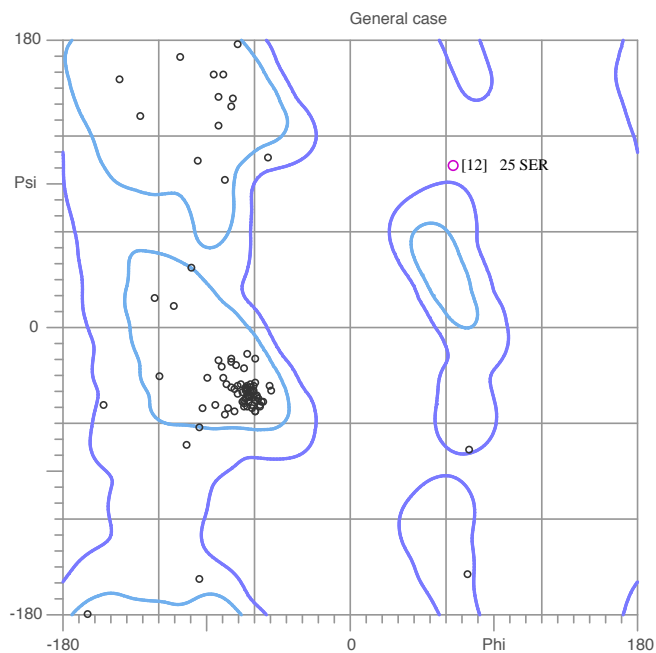


92.5% (99/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[11] 24 THR (75.0, 124.9)
[11] 90 ASN (-130.2, -46.5)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 12

