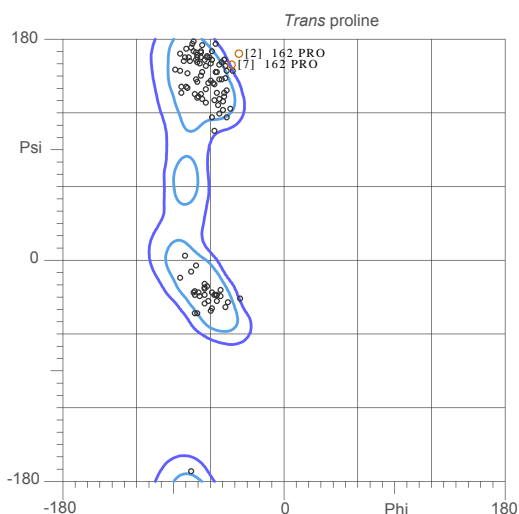
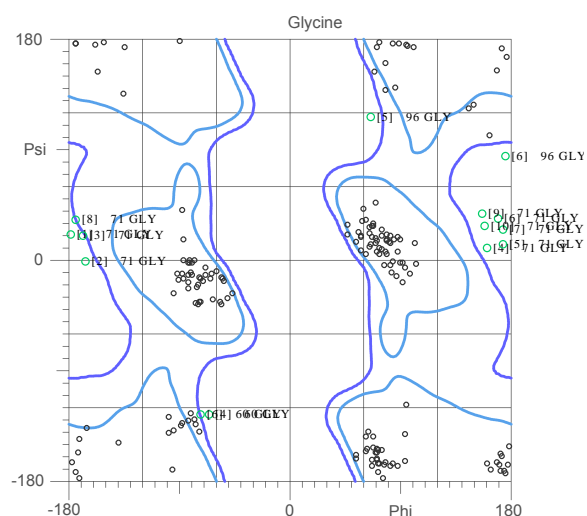
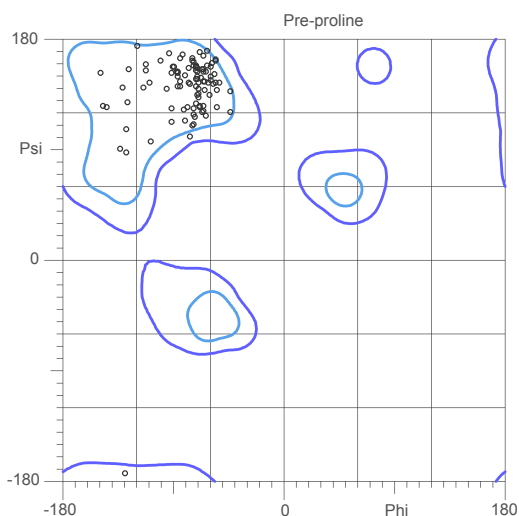
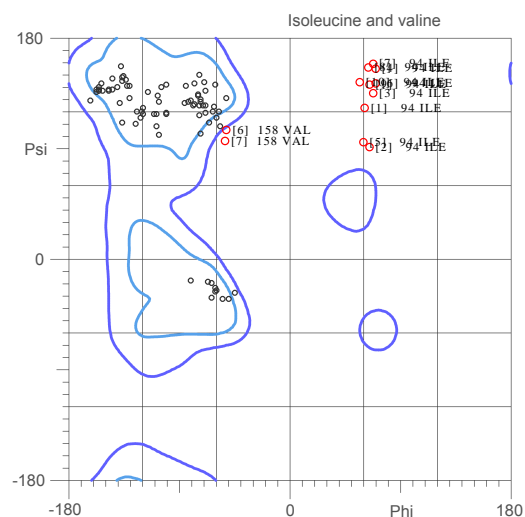
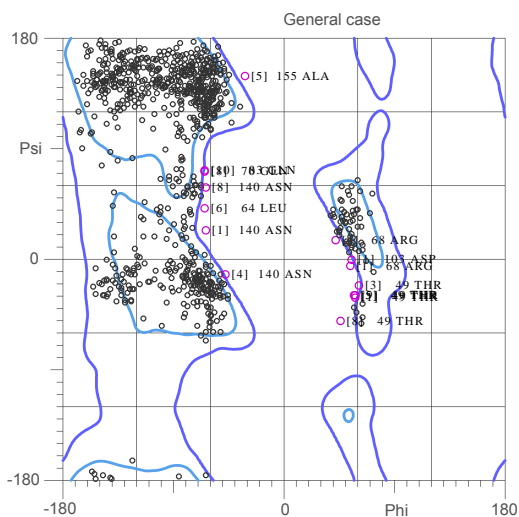


MolProbity Ramachandran analysis

7act.H.pdb, all models



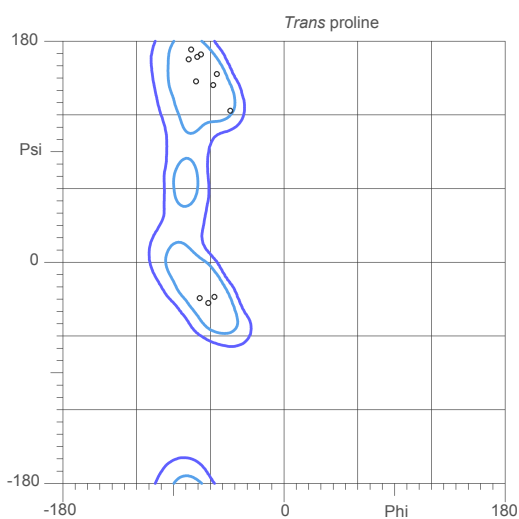
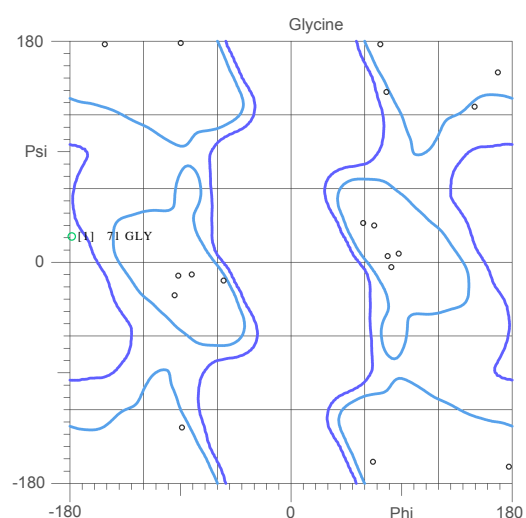
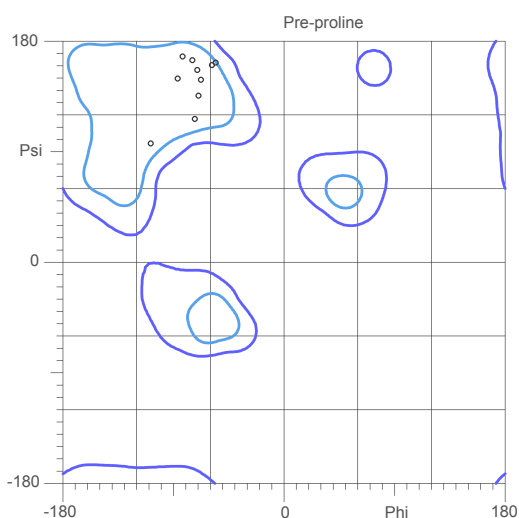
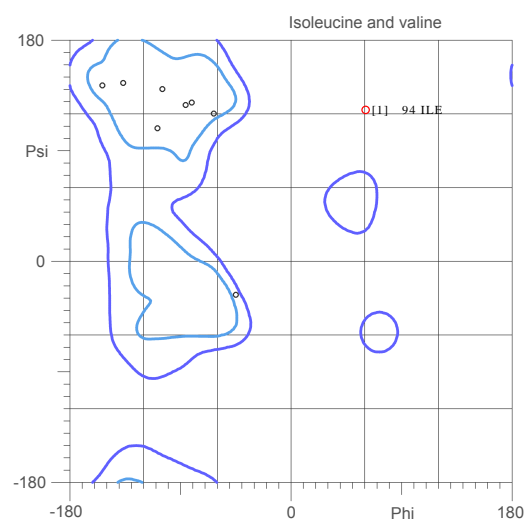
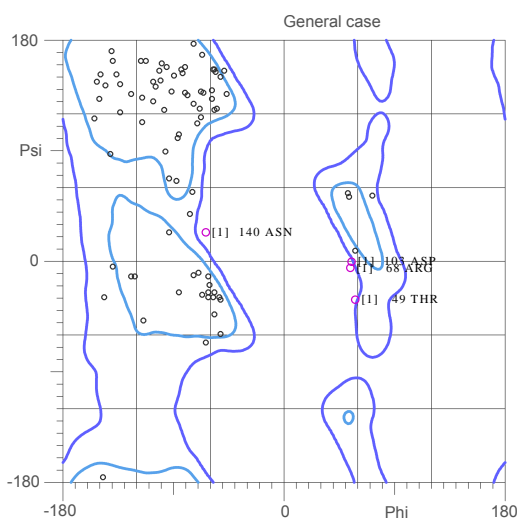
85.5% (1154/1350) of all residues were in favored (98%) regions.
96.8% (1307/1350) of all residues were in allowed (>99.8%) regions.

