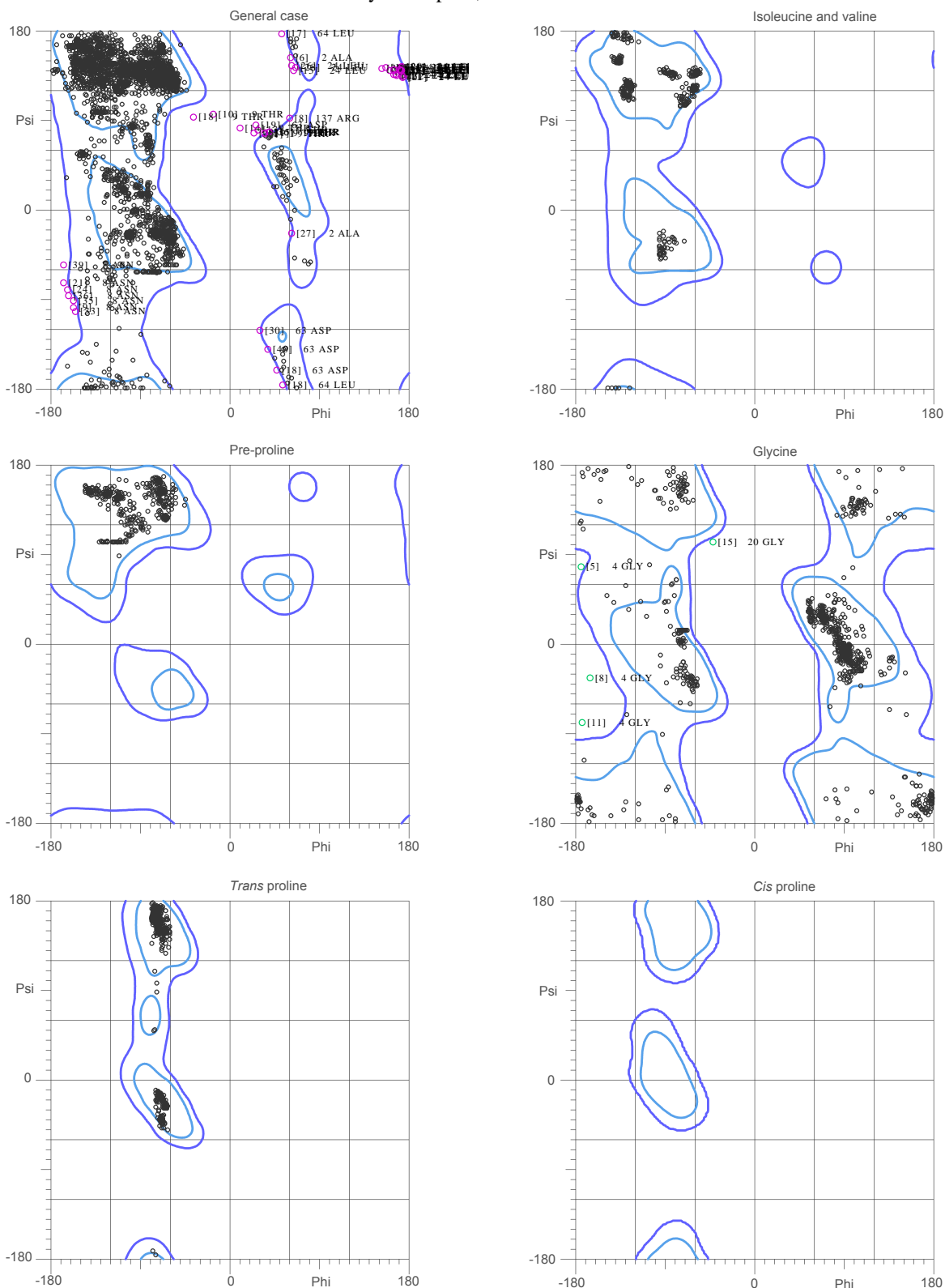


MolProbity Ramachandran analysis

6yi3.H.pdb, all models



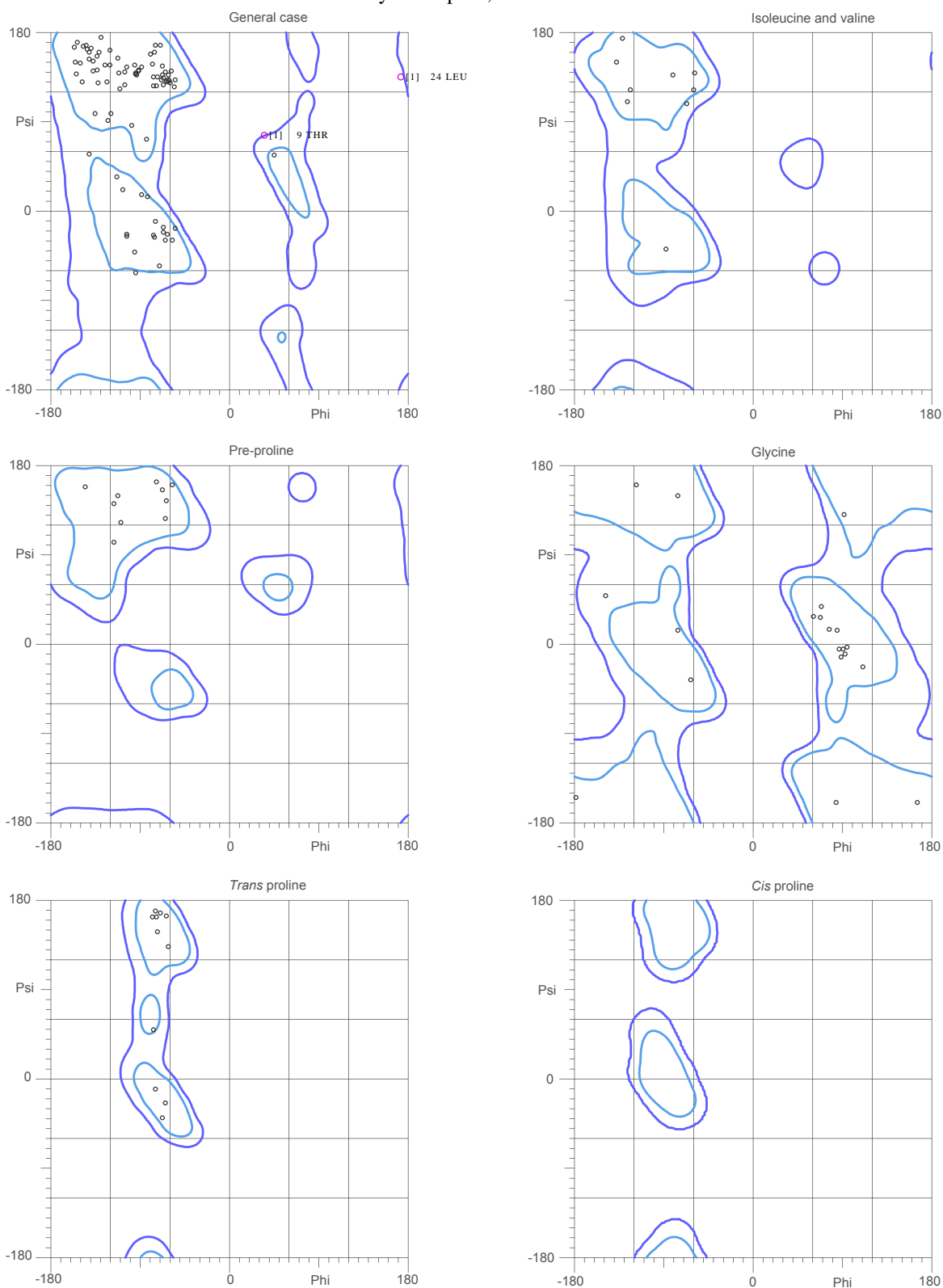
94.0% (5189/5520) of all residues were in favored (90%) regions.
9% (508/5520) of all residues were in allowed (10%) regions.

There were 52 outliers (phi, psi):

(1) 9 THR (35.1, 77.1)	(19) 43 ASP (57.6, -54.5)
(2) 24 LEU (175.8, 158.9)	(20) 64 LEU (17.6, -176.7)
(3) 4 GLY (175.2, 79.1)	(21) 43 ASP (26.6, 94.3)
(4) 24 LEU (168.5, 141.9)	(22) 43 ASP (175.7, 158.9)
(5) 2 ALA (16.9, 154.2)	(23) 8 ASN (168.2, -71.7)
(6) 24 LEU (167.5, 137.4)	(24) 24 LEU (175.3, 158.9)
(7) 4 GLY (168.5, 14.7)	(25) 24 LEU (168.4, 146.7)
(8) 24 LEU (177.5, 148.5)	(26) 24 LEU (168.5, 146.7)
(9) 137 ARG (168.5, 93.8)	(27) 24 LEU (175.6, 146.7)
(10) 8 ASN (176.9, 106.5)	(28) 24 LEU (168.3, 146.3)
(11) 24 LEU (167.7, 137.4)	(29) 24 LEU (168.5, 146.3)
(12) 4 GLY (176.2, 106.8)	(30) 24 LEU (168.5, 146.3)
(13) 24 LEU (177.5, 144.4)	(31) 43 ASP (16.7, -114.4)
(14) 9 THR (16.9, 89.1)	(32) 9 THR (15.7, 76.7)
(15) 24 LEU (177.4, 144.2)	(33) 24 LEU (175.6, 146.3)
(16) 9 THR (16.9, 76.2)	(34) 8 ASN (158.1, -100.2)
(17) 20 GLY (-62.1, 103.0)	(35) 8 ASN (158.4, -91.8)
(18) 24 LEU (168.2, 144.2)	(36) 24 LEU (177.7, 146.4)
(19) 43 ASP (16.5, -148.8)	(37) 8 ASN (162.1, 48.8)
(20) 24 LEU (175.9, 144.8)	(38) 9 THR (16.9, 76.2)
(21) 24 LEU (175.3, 144.2)	(39) 24 LEU (175.9, 144.8)
(22) 7 ASN (168.7, -51.3)	(40) 24 LEU (175.3, 144.2)
(23) 24 LEU (175.3, 144.2)	(41) 43 ASP (16.5, -148.8)
(24) 43 ASP (16.5, -148.8)	

MolProbity Ramachandran analysis

6yi3.H.pdb, model 1



95.7% (132/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[1] 9 THR (35.1, 77.1)

