Supplementary information to:

Original article

UNVEILING THE Ro60-Ro52 COMPLEX

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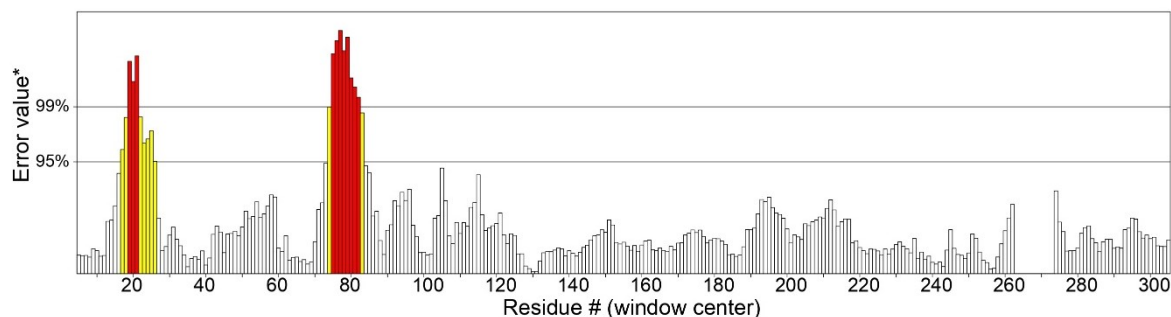   E-mail: Pilar.Gonzalez-Cabo@uv.es
    David Gimenez-Romero, Department of Physical Chemistry, Faculty of Chemistry,
    University of Valencia, C/ Doctor Moliner 50, 46100, Burjassot, Spain.
    E-mail: giroda@uv.es

Program: ERRAT2
File: Ro60Ro52_2.pdb
Chain#:B
Overall quality factor**: 93.868

*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

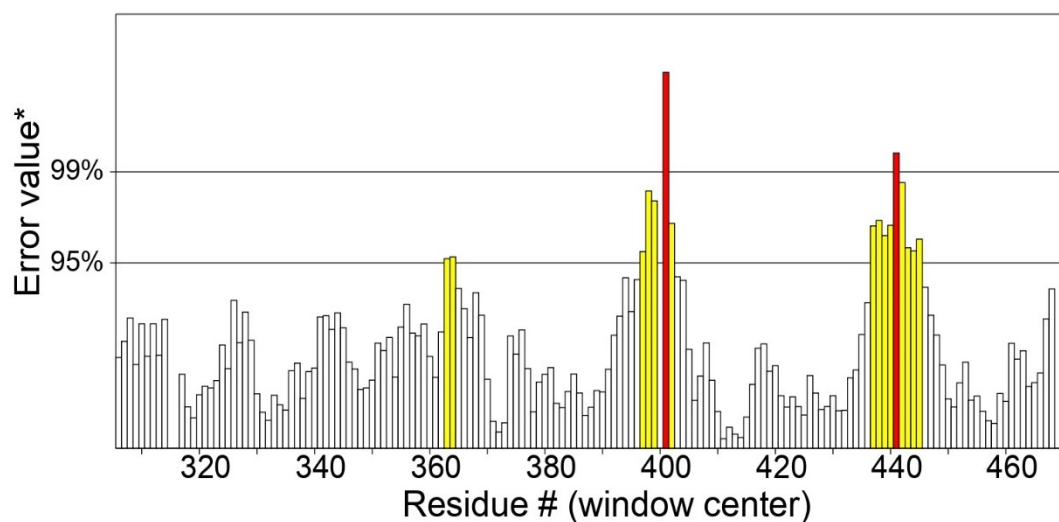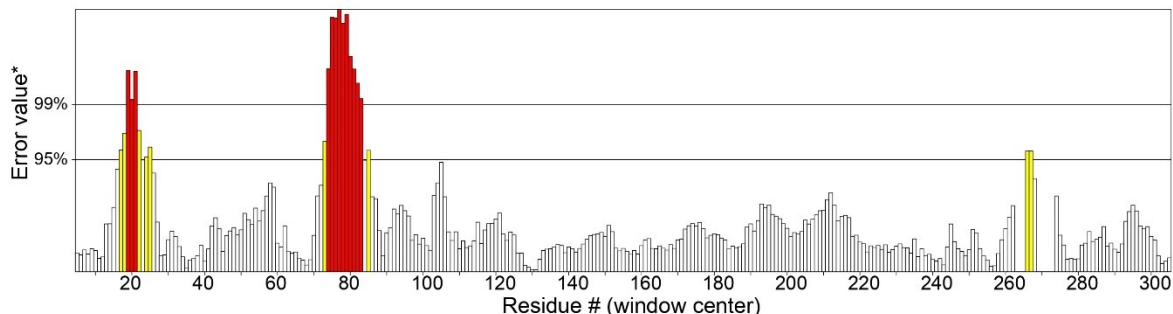**Figure S1:** ERRAT2 values for the first 300 residues of the B-chain of Ro52

Program: ERRAT2
File: Ro60Ro52_2.pdb
Chain#:B
Overall quality factor**: 93.868

*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

Figure S2: ERRAT2 values for residues 301 to the last residue of the B-chain of Ro52
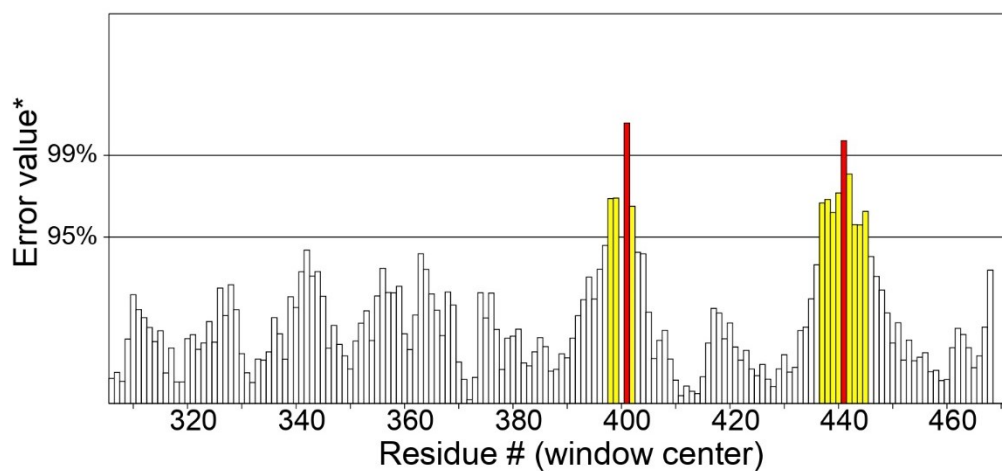
Program: ERRAT2
File: Ro60Ro52_2.pdb
Chain#:A
Overall quality factor**: 93.868

*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

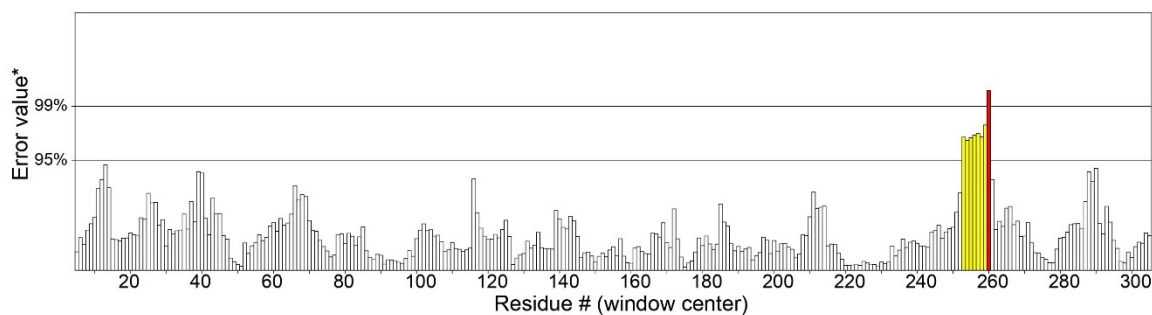**Figure S3:** ERRAT2 values for the first 300 residues of the A-chain of Ro52