There were 43 outliers (phi, psi):

[11] 49 THR (58.5, -31.6)	[5] 94 ILE (60.2, 97.0)
[11] 48 ARG (54.6, -6.9)	[5] 96 GLY (66.9, 117.4)
[11] 71 GLY (-179.1, 21.9)	[5] 155 ALA (-52.2, 106.3)
[11] 94 ILE (61.3, 124.9)	[6] 60 GLY (-73.0, -126.9)
[11] 100 ASP (56.8, -0.3)	[6] 64 LEU (-65.7, -42.9)
[11] 140 ASN (64.9, 24.4)	[6] 71 GLY (170.1, 35.0)
[12] 71 GLY (-107.4, -1.3)	[6] 94 ILE (78.5, 140.0)
[12] 94 ILE (68.6, 92.1)	[6] 96 GLY (176.2, 95.7)
[12] 162 PRO (-37.7, 149.6)	[6] 158 VAL (-102.2, 100.4)
[12] 49 THR (61.2, -21.8)	[7] 71 GLY (174.9, 28.7)
[13] 71 GLY (-149.2, 20.1)	[7] 94 ILE (68.1, 100.9)
[13] 94 ILE (68.6, 136.8)	[7] 158 VAL (-51.5, 97.4)
[14] 60 GLY (-68.6, -126.8)	[7] 162 PRO (-42.1, 160.4)
[14] 48 ARG (52.7, 16.9)	[8] 49 THR (66.2, -30.2)
[14] 71 GLY (161.9, 10.8)	[8] 70 GLN (-45.4, 72.4)
[14] 94 ILE (70.8, 166.1)	[8] 71 GLY (-175.2, 34.0)
[15] 140 ASN (-44.6, -22.5)	[8] 94 ILE (64.4, 157.8)
[15] 49 THR (57.2, -29.8)	[8] 140 ASN (-64.5, 59.4)
[15] 71 GLY (173.6, 13.7)	[9] 49 THR (58.5, -29.3)
	[9] 71 GLY (157.1, 38.2)
	[9] 94 ILE (65.9, 161.7)
	[10] 71 GLY (-139.2, 28.8)
	[10] 85 GLN (-65.0, 75.8)
	[10] 94 ILE (57.0, 145.1)

MolProbity Ramachandran analysis

7act.H.pdb, model 1



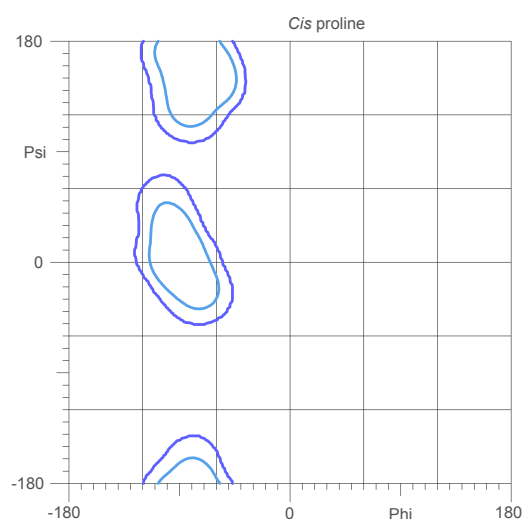
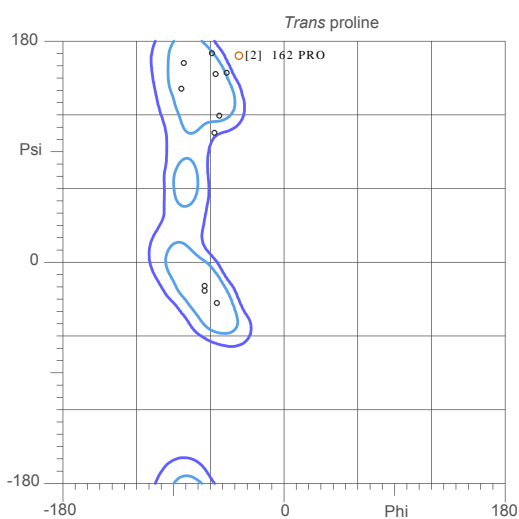
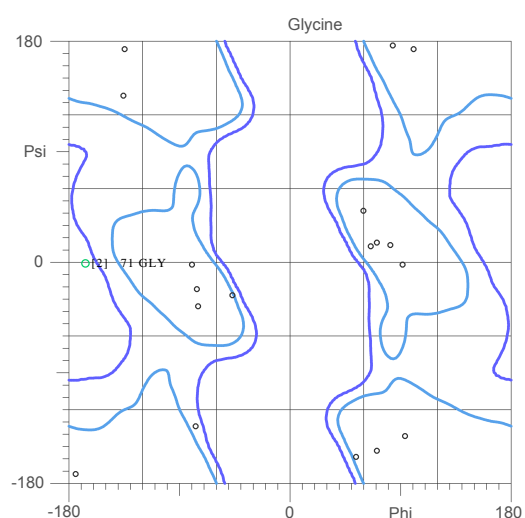
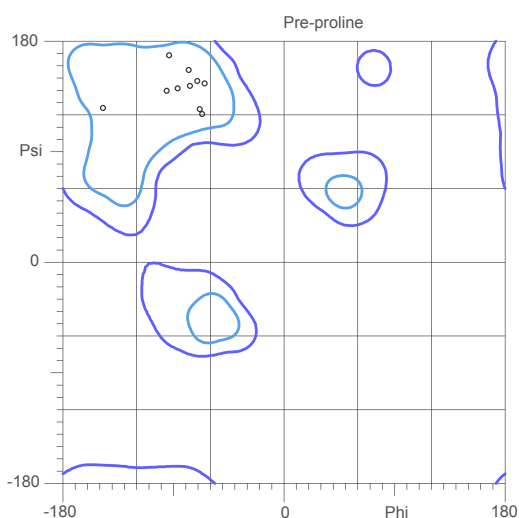
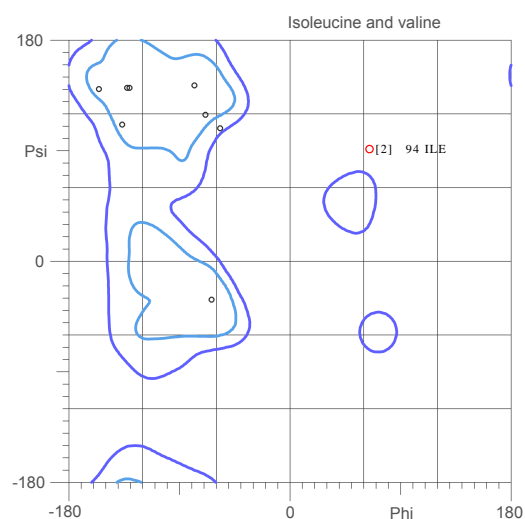
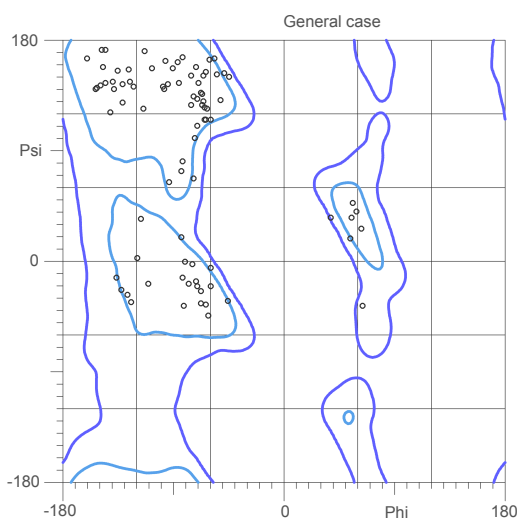
87.4% (118/135) of all residues were in favored (98%) regions.
95.6% (129/135) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

