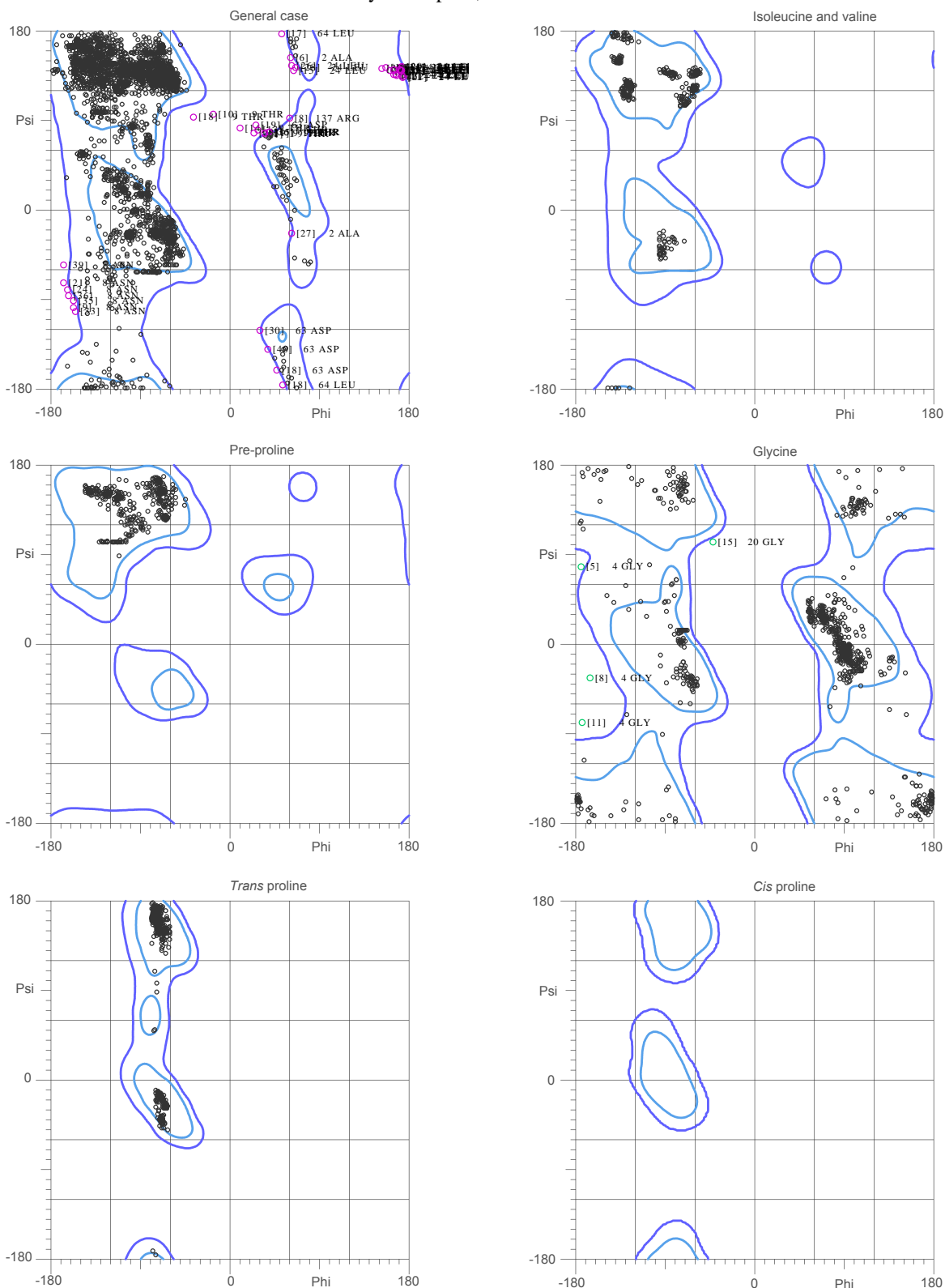


# MolProbity Ramachandran analysis

6yi3.H.pdb, all models



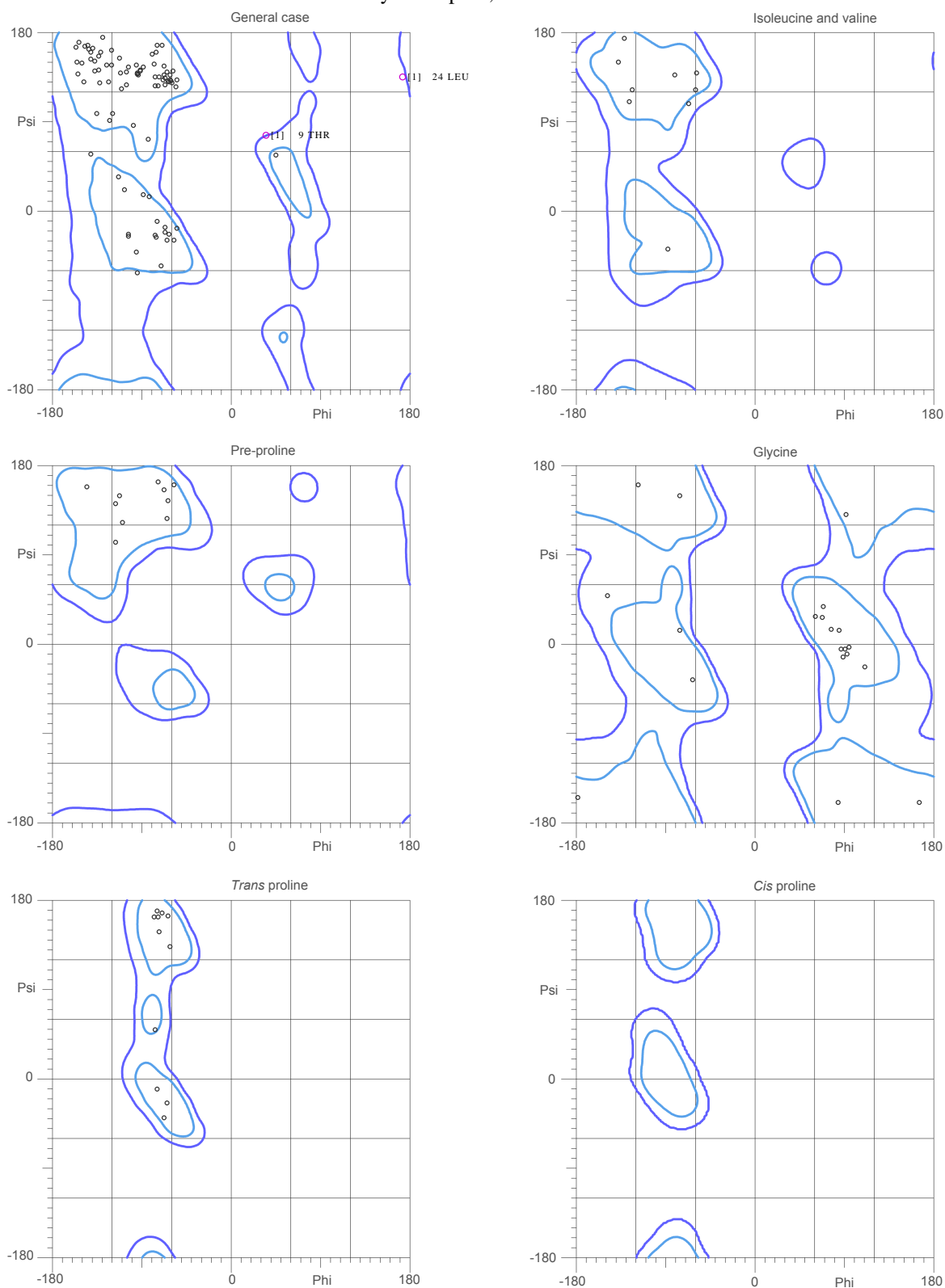
94.0% (5189/5520) of all residues were in favored (90%) regions.  
9% (508/5520) of all residues were in allowed (10%) regions.

There were 52 outliers (phi, psi):

