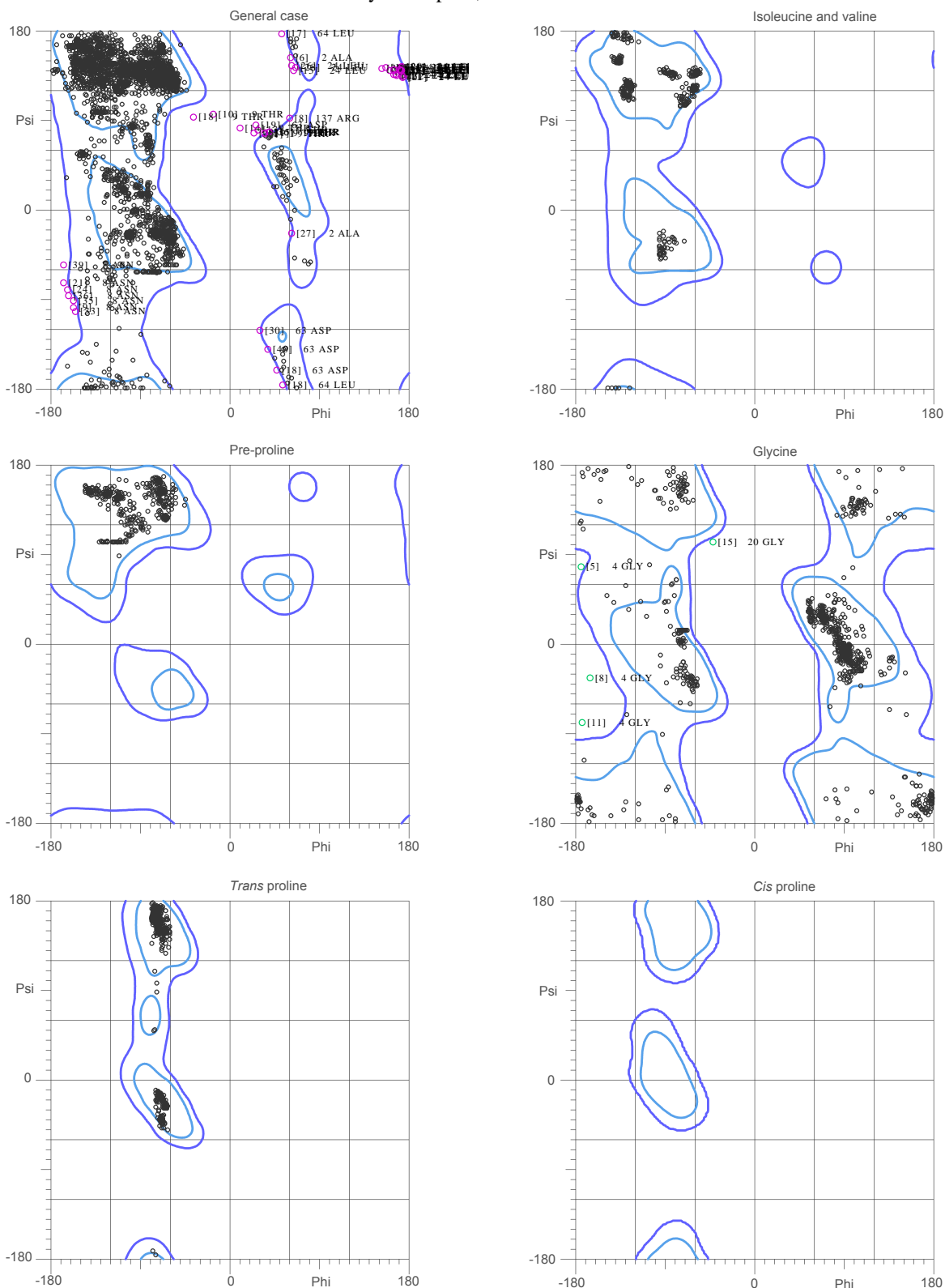


MolProbity Ramachandran analysis

6yi3.H.pdb, all models



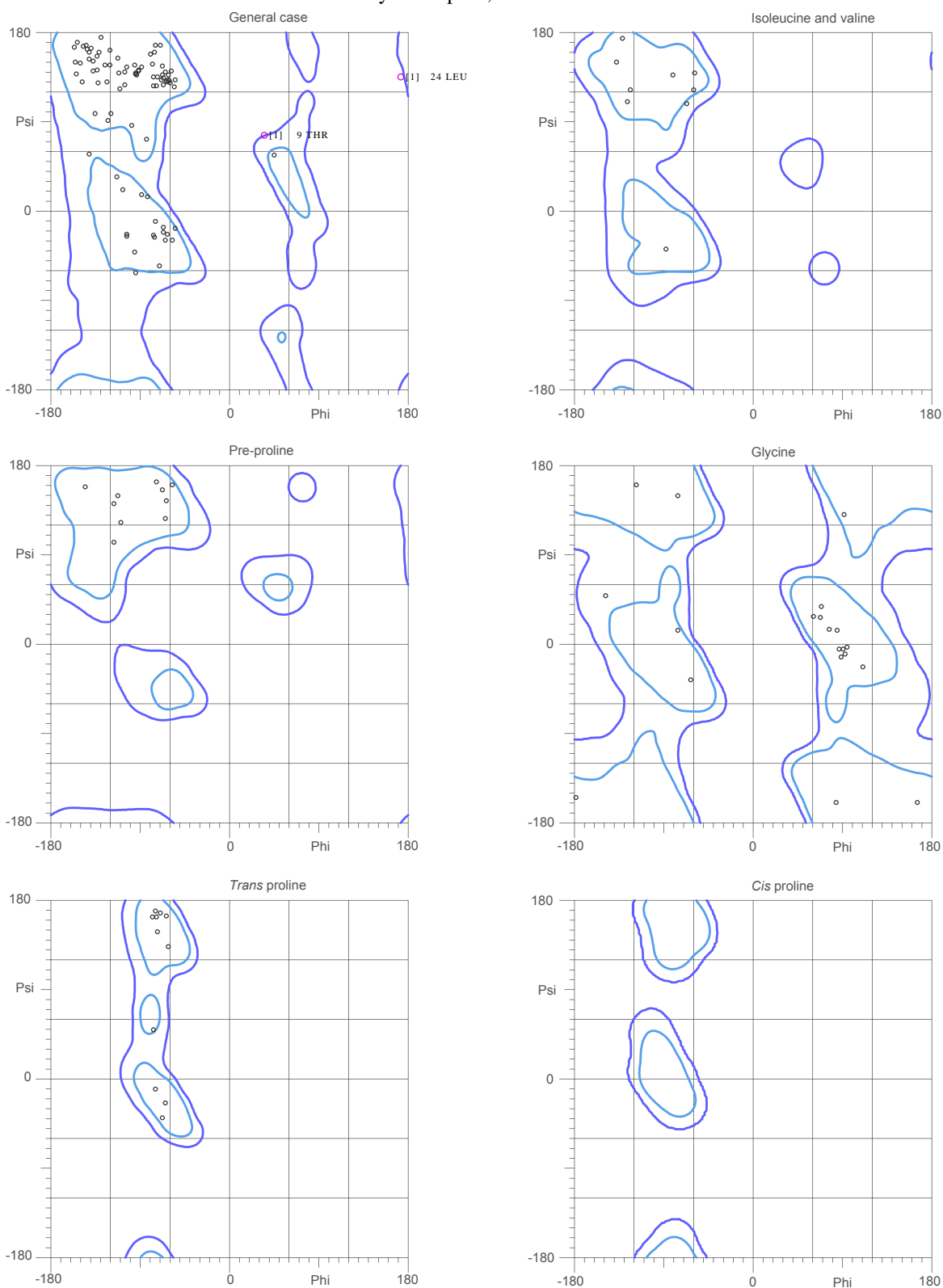
94.0% (5189/5520) of all residues were in favored (90%) regions.
9% (508/5520) of all residues were in allowed (5%) regions.

There were 52 outliers (phi, psi):

(1) 9 THR (35.1, 77.1)	(191) 63 ASP (57.6, -161.5)
(2) 24 LEU (175.8, 158.9)	(192) 64 LEU (175.8, -175.7)
(3) 4 GLY (175.2, 79.1)	(193) 63 ASP (58.6, 84.3)
(4) 24 LEU (168.5, 141.9)	(194) 63 ASP (57.7, 156.9)
(5) 2 ALA (161.9, 161.2)	(195) 63 ASP (58.2, -71.7)
(6) 24 LEU (167.5, 137.4)	(196) 63 ASP (57.5, 154.3)
(7) 4 GLY (168.5, 14.7)	(197) 63 ASP (58.7, 89.8)
(8) 24 LEU (177.5, 168.5)	(198) 63 ASP (57.5, 168.5)
(9) 137 ARG (168.5, 93.8)	(199) 63 ASP (58.5, 168.5)
(10) 8 ASP (168.5, 168.5)	(200) 63 ASP (58.5, 168.5)
(11) 24 LEU (168.5, 168.5)	(201) 63 ASP (58.5, 168.5)
(12) 4 GLY (168.5, 168.5)	(202) 63 ASP (58.5, 168.5)
(13) 24 LEU (177.5, 168.5)	(203) 63 ASP (58.5, 168.5)
(14) 9 THR (168.5, 168.5)	(204) 63 ASP (58.5, 168.5)
(15) 24 LEU (177.5, 168.5)	(205) 63 ASP (58.5, 168.5)
(16) 9 THR (168.5, 168.5)	(206) 63 ASP (58.5, 168.5)
(17) 24 LEU (177.5, 168.5)	(207) 63 ASP (58.5, 168.5)
(18) 9 THR (168.5, 168.5)	(208) 63 ASP (58.5, 168.5)
(19) 24 LEU (177.5, 168.5)	(209) 63 ASP (58.5, 168.5)
(20) 9 THR (168.5, 168.5)	(210) 63 ASP (58.5, 168.5)
(21) 24 LEU (177.5, 168.5)	(211) 63 ASP (58.5, 168.5)
(22) 9 THR (168.5, 168.5)	(212) 63 ASP (58.5, 168.5)
(23) 24 LEU (177.5, 168.5)	(213) 63 ASP (58.5, 168.5)
(24) 9 THR (168.5, 168.5)	(214) 63 ASP (58.5, 168.5)
(25) 24 LEU (177.5, 168.5)	(215) 63 ASP (58.5, 168.5)
(26) 9 THR (168.5, 168.5)	(216) 63 ASP (58.5, 168.5)
(27) 24 LEU (177.5, 168.5)	(217) 63 ASP (58.5, 168.5)
(28) 9 THR (168.5, 168.5)	(218) 63 ASP (58.5, 168.5)
(29) 24 LEU (177.5, 168.5)	(219) 63 ASP (58.5, 168.5)
(30) 9 THR (168.5, 168.5)	(220) 63 ASP (58.5, 168.5)
(31) 24 LEU (177.5, 168.5)	(221) 63 ASP (58.5, 168.5)
(32) 9 THR (168.5, 168.5)	(222) 63 ASP (58.5, 168.5)
(33) 24 LEU (177.5, 168.5)	(223) 63 ASP (58.5, 168.5)
(34) 9 THR (168.5, 168.5)	(224) 63 ASP (58.5, 168.5)
(35) 24 LEU (177.5, 168.5)	(225) 63 ASP (58.5, 168.5)
(36) 9 THR (168.5, 168.5)	(226) 63 ASP (58.5, 168.5)
(37) 24 LEU (177.5, 168.5)	(227) 63 ASP (58.5, 168.5)
(38) 9 THR (168.5, 168.5)	(228) 63 ASP (58.5, 168.5)
(39) 24 LEU (177.5, 168.5)	(229) 63 ASP (58.5, 168.5)
(40) 9 THR (168.5, 168.5)	(230) 63 ASP (58.5, 168.5)
(41) 24 LEU (177.5, 168.5)	(231) 63 ASP (58.5, 168.5)
(42) 9 THR (168.5, 168.5)	(232) 63 ASP (58.5, 168.5)
(43) 24 LEU (177.5, 168.5)	(233) 63 ASP (58.5, 168.5)
(44) 9 THR (168.5, 168.5)	(234) 63 ASP (58.5, 168.5)
(45) 24 LEU (177.5, 168.5)	(235) 63 ASP (58.5, 168.5)
(46) 9 THR (168.5, 168.5)	(236) 63 ASP (58.5, 168.5)
(47) 24 LEU (177.5, 168.5)	(237) 63 ASP (58.5, 168.5)
(48) 9 THR (168.5, 168.5)	(238) 63 ASP (58.5, 168.5)
(49) 24 LEU (177.5, 168.5)	(239) 63 ASP (58.5, 168.5)
(50) 9 THR (168.5, 168.5)	(240) 63 ASP (58.5, 168.5)
(51) 24 LEU (177.5, 168.5)	(241) 63 ASP (58.5, 168.5)
(52) 9 THR (168.5, 168.5)	(242) 63 ASP (58.5, 168.5)
(53) 24 LEU (177.5, 168.5)	(243) 63 ASP (58.5, 168.5)
(54) 9 THR (168.5, 168.5)	(244) 63 ASP (58.5, 168.5)
(55) 24 LEU (177.5, 168.5)	(245) 63 ASP (58.5, 168.5)
(56) 9 THR (168.5, 168.5)	(246) 63 ASP (58.5, 168.5)
(57) 24 LEU (177.5, 168.5)	(247) 63 ASP (58.5, 168.5)
(58) 9 THR (168.5, 168.5)	(248) 63 ASP (58.5, 168.5)
(59) 24 LEU (177.5, 168.5)	(249) 63 ASP (58.5, 168.5)
(60) 9 THR (168.5, 168.5)	(250) 63 ASP (58.5, 168.5)