- [1] 49 THR (58.5, -31.6)
- [1] 68 ARG (54.6, -6.0)
- [1] 71 GLY (-179.3, 21.5)
- [1] 94 ILE (61.3, 124.9)
- [1] 103 ASP (56.0, -0.3)
- [1] 140 ASN (-64.5, 24.4)

MolProbity Ramachandran analysis

7act.H.pdb, model 2



87.4% (118/135) of all residues were in favored (98%) regions.
97.8% (132/135) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

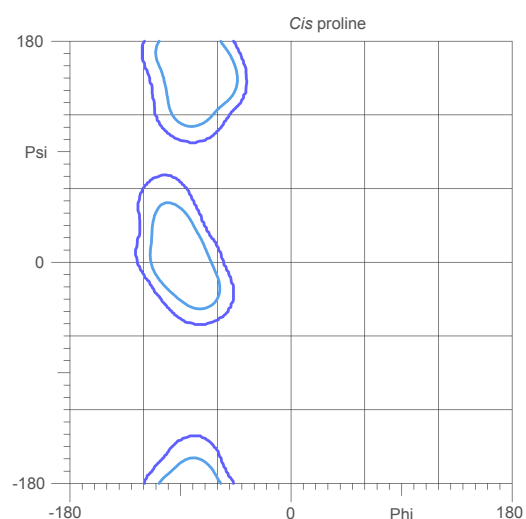
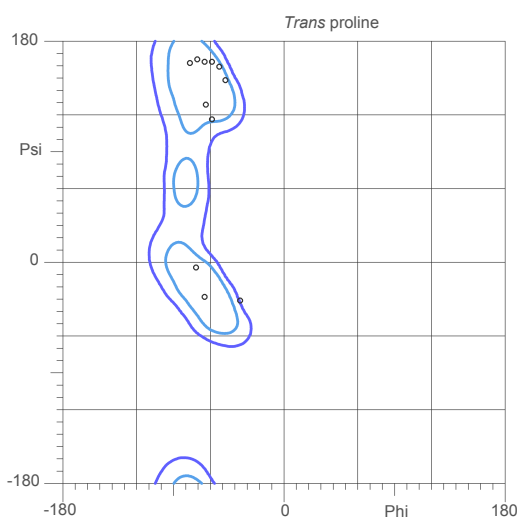
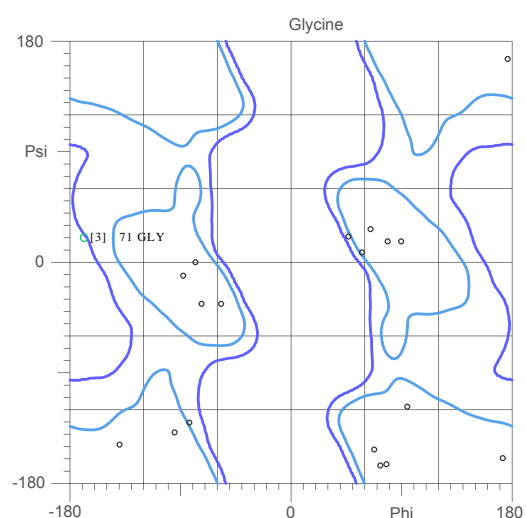
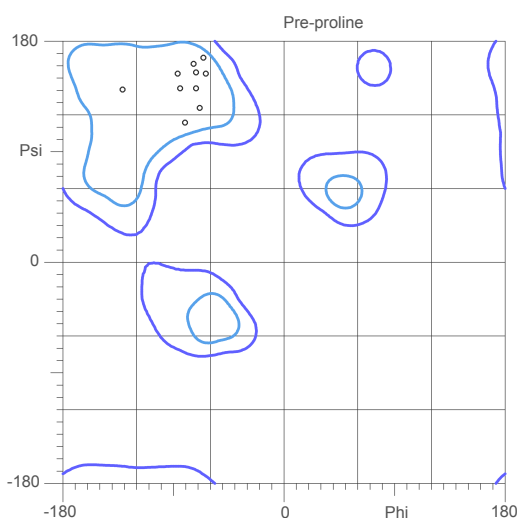
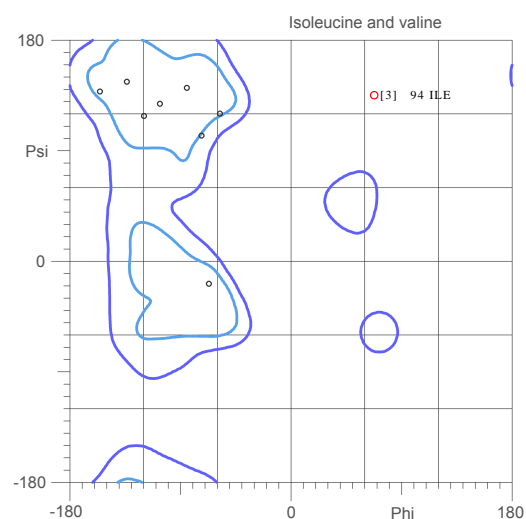
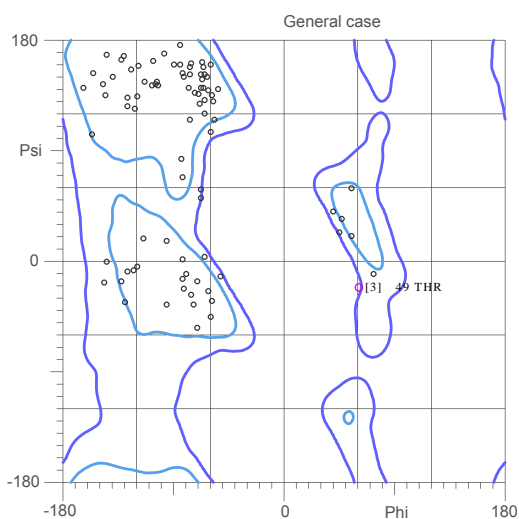
[2] 71 GLY (-167.4, -1.3)

[2] 94 ILE (65.6, 92.1)

[2] 162 PRO (-37.7, 169.6)

