



Full wwPDB EM Validation Report ⓘ

Mar 28, 2026 – 12:11 AM UTC

PDB ID : 8SS2 / pdb_00008ss2
EMDB ID : EMD-40741
Title : Structure of AMPA receptor GluA2 complex with auxiliary subunits TARP gamma-5 and cornichon-2 bound to competitive antagonist ZK and channel blocker spermidine (closed state)
Authors : Gangwar, S.P.; Yen, L.Y.; Yelshanskaya, M.V.; Sobolevsky, A.I.
Deposited on : 2023-05-08
Resolution : 3.58 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

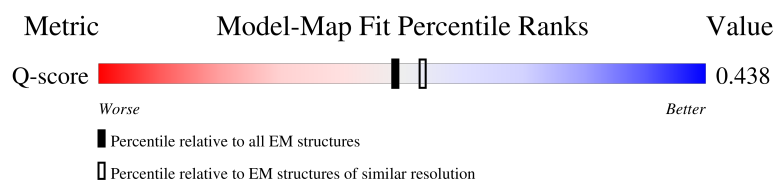
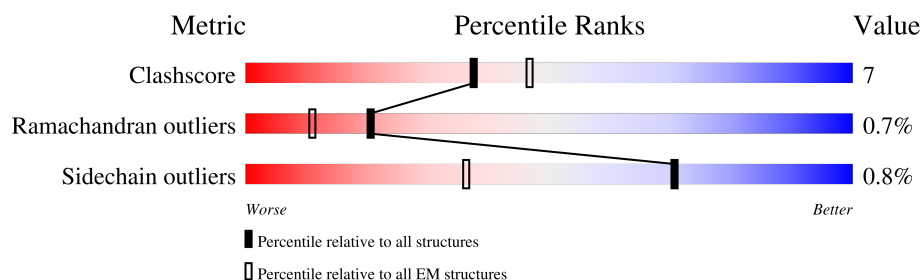
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

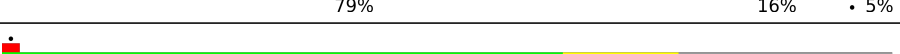
The reported resolution of this entry is 3.58 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	12629 (3.08 - 4.08)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1026	
1	B	1026	
1	C	1026	
1	D	1026	

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Mol	Chain	Length	Quality of chain
2	E	160	
2	F	160	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	CLR	A	1105	X	-	-	-
5	CLR	C	1105	X	-	-	-
6	AJP	A	1106	X	-	X	-
6	AJP	C	1106	X	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 31146 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Glutamate receptor 2, Voltage-dependent calcium channel gamma-5 subunit chimera.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	978	Total	C	N	O	S	0	0
			7714	4982	1270	1422	40		
1	B	783	Total	C	N	O	S	0	0
			6177	3969	1022	1156	30		
1	C	978	Total	C	N	O	S	0	0
			7714	4982	1270	1422	40		
1	D	783	Total	C	N	O	S	0	0
			6177	3969	1022	1156	30		

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	GLU	ASN	conflict	UNP P19491
A	382	LEU	VAL	conflict	UNP P19491
A	?	-	LEU	deletion	UNP P19491
A	?	-	THR	deletion	UNP P19491
A	?	-	GLU	deletion	UNP P19491
A	?	-	LEU	deletion	UNP P19491
A	?	-	PRO	deletion	UNP P19491
A	?	-	SER	deletion	UNP P19491
A	384	GLU	GLY	conflict	UNP P19491
A	385	ASP	ASN	conflict	UNP P19491
A	392	GLN	ASN	conflict	UNP P19491
A	754	SER	ASN	conflict	UNP P19491
A	758	VAL	LEU	conflict	UNP P19491
A	827	GLY	-	linker	UNP P19491
A	828	THR	-	linker	UNP P19491
A	829	GLY	-	linker	UNP P19491
A	830	SER	-	linker	UNP P19491
A	831	ALA	-	linker	UNP P19491
B	241	GLU	ASN	conflict	UNP P19491
B	382	LEU	VAL	conflict	UNP P19491
B	?	-	LEU	deletion	UNP P19491

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	THR	deletion	UNP P19491
B	?	-	GLU	deletion	UNP P19491
B	?	-	LEU	deletion	UNP P19491
B	?	-	PRO	deletion	UNP P19491
B	?	-	SER	deletion	UNP P19491
B	384	GLU	GLY	conflict	UNP P19491
B	385	ASP	ASN	conflict	UNP P19491
B	392	GLN	ASN	conflict	UNP P19491
B	754	SER	ASN	conflict	UNP P19491
B	758	VAL	LEU	conflict	UNP P19491
B	827	GLY	-	linker	UNP P19491
B	828	THR	-	linker	UNP P19491
B	829	GLY	-	linker	UNP P19491
B	830	SER	-	linker	UNP P19491
B	831	ALA	-	linker	UNP P19491
C	241	GLU	ASN	conflict	UNP P19491
C	382	LEU	VAL	conflict	UNP P19491
C	?	-	LEU	deletion	UNP P19491
C	?	-	THR	deletion	UNP P19491
C	?	-	GLU	deletion	UNP P19491
C	?	-	LEU	deletion	UNP P19491
C	?	-	PRO	deletion	UNP P19491
C	?	-	SER	deletion	UNP P19491
C	384	GLU	GLY	conflict	UNP P19491
C	385	ASP	ASN	conflict	UNP P19491
C	392	GLN	ASN	conflict	UNP P19491
C	754	SER	ASN	conflict	UNP P19491
C	758	VAL	LEU	conflict	UNP P19491
C	827	GLY	-	linker	UNP P19491
C	828	THR	-	linker	UNP P19491
C	829	GLY	-	linker	UNP P19491
C	830	SER	-	linker	UNP P19491
C	831	ALA	-	linker	UNP P19491
D	241	GLU	ASN	conflict	UNP P19491
D	382	LEU	VAL	conflict	UNP P19491
D	?	-	LEU	deletion	UNP P19491
D	?	-	THR	deletion	UNP P19491
D	?	-	GLU	deletion	UNP P19491
D	?	-	LEU	deletion	UNP P19491
D	?	-	PRO	deletion	UNP P19491
D	?	-	SER	deletion	UNP P19491
D	384	GLU	GLY	conflict	UNP P19491

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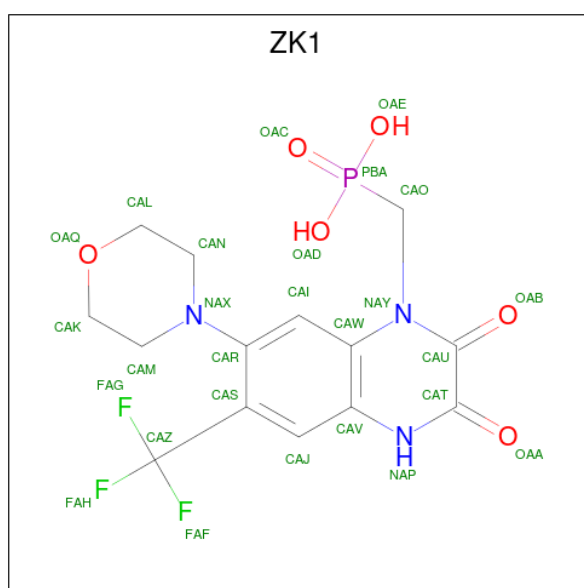
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Chain	Residue	Modelled	Actual	Comment	Reference
D	385	ASP	ASN	conflict	UNP P19491
D	392	GLN	ASN	conflict	UNP P19491
D	754	SER	ASN	conflict	UNP P19491
D	758	VAL	LEU	conflict	UNP P19491
D	827	GLY	-	linker	UNP P19491
D	828	THR	-	linker	UNP P19491
D	829	GLY	-	linker	UNP P19491
D	830	SER	-	linker	UNP P19491
D	831	ALA	-	linker	UNP P19491

- Molecule 2 is a protein called Protein cornichon homolog 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	140	Total	C	N	O	S	0	0
			1166	787	175	191	13		
2	F	140	Total	C	N	O	S	0	0
			1166	787	175	191	13		

- Molecule 3 is {[7-morpholin-4-yl-2,3-dioxo-6-(trifluoromethyl)-3,4-dihydroquinoxalin-1(2H)-yl]methyl}phosphonic acid (CCD ID: ZK1) (formula: C₁₄H₁₅F₃N₃O₆P) (labeled as "Ligand of Interest" by depositor).



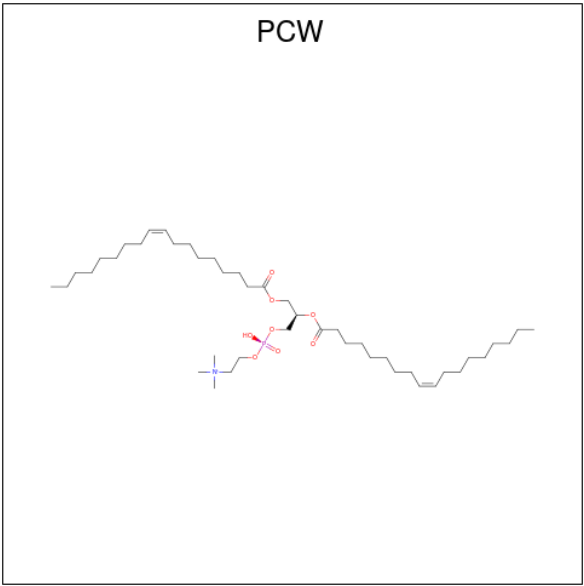
Mol	Chain	Residues	Atoms						AltConf
3	A	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	
3	B	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	

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Mol	Chain	Residues	Atoms						AltConf
3	C	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	
3	D	1	Total	C	F	N	O	P	0
			27	14	3	3	6	1	

- Molecule 4 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PCW) (formula: C₄₄H₈₅NO₈P).



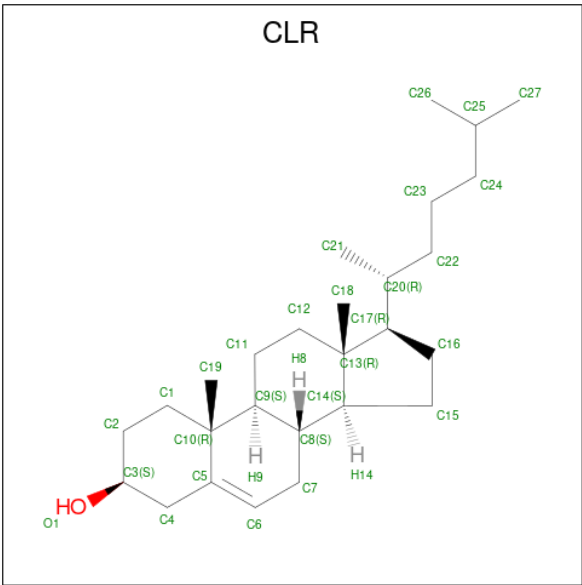
Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total 40	C 30	N 1	O 8	P 1	0
4	A	1	Total 43	C 33	N 1	O 8	P 1	0
4	A	1	Total C 11 11					0
4	A	1	Total 51	C 41	N 1	O 8	P 1	0
4	A	1	Total C 11 11					0
4	A	1	Total 39	C 29	N 1	O 8	P 1	0
4	A	1	Total C 11 11					0
4	B	1	Total 43	C 33	N 1	O 8	P 1	0
4	B	1	Total 32	C 22	N 1	O 8	P 1	0

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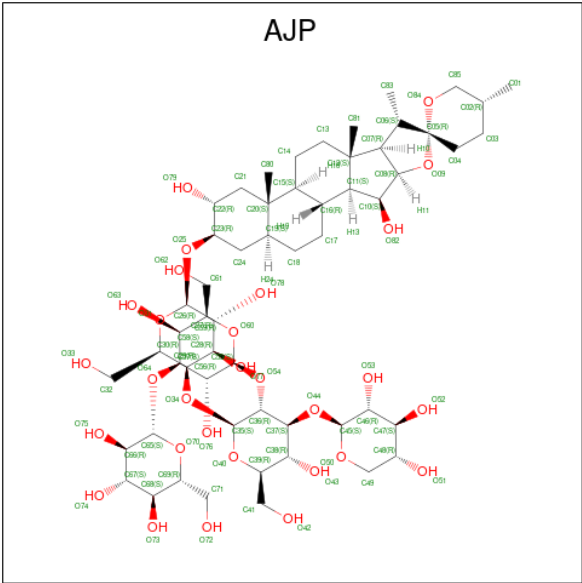
Mol	Chain	Residues	Atoms					AltConf
4	B	1	Total	C	N	O	P	0
			41	31	1	8	1	
4	B	1	Total	C				0
			11	11				
4	C	1	Total	C	N	O	P	0
			40	30	1	8	1	
4	C	1	Total	C	N	O	P	0
			43	33	1	8	1	
4	C	1	Total	C				0
			11	11				
4	C	1	Total	C	N	O	P	0
			51	41	1	8	1	
4	C	1	Total	C				0
			11	11				
4	C	1	Total	C	N	O	P	0
			39	29	1	8	1	
4	C	1	Total	C				0
			11	11				
4	D	1	Total	C	N	O	P	0
			43	33	1	8	1	
4	D	1	Total	C	N	O	P	0
			32	22	1	8	1	
4	D	1	Total	C	N	O	P	0
			41	31	1	8	1	
4	D	1	Total	C				0
			11	11				
4	E	1	Total	C				0
			11	11				
4	E	1	Total	C	N	O	P	0
			43	33	1	8	1	
4	F	1	Total	C				0
			11	11				
4	F	1	Total	C	N	O	P	0
			43	33	1	8	1	

- Molecule 5 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



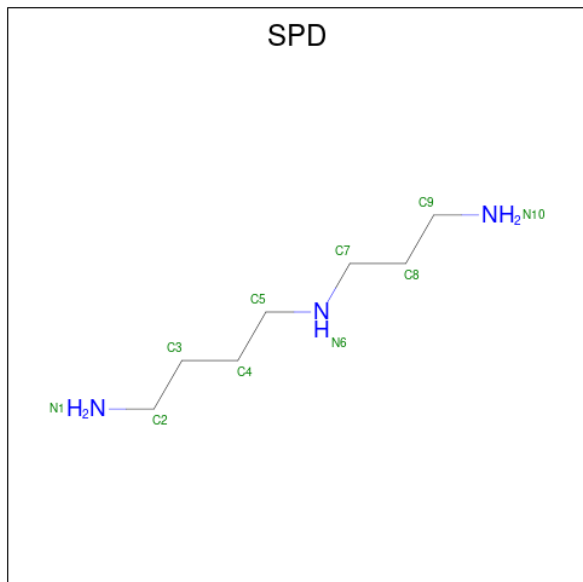
Mol	Chain	Residues	Atoms			AltConf
5	A	1	Total	C	O	0
			28	27	1	
5	C	1	Total	C	O	0
			28	27	1	

- Molecule 6 is Digitonin (CCD ID: AJP) (formula: C₅₆H₉₂O₂₉).



Mol	Chain	Residues	Atoms			AltConf
6	A	1	Total	C	O	0
			42	33	9	
6	C	1	Total	C	O	0
			42	33	9	

- Molecule 7 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$) (labeled as "Ligand of Interest" by depositor).

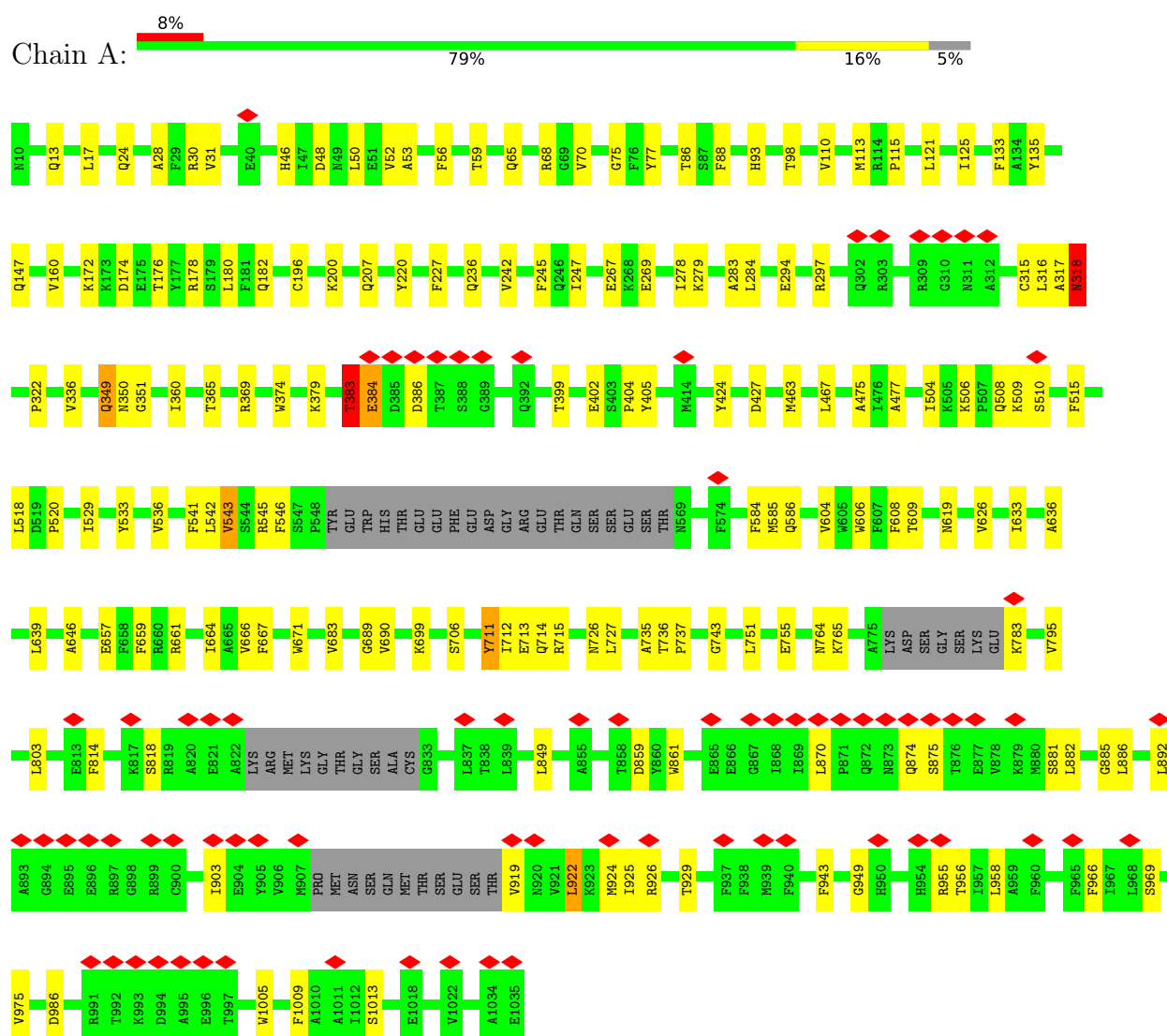


Mol	Chain	Residues	Atoms			AltConf
7	A	1	Total	C	N	0
			10	7	3	

3 Residue-property plots

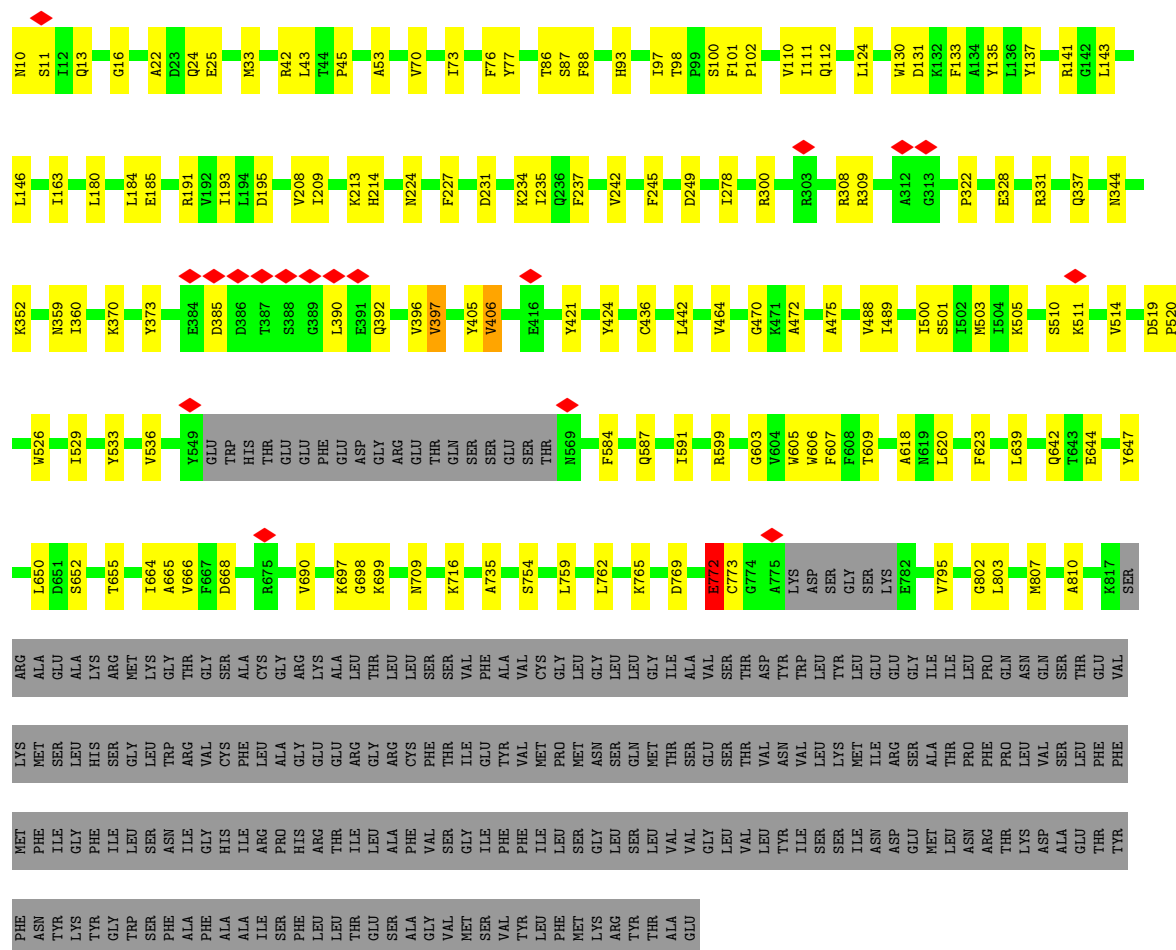
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Glutamate receptor 2, Voltage-dependent calcium channel gamma-5 subunit chimera

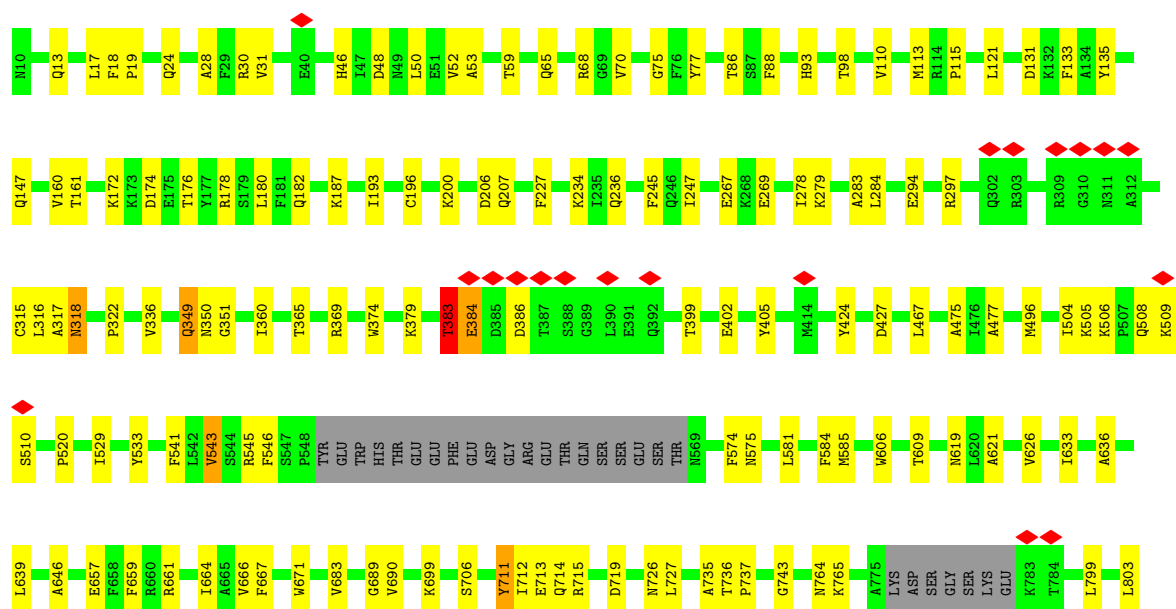
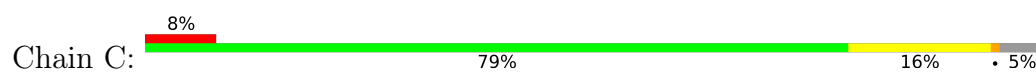


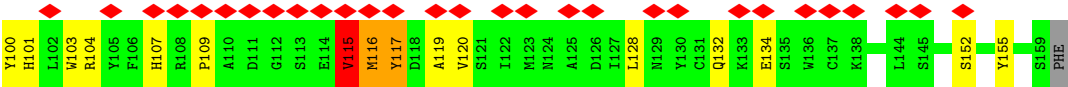
- Molecule 1: Glutamate receptor 2, Voltage-dependent calcium channel gamma-5 subunit chimera



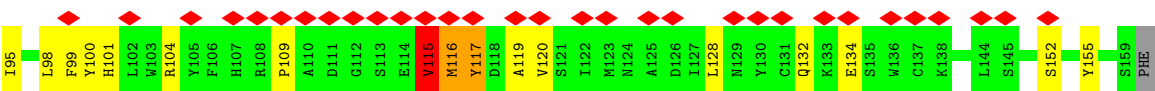
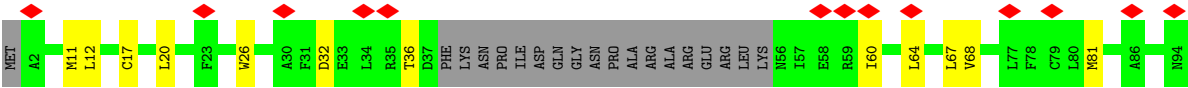


- Molecule 1: Glutamate receptor 2, Voltage-dependent calcium channel gamma-5 subunit chimera





• Molecule 2: Protein cornichon homolog 2



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	55275	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	58	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.107	Depositor
Minimum map value	-0.718	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.13	Depositor
Map size ($\text{\AA}$)	345.28, 345.28, 345.28	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.83, 0.83, 0.83	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SPD, PCW, AJP, CLR, ZK1

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.53	1/7880 (0.0%)	0.92	12/10648 (0.1%)
1	B	0.54	1/6308 (0.0%)	0.90	5/8523 (0.1%)
1	C	0.54	1/7880 (0.0%)	0.92	12/10648 (0.1%)
1	D	0.54	1/6308 (0.0%)	0.90	5/8523 (0.1%)
2	E	0.32	0/1203	0.81	0/1636
2	F	0.32	0/1203	0.82	0/1636
All	All	0.52	4/30782 (0.0%)	0.90	34/41614 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
1	B	0	7
1	C	0	7
1	D	0	7
2	E	0	4
2	F	0	4
All	All	0	36

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	402	GLU	C-N	-5.59	1.22	1.33
1	A	402	GLU	C-N	-5.56	1.22	1.33
1	D	237	PHE	CA-C	-5.53	1.44	1.52
1	B	237	PHE	CA-C	-5.47	1.44	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	317	ALA	CA-C-N	8.48	132.81	120.51
1	A	317	ALA	C-N-CA	8.48	132.81	120.51
1	C	317	ALA	CA-C-N	8.44	132.75	120.51
1	C	317	ALA	C-N-CA	8.44	132.75	120.51
1	A	53	ALA	N-CA-C	-6.39	104.71	114.16
1	C	53	ALA	N-CA-C	-6.38	104.72	114.16
1	C	666	VAL	N-CA-C	-6.26	104.18	111.00
1	A	666	VAL	N-CA-C	-6.25	104.19	111.00
1	D	514	VAL	CA-C-N	6.04	129.47	120.17
1	D	514	VAL	C-N-CA	6.04	129.47	120.17
1	B	514	VAL	CA-C-N	6.02	129.44	120.17
1	B	514	VAL	C-N-CA	6.02	129.44	120.17
1	B	699	LYS	N-CA-C	-6.01	105.50	114.64
1	D	699	LYS	N-CA-C	-6.01	105.51	114.64
1	D	666	VAL	N-CA-C	-5.97	105.25	111.58
1	B	666	VAL	N-CA-C	-5.95	105.28	111.58
1	A	247	ILE	N-CA-C	-5.78	107.87	113.53
1	C	247	ILE	N-CA-C	-5.75	107.89	113.53
1	A	924	MET	N-CA-C	-5.66	106.51	113.41
1	C	924	MET	N-CA-C	-5.63	106.54	113.41
1	B	53	ALA	N-CA-C	-5.58	104.29	113.50
1	D	53	ALA	N-CA-C	-5.56	104.32	113.50
1	C	383	THR	CA-C-N	5.55	132.14	121.54
1	C	383	THR	C-N-CA	5.55	132.14	121.54
1	A	383	THR	CA-C-N	5.54	132.12	121.54
1	A	383	THR	C-N-CA	5.54	132.12	121.54
1	A	543	VAL	N-CA-C	-5.48	107.46	113.43
1	C	543	VAL	N-CA-C	-5.47	107.46	113.43
1	A	68	ARG	N-CA-C	-5.44	106.37	114.64
1	C	68	ARG	N-CA-C	-5.41	106.42	114.64
1	A	919	VAL	CA-C-N	5.36	130.43	122.82
1	A	919	VAL	C-N-CA	5.36	130.43	122.82
1	C	919	VAL	CA-C-N	5.33	130.38	122.82
1	C	919	VAL	C-N-CA	5.33	130.38	122.82

There are no chirality outliers.

