MolProbity Ramachandran analysis

6yi3.H.pdb, all models

http://kinemage.biochem.duke.edu
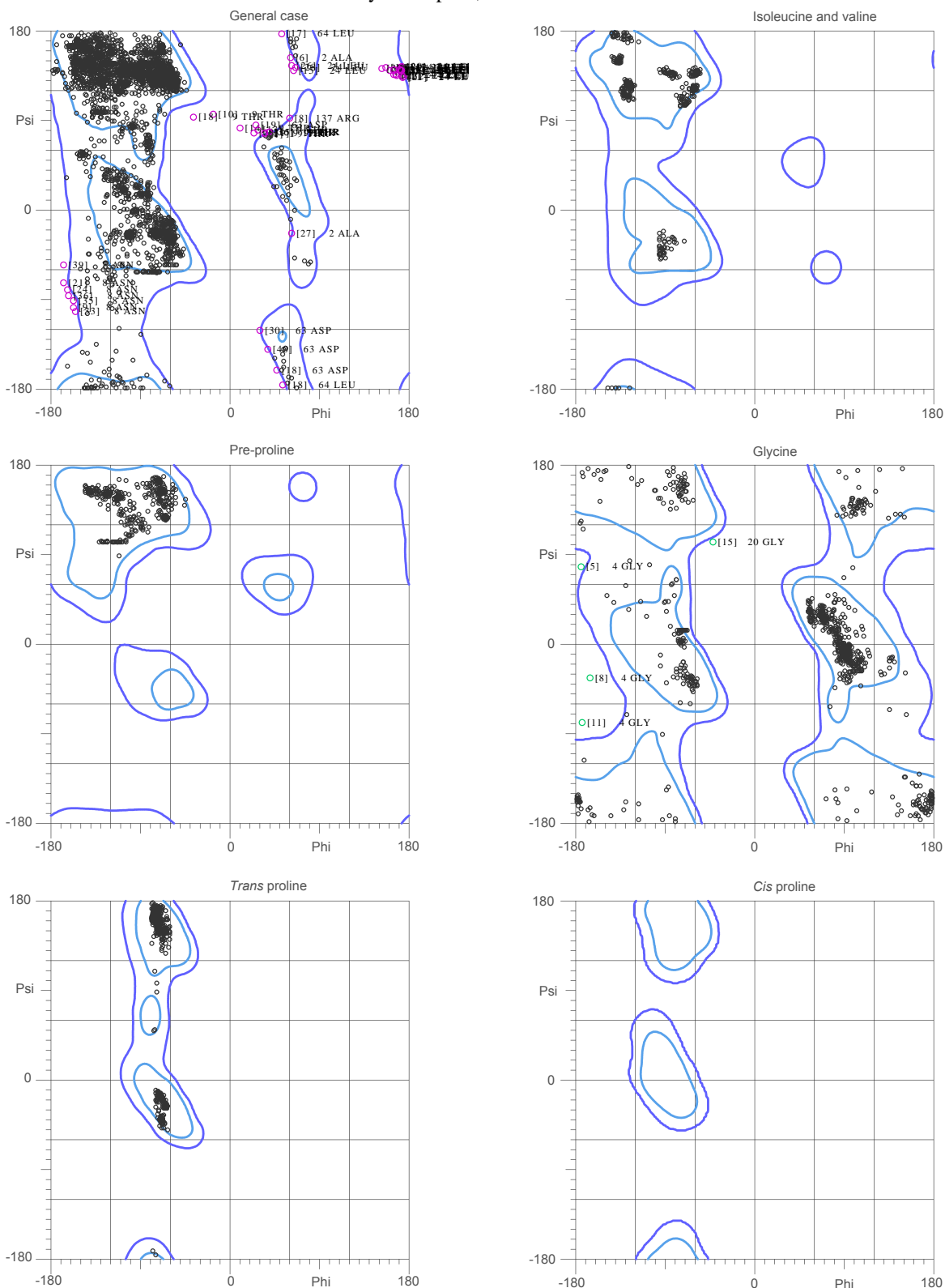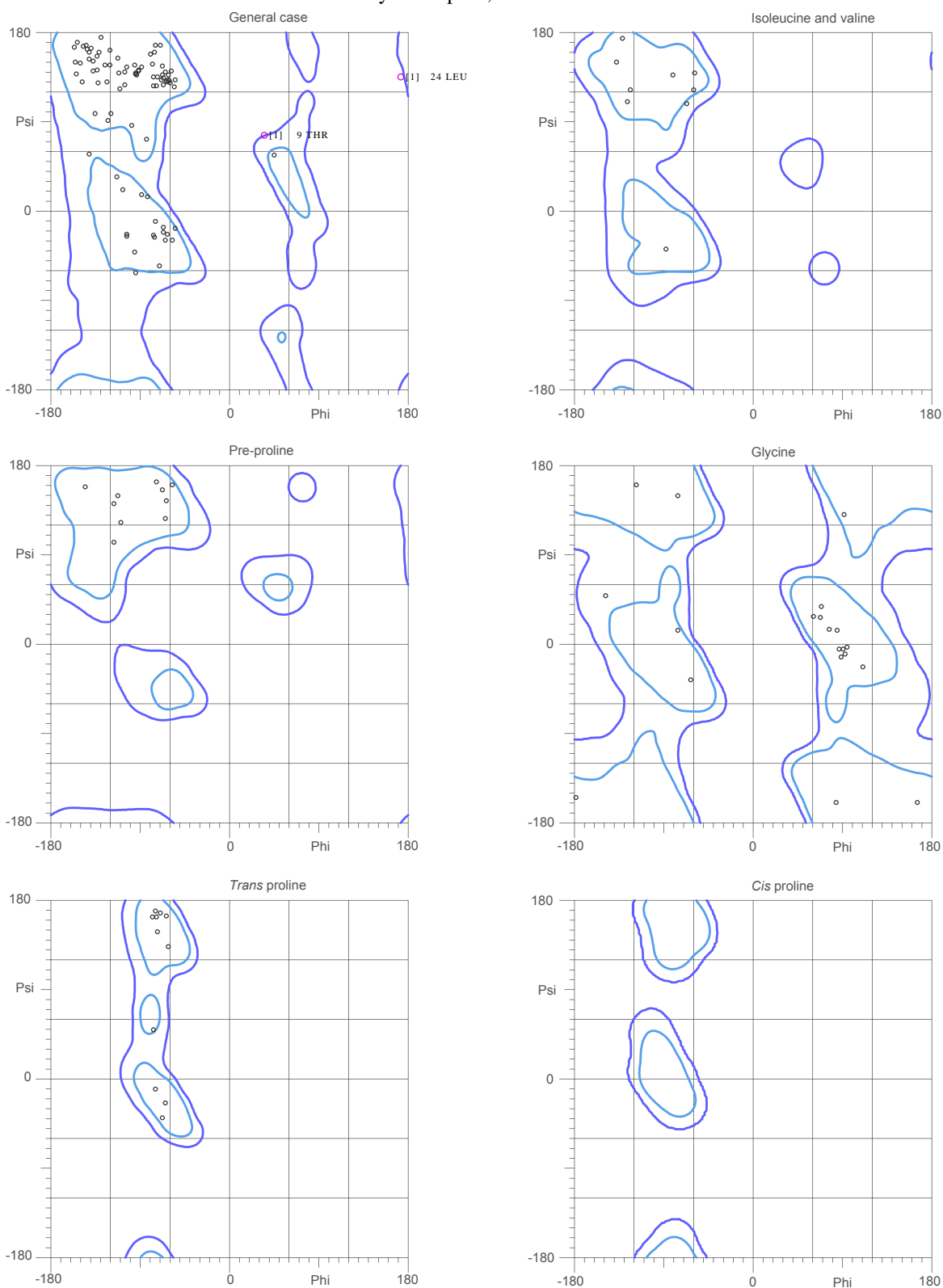
Lovell, Davis, et al. Proteins 50:437 (2003)