(1) 9 THR (35.1, 77.1)	(19) 63 ASP (57.6, -161.5)
(2) 24 LEU (175.8, 158.9)	(20) 64 LEU (175.6, -176.7)
(3) 4 GLY (175.2, 79.1)	(21) 63 ASP (26.6, 84.3)
(4) 24 LEU (168.5, 141.9)	(22) 63 ASP (175.7, 158.9)
(5) 2 ALA (161.9, 161.2)	(23) 63 ASP (168.5, -177.7)
(6) 24 LEU (167.5, 137.4)	(24) 63 ASP (168.4, 166.7)
(7) 4 GLY (166.5, 14.7)	(25) 63 ASP (168.5, 166.7)
(8) 24 LEU (175.7, 168.5)	(26) 63 ASP (175.6, 167.7)
(9) 137 ARG (168.5, 93.8)	(27) 2 ALA (165.5, 151.5)
(10) 63 ASP (168.5, 93.8)	(28) 9 THR (161.4, 78.1)
(11) 24 LEU (167.7, 137.4)	(29) 24 LEU (168.5, 166.7)
(12) 4 GLY (175.2, 79.1)	(30) 63 ASP (168.5, -177.7)
(13) 24 LEU (175.8, 158.9)	(31) 9 THR (161.4, 78.1)
(14) 24 LEU (175.8, 158.9)	(32) 63 ASP (175.6, 167.7)
(15) 9 THR (161.4, 78.1)	(33) 63 ASP (175.7, 158.9)
(16) 24 LEU (175.8, 158.9)	(34) 63 ASP (168.5, -177.7)
(17) 4 GLY (175.2, 79.1)	(35) 63 ASP (168.4, 166.7)
(18) 24 LEU (168.5, 141.9)	(36) 9 THR (161.4, 78.1)
(37) 63 ASP (168.5, -177.7)	(37) 63 ASP (168.5, -177.7)
(38) 24 LEU (175.8, 158.9)	(38) 24 LEU (175.8, 158.9)
(39) 4 GLY (175.2, 79.1)	(39) 4 GLY (175.2, 79.1)
(40) 24 LEU (168.5, 141.9)	(40) 24 LEU (168.5, 141.9)
(41) 2 ALA (161.9, 161.2)	(41) 2 ALA (161.9, 161.2)
(42) 24 LEU (167.5, 137.4)	(42) 24 LEU (167.5, 137.4)
(43) 4 GLY (166.5, 14.7)	(43) 4 GLY (166.5, 14.7)
(44) 24 LEU (175.7, 168.5)	(44) 24 LEU (175.7, 168.5)
(45) 137 ARG (168.5, 93.8)	(45) 137 ARG (168.5, 93.8)
(46) 63 ASP (168.5, 93.8)	(46) 63 ASP (168.5, 93.8)
(47) 24 LEU (167.7, 137.4)	(47) 24 LEU (167.7, 137.4)
(48) 4 GLY (175.2, 79.1)	(48) 4 GLY (175.2, 79.1)
(49) 24 LEU (175.8, 158.9)	(49) 24 LEU (175.8, 158.9)
(50) 24 LEU (175.8, 158.9)	(50) 24 LEU (175.8, 158.9)
(51) 9 THR (161.4, 78.1)	(51) 9 THR (161.4, 78.1)
(52) 63 ASP (175.6, 167.7)	(52) 63 ASP (175.6, 167.7)
(53) 63 ASP (175.7, 158.9)	(53) 63 ASP (175.7, 158.9)
(54) 63 ASP (168.5, -177.7)	(54) 63 ASP (168.5, -177.7)
(55) 63 ASP (168.4, 166.7)	(55) 63 ASP (168.4, 166.7)
(56) 9 THR (161.4, 78.1)	(56) 9 THR (161.4, 78.1)
(57) 24 LEU (168.5, 166.7)	(57) 24 LEU (168.5, 166.7)
(58) 63 ASP (168.5, -177.7)	(58) 63 ASP (168.5, -177.7)
(59) 63 ASP (168.4, 166.7)	(59) 63 ASP (168.4, 166.7)
(60) 9 THR (161.4, 78.1)	(60) 9 THR (161.4, 78.1)
(61) 24 LEU (167.5, 137.4)	(61) 24 LEU (167.5, 137.4)
(62) 4 GLY (166.5, 14.7)	(62) 4 GLY (166.5, 14.7)
(63) 24 LEU (175.7, 168.5)	(63) 24 LEU (175.7, 168.5)
(64) 137 ARG (168.5, 93.8)	(64) 137 ARG (168.5, 93.8)
(65) 63 ASP (168.5, 93.8)	(65) 63 ASP (168.5, 93.8)
(66) 24 LEU (167.7, 137.4)	(66) 24 LEU (167.7, 137.4)
(67) 4 GLY (175.2, 79.1)	(67) 4 GLY (175.2, 79.1)
(68) 24 LEU (175.8, 158.9)	(68) 24 LEU (175.8, 158.9)
(69) 24 LEU (175.8, 158.9)	(69) 24 LEU (175.8, 158.9)
(70) 9 THR (161.4, 78.1)	(70) 9 THR (161.4, 78.1)
(71) 63 ASP (175.6, 167.7)	(71) 63 ASP (175.6, 167.7)
(72) 63 ASP (175.7, 158.9)	(72) 63 ASP (175.7, 158.9)
(73) 63 ASP (168.5, -177.7)	(73) 63 ASP (168.5, -177.7)
(74) 63 ASP (168.4, 166.7)	(74) 63 ASP (168.4, 166.7)
(75) 9 THR (161.4, 78.1)	(75) 9 THR (161.4, 78.1)
(76) 24 LEU (168.5, 166.7)	(76) 24 LEU (168.5, 166.7)
(77) 63 ASP (168.5, -177.7)	(77) 63 ASP (168.5, -177.7)
(78) 63 ASP (168.4, 166.7)	(78) 63 ASP (168.4, 166.7)
(79) 9 THR (161.4, 78.1)	(79) 9 THR (161.4, 78.1)
(80) 24 LEU (167.5, 137.4)	(80) 24 LEU (167.5, 137.4)
(81) 4 GLY (166.5, 14.7)	(81) 4 GLY (166.5, 14.7)
(82) 24 LEU (175.7, 168.5)	(82) 24 LEU (175.7, 168.5)
(83) 137 ARG (168.5, 93.8)	(83) 137 ARG (168.5, 93.8)
(84) 63 ASP (168.5, 93.8)	(84) 63 ASP (168.5, 93.8)
(85) 24 LEU (167.7, 137.4)	(85) 24 LEU (167.7, 137.4)
(86) 4 GLY (175.2, 79.1)	(86) 4 GLY (175.2, 79.1)
(87) 24 LEU (175.8, 158.9)	(87) 24 LEU (175.8, 158.9)
(88) 24 LEU (175.8, 158.9)	(88) 24 LEU (175.8, 158.9)
(89) 9 THR (161.4, 78.1)	(89) 9 THR (161.4, 78.1)
(90) 63 ASP (175.6, 167.7)	(90) 63 ASP (175.6, 167.7)
(91) 63 ASP (175.7, 158.9)	(91) 63 ASP (175.7, 158.9)
(92) 63 ASP (168.5, -177.7)	(92) 63 ASP (168.5, -177.7)
(93) 63 ASP (168.4, 166.7)	(93) 63 ASP (168.4, 166.7)
(94) 9 THR (161.4, 78.1)	(94) 9 THR (161.4, 78.1)
(95) 24 LEU (168.5, 166.7)	(95) 24 LEU (168.5, 166.7)
(96) 63 ASP (168.5, -177.7)	(96) 63 ASP (168.5, -177.7)
(97) 63 ASP (168.4, 166.7)	(97) 63 ASP (168.4, 166.7)
(98) 9 THR (161.4, 78.1)	(98) 9 THR (161.4, 78.1)
(99) 24 LEU (167.5, 137.4)	(99) 24 LEU (167.5, 137.4)
(100) 4 GLY (166.5, 14.7)	(100) 4 GLY (166.5, 14.7)
(101) 24 LEU (175.7, 168.5)	(101) 24 LEU (175.7, 168.5)
(102) 137 ARG (168.5, 93.8)	(102) 137 ARG (168.5, 93.8)
(103) 63 ASP (168.5, 93.8)	(103) 63 ASP (168.5, 93.8)
(104) 24 LEU (167.7, 137.4)	(104) 24 LEU (167.7, 137.4)
(105) 4 GLY (175.2, 79.1)	(105) 4 GLY (175.2, 79.1)
(106) 24 LEU (175.8, 158.9)	(106) 24 LEU (175.8, 158.9)
(107) 24 LEU (175.8, 158.9)	(107) 24 LEU (175.8, 158.9)
(108) 9 THR (161.4, 78.1)	(108) 9 THR (161.4, 78.1)
(109) 63 ASP (175.6, 167.7)	(109) 63 ASP (175.6, 167.7)
(110) 63 ASP (175.7, 158.9)	(110) 63 ASP (175.7, 158.9)
(111) 63 ASP (168.5, -177.7)	(111) 63 ASP (168.5, -177.7)
(112) 63 ASP (168.4, 166.7)	(112) 63 ASP (168.4, 166.7)
(113) 9 THR (161.4, 78.1)	(113) 9 THR (161.4, 78.1)
(114) 24 LEU (168.5, 166.7)	(114) 24 LEU (168.5, 166.7)
(115) 63 ASP (168.5, -177.7)	(115) 63 ASP (168.5, -177.7)
(116) 63 ASP (168.4, 166.7)	(116) 63 ASP (168.4, 166.7)
(117) 9 THR (161.4, 78.1)	(117) 9 THR (161.4, 78.1)
(118) 24 LEU (167.5, 137.4)	(118) 24 LEU (167.5, 137.4)
(119) 4 GLY (166.5, 14.7)	(119) 4 GLY (166.5, 14.7)
(120) 24 LEU (175.7, 168.5)	(120) 24 LEU (175.7, 168.5)
(121) 137 ARG (168.5, 93.8)	(121) 137 ARG (168.5, 93.8)
(122) 63 ASP (168.5, 93.8)	(122) 63 ASP (168.5, 93.8)
(123) 24 LEU (167.7, 137.4)	(123) 24 LEU (167.7, 137.4)
(124) 4 GLY (175.2, 79.1)	(124) 4 GLY (175.2, 79.1)
(125) 24 LEU (175.8, 158.9)	(125) 24 LEU (175.8, 158.9)
(126) 24 LEU (175.8, 158.9)	(126) 24 LEU (175.8, 158.9)
(127) 9 THR (161.4, 78.1)	(127) 9 THR (161.4, 78.1)
(128) 63 ASP (175.6, 167.7)	(128) 63 ASP (175.6, 167.7)
(129) 63 ASP (175.7, 158.9)	(129) 63 ASP (175.7, 158.9)
(130) 63 ASP (168.5, -177.7)	(130) 63 ASP (168.5, -177.7)
(131) 63 ASP (168.4, 166.7)	(131) 63 ASP (168.4, 166.7)
(132) 9 THR (161.4, 78.1)	(132) 9 THR (161.4, 78.1)
(133) 24 LEU (168.5, 166.7)	(133) 24 LEU (168.5, 166.7)
(134) 63 ASP (168.5, -177.7)	(134) 63 ASP (168.5, -177.7)
(135) 63 ASP (168.4, 166.7)	(135) 63 ASP (168.4, 166.7)
(136) 9 THR (161.4, 78.1)	(136) 9 THR (161.4, 78.1)
(137) 24 LEU (167.5, 137.4)	(137) 24 LEU (167.5, 137.4)
(138) 4 GLY (166.5, 14.7)	(138) 4 GLY (166.5, 14.7)
(139) 24 LEU (175.7, 168.5)	(139) 24 LEU (175.7, 168.5)
(140) 137 ARG (168.5, 93.8)	(140) 137 ARG (168.5, 93.8)
(141) 63 ASP (168.5, 93.8)	(141) 63 ASP (168.5, 93.8)
(142) 24 LEU (167.7, 137.4)	(142) 24 LEU (167.7, 137.4)
(143) 4 GLY (175.2, 79.1)	(143) 4 GLY (175.2, 79.1)
(144) 24 LEU (175.8, 158.9)	(144) 24 LEU (175.8, 158.9)
(145) 24 LEU (175.8, 158.9)	(145) 24 LEU (175.8, 158.9)
(146) 9 THR (161.4, 78.1)	(146) 9 THR (161.4, 78.1)
(147) 63 ASP (175.6, 167.7)	(147) 63 ASP (175.6, 167.7)
(148) 63 ASP (175.7, 158.9)	(148) 63 ASP (175.7, 158.9)
(149) 63 ASP (168.5, -177.7)	(149) 63 ASP (168.5, -177.7)
(150) 63 ASP (168.4, 166.7)	(150) 63 ASP (168.4, 166.7)
(151) 9 THR (161.4, 78.1)	(151) 9 THR (161.4, 78.1)
(152) 24 LEU (168.5, 166.7)	(152) 24 LEU (168.5, 166.7)
(153) 63 ASP (168.5, -177.7)	(153) 63 ASP (168.5, -177.7)
(154) 63 ASP (168.4, 166.7)	(154) 63 ASP (168.4, 166.7)
(155) 9 THR (161.4, 78.1)	(155) 9 THR (161.4, 78.1)
(156) 24 LEU (167.5, 137.4)	(156) 24 LEU (167.5, 137.4)
(157) 4 GLY (166.5, 14.7)	(157) 4 GLY (166.5, 14.7)
(158) 24 LEU (175.7, 168.5)	(158) 24 LEU (175.7, 168.5)
(159) 137 ARG (168.5, 93.8)	(159) 137 ARG (168.5, 93.8)
(160) 63 ASP (168.5, 93.8)	(160) 63 ASP (168.5, 93.8)
(161) 24 LEU (167.7, 137.4)	(161) 24 LEU (167.7, 137.4)
(162) 4 GLY (175.2, 79.1)	(162) 4 GLY (175.2, 79.1)
(163) 24 LEU (175.8, 158.9)	(163) 24 LEU (175.8, 158.9)
(164) 24 LEU (175.8, 158.9)	(164) 24 LEU (175.8, 158.9)
(165) 9 THR (161.4, 78.1)	(165) 9 THR (161.4, 78.1)
(166) 63 ASP (175.6, 167.7)	(166) 63 ASP (175.6, 167.7)
(167) 63 ASP (175.7, 158.9)	(167) 63 ASP (175.7, 158.9)
(168) 63 ASP (168.5, -177.7)	(168) 63 ASP (168.5, -177.7)
(169) 63 ASP (168.4, 166.7)	(169) 63 ASP (168.4, 166.7)
(170) 9 THR (161.4, 78.1)	(170) 9 THR (161.4, 78.1)
(171) 24 LEU (168.5, 166.7)	(171) 24 LEU (168.5, 166.7)
(172) 63 ASP (168.5, -177.7)	(172) 63 ASP (168.5, -177.7)
(173) 63 ASP (168.4, 166.7)	(173) 63 ASP (168.4, 166.7)
(174) 9 THR (161.4, 78.1)	(174) 9 THR (161.4, 78.1)
(175) 24 LEU (167.5, 137.4)	(175) 24 LEU (167.5, 137.4)
(176) 4 GLY (166.5, 14.7)	(176) 4 GLY (166.5, 14.7)
(177) 24 LEU (175.7, 168.5)	(177) 24 LEU (175.7, 168.5)
(178) 137 ARG (168.5, 93.8)	(178) 137 ARG (168.5, 93.8)
(179) 63 ASP (168.5, 93.8)	(179) 63 ASP (168.5, 93.8)
(180) 24 LEU (167.7, 137.4)	(180) 24 LEU (167.7, 137.4)
(181) 4 GLY (175.2, 79.1)	(181) 4 GLY (175.2, 79.1)
(182) 24 LEU (175.8, 158.9)	(182) 24 LEU (175.8, 158.9)
(183) 24 LEU (175.8, 158.9)	(183) 24 LEU (175.8, 158.9)
(184) 9 THR (161.4, 78.1)	(184) 9 THR (161.4, 78.1)
(185) 63 ASP (175.6, 167.7)	(185) 63 ASP (175.6, 167.7)
(186) 63 ASP (175.7, 158.9)	(186) 63 ASP (175.7, 158.9)
(187) 63 ASP (168.5, -177.7)	(187) 63 ASP (168.5, -177.7)
(188) 63 ASP (168.4, 166.7)	(188) 63 ASP (168.4, 166.7)
(189) 9 THR (161.4, 78.1)	(189) 9 THR (161.4, 78.1)
(190) 24 LEU (168.5, 166.7)	(190) 24 LEU (168.5, 166.7)
(191) 63 ASP (168.5, -177.7)	(191) 63 ASP (168.5, -177.7)
(192) 63 ASP (168.4, 166.7)	(192) 63 ASP (168.4, 166.7)
(193) 9 THR (161.4, 78.1)	(193) 9 THR (161.4, 78.1)
(194) 24 LEU (167.5, 137.4)	(194) 24 LEU (167.5, 137.4)
(195) 4 GLY (166.5, 14.7)	(195) 4 GLY (166.5, 14.7)
(196) 24 LEU (175.7, 168.5)	(196) 24 LEU (175.7, 168.5)
(197) 137 ARG (168.5, 93.8)	(197) 137 ARG (168.5, 93.8)
(198) 63 ASP (168.5, 93.8)	(198) 63 ASP (168.5, 93.8)
(199) 24 LEU (167.7, 137.4)	(199) 24 LEU (167.7, 137.4)
(200) 4 GLY (175.2, 79.1)	(200) 4 GLY (175.2, 79.1)
(201) 24 LEU (175.8, 158.9)	(201) 24 LEU (175.8, 158.9)
(202) 24 LEU (175.8, 158.9)	(202) 24 LEU (175.8, 158.9)
(203) 9 THR (161.4, 78.1)	(203) 9 THR (161.4, 78.1)
(204) 63 ASP (175.6, 167.7)	(204) 63 ASP (175.6, 167.7)
(205) 63 ASP (175.7, 158.9)	(205) 63 ASP (175.7, 158.9)
(206) 63 ASP (168.5, -177.7)	(206) 63 ASP (168.5, -177.7)
(207) 63 ASP (168.4, 166.7)	(207) 63 ASP (168.4, 166.7)
(208) 9 THR (161.4, 78.1)	(208) 9 THR (161.4, 78.1)
(209) 24 LEU (168.5, 166.7)	(209) 24 LEU (168.5, 166.7)
(210) 63 ASP (168.5, -177.7)	(210) 63 ASP (168.5, -177.7)
(211) 63 ASP (168.4, 166.7)	(211) 63 ASP (168.4, 166.7)
(212) 9 THR (161.4, 78.1)	(212) 9 THR (161.4, 78.1)
(213) 24 LEU (167.5, 137.4)	(213) 24 LEU (167.5, 137.4)
(214) 4 GLY (166.5, 14.7)	(214) 4 GLY (166.5, 14.7)
(215) 24 LEU (175.7, 168.5)	(215) 24 LEU (175.7, 168.5)
(216) 137 ARG (168.5, 93.8)	(216) 137 ARG (168.5, 93.8)
(217) 63 ASP (168.5, 93.8)	(217) 63 ASP (168.5, 93.8)
(218) 24 LEU (167.7, 137.4)	(218) 24 LEU (167.7, 137.4)
(219) 4 GLY (175.2, 79.1)	(219) 4 GLY (175.2, 79.1)
(220) 24 LEU (175.8, 158.9)	(220) 24 LEU (175.8, 158.9)
(221) 24 LEU (175.8, 158.9)	(221) 24 LEU (175.8, 158.9)
(222) 9 THR (161.4, 78.1)	(222) 9 THR (161.4, 78.1)
(223) 63 ASP (175.6, 167.7)	(223) 63 ASP (175.6, 167.7)
(224) 63 ASP (175.7, 158.9)	(224) 63 ASP (175.7, 158.9)
(225) 63 ASP (168.5, -177.7)	(225) 63 ASP (168.5, -177.7)
(226) 63 ASP (168.4, 166.7)	(226) 63 ASP (168.4, 166.7)
(227) 9 THR (161.4, 78.1)	(227) 9 THR (161.4, 78.1)
(228) 24 LEU (168.5, 166.7)	(228) 24 LEU (168.5, 166.7)
(229) 63 ASP (168.5, -177.7)	(229) 63 ASP (168.5, -177.7)
(230) 63 ASP (168.4, 166.7)	(230) 63 ASP (168.4, 166.7)
(231) 9 THR (161.4, 78.1)	(231) 9 THR (161.4, 78.1)