All (36) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	267	GLU	Peptide
1	A	318	ASN	Peptide
1	A	383	THR	Peptide
1	A	506	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	A	546	PHE	Peptide
1	A	711	TYR	Peptide
1	A	874	GLN	Peptide
1	B	133	PHE	Peptide
1	B	224	ASN	Peptide
1	B	392	GLN	Peptide
1	B	436	CYS	Peptide
1	B	510	SER	Peptide
1	B	697	LYS	Peptide
1	B	772	GLU	Peptide
1	C	267	GLU	Peptide
1	C	318	ASN	Peptide
1	C	383	THR	Peptide
1	C	506	LYS	Peptide
1	C	546	PHE	Peptide
1	C	711	TYR	Peptide
1	C	874	GLN	Peptide
1	D	133	PHE	Peptide
1	D	224	ASN	Peptide
1	D	392	GLN	Peptide
1	D	436	CYS	Peptide
1	D	510	SER	Peptide
1	D	697	LYS	Peptide
1	D	772	GLU	Peptide
2	E	109	PRO	Peptide
2	E	115	VAL	Peptide
2	E	116	MET	Peptide
2	E	119	ALA	Peptide
2	F	109	PRO	Peptide
2	F	115	VAL	Peptide
2	F	116	MET	Peptide
2	F	119	ALA	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7714	0	7731	101	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	6177	0	6164	93	0
1	C	7714	0	7731	94	0
1	D	6177	0	6164	87	0
2	E	1166	0	1152	17	0
2	F	1166	0	1152	18	0
3	A	27	0	13	0	0
3	B	27	0	13	0	0
3	C	27	0	13	1	0
3	D	27	0	13	0	0
4	A	206	0	282	8	0
4	B	127	0	161	3	0
4	C	206	0	282	5	0
4	D	127	0	161	5	0
4	E	54	0	73	2	0
4	F	54	0	73	0	0
5	A	28	0	37	4	0
5	C	28	0	37	3	0
6	A	42	0	0	33	0
6	C	42	0	0	36	0
7	A	10	0	19	2	0
All	All	31146	0	31271	467	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (467) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:1106:AJP:C19	6:C:1106:AJP:C24	1.77	1.61
6:A:1106:AJP:C14	6:A:1106:AJP:C15	1.79	1.60
6:C:1106:AJP:C15	6:C:1106:AJP:C14	1.79	1.59
6:C:1106:AJP:C18	6:C:1106:AJP:C17	1.81	1.58
5:A:1105:CLR:C15	5:A:1105:CLR:C16	1.77	1.58
6:A:1106:AJP:C19	6:A:1106:AJP:C24	1.77	1.58
5:C:1105:CLR:C15	5:C:1105:CLR:C16	1.78	1.54
6:A:1106:AJP:C18	6:A:1106:AJP:C17	1.81	1.54
6:C:1106:AJP:C22	6:C:1106:AJP:C21	1.81	1.53
6:A:1106:AJP:C22	6:A:1106:AJP:C21	1.81	1.53
6:A:1106:AJP:C10	6:A:1106:AJP:C11	1.85	1.50
6:C:1106:AJP:C10	6:C:1106:AJP:C11	1.86	1.50
6:A:1106:AJP:C28	6:A:1106:AJP:C27	1.89	1.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:1106:AJP:C27	6:C:1106:AJP:C28	1.94	1.41
6:A:1106:AJP:C11	6:A:1106:AJP:C12	2.09	1.31
6:C:1106:AJP:C11	6:C:1106:AJP:C12	2.09	1.29
6:C:1106:AJP:C30	6:C:1106:AJP:O31	1.82	1.27
6:A:1106:AJP:O31	6:A:1106:AJP:C30	1.82	1.27
6:C:1106:AJP:C08	6:C:1106:AJP:C07	2.22	1.17
6:A:1106:AJP:C07	6:A:1106:AJP:C08	2.22	1.17
6:A:1106:AJP:C26	6:A:1106:AJP:C23	2.32	1.08
6:C:1106:AJP:C26	6:C:1106:AJP:C23	2.33	1.05
6:A:1106:AJP:C05	6:A:1106:AJP:O09	2.06	1.03
6:A:1106:AJP:C26	6:A:1106:AJP:O25	2.05	1.03
6:C:1106:AJP:C05	6:C:1106:AJP:O09	2.06	1.03
6:C:1106:AJP:C26	6:C:1106:AJP:O25	2.07	1.01
6:C:1106:AJP:C18	6:C:1106:AJP:C16	2.47	0.90
6:C:1106:AJP:C24	6:C:1106:AJP:C20	2.52	0.88
6:A:1106:AJP:C27	6:A:1106:AJP:C29	2.52	0.85
6:A:1106:AJP:C24	6:A:1106:AJP:C20	2.53	0.84
6:A:1106:AJP:C18	6:A:1106:AJP:C16	2.48	0.81
6:A:1106:AJP:C21	6:A:1106:AJP:C23	2.55	0.80
6:A:1106:AJP:C08	6:A:1106:AJP:C05	2.59	0.80
6:C:1106:AJP:C08	6:C:1106:AJP:C05	2.60	0.79
6:C:1106:AJP:C12	6:C:1106:AJP:C16	2.60	0.79
6:C:1106:AJP:C30	6:C:1106:AJP:C26	2.61	0.78
6:A:1106:AJP:C12	6:A:1106:AJP:C16	2.59	0.77
6:C:1106:AJP:C21	6:C:1106:AJP:C23	2.57	0.77
6:C:1106:AJP:C24	6:C:1106:AJP:C18	2.64	0.76
6:A:1106:AJP:C24	6:A:1106:AJP:C18	2.65	0.75
6:A:1106:AJP:C30	6:A:1106:AJP:C26	2.64	0.74
6:C:1106:AJP:C27	6:C:1106:AJP:C29	2.61	0.72
1:A:543:VAL:HG13	1:B:810:ALA:HB2	1.70	0.72
6:A:1106:AJP:C19	6:A:1106:AJP:C23	2.70	0.69
6:C:1106:AJP:C19	6:C:1106:AJP:C23	2.70	0.68
1:B:606:TRP:HB3	1:C:585:MET:HG2	1.76	0.67
1:A:178:ARG:O	1:A:182:GLN:NE2	2.29	0.66
6:C:1106:AJP:C28	6:C:1106:AJP:C26	2.73	0.66
1:C:178:ARG:O	1:C:182:GLN:NE2	2.28	0.65
1:A:30:ARG:NH2	1:A:269:GLU:O	2.30	0.64
1:C:30:ARG:NH2	1:C:269:GLU:O	2.31	0.64
1:D:163:ILE:HG21	1:D:180:LEU:HD11	1.80	0.64
6:A:1106:AJP:C15	6:A:1106:AJP:C13	2.70	0.64
1:B:163:ILE:HG21	1:B:180:LEU:HD11	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:VAL:O	1:B:308:ARG:NH2	2.32	0.63
6:C:1106:AJP:C11	6:C:1106:AJP:C08	2.74	0.62
6:A:1106:AJP:C11	6:A:1106:AJP:C08	2.73	0.61
6:A:1106:AJP:C28	6:A:1106:AJP:C26	2.74	0.61
1:D:70:VAL:O	1:D:308:ARG:NH2	2.32	0.61
1:C:1005:TRP:HB3	4:C:1103:PCW:H31	1.83	0.60
1:B:24:GLN:HE21	1:B:278:ILE:HD12	1.67	0.60
1:D:24:GLN:HE21	1:D:278:ILE:HD12	1.67	0.60
1:A:803:LEU:HD11	1:D:536:VAL:HG22	1.84	0.60
6:C:1106:AJP:C15	6:C:1106:AJP:C13	2.71	0.60
1:C:46:HIS:HD2	1:C:65:GLN:HE22	1.50	0.59
6:A:1106:AJP:C11	6:A:1106:AJP:C07	2.77	0.59
1:B:249:ASP:HB2	1:B:359:ASN:HD21	1.67	0.59
6:C:1106:AJP:C11	6:C:1106:AJP:C07	2.78	0.59
1:D:639:LEU:HB3	1:D:647:TYR:HE1	1.67	0.59
1:A:586:GLN:O	7:A:1111:SPD:N6	2.31	0.59
1:A:46:HIS:HD2	1:A:65:GLN:HE22	1.50	0.58
1:B:639:LEU:HB3	1:B:647:TYR:HE1	1.67	0.58
2:E:104:ARG:NH1	2:E:134:GLU:OE2	2.36	0.58
1:B:102:PRO:HA	1:B:112:GLN:HG2	1.85	0.58
1:D:102:PRO:HA	1:D:112:GLN:HG2	1.85	0.58
2:F:104:ARG:NH1	2:F:134:GLU:OE2	2.36	0.58
6:C:1106:AJP:C19	6:C:1106:AJP:C17	2.64	0.58
6:A:1106:AJP:C14	6:A:1106:AJP:C16	2.76	0.57
1:A:949:GLY:HA2	1:A:958:LEU:HD13	1.85	0.57
6:C:1106:AJP:C14	6:C:1106:AJP:C16	2.76	0.57
1:D:249:ASP:HB2	1:D:359:ASN:HD21	1.67	0.57
2:F:26:TRP:HD1	2:F:67:LEU:HD11	1.68	0.57
1:D:501:SER:OG	1:D:709:ASN:ND2	2.37	0.57
1:C:949:GLY:HA2	1:C:958:LEU:HD13	1.85	0.57
2:E:26:TRP:HD1	2:E:67:LEU:HD11	1.68	0.57
1:A:508:GLN:NE2	1:A:509:LYS:O	2.38	0.57
1:B:501:SER:OG	1:B:709:ASN:ND2	2.37	0.57
6:C:1106:AJP:C08	6:C:1106:AJP:C06	2.81	0.57
1:A:174:ASP:OD1	1:A:207:GLN:NE2	2.38	0.56
1:A:986:ASP:HB2	1:B:511:LYS:HG3	1.86	0.56
1:C:690:VAL:HG21	1:C:712:ILE:HD13	1.88	0.56
1:C:13:GLN:HG3	1:C:70:VAL:HG12	1.87	0.56
6:A:1106:AJP:C14	6:A:1106:AJP:C11	2.83	0.56
1:B:488:VAL:HG23	1:B:489:ILE:HG13	1.86	0.56
1:C:508:GLN:NE2	1:C:509:LYS:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:706:SER:OG	1:C:726:ASN:ND2	2.39	0.56
1:A:13:GLN:HG3	1:A:70:VAL:HG12	1.87	0.56
1:D:488:VAL:HG23	1:D:489:ILE:HG13	1.86	0.56
1:D:503:MET:HE1	1:D:690:VAL:HG22	1.88	0.56
1:B:503:MET:HE1	1:B:690:VAL:HG22	1.88	0.56
1:A:690:VAL:HG21	1:A:712:ILE:HD13	1.88	0.55
1:C:174:ASP:OD1	1:C:207:GLN:NE2	2.38	0.55
1:C:475:ALA:HB3	1:C:735:ALA:HB3	1.87	0.55
1:A:706:SER:OG	1:A:726:ASN:ND2	2.39	0.55
1:B:599:ARG:NH1	1:C:574:PHE:O	2.39	0.55
1:D:328:GLU:OE1	1:D:331:ARG:NH2	2.34	0.55
6:C:1106:AJP:C14	6:C:1106:AJP:C11	2.83	0.55
1:A:475:ALA:HB3	1:A:735:ALA:HB3	1.87	0.55
1:B:86:THR:HG22	1:B:110:VAL:HG21	1.88	0.55
1:C:520:PRO:O	1:C:619:ASN:ND2	2.40	0.54
1:B:618:ALA:HA	1:C:621:ALA:HB2	1.89	0.54
1:A:520:PRO:O	1:A:619:ASN:ND2	2.40	0.54
1:D:86:THR:HG22	1:D:110:VAL:HG21	1.88	0.54
2:E:100:TYR:O	2:E:104:ARG:N	2.39	0.54
1:B:328:GLU:OE1	1:B:331:ARG:NH2	2.34	0.54
1:B:208:VAL:HG13	1:B:213:LYS:HB2	1.90	0.54
1:A:604:VAL:HG21	1:B:802:GLY:HA3	1.90	0.54
1:B:10:ASN:OD1	1:B:300:ARG:NH1	2.41	0.54
1:A:585:MET:HG2	1:D:606:TRP:HB3	1.90	0.54
1:C:236:GLN:NE2	1:C:365:THR:O	2.42	0.54
1:A:236:GLN:NE2	1:A:365:THR:O	2.42	0.53
1:A:586:GLN:HB3	7:A:1111:SPD:H81	1.90	0.53
1:D:10:ASN:OD1	1:D:300:ARG:NH1	2.41	0.53
1:D:208:VAL:HG13	1:D:213:LYS:HB2	1.90	0.53
6:A:1106:AJP:C08	6:A:1106:AJP:C06	2.81	0.53
1:B:716:LYS:NZ	1:B:772:GLU:OE2	2.35	0.53
1:C:161:THR:HG21	1:C:187:LYS:HZ1	1.72	0.53
6:A:1106:AJP:C17	6:A:1106:AJP:C10	2.86	0.53
1:A:536:VAL:HG22	1:B:803:LEU:HD21	1.90	0.53
1:B:396:VAL:HB	1:B:472:ALA:HA	1.91	0.53
1:D:235:ILE:HD12	1:D:242:VAL:HG21	1.91	0.53
1:C:86:THR:HG22	1:C:110:VAL:HG11	1.91	0.53
6:C:1106:AJP:C17	6:C:1106:AJP:C10	2.86	0.53
1:D:396:VAL:HB	1:D:472:ALA:HA	1.91	0.53
2:E:68:VAL:HG21	2:E:117:TYR:HB2	1.91	0.52
1:B:536:VAL:HG11	1:B:605:TRP:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:882:LEU:HD11	1:C:922:LEU:HD21	1.92	0.52
1:D:536:VAL:HG11	1:D:605:TRP:HB2	1.91	0.52
1:A:1005:TRP:HB3	4:A:1103:PCW:H31	1.90	0.52
1:D:716:LYS:NZ	1:D:772:GLU:OE2	2.35	0.52
1:A:427:ASP:OD2	1:A:765:LYS:NZ	2.43	0.51
1:A:882:LEU:HD11	1:A:922:LEU:HD21	1.92	0.51
1:B:13:GLN:HG3	1:B:70:VAL:HG12	1.92	0.51
1:B:235:ILE:HD12	1:B:242:VAL:HG21	1.91	0.51
1:C:975:VAL:HG21	5:C:1105:CLR:H211	1.92	0.51
1:A:147:GLN:HE21	1:B:143:LEU:HD21	1.75	0.51
1:C:427:ASP:OD2	1:C:765:LYS:NZ	2.43	0.51
1:B:464:VAL:HG13	1:B:489:ILE:HD11	1.92	0.51
1:C:955:ARG:HB3	1:C:958:LEU:HD11	1.92	0.51
1:A:86:THR:HG22	1:A:110:VAL:HG11	1.91	0.51
1:A:315:CYS:SG	1:A:316:LEU:N	2.84	0.51
1:B:536:VAL:HG22	1:C:803:LEU:HD11	1.92	0.51
2:F:68:VAL:HG21	2:F:117:TYR:HB2	1.92	0.51
1:D:765:LYS:HA	1:D:769:ASP:HB2	1.93	0.51
1:D:13:GLN:HG3	1:D:70:VAL:HG12	1.92	0.50
1:A:172:LYS:HB3	1:A:176:THR:HG23	1.94	0.50
1:A:405:TYR:HA	1:A:424:TYR:HB3	1.94	0.50
1:B:22:ALA:HB1	1:B:25:GLU:HB2	1.93	0.50
6:C:1106:AJP:C22	6:C:1106:AJP:C20	2.80	0.50
1:D:464:VAL:HG13	1:D:489:ILE:HD11	1.92	0.50
1:B:93:HIS:CD2	1:B:322:PRO:HB3	2.46	0.50
1:D:93:HIS:CD2	1:D:322:PRO:HB3	2.46	0.50
1:D:337:GLN:HG2	1:D:344:ASN:HD21	1.76	0.50
1:C:405:TYR:HA	1:C:424:TYR:HB3	1.94	0.50
1:A:955:ARG:HB3	1:A:958:LEU:HD11	1.93	0.50
1:B:337:GLN:HG2	1:B:344:ASN:HD21	1.76	0.50
1:D:359:ASN:HA	1:D:373:TYR:HA	1.94	0.50
2:E:128:LEU:O	2:E:132:GLN:N	2.44	0.50
1:B:765:LYS:HA	1:B:769:ASP:HB2	1.93	0.50
1:C:172:LYS:HB3	1:C:176:THR:HG23	1.94	0.50
1:A:1009:PHE:O	1:A:1013:SER:N	2.42	0.50
1:C:77:TYR:HE1	1:C:98:THR:HG21	1.77	0.50
1:D:22:ALA:HB1	1:D:25:GLU:HB2	1.93	0.50
1:C:886:LEU:HG	1:C:929:THR:HG23	1.94	0.50
1:B:141:ARG:NH2	1:B:195:ASP:O	2.45	0.49
1:C:315:CYS:SG	1:C:316:LEU:N	2.84	0.49
2:E:101:HIS:HA	2:E:104:ARG:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:TYR:HE1	1:A:98:THR:HG21	1.77	0.49
1:C:1009:PHE:O	1:C:1013:SER:N	2.42	0.49
1:C:606:TRP:CG	1:D:587:GLN:HG3	2.47	0.49
2:F:100:TYR:O	2:F:104:ARG:N	2.39	0.49
1:A:955:ARG:HE	1:A:956:THR:H	1.61	0.49
1:A:814:PHE:O	1:A:818:SER:OG	2.30	0.49
6:A:1106:AJP:C19	6:A:1106:AJP:C17	2.65	0.49
1:B:135:TYR:HD1	1:B:193:ILE:HG23	1.78	0.49
1:C:870:LEU:HB2	1:C:875:SER:HB3	1.95	0.49
1:A:24:GLN:HE21	1:A:278:ILE:HD12	1.77	0.49
1:A:633:ILE:HG21	1:A:639:LEU:HD12	1.95	0.49
1:A:764:ASN:HD22	1:D:664:ILE:HD11	1.78	0.49
1:B:227:PHE:HB2	1:B:245:PHE:H	1.78	0.49
1:B:359:ASN:HA	1:B:373:TYR:HA	1.94	0.49
1:C:529:ILE:O	1:C:533:TYR:N	2.45	0.49
1:A:755:GLU:OE2	1:D:482:THR:OG1	2.20	0.49
1:A:886:LEU:HG	1:A:929:THR:HG23	1.94	0.49
1:D:227:PHE:HB2	1:D:245:PHE:H	1.78	0.49
2:F:101:HIS:HA	2:F:104:ARG:HB3	1.94	0.49
1:B:664:ILE:HD11	1:C:764:ASN:HD22	1.77	0.48
1:A:529:ILE:O	1:A:533:TYR:N	2.45	0.48
1:C:316:LEU:O	1:D:60:ASN:ND2	2.46	0.48
1:A:736:THR:HG21	1:A:743:GLY:HA2	1.94	0.48
1:C:113:MET:HE3	1:C:113:MET:HB2	1.69	0.48
2:F:100:TYR:OH	2:F:104:ARG:NH1	2.46	0.48
1:D:141:ARG:NH2	1:D:195:ASP:O	2.45	0.48
1:A:542:LEU:HD22	1:B:807:MET:HE3	1.96	0.48
1:A:870:LEU:HB2	1:A:875:SER:HB3	1.95	0.48
1:D:135:TYR:HD1	1:D:193:ILE:HG23	1.78	0.48
2:E:100:TYR:OH	2:E:104:ARG:NH1	2.46	0.48
2:F:60:ILE:HG23	2:F:64:LEU:HD12	1.96	0.48
1:A:657:GLU:HB3	1:A:661:ARG:HH12	1.79	0.48
1:B:141:ARG:NH2	1:B:195:ASP:OD2	2.47	0.48
1:C:606:TRP:CD1	1:D:587:GLN:HG3	2.48	0.48
1:C:955:ARG:HE	1:C:956:THR:H	1.61	0.48
1:D:141:ARG:NH2	1:D:195:ASP:OD2	2.47	0.48
1:D:385:ASP:OD1	1:D:385:ASP:N	2.47	0.48
1:C:24:GLN:HE21	1:C:278:ILE:HD12	1.77	0.48
1:A:227:PHE:HB2	1:A:245:PHE:H	1.79	0.48
1:D:639:LEU:O	1:D:647:TYR:OH	2.23	0.48
1:D:77:TYR:HE1	1:D:98:THR:HG21	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:17:CYS:HA	2:F:20:LEU:HB2	1.97	0.47
1:A:795:VAL:HG21	1:D:611:ILE:HG21	1.96	0.47
1:A:925:ILE:O	1:A:929:THR:N	2.47	0.47
1:B:754:SER:HB2	1:B:759:LEU:HD12	1.96	0.47
1:C:28:ALA:HA	1:C:31:VAL:HG12	1.96	0.47
1:B:475:ALA:HB3	1:B:735:ALA:HB3	1.96	0.47
1:C:227:PHE:HB2	1:C:245:PHE:H	1.79	0.47
1:C:633:ILE:HG21	1:C:639:LEU:HD12	1.95	0.47
1:D:754:SER:HB2	1:D:759:LEU:HD12	1.96	0.47
1:D:584:PHE:HA	1:D:609:THR:HG21	1.97	0.47
1:A:713:GLU:HG3	1:A:714:GLN:HG3	1.97	0.47
1:D:209:ILE:HA	1:D:214:HIS:HD2	1.80	0.47
2:E:60:ILE:HG23	2:E:64:LEU:HD12	1.96	0.47
1:A:28:ALA:HA	1:A:31:VAL:HG12	1.95	0.47
1:B:77:TYR:HE1	1:B:98:THR:HG21	1.79	0.47
1:B:209:ILE:HA	1:B:214:HIS:HD2	1.80	0.47
1:C:736:THR:HG21	1:C:743:GLY:HA2	1.94	0.47
1:C:814:PHE:O	1:C:818:SER:OG	2.30	0.47
2:F:95:ILE:HA	2:F:98:LEU:HB3	1.97	0.47
2:F:152:SER:HA	2:F:155:TYR:HB3	1.97	0.47
1:B:584:PHE:HA	1:B:609:THR:HG21	1.97	0.47
1:C:657:GLU:HB3	1:C:661:ARG:HH12	1.79	0.47
1:C:925:ILE:O	1:C:929:THR:N	2.47	0.47
1:A:59:THR:HG21	1:B:88:PHE:HZ	1.80	0.47
1:C:196:CYS:HB3	1:C:200:LYS:HB3	1.97	0.47
2:E:17:CYS:HA	2:E:20:LEU:HB2	1.96	0.47
1:A:196:CYS:HB3	1:A:200:LYS:HB3	1.97	0.46
1:B:406:VAL:HG23	1:B:421:TYR:HB3	1.97	0.46
1:C:93:HIS:CD2	1:C:322:PRO:HB3	2.51	0.46
1:D:716:LYS:HB3	1:D:772:GLU:HG2	1.97	0.46
4:B:1102:PCW:H341	4:B:1102:PCW:H372	1.70	0.46
1:B:385:ASP:OD1	1:B:385:ASP:N	2.47	0.46
1:C:543:VAL:HG13	1:D:810:ALA:HB2	1.97	0.46
4:C:1109:PCW:H121	4:C:1109:PCW:H31	1.68	0.46
1:D:25:GLU:HG2	1:D:76:PHE:HE2	1.80	0.46
1:D:475:ALA:HB3	1:D:735:ALA:HB3	1.96	0.46
1:C:294:GLU:OE1	1:C:297:ARG:NH2	2.48	0.46
1:A:48:ASP:N	1:A:48:ASP:OD1	2.47	0.46
1:C:713:GLU:HG3	1:C:714:GLN:HG3	1.97	0.46
2:F:32:ASP:O	2:F:36:THR:OG1	2.27	0.46
6:C:1106:AJP:C12	6:C:1106:AJP:C08	2.89	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:405:TYR:HA	1:D:424:TYR:H	1.80	0.46
1:D:406:VAL:HG23	1:D:421:TYR:HB3	1.97	0.46
1:A:903:ILE:HG13	1:A:926:ARG:HH21	1.81	0.46
1:B:603:GLY:HA2	1:C:581:LEU:HD11	1.97	0.46
1:C:59:THR:HG23	1:C:88:PHE:HE2	1.80	0.46
1:D:77:TYR:HE2	1:D:101:PHE:HB2	1.81	0.46
2:E:95:ILE:HA	2:E:98:LEU:HB3	1.97	0.46
2:E:152:SER:HA	2:E:155:TYR:HB3	1.97	0.46
1:A:59:THR:HG23	1:A:88:PHE:HE2	1.80	0.46
1:A:294:GLU:OE1	1:A:297:ARG:NH2	2.48	0.46
1:B:77:TYR:HE2	1:B:101:PHE:HB2	1.80	0.46
1:C:279:LYS:O	1:C:283:ALA:N	2.46	0.46
1:C:369:ARG:NH1	1:C:386:ASP:O	2.49	0.46
4:C:1103:PCW:H151	4:C:1103:PCW:H122	1.57	0.46
1:D:231:ASP:HB3	1:D:234:LYS:HE2	1.97	0.46
1:A:93:HIS:CD2	1:A:322:PRO:HB3	2.51	0.46
2:E:64:LEU:HD23	2:E:67:LEU:HD12	1.98	0.46
1:A:52:VAL:HG11	1:A:77:TYR:HA	1.97	0.45
1:A:369:ARG:NH1	1:A:386:ASP:O	2.49	0.45
1:A:463:MET:HE2	1:A:463:MET:HB3	1.70	0.45
1:C:52:VAL:HG11	1:C:77:TYR:HA	1.97	0.45
1:A:294:GLU:HG2	1:A:336:VAL:HG13	1.98	0.45
1:A:404:PRO:O	1:A:424:TYR:N	2.46	0.45
1:B:639:LEU:O	1:B:647:TYR:OH	2.23	0.45
1:C:903:ILE:HG13	1:C:926:ARG:HH21	1.81	0.45
4:D:1102:PCW:H162	4:D:1102:PCW:H131	1.72	0.45
1:A:803:LEU:HD21	1:D:536:VAL:HG13	1.98	0.45
1:B:143:LEU:HD23	1:B:146:LEU:HD23	1.98	0.45
1:B:337:GLN:HE21	1:B:344:ASN:HD21	1.64	0.45
1:A:859:ASP:OD1	1:A:859:ASP:N	2.49	0.45
1:B:137:TYR:HA	1:B:195:ASP:HB3	1.98	0.45
1:C:48:ASP:OD1	1:C:48:ASP:N	2.47	0.45
1:C:711:TYR:HE1	1:C:715:ARG:HH21	1.65	0.45
1:D:529:ILE:O	1:D:533:TYR:N	2.49	0.45
2:F:128:LEU:O	2:F:132:GLN:N	2.44	0.45
1:A:509:LYS:HG3	1:A:510:SER:H	1.82	0.45
1:B:185:GLU:OE1	1:B:213:LYS:NZ	2.49	0.45
1:B:25:GLU:HG2	1:B:76:PHE:HE2	1.80	0.45
1:B:716:LYS:HB3	1:B:772:GLU:HG2	1.97	0.45
1:A:543:VAL:HG21	1:B:807:MET:HG2	1.98	0.45
1:A:783:LYS:HE2	1:D:630:VAL:HG11	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:1106:AJP:C24	6:C:1106:AJP:C80	2.95	0.45
1:D:126:GLU:OE2	1:D:156:LYS:NZ	2.33	0.45
1:D:337:GLN:HE21	1:D:344:ASN:HD21	1.64	0.45
2:E:32:ASP:O	2:E:36:THR:OG1	2.27	0.45
1:B:100:SER:OG	1:B:101:PHE:N	2.43	0.45
1:C:206:ASP:OD1	1:C:234:LYS:NZ	2.39	0.45
1:D:137:TYR:HA	1:D:195:ASP:HB3	1.98	0.45
1:B:405:TYR:HA	1:B:424:TYR:H	1.80	0.45
1:B:529:ILE:O	1:B:533:TYR:N	2.49	0.45
1:B:639:LEU:HB3	1:B:647:TYR:CE1	2.50	0.45
1:C:861:TRP:CD1	1:C:885:GLY:HA2	2.53	0.45
1:D:77:TYR:CE1	1:D:98:THR:HG21	2.53	0.45
1:A:584:PHE:HA	1:A:609:THR:HG21	1.99	0.44
1:B:231:ASP:HB3	1:B:234:LYS:HE2	1.98	0.44
1:C:509:LYS:HG3	1:C:510:SER:H	1.82	0.44
1:D:143:LEU:HD23	1:D:146:LEU:HD23	1.98	0.44
1:D:599:ARG:O	1:D:603:GLY:N	2.50	0.44
1:C:294:GLU:HG2	1:C:336:VAL:HG13	1.98	0.44
1:C:859:ASP:N	1:C:859:ASP:OD1	2.50	0.44
1:D:639:LEU:HB3	1:D:647:TYR:CE1	2.51	0.44
6:A:1106:AJP:C26	6:A:1106:AJP:C29	2.91	0.44
1:B:397:VAL:HG13	1:B:442:LEU:HA	2.00	0.44
1:B:599:ARG:O	1:B:603:GLY:N	2.50	0.44
2:F:64:LEU:HD23	2:F:67:LEU:HD12	1.98	0.44
1:A:608:PHE:HD1	1:B:795:VAL:HG12	1.82	0.44
1:B:130:TRP:CD2	1:B:191:ARG:HD3	2.53	0.44
4:C:1107:PCW:H382	4:C:1107:PCW:H411	1.74	0.44
1:A:467:LEU:HD13	1:A:475:ALA:HB2	2.00	0.44
1:A:93:HIS:HD2	1:A:322:PRO:HB3	1.83	0.44
1:B:77:TYR:CE1	1:B:98:THR:HG21	2.52	0.44
1:A:861:TRP:CD1	1:A:885:GLY:HA2	2.52	0.44
1:B:11:SER:HA	1:B:42:ARG:HB3	2.00	0.44
1:B:500:ILE:HD12	1:B:655:THR:HG23	2.00	0.43
1:D:397:VAL:HG13	1:D:442:LEU:HA	2.00	0.43
1:A:646:ALA:N	1:A:699:LYS:O	2.39	0.43
1:A:711:TYR:HE1	1:A:715:ARG:HH21	1.65	0.43
1:B:16:GLY:H	1:B:73:ILE:HG23	1.83	0.43
1:A:56:PHE:N	1:B:87:SER:OG	2.45	0.43
1:C:93:HIS:HD2	1:C:322:PRO:HB3	1.83	0.43
4:A:1104:PCW:H172	5:A:1105:CLR:H193	2.01	0.43
1:C:584:PHE:HA	1:C:609:THR:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:975:VAL:HG21	5:A:1105:CLR:H211	1.99	0.43
6:A:1106:AJP:C24	6:A:1106:AJP:C80	2.96	0.43
1:C:113:MET:HB3	1:C:284:LEU:HD12	2.01	0.43
1:C:383:THR:OG1	1:C:384:GLU:N	2.51	0.43
1:D:11:SER:HA	1:D:42:ARG:HB3	2.00	0.43
1:D:500:ILE:HD12	1:D:655:THR:HG23	2.01	0.43
1:A:383:THR:OG1	1:A:384:GLU:N	2.51	0.43
1:C:349:GLN:O	1:C:351:GLY:N	2.51	0.43
1:A:360:ILE:HD11	1:A:374:TRP:HB2	2.00	0.43
4:D:1102:PCW:H341	4:D:1102:PCW:H372	1.65	0.43
4:A:1107:PCW:H62	4:A:1107:PCW:H41	1.84	0.43
1:B:526:TRP:HB3	4:B:1102:PCW:H121	2.01	0.43
1:B:536:VAL:HG13	1:C:803:LEU:HD21	2.00	0.43
1:C:683:VAL:HG11	1:C:689:GLY:HA2	2.00	0.43
1:D:97:ILE:HA	1:D:111:ILE:HB	2.01	0.43
2:E:12:LEU:HD23	2:E:81:MET:HE1	2.01	0.43
4:E:202:PCW:H82	4:E:202:PCW:H41	1.89	0.43
1:D:130:TRP:CD2	1:D:191:ARG:HD3	2.53	0.43
1:A:113:MET:HE3	1:A:113:MET:HB2	1.69	0.42
1:C:467:LEU:HD13	1:C:475:ALA:HB2	2.00	0.42
1:B:599:ARG:HH22	1:C:575:ASN:ND2	2.17	0.42
1:C:17:LEU:HB2	1:C:75:GLY:HA3	2.02	0.42
1:D:16:GLY:H	1:D:73:ILE:HG23	1.83	0.42
1:D:519:ASP:HB3	1:D:623:PHE:HE2	1.84	0.42
1:A:176:THR:O	1:A:180:LEU:N	2.50	0.42
1:A:349:GLN:O	1:A:351:GLY:N	2.51	0.42
1:C:508:GLN:CD	1:C:509:LYS:H	2.27	0.42
5:A:1105:CLR:H213	5:A:1105:CLR:H161	1.86	0.42
1:D:33:MET:HE1	1:D:45:PRO:HG3	2.01	0.42
1:D:185:GLU:OE1	1:D:213:LYS:NZ	2.49	0.42
2:F:12:LEU:HD23	2:F:81:MET:HE1	2.01	0.42
1:A:508:GLN:CD	1:A:509:LYS:H	2.27	0.42
1:A:751:LEU:HD11	1:D:481:ILE:HG22	2.02	0.42
1:B:519:ASP:HB3	1:B:623:PHE:HE2	1.84	0.42
2:F:26:TRP:CD1	2:F:67:LEU:HD11	2.52	0.42
1:A:17:LEU:HB2	1:A:75:GLY:HA3	2.01	0.42
1:A:606:TRP:CD1	1:B:587:GLN:HG3	2.55	0.42
1:B:33:MET:HE1	1:B:45:PRO:HG3	2.01	0.42
1:C:193:ILE:HD13	1:C:193:ILE:HG21	1.85	0.42
1:D:526:TRP:HB3	4:D:1102:PCW:H121	2.00	0.42
1:A:133:PHE:CD2	1:A:160:VAL:HG22	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:659:PHE:HB3	1:A:671:TRP:HB2	2.02	0.42
1:B:536:VAL:HG21	1:C:799:LEU:HD11	2.02	0.42
1:C:360:ILE:HD11	1:C:374:TRP:HB2	2.00	0.42
1:C:849:LEU:HD21	1:C:943:PHE:HB2	2.02	0.42
1:C:881:SER:HB2	1:C:892:LEU:HB3	2.01	0.42
6:C:1106:AJP:C26	6:C:1106:AJP:C29	2.94	0.42
1:C:133:PHE:CD2	1:C:160:VAL:HG22	2.55	0.42
1:D:180:LEU:HA	1:D:180:LEU:HD12	1.87	0.42
2:E:103:TRP:O	2:E:107:HIS:N	2.37	0.42
1:A:113:MET:HB3	1:A:284:LEU:HD12	2.00	0.42
1:A:683:VAL:HG11	1:A:689:GLY:HA2	2.00	0.42
4:A:1109:PCW:H42	4:A:1109:PCW:H83	1.88	0.42
1:B:642:GLN:OE1	1:B:644:GLU:N	2.53	0.42
1:C:399:THR:HA	1:C:477:ALA:HB2	2.02	0.42
4:D:1103:PCW:H411	4:D:1103:PCW:H382	1.83	0.42
2:E:26:TRP:CD1	2:E:67:LEU:HD11	2.52	0.42
2:F:95:ILE:O	2:F:99:PHE:N	2.40	0.42
1:D:642:GLN:OE1	1:D:644:GLU:N	2.53	0.41
1:A:279:LYS:O	1:A:283:ALA:N	2.46	0.41
1:A:515:PHE:HB3	1:A:518:LEU:HD12	2.02	0.41
1:A:881:SER:HB2	1:A:892:LEU:HB3	2.01	0.41
1:D:520:PRO:HG2	1:D:620:LEU:HD12	2.03	0.41
1:A:664:ILE:HB	1:A:667:PHE:HD2	1.85	0.41
1:B:359:ASN:HB2	1:B:370:LYS:HE2	2.03	0.41
5:C:1105:CLR:H221	1:D:800:VAL:HG12	2.02	0.41
1:D:359:ASN:HB2	1:D:370:LYS:HE2	2.02	0.41
1:A:318:ASN:HD22	1:A:318:ASN:HA	1.55	0.41
4:A:1103:PCW:H172	4:A:1103:PCW:H142	1.88	0.41
1:C:496:MET:HE3	1:C:496:MET:HB2	1.94	0.41
1:C:664:ILE:HB	1:C:667:PHE:HD2	1.85	0.41
1:C:667:PHE:HE1	1:C:727:LEU:HD13	1.85	0.41
1:A:585:MET:HE2	1:D:607:PHE:HD1	1.84	0.41
4:A:1103:PCW:H151	4:A:1103:PCW:H122	1.53	0.41
1:B:97:ILE:HA	1:B:111:ILE:HB	2.01	0.41
1:B:131:ASP:OD1	1:B:131:ASP:N	2.52	0.41
6:C:1106:AJP:C24	6:C:1106:AJP:C21	2.87	0.41
4:D:1103:PCW:H82	4:D:1103:PCW:H42	1.86	0.41
6:A:1106:AJP:C12	6:A:1106:AJP:C08	2.89	0.41
1:B:505:LYS:HD2	1:B:698:GLY:H	1.86	0.41
1:B:607:PHE:HD1	1:C:585:MET:HE2	1.85	0.41
6:C:1106:AJP:C14	6:C:1106:AJP:C20	2.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:184:LEU:HD23	1:B:184:LEU:HA	1.93	0.41
1:B:308:ARG:HB3	1:B:309:ARG:H	1.68	0.41
1:C:659:PHE:HB3	1:C:671:TRP:HB2	2.02	0.41
1:D:124:LEU:HD13	1:D:360:ILE:HD13	2.01	0.41
1:D:665:ALA:HA	1:D:668:ASP:HB3	2.03	0.41
1:A:399:THR:HA	1:A:477:ALA:HB2	2.02	0.41
1:B:124:LEU:HD13	1:B:360:ILE:HD13	2.01	0.41
4:B:1102:PCW:H83	4:B:1102:PCW:H42	1.87	0.41
1:C:18:PHE:HA	1:C:19:PRO:HD3	1.97	0.41
2:E:60:ILE:HD13	2:E:60:ILE:HA	1.92	0.41
2:F:11:MET:HE2	2:F:11:MET:HB3	1.98	0.41
1:A:636:ALA:HB2	1:A:727:LEU:HD21	2.03	0.41
1:A:849:LEU:HD21	1:A:943:PHE:HB2	2.02	0.41
4:A:1103:PCW:H372	4:A:1103:PCW:H341	1.94	0.41
1:B:520:PRO:HG2	1:B:620:LEU:HD12	2.02	0.41
1:B:650:LEU:HD23	1:B:652:SER:H	1.86	0.41
1:C:505:LYS:NZ	1:C:719:ASP:OD1	2.48	0.41
1:C:646:ALA:N	1:C:699:LYS:O	2.39	0.41
3:C:1101:ZK1:HAI	3:C:1101:ZK1:HAOA	1.81	0.41
1:D:100:SER:OG	1:D:101:PHE:N	2.43	0.41
1:D:131:ASP:N	1:D:131:ASP:OD1	2.52	0.41
1:D:363:LEU:HD12	1:D:363:LEU:HA	1.80	0.41
1:A:220:TYR:HB2	1:A:242:VAL:HG22	2.04	0.41
1:B:665:ALA:HA	1:B:668:ASP:HB3	2.03	0.41
1:B:772:GLU:N	1:B:772:GLU:OE1	2.54	0.41
1:C:176:THR:O	1:C:180:LEU:N	2.50	0.41
1:D:112:GLN:HE21	1:D:352:LYS:HD3	1.86	0.41
2:F:60:ILE:HD13	2:F:60:ILE:HA	1.92	0.41
1:A:667:PHE:HE1	1:A:727:LEU:HD13	1.85	0.40
1:D:772:GLU:N	1:D:772:GLU:OE1	2.54	0.40
4:E:202:PCW:H342	4:E:202:PCW:H372	1.79	0.40
1:A:966:PHE:O	1:A:969:SER:OG	2.35	0.40
1:C:147:GLN:HE21	1:D:143:LEU:HD21	1.86	0.40
4:C:1103:PCW:H172	4:C:1103:PCW:H142	1.73	0.40
1:B:42:ARG:HE	1:B:43:LEU:H	1.69	0.40
1:B:112:GLN:HE21	1:B:352:LYS:HD3	1.87	0.40
1:C:541:PHE:HE1	1:C:545:ARG:HE	1.68	0.40
1:C:636:ALA:HB2	1:C:727:LEU:HD21	2.03	0.40
1:A:125:ILE:HD13	1:A:133:PHE:CZ	2.57	0.40
4:A:1109:PCW:H121	4:A:1109:PCW:H31	1.67	0.40
1:C:131:ASP:OD1	1:C:131:ASP:N	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:501:SER:HG	1:D:709:ASN:HD22	1.67	0.40
1:A:541:PHE:HE1	1:A:545:ARG:HE	1.68	0.40
1:D:308:ARG:HB3	1:D:309:ARG:H	1.68	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	968/1026 (94%)	813 (84%)	148 (15%)	7 (1%)	18	51
1	B	777/1026 (76%)	654 (84%)	120 (15%)	3 (0%)	30	60
1	C	968/1026 (94%)	812 (84%)	149 (15%)	7 (1%)	18	51
1	D	777/1026 (76%)	654 (84%)	120 (15%)	3 (0%)	30	60
2	E	136/160 (85%)	119 (88%)	14 (10%)	3 (2%)	5	30
2	F	136/160 (85%)	119 (88%)	14 (10%)	3 (2%)	5	30
All	All	3762/4424 (85%)	3171 (84%)	565 (15%)	26 (1%)	20	51