Program: ERRAT2
File: Ro60Ro52_2.pdb
Chain#:A
Overall quality factor**: 93.868

*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

Figure S4: ERRAT2 values for residues 301 to the last residue of the A-chain of Ro52
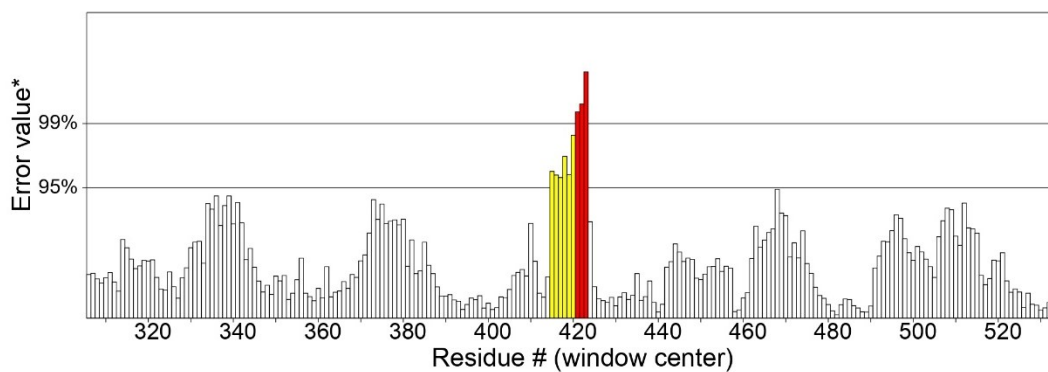
Program: ERRAT2
File: Ro60Ro52_2.pdb
Chain#:C
Overall quality factor**: 93.868

*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

Figure S5: ERRAT2 values for the first 300 residues of Ro60

Program: ERRAT2
File: Ro60Ro52_2.pdb
Chain#:C
Overall quality factor**: 93.868

*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.
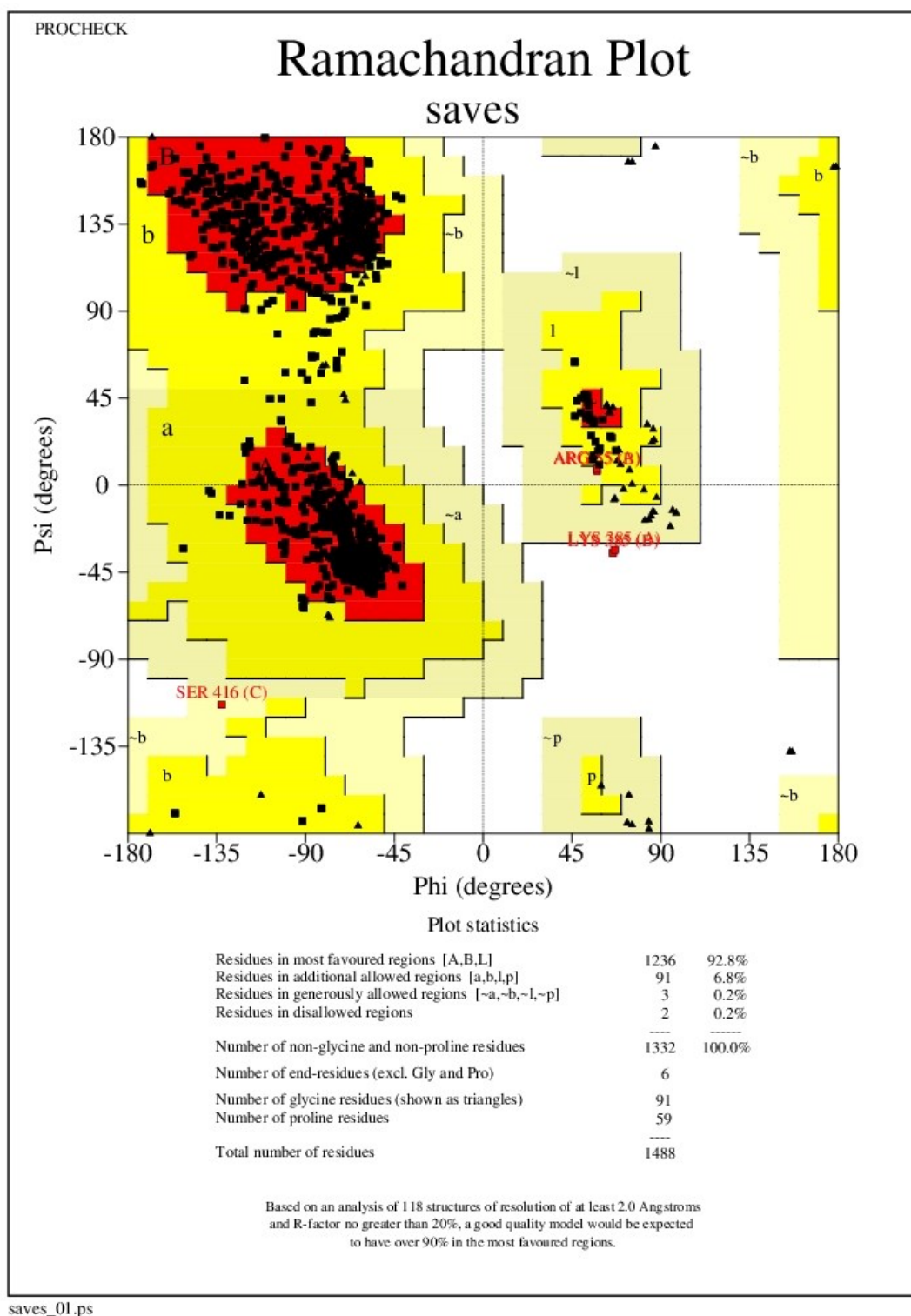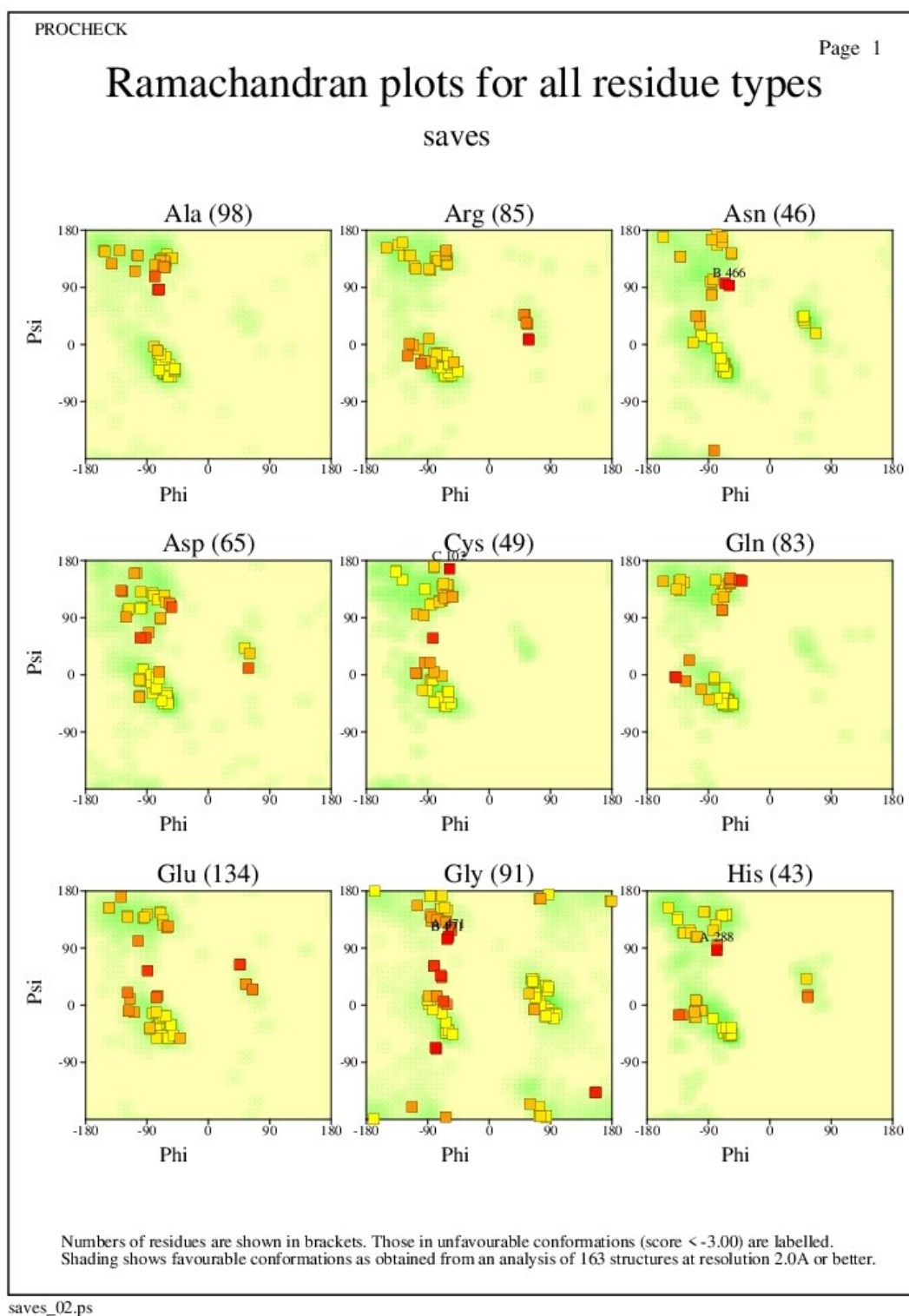
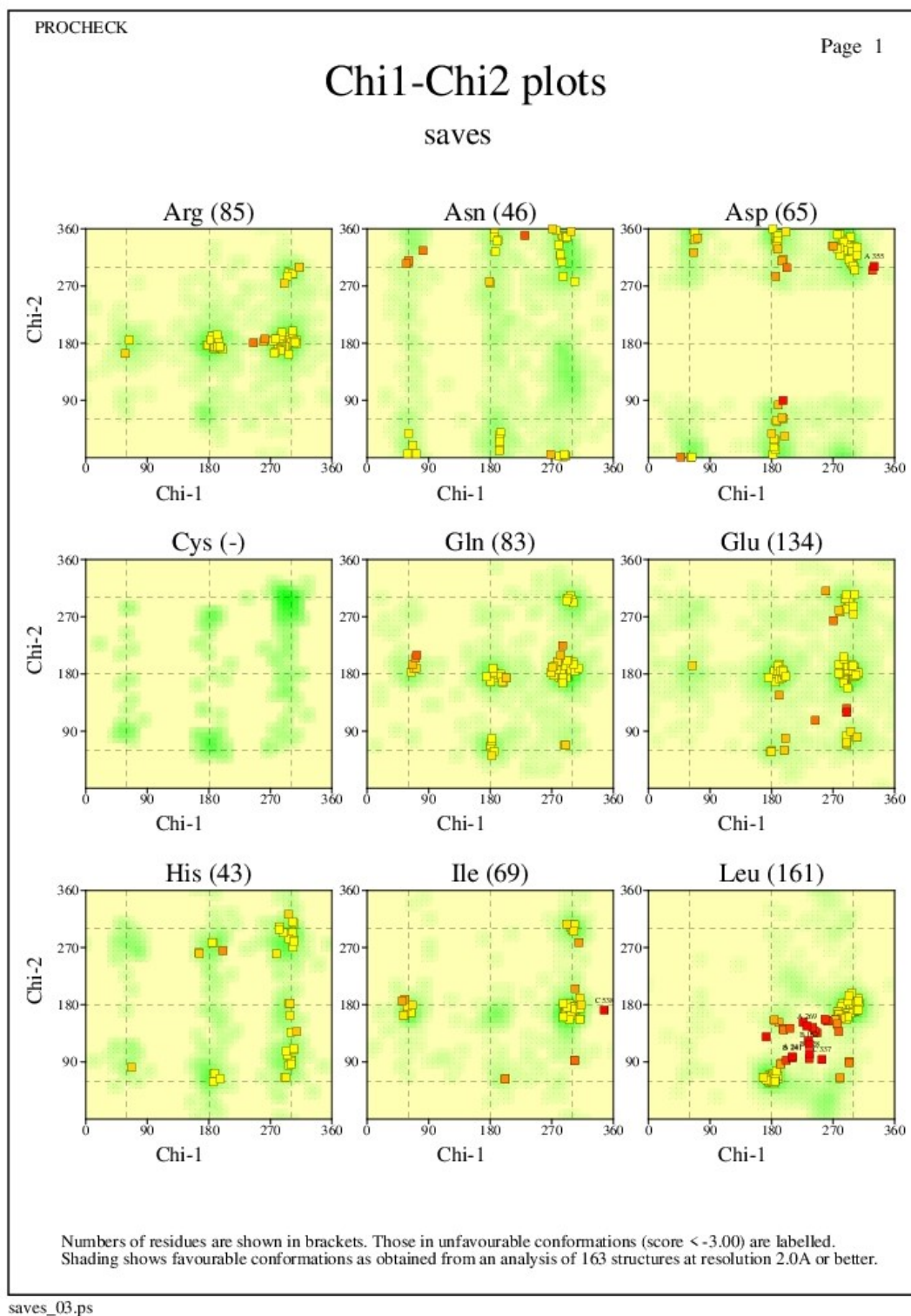**Figure S6:** ERRAT2 values for residues 301 to the last residue of Ro60