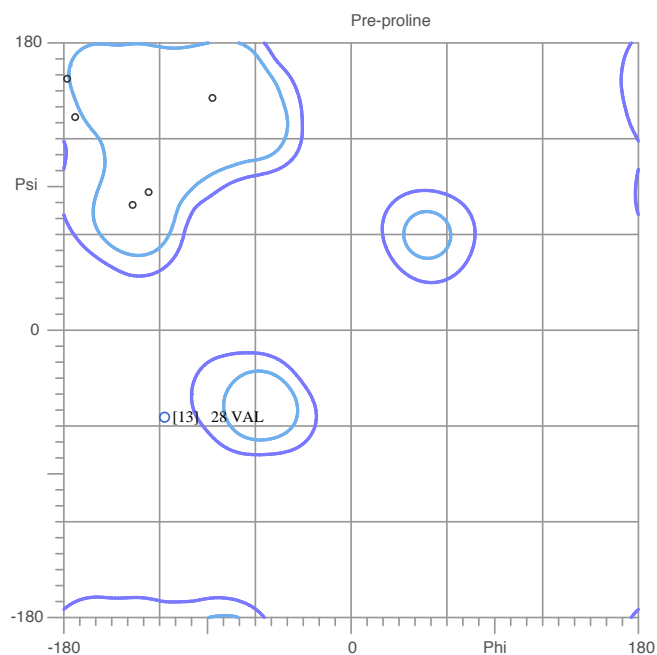
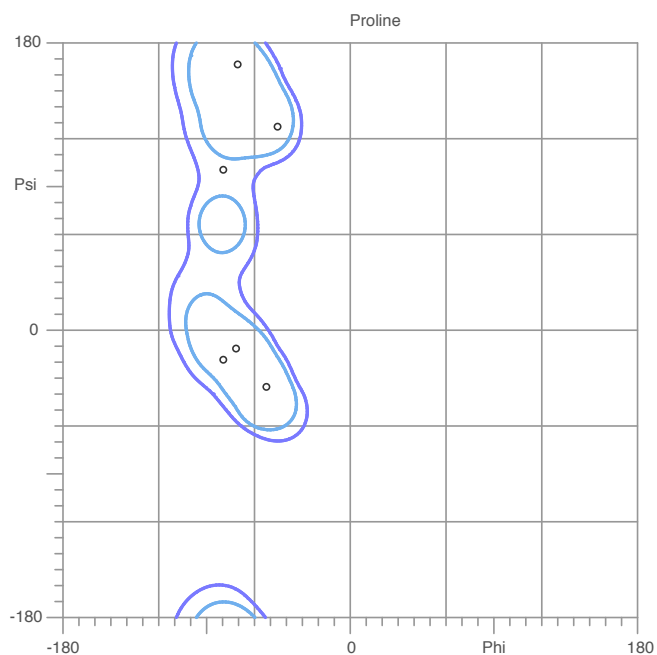
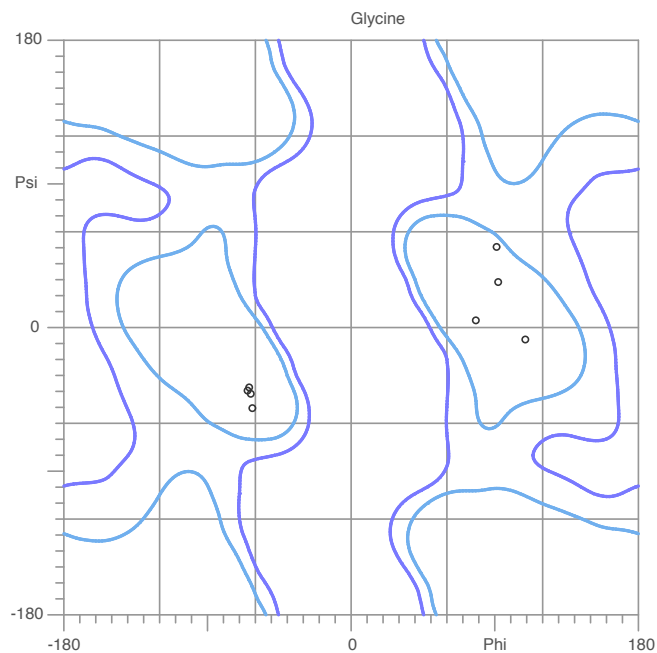
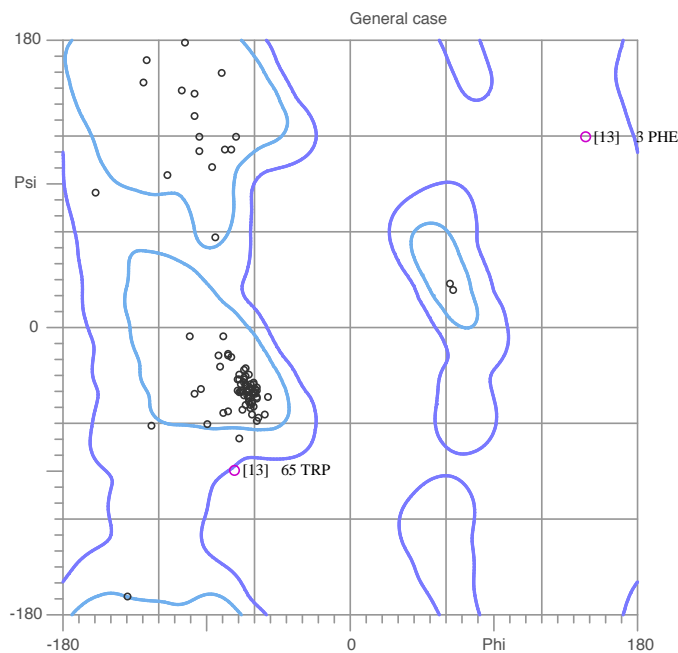


