wwPDB EM Validation Summary Report

Aug 6, 2026 – 05:35 AM JST

PDB ID	:	6KAF / pdb_00006kaf
EMDB ID	:	EMD-9957
Title	:	C2S2M2N2-type PSII-LHCII
Authors	:	Chang, S.H.; Shen, L.L.; Huang, Z.H.; Wang, W.D.; Han, G.Y.; Shen, J.R.; Zhang, X.
Deposited on	:	2019-06-22
Resolution	:	3.73 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 ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

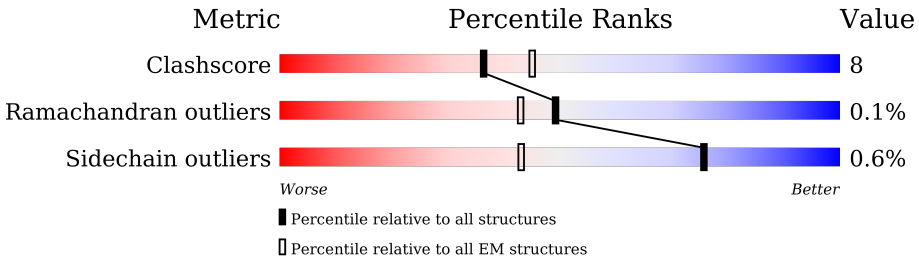
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using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

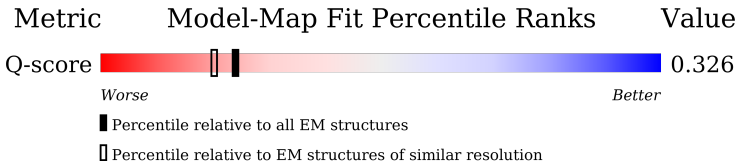
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.73 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.





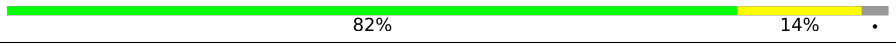
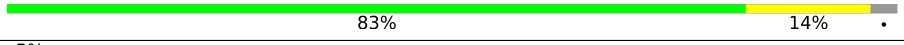
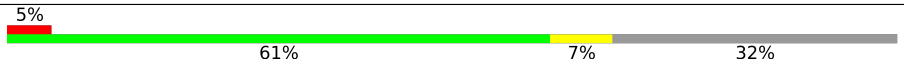
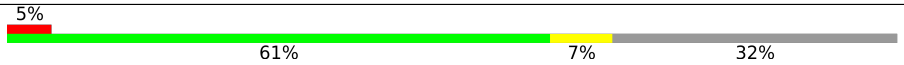
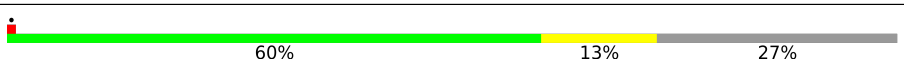
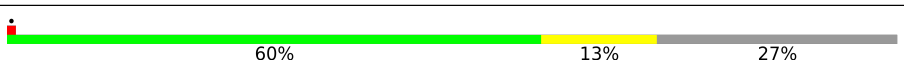
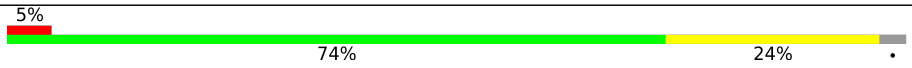
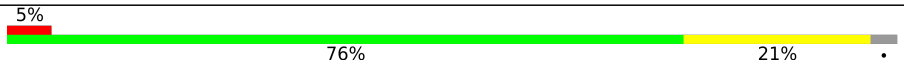
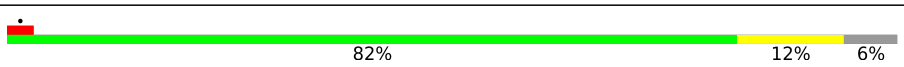
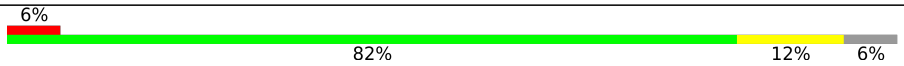
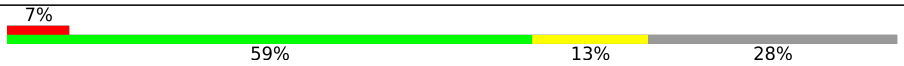
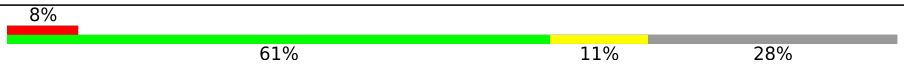
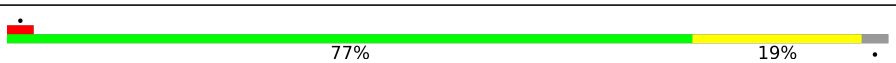
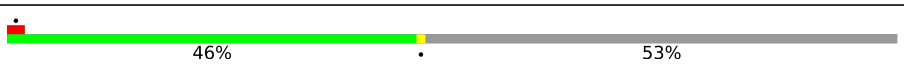
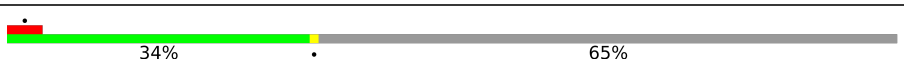
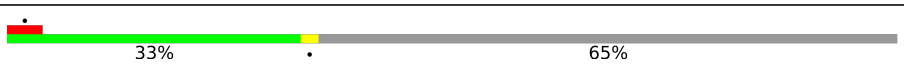
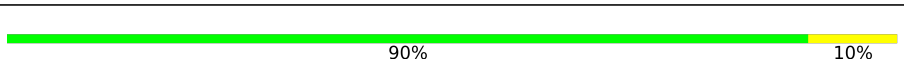
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10415 (3.23 - 4.23)

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	R	280	16% 64% 16% 20%
1	r	280	15% 64% 15% 20%
2	A	352	80% 14% 5%
2	a	352	82% 13% 5%

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Mol	Chain	Length	Quality of chain
3	D	352	
3	d	352	
4	F	44	
4	f	44	
5	H	88	
5	h	88	
6	I	37	
6	i	37	
7	J	50	
7	j	50	
8	K	46	
8	k	46	
9	L	38	
9	l	38	
10	M	34	
10	m	34	
11	O	291	
11	o	291	
12	T	31	
12	t	31	
13	W	115	
13	w	115	
14	X	101	
14	x	101	
15	Z	62	

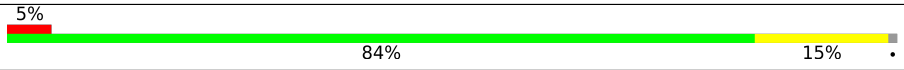
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Mol	Chain	Length	Quality of chain
15	z	62	85% 15%
16	Y	33	9% 85% 6% 9%
16	y	33	9% 85% 6% 9%
17	E	82	72% 11% 17%
17	e	82	72% 11% 17%
18	1	257	30% 73% 12% 15%
18	2	257	63% 74% 10% 15%
18	3	257	58% 73% 12% 15%
18	4	257	30% 68% 16% 15%
18	5	257	63% 72% 12% 15%
18	6	257	57% 73% 12% 15%
18	G	257	6% 70% 15% 15%
18	N	257	73% 11% 16%
18	P	257	61% 72% 12% 15%
18	Q	257	80% 72% 13% 15%
18	U	257	67% 17% 15%
18	V	257	69% 70% 14% 15%
18	g	257	7% 73% 11% 15%
18	n	257	76% 9% 15%
18	p	257	60% 71% 12% 15%
18	q	257	80% 72% 13% 15%
18	u	257	65% 20% 15%
18	v	257	68% 73% 12% 15%
19	S	289	68% 13% 18%
19	s	289	69% 12% 18%

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Mol	Chain	Length	Quality of chain
20	C	461	
20	c	461	
21	B	508	
21	b	508	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
29	CL	A	402	-	-	X	-
29	CL	a	402	-	-	X	-
29	CL	a	403	-	-	X	-

2 Entry composition (i)

There are 37 unique types of molecules in this entry. The entry contains 104363 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 CP29.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	r	223	Total	C	N	O	S	0	0
			1701	1081	286	329	5		
1	R	223	Total	C	N	O	S	0	0
			1698	1080	285	328	5		

- Molecule 2 is a protein called Photosystem II protein D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	a	333	Total	C	N	O	S	0	0
			2614	1707	430	462	15		
2	A	333	Total	C	N	O	S	0	0
			2614	1707	430	462	15		

- Molecule 3 is a protein called Photosystem II D2 protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	341	Total	C	N	O	S	0	0
			2714	1791	447	464	12		
3	D	341	Total	C	N	O	S	0	0
			2714	1791	447	464	12		

- Molecule 4 is a protein called Cytochrome b559 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	f	30	Total	C	N	O	S	0	0
			243	165	41	36	1		
4	F	30	Total	C	N	O	S	0	0
			243	165	41	36	1		

- Molecule 5 is a protein called Photosystem II reaction center protein H.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	h	64	Total 488	C 327	N 72	O 87	S 2	0	0
5	H	64	Total 488	C 327	N 72	O 87	S 2	0	0

- Molecule 6 is a protein called Photosystem II reaction center protein I.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	i	34	Total 275	C 189	N 41	O 43	S 2	0	0
6	I	34	Total 275	C 189	N 41	O 43	S 2	0	0

- Molecule 7 is a protein called Photosystem II reaction center protein J, PsbJ.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	j	31	Total 245	C 168	N 36	O 39	S 2	0	0
7	J	31	Total 245	C 168	N 36	O 39	S 2	0	0

- Molecule 8 is a protein called Photosystem II reaction center protein K.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	k	36	Total 288	C 203	N 41	O 44	0	0
8	K	36	Total 288	C 203	N 41	O 44	0	0

- Molecule 9 is a protein called Photosystem II reaction center protein L.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	l	37	Total 306	C 205	N 50	O 51	0	0
9	L	37	Total 306	C 205	N 50	O 51	0	0

- Molecule 10 is a protein called Photosystem II reaction center protein M.

Mol	Chain	Residues	Atoms				AltConf	Trace
10	m	32	Total 248	C 168	N 35	O 45	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace
10	M	32	Total 248	C 168	N 35	O 45	0	0

- Molecule 11 is a protein called Oxygen-evolving enhancer protein 1 of photosystem II.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	o	210	Total 1592	C 1016	N 254	O 318	S 4	0	0
11	O	210	Total 1592	C 1016	N 254	O 318	S 4	0	0

- Molecule 12 is a protein called Photosystem II reaction center protein T.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	t	30	Total 247	C 171	N 36	O 38	S 2	0	0
12	T	30	Total 247	C 171	N 36	O 38	S 2	0	0

- Molecule 13 is a protein called Photosystem II reaction center W protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	w	54	Total 417	C 269	N 67	O 79	S 2	0	0
13	W	54	Total 417	C 269	N 67	O 79	S 2	0	0

- Molecule 14 is a protein called 4.1 kDa photosystem II subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	x	35	Total 242	C 159	N 39	O 44	0	0
14	X	35	Total 242	C 159	N 39	O 44	0	0

- Molecule 15 is a protein called Photosystem II reaction center protein Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	z	62	Total 465	C 319	N 69	O 76	S 1	0	0
15	Z	62	Total 465	C 319	N 69	O 76	S 1	0	0

- Molecule 16 is a protein called Photosystem II reaction center protein 30, Psb30.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	Y	30	Total 208	C 137	N 34	O 37	0	0
16	y	30	Total 208	C 137	N 34	O 37	0	0

- Molecule 17 is a protein called Cytochrome b559 subunit alpha.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	E	68	Total 555	C 366	N 90	O 99	0	0
17	e	68	Total 555	C 366	N 90	O 99	0	0

- Molecule 18 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	1	218	Total 1669	C 1081	N 271	O 312	S 5	0	0
18	2	218	Total 1669	C 1081	N 271	O 312	S 5	0	0
18	3	219	Total 1675	C 1084	N 272	O 314	S 5	0	0
18	4	218	Total 1669	C 1081	N 271	O 312	S 5	0	0
18	5	218	Total 1669	C 1081	N 271	O 312	S 5	0	0
18	6	219	Total 1675	C 1084	N 272	O 314	S 5	0	0
18	v	218	Total 1669	C 1081	N 271	O 312	S 5	0	0
18	p	218	Total 1669	C 1081	N 271	O 312	S 5	0	0
18	q	219	Total 1675	C 1084	N 272	O 314	S 5	0	0
18	V	218	Total 1669	C 1081	N 271	O 312	S 5	0	0
18	P	218	Total 1669	C 1081	N 271	O 312	S 5	0	0
18	Q	219	Total 1675	C 1084	N 272	O 314	S 5	0	0
18	U	218	Total 1669	C 1081	N 271	O 312	S 5	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	217	Total	C	N	O	S	0	0
			1661	1075	270	311	5		
18	G	219	Total	C	N	O	S	0	0
			1675	1084	272	314	5		
18	u	218	Total	C	N	O	S	0	0
			1669	1081	271	312	5		
18	n	218	Total	C	N	O	S	0	0
			1669	1081	271	312	5		
18	g	219	Total	C	N	O	S	0	0
			1675	1084	272	314	5		

- Molecule 19 is a protein called Chlorophyll a-b binding protein, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	236	Total	C	N	O	S	0	0
			1797	1166	290	337	4		
19	s	236	Total	C	N	O	S	0	0
			1797	1166	290	337	4		

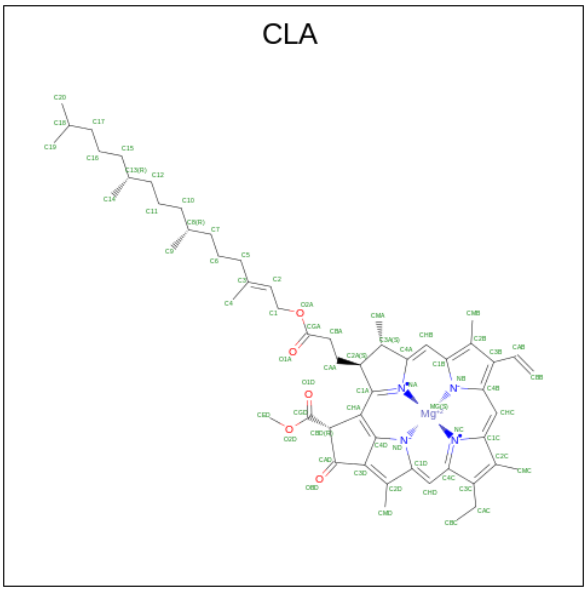
- Molecule 20 is a protein called Photosystem II CP43 reaction center protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	C	450	Total	C	N	O	S	0	0
			3502	2290	585	610	17		
20	c	450	Total	C	N	O	S	0	0
			3502	2290	585	610	17		

- Molecule 21 is a protein called Photosystem II CP47 reaction center protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	B	503	Total	C	N	O	S	0	0
			3937	2575	658	692	12		
21	b	503	Total	C	N	O	S	0	0
			3937	2575	658	692	12		

- Molecule 22 is CHLOROPHYLL A (CCD ID: CLA) (formula: $C_{55}H_{72}MgN_4O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
22	r	1	Total 49	C 39	Mg 1	N 4	O 5	0
22	r	1	Total 60	C 50	Mg 1	N 4	O 5	0
22	r	1	Total 60	C 50	Mg 1	N 4	O 5	0
22	r	1	Total 48	C 38	Mg 1	N 4	O 5	0
22	r	1	Total 58	C 48	Mg 1	N 4	O 5	0
22	r	1	Total 65	C 55	Mg 1	N 4	O 5	0
22	r	1	Total 49	C 39	Mg 1	N 4	O 5	0
22	r	1	Total 49	C 39	Mg 1	N 4	O 5	0
22	r	1	Total 60	C 50	Mg 1	N 4	O 5	0
22	r	1	Total 45	C 35	Mg 1	N 4	O 5	0
22	a	1	Total 65	C 55	Mg 1	N 4	O 5	0
22	a	1	Total 65	C 55	Mg 1	N 4	O 5	0
22	a	1	Total 50	C 40	Mg 1	N 4	O 5	0
22	a	1	Total 60	C 50	Mg 1	N 4	O 5	0

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Mol	Chain	Residues	Atoms					AltConf
22	d	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	x	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	A	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	A	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	A	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	A	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	1	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	1	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	1	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	1	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	1	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	1	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	1	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	1	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	2	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	2	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	2	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	2	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	2	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	2	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	2	1	Total	C	Mg	N	O	0
			60	50	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	2	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	3	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	3	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	3	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	3	1	Total	C	Mg	N	O	0
			64	54	1	4	5	
22	3	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	3	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	3	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	3	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	4	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	4	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	4	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	4	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	4	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	4	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	4	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	4	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	5	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	5	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	5	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	5	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	5	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	5	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	5	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	5	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	6	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	6	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	6	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	6	1	Total	C	Mg	N	O	0
			64	54	1	4	5	
22	6	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	6	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	6	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	6	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	v	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	v	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	v	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	v	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	v	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	v	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	v	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	v	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	p	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	p	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	p	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	p	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	p	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	p	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	p	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	p	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	q	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	q	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	q	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	q	1	Total	C	Mg	N	O	0
			64	54	1	4	5	
22	q	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	q	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	q	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	q	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	V	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	V	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	V	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	V	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	V	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	V	1	Total	C	Mg	N	O	0
			60	50	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	V	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	V	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	P	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	P	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	P	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	P	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	P	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	P	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	P	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	P	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	Q	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	Q	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	Q	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	Q	1	Total	C	Mg	N	O	0
			64	54	1	4	5	
22	Q	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	Q	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	Q	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	Q	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	U	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	U	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	U	1	Total	C	Mg	N	O	0
			50	40	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	U	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	U	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	U	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	U	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	U	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	N	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	N	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	N	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	N	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	N	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	N	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	N	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	N	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	G	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	G	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	G	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	G	1	Total	C	Mg	N	O	0
			64	54	1	4	5	
22	G	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	G	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	G	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	G	1	Total	C	Mg	N	O	0
			48	38	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	u	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	u	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	u	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	u	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	u	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	u	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	u	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	u	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	n	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	n	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	n	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	n	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	n	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	n	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	n	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	n	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	g	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	g	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	g	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	g	1	Total	C	Mg	N	O	0
			64	54	1	4	5	
22	g	1	Total	C	Mg	N	O	0
			60	50	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	g	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	g	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	g	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			49	39	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			48	38	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			58	48	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			49	39	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			49	39	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			60	50	1	4	5	
22	R	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
22	S	1	Total	C	Mg	N	O	0
			61	51	1	4	5	
22	S	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
22	S	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	S	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
22	S	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
22	S	1	Total	C	Mg	N	O	0
			56	46	1	4	5	
22	S	1	Total	C	Mg	N	O	0
			49	39	1	4	5	
22	S	1	Total	C	Mg	N	O	0
			55	45	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	S	1	Total	C	Mg	N	O	0
			49	39	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	C	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	B	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	D	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	X	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	

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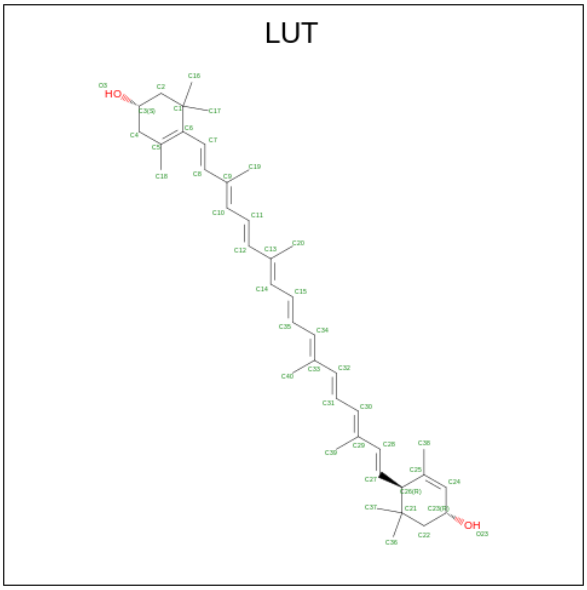
Mol	Chain	Residues	Atoms					AltConf
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	b	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	c	1	Total	C	Mg	N	O	0
			65	55	1	4	5	
22	s	1	Total	C	Mg	N	O	0
			61	51	1	4	5	
22	s	1	Total	C	Mg	N	O	0
			45	35	1	4	5	

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Mol	Chain	Residues	Atoms					AltConf
22	s	1	Total	C	Mg	N	O	0
			50	40	1	4	5	
22	s	1	Total	C	Mg	N	O	0
			45	35	1	4	5	
22	s	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
22	s	1	Total	C	Mg	N	O	0
			56	46	1	4	5	
22	s	1	Total	C	Mg	N	O	0
			49	39	1	4	5	
22	s	1	Total	C	Mg	N	O	0
			55	45	1	4	5	
22	s	1	Total	C	Mg	N	O	0
			49	39	1	4	5	

- Molecule 23 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
23	r	1	Total	C	O	0
			42	40	2	
23	1	1	Total	C	O	0
			42	40	2	
23	1	1	Total	C	O	0
			42	40	2	
23	2	1	Total	C	O	0
			42	40	2	

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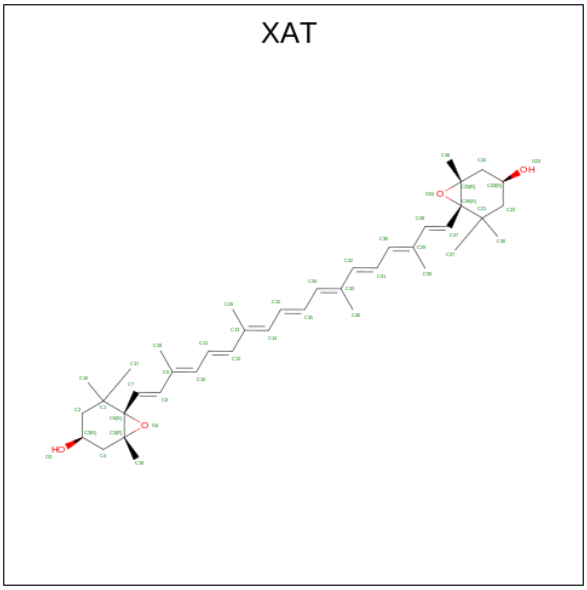
Mol	Chain	Residues	Atoms			AltConf
23	2	1	Total	C	O	0
			42	40	2	
23	4	1	Total	C	O	0
			42	40	2	
23	4	1	Total	C	O	0
			42	40	2	
23	5	1	Total	C	O	0
			42	40	2	
23	5	1	Total	C	O	0
			42	40	2	
23	v	1	Total	C	O	0
			42	40	2	
23	v	1	Total	C	O	0
			42	40	2	
23	p	1	Total	C	O	0
			42	40	2	
23	p	1	Total	C	O	0
			42	40	2	
23	V	1	Total	C	O	0
			42	40	2	
23	V	1	Total	C	O	0
			42	40	2	
23	P	1	Total	C	O	0
			42	40	2	
23	P	1	Total	C	O	0
			42	40	2	
23	U	1	Total	C	O	0
			42	40	2	
23	U	1	Total	C	O	0
			42	40	2	
23	N	1	Total	C	O	0
			42	40	2	
23	N	1	Total	C	O	0
			42	40	2	
23	u	1	Total	C	O	0
			42	40	2	
23	u	1	Total	C	O	0
			42	40	2	
23	n	1	Total	C	O	0
			42	40	2	
23	n	1	Total	C	O	0
			42	40	2	

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Mol	Chain	Residues	Atoms	AltConf
23	R	1	Total C O 42 40 2	0
23	S	1	Total C O 42 40 2	0
23	S	1	Total C O 42 40 2	0
23	s	1	Total C O 42 40 2	0
23	s	1	Total C O 42 40 2	0

- Molecule 24 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: $C_{40}H_{56}O_4$).



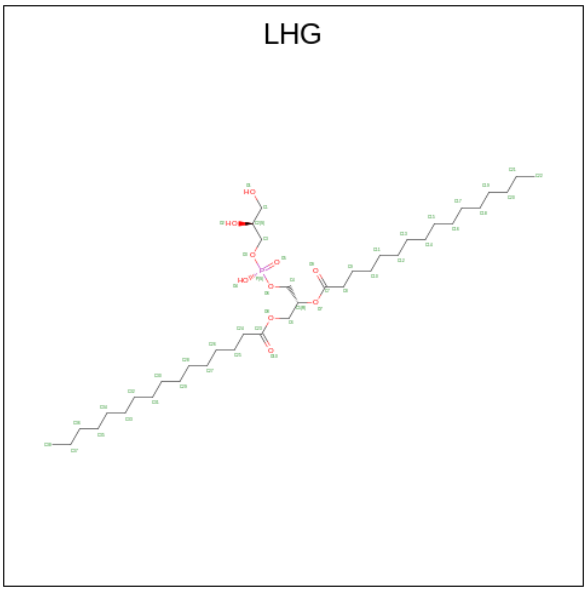
Mol	Chain	Residues	Atoms	AltConf
24	r	1	Total C O 44 40 4	0
24	1	1	Total C O 44 40 4	0
24	2	1	Total C O 44 40 4	0
24	3	1	Total C O 44 40 4	0
24	4	1	Total C O 44 40 4	0
24	5	1	Total C O 44 40 4	0

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Mol	Chain	Residues	Atoms	AltConf
24	6	1	Total C O 44 40 4	0
24	v	1	Total C O 44 40 4	0
24	p	1	Total C O 44 40 4	0
24	q	1	Total C O 44 40 4	0
24	V	1	Total C O 44 40 4	0
24	P	1	Total C O 44 40 4	0
24	Q	1	Total C O 44 40 4	0
24	U	1	Total C O 44 40 4	0
24	N	1	Total C O 44 40 4	0
24	G	1	Total C O 44 40 4	0
24	u	1	Total C O 44 40 4	0
24	n	1	Total C O 44 40 4	0
24	g	1	Total C O 44 40 4	0
24	R	1	Total C O 44 40 4	0

- Molecule 25 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: $C_{38}H_{75}O_{10}P$).



Mol	Chain	Residues	Atoms				AltConf
25	r	1	Total	C	O	P	0
			42	31	10	1	
25	a	1	Total	C	O	P	0
			43	32	10	1	
25	d	1	Total	C	O	P	0
			46	35	10	1	
25	d	1	Total	C	O	P	0
			49	38	10	1	
25	l	1	Total	C	O	P	0
			49	38	10	1	
25	A	1	Total	C	O	P	0
			43	32	10	1	
25	L	1	Total	C	O	P	0
			49	38	10	1	
25	1	1	Total	C	O	P	0
			49	38	10	1	
25	2	1	Total	C	O	P	0
			49	38	10	1	
25	3	1	Total	C	O	P	0
			49	38	10	1	
25	4	1	Total	C	O	P	0
			49	38	10	1	
25	5	1	Total	C	O	P	0
			49	38	10	1	
25	6	1	Total	C	O	P	0
			49	38	10	1	
25	v	1	Total	C	O	P	0
			49	38	10	1	

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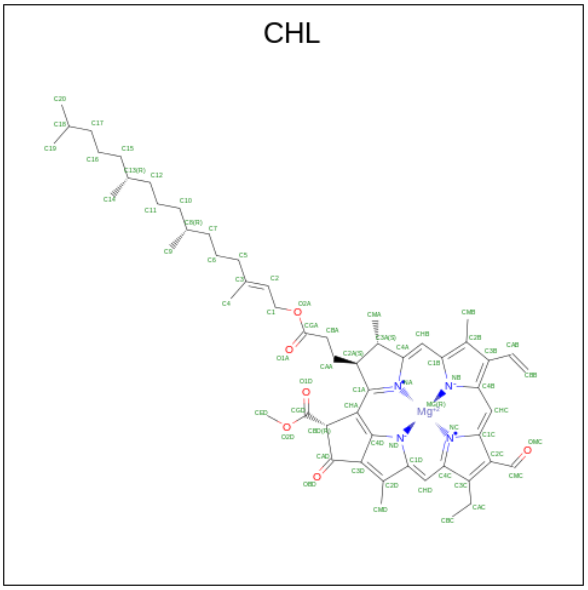
Mol	Chain	Residues	Atoms				AltConf
25	p	1	Total	C	O	P	0
			49	38	10	1	
25	q	1	Total	C	O	P	0
			49	38	10	1	
25	V	1	Total	C	O	P	0
			49	38	10	1	
25	P	1	Total	C	O	P	0
			49	38	10	1	
25	Q	1	Total	C	O	P	0
			49	38	10	1	
25	U	1	Total	C	O	P	0
			49	38	10	1	
25	N	1	Total	C	O	P	0
			49	38	10	1	
25	G	1	Total	C	O	P	0
			49	38	10	1	
25	u	1	Total	C	O	P	0
			49	38	10	1	
25	n	1	Total	C	O	P	0
			49	38	10	1	
25	g	1	Total	C	O	P	0
			49	38	10	1	
25	R	1	Total	C	O	P	0
			42	31	10	1	
25	S	1	Total	C	O	P	0
			49	38	10	1	
25	C	1	Total	C	O	P	0
			49	38	10	1	
25	C	1	Total	C	O	P	0
			49	38	10	1	
25	C	1	Total	C	O	P	0
			49	38	10	1	
25	B	1	Total	C	O	P	0
			47	36	10	1	
25	B	1	Total	C	O	P	0
			49	38	10	1	
25	D	1	Total	C	O	P	0
			46	35	10	1	
25	D	1	Total	C	O	P	0
			49	38	10	1	
25	b	1	Total	C	O	P	0
			47	36	10	1	

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Mol	Chain	Residues	Atoms				AltConf
25	b	1	Total	C	O	P	0
			49	38	10	1	
25	c	1	Total	C	O	P	0
			49	38	10	1	
25	c	1	Total	C	O	P	0
			49	38	10	1	
25	c	1	Total	C	O	P	0
			49	38	10	1	
25	s	1	Total	C	O	P	0
			49	38	10	1	

- Molecule 26 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
26	r	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	r	1	Total	C	Mg	N	O	0
			56	45	1	4	6	
26	r	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
26	r	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	1	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	1	1	Total	C	Mg	N	O	0
			48	37	1	4	6	

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Mol	Chain	Residues	Atoms					AltConf
26	1	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	1	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	1	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	1	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	2	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	2	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	2	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	2	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	2	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	2	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	3	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	3	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	3	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	3	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	3	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	3	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
26	4	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	4	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	4	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	4	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	4	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

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Mol	Chain	Residues	Atoms					AltConf
26	5	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	5	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	5	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	5	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	5	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	5	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	6	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	6	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	6	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	6	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	6	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	6	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	6	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
26	v	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	v	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	v	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	v	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	v	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	v	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	p	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	p	1	Total	C	Mg	N	O	0
			48	37	1	4	6	

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Mol	Chain	Residues	Atoms					AltConf
26	p	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	p	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	p	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	p	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	p	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	q	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	q	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	q	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	q	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	q	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
26	V	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	V	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	V	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	V	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	V	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	V	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	P	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	P	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	P	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	P	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	P	1	Total	C	Mg	N	O	0
			66	55	1	4	6	

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Mol	Chain	Residues	Atoms					AltConf
26	P	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	Q	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	Q	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	Q	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	Q	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	Q	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	Q	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
26	U	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	U	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	U	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	U	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	U	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	U	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	N	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	N	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	N	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	N	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	N	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	G	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	G	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	G	1	Total	C	Mg	N	O	0
			50	39	1	4	6	

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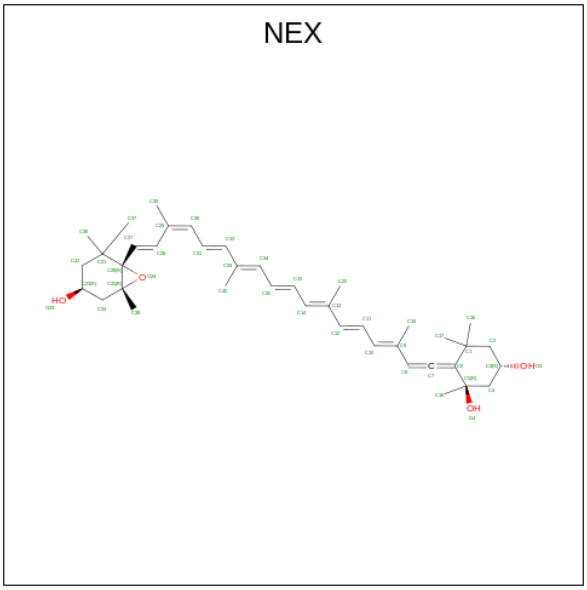
Mol	Chain	Residues	Atoms					AltConf
26	G	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	G	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	G	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
26	u	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	u	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	u	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	u	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	u	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	u	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	n	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	n	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	n	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	n	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	n	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	n	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	g	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	g	1	Total	C	Mg	N	O	0
			48	37	1	4	6	
26	g	1	Total	C	Mg	N	O	0
			50	39	1	4	6	
26	g	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	g	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	g	1	Total	C	Mg	N	O	0
			61	50	1	4	6	

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Mol	Chain	Residues	Atoms					AltConf
26	R	1	Total	C	Mg	N	O	0
			66	55	1	4	6	
26	R	1	Total	C	Mg	N	O	0
			56	45	1	4	6	
26	R	1	Total	C	Mg	N	O	0
			61	50	1	4	6	
26	S	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
26	S	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
26	S	1	Total	C	Mg	N	O	0
			58	47	1	4	6	
26	S	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
26	s	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
26	s	1	Total	C	Mg	N	O	0
			46	35	1	4	6	
26	s	1	Total	C	Mg	N	O	0
			58	47	1	4	6	
26	s	1	Total	C	Mg	N	O	0
			46	35	1	4	6	

- Molecule 27 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: $C_{40}H_{56}O_4$).



Mol	Chain	Residues	Atoms			AltConf
27	r	1	Total	C	O	0
			44	40	4	
27	r	1	Total	C	O	0
			44	40	4	
27	2	1	Total	C	O	0
			44	40	4	
27	5	1	Total	C	O	0
			44	40	4	
27	v	1	Total	C	O	0
			44	40	4	
27	p	1	Total	C	O	0
			44	40	4	
27	V	1	Total	C	O	0
			44	40	4	
27	P	1	Total	C	O	0
			44	40	4	
27	U	1	Total	C	O	0
			44	40	4	
27	N	1	Total	C	O	0
			44	40	4	
27	u	1	Total	C	O	0
			44	40	4	
27	u	1	Total	C	O	0
			44	40	4	
27	n	1	Total	C	O	0
			44	40	4	
27	R	1	Total	C	O	0
			44	40	4	
27	S	1	Total	C	O	0
			44	40	4	
27	s	1	Total	C	O	0
			44	40	4	

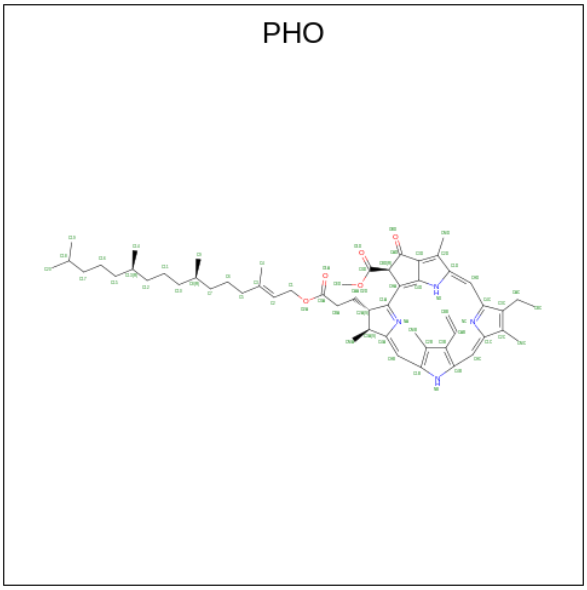
- Molecule 28 is FE (II) ION (CCD ID: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		AltConf
28	a	1	Total	Fe	0
			1	1	
28	A	1	Total	Fe	0
			1	1	

- Molecule 29 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

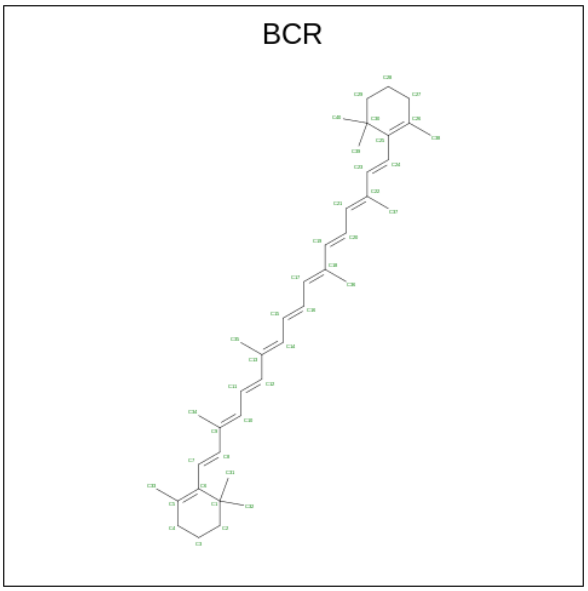
Mol	Chain	Residues	Atoms	AltConf
29	a	2	Total Cl 2 2	0
29	A	2	Total Cl 2 2	0

- Molecule 30 is PHEOPHYTIN A (CCD ID: PHO) (formula: $C_{55}H_{74}N_4O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	AltConf
30	a	1	Total C N O 64 55 4 5	0
30	d	1	Total C N O 64 55 4 5	0
30	A	1	Total C N O 64 55 4 5	0
30	D	1	Total C N O 64 55 4 5	0

- Molecule 31 is BETA-CAROTENE (CCD ID: BCR) (formula: $C_{40}H_{56}$).



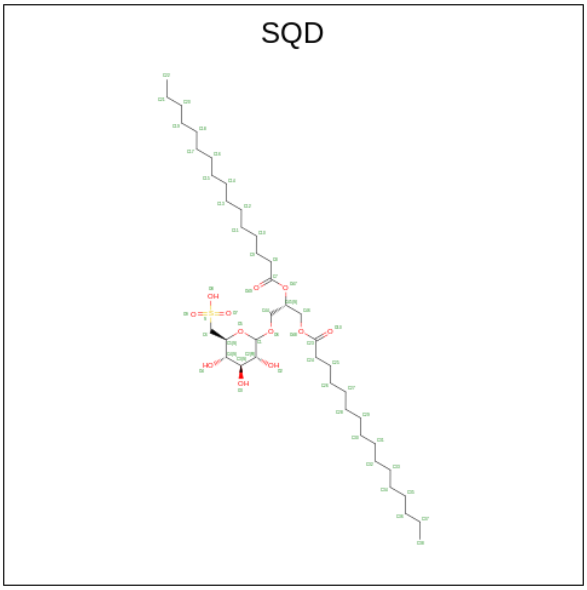
Mol	Chain	Residues	Atoms	AltConf
31	a	1	Total C 40 40	0
31	d	1	Total C 40 40	0
31	k	1	Total C 40 40	0
31	t	1	Total C 40 40	0
31	x	1	Total C 40 40	0
31	z	1	Total C 40 40	0
31	A	1	Total C 40 40	0
31	K	1	Total C 40 40	0
31	T	1	Total C 40 40	0
31	C	1	Total C 40 40	0
31	C	1	Total C 40 40	0
31	C	1	Total C 40 40	0
31	B	1	Total C 40 40	0
31	B	1	Total C 40 40	0

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Mol	Chain	Residues	Atoms	AltConf
31	B	1	Total C 40 40	0
31	D	1	Total C 40 40	0
31	X	1	Total C 40 40	0
31	b	1	Total C 40 40	0
31	b	1	Total C 40 40	0
31	b	1	Total C 40 40	0
31	c	1	Total C 40 40	0
31	c	1	Total C 40 40	0

- Molecule 32 is 1,2-DI-O-ACYL-3-O-[6-DEOXY-6-SULFO-ALPHA-D-GLUCOPYRANOSYL]-SN-GLYCEROL (CCD ID: SQD) (formula: $C_{41}H_{78}O_{12}S$).



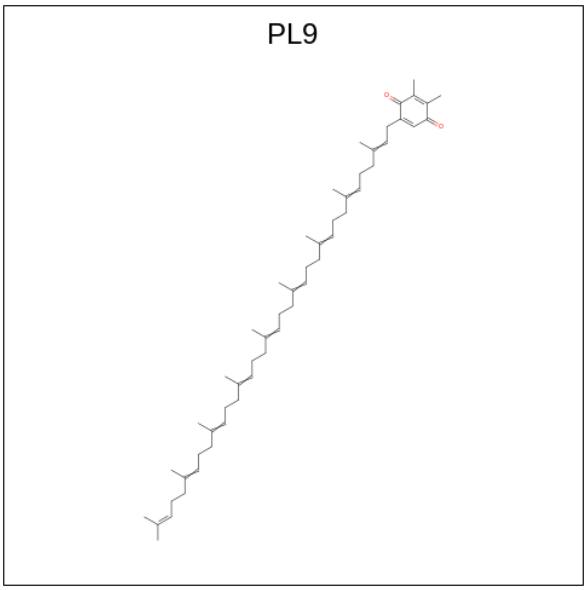
Mol	Chain	Residues	Atoms	AltConf
32	a	1	Total C O S 50 37 12 1	0
32	a	1	Total C O S 54 41 12 1	0
32	l	1	Total C O S 54 41 12 1	0

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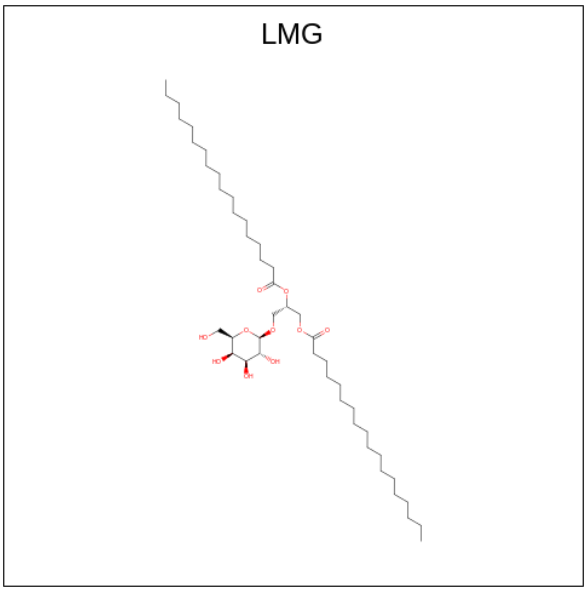
Mol	Chain	Residues	Atoms				AltConf
32	m	1	Total	C	O	S	0
			42	29	12	1	
32	A	1	Total	C	O	S	0
			54	41	12	1	
32	L	1	Total	C	O	S	0
			54	41	12	1	
32	M	1	Total	C	O	S	0
			42	29	12	1	
32	C	1	Total	C	O	S	0
			50	37	12	1	

- Molecule 33 is 2,3-DIMETHYL-5-(3,7,11,15,19,23,27,31,35-NONAMETHYL-2,6,10,14,18,22,26,30,34-HEXATRIACONTANONAENYL-2,5-CYCLOHEXADIENE-1,4-DIONE-2,3-DIMETHYL-5-SOLANESYL-1,4-BENZOQUINONE (CCD ID: PL9) (formula: $C_{53}H_{80}O_2$).



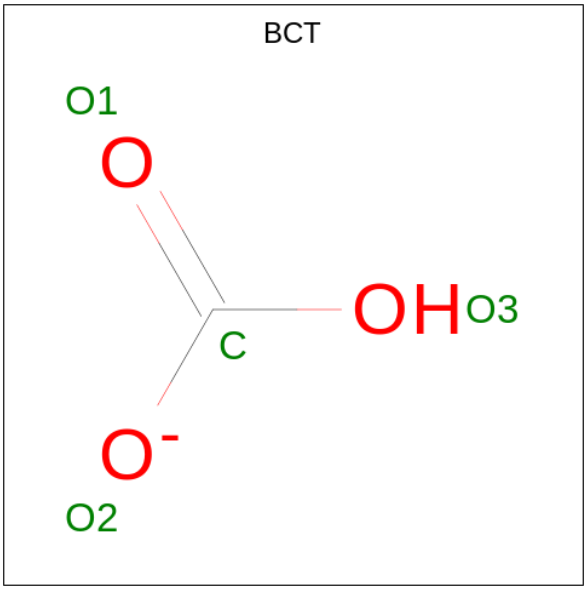
Mol	Chain	Residues	Atoms			AltConf
33	a	1	Total	C	O	0
			13	11	2	
33	d	1	Total	C	O	0
			55	53	2	
33	A	1	Total	C	O	0
			13	11	2	
33	D	1	Total	C	O	0
			55	53	2	

- Molecule 34 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (CCD ID: LMG) (formula: $C_{45}H_{86}O_{10}$).



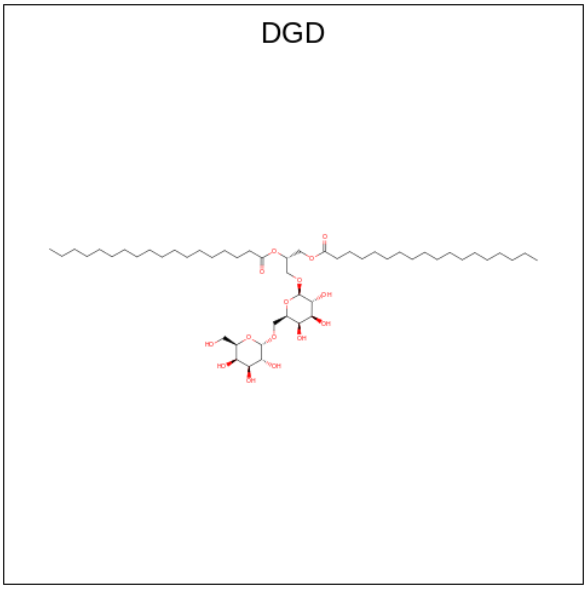
Mol	Chain	Residues	Atoms	AltConf
34	a	1	Total C O 40 30 10	0
34	d	1	Total C O 46 36 10	0
34	w	1	Total C O 48 38 10	0
34	A	1	Total C O 40 30 10	0
34	W	1	Total C O 48 38 10	0
34	C	1	Total C O 51 41 10	0
34	C	1	Total C O 51 41 10	0
34	B	1	Total C O 51 41 10	0
34	B	1	Total C O 55 45 10	0
34	D	1	Total C O 46 36 10	0
34	b	1	Total C O 51 41 10	0
34	b	1	Total C O 55 45 10	0
34	c	1	Total C O 51 41 10	0
34	c	1	Total C O 51 41 10	0

- Molecule 35 is BICARBONATE ION (CCD ID: BCT) (formula: CHO_3).



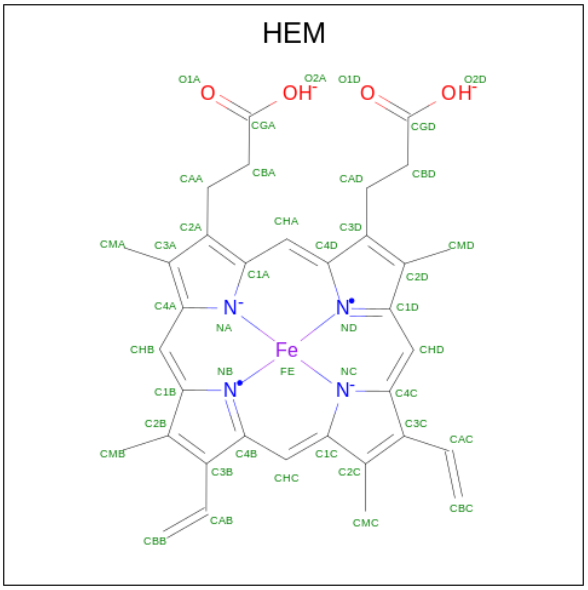
Mol	Chain	Residues	Atoms			AltConf
35	a	1	Total	C	O	0
			4	1	3	
35	D	1	Total	C	O	0
			4	1	3	

- Molecule 36 is DIGALACTOSYL DIACYL GLYCEROL (DGDG) (CCD ID: DGD) (formula: $C_{51}H_{96}O_{15}$).



Mol	Chain	Residues	Atoms	AltConf
36	a	1	Total C O 59 44 15	0
36	A	1	Total C O 59 44 15	0
36	J	1	Total C O 60 45 15	0
36	C	1	Total C O 55 40 15	0
36	C	1	Total C O 62 47 15	0
36	B	1	Total C O 62 47 15	0
36	b	1	Total C O 62 47 15	0
36	c	1	Total C O 55 40 15	0
36	c	1	Total C O 62 47 15	0
36	c	1	Total C O 60 45 15	0

- Molecule 37 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms	AltConf
37	E	1	Total C Fe N O 43 34 1 4 4	0

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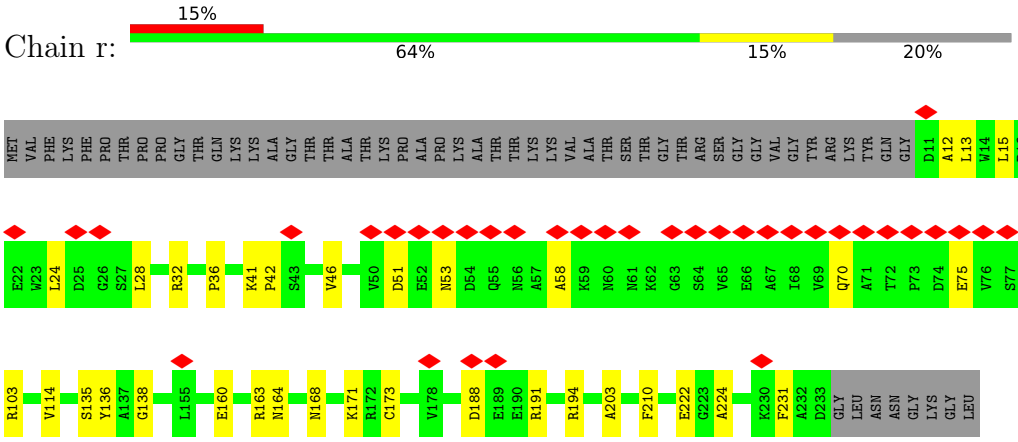
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Mol	Chain	Residues	Atoms					AltConf
37	e	1	Total	C	Fe	N	O	0
			43	34	1	4	4	

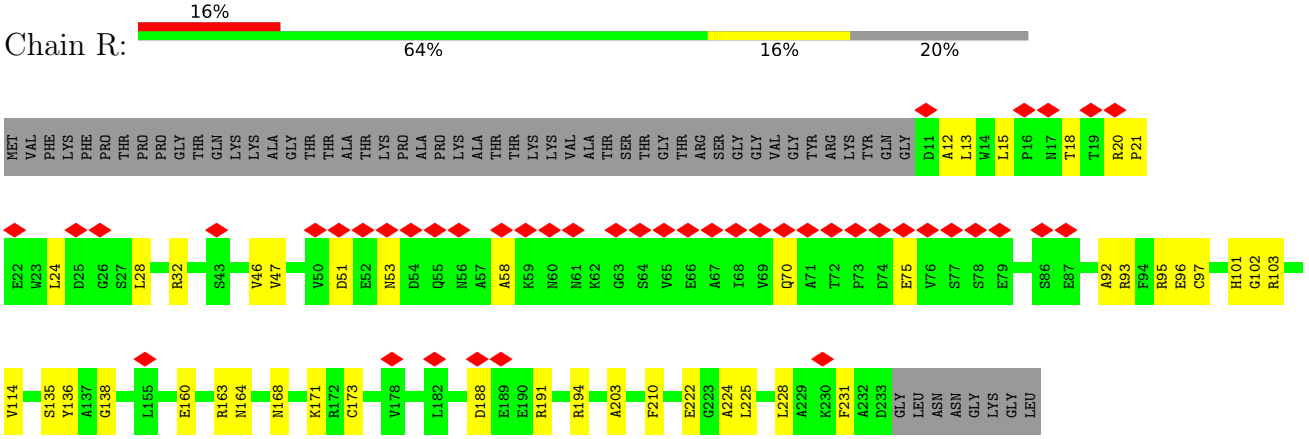
3 Residue-property plots (i)

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.

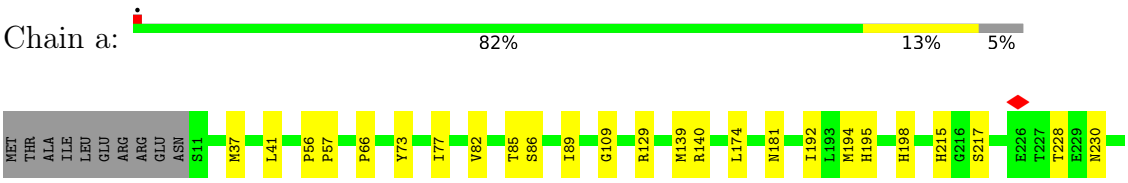
• Molecule 1: Chlorophyll a-b binding protein CP29



• Molecule 1: Chlorophyll a-b binding protein CP29

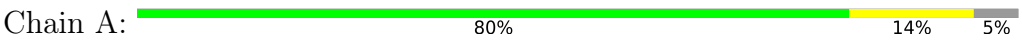


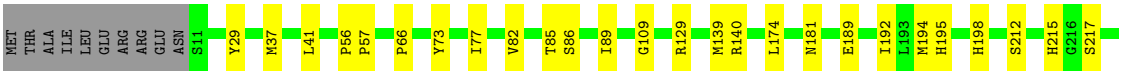
• Molecule 2: Photosystem II protein D1





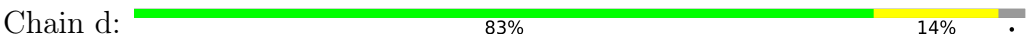
• Molecule 2: Photosystem II protein D1







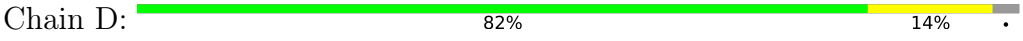
• Molecule 3: Photosystem II D2 protein



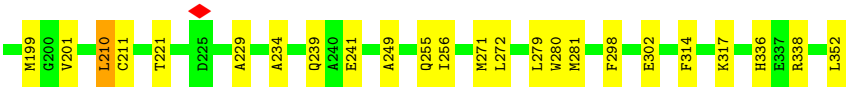




• Molecule 3: Photosystem II D2 protein

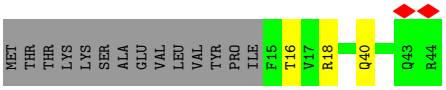






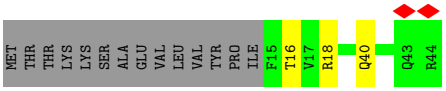
• Molecule 4: Cytochrome b559 subunit beta





• Molecule 4: Cytochrome b559 subunit beta

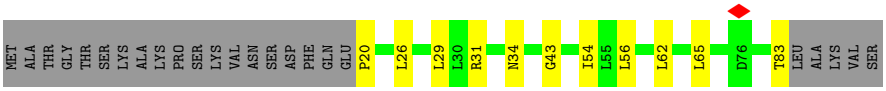




• Molecule 5: Photosystem II reaction center protein H

Chain h:

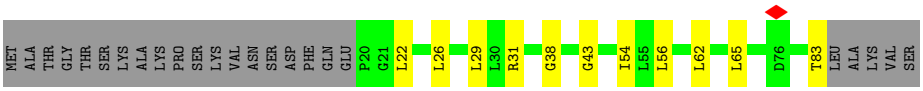




• Molecule 5: Photosystem II reaction center protein H

Chain H:

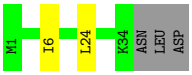




• Molecule 6: Photosystem II reaction center protein I

Chain i:

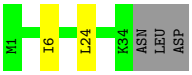




• Molecule 6: Photosystem II reaction center protein I

Chain I:

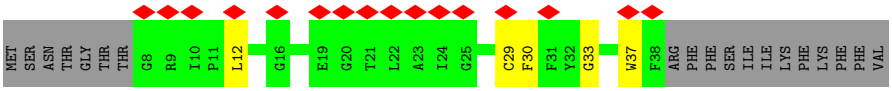




• Molecule 7: Photosystem II reaction center protein J, PsbJ

Chain j:

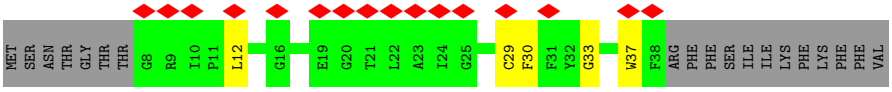




• Molecule 7: Photosystem II reaction center protein J, PsbJ

Chain J:





• Molecule 8: Photosystem II reaction center protein K

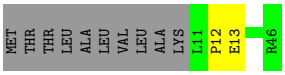
Chain k:





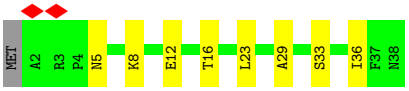
• Molecule 8: Photosystem II reaction center protein K





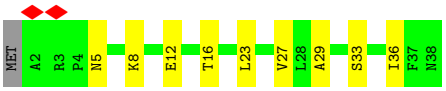
• Molecule 9: Photosystem II reaction center protein L



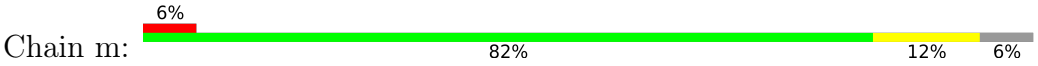


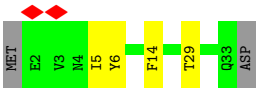
• Molecule 9: Photosystem II reaction center protein L



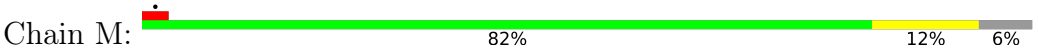


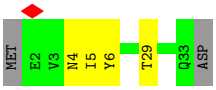
• Molecule 10: Photosystem II reaction center protein M





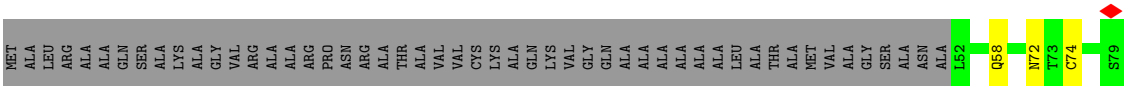
• Molecule 10: Photosystem II reaction center protein M

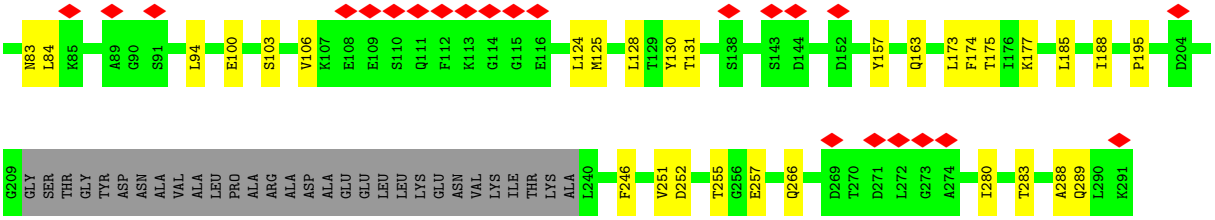




• Molecule 11: Oxygen-evolving enhancer protein 1 of photosystem II





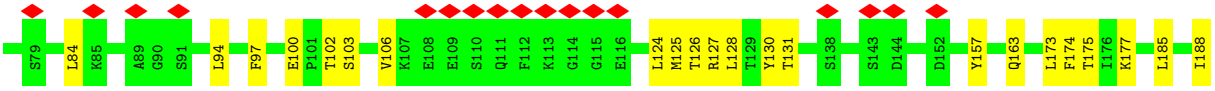


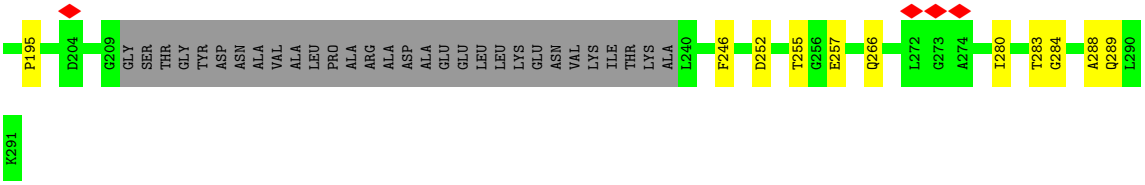
• Molecule 11: Oxygen-evolving enhancer protein 1 of photosystem II

Chain O:









• Molecule 12: Photosystem II reaction center protein T

Chain t:





• Molecule 12: Photosystem II reaction center protein T

Chain T:

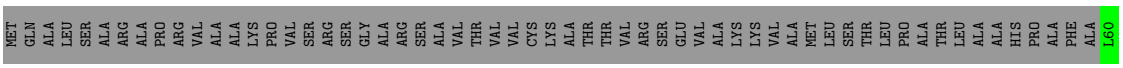


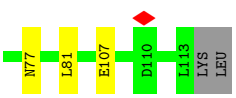


• Molecule 13: Photosystem II reaction center W protein, chloroplastic

Chain w:

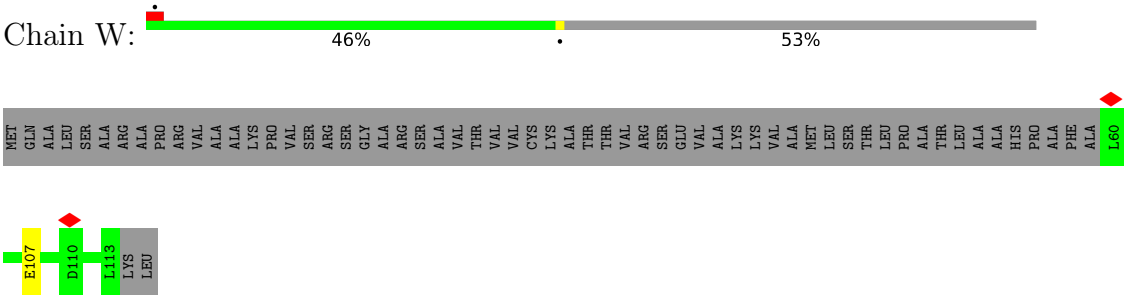






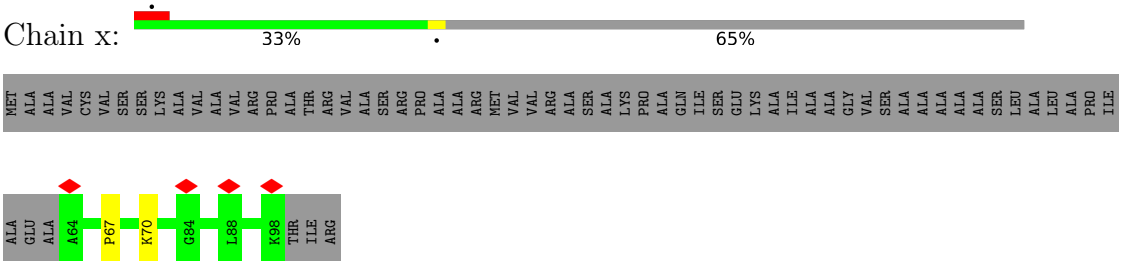
• Molecule 13: Photosystem II reaction center W protein, chloroplastic

Chain W:



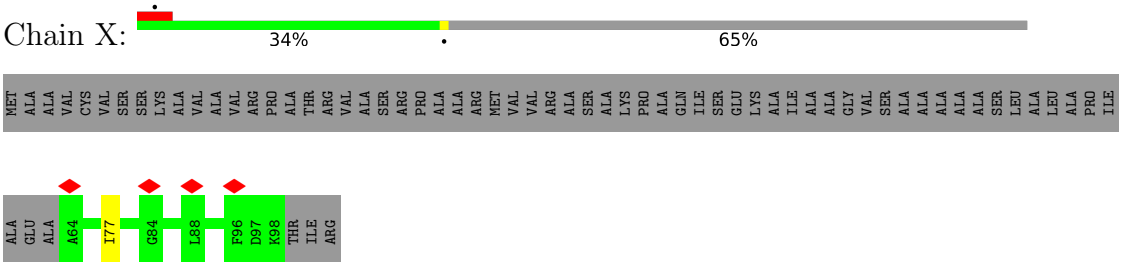
• Molecule 14: 4.1 kDa photosystem II subunit

Chain x:



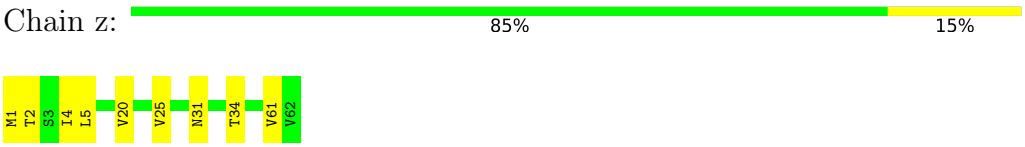
• Molecule 14: 4.1 kDa photosystem II subunit

Chain X:



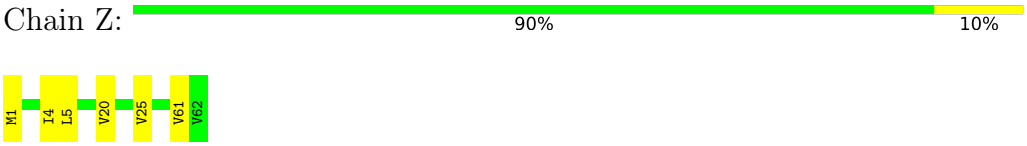
• Molecule 15: Photosystem II reaction center protein Z

Chain z:



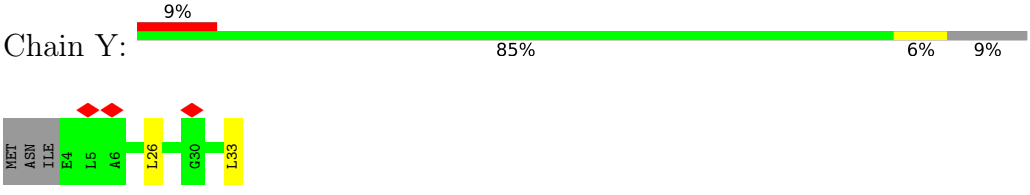
• Molecule 15: Photosystem II reaction center protein Z

Chain Z:



• Molecule 16: Photosystem II reaction center protein 30, Psb30

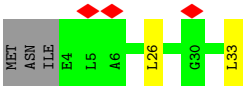
Chain Y:



• Molecule 16: Photosystem II reaction center protein 30, Psb30

Chain y:

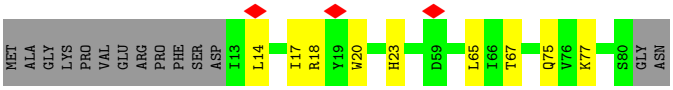




• Molecule 17: Cytochrome b559 subunit alpha

Chain E:

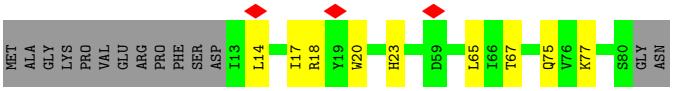




• Molecule 17: Cytochrome b559 subunit alpha

Chain e:

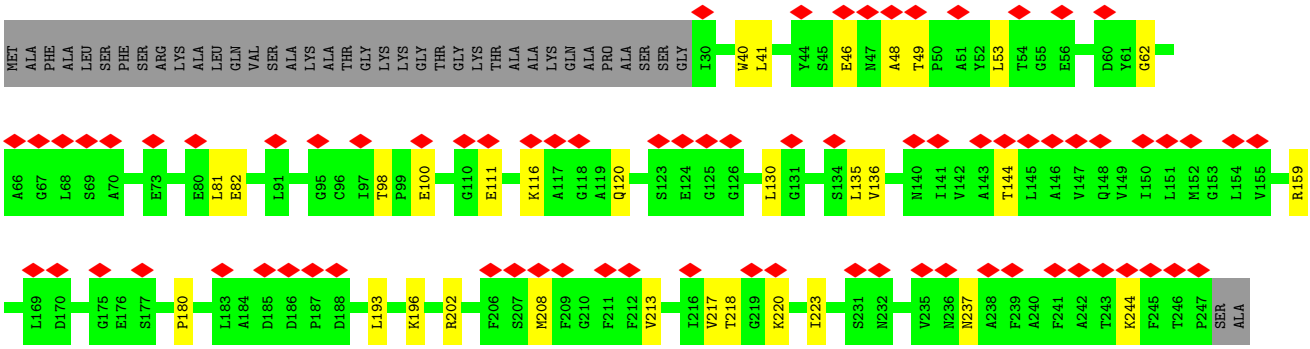




• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain 1:

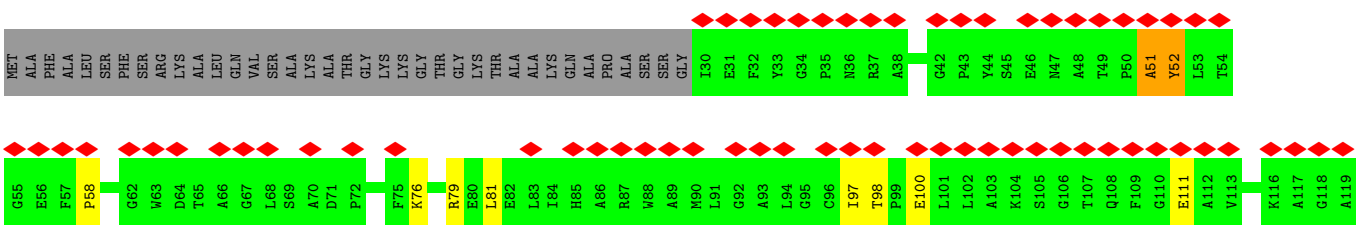




• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain 2:



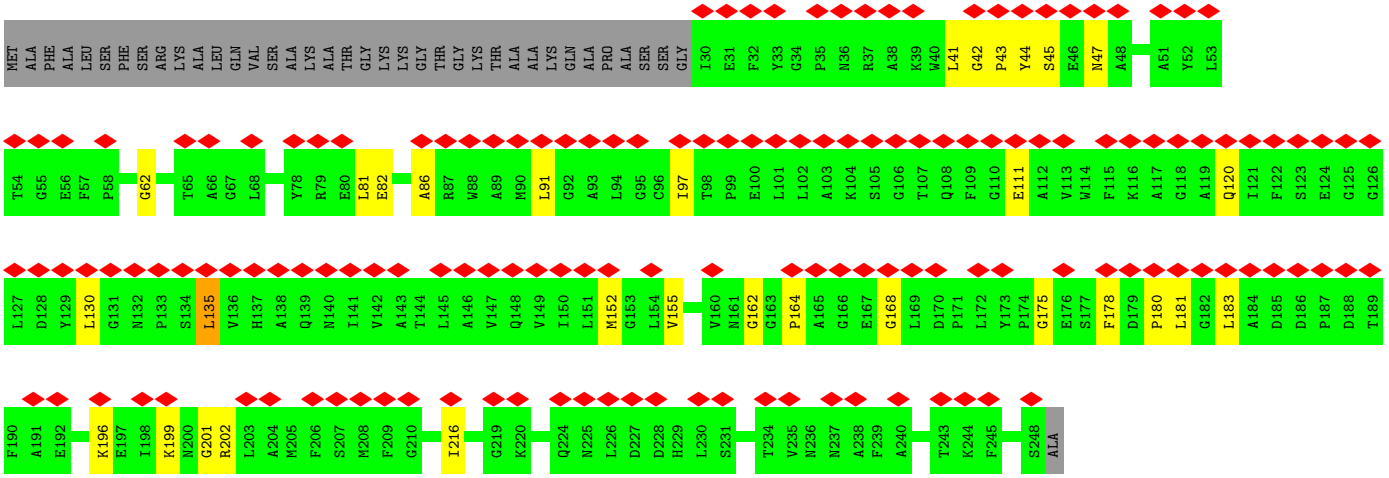




• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain 3:

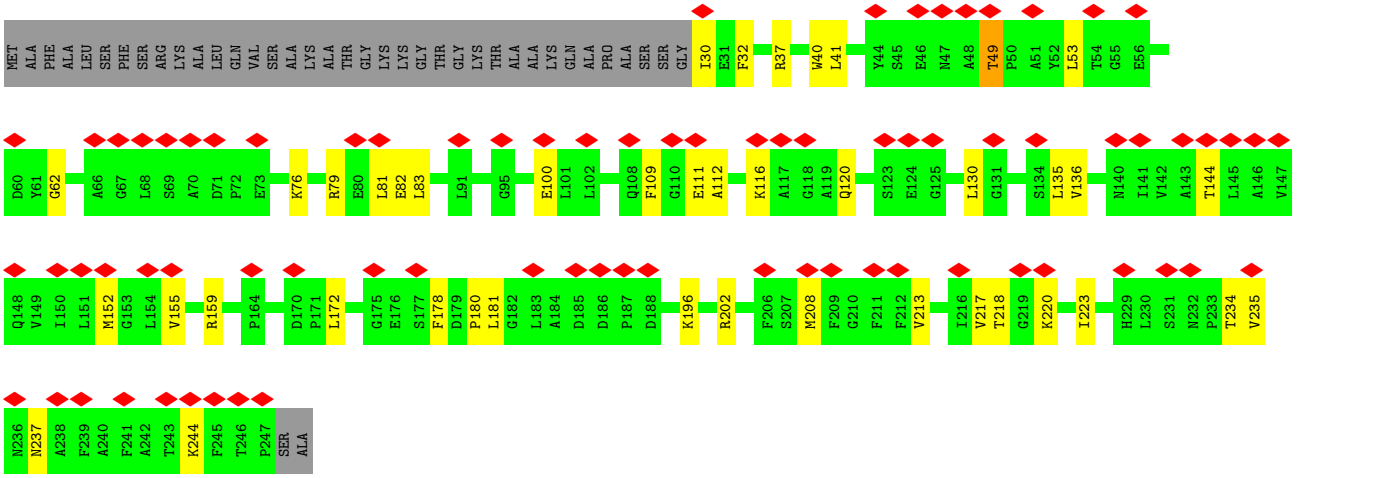




• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

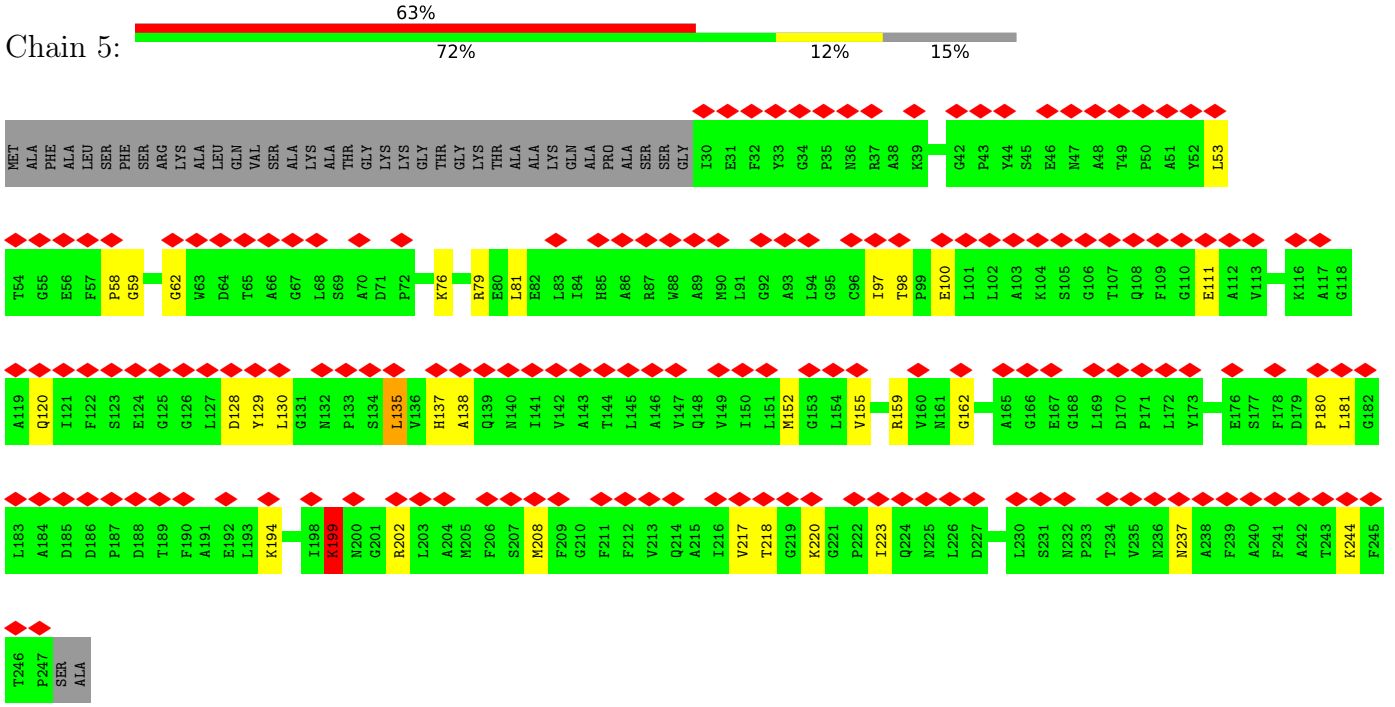
Chain 4:





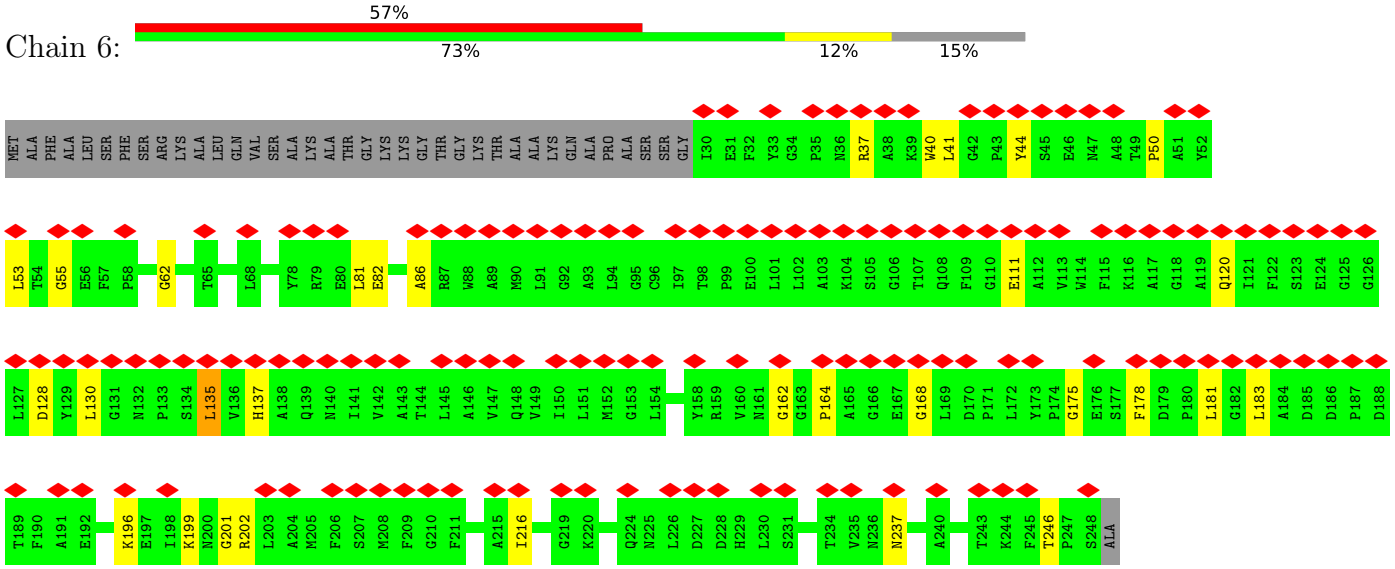
• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain 5:



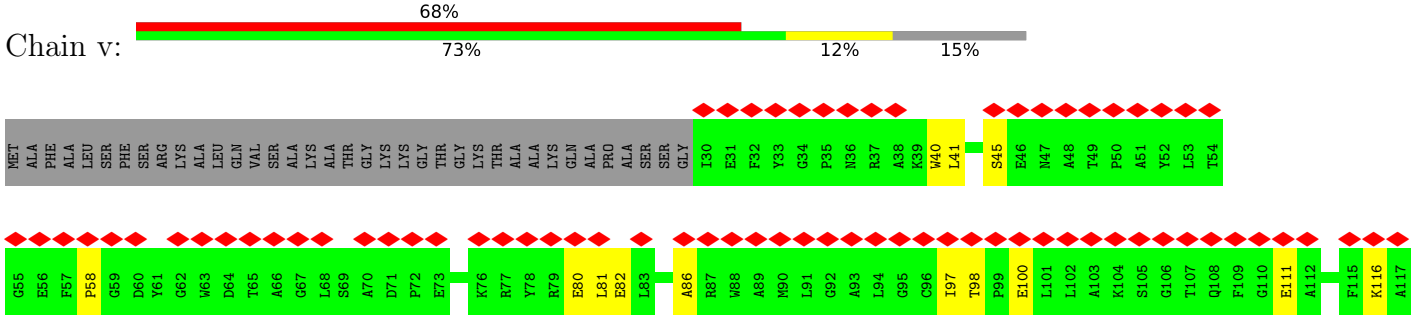
• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

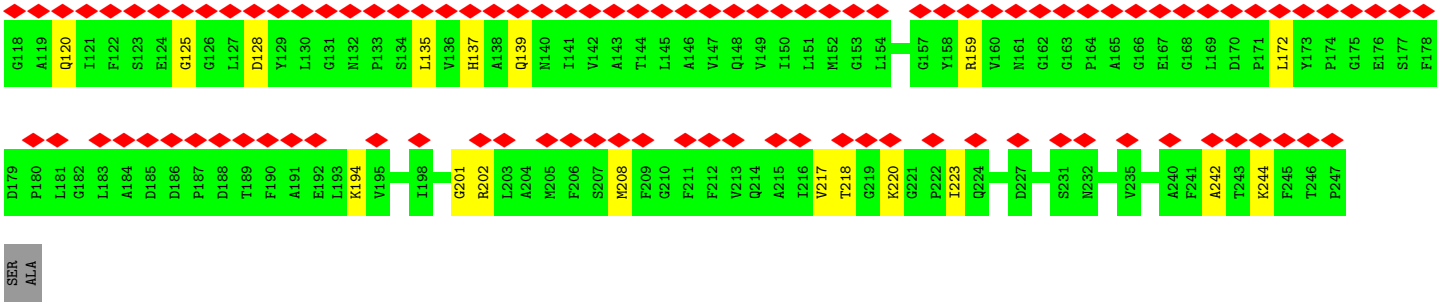
Chain 6:



• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain v:

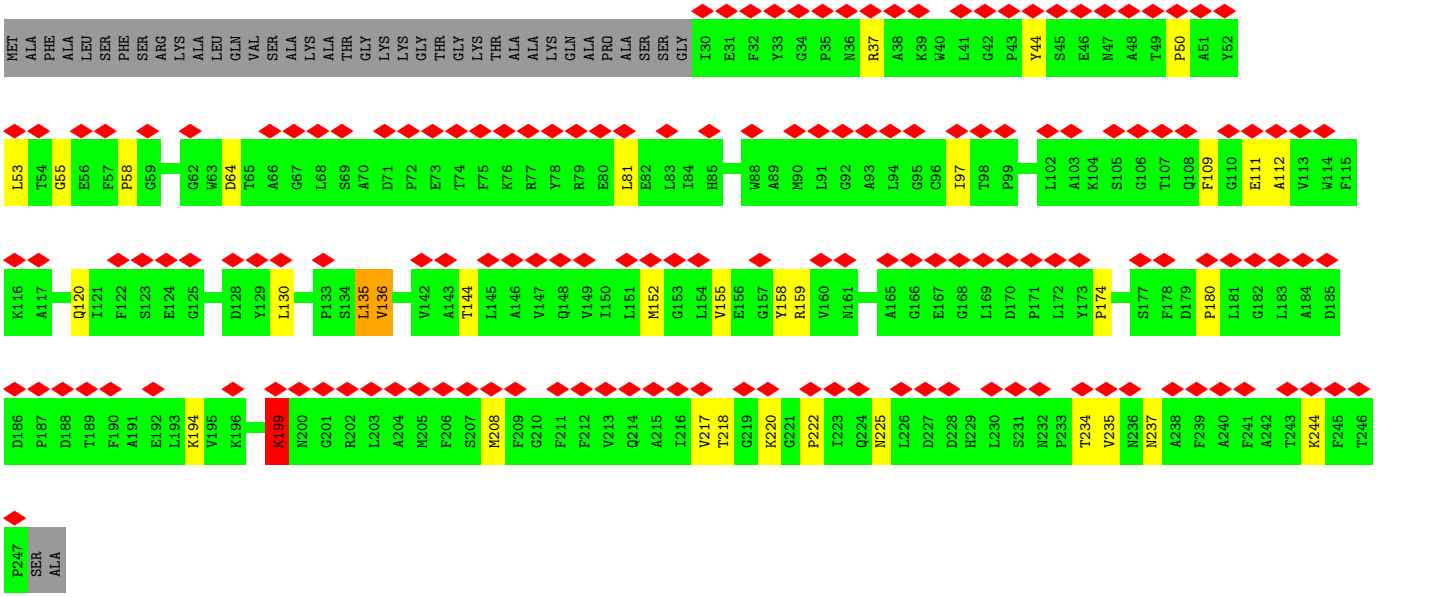




• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain p:

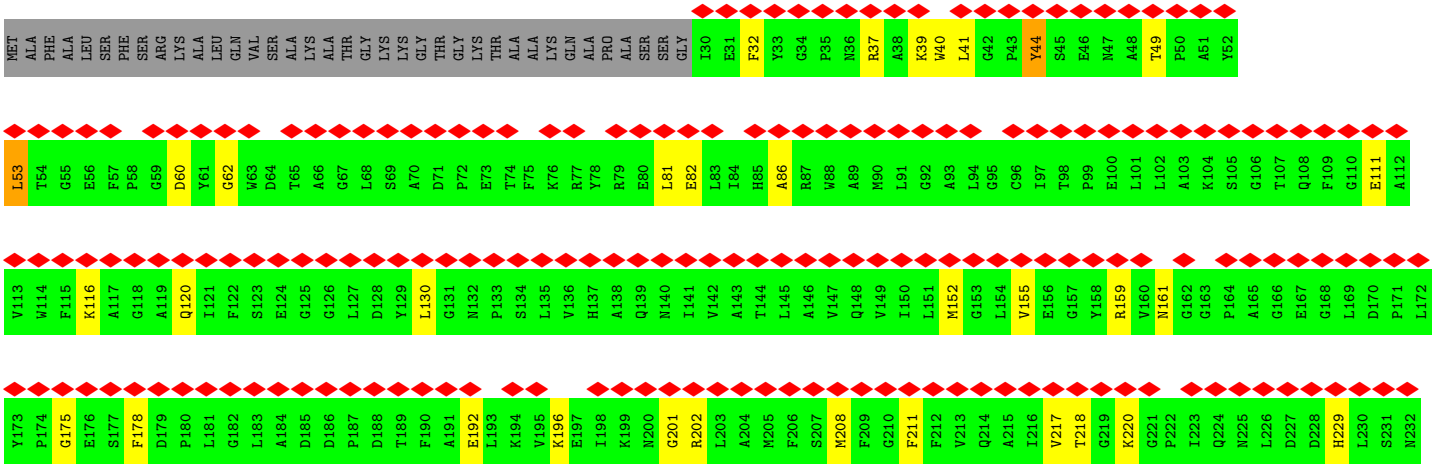


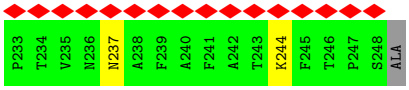


• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain q:



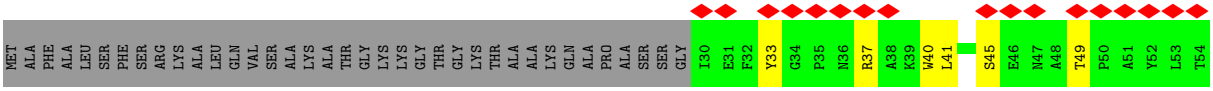


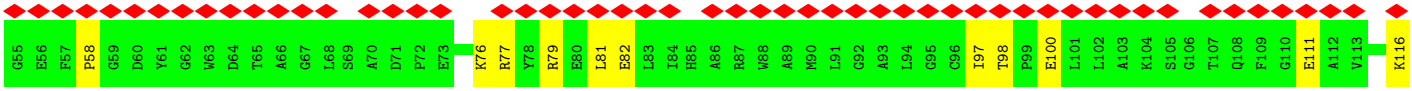


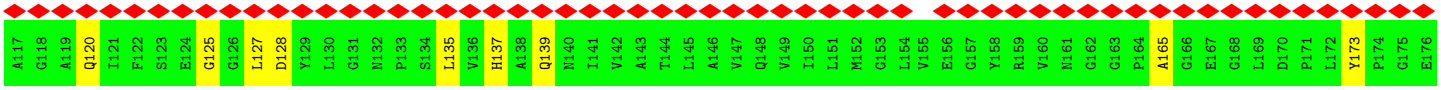
• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

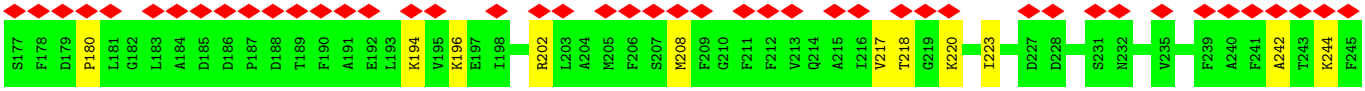
Chain V:









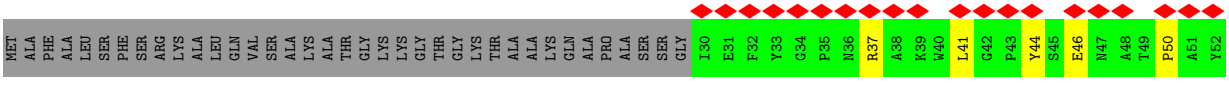


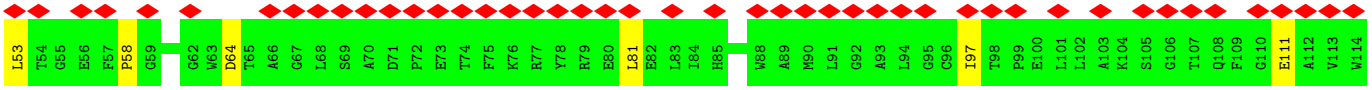


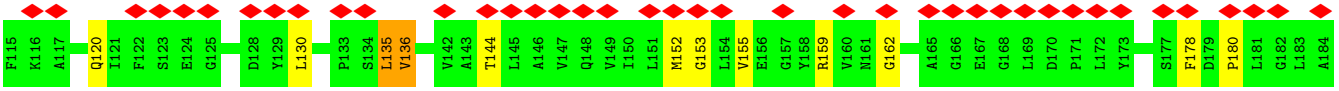
• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain P:







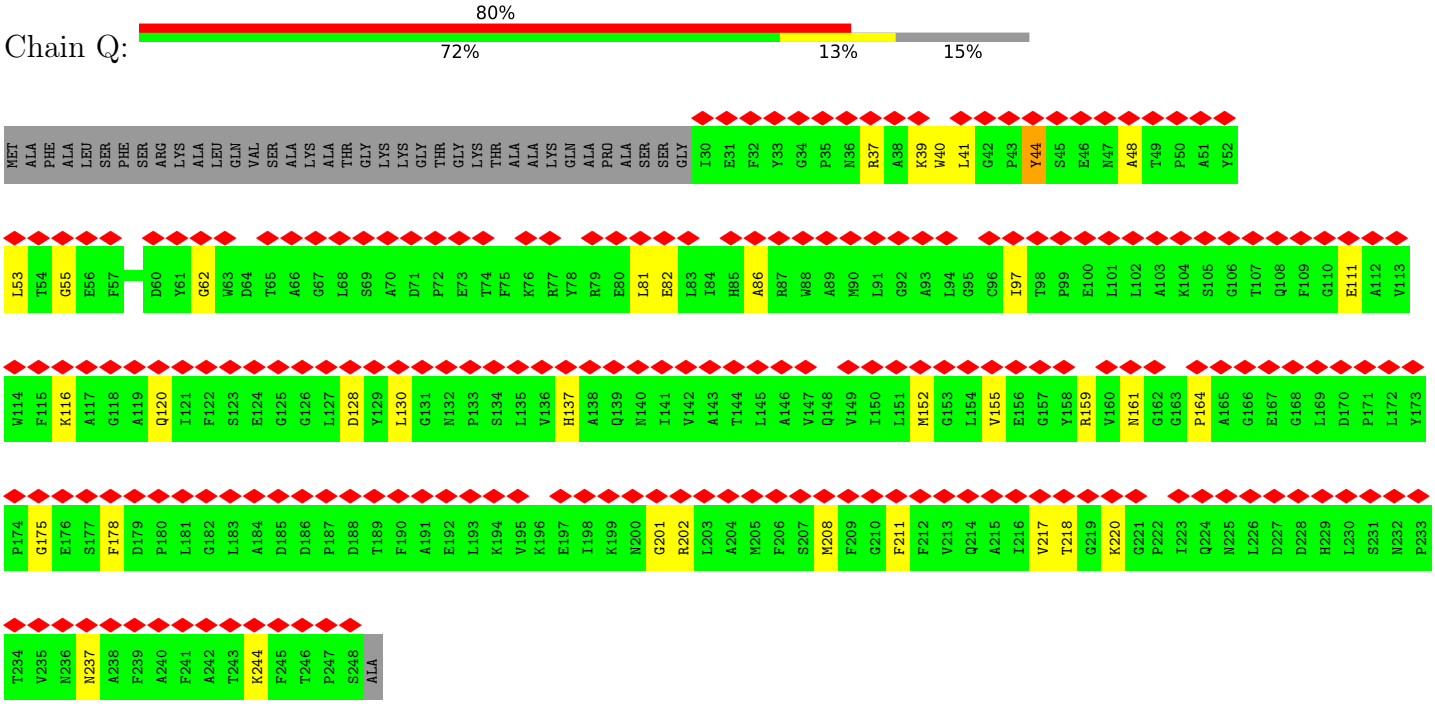






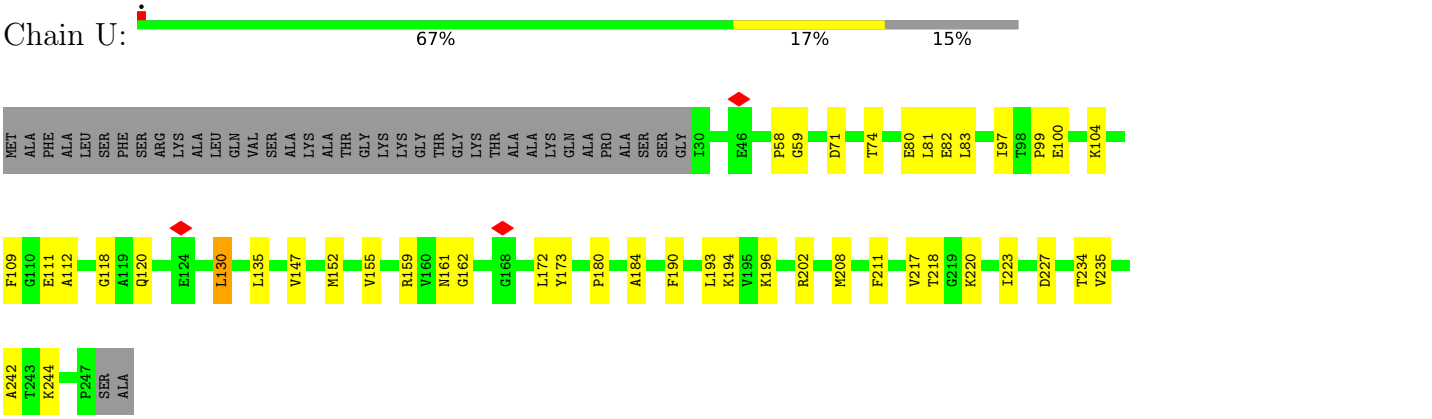
• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain Q:



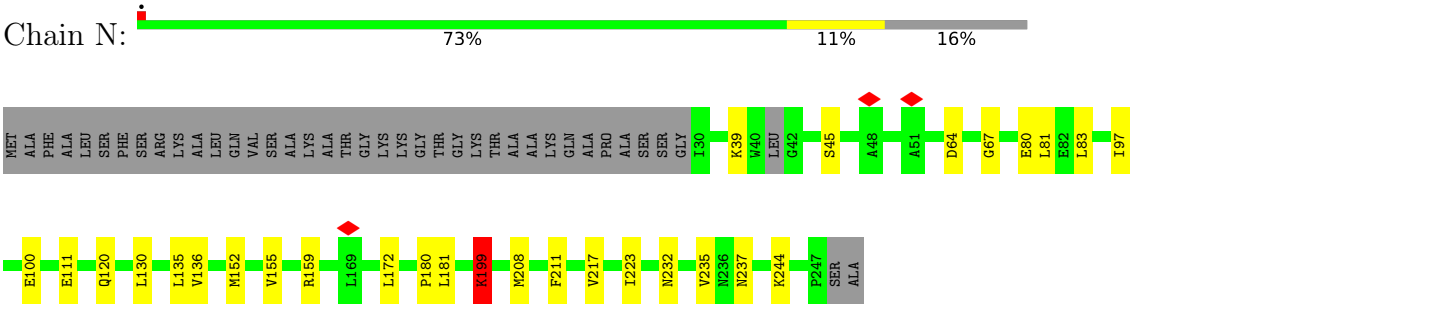
• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain U:



• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

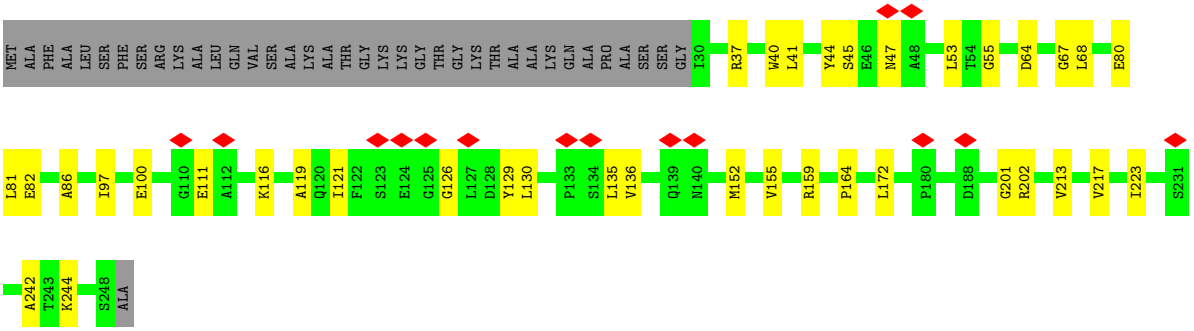
Chain N:



• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain G:

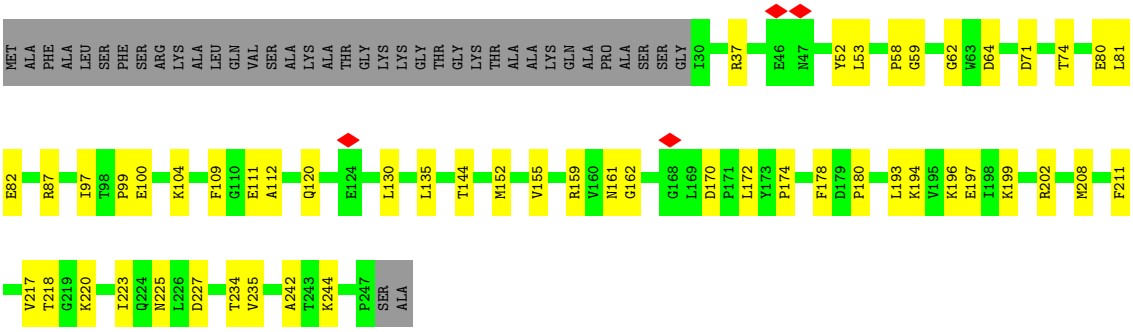




• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain u:

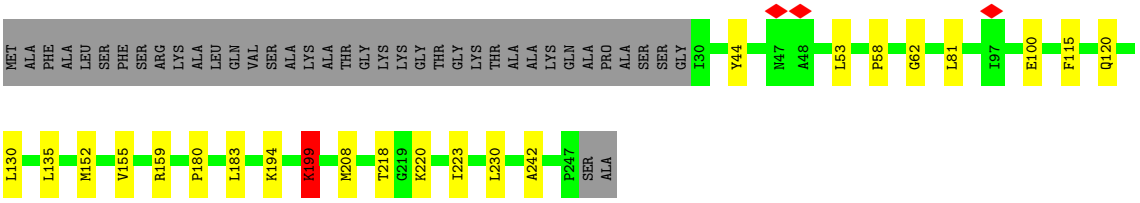




• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain n:

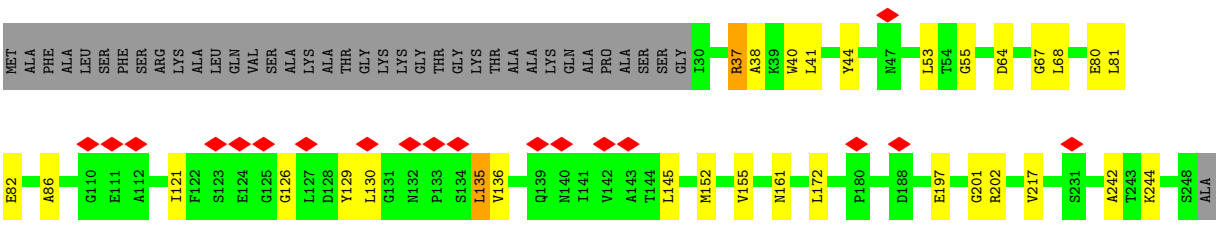




• Molecule 18: Chlorophyll a-b binding protein, chloroplastic

Chain g:

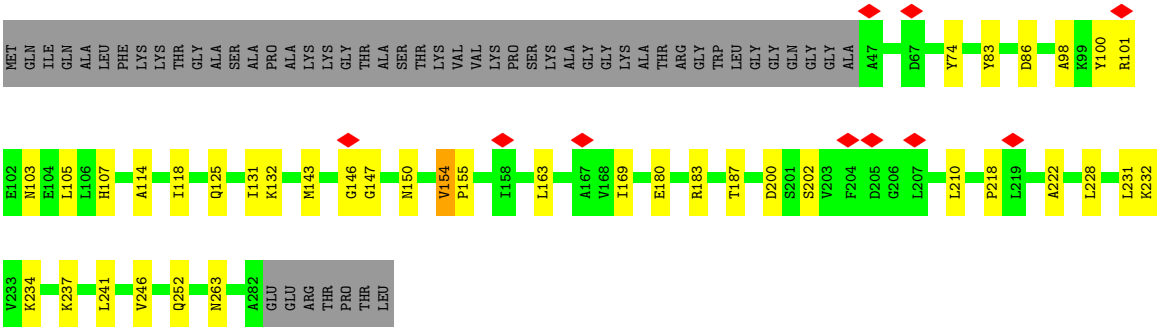




• Molecule 19: Chlorophyll a-b binding protein, chloroplastic

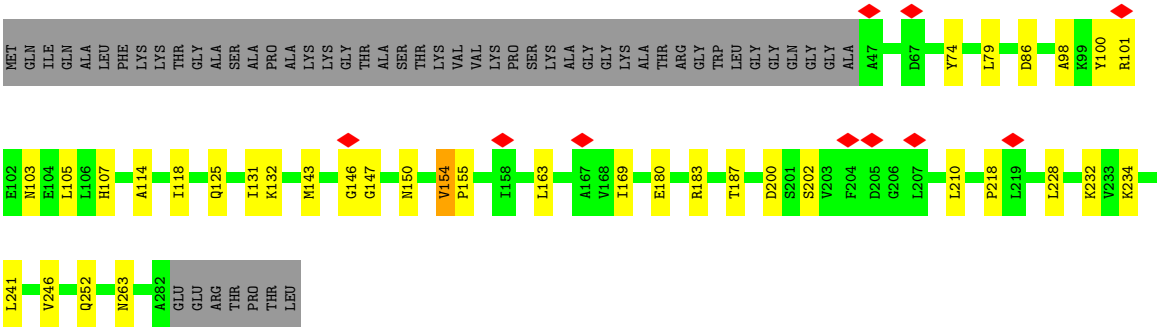
Chain S:



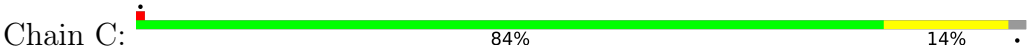


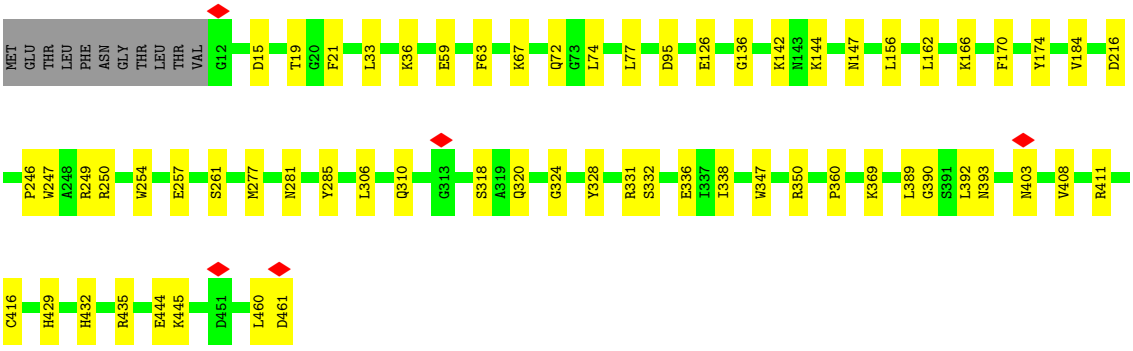
• Molecule 19: Chlorophyll a-b binding protein, chloroplastic



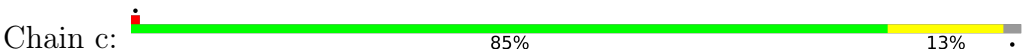


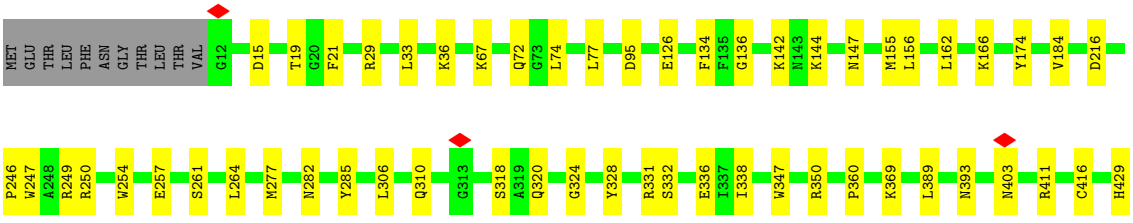
• Molecule 20: Photosystem II CP43 reaction center protein

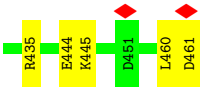




• Molecule 20: Photosystem II CP43 reaction center protein



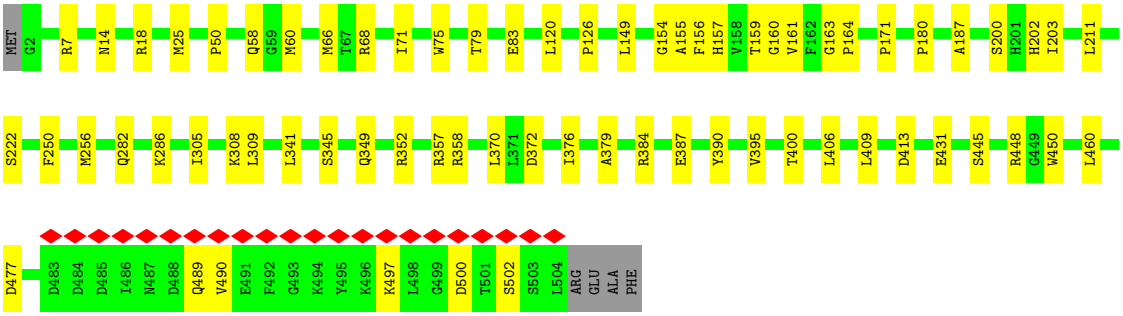




• Molecule 21: Photosystem II CP47 reaction center protein

Chain B:

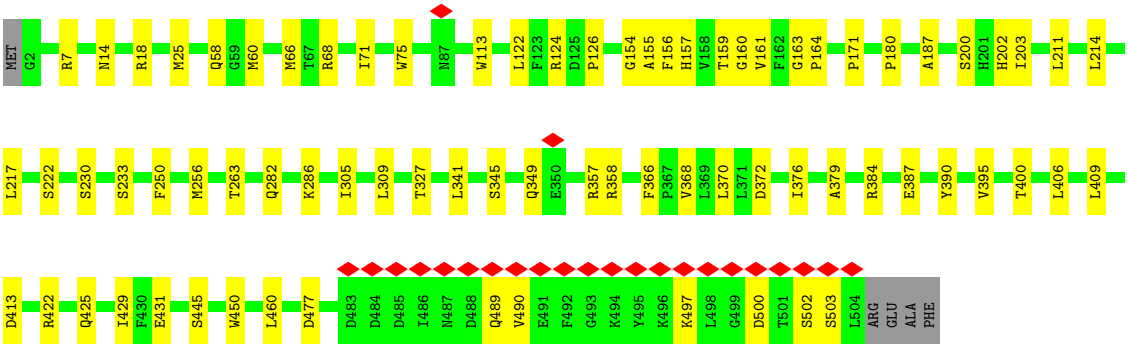




• Molecule 21: Photosystem II CP47 reaction center protein

Chain b:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	89018	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.181	Depositor
Minimum map value	-1.592	Depositor
Average map value	-0.003	Depositor
Map value standard deviation	0.139	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	392.1, 392.1, 392.1	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.307, 1.307, 1.307	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: SQD, XAT, BCR, CHL, PL9, CLA, BCT, LUT, FE2, LHG, NEX, LMG, PHO, HEM, CL, DGD

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	R	0.21	0/1736	0.56	0/2357
1	r	0.21	0/1739	0.57	0/2361
2	A	0.28	0/2696	0.51	0/3676
2	a	0.29	0/2696	0.53	0/3676
3	D	0.29	0/2808	0.61	0/3830
3	d	0.29	0/2808	0.61	0/3830
4	F	0.25	0/250	0.56	0/338
4	f	0.26	0/250	0.56	0/338
5	H	0.25	0/499	0.51	0/683
5	h	0.25	0/499	0.52	0/683
6	I	0.31	0/283	0.57	0/383
6	i	0.31	0/283	0.57	0/383
7	J	0.18	0/254	0.47	0/345
7	j	0.17	0/254	0.47	0/345
8	K	0.33	0/300	0.74	0/414
8	k	0.35	0/300	0.73	0/414
9	L	0.26	0/314	0.52	0/427
9	l	0.26	0/314	0.55	0/427
10	M	0.24	0/252	0.48	0/345
10	m	0.24	0/252	0.48	0/345
11	O	0.21	0/1620	0.53	0/2184
11	o	0.21	0/1620	0.53	0/2184
12	T	0.22	0/254	0.54	0/343
12	t	0.21	0/254	0.54	0/343
13	W	0.24	0/428	0.48	0/581
13	w	0.24	0/428	0.48	0/581
14	X	0.21	0/244	0.40	0/330
14	x	0.21	0/244	0.40	0/330
15	Z	0.19	0/476	0.41	0/654
15	z	0.19	0/476	0.41	0/654
16	Y	0.19	0/208	0.48	0/285
16	y	0.19	0/208	0.48	0/285

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
17	E	0.22	0/571	0.54	0/780
17	e	0.22	0/571	0.51	0/780
18	1	0.22	0/1717	0.55	0/2337
18	2	0.25	0/1717	0.63	3/2337 (0.1%)
18	3	0.20	0/1723	0.52	0/2345
18	4	0.22	0/1717	0.56	0/2337
18	5	0.24	0/1717	0.56	1/2337 (0.0%)
18	6	0.21	0/1723	0.54	0/2345
18	G	0.23	0/1723	0.56	0/2345
18	N	0.24	0/1708	0.55	1/2323 (0.0%)
18	P	0.22	0/1717	0.55	1/2337 (0.0%)
18	Q	0.20	0/1723	0.57	0/2345
18	U	0.25	0/1717	0.56	0/2337
18	V	0.21	0/1717	0.53	0/2337
18	g	0.23	0/1723	0.61	0/2345
18	n	0.23	0/1717	0.59	1/2337 (0.0%)
18	p	0.23	0/1717	0.57	1/2337 (0.0%)
18	q	0.21	0/1723	0.57	0/2345
18	u	0.26	0/1717	0.59	0/2337
18	v	0.22	0/1717	0.55	0/2337
19	S	0.25	0/1849	0.65	2/2521 (0.1%)
19	s	0.25	0/1849	0.66	2/2521 (0.1%)
20	C	0.26	0/3623	0.47	0/4936
20	c	0.26	0/3623	0.47	0/4936
21	B	0.23	0/4067	0.45	0/5533
21	b	0.23	0/4067	0.46	0/5533
All	All	0.24	0/76400	0.54	12/103994 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	r	0	1
18	1	0	1
18	2	0	2
18	3	0	1
18	4	0	2
18	5	0	1
18	6	0	2
18	N	0	1

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
18	P	0	1
18	Q	0	1
18	U	0	1
18	V	0	1
18	g	0	1
18	n	0	1
18	p	0	1
18	q	0	1
18	u	0	1
18	v	0	1
All	All	0	21

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
18	2	199	LYS	CD-CE-NZ	-6.37	91.50	111.90
18	5	199	LYS	CD-CE-NZ	-6.22	91.99	111.90
18	n	199	LYS	CD-CE-NZ	-5.93	92.92	111.90
18	p	199	LYS	CD-CE-NZ	-5.74	93.54	111.90
18	2	51	ALA	CA-C-N	5.30	131.65	121.54

There are no chirality outliers.

5 of 21 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
18	1	135	LEU	Peptide
18	2	51	ALA	Peptide
18	2	52	TYR	Peptide
18	3	135	LEU	Peptide
1	r	15	LEU	Peptide

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.

