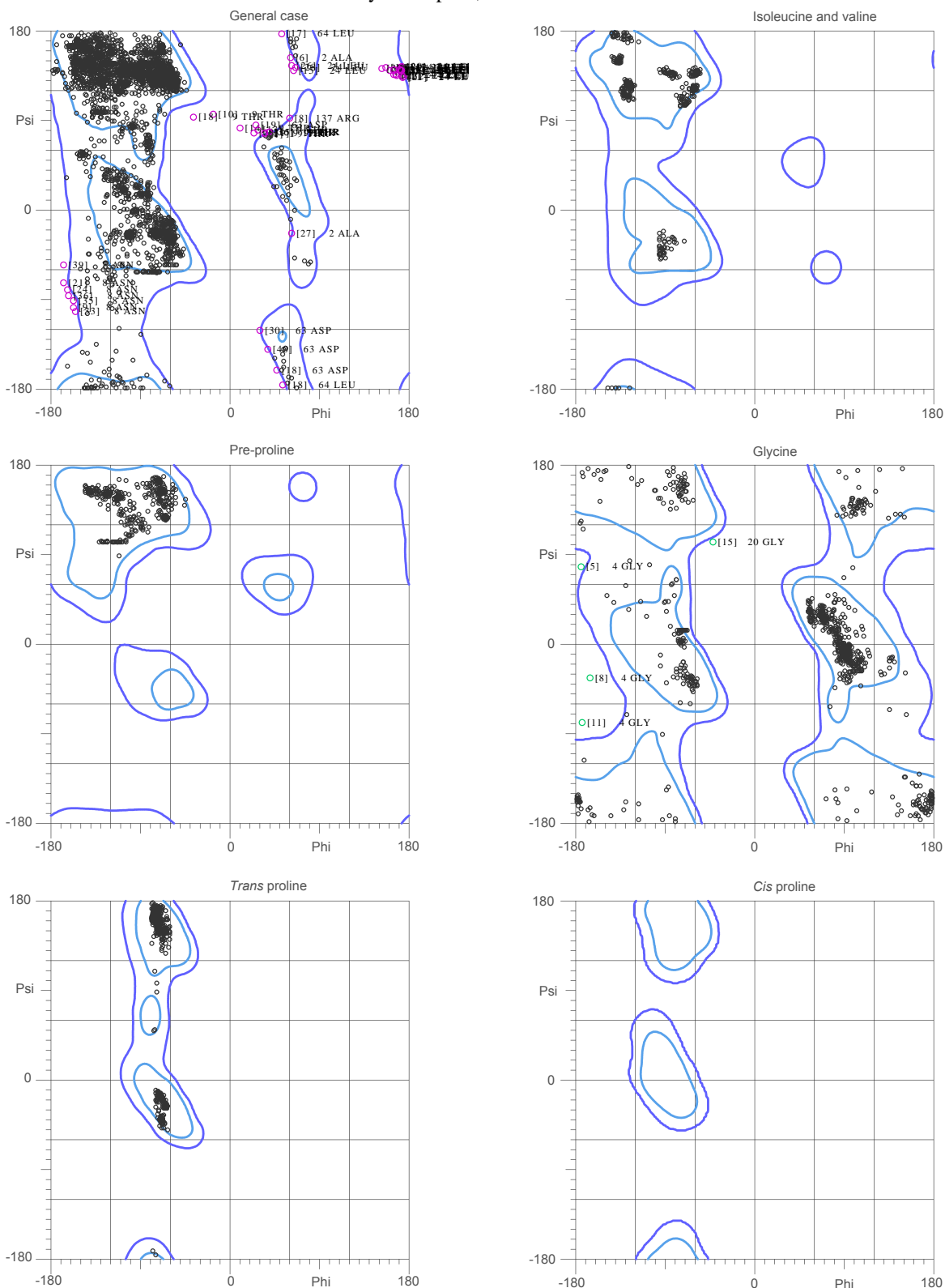


MolProbity Ramachandran analysis

6yi3.H.pdb, all models



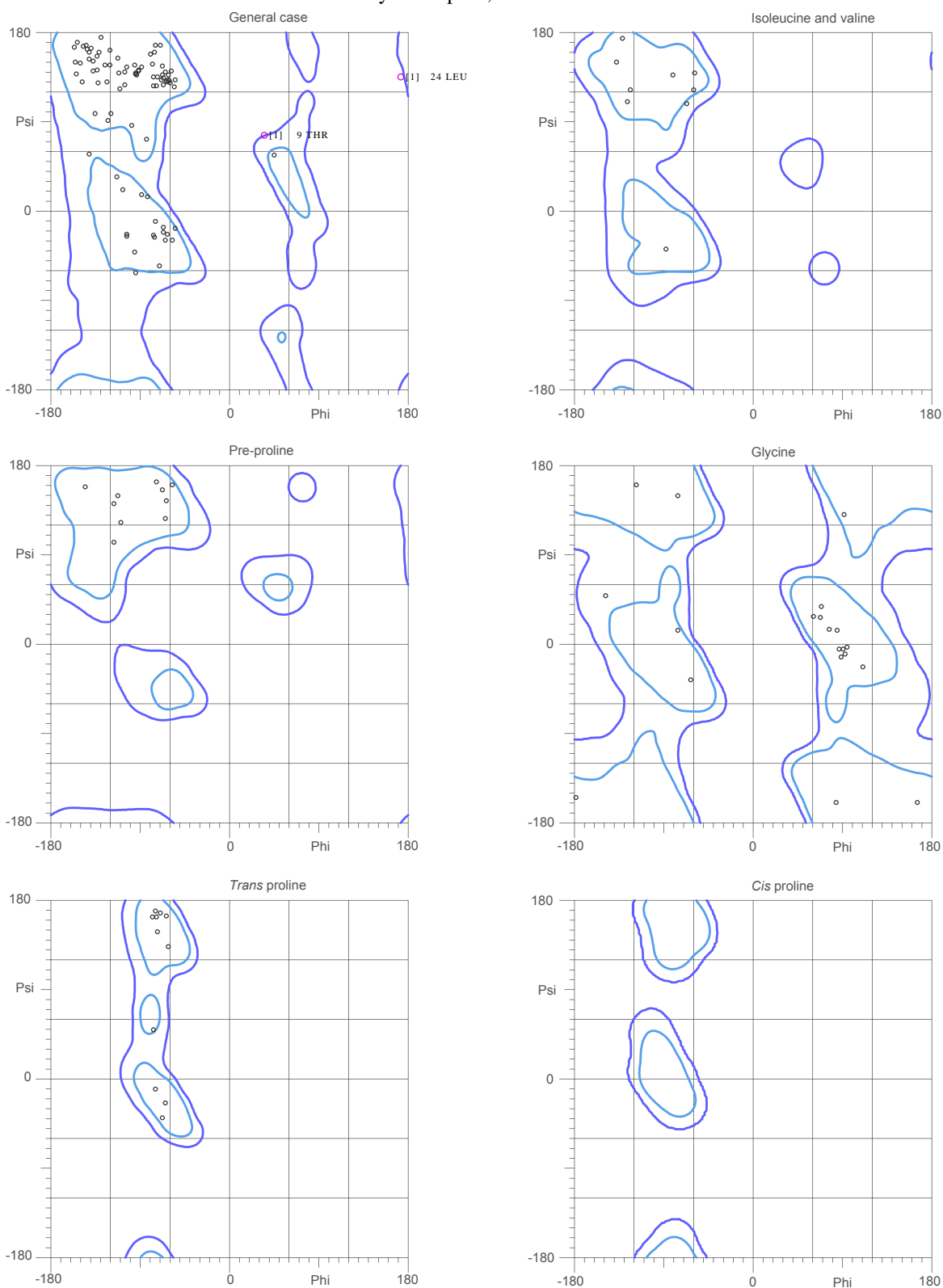
94.0% (5189/5520) of all residues were in favored (90%) regions.
9% (508/5520) of all residues were in allowed (5%) regions.

There were 52 outliers (phi, psi):

(1) 9 THR (35.1, 77.1)
(2) 24 LEU (175.8, 158.9)
(3) 4 GLY (175.2, 79.1)
(4) 24 LEU (168.5, 141.9)
(5) 2 ALA (161.9, 154.2)
(6) 24 LEU (167.5, 137.4)
(7) 4 GLY (168.5, 13.7)
(8) 24 LEU (177.5, 148.5)
(9) 137 ARG (168.5, 93.8)
(10) 8 ASN (175.5, 106.5)
(11) 24 LEU (167.5, 137.4)
(12) 4 GLY (175.2, 79.1)
(13) 24 LEU (177.5, 148.5)
(14) 9 THR (25.0, 39.1)
(15) 24 LEU (161.9, 154.2)
(16) 9 THR (168.5, 93.8)
(17) 24 LEU (177.5, 148.5)
(18) 20 GLY (162.1, 103.0)
(19) 24 LEU (168.5, 141.9)
(20) 40 LEU (152.9, 179.7)
(21) 9 THR (177.2, 164.9)
(22) 24 LEU (157.2, 144.4)
(23) 43 ASP (174.6, 161.5)
(24) 40 LEU (174.6, 161.5)
(25) 43 ASP (168.5, 94.3)
(26) 43 ASP (177.7, 104.9)
(27) 8 ASN (168.5, 93.8)
(28) 43 ASP (168.5, 94.3)
(29) 8 ASN (168.5, 93.8)
(30) 24 LEU (168.5, 141.9)
(31) 8 ASN (168.5, 93.8)
(32) 24 LEU (168.5, 141.9)
(33) 8 ASN (168.5, 93.8)
(34) 24 LEU (168.5, 141.9)
(35) 8 ASN (168.5, 93.8)
(36) 24 LEU (168.5, 141.9)
(37) 8 ASN (168.5, 93.8)
(38) 24 LEU (168.5, 141.9)
(39) 8 ASN (168.5, 93.8)
(40) 24 LEU (168.5, 141.9)
(41) 8 ASN (168.5, 93.8)
(42) 24 LEU (168.5, 141.9)
(43) 8 ASN (168.5, 93.8)
(44) 24 LEU (168.5, 141.9)
(45) 8 ASN (168.5, 93.8)
(46) 24 LEU (168.5, 141.9)
(47) 8 ASN (168.5, 93.8)
(48) 24 LEU (168.5, 141.9)
(49) 8 ASN (168.5, 93.8)
(50) 24 LEU (168.5, 141.9)