89.7% (96/107) of all residues were in favored (98%) regions.
98.1% (105/107) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):
[12] 8 MET (77.0, 109.4)
[12] 25 SER (64.6, 102.8)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 13



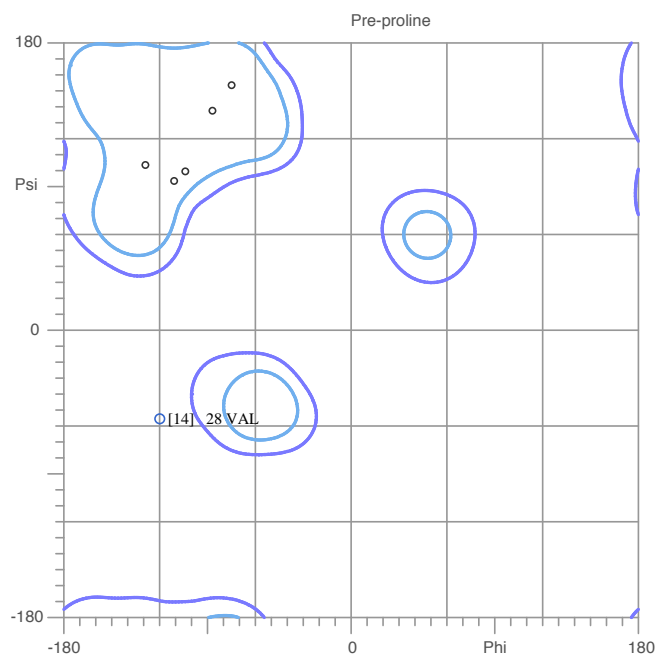
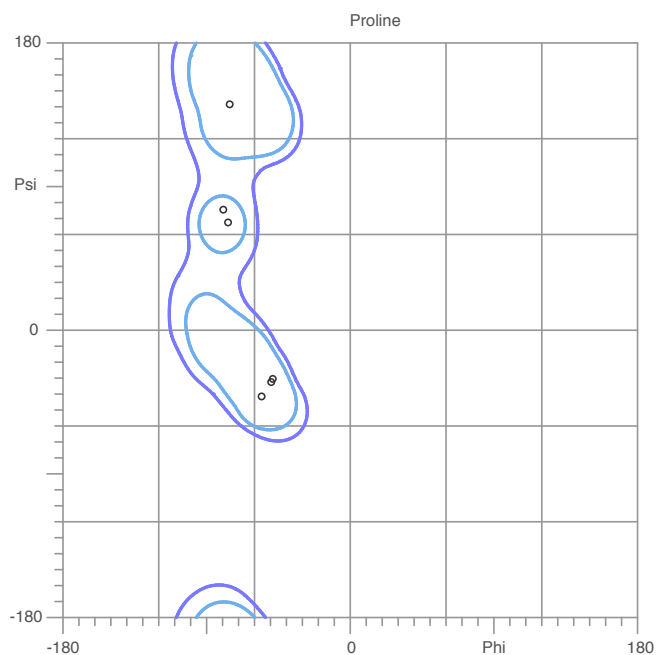
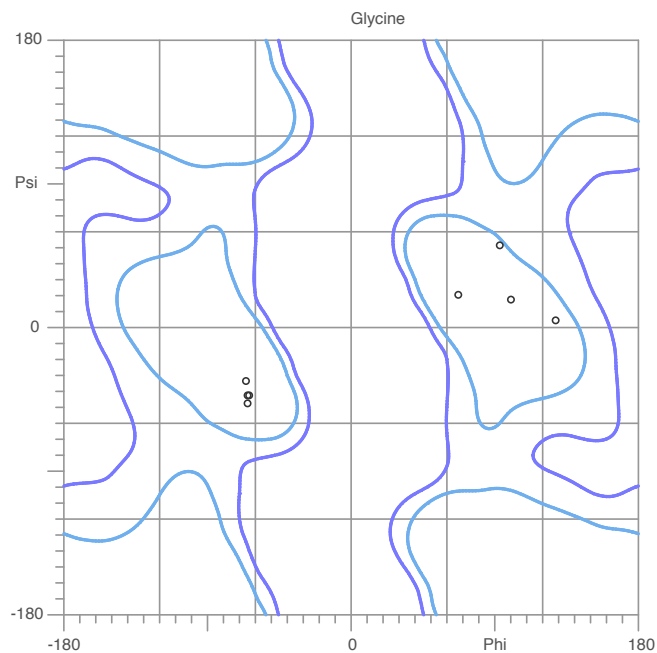
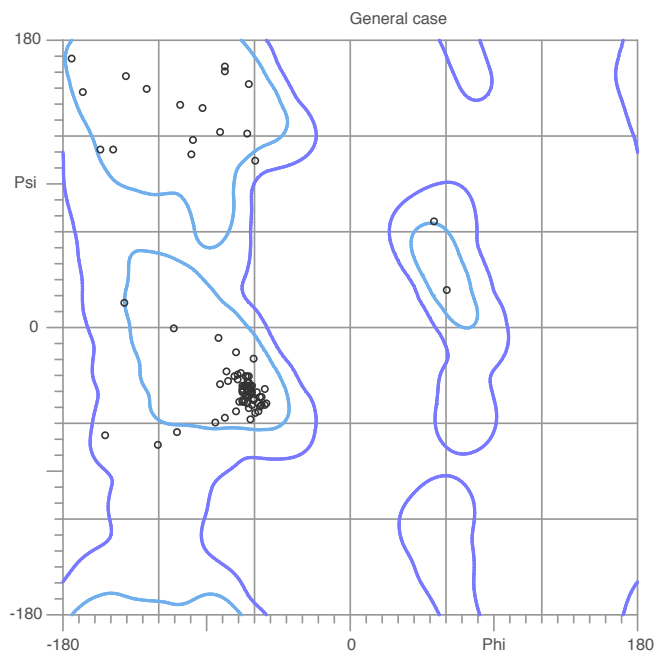
91.6% (98/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [13] 3 PHE (147.4, 121.0)
- [13] 28 VAL (-117.2, -54.8)
- [13] 65 TRP (-73.1, -89.7)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 14