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	R	1698	0	1653	34	0
1	r	1701	0	1656	31	0
2	A	2614	0	2516	41	0
2	a	2614	0	2516	38	0
3	D	2714	0	2596	40	0
3	d	2714	0	2596	38	0
4	F	243	0	252	4	0
4	f	243	0	252	4	0
5	H	488	0	515	9	0
5	h	488	0	515	9	0
6	I	275	0	287	1	0
6	i	275	0	287	1	0
7	J	245	0	236	5	0
7	j	245	0	236	5	0
8	K	288	0	295	1	0
8	k	288	0	295	2	0
9	L	306	0	313	7	0
9	l	306	0	313	6	0
10	M	248	0	266	4	0
10	m	248	0	266	4	0
11	O	1592	0	1592	25	0
11	o	1592	0	1592	22	0
12	T	247	0	260	6	0
12	t	247	0	260	7	0
13	W	417	0	387	1	0
13	w	417	0	387	2	0
14	X	242	0	266	1	0
14	x	242	0	266	1	0
15	Z	465	0	499	4	0
15	z	465	0	499	6	0
16	Y	208	0	239	2	0
16	y	208	0	239	2	0
17	E	555	0	550	6	0
17	e	555	0	550	7	0
18	1	1669	0	1612	21	0
18	2	1669	0	1612	16	0
18	3	1675	0	1616	22	0
18	4	1669	0	1612	28	0
18	5	1669	0	1612	22	0
18	6	1675	0	1616	23	0
18	G	1675	0	1617	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	N	1661	0	1600	19	0
18	P	1669	0	1612	26	0
18	Q	1675	0	1617	24	0
18	U	1669	0	1612	27	0
18	V	1669	0	1612	24	0
18	g	1675	0	1617	21	0
18	n	1669	0	1612	16	0
18	p	1669	0	1612	23	0
18	q	1675	0	1617	24	0
18	u	1669	0	1612	32	0
18	v	1669	0	1612	18	0
19	S	1797	0	1744	25	0
19	s	1797	0	1743	24	0
20	C	3502	0	3373	46	0
20	c	3502	0	3373	44	0
21	B	3937	0	3814	50	0
21	b	3937	0	3814	55	0
22	1	473	0	468	16	0
22	2	473	0	466	22	0
22	3	477	0	475	15	0
22	4	473	0	468	19	0
22	5	473	0	466	19	0
22	6	477	0	474	12	0
22	A	240	0	242	8	0
22	B	1040	0	1150	29	0
22	C	845	0	933	25	0
22	D	65	0	71	3	0
22	G	477	0	475	9	0
22	N	473	0	466	15	0
22	P	473	0	466	17	0
22	Q	477	0	475	14	0
22	R	543	0	489	14	0
22	S	465	0	391	10	0
22	U	473	0	468	11	0
22	V	473	0	468	16	0
22	X	65	0	70	1	0
22	a	240	0	242	6	0
22	b	1040	0	1149	33	0
22	c	845	0	933	23	0
22	d	65	0	71	2	0
22	g	477	0	474	5	0
22	n	473	0	466	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	p	473	0	466	14	0
22	q	477	0	474	10	0
22	r	543	0	487	19	0
22	s	465	0	391	13	0
22	u	473	0	468	14	0
22	v	473	0	468	14	0
22	x	65	0	70	0	0
23	1	84	0	112	5	0
23	2	84	0	112	8	0
23	4	84	0	112	9	0
23	5	84	0	112	14	0
23	N	84	0	112	9	0
23	P	84	0	112	7	0
23	R	42	0	56	2	0
23	S	84	0	112	9	0
23	U	84	0	112	4	0
23	V	84	0	112	11	0
23	n	84	0	112	7	0
23	p	84	0	112	5	0
23	r	42	0	55	4	0
23	s	84	0	111	10	0
23	u	84	0	112	6	0
23	v	84	0	112	7	0
24	1	44	0	56	2	0
24	2	44	0	56	5	0
24	3	44	0	56	2	0
24	4	44	0	56	1	0
24	5	44	0	56	3	0
24	6	44	0	56	4	0
24	G	44	0	56	3	0
24	N	44	0	56	2	0
24	P	44	0	56	4	0
24	Q	44	0	56	0	0
24	R	44	0	56	3	0
24	U	44	0	56	5	0
24	V	44	0	56	4	0
24	g	44	0	56	5	0
24	n	44	0	56	1	0
24	p	44	0	56	3	0
24	q	44	0	56	1	0
24	r	44	0	56	4	0
24	u	44	0	56	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	v	44	0	56	3	0
25	1	49	0	74	0	0
25	2	49	0	74	3	0
25	3	49	0	74	3	0
25	4	49	0	74	1	0
25	5	49	0	74	1	0
25	6	49	0	74	3	0
25	A	43	0	56	3	0
25	B	96	0	139	0	0
25	C	147	0	222	5	0
25	D	95	0	138	11	0
25	G	49	0	74	0	0
25	L	49	0	74	2	0
25	N	49	0	74	4	0
25	P	49	0	74	1	0
25	Q	49	0	74	4	0
25	R	42	0	57	0	0
25	S	49	0	71	5	0
25	U	49	0	74	4	0
25	V	49	0	74	6	0
25	a	43	0	56	1	0
25	b	96	0	139	0	0
25	c	147	0	222	7	0
25	d	95	0	138	12	0
25	g	49	0	74	2	0
25	l	49	0	74	1	0
25	n	49	0	74	1	0
25	p	49	0	74	2	0
25	q	49	0	74	2	0
25	r	42	0	57	1	0
25	s	49	0	71	3	0
25	u	49	0	74	2	0
25	v	49	0	74	4	0
26	1	362	0	347	10	0
26	2	362	0	349	12	0
26	3	357	0	335	16	0
26	4	296	0	277	11	0
26	5	362	0	349	12	0
26	6	423	0	405	20	0
26	G	357	0	335	13	0
26	N	296	0	280	12	0
26	P	362	0	349	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
26	Q	357	0	335	9	0
26	R	183	0	174	5	0
26	S	196	0	141	4	0
26	U	380	0	384	17	0
26	V	362	0	347	15	0
26	g	357	0	335	12	0
26	n	362	0	349	13	0
26	p	428	0	419	12	0
26	q	291	0	265	13	0
26	r	231	0	207	7	0
26	s	196	0	141	2	0
26	u	362	0	347	11	0
26	v	362	0	347	14	0
27	2	44	0	56	1	0
27	5	44	0	56	2	0
27	N	44	0	56	2	0
27	P	44	0	54	1	0
27	R	44	0	54	3	0
27	S	44	0	55	3	0
27	U	44	0	56	0	0
27	V	44	0	56	3	0
27	n	44	0	56	2	0
27	p	44	0	54	4	0
27	r	88	0	110	7	0
27	s	44	0	55	4	0
27	u	88	0	112	3	0
27	v	44	0	56	2	0
28	A	1	0	0	0	0
28	a	1	0	0	0	0
29	A	2	0	0	2	0
29	a	2	0	0	4	0
30	A	64	0	74	4	0
30	D	64	0	74	1	0
30	a	64	0	74	2	0
30	d	64	0	74	1	0
31	A	40	0	56	4	0
31	B	120	0	168	11	0
31	C	120	0	168	4	0
31	D	40	0	55	1	0
31	K	40	0	56	2	0
31	T	40	0	56	5	0
31	X	40	0	56	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	a	40	0	56	3	0
31	b	120	0	168	12	0
31	c	80	0	112	1	0
31	d	40	0	55	0	0
31	k	40	0	56	2	0
31	t	40	0	56	6	0
31	x	40	0	56	3	0
31	z	40	0	56	2	0
32	A	54	0	77	3	0
32	C	50	0	66	2	0
32	L	54	0	76	2	0
32	M	42	0	48	1	0
32	a	104	0	143	6	0
32	l	54	0	76	3	0
32	m	42	0	48	1	0
33	A	13	0	7	0	0
33	D	55	0	80	3	0
33	a	13	0	7	0	0
33	d	55	0	80	3	0
34	A	40	0	50	1	0
34	B	106	0	157	4	0
34	C	102	0	144	4	0
34	D	46	0	61	0	0
34	W	48	0	66	2	0
34	a	40	0	50	1	0
34	b	106	0	157	5	0
34	c	102	0	144	3	0
34	d	46	0	61	0	0
34	w	48	0	66	2	0
35	D	4	0	1	1	0
35	a	4	0	1	1	0
36	A	59	0	76	2	0
36	B	62	0	80	6	0
36	C	117	0	150	7	0
36	J	60	0	78	2	0
36	a	59	0	76	2	0
36	b	62	0	80	7	0
36	c	177	0	228	8	0
37	E	43	0	30	1	0
37	e	43	0	30	1	0
All	All	104363	0	104847	1605	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 8.

The worst 5 of 1605 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)
18:v:208:MET:HE2	23:v:310:LUT:H10	1.67	0.74
11:o:125:MET:SD	11:o:163:GLN:NE2	2.61	0.73
11:O:125:MET:SD	11:O:163:GLN:NE2	2.62	0.73
18:V:208:MET:HE2	23:V:310:LUT:H10	1.72	0.72
22:2:304:CLA:H52	23:2:309:LUT:H30	1.71	0.71

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	R	221/280 (79%)	201 (91%)	20 (9%)	0	100	100
1	r	221/280 (79%)	197 (89%)	24 (11%)	0	100	100
2	A	331/352 (94%)	314 (95%)	17 (5%)	0	100	100
2	a	331/352 (94%)	316 (96%)	15 (4%)	0	100	100
3	D	339/352 (96%)	304 (90%)	35 (10%)	0	100	100
3	d	339/352 (96%)	307 (91%)	32 (9%)	0	100	100
4	F	28/44 (64%)	27 (96%)	1 (4%)	0	100	100
4	f	28/44 (64%)	27 (96%)	1 (4%)	0	100	100
5	H	62/88 (70%)	61 (98%)	1 (2%)	0	100	100
5	h	62/88 (70%)	61 (98%)	1 (2%)	0	100	100
6	I	32/37 (86%)	29 (91%)	3 (9%)	0	100	100
6	i	32/37 (86%)	29 (91%)	3 (9%)	0	100	100
7	J	29/50 (58%)	27 (93%)	2 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	j	29/50 (58%)	27 (93%)	2 (7%)	0	100	100
8	K	34/46 (74%)	30 (88%)	4 (12%)	0	100	100
8	k	34/46 (74%)	30 (88%)	4 (12%)	0	100	100
9	L	35/38 (92%)	34 (97%)	1 (3%)	0	100	100
9	l	35/38 (92%)	34 (97%)	1 (3%)	0	100	100
10	M	30/34 (88%)	30 (100%)	0	0	100	100
10	m	30/34 (88%)	30 (100%)	0	0	100	100
11	O	206/291 (71%)	176 (85%)	30 (15%)	0	100	100
11	o	206/291 (71%)	175 (85%)	31 (15%)	0	100	100
12	T	28/31 (90%)	25 (89%)	3 (11%)	0	100	100
12	t	28/31 (90%)	26 (93%)	2 (7%)	0	100	100
13	W	52/115 (45%)	49 (94%)	3 (6%)	0	100	100
13	w	52/115 (45%)	49 (94%)	3 (6%)	0	100	100
14	X	33/101 (33%)	33 (100%)	0	0	100	100
14	x	33/101 (33%)	33 (100%)	0	0	100	100
15	Z	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
15	z	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
16	Y	28/33 (85%)	26 (93%)	2 (7%)	0	100	100
16	y	28/33 (85%)	26 (93%)	2 (7%)	0	100	100
17	E	66/82 (80%)	58 (88%)	8 (12%)	0	100	100
17	e	66/82 (80%)	57 (86%)	9 (14%)	0	100	100
18	1	216/257 (84%)	188 (87%)	27 (12%)	1 (0%)	24	56
18	2	216/257 (84%)	188 (87%)	27 (12%)	1 (0%)	24	56
18	3	217/257 (84%)	191 (88%)	26 (12%)	0	100	100
18	4	216/257 (84%)	189 (88%)	26 (12%)	1 (0%)	24	56
18	5	216/257 (84%)	190 (88%)	26 (12%)	0	100	100
18	6	217/257 (84%)	190 (88%)	27 (12%)	0	100	100
18	G	217/257 (84%)	185 (85%)	32 (15%)	0	100	100
18	N	213/257 (83%)	188 (88%)	24 (11%)	1 (0%)	24	56
18	P	216/257 (84%)	188 (87%)	27 (12%)	1 (0%)	24	56
18	Q	217/257 (84%)	184 (85%)	33 (15%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	U	216/257 (84%)	187 (87%)	29 (13%)	0	100	100
18	V	216/257 (84%)	187 (87%)	29 (13%)	0	100	100
18	g	217/257 (84%)	183 (84%)	34 (16%)	0	100	100
18	n	216/257 (84%)	184 (85%)	32 (15%)	0	100	100
18	p	216/257 (84%)	186 (86%)	28 (13%)	2 (1%)	14	45
18	q	217/257 (84%)	186 (86%)	31 (14%)	0	100	100
18	u	216/257 (84%)	183 (85%)	33 (15%)	0	100	100
18	v	216/257 (84%)	186 (86%)	30 (14%)	0	100	100
19	S	234/289 (81%)	201 (86%)	33 (14%)	0	100	100
19	s	234/289 (81%)	202 (86%)	32 (14%)	0	100	100
20	C	448/461 (97%)	429 (96%)	19 (4%)	0	100	100
20	c	448/461 (97%)	430 (96%)	18 (4%)	0	100	100
21	B	501/508 (99%)	472 (94%)	29 (6%)	0	100	100
21	b	501/508 (99%)	470 (94%)	31 (6%)	0	100	100
All	All	9485/11214 (85%)	8533 (90%)	945 (10%)	7 (0%)	49	78

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	2	52	TYR
18	p	136	VAL
18	P	136	VAL
18	1	136	VAL
18	N	136	VAL

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	R	175/218 (80%)	175 (100%)	0	100	100
1	r	176/218 (81%)	176 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	272/289 (94%)	272 (100%)	0	100	100
2	a	272/289 (94%)	272 (100%)	0	100	100
3	D	272/281 (97%)	270 (99%)	2 (1%)	76	77
3	d	272/281 (97%)	270 (99%)	2 (1%)	76	77
4	F	24/37 (65%)	24 (100%)	0	100	100
4	f	24/37 (65%)	24 (100%)	0	100	100
5	H	55/75 (73%)	54 (98%)	1 (2%)	51	66
5	h	55/75 (73%)	54 (98%)	1 (2%)	51	66
6	I	31/34 (91%)	30 (97%)	1 (3%)	34	56
6	i	31/34 (91%)	30 (97%)	1 (3%)	34	56
7	J	24/42 (57%)	24 (100%)	0	100	100
7	j	24/42 (57%)	24 (100%)	0	100	100
8	K	30/38 (79%)	30 (100%)	0	100	100
8	k	30/38 (79%)	30 (100%)	0	100	100
9	L	34/35 (97%)	34 (100%)	0	100	100
9	l	34/35 (97%)	34 (100%)	0	100	100
10	M	28/30 (93%)	28 (100%)	0	100	100
10	m	28/30 (93%)	28 (100%)	0	100	100
11	O	174/223 (78%)	174 (100%)	0	100	100
11	o	174/223 (78%)	174 (100%)	0	100	100
12	T	27/28 (96%)	27 (100%)	0	100	100
12	t	27/28 (96%)	27 (100%)	0	100	100
13	W	42/87 (48%)	42 (100%)	0	100	100
13	w	42/87 (48%)	42 (100%)	0	100	100
14	X	25/67 (37%)	25 (100%)	0	100	100
14	x	25/67 (37%)	25 (100%)	0	100	100
15	Z	52/52 (100%)	52 (100%)	0	100	100
15	z	52/52 (100%)	52 (100%)	0	100	100
16	Y	24/27 (89%)	24 (100%)	0	100	100
16	y	24/27 (89%)	24 (100%)	0	100	100
17	E	60/71 (84%)	60 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	e	60/71 (84%)	60 (100%)	0	100	100
18	1	169/194 (87%)	168 (99%)	1 (1%)	78	79
18	2	169/194 (87%)	166 (98%)	3 (2%)	51	66
18	3	170/194 (88%)	168 (99%)	2 (1%)	63	71
18	4	169/194 (87%)	168 (99%)	1 (1%)	78	79
18	5	169/194 (87%)	166 (98%)	3 (2%)	51	66
18	6	170/194 (88%)	169 (99%)	1 (1%)	78	79
18	G	170/194 (88%)	168 (99%)	2 (1%)	63	71
18	N	168/194 (87%)	165 (98%)	3 (2%)	51	66
18	P	169/194 (87%)	166 (98%)	3 (2%)	51	66
18	Q	170/194 (88%)	168 (99%)	2 (1%)	63	71
18	U	169/194 (87%)	167 (99%)	2 (1%)	63	71
18	V	169/194 (87%)	168 (99%)	1 (1%)	78	79
18	g	170/194 (88%)	167 (98%)	3 (2%)	51	66
18	n	169/194 (87%)	167 (99%)	2 (1%)	63	71
18	p	169/194 (87%)	166 (98%)	3 (2%)	51	66
18	q	170/194 (88%)	168 (99%)	2 (1%)	63	71
18	u	169/194 (87%)	167 (99%)	2 (1%)	63	71
18	v	169/194 (87%)	168 (99%)	1 (1%)	78	79
19	S	181/217 (83%)	180 (99%)	1 (1%)	78	79
19	s	181/217 (83%)	180 (99%)	1 (1%)	78	79
20	C	352/362 (97%)	352 (100%)	0	100	100
20	c	352/362 (97%)	352 (100%)	0	100	100
21	B	403/407 (99%)	403 (100%)	0	100	100
21	b	403/407 (99%)	403 (100%)	0	100	100
All	All	7618/8732 (87%)	7571 (99%)	47 (1%)	76	79

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	Q	130	LEU
18	G	130	LEU
18	U	97	ILE

Continued on next page...

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Mol	Chain	Res	Type
18	N	130	LEU
18	u	130	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 136 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	239	GLN
3	D	350	ASN
20	c	320	GLN
18	6	236	ASN
18	6	120	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 552 ligands modelled in this entry, 6 are monoatomic - leaving 546 for Mogul analysis.

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	$\#\|Z\| > 2$
22	CLA	b	608	-	69,73,73	1.24	9 (13%)	83,113,113	1.40	8 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
22	CLA	v	302	-	69,73,73	1.26	10 (14%)	83,113,113	1.31	7 (8%)
25	LHG	C	522	-	48,48,48	0.89	4 (8%)	51,54,54	1.09	2 (3%)
22	CLA	s	308	-	59,63,73	1.33	9 (15%)	71,101,113	1.40	5 (7%)
23	LUT	2	309	-	42,43,43	0.76	0	51,60,60	1.68	14 (27%)
26	CHL	U	319	-	70,74,74	1.93	20 (28%)	80,114,114	2.63	24 (30%)
27	NEX	r	618	22,1	38,46,46	1.04	2 (5%)	50,70,70	2.49	16 (32%)
26	CHL	6	315	-	70,74,74	1.96	20 (28%)	80,114,114	2.61	25 (31%)
22	CLA	R	309	-	53,57,73	1.41	7 (13%)	62,93,113	1.48	10 (16%)
22	CLA	b	606	-	69,73,73	1.24	9 (13%)	83,113,113	1.36	6 (7%)
22	CLA	C	503	-	69,73,73	1.25	9 (13%)	83,113,113	1.35	8 (9%)
25	LHG	5	312	-	48,48,48	0.90	3 (6%)	51,54,54	1.07	2 (3%)
34	LMG	b	621	-	51,51,55	1.18	6 (11%)	59,59,63	1.44	7 (11%)
26	CHL	n	317	-	70,74,74	1.94	21 (30%)	80,114,114	2.69	25 (31%)
23	LUT	V	309	-	42,43,43	0.78	0	51,60,60	1.63	13 (25%)
31	BCR	b	618	-	41,41,41	4.74	24 (58%)	56,56,56	2.46	23 (41%)
26	CHL	Q	311	-	70,74,74	1.92	20 (28%)	80,114,114	2.70	27 (33%)
25	LHG	R	314	-	41,41,48	0.96	3 (7%)	44,47,54	1.09	2 (4%)
22	CLA	r	601	27	53,57,73	1.44	10 (18%)	62,93,113	1.51	6 (9%)
22	CLA	G	304	18	68,72,73	1.25	9 (13%)	81,111,113	1.39	10 (12%)
32	SQD	a	413	-	53,54,54	0.95	5 (9%)	62,65,65	1.51	9 (14%)
22	CLA	g	302	-	69,73,73	1.26	9 (13%)	83,113,113	1.29	5 (6%)
22	CLA	1	304	-	64,68,73	1.28	10 (15%)	77,107,113	1.36	6 (7%)
26	CHL	2	316	-	70,74,74	1.95	20 (28%)	80,114,114	2.61	23 (28%)
22	CLA	p	307	-	64,68,73	1.29	7 (10%)	77,107,113	1.36	6 (7%)
22	CLA	b	603	-	69,73,73	1.24	9 (13%)	83,113,113	1.34	5 (6%)
26	CHL	3	311	-	70,74,74	1.90	18 (25%)	80,114,114	2.71	27 (33%)
27	NEX	2	319	-	38,46,46	0.93	1 (2%)	50,70,70	2.45	14 (28%)
25	LHG	D	407	3	48,48,48	0.90	4 (8%)	51,54,54	1.07	3 (5%)
23	LUT	5	309	-	42,43,43	0.76	0	51,60,60	1.75	13 (25%)
24	XAT	4	311	-	39,47,47	2.54	17 (43%)	54,74,74	12.07	21 (38%)
22	CLA	p	309	-	52,56,73	1.42	9 (17%)	62,92,113	1.45	5 (8%)
24	XAT	1	311	-	39,47,47	2.54	17 (43%)	54,74,74	12.16	18 (33%)
22	CLA	3	307	-	69,73,73	1.24	10 (14%)	83,113,113	1.34	6 (7%)
22	CLA	B	602	-	69,73,73	1.25	10 (14%)	83,113,113	1.37	9 (10%)
22	CLA	g	306	22	64,68,73	1.31	8 (12%)	77,107,113	1.27	4 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
24	XAT	P	312	-	39,47,47	2.59	18 (46%)	54,74,74	11.98	19 (35%)
22	CLA	c	512	-	69,73,73	1.26	11 (15%)	83,113,113	1.40	8 (9%)
22	CLA	N	306	-	64,68,73	1.29	7 (10%)	77,107,113	1.39	8 (10%)
22	CLA	U	303	-	54,58,73	1.40	9 (16%)	65,95,113	1.43	8 (12%)
25	LHG	b	622	-	46,46,48	0.91	4 (8%)	49,52,54	1.04	2 (4%)
22	CLA	B	611	-	69,73,73	1.26	9 (13%)	83,113,113	1.39	7 (8%)
33	PL9	d	404	-	55,55,55	1.54	6 (10%)	68,69,69	1.68	18 (26%)
31	BCR	b	620	-	41,41,41	4.77	24 (58%)	56,56,56	2.21	21 (37%)
26	CHL	2	318	-	70,74,74	1.90	20 (28%)	80,114,114	2.66	25 (31%)
22	CLA	5	301	-	69,73,73	1.24	10 (14%)	83,113,113	1.30	8 (9%)
35	BCT	a	414	-	2,3,3	1.35	0	2,3,3	0.20	0
22	CLA	v	304	-	64,68,73	1.28	8 (12%)	77,107,113	1.39	8 (10%)
22	CLA	C	513	-	69,73,73	1.27	11 (15%)	83,113,113	1.41	8 (9%)
25	LHG	s	312	19	48,48,48	0.89	4 (8%)	51,54,54	1.14	3 (5%)
34	LMG	a	412	-	40,40,55	1.30	6 (15%)	48,48,63	1.16	2 (4%)
23	LUT	1	310	-	42,43,43	0.80	0	51,60,60	1.74	14 (27%)
25	LHG	b	623	21	48,48,48	0.90	4 (8%)	51,54,54	1.06	2 (3%)
22	CLA	q	303	-	54,58,73	1.40	9 (16%)	65,95,113	1.49	9 (13%)
22	CLA	c	513	-	69,73,73	1.24	10 (14%)	83,113,113	1.34	6 (7%)
22	CLA	b	615	-	69,73,73	1.22	10 (14%)	83,113,113	1.38	7 (8%)
22	CLA	1	308	-	52,56,73	1.41	9 (17%)	62,92,113	1.44	5 (8%)
22	CLA	Q	303	-	54,58,73	1.41	8 (14%)	65,95,113	1.41	5 (7%)
26	CHL	v	314	-	52,56,74	2.20	16 (30%)	58,92,114	3.11	23 (39%)
31	BCR	c	516	-	41,41,41	4.76	24 (58%)	56,56,56	2.30	21 (37%)
33	PL9	A	410	-	13,13,55	3.64	7 (53%)	17,17,69	1.47	3 (17%)
22	CLA	5	304	18	69,73,73	1.23	10 (14%)	83,113,113	1.40	8 (9%)
34	LMG	b	624	21	55,55,55	1.17	6 (10%)	63,63,63	1.07	2 (3%)
22	CLA	B	606	-	69,73,73	1.25	9 (13%)	83,113,113	1.37	5 (6%)
22	CLA	U	302	-	69,73,73	1.26	9 (13%)	83,113,113	1.31	4 (4%)
22	CLA	2	304	18	69,73,73	1.22	10 (14%)	83,113,113	1.37	7 (8%)
22	CLA	q	301	-	69,73,73	1.28	10 (14%)	83,113,113	1.30	8 (9%)
22	CLA	G	306	22	64,68,73	1.30	8 (12%)	77,107,113	1.28	4 (5%)
26	CHL	u	314	-	52,56,74	2.20	20 (38%)	58,92,114	3.03	24 (41%)
22	CLA	Q	301	-	69,73,73	1.28	10 (14%)	83,113,113	1.31	8 (9%)
26	CHL	6	314	-	54,58,74	2.28	19 (35%)	59,94,114	2.84	25 (42%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
22	CLA	s	301	19	65,69,73	1.26	11 (16%)	78,108,113	1.37	11 (14%)
24	XAT	Q	309	-	39,47,47	2.60	18 (46%)	54,74,74	11.94	19 (35%)
22	CLA	6	307	22	64,68,73	1.30	8 (12%)	77,107,113	1.33	5 (6%)
25	LHG	L	101	-	48,48,48	0.89	3 (6%)	51,54,54	1.11	3 (5%)
22	CLA	v	303	-	54,58,73	1.41	9 (16%)	65,95,113	1.48	5 (7%)
27	NEX	R	301	22,1	38,46,46	1.03	2 (5%)	50,70,70	2.42	13 (26%)
36	DGD	B	601	21	63,63,67	1.22	7 (11%)	77,77,81	1.07	3 (3%)
31	BCR	C	517	-	41,41,41	4.69	24 (58%)	56,56,56	2.67	24 (42%)
22	CLA	n	304	18	69,73,73	1.22	10 (14%)	83,113,113	1.40	9 (10%)
22	CLA	V	302	-	69,73,73	1.26	10 (14%)	83,113,113	1.29	5 (6%)
22	CLA	G	308	-	52,56,73	1.43	9 (17%)	62,92,113	1.47	6 (9%)
22	CLA	C	506	-	69,73,73	1.24	9 (13%)	83,113,113	1.35	6 (7%)
26	CHL	4	315	-	54,58,74	2.25	19 (35%)	59,94,114	2.84	21 (35%)
23	LUT	p	310	-	42,43,43	0.74	0	51,60,60	1.72	14 (27%)
27	NEX	s	317	19	38,46,46	0.87	1 (2%)	50,70,70	2.39	16 (32%)
22	CLA	C	511	-	69,73,73	1.23	10 (14%)	83,113,113	1.39	11 (13%)
26	CHL	U	317	-	70,74,74	1.88	19 (27%)	80,114,114	2.65	22 (27%)
26	CHL	3	314	-	70,74,74	1.97	20 (28%)	80,114,114	2.59	23 (28%)
22	CLA	c	502	-	69,73,73	1.25	9 (13%)	83,113,113	1.34	7 (8%)
36	DGD	C	520	-	63,63,67	1.22	6 (9%)	77,77,81	1.16	4 (5%)
26	CHL	U	315	-	70,74,74	1.87	18 (25%)	80,114,114	2.75	26 (32%)
22	CLA	C	508	-	69,73,73	1.26	10 (14%)	83,113,113	1.38	7 (8%)
31	BCR	d	403	3	41,41,41	4.76	24 (58%)	56,56,56	2.26	23 (41%)
24	XAT	p	312	-	39,47,47	2.59	18 (46%)	54,74,74	11.83	18 (33%)
24	XAT	r	612	-	39,47,47	2.52	17 (43%)	54,74,74	11.45	25 (46%)
26	CHL	g	311	-	70,74,74	1.90	19 (27%)	80,114,114	2.66	25 (31%)
22	CLA	P	303	-	69,73,73	1.24	9 (13%)	83,113,113	1.33	5 (6%)
26	CHL	n	318	-	70,74,74	1.96	20 (28%)	80,114,114	2.59	26 (32%)
37	HEM	E	101	4,17	50,50,50	1.43	6 (12%)	66,82,82	1.21	4 (6%)
36	DGD	J	101	-	61,61,67	1.26	6 (9%)	75,75,81	1.17	3 (4%)
25	LHG	V	312	-	48,48,48	0.90	4 (8%)	51,54,54	1.10	2 (3%)
25	LHG	d	406	3	48,48,48	0.90	4 (8%)	51,54,54	1.07	3 (5%)
25	LHG	6	311	-	48,48,48	0.90	4 (8%)	51,54,54	1.12	2 (3%)
31	BCR	t	101	-	41,41,41	4.79	24 (58%)	56,56,56	2.38	22 (39%)
26	CHL	N	313	-	70,74,74	1.91	19 (27%)	80,114,114	2.63	25 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
30	PHO	D	401	-	58,69,69	1.98	9 (15%)	56,99,99	1.79	9 (16%)
22	CLA	B	603	-	69,73,73	1.24	9 (13%)	83,113,113	1.34	5 (6%)
22	CLA	r	609	26	64,68,73	1.30	7 (10%)	77,107,113	1.46	9 (11%)
22	CLA	b	607	-	69,73,73	1.25	9 (13%)	83,113,113	1.42	7 (8%)
22	CLA	r	610	-	49,53,73	1.48	8 (16%)	59,89,113	1.51	4 (6%)
22	CLA	n	303	-	54,58,73	1.40	9 (16%)	65,95,113	1.43	8 (12%)
31	BCR	T	101	-	41,41,41	4.79	24 (58%)	56,56,56	2.38	22 (39%)
34	LMG	C	502	-	51,51,55	1.15	4 (7%)	59,59,63	1.16	3 (5%)
26	CHL	R	317	-	65,69,74	2.02	21 (32%)	74,108,114	2.57	23 (31%)
25	LHG	P	313	-	48,48,48	0.90	4 (8%)	51,54,54	1.07	2 (3%)
22	CLA	s	302	-	49,53,73	1.50	8 (16%)	59,89,113	1.49	6 (10%)
26	CHL	S	313	-	50,54,74	2.31	18 (36%)	56,90,114	3.06	23 (41%)
24	XAT	v	311	-	39,47,47	2.56	18 (46%)	54,74,74	12.01	19 (35%)
26	CHL	p	320	-	70,74,74	1.88	19 (27%)	80,114,114	2.69	24 (30%)
22	CLA	4	306	-	64,68,73	1.32	9 (14%)	77,107,113	1.33	7 (9%)
22	CLA	U	305	-	64,68,73	1.29	10 (15%)	77,107,113	1.31	4 (5%)
26	CHL	4	317	-	70,74,74	1.89	20 (28%)	80,114,114	2.67	25 (31%)
36	DGD	b	601	21	63,63,67	1.23	7 (11%)	77,77,81	1.06	3 (3%)
22	CLA	A	406	-	54,58,73	1.41	10 (18%)	65,95,113	1.44	6 (9%)
22	CLA	C	514	-	69,73,73	1.24	10 (14%)	83,113,113	1.34	5 (6%)
23	LUT	u	309	-	42,43,43	0.75	0	51,60,60	1.52	10 (19%)
22	CLA	6	304	-	54,58,73	1.41	10 (18%)	65,95,113	1.43	9 (13%)
22	CLA	5	303	-	54,58,73	1.40	9 (16%)	65,95,113	1.45	6 (9%)
26	CHL	5	317	-	70,74,74	1.87	18 (25%)	80,114,114	2.72	25 (31%)
26	CHL	n	316	-	70,74,74	1.92	20 (28%)	80,114,114	2.63	23 (28%)
22	CLA	4	304	-	64,68,73	1.28	10 (15%)	77,107,113	1.36	5 (6%)
22	CLA	B	617	-	69,73,73	1.25	9 (13%)	83,113,113	1.37	8 (9%)
22	CLA	b	614	-	69,73,73	1.25	10 (14%)	83,113,113	1.30	8 (9%)
22	CLA	5	302	-	69,73,73	1.26	8 (11%)	83,113,113	1.32	6 (7%)
22	CLA	b	609	-	69,73,73	1.25	11 (15%)	83,113,113	1.32	7 (8%)
22	CLA	q	306	22	64,68,73	1.29	6 (9%)	77,107,113	1.31	4 (5%)
24	XAT	u	311	-	39,47,47	2.54	18 (46%)	54,74,74	11.77	18 (33%)
22	CLA	U	304	-	64,68,73	1.28	9 (14%)	77,107,113	1.39	8 (10%)
26	CHL	u	318	-	70,74,74	1.87	18 (25%)	80,114,114	2.66	26 (32%)
32	SQD	L	102	9	53,54,54	0.93	4 (7%)	62,65,65	1.80	12 (19%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
22	CLA	b	602	-	69,73,73	1.24	10 (14%)	83,113,113	1.35	6 (7%)
31	BCR	B	618	-	41,41,41	4.74	24 (58%)	56,56,56	2.45	22 (39%)
24	XAT	2	311	-	39,47,47	2.58	18 (46%)	54,74,74	11.93	19 (35%)
22	CLA	v	301	-	69,73,73	1.26	10 (14%)	83,113,113	1.26	5 (6%)
22	CLA	b	612	-	69,73,73	1.25	10 (14%)	83,113,113	1.42	7 (8%)
22	CLA	C	515	-	69,73,73	1.24	9 (13%)	83,113,113	1.38	7 (8%)
23	LUT	S	311	-	42,43,43	0.77	0	51,60,60	1.64	17 (33%)
22	CLA	B	607	-	69,73,73	1.25	9 (13%)	83,113,113	1.41	7 (8%)
22	CLA	B	615	-	69,73,73	1.21	10 (14%)	83,113,113	1.38	7 (8%)
25	LHG	l	101	-	48,48,48	0.89	3 (6%)	51,54,54	1.11	3 (5%)
25	LHG	4	312	-	48,48,48	0.90	4 (8%)	51,54,54	1.07	2 (3%)
22	CLA	B	612	-	69,73,73	1.26	10 (14%)	83,113,113	1.43	7 (8%)
22	CLA	R	304	-	64,68,73	1.29	7 (10%)	77,107,113	1.36	4 (5%)
26	CHL	U	316	18	70,74,74	1.88	20 (28%)	80,114,114	2.80	27 (33%)
22	CLA	P	309	-	52,56,73	1.43	9 (17%)	62,92,113	1.45	5 (8%)
26	CHL	1	315	-	54,58,74	2.22	19 (35%)	59,94,114	2.87	21 (35%)
23	LUT	U	310	-	42,43,43	0.79	0	51,60,60	1.61	9 (17%)
22	CLA	c	514	-	69,73,73	1.24	10 (14%)	83,113,113	1.37	8 (9%)
22	CLA	r	605	-	62,66,73	1.30	9 (14%)	74,104,113	1.42	5 (6%)
22	CLA	x	201	14	69,73,73	1.24	9 (13%)	83,113,113	1.38	8 (9%)
22	CLA	S	301	19	65,69,73	1.25	9 (13%)	78,108,113	1.36	10 (12%)
26	CHL	Q	312	-	52,56,74	2.27	18 (34%)	58,92,114	3.01	24 (41%)
23	LUT	4	309	-	42,43,43	0.73	0	51,60,60	1.60	11 (21%)
31	BCR	C	518	-	41,41,41	4.75	24 (58%)	56,56,56	2.29	19 (33%)
26	CHL	P	319	-	70,74,74	1.89	20 (28%)	80,114,114	2.67	23 (28%)
22	CLA	G	305	22	64,68,73	1.27	9 (14%)	77,107,113	1.44	6 (7%)
26	CHL	1	317	18	70,74,74	1.91	20 (28%)	80,114,114	2.78	28 (35%)
22	CLA	X	202	14	69,73,73	1.23	9 (13%)	83,113,113	1.36	8 (9%)
22	CLA	S	308	-	59,63,73	1.34	9 (15%)	71,101,113	1.39	5 (7%)
22	CLA	R	307	-	69,73,73	1.24	9 (13%)	83,113,113	1.30	4 (4%)
22	CLA	1	306	-	64,68,73	1.30	10 (15%)	77,107,113	1.36	8 (10%)
22	CLA	b	613	-	69,73,73	1.27	12 (17%)	83,113,113	1.34	10 (12%)
23	LUT	r	611	1	42,43,43	0.75	0	51,60,60	1.66	10 (19%)
25	LHG	n	312	-	48,48,48	0.90	4 (8%)	51,54,54	1.03	2 (3%)
23	LUT	P	311	-	42,43,43	0.76	0	51,60,60	1.58	12 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
22	CLA	3	302	-	69,73,73	1.25	8 (11%)	83,113,113	1.32	6 (7%)
22	CLA	N	308	-	52,56,73	1.44	9 (17%)	62,92,113	1.41	5 (8%)
22	CLA	r	604	-	52,56,73	1.43	8 (15%)	62,92,113	1.51	6 (9%)
23	LUT	n	309	-	42,43,43	0.74	0	51,60,60	1.62	11 (21%)
26	CHL	q	313	-	54,58,74	2.17	18 (33%)	59,94,114	2.96	22 (37%)
22	CLA	u	307	-	69,73,73	1.22	9 (13%)	83,113,113	1.37	7 (8%)
26	CHL	Q	313	-	54,58,74	2.19	19 (35%)	59,94,114	2.94	23 (38%)
26	CHL	S	315	19	62,66,74	2.15	19 (30%)	70,104,114	2.67	23 (32%)
22	CLA	b	611	-	69,73,73	1.27	9 (13%)	83,113,113	1.39	7 (8%)
34	LMG	d	407	3	46,46,55	1.26	6 (13%)	54,54,63	1.01	2 (3%)
22	CLA	3	306	22	64,68,73	1.29	8 (12%)	77,107,113	1.33	5 (6%)
23	LUT	s	311	-	42,43,43	0.76	0	51,60,60	1.65	16 (31%)
22	CLA	2	307	-	64,68,73	1.28	9 (14%)	77,107,113	1.39	6 (7%)
22	CLA	4	307	-	69,73,73	1.24	10 (14%)	83,113,113	1.39	8 (9%)
22	CLA	4	308	-	52,56,73	1.42	9 (17%)	62,92,113	1.46	5 (8%)
25	LHG	q	310	-	48,48,48	0.89	4 (8%)	51,54,54	1.05	2 (3%)
26	CHL	q	312	-	52,56,74	2.34	20 (38%)	58,92,114	3.08	24 (41%)
26	CHL	u	317	18	70,74,74	1.87	20 (28%)	80,114,114	2.77	27 (33%)
22	CLA	c	505	-	69,73,73	1.23	9 (13%)	83,113,113	1.36	6 (7%)
22	CLA	B	614	-	69,73,73	1.25	10 (14%)	83,113,113	1.31	8 (9%)
25	LHG	Q	310	-	48,48,48	0.90	4 (8%)	51,54,54	1.06	2 (3%)
26	CHL	5	318	-	70,74,74	1.90	20 (28%)	80,114,114	2.65	25 (31%)
22	CLA	G	302	-	69,73,73	1.25	8 (11%)	83,113,113	1.29	5 (6%)
26	CHL	u	315	-	54,58,74	2.13	18 (33%)	59,94,114	2.91	23 (38%)
30	PHO	A	407	-	58,69,69	2.02	10 (17%)	56,99,99	1.63	9 (16%)
22	CLA	6	303	-	69,73,73	1.24	8 (11%)	83,113,113	1.26	5 (6%)
22	CLA	R	306	-	62,66,73	1.30	9 (14%)	74,104,113	1.42	5 (6%)
36	DGD	c	519	-	61,61,67	1.25	6 (9%)	75,75,81	1.17	3 (4%)
22	CLA	B	609	-	69,73,73	1.25	11 (15%)	83,113,113	1.32	7 (8%)
27	NEX	v	319	-	38,46,46	0.89	1 (2%)	50,70,70	2.45	14 (28%)
22	CLA	4	303	-	54,58,73	1.41	9 (16%)	65,95,113	1.43	9 (13%)
26	CHL	n	313	18	70,74,74	1.94	18 (25%)	80,114,114	2.66	27 (33%)
31	BCR	c	515	-	41,41,41	4.70	24 (58%)	56,56,56	2.67	23 (41%)
22	CLA	N	305	18	64,68,73	1.25	9 (14%)	77,107,113	1.80	12 (15%)
26	CHL	q	311	-	70,74,74	1.90	19 (27%)	80,114,114	2.68	26 (32%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
26	CHL	N	314	-	52,56,74	2.31	19 (36%)	58,92,114	3.03	23 (39%)
22	CLA	s	305	-	59,63,73	1.35	9 (15%)	71,101,113	1.37	6 (8%)
27	NEX	U	318	-	38,46,46	0.96	1 (2%)	50,70,70	2.38	12 (24%)
23	LUT	R	312	-	42,43,43	0.73	0	51,60,60	1.52	11 (21%)
22	CLA	c	509	-	69,73,73	1.28	12 (17%)	83,113,113	1.44	9 (10%)
26	CHL	P	317	-	70,74,74	1.95	21 (30%)	80,114,114	2.66	27 (33%)
26	CHL	r	614	-	70,74,74	1.89	17 (24%)	80,114,114	2.68	25 (31%)
22	CLA	5	305	18	64,68,73	1.26	9 (14%)	77,107,113	1.92	11 (14%)
22	CLA	p	302	-	69,73,73	1.24	10 (14%)	83,113,113	1.33	8 (9%)
22	CLA	6	305	18	68,72,73	1.25	9 (13%)	81,111,113	1.36	10 (12%)
26	CHL	v	317	18	70,74,74	1.92	19 (27%)	80,114,114	2.78	30 (37%)
22	CLA	B	605	21	69,73,73	1.25	9 (13%)	83,113,113	1.66	11 (13%)
22	CLA	N	302	-	69,73,73	1.28	9 (13%)	83,113,113	1.30	6 (7%)
32	SQD	l	102	9	53,54,54	0.93	4 (7%)	62,65,65	1.80	12 (19%)
22	CLA	A	404	-	69,73,73	1.26	11 (15%)	83,113,113	1.44	9 (10%)
26	CHL	p	317	-	70,74,74	1.93	19 (27%)	80,114,114	2.65	24 (30%)
22	CLA	P	308	-	64,68,73	1.29	10 (15%)	77,107,113	1.37	5 (6%)
22	CLA	p	306	18	64,68,73	1.25	7 (10%)	77,107,113	1.97	15 (19%)
22	CLA	b	617	21	69,73,73	1.29	10 (14%)	83,113,113	1.49	12 (14%)
22	CLA	g	303	-	54,58,73	1.42	9 (16%)	65,95,113	1.51	7 (10%)
26	CHL	1	313	-	70,74,74	1.96	20 (28%)	80,114,114	2.60	26 (32%)
25	LHG	A	413	2	42,42,48	0.93	3 (7%)	45,48,54	1.11	2 (4%)
32	SQD	m	101	-	41,42,54	1.06	5 (12%)	50,53,65	1.75	11 (22%)
22	CLA	Q	308	-	52,56,73	1.43	8 (15%)	62,92,113	1.42	6 (9%)
22	CLA	A	408	-	64,68,73	1.29	12 (18%)	77,107,113	1.49	9 (11%)
26	CHL	G	313	-	54,58,74	2.18	18 (33%)	59,94,114	2.96	21 (35%)
27	NEX	r	617	-	38,46,46	1.01	3 (7%)	50,70,70	2.42	17 (34%)
22	CLA	P	305	18	69,73,73	1.22	8 (11%)	83,113,113	1.33	6 (7%)
25	LHG	G	310	-	48,48,48	0.89	4 (8%)	51,54,54	1.10	2 (3%)
22	CLA	P	306	18	64,68,73	1.24	7 (10%)	77,107,113	1.88	11 (14%)
22	CLA	n	301	-	69,73,73	1.25	10 (14%)	83,113,113	1.34	8 (9%)
26	CHL	v	313	-	70,74,74	1.94	20 (28%)	80,114,114	2.67	26 (32%)
22	CLA	5	308	-	52,56,73	1.42	8 (15%)	62,92,113	1.43	5 (8%)
24	XAT	q	309	-	39,47,47	2.58	18 (46%)	54,74,74	11.94	18 (33%)
22	CLA	a	408	-	64,68,73	1.29	12 (18%)	77,107,113	1.50	9 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
22	CLA	C	510	-	69,73,73	1.28	12 (17%)	83,113,113	1.44	9 (10%)
22	CLA	u	304	-	64,68,73	1.29	11 (17%)	77,107,113	1.39	8 (10%)
22	CLA	g	305	22	64,68,73	1.28	8 (12%)	77,107,113	1.42	9 (11%)
34	LMG	B	621	-	51,51,55	1.18	6 (11%)	59,59,63	1.44	6 (10%)
34	LMG	D	408	3	46,46,55	1.26	6 (13%)	54,54,63	1.02	2 (3%)
25	LHG	C	524	-	48,48,48	0.90	4 (8%)	51,54,54	1.13	2 (3%)
22	CLA	N	307	-	64,68,73	1.28	10 (15%)	77,107,113	1.38	5 (6%)
26	CHL	6	301	-	70,74,74	1.92	20 (28%)	80,114,114	2.67	25 (31%)
31	BCR	x	202	-	41,41,41	4.78	24 (58%)	56,56,56	2.27	18 (32%)
22	CLA	p	303	-	69,73,73	1.25	9 (13%)	83,113,113	1.36	6 (7%)
26	CHL	S	316	-	50,54,74	2.35	19 (38%)	56,90,114	2.98	23 (41%)
22	CLA	3	304	18	68,72,73	1.26	10 (14%)	81,111,113	1.37	10 (12%)
26	CHL	s	313	-	50,54,74	2.33	18 (36%)	56,90,114	3.04	23 (41%)
25	LHG	D	406	3	45,45,48	0.92	4 (8%)	48,51,54	1.08	2 (4%)
26	CHL	q	315	-	65,69,74	2.01	20 (30%)	74,108,114	2.74	26 (35%)
30	PHO	d	401	-	58,69,69	1.98	9 (15%)	56,99,99	1.80	9 (16%)
25	LHG	B	622	-	46,46,48	0.91	4 (8%)	49,52,54	1.06	2 (4%)
25	LHG	p	313	-	48,48,48	0.90	4 (8%)	51,54,54	1.04	2 (3%)
26	CHL	Q	315	18	70,74,74	1.88	18 (25%)	80,114,114	2.70	25 (31%)
22	CLA	P	302	-	69,73,73	1.24	10 (14%)	83,113,113	1.34	8 (9%)
26	CHL	Q	314	-	70,74,74	1.94	19 (27%)	80,114,114	2.59	25 (31%)
22	CLA	q	308	-	52,56,73	1.42	8 (15%)	62,92,113	1.46	6 (9%)
22	CLA	S	304	19	49,53,73	1.48	8 (16%)	59,89,113	1.43	4 (6%)
26	CHL	s	315	19	62,66,74	2.14	19 (30%)	70,104,114	2.68	23 (32%)
22	CLA	n	302	-	69,73,73	1.28	9 (13%)	83,113,113	1.30	6 (7%)
22	CLA	2	302	-	69,73,73	1.27	9 (13%)	83,113,113	1.30	6 (7%)
26	CHL	u	316	-	70,74,74	1.91	18 (25%)	80,114,114	2.76	30 (37%)
25	LHG	u	312	-	48,48,48	0.88	4 (8%)	51,54,54	1.13	3 (5%)
26	CHL	U	314	-	54,58,74	2.15	19 (35%)	59,94,114	2.95	23 (38%)
25	LHG	c	521	-	48,48,48	0.90	4 (8%)	51,54,54	1.08	2 (3%)
26	CHL	Q	316	-	65,69,74	2.00	20 (30%)	74,108,114	2.72	25 (33%)
27	NEX	P	301	18	38,46,46	0.94	1 (2%)	50,70,70	2.35	18 (36%)
22	CLA	U	307	-	69,73,73	1.24	9 (13%)	83,113,113	1.37	6 (7%)
22	CLA	q	302	-	69,73,73	1.24	8 (11%)	83,113,113	1.28	5 (6%)
37	HEM	e	101	4,17	50,50,50	1.44	6 (12%)	66,82,82	1.20	4 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
22	CLA	g	301	-	69,73,73	1.25	10 (14%)	83,113,113	1.37	7 (8%)
23	LUT	1	309	-	42,43,43	0.72	0	51,60,60	1.57	10 (19%)
25	LHG	2	312	-	48,48,48	0.89	4 (8%)	51,54,54	1.09	2 (3%)
26	CHL	6	317	-	65,69,74	1.99	19 (29%)	74,108,114	2.80	25 (33%)
22	CLA	G	303	-	54,58,73	1.41	9 (16%)	65,95,113	1.49	7 (10%)
24	XAT	g	309	-	39,47,47	2.53	17 (43%)	54,74,74	11.71	20 (37%)
25	LHG	v	312	-	48,48,48	0.90	4 (8%)	51,54,54	1.12	2 (3%)
22	CLA	B	610	-	69,73,73	1.23	10 (14%)	83,113,113	1.35	7 (8%)
22	CLA	V	307	-	69,73,73	1.24	10 (14%)	83,113,113	1.36	6 (7%)
31	BCR	X	201	-	41,41,41	4.79	24 (58%)	56,56,56	2.26	17 (30%)
25	LHG	3	310	-	48,48,48	0.89	4 (8%)	51,54,54	1.11	2 (3%)
22	CLA	S	305	-	59,63,73	1.35	9 (15%)	71,101,113	1.37	5 (7%)
26	CHL	V	315	-	54,58,74	2.27	19 (35%)	59,94,114	2.87	23 (38%)
27	NEX	V	319	-	38,46,46	0.91	1 (2%)	50,70,70	2.46	16 (32%)
22	CLA	v	308	-	52,56,73	1.42	8 (15%)	62,92,113	1.43	4 (6%)
26	CHL	g	315	18	70,74,74	1.89	18 (25%)	80,114,114	2.69	25 (31%)
22	CLA	3	301	-	69,73,73	1.26	10 (14%)	83,113,113	1.31	8 (9%)
22	CLA	S	309	-	53,57,73	1.42	10 (18%)	62,93,113	1.42	4 (6%)
26	CHL	3	312	-	52,56,74	2.35	20 (38%)	58,92,114	3.02	26 (44%)
22	CLA	G	301	-	69,73,73	1.25	10 (14%)	83,113,113	1.35	7 (8%)
22	CLA	b	616	21	69,73,73	1.24	8 (11%)	83,113,113	1.38	8 (9%)
27	NEX	u	320	-	38,46,46	0.89	2 (5%)	50,70,70	2.32	18 (36%)
22	CLA	S	302	-	49,53,73	1.51	8 (16%)	59,89,113	1.49	6 (10%)
24	XAT	U	311	-	39,47,47	2.51	17 (43%)	54,74,74	11.93	20 (37%)
26	CHL	V	317	18	70,74,74	1.92	19 (27%)	80,114,114	2.78	29 (36%)
22	CLA	U	306	-	64,68,73	1.31	10 (15%)	77,107,113	1.34	6 (7%)
26	CHL	g	312	-	52,56,74	2.25	18 (34%)	58,92,114	3.08	24 (41%)
31	BCR	a	409	-	41,41,41	4.73	24 (58%)	56,56,56	2.22	22 (39%)
27	NEX	5	319	-	38,46,46	0.91	1 (2%)	50,70,70	2.43	16 (32%)
22	CLA	4	305	-	64,68,73	1.29	9 (14%)	77,107,113	1.34	7 (9%)
22	CLA	v	306	-	64,68,73	1.30	9 (14%)	77,107,113	1.35	7 (9%)
22	CLA	s	304	19	49,53,73	1.47	8 (16%)	59,89,113	1.44	4 (6%)
33	PL9	a	411	-	13,13,55	3.63	7 (53%)	17,17,69	1.48	3 (17%)
26	CHL	R	315	-	70,74,74	1.89	16 (22%)	80,114,114	2.67	26 (32%)
31	BCR	C	516	-	41,41,41	4.76	24 (58%)	56,56,56	2.30	20 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
23	LUT	n	310	-	42,43,43	0.79	0	51,60,60	1.75	14 (27%)
24	XAT	6	310	-	39,47,47	2.56	18 (46%)	54,74,74	11.74	17 (31%)
32	SQD	M	101	-	41,42,54	1.06	5 (12%)	50,53,65	1.74	11 (22%)
31	BCR	k	101	-	41,41,41	4.73	25 (60%)	56,56,56	2.52	19 (33%)
22	CLA	1	303	-	54,58,73	1.40	10 (18%)	65,95,113	1.46	9 (13%)
26	CHL	v	316	-	70,74,74	1.89	19 (27%)	80,114,114	2.68	26 (32%)
22	CLA	C	505	-	69,73,73	1.25	11 (15%)	83,113,113	1.34	6 (7%)
22	CLA	V	301	-	69,73,73	1.27	10 (14%)	83,113,113	1.24	5 (6%)
22	CLA	A	405	-	69,73,73	1.27	10 (14%)	83,113,113	1.39	9 (10%)
36	DGD	C	519	-	56,56,67	1.30	8 (14%)	70,70,81	1.19	5 (7%)
22	CLA	U	308	-	52,56,73	1.42	8 (15%)	62,92,113	1.46	5 (8%)
22	CLA	3	303	-	54,58,73	1.41	8 (14%)	65,95,113	1.47	8 (12%)
24	XAT	R	313	-	39,47,47	2.54	17 (43%)	54,74,74	11.48	22 (40%)
22	CLA	u	303	-	54,58,73	1.41	9 (16%)	65,95,113	1.47	8 (12%)
22	CLA	V	306	-	64,68,73	1.32	9 (14%)	77,107,113	1.34	7 (9%)
26	CHL	5	314	-	52,56,74	2.33	20 (38%)	58,92,114	3.05	23 (39%)
22	CLA	a	405	-	69,73,73	1.27	10 (14%)	83,113,113	1.39	7 (8%)
22	CLA	C	509	20	69,73,73	1.23	10 (14%)	83,113,113	1.43	10 (12%)
25	LHG	B	623	21	48,48,48	0.90	4 (8%)	51,54,54	1.06	2 (3%)
22	CLA	q	305	22	64,68,73	1.29	9 (14%)	77,107,113	1.34	4 (5%)
34	LMG	w	201	-	48,48,55	1.23	6 (12%)	56,56,63	1.12	4 (7%)
26	CHL	s	316	-	50,54,74	2.35	19 (38%)	56,90,114	2.99	23 (41%)
34	LMG	C	521	-	51,51,55	1.20	6 (11%)	59,59,63	1.07	2 (3%)
22	CLA	Q	305	22	64,68,73	1.29	9 (14%)	77,107,113	1.30	5 (6%)
22	CLA	S	307	-	53,57,73	1.42	8 (15%)	62,93,113	1.49	8 (12%)
24	XAT	3	309	-	39,47,47	2.56	18 (46%)	54,74,74	11.80	17 (31%)
24	XAT	G	309	-	39,47,47	2.53	17 (43%)	54,74,74	11.82	19 (35%)
22	CLA	1	301	-	69,73,73	1.26	10 (14%)	83,113,113	1.31	7 (8%)
22	CLA	V	304	-	64,68,73	1.28	8 (12%)	77,107,113	1.38	9 (11%)
23	LUT	s	310	19	42,43,43	0.79	0	51,60,60	1.72	13 (25%)
26	CHL	5	316	-	70,74,74	1.95	19 (27%)	80,114,114	2.60	24 (30%)
26	CHL	N	316	-	70,74,74	1.87	19 (27%)	80,114,114	2.71	24 (30%)
32	SQD	C	501	-	49,50,54	1.00	5 (10%)	58,61,65	1.75	11 (18%)
22	CLA	s	307	-	53,57,73	1.42	9 (16%)	62,93,113	1.49	8 (12%)
22	CLA	D	403	3	69,73,73	1.24	10 (14%)	83,113,113	1.28	6 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
22	CLA	S	303	19	54,58,73	1.40	9 (16%)	65,95,113	1.47	8 (12%)
25	LHG	a	415	2	42,42,48	0.93	3 (7%)	45,48,54	1.10	2 (4%)
22	CLA	q	304	18	68,72,73	1.25	9 (13%)	81,111,113	1.47	9 (11%)
22	CLA	s	309	-	53,57,73	1.39	9 (16%)	62,93,113	1.41	4 (6%)
26	CHL	v	315	-	54,58,74	2.22	18 (33%)	59,94,114	2.89	24 (40%)
22	CLA	c	507	-	69,73,73	1.27	10 (14%)	83,113,113	1.39	8 (9%)
22	CLA	2	305	18	64,68,73	1.25	8 (12%)	77,107,113	1.91	13 (16%)
22	CLA	Q	304	18	68,72,73	1.25	9 (13%)	81,111,113	1.40	10 (12%)
27	NEX	n	319	-	38,46,46	0.96	2 (5%)	50,70,70	2.64	17 (34%)
26	CHL	P	314	18	70,74,74	1.98	19 (27%)	80,114,114	2.64	25 (31%)
34	LMG	A	411	-	40,40,55	1.30	6 (15%)	48,48,63	1.16	2 (4%)
23	LUT	u	310	-	42,43,43	0.78	0	51,60,60	1.60	10 (19%)
22	CLA	a	404	-	69,73,73	1.26	11 (15%)	83,113,113	1.45	9 (10%)
26	CHL	n	314	-	52,56,74	2.32	20 (38%)	58,92,114	3.02	23 (39%)
23	LUT	P	310	-	42,43,43	0.73	0	51,60,60	1.67	14 (27%)
22	CLA	n	307	-	64,68,73	1.29	10 (15%)	77,107,113	1.37	5 (6%)
26	CHL	G	312	-	52,56,74	2.31	21 (40%)	58,92,114	3.10	23 (39%)
26	CHL	P	316	-	54,58,74	2.23	20 (37%)	59,94,114	2.92	23 (38%)
26	CHL	V	313	-	70,74,74	1.96	19 (27%)	80,114,114	2.64	24 (30%)
22	CLA	R	311	-	49,53,73	1.48	8 (16%)	59,89,113	1.51	4 (6%)
22	CLA	u	301	-	69,73,73	1.25	9 (13%)	83,113,113	1.31	7 (8%)
22	CLA	b	604	-	69,73,73	1.24	9 (13%)	83,113,113	1.33	8 (9%)
22	CLA	n	305	18	64,68,73	1.26	7 (10%)	77,107,113	1.96	15 (19%)
22	CLA	a	406	-	54,58,73	1.42	10 (18%)	65,95,113	1.44	7 (10%)
22	CLA	r	603	-	64,68,73	1.29	9 (14%)	77,107,113	1.36	4 (5%)
26	CHL	6	312	-	70,74,74	1.91	19 (27%)	80,114,114	2.72	27 (33%)
26	CHL	g	316	-	65,69,74	1.97	19 (29%)	74,108,114	2.73	27 (36%)
25	LHG	r	613	-	41,41,48	0.96	3 (7%)	44,47,54	1.09	2 (4%)
32	SQD	A	412	-	53,54,54	0.95	5 (9%)	62,65,65	1.50	10 (16%)
26	CHL	P	318	-	70,74,74	1.87	19 (27%)	80,114,114	2.68	24 (30%)
26	CHL	1	314	22	52,56,74	2.24	19 (36%)	58,92,114	3.09	23 (39%)
36	DGD	c	518	-	63,63,67	1.22	6 (9%)	77,77,81	1.15	5 (6%)
26	CHL	r	619	1	52,56,74	2.19	20 (38%)	58,92,114	3.10	23 (39%)
22	CLA	r	607	1	53,57,73	1.40	8 (15%)	62,93,113	1.53	8 (12%)
25	LHG	g	310	-	48,48,48	0.89	4 (8%)	51,54,54	1.09	2 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
31	BCR	z	101	-	41,41,41	4.76	24 (58%)	56,56,56	2.32	20 (35%)
27	NEX	N	318	-	38,46,46	0.93	2 (5%)	50,70,70	2.40	17 (34%)
24	XAT	N	311	-	39,47,47	2.53	17 (43%)	54,74,74	11.91	18 (33%)
22	CLA	b	610	-	69,73,73	1.23	10 (14%)	83,113,113	1.33	7 (8%)
26	CHL	p	314	18	70,74,74	1.95	18 (25%)	80,114,114	2.67	26 (32%)
33	PL9	D	405	-	55,55,55	1.54	6 (10%)	68,69,69	1.68	18 (26%)
25	LHG	1	312	-	48,48,48	0.89	4 (8%)	51,54,54	1.09	2 (3%)
34	LMG	W	201	-	48,48,55	1.23	6 (12%)	56,56,63	1.12	4 (7%)
22	CLA	s	303	19	54,58,73	1.40	9 (16%)	65,95,113	1.47	7 (10%)
35	BCT	D	402	-	2,3,3	1.35	0	2,3,3	0.19	0
31	BCR	K	101	-	41,41,41	4.72	24 (58%)	56,56,56	2.53	19 (33%)
31	BCR	B	619	-	41,41,41	4.74	24 (58%)	56,56,56	2.26	22 (39%)
22	CLA	P	307	-	64,68,73	1.28	7 (10%)	77,107,113	1.36	8 (10%)
22	CLA	R	303	-	64,68,73	1.30	9 (14%)	77,107,113	1.35	7 (9%)
26	CHL	p	316	-	54,58,74	2.22	19 (35%)	59,94,114	2.96	25 (42%)
22	CLA	s	306	-	60,64,73	1.35	10 (16%)	72,102,113	1.40	9 (12%)
26	CHL	g	314	-	70,74,74	1.97	19 (27%)	80,114,114	2.63	26 (32%)
24	XAT	5	311	-	39,47,47	2.58	18 (46%)	54,74,74	11.93	19 (35%)
26	CHL	S	314	-	50,54,74	2.26	19 (38%)	56,90,114	3.12	21 (37%)
31	BCR	D	404	3	41,41,41	4.77	24 (58%)	56,56,56	2.26	23 (41%)
26	CHL	v	318	-	70,74,74	1.93	19 (27%)	80,114,114	2.59	24 (30%)
22	CLA	1	305	-	64,68,73	1.28	8 (12%)	77,107,113	1.37	7 (9%)
23	LUT	U	309	-	42,43,43	0.74	0	51,60,60	1.54	10 (19%)
22	CLA	n	308	-	52,56,73	1.45	8 (15%)	62,92,113	1.52	8 (12%)
26	CHL	G	316	-	65,69,74	1.96	20 (30%)	74,108,114	2.76	25 (33%)
22	CLA	R	308	1	53,57,73	1.39	7 (13%)	62,93,113	1.53	6 (9%)
22	CLA	5	306	-	64,68,73	1.28	8 (12%)	77,107,113	1.39	7 (9%)
26	CHL	2	317	-	70,74,74	1.87	17 (24%)	80,114,114	2.71	26 (32%)
26	CHL	G	314	-	70,74,74	1.95	20 (28%)	80,114,114	2.57	24 (30%)
22	CLA	V	303	-	54,58,73	1.41	10 (18%)	65,95,113	1.51	8 (12%)
22	CLA	G	307	-	69,73,73	1.24	9 (13%)	83,113,113	1.36	5 (6%)
22	CLA	v	305	-	64,68,73	1.29	8 (12%)	77,107,113	1.33	5 (6%)
23	LUT	5	310	-	42,43,43	0.77	0	51,60,60	1.64	12 (23%)
26	CHL	r	616	-	65,69,74	2.03	20 (30%)	74,108,114	2.56	22 (29%)
22	CLA	B	608	-	69,73,73	1.23	8 (11%)	83,113,113	1.39	8 (9%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
25	LHG	c	523	-	48,48,48	0.90	4 (8%)	51,54,54	1.12	2 (3%)
27	NEX	u	319	-	38,46,46	0.93	1 (2%)	50,70,70	2.45	18 (36%)
22	CLA	B	613	-	69,73,73	1.26	12 (17%)	83,113,113	1.34	9 (10%)
22	CLA	U	301	-	69,73,73	1.24	10 (14%)	83,113,113	1.31	8 (9%)
22	CLA	3	305	22	64,68,73	1.28	9 (14%)	77,107,113	1.42	8 (10%)
31	BCR	A	409	-	41,41,41	4.74	24 (58%)	56,56,56	2.25	22 (39%)
22	CLA	c	510	-	69,73,73	1.22	9 (13%)	83,113,113	1.38	9 (10%)
22	CLA	C	507	-	69,73,73	1.23	10 (14%)	83,113,113	1.49	11 (13%)
22	CLA	P	304	-	54,58,73	1.40	9 (16%)	65,95,113	1.44	6 (9%)
26	CHL	V	314	-	52,56,74	2.27	20 (38%)	58,92,114	3.09	24 (41%)
23	LUT	p	311	-	42,43,43	0.76	0	51,60,60	1.54	12 (23%)
22	CLA	d	402	3	69,73,73	1.24	10 (14%)	83,113,113	1.29	6 (7%)
26	CHL	q	314	18	70,74,74	1.89	19 (27%)	80,114,114	2.72	24 (30%)
26	CHL	p	318	-	70,74,74	1.86	19 (27%)	80,114,114	2.72	23 (28%)
26	CHL	n	315	-	54,58,74	2.21	19 (35%)	59,94,114	2.95	23 (38%)
23	LUT	N	310	-	42,43,43	0.78	0	51,60,60	1.69	15 (29%)
26	CHL	V	316	-	70,74,74	1.94	19 (27%)	80,114,114	2.60	25 (31%)
22	CLA	6	309	-	52,56,73	1.42	8 (15%)	62,92,113	1.41	5 (8%)
26	CHL	N	315	-	54,58,74	2.16	19 (35%)	59,94,114	2.97	23 (38%)
22	CLA	c	503	-	69,73,73	1.27	11 (15%)	83,113,113	1.47	8 (9%)
26	CHL	6	316	18	70,74,74	1.90	20 (28%)	80,114,114	2.72	23 (28%)
22	CLA	5	307	-	64,68,73	1.28	10 (15%)	77,107,113	1.38	6 (7%)
22	CLA	g	308	-	52,56,73	1.43	9 (17%)	62,92,113	1.45	6 (9%)
22	CLA	2	301	-	69,73,73	1.25	10 (14%)	83,113,113	1.31	9 (10%)
22	CLA	p	305	18	69,73,73	1.22	8 (11%)	83,113,113	1.34	6 (7%)
22	CLA	4	301	-	69,73,73	1.26	10 (14%)	83,113,113	1.33	8 (9%)
23	LUT	N	309	-	42,43,43	0.72	0	51,60,60	1.55	11 (21%)
26	CHL	u	313	-	70,74,74	1.94	20 (28%)	80,114,114	2.59	26 (32%)
22	CLA	q	307	-	69,73,73	1.23	9 (13%)	83,113,113	1.36	6 (7%)
26	CHL	4	314	-	52,56,74	2.19	19 (36%)	58,92,114	3.15	24 (41%)
36	DGD	a	416	-	60,60,67	1.27	7 (11%)	74,74,81	1.25	6 (8%)
22	CLA	Q	307	-	69,73,73	1.23	9 (13%)	83,113,113	1.33	6 (7%)
26	CHL	U	313	-	70,74,74	1.96	19 (27%)	80,114,114	2.62	25 (31%)
27	NEX	p	301	18	38,46,46	0.98	2 (5%)	50,70,70	2.43	19 (38%)
26	CHL	3	313	-	54,58,74	2.25	19 (35%)	59,94,114	2.86	24 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
23	LUT	v	310	-	42,43,43	0.77	0	51,60,60	1.63	10 (19%)
22	CLA	c	508	20	69,73,73	1.24	10 (14%)	83,113,113	1.42	10 (12%)
36	DGD	A	414	-	60,60,67	1.27	7 (11%)	74,74,81	1.25	6 (8%)
22	CLA	4	302	-	69,73,73	1.27	9 (13%)	83,113,113	1.26	6 (7%)
32	SQD	a	410	-	49,50,54	1.01	5 (10%)	58,61,65	1.74	11 (18%)
22	CLA	p	308	-	64,68,73	1.29	10 (15%)	77,107,113	1.39	5 (6%)
23	LUT	v	309	-	42,43,43	0.79	0	51,60,60	1.65	12 (23%)
22	CLA	c	504	-	69,73,73	1.25	11 (15%)	83,113,113	1.34	6 (7%)
26	CHL	V	318	-	70,74,74	1.95	20 (28%)	80,114,114	2.58	24 (30%)
26	CHL	6	313	-	52,56,74	2.34	20 (38%)	58,92,114	3.04	26 (44%)
24	XAT	n	311	-	39,47,47	2.53	18 (46%)	54,74,74	11.76	23 (42%)
22	CLA	r	602	-	64,68,73	1.30	9 (14%)	77,107,113	1.34	5 (6%)
23	LUT	S	310	-	42,43,43	0.77	0	51,60,60	1.69	14 (27%)
22	CLA	N	304	18	69,73,73	1.22	10 (14%)	83,113,113	1.39	9 (10%)
34	LMG	c	501	-	51,51,55	1.15	5 (9%)	59,59,63	1.16	3 (5%)
25	LHG	d	405	3	45,45,48	0.92	4 (8%)	48,51,54	1.07	2 (4%)
26	CHL	N	317	-	70,74,74	1.95	20 (28%)	80,114,114	2.59	25 (31%)
22	CLA	B	604	-	69,73,73	1.23	8 (11%)	83,113,113	1.32	8 (9%)
22	CLA	1	302	-	69,73,73	1.28	8 (11%)	83,113,113	1.23	6 (7%)
26	CHL	G	315	18	70,74,74	1.89	20 (28%)	80,114,114	2.69	24 (30%)
22	CLA	2	306	-	64,68,73	1.28	8 (12%)	77,107,113	1.39	7 (9%)
25	LHG	C	523	-	48,48,48	0.89	3 (6%)	51,54,54	1.07	2 (3%)
22	CLA	V	305	-	64,68,73	1.29	9 (14%)	77,107,113	1.38	5 (6%)
26	CHL	p	315	-	52,56,74	2.39	20 (38%)	58,92,114	2.92	22 (37%)
22	CLA	u	308	-	52,56,73	1.42	8 (15%)	62,92,113	1.45	6 (9%)
31	BCR	b	619	-	41,41,41	4.74	24 (58%)	56,56,56	2.27	20 (35%)
22	CLA	S	306	-	60,64,73	1.35	10 (16%)	72,102,113	1.41	7 (9%)
22	CLA	N	301	-	69,73,73	1.26	10 (14%)	83,113,113	1.35	7 (8%)
22	CLA	6	308	-	69,73,73	1.25	10 (14%)	83,113,113	1.34	6 (7%)
26	CHL	G	311	-	70,74,74	1.88	19 (27%)	80,114,114	2.71	27 (33%)
25	LHG	U	312	-	48,48,48	0.89	4 (8%)	51,54,54	1.17	3 (5%)
30	PHO	a	407	-	58,69,69	2.01	11 (18%)	56,99,99	1.62	9 (16%)
22	CLA	Q	302	-	69,73,73	1.24	8 (11%)	83,113,113	1.27	5 (6%)
26	CHL	r	615	-	60,64,74	2.06	20 (33%)	68,102,114	2.92	24 (35%)
22	CLA	2	308	-	52,56,73	1.42	9 (17%)	62,92,113	1.47	5 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
34	LMG	c	520	-	51,51,55	1.20	6 (11%)	59,59,63	1.08	2 (3%)
25	LHG	N	312	-	48,48,48	0.89	4 (8%)	51,54,54	1.09	2 (3%)
22	CLA	3	308	-	52,56,73	1.43	8 (15%)	62,92,113	1.41	5 (8%)
22	CLA	C	504	-	69,73,73	1.28	11 (15%)	83,113,113	1.48	8 (9%)
22	CLA	V	308	-	52,56,73	1.42	8 (15%)	62,92,113	1.45	4 (6%)
26	CHL	R	316	-	60,64,74	2.06	19 (31%)	68,102,114	2.94	24 (35%)
34	LMG	B	624	21	55,55,55	1.16	6 (10%)	63,63,63	1.07	2 (3%)
22	CLA	g	307	-	69,73,73	1.24	9 (13%)	83,113,113	1.35	5 (6%)
22	CLA	u	305	-	64,68,73	1.29	10 (15%)	77,107,113	1.31	5 (6%)
26	CHL	5	313	18	70,74,74	2.02	20 (28%)	80,114,114	2.65	24 (30%)
22	CLA	u	306	-	64,68,73	1.31	10 (15%)	77,107,113	1.36	5 (6%)
22	CLA	g	304	18	68,72,73	1.26	9 (13%)	81,111,113	1.38	9 (11%)
22	CLA	R	305	-	52,56,73	1.44	8 (15%)	62,92,113	1.51	6 (9%)
22	CLA	2	303	-	54,58,73	1.39	9 (16%)	65,95,113	1.43	5 (7%)
22	CLA	C	512	8,20	69,73,73	1.26	9 (13%)	83,113,113	1.21	5 (6%)
26	CHL	1	316	-	70,74,74	1.92	20 (28%)	80,114,114	2.67	25 (31%)
22	CLA	6	306	22	64,68,73	1.28	9 (14%)	77,107,113	1.41	8 (10%)
25	LHG	S	312	19	48,48,48	0.89	4 (8%)	51,54,54	1.13	3 (5%)
22	CLA	Q	306	22	64,68,73	1.29	7 (10%)	77,107,113	1.28	3 (3%)
25	LHG	c	522	-	48,48,48	0.90	3 (6%)	51,54,54	1.07	2 (3%)
23	LUT	4	310	-	42,43,43	0.83	1 (2%)	51,60,60	1.79	14 (27%)
22	CLA	r	606	-	69,73,73	1.24	9 (13%)	83,113,113	1.29	5 (6%)
22	CLA	N	303	-	54,58,73	1.40	9 (16%)	65,95,113	1.53	7 (10%)
22	CLA	c	506	-	69,73,73	1.23	10 (14%)	83,113,113	1.50	11 (13%)
22	CLA	1	307	-	69,73,73	1.24	11 (15%)	83,113,113	1.37	8 (9%)
22	CLA	r	608	-	53,57,73	1.40	8 (15%)	62,93,113	1.47	8 (12%)
26	CHL	s	314	-	50,54,74	2.26	18 (36%)	56,90,114	3.11	22 (39%)
27	NEX	S	317	19	38,46,46	0.88	1 (2%)	50,70,70	2.45	17 (34%)
22	CLA	R	302	27	53,57,73	1.44	9 (16%)	62,93,113	1.49	6 (9%)
24	XAT	V	311	-	39,47,47	2.58	18 (46%)	54,74,74	12.00	18 (33%)
26	CHL	1	318	-	70,74,74	1.90	20 (28%)	80,114,114	2.64	25 (31%)
26	CHL	3	315	18	70,74,74	1.91	19 (27%)	80,114,114	2.67	23 (28%)
22	CLA	B	616	21	69,73,73	1.23	9 (13%)	83,113,113	1.38	8 (9%)
22	CLA	b	605	21	69,73,73	1.24	9 (13%)	83,113,113	1.66	10 (12%)
26	CHL	3	316	-	65,69,74	2.00	19 (29%)	74,108,114	2.75	25 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
26	CHL	4	316	18	70,74,74	1.92	20 (28%)	80,114,114	2.75	28 (35%)
22	CLA	v	307	-	69,73,73	1.24	10 (14%)	83,113,113	1.35	6 (7%)
26	CHL	5	315	-	54,58,74	2.16	20 (37%)	59,94,114	3.06	23 (38%)
31	BCR	B	620	-	41,41,41	4.75	24 (58%)	56,56,56	2.28	23 (41%)
22	CLA	c	511	8,20	69,73,73	1.26	10 (14%)	83,113,113	1.22	5 (6%)
22	CLA	n	306	-	64,68,73	1.27	7 (10%)	77,107,113	1.39	8 (10%)
26	CHL	2	314	-	52,56,74	2.36	20 (38%)	58,92,114	3.15	24 (41%)
22	CLA	u	302	-	69,73,73	1.26	9 (13%)	83,113,113	1.30	5 (6%)
23	LUT	2	310	-	42,43,43	0.78	0	51,60,60	1.64	12 (23%)
26	CHL	p	319	-	70,74,74	1.91	20 (28%)	80,114,114	2.64	24 (30%)
26	CHL	2	313	18	70,74,74	2.00	20 (28%)	80,114,114	2.65	25 (31%)
22	CLA	6	302	-	69,73,73	1.25	9 (13%)	83,113,113	1.29	8 (9%)
26	CHL	2	315	-	54,58,74	2.17	19 (35%)	59,94,114	3.04	22 (37%)
26	CHL	4	313	-	70,74,74	1.96	20 (28%)	80,114,114	2.57	25 (31%)
36	DGD	c	517	-	56,56,67	1.30	8 (14%)	70,70,81	1.19	5 (7%)
22	CLA	p	304	-	54,58,73	1.41	8 (14%)	65,95,113	1.42	6 (9%)
22	CLA	R	310	-	64,68,73	1.31	7 (10%)	77,107,113	1.43	7 (9%)
26	CHL	g	313	-	54,58,74	2.17	17 (31%)	59,94,114	3.02	20 (33%)
26	CHL	P	315	-	52,56,74	2.43	20 (38%)	58,92,114	2.90	21 (36%)
23	LUT	V	310	-	42,43,43	0.78	0	51,60,60	1.62	12 (23%)

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
22	CLA	b	608	-	-	11/39/115/115	-
22	CLA	v	302	-	-	14/39/115/115	-
25	LHG	C	522	-	-	16/53/53/53	-
22	CLA	s	308	-	-	9/27/103/115	-
23	LUT	2	309	-	-	4/29/67/67	0/2/2/2
26	CHL	U	319	-	-	22/41/117/117	-
27	NEX	r	618	22,1	-	7/27/83/83	0/3/3/3
26	CHL	6	315	-	-	17/41/117/117	-
22	CLA	R	309	-	-	7/20/96/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	CLA	b	606	-	-	20/39/115/115	-
22	CLA	C	503	-	-	9/39/115/115	-
25	LHG	5	312	-	-	23/53/53/53	-
34	LMG	b	621	-	-	24/46/66/70	0/1/1/1
26	CHL	n	317	-	-	18/41/117/117	-
23	LUT	V	309	-	-	2/29/67/67	0/2/2/2
31	BCR	b	618	-	-	8/29/63/63	0/2/2/2
26	CHL	Q	311	-	-	19/41/117/117	-
25	LHG	R	314	-	-	24/46/46/53	-
22	CLA	r	601	27	-	9/20/96/115	-
22	CLA	G	304	18	-	10/38/114/115	-
32	SQD	a	413	-	-	22/49/69/69	0/1/1/1
22	CLA	g	302	-	-	15/39/115/115	-
22	CLA	1	304	-	-	9/33/109/115	-
26	CHL	2	316	-	-	19/41/117/117	-
22	CLA	p	307	-	-	9/33/109/115	-
22	CLA	b	603	-	-	14/39/115/115	-
26	CHL	3	311	-	-	16/41/117/117	-
27	NEX	2	319	-	-	7/27/83/83	0/3/3/3
25	LHG	D	407	3	-	18/53/53/53	-
23	LUT	5	309	-	-	4/29/67/67	0/2/2/2
24	XAT	4	311	-	-	8/31/93/93	0/4/4/4
22	CLA	p	309	-	-	8/19/95/115	-
24	XAT	1	311	-	-	7/31/93/93	0/4/4/4
22	CLA	3	307	-	-	12/39/115/115	-
22	CLA	B	602	-	-	21/39/115/115	-
22	CLA	g	306	22	-	15/33/109/115	-
24	XAT	P	312	-	-	8/31/93/93	0/4/4/4
22	CLA	c	512	-	-	9/39/115/115	-
22	CLA	N	306	-	-	9/33/109/115	-
22	CLA	U	303	-	-	7/21/97/115	-
25	LHG	b	622	-	-	22/51/51/53	-
22	CLA	B	611	-	-	16/39/115/115	-
33	PL9	d	404	-	-	9/53/73/73	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	BCR	b	620	-	-	12/29/63/63	0/2/2/2
26	CHL	2	318	-	-	20/41/117/117	-
22	CLA	5	301	-	-	12/39/115/115	-
22	CLA	v	304	-	-	14/33/109/115	-
22	CLA	C	513	-	-	10/39/115/115	-
25	LHG	s	312	19	-	17/53/53/53	-
34	LMG	a	412	-	-	8/35/55/70	0/1/1/1
23	LUT	1	310	-	-	0/29/67/67	0/2/2/2
25	LHG	b	623	21	-	24/53/53/53	-
22	CLA	q	303	-	-	10/21/97/115	-
22	CLA	c	513	-	-	10/39/115/115	-
22	CLA	b	615	-	-	20/39/115/115	-
22	CLA	1	308	-	-	13/19/95/115	-
22	CLA	Q	303	-	-	12/21/97/115	-
26	CHL	v	314	-	-	14/20/96/117	-
31	BCR	c	516	-	-	11/29/63/63	0/2/2/2
33	PL9	A	410	-	-	0/5/18/73	0/1/1/1
22	CLA	5	304	18	-	14/39/115/115	-
34	LMG	b	624	21	-	22/50/70/70	0/1/1/1
22	CLA	B	606	-	-	20/39/115/115	-
22	CLA	U	302	-	-	14/39/115/115	-
22	CLA	2	304	18	-	11/39/115/115	-
22	CLA	q	301	-	-	17/39/115/115	-
22	CLA	G	306	22	-	11/33/109/115	-
26	CHL	u	314	-	-	13/20/96/117	-
22	CLA	Q	301	-	-	16/39/115/115	-
26	CHL	6	314	-	-	13/22/98/117	-
22	CLA	s	301	19	-	17/35/111/115	-
24	XAT	Q	309	-	-	10/31/93/93	0/4/4/4
22	CLA	6	307	22	-	18/33/109/115	-
25	LHG	L	101	-	-	28/53/53/53	-
22	CLA	v	303	-	-	9/21/97/115	-
27	NEX	R	301	22,1	-	10/27/83/83	0/3/3/3
36	DGD	B	601	21	-	22/51/91/95	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	BCR	C	517	-	-	14/29/63/63	0/2/2/2
22	CLA	n	304	18	-	15/39/115/115	-
22	CLA	V	302	-	-	14/39/115/115	-
22	CLA	G	308	-	-	11/19/95/115	-
22	CLA	C	506	-	-	15/39/115/115	-
26	CHL	4	315	-	-	8/22/98/117	-
23	LUT	p	310	-	-	2/29/67/67	0/2/2/2
27	NEX	s	317	19	-	4/27/83/83	0/3/3/3
22	CLA	C	511	-	-	14/39/115/115	-
26	CHL	U	317	-	-	20/41/117/117	-
26	CHL	3	314	-	-	18/41/117/117	-
22	CLA	c	502	-	-	10/39/115/115	-
36	DGD	C	520	-	-	31/51/91/95	0/2/2/2
26	CHL	U	315	-	-	16/41/117/117	-
22	CLA	C	508	-	-	22/39/115/115	-
31	BCR	d	403	3	-	12/29/63/63	0/2/2/2
24	XAT	p	312	-	-	7/31/93/93	0/4/4/4
24	XAT	r	612	-	-	7/31/93/93	0/4/4/4
26	CHL	g	311	-	-	21/41/117/117	-
22	CLA	P	303	-	-	15/39/115/115	-
26	CHL	n	318	-	-	25/41/117/117	-
37	HEM	E	101	4,17	-	2/14/54/54	-
36	DGD	J	101	-	-	21/49/89/95	0/2/2/2
25	LHG	V	312	-	-	18/53/53/53	-
25	LHG	d	406	3	-	19/53/53/53	-
25	LHG	6	311	-	-	19/53/53/53	-
31	BCR	t	101	-	-	12/29/63/63	0/2/2/2
26	CHL	N	313	-	-	14/41/117/117	-
30	PHO	D	401	-	-	11/37/103/103	0/5/6/6
22	CLA	B	603	-	-	16/39/115/115	-
22	CLA	r	609	26	-	12/33/109/115	-
22	CLA	b	607	-	-	15/39/115/115	-
22	CLA	r	610	-	-	10/15/91/115	-
22	CLA	n	303	-	-	7/21/97/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	BCR	T	101	-	-	12/29/63/63	0/2/2/2
34	LMG	C	502	-	-	26/46/66/70	0/1/1/1
26	CHL	R	317	-	-	16/35/111/117	-
25	LHG	P	313	-	-	24/53/53/53	-
22	CLA	s	302	-	-	6/15/91/115	-
26	CHL	S	313	-	-	7/17/93/117	-
24	XAT	v	311	-	-	11/31/93/93	0/4/4/4
26	CHL	p	320	-	-	20/41/117/117	-
22	CLA	4	306	-	-	16/33/109/115	-
22	CLA	U	305	-	-	12/33/109/115	-
26	CHL	4	317	-	-	16/41/117/117	-
36	DGD	b	601	21	-	21/51/91/95	0/2/2/2
22	CLA	A	406	-	-	9/21/97/115	-
22	CLA	C	514	-	-	14/39/115/115	-
23	LUT	u	309	-	-	2/29/67/67	0/2/2/2
22	CLA	6	304	-	-	11/21/97/115	-
22	CLA	5	303	-	-	7/21/97/115	-
26	CHL	5	317	-	-	17/41/117/117	-
26	CHL	n	316	-	-	27/41/117/117	-
22	CLA	4	304	-	-	11/33/109/115	-
22	CLA	B	617	-	-	11/39/115/115	-
22	CLA	b	614	-	-	16/39/115/115	-
22	CLA	5	302	-	-	18/39/115/115	-
22	CLA	b	609	-	-	12/39/115/115	-
22	CLA	q	306	22	-	14/33/109/115	-
24	XAT	u	311	-	-	7/31/93/93	0/4/4/4
22	CLA	U	304	-	-	7/33/109/115	-
26	CHL	u	318	-	-	20/41/117/117	-
32	SQD	L	102	9	-	21/49/69/69	0/1/1/1
22	CLA	b	602	-	-	19/39/115/115	-
31	BCR	B	618	-	-	8/29/63/63	0/2/2/2
24	XAT	2	311	-	-	6/31/93/93	0/4/4/4
22	CLA	v	301	-	-	13/39/115/115	-
22	CLA	b	612	-	-	15/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	CLA	C	515	-	-	12/39/115/115	-
23	LUT	S	311	-	-	8/29/67/67	0/2/2/2
22	CLA	B	607	-	-	15/39/115/115	-
22	CLA	B	615	-	-	19/39/115/115	-
25	LHG	l	101	-	-	27/53/53/53	-
25	LHG	4	312	-	-	18/53/53/53	-
22	CLA	B	612	-	-	17/39/115/115	-
22	CLA	R	304	-	-	13/33/109/115	-
26	CHL	U	316	18	-	13/41/117/117	-
22	CLA	P	309	-	-	12/19/95/115	-
26	CHL	1	315	-	-	8/22/98/117	-
23	LUT	U	310	-	-	3/29/67/67	0/2/2/2
22	CLA	c	514	-	-	11/39/115/115	-
22	CLA	r	605	-	-	9/31/107/115	-
22	CLA	x	201	14	-	10/39/115/115	-
22	CLA	S	301	19	-	17/35/111/115	-
26	CHL	Q	312	-	-	16/20/96/117	-
23	LUT	4	309	-	-	2/29/67/67	0/2/2/2
31	BCR	C	518	-	-	11/29/63/63	0/2/2/2
26	CHL	P	319	-	-	22/41/117/117	-
22	CLA	G	305	22	-	12/33/109/115	-
26	CHL	1	317	18	-	21/41/117/117	-
22	CLA	X	202	14	-	9/39/115/115	-
22	CLA	S	308	-	-	9/27/103/115	-
22	CLA	R	307	-	-	18/39/115/115	-
22	CLA	1	306	-	-	16/33/109/115	-
22	CLA	b	613	-	-	16/39/115/115	-
23	LUT	r	611	1	-	2/29/67/67	0/2/2/2
25	LHG	n	312	-	-	19/53/53/53	-
23	LUT	P	311	-	-	3/29/67/67	0/2/2/2
22	CLA	3	302	-	-	15/39/115/115	-
22	CLA	N	308	-	-	16/19/95/115	-
22	CLA	r	604	-	-	9/19/95/115	-
23	LUT	n	309	-	-	0/29/67/67	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	CHL	q	313	-	-	11/22/98/117	-
22	CLA	u	307	-	-	16/39/115/115	-
26	CHL	Q	313	-	-	11/22/98/117	-
26	CHL	S	315	19	-	17/32/108/117	-
22	CLA	b	611	-	-	16/39/115/115	-
34	LMG	d	407	3	-	17/41/61/70	0/1/1/1
22	CLA	3	306	22	-	18/33/109/115	-
23	LUT	s	311	-	-	7/29/67/67	0/2/2/2
22	CLA	2	307	-	-	10/33/109/115	-
22	CLA	4	307	-	-	9/39/115/115	-
22	CLA	4	308	-	-	13/19/95/115	-
25	LHG	q	310	-	-	22/53/53/53	-
26	CHL	q	312	-	-	14/20/96/117	-
26	CHL	u	317	18	-	13/41/117/117	-
22	CLA	c	505	-	-	11/39/115/115	-
22	CLA	B	614	-	-	14/39/115/115	-
25	LHG	Q	310	-	-	19/53/53/53	-
26	CHL	5	318	-	-	18/41/117/117	-
22	CLA	G	302	-	-	19/39/115/115	-
26	CHL	u	315	-	-	10/22/98/117	-
30	PHO	A	407	-	-	10/37/103/103	0/5/6/6
22	CLA	6	303	-	-	14/39/115/115	-
22	CLA	R	306	-	-	9/31/107/115	-
36	DGD	c	519	-	-	21/49/89/95	0/2/2/2
22	CLA	B	609	-	-	12/39/115/115	-
27	NEX	v	319	-	-	4/27/83/83	0/3/3/3
22	CLA	4	303	-	-	11/21/97/115	-
26	CHL	n	313	18	-	21/41/117/117	-
31	BCR	c	515	-	-	14/29/63/63	0/2/2/2
22	CLA	N	305	18	-	14/33/109/115	-
26	CHL	q	311	-	-	18/41/117/117	-
26	CHL	N	314	-	-	12/20/96/117	-
22	CLA	s	305	-	-	7/27/103/115	-
27	NEX	U	318	-	-	3/27/83/83	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	LUT	R	312	-	-	4/29/67/67	0/2/2/2
22	CLA	c	509	-	-	10/39/115/115	-
26	CHL	P	317	-	-	17/41/117/117	-
26	CHL	r	614	-	-	20/41/117/117	-
22	CLA	5	305	18	-	13/33/109/115	-
22	CLA	p	302	-	-	17/39/115/115	-
22	CLA	6	305	18	-	19/38/114/115	-
26	CHL	v	317	18	-	12/41/117/117	-
22	CLA	B	605	21	-	20/39/115/115	-
22	CLA	N	302	-	-	20/39/115/115	-
32	SQD	l	102	9	-	21/49/69/69	0/1/1/1
22	CLA	A	404	-	-	15/39/115/115	-
26	CHL	p	317	-	-	16/41/117/117	-
22	CLA	P	308	-	-	15/33/109/115	-
22	CLA	p	306	18	-	13/33/109/115	-
22	CLA	b	617	21	-	14/39/115/115	-
22	CLA	g	303	-	-	13/21/97/115	-
26	CHL	1	313	-	-	12/41/117/117	-
25	LHG	A	413	2	-	27/47/47/53	-
32	SQD	m	101	-	-	21/37/57/69	0/1/1/1
22	CLA	Q	308	-	-	11/19/95/115	-
22	CLA	A	408	-	-	12/33/109/115	-
26	CHL	G	313	-	-	9/22/98/117	-
27	NEX	r	617	-	-	2/27/83/83	0/3/3/3
22	CLA	P	305	18	-	12/39/115/115	-
25	LHG	G	310	-	-	19/53/53/53	-
22	CLA	P	306	18	-	12/33/109/115	-
22	CLA	n	301	-	-	14/39/115/115	-
26	CHL	v	313	-	-	17/41/117/117	-
22	CLA	5	308	-	-	5/19/95/115	-
24	XAT	q	309	-	-	12/31/93/93	0/4/4/4
22	CLA	a	408	-	-	11/33/109/115	-
22	CLA	C	510	-	-	9/39/115/115	-
22	CLA	u	304	-	-	5/33/109/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	CLA	g	305	22	-	12/33/109/115	-
34	LMG	B	621	-	-	20/46/66/70	0/1/1/1
34	LMG	D	408	3	-	17/41/61/70	0/1/1/1
25	LHG	C	524	-	-	13/53/53/53	-
22	CLA	N	307	-	-	15/33/109/115	-
26	CHL	6	301	-	-	22/41/117/117	-
31	BCR	x	202	-	-	9/29/63/63	0/2/2/2
22	CLA	p	303	-	-	8/39/115/115	-
26	CHL	S	316	-	-	13/17/93/117	-
22	CLA	3	304	18	-	15/38/114/115	-
26	CHL	s	313	-	-	7/17/93/117	-
25	LHG	D	406	3	-	28/50/50/53	-
26	CHL	q	315	-	-	13/35/111/117	-
30	PHO	d	401	-	-	11/37/103/103	0/5/6/6
25	LHG	B	622	-	-	21/51/51/53	-
25	LHG	p	313	-	-	22/53/53/53	-
26	CHL	Q	315	18	-	20/41/117/117	-
22	CLA	P	302	-	-	18/39/115/115	-
26	CHL	Q	314	-	-	22/41/117/117	-
22	CLA	q	308	-	-	13/19/95/115	-
22	CLA	S	304	19	-	11/15/91/115	-
26	CHL	s	315	19	-	17/32/108/117	-
22	CLA	n	302	-	-	16/39/115/115	-
22	CLA	2	302	-	-	14/39/115/115	-
26	CHL	u	316	-	-	24/41/117/117	-
25	LHG	u	312	-	-	25/53/53/53	-
26	CHL	U	314	-	-	12/22/98/117	-
25	LHG	c	521	-	-	14/53/53/53	-
26	CHL	Q	316	-	-	14/35/111/117	-
27	NEX	P	301	18	-	3/27/83/83	0/3/3/3
22	CLA	U	307	-	-	17/39/115/115	-
22	CLA	q	302	-	-	13/39/115/115	-
37	HEM	e	101	4,17	-	3/14/54/54	-
22	CLA	g	301	-	-	14/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	LUT	1	309	-	-	2/29/67/67	0/2/2/2
25	LHG	2	312	-	-	24/53/53/53	-
26	CHL	6	317	-	-	18/35/111/117	-
22	CLA	G	303	-	-	12/21/97/115	-
24	XAT	g	309	-	-	10/31/93/93	0/4/4/4
25	LHG	v	312	-	-	19/53/53/53	-
22	CLA	B	610	-	-	18/39/115/115	-
22	CLA	V	307	-	-	10/39/115/115	-
31	BCR	X	201	-	-	9/29/63/63	0/2/2/2
25	LHG	3	310	-	-	18/53/53/53	-
22	CLA	S	305	-	-	8/27/103/115	-
26	CHL	V	315	-	-	8/22/98/117	-
27	NEX	V	319	-	-	6/27/83/83	0/3/3/3
22	CLA	v	308	-	-	11/19/95/115	-
26	CHL	g	315	18	-	23/41/117/117	-
22	CLA	3	301	-	-	14/39/115/115	-
22	CLA	S	309	-	-	4/20/96/115	-
26	CHL	3	312	-	-	10/20/96/117	-
22	CLA	G	301	-	-	19/39/115/115	-
22	CLA	b	616	21	-	11/39/115/115	-
27	NEX	u	320	-	-	2/27/83/83	0/3/3/3
22	CLA	S	302	-	-	6/15/91/115	-
24	XAT	U	311	-	-	7/31/93/93	0/4/4/4
26	CHL	V	317	18	-	14/41/117/117	-
22	CLA	U	306	-	-	12/33/109/115	-
26	CHL	g	312	-	-	12/20/96/117	-
31	BCR	a	409	-	-	2/29/63/63	0/2/2/2
27	NEX	5	319	-	-	8/27/83/83	0/3/3/3
22	CLA	4	305	-	-	8/33/109/115	-
22	CLA	v	306	-	-	15/33/109/115	-
22	CLA	s	304	19	-	11/15/91/115	-
33	PL9	a	411	-	-	0/5/18/73	0/1/1/1
26	CHL	R	315	-	-	20/41/117/117	-
31	BCR	C	516	-	-	8/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	LUT	n	310	-	-	3/29/67/67	0/2/2/2
24	XAT	6	310	-	-	8/31/93/93	0/4/4/4
32	SQD	M	101	-	-	22/37/57/69	0/1/1/1
31	BCR	k	101	-	-	13/29/63/63	0/2/2/2
22	CLA	1	303	-	-	10/21/97/115	-
26	CHL	v	316	-	-	17/41/117/117	-
22	CLA	C	505	-	-	19/39/115/115	-
22	CLA	V	301	-	-	14/39/115/115	-
22	CLA	A	405	-	-	12/39/115/115	-
36	DGD	C	519	-	-	23/44/84/95	0/2/2/2
22	CLA	U	308	-	-	12/19/95/115	-
22	CLA	3	303	-	-	12/21/97/115	-
24	XAT	R	313	-	-	8/31/93/93	0/4/4/4
22	CLA	u	303	-	-	8/21/97/115	-
22	CLA	V	306	-	-	7/33/109/115	-
26	CHL	5	314	-	-	13/20/96/117	-
22	CLA	a	405	-	-	12/39/115/115	-
22	CLA	C	509	20	-	16/39/115/115	-
25	LHG	B	623	21	-	21/53/53/53	-
22	CLA	q	305	22	-	14/33/109/115	-
34	LMG	w	201	-	-	22/43/63/70	0/1/1/1
26	CHL	s	316	-	-	13/17/93/117	-
34	LMG	C	521	-	-	19/46/66/70	0/1/1/1
22	CLA	Q	305	22	-	18/33/109/115	-
22	CLA	S	307	-	-	6/20/96/115	-
24	XAT	3	309	-	-	8/31/93/93	0/4/4/4
24	XAT	G	309	-	-	10/31/93/93	0/4/4/4
22	CLA	1	301	-	-	9/39/115/115	-
22	CLA	V	304	-	-	12/33/109/115	-
23	LUT	s	310	19	-	2/29/67/67	0/2/2/2
26	CHL	5	316	-	-	20/41/117/117	-
26	CHL	N	316	-	-	19/41/117/117	-
32	SQD	C	501	-	-	27/45/65/69	0/1/1/1
22	CLA	s	307	-	-	6/20/96/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	CLA	D	403	3	-	17/39/115/115	-
22	CLA	S	303	19	-	6/21/97/115	-
25	LHG	a	415	2	-	26/47/47/53	-
22	CLA	q	304	18	-	15/38/114/115	-
22	CLA	s	309	-	-	4/20/96/115	-
26	CHL	v	315	-	-	8/22/98/117	-
22	CLA	c	507	-	-	22/39/115/115	-
22	CLA	2	305	18	-	13/33/109/115	-
22	CLA	Q	304	18	-	14/38/114/115	-
27	NEX	n	319	-	-	7/27/83/83	0/3/3/3
26	CHL	P	314	18	-	16/41/117/117	-
34	LMG	A	411	-	-	11/35/55/70	0/1/1/1
23	LUT	u	310	-	-	2/29/67/67	0/2/2/2
22	CLA	a	404	-	-	15/39/115/115	-
26	CHL	n	314	-	-	11/20/96/117	-
23	LUT	P	310	-	-	2/29/67/67	0/2/2/2
22	CLA	n	307	-	-	13/33/109/115	-
26	CHL	G	312	-	-	8/20/96/117	-
26	CHL	P	316	-	-	9/22/98/117	-
26	CHL	V	313	-	-	20/41/117/117	-
22	CLA	R	311	-	-	10/15/91/115	-
22	CLA	u	301	-	-	9/39/115/115	-
22	CLA	b	604	-	-	18/39/115/115	-
22	CLA	n	305	18	-	13/33/109/115	-
22	CLA	a	406	-	-	10/21/97/115	-
22	CLA	r	603	-	-	13/33/109/115	-
26	CHL	6	312	-	-	17/41/117/117	-
26	CHL	g	316	-	-	17/35/111/117	-
25	LHG	r	613	-	-	19/46/46/53	-
32	SQD	A	412	-	-	21/49/69/69	0/1/1/1
26	CHL	P	318	-	-	19/41/117/117	-
26	CHL	1	314	22	-	16/20/96/117	-
36	DGD	c	518	-	-	31/51/91/95	0/2/2/2
26	CHL	r	619	1	-	10/20/96/117	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	CLA	r	607	1	-	11/20/96/115	-
25	LHG	g	310	-	-	20/53/53/53	-
31	BCR	z	101	-	-	8/29/63/63	0/2/2/2
27	NEX	N	318	-	-	9/27/83/83	0/3/3/3
24	XAT	N	311	-	-	8/31/93/93	0/4/4/4
22	CLA	b	610	-	-	18/39/115/115	-
26	CHL	p	314	18	-	13/41/117/117	-
33	PL9	D	405	-	-	9/53/73/73	0/1/1/1
25	LHG	1	312	-	-	14/53/53/53	-
34	LMG	W	201	-	-	21/43/63/70	0/1/1/1
22	CLA	s	303	19	-	6/21/97/115	-
31	BCR	K	101	-	-	13/29/63/63	0/2/2/2
31	BCR	B	619	-	-	14/29/63/63	0/2/2/2
22	CLA	P	307	-	-	12/33/109/115	-
22	CLA	R	303	-	-	9/33/109/115	-
26	CHL	p	316	-	-	9/22/98/117	-
22	CLA	s	306	-	-	7/29/105/115	-
26	CHL	g	314	-	-	22/41/117/117	-
24	XAT	5	311	-	-	6/31/93/93	0/4/4/4
26	CHL	S	314	-	-	9/17/93/117	-
31	BCR	D	404	3	-	13/29/63/63	0/2/2/2
26	CHL	v	318	-	-	22/41/117/117	-
22	CLA	1	305	-	-	10/33/109/115	-
23	LUT	U	309	-	-	4/29/67/67	0/2/2/2
22	CLA	n	308	-	-	13/19/95/115	-
26	CHL	G	316	-	-	15/35/111/117	-
22	CLA	R	308	1	-	12/20/96/115	-
22	CLA	5	306	-	-	13/33/109/115	-
26	CHL	2	317	-	-	13/41/117/117	-
26	CHL	G	314	-	-	17/41/117/117	-
22	CLA	V	303	-	-	8/21/97/115	-
22	CLA	G	307	-	-	14/39/115/115	-
22	CLA	v	305	-	-	9/33/109/115	-
23	LUT	5	310	-	-	1/29/67/67	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	CHL	r	616	-	-	16/35/111/117	-
22	CLA	B	608	-	-	14/39/115/115	-
25	LHG	c	523	-	-	17/53/53/53	-
27	NEX	u	319	-	-	7/27/83/83	0/3/3/3
22	CLA	B	613	-	-	16/39/115/115	-
22	CLA	U	301	-	-	10/39/115/115	-
22	CLA	3	305	22	-	11/33/109/115	-
31	BCR	A	409	-	-	3/29/63/63	0/2/2/2
22	CLA	c	510	-	-	15/39/115/115	-
22	CLA	C	507	-	-	19/39/115/115	-
22	CLA	P	304	-	-	12/21/97/115	-
26	CHL	V	314	-	-	13/20/96/117	-
23	LUT	p	311	-	-	3/29/67/67	0/2/2/2
22	CLA	d	402	3	-	15/39/115/115	-
26	CHL	q	314	18	-	23/41/117/117	-
26	CHL	p	318	-	-	19/41/117/117	-
26	CHL	n	315	-	-	12/22/98/117	-
23	LUT	N	310	-	-	1/29/67/67	0/2/2/2
26	CHL	V	316	-	-	19/41/117/117	-
22	CLA	6	309	-	-	12/19/95/115	-
26	CHL	N	315	-	-	9/22/98/117	-
22	CLA	c	503	-	-	22/39/115/115	-
26	CHL	6	316	18	-	23/41/117/117	-
22	CLA	5	307	-	-	12/33/109/115	-
22	CLA	g	308	-	-	10/19/95/115	-
22	CLA	2	301	-	-	13/39/115/115	-
22	CLA	p	305	18	-	13/39/115/115	-
22	CLA	4	301	-	-	9/39/115/115	-
23	LUT	N	309	-	-	2/29/67/67	0/2/2/2
26	CHL	u	313	-	-	16/41/117/117	-
22	CLA	q	307	-	-	17/39/115/115	-
26	CHL	4	314	-	-	12/20/96/117	-
36	DGD	a	416	-	-	24/48/88/95	0/2/2/2
22	CLA	Q	307	-	-	12/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	CHL	U	313	-	-	17/41/117/117	-
27	NEX	p	301	18	-	3/27/83/83	0/3/3/3
26	CHL	3	313	-	-	16/22/98/117	-
23	LUT	v	310	-	-	0/29/67/67	0/2/2/2
22	CLA	c	508	20	-	16/39/115/115	-
36	DGD	A	414	-	-	22/48/88/95	0/2/2/2
22	CLA	4	302	-	-	15/39/115/115	-
32	SQD	a	410	-	-	25/45/65/69	0/1/1/1
22	CLA	p	308	-	-	13/33/109/115	-
23	LUT	v	309	-	-	2/29/67/67	0/2/2/2
22	CLA	c	504	-	-	19/39/115/115	-
26	CHL	V	318	-	-	19/41/117/117	-
26	CHL	6	313	-	-	10/20/96/117	-
24	XAT	n	311	-	-	9/31/93/93	0/4/4/4
22	CLA	r	602	-	-	9/33/109/115	-
23	LUT	S	310	-	-	2/29/67/67	0/2/2/2
22	CLA	N	304	18	-	19/39/115/115	-
34	LMG	c	501	-	-	25/46/66/70	0/1/1/1
25	LHG	d	405	3	-	26/50/50/53	-
26	CHL	N	317	-	-	22/41/117/117	-
22	CLA	B	604	-	-	17/39/115/115	-
22	CLA	1	302	-	-	14/39/115/115	-
26	CHL	G	315	18	-	19/41/117/117	-
22	CLA	2	306	-	-	11/33/109/115	-
25	LHG	C	523	-	-	24/53/53/53	-
22	CLA	V	305	-	-	10/33/109/115	-
26	CHL	p	315	-	-	8/20/96/117	-
22	CLA	u	308	-	-	12/19/95/115	-
31	BCR	b	619	-	-	14/29/63/63	0/2/2/2
22	CLA	S	306	-	-	8/29/105/115	-
22	CLA	N	301	-	-	14/39/115/115	-
22	CLA	6	308	-	-	12/39/115/115	-
26	CHL	G	311	-	-	18/41/117/117	-
25	LHG	U	312	-	-	29/53/53/53	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	PHO	a	407	-	-	10/37/103/103	0/5/6/6
22	CLA	Q	302	-	-	13/39/115/115	-
26	CHL	r	615	-	-	12/29/105/117	-
22	CLA	2	308	-	-	8/19/95/115	-
34	LMG	c	520	-	-	21/46/66/70	0/1/1/1
25	LHG	N	312	-	-	16/53/53/53	-
22	CLA	3	308	-	-	12/19/95/115	-
22	CLA	C	504	-	-	23/39/115/115	-
22	CLA	V	308	-	-	11/19/95/115	-
26	CHL	R	316	-	-	13/29/105/117	-
34	LMG	B	624	21	-	21/50/70/70	0/1/1/1
22	CLA	g	307	-	-	14/39/115/115	-
22	CLA	u	305	-	-	14/33/109/115	-
26	CHL	5	313	18	-	21/41/117/117	-
22	CLA	u	306	-	-	12/33/109/115	-
22	CLA	g	304	18	-	9/38/114/115	-
22	CLA	R	305	-	-	9/19/95/115	-
22	CLA	2	303	-	-	8/21/97/115	-
22	CLA	C	512	8,20	-	22/39/115/115	-
26	CHL	1	316	-	-	23/41/117/117	-
22	CLA	6	306	22	-	15/33/109/115	-
25	LHG	S	312	19	-	17/53/53/53	-
22	CLA	Q	306	22	-	13/33/109/115	-
25	LHG	c	522	-	-	24/53/53/53	-
23	LUT	4	310	-	-	0/29/67/67	0/2/2/2
22	CLA	r	606	-	-	18/39/115/115	-
22	CLA	N	303	-	-	7/21/97/115	-
22	CLA	c	506	-	-	19/39/115/115	-
22	CLA	1	307	-	-	13/39/115/115	-
22	CLA	r	608	-	-	7/20/96/115	-
26	CHL	s	314	-	-	8/17/93/117	-
27	NEX	S	317	19	-	4/27/83/83	0/3/3/3
22	CLA	R	302	27	-	10/20/96/115	-
24	XAT	V	311	-	-	11/31/93/93	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	CHL	1	318	-	-	16/41/117/117	-
26	CHL	3	315	18	-	23/41/117/117	-
22	CLA	B	616	21	-	8/39/115/115	-
22	CLA	b	605	21	-	18/39/115/115	-
26	CHL	3	316	-	-	18/35/111/117	-
26	CHL	4	316	18	-	16/41/117/117	-
22	CLA	v	307	-	-	12/39/115/115	-
26	CHL	5	315	-	-	8/22/98/117	-
31	BCR	B	620	-	-	12/29/63/63	0/2/2/2
22	CLA	c	511	8,20	-	20/39/115/115	-
22	CLA	n	306	-	-	9/33/109/115	-
26	CHL	2	314	-	-	9/20/96/117	-
22	CLA	u	302	-	-	16/39/115/115	-
23	LUT	2	310	-	-	1/29/67/67	0/2/2/2
26	CHL	p	319	-	-	17/41/117/117	-
26	CHL	2	313	18	-	20/41/117/117	-
22	CLA	6	302	-	-	17/39/115/115	-
26	CHL	2	315	-	-	7/22/98/117	-
26	CHL	4	313	-	-	18/41/117/117	-
36	DGD	c	517	-	-	22/44/84/95	0/2/2/2
22	CLA	p	304	-	-	12/21/97/115	-
22	CLA	R	310	-	-	12/33/109/115	-
26	CHL	g	313	-	-	10/22/98/117	-
26	CHL	P	315	-	-	11/20/96/117	-
23	LUT	V	310	-	-	0/29/67/67	0/2/2/2

The worst 5 of 5975 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	A	409	BCR	C26-C25	15.51	1.61	1.34
31	a	409	BCR	C26-C25	15.51	1.61	1.34
31	b	619	BCR	C5-C6	15.49	1.61	1.34
31	B	619	BCR	C5-C6	15.47	1.61	1.34
31	x	202	BCR	C5-C6	15.45	1.61	1.34

The worst 5 of 6551 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	1	311	XAT	O4-C5-C4	60.27	158.66	113.38
24	2	311	XAT	O4-C5-C4	60.01	158.46	113.38
24	n	311	XAT	O24-C25-C24	59.81	158.31	113.38
24	N	311	XAT	O24-C25-C24	59.80	158.31	113.38
24	4	311	XAT	O4-C5-C4	59.80	158.31	113.38

There are no chirality outliers.

5 of 7284 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
22	r	601	CLA	C2B-C3B-CAB-CBB
22	r	601	CLA	C4B-C3B-CAB-CBB
22	r	604	CLA	C1A-C2A-CAA-CBA
22	r	605	CLA	C4B-C3B-CAB-CBB
22	r	606	CLA	CBD-CGD-O2D-CED

There are no ring outliers.

459 monomers are involved in 949 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	b	608	CLA	3	0
22	v	302	CLA	6	0
25	C	522	LHG	3	0
23	2	309	LUT	4	0
26	U	319	CHL	6	0
27	r	618	NEX	3	0
26	6	315	CHL	7	0
22	b	606	CLA	3	0
22	C	503	CLA	1	0
25	5	312	LHG	1	0
34	b	621	LMG	4	0
26	n	317	CHL	1	0
23	V	309	LUT	5	0
31	b	618	BCR	5	0
26	Q	311	CHL	2	0
22	r	601	CLA	1	0
32	a	413	SQD	3	0
22	g	302	CLA	1	0
26	2	316	CHL	6	0
22	p	307	CLA	2	0
22	b	603	CLA	6	0
26	3	311	CHL	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	2	319	NEX	1	0
25	D	407	LHG	7	0
23	5	309	LUT	6	0
24	4	311	XAT	1	0
22	p	309	CLA	2	0
24	1	311	XAT	2	0
22	3	307	CLA	2	0
22	B	602	CLA	4	0
24	P	312	XAT	4	0
22	c	512	CLA	1	0
22	N	306	CLA	1	0
33	d	404	PL9	3	0
31	b	620	BCR	3	0
26	2	318	CHL	6	0
22	5	301	CLA	4	0
35	a	414	BCT	1	0
22	v	304	CLA	3	0
22	C	513	CLA	1	0
25	s	312	LHG	3	0
34	a	412	LMG	1	0
23	1	310	LUT	3	0
22	q	303	CLA	2	0
22	c	513	CLA	3	0
22	b	615	CLA	1	0
22	1	308	CLA	2	0
22	Q	303	CLA	1	0
22	5	304	CLA	2	0
34	b	624	LMG	1	0
22	B	606	CLA	4	0
22	U	302	CLA	2	0
22	2	304	CLA	3	0
22	q	301	CLA	1	0
26	u	314	CHL	1	0
22	Q	301	CLA	3	0
26	6	314	CHL	2	0
22	s	301	CLA	2	0
22	6	307	CLA	2	0
25	L	101	LHG	2	0
22	v	303	CLA	1	0
27	R	301	NEX	3	0
36	B	601	DGD	6	0
31	C	517	BCR	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	n	304	CLA	1	0
22	V	302	CLA	3	0
22	C	506	CLA	3	0
23	p	310	LUT	1	0
27	s	317	NEX	4	0
22	C	511	CLA	3	0
26	U	317	CHL	6	0
26	3	314	CHL	6	0
22	c	502	CLA	1	0
36	C	520	DGD	3	0
26	U	315	CHL	5	0
22	C	508	CLA	2	0
24	p	312	XAT	3	0
24	r	612	XAT	4	0
26	g	311	CHL	6	0
22	P	303	CLA	4	0
26	n	318	CHL	6	0
37	E	101	HEM	1	0
36	J	101	DGD	2	0
25	V	312	LHG	6	0
25	d	406	LHG	7	0
25	6	311	LHG	3	0
31	t	101	BCR	6	0
26	N	313	CHL	5	0
30	D	401	PHO	1	0
22	B	603	CLA	3	0
22	r	609	CLA	3	0
22	b	607	CLA	1	0
22	r	610	CLA	2	0
22	n	303	CLA	1	0
31	T	101	BCR	5	0
34	C	502	LMG	1	0
26	R	317	CHL	3	0
25	P	313	LHG	1	0
22	s	302	CLA	1	0
26	S	313	CHL	1	0
24	v	311	XAT	3	0
26	p	320	CHL	2	0
22	4	306	CLA	5	0
22	U	305	CLA	2	0
26	4	317	CHL	5	0
36	b	601	DGD	7	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	A	406	CLA	2	0
22	C	514	CLA	2	0
23	u	309	LUT	2	0
22	6	304	CLA	1	0
22	5	303	CLA	1	0
26	5	317	CHL	3	0
26	n	316	CHL	6	0
22	b	614	CLA	4	0
22	5	302	CLA	6	0
22	q	306	CLA	1	0
24	u	311	XAT	3	0
22	U	304	CLA	1	0
26	u	318	CHL	6	0
32	L	102	SQD	2	0
22	b	602	CLA	4	0
31	B	618	BCR	6	0
24	2	311	XAT	5	0
22	v	301	CLA	1	0
22	b	612	CLA	1	0
22	C	515	CLA	3	0
23	S	311	LUT	5	0
22	B	607	CLA	2	0
22	B	615	CLA	1	0
25	l	101	LHG	1	0
25	4	312	LHG	1	0
22	R	304	CLA	4	0
22	P	309	CLA	2	0
23	U	310	LUT	3	0
22	c	514	CLA	3	0
22	S	301	CLA	2	0
23	4	309	LUT	4	0
31	C	518	BCR	1	0
26	P	319	CHL	9	0
26	1	317	CHL	2	0
22	X	202	CLA	1	0
22	R	307	CLA	1	0
22	1	306	CLA	2	0
22	b	613	CLA	3	0
23	r	611	LUT	4	0
25	n	312	LHG	1	0
23	P	311	LUT	4	0
22	3	302	CLA	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	N	308	CLA	1	0
22	r	604	CLA	2	0
23	n	309	LUT	3	0
26	q	313	CHL	1	0
22	u	307	CLA	2	0
26	S	315	CHL	2	0
22	3	306	CLA	2	0
23	s	311	LUT	4	0
22	2	307	CLA	4	0
22	4	307	CLA	4	0
22	4	308	CLA	1	0
25	q	310	LHG	2	0
26	u	317	CHL	1	0
22	c	505	CLA	2	0
22	B	614	CLA	4	0
25	Q	310	LHG	4	0
26	5	318	CHL	5	0
22	G	302	CLA	3	0
30	A	407	PHO	4	0
22	6	303	CLA	1	0
36	c	519	DGD	1	0
22	B	609	CLA	1	0
27	v	319	NEX	2	0
26	n	313	CHL	3	0
31	c	515	BCR	1	0
22	N	305	CLA	1	0
26	q	311	CHL	7	0
22	s	305	CLA	4	0
23	R	312	LUT	2	0
22	c	509	CLA	3	0
26	P	317	CHL	5	0
26	r	614	CHL	2	0
22	5	305	CLA	2	0
22	p	302	CLA	2	0
22	6	305	CLA	3	0
26	v	317	CHL	1	0
22	B	605	CLA	2	0
22	N	302	CLA	5	0
32	l	102	SQD	3	0
22	A	404	CLA	1	0
26	p	317	CHL	4	0
22	P	308	CLA	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	p	306	CLA	1	0
22	b	617	CLA	2	0
22	g	303	CLA	1	0
26	1	313	CHL	1	0
25	A	413	LHG	3	0
32	m	101	SQD	1	0
22	Q	308	CLA	2	0
22	A	408	CLA	1	0
27	r	617	NEX	4	0
22	P	305	CLA	2	0
22	P	306	CLA	1	0
22	n	301	CLA	3	0
26	v	313	CHL	1	0
22	5	308	CLA	1	0
24	q	309	XAT	1	0
22	a	408	CLA	1	0
22	C	510	CLA	4	0
34	B	621	LMG	3	0
25	C	524	LHG	2	0
22	N	307	CLA	3	0
26	6	301	CHL	5	0
31	x	202	BCR	3	0
22	p	303	CLA	3	0
22	3	304	CLA	3	0
25	D	406	LHG	4	0
26	q	315	CHL	3	0
30	d	401	PHO	1	0
25	p	313	LHG	2	0
26	Q	315	CHL	4	0
22	P	302	CLA	3	0
26	Q	314	CHL	1	0
22	q	308	CLA	3	0
22	S	304	CLA	2	0
26	s	315	CHL	1	0
22	n	302	CLA	6	0
22	2	302	CLA	5	0
26	u	316	CHL	3	0
25	u	312	LHG	2	0
26	U	314	CHL	2	0
25	c	521	LHG	4	0
26	Q	316	CHL	2	0
27	P	301	NEX	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	U	307	CLA	1	0
22	q	302	CLA	2	0
37	e	101	HEM	1	0
22	g	301	CLA	1	0
23	1	309	LUT	2	0
25	2	312	LHG	3	0
26	6	317	CHL	2	0
22	G	303	CLA	1	0
24	g	309	XAT	5	0
25	v	312	LHG	4	0
22	B	610	CLA	4	0
22	V	307	CLA	2	0
31	X	201	BCR	4	0
25	3	310	LHG	3	0
22	S	305	CLA	2	0
27	V	319	NEX	3	0
26	g	315	CHL	3	0
22	3	301	CLA	3	0
26	3	312	CHL	1	0
22	G	301	CLA	2	0
22	b	616	CLA	1	0
27	u	320	NEX	2	0
22	S	302	CLA	1	0
24	U	311	XAT	5	0
26	V	317	CHL	2	0
22	U	306	CLA	4	0
26	g	312	CHL	1	0
31	a	409	BCR	3	0
27	5	319	NEX	2	0
22	v	306	CLA	1	0
22	s	304	CLA	2	0
26	R	315	CHL	1	0
31	C	516	BCR	2	0
23	n	310	LUT	4	0
24	6	310	XAT	4	0
32	M	101	SQD	1	0
31	k	101	BCR	2	0
22	1	303	CLA	1	0
26	v	316	CHL	7	0
22	C	505	CLA	4	0
22	V	301	CLA	3	0
22	A	405	CLA	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	C	519	DGD	4	0
22	3	303	CLA	2	0
24	R	313	XAT	3	0
22	V	306	CLA	2	0
26	5	314	CHL	1	0
22	a	405	CLA	3	0
22	C	509	CLA	1	0
34	w	201	LMG	2	0
34	C	521	LMG	3	0
22	Q	305	CLA	1	0
22	S	307	CLA	1	0
24	3	309	XAT	2	0
24	G	309	XAT	3	0
22	1	301	CLA	3	0
22	V	304	CLA	2	0
23	s	310	LUT	6	0
26	5	316	CHL	3	0
26	N	316	CHL	2	0
32	C	501	SQD	2	0
22	s	307	CLA	2	0
22	D	403	CLA	3	0
25	a	415	LHG	1	0
22	c	507	CLA	2	0
22	2	305	CLA	3	0
27	n	319	NEX	2	0
34	A	411	LMG	1	0
23	u	310	LUT	4	0
22	a	404	CLA	1	0
23	P	310	LUT	3	0
22	n	307	CLA	1	0
26	G	312	CHL	1	0
26	V	313	CHL	7	0
22	R	311	CLA	2	0
22	u	301	CLA	5	0
22	b	604	CLA	5	0
22	n	305	CLA	1	0
22	a	406	CLA	2	0
22	r	603	CLA	4	0
26	6	312	CHL	2	0
25	r	613	LHG	1	0
32	A	412	SQD	3	0
26	P	318	CHL	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	1	314	CHL	1	0
36	c	518	DGD	3	0
22	r	607	CLA	1	0
25	g	310	LHG	2	0
31	z	101	BCR	2	0
27	N	318	NEX	2	0
24	N	311	XAT	2	0
22	b	610	CLA	2	0
26	p	314	CHL	3	0
33	D	405	PL9	3	0
34	W	201	LMG	2	0
35	D	402	BCT	1	0
31	K	101	BCR	2	0
31	B	619	BCR	4	0
22	P	307	CLA	2	0
22	R	303	CLA	2	0
22	s	306	CLA	3	0
26	g	314	CHL	2	0
24	5	311	XAT	3	0
26	S	314	CHL	1	0
31	D	404	BCR	1	0
26	v	318	CHL	7	0
22	1	305	CLA	1	0
23	U	309	LUT	1	0
22	n	308	CLA	2	0
26	G	316	CHL	2	0
22	R	308	CLA	1	0
22	5	306	CLA	2	0
26	2	317	CHL	1	0
26	G	314	CHL	4	0
22	V	303	CLA	2	0
22	G	307	CLA	3	0
22	v	305	CLA	1	0
23	5	310	LUT	8	0
26	r	616	CHL	4	0
22	B	608	CLA	1	0
25	c	523	LHG	3	0
27	u	319	NEX	1	0
22	B	613	CLA	3	0
22	U	301	CLA	2	0
31	A	409	BCR	4	0
22	c	510	CLA	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	C	507	CLA	1	0
22	P	304	CLA	1	0
23	p	311	LUT	4	0
22	d	402	CLA	2	0
26	q	314	CHL	2	0
23	N	310	LUT	4	0
26	V	316	CHL	4	0
22	6	309	CLA	1	0
22	c	503	CLA	1	0
26	6	316	CHL	2	0
22	5	307	CLA	2	0
22	2	301	CLA	4	0
22	p	305	CLA	2	0
22	4	301	CLA	4	0
23	N	309	LUT	5	0
26	u	313	CHL	1	0
22	q	307	CLA	2	0
26	4	314	CHL	1	0
36	a	416	DGD	2	0
22	Q	307	CLA	3	0
26	U	313	CHL	1	0
27	p	301	NEX	4	0
26	3	313	CHL	2	0
23	v	310	LUT	4	0
22	c	508	CLA	1	0
36	A	414	DGD	2	0
22	4	302	CLA	5	0
32	a	410	SQD	3	0
22	p	308	CLA	1	0
23	v	309	LUT	3	0
22	c	504	CLA	4	0
26	V	318	CHL	4	0
26	6	313	CHL	1	0
24	n	311	XAT	1	0
22	r	602	CLA	3	0
23	S	310	LUT	4	0
34	c	501	LMG	1	0
25	d	405	LHG	5	0
26	N	317	CHL	5	0
22	B	604	CLA	4	0
22	1	302	CLA	4	0
26	G	315	CHL	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
22	2	306	CLA	2	0
22	V	305	CLA	1	0
26	p	315	CHL	1	0
31	b	619	BCR	4	0
22	S	306	CLA	2	0
22	N	301	CLA	3	0
22	6	308	CLA	1	0
26	G	311	CHL	4	0
25	U	312	LHG	4	0
30	a	407	PHO	2	0
22	Q	302	CLA	4	0
26	r	615	CHL	2	0
22	2	308	CLA	1	0
34	c	520	LMG	2	0
25	N	312	LHG	4	0
22	C	504	CLA	2	0
22	V	308	CLA	1	0
26	R	316	CHL	1	0
34	B	624	LMG	1	0
22	g	307	CLA	1	0
22	u	305	CLA	4	0
26	5	313	CHL	2	0
22	u	306	CLA	2	0
22	g	304	CLA	1	0
22	R	305	CLA	2	0
22	2	303	CLA	1	0
22	C	512	CLA	3	0
26	1	316	CHL	3	0
25	S	312	LHG	5	0
23	4	310	LUT	5	0
22	r	606	CLA	4	0
22	N	303	CLA	1	0
22	c	506	CLA	1	0
22	1	307	CLA	3	0
26	s	314	CHL	1	0
27	S	317	NEX	3	0
22	R	302	CLA	1	0
24	V	311	XAT	4	0
26	1	318	CHL	5	0
26	3	315	CHL	3	0
22	b	605	CLA	1	0
26	3	316	CHL	1	0

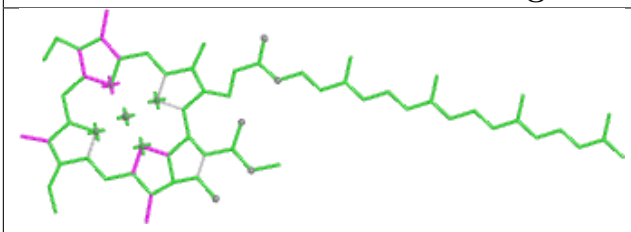
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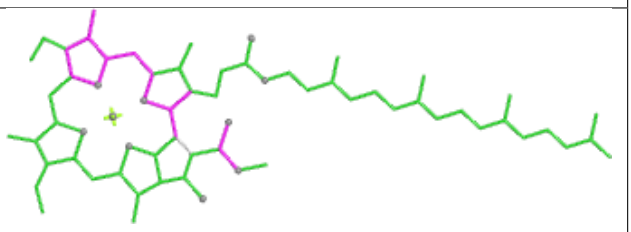
Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	4	316	CHL	2	0
22	v	307	CLA	2	0
31	B	620	BCR	1	0
22	c	511	CLA	3	0
22	n	306	CLA	1	0
26	2	314	CHL	1	0
22	u	302	CLA	2	0
23	2	310	LUT	4	0
26	p	319	CHL	4	0
26	2	313	CHL	1	0
22	6	302	CLA	3	0
26	4	313	CHL	3	0
36	c	517	DGD	4	0
22	p	304	CLA	1	0
22	R	310	CLA	2	0
26	P	315	CHL	1	0
23	V	310	LUT	6	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.