All (26) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	350	ASN
1	C	350	ASN
1	A	349	GLN
1	A	384	GLU
1	B	773	CYS
1	C	349	GLN
1	C	384	GLU
1	D	773	CYS
2	E	116	MET

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Mol	Chain	Res	Type
2	F	116	MET
1	A	115	PRO
1	C	115	PRO
2	E	115	VAL
2	E	117	TYR
2	F	117	TYR
1	A	135	TYR
1	B	772	GLU
1	C	135	TYR
1	D	772	GLU
2	F	115	VAL
1	A	379	LYS
1	C	379	LYS
1	A	737	PRO
1	C	737	PRO
1	B	470	GLY
1	D	470	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	834/877 (95%)	828 (99%)	6 (1%)	76	78
1	B	668/877 (76%)	663 (99%)	5 (1%)	76	78
1	C	834/877 (95%)	828 (99%)	6 (1%)	76	78
1	D	668/877 (76%)	663 (99%)	5 (1%)	76	78
2	E	126/143 (88%)	124 (98%)	2 (2%)	55	69
2	F	126/143 (88%)	124 (98%)	2 (2%)	55	69
All	All	3256/3794 (86%)	3230 (99%)	26 (1%)	70	77

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	LEU

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Mol	Chain	Res	Type
1	A	121	LEU
1	A	318	ASN
1	A	504	ILE
1	A	626	VAL
1	A	922	LEU
1	B	390	LEU
1	B	397	VAL
1	B	406	VAL
1	B	591	ILE
1	B	762	LEU
1	C	50	LEU
1	C	121	LEU
1	C	318	ASN
1	C	504	ILE
1	C	626	VAL
1	C	922	LEU
1	D	390	LEU
1	D	397	VAL
1	D	406	VAL
1	D	591	ILE
1	D	762	LEU
2	E	115	VAL
2	E	120	VAL
2	F	115	VAL
2	F	120	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (69) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	GLN
1	A	46	HIS
1	A	60	ASN
1	A	93	HIS
1	A	107	HIS
1	A	147	GLN
1	A	167	ASN
1	A	202	ASN
1	A	290	GLN
1	A	318	ASN
1	A	344	ASN
1	A	359	ASN
1	A	508	GLN

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Mol	Chain	Res	Type
1	A	575	ASN
1	A	726	ASN
1	A	764	ASN
1	A	950	HIS
1	A	985	ASN
1	B	24	GLN
1	B	112	GLN
1	B	170	ASN
1	B	224	ASN
1	B	302	GLN
1	B	311	ASN
1	B	318	ASN
1	B	344	ASN
1	B	350	ASN
1	B	418	ASN
1	B	461	ASN
1	B	764	ASN
1	B	791	ASN
1	C	13	GLN
1	C	46	HIS
1	C	107	HIS
1	C	167	ASN
1	C	202	ASN
1	C	290	GLN
1	C	318	ASN
1	C	344	ASN
1	C	359	ASN
1	C	508	GLN
1	C	575	ASN
1	C	726	ASN
1	C	764	ASN
1	C	985	ASN
1	D	24	GLN
1	D	60	ASN
1	D	112	GLN
1	D	170	ASN
1	D	224	ASN
1	D	274	HIS
1	D	302	GLN
1	D	311	ASN
1	D	318	ASN
1	D	335	GLN

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Mol	Chain	Res	Type
1	D	344	ASN
1	D	418	ASN
1	D	461	ASN
1	D	764	ASN
1	D	791	ASN
2	E	75	HIS
2	E	94	ASN
2	E	107	HIS
2	E	129	ASN
2	E	132	GLN
2	F	75	HIS
2	F	94	ASN
2	F	107	HIS
2	F	132	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

35 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	AJP	A	1106	-	48,48,95	18.69	38 (79%)	72,78,149	3.60	40 (55%)
4	PCW	C	1108	-	10,10,53	0.83	0	9,9,61	0.32	0
4	PCW	C	1102	-	39,39,53	1.26	4 (10%)	45,47,61	1.08	3 (6%)
3	ZK1	D	1101	-	29,29,29	3.42	9 (31%)	45,45,45	1.91	11 (24%)
4	PCW	A	1103	-	42,42,53	1.27	5 (11%)	48,50,61	1.04	3 (6%)
4	PCW	D	1102	-	42,42,53	1.22	3 (7%)	48,50,61	1.12	3 (6%)
4	PCW	C	1107	-	50,50,53	1.17	4 (8%)	56,58,61	1.07	4 (7%)
4	PCW	D	1104	-	40,40,53	1.27	4 (10%)	46,48,61	1.22	3 (6%)
3	ZK1	C	1101	-	29,29,29	3.53	10 (34%)	45,45,45	1.76	9 (20%)
4	PCW	F	201	-	10,10,53	0.80	0	9,9,61	0.33	0
4	PCW	F	202	-	42,42,53	1.27	4 (9%)	48,50,61	1.10	3 (6%)
6	AJP	C	1106	-	48,48,95	18.94	40 (83%)	72,78,149	3.54	39 (54%)
4	PCW	B	1104	-	40,40,53	1.27	4 (10%)	46,48,61	1.23	3 (6%)
7	SPD	A	1111	-	9,9,9	0.39	0	8,8,8	0.89	0
4	PCW	E	202	-	42,42,53	1.27	4 (9%)	48,50,61	1.09	3 (6%)
3	ZK1	B	1101	-	29,29,29	3.42	9 (31%)	45,45,45	1.93	10 (22%)
4	PCW	A	1110	-	10,10,53	0.82	0	9,9,61	0.39	0
4	PCW	C	1103	-	42,42,53	1.27	5 (11%)	48,50,61	1.06	3 (6%)
4	PCW	B	1102	-	42,42,53	1.21	3 (7%)	48,50,61	1.14	3 (6%)
4	PCW	C	1104	-	10,10,53	0.82	0	9,9,61	0.38	0
4	PCW	A	1109	-	38,38,53	1.30	4 (10%)	44,46,61	1.18	4 (9%)
4	PCW	E	201	-	10,10,53	0.80	0	9,9,61	0.34	0
4	PCW	D	1103	-	31,31,53	1.29	2 (6%)	37,39,61	1.37	2 (5%)
4	PCW	B	1105	-	10,10,53	0.82	0	9,9,61	0.35	0
5	CLR	C	1105	-	31,31,31	9.43	22 (70%)	48,48,48	3.79	25 (52%)
4	PCW	C	1110	-	10,10,53	0.83	0	9,9,61	0.39	0
4	PCW	C	1109	-	38,38,53	1.31	5 (13%)	44,46,61	1.19	3 (6%)
4	PCW	A	1104	-	10,10,53	0.82	0	9,9,61	0.38	0
4	PCW	D	1105	-	10,10,53	0.82	0	9,9,61	0.35	0
4	PCW	A	1102	-	39,39,53	1.26	4 (10%)	45,47,61	1.08	3 (6%)
4	PCW	A	1108	-	10,10,53	0.83	0	9,9,61	0.33	0
5	CLR	A	1105	-	31,31,31	9.41	22 (70%)	48,48,48	3.95	24 (50%)
4	PCW	B	1103	-	31,31,53	1.28	2 (6%)	37,39,61	1.24	2 (5%)
4	PCW	A	1107	-	50,50,53	1.17	4 (8%)	56,58,61	1.06	4 (7%)
3	ZK1	A	1101	-	29,29,29	3.50	10 (34%)	45,45,45	1.74	9 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	AJP	A	1106	-	12/12/18/38	0/6/117/220	0/7/7/11
4	PCW	C	1108	-	-	3/8/8/57	-
4	PCW	C	1102	-	-	19/43/43/57	-
3	ZK1	D	1101	-	-	5/13/23/23	0/3/3/3
4	PCW	A	1103	-	-	26/46/46/57	-
4	PCW	D	1102	-	-	29/46/46/57	-
4	PCW	C	1107	-	-	25/54/54/57	-
4	PCW	D	1104	-	-	24/44/44/57	-
3	ZK1	C	1101	-	-	5/13/23/23	0/3/3/3
4	PCW	F	201	-	-	4/8/8/57	-
4	PCW	F	202	-	-	25/46/46/57	-
6	AJP	C	1106	-	12/12/18/38	0/6/117/220	0/7/7/11
4	PCW	B	1104	-	-	23/44/44/57	-
7	SPD	A	1111	-	-	3/7/7/7	-
4	PCW	E	202	-	-	24/46/46/57	-
3	ZK1	B	1101	-	-	4/13/23/23	0/3/3/3
4	PCW	A	1110	-	-	5/8/8/57	-
4	PCW	C	1103	-	-	32/46/46/57	-
4	PCW	B	1102	-	-	28/46/46/57	-
4	PCW	C	1104	-	-	2/8/8/57	-
4	PCW	A	1109	-	-	27/42/42/57	-
4	PCW	E	201	-	-	4/8/8/57	-
4	PCW	D	1103	-	-	18/34/34/57	-
4	PCW	B	1105	-	-	5/8/8/57	-
5	CLR	C	1105	-	2/2/10/11	7/10/68/68	0/4/4/4
4	PCW	C	1110	-	-	4/8/8/57	-
4	PCW	C	1109	-	-	28/42/42/57	-
4	PCW	A	1104	-	-	1/8/8/57	-
4	PCW	D	1105	-	-	5/8/8/57	-
4	PCW	A	1102	-	-	18/43/43/57	-
4	PCW	A	1108	-	-	3/8/8/57	-
5	CLR	A	1105	-	2/2/10/11	6/10/68/68	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PCW	B	1103	-	-	18/34/34/57	-
4	PCW	A	1107	-	-	26/54/54/57	-
3	ZK1	A	1101	-	-	4/13/23/23	0/3/3/3

All (221) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1106	AJP	O78-C27	-54.22	0.08	1.43
6	A	1106	AJP	O78-C27	-51.45	0.15	1.43
6	A	1106	AJP	O25-C23	-51.28	0.49	1.44
6	C	1106	AJP	O25-C23	-51.06	0.50	1.44
6	C	1106	AJP	C07-C08	41.66	2.22	1.53
6	A	1106	AJP	C07-C08	41.62	2.22	1.53
6	A	1106	AJP	C16-C11	-37.47	1.02	1.54
6	C	1106	AJP	C16-C11	-37.39	1.02	1.54
6	C	1106	AJP	O09-C05	30.33	2.06	1.42
6	A	1106	AJP	O09-C05	30.32	2.06	1.42
5	A	1105	CLR	C8-C14	-29.32	0.98	1.53
5	C	1105	CLR	C8-C14	-29.26	0.98	1.53
6	C	1106	AJP	C12-C11	29.13	2.09	1.56
6	A	1106	AJP	C12-C11	28.99	2.09	1.56
6	C	1106	AJP	C28-C27	27.50	1.94	1.52
6	A	1106	AJP	C28-C27	24.33	1.89	1.52
6	C	1106	AJP	O31-C30	24.05	1.82	1.44
6	A	1106	AJP	O31-C30	23.62	1.82	1.44
6	C	1106	AJP	O25-C26	23.30	2.07	1.41
6	A	1106	AJP	O25-C26	22.71	2.05	1.41
6	C	1106	AJP	C29-C28	-22.41	1.10	1.52
6	A	1106	AJP	C29-C28	-22.17	1.10	1.52
6	A	1106	AJP	C13-C12	-21.77	1.16	1.54
5	C	1105	CLR	C12-C11	-21.77	1.10	1.53
6	C	1106	AJP	C17-C16	-21.61	1.15	1.53
6	A	1106	AJP	C17-C16	-21.58	1.15	1.53
6	C	1106	AJP	C13-C12	-21.53	1.16	1.54
5	A	1105	CLR	C12-C11	-21.42	1.10	1.53
5	A	1105	CLR	C7-C8	-20.10	1.20	1.53
5	C	1105	CLR	C7-C8	-20.05	1.20	1.53
6	A	1106	AJP	C20-C19	-19.87	1.24	1.55
6	C	1106	AJP	C20-C19	-19.51	1.25	1.55
6	A	1106	AJP	C21-C22	19.27	1.81	1.53
6	C	1106	AJP	C21-C22	19.10	1.81	1.53
6	A	1106	AJP	C22-C23	-18.36	1.20	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	1106	AJP	C22-C23	-18.27	1.20	1.52
6	A	1106	AJP	O09-C08	-18.17	1.12	1.43
6	C	1106	AJP	O09-C08	-18.11	1.12	1.43
6	C	1106	AJP	C11-C10	16.37	1.86	1.53
6	A	1106	AJP	C11-C10	16.24	1.85	1.53
6	C	1106	AJP	C14-C15	15.59	1.79	1.53
6	A	1106	AJP	C14-C15	15.54	1.79	1.53
6	A	1106	AJP	C24-C19	14.95	1.77	1.53
6	C	1106	AJP	C24-C19	14.90	1.77	1.53
6	A	1106	AJP	O82-C10	-13.71	1.09	1.43
6	C	1106	AJP	O82-C10	-13.70	1.09	1.43
6	A	1106	AJP	C12-C07	-13.33	1.31	1.56
6	C	1106	AJP	C12-C07	-12.93	1.32	1.56
6	A	1106	AJP	O77-C28	-12.79	1.16	1.43
5	C	1105	CLR	C12-C13	-12.23	1.32	1.54
6	A	1106	AJP	C18-C17	11.99	1.81	1.52
6	C	1106	AJP	C18-C17	11.96	1.81	1.52
5	A	1105	CLR	C12-C13	-11.85	1.33	1.54
6	C	1106	AJP	O31-C26	-11.15	1.13	1.41
5	A	1105	CLR	C20-C17	-11.09	1.35	1.54
3	C	1101	ZK1	CAU-CAT	-11.07	1.38	1.53
5	C	1105	CLR	C20-C17	-10.92	1.35	1.54
3	A	1101	ZK1	CAU-CAT	-10.86	1.38	1.53
6	C	1106	AJP	O77-C28	-10.47	1.21	1.43
3	B	1101	ZK1	CAU-CAT	-10.25	1.39	1.53
3	D	1101	ZK1	CAU-CAT	-10.23	1.39	1.53
5	A	1105	CLR	C7-C6	10.08	1.70	1.50
5	C	1105	CLR	C7-C6	10.07	1.70	1.50
6	A	1106	AJP	C81-C12	9.96	1.70	1.54
6	C	1106	AJP	C81-C12	9.90	1.70	1.54
6	A	1106	AJP	C07-C06	-9.71	1.26	1.54
6	C	1106	AJP	C07-C06	-9.62	1.27	1.54
5	C	1105	CLR	C15-C14	9.46	1.73	1.54
5	A	1105	CLR	C15-C14	9.41	1.73	1.54
5	C	1105	CLR	C10-C5	-9.26	1.35	1.52
6	C	1106	AJP	C20-C15	9.17	1.72	1.56
6	A	1106	AJP	C20-C15	9.17	1.72	1.56
5	A	1105	CLR	C10-C5	-9.01	1.35	1.52
6	C	1106	AJP	C80-C20	8.99	1.69	1.54
5	A	1105	CLR	C4-C5	8.93	1.69	1.51
5	A	1105	CLR	C13-C14	8.83	1.71	1.55
5	C	1105	CLR	C4-C5	8.83	1.69	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1101	ZK1	OAA-CAT	8.82	1.40	1.23
5	C	1105	CLR	C16-C15	8.80	1.78	1.54
6	A	1106	AJP	O31-C26	-8.80	1.19	1.41
3	B	1101	ZK1	OAA-CAT	8.75	1.40	1.23
5	A	1105	CLR	C16-C15	8.74	1.77	1.54
5	C	1105	CLR	C13-C14	8.74	1.71	1.55
6	A	1106	AJP	C80-C20	8.73	1.68	1.54
5	A	1105	CLR	C13-C17	8.68	1.71	1.55
5	C	1105	CLR	C13-C17	8.56	1.70	1.55
3	A	1101	ZK1	OAA-CAT	8.54	1.39	1.23
3	C	1101	ZK1	OAA-CAT	8.44	1.39	1.23
3	B	1101	ZK1	OAB-CAU	8.19	1.39	1.23
3	D	1101	ZK1	OAB-CAU	8.15	1.39	1.23
3	A	1101	ZK1	OAB-CAU	8.06	1.39	1.23
3	C	1101	ZK1	OAB-CAU	8.04	1.39	1.23
5	A	1105	CLR	C16-C17	6.81	1.68	1.54
5	C	1105	CLR	C16-C17	6.61	1.67	1.54
6	A	1106	AJP	C32-C30	-6.54	1.35	1.51
6	C	1106	AJP	C32-C30	-6.12	1.36	1.51
6	A	1106	AJP	C13-C14	-6.11	1.41	1.53
6	C	1106	AJP	C13-C14	-6.01	1.41	1.53
5	C	1105	CLR	C1-C10	5.39	1.64	1.54
6	C	1106	AJP	C01-C02	5.25	1.69	1.52
6	A	1106	AJP	C01-C02	5.23	1.69	1.52
5	A	1105	CLR	C1-C10	5.18	1.63	1.54
6	C	1106	AJP	O84-C85	5.10	1.51	1.43
6	A	1106	AJP	O84-C85	4.95	1.50	1.43
6	C	1106	AJP	C04-C05	-4.85	1.44	1.51
6	A	1106	AJP	C04-C05	-4.71	1.44	1.51
6	A	1106	AJP	C18-C19	-4.69	1.41	1.53
6	C	1106	AJP	C18-C19	-4.63	1.42	1.53
3	C	1101	ZK1	CAW-NAY	-4.39	1.33	1.41
3	A	1101	ZK1	CAW-NAY	-4.34	1.33	1.41
3	D	1101	ZK1	CAW-NAY	-4.31	1.33	1.41
3	B	1101	ZK1	CAW-NAY	-4.27	1.33	1.41
3	C	1101	ZK1	CAU-NAY	-4.19	1.30	1.38
5	C	1105	CLR	C22-C20	4.16	1.64	1.54
3	A	1101	ZK1	CAU-NAY	-4.15	1.30	1.38
5	A	1105	CLR	C2-C3	-4.14	1.42	1.51
5	A	1105	CLR	C22-C20	4.12	1.64	1.54
5	C	1105	CLR	C2-C3	-3.96	1.42	1.51
6	A	1106	AJP	C26-C27	-3.95	1.40	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1105	CLR	C11-C9	3.95	1.60	1.53
3	B	1101	ZK1	CAU-NAY	-3.93	1.31	1.38
3	D	1101	ZK1	CAU-NAY	-3.92	1.31	1.38
3	A	1101	ZK1	CAV-NAP	-3.85	1.33	1.39
3	C	1101	ZK1	CAV-NAP	-3.85	1.33	1.39
3	B	1101	ZK1	CAV-NAP	-3.80	1.33	1.39
3	D	1101	ZK1	CAV-NAP	-3.79	1.33	1.39
5	C	1105	CLR	C11-C9	3.77	1.60	1.53
5	A	1105	CLR	C6-C5	3.72	1.40	1.33
3	C	1101	ZK1	CAV-CAW	-3.68	1.36	1.40
3	A	1101	ZK1	CAV-CAW	-3.68	1.36	1.40
5	C	1105	CLR	C1-C2	3.62	1.60	1.53
5	A	1105	CLR	C1-C2	3.61	1.60	1.53
5	C	1105	CLR	C6-C5	3.58	1.40	1.33
4	C	1109	PCW	O3-C11	3.46	1.43	1.33
3	B	1101	ZK1	CAV-CAW	-3.45	1.36	1.40
3	D	1101	ZK1	CAV-CAW	-3.45	1.36	1.40
6	A	1106	AJP	C83-C06	3.44	1.60	1.53
4	A	1109	PCW	O3-C11	3.43	1.43	1.33
4	C	1107	PCW	O3-C11	3.43	1.43	1.33
4	A	1107	PCW	O3-C11	3.42	1.43	1.33
4	D	1102	PCW	O3-C11	3.37	1.43	1.33
6	A	1106	AJP	O79-C22	3.35	1.50	1.43
3	A	1101	ZK1	CAT-NAP	-3.30	1.31	1.35
3	C	1101	ZK1	CAT-NAP	-3.28	1.31	1.35
4	B	1102	PCW	O3-C11	3.28	1.42	1.33
4	C	1102	PCW	O3-C11	3.28	1.42	1.33
4	A	1102	PCW	O3-C11	3.28	1.42	1.33
4	C	1103	PCW	O3-C11	3.24	1.42	1.33
4	A	1103	PCW	O3-C11	3.23	1.42	1.33
6	C	1106	AJP	O79-C22	3.18	1.50	1.43
4	B	1104	PCW	O3-C11	3.15	1.42	1.33
4	D	1104	PCW	O3-C11	3.12	1.42	1.33
4	F	202	PCW	O3-C11	3.11	1.42	1.33
4	E	202	PCW	O3-C11	3.07	1.42	1.33
5	A	1105	CLR	C18-C13	3.06	1.59	1.54
6	C	1106	AJP	C26-C27	-3.06	1.43	1.52
4	B	1103	PCW	O2-C31	3.03	1.42	1.34
4	B	1104	PCW	O2-C31	3.02	1.42	1.34
4	D	1104	PCW	O2-C31	2.97	1.42	1.34
6	C	1106	AJP	C83-C06	2.97	1.59	1.53
3	B	1101	ZK1	CAT-NAP	-2.96	1.31	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	1103	PCW	O2-C31	2.96	1.42	1.34
4	D	1103	PCW	O2-C31	2.96	1.42	1.34
3	D	1101	ZK1	CAT-NAP	-2.95	1.31	1.35
4	A	1103	PCW	O2-C31	2.95	1.42	1.34
4	C	1109	PCW	O2-C31	2.94	1.42	1.34
4	E	202	PCW	O2-C31	2.94	1.42	1.34
4	F	202	PCW	O2-C31	2.92	1.42	1.34
4	D	1102	PCW	O2-C31	2.91	1.42	1.34
4	B	1102	PCW	O2-C31	2.86	1.42	1.34
4	C	1102	PCW	O2-C31	2.85	1.42	1.34
4	A	1102	PCW	O2-C2	-2.84	1.39	1.46
4	A	1102	PCW	O2-C31	2.83	1.42	1.34
5	C	1105	CLR	C18-C13	2.83	1.59	1.54
4	C	1102	PCW	O2-C2	-2.82	1.40	1.46
4	A	1109	PCW	O2-C31	2.80	1.42	1.34
4	C	1107	PCW	O2-C31	2.78	1.42	1.34
4	D	1104	PCW	O2-C2	-2.76	1.40	1.46
4	F	202	PCW	O2-C2	-2.75	1.40	1.46
4	A	1107	PCW	O2-C31	2.75	1.42	1.34
4	B	1102	PCW	O2-C2	-2.74	1.40	1.46
4	A	1109	PCW	O2-C2	-2.74	1.40	1.46
4	C	1107	PCW	O2-C2	-2.74	1.40	1.46
4	D	1102	PCW	O2-C2	-2.72	1.40	1.46
4	E	202	PCW	O2-C2	-2.72	1.40	1.46
4	A	1107	PCW	O2-C2	-2.72	1.40	1.46
4	B	1104	PCW	O2-C2	-2.70	1.40	1.46
4	C	1103	PCW	O2-C2	-2.63	1.40	1.46
4	A	1103	PCW	O2-C2	-2.61	1.40	1.46
4	C	1109	PCW	O2-C2	-2.60	1.40	1.46
6	A	1106	AJP	C16-C15	-2.58	1.48	1.53
6	C	1106	AJP	C16-C15	-2.46	1.49	1.53
5	C	1105	CLR	C4-C3	2.37	1.56	1.52
6	C	1106	AJP	O84-C05	2.37	1.45	1.42
5	A	1105	CLR	C10-C9	2.36	1.59	1.56
4	D	1103	PCW	O2-C2	-2.32	1.41	1.46
4	B	1103	PCW	O2-C2	-2.19	1.41	1.46
5	A	1105	CLR	C4-C3	2.19	1.56	1.52
5	C	1105	CLR	C10-C9	2.15	1.59	1.56
4	E	202	PCW	P-O4P	2.14	1.67	1.59
4	F	202	PCW	P-O4P	2.14	1.67	1.59
3	C	1101	ZK1	PBA-OAE	-2.12	1.50	1.55
4	C	1103	PCW	P-O3P	2.11	1.67	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1103	PCW	P-O3P	2.09	1.67	1.59
4	A	1109	PCW	P-O4P	2.09	1.67	1.59
4	A	1102	PCW	P-O4P	2.09	1.67	1.59
3	A	1101	ZK1	PBA-OAE	-2.08	1.50	1.55
4	D	1104	PCW	P-O4P	2.07	1.67	1.59
4	C	1107	PCW	P-O4P	2.07	1.67	1.59
4	C	1102	PCW	P-O4P	2.07	1.67	1.59
6	C	1106	AJP	C24-C23	2.07	1.56	1.52
3	D	1101	ZK1	PBA-OAD	-2.07	1.50	1.55
3	C	1101	ZK1	PBA-OAD	-2.06	1.50	1.55
4	C	1103	PCW	P-O4P	2.05	1.67	1.59
4	A	1107	PCW	P-O4P	2.05	1.67	1.59
4	A	1103	PCW	P-O4P	2.05	1.67	1.59
4	B	1104	PCW	P-O4P	2.05	1.67	1.59
4	C	1109	PCW	P-O4P	2.04	1.67	1.59
3	B	1101	ZK1	PBA-OAD	-2.03	1.50	1.55
4	C	1109	PCW	P-O3P	2.02	1.67	1.59
3	A	1101	ZK1	PBA-OAD	-2.02	1.50	1.55