[1] 24 LEU (173.8, 136.0)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 2



92.0% (127/138) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 3



97.1% (134/138) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 4



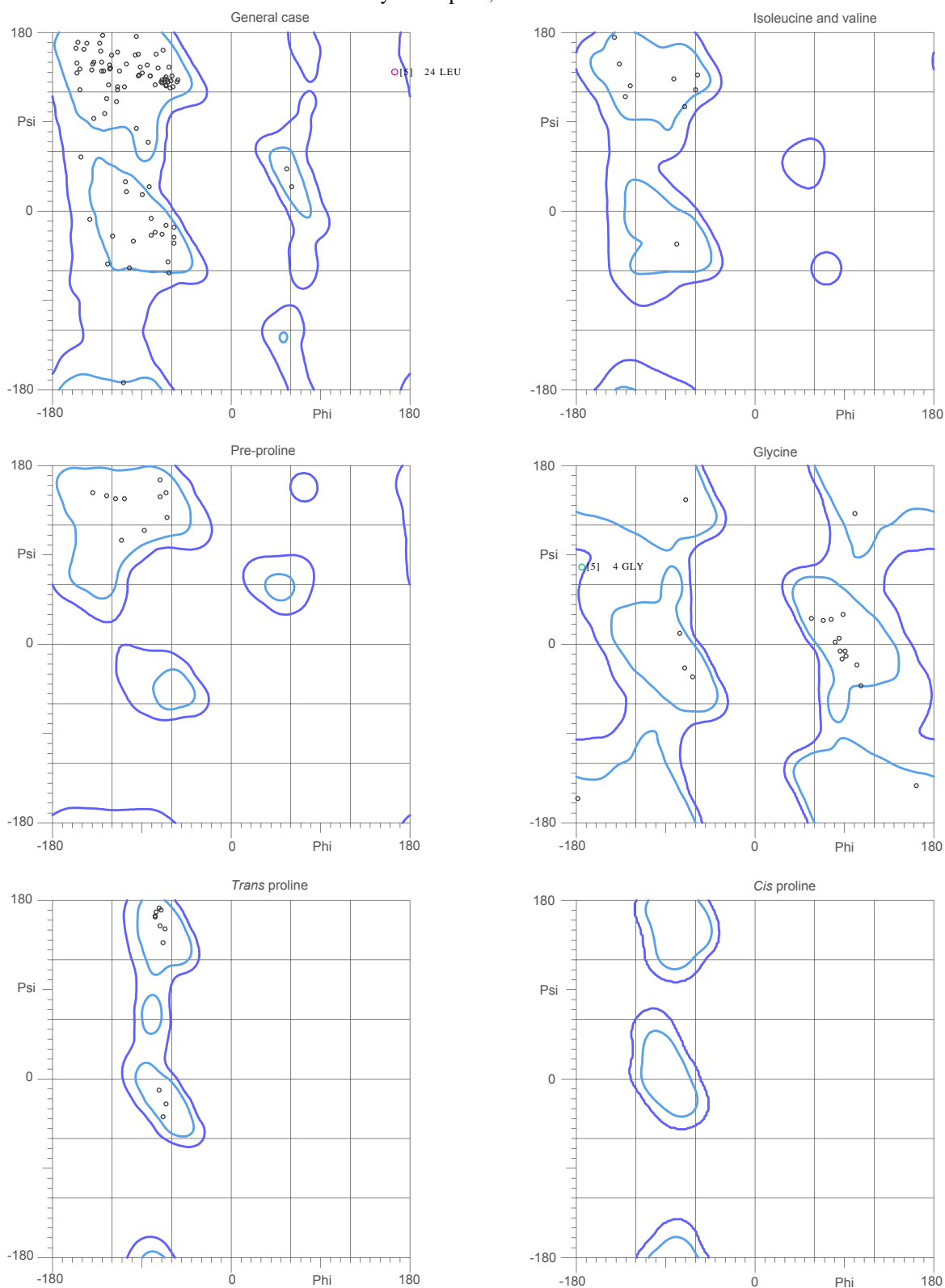
94.2% (130/138) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 5



93.5% (129/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[5] 4 GLY (-175.2, 78.1)

[5] 24 LEU (165.3, 141.9)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 6



94.9% (131/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[6] 2 ALA (61.9, 154.2)

[6] 24 LEU (167.5, 137.4)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 7



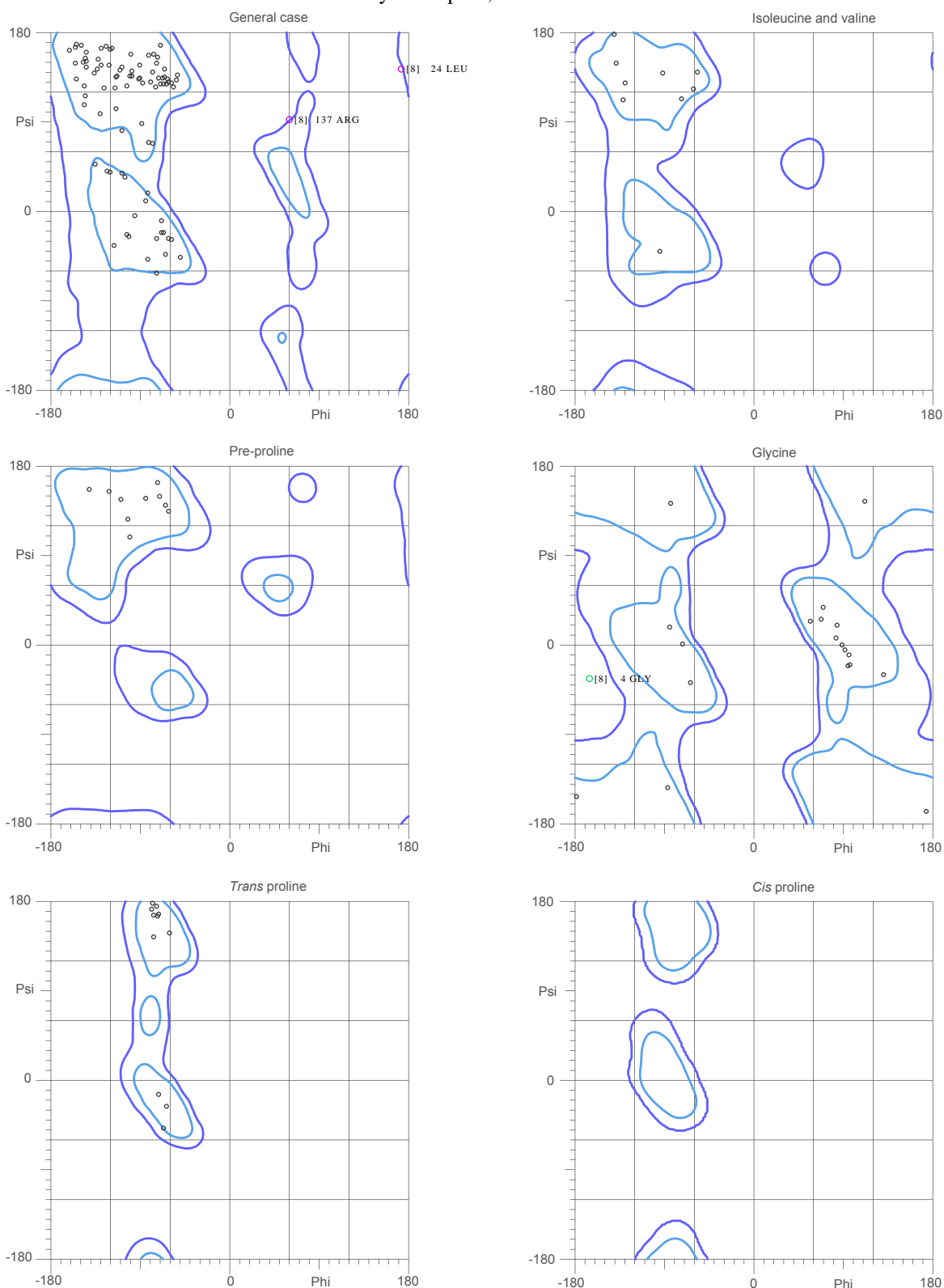
94.2% (130/138) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 8



94.9% (131/138) of all residues were in favored (98%) regions.
97.8% (135/138) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [8] 4 GLY (-166.3, -34.7)
- [8] 24 LEU (173.7, 144.5)
- [8] 137 ARG (60.3, 93.0)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 9



92.8% (128/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

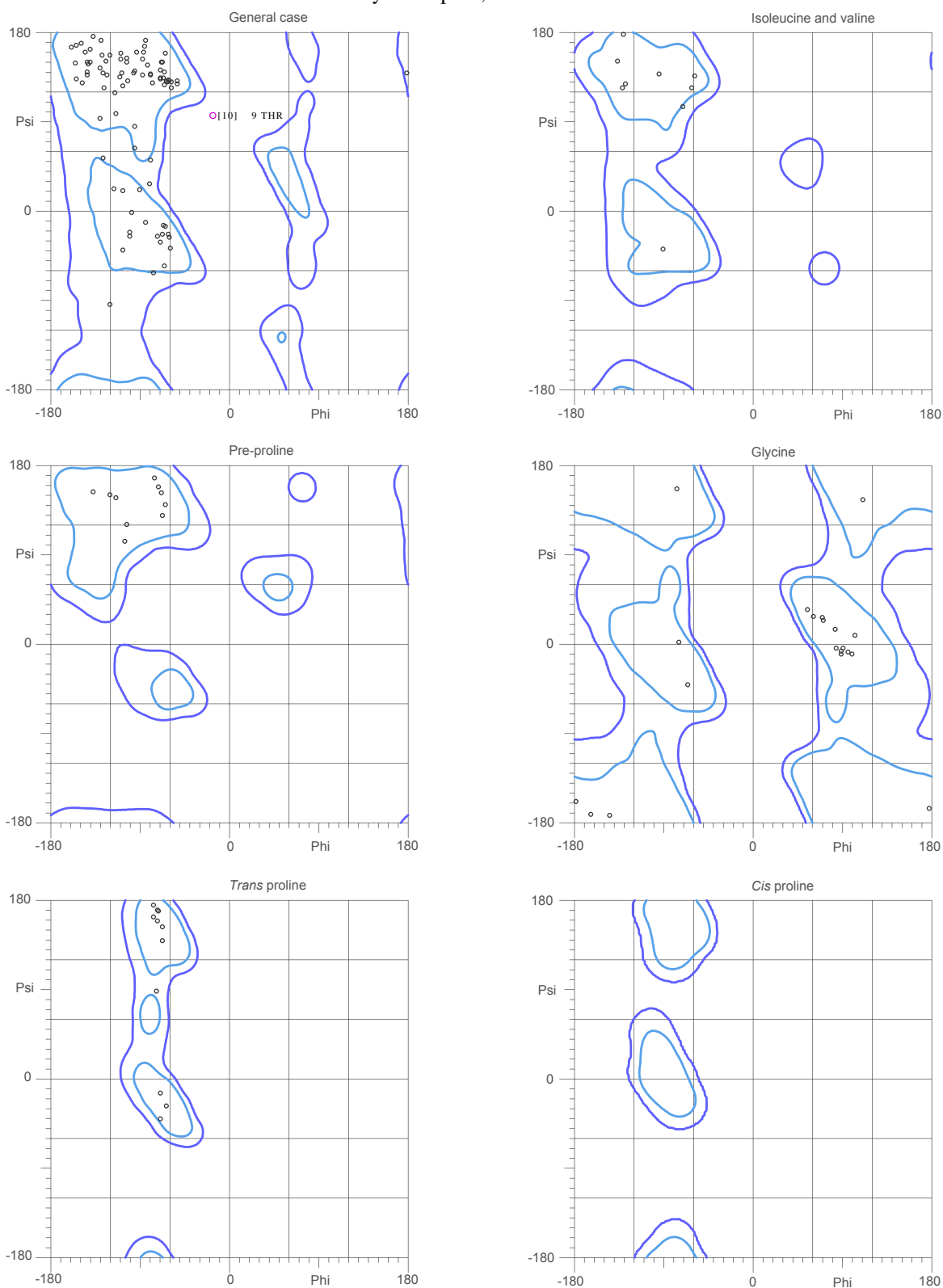
There were 2 outliers (phi, psi):

[9] 8 ASN (-158.6, -98.3)

[9] 24 LEU (165.7, 137.4)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 10



94.2% (130/138) of all residues were in favored (98%) regions.