# 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



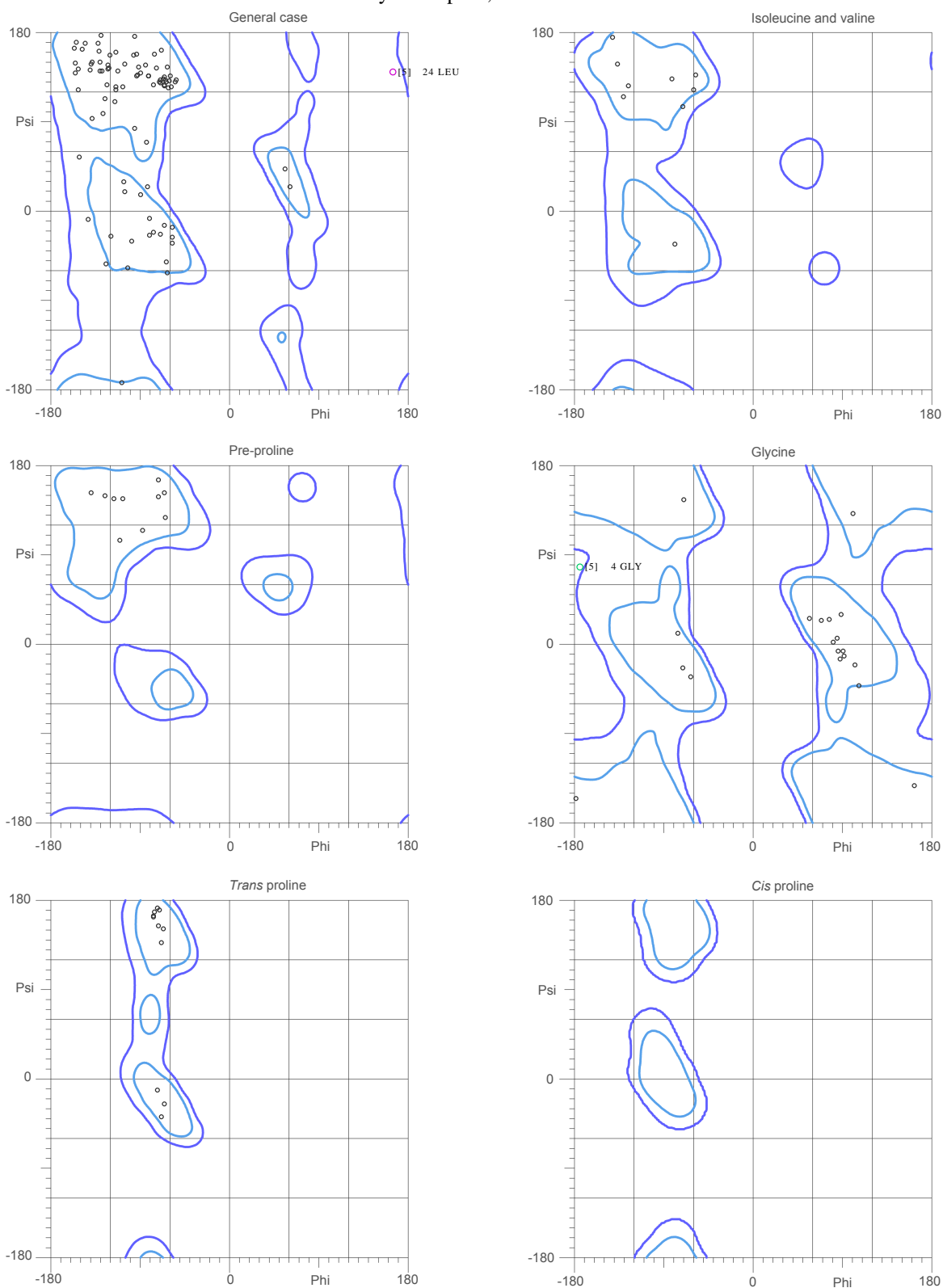
94.2% (130/138) of all residues were in favored (98%) regions.

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.

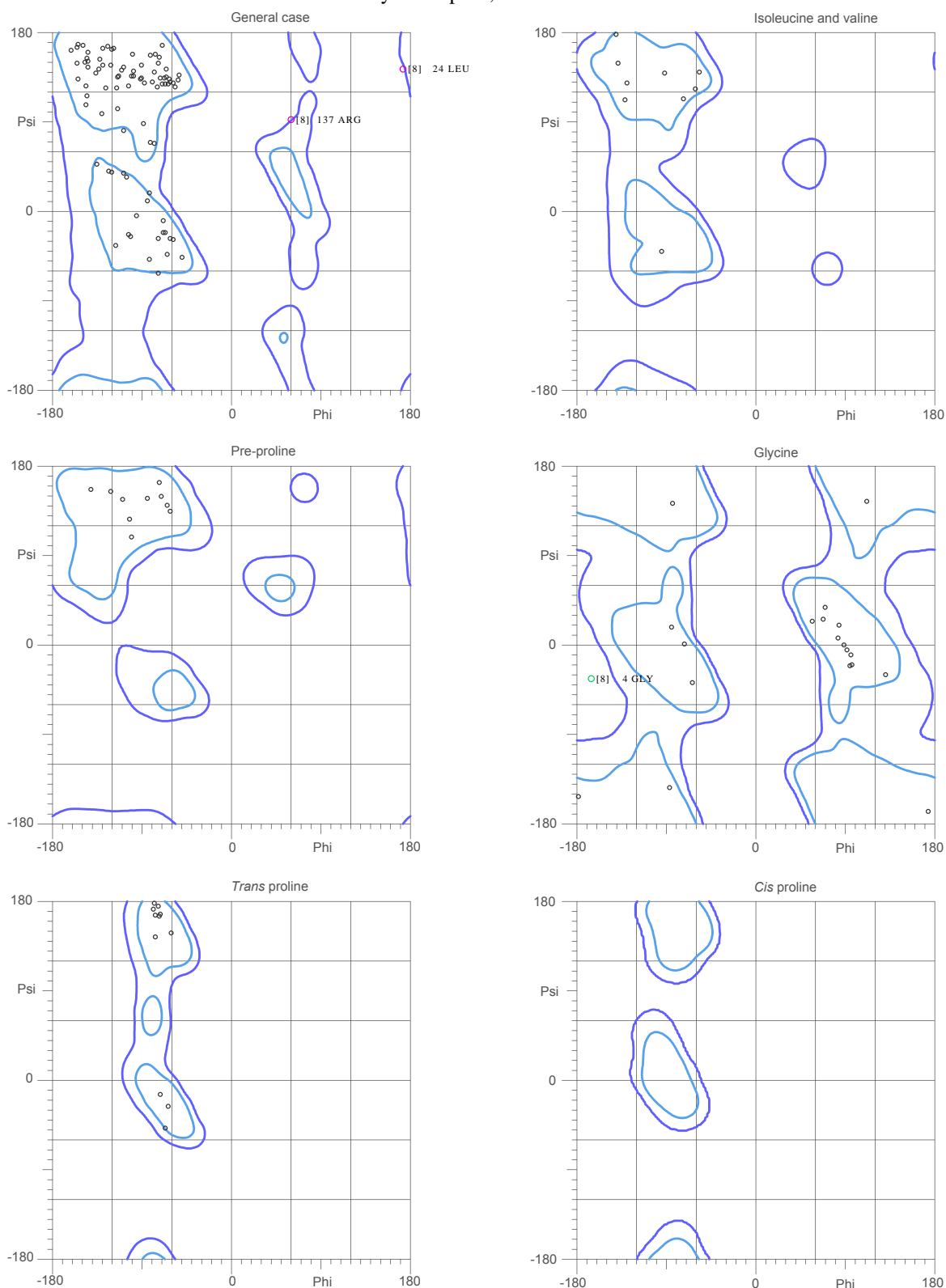
100.0% (138/138) of all residues were in allowed (>99.8%) regions.

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.