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



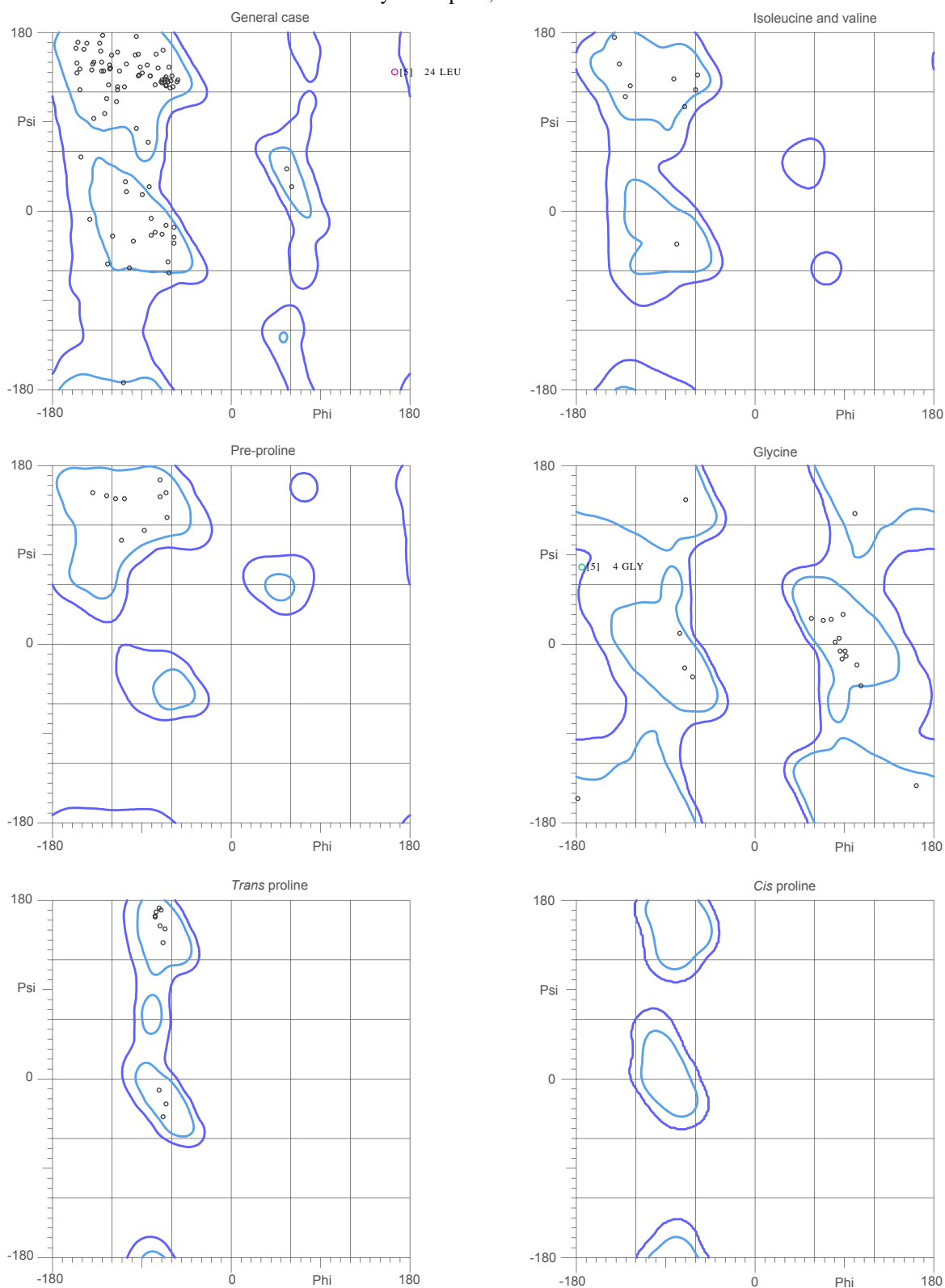
94.2% (130/138) of all residues were in favored (98%) regions.

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



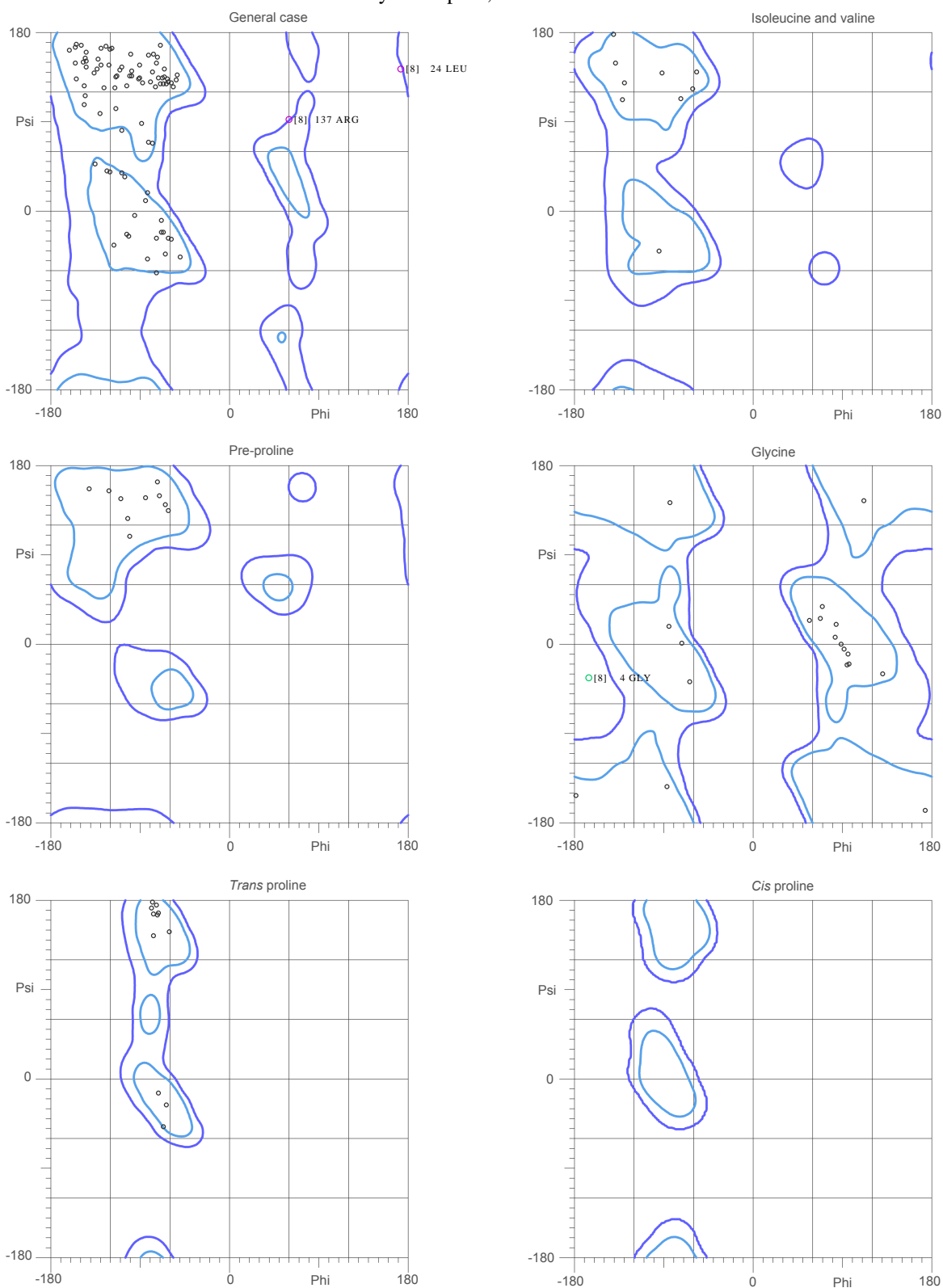
94.2% (130/138) of all residues were in favored (98%) regions.

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.