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



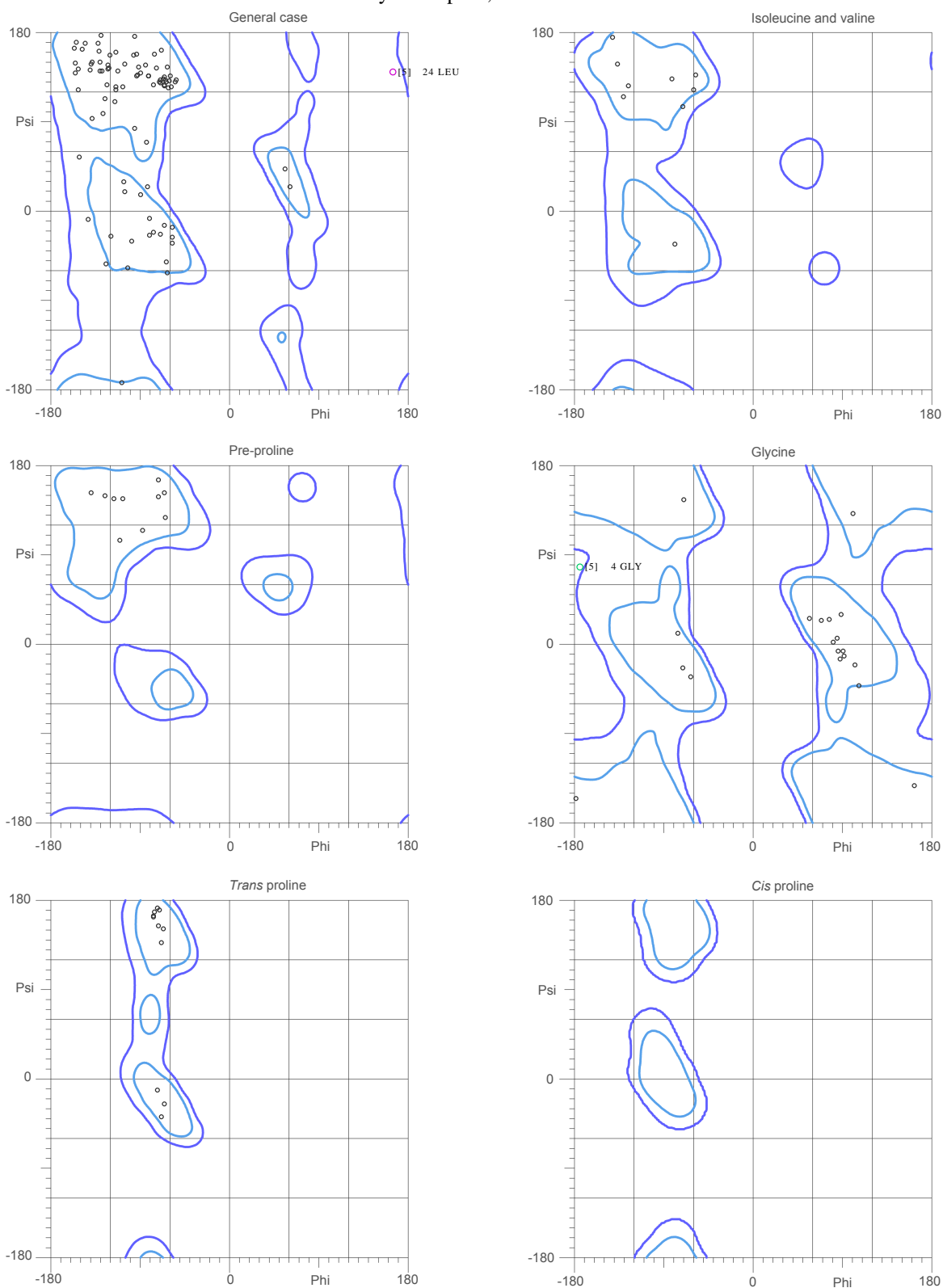
94.2% (130/138) of all residues were in favored (98%) regions.

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



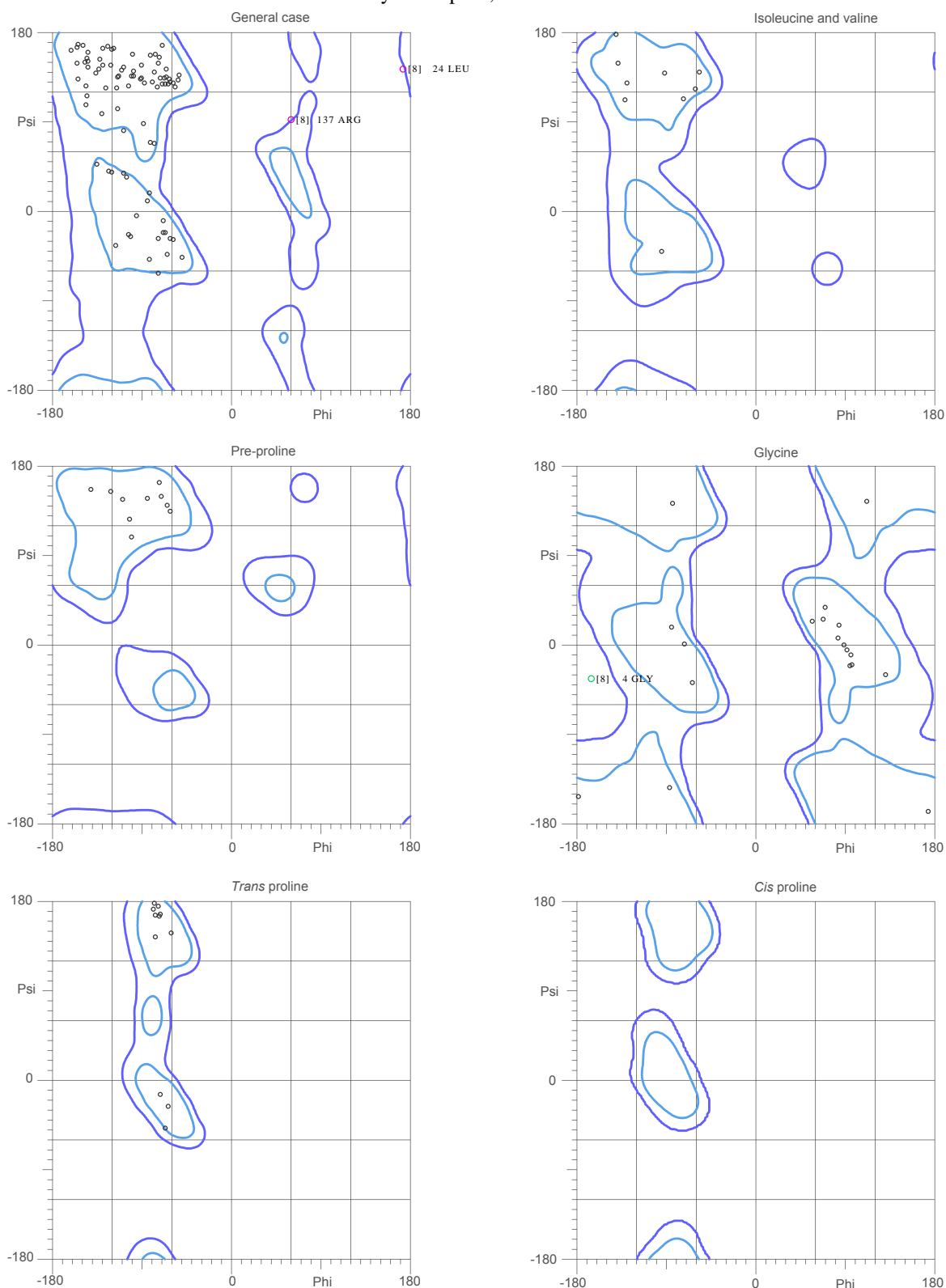
94.2% (130/138) of all residues were in favored (98%) regions.

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.

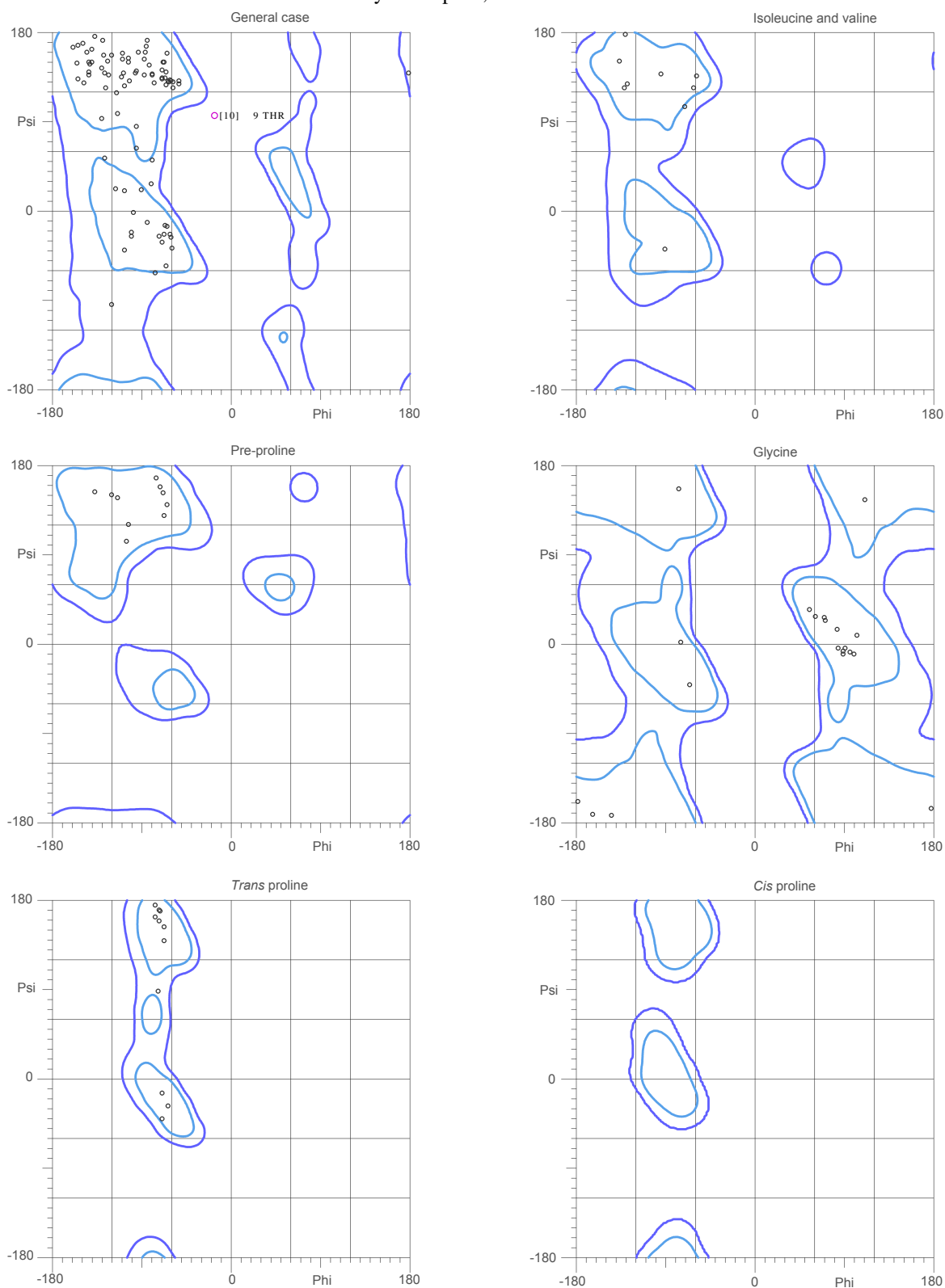
There were 2 outliers (phi, psi):