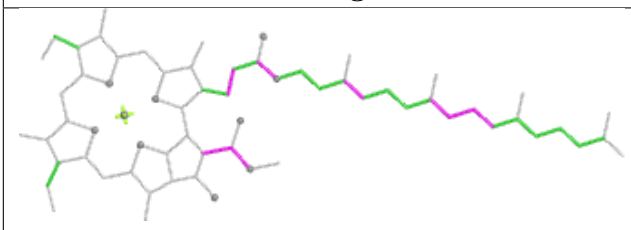
Ligand CLA b 608



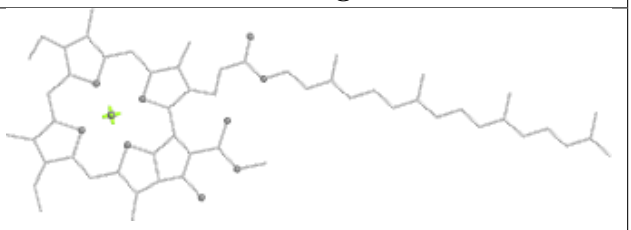
Bond lengths



Bond angles

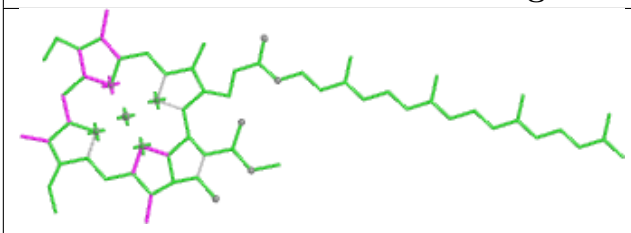


Torsions

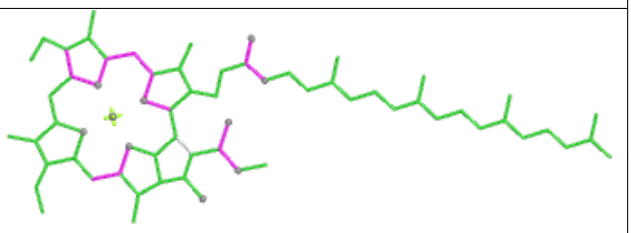


Rings

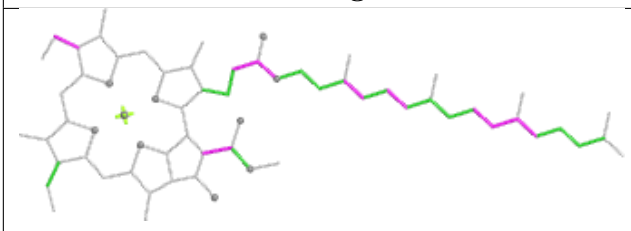
Ligand CLA v 302



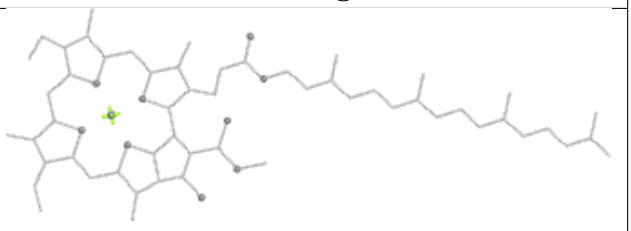
Bond lengths



Bond angles

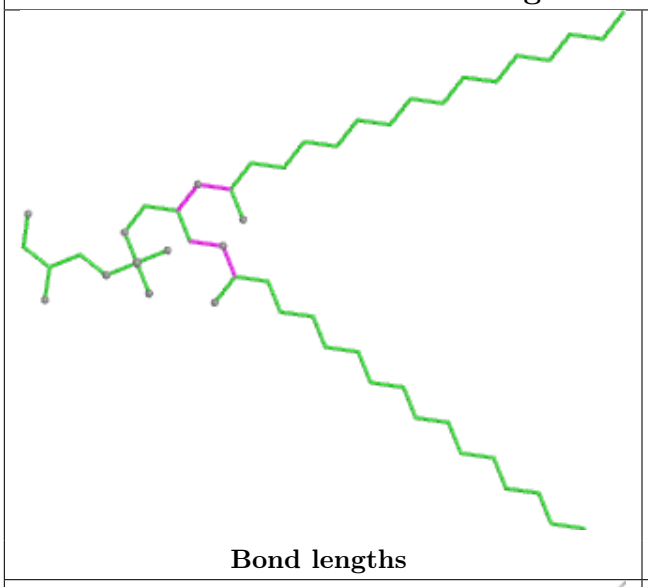


Torsions

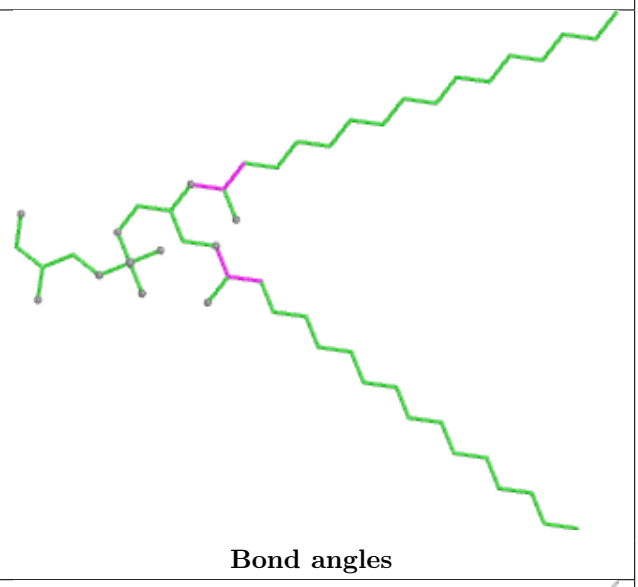


Rings

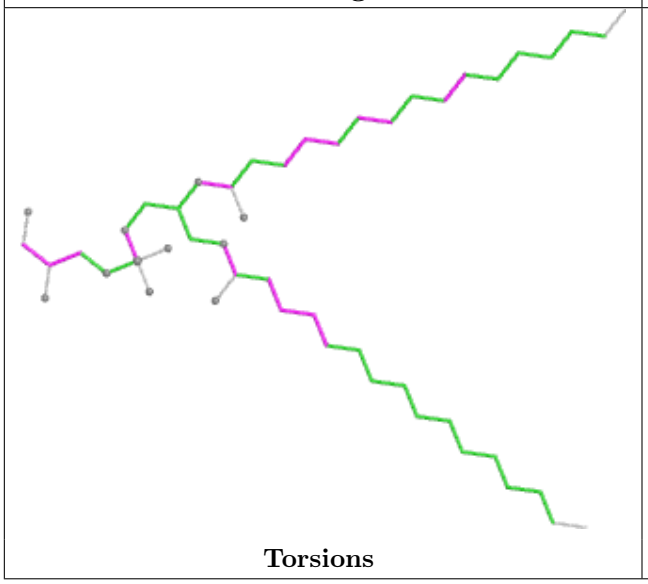
Ligand LHG C 522



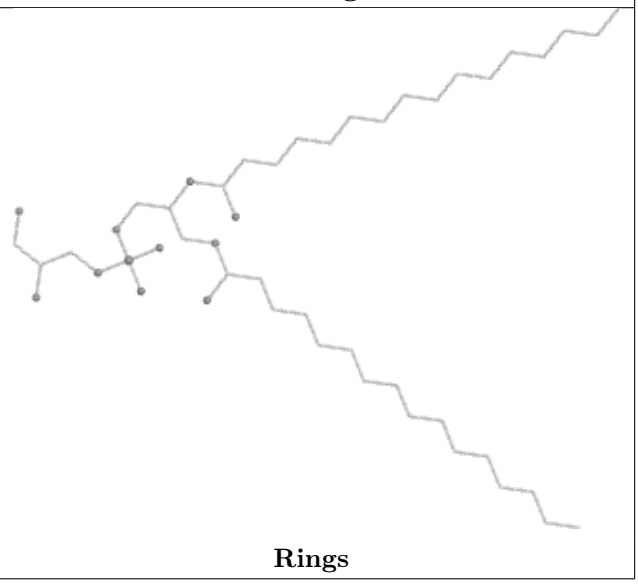
Bond lengths



Bond angles

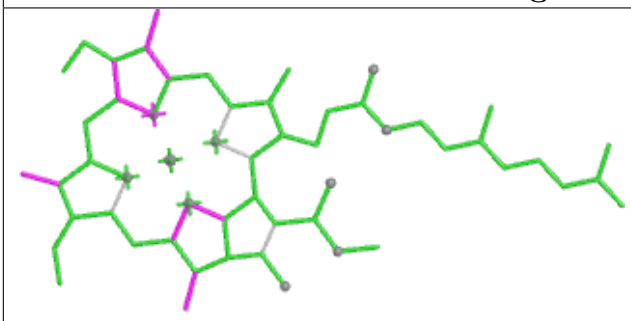


Torsions

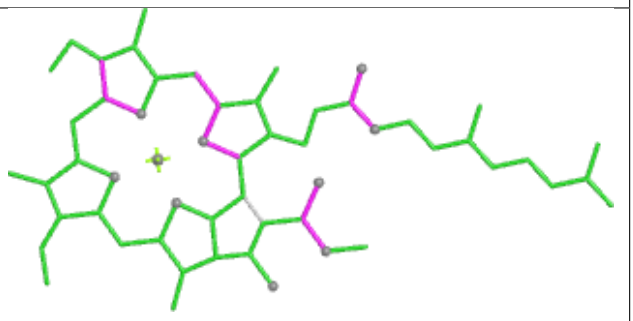


Rings

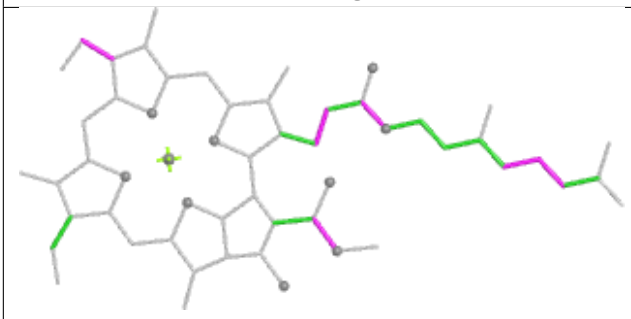
Ligand CLA s 308



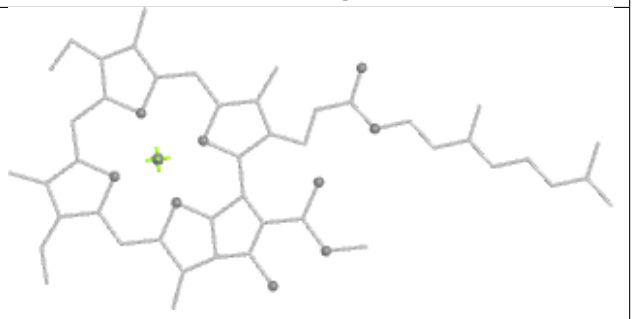
Bond lengths



Bond angles

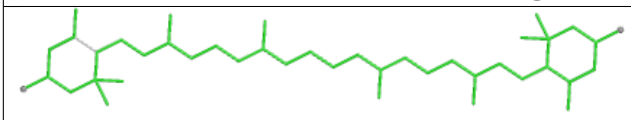


Torsions

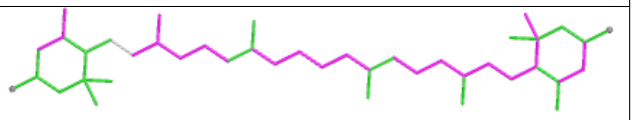


Rings

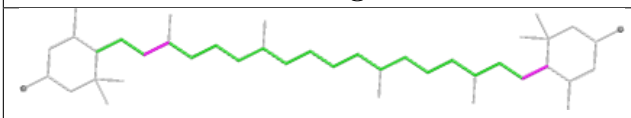
Ligand LUT 2 309



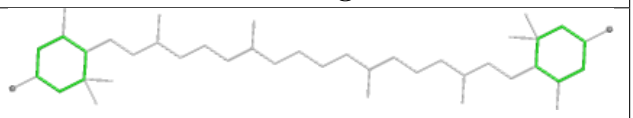
Bond lengths



Bond angles

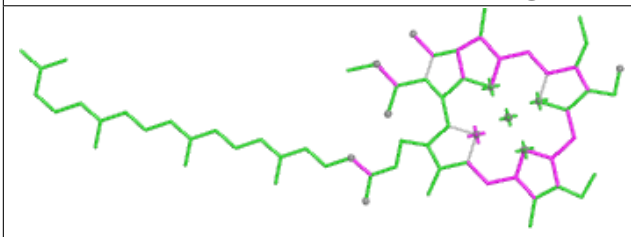


Torsions

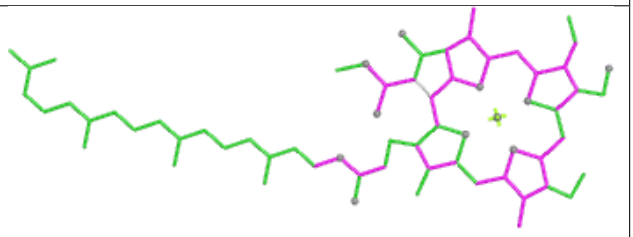


Rings

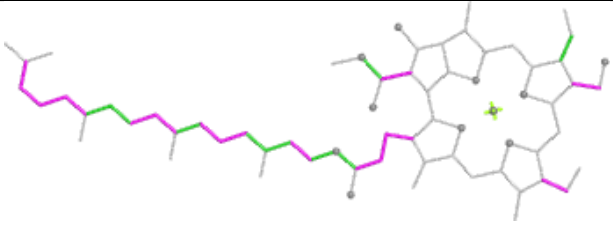
Ligand CHL U 319



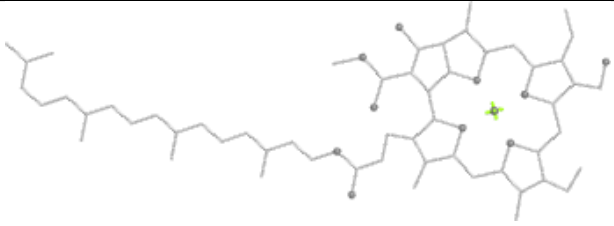
Bond lengths



Bond angles

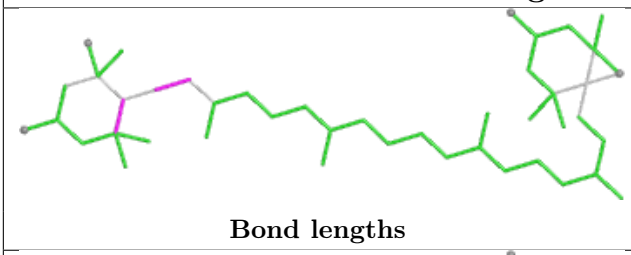


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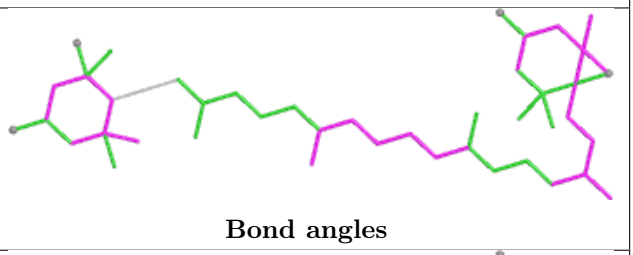


Rings

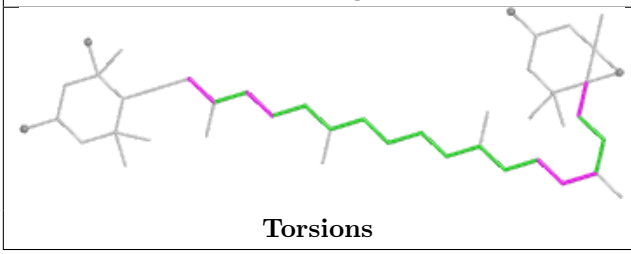
Ligand NEX r 618



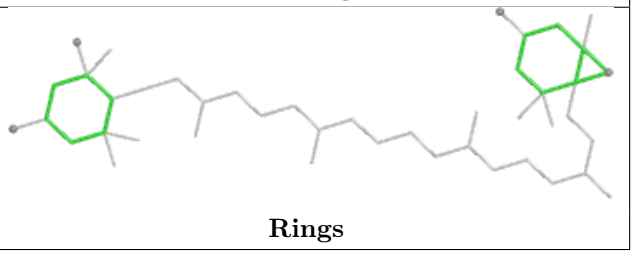
Bond lengths



Bond angles

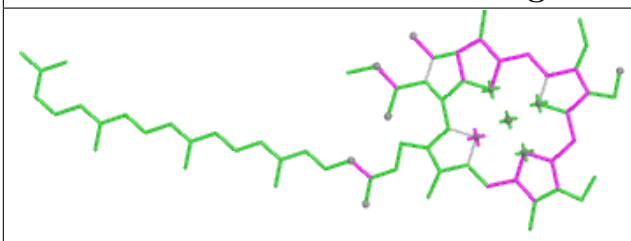


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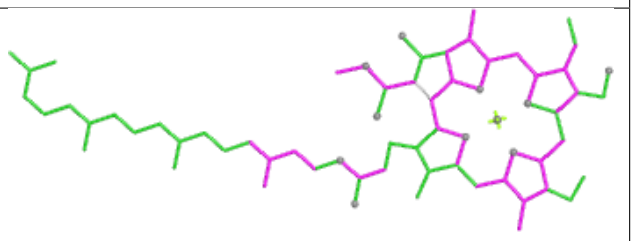


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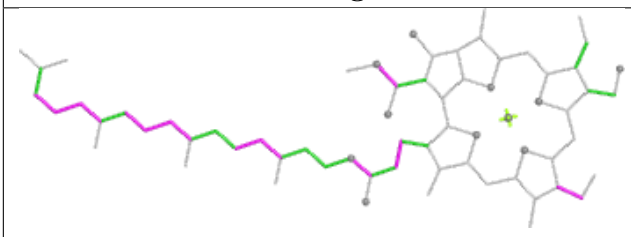
Ligand CHL 6 315



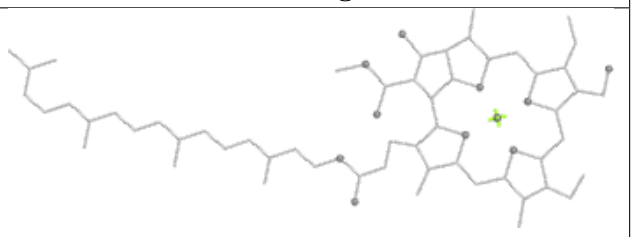
Bond lengths



Bond angles

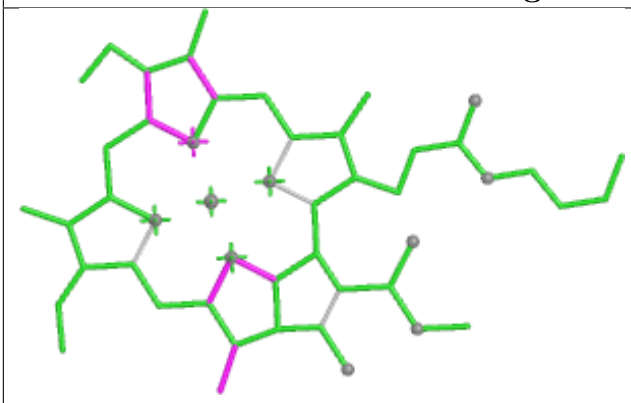


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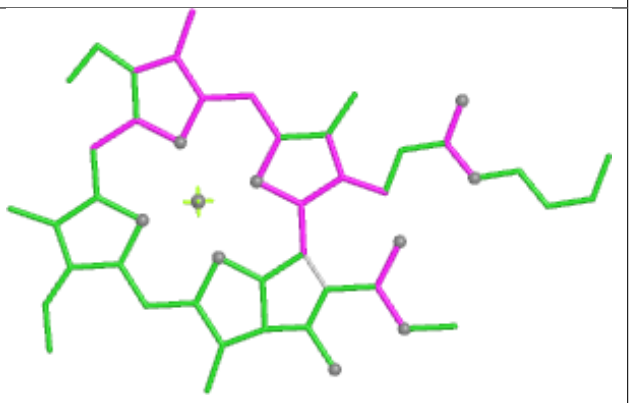


Rings

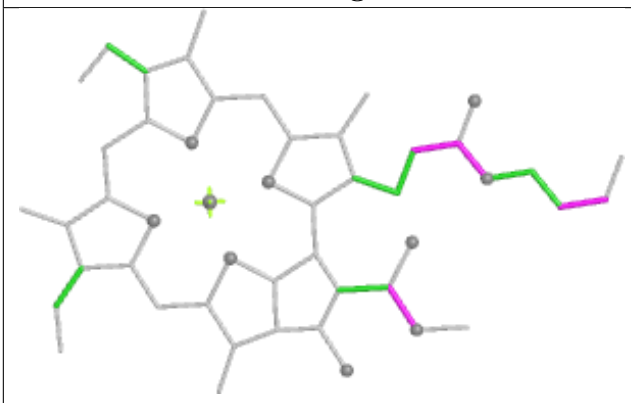
Ligand CLA R 309



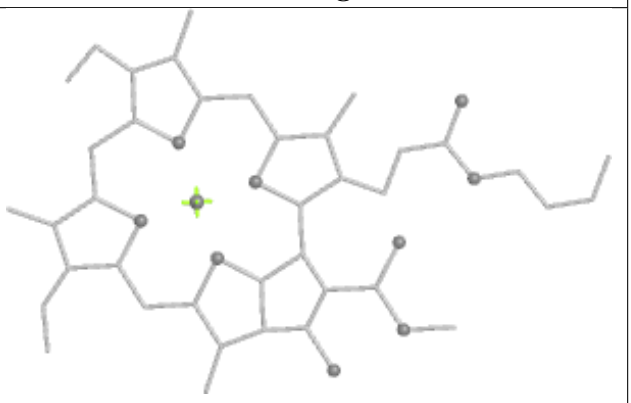
Bond lengths



Bond angles

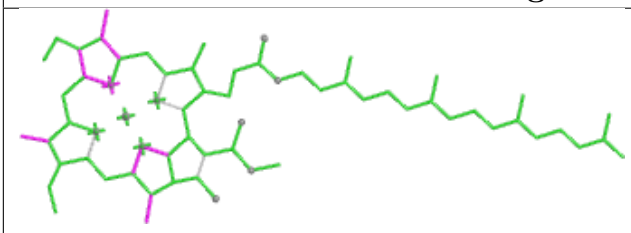


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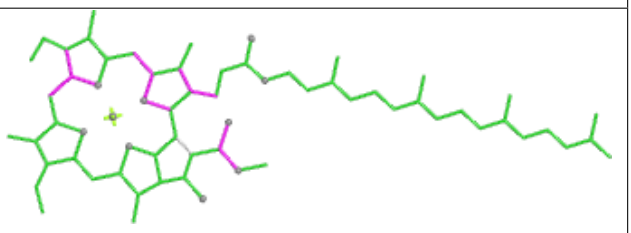


Rings

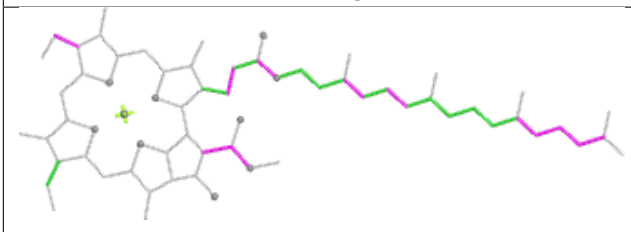
Ligand CLA b 606



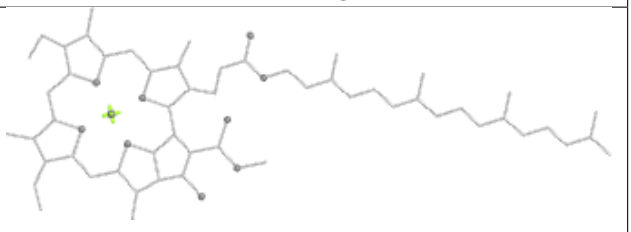
Bond lengths



Bond angles

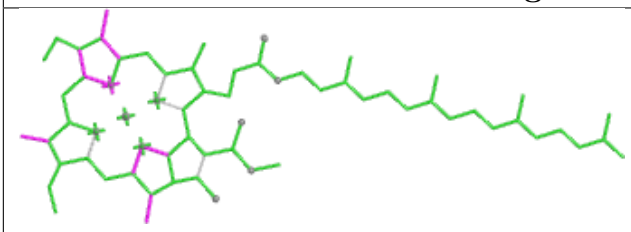


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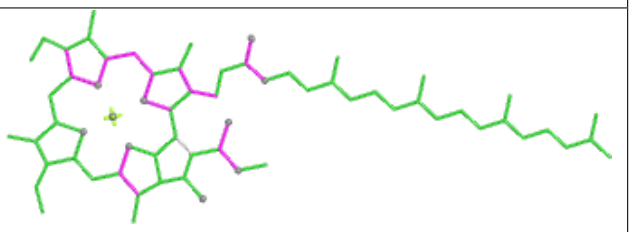


Rings

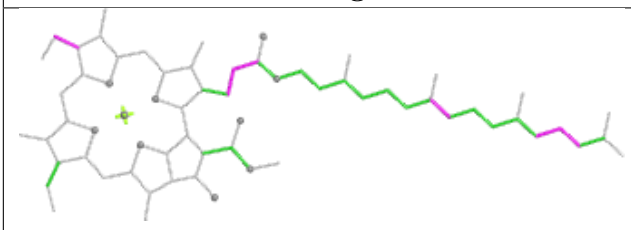
Ligand CLA C 503



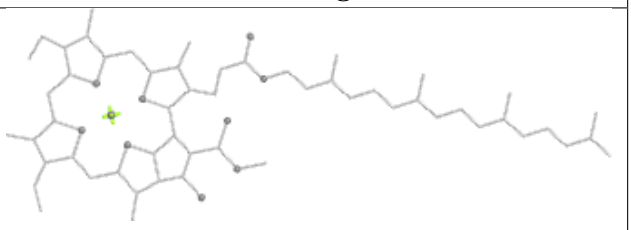
Bond lengths



Bond angles

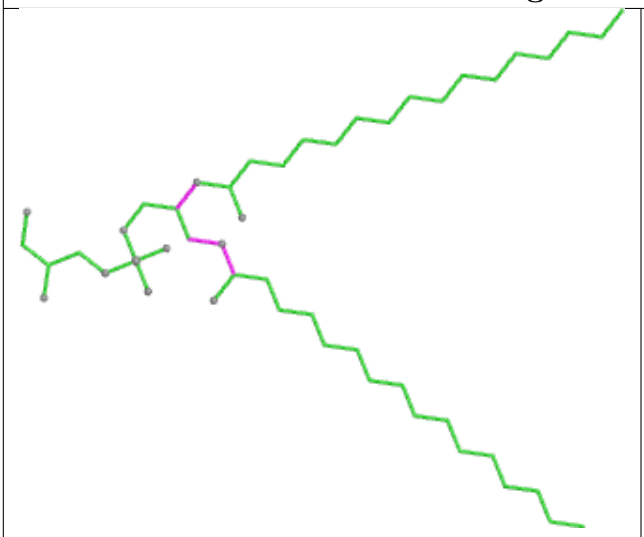


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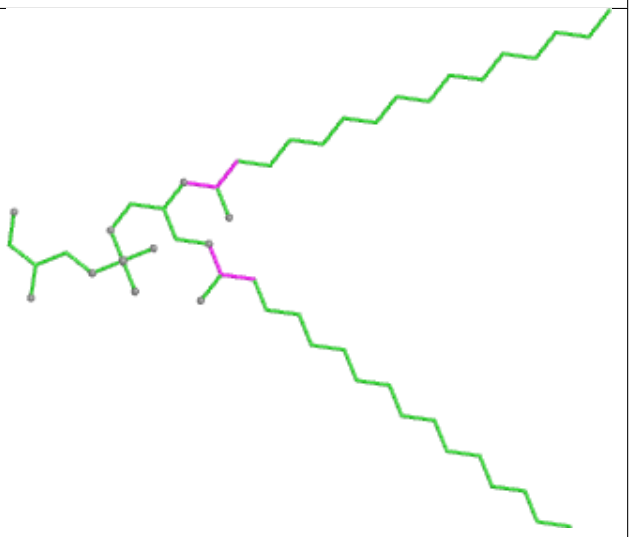


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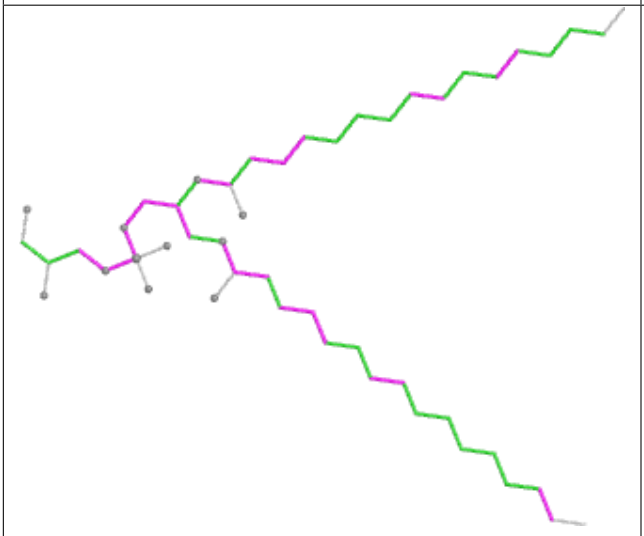
Ligand LHG 5 312



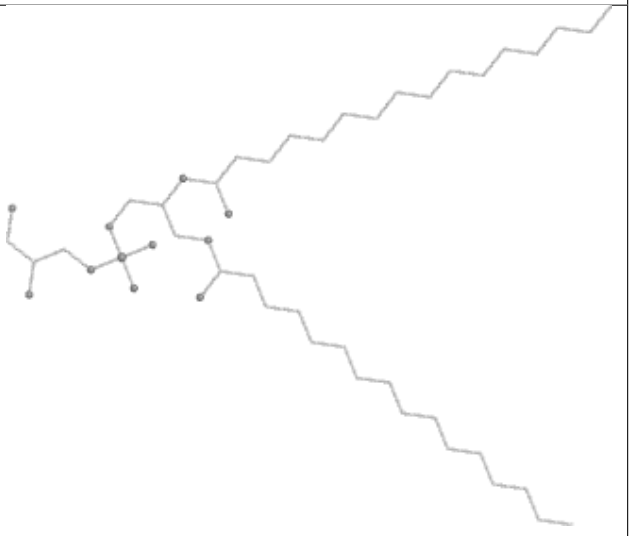
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Bond angles

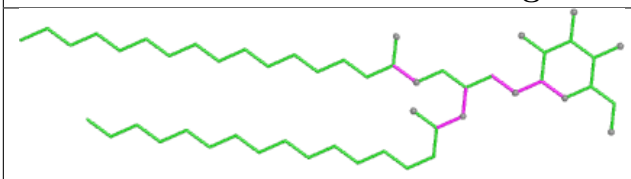


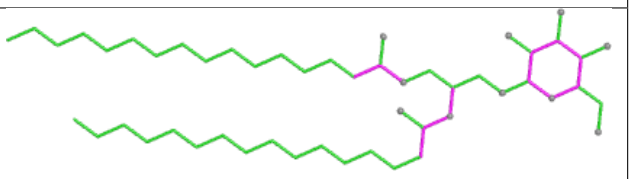
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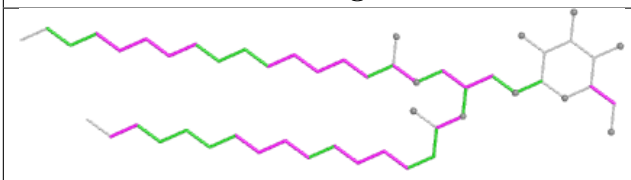


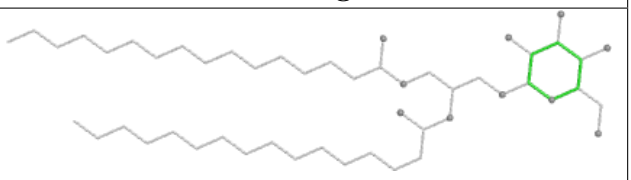
Rings

Ligand LMG b 621

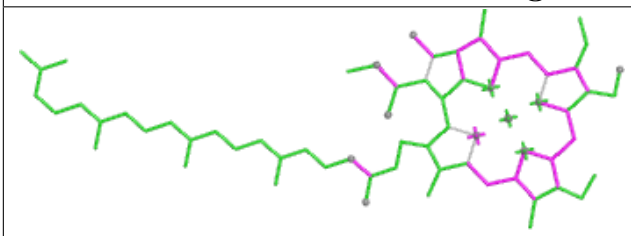

Bond lengths

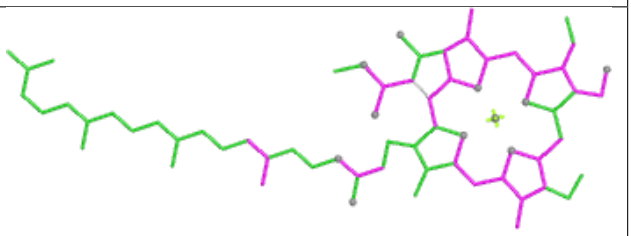

Bond angles

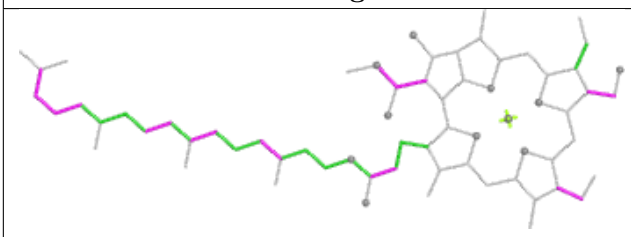

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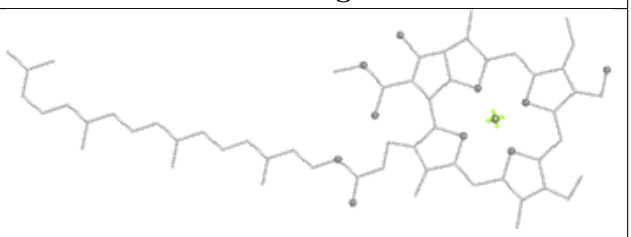

Rings

Ligand CHL n 317


Bond lengths

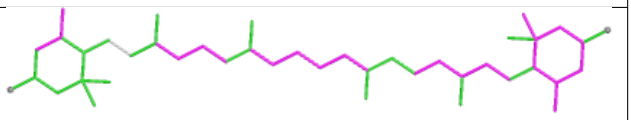

Bond angles

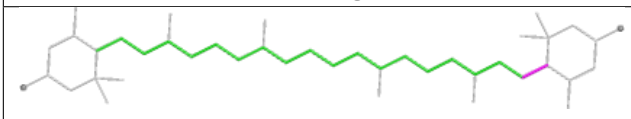

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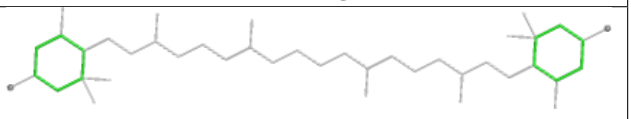

Rings

Ligand LUT V 309

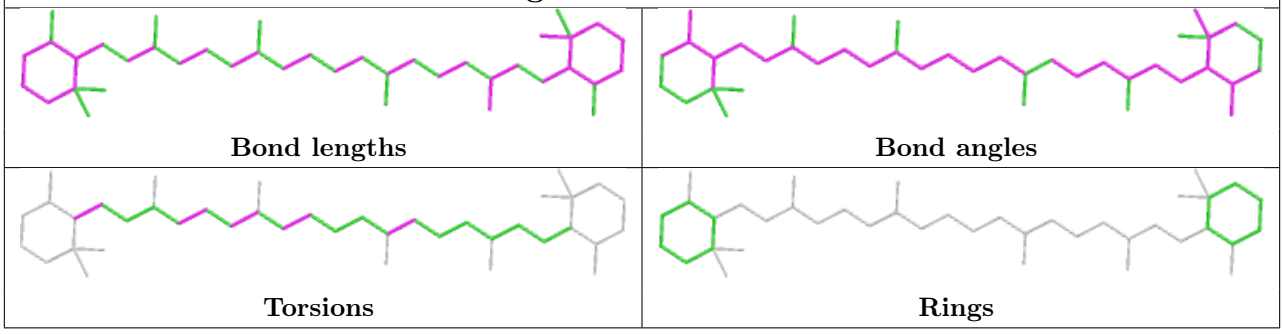

Bond lengths


Bond angles

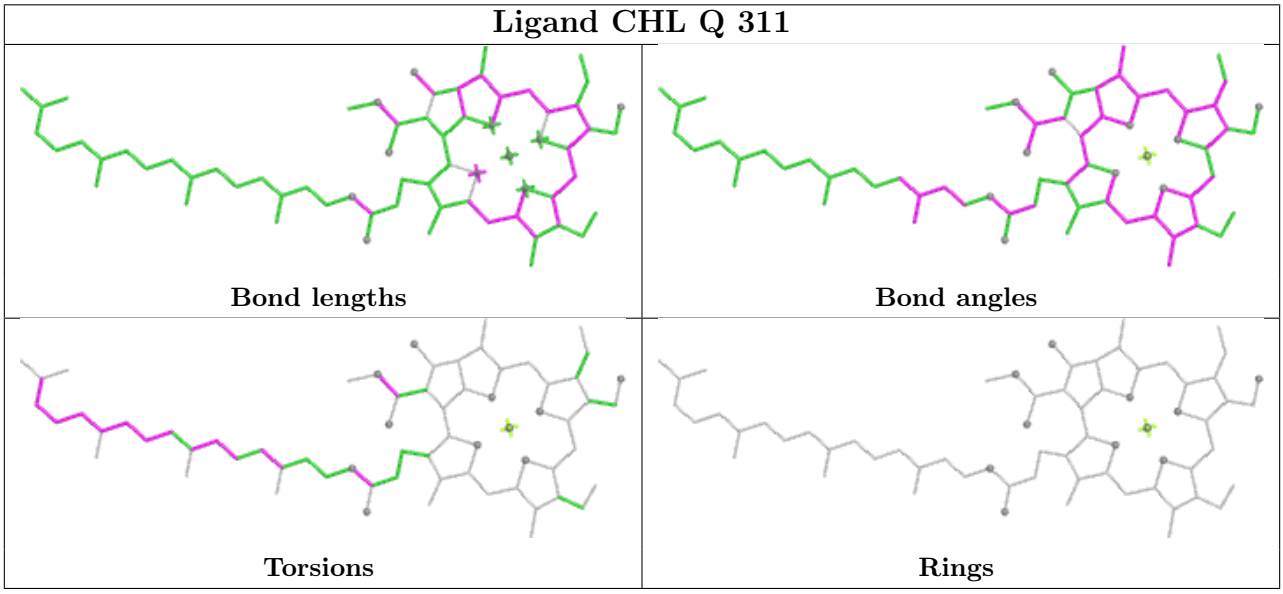

Torsions


Rings

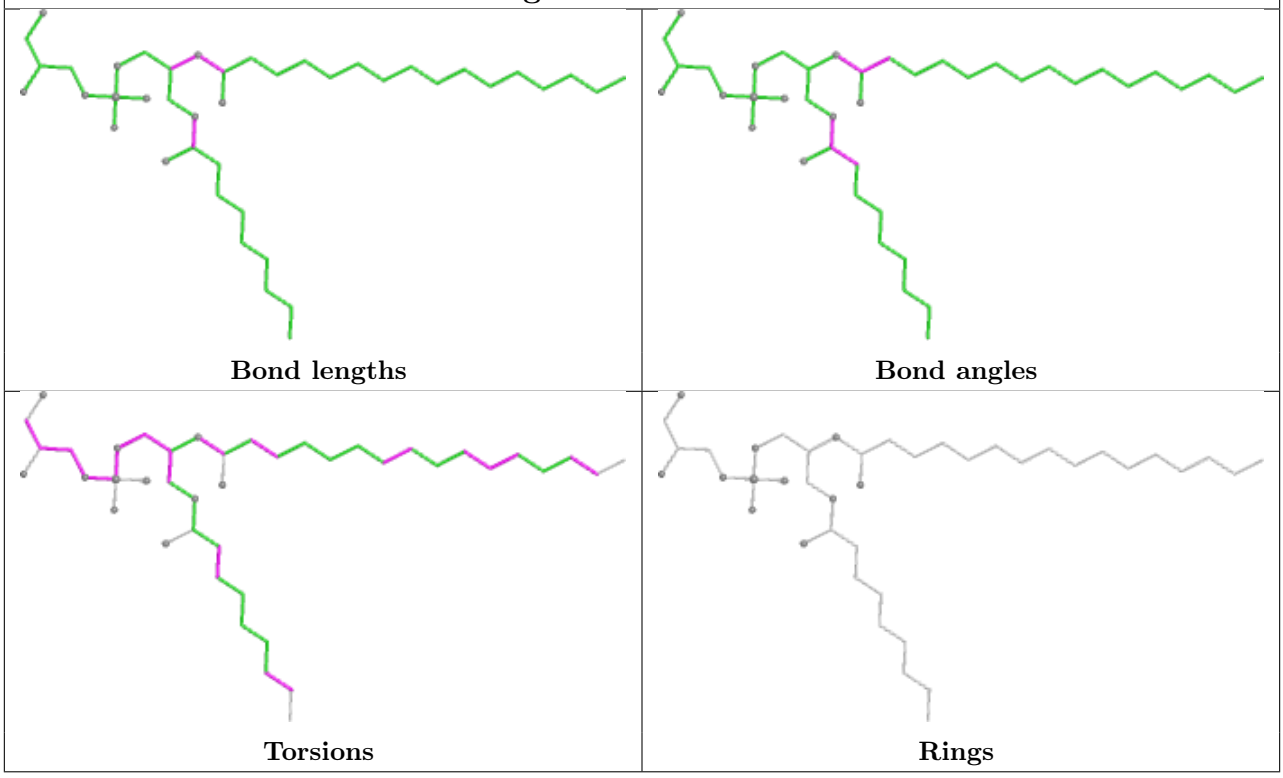
Ligand BCR b 618



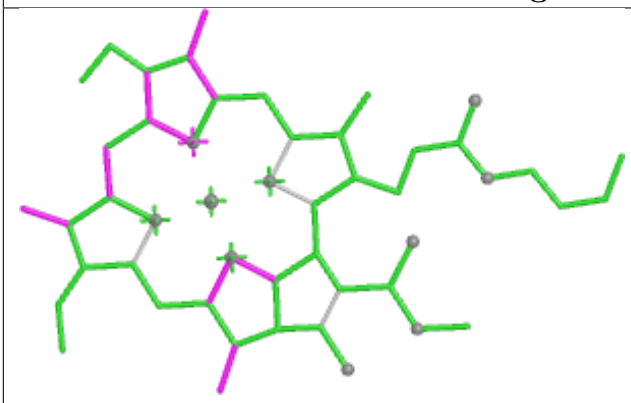
Ligand CHL Q 311



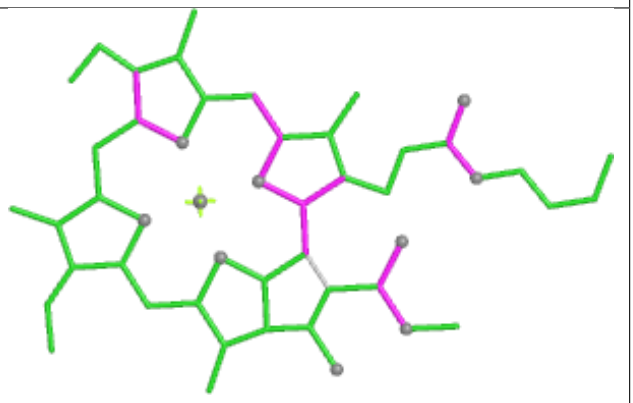
Ligand LHG R 314



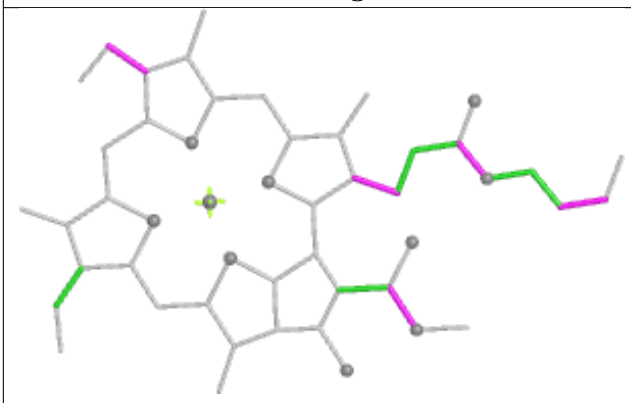
Ligand CLA r 601



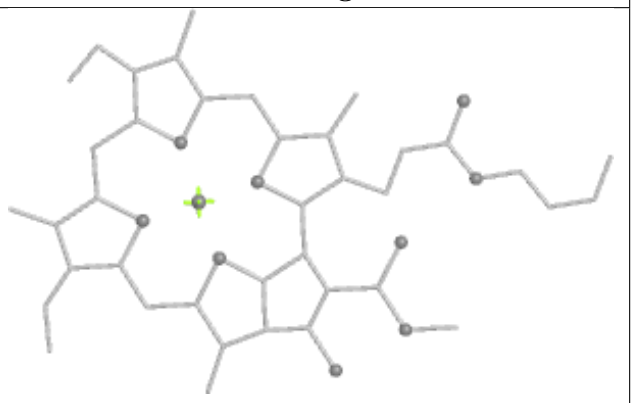
Bond lengths



Bond angles

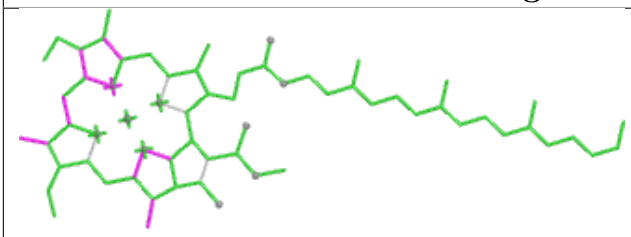


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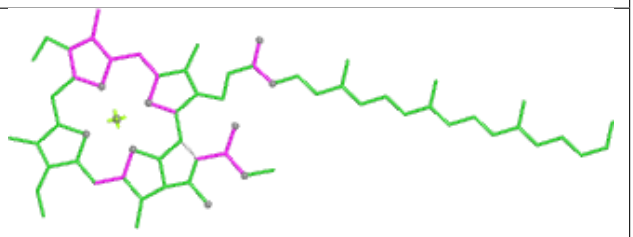


Rings

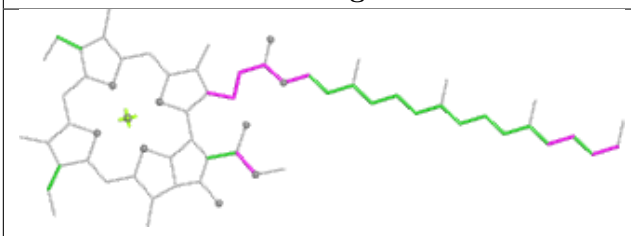
Ligand CLA G 304



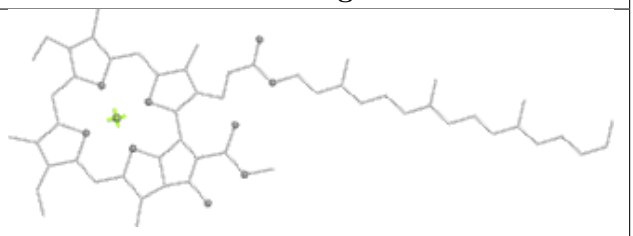
Bond lengths



Bond angles

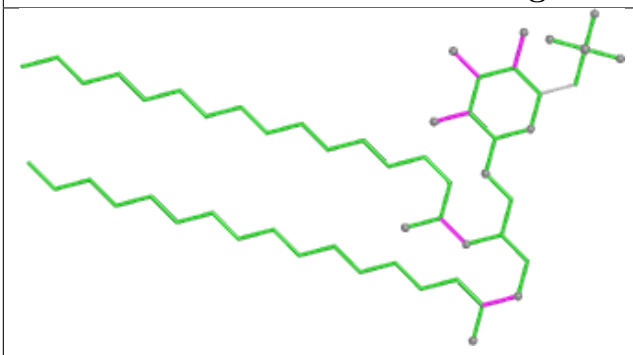


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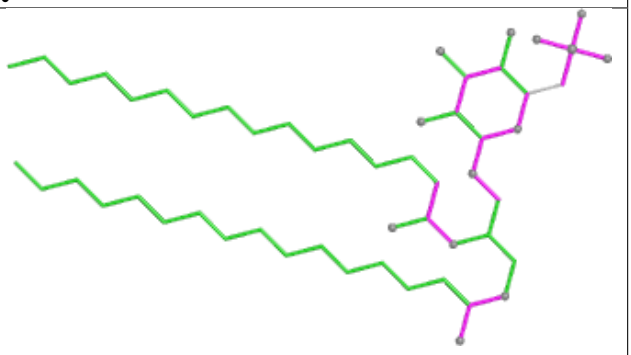


Rings

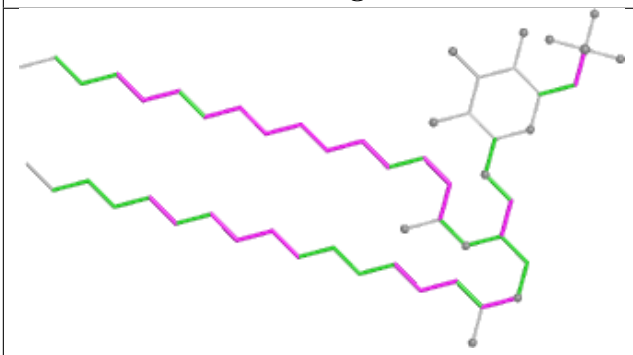
Ligand SQD a 413



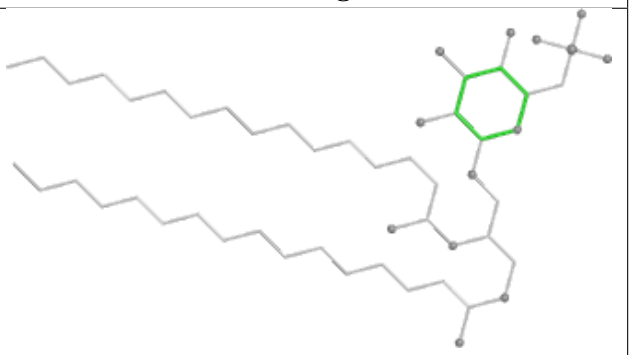
Bond lengths



Bond angles

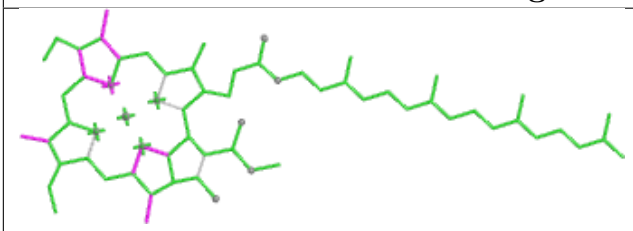


Torsions

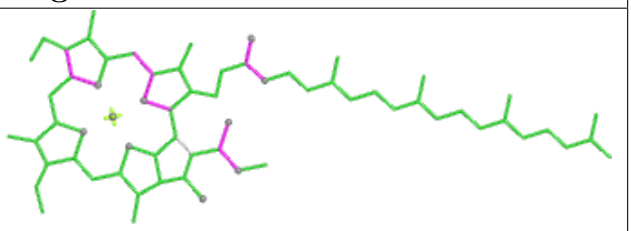


Rings

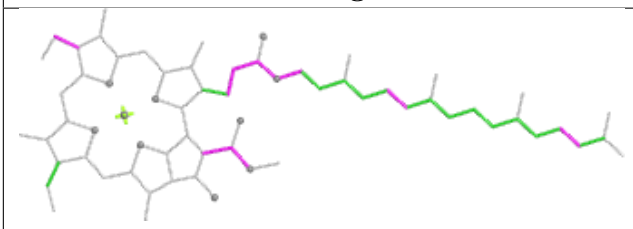
Ligand CLA g 302



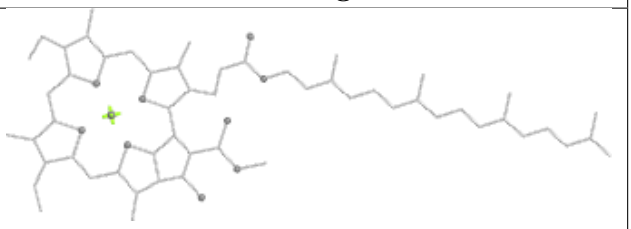
Bond lengths



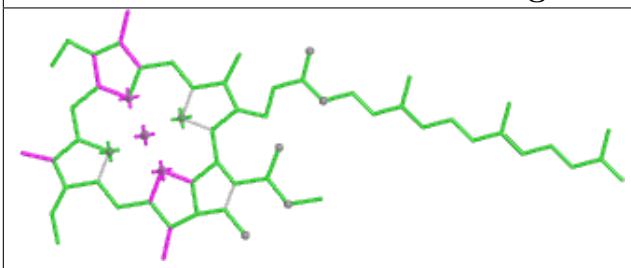
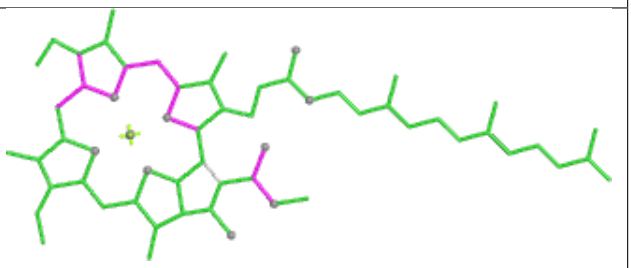
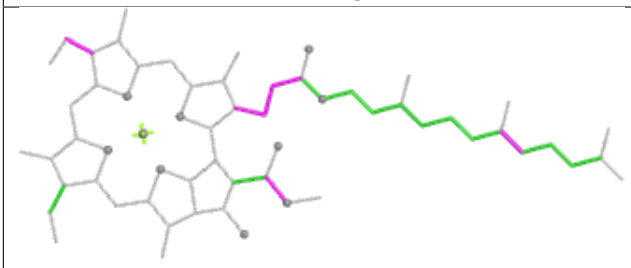
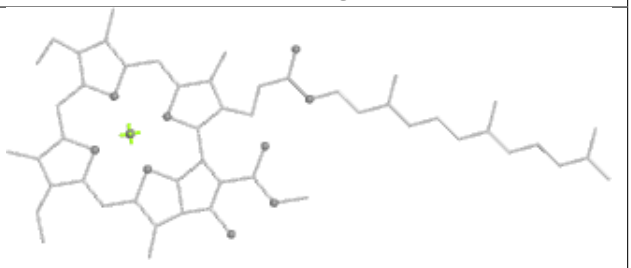
Bond angles

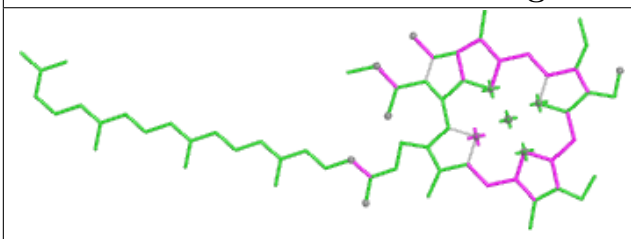
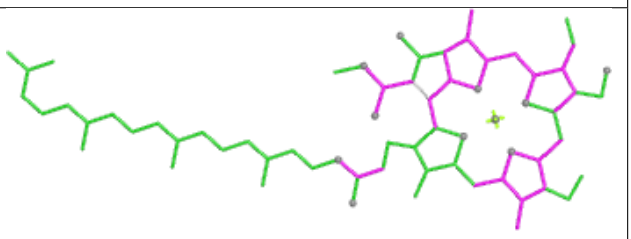
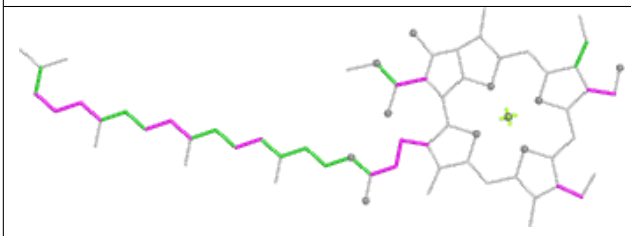
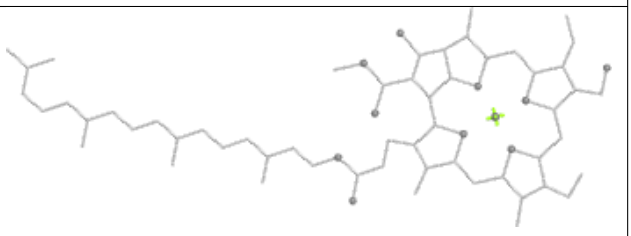


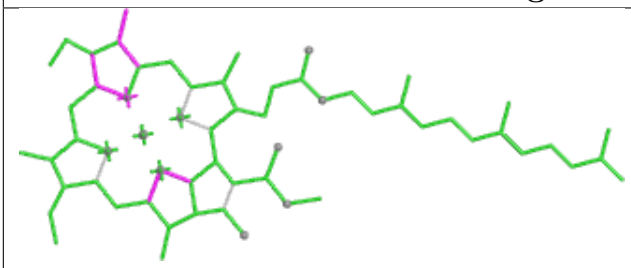
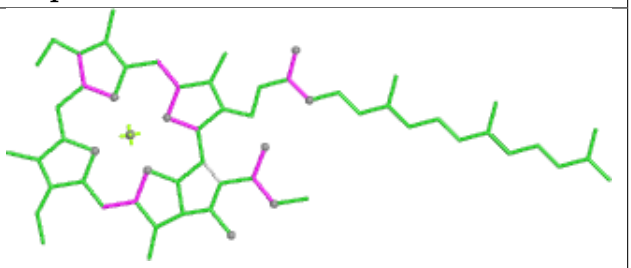
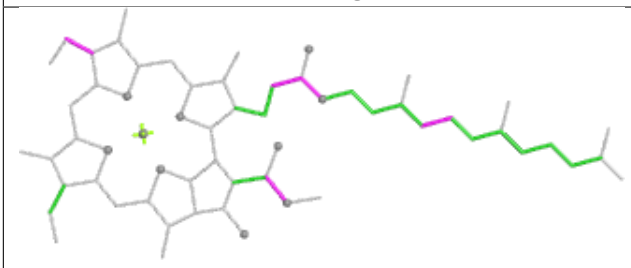
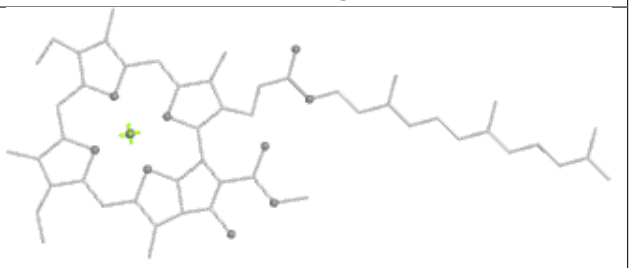
Torsions

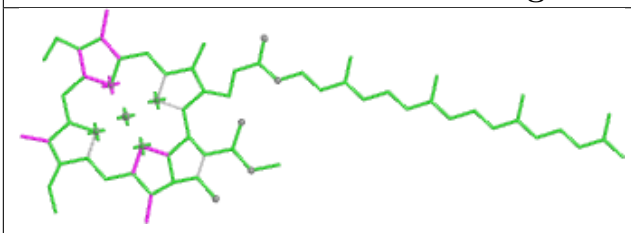
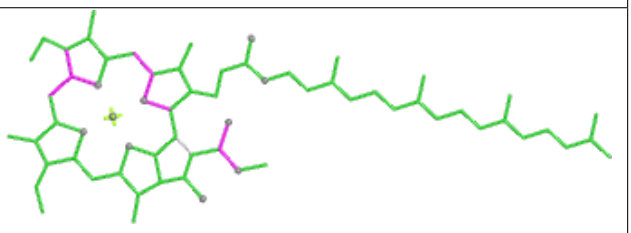
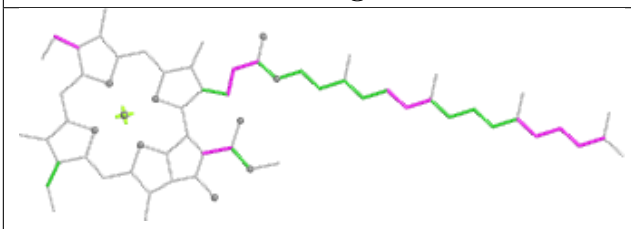
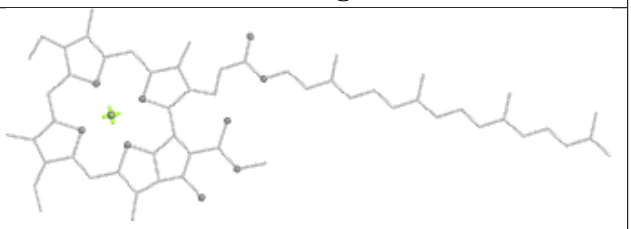


Rings

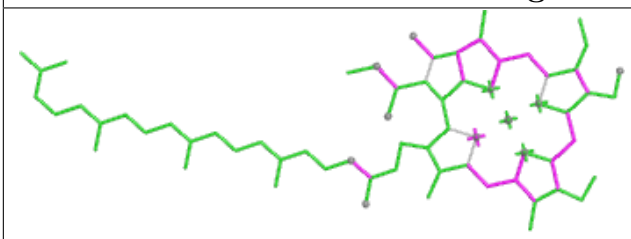
Ligand CLA 1 304	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

Ligand CHL 2 316	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

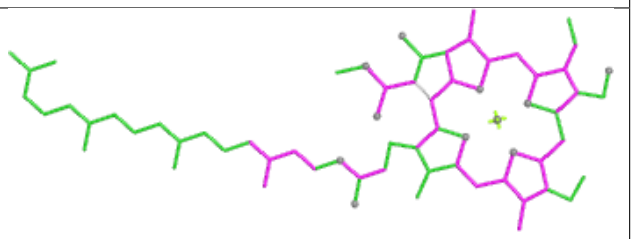
Ligand CLA p 307	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA b 603	
	
Bond lengths	Bond angles
	
Torsions	Rings

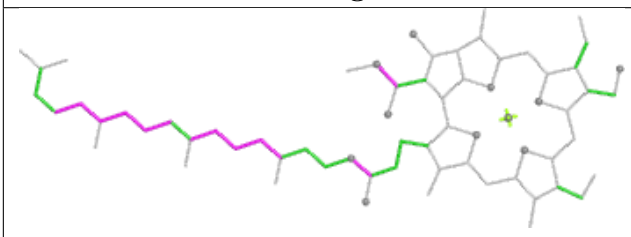
Ligand CHL 3 311



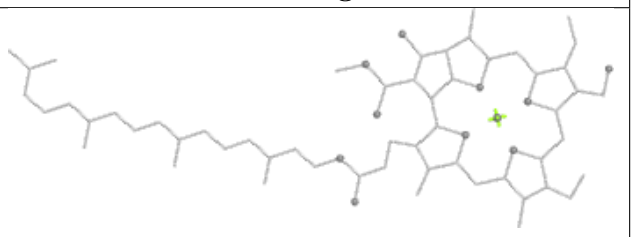
Bond lengths



Bond angles

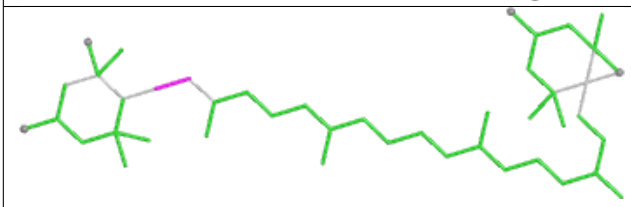


Torsions

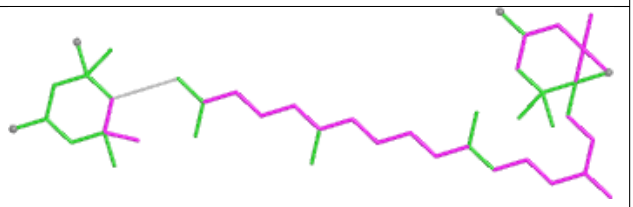


Rings

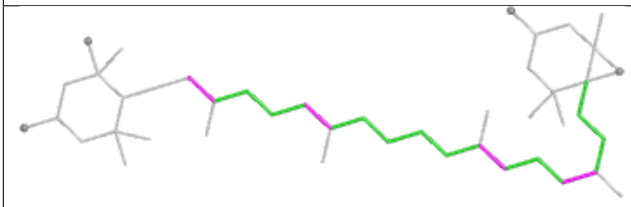
Ligand NEX 2 319



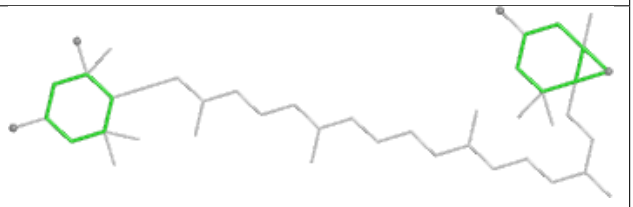
Bond lengths



Bond angles

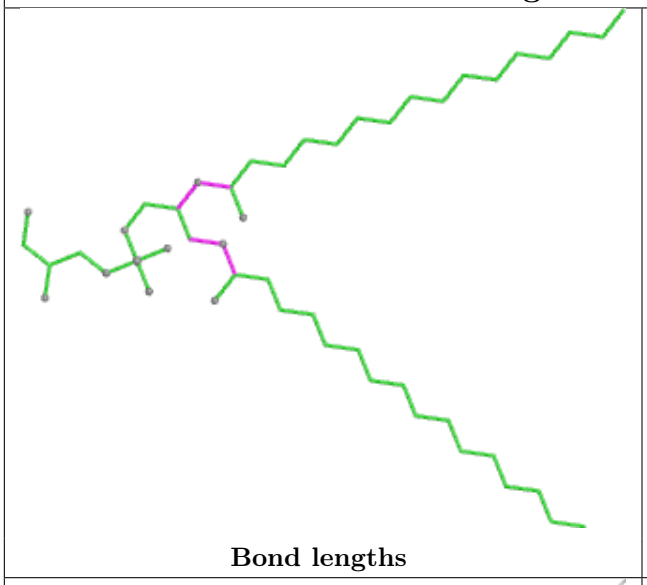


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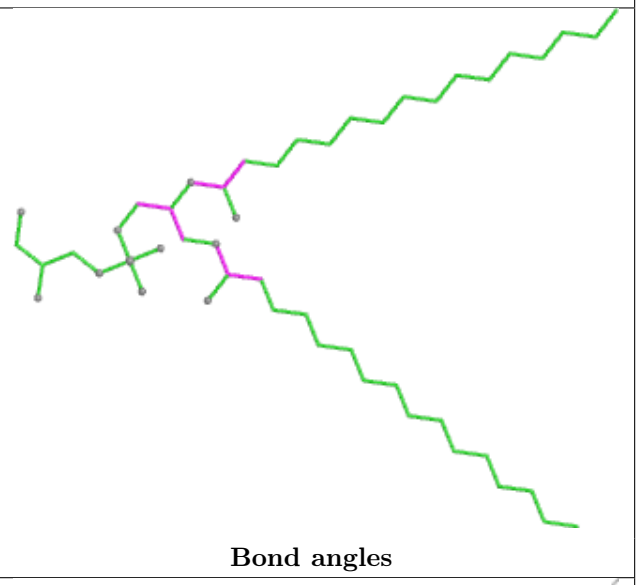


Rings

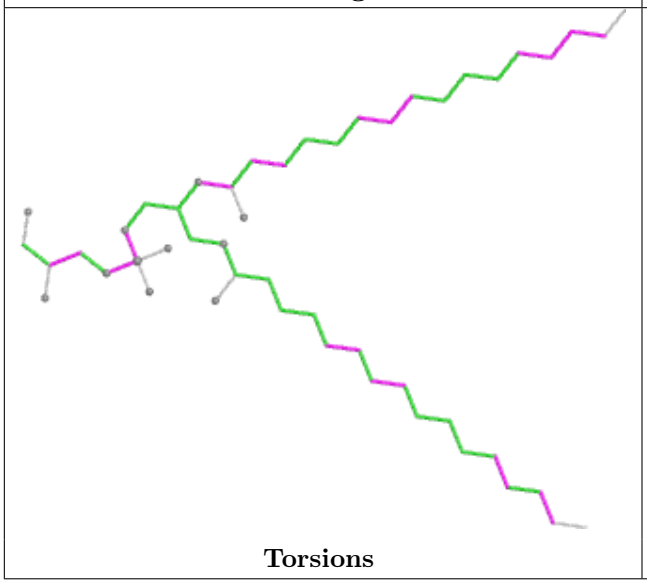
Ligand LHG D 407



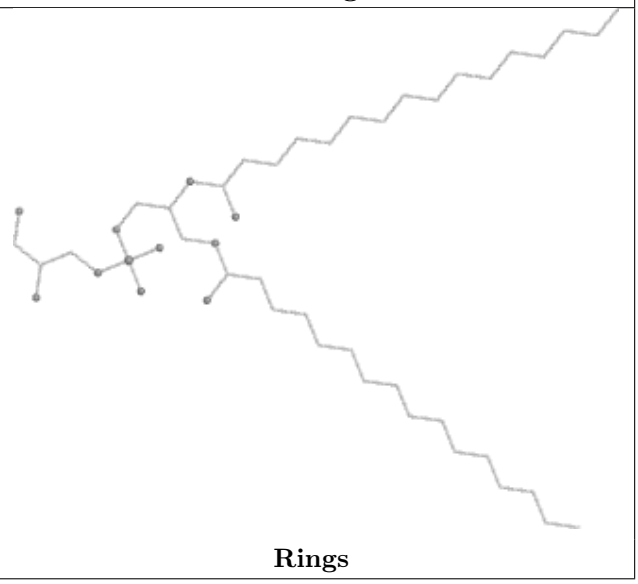
Bond lengths



Bond angles

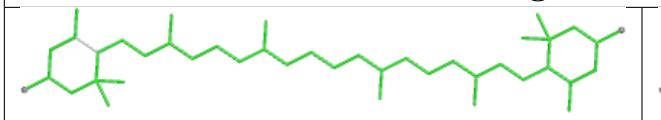


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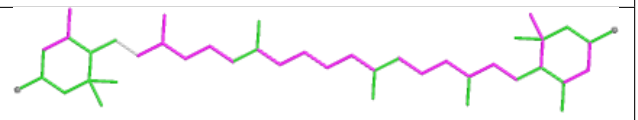


Rings

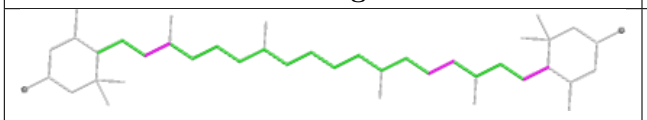
Ligand LUT 5 309



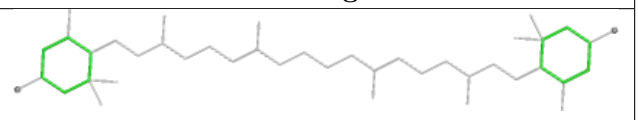
Bond lengths



Bond angles

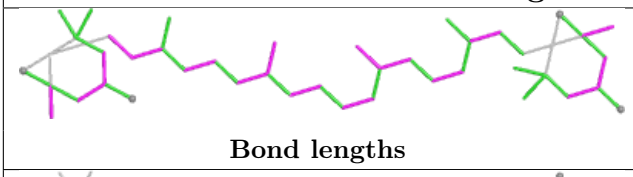


Torsions

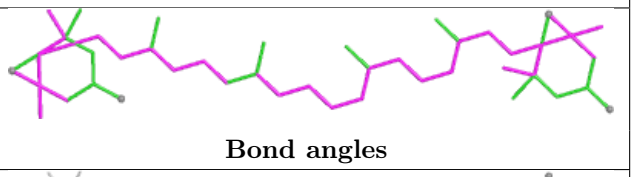


Rings

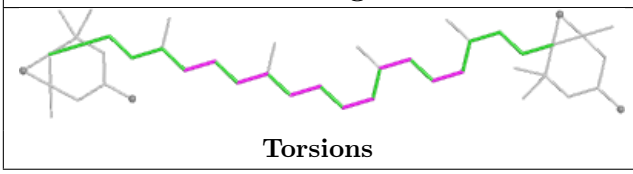
Ligand XAT 4 311



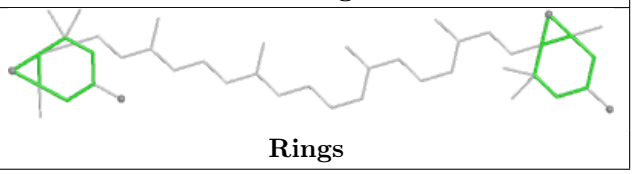
Bond lengths



Bond angles

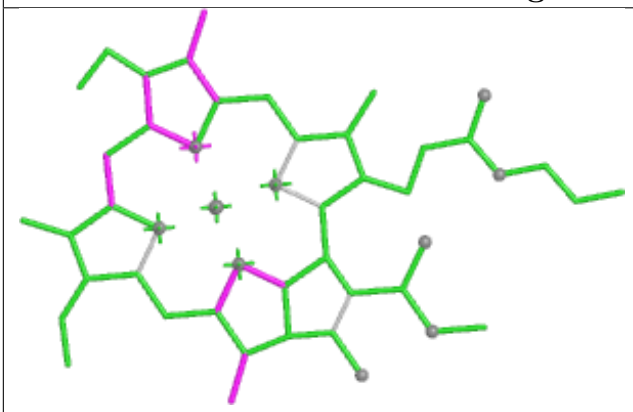


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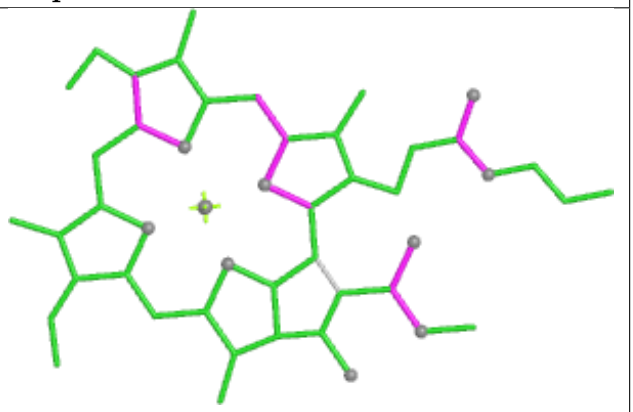


Rings

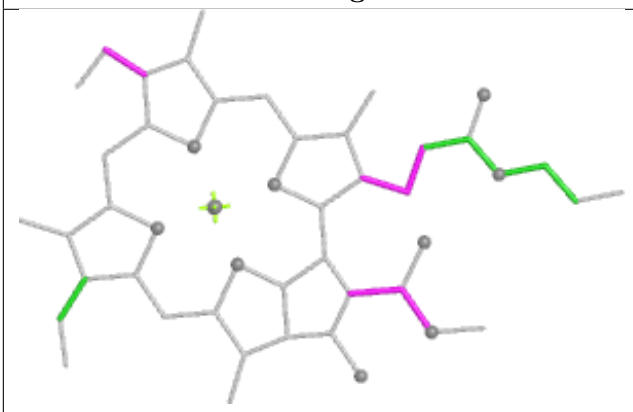
Ligand CLA p 309



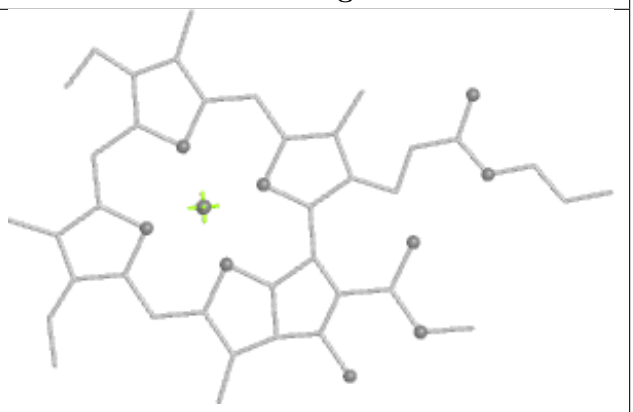
Bond lengths



Bond angles

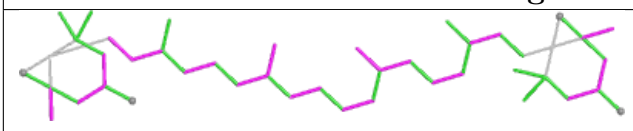


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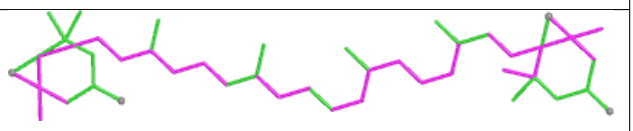


Rings

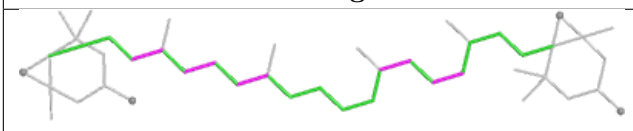
Ligand XAT 1 311



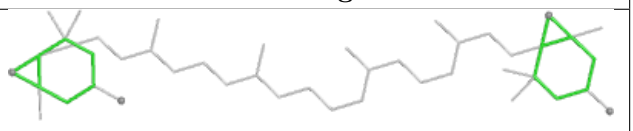
Bond lengths



Bond angles

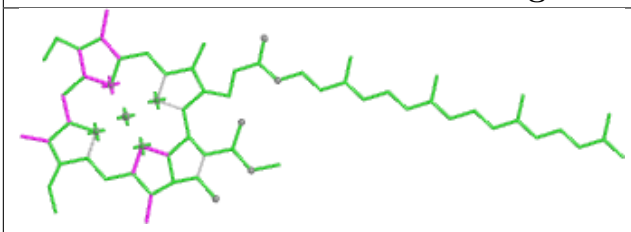


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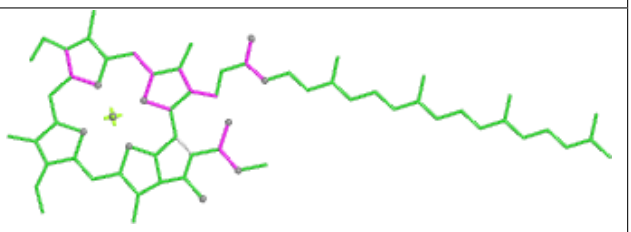


Rings

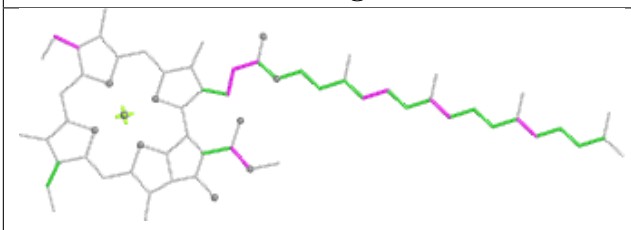
Ligand CLA 3 307



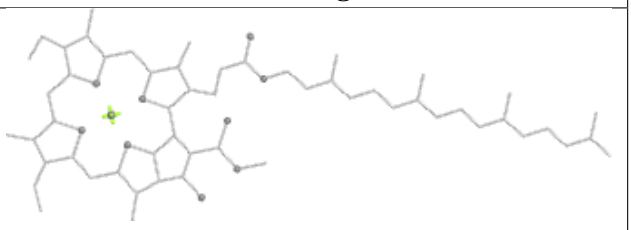
Bond lengths



Bond angles

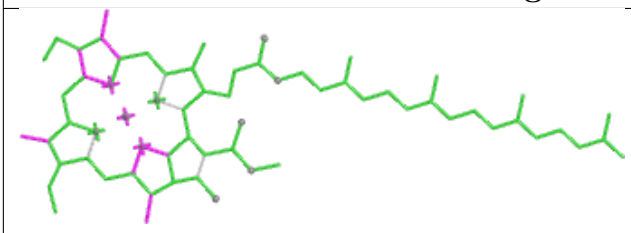


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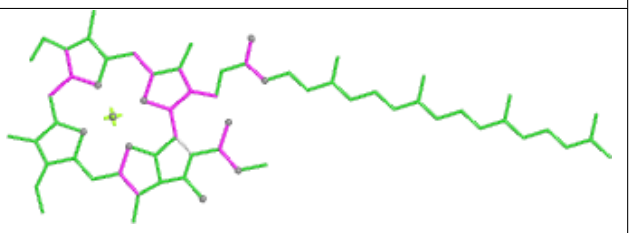


Rings

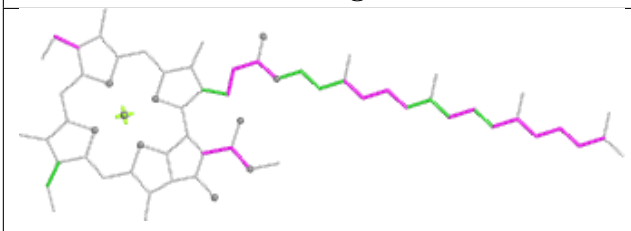
Ligand CLA B 602



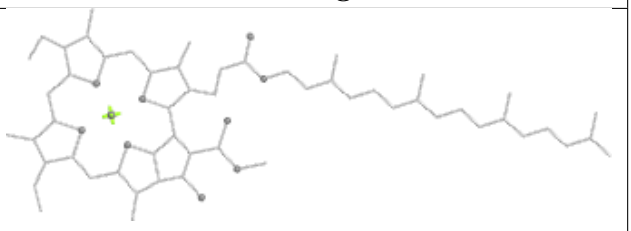
Bond lengths



Bond angles

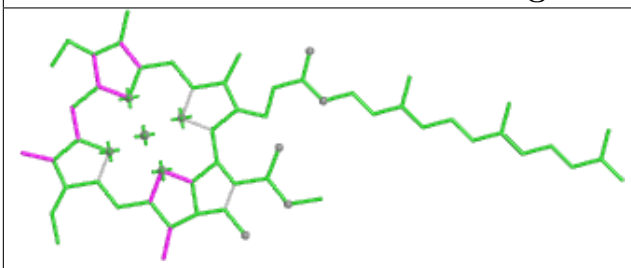


Torsions

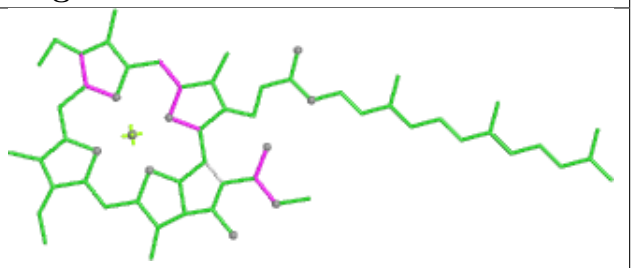


Rings

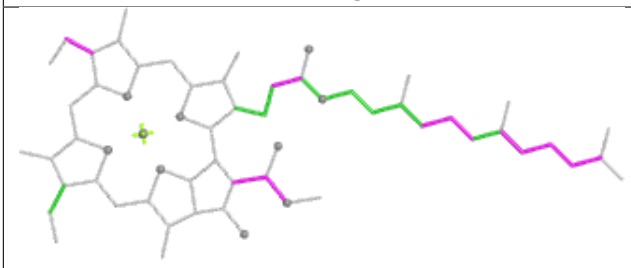
Ligand CLA g 306



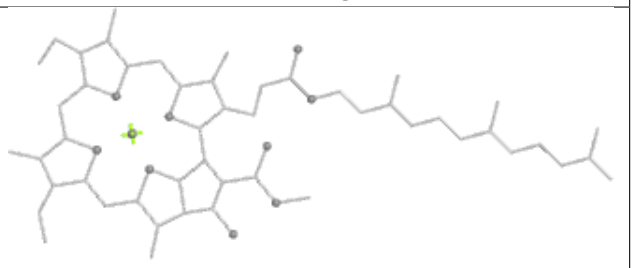
Bond lengths



Bond angles

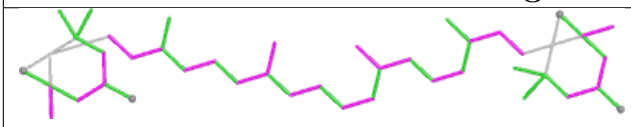


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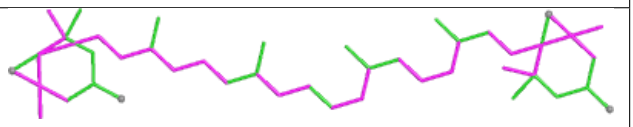


Rings

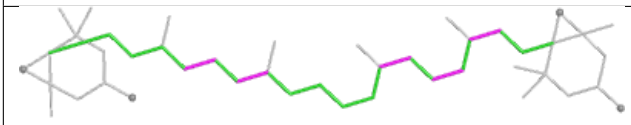
Ligand XAT P 312



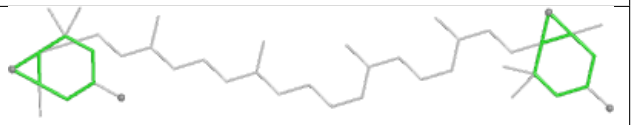
Bond lengths



Bond angles

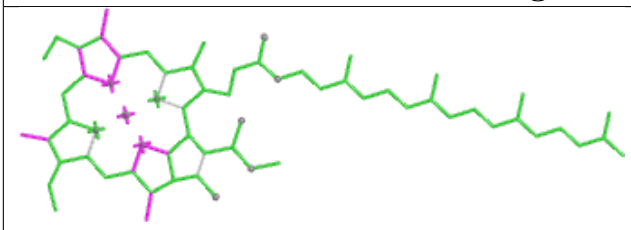


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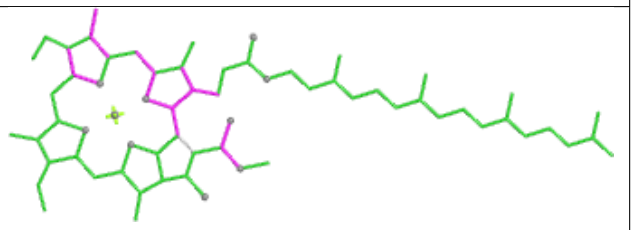


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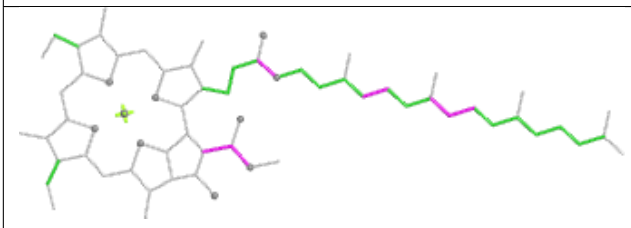
Ligand CLA c 512



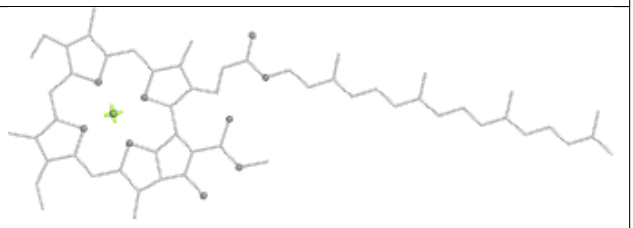
Bond lengths



Bond angles

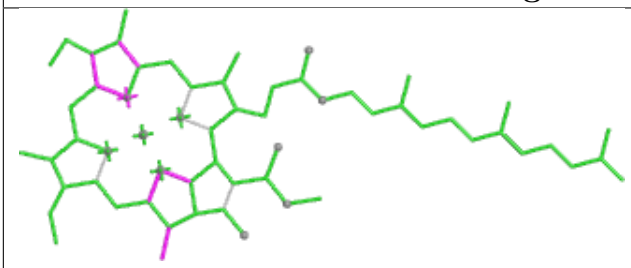


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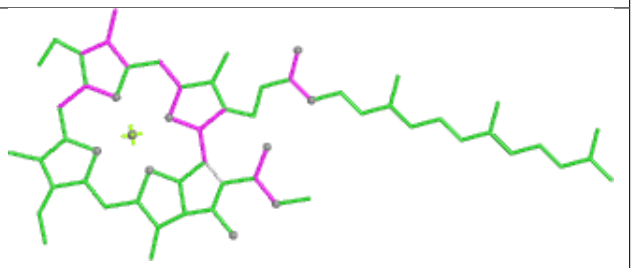


Rings

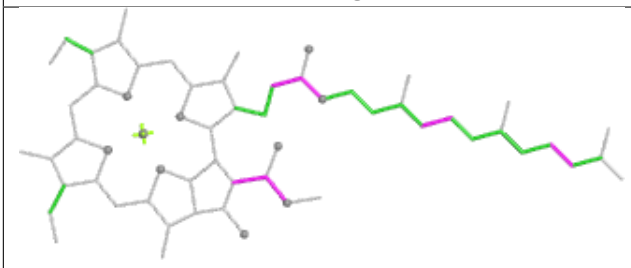
Ligand CLA N 306



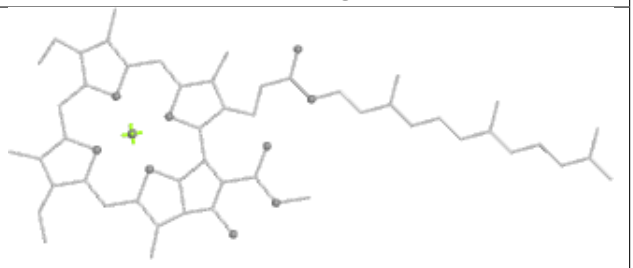
Bond lengths



Bond angles

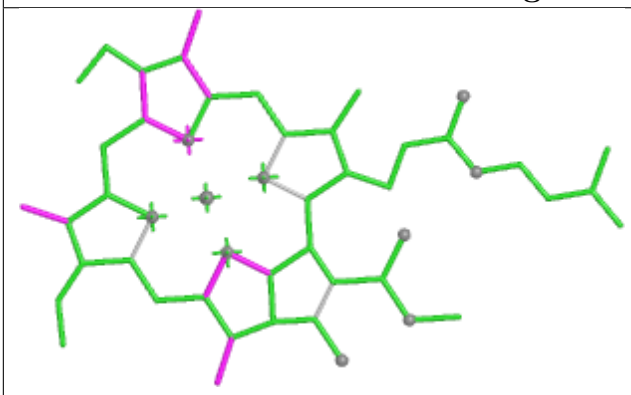


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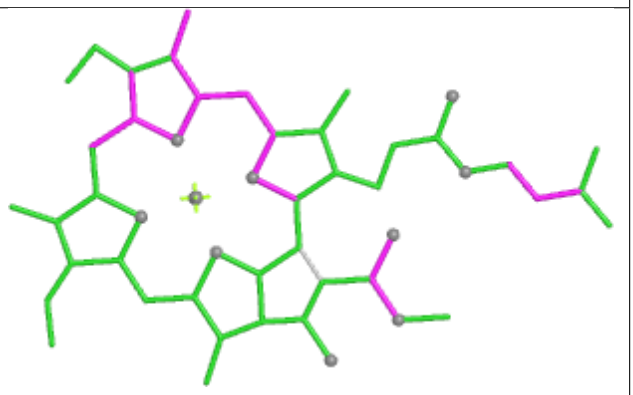


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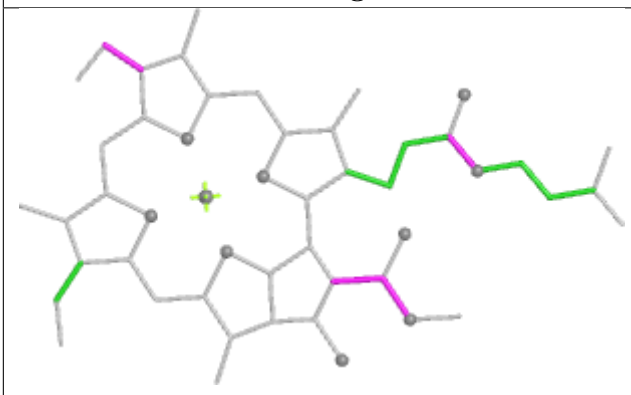
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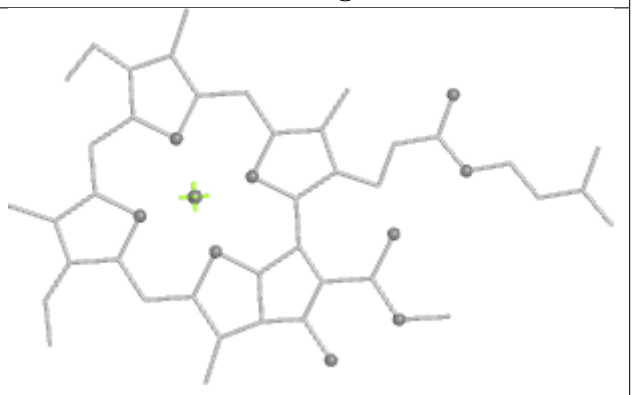
Bond lengths



Bond angles

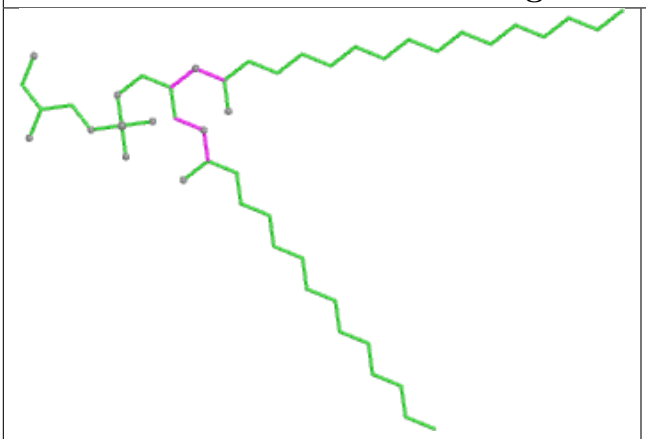


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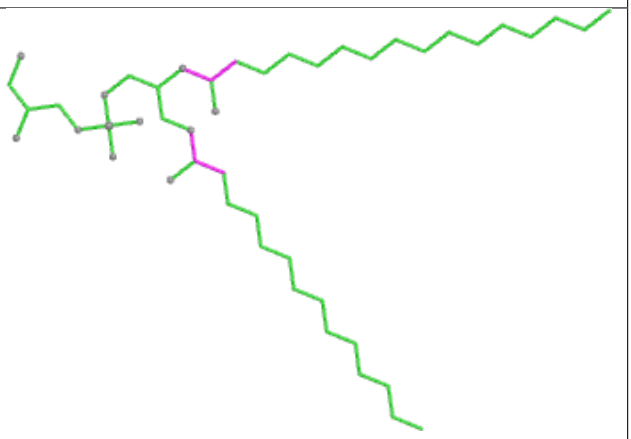


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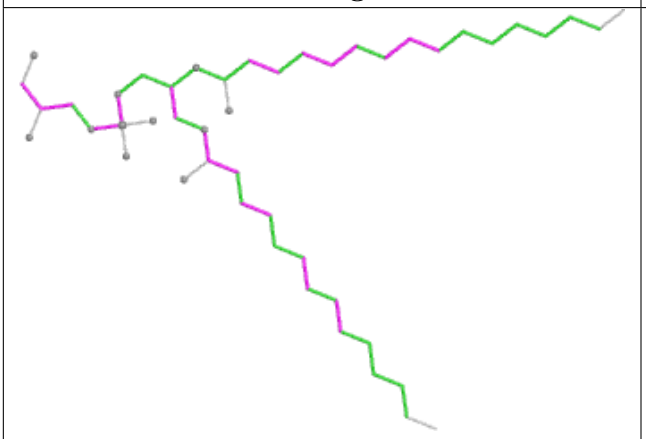
Ligand LHG b 622



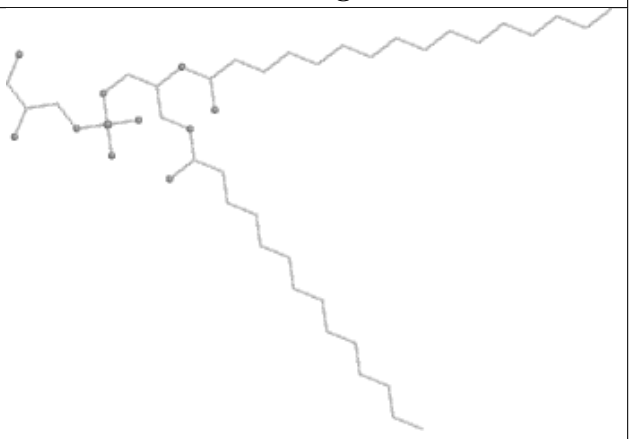
Bond lengths



Bond angles

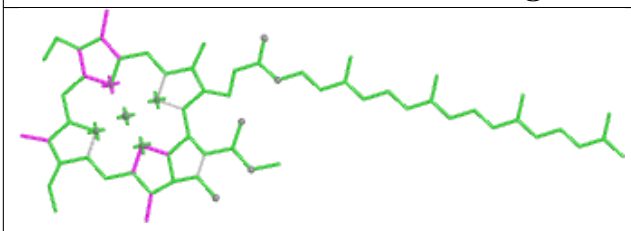


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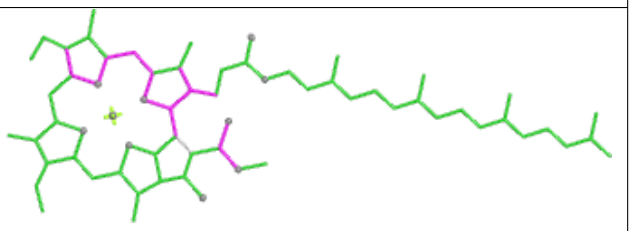


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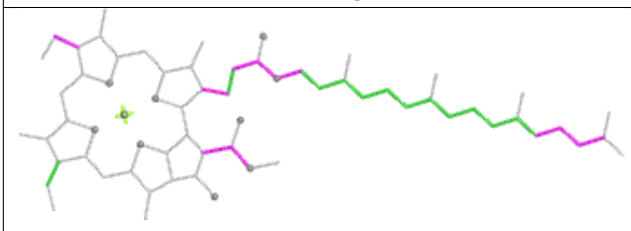
Ligand CLA B 611



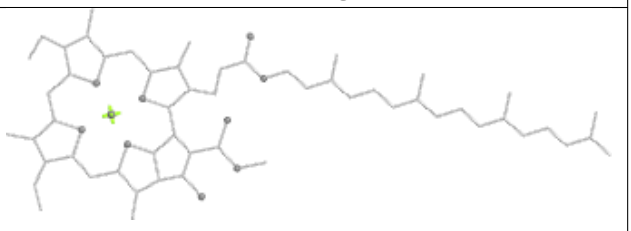
Bond lengths



Bond angles



Torsions

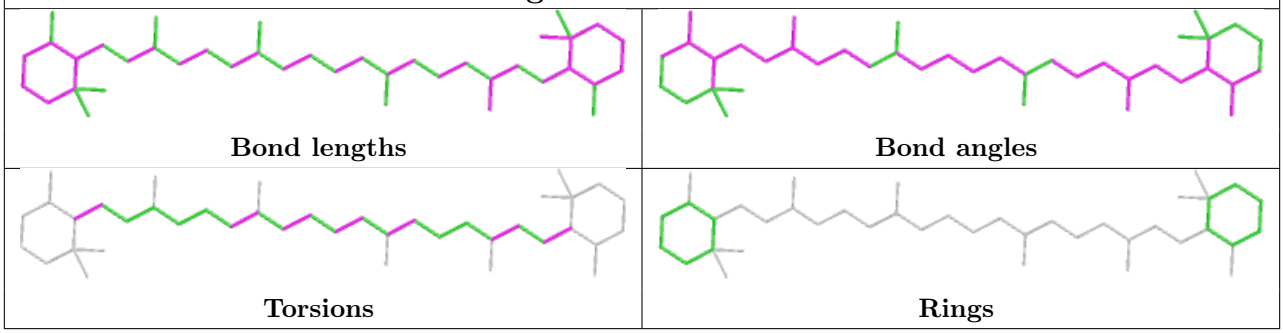


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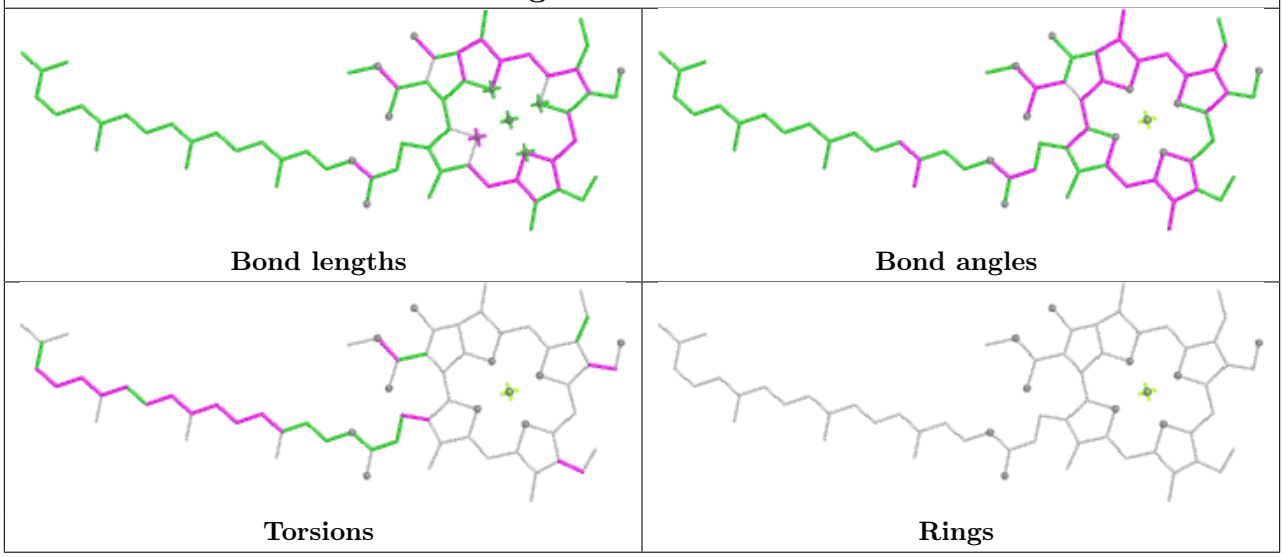
Ligand PL9 d 404



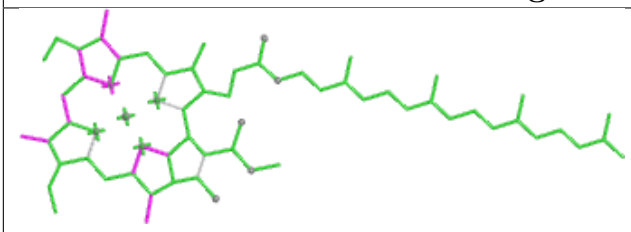
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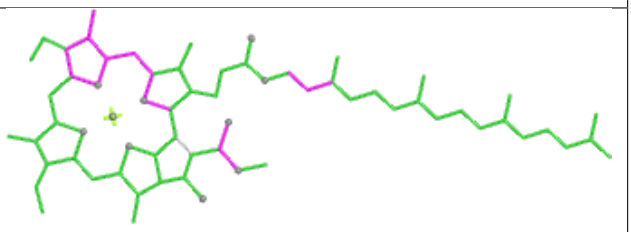
Ligand CHL 2 318



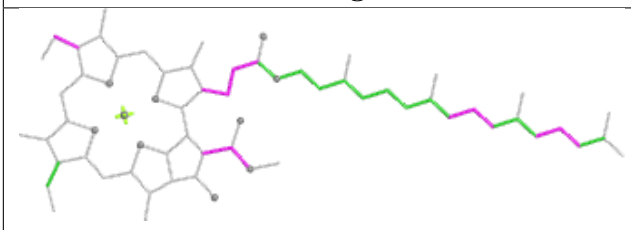
Ligand CLA 5 301



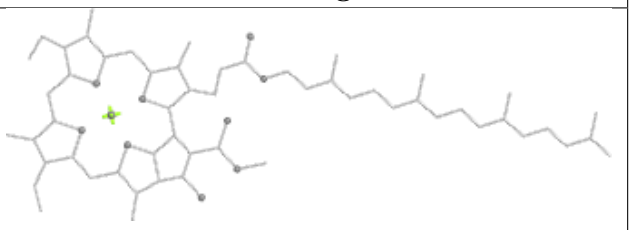
Bond lengths



Bond angles

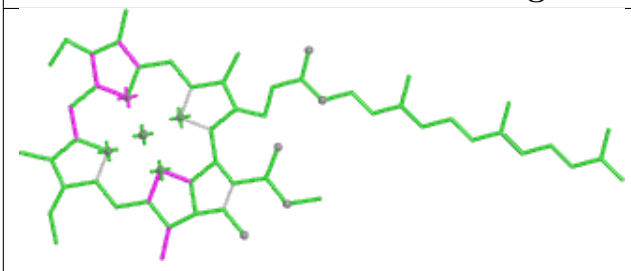


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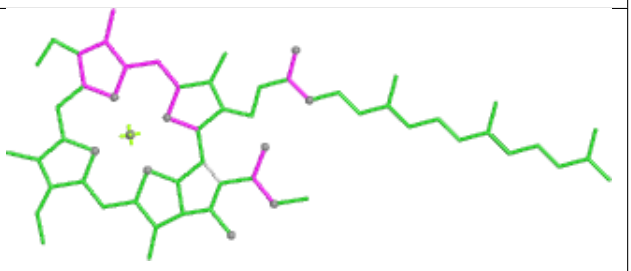


Rings

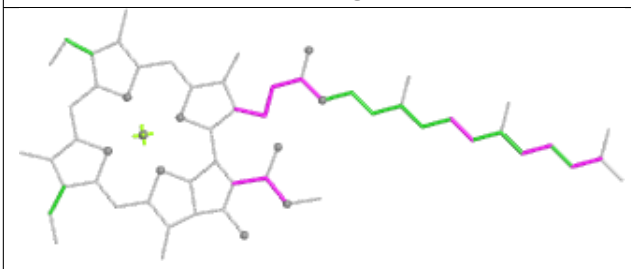
Ligand CLA v 304



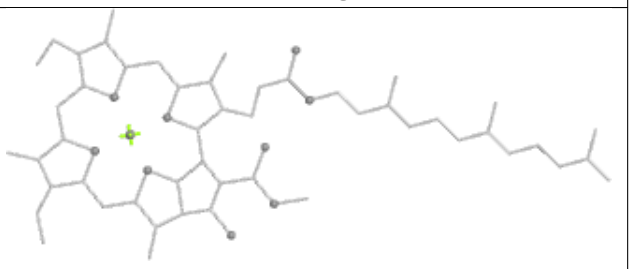
Bond lengths



Bond angles

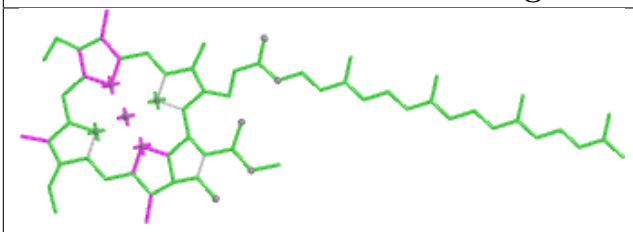


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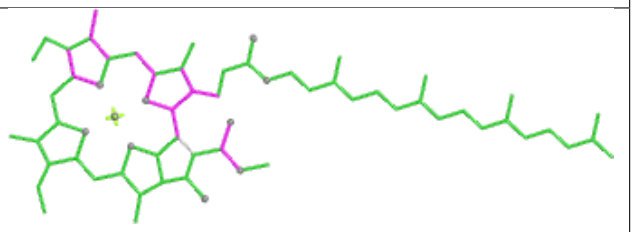


Rings

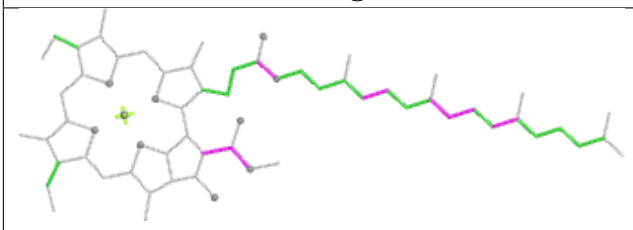
Ligand CLA C 513



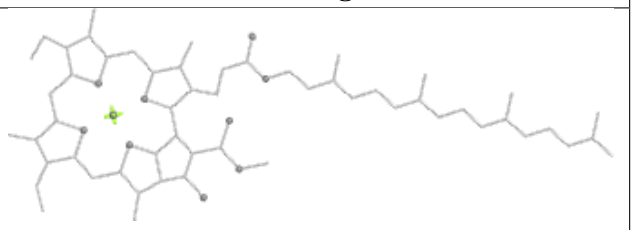
Bond lengths



Bond angles

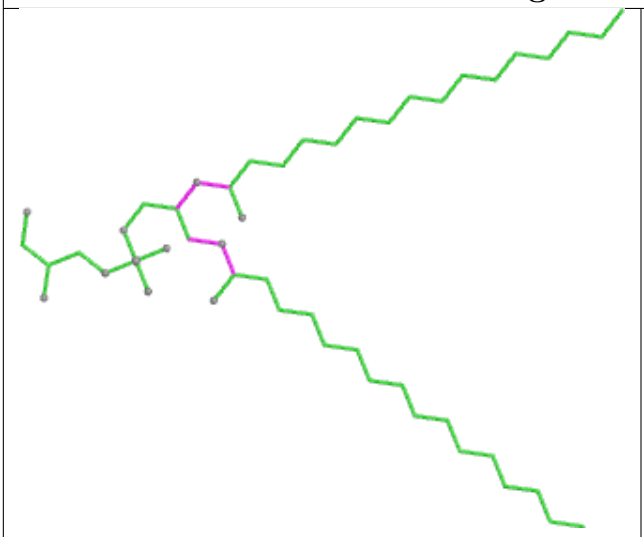


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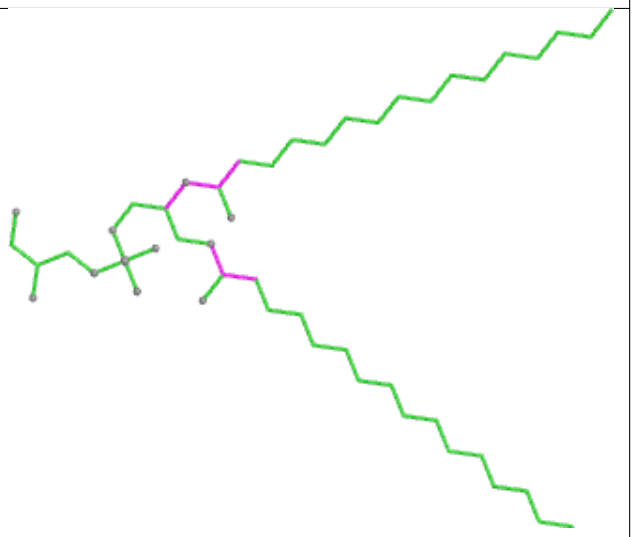