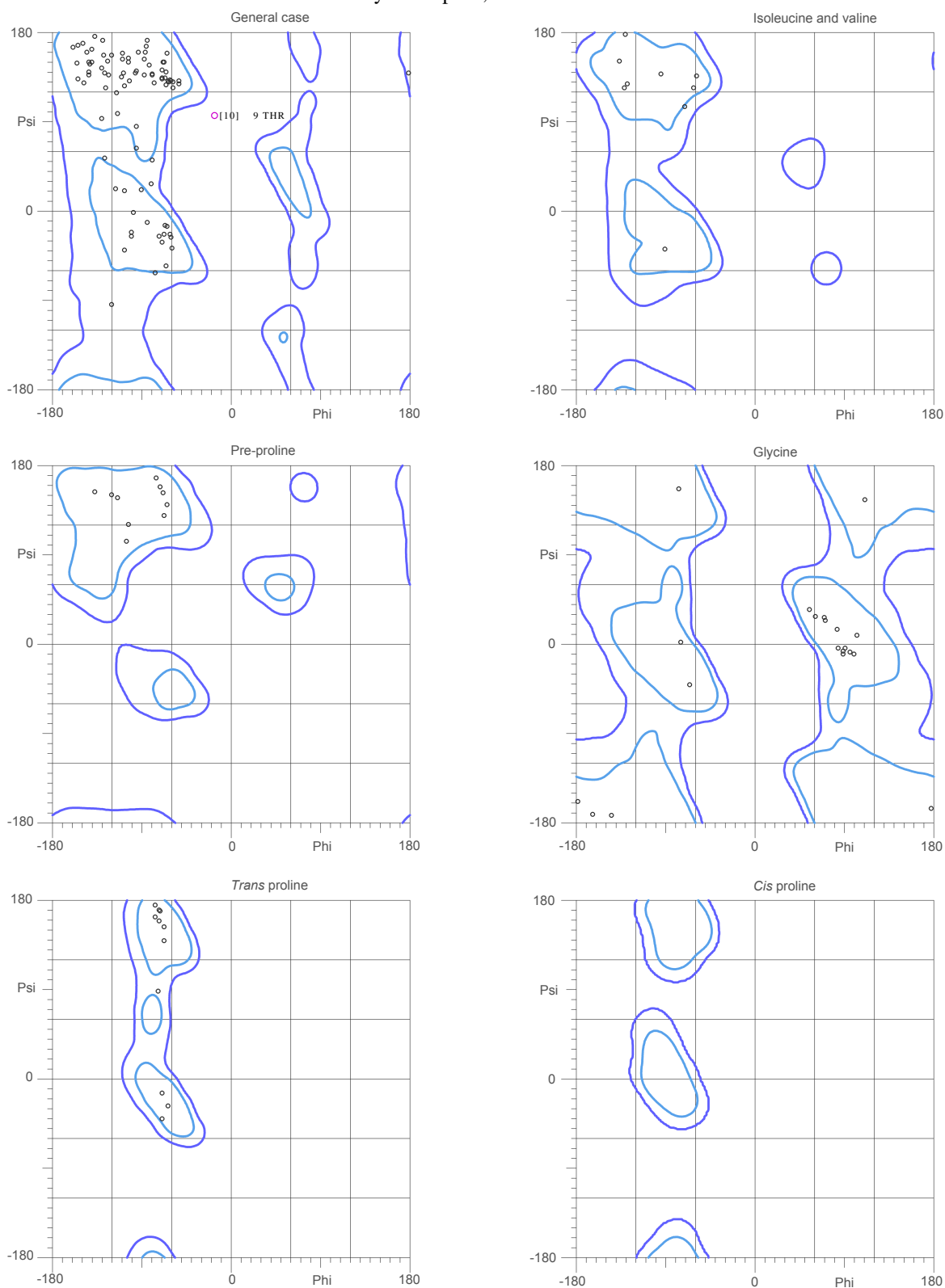
There were 2 outliers (phi, psi):

[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.

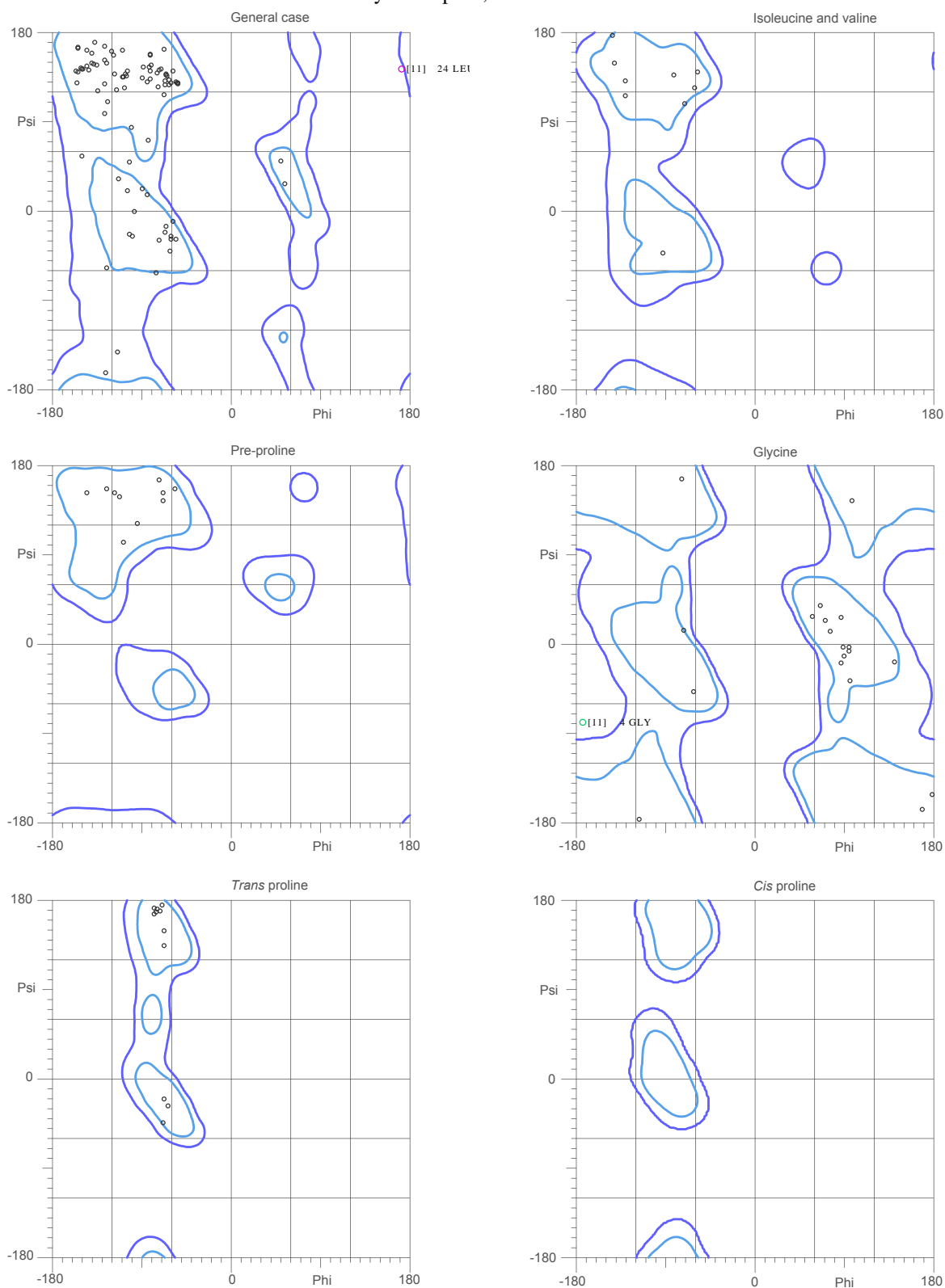
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

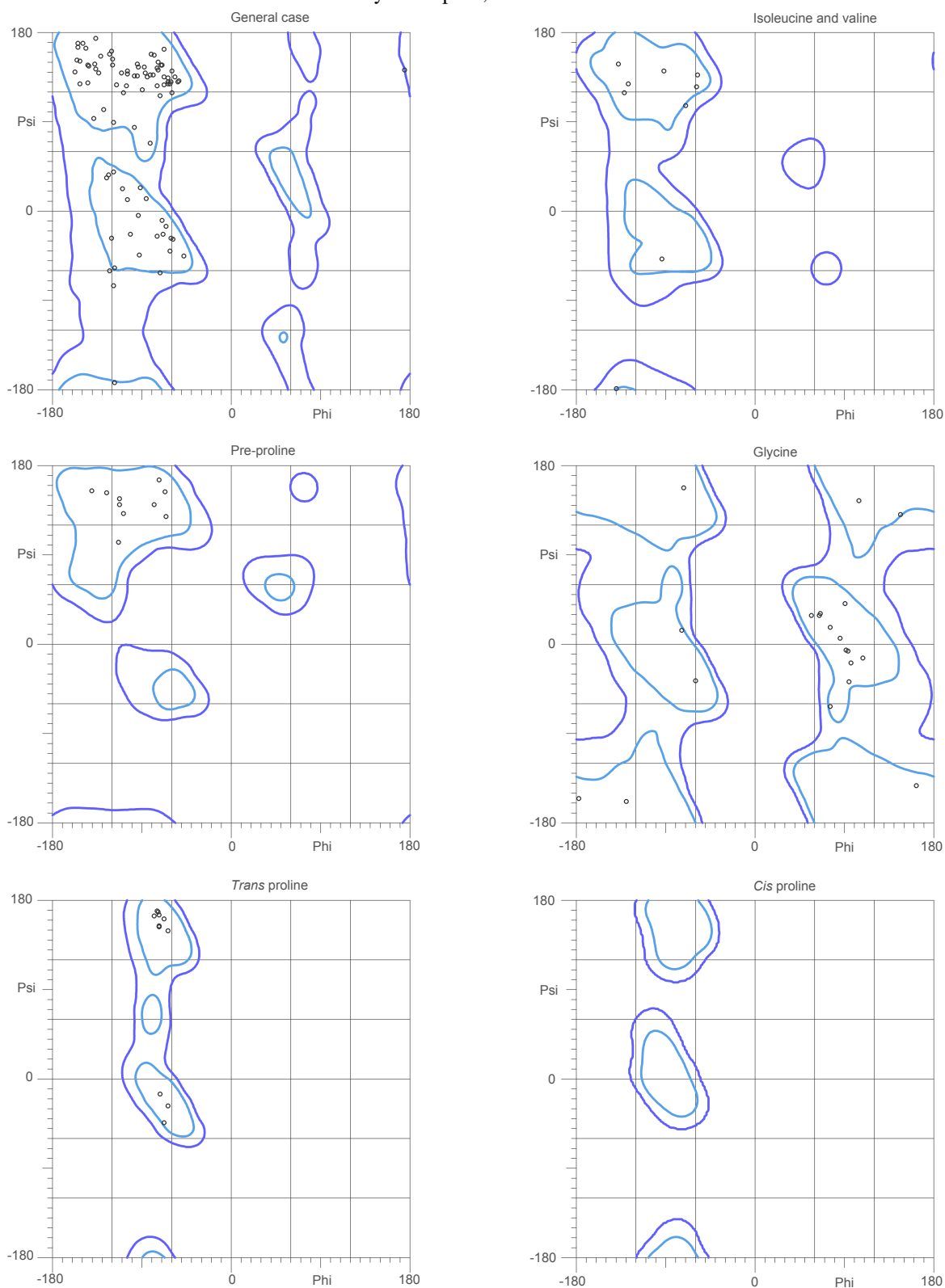
There were 2 outliers (phi, psi):