Figure S7: Ramachandran plot and statistics for the Ro60-Ro52 complex obtained with PROCHECK
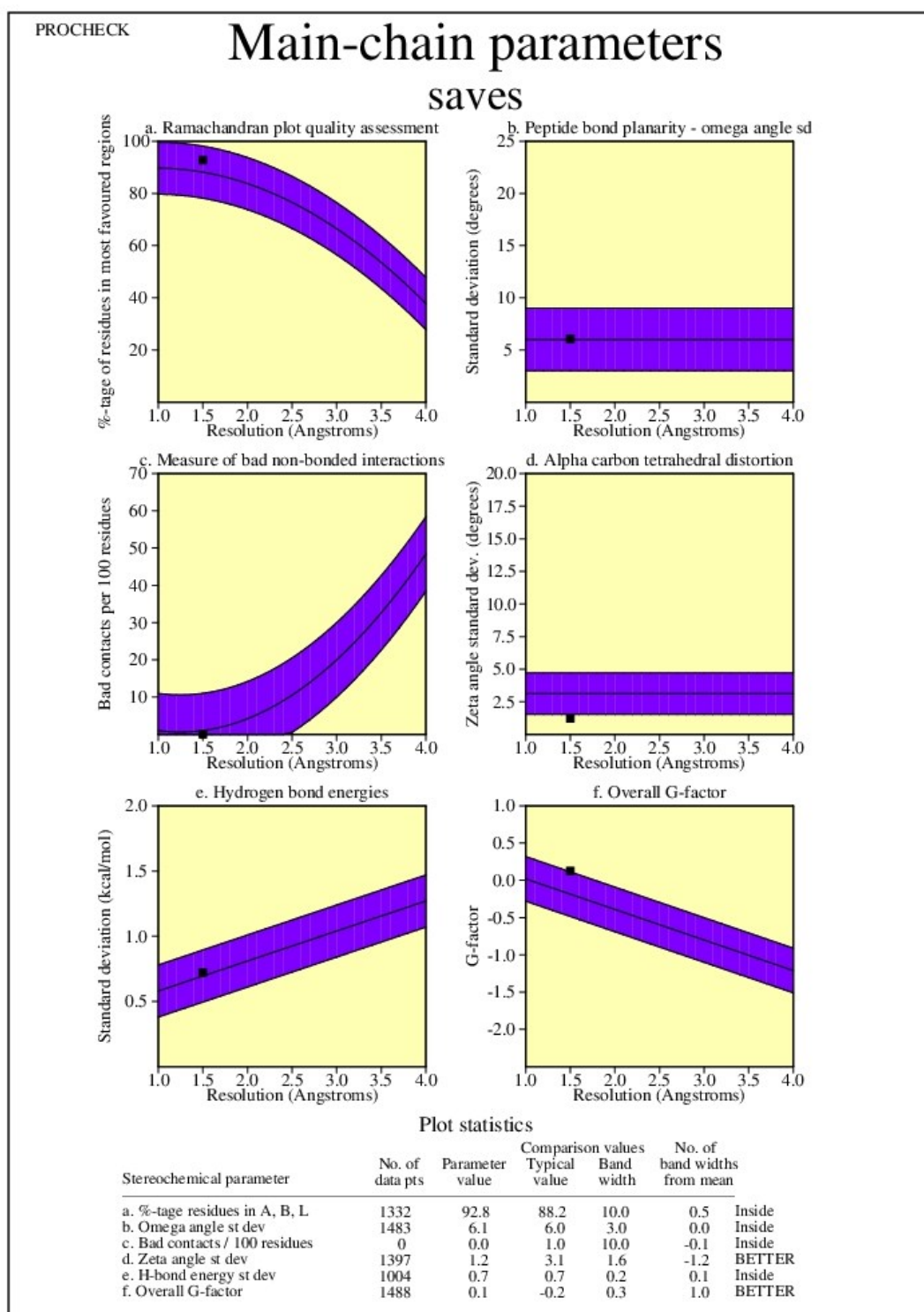
Figure S8: Ramachandran plot for the Alanine to Histidine residues of the Ro60-Ro52 complex obtained with PROCHECK
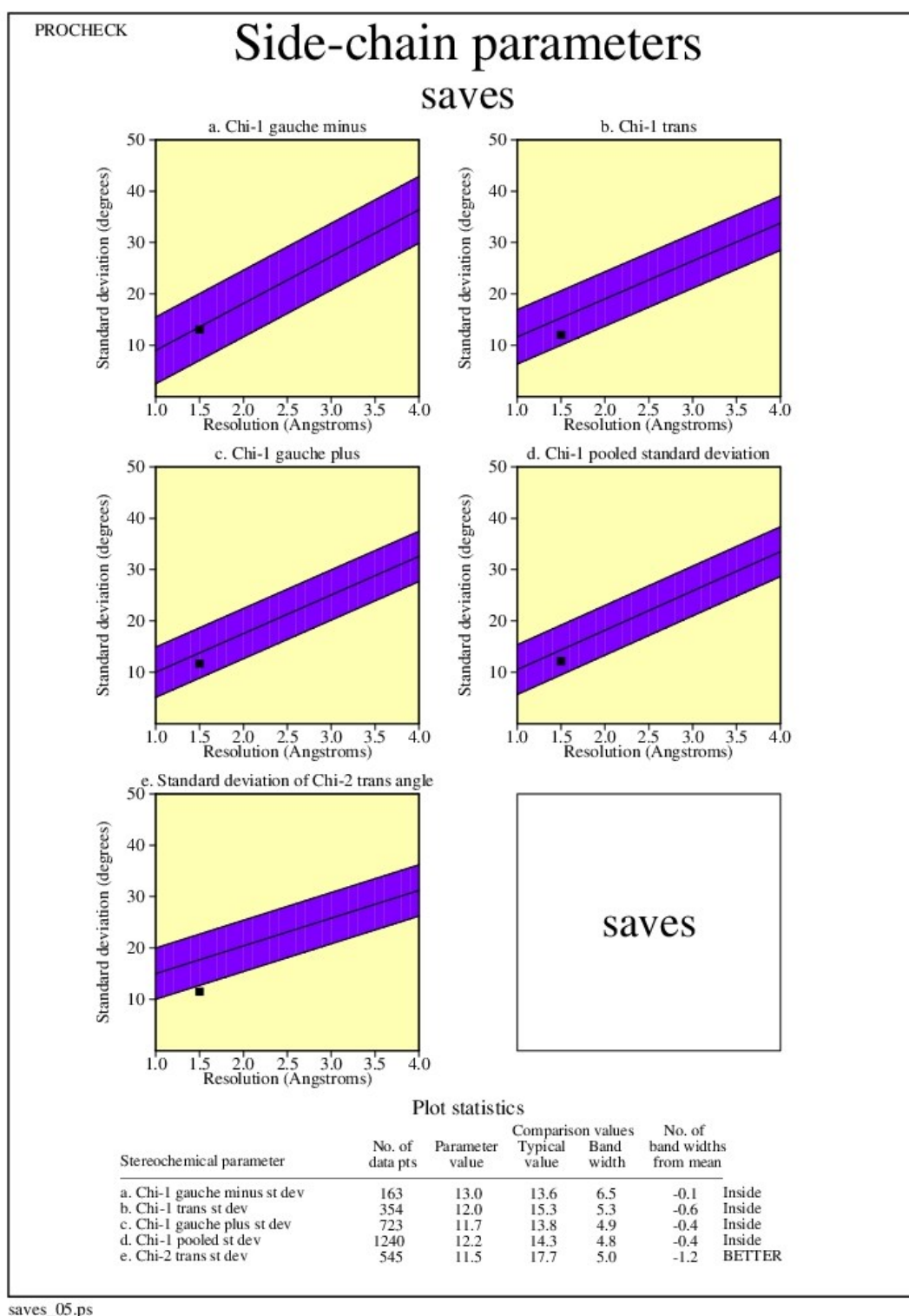
Figure S9: $X_1 - X_2$ plots of some residues of the Ro60-Ro52 complex obtained with PROCHECK