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

General case

Isoleucine and valine

Pre-proline

Glycine

Trans proline

Cis proline

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

General case

Isoleucine and valine

Pre-proline

Glycine

Trans proline

Cis proline

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

General case

Isoleucine and valine

Pre-proline

Glycine
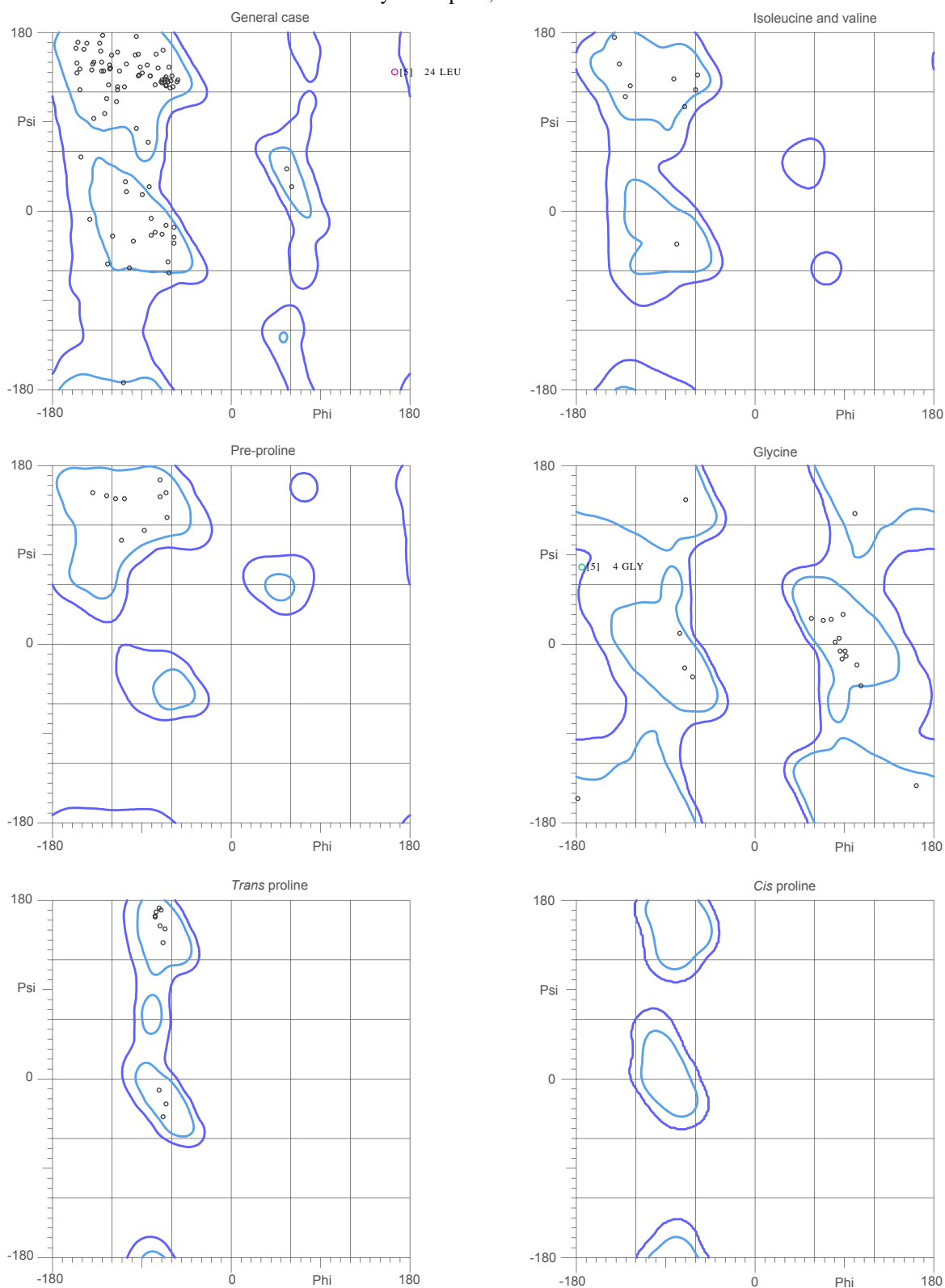
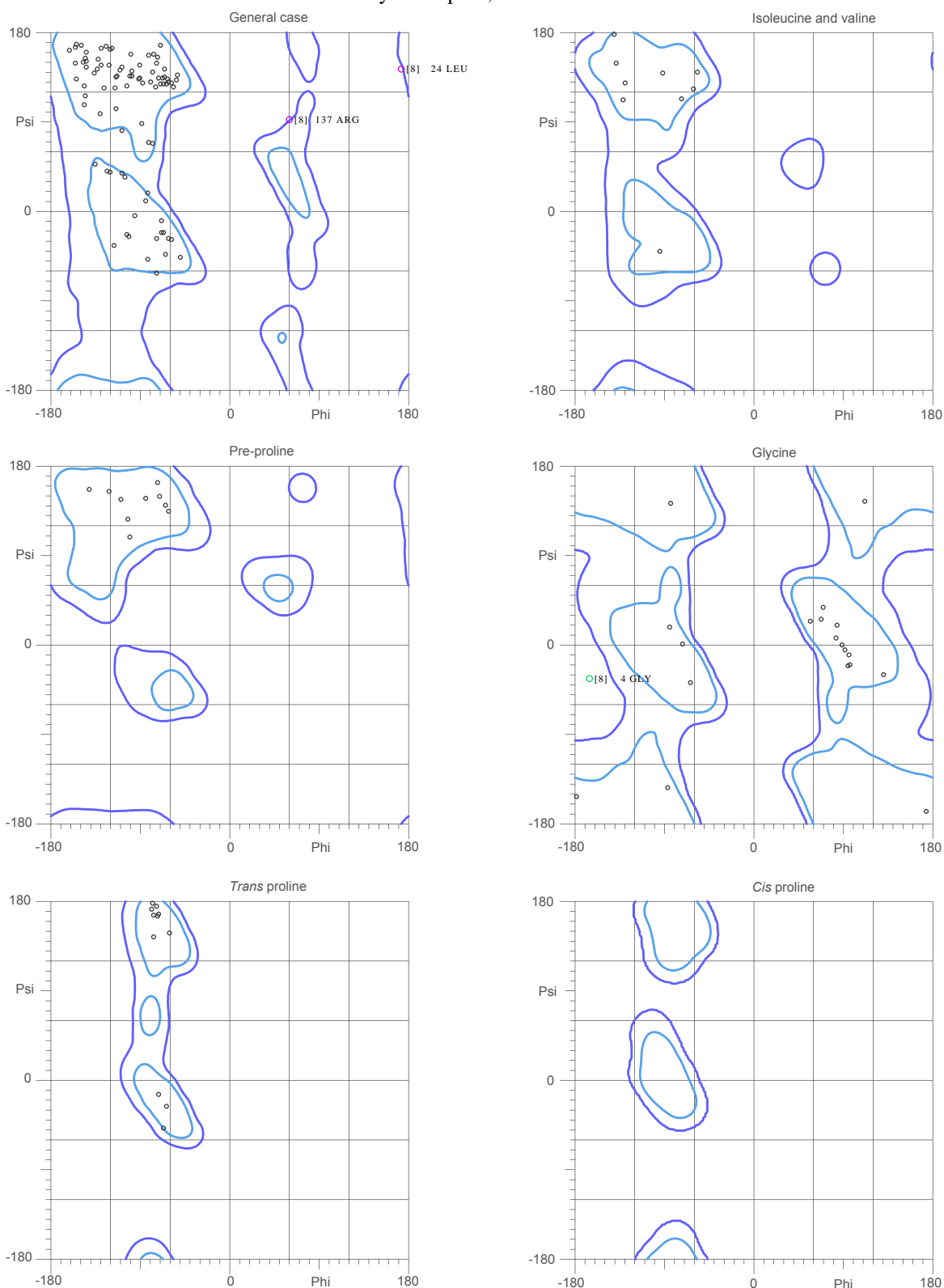*Trans* proline

Cis proline

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

General case

Isoleucine and valine

Pre-proline

Glycine

Trans proline

Cis proline

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.

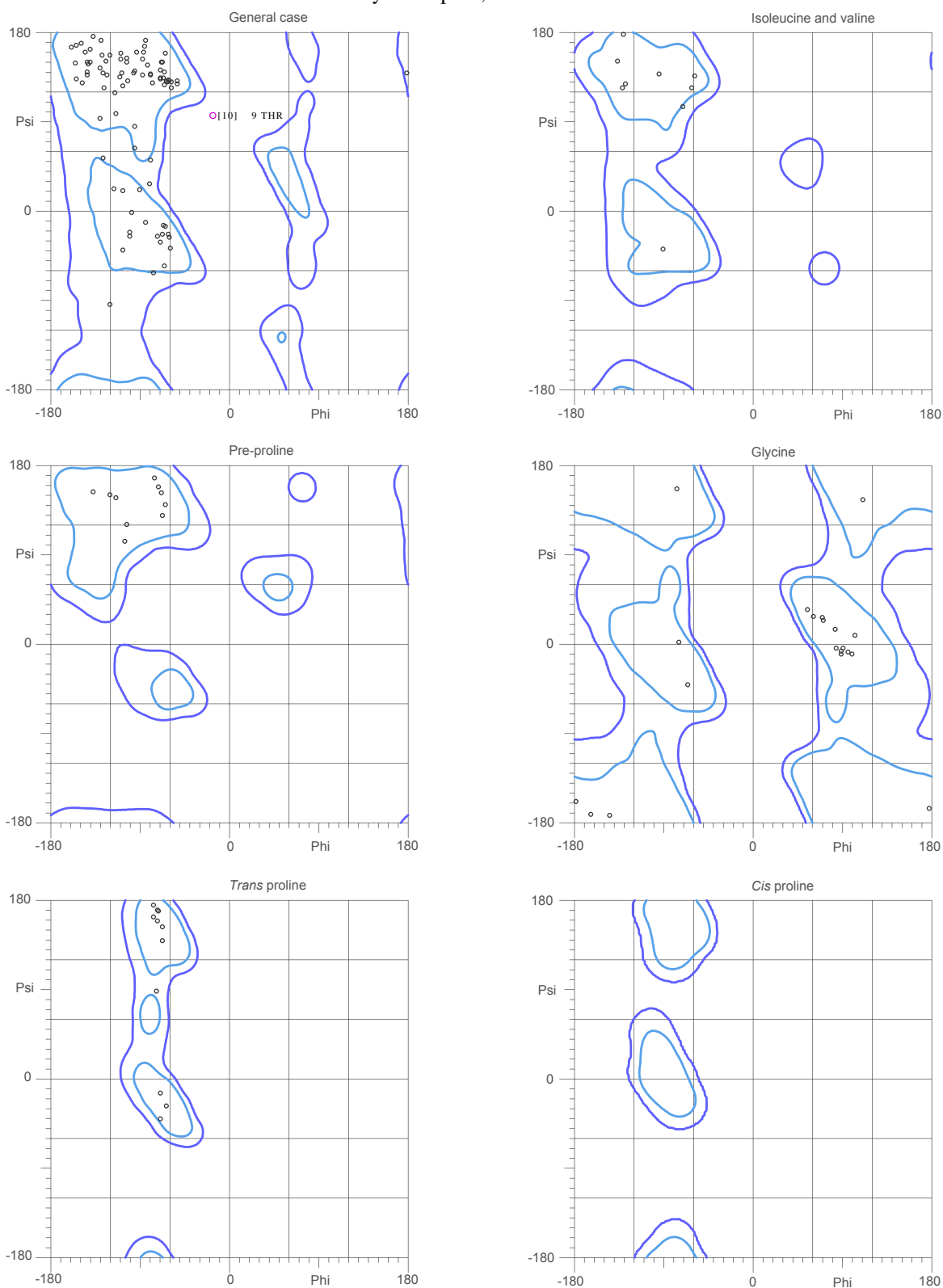98.6% (136/138) of all residues were in allowed (>99.8%) regions.

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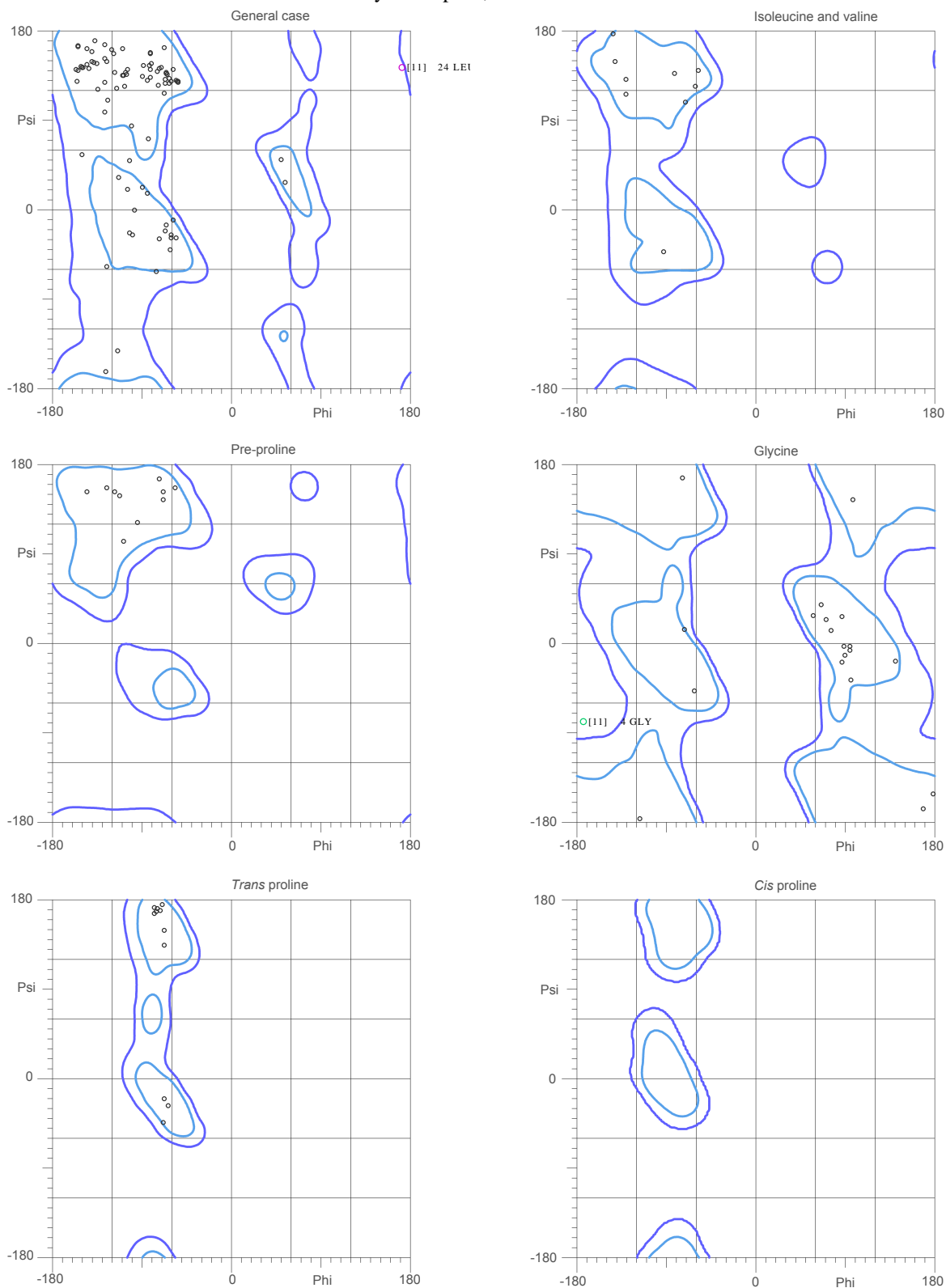
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