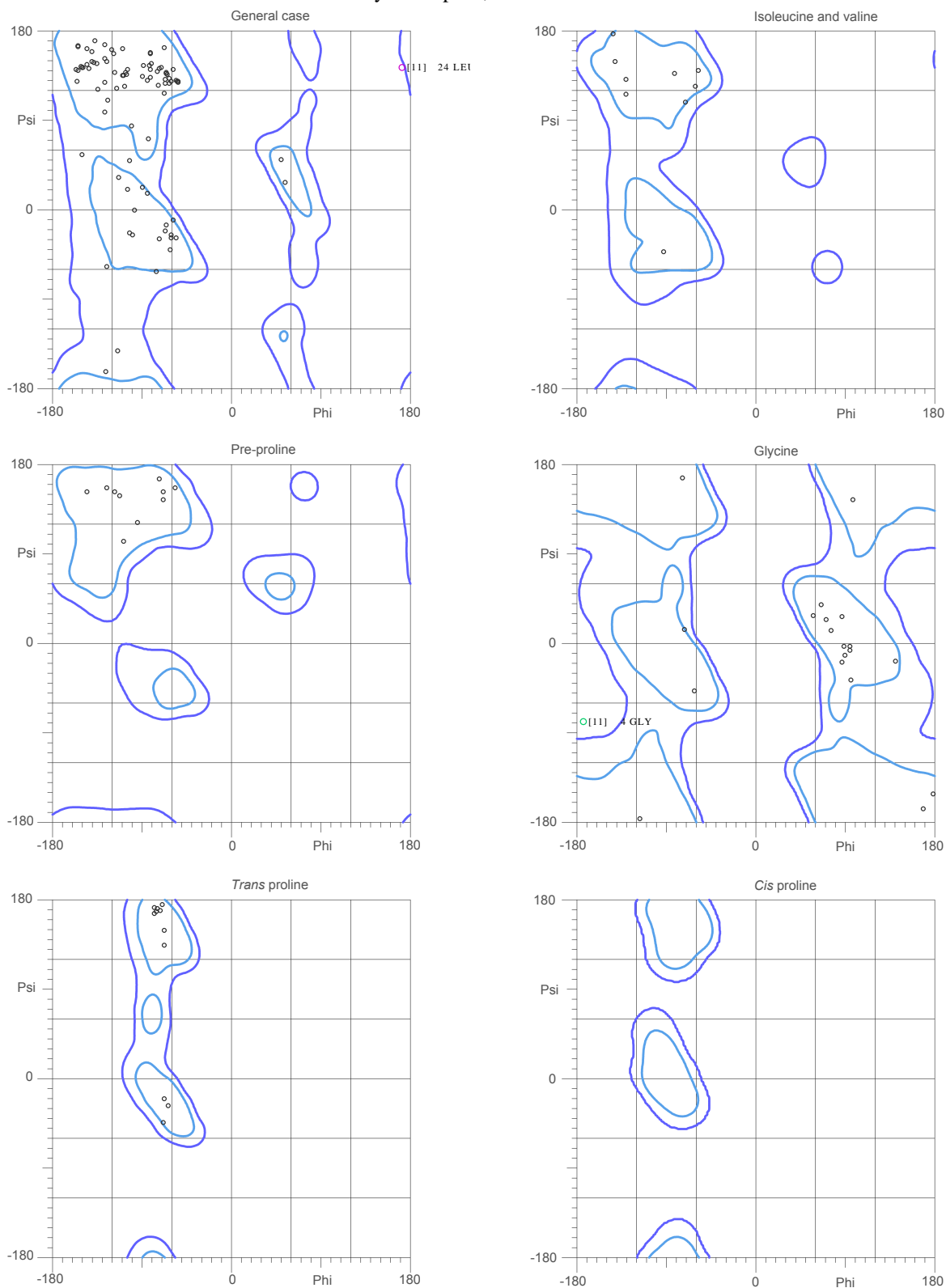
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[10] 9 THR (-17.7, 97.4)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 11



93.5% (129/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

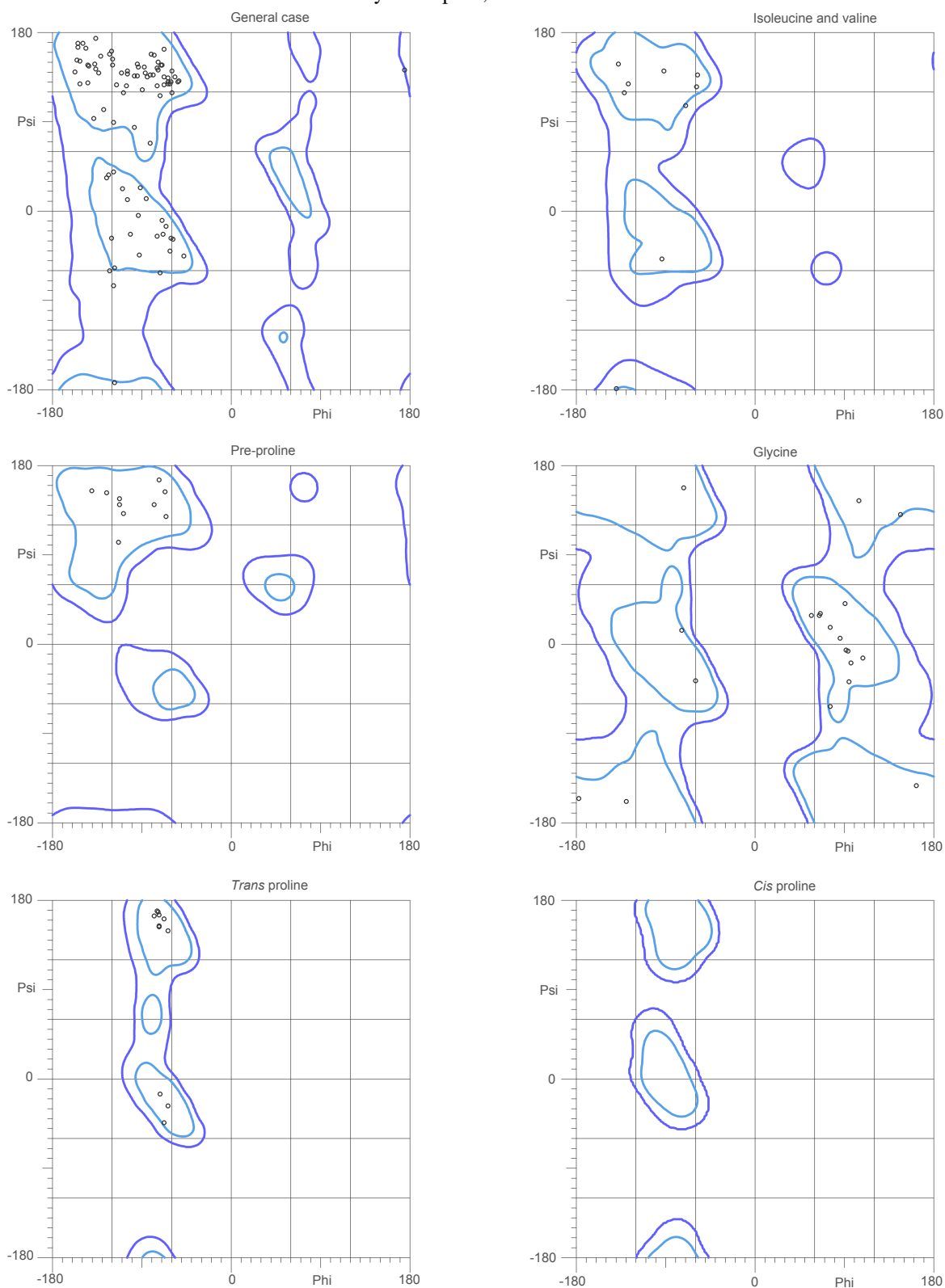
There were 2 outliers (phi, psi):

[11] 4 GLY (-174.2, -79.0)

[11] 24 LEU (172.6, 144.8)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 12



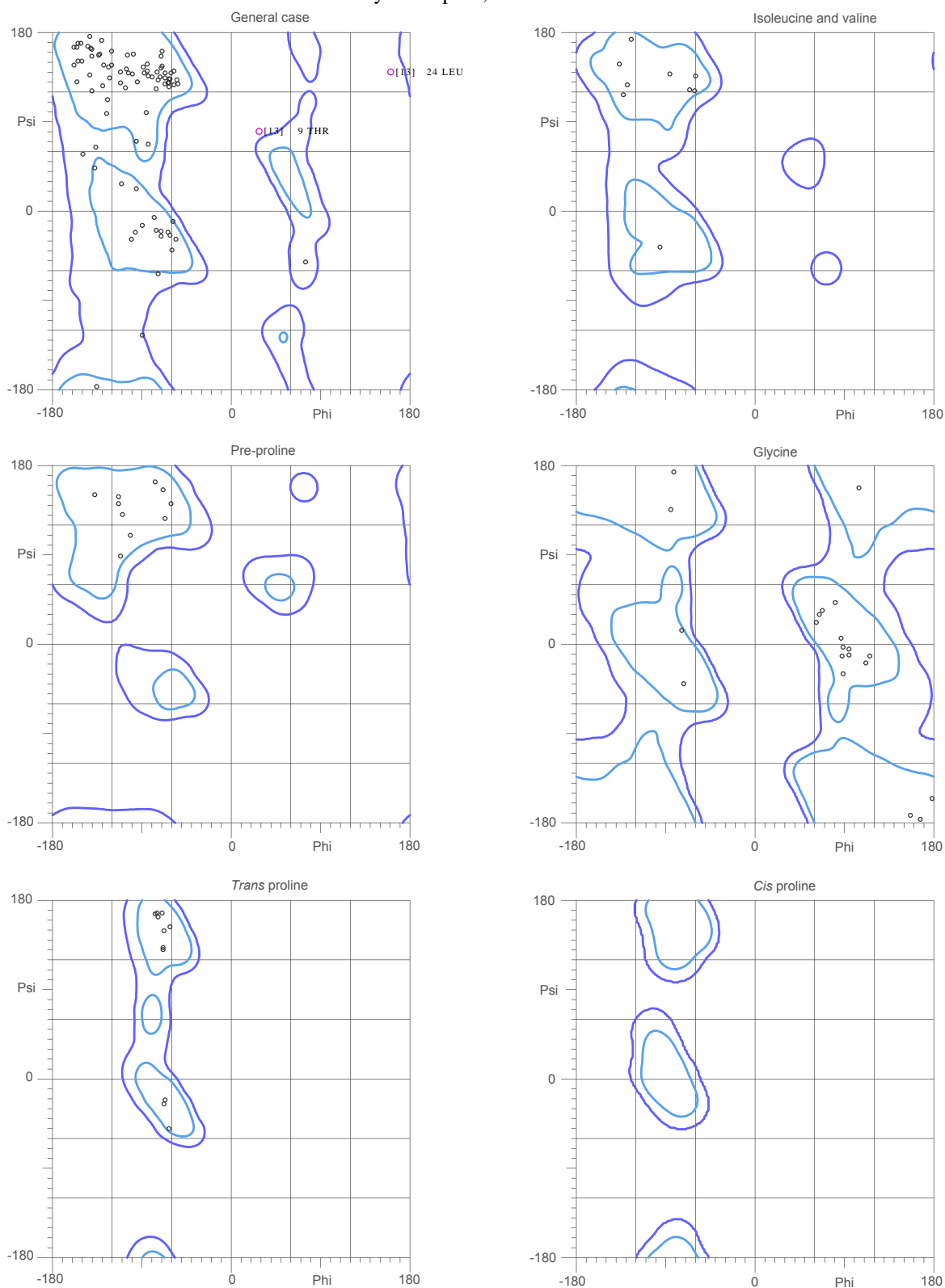
97.1% (134/138) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 13



