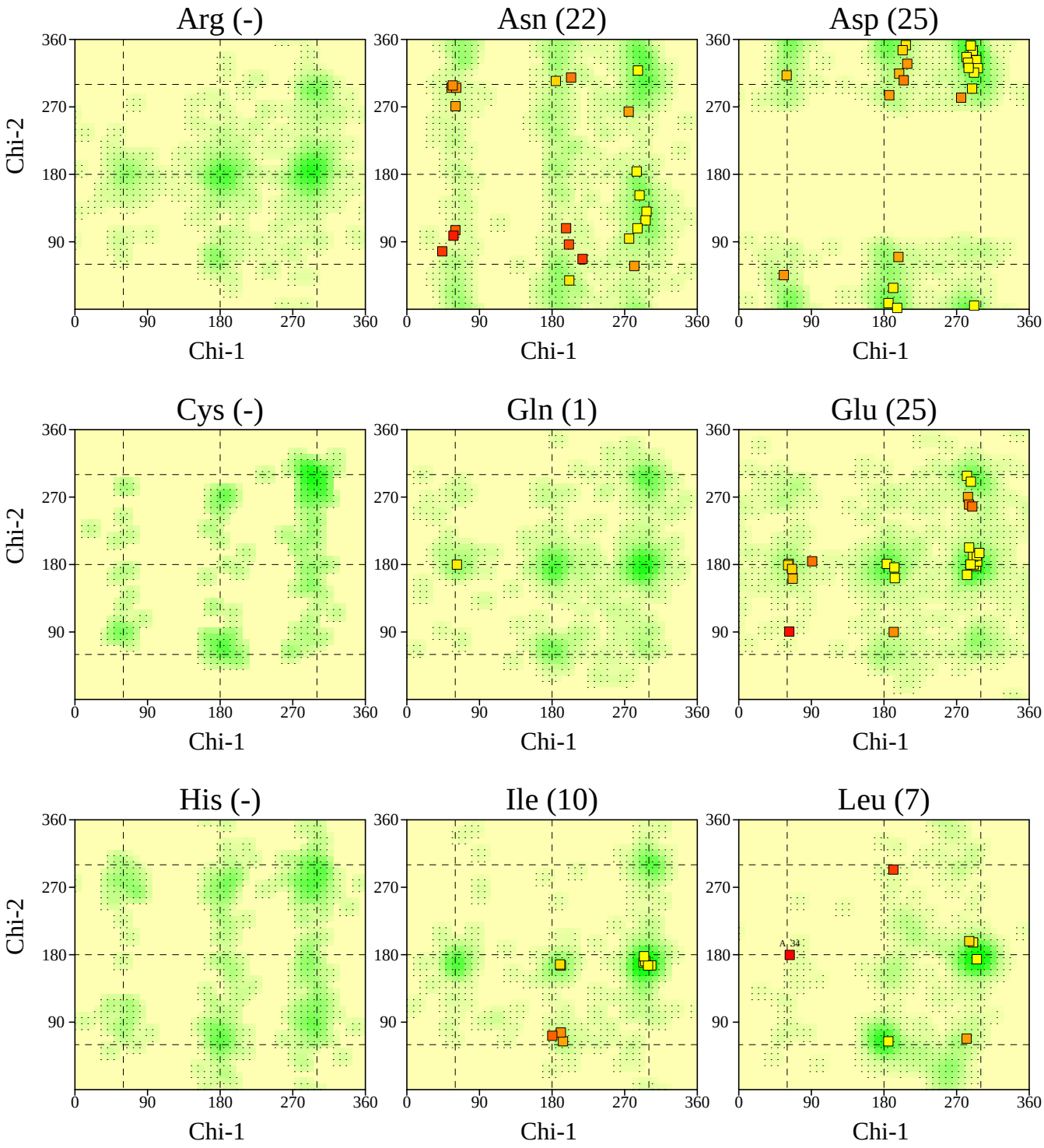
Chi1-Chi2 plots

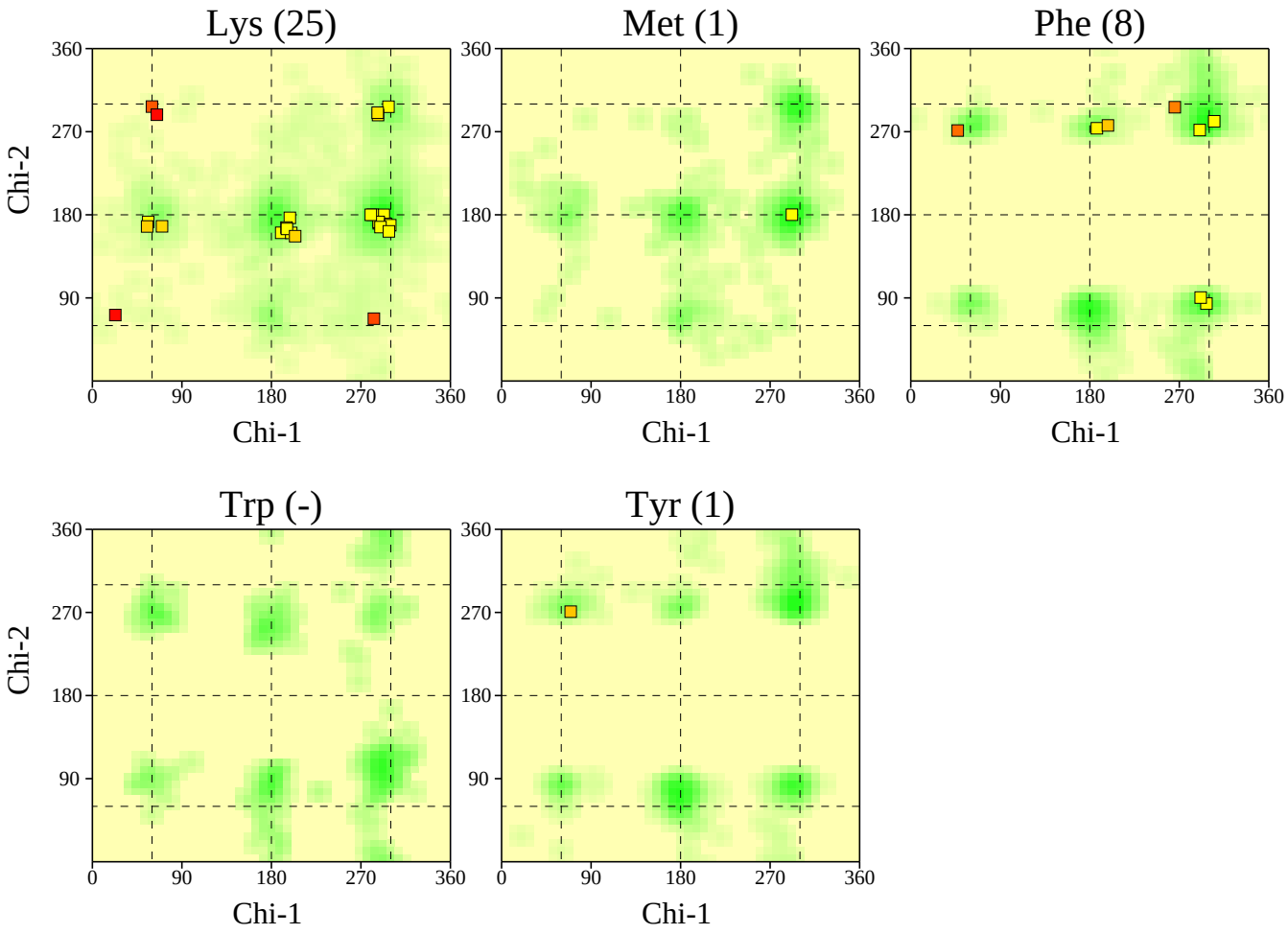
23_128_72



Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0A or better.