There were 1 outliers (phi, psi):

    [10]   9 THR (-17.7, 97.4)

MolProbity Ramachandran analysis

6yi3.H.pdb, model 11

General case

Isoleucine and valine

Pre-proline

Glycine

Trans proline

Cis proline

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.
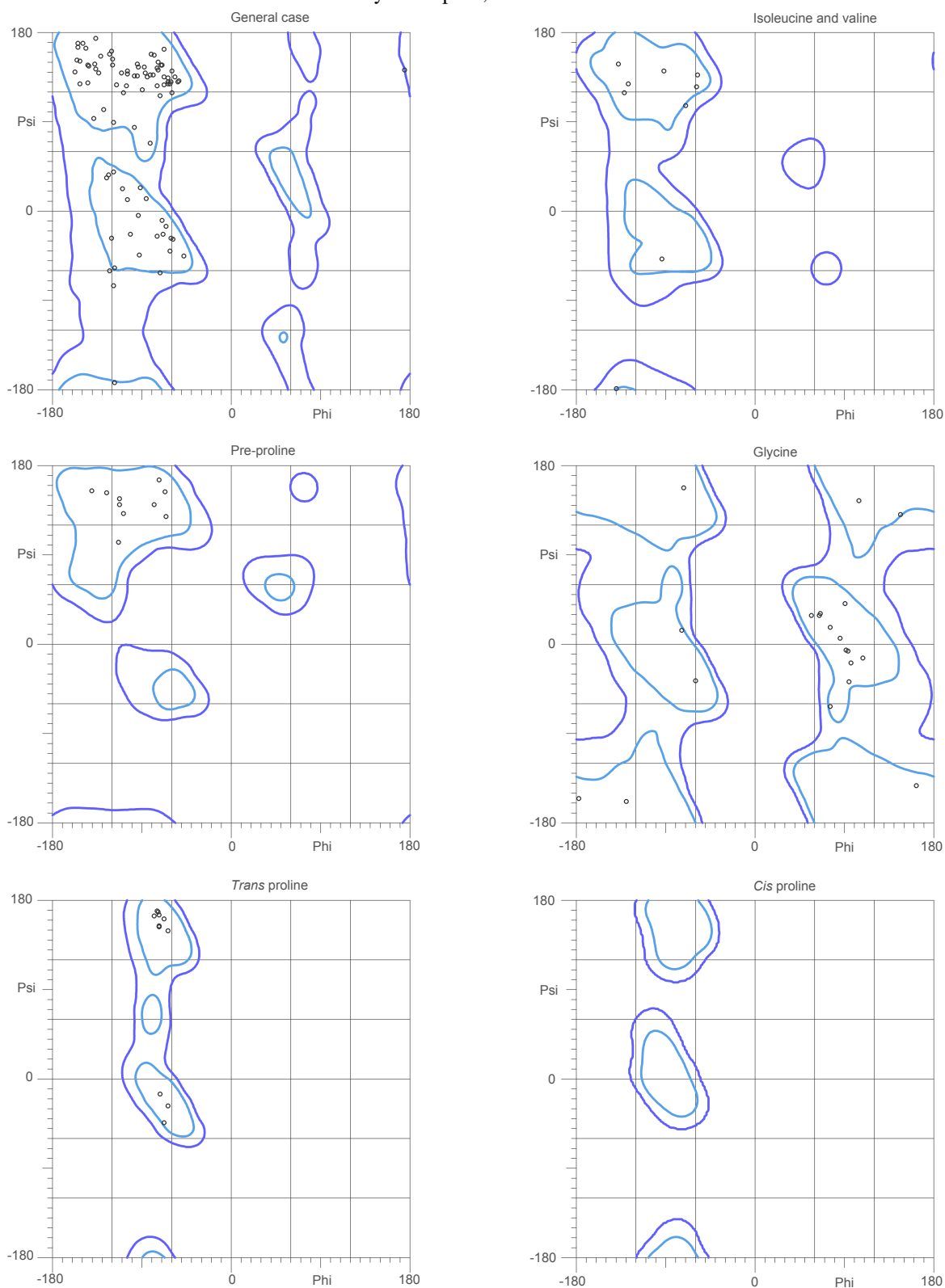
There were 2 outliers (phi, psi):

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

    [11]   24 LEU (172.6, 144.8)

MolProbity Ramachandran analysis
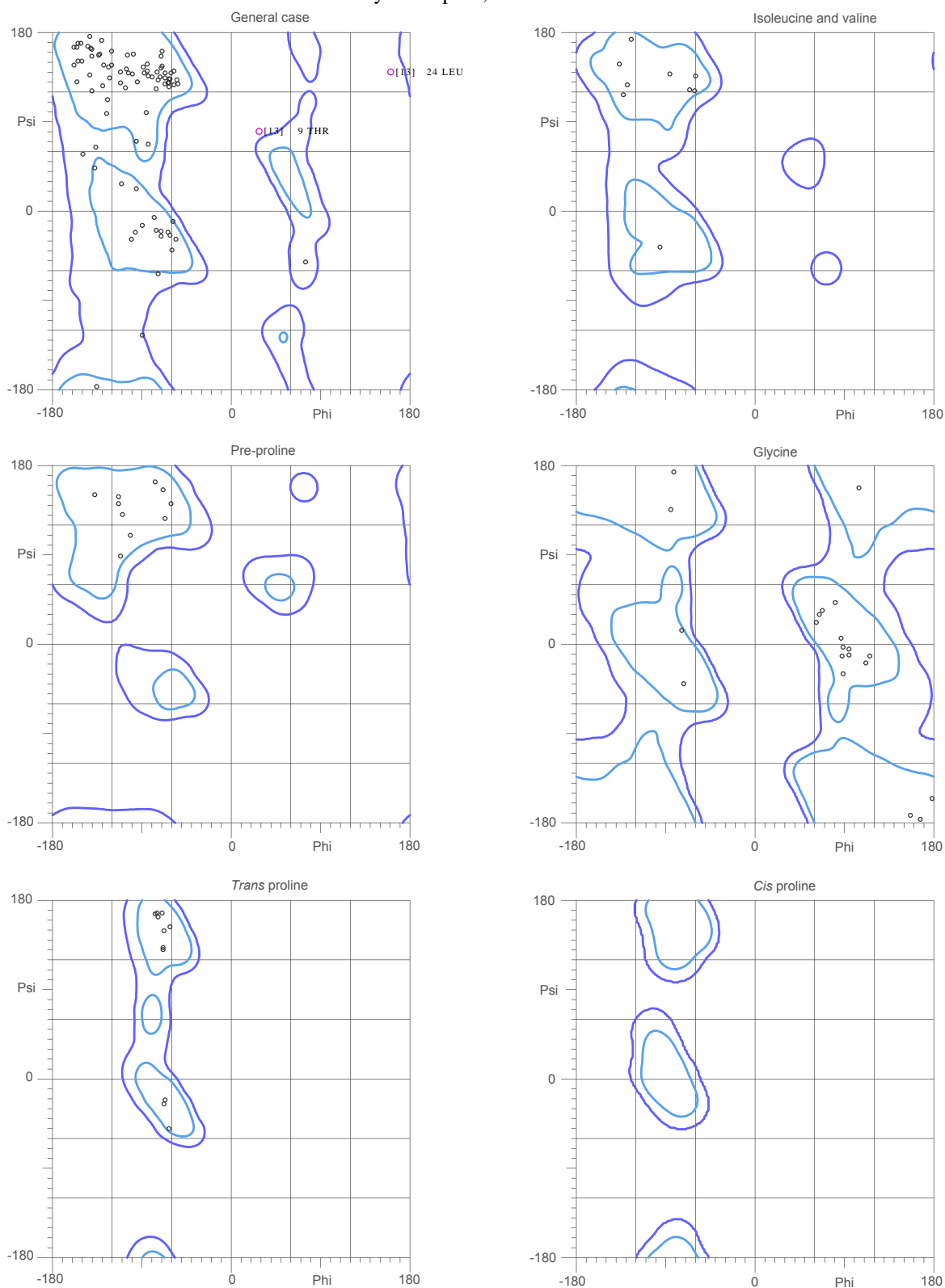
6yi3.H.pdb, model 12

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.