[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.

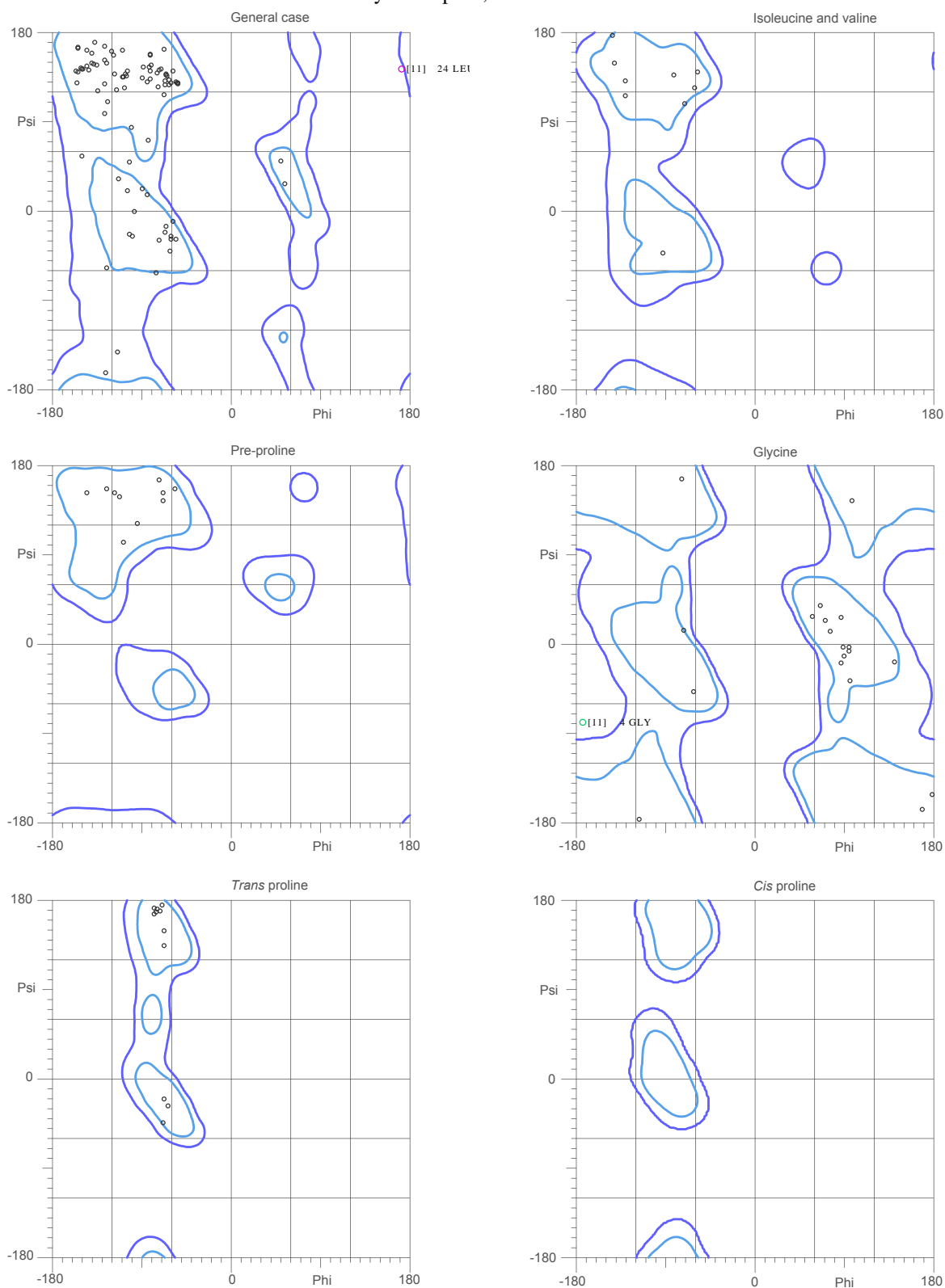
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

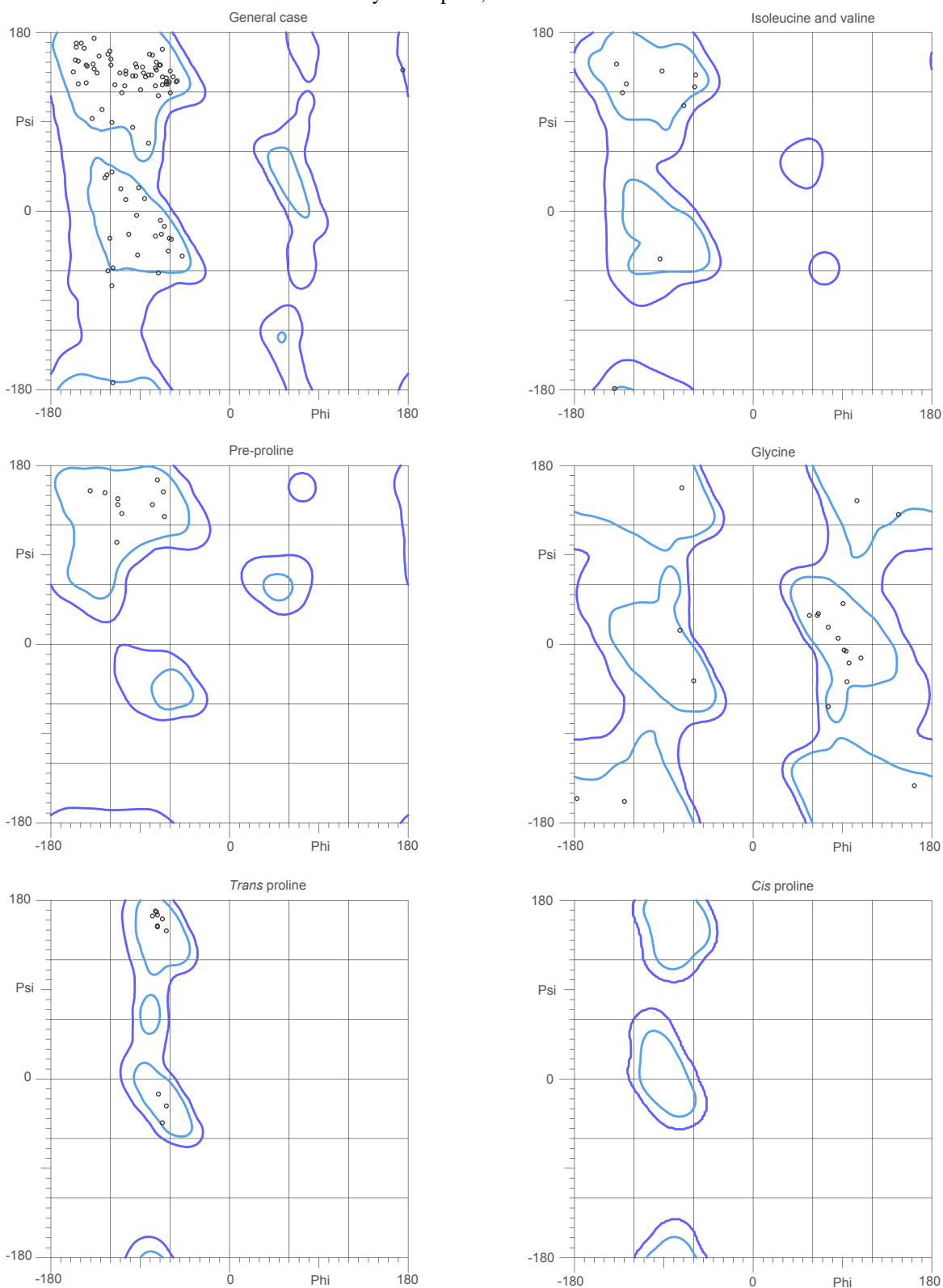
There were 2 outliers (phi, psi):

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

[11] 24 LEU (172.6, 144.8)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 12