93.5% (100/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

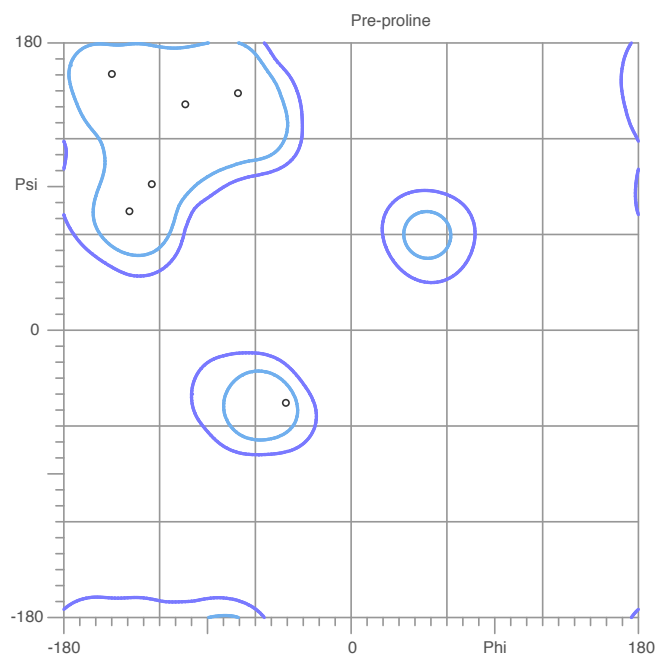
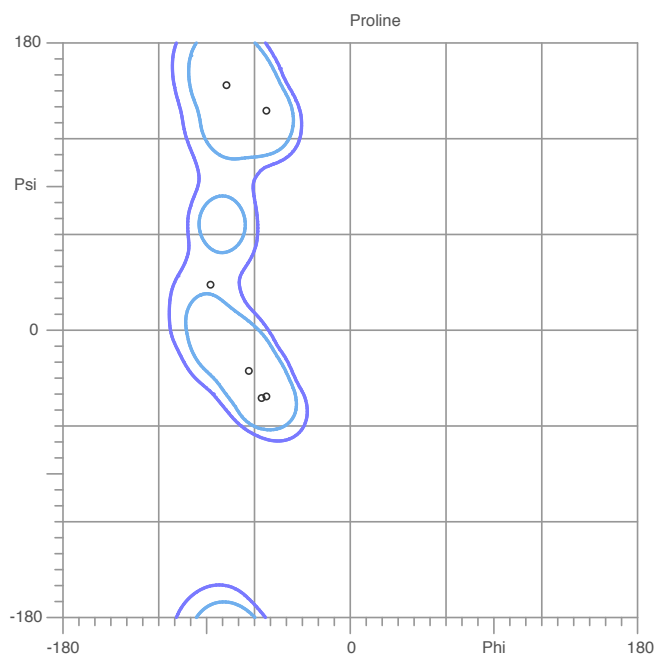
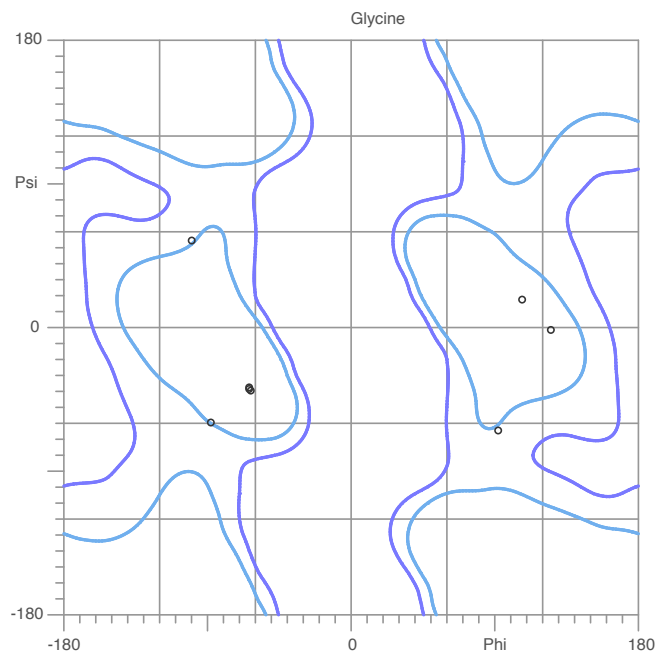
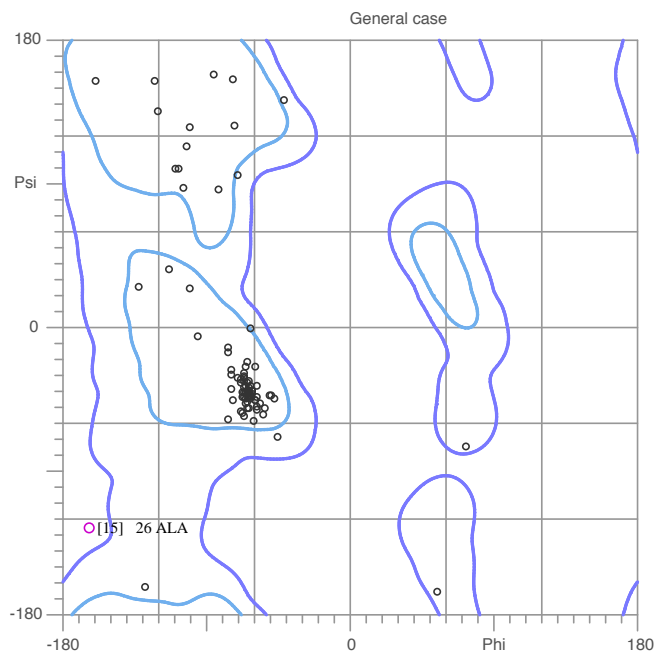
There were 1 outliers (phi, psi):
[14] 28 VAL (-120.1, -55.3)