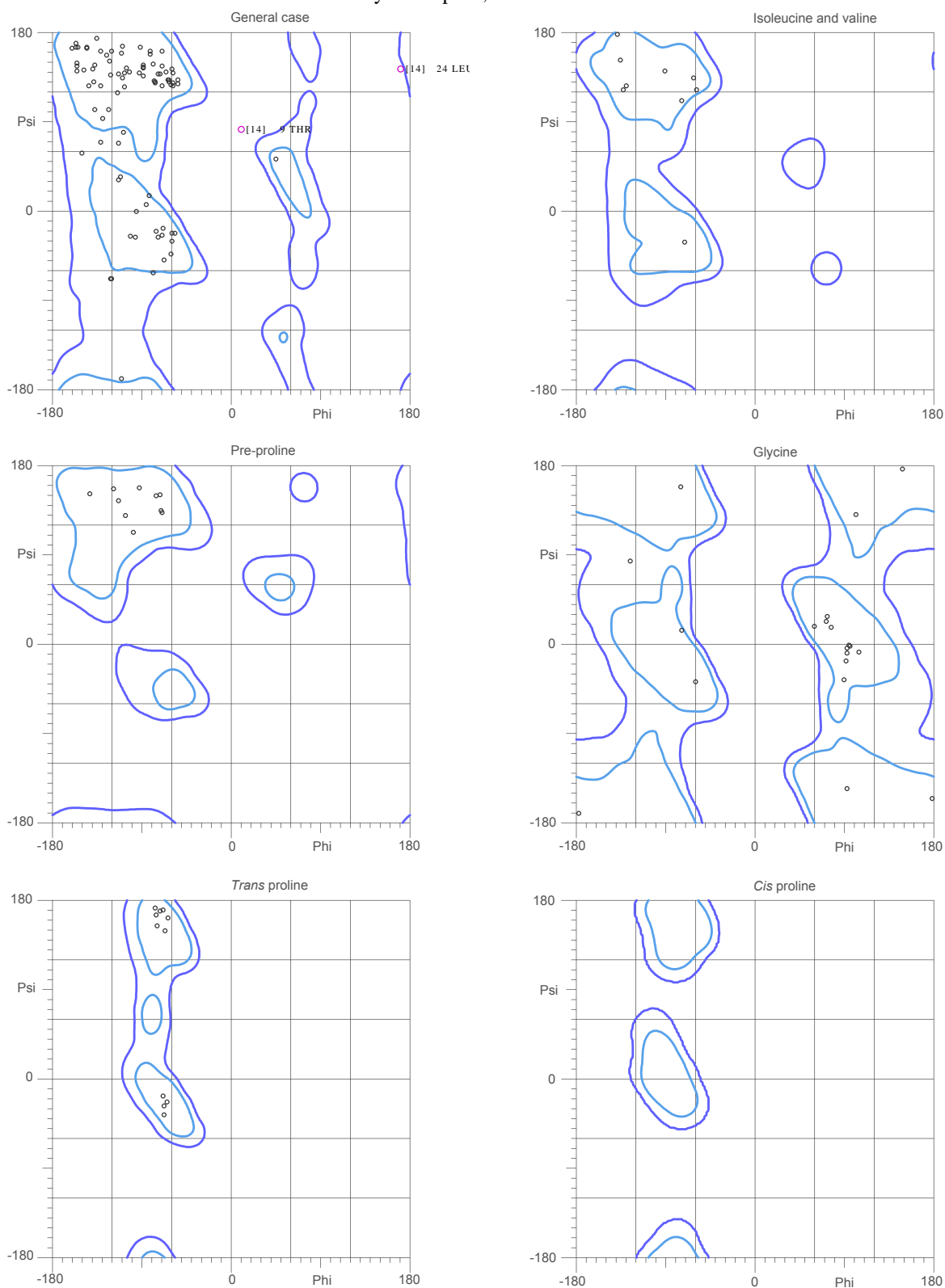98.6% (136/138) of all residues were in allowed (>99.8%) regions.

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

General case

Isoleucine and valine

Pre-proline

Glycine

Trans proline

Cis proline

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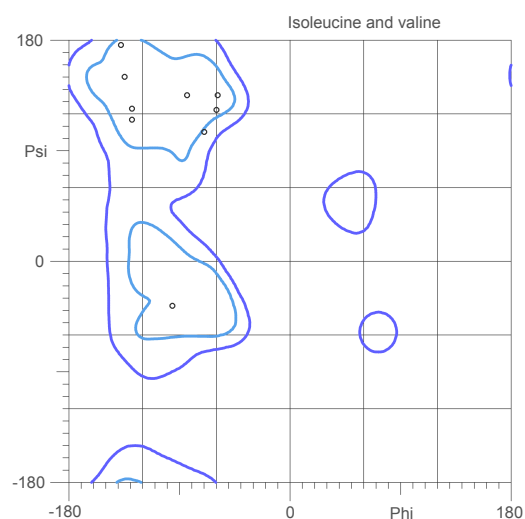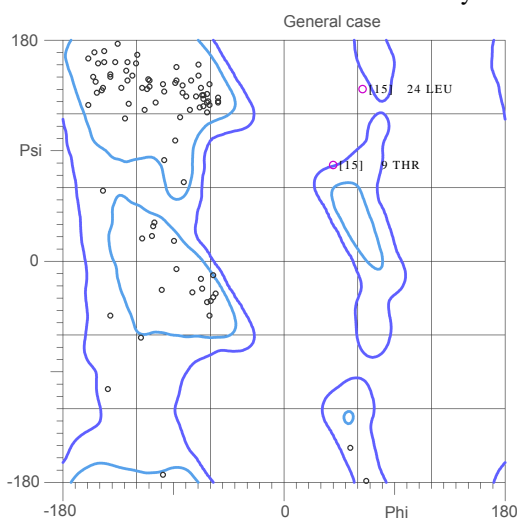
92.0% (127/138) of all residues were in favored (98%) regions.

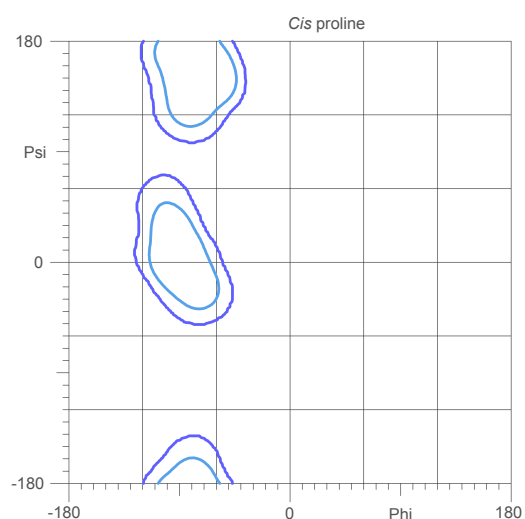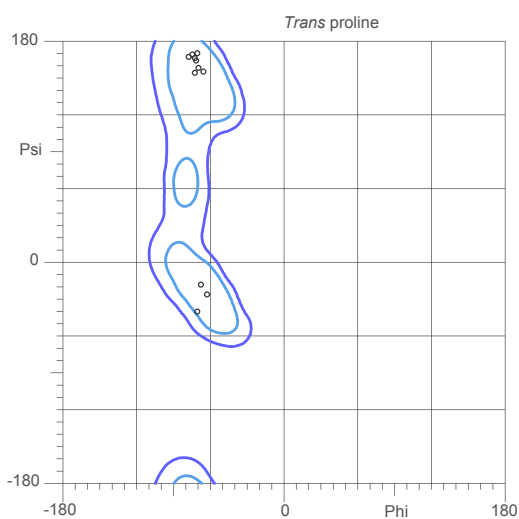97.8% (135/138) of all residues were in allowed (>99.8%) regions.

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.

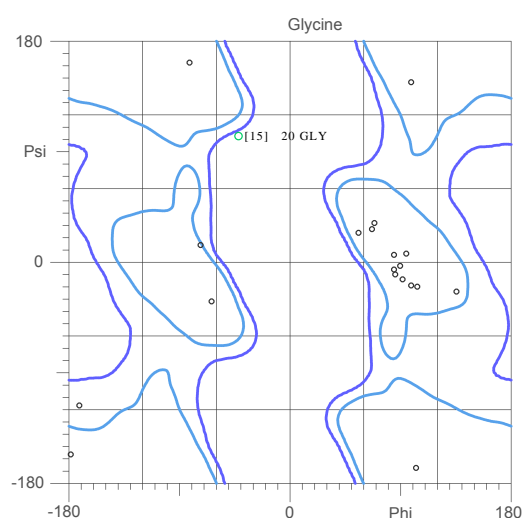100.0% (138/138) of all residues were in allowed (>99.8%) regions.

There were no outliers.

MolProbity Ramachandran analysis

6yi3.H.pdb, model 17

General case

Isoleucine and valine

Pre-proline

Glycine

Trans proline

Cis proline

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

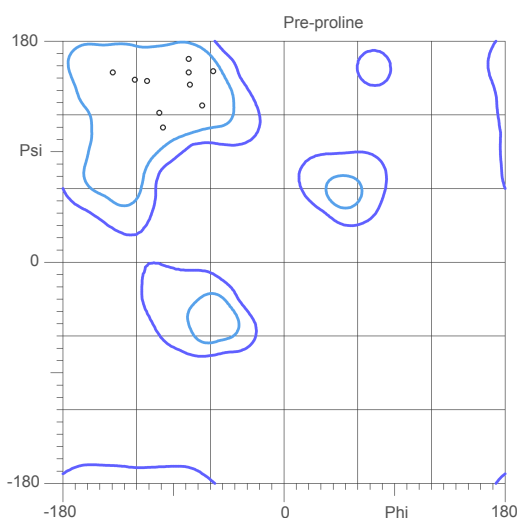99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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)