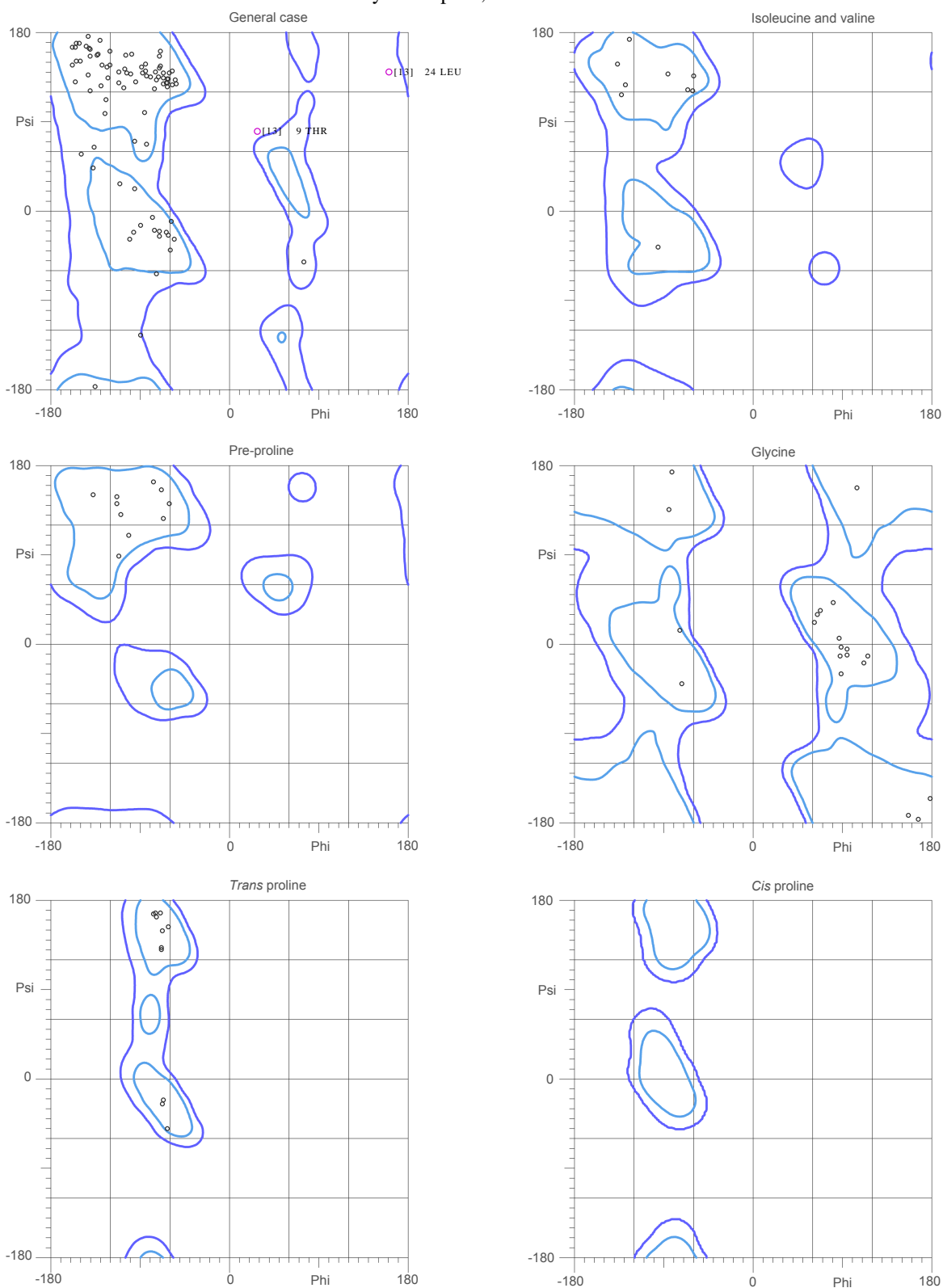
97.1% (134/138) of all residues were in favored (98%) regions.

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.

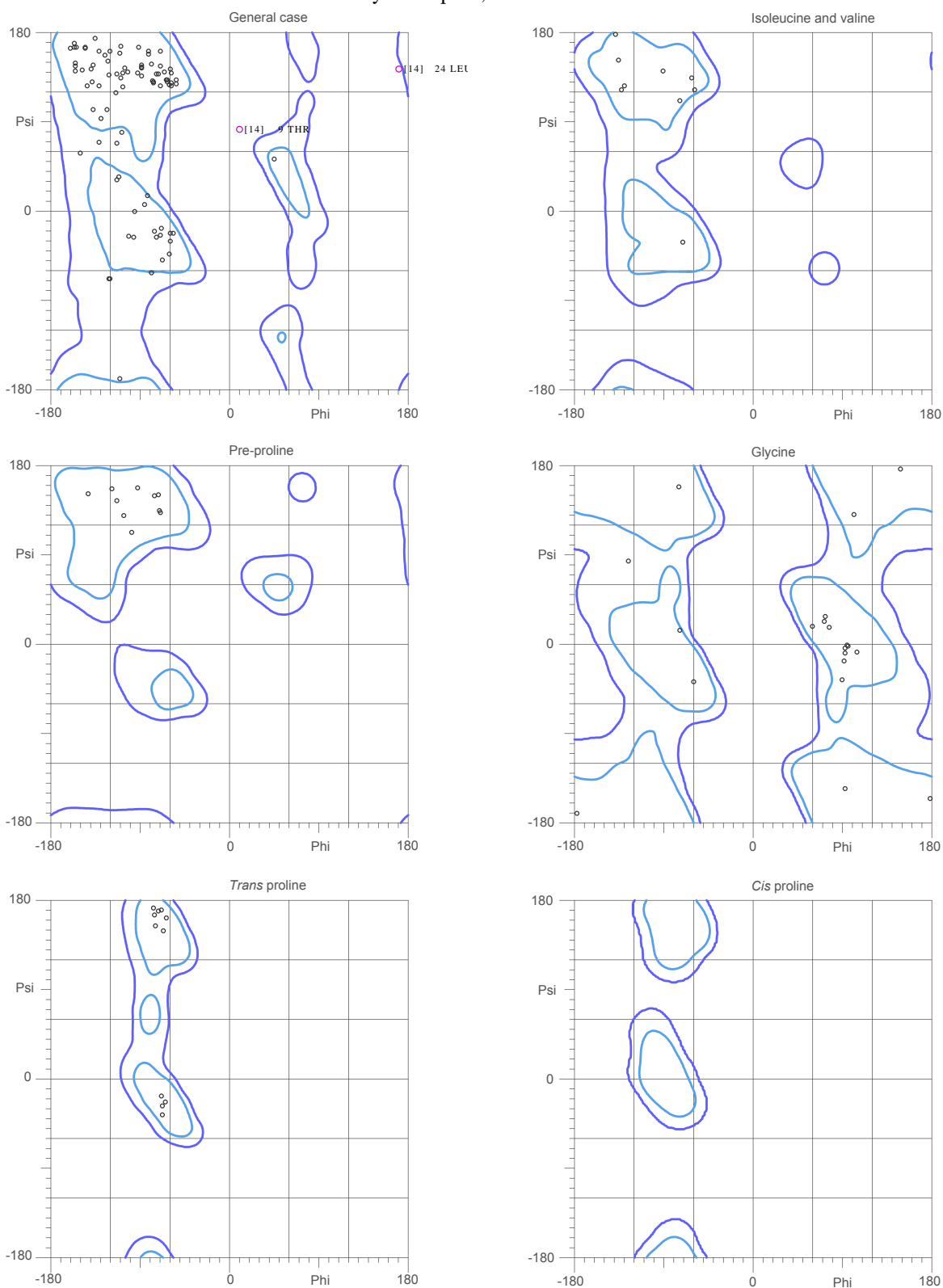
There were 2 outliers (phi, psi):

[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.

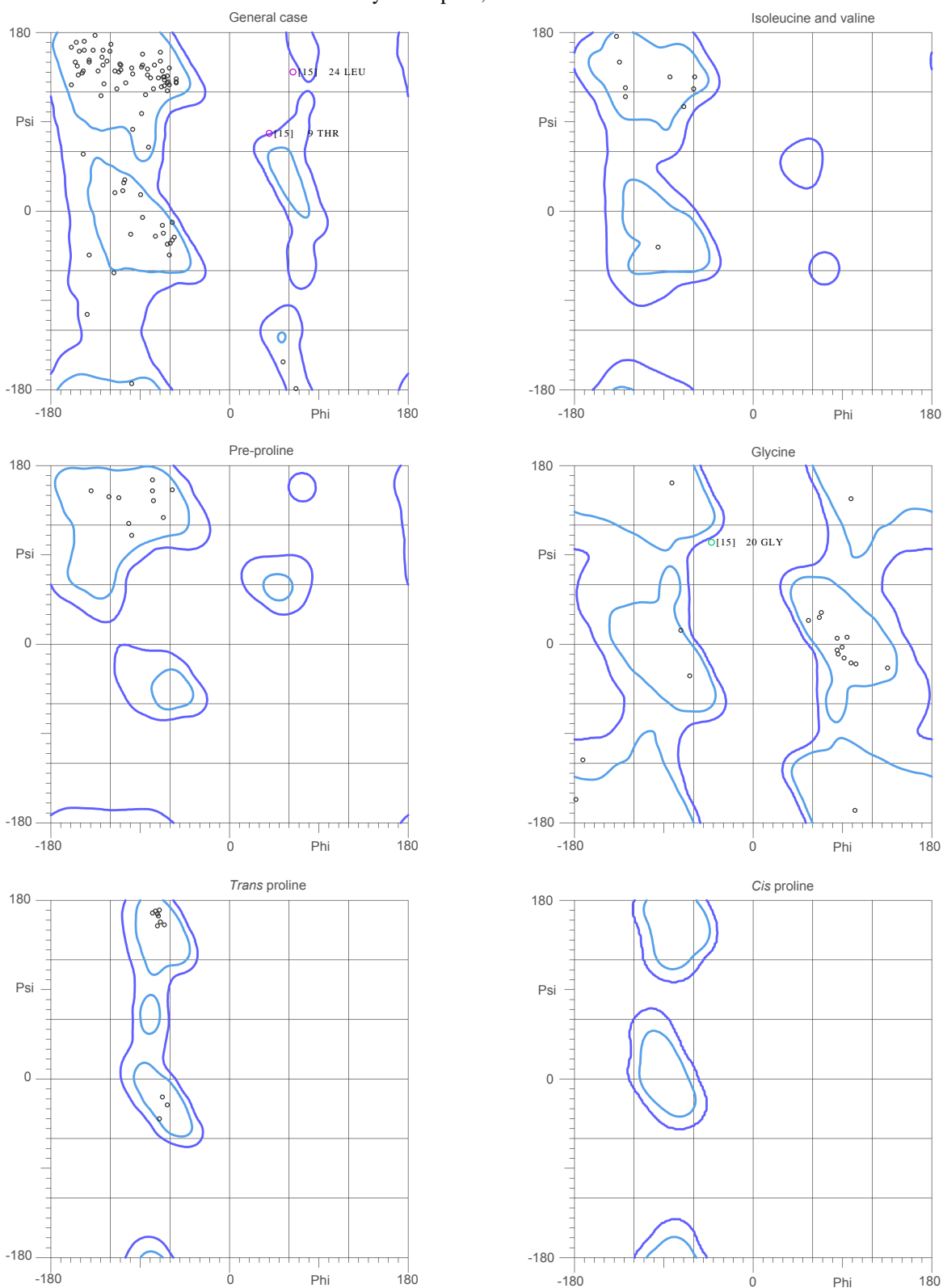
There were 2 outliers (phi, psi):

