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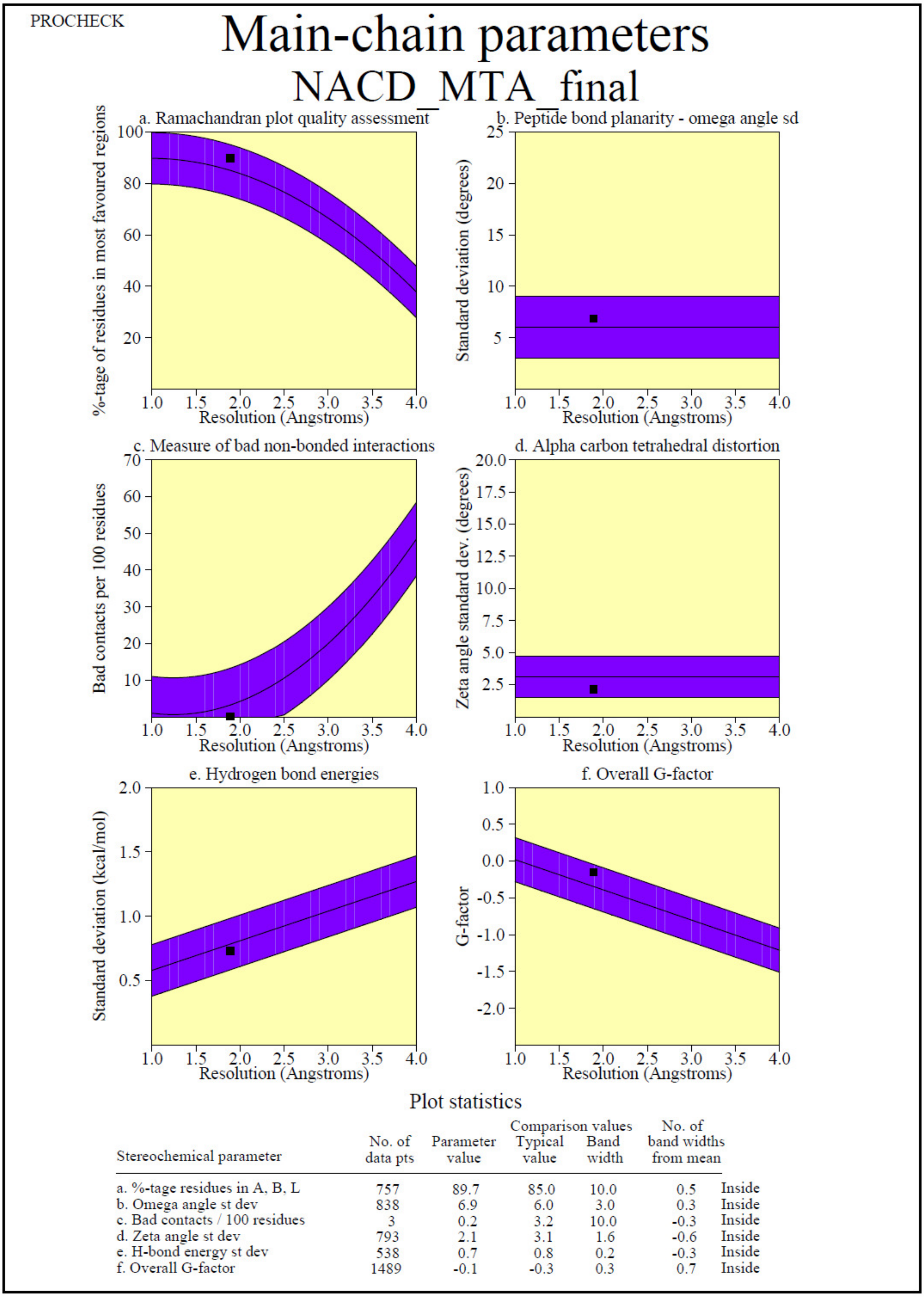
Appendix I: PROCHECK results for the *Pf*SpdS-NACD-MTA crystal structure



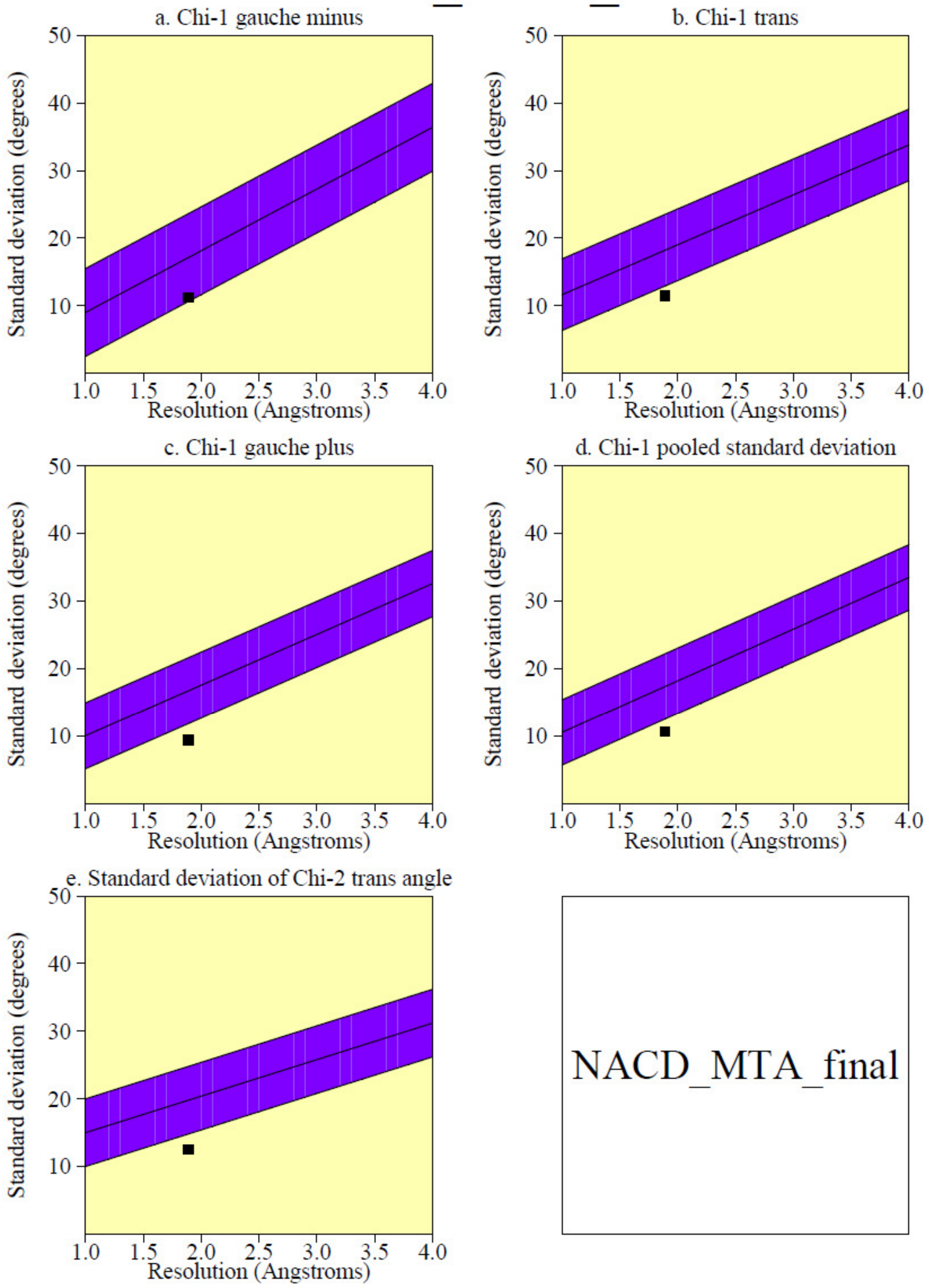
Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values Typical value	Band width	No. of band widths from mean	
a. %-tage residues in A, B, L	757	89.7	85.0	10.0	0.5	Inside
b. Omega angle st dev	838	6.9	6.0	3.0	0.3	Inside
c. Bad contacts / 100 residues	3	0.2	3.2	10.0	-0.3	Inside
d. Zeta angle st dev	793	2.1	3.1	1.6	-0.6	Inside
e. H-bond energy st dev	538	0.7	0.8	0.2	-0.3	Inside
f. Overall G-factor	1489	-0.1	-0.3	0.3	0.7	Inside