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

[11] 24 LEU (172.6, 144.8)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 12



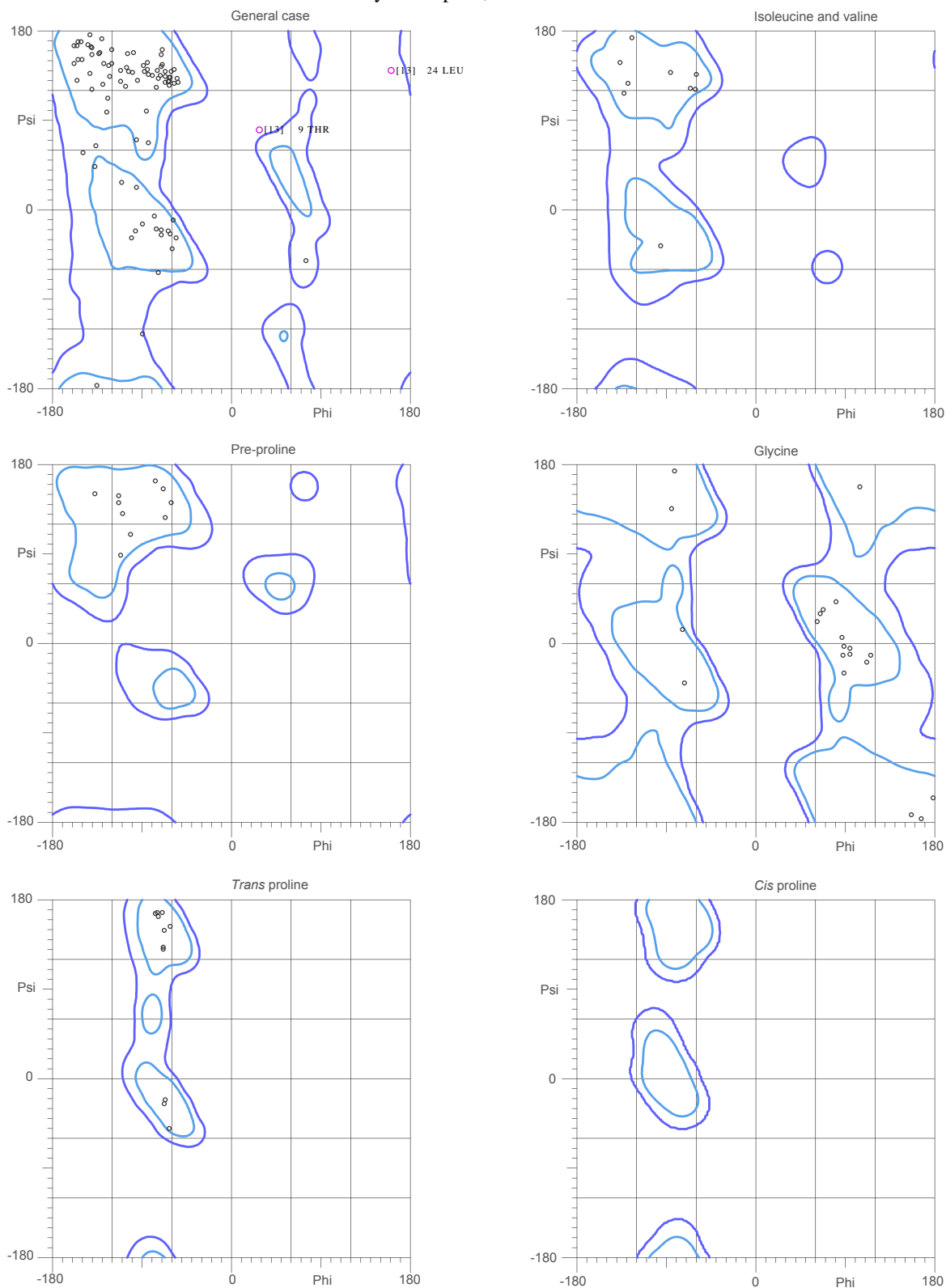
97.1% (134/138) of all residues were in favored (98%) regions.

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.

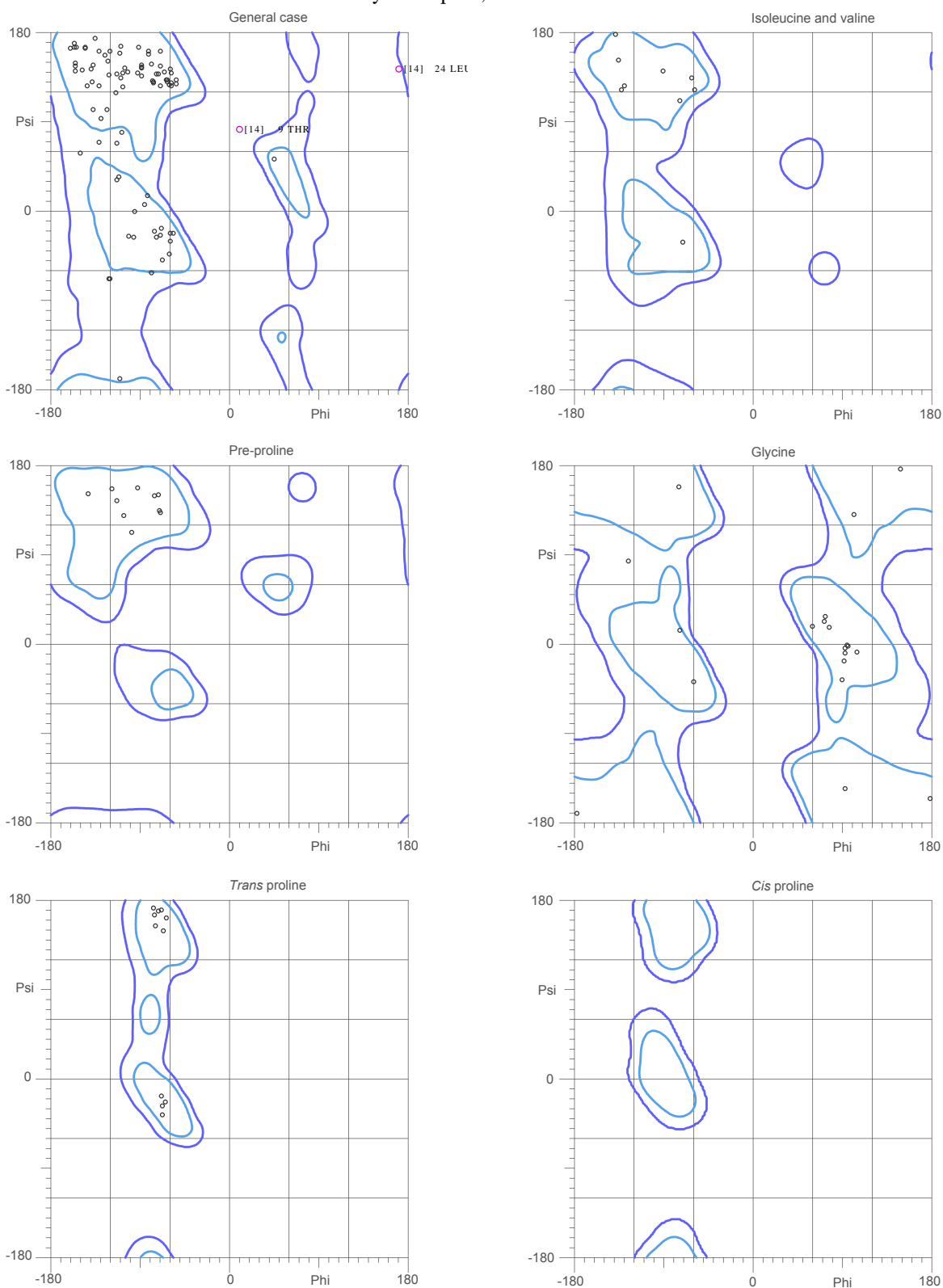
There were 2 outliers (phi, psi):

[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.