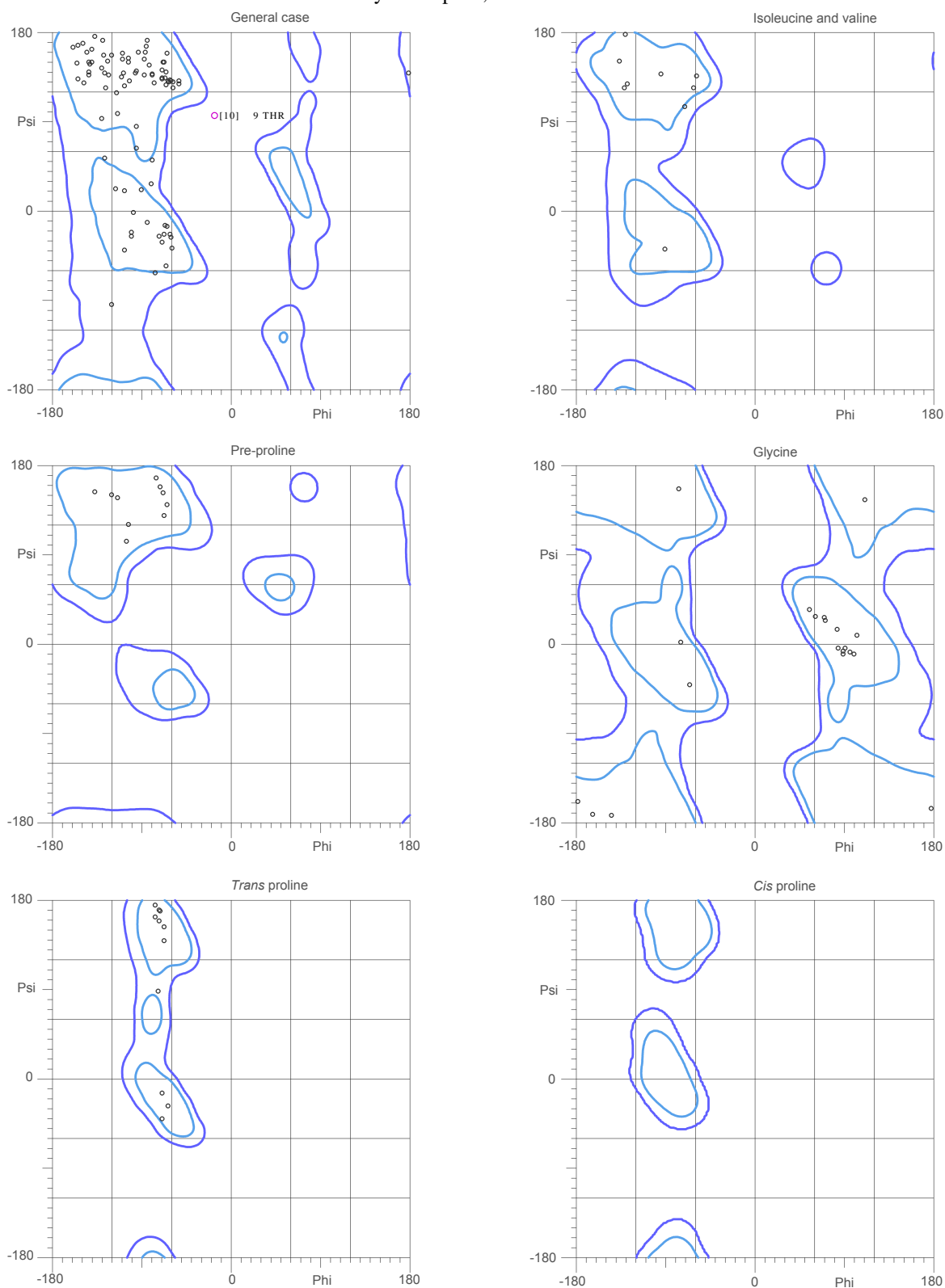
There were 2 outliers (phi, psi):

[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.

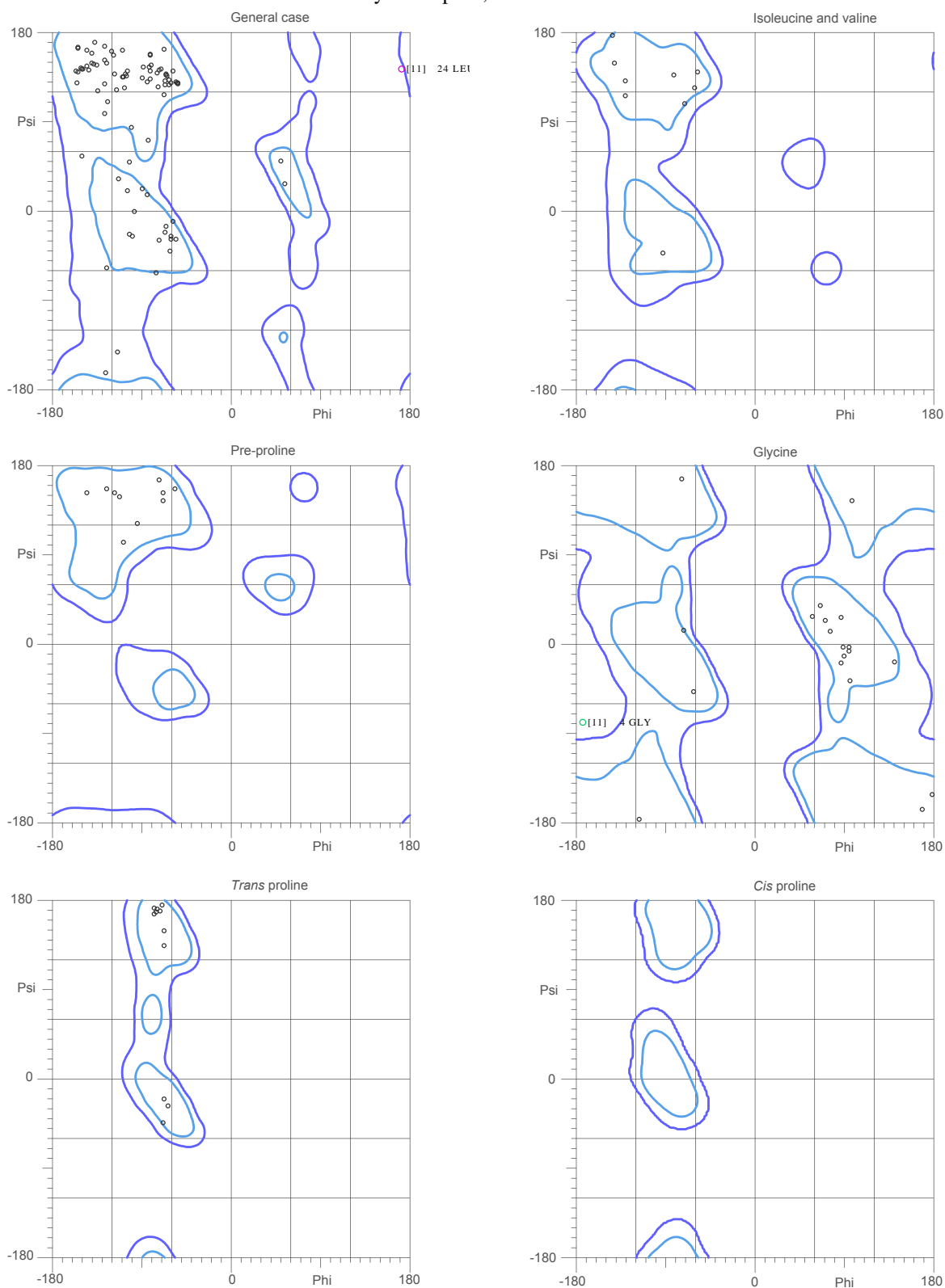
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

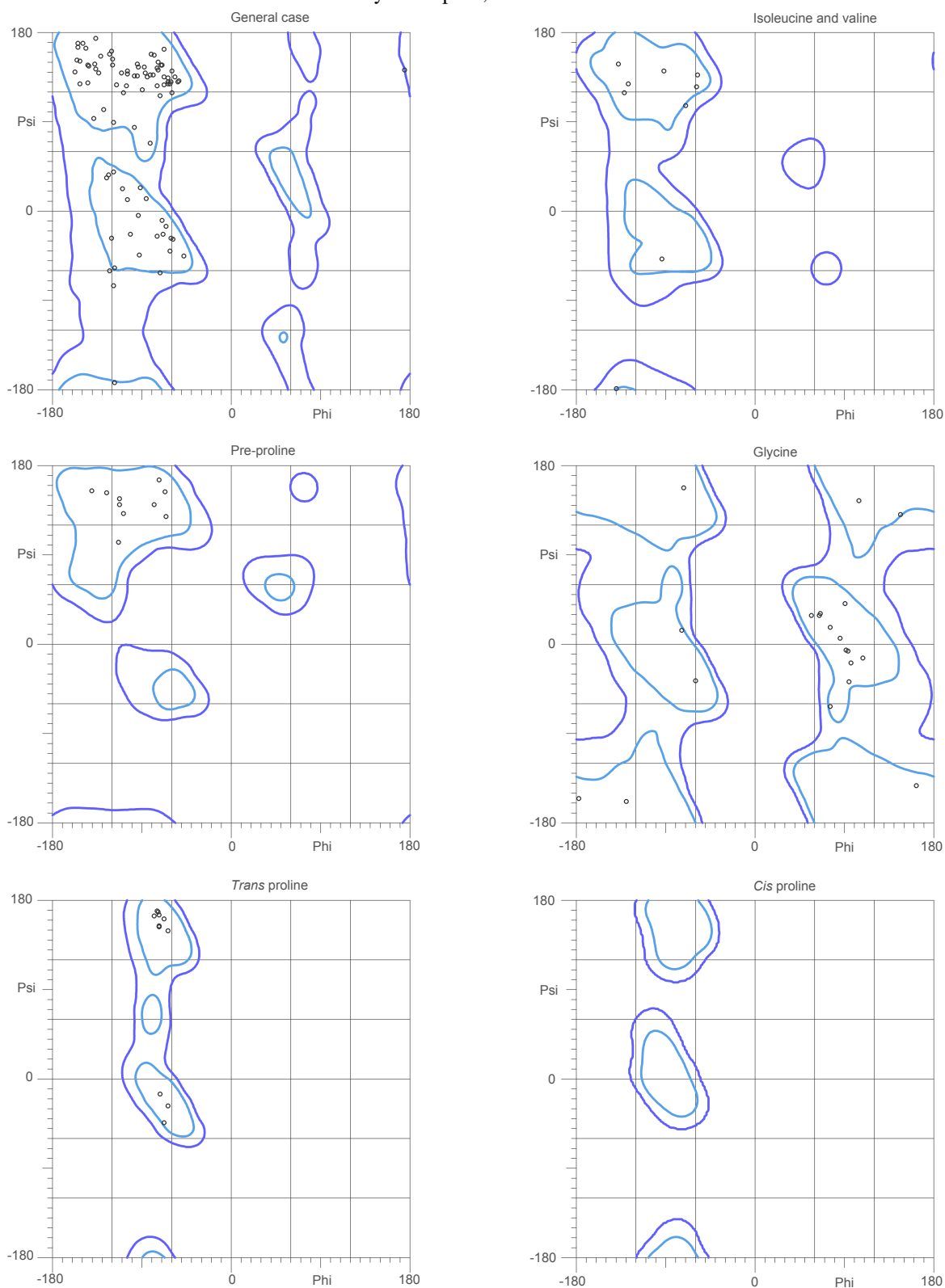
There were 2 outliers (phi, psi):

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

[11] 24 LEU (172.6, 144.8)

# MolProbity Ramachandran analysis

6yi3.H.pdb, model 12



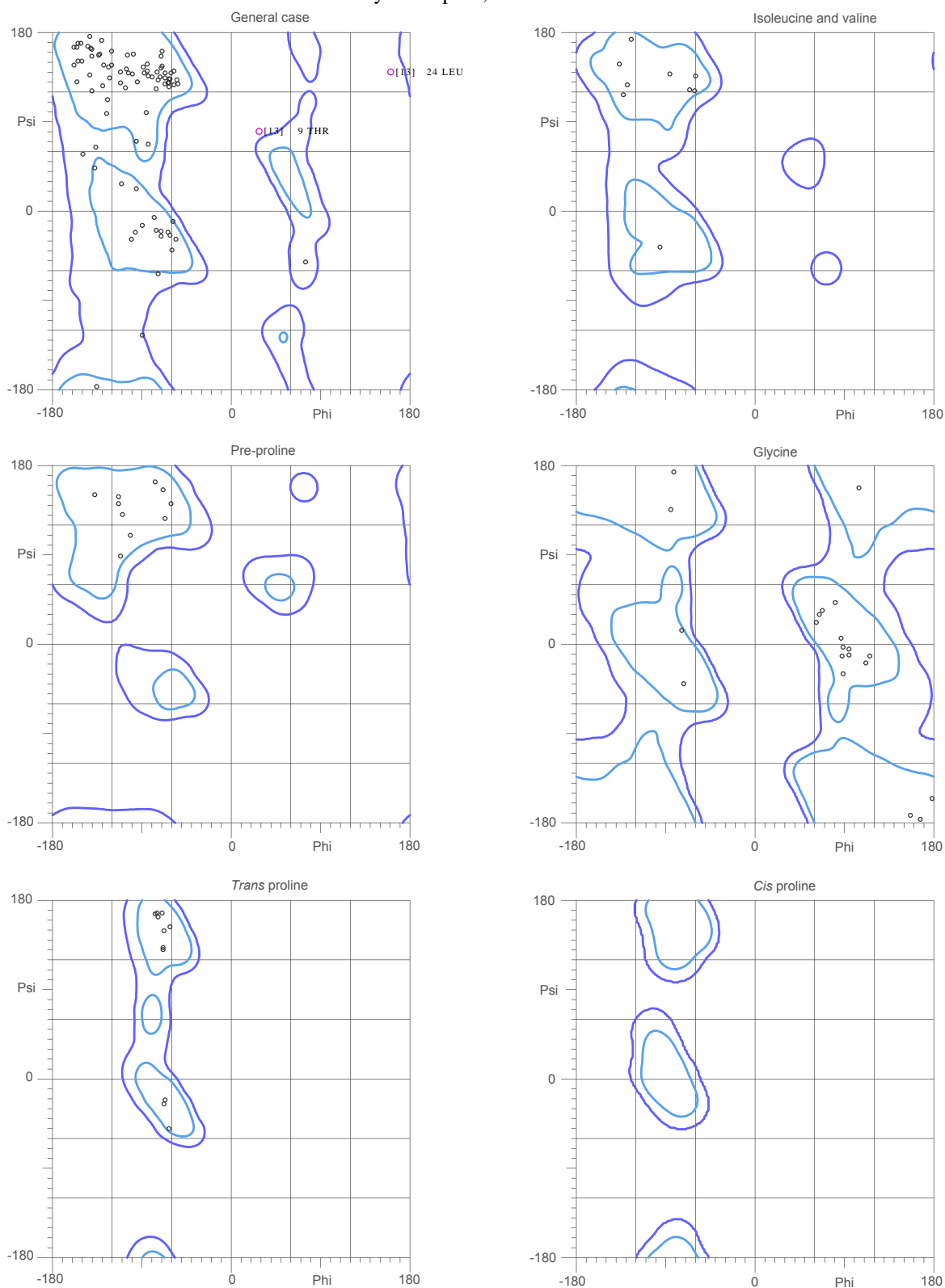
97.1% (134/138) of all residues were in favored (98%) regions.