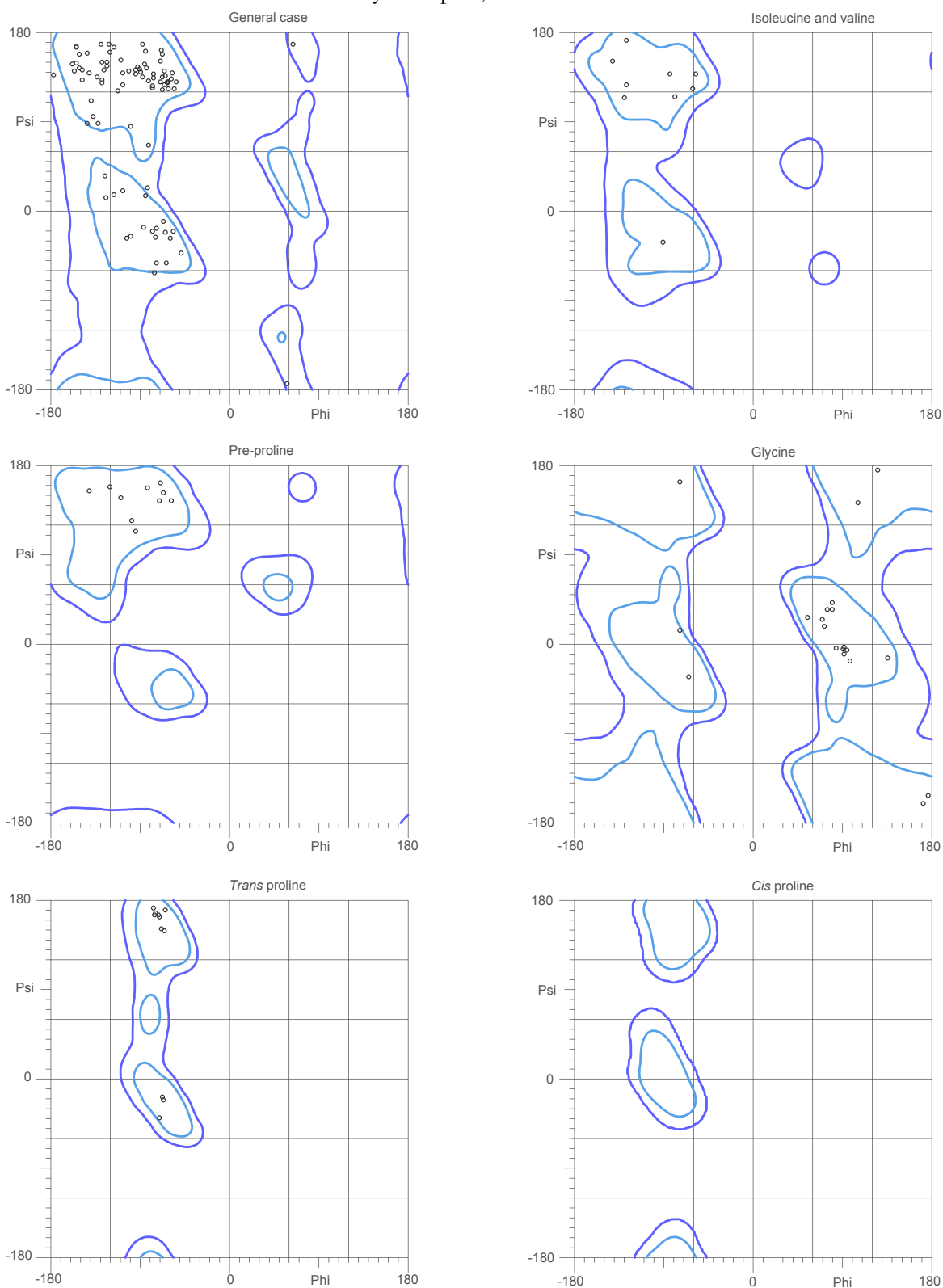# MolProbity Ramachandran analysis

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

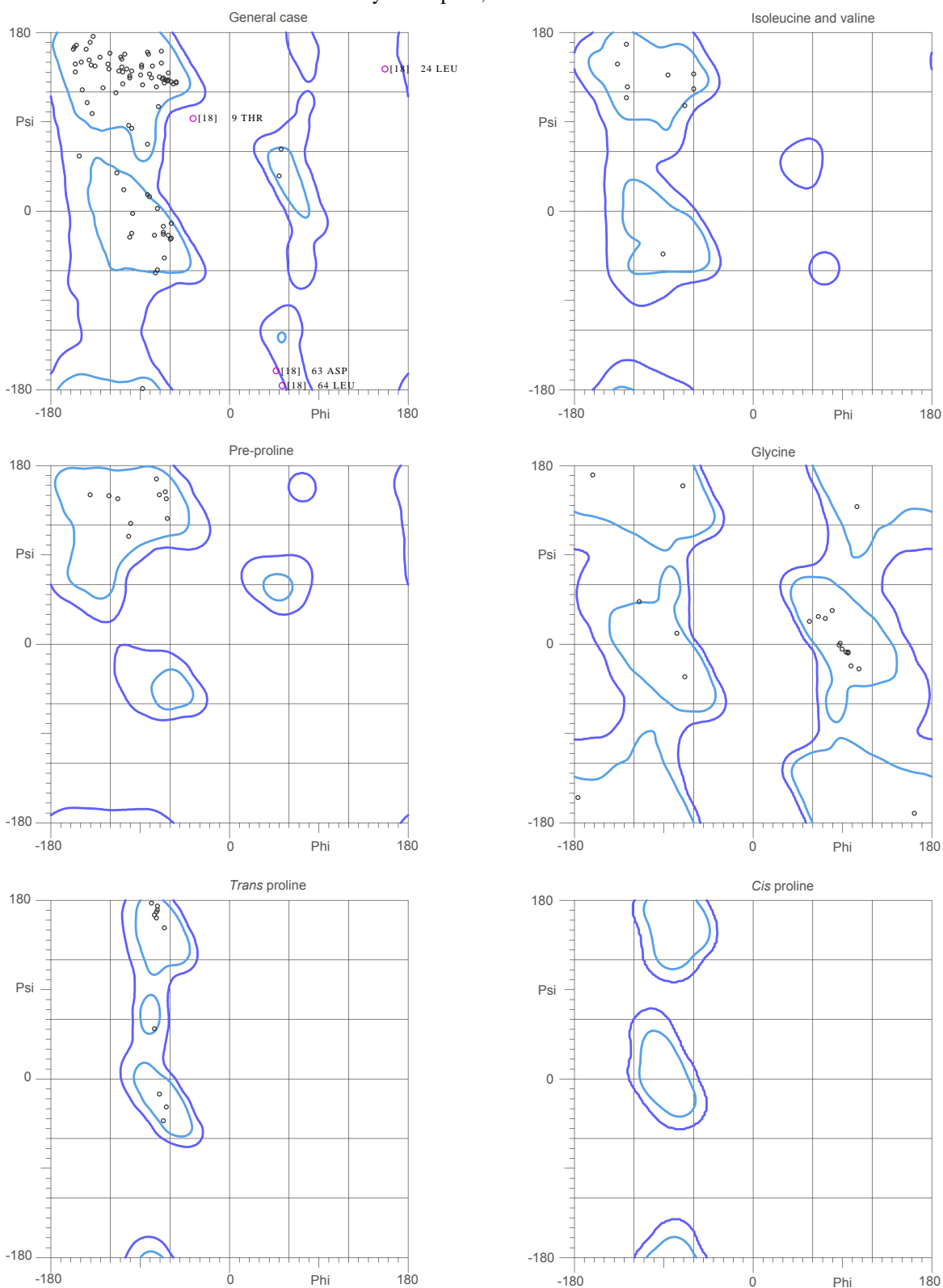94.2% (130/138) of all residues were in favored (98%) regions.

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
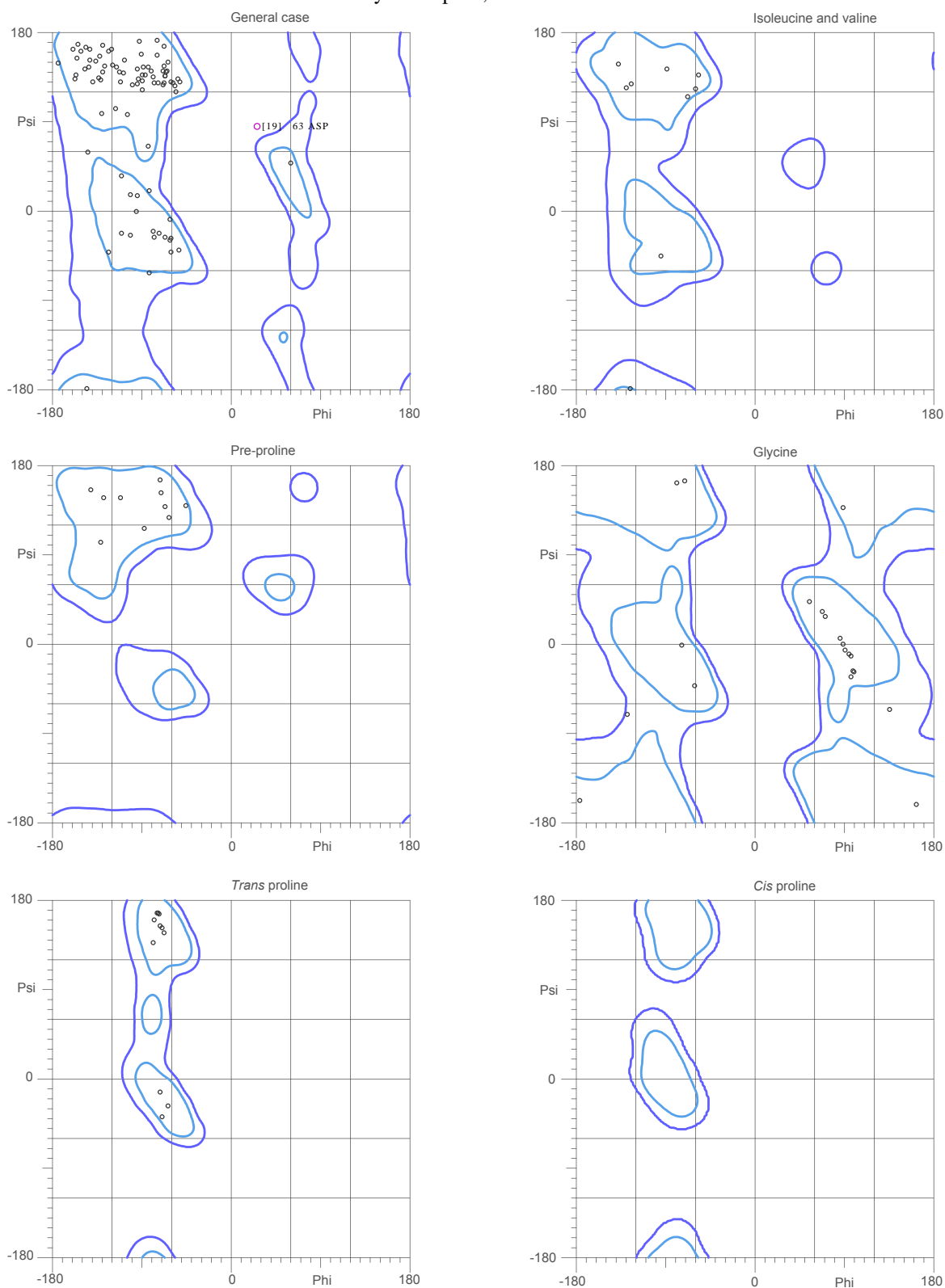
6yi3.H.pdb, model 22