MolProbity Ramachandran analysis

7act.H.pdb, model 3



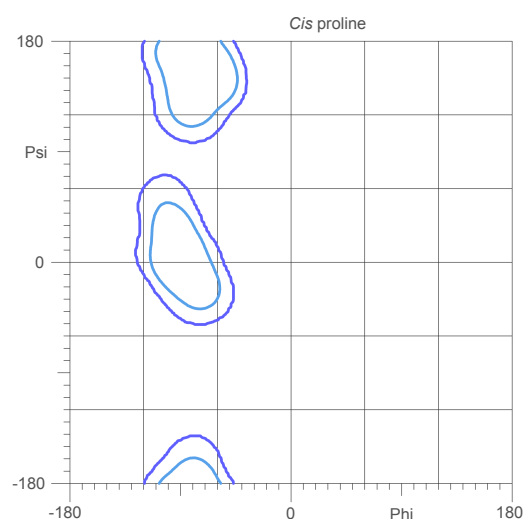
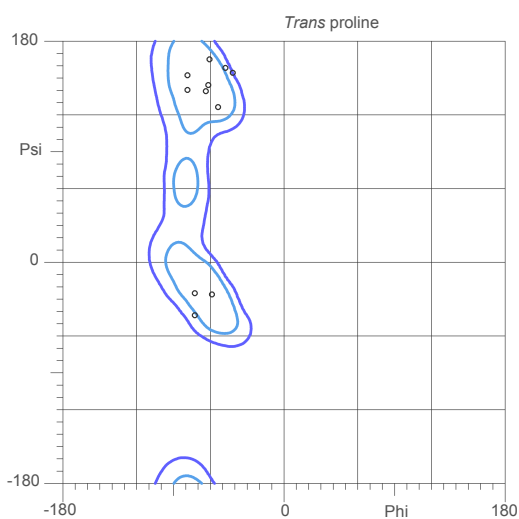
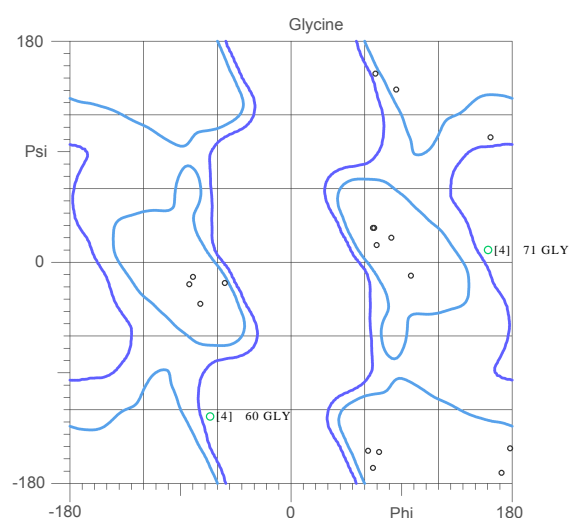
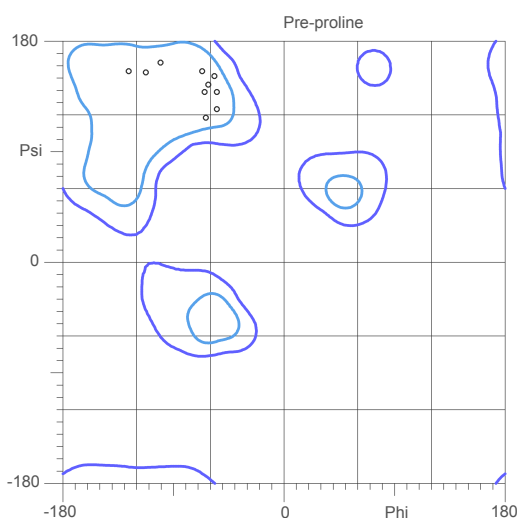
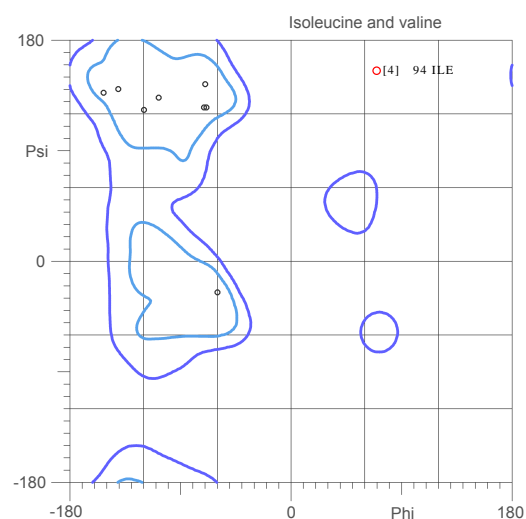
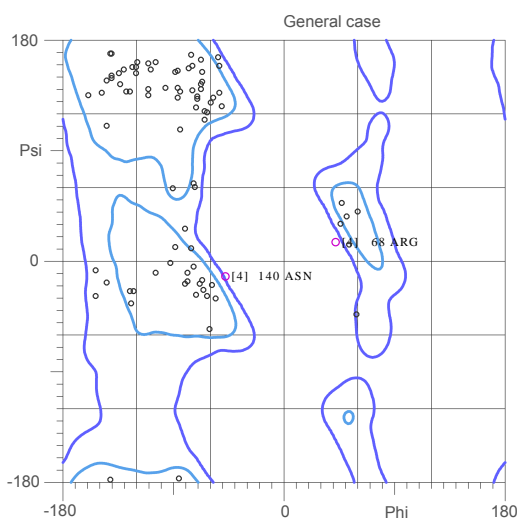
87.4% (118/135) of all residues were in favored (98%) regions.
97.8% (132/135) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [3] 49 THR (61.3, -21.8)
- [3] 71 GLY (-169.2, 20.1)
- [3] 94 ILE (68.4, 136.8)