All (216) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1105	CLR	C18-C13-C17	-12.88	88.31	111.68
5	C	1105	CLR	C18-C13-C17	-11.67	90.52	111.68
6	A	1106	AJP	C04-C05-C06	10.38	134.46	115.66
6	C	1106	AJP	C04-C05-C06	10.25	134.22	115.66
6	A	1106	AJP	O78-C27-C28	9.43	129.29	110.05
5	A	1105	CLR	C4-C5-C6	-8.75	108.71	120.57
5	C	1105	CLR	C4-C5-C6	-8.51	109.03	120.57
6	C	1106	AJP	C26-O31-C30	8.23	122.25	113.13
6	C	1106	AJP	C83-C06-C05	-8.17	101.77	114.94
5	A	1105	CLR	C19-C10-C9	-8.16	102.51	111.66
6	C	1106	AJP	C13-C12-C07	8.04	126.80	115.36
5	C	1105	CLR	C19-C10-C9	-7.88	102.82	111.66
6	A	1106	AJP	C13-C12-C07	7.73	126.37	115.36
5	A	1105	CLR	C12-C13-C17	7.72	127.97	116.60
6	A	1106	AJP	C26-O31-C30	7.68	121.64	113.13
6	C	1106	AJP	C81-C12-C13	-7.18	100.03	110.61
6	A	1106	AJP	C83-C06-C05	-6.96	103.72	114.94
6	C	1106	AJP	O78-C27-C26	-6.83	93.79	110.08
5	A	1105	CLR	C10-C5-C6	-6.83	112.95	122.93
5	A	1105	CLR	C11-C12-C13	6.73	124.10	112.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	1105	CLR	C11-C12-C13	6.69	124.04	112.74
5	C	1105	CLR	C10-C5-C6	-6.64	113.24	122.93
5	A	1105	CLR	C7-C6-C5	-6.63	113.83	125.02
6	C	1106	AJP	O09-C05-C06	-6.60	95.78	104.56
5	C	1105	CLR	C12-C13-C17	6.59	126.30	116.60
6	A	1106	AJP	C81-C12-C13	-6.58	100.91	110.61
5	C	1105	CLR	C7-C6-C5	-6.55	113.96	125.02
6	A	1106	AJP	O09-C05-C06	-6.51	95.91	104.56
5	A	1105	CLR	C14-C8-C9	6.27	117.28	109.09
5	C	1105	CLR	C13-C14-C8	6.21	123.22	114.41
6	C	1106	AJP	O78-C27-C28	-6.13	97.55	110.05
5	C	1105	CLR	C14-C8-C9	6.07	117.02	109.09
5	A	1105	CLR	C13-C14-C8	6.05	123.00	114.41
6	A	1106	AJP	O09-C08-C10	5.99	122.32	110.20
6	C	1106	AJP	O09-C08-C10	5.93	122.19	110.20
6	A	1106	AJP	C81-C12-C07	-5.56	99.50	111.58
6	C	1106	AJP	C81-C12-C07	-5.50	99.63	111.58
5	A	1105	CLR	C11-C9-C10	5.48	119.84	113.08
6	C	1106	AJP	C21-C20-C19	5.15	112.16	107.23
3	B	1101	ZK1	CAN-NAX-CAM	5.12	123.08	111.57
6	A	1106	AJP	C24-C23-C22	5.09	116.39	111.07
3	D	1101	ZK1	CAN-NAX-CAM	5.09	123.01	111.57
4	D	1103	PCW	O2-C31-C32	5.05	122.39	111.48
3	B	1101	ZK1	CAI-CAR-NAX	-5.04	115.24	122.59
6	A	1106	AJP	O78-C27-C26	-5.00	98.15	110.08
3	D	1101	ZK1	CAI-CAR-NAX	-4.99	115.33	122.59
6	A	1106	AJP	O31-C30-C32	4.88	114.65	106.83
6	C	1106	AJP	C11-C12-C07	4.74	107.31	100.16
6	A	1106	AJP	C12-C11-C16	-4.58	107.52	113.90
4	D	1102	PCW	O2-C31-C32	4.43	121.06	111.48
4	B	1102	PCW	O2-C31-C32	4.42	121.05	111.48
6	A	1106	AJP	C21-C20-C19	4.41	111.44	107.23
6	C	1106	AJP	O31-C30-C32	4.40	113.89	106.83
6	A	1106	AJP	C11-C12-C07	4.37	106.75	100.16
3	B	1101	ZK1	CAS-CAR-NAX	4.35	124.90	119.92
3	A	1101	ZK1	CAN-NAX-CAM	4.34	121.34	111.57
3	C	1101	ZK1	CAN-NAX-CAM	4.30	121.25	111.57
4	A	1107	PCW	O2-C31-C32	4.28	120.75	111.48
4	B	1104	PCW	O2-C31-C32	4.27	120.73	111.48
3	D	1101	ZK1	CAS-CAR-NAX	4.27	124.81	119.92
3	C	1101	ZK1	CAI-CAR-NAX	-4.26	116.39	122.59
4	C	1107	PCW	O2-C31-C32	4.25	120.67	111.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1103	PCW	O2-C31-C32	4.24	120.65	111.48
6	C	1106	AJP	C12-C11-C16	-4.23	108.00	113.90
6	A	1106	AJP	C28-C29-C30	4.21	118.32	111.19
4	D	1104	PCW	O2-C31-C32	4.20	120.56	111.48
6	A	1106	AJP	O31-C30-C29	-4.17	103.78	110.14
4	C	1109	PCW	O2-C31-C32	4.09	120.32	111.48
5	C	1105	CLR	C8-C7-C6	4.05	118.37	112.76
3	A	1101	ZK1	CAI-CAR-NAX	-4.01	116.75	122.59
4	F	202	PCW	C8-N-C6	3.97	119.41	108.98
4	E	202	PCW	C8-N-C6	3.91	119.23	108.98
4	E	202	PCW	O2-C31-C32	3.90	119.93	111.48
6	A	1106	AJP	O09-C05-C04	-3.90	100.63	108.54
5	C	1105	CLR	C15-C14-C8	3.89	125.31	119.10
6	C	1106	AJP	C14-C13-C12	3.88	119.28	112.74
4	F	202	PCW	O2-C31-C32	3.88	119.87	111.48
4	A	1109	PCW	O2-C31-C32	3.87	119.85	111.48
4	A	1103	PCW	O2-C31-C32	3.86	119.84	111.48
6	C	1106	AJP	C21-C22-C23	3.86	115.63	110.46
6	C	1106	AJP	O31-C30-C29	-3.85	104.27	110.14
3	C	1101	ZK1	CAV-NAP-CAT	-3.84	119.44	124.82
4	D	1103	PCW	C8-N-C6	3.84	119.06	108.98
6	A	1106	AJP	C14-C13-C12	3.84	119.21	112.74
6	A	1106	AJP	C13-C12-C11	3.83	115.60	108.11
4	C	1103	PCW	O2-C31-C32	3.83	119.77	111.48
4	A	1102	PCW	O2-C31-C32	3.83	119.76	111.48
4	B	1102	PCW	C8-N-C6	3.83	119.03	108.98
4	D	1102	PCW	C8-N-C6	3.81	119.00	108.98
4	C	1102	PCW	O2-C31-C32	3.81	119.73	111.48
6	C	1106	AJP	O09-C05-C04	-3.81	100.81	108.54
5	C	1105	CLR	C12-C13-C14	3.80	112.94	107.25
4	A	1109	PCW	C8-N-C6	3.75	118.84	108.98
4	B	1103	PCW	C8-N-C6	3.75	118.83	108.98
3	A	1101	ZK1	CAV-NAP-CAT	-3.74	119.58	124.82
3	C	1101	ZK1	CAS-CAR-NAX	3.74	124.21	119.92
4	C	1109	PCW	C8-N-C6	3.72	118.75	108.98
6	A	1106	AJP	C81-C12-C11	-3.70	103.54	111.58
6	A	1106	AJP	C03-C02-C85	3.67	113.04	108.59
4	B	1104	PCW	C8-N-C6	3.65	118.56	108.98
4	C	1107	PCW	C8-N-C6	3.63	118.52	108.98
4	D	1104	PCW	C8-N-C6	3.63	118.52	108.98
4	C	1102	PCW	C8-N-C6	3.60	118.42	108.98
4	A	1102	PCW	C8-N-C6	3.59	118.42	108.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1105	CLR	C16-C15-C14	-3.59	98.12	105.14
3	D	1101	ZK1	CAV-NAP-CAT	-3.59	119.80	124.82
4	A	1107	PCW	C8-N-C6	3.58	118.39	108.98
6	C	1106	AJP	C81-C12-C11	-3.57	103.81	111.58
6	A	1106	AJP	O25-C26-C27	3.57	116.88	108.09
3	B	1101	ZK1	CAV-NAP-CAT	-3.54	119.86	124.82
6	C	1106	AJP	C13-C12-C11	3.53	115.00	108.11
6	C	1106	AJP	C24-C23-C22	3.51	114.74	111.07
5	C	1105	CLR	C16-C15-C14	-3.48	98.34	105.14
3	A	1101	ZK1	CAS-CAR-NAX	3.46	123.88	119.92
5	A	1105	CLR	C8-C7-C6	3.43	117.52	112.76
6	C	1106	AJP	C03-C02-C85	3.42	112.75	108.59
5	C	1105	CLR	C11-C9-C10	3.41	117.29	113.08
6	A	1106	AJP	C15-C20-C19	3.40	113.24	108.51
6	A	1106	AJP	O77-C28-C29	3.40	118.30	109.86
6	A	1106	AJP	C12-C07-C06	3.34	130.38	120.50
5	A	1105	CLR	C12-C13-C14	3.33	112.23	107.25
6	C	1106	AJP	C12-C07-C06	3.32	130.30	120.50
6	C	1106	AJP	C29-C28-C27	3.26	115.37	110.67
5	A	1105	CLR	C15-C14-C8	3.25	124.28	119.10
4	C	1103	PCW	C8-N-C6	3.24	117.48	108.98
4	C	1109	PCW	O3-C11-C12	3.21	121.63	111.83
4	A	1109	PCW	O3-C11-C12	3.19	121.55	111.83
4	A	1103	PCW	C8-N-C6	3.14	117.23	108.98
5	C	1105	CLR	C17-C13-C14	3.13	103.69	100.10
5	C	1105	CLR	C7-C8-C9	3.12	113.33	109.72
6	C	1106	AJP	O31-C26-C27	3.09	116.73	110.37
5	C	1105	CLR	C10-C9-C8	3.05	117.17	112.71
6	A	1106	AJP	O25-C26-O31	-3.05	102.67	110.69
6	A	1106	AJP	C05-C06-C07	-3.04	98.89	103.37
5	A	1105	CLR	C22-C20-C17	-3.00	104.11	110.33
5	A	1105	CLR	C1-C10-C9	2.98	112.67	108.74
4	D	1104	PCW	O3-C11-C12	2.96	120.86	111.83
3	C	1101	ZK1	FAG-CAZ-CAS	-2.96	107.40	112.65
5	A	1105	CLR	C17-C13-C14	2.95	103.48	100.10
6	C	1106	AJP	O84-C05-O09	-2.94	102.88	109.88
6	C	1106	AJP	C28-C29-C30	2.94	116.16	111.19
4	B	1104	PCW	O3-C11-C12	2.94	120.78	111.83
5	A	1105	CLR	C16-C17-C13	2.92	107.27	103.84
6	A	1106	AJP	C21-C22-C23	2.91	114.35	110.46
4	C	1107	PCW	O3-C11-C12	2.91	120.69	111.83
6	C	1106	AJP	C15-C20-C19	2.90	112.54	108.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1101	ZK1	FAG-CAZ-CAS	-2.87	107.57	112.65
4	A	1107	PCW	O3-C11-C12	2.86	120.56	111.83
3	B	1101	ZK1	CAT-CAU-NAY	2.86	120.51	117.41
4	A	1103	PCW	O3-C11-C12	2.85	120.52	111.83
6	C	1106	AJP	O25-C26-O31	-2.84	103.22	110.69
3	D	1101	ZK1	CAT-CAU-NAY	2.80	120.45	117.41
3	A	1101	ZK1	CAT-CAU-NAY	2.79	120.44	117.41
5	A	1105	CLR	C7-C8-C9	2.78	112.94	109.72
4	C	1103	PCW	O3-C11-C12	2.75	120.23	111.83
3	B	1101	ZK1	CAW-NAY-CAU	-2.74	119.46	122.84
3	B	1101	ZK1	OAA-CAT-CAU	2.74	121.26	119.21
6	C	1106	AJP	O77-C28-C29	2.73	116.66	109.86
5	C	1105	CLR	C12-C11-C9	2.72	117.76	113.14
3	C	1101	ZK1	CAU-CAT-NAP	2.72	120.23	117.46
5	C	1105	CLR	C22-C20-C17	-2.71	104.71	110.33
3	C	1101	ZK1	CAT-CAU-NAY	2.71	120.35	117.41
3	B	1101	ZK1	CAO-NAY-CAU	2.70	119.30	116.55
6	C	1106	AJP	C80-C20-C15	-2.70	107.55	111.18
3	D	1101	ZK1	CAW-NAY-CAU	-2.69	119.53	122.84
5	A	1105	CLR	C10-C9-C8	2.69	116.64	112.71
3	D	1101	ZK1	OAA-CAT-CAU	2.68	121.22	119.21
6	A	1106	AJP	C80-C20-C21	-2.66	105.08	108.99
4	E	202	PCW	O3-C11-C12	2.65	119.92	111.83
4	F	202	PCW	O3-C11-C12	2.64	119.88	111.83
3	D	1101	ZK1	CAO-NAY-CAU	2.63	119.22	116.55
6	C	1106	AJP	C03-C04-C05	2.58	115.97	111.93
6	A	1106	AJP	O84-C05-O09	-2.56	103.79	109.88
6	A	1106	AJP	C03-C04-C05	2.53	115.90	111.93
6	A	1106	AJP	C17-C16-C11	2.52	115.84	112.29
3	C	1101	ZK1	CAW-NAY-CAU	-2.49	119.78	122.84
3	A	1101	ZK1	CAU-CAT-NAP	2.48	120.00	117.46
4	A	1102	PCW	O3-C11-C12	2.47	119.37	111.83
3	A	1101	ZK1	CAW-NAY-CAU	-2.47	119.80	122.84
6	C	1106	AJP	C80-C20-C21	-2.46	105.38	108.99
5	C	1105	CLR	C16-C17-C13	2.46	106.73	103.84
4	C	1102	PCW	O3-C11-C12	2.45	119.30	111.83
6	A	1106	AJP	O09-C08-C07	-2.44	98.46	104.08
6	A	1106	AJP	C20-C15-C16	-2.43	109.96	112.43
5	A	1105	CLR	C12-C11-C9	2.42	117.25	113.14
6	A	1106	AJP	C14-C15-C20	-2.42	111.19	113.91
5	C	1105	CLR	C4-C5-C10	-2.42	113.33	116.42
4	D	1102	PCW	O3-C11-C12	2.40	119.14	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	1106	AJP	C80-C20-C15	-2.40	107.96	111.18
6	C	1106	AJP	C17-C16-C11	2.38	115.65	112.29
3	C	1101	ZK1	CAO-NAY-CAU	2.37	118.96	116.55
4	B	1102	PCW	O3-C11-C12	2.35	119.01	111.83
6	A	1106	AJP	O84-C85-C02	-2.35	109.16	112.17
5	A	1105	CLR	C21-C20-C22	-2.34	106.71	110.34
5	C	1105	CLR	C21-C20-C22	-2.33	106.72	110.34
5	C	1105	CLR	C9-C10-C5	2.33	113.07	109.65
3	A	1101	ZK1	CAO-NAY-CAU	2.28	118.87	116.55
3	D	1101	ZK1	CAU-CAT-NAP	2.26	119.77	117.46
3	B	1101	ZK1	FAG-CAZ-CAS	-2.24	108.68	112.65
6	A	1106	AJP	C29-C30-C32	2.24	116.64	112.50
5	A	1105	CLR	C9-C10-C5	2.23	112.91	109.65
3	B	1101	ZK1	CAU-CAT-NAP	2.22	119.73	117.46
6	C	1106	AJP	O09-C08-C07	-2.21	98.99	104.08
3	D	1101	ZK1	FAG-CAZ-CAS	-2.19	108.77	112.65
5	A	1105	CLR	C2-C1-C10	-2.14	108.23	112.78
5	C	1105	CLR	C1-C2-C3	2.12	113.30	110.48
4	A	1109	PCW	C2-O2-C31	-2.11	112.74	117.80
5	C	1105	CLR	C1-C10-C9	2.11	111.53	108.74
3	D	1101	ZK1	FAF-CAZ-CAS	-2.09	108.94	112.65
6	C	1106	AJP	O84-C85-C02	-2.08	109.50	112.17
6	C	1106	AJP	C20-C15-C16	-2.07	110.33	112.43
6	A	1106	AJP	C14-C15-C16	2.06	114.65	111.78
6	C	1106	AJP	C11-C10-C08	2.05	107.49	103.05
6	C	1106	AJP	C18-C19-C20	2.04	115.74	112.31
4	A	1107	PCW	C2-O2-C31	-2.04	112.91	117.80
4	C	1107	PCW	C2-O2-C31	-2.03	112.93	117.80

All (28) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	1105	CLR	C9
5	A	1105	CLR	C17
5	C	1105	CLR	C9
5	C	1105	CLR	C17
6	A	1106	AJP	C05
6	A	1106	AJP	C19
6	A	1106	AJP	C26
6	A	1106	AJP	C16
6	A	1106	AJP	C02
6	A	1106	AJP	C27

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Mol	Chain	Res	Type	Atom
6	A	1106	AJP	C20
6	A	1106	AJP	C06
6	A	1106	AJP	C23
6	A	1106	AJP	C12
6	A	1106	AJP	C11
6	A	1106	AJP	C15
6	C	1106	AJP	C05
6	C	1106	AJP	C19
6	C	1106	AJP	C26
6	C	1106	AJP	C16
6	C	1106	AJP	C02
6	C	1106	AJP	C23
6	C	1106	AJP	C27
6	C	1106	AJP	C20
6	C	1106	AJP	C06
6	C	1106	AJP	C12
6	C	1106	AJP	C11
6	C	1106	AJP	C15

All (460) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1102	PCW	C32-C31-O2-C2
4	A	1102	PCW	C4-O4P-P-O1P
4	A	1102	PCW	C4-O4P-P-O3P
4	A	1103	PCW	C1-O3P-P-O1P
4	A	1103	PCW	C1-O3P-P-O2P
4	A	1103	PCW	C1-O3P-P-O4P
4	A	1107	PCW	C1-O3P-P-O1P
4	A	1107	PCW	C1-O3P-P-O2P
4	A	1107	PCW	C1-O3P-P-O4P
4	A	1107	PCW	C4-O4P-P-O1P
4	A	1107	PCW	C4-O4P-P-O2P
4	A	1107	PCW	C4-O4P-P-O3P
4	A	1109	PCW	O4P-C4-C5-N
4	A	1109	PCW	C12-C11-O3-C3
4	A	1109	PCW	O11-C11-O3-C3
4	A	1109	PCW	C32-C31-O2-C2
4	A	1109	PCW	C1-O3P-P-O1P
4	A	1109	PCW	C1-O3P-P-O2P
4	A	1109	PCW	C1-O3P-P-O4P
4	A	1109	PCW	C4-O4P-P-O1P

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Mol	Chain	Res	Type	Atoms
4	A	1109	PCW	C4-O4P-P-O2P
4	A	1109	PCW	C4-O4P-P-O3P
4	B	1102	PCW	O4P-C4-C5-N
4	B	1102	PCW	C32-C31-O2-C2
4	B	1102	PCW	O31-C31-O2-C2
4	B	1102	PCW	C1-O3P-P-O1P
4	B	1102	PCW	C1-O3P-P-O4P
4	B	1102	PCW	C4-O4P-P-O1P
4	B	1102	PCW	C4-O4P-P-O3P
4	B	1103	PCW	C5-C4-O4P-P
4	B	1103	PCW	C32-C31-O2-C2
4	B	1103	PCW	C1-O3P-P-O1P
4	B	1103	PCW	C4-O4P-P-O1P
4	B	1103	PCW	C4-O4P-P-O3P
4	B	1104	PCW	C32-C31-O2-C2
4	B	1105	PCW	C20-C21-C22-C23
4	C	1102	PCW	C32-C31-O2-C2
4	C	1102	PCW	C4-O4P-P-O1P
4	C	1102	PCW	C4-O4P-P-O3P
4	C	1103	PCW	C1-O3P-P-O1P
4	C	1103	PCW	C1-O3P-P-O2P
4	C	1103	PCW	C1-O3P-P-O4P
4	C	1103	PCW	C4-O4P-P-O1P
4	C	1103	PCW	C4-O4P-P-O2P
4	C	1103	PCW	C4-O4P-P-O3P
4	C	1107	PCW	C1-O3P-P-O1P
4	C	1107	PCW	C1-O3P-P-O2P
4	C	1107	PCW	C1-O3P-P-O4P
4	C	1107	PCW	C4-O4P-P-O1P
4	C	1107	PCW	C4-O4P-P-O2P
4	C	1107	PCW	C4-O4P-P-O3P
4	C	1109	PCW	O4P-C4-C5-N
4	C	1109	PCW	C12-C11-O3-C3
4	C	1109	PCW	O11-C11-O3-C3
4	C	1109	PCW	C32-C31-O2-C2
4	C	1109	PCW	C1-O3P-P-O1P
4	C	1109	PCW	C1-O3P-P-O4P
4	C	1109	PCW	C4-O4P-P-O1P
4	C	1109	PCW	C4-O4P-P-O2P
4	C	1109	PCW	C4-O4P-P-O3P
4	D	1102	PCW	O4P-C4-C5-N
4	D	1102	PCW	O31-C31-O2-C2

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Mol	Chain	Res	Type	Atoms
4	D	1102	PCW	C1-O3P-P-O4P
4	D	1102	PCW	C4-O4P-P-O1P
4	D	1102	PCW	C4-O4P-P-O3P
4	D	1103	PCW	C5-C4-O4P-P
4	D	1103	PCW	C32-C31-O2-C2
4	D	1103	PCW	C1-O3P-P-O1P
4	D	1103	PCW	C4-O4P-P-O1P
4	D	1103	PCW	C4-O4P-P-O3P
4	D	1104	PCW	O3P-C1-C2-O2
4	D	1104	PCW	C32-C31-O2-C2
4	D	1104	PCW	O31-C31-O2-C2
4	D	1105	PCW	C20-C21-C22-C23
4	E	202	PCW	O4P-C4-C5-N
4	E	202	PCW	C4-O4P-P-O2P
4	F	202	PCW	O4P-C4-C5-N
4	E	202	PCW	O11-C11-O3-C3
4	F	202	PCW	O11-C11-O3-C3
4	A	1102	PCW	O31-C31-O2-C2
4	A	1109	PCW	O31-C31-O2-C2
4	B	1103	PCW	O31-C31-O2-C2
4	B	1104	PCW	O31-C31-O2-C2
4	C	1102	PCW	O31-C31-O2-C2
4	C	1109	PCW	O31-C31-O2-C2
4	D	1103	PCW	O31-C31-O2-C2
4	E	202	PCW	O31-C31-O2-C2
4	F	202	PCW	O31-C31-O2-C2
4	A	1103	PCW	C12-C11-O3-C3
4	D	1102	PCW	C32-C31-O2-C2
4	E	202	PCW	C32-C31-O2-C2
4	F	202	PCW	C32-C31-O2-C2
4	B	1103	PCW	O11-C11-O3-C3
4	D	1103	PCW	O11-C11-O3-C3
4	B	1102	PCW	C12-C11-O3-C3
4	D	1102	PCW	C12-C11-O3-C3
4	E	202	PCW	C12-C11-O3-C3
4	F	202	PCW	C12-C11-O3-C3
4	A	1107	PCW	C12-C11-O3-C3
4	C	1103	PCW	C12-C11-O3-C3
4	C	1107	PCW	C12-C11-O3-C3
4	A	1103	PCW	O11-C11-O3-C3
4	D	1102	PCW	O11-C11-O3-C3
4	B	1103	PCW	C12-C11-O3-C3

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Mol	Chain	Res	Type	Atoms
4	D	1103	PCW	C12-C11-O3-C3
4	B	1102	PCW	O11-C11-O3-C3
4	C	1103	PCW	O11-C11-O3-C3
4	C	1103	PCW	C12-C13-C14-C15
4	A	1107	PCW	O11-C11-O3-C3
4	C	1107	PCW	O11-C11-O3-C3
4	A	1103	PCW	C12-C13-C14-C15
5	A	1105	CLR	C17-C20-C22-C23
5	A	1105	CLR	C21-C20-C22-C23
4	A	1107	PCW	C32-C33-C34-C35
4	C	1103	PCW	C4-C5-N-C7
4	C	1103	PCW	C4-C5-N-C8
4	B	1104	PCW	O3P-C1-C2-O2
7	A	1111	SPD	N6-C7-C8-C9
4	C	1103	PCW	C31-C32-C33-C34
4	C	1107	PCW	C32-C33-C34-C35
4	A	1103	PCW	C31-C32-C33-C34
4	D	1103	PCW	C31-C32-C33-C34
4	E	202	PCW	C11-C12-C13-C14
4	F	202	PCW	C11-C12-C13-C14
4	B	1103	PCW	C33-C34-C35-C36
4	B	1104	PCW	C31-C32-C33-C34
4	D	1104	PCW	C31-C32-C33-C34
4	A	1109	PCW	C11-C12-C13-C14
4	C	1109	PCW	C11-C12-C13-C14
4	C	1103	PCW	C17-C18-C19-C20
4	A	1102	PCW	C31-C32-C33-C34
4	B	1103	PCW	C3-C2-O2-C31
4	D	1103	PCW	C3-C2-O2-C31
4	D	1103	PCW	C33-C34-C35-C36
4	D	1102	PCW	C34-C35-C36-C37
4	A	1103	PCW	C34-C35-C36-C37
4	A	1108	PCW	C14-C15-C16-C17
4	B	1102	PCW	C35-C36-C37-C38
4	B	1104	PCW	C33-C34-C35-C36
4	C	1102	PCW	C35-C36-C37-C38
4	C	1108	PCW	C14-C15-C16-C17
4	A	1102	PCW	C35-C36-C37-C38
4	D	1104	PCW	C33-C34-C35-C36
4	C	1102	PCW	C31-C32-C33-C34
4	F	202	PCW	C32-C33-C34-C35
4	C	1103	PCW	C32-C31-O2-C2

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Mol	Chain	Res	Type	Atoms
4	A	1102	PCW	C34-C35-C36-C37
4	A	1107	PCW	C24-C25-C26-C27
4	C	1102	PCW	C34-C35-C36-C37
4	D	1102	PCW	C35-C36-C37-C38
4	B	1105	PCW	C15-C16-C17-C18
4	C	1107	PCW	C24-C25-C26-C27
4	E	202	PCW	C34-C35-C36-C37
4	A	1103	PCW	C11-C12-C13-C14
4	B	1103	PCW	C31-C32-C33-C34
4	C	1103	PCW	C11-C12-C13-C14
4	E	202	PCW	C12-C13-C14-C15
4	E	202	PCW	C32-C33-C34-C35
4	A	1103	PCW	C32-C33-C34-C35
4	C	1109	PCW	C31-C32-C33-C34
4	B	1104	PCW	C34-C35-C36-C37
4	E	202	PCW	C33-C34-C35-C36
4	F	202	PCW	C12-C13-C14-C15
4	A	1103	PCW	C13-C14-C15-C16
4	A	1109	PCW	C34-C35-C36-C37
4	C	1103	PCW	C41-C42-C43-C44
4	D	1104	PCW	C34-C35-C36-C37
4	C	1109	PCW	C12-C13-C14-C15
4	D	1105	PCW	C15-C16-C17-C18
4	C	1103	PCW	C33-C34-C35-C36
5	A	1105	CLR	C23-C24-C25-C27
4	A	1103	PCW	C32-C31-O2-C2
4	C	1103	PCW	O31-C31-O2-C2
4	A	1109	PCW	C36-C37-C38-C39
4	C	1108	PCW	C16-C17-C18-C19
4	C	1107	PCW	C15-C16-C17-C18
4	B	1103	PCW	C32-C33-C34-C35
4	E	202	PCW	C13-C14-C15-C16
4	C	1103	PCW	C4-C5-N-C6
4	A	1109	PCW	C12-C13-C14-C15
4	F	202	PCW	C13-C14-C15-C16
4	A	1109	PCW	C32-C33-C34-C35
4	A	1103	PCW	C33-C34-C35-C36
4	E	202	PCW	C14-C15-C16-C17
4	F	202	PCW	C14-C15-C16-C17
4	E	201	PCW	C15-C16-C17-C18
5	C	1105	CLR	C23-C24-C25-C27
4	C	1102	PCW	C13-C14-C15-C16

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Mol	Chain	Res	Type	Atoms
4	C	1109	PCW	C34-C35-C36-C37
4	C	1109	PCW	C33-C34-C35-C36
4	A	1102	PCW	O2-C2-C3-O3
4	A	1108	PCW	C16-C17-C18-C19
4	C	1102	PCW	O2-C2-C3-O3
4	C	1109	PCW	C36-C37-C38-C39
4	F	201	PCW	C15-C16-C17-C18
4	A	1104	PCW	C19-C20-C21-C22
4	A	1103	PCW	C2-C1-O3P-P
4	C	1103	PCW	C2-C1-O3P-P
4	F	201	PCW	C13-C14-C15-C16
4	E	201	PCW	C13-C14-C15-C16
4	A	1102	PCW	C33-C34-C35-C36
4	A	1107	PCW	C14-C15-C16-C17
4	A	1107	PCW	C15-C16-C17-C18
4	C	1103	PCW	C34-C35-C36-C37
4	C	1110	PCW	C14-C15-C16-C17
4	C	1103	PCW	C14-C15-C16-C17
5	A	1105	CLR	C16-C17-C20-C21
5	C	1105	CLR	C16-C17-C20-C21
4	A	1107	PCW	C23-C24-C25-C26
4	B	1104	PCW	C15-C16-C17-C18
4	C	1107	PCW	C14-C15-C16-C17
4	A	1102	PCW	C13-C14-C15-C16
4	A	1103	PCW	O3P-C1-C2-C3
4	C	1103	PCW	O3P-C1-C2-C3
4	C	1109	PCW	O3P-C1-C2-C3
4	C	1107	PCW	C42-C43-C44-C45
4	A	1103	PCW	O31-C31-O2-C2
4	A	1109	PCW	C31-C32-C33-C34
4	B	1102	PCW	C34-C35-C36-C37
4	C	1109	PCW	C32-C33-C34-C35
4	A	1107	PCW	C13-C14-C15-C16
4	A	1109	PCW	C1-C2-C3-O3
4	C	1107	PCW	C1-C2-C3-O3
4	E	202	PCW	C1-C2-C3-O3
4	A	1103	PCW	C40-C41-C42-C43
4	C	1103	PCW	C16-C17-C18-C19
4	D	1102	PCW	C36-C37-C38-C39
4	C	1108	PCW	C13-C14-C15-C16
4	A	1107	PCW	C33-C34-C35-C36
4	A	1110	PCW	C14-C15-C16-C17

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Mol	Chain	Res	Type	Atoms
4	C	1104	PCW	C19-C20-C21-C22
4	A	1110	PCW	C20-C21-C22-C23
4	C	1110	PCW	C20-C21-C22-C23
4	C	1107	PCW	C13-C14-C15-C16
4	A	1109	PCW	C13-C14-C15-C16
4	A	1103	PCW	C41-C42-C43-C44
4	A	1108	PCW	C13-C14-C15-C16
4	B	1104	PCW	C13-C14-C15-C16
4	C	1107	PCW	C23-C24-C25-C26
4	E	202	PCW	C41-C42-C43-C44
4	A	1107	PCW	O3P-C1-C2-O2
4	C	1107	PCW	O3P-C1-C2-O2
4	C	1109	PCW	C13-C14-C15-C16
4	D	1104	PCW	C15-C16-C17-C18
4	F	202	PCW	C33-C34-C35-C36
4	F	202	PCW	C34-C35-C36-C37
4	C	1103	PCW	C13-C14-C15-C16
4	B	1104	PCW	O2-C2-C3-O3
4	D	1102	PCW	C33-C34-C35-C36
4	D	1104	PCW	C13-C14-C15-C16
4	D	1102	PCW	O3-C11-C12-C13
4	A	1103	PCW	C16-C17-C18-C19
4	A	1107	PCW	C31-C32-C33-C34
4	B	1102	PCW	O3-C11-C12-C13
4	D	1104	PCW	C11-C12-C13-C14
4	A	1109	PCW	C33-C34-C35-C36
4	E	201	PCW	C14-C15-C16-C17
4	B	1104	PCW	O3P-C1-C2-C3
4	D	1104	PCW	O3P-C1-C2-C3
4	E	202	PCW	C17-C18-C19-C20
4	F	202	PCW	C17-C18-C19-C20
4	F	201	PCW	C14-C15-C16-C17
4	A	1102	PCW	C1-C2-C3-O3
4	A	1107	PCW	C1-C2-C3-O3
4	B	1102	PCW	C1-C2-C3-O3
4	B	1104	PCW	C1-C2-C3-O3
4	C	1102	PCW	C1-C2-C3-O3
4	C	1109	PCW	C1-C2-C3-O3
4	D	1102	PCW	C1-C2-C3-O3
4	D	1104	PCW	C1-C2-C3-O3
4	F	202	PCW	C1-C2-C3-O3
4	A	1109	PCW	C15-C16-C17-C18

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Mol	Chain	Res	Type	Atoms
4	C	1102	PCW	C33-C34-C35-C36
4	C	1109	PCW	C15-C16-C17-C18
5	C	1105	CLR	C21-C20-C22-C23
4	A	1103	PCW	O3P-C1-C2-O2
4	C	1109	PCW	O3P-C1-C2-O2
4	D	1105	PCW	C16-C17-C18-C19
4	A	1107	PCW	O2-C2-C3-O3
4	D	1102	PCW	O2-C2-C3-O3
4	D	1104	PCW	O2-C2-C3-O3
4	D	1102	PCW	C12-C13-C14-C15
4	F	202	PCW	C39-C40-C41-C42
4	B	1102	PCW	C11-C12-C13-C14
4	F	202	PCW	C31-C32-C33-C34
4	A	1107	PCW	C42-C43-C44-C45
4	A	1103	PCW	C14-C15-C16-C17
4	E	202	PCW	C39-C40-C41-C42
4	A	1109	PCW	C39-C40-C41-C42
4	C	1109	PCW	C39-C40-C41-C42
3	A	1101	ZK1	NAY-CAO-PBA-OAD
3	A	1101	ZK1	NAY-CAO-PBA-OAE
3	B	1101	ZK1	NAY-CAO-PBA-OAD
3	B	1101	ZK1	NAY-CAO-PBA-OAE
3	C	1101	ZK1	NAY-CAO-PBA-OAD
3	C	1101	ZK1	NAY-CAO-PBA-OAE
3	D	1101	ZK1	NAY-CAO-PBA-OAD
3	D	1101	ZK1	NAY-CAO-PBA-OAE
4	A	1107	PCW	O3P-C1-C2-C3
4	B	1103	PCW	O3P-C1-C2-C3
4	C	1107	PCW	O3P-C1-C2-C3
5	C	1105	CLR	C23-C24-C25-C26
4	D	1105	PCW	C14-C15-C16-C17
4	D	1102	PCW	C11-C12-C13-C14
5	A	1105	CLR	C23-C24-C25-C26
4	A	1110	PCW	C15-C16-C17-C18
4	D	1103	PCW	C4-C5-N-C6
3	D	1101	ZK1	CAI-CAR-NAX-CAN
4	A	1103	PCW	C36-C37-C38-C39
4	B	1103	PCW	O3P-C1-C2-O2
4	C	1103	PCW	O3P-C1-C2-O2
4	B	1102	PCW	C5-C4-O4P-P
4	D	1102	PCW	C5-C4-O4P-P
4	D	1104	PCW	C32-C33-C34-C35

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Mol	Chain	Res	Type	Atoms
4	B	1102	PCW	C36-C37-C38-C39
4	E	202	PCW	O2-C2-C3-O3
4	B	1105	PCW	C14-C15-C16-C17
4	A	1103	PCW	C4-C5-N-C8
3	B	1101	ZK1	CAI-CAR-NAX-CAN
4	B	1102	PCW	C41-C42-C43-C44
4	A	1102	PCW	O4P-C4-C5-N
4	A	1107	PCW	O4P-C4-C5-N
4	B	1104	PCW	O4P-C4-C5-N
4	C	1102	PCW	O4P-C4-C5-N
4	C	1107	PCW	O4P-C4-C5-N
4	D	1104	PCW	O4P-C4-C5-N
3	A	1101	ZK1	CAI-CAR-NAX-CAN
3	C	1101	ZK1	CAI-CAR-NAX-CAN
4	C	1103	PCW	C40-C41-C42-C43
4	A	1109	PCW	O3P-C1-C2-C3
4	E	202	PCW	O3P-C1-C2-C3
4	E	202	PCW	C37-C38-C39-C40
4	F	202	PCW	C2-C1-O3P-P
4	A	1109	PCW	O3P-C1-C2-O2
4	E	202	PCW	O3P-C1-C2-O2
4	B	1105	PCW	C16-C17-C18-C19
4	A	1109	PCW	O2-C2-C3-O3
4	B	1102	PCW	O2-C2-C3-O3
4	C	1107	PCW	O2-C2-C3-O3
4	C	1109	PCW	O2-C2-C3-O3
4	F	202	PCW	O2-C2-C3-O3
4	A	1102	PCW	O11-C11-O3-C3
4	C	1102	PCW	O11-C11-O3-C3
4	A	1102	PCW	C1-O3P-P-O2P
4	A	1103	PCW	C4-O4P-P-O2P
4	B	1102	PCW	C1-O3P-P-O2P
4	B	1103	PCW	C1-O3P-P-O2P
4	B	1103	PCW	C1-O3P-P-O4P
4	B	1104	PCW	C1-O3P-P-O1P
4	B	1104	PCW	C4-O4P-P-O2P
4	B	1104	PCW	C4-O4P-P-O3P
4	C	1102	PCW	C1-O3P-P-O2P
4	C	1109	PCW	C1-O3P-P-O2P
4	D	1102	PCW	C1-O3P-P-O2P
4	D	1103	PCW	C1-O3P-P-O4P
4	D	1104	PCW	C4-O4P-P-O2P