Figure S10: Parameters and statistics of the main chain of the Ro60-Ro52 complex obtained with PROCHECK

Side-chain parameters
saves

PROCHECK

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	163	13.0	13.6	6.5	-0.1	Inside
b. Chi-1 trans st dev	354	12.0	15.3	5.3	-0.6	Inside
c. Chi-1 gauche plus st dev	723	11.7	13.8	4.9	-0.4	Inside
d. Chi-1 pooled st dev	1240	12.2	14.3	4.8	-0.4	Inside
e. Chi-2 trans st dev	545	11.5	17.7	5.0	-1.2	BETTER

saves_05.ps

Figure S11: Parameters and statistics of the side chain of the Ro60-Ro52 complex obtained with PROCHECK
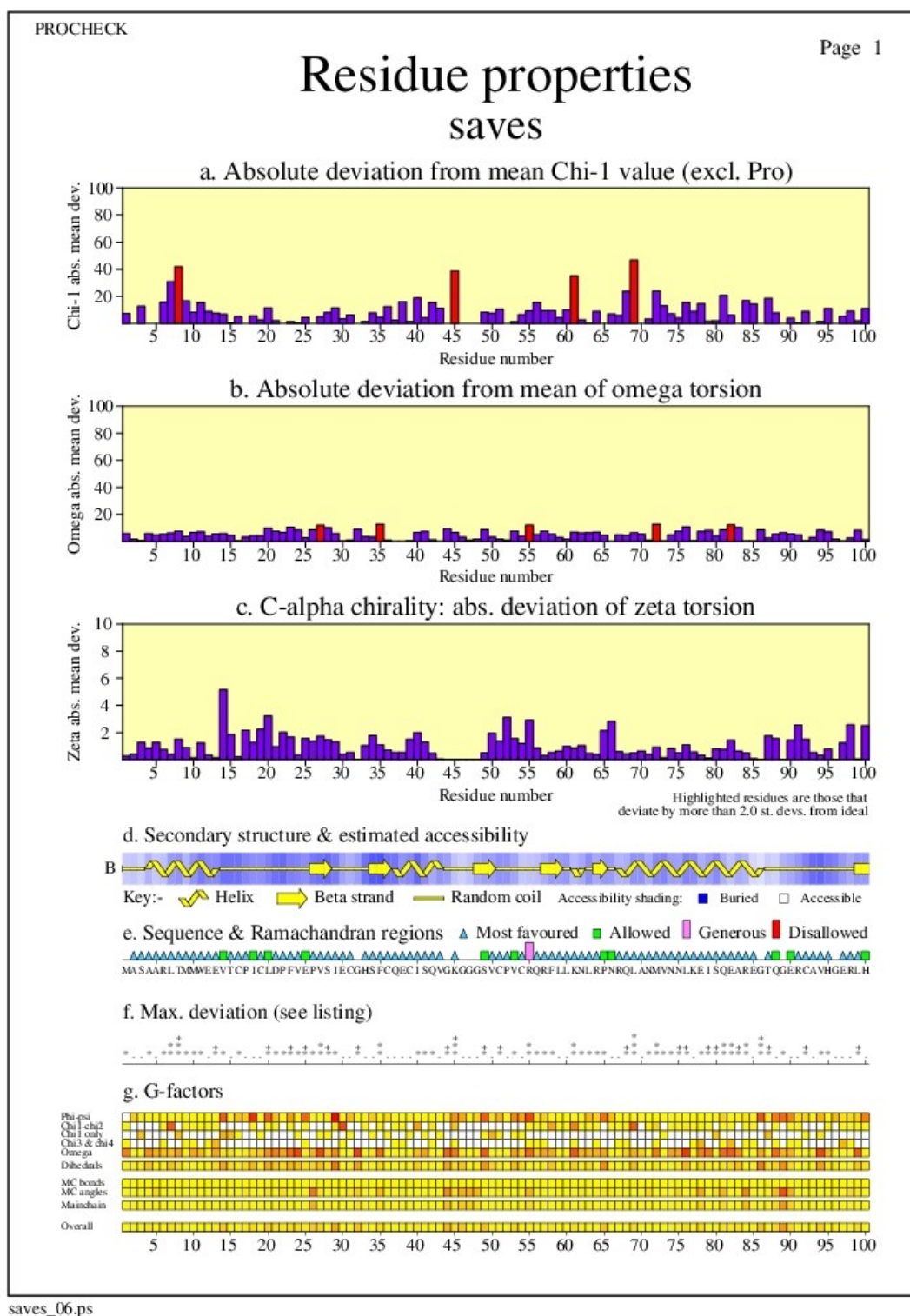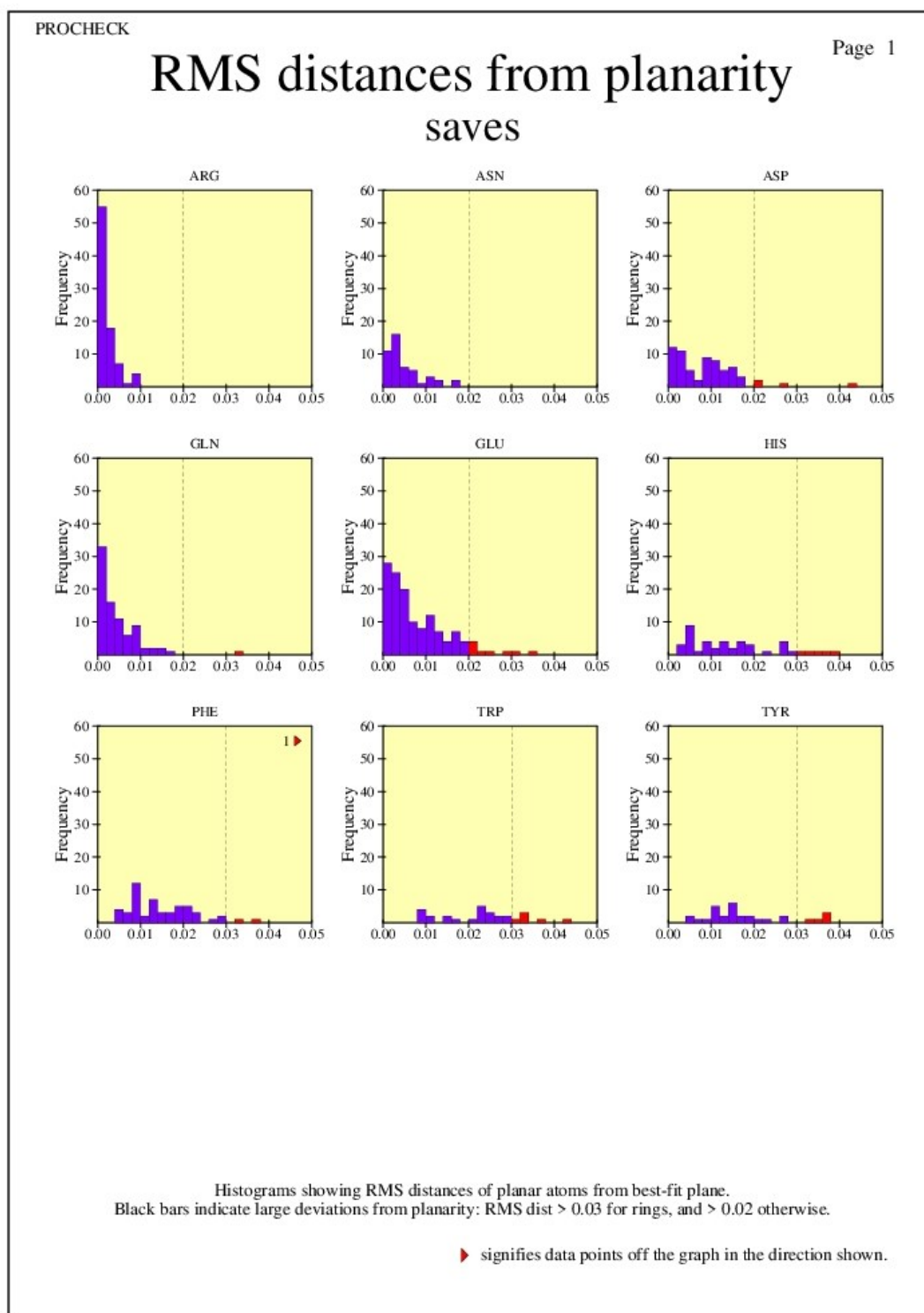