MolProbity Ramachandran analysis

7act.H.pdb, model 4



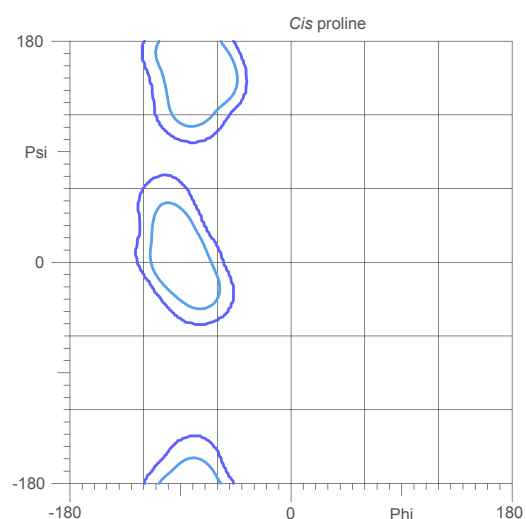
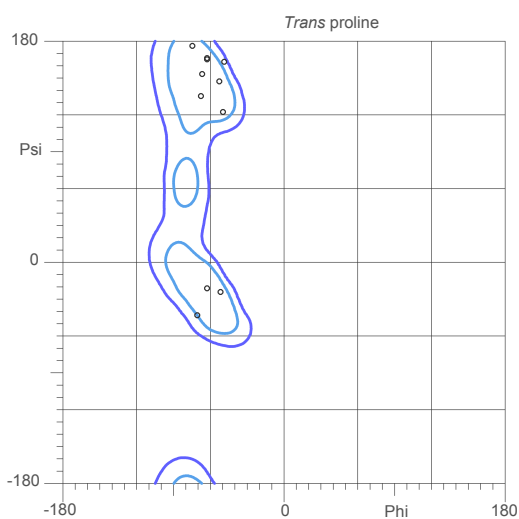
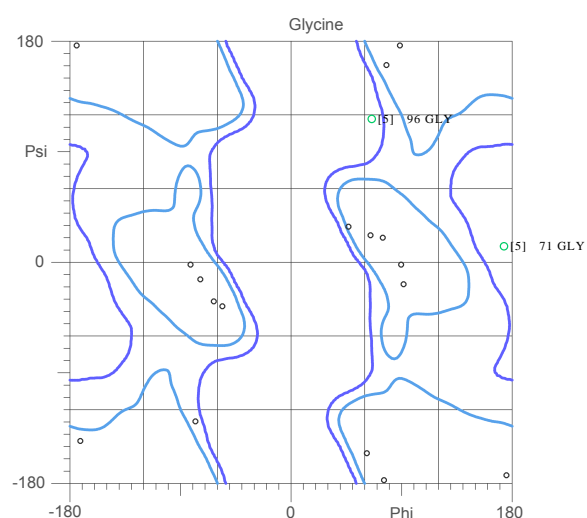
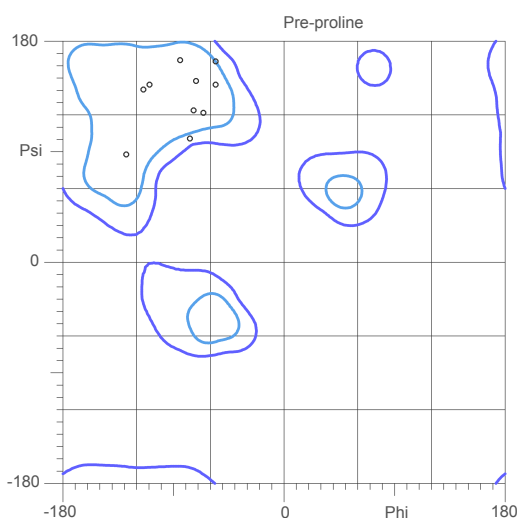
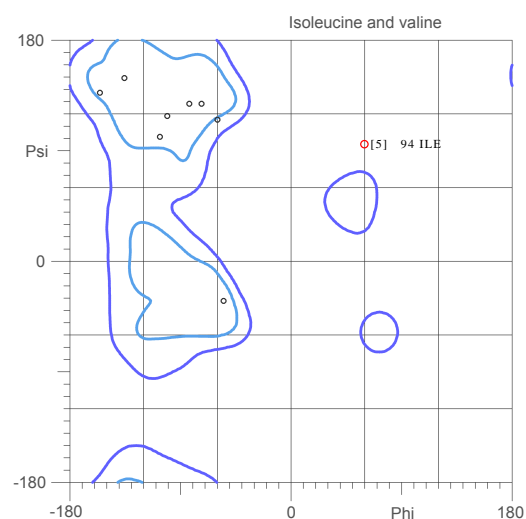
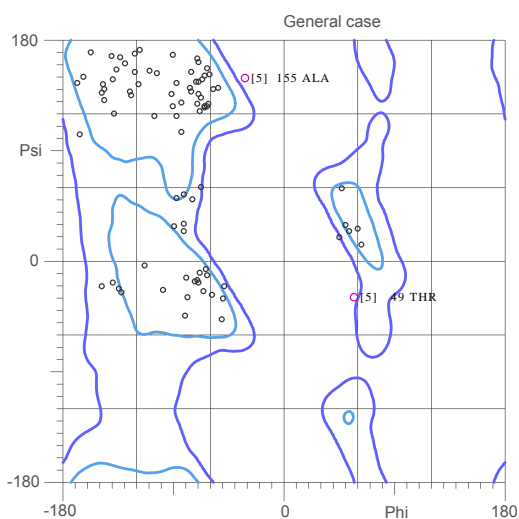
83.7% (113/135) of all residues were in favored (98%) regions.
96.3% (130/135) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [4] 60 GLY (-66.0, -126.8)
- [4] 68 ARG (42.9, 16.5)
- [4] 71 GLY (161.9, 10.8)
- [4] 94 ILE (70.8, 156.3)
- [4] 140 ASN (-48.0, -12.5)

MolProbity Ramachandran analysis

7act.H.pdb, model 5



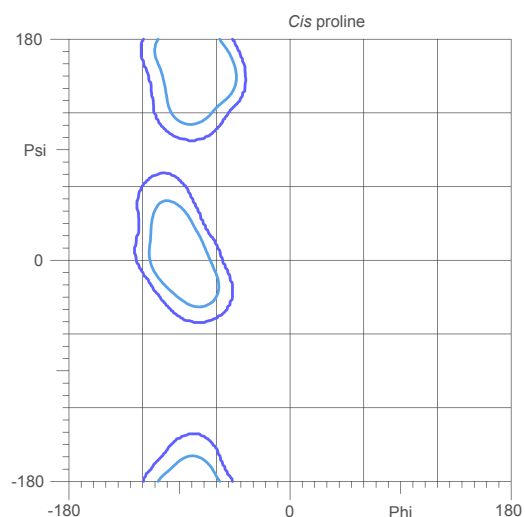
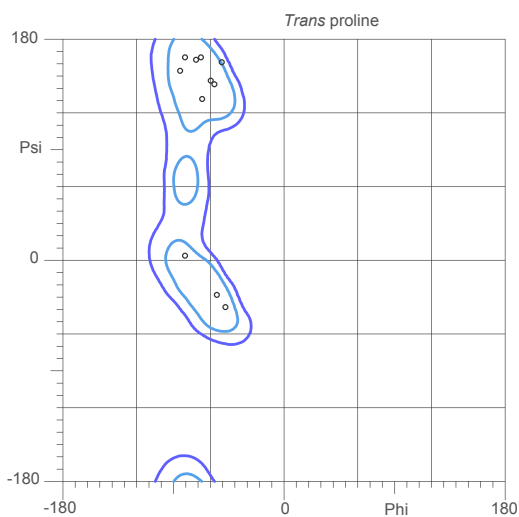
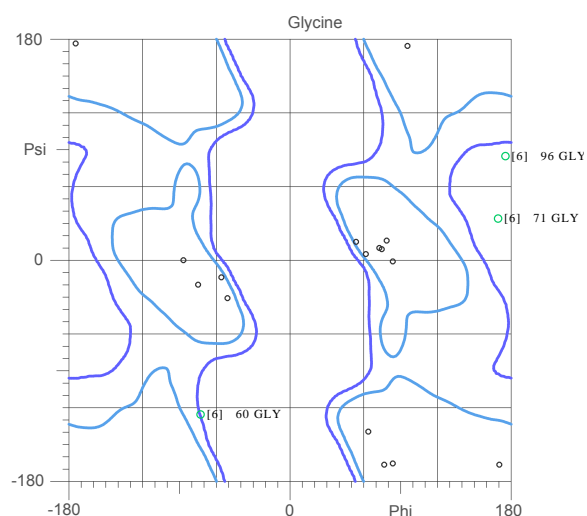
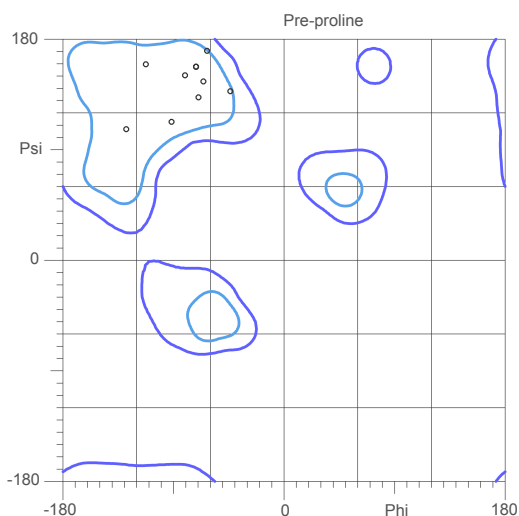
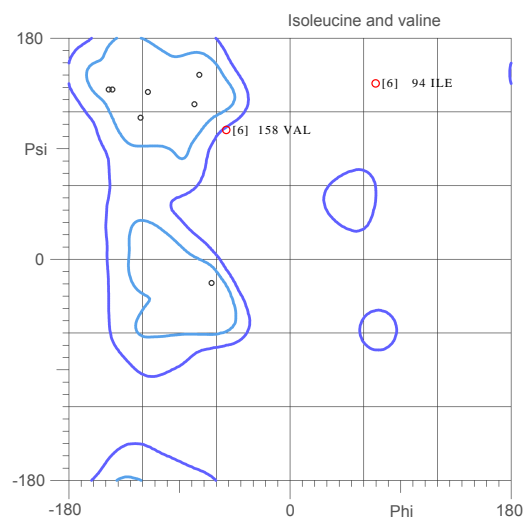
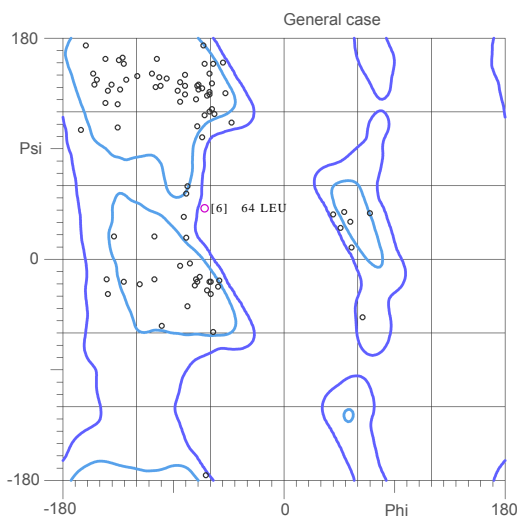
83.0% (112/135) of all residues were in favored (98%) regions.
96.3% (130/135) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [5] 49 THR (57.2, -29.8)
- [5] 71 GLY (174.8, 13.7)
- [5] 94 ILE (60.2, 97.0)
- [5] 96 GLY (66.9, 117.4)
- [5] 155 ALA (-32.5, 150.3)