[14] 9 THR (10.2, 83.8)

[14] 24 LEU (171.6, 144.2)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 15



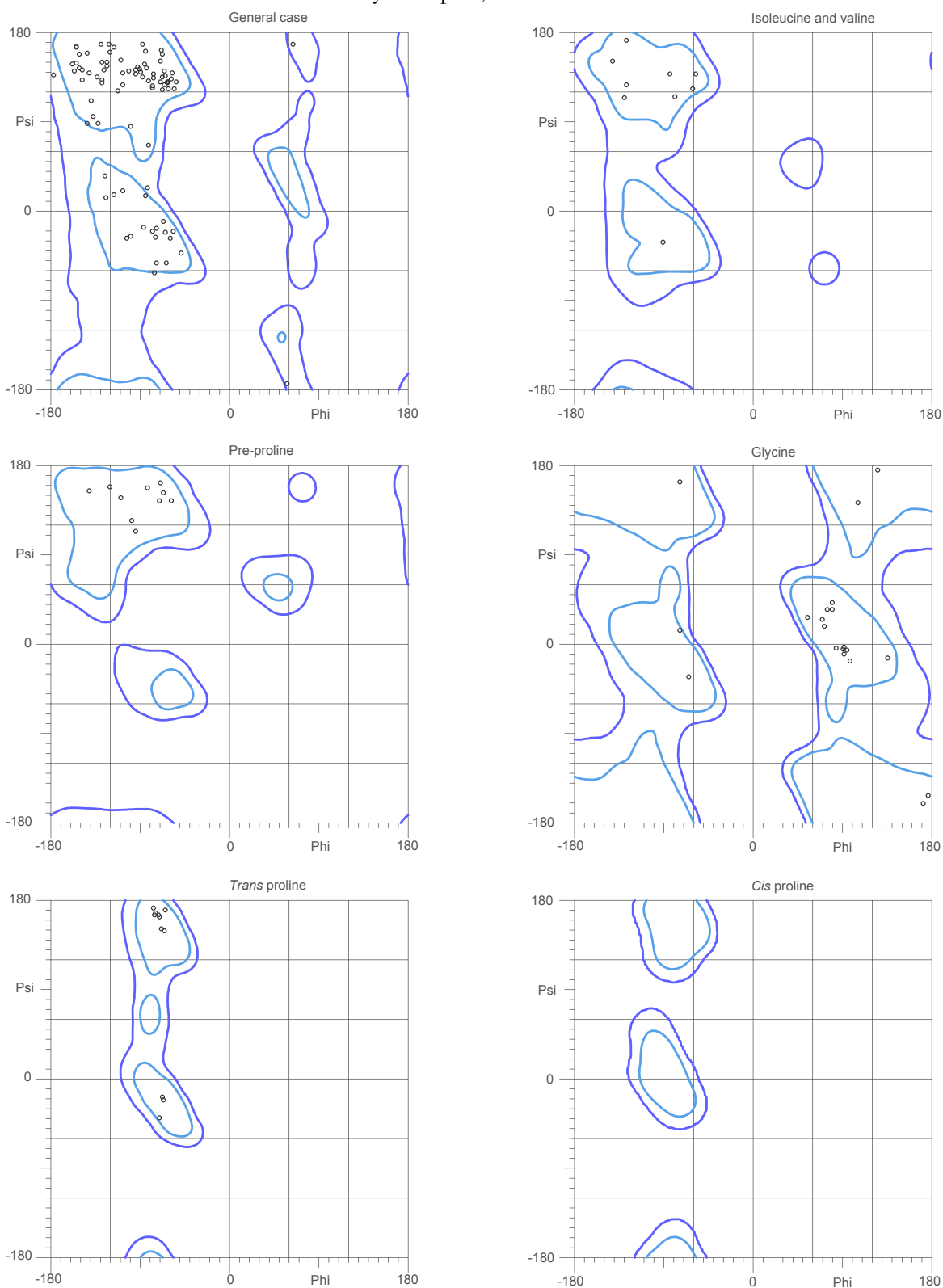
92.0% (127/138) of all residues were in favored (98%) regions.
97.8% (135/138) of all residues were in allowed (>99.8%) regions.

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.

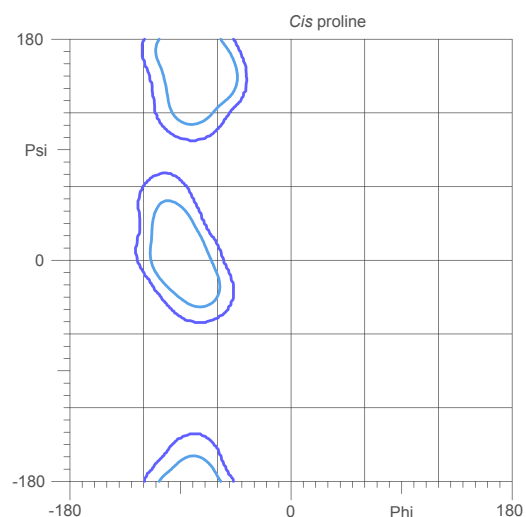
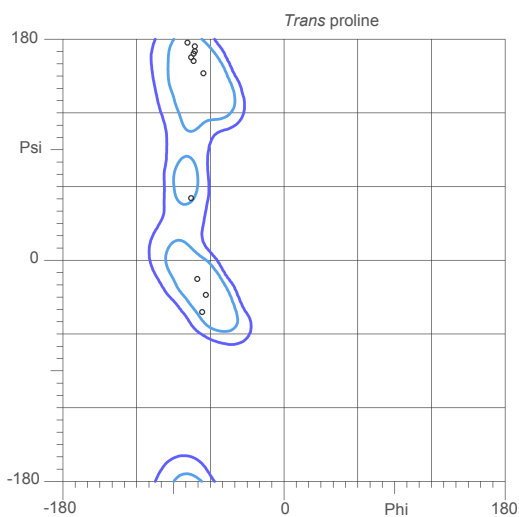
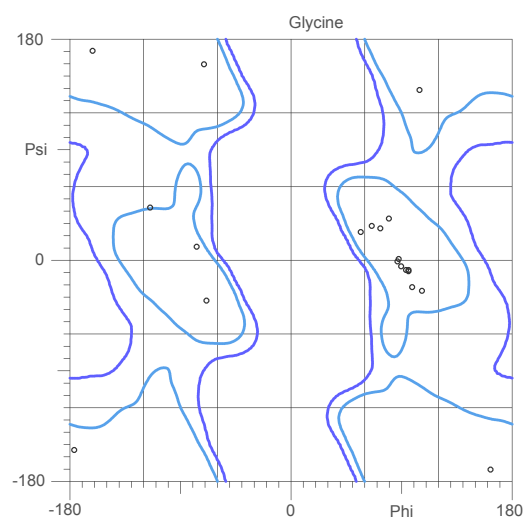
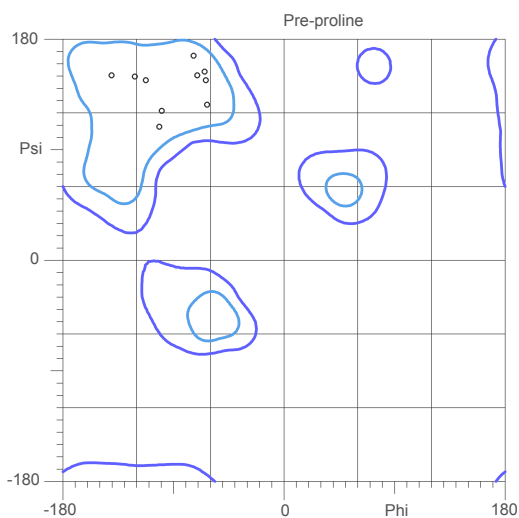
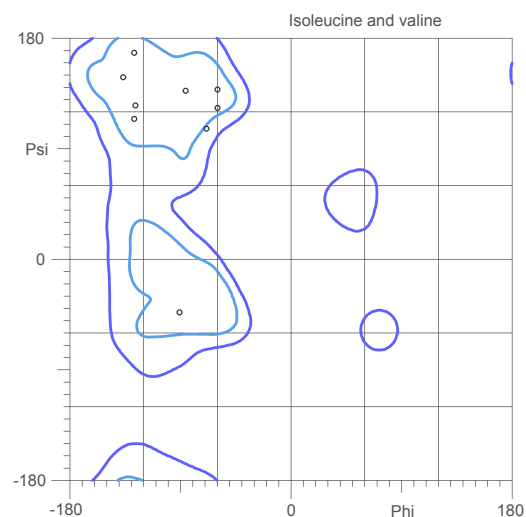
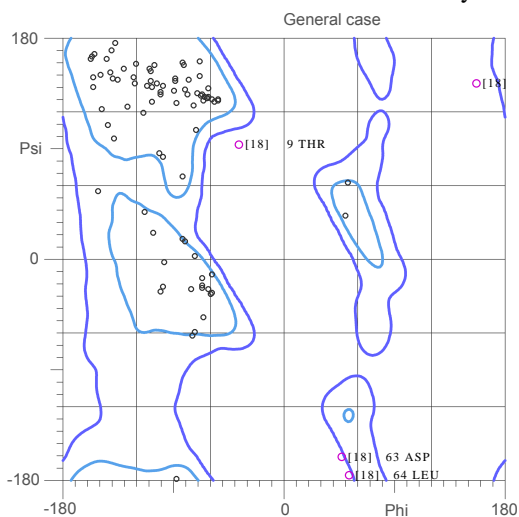
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[17] 64 LEU (52.9, 178.7)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 18