PROCHECK

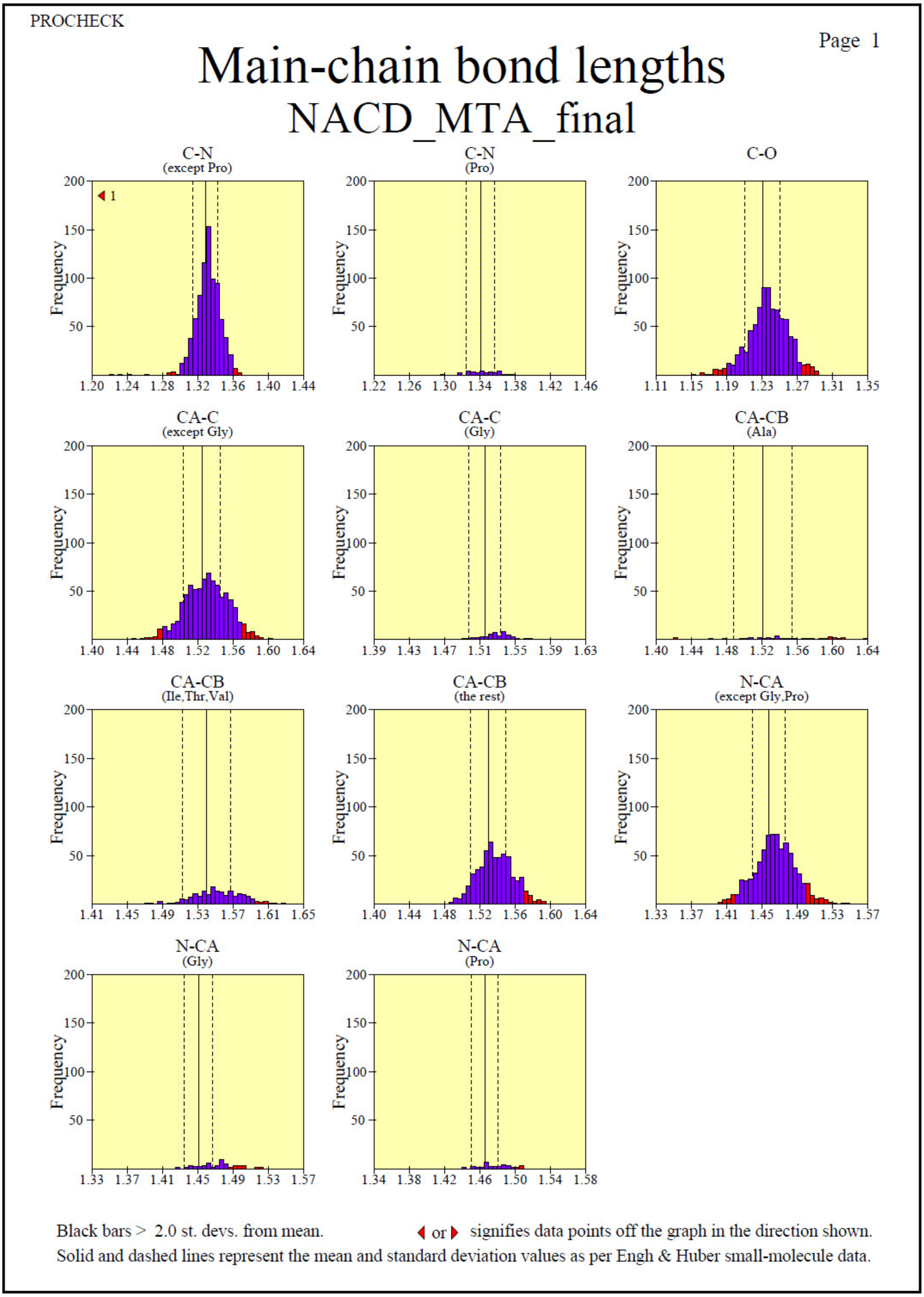
Side-chain parameters

NACD_MTA_final



Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values Typical value	Band width	No. of band widths from mean	
a. Chi-1 gauche minus st dev	125	11.2	17.1	6.5	-0.9	Inside
b. Chi-1 trans st dev	230	11.5	18.2	5.3	-1.3	BETTER
c. Chi-1 gauche plus st dev	371	9.3	16.7	4.9	-1.5	BETTER
d. Chi-1 pooled st dev	726	10.6	17.3	4.8	-1.4	BETTER
e. Chi-2 trans st dev	243	12.5	19.8	5.0	-1.5	BETTER



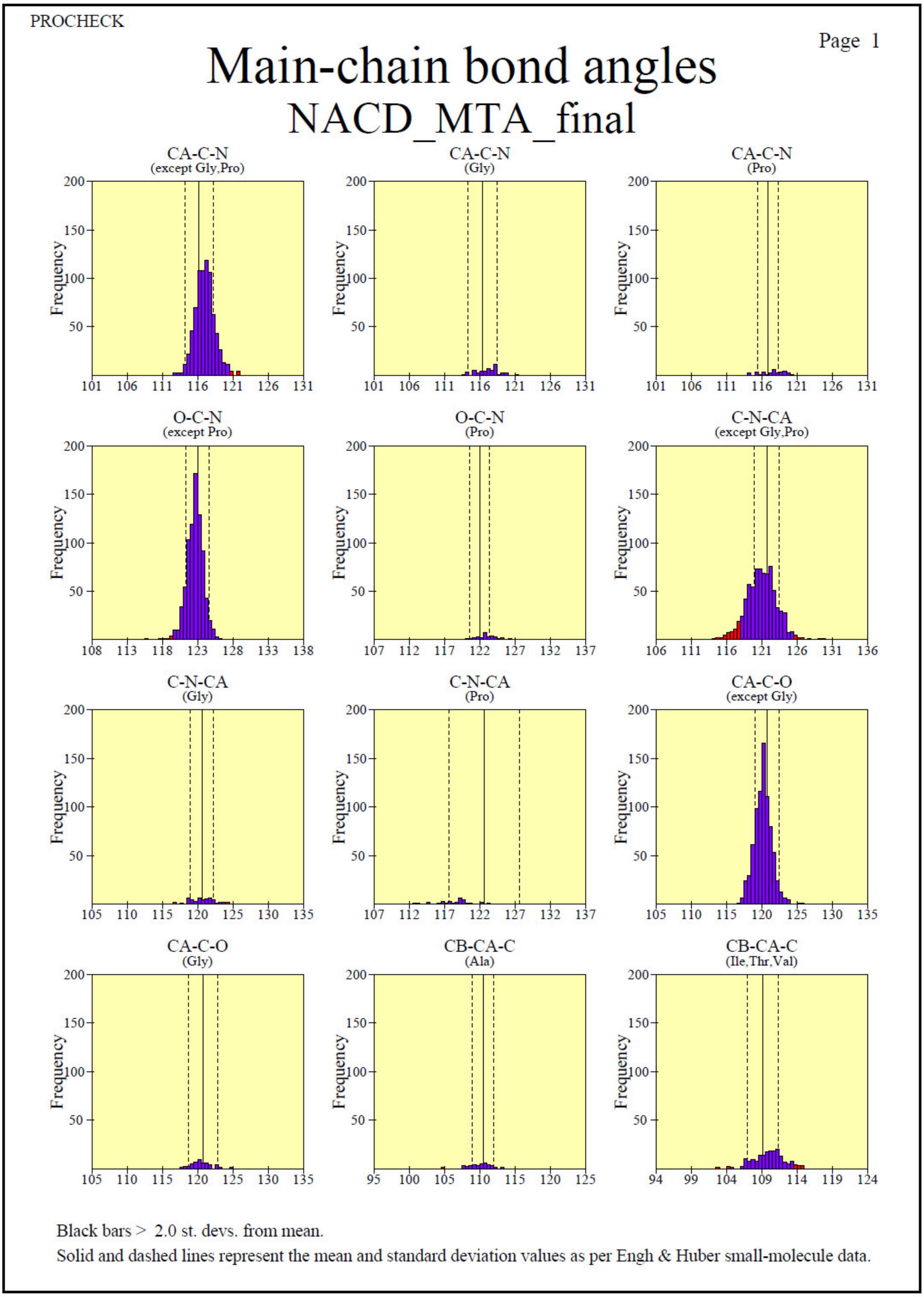
PROCHECK

Page 1

Main-chain bond lengths

NACD_MTA_final

Black bars > 2.0 st. devs. from mean. ◀ or ▶ signifies data points off the graph in the direction shown.
Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.



PROCHECK

Page 1

Main-chain bond angles

NACD_MTA_final

Black bars > 2.0 st. devs. from mean.

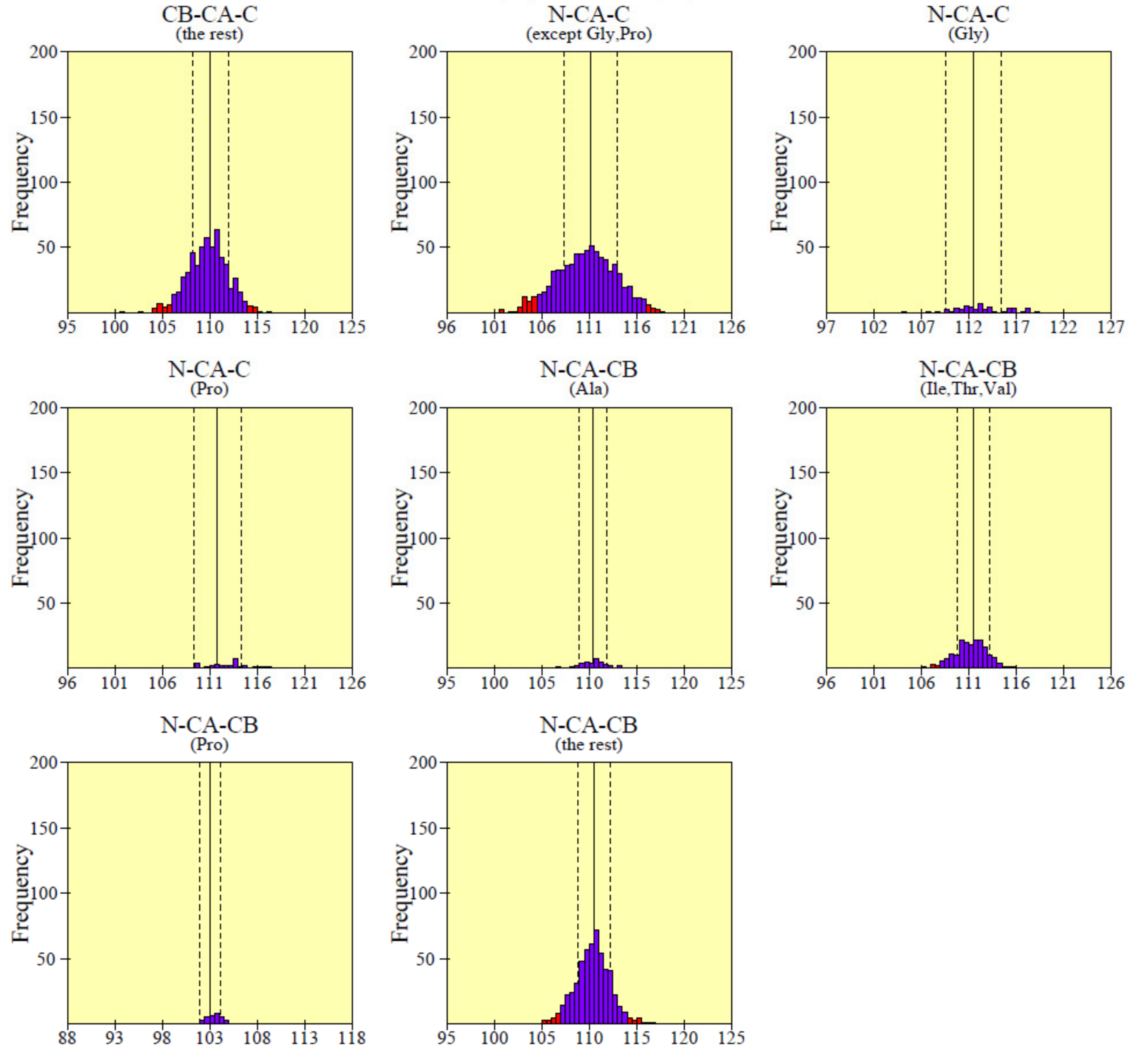
Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