94.9% (131/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

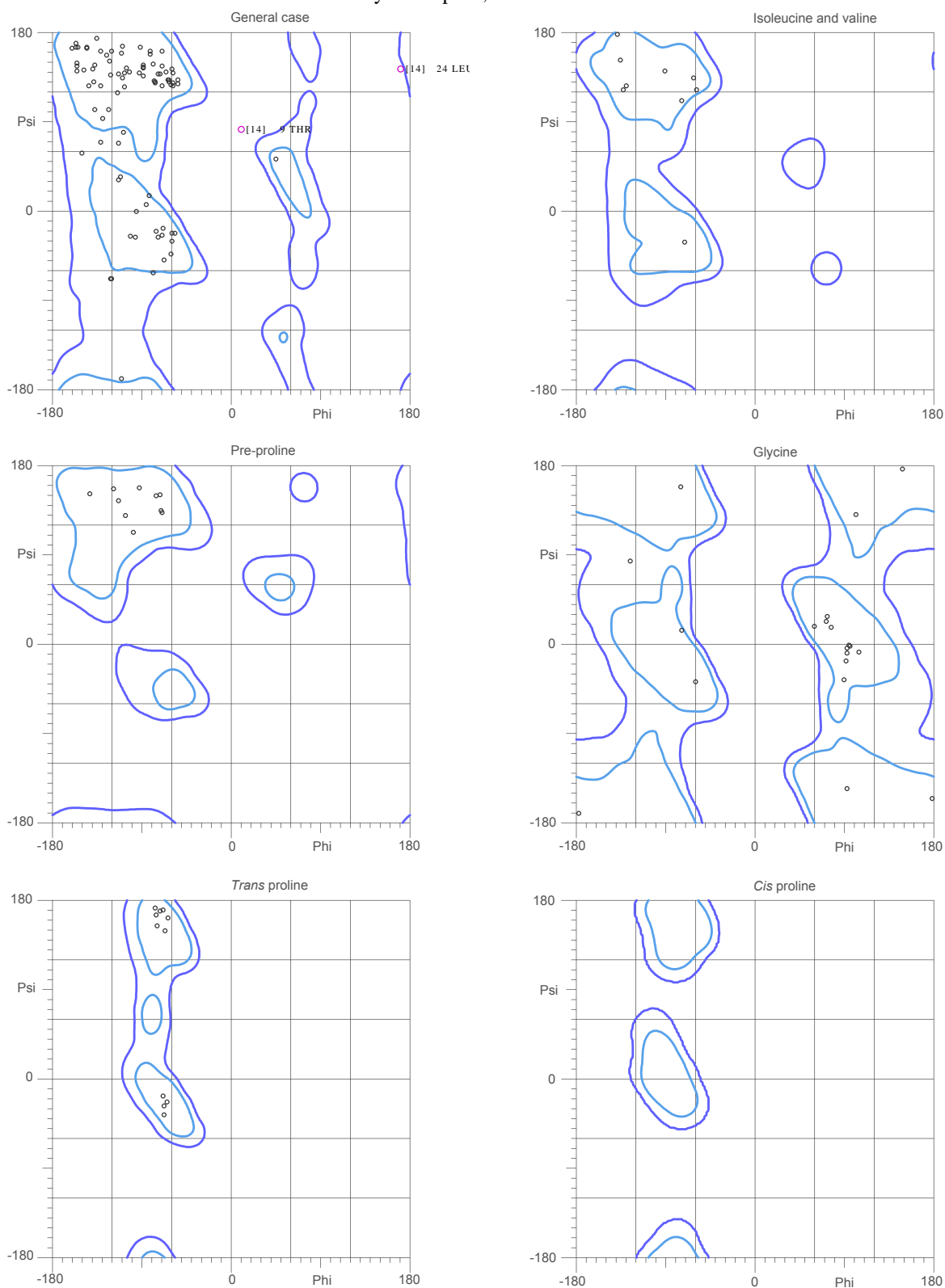
There were 2 outliers (phi, psi):

[13] 9 THR (28.3, 81.1)

[13] 24 LEU (161.0, 141.8)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 14



92.0% (127/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

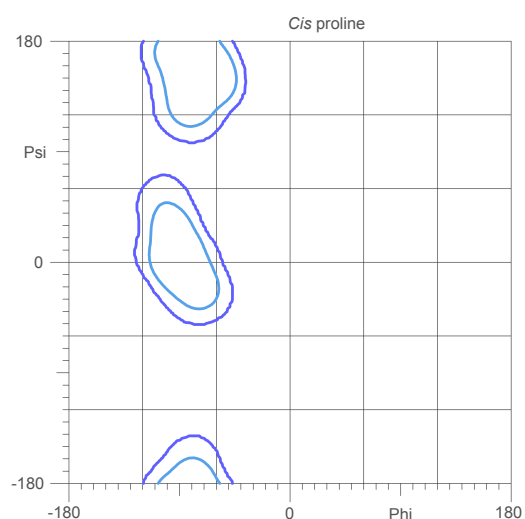
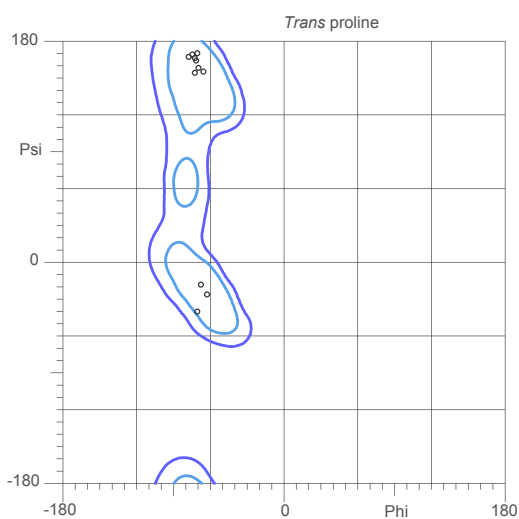
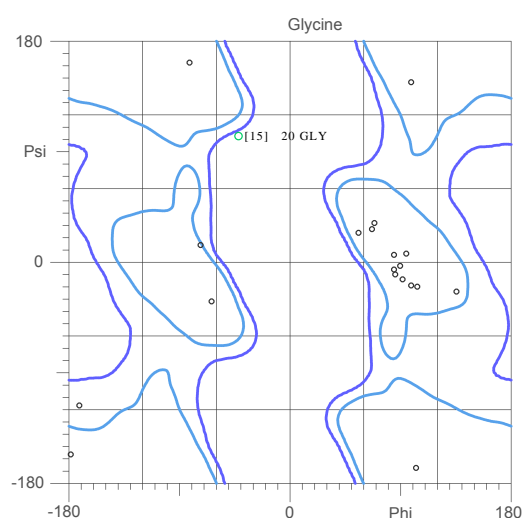
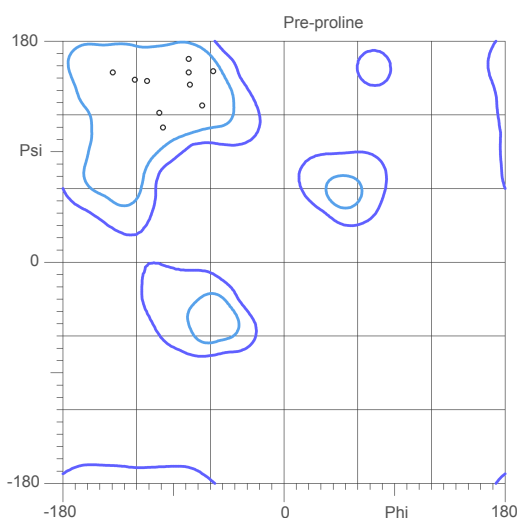
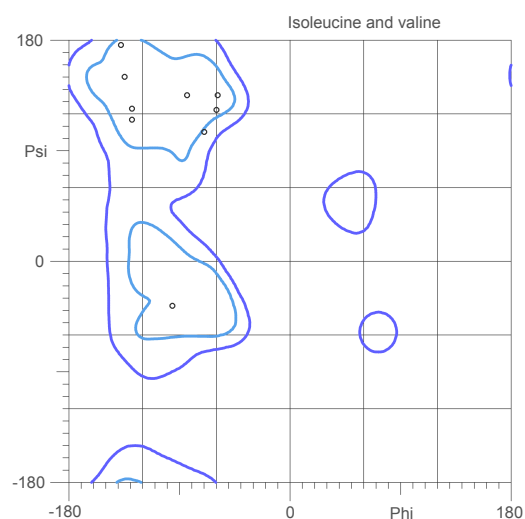
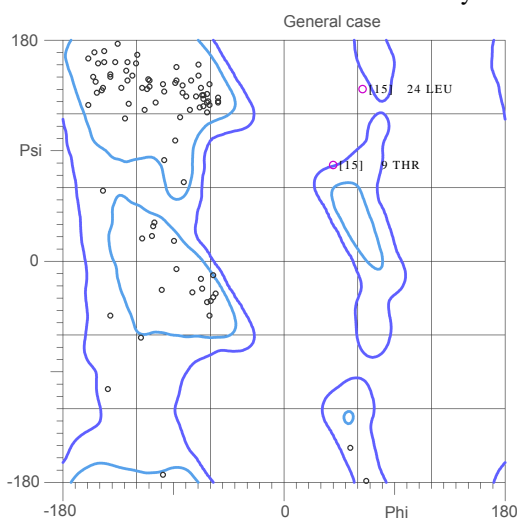
There were 2 outliers (phi, psi):

[14] 9 THR (10.2, 83.8)

[14] 24 LEU (171.6, 144.2)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 15



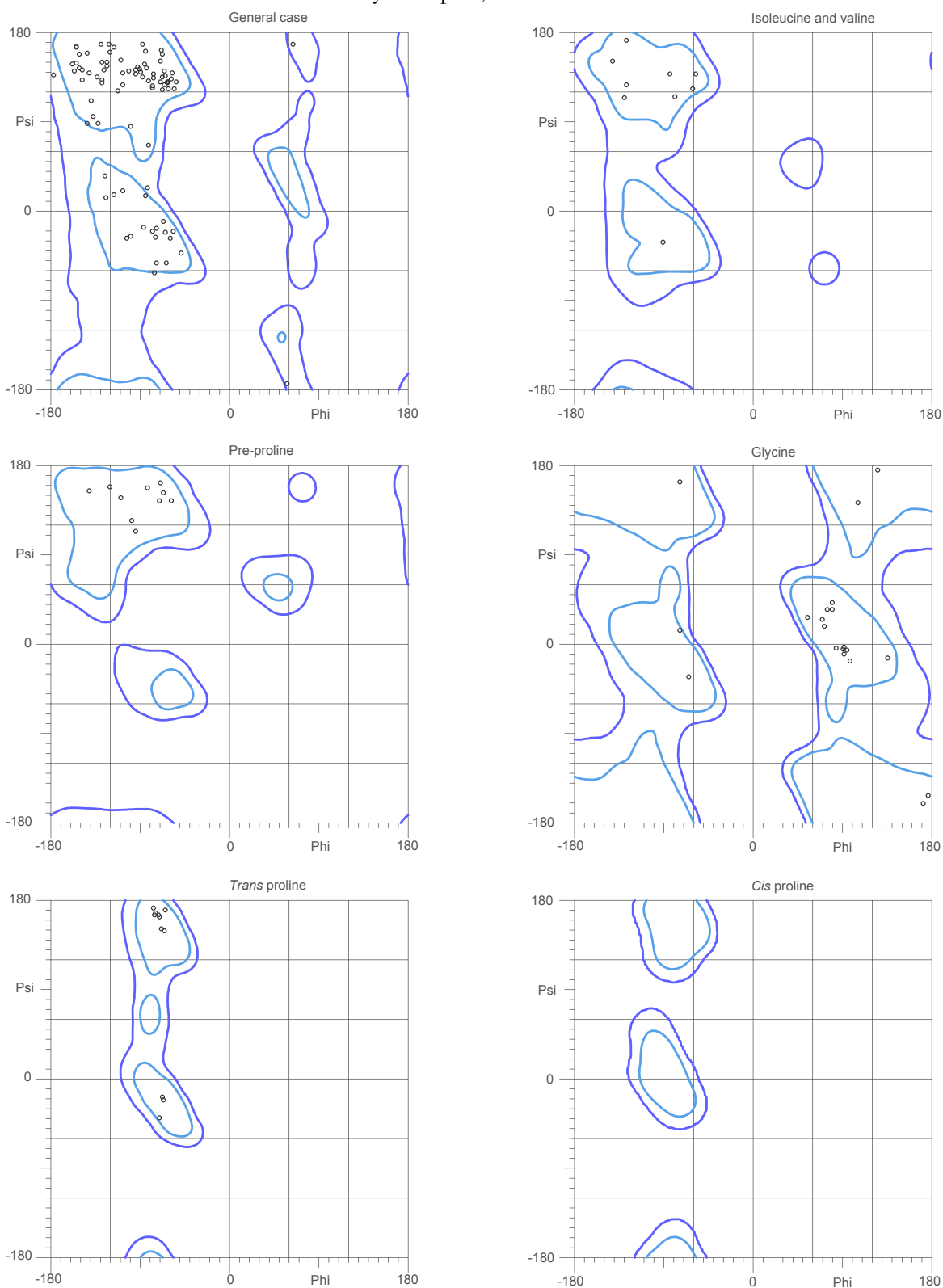
92.0% (127/138) of all residues were in favored (98%) regions.
97.8% (135/138) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [15] 9 THR (40.5, 79.6)
- [15] 20 GLY (-42.1, 103.0)
- [15] 24 LEU (64.2, 141.5)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 16



96.4% (133/138) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 17



96.4% (133/138) of all residues were in favored (98%) regions.