Chi1-Chi2 plots

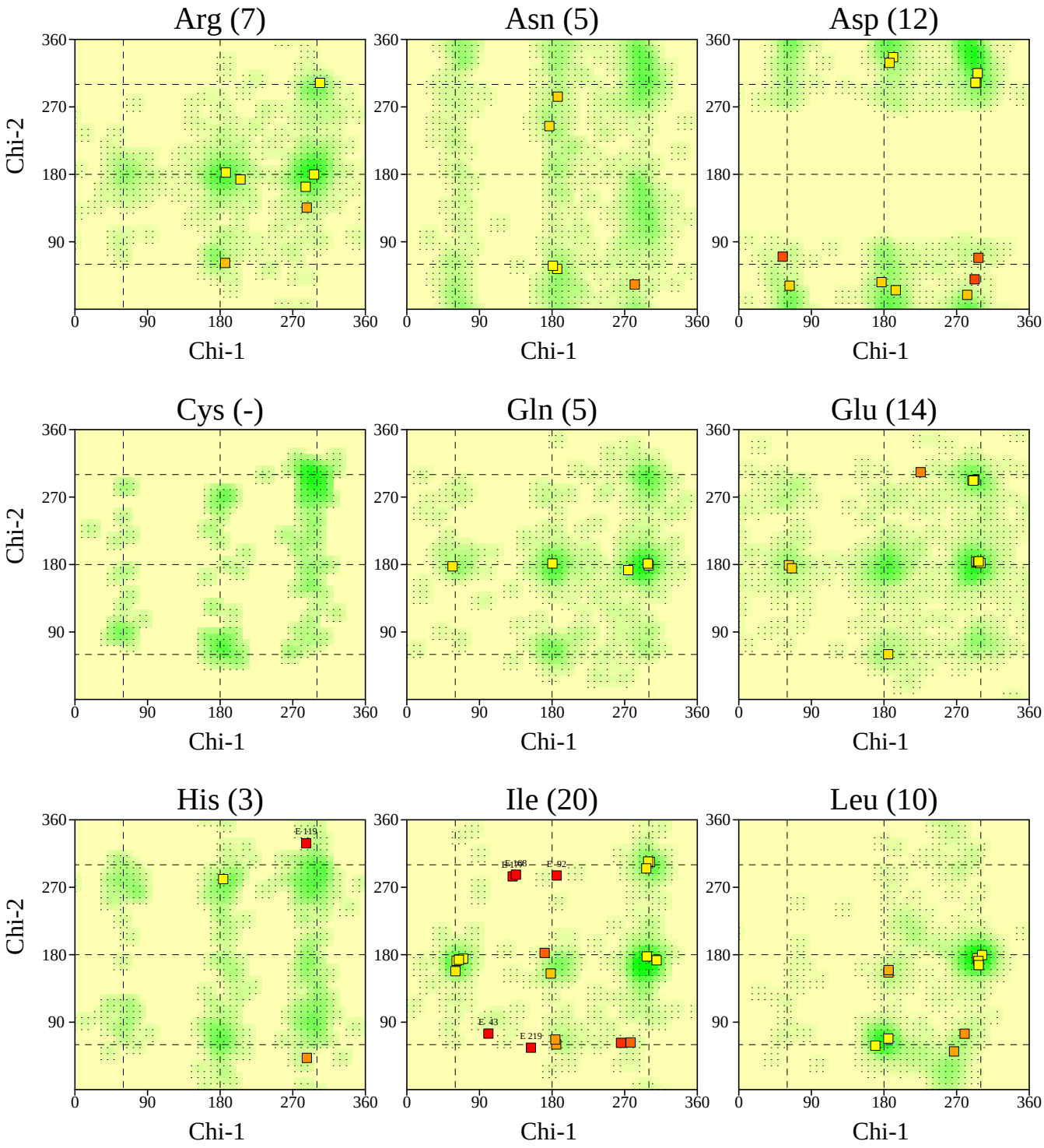
23_128_72



Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0A or better.