MolProbity Ramachandran analysis

7act.H.pdb, model 6



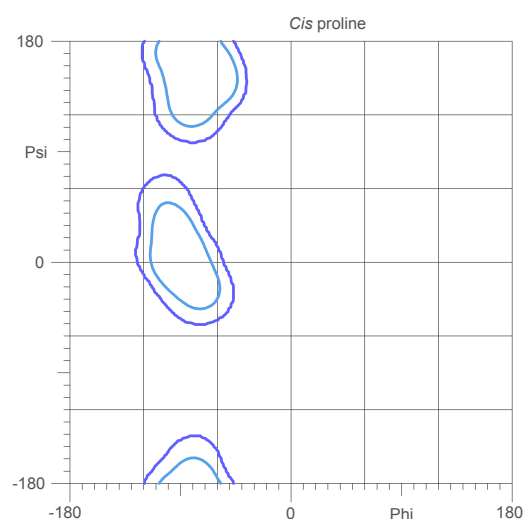
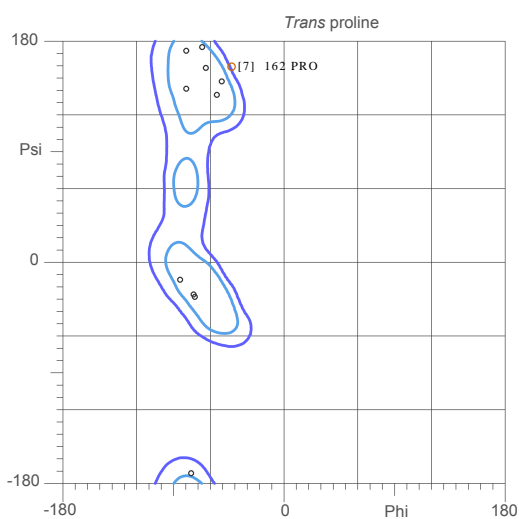
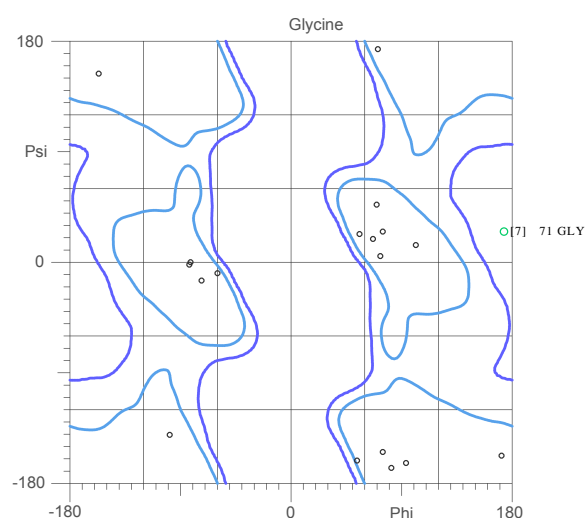
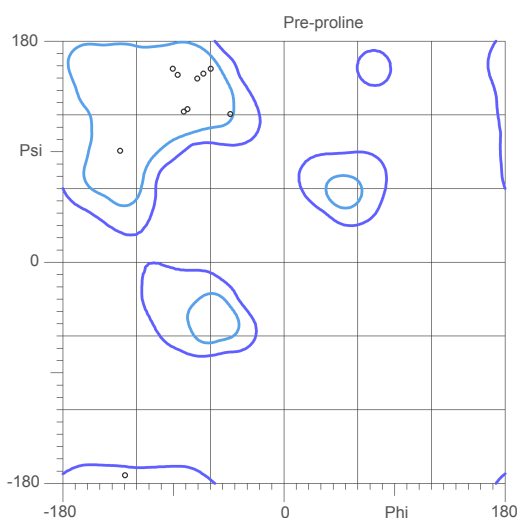
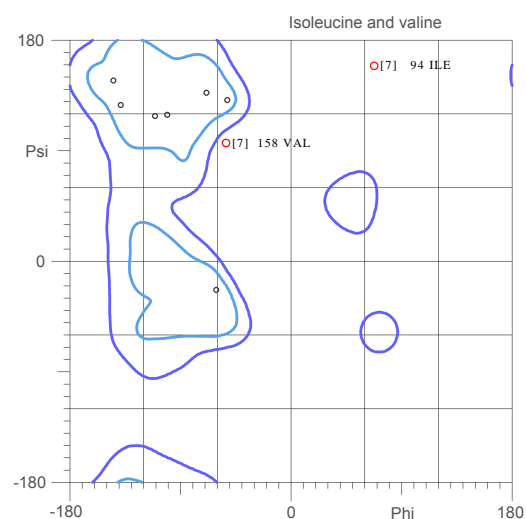
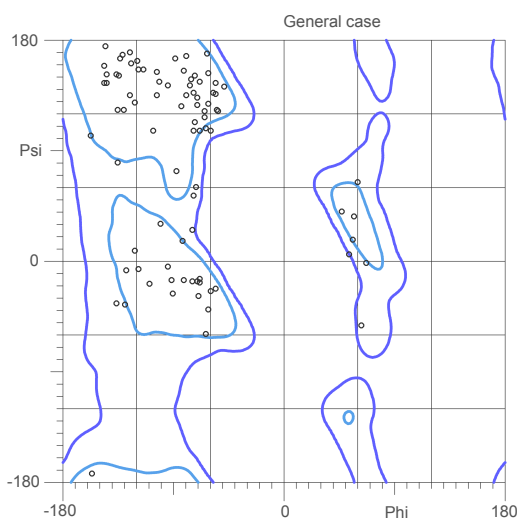
83.7% (113/135) of all residues were in favored (98%) regions.
95.6% (129/135) of all residues were in allowed (>99.8%) regions.

There were 6 outliers (phi, psi):

- [6] 60 GLY (-73.0, -126.9)
- [6] 64 LEU (-65.7, 42.9)
- [6] 71 GLY (170.1, 35.0)
- [6] 94 ILE (70.5, 145.0)
- [6] 96 GLY (176.2, 85.7)
- [6] 158 VAL (-52.8, 106.4)

