



Full wwPDB EM Validation Report ⓘ

Mar 7, 2026 – 04:47 AM UTC

PDB ID : 8HLV / pdb_00008hlv
EMDB ID : EMD-34883
Title : Bry-LHCII homotrimer of Bryopsis corticulans
Authors : Li, Z.H.; Shen, J.R.; Wang, W.D.
Deposited on : 2022-12-01
Resolution : 2.55 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

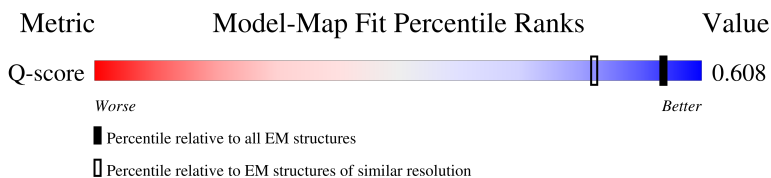
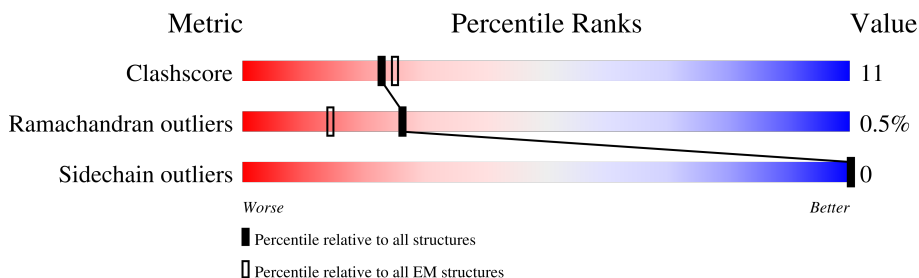
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.55 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	7475 (2.05 - 3.05)

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	249	
1	B	249	
1	C	249	

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	CHL	A	305	X	-	-	-
5	CHL	A	306	X	-	-	-
5	CHL	A	309	X	-	-	-
5	CHL	A	310	X	-	-	-
5	CHL	A	311	X	-	-	-
5	CHL	A	312	X	-	-	-
5	CHL	A	313	X	-	-	-
5	CHL	A	318	X	-	-	-
5	CHL	B	305	X	-	-	-
5	CHL	B	306	X	-	-	-
5	CHL	B	309	X	-	-	-
5	CHL	B	310	X	-	-	-
5	CHL	B	311	X	-	-	-
5	CHL	B	312	X	-	-	-
5	CHL	B	313	X	-	-	-
5	CHL	B	318	X	-	-	-
5	CHL	C	305	X	-	-	-
5	CHL	C	306	X	-	-	-
5	CHL	C	309	X	-	-	-
5	CHL	C	310	X	-	-	-
5	CHL	C	311	X	-	-	-
5	CHL	C	312	X	-	-	-
5	CHL	C	313	X	-	-	-
5	CHL	C	318	X	-	-	-
6	CLA	A	307	X	-	-	-
6	CLA	A	308	X	-	-	-
6	CLA	A	314	X	-	-	-
6	CLA	A	315	X	-	-	-
6	CLA	A	316	X	-	-	-
6	CLA	A	317	X	-	-	-
6	CLA	B	307	X	-	-	-
6	CLA	B	308	X	-	-	-
6	CLA	B	314	X	-	-	-
6	CLA	B	315	X	-	-	-
6	CLA	B	316	X	-	-	-
6	CLA	B	317	X	-	-	-
6	CLA	C	307	X	-	-	-
6	CLA	C	308	X	-	-	-
6	CLA	C	314	X	-	-	-
6	CLA	C	315	X	-	-	-
6	CLA	C	316	X	-	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	CLA	C	317	X	-	-	-

2 Entry composition [i](#)

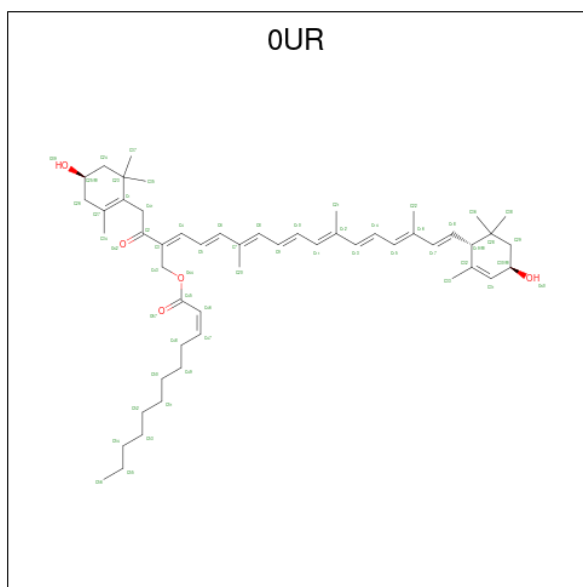
There are 7 unique types of molecules in this entry. The entry contains 8136 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Siphonaxanthin chlorophyll a/b binding light-harvesting complex II, Bry-Lhcb1.

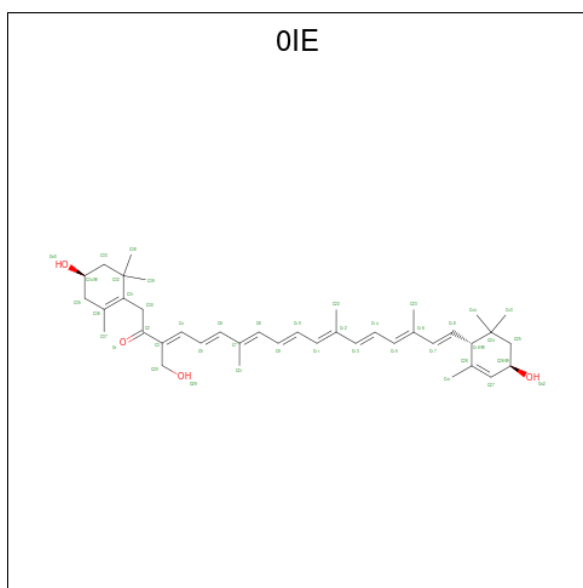
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	223	Total	C	N	O	S	0	0
			1690	1097	268	315	10		
1	B	223	Total	C	N	O	S	0	0
			1690	1097	268	315	10		
1	C	223	Total	C	N	O	S	0	0
			1690	1097	268	315	10		

- Molecule 2 is Siphonein (CCD ID: 0UR) (formula: C₅₂H₇₆O₅) (labeled as "Ligand of Interest" by depositor).



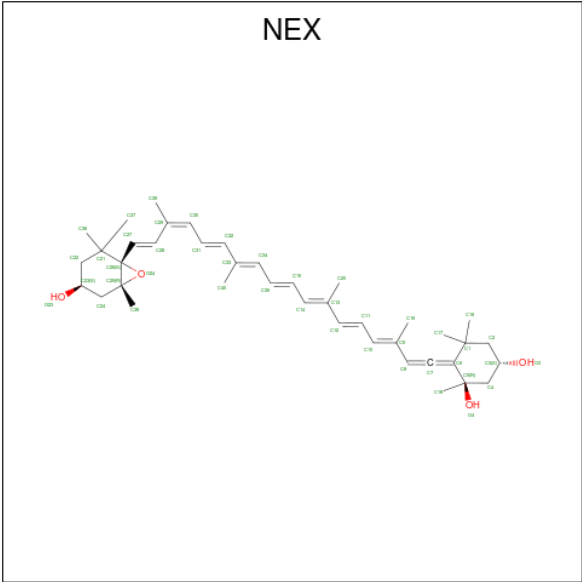
Mol	Chain	Residues	Atoms			AltConf
2	A	1	Total	C	O	0
			52	47	5	
2	B	1	Total	C	O	0
			52	47	5	
2	C	1	Total	C	O	0
			52	47	5	

- Molecule 3 is Siphonaxanthin (CCD ID: 0IE) (formula: $C_{40}H_{56}O_4$).



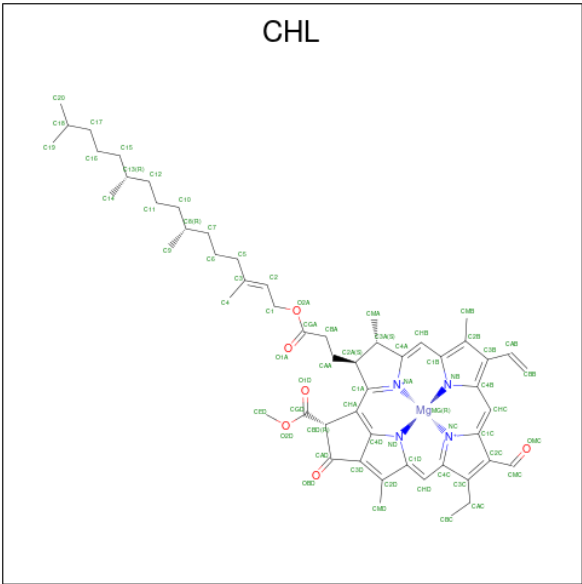
Mol	Chain	Residues	Atoms			AltConf
3	A	1	Total	C	O	0
			44	40	4	
3	A	1	Total	C	O	0
			44	40	4	
3	B	1	Total	C	O	0
			44	40	4	
3	B	1	Total	C	O	0
			44	40	4	
3	C	1	Total	C	O	0
			44	40	4	
3	C	1	Total	C	O	0
			44	40	4	

- Molecule 4 is (1R,3R)-6-[(3E,5E,7E,9E,11E,13E,15E,17E)-18-[(1S,4R,6R)-4-HYDROXY-2,2,6-TRIMETHYL-7-OXABICYCLO[4.1.0]HEPT-1-YL]-3,7,12,16-TETRAMETHYLOCTADECA-1,3,5,7,9,11,13,15,17-NONAENYLIDENE]-1,5,5-TRIMETHYLCYCLOHEXANE-1,3-DIOL (CCD ID: NEX) (formula: $C_{40}H_{56}O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
4	A	1	Total	C	O	0
			44	40	4	
4	B	1	Total	C	O	0
			44	40	4	
4	C	1	Total	C	O	0
			44	40	4	

- Molecule 5 is CHLOROPHYLL B (CCD ID: CHL) (formula: $C_{55}H_{70}MgN_4O_6$) (labeled as "Ligand of Interest" by depositor).



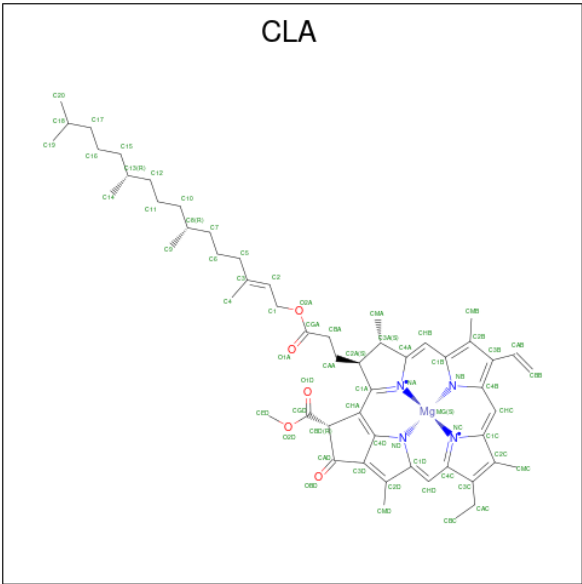
Mol	Chain	Residues	Atoms					AltConf
5	A	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
5	A	1	Total	C	Mg	N	O	0
			64	53	1	4	6	
5	A	1	Total	C	Mg	N	O	0
			43	34	1	4	4	
5	A	1	Total	C	Mg	N	O	0
			51	40	1	4	6	
5	A	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
5	A	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
5	A	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
5	A	1	Total	C	Mg	N	O	0
			44	35	1	4	4	
5	B	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
5	B	1	Total	C	Mg	N	O	0
			64	53	1	4	6	
5	B	1	Total	C	Mg	N	O	0
			43	34	1	4	4	
5	B	1	Total	C	Mg	N	O	0
			51	40	1	4	6	
5	B	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
5	B	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
5	B	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
5	B	1	Total	C	Mg	N	O	0
			47	36	1	4	6	
5	C	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
5	C	1	Total	C	Mg	N	O	0
			64	53	1	4	6	
5	C	1	Total	C	Mg	N	O	0
			43	34	1	4	4	
5	C	1	Total	C	Mg	N	O	0
			51	40	1	4	6	
5	C	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
5	C	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

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Mol	Chain	Residues	Atoms					AltConf
5	C	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
5	C	1	Total	C	Mg	N	O	0
			44	35	1	4	4	

- Molecule 6 is CHLOROPHYLL A (CCD ID: CLA) (formula: C₅₅H₇₂MgN₄O₅) (labeled as "Ligand of Interest" by depositor).



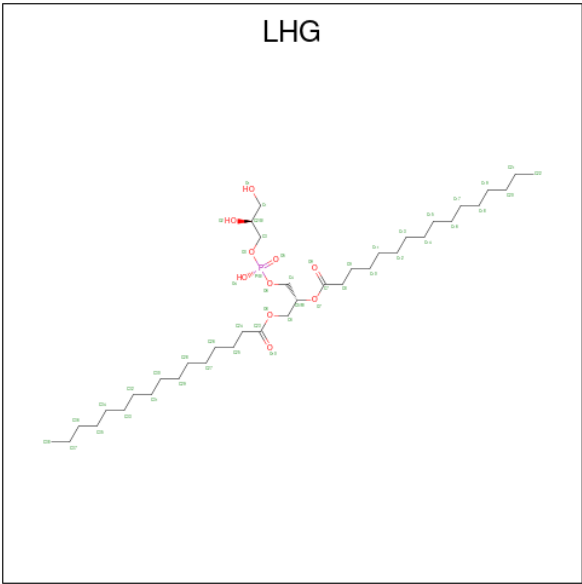
Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
6	A	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
6	A	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
6	A	1	Total	C	Mg	N	O	0
			63	53	1	4	5	
6	A	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
6	A	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
6	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
6	B	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
6	B	1	Total	C	Mg	N	O	0
			55	45	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
6	B	1	Total	C	Mg	N	O	0
			63	53	1	4	5	
6	B	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
6	B	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
6	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
6	C	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
6	C	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
6	C	1	Total	C	Mg	N	O	0
			63	53	1	4	5	
6	C	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
6	C	1	Total	C	Mg	N	O	0
			55	45	1	4	5	

- Molecule 7 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: C₃₈H₇₅O₁₀P).



Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	O	P	0
			43	32	10	1	
7	B	1	Total	C	O	P	0
			43	32	10	1	

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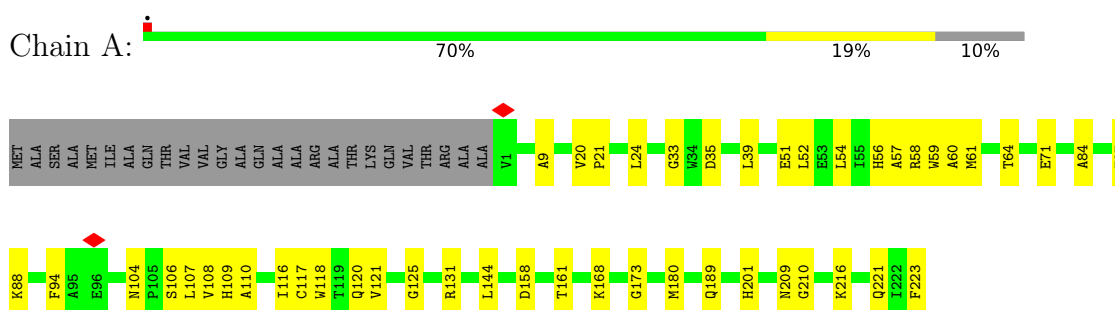
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Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
7	C	1	43	32	10	1	0

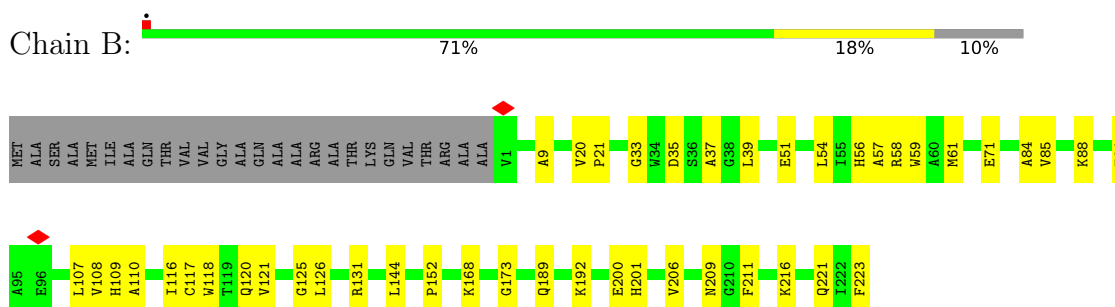
3 Residue-property plots [i](#)

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.

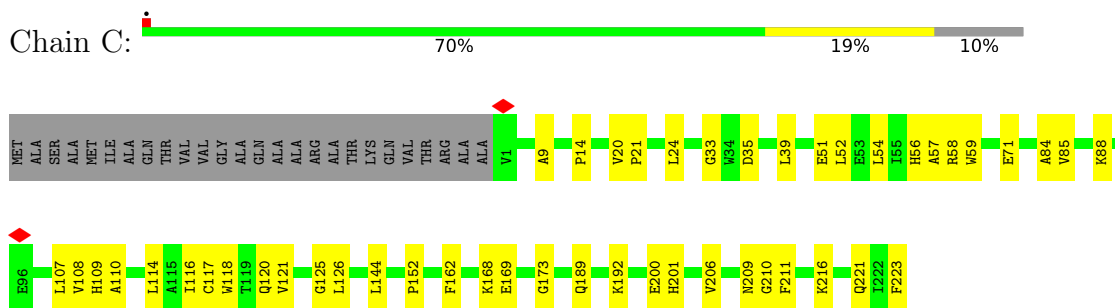
- Molecule 1: Siphonaxanthin chlorophyll a/b binding light-harvesting complex II, Bry-Lhcb1



- Molecule 1: Siphonaxanthin chlorophyll a/b binding light-harvesting complex II, Bry-Lhcb1



- Molecule 1: Siphonaxanthin chlorophyll a/b binding light-harvesting complex II, Bry-Lhcb1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	614955	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.903	Depositor
Minimum map value	-0.282	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.024	Depositor
Recommended contour level	0.207	Depositor
Map size ($\text{\AA}$)	266.24, 266.24, 266.24	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.04, 1.04, 1.04	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NEX, LHG, CHL, OIE, CLA, OUR

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	0.16	0/1743	0.27	0/2371
1	B	0.16	0/1743	0.28	0/2371
1	C	0.15	0/1743	0.26	0/2371
All	All	0.16	0/5229	0.27	0/7113

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1690	0	1593	39	0
1	B	1690	0	1593	39	0
1	C	1690	0	1593	41	0
2	A	52	0	0	3	0
2	B	52	0	0	3	0
2	C	52	0	0	3	0
3	A	88	0	0	1	0
3	B	88	0	0	0	0
3	C	88	0	0	0	0
4	A	44	0	56	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	44	0	56	3	0
4	C	44	0	56	3	0
5	A	461	0	425	23	0
5	B	464	0	425	25	0
5	C	461	0	425	28	0
6	A	333	0	305	13	0
6	B	333	0	305	15	0
6	C	333	0	305	15	0
7	A	43	0	56	1	0
7	B	43	0	56	1	0
7	C	43	0	56	0	0
All	All	8136	0	7305	173	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 11.

All (173) 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)
4:A:304:NEX:H403	5:A:310:CHL:HBA2	1.49	0.95
5:A:306:CHL:H51	5:A:306:CHL:HBB1	1.51	0.93
5:C:306:CHL:HBB1	5:C:306:CHL:H51	1.51	0.91
4:B:304:NEX:H403	5:B:310:CHL:HBA2	1.57	0.85
4:A:304:NEX:H403	5:A:310:CHL:CBA	2.09	0.81
4:C:304:NEX:H403	5:C:310:CHL:HBA2	1.62	0.81
4:C:304:NEX:H403	5:C:310:CHL:CBA	2.16	0.74
4:B:304:NEX:H403	5:B:310:CHL:CBA	2.16	0.74
1:A:209:ASN:HD22	1:C:114:LEU:HD21	1.60	0.67
1:B:192:LYS:NZ	1:B:200:GLU:OE2	2.29	0.65
1:B:61:MET:HE3	6:B:314:CLA:CMC	2.26	0.64
1:B:61:MET:HE3	6:B:314:CLA:HMC2	1.78	0.64
1:C:206:VAL:O	1:C:209:ASN:ND2	2.32	0.62
1:B:206:VAL:O	1:B:209:ASN:ND2	2.33	0.61
1:C:192:LYS:NZ	1:C:200:GLU:OE2	2.31	0.61
1:A:180:MET:HG2	3:A:302:OIE:C6	2.32	0.60
1:C:221:GLN:NE2	1:C:223:PHE:OXT	2.37	0.58
1:A:54:LEU:HD23	1:A:144:LEU:HB3	1.86	0.58
1:B:54:LEU:HD23	1:B:144:LEU:HB3	1.85	0.58
1:C:201:HIS:CD2	5:C:318:CHL:NC	2.71	0.58
1:C:21:PRO:HG2	1:C:35:ASP:HB3	1.86	0.57
1:B:189:GLN:NE2	1:B:216:LYS:O	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:189:GLN:NE2	1:C:216:LYS:O	2.33	0.57
1:C:54:LEU:HD23	1:C:144:LEU:HB3	1.86	0.57
1:C:210:GLY:H	5:C:318:CHL:HED1	1.70	0.57
6:C:307:CLA:HAC1	5:C:311:CHL:HBB2	1.87	0.56
1:C:58:ARG:NH1	5:C:312:CHL:OBD	2.37	0.56
1:B:61:MET:HE1	6:B:314:CLA:CHC	2.34	0.56
1:A:221:GLN:NE2	1:A:223:PHE:OXT	2.38	0.56
1:B:221:GLN:NE2	1:B:223:PHE:OXT	2.38	0.56
6:B:307:CLA:HAC1	5:B:311:CHL:HBB2	1.87	0.56
1:A:21:PRO:HG2	1:A:35:ASP:HB3	1.88	0.55
1:A:189:GLN:NE2	1:A:216:LYS:O	2.35	0.55
5:A:318:CHL:HBD	1:C:118:TRP:HZ2	1.72	0.55
1:A:61:MET:HE1	6:A:314:CLA:CAB	2.36	0.55
1:A:20:VAL:HG13	1:A:33:GLY:HA3	1.89	0.55
1:A:125:GLY:HA2	5:A:313:CHL:HAB	1.89	0.55
1:B:21:PRO:HG2	1:B:35:ASP:HB3	1.89	0.55
1:B:118:TRP:HZ2	5:C:318:CHL:HBD	1.72	0.55
6:A:307:CLA:HAC1	5:A:311:CHL:HBB2	1.89	0.54
1:B:125:GLY:HA2	5:B:313:CHL:HAB	1.90	0.54
5:C:312:CHL:HBB1	5:C:312:CHL:HHC	1.90	0.54
2:B:301:0UR:C15	6:B:314:CLA:H72	2.39	0.53
1:A:61:MET:HE2	2:A:301:0UR:C11	2.39	0.53
1:C:56:HIS:HE1	6:C:307:CLA:C4D	2.22	0.53
1:B:117:CYS:O	1:B:121:VAL:HG23	2.09	0.53
1:B:201:HIS:CD2	5:B:318:CHL:NC	2.77	0.53
6:C:307:CLA:HBC1	5:C:313:CHL:CBC	2.39	0.52
1:C:117:CYS:O	1:C:121:VAL:HG23	2.09	0.52
1:B:58:ARG:NH1	5:B:312:CHL:OBD	2.33	0.52
1:B:56:HIS:HE1	6:B:307:CLA:C4D	2.23	0.52
6:B:307:CLA:H12	1:C:39:LEU:HD11	1.92	0.52
1:A:118:TRP:HZ2	5:B:318:CHL:HBD	1.75	0.51
2:C:301:0UR:C15	6:C:314:CLA:H72	2.40	0.51
5:A:312:CHL:HBB1	5:A:312:CHL:HHC	1.91	0.51
2:A:301:0UR:C15	6:A:314:CLA:H72	2.40	0.51
1:B:57:ALA:HB1	1:B:173:GLY:HA3	1.93	0.51
6:B:307:CLA:HBC1	5:B:313:CHL:CBC	2.41	0.50
1:A:120:GLN:OE1	5:A:311:CHL:HMC	2.12	0.50
5:B:312:CHL:HHC	5:B:312:CHL:HBB1	1.92	0.50
2:C:301:0UR:C13	6:C:314:CLA:HAB	2.41	0.50
1:C:125:GLY:HA2	5:C:313:CHL:HAB	1.92	0.50
1:A:57:ALA:O	1:A:61:MET:HG3	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:85:VAL:HG23	1:C:88:LYS:HB2	1.93	0.49
1:B:59:TRP:CE2	5:B:312:CHL:HED2	2.47	0.49
1:C:57:ALA:HB1	1:C:173:GLY:HA3	1.95	0.49
1:A:107:LEU:O	1:A:109:HIS:N	2.45	0.49
1:A:210:GLY:H	5:A:318:CHL:HED1	1.77	0.49
6:A:307:CLA:H12	1:B:39:LEU:HD11	1.94	0.49
1:A:168:LYS:HD3	6:A:316:CLA:HAA2	1.95	0.48
1:B:85:VAL:HG23	1:B:88:LYS:HB2	1.96	0.48
1:A:58:ARG:NH1	5:A:312:CHL:OBD	2.37	0.48
1:B:110:ALA:HB1	1:B:116:ILE:HD11	1.95	0.48
2:B:301:0UR:C13	6:B:314:CLA:HAB	2.43	0.48
1:B:9:ALA:HB1	5:B:305:CHL:HBC1	1.93	0.48
5:A:311:CHL:H92	5:A:313:CHL:H193	1.95	0.48
1:C:120:GLN:OE1	5:C:311:CHL:HMC	2.12	0.48
5:C:312:CHL:H143	5:C:312:CHL:H162	1.69	0.48
1:A:59:TRP:CE2	5:A:312:CHL:HED2	2.48	0.48
1:C:20:VAL:HG13	1:C:33:GLY:HA3	1.94	0.48
1:C:107:LEU:O	1:C:109:HIS:N	2.46	0.48
1:B:120:GLN:OE1	5:B:311:CHL:HMC	2.14	0.48
1:C:59:TRP:CE2	5:C:312:CHL:HED2	2.48	0.48
5:A:313:CHL:HMB2	5:B:305:CHL:HHB	1.96	0.47
1:A:104:ASN:OD1	1:A:106:SER:OG	2.22	0.47
1:A:201:HIS:HB2	6:A:317:CLA:HAA2	1.96	0.47
1:B:107:LEU:O	1:B:109:HIS:N	2.46	0.47
5:B:311:CHL:H92	5:B:313:CHL:H193	1.96	0.47
1:A:87:PHE:HE1	1:A:88:LYS:NZ	2.13	0.47
1:C:56:HIS:HE1	6:C:307:CLA:ND	2.06	0.47
1:C:9:ALA:HB1	5:C:305:CHL:HBC1	1.97	0.46
1:C:168:LYS:HD3	6:C:316:CLA:HAA2	1.96	0.46
5:C:305:CHL:H41	5:C:305:CHL:H61	1.74	0.46
1:A:64:THR:HA	1:A:180:MET:HE1	1.98	0.46
1:A:39:LEU:HD11	6:C:307:CLA:H12	1.97	0.46
5:A:306:CHL:H142	5:A:306:CHL:H112	1.65	0.46
1:B:71:GLU:HA	1:B:84:ALA:HB1	1.98	0.46
1:A:117:CYS:O	1:A:121:VAL:HG23	2.15	0.46
6:C:315:CLA:H2	6:C:316:CLA:HMD2	1.98	0.46
1:B:56:HIS:HE1	6:B:307:CLA:ND	2.09	0.46
1:A:60:ALA:O	1:A:64:THR:HG23	2.16	0.46
5:B:306:CHL:HBB1	5:B:306:CHL:HHC	1.96	0.46
1:B:201:HIS:HB2	6:B:317:CLA:HAA2	1.98	0.46
1:A:24:LEU:HD11	1:A:35:ASP:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:ALA:HB1	5:A:305:CHL:HBC1	1.98	0.45
1:A:57:ALA:HB1	1:A:173:GLY:HA3	1.98	0.45
5:A:305:CHL:H41	5:A:305:CHL:H61	1.75	0.45
1:B:20:VAL:HG13	1:B:33:GLY:HA3	1.98	0.45
7:A:319:LHG:H272	7:A:319:LHG:H242	1.56	0.45
1:C:201:HIS:HB2	6:C:317:CLA:HAA2	1.98	0.45
5:C:310:CHL:HMB1	5:C:313:CHL:HMC	1.98	0.45
1:A:51:GLU:HA	1:A:144:LEU:HD21	1.98	0.45
5:A:305:CHL:HBA1	5:A:305:CHL:H3A	1.73	0.45
5:B:313:CHL:HMB2	5:C:305:CHL:HHB	2.00	0.45
1:A:71:GLU:HA	1:A:84:ALA:HB1	1.99	0.44
1:A:158:ASP:HB3	1:A:161:THR:OG1	2.18	0.44
1:C:152:PRO:HD2	2:C:301:OUR:C30	2.48	0.44
1:B:201:HIS:CG	6:B:317:CLA:HAA2	2.52	0.44
5:A:312:CHL:H162	5:A:312:CHL:H143	1.69	0.44
1:B:168:LYS:HD3	6:B:316:CLA:HAA2	1.99	0.43
6:A:307:CLA:HBC1	5:A:313:CHL:CBC	2.49	0.43
6:B:307:CLA:H142	6:B:307:CLA:H111	1.75	0.43
1:A:201:HIS:CG	6:A:317:CLA:HAA2	2.54	0.43
1:C:14:PRO:HD2	5:C:305:CHL:HBB1	2.00	0.43
1:C:201:HIS:CG	6:C:317:CLA:HAA2	2.53	0.43
2:A:301:OUR:C13	6:A:314:CLA:HAB	2.48	0.43
5:B:312:CHL:H162	5:B:312:CHL:H143	1.69	0.43
1:C:51:GLU:HA	1:C:144:LEU:HD21	2.00	0.43
1:B:51:GLU:HA	1:B:144:LEU:HD21	1.99	0.43
1:B:131:ARG:NH2	5:B:313:CHL:O1D	2.47	0.43
6:A:307:CLA:H72	6:A:307:CLA:H112	1.74	0.42
1:A:210:GLY:N	6:A:317:CLA:O1A	2.52	0.42
1:C:24:LEU:HD11	1:C:35:ASP:HB2	2.01	0.42
1:A:94:PHE:HZ	1:B:211:PHE:HB3	1.84	0.42
1:C:71:GLU:HA	1:C:84:ALA:HB1	2.01	0.42
1:C:162:PHE:CZ	6:C:314:CLA:HED2	2.54	0.42
5:C:311:CHL:H92	5:C:313:CHL:H193	2.02	0.42
6:A:307:CLA:H142	6:A:307:CLA:H111	1.76	0.42
1:A:54:LEU:HB3	1:A:144:LEU:HD22	2.02	0.42
1:C:51:GLU:HA	1:C:144:LEU:HD11	2.01	0.42
5:C:306:CHL:H142	5:C:306:CHL:H112	1.65	0.42
1:A:131:ARG:NH2	5:A:313:CHL:O1D	2.47	0.42
5:A:306:CHL:H141	5:A:306:CHL:H162	1.73	0.42
1:B:54:LEU:HB3	1:B:144:LEU:HD22	2.02	0.42
1:B:94:PHE:HZ	1:C:211:PHE:HB3	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:ALA:HB1	1:A:116:ILE:HD11	2.02	0.41
5:A:305:CHL:HBB1	5:A:305:CHL:HHC	2.02	0.41
5:C:305:CHL:HBB1	5:C:305:CHL:HHC	2.02	0.41
1:C:125:GLY:CA	5:C:313:CHL:HAB	2.51	0.41
1:B:118:TRP:CZ2	5:C:318:CHL:HBD	2.54	0.41
5:B:312:CHL:H172	5:B:312:CHL:HBA1	2.02	0.41
1:C:210:GLY:N	6:C:317:CLA:O1A	2.53	0.41
1:C:54:LEU:HB3	1:C:144:LEU:HD22	2.02	0.41
6:B:307:CLA:OBD	5:B:313:CHL:CGA	2.68	0.41
5:B:313:CHL:H62	5:B:313:CHL:H2	1.91	0.41
1:C:169:GLU:HB2	6:C:314:CLA:CHB	2.51	0.41
7:B:319:LHG:H272	7:B:319:LHG:H242	1.58	0.41
1:C:126:LEU:HB2	4:C:304:NEX:C20	2.49	0.41
5:C:305:CHL:HBA1	5:C:305:CHL:H3A	1.76	0.41
1:A:56:HIS:CE1	6:A:307:CLA:ND	2.88	0.41
5:B:306:CHL:H141	5:B:306:CHL:H162	1.68	0.41
1:B:120:GLN:HE22	5:B:311:CHL:CMC	2.34	0.40
1:B:152:PRO:HD2	2:B:301:OUR:C30	2.51	0.40
6:C:307:CLA:H142	6:C:307:CLA:H111	1.76	0.40
1:A:52:LEU:HD11	1:B:37:ALA:HA	2.02	0.40
1:C:52:LEU:HD23	5:C:313:CHL:OBD	2.21	0.40
1:C:110:ALA:HB1	1:C:116:ILE:HD11	2.03	0.40
5:C:305:CHL:H12	5:C:305:CHL:H51	1.78	0.40
5:B:305:CHL:HBA1	5:B:305:CHL:H3A	1.76	0.40
5:C:306:CHL:H141	5:C:306:CHL:H162	1.73	0.40
5:A:305:CHL:H12	5:A:305:CHL:H51	1.76	0.40
1:B:126:LEU:HB2	4:B:304:NEX:C20	2.52	0.40
5:B:305:CHL:HHC	5:B:305:CHL:HBB1	2.02	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	221/249 (89%)	215 (97%)	5 (2%)	1 (0%)	24	34
1	B	221/249 (89%)	216 (98%)	4 (2%)	1 (0%)	24	34
1	C	221/249 (89%)	215 (97%)	5 (2%)	1 (0%)	24	34
All	All	663/747 (89%)	646 (97%)	14 (2%)	3 (0%)	26	34

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	108	VAL
1	C	108	VAL
1	B	108	VAL

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	165/184 (90%)	165 (100%)	0	100	100
1	B	165/184 (90%)	165 (100%)	0	100	100
1	C	165/184 (90%)	165 (100%)	0	100	100
All	All	495/552 (90%)	495 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
1	B	172	ASN
1	C	111	GLN

5.3.3 RNA ⓘ

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](#)

57 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	$\# Z > 2$
5	CHL	C	309	1	37,51,74	4.19	17 (45%)	30,86,114	3.94	17 (56%)
6	CLA	C	315	7	67,71,73	1.17	9 (13%)	79,110,113	1.28	4 (5%)
6	CLA	A	314	1	59,63,73	1.26	9 (15%)	70,101,113	1.34	9 (12%)
2	OUR	A	301	-	50,53,58	1.01	1 (2%)	59,72,77	1.67	14 (23%)
5	CHL	B	311	-	55,69,74	3.49	18 (32%)	51,107,114	3.25	23 (45%)
6	CLA	B	307	-	69,73,73	1.15	8 (11%)	82,113,113	1.26	6 (7%)
6	CLA	C	314	1	59,63,73	1.26	9 (15%)	70,101,113	1.33	9 (12%)
3	OIE	A	303	-	42,45,45	1.13	6 (14%)	51,63,63	1.56	10 (19%)
5	CHL	B	312	-	60,74,74	3.33	18 (30%)	58,114,114	3.04	20 (34%)
5	CHL	B	306	1	58,72,74	3.43	18 (31%)	55,111,114	2.86	18 (32%)
5	CHL	C	312	-	60,74,74	3.31	18 (30%)	58,114,114	3.04	20 (34%)
5	CHL	C	306	1	58,72,74	3.44	19 (32%)	55,111,114	2.91	19 (34%)
6	CLA	A	316	1	49,53,73	1.37	9 (18%)	58,89,113	1.44	4 (6%)
5	CHL	B	313	1	60,74,74	3.35	18 (30%)	58,114,114	2.91	19 (32%)
6	CLA	A	315	7	67,71,73	1.18	8 (11%)	79,110,113	1.30	5 (6%)
3	OIE	A	302	-	42,45,45	1.12	6 (14%)	51,63,63	1.58	10 (19%)
5	CHL	C	313	1	60,74,74	3.35	18 (30%)	58,114,114	2.91	19 (32%)
6	CLA	A	317	1	59,63,73	1.26	8 (13%)	69,100,113	1.34	4 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CLA	B	308	-	54,58,73	1.30	8 (14%)	64,95,113	1.39	7 (10%)
4	NEX	C	304	-	40,46,46	1.67	3 (7%)	50,70,70	1.07	4 (8%)
2	OUR	B	301	-	50,53,58	1.01	1 (2%)	59,72,77	1.75	14 (23%)
5	CHL	A	305	1	60,74,74	3.34	18 (30%)	58,114,114	2.95	20 (34%)
5	CHL	B	309	1	37,51,74	4.19	17 (45%)	30,86,114	3.95	16 (53%)
4	NEX	B	304	-	40,46,46	1.63	3 (7%)	50,70,70	1.03	4 (8%)
5	CHL	A	311	-	55,69,74	3.50	18 (32%)	51,107,114	3.23	22 (43%)
6	CLA	A	308	-	54,58,73	1.30	9 (16%)	64,95,113	1.39	7 (10%)
3	OIE	C	303	-	42,45,45	1.13	6 (14%)	51,63,63	1.52	10 (19%)
3	OIE	B	303	-	42,45,45	1.13	6 (14%)	51,63,63	1.55	11 (21%)
5	CHL	B	305	1	60,74,74	3.33	18 (30%)	58,114,114	2.95	20 (34%)
5	CHL	A	310	-	45,59,74	3.83	19 (42%)	40,96,114	3.63	19 (47%)
5	CHL	B	318	-	41,55,74	4.10	18 (43%)	35,91,114	3.50	16 (45%)
4	NEX	A	304	-	40,46,46	1.56	2 (5%)	50,70,70	0.95	3 (6%)
5	CHL	C	318	-	38,52,74	4.18	17 (44%)	31,87,114	3.63	15 (48%)
2	OUR	C	301	-	50,53,58	1.01	1 (2%)	59,72,77	1.72	14 (23%)
5	CHL	A	313	1	60,74,74	3.36	18 (30%)	58,114,114	2.90	18 (31%)
5	CHL	B	310	-	45,59,74	3.84	18 (40%)	40,96,114	3.64	18 (45%)
6	CLA	C	316	1	49,53,73	1.37	9 (18%)	58,89,113	1.44	4 (6%)
3	OIE	C	302	-	42,45,45	1.12	6 (14%)	51,63,63	1.55	9 (17%)
6	CLA	B	315	7	67,71,73	1.18	8 (11%)	79,110,113	1.28	5 (6%)
6	CLA	B	317	1	59,63,73	1.25	9 (15%)	69,100,113	1.33	4 (5%)
6	CLA	C	307	-	69,73,73	1.15	8 (11%)	82,113,113	1.26	5 (6%)
5	CHL	C	305	1	60,74,74	3.34	18 (30%)	58,114,114	2.92	20 (34%)
7	LHG	A	319	6	42,42,48	1.21	5 (11%)	45,48,54	1.37	4 (8%)
6	CLA	C	317	1	59,63,73	1.25	9 (15%)	69,100,113	1.35	4 (5%)
5	CHL	C	311	-	55,69,74	3.50	18 (32%)	51,107,114	3.25	21 (41%)
6	CLA	B	314	1	59,63,73	1.26	9 (15%)	70,101,113	1.34	9 (12%)
7	LHG	B	319	6	42,42,48	1.21	5 (11%)	45,48,54	1.36	4 (8%)
7	LHG	C	319	6	42,42,48	1.20	5 (11%)	45,48,54	1.35	4 (8%)
5	CHL	A	309	1	37,51,74	4.19	18 (48%)	30,86,114	3.94	17 (56%)
6	CLA	C	308	-	54,58,73	1.31	9 (16%)	64,95,113	1.39	7 (10%)
5	CHL	C	310	-	45,59,74	3.83	18 (40%)	40,96,114	3.63	19 (47%)
3	OIE	B	302	-	42,45,45	1.12	6 (14%)	51,63,63	1.55	10 (19%)
6	CLA	B	316	1	49,53,73	1.38	9 (18%)	58,89,113	1.44	4 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	CHL	A	318	-	38,52,74	4.17	18 (47%)	31,87,114	3.64	15 (48%)
5	CHL	A	312	-	60,74,74	3.31	18 (30%)	58,114,114	3.03	20 (34%)
6	CLA	A	307	-	69,73,73	1.15	9 (13%)	82,113,113	1.30	7 (8%)
5	CHL	A	306	1	58,72,74	3.43	18 (31%)	55,111,114	2.91	18 (32%)

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
5	CHL	C	309	1	3/3/15/26	3/12/110/137	-
6	CLA	C	315	7	1/1/14/20	5/37/113/115	-
6	CLA	A	314	1	1/1/13/20	4/27/103/115	-
2	OUR	A	301	-	-	9/42/81/86	0/2/2/2
5	CHL	B	311	-	3/3/18/26	21/33/131/137	-
6	CLA	B	307	-	1/1/15/20	6/39/115/115	-
6	CLA	C	314	1	1/1/13/20	4/27/103/115	-
3	OIE	A	303	-	-	6/33/72/72	0/2/2/2
5	CHL	B	312	-	3/3/20/26	13/39/137/137	-
5	CHL	B	306	1	3/3/19/26	12/37/135/137	-
5	CHL	C	312	-	3/3/20/26	15/39/137/137	-
5	CHL	C	306	1	3/3/19/26	17/37/135/137	-
6	CLA	A	316	1	1/1/11/20	6/15/91/115	-
5	CHL	B	313	1	3/3/20/26	14/39/137/137	-
6	CLA	A	315	7	1/1/14/20	6/37/113/115	-
5	CHL	C	313	1	3/3/20/26	14/39/137/137	-
6	CLA	A	317	1	1/1/12/20	7/27/103/115	-
6	CLA	B	308	-	1/1/12/20	5/21/97/115	-
3	OIE	A	302	-	-	7/33/72/72	0/2/2/2
4	NEX	C	304	-	-	2/27/83/83	0/3/3/3
5	CHL	A	305	1	3/3/20/26	18/39/137/137	-
5	CHL	B	309	1	3/3/15/26	3/12/110/137	-
2	OUR	B	301	-	-	9/42/81/86	0/2/2/2
5	CHL	A	311	-	3/3/18/26	20/33/131/137	-
4	NEX	B	304	-	-	2/27/83/83	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	CLA	A	308	-	1/1/12/20	7/21/97/115	-
6	CLA	B	315	7	1/1/14/20	6/37/113/115	-
5	CHL	B	305	1	3/3/20/26	19/39/137/137	-
3	OIE	B	303	-	-	9/33/72/72	0/2/2/2
5	CHL	A	310	-	3/3/17/26	8/21/119/137	-
5	CHL	B	318	-	3/3/16/26	6/17/115/137	-
5	CHL	C	318	-	3/3/15/26	3/13/111/137	-
3	OIE	C	303	-	-	8/33/72/72	0/2/2/2
6	CLA	C	316	1	1/1/11/20	3/15/91/115	-
5	CHL	A	313	1	3/3/20/26	14/39/137/137	-
5	CHL	B	310	-	3/3/17/26	8/21/119/137	-
2	OUR	C	301	-	-	10/42/81/86	0/2/2/2
6	CLA	B	317	1	1/1/12/20	4/27/103/115	-
6	CLA	C	307	-	1/1/15/20	6/39/115/115	-
3	OIE	C	302	-	-	8/33/72/72	0/2/2/2
4	NEX	A	304	-	-	3/27/83/83	0/3/3/3
5	CHL	C	305	1	3/3/20/26	17/39/137/137	-
7	LHG	A	319	6	-	24/47/47/53	-
6	CLA	C	317	1	1/1/12/20	6/27/103/115	-
5	CHL	C	311	-	3/3/18/26	20/33/131/137	-
6	CLA	B	314	1	1/1/13/20	4/27/103/115	-
7	LHG	B	319	6	-	24/47/47/53	-
7	LHG	C	319	6	-	22/47/47/53	-
5	CHL	A	309	1	3/3/15/26	4/12/110/137	-
6	CLA	C	308	-	1/1/12/20	5/21/97/115	-
5	CHL	C	310	-	3/3/17/26	8/21/119/137	-
3	OIE	B	302	-	-	6/33/72/72	0/2/2/2
6	CLA	B	316	1	1/1/11/20	4/15/91/115	-
5	CHL	A	318	-	3/3/15/26	3/13/111/137	-
5	CHL	A	312	-	3/3/20/26	14/39/137/137	-
6	CLA	A	307	-	1/1/15/20	5/39/115/115	-
5	CHL	A	306	1	3/3/19/26	17/37/135/137	-