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MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 15



90.7% (97/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

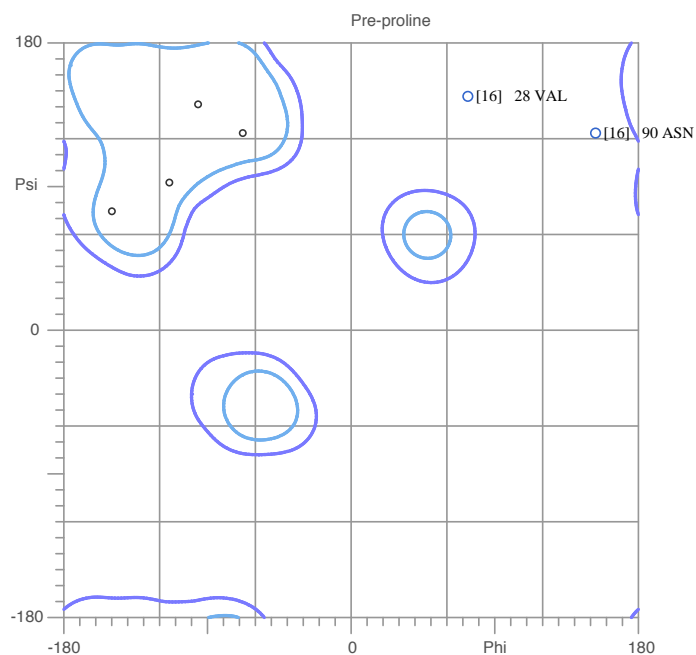
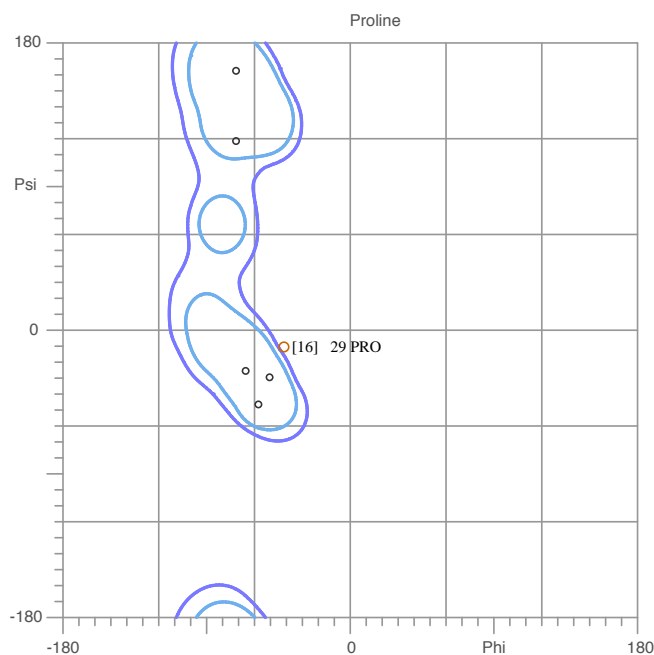
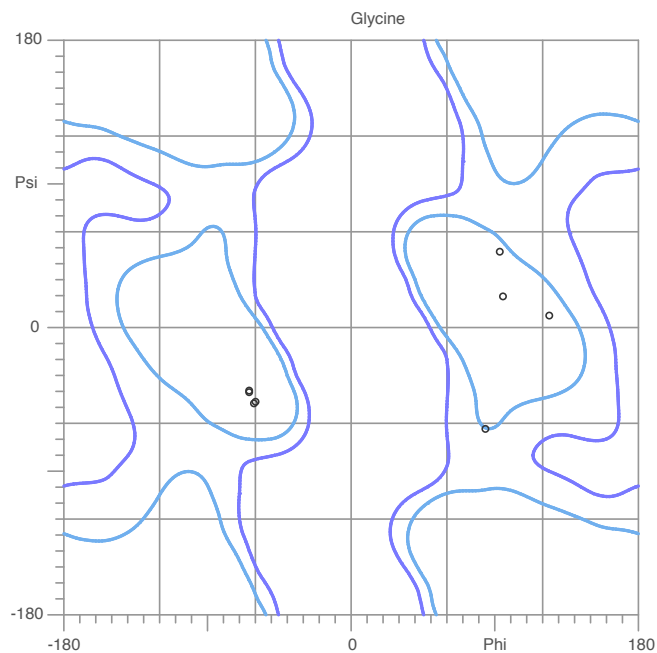
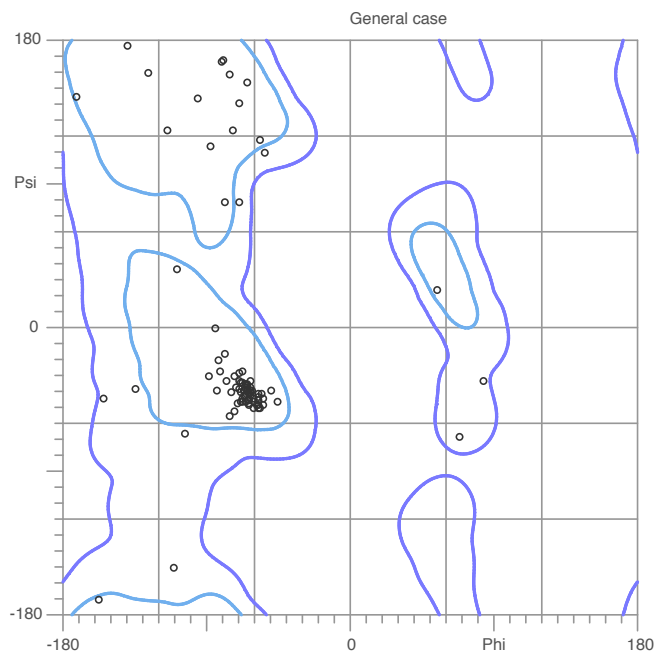
There were 1 outliers (phi, psi):
[15] 26 ALA (-164.6, -125.3)