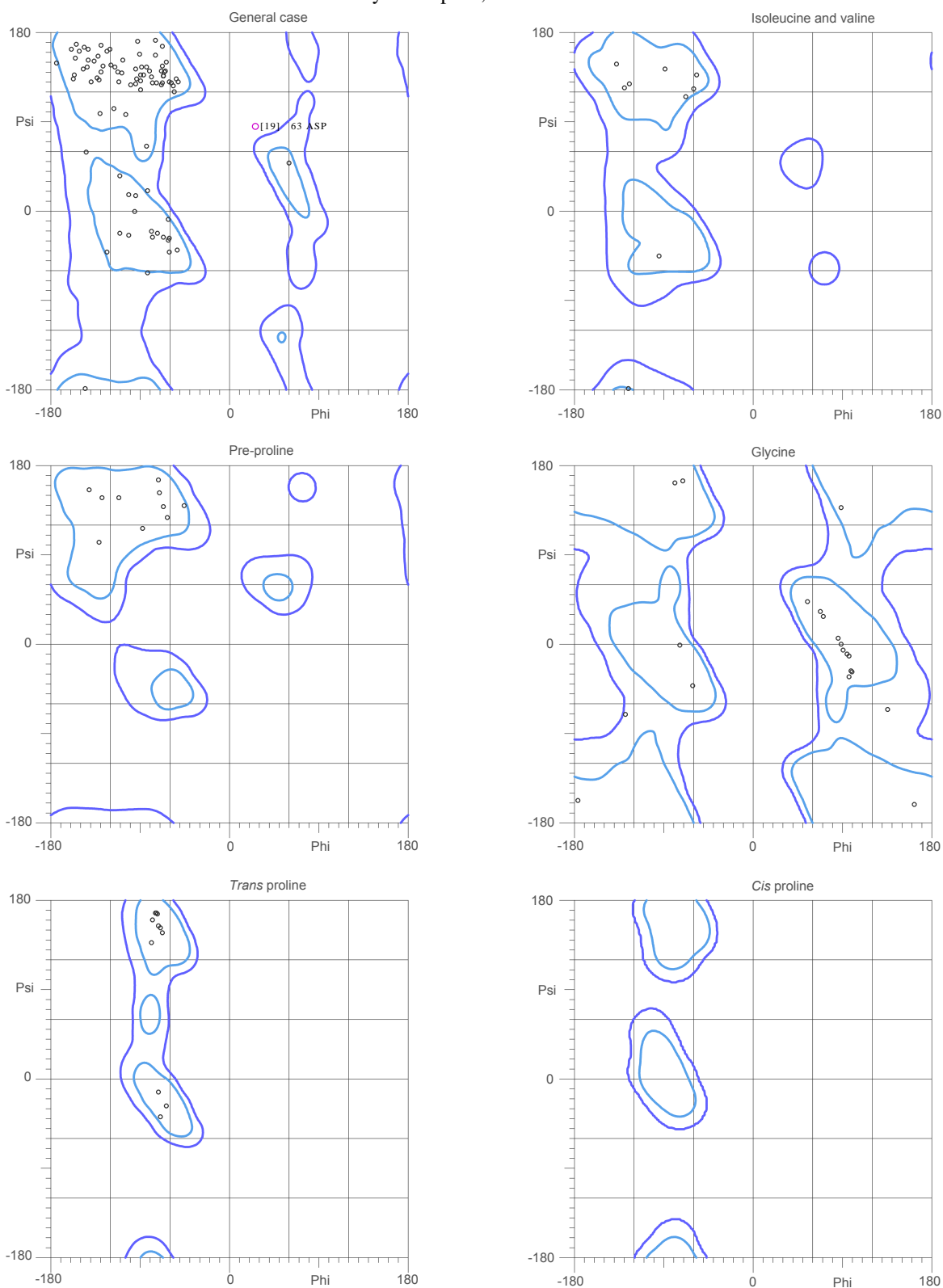
93.5% (129/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

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.

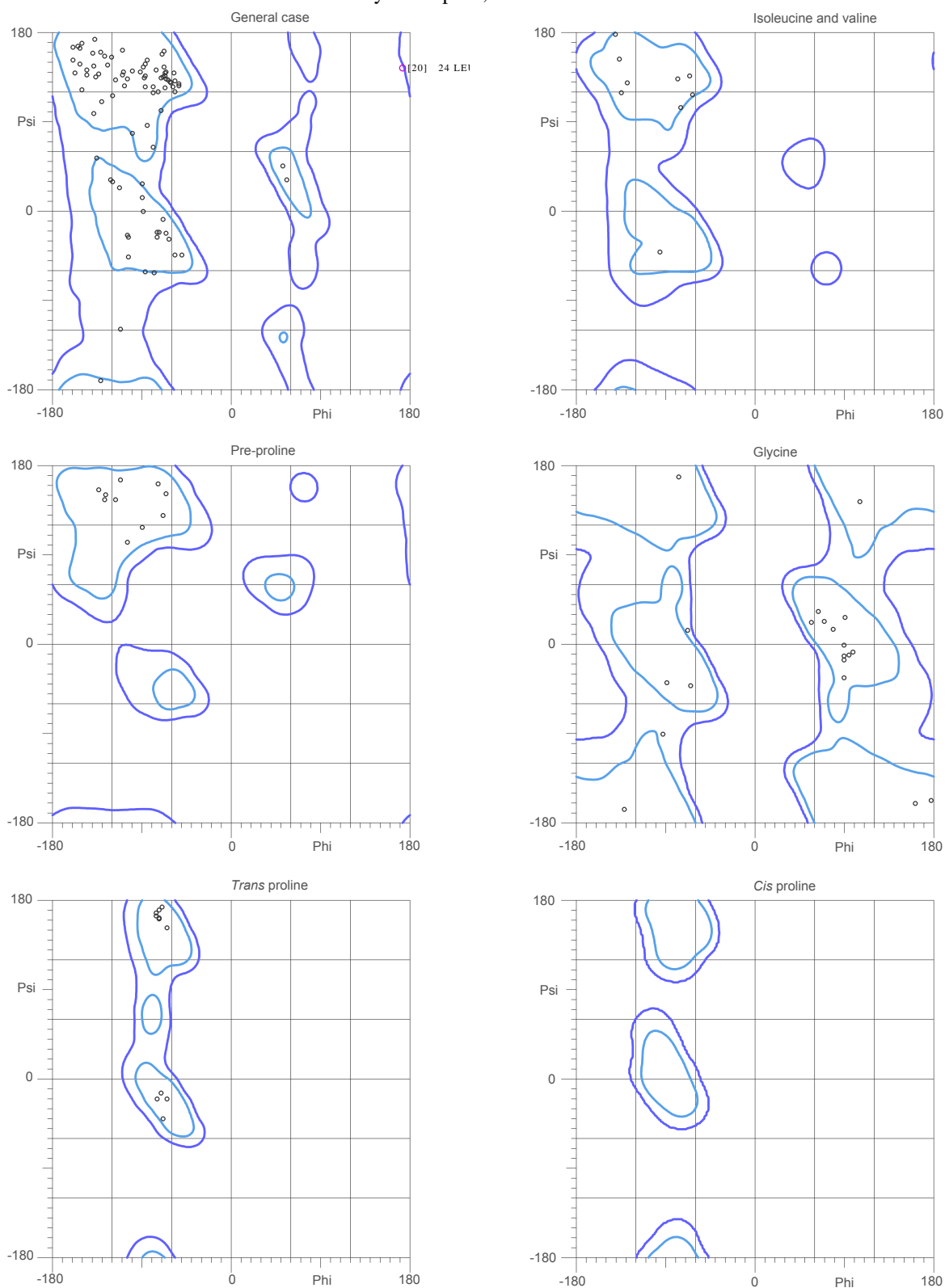
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

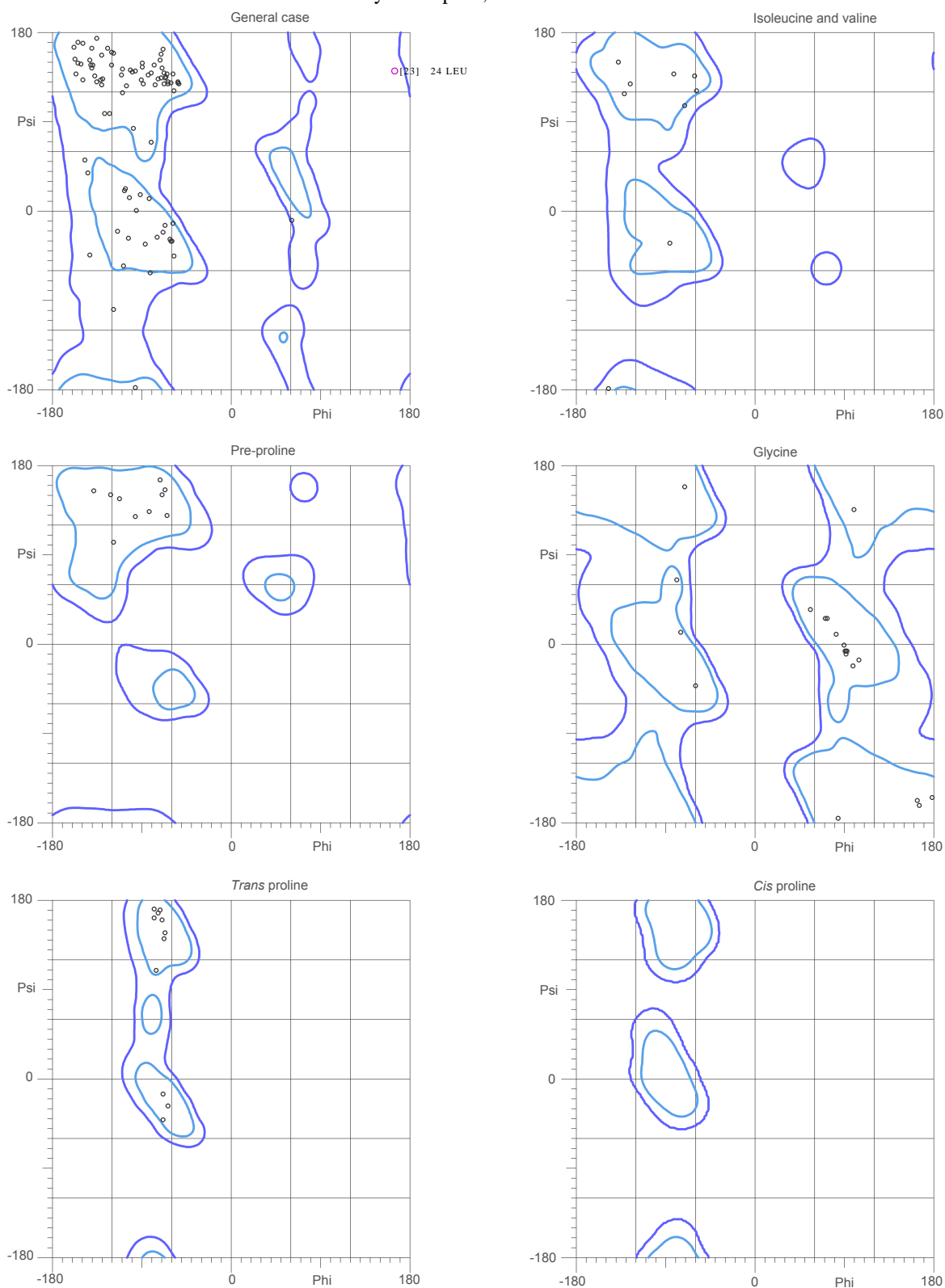
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