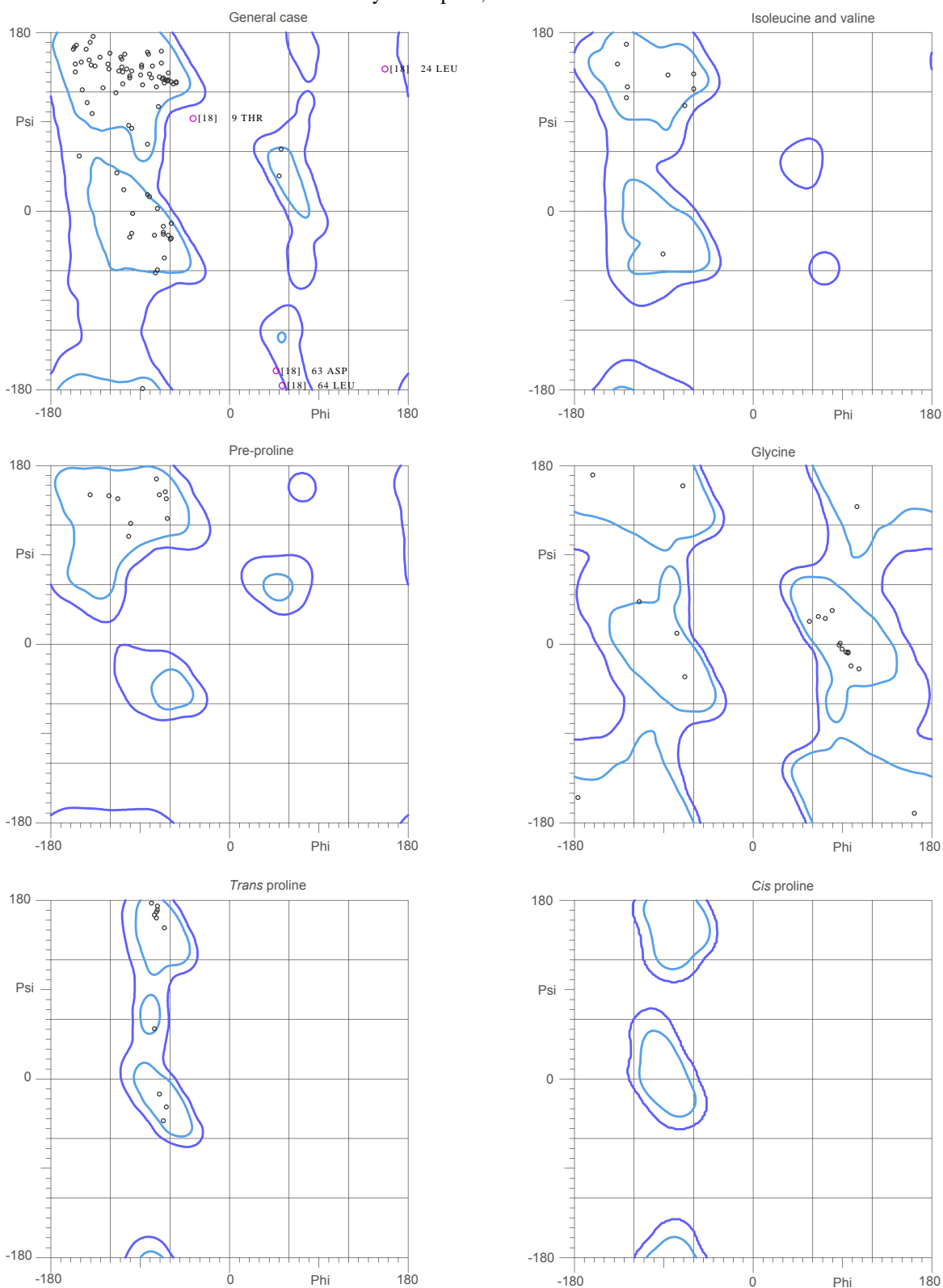
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[17] 64 LEU (52.9, 178.7)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 18



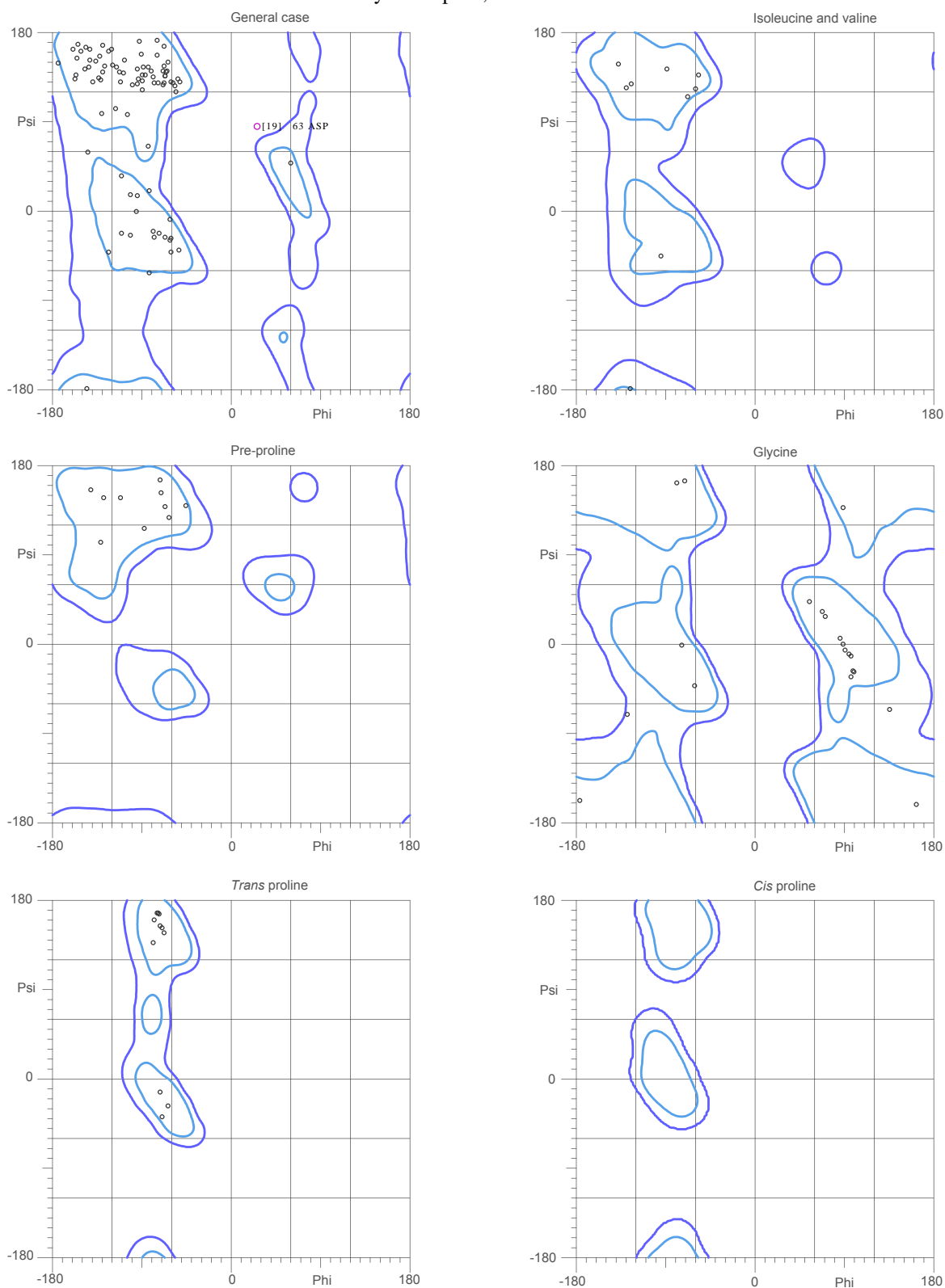
93.5% (129/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

There were 4 outliers (phi, psi):

[18] 9 THR (-37.2, 94.9)
[18] 24 LEU (157.2, 144.8)
[18] 63 ASP (47.0, -161.5)
[18] 64 LEU (53.5, -176.7)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 19



94.9% (131/138) of all residues were in favored (98%) regions.

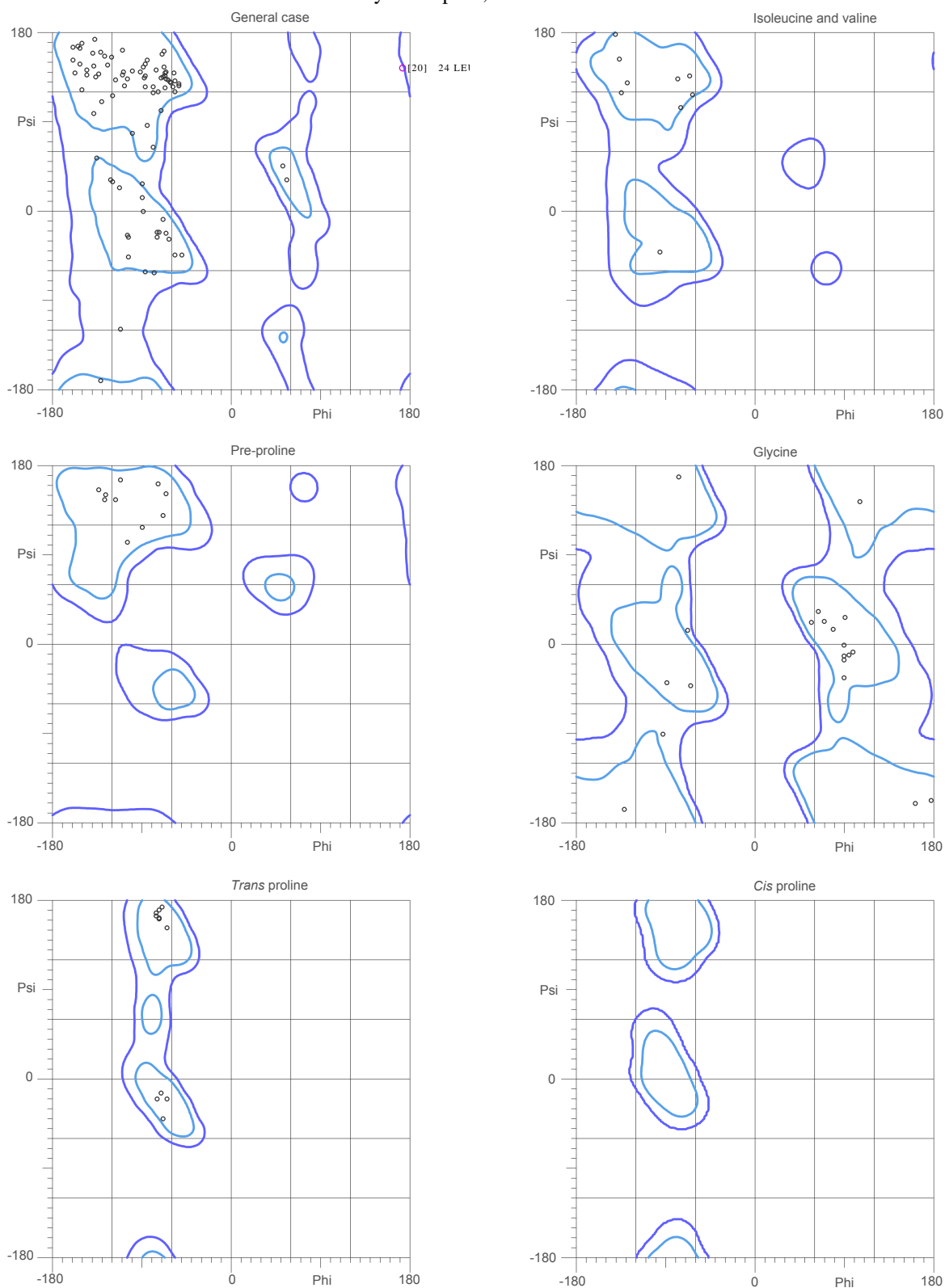
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[19] 63 ASP (26.6, 86.3)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 20



94.2% (130/138) of all residues were in favored (98%) regions.