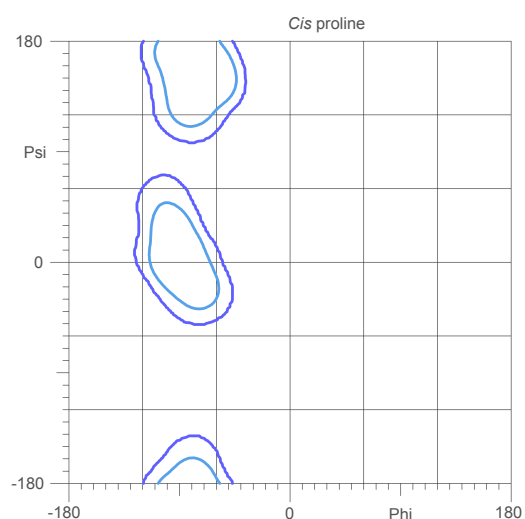
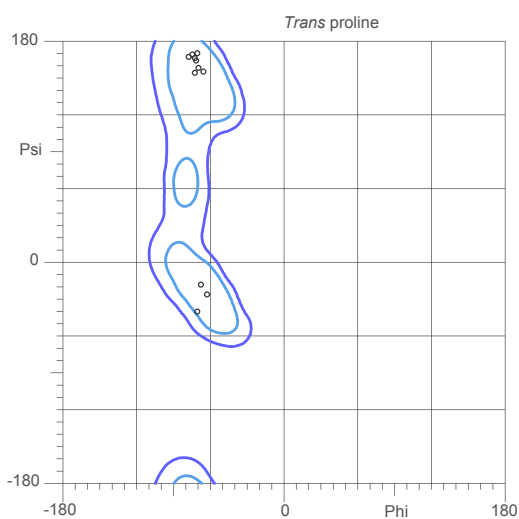
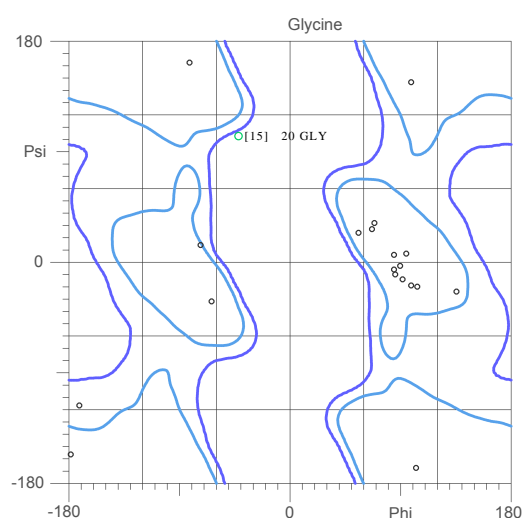
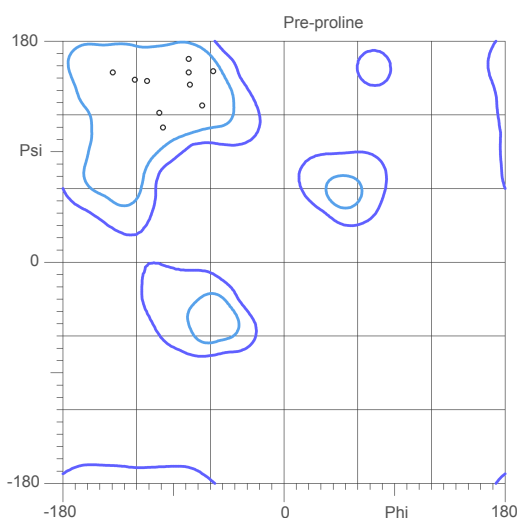
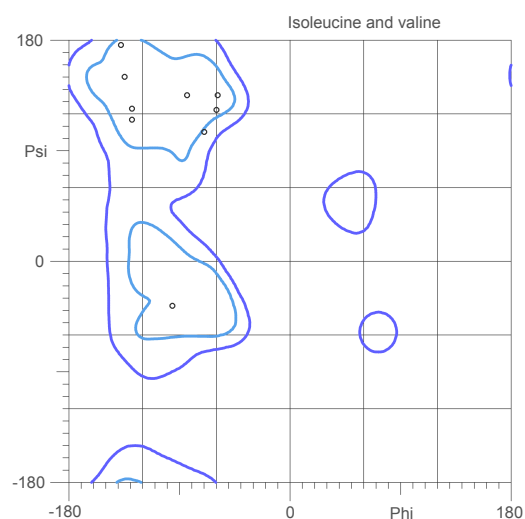
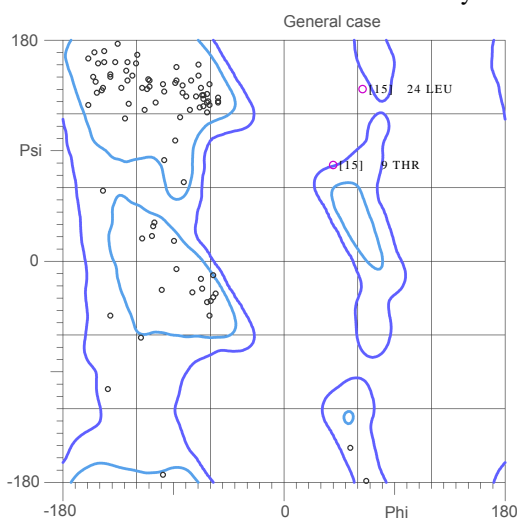
There were 2 outliers (phi, psi):

[14] 9 THR (10.2, 83.8)

[14] 24 LEU (171.6, 144.2)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 15



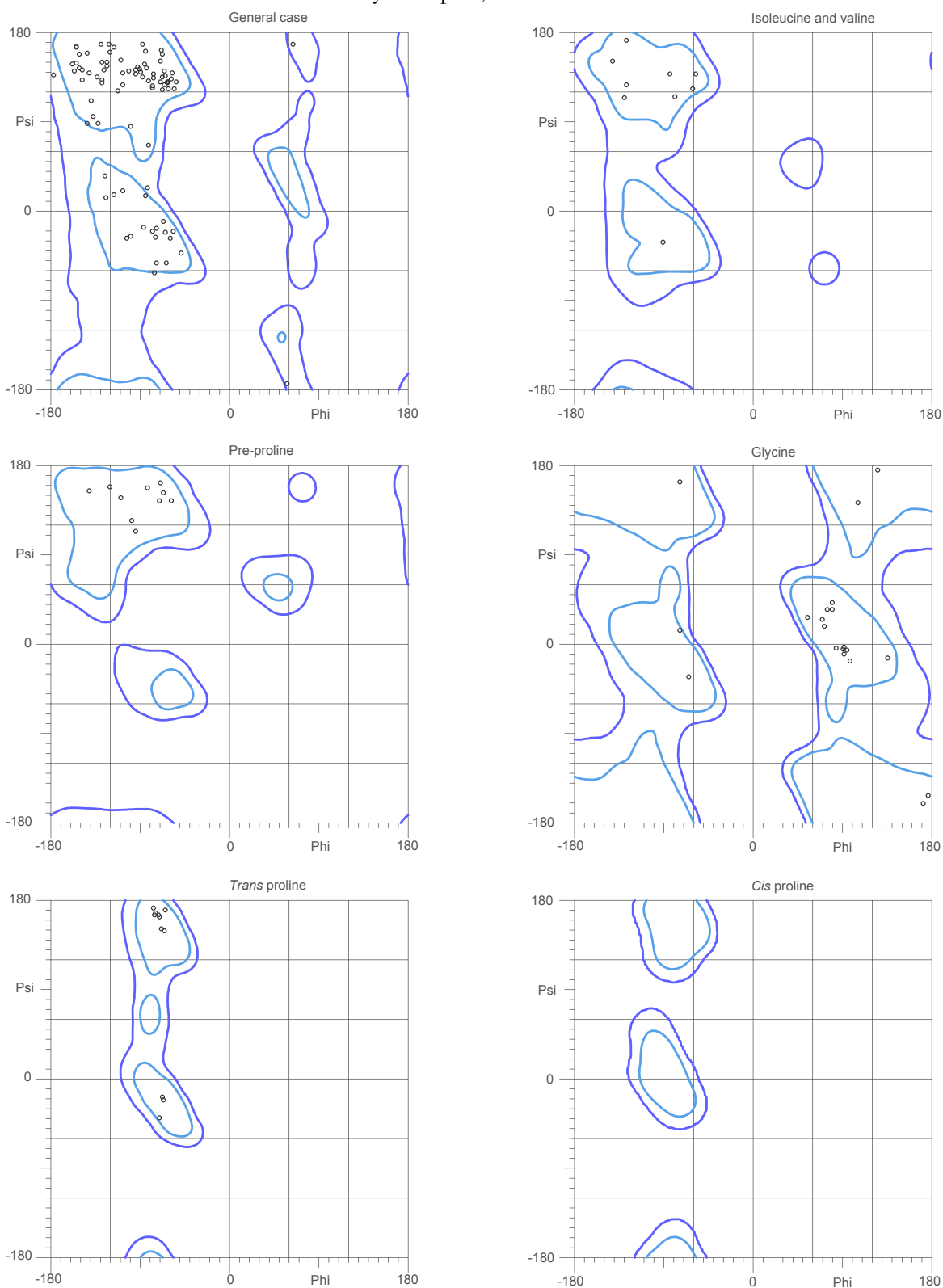
92.0% (127/138) of all residues were in favored (98%) regions.
97.8% (135/138) of all residues were in allowed (>99.8%) regions.

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.

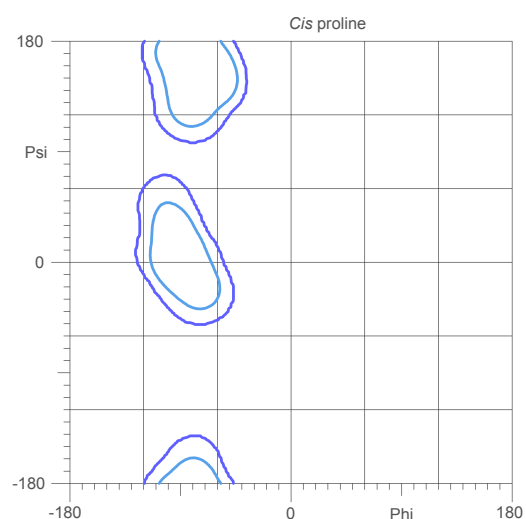
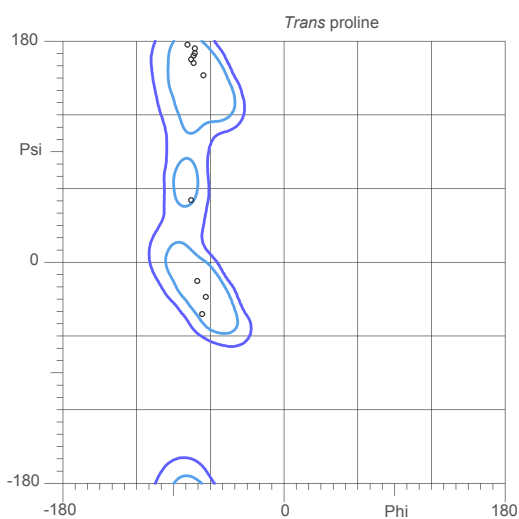
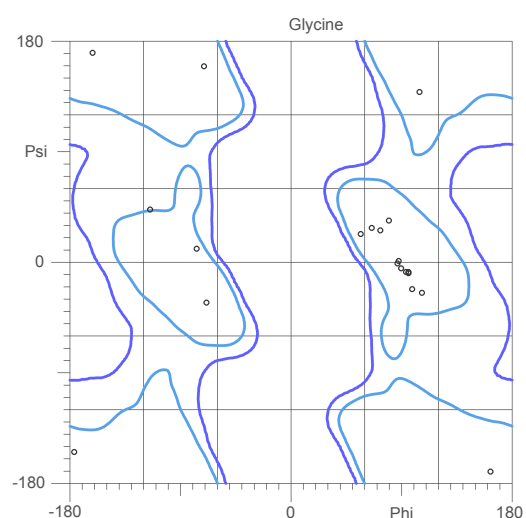
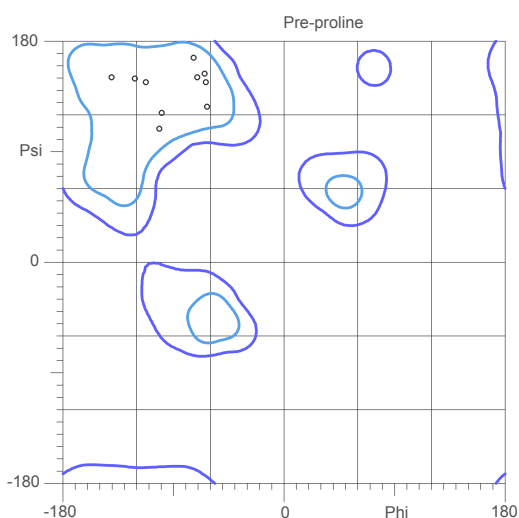
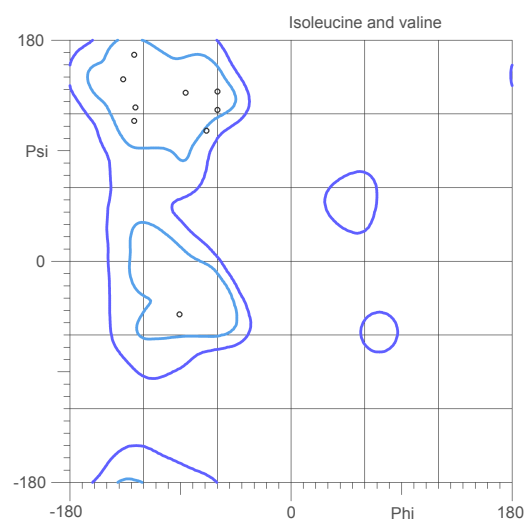
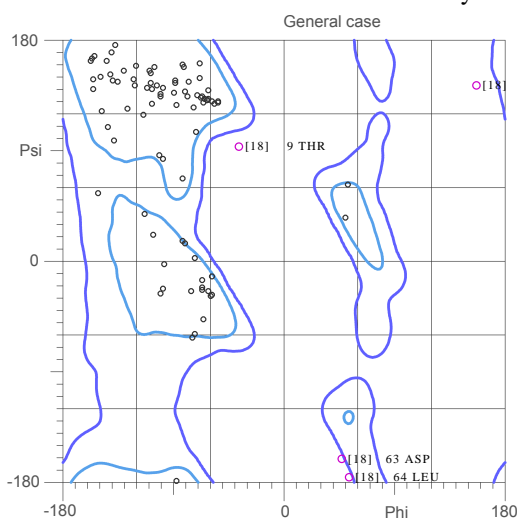
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[17] 64 LEU (52.9, 178.7)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 18