All (649) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	318	CHL	C2C-C3C	12.04	1.48	1.36
5	C	318	CHL	C2C-C3C	12.04	1.48	1.36
5	A	306	CHL	C2C-C3C	12.03	1.48	1.36
5	B	306	CHL	C2C-C3C	12.03	1.48	1.36
5	C	306	CHL	C2C-C3C	12.03	1.48	1.36
5	A	318	CHL	C2C-C3C	11.96	1.48	1.36
5	C	313	CHL	C2C-C3C	11.57	1.47	1.36
5	B	313	CHL	C2C-C3C	11.52	1.47	1.36
5	A	313	CHL	C2C-C3C	11.50	1.47	1.36
5	B	312	CHL	C2C-C3C	11.43	1.47	1.36
5	A	309	CHL	C2C-C3C	11.39	1.47	1.36
5	C	311	CHL	C2C-C3C	11.39	1.47	1.36
5	A	311	CHL	C2C-C3C	11.37	1.47	1.36
5	B	309	CHL	C2C-C3C	11.36	1.47	1.36
5	B	311	CHL	C2C-C3C	11.35	1.47	1.36
5	C	309	CHL	C2C-C3C	11.33	1.47	1.36
5	B	305	CHL	C2C-C3C	11.32	1.47	1.36
5	C	305	CHL	C2C-C3C	11.32	1.47	1.36
5	B	310	CHL	C2C-C3C	11.29	1.47	1.36
5	A	312	CHL	C2C-C3C	11.27	1.47	1.36
5	A	305	CHL	C2C-C3C	11.25	1.47	1.36
5	C	312	CHL	C2C-C3C	11.25	1.47	1.36
5	C	310	CHL	C2C-C3C	11.23	1.47	1.36
5	A	310	CHL	C2C-C3C	11.22	1.47	1.36
4	C	304	NEX	C7-C6	8.51	1.40	1.30
5	C	309	CHL	C1A-CHA	8.32	1.49	1.40
4	B	304	NEX	C7-C6	8.29	1.40	1.30
5	B	312	CHL	C1A-CHA	8.28	1.49	1.40
5	B	305	CHL	C1A-CHA	8.28	1.49	1.40
5	C	305	CHL	C1A-CHA	8.28	1.49	1.40
5	C	311	CHL	C1A-CHA	8.27	1.49	1.40
5	A	305	CHL	C1A-CHA	8.26	1.49	1.40
5	C	306	CHL	C1B-C2B	8.24	1.48	1.39
5	A	318	CHL	C1A-CHA	8.24	1.49	1.40
5	C	318	CHL	C1A-CHA	8.24	1.49	1.40
5	B	309	CHL	C1A-CHA	8.24	1.49	1.40
5	B	310	CHL	C3B-C4B	8.22	1.49	1.41
5	C	312	CHL	C1A-CHA	8.22	1.49	1.40
5	A	309	CHL	C1A-CHA	8.21	1.49	1.40
5	A	311	CHL	C1A-CHA	8.21	1.49	1.40
5	A	309	CHL	C3B-C4B	8.21	1.49	1.41
5	A	306	CHL	C1B-C2B	8.20	1.48	1.39
5	A	312	CHL	C1A-CHA	8.20	1.49	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	310	CHL	C3B-C4B	8.19	1.49	1.41
5	B	311	CHL	C1A-CHA	8.18	1.49	1.40
5	C	310	CHL	C3B-C4B	8.11	1.49	1.41
5	B	309	CHL	C3B-C4B	8.11	1.49	1.41
5	C	309	CHL	C3B-C4B	8.10	1.49	1.41
5	B	312	CHL	C3B-C4B	8.09	1.49	1.41
5	C	312	CHL	C3B-C4B	8.09	1.49	1.41
5	C	305	CHL	C3B-C4B	8.08	1.49	1.41
5	A	305	CHL	C3B-C4B	8.07	1.49	1.41
5	A	312	CHL	C3B-C4B	8.06	1.49	1.41
4	A	304	NEX	C7-C6	8.05	1.40	1.30
5	B	305	CHL	C3B-C4B	8.05	1.49	1.41
5	B	318	CHL	C1B-C2B	8.04	1.48	1.39
5	B	306	CHL	C3B-C4B	8.03	1.49	1.41
5	B	311	CHL	C3B-C4B	8.02	1.49	1.41
5	B	305	CHL	C1B-C2B	8.00	1.48	1.39
5	C	318	CHL	C1B-C2B	7.99	1.48	1.39
5	A	305	CHL	C1B-C2B	7.98	1.48	1.39
5	B	310	CHL	C1A-CHA	7.97	1.49	1.40
5	A	310	CHL	C1A-CHA	7.95	1.49	1.40
5	A	311	CHL	C3B-C4B	7.95	1.49	1.41
5	A	318	CHL	C1B-C2B	7.94	1.48	1.39
5	C	311	CHL	C3B-C4B	7.93	1.49	1.41
5	C	305	CHL	C1B-C2B	7.93	1.48	1.39
5	C	309	CHL	C1B-C2B	7.91	1.48	1.39
5	B	318	CHL	C1A-CHA	7.90	1.49	1.40
5	C	310	CHL	C1A-CHA	7.86	1.48	1.40
5	C	311	CHL	C1B-C2B	7.86	1.48	1.39
5	B	306	CHL	C1B-C2B	7.84	1.48	1.39
5	A	311	CHL	C1B-C2B	7.84	1.48	1.39
5	A	318	CHL	C3B-C4B	7.83	1.49	1.41
5	A	309	CHL	C1B-C2B	7.82	1.48	1.39
5	B	309	CHL	C1B-C2B	7.79	1.48	1.39
5	B	311	CHL	C1B-C2B	7.79	1.48	1.39
5	A	306	CHL	C1A-CHA	7.76	1.48	1.40
5	C	318	CHL	C3B-C4B	7.76	1.48	1.41
5	C	306	CHL	C1A-CHA	7.73	1.48	1.40
5	A	313	CHL	C1D-C2D	7.71	1.48	1.39
5	B	313	CHL	C1D-C2D	7.70	1.48	1.39
5	C	313	CHL	C1D-C2D	7.70	1.48	1.39
5	B	310	CHL	C1B-C2B	7.69	1.48	1.39
5	A	310	CHL	C1B-C2B	7.67	1.48	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	310	CHL	C1B-C2B	7.66	1.48	1.39
5	B	306	CHL	C1A-CHA	7.65	1.48	1.40
5	C	306	CHL	C3B-C4B	7.65	1.48	1.41
5	C	312	CHL	C1B-C2B	7.65	1.48	1.39
5	B	312	CHL	C1B-C2B	7.65	1.48	1.39
5	A	312	CHL	C1B-C2B	7.64	1.48	1.39
5	A	306	CHL	C3B-C4B	7.62	1.48	1.41
5	B	318	CHL	C3B-C4B	7.61	1.48	1.41
5	A	313	CHL	C3B-C4B	7.55	1.48	1.41
5	B	318	CHL	C1D-C2D	7.52	1.48	1.39
5	C	313	CHL	C3B-C4B	7.48	1.48	1.41
5	B	313	CHL	C3B-C4B	7.44	1.48	1.41
5	C	313	CHL	C1B-C2B	7.42	1.48	1.39
5	B	313	CHL	C1B-C2B	7.41	1.48	1.39
5	A	313	CHL	C1B-C2B	7.38	1.47	1.39
5	A	318	CHL	C1D-C2D	7.26	1.47	1.39
5	C	318	CHL	C1D-C2D	7.26	1.47	1.39
5	C	306	CHL	C1D-C2D	7.17	1.47	1.39
5	B	306	CHL	C1D-C2D	7.16	1.47	1.39
5	A	305	CHL	C1D-C2D	7.13	1.47	1.39
5	C	305	CHL	C1D-C2D	7.12	1.47	1.39
5	A	312	CHL	C1D-C2D	7.12	1.47	1.39
5	C	309	CHL	C1D-C2D	7.11	1.47	1.39
5	A	306	CHL	C1D-C2D	7.11	1.47	1.39
5	A	309	CHL	C1D-C2D	7.10	1.47	1.39
5	B	309	CHL	C1D-C2D	7.10	1.47	1.39
5	B	312	CHL	C1D-C2D	7.07	1.47	1.39
5	C	312	CHL	C1D-C2D	7.01	1.47	1.39
5	A	311	CHL	C1D-C2D	7.00	1.47	1.39
5	B	305	CHL	C1D-C2D	6.99	1.47	1.39
5	C	311	CHL	C1D-C2D	6.98	1.47	1.39
5	B	311	CHL	C1D-C2D	6.97	1.47	1.39
5	C	310	CHL	C1D-C2D	6.86	1.47	1.39
5	B	310	CHL	C1D-C2D	6.83	1.47	1.39
5	A	310	CHL	C1D-C2D	6.80	1.47	1.39
5	A	313	CHL	C1A-CHA	6.71	1.47	1.40
5	B	313	CHL	C1A-CHA	6.69	1.47	1.40
5	C	313	CHL	C1A-CHA	6.68	1.47	1.40
5	B	313	CHL	C3A-C2A	-6.15	1.49	1.54
5	A	313	CHL	C3A-C2A	-6.10	1.49	1.54
5	C	313	CHL	C3A-C2A	-6.09	1.49	1.54
5	A	310	CHL	C3A-C2A	-5.83	1.49	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	318	CHL	C3A-C2A	-5.82	1.49	1.54
5	C	306	CHL	C3A-C2A	-5.79	1.49	1.54
5	A	306	CHL	C3A-C2A	-5.79	1.49	1.54
5	C	310	CHL	C3A-C2A	-5.77	1.49	1.54
5	B	310	CHL	C3A-C2A	-5.77	1.49	1.54
5	A	306	CHL	C3B-C2B	5.72	1.48	1.40
5	C	306	CHL	C3B-C2B	5.70	1.48	1.40
5	A	311	CHL	C3A-C2A	-5.67	1.49	1.54
5	A	318	CHL	C3A-C2A	-5.66	1.49	1.54
5	B	306	CHL	C3A-C2A	-5.64	1.49	1.54
5	C	311	CHL	C3A-C2A	-5.64	1.49	1.54
5	A	305	CHL	C3A-C2A	-5.62	1.49	1.54
5	C	318	CHL	C3A-C2A	-5.59	1.49	1.54
5	B	311	CHL	C3A-C2A	-5.57	1.49	1.54
5	B	312	CHL	C3A-C2A	-5.55	1.49	1.54
5	C	305	CHL	C3A-C2A	-5.54	1.49	1.54
5	C	312	CHL	C3A-C2A	-5.53	1.49	1.54
5	C	309	CHL	C3A-C2A	-5.52	1.49	1.54
5	A	309	CHL	C3A-C2A	-5.50	1.50	1.54
5	B	309	CHL	C3A-C2A	-5.46	1.50	1.54
5	A	310	CHL	C3B-C2B	5.46	1.47	1.40
5	A	318	CHL	C3B-C2B	5.46	1.47	1.40
5	A	312	CHL	C3A-C2A	-5.45	1.50	1.54
5	C	310	CHL	C3B-C2B	5.45	1.47	1.40
5	B	313	CHL	C3B-C2B	5.43	1.47	1.40
5	B	305	CHL	C3A-C2A	-5.42	1.50	1.54
5	A	309	CHL	C3B-C2B	5.42	1.47	1.40
5	B	309	CHL	C3B-C2B	5.41	1.47	1.40
5	B	310	CHL	C3B-C2B	5.41	1.47	1.40
5	C	309	CHL	C3B-C2B	5.41	1.47	1.40
5	B	306	CHL	C3B-C2B	5.38	1.47	1.40
5	C	318	CHL	C3B-C2B	5.38	1.47	1.40
5	C	311	CHL	C3B-C2B	5.38	1.47	1.40
5	A	313	CHL	C3B-C2B	5.37	1.47	1.40
5	B	311	CHL	C3B-C2B	5.35	1.47	1.40
5	A	311	CHL	C3B-C2B	5.35	1.47	1.40
5	C	313	CHL	C3B-C2B	5.34	1.47	1.40
5	B	318	CHL	C3B-C2B	5.33	1.47	1.40
5	C	312	CHL	C3B-C2B	5.33	1.47	1.40
5	B	313	CHL	C3D-C2D	5.33	1.48	1.39
5	B	312	CHL	C3B-C2B	5.32	1.47	1.40
5	A	313	CHL	C3D-C2D	5.30	1.48	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	312	CHL	C3B-C2B	5.28	1.47	1.40
5	A	305	CHL	C3B-C2B	5.28	1.47	1.40
5	C	313	CHL	C3D-C2D	5.27	1.48	1.39
5	B	305	CHL	C3B-C2B	5.27	1.47	1.40
5	A	306	CHL	C3D-C2D	5.21	1.48	1.39
5	B	306	CHL	C3D-C2D	5.20	1.48	1.39
5	A	311	CHL	C3D-C2D	5.19	1.48	1.39
5	C	306	CHL	C3D-C2D	5.19	1.48	1.39
5	B	318	CHL	C3D-C2D	5.19	1.48	1.39
5	C	305	CHL	C3B-C2B	5.17	1.47	1.40
5	C	313	CHL	CHA-CBD	-5.15	1.45	1.51
5	A	313	CHL	CHA-CBD	-5.15	1.45	1.51
5	B	313	CHL	CHA-CBD	-5.15	1.45	1.51
5	C	311	CHL	C3D-C2D	5.15	1.48	1.39
5	B	311	CHL	C3D-C2D	5.13	1.48	1.39
5	B	309	CHL	C3D-C2D	5.12	1.48	1.39
5	A	318	CHL	C3D-C2D	5.11	1.48	1.39
5	C	305	CHL	C3D-C2D	5.11	1.48	1.39
5	C	318	CHL	C3D-C2D	5.09	1.48	1.39
5	C	309	CHL	O2D-CGD	5.08	1.45	1.33
5	B	305	CHL	C3D-C2D	5.08	1.48	1.39
5	B	309	CHL	O2D-CGD	5.07	1.45	1.33
5	A	309	CHL	C3D-C2D	5.06	1.48	1.39
5	C	309	CHL	C3D-C2D	5.06	1.48	1.39
5	B	306	CHL	O2D-CGD	5.06	1.45	1.33
5	B	310	CHL	O2D-CGD	5.06	1.45	1.33
5	C	311	CHL	O2D-CGD	5.05	1.45	1.33
5	C	310	CHL	O2D-CGD	5.05	1.45	1.33
5	A	305	CHL	C3D-C2D	5.05	1.48	1.39
5	C	306	CHL	O2D-CGD	5.05	1.45	1.33
5	A	306	CHL	O2D-CGD	5.05	1.45	1.33
5	A	305	CHL	O2D-CGD	5.05	1.45	1.33
5	A	309	CHL	O2D-CGD	5.04	1.45	1.33
5	B	311	CHL	O2D-CGD	5.04	1.45	1.33
5	A	310	CHL	O2D-CGD	5.04	1.45	1.33
5	A	311	CHL	O2D-CGD	5.03	1.45	1.33
5	A	312	CHL	C3D-C2D	5.03	1.48	1.39
5	C	312	CHL	O2D-CGD	5.03	1.45	1.33
5	C	305	CHL	O2D-CGD	5.03	1.45	1.33
5	A	312	CHL	O2D-CGD	5.03	1.45	1.33
5	B	312	CHL	C3D-C2D	5.02	1.48	1.39
5	B	312	CHL	O2D-CGD	5.00	1.45	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	305	CHL	O2D-CGD	5.00	1.45	1.33
5	B	318	CHL	O2D-CGD	5.00	1.45	1.33
5	C	312	CHL	C3D-C2D	4.98	1.48	1.39
5	B	305	CHL	OBD-CAD	4.97	1.28	1.22
5	A	310	CHL	C3D-C2D	4.97	1.48	1.39
5	A	311	CHL	OBD-CAD	4.97	1.28	1.22
5	B	310	CHL	C3D-C2D	4.96	1.48	1.39
5	A	313	CHL	O2D-CGD	4.94	1.45	1.33
5	B	318	CHL	OBD-CAD	4.94	1.28	1.22
5	C	305	CHL	OBD-CAD	4.93	1.28	1.22
5	C	313	CHL	O2D-CGD	4.93	1.45	1.33
5	B	311	CHL	OBD-CAD	4.93	1.28	1.22
5	C	310	CHL	C3D-C2D	4.93	1.48	1.39
5	B	313	CHL	O2D-CGD	4.91	1.45	1.33
5	C	311	CHL	OBD-CAD	4.90	1.28	1.22
5	A	318	CHL	OBD-CAD	4.90	1.28	1.22
5	B	309	CHL	OBD-CAD	4.90	1.28	1.22
5	C	318	CHL	O2D-CGD	4.90	1.45	1.33
5	A	313	CHL	CHB-C4A	-4.90	1.32	1.38
5	C	318	CHL	OBD-CAD	4.89	1.28	1.22
5	C	309	CHL	OBD-CAD	4.89	1.28	1.22
5	A	305	CHL	OBD-CAD	4.89	1.28	1.22
5	C	313	CHL	CHB-C4A	-4.89	1.32	1.38
5	A	318	CHL	O2D-CGD	4.89	1.45	1.33
5	A	312	CHL	OBD-CAD	4.87	1.28	1.22
5	C	312	CHL	OBD-CAD	4.86	1.28	1.22
5	A	309	CHL	OBD-CAD	4.86	1.28	1.22
5	B	313	CHL	CHB-C4A	-4.85	1.32	1.38
5	A	313	CHL	OBD-CAD	4.83	1.28	1.22
5	A	310	CHL	CHC-C4B	4.82	1.47	1.39
5	C	313	CHL	OBD-CAD	4.79	1.28	1.22
5	B	313	CHL	OBD-CAD	4.79	1.28	1.22
5	C	310	CHL	CHC-C4B	4.78	1.47	1.39
5	B	312	CHL	OBD-CAD	4.78	1.28	1.22
5	B	310	CHL	CHC-C4B	4.77	1.47	1.39
5	B	318	CHL	CHD-C4C	4.77	1.48	1.39
5	B	310	CHL	OBD-CAD	4.75	1.28	1.22
5	C	310	CHL	OBD-CAD	4.73	1.28	1.22
5	B	318	CHL	CHD-C1D	4.68	1.47	1.39
5	A	310	CHL	OBD-CAD	4.68	1.28	1.22
5	C	313	CHL	CHD-C4C	4.67	1.48	1.39
5	B	309	CHL	CHC-C4B	4.67	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	309	CHL	CHC-C4B	4.67	1.47	1.39
5	B	313	CHL	CHD-C4C	4.66	1.48	1.39
5	C	309	CHL	CHC-C4B	4.65	1.47	1.39
5	A	313	CHL	CHD-C4C	4.64	1.48	1.39
5	C	318	CHL	CHD-C4C	4.61	1.48	1.39
5	B	313	CHL	CHD-C1D	4.61	1.47	1.39
5	A	311	CHL	CHC-C4B	4.60	1.47	1.39
5	A	313	CHL	CHD-C1D	4.59	1.47	1.39
5	B	311	CHL	CHC-C4B	4.59	1.47	1.39
5	A	318	CHL	CHD-C4C	4.58	1.48	1.39
5	C	313	CHL	CHD-C1D	4.58	1.47	1.39
5	B	306	CHL	CHC-C4B	4.57	1.47	1.39
5	A	306	CHL	OBD-CAD	4.56	1.28	1.22
5	C	306	CHL	OBD-CAD	4.56	1.28	1.22
5	A	311	CHL	CHB-C4A	-4.55	1.33	1.38
5	C	311	CHL	CHC-C4B	4.54	1.47	1.39
5	B	311	CHL	CHB-C4A	-4.54	1.33	1.38
5	C	306	CHL	CHD-C4C	4.53	1.48	1.39
5	C	318	CHL	CHD-C1D	4.53	1.47	1.39
5	B	312	CHL	CHC-C4B	4.53	1.47	1.39
5	A	306	CHL	CHD-C4C	4.52	1.48	1.39
5	B	311	CHL	CHD-C4C	4.50	1.48	1.39
5	A	309	CHL	CHB-C4A	-4.50	1.33	1.38
5	A	305	CHL	CHC-C4B	4.49	1.46	1.39
5	C	311	CHL	CHD-C4C	4.49	1.48	1.39
5	A	311	CHL	CHD-C4C	4.49	1.48	1.39
5	C	305	CHL	CHC-C4B	4.49	1.46	1.39
5	A	305	CHL	CHD-C4C	4.48	1.48	1.39
5	C	311	CHL	CHB-C4A	-4.48	1.33	1.38
5	B	306	CHL	CHD-C4C	4.47	1.48	1.39
5	A	312	CHL	CHC-C4B	4.47	1.46	1.39
5	B	309	CHL	CHB-C4A	-4.47	1.33	1.38
5	C	305	CHL	CHD-C4C	4.47	1.47	1.39
5	B	305	CHL	CHC-C4B	4.47	1.46	1.39
5	A	318	CHL	CHD-C1D	4.46	1.46	1.39
5	B	306	CHL	OBD-CAD	4.46	1.28	1.22
5	A	310	CHL	CHB-C4A	-4.46	1.33	1.38
5	C	312	CHL	CHC-C4B	4.45	1.46	1.39
5	B	313	CHL	CHC-C4B	4.45	1.46	1.39
5	B	310	CHL	CHB-C4A	-4.45	1.33	1.38
5	C	312	CHL	CHB-C4A	-4.44	1.33	1.38
5	A	312	CHL	CHB-C4A	-4.44	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	312	CHL	CHB-C4A	-4.44	1.33	1.38
5	B	312	CHL	CHD-C4C	4.44	1.47	1.39
5	A	305	CHL	CHB-C4A	-4.44	1.33	1.38
5	B	309	CHL	CHD-C4C	4.44	1.47	1.39
5	C	312	CHL	CHD-C4C	4.44	1.47	1.39
5	B	305	CHL	CHD-C4C	4.44	1.47	1.39
5	C	318	CHL	CHB-C4A	-4.43	1.33	1.38
5	C	310	CHL	CHB-C4A	-4.43	1.33	1.38
5	C	305	CHL	CHB-C4A	-4.43	1.33	1.38
5	A	313	CHL	CHC-C4B	4.43	1.46	1.39
5	A	312	CHL	CHD-C4C	4.43	1.47	1.39
5	C	306	CHL	CHC-C4B	4.42	1.46	1.39
5	A	306	CHL	CHC-C4B	4.41	1.46	1.39
5	A	313	CHL	O2A-CGA	4.40	1.46	1.33
5	B	313	CHL	O2A-CGA	4.40	1.46	1.33
5	A	309	CHL	CHD-C4C	4.40	1.47	1.39
5	C	313	CHL	CHC-C4B	4.39	1.46	1.39
5	C	309	CHL	CHD-C4C	4.39	1.47	1.39
5	C	310	CHL	CHD-C4C	4.38	1.47	1.39
5	B	305	CHL	CHB-C4A	-4.38	1.33	1.38
5	A	311	CHL	CHD-C1D	4.38	1.46	1.39
5	C	313	CHL	O2A-CGA	4.38	1.46	1.33
5	A	305	CHL	CHD-C1D	4.38	1.46	1.39
5	C	309	CHL	CHB-C4A	-4.37	1.33	1.38
5	C	311	CHL	CHD-C1D	4.37	1.46	1.39
5	A	318	CHL	CHB-C4A	-4.37	1.33	1.38
5	B	311	CHL	CHD-C1D	4.37	1.46	1.39
5	B	318	CHL	CHB-C4A	-4.37	1.33	1.38
5	A	311	CHL	O2A-CGA	4.37	1.46	1.33
5	C	310	CHL	CHC-C1C	4.37	1.47	1.39
5	A	306	CHL	CHD-C1D	4.36	1.46	1.39
5	A	306	CHL	CHB-C1B	4.36	1.46	1.39
5	A	310	CHL	CHD-C4C	4.36	1.47	1.39
5	C	311	CHL	O2A-CGA	4.36	1.46	1.33
5	C	306	CHL	CHB-C1B	4.36	1.46	1.39
5	B	311	CHL	O2A-CGA	4.36	1.46	1.33
5	C	305	CHL	CHD-C1D	4.36	1.46	1.39
5	C	318	CHL	CHC-C4B	4.35	1.46	1.39
5	B	310	CHL	CHD-C4C	4.34	1.47	1.39
5	B	306	CHL	CHB-C4A	-4.34	1.33	1.38
5	A	318	CHL	CHC-C4B	4.33	1.46	1.39
5	B	306	CHL	CHD-C1D	4.33	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	306	CHL	CHD-C1D	4.32	1.46	1.39
5	B	305	CHL	O2A-CGA	4.32	1.45	1.33
5	B	306	CHL	CHB-C1B	4.32	1.46	1.39
5	B	305	CHL	CHD-C1D	4.32	1.46	1.39
5	C	309	CHL	CHD-C1D	4.31	1.46	1.39
2	B	301	0UR	O44-C45	4.31	1.44	1.34
5	A	310	CHL	CHC-C1C	4.31	1.47	1.39
5	B	318	CHL	CHB-C1B	4.31	1.46	1.39
5	A	309	CHL	CHD-C1D	4.30	1.46	1.39
5	B	310	CHL	CHC-C1C	4.30	1.47	1.39
5	A	305	CHL	O2A-CGA	4.30	1.45	1.33
5	B	318	CHL	CHC-C4B	4.29	1.46	1.39
5	A	312	CHL	CHD-C1D	4.28	1.46	1.39
2	C	301	0UR	O44-C45	4.28	1.44	1.34
2	A	301	0UR	O44-C45	4.28	1.44	1.34
5	B	309	CHL	CHB-C1B	4.28	1.46	1.39
5	B	309	CHL	CHD-C1D	4.28	1.46	1.39
5	C	310	CHL	CHB-C1B	4.28	1.46	1.39
5	C	310	CHL	O2A-CGA	4.28	1.45	1.33
5	C	312	CHL	O2A-CGA	4.27	1.45	1.33
5	C	318	CHL	CHB-C1B	4.27	1.46	1.39
5	C	312	CHL	CHD-C1D	4.27	1.46	1.39
5	B	312	CHL	O2A-CGA	4.27	1.45	1.33
5	A	310	CHL	O2A-CGA	4.27	1.45	1.33
5	A	310	CHL	CHB-C1B	4.27	1.46	1.39
5	B	310	CHL	O2A-CGA	4.26	1.45	1.33
5	C	305	CHL	O2A-CGA	4.26	1.45	1.33
5	B	310	CHL	CHB-C1B	4.25	1.46	1.39
5	B	312	CHL	CHD-C1D	4.25	1.46	1.39
5	A	312	CHL	O2A-CGA	4.25	1.45	1.33
4	B	304	NEX	C7-C8	4.25	1.38	1.31
5	A	305	CHL	CHB-C1B	4.24	1.46	1.39
5	A	309	CHL	CHB-C1B	4.24	1.46	1.39
5	C	312	CHL	CHB-C1B	4.24	1.46	1.39
5	C	305	CHL	CHB-C1B	4.24	1.46	1.39
5	C	306	CHL	CHB-C4A	-4.23	1.33	1.38
5	A	312	CHL	CHB-C1B	4.23	1.46	1.39
5	C	309	CHL	CHB-C1B	4.23	1.46	1.39
5	A	311	CHL	CHC-C1C	4.22	1.47	1.39
5	A	309	CHL	CHC-C1C	4.21	1.47	1.39
5	C	306	CHL	O2A-CGA	4.21	1.45	1.33
5	B	311	CHL	CHC-C1C	4.21	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	312	CHL	CHB-C1B	4.20	1.46	1.39
5	B	309	CHL	CHC-C1C	4.20	1.47	1.39
5	B	306	CHL	CHC-C1C	4.20	1.47	1.39
5	A	306	CHL	O2A-CGA	4.19	1.45	1.33
5	A	318	CHL	CHB-C1B	4.19	1.46	1.39
5	C	311	CHL	CHC-C1C	4.19	1.47	1.39
5	B	318	CHL	O2A-CGA	4.19	1.46	1.33
5	A	306	CHL	CHB-C4A	-4.19	1.33	1.38
5	B	310	CHL	CHD-C1D	4.18	1.46	1.39
5	B	306	CHL	O2A-CGA	4.18	1.45	1.33
5	C	309	CHL	CHC-C1C	4.18	1.47	1.39
5	B	305	CHL	CHB-C1B	4.17	1.46	1.39
5	C	311	CHL	CHB-C1B	4.17	1.46	1.39
5	C	313	CHL	CHB-C1B	4.17	1.46	1.39
5	A	310	CHL	CHD-C1D	4.16	1.46	1.39
5	B	312	CHL	CHC-C1C	4.16	1.47	1.39
5	A	313	CHL	CHB-C1B	4.16	1.46	1.39
5	B	311	CHL	CHB-C1B	4.13	1.46	1.39
5	C	310	CHL	CHD-C1D	4.13	1.46	1.39
5	A	306	CHL	CHC-C1C	4.13	1.47	1.39
5	A	311	CHL	CHB-C1B	4.13	1.46	1.39
5	C	306	CHL	CHC-C1C	4.12	1.47	1.39
5	B	313	CHL	CHB-C1B	4.11	1.46	1.39
5	B	305	CHL	CHC-C1C	4.10	1.47	1.39
5	C	313	CHL	CHC-C1C	4.10	1.47	1.39
5	A	305	CHL	CHC-C1C	4.09	1.47	1.39
4	C	304	NEX	C7-C8	4.09	1.38	1.31
5	B	313	CHL	CHC-C1C	4.09	1.47	1.39
5	C	312	CHL	CHC-C1C	4.09	1.47	1.39
5	A	313	CHL	CHC-C1C	4.09	1.47	1.39
5	A	312	CHL	CHC-C1C	4.07	1.47	1.39
5	C	305	CHL	CHC-C1C	4.04	1.47	1.39
5	B	318	CHL	CHC-C1C	4.03	1.47	1.39
5	C	318	CHL	CHC-C1C	4.02	1.47	1.39
5	A	318	CHL	CHC-C1C	3.97	1.47	1.39
4	A	304	NEX	C7-C8	3.65	1.37	1.31
5	B	306	CHL	CHA-CBD	-3.63	1.47	1.51
5	C	306	CHL	CHA-CBD	-3.57	1.47	1.51
5	A	306	CHL	CHA-CBD	-3.54	1.47	1.51
6	B	317	CLA	C1D-ND	3.47	1.42	1.37
6	C	317	CLA	C1D-ND	3.43	1.42	1.37
6	A	317	CLA	C1D-ND	3.41	1.42	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	C	315	CLA	C1D-ND	3.40	1.42	1.37
6	C	307	CLA	C1D-ND	3.40	1.42	1.37
6	B	316	CLA	C1D-ND	3.40	1.42	1.37
6	A	315	CLA	C1D-ND	3.38	1.42	1.37
6	A	316	CLA	C1D-ND	3.37	1.42	1.37
6	B	315	CLA	C1D-ND	3.37	1.42	1.37
6	B	314	CLA	C1D-ND	3.36	1.42	1.37
6	B	308	CLA	C1D-ND	3.35	1.42	1.37
6	C	314	CLA	C1D-ND	3.35	1.42	1.37
6	A	307	CLA	C1D-ND	3.35	1.42	1.37
6	C	316	CLA	C1D-ND	3.35	1.42	1.37
6	B	307	CLA	C1D-ND	3.34	1.42	1.37
6	A	314	CLA	C1D-ND	3.34	1.42	1.37
6	A	308	CLA	C1D-ND	3.32	1.42	1.37
6	C	308	CLA	C1D-ND	3.31	1.42	1.37
5	A	311	CHL	CHA-CBD	-3.29	1.47	1.51
5	B	318	CHL	CHA-CBD	-3.26	1.47	1.51
5	C	311	CHL	CHA-CBD	-3.22	1.47	1.51
7	A	319	LHG	C26-C25	-3.21	1.35	1.51
7	C	319	LHG	C26-C25	-3.20	1.35	1.51
7	B	319	LHG	C26-C25	-3.19	1.35	1.51
5	B	311	CHL	CHA-CBD	-3.17	1.48	1.51
5	C	310	CHL	CHA-CBD	-3.15	1.48	1.51
5	B	310	CHL	CHA-CBD	-3.14	1.48	1.51
5	A	318	CHL	CHA-CBD	-3.12	1.48	1.51
5	C	305	CHL	CHA-CBD	-3.11	1.48	1.51
5	A	305	CHL	CHA-CBD	-3.10	1.48	1.51
5	A	310	CHL	CHA-CBD	-3.10	1.48	1.51
5	B	309	CHL	CHA-CBD	-3.07	1.48	1.51
5	C	318	CHL	CHA-CBD	-3.03	1.48	1.51
5	B	312	CHL	CHA-CBD	-3.02	1.48	1.51
5	C	312	CHL	CHA-CBD	-3.00	1.48	1.51
5	C	309	CHL	CHA-CBD	-2.98	1.48	1.51
5	B	305	CHL	CHA-CBD	-2.98	1.48	1.51
5	A	312	CHL	CHA-CBD	-2.95	1.48	1.51
6	C	314	CLA	C4B-NB	2.94	1.41	1.37
6	A	317	CLA	C4B-NB	2.94	1.41	1.37
6	A	314	CLA	C4B-NB	2.91	1.41	1.37
6	C	308	CLA	C4B-NB	2.91	1.41	1.37
6	B	307	CLA	C4B-NB	2.91	1.41	1.37
6	B	308	CLA	C4B-NB	2.90	1.41	1.37
5	A	309	CHL	CHA-CBD	-2.90	1.48	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	314	CLA	C4B-NB	2.89	1.41	1.37
6	C	317	CLA	C4B-NB	2.87	1.41	1.37
6	B	316	CLA	C4B-NB	2.86	1.41	1.37
6	B	317	CLA	C4B-NB	2.86	1.41	1.37
6	A	316	CLA	C4B-NB	2.85	1.41	1.37
6	C	307	CLA	C4B-NB	2.85	1.41	1.37
6	A	315	CLA	C4B-NB	2.84	1.41	1.37
6	A	307	CLA	C4B-NB	2.83	1.41	1.37
6	C	316	CLA	C4B-NB	2.82	1.41	1.37
6	C	315	CLA	C4B-NB	2.79	1.41	1.37
6	B	315	CLA	C4B-NB	2.79	1.41	1.37
6	A	308	CLA	C4B-NB	2.77	1.41	1.37
6	C	316	CLA	C1B-C2B	2.72	1.49	1.43
6	A	316	CLA	C1B-C2B	2.72	1.49	1.43
6	B	316	CLA	C1B-C2B	2.71	1.49	1.43
6	C	307	CLA	C1B-C2B	2.67	1.49	1.43
6	B	315	CLA	C1B-C2B	2.67	1.49	1.43
6	C	315	CLA	C1B-C2B	2.67	1.49	1.43
6	B	307	CLA	C1B-C2B	2.66	1.49	1.43
6	B	317	CLA	C1B-C2B	2.66	1.49	1.43
6	A	307	CLA	C1B-C2B	2.66	1.49	1.43
6	C	317	CLA	C1B-C2B	2.66	1.49	1.43
6	A	315	CLA	C1B-C2B	2.66	1.49	1.43
6	A	317	CLA	C1B-C2B	2.65	1.49	1.43
7	A	319	LHG	O7-C5	-2.62	1.40	1.46
7	B	319	LHG	O7-C5	-2.60	1.40	1.46
6	C	308	CLA	C1B-C2B	2.60	1.49	1.43
7	C	319	LHG	O7-C5	-2.58	1.40	1.46
6	B	308	CLA	C1B-C2B	2.57	1.49	1.43
6	B	314	CLA	C3B-C4B	2.56	1.50	1.42
6	A	308	CLA	C1B-C2B	2.56	1.49	1.43
7	C	319	LHG	O8-C6	-2.55	1.39	1.45
6	A	314	CLA	C3B-C4B	2.55	1.50	1.42
6	B	314	CLA	CHC-C1C	2.55	1.43	1.38
7	B	319	LHG	O8-C6	-2.54	1.39	1.45
6	A	314	CLA	CHC-C1C	2.54	1.43	1.38
6	C	314	CLA	C3B-C4B	2.53	1.50	1.42
7	A	319	LHG	O8-C6	-2.53	1.39	1.45
6	C	314	CLA	CHC-C1C	2.50	1.43	1.38
3	C	303	OIE	C6-C7	-2.39	1.40	1.46
3	B	303	OIE	C6-C7	-2.38	1.40	1.46
3	B	302	OIE	C13-C12	-2.38	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	302	0IE	C17-C16	-2.36	1.40	1.46
3	B	302	0IE	C17-C16	-2.36	1.40	1.46
3	C	303	0IE	C13-C12	-2.34	1.40	1.46
3	A	303	0IE	C6-C7	-2.33	1.41	1.46
3	C	302	0IE	C13-C12	-2.33	1.41	1.46
3	A	302	0IE	C13-C12	-2.33	1.41	1.46
3	B	303	0IE	C17-C16	-2.32	1.41	1.46
3	C	303	0IE	C17-C16	-2.32	1.41	1.46
3	A	303	0IE	C15-C16	2.30	1.41	1.35
3	B	303	0IE	C13-C12	-2.29	1.41	1.46
6	A	317	CLA	C3B-C4B	2.28	1.49	1.42
3	C	302	0IE	C6-C7	-2.28	1.41	1.46
3	A	302	0IE	C8-C7	2.27	1.41	1.35
6	A	314	CLA	MG-NB	-2.27	2.01	2.05
6	C	314	CLA	MG-NB	-2.27	2.01	2.05
3	A	303	0IE	C17-C16	-2.27	1.41	1.46
6	C	308	CLA	C3B-C4B	2.27	1.49	1.42
3	B	303	0IE	C15-C16	2.26	1.41	1.35
3	A	302	0IE	C17-C16	-2.26	1.41	1.46
3	A	303	0IE	C11-C12	2.26	1.41	1.35
6	B	308	CLA	C3B-C4B	2.25	1.49	1.42
3	A	303	0IE	C8-C7	2.25	1.41	1.35
6	B	314	CLA	MG-NB	-2.25	2.01	2.05
3	C	303	0IE	C15-C16	2.24	1.41	1.35
3	B	303	0IE	C8-C7	2.24	1.41	1.35
6	A	308	CLA	CMB-C2B	-2.23	1.46	1.50
6	A	317	CLA	CHC-C1C	2.23	1.43	1.38
6	B	316	CLA	C3B-C4B	2.23	1.49	1.42
6	A	316	CLA	C3B-C4B	2.23	1.49	1.42
6	C	316	CLA	CMC-C2C	-2.23	1.46	1.50
3	A	303	0IE	C13-C12	-2.22	1.41	1.46
3	B	302	0IE	C8-C7	2.22	1.40	1.35
3	A	302	0IE	C6-C7	-2.22	1.41	1.46
3	C	302	0IE	C11-C12	2.22	1.40	1.35
6	B	314	CLA	CMB-C2B	-2.22	1.46	1.50
3	B	303	0IE	C11-C12	2.22	1.40	1.35
6	B	316	CLA	CMC-C2C	-2.22	1.46	1.50
3	B	302	0IE	C6-C7	-2.22	1.41	1.46
6	A	315	CLA	C3B-C4B	2.22	1.49	1.42
6	C	315	CLA	MG-NB	-2.22	2.01	2.05
6	A	316	CLA	CMC-C2C	-2.21	1.46	1.50
6	A	308	CLA	C3B-C4B	2.21	1.49	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	315	CLA	C3B-C4B	2.21	1.49	1.42
6	C	316	CLA	C3B-C4B	2.21	1.49	1.42
7	A	319	LHG	O8-C23	2.21	1.39	1.33
6	C	315	CLA	C3B-C4B	2.21	1.49	1.42
6	B	315	CLA	MG-NB	-2.21	2.01	2.05
6	A	314	CLA	CMB-C2B	-2.21	1.46	1.50
6	B	308	CLA	CMB-C2B	-2.21	1.46	1.50
6	B	317	CLA	C3B-C4B	2.20	1.49	1.42
7	C	319	LHG	O8-C23	2.20	1.39	1.33
7	B	319	LHG	O8-C23	2.20	1.39	1.33
6	C	308	CLA	CHC-C1C	2.20	1.42	1.38
6	C	308	CLA	MG-NB	-2.20	2.01	2.05
6	B	308	CLA	CHC-C1C	2.20	1.42	1.38
3	C	302	0IE	C8-C7	2.20	1.40	1.35
3	A	302	0IE	C11-C12	2.20	1.40	1.35
6	C	314	CLA	CMB-C2B	-2.19	1.46	1.50
3	C	302	0IE	C15-C16	2.19	1.40	1.35
6	B	308	CLA	MG-NB	-2.19	2.01	2.05
6	C	317	CLA	C3B-C4B	2.19	1.49	1.42
3	B	302	0IE	C11-C12	2.19	1.40	1.35
6	A	315	CLA	MG-NB	-2.19	2.01	2.05
6	B	315	CLA	CHC-C1C	2.18	1.42	1.38
6	A	317	CLA	MG-NB	-2.18	2.01	2.05
6	B	307	CLA	C3B-C4B	2.18	1.49	1.42
6	B	316	CLA	MG-NB	-2.18	2.01	2.05
6	A	308	CLA	MG-NB	-2.18	2.01	2.05
6	A	316	CLA	CHC-C1C	2.18	1.42	1.38
6	C	307	CLA	C3B-C4B	2.18	1.49	1.42
6	A	315	CLA	CHC-C1C	2.18	1.42	1.38
3	C	303	0IE	C11-C12	2.18	1.40	1.35
6	A	308	CLA	CHC-C1C	2.18	1.42	1.38
6	A	314	CLA	CMD-C2D	-2.17	1.46	1.50
6	A	307	CLA	C3B-C4B	2.17	1.49	1.42
6	C	314	CLA	CMD-C2D	-2.17	1.46	1.50
3	A	302	0IE	C15-C16	2.17	1.40	1.35
6	C	308	CLA	CMB-C2B	-2.16	1.46	1.50
3	C	303	0IE	C8-C7	2.16	1.40	1.35
6	B	316	CLA	CMD-C2D	-2.15	1.46	1.50
6	C	316	CLA	CMD-C2D	-2.15	1.46	1.50
6	B	317	CLA	MG-NB	-2.15	2.01	2.05
3	B	302	0IE	C15-C16	2.15	1.40	1.35
6	C	317	CLA	MG-NB	-2.15	2.01	2.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	314	CLA	CMD-C2D	-2.15	1.46	1.50
6	B	307	CLA	CMD-C2D	-2.15	1.46	1.50
6	C	308	CLA	CMD-C2D	-2.15	1.46	1.50
6	C	307	CLA	MG-NB	-2.15	2.01	2.05
6	C	307	CLA	CMB-C2B	-2.15	1.46	1.50
6	B	307	CLA	MG-NB	-2.15	2.01	2.05
6	A	315	CLA	CMD-C2D	-2.14	1.46	1.50
6	B	315	CLA	CMD-C2D	-2.14	1.46	1.50
6	A	316	CLA	CMD-C2D	-2.14	1.46	1.50
6	C	316	CLA	CHC-C1C	2.14	1.42	1.38
6	A	308	CLA	CMD-C2D	-2.14	1.46	1.50
7	C	319	LHG	O7-C7	2.13	1.40	1.34
6	B	316	CLA	CHC-C1C	2.13	1.42	1.38
6	A	317	CLA	CMD-C2D	-2.13	1.46	1.50
6	C	316	CLA	MG-NB	-2.13	2.01	2.05
6	B	308	CLA	CMD-C2D	-2.13	1.46	1.50
6	C	317	CLA	CHC-C1C	2.13	1.42	1.38
7	A	319	LHG	O7-C7	2.13	1.40	1.34
6	C	315	CLA	CHC-C1C	2.12	1.42	1.38
6	A	307	CLA	CMD-C2D	-2.12	1.46	1.50
6	C	315	CLA	CMD-C2D	-2.12	1.46	1.50
6	A	317	CLA	CMB-C2B	-2.12	1.46	1.50
6	B	314	CLA	C1B-C2B	2.12	1.48	1.43
7	B	319	LHG	O7-C7	2.11	1.40	1.34
6	B	317	CLA	CHC-C1C	2.11	1.42	1.38
6	A	314	CLA	C1B-C2B	2.11	1.48	1.43
6	C	317	CLA	CMD-C2D	-2.11	1.46	1.50
6	B	317	CLA	CMD-C2D	-2.11	1.46	1.50
6	C	315	CLA	CMB-C2B	-2.10	1.46	1.50
6	C	314	CLA	C1B-C2B	2.09	1.48	1.43
6	A	315	CLA	CMB-C2B	-2.09	1.46	1.50
6	A	316	CLA	MG-NB	-2.09	2.01	2.05
6	C	307	CLA	CMD-C2D	-2.09	1.46	1.50
6	B	316	CLA	CMB-C2B	-2.08	1.46	1.50
6	B	315	CLA	CMB-C2B	-2.07	1.46	1.50
6	B	317	CLA	CMB-C2B	-2.06	1.46	1.50
6	A	307	CLA	MG-NB	-2.06	2.01	2.05
6	B	307	CLA	CHC-C1C	2.05	1.42	1.38
6	C	317	CLA	CMB-C2B	-2.05	1.46	1.50
6	C	316	CLA	CMB-C2B	-2.05	1.46	1.50
6	B	307	CLA	CMB-C2B	-2.04	1.46	1.50
6	A	316	CLA	CMB-C2B	-2.04	1.46	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	314	CLA	CMC-C2C	-2.04	1.46	1.50
6	A	307	CLA	CMB-C2B	-2.04	1.46	1.50
6	B	314	CLA	CMC-C2C	-2.04	1.46	1.50
6	B	317	CLA	CMC-C2C	-2.04	1.46	1.50
6	C	314	CLA	CMC-C2C	-2.04	1.46	1.50
6	A	307	CLA	CMC-C2C	-2.03	1.46	1.50
5	A	318	CHL	CMC-C2C	2.03	1.49	1.44
4	C	304	NEX	C1-C6	2.03	1.57	1.54
6	A	308	CLA	CMC-C2C	-2.03	1.46	1.50
5	A	309	CHL	CBD-CGD	-2.03	1.50	1.52
6	C	307	CLA	CHC-C1C	2.02	1.42	1.38
6	C	308	CLA	CMC-C2C	-2.01	1.46	1.50
6	C	317	CLA	CMC-C2C	-2.01	1.46	1.50
6	C	315	CLA	CMC-C2C	-2.01	1.46	1.50
5	C	306	CHL	CMC-C2C	2.01	1.49	1.44
4	B	304	NEX	C1-C6	2.01	1.57	1.54
6	A	307	CLA	CHC-C1C	2.01	1.42	1.38
5	A	310	CHL	CBD-CGD	-2.00	1.50	1.52