PROCHECK

Page 2

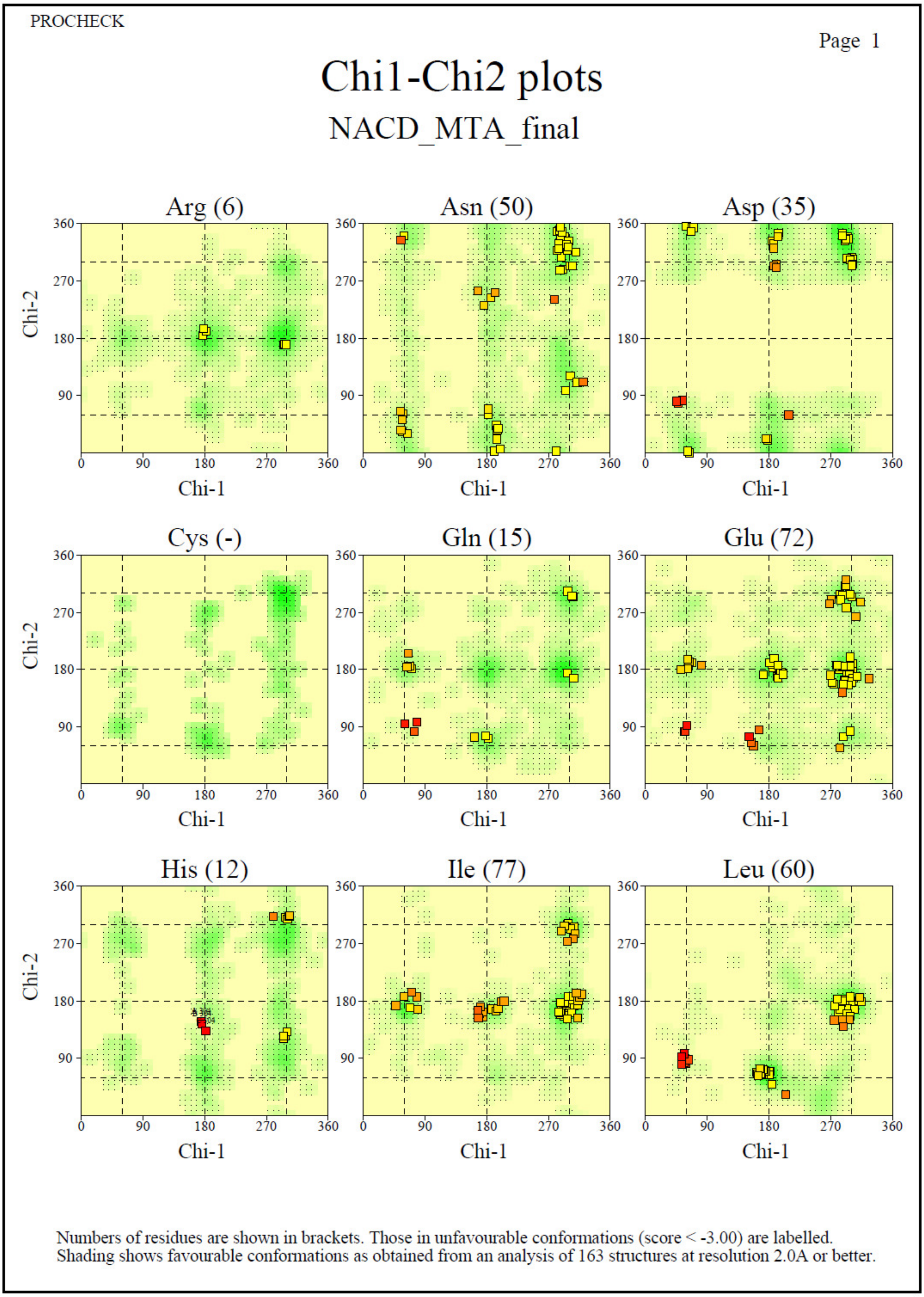
Main-chain bond angles

NACD_MTA_final



Black bars > 2.0 st. devs. from mean.

Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.



PROCHECK

Page 1

Chi1-Chi2 plots

NACD_MTA_final

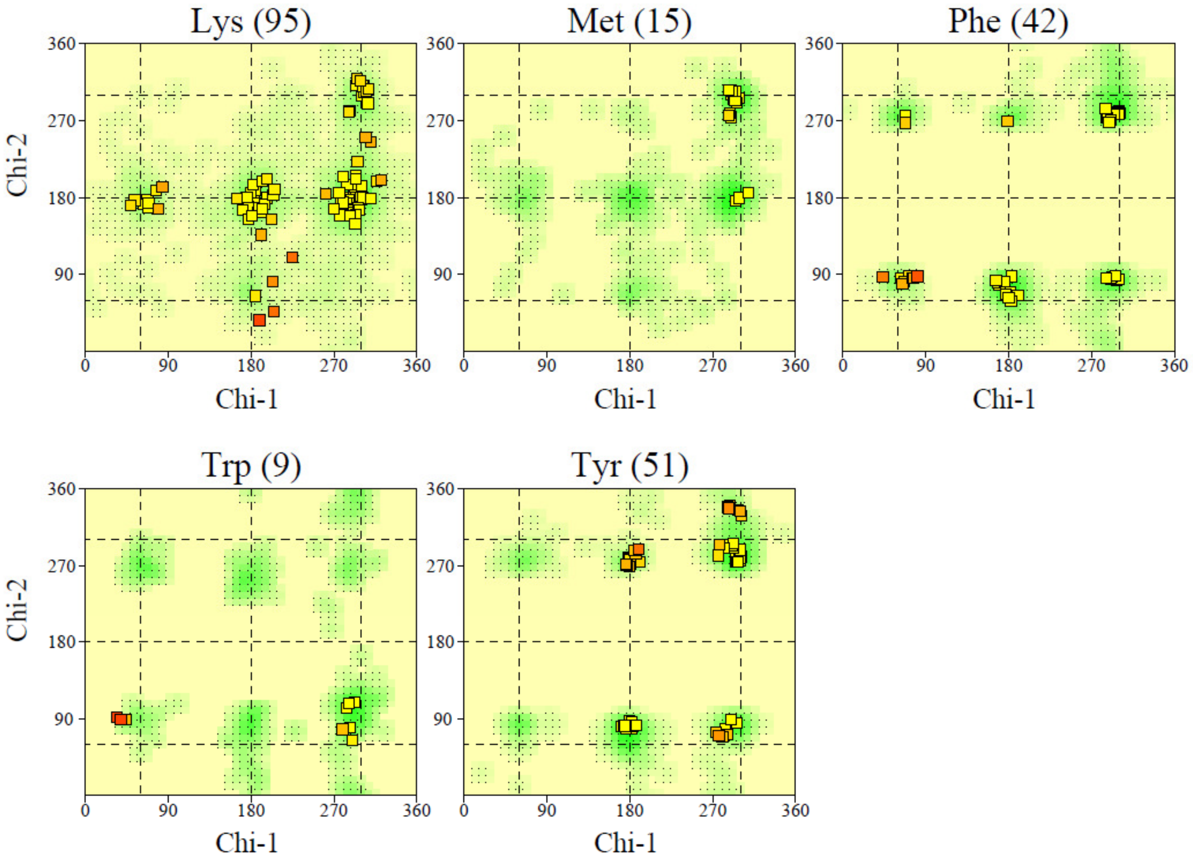
Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0A or better.

PROCHECK

Page 2

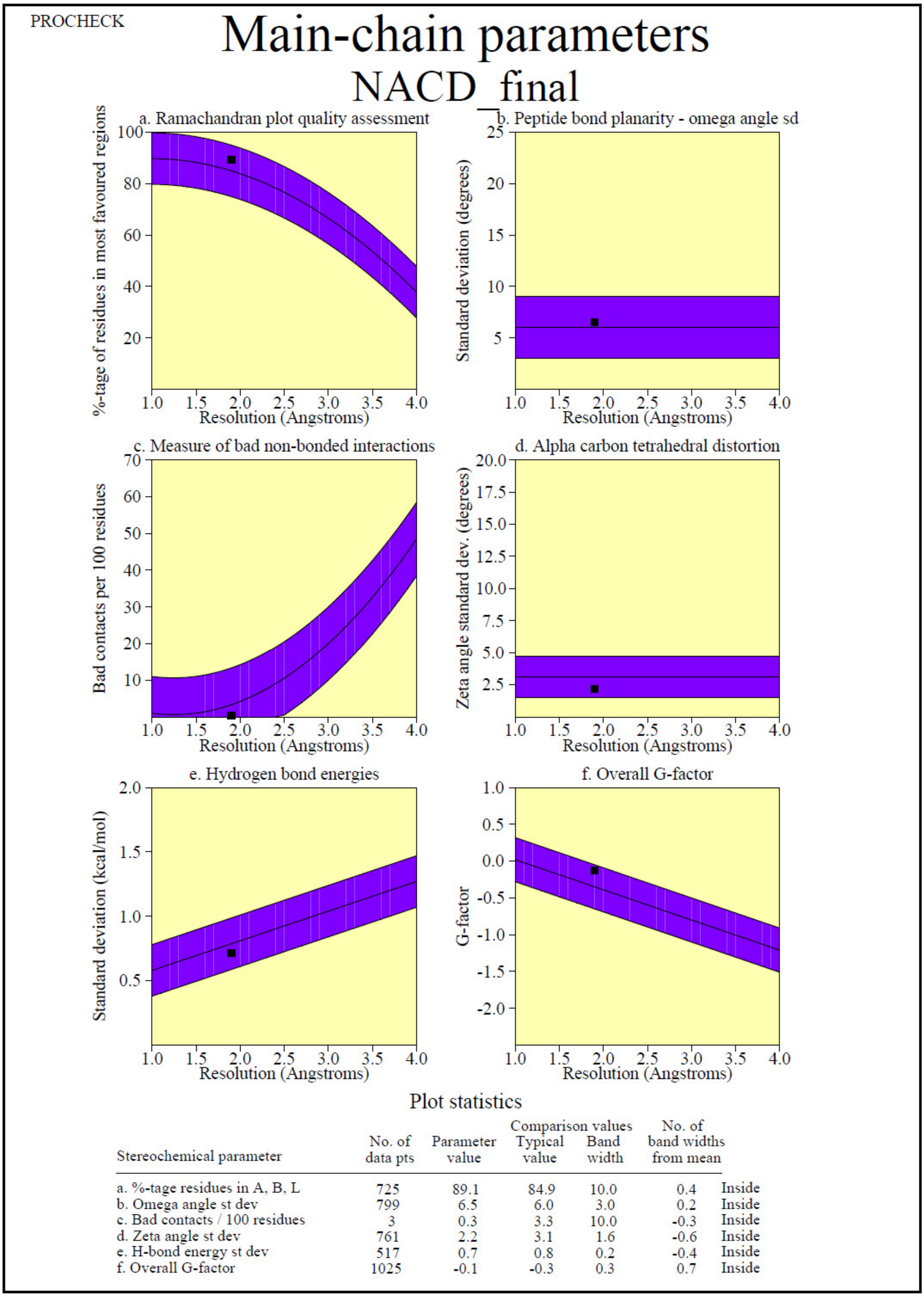
Chi1-Chi2 plots

NACD_MTA_final



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.