Rings

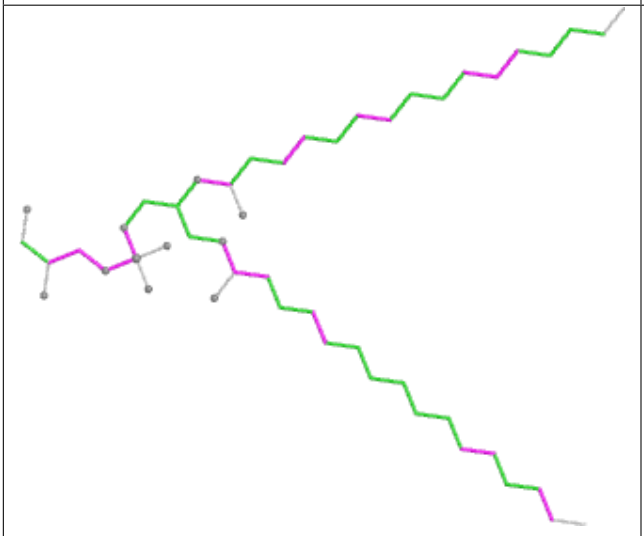
Ligand LHG s 312



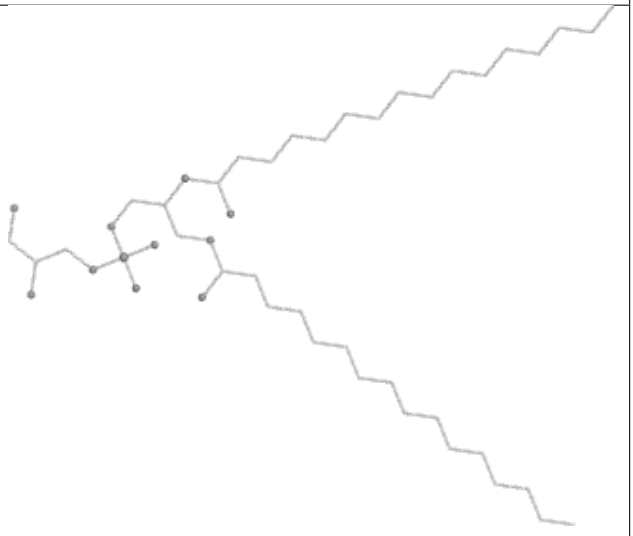
Bond lengths



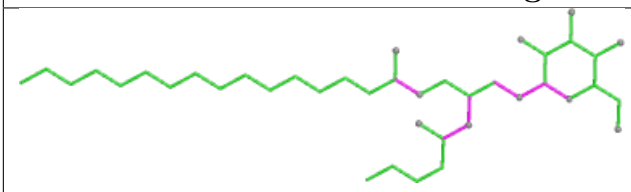
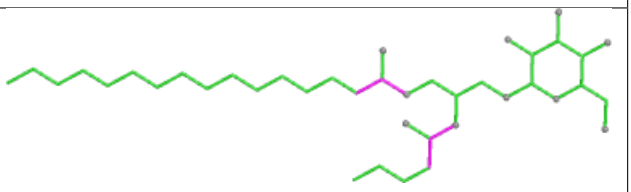
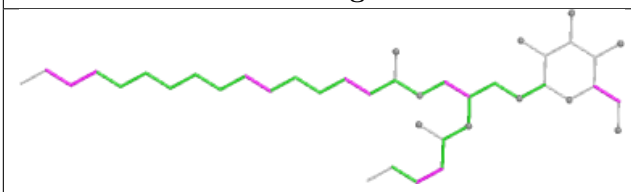
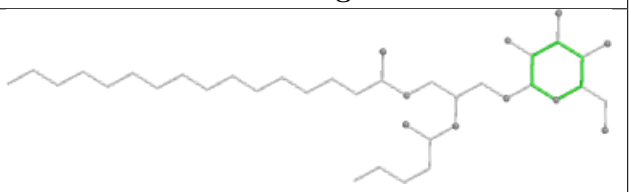
Bond angles

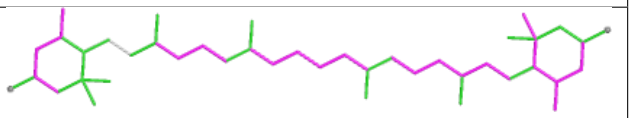
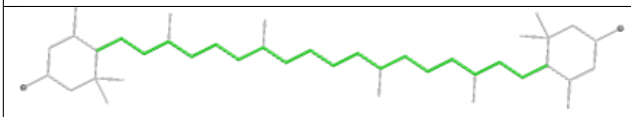
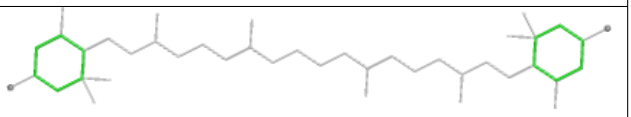


Torsions

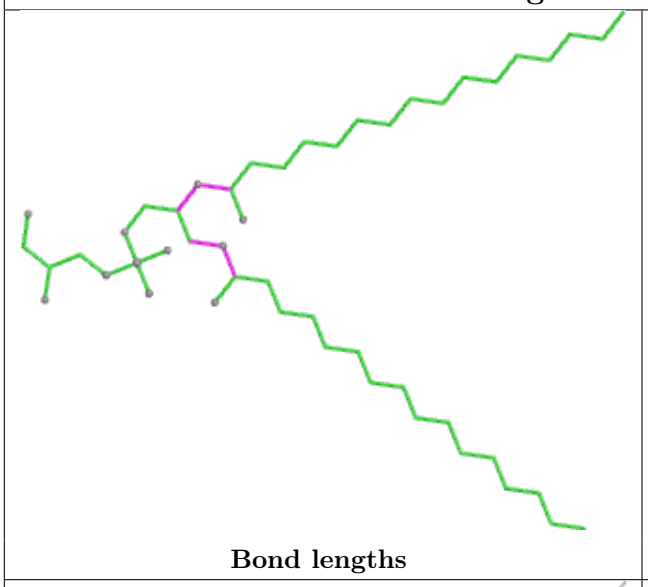


Rings

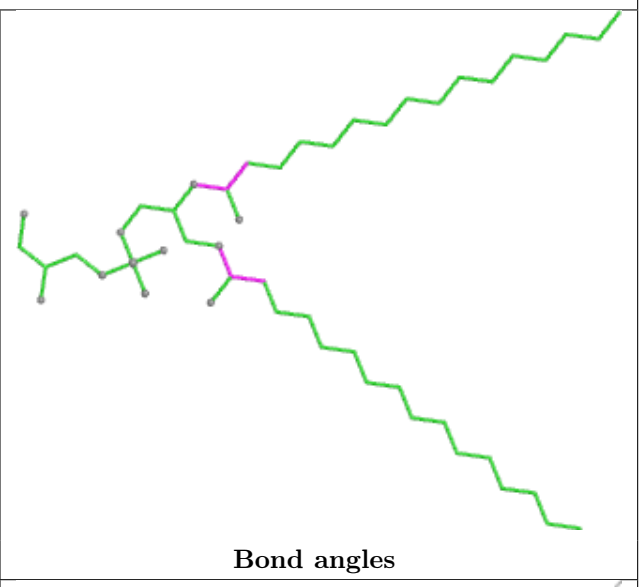
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 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand LUT 1 310	
 Bond lengths	 Bond angles
 Torsions	 Rings

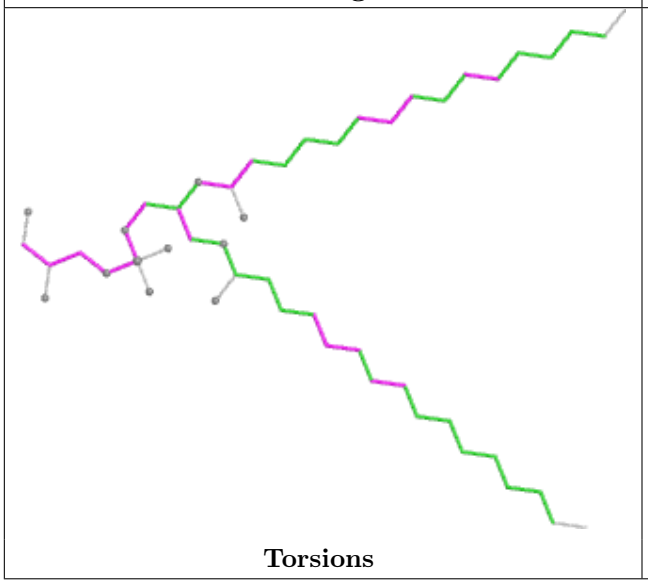
Ligand LHG b 623



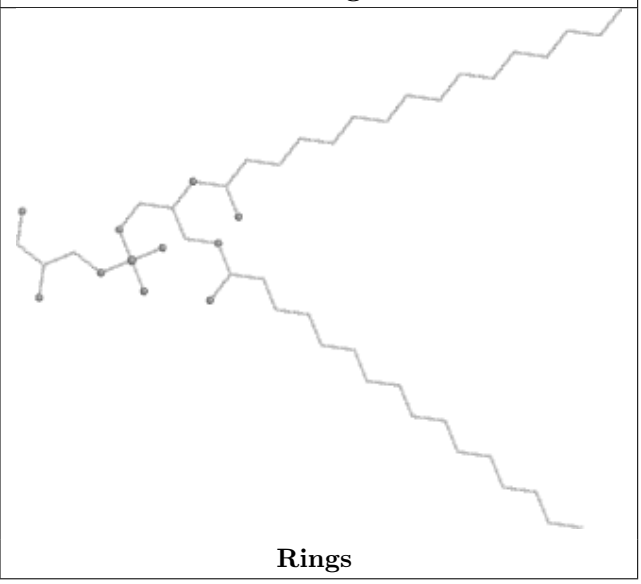
Bond lengths



Bond angles

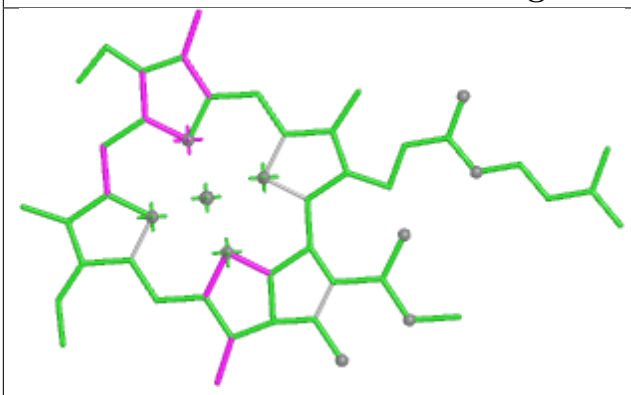


Torsions

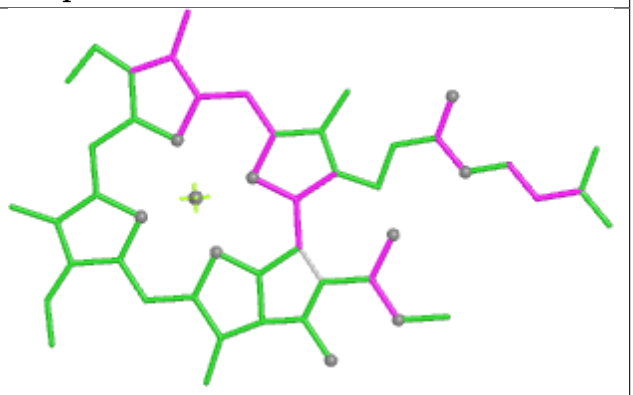


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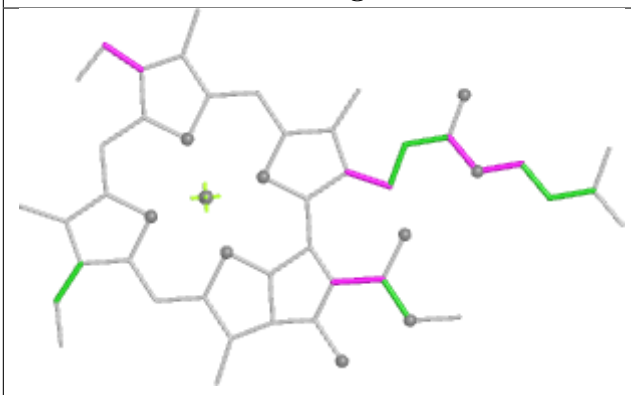
Ligand CLA q 303



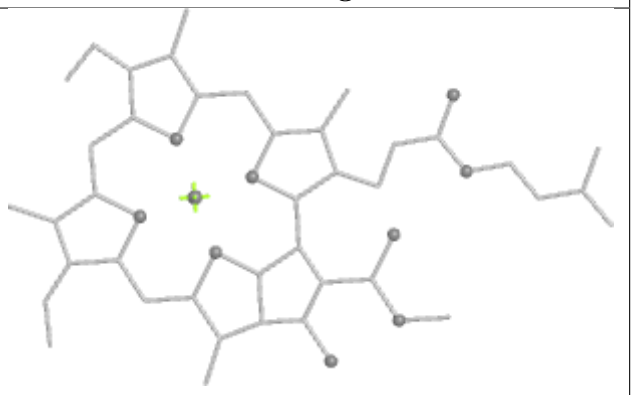
Bond lengths



Bond angles

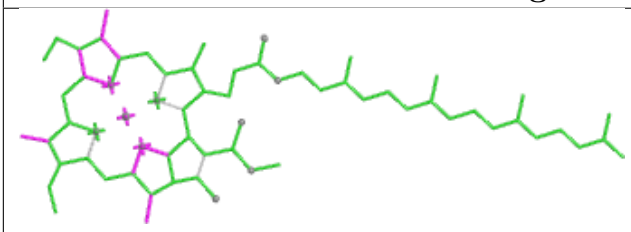


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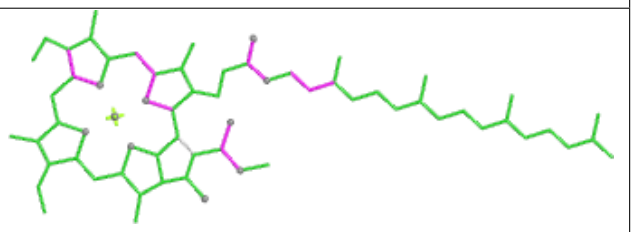


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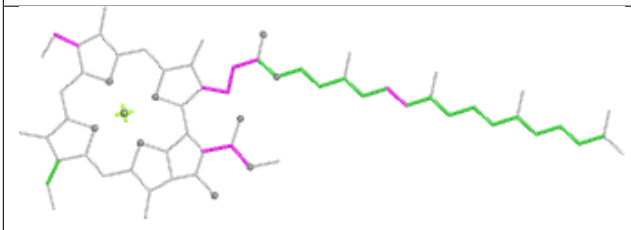
Ligand CLA c 513



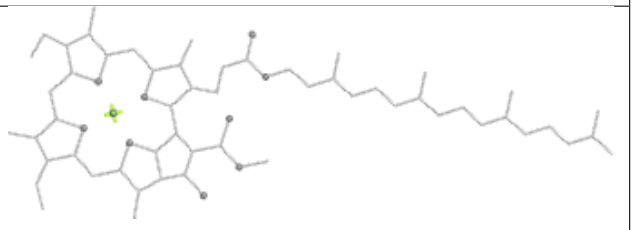
Bond lengths



Bond angles

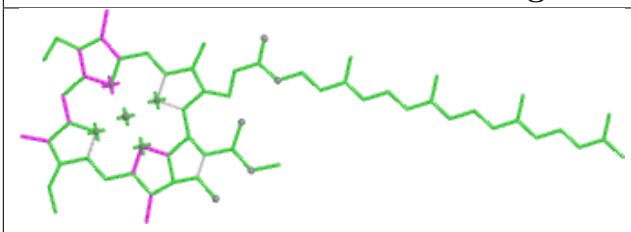


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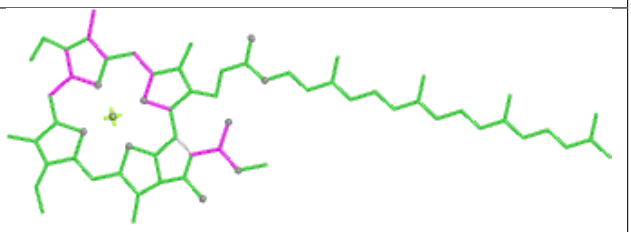


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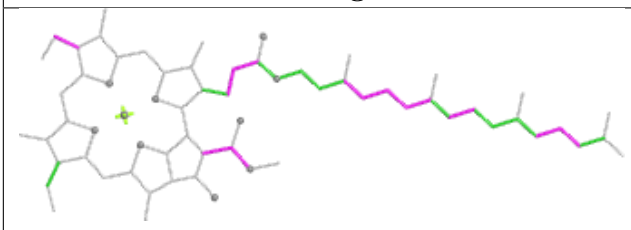
Ligand CLA b 615



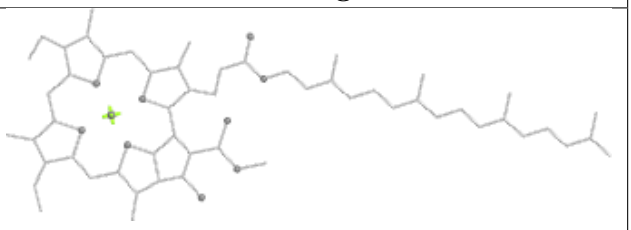
Bond lengths



Bond angles

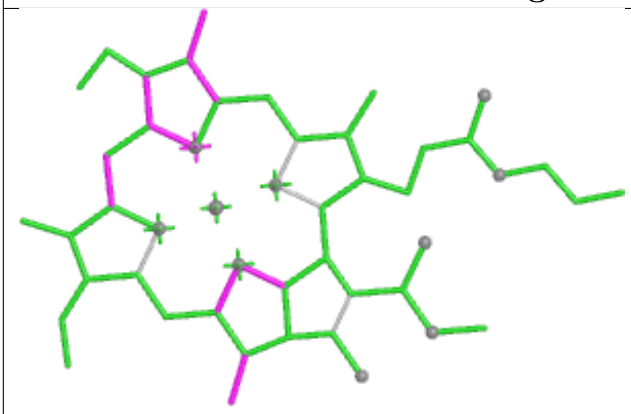


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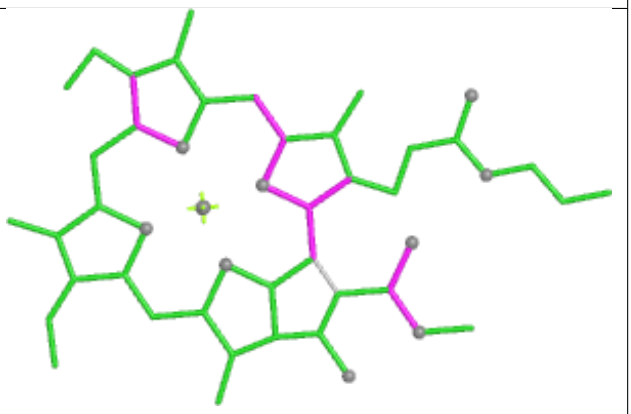


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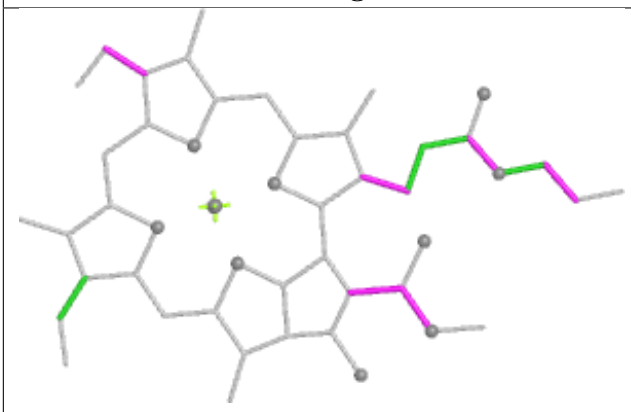
Ligand CLA 1 308



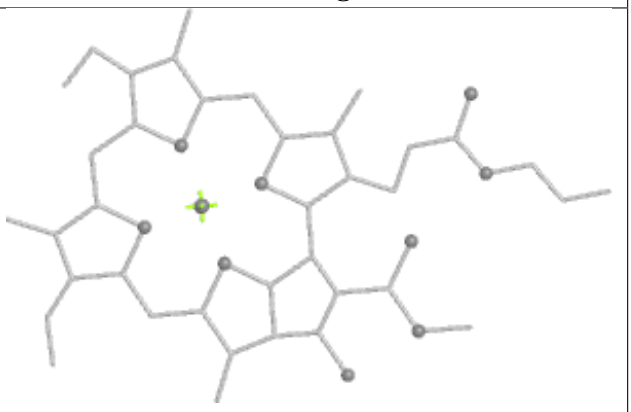
Bond lengths



Bond angles

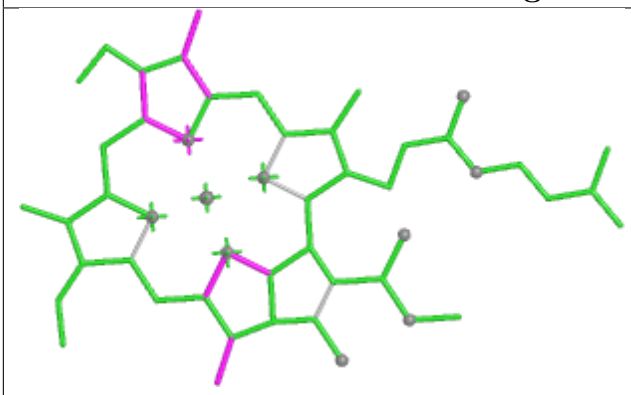


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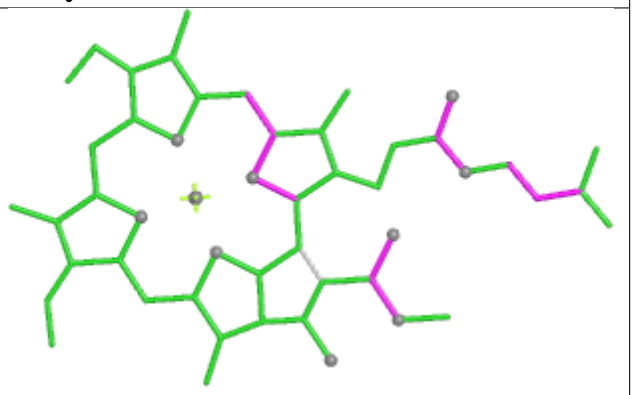


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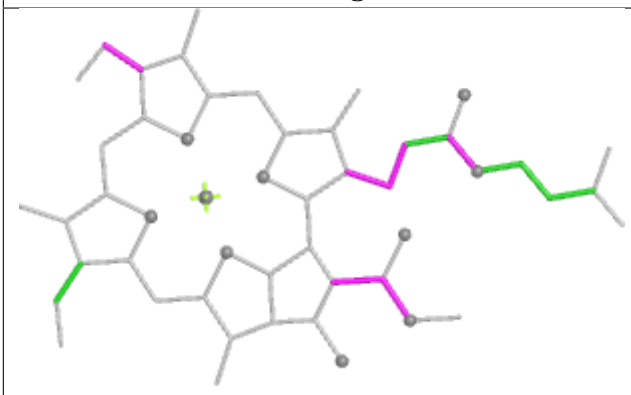
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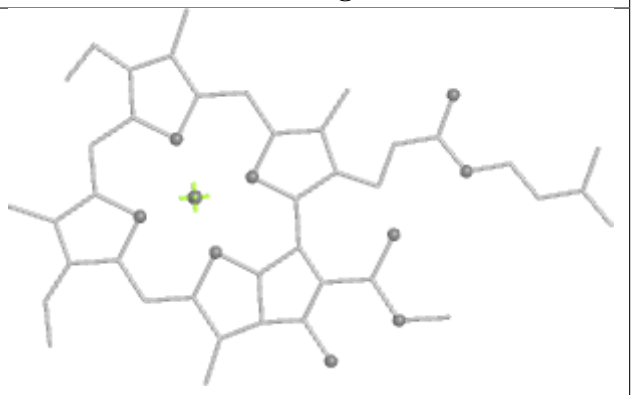
Bond lengths



Bond angles

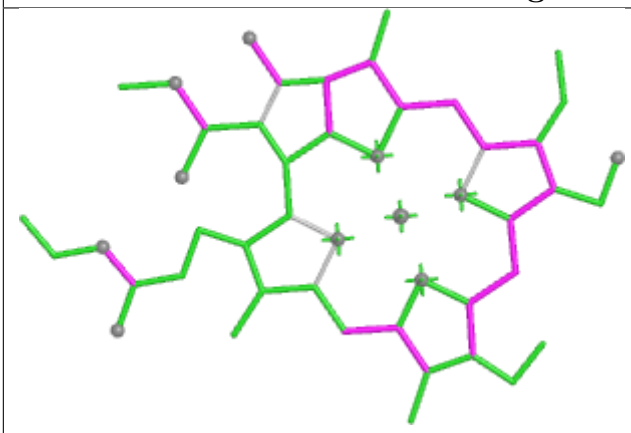


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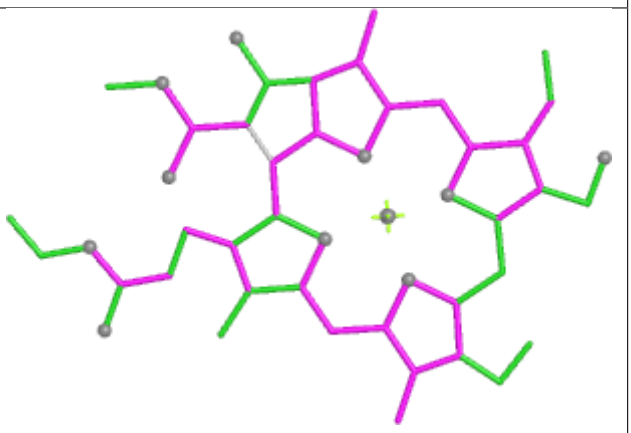


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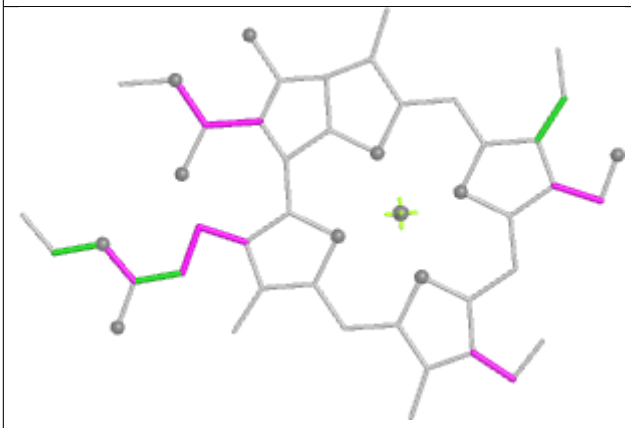
Ligand CHL v 314



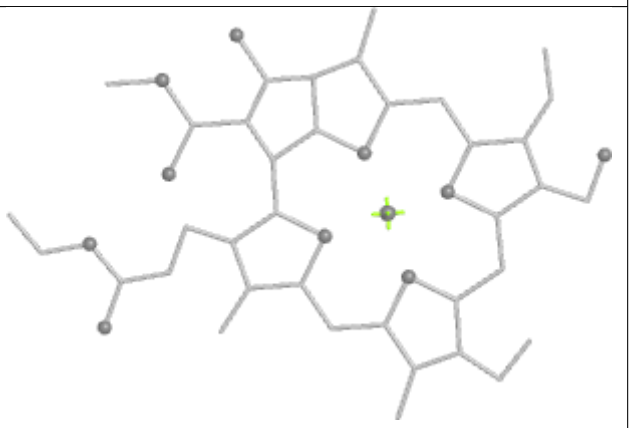
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Bond angles

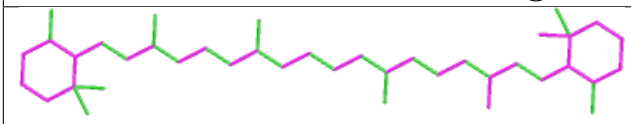


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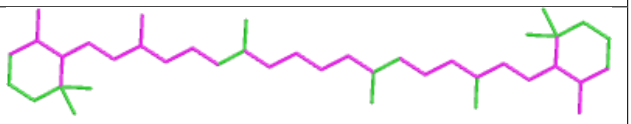


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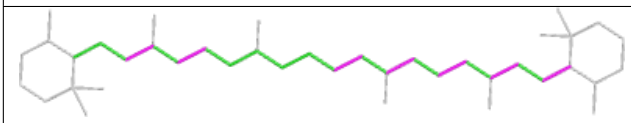
Ligand BCR c 516



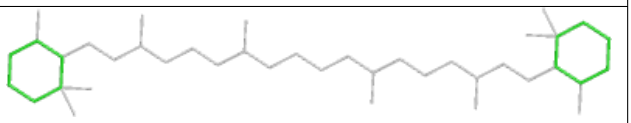
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Bond angles

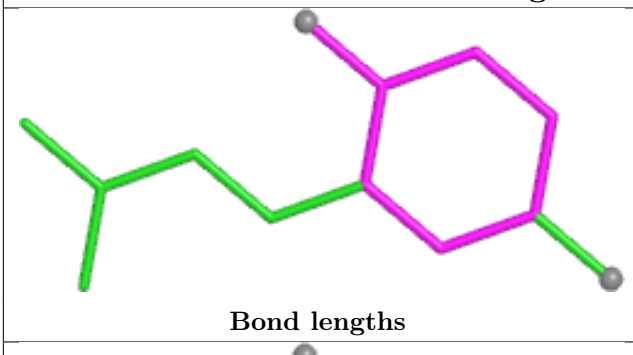


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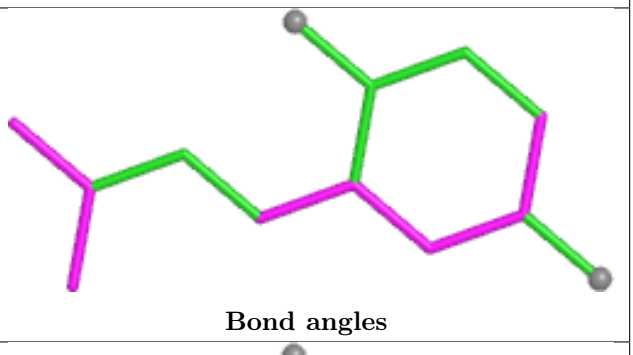


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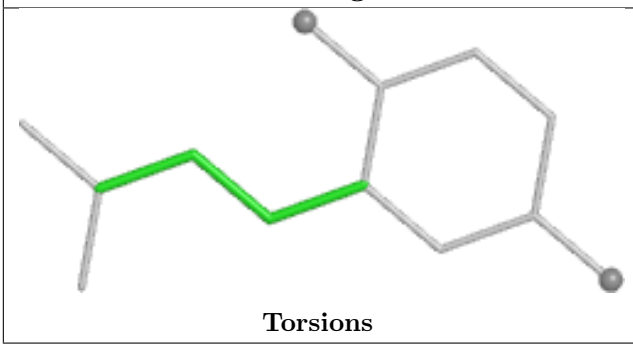
Ligand PL9 A 410



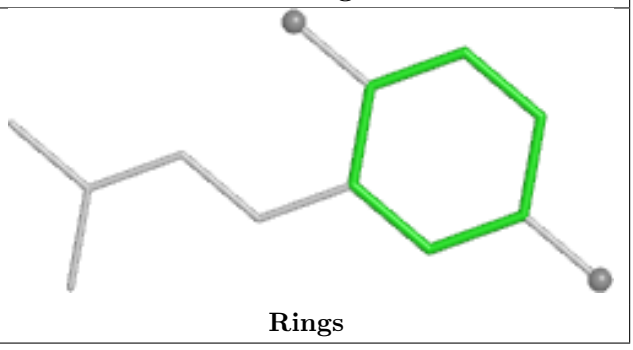
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Bond angles

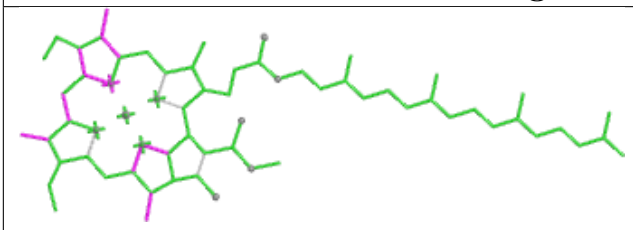


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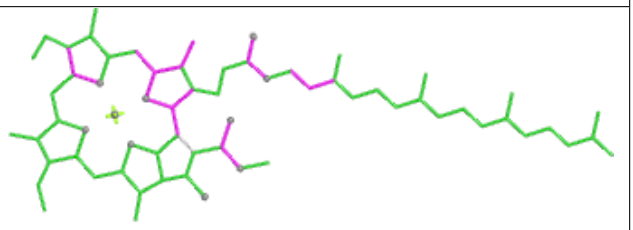


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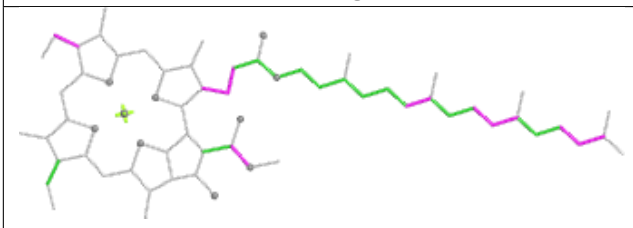
Ligand CLA 5 304



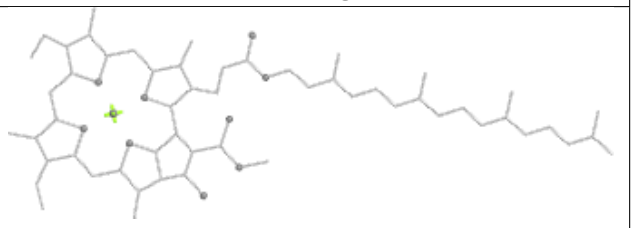
Bond lengths



Bond angles

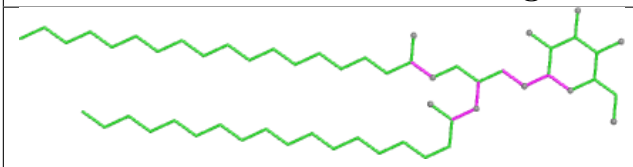


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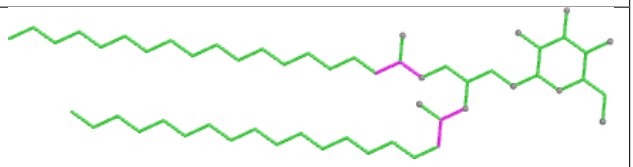


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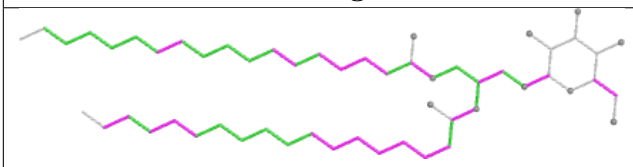
Ligand LMG b 624



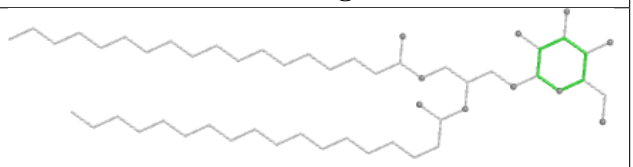
Bond lengths



Bond angles

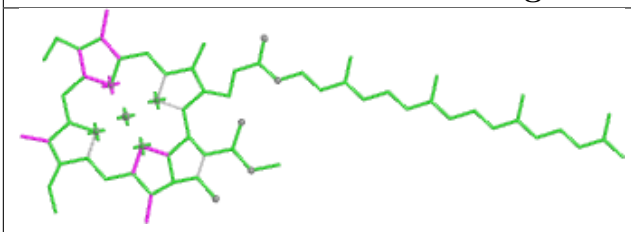


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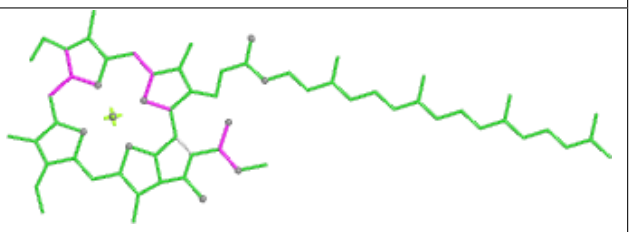


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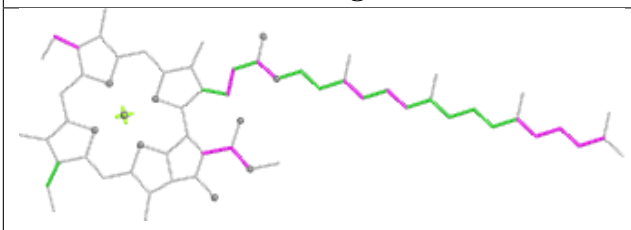
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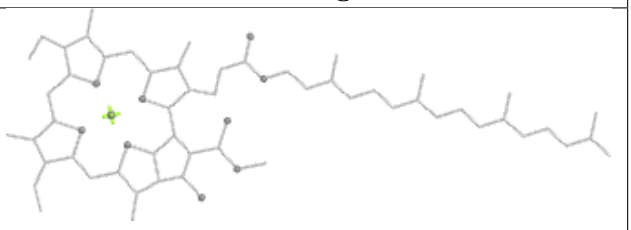
Bond lengths



Bond angles

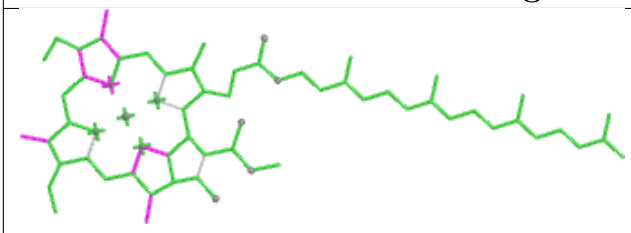


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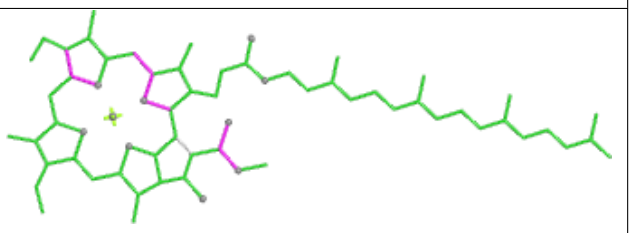


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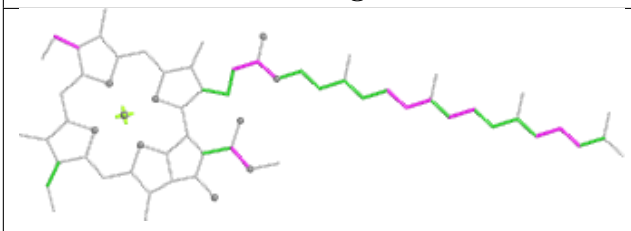
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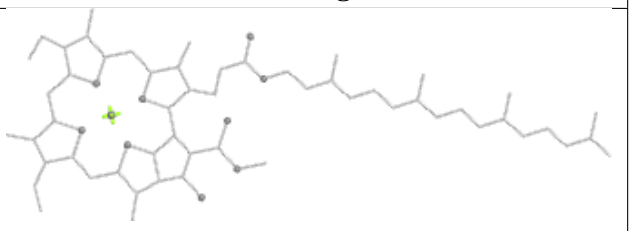
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Bond angles

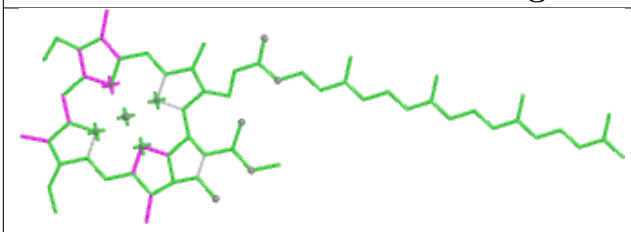


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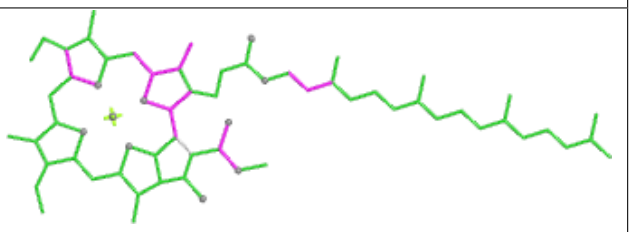


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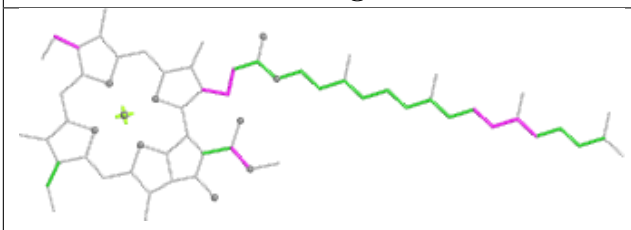
Ligand CLA 2 304



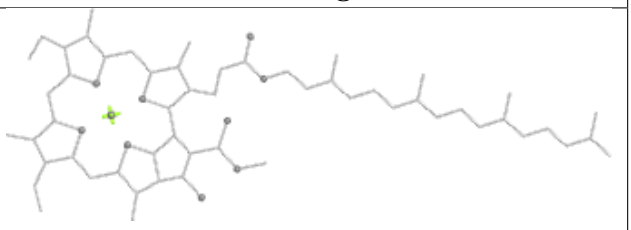
Bond lengths



Bond angles

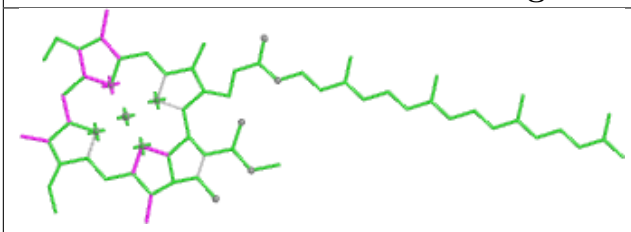


Torsions

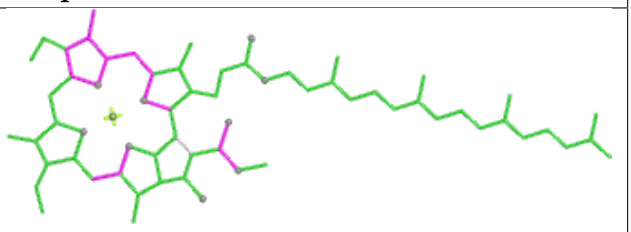


Rings

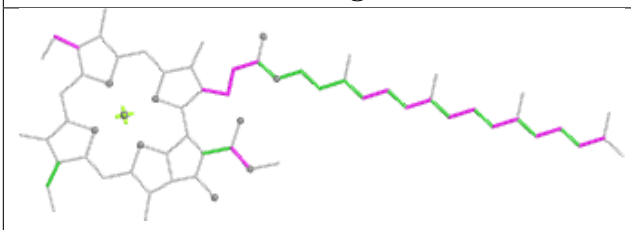
Ligand CLA q 301



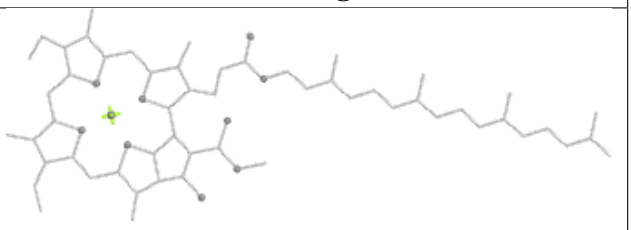
Bond lengths



Bond angles

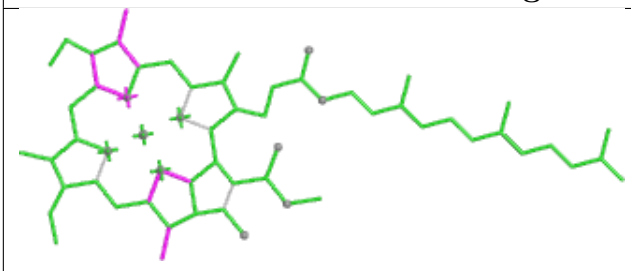


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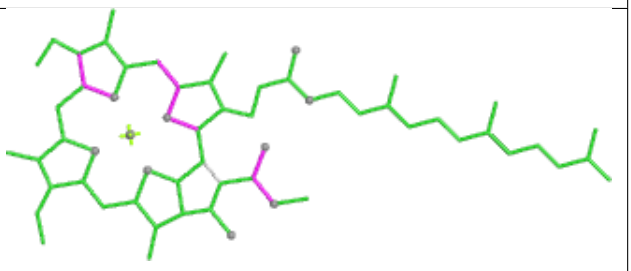


Rings

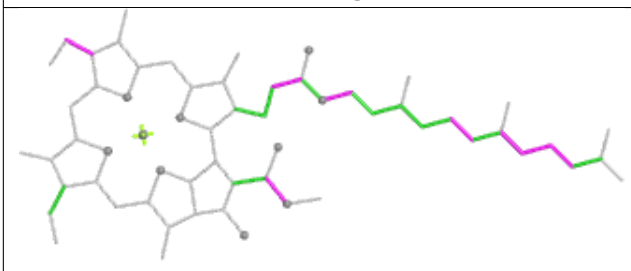
Ligand CLA G 306



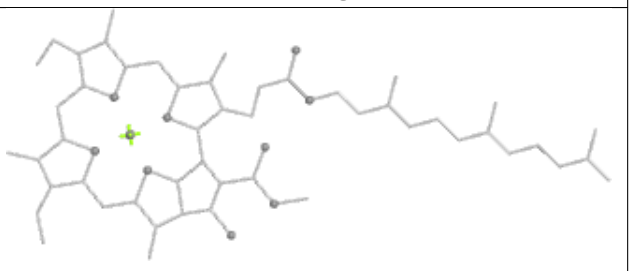
Bond lengths



Bond angles

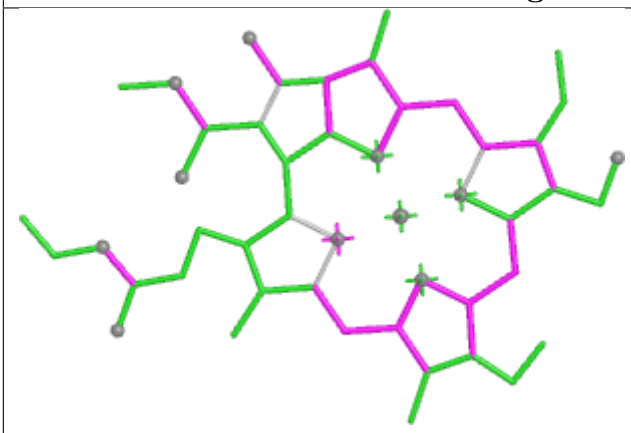


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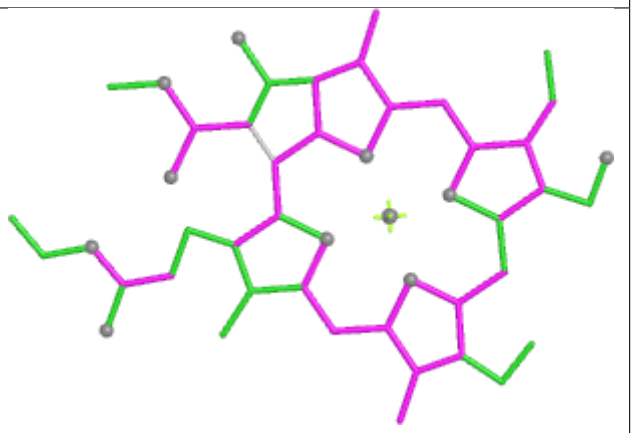


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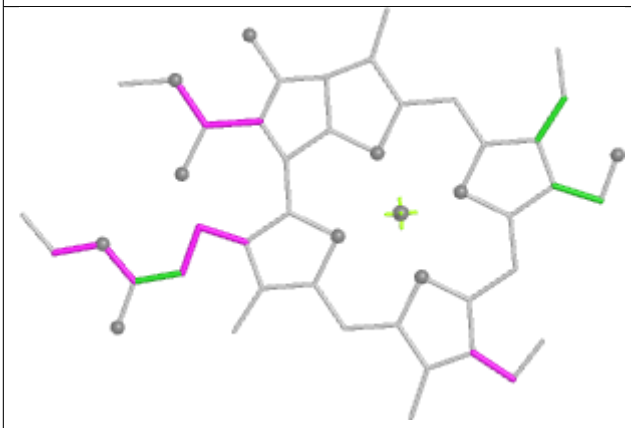
Ligand CHL u 314



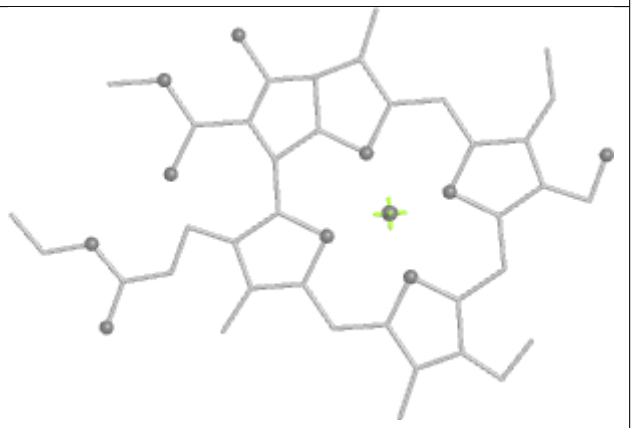
Bond lengths



Bond angles

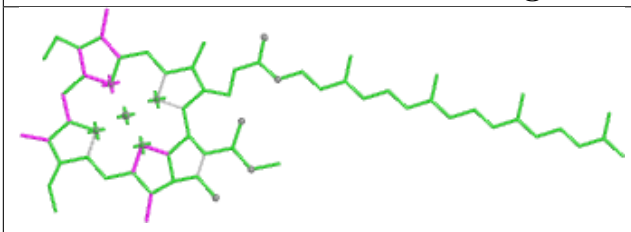


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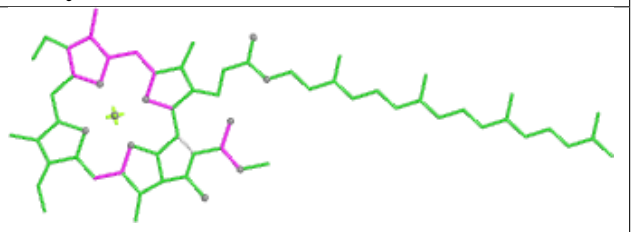


Rings

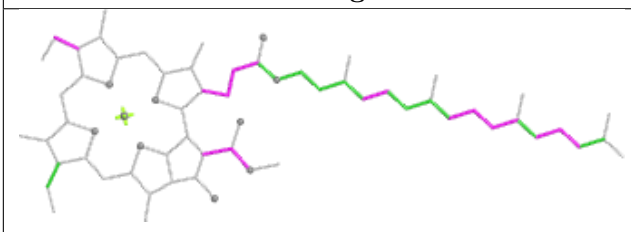
Ligand CLA Q 301



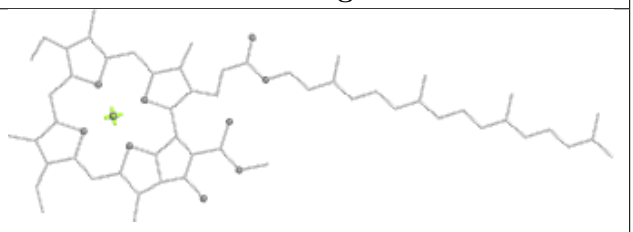
Bond lengths



Bond angles

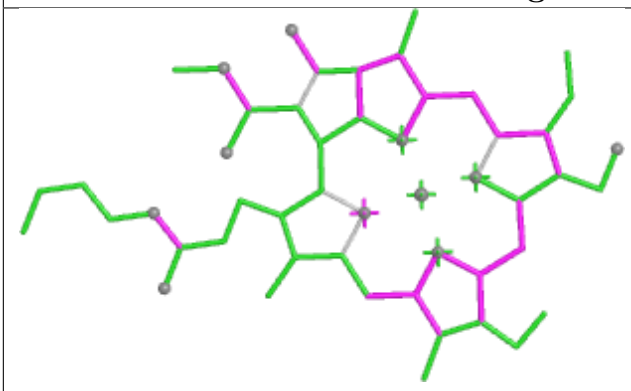


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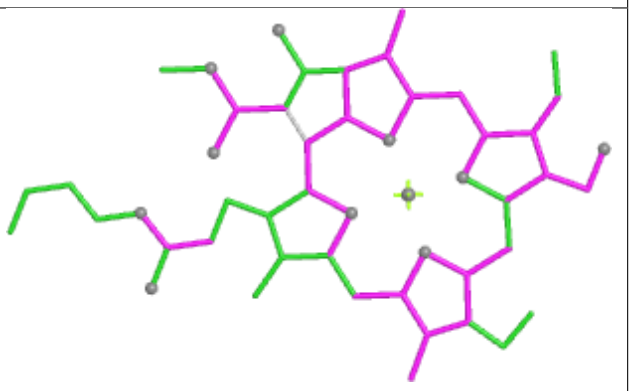


Rings

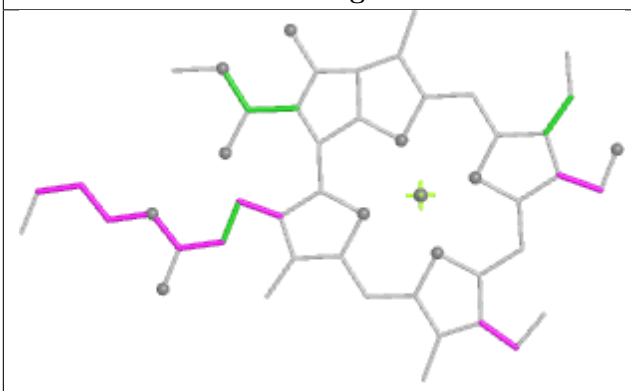
Ligand CHL 6 314



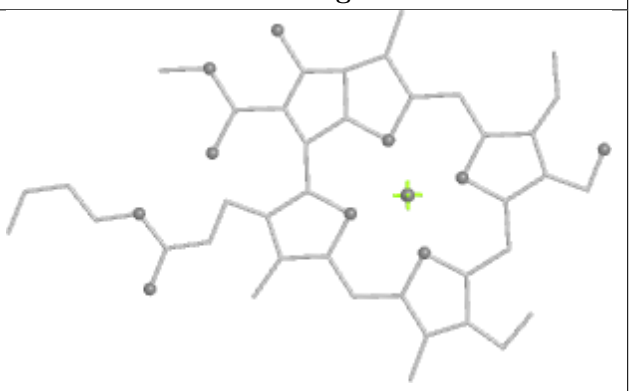
Bond lengths



Bond angles

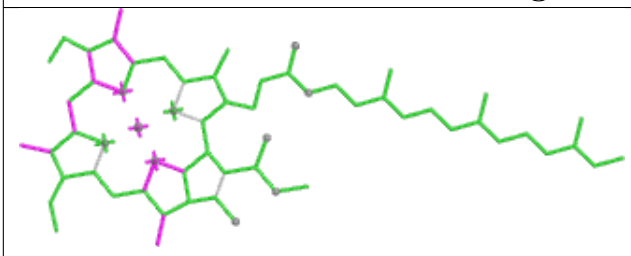


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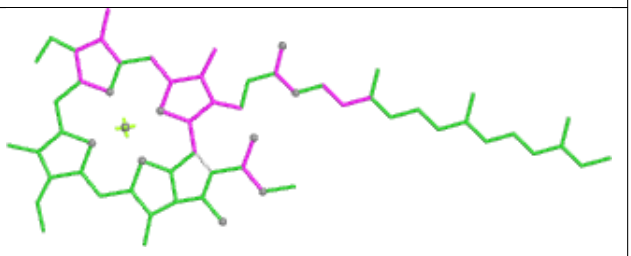


Rings

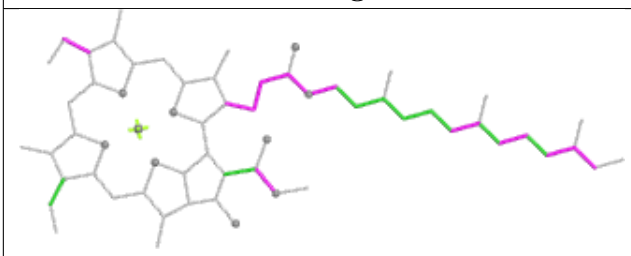
Ligand CLA s 301



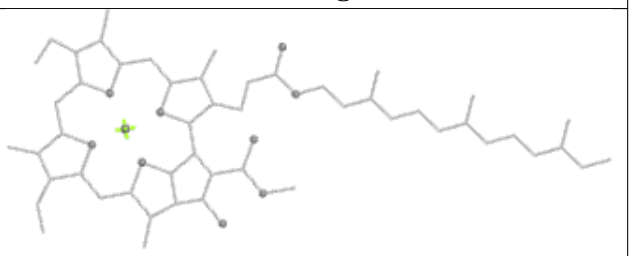
Bond lengths



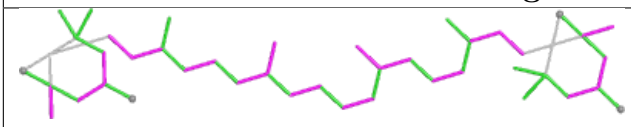
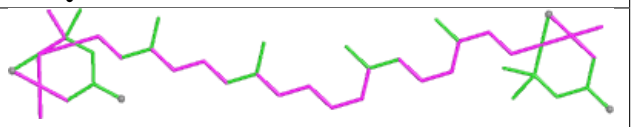
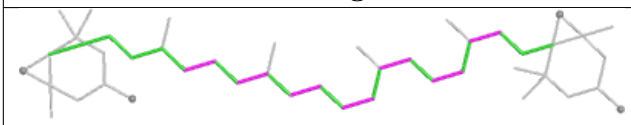
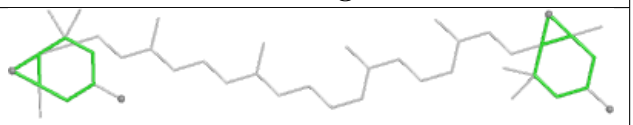
Bond angles

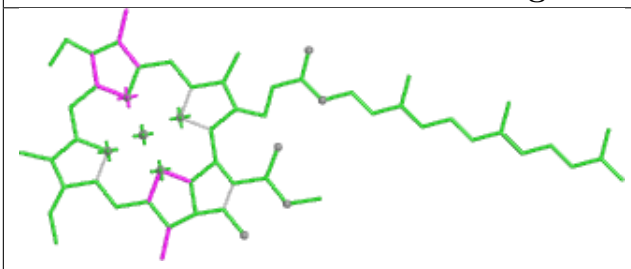
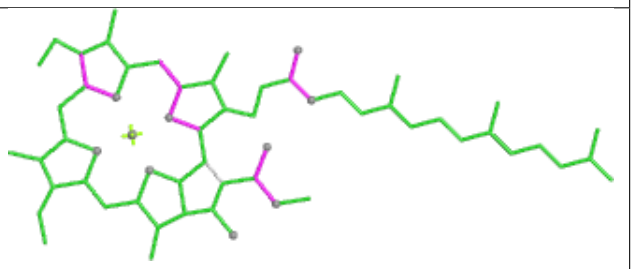
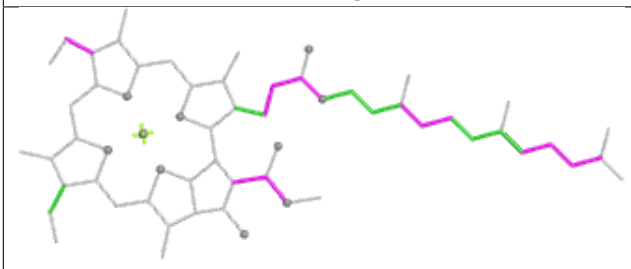
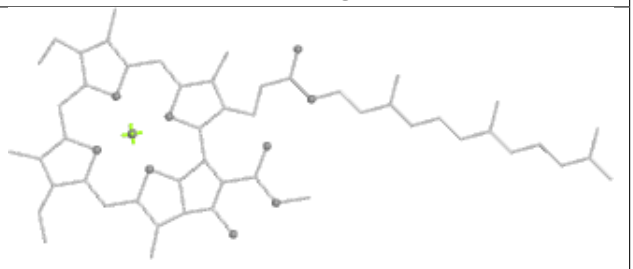


Torsions

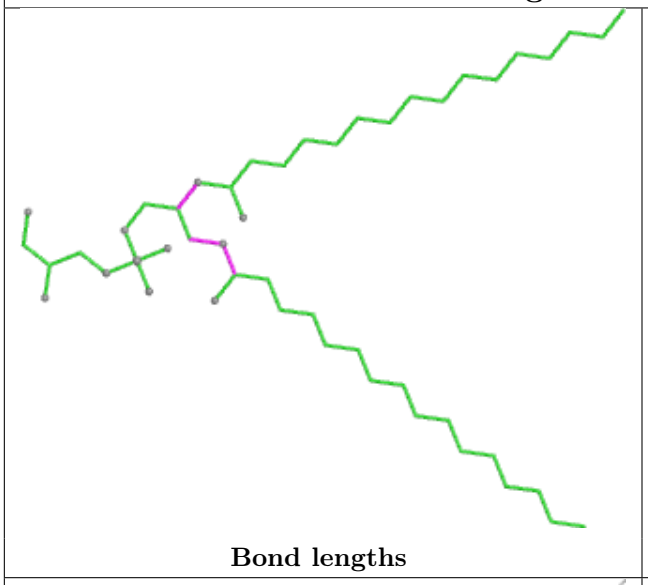


Rings

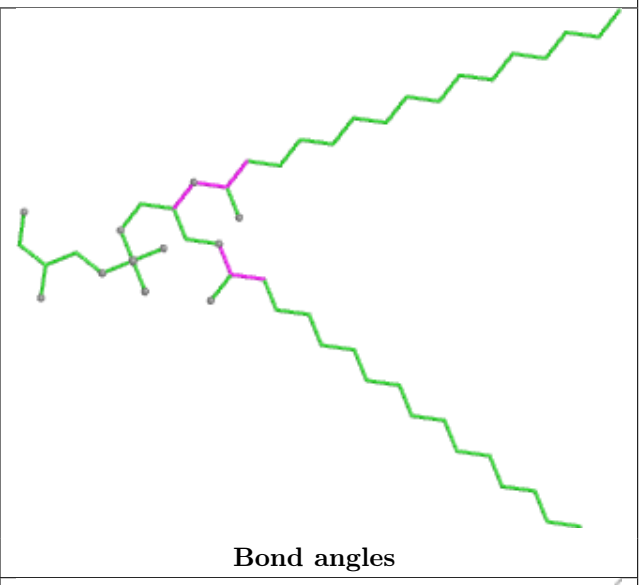
Ligand XAT Q 309	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

Ligand CLA 6 307	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

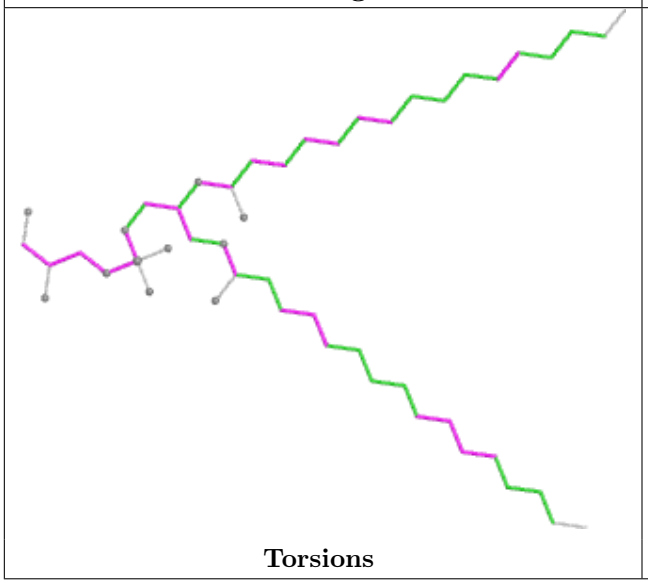
Ligand LHG L 101



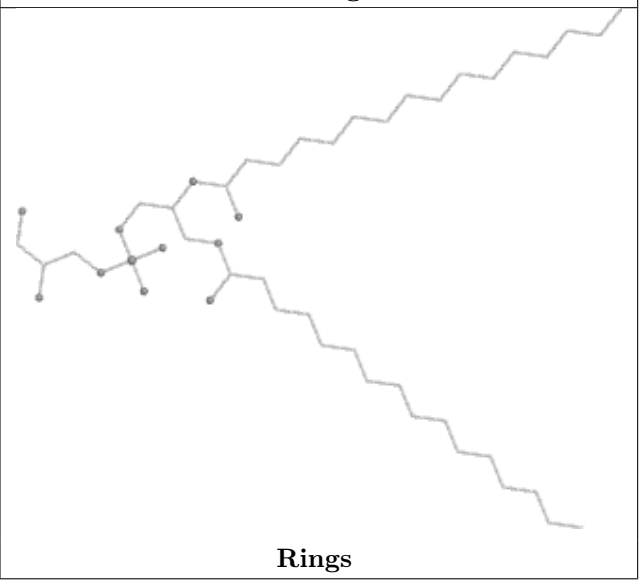
Bond lengths



Bond angles

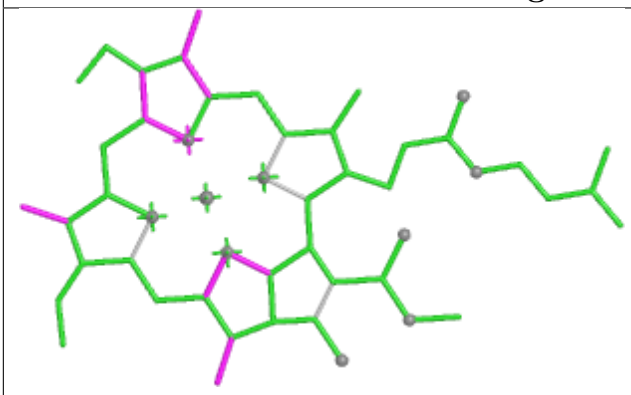


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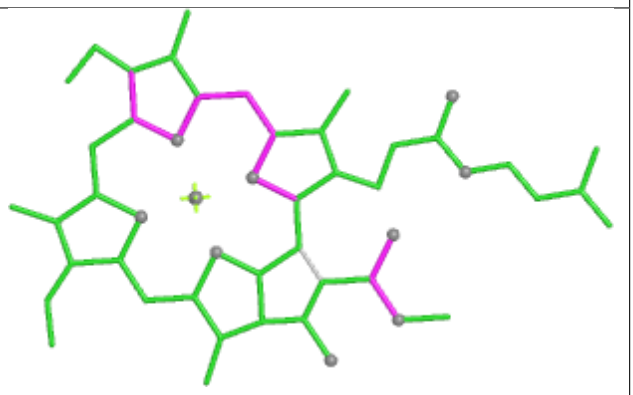


Rings

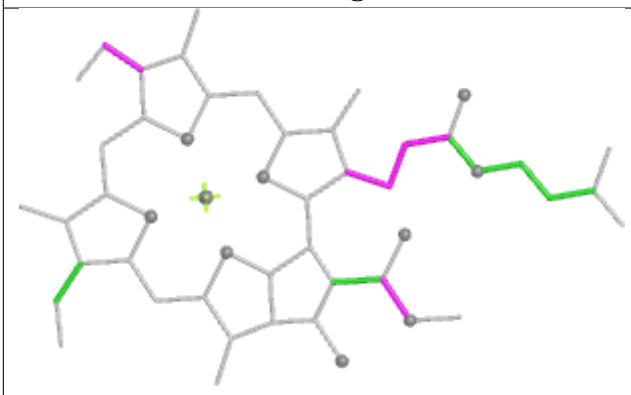
Ligand CLA v 303



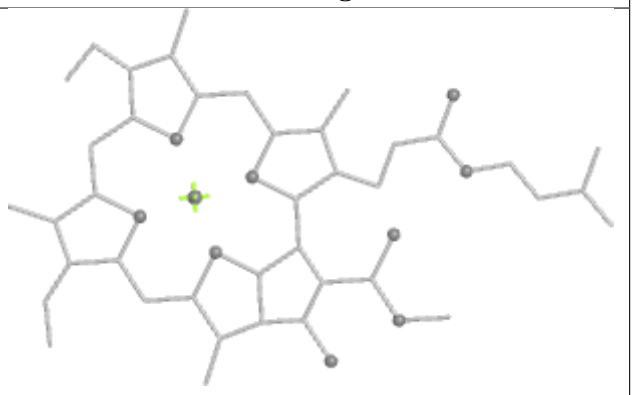
Bond lengths



Bond angles



Torsions

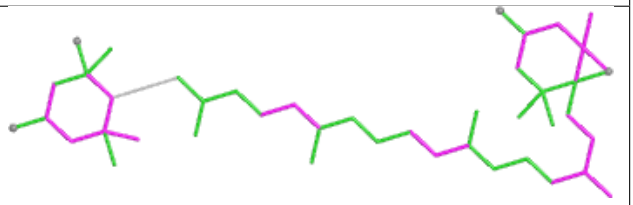


Rings

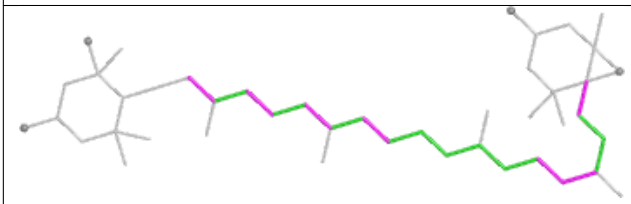
Ligand NEX R 301



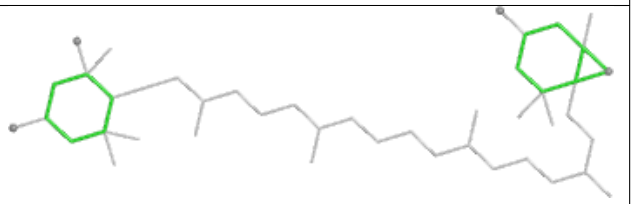
Bond lengths



Bond angles

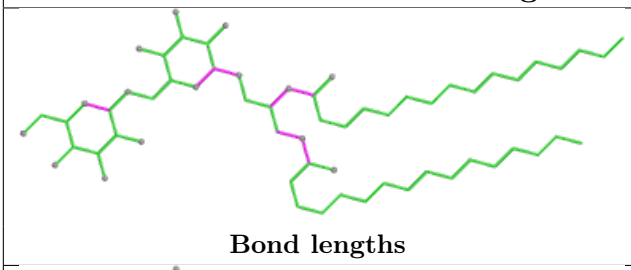


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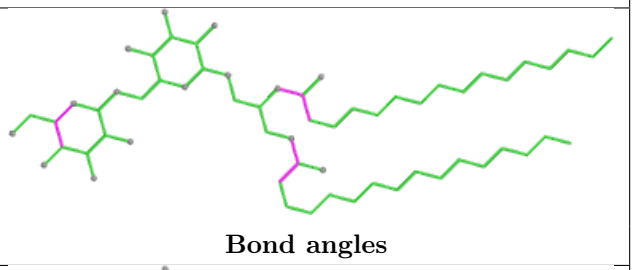


Rings

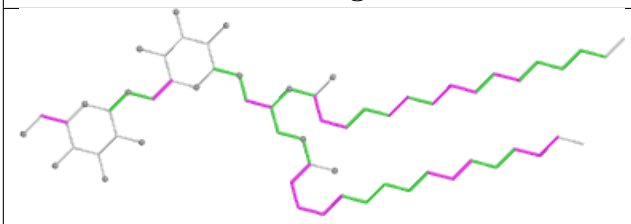
Ligand DGD B 601



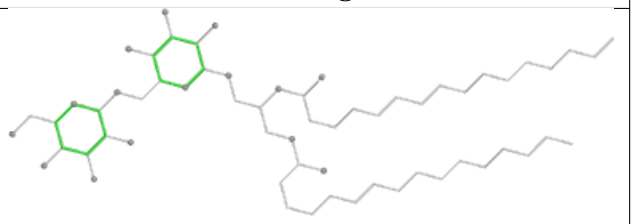
Bond lengths



Bond angles

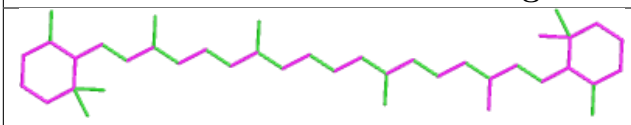


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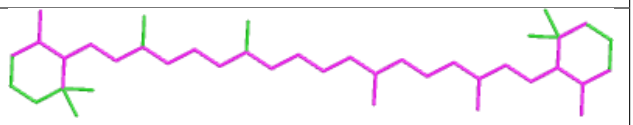


Rings

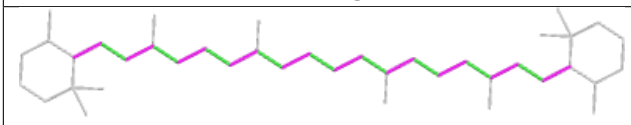
Ligand BCR C 517



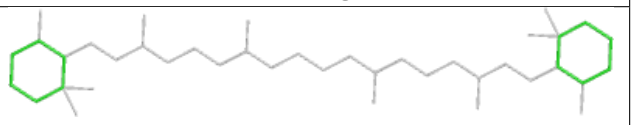
Bond lengths



Bond angles

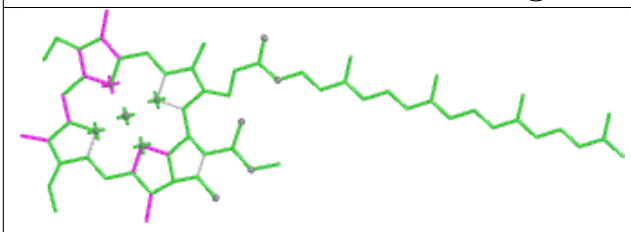


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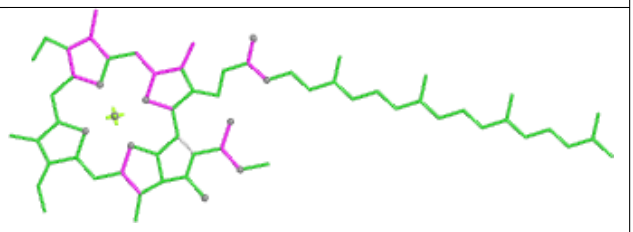


Rings

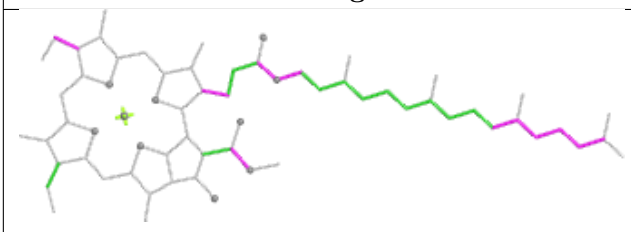
Ligand CLA n 304



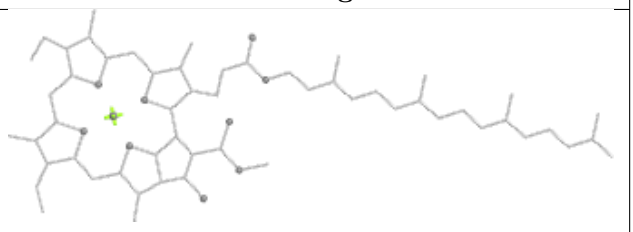
Bond lengths



Bond angles

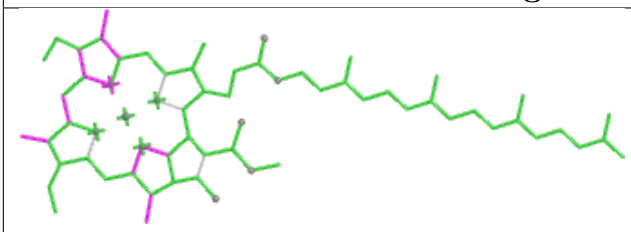


Torsions

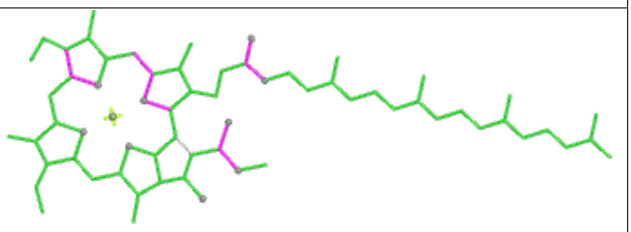


Rings

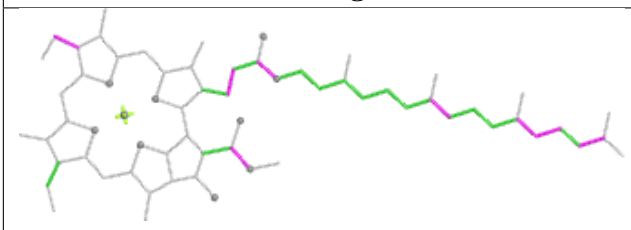
Ligand CLA V 302



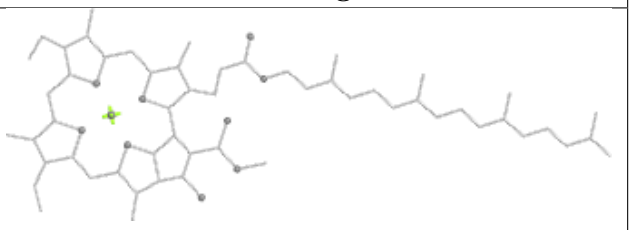
Bond lengths



Bond angles

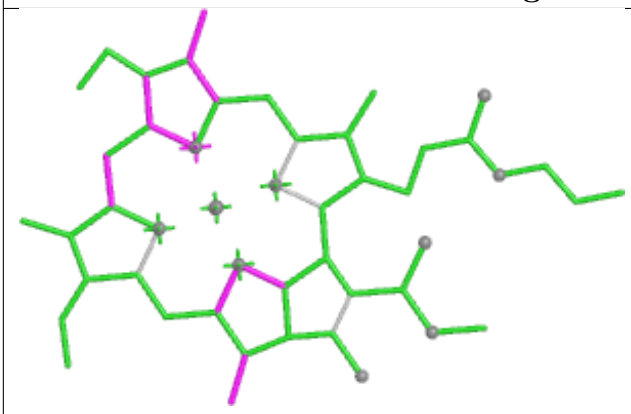


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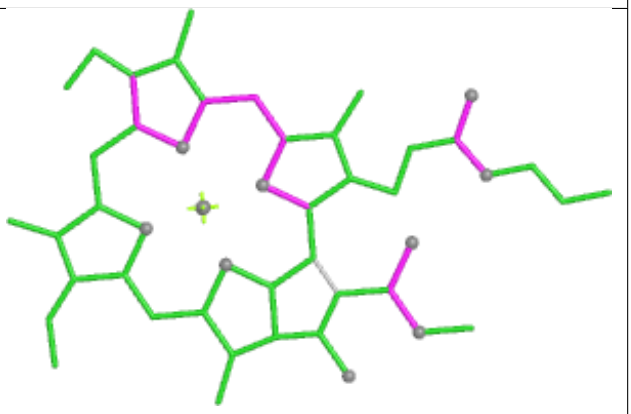


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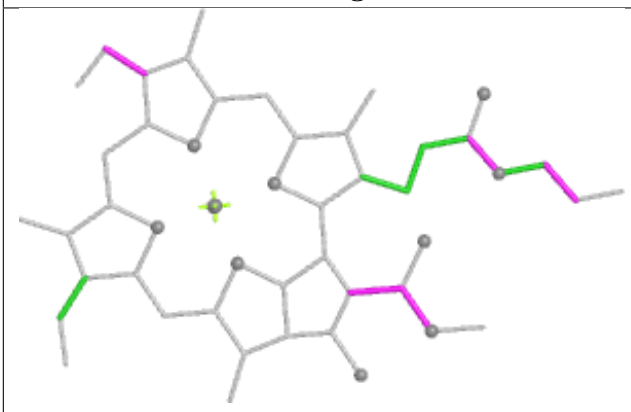
Ligand CLA G 308



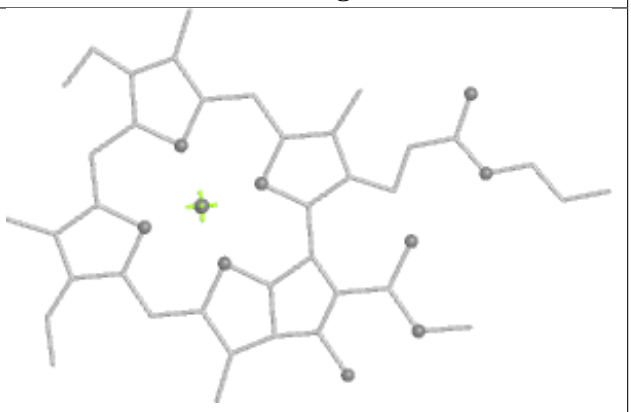
Bond lengths



Bond angles

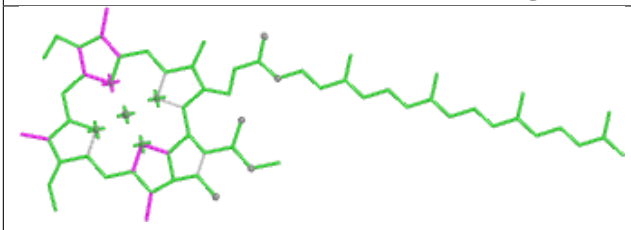


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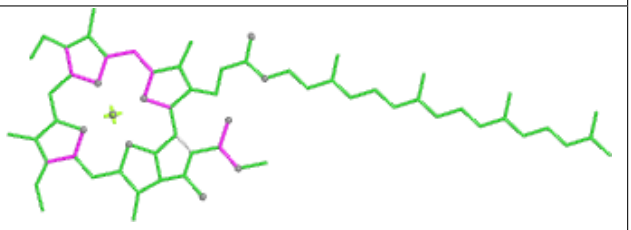


Rings

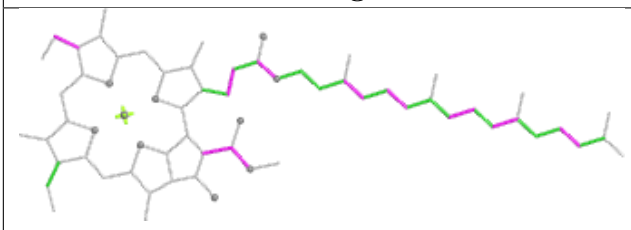
Ligand CLA C 506



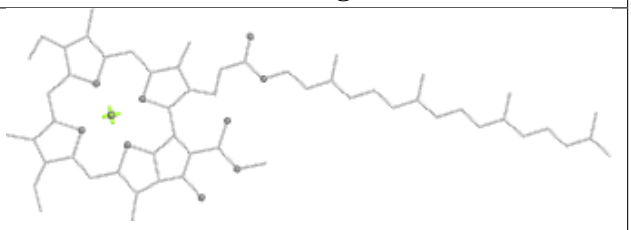
Bond lengths



Bond angles

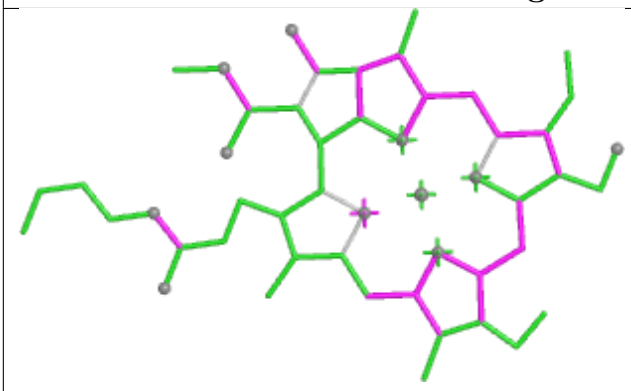


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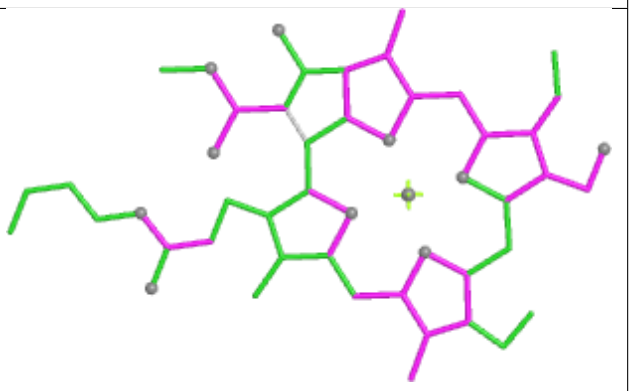


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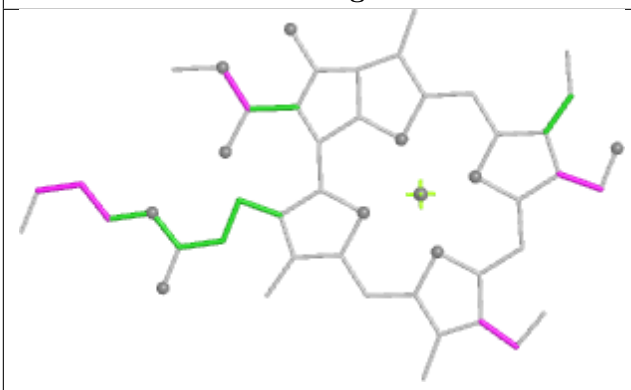
Ligand CHL 4 315



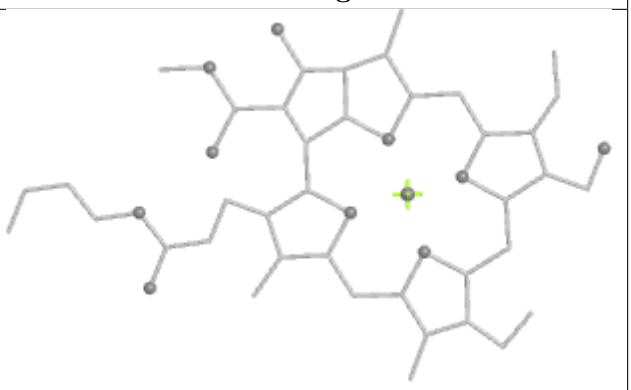
Bond lengths



Bond angles

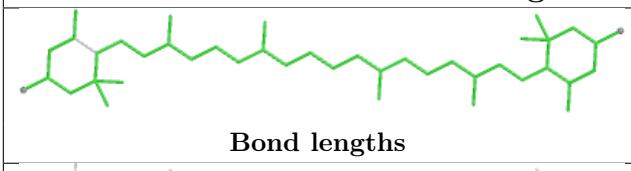


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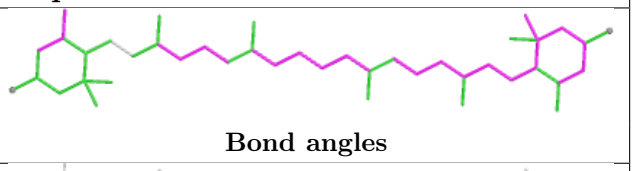


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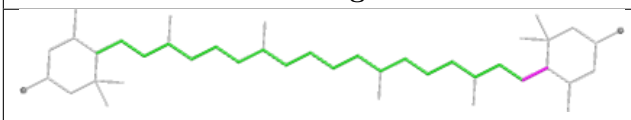
Ligand LUT p 310



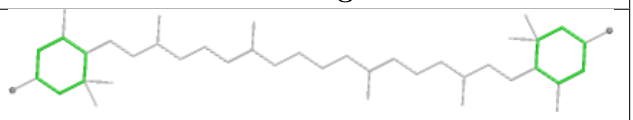
Bond lengths



Bond angles

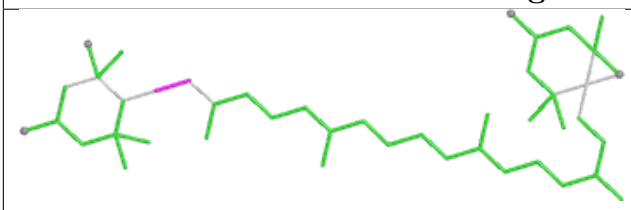


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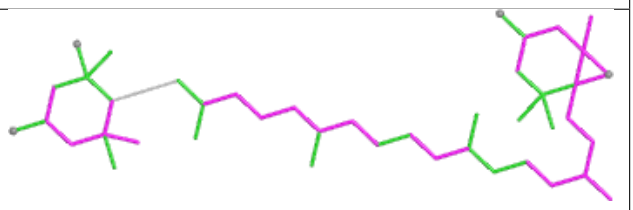


Rings

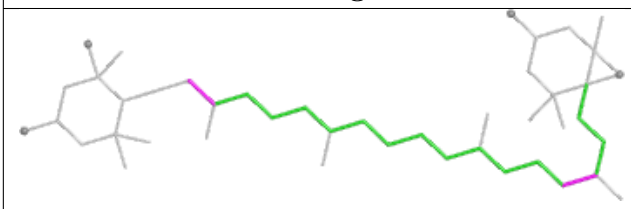
Ligand NEX s 317



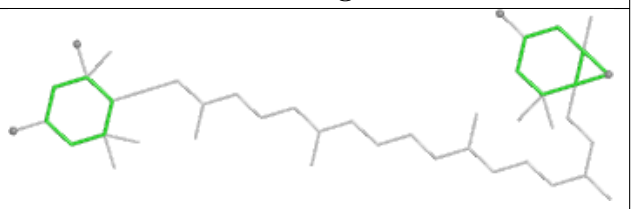
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Bond angles

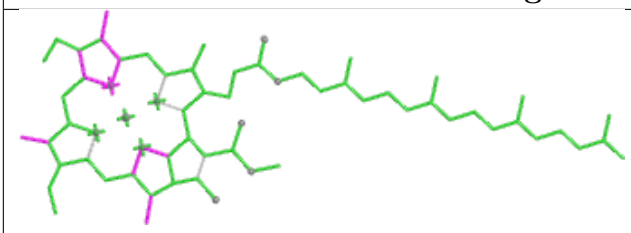


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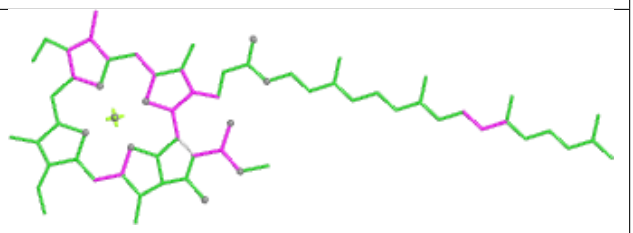


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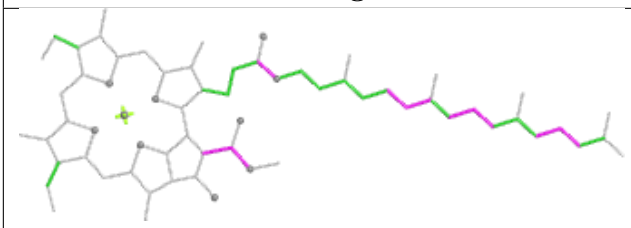
Ligand CLA C 511



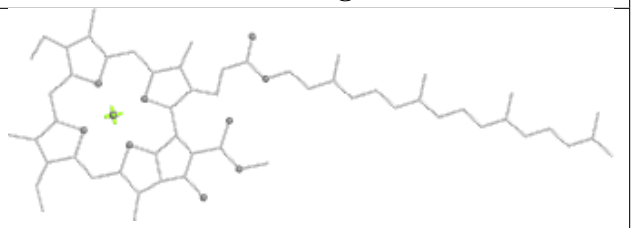
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Bond angles

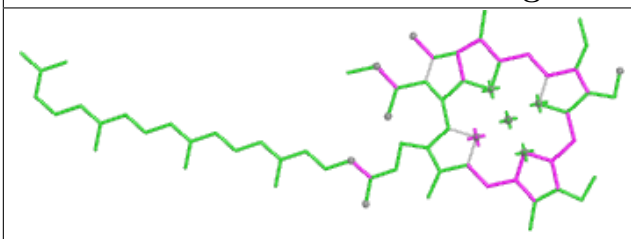


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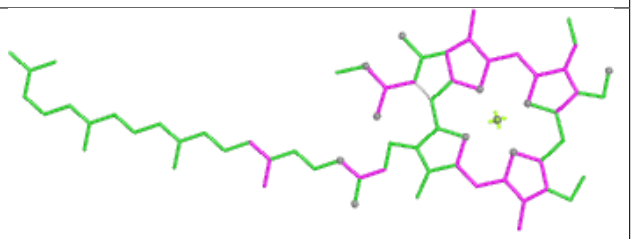


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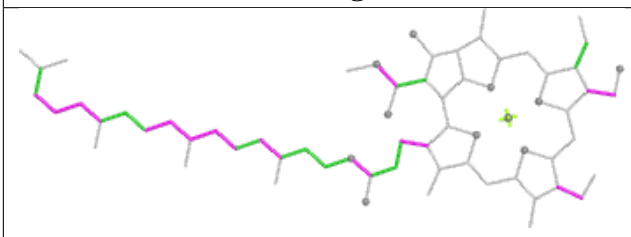
Ligand CHL U 317



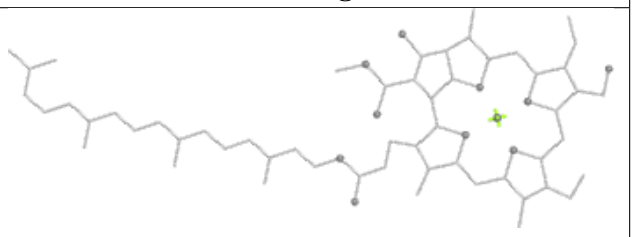
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Bond angles

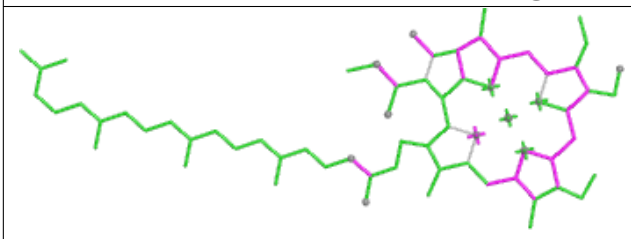


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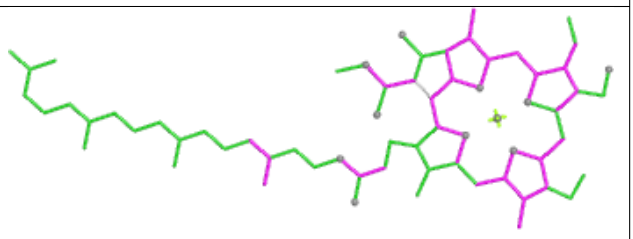


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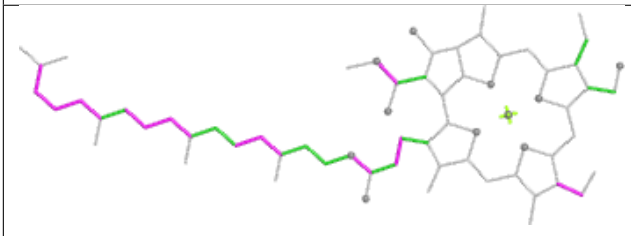
Ligand CHL 3 314



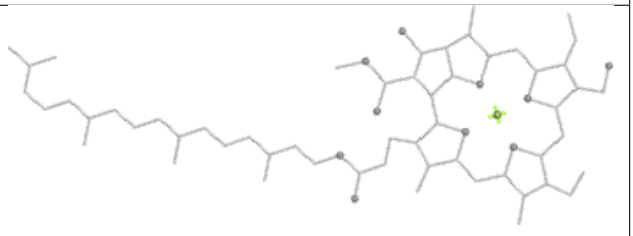
Bond lengths



Bond angles

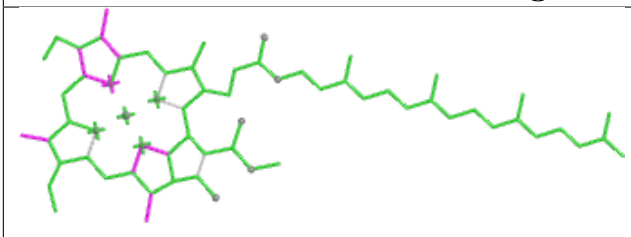


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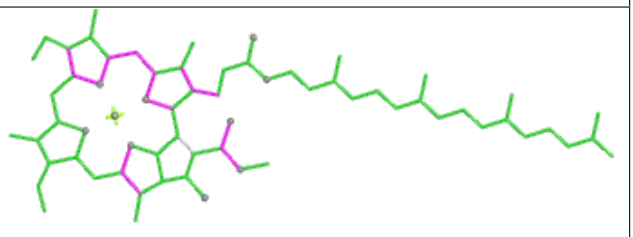


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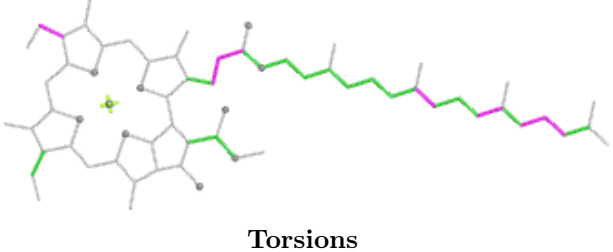
Ligand CLA c 502



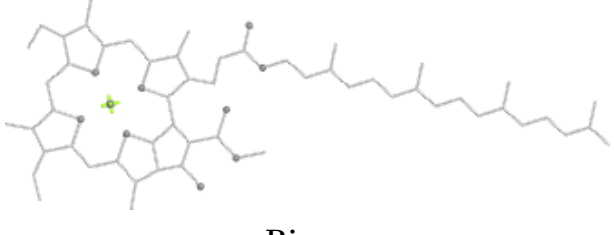
Bond lengths



Bond angles

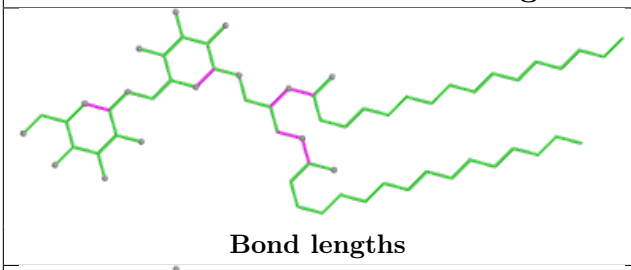


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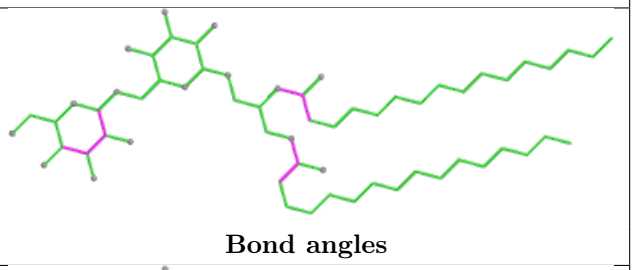


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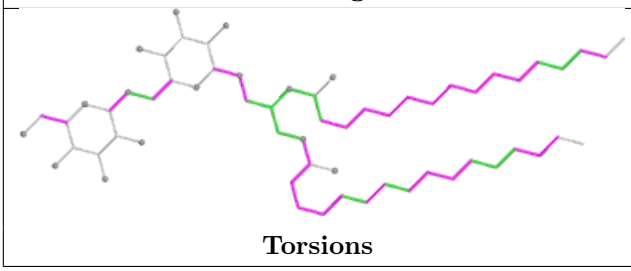
Ligand DGD C 520



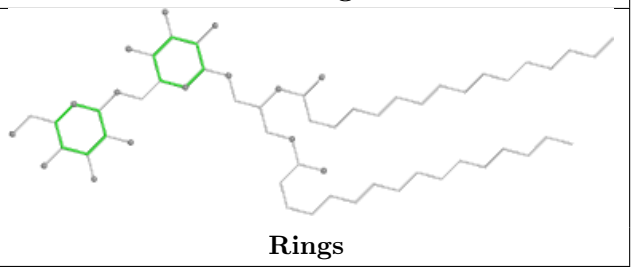
Bond lengths



Bond angles

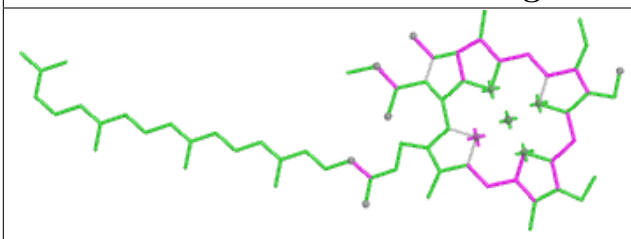


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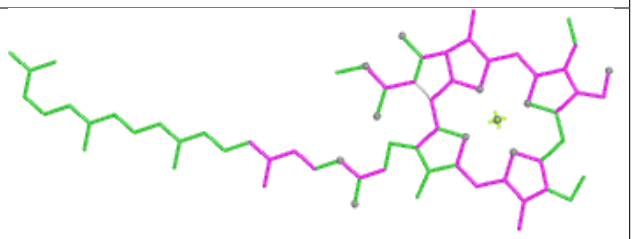


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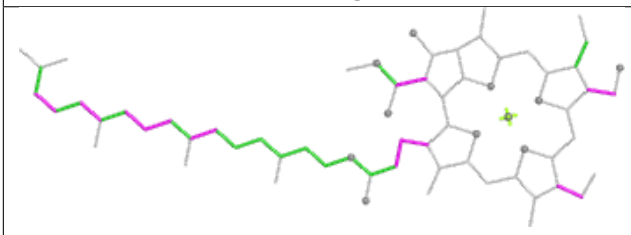
Ligand CHL U 315



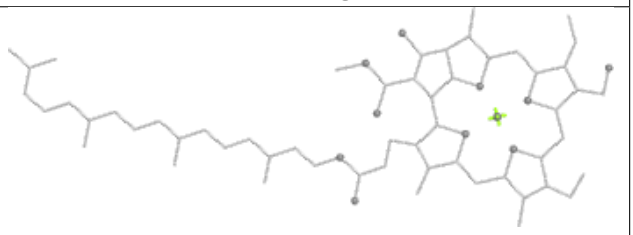
Bond lengths



Bond angles

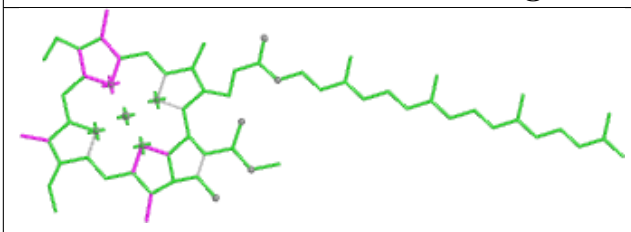


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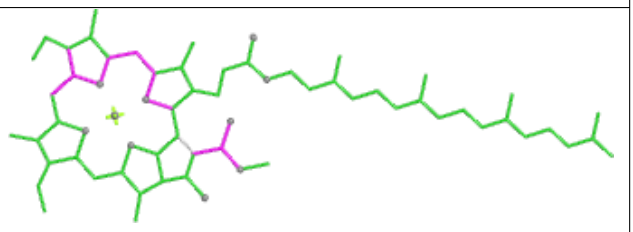


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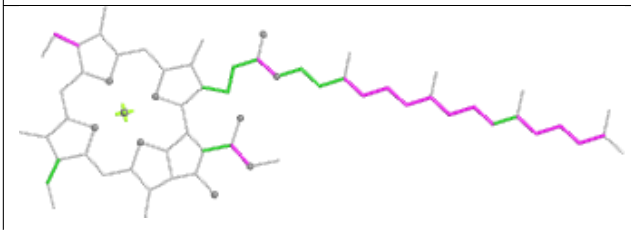
Ligand CLA C 508



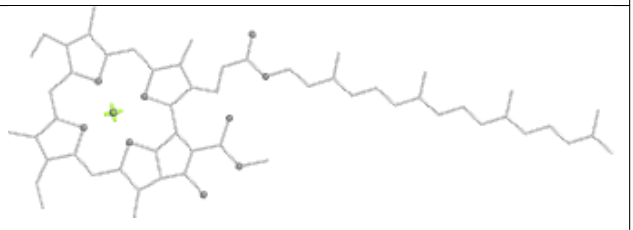
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Bond angles

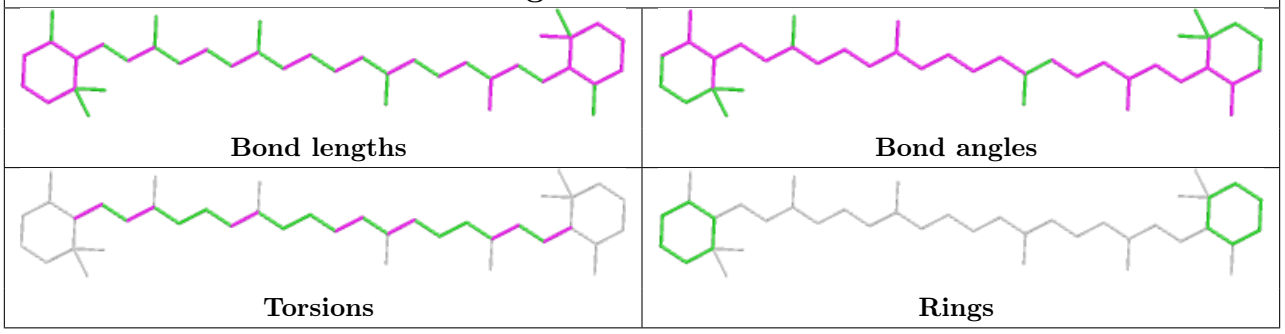


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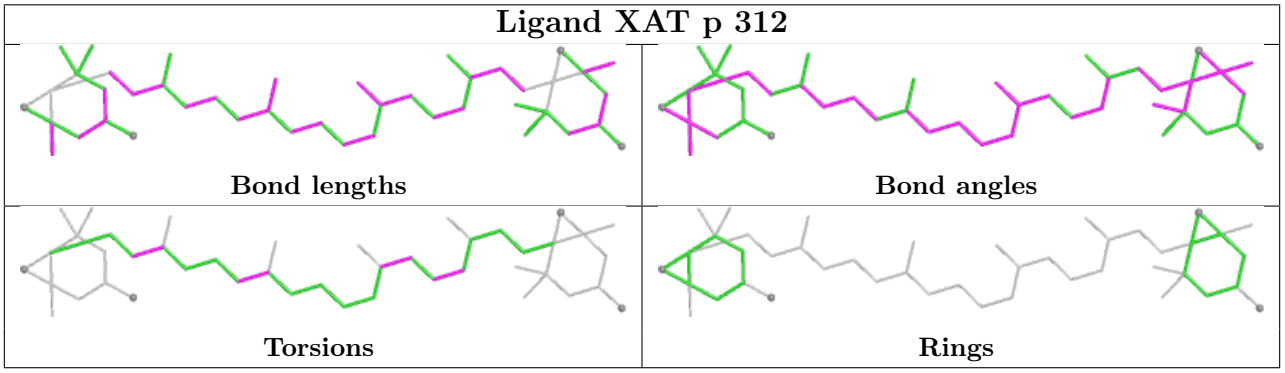


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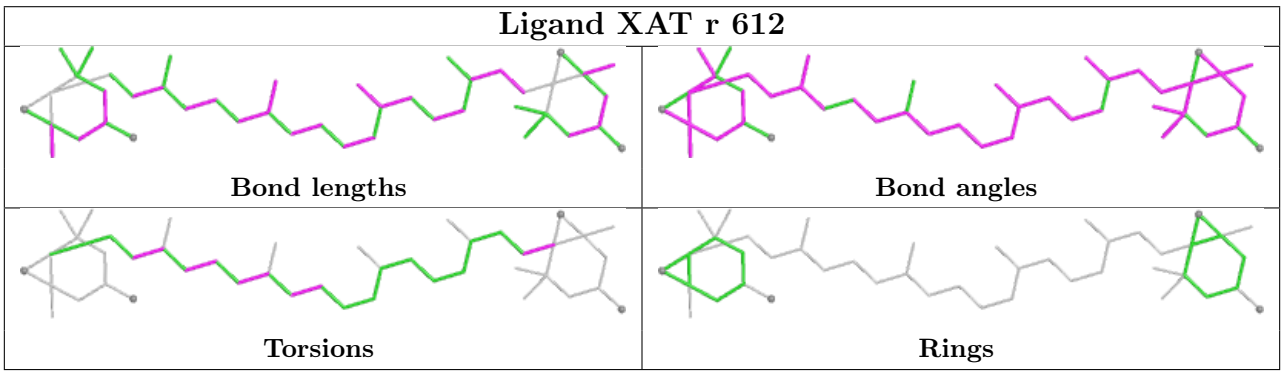
Ligand BCR d 403



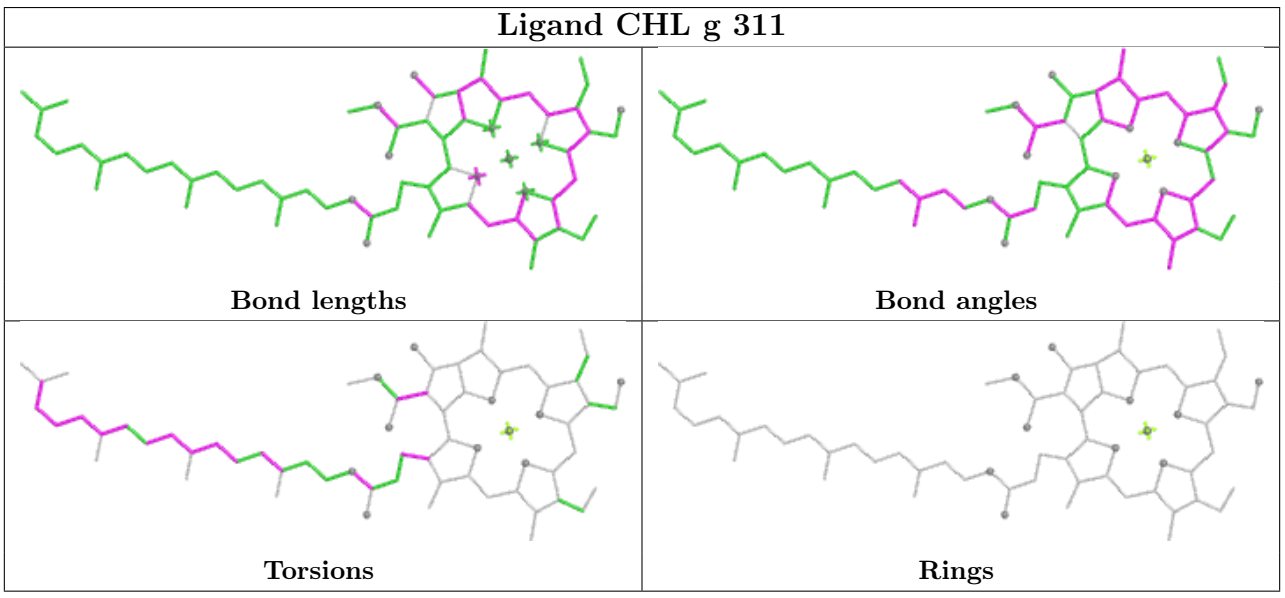
Ligand XAT p 312

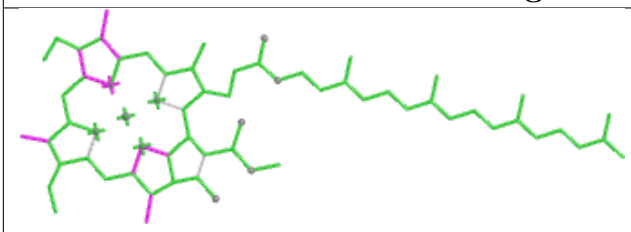
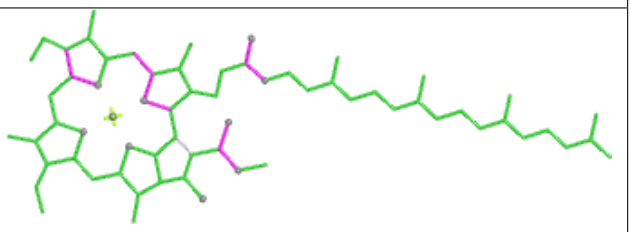
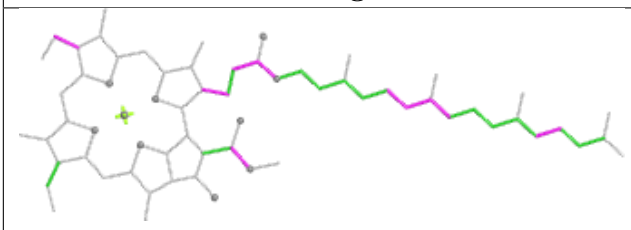
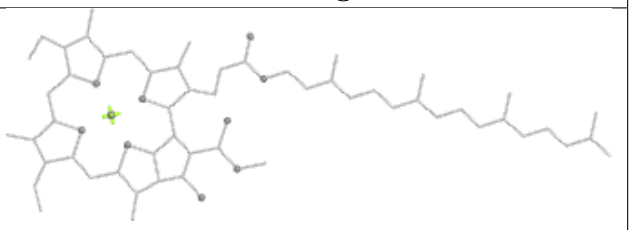


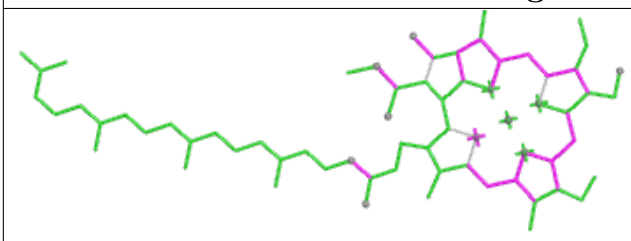
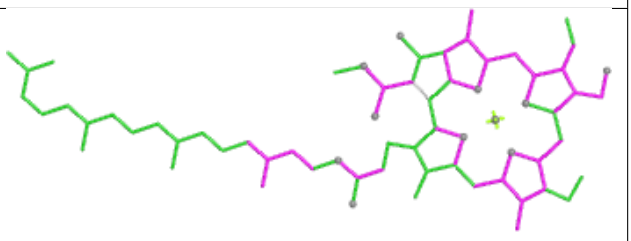
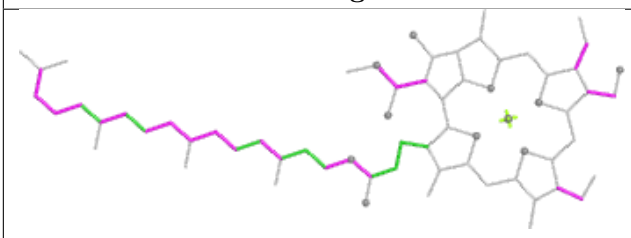
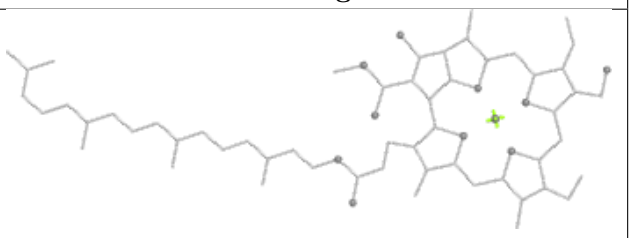
Ligand XAT r 612



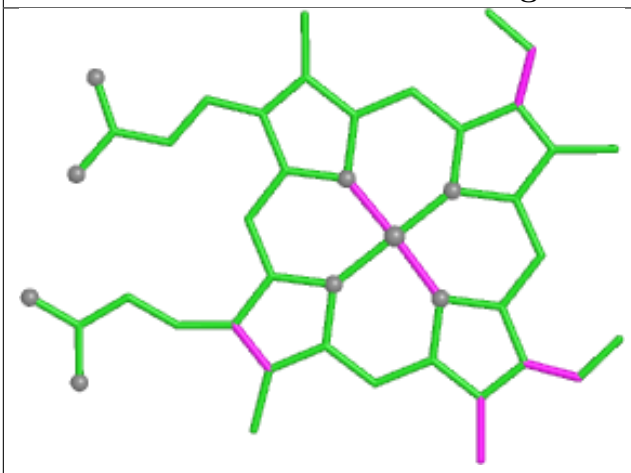
Ligand CHL g 311



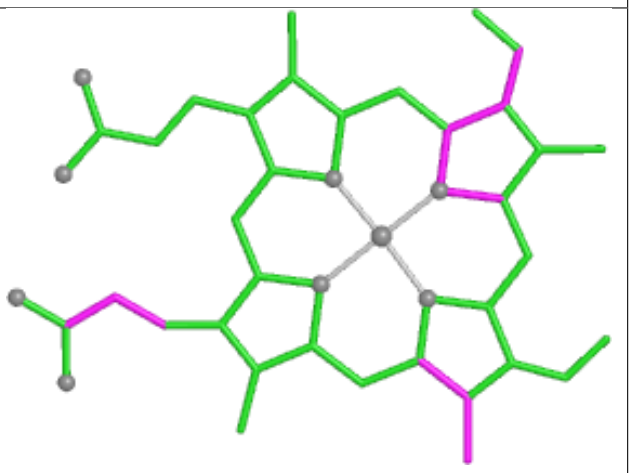
Ligand CLA P 303	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CHL n 318	
 Bond lengths	 Bond angles
 Torsions	 Rings