All (678) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	311	CHL	C4D-ND-C1D	10.25	113.00	105.22
5	B	311	CHL	C4D-ND-C1D	10.18	112.94	105.22
5	A	311	CHL	C4D-ND-C1D	10.13	112.91	105.22
5	C	318	CHL	C4D-ND-C1D	10.10	112.88	105.22
5	A	305	CHL	C4D-ND-C1D	10.06	112.86	105.22
5	C	312	CHL	C4D-ND-C1D	10.05	112.85	105.22
5	C	305	CHL	C4D-ND-C1D	10.04	112.84	105.22
5	B	312	CHL	C4D-ND-C1D	10.03	112.83	105.22
5	A	312	CHL	C4D-ND-C1D	10.03	112.83	105.22
5	B	318	CHL	C4D-ND-C1D	10.01	112.82	105.22
5	A	318	CHL	C4D-ND-C1D	10.01	112.82	105.22
5	B	305	CHL	C4D-ND-C1D	9.97	112.79	105.22
5	B	310	CHL	C4D-ND-C1D	9.92	112.74	105.22
5	C	310	CHL	C4D-ND-C1D	9.91	112.74	105.22
5	B	309	CHL	C4D-ND-C1D	9.90	112.73	105.22
5	B	306	CHL	C4D-ND-C1D	9.89	112.72	105.22
5	A	309	CHL	C4D-ND-C1D	9.88	112.72	105.22
5	C	309	CHL	C4D-ND-C1D	9.88	112.71	105.22
5	A	310	CHL	C4D-ND-C1D	9.79	112.65	105.22
5	A	306	CHL	C4D-ND-C1D	9.77	112.64	105.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	306	CHL	C4D-ND-C1D	9.76	112.63	105.22
5	B	313	CHL	C4D-ND-C1D	9.66	112.55	105.22
5	C	313	CHL	C4D-ND-C1D	9.65	112.54	105.22
5	A	313	CHL	C4D-ND-C1D	9.58	112.49	105.22
5	B	318	CHL	O2D-CGD-CBD	9.54	121.43	110.95
5	A	318	CHL	O2D-CGD-CBD	9.23	121.09	110.95
5	C	318	CHL	O2D-CGD-CBD	9.08	120.92	110.95
5	B	310	CHL	C1C-C2C-CMC	8.90	142.84	126.80
5	A	310	CHL	C1C-C2C-CMC	8.86	142.78	126.80
5	C	306	CHL	O2D-CGD-CBD	8.84	120.66	110.95
5	A	306	CHL	O2D-CGD-CBD	8.83	120.65	110.95
5	C	310	CHL	C1C-C2C-CMC	8.82	142.70	126.80
5	B	306	CHL	O2D-CGD-CBD	8.53	120.32	110.95
5	C	311	CHL	O2D-CGD-CBD	8.52	120.31	110.95
5	A	310	CHL	O2D-CGD-CBD	8.48	120.27	110.95
5	C	310	CHL	O2D-CGD-CBD	8.47	120.25	110.95
5	A	311	CHL	O2D-CGD-CBD	8.46	120.24	110.95
5	B	305	CHL	O2D-CGD-CBD	8.45	120.23	110.95
5	B	311	CHL	O2D-CGD-CBD	8.43	120.21	110.95
5	C	305	CHL	O2D-CGD-CBD	8.42	120.20	110.95
5	B	309	CHL	O2D-CGD-CBD	8.40	120.18	110.95
5	B	310	CHL	O2D-CGD-CBD	8.40	120.18	110.95
5	A	305	CHL	O2D-CGD-CBD	8.39	120.16	110.95
5	C	313	CHL	CHA-C1A-C2A	-8.34	113.72	133.31
5	A	313	CHL	CHA-C1A-C2A	-8.33	113.76	133.31
5	B	313	CHL	CHA-C1A-C2A	-8.32	113.78	133.31
5	A	309	CHL	O2D-CGD-CBD	8.31	120.08	110.95
5	C	309	CHL	O2D-CGD-CBD	8.29	120.06	110.95
5	B	310	CHL	CHA-C1A-C2A	-8.21	114.03	133.31
5	C	310	CHL	CHA-C1A-C2A	-8.20	114.05	133.31
5	B	318	CHL	CHA-C1A-C2A	-8.20	114.07	133.31
5	A	310	CHL	CHA-C1A-C2A	-8.19	114.08	133.31
5	A	306	CHL	CHA-C1A-C2A	-8.15	114.18	133.31
5	C	306	CHL	CHA-C1A-C2A	-8.14	114.20	133.31
5	B	306	CHL	CHA-C1A-C2A	-8.10	114.30	133.31
5	B	309	CHL	CHA-C1A-C2A	-7.91	114.75	133.31
5	B	312	CHL	CHA-C1A-C2A	-7.90	114.76	133.31
5	C	309	CHL	CHA-C1A-C2A	-7.89	114.77	133.31
5	A	309	CHL	CHA-C1A-C2A	-7.88	114.81	133.31
5	A	305	CHL	CHA-C1A-C2A	-7.87	114.83	133.31
5	A	312	CHL	CHA-C1A-C2A	-7.87	114.83	133.31
5	C	305	CHL	CHA-C1A-C2A	-7.85	114.87	133.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	312	CHL	CHA-C1A-C2A	-7.85	114.88	133.31
5	B	305	CHL	CHA-C1A-C2A	-7.84	114.91	133.31
5	C	311	CHL	CHA-C1A-C2A	-7.75	115.12	133.31
5	B	311	CHL	CHA-C1A-C2A	-7.74	115.14	133.31
5	A	311	CHL	CHA-C1A-C2A	-7.72	115.17	133.31
5	C	318	CHL	CHA-C1A-C2A	-7.70	115.24	133.31
5	A	312	CHL	O2D-CGD-CBD	7.64	119.34	110.95
5	A	318	CHL	CHA-C1A-C2A	-7.62	115.42	133.31
5	B	312	CHL	O2D-CGD-CBD	7.62	119.31	110.95
5	A	313	CHL	O2D-CGD-CBD	7.47	119.16	110.95
5	C	312	CHL	O2D-CGD-CBD	7.46	119.15	110.95
5	C	313	CHL	O2D-CGD-CBD	7.42	119.10	110.95
5	B	309	CHL	C1C-C2C-CMC	7.41	140.15	126.80
5	B	313	CHL	O2D-CGD-CBD	7.40	119.08	110.95
5	B	313	CHL	C1B-CHB-C4A	-7.40	116.56	121.32
5	C	313	CHL	C1B-CHB-C4A	-7.40	116.56	121.32
5	A	313	CHL	C1B-CHB-C4A	-7.39	116.57	121.32
5	A	309	CHL	C1C-C2C-CMC	7.39	140.12	126.80
5	C	309	CHL	C1C-C2C-CMC	7.38	140.10	126.80
5	B	305	CHL	C1C-C2C-CMC	7.16	139.71	126.80
5	A	305	CHL	C1C-C2C-CMC	7.11	139.61	126.80
5	C	305	CHL	C1C-C2C-CMC	6.98	139.38	126.80
5	B	311	CHL	C1C-C2C-CMC	6.86	139.17	126.80
5	B	312	CHL	C1C-C2C-CMC	6.78	139.02	126.80
5	A	311	CHL	C1C-C2C-CMC	6.73	138.93	126.80
6	B	317	CLA	C4A-NA-C1A	6.70	109.74	106.68
6	B	316	CLA	C4A-NA-C1A	6.69	109.73	106.68
5	C	312	CHL	C1C-C2C-CMC	6.69	138.86	126.80
5	A	312	CHL	C1C-C2C-CMC	6.68	138.84	126.80
6	A	317	CLA	C4A-NA-C1A	6.67	109.72	106.68
5	C	311	CHL	C1C-C2C-CMC	6.64	138.77	126.80
6	C	316	CLA	C4A-NA-C1A	6.63	109.70	106.68
6	A	316	CLA	C4A-NA-C1A	6.62	109.70	106.68
6	C	317	CLA	C4A-NA-C1A	6.58	109.68	106.68
6	B	308	CLA	C4A-NA-C1A	6.43	109.61	106.68
6	C	315	CLA	C4A-NA-C1A	6.43	109.61	106.68
5	B	313	CHL	C1C-C2C-CMC	6.40	138.33	126.80
5	C	313	CHL	C1C-C2C-CMC	6.40	138.33	126.80
6	A	315	CLA	C4A-NA-C1A	6.40	109.60	106.68
6	C	308	CLA	C4A-NA-C1A	6.38	109.59	106.68
5	A	313	CHL	C1C-C2C-CMC	6.36	138.27	126.80
6	A	308	CLA	C4A-NA-C1A	6.32	109.56	106.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	307	CLA	C4A-NA-C1A	6.28	109.54	106.68
6	B	315	CLA	C4A-NA-C1A	6.21	109.51	106.68
6	C	307	CLA	C4A-NA-C1A	6.18	109.50	106.68
6	B	307	CLA	C4A-NA-C1A	6.12	109.47	106.68
5	A	311	CHL	C1B-CHB-C4A	-5.80	117.59	121.32
5	C	311	CHL	C1B-CHB-C4A	-5.79	117.60	121.32
5	C	312	CHL	C1B-CHB-C4A	-5.76	117.62	121.32
5	B	311	CHL	C1B-CHB-C4A	-5.73	117.64	121.32
5	B	310	CHL	C1A-CHA-C4D	-5.71	109.45	118.98
5	B	312	CHL	C1B-CHB-C4A	-5.71	117.65	121.32
5	A	310	CHL	C1A-CHA-C4D	-5.70	109.47	118.98
5	C	310	CHL	C1A-CHA-C4D	-5.67	109.51	118.98
5	A	312	CHL	C1B-CHB-C4A	-5.64	117.69	121.32
5	C	309	CHL	C1A-CHA-C4D	-5.63	109.59	118.98
5	A	309	CHL	C1A-CHA-C4D	-5.59	109.65	118.98
5	B	309	CHL	C1A-CHA-C4D	-5.59	109.66	118.98
5	B	312	CHL	C1A-CHA-C4D	-5.56	109.70	118.98
5	A	312	CHL	C6-C7-C8	-5.56	97.49	115.97
5	A	312	CHL	C1A-CHA-C4D	-5.55	109.72	118.98
5	C	312	CHL	C1A-CHA-C4D	-5.55	109.73	118.98
5	B	305	CHL	C1A-CHA-C4D	-5.53	109.76	118.98
5	C	311	CHL	C1A-CHA-C4D	-5.53	109.76	118.98
5	A	305	CHL	C1A-CHA-C4D	-5.53	109.76	118.98
5	C	305	CHL	C1A-CHA-C4D	-5.51	109.79	118.98
5	B	312	CHL	C6-C7-C8	-5.51	97.66	115.97
5	B	311	CHL	C1A-CHA-C4D	-5.47	109.86	118.98
5	A	311	CHL	C1A-CHA-C4D	-5.45	109.89	118.98
5	C	312	CHL	C6-C7-C8	-5.44	97.88	115.97
2	B	301	OUR	C43-C3-C4	-5.42	118.63	125.03
5	B	318	CHL	C1A-CHA-C4D	-5.41	109.96	118.98
5	C	306	CHL	C1A-CHA-C4D	-5.40	109.97	118.98
5	A	306	CHL	C1A-CHA-C4D	-5.39	109.98	118.98
5	A	309	CHL	C1B-CHB-C4A	-5.37	117.87	121.32
6	B	314	CLA	C4A-NA-C1A	5.37	109.13	106.68
5	B	309	CHL	C1B-CHB-C4A	-5.36	117.88	121.32
5	C	309	CHL	C1B-CHB-C4A	-5.36	117.88	121.32
2	C	301	OUR	C43-C3-C4	-5.31	118.76	125.03
5	B	306	CHL	C1B-CHB-C4A	-5.30	117.91	121.32
5	B	306	CHL	C1A-CHA-C4D	-5.30	110.14	118.98
6	A	314	CLA	C4A-NA-C1A	5.29	109.09	106.68
7	A	319	LHG	C11-C10-C9	-5.28	87.68	114.37
5	C	318	CHL	C1A-CHA-C4D	-5.27	110.19	118.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	314	CLA	C4A-NA-C1A	5.26	109.08	106.68
5	A	310	CHL	C1B-CHB-C4A	-5.21	117.97	121.32
5	C	312	CHL	OBD-CAD-CBD	5.21	133.46	125.82
5	C	310	CHL	C1B-CHB-C4A	-5.20	117.98	121.32
5	A	318	CHL	C1A-CHA-C4D	-5.19	110.32	118.98
5	B	318	CHL	C1B-CHB-C4A	-5.17	118.00	121.32
2	A	301	OUR	C43-C3-C4	-5.12	118.98	125.03
5	B	310	CHL	C1B-CHB-C4A	-5.08	118.06	121.32
5	B	312	CHL	OBD-CAD-CBD	5.06	133.25	125.82
5	C	318	CHL	C1B-CHB-C4A	-5.02	118.10	121.32
5	A	312	CHL	OBD-CAD-CBD	4.97	133.11	125.82
5	A	318	CHL	C1B-CHB-C4A	-4.89	118.18	121.32
5	A	306	CHL	C1B-CHB-C4A	-4.86	118.20	121.32
7	B	319	LHG	C11-C10-C9	-4.83	89.98	114.37
5	B	305	CHL	OBD-CAD-CBD	4.80	132.88	125.82
5	C	306	CHL	C1B-CHB-C4A	-4.80	118.24	121.32
7	C	319	LHG	C11-C10-C9	-4.79	90.16	114.37
5	C	312	CHL	OBD-CAD-C3D	-4.71	120.55	127.89
5	A	305	CHL	C1B-CHB-C4A	-4.71	118.30	121.32
5	C	311	CHL	OBD-CAD-CBD	4.69	132.71	125.82
5	A	311	CHL	C11-C10-C8	-4.68	100.43	115.97
5	B	311	CHL	OBD-CAD-CBD	4.65	132.65	125.82
5	B	311	CHL	C11-C10-C8	-4.64	100.53	115.97
5	A	305	CHL	OBD-CAD-CBD	4.64	132.63	125.82
5	B	309	CHL	OBD-CAD-CBD	4.61	132.59	125.82
5	B	310	CHL	OBD-CAD-CBD	4.61	132.59	125.82
5	B	312	CHL	OBD-CAD-C3D	-4.59	120.74	127.89
5	A	310	CHL	OBD-CAD-CBD	4.58	132.54	125.82
5	A	309	CHL	OBD-CAD-CBD	4.57	132.53	125.82
5	C	309	CHL	OBD-CAD-CBD	4.57	132.53	125.82
5	C	310	CHL	OBD-CAD-CBD	4.55	132.50	125.82
5	A	312	CHL	OBD-CAD-C3D	-4.55	120.80	127.89
5	C	305	CHL	OBD-CAD-CBD	4.54	132.49	125.82
5	A	311	CHL	OBD-CAD-CBD	4.48	132.40	125.82
5	C	311	CHL	C11-C10-C8	-4.47	101.10	115.97
5	C	311	CHL	OBD-CAD-C3D	-4.47	120.92	127.89
5	C	305	CHL	C1B-CHB-C4A	-4.45	118.46	121.32
5	B	305	CHL	C1B-CHB-C4A	-4.43	118.47	121.32
5	B	311	CHL	OBD-CAD-C3D	-4.38	121.06	127.89
5	B	305	CHL	OBD-CAD-C3D	-4.38	121.06	127.89
5	C	309	CHL	C1A-CHA-CBD	4.38	143.57	132.36
5	C	312	CHL	C1A-CHA-CBD	4.37	143.56	132.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	312	CHL	C1A-CHA-CBD	4.37	143.54	132.36
5	B	313	CHL	OBD-CAD-CBD	4.36	132.22	125.82
5	A	312	CHL	C1A-CHA-CBD	4.35	143.50	132.36
5	A	313	CHL	OBD-CAD-CBD	4.35	132.20	125.82
5	C	313	CHL	OBD-CAD-CBD	4.35	132.20	125.82
5	A	309	CHL	C1A-CHA-CBD	4.34	143.48	132.36
5	A	310	CHL	OBD-CAD-C3D	-4.34	121.13	127.89
5	B	310	CHL	C1A-CHA-CBD	4.33	143.46	132.36
5	B	305	CHL	C1A-CHA-CBD	4.33	143.46	132.36
3	A	302	0IE	C20-C3-C4	-4.31	118.76	124.72
5	A	310	CHL	C1A-CHA-CBD	4.30	143.38	132.36
5	B	309	CHL	C1A-CHA-CBD	4.30	143.38	132.36
5	A	305	CHL	C1A-CHA-CBD	4.28	143.33	132.36
5	C	310	CHL	C1A-CHA-CBD	4.28	143.33	132.36
5	A	311	CHL	OBD-CAD-C3D	-4.28	121.22	127.89
5	C	318	CHL	C1A-CHA-CBD	4.28	143.31	132.36
5	B	310	CHL	OBD-CAD-C3D	-4.27	121.23	127.89
5	C	310	CHL	OBD-CAD-C3D	-4.26	121.24	127.89
5	A	318	CHL	C1A-CHA-CBD	4.26	143.27	132.36
5	C	311	CHL	C1A-CHA-CBD	4.26	143.27	132.36
5	C	305	CHL	C1A-CHA-CBD	4.25	143.26	132.36
5	B	309	CHL	OBD-CAD-C3D	-4.25	121.27	127.89
5	A	305	CHL	OBD-CAD-C3D	-4.24	121.28	127.89
5	B	311	CHL	C1A-CHA-CBD	4.24	143.21	132.36
5	A	309	CHL	OBD-CAD-C3D	-4.23	121.29	127.89
5	C	313	CHL	C1A-CHA-C4D	-4.21	111.96	118.98
5	A	311	CHL	C1A-CHA-CBD	4.21	143.14	132.36
5	B	313	CHL	C1A-CHA-C4D	-4.19	111.99	118.98
5	A	313	CHL	C1A-CHA-C4D	-4.18	112.01	118.98
5	C	305	CHL	OBD-CAD-C3D	-4.18	121.37	127.89
5	A	313	CHL	OBD-CAD-C3D	-4.17	121.39	127.89
5	B	313	CHL	OBD-CAD-C3D	-4.16	121.41	127.89
5	C	313	CHL	OBD-CAD-C3D	-4.16	121.41	127.89
5	C	309	CHL	OBD-CAD-C3D	-4.15	121.41	127.89
5	A	318	CHL	OBD-CAD-CBD	4.09	131.83	125.82
5	B	318	CHL	C1A-CHA-CBD	4.06	142.76	132.36
3	C	302	0IE	C20-C3-C4	-4.04	119.14	124.72
3	B	303	0IE	C10-C9-C8	3.96	131.61	123.52
3	B	302	0IE	C20-C3-C4	-3.95	119.26	124.72
5	C	306	CHL	C1A-CHA-CBD	3.93	142.43	132.36
5	A	306	CHL	C1A-CHA-CBD	3.93	142.42	132.36
5	C	306	CHL	OBD-CAD-C3D	-3.90	121.80	127.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	303	OIE	C10-C9-C8	3.89	131.49	123.52
3	C	302	OIE	C9-C10-C11	3.89	131.47	123.52
5	A	306	CHL	OBD-CAD-C3D	-3.88	121.84	127.89
5	C	318	CHL	OBD-CAD-CBD	3.87	131.50	125.82
5	B	306	CHL	OBD-CAD-C3D	-3.85	121.89	127.89
3	A	302	OIE	C10-C9-C8	3.85	131.40	123.52
5	B	306	CHL	C1A-CHA-CBD	3.85	142.22	132.36
5	C	306	CHL	OBD-CAD-CBD	3.82	131.44	125.82
5	A	306	CHL	OBD-CAD-CBD	3.82	131.43	125.82
5	B	318	CHL	CMD-C2D-C3D	-3.82	117.06	124.68
3	A	303	OIE	C20-C3-C4	-3.77	119.50	124.72
7	C	319	LHG	O7-C7-C8	3.74	119.58	111.48
5	B	306	CHL	C1C-C2C-CMC	3.73	133.53	126.80
5	B	306	CHL	OBD-CAD-CBD	3.73	131.30	125.82
7	B	319	LHG	O7-C7-C8	3.72	119.54	111.48
5	A	306	CHL	C1C-C2C-CMC	3.71	133.49	126.80
5	A	306	CHL	C4-C3-C5	3.69	121.64	115.23
5	C	306	CHL	C1C-C2C-CMC	3.68	133.44	126.80
5	C	306	CHL	C4-C3-C5	3.68	121.62	115.23
2	C	301	OUR	C34-C27-C1	-3.67	119.88	124.45
3	B	303	OIE	C20-C3-C4	-3.66	119.66	124.72
2	A	301	OUR	C34-C27-C1	-3.66	119.89	124.45
5	C	318	CHL	CMD-C2D-C3D	-3.65	117.38	124.68
3	C	303	OIE	C23-C16-C15	-3.65	116.90	122.82
5	A	318	CHL	CMD-C2D-C3D	-3.63	117.42	124.68
5	A	312	CHL	C1-C2-C3	-3.63	120.24	126.20
5	B	313	CHL	CMD-C2D-C3D	-3.63	117.43	124.68
7	A	319	LHG	C18-C17-C16	-3.63	96.02	114.37
5	C	313	CHL	CMD-C2D-C3D	-3.63	117.44	124.68
5	C	312	CHL	C1-C2-C3	-3.62	120.26	126.20
3	B	303	OIE	C23-C16-C15	-3.61	116.96	122.82
3	A	303	OIE	C23-C16-C15	-3.61	116.97	122.82
3	C	303	OIE	C9-C10-C11	3.61	130.90	123.52
5	A	313	CHL	CMD-C2D-C3D	-3.61	117.48	124.68
5	B	312	CHL	C1-C2-C3	-3.61	120.29	126.20
2	B	301	OUR	O44-C45-C46	3.60	120.44	111.55
7	B	319	LHG	C18-C17-C16	-3.60	96.16	114.37
2	B	301	OUR	C34-C27-C1	-3.57	120.00	124.45
3	B	302	OIE	C9-C10-C11	3.57	130.82	123.52
7	C	319	LHG	C18-C17-C16	-3.57	96.34	114.37
7	A	319	LHG	O7-C7-C8	3.56	119.18	111.48
2	B	301	OUR	C10-C11-C12	-3.56	122.29	127.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	0UR	O44-C45-C46	3.54	120.29	111.55
3	A	302	0IE	C23-C16-C15	-3.53	117.09	122.82
3	C	303	0IE	C20-C3-C4	-3.53	119.83	124.72
3	B	302	0IE	C23-C16-C15	-3.53	117.09	122.82
5	C	312	CHL	CMD-C2D-C3D	-3.53	117.63	124.68
2	C	301	0UR	O44-C45-C46	3.53	120.25	111.55
3	B	302	0IE	C10-C9-C8	3.52	130.72	123.52
5	B	310	CHL	CMD-C2D-C3D	-3.52	117.65	124.68
5	B	312	CHL	CMD-C2D-C3D	-3.51	117.67	124.68
5	C	310	CHL	CMD-C2D-C3D	-3.51	117.67	124.68
5	B	305	CHL	CMD-C2D-C3D	-3.49	117.71	124.68
2	C	301	0UR	C10-C11-C12	-3.49	122.39	127.28
3	C	303	0IE	C10-C9-C8	3.48	130.63	123.52
5	A	305	CHL	CMD-C2D-C3D	-3.48	117.74	124.68
5	A	312	CHL	CMD-C2D-C3D	-3.48	117.74	124.68
5	C	305	CHL	CMD-C2D-C3D	-3.46	117.77	124.68
5	A	310	CHL	CMD-C2D-C3D	-3.44	117.80	124.68
3	C	302	0IE	C23-C16-C15	-3.43	117.25	122.82
5	B	309	CHL	CMD-C2D-C3D	-3.43	117.83	124.68
5	B	313	CHL	C1-C2-C3	-3.43	120.58	126.20
5	C	313	CHL	C1-C2-C3	-3.42	120.59	126.20
5	C	309	CHL	CMD-C2D-C3D	-3.42	117.85	124.68
3	A	303	0IE	C9-C10-C11	3.42	130.51	123.52
5	A	313	CHL	C1-C2-C3	-3.41	120.60	126.20
5	A	309	CHL	CMD-C2D-C3D	-3.41	117.88	124.68
6	C	314	CLA	C3B-C4B-NB	-3.41	107.49	110.53
5	A	318	CHL	OBD-CAD-C3D	-3.40	122.59	127.89
6	A	314	CLA	C3B-C4B-NB	-3.40	107.50	110.53
6	B	314	CLA	C3B-C4B-NB	-3.39	107.50	110.53
3	C	302	0IE	C10-C9-C8	3.35	130.37	123.52
5	A	310	CHL	C1-C2-C3	-3.35	121.35	126.76
5	C	305	CHL	C1-C2-C3	-3.34	120.72	126.20
5	B	310	CHL	C1-C2-C3	-3.34	121.36	126.76
5	A	306	CHL	CMD-C2D-C3D	-3.34	118.02	124.68
5	B	306	CHL	CMD-C2D-C3D	-3.34	118.02	124.68
5	C	306	CHL	CMD-C2D-C3D	-3.34	118.02	124.68
5	C	310	CHL	C1-C2-C3	-3.33	121.37	126.76
5	B	318	CHL	OBD-CAD-CBD	3.33	130.71	125.82
5	A	311	CHL	CMD-C2D-C3D	-3.33	118.03	124.68
5	B	305	CHL	C1-C2-C3	-3.32	120.76	126.20
5	B	311	CHL	CMD-C2D-C3D	-3.32	118.06	124.68
5	A	305	CHL	C1-C2-C3	-3.31	120.77	126.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	0IE	C9-C10-C11	3.31	130.29	123.52
5	C	311	CHL	CMD-C2D-C3D	-3.30	118.09	124.68
3	B	303	0IE	C9-C10-C11	3.27	130.22	123.52
5	C	312	CHL	OMC-CMC-C2C	-3.24	119.49	125.12
5	B	312	CHL	OMC-CMC-C2C	-3.24	119.50	125.12
5	C	318	CHL	OBD-CAD-C3D	-3.23	122.85	127.89
6	B	315	CLA	O2D-CGD-O1D	-3.21	117.61	123.85
5	B	306	CHL	C4-C3-C5	3.20	120.78	115.23
5	A	312	CHL	OMC-CMC-C2C	-3.20	119.56	125.12
6	A	315	CLA	O2D-CGD-O1D	-3.16	117.70	123.85
5	B	313	CHL	CBC-CAC-C3C	-3.14	108.38	112.87
5	A	313	CHL	CBC-CAC-C3C	-3.12	108.40	112.87
5	C	313	CHL	CBC-CAC-C3C	-3.12	108.41	112.87
6	A	307	CLA	O2D-CGD-O1D	-3.10	117.81	123.85
2	B	301	0UR	C28-C19-C18	-3.10	109.26	112.83
2	A	301	0UR	C19-C18-C17	-3.05	119.83	124.58
2	C	301	0UR	C48-C47-C46	-3.05	119.57	125.92
5	B	311	CHL	O2A-CGA-CBA	3.05	121.13	111.83
2	A	301	0UR	C48-C47-C46	-3.05	119.58	125.92
5	A	309	CHL	OMC-CMC-C2C	-3.04	119.83	125.12
5	C	309	CHL	OMC-CMC-C2C	-3.04	119.83	125.12
6	C	315	CLA	O2D-CGD-O1D	-3.03	117.95	123.85
5	B	309	CHL	OMC-CMC-C2C	-3.03	119.87	125.12
6	B	308	CLA	O2D-CGD-O1D	-3.03	117.96	123.85
2	C	301	0UR	C19-C18-C17	-3.01	119.89	124.58
5	C	313	CHL	C1A-CHA-CBD	3.01	140.07	132.36
5	A	313	CHL	C1A-CHA-CBD	3.01	140.07	132.36
5	C	311	CHL	OMC-CMC-C2C	-3.01	119.89	125.12
5	B	313	CHL	C1A-CHA-CBD	3.01	140.06	132.36
5	A	311	CHL	O2A-CGA-CBA	3.00	120.99	111.83
2	B	301	0UR	C19-C18-C17	-3.00	119.91	124.58
3	B	303	0IE	C6-C7-C8	3.00	123.73	119.01
5	B	318	CHL	O1D-CGD-CBD	-3.00	120.17	124.72
5	B	318	CHL	OBD-CAD-C3D	-2.99	123.22	127.89
5	A	305	CHL	OMC-CMC-C2C	-2.99	119.92	125.12
6	A	308	CLA	O2D-CGD-O1D	-2.99	118.03	123.85
3	C	302	0IE	C13-C12-C11	2.99	123.71	119.01
5	B	311	CHL	OMC-CMC-C2C	-2.99	119.94	125.12
5	B	305	CHL	OMC-CMC-C2C	-2.97	119.96	125.12
6	A	317	CLA	C3B-C4B-NB	-2.97	107.88	110.53
6	A	314	CLA	CMB-C2B-C1B	-2.97	120.90	125.42
6	C	308	CLA	O2D-CGD-O1D	-2.97	118.07	123.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	311	CHL	O2A-CGA-CBA	2.96	120.86	111.83
3	A	303	0IE	C6-C7-C8	2.96	123.66	119.01
6	C	314	CLA	CMB-C2B-C1B	-2.95	120.92	125.42
6	B	314	CLA	CMB-C2B-C1B	-2.95	120.92	125.42
3	C	303	0IE	C13-C12-C11	2.94	123.64	119.01
2	B	301	0UR	C48-C47-C46	-2.94	119.79	125.92
5	A	318	CHL	C1C-C2C-CMC	2.94	132.11	126.80
2	B	301	0UR	C9-C8-C7	-2.94	123.15	127.28
5	A	306	CHL	C1-C2-C3	-2.93	121.40	126.20
5	A	311	CHL	OMC-CMC-C2C	-2.92	120.04	125.12
5	C	305	CHL	OMC-CMC-C2C	-2.92	120.04	125.12
3	C	303	0IE	C22-C12-C11	-2.92	118.09	122.82
3	C	302	0IE	C22-C12-C11	-2.91	118.10	122.82
6	C	307	CLA	O2D-CGD-O1D	-2.90	118.19	123.85
6	A	316	CLA	O2D-CGD-O1D	-2.90	118.21	123.85
5	C	306	CHL	C1-C2-C3	-2.89	121.47	126.20
6	B	307	CLA	O2D-CGD-O1D	-2.89	118.23	123.85
5	C	318	CHL	C1C-C2C-CMC	2.88	132.00	126.80
3	B	302	0IE	C22-C12-C11	-2.88	118.15	122.82
3	B	303	0IE	C21-C7-C8	-2.88	118.15	122.82
6	C	317	CLA	O2D-CGD-O1D	-2.88	118.24	123.85
3	B	302	0IE	C13-C12-C11	2.88	123.54	119.01
6	A	317	CLA	O2D-CGD-O1D	-2.87	118.26	123.85
7	B	319	LHG	O8-C23-C24	2.87	120.58	111.83
6	B	316	CLA	O2D-CGD-O1D	-2.86	118.27	123.85
5	C	318	CHL	O1D-CGD-CBD	-2.86	120.39	124.72
3	B	303	0IE	C22-C12-C11	-2.86	118.18	122.82
3	C	303	0IE	C6-C7-C8	2.86	123.50	119.01
3	A	303	0IE	C21-C7-C8	-2.86	118.19	122.82
3	A	303	0IE	C22-C12-C11	-2.86	118.19	122.82
3	A	303	0IE	C13-C12-C11	2.86	123.50	119.01
3	A	302	0IE	C21-C7-C8	-2.85	118.19	122.82
5	A	318	CHL	O1D-CGD-CBD	-2.85	120.40	124.72
7	C	319	LHG	O8-C23-C24	2.84	120.51	111.83
6	C	316	CLA	O2D-CGD-O1D	-2.83	118.34	123.85
3	A	302	0IE	C22-C12-C11	-2.82	118.24	122.82
5	C	312	CHL	O2A-CGA-CBA	2.82	120.44	111.83
3	C	302	0IE	C21-C7-C8	-2.82	118.25	122.82
5	B	313	CHL	OMC-CMC-C2C	-2.82	120.22	125.12
6	A	314	CLA	O2D-CGD-O1D	-2.82	118.36	123.85
3	A	302	0IE	C13-C12-C11	2.82	123.44	119.01
3	B	303	0IE	C13-C12-C11	2.82	123.44	119.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	314	CLA	O2D-CGD-O1D	-2.82	118.37	123.85
5	A	312	CHL	O2A-CGA-CBA	2.81	120.42	111.83
5	B	305	CHL	C4-C3-C5	2.81	120.11	115.23
3	B	302	0IE	C21-C7-C8	-2.81	118.26	122.82
5	B	312	CHL	CBC-CAC-C3C	-2.81	108.85	112.87
5	C	312	CHL	CBC-CAC-C3C	-2.81	108.86	112.87
5	B	311	CHL	C1-C2-C3	-2.81	121.60	126.20
6	A	315	CLA	C3B-C4B-NB	-2.80	108.03	110.53
5	A	306	CHL	O1D-CGD-CBD	-2.80	120.47	124.72
5	B	318	CHL	O2D-CGD-O1D	-2.80	118.40	123.85
5	C	311	CHL	C1-C2-C3	-2.80	121.61	126.20
5	A	312	CHL	CBC-CAC-C3C	-2.80	108.87	112.87
7	A	319	LHG	O8-C23-C24	2.80	120.37	111.83
5	C	313	CHL	OMC-CMC-C2C	-2.80	120.26	125.12
5	C	310	CHL	OMC-CMC-C2C	-2.80	120.26	125.12
5	A	313	CHL	OMC-CMC-C2C	-2.79	120.27	125.12
5	C	306	CHL	C11-C10-C8	-2.79	106.68	115.97
5	A	306	CHL	C11-C10-C8	-2.79	106.69	115.97
3	C	303	0IE	C21-C7-C8	-2.79	118.30	122.82
5	B	311	CHL	O1D-CGD-CBD	-2.79	120.50	124.72
6	C	314	CLA	O2D-CGD-O1D	-2.78	118.44	123.85
5	B	312	CHL	O2A-CGA-CBA	2.78	120.31	111.83
5	A	311	CHL	C1-C2-C3	-2.78	121.64	126.20
5	C	306	CHL	O1D-CGD-CBD	-2.77	120.52	124.72
6	B	317	CLA	O2D-CGD-O1D	-2.77	118.45	123.85
5	A	310	CHL	OMC-CMC-C2C	-2.77	120.31	125.12
5	C	311	CHL	O1D-CGD-CBD	-2.76	120.54	124.72
5	C	305	CHL	C4-C3-C5	2.76	120.02	115.23
5	A	311	CHL	O1D-CGD-CBD	-2.76	120.54	124.72
3	A	302	0IE	C6-C7-C8	2.76	123.34	119.01
5	B	305	CHL	CBC-CAC-C3C	-2.75	108.93	112.87
5	A	305	CHL	C4-C3-C5	2.75	120.00	115.23
5	B	310	CHL	OMC-CMC-C2C	-2.75	120.34	125.12
5	A	318	CHL	O2D-CGD-O1D	-2.74	118.51	123.85
6	B	315	CLA	C3B-C4B-NB	-2.74	108.09	110.53
6	C	315	CLA	C3B-C4B-NB	-2.73	108.10	110.53
5	B	309	CHL	O1D-CGD-CBD	-2.72	120.59	124.72
4	C	304	NEX	C16-C1-C6	2.72	112.90	110.47
5	C	310	CHL	O2A-CGA-CBA	2.72	120.11	111.83
5	A	309	CHL	O1D-CGD-CBD	-2.71	120.61	124.72
6	B	317	CLA	C3B-C4B-NB	-2.71	108.11	110.53
5	C	310	CHL	O1D-CGD-CBD	-2.71	120.61	124.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	310	CHL	O2A-CGA-CBA	2.71	120.10	111.83
5	A	310	CHL	O1D-CGD-CBD	-2.71	120.61	124.72
5	B	306	CHL	C1-C2-C3	-2.71	121.76	126.20
5	B	310	CHL	O1D-CGD-CBD	-2.71	120.62	124.72
6	C	317	CLA	C3B-C4B-NB	-2.70	108.12	110.53
3	C	302	0IE	C6-C7-C8	2.70	123.26	119.01
5	A	310	CHL	O2A-CGA-CBA	2.70	120.07	111.83
5	C	309	CHL	O1D-CGD-CBD	-2.70	120.63	124.72
2	C	301	0UR	C28-C19-C18	-2.69	109.74	112.83
5	C	306	CHL	O2A-CGA-CBA	2.67	119.97	111.83
5	A	306	CHL	O2A-CGA-CBA	2.66	119.96	111.83
2	B	301	0UR	C5-C4-C3	-2.66	123.73	126.92
4	C	304	NEX	C24-C23-C22	2.66	115.77	110.79
3	B	302	0IE	C6-C7-C8	2.66	123.19	119.01
5	B	306	CHL	O1D-CGD-CBD	-2.65	120.70	124.72
2	C	301	0UR	C5-C4-C3	-2.65	123.75	126.92
5	C	318	CHL	O2D-CGD-O1D	-2.65	118.69	123.85
6	B	316	CLA	C3B-C4B-NB	-2.65	108.17	110.53
2	A	301	0UR	C28-C19-C18	-2.64	109.79	112.83
4	B	304	NEX	C16-C1-C6	2.63	112.83	110.47
5	A	305	CHL	CBC-CAC-C3C	-2.63	109.11	112.87
5	C	313	CHL	O2A-CGA-CBA	2.62	119.84	111.83
6	A	316	CLA	C3B-C4B-NB	-2.62	108.19	110.53
6	C	316	CLA	C3B-C4B-NB	-2.62	108.19	110.53
5	A	313	CHL	O2A-CGA-CBA	2.62	119.81	111.83
5	B	313	CHL	O2A-CGA-CBA	2.61	119.81	111.83
3	A	303	0IE	C17-C16-C15	2.61	123.12	119.01
5	C	305	CHL	CBC-CAC-C3C	-2.61	109.14	112.87
6	A	316	CLA	CHB-C4A-NA	2.60	128.15	124.40
5	A	305	CHL	O1D-CGD-CBD	-2.60	120.78	124.72
5	A	313	CHL	C6-C7-C8	-2.60	107.32	115.97
5	A	306	CHL	CBC-CAC-C3C	-2.60	109.15	112.87
5	B	313	CHL	C6-C7-C8	-2.60	107.33	115.97
6	A	307	CLA	CHB-C4A-NA	2.60	128.15	124.40
5	C	313	CHL	C6-C7-C8	-2.59	107.36	115.97
5	C	305	CHL	O1D-CGD-CBD	-2.58	120.81	124.72
5	C	306	CHL	O2D-CGD-O1D	-2.58	118.82	123.85
5	C	306	CHL	CBC-CAC-C3C	-2.58	109.18	112.87
6	B	316	CLA	CHB-C4A-NA	2.57	128.11	124.40
2	C	301	0UR	C9-C8-C7	-2.57	123.67	127.28
6	C	316	CLA	CHB-C4A-NA	2.56	128.10	124.40
3	B	303	0IE	C17-C16-C15	2.56	123.04	119.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	308	CLA	C3B-C4B-NB	-2.56	108.24	110.53
5	A	306	CHL	O2D-CGD-O1D	-2.55	118.88	123.85
5	B	305	CHL	O1D-CGD-CBD	-2.55	120.86	124.72
5	A	318	CHL	C4D-CHA-CBD	-2.54	106.41	108.97
2	C	301	0UR	C29-C30-C31	-2.54	107.42	111.18
5	C	311	CHL	C7-C6-C5	-2.54	106.50	113.26
2	A	301	0UR	O42-C2-C41	-2.54	116.51	120.41
5	B	305	CHL	O2D-CGD-O1D	-2.53	118.91	123.85
4	A	304	NEX	C16-C1-C6	2.53	112.74	110.47
6	A	308	CLA	C3B-C4B-NB	-2.53	108.27	110.53
5	A	306	CHL	CMA-C3A-C4A	-2.52	109.17	114.61
6	C	307	CLA	C3B-C4B-NB	-2.52	108.28	110.53
6	C	307	CLA	CHB-C4A-NA	2.52	128.04	124.40
6	B	307	CLA	C3B-C4B-NB	-2.52	108.28	110.53
6	B	308	CLA	C3B-C4B-NB	-2.52	108.28	110.53
4	B	304	NEX	C24-C23-C22	2.52	115.50	110.79
6	C	317	CLA	CHB-C4A-NA	2.51	128.03	124.40
5	C	306	CHL	CMA-C3A-C4A	-2.51	109.20	114.61
6	A	317	CLA	CHB-C4A-NA	2.51	128.03	124.40
5	B	305	CHL	O2A-CGA-CBA	2.51	119.49	111.83
5	B	306	CHL	O2A-CGA-CBA	2.51	119.48	111.83
3	C	303	0IE	C17-C16-C15	2.50	122.94	119.01
5	B	306	CHL	O2D-CGD-O1D	-2.50	118.98	123.85
5	C	305	CHL	O2D-CGD-O1D	-2.50	118.99	123.85
5	B	306	CHL	CBC-CAC-C3C	-2.49	109.31	112.87
2	A	301	0UR	C5-C4-C3	-2.49	123.94	126.92
2	A	301	0UR	C29-C30-C31	-2.49	107.49	111.18
5	B	311	CHL	C7-C6-C5	-2.48	106.64	113.26
6	B	307	CLA	CHB-C4A-NA	2.48	127.98	124.40
5	C	305	CHL	O2A-CGA-CBA	2.48	119.40	111.83
2	C	301	0UR	O42-C2-C41	-2.48	116.60	120.41
5	A	305	CHL	O2D-CGD-O1D	-2.46	119.06	123.85
6	B	317	CLA	CHB-C4A-NA	2.46	127.94	124.40
5	A	305	CHL	O2A-CGA-CBA	2.46	119.32	111.83
5	B	318	CHL	C1C-C2C-CMC	2.45	131.23	126.80
5	C	318	CHL	C4D-CHA-CBD	-2.45	106.50	108.97
5	A	311	CHL	C7-C6-C5	-2.45	106.73	113.26
2	B	301	0UR	C29-C30-C31	-2.44	107.56	111.18
6	A	314	CLA	CMB-C2B-C3B	2.43	132.27	126.55
5	A	310	CHL	O2D-CGD-O1D	-2.43	119.12	123.85
5	B	312	CHL	O1D-CGD-CBD	-2.43	121.04	124.72
5	C	310	CHL	O2D-CGD-O1D	-2.42	119.14	123.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	315	CLA	CHB-C4A-NA	2.42	127.89	124.40
5	B	310	CHL	CBC-CAC-C3C	-2.42	109.41	112.87
5	A	312	CHL	O1D-CGD-CBD	-2.41	121.06	124.72
5	B	318	CHL	CBC-CAC-C3C	-2.41	109.42	112.87
6	B	314	CLA	CMB-C2B-C3B	2.41	132.23	126.55
5	C	311	CHL	O2D-CGD-O1D	-2.41	119.15	123.85
6	B	308	CLA	CHB-C4A-NA	2.41	127.88	124.40
6	C	308	CLA	CHB-C4A-NA	2.41	127.88	124.40
6	C	314	CLA	CMB-C2B-C3B	2.41	132.21	126.55
6	A	314	CLA	O2A-CGA-O1A	-2.41	117.61	123.63
4	B	304	NEX	C1-C2-C3	2.40	118.86	113.59
6	C	314	CLA	O2A-CGA-O1A	-2.40	117.62	123.63
6	C	315	CLA	CHB-C4A-NA	2.40	127.87	124.40
6	B	314	CLA	O2A-CGA-O1A	-2.40	117.63	123.63
6	A	308	CLA	CHB-C4A-NA	2.40	127.86	124.40
3	A	302	OIE	C4-C3-C2	2.39	122.24	120.16
6	C	308	CLA	C1-C2-C3	-2.39	122.89	126.76
5	B	310	CHL	O2D-CGD-O1D	-2.39	119.20	123.85
2	A	301	OUR	C9-C8-C7	-2.39	123.93	127.28
6	B	308	CLA	C1-C2-C3	-2.39	122.90	126.76
5	A	311	CHL	O2D-CGD-O1D	-2.38	119.22	123.85
5	B	306	CHL	CMA-C3A-C4A	-2.38	109.49	114.61
5	B	309	CHL	O2D-CGD-O1D	-2.37	119.23	123.85
5	C	312	CHL	O1D-CGD-CBD	-2.37	121.13	124.72
5	A	313	CHL	O2D-CGD-O1D	-2.37	119.24	123.85
6	B	315	CLA	CHB-C4A-NA	2.36	127.80	124.40
5	C	313	CHL	O2D-CGD-O1D	-2.35	119.27	123.85
5	B	311	CHL	C4-C3-C5	2.35	119.31	115.23
6	A	308	CLA	C1-C2-C3	-2.35	122.96	126.76
2	A	301	OUR	C10-C11-C12	-2.35	123.98	127.28
6	A	315	CLA	C1-C2-C3	-2.35	122.35	126.20
6	B	314	CLA	CHB-C4A-NA	2.35	127.79	124.40
6	B	315	CLA	C1-C2-C3	-2.35	122.35	126.20
5	B	311	CHL	O2D-CGD-O1D	-2.34	119.29	123.85
5	C	313	CHL	CMA-C3A-C4A	-2.34	109.57	114.61
5	A	310	CHL	CBC-CAC-C3C	-2.34	109.53	112.87
5	A	311	CHL	C1-O2A-CGA	2.33	122.30	116.65
5	C	309	CHL	O2D-CGD-O1D	-2.33	119.31	123.85
5	A	309	CHL	O2D-CGD-O1D	-2.33	119.31	123.85
5	A	313	CHL	CMA-C3A-C4A	-2.33	109.59	114.61
2	B	301	OUR	O44-C45-O57	-2.33	118.06	122.96
5	B	313	CHL	CMA-C3A-C4A	-2.33	109.60	114.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	314	CLA	CHB-C4A-NA	2.32	127.75	124.40
5	B	313	CHL	O2D-CGD-O1D	-2.32	119.34	123.85
2	C	301	0UR	O44-C45-O57	-2.31	118.10	122.96
5	C	310	CHL	C5-C3-C4	2.31	119.91	114.59
5	A	310	CHL	C5-C3-C4	2.30	119.89	114.59
6	C	314	CLA	CHB-C4A-NA	2.30	127.72	124.40
5	B	310	CHL	C5-C3-C4	2.30	119.89	114.59
3	B	302	0IE	C17-C16-C15	2.30	122.63	119.01
5	A	311	CHL	C4-C3-C5	2.30	119.21	115.23
4	C	304	NEX	C1-C2-C3	2.30	118.63	113.59
5	A	318	CHL	CBC-CAC-C3C	-2.29	109.59	112.87
4	C	304	NEX	C38-C25-C24	-2.29	111.67	114.24
5	A	311	CHL	CMA-C3A-C4A	-2.28	109.70	114.61
2	A	301	0UR	O44-C45-O57	-2.28	118.17	122.96
5	B	311	CHL	CMA-C3A-C4A	-2.27	109.72	114.61
5	C	311	CHL	C1-O2A-CGA	2.26	122.13	116.65
5	A	309	CHL	CMA-C3A-C4A	-2.26	109.74	114.61
5	C	309	CHL	CBC-CAC-C3C	-2.26	109.64	112.87
5	B	309	CHL	CMA-C3A-C4A	-2.26	109.74	114.61
5	C	311	CHL	C4-C3-C5	2.26	119.14	115.23
5	C	318	CHL	CBC-CAC-C3C	-2.25	109.64	112.87
5	C	310	CHL	CBC-CAC-C3C	-2.25	109.65	112.87
6	A	307	CLA	C3B-C4B-NB	-2.25	108.52	110.53
6	B	314	CLA	CHB-C1B-NB	2.25	127.42	124.05
5	C	312	CHL	C4D-CHA-CBD	-2.24	106.71	108.97
5	B	311	CHL	C1-O2A-CGA	2.24	122.07	116.65
5	C	312	CHL	C3D-C4D-ND	-2.24	109.35	112.94
5	C	309	CHL	CMA-C3A-C4A	-2.23	109.80	114.61
5	B	306	CHL	C1-O2A-CGA	2.23	122.05	116.65
5	B	312	CHL	C3D-C4D-ND	-2.23	109.36	112.94
4	A	304	NEX	C24-C23-C22	2.22	114.95	110.79
5	B	309	CHL	CBC-CAC-C3C	-2.22	109.69	112.87
5	C	311	CHL	C3D-C4D-ND	-2.22	109.38	112.94
5	B	311	CHL	C3D-C4D-ND	-2.22	109.38	112.94
2	C	301	0UR	C15-C14-C13	-2.21	116.79	123.20
3	A	302	0IE	C17-C16-C15	2.21	122.48	119.01
6	A	314	CLA	CHB-C1B-NB	2.21	127.36	124.05
6	C	314	CLA	CHB-C1B-NB	2.21	127.36	124.05
5	B	312	CHL	C4D-CHA-CBD	-2.20	106.75	108.97
5	A	312	CHL	C3D-C4D-ND	-2.19	109.42	112.94
5	A	318	CHL	C3D-C4D-ND	-2.19	109.42	112.94
5	B	305	CHL	C3D-C4D-ND	-2.19	109.42	112.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	309	CHL	C3D-C4D-ND	-2.19	109.43	112.94
5	A	312	CHL	O2D-CGD-O1D	-2.18	119.60	123.85
5	A	311	CHL	C3D-C4D-ND	-2.18	109.43	112.94
5	C	318	CHL	C3D-C4D-ND	-2.18	109.44	112.94
2	B	301	0UR	C15-C14-C13	-2.17	116.90	123.20
5	B	305	CHL	C4D-CHA-CBD	-2.17	106.78	108.97
5	C	309	CHL	C3D-C4D-ND	-2.17	109.46	112.94
3	C	302	0IE	C17-C16-C15	2.16	122.41	119.01
5	B	312	CHL	O2D-CGD-O1D	-2.16	119.64	123.85
5	A	312	CHL	C4D-CHA-CBD	-2.16	106.79	108.97
5	A	305	CHL	C3D-C4D-ND	-2.16	109.47	112.94
5	C	305	CHL	C3D-C4D-ND	-2.16	109.47	112.94
4	A	304	NEX	C1-C2-C3	2.16	118.33	113.59
6	A	307	CLA	O2D-CGD-CBD	2.15	114.99	111.23
5	C	311	CHL	CMA-C3A-C4A	-2.15	109.99	114.61
5	B	309	CHL	C3D-C4D-ND	-2.14	109.50	112.94
6	A	308	CLA	CMB-C2B-C1B	-2.14	122.17	125.42
5	A	309	CHL	CBC-CAC-C3C	-2.13	109.82	112.87
4	B	304	NEX	C38-C25-C24	-2.13	111.84	114.24
5	B	311	CHL	CBC-CAC-C3C	-2.13	109.82	112.87
6	C	314	CLA	C1-C2-C3	-2.13	122.71	126.20
6	A	307	CLA	O2A-CGA-O1A	-2.13	118.31	123.63
5	C	312	CHL	O2D-CGD-O1D	-2.12	119.72	123.85
6	A	314	CLA	C1-C2-C3	-2.12	122.72	126.20
6	B	314	CLA	C1-C2-C3	-2.12	122.72	126.20
2	B	301	0UR	C41-C2-C3	2.11	124.88	119.12
5	C	309	CHL	C4D-CHA-CBD	-2.11	106.84	108.97
2	B	301	0UR	O42-C2-C41	-2.10	117.17	120.41
5	A	312	CHL	CMA-C3A-C4A	-2.10	110.08	114.61
5	C	312	CHL	CMA-C3A-C4A	-2.10	110.08	114.61
3	C	303	0IE	C20-C3-C2	2.10	119.83	115.01
6	A	307	CLA	C1-C2-C3	-2.10	122.76	126.20
5	B	305	CHL	CMA-C3A-C4A	-2.10	110.09	114.61
6	B	307	CLA	O2A-CGA-O1A	-2.10	118.38	123.63
5	B	313	CHL	O1D-CGD-CBD	-2.10	121.54	124.72
5	B	310	CHL	C3D-C4D-ND	-2.09	109.58	112.94
6	C	307	CLA	O2A-CGA-O1A	-2.09	118.40	123.63
5	A	309	CHL	C4D-CHA-CBD	-2.09	106.86	108.97
5	B	312	CHL	CMA-C3A-C4A	-2.08	110.12	114.61
6	B	307	CLA	C1-C2-C3	-2.08	122.78	126.20
5	A	313	CHL	O1D-CGD-CBD	-2.08	121.57	124.72
3	B	303	0IE	C33-C32-C31	2.08	113.36	110.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	0UR	C15-C14-C13	-2.08	117.18	123.20
2	C	301	0UR	C41-C2-C3	2.07	124.77	119.12
5	A	310	CHL	C3D-C4D-ND	-2.07	109.62	112.94
3	B	302	0IE	C19-C18-C17	2.07	127.80	124.58
5	B	318	CHL	CAA-CBA-CGA	-2.07	107.33	113.21
5	C	310	CHL	C3D-C4D-ND	-2.06	109.63	112.94
6	C	308	CLA	CMB-C2B-C1B	-2.06	122.28	125.42
6	B	308	CLA	CMB-C2B-C1B	-2.06	122.28	125.42
5	C	313	CHL	O1D-CGD-CBD	-2.06	121.60	124.72
5	A	310	CHL	CMA-C3A-C4A	-2.06	110.18	114.61
5	A	311	CHL	CBC-CAC-C3C	-2.05	109.93	112.87
5	C	305	CHL	CMA-C3A-C4A	-2.05	110.19	114.61
5	B	318	CHL	O2A-CGA-CBA	2.05	119.89	112.14
6	B	308	CLA	O2A-CGA-O1A	-2.05	118.51	123.63
5	A	305	CHL	CMA-C3A-C4A	-2.04	110.21	114.61
6	A	308	CLA	O2A-CGA-O1A	-2.04	118.52	123.63
5	A	305	CHL	C4D-CHA-CBD	-2.04	106.91	108.97
3	B	303	0IE	C20-C3-C2	2.04	119.69	115.01
3	A	303	0IE	C20-C3-C2	2.03	119.68	115.01
5	C	310	CHL	CMA-C3A-C4A	-2.03	110.25	114.61
5	C	313	CHL	C4-C3-C5	2.02	118.74	115.23
5	B	313	CHL	C4-C3-C5	2.02	118.74	115.23
2	A	301	0UR	C41-C2-C3	2.02	124.63	119.12
5	B	318	CHL	CMA-C3A-C4A	-2.02	110.26	114.61
5	B	311	CHL	C4D-CHA-CBD	-2.02	106.93	108.97
6	C	308	CLA	O2A-CGA-O1A	-2.01	118.60	123.63
5	C	306	CHL	CMB-C2B-C3B	2.01	128.70	124.68
5	C	305	CHL	C4D-CHA-CBD	-2.00	106.95	108.97