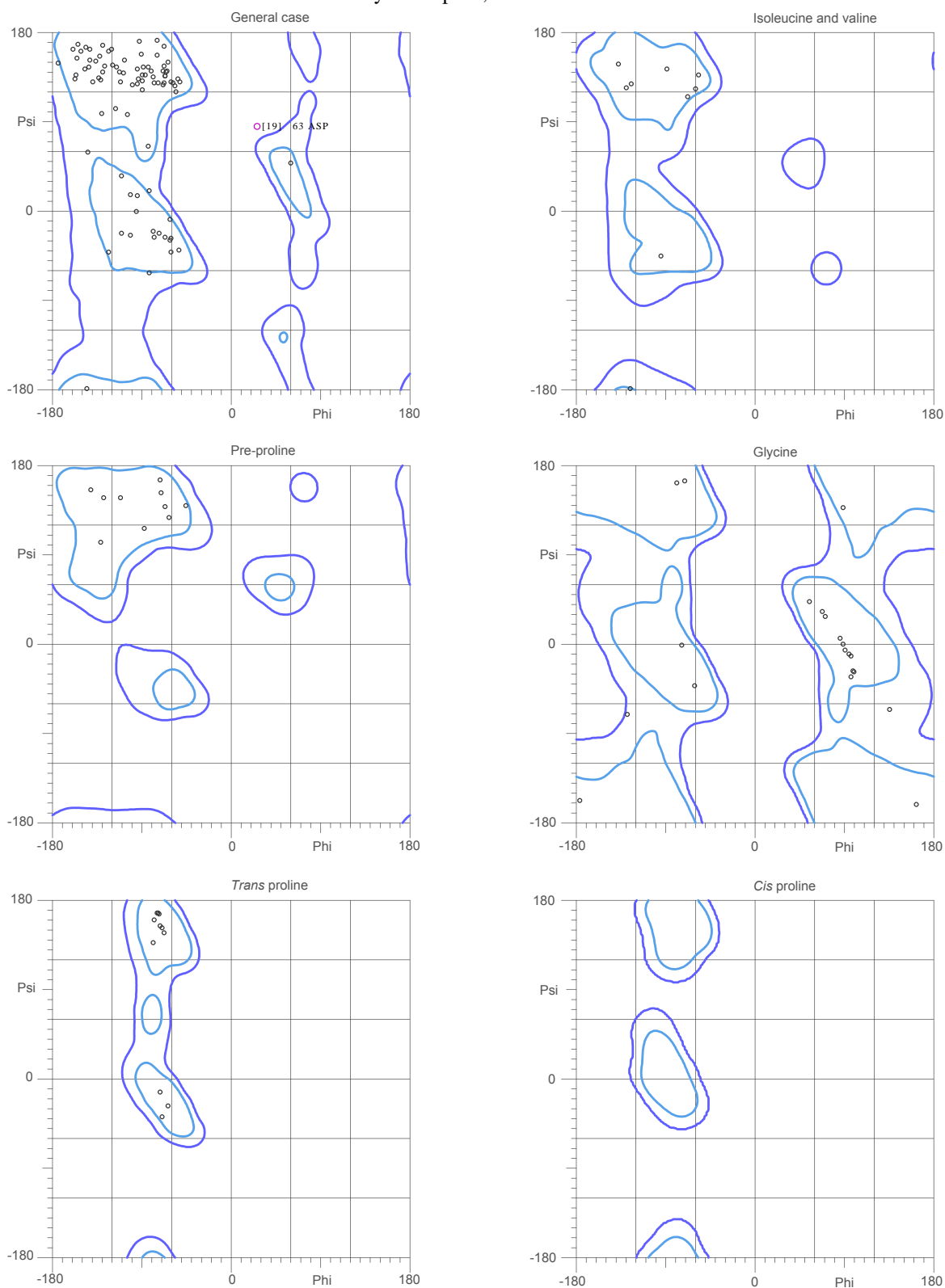
93.5% (129/138) of all residues were in favored (98%) regions.
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

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.

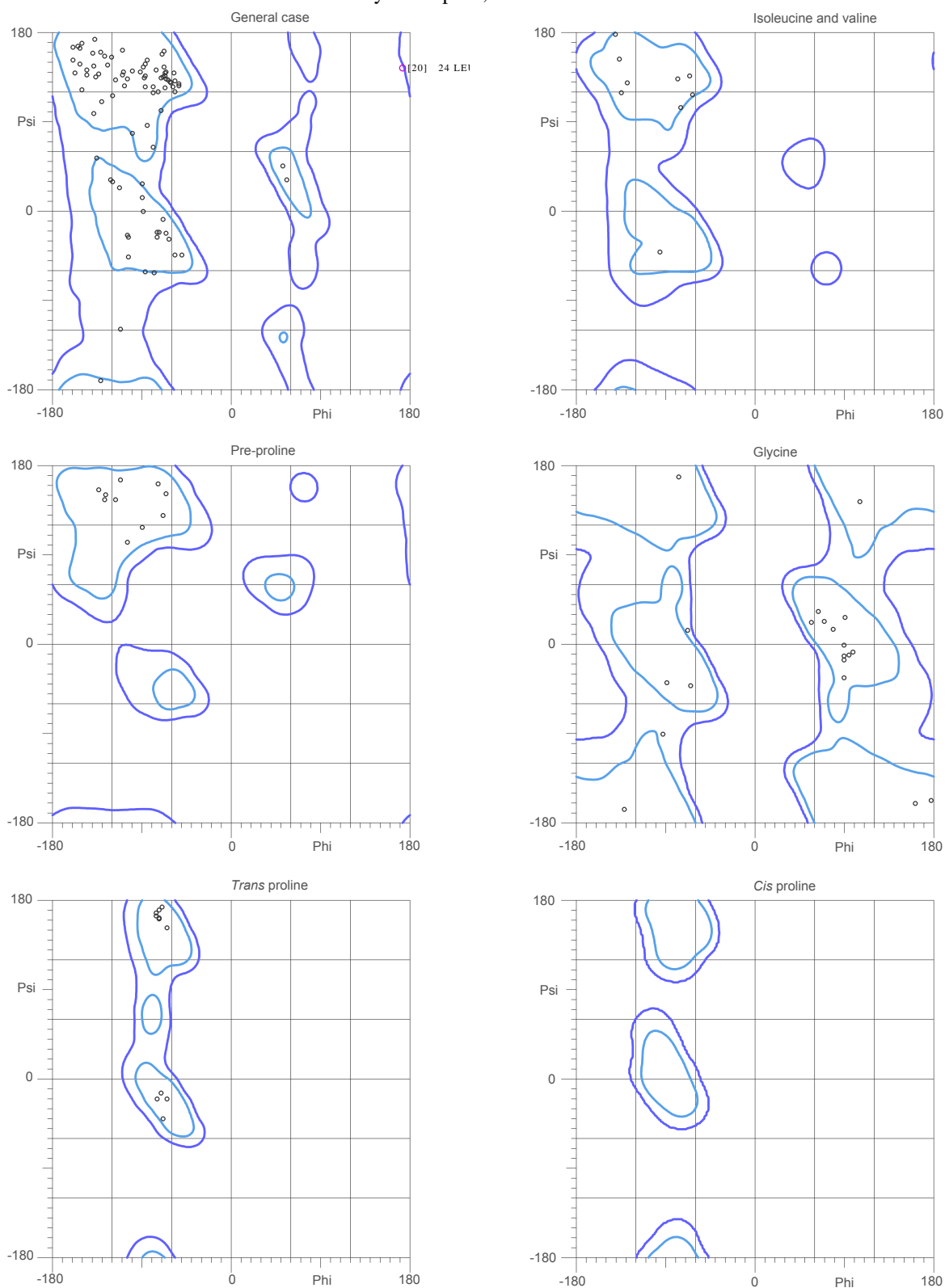
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