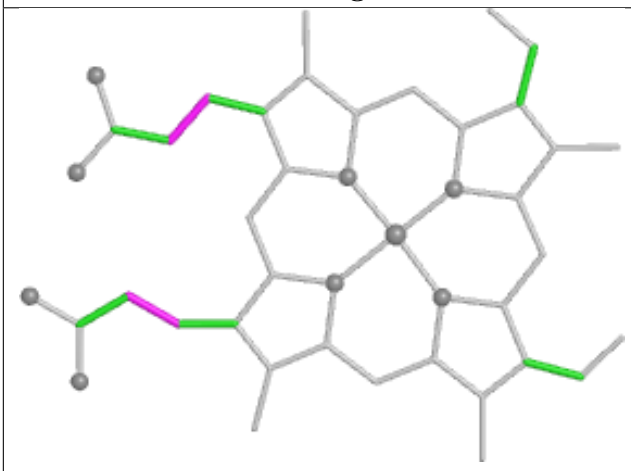
Ligand HEM E 101



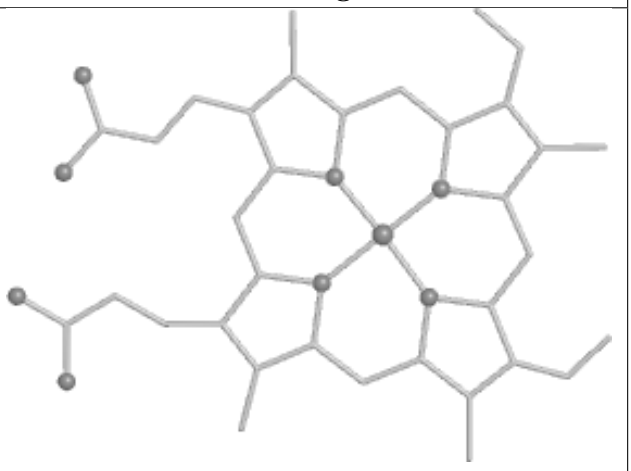
Bond lengths



Bond angles

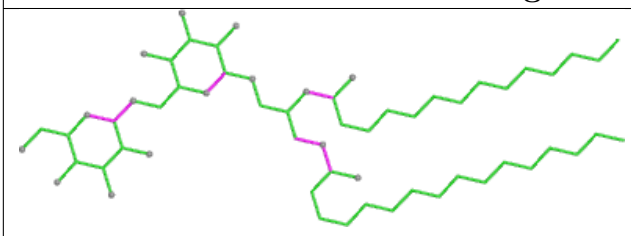


Torsions

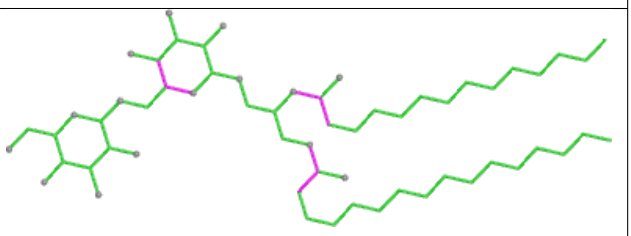


Rings

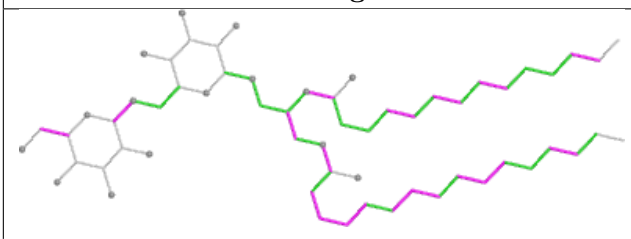
Ligand DGD J 101



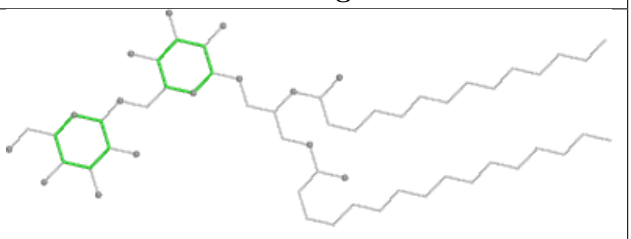
Bond lengths



Bond angles

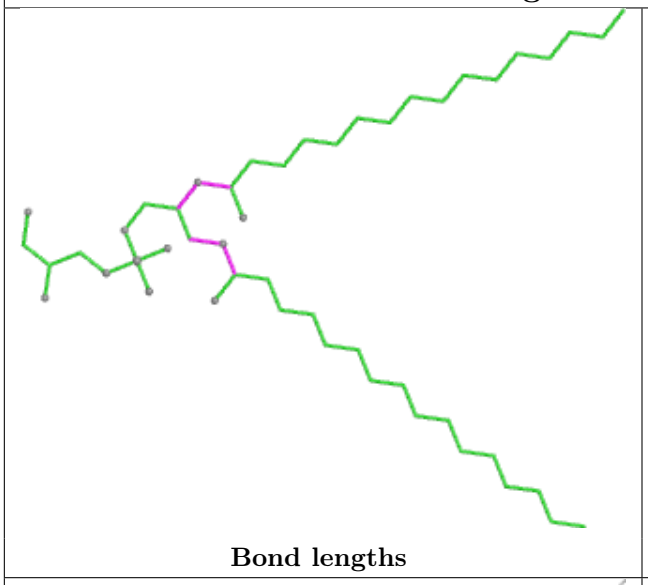


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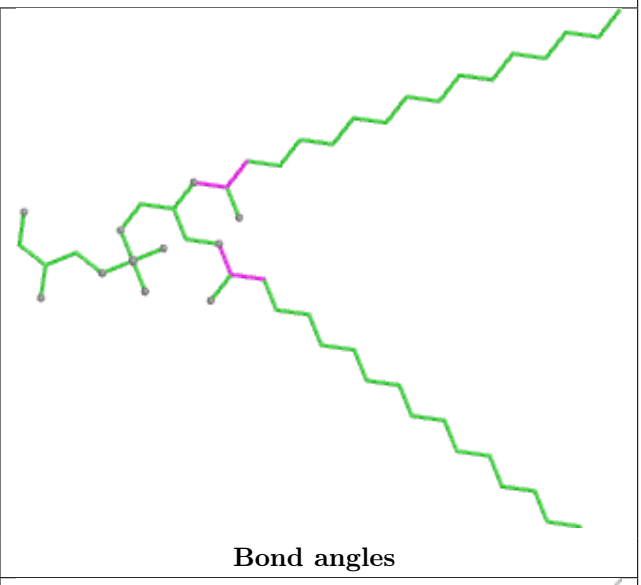


Rings

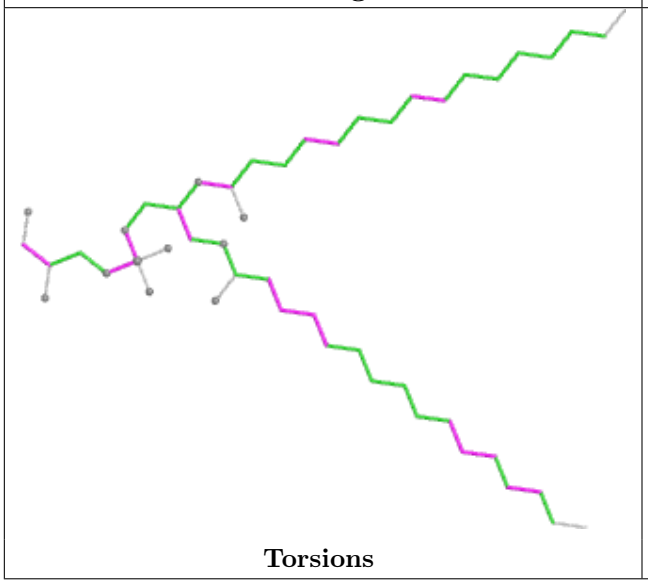
Ligand LHG V 312



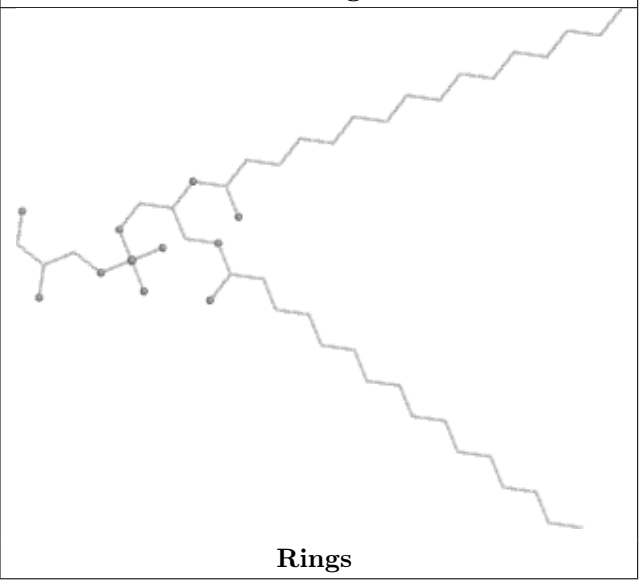
Bond lengths



Bond angles

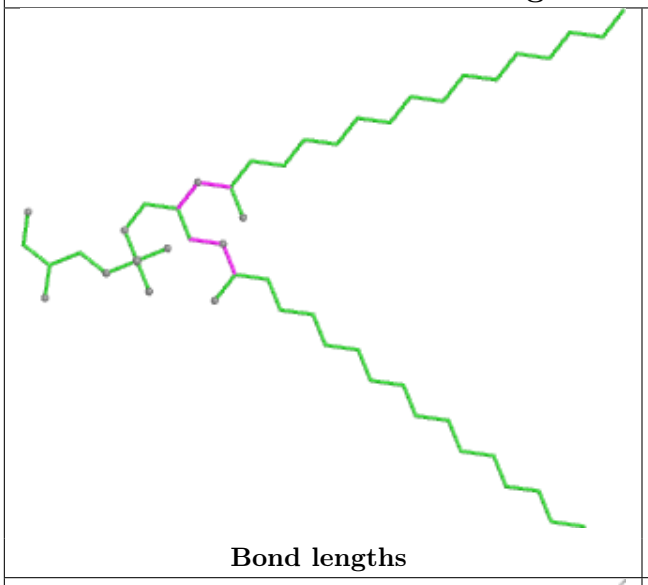


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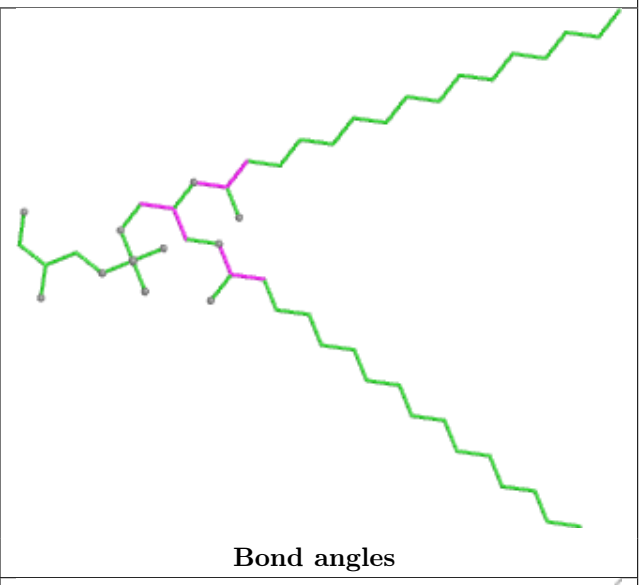


Rings

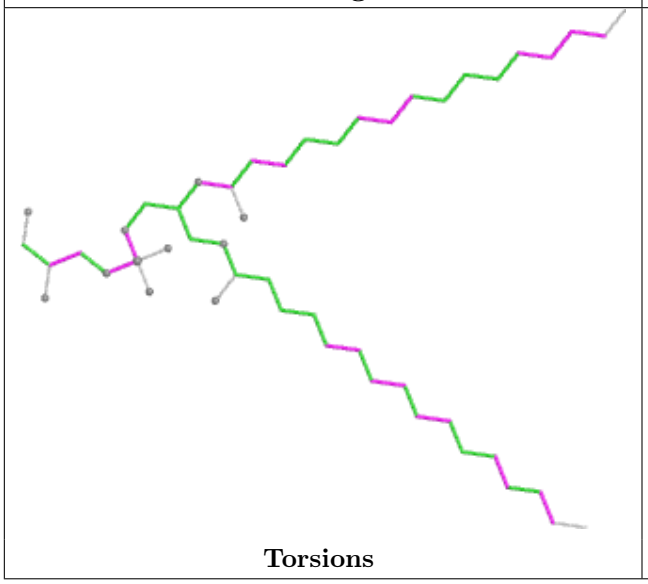
Ligand LHG d 406



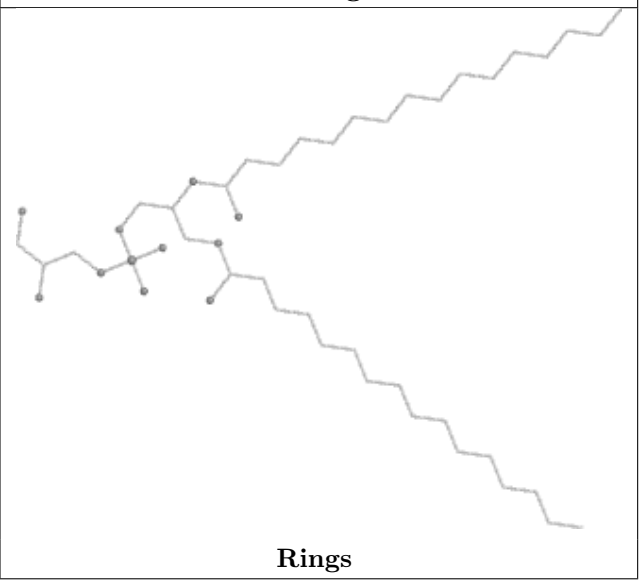
Bond lengths



Bond angles

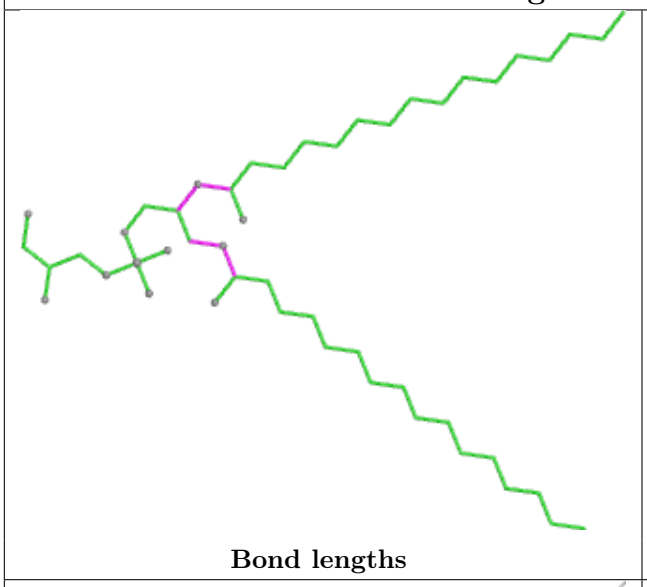


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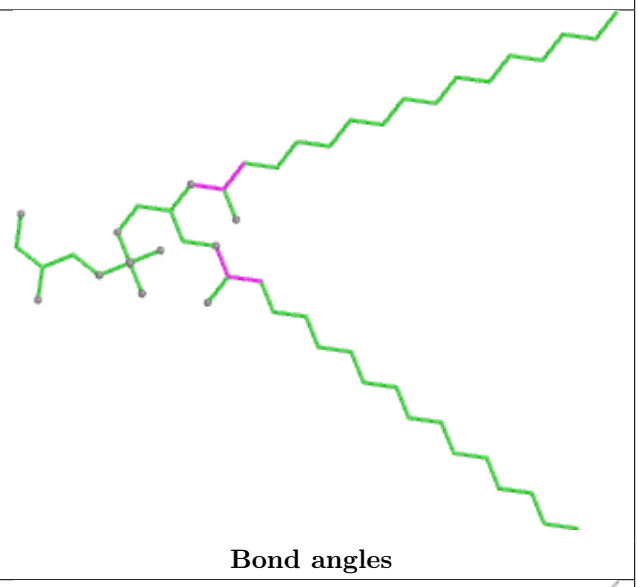


Rings

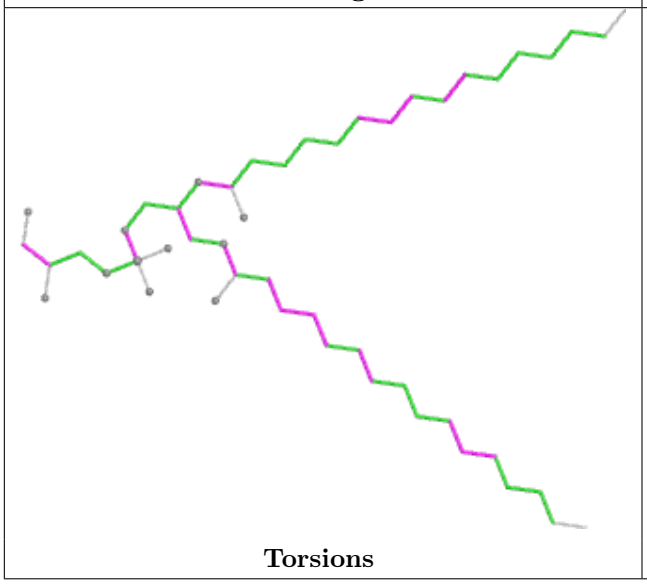
Ligand LHG 6 311



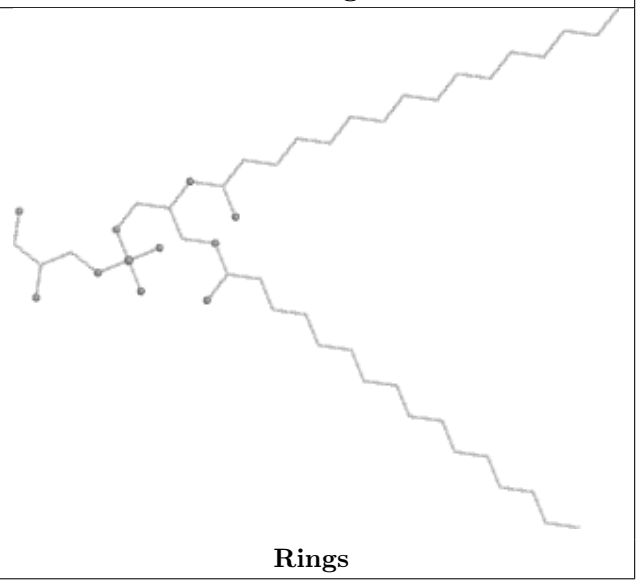
Bond lengths



Bond angles

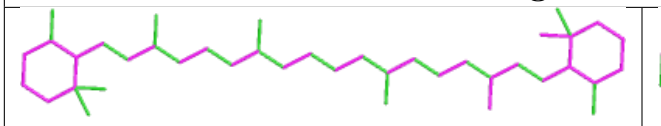


Torsions



Rings

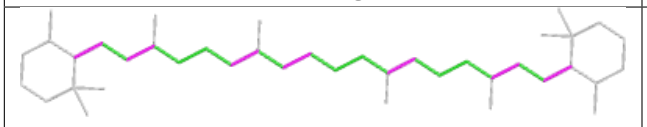
Ligand BCR t 101



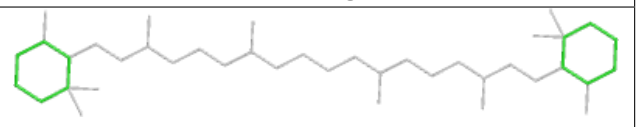
Bond lengths



Bond angles

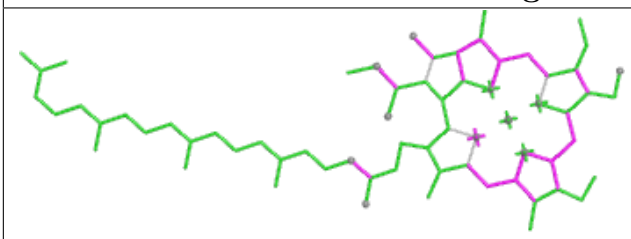


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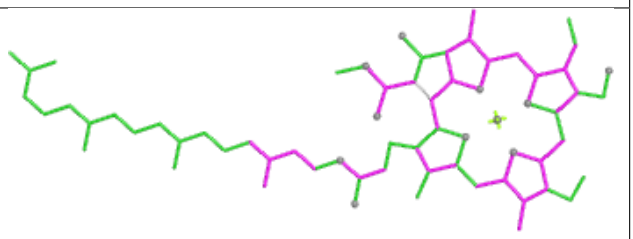


Rings

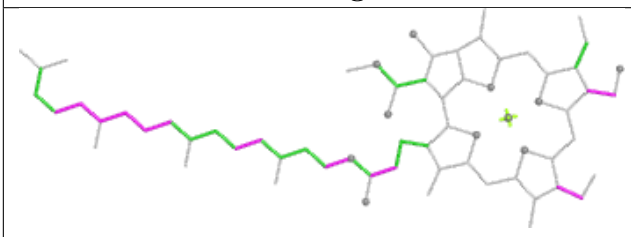
Ligand CHL N 313



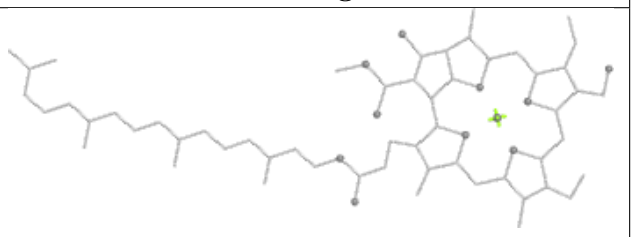
Bond lengths



Bond angles

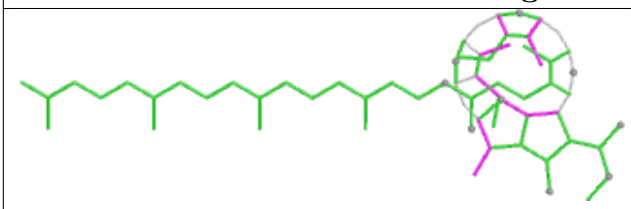


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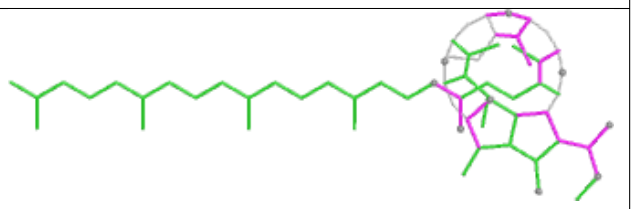


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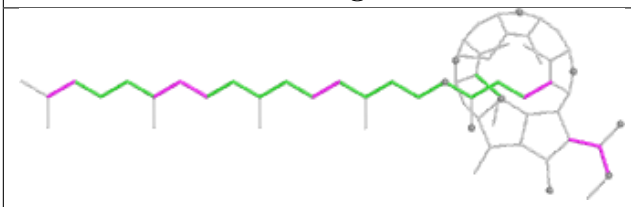
Ligand PHO D 401



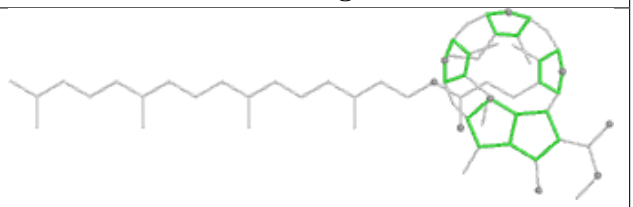
Bond lengths



Bond angles

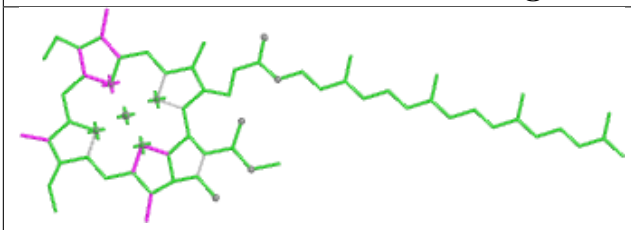


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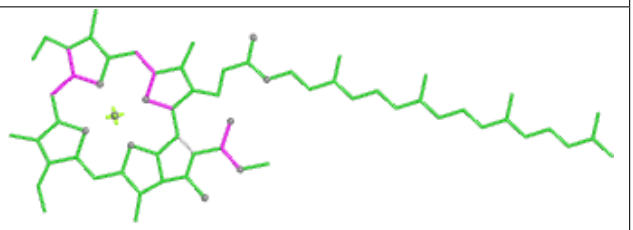


Rings

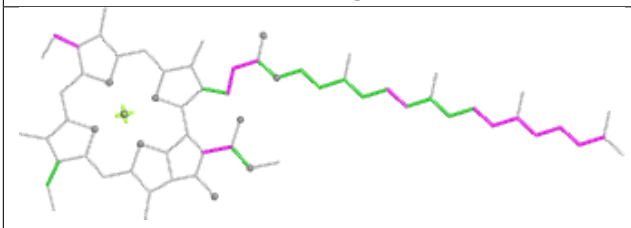
Ligand CLA B 603



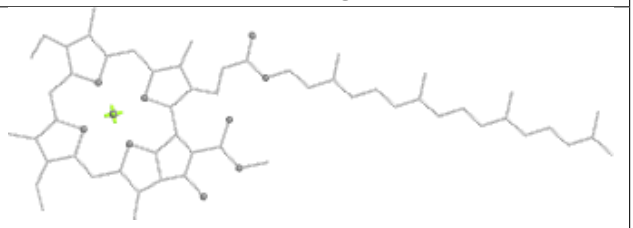
Bond lengths



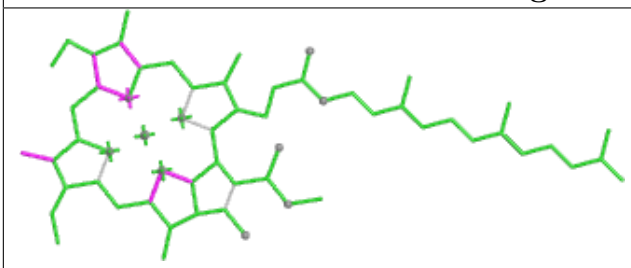
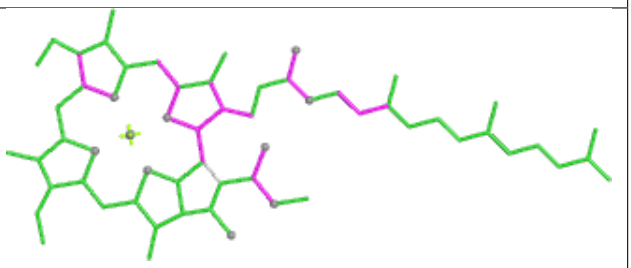
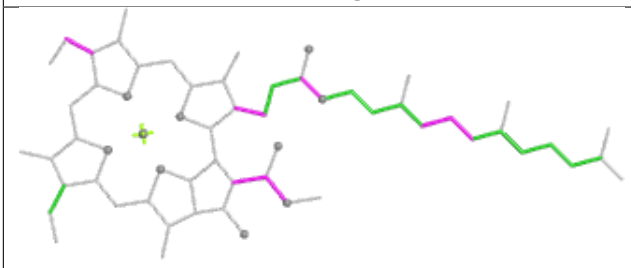
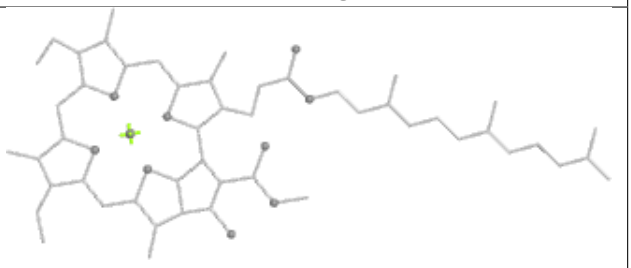
Bond angles

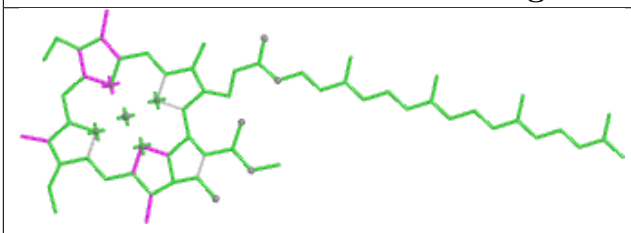
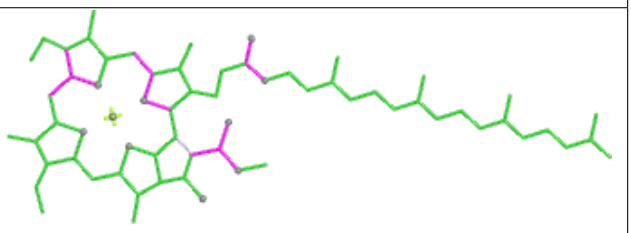
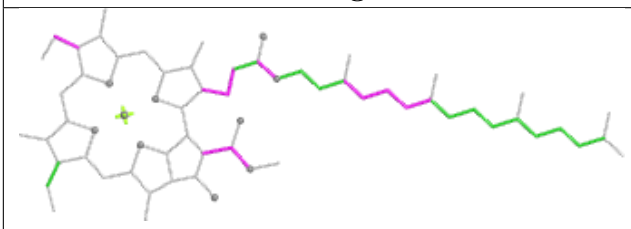
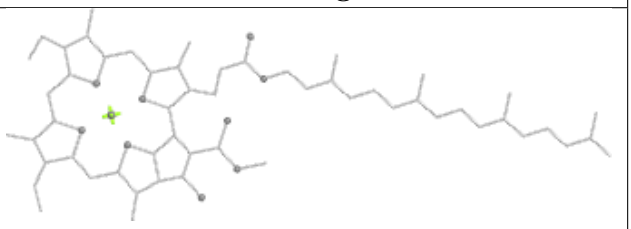


Torsions

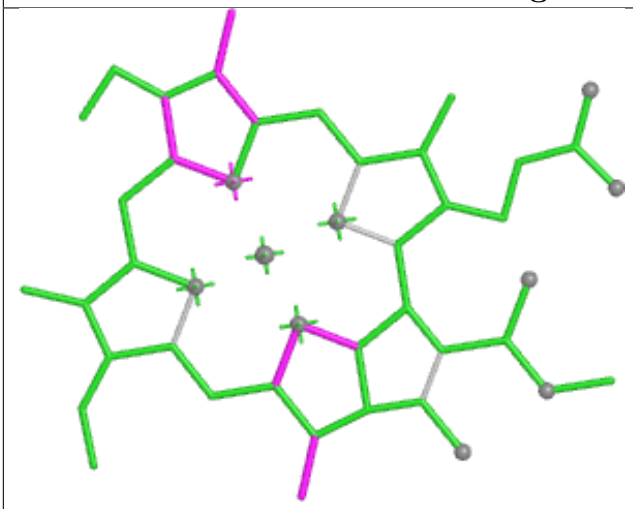


Rings

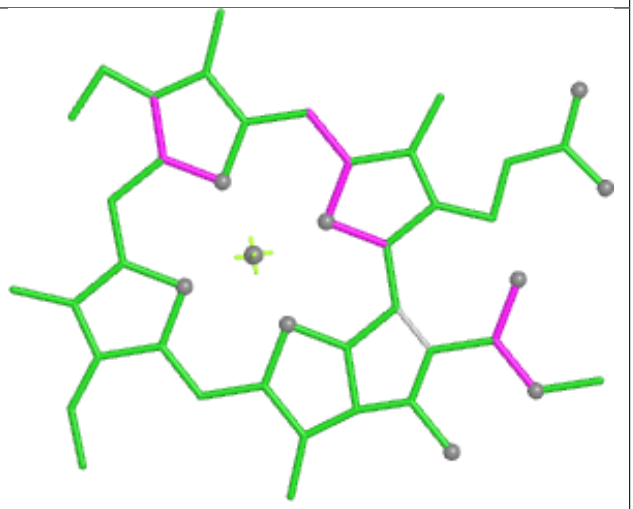
Ligand CLA r 609	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

Ligand CLA b 607	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

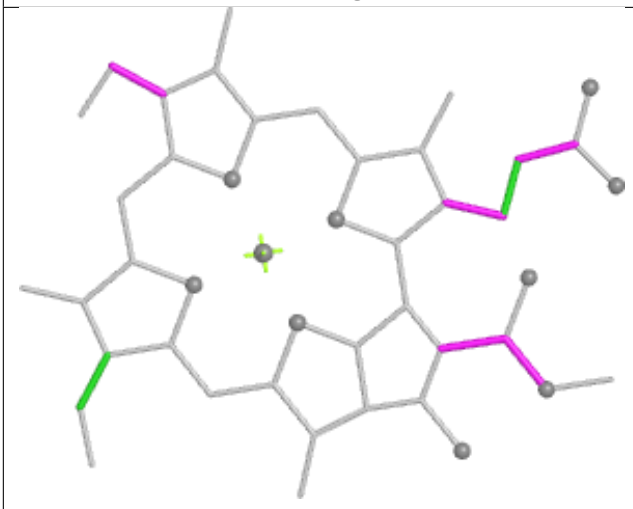
Ligand CLA r 610



Bond lengths



Bond angles

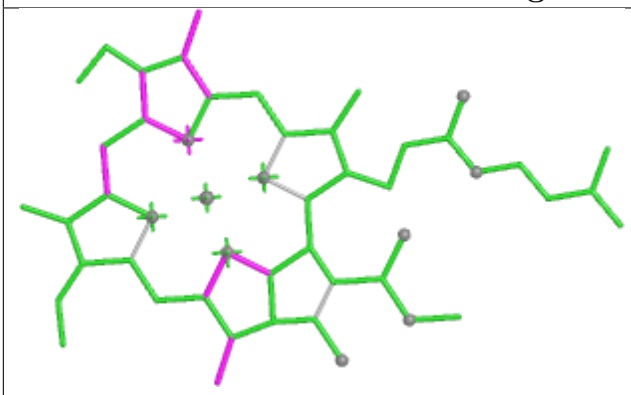


Torsions

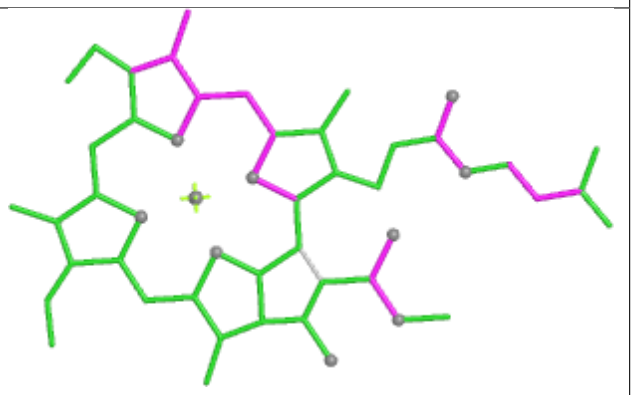


Rings

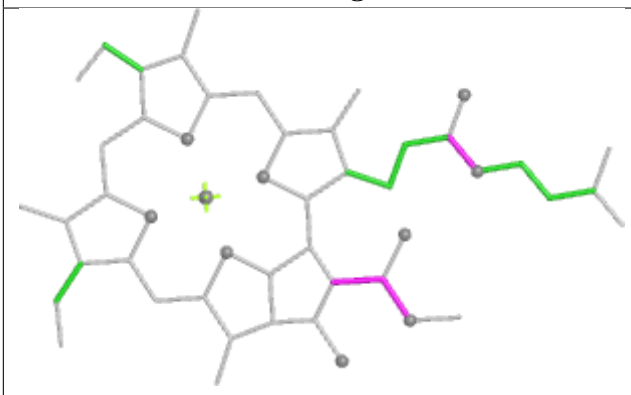
Ligand CLA n 303



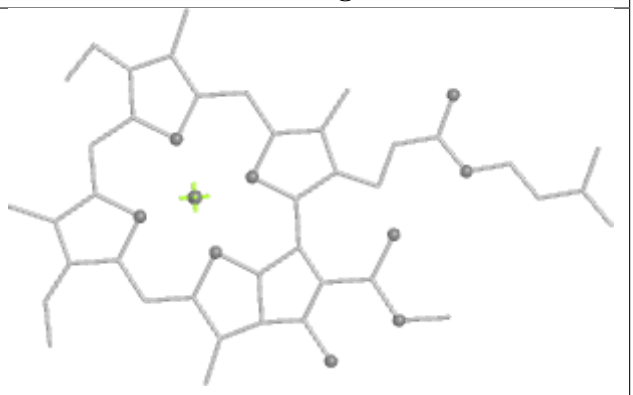
Bond lengths



Bond angles

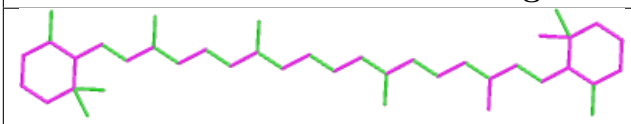


Torsions

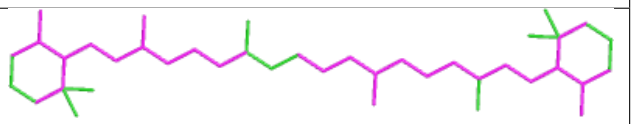


Rings

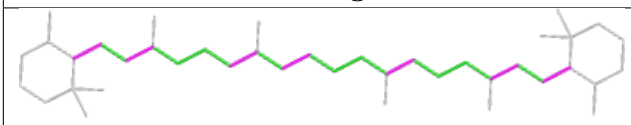
Ligand BCR T 101



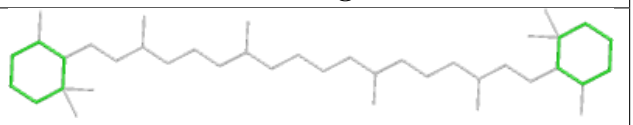
Bond lengths



Bond angles

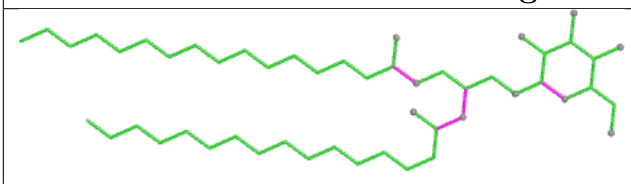


Torsions

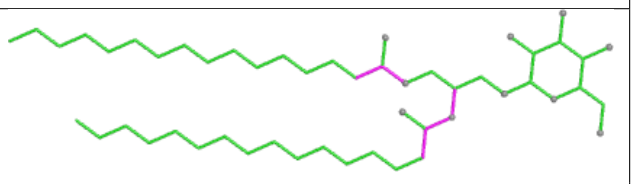


Rings

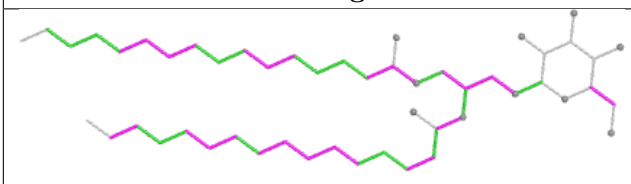
Ligand LMG C 502



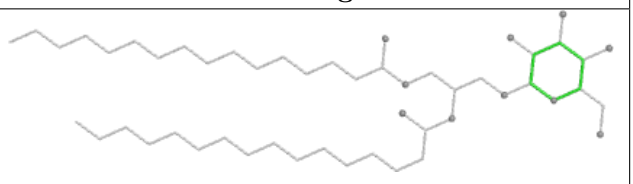
Bond lengths



Bond angles

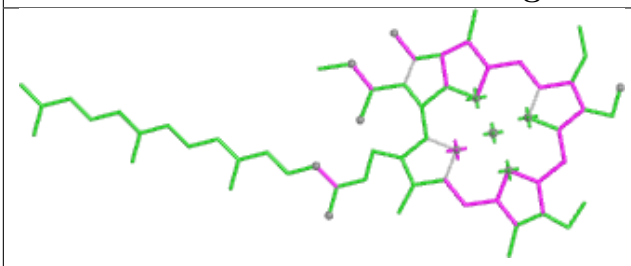


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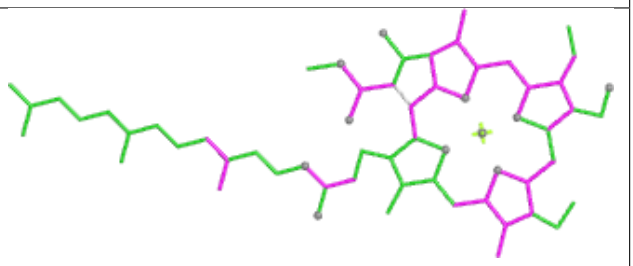


Rings

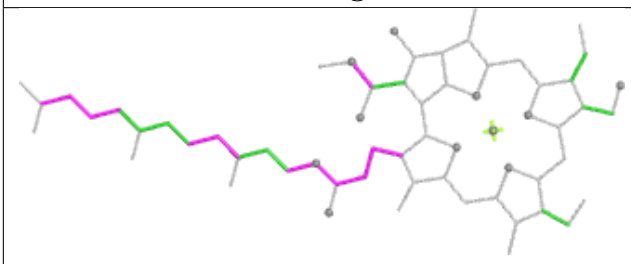
Ligand CHL R 317



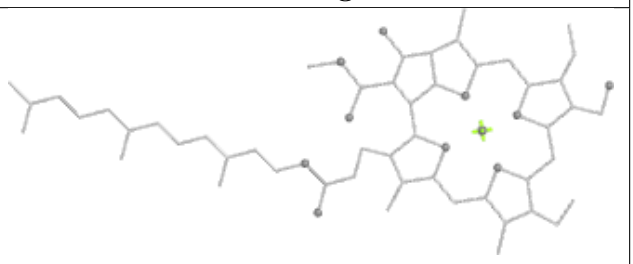
Bond lengths



Bond angles

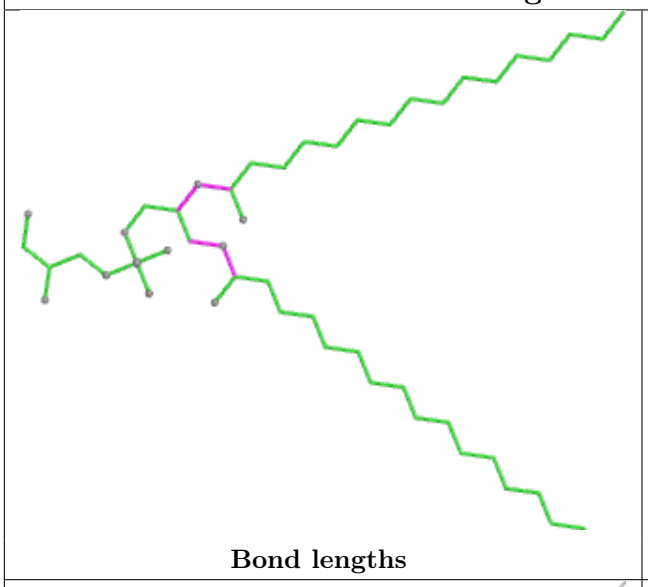


Torsions

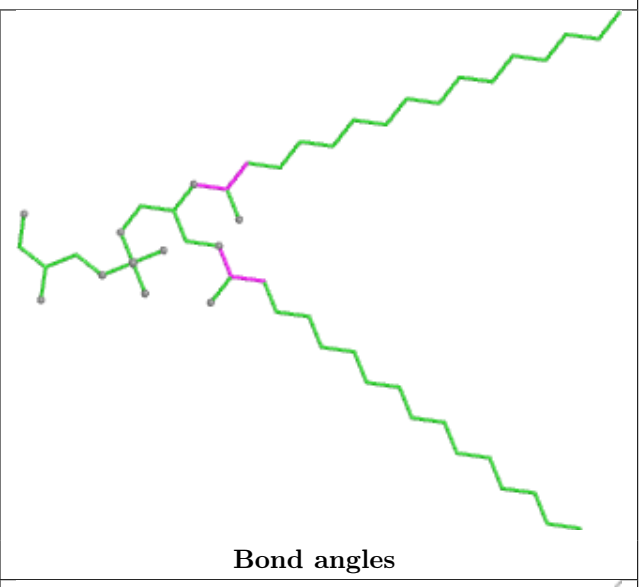


Rings

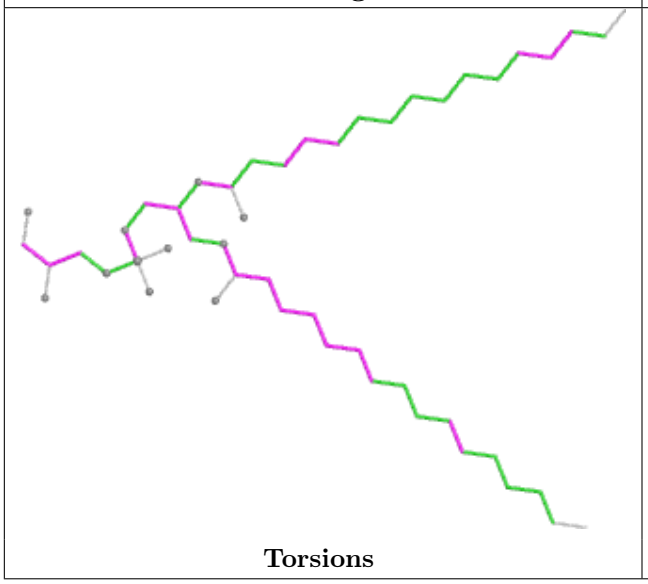
Ligand LHG P 313



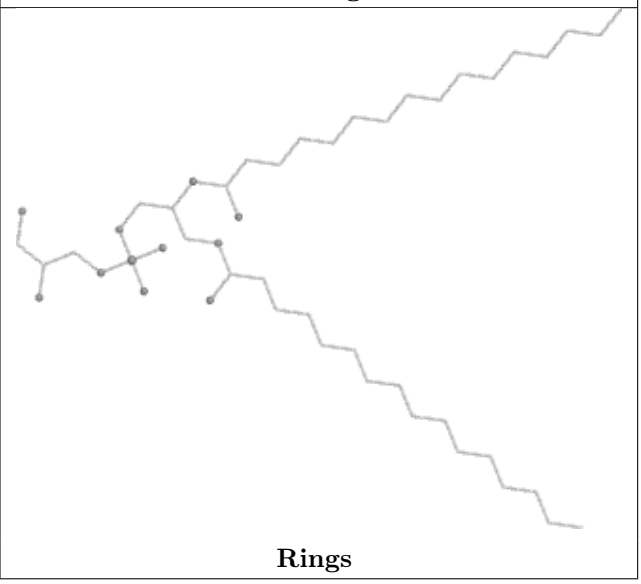
Bond lengths



Bond angles

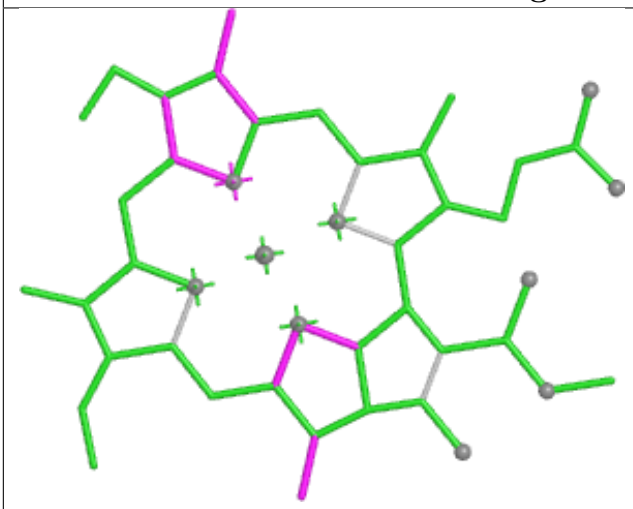


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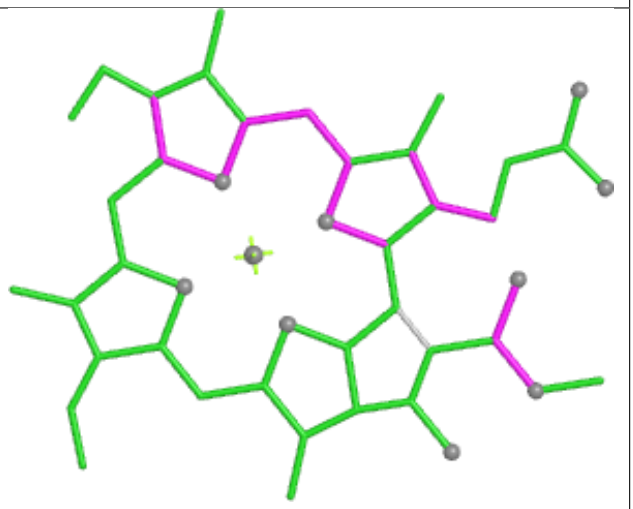


Rings

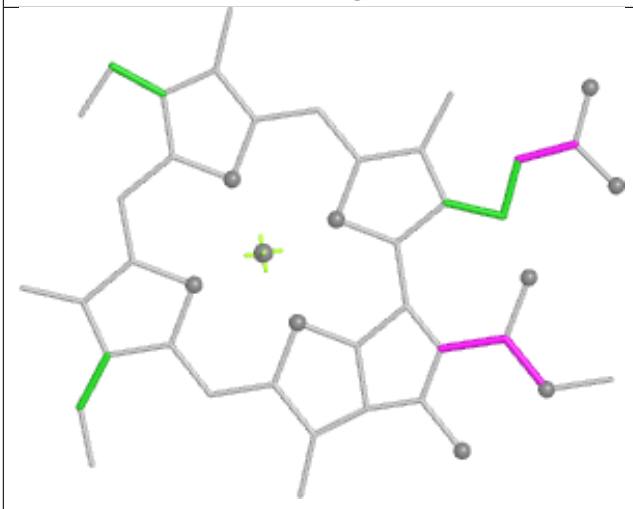
Ligand CLA s 302



Bond lengths



Bond angles

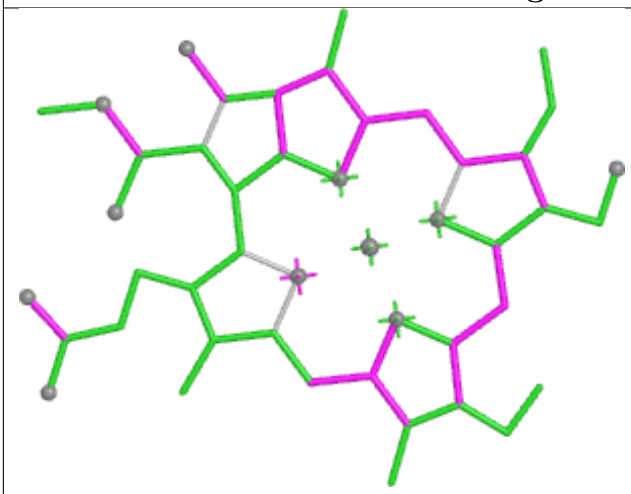


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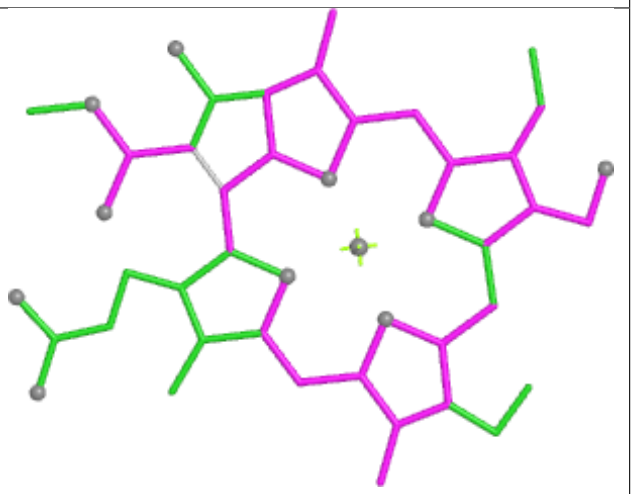


Rings

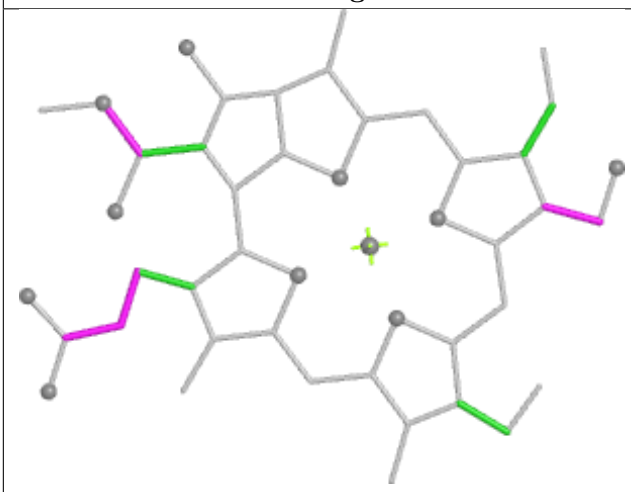
Ligand CHL S 313



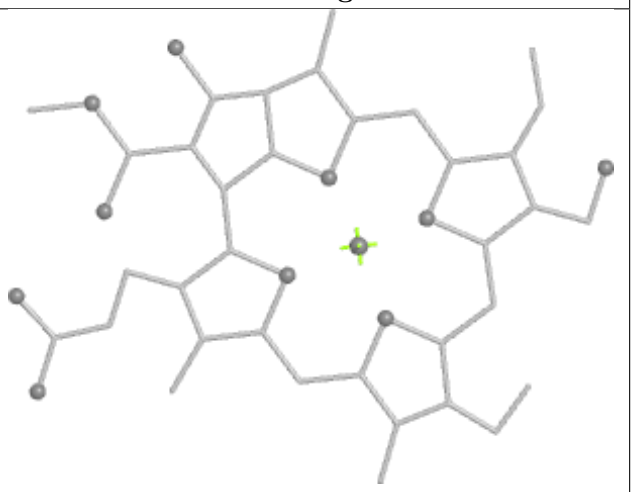
Bond lengths



Bond angles

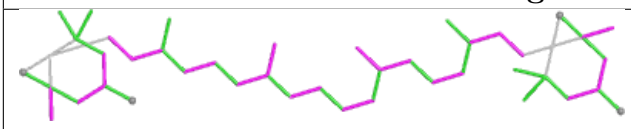


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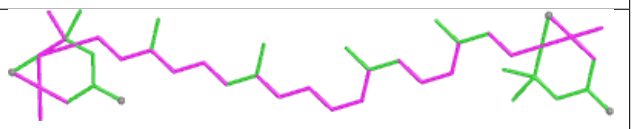


Rings

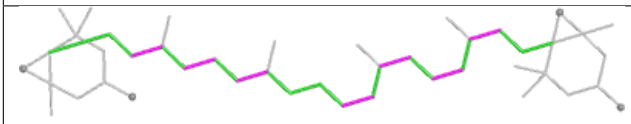
Ligand XAT v 311



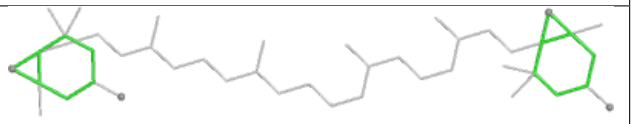
Bond lengths



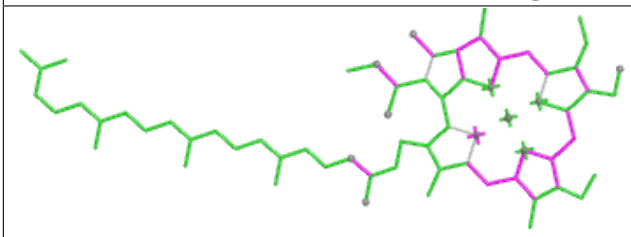
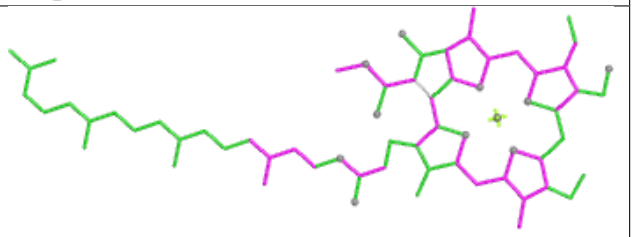
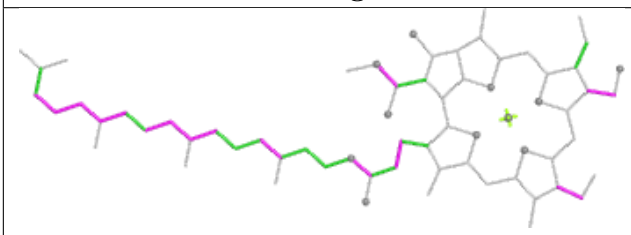
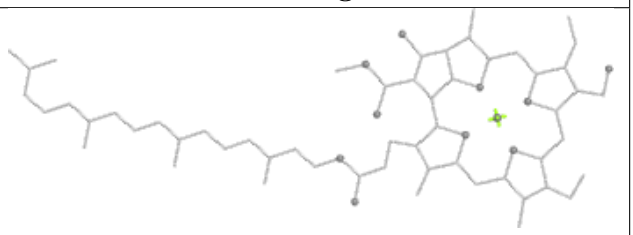
Bond angles

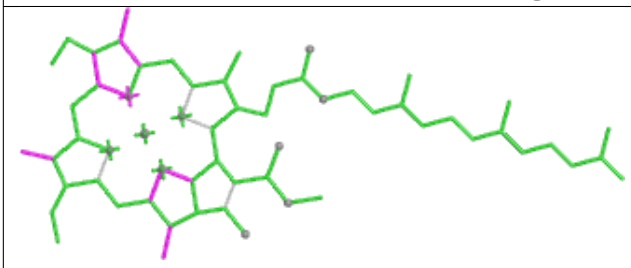
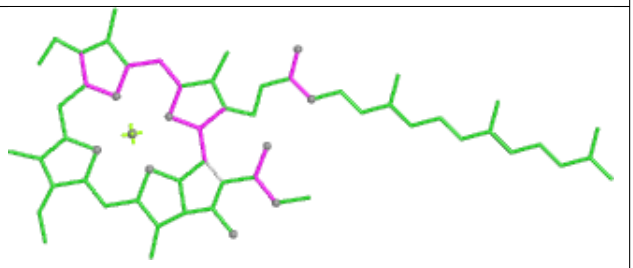
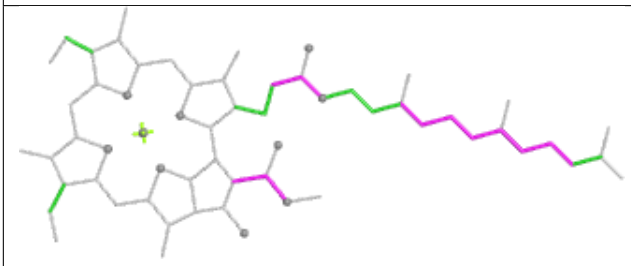
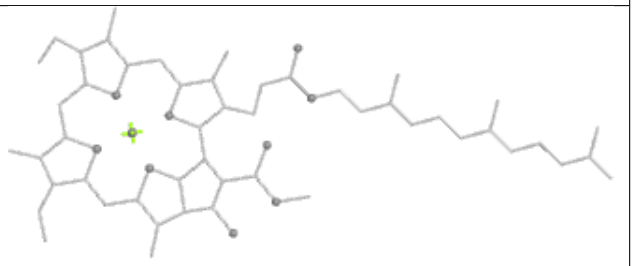


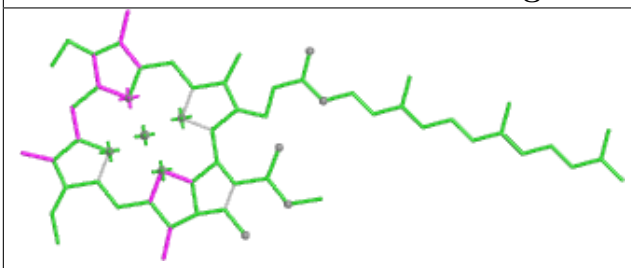
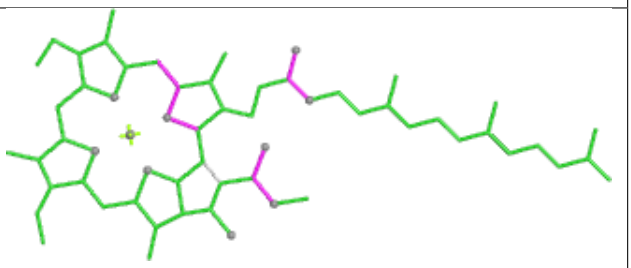
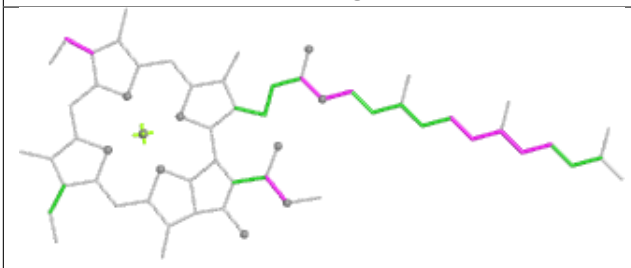
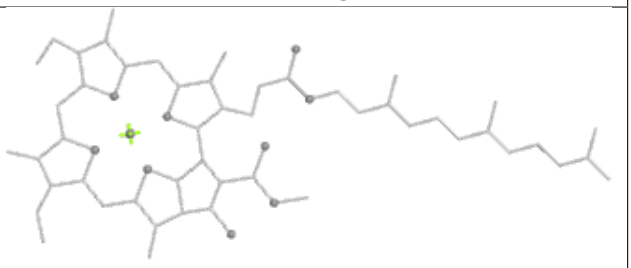
Torsions

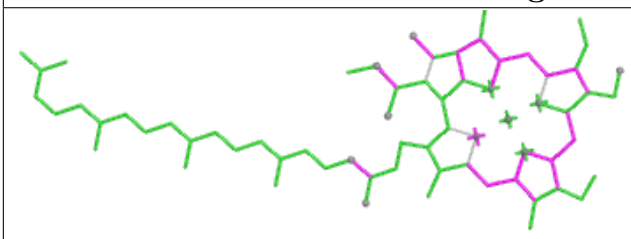
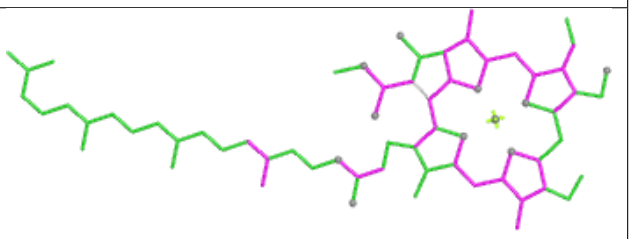
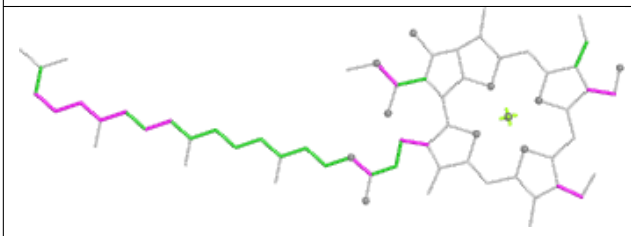
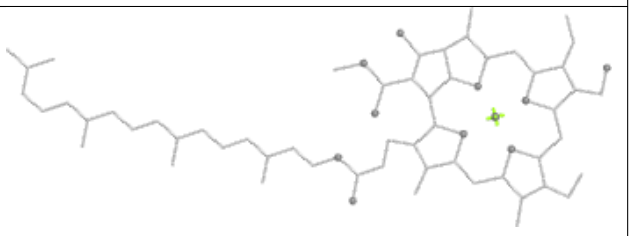


Rings

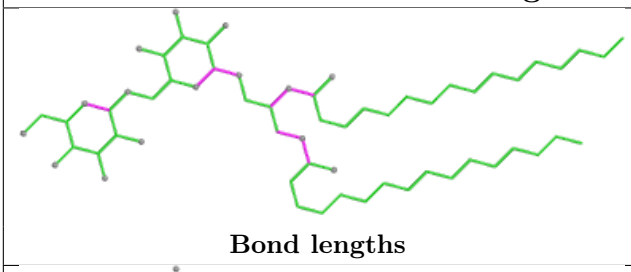
Ligand CHL p 320	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA 4 306	
 Bond lengths	 Bond angles
 Torsions	 Rings

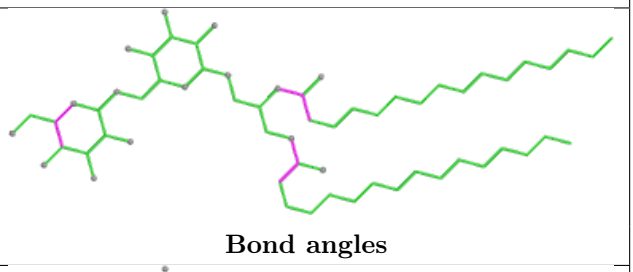
Ligand CLA U 305	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

Ligand CHL 4 317	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

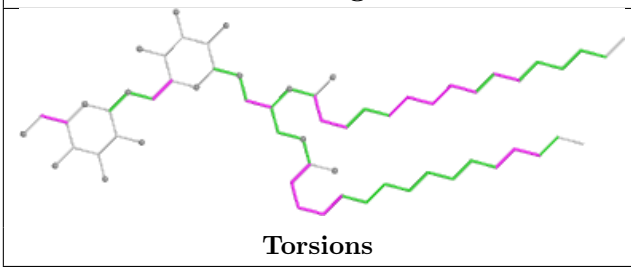
Ligand DGD b 601



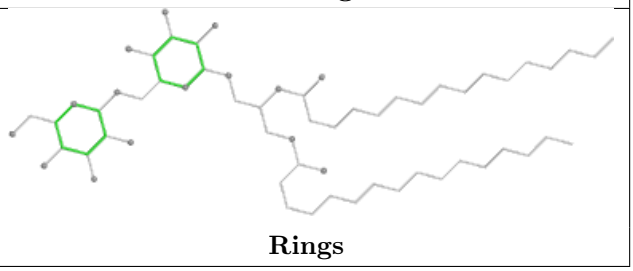
Bond lengths



Bond angles

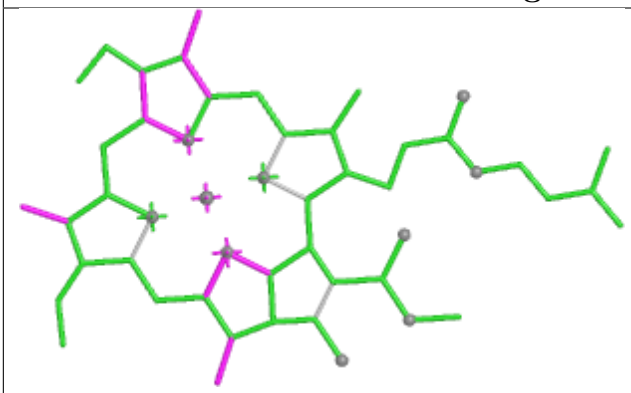


Torsions

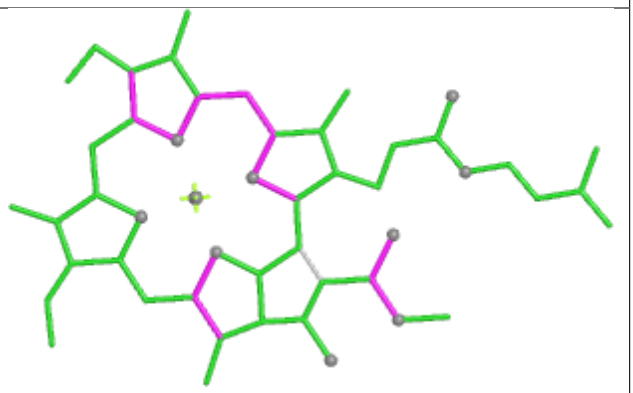


Rings

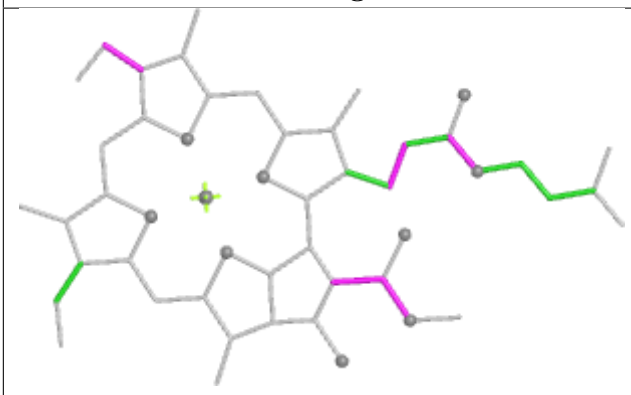
Ligand CLA A 406



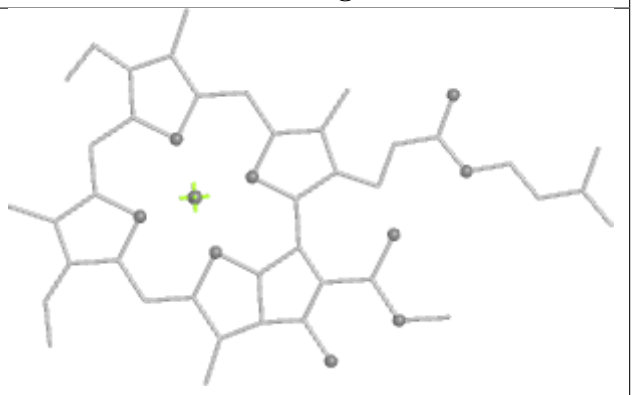
Bond lengths



Bond angles

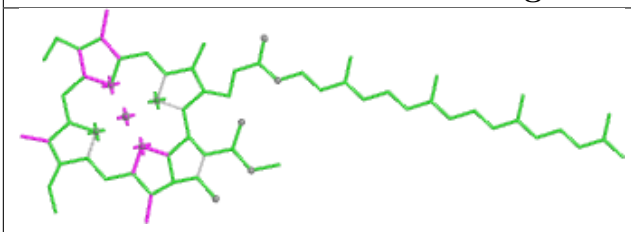


Torsions

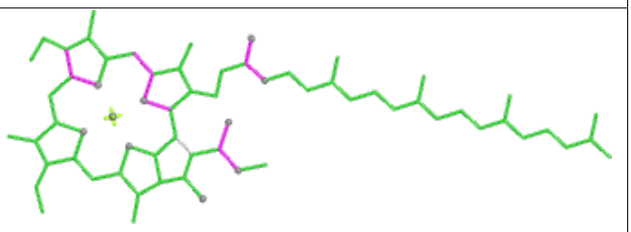


Rings

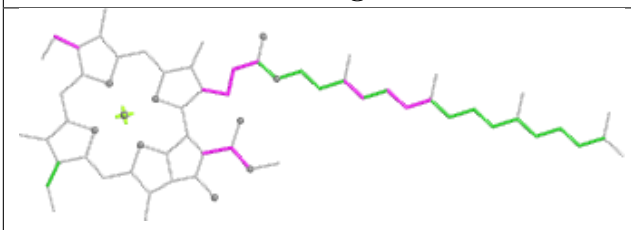
Ligand CLA C 514



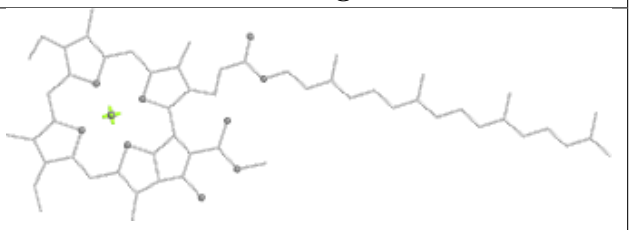
Bond lengths



Bond angles



Torsions

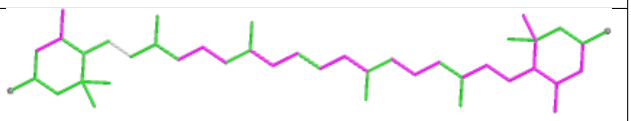


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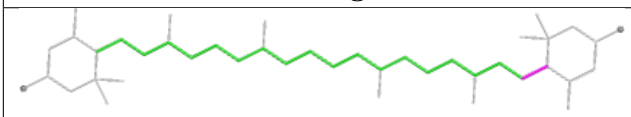
Ligand LUT u 309



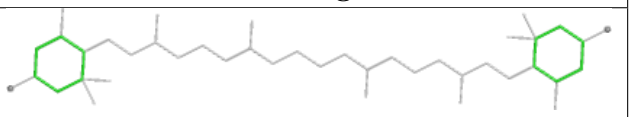
Bond lengths



Bond angles

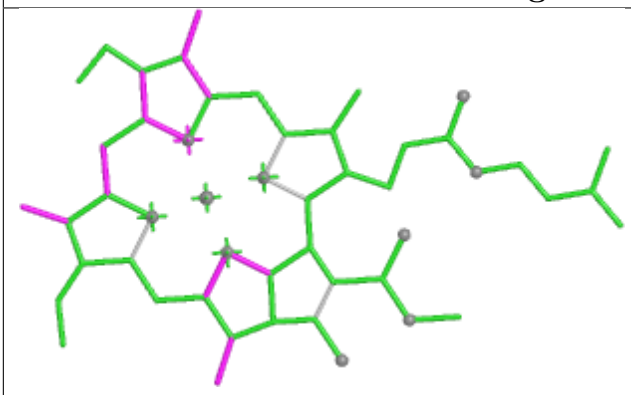


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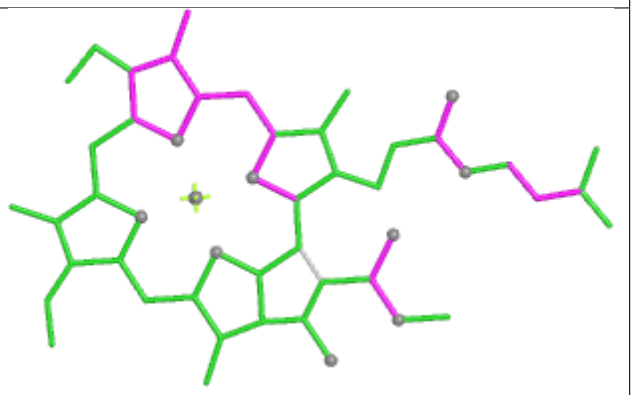


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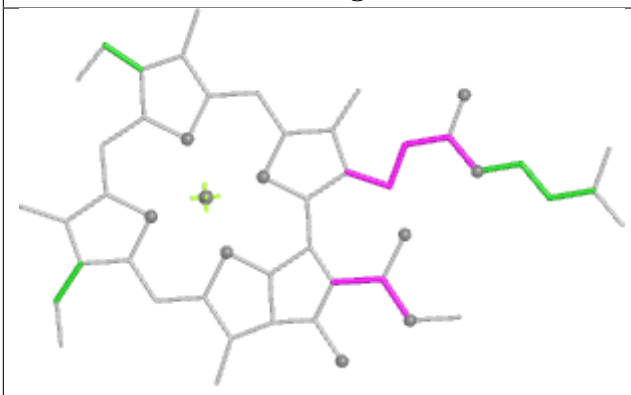
Ligand CLA 6 304



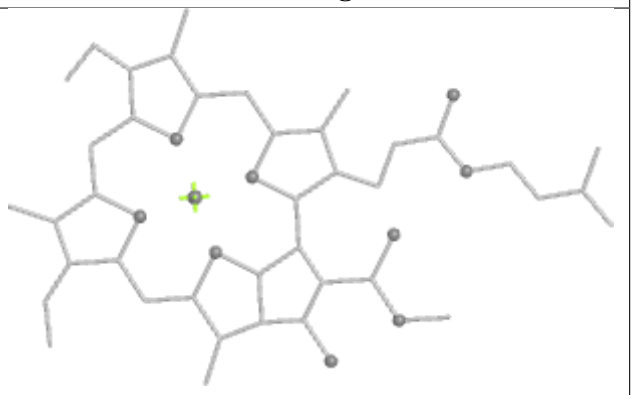
Bond lengths



Bond angles

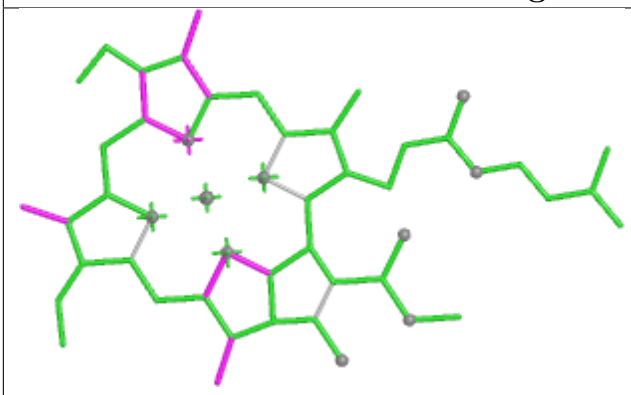


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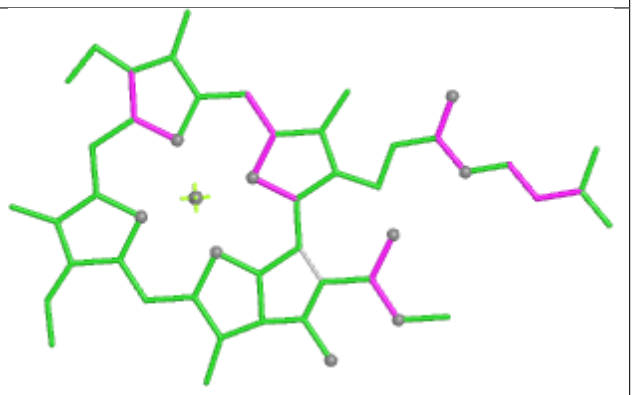


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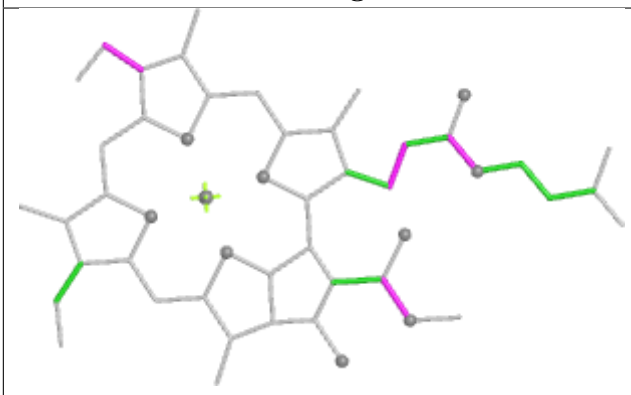
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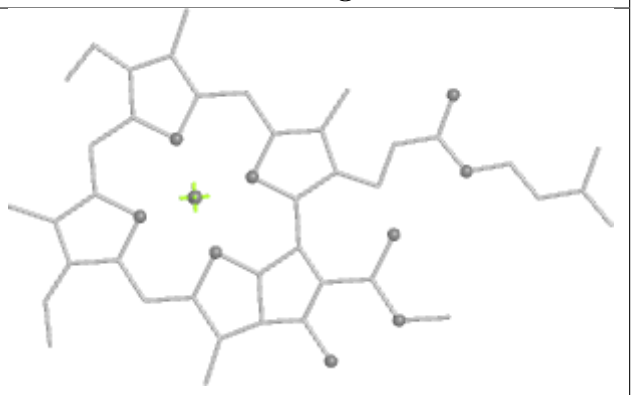
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Bond angles

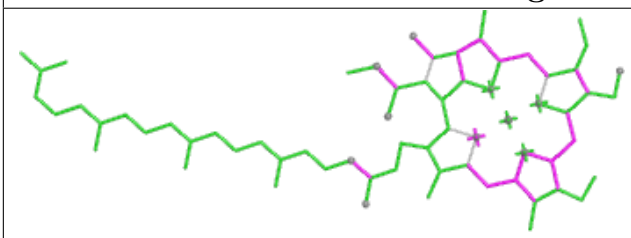


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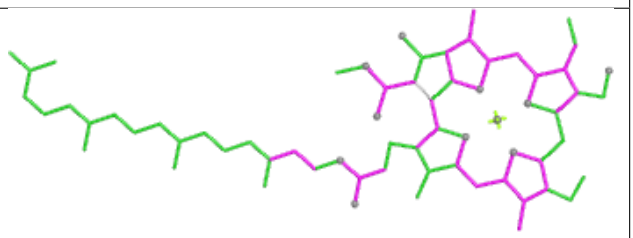


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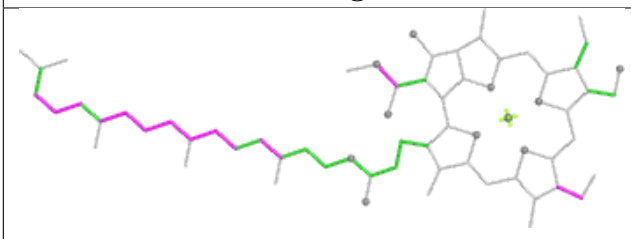
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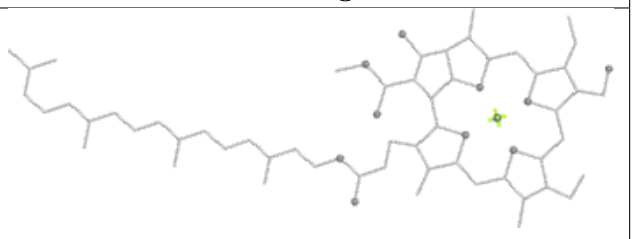
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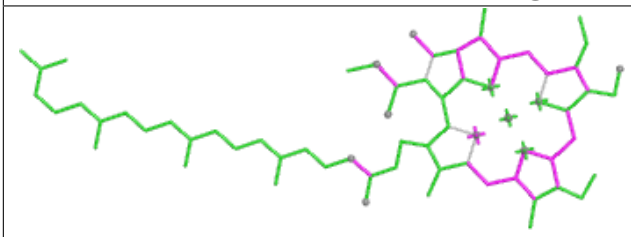
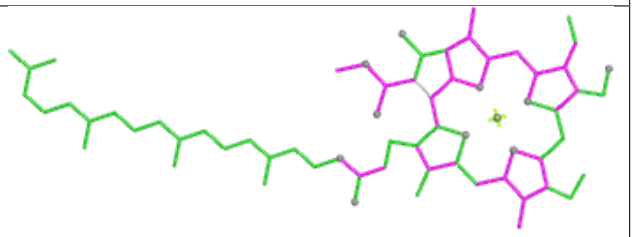
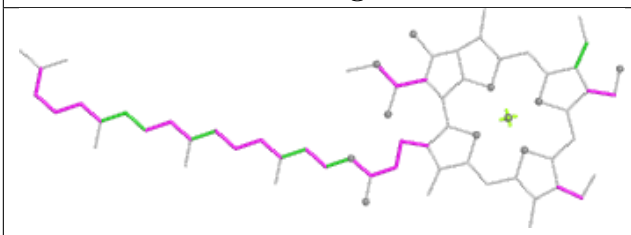
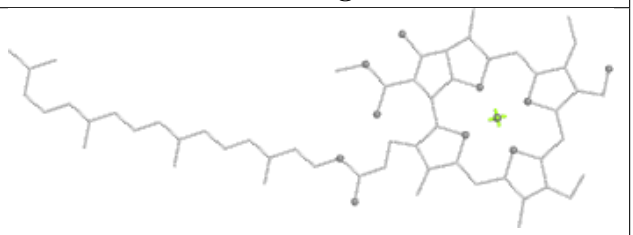
Bond angles

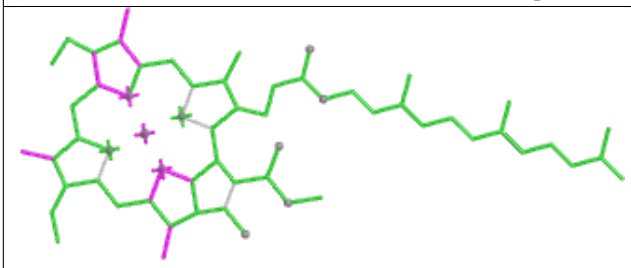
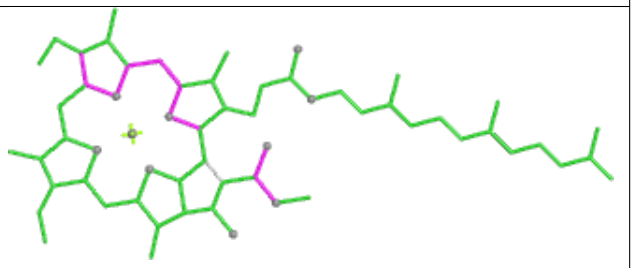
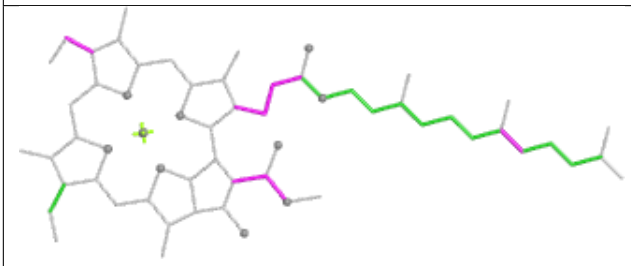
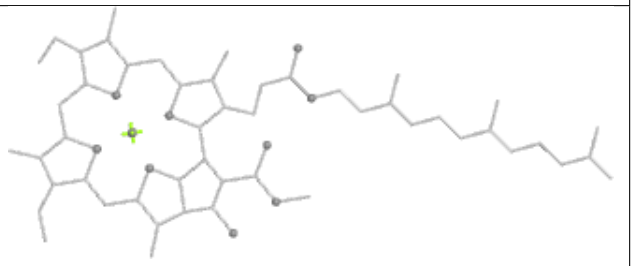


Torsions

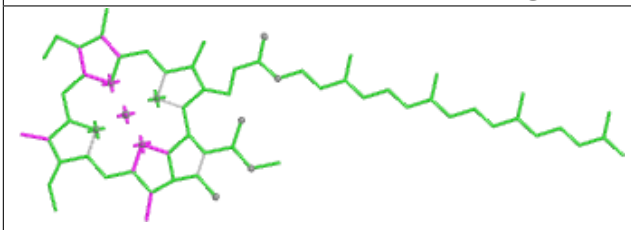


Rings

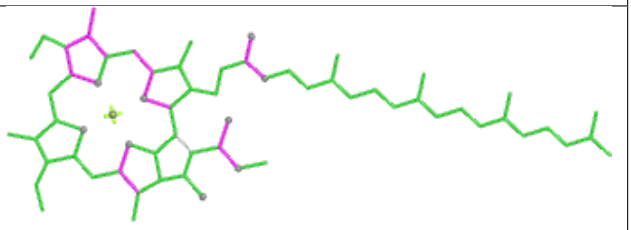
Ligand CHL n 316	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA 4 304	
	
Bond lengths	Bond angles
	
Torsions	Rings

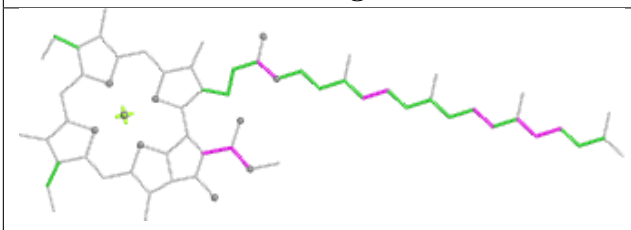
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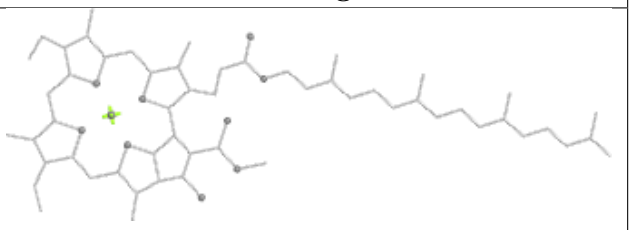
Bond lengths



Bond angles

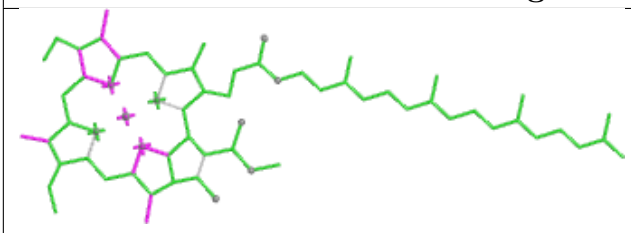


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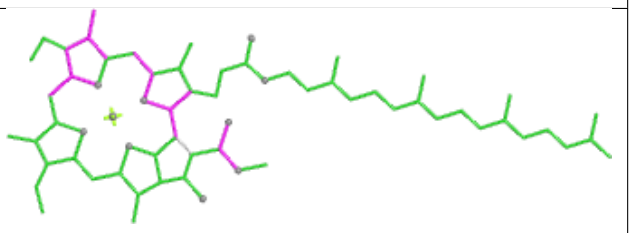


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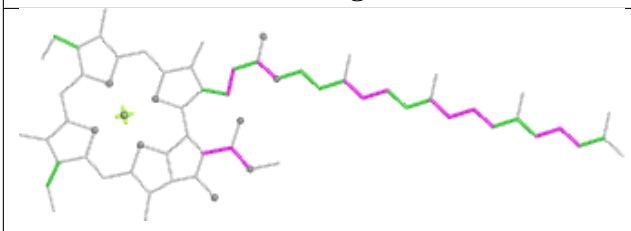
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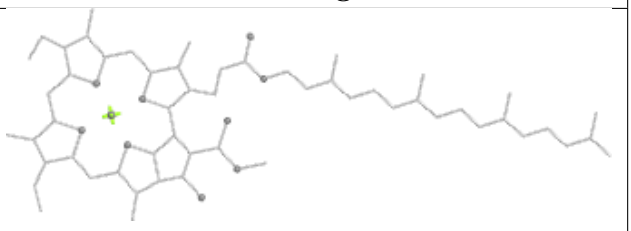
Bond lengths



Bond angles

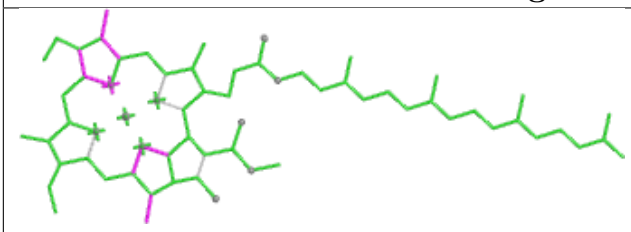


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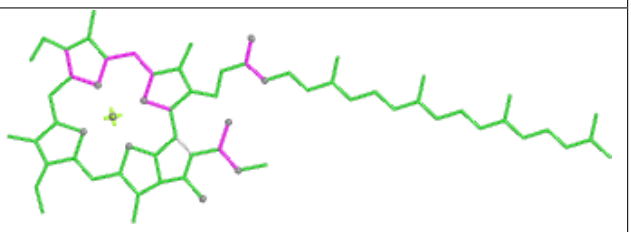


Rings

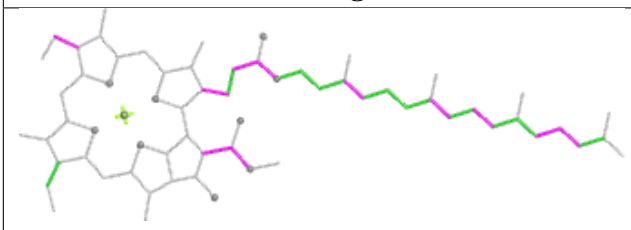
Ligand CLA 5 302



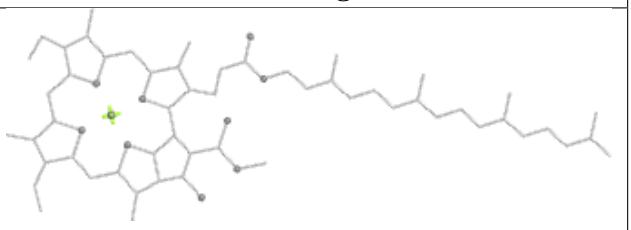
Bond lengths



Bond angles

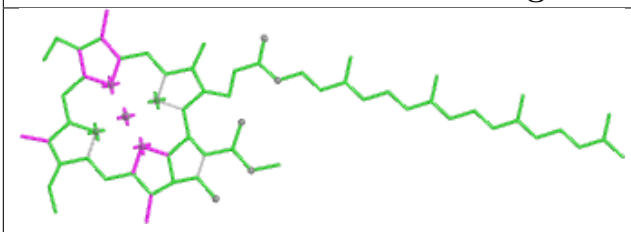


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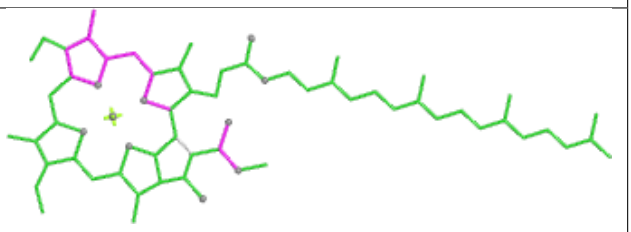


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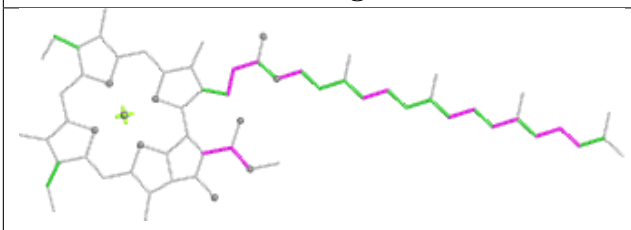
Ligand CLA b 609



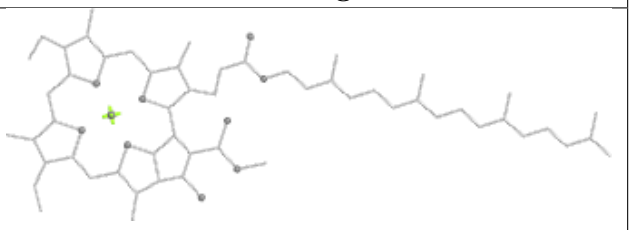
Bond lengths



Bond angles

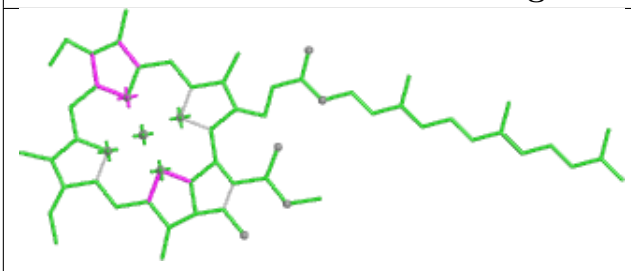


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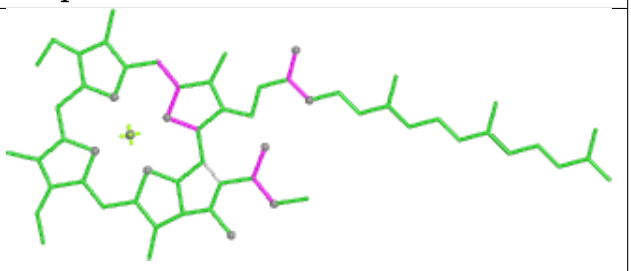


Rings

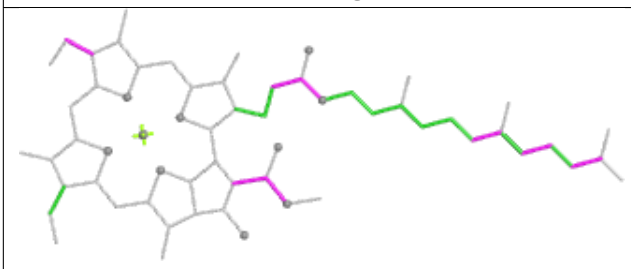
Ligand CLA q 306



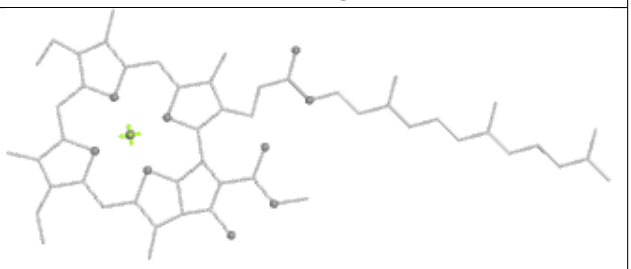
Bond lengths



Bond angles

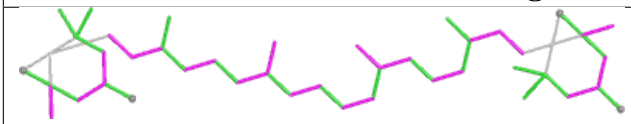


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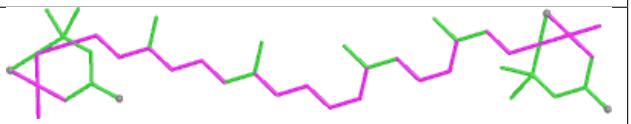


Rings

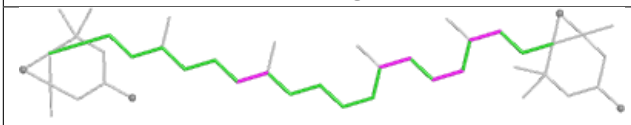
Ligand XAT u 311



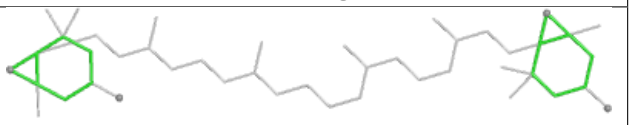
Bond lengths



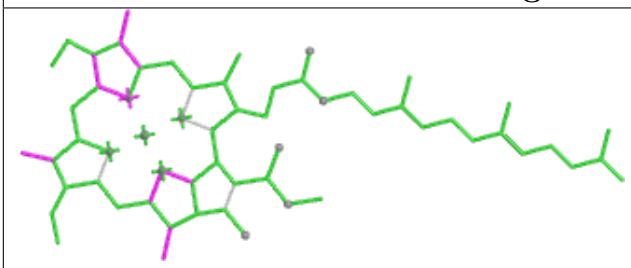
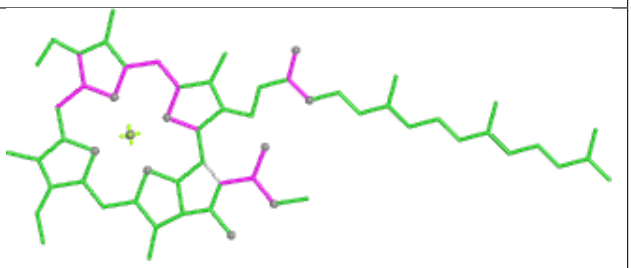
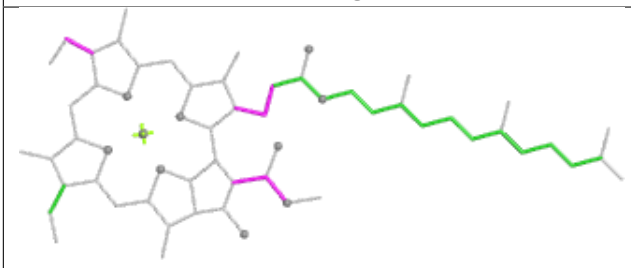
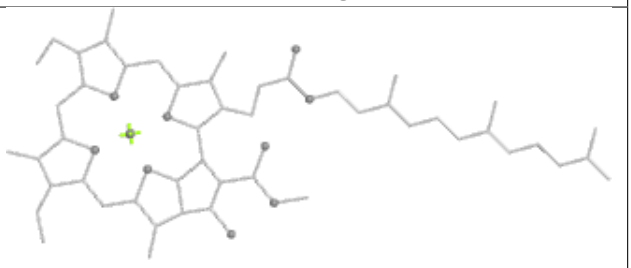
Bond angles

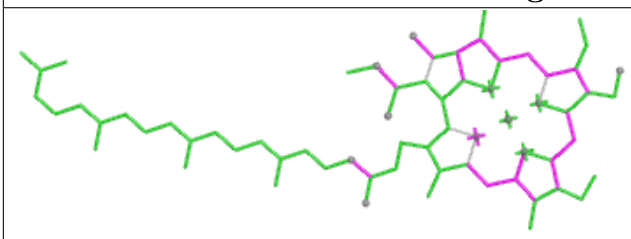
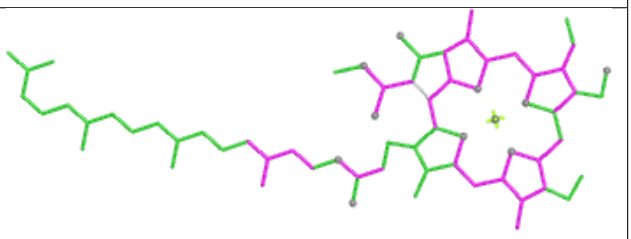
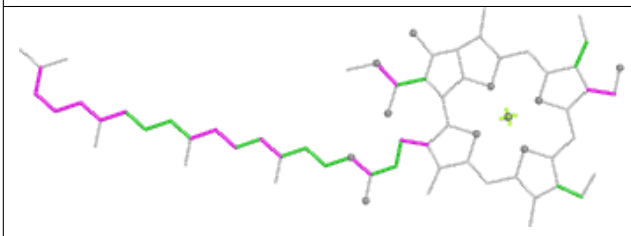
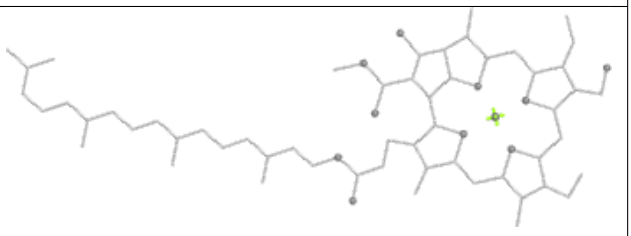


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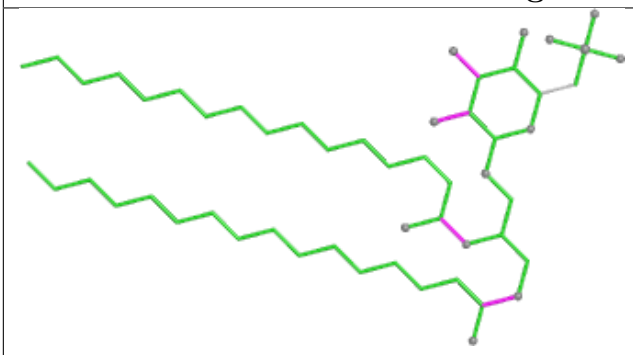


Rings

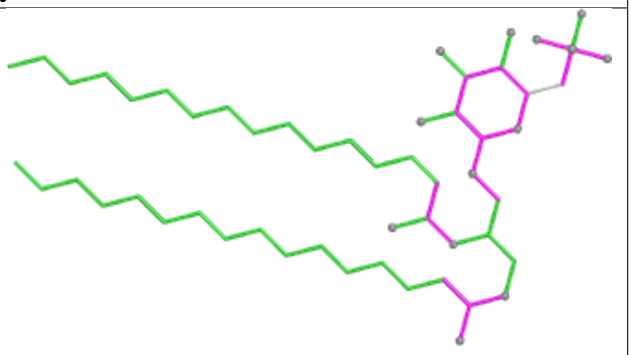
Ligand CLA U 304	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

Ligand CHL u 318	
	
Bond lengths	**Bond angles**
	
Torsions	**Rings**

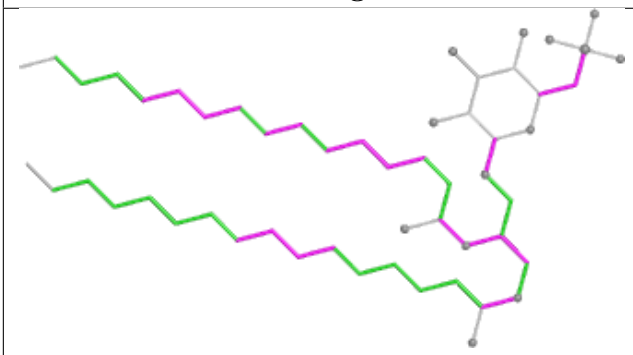
Ligand SQD L 102



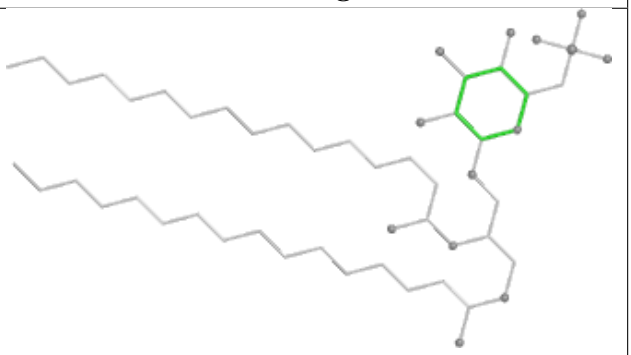
Bond lengths



Bond angles

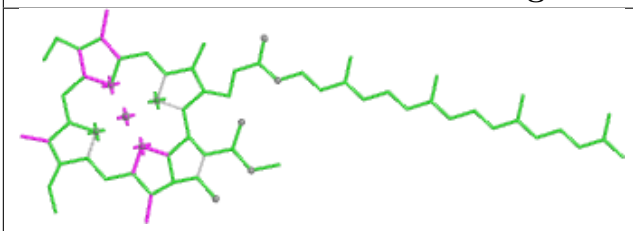


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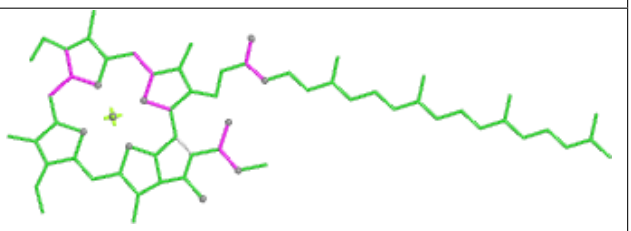


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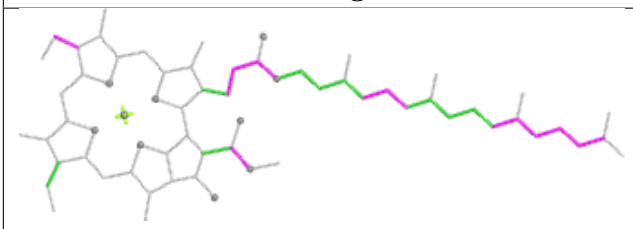
Ligand CLA b 602



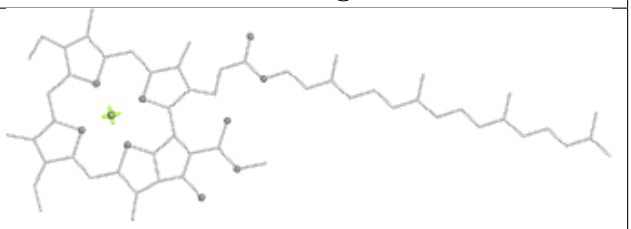
Bond lengths



Bond angles

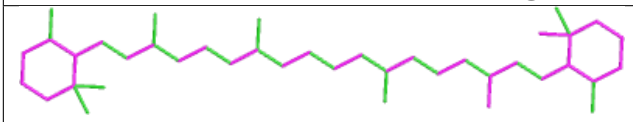


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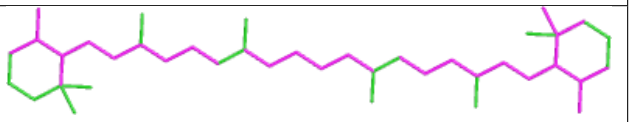


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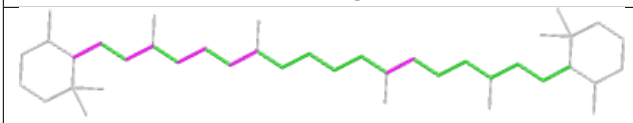
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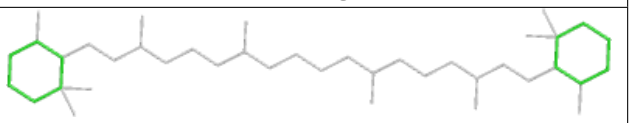
Bond lengths



Bond angles

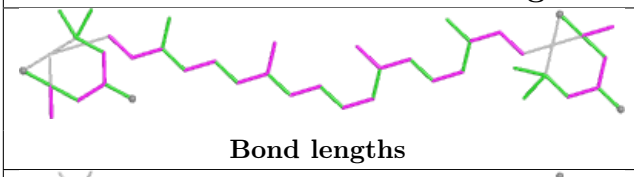


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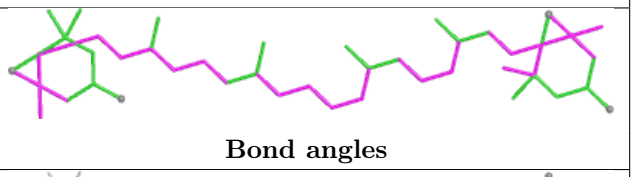


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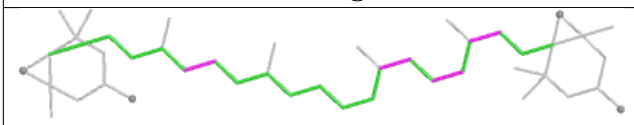
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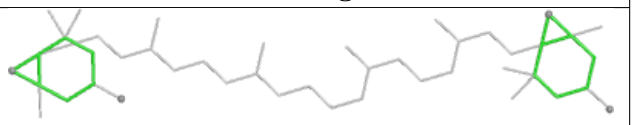
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Bond angles

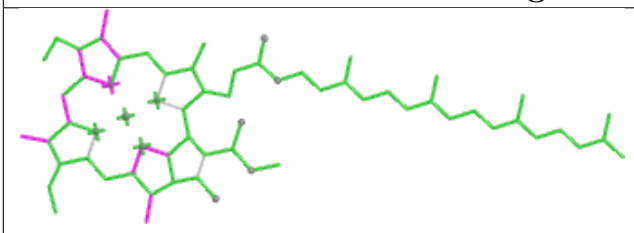


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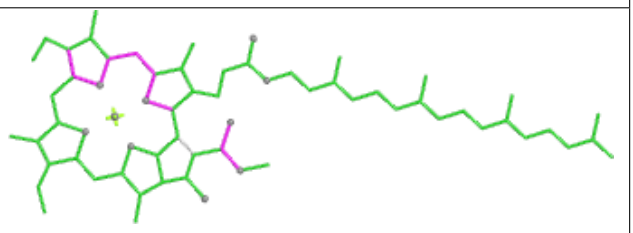


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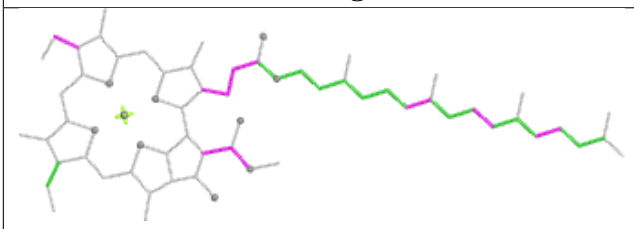
Ligand CLA v 301



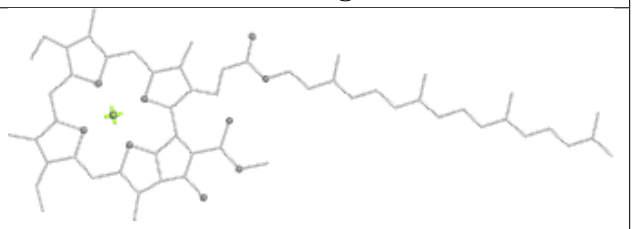
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Bond angles

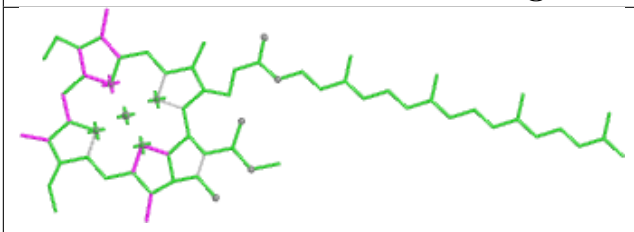


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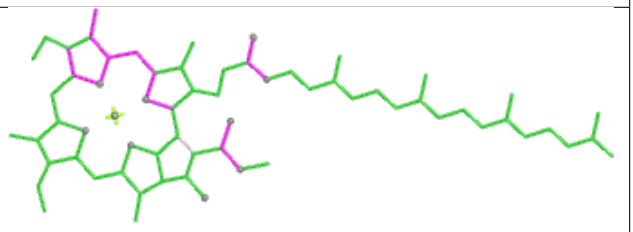


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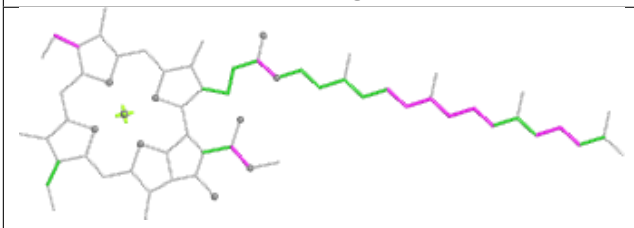
Ligand CLA b 612



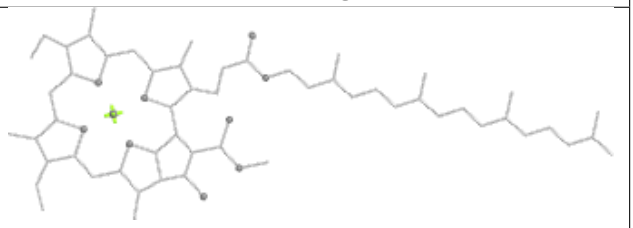
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Bond angles

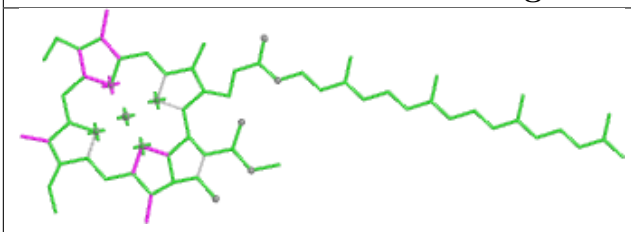


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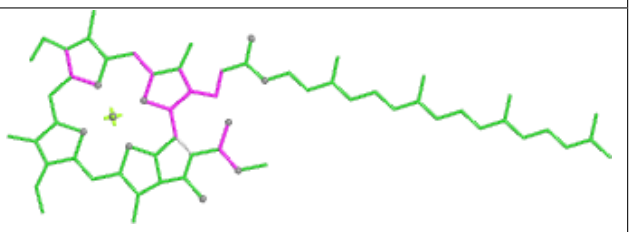


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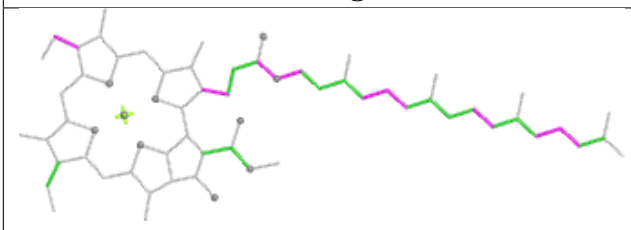
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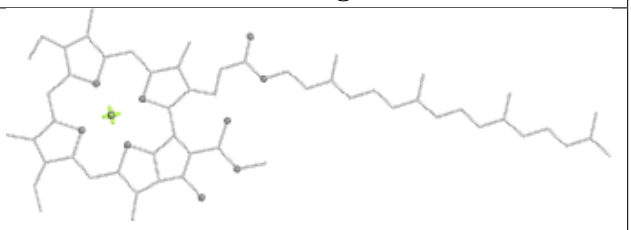
Bond lengths



Bond angles



Torsions



Rings

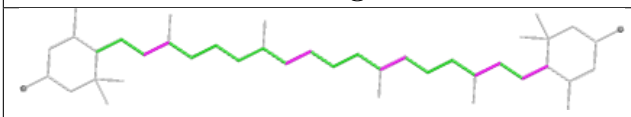
Ligand LUT S 311



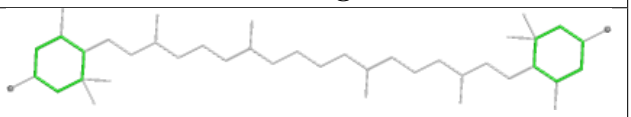
Bond lengths



Bond angles

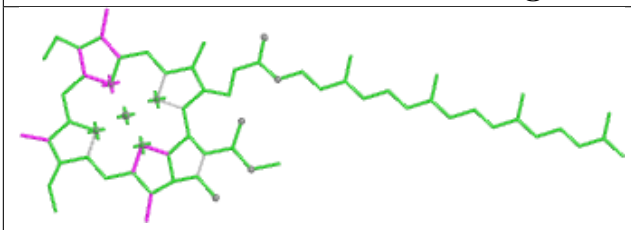


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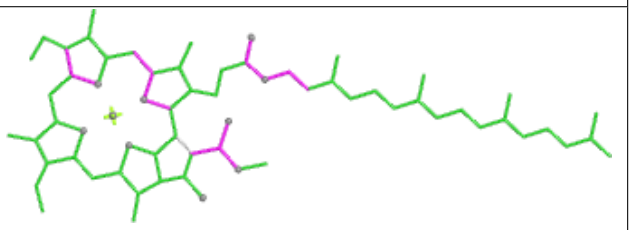


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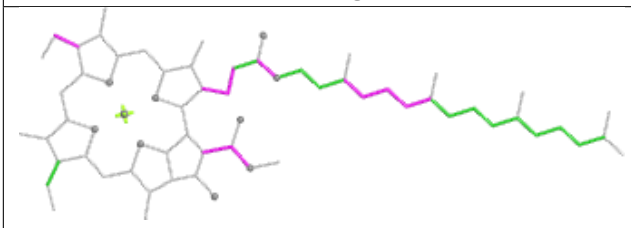
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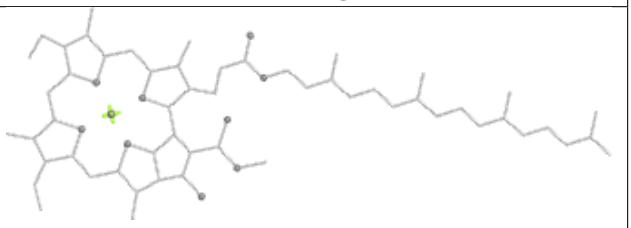
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Bond angles

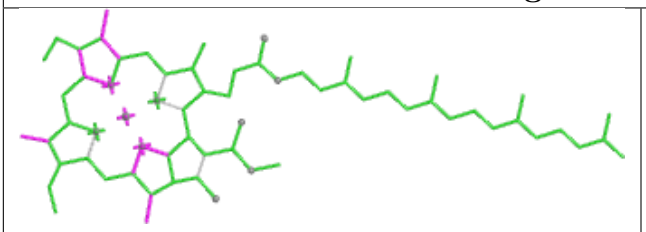


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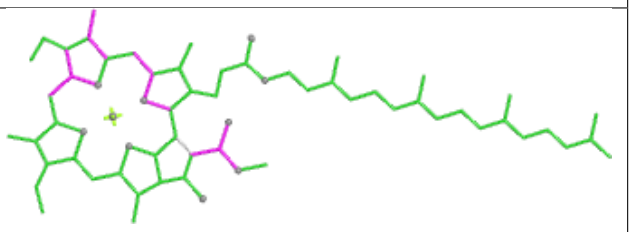