All (90) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	305	CHL	ND
5	A	305	CHL	NA
5	A	305	CHL	NC
5	A	306	CHL	ND
5	A	306	CHL	NA
5	A	306	CHL	NC
5	A	309	CHL	ND
5	A	309	CHL	NA
5	A	309	CHL	NC
5	A	310	CHL	ND

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Mol	Chain	Res	Type	Atom
5	A	310	CHL	NA
5	A	310	CHL	NC
5	A	311	CHL	ND
5	A	311	CHL	NA
5	A	311	CHL	NC
5	A	312	CHL	ND
5	A	312	CHL	NA
5	A	312	CHL	NC
5	A	313	CHL	ND
5	A	313	CHL	NA
5	A	313	CHL	NC
5	A	318	CHL	ND
5	A	318	CHL	NA
5	A	318	CHL	NC
5	B	305	CHL	ND
5	B	305	CHL	NA
5	B	305	CHL	NC
5	B	306	CHL	ND
5	B	306	CHL	NA
5	B	306	CHL	NC
5	B	309	CHL	ND
5	B	309	CHL	NA
5	B	309	CHL	NC
5	B	310	CHL	ND
5	B	310	CHL	NA
5	B	310	CHL	NC
5	B	311	CHL	ND
5	B	311	CHL	NA
5	B	311	CHL	NC
5	B	312	CHL	ND
5	B	312	CHL	NA
5	B	312	CHL	NC
5	B	313	CHL	ND
5	B	313	CHL	NA
5	B	313	CHL	NC
5	B	318	CHL	ND
5	B	318	CHL	NA
5	B	318	CHL	NC
5	C	305	CHL	ND
5	C	305	CHL	NA
5	C	305	CHL	NC
5	C	306	CHL	ND

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Mol	Chain	Res	Type	Atom
5	C	306	CHL	NA
5	C	306	CHL	NC
5	C	309	CHL	ND
5	C	309	CHL	NA
5	C	309	CHL	NC
5	C	310	CHL	ND
5	C	310	CHL	NA
5	C	310	CHL	NC
5	C	311	CHL	ND
5	C	311	CHL	NA
5	C	311	CHL	NC
5	C	312	CHL	ND
5	C	312	CHL	NA
5	C	312	CHL	NC
5	C	313	CHL	ND
5	C	313	CHL	NA
5	C	313	CHL	NC
5	C	318	CHL	ND
5	C	318	CHL	NA
5	C	318	CHL	NC
6	A	307	CLA	ND
6	A	308	CLA	ND
6	A	314	CLA	ND
6	A	315	CLA	ND
6	A	316	CLA	ND
6	A	317	CLA	ND
6	B	307	CLA	ND
6	B	308	CLA	ND
6	B	314	CLA	ND
6	B	315	CLA	ND
6	B	316	CLA	ND
6	B	317	CLA	ND
6	C	307	CLA	ND
6	C	308	CLA	ND
6	C	314	CLA	ND
6	C	315	CLA	ND
6	C	316	CLA	ND
6	C	317	CLA	ND

All (533) torsion outliers are listed below:

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Mol	Chain	Res	Type	Atoms
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Mol	Chain	Res	Type	Atoms
2	A	301	0UR	C46-C45-O44-C43
2	A	301	0UR	O57-C45-O44-C43
2	B	301	0UR	C46-C45-O44-C43
2	B	301	0UR	O57-C45-O44-C43
2	C	301	0UR	C46-C45-O44-C43
2	C	301	0UR	O57-C45-O44-C43
3	A	302	0IE	O1-C2-C3-C20
3	A	303	0IE	C14-C15-C16-C17
3	A	303	0IE	C14-C15-C16-C23
3	B	302	0IE	O1-C2-C3-C20
3	B	303	0IE	C14-C15-C16-C23
3	C	302	0IE	O1-C2-C3-C20
3	C	302	0IE	C15-C16-C17-C18
3	C	303	0IE	C14-C15-C16-C17
3	C	303	0IE	C14-C15-C16-C23
3	C	303	0IE	C16-C17-C18-C19
5	A	311	CHL	C1A-C2A-CAA-CBA
5	A	312	CHL	CBD-CGD-O2D-CED
5	A	313	CHL	CBD-CGD-O2D-CED
5	B	311	CHL	C1A-C2A-CAA-CBA
5	B	312	CHL	CBD-CGD-O2D-CED
5	B	313	CHL	CBD-CGD-O2D-CED
5	C	311	CHL	C1A-C2A-CAA-CBA
5	C	312	CHL	CBD-CGD-O2D-CED
5	C	313	CHL	CBD-CGD-O2D-CED
6	A	307	CLA	CHA-CBD-CGD-O1D
6	A	307	CLA	CHA-CBD-CGD-O2D
6	A	317	CLA	C4B-C3B-CAB-CBB
6	B	307	CLA	CHA-CBD-CGD-O1D
6	B	307	CLA	CHA-CBD-CGD-O2D
6	C	307	CLA	CHA-CBD-CGD-O1D
6	C	307	CLA	CHA-CBD-CGD-O2D
7	A	319	LHG	C3-O3-P-O5
7	A	319	LHG	C3-O3-P-O6
7	A	319	LHG	C4-O6-P-O5
7	B	319	LHG	C3-O3-P-O5
7	B	319	LHG	C3-O3-P-O6
7	C	319	LHG	C3-O3-P-O5
5	A	313	CHL	O1D-CGD-O2D-CED
5	B	313	CHL	O1D-CGD-O2D-CED
5	C	313	CHL	O1D-CGD-O2D-CED

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Mol	Chain	Res	Type	Atoms
6	A	314	CLA	CBD-CGD-O2D-CED
6	B	314	CLA	CBD-CGD-O2D-CED
6	C	314	CLA	CBD-CGD-O2D-CED
6	C	317	CLA	CBD-CGD-O2D-CED
7	A	319	LHG	O10-C23-O8-C6
7	B	319	LHG	O10-C23-O8-C6
7	C	319	LHG	O10-C23-O8-C6
5	A	312	CHL	O1D-CGD-O2D-CED
5	B	312	CHL	O1D-CGD-O2D-CED
5	A	311	CHL	C3-C5-C6-C7
5	B	311	CHL	C3-C5-C6-C7
5	C	311	CHL	C3-C5-C6-C7
5	C	312	CHL	O1D-CGD-O2D-CED
7	B	319	LHG	C24-C23-O8-C6
7	C	319	LHG	C24-C23-O8-C6
6	A	308	CLA	CBD-CGD-O2D-CED
6	A	317	CLA	CBD-CGD-O2D-CED
5	A	312	CHL	C2A-CAA-CBA-CGA
7	A	319	LHG	C24-C23-O8-C6
7	B	319	LHG	C24-C25-C26-C27
7	C	319	LHG	C24-C25-C26-C27
7	A	319	LHG	C24-C25-C26-C27
6	A	315	CLA	C3-C5-C6-C7
6	C	317	CLA	O1D-CGD-O2D-CED
6	A	314	CLA	O1D-CGD-O2D-CED
6	B	314	CLA	O1D-CGD-O2D-CED
6	C	314	CLA	O1D-CGD-O2D-CED
6	B	315	CLA	C3-C5-C6-C7
6	C	315	CLA	C3-C5-C6-C7
5	A	309	CHL	CBD-CGD-O2D-CED
5	C	309	CHL	CBD-CGD-O2D-CED
5	C	318	CHL	CBD-CGD-O2D-CED
6	B	317	CLA	CBD-CGD-O2D-CED
5	A	305	CHL	CBD-CGD-O2D-CED
5	A	318	CHL	CBD-CGD-O2D-CED
5	B	305	CHL	CBD-CGD-O2D-CED
5	B	309	CHL	CBD-CGD-O2D-CED
6	B	308	CLA	CBD-CGD-O2D-CED
6	C	308	CLA	CBD-CGD-O2D-CED
6	A	317	CLA	O1D-CGD-O2D-CED
5	A	305	CHL	C11-C12-C13-C14
5	A	306	CHL	C11-C12-C13-C14

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Mol	Chain	Res	Type	Atoms
5	A	311	CHL	C6-C7-C8-C9
5	A	313	CHL	C11-C10-C8-C9
5	A	313	CHL	C11-C12-C13-C14
5	B	305	CHL	C11-C10-C8-C9
5	B	305	CHL	C11-C12-C13-C14
5	B	306	CHL	C6-C7-C8-C9
5	B	311	CHL	C6-C7-C8-C9
5	B	313	CHL	C11-C10-C8-C9
5	B	313	CHL	C11-C12-C13-C14
5	C	306	CHL	C11-C12-C13-C14
5	C	311	CHL	C6-C7-C8-C9
5	C	313	CHL	C11-C10-C8-C9
5	C	313	CHL	C11-C12-C13-C14
2	A	301	0UR	C5-C6-C7-C20
2	C	301	0UR	C5-C6-C7-C20
3	C	302	0IE	C23-C16-C17-C18
5	B	312	CHL	C2A-CAA-CBA-CGA
5	A	311	CHL	CBD-CGD-O2D-CED
5	B	311	CHL	C8-C10-C11-C12
5	C	311	CHL	C8-C10-C11-C12
5	A	306	CHL	C5-C6-C7-C8
5	C	306	CHL	C5-C6-C7-C8
5	A	311	CHL	C5-C6-C7-C8
5	A	311	CHL	C8-C10-C11-C12
5	C	312	CHL	C8-C10-C11-C12
7	A	319	LHG	C7-C8-C9-C10
7	C	319	LHG	C23-C24-C25-C26
6	A	308	CLA	O1D-CGD-O2D-CED
5	A	312	CHL	C8-C10-C11-C12
5	B	311	CHL	C5-C6-C7-C8
5	C	305	CHL	C13-C15-C16-C17
5	A	310	CHL	C2A-CAA-CBA-CGA
5	B	310	CHL	C2A-CAA-CBA-CGA
5	C	310	CHL	C2A-CAA-CBA-CGA
5	C	312	CHL	C2A-CAA-CBA-CGA
6	B	308	CLA	C2A-CAA-CBA-CGA
6	C	308	CLA	C2A-CAA-CBA-CGA
5	B	312	CHL	C8-C10-C11-C12
7	B	319	LHG	C7-C8-C9-C10
7	B	319	LHG	C23-C24-C25-C26
5	C	311	CHL	C5-C6-C7-C8
5	A	312	CHL	C15-C16-C17-C18

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Mol	Chain	Res	Type	Atoms
5	A	313	CHL	C5-C6-C7-C8
5	B	306	CHL	C5-C6-C7-C8
5	B	313	CHL	C5-C6-C7-C8
5	C	313	CHL	C5-C6-C7-C8
7	A	319	LHG	C23-C24-C25-C26
5	A	305	CHL	C13-C15-C16-C17
5	A	312	CHL	C13-C15-C16-C17
5	B	305	CHL	C13-C15-C16-C17
5	C	312	CHL	C15-C16-C17-C18
6	B	307	CLA	C8-C10-C11-C12
5	C	305	CHL	CBD-CGD-O2D-CED
5	B	312	CHL	C13-C15-C16-C17
5	C	312	CHL	C13-C15-C16-C17
6	A	315	CLA	CBA-CGA-O2A-C1
5	B	312	CHL	C15-C16-C17-C18
3	A	302	0IE	C14-C15-C16-C23
3	B	302	0IE	C14-C15-C16-C23
3	B	303	0IE	C10-C11-C12-C22
3	C	302	0IE	C14-C15-C16-C23
5	A	306	CHL	C8-C10-C11-C12
5	C	306	CHL	C8-C10-C11-C12
2	B	301	0UR	C5-C6-C7-C20
5	A	318	CHL	C2A-CAA-CBA-CGA
5	C	318	CHL	C2A-CAA-CBA-CGA
2	A	301	0UR	C5-C6-C7-C8
2	C	301	0UR	C5-C6-C7-C8
7	B	319	LHG	O1-C1-C2-C3
7	C	319	LHG	O1-C1-C2-C3
6	A	307	CLA	C8-C10-C11-C12
6	C	307	CLA	C8-C10-C11-C12
3	A	302	0IE	C14-C15-C16-C17
3	B	302	0IE	C14-C15-C16-C17
3	B	303	0IE	C10-C11-C12-C13
3	B	303	0IE	C14-C15-C16-C17
3	C	302	0IE	C14-C15-C16-C17
5	C	309	CHL	O1D-CGD-O2D-CED
5	A	309	CHL	O1D-CGD-O2D-CED
5	C	318	CHL	O1D-CGD-O2D-CED
6	B	317	CLA	O1D-CGD-O2D-CED
6	B	308	CLA	CBA-CGA-O2A-C1
6	B	315	CLA	CBA-CGA-O2A-C1
5	A	313	CHL	C16-C17-C18-C19

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Mol	Chain	Res	Type	Atoms
5	B	305	CHL	C16-C17-C18-C20
5	B	313	CHL	C16-C17-C18-C19
5	C	305	CHL	C16-C17-C18-C19
5	C	313	CHL	C16-C17-C18-C19
3	C	303	0IE	C11-C10-C9-C8
6	C	308	CLA	O1D-CGD-O2D-CED
7	C	319	LHG	C27-C28-C29-C30
5	A	305	CHL	C16-C17-C18-C19
5	A	305	CHL	C16-C17-C18-C20
5	A	313	CHL	C16-C17-C18-C20
5	B	305	CHL	C16-C17-C18-C19
5	B	313	CHL	C16-C17-C18-C20
5	C	305	CHL	C16-C17-C18-C20
5	C	313	CHL	C16-C17-C18-C20
5	B	305	CHL	O1D-CGD-O2D-CED
6	B	308	CLA	O1D-CGD-O2D-CED
5	A	311	CHL	C3A-C2A-CAA-CBA
5	B	311	CHL	C3A-C2A-CAA-CBA
5	C	311	CHL	C3A-C2A-CAA-CBA
5	A	305	CHL	O1D-CGD-O2D-CED
5	B	309	CHL	O1D-CGD-O2D-CED
5	A	311	CHL	CBA-CGA-O2A-C1
5	C	311	CHL	CBA-CGA-O2A-C1
6	A	315	CLA	O1A-CGA-O2A-C1
5	A	318	CHL	O1D-CGD-O2D-CED
7	C	319	LHG	C12-C13-C14-C15
6	A	317	CLA	C2B-C3B-CAB-CBB
5	B	311	CHL	CBA-CGA-O2A-C1
6	B	308	CLA	O1A-CGA-O2A-C1
6	B	315	CLA	O1A-CGA-O2A-C1
6	C	317	CLA	C6-C7-C8-C10
3	C	303	0IE	C4-C5-C6-C7
5	A	305	CHL	C11-C10-C8-C9
5	A	306	CHL	C10-C11-C12-C13
5	C	306	CHL	C10-C11-C12-C13
5	A	311	CHL	O1A-CGA-O2A-C1
5	C	311	CHL	O1A-CGA-O2A-C1
7	C	319	LHG	C26-C27-C28-C29
5	C	305	CHL	C15-C16-C17-C18
5	A	310	CHL	CBA-CGA-O2A-C1
6	A	308	CLA	C2A-CAA-CBA-CGA
5	B	312	CHL	C16-C17-C18-C19

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Mol	Chain	Res	Type	Atoms
5	B	312	CHL	C16-C17-C18-C20
7	A	319	LHG	C27-C28-C29-C30
7	C	319	LHG	C7-C8-C9-C10
5	B	318	CHL	CBD-CGD-O2D-CED
5	B	311	CHL	O1A-CGA-O2A-C1
7	B	319	LHG	C12-C13-C14-C15
5	A	305	CHL	C15-C16-C17-C18
5	B	311	CHL	C10-C11-C12-C13
5	B	310	CHL	CBA-CGA-O2A-C1
5	C	310	CHL	CBA-CGA-O2A-C1
7	A	319	LHG	C10-C11-C12-C13
5	A	306	CHL	C2A-CAA-CBA-CGA
5	C	306	CHL	C2A-CAA-CBA-CGA
5	B	310	CHL	CBD-CGD-O2D-CED
5	A	311	CHL	C10-C11-C12-C13
7	C	319	LHG	C10-C11-C12-C13
7	C	319	LHG	O1-C1-C2-O2
7	A	319	LHG	C11-C10-C9-C8
5	C	311	CHL	C10-C11-C12-C13
5	B	311	CHL	CBD-CGD-O2D-CED
5	A	311	CHL	C6-C7-C8-C10
5	A	313	CHL	C11-C12-C13-C15
5	B	305	CHL	C6-C7-C8-C10
5	B	311	CHL	C6-C7-C8-C10
5	B	313	CHL	C11-C12-C13-C15
5	C	313	CHL	C11-C12-C13-C15
5	C	312	CHL	C16-C17-C18-C20
5	C	305	CHL	C4-C3-C5-C6
7	A	319	LHG	C26-C27-C28-C29
3	B	302	OIE	C13-C14-C15-C16
7	B	319	LHG	C27-C28-C29-C30
5	A	311	CHL	O1D-CGD-O2D-CED
7	A	319	LHG	C12-C13-C14-C15
7	B	319	LHG	C10-C11-C12-C13
5	A	312	CHL	C16-C17-C18-C20
5	A	306	CHL	CHA-CBD-CGD-O1D
5	A	306	CHL	CHA-CBD-CGD-O2D
5	C	306	CHL	CHA-CBD-CGD-O1D
5	C	306	CHL	CHA-CBD-CGD-O2D
5	A	310	CHL	O1A-CGA-O2A-C1
5	B	310	CHL	O1A-CGA-O2A-C1
5	C	310	CHL	O1A-CGA-O2A-C1

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Mol	Chain	Res	Type	Atoms
5	C	311	CHL	C11-C12-C13-C15
5	A	311	CHL	C11-C12-C13-C15
5	B	313	CHL	C2-C3-C5-C6
5	C	312	CHL	C16-C17-C18-C19
5	B	311	CHL	C12-C13-C15-C16
2	A	301	0UR	O44-C45-C46-C47
5	B	311	CHL	C11-C12-C13-C15
2	A	301	0UR	C46-C47-C48-C49
5	A	306	CHL	C15-C16-C17-C18
5	B	306	CHL	C15-C16-C17-C18
5	C	306	CHL	C15-C16-C17-C18
5	C	311	CHL	C12-C13-C15-C16
5	C	311	CHL	CBD-CGD-O2D-CED
5	A	311	CHL	C12-C13-C15-C16
7	B	319	LHG	C26-C27-C28-C29
5	B	305	CHL	C4-C3-C5-C6
5	A	313	CHL	C2-C3-C5-C6
5	C	313	CHL	C2-C3-C5-C6
7	C	319	LHG	C13-C14-C15-C16
5	B	306	CHL	C11-C12-C13-C14
5	B	305	CHL	C15-C16-C17-C18
6	B	317	CLA	C6-C7-C8-C10
7	A	319	LHG	O6-C4-C5-C6
7	B	319	LHG	O6-C4-C5-C6
7	C	319	LHG	O6-C4-C5-C6
5	B	305	CHL	C11-C12-C13-C15
5	C	311	CHL	C6-C7-C8-C10
5	C	305	CHL	O1D-CGD-O2D-CED
5	A	312	CHL	C16-C17-C18-C19
5	A	305	CHL	C3A-C2A-CAA-CBA
5	B	305	CHL	C3A-C2A-CAA-CBA
5	C	305	CHL	C3A-C2A-CAA-CBA
7	B	319	LHG	C13-C14-C15-C16
6	C	308	CLA	CBA-CGA-O2A-C1
3	C	302	0IE	C13-C14-C15-C16
5	A	305	CHL	C3-C5-C6-C7
5	A	305	CHL	C1A-C2A-CAA-CBA
5	B	305	CHL	C1A-C2A-CAA-CBA
5	C	305	CHL	C1A-C2A-CAA-CBA
5	A	305	CHL	C4-C3-C5-C6
5	A	313	CHL	C4-C3-C5-C6
5	B	313	CHL	C4-C3-C5-C6

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Mol	Chain	Res	Type	Atoms
5	C	313	CHL	C4-C3-C5-C6
7	B	319	LHG	O6-C4-C5-O7
7	C	319	LHG	O6-C4-C5-O7
2	B	301	0UR	O44-C45-C46-C47
7	A	319	LHG	C13-C14-C15-C16
5	C	305	CHL	C11-C12-C13-C14
7	B	319	LHG	O1-C1-C2-O2
2	A	301	0UR	O42-C2-C3-C4
2	B	301	0UR	O42-C2-C3-C4
2	C	301	0UR	O42-C2-C3-C4
3	A	302	0IE	O1-C2-C3-C4
3	B	302	0IE	O1-C2-C3-C4
3	C	302	0IE	O1-C2-C3-C4
5	C	305	CHL	C3-C5-C6-C7
5	B	310	CHL	O1D-CGD-O2D-CED
5	A	305	CHL	C11-C12-C13-C15
5	A	311	CHL	C11-C10-C8-C7
5	A	312	CHL	C6-C7-C8-C10
5	B	311	CHL	C11-C10-C8-C7
5	B	312	CHL	C6-C7-C8-C10
5	C	311	CHL	C11-C10-C8-C7
5	C	312	CHL	C6-C7-C8-C10
2	B	301	0UR	C5-C6-C7-C8
6	A	317	CLA	C2A-CAA-CBA-CGA
7	B	319	LHG	C9-C10-C11-C12
5	B	318	CHL	O1D-CGD-O2D-CED
6	A	308	CLA	CBA-CGA-O2A-C1
2	C	301	0UR	C46-C47-C48-C49
3	A	303	0IE	C13-C14-C15-C16
6	B	307	CLA	C10-C11-C12-C13
7	A	319	LHG	O6-C4-C5-O7
6	C	308	CLA	O1A-CGA-O2A-C1
5	B	312	CHL	C4-C3-C5-C6
5	C	312	CHL	C4-C3-C5-C6
6	A	307	CLA	C10-C11-C12-C13
6	C	307	CLA	C10-C11-C12-C13
5	B	311	CHL	O1D-CGD-O2D-CED
5	B	306	CHL	C11-C10-C8-C9
5	C	305	CHL	C11-C10-C8-C9
3	A	303	0IE	C16-C17-C18-C19
3	B	303	0IE	C16-C17-C18-C19
3	C	302	0IE	C16-C17-C18-C19

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Mol	Chain	Res	Type	Atoms
5	B	318	CHL	CAA-CBA-CGA-O2A
2	A	301	0UR	O42-C2-C3-C43
7	C	319	LHG	O2-C2-C3-O3
5	B	305	CHL	C3-C5-C6-C7
6	A	314	CLA	C1A-C2A-CAA-CBA
6	B	314	CLA	C1A-C2A-CAA-CBA
6	C	314	CLA	C1A-C2A-CAA-CBA
5	C	311	CHL	O1D-CGD-O2D-CED
5	C	305	CHL	C2-C3-C5-C6
5	A	313	CHL	C11-C10-C8-C7
5	B	313	CHL	C11-C10-C8-C7
5	C	313	CHL	C11-C10-C8-C7
6	A	308	CLA	O1A-CGA-O2A-C1
5	A	312	CHL	C4-C3-C5-C6
3	A	303	0IE	C3-C4-C5-C6
6	A	316	CLA	CBD-CGD-O2D-CED
5	B	318	CHL	CAD-CBD-CGD-O2D
6	A	308	CLA	CAD-CBD-CGD-O2D
2	A	301	0UR	O57-C45-C46-C47
6	A	317	CLA	C11-C10-C8-C7
3	A	302	0IE	C13-C14-C15-C16
3	B	303	0IE	C13-C14-C15-C16
5	A	309	CHL	CHA-CBD-CGD-O2D
5	A	311	CHL	CHA-CBD-CGD-O2D
5	B	305	CHL	CHA-CBD-CGD-O1D
5	B	305	CHL	CHA-CBD-CGD-O2D
5	B	306	CHL	CHA-CBD-CGD-O1D
5	B	306	CHL	CHA-CBD-CGD-O2D
5	B	309	CHL	CHA-CBD-CGD-O2D
5	B	311	CHL	CHA-CBD-CGD-O1D
5	B	311	CHL	CHA-CBD-CGD-O2D
5	B	318	CHL	CAD-CBD-CGD-O1D
5	C	309	CHL	CHA-CBD-CGD-O2D
5	C	311	CHL	CHA-CBD-CGD-O2D
6	A	308	CLA	CAD-CBD-CGD-O1D
6	A	316	CLA	CHA-CBD-CGD-O1D
6	A	316	CLA	CHA-CBD-CGD-O2D
6	B	316	CLA	CHA-CBD-CGD-O1D
6	B	316	CLA	CHA-CBD-CGD-O2D
6	C	316	CLA	CHA-CBD-CGD-O2D
7	A	319	LHG	C4-O6-P-O3
7	A	319	LHG	C4-O6-P-O4

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Mol	Chain	Res	Type	Atoms
7	B	319	LHG	C4-O6-P-O3
7	B	319	LHG	C4-O6-P-O4
7	B	319	LHG	C4-O6-P-O5
7	C	319	LHG	C3-O3-P-O6
5	B	312	CHL	C2-C3-C5-C6
5	C	312	CHL	C2-C3-C5-C6
5	C	306	CHL	O1A-CGA-O2A-C1
5	A	306	CHL	O1A-CGA-O2A-C1
5	C	305	CHL	C5-C6-C7-C8
6	C	317	CLA	CBA-CGA-O2A-C1
5	A	311	CHL	C11-C10-C8-C9
5	B	311	CHL	C11-C10-C8-C9
5	B	312	CHL	C14-C13-C15-C16
5	C	312	CHL	C14-C13-C15-C16
5	A	305	CHL	C6-C7-C8-C10
5	B	306	CHL	C6-C7-C8-C10
5	C	305	CHL	C6-C7-C8-C10
4	A	304	NEX	C11-C10-C9-C8
5	B	305	CHL	C2-C3-C5-C6
7	B	319	LHG	C29-C30-C31-C32
7	A	319	LHG	C25-C26-C27-C28
5	A	306	CHL	CBA-CGA-O2A-C1
5	C	306	CHL	CBA-CGA-O2A-C1
6	C	317	CLA	O1A-CGA-O2A-C1
5	B	306	CHL	C13-C15-C16-C17
6	A	317	CLA	C6-C7-C8-C10
2	B	301	0UR	O57-C45-C46-C47
6	A	316	CLA	O1D-CGD-O2D-CED
5	B	306	CHL	C2A-CAA-CBA-CGA
7	B	319	LHG	C31-C32-C33-C34
7	C	319	LHG	C9-C10-C11-C12
5	A	312	CHL	C6-C7-C8-C9
5	C	311	CHL	C11-C10-C8-C9
5	A	305	CHL	C5-C6-C7-C8
2	C	301	0UR	C47-C48-C49-C50
5	A	306	CHL	C4-C3-C5-C6
5	C	306	CHL	C4-C3-C5-C6
3	B	303	0IE	C3-C4-C5-C6
6	A	315	CLA	C6-C7-C8-C10
7	B	319	LHG	O2-C2-C3-O3
2	B	301	0UR	C46-C47-C48-C49
5	A	312	CHL	C2-C3-C5-C6

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Mol	Chain	Res	Type	Atoms
3	B	303	0IE	C20-C3-C4-C5
3	C	303	0IE	C20-C3-C4-C5
3	C	303	0IE	C10-C11-C12-C22
4	A	304	NEX	C39-C29-C30-C31
4	B	304	NEX	C39-C29-C30-C31
4	C	304	NEX	C39-C29-C30-C31
7	C	319	LHG	C11-C10-C9-C8
5	A	310	CHL	C2-C1-O2A-CGA
5	B	310	CHL	C2-C1-O2A-CGA
5	C	311	CHL	C2-C1-O2A-CGA
5	A	305	CHL	C2-C3-C5-C6
6	C	317	CLA	C2A-CAA-CBA-CGA
2	C	301	0UR	O44-C45-C46-C47
5	C	310	CHL	O1D-CGD-O2D-CED
5	A	312	CHL	C14-C13-C15-C16
6	A	307	CLA	C11-C12-C13-C14
6	A	315	CLA	C6-C7-C8-C9
6	B	307	CLA	C11-C12-C13-C14
6	B	315	CLA	C6-C7-C8-C9
6	C	307	CLA	C11-C12-C13-C14
5	A	306	CHL	C1A-C2A-CAA-CBA
5	B	306	CHL	C1A-C2A-CAA-CBA
5	C	306	CHL	C1A-C2A-CAA-CBA
7	A	319	LHG	C29-C30-C31-C32
7	C	319	LHG	C29-C30-C31-C32
4	A	304	NEX	C28-C29-C30-C31
4	B	304	NEX	C28-C29-C30-C31
4	C	304	NEX	C28-C29-C30-C31
5	A	310	CHL	O1D-CGD-O2D-CED
5	A	306	CHL	C11-C12-C13-C15
5	A	313	CHL	C12-C13-C15-C16
5	B	313	CHL	C12-C13-C15-C16
5	C	306	CHL	C11-C12-C13-C15
5	C	313	CHL	C12-C13-C15-C16
7	A	319	LHG	C15-C16-C17-C18
5	A	313	CHL	C10-C11-C12-C13
5	B	313	CHL	C10-C11-C12-C13
3	A	302	0IE	C5-C6-C7-C21
5	B	305	CHL	C5-C6-C7-C8
5	C	313	CHL	C10-C11-C12-C13
6	C	316	CLA	CAA-CBA-CGA-O2A
6	B	317	CLA	C2A-CAA-CBA-CGA

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Mol	Chain	Res	Type	Atoms
5	A	313	CHL	C13-C15-C16-C17
5	B	313	CHL	C13-C15-C16-C17
5	C	313	CHL	C13-C15-C16-C17
5	A	311	CHL	CAA-CBA-CGA-O2A
5	A	305	CHL	CHA-CBD-CGD-O1D
5	A	305	CHL	CHA-CBD-CGD-O2D
5	A	309	CHL	CHA-CBD-CGD-O1D
5	C	305	CHL	CHA-CBD-CGD-O1D
5	C	305	CHL	CHA-CBD-CGD-O2D
6	C	316	CLA	CAA-CBA-CGA-O1A
5	B	311	CHL	CAA-CBA-CGA-O2A
7	A	319	LHG	C9-C10-C11-C12
6	B	315	CLA	C6-C7-C8-C10
5	C	311	CHL	CAA-CBA-CGA-O2A
5	B	306	CHL	C14-C13-C15-C16
6	C	315	CLA	C6-C7-C8-C9
6	B	316	CLA	CAA-CBA-CGA-O2A
5	A	311	CHL	C2-C1-O2A-CGA
5	B	311	CHL	C2-C1-O2A-CGA
5	C	310	CHL	C2-C1-O2A-CGA
6	C	315	CLA	C3A-C2A-CAA-CBA
7	B	319	LHG	C11-C10-C9-C8
6	A	316	CLA	CAA-CBA-CGA-O2A
5	A	306	CHL	C2-C3-C5-C6
5	C	306	CHL	C2-C3-C5-C6
6	A	316	CLA	CAA-CBA-CGA-O1A
7	A	319	LHG	C2-C3-O3-P
5	C	312	CHL	C10-C11-C12-C13
7	A	319	LHG	C31-C32-C33-C34
6	B	316	CLA	CAA-CBA-CGA-O1A
3	C	303	OIE	C3-C4-C5-C6
5	A	312	CHL	C10-C11-C12-C13
5	B	312	CHL	C6-C7-C8-C9
6	B	307	CLA	C11-C10-C8-C7
6	C	307	CLA	C11-C10-C8-C7
6	C	315	CLA	C6-C7-C8-C10
5	C	310	CHL	CBD-CGD-O2D-CED
6	A	315	CLA	C2-C1-O2A-CGA
2	B	301	OURL	O42-C2-C3-C43
2	C	301	OURL	O42-C2-C3-C43
5	A	306	CHL	CAA-CBA-CGA-O2A
5	C	306	CHL	CAA-CBA-CGA-O2A

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Mol	Chain	Res	Type	Atoms
5	B	311	CHL	C2A-CAA-CBA-CGA
5	C	311	CHL	C2A-CAA-CBA-CGA
5	A	310	CHL	CBD-CGD-O2D-CED
6	C	314	CLA	C2A-CAA-CBA-CGA
5	A	310	CHL	CAA-CBA-CGA-O2A
5	C	310	CHL	CAA-CBA-CGA-O2A
5	C	312	CHL	C6-C7-C8-C9
6	C	315	CLA	C1A-C2A-CAA-CBA
5	B	310	CHL	CAA-CBA-CGA-O2A
6	A	314	CLA	C2A-CAA-CBA-CGA
6	B	314	CLA	C2A-CAA-CBA-CGA
6	B	315	CLA	C2-C1-O2A-CGA
5	B	305	CHL	C11-C10-C8-C7
7	C	319	LHG	C2-C3-O3-P
5	B	318	CHL	CAA-CBA-CGA-O1A
2	C	301	OUR	O57-C45-C46-C47
5	B	310	CHL	CAA-CBA-CGA-O1A
3	A	303	OIE	C7-C8-C9-C10
3	A	302	OIE	C5-C6-C7-C8
3	B	302	OIE	C15-C16-C17-C18
3	B	303	OIE	C12-C13-C14-C15
5	C	306	CHL	CAA-CBA-CGA-O1A
5	A	311	CHL	C2A-CAA-CBA-CGA
5	A	306	CHL	CAA-CBA-CGA-O1A
5	A	310	CHL	CAA-CBA-CGA-O1A
5	A	306	CHL	C13-C15-C16-C17
5	C	310	CHL	CAA-CBA-CGA-O1A
5	C	306	CHL	C13-C15-C16-C17
5	C	312	CHL	C5-C6-C7-C8
7	C	319	LHG	C14-C15-C16-C17

There are no ring outliers.

43 monomers are involved in 118 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	315	CLA	1	0
6	A	314	CLA	3	0
2	A	301	OUR	3	0
5	B	311	CHL	4	0
6	B	307	CLA	7	0
6	C	314	CLA	4	0
5	B	312	CHL	5	0

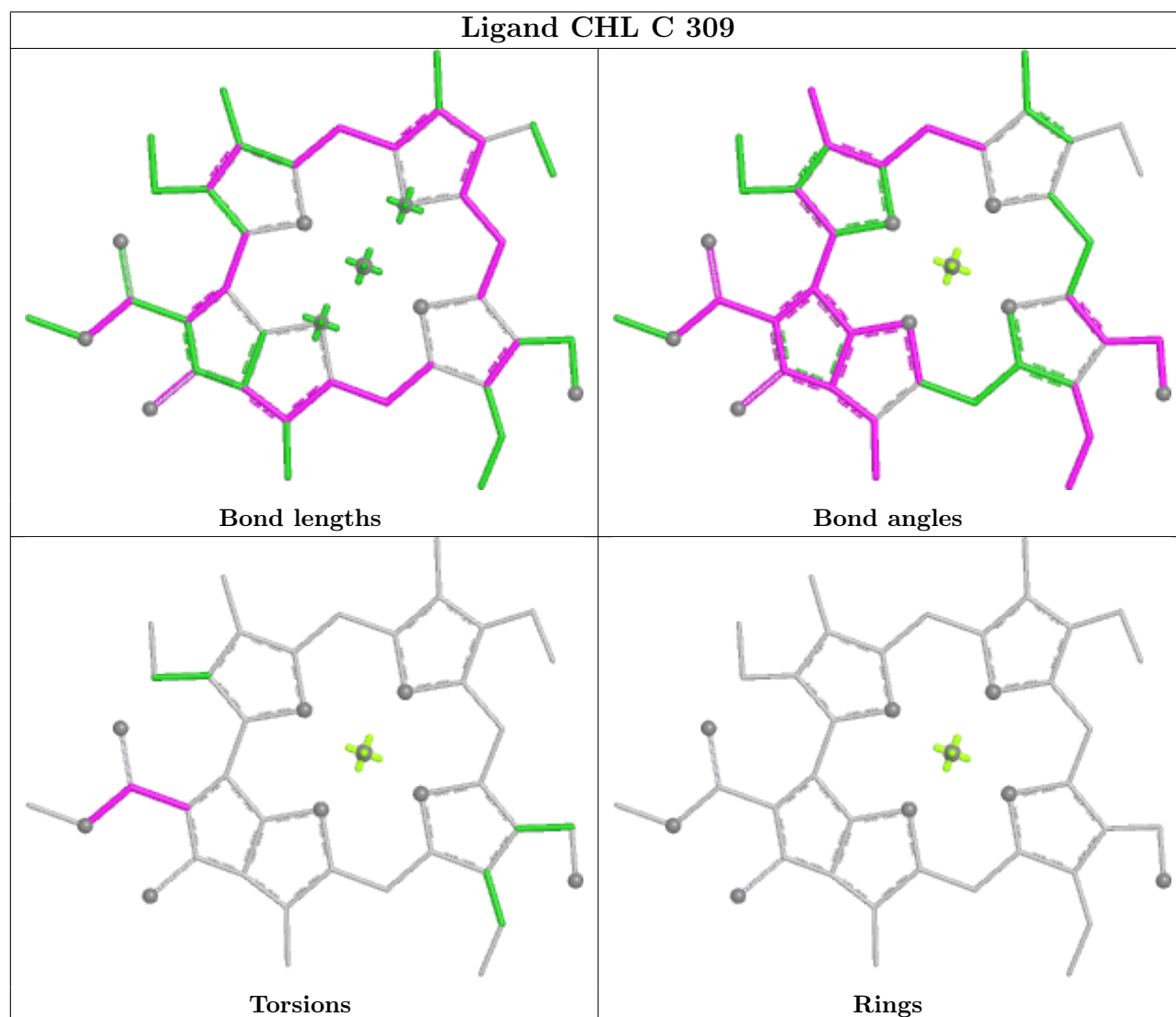
Continued on next page...