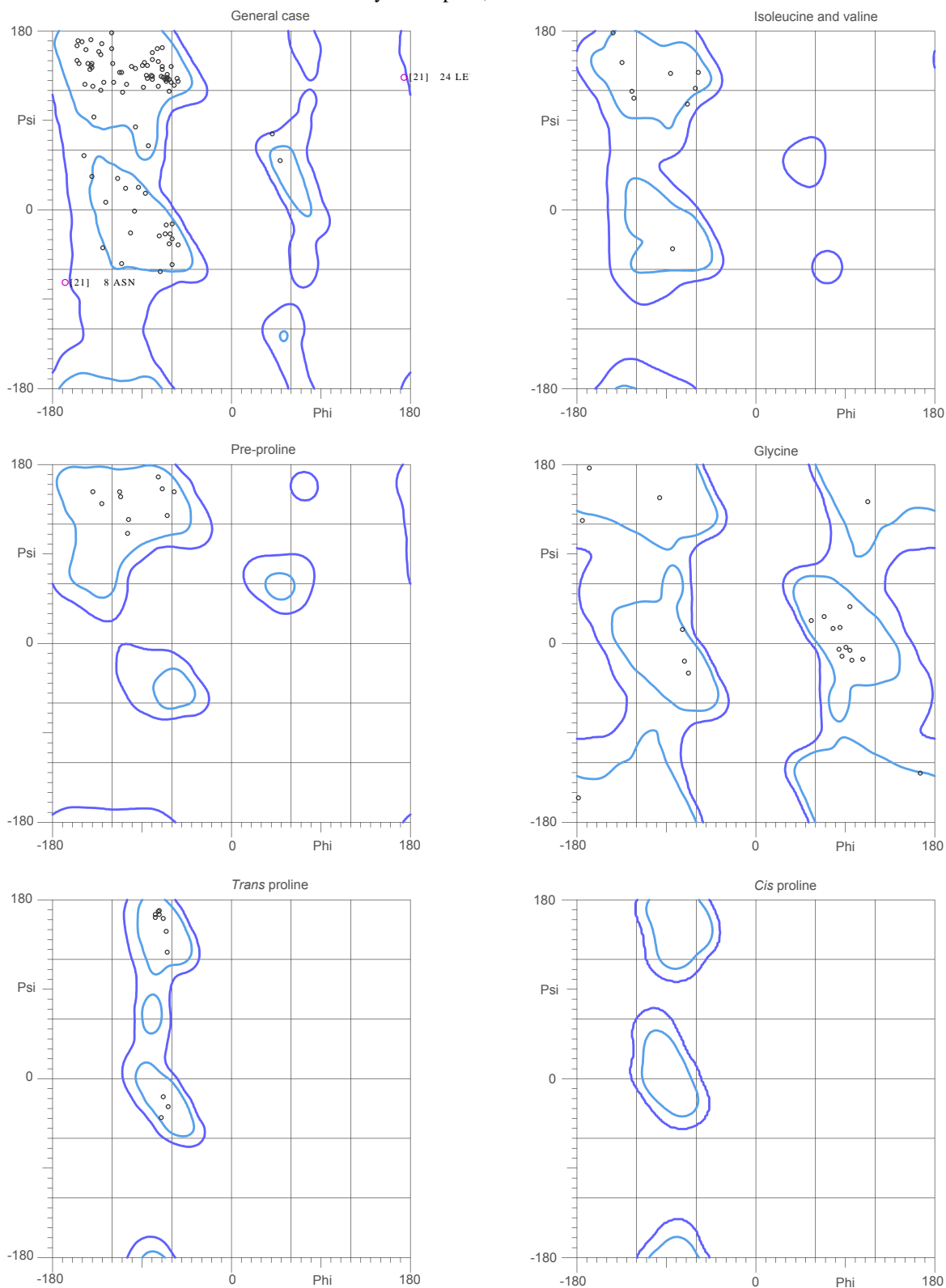
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[20] 24 LEU (173.7, 145.6)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 21



92.8% (128/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[21] 8 ASN (-168.2, -73.7)

[21] 24 LEU (174.5, 134.2)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 22



94.2% (130/138) of all residues were in favored (98%) regions.

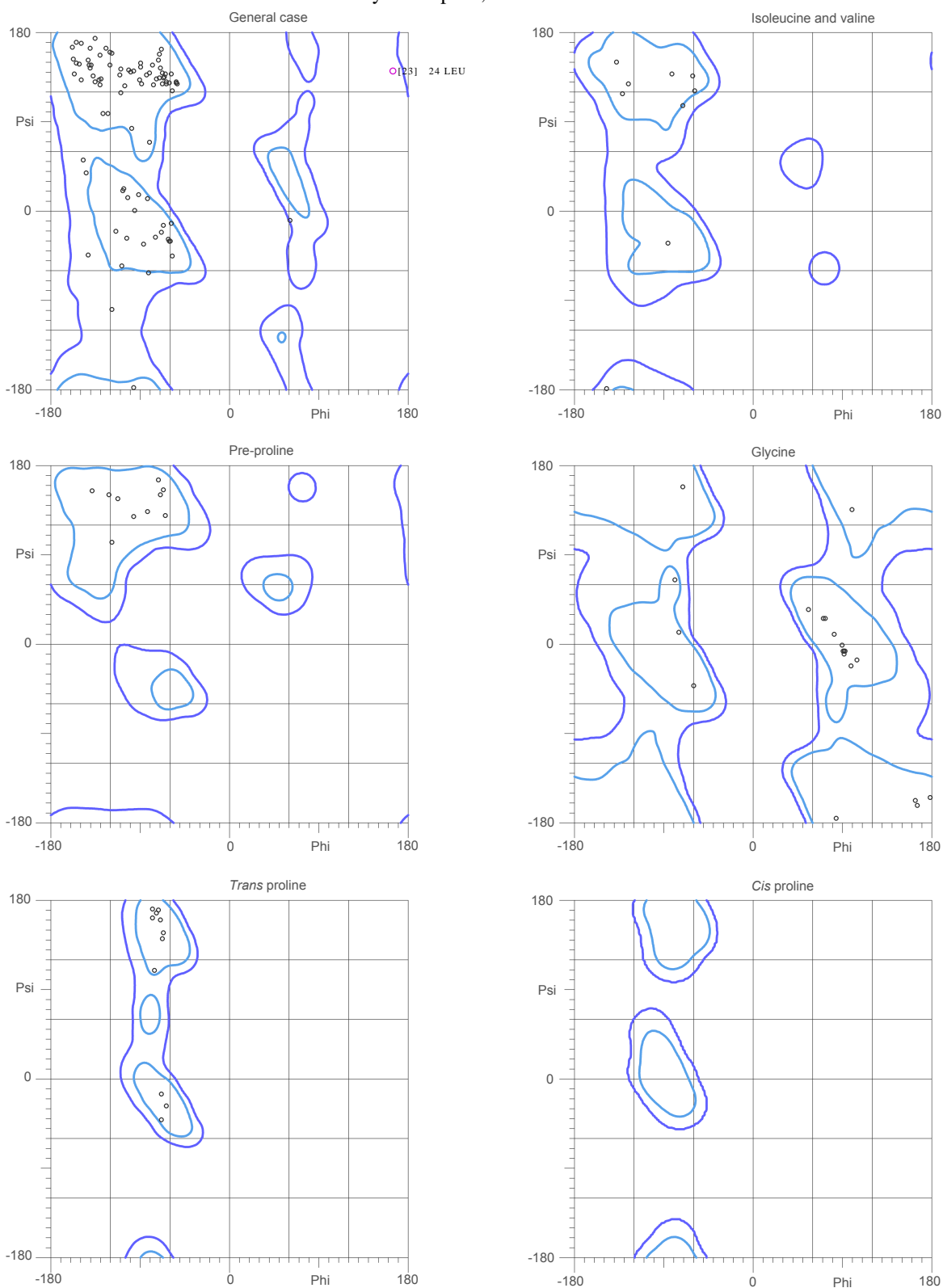
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[22] 24 LEU (168.6, 136.7)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 23



94.2% (130/138) of all residues were in favored (98%) regions.