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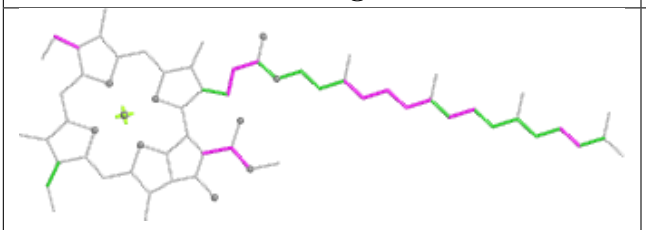
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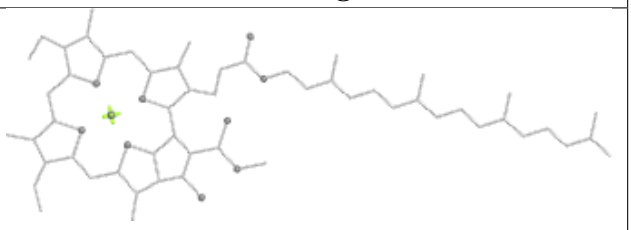
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Bond angles

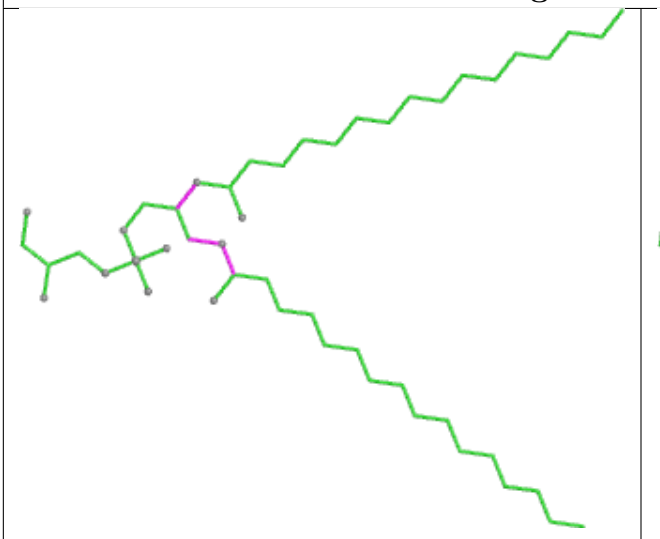


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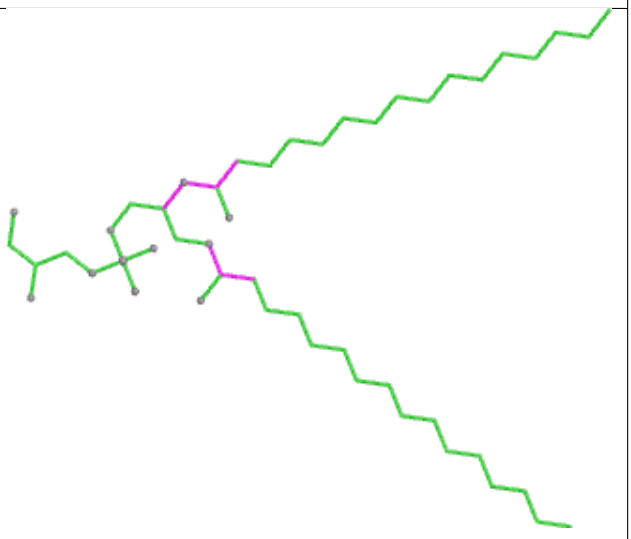


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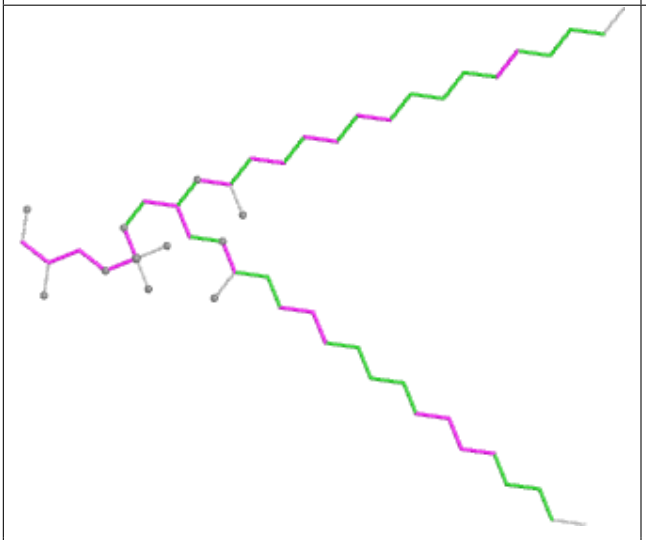
Ligand LHG l 101



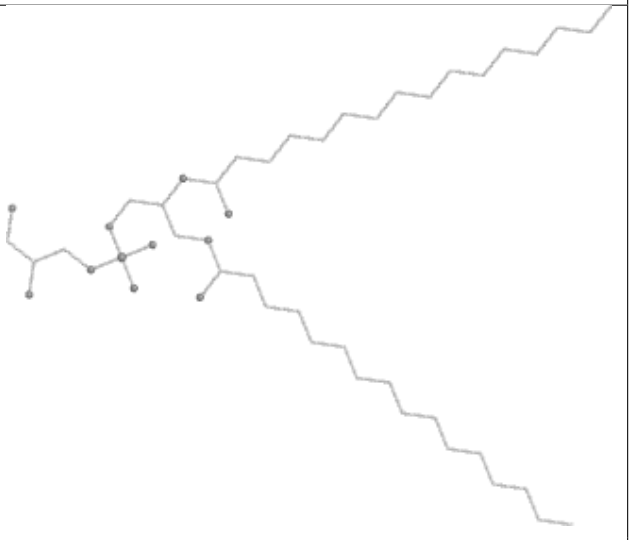
Bond lengths



Bond angles

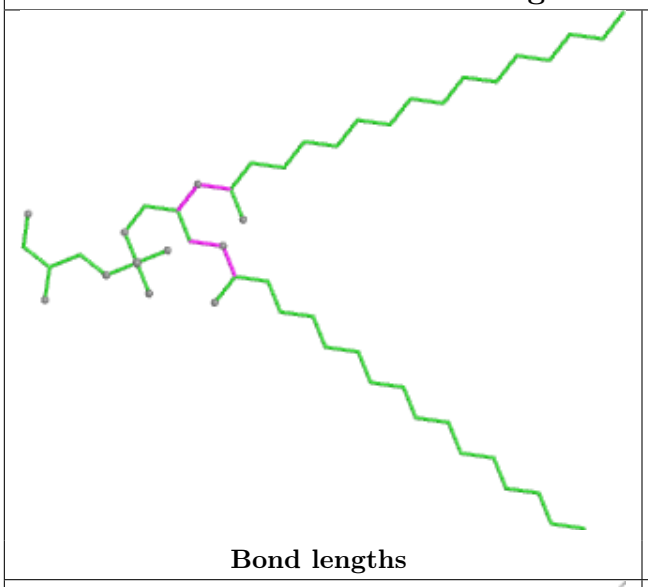


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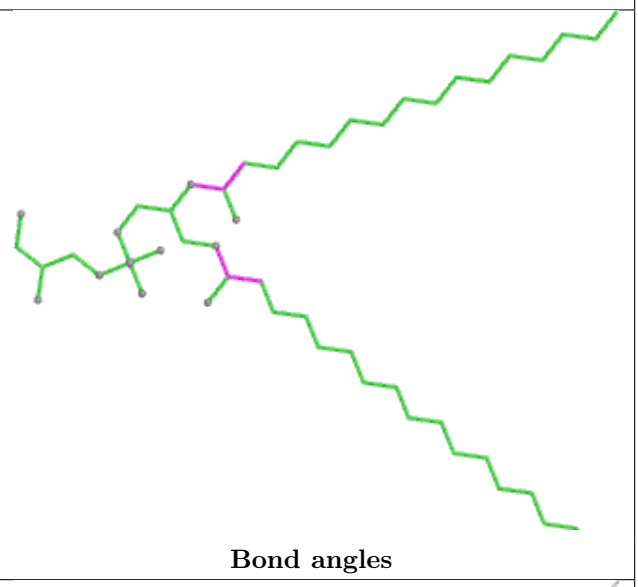


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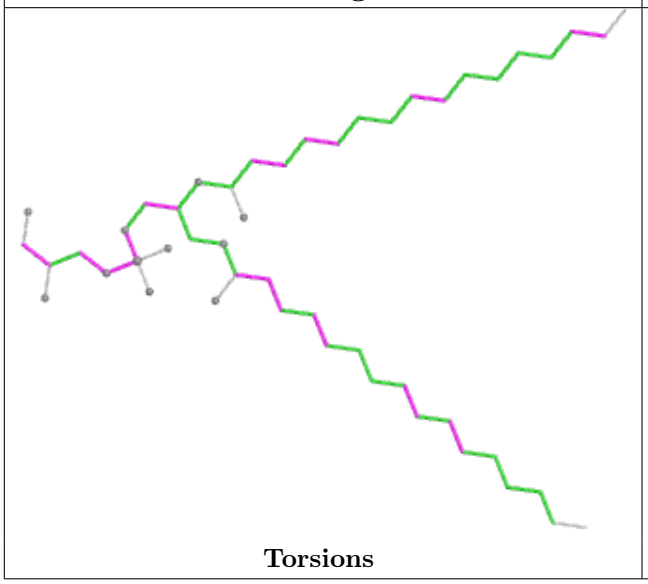
Ligand LHG 4 312



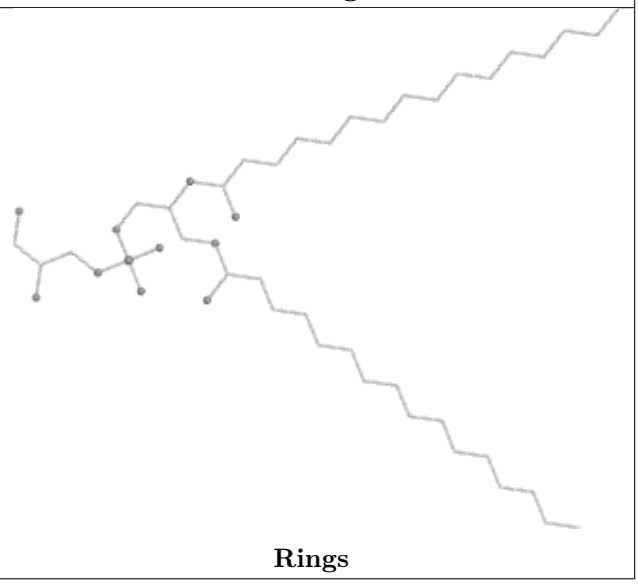
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Bond angles

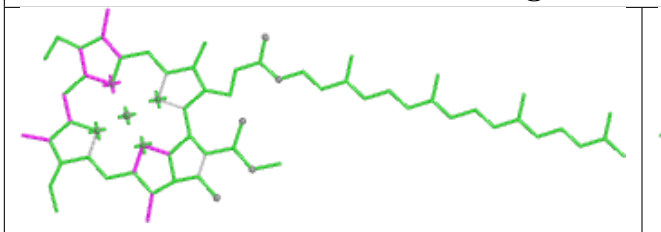


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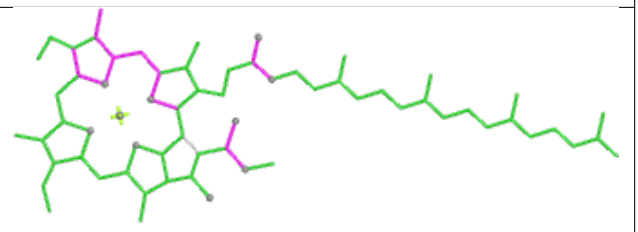


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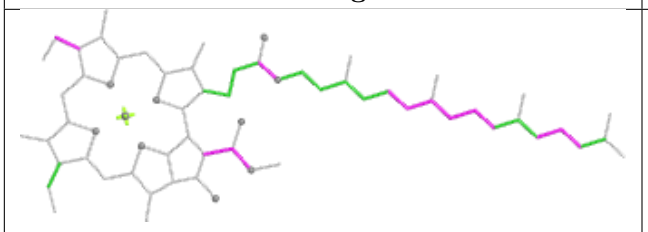
Ligand CLA B 612



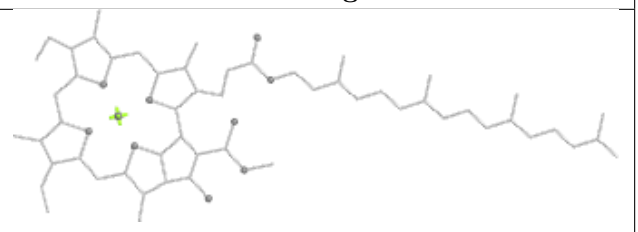
Bond lengths



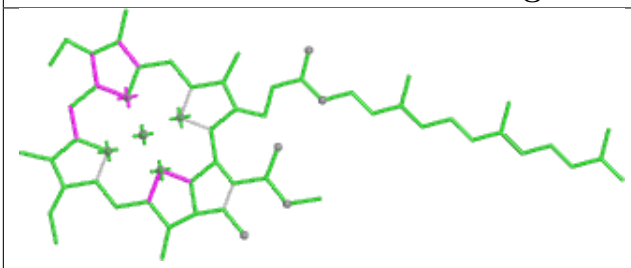
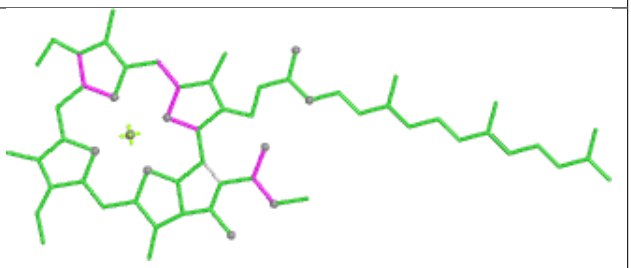
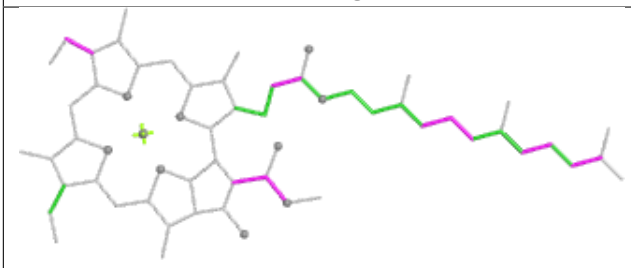
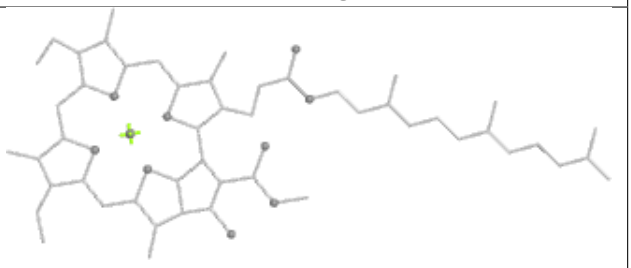
Bond angles

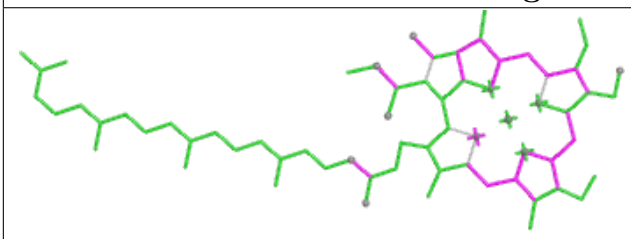
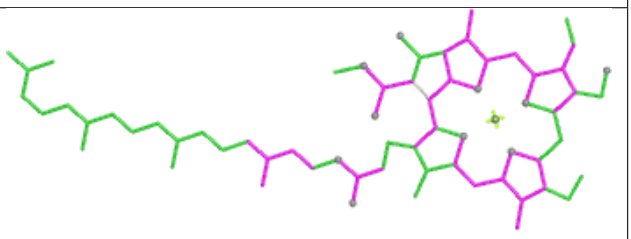
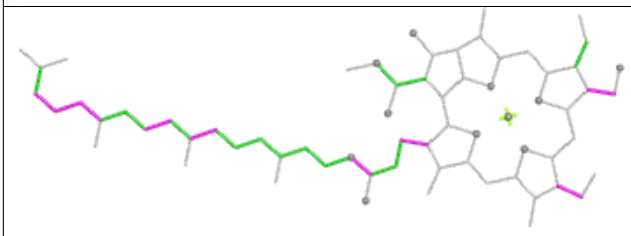
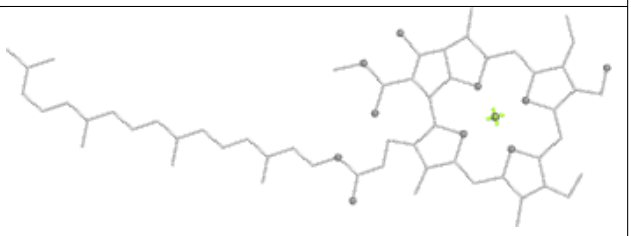


Torsions

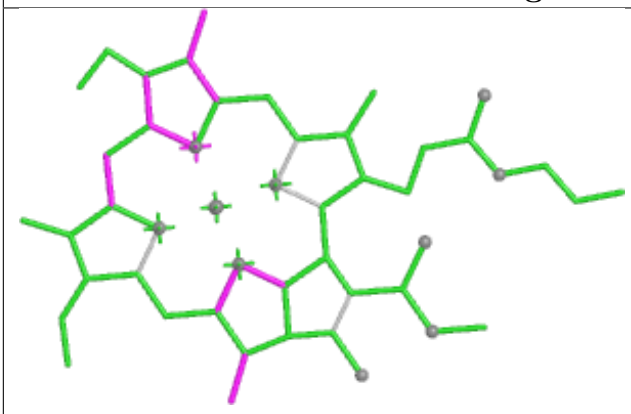


Rings

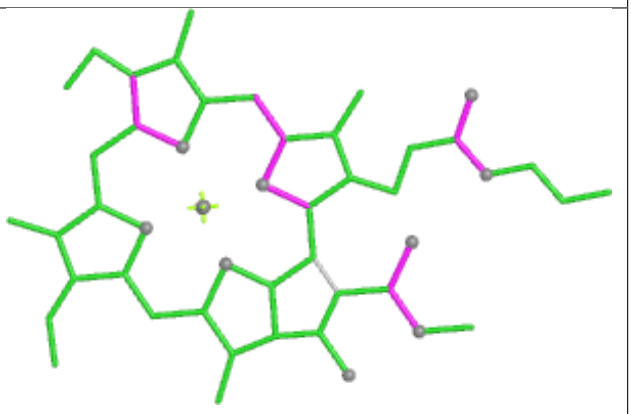
Ligand CLA R 304	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CHL U 316	
 Bond lengths	 Bond angles
 Torsions	 Rings

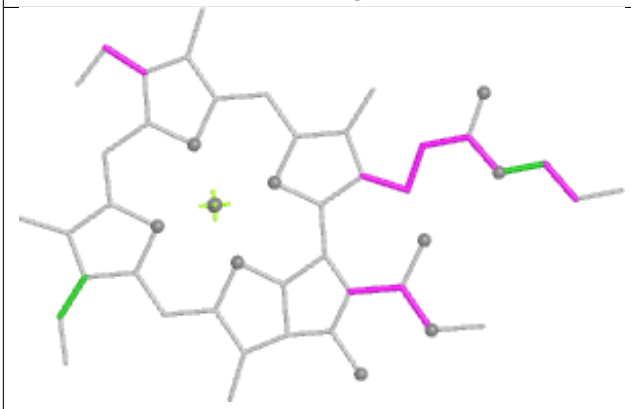
Ligand CLA P 309



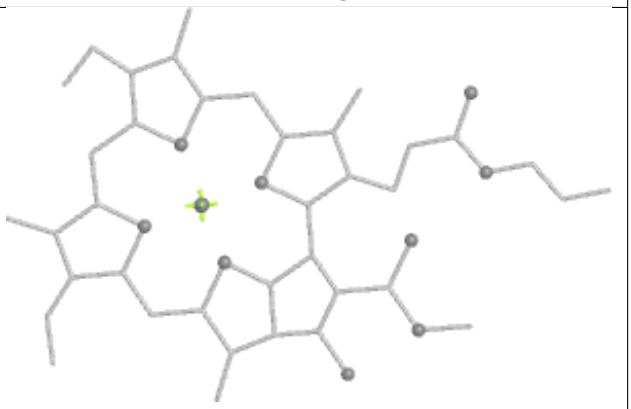
Bond lengths



Bond angles

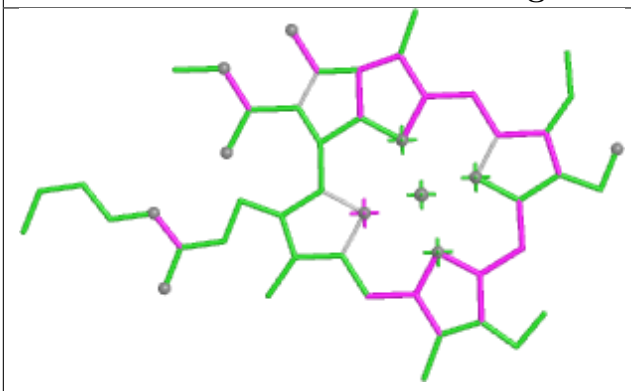


Torsions

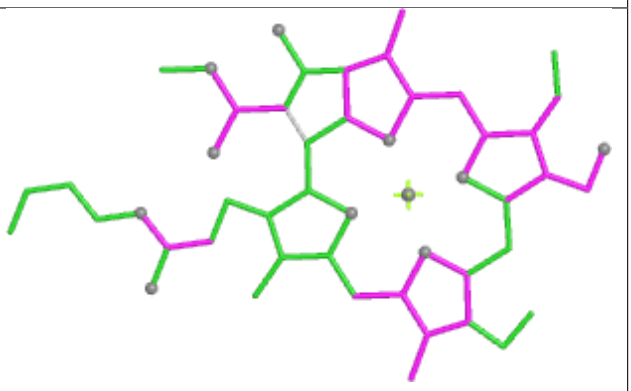


Rings

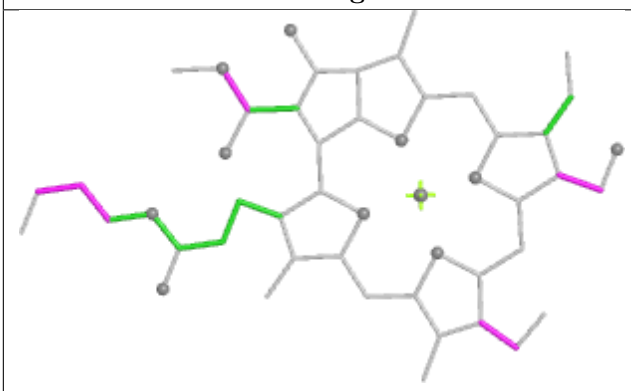
Ligand CHL 1 315



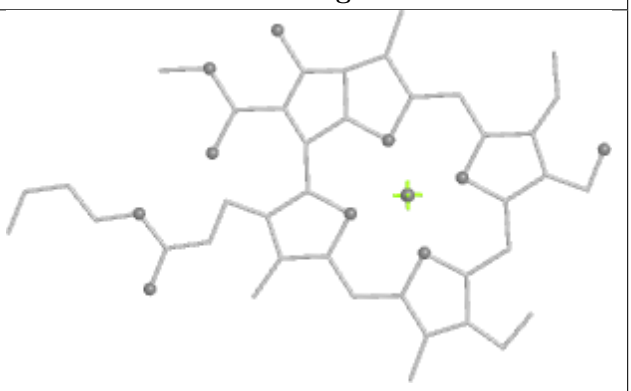
Bond lengths



Bond angles

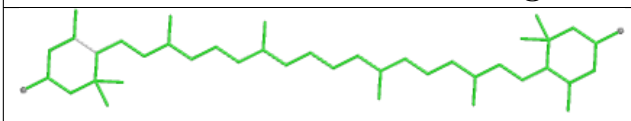


Torsions

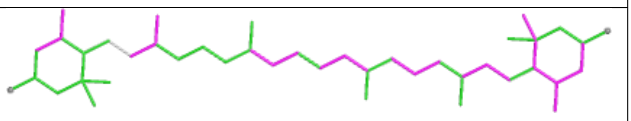


Rings

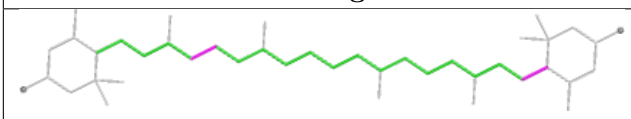
Ligand LUT U 310



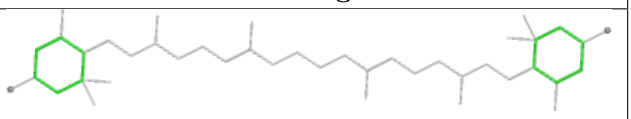
Bond lengths



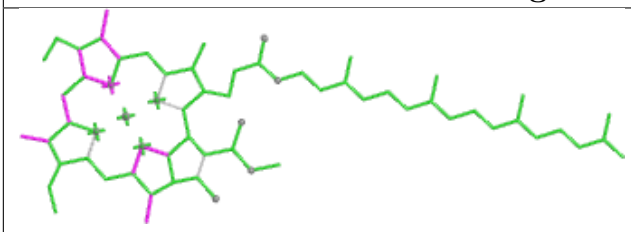
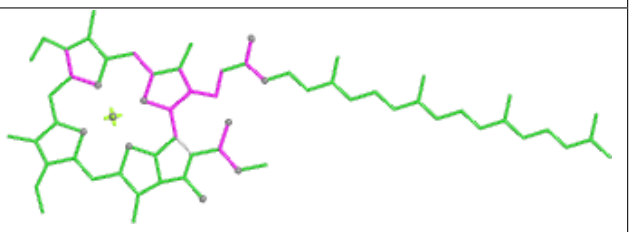
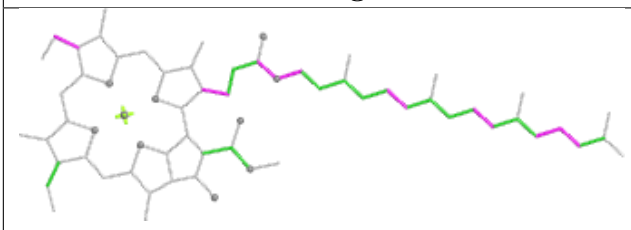
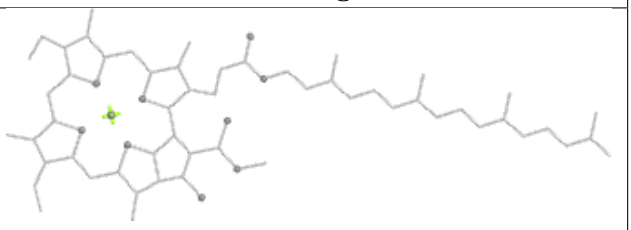
Bond angles

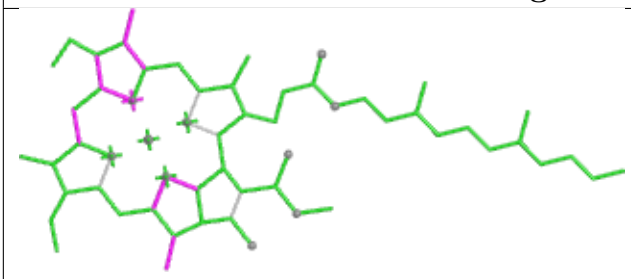
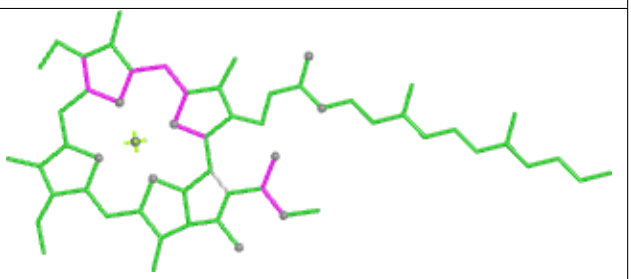
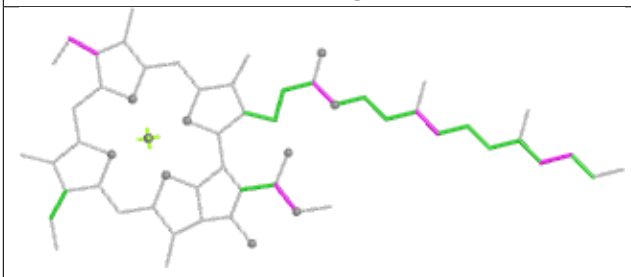
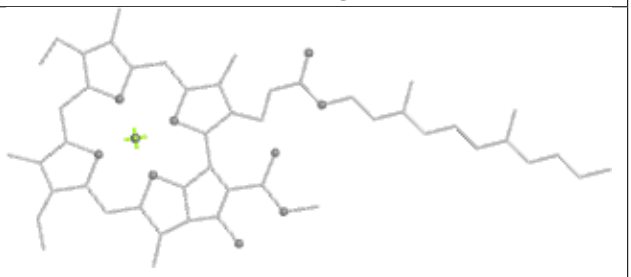


Torsions

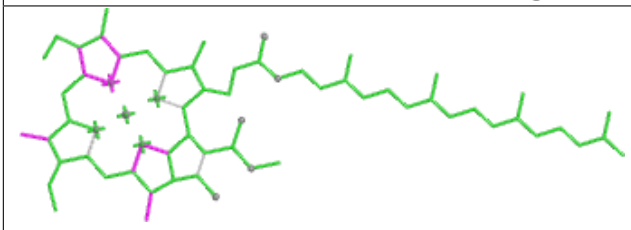


Rings

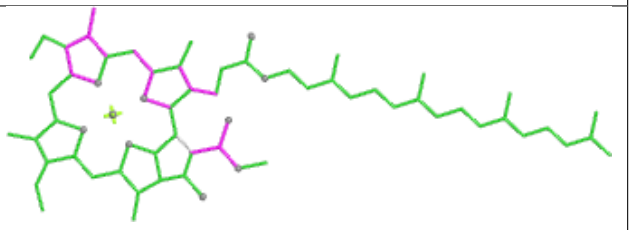
Ligand CLA c 514	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA r 605	
	
Bond lengths	Bond angles
	
Torsions	Rings

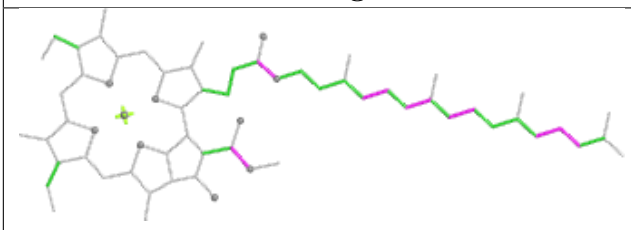
Ligand CLA x 201



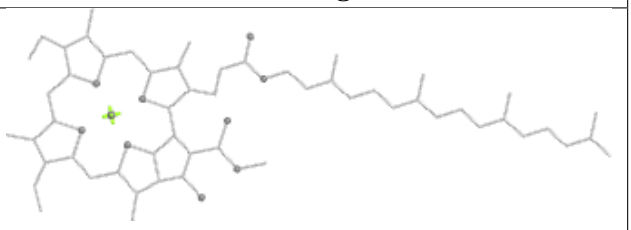
Bond lengths



Bond angles

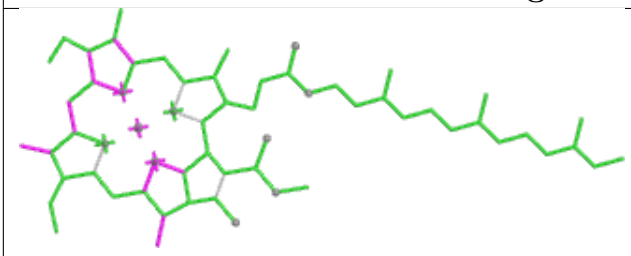


Torsions

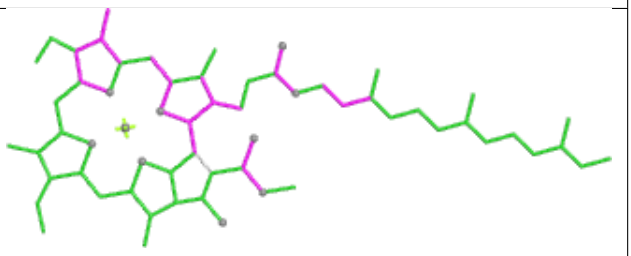


Rings

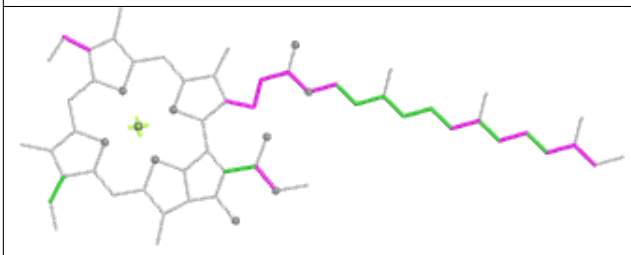
Ligand CLA S 301



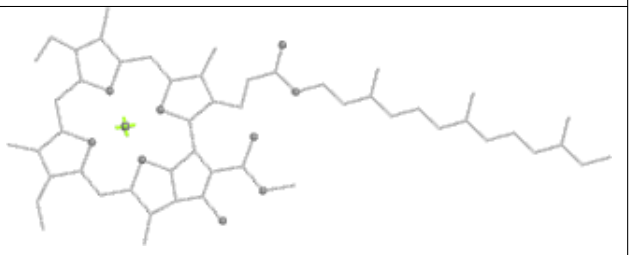
Bond lengths



Bond angles

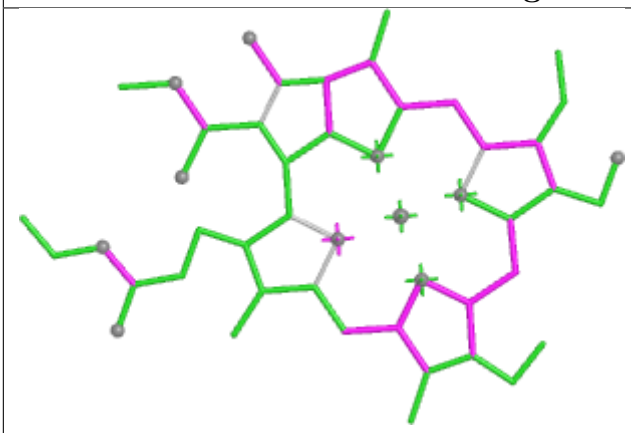


Torsions

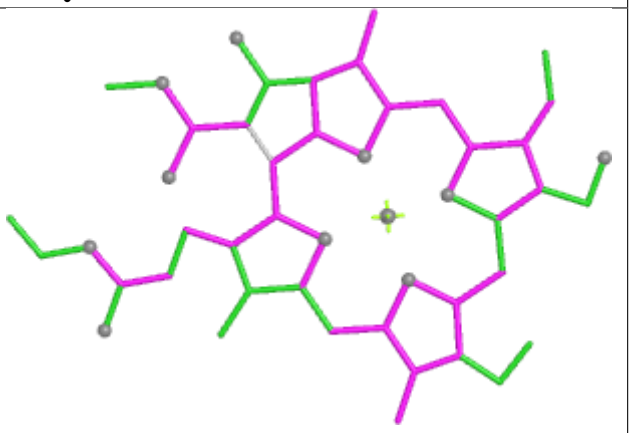


Rings

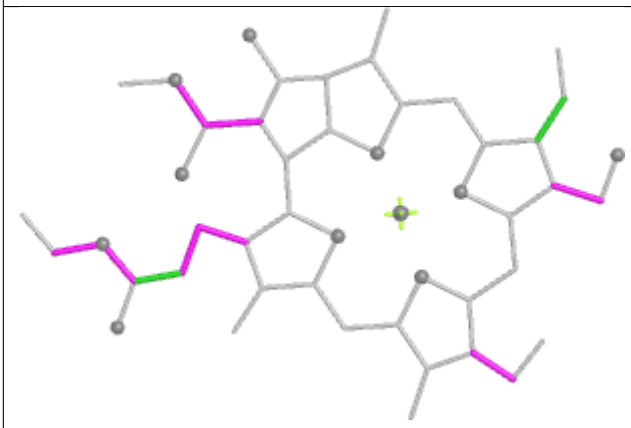
Ligand CHL Q 312



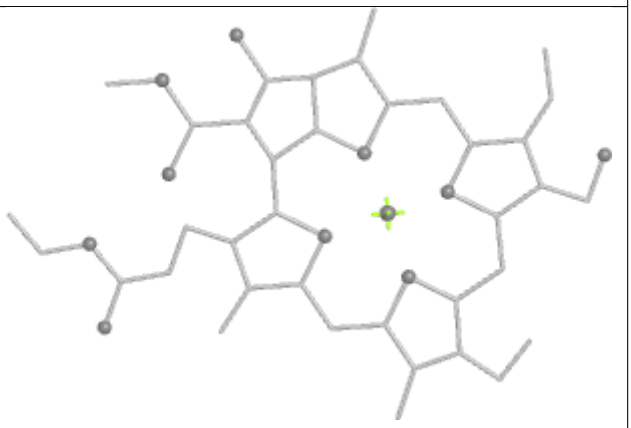
Bond lengths



Bond angles

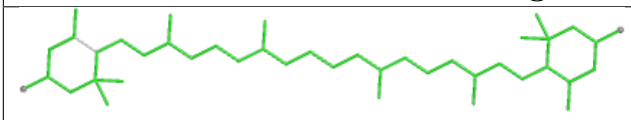


Torsions

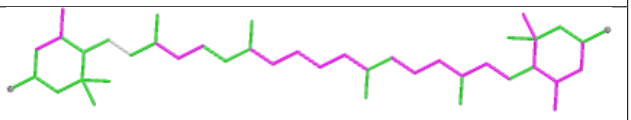


Rings

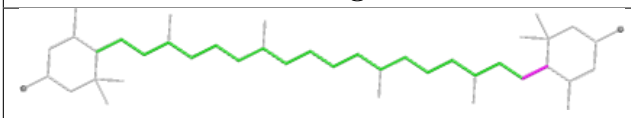
Ligand LUT 4 309



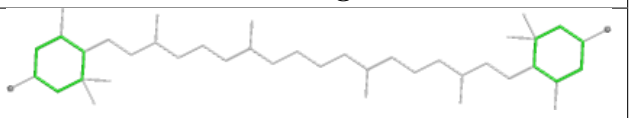
Bond lengths



Bond angles

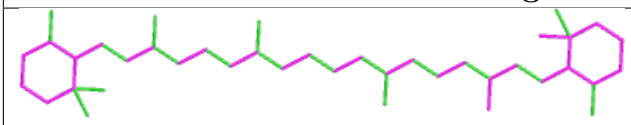


Torsions

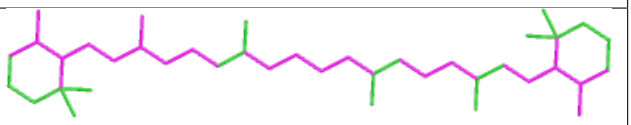


Rings

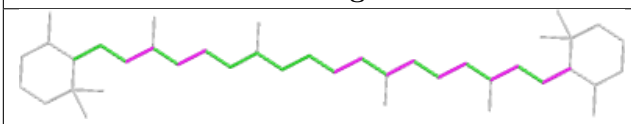
Ligand BCR C 518



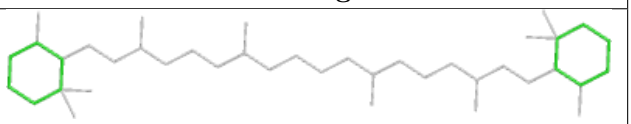
Bond lengths



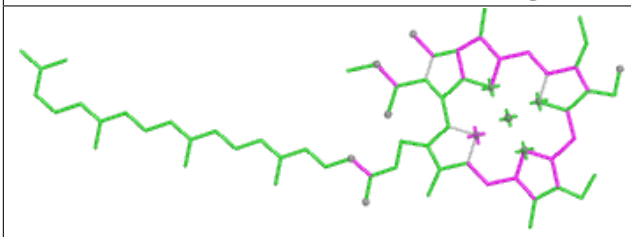
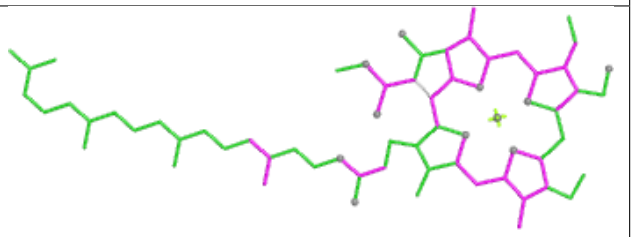
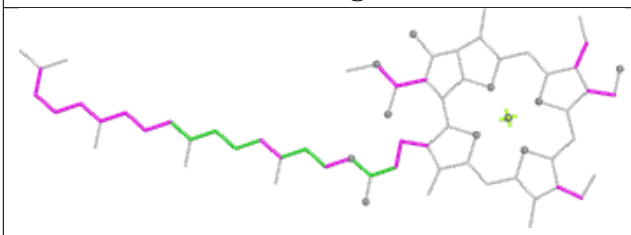
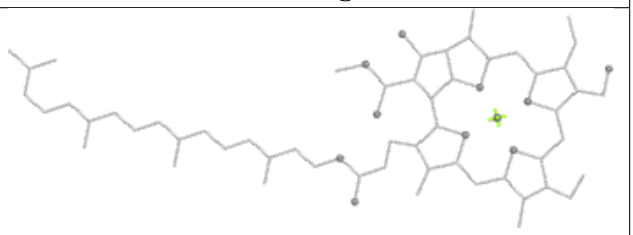
Bond angles

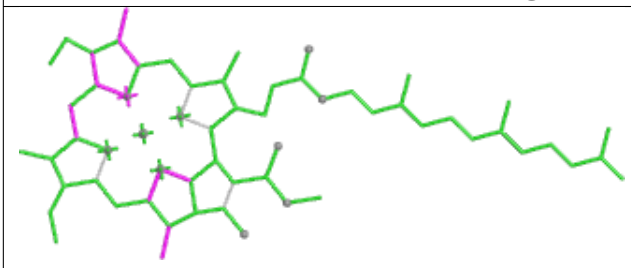
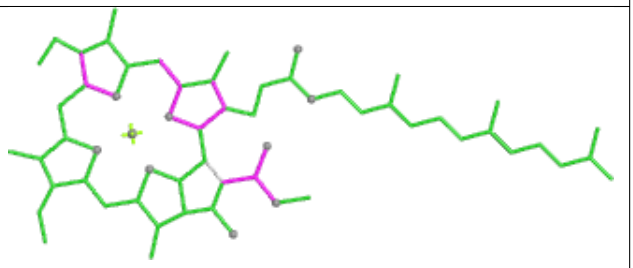
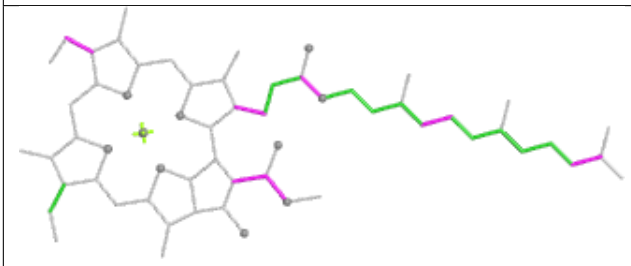
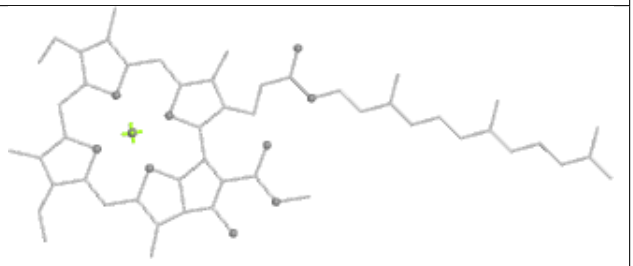


Torsions

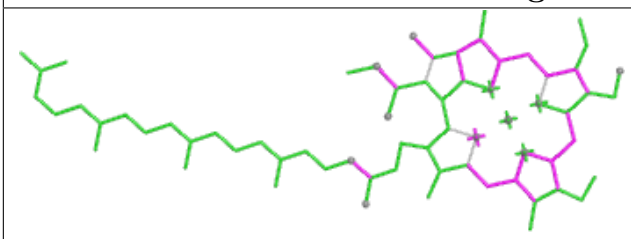


Rings

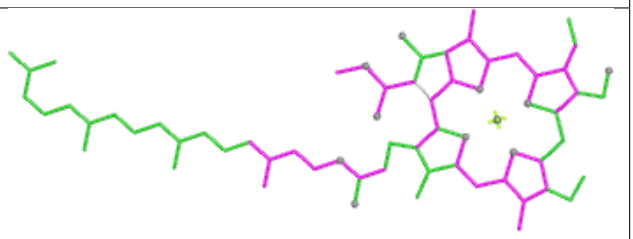
Ligand CHL P 319	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA G 305	
 Bond lengths	 Bond angles
 Torsions	 Rings

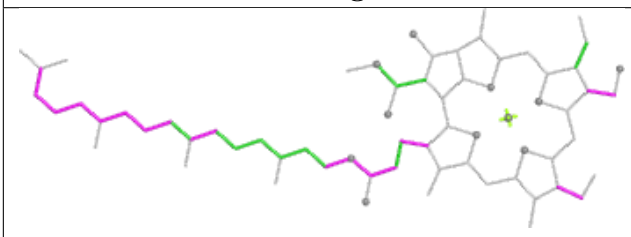
Ligand CHL 1 317



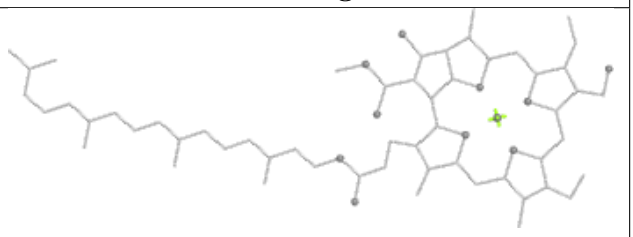
Bond lengths



Bond angles

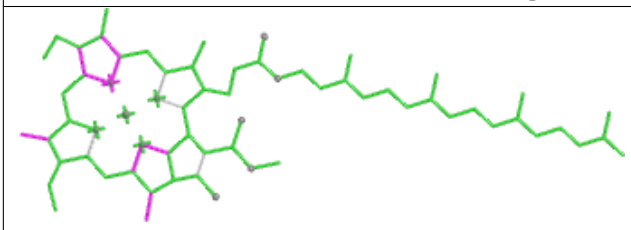


Torsions

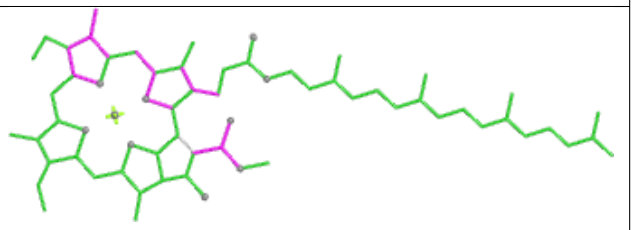


Rings

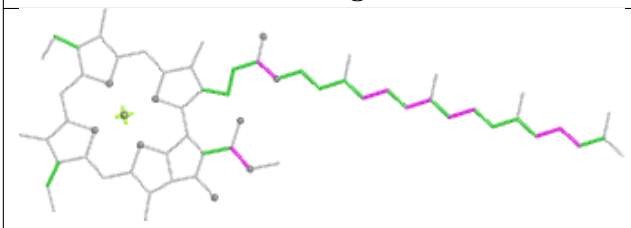
Ligand CLA X 202



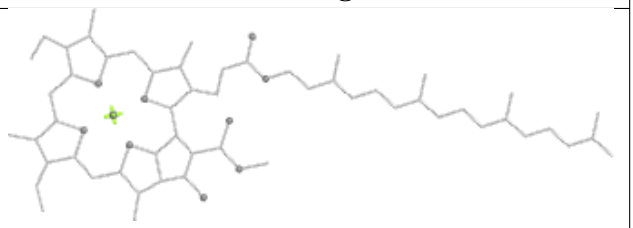
Bond lengths



Bond angles

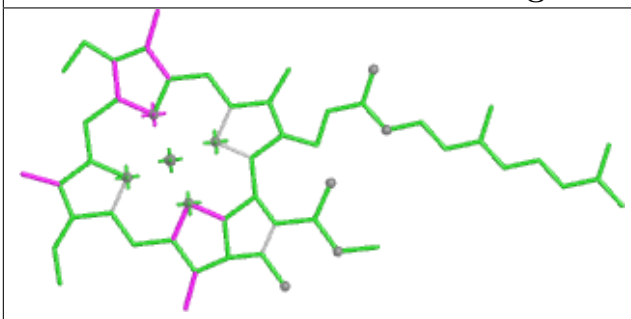


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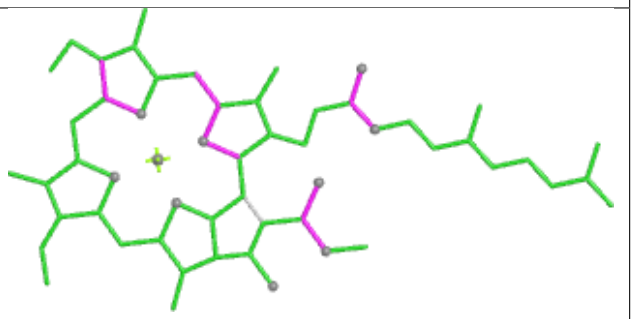


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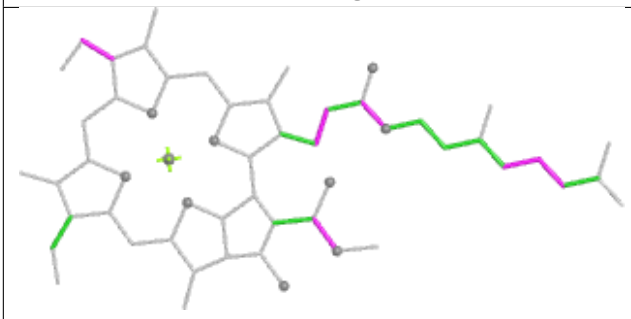
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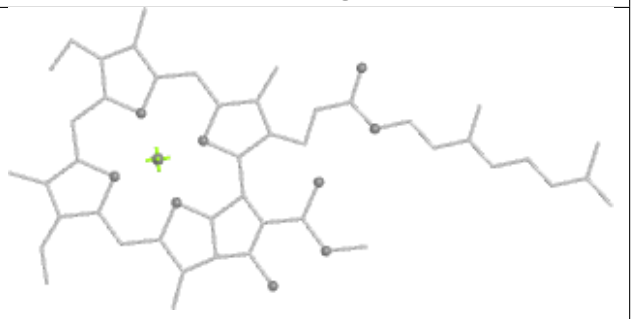
Bond lengths



Bond angles

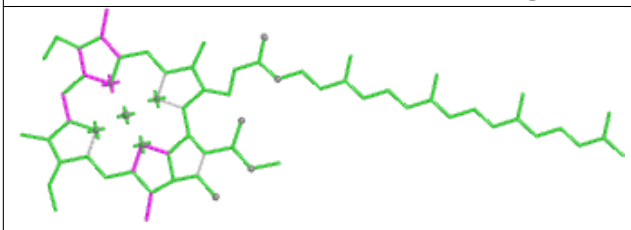


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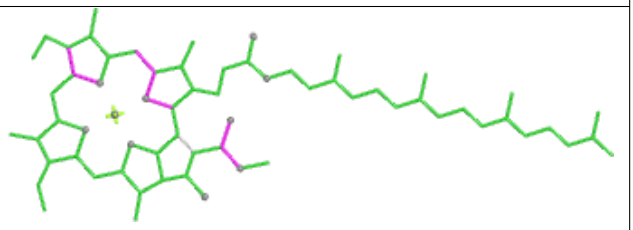


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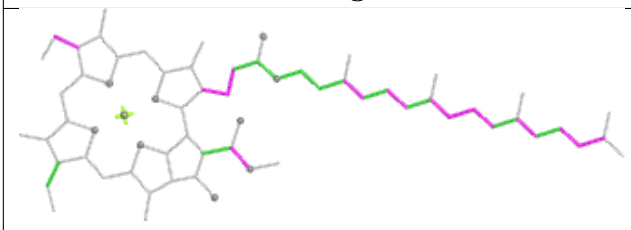
Ligand CLA R 307



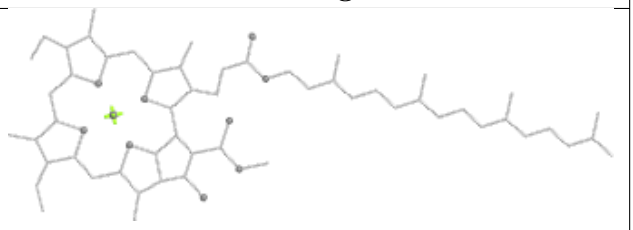
Bond lengths



Bond angles

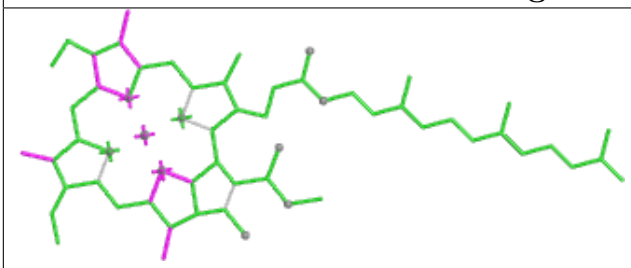


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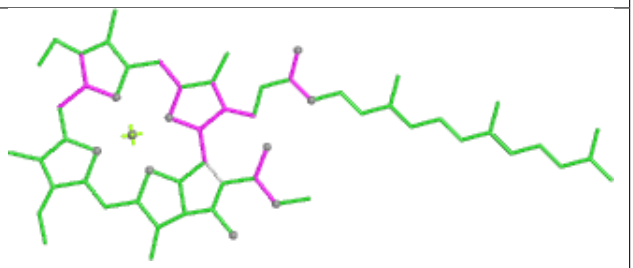


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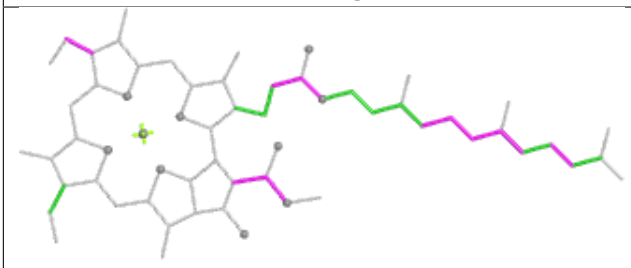
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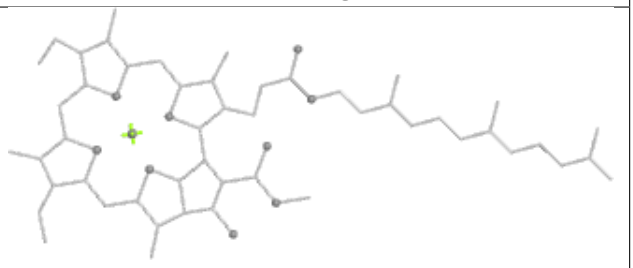
Bond lengths



Bond angles

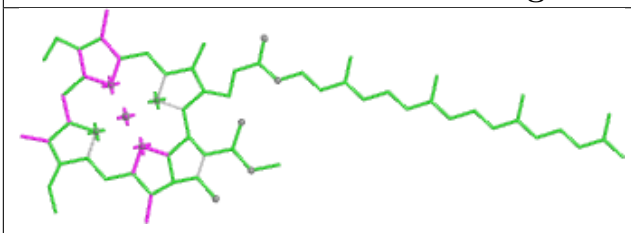


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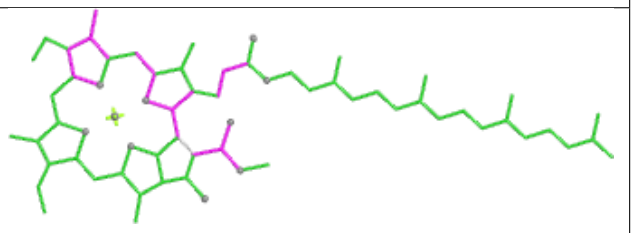


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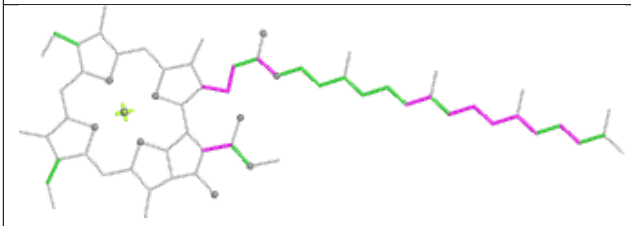
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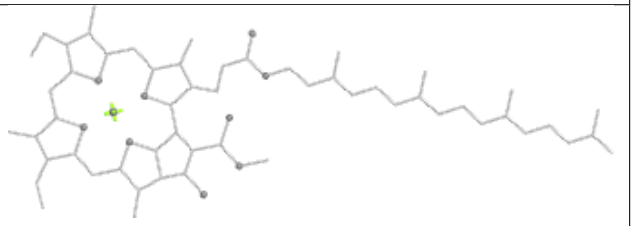
Bond lengths



Bond angles



Torsions

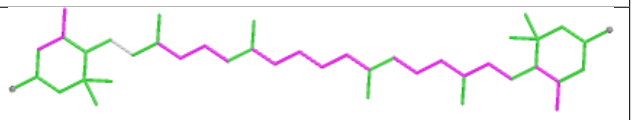


Rings

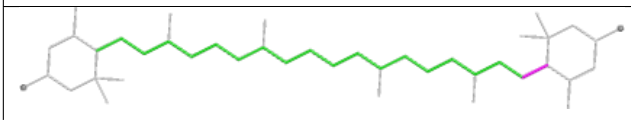
Ligand LUT r 611



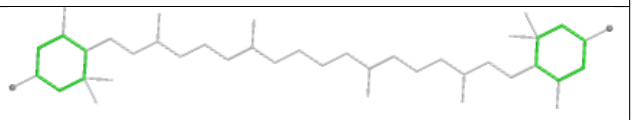
Bond lengths



Bond angles

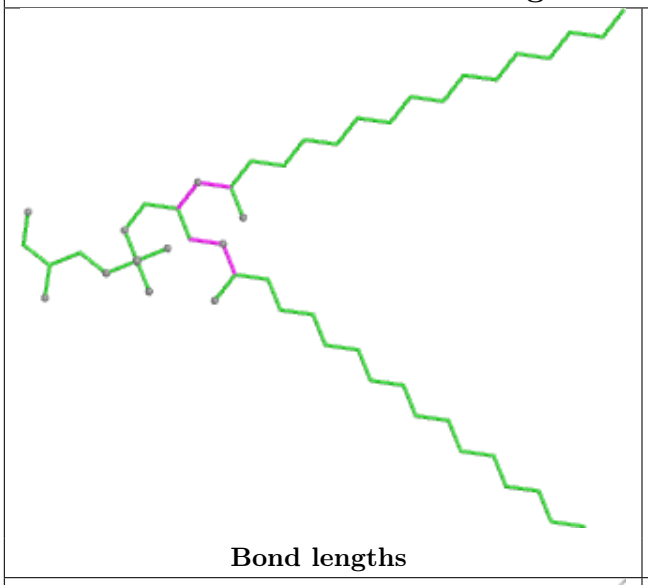


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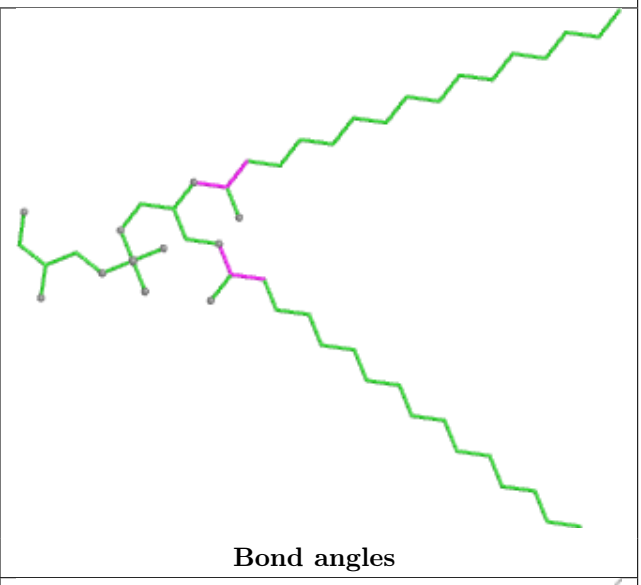


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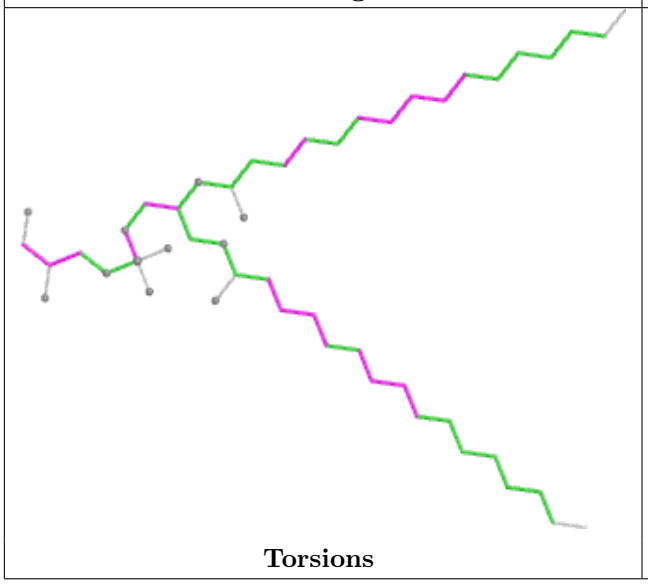
Ligand LHG n 312



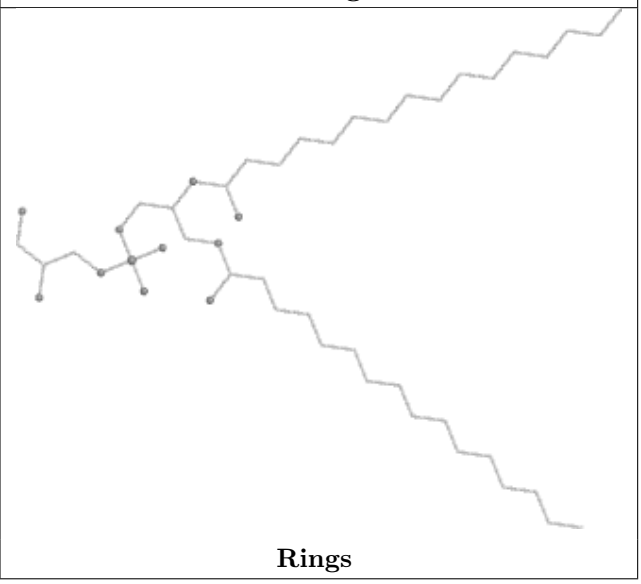
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Bond angles

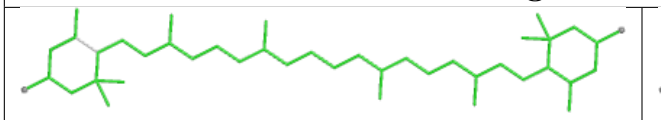


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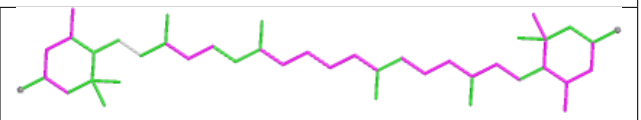


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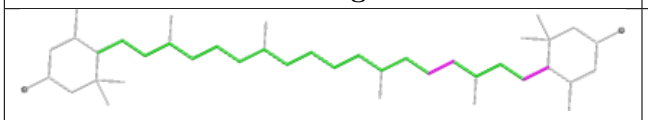
Ligand LUT P 311



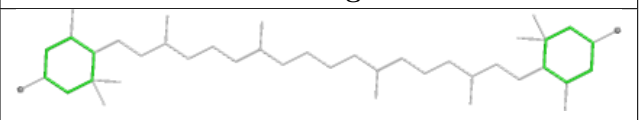
Bond lengths



Bond angles

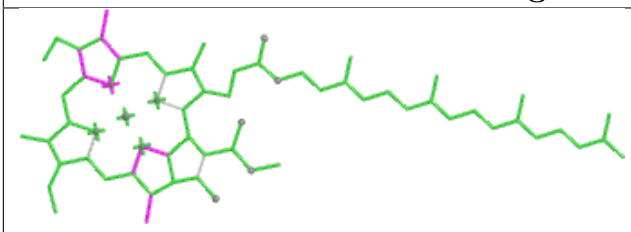


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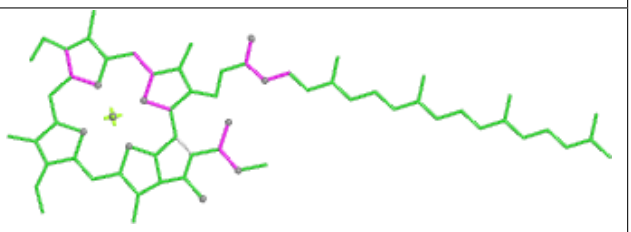


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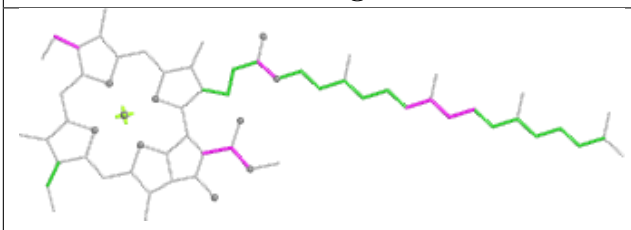
Ligand CLA 3 302



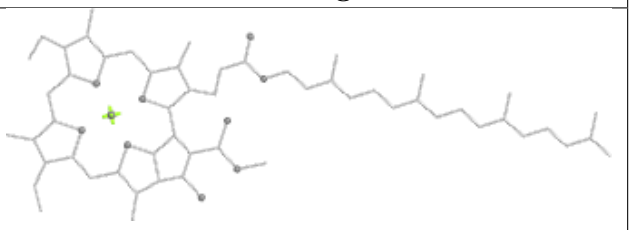
Bond lengths



Bond angles

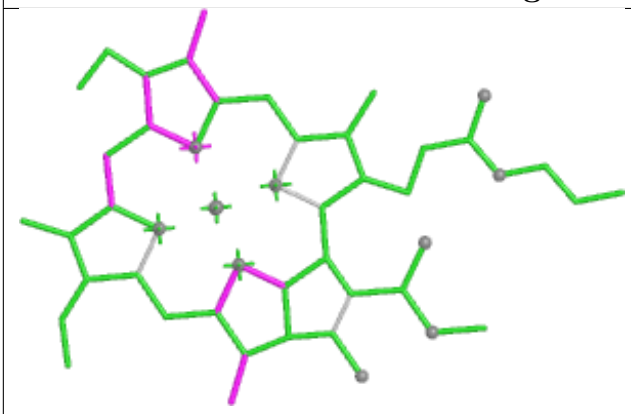


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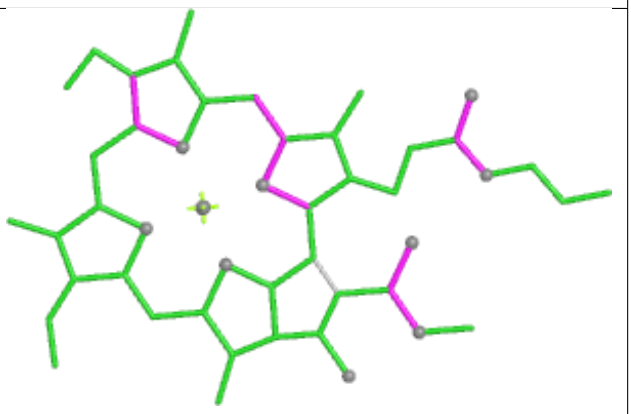


Rings

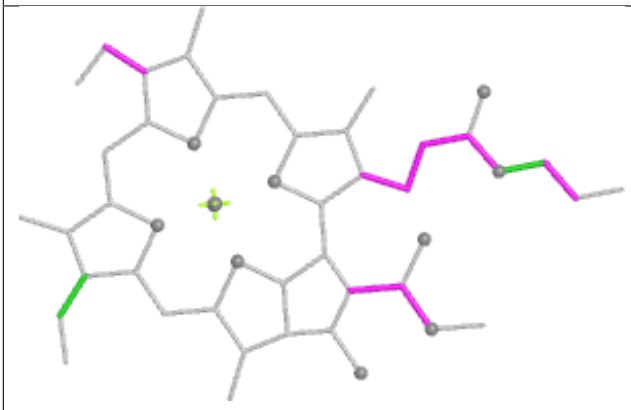
Ligand CLA N 308



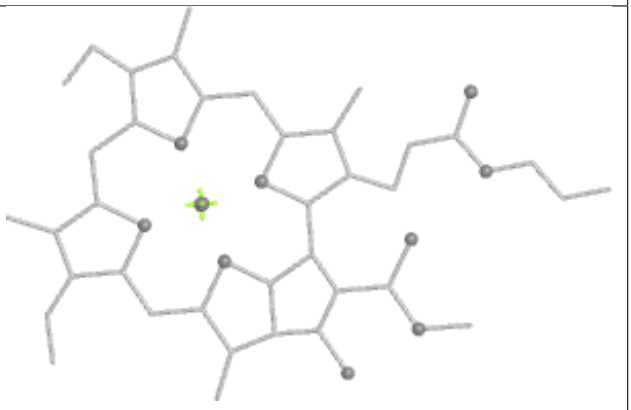
Bond lengths



Bond angles

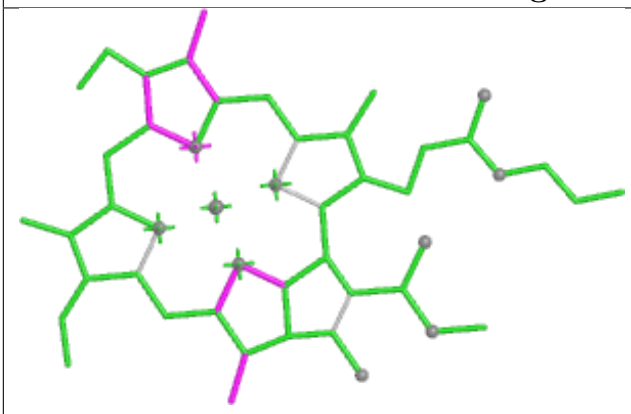


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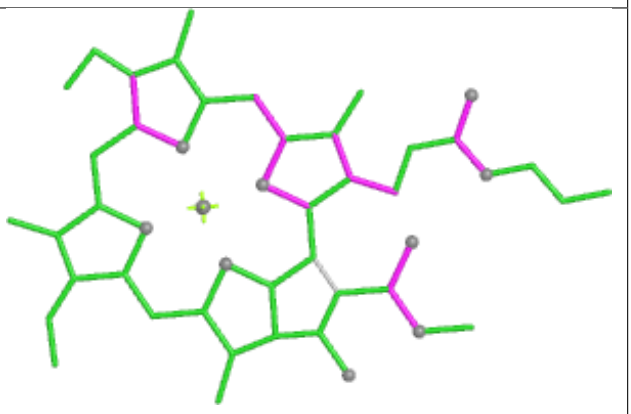


Rings

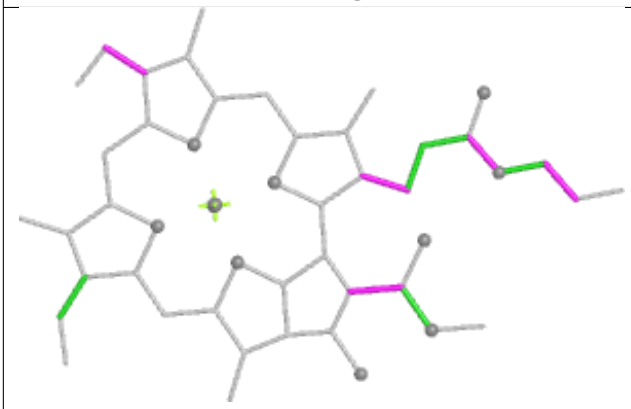
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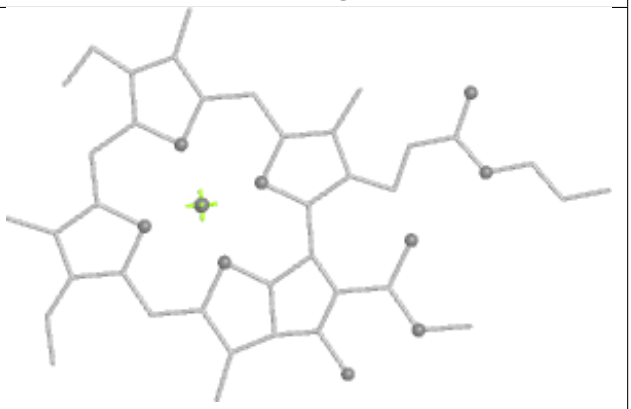
Bond lengths



Bond angles

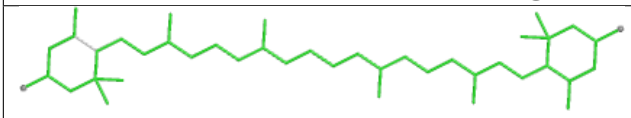


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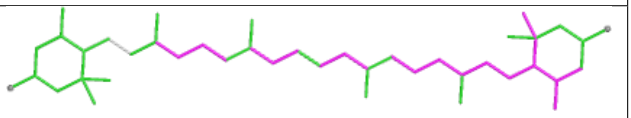


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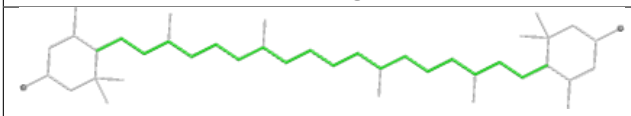
Ligand LUT n 309



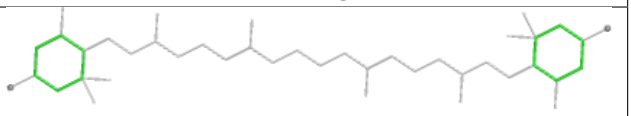
Bond lengths



Bond angles

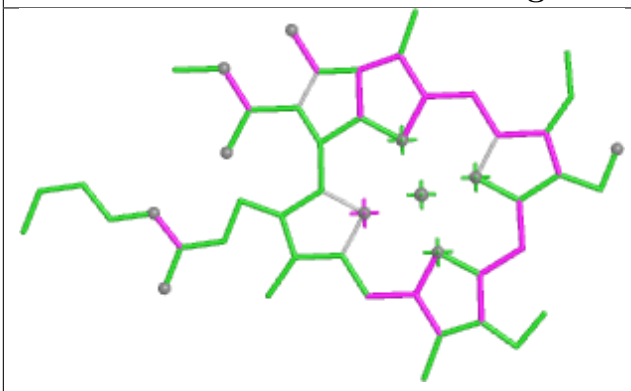


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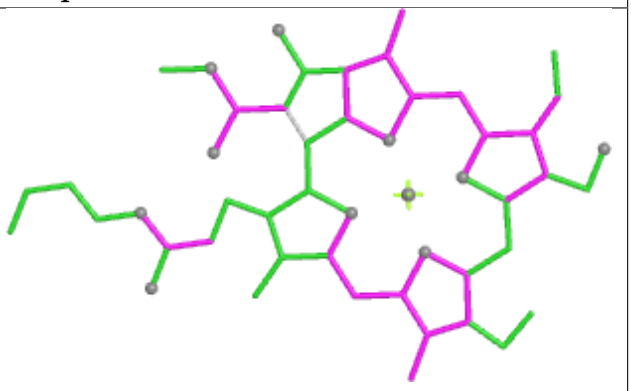


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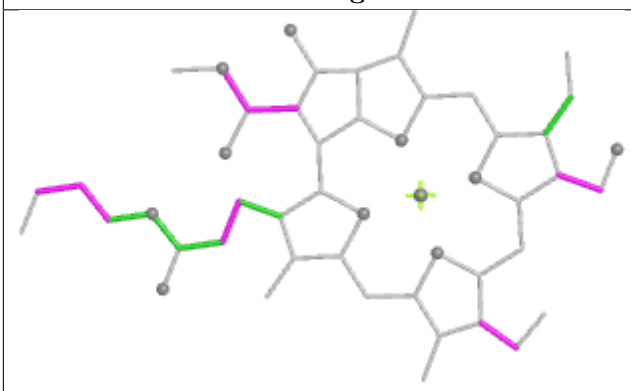
Ligand CHL q 313



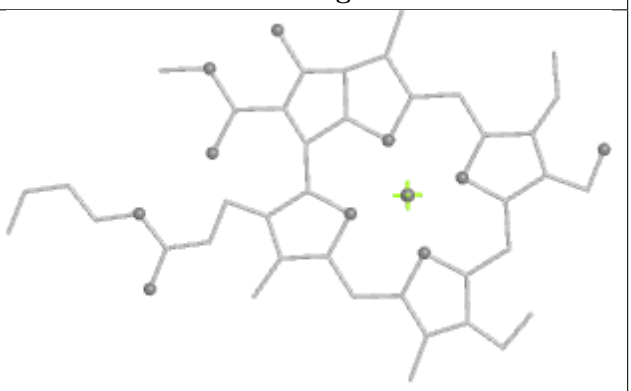
Bond lengths



Bond angles

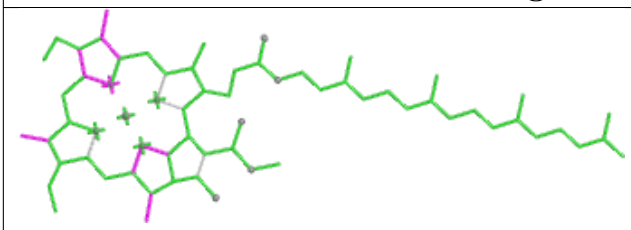


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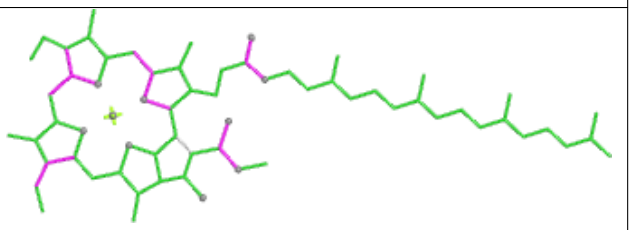


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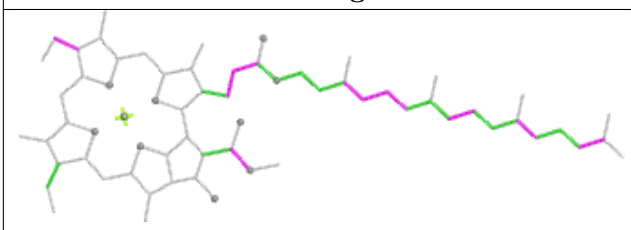
Ligand CLA u 307



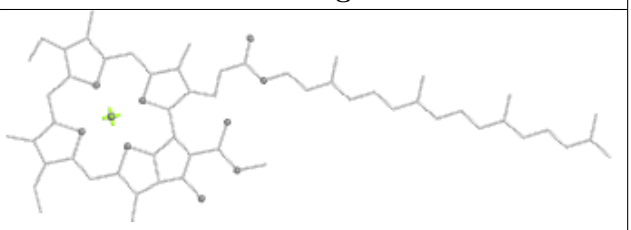
Bond lengths



Bond angles

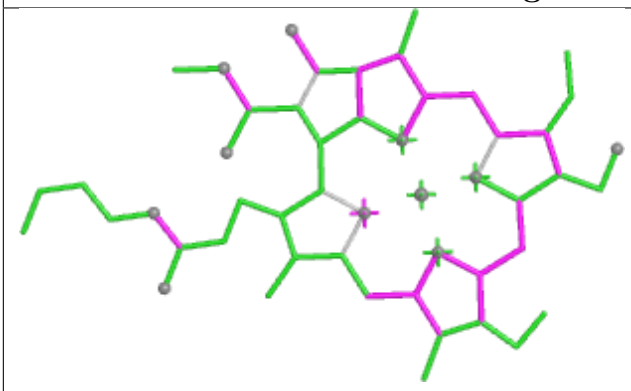


Torsions

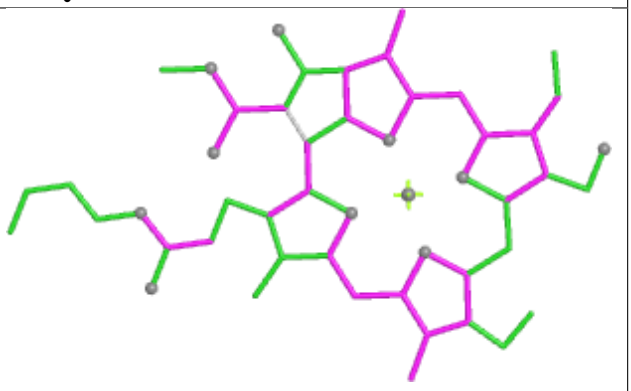


Rings

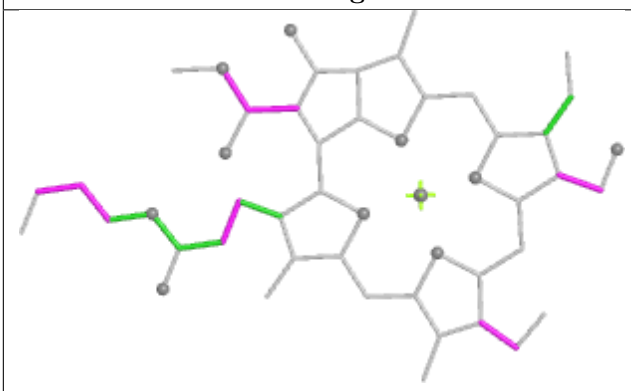
Ligand CHL Q 313



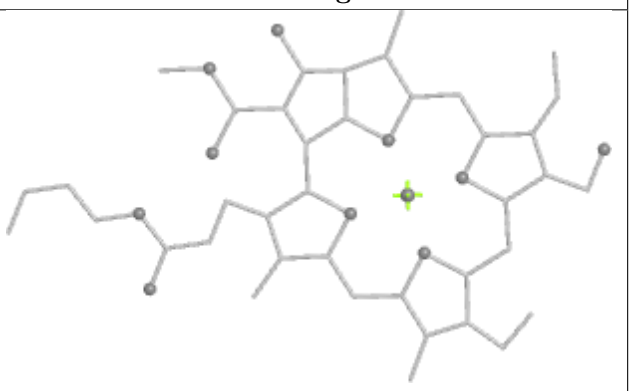
Bond lengths



Bond angles

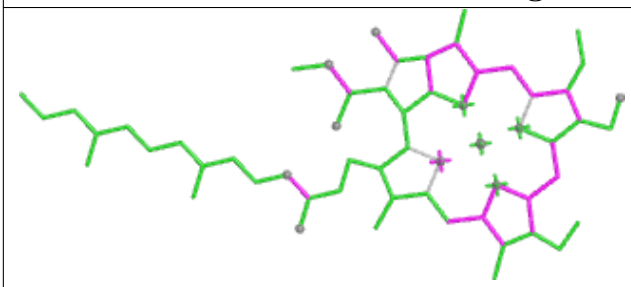


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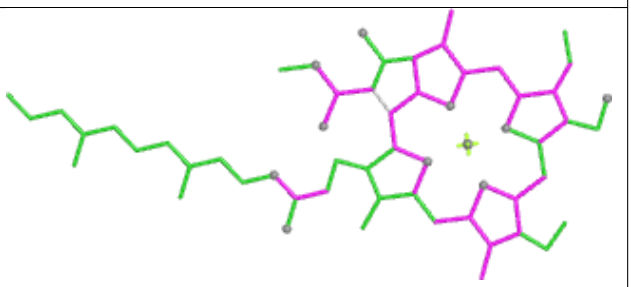


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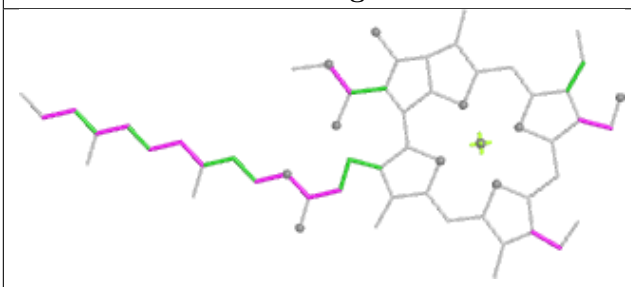
Ligand CHL S 315



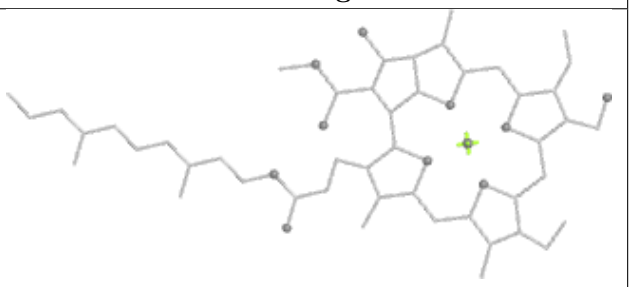
Bond lengths



Bond angles

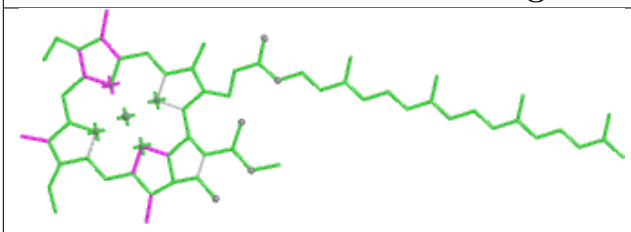


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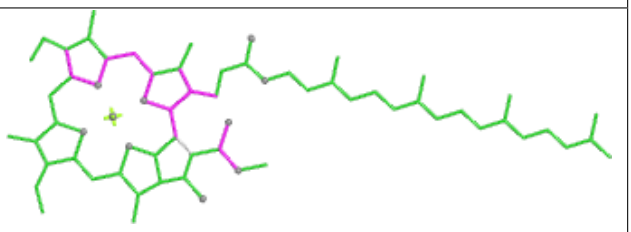


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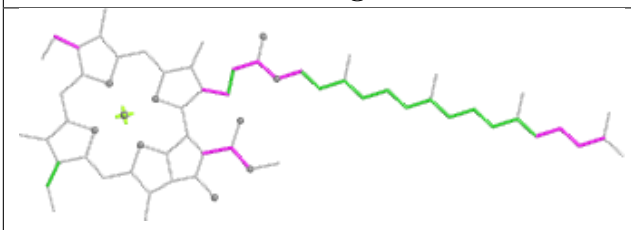
Ligand CLA b 611



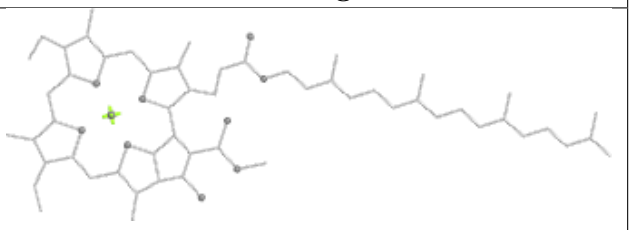
Bond lengths



Bond angles

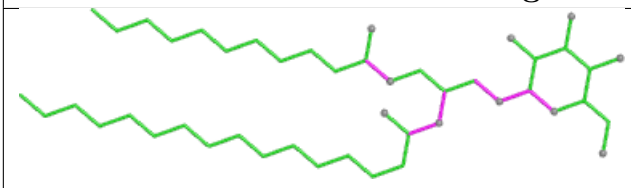


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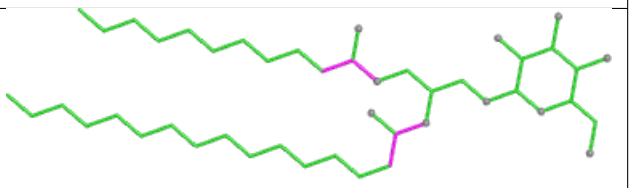


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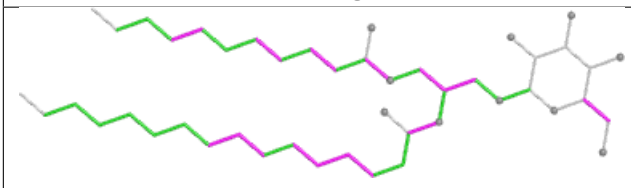
Ligand LMG d 407



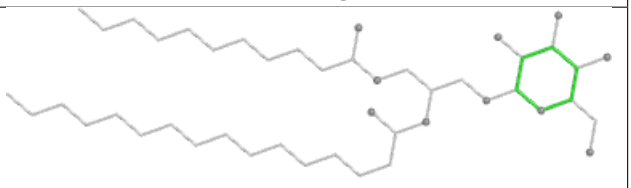
Bond lengths



Bond angles

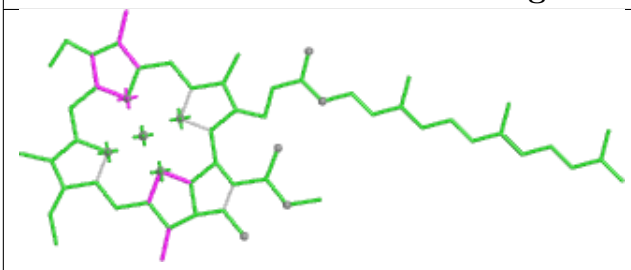


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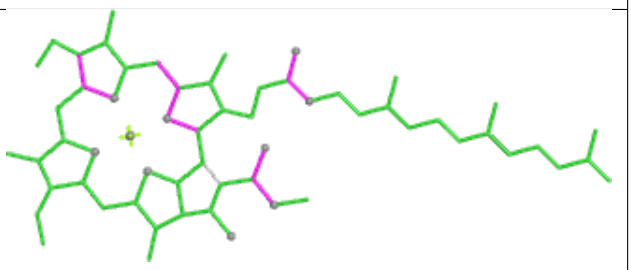


Rings

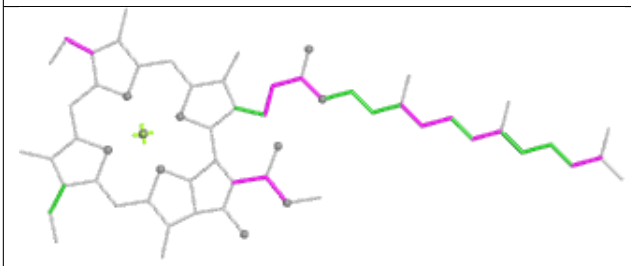
Ligand CLA 3 306



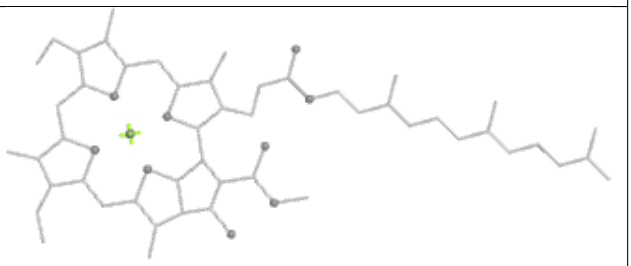
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Bond angles

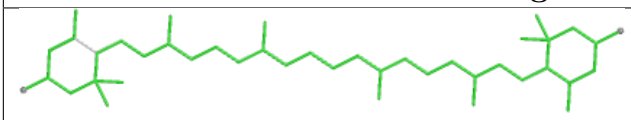


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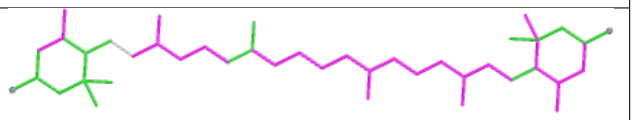


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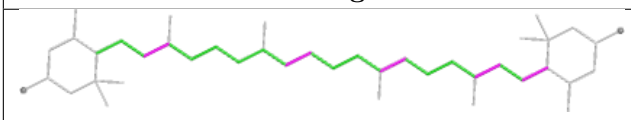
Ligand LUT s 311



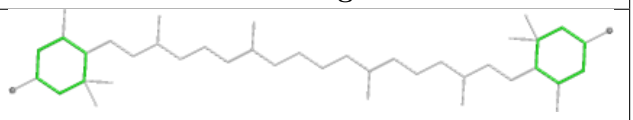
Bond lengths



Bond angles

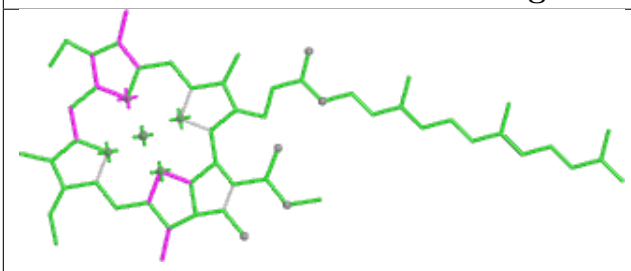


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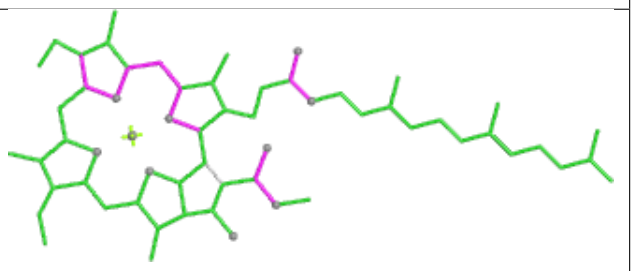


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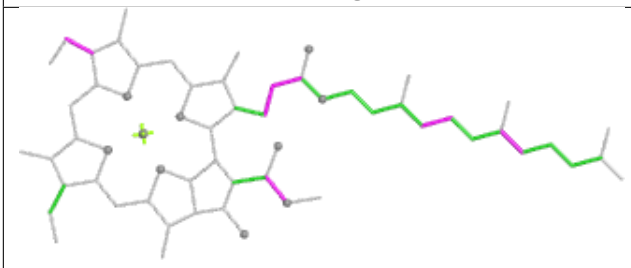
Ligand CLA 2 307



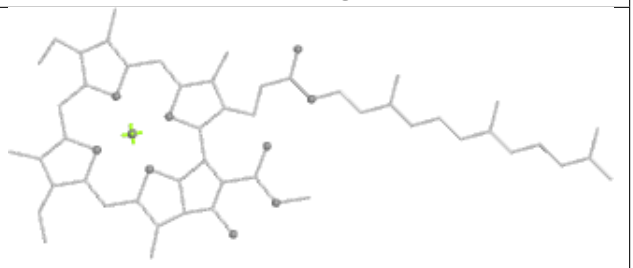
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Bond angles

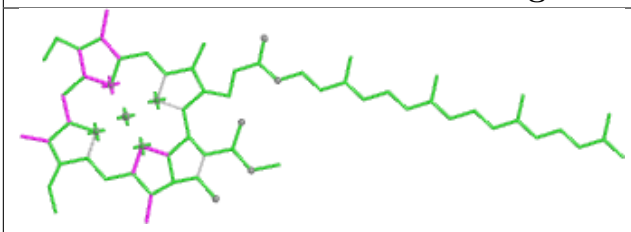


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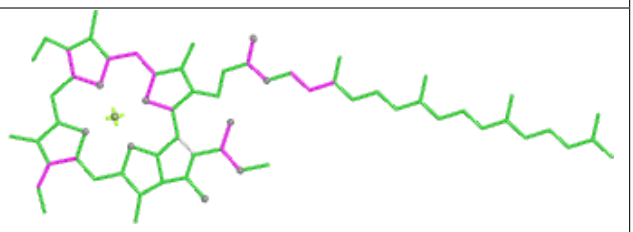


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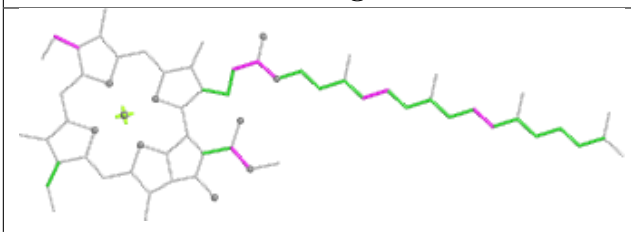
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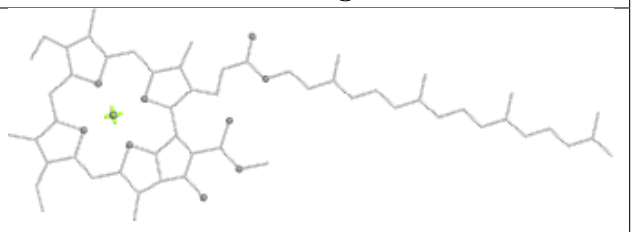
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Bond angles

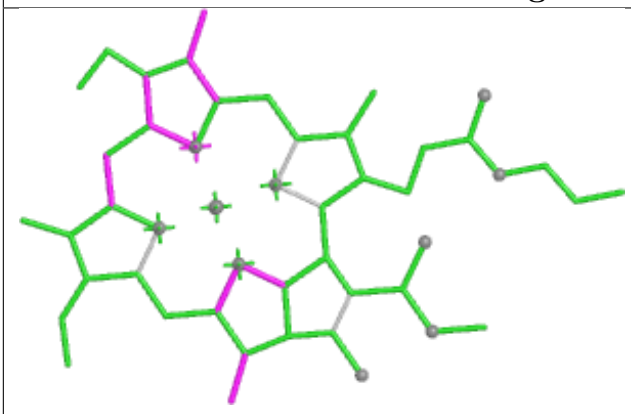


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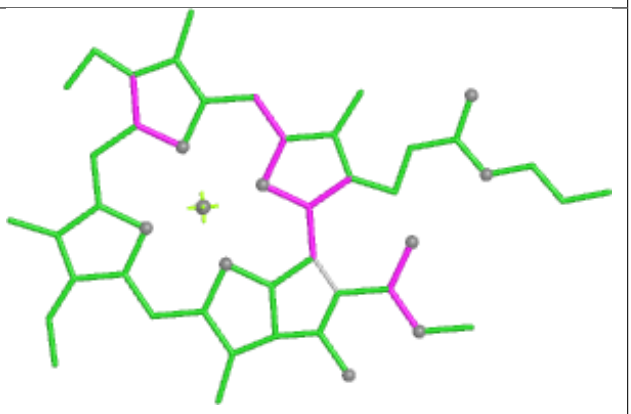


Rings

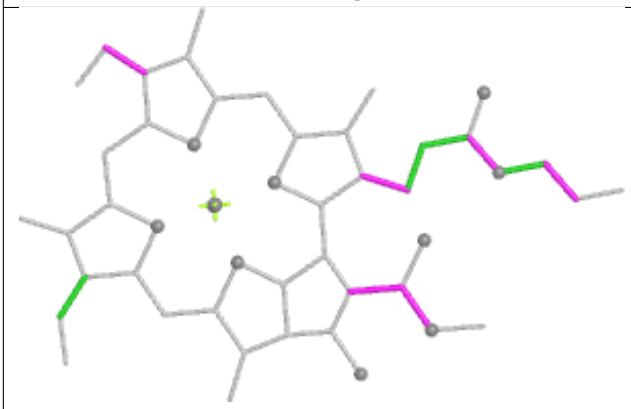
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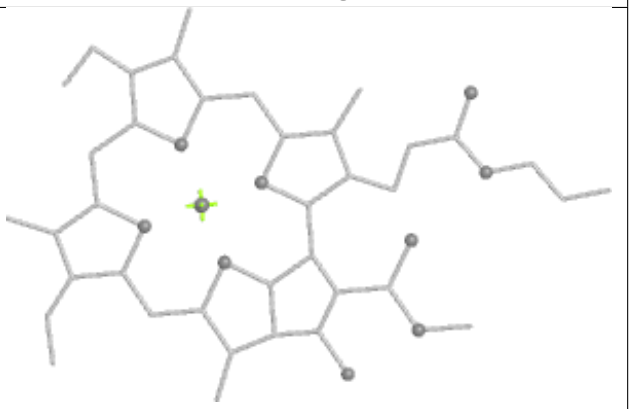
Bond lengths



Bond angles

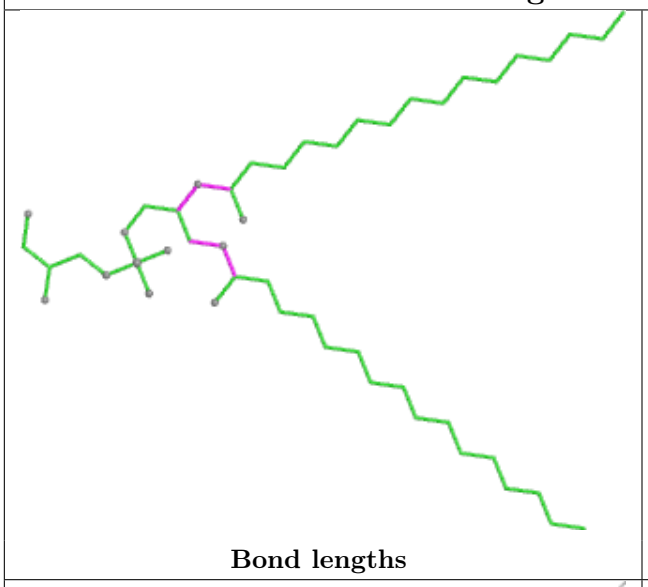


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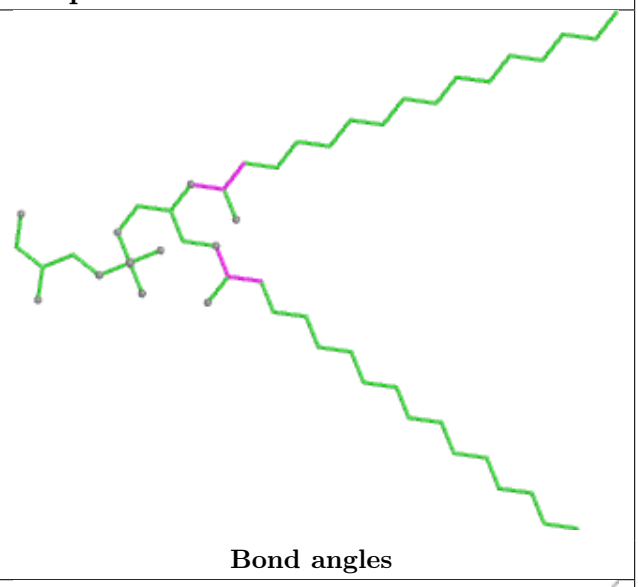


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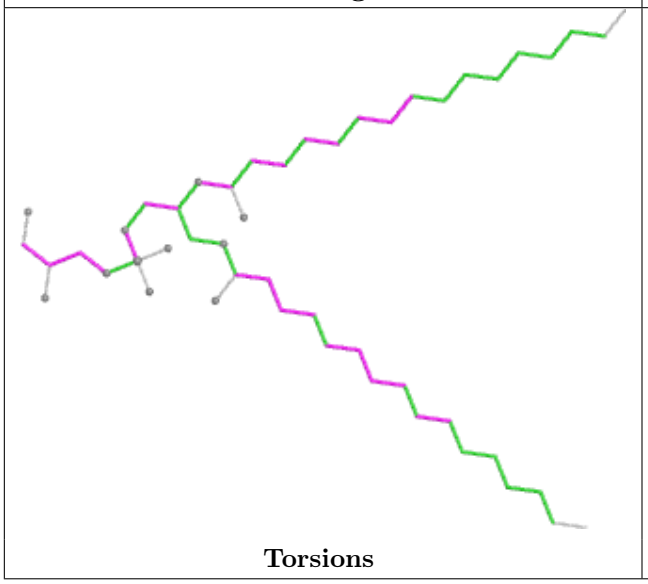
Ligand LHG q 310



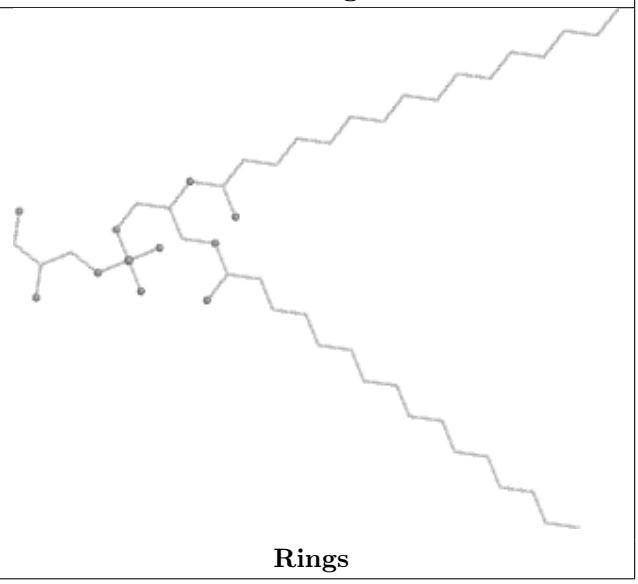
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Bond angles

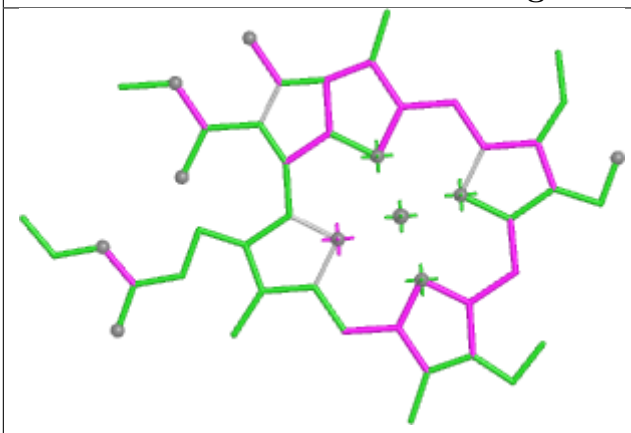


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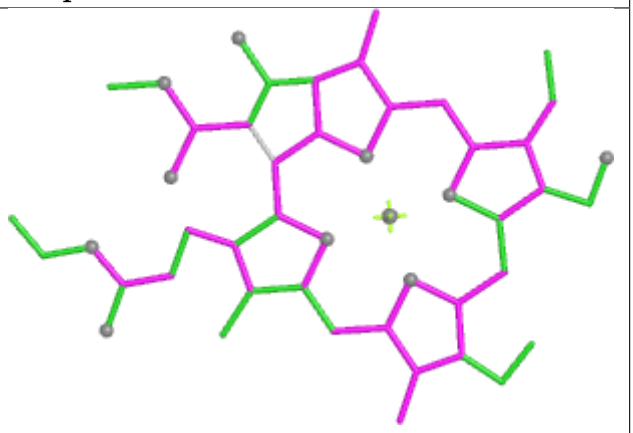


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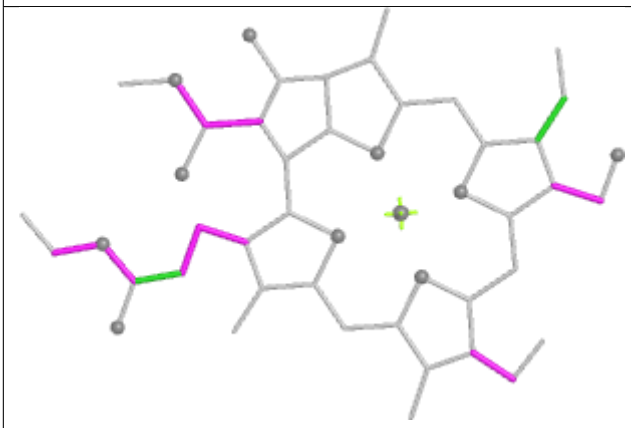
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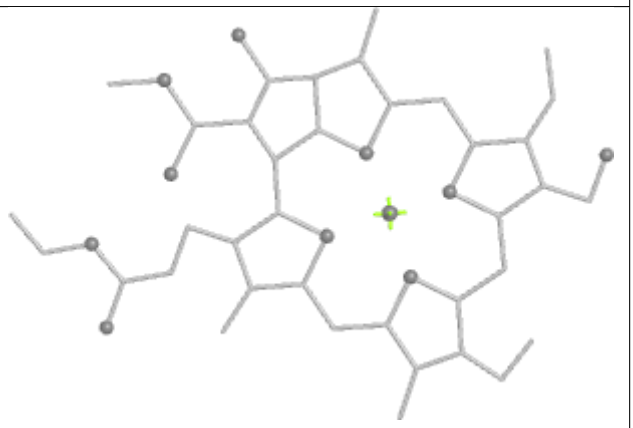
Bond lengths



Bond angles

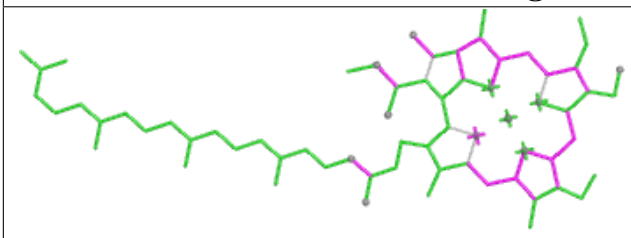


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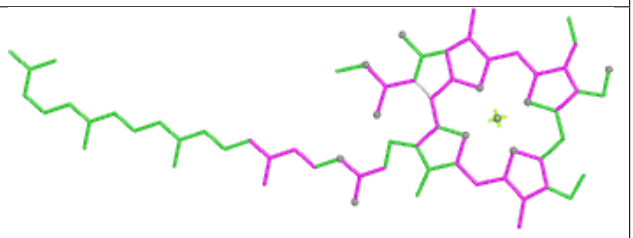


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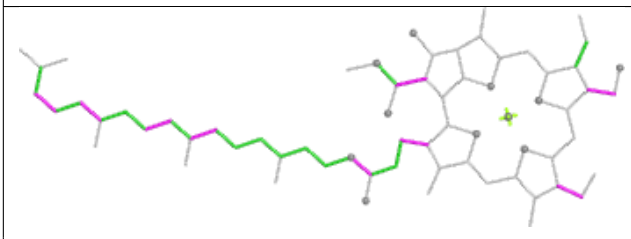
Ligand CHL u 317



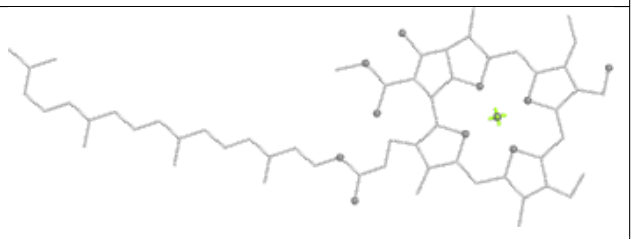
Bond lengths



Bond angles

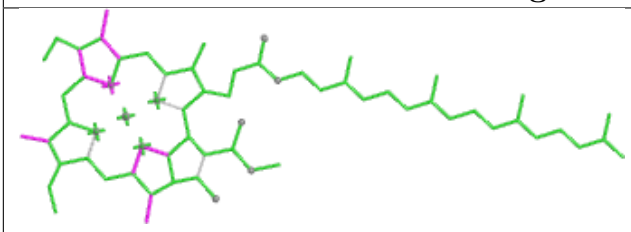


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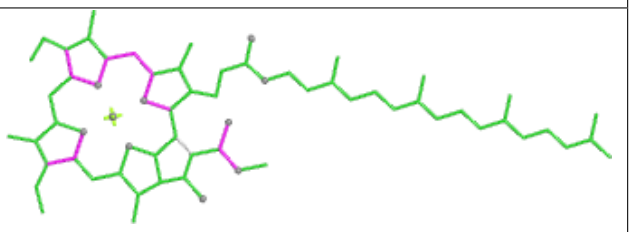


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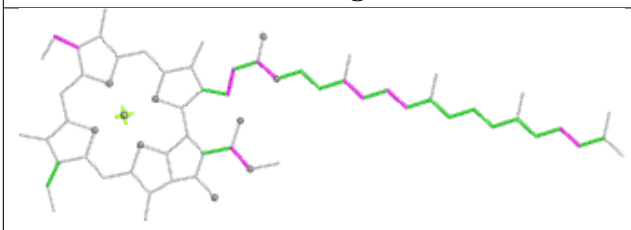
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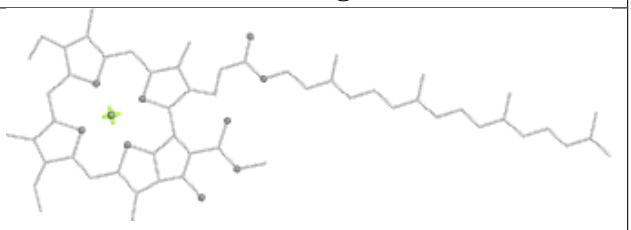
Bond lengths



Bond angles

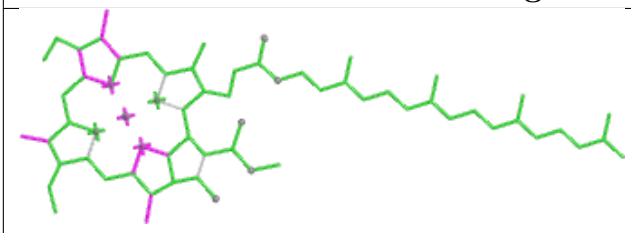


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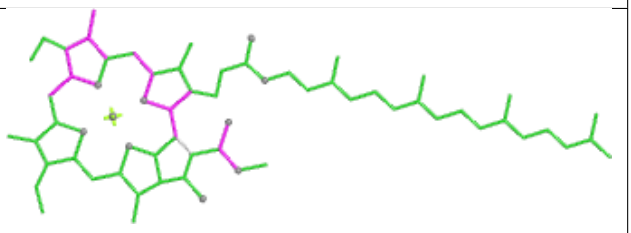


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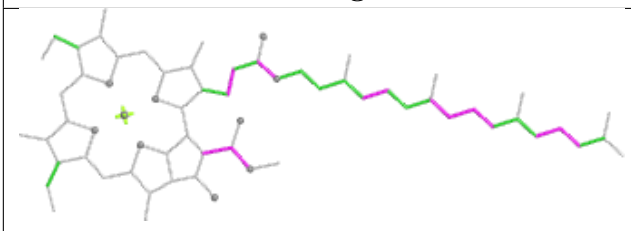
Ligand CLA B 614



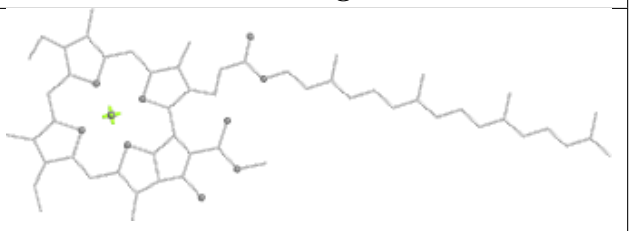
Bond lengths



Bond angles

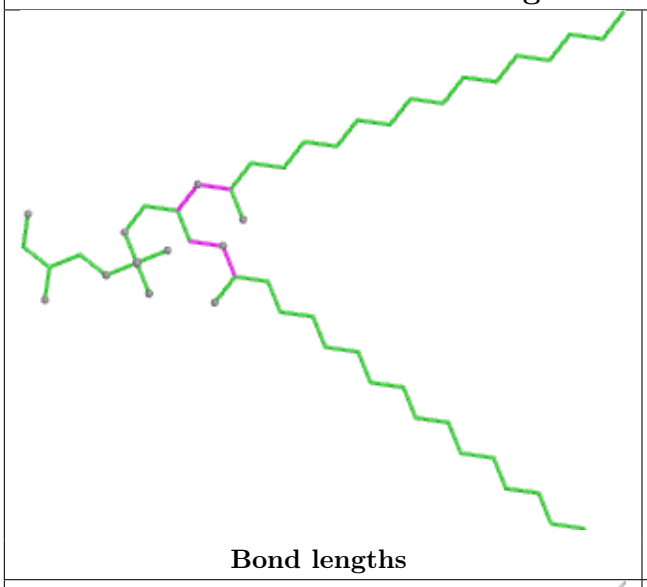


Torsions

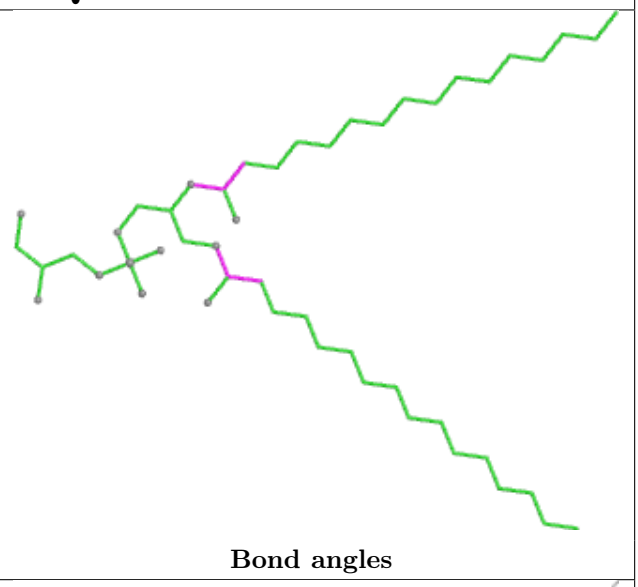


Rings

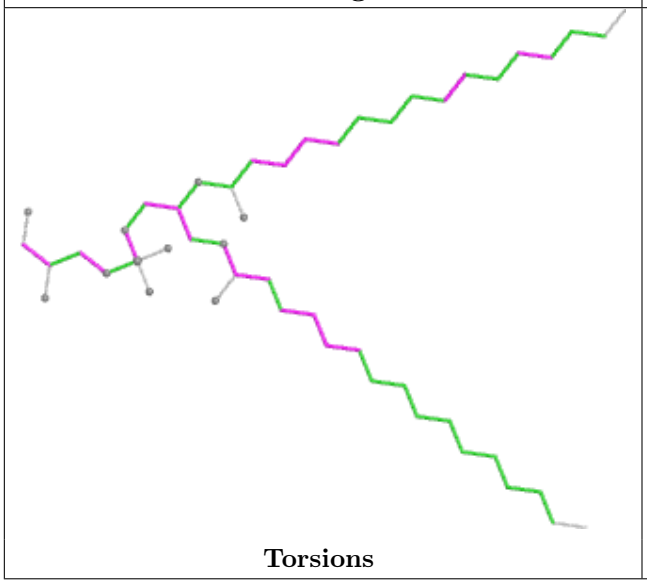
Ligand LHG Q 310



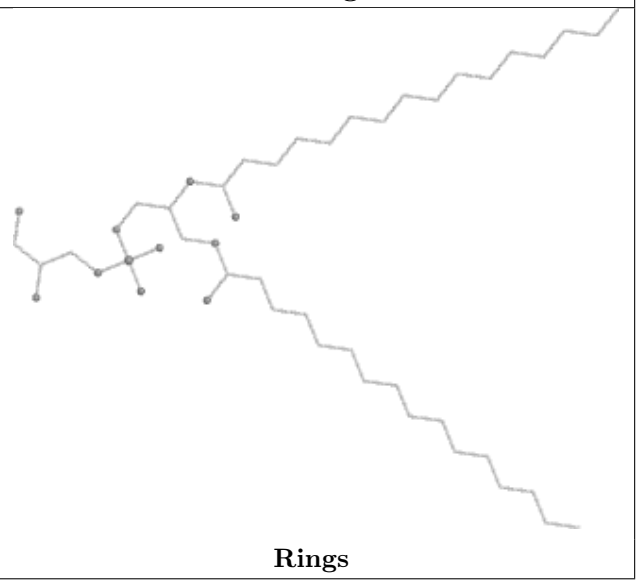
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Bond angles