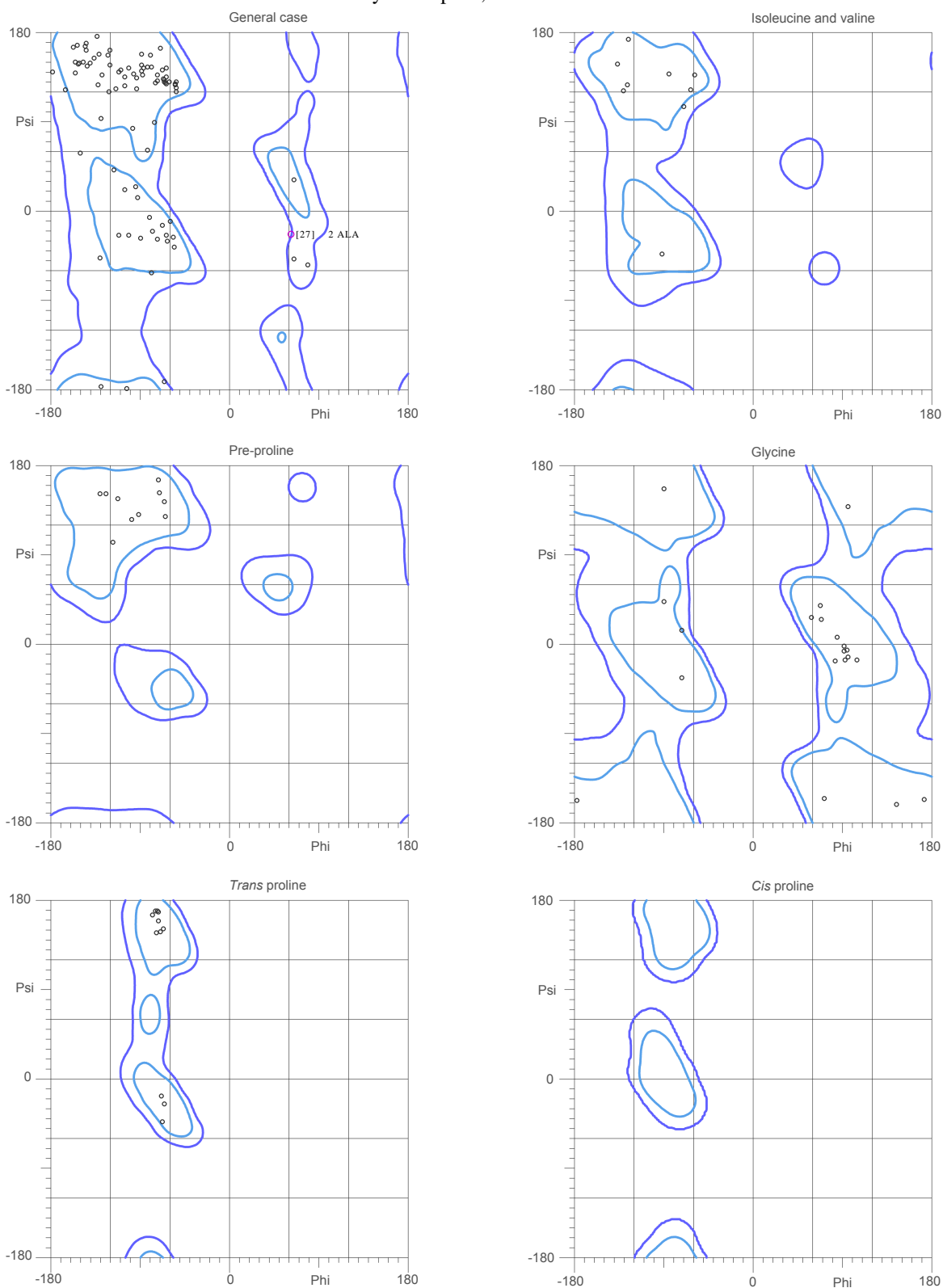
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

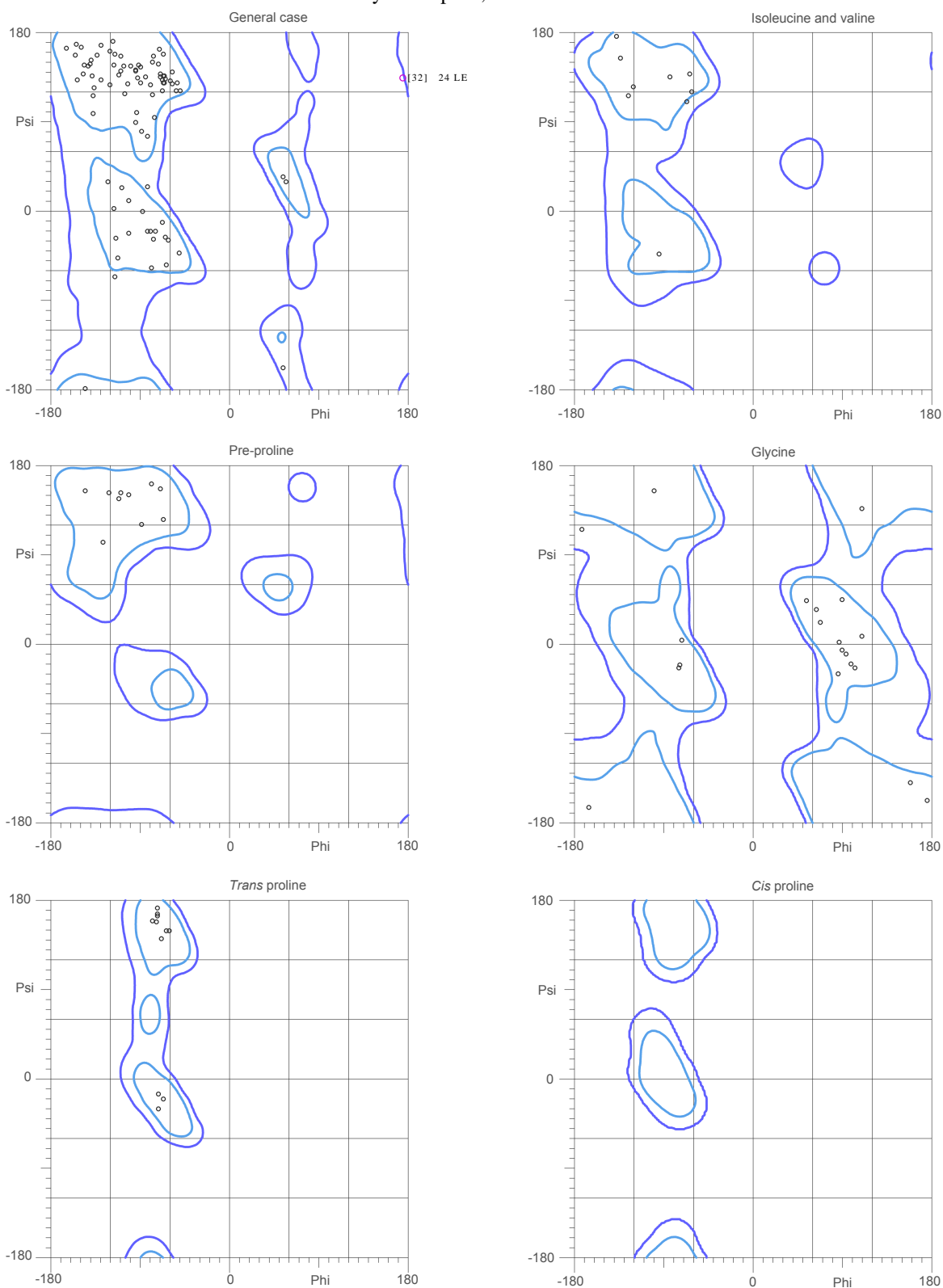
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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