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MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 16



88.8% (95/107) of all residues were in favored (98%) regions.
97.2% (104/107) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

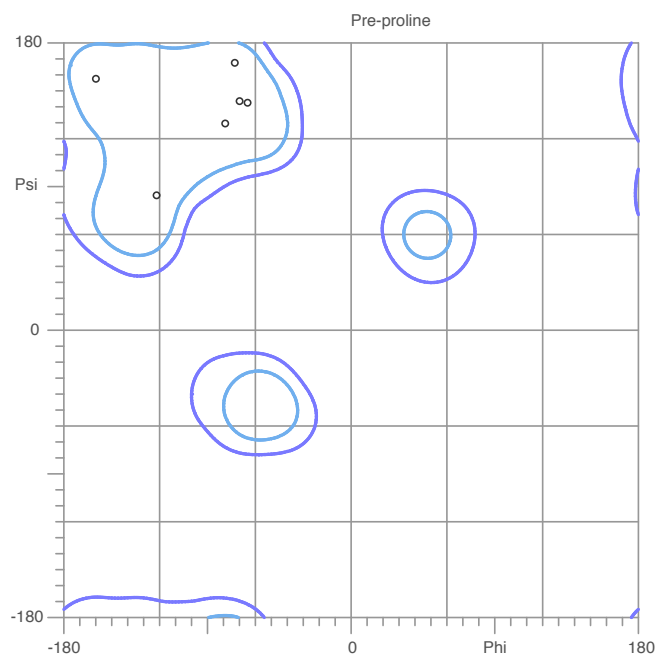
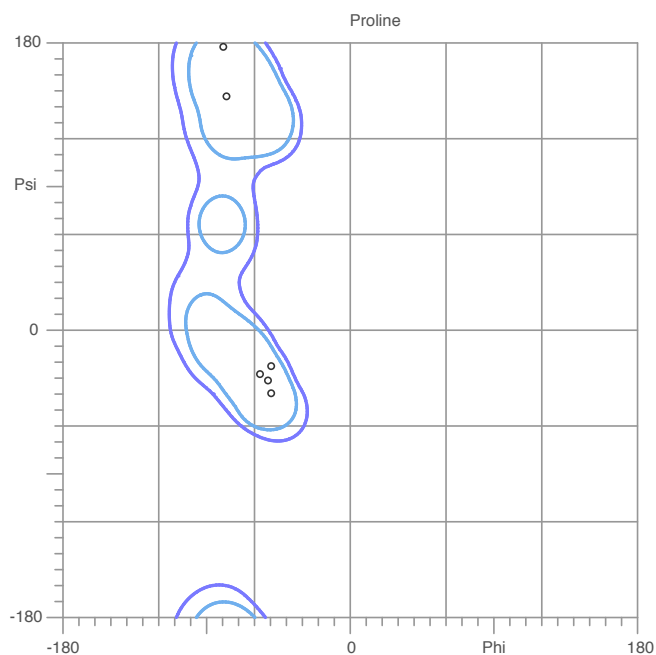
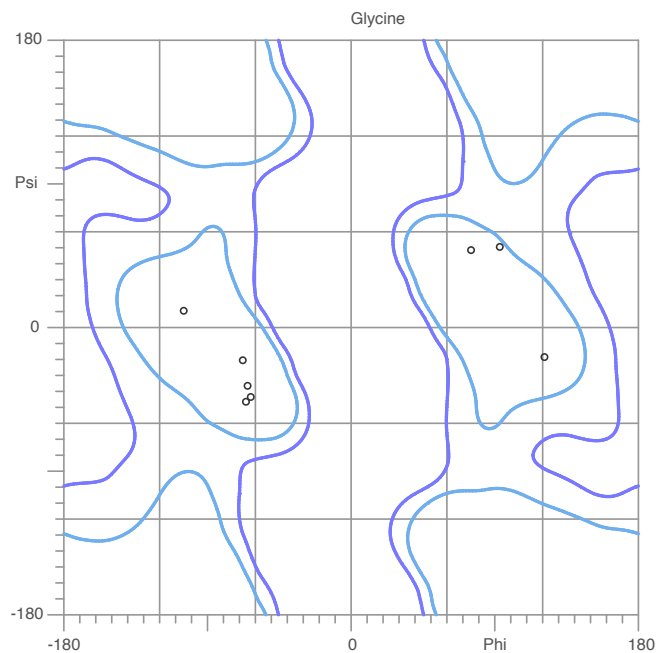
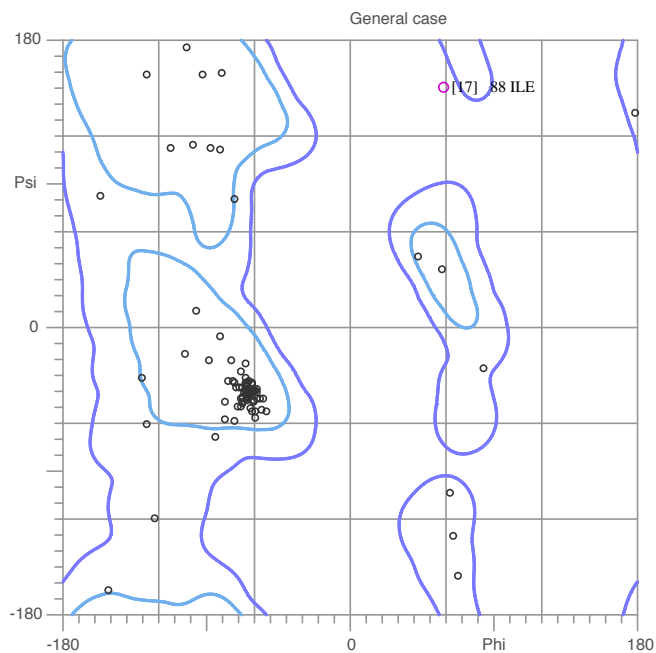
[16] 28 VAL (73.7, 147.5)