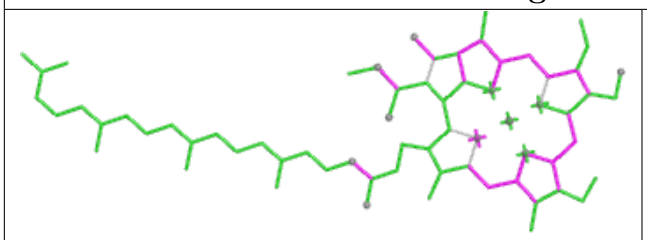


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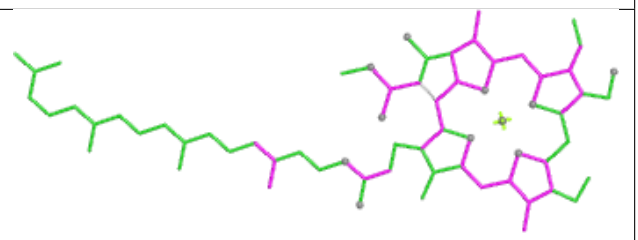


Rings

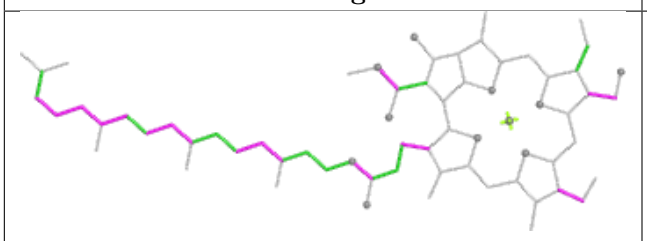
Ligand CHL 5 318



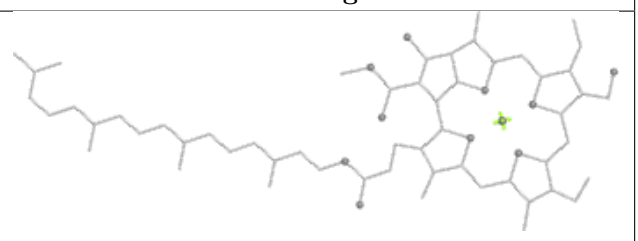
Bond lengths



Bond angles

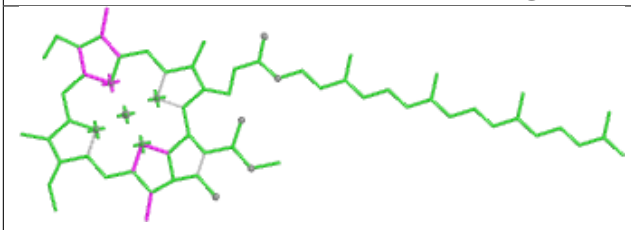


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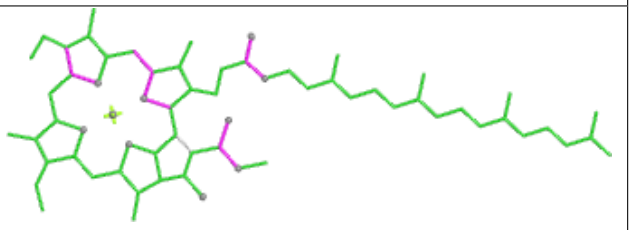


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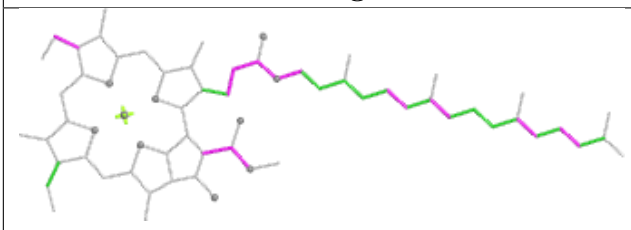
Ligand CLA G 302



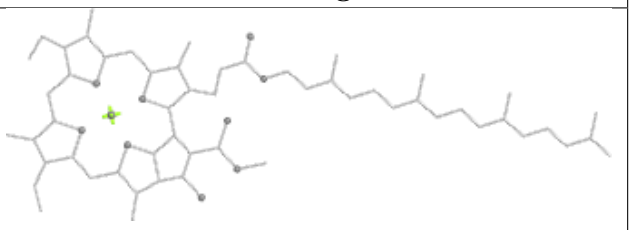
Bond lengths



Bond angles

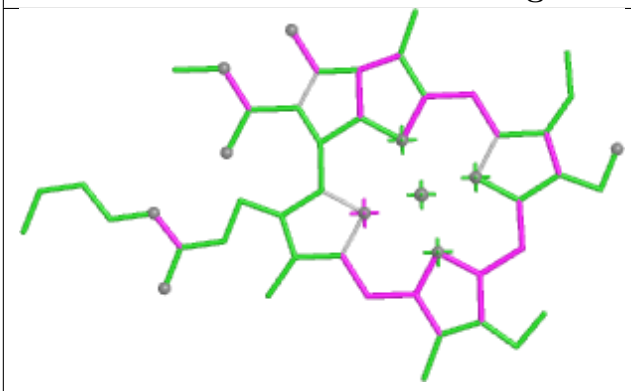


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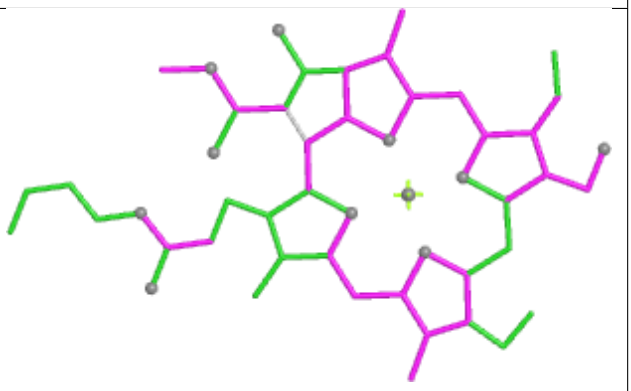


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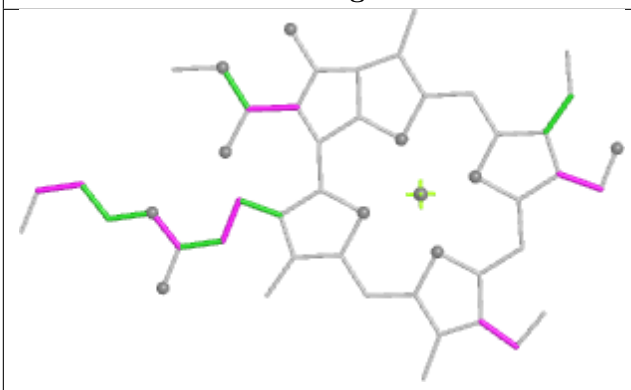
Ligand CHL u 315



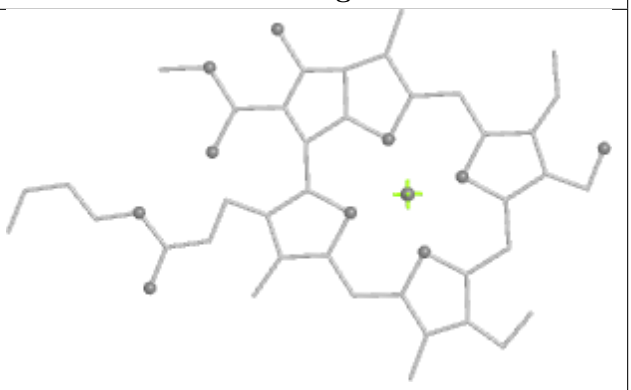
Bond lengths



Bond angles

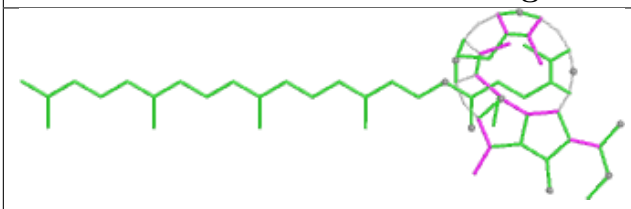


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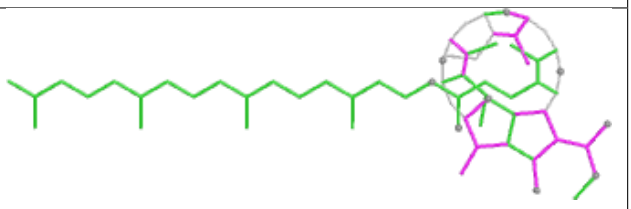


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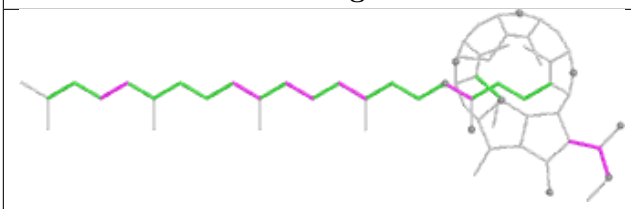
Ligand PHO A 407



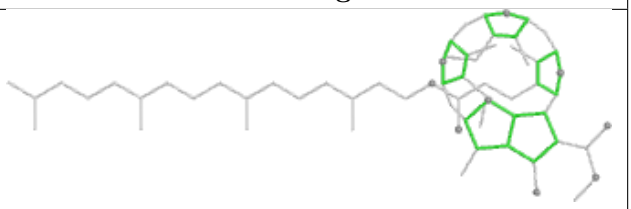
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Bond angles

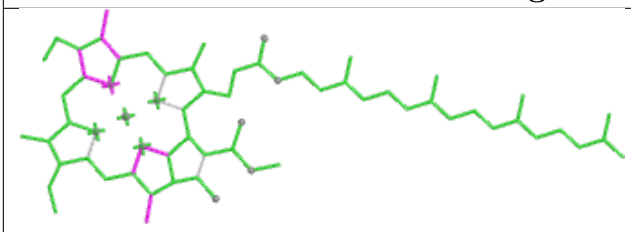


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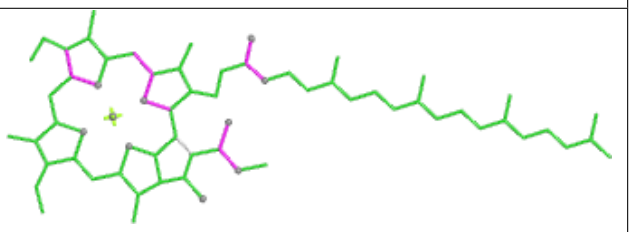


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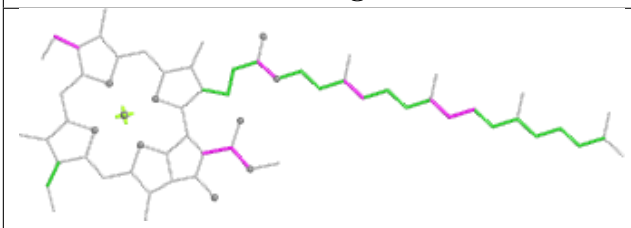
Ligand CLA 6 303



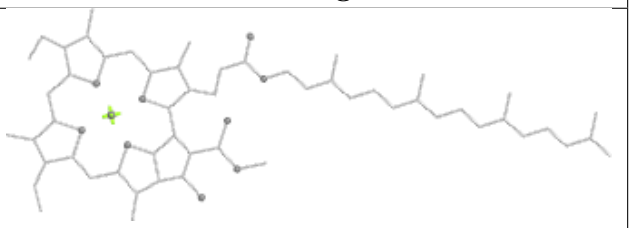
Bond lengths



Bond angles

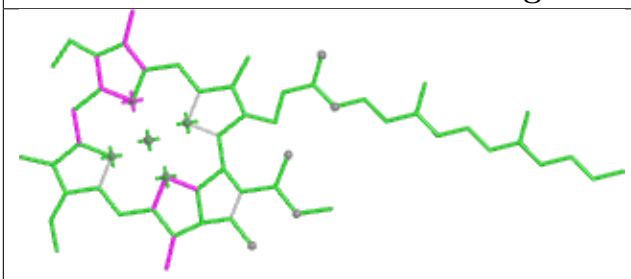


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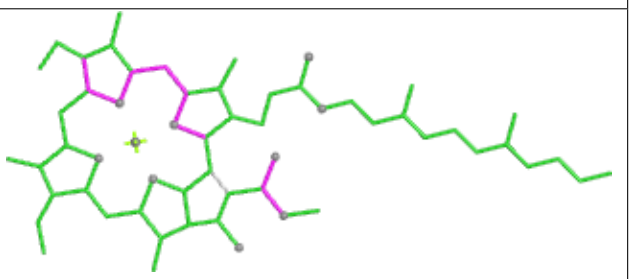


Rings

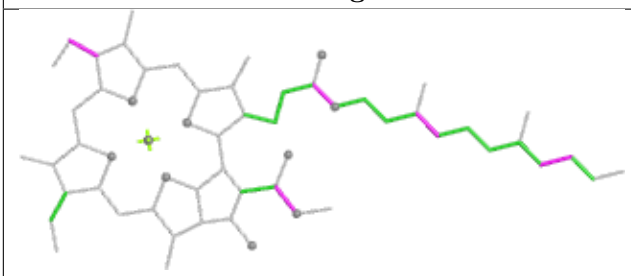
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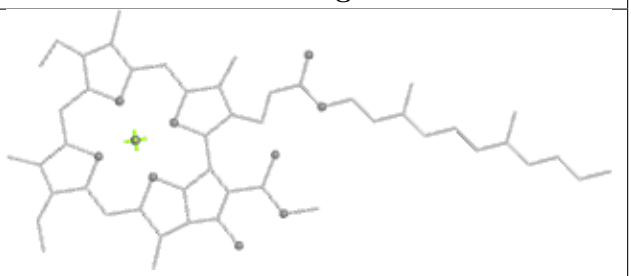
Bond lengths



Bond angles

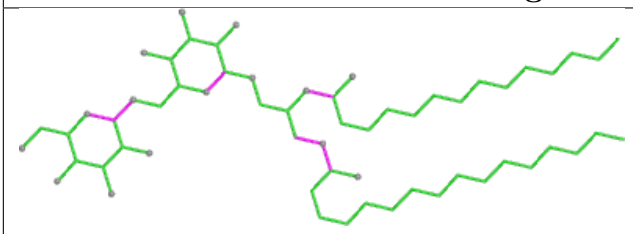


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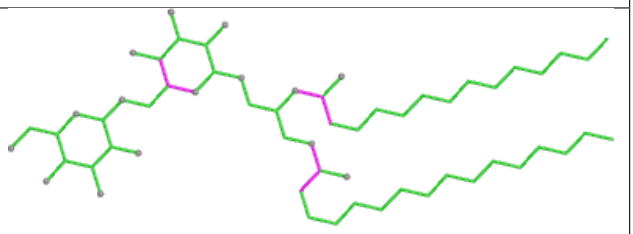


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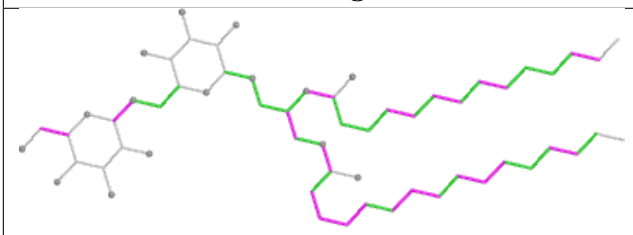
Ligand DGD c 519



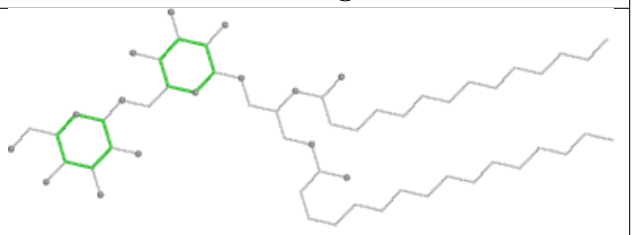
Bond lengths



Bond angles

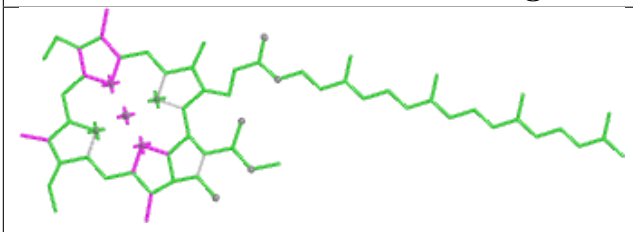


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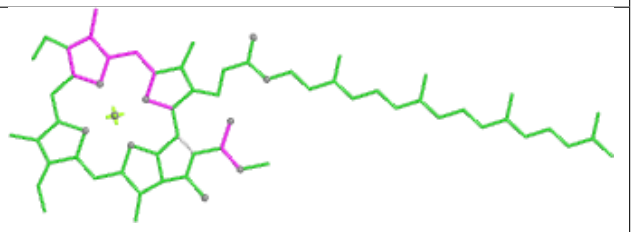


Rings

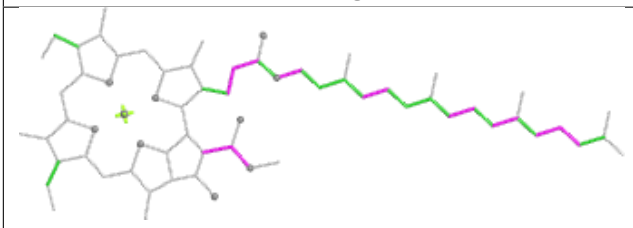
Ligand CLA B 609



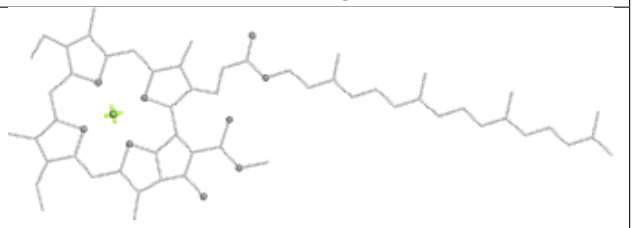
Bond lengths



Bond angles

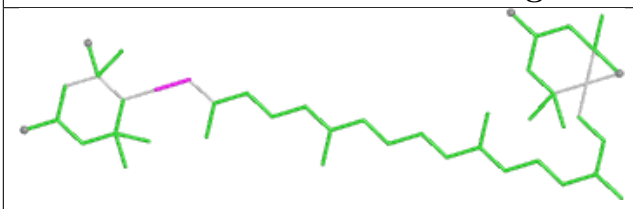


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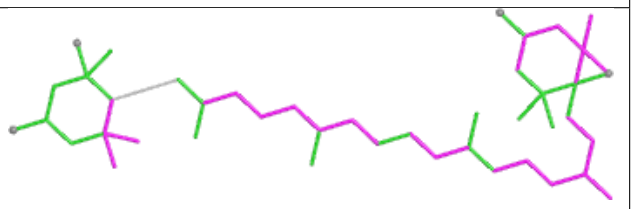


Rings

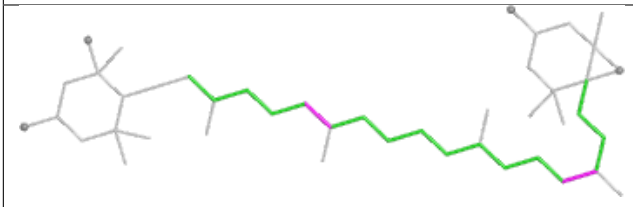
Ligand NEX v 319



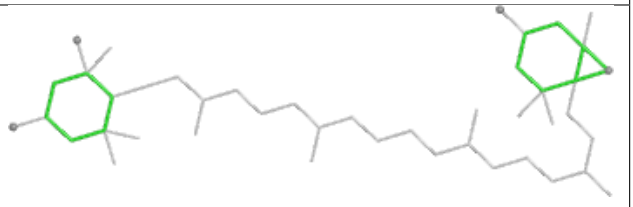
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Bond angles

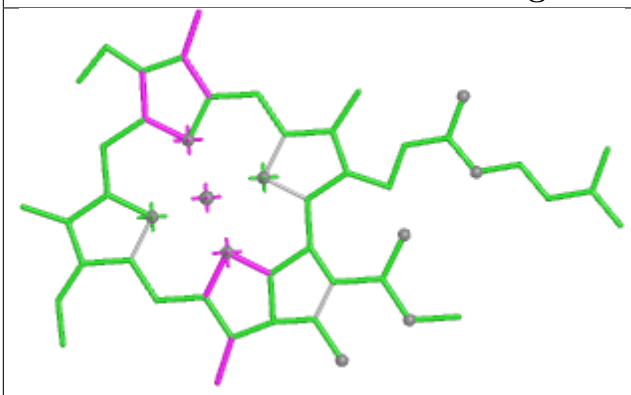


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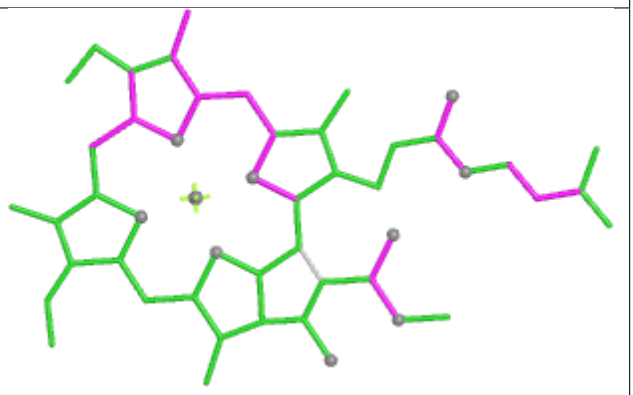


Rings

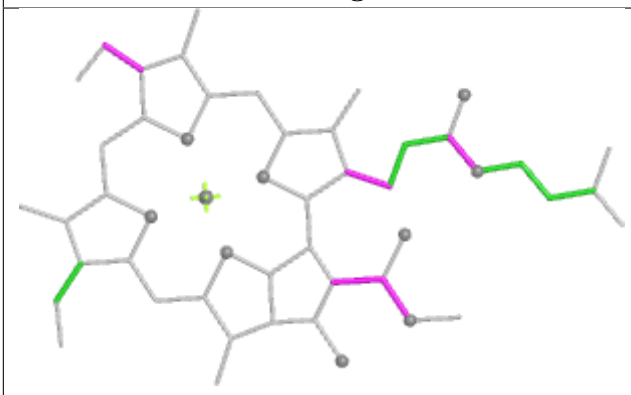
Ligand CLA 4 303



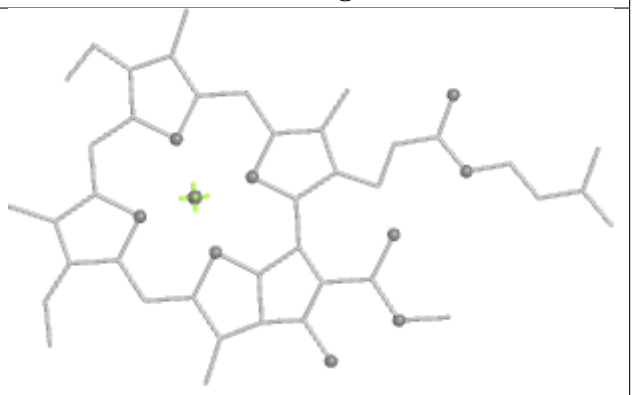
Bond lengths



Bond angles

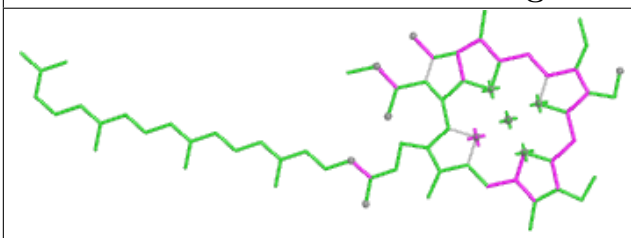


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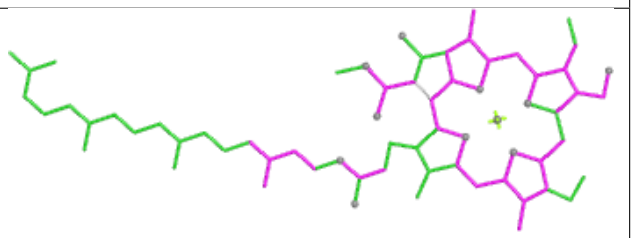


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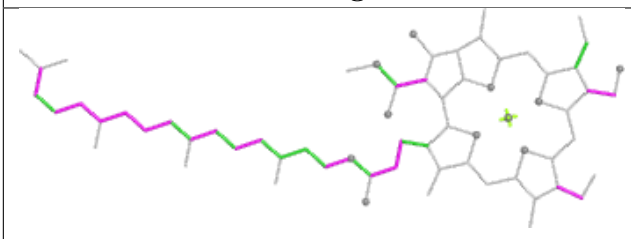
Ligand CHL n 313



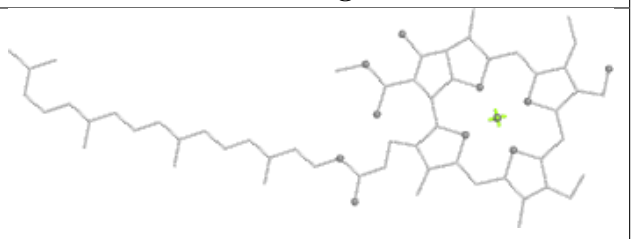
Bond lengths



Bond angles

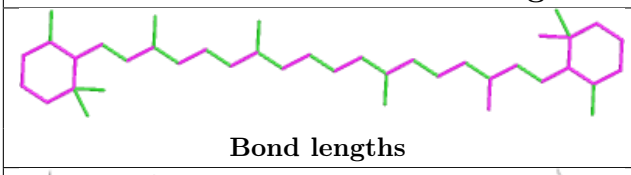


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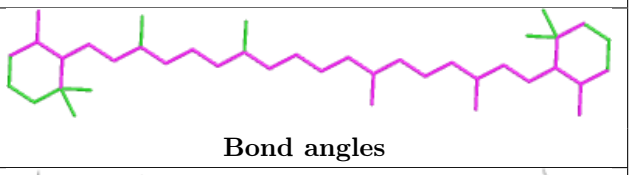


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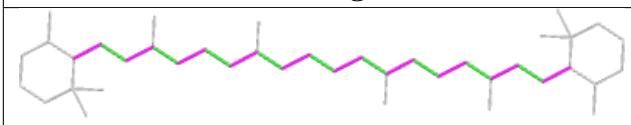
Ligand BCR c 515



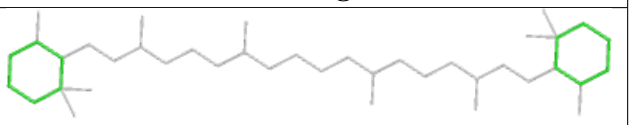
Bond lengths



Bond angles

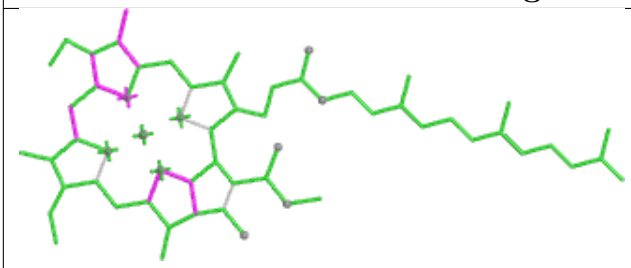


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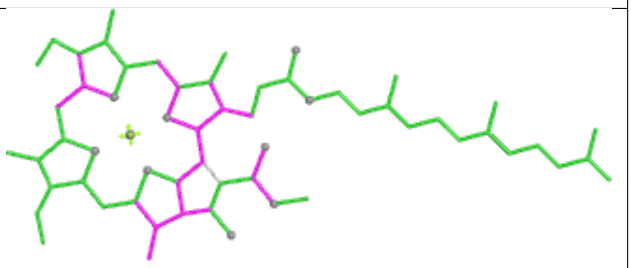


Rings

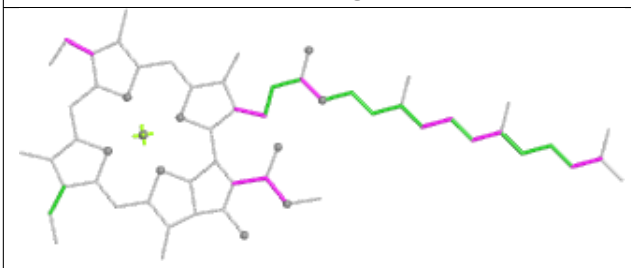
Ligand CLA N 305



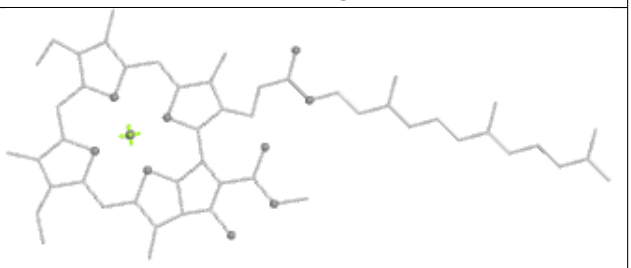
Bond lengths



Bond angles

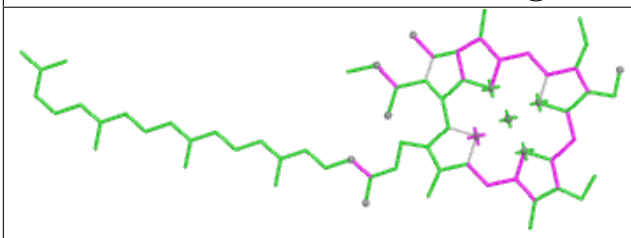


Torsions

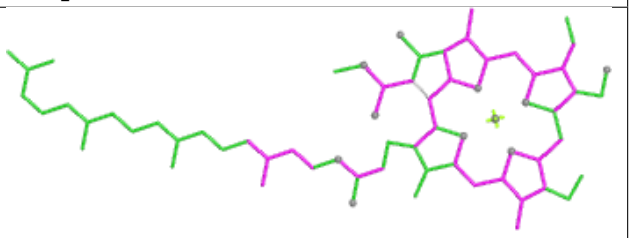


Rings

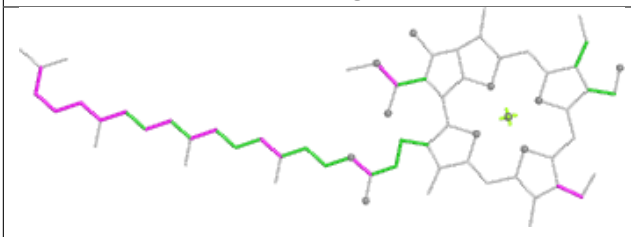
Ligand CHL q 311



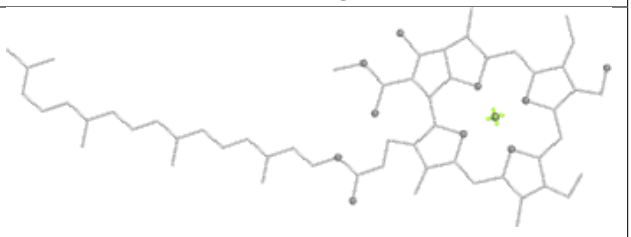
Bond lengths



Bond angles

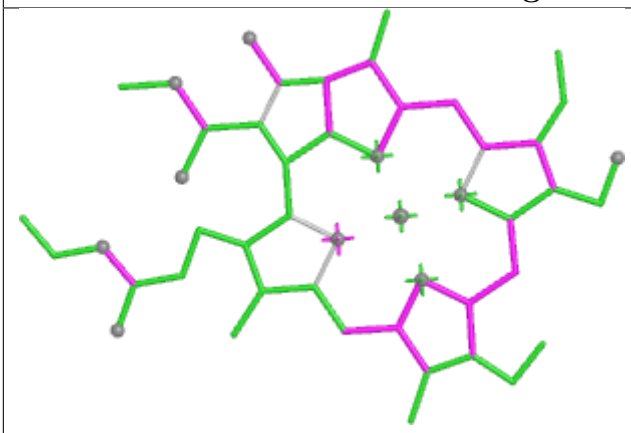


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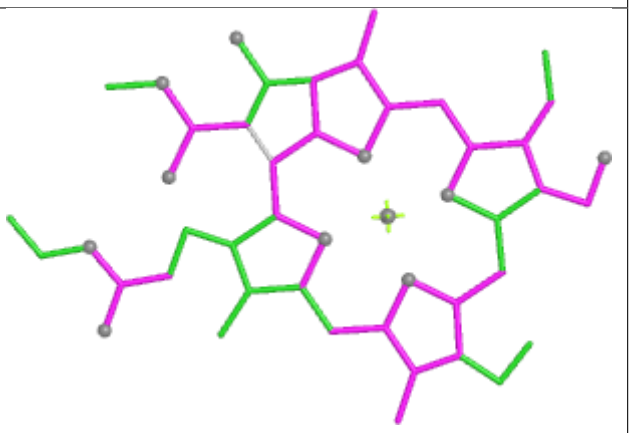


Rings

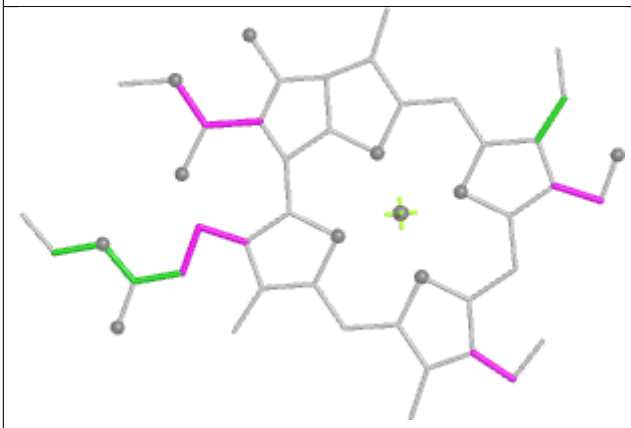
Ligand CHL N 314



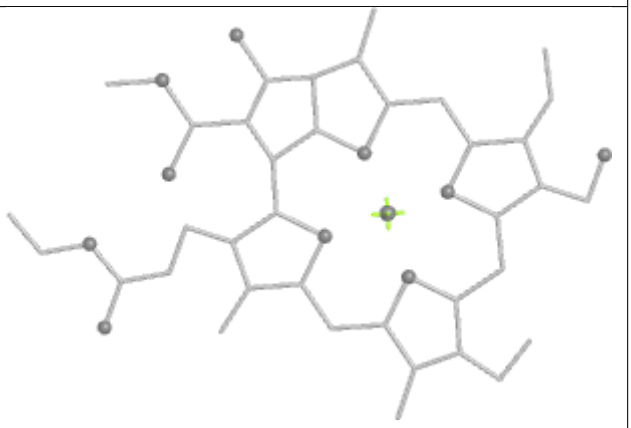
Bond lengths



Bond angles

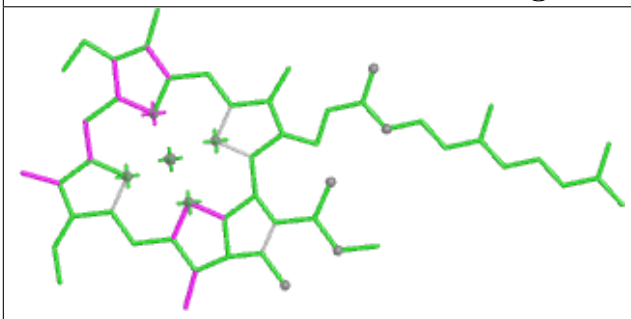


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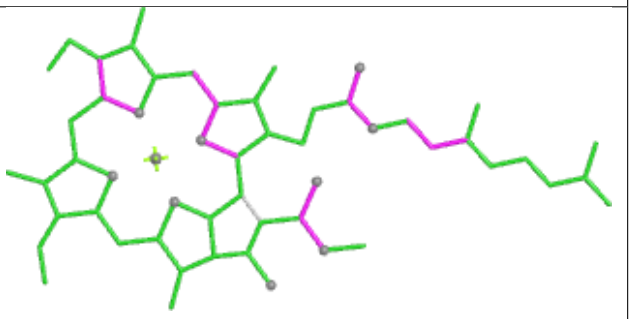


Rings

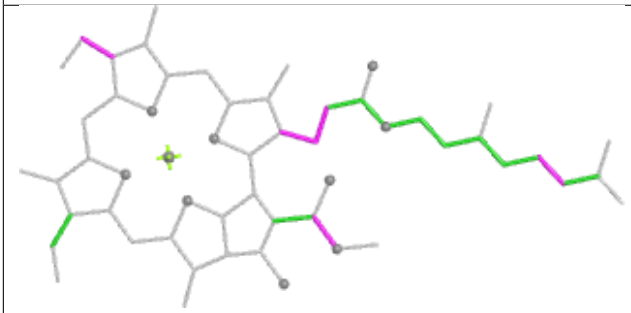
Ligand CLA s 305



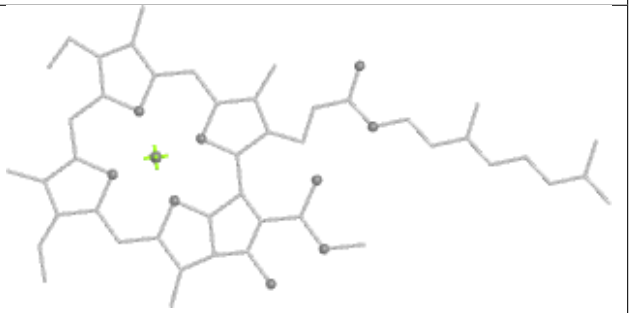
Bond lengths



Bond angles

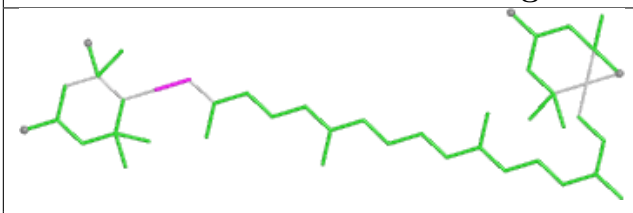


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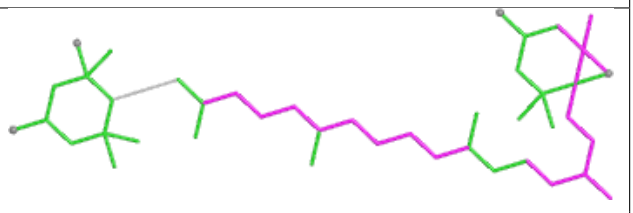


Rings

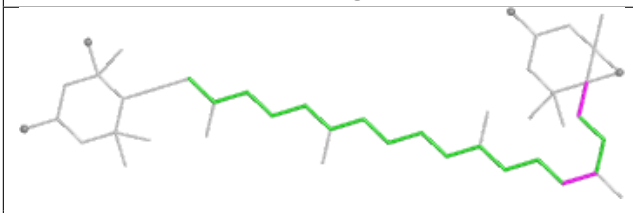
Ligand NEX U 318



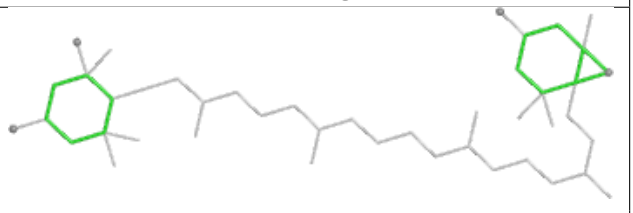
Bond lengths



Bond angles

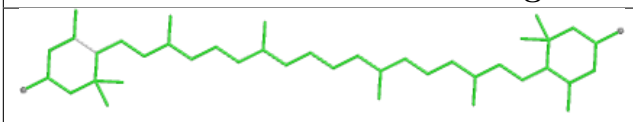


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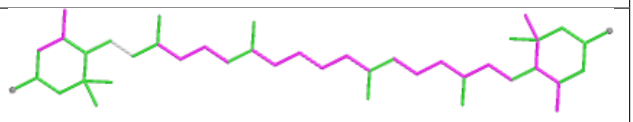


Rings

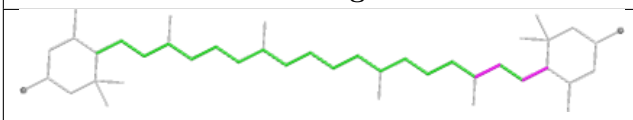
Ligand LUT R 312



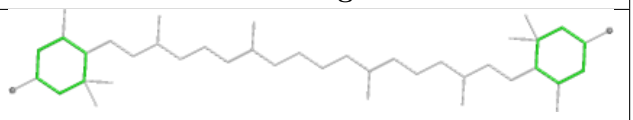
Bond lengths



Bond angles

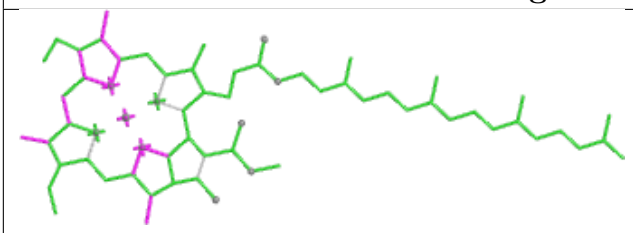


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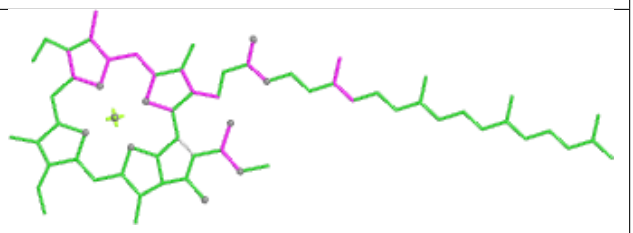


Rings

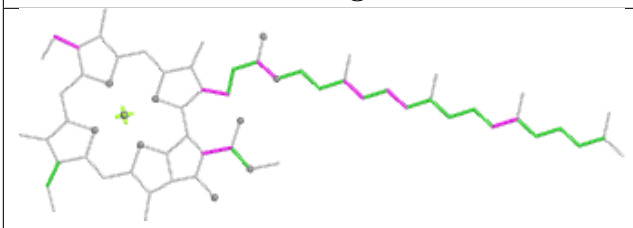
Ligand CLA c 509



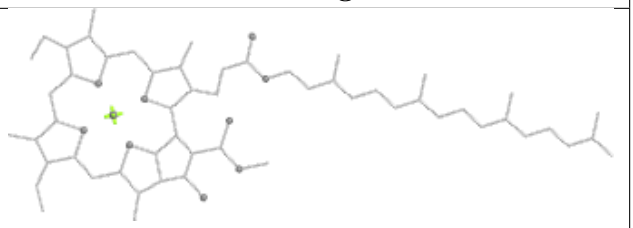
Bond lengths



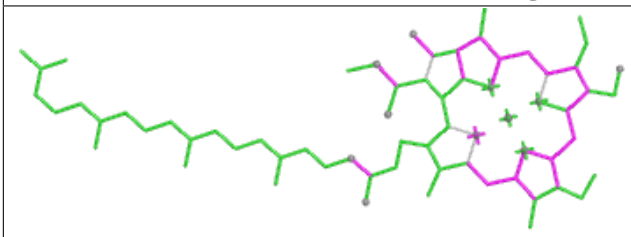
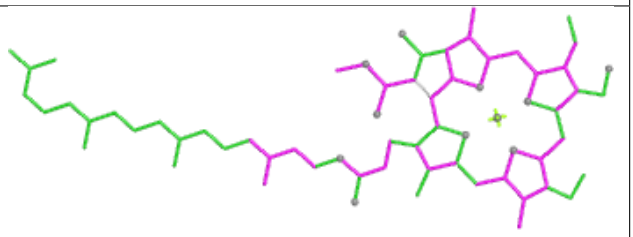
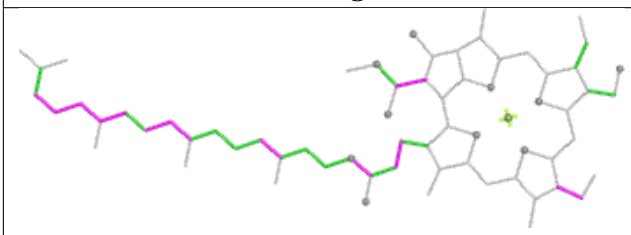
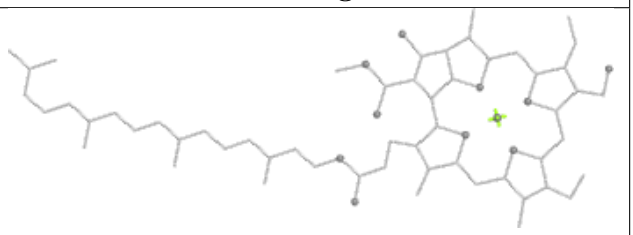
Bond angles

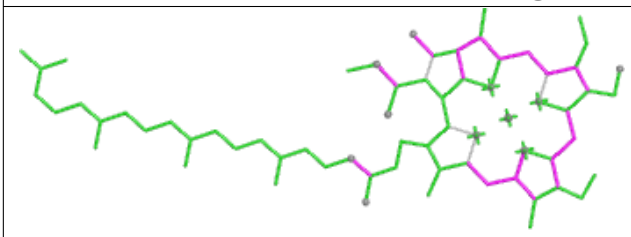
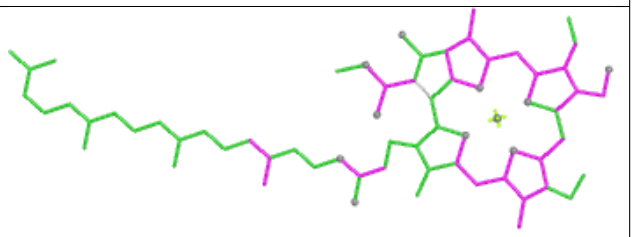
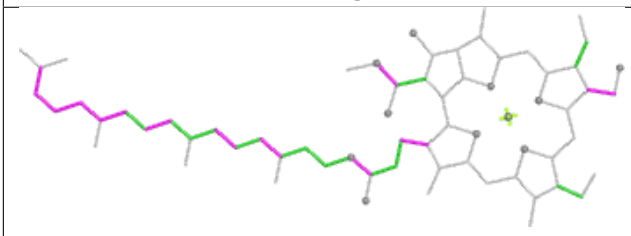
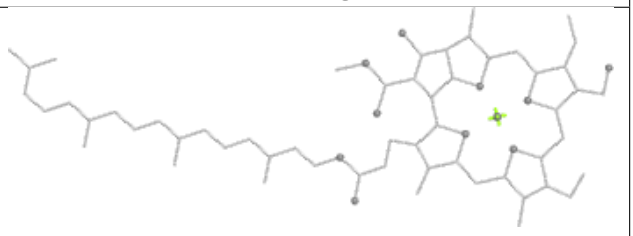


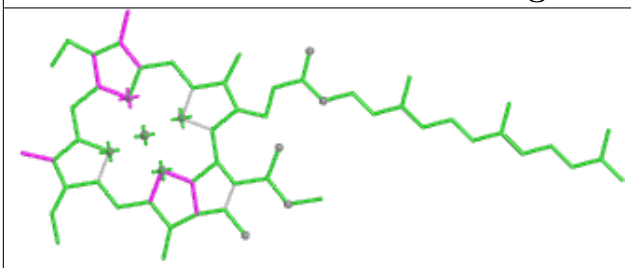
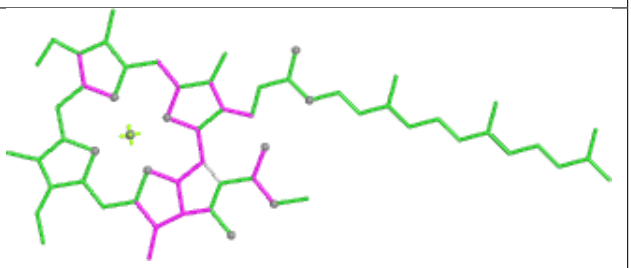
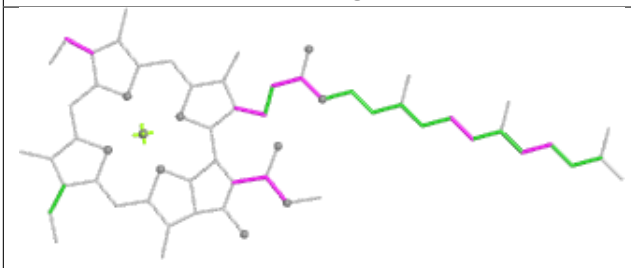
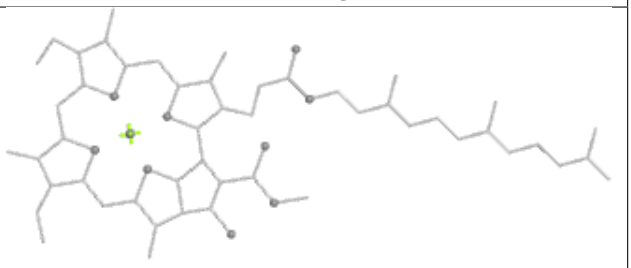
Torsions

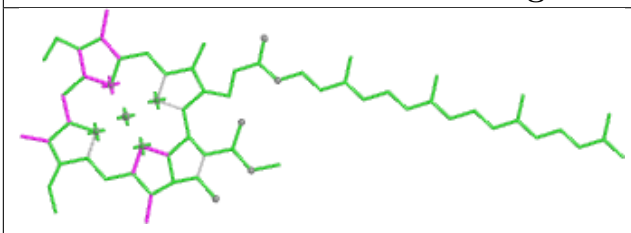
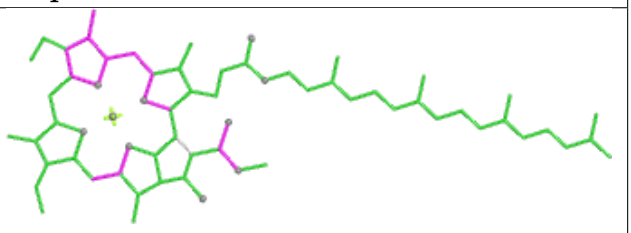
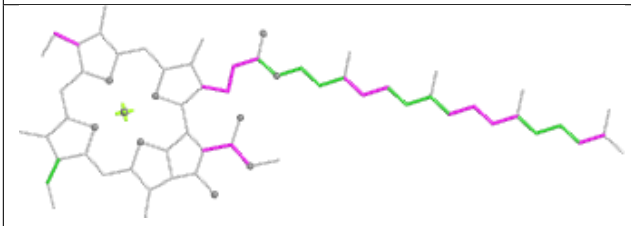
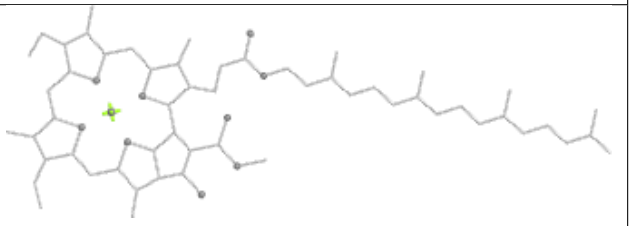


Rings

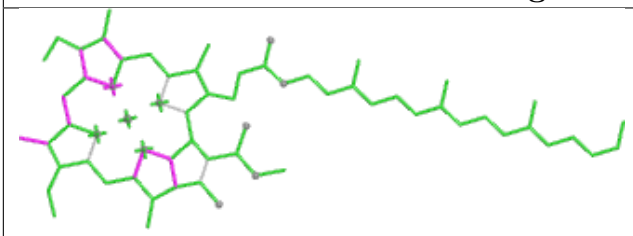
Ligand CHL P 317	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CHL r 614	
	
Bond lengths	Bond angles
	
Torsions	Rings

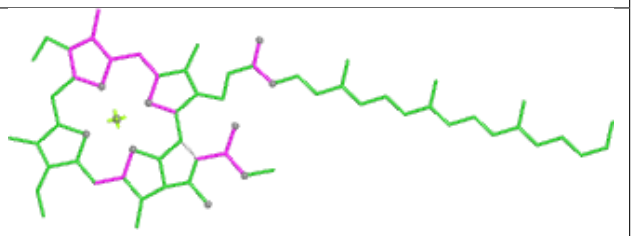
Ligand CLA 5 305	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA p 302	
 Bond lengths	 Bond angles
 Torsions	 Rings

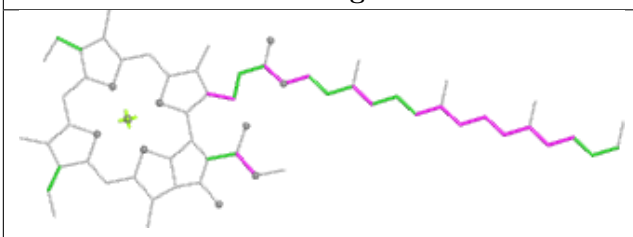
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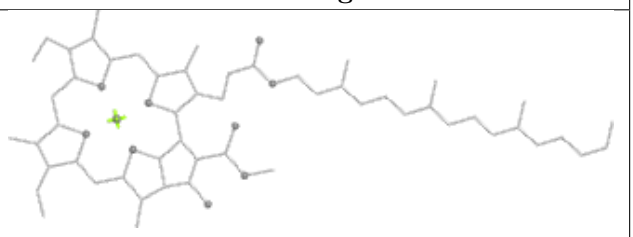
Bond lengths



Bond angles

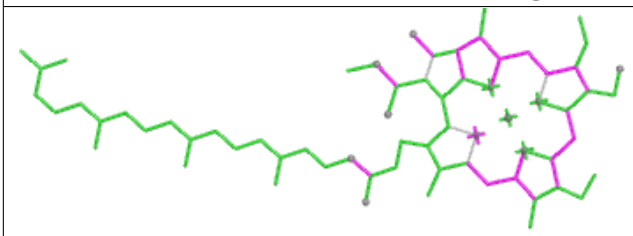


Torsions

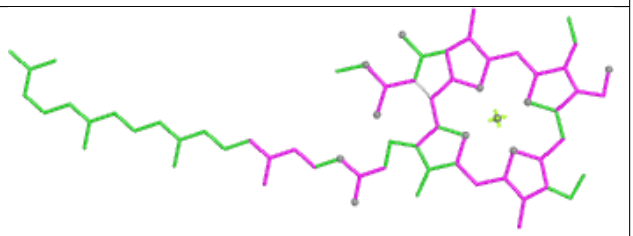


Rings

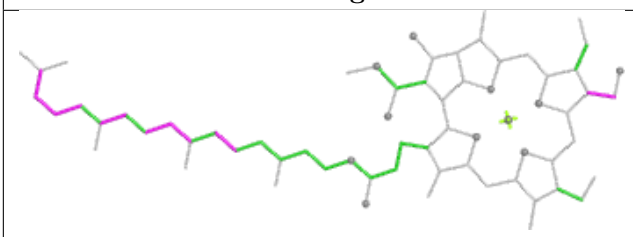
Ligand CHL v 317



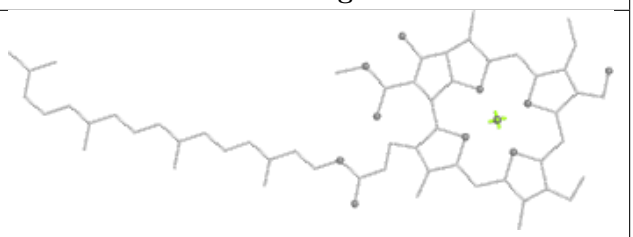
Bond lengths



Bond angles

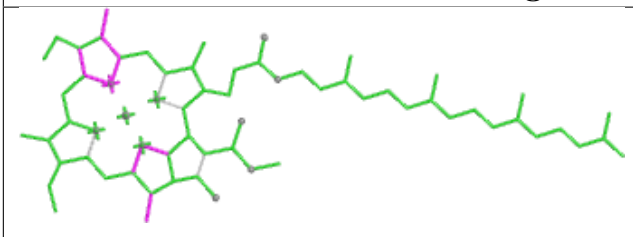


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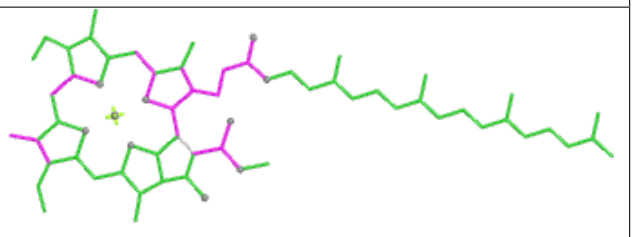


Rings

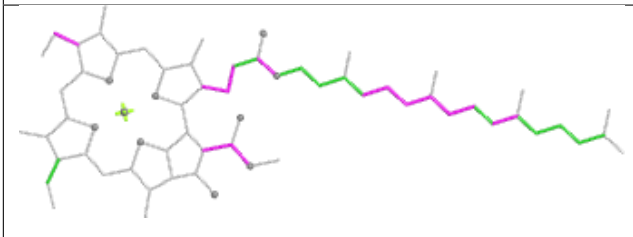
Ligand CLA B 605



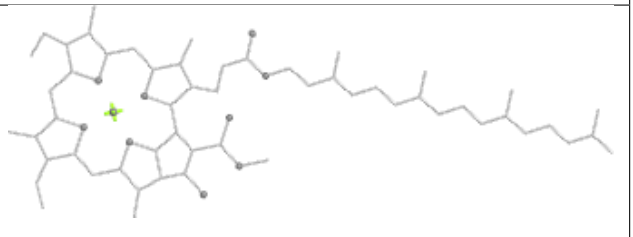
Bond lengths



Bond angles

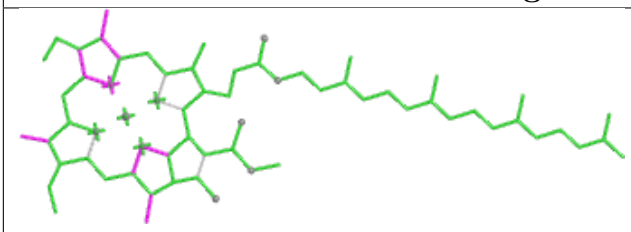


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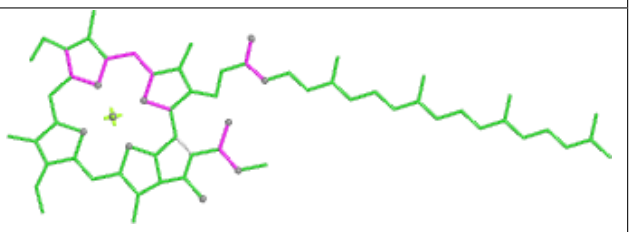


Rings

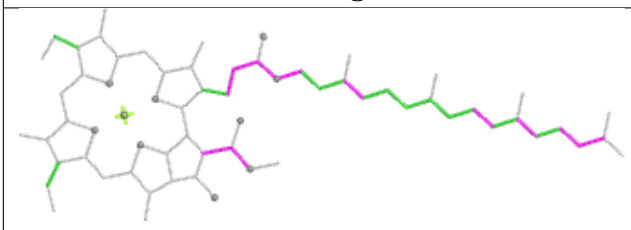
Ligand CLA N 302



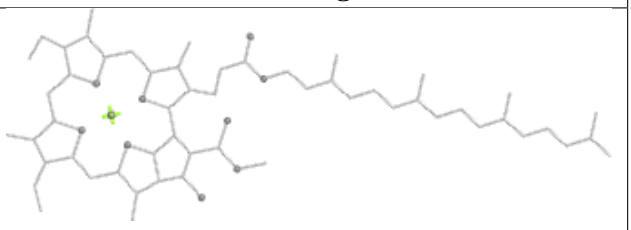
Bond lengths



Bond angles

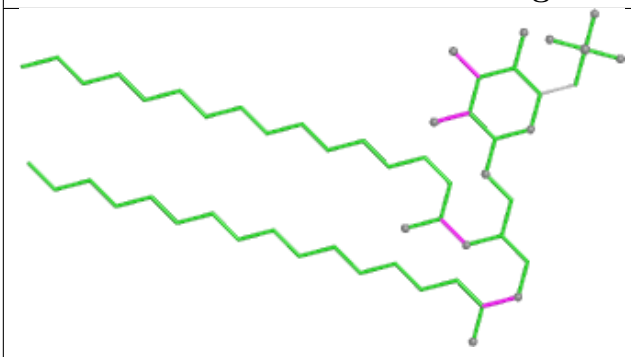


Torsions

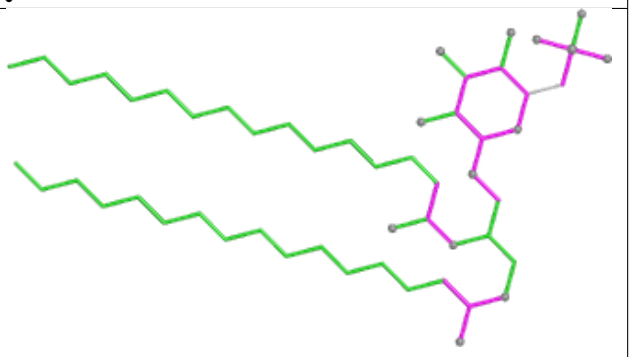


Rings

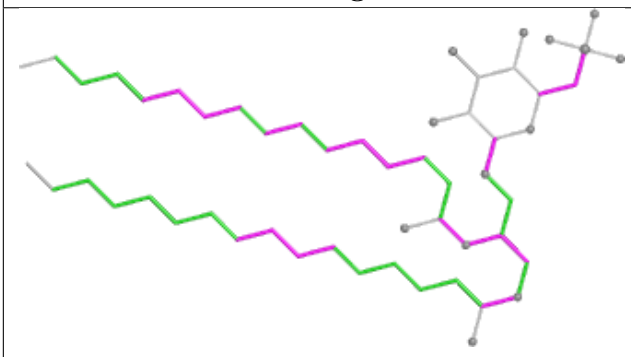
Ligand SQD l 102



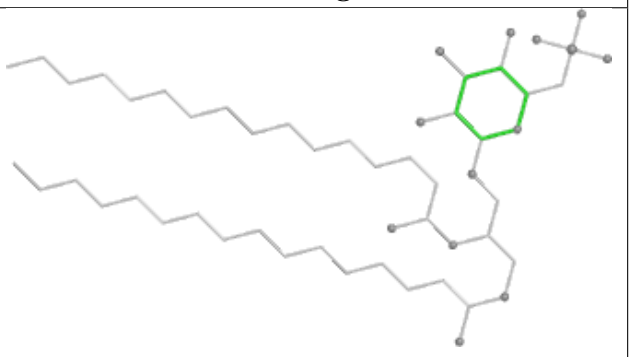
Bond lengths



Bond angles

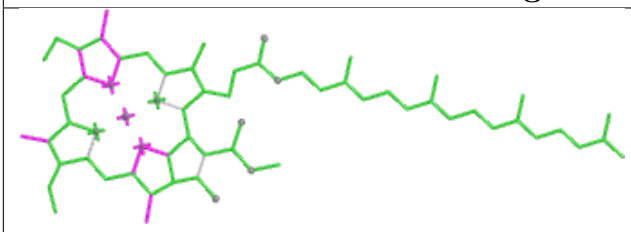


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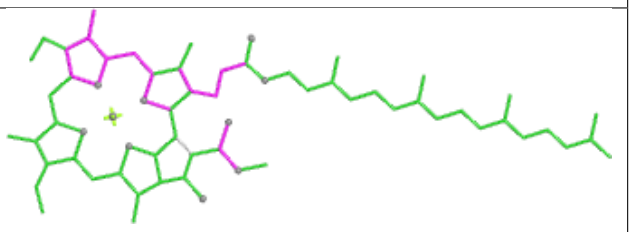


Rings

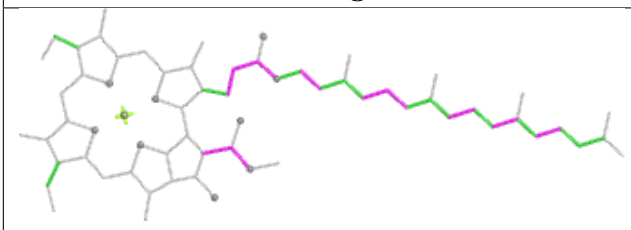
Ligand CLA A 404



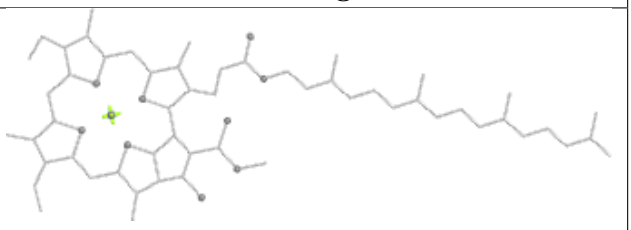
Bond lengths



Bond angles

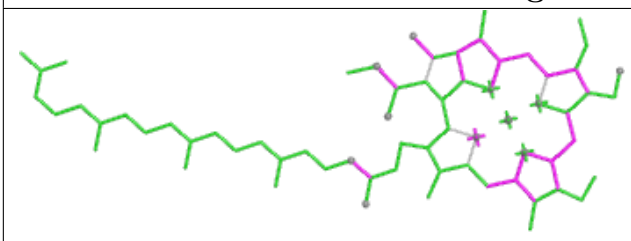


Torsions

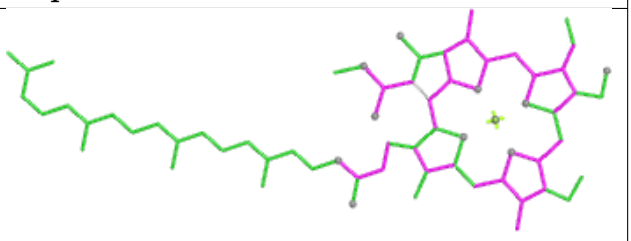


Rings

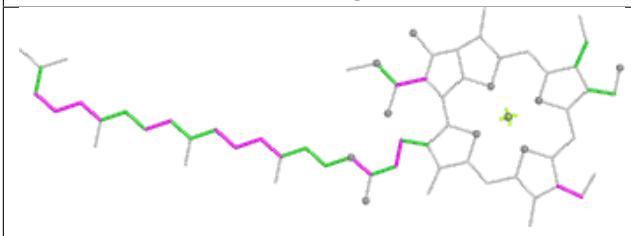
Ligand CHL p 317



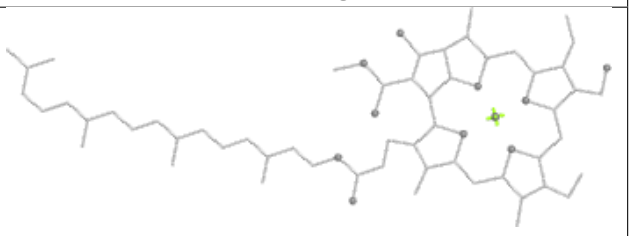
Bond lengths



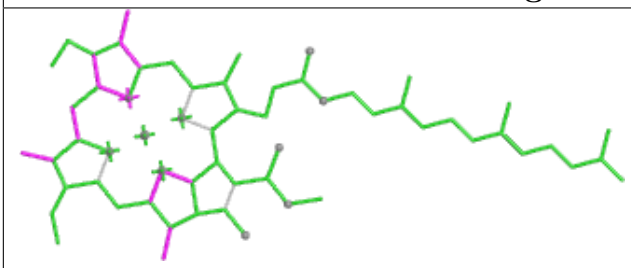
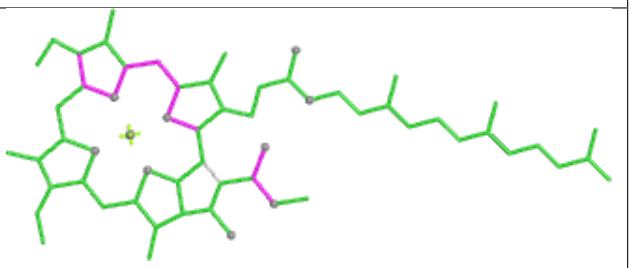
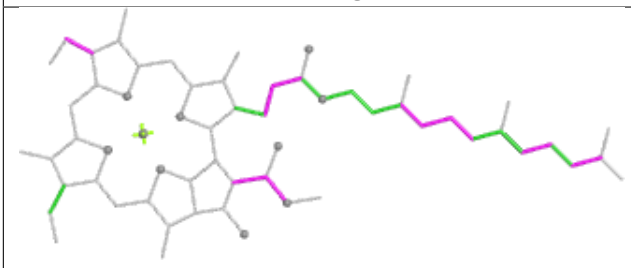
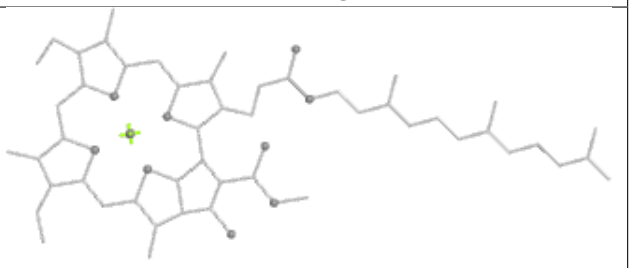
Bond angles

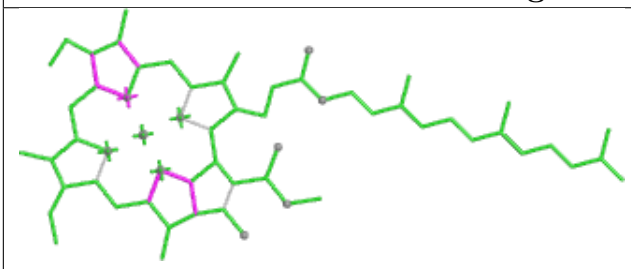
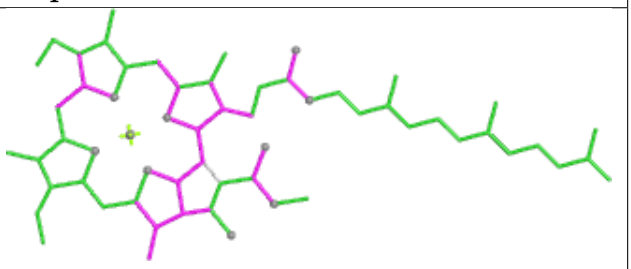
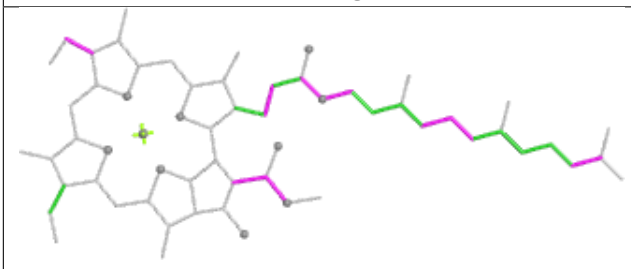
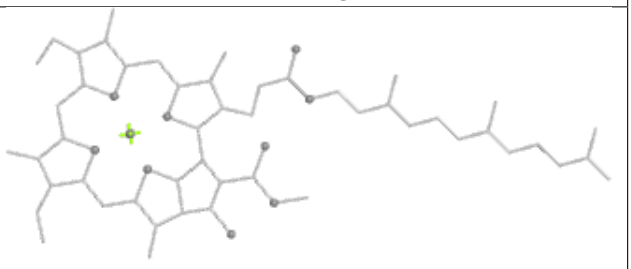


Torsions

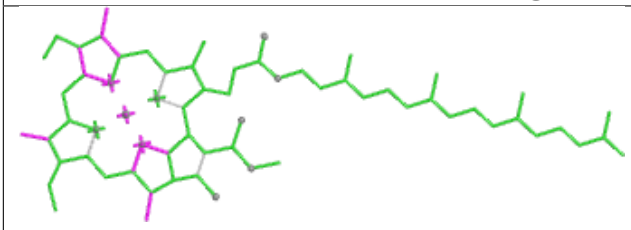


Rings

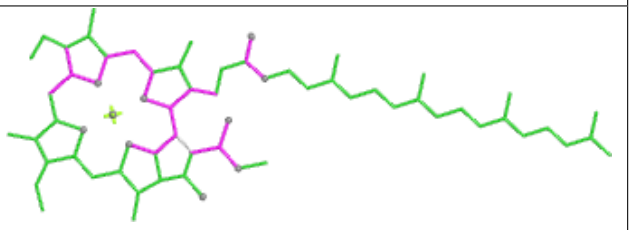
Ligand CLA P 308	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA p 306	
	
Bond lengths	Bond angles
	
Torsions	Rings

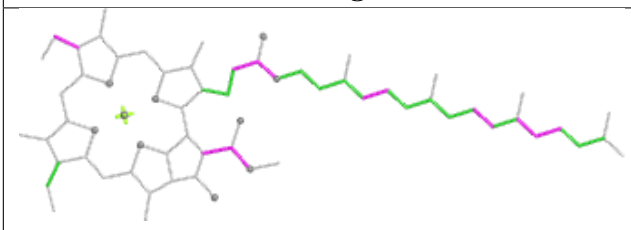
Ligand CLA b 617



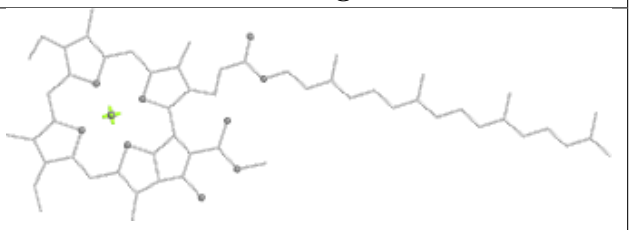
Bond lengths



Bond angles

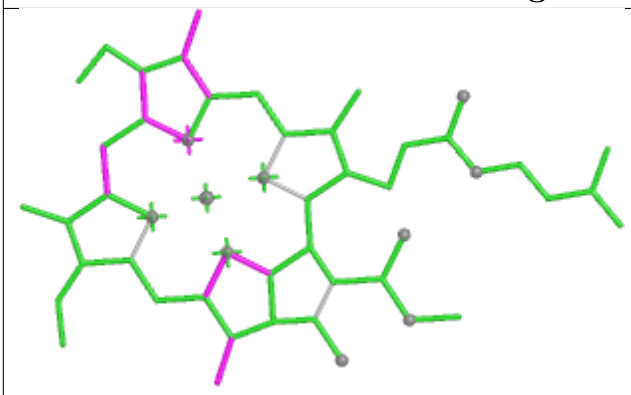


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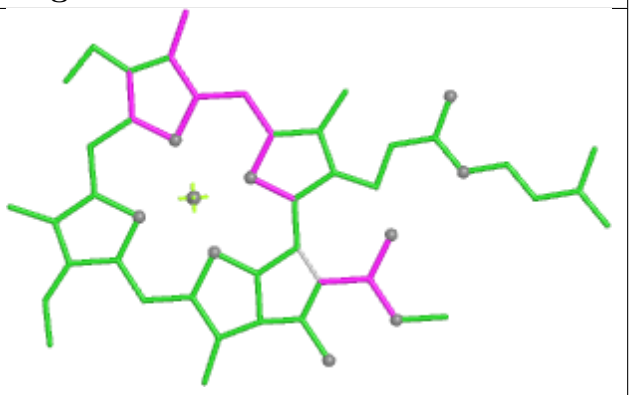


Rings

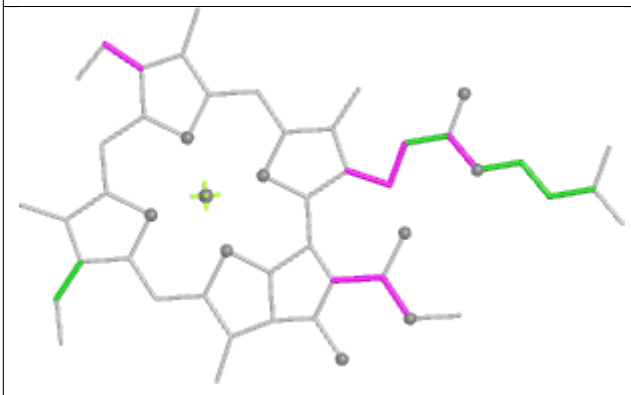
Ligand CLA g 303



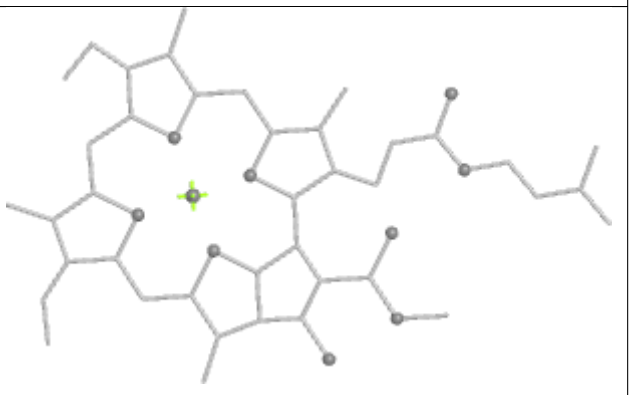
Bond lengths



Bond angles

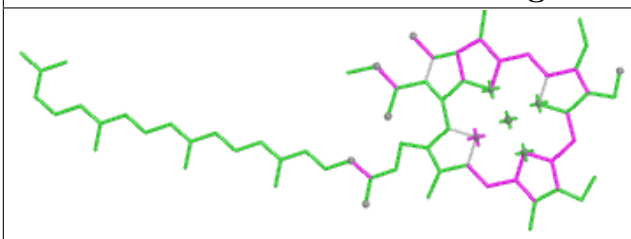


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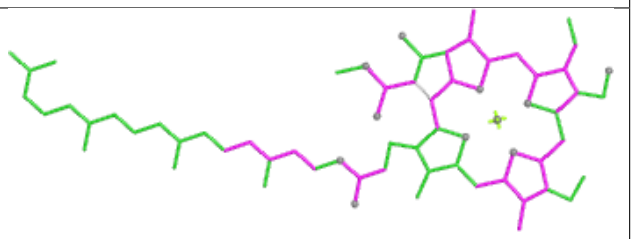


Rings

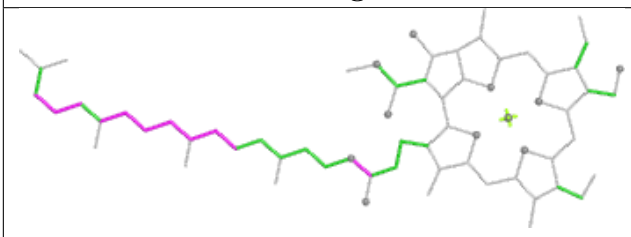
Ligand CHL 1 313



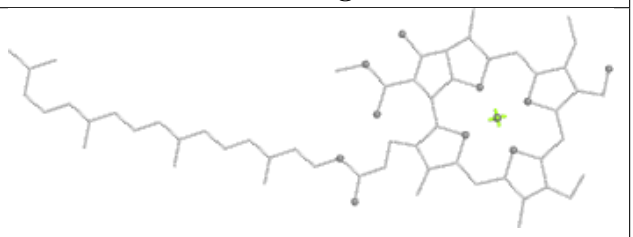
Bond lengths



Bond angles

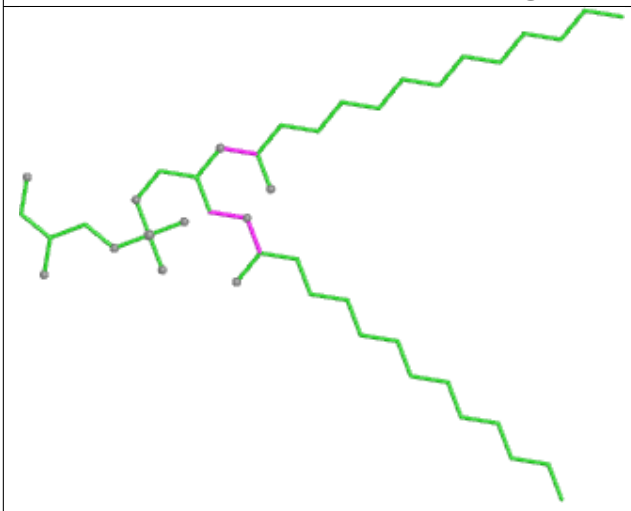


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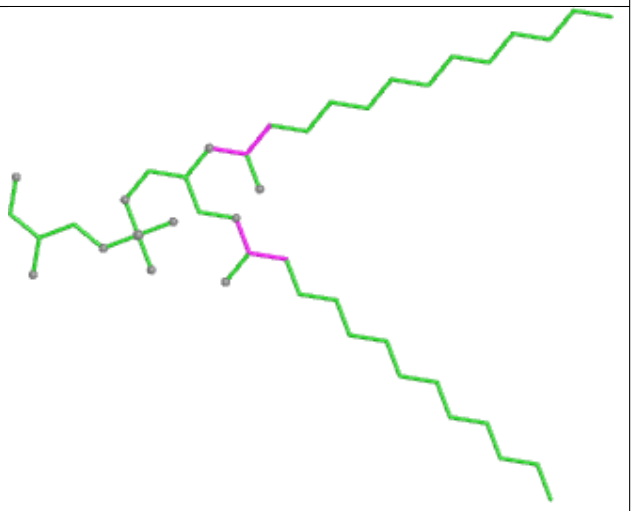


Rings

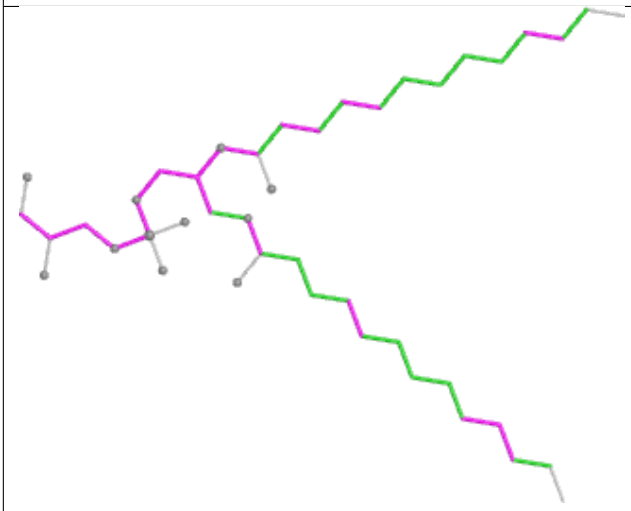
Ligand LHG A 413



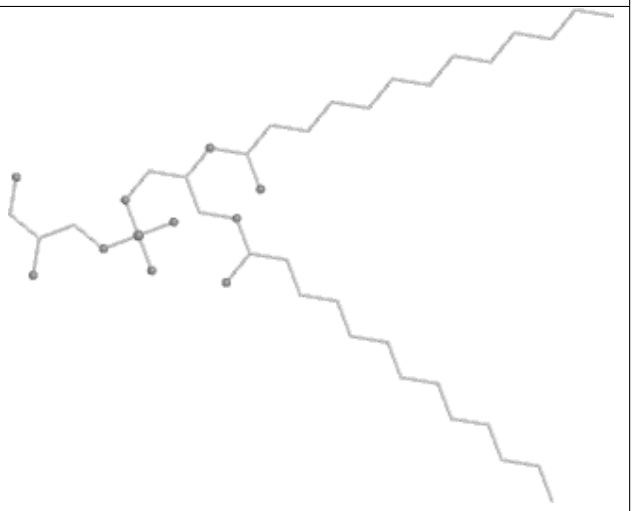
Bond lengths



Bond angles

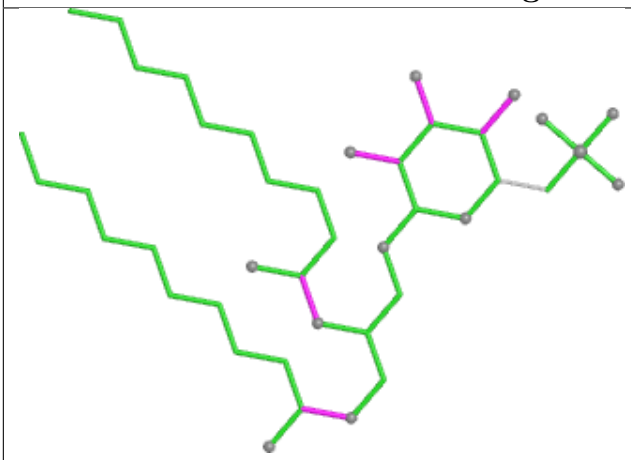


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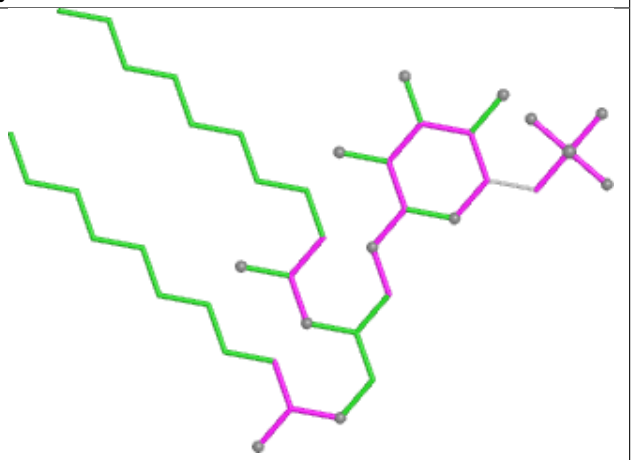


Rings

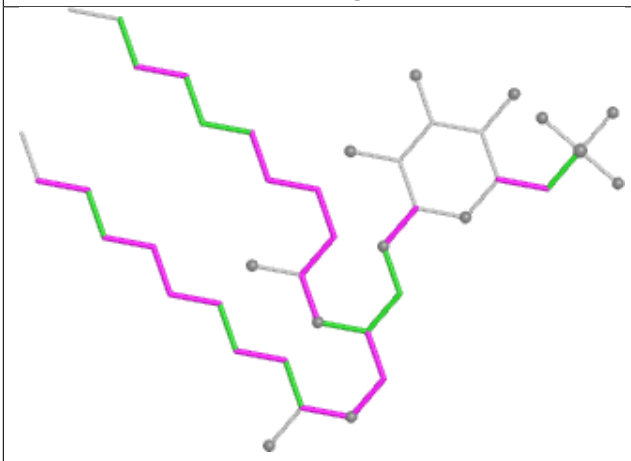
Ligand SQD m 101



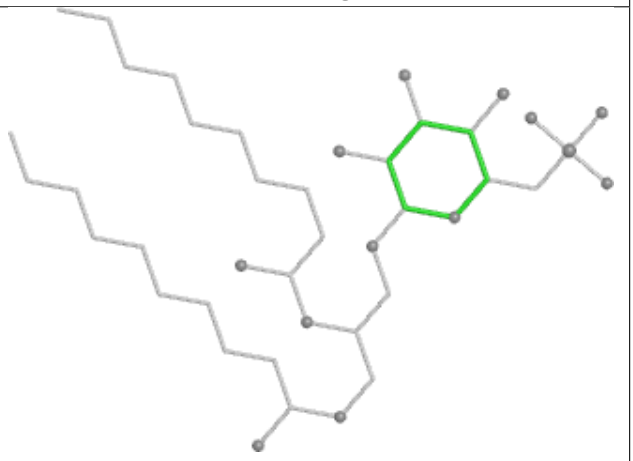
Bond lengths



Bond angles

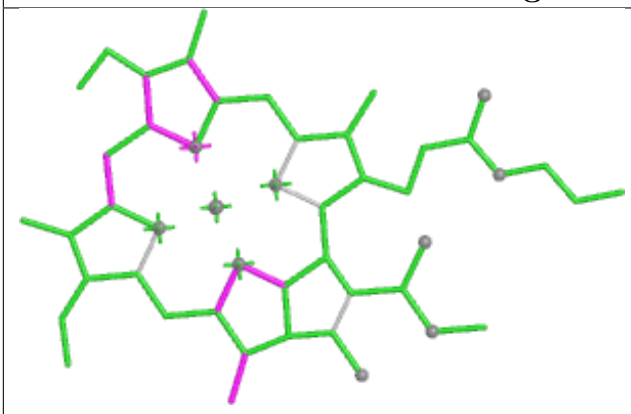


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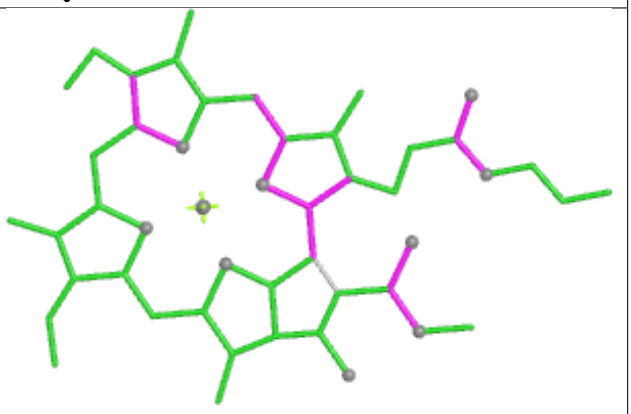


Rings

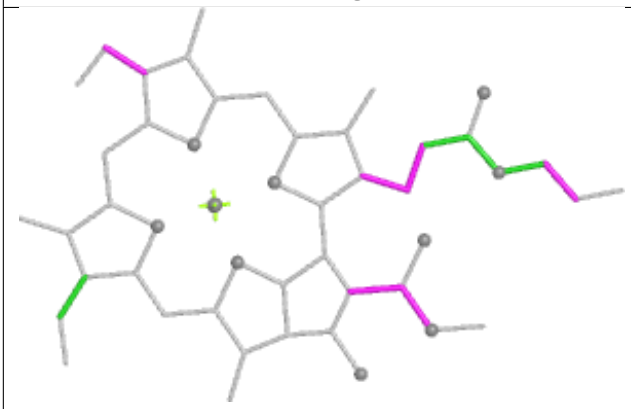
Ligand CLA Q 308



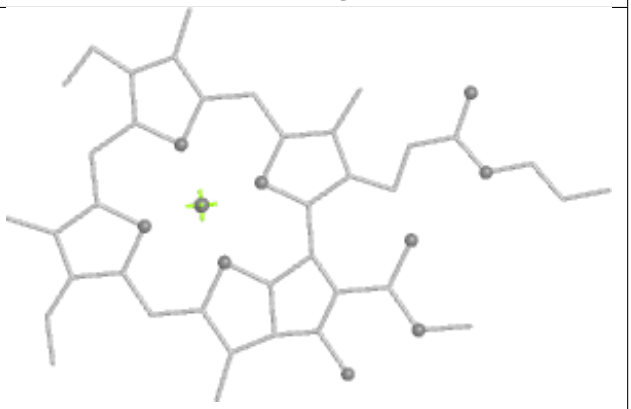
Bond lengths



Bond angles

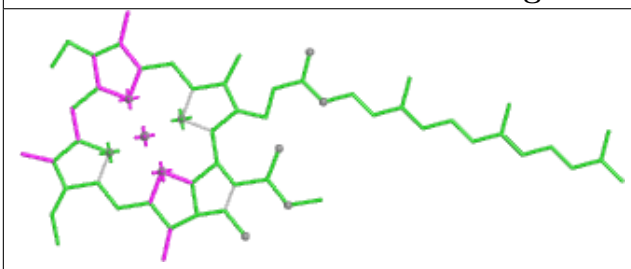


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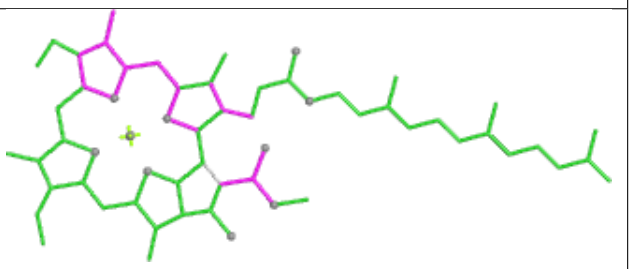


Rings

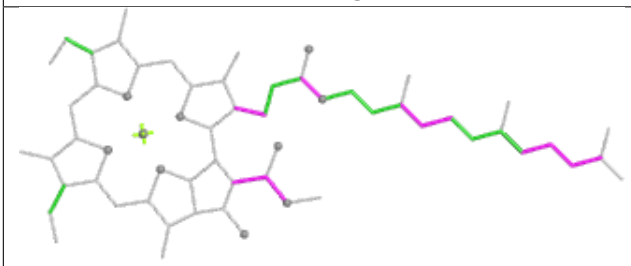
Ligand CLA A 408



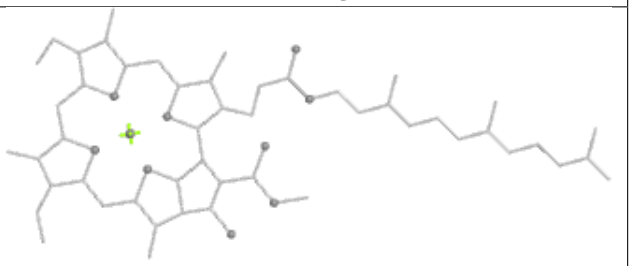
Bond lengths



Bond angles

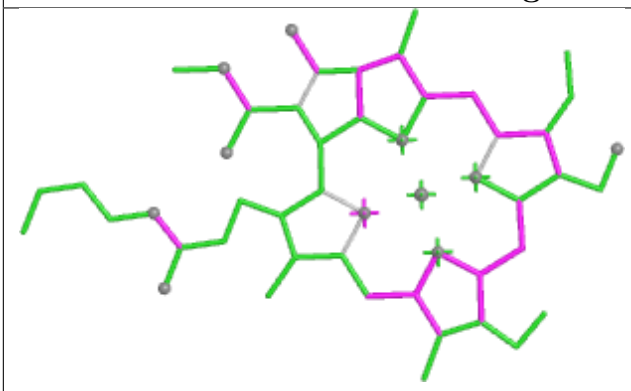


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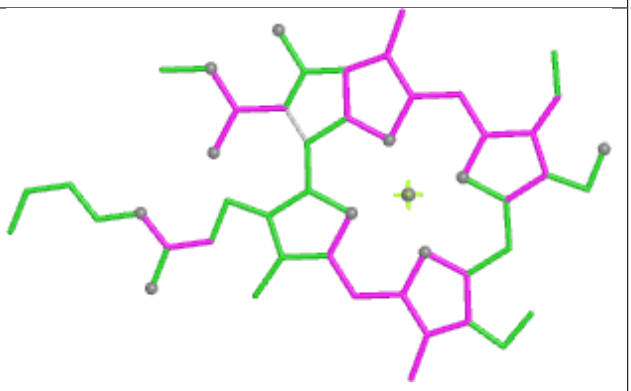


Rings

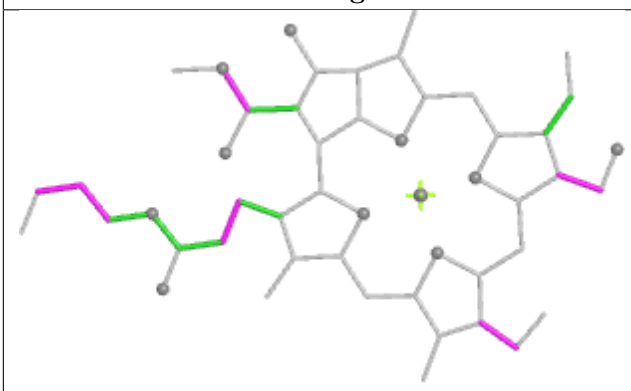
Ligand CHL G 313



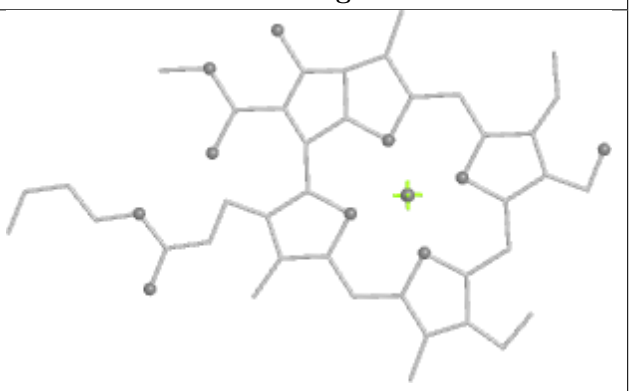
Bond lengths



Bond angles

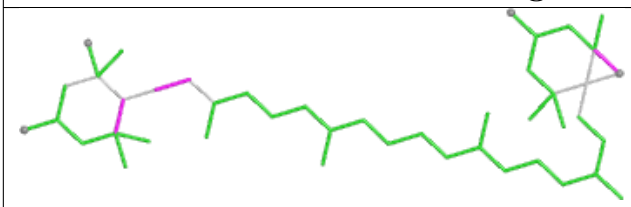


Torsions

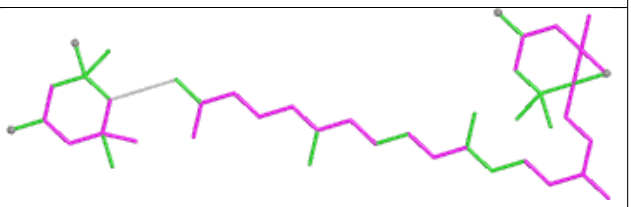


Rings

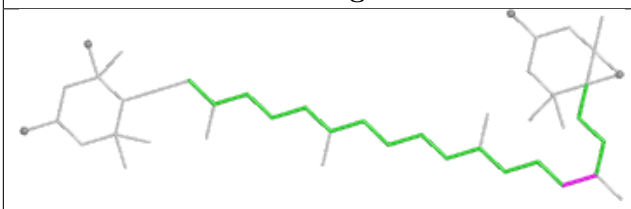
Ligand NEX r 617



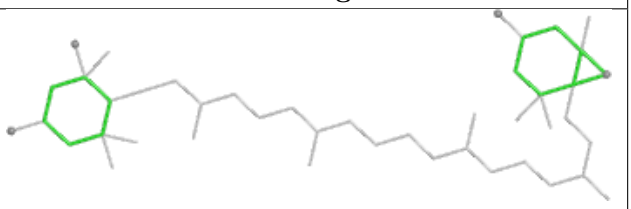
Bond lengths



Bond angles

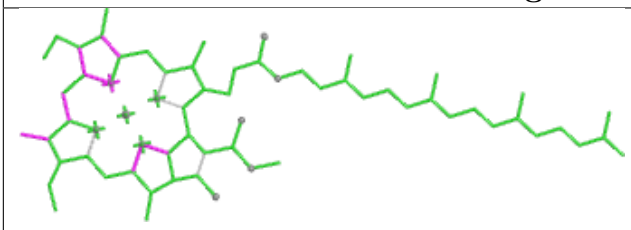


Torsions

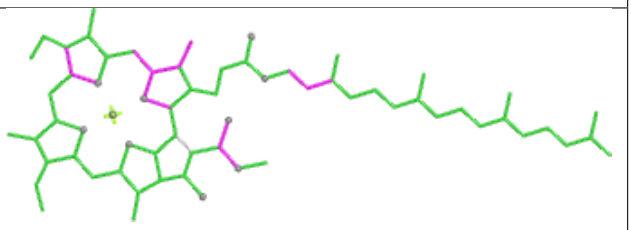


Rings

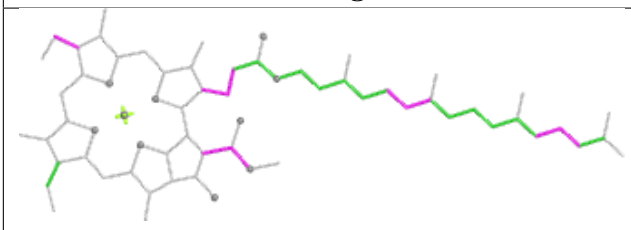
Ligand CLA P 305



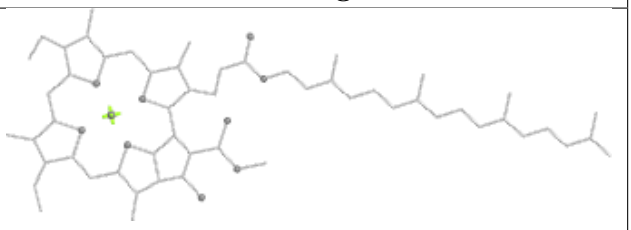
Bond lengths



Bond angles

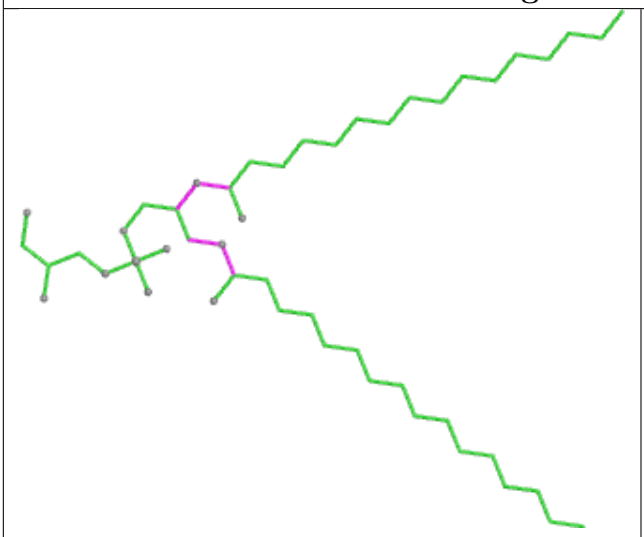


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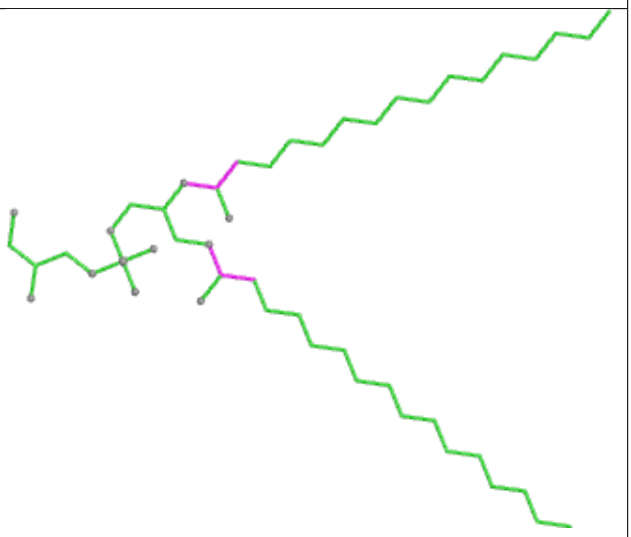


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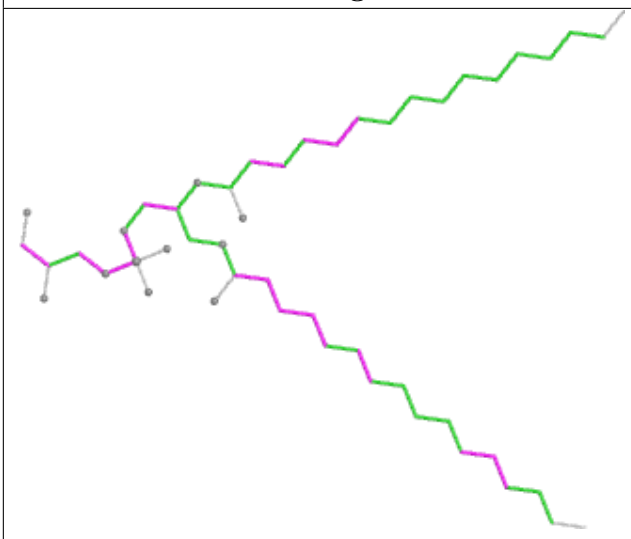
Ligand LHG G 310



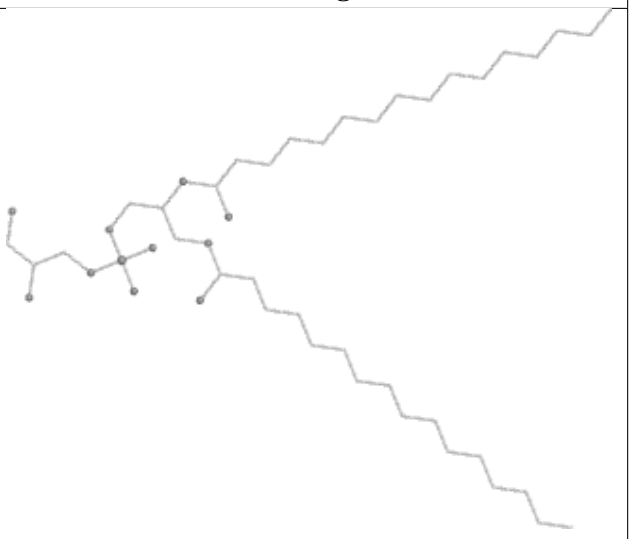
Bond lengths



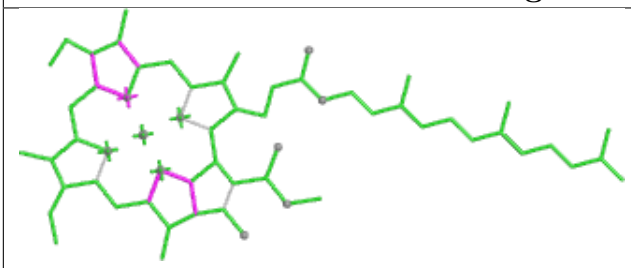
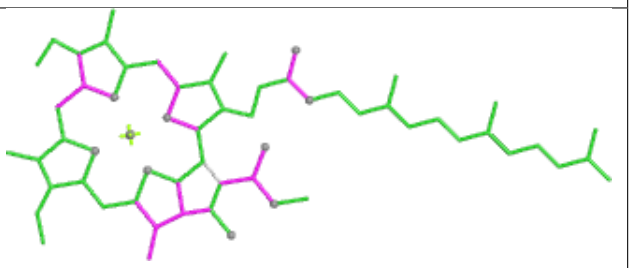
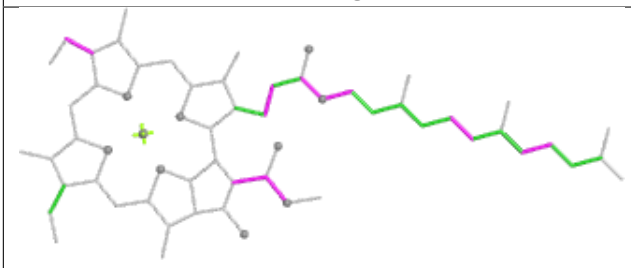
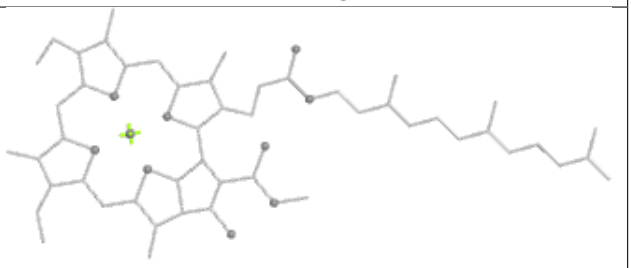
Bond angles

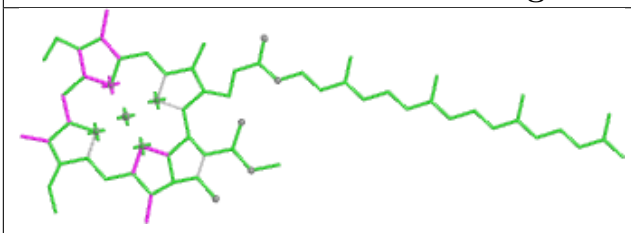
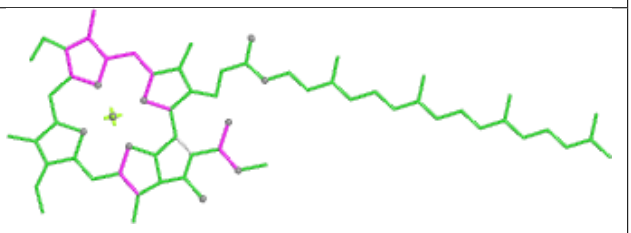
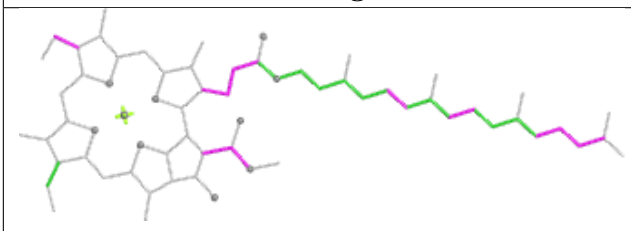
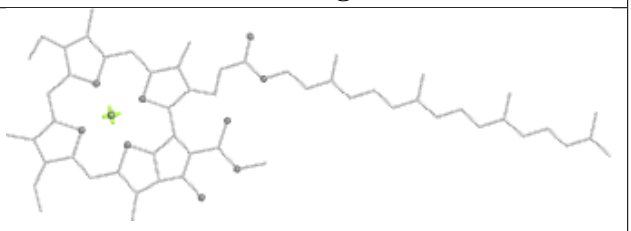


Torsions

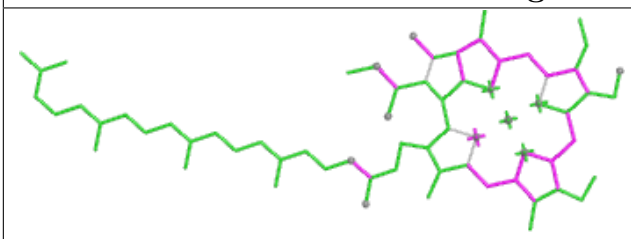


Rings

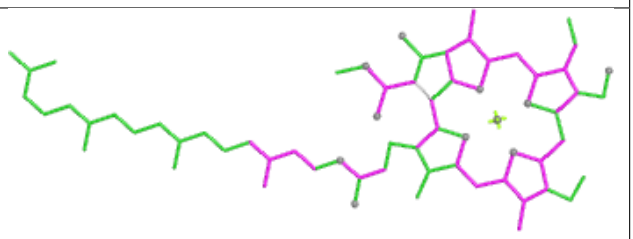
Ligand CLA P 306	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA n 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

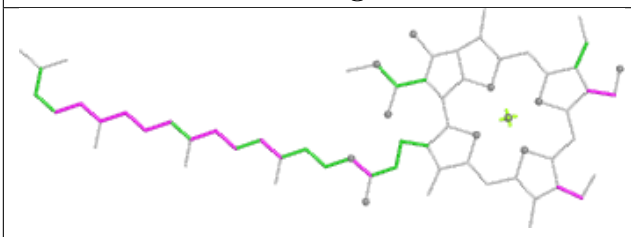
Ligand CHL v 313



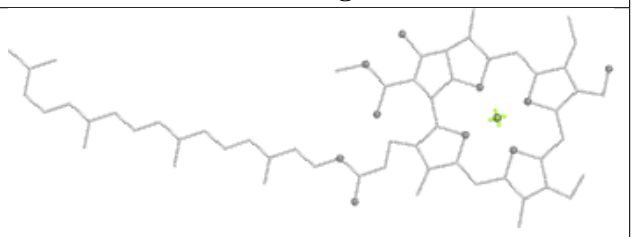
Bond lengths



Bond angles

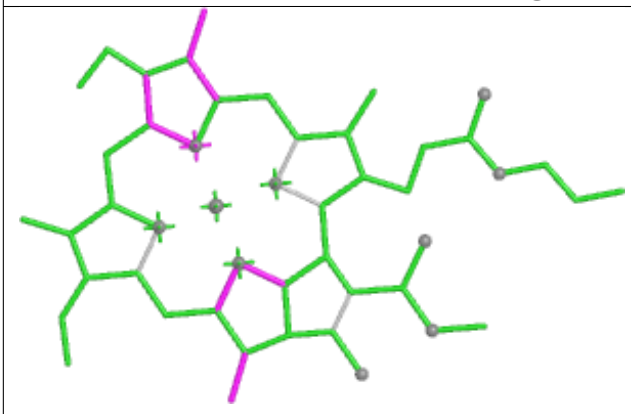


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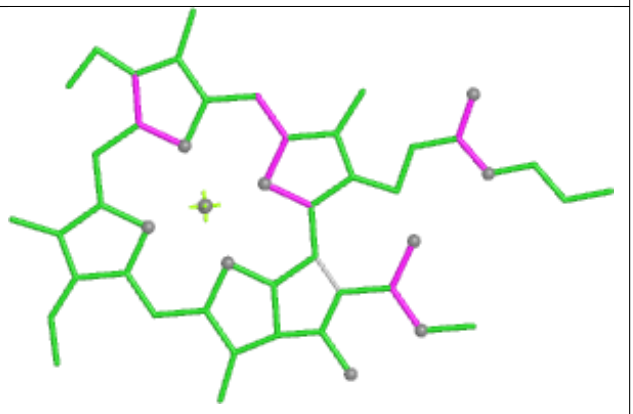


Rings

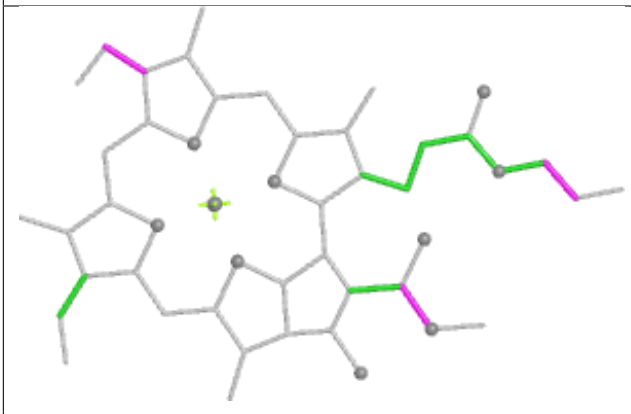
Ligand CLA 5 308



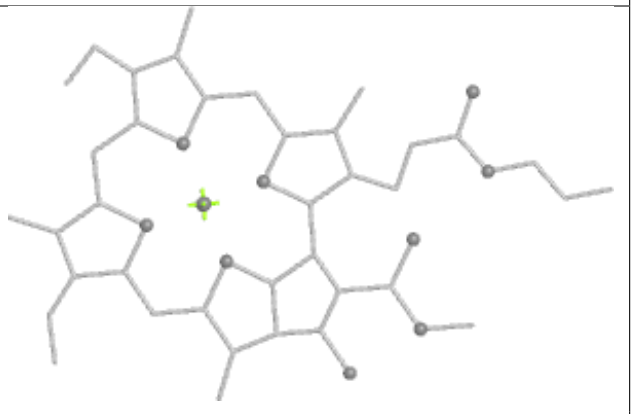
Bond lengths



Bond angles

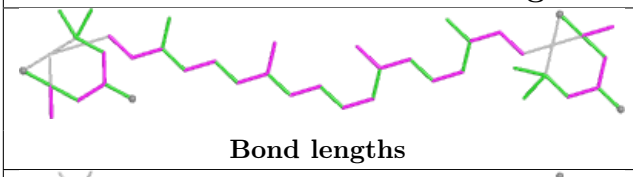


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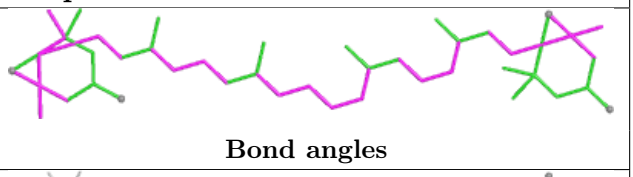


Rings

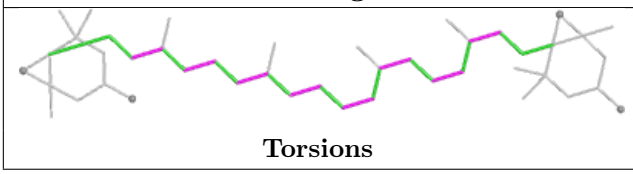
Ligand XAT q 309



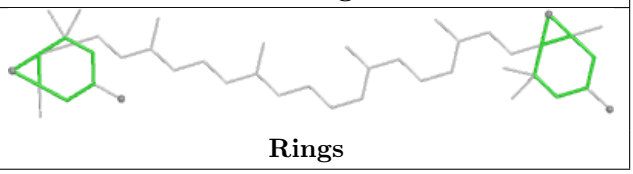
Bond lengths



Bond angles

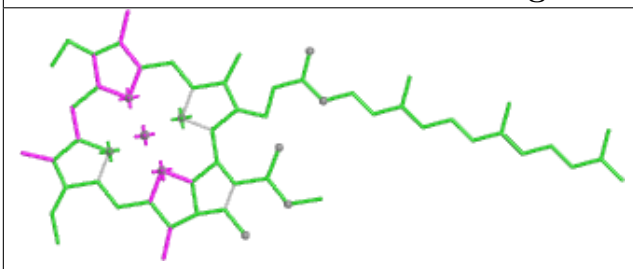


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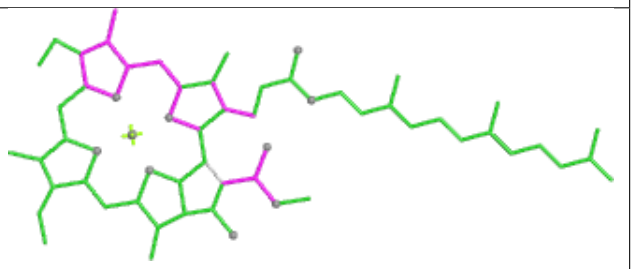