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.

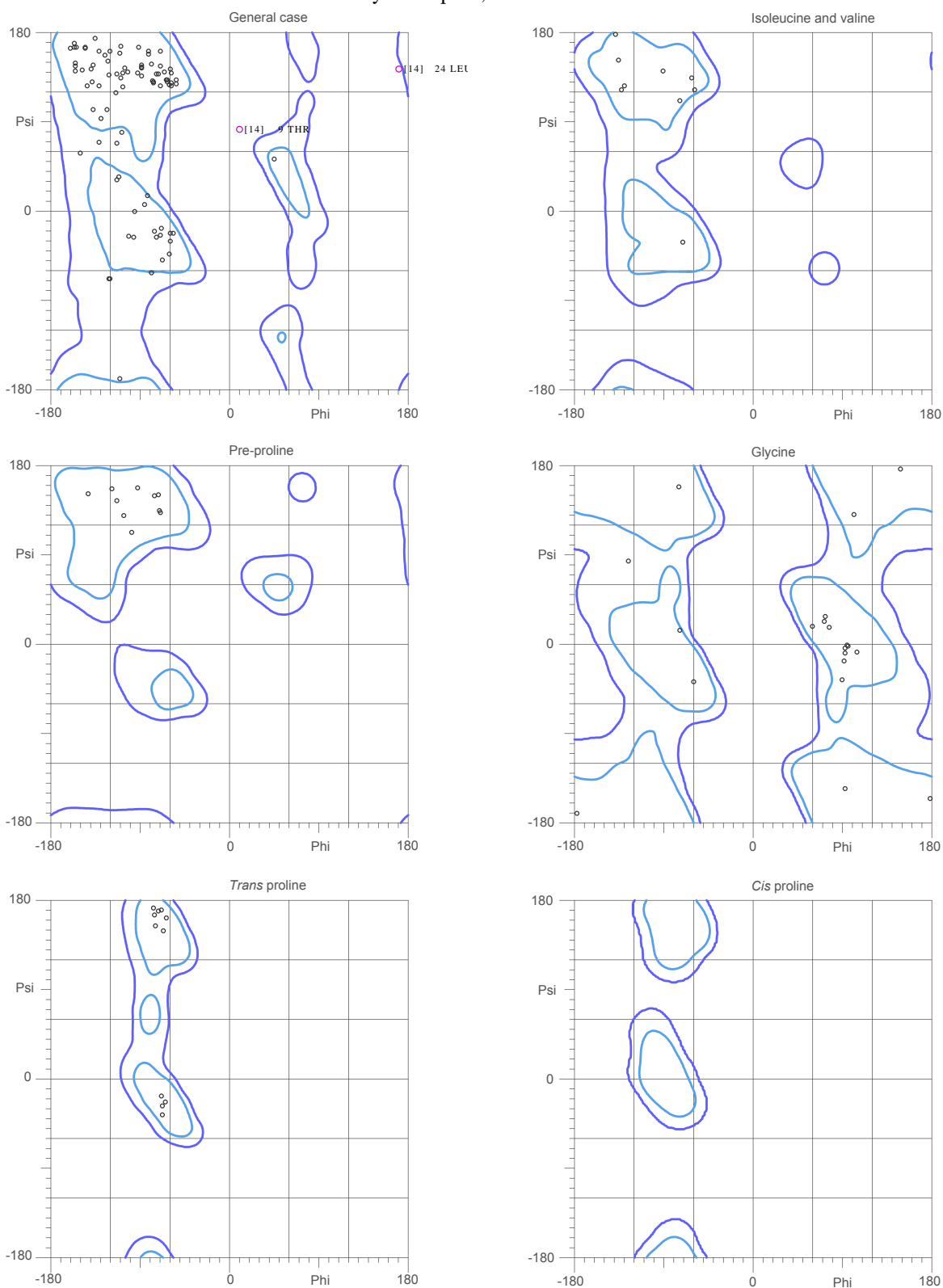
There were 2 outliers (phi, psi):

[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.

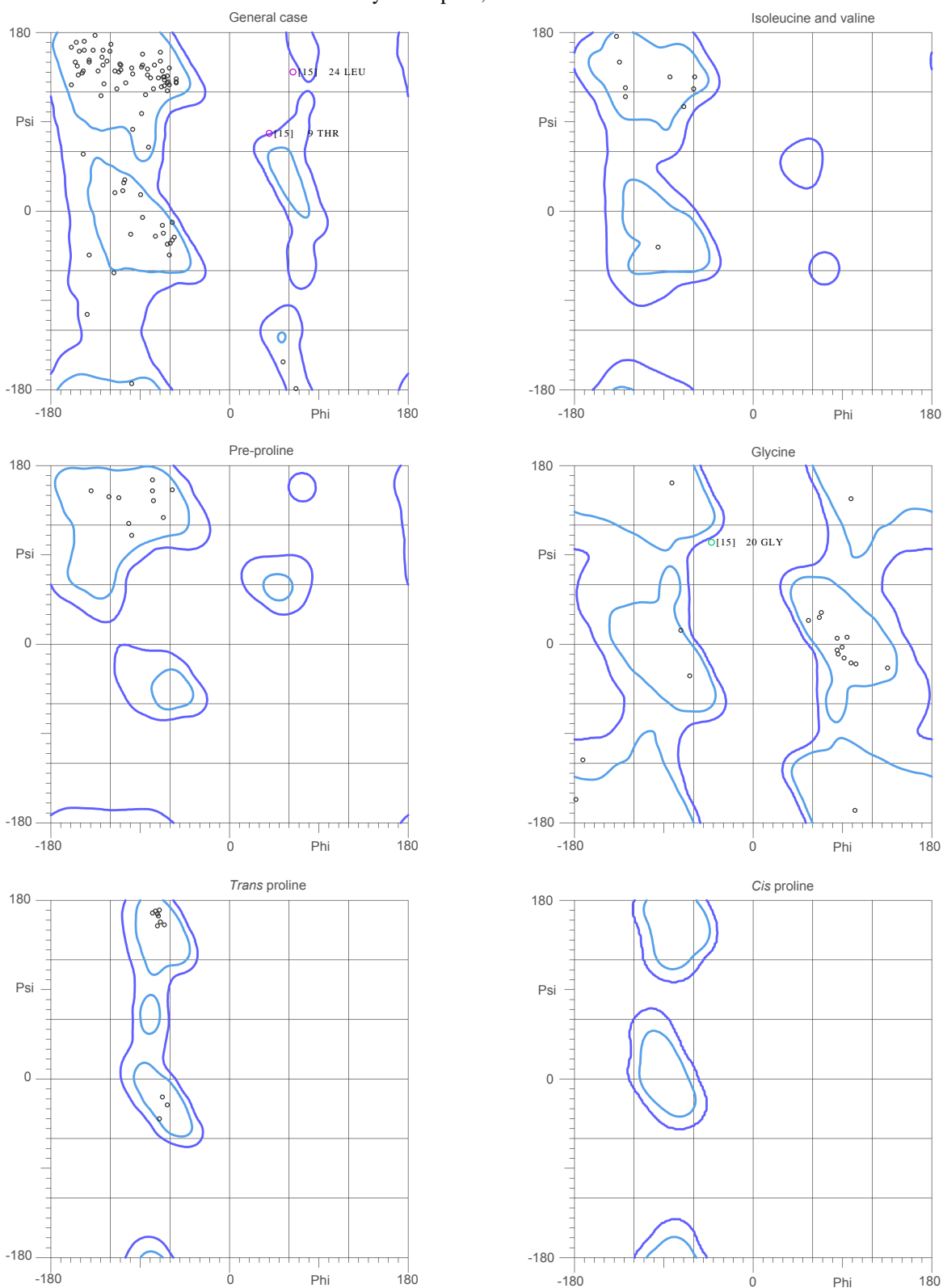
There were 2 outliers (phi, psi):

[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.

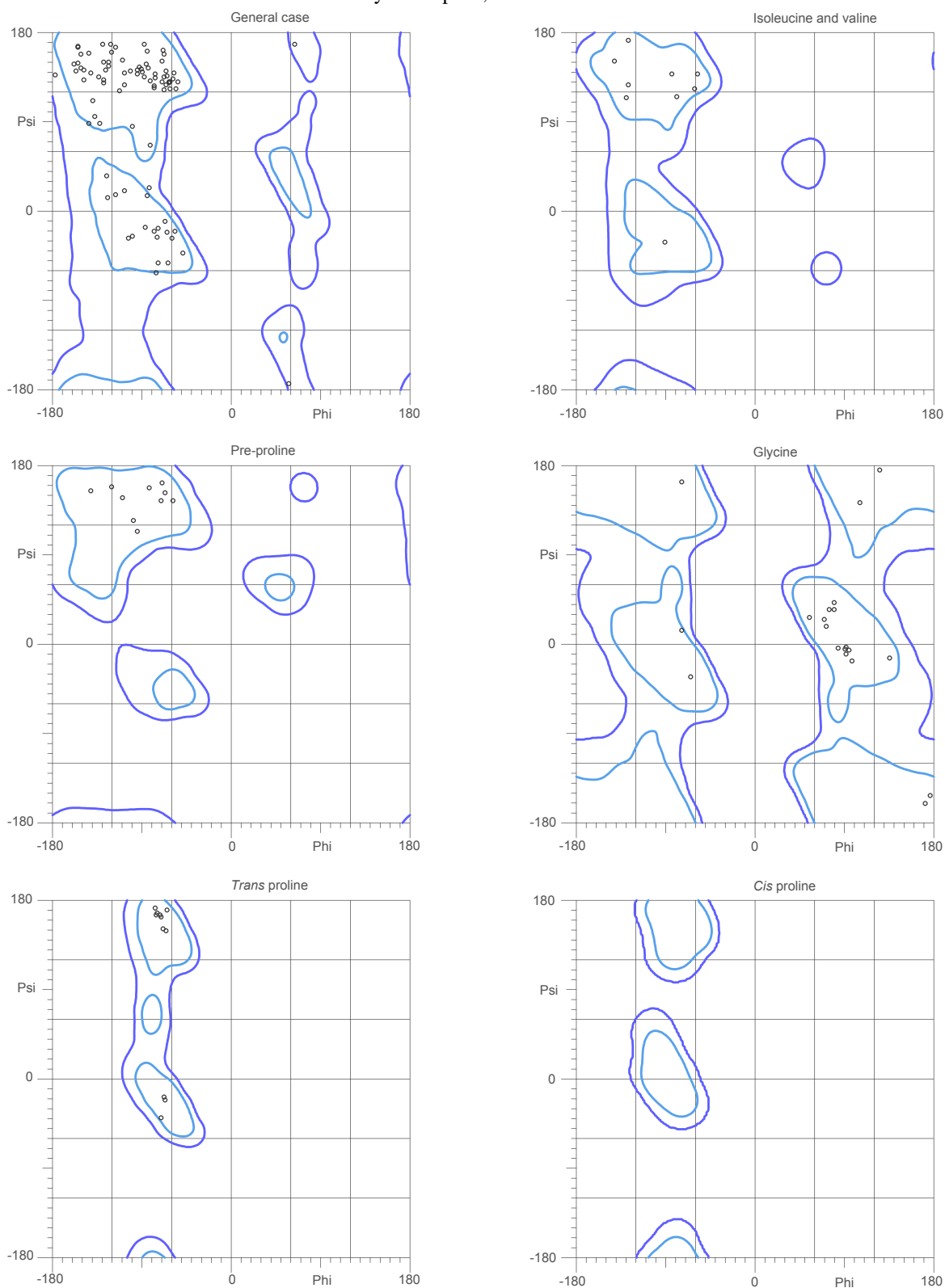
There were 3 outliers (phi, psi):

[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.