MolProbity Ramachandran analysis

7act.H.pdb, model 7



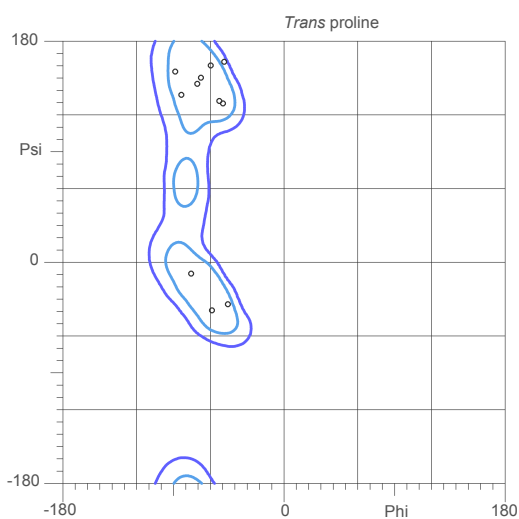
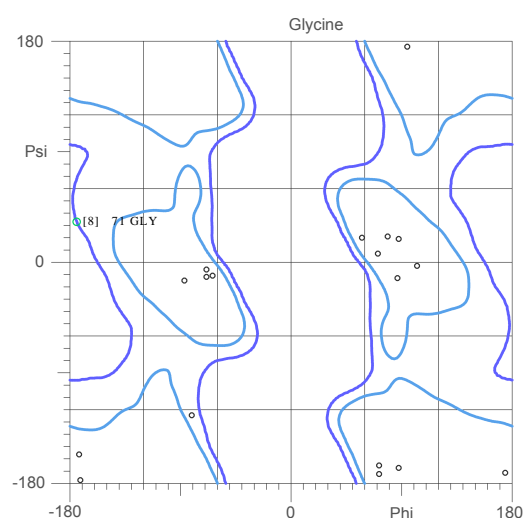
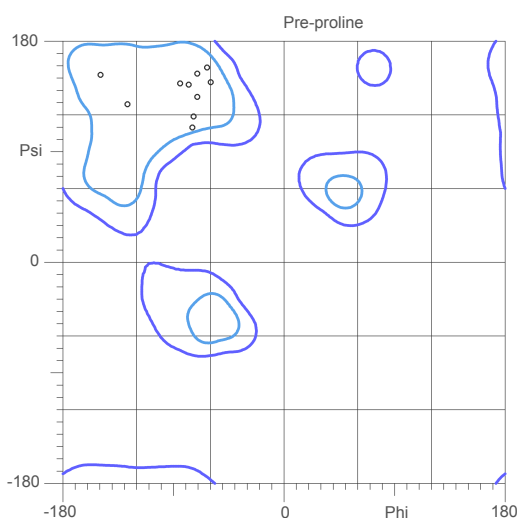
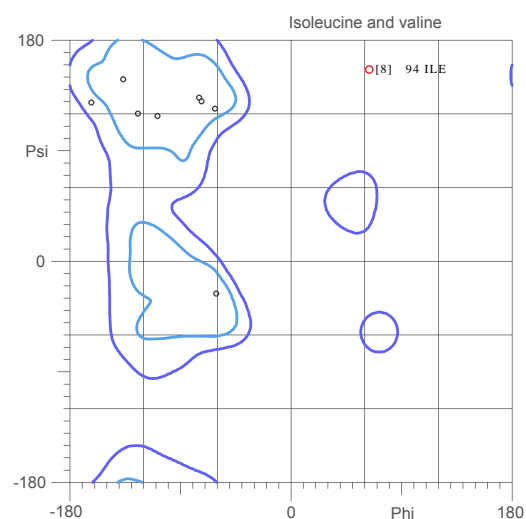
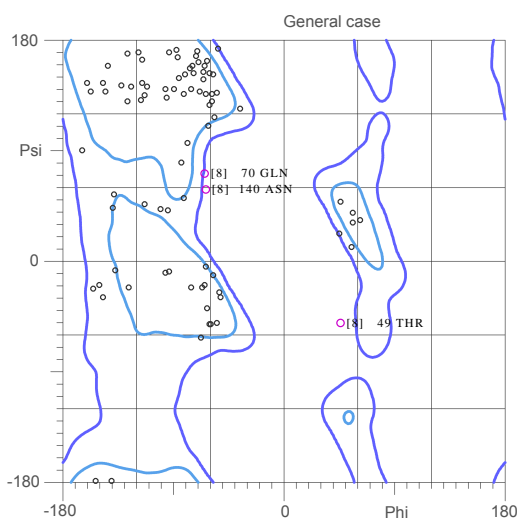
85.9% (116/135) of all residues were in favored (98%) regions.
97.0% (131/135) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

- [7] 71 GLY (174.9, 25.7)
- [7] 94 ILE (68.1, 160.9)
- [7] 158 VAL (-53.5, 97.8)
- [7] 162 PRO (-43.3, 160.4)

MolProbity Ramachandran analysis

7act.H.pdb, model 8



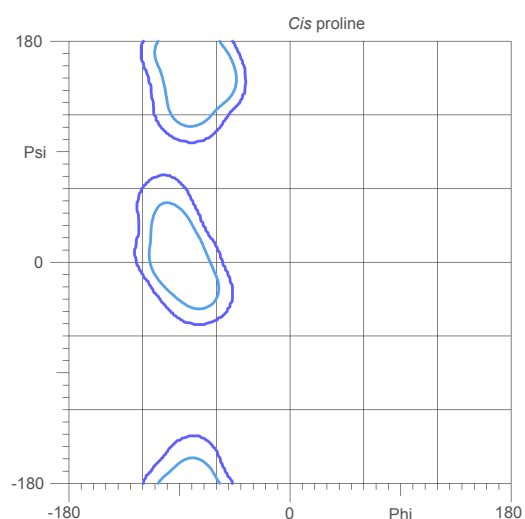
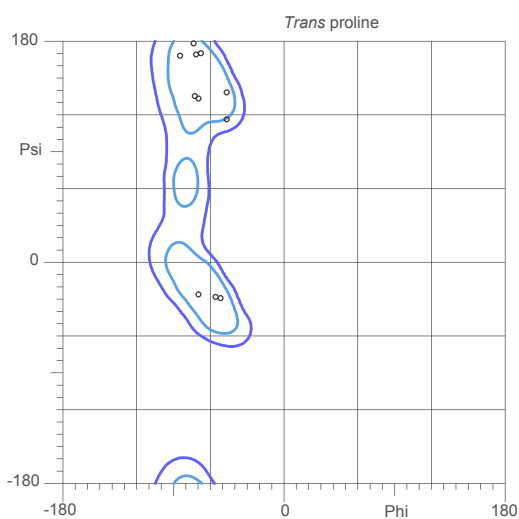
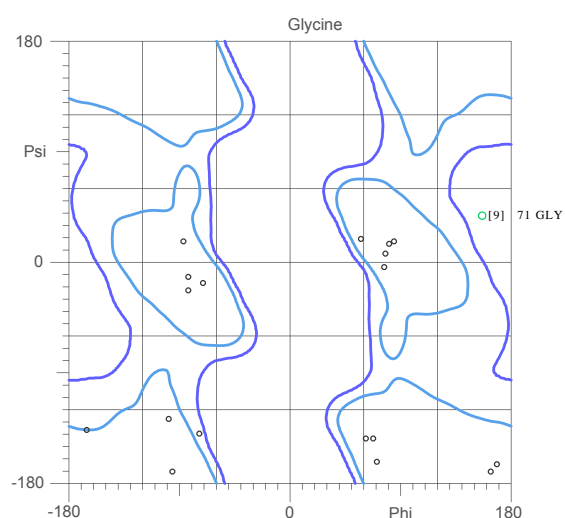
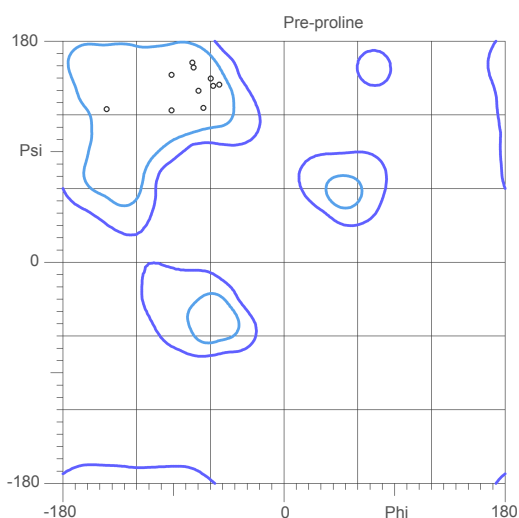
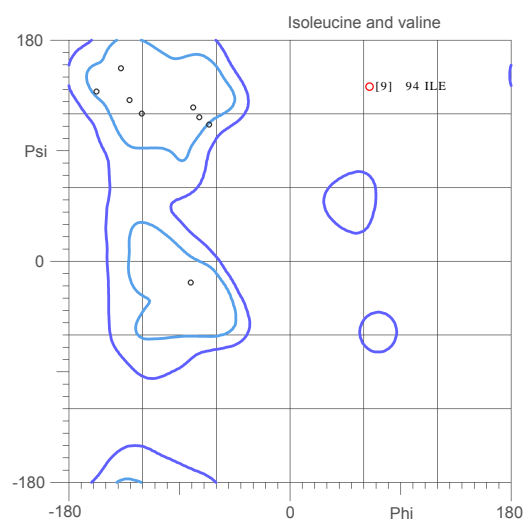
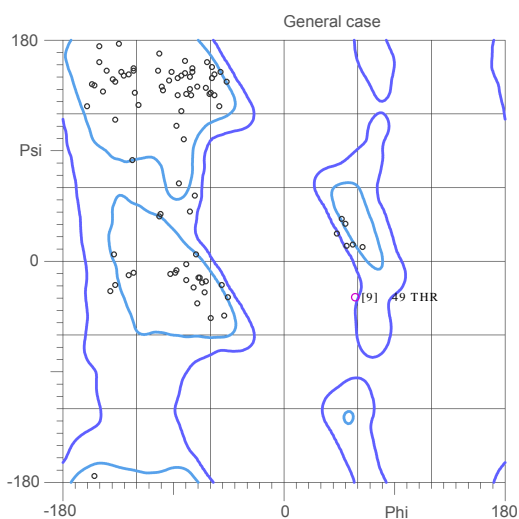
83.0% (112/135) of all residues were in favored (98%) regions.
96.3% (130/135) of all residues were in allowed (>99.8%) regions.