[16] 29 PRO (-42.3, -10.0)

[16] 90 ASN (153.1, 124.5)

MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 17



88.8% (95/107) of all residues were in favored (98%) regions.
99.1% (106/107) of all residues were in allowed (>99.8%) regions.

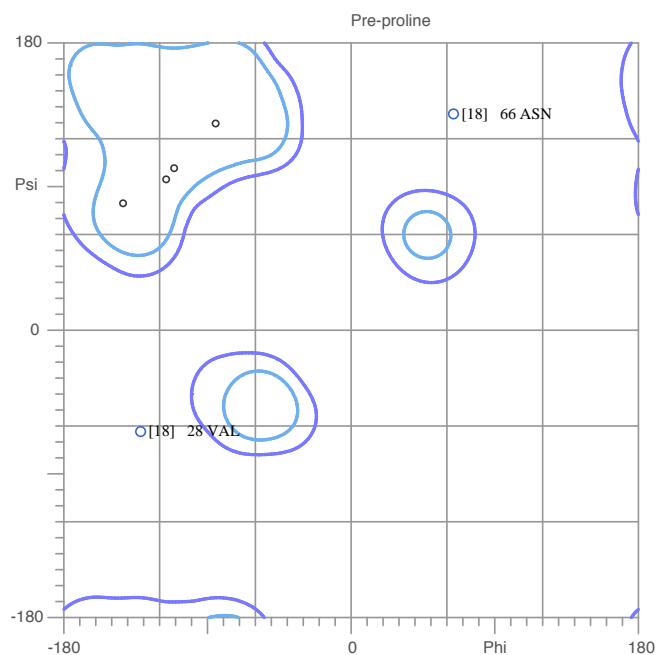
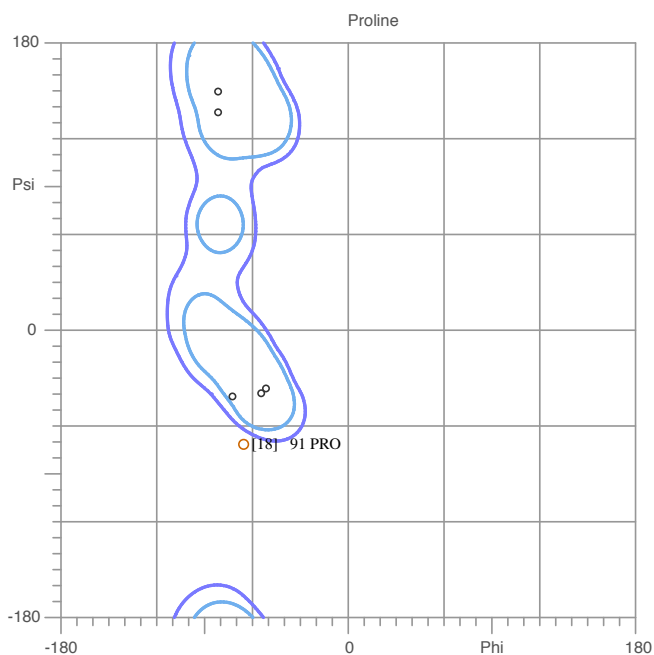
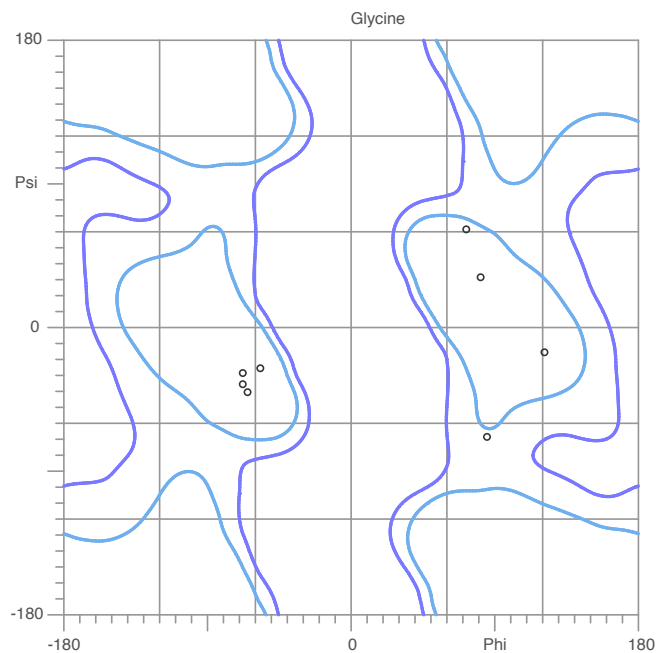
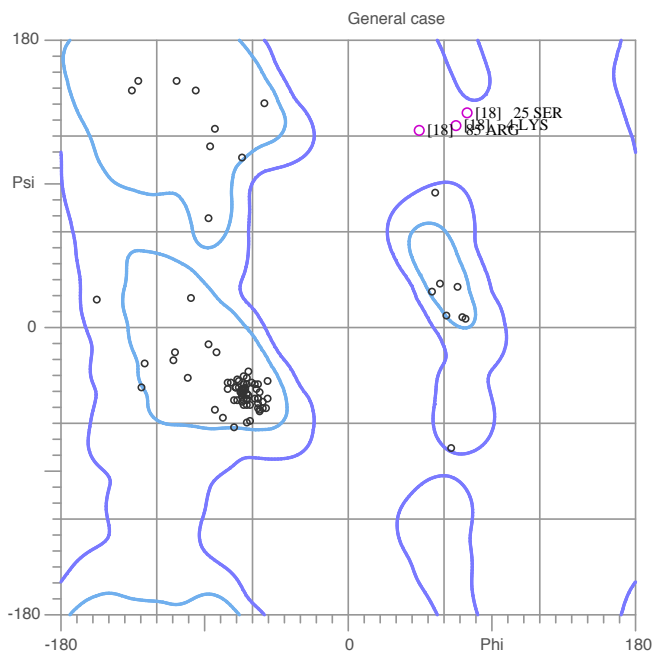
There were 1 outliers (phi, psi):
[17] 88 ILE (58.4, 151.2)

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MolProbity Ramachandran analysis

STR65_R3Cons_em_bcr3.pdb, model 18



89.7% (96/107) of all residues were in favored (98%) regions.
94.4% (101/107) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):
[18] 4 LYS (67.2, 127.9)

[18] 25 SER (74.4, 135.3)
[18] 28 VAL (-132.2, -63.9)
[18] 66 ASN (64.8, 136.1)
[18] 85 ARG (44.1, 124.1)
[18] 91 PRO (-66.9, -71.4)