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Mol	Chain	Res	Type	Atoms
4	D	1104	PCW	C4-O4P-P-O3P
4	E	202	PCW	C4-O4P-P-O1P
4	E	202	PCW	C4-O4P-P-O3P
4	F	202	PCW	C1-O3P-P-O1P
4	F	202	PCW	C1-O3P-P-O4P
4	F	202	PCW	C4-O4P-P-O1P
4	B	1104	PCW	C32-C33-C34-C35
4	D	1102	PCW	C15-C16-C17-C18
4	A	1102	PCW	C12-C11-O3-C3
4	D	1105	PCW	C19-C20-C21-C22
5	C	1105	CLR	C17-C20-C22-C23
4	B	1104	PCW	C19-C20-C21-C22
4	D	1104	PCW	C19-C20-C21-C22
4	D	1102	PCW	C13-C14-C15-C16
4	D	1104	PCW	C12-C13-C14-C15
4	F	202	PCW	C41-C42-C43-C44
4	C	1102	PCW	C12-C11-O3-C3
4	C	1102	PCW	C14-C15-C16-C17
4	B	1103	PCW	C36-C37-C38-C39
7	A	1111	SPD	C4-C5-N6-C7
4	B	1102	PCW	O11-C11-C12-C13
4	D	1102	PCW	O11-C11-C12-C13
4	D	1104	PCW	C12-C11-O3-C3
4	C	1103	PCW	C32-C33-C34-C35
4	C	1109	PCW	C14-C15-C16-C17
4	B	1105	PCW	C19-C20-C21-C22
4	C	1107	PCW	O3-C11-C12-C13
4	A	1109	PCW	C14-C15-C16-C17
4	A	1107	PCW	C19-C20-C21-C22
4	C	1107	PCW	C19-C20-C21-C22
4	F	202	PCW	C37-C38-C39-C40
5	C	1105	CLR	C22-C23-C24-C25
4	C	1107	PCW	C2-C1-O3P-P
4	A	1102	PCW	C37-C38-C39-C40
4	C	1102	PCW	C37-C38-C39-C40
4	D	1103	PCW	C4-C5-N-C7
4	F	202	PCW	O3P-C1-C2-O2
4	C	1103	PCW	C36-C37-C38-C39
4	D	1104	PCW	C36-C37-C38-C39
4	A	1107	PCW	C2-C1-O3P-P
4	D	1102	PCW	C2-C1-O3P-P
4	D	1103	PCW	C2-C1-O3P-P

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Mol	Chain	Res	Type	Atoms
4	E	202	PCW	C2-C1-O3P-P
4	B	1102	PCW	C33-C34-C35-C36
4	A	1103	PCW	C4-C5-N-C7
4	D	1102	PCW	C14-C15-C16-C17
4	A	1102	PCW	C42-C43-C44-C45
4	B	1104	PCW	C12-C13-C14-C15
4	B	1102	PCW	C2-C1-O3P-P
4	D	1104	PCW	O11-C11-O3-C3
3	A	1101	ZK1	NAY-CAO-PBA-OAC
3	B	1101	ZK1	NAY-CAO-PBA-OAC
3	C	1101	ZK1	NAY-CAO-PBA-OAC
3	D	1101	ZK1	NAY-CAO-PBA-OAC
4	D	1102	PCW	C39-C40-C41-C42
4	A	1107	PCW	O3-C11-C12-C13
4	D	1103	PCW	C36-C37-C38-C39
4	F	202	PCW	O3P-C1-C2-C3
4	A	1109	PCW	C37-C38-C39-C40
4	B	1104	PCW	C36-C37-C38-C39
4	A	1103	PCW	C37-C38-C39-C40
4	A	1110	PCW	C19-C20-C21-C22
4	C	1103	PCW	C37-C38-C39-C40
4	B	1102	PCW	C39-C40-C41-C42
4	E	201	PCW	C19-C20-C21-C22
4	F	201	PCW	C19-C20-C21-C22
4	C	1102	PCW	C40-C41-C42-C43
4	C	1110	PCW	C19-C20-C21-C22
4	B	1104	PCW	C2-C1-O3P-P
4	B	1103	PCW	C4-C5-N-C6
4	C	1107	PCW	C36-C37-C38-C39
4	B	1104	PCW	C37-C38-C39-C40
4	C	1104	PCW	C17-C18-C19-C20
4	C	1107	PCW	C5-C4-O4P-P
4	B	1102	PCW	C12-C13-C14-C15
4	A	1107	PCW	C36-C37-C38-C39
4	C	1109	PCW	C37-C38-C39-C40
4	C	1109	PCW	C35-C36-C37-C38
4	D	1103	PCW	C32-C33-C34-C35
7	A	1111	SPD	C8-C7-N6-C5
4	C	1110	PCW	C15-C16-C17-C18
4	B	1102	PCW	O2-C31-C32-C33
4	D	1102	PCW	O2-C31-C32-C33
4	D	1103	PCW	C4-C5-N-C8

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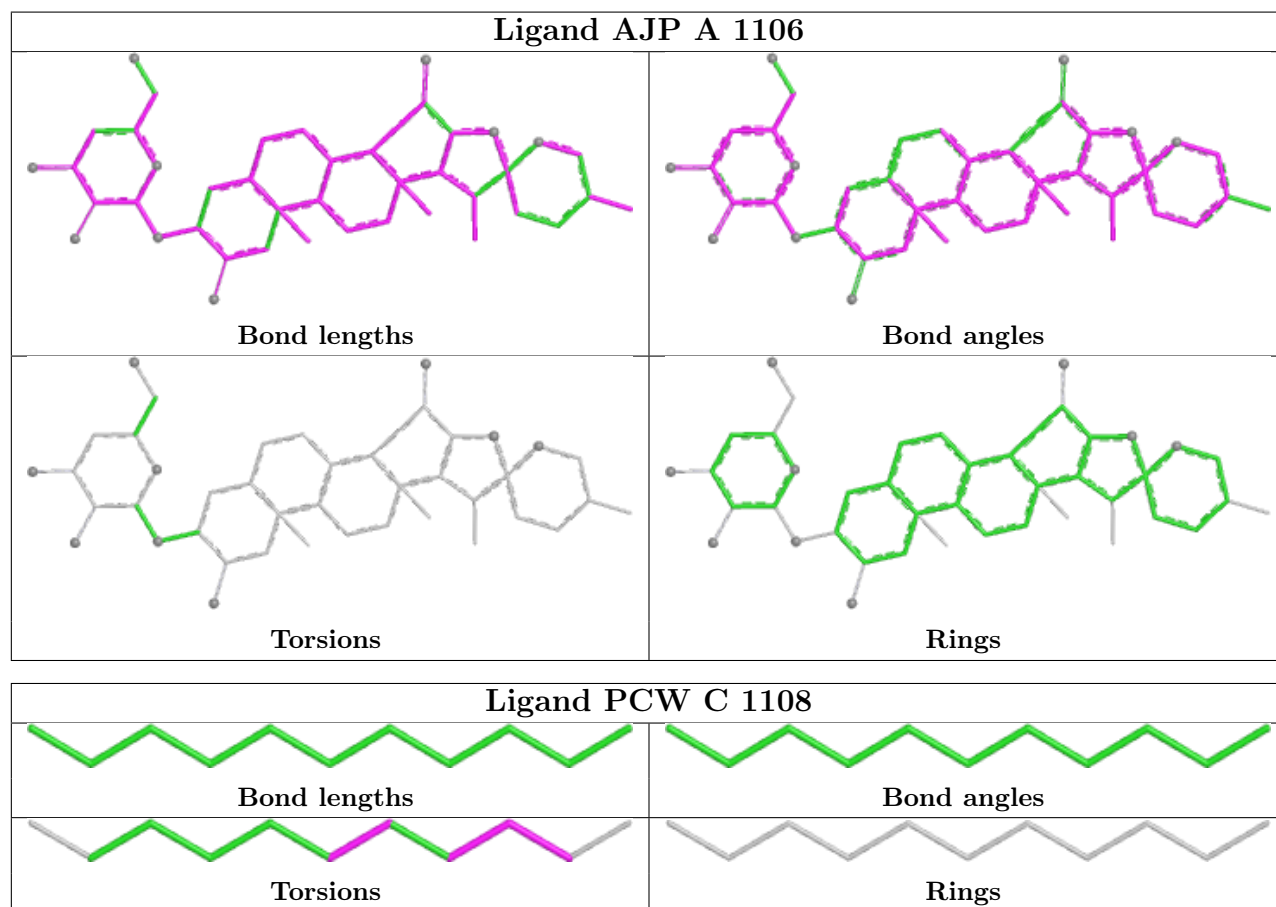
Mol	Chain	Res	Type	Atoms
4	A	1102	PCW	C14-C15-C16-C17
4	B	1102	PCW	C40-C41-C42-C43
4	D	1104	PCW	C37-C38-C39-C40
5	A	1105	CLR	C22-C23-C24-C25
4	A	1110	PCW	C13-C14-C15-C16
3	C	1101	ZK1	CAI-CAR-NAX-CAM
5	C	1105	CLR	C20-C22-C23-C24
4	C	1103	PCW	O3-C11-C12-C13
3	D	1101	ZK1	CAS-CAR-NAX-CAN
4	B	1104	PCW	C14-C15-C16-C17
4	B	1104	PCW	C35-C36-C37-C38
4	D	1104	PCW	C35-C36-C37-C38
4	D	1104	PCW	C14-C15-C16-C17
4	B	1102	PCW	O31-C31-C32-C33
4	D	1102	PCW	C41-C42-C43-C44
4	D	1102	PCW	O31-C31-C32-C33
4	D	1102	PCW	C40-C41-C42-C43
4	B	1102	PCW	C17-C18-C19-C20
4	C	1102	PCW	C11-C12-C13-C14
4	C	1103	PCW	C39-C40-C41-C42

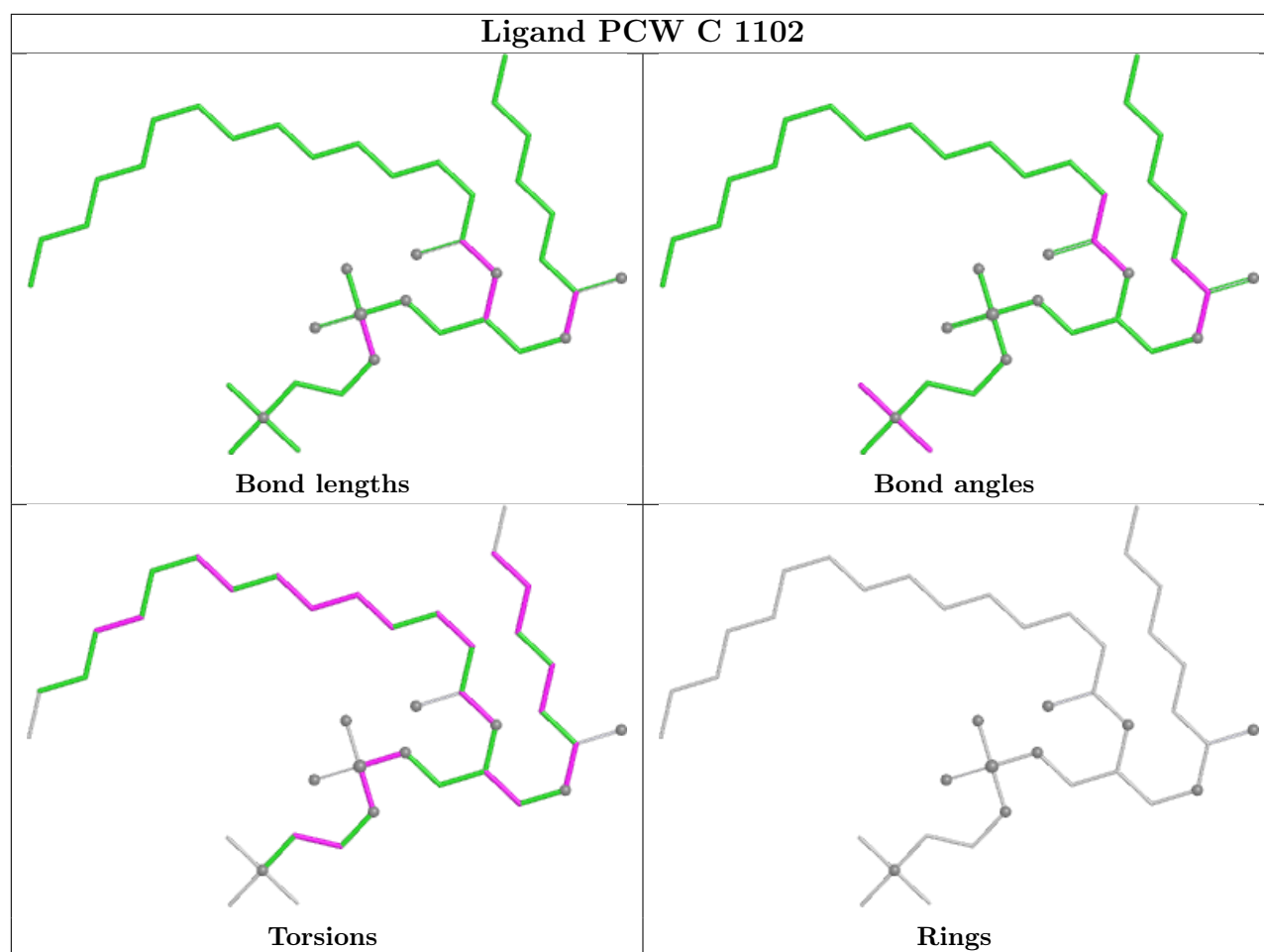
There are no ring outliers.

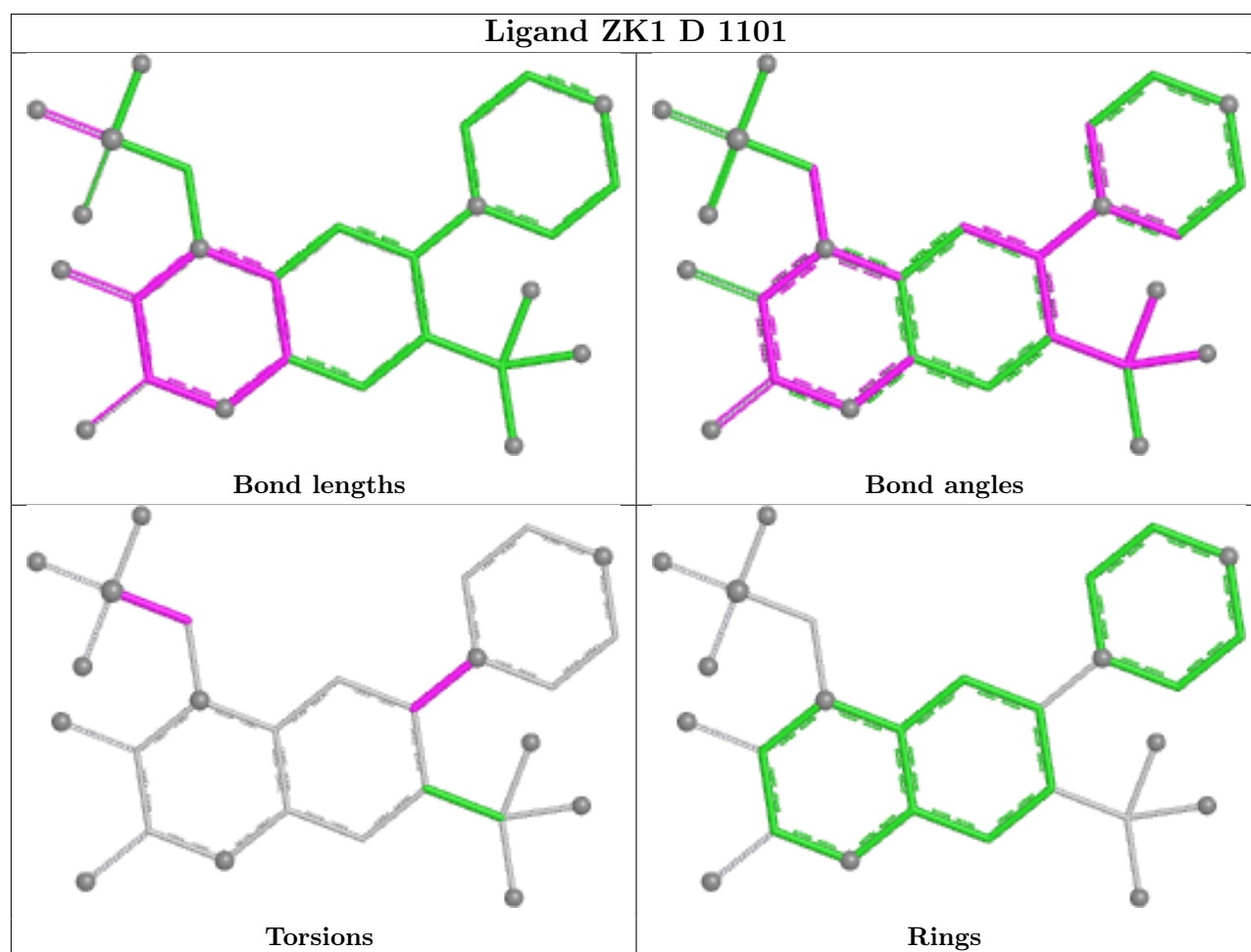
17 monomers are involved in 101 short contacts:

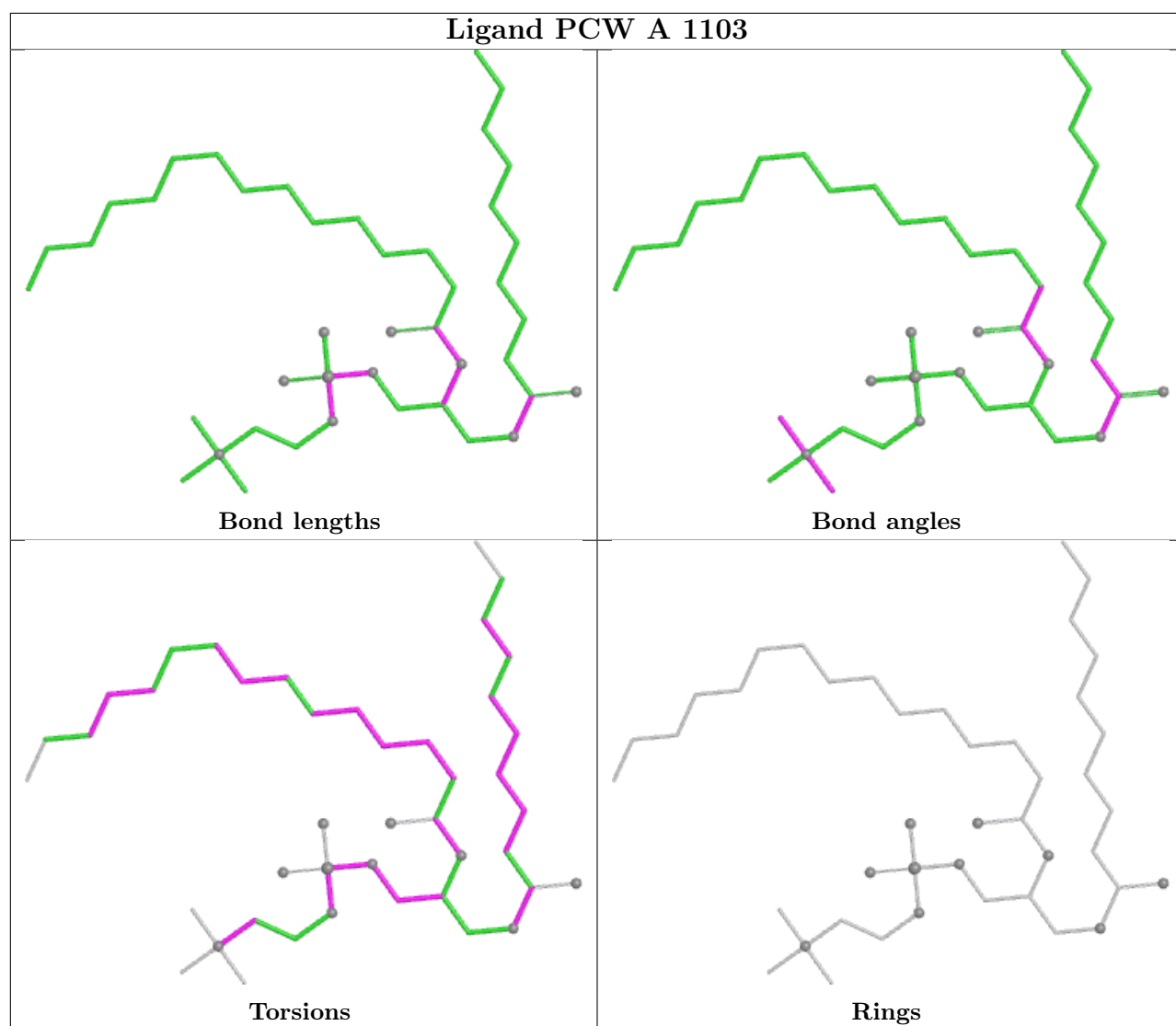
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1106	AJP	33	0
4	A	1103	PCW	4	0
4	D	1102	PCW	3	0
4	C	1107	PCW	1	0
3	C	1101	ZK1	1	0
6	C	1106	AJP	36	0
7	A	1111	SPD	2	0
4	E	202	PCW	2	0
4	C	1103	PCW	3	0
4	B	1102	PCW	3	0
4	A	1109	PCW	2	0
4	D	1103	PCW	2	0
5	C	1105	CLR	3	0
4	C	1109	PCW	1	0
4	A	1104	PCW	1	0
5	A	1105	CLR	4	0
4	A	1107	PCW	1	0

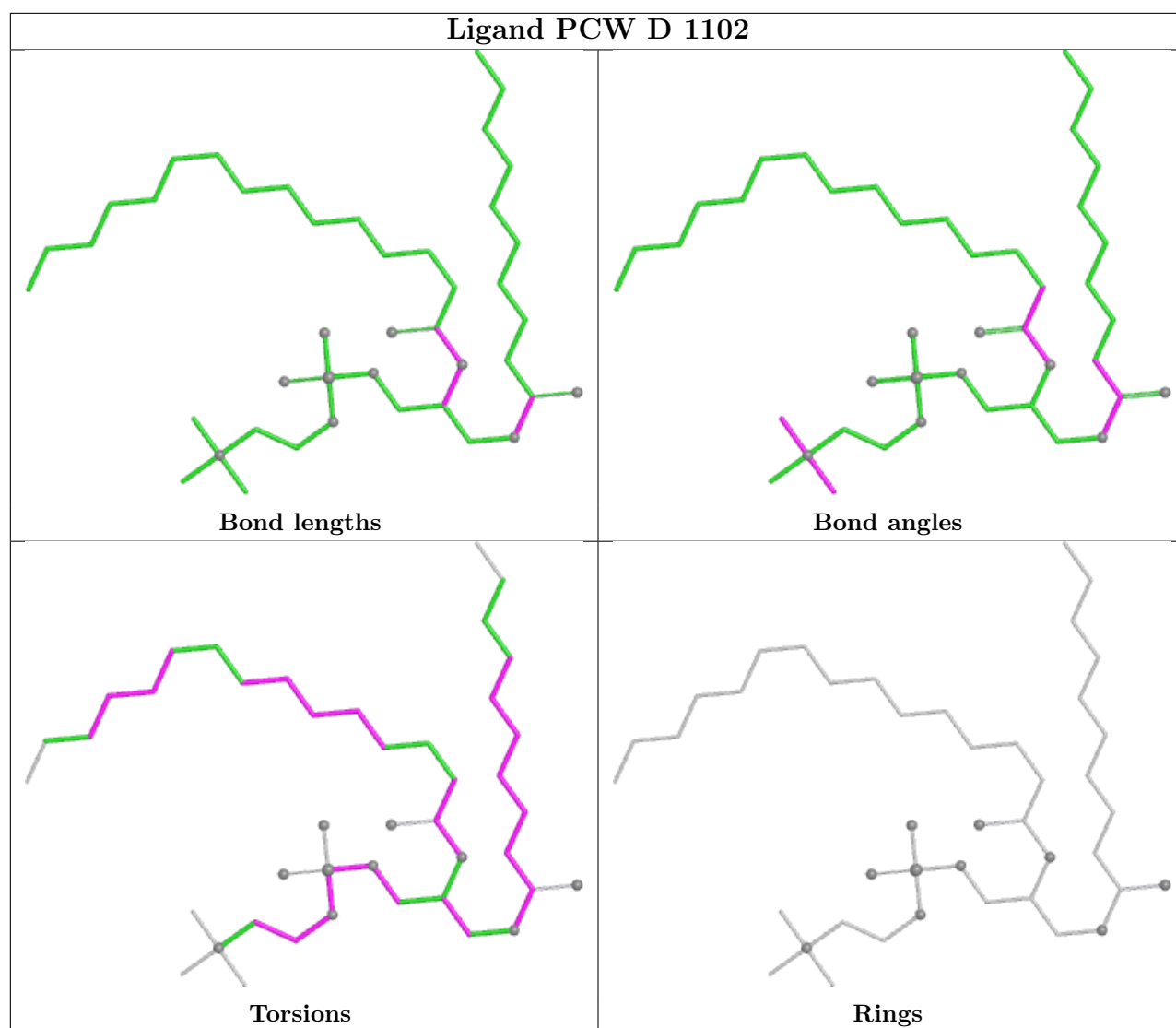
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