Figure S12: Properties of the residues of the Ro60-Ro52 complex obtained with PROCHECK
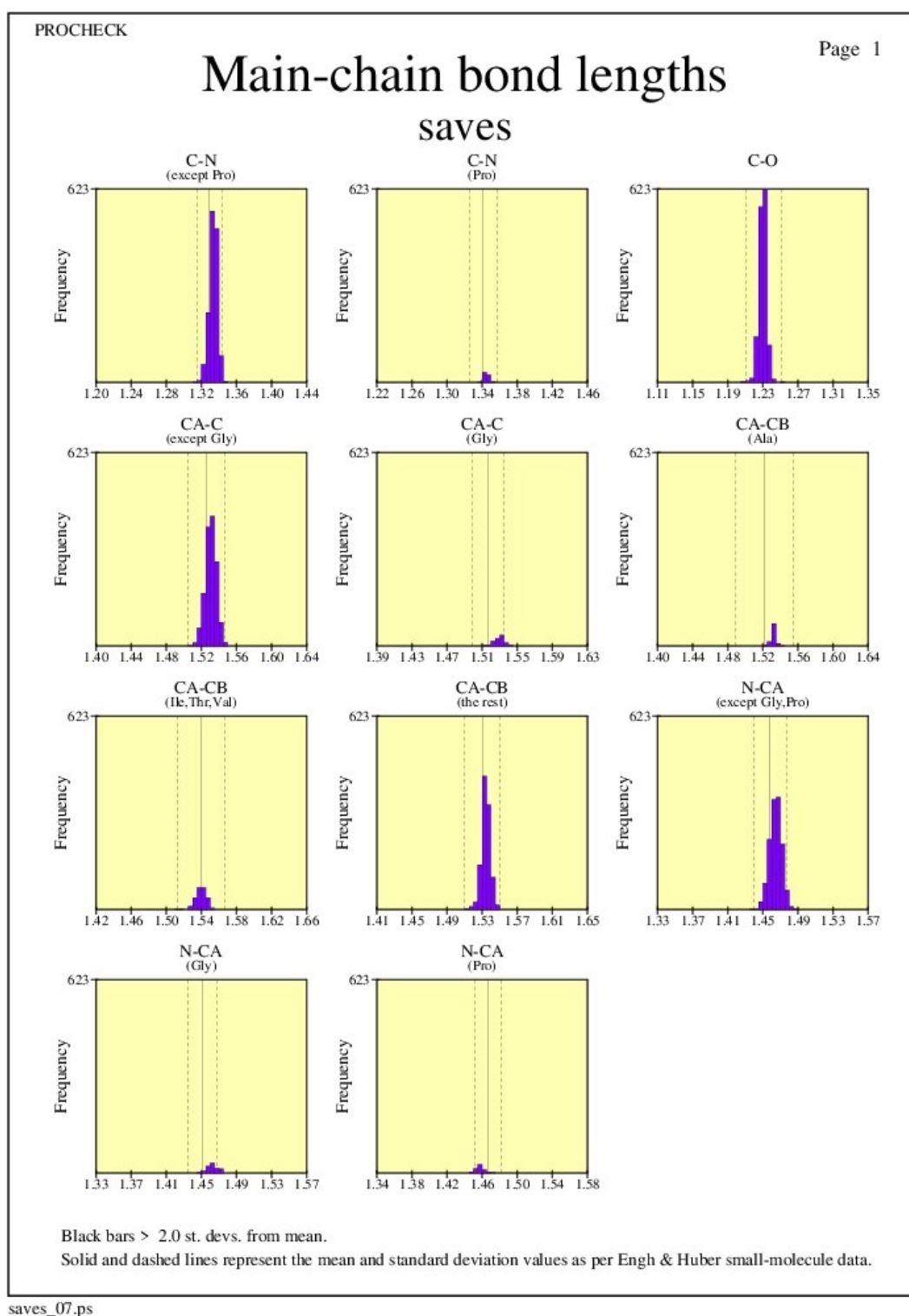
Figure S13: Main chain bond lengths of the Ro60-Ro52 complex obtained with PROCHECK
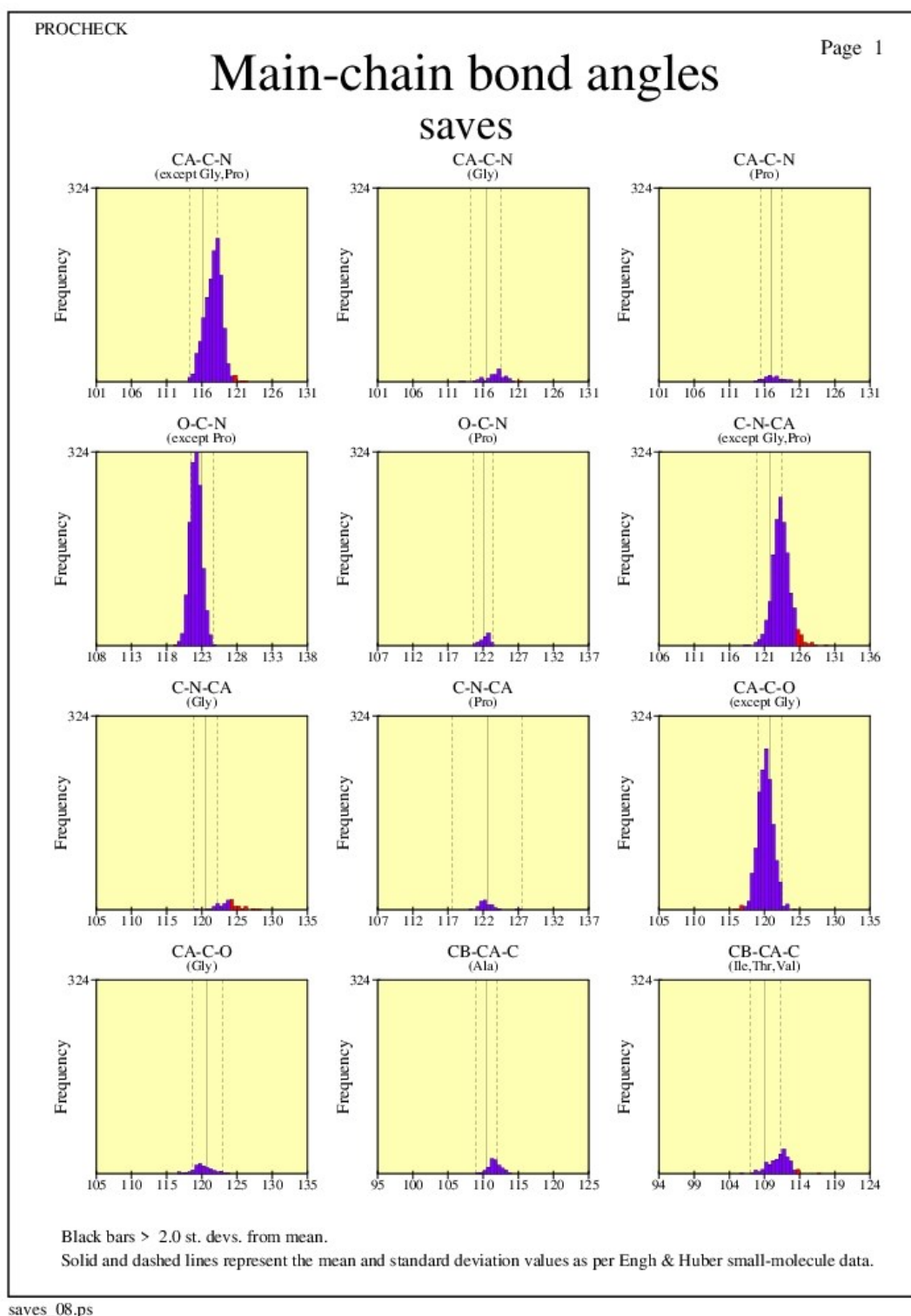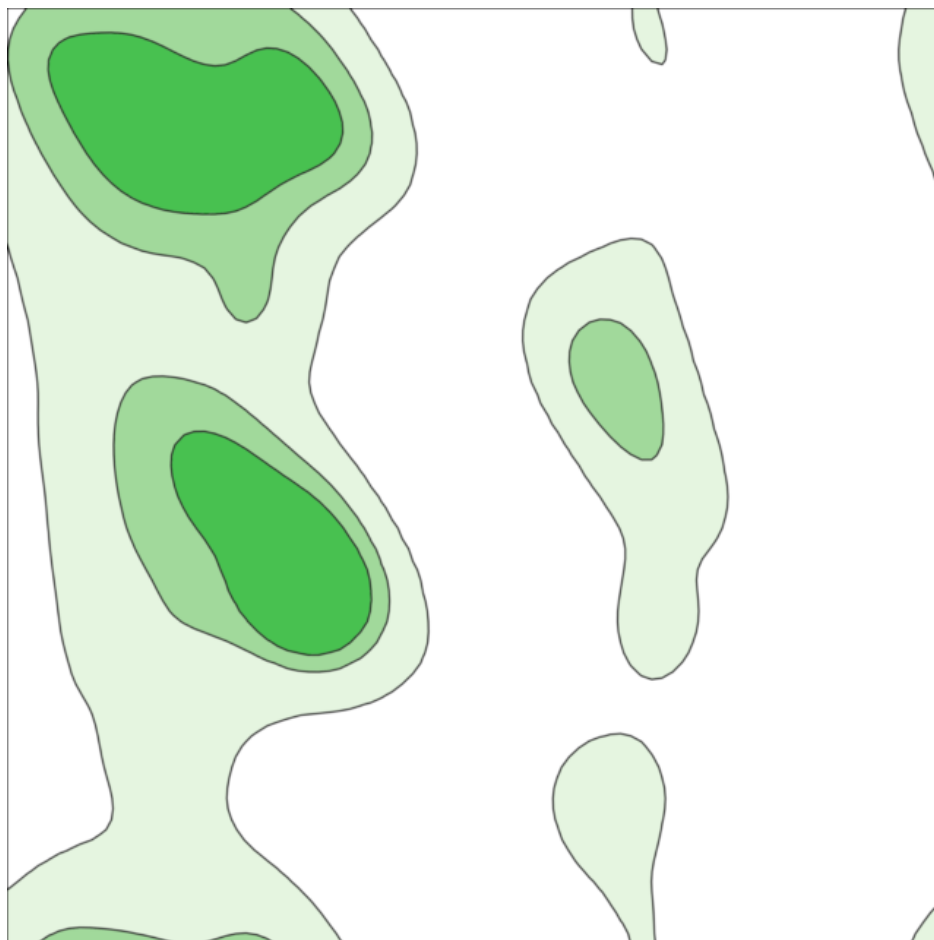