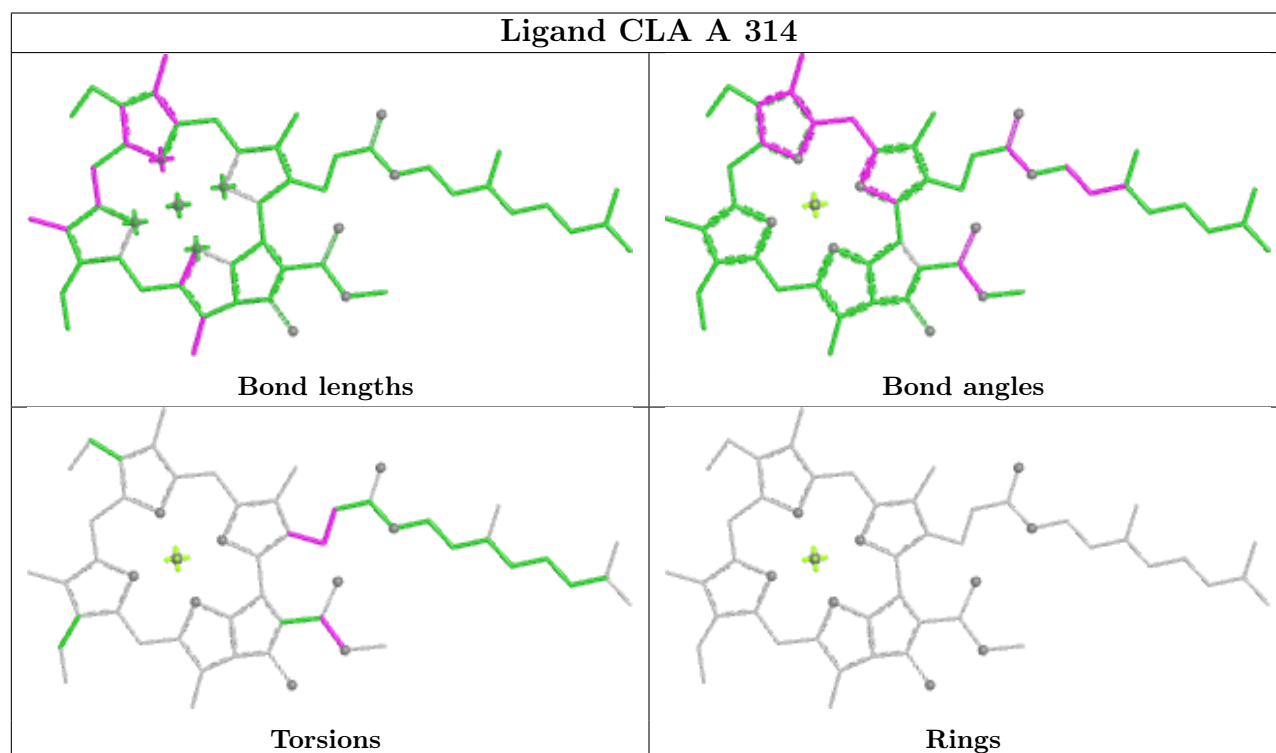
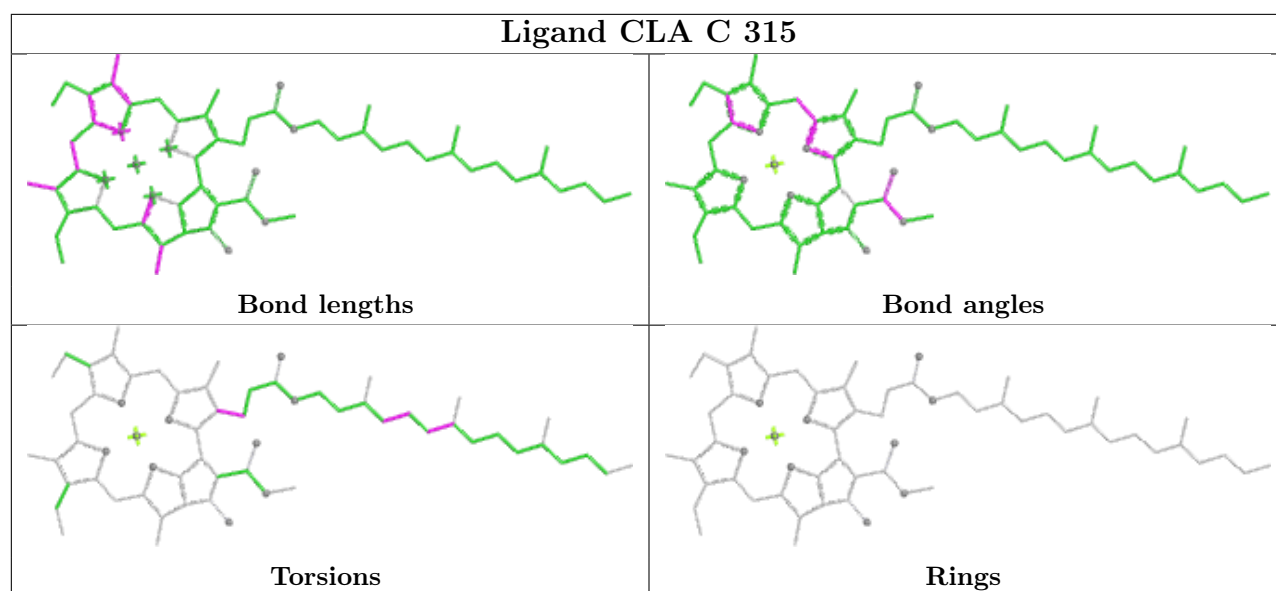
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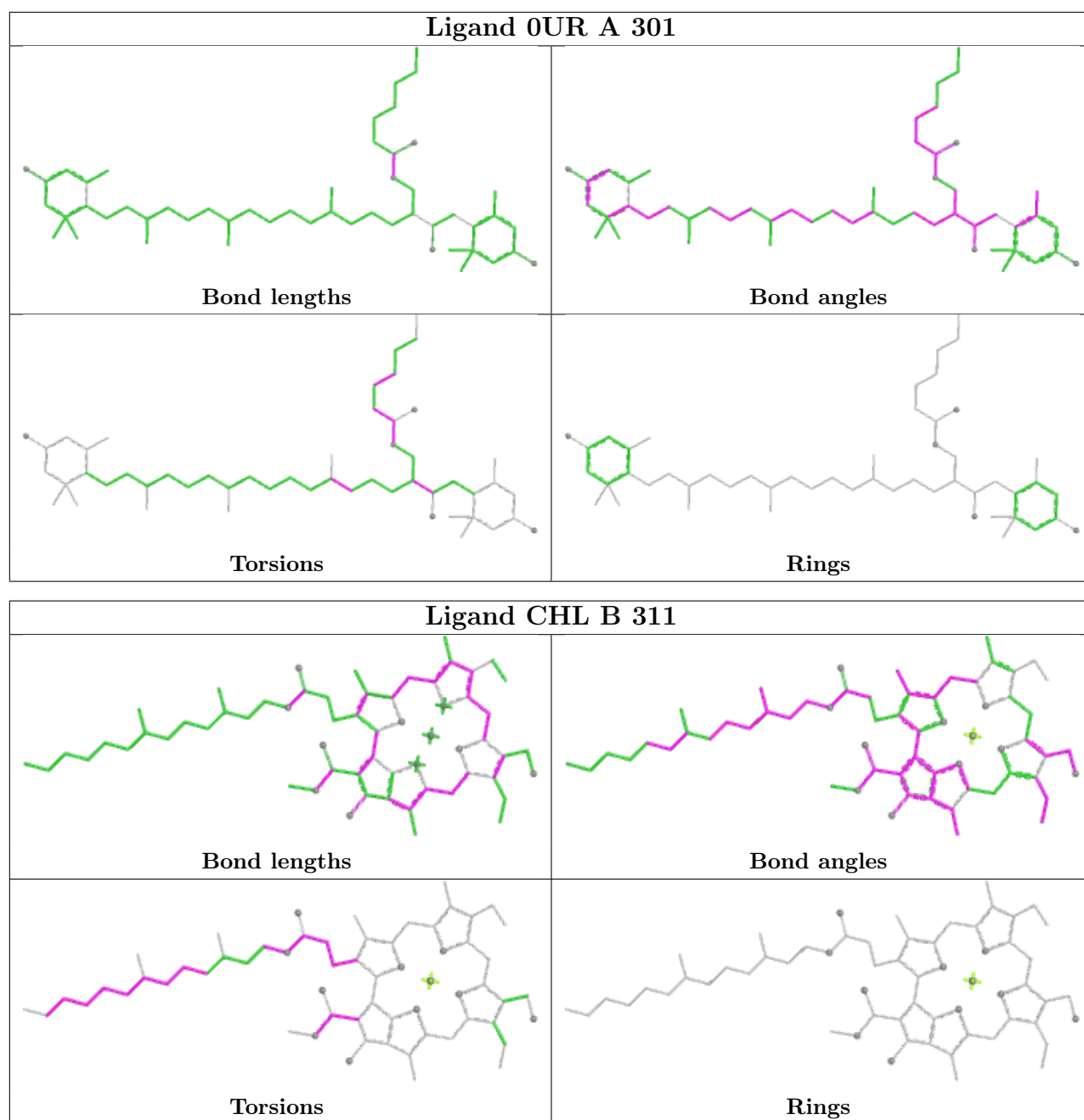
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	306	CHL	2	0
5	C	312	CHL	4	0
5	C	306	CHL	3	0
6	A	316	CLA	1	0
5	B	313	CHL	7	0
3	A	302	0IE	1	0
5	C	313	CHL	6	0
6	A	317	CLA	3	0
4	C	304	NEX	3	0
2	B	301	0UR	3	0
5	A	305	CHL	5	0
4	B	304	NEX	3	0
5	A	311	CHL	3	0
5	B	305	CHL	4	0
5	A	310	CHL	2	0
5	B	318	CHL	2	0
4	A	304	NEX	2	0
5	C	318	CHL	4	0
2	C	301	0UR	3	0
5	A	313	CHL	5	0
5	B	310	CHL	2	0
6	C	316	CLA	2	0
6	B	317	CLA	2	0
6	C	307	CLA	6	0
5	C	305	CHL	7	0
7	A	319	LHG	1	0
6	C	317	CLA	3	0
5	C	311	CHL	3	0
6	B	314	CLA	5	0
7	B	319	LHG	1	0
5	C	310	CHL	3	0
6	B	316	CLA	1	0
5	A	318	CHL	2	0
5	A	312	CHL	4	0
6	A	307	CLA	6	0
5	A	306	CHL	3	0

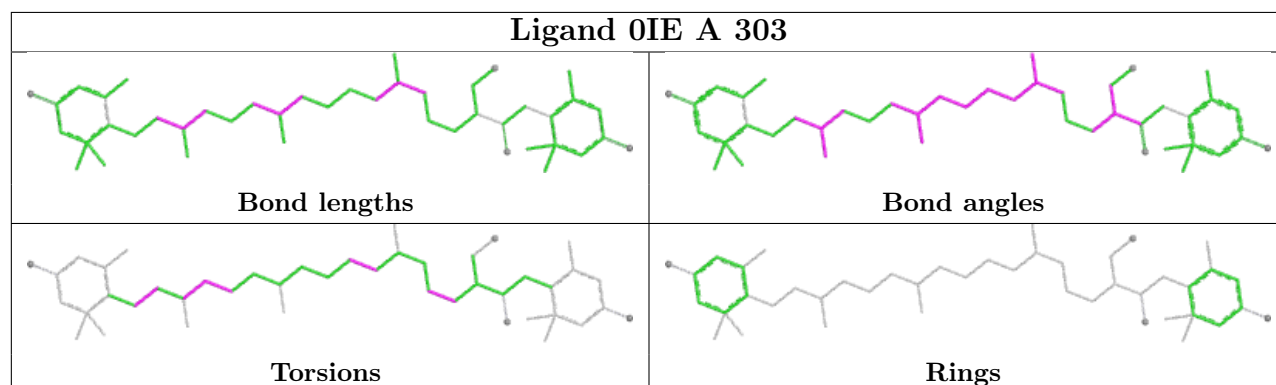
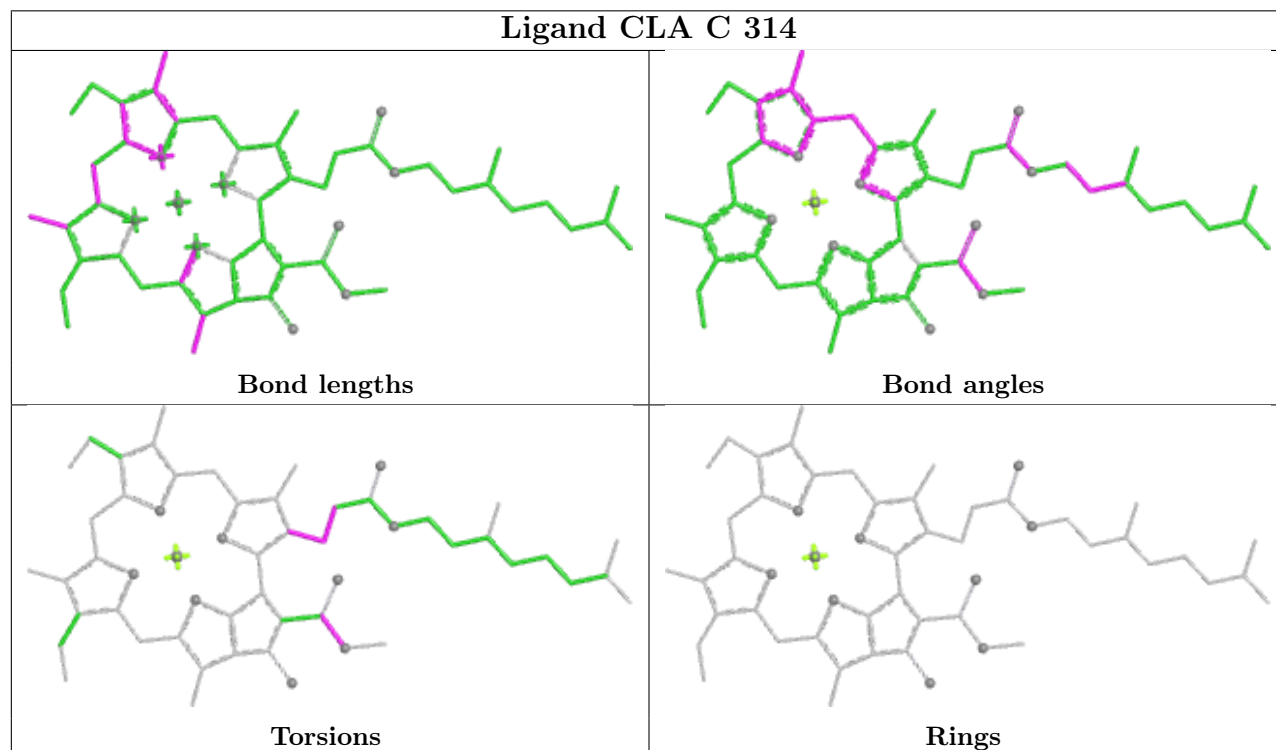
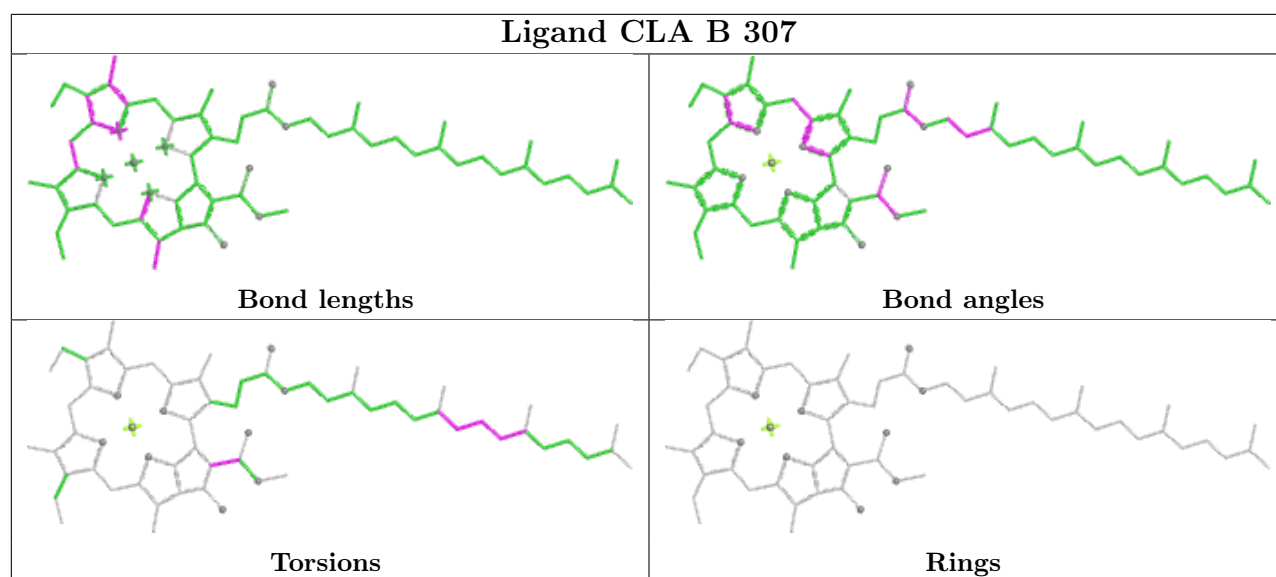
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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

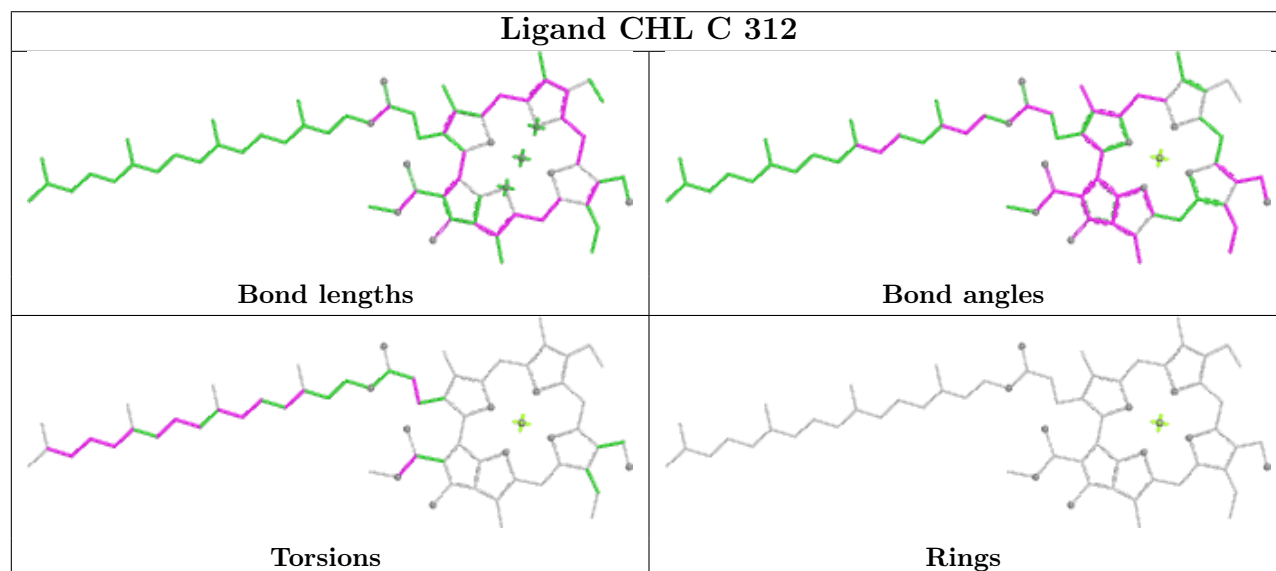
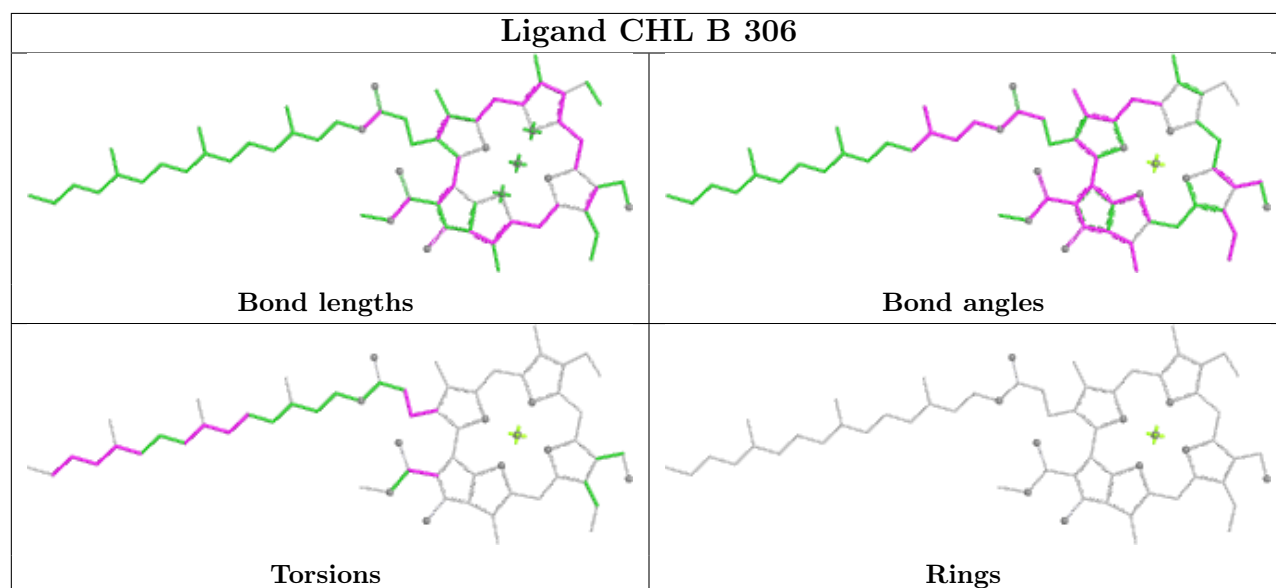
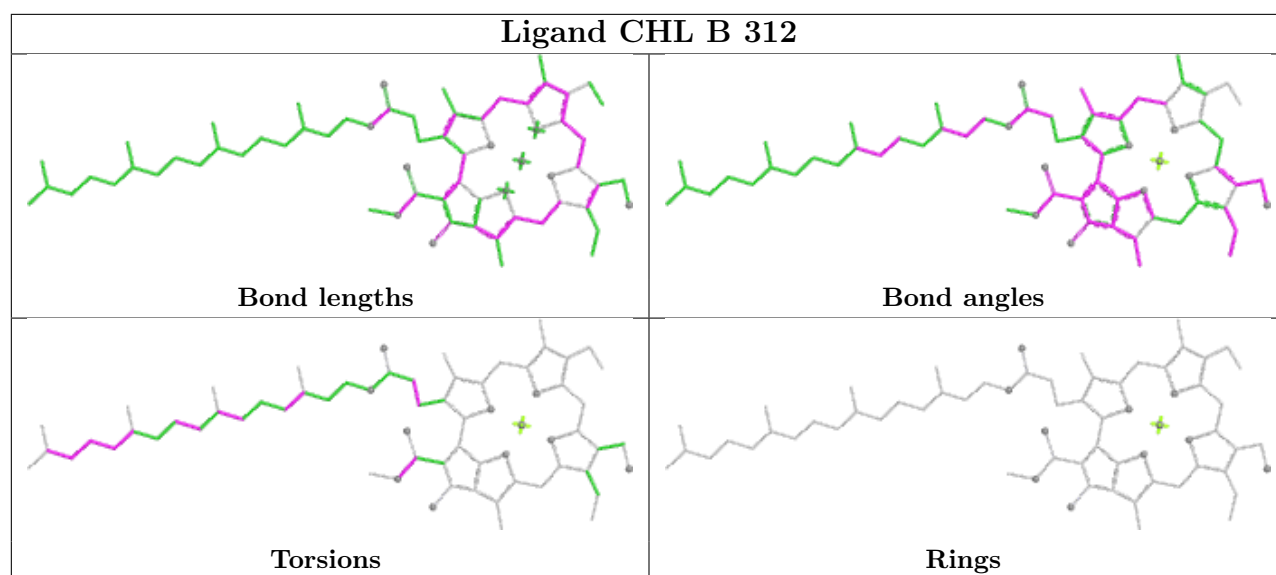
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

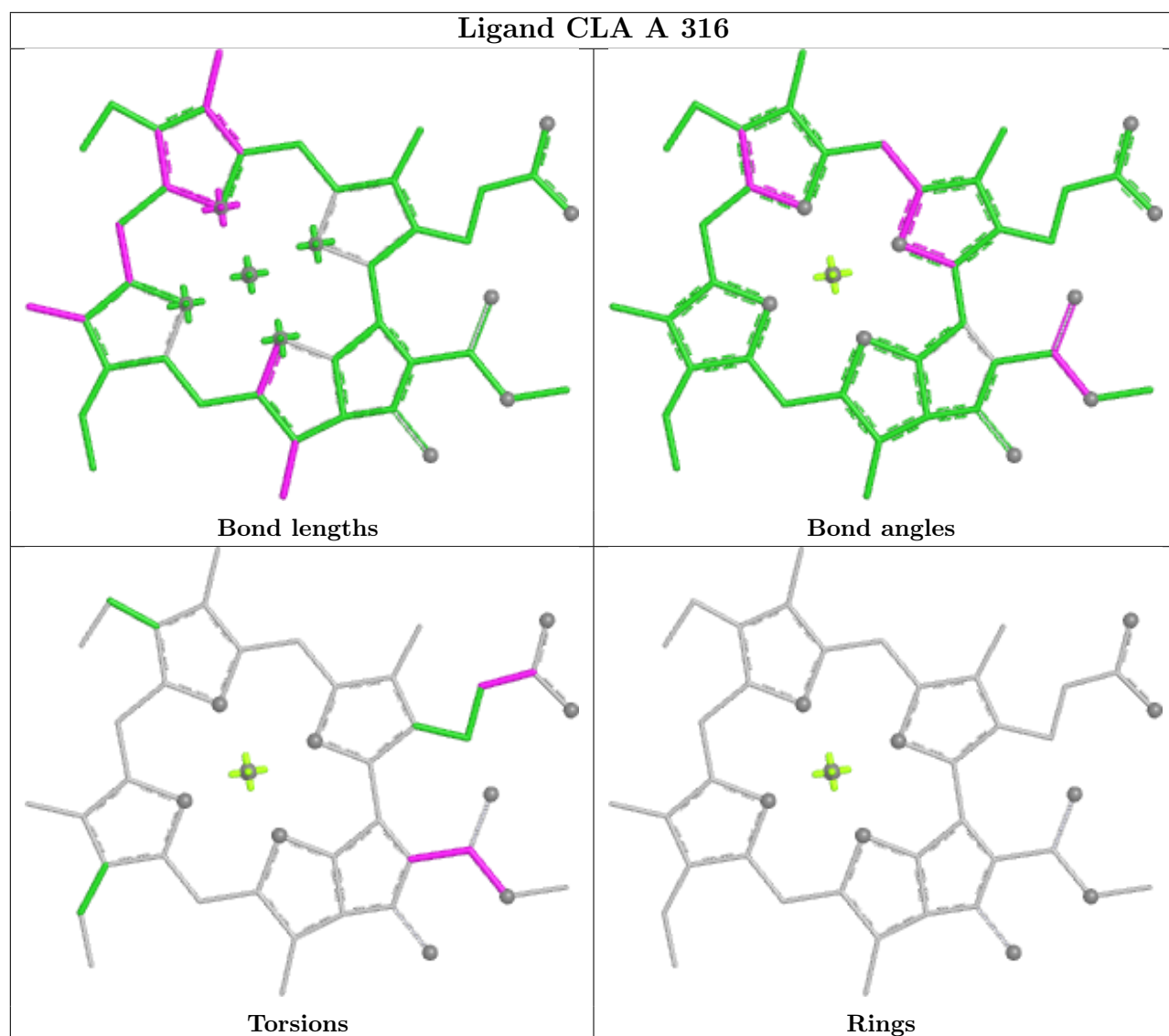
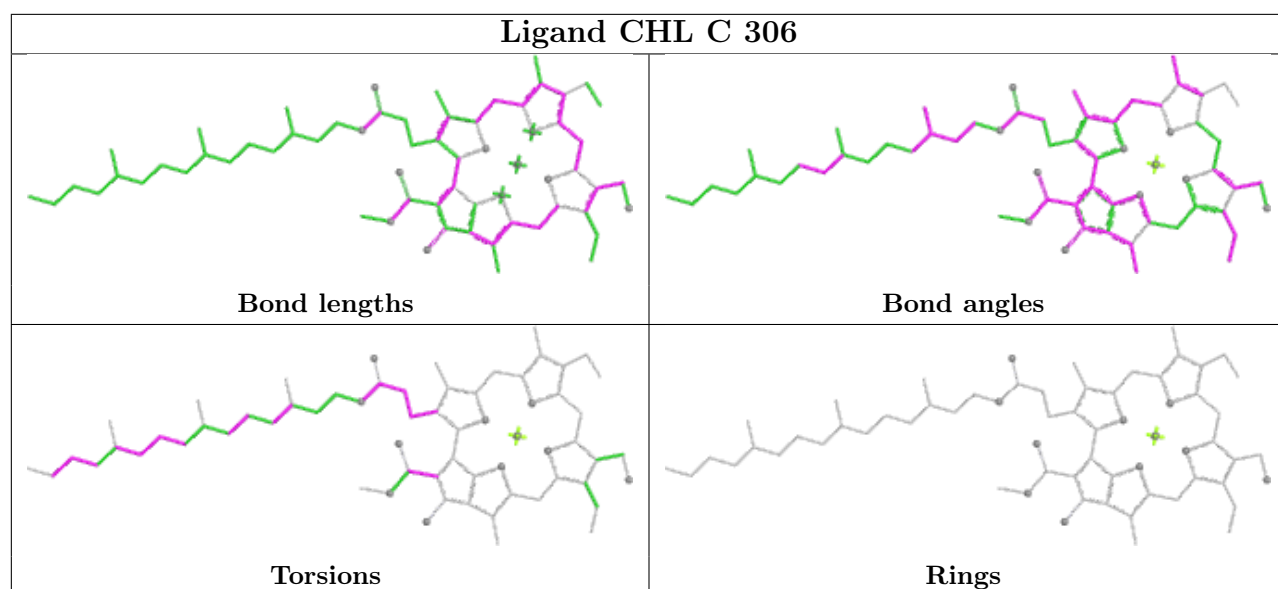


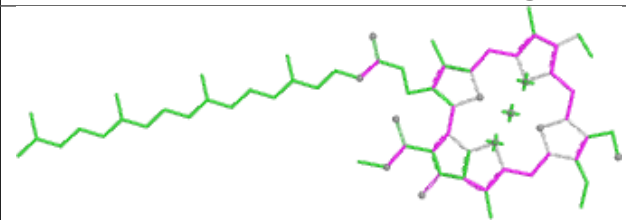
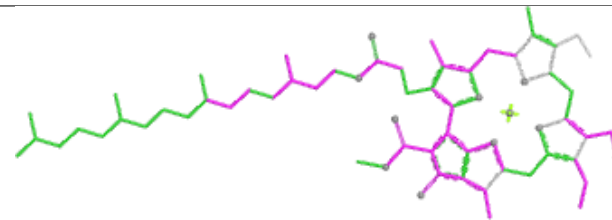
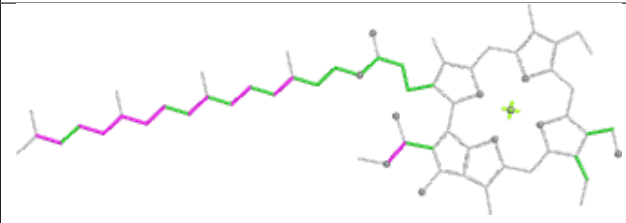
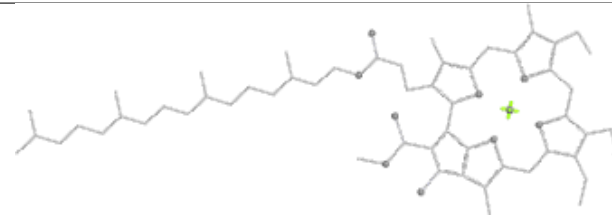


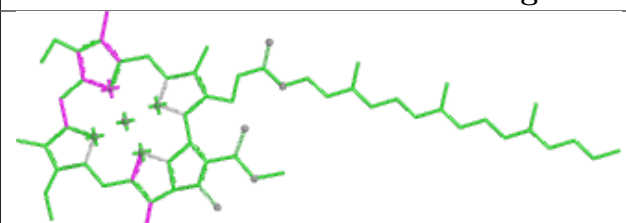
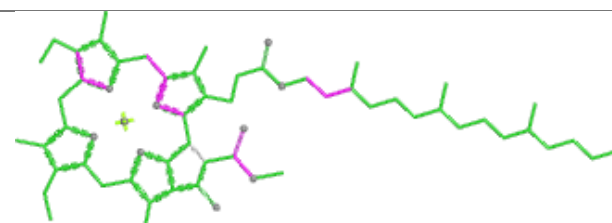
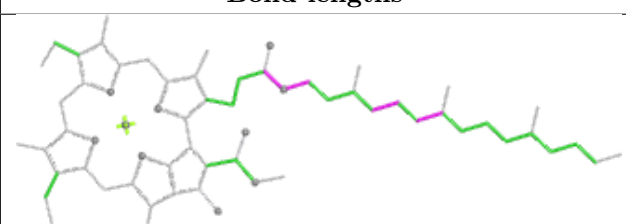
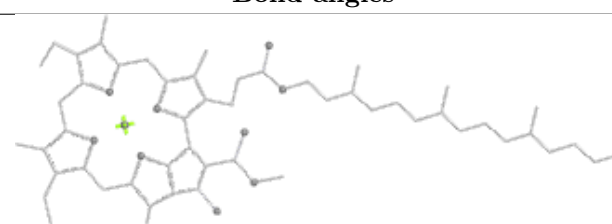


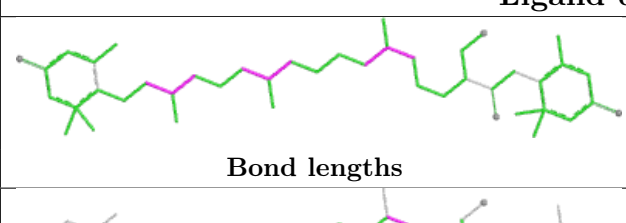
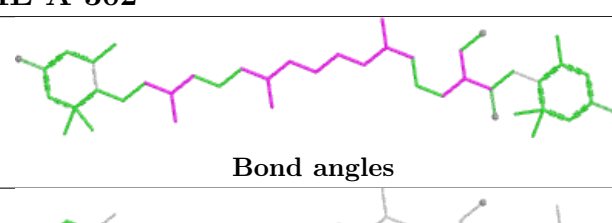
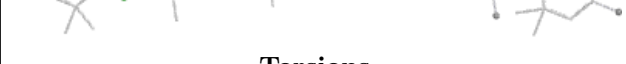


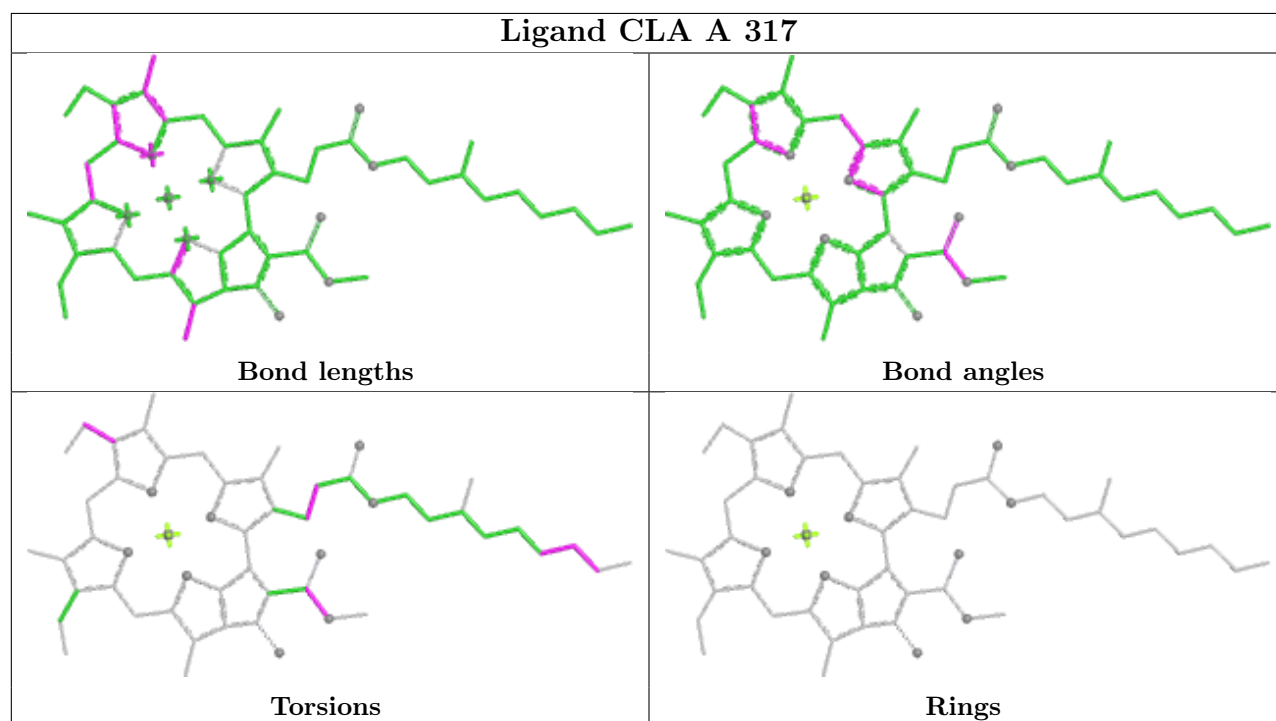
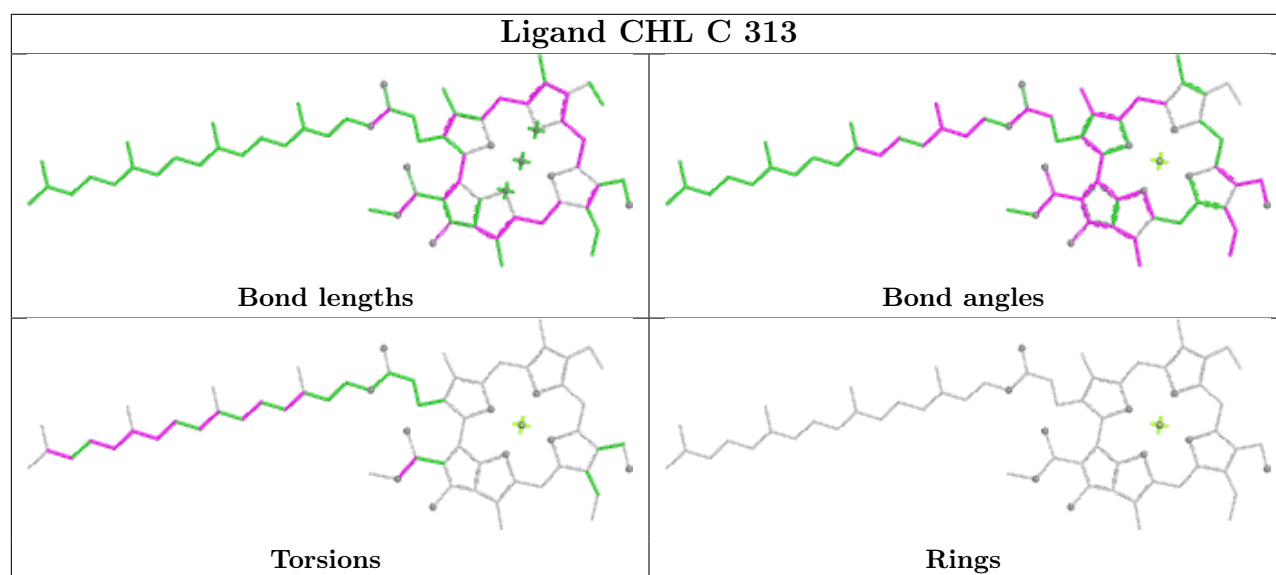




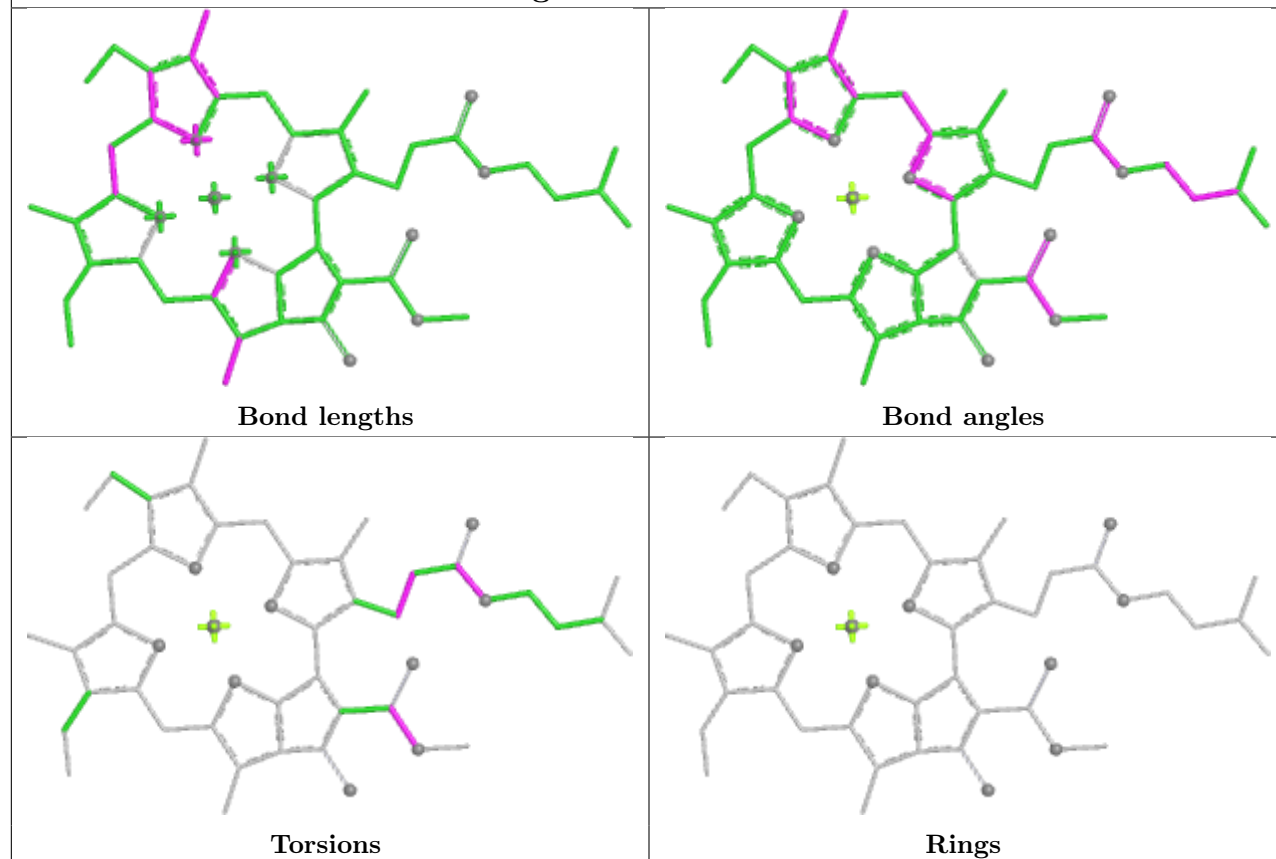
Ligand CHL B 313	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA A 315	
	
Bond lengths	Bond angles
	
Torsions	Rings

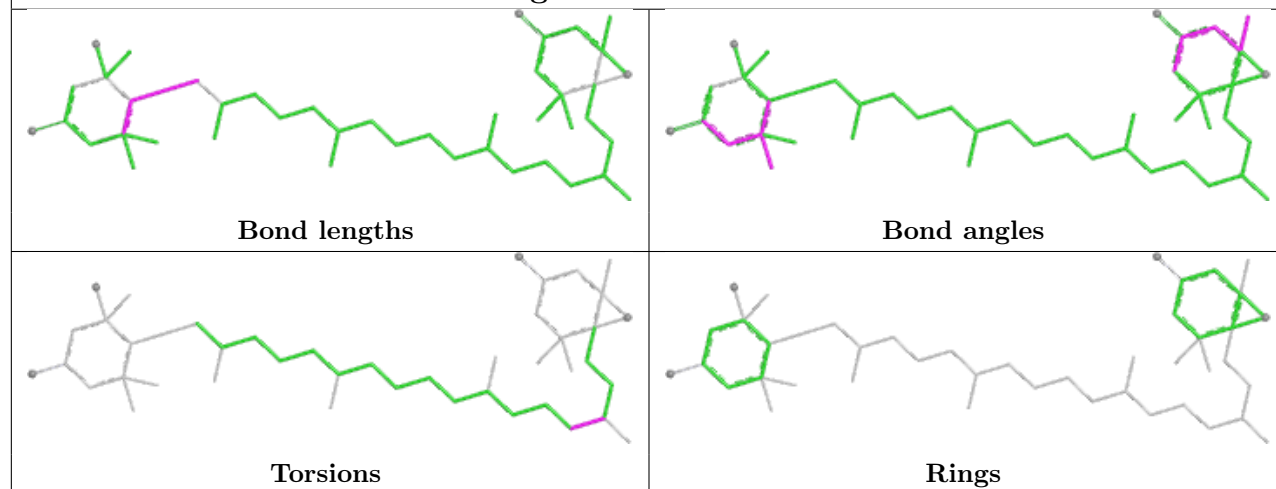
Ligand OIE A 302	
	
Bond lengths	Bond angles
	
Torsions	Rings

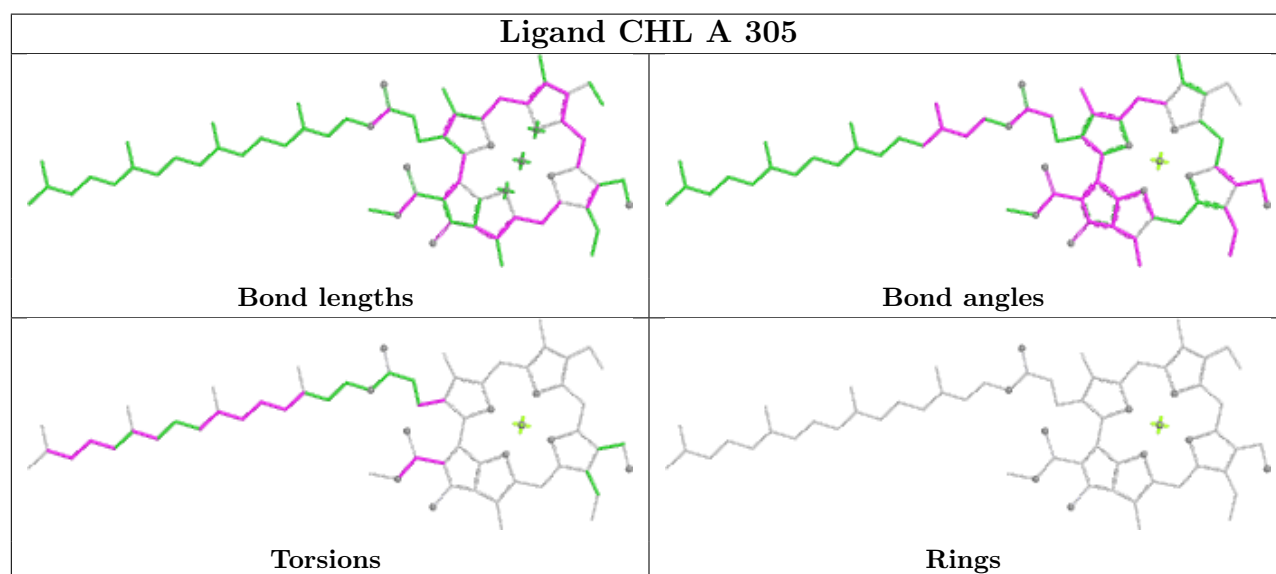
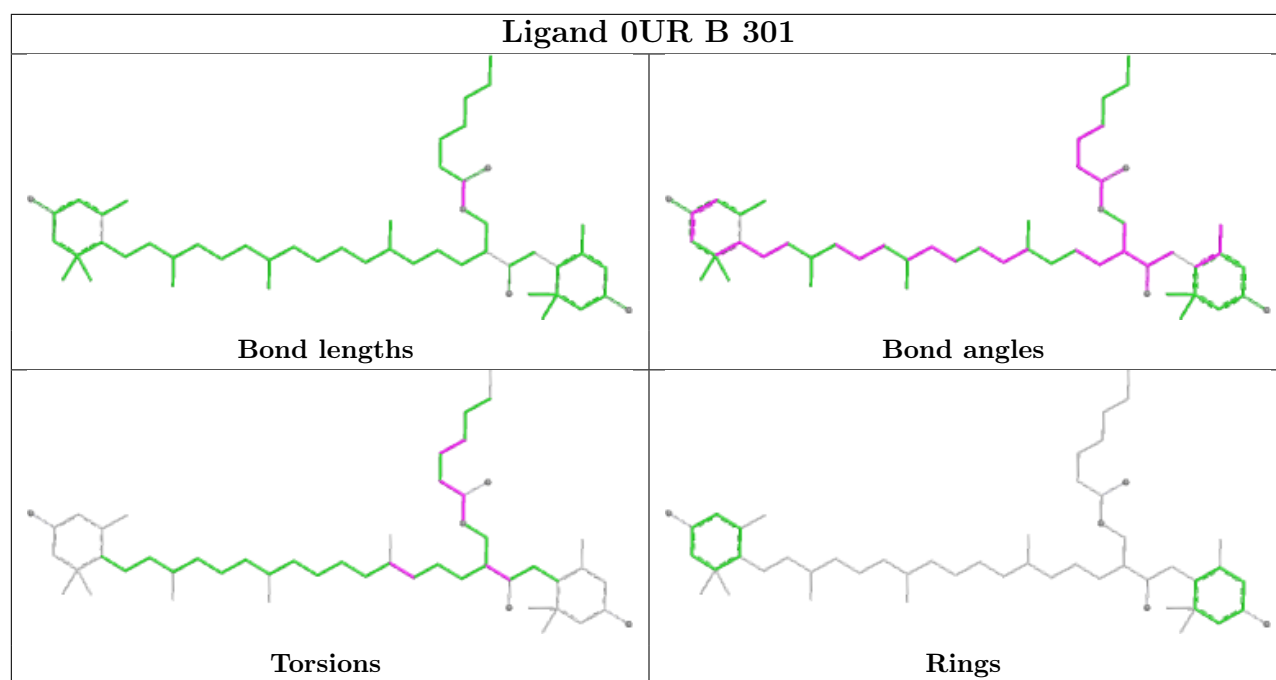