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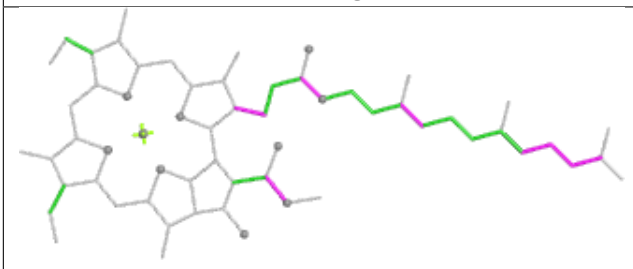
Ligand CLA a 408



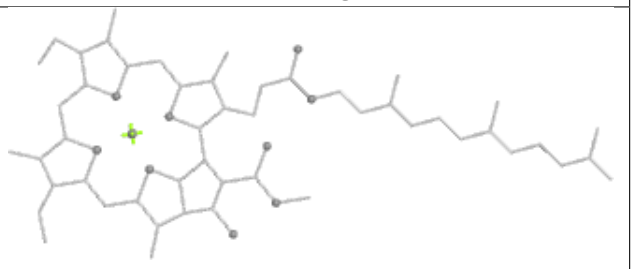
Bond lengths



Bond angles

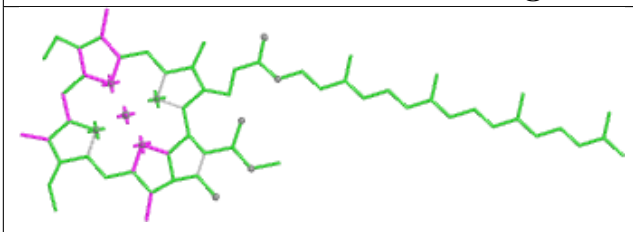


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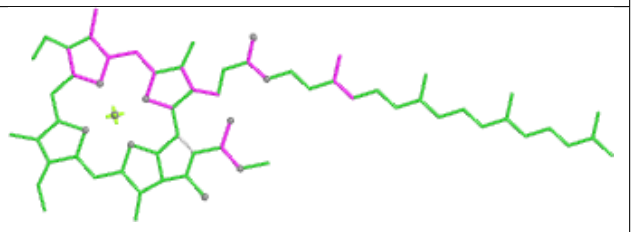


Rings

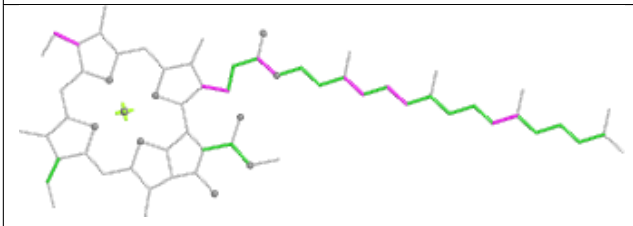
Ligand CLA C 510



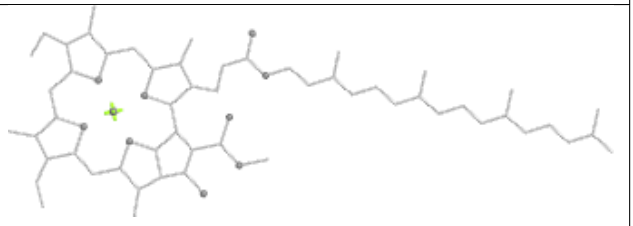
Bond lengths



Bond angles

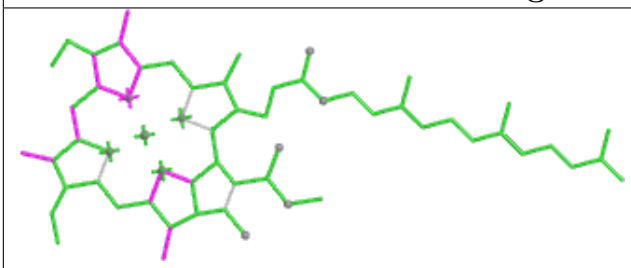


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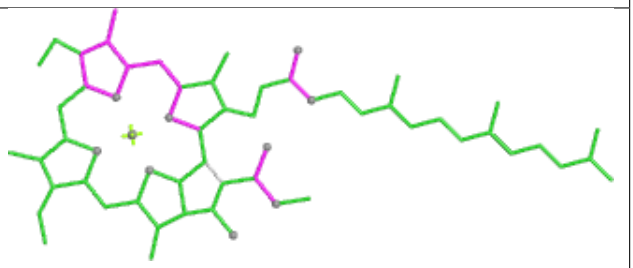


Rings

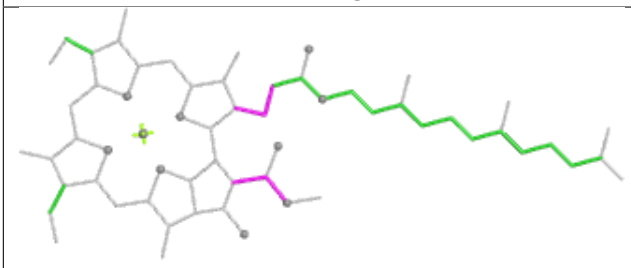
Ligand CLA u 304



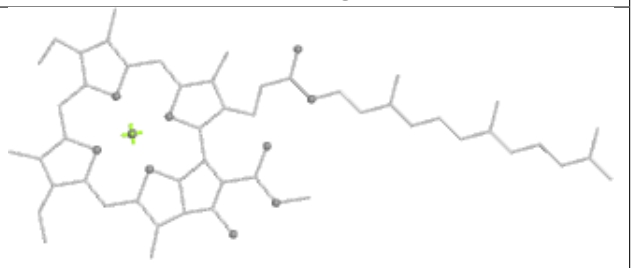
Bond lengths



Bond angles

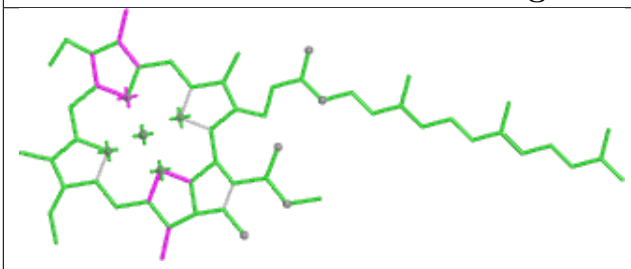


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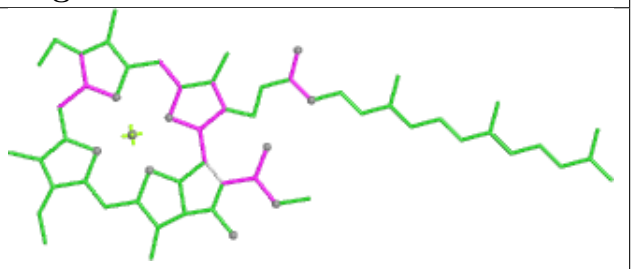


Rings

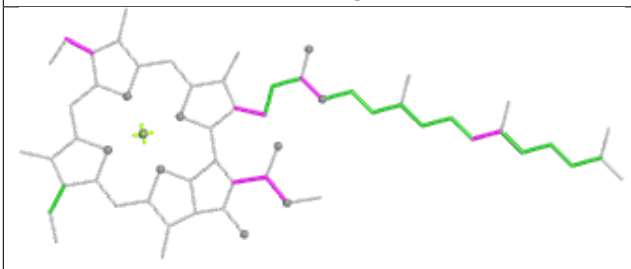
Ligand CLA g 305



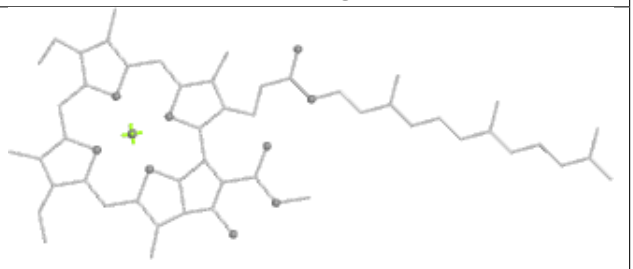
Bond lengths



Bond angles

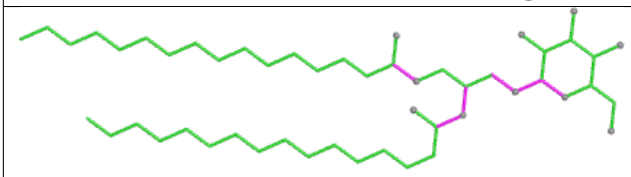


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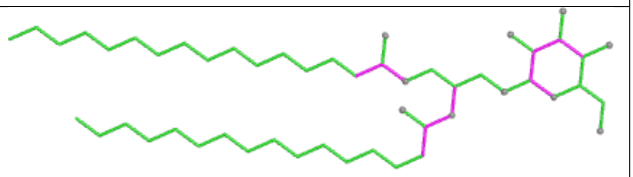


Rings

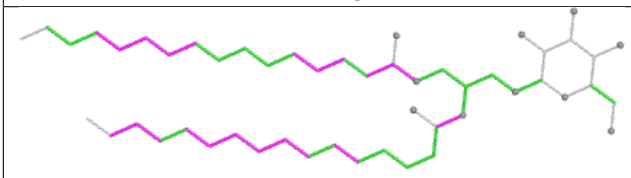
Ligand LMG B 621



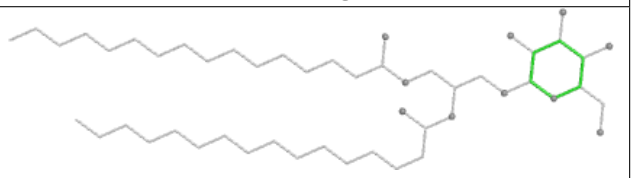
Bond lengths



Bond angles

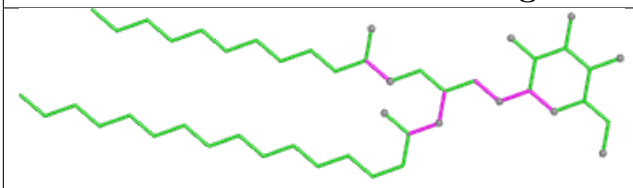


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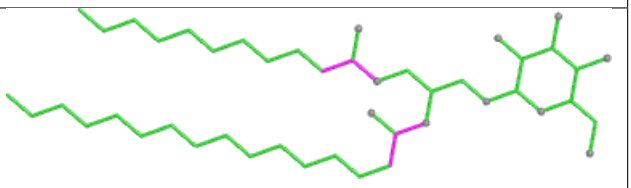


Rings

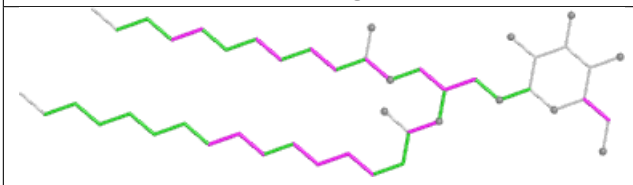
Ligand LMG D 408



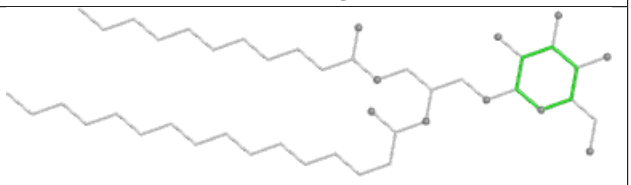
Bond lengths



Bond angles

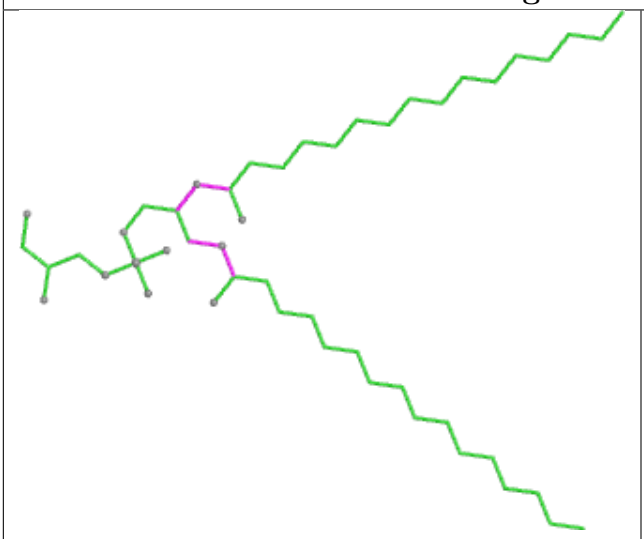


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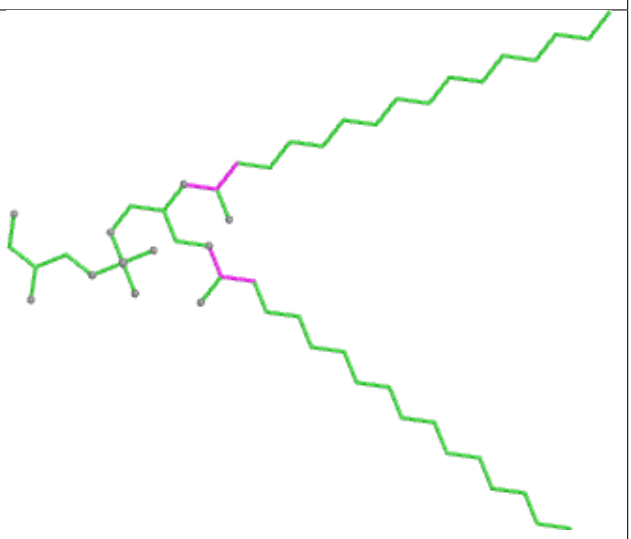


Rings

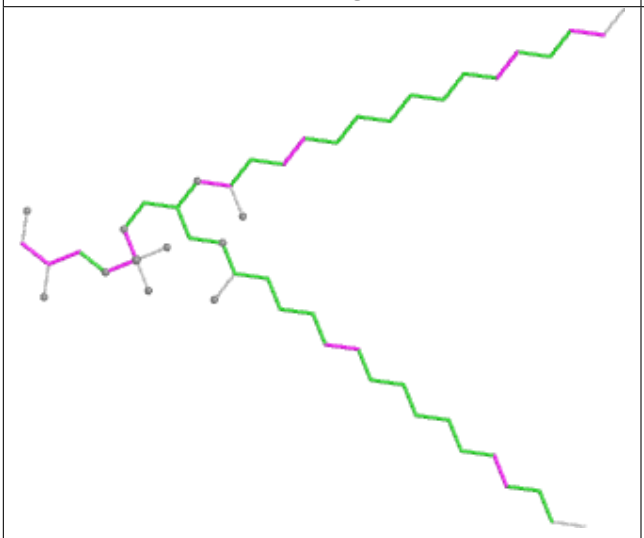
Ligand LHG C 524



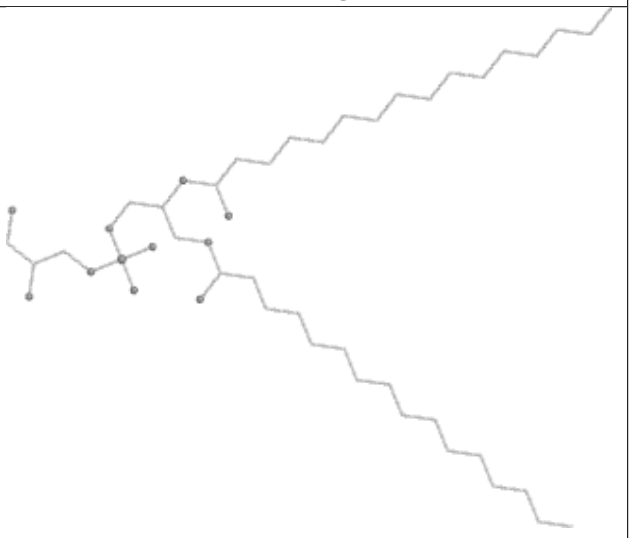
Bond lengths



Bond angles

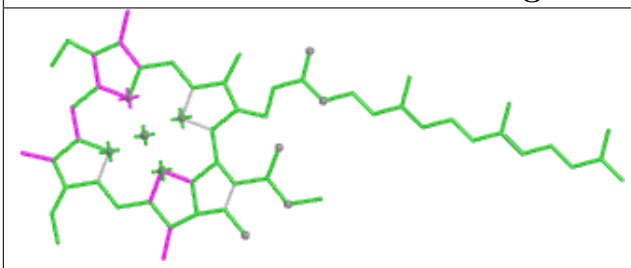


Torsions

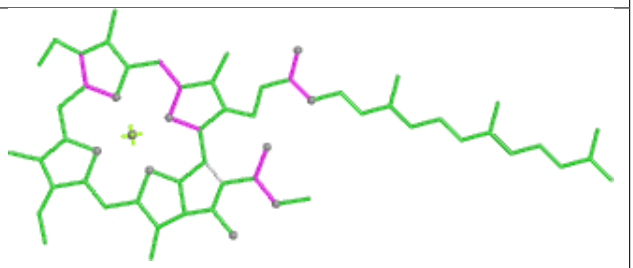


Rings

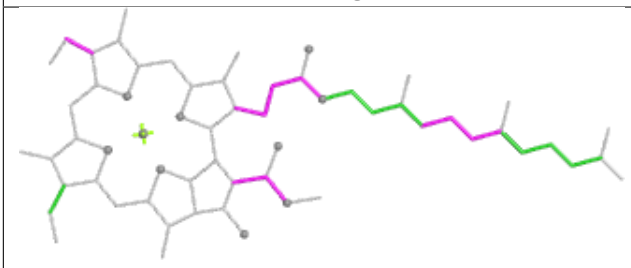
Ligand CLA N 307



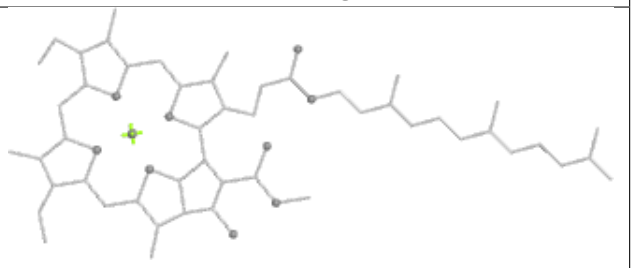
Bond lengths



Bond angles

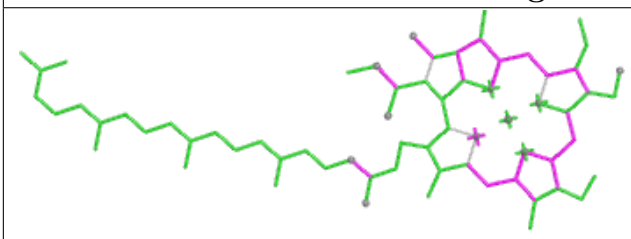


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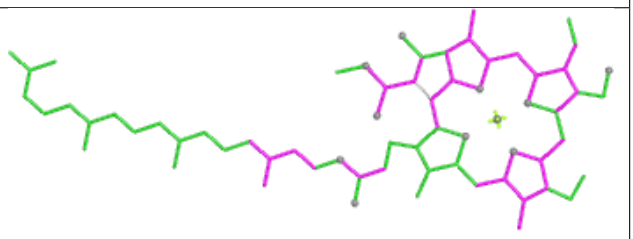


Rings

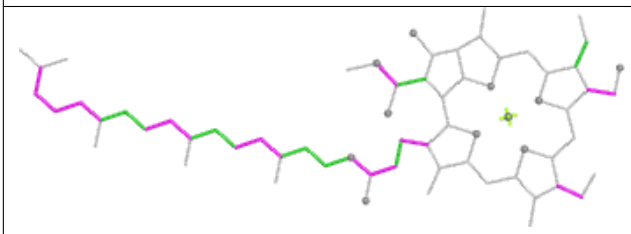
Ligand CHL 6 301



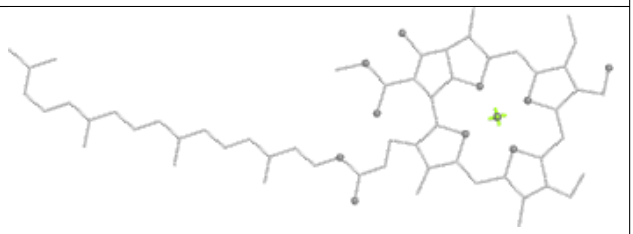
Bond lengths



Bond angles

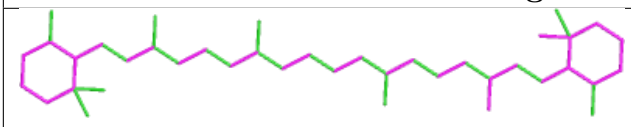


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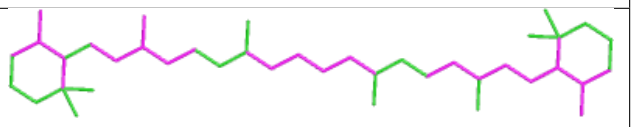


Rings

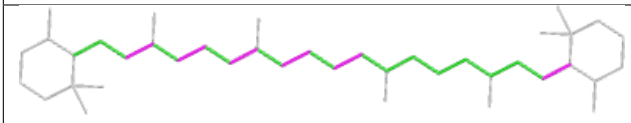
Ligand BCR x 202



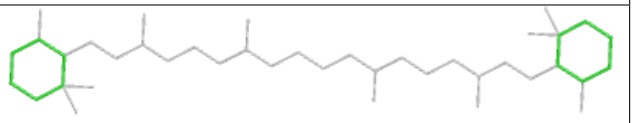
Bond lengths



Bond angles

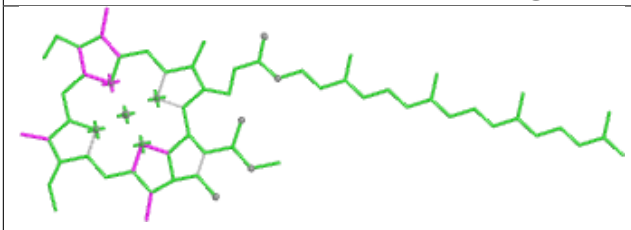


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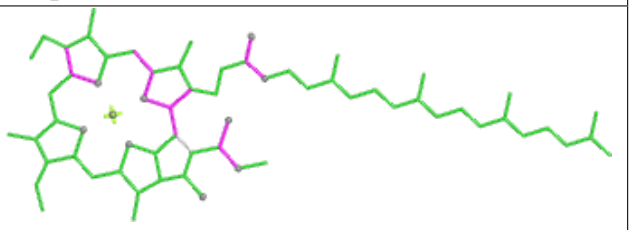


Rings

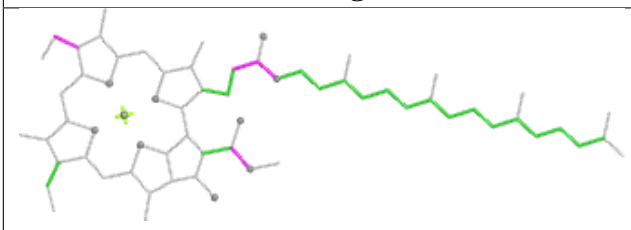
Ligand CLA p 303



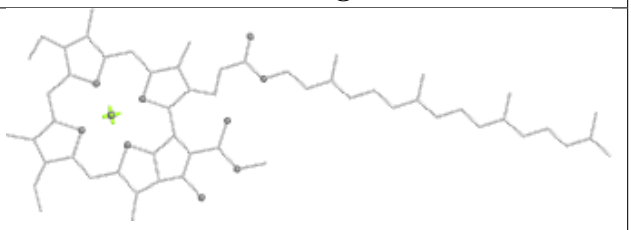
Bond lengths



Bond angles

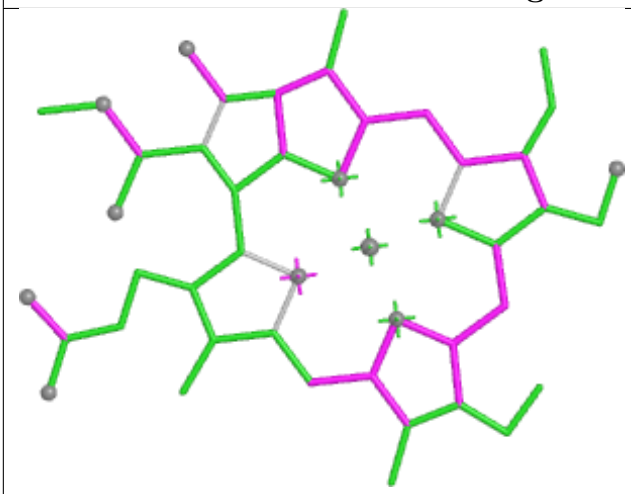


Torsions



Rings

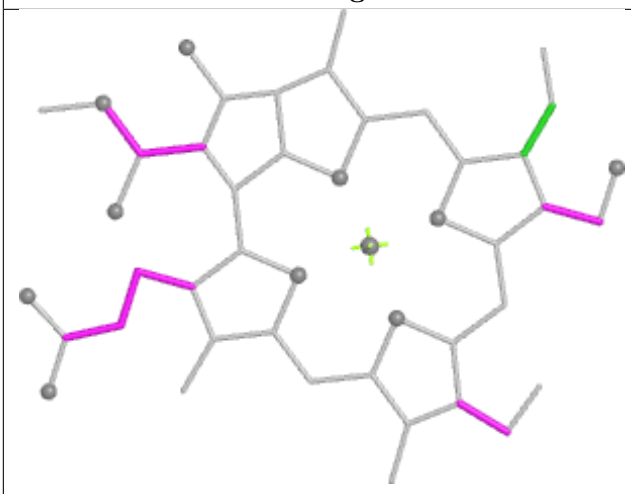
Ligand CHL S 316



Bond lengths



Bond angles

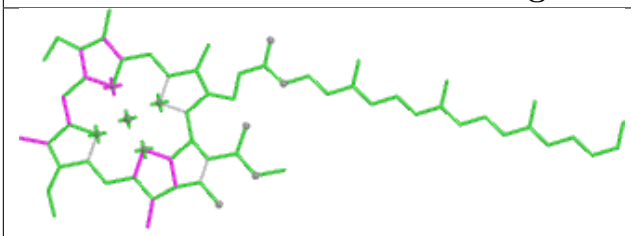


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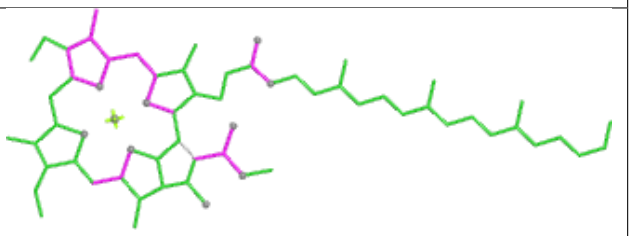


Rings

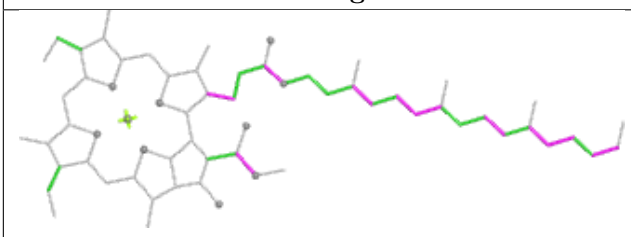
Ligand CLA 3 304



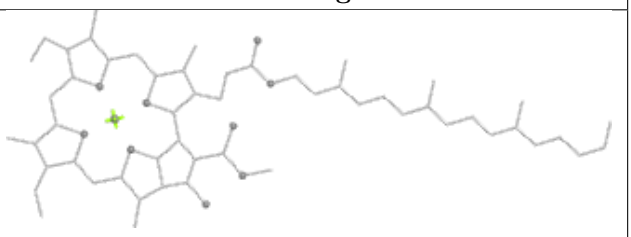
Bond lengths



Bond angles

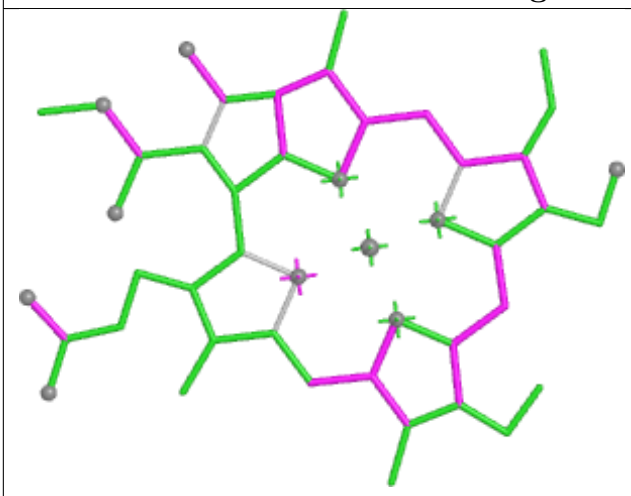


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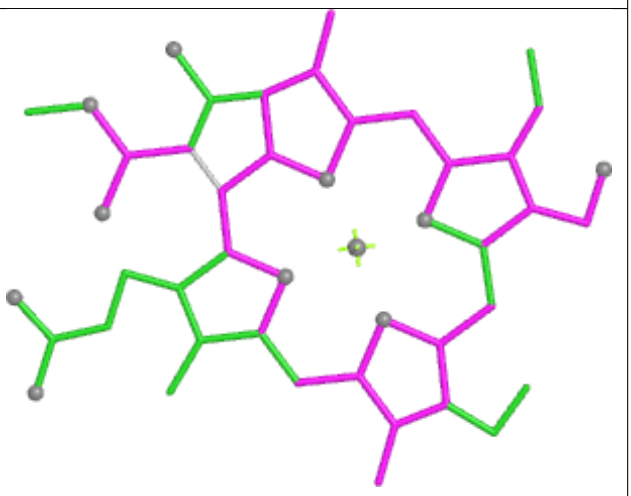


Rings

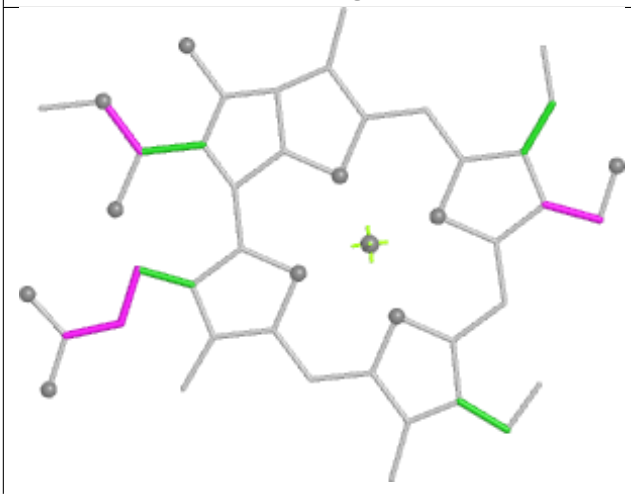
Ligand CHL s 313



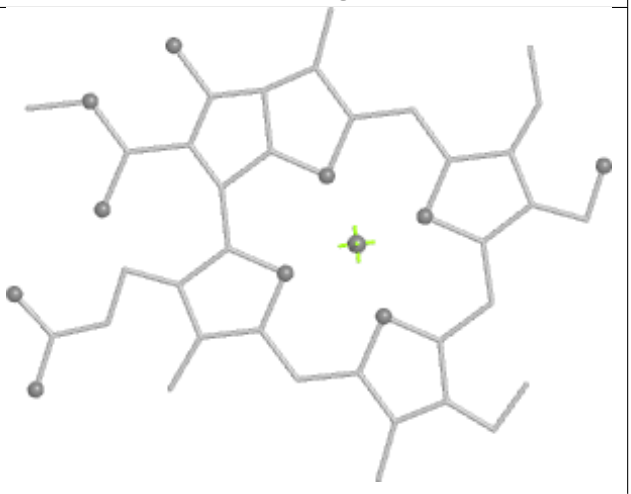
Bond lengths



Bond angles

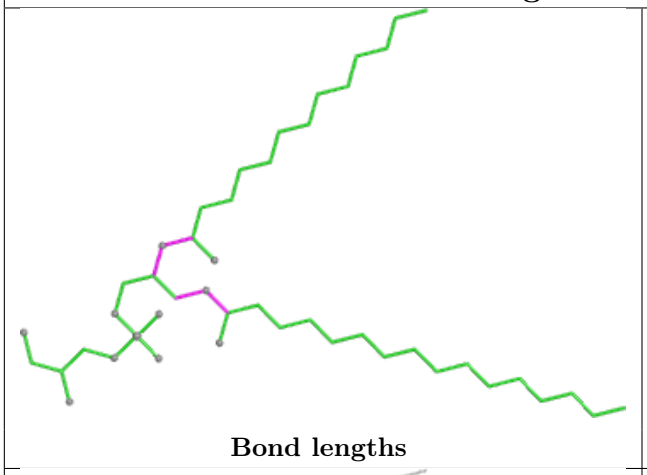


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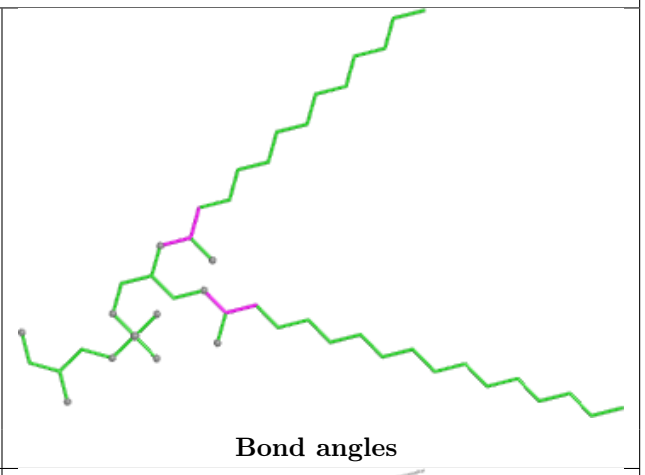


Rings

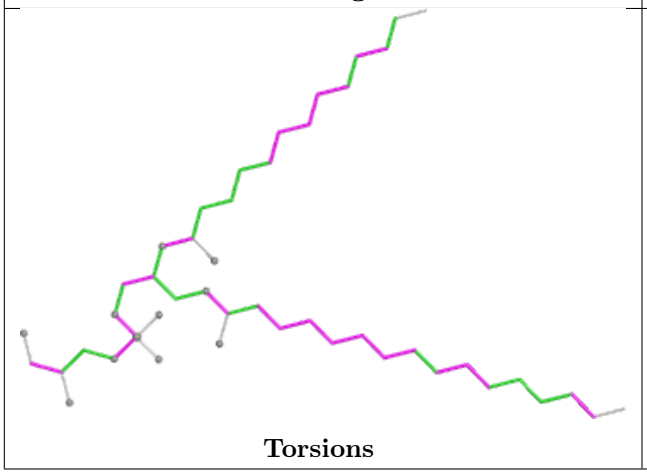
Ligand LHG D 406



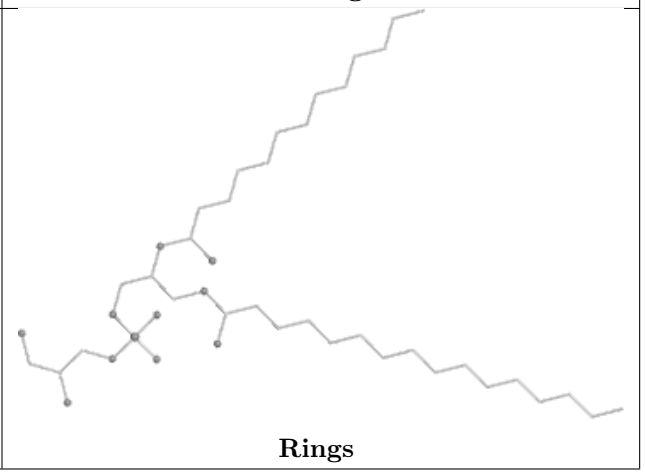
Bond lengths



Bond angles

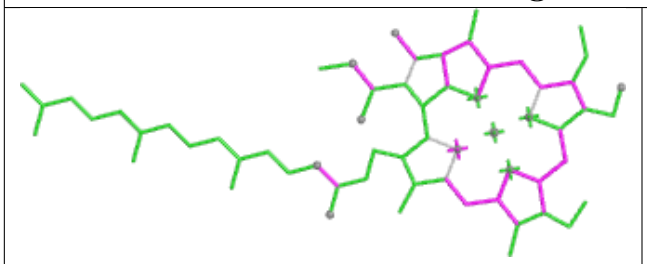


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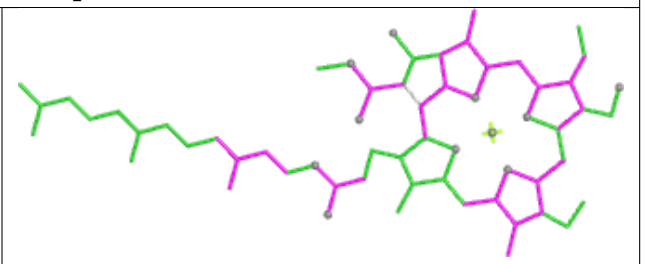


Rings

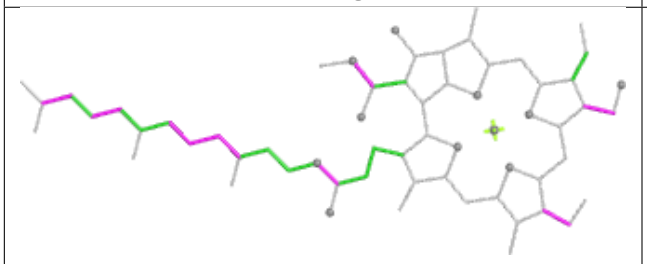
Ligand CHL q 315



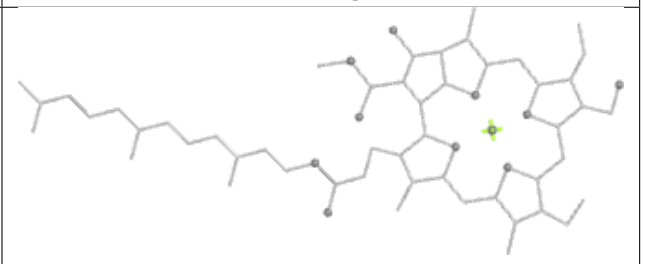
Bond lengths



Bond angles

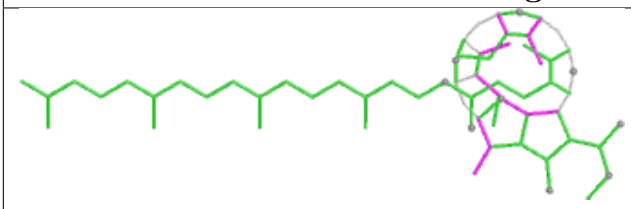


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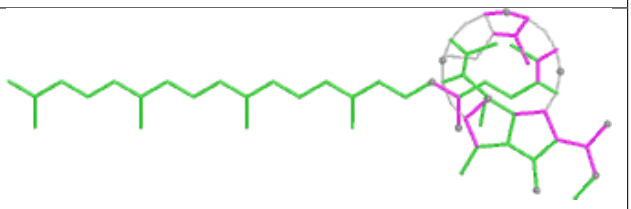


Rings

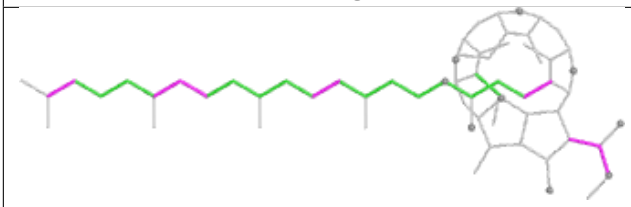
Ligand PHO d 401



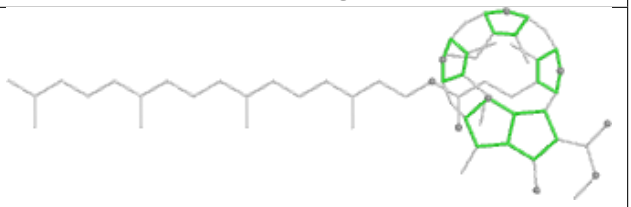
Bond lengths



Bond angles

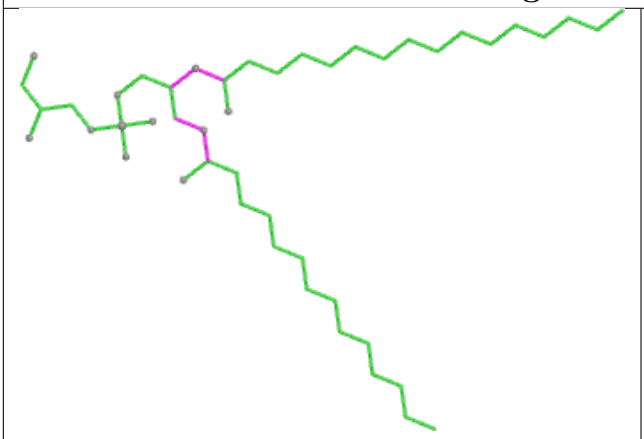


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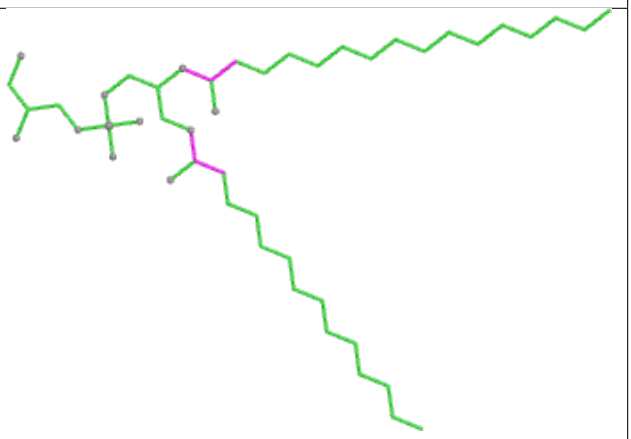


Rings

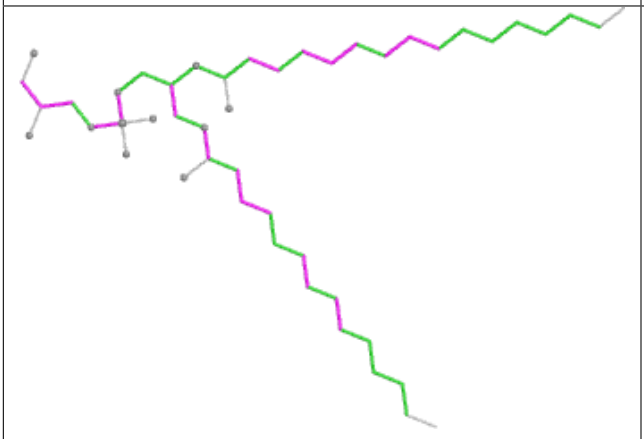
Ligand LHG B 622



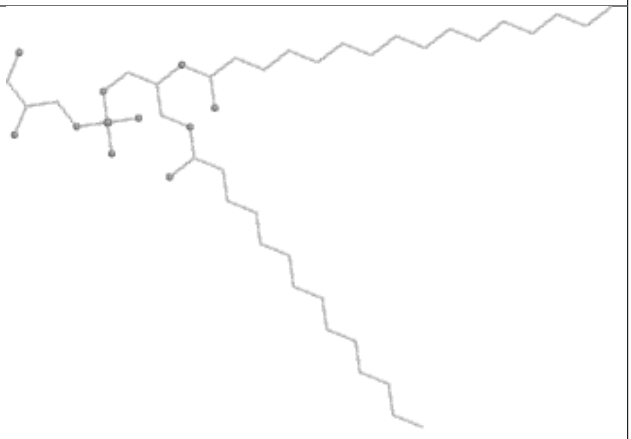
Bond lengths



Bond angles

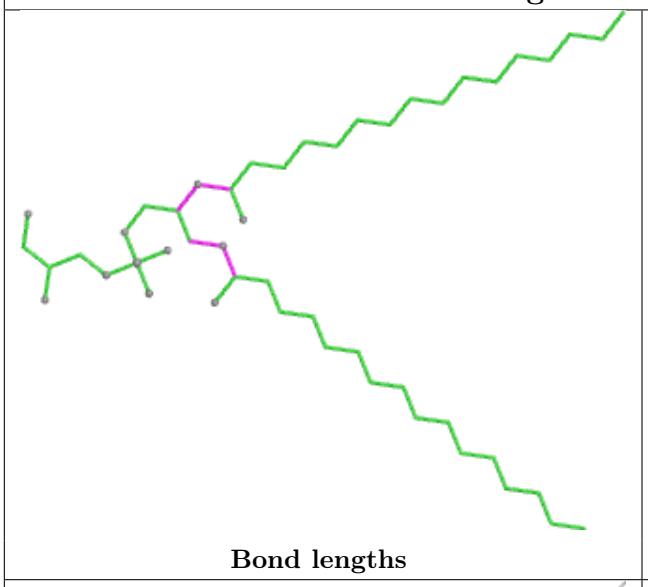


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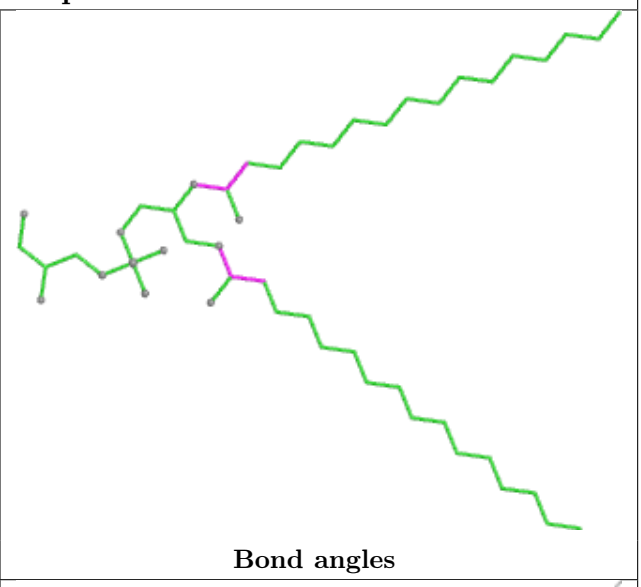


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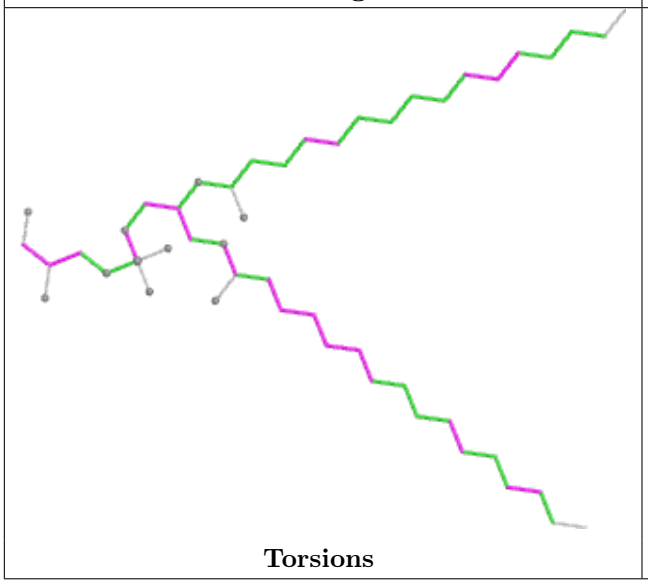
Ligand LHG p 313



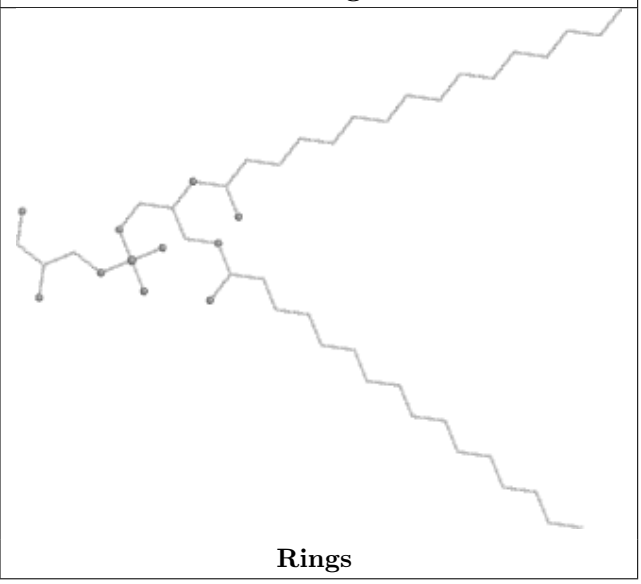
Bond lengths



Bond angles

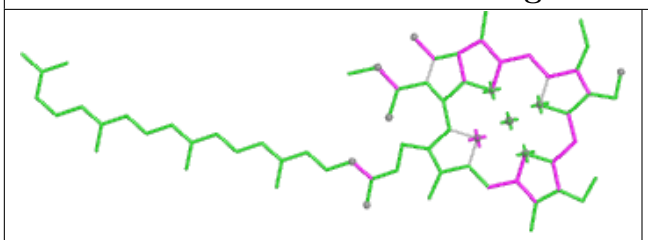


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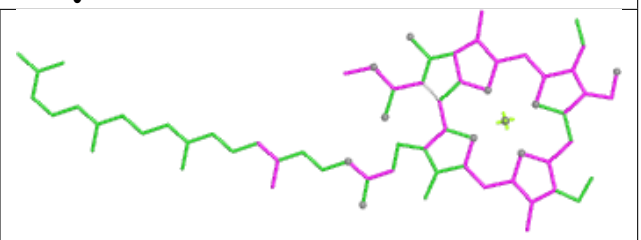


Rings

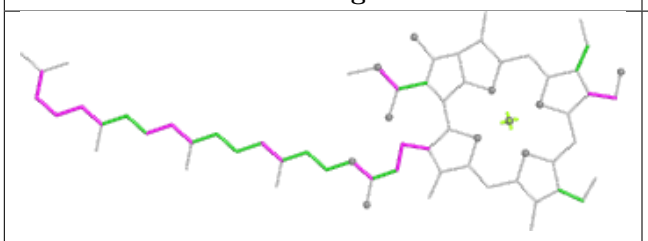
Ligand CHL Q 315



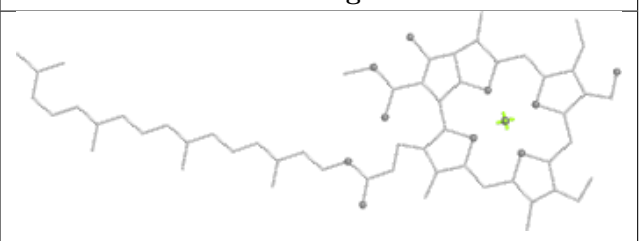
Bond lengths



Bond angles

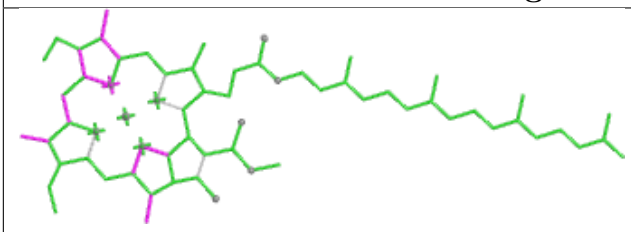


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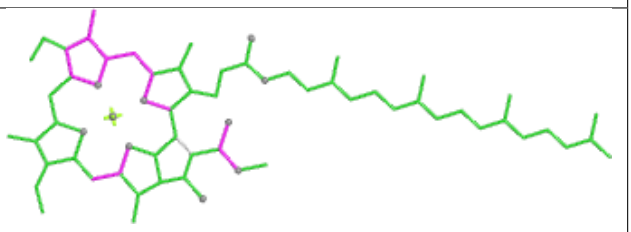


Rings

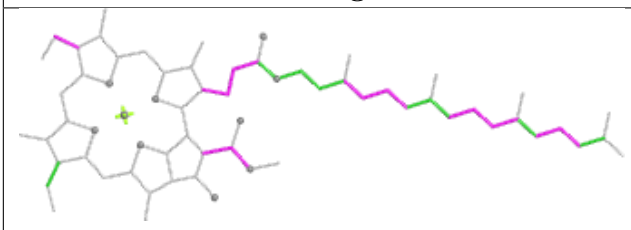
Ligand CLA P 302



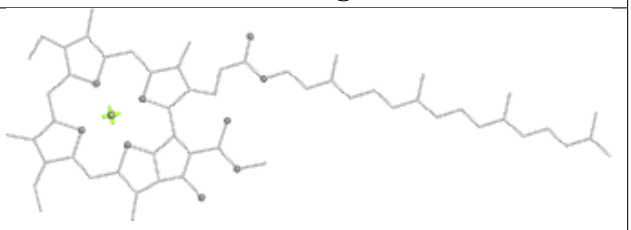
Bond lengths



Bond angles

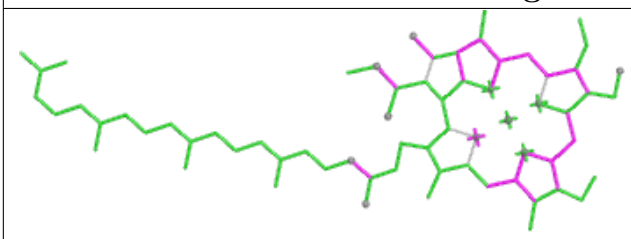


Torsions

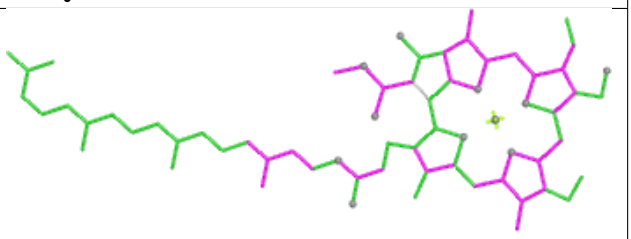


Rings

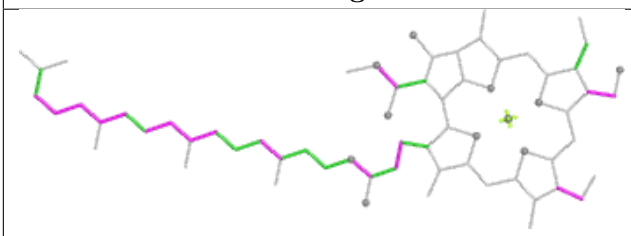
Ligand CHL Q 314



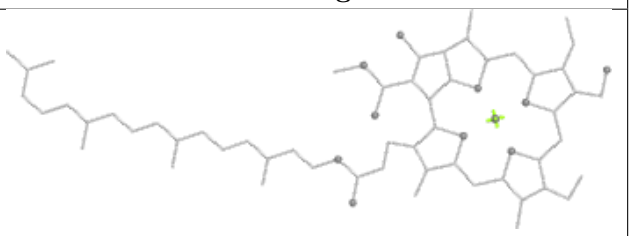
Bond lengths



Bond angles

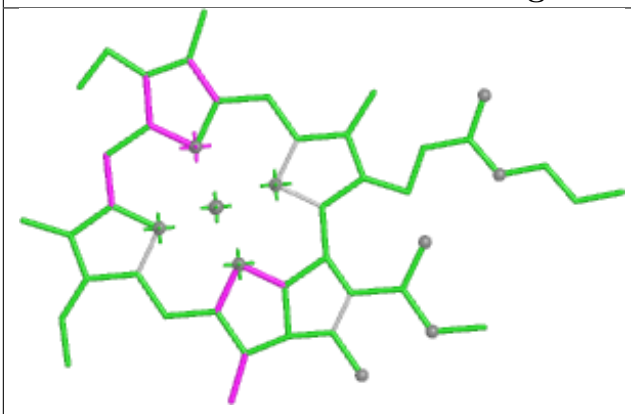


Torsions

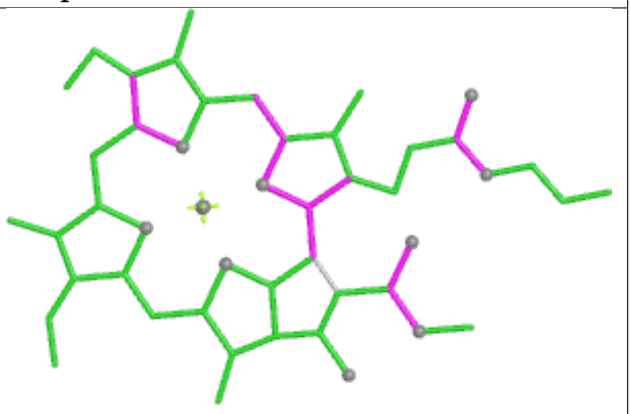


Rings

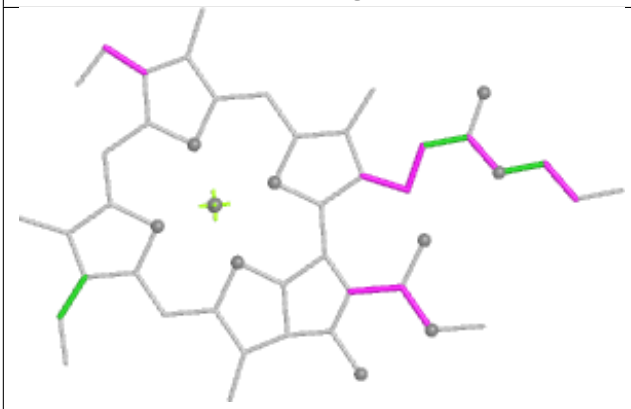
Ligand CLA q 308



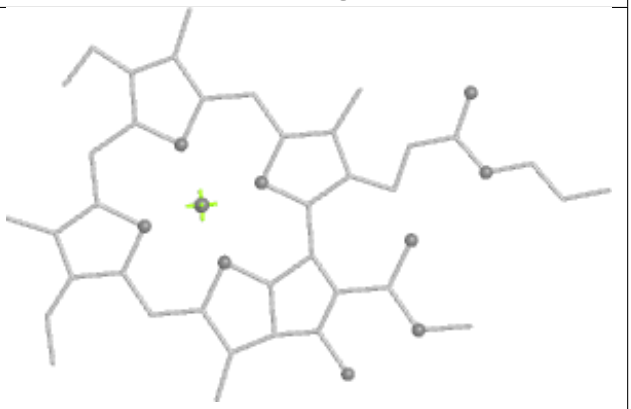
Bond lengths



Bond angles

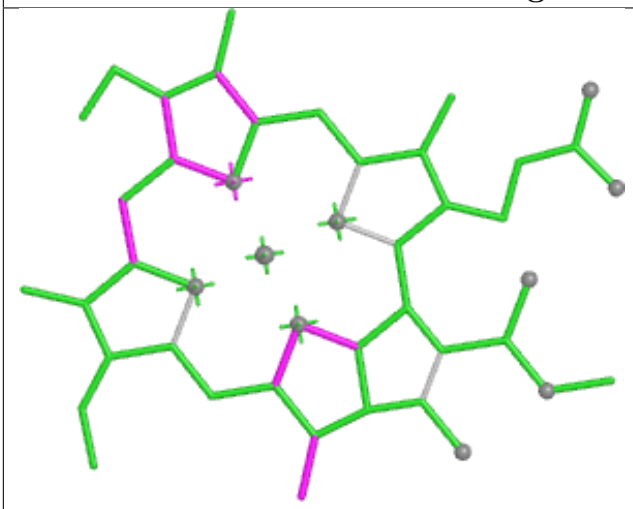


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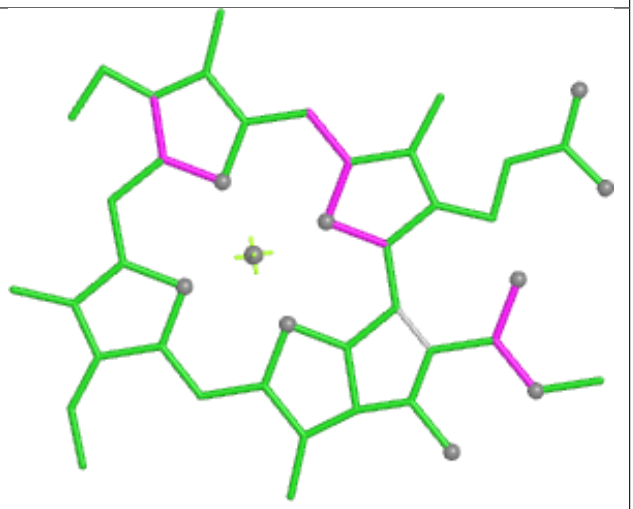


Rings

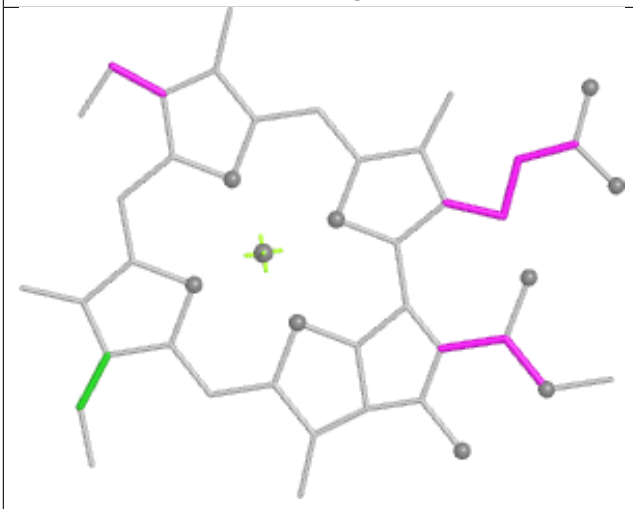
Ligand CLA S 304



Bond lengths



Bond angles

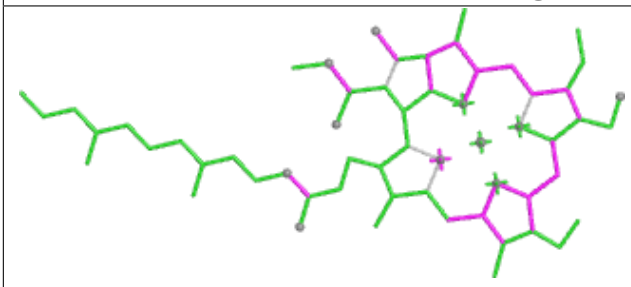


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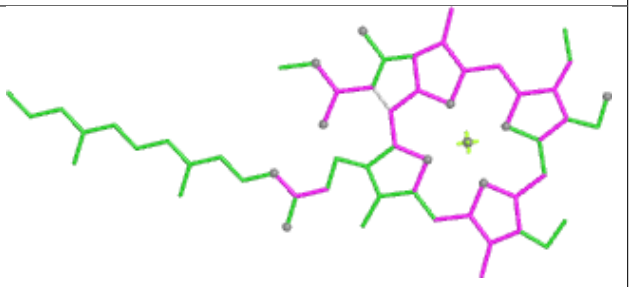


Rings

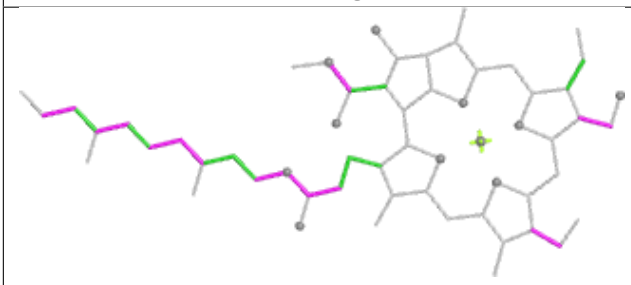
Ligand CHL s 315



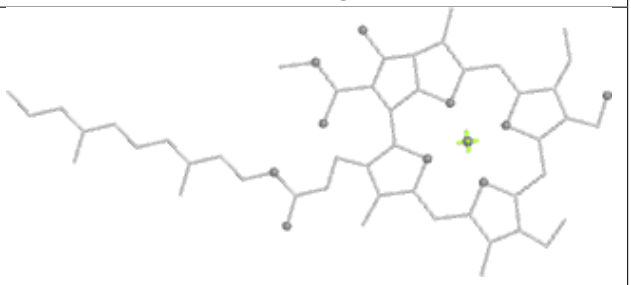
Bond lengths



Bond angles

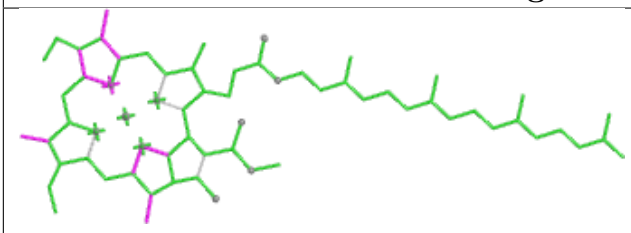


Torsions

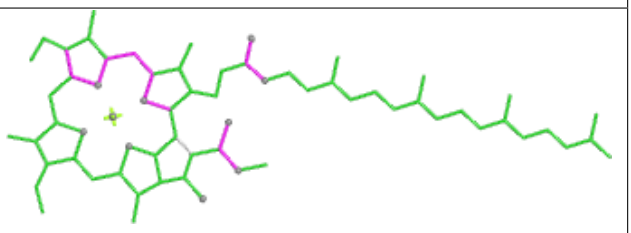


Rings

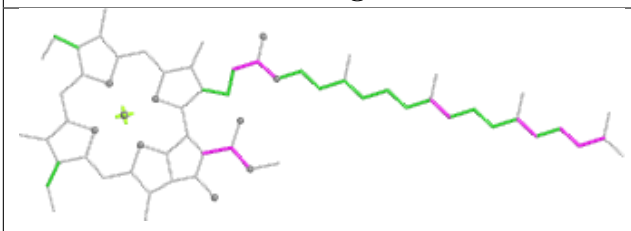
Ligand CLA n 302



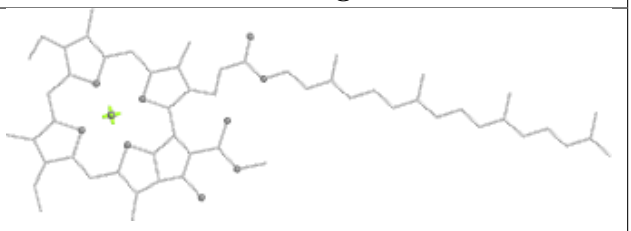
Bond lengths



Bond angles

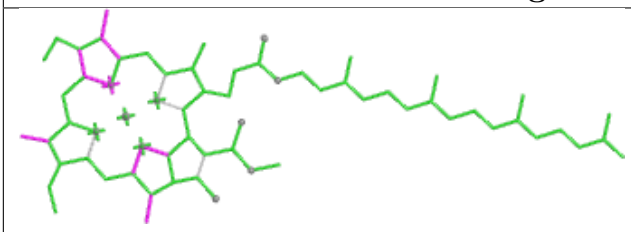


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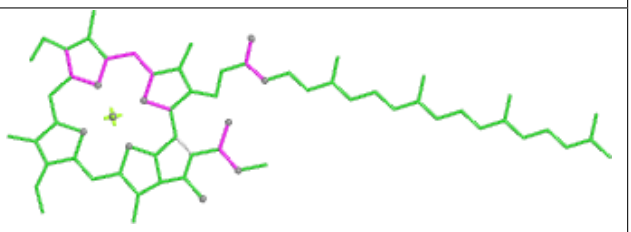


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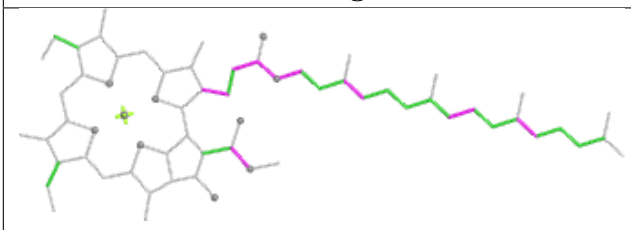
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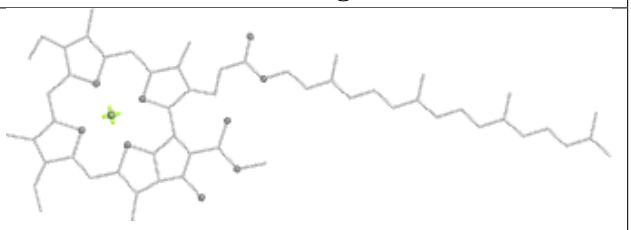
Bond lengths



Bond angles

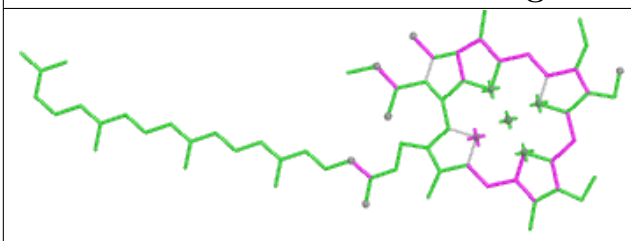


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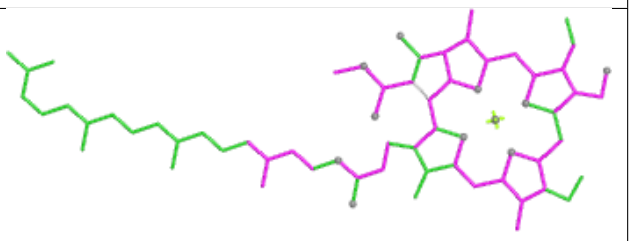


Rings

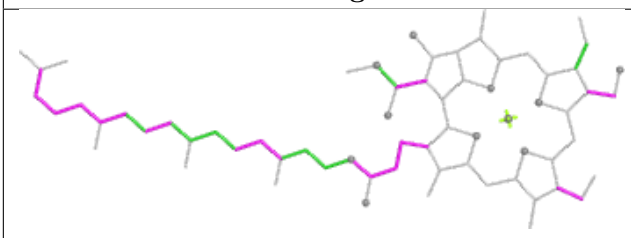
Ligand CHL u 316



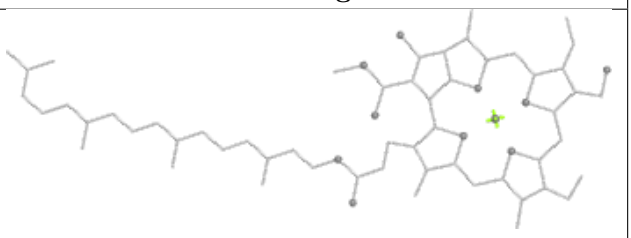
Bond lengths



Bond angles

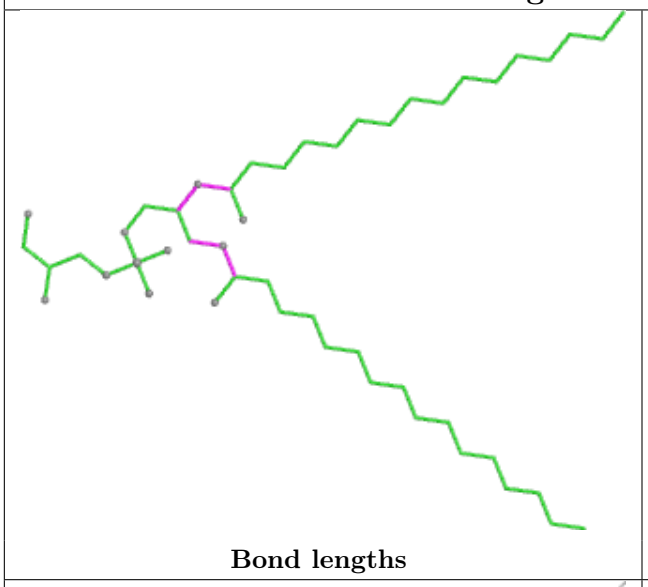


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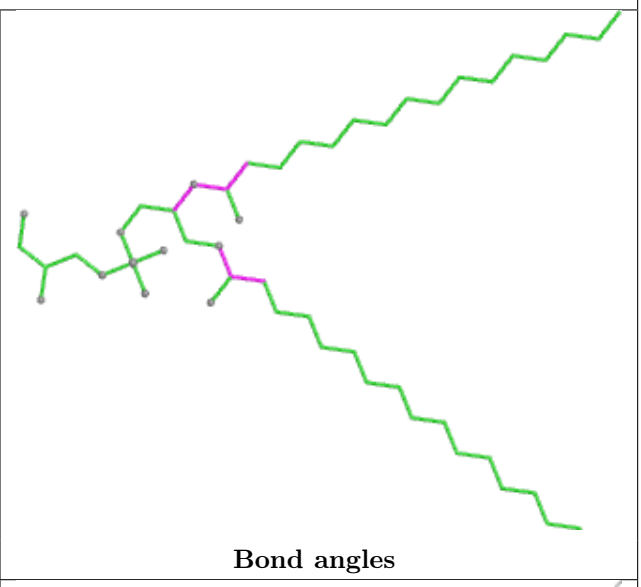


Rings

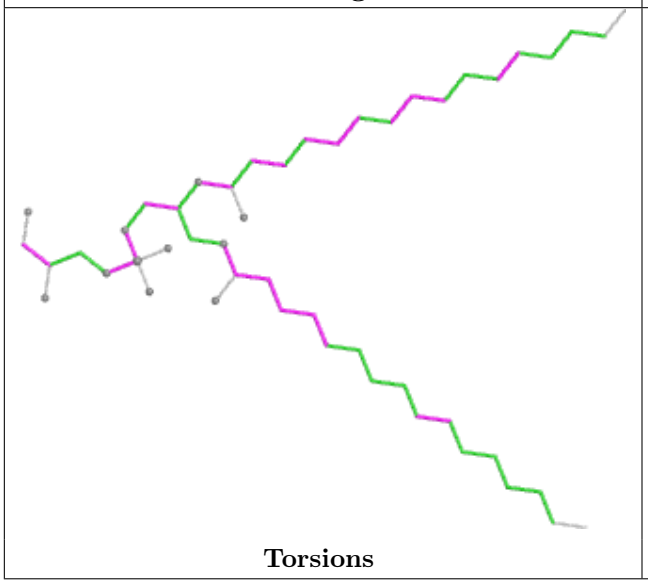
Ligand LHG u 312



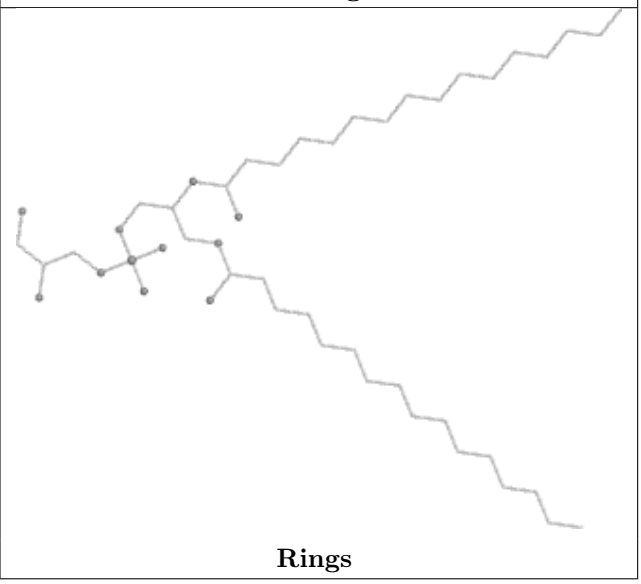
Bond lengths



Bond angles

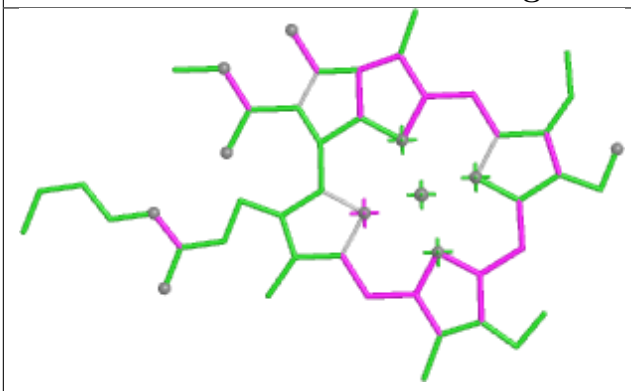


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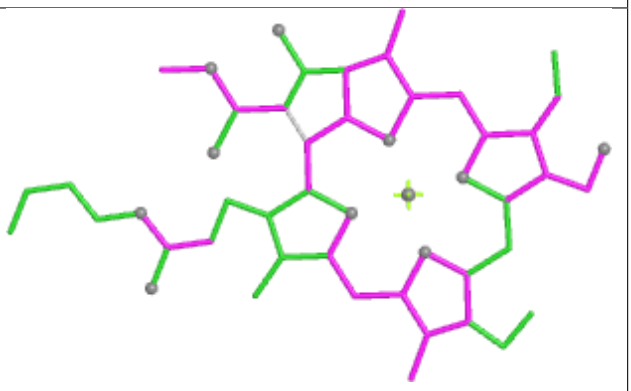


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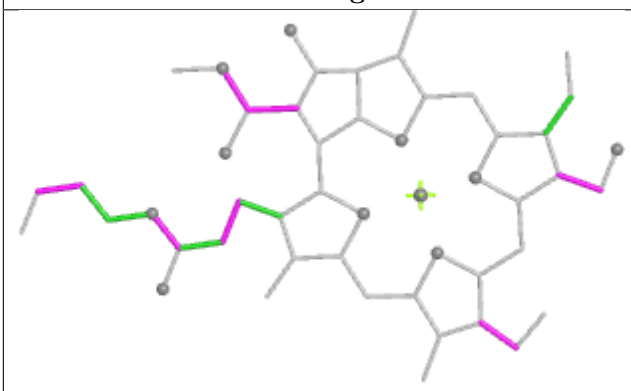
Ligand CHL U 314



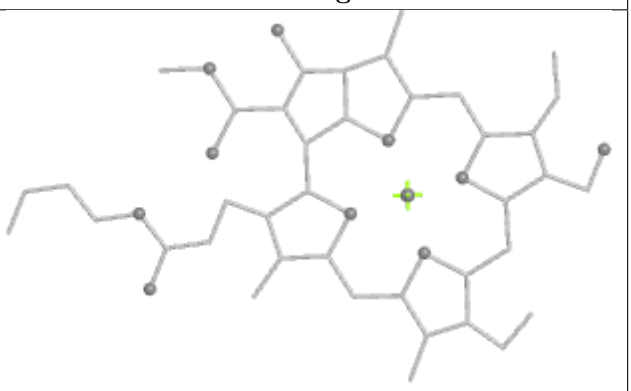
Bond lengths



Bond angles

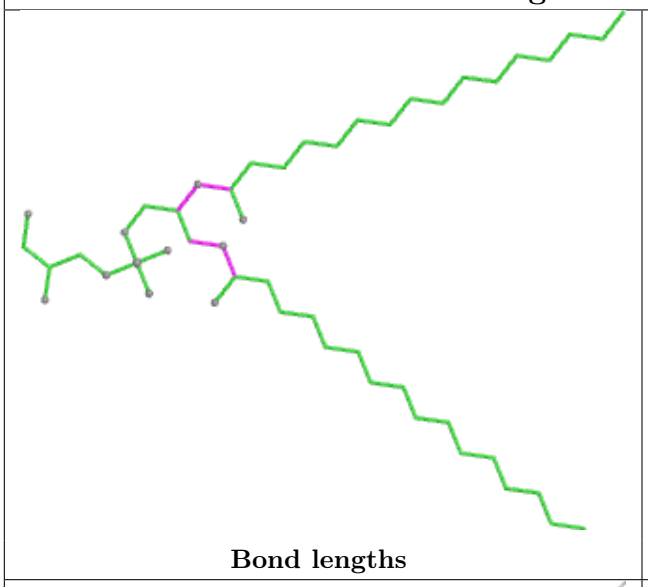


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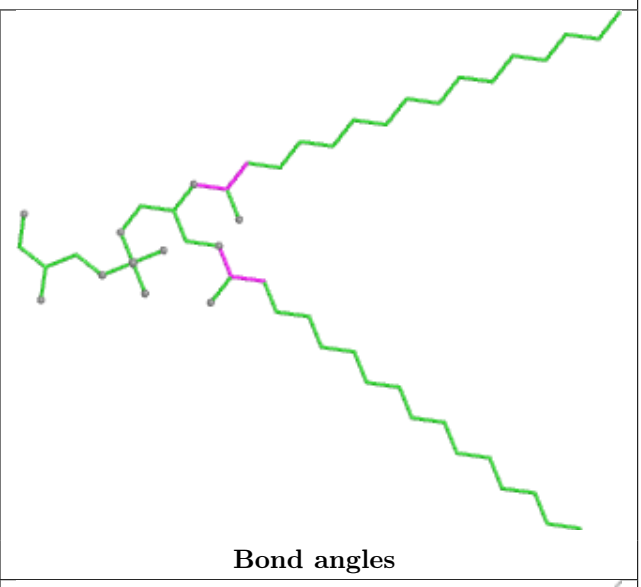


Rings

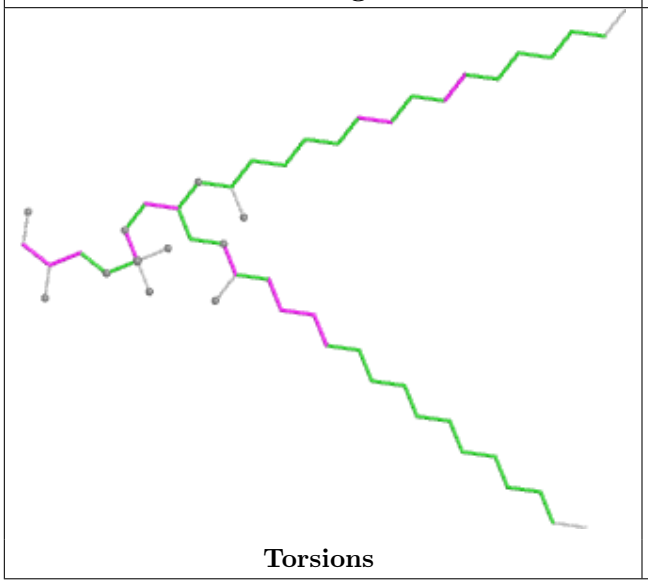
Ligand LHG c 521



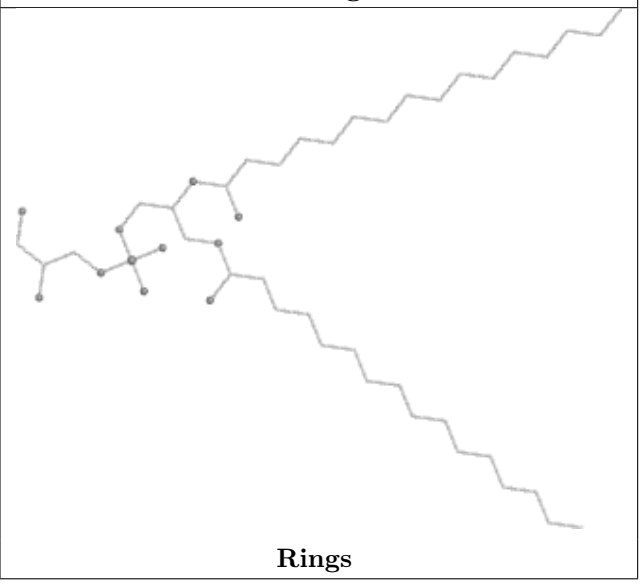
Bond lengths



Bond angles

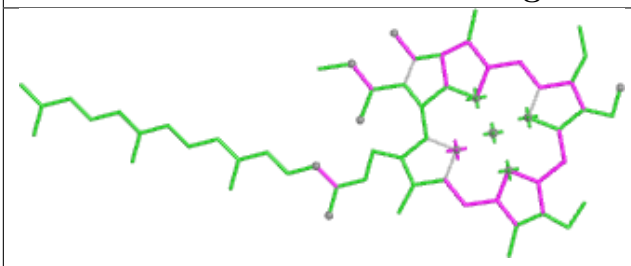


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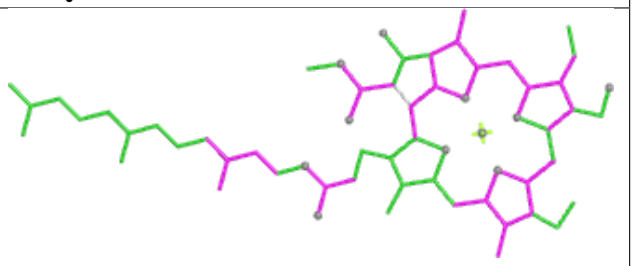


Rings

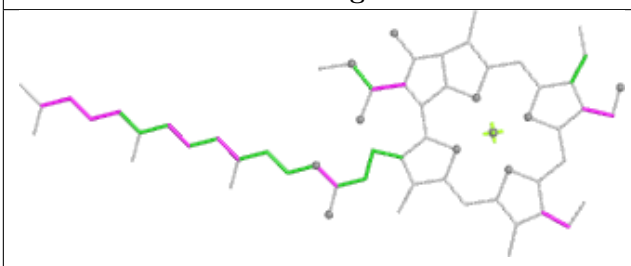
Ligand CHL Q 316



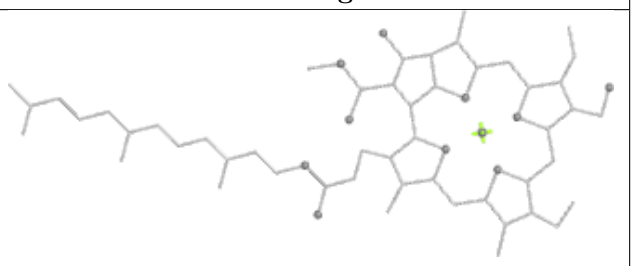
Bond lengths



Bond angles

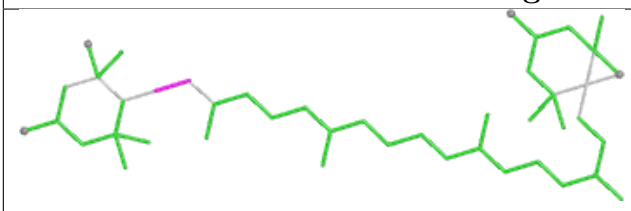


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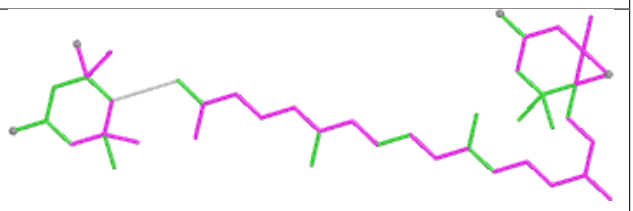


Rings

Ligand NEX P 301



Bond lengths



Bond angles

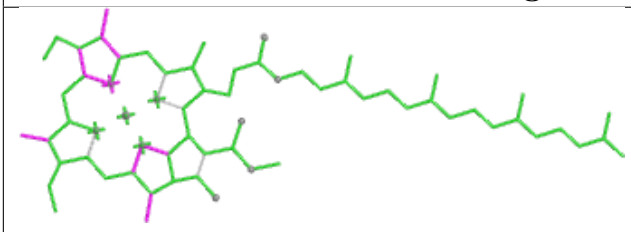


Torsions

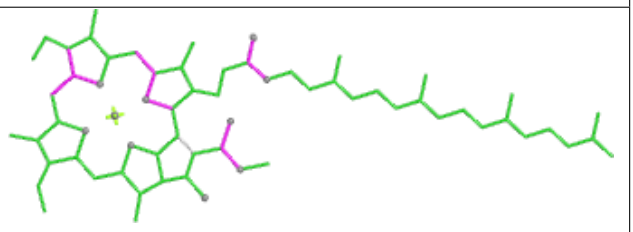


Rings

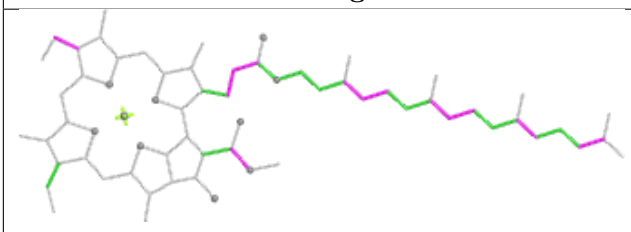
Ligand CLA U 307



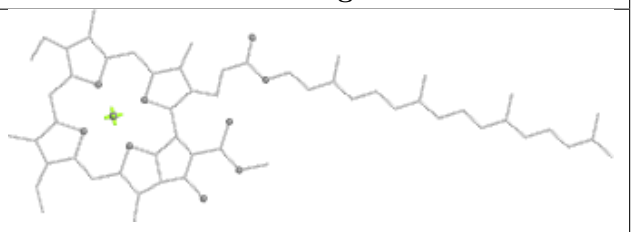
Bond lengths



Bond angles

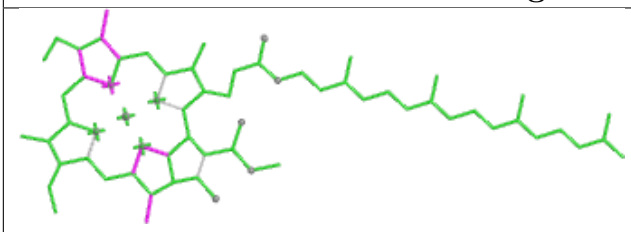


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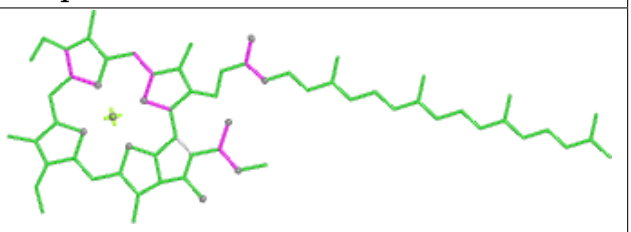


Rings

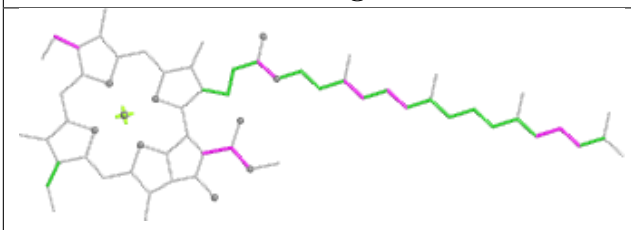
Ligand CLA q 302



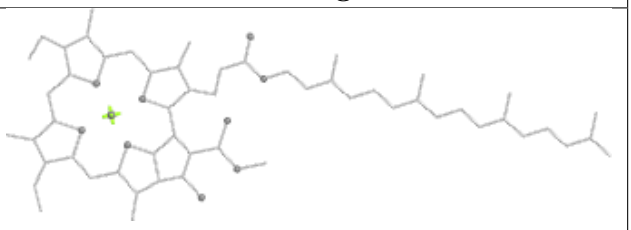
Bond lengths



Bond angles

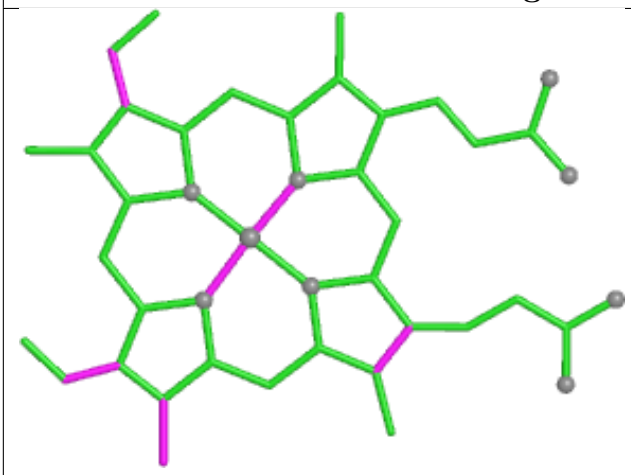


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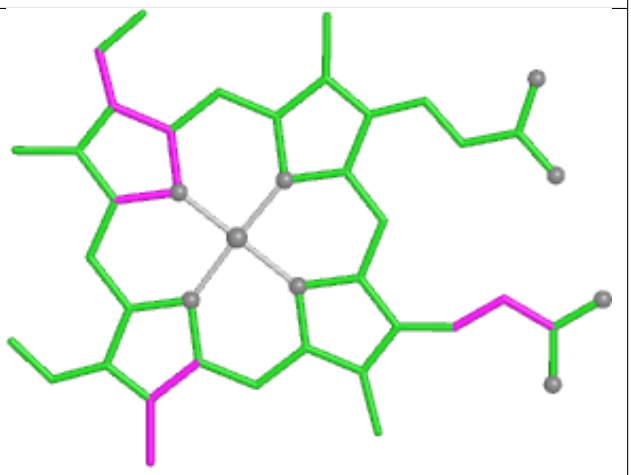


Rings

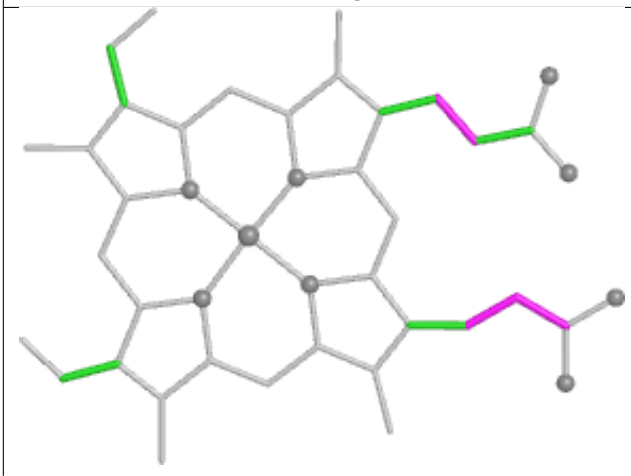
Ligand HEM e 101



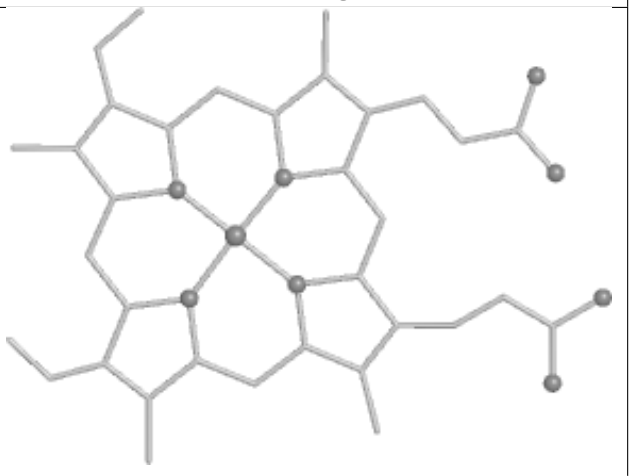
Bond lengths



Bond angles

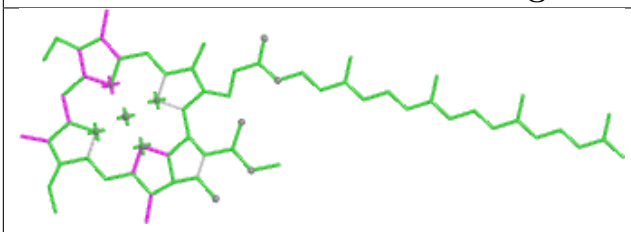


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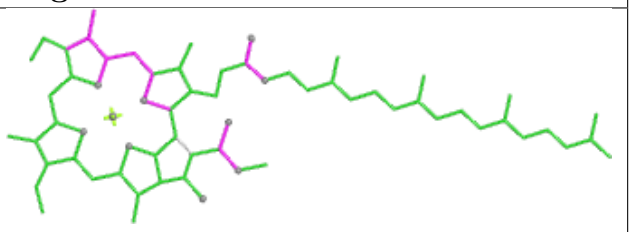


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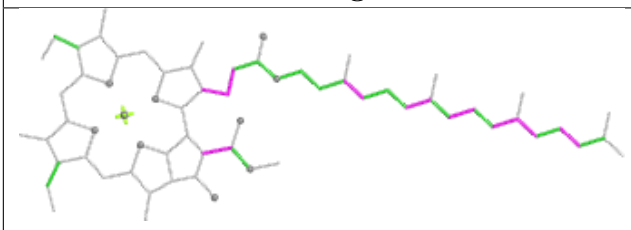
Ligand CLA g 301



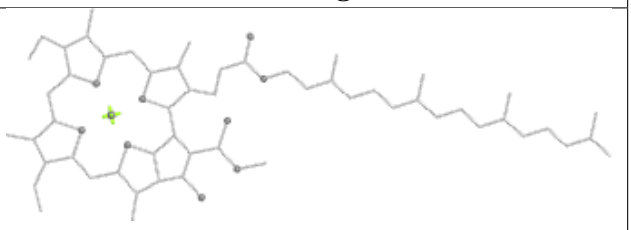
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Bond angles



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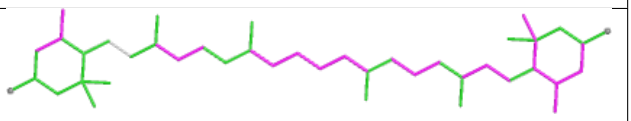


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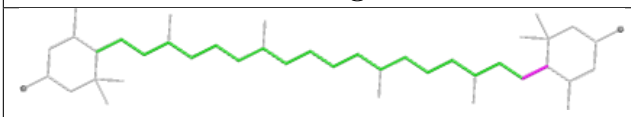
Ligand LUT 1 309



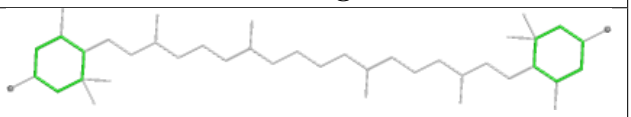
Bond lengths



Bond angles

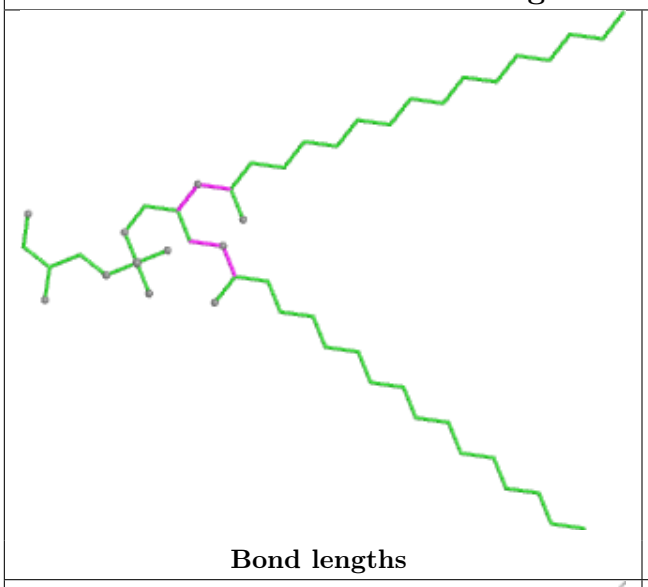


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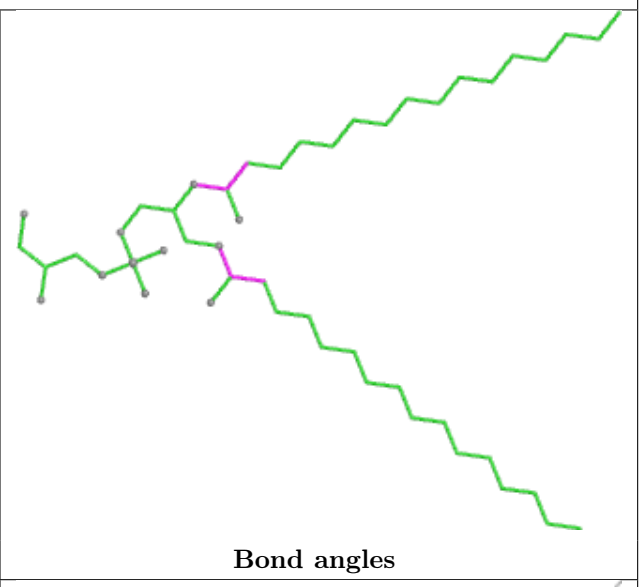


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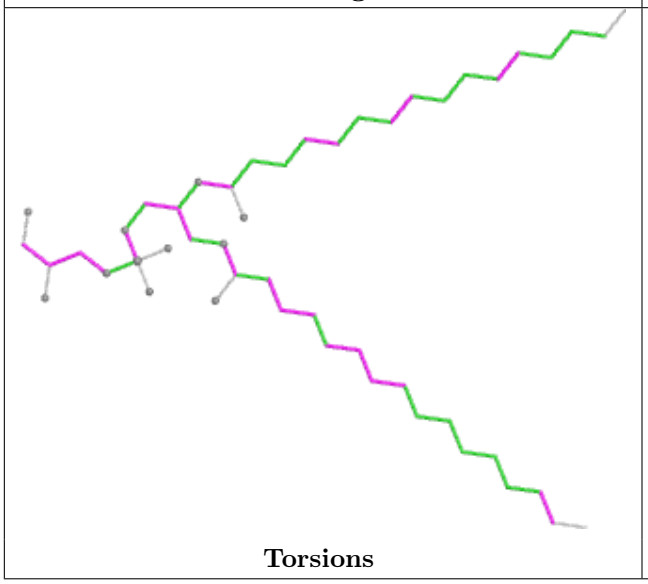
Ligand LHG 2 312



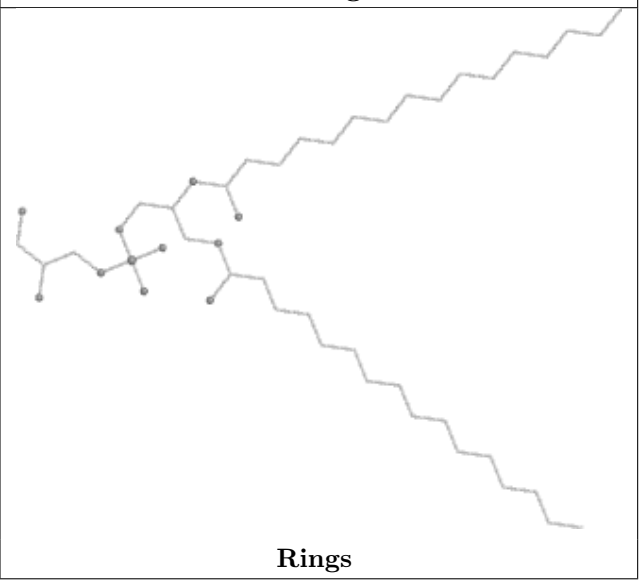
Bond lengths



Bond angles

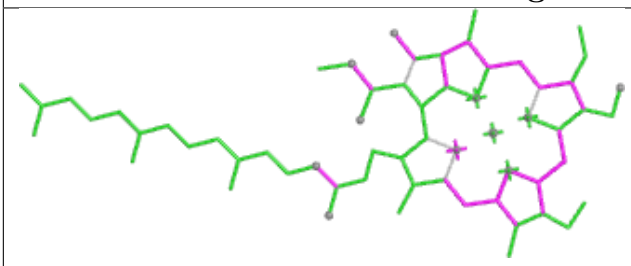


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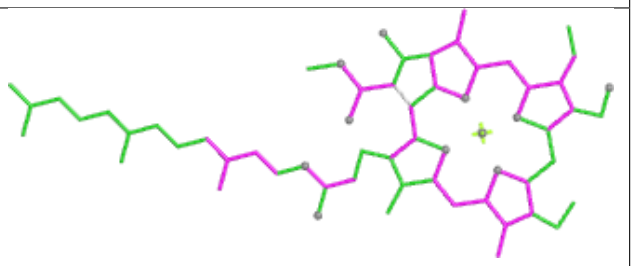


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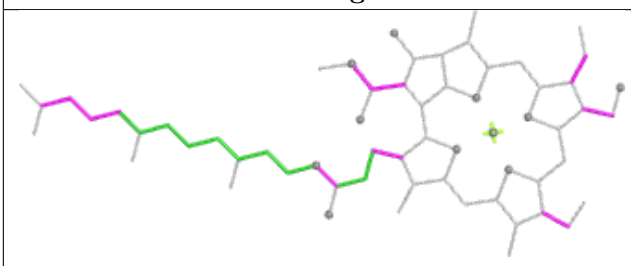
Ligand CHL 6 317



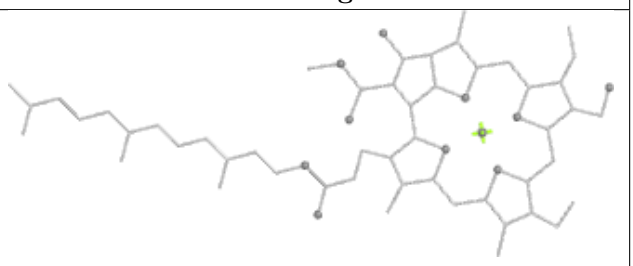
Bond lengths



Bond angles

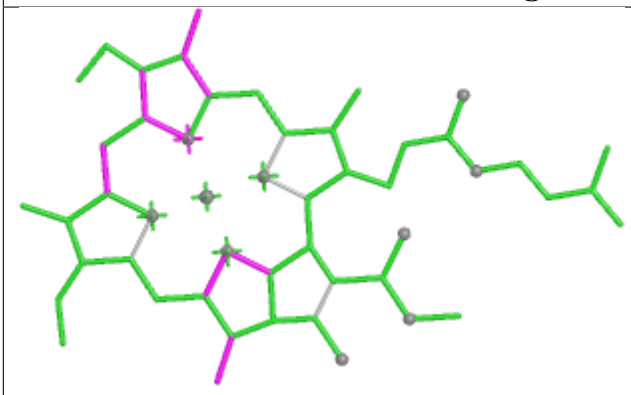


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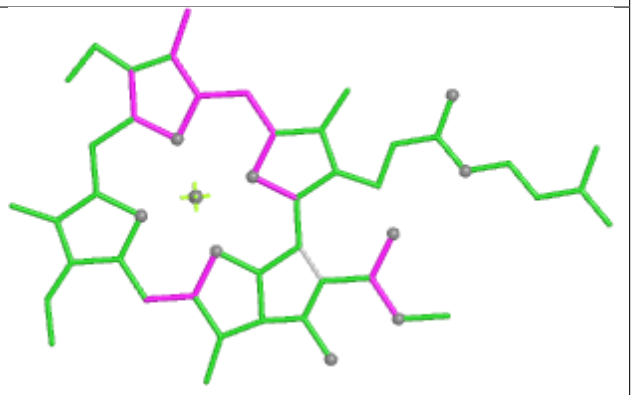


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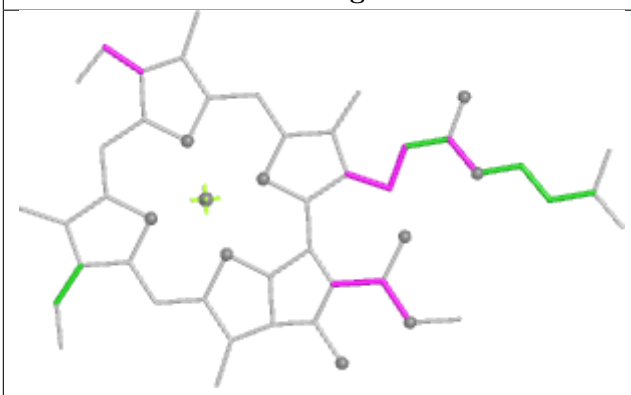
Ligand CLA G 303



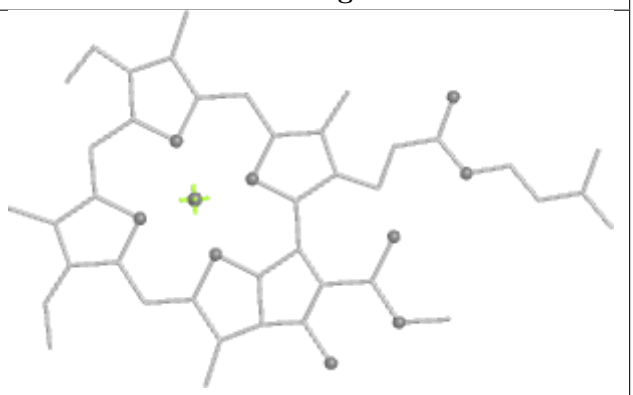
Bond lengths



Bond angles

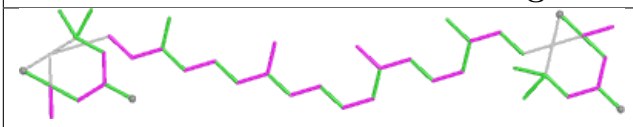


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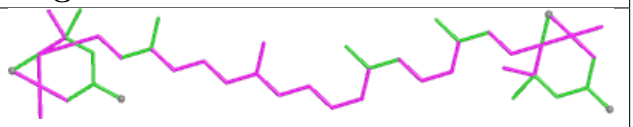


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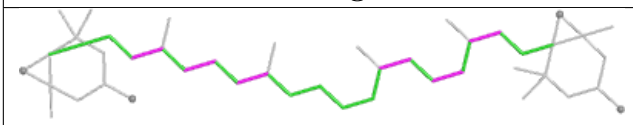
Ligand XAT g 309



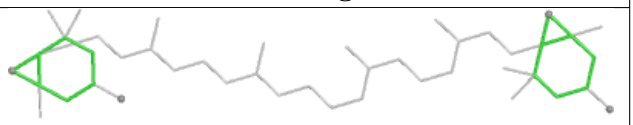
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Bond angles

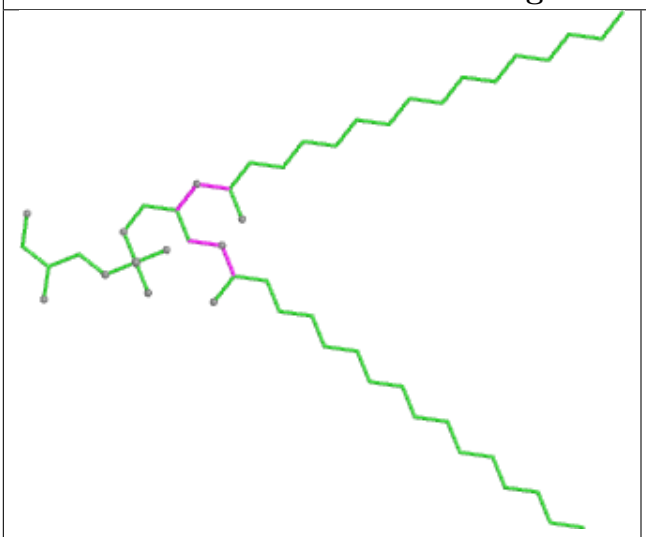


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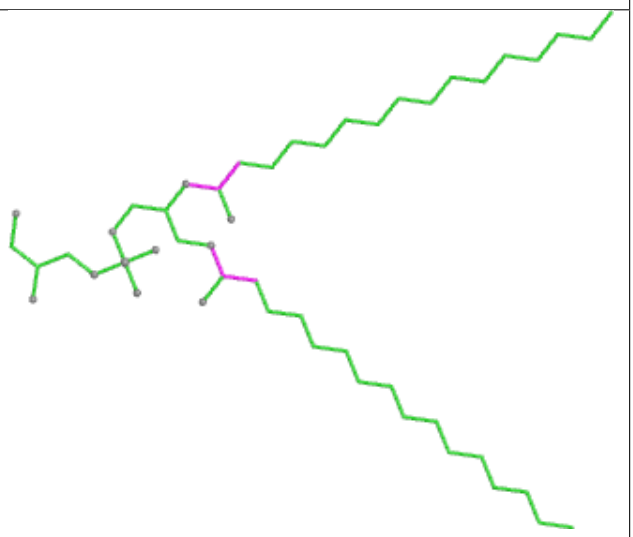


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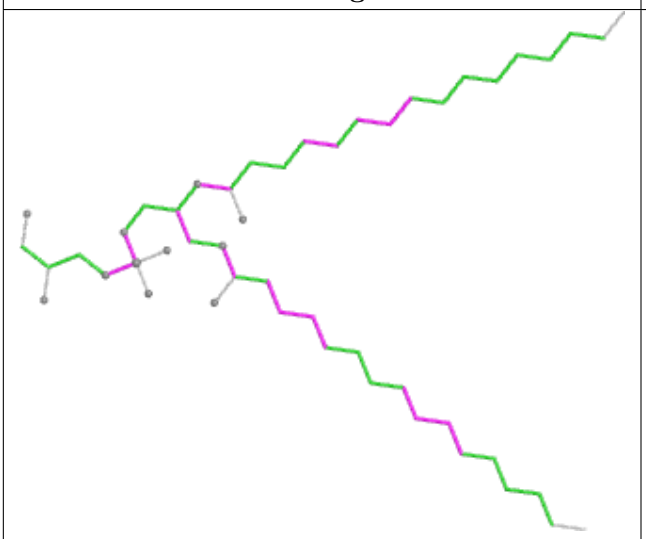
Ligand LHG v 312



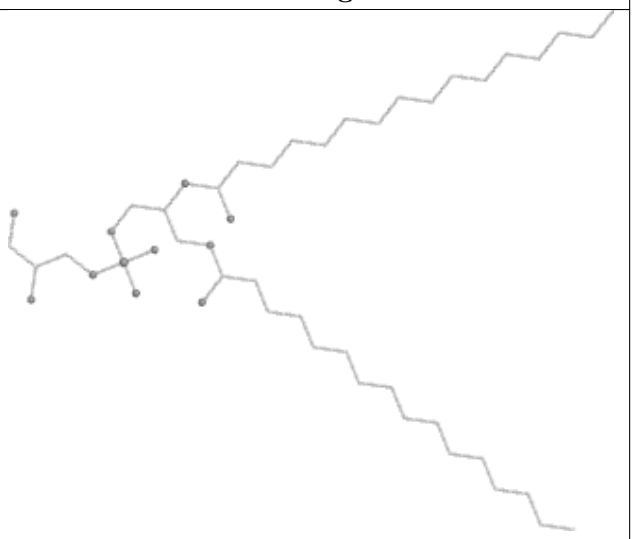
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Bond angles

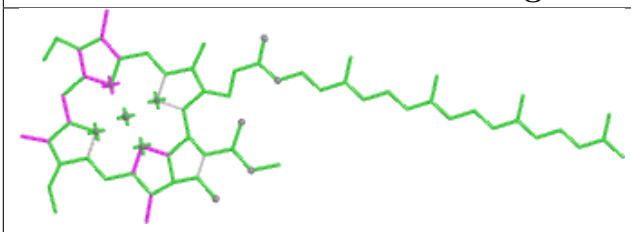


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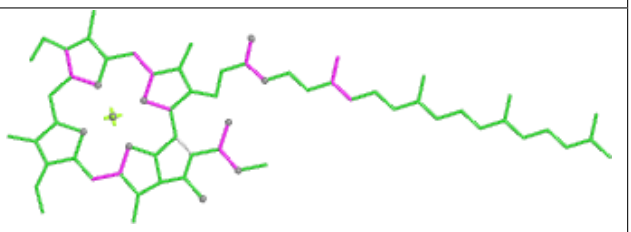


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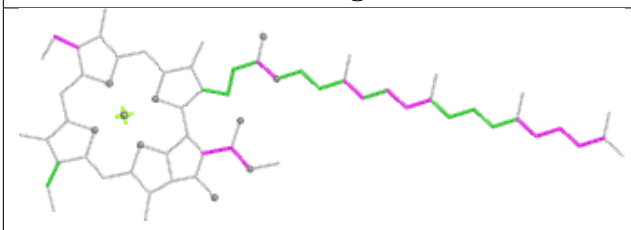
Ligand CLA B 610



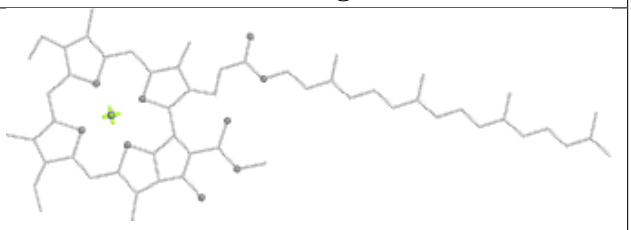
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Bond angles

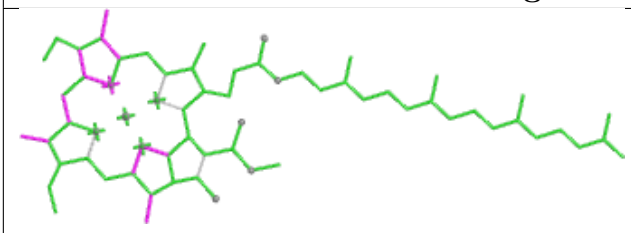


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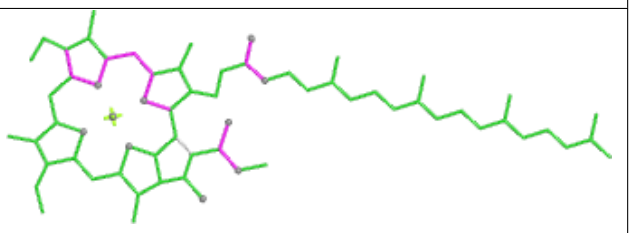


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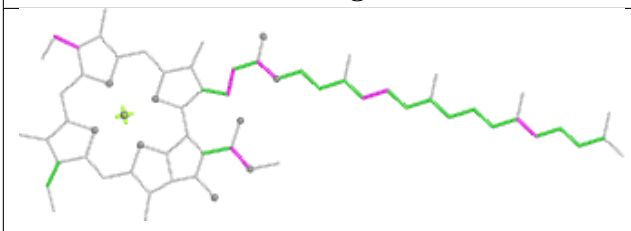
Ligand CLA V 307



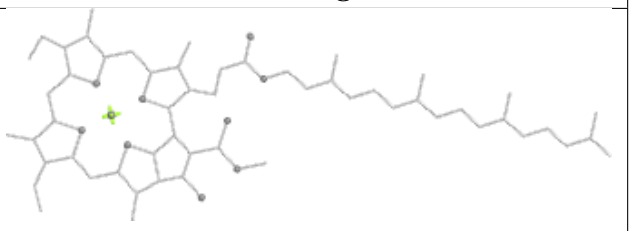
Bond lengths



Bond angles