Appendix II: PROCHECK results for the *Pf*SpdS-NACD crystal structure



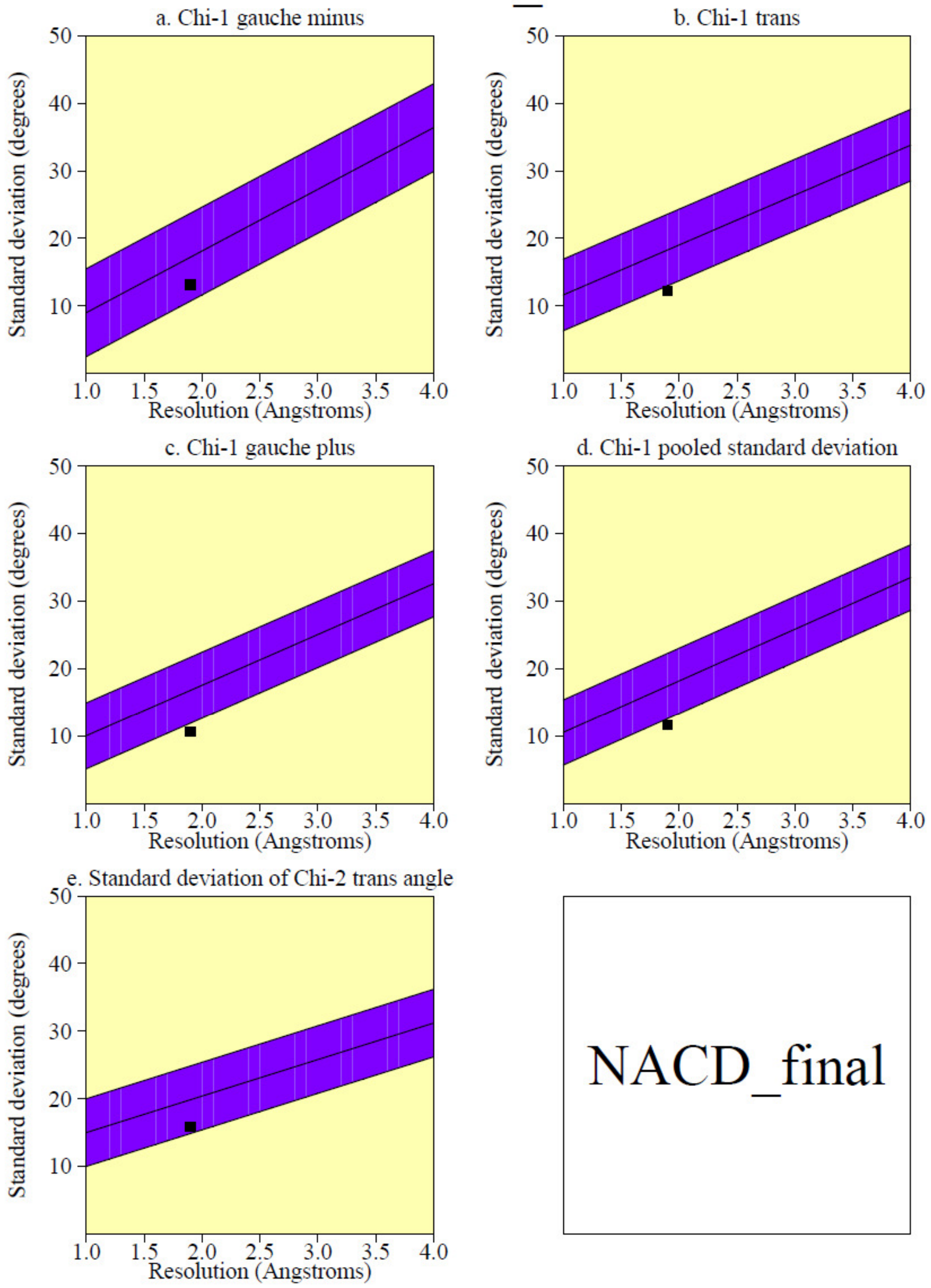
Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values Typical value	Band width	No. of band widths from mean	
a. %-tage residues in A, B, L	725	89.1	84.9	10.0	0.4	Inside
b. Omega angle st dev	799	6.5	6.0	3.0	0.2	Inside
c. Bad contacts / 100 residues	3	0.3	3.3	10.0	-0.3	Inside
d. Zeta angle st dev	761	2.2	3.1	1.6	-0.6	Inside
e. H-bond energy st dev	517	0.7	0.8	0.2	-0.4	Inside
f. Overall G-factor	1025	-0.1	-0.3	0.3	0.7	Inside

PROCHECK

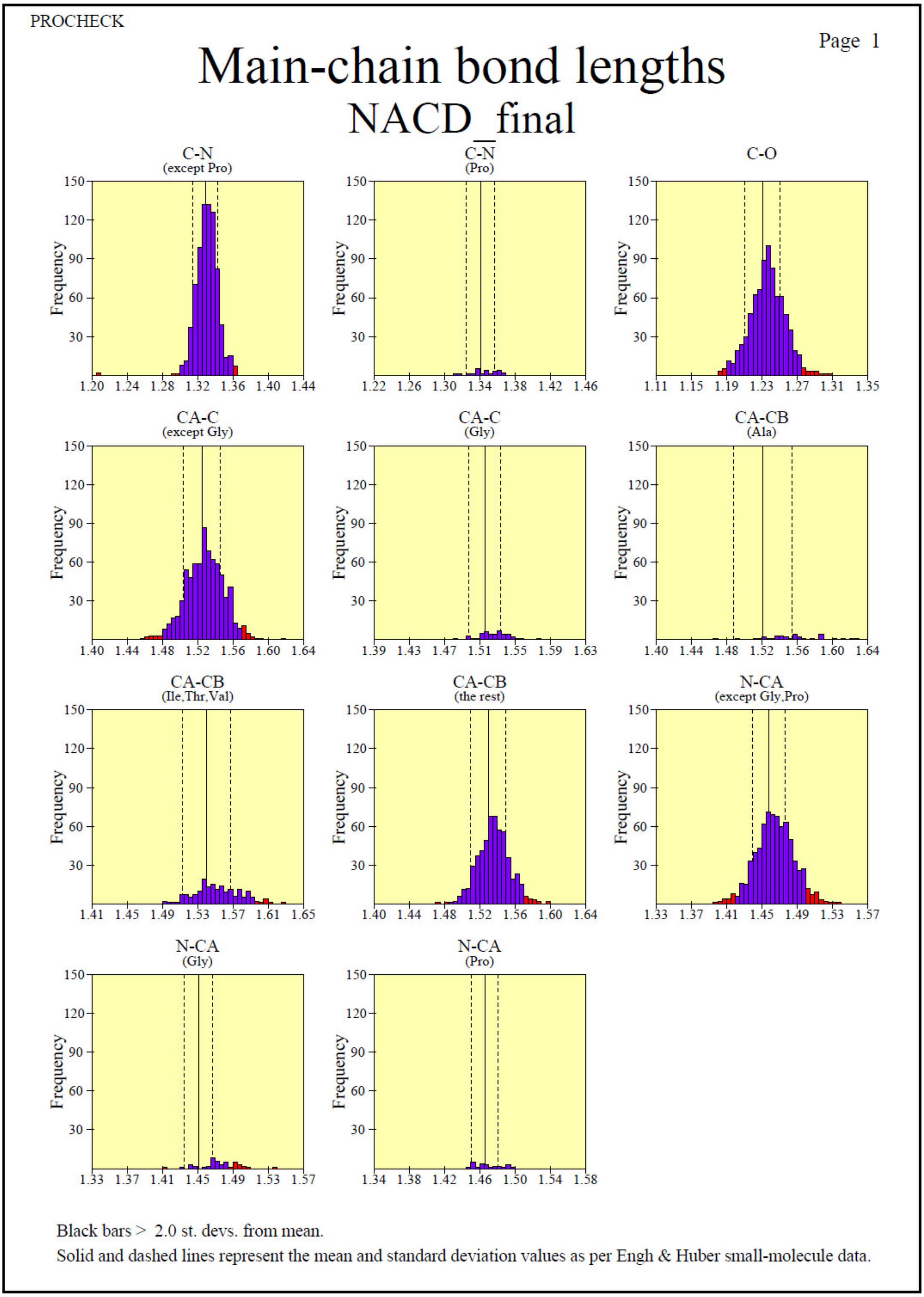
Side-chain parameters

NACD_final



Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values Typical value	Band width	No. of band widths from mean	
a. Chi-1 gauche minus st dev	108	13.1	17.2	6.5	-0.6	Inside
b. Chi-1 trans st dev	233	12.3	18.3	5.3	-1.1	BETTER
c. Chi-1 gauche plus st dev	363	10.7	16.8	4.9	-1.2	BETTER
d. Chi-1 pooled st dev	704	11.7	17.4	4.8	-1.2	BETTER
e. Chi-2 trans st dev	236	15.9	19.9	5.0	-0.8	Inside