Ligand CLA B 308

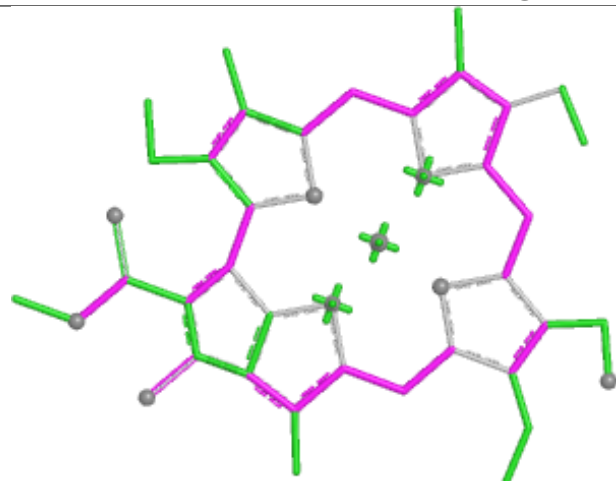


Ligand NEX C 304

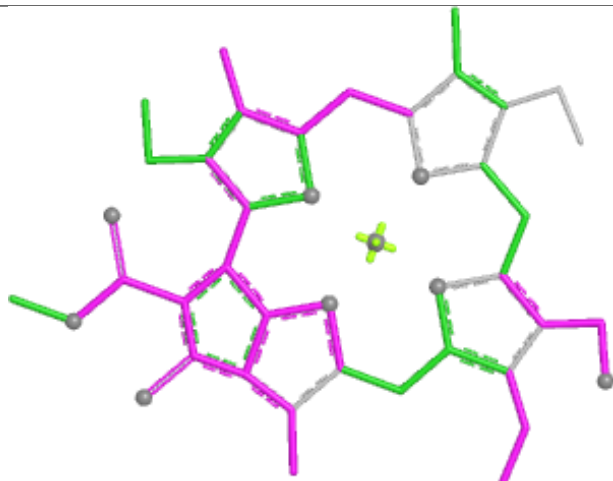




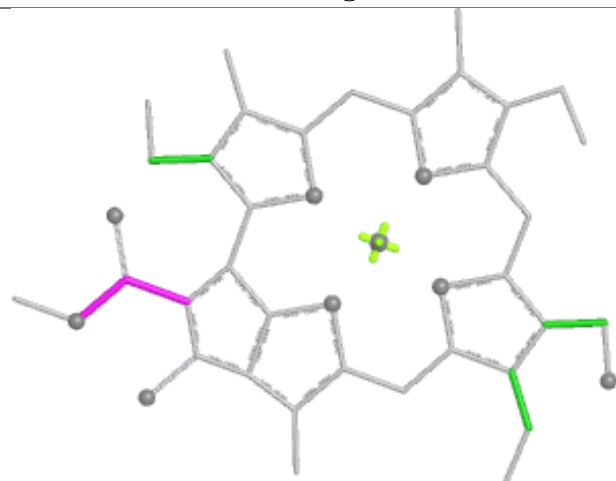
Ligand CHL B 309



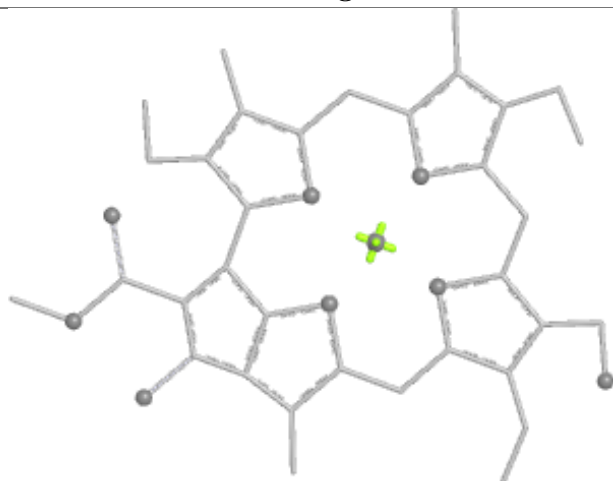
Bond lengths



Bond angles

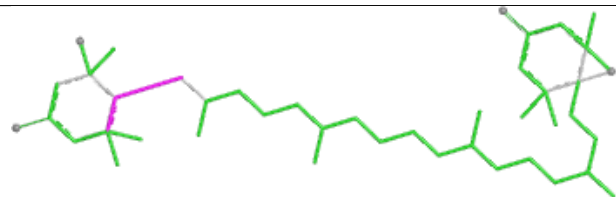


Torsions

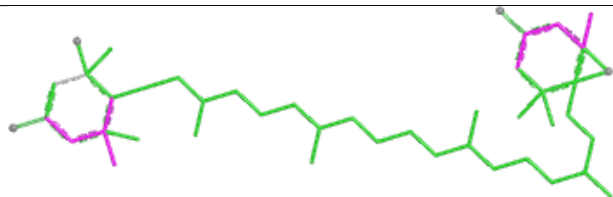


Rings

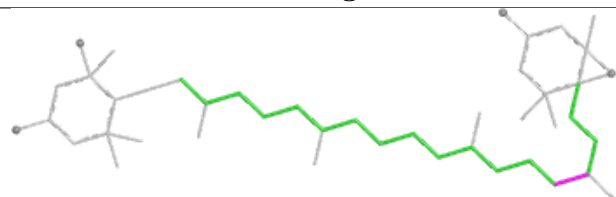
Ligand NEX B 304



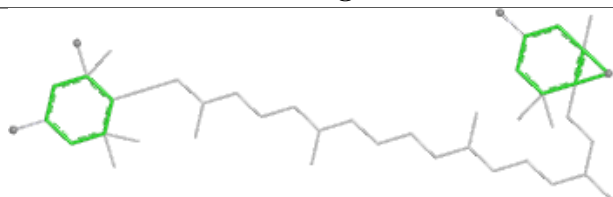
Bond lengths



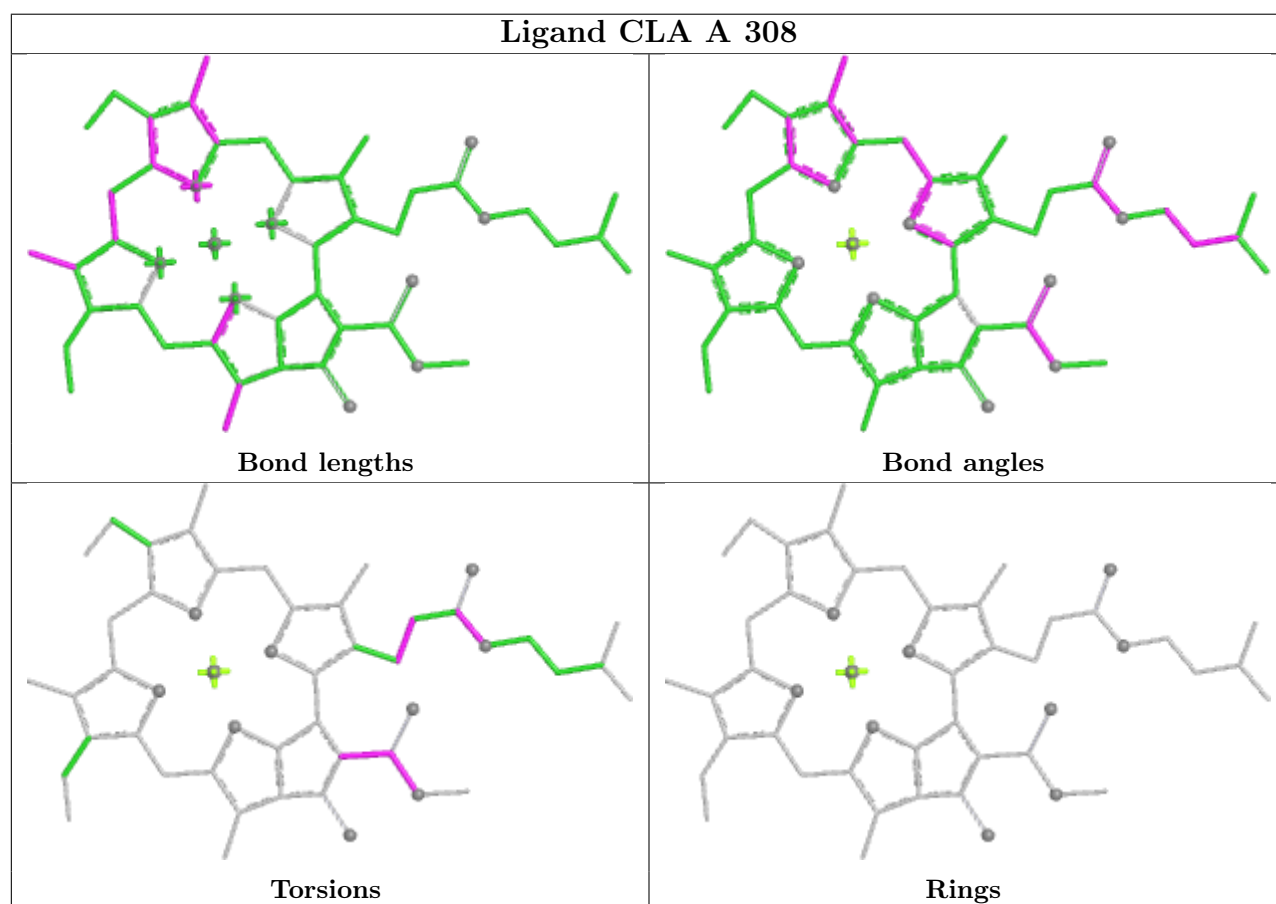
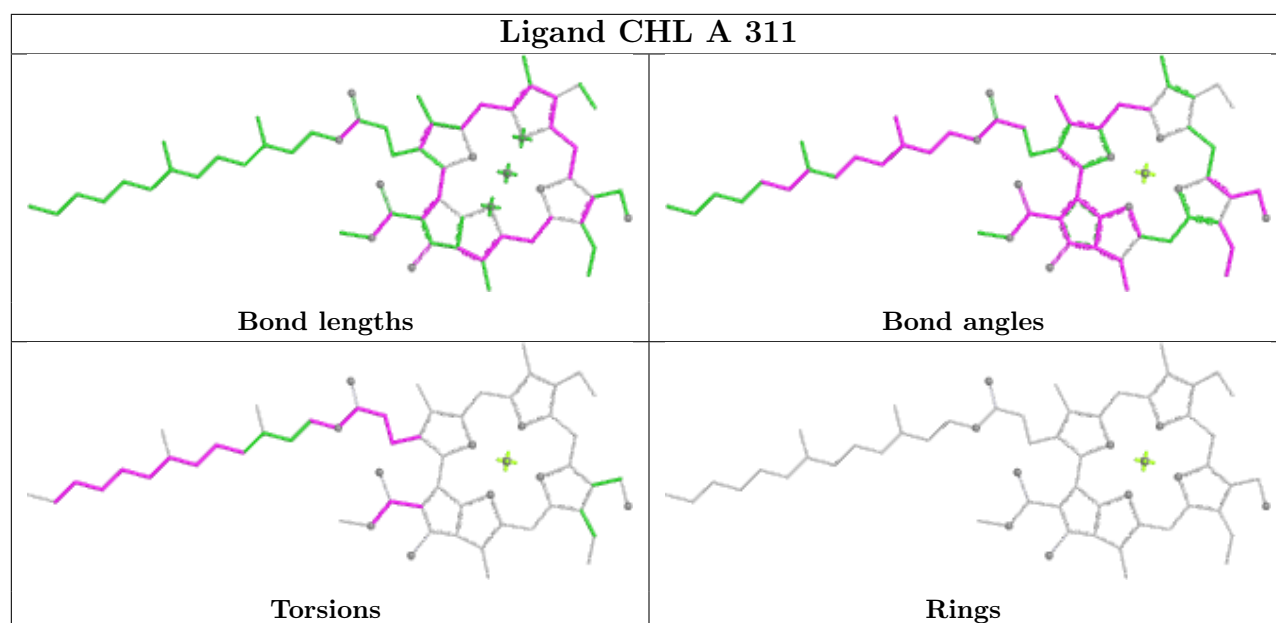
Bond angles

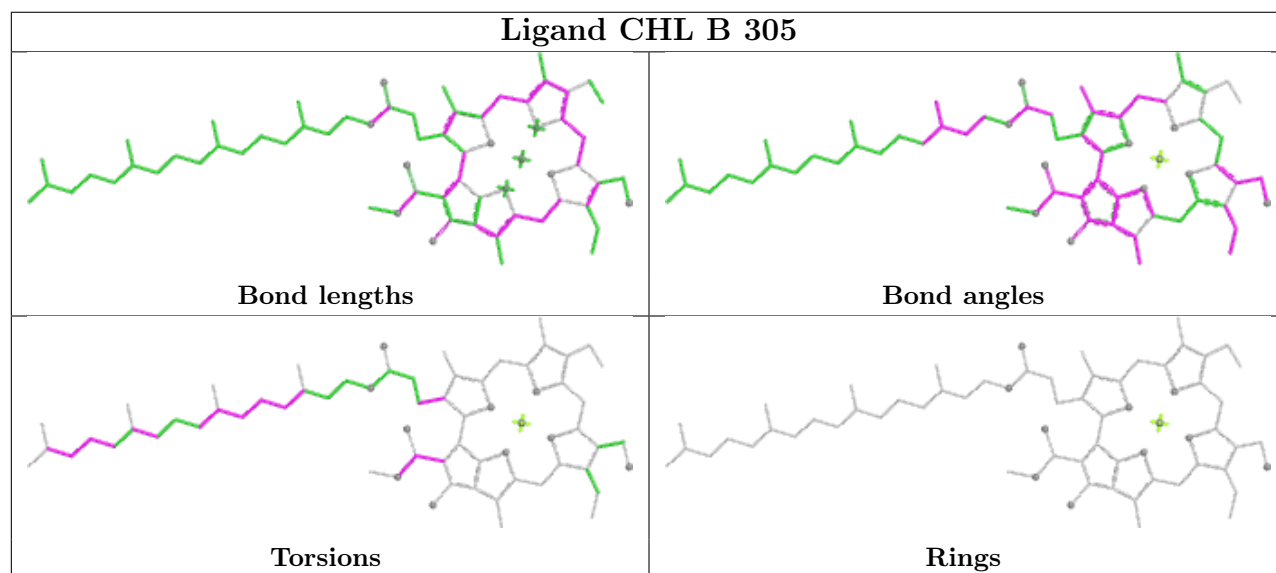
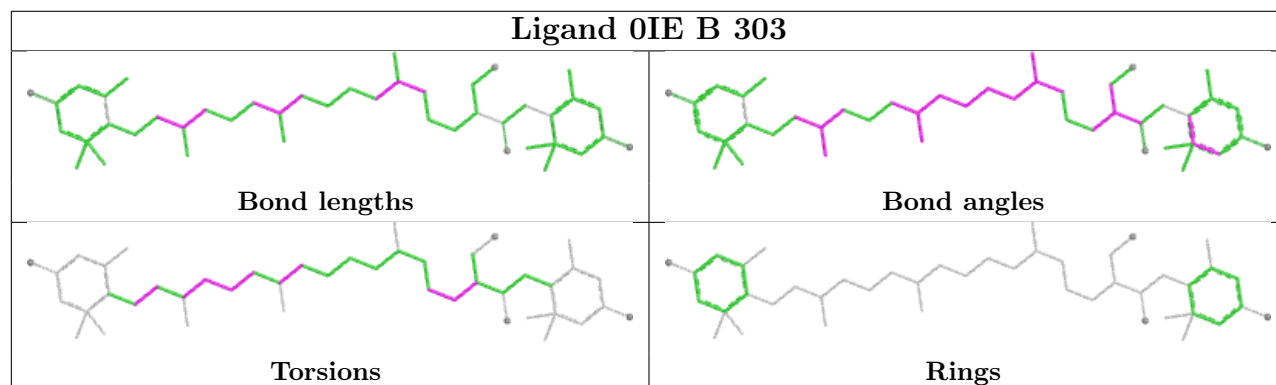
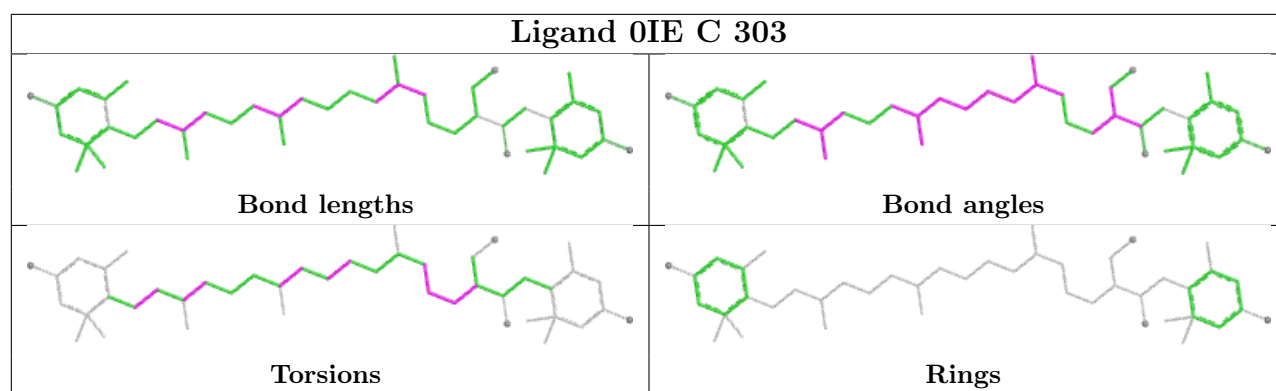


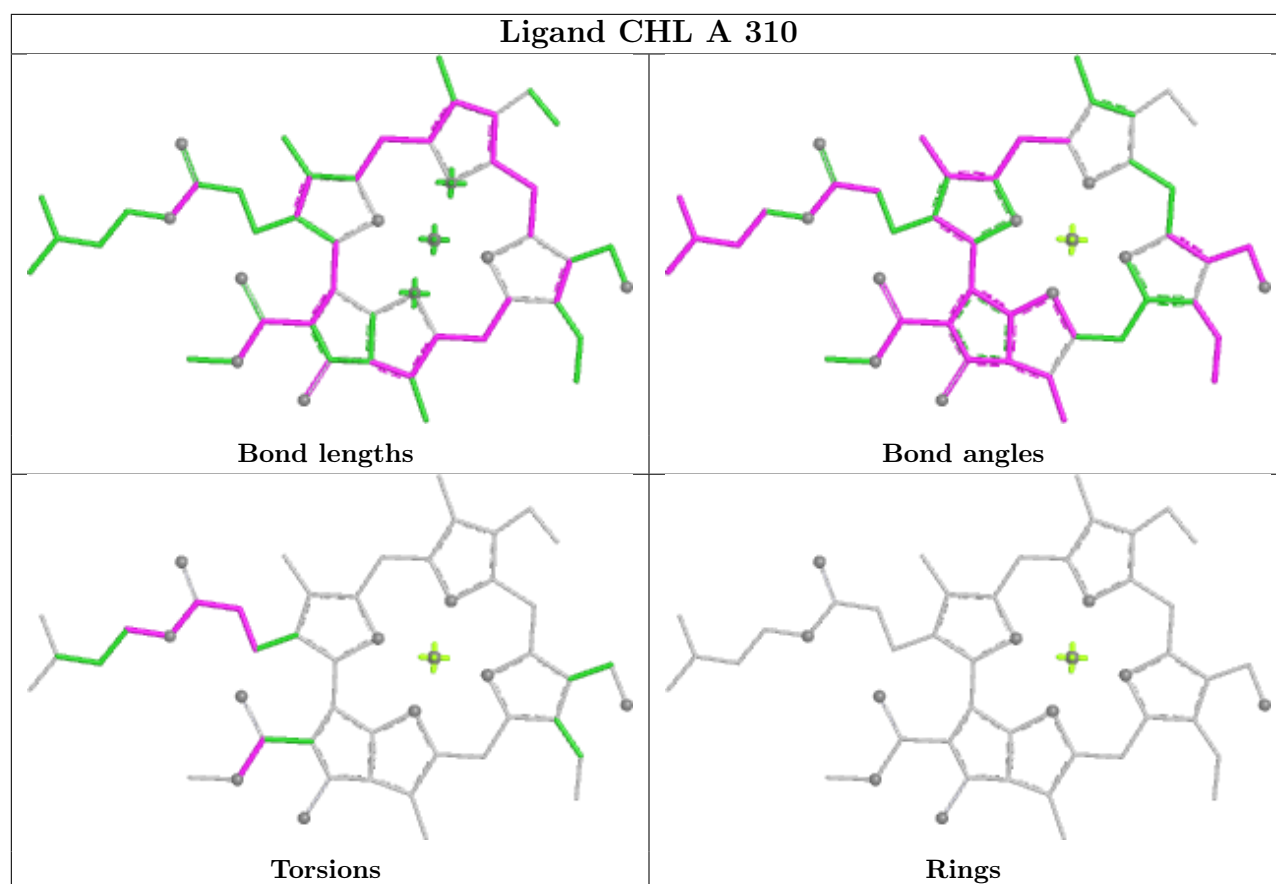
Torsions



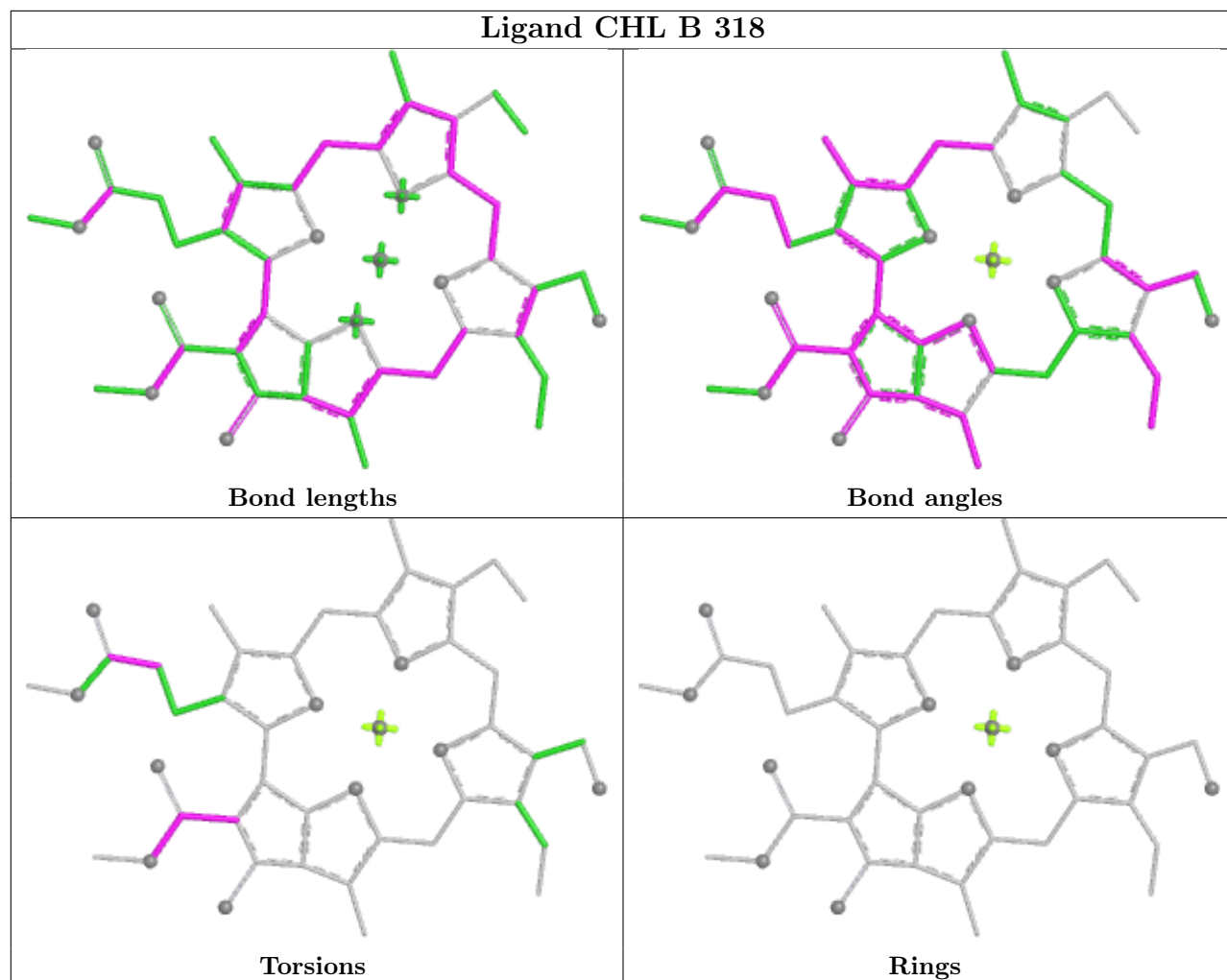
Rings



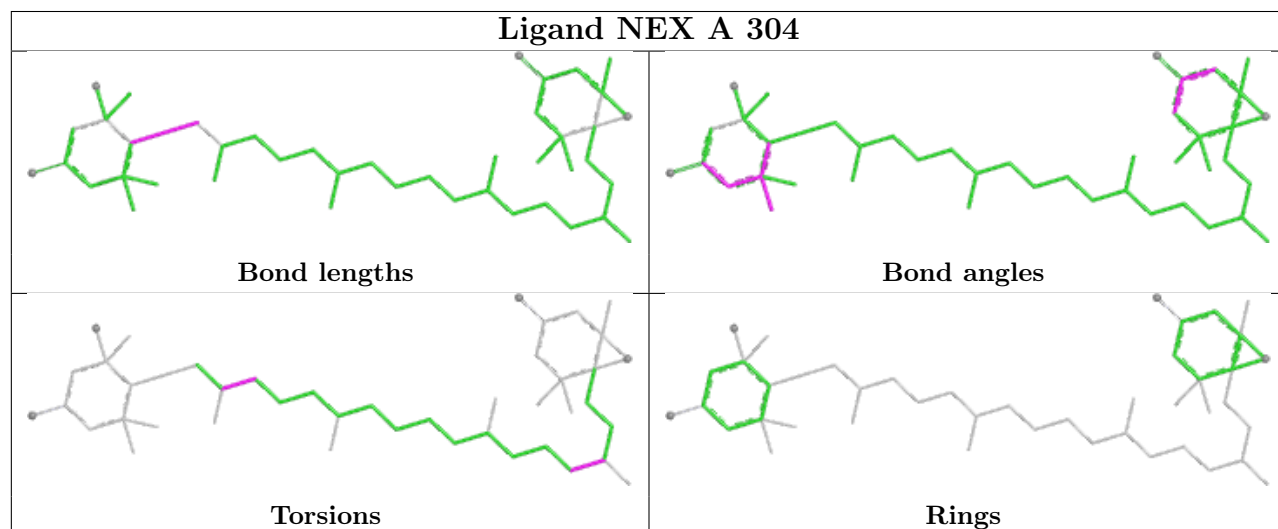


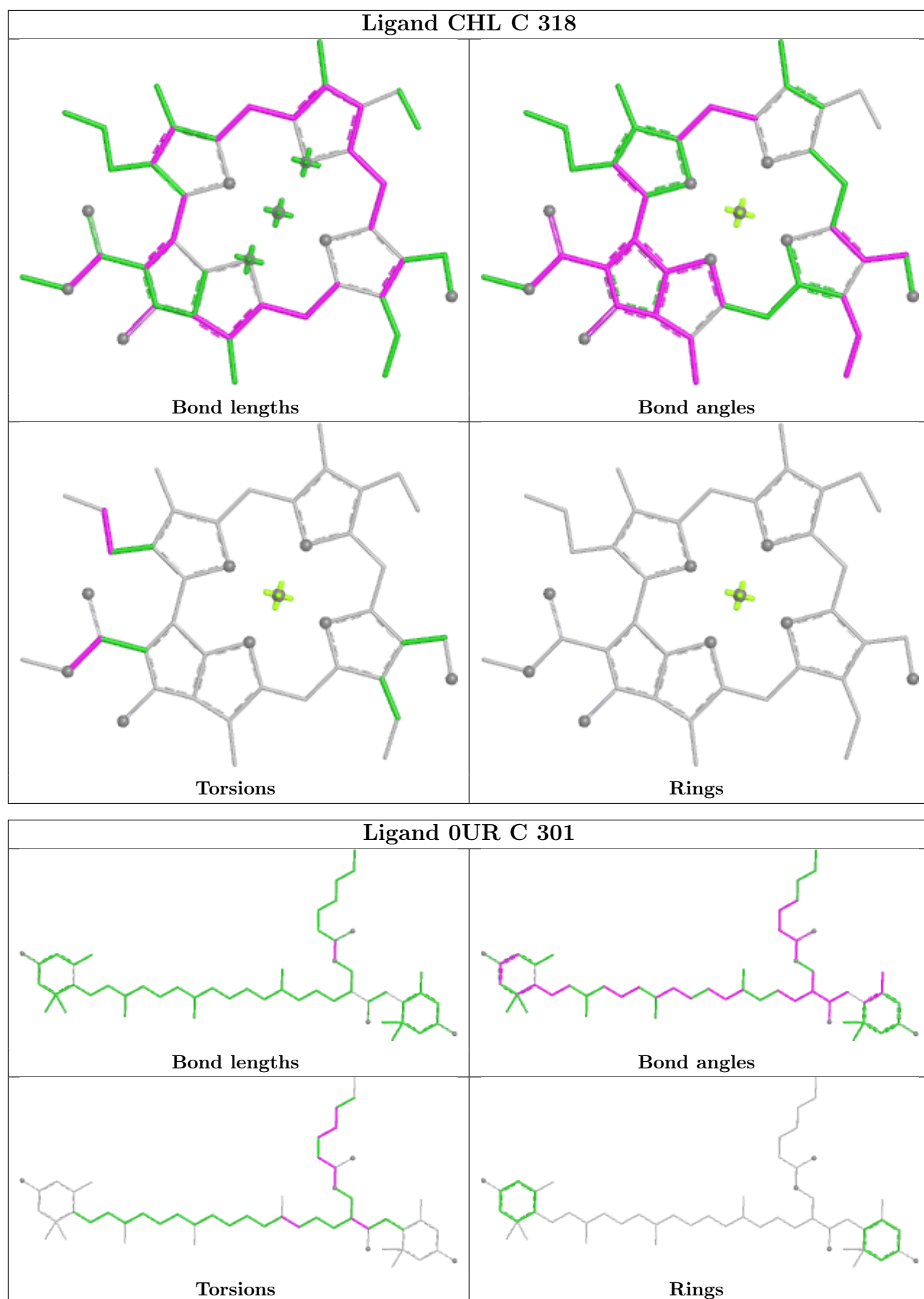


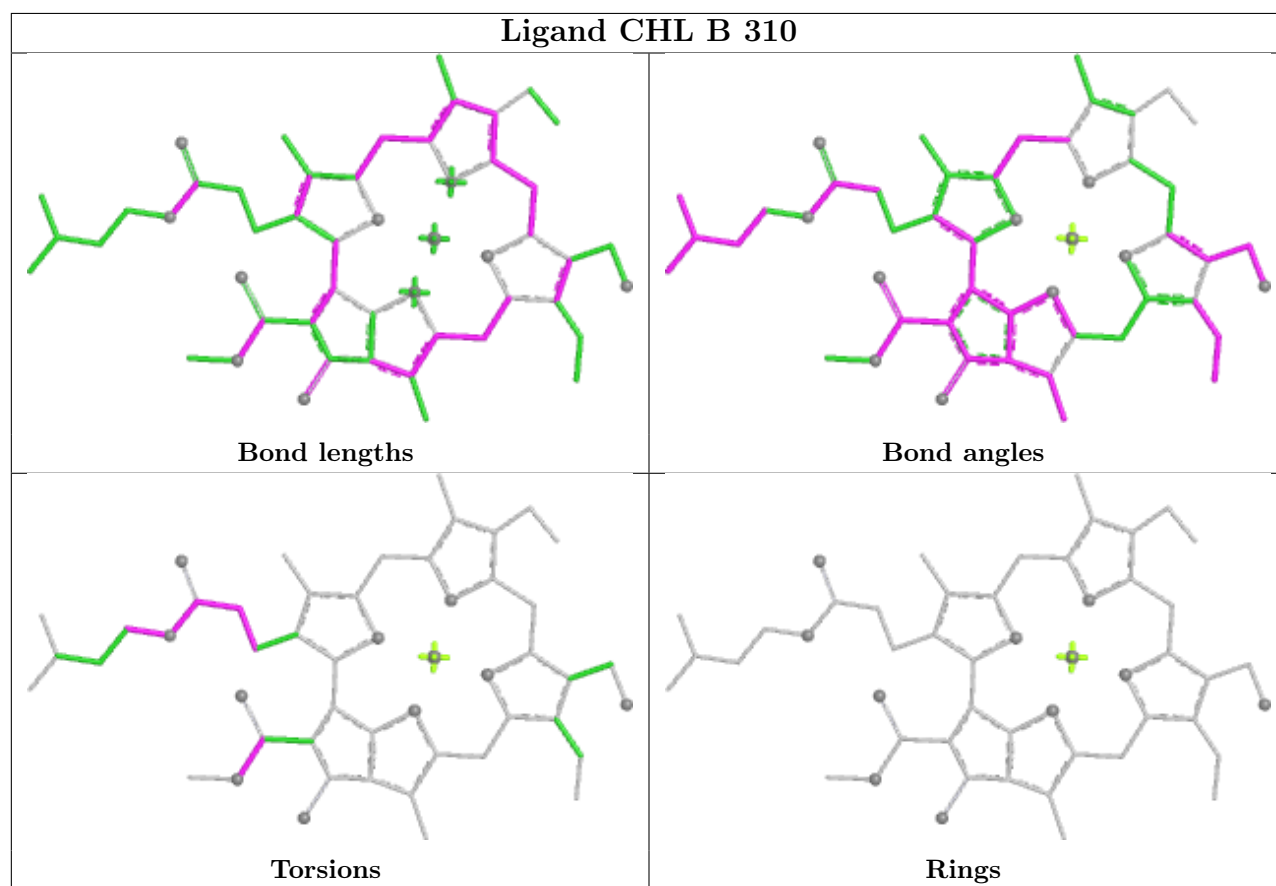
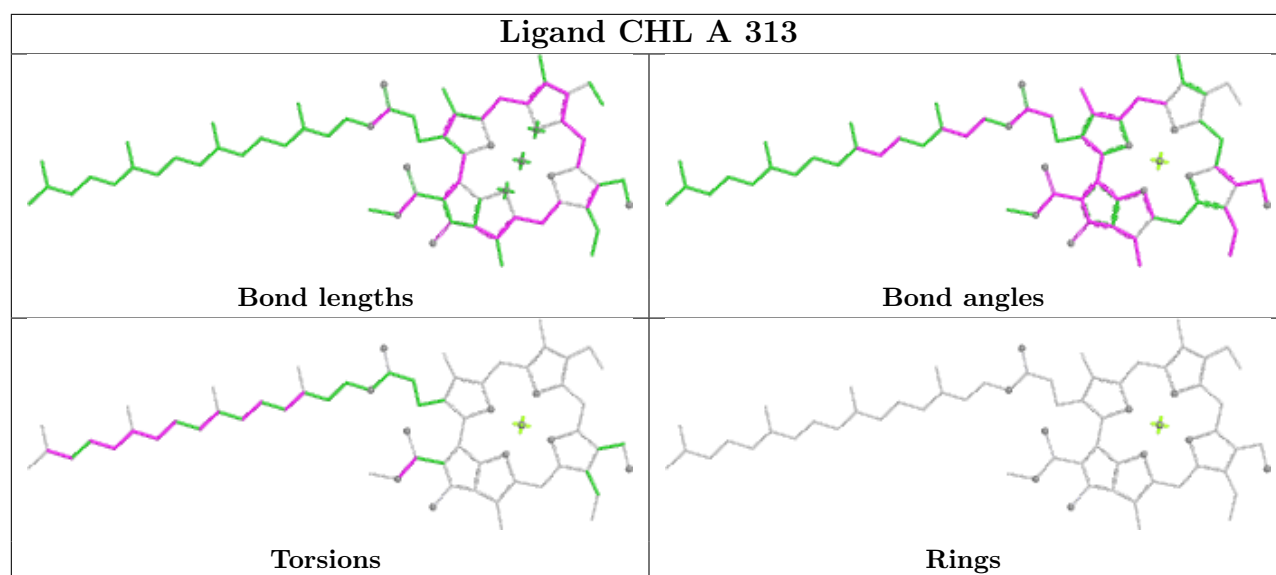
Ligand CHL B 318



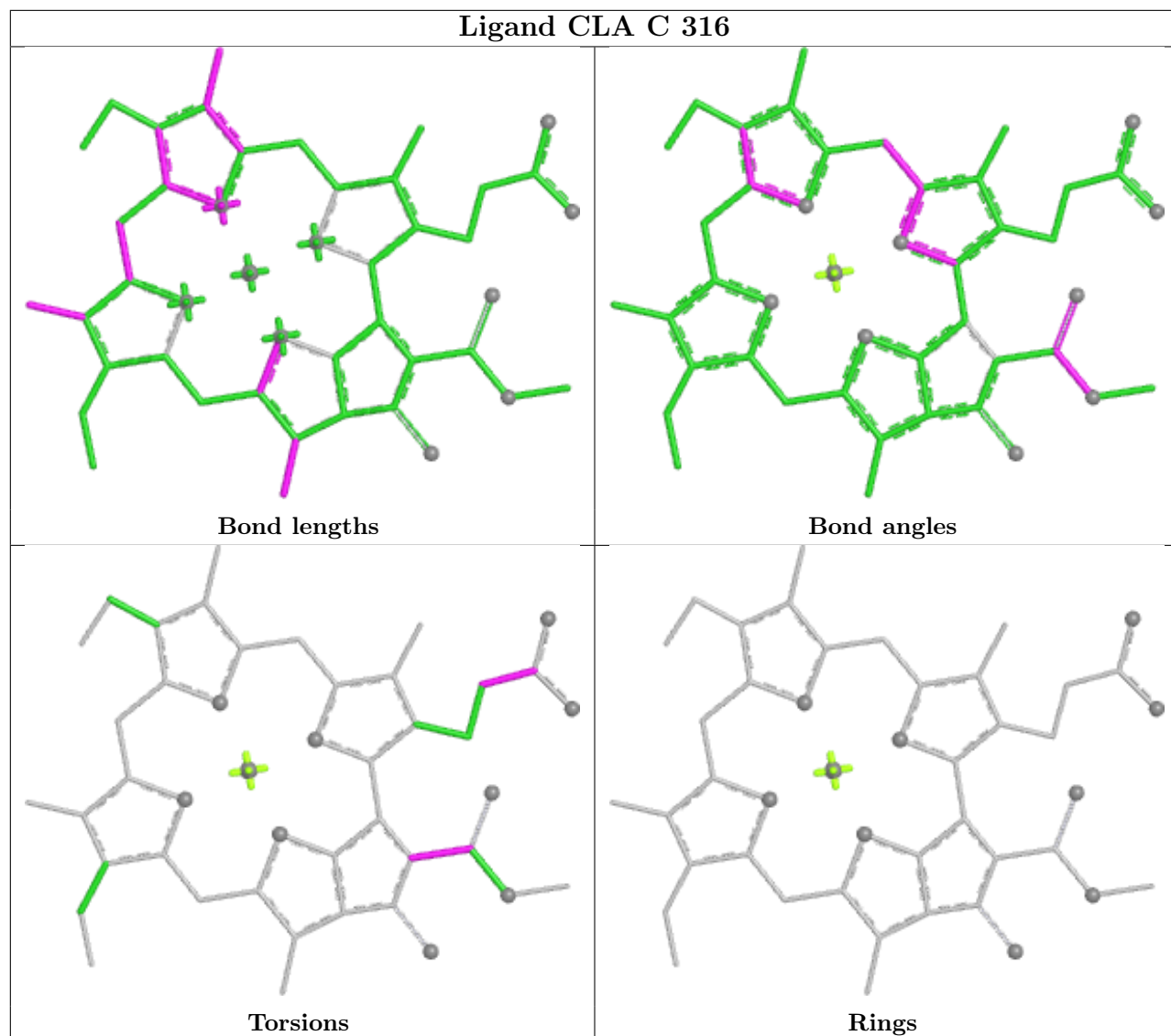
Ligand NEX A 304



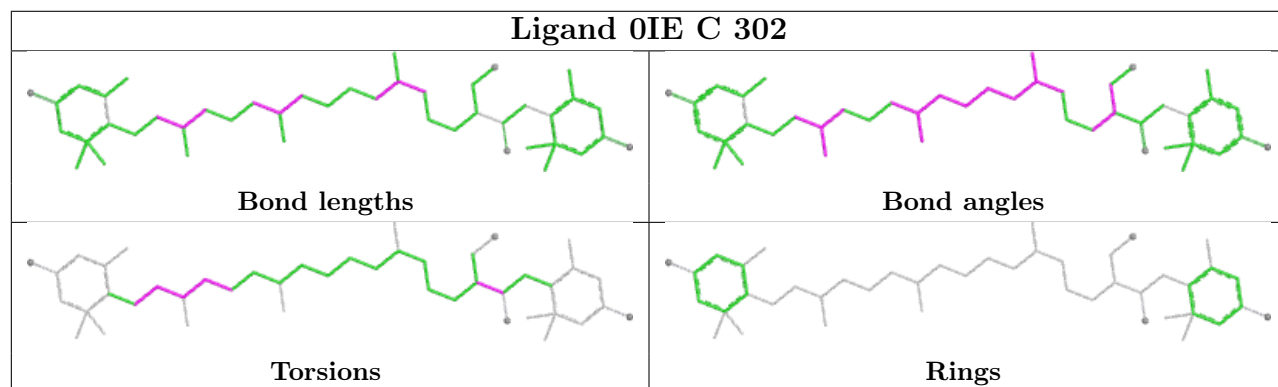


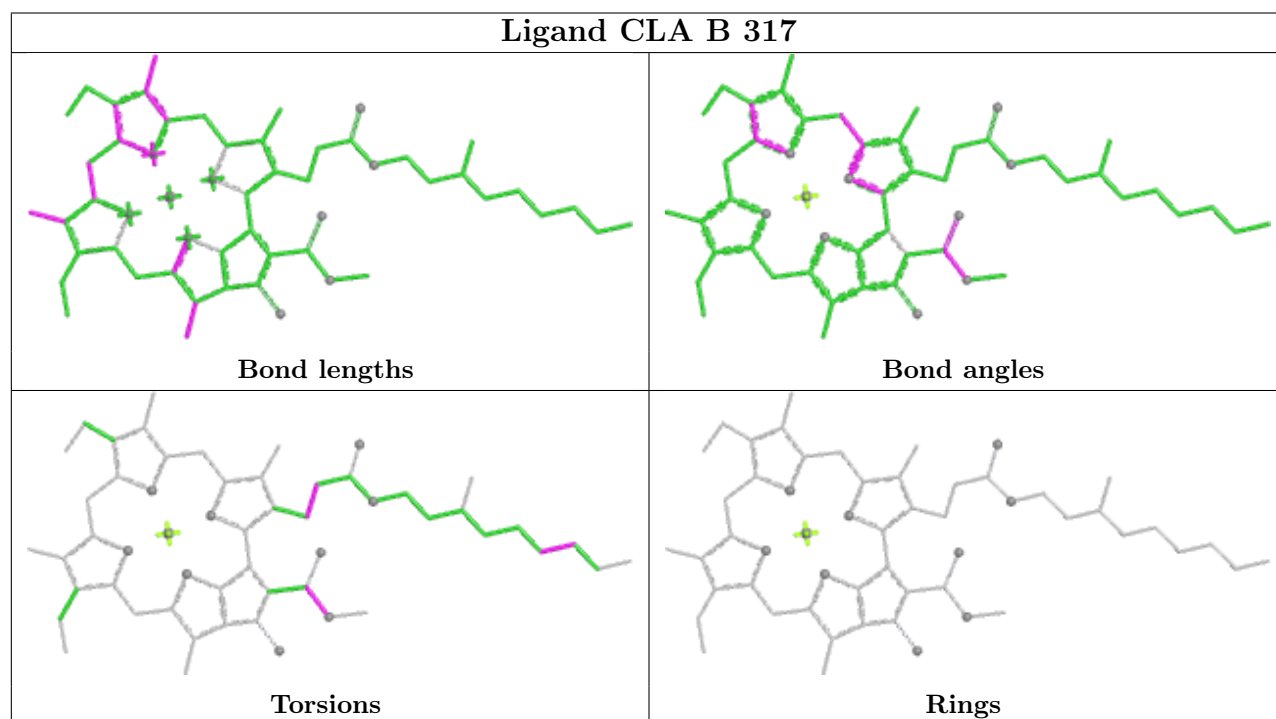
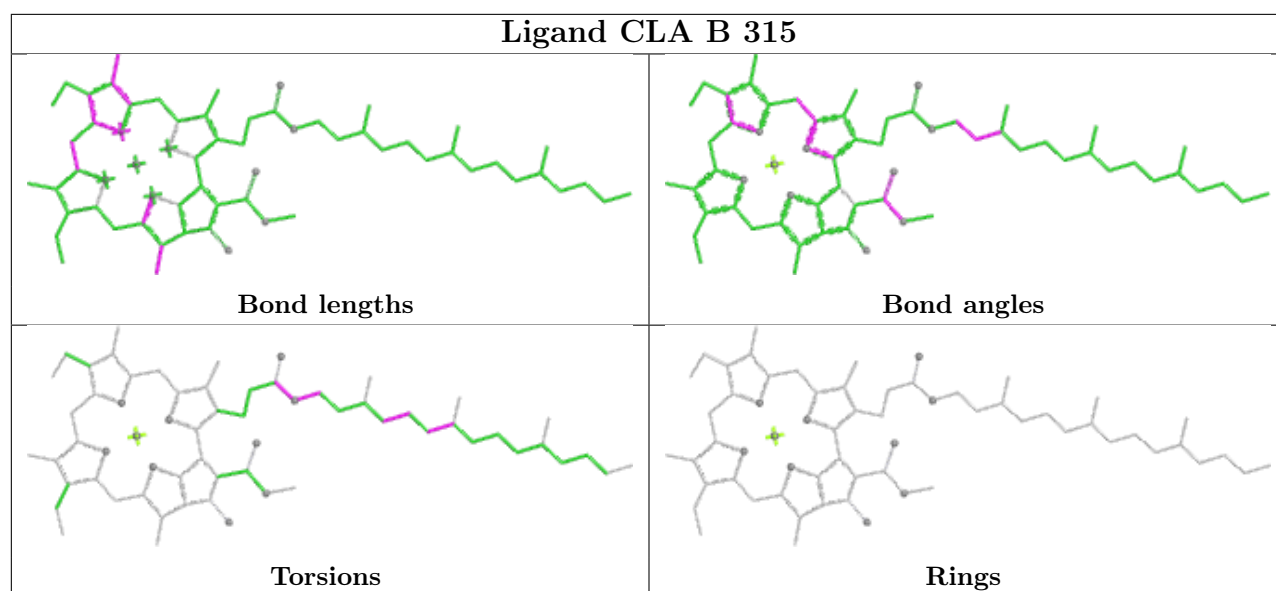