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

General case

Isoleucine and valine

Pre-proline

Glycine

Trans proline

Cis proline

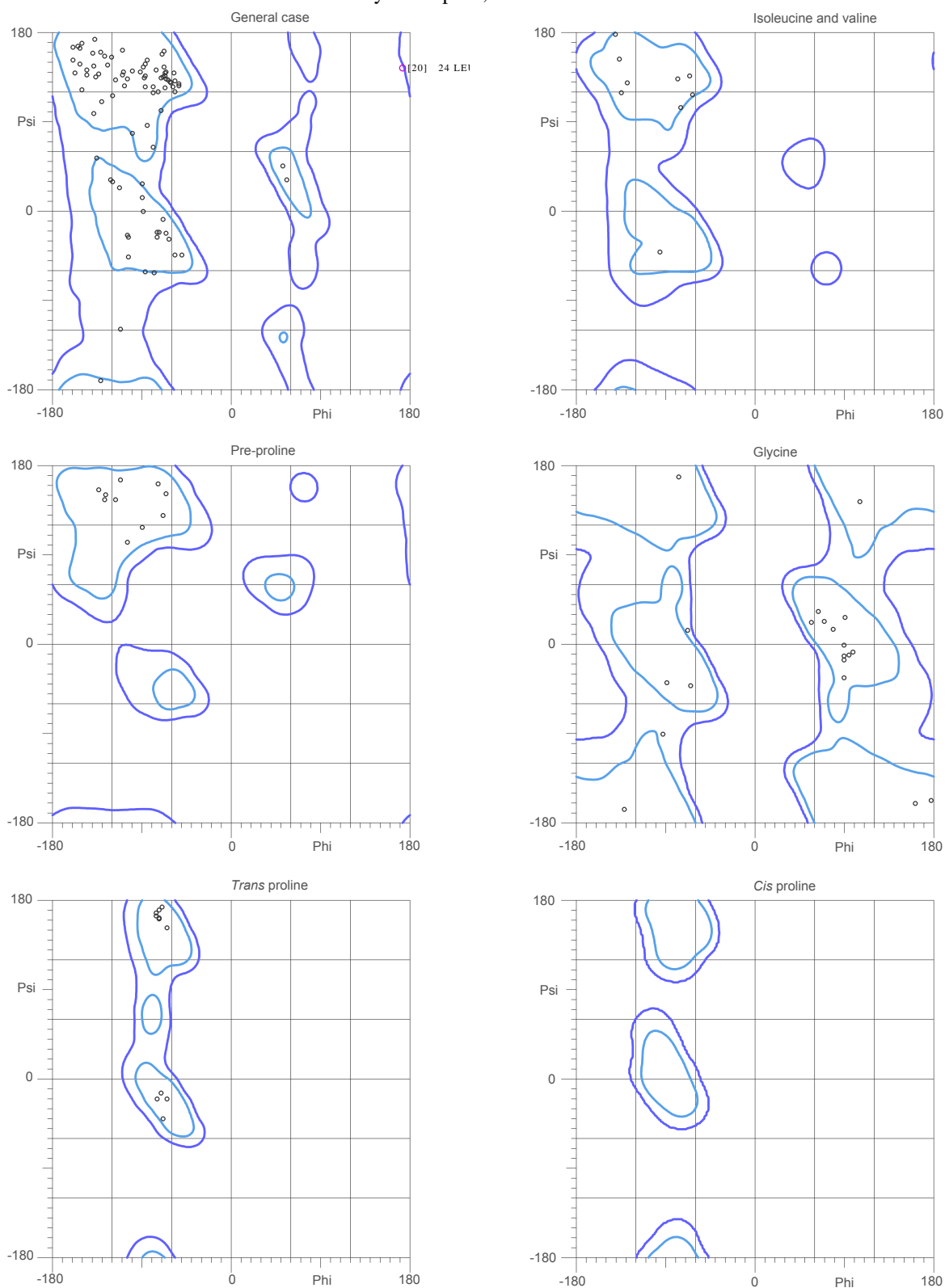94.2% (130/138) of all residues were in favored (98%) regions.
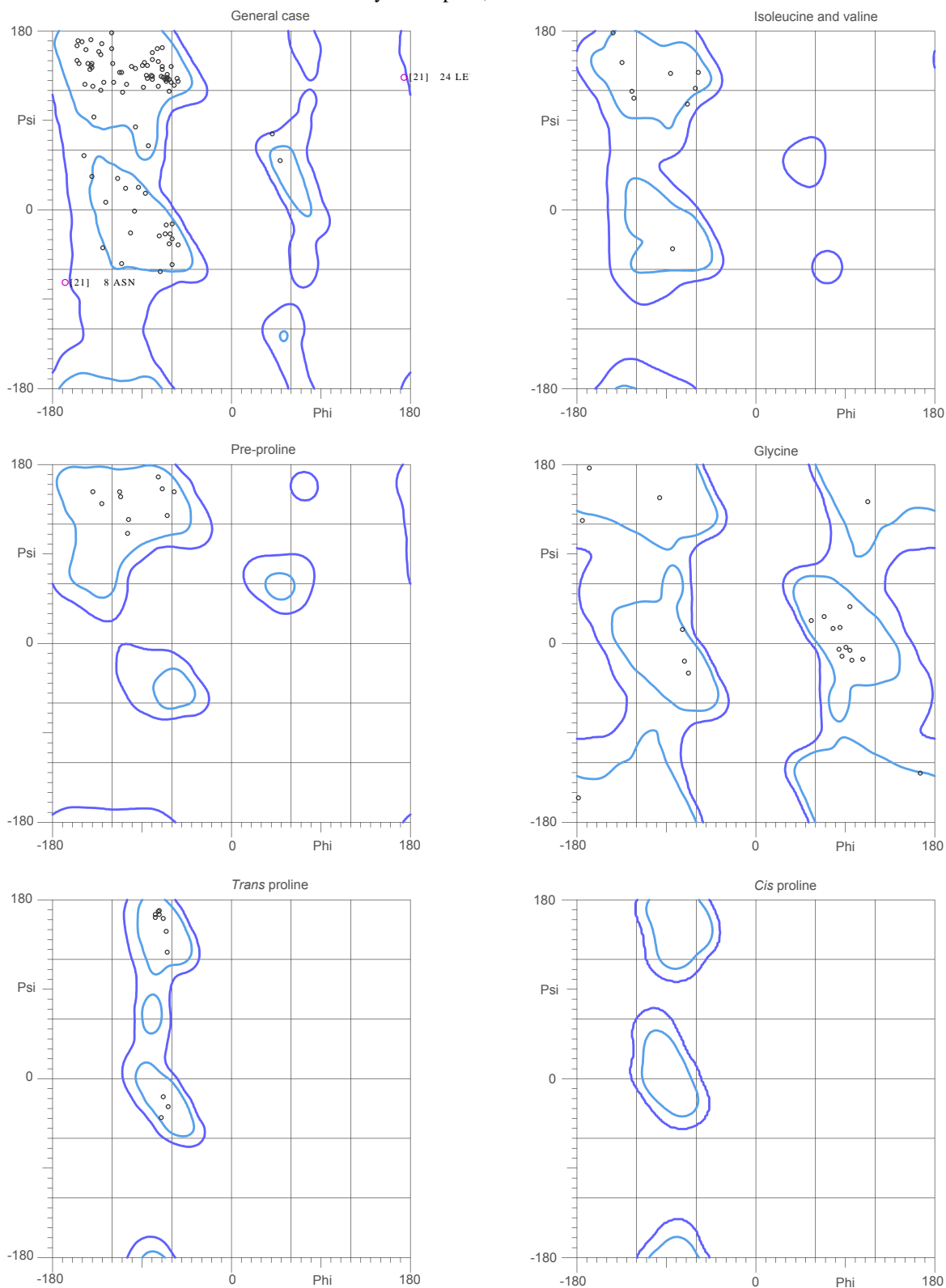
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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

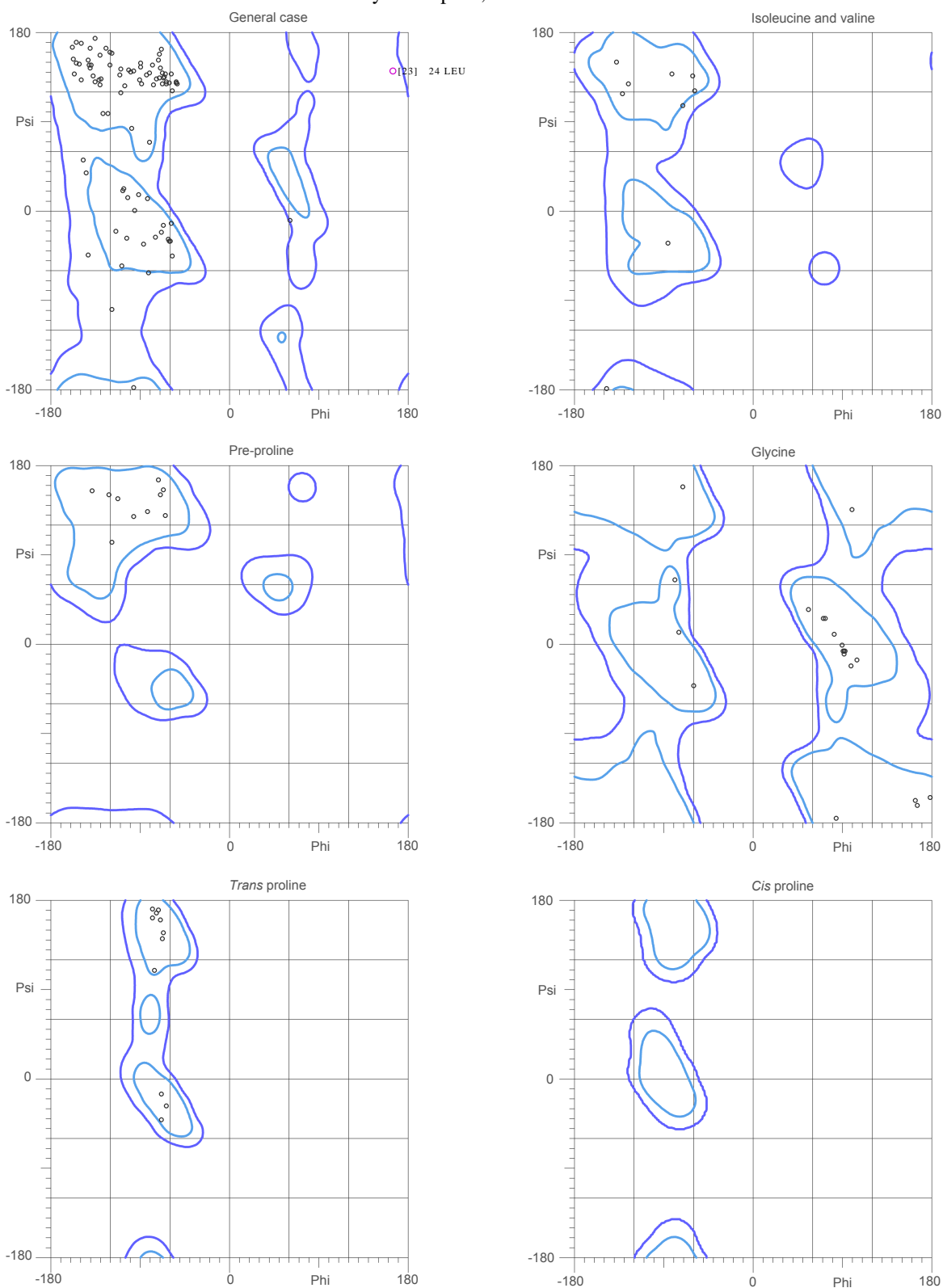94.2% (130/138) of all residues were in favored (98%) regions.