PROCHECK

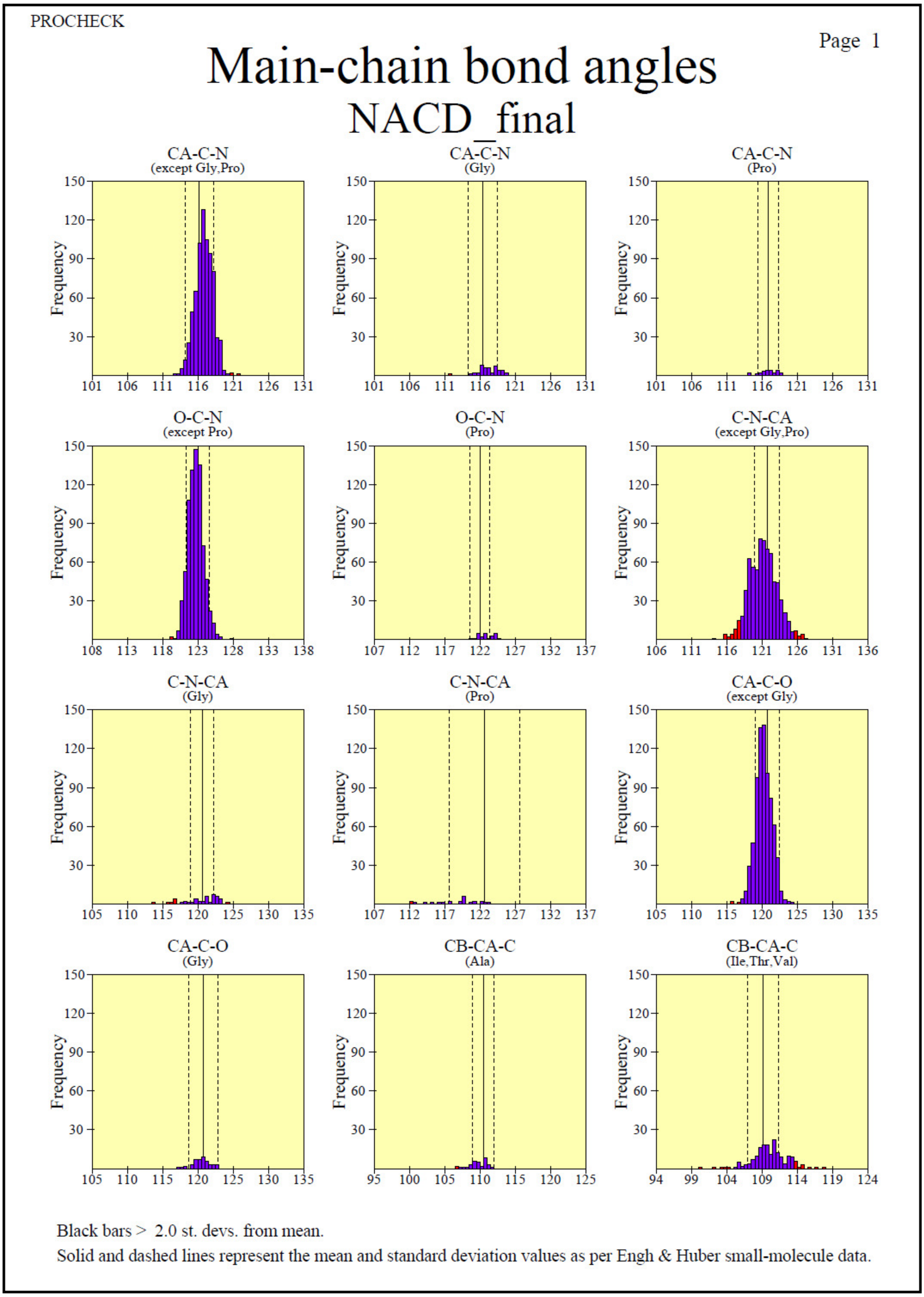
Page 1

Main-chain bond lengths

NACD_final

Black bars > 2.0 st. devs. from mean.

Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.



PROCHECK

Page 1

Main-chain bond angles

NACD_final

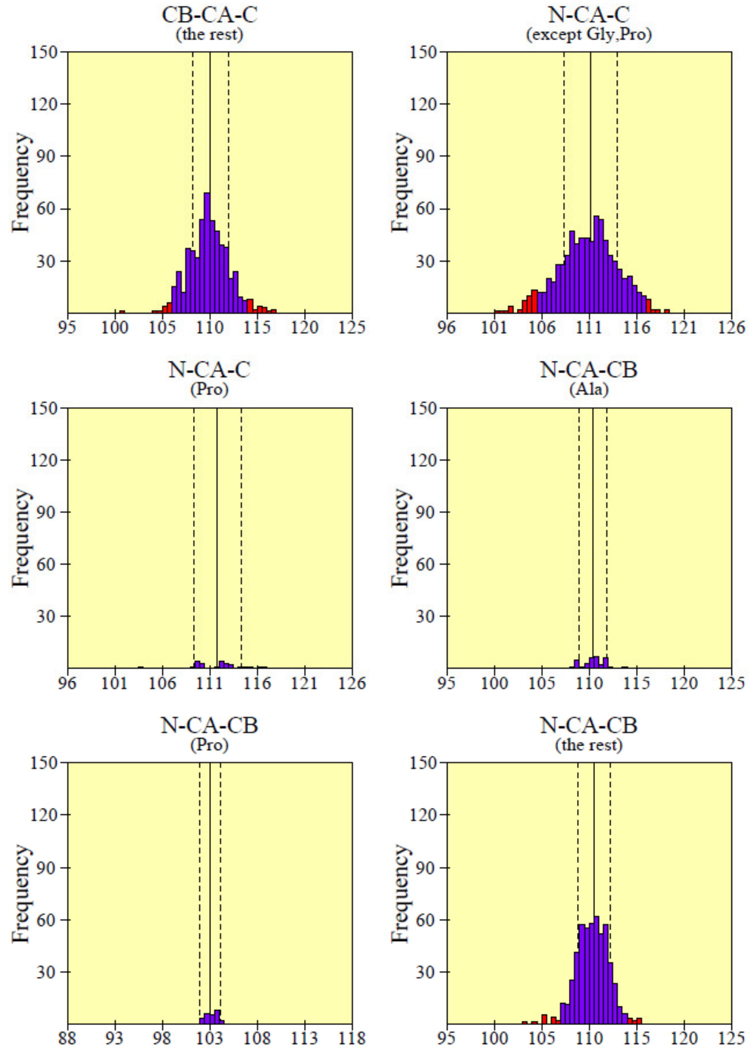
Black bars > 2.0 st. devs. from mean.
Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

PROCHECK

Page 2

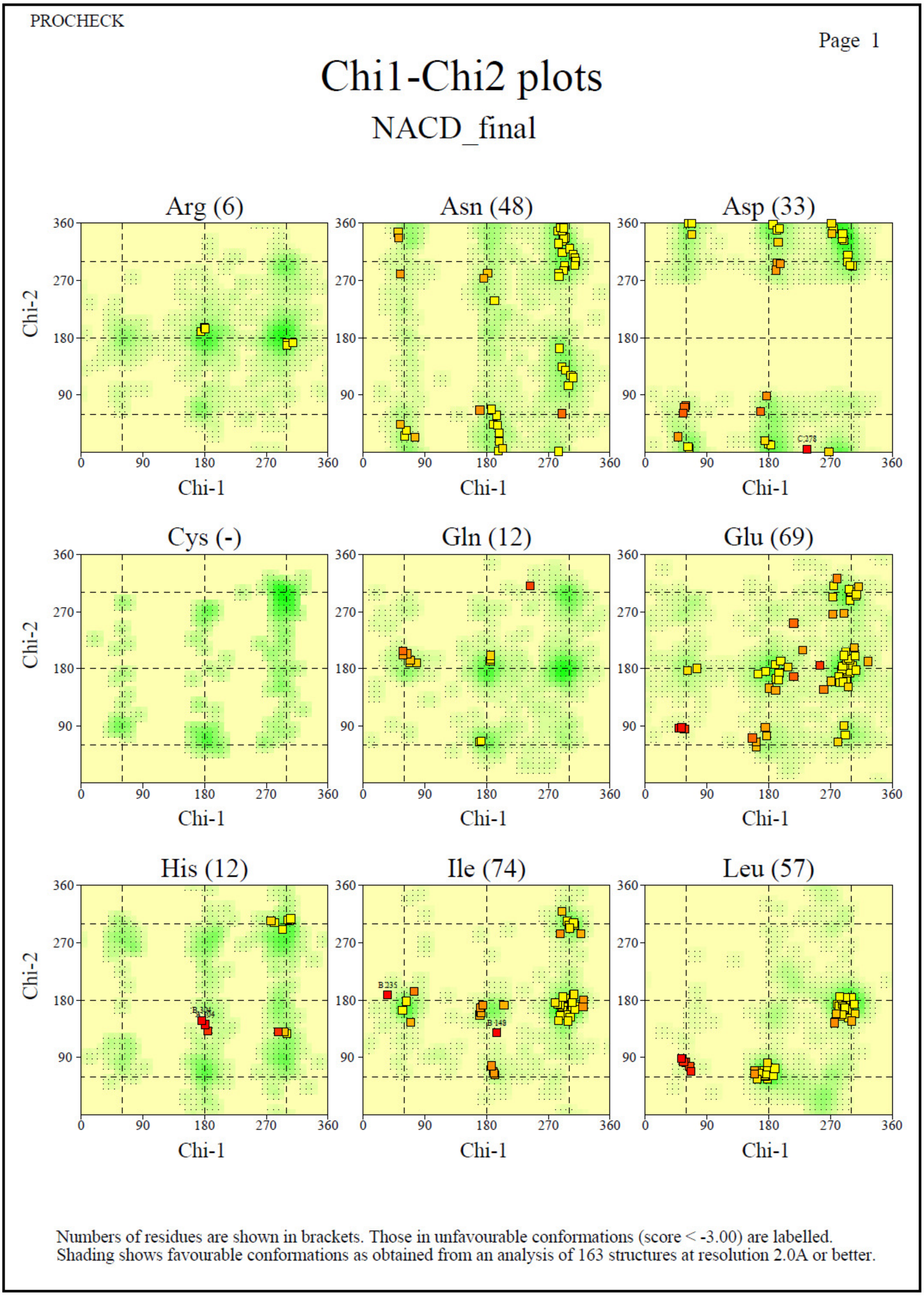
Main-chain bond angles

NACD_final



Black bars > 2.0 st. devs. from mean.

Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.