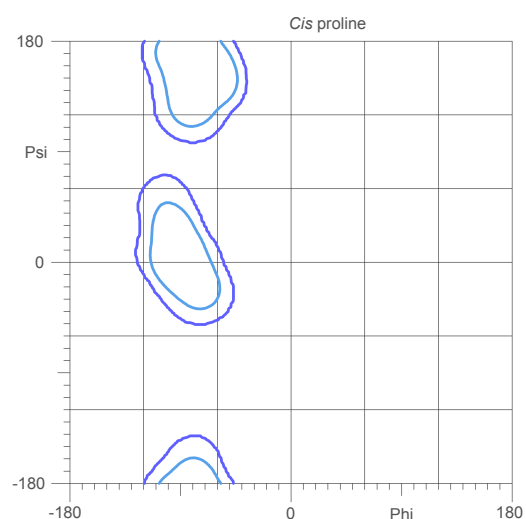
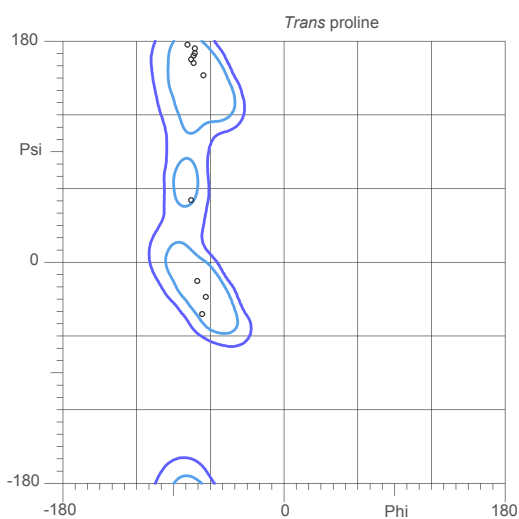
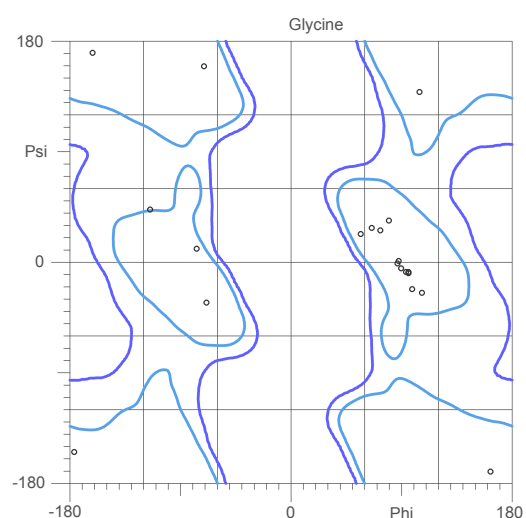
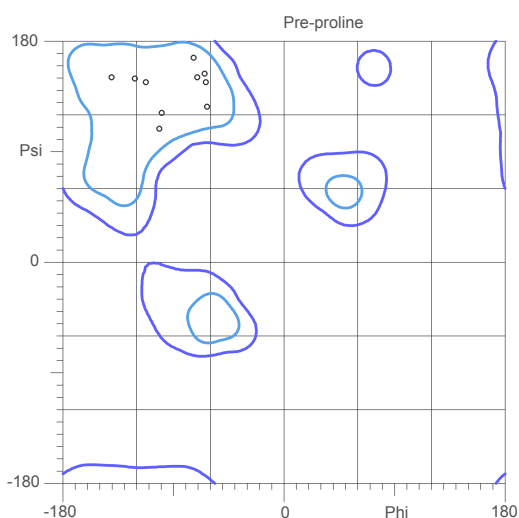
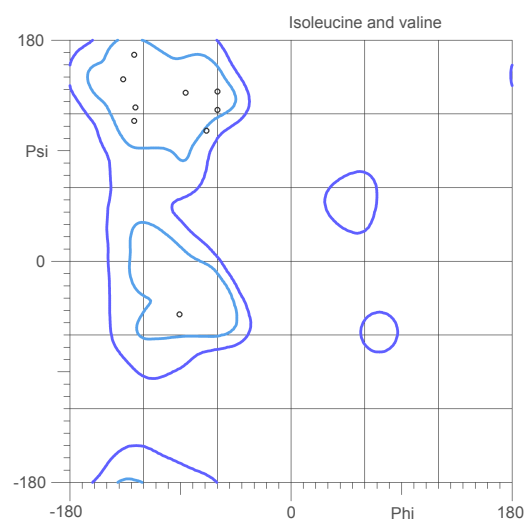
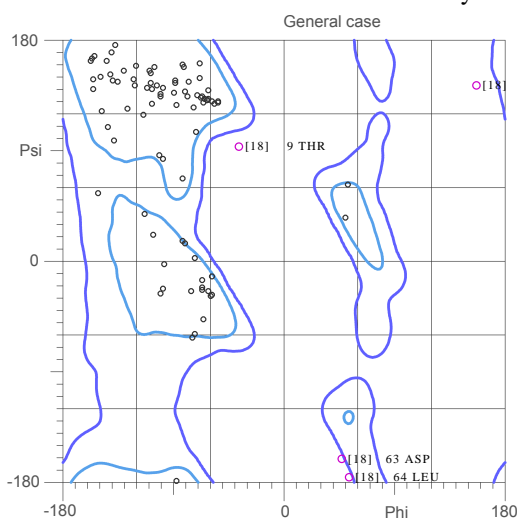
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

[17] 64 LEU (52.9, 178.7)

# MolProbity Ramachandran analysis

6yi3.H.pdb, model 18



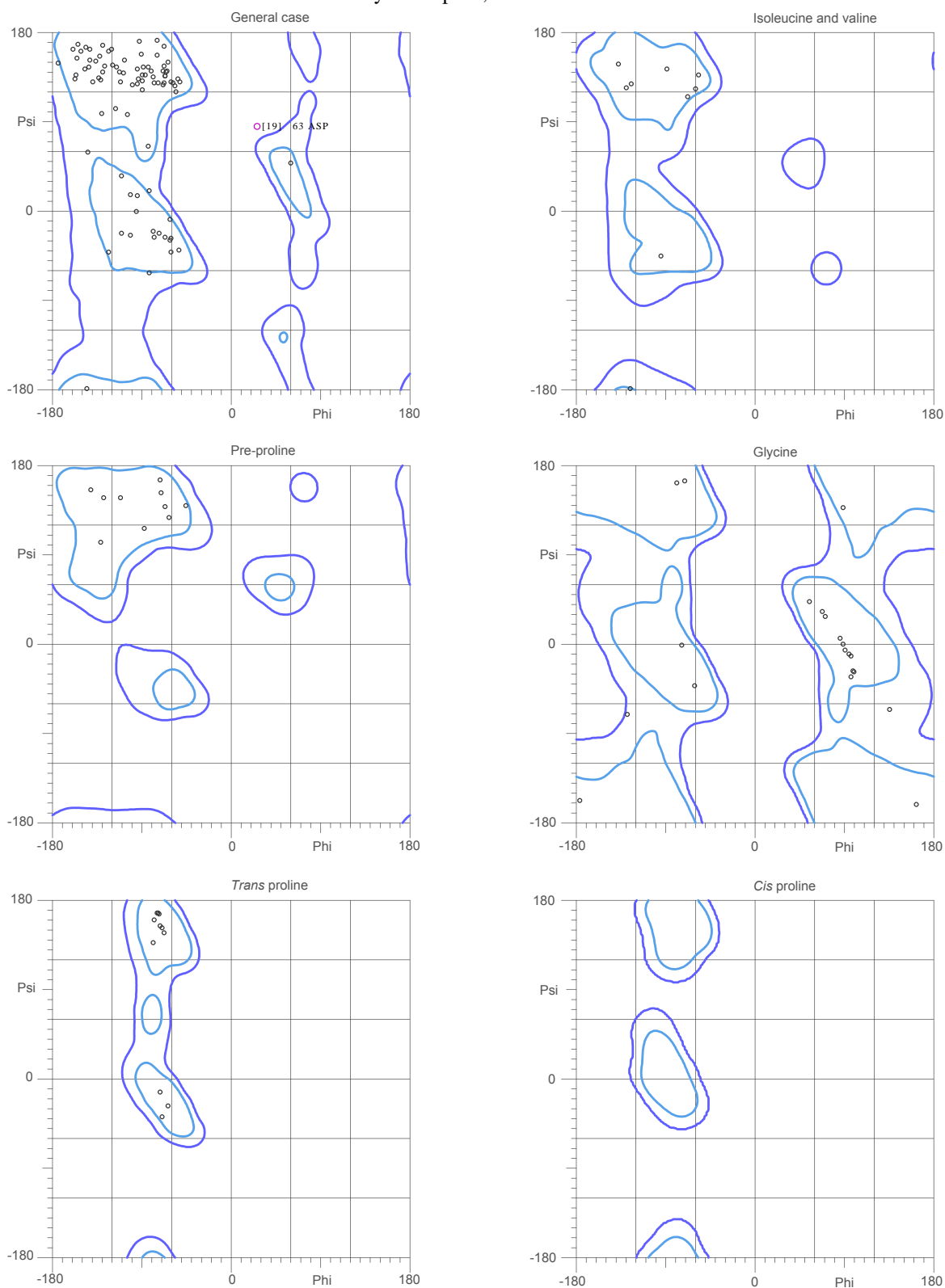
93.5% (129/138) of all residues were in favored (98%) regions.  
97.1% (134/138) of all residues were in allowed (>99.8%) regions.

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.

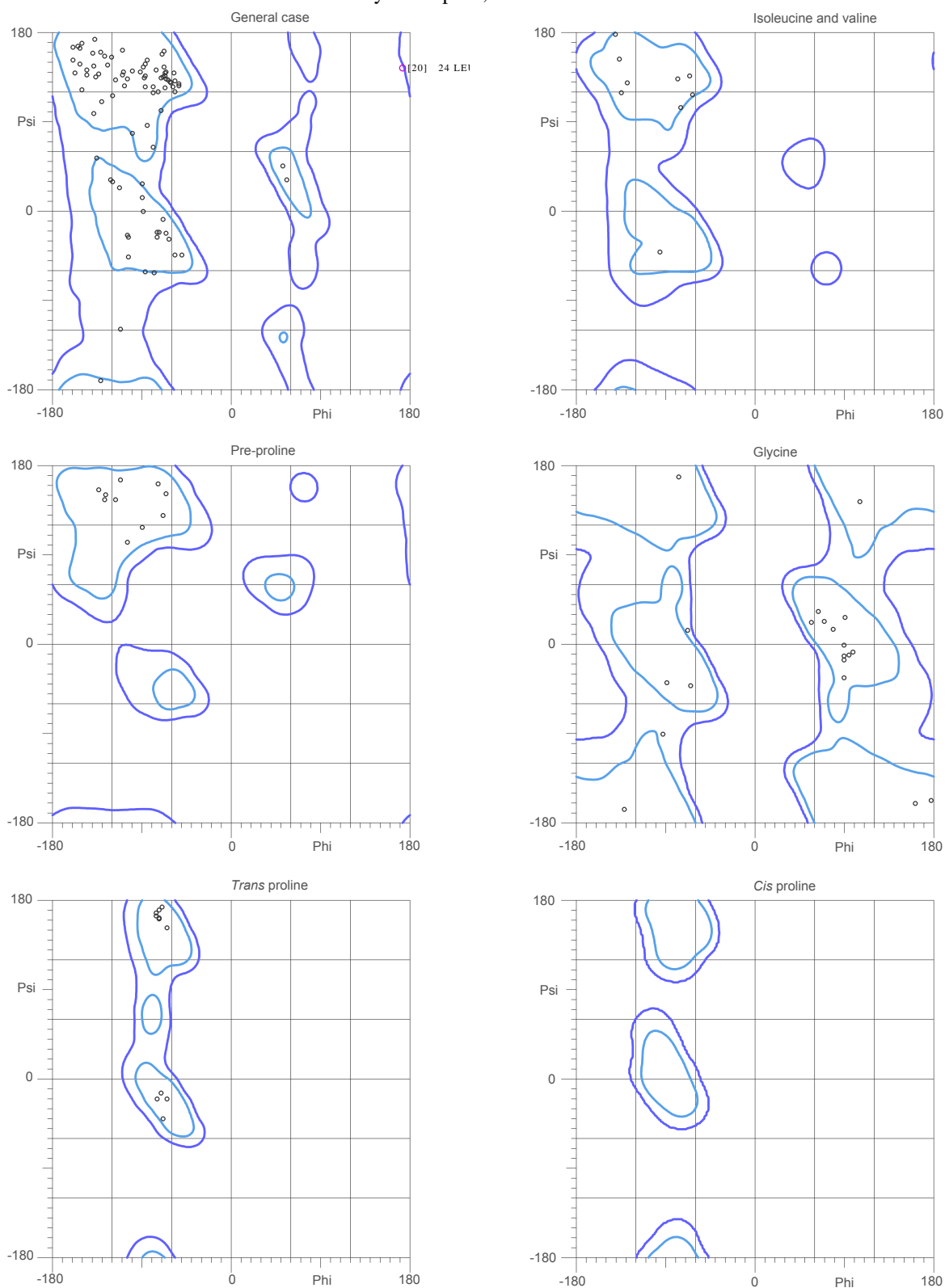
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