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

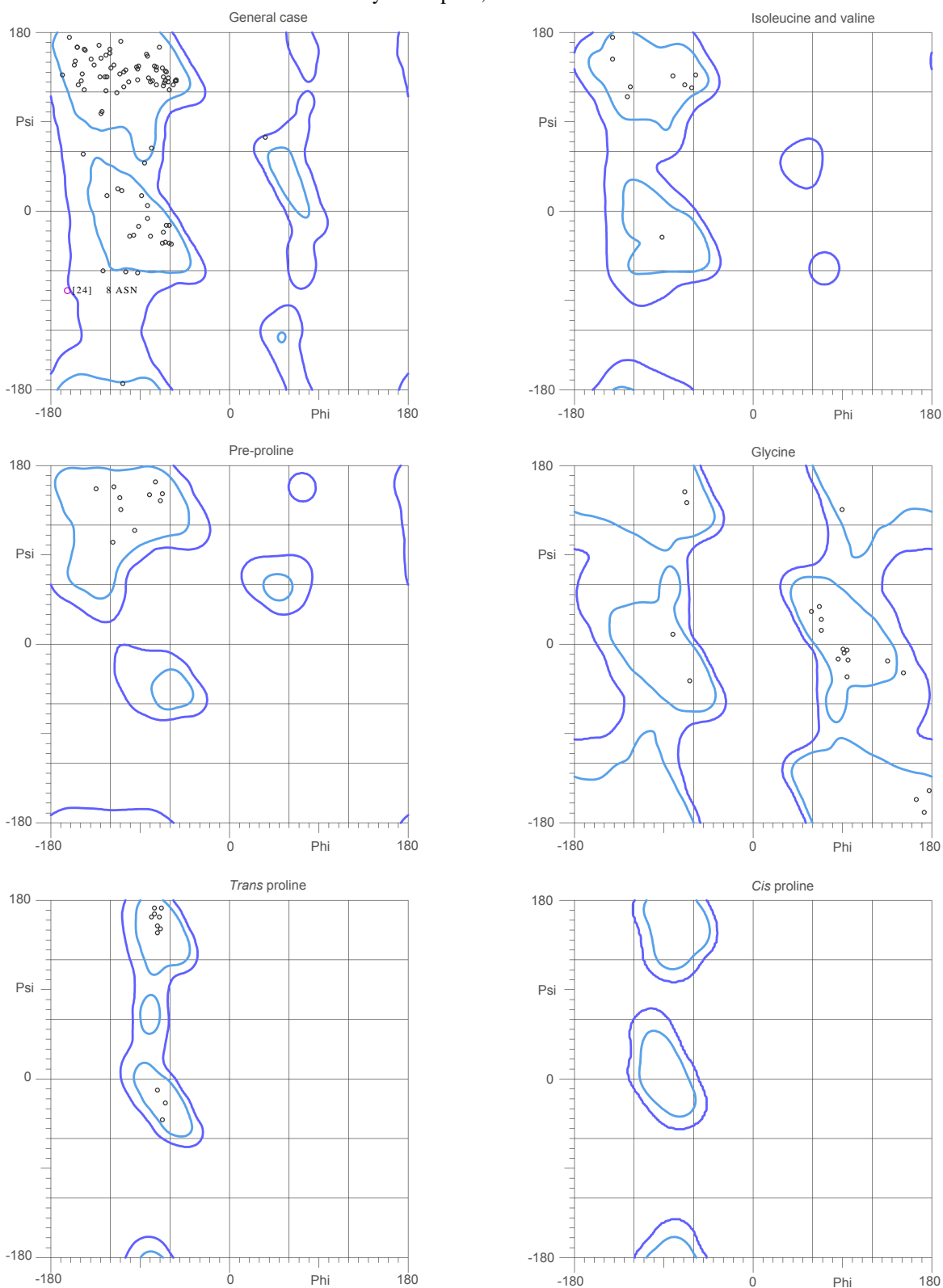92.8% (128/138) of all residues were in favored (98%) regions.

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

General case

Isoleucine and valine

Pre-proline

Glycine

Trans proline

Cis proline

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

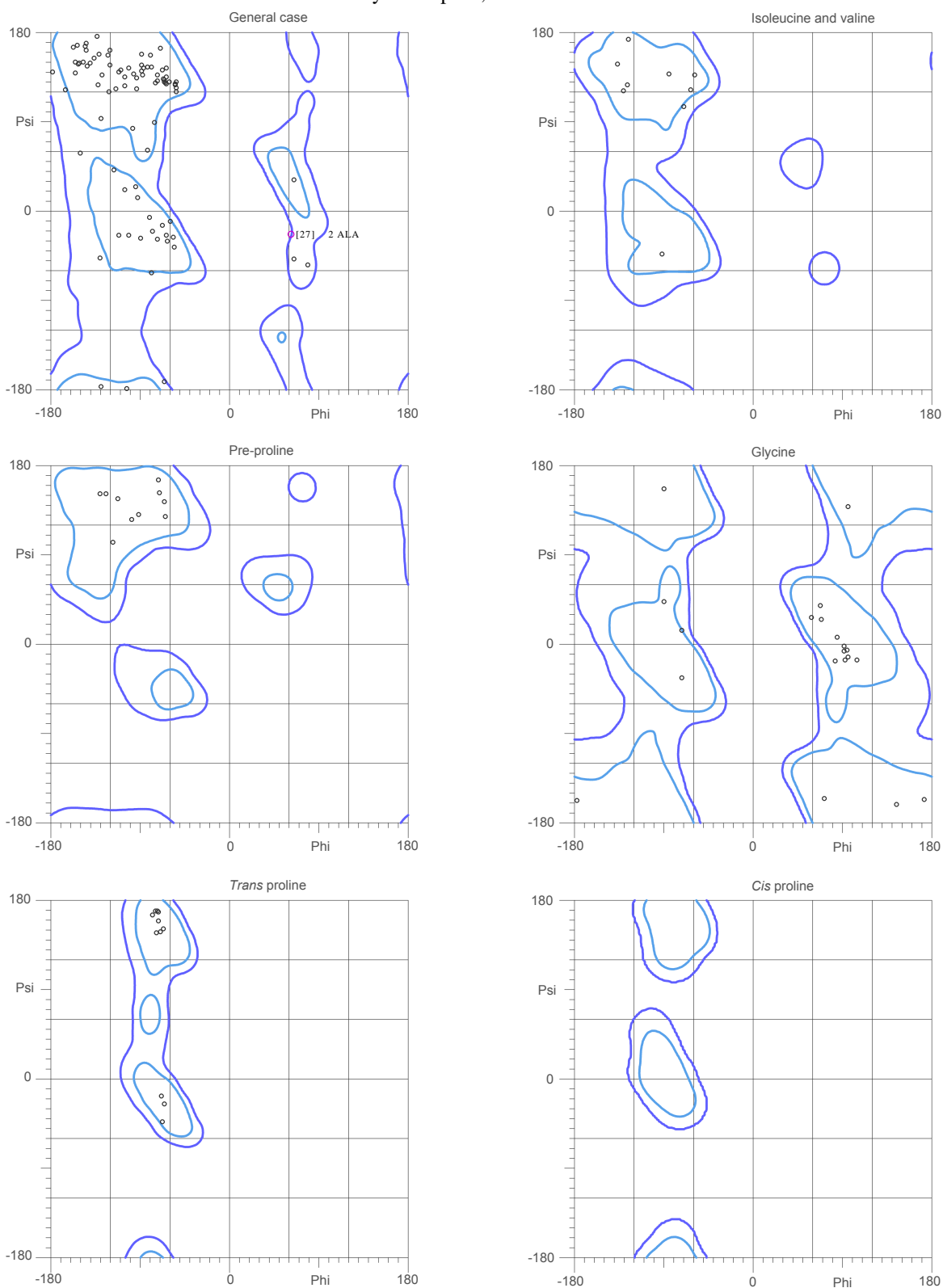93.5% (129/138) of all residues were in favored (98%) regions.

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

General case

Isoleucine and valine

Pre-proline

Glycine

Trans proline

Cis proline

94.9% (131/138) of all residues were in favored (98%) regions.
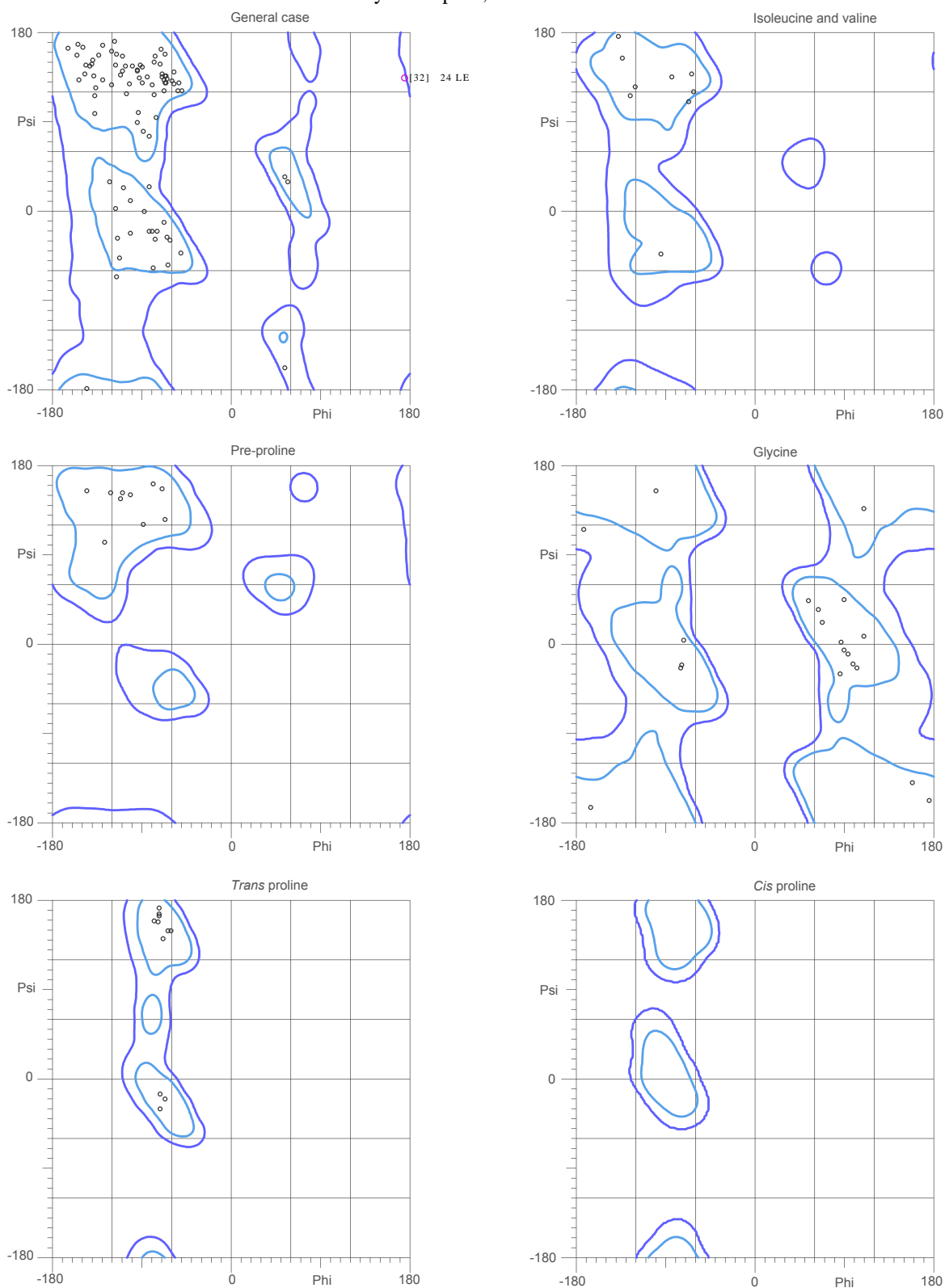
99.3% (137/138) of all residues were in allowed (>99.8%) regions.