PROCHECK

Page 1

Chi1-Chi2 plots

NACD_final

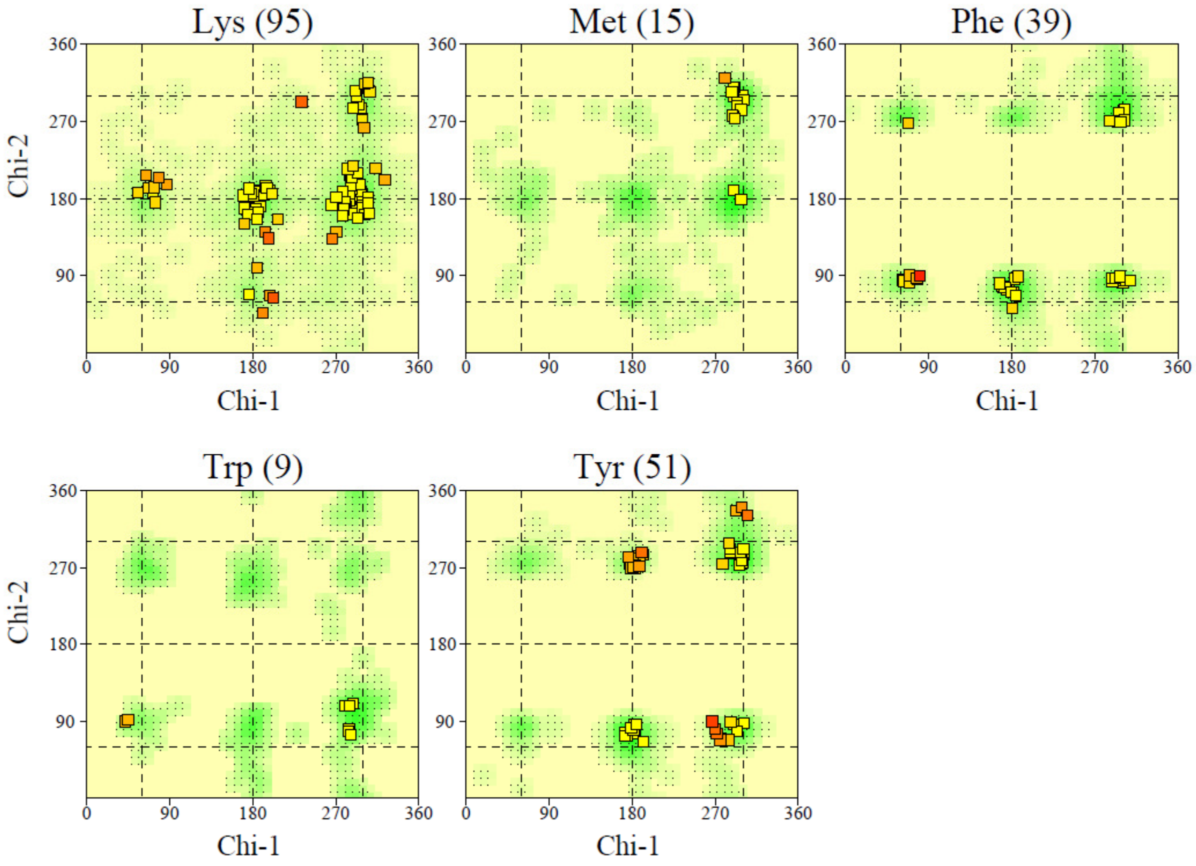
Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0A or better.

PROCHECK

Page 2

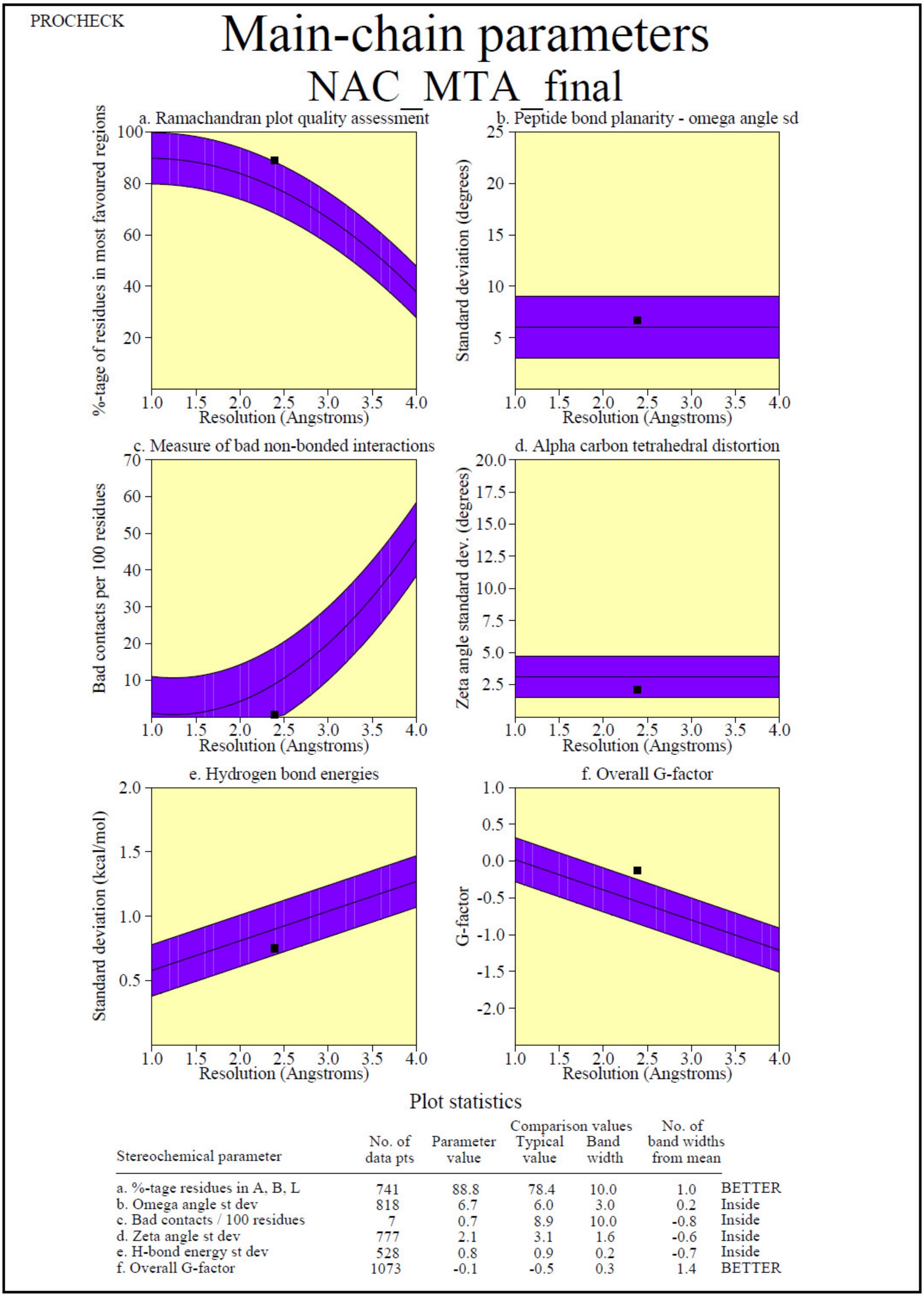
Chi1-Chi2 plots

NACD_final



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.

Appendix III: PROCHECK results for the *Pf*SpdS-NAC-MTA crystal structure



Main-chain parameters

NAC_MTA_final

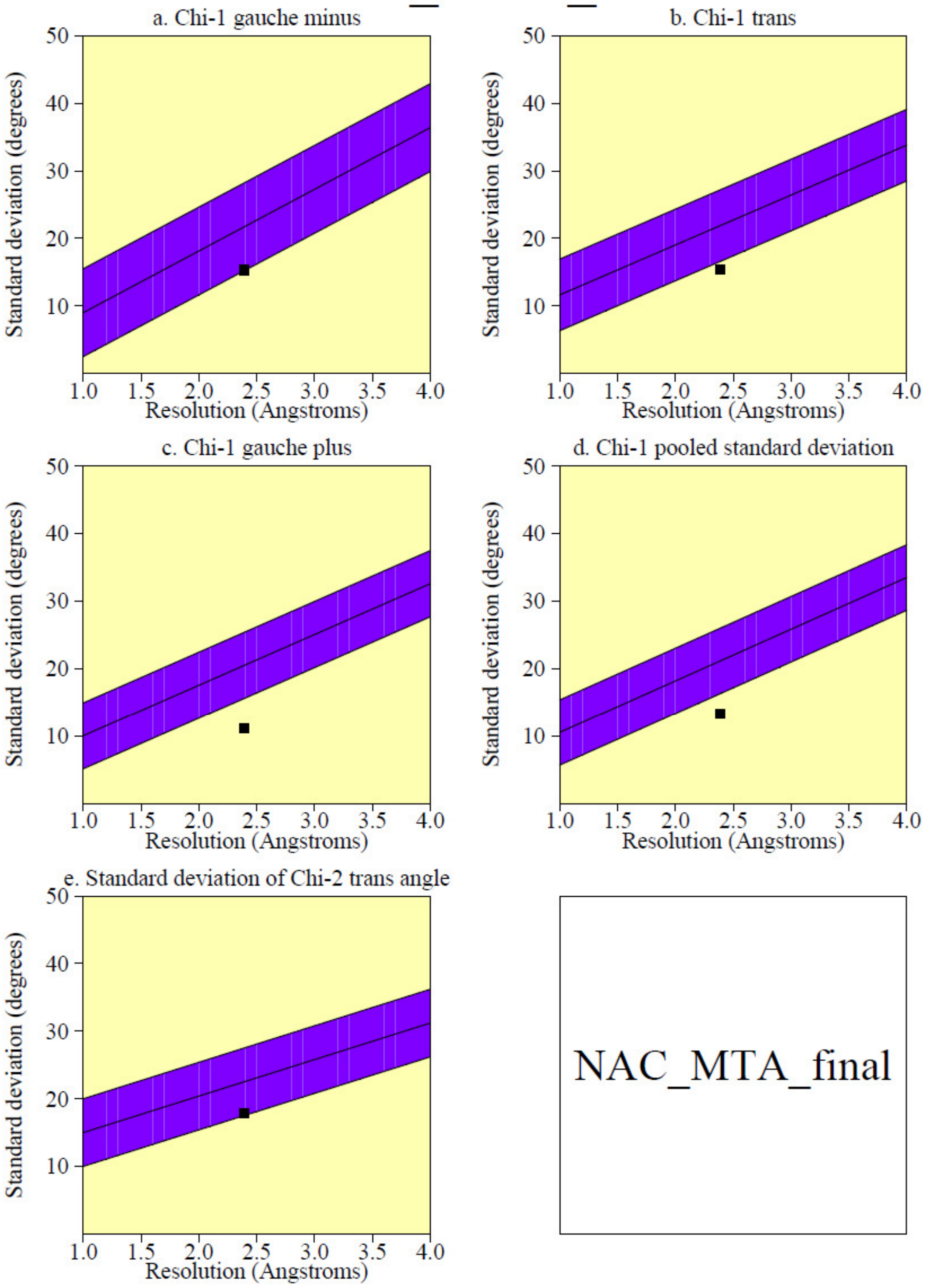
Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values Typical value	Band width	No. of band widths from mean	
a. %-tage residues in A, B, L	741	88.8	78.4	10.0	1.0	BETTER
b. Omega angle st dev	818	6.7	6.0	3.0	0.2	Inside
c. Bad contacts / 100 residues	7	0.7	8.9	10.0	-0.8	Inside
d. Zeta angle st dev	777	2.1	3.1	1.6	-0.6	Inside
e. H-bond energy st dev	528	0.8	0.9	0.2	-0.7	Inside
f. Overall G-factor	1073	-0.1	-0.5	0.3	1.4	BETTER