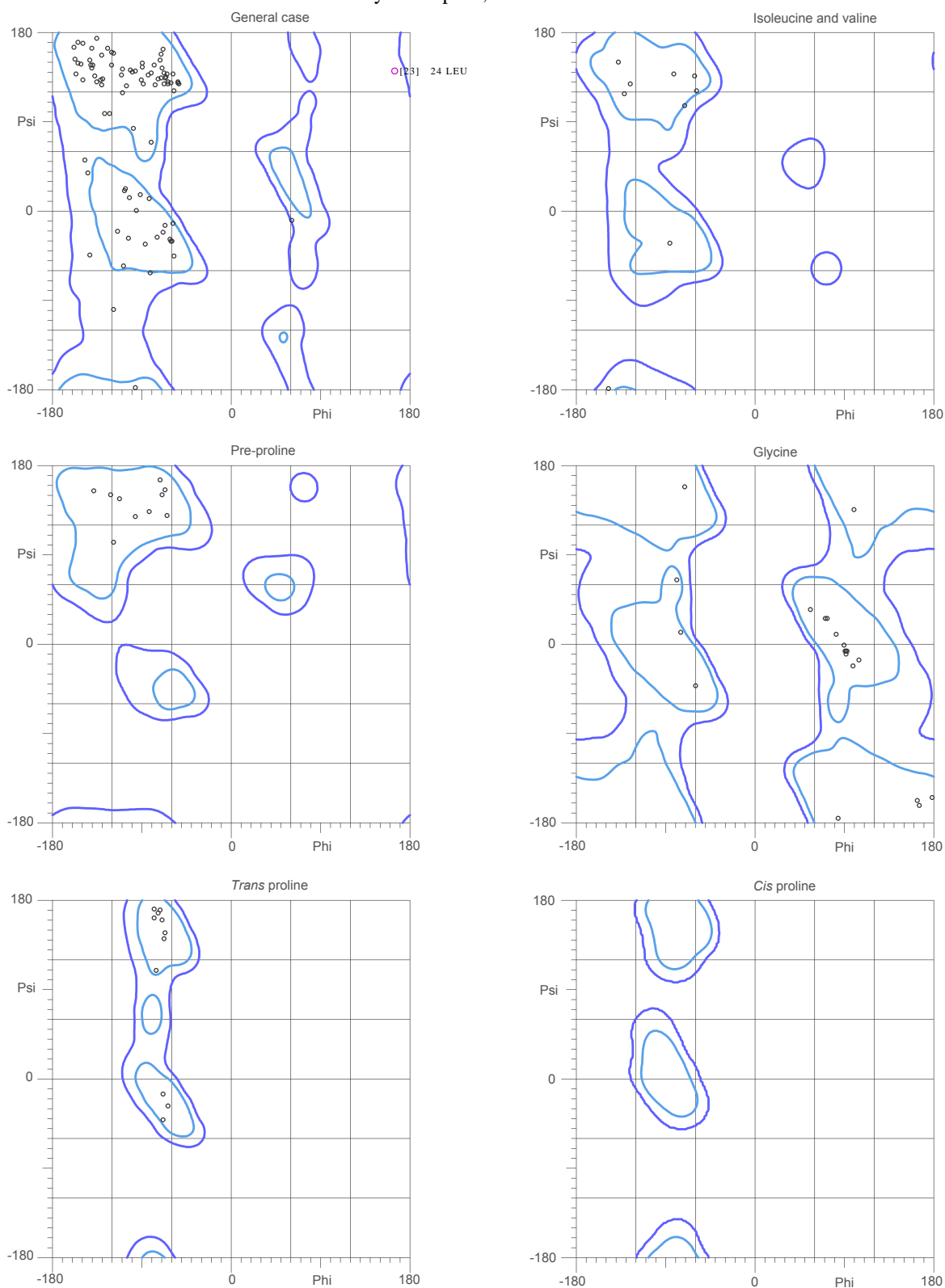
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

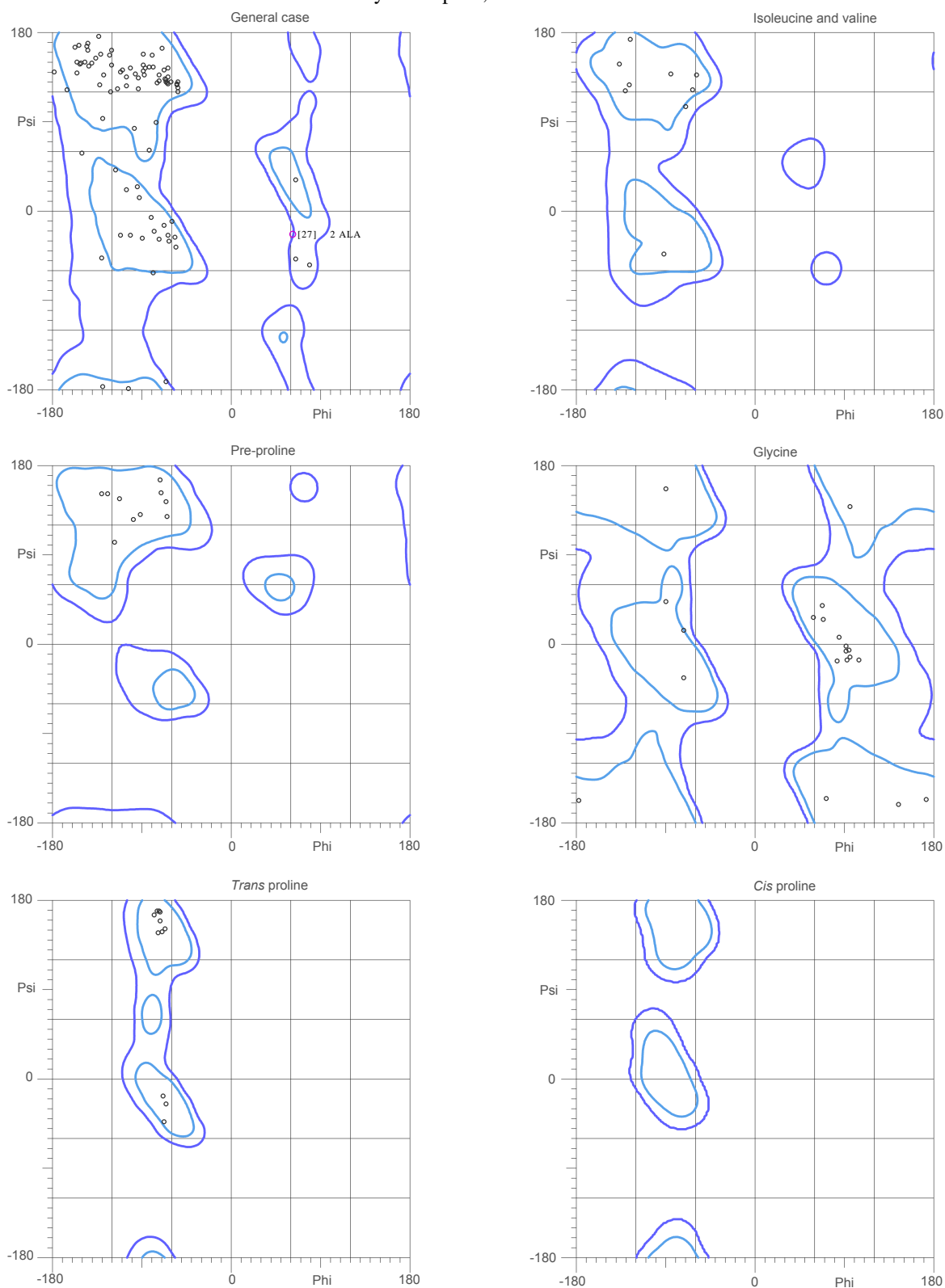
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

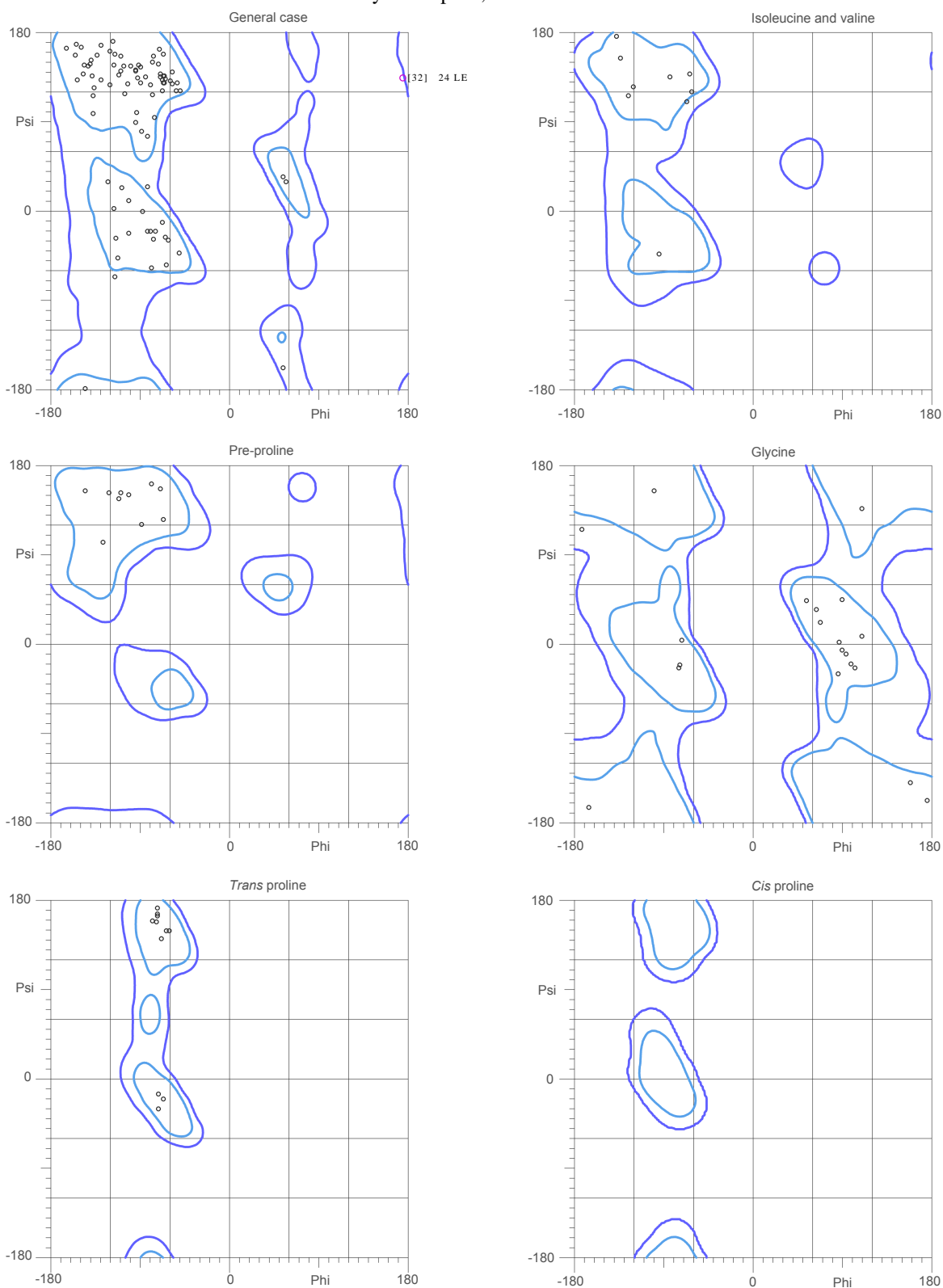
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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