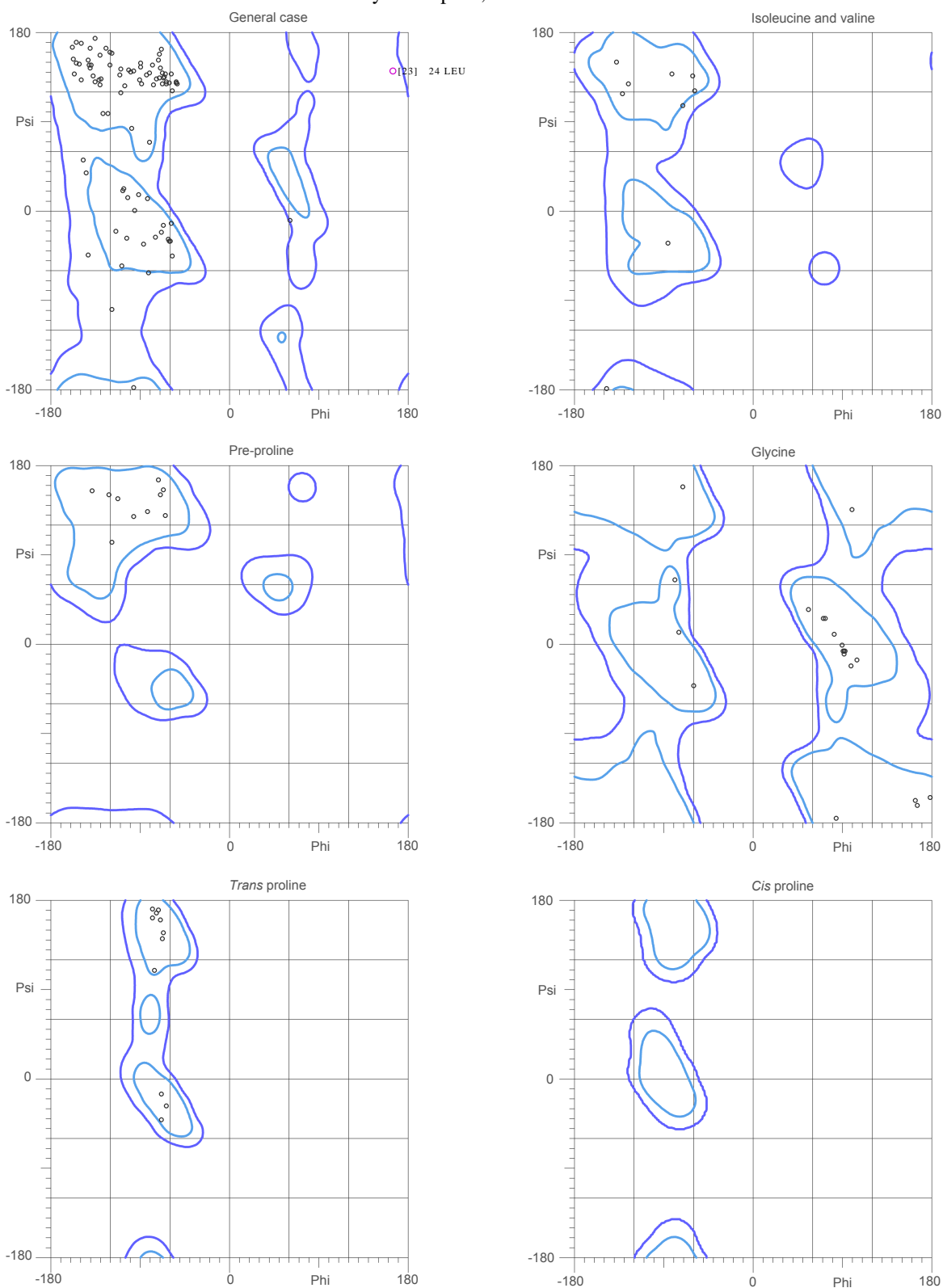
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

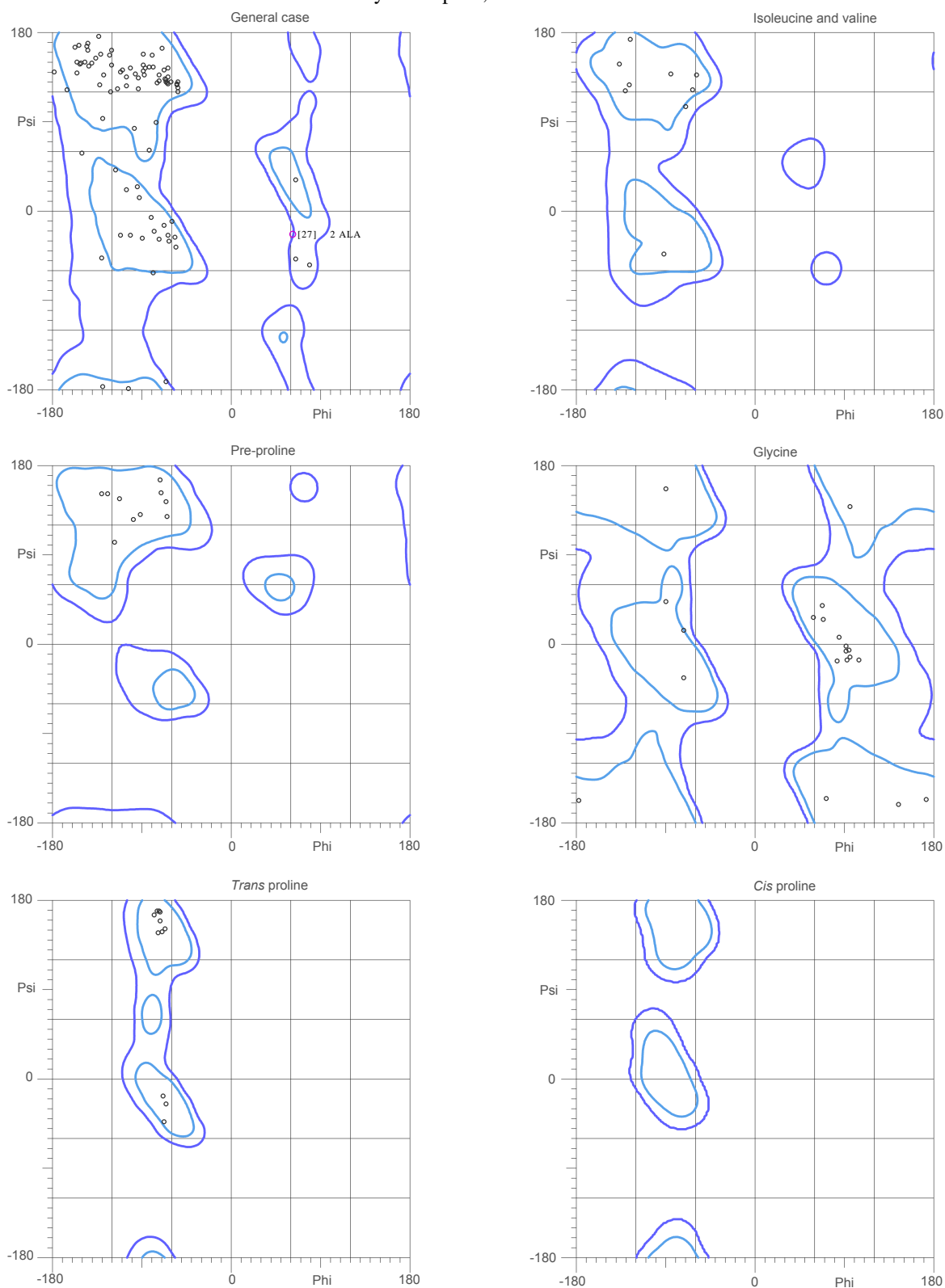
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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.

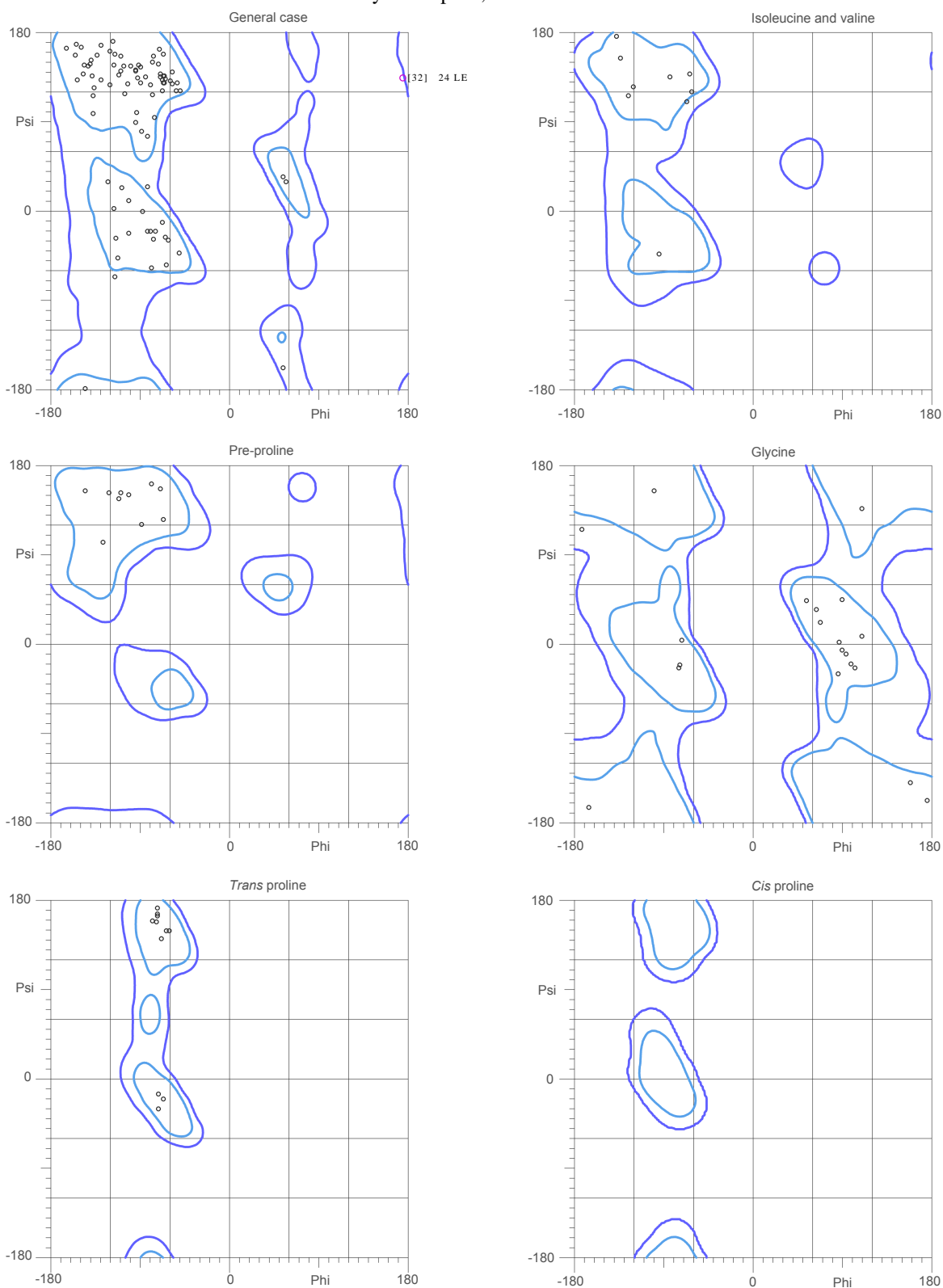
There were 1 outliers (phi, psi):