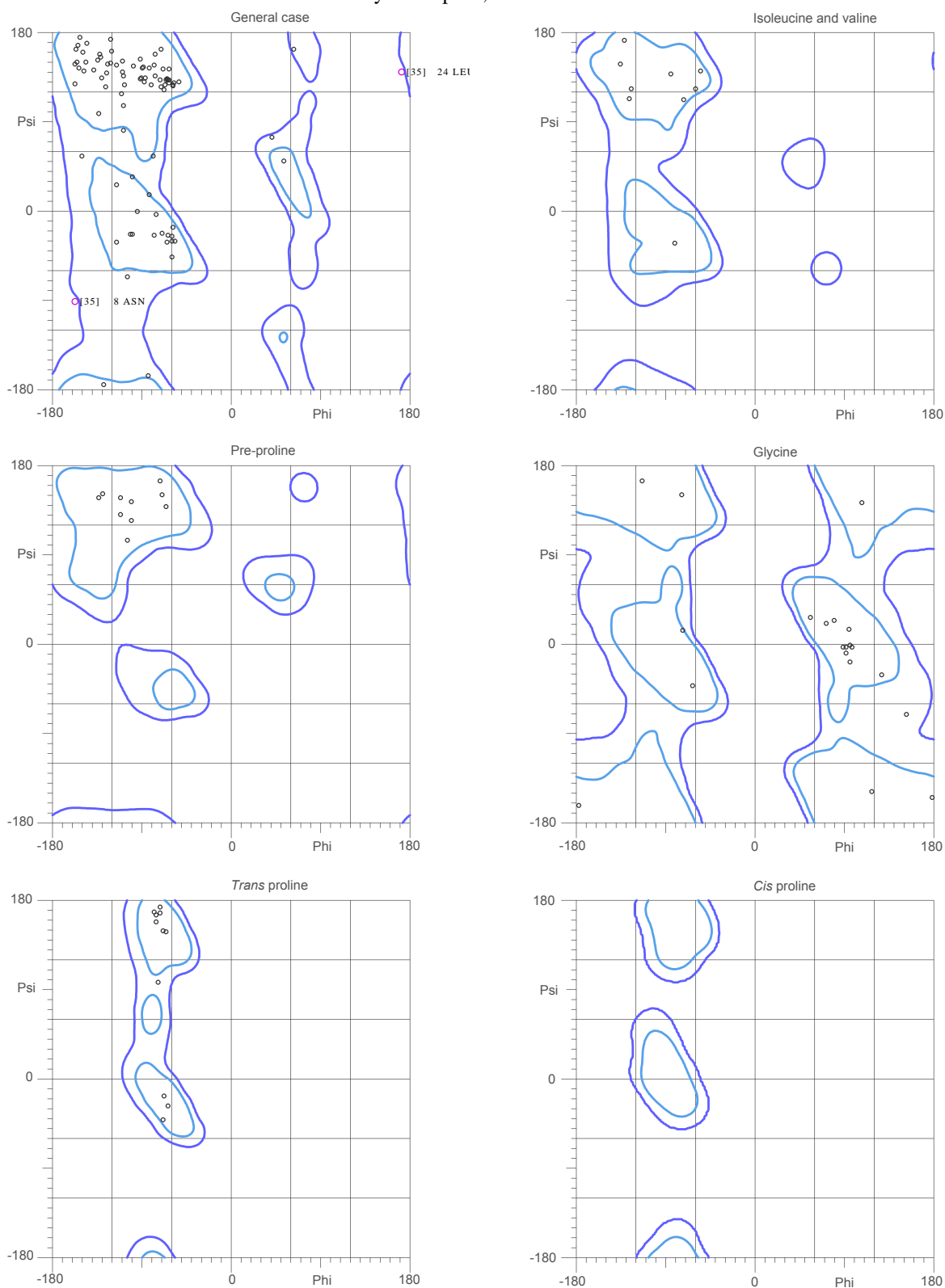
95.7% (132/138) of all residues were in favored (98%) regions.

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



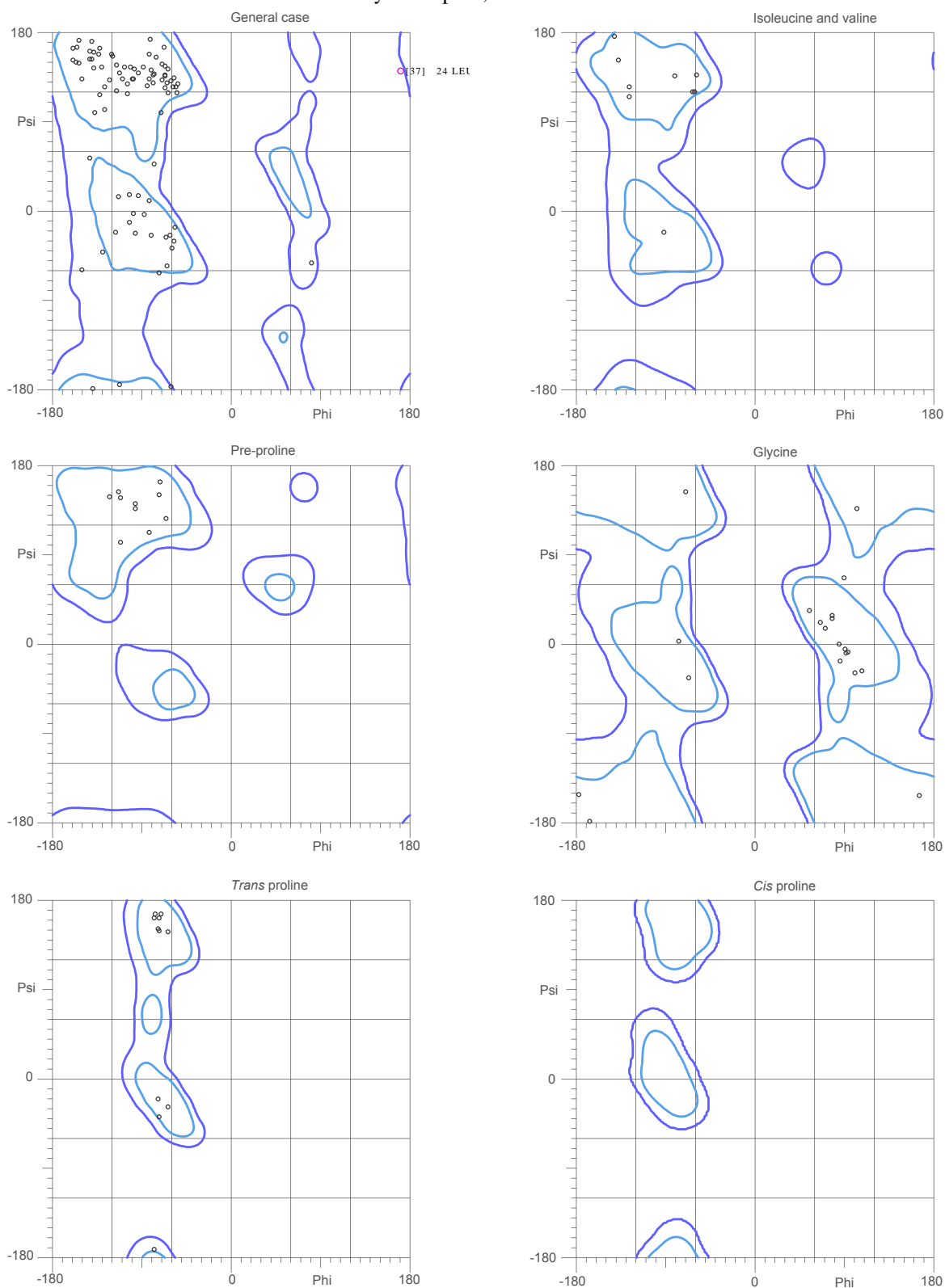
91.3% (126/138) of all residues were in favored (98%) regions.
97.8% (135/138) of all residues were in allowed (>99.8%) regions.

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



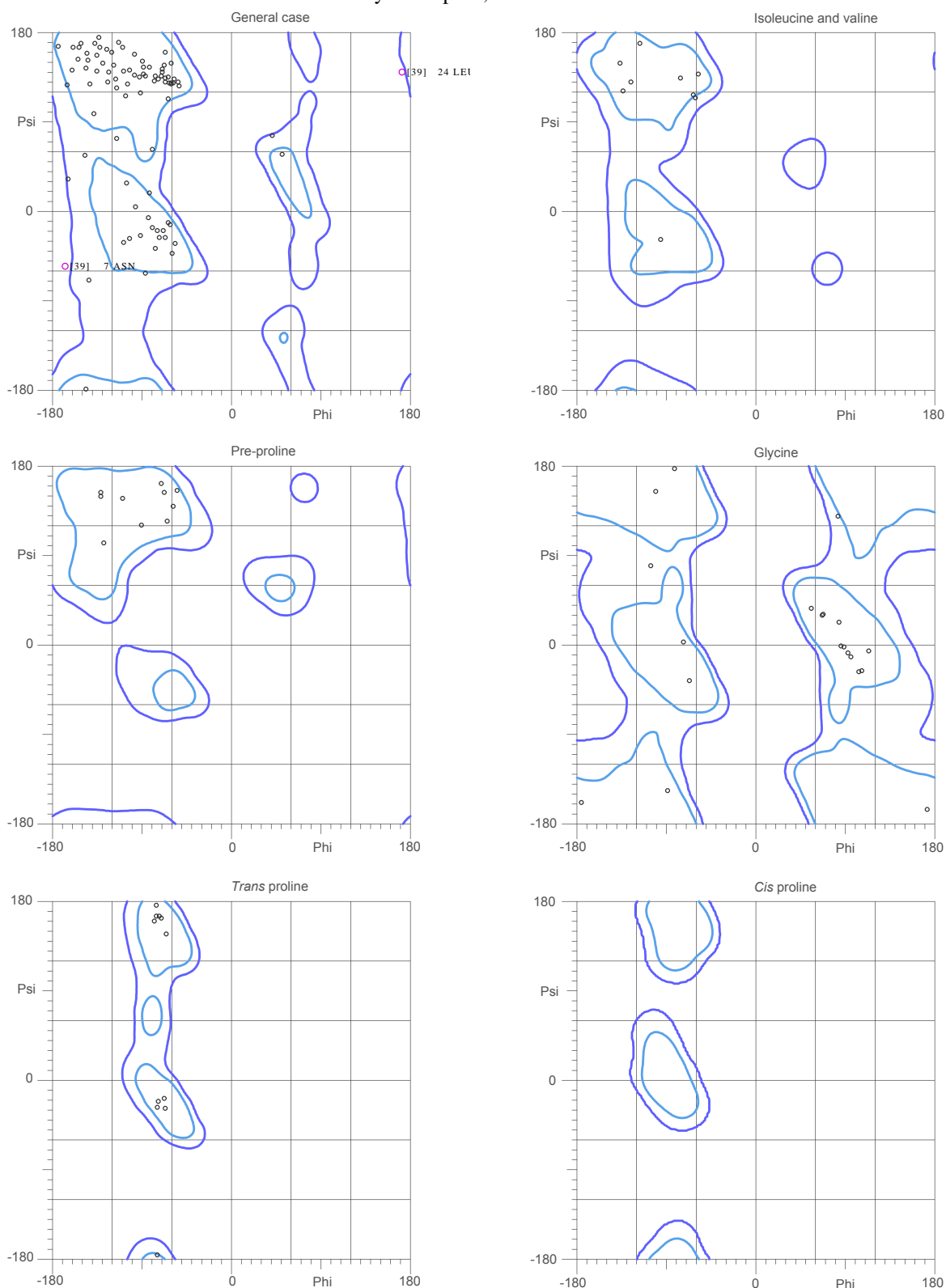
94.2% (130/138) of all residues were in favored (98%) regions.

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)