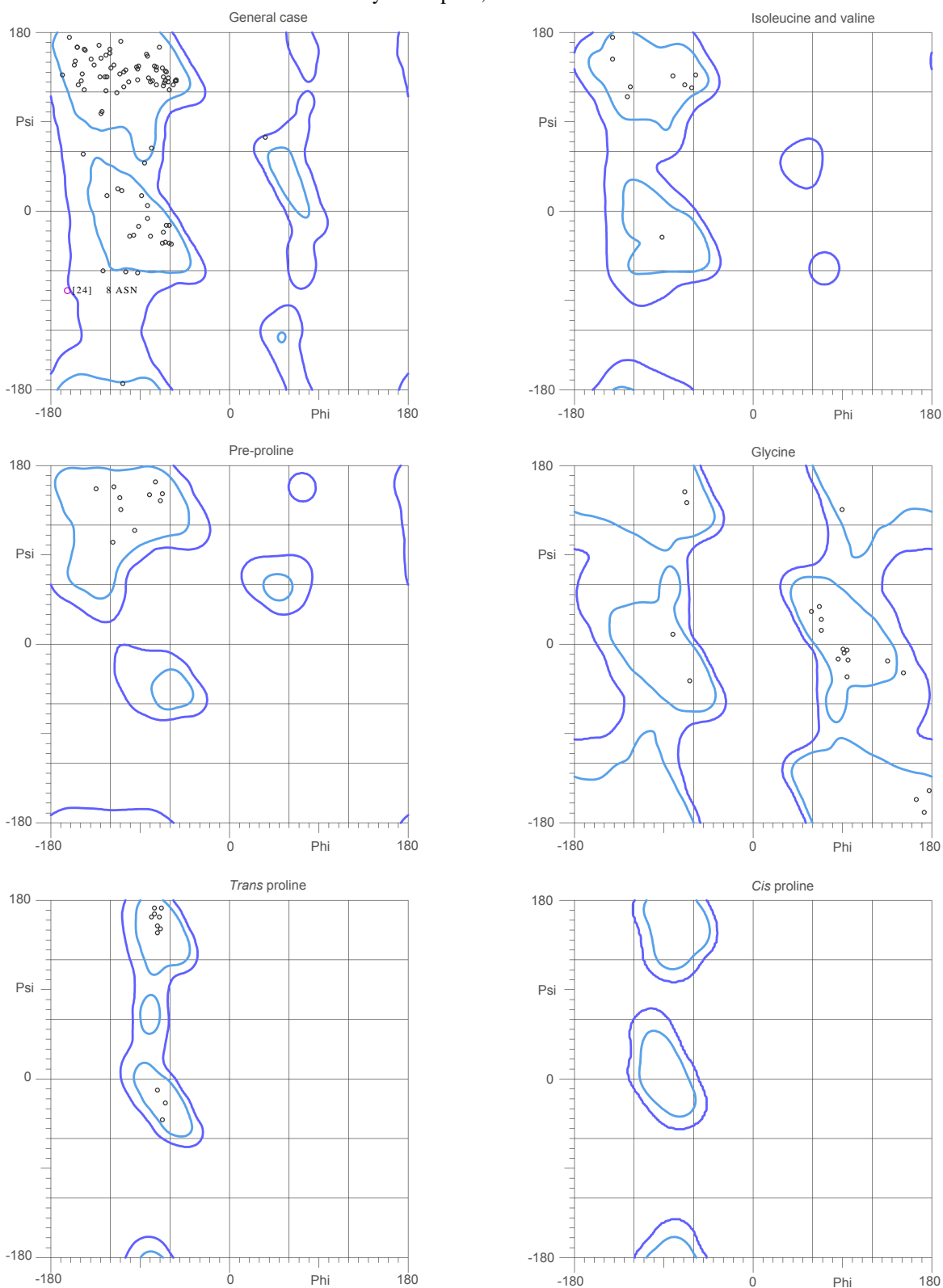
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[23] 24 LEU (165.3, 142.2)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 24



93.5% (129/138) of all residues were in favored (98%) regions.

99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[24] 8 ASN (-164.7, -80.6)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 25



94.2% (130/138) of all residues were in favored (98%) regions.

99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[25] 24 LEU (173.0, 142.7)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 26



94.2% (130/138) of all residues were in favored (98%) regions.

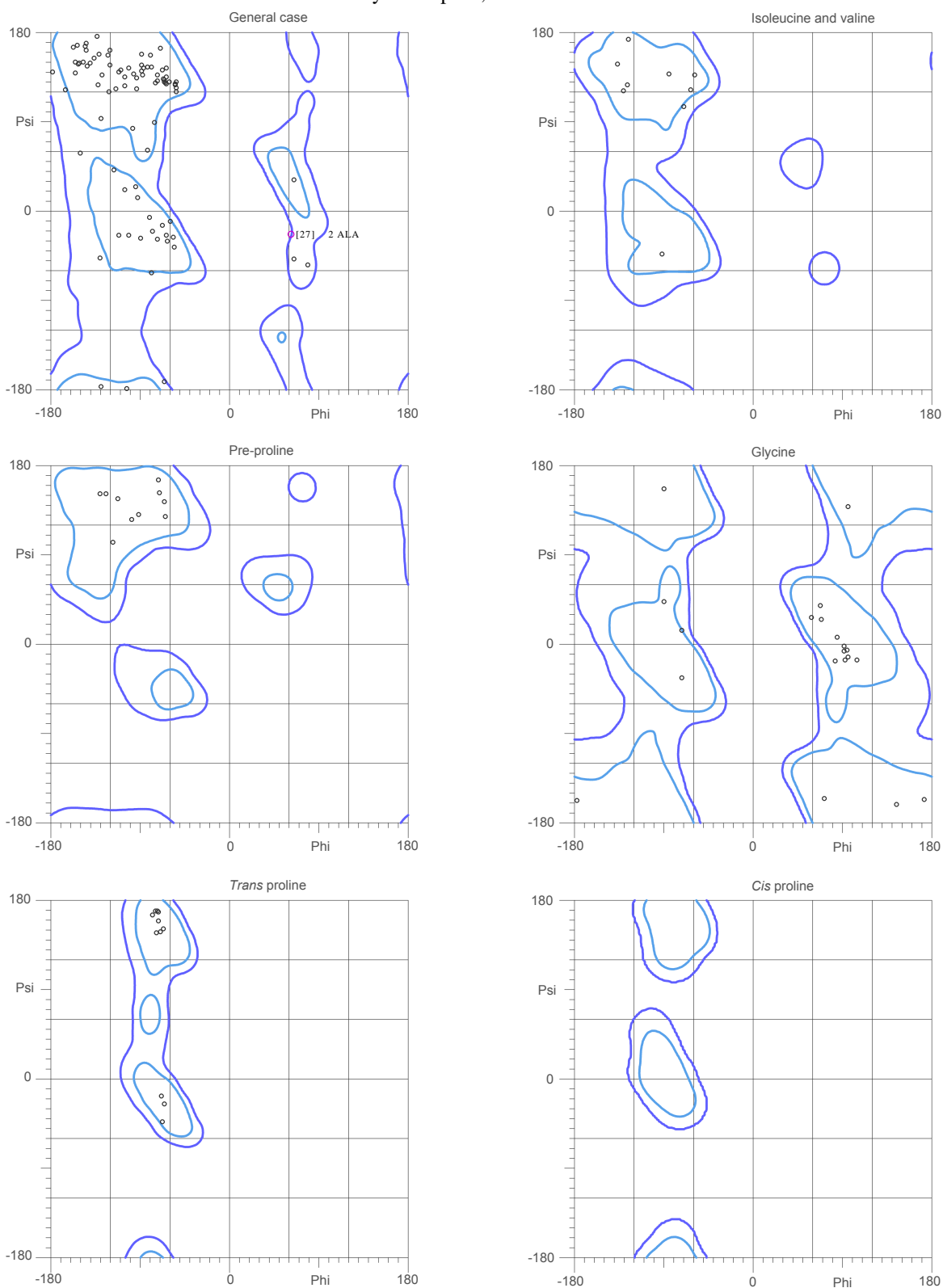
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[26] 24 LEU (62.5, 146.3)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 27



92.8% (128/138) of all residues were in favored (98%) regions.

99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[27] 2 ALA (62.0, -23.2)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 28



92.8% (128/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[28] 9 THR (24.6, 78.8)

[28] 24 LEU (66.5, 144.2)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 29



93.5% (129/138) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 30



92.8% (128/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[30] 24 LEU (153.7, 143.4)

[30] 63 ASP (30.7, -121.6)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 31



94.9% (131/138) of all residues were in favored (98%) regions.

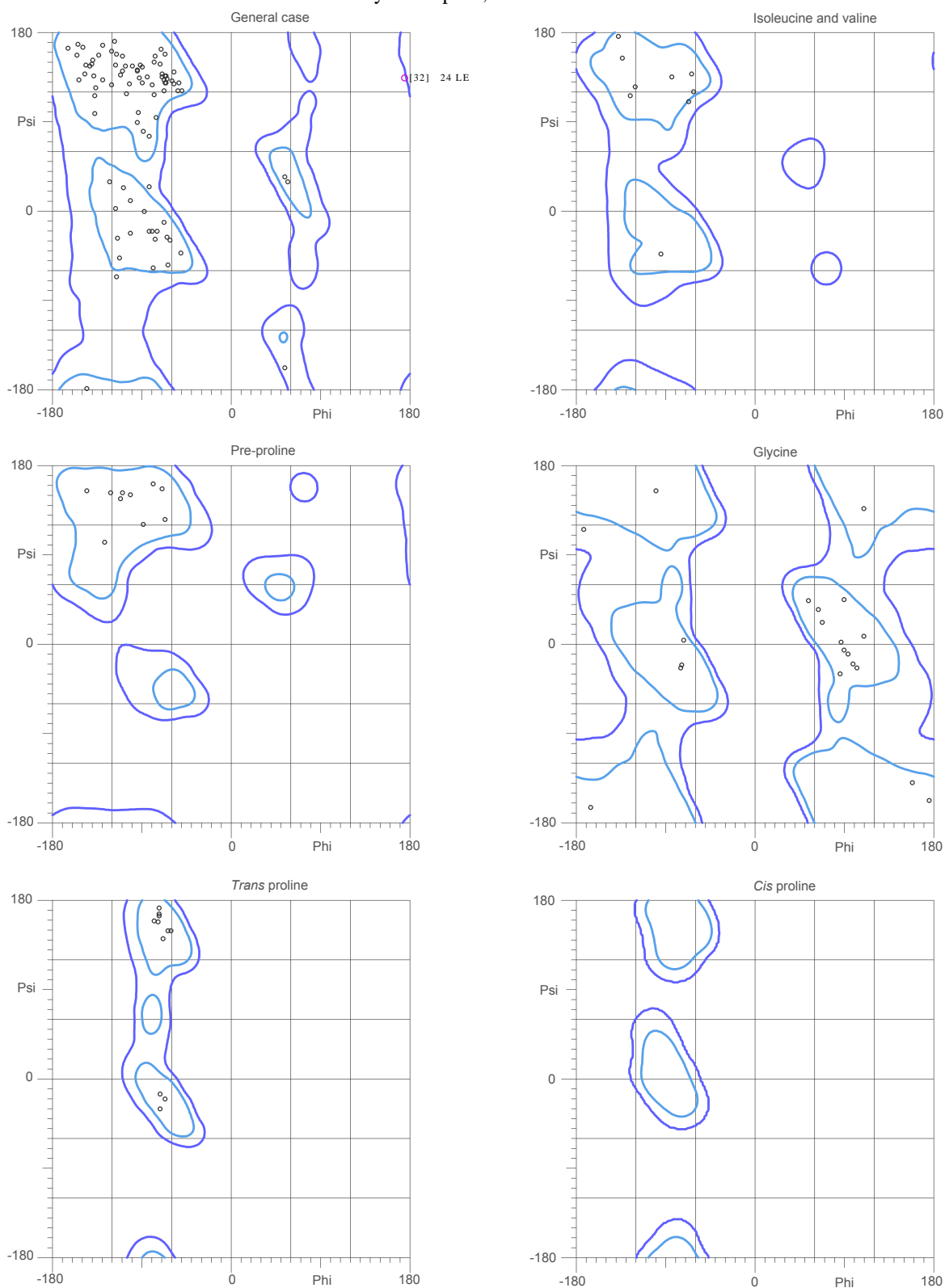
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[31] 9 THR (35.7, 78.9)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 32



96.4% (133/138) of all residues were in favored (98%) regions.

99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[32] 24 LEU (176.0, 135.2)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 33



95.7% (132/138) of all residues were in favored (98%) regions.