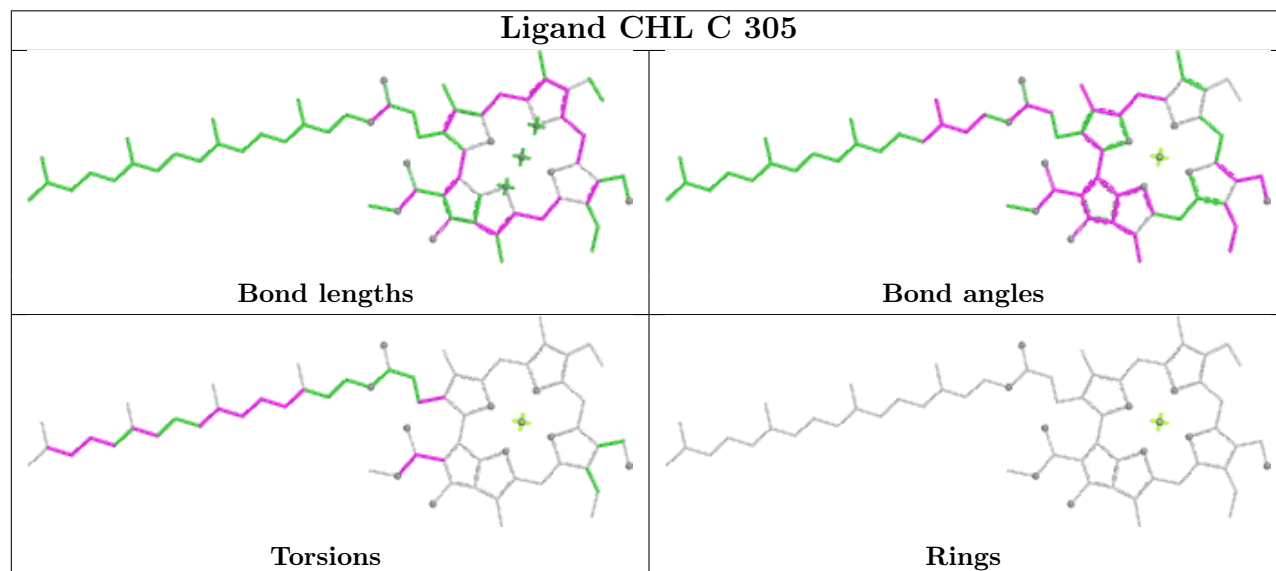
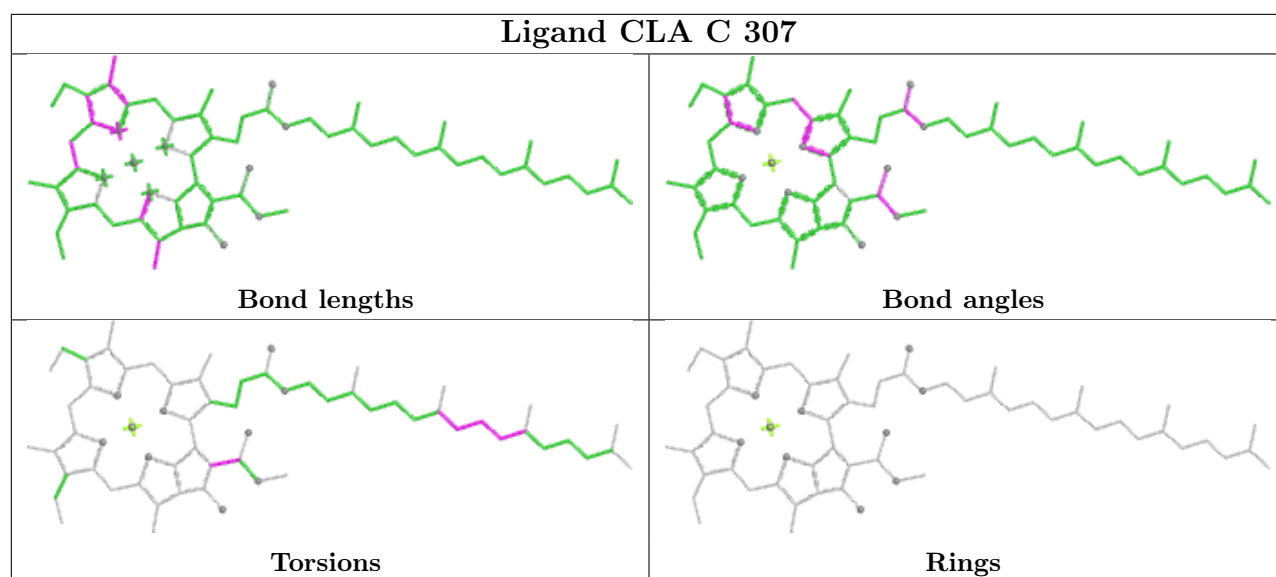
Ligand CLA C 316

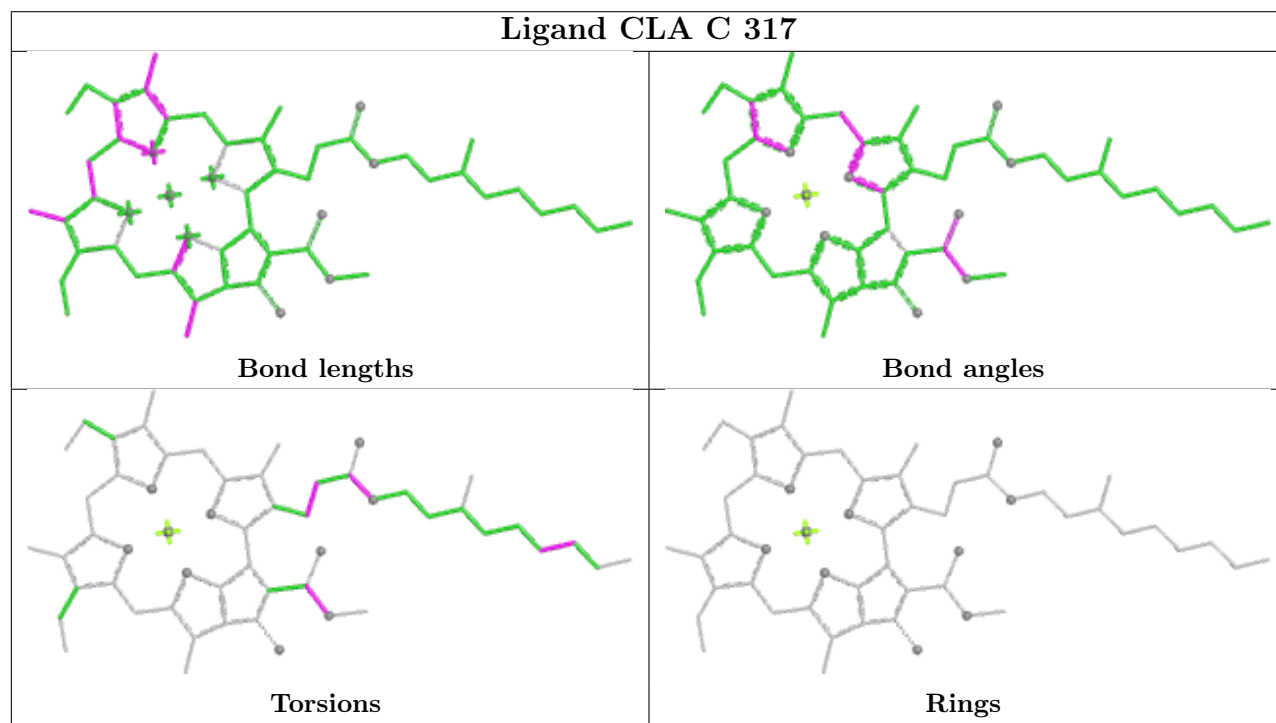
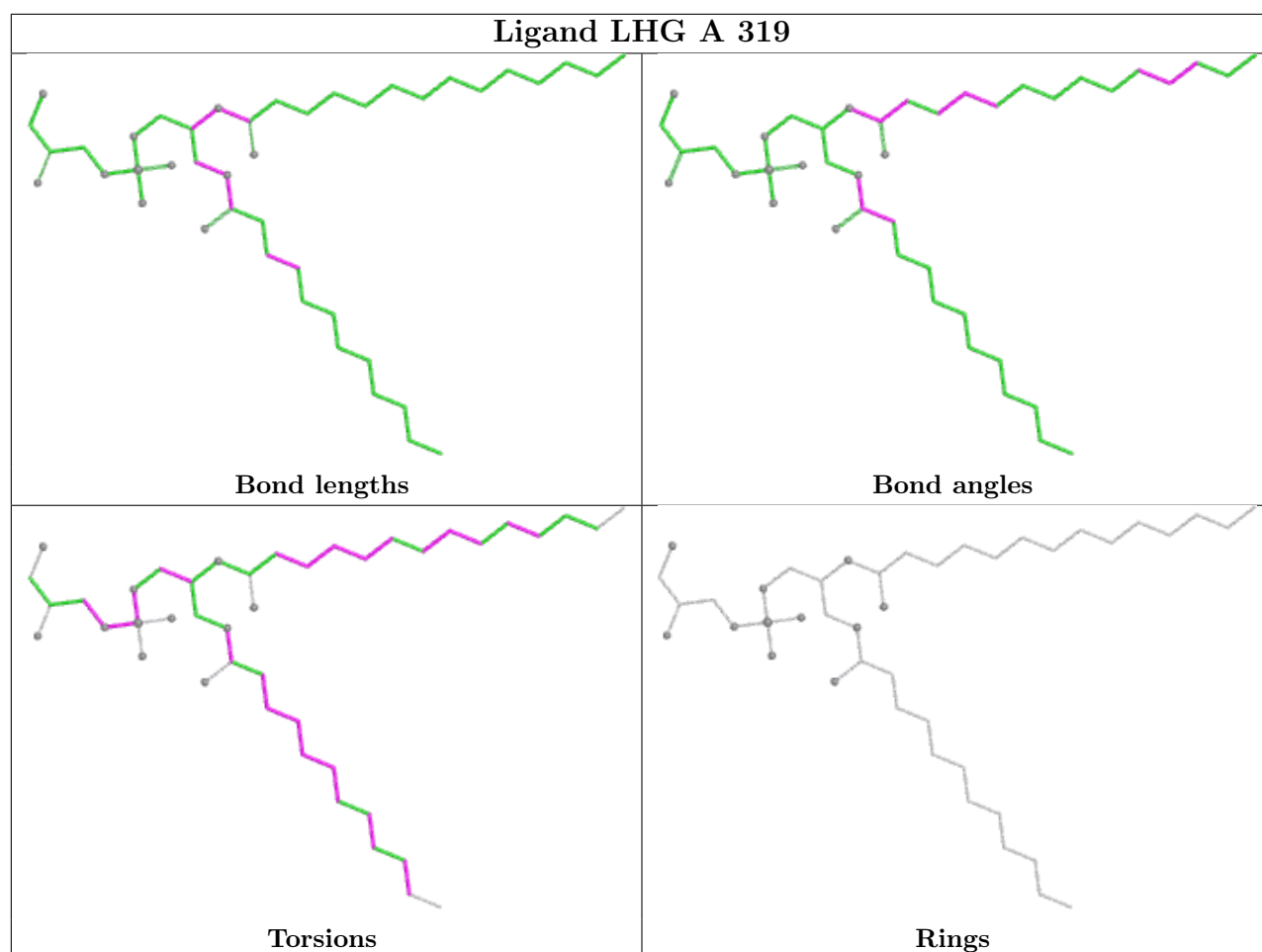


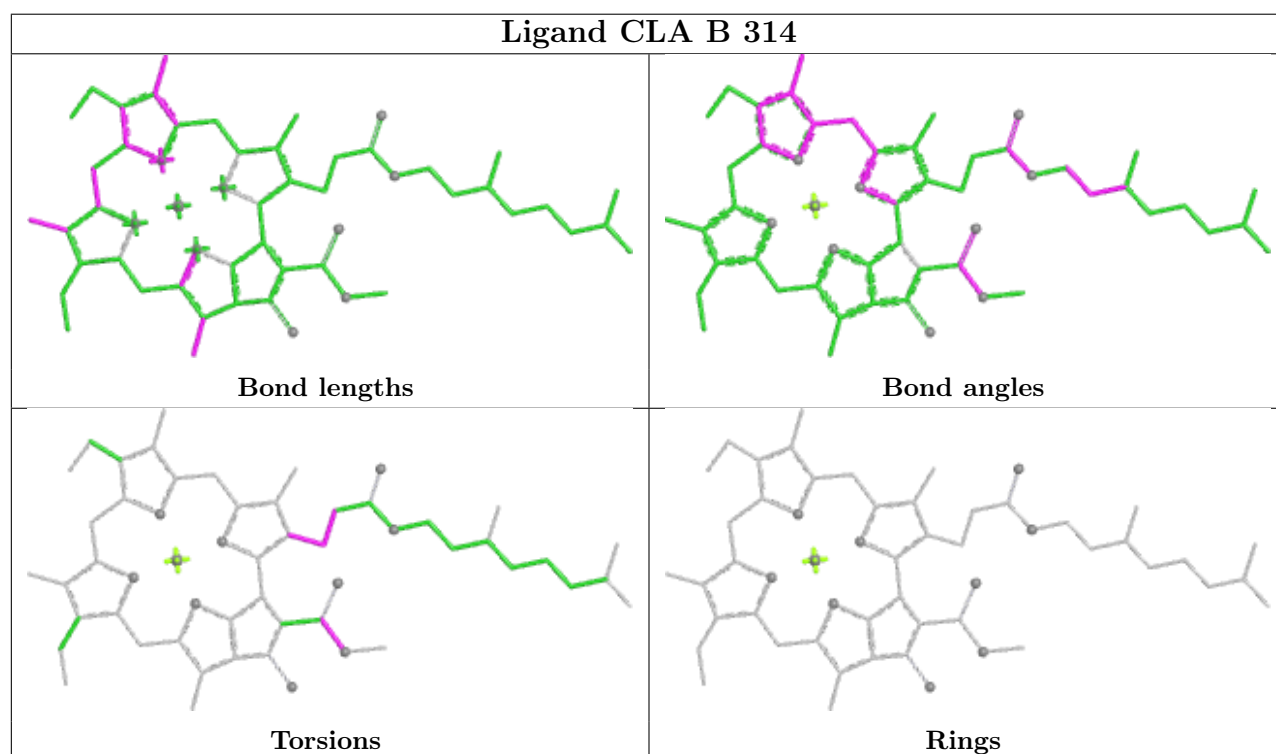
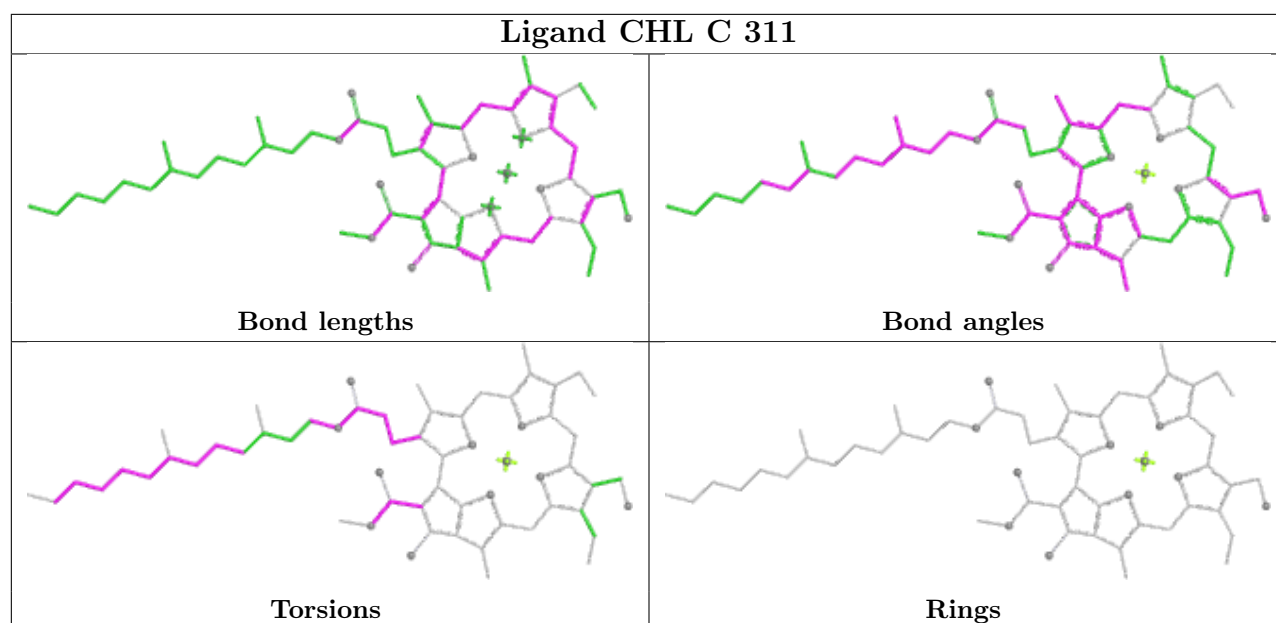
Ligand OIE C 302

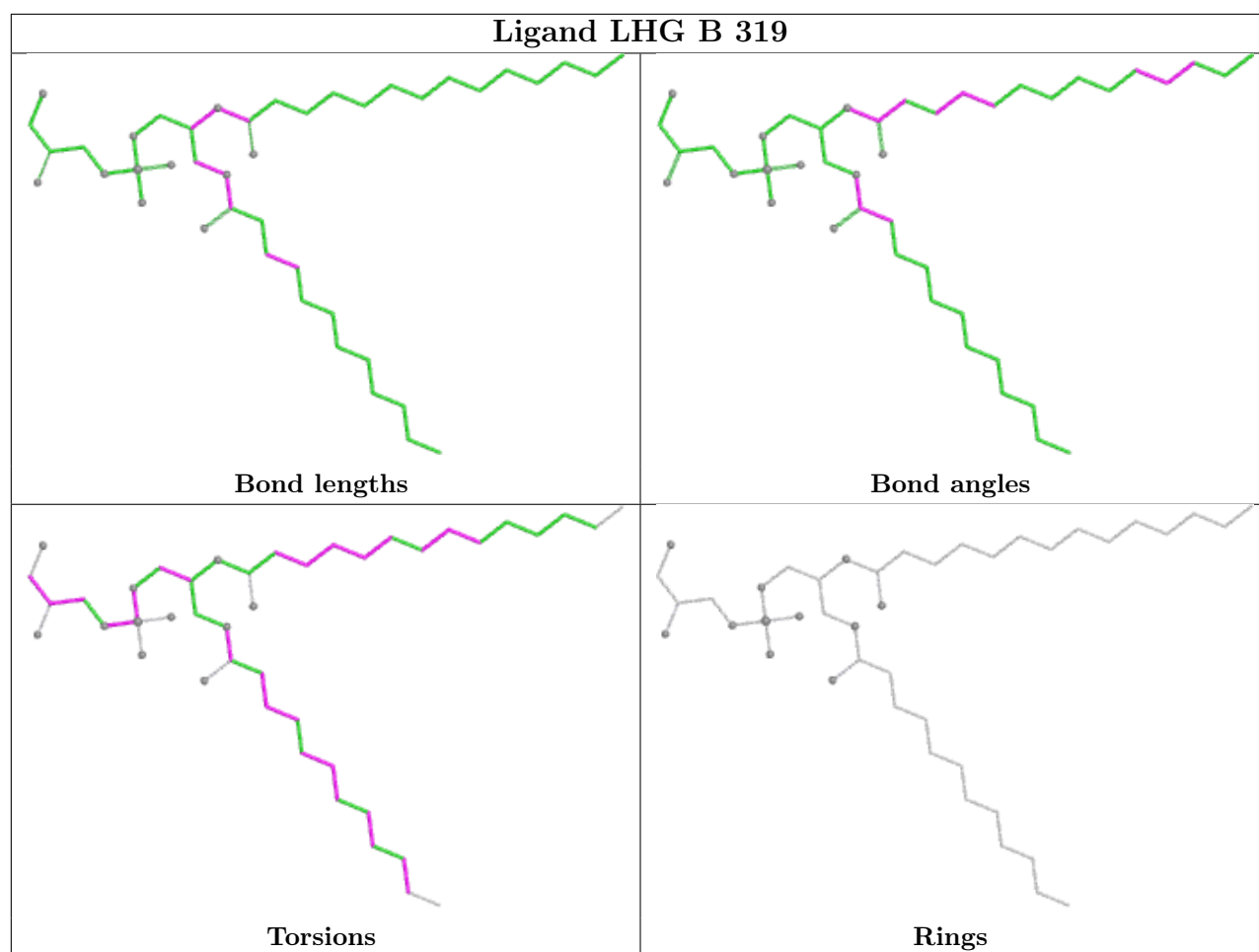


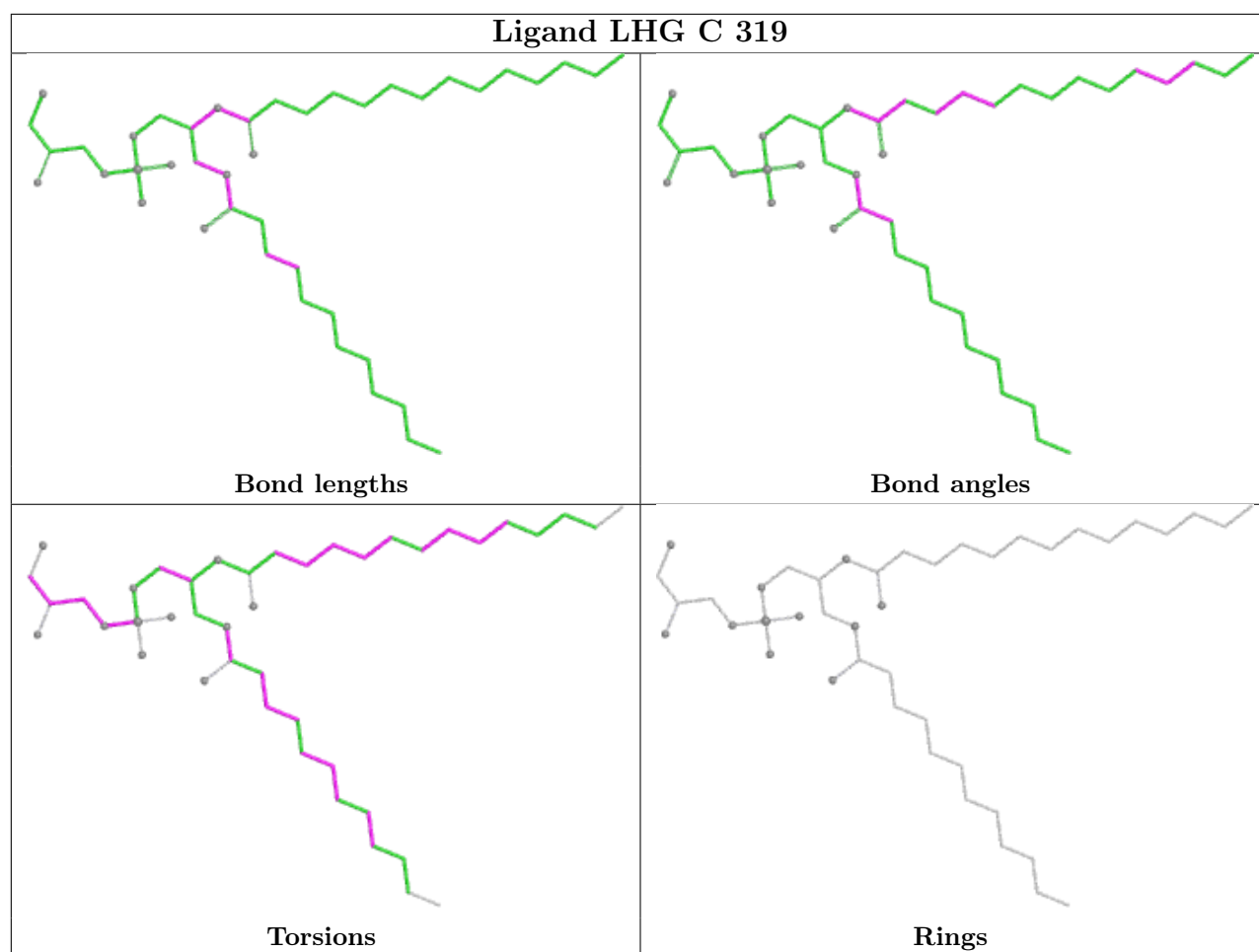




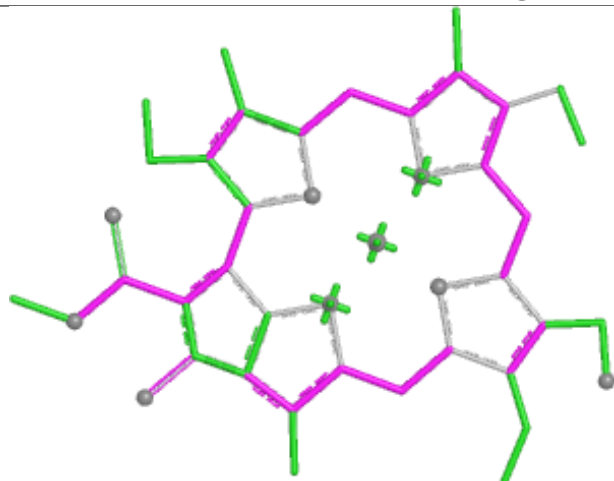




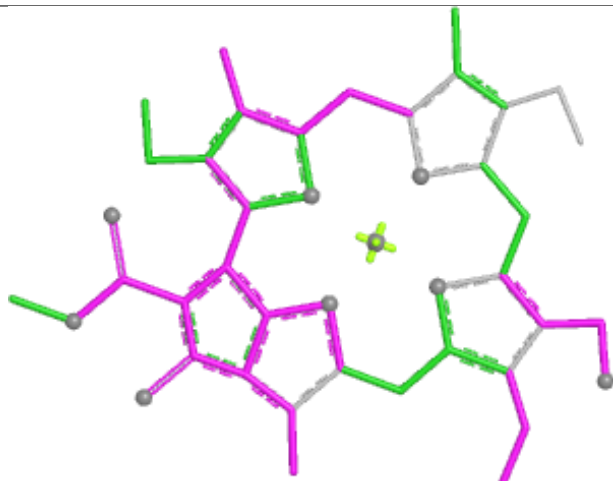




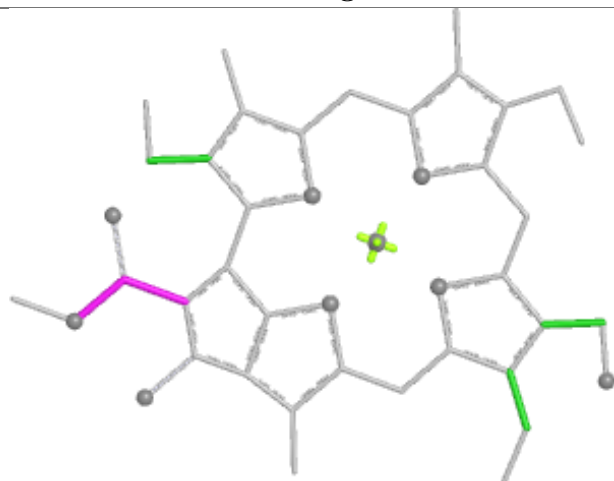
Ligand CHL A 309



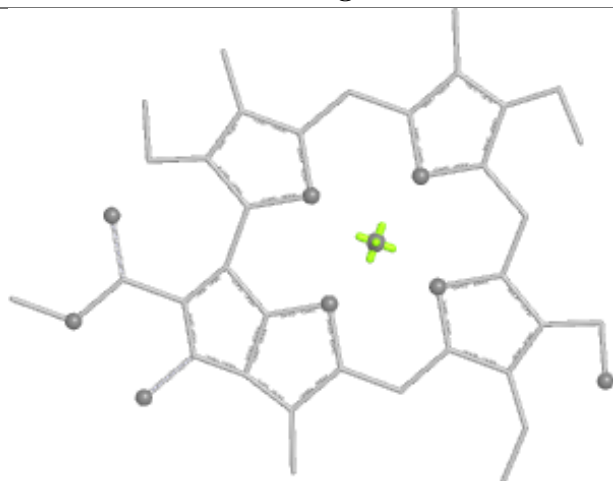
Bond lengths



Bond angles

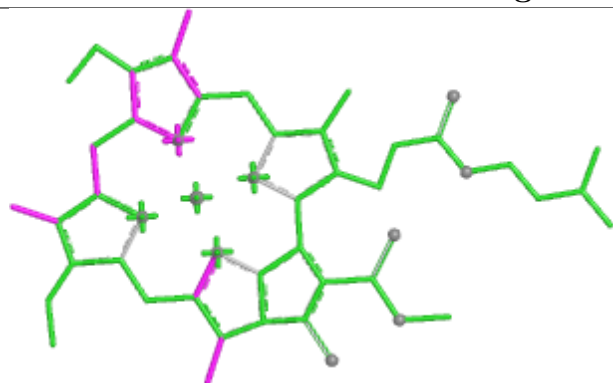


Torsions

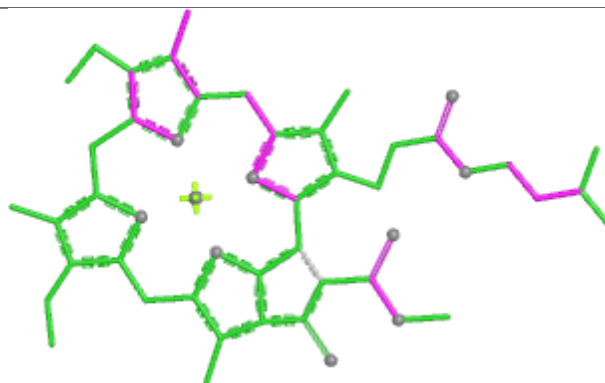


Rings

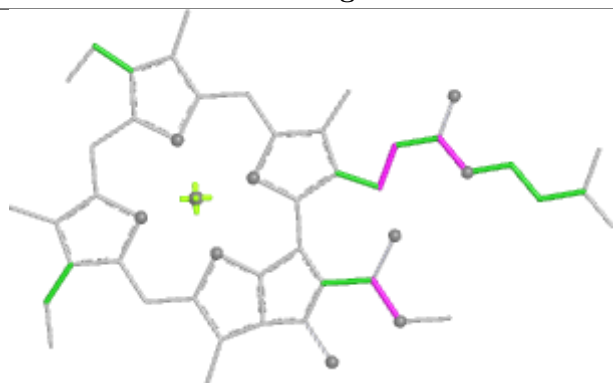
Ligand CLA C 308



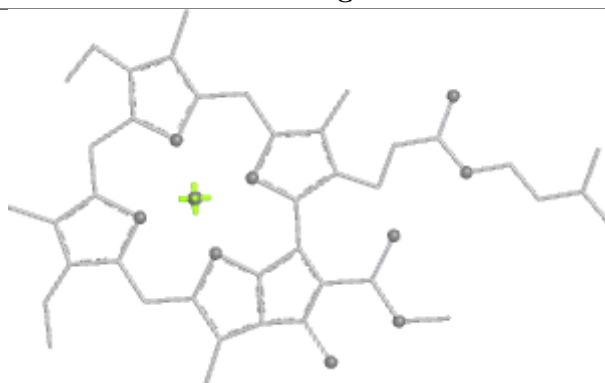
Bond lengths



Bond angles

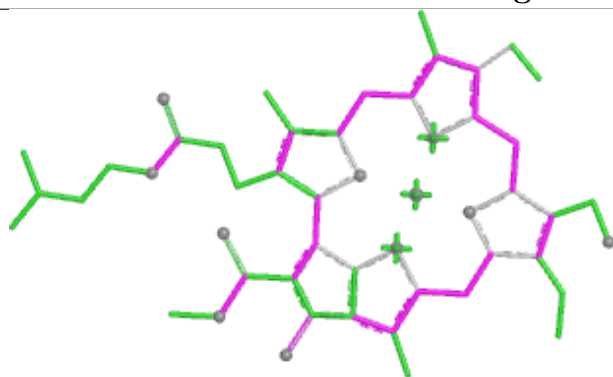


Torsions

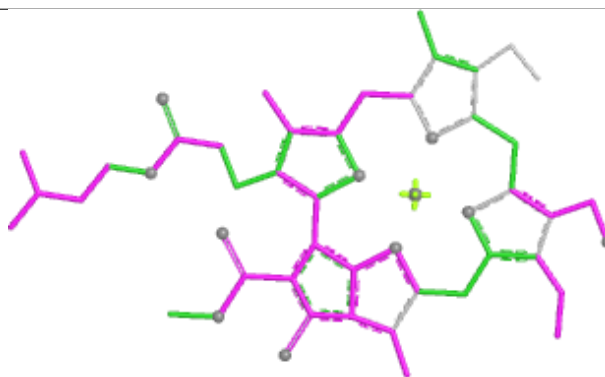


Rings

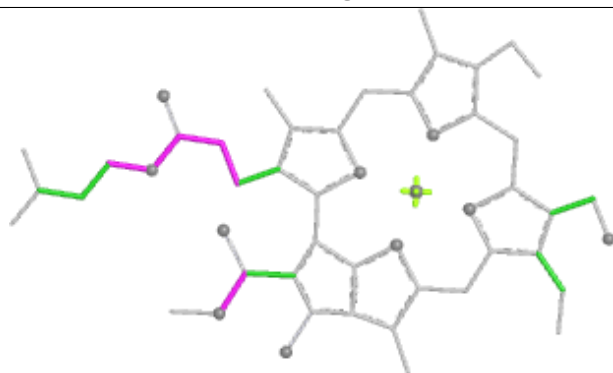
Ligand CHL C 310



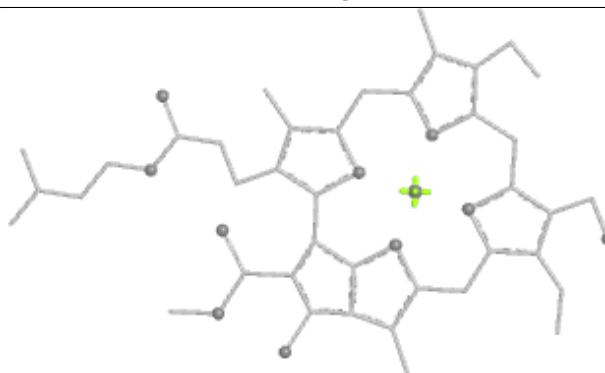
Bond lengths



Bond angles

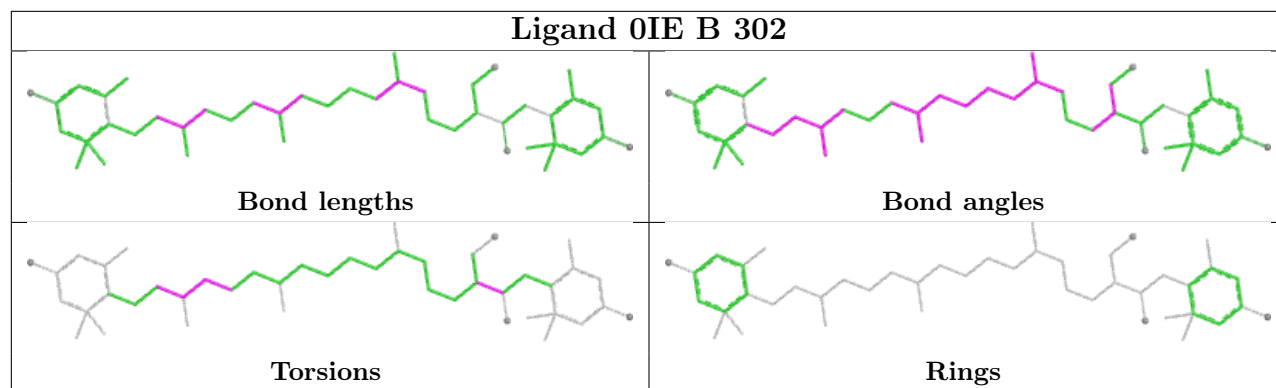


Torsions

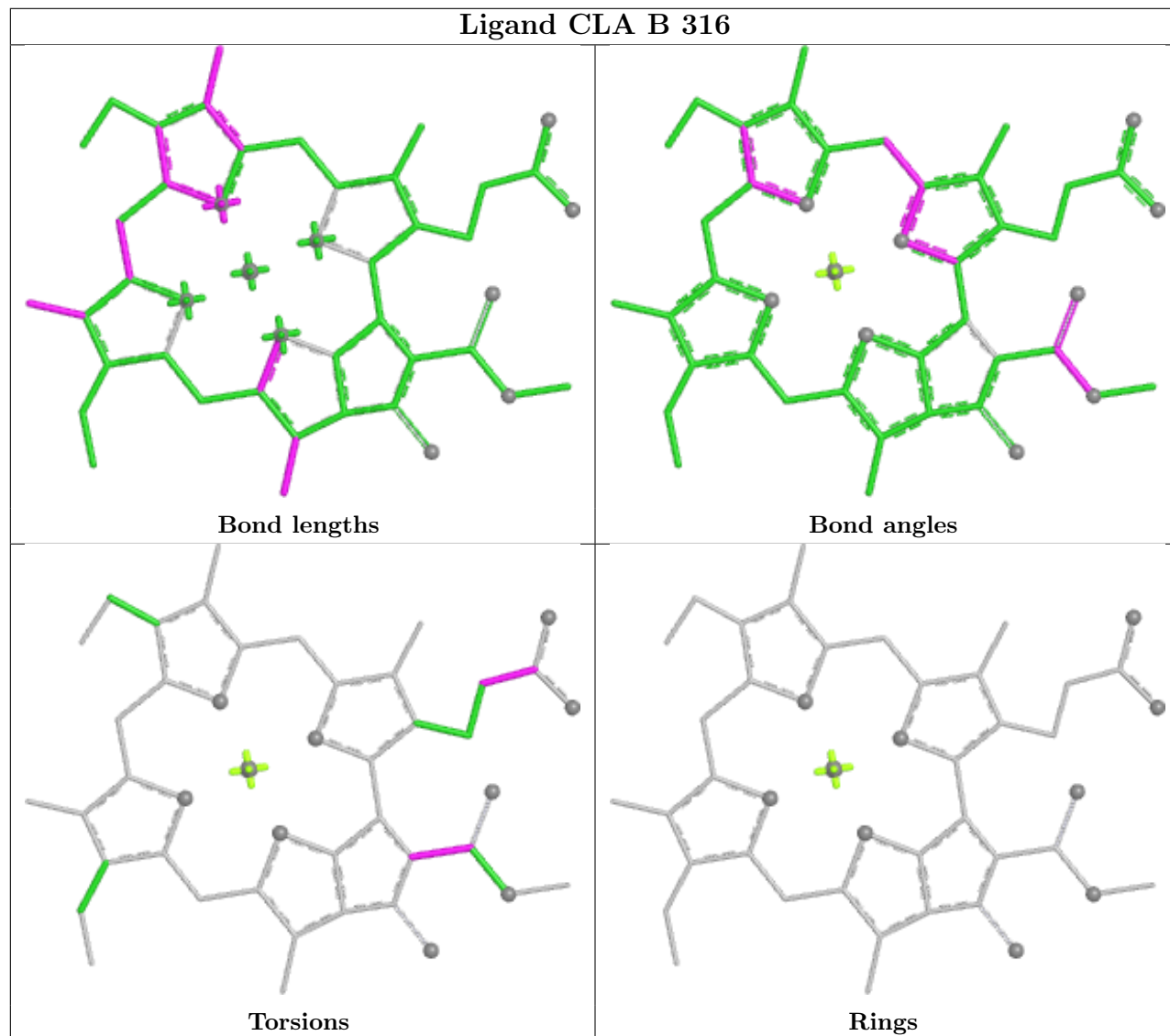


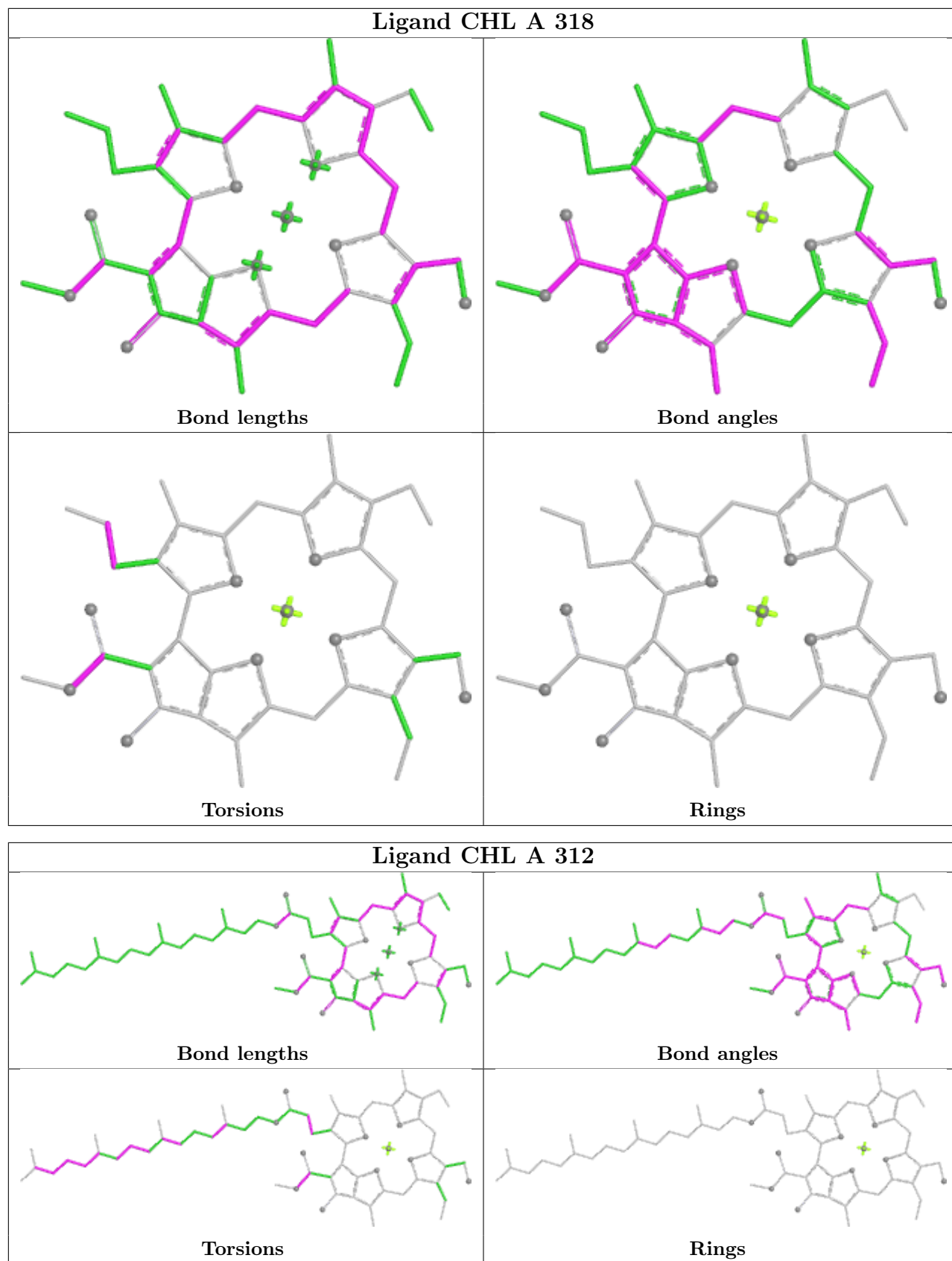
Rings

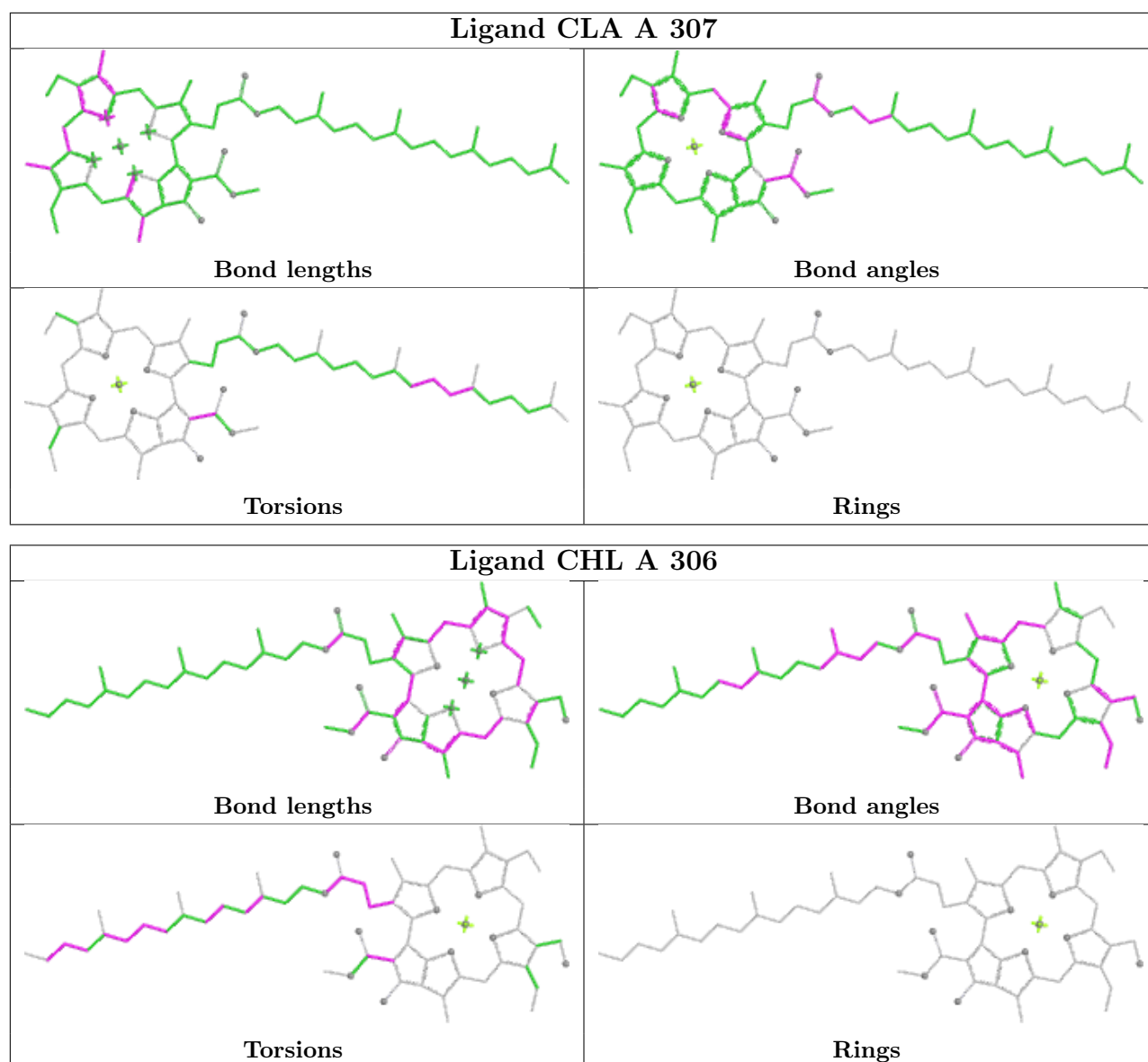
Ligand 0IE B 302



Ligand CLA B 316







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.