PROCHECK

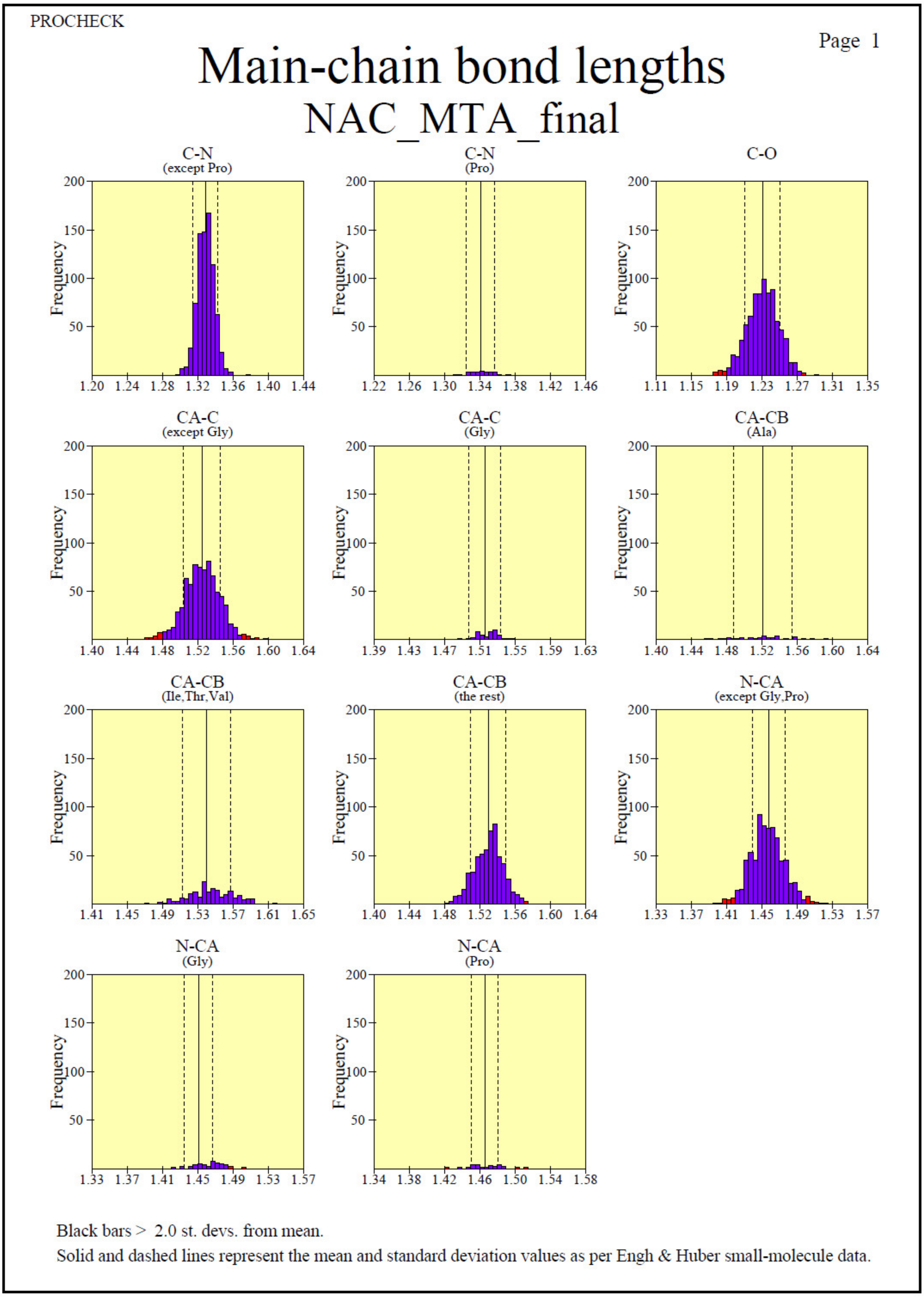
Side-chain parameters

NAC_MTA_final



Plot statistics

Stereochemical parameter	No. of data pts	Parameter value	Comparison values Typical value	Band width	No. of band widths from mean	
a. Chi-1 gauche minus st dev	123	15.3	21.7	6.5	-1.0	Inside
b. Chi-1 trans st dev	234	15.3	21.9	5.3	-1.2	BETTER
c. Chi-1 gauche plus st dev	360	11.2	20.5	4.9	-1.9	BETTER
d. Chi-1 pooled st dev	717	13.3	21.2	4.8	-1.6	BETTER
e. Chi-2 trans st dev	238	17.9	22.5	5.0	-0.9	Inside



PROCHECK

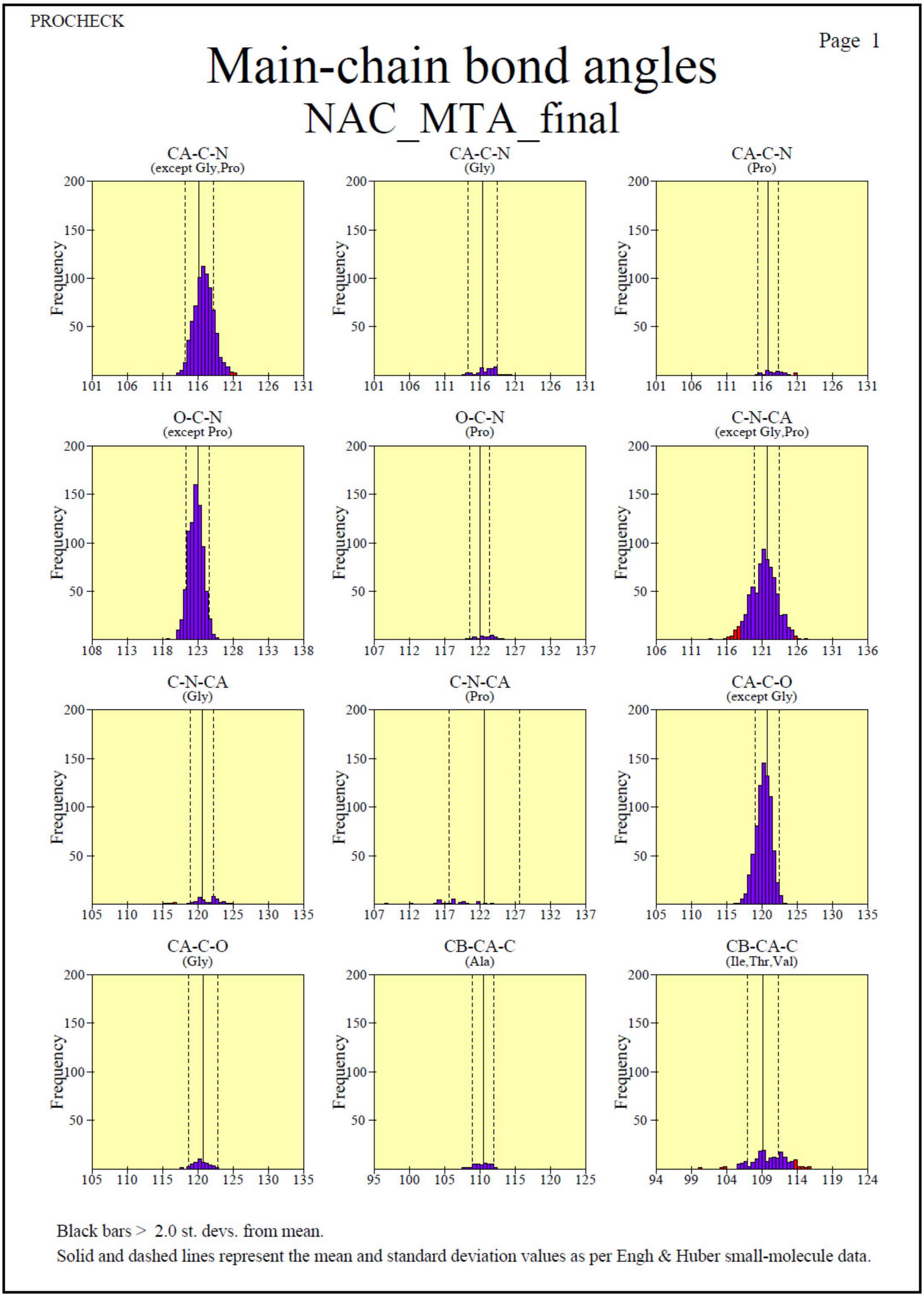
Page 1

Main-chain bond lengths

NAC_MTA_final

Black bars > 2.0 st. devs. from mean.

Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.



PROCHECK

Page 1

Main-chain bond angles

NAC_MTA_final

Black bars > 2.0 st. devs. from mean.