99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[33] 8 ASN (-156.1, -102.5)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 34



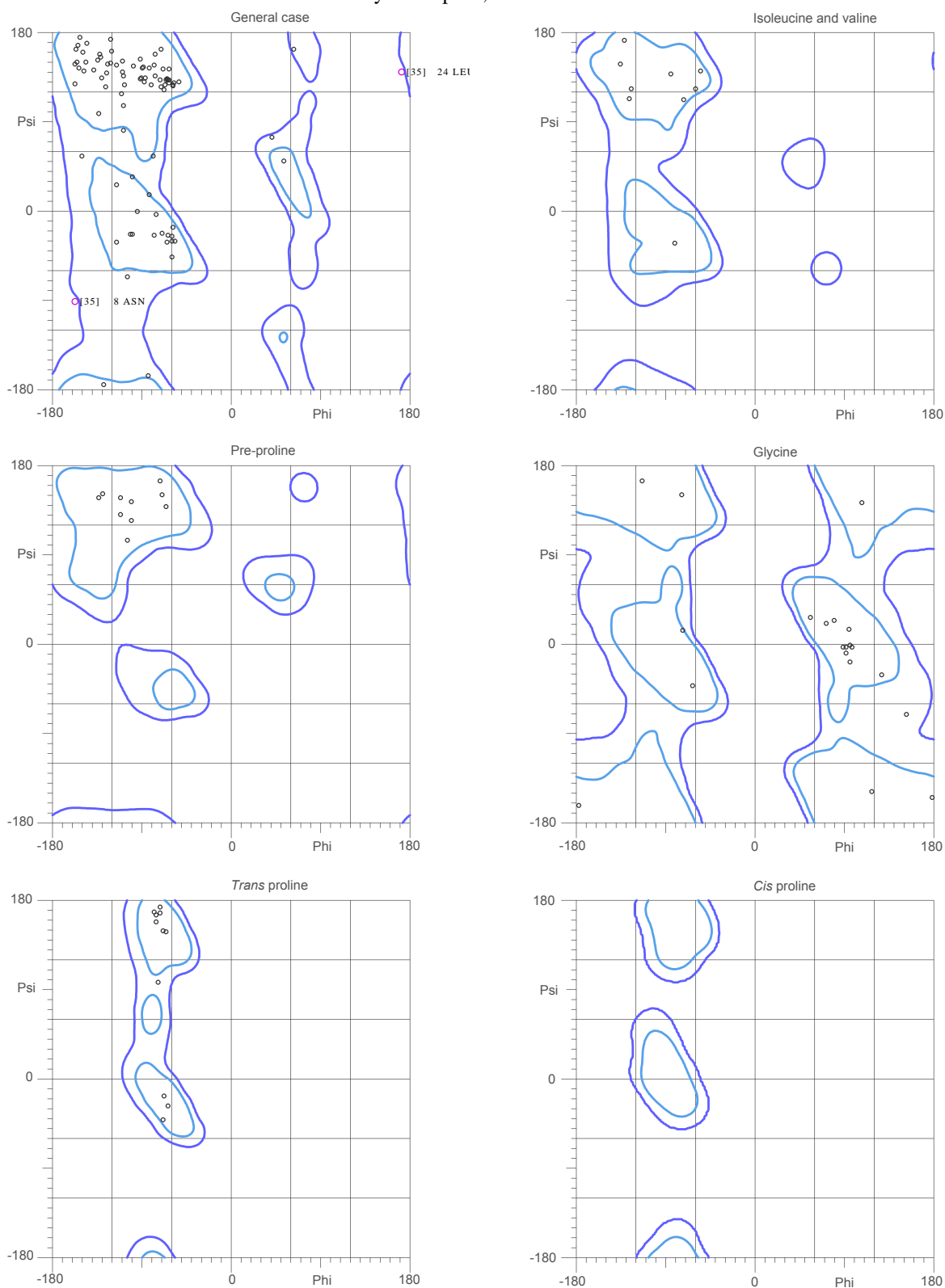
95.7% (132/138) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 35



92.0% (127/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[35] 8 ASN (-158.4, -91.8)

[35] 24 LEU (172.7, 141.6)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 36



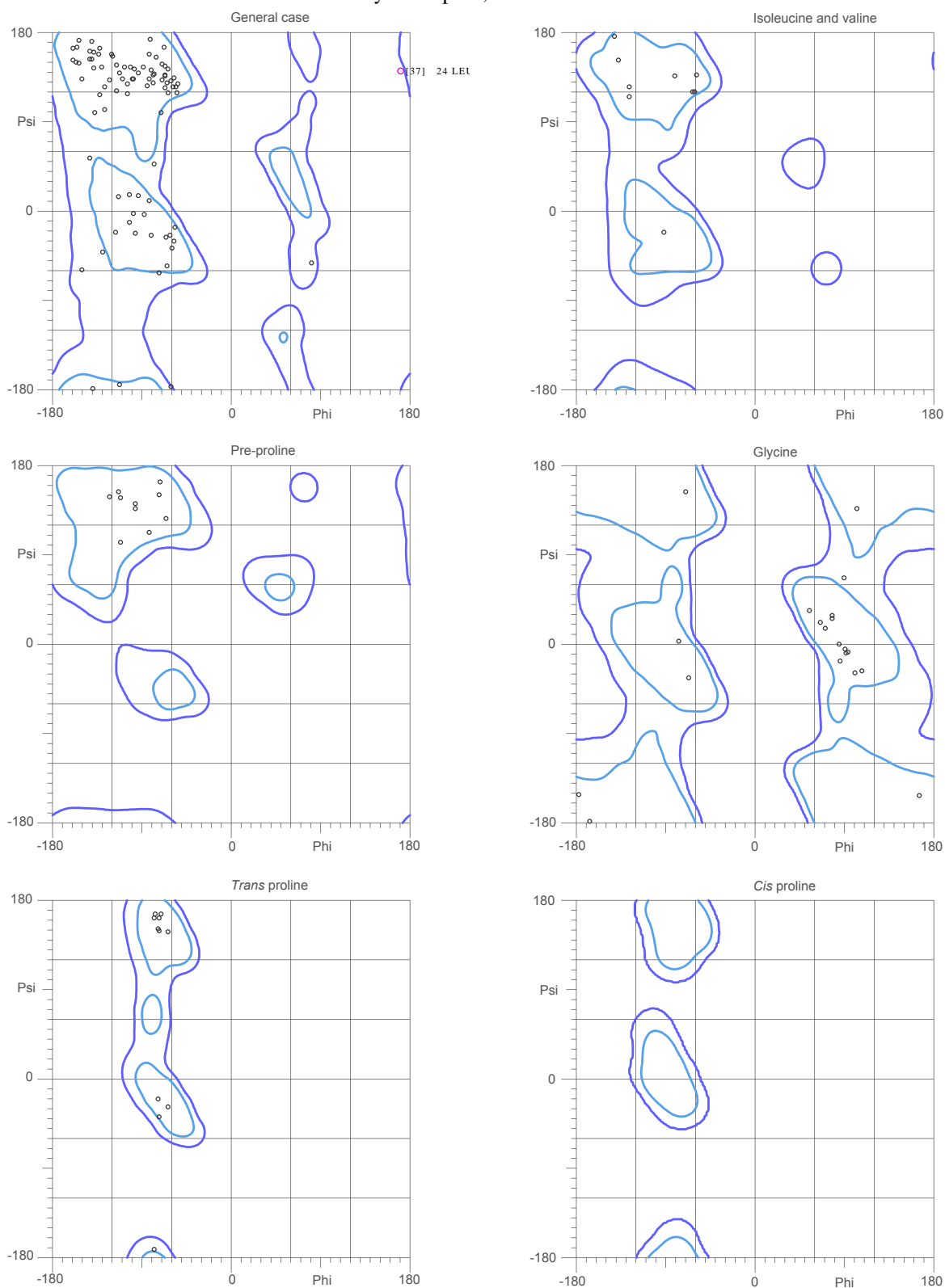
91.3% (126/138) of all residues were in favored (98%) regions.
97.8% (135/138) of all residues were in allowed (>99.8%) regions.

There were 3 outliers (phi, psi):

- [36] 8 ASN (-163.1, -86.8)
- [36] 9 THR (39.4, 79.0)
- [36] 24 LEU (173.9, 141.0)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 37



92.0% (127/138) of all residues were in favored (98%) regions.

99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[37] 24 LEU (171.3, 142.2)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 38



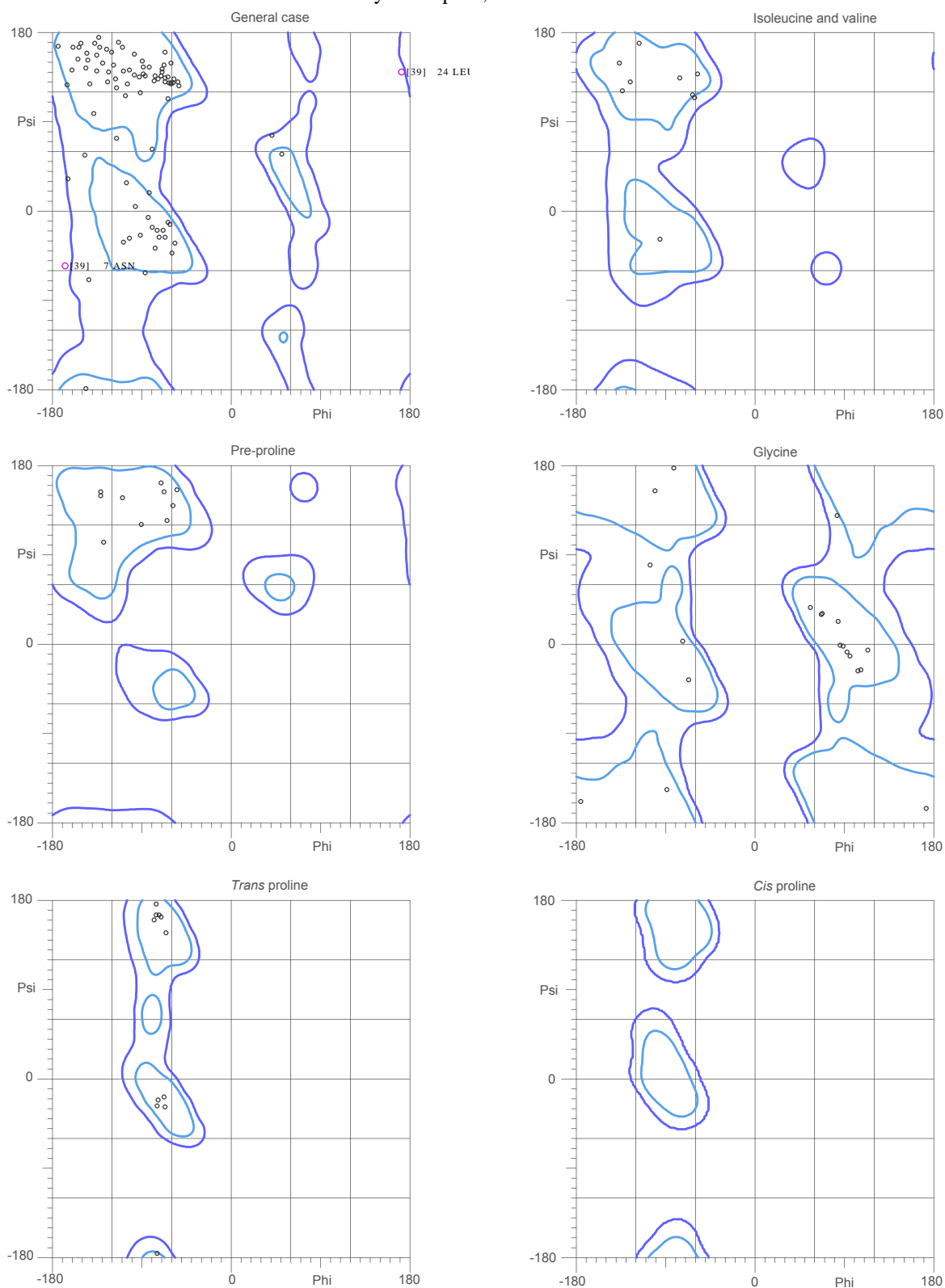
94.2% (130/138) of all residues were in favored (98%) regions.

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

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 39



90.6% (125/138) of all residues were in favored (98%) regions.

98.6% (136/138) of all residues were in allowed (>99.8%) regions.

There were 2 outliers (phi, psi):

[39] 7 ASN (-168.7, -55.3)

[39] 24 LEU (172.3, 141.7)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 40



94.2% (130/138) of all residues were in favored (98%) regions.

99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[40] 63 ASP (38.5, -140.8)