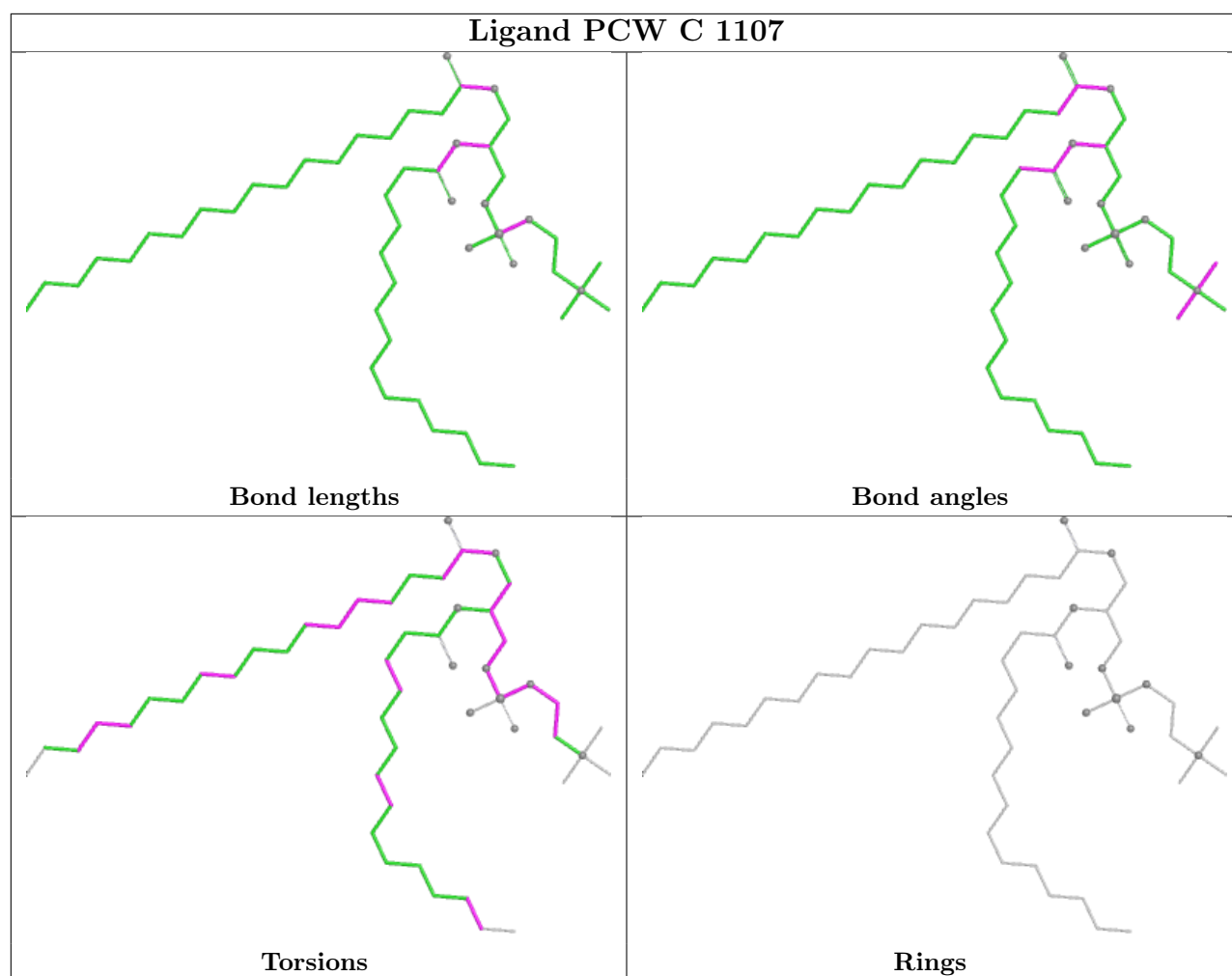


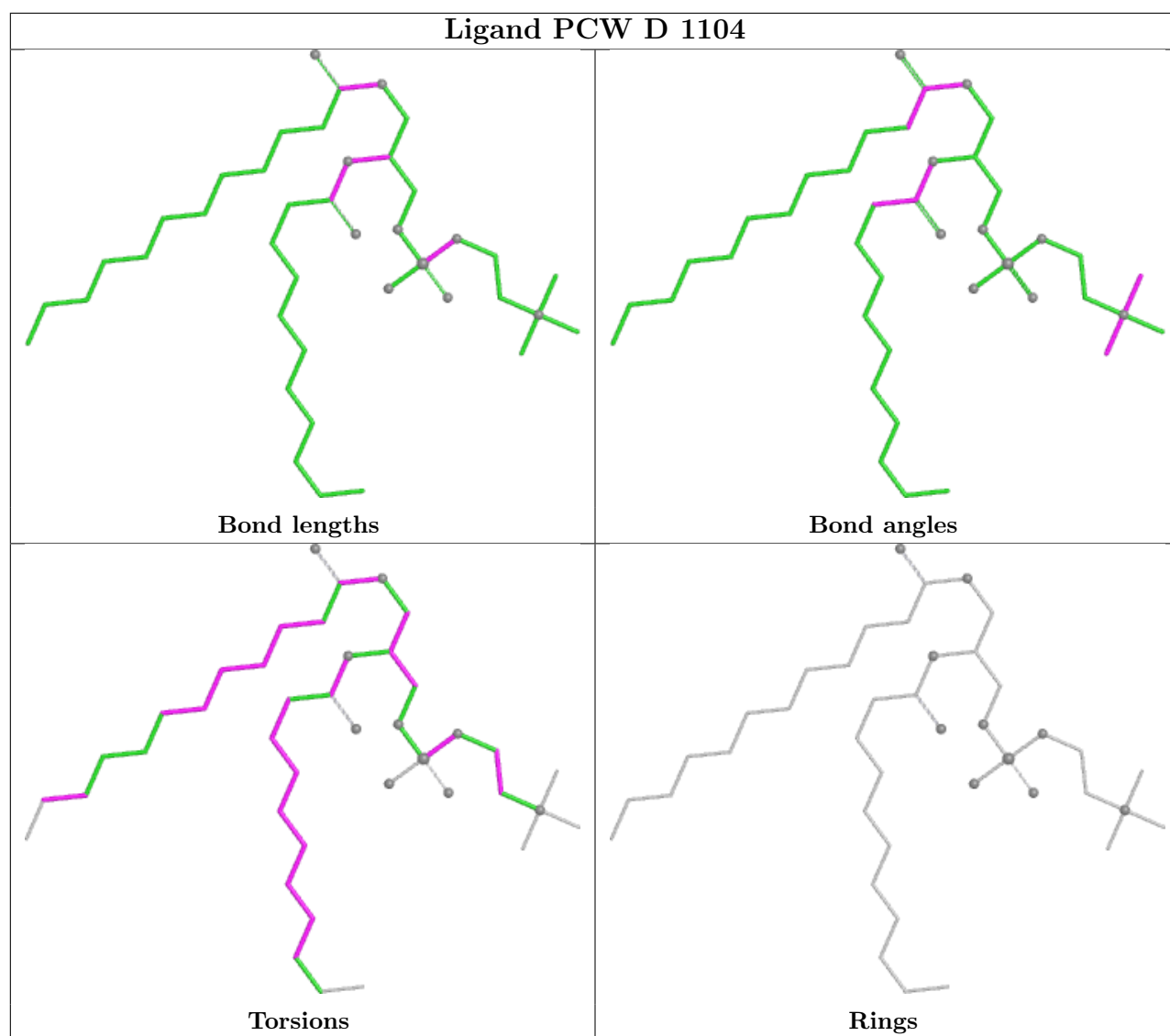


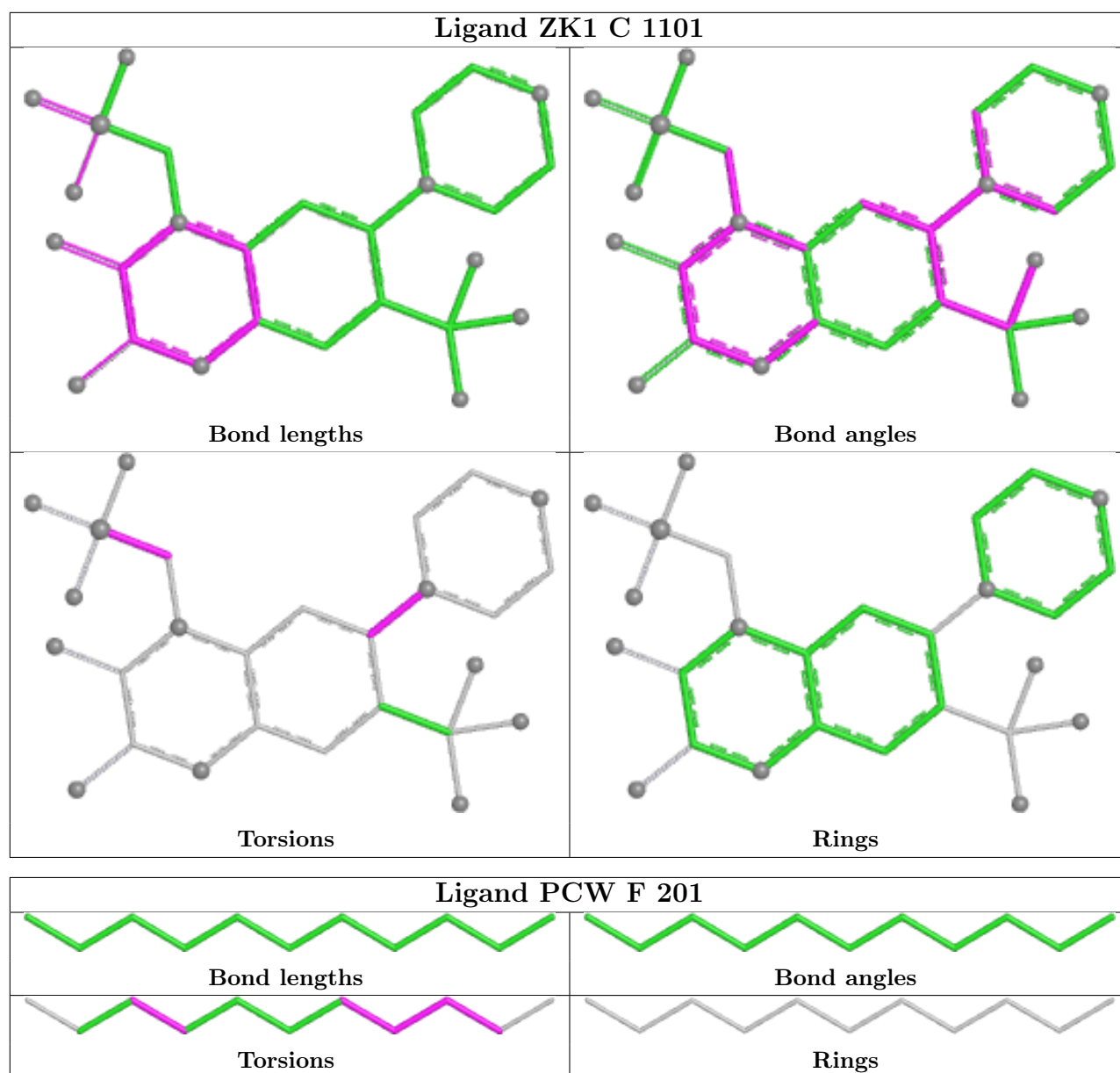


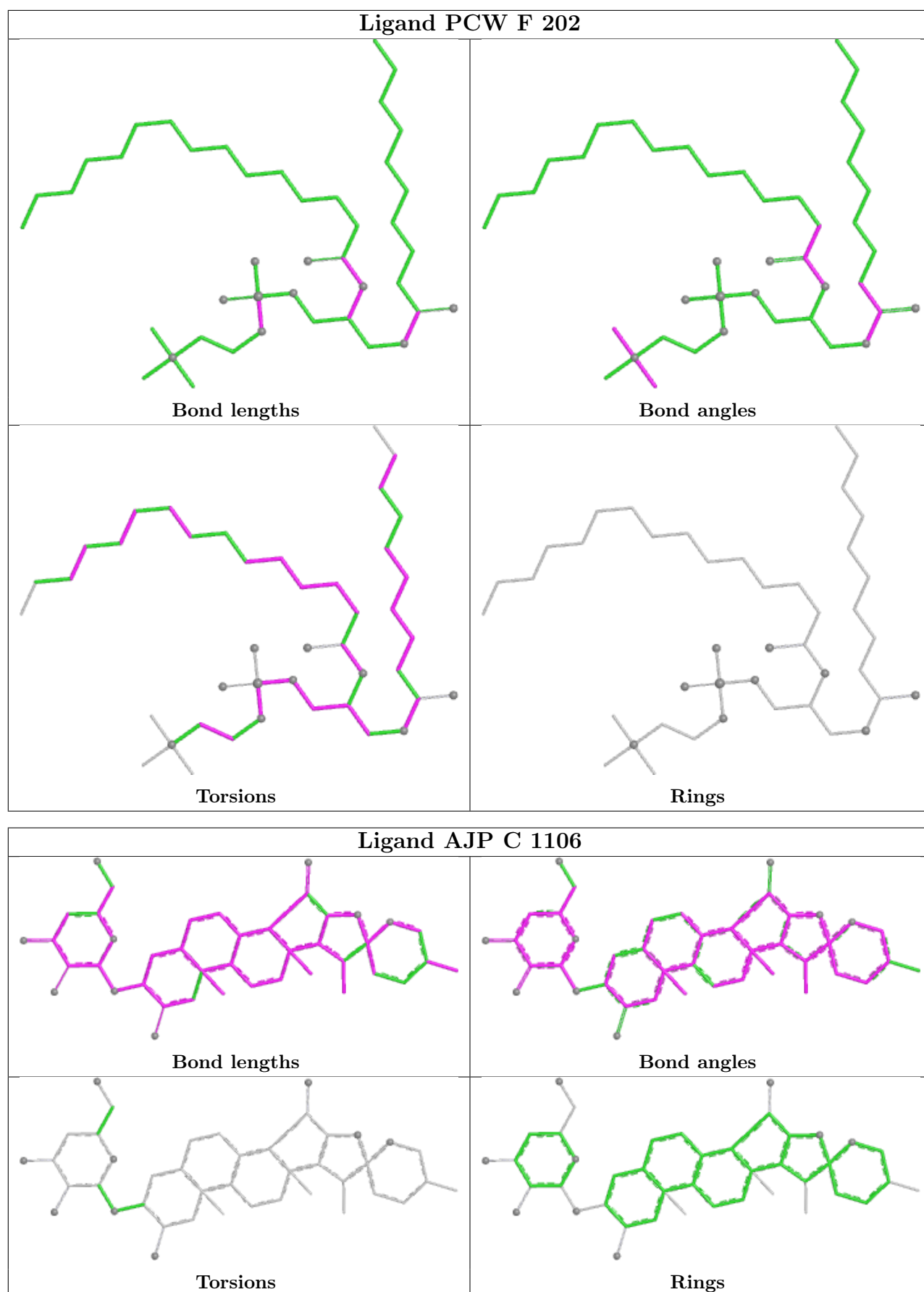


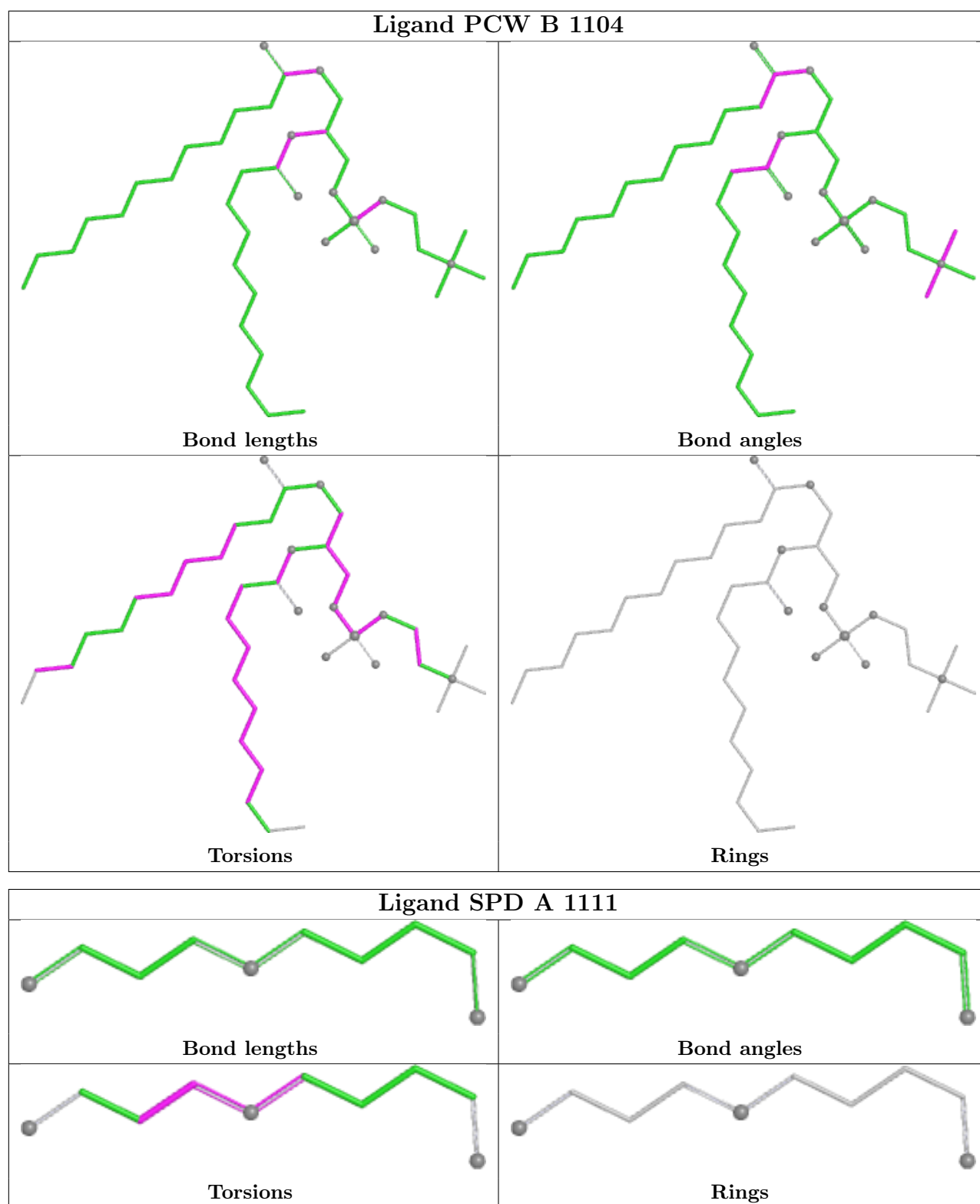


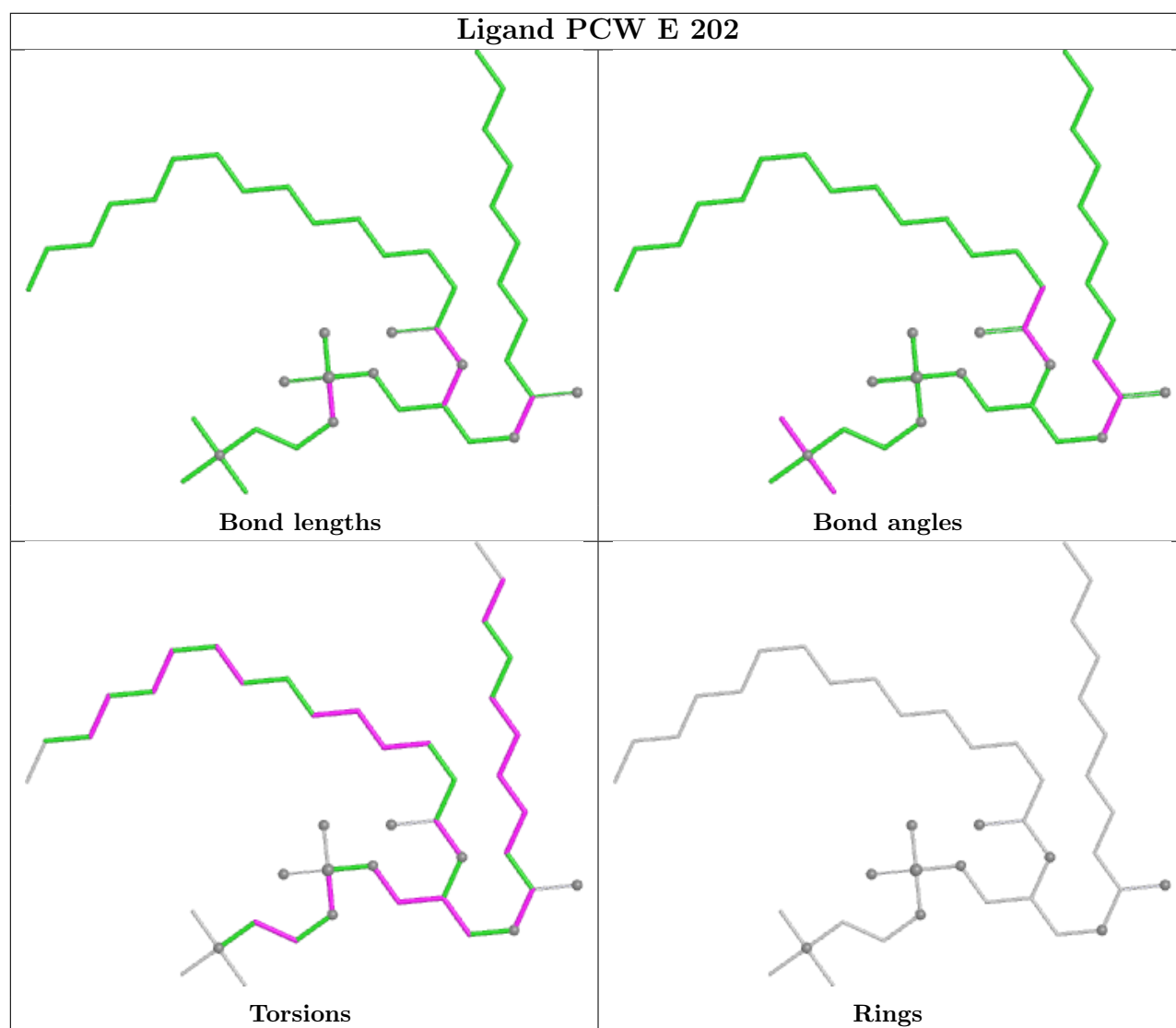


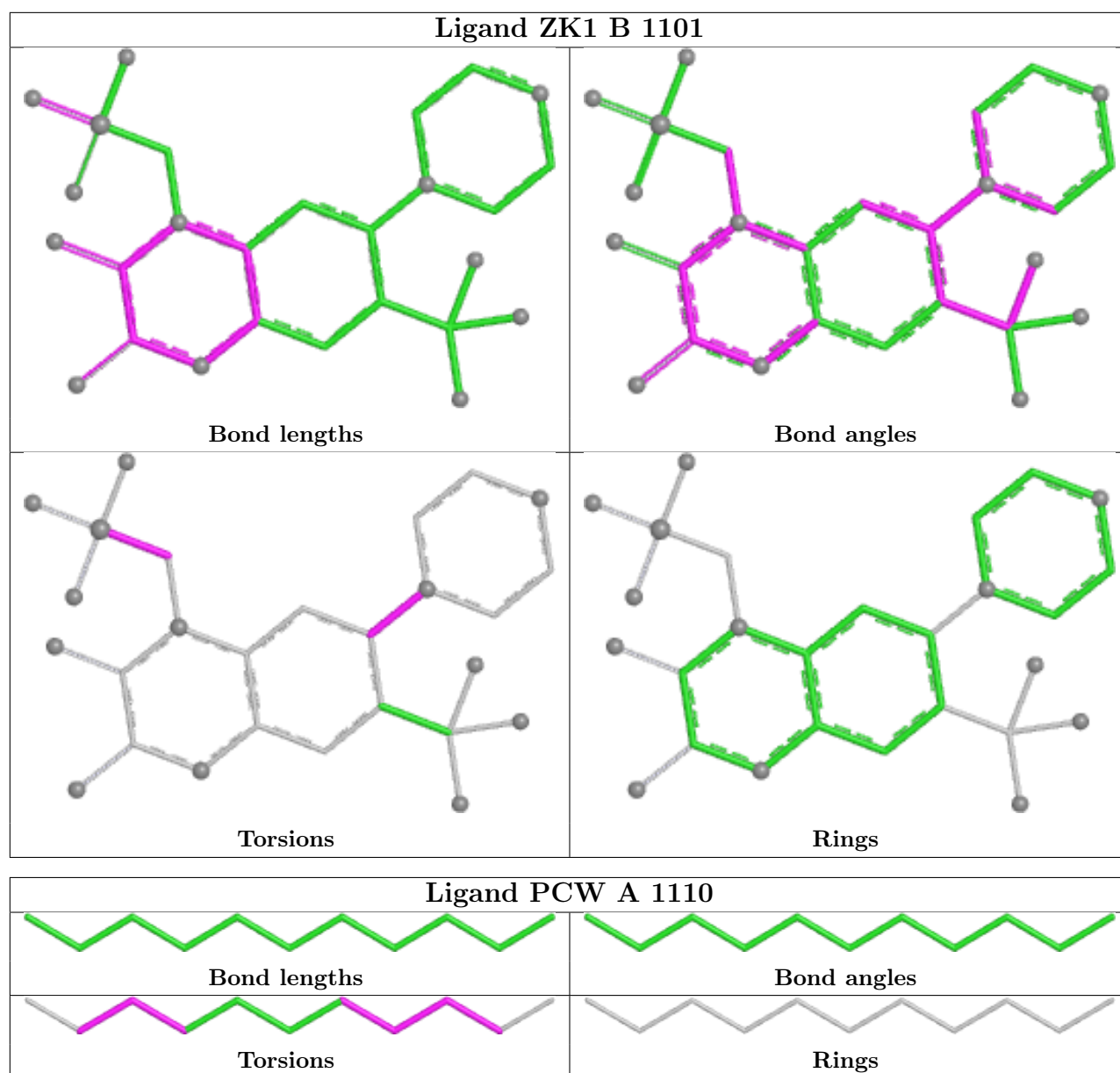


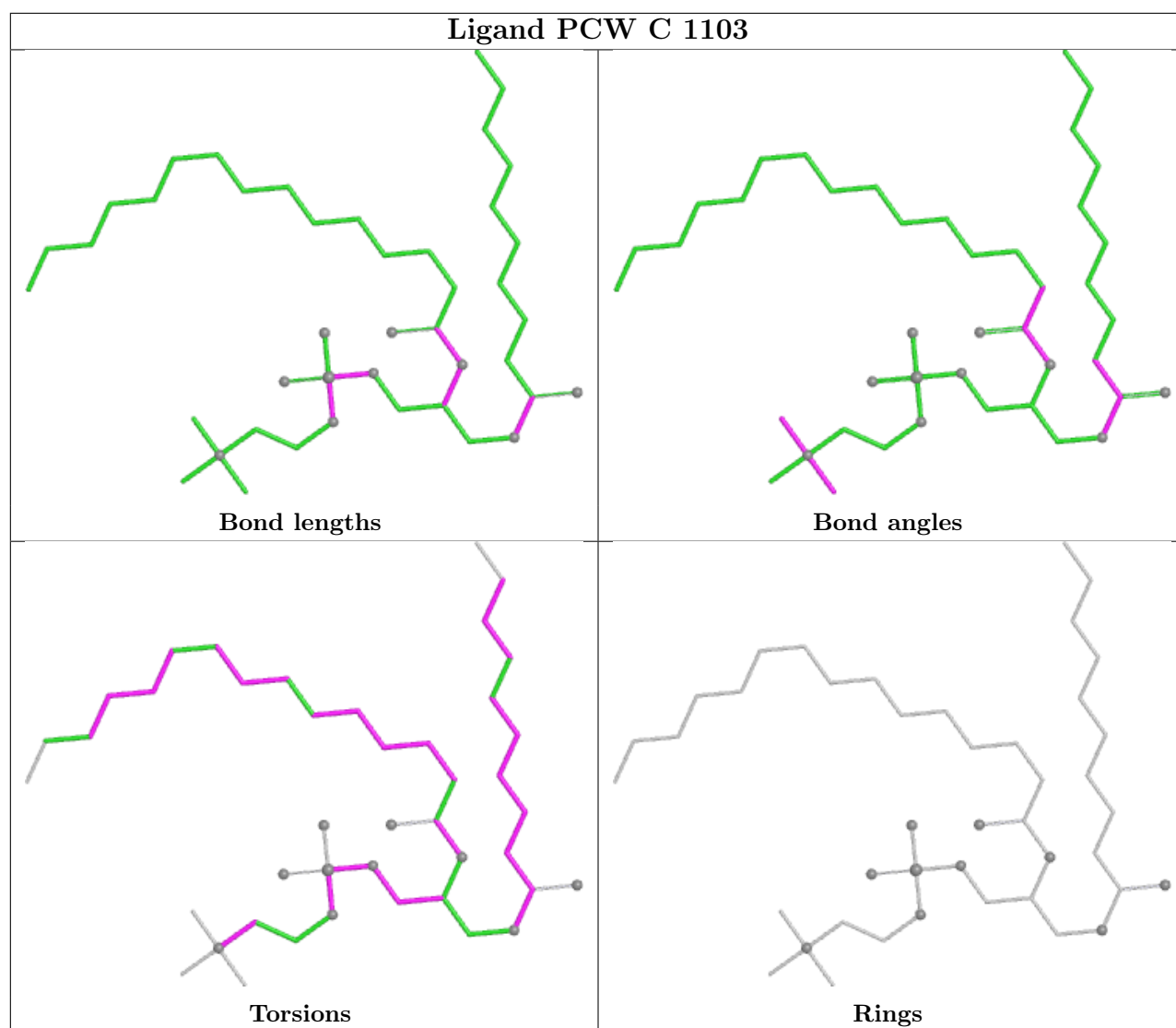


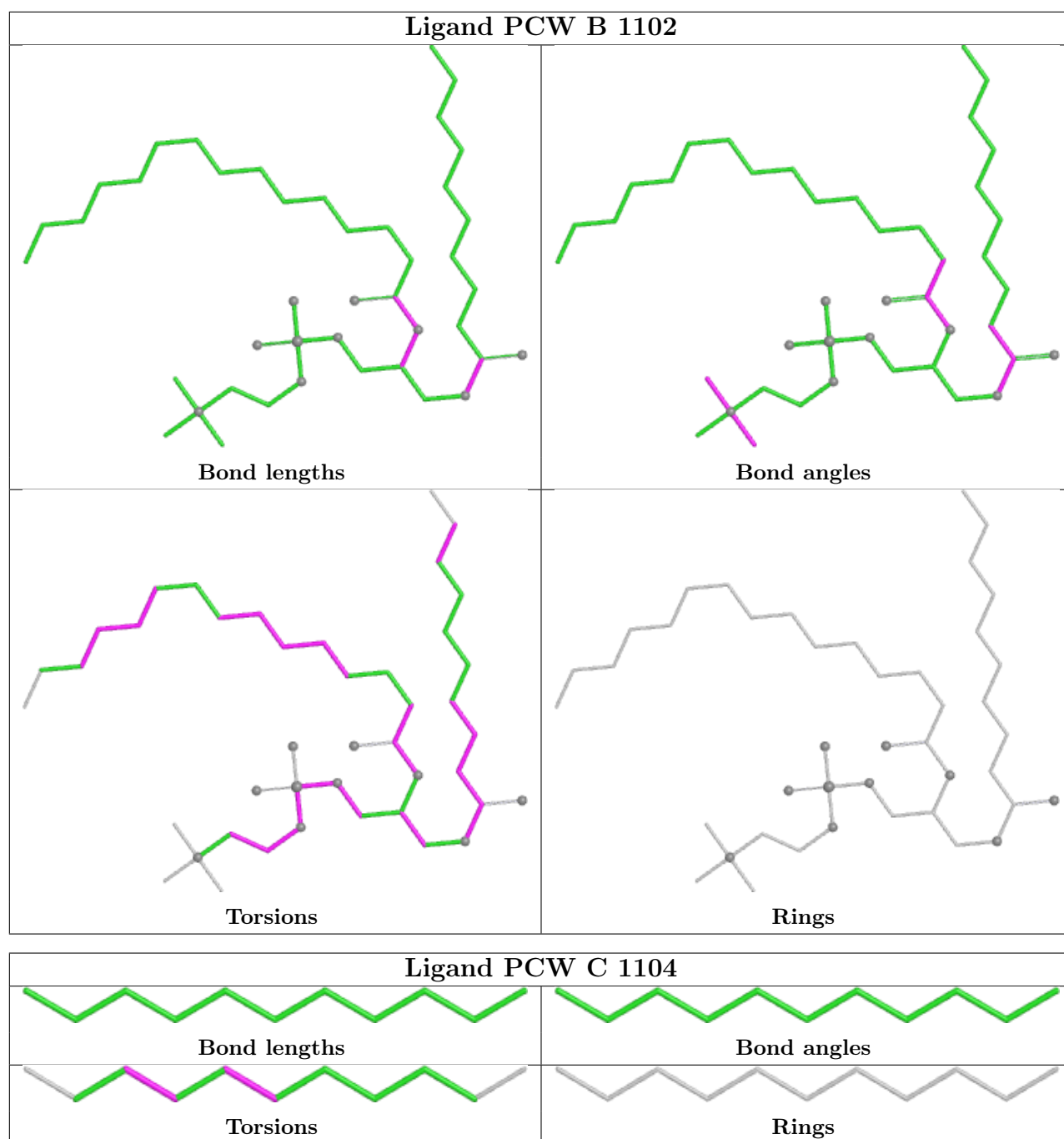


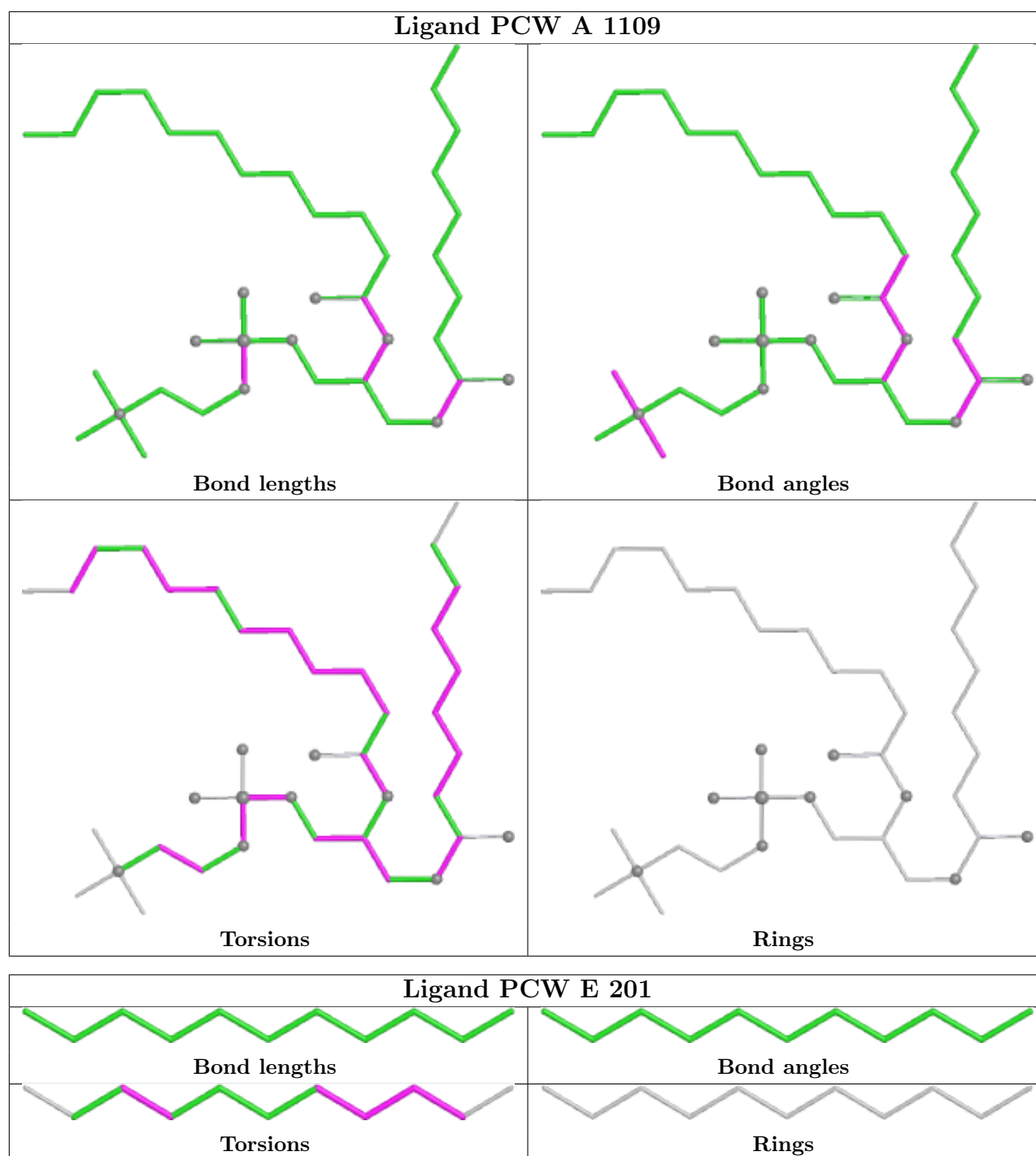


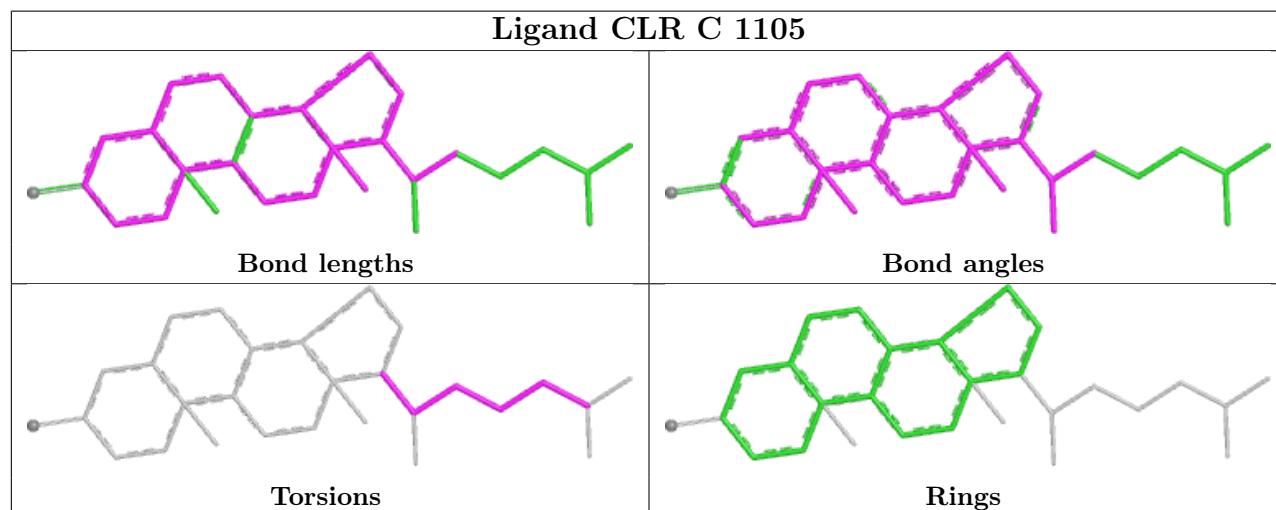
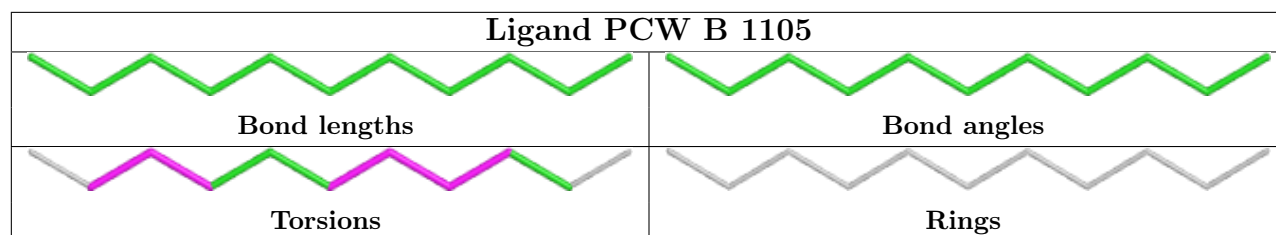
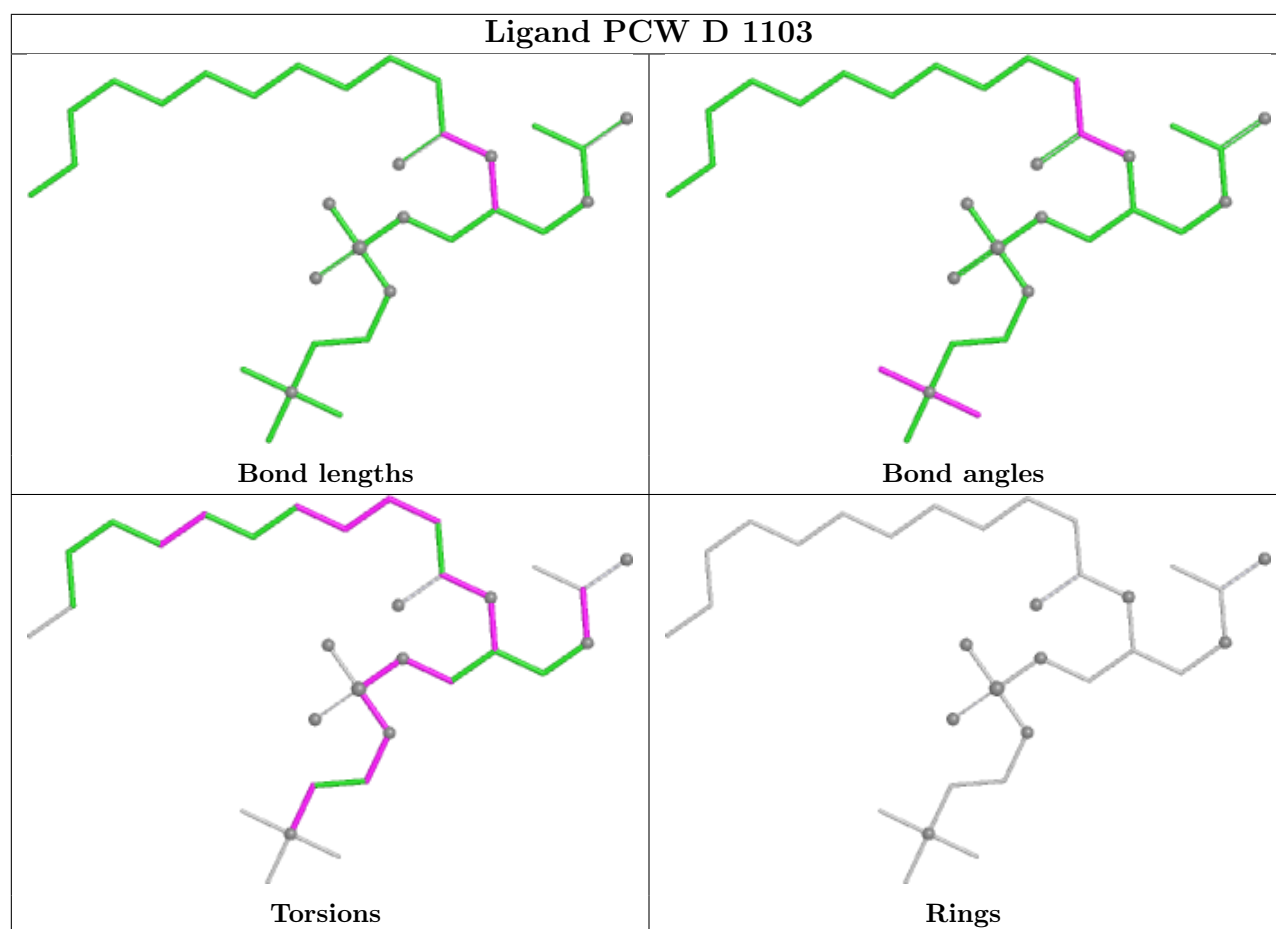