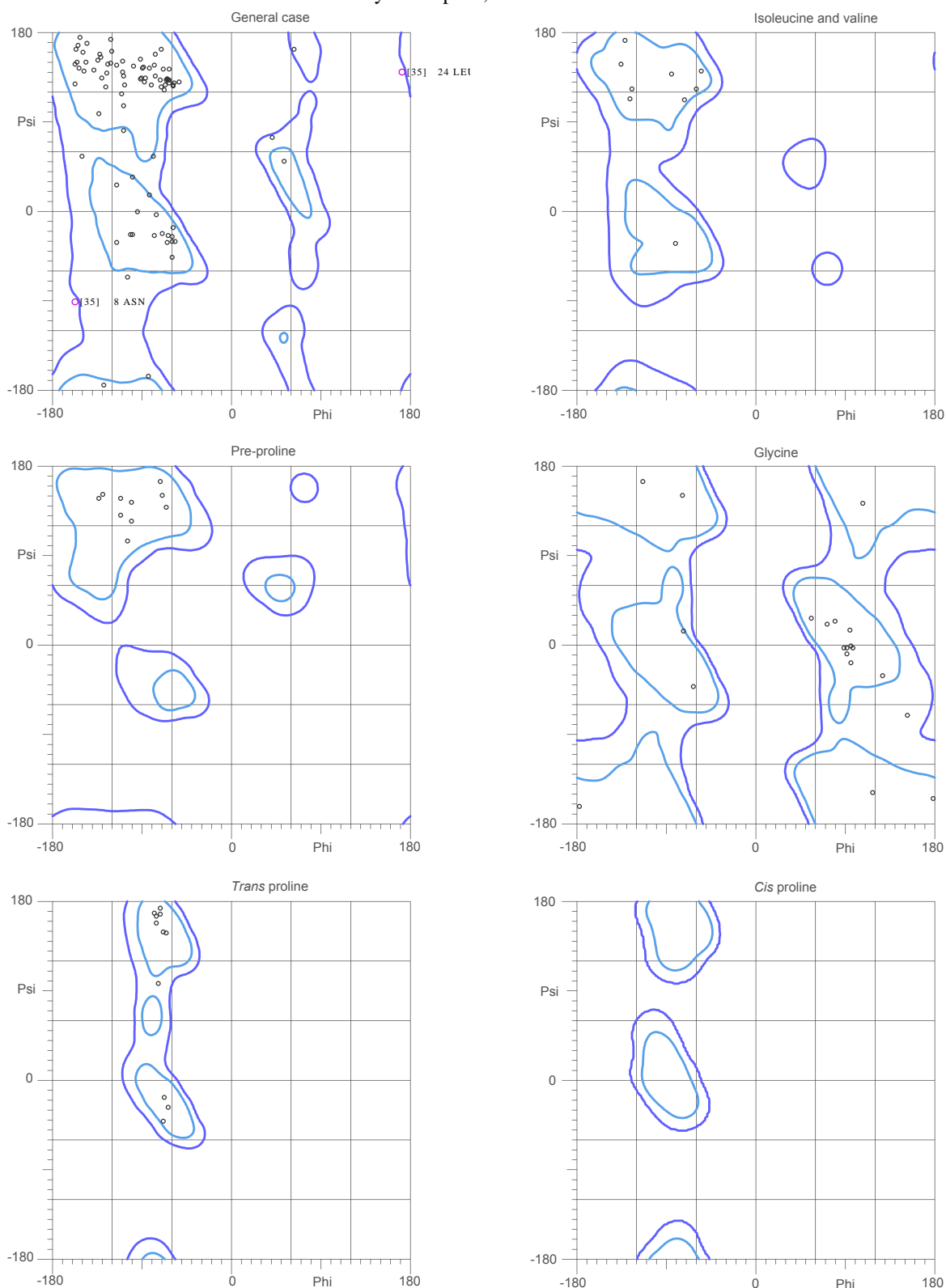
95.7% (132/138) of all residues were in favored (98%) regions.

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



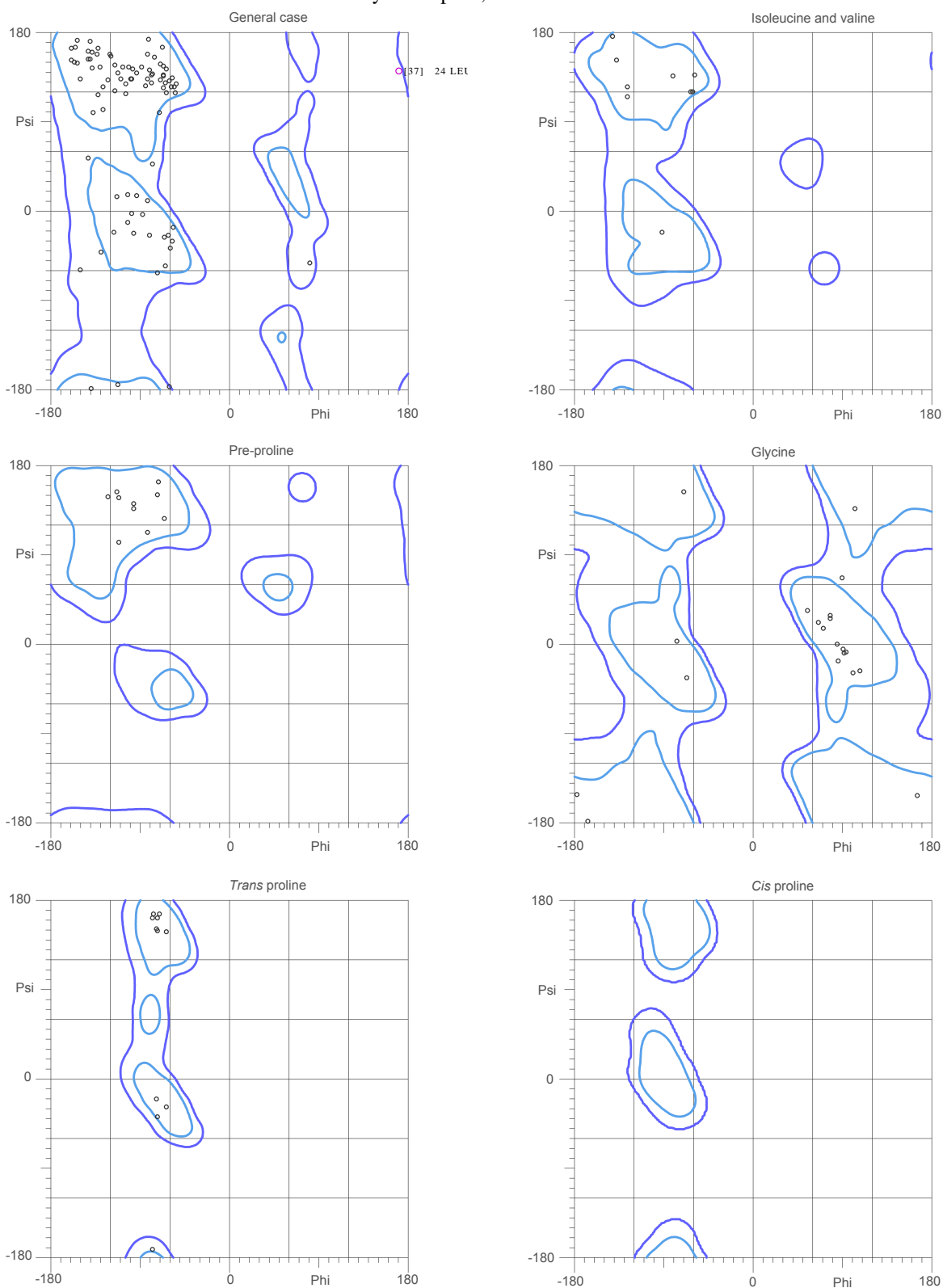
91.3% (126/138) of all residues were in favored (98%) regions.
97.8% (135/138) of all residues were in allowed (>99.8%) regions.

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



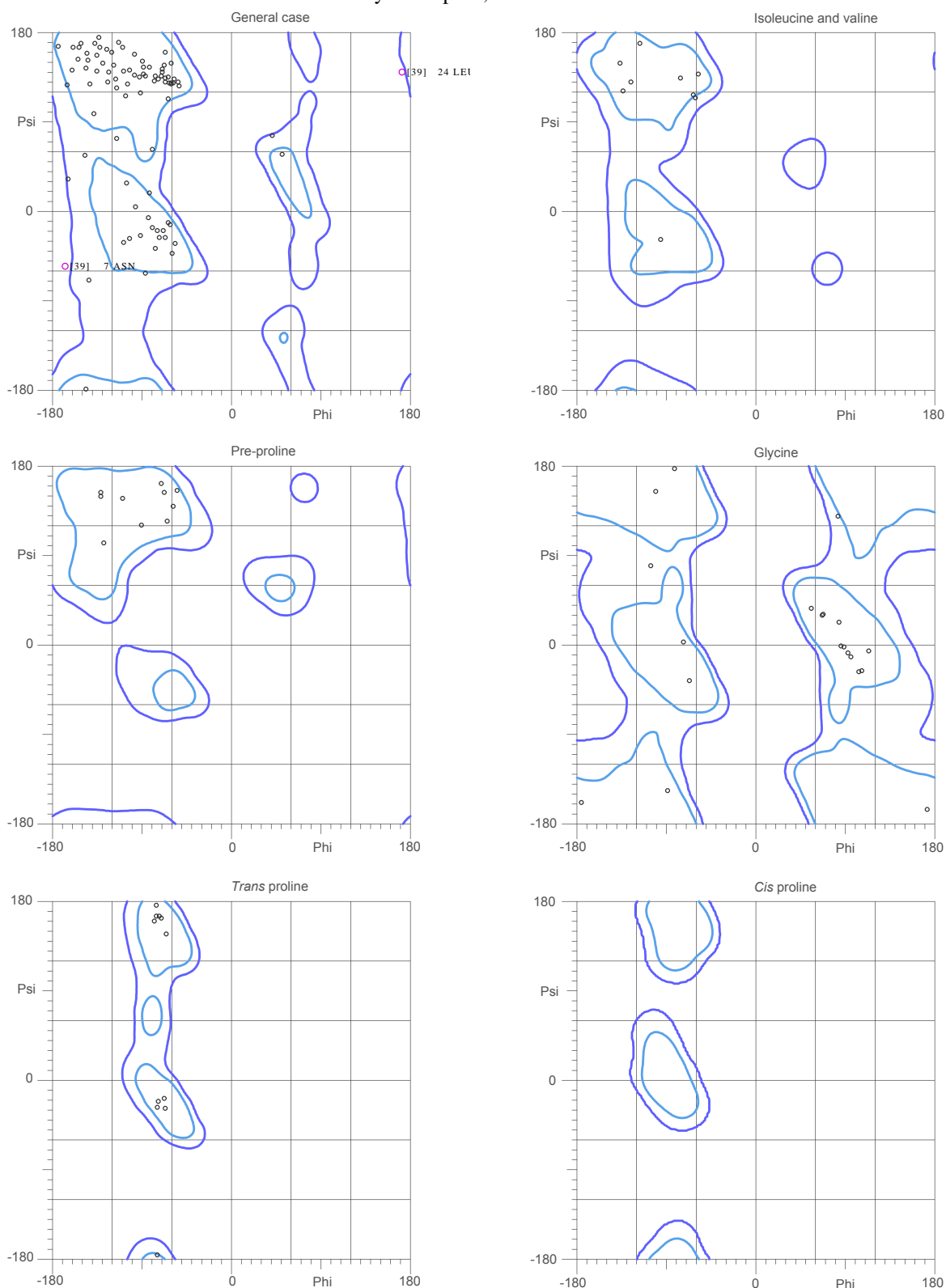
94.2% (130/138) of all residues were in favored (98%) regions.

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)