wwPDB EM Validation Summary Report (i)

Aug 6, 2026 – 09:07 PM JST

PDB ID	:	8IX1 / pdb_00008ix1
EMDB ID	:	EMD-35786
Title	:	Cryo-EM structure of protonated LHCII nanodisc at low pH value
Authors	:	Ruan, M.X.; Ding, W.
Deposited on	:	2023-03-31
Resolution	:	2.63 Å(reported)

This is a wwPDB EM Validation Summary 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 (i) 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 (i)) were used in the production of this report:

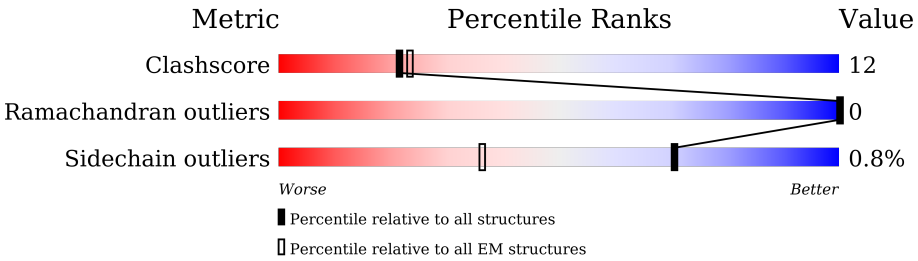
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using 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)	:	2.50

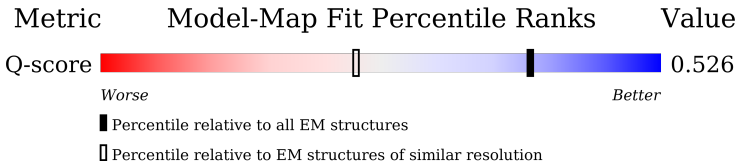
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.63 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	8888 (2.13 - 3.13)

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 <=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	G	218	83% 17% •
1	N	218	83% 17%
1	Y	218	86% 13% •

2 Entry composition (i)

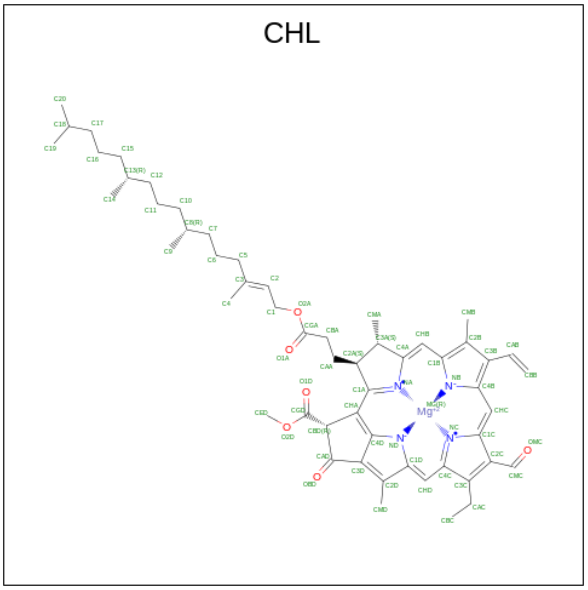
There are 7 unique types of molecules in this entry. The entry contains 7896 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	G	218	1661	1079	270	305	7	0	0
			Total	C	N	O	S		
1	N	218	1661	1079	270	305	7	0	0
			Total	C	N	O	S		
1	Y	218	1661	1079	270	305	7	0	0

- Molecule 2 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
			Total	C	Mg	N	O	
2	G	1	51	40	1	4	6	0
			Total	C	Mg	N	O	
2	G	1	48	37	1	4	6	0
			Total	C	Mg	N	O	
2	G	1	50	39	1	4	6	0

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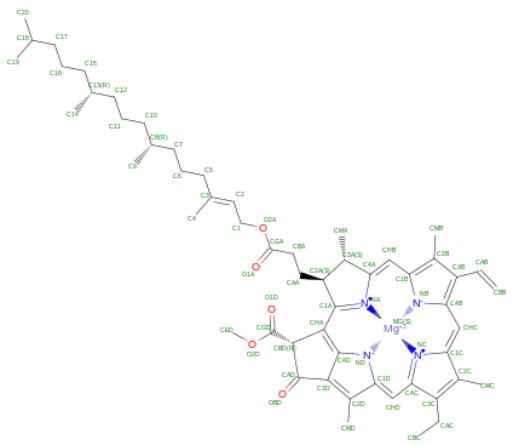
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
2	G	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	G	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	G	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	N	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	N	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	N	1	48	37	1	4	6	0
			Total	C	Mg	N	O	
2	N	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	N	1	51	40	1	4	6	0
			Total	C	Mg	N	O	
2	N	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	N	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	Y	1	49	38	1	4	6	0
			Total	C	Mg	N	O	
2	Y	1	48	37	1	4	6	0
			Total	C	Mg	N	O	
2	Y	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	Y	1	50	39	1	4	6	0
			Total	C	Mg	N	O	
2	Y	1	53	42	1	4	6	0

- Molecule 3 is CHLOROPHYLL A (CCD ID: CLA) (formula: $C_{55}H_{72}MgN_4O_5$) (labeled as "Ligand of Interest" by depositor).

CLA



Mol	Chain	Residues	Atoms					AltConf
3	G	1	Total 65	C 55	Mg 1	N 4	O 5	0
3	G	1	Total 49	C 39	Mg 1	N 4	O 5	0
3	G	1	Total 49	C 39	Mg 1	N 4	O 5	0
3	G	1	Total 65	C 55	Mg 1	N 4	O 5	0
3	G	1	Total 49	C 39	Mg 1	N 4	O 5	0
3	G	1	Total 65	C 55	Mg 1	N 4	O 5	0
3	G	1	Total 49	C 39	Mg 1	N 4	O 5	0
3	G	1	Total 49	C 39	Mg 1	N 4	O 5	0
3	N	1	Total 65	C 55	Mg 1	N 4	O 5	0
3	N	1	Total 49	C 39	Mg 1	N 4	O 5	0
3	N	1	Total 49	C 39	Mg 1	N 4	O 5	0
3	N	1	Total 65	C 55	Mg 1	N 4	O 5	0
3	N	1	Total 49	C 39	Mg 1	N 4	O 5	0
3	N	1	Total 65	C 55	Mg 1	N 4	O 5	0

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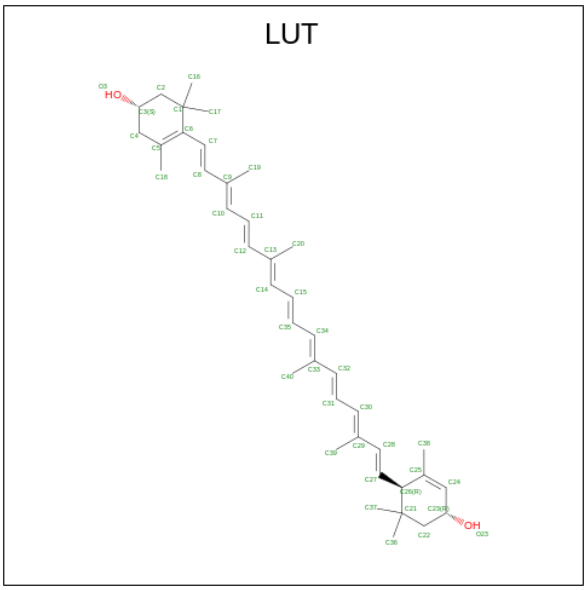
Mol	Chain	Residues	Atoms					AltConf
			Total	C	Mg	N	O	
3	N	1	49	39	1	4	5	0
			Total	C	Mg	N	O	
3	N	1	49	39	1	4	5	0
			Total	C	Mg	N	O	
3	Y	1	65	55	1	4	5	0
			Total	C	Mg	N	O	
3	Y	1	49	39	1	4	5	0
			Total	C	Mg	N	O	
3	Y	1	49	39	1	4	5	0
			Total	C	Mg	N	O	
3	Y	1	65	55	1	4	5	0
			Total	C	Mg	N	O	
3	Y	1	65	55	1	4	5	0
			Total	C	Mg	N	O	
3	Y	1	65	55	1	4	5	0
			Total	C	Mg	N	O	
3	Y	1	65	55	1	4	5	0
			Total	C	Mg	N	O	
3	Y	1	49	39	1	4	5	0

- Molecule 4 is (3R,3'R,6S)-4,5-DIDEHYDRO-5,6-DIHYDRO-BETA,BETA-CAROTENE-3,3'-DIOL (CCD ID: LUT) (formula: $C_{40}H_{56}O_2$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
4	G	1	42	40	2	0

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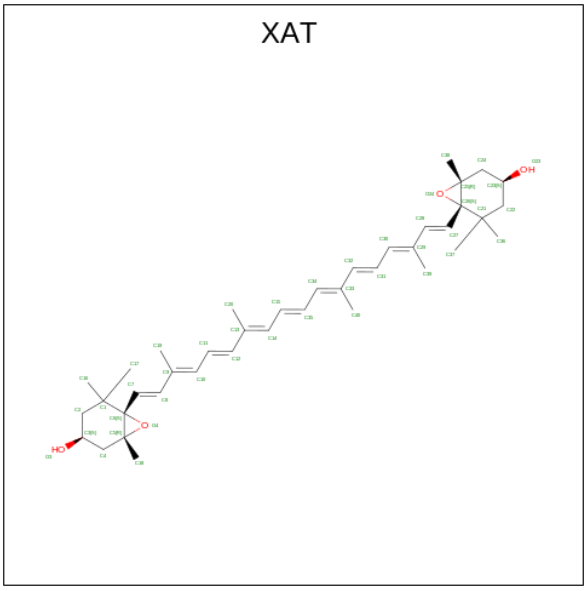
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
4	G	1	42	40	2	0
4	N	1	42	40	2	0
4	N	1	42	40	2	0
4	Y	1	42	40	2	0
4	Y	1	42	40	2	0

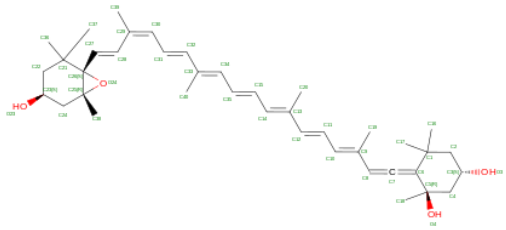
- Molecule 5 is (3S,5R,6S,3'S,5'R,6'S)-5,6,5',6'-DIEPOXY-5,6,5',6'- TETRAHYDRO-BETA, BETA-CAROTENE-3,3'-DIOL (CCD ID: XAT) (formula: $C_{40}H_{56}O_4$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
5	G	1	44	40	4	0
5	N	1	44	40	4	0
5	N	1	44	40	4	0

- Molecule 6 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).

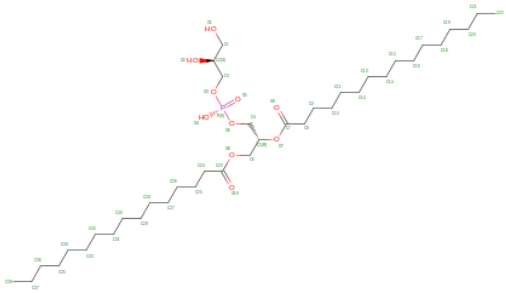
NEX



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
6	G	1	44	40	4	0
			Total	C	O	
6	N	1	44	40	4	0
			Total	C	O	
6	Y	1	44	40	4	0

- Molecule 7 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: $C_{38}H_{75}O_{10}P$).

LHG



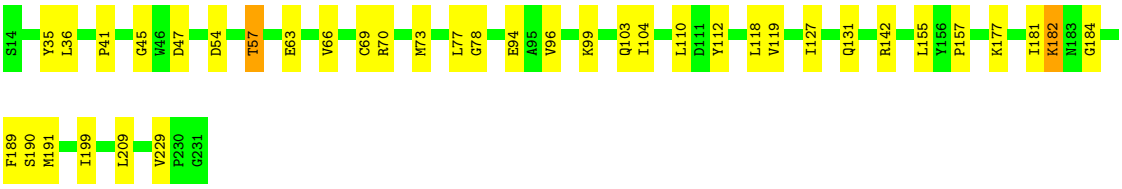
Mol	Chain	Residues	Atoms				AltConf
			Total	C	O	P	
7	G	1	49	38	10	1	0
			Total	C	O	P	
7	N	1	49	38	10	1	0
			Total	C	O	P	
7	Y	1	49	38	10	1	0

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.

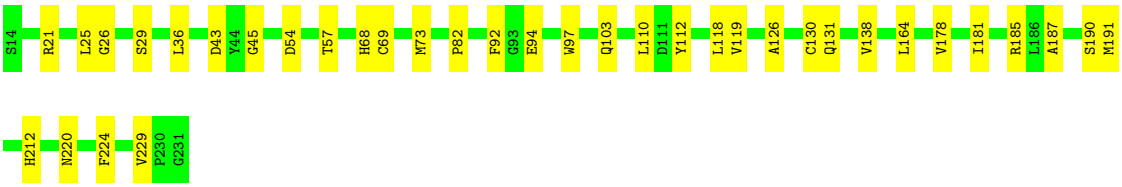
• Molecule 1: Chlorophyll a-b binding protein, chloroplastic

Chain G: 83% 17%



• Molecule 1: Chlorophyll a-b binding protein, chloroplastic

Chain N: 83% 17%



• Molecule 1: Chlorophyll a-b binding protein, chloroplastic

Chain Y: 86% 13%

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	860690	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 ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	22500	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.570	Depositor
Minimum map value	-0.196	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.022	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	220.0, 220.0, 220.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.1, 1.1, 1.1	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: CLA, XAT, LHG, CHL, NEX, LUT

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	G	0.36	0/1713	0.64	0/2333
1	N	0.36	0/1713	0.64	0/2333
1	Y	0.36	0/1713	0.66	0/2333
All	All	0.36	0/5139	0.65	0/6999

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	G	1661	0	1591	41	0
1	N	1661	0	1592	28	0
1	Y	1661	0	1592	38	0
2	G	299	0	218	15	0
2	N	349	0	255	8	0
2	Y	250	0	182	14	0
3	G	440	0	411	23	0
3	N	440	0	411	6	0
3	Y	472	0	477	25	0
4	G	84	0	112	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	N	84	0	112	11	0
4	Y	84	0	112	12	0
5	G	44	0	56	4	0
5	N	88	0	112	6	0
6	G	44	0	56	4	0
6	N	44	0	56	3	0
6	Y	44	0	56	5	0
7	G	49	0	74	4	0
7	N	49	0	74	1	0
7	Y	49	0	74	2	0
All	All	7896	0	7623	182	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 12.

The worst 5 of 182 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)
1:Y:54:ASP:HB2	1:Y:57:THR:CG2	1.51	1.39
1:G:54:ASP:HB2	1:G:57:THR:CG2	1.67	1.22
1:Y:54:ASP:HB2	1:Y:57:THR:HG21	1.38	1.04
1:Y:54:ASP:CB	1:Y:57:THR:CG2	2.40	0.99
3:Y:610:CLA:H122	3:Y:611:CLA:HBB1	1.46	0.97

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	G	216/218 (99%)	208 (96%)	8 (4%)	0	100 100
1	N	216/218 (99%)	205 (95%)	11 (5%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Y	216/218 (99%)	207 (96%)	9 (4%)	0	100	100
All	All	648/654 (99%)	620 (96%)	28 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	G	168/168 (100%)	166 (99%)	2 (1%)	63	78
1	N	168/168 (100%)	168 (100%)	0	100	100
1	Y	168/168 (100%)	166 (99%)	2 (1%)	63	78
All	All	504/504 (100%)	500 (99%)	4 (1%)	70	84

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	57	THR
1	G	182	LYS
1	Y	57	THR
1	Y	71	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	Y	197	GLN
1	Y	68	HIS
1	N	208	ASN
1	N	197	GLN
1	Y	61	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

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	$\#\|Z\| > 2$
4	LUT	G	615	-	42,43,43	0.78	0	51,60,60	1.77	17 (33%)
2	CHL	G	608	1	54,58,74	1.47	10 (18%)	59,94,114	1.67	12 (20%)
2	CHL	N	309	-	54,58,74	1.41	7 (12%)	59,94,114	1.34	7 (11%)
5	XAT	G	616	-	39,47,47	0.96	2 (5%)	54,74,74	2.79	17 (31%)
3	CLA	Y	602	1	69,73,73	1.26	6 (8%)	83,113,113	1.23	10 (12%)
5	XAT	N	318	-	39,47,47	0.92	0	54,74,74	2.81	22 (40%)
5	XAT	N	321	-	39,47,47	0.98	2 (5%)	54,74,74	2.83	19 (35%)
3	CLA	Y	613	-	53,57,73	1.43	6 (11%)	62,93,113	1.41	9 (14%)
6	NEX	G	617	-	38,46,46	1.10	2 (5%)	50,70,70	2.98	17 (34%)
2	CHL	Y	608	1	57,61,74	1.34	9 (15%)	64,98,114	1.57	6 (9%)
3	CLA	G	610	-	53,57,73	1.39	9 (16%)	62,93,113	1.43	6 (9%)
3	CLA	N	311	1	69,73,73	1.26	7 (10%)	83,113,113	1.15	5 (6%)
2	CHL	Y	605	-	52,56,74	1.41	8 (15%)	58,92,114	1.49	7 (12%)
2	CHL	Y	601	-	53,57,74	1.42	7 (13%)	59,93,114	1.27	7 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	CHL	N	301	-	54,58,74	1.43	7 (12%)	59,94,114	1.41	10 (16%)
6	NEX	N	319	-	38,46,46	0.91	1 (2%)	50,70,70	2.35	17 (34%)
3	CLA	G	602	1	69,73,73	1.26	6 (8%)	83,113,113	1.22	6 (7%)
3	CLA	Y	609	1	69,73,73	1.26	7 (10%)	83,113,113	1.36	10 (12%)
2	CHL	G	601	-	55,59,74	1.40	7 (12%)	62,96,114	1.19	7 (11%)
3	CLA	Y	610	7	69,73,73	1.23	8 (11%)	83,113,113	1.19	9 (10%)
2	CHL	N	310	-	54,58,74	1.40	7 (12%)	59,94,114	1.34	7 (11%)
2	CHL	G	606	-	54,58,74	1.39	8 (14%)	59,94,114	1.39	6 (10%)
2	CHL	N	302	-	54,58,74	1.43	8 (14%)	59,94,114	1.23	7 (11%)
3	CLA	Y	611	-	69,73,73	1.38	8 (11%)	83,113,113	1.15	5 (6%)
3	CLA	G	604	-	53,57,73	1.42	7 (13%)	62,93,113	1.33	8 (12%)
7	LHG	Y	617	3	48,48,48	0.88	2 (4%)	51,54,54	1.03	1 (1%)
3	CLA	G	609	1	69,73,73	1.23	9 (13%)	83,113,113	1.33	8 (9%)
3	CLA	N	314	-	53,57,73	1.42	9 (16%)	62,93,113	1.30	6 (9%)
3	CLA	Y	603	-	53,57,73	1.43	8 (15%)	62,93,113	1.45	6 (9%)
3	CLA	Y	604	-	53,57,73	1.42	9 (16%)	62,93,113	1.38	8 (12%)
2	CHL	Y	606	-	54,58,74	1.39	9 (16%)	59,94,114	1.26	4 (6%)
4	LUT	Y	615	-	42,43,43	0.79	0	51,60,60	1.70	15 (29%)
2	CHL	Y	607	-	54,58,74	1.45	8 (14%)	59,94,114	1.44	6 (10%)
7	LHG	G	618	-	48,48,48	0.93	2 (4%)	51,54,54	0.93	2 (3%)
2	CHL	G	605	1	52,56,74	1.41	7 (13%)	58,92,114	1.74	11 (18%)
6	NEX	Y	616	-	38,46,46	0.91	1 (2%)	50,70,70	2.48	16 (32%)
3	CLA	N	303	1	69,73,73	1.28	8 (11%)	83,113,113	1.12	7 (8%)
3	CLA	N	315	1	53,57,73	1.44	7 (13%)	62,93,113	1.18	6 (9%)
3	CLA	G	603	-	53,57,73	1.43	7 (13%)	62,93,113	1.47	5 (8%)
4	LUT	N	316	-	42,43,43	1.58	8 (19%)	51,60,60	1.48	10 (19%)
2	CHL	N	306	-	52,56,74	1.40	7 (13%)	58,92,114	1.51	9 (15%)
4	LUT	Y	614	-	42,43,43	1.58	8 (19%)	51,60,60	1.49	10 (19%)
2	CHL	G	607	-	54,58,74	1.41	9 (16%)	59,94,114	1.66	8 (13%)
3	CLA	G	613	1	53,57,73	1.46	8 (15%)	62,93,113	1.18	7 (11%)
3	CLA	N	305	-	53,57,73	1.43	9 (16%)	62,93,113	1.32	7 (11%)
4	LUT	N	317	-	42,43,43	0.97	1 (2%)	51,60,60	2.08	11 (21%)
3	CLA	G	611	1	69,73,73	1.25	10 (14%)	83,113,113	1.27	10 (12%)
4	LUT	G	614	-	42,43,43	1.58	8 (19%)	51,60,60	1.50	10 (19%)
7	LHG	N	320	3	48,48,48	0.88	2 (4%)	51,54,54	1.12	4 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	CHL	N	308	-	55,59,74	1.42	6 (10%)	62,96,114	1.29	5 (8%)
2	CHL	G	619	-	54,58,74	1.42	8 (14%)	59,94,114	1.38	8 (13%)
3	CLA	G	612	-	53,57,73	1.42	8 (15%)	62,93,113	1.30	7 (11%)
3	CLA	N	304	-	53,57,73	1.45	7 (13%)	62,93,113	1.40	6 (9%)
3	CLA	N	312	7	53,57,73	1.41	7 (13%)	62,93,113	1.38	5 (8%)
3	CLA	Y	612	-	69,73,73	1.28	9 (13%)	83,113,113	1.20	7 (8%)
2	CHL	N	307	-	54,58,74	1.46	8 (14%)	59,94,114	1.47	7 (11%)
3	CLA	N	313	1	69,73,73	1.24	9 (13%)	83,113,113	1.20	8 (9%)

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
4	LUT	G	615	-	-	2/29/67/67	0/2/2/2
2	CHL	G	608	1	-	8/22/98/117	-
2	CHL	N	309	-	-	6/22/98/117	-
5	XAT	G	616	-	-	2/31/93/93	0/4/4/4
3	CLA	Y	602	1	-	14/39/115/115	-
5	XAT	N	318	-	-	1/31/93/93	0/4/4/4
5	XAT	N	321	-	-	6/31/93/93	0/4/4/4
3	CLA	Y	613	-	-	10/20/96/115	-
6	NEX	G	617	-	-	7/27/83/83	0/3/3/3
2	CHL	Y	608	1	-	12/26/102/117	-
3	CLA	G	610	-	-	9/20/96/115	-
3	CLA	N	311	1	-	13/39/115/115	-
2	CHL	Y	605	-	-	14/20/96/117	-
2	CHL	Y	601	-	-	3/21/97/117	-
2	CHL	N	301	-	-	10/22/98/117	-
6	NEX	N	319	-	-	6/27/83/83	0/3/3/3
3	CLA	G	602	1	-	15/39/115/115	-
3	CLA	Y	609	1	-	12/39/115/115	-
2	CHL	G	601	-	-	3/23/99/117	-
3	CLA	Y	610	7	-	16/39/115/115	-
2	CHL	N	310	-	-	7/22/98/117	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CHL	G	606	-	-	6/22/98/117	-
2	CHL	N	302	-	-	6/22/98/117	-
3	CLA	Y	611	-	-	13/39/115/115	-
3	CLA	G	604	-	-	10/20/96/115	-
7	LHG	Y	617	3	-	22/53/53/53	-
3	CLA	G	609	1	-	15/39/115/115	-
3	CLA	N	314	-	-	10/20/96/115	-
3	CLA	Y	603	-	-	5/20/96/115	-
3	CLA	Y	604	-	-	8/20/96/115	-
2	CHL	Y	606	-	-	14/22/98/117	-
4	LUT	Y	615	-	-	1/29/67/67	0/2/2/2
2	CHL	Y	607	-	-	9/22/98/117	-
7	LHG	G	618	-	-	7/53/53/53	-
2	CHL	G	605	1	-	6/20/96/117	-
6	NEX	Y	616	-	-	3/27/83/83	0/3/3/3
3	CLA	N	303	1	-	11/39/115/115	-
3	CLA	N	315	1	-	12/20/96/115	-
3	CLA	G	603	-	-	6/20/96/115	-
4	LUT	N	316	-	-	7/29/67/67	0/2/2/2
2	CHL	N	306	-	-	6/20/96/117	-
4	LUT	Y	614	-	-	7/29/67/67	0/2/2/2
2	CHL	G	607	-	-	8/22/98/117	-
3	CLA	G	613	1	-	8/20/96/115	-
3	CLA	N	305	-	-	8/20/96/115	-
4	LUT	N	317	-	-	3/29/67/67	0/2/2/2
3	CLA	G	611	1	-	22/39/115/115	-
4	LUT	G	614	-	-	7/29/67/67	0/2/2/2
7	LHG	N	320	3	-	27/53/53/53	-
2	CHL	N	308	-	-	5/23/99/117	-
2	CHL	G	619	-	-	8/22/98/117	-
3	CLA	G	612	-	-	10/20/96/115	-
3	CLA	N	304	-	-	12/20/96/115	-
3	CLA	N	312	7	-	10/20/96/115	-
3	CLA	Y	612	-	-	15/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CHL	N	307	-	-	4/22/98/117	-
3	CLA	N	313	1	-	12/39/115/115	-

The worst 5 of 367 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Y	611	CLA	MG-NB	-4.80	1.96	2.05
2	Y	607	CHL	C1D-ND	4.19	1.42	1.37
7	G	618	LHG	O8-C23	4.15	1.45	1.33
7	G	618	LHG	O7-C7	4.12	1.45	1.34
3	Y	602	CLA	C1D-ND	4.06	1.42	1.37

The worst 5 of 493 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	G	617	NEX	O24-C25-C24	10.71	121.42	113.38
5	G	616	XAT	O24-C25-C24	9.66	120.64	113.38
5	N	321	XAT	O24-C25-C24	9.22	120.31	113.38
6	G	617	NEX	C38-C25-C26	-8.91	107.33	122.26
5	N	318	XAT	O4-C5-C4	8.61	119.85	113.38

There are no chirality outliers.

5 of 519 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	601	CHL	CHA-CBD-CGD-O1D
2	G	601	CHL	CHA-CBD-CGD-O2D
2	G	605	CHL	CAD-CBD-CGD-O1D
2	G	605	CHL	CAD-CBD-CGD-O2D
2	G	606	CHL	C1C-C2C-CMC-OMC

There are no ring outliers.