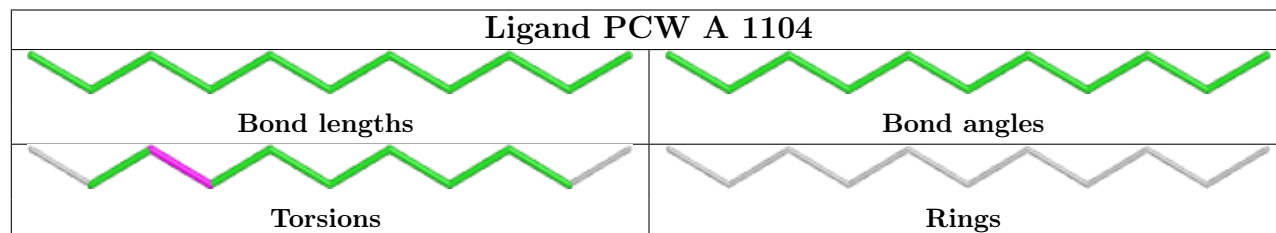
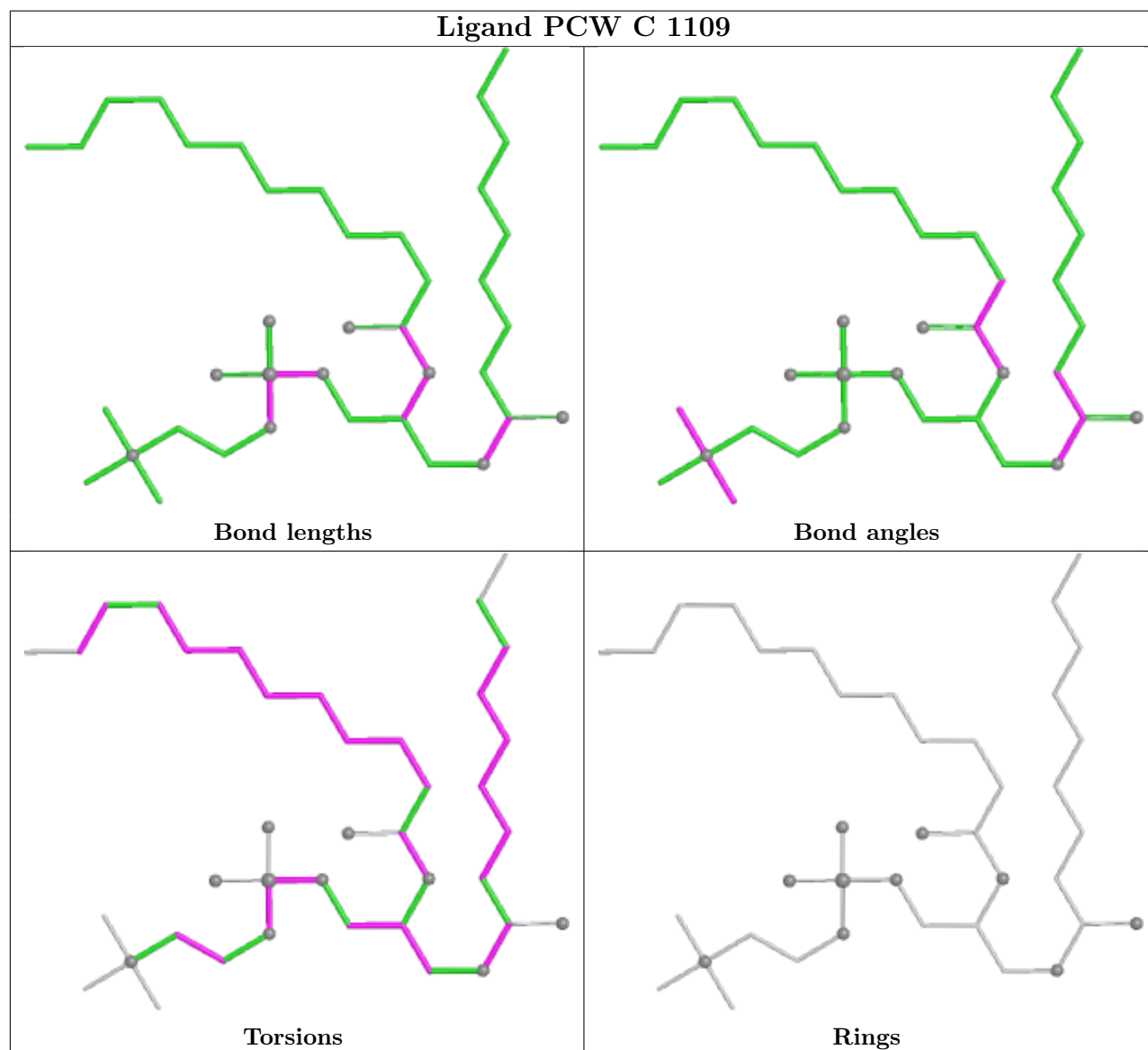
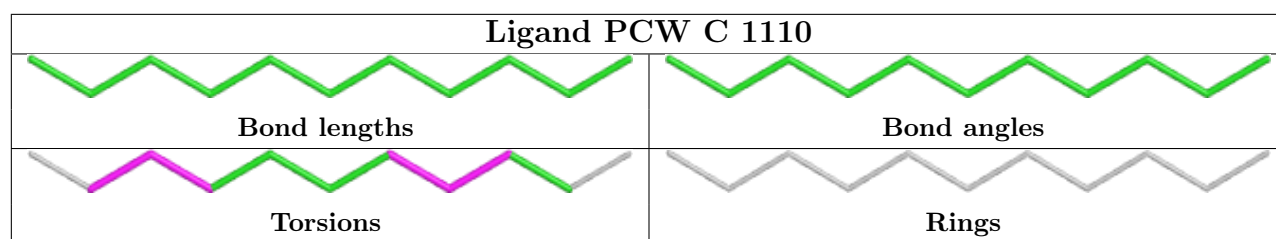


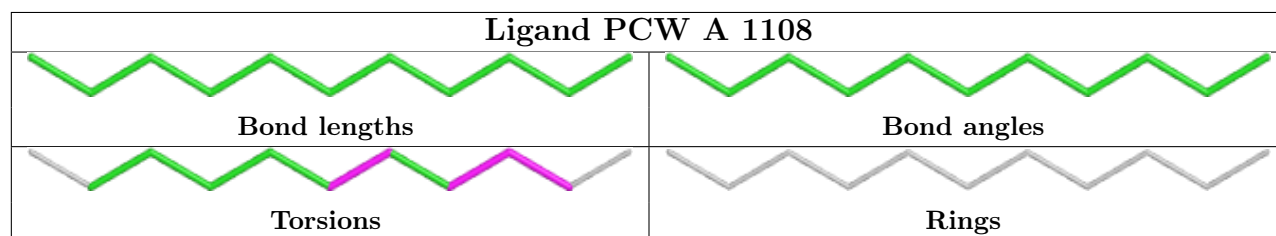
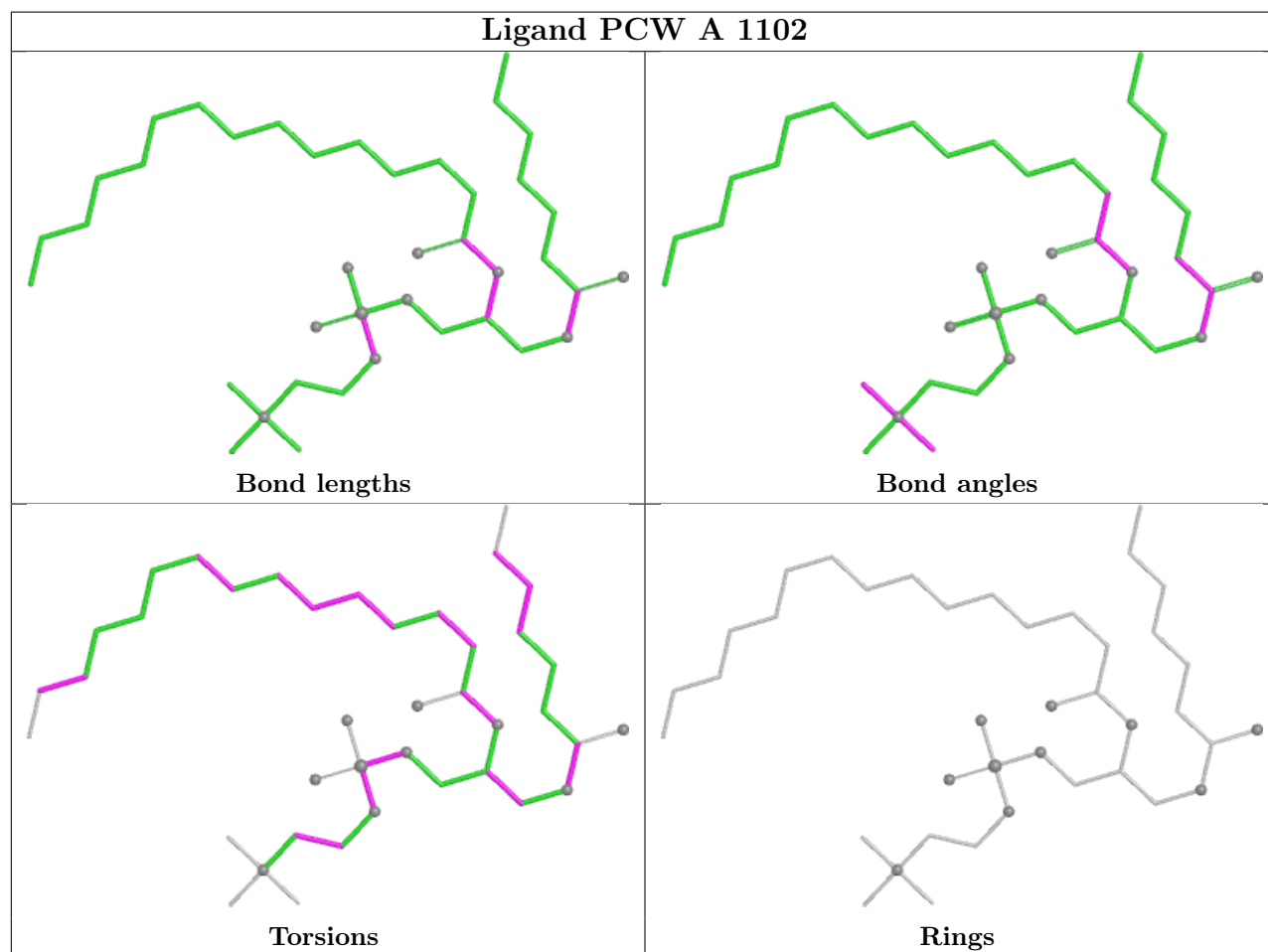
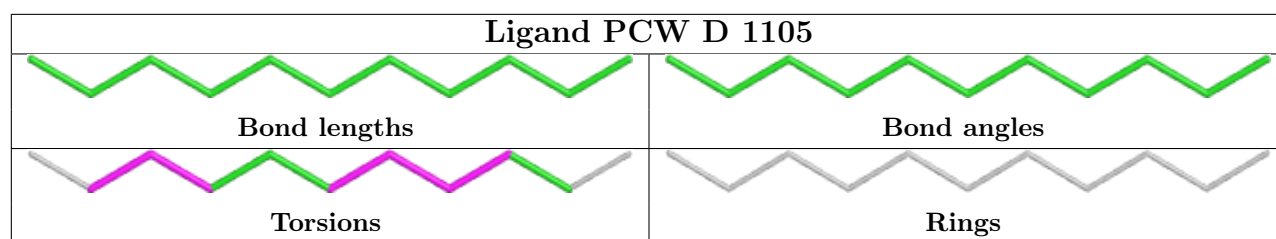


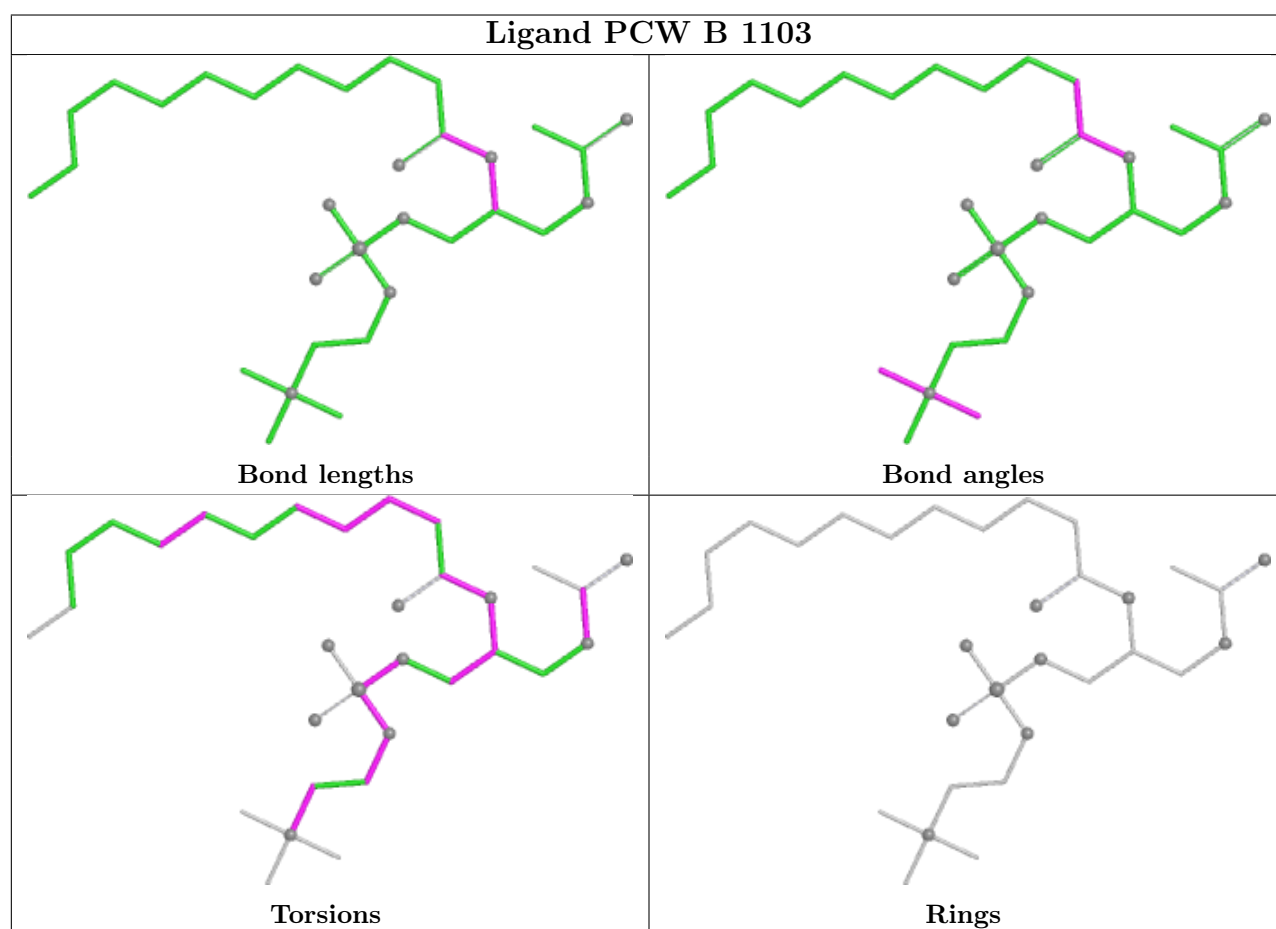
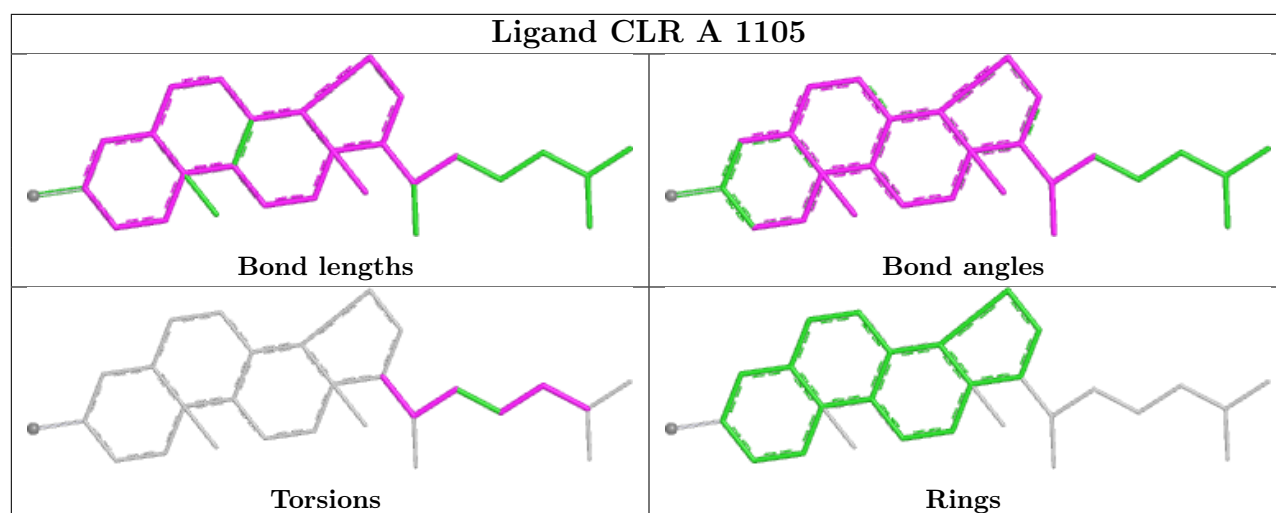


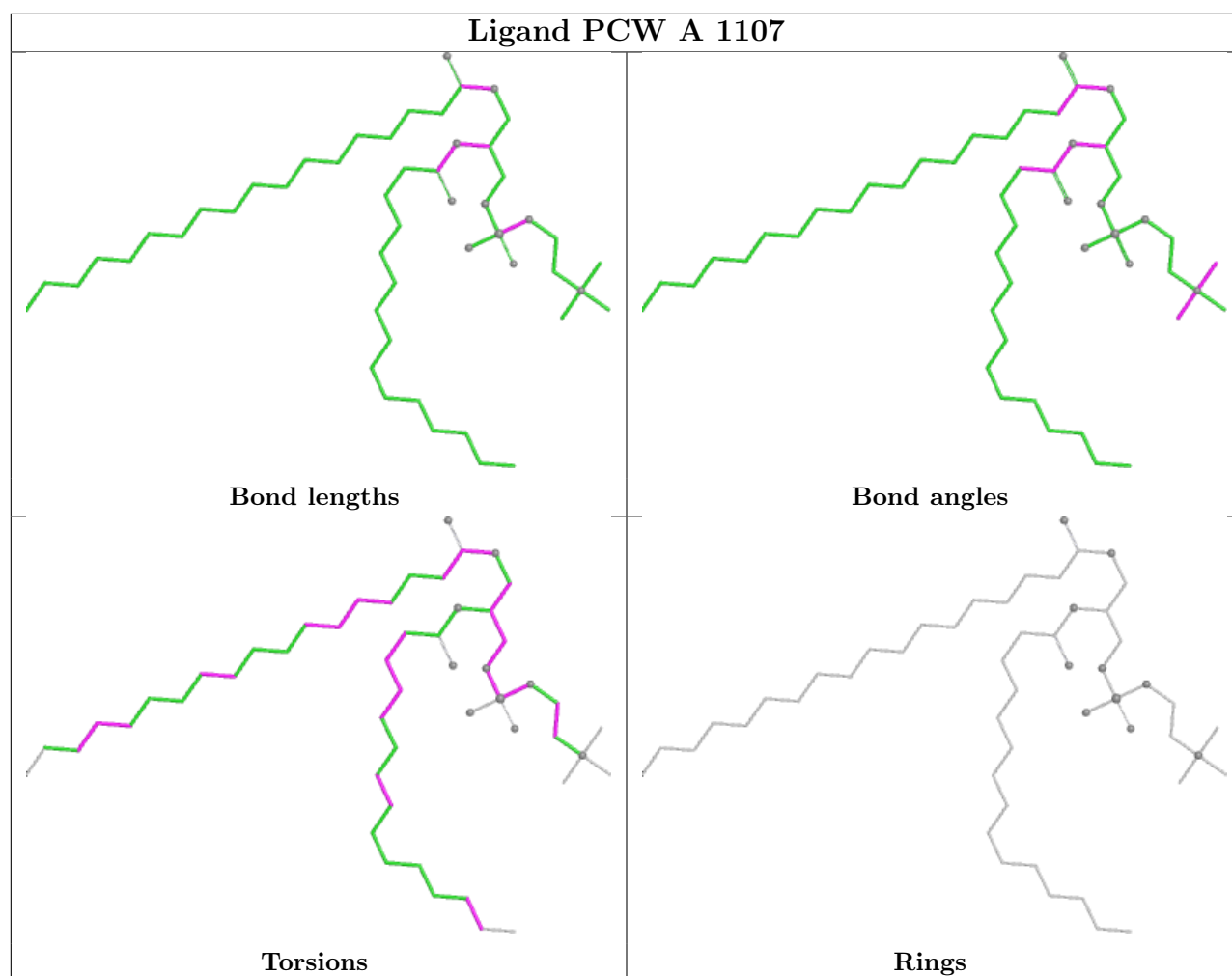


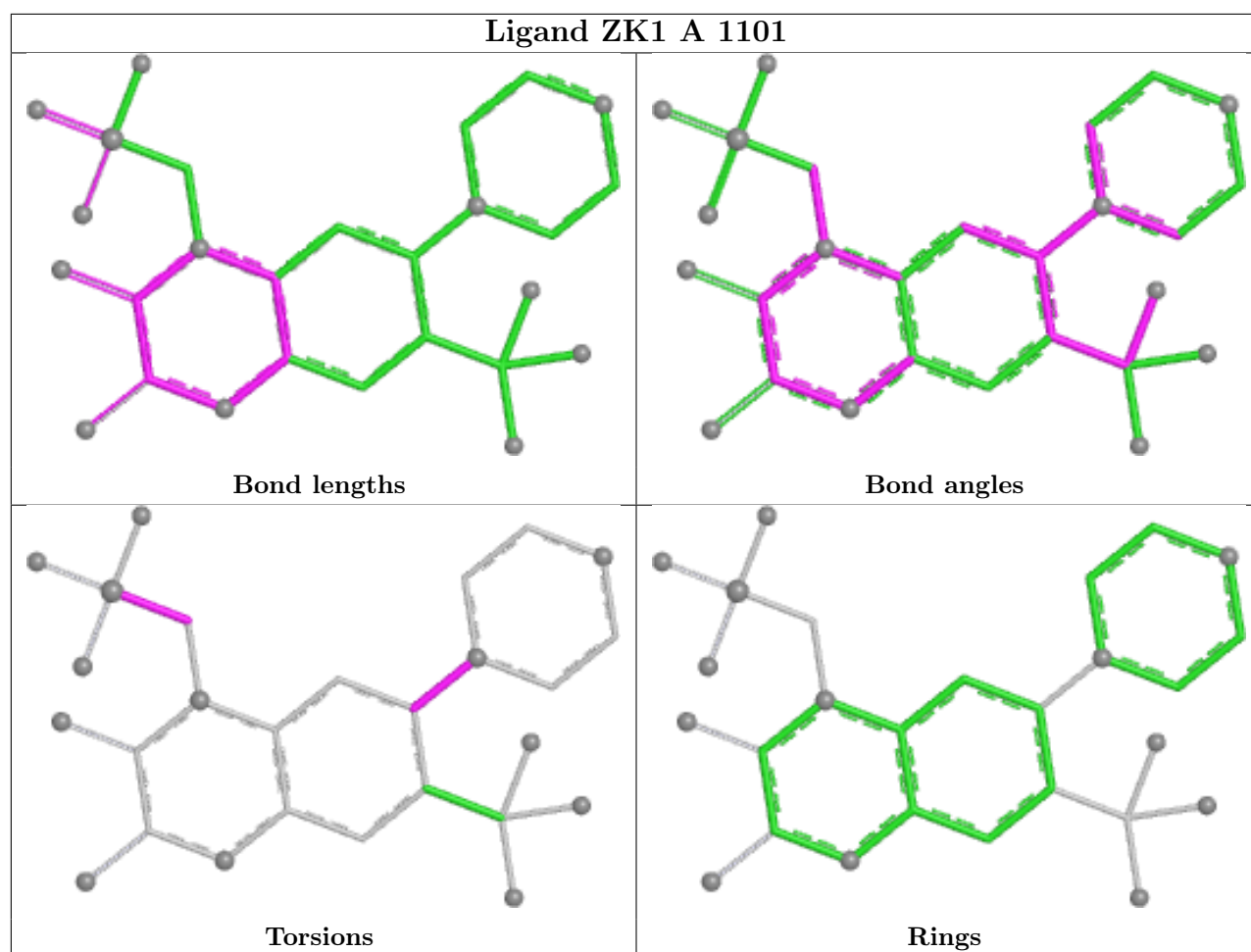












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

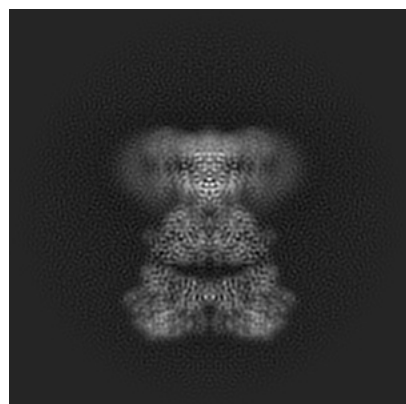
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-40741. These allow visual inspection of the internal detail of the map and identification of artifacts.

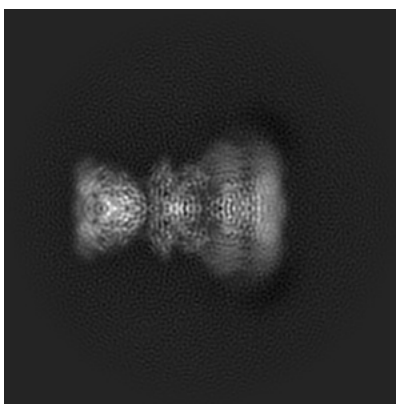
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

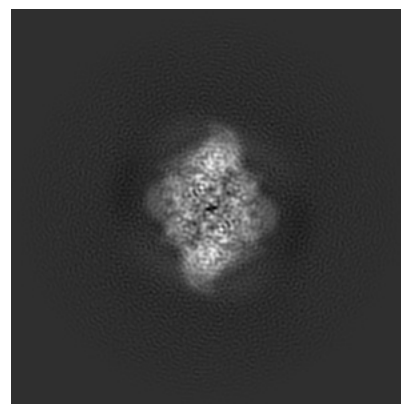
6.1.1 Primary map



X

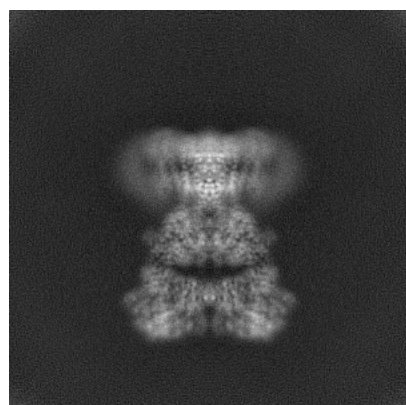


Y

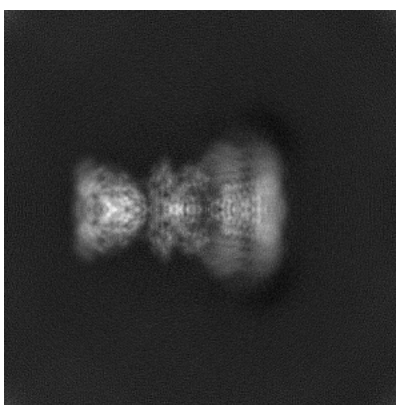


Z

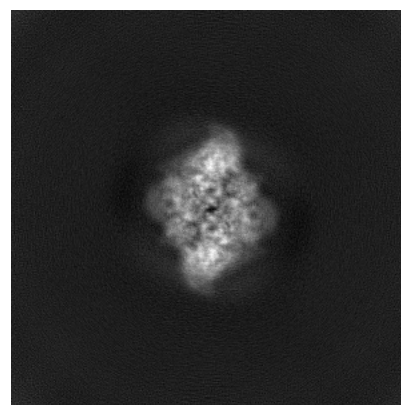
6.1.2 Raw map



X



Y

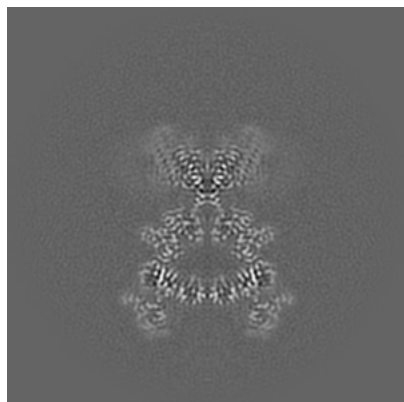


Z

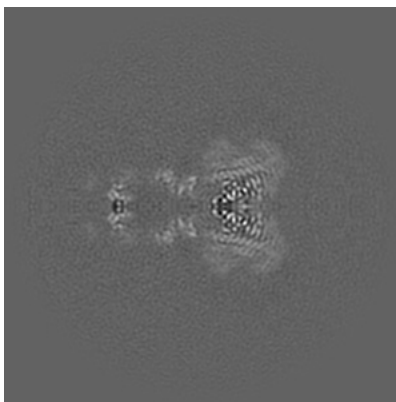
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

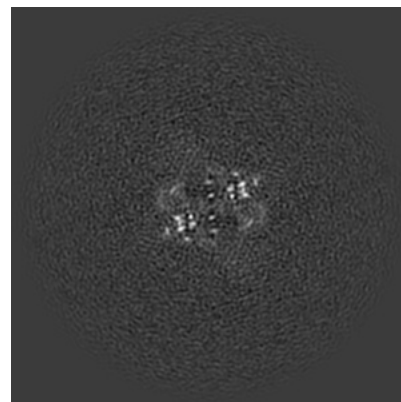
6.2.1 Primary map



X Index: 208

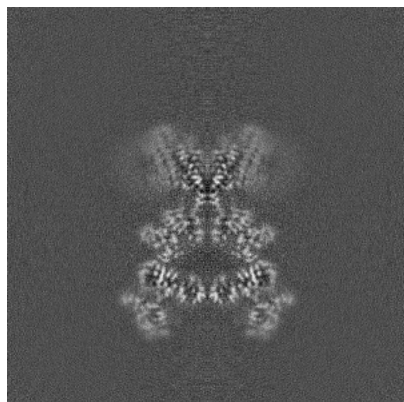


Y Index: 208

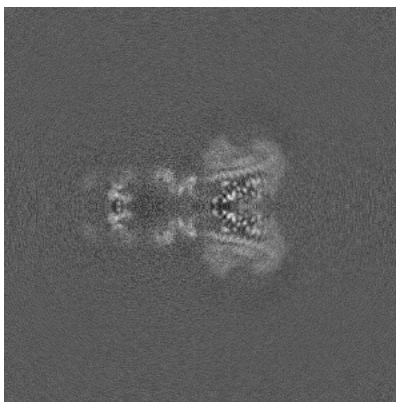


Z Index: 208

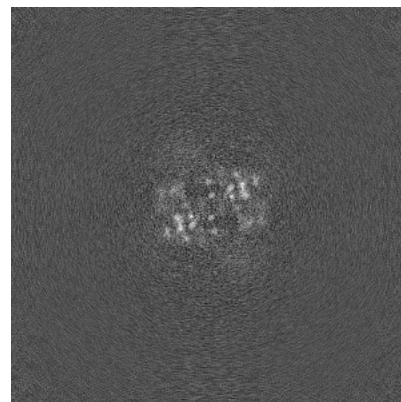
6.2.2 Raw map



X Index: 208



Y Index: 208

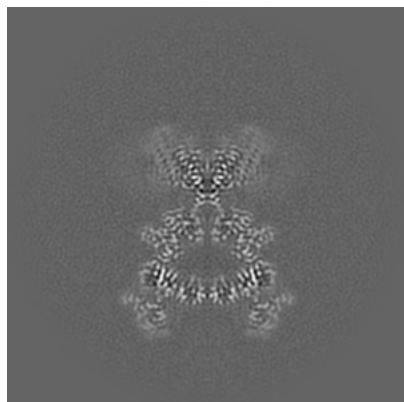


Z Index: 208

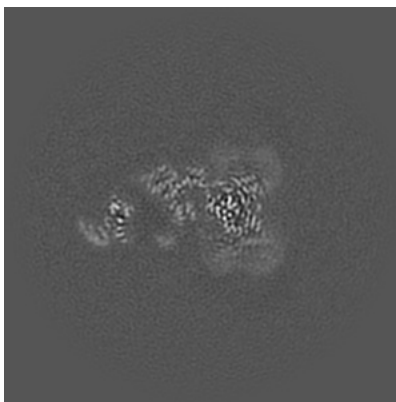
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