There were 5 outliers (phi, psi):

- [8] 49 THR (46.2, -50.2)
- [8] 70 GLN (-65.4, 72.4)
- [8] 71 GLY (-175.2, 34.0)
- [8] 94 ILE (64.6, 157.8)
- [8] 140 ASN (-64.5, 59.6)

MolProbity Ramachandran analysis

7act.H.pdb, model 9



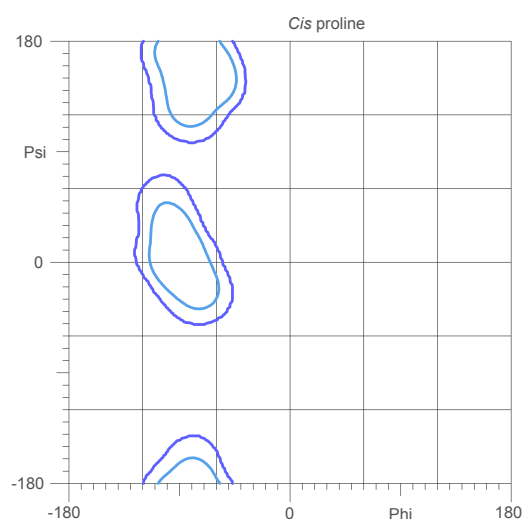
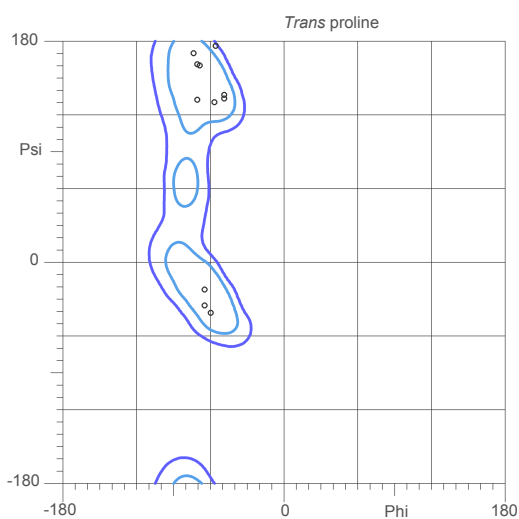
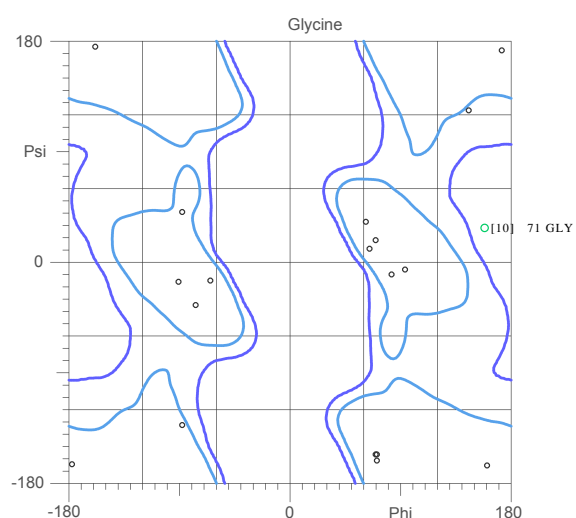
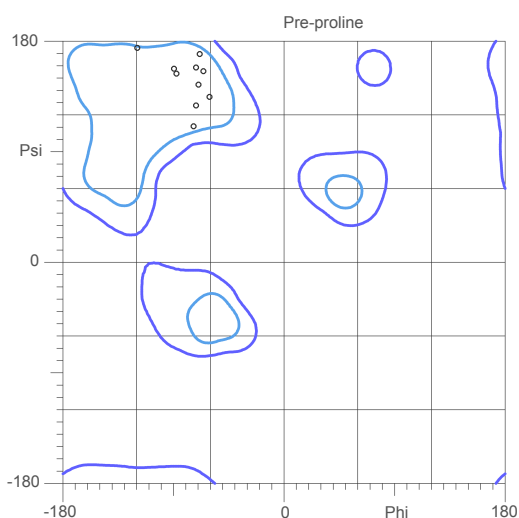
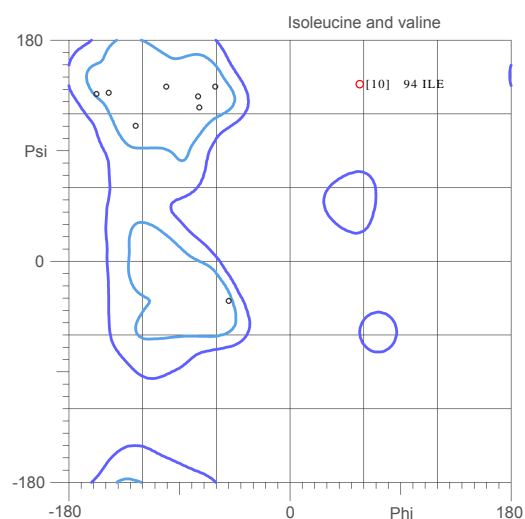
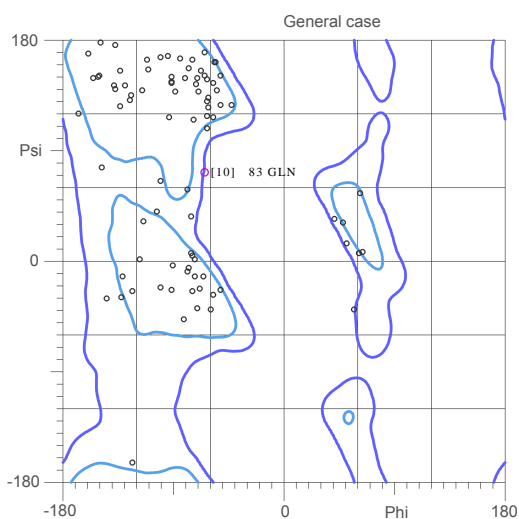
88.1% (119/135) of all residues were in favored (98%) regions.
97.8% (132/135) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [9] 49 THR (58.5, -29.3)
- [9] 71 GLY (157.1, 38.2)
- [9] 94 ILE (65.9, 143.7)

MolProbity Ramachandran analysis

7act.H.pdb, model 10



85.2% (115/135) of all residues were in favored (98%) regions.
97.8% (132/135) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

[10] 71 GLY (159.2, 28.9)

[10] 83 GLN (-65.0, 73.8)

[10] 94 ILE (57.9, 145.1)