Chi1-Chi2 plots

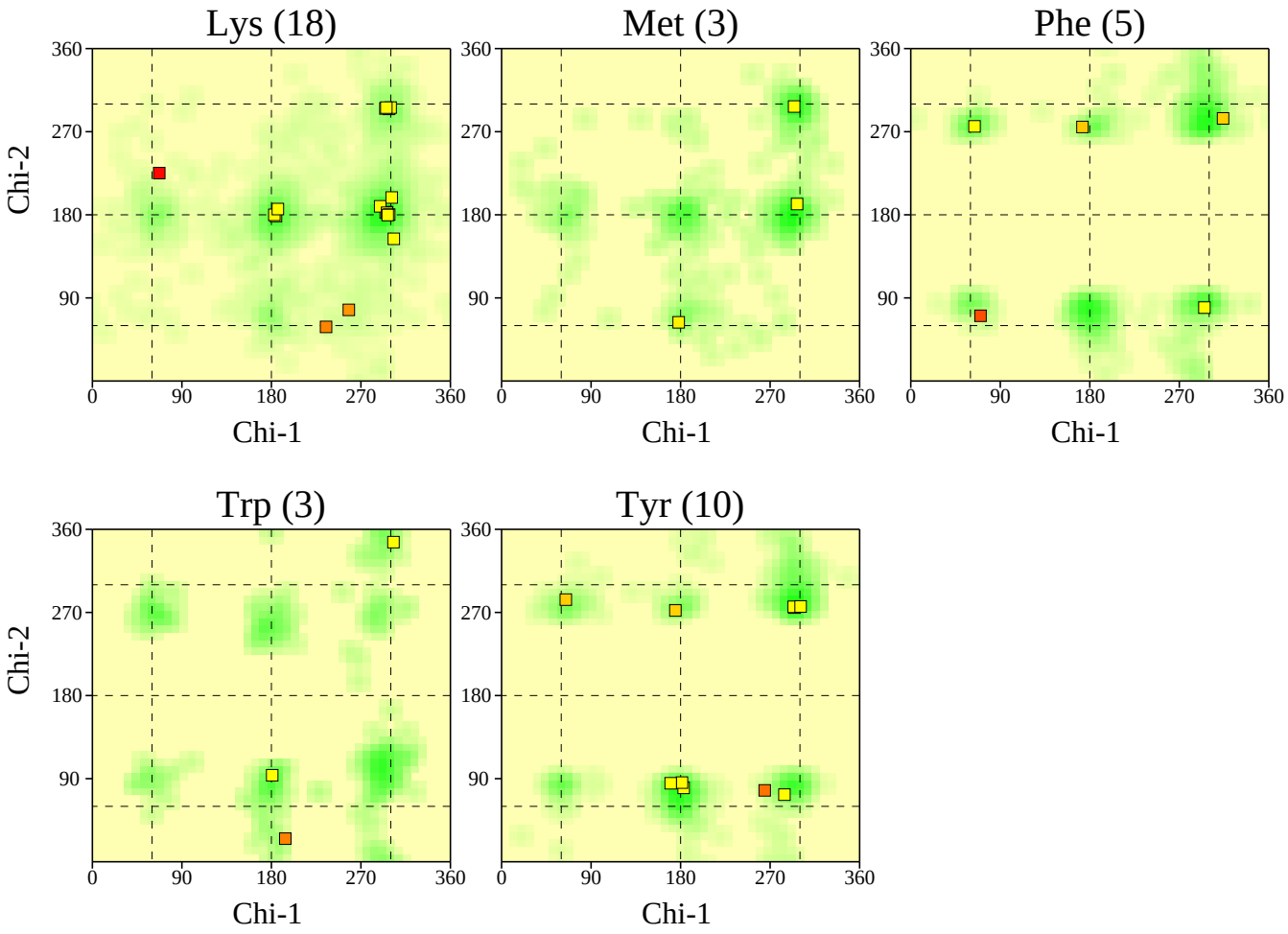
Model_12



Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0A or better.

Chi1-Chi2 plots

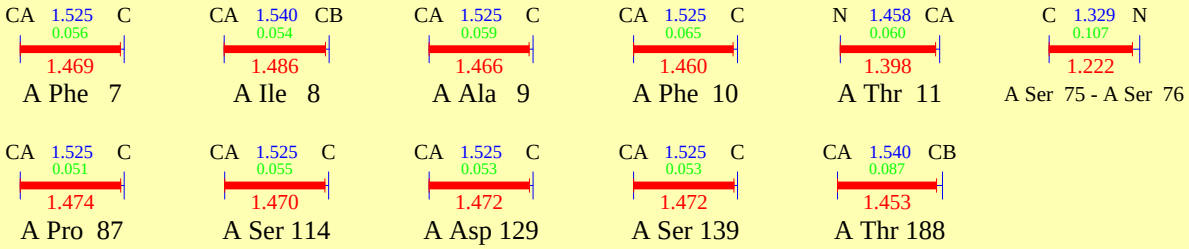
Model_12



Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0A or better.