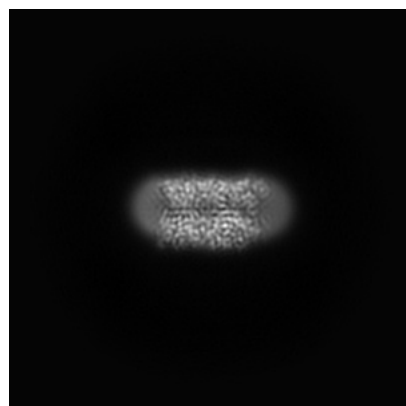
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-34883. These allow visual inspection of the internal detail of the map and identification of artifacts.

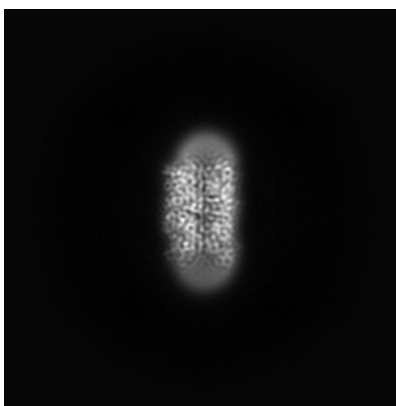
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

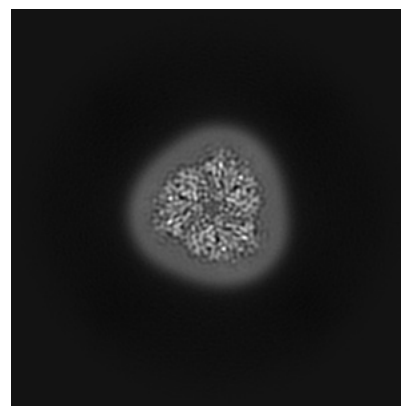
6.1.1 Primary map



X

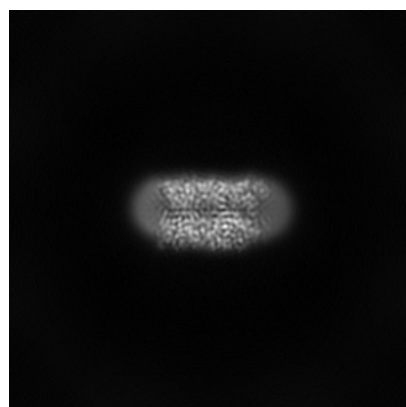


Y

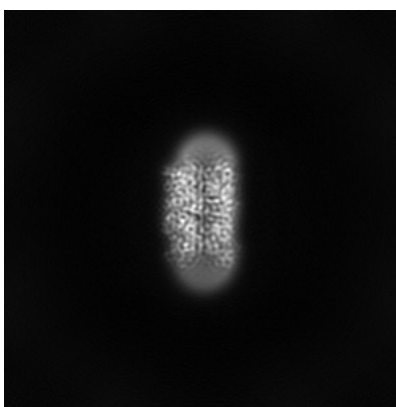


Z

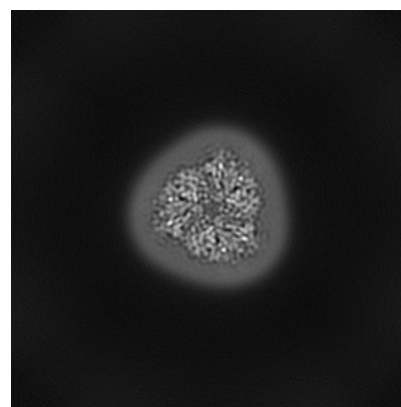
6.1.2 Raw map



X



Y

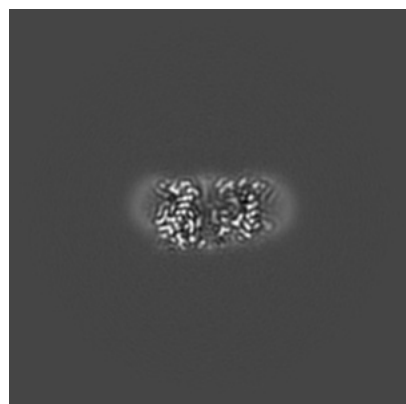


Z

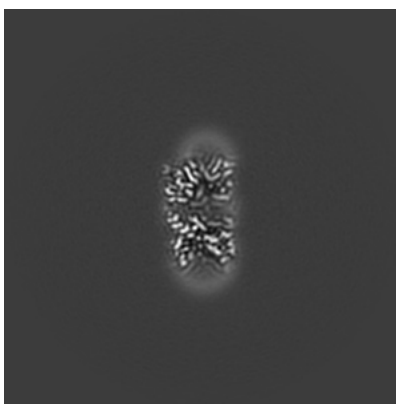
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

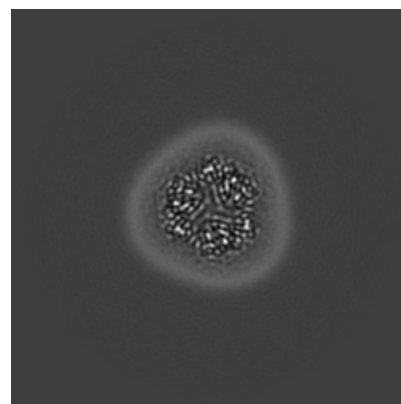
6.2.1 Primary map



X Index: 128

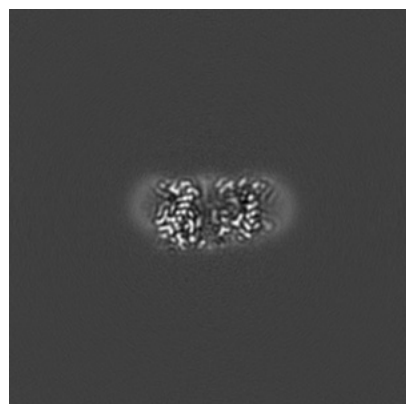


Y Index: 128

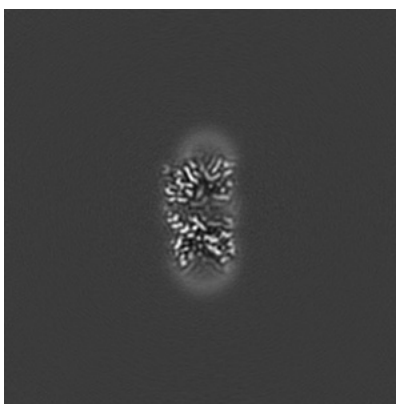


Z Index: 128

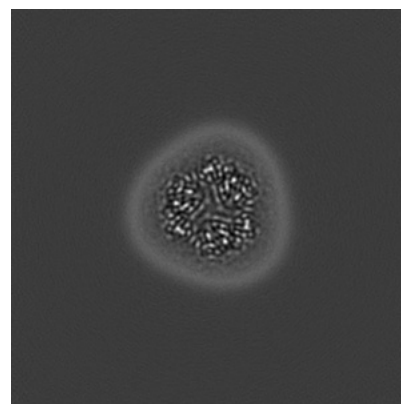
6.2.2 Raw map



X Index: 128



Y Index: 128

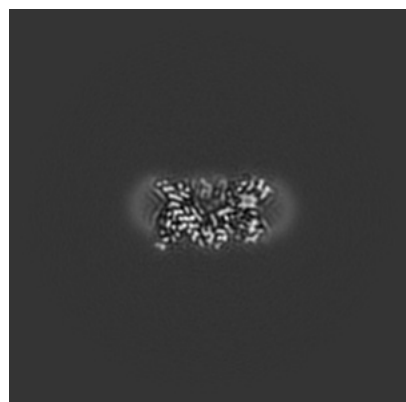


Z Index: 128

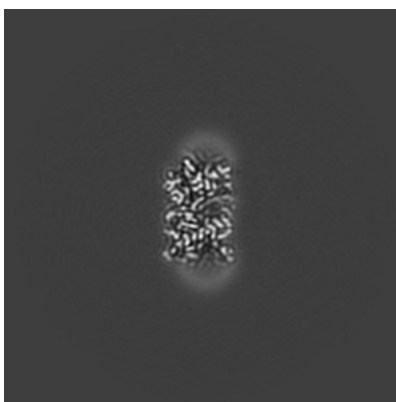
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

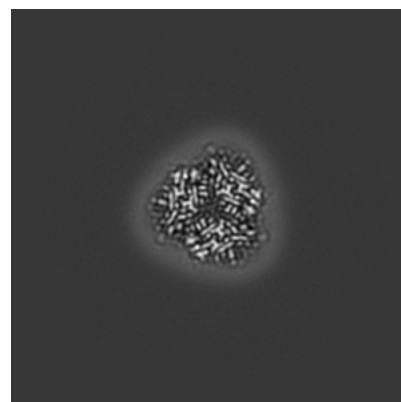
6.3.1 Primary map



X Index: 134

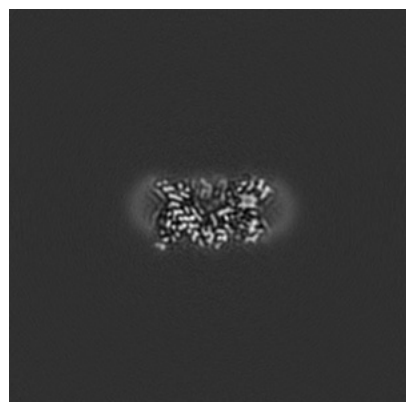


Y Index: 137

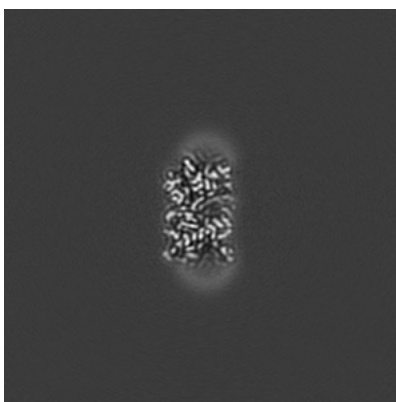


Z Index: 117

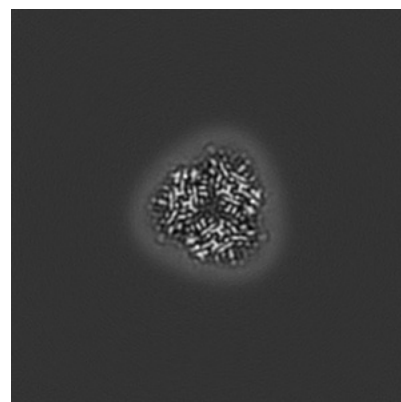
6.3.2 Raw map



X Index: 134



Y Index: 137

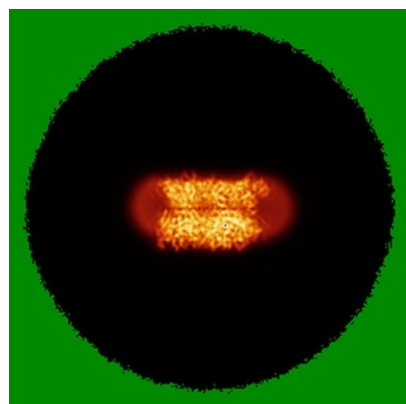


Z Index: 117

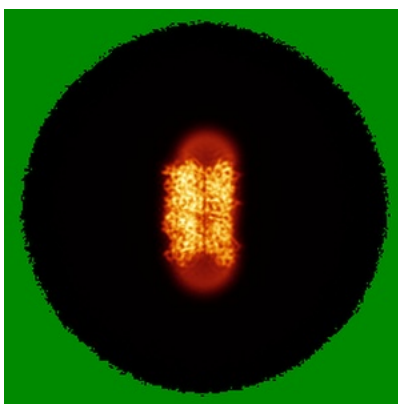
The images above show the largest variance slices of the map in three orthogonal directions.

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

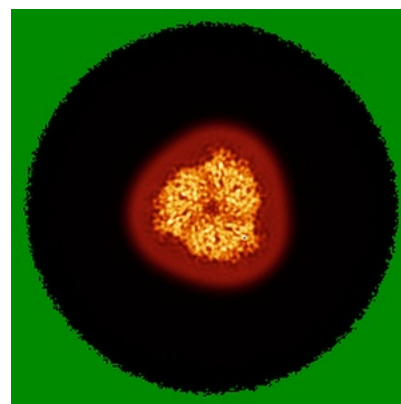
6.4.1 Primary map



X

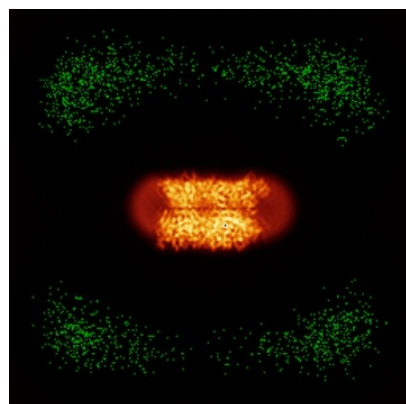


Y

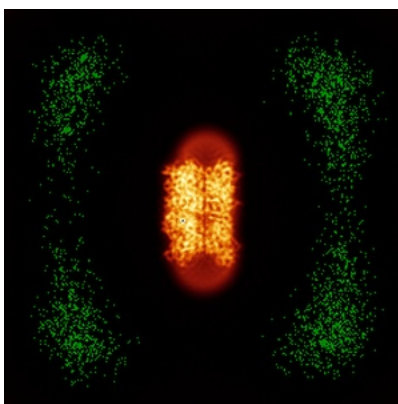


Z

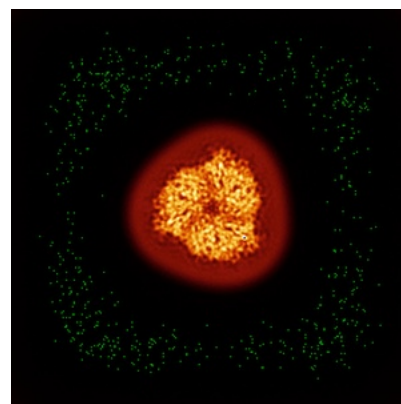
6.4.2 Raw map



X



Y

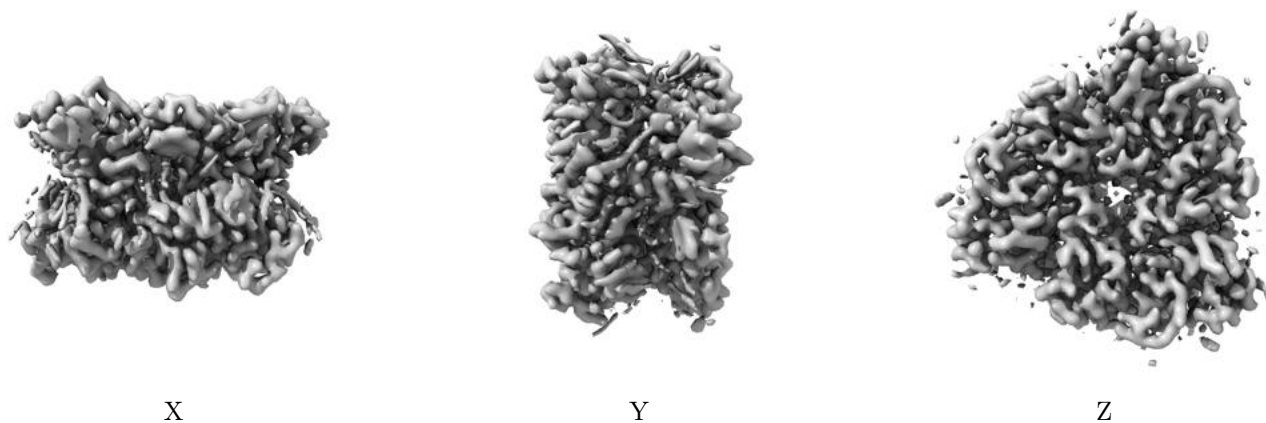


Z

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.

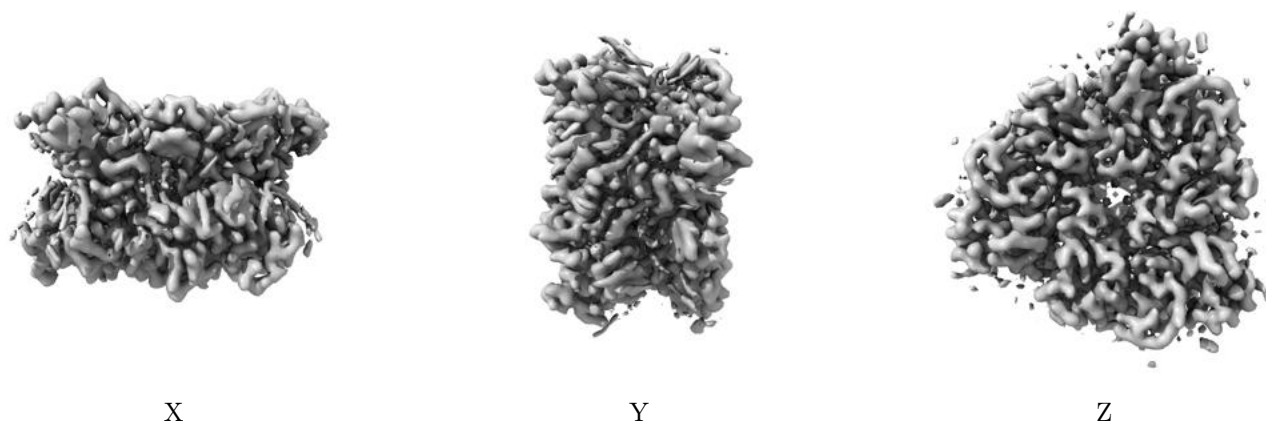
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.207. 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.

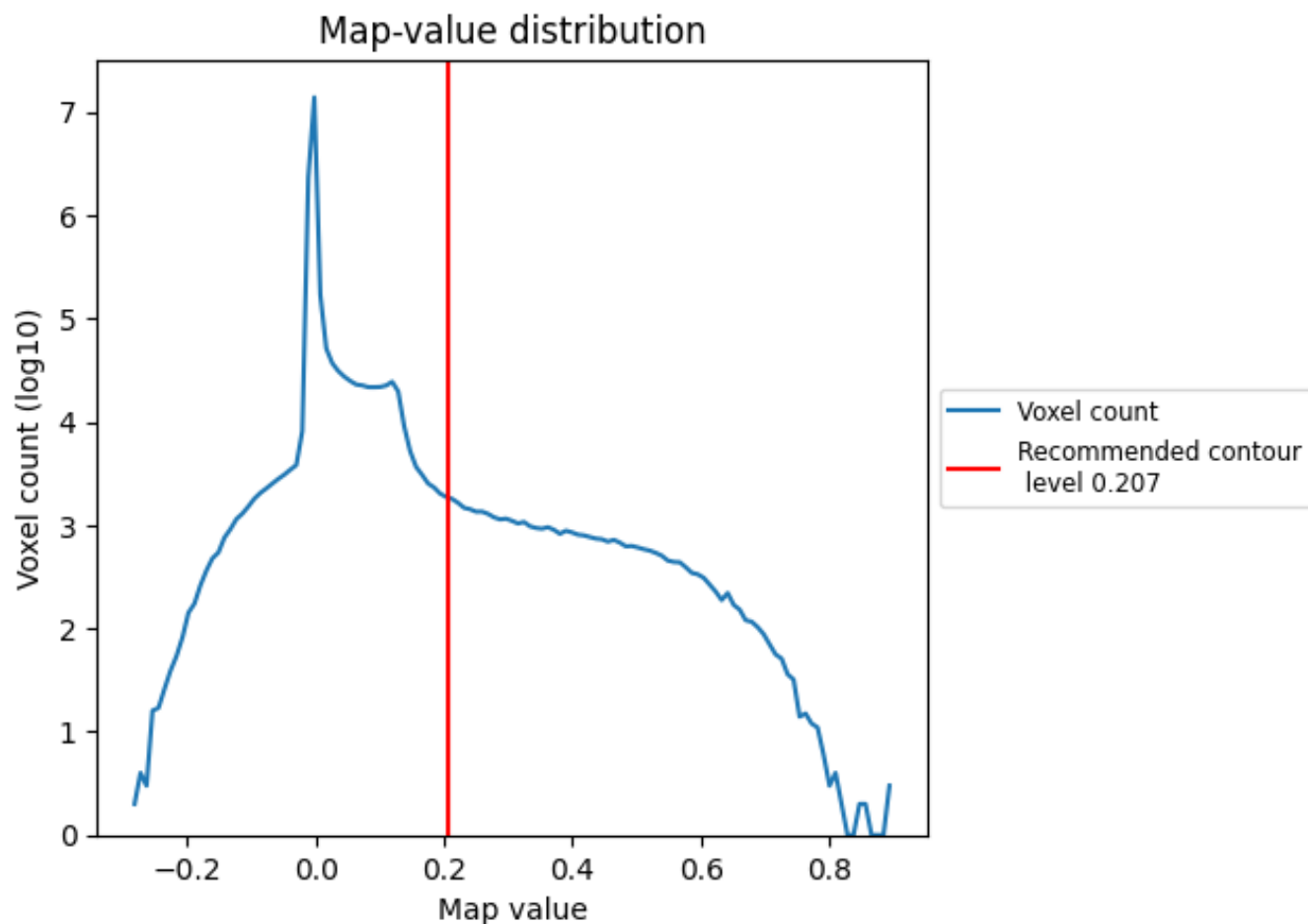
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

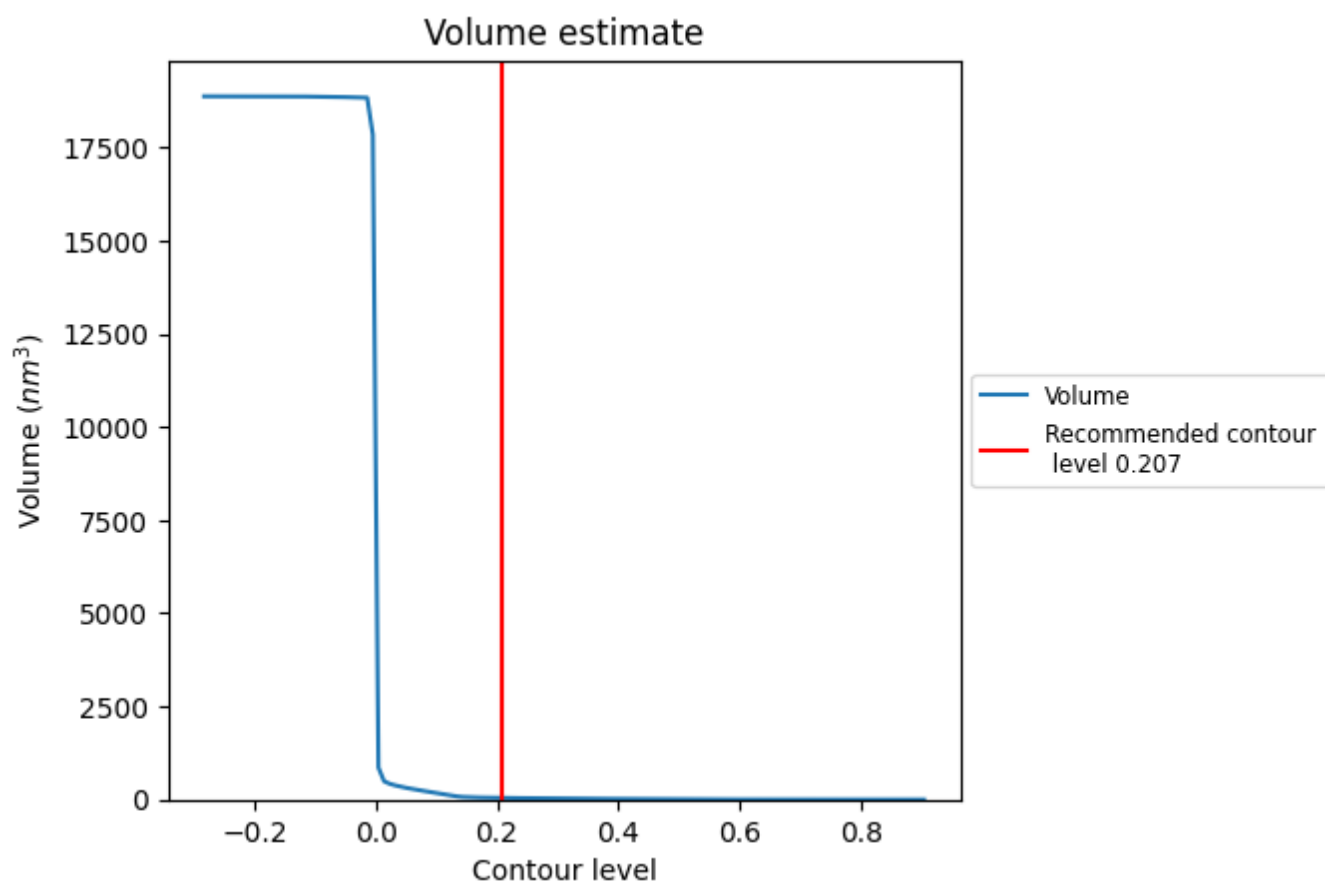
This section contains the results of statistical analysis of the map.

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.

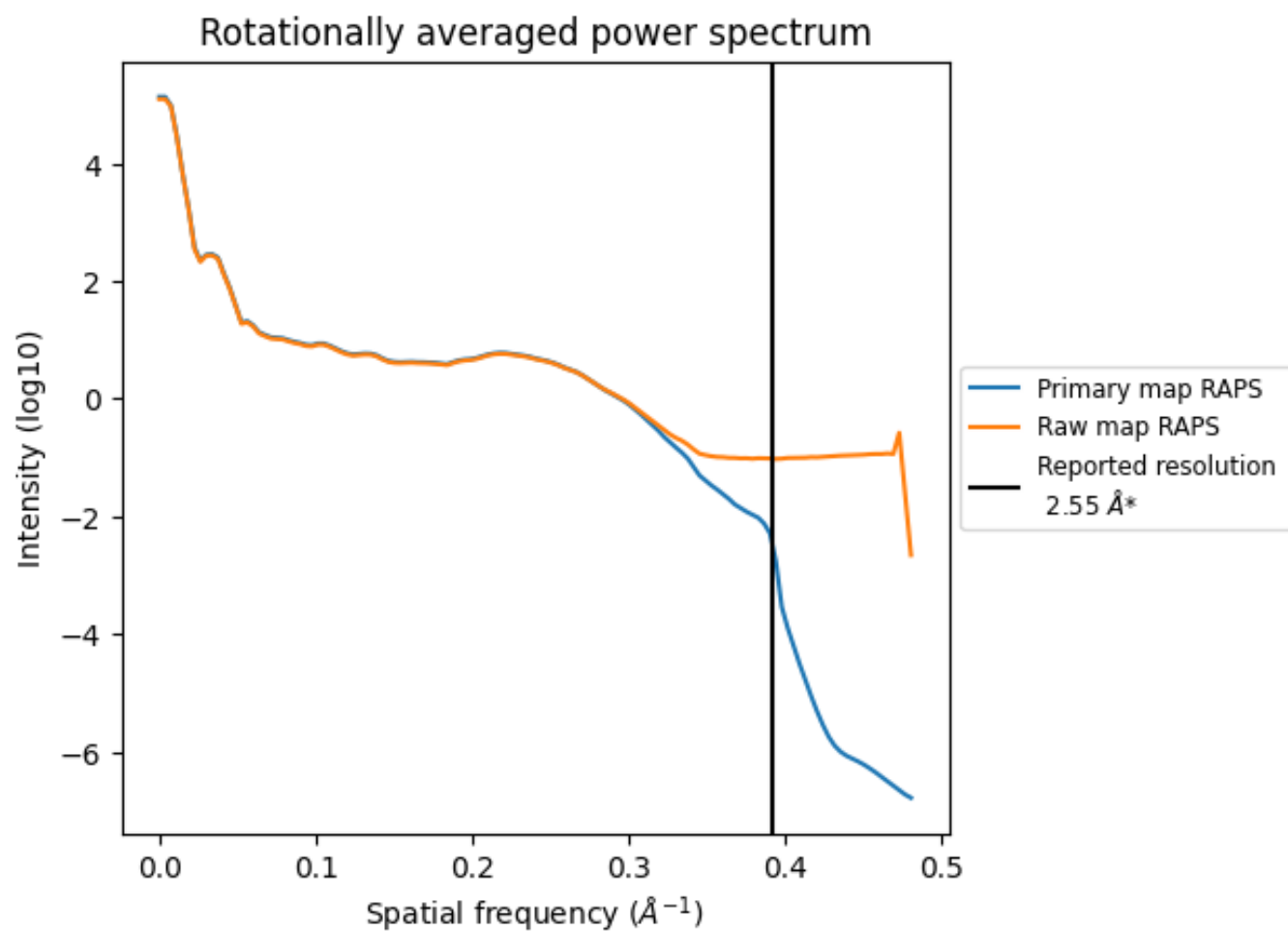
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 45 nm^3 ; this corresponds to an approximate mass of 41 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 ⓘ

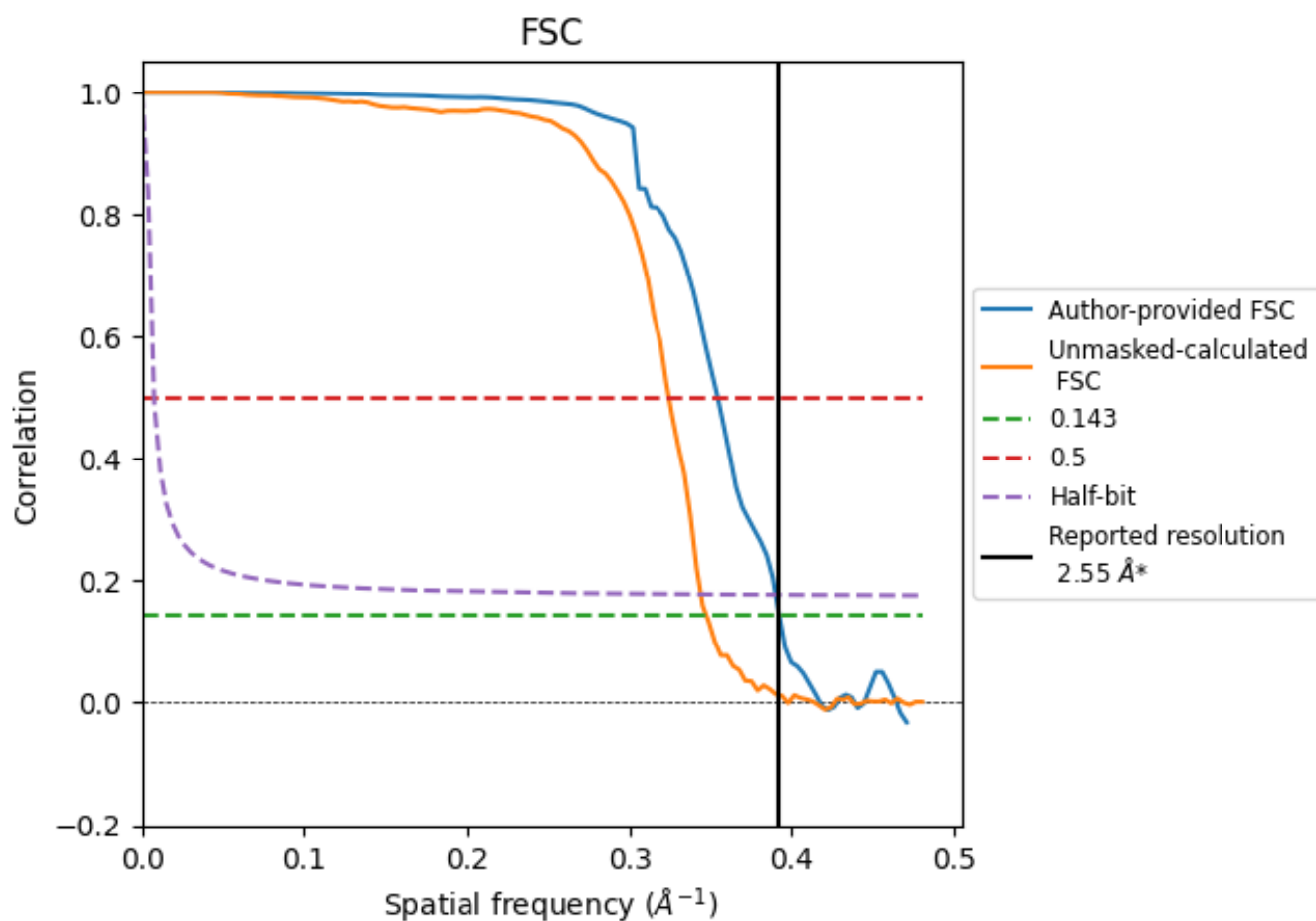


*Reported resolution corresponds to spatial frequency of 0.392 Å⁻¹

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 0.392 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

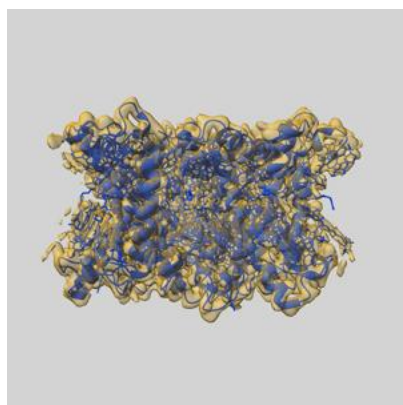
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.55	-	-
Author-provided FSC curve	2.55	2.82	2.56
Unmasked-calculated*	2.87	3.08	2.90

*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 2.87 differs from the reported value 2.55 by more than 10 %

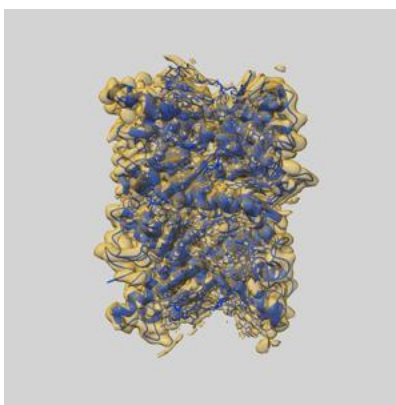
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-34883 and PDB model 8HLV. Per-residue inclusion information can be found in [section 3](#) on [page 12](#).

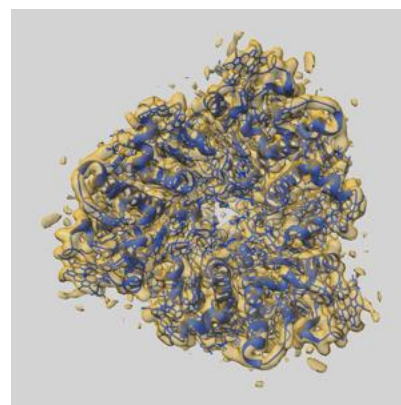
9.1 Map-model overlay [i](#)



X



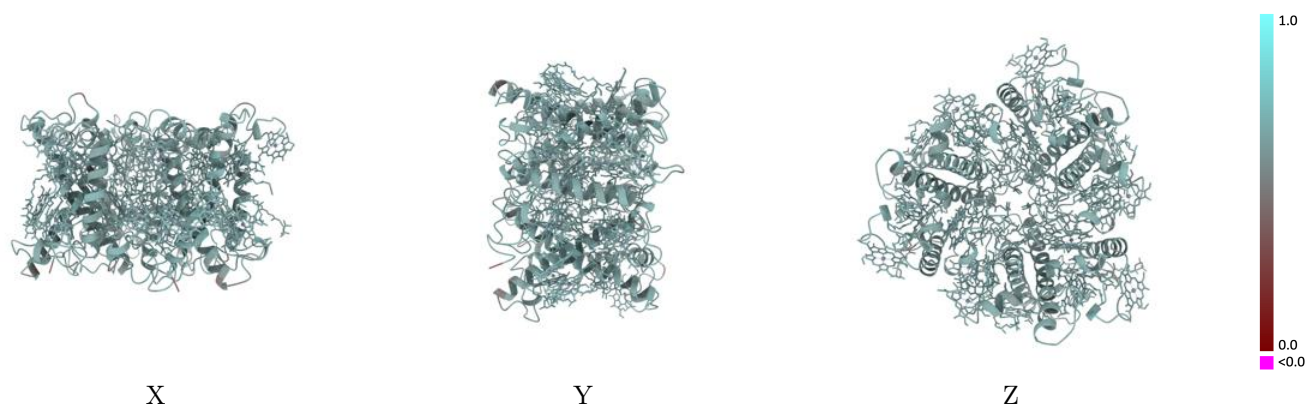
Y



Z

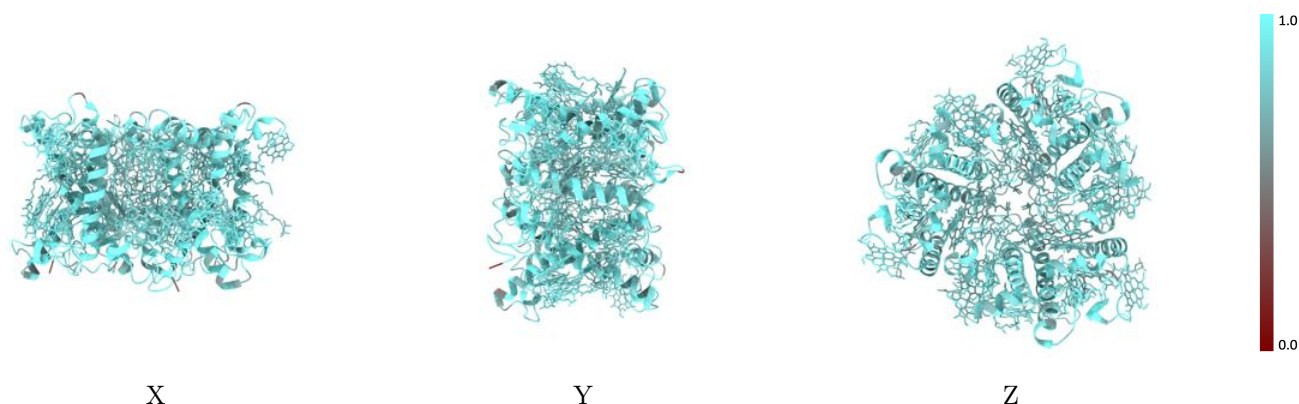
The images above show the 3D surface view of the map at the recommended contour level 0.207 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



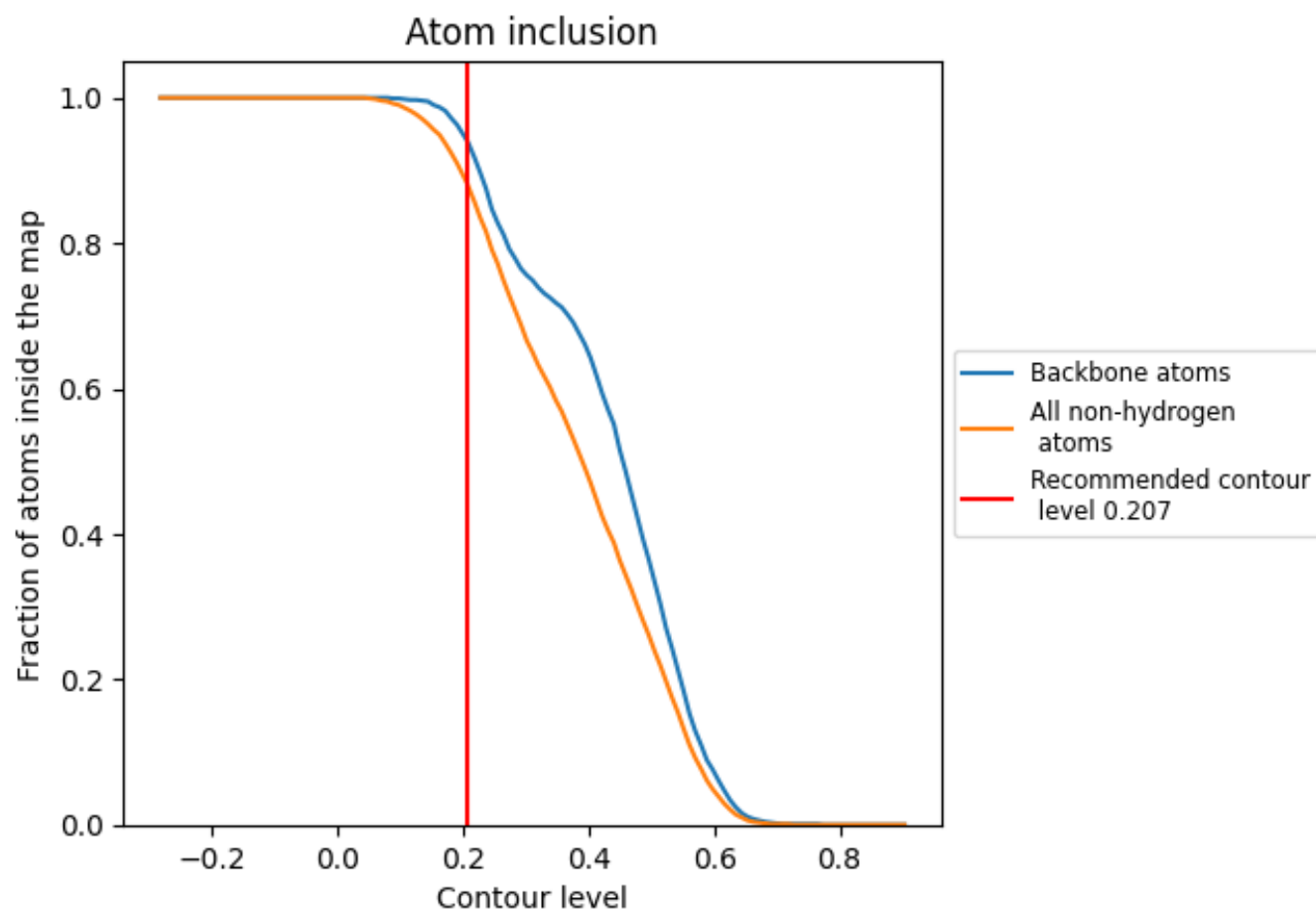
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.207).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 88% 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 (0.207) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8810	0.6080
A	0.8820	0.6080
B	0.8820	0.6090
C	0.8790	0.6070