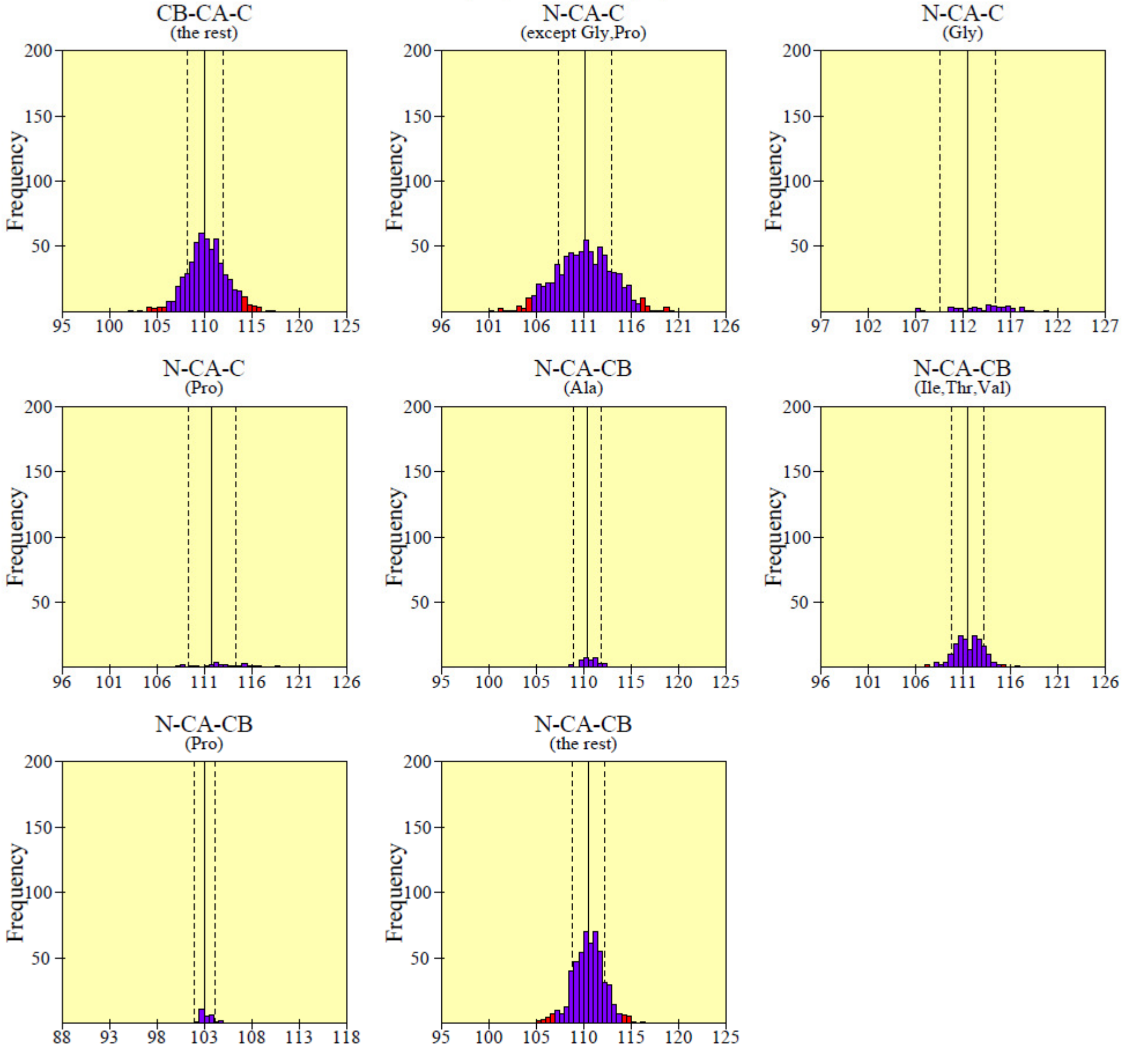
Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

PROCHECK

Page 2

Main-chain bond angles

NAC_MTA_final



Black bars > 2.0 st. devs. from mean.

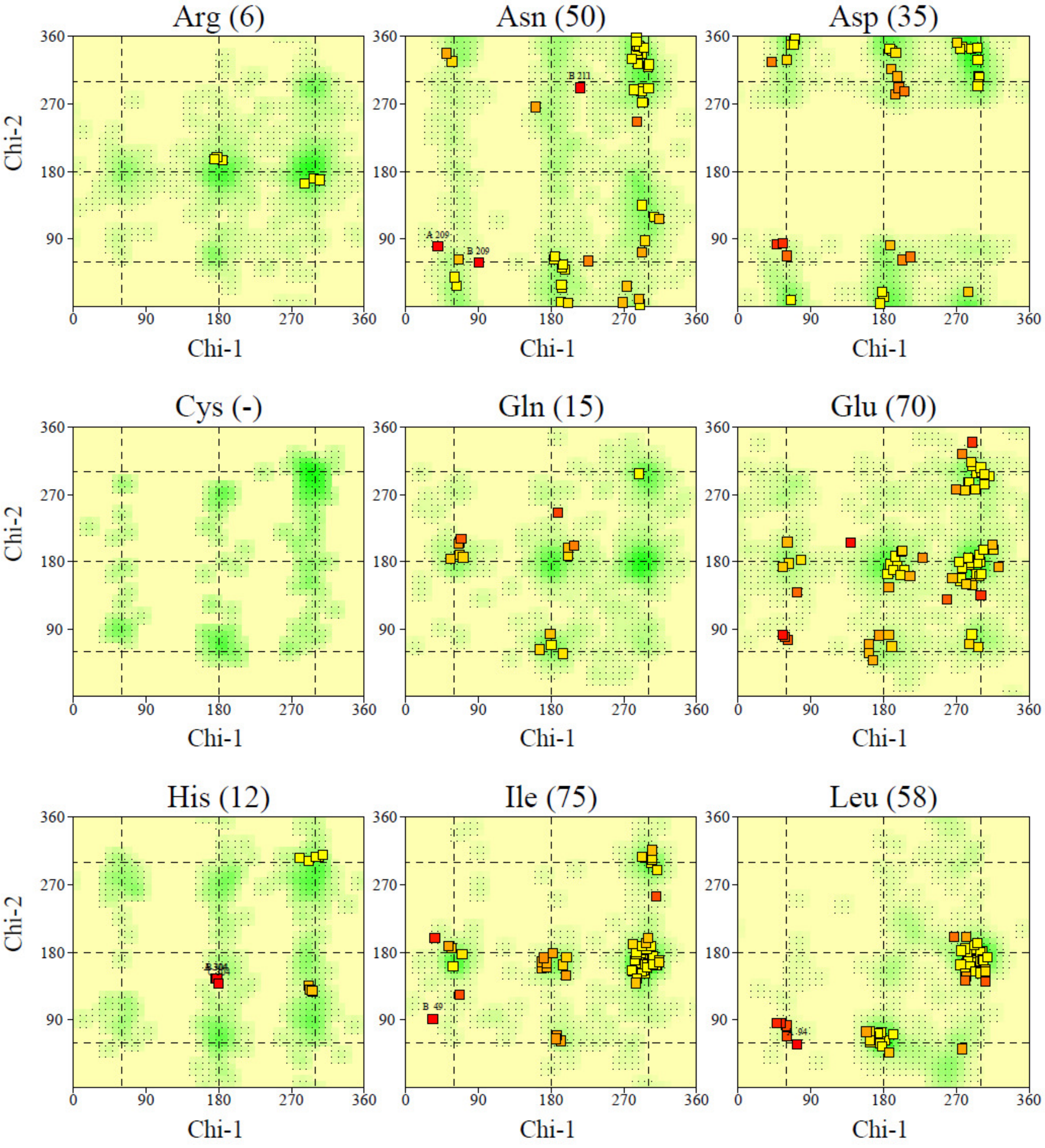
Solid and dashed lines represent the mean and standard deviation values as per Engh & Huber small-molecule data.

PROCHECK

Page 1

Chi1-Chi2 plots

NAC_MTA_final



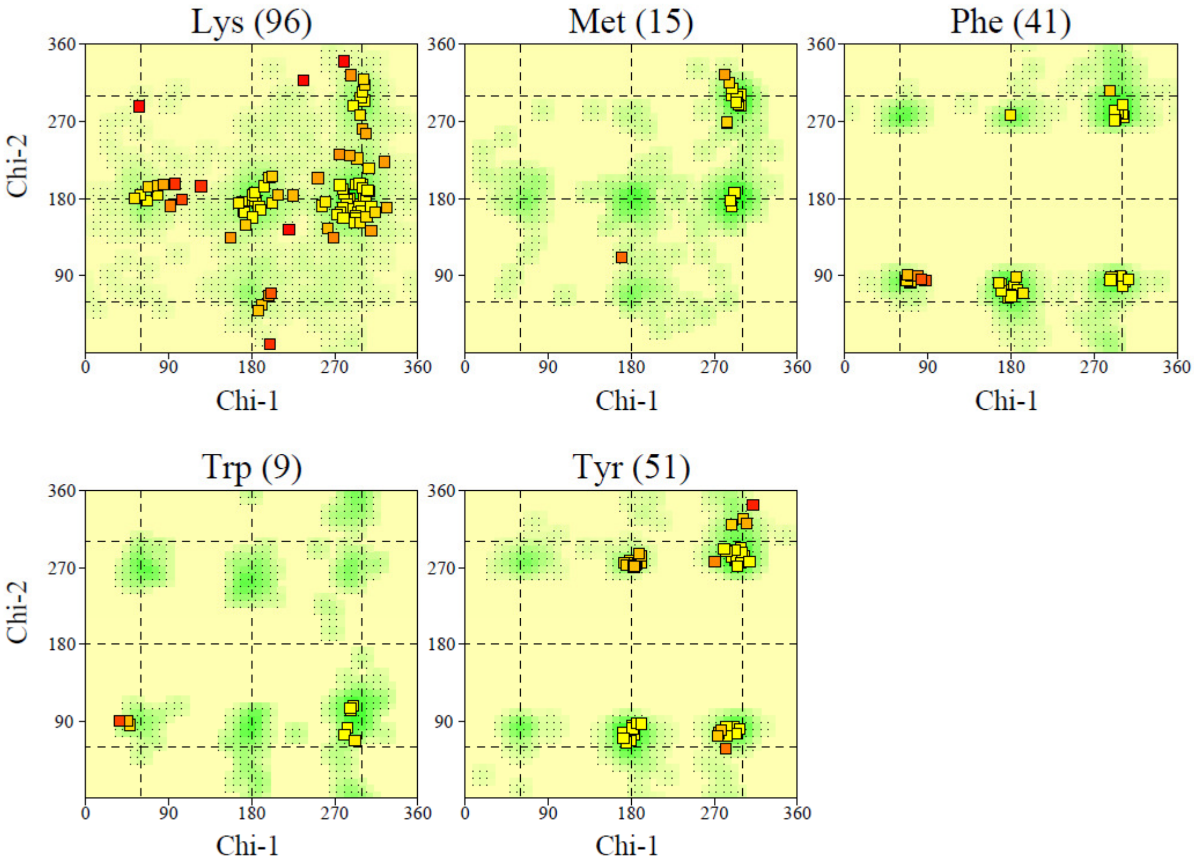
Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
Shading shows favourable conformations as obtained from an analysis of 163 structures at resolution 2.0A or better.

PROCHECK

Page 2

Chi1-Chi2 plots

NAC_MTA_final



Numbers of residues are shown in brackets. Those in unfavourable conformations (score < -3.00) are labelled.
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