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
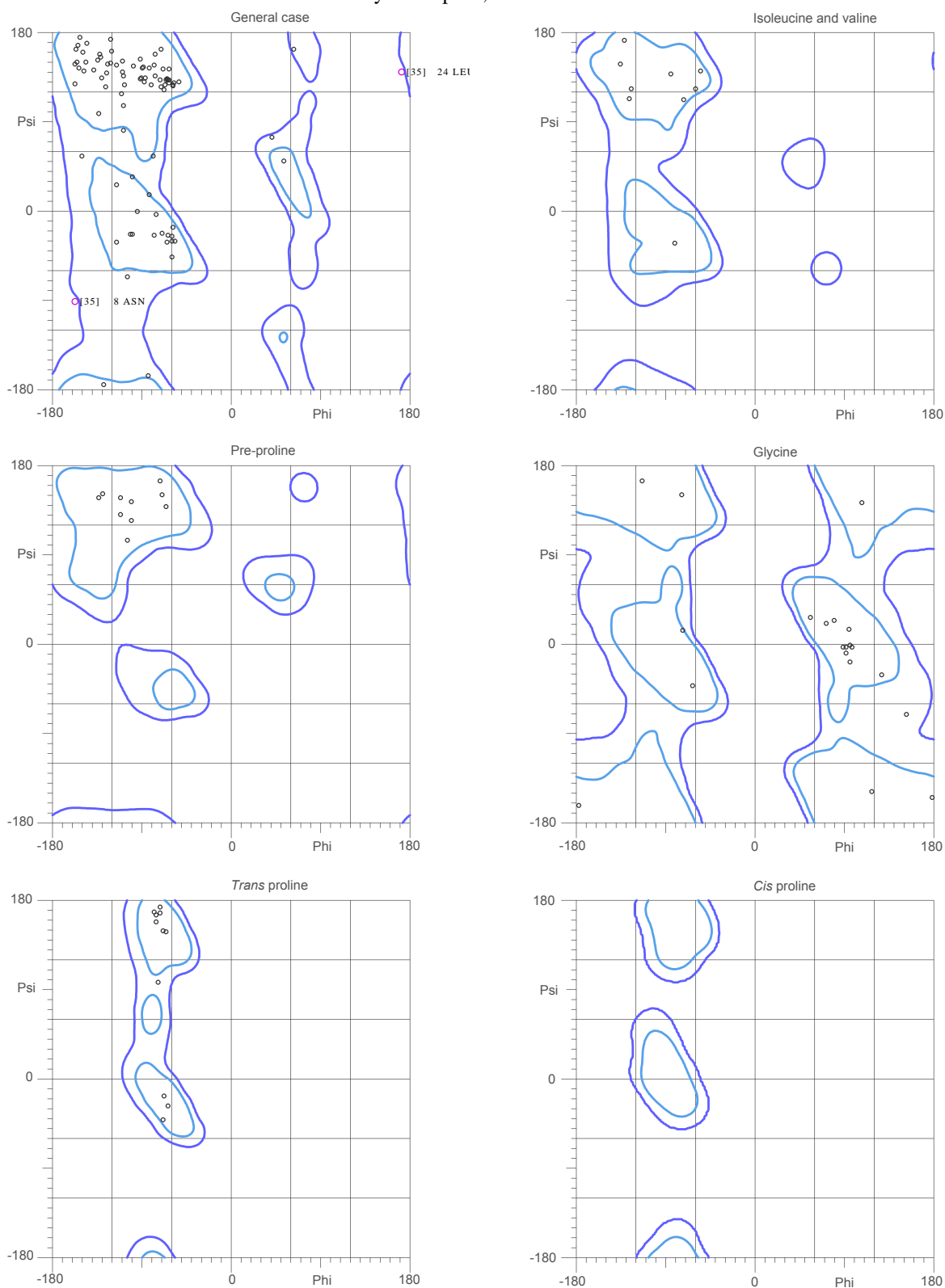
6yi3.H.pdb, model 34

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

General case

Isoleucine and valine

Pre-proline

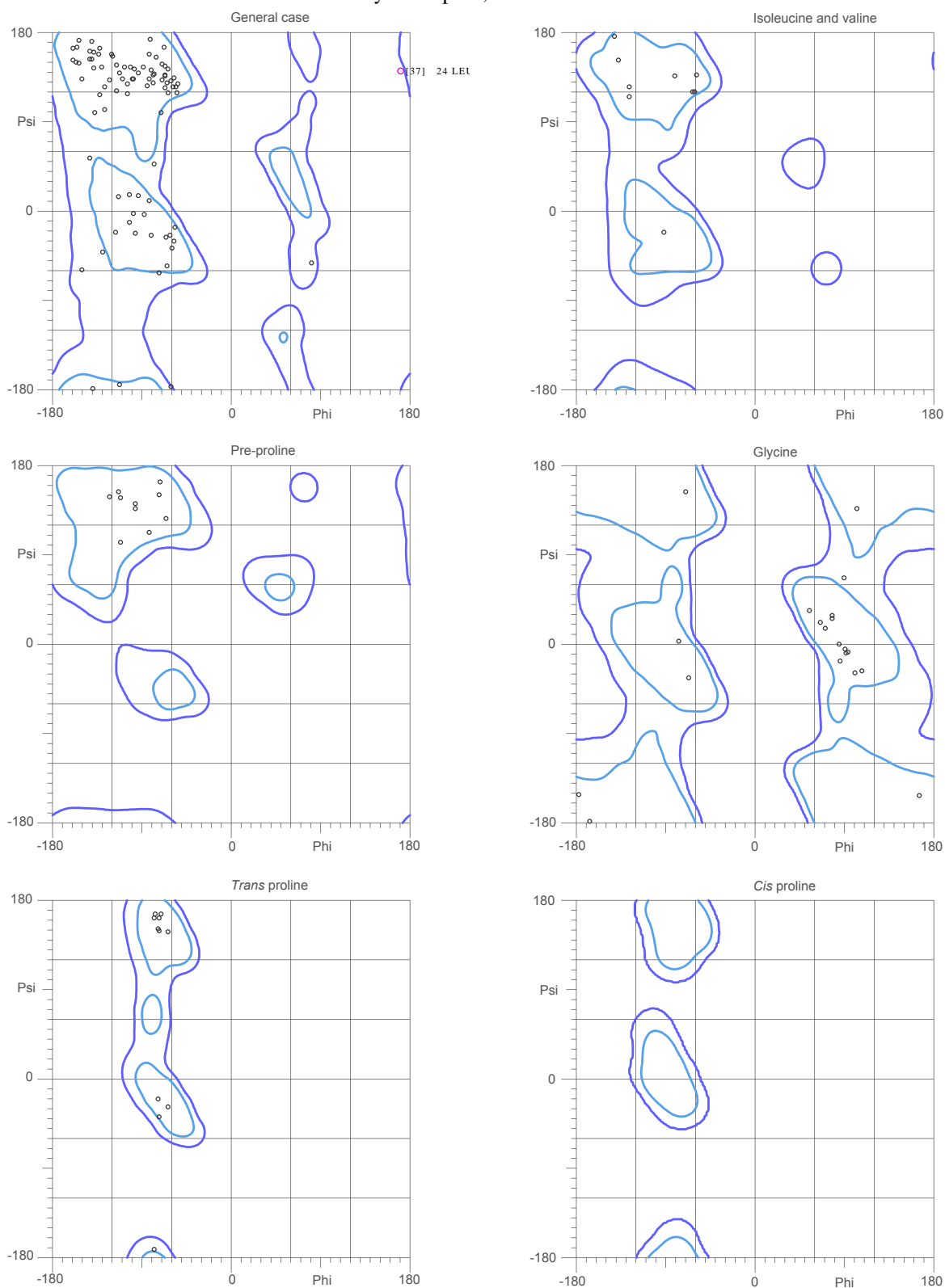Glycine

Trans proline

Cis proline

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)

Lovell, Davis, et al. Proteins 50:437 (2003)

MolProbity Ramachandran analysis
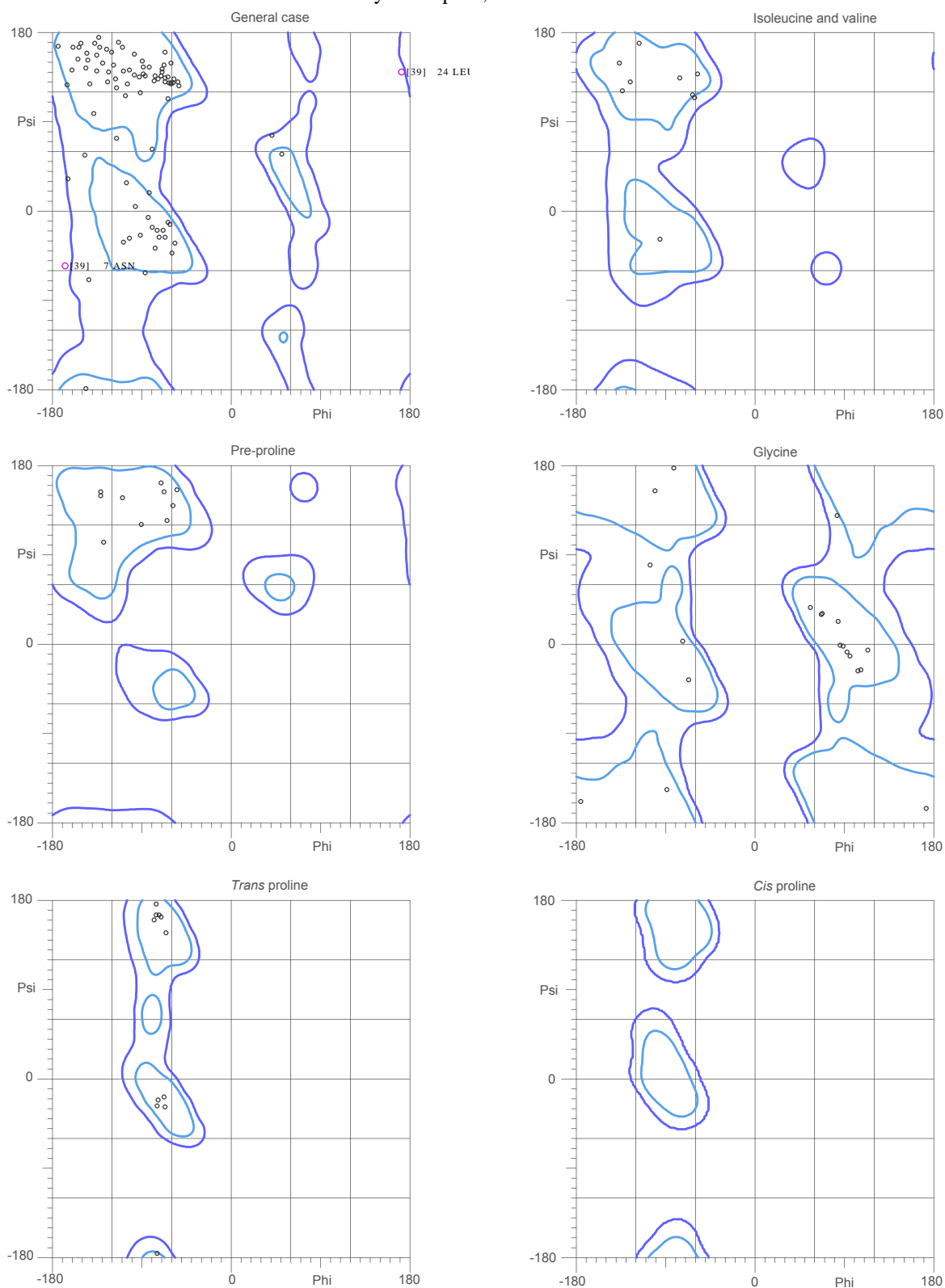
6yi3.H.pdb, model 38

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)