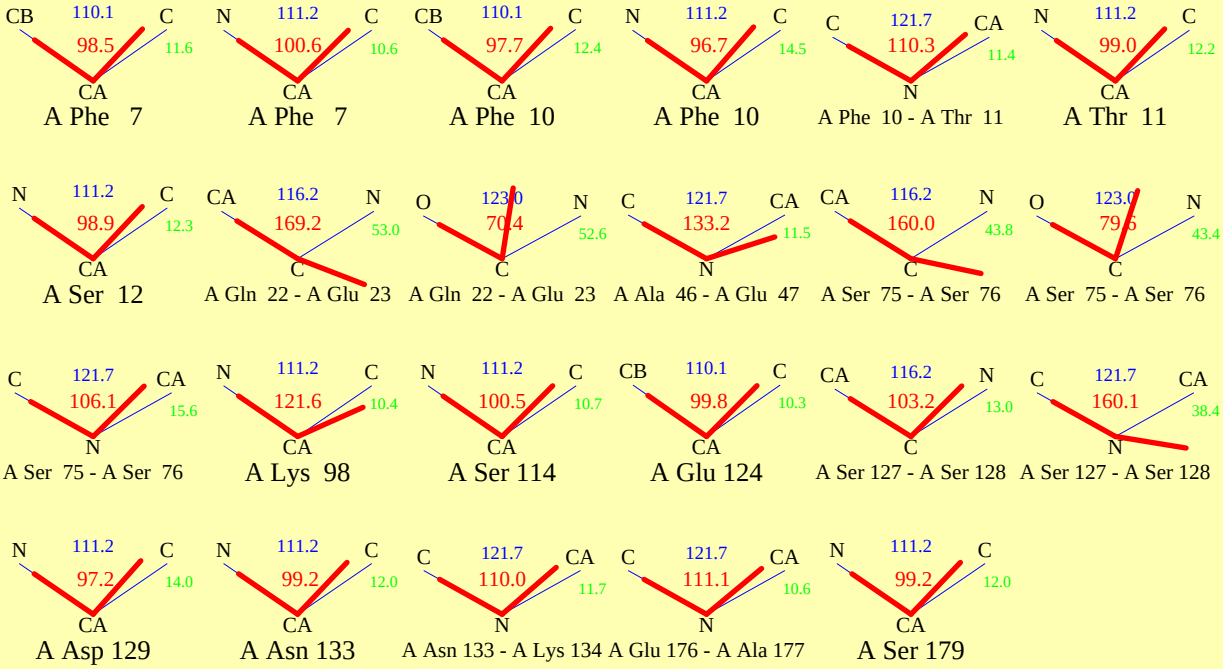
Distorted geometry
23_128_72

Main-chain bond lengths



Bonds differing by > 0.05A from small-molecule values. Values shown: "ideal", difference, actual

Main-chain bond angles



Bond angles differing by > 10.0 degrees from small-molec values. Values shown: "ideal", actual, diff.

Distorted geometry
Model_12

Main-chain bond lengths

E Gly 59 - E Ser 60

E Val 74 - E Val 75

E Val 75

E Val 75

E Val 75 - E Leu 76

E Leu 81

E Leu 81 - E Asp 82

E Ile 92

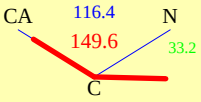
E Gly 164 - E Tyr 165

E Ile 167 - E Ile 168

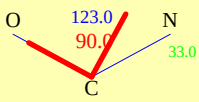
E Glu 189

Bonds differing by > 0.05A from small-molecule values. Values shown: "ideal", difference, actual

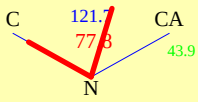
Main-chain bond angles



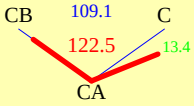
E Gly 59 - E Ser 60



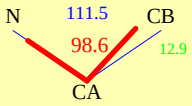
E Gly 59 - E Ser 60



E Gly 59 - E Ser 60



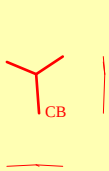
E Val 75



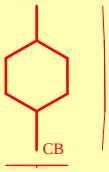
E Val 75

Bond angles differing by > 10.0 degrees from small-molec values. Values shown: "ideal", actual, diff.

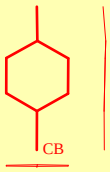
Planar groups



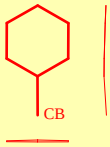
0.024
E Asp 65



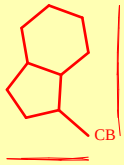
0.037
E Tyr 69



0.030
E Tyr 73

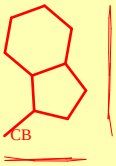


0.034
E Phe 78

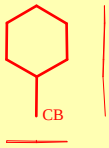


0.035
E Trp 83

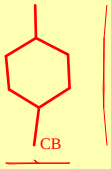
0.024
E Glu 90



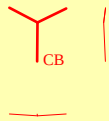
0.048
E Trp 122



0.031
E Phe 137

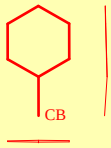


0.054
E Tyr 165



0.031
E Asp 170

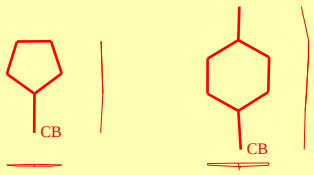
0.028
E Gln 178



0.033
E Phe 200

Distorted geometry
Model_12

Planar groups (contd)



0.031 E His 204

0.092 E Tyr 229

Sidechains with RMS dist. from planarity > 0.03A for rings, or > 0.02A otherwise. Value shown is RMS dist.