[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



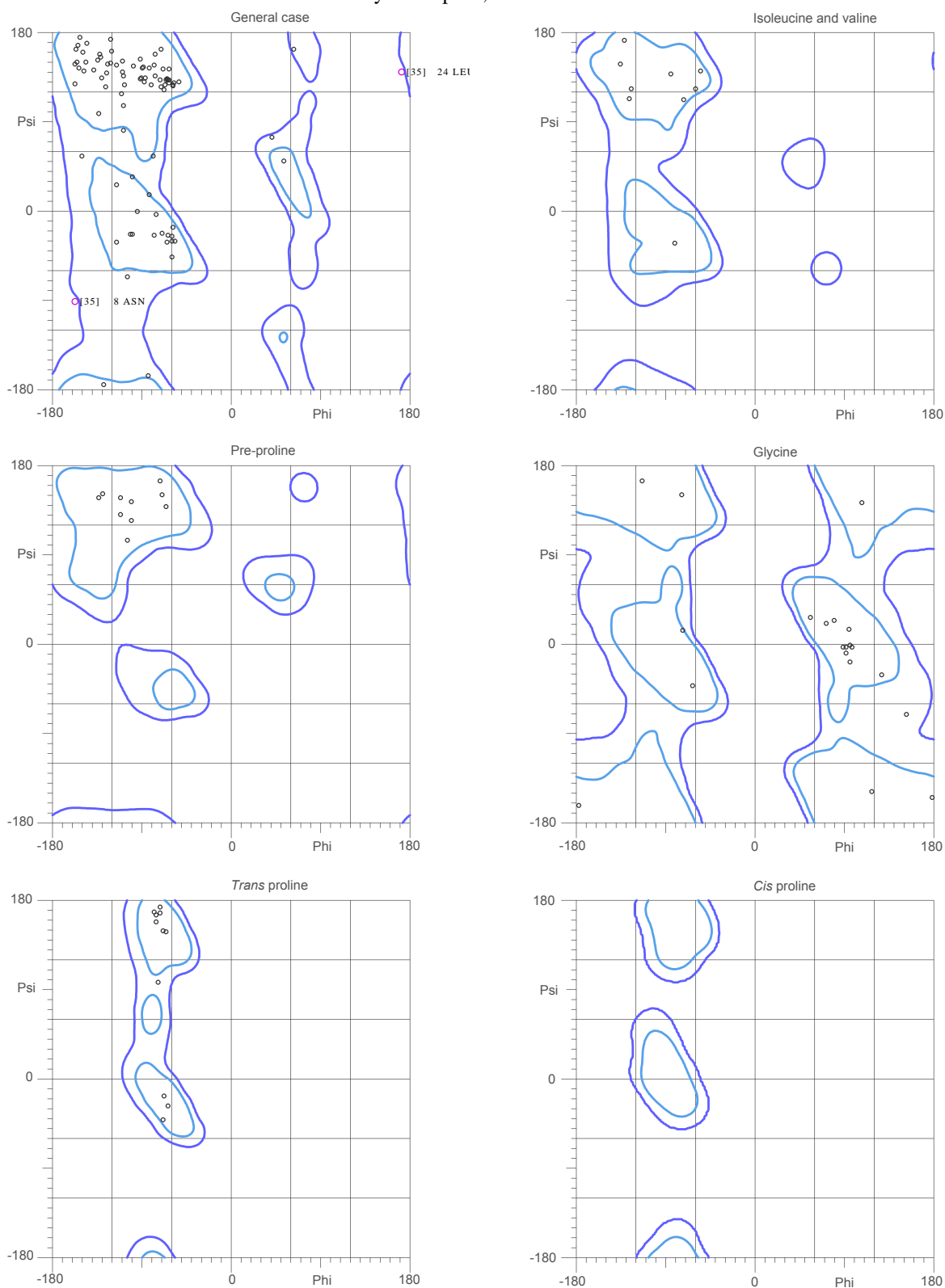
95.7% (132/138) of all residues were in favored (98%) regions.

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



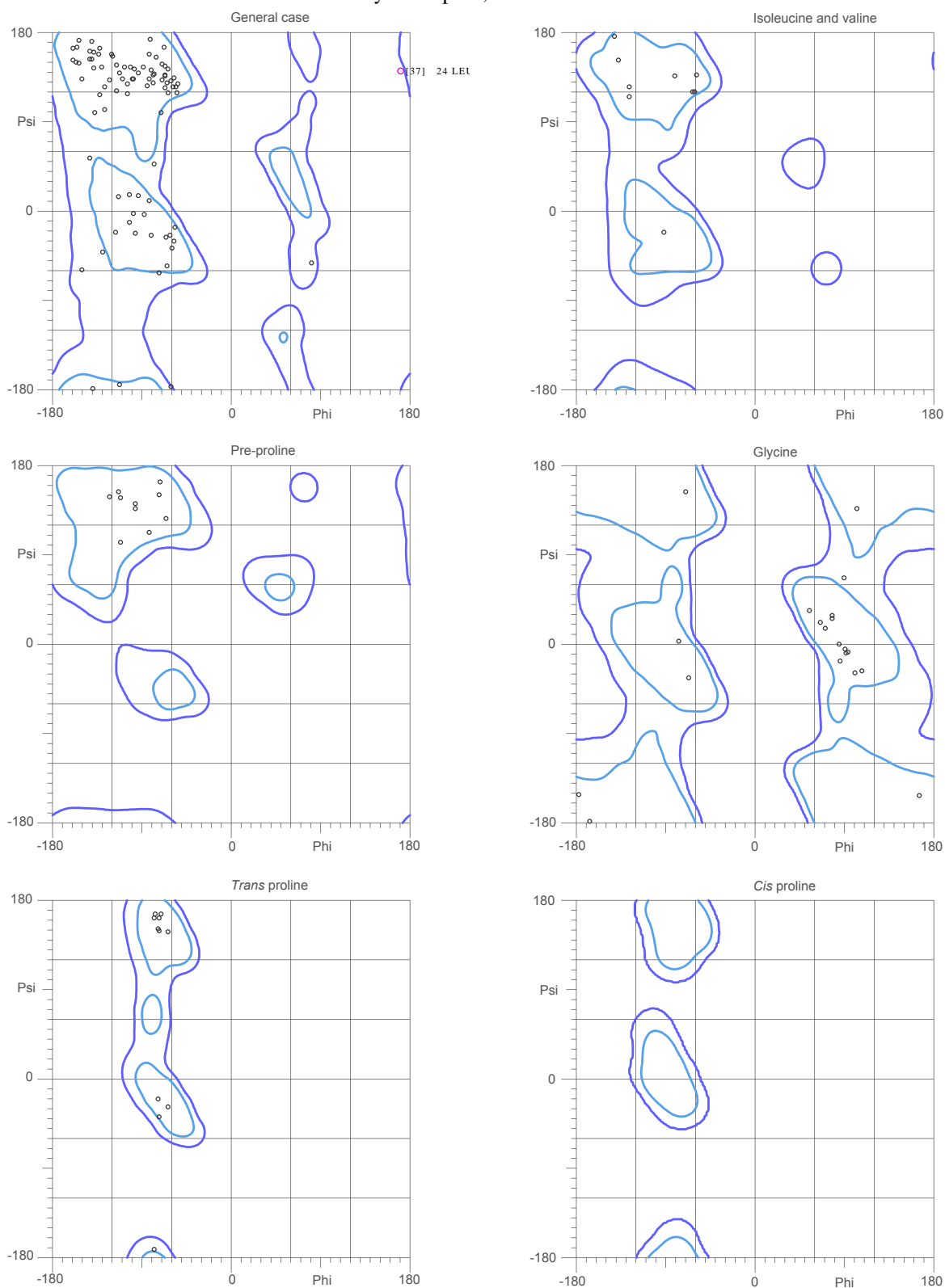
91.3% (126/138) of all residues were in favored (98%) regions.  
97.8% (135/138) of all residues were in allowed (>99.8%) regions.

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



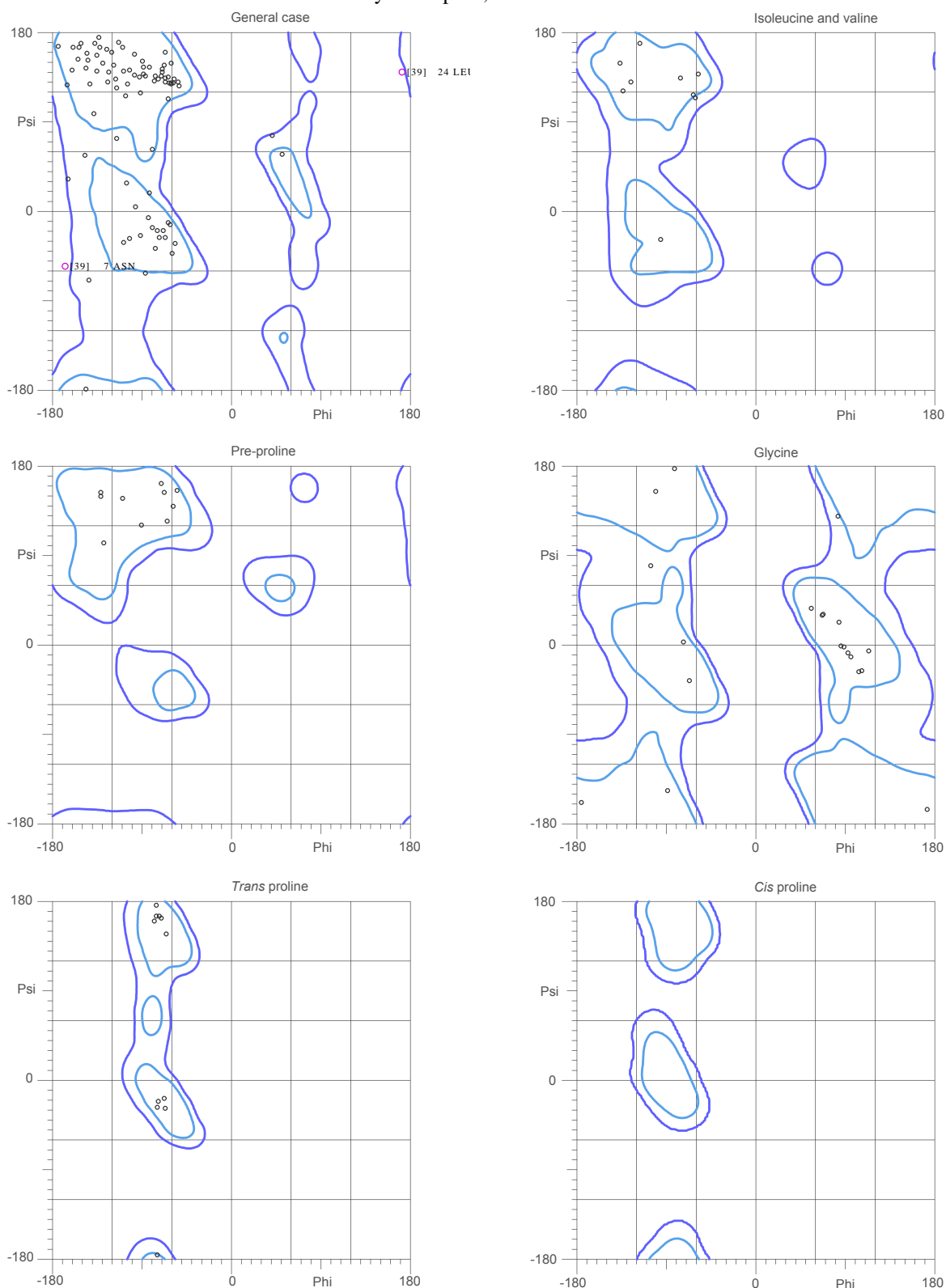
94.2% (130/138) of all residues were in favored (98%) regions.

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)