Figure S14: Bond angles of the main chain of the Ro60-Ro52 complex obtained with PROCHECK
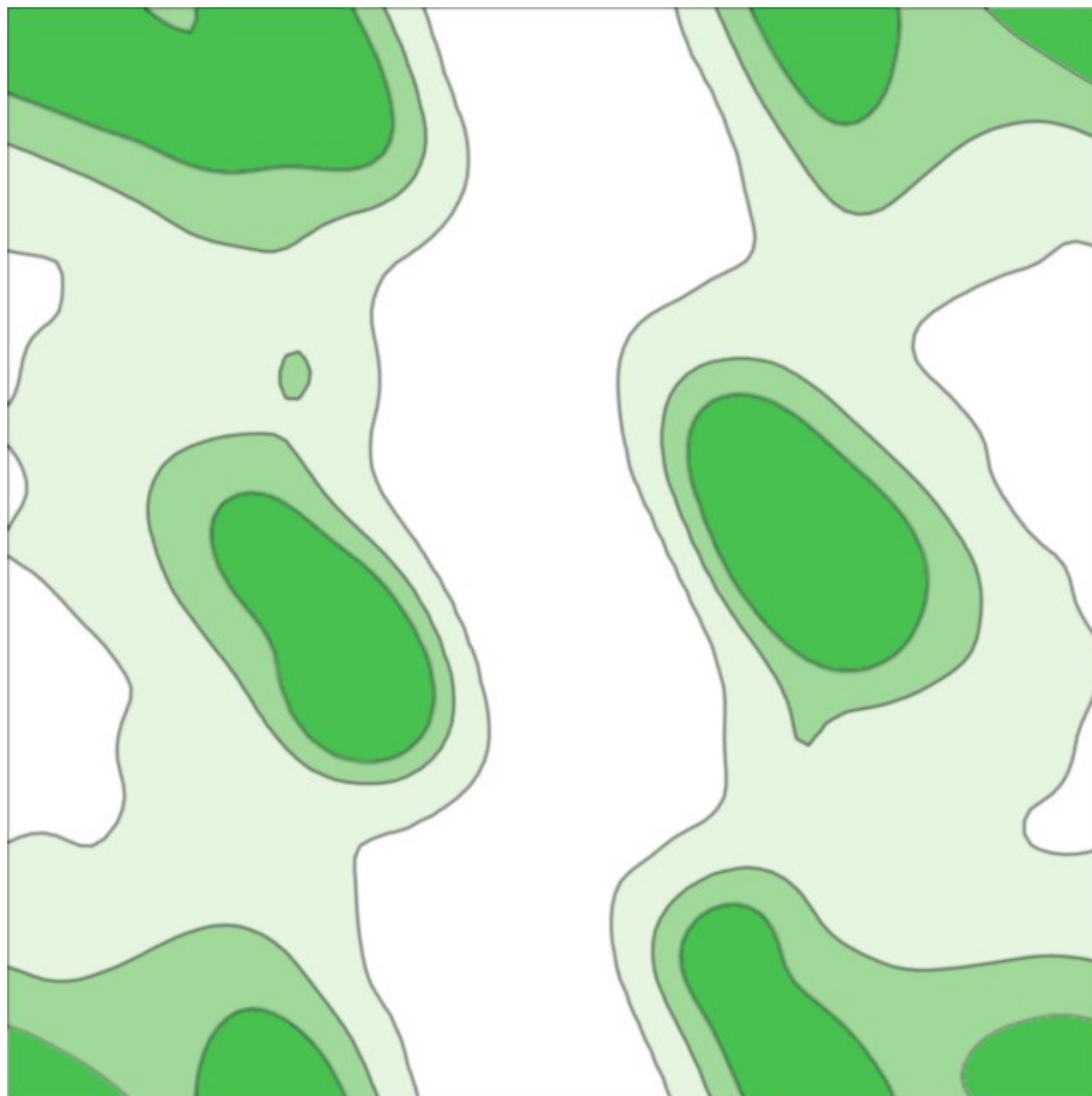
Figure S15: Planarity results of the Ro60-Ro52 complex obtained with PROCHECK
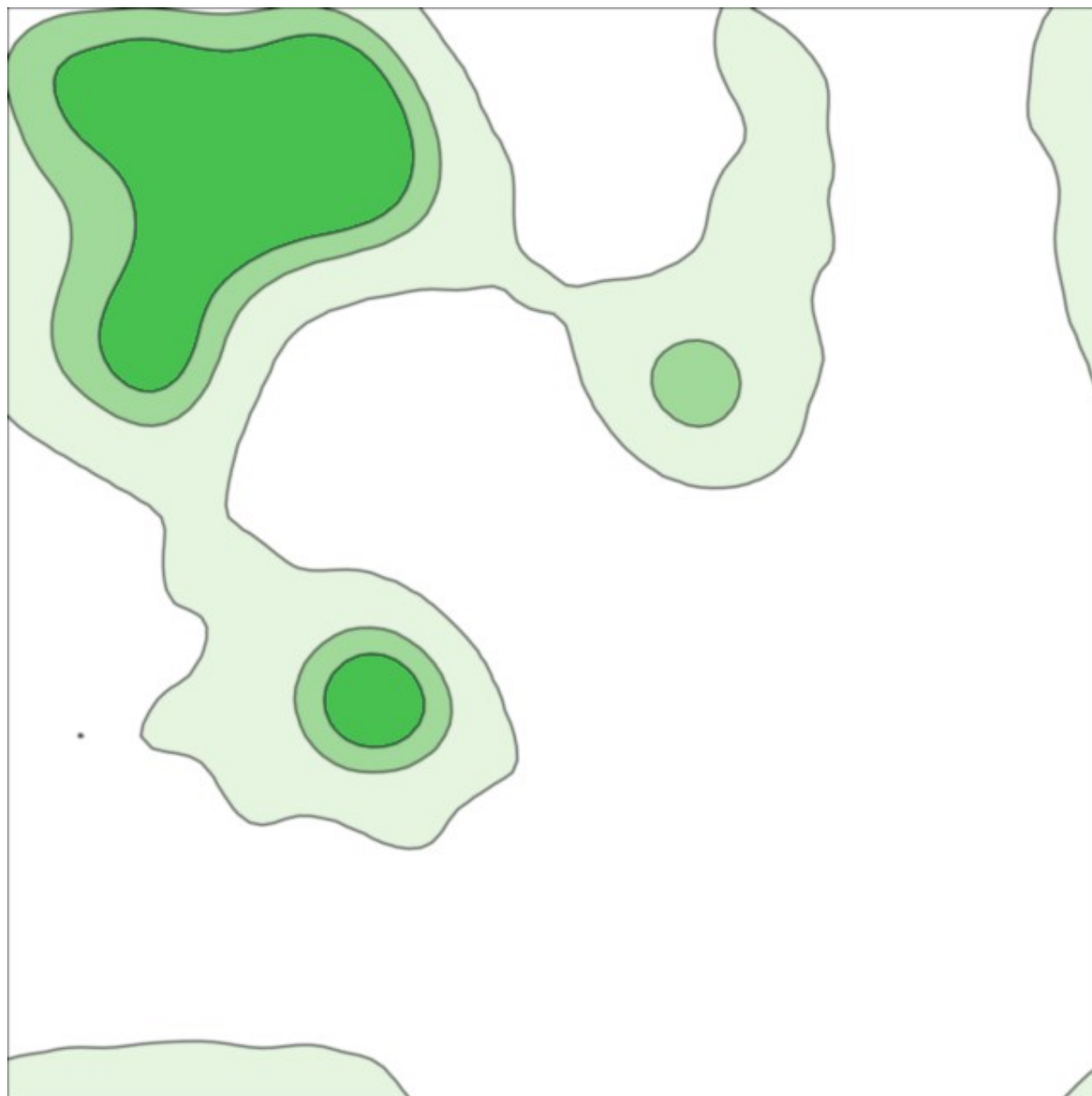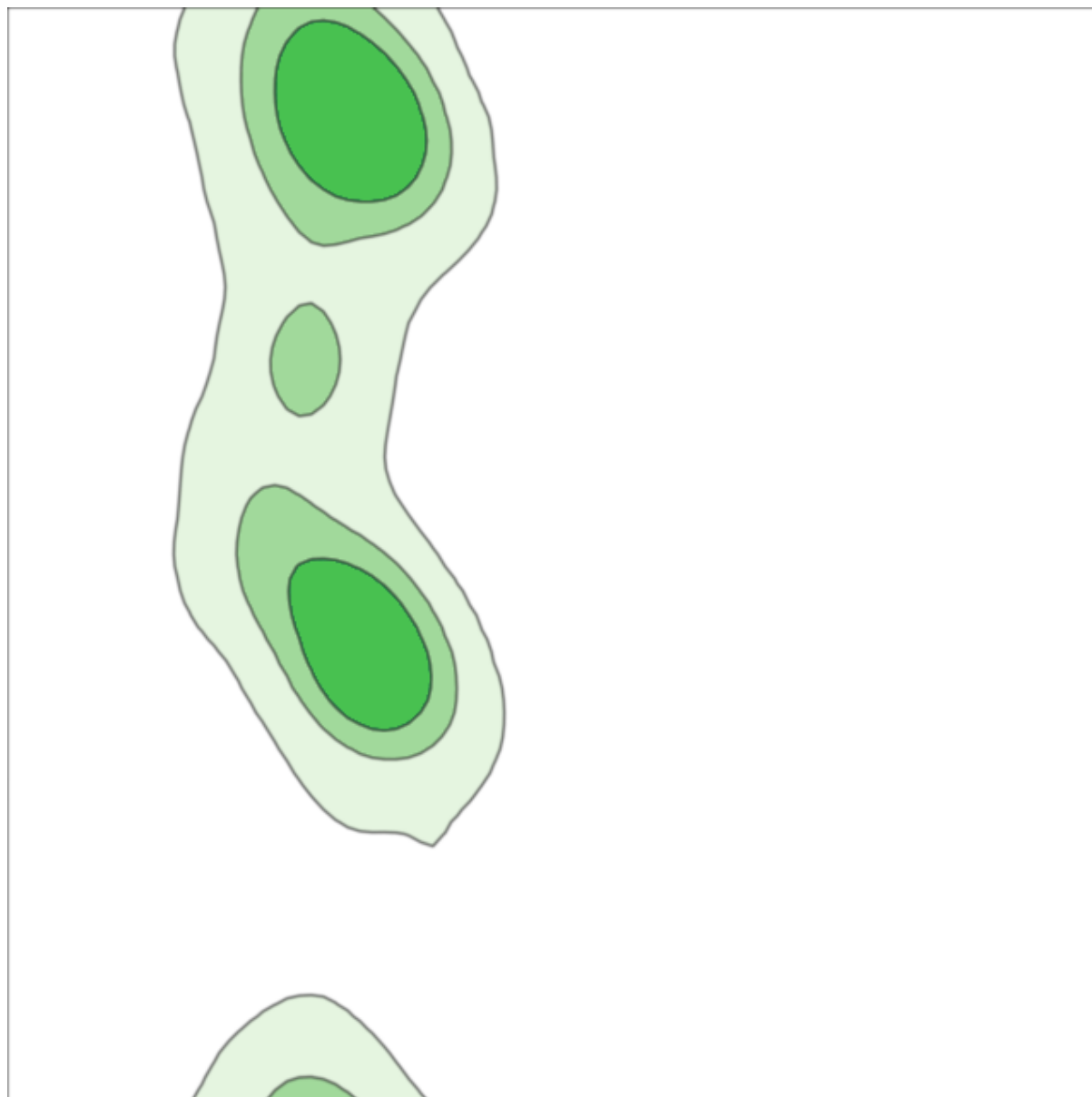
Swiss-Model