47 monomers are involved in 125 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	615	LUT	4	0
2	G	608	CHL	1	0
5	G	616	XAT	4	0
3	Y	602	CLA	5	0
5	N	318	XAT	4	0

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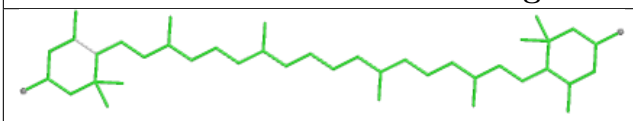
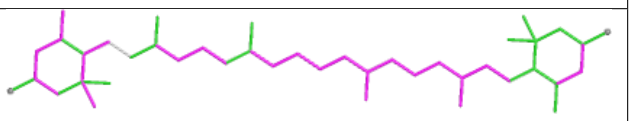
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	N	321	XAT	2	0
3	Y	613	CLA	1	0
6	G	617	NEX	4	0
2	Y	608	CHL	1	0
3	G	610	CLA	1	0
3	N	311	CLA	2	0
2	Y	605	CHL	4	0
2	N	301	CHL	4	0
6	N	319	NEX	3	0
3	G	602	CLA	4	0
3	Y	609	CLA	6	0
2	G	601	CHL	2	0
3	Y	610	CLA	8	0
2	N	310	CHL	1	0
2	G	606	CHL	6	0
2	N	302	CHL	2	0
3	Y	611	CLA	4	0
3	G	604	CLA	4	0
7	Y	617	LHG	2	0
3	G	609	CLA	11	0
3	N	314	CLA	1	0
2	Y	606	CHL	9	0
4	Y	615	LUT	4	0
2	Y	607	CHL	1	0
7	G	618	LHG	4	0
2	G	605	CHL	1	0
6	Y	616	NEX	5	0
3	G	603	CLA	1	0
4	N	316	LUT	7	0
2	N	306	CHL	1	0
4	Y	614	LUT	8	0
2	G	607	CHL	3	0
3	N	305	CLA	1	0
4	N	317	LUT	4	0
3	G	611	CLA	3	0
4	G	614	LUT	8	0
7	N	320	LHG	1	0
2	G	619	CHL	2	0
3	G	612	CLA	2	0
3	N	312	CLA	1	0
3	Y	612	CLA	5	0
3	N	313	CLA	1	0

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

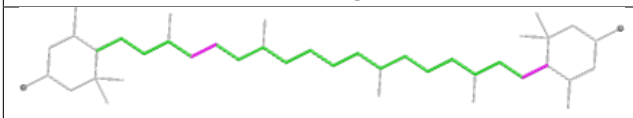
Ligand LUT G 615



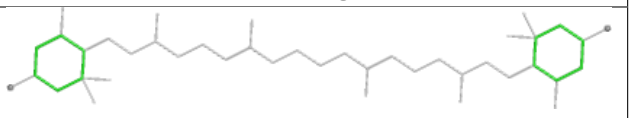
Bond lengths



Bond angles

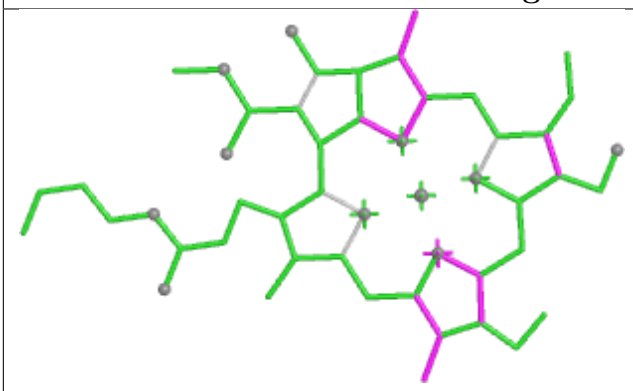


Torsions

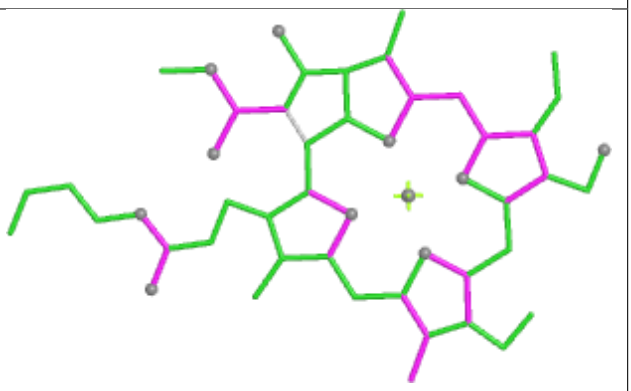


Rings

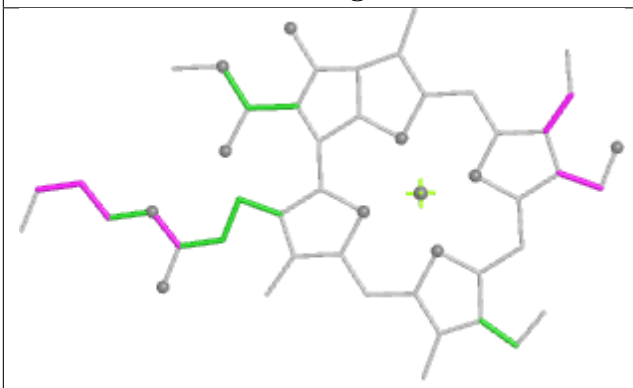
Ligand CHL G 608



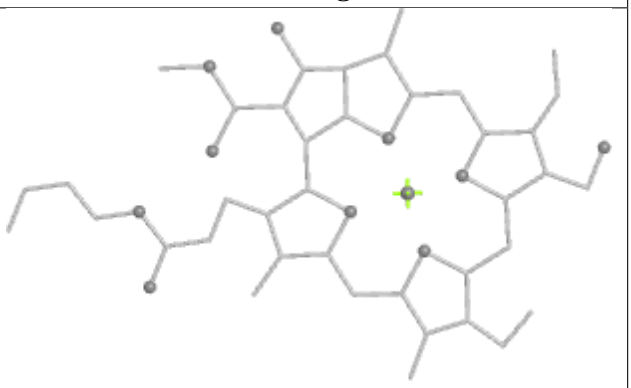
Bond lengths



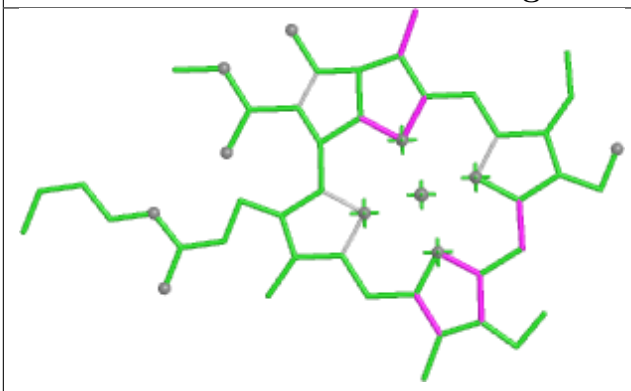
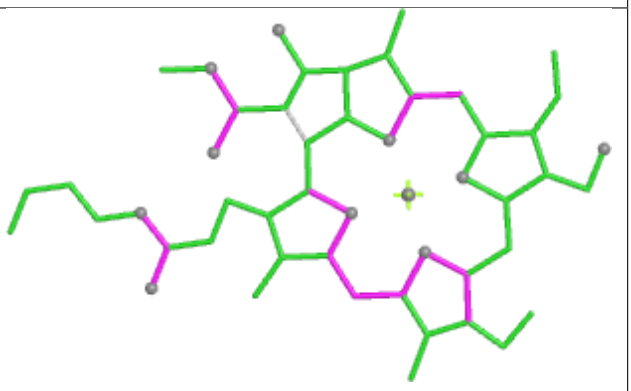
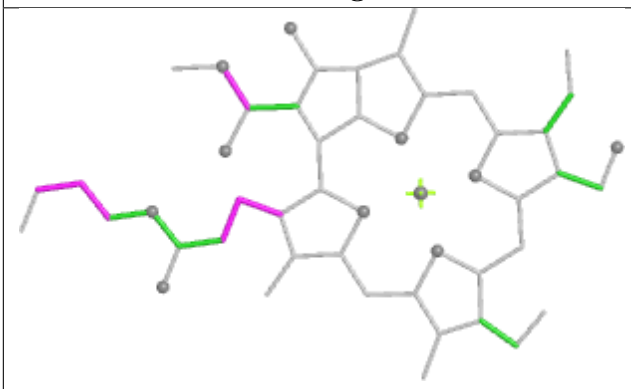
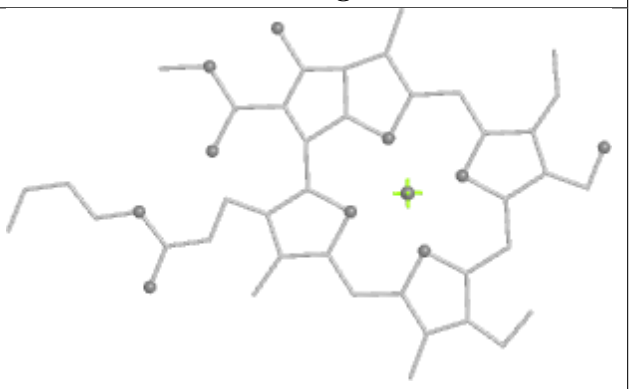
Bond angles

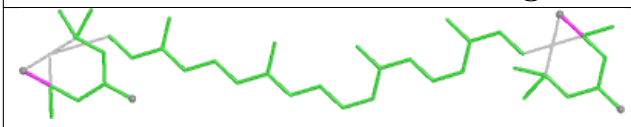
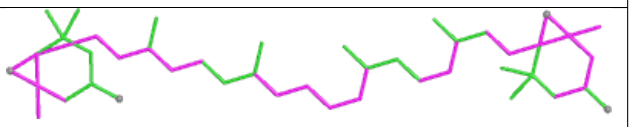
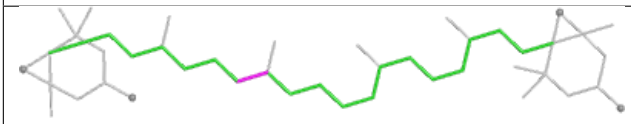
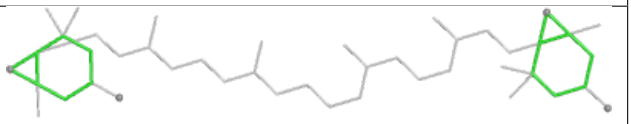


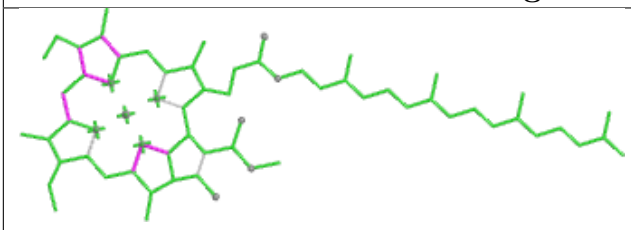
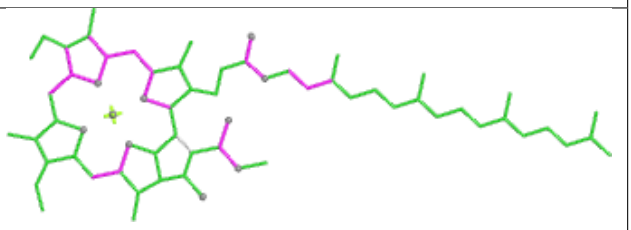
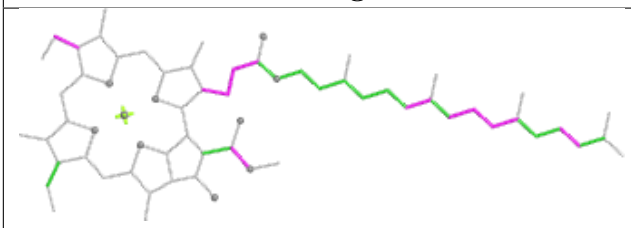
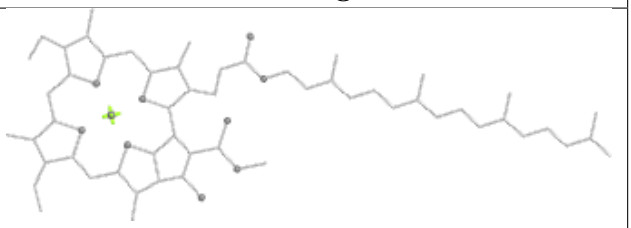
Torsions

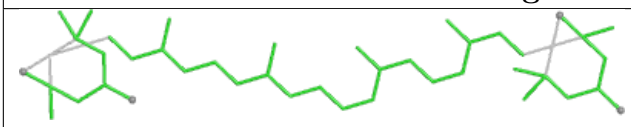
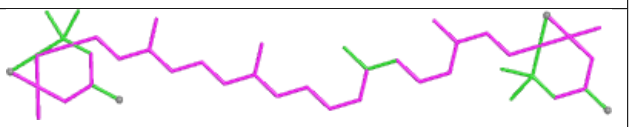
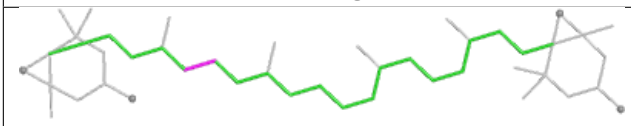
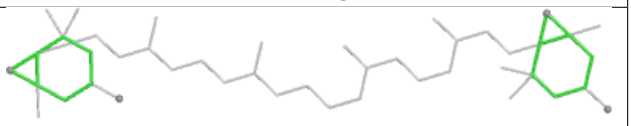


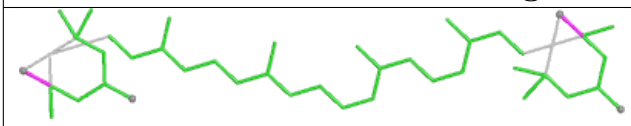
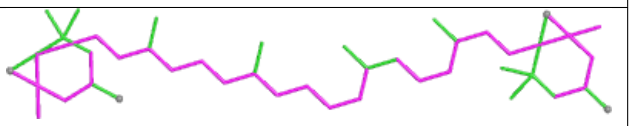
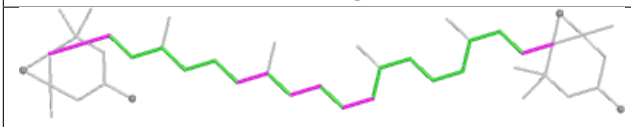
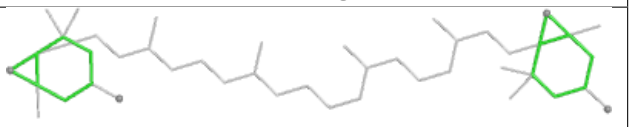
Rings

Ligand CHL N 309	
 Bond lengths	 Bond angles
 Torsions	 Rings

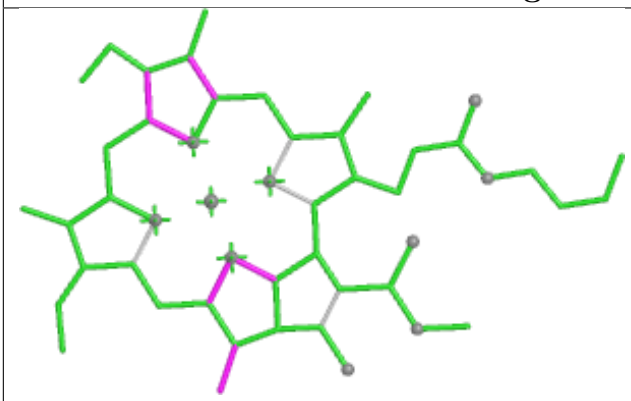
Ligand XAT G 616	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA Y 602	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand XAT N 318	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand XAT N 321	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA Y 613



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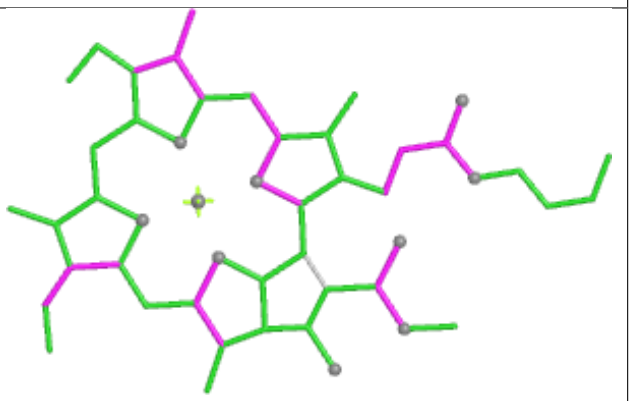
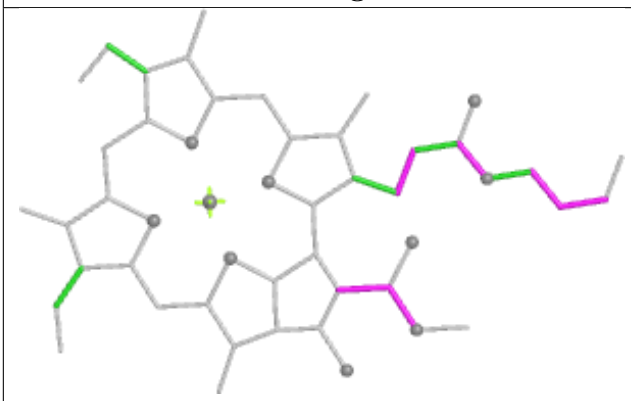


Bond angles



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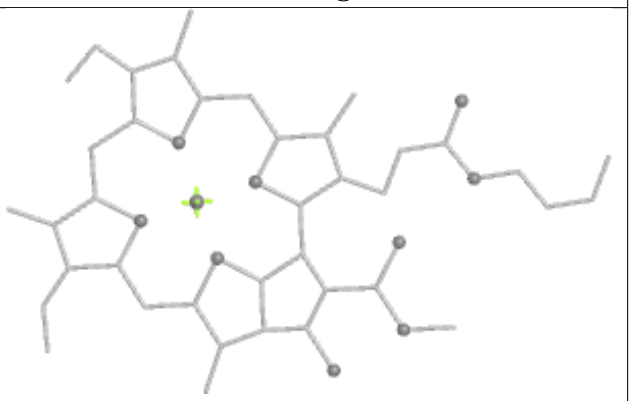
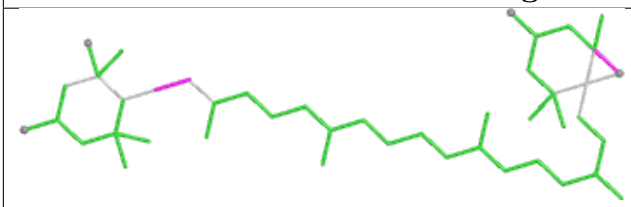


Rings

Ligand NEX G 617



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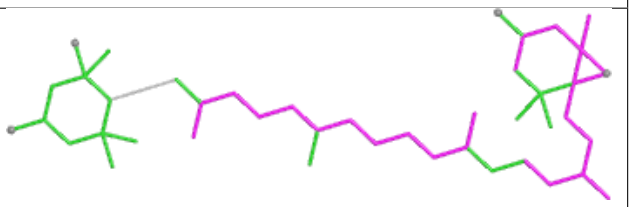

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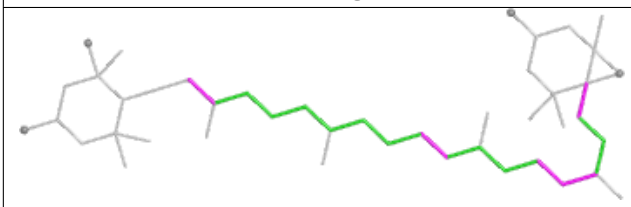

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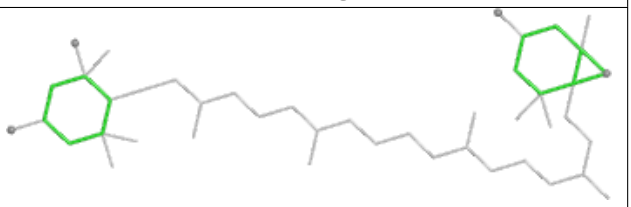
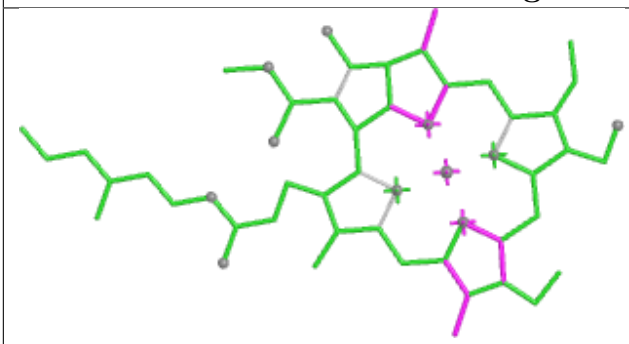
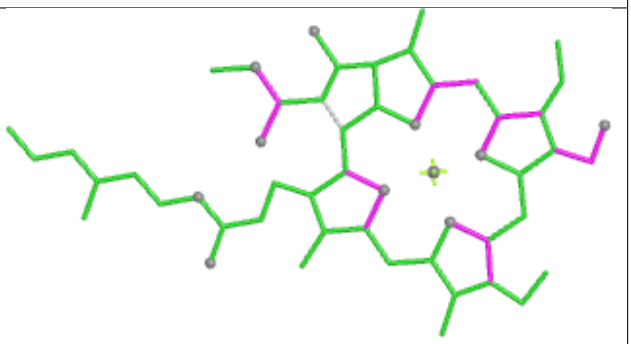
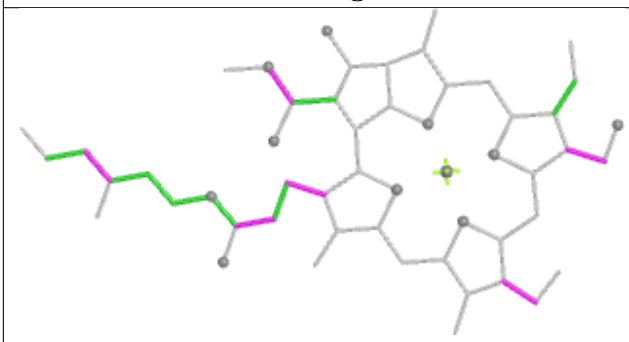
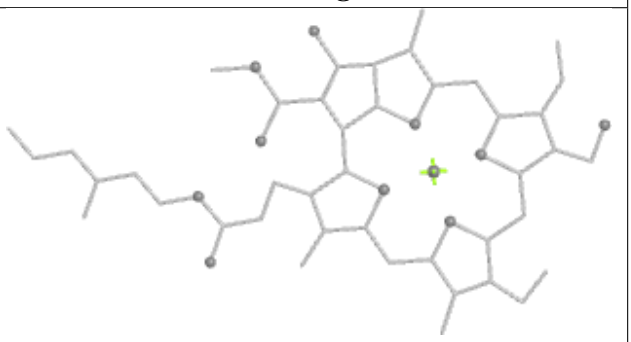
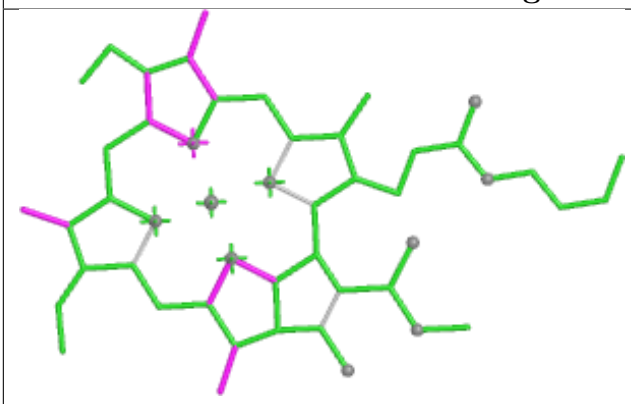
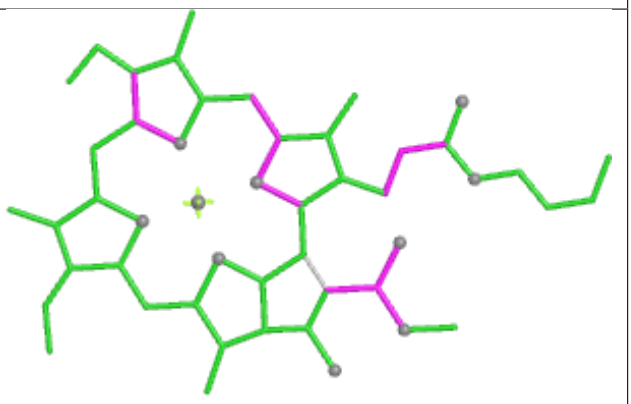
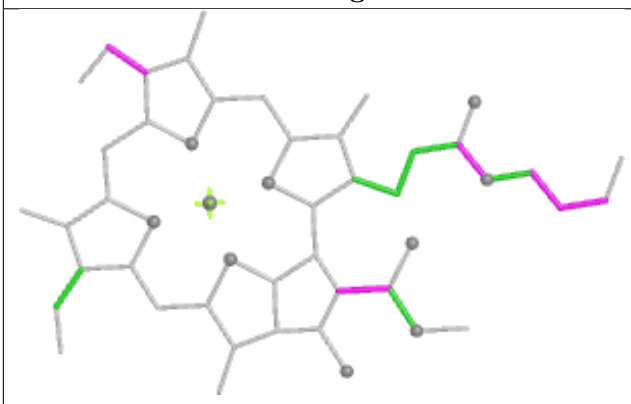
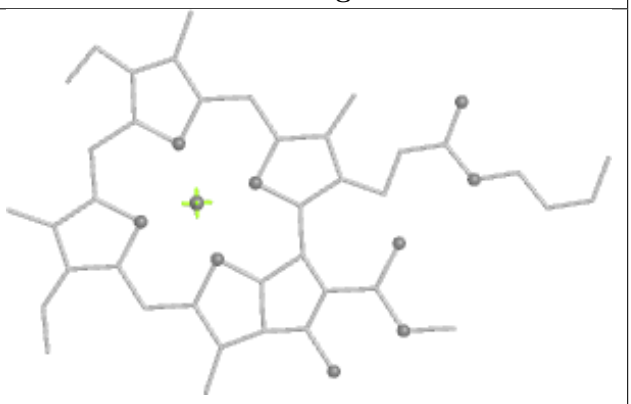
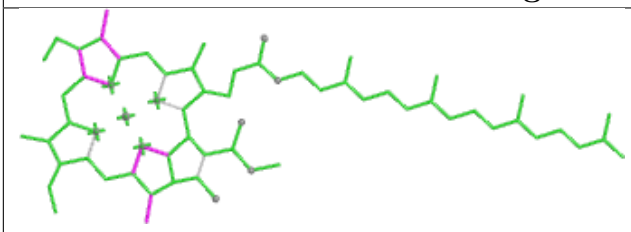


Rings

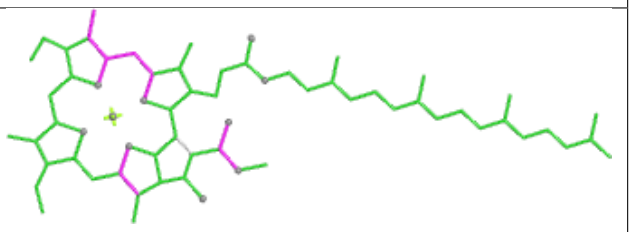
Ligand CHL Y 608	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA G 610	
 Bond lengths	 Bond angles
 Torsions	 Rings