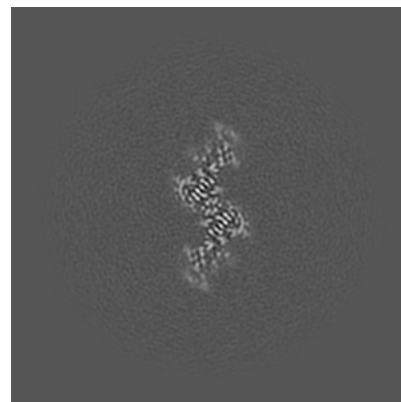
6.3.1 Primary map



X Index: 208

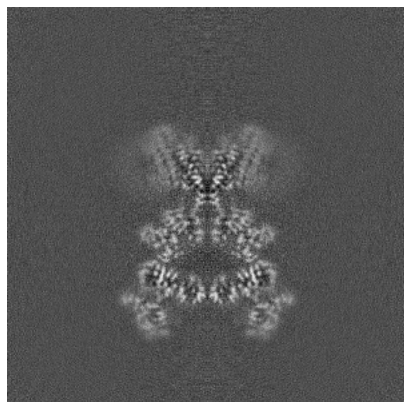


Y Index: 217

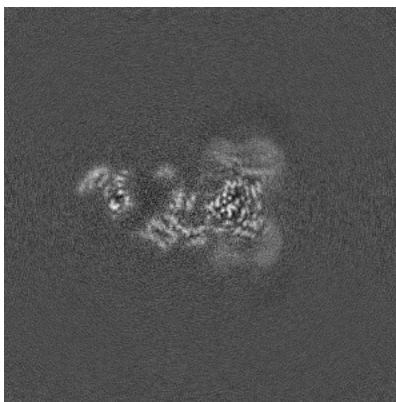


Z Index: 121

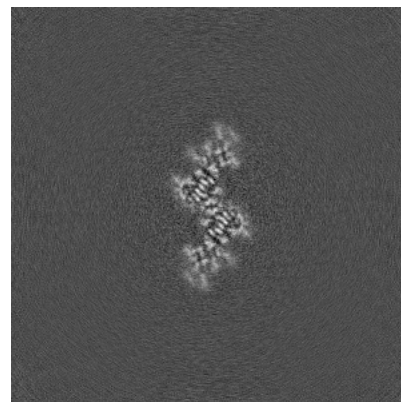
6.3.2 Raw map



X Index: 208



Y Index: 199

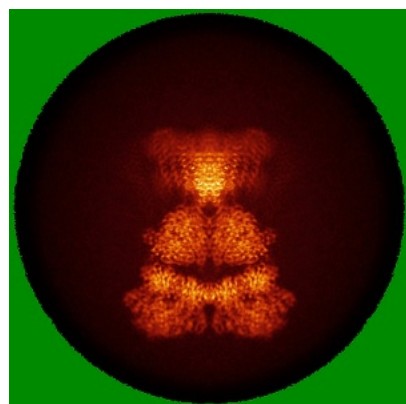


Z Index: 122

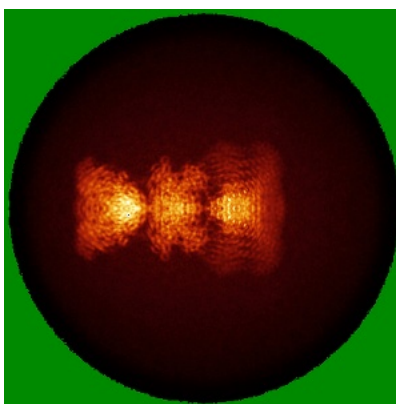
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

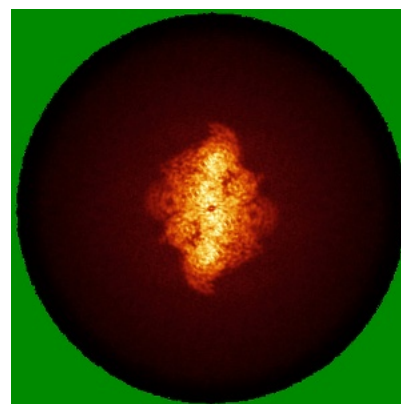
6.4.1 Primary map



X

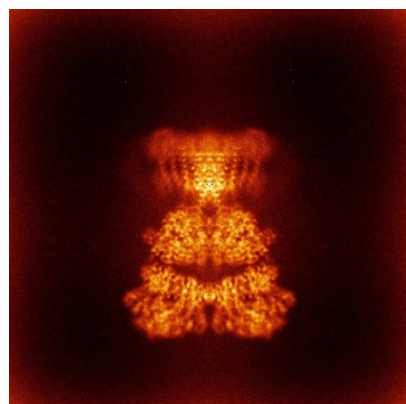


Y

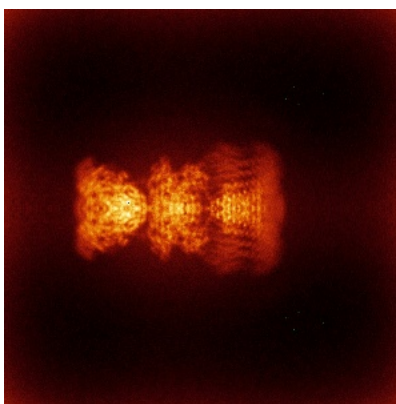


Z

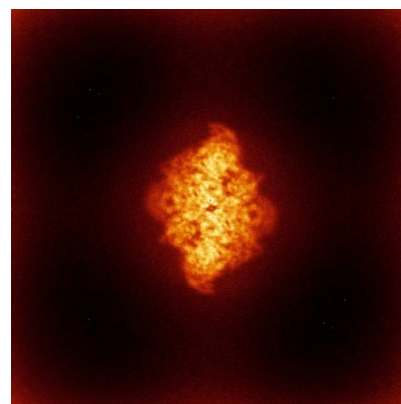
6.4.2 Raw map



X



Y

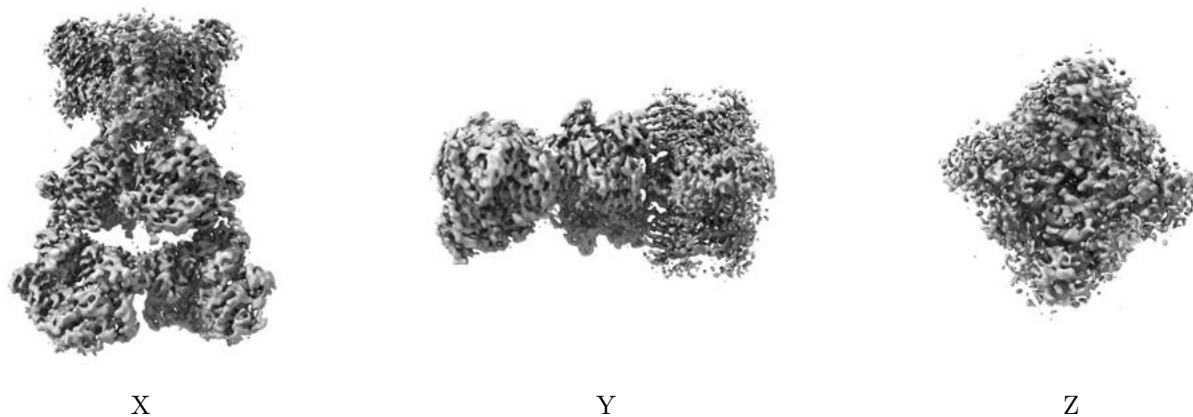


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

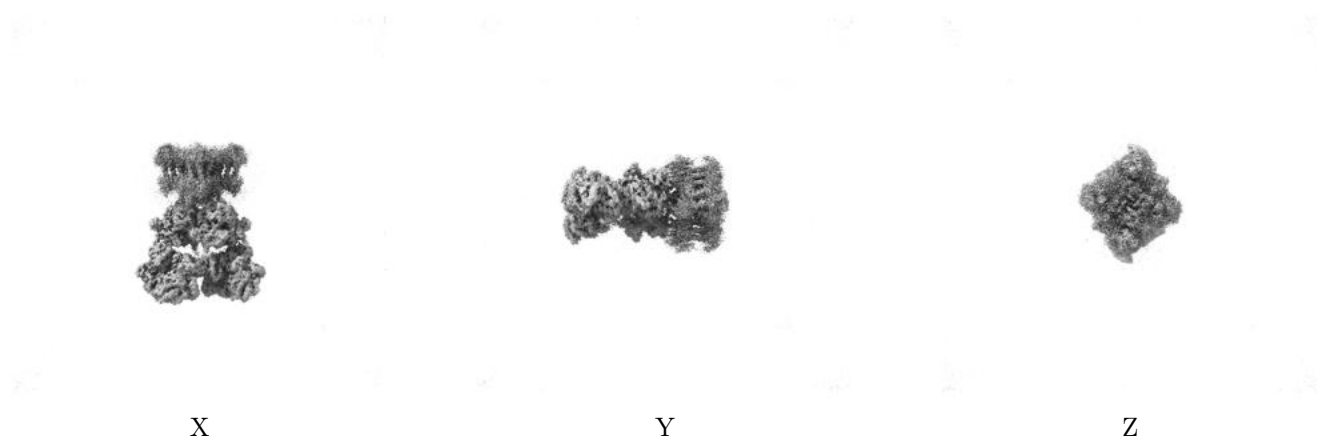
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

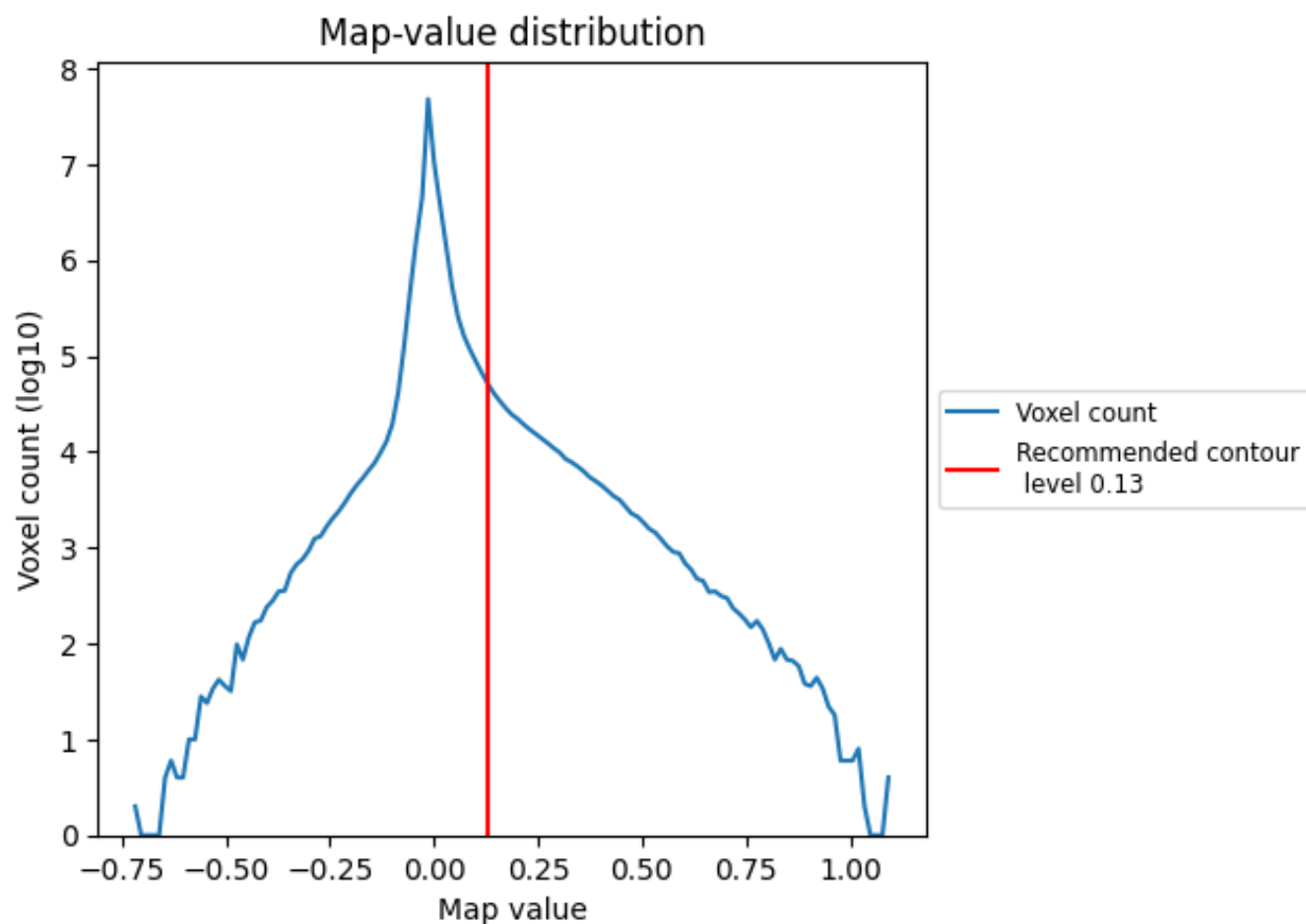
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

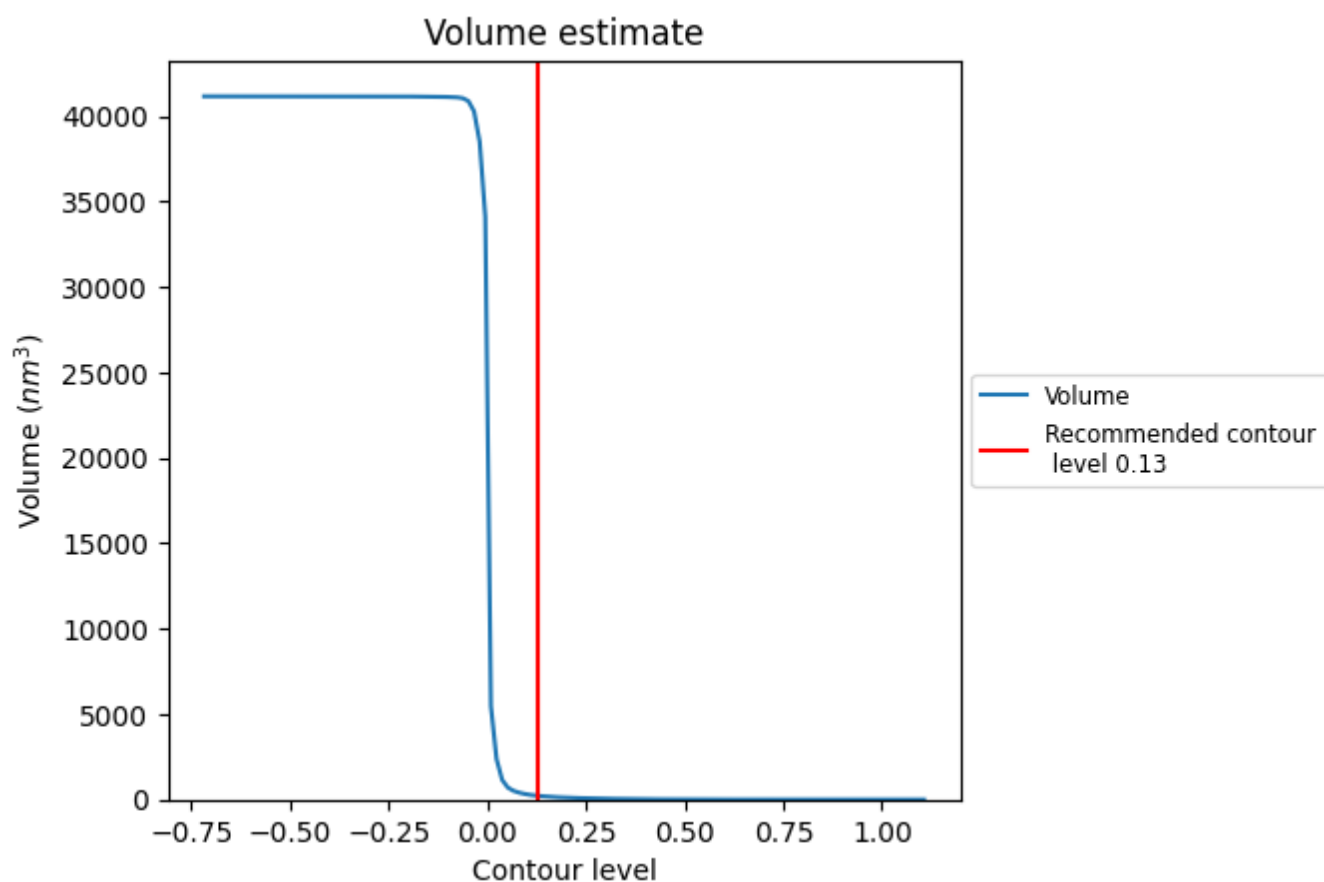
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

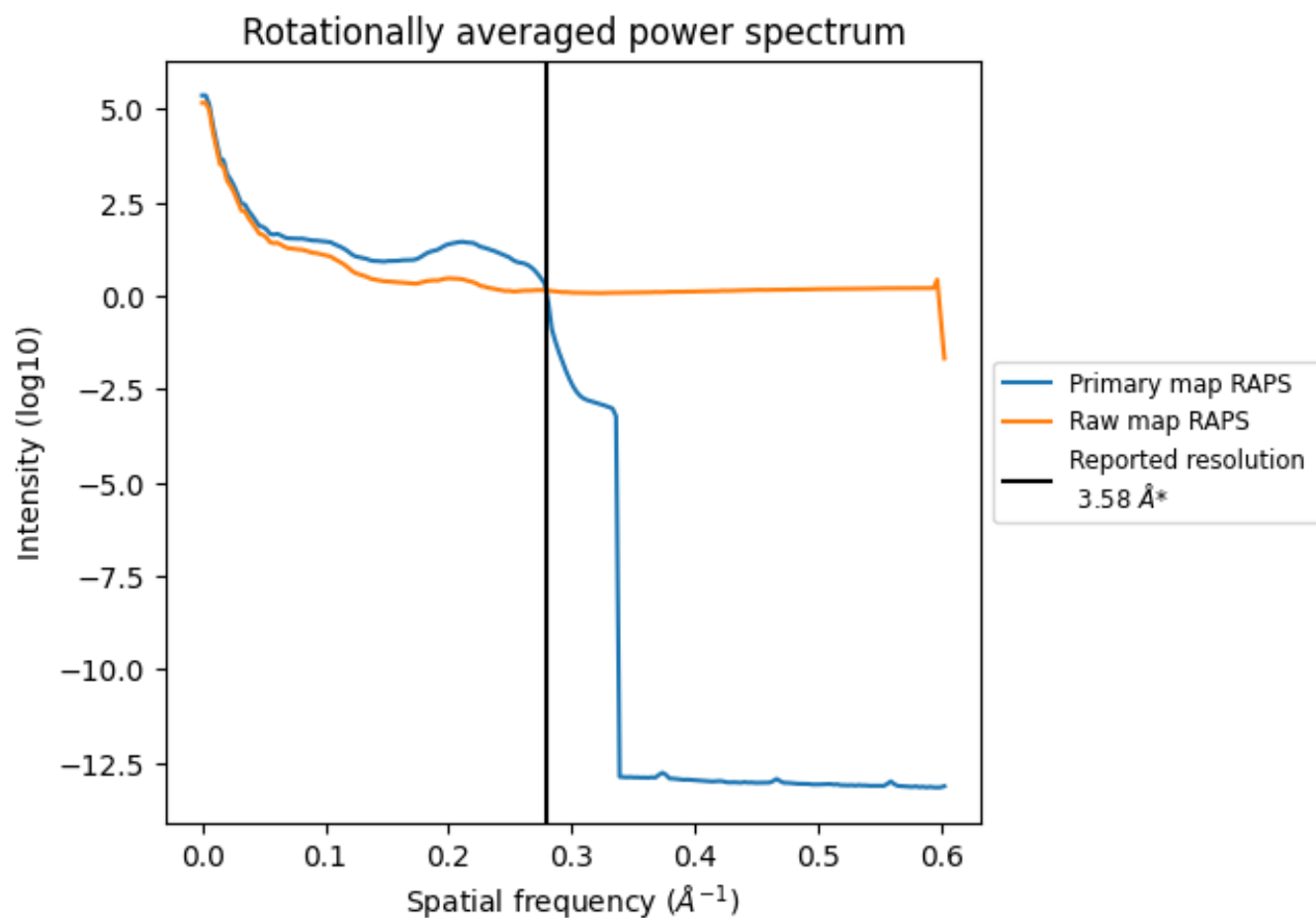
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 216 nm³; this corresponds to an approximate mass of 195 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

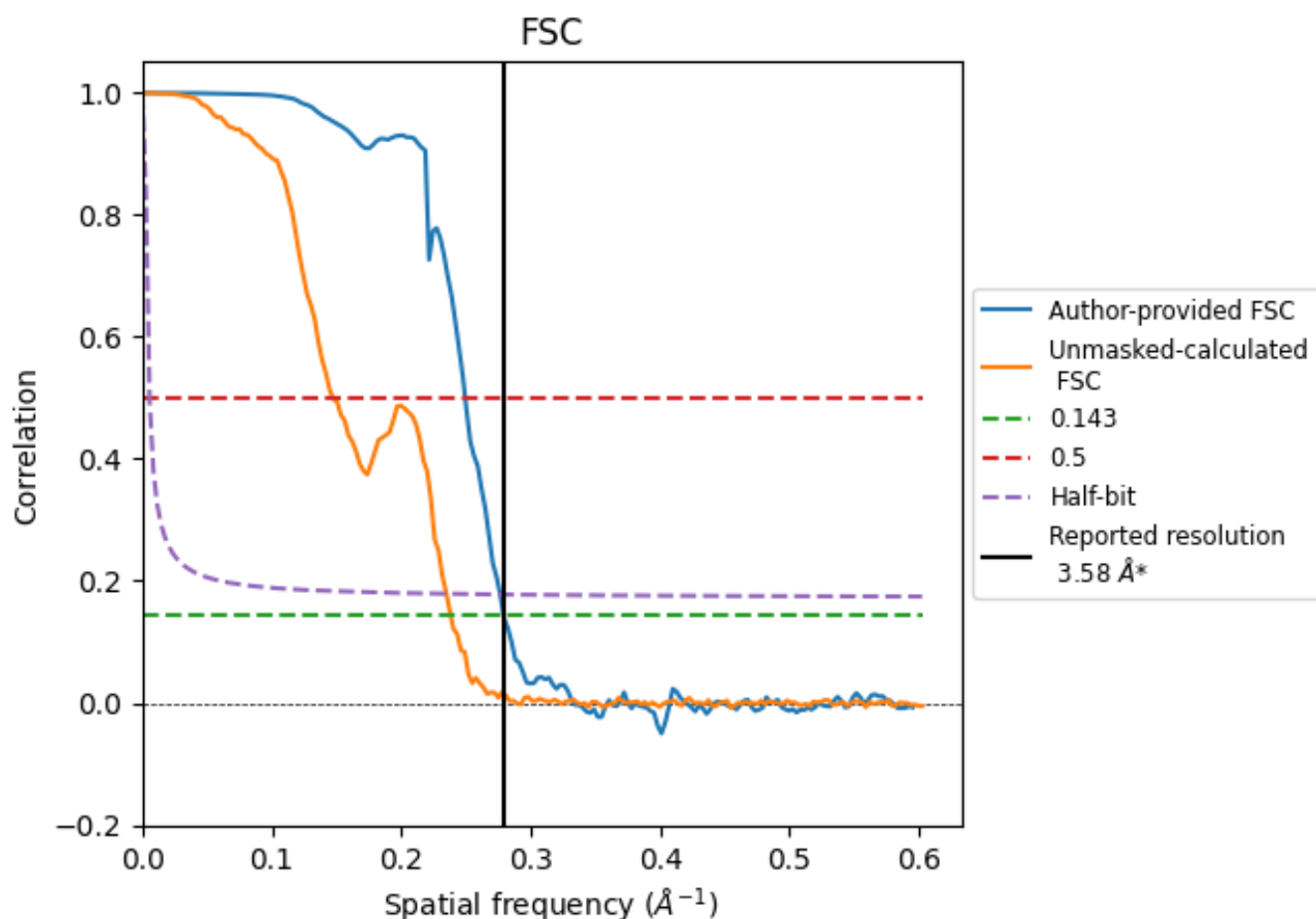


*Reported resolution corresponds to spatial frequency of 0.279 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.279 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

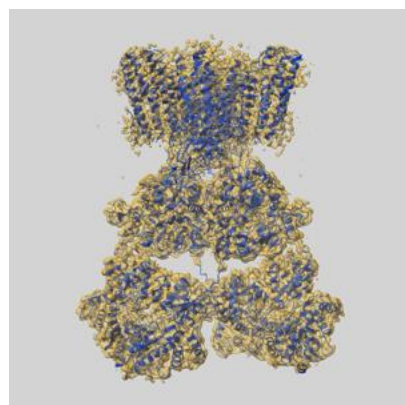
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.58	-	-
Author-provided FSC curve	3.58	4.01	3.62
Unmasked-calculated*	4.20	6.79	4.26

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.20 differs from the reported value 3.58 by more than 10 %

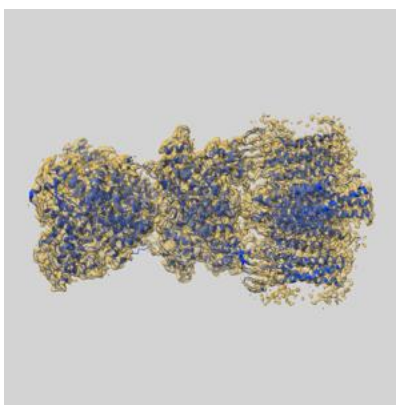
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-40741 and PDB model 8SS2. Per-residue inclusion information can be found in section 3 on page 11.

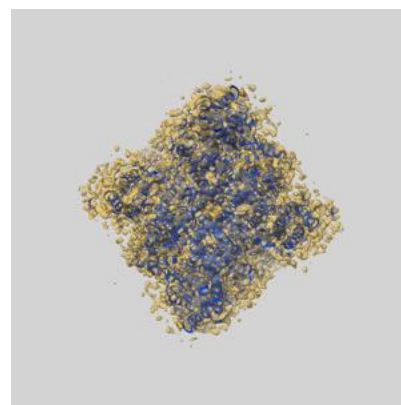
9.1 Map-model overlay [i](#)



X



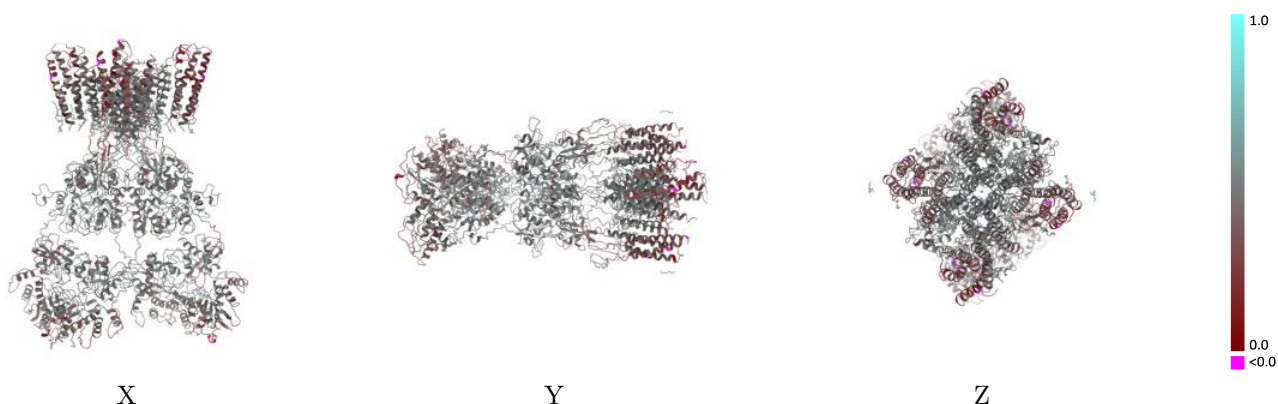
Y



Z

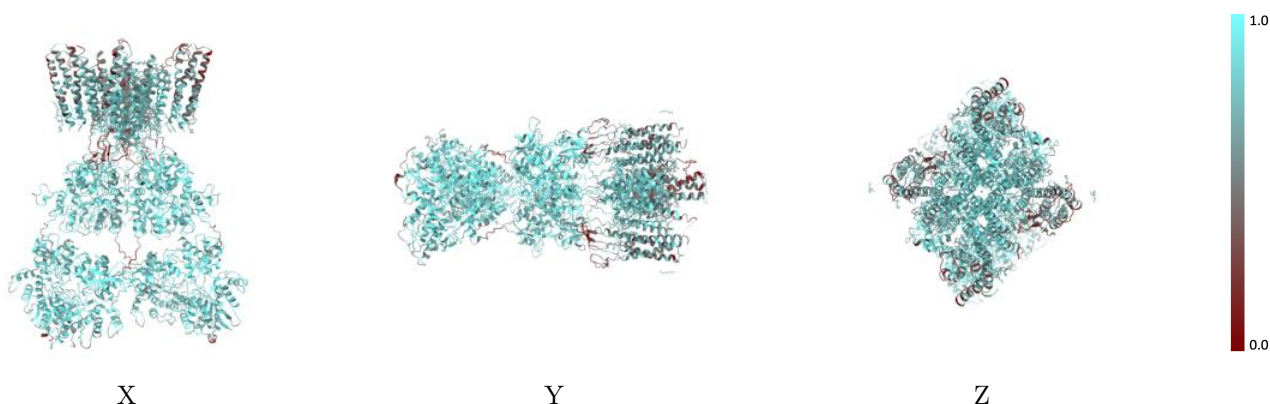
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



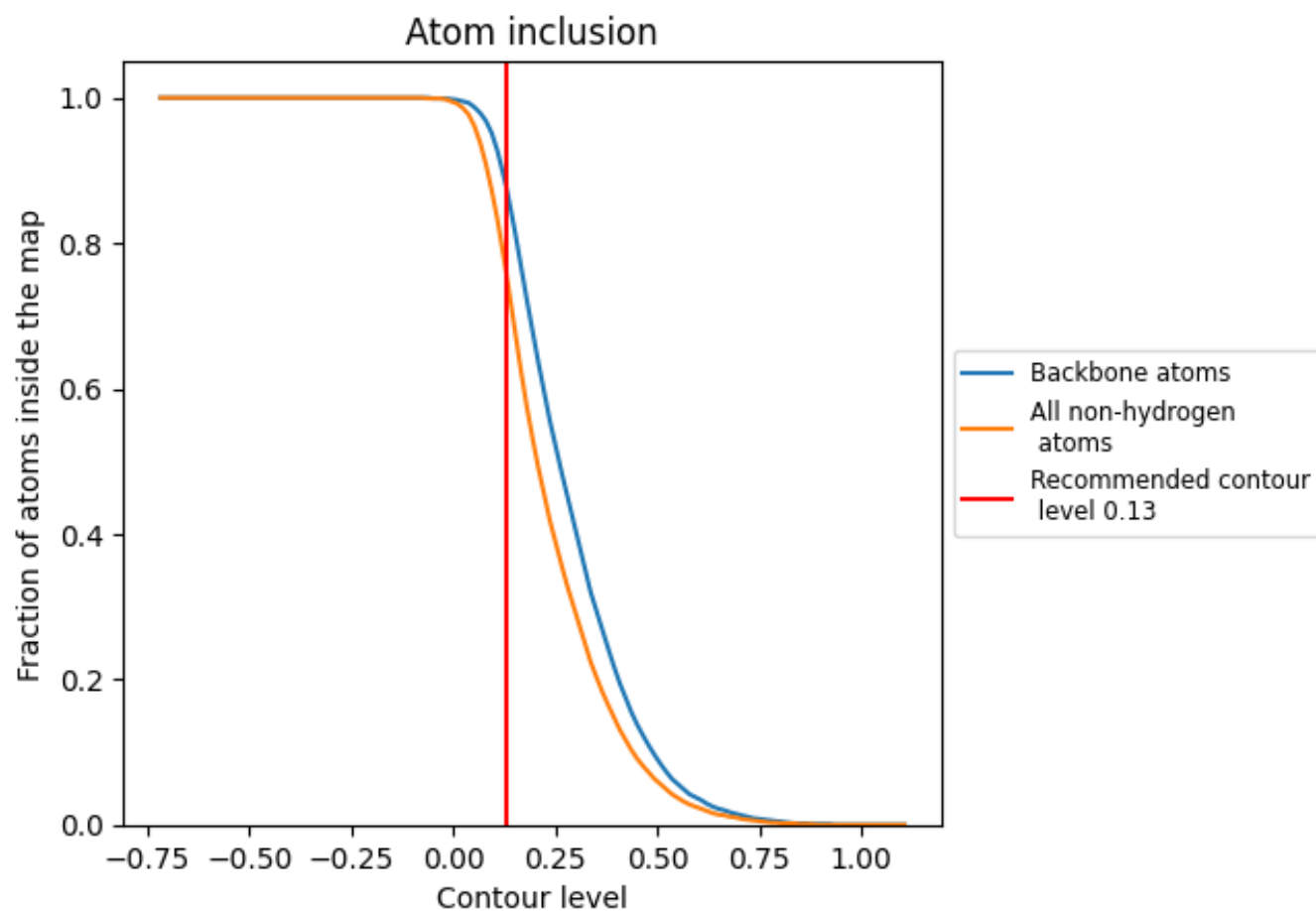
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 76% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7600	0.4380
A	0.7560	0.4420
B	0.8040	0.4580
C	0.7530	0.4380
D	0.8050	0.4550
E	0.5710	0.3300
F	0.5710	0.3270

1.0

0.0

<0.0