Figure S16: Ramachandran plot for the Ro60-Ro52 complex obtained with SWISS-MODEL Structure Assessment

Figure S17: Ramachandran plot for the Gly residues of the Ro60-Ro52 complex obtained with SWISS-MODEL Structure Assessment

Figure S18: Ramachandran plot for the residues apearing before Pro in the Ro60-Ro52 complex obtained with SWISS-MODEL Structure Assessment

Figure S19: Ramachandran plot for the Pro residues of the Ro60-Ro52 complex obtained with SWISS-MODEL Structure Assessment
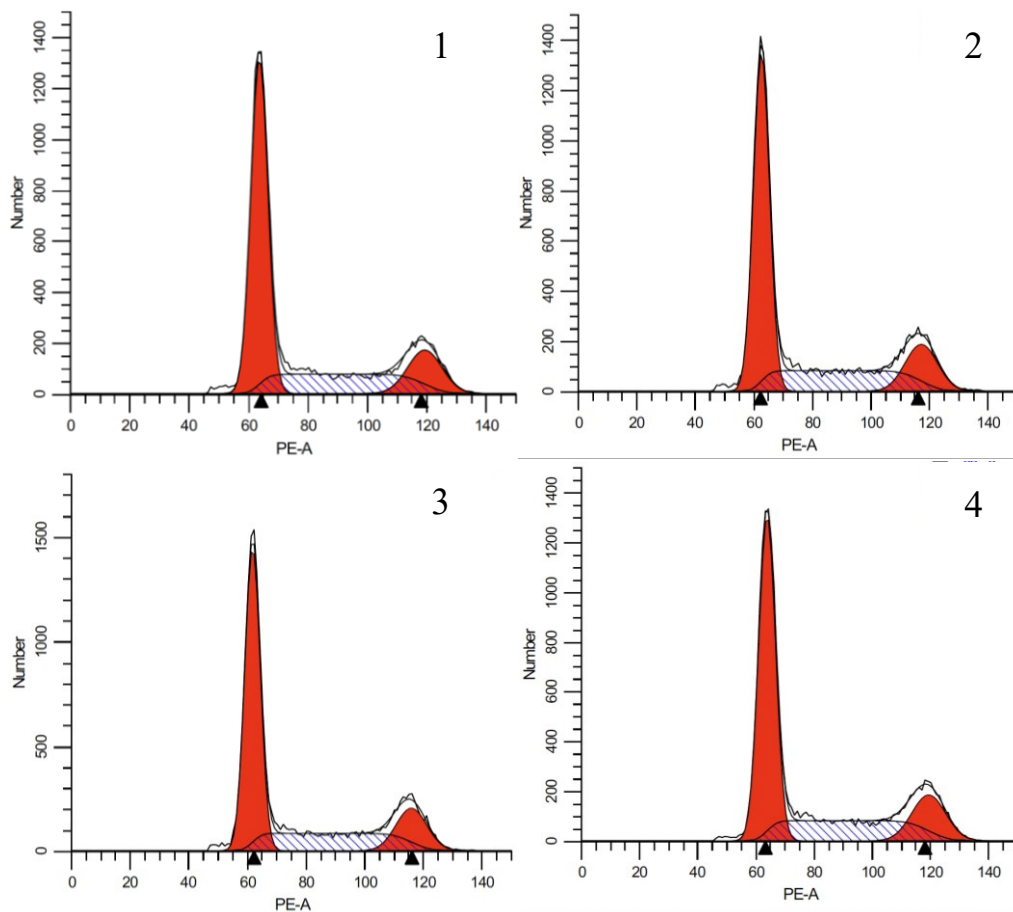
Cell Cycle	1	2	3	4	Mean	SD
G0/G1	58,84	56,95	57,20	56,94	57,48	0,91
S	25,96	27,30	26,81	26,99	26,77	0,57
G2/M	15,20	15,76	15,99	16,07	15,76	0,39

Figure S20: Analysis of the cell cycle in HeLa cells by Flow Cytometry. Each histogram represents one biological independent experiment (n=4). The table displays the results from the 4 experiments (numbered 1-4), the mean as well as the standard deviation (SD). The values refer to the percentage of cells in each of the phases of the cell cycle.