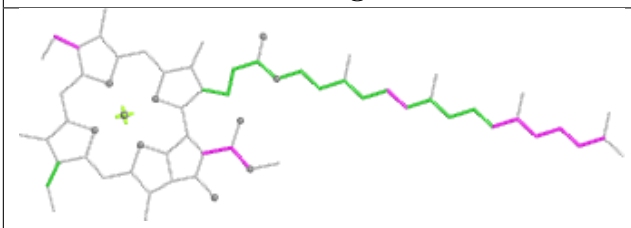
Ligand CLA N 311



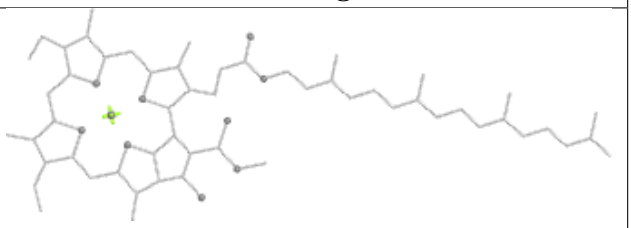
Bond lengths



Bond angles

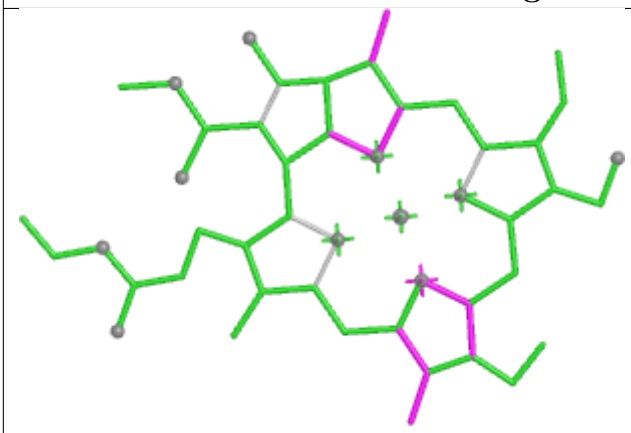


Torsions

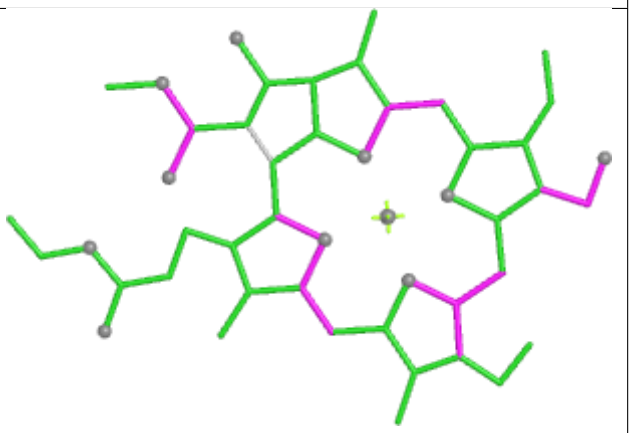


Rings

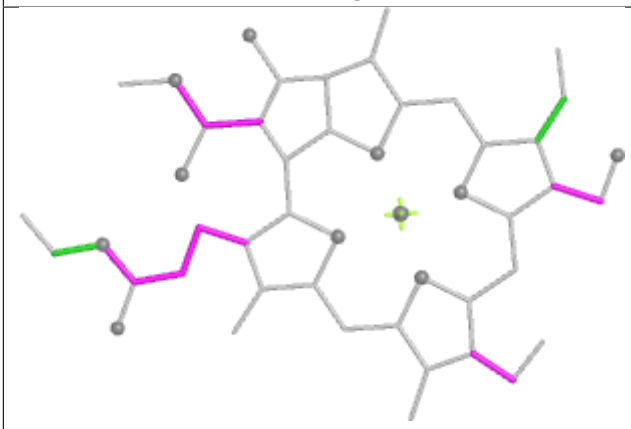
Ligand CHL Y 605



Bond lengths



Bond angles



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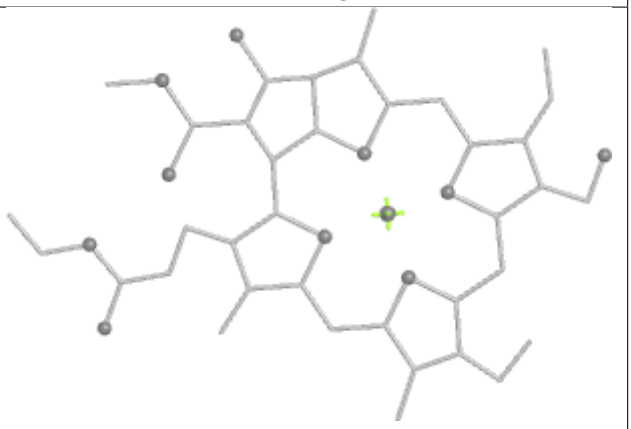
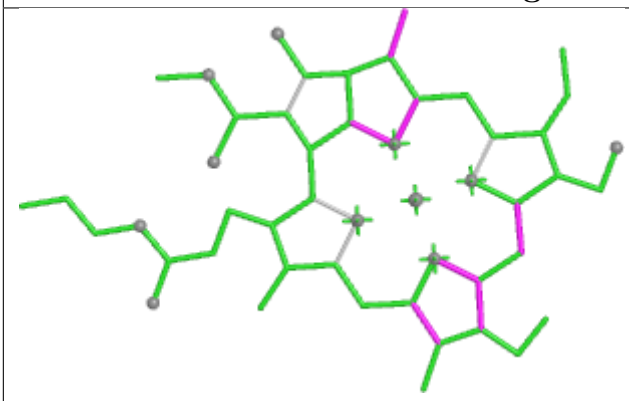
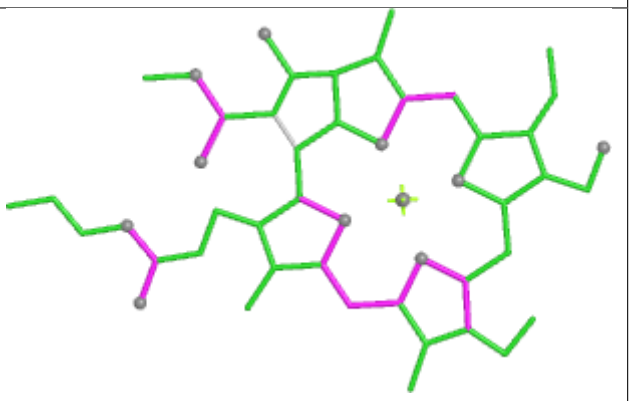
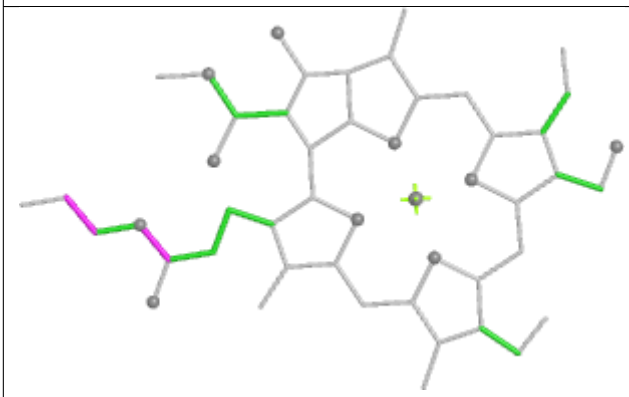
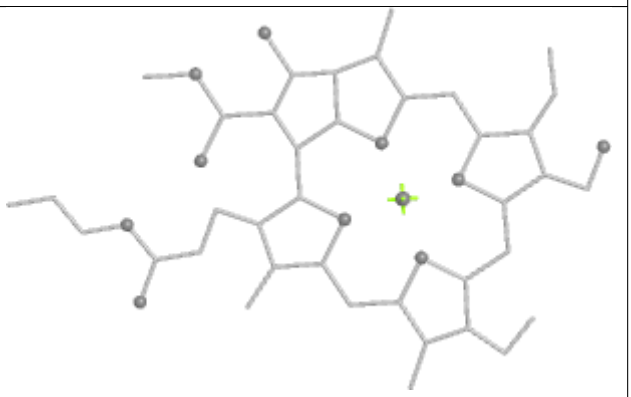
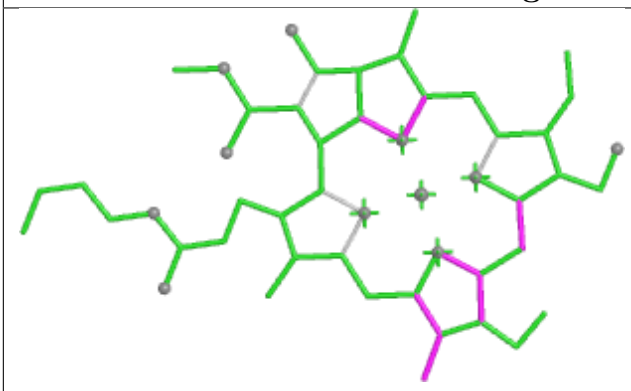
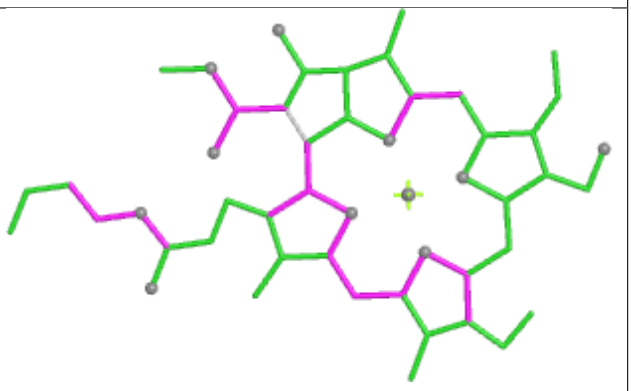
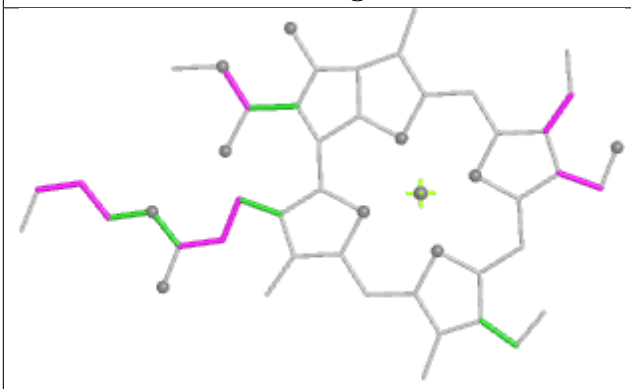
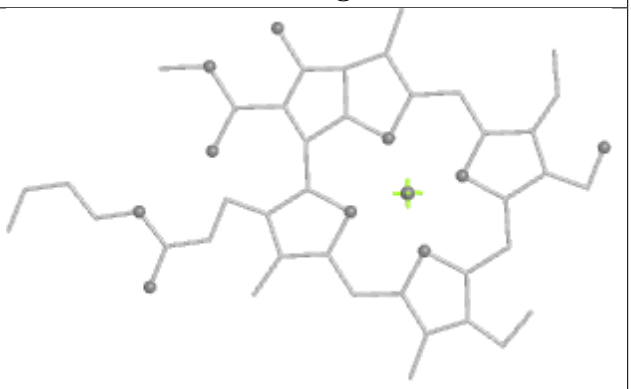
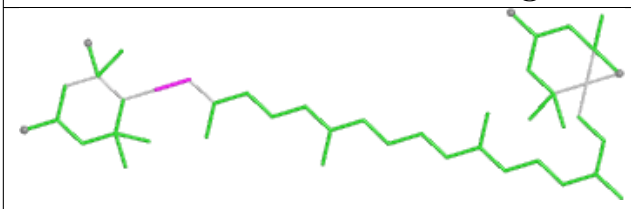
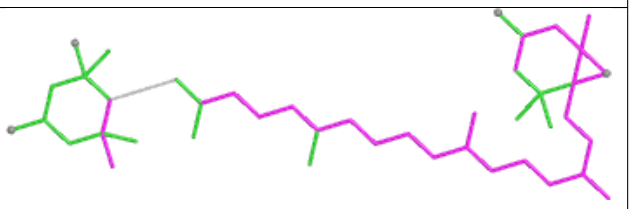
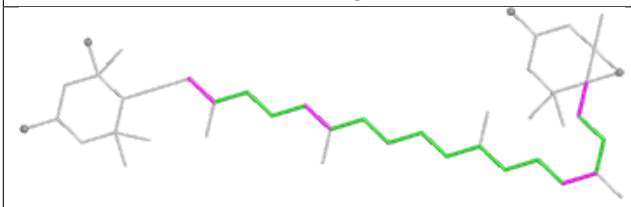
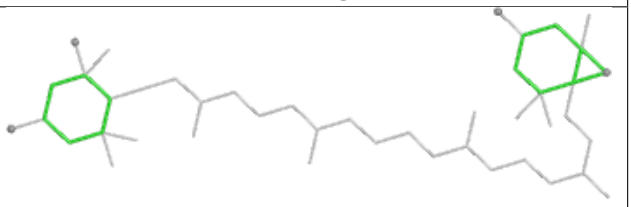
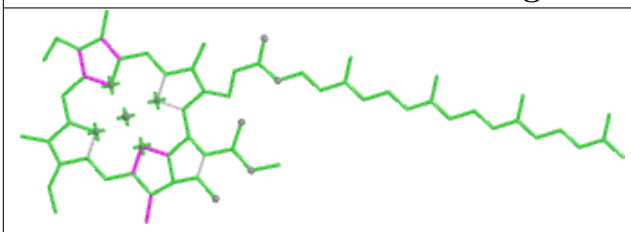
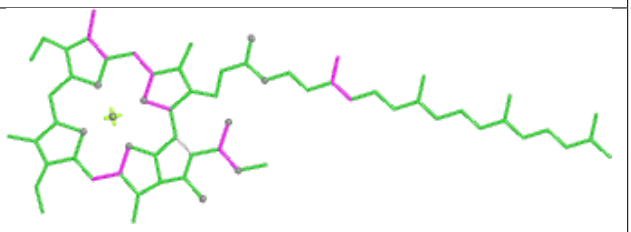
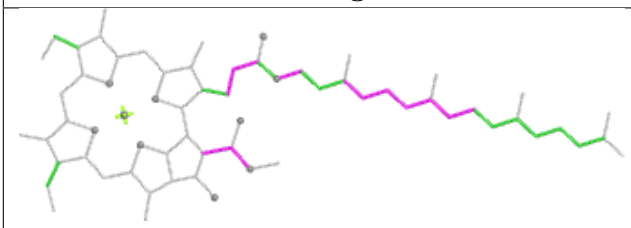
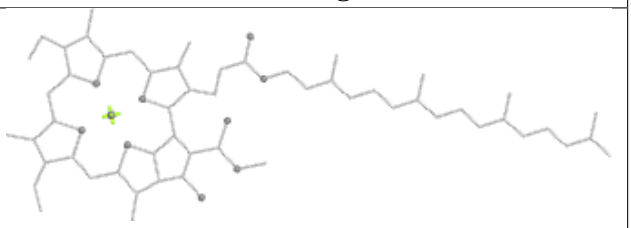


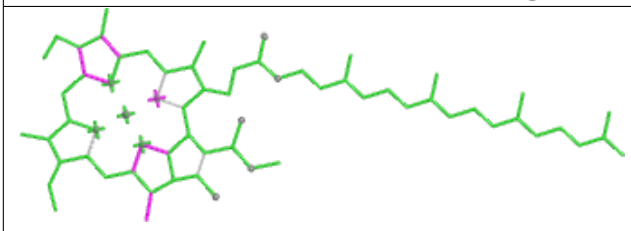
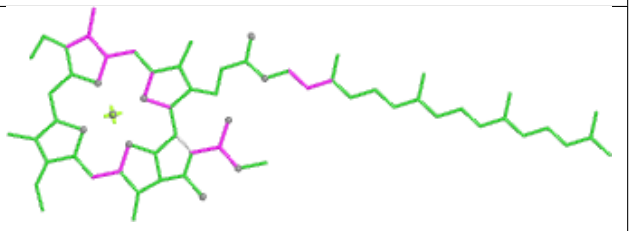
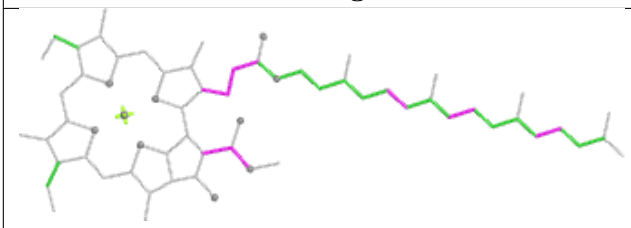
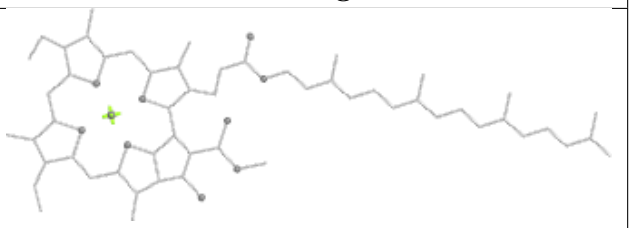
Rings

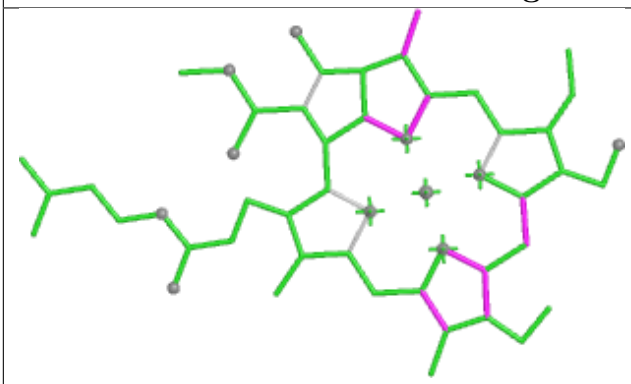
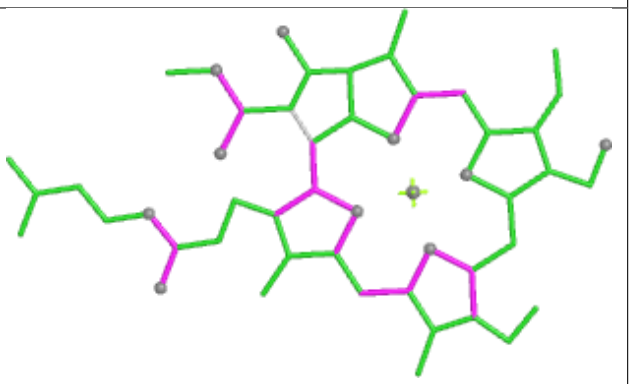
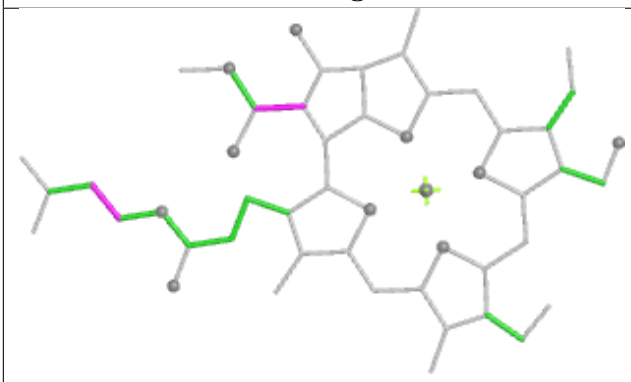
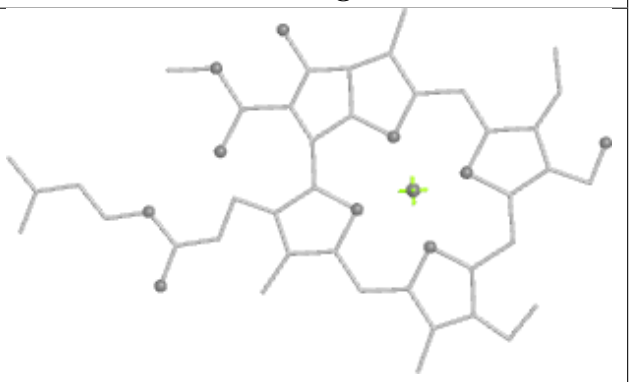
Ligand CHL Y 601	
 Bond lengths	 Bond angles
 Torsions	 Rings

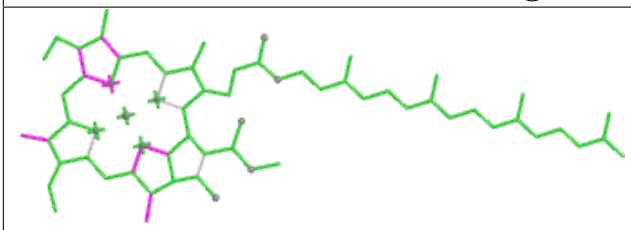
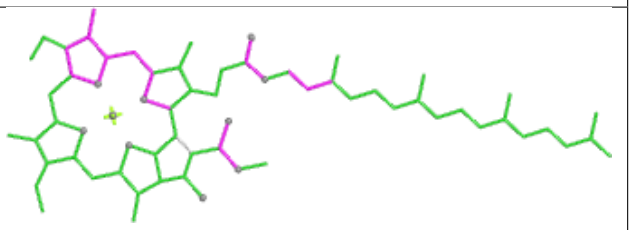
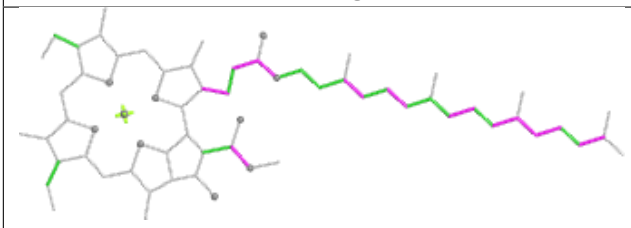
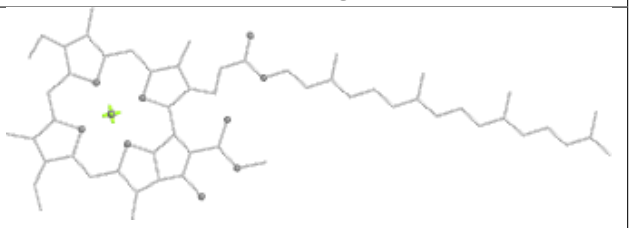
Ligand CHL N 301	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand NEX N 319	
 Bond lengths	 Bond angles
 Torsions	 Rings

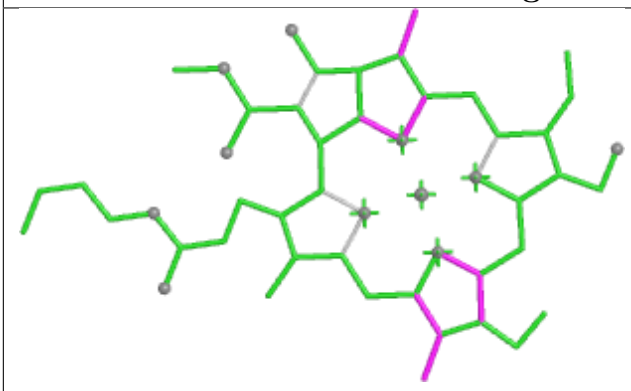
Ligand CLA G 602	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA Y 609	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CHL G 601	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA Y 610	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CHL N 310



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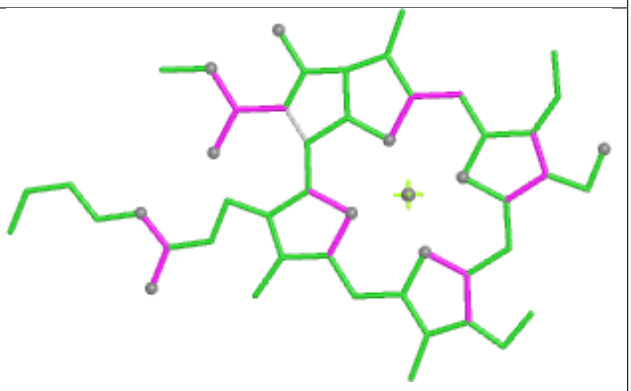
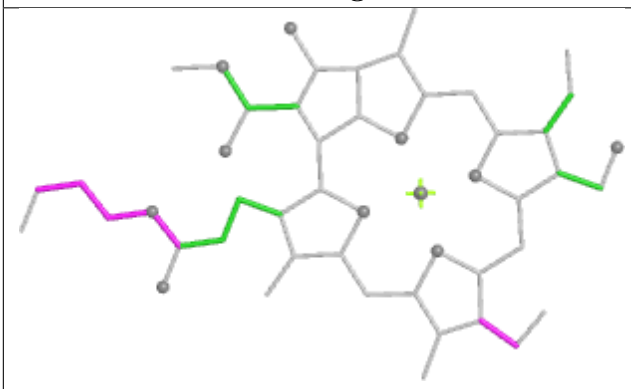


Bond angles



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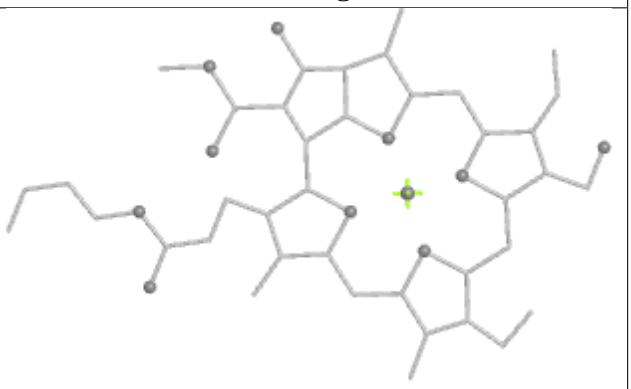
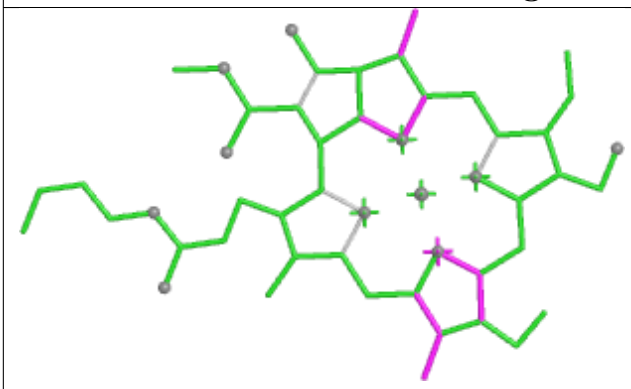


Rings

Ligand CHL G 606



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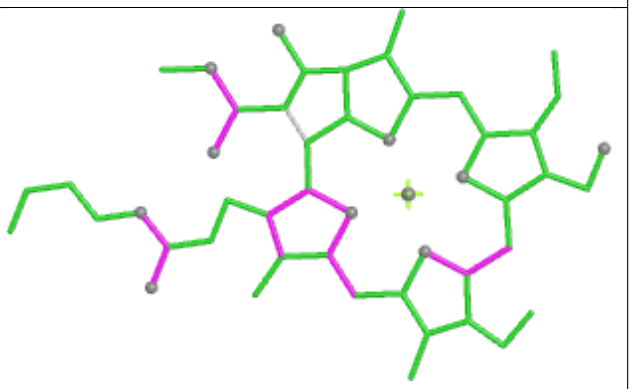

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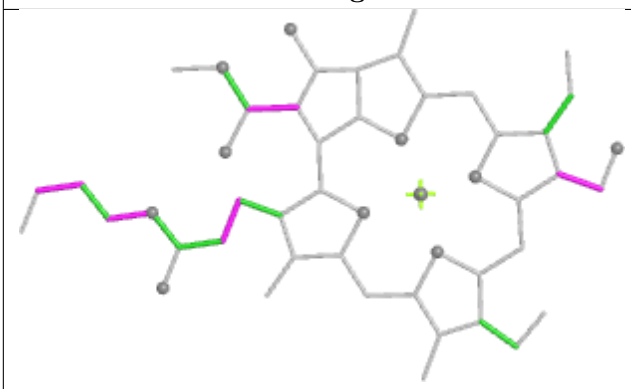

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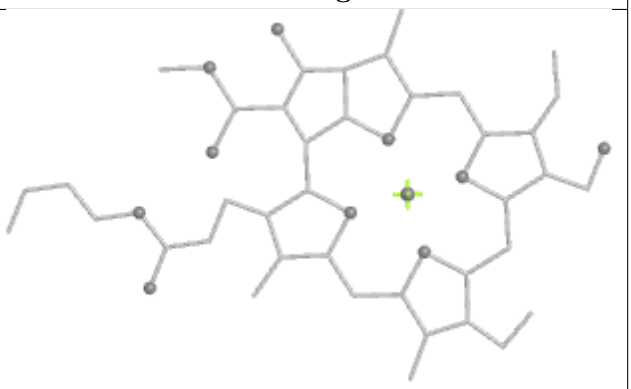
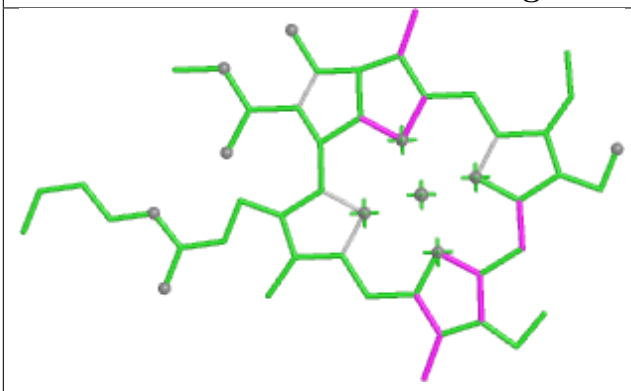
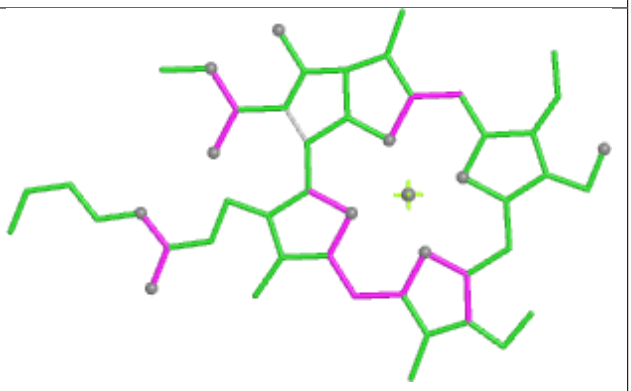
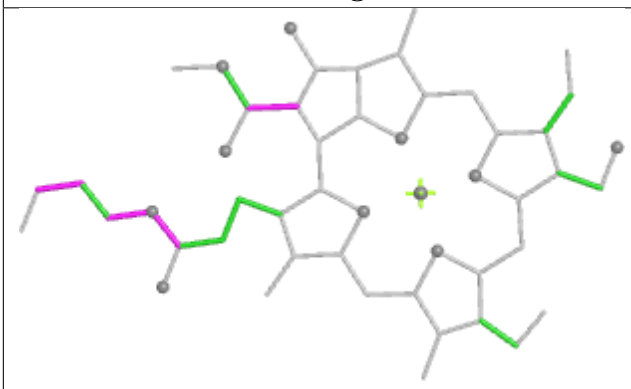
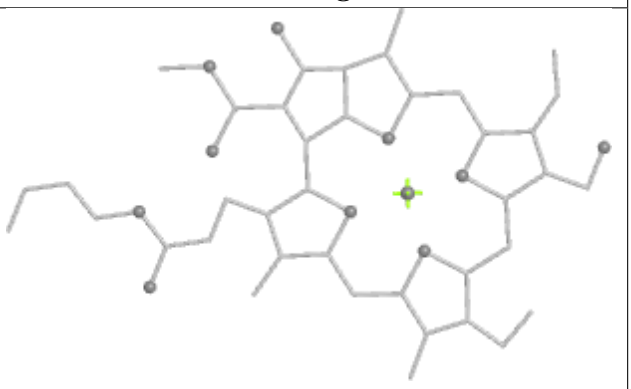
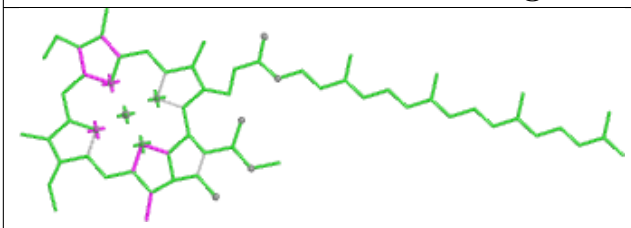
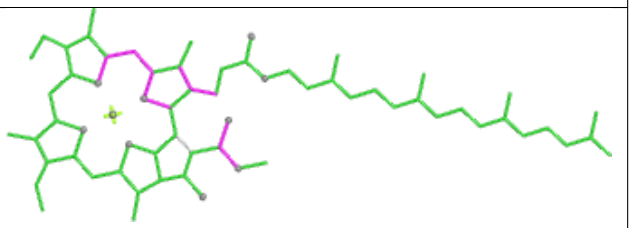
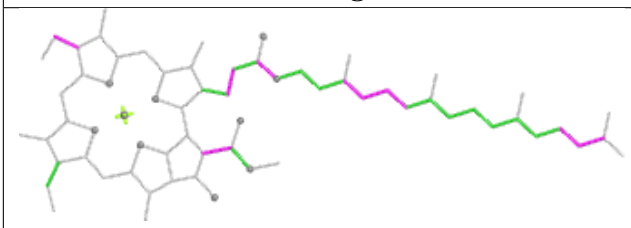
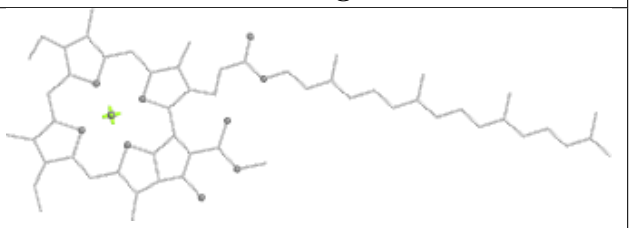
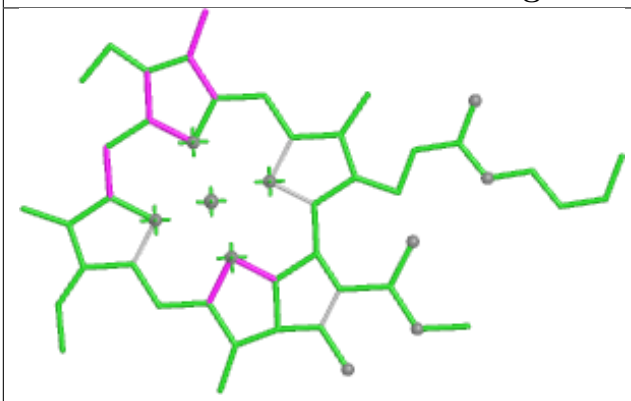
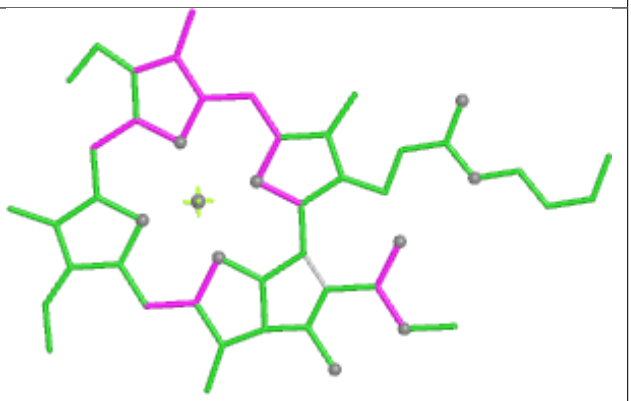
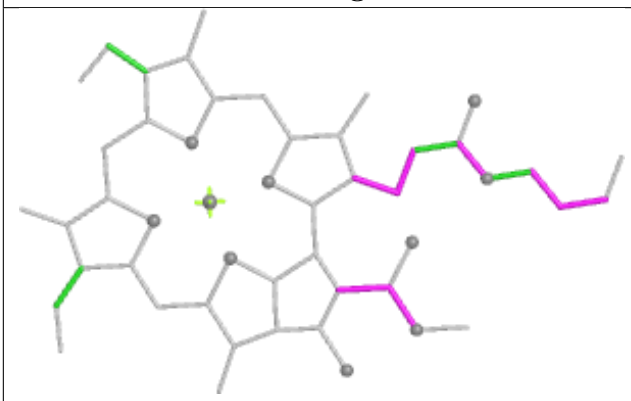
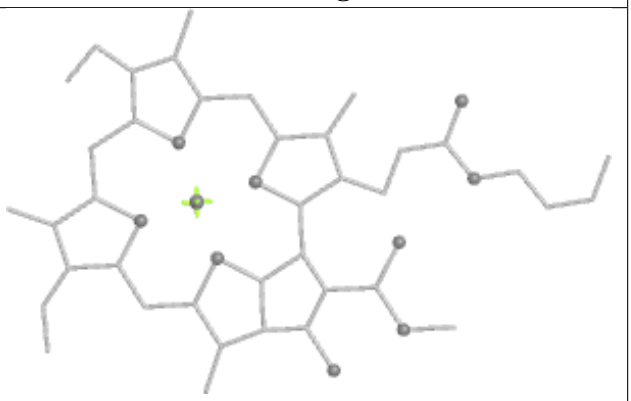


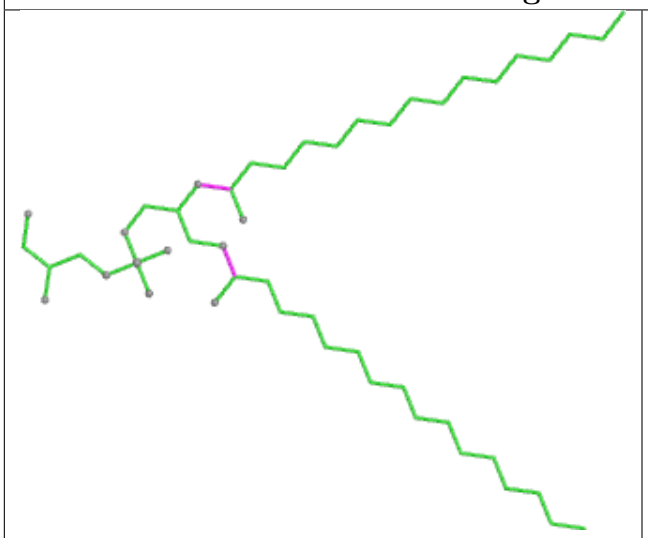
Rings

Ligand CHL N 302	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA Y 611	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA G 604	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LHG Y 617



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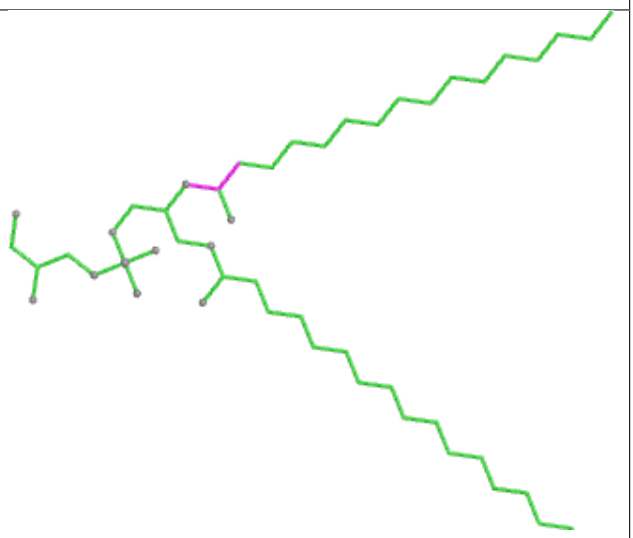
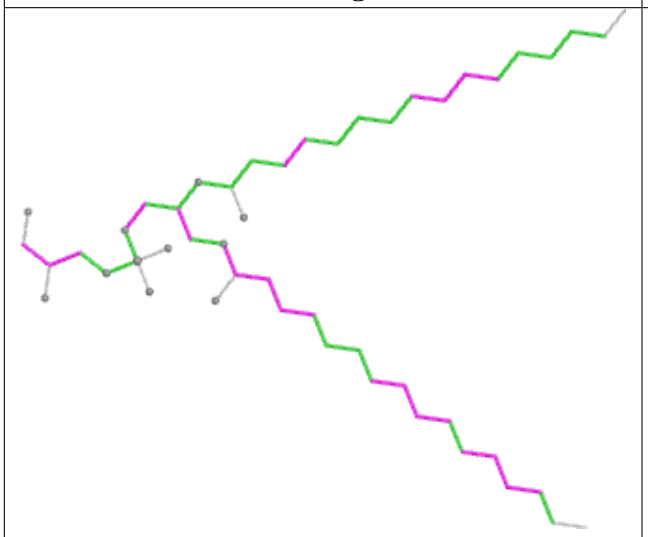
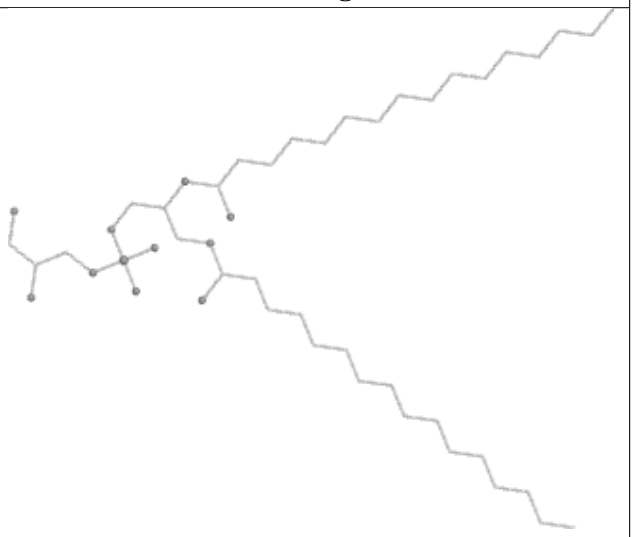


Bond angles

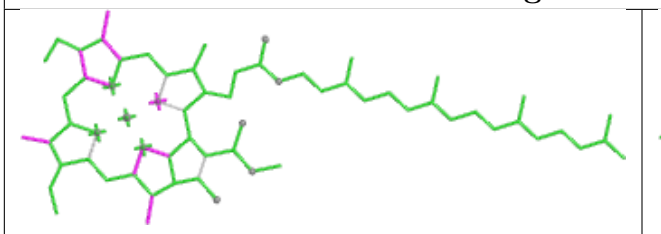


Torsions



Rings

Ligand CLA G 609



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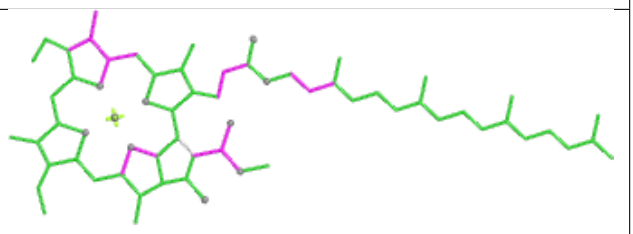
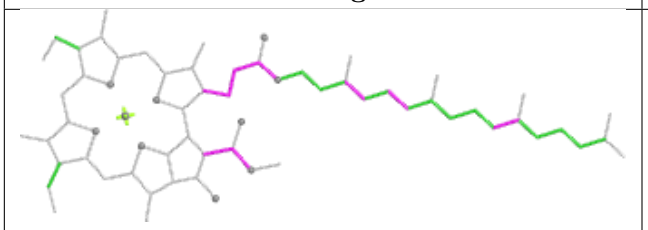


Bond angles



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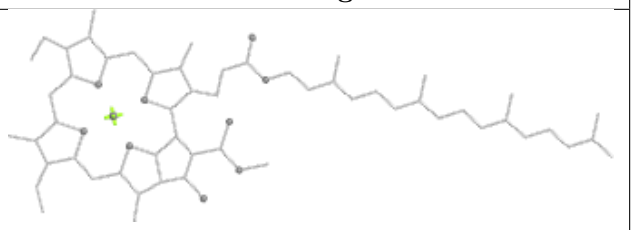
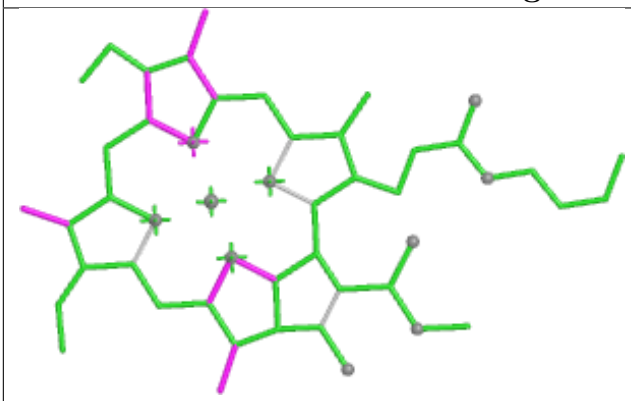
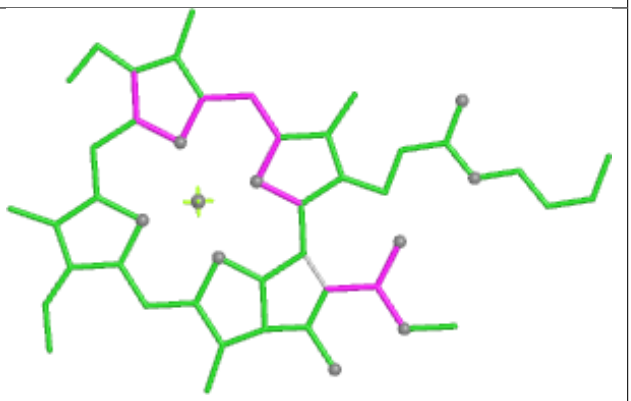
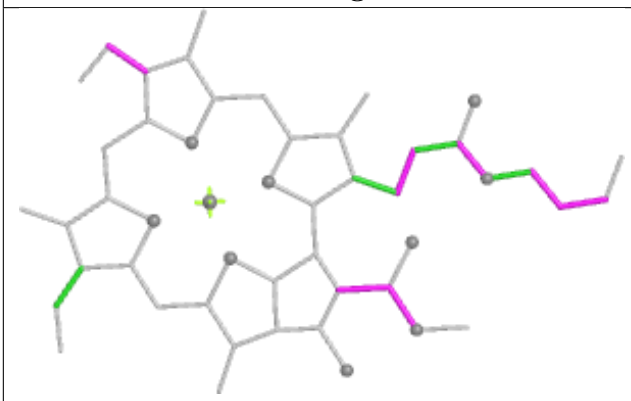
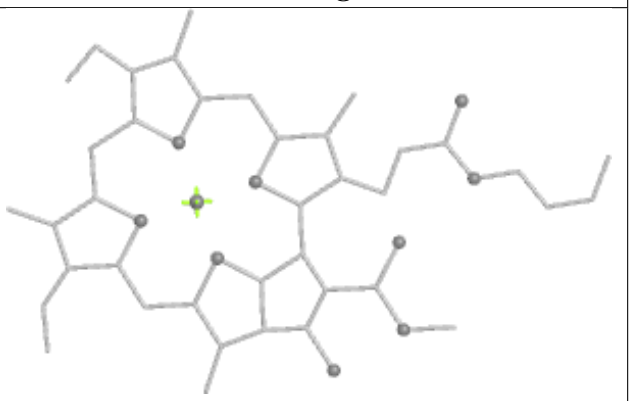


Rings

Ligand CLA N 314	
 Bond lengths	 Bond angles
 Torsions	 Rings

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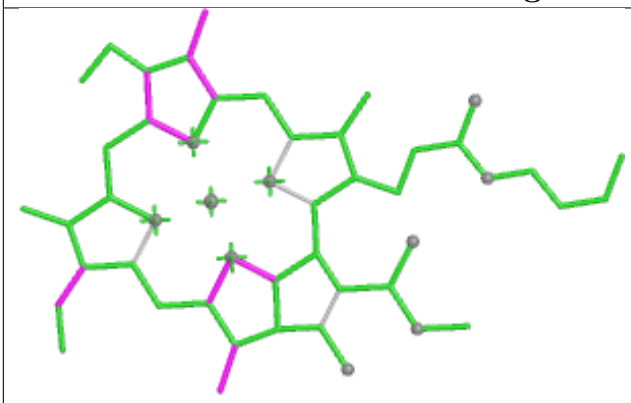
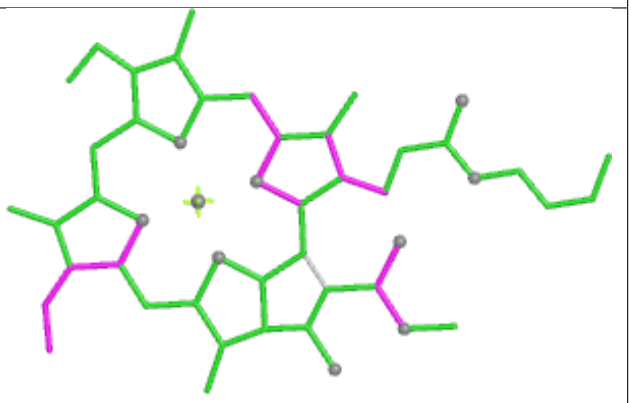
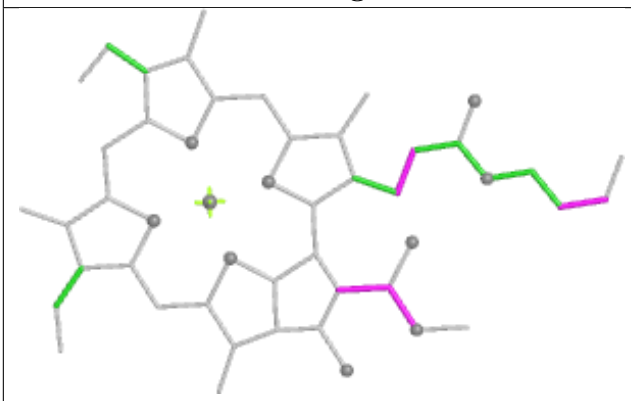
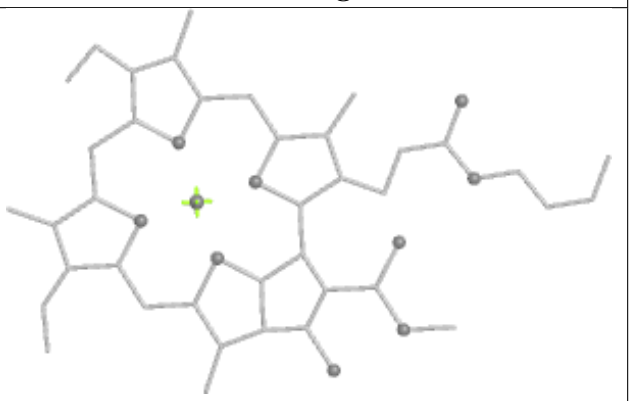
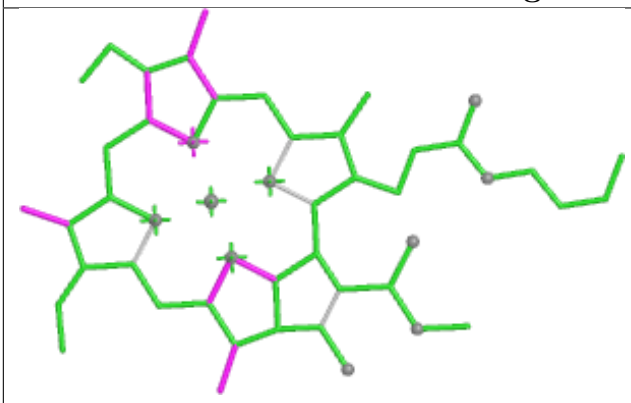
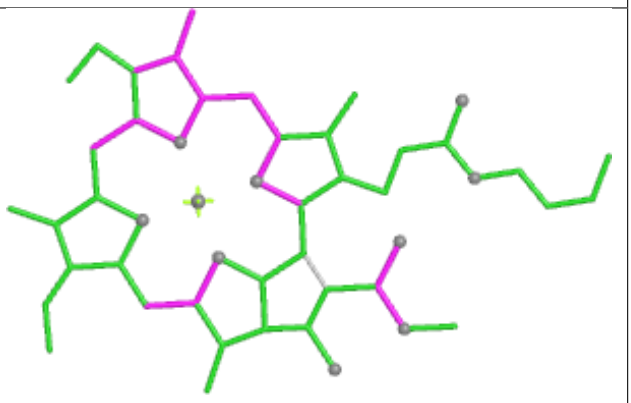
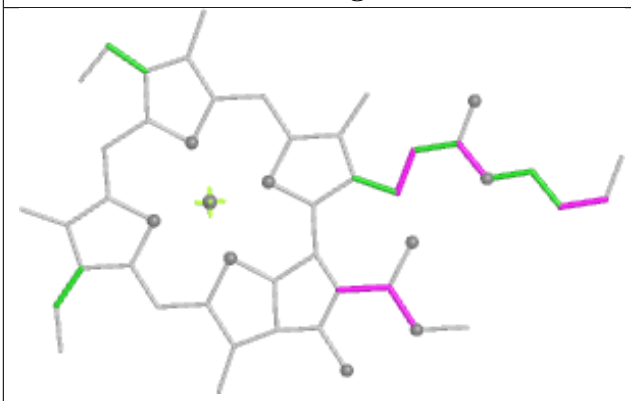
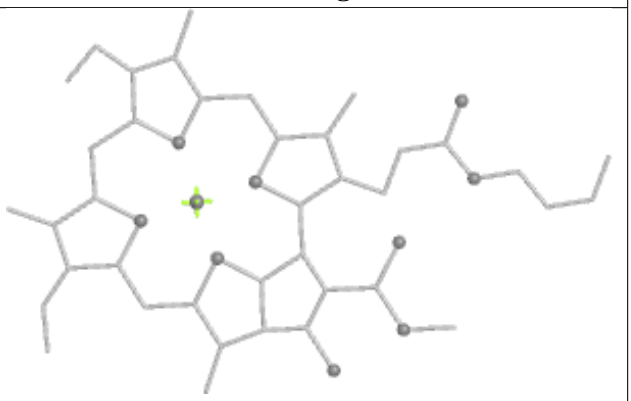
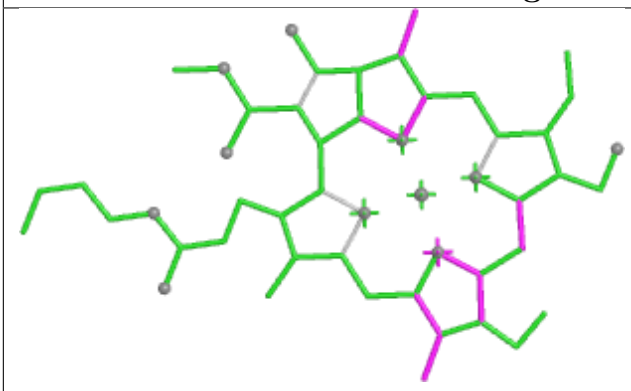
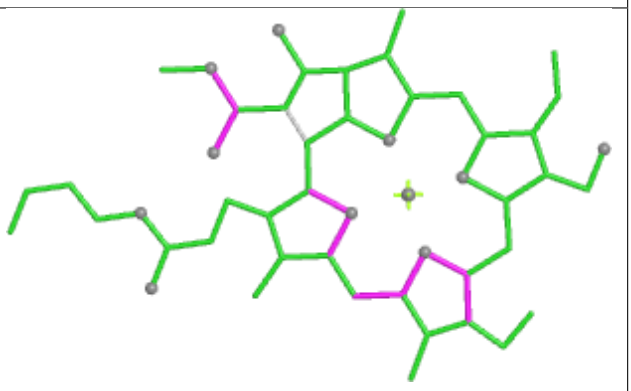
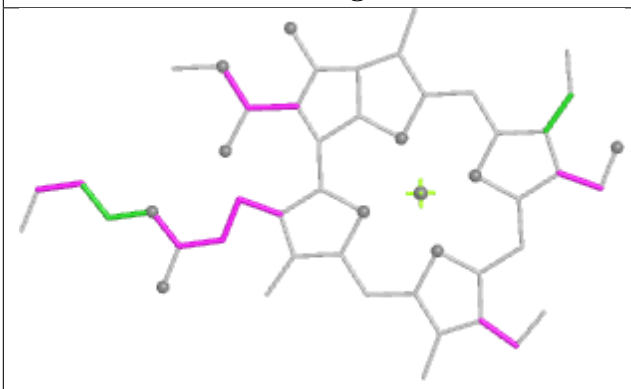
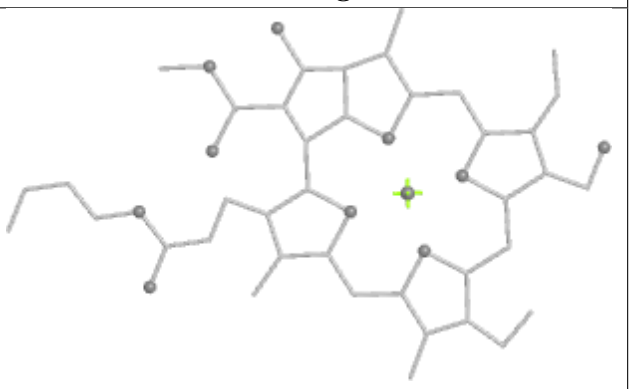
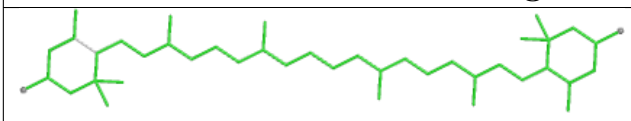
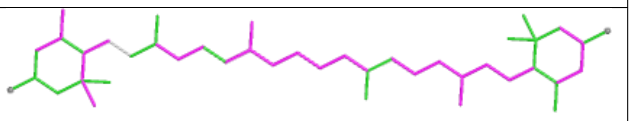
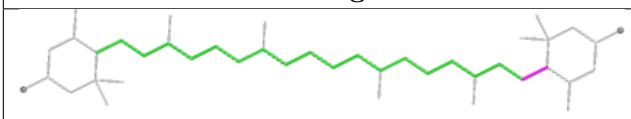
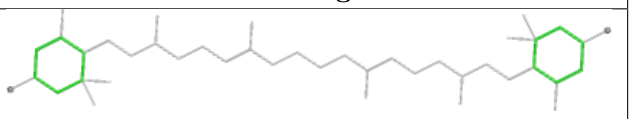
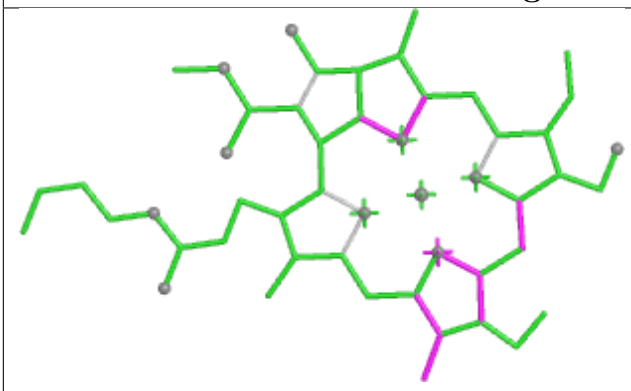
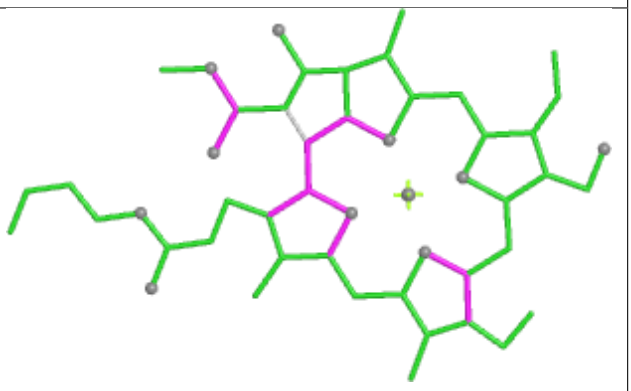
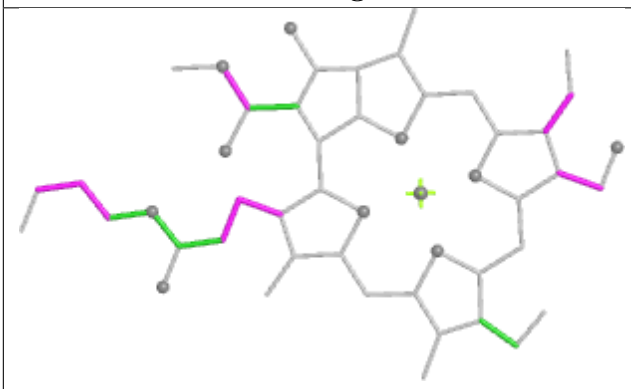
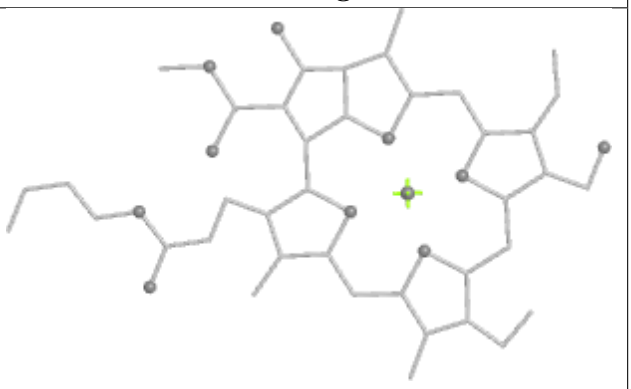
 Bond lengths	 Bond angles
 Torsions	 Rings

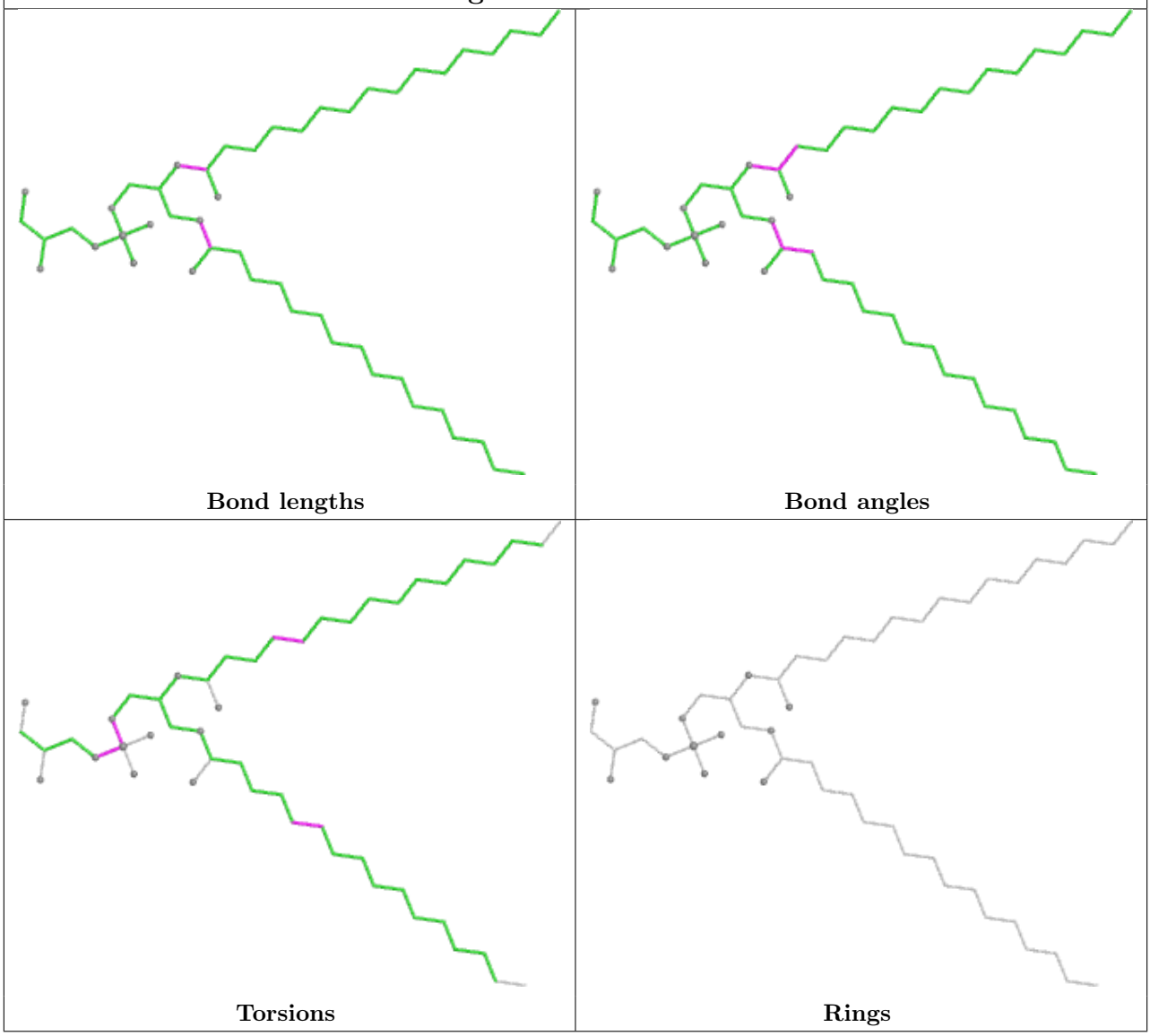
Ligand CLA Y 604	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CHL Y 606	
 Bond lengths	 Bond angles
 Torsions	 Rings

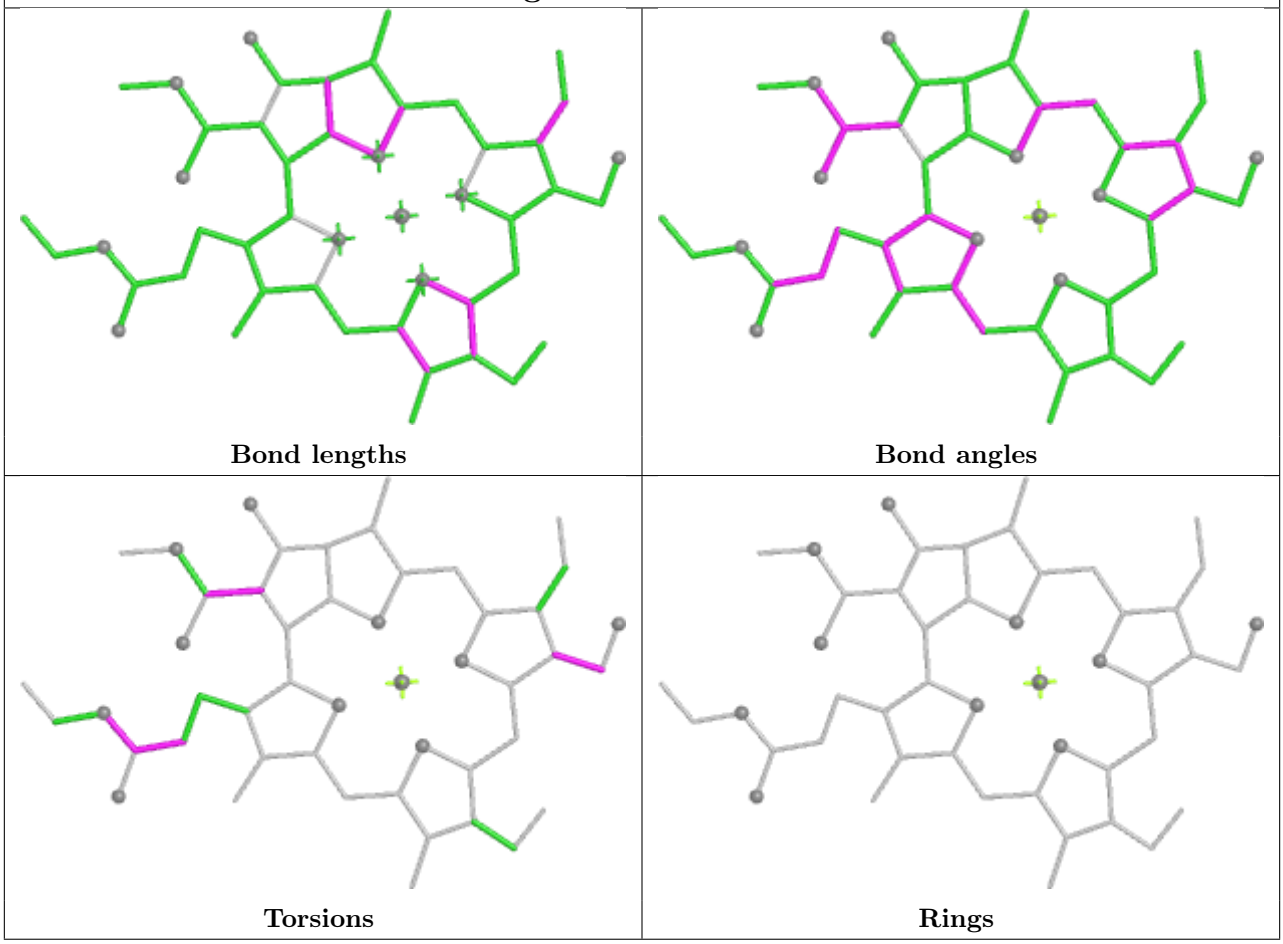
Ligand LUT Y 615	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CHL Y 607	
 Bond lengths	 Bond angles
 Torsions	 Rings

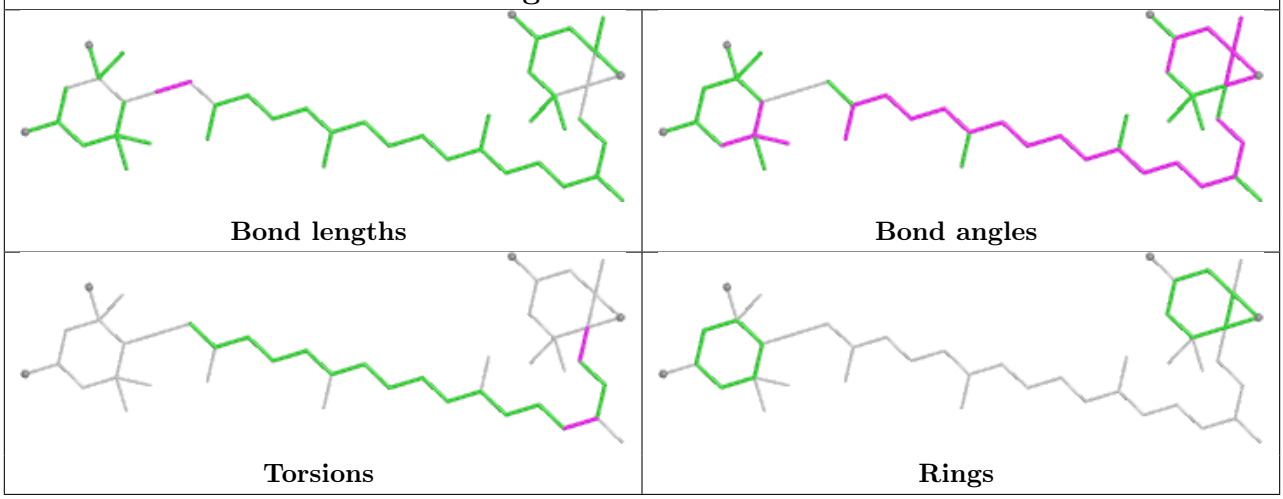
Ligand LHG G 618



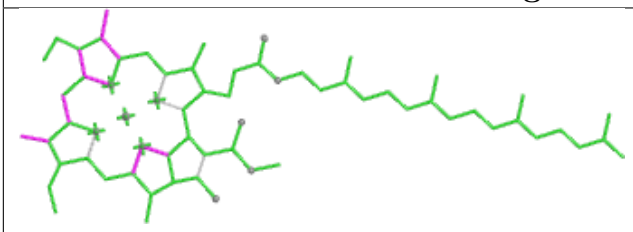
Ligand CHL G 605



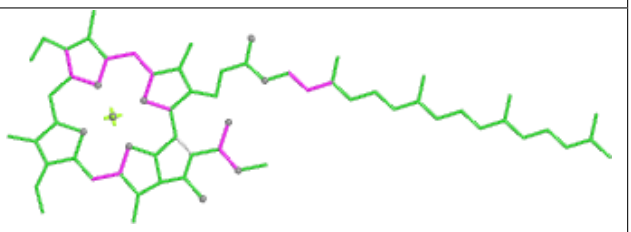
Ligand NEX Y 616



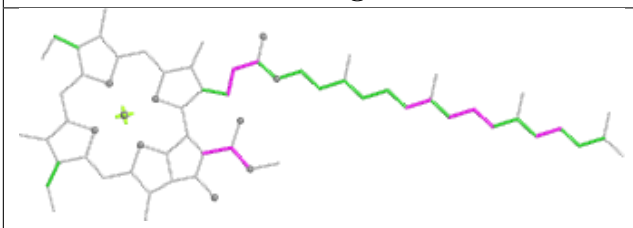
Ligand CLA N 303



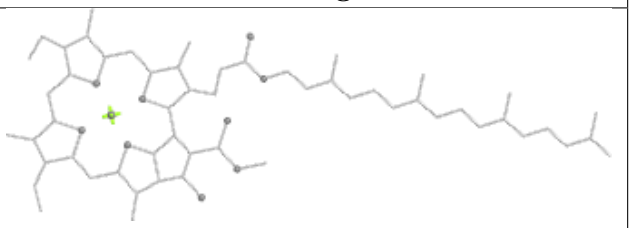
Bond lengths



Bond angles

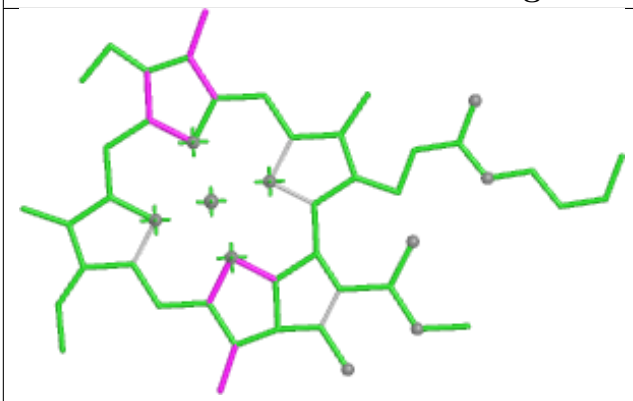


Torsions



Rings

Ligand CLA N 315



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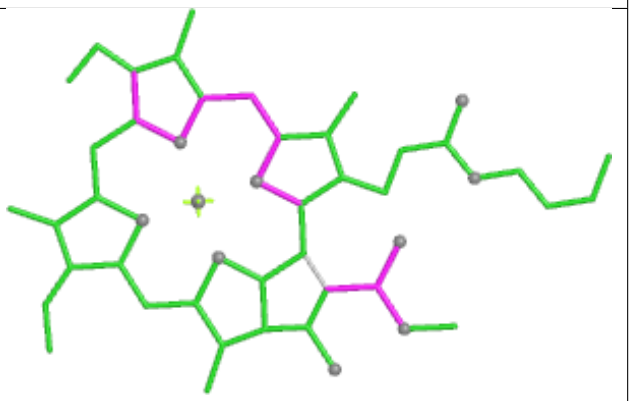
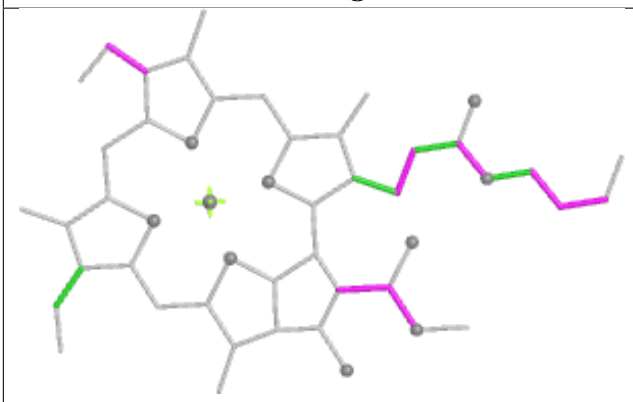
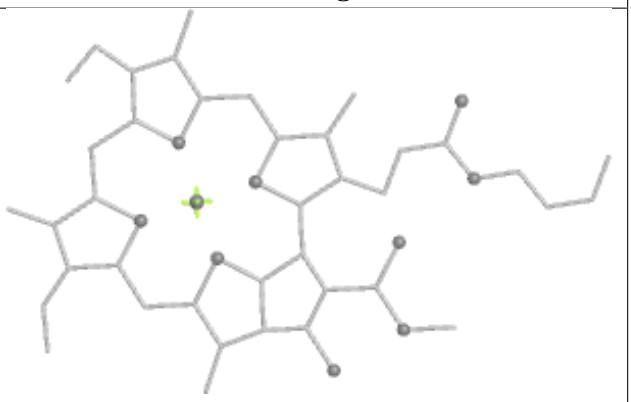


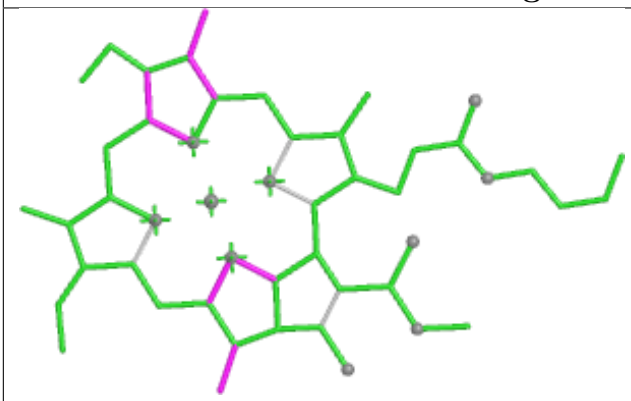
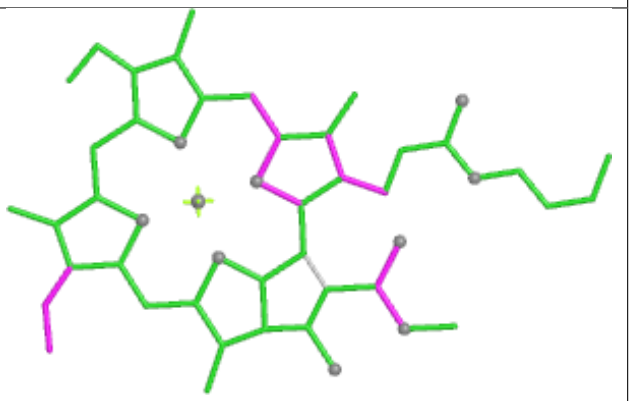
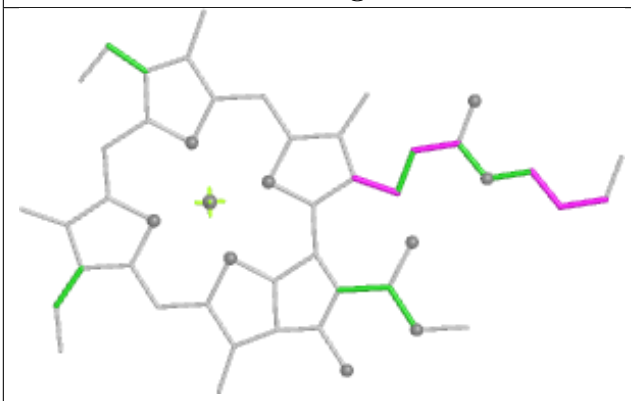
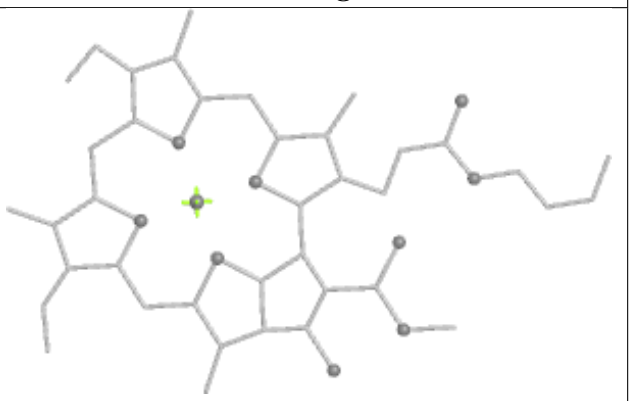
Bond angles

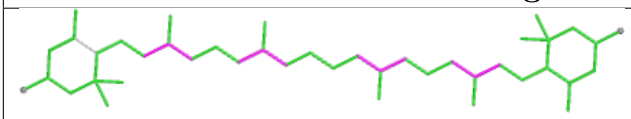
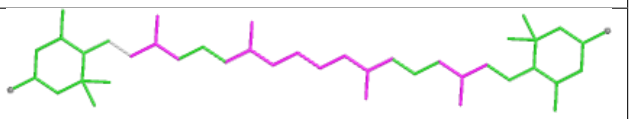
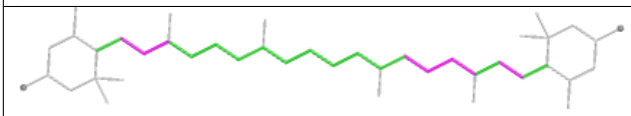
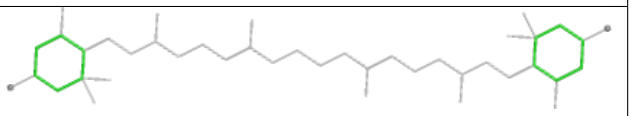


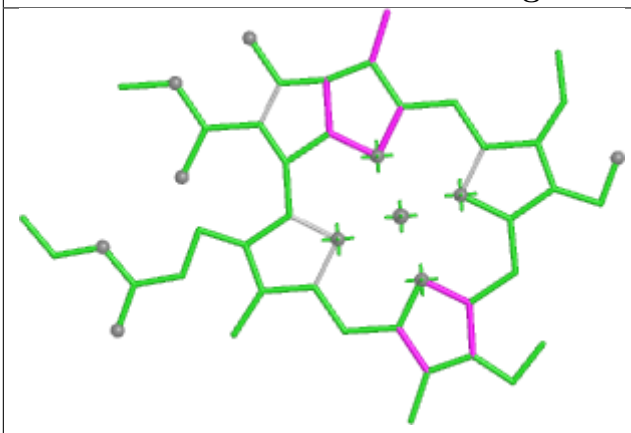
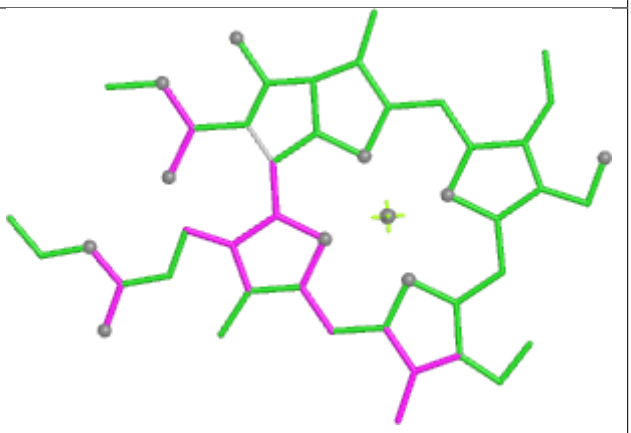
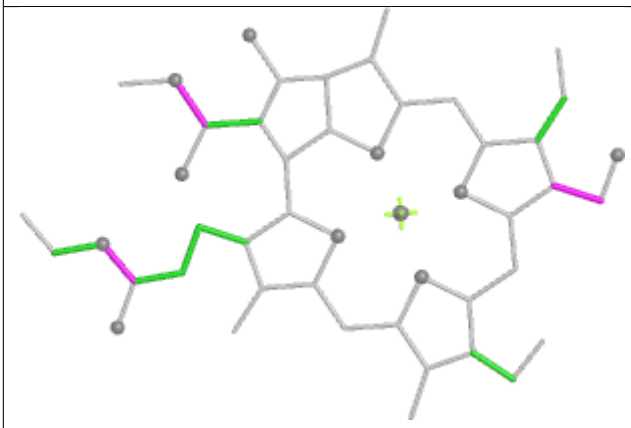
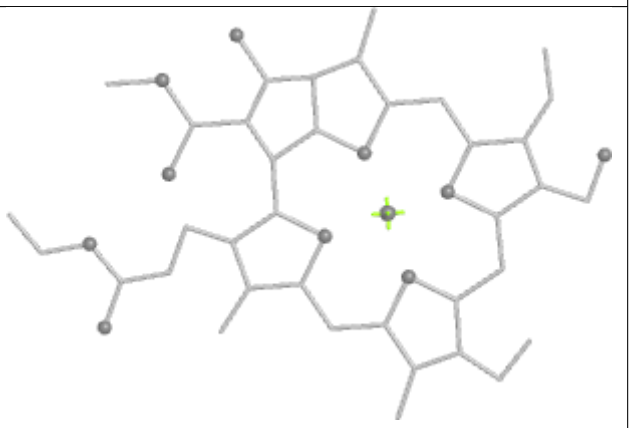
Torsions

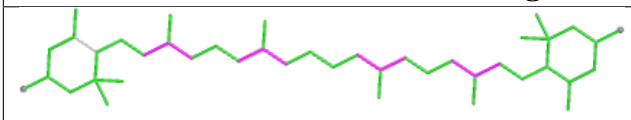
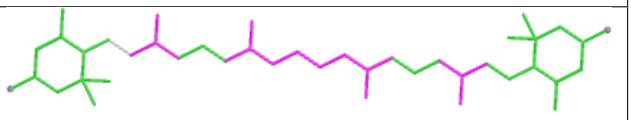
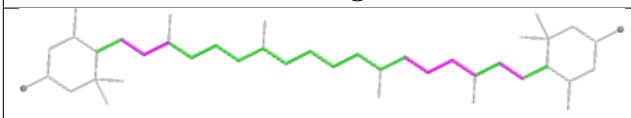
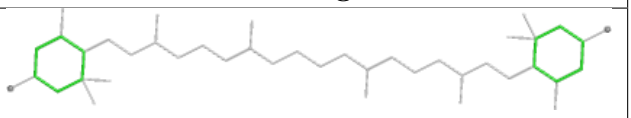


Rings

Ligand CLA G 603	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LUT N 316	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CHL N 306	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LUT Y 614	
 Bond lengths	 Bond angles
 Torsions	 Rings

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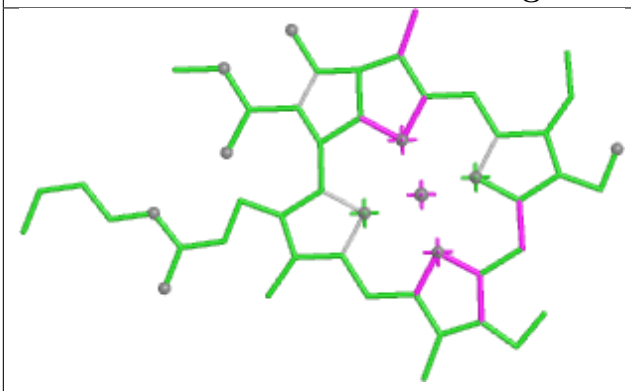
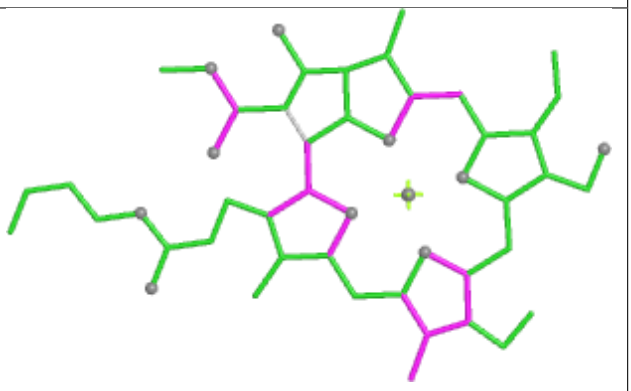
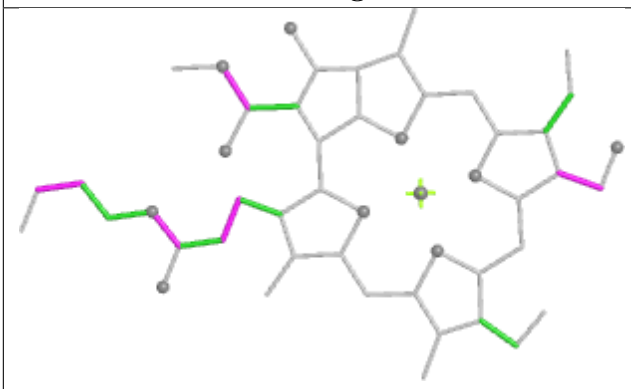
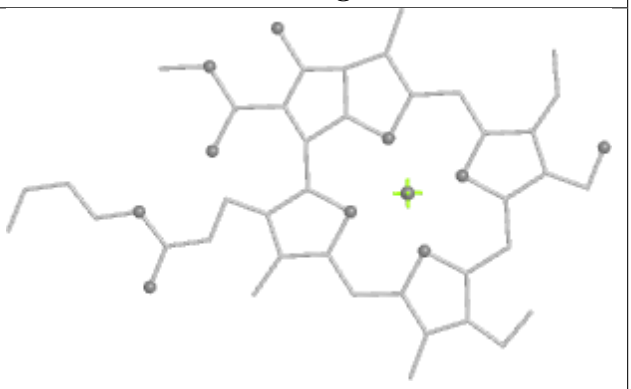
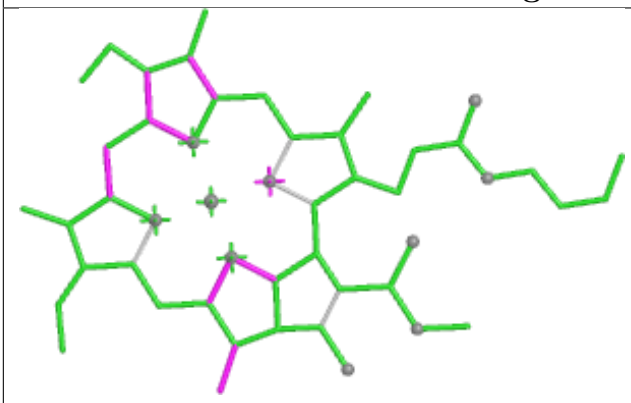
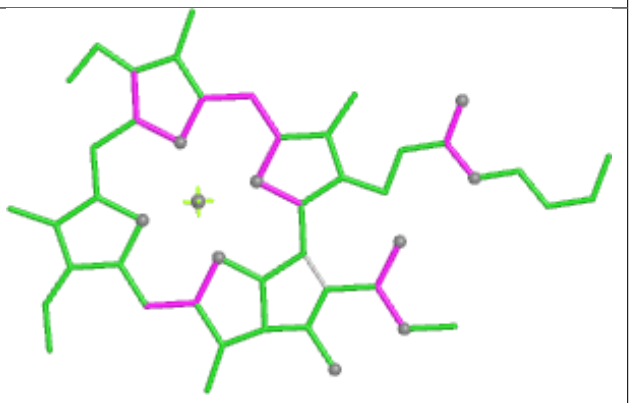
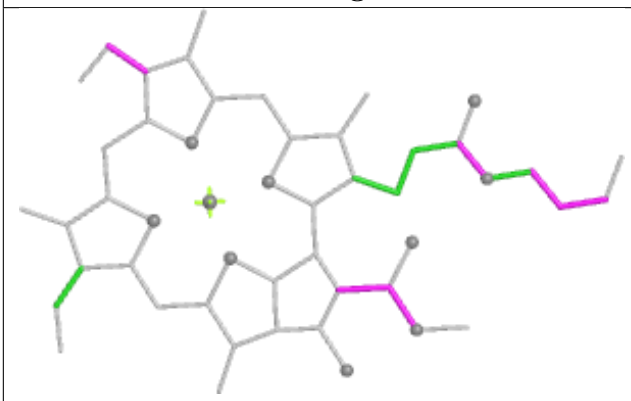
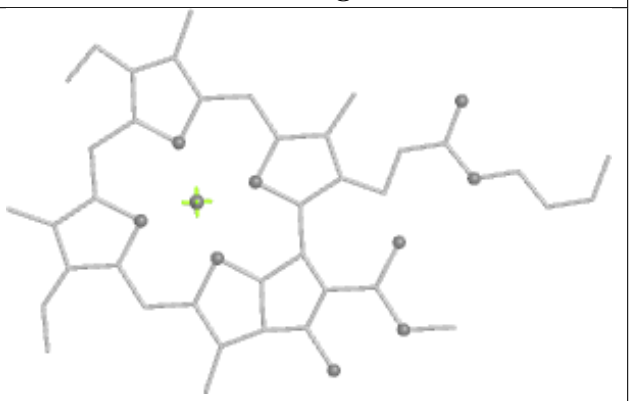
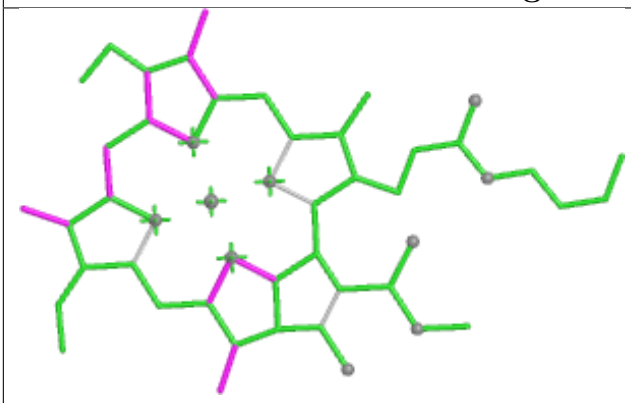
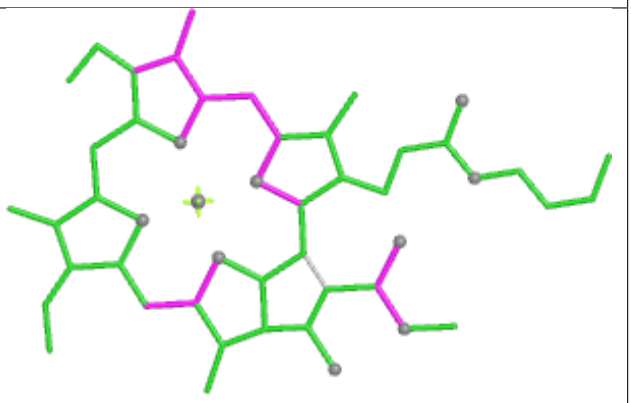
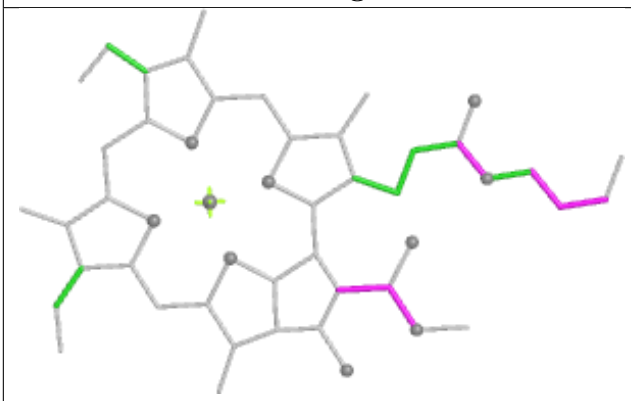
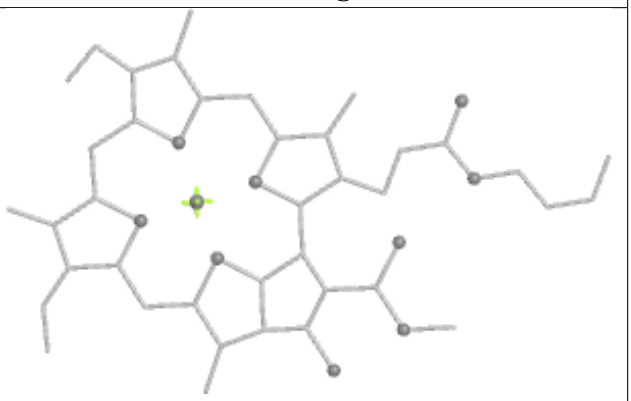
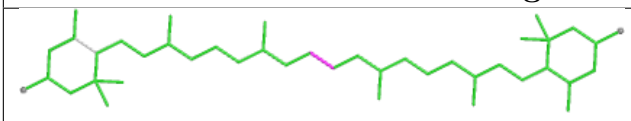
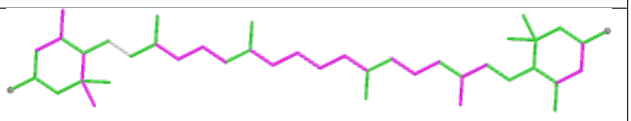
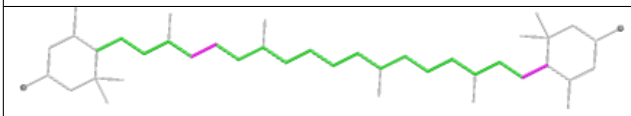
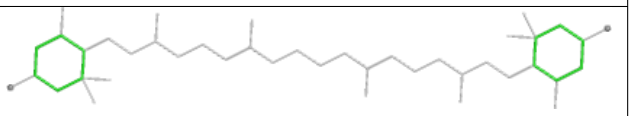
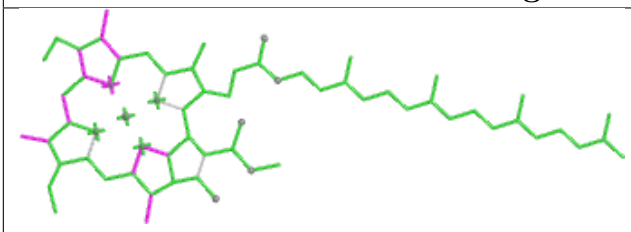
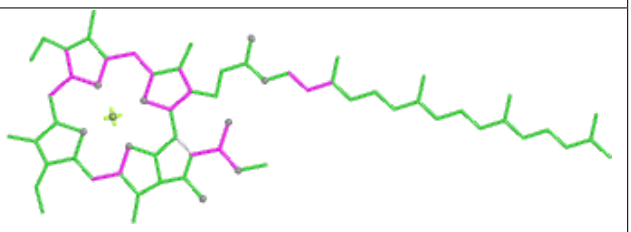
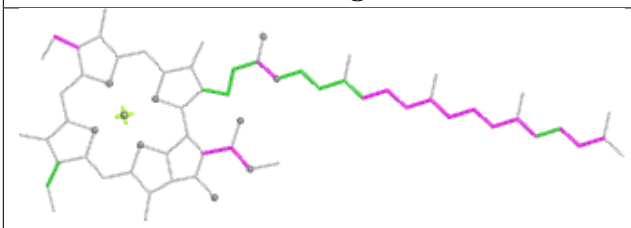
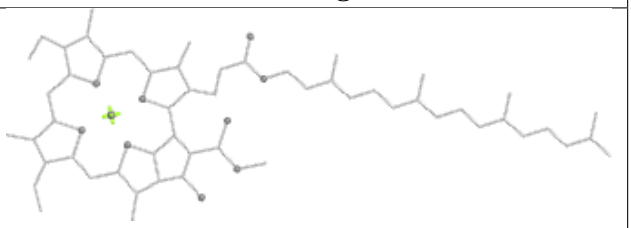
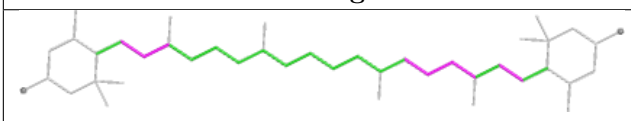
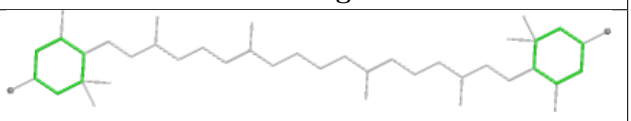
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA G 613	
 Bond lengths	 Bond angles
 Torsions	 Rings

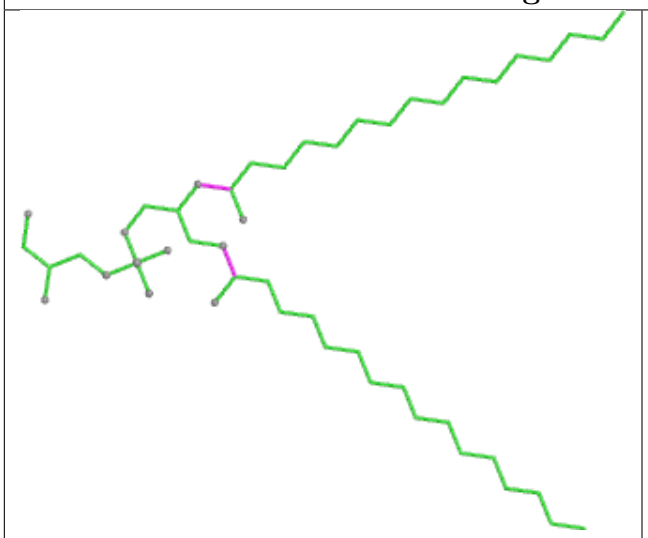
Ligand CLA N 305	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LUT N 317	
 Bond lengths	 Bond angles
 Torsions	 Rings

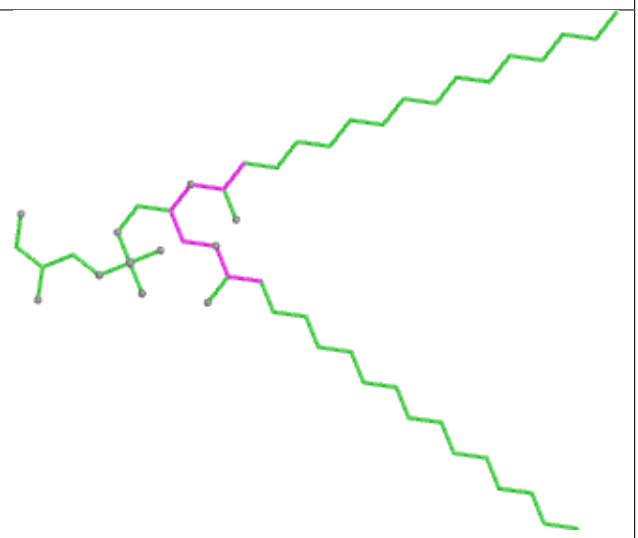
Ligand CLA G 611	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LUT G 614	
Bond lengths	Bond angles
 Torsions	 Rings

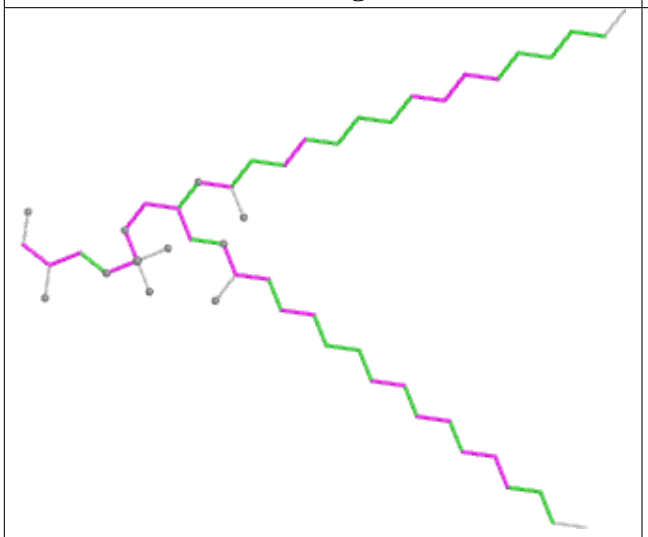
Ligand LHG N 320



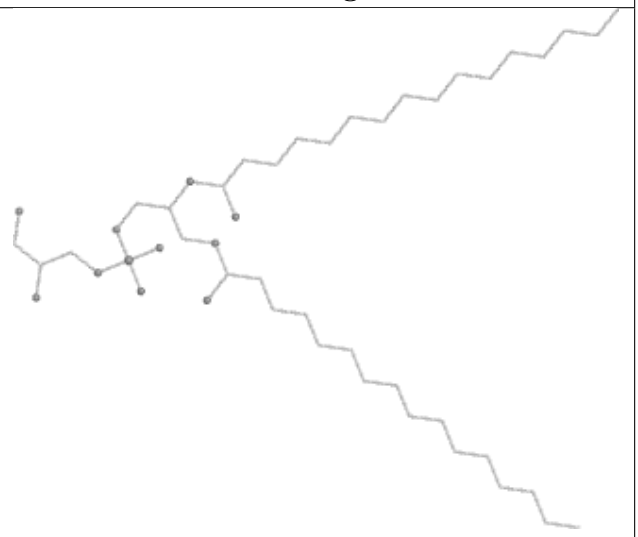
Bond lengths



Bond angles

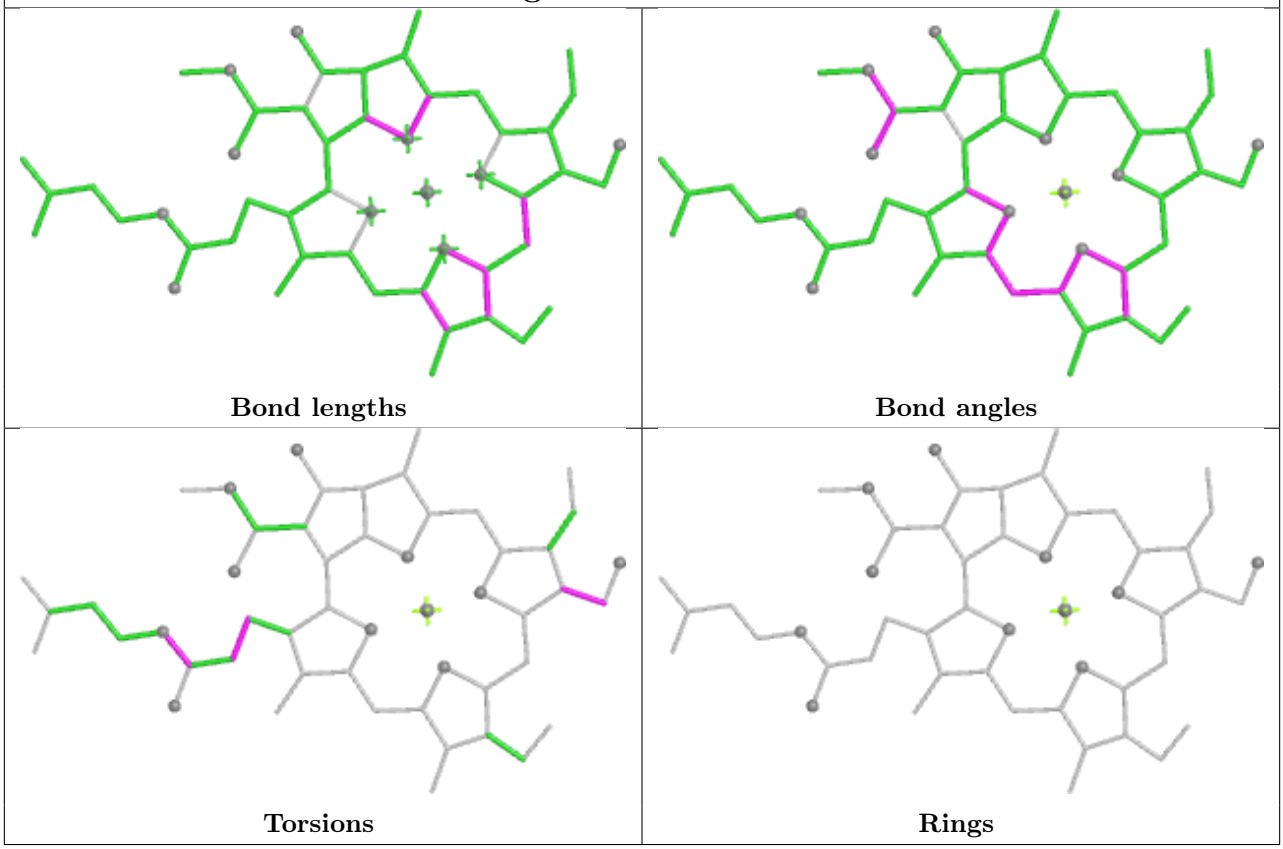


Torsions

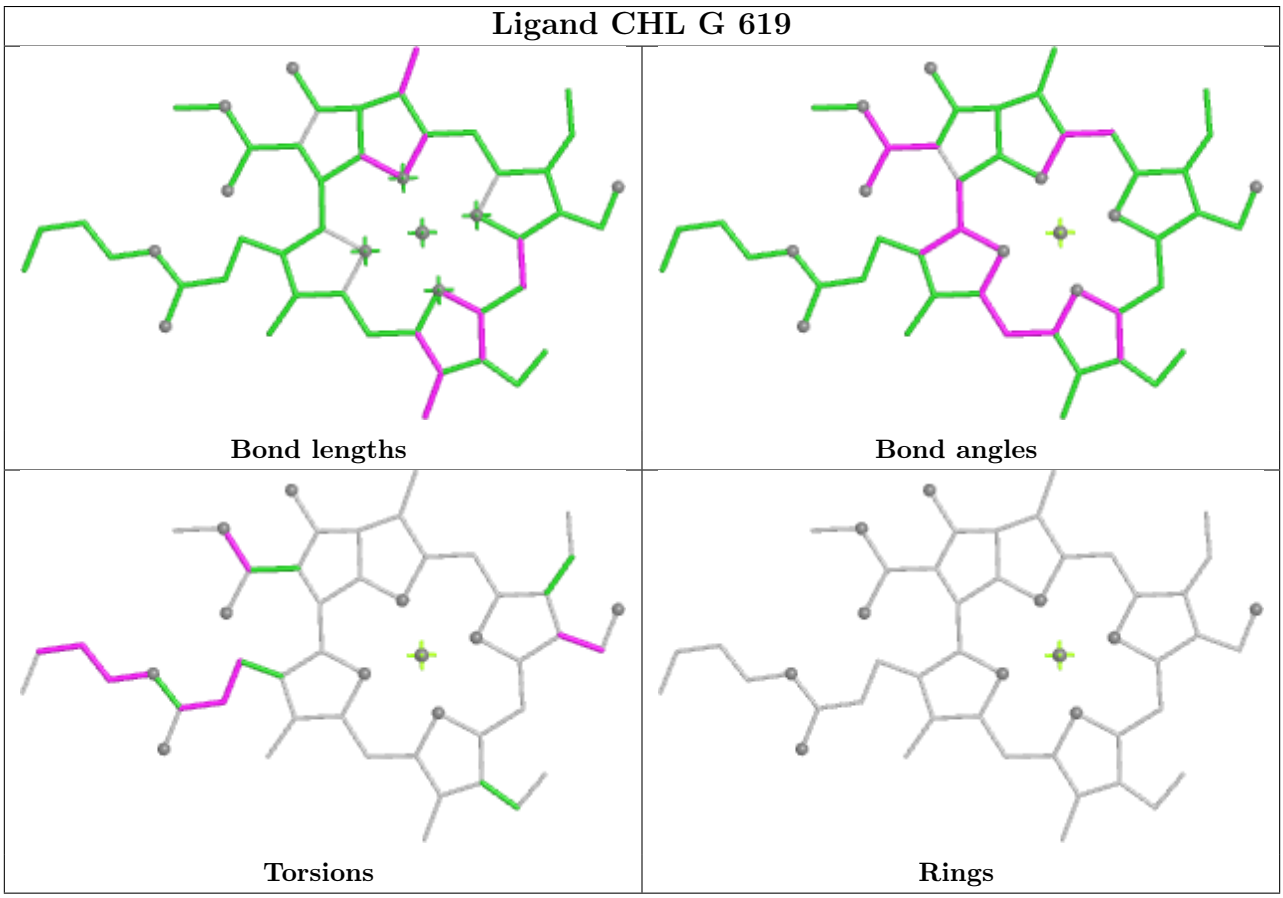


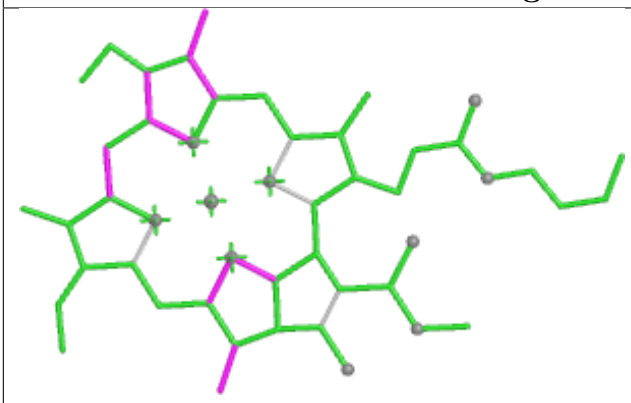
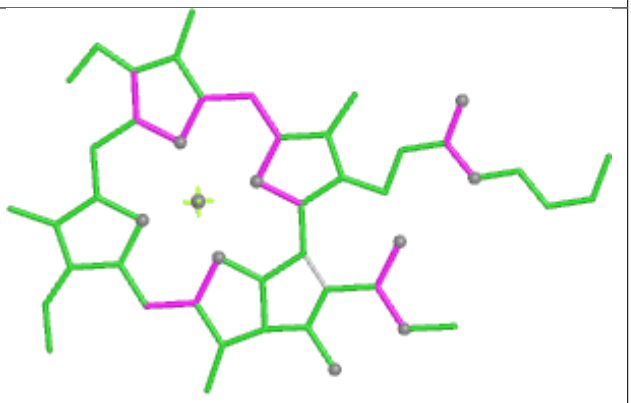
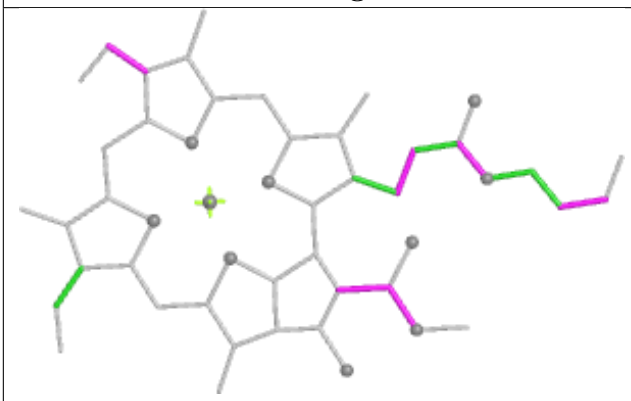
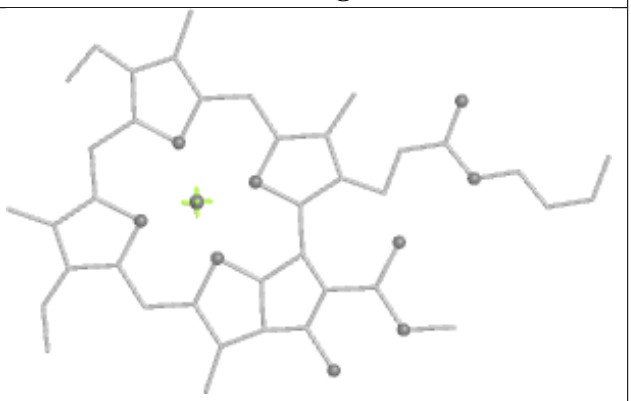
Rings

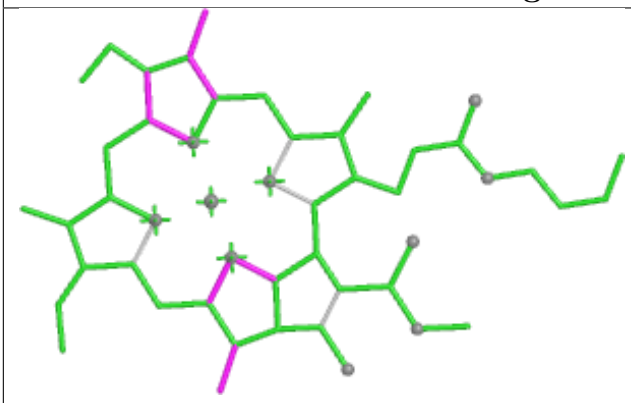
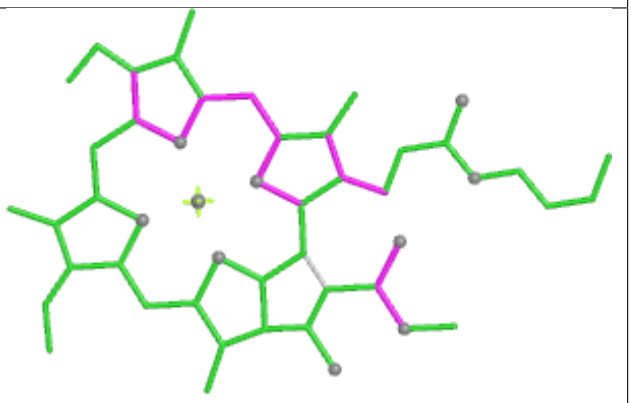
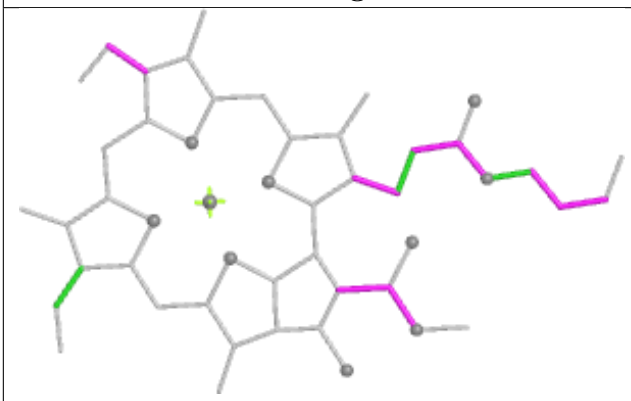
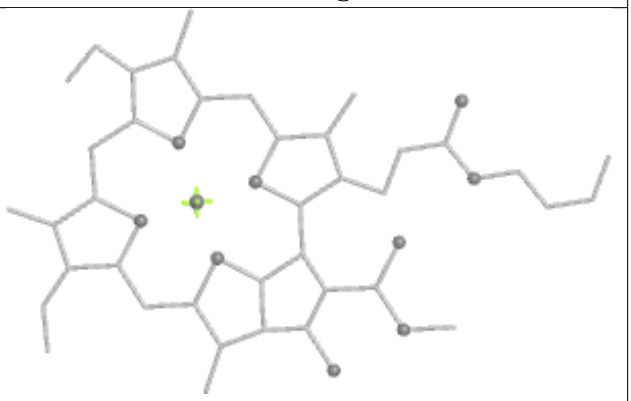
Ligand CHL N 308

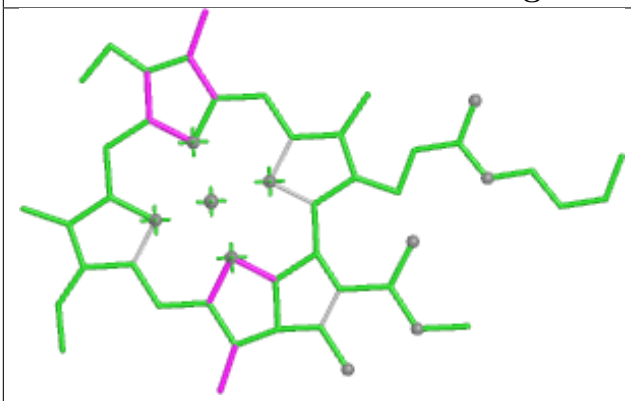
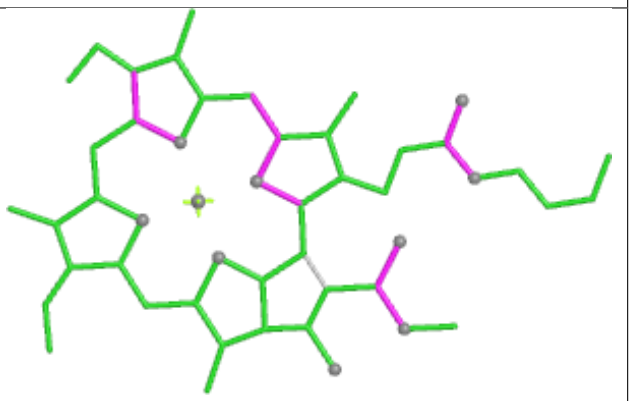
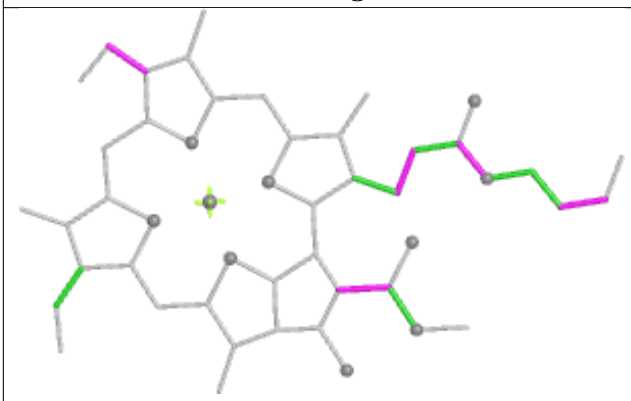
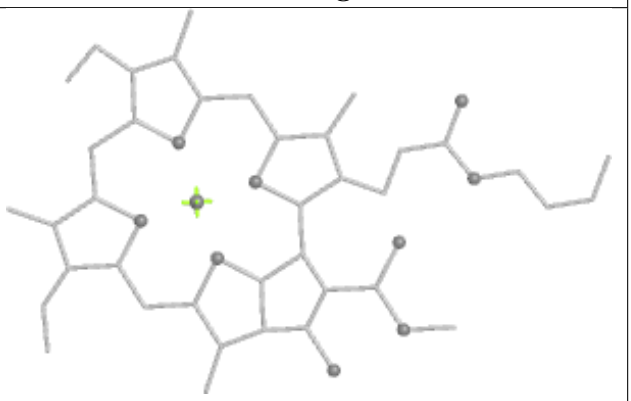


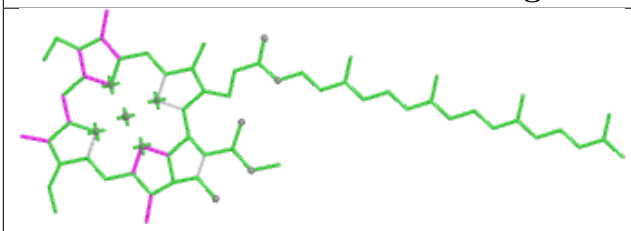
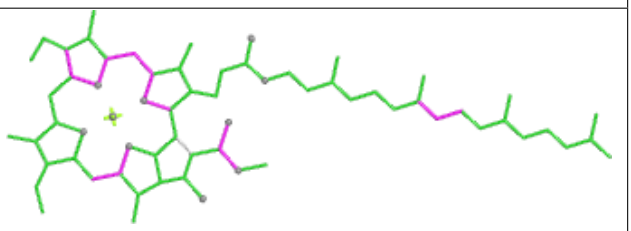
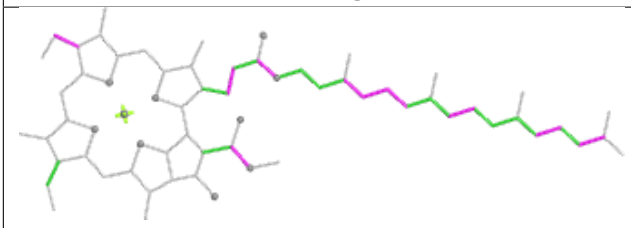
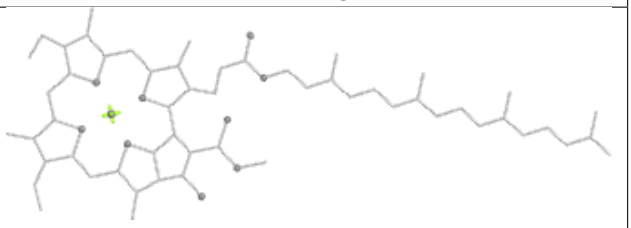
Ligand CHL G 619

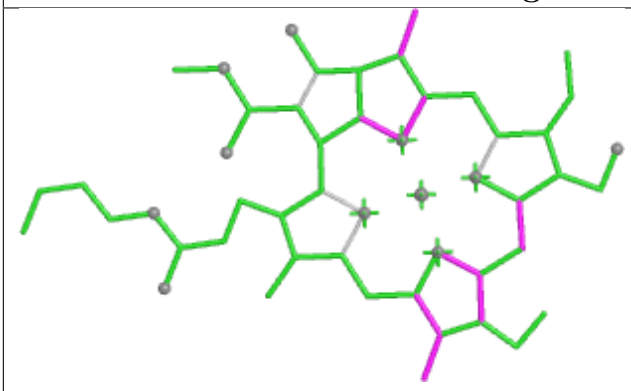
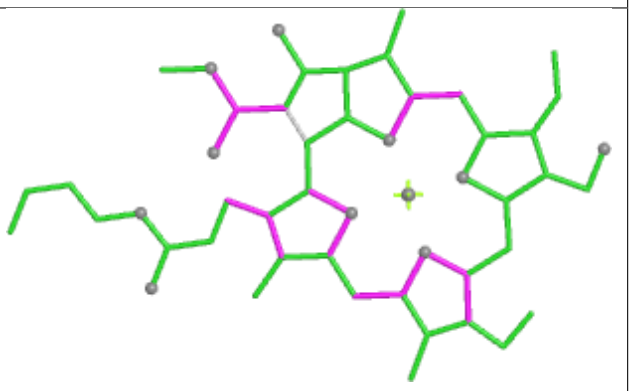
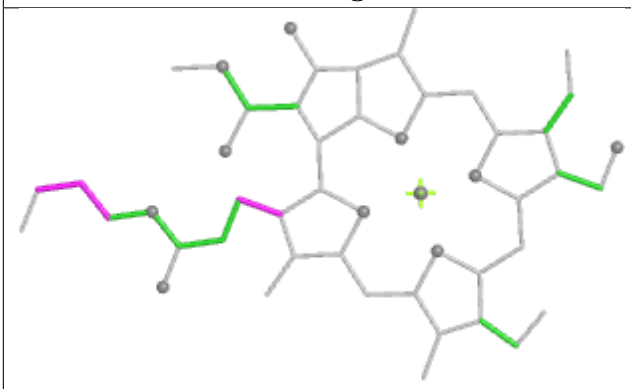
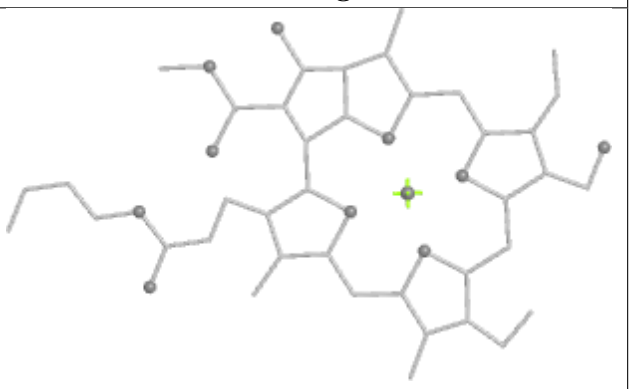


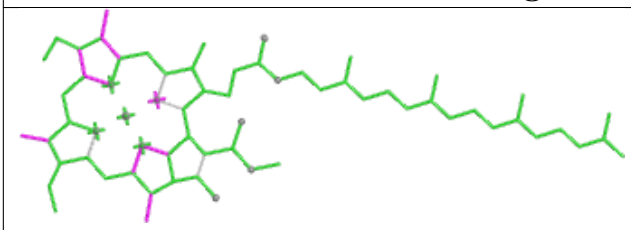
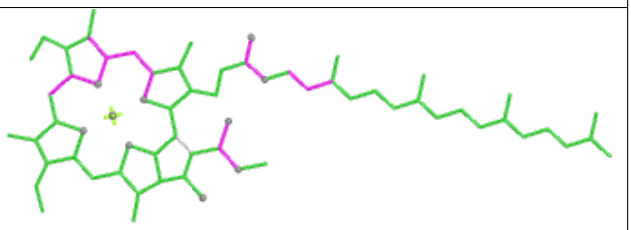
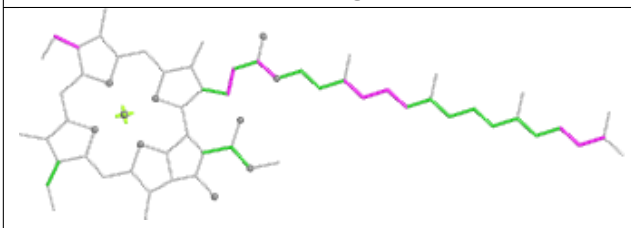
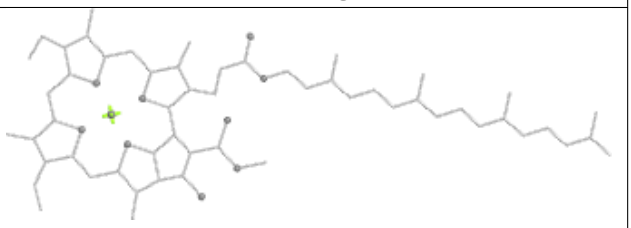
Ligand CLA G 612	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA N 304	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA N 312	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA Y 612	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CHL N 307	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA N 313	
 Bond lengths	 Bond angles
 Torsions	 Rings

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.

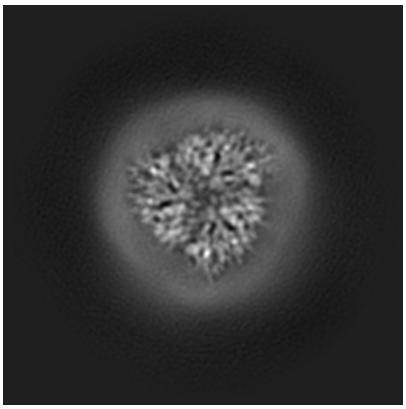
6 Map visualisation (i)

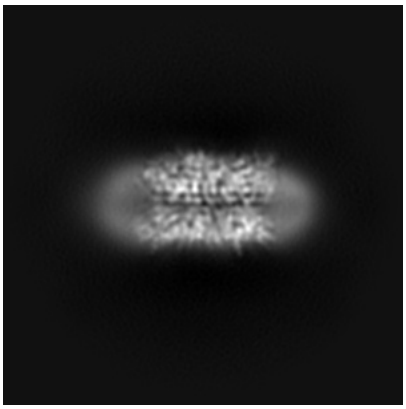
This section contains visualisations of the EMDB entry EMD-35786. These allow visual inspection of the internal detail of the map and identification of artifacts.

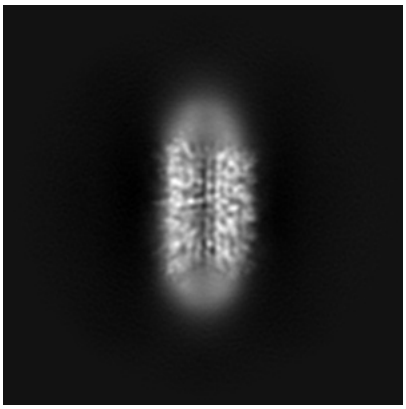
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections (i)

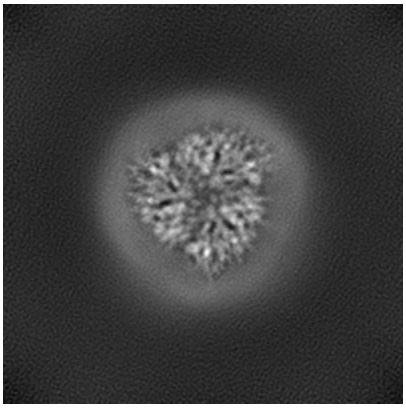
6.1.1 Primary map

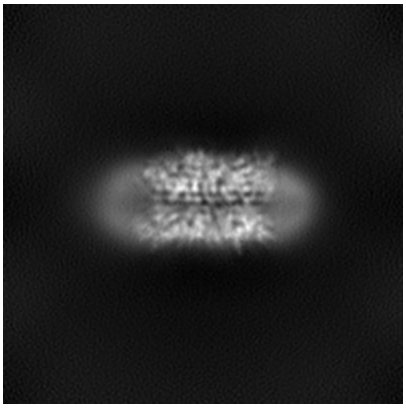

X

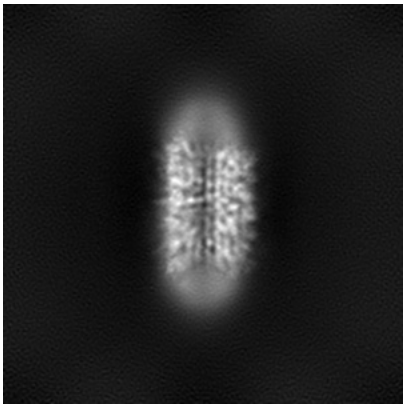

Y


Z

6.1.2 Raw map


X

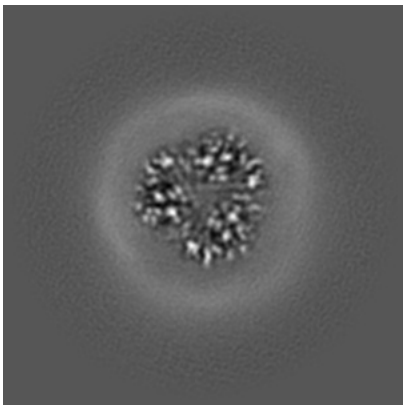

Y

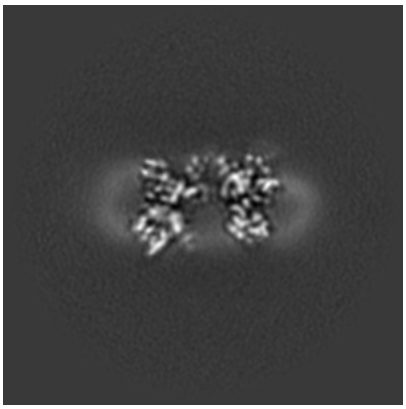

Z

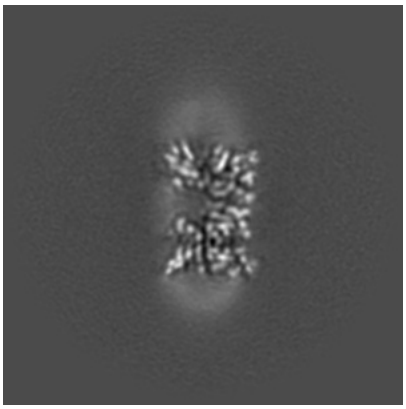
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

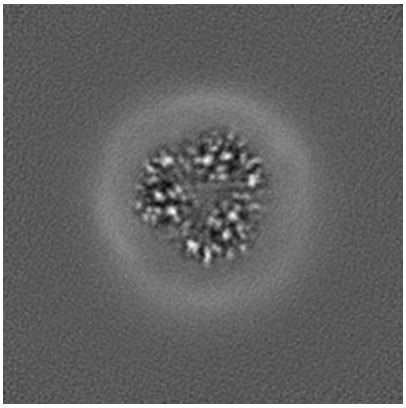
6.2.1 Primary map

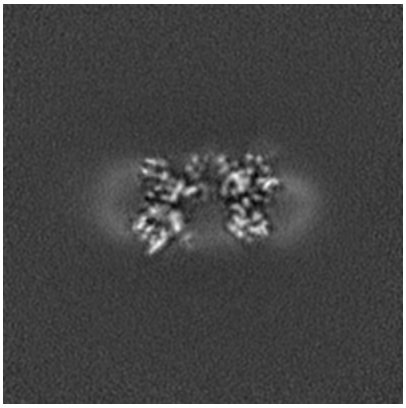

X Index: 100

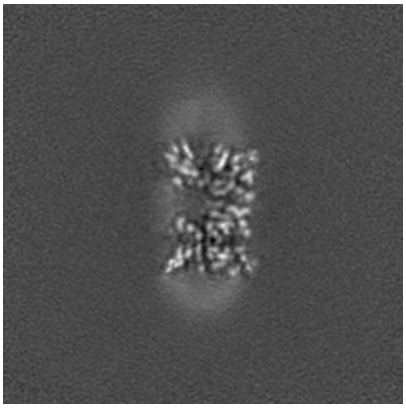

Y Index: 100


Z Index: 100

6.2.2 Raw map


X Index: 100

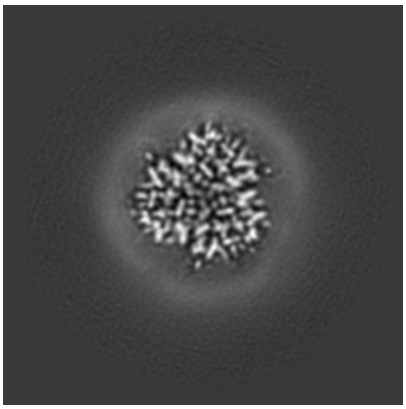

Y Index: 100


Z Index: 100

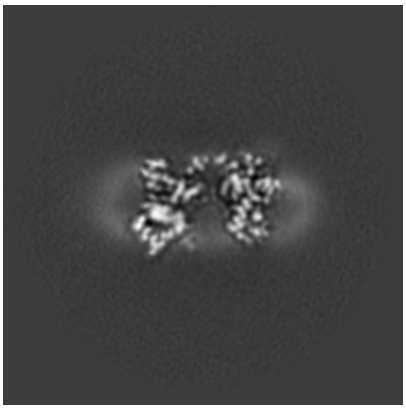
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

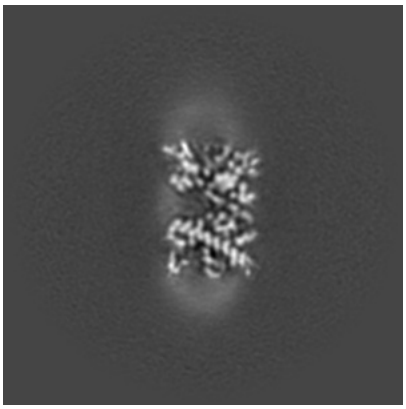
6.3.1 Primary map



X Index: 108

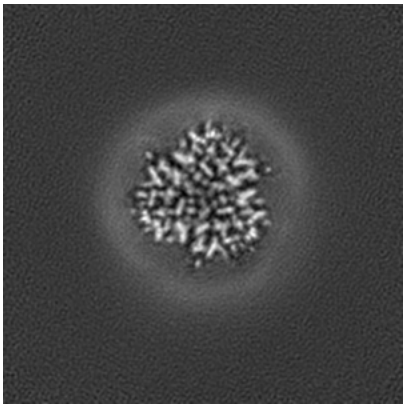


Y Index: 101

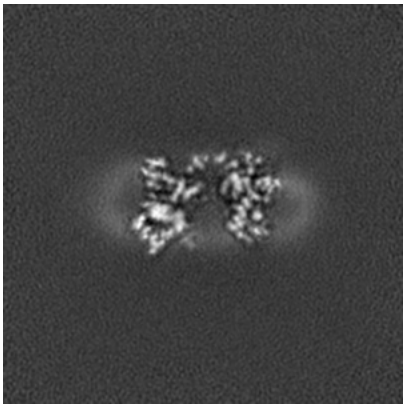


Z Index: 97

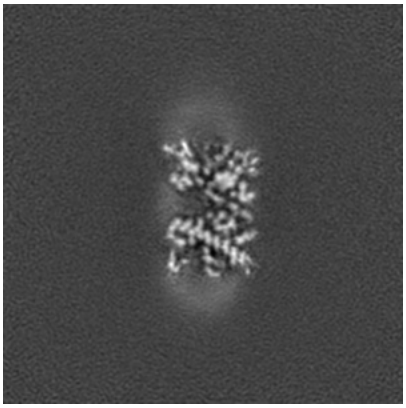
6.3.2 Raw map



X Index: 108



Y Index: 101

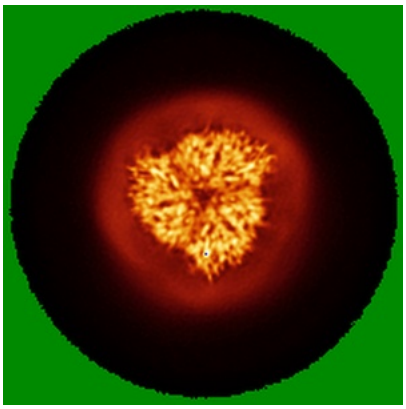


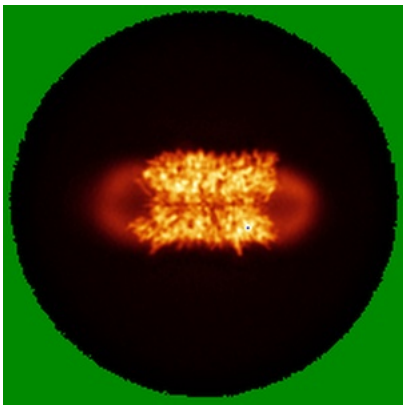
Z Index: 97

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

6.4 Orthogonal standard-deviation projections (False-color) (i)

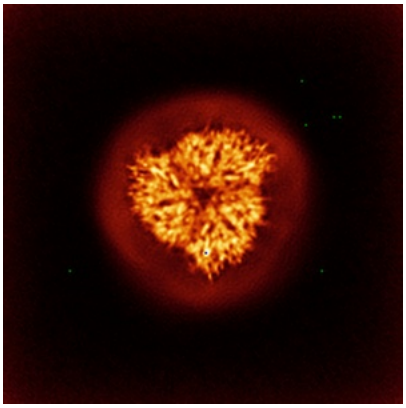
6.4.1 Primary map

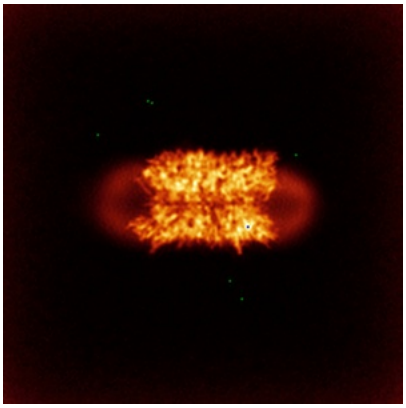

X

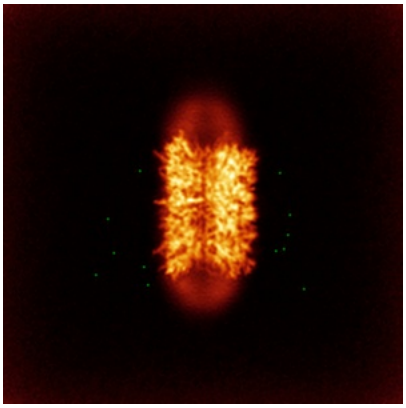

Y

Z

6.4.2 Raw map


X

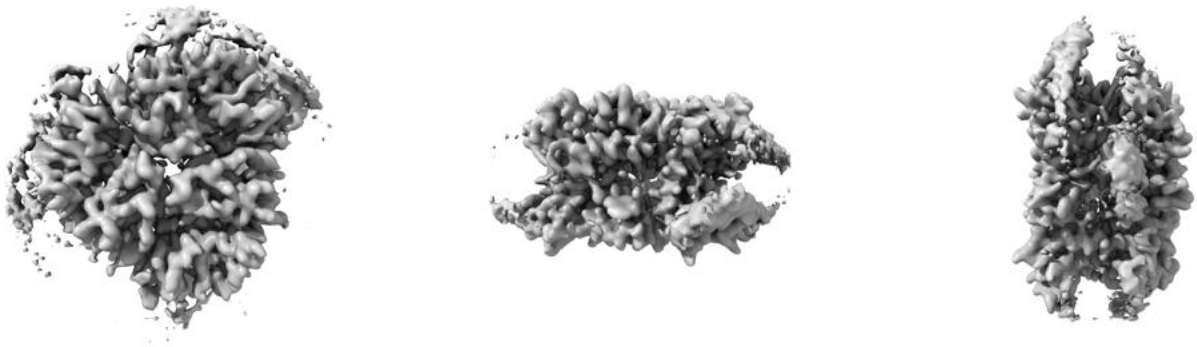

Y


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



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. 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

X Y Z

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.

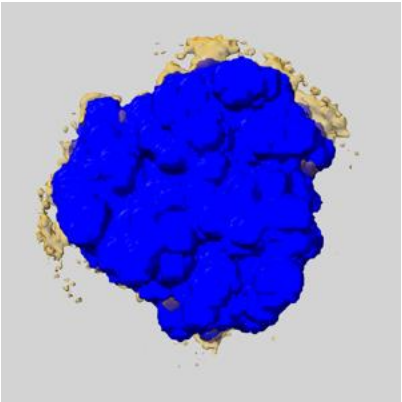
6.6 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

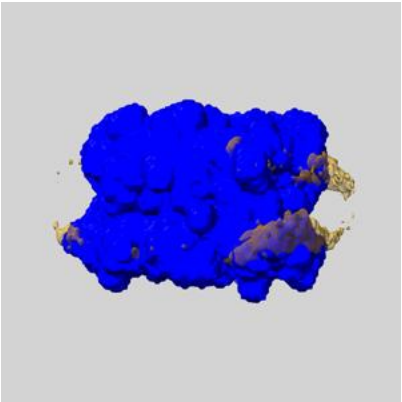
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

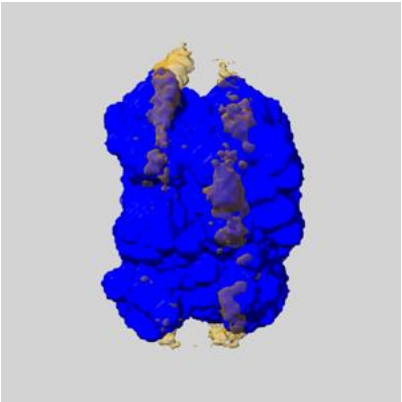
6.6.1 emd_35786_msk_1.map (i)



X



Y

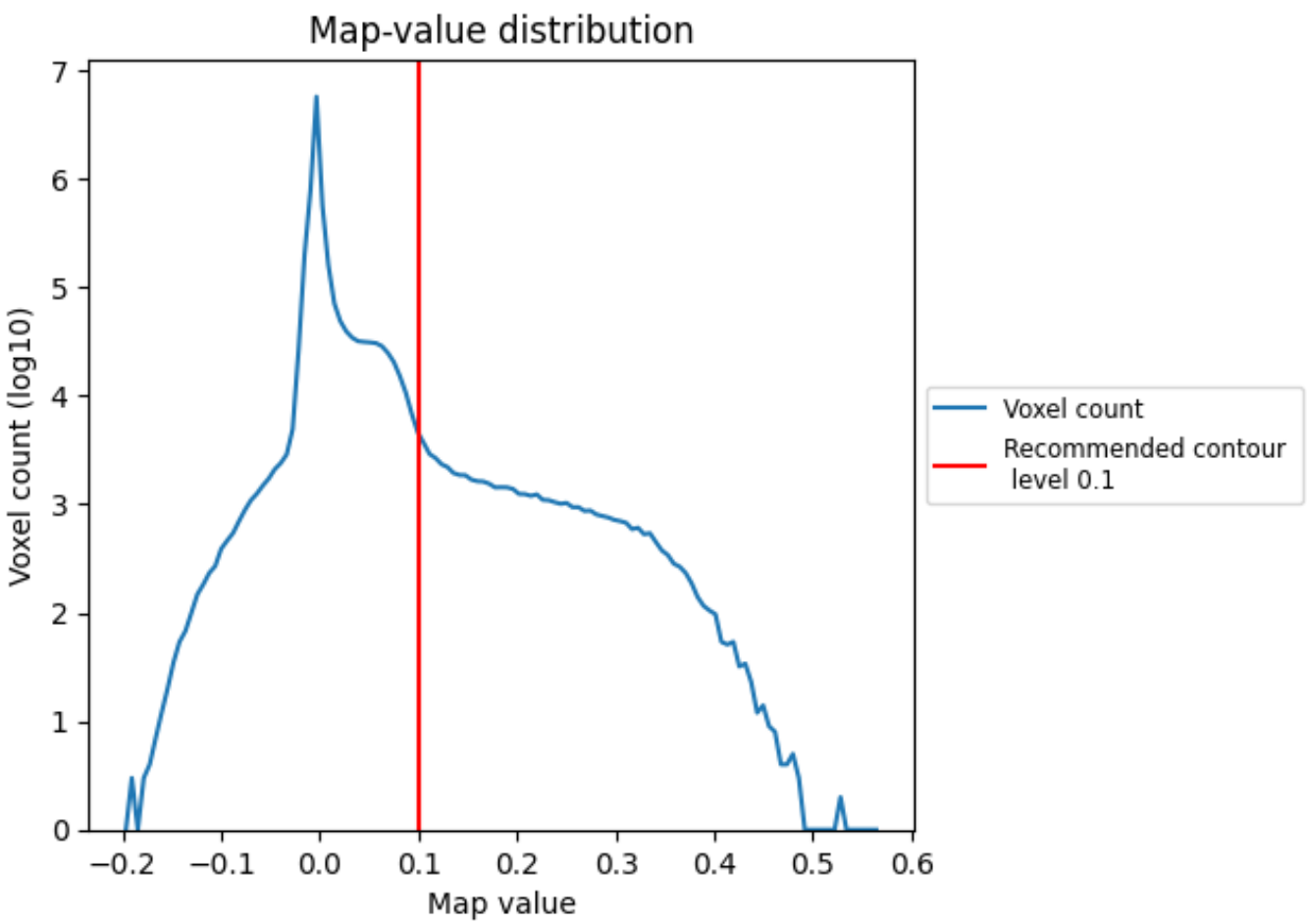


Z

7 Map analysis (i)

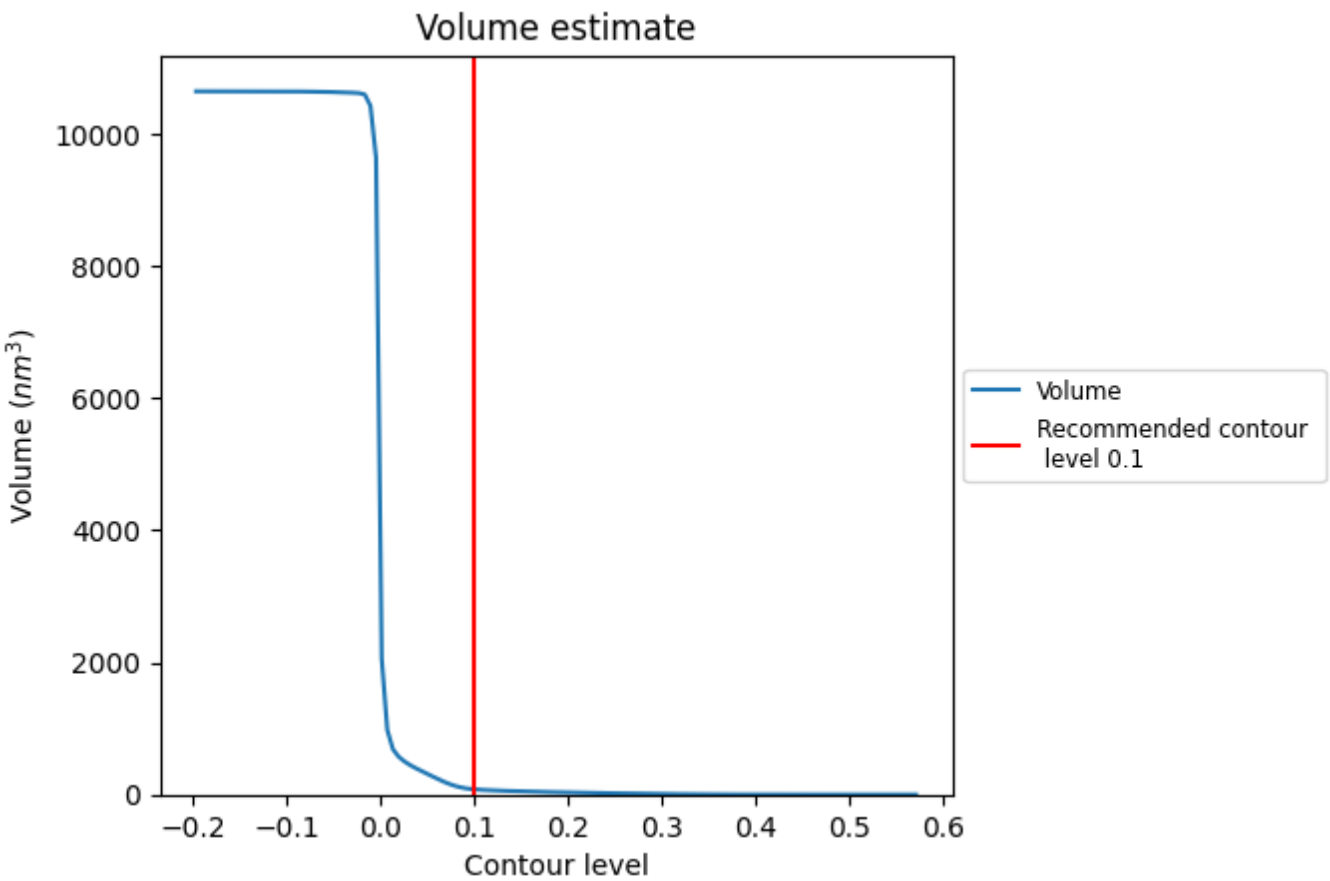
This section contains the results of statistical analysis of the map.

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.

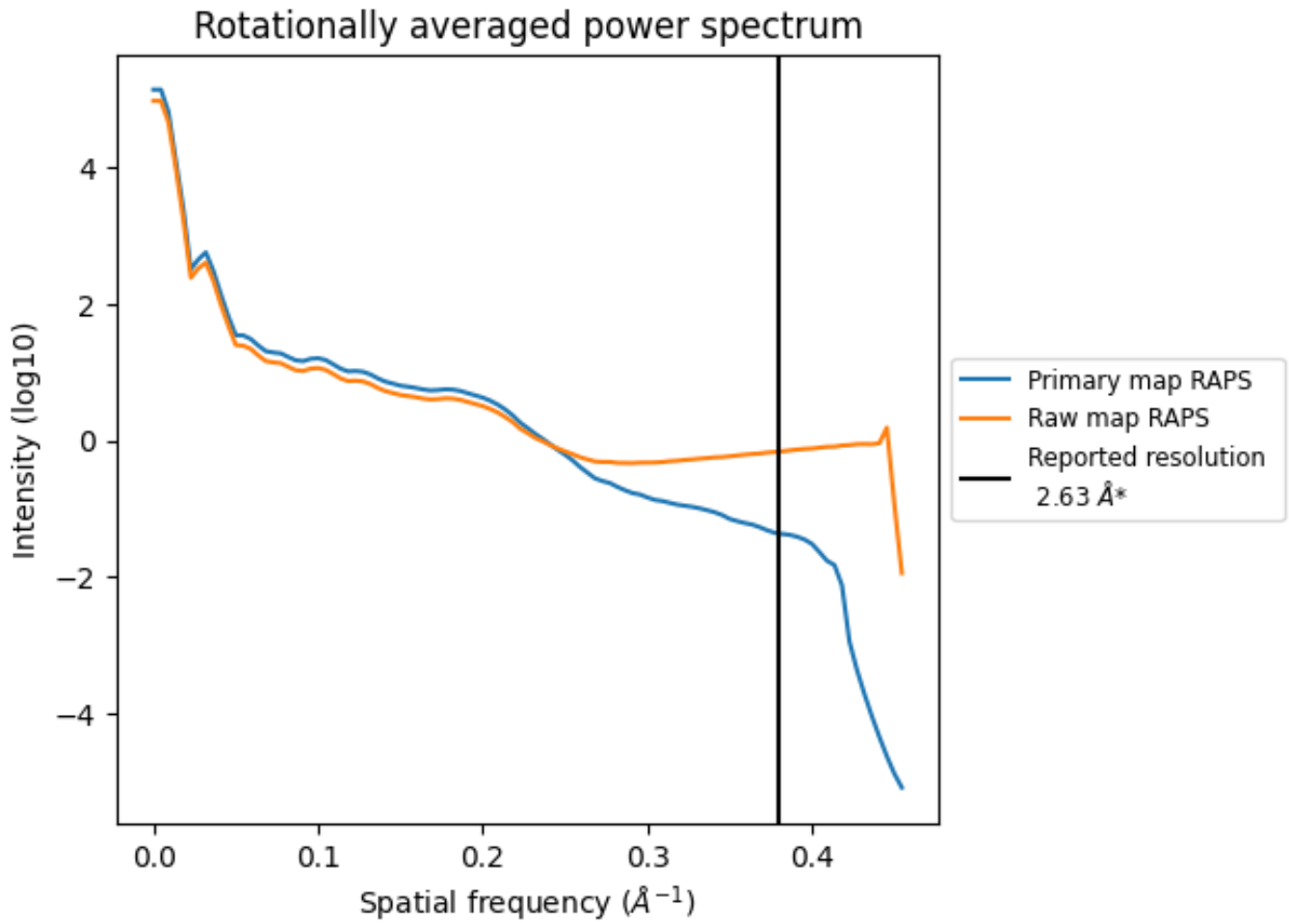
7.2 Volume estimate (i)



The volume at the recommended contour level is 79 nm^3; this corresponds to an approximate mass of 72 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 (i)

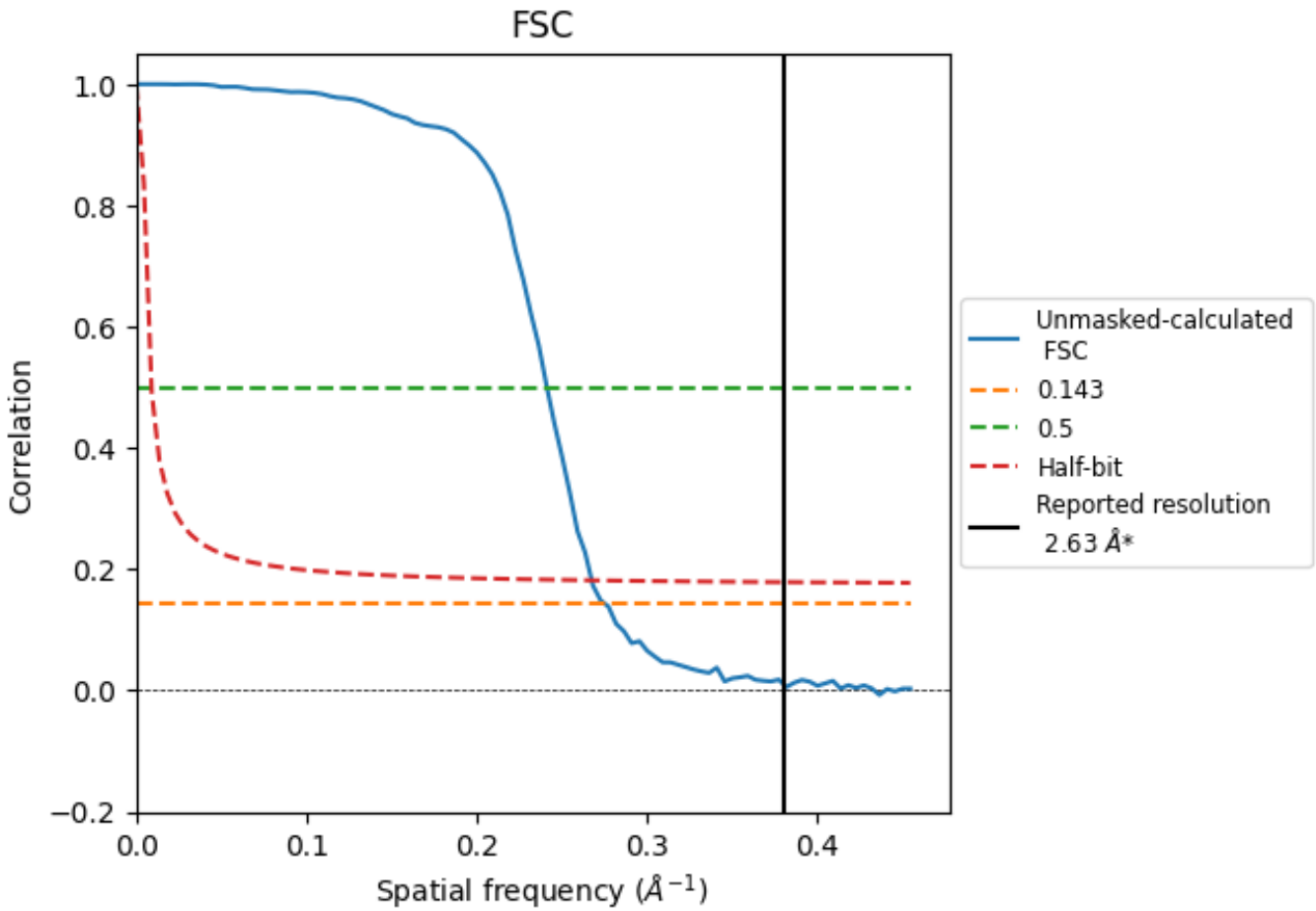


*Reported resolution corresponds to spatial frequency of 0.380 Å^{-1}

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 0.380 Å^{-1}

8.2 Resolution estimates (i)

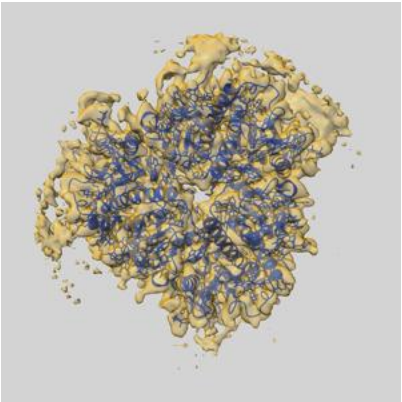
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.63	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.64	4.15	3.74

*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 3.64 differs from the reported value 2.63 by more than 10 %

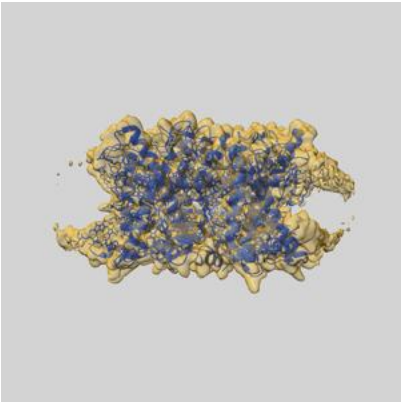
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-35786 and PDB model 8IX1. Per-residue inclusion information can be found in section 3 on page 10.

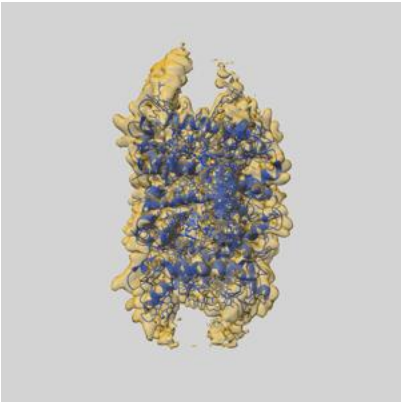
9.1 Map-model overlay (i)



X



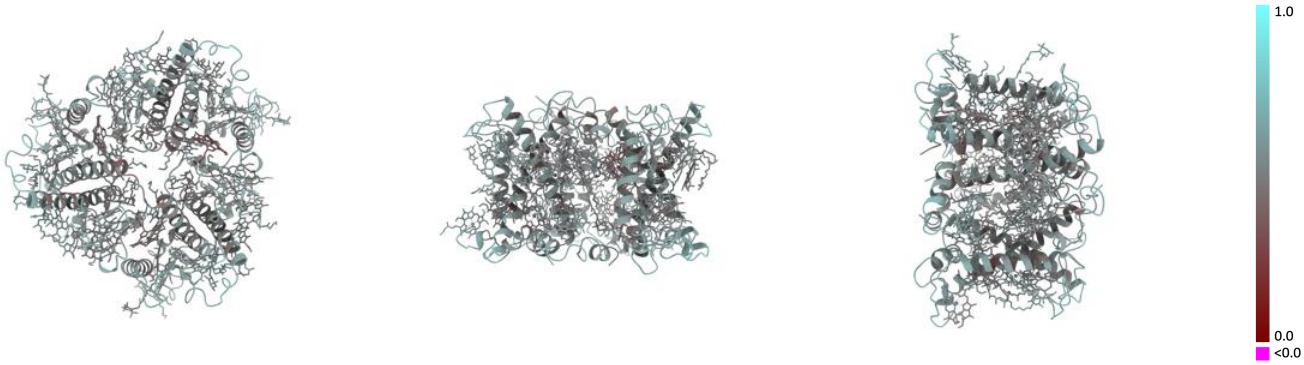
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1 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.

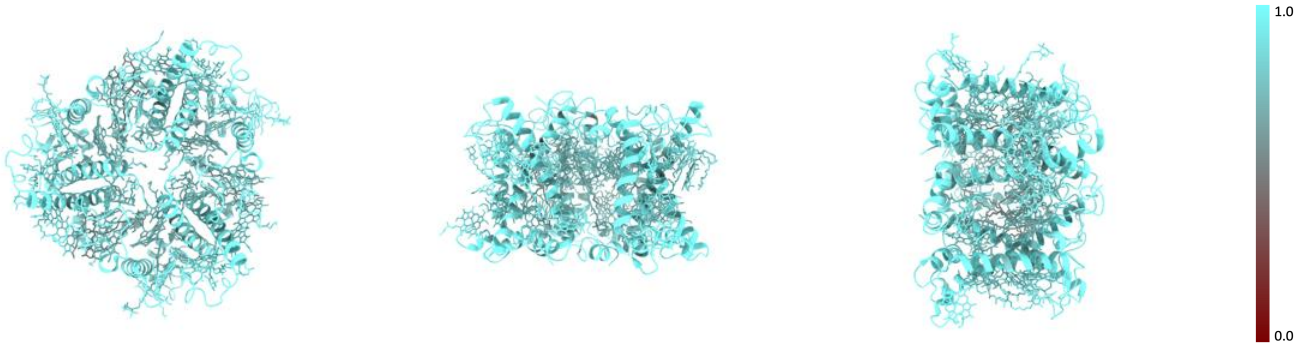
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

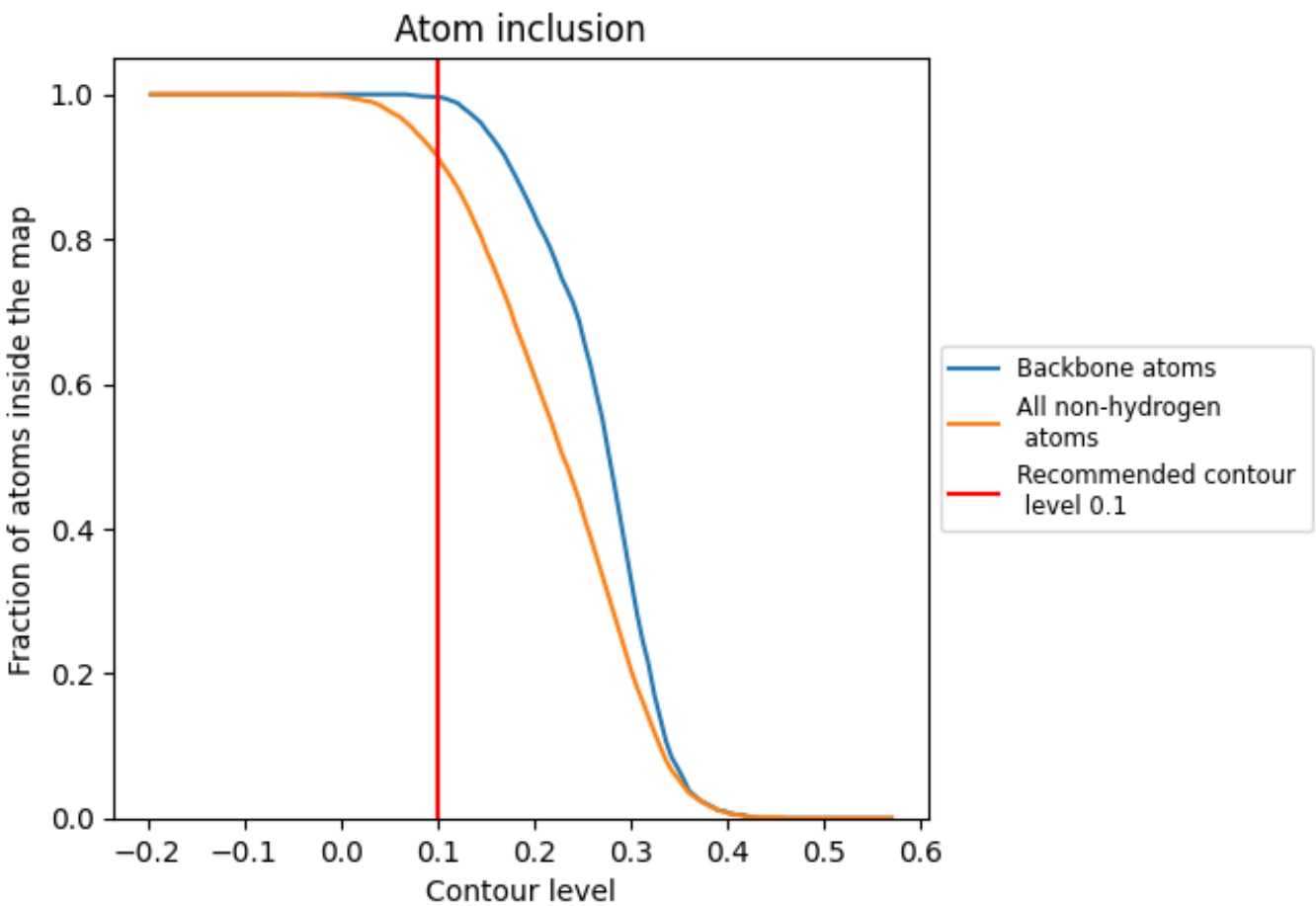
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 100% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9150	0.5260
G	0.9130	0.5280
N	0.9080	0.5190
Y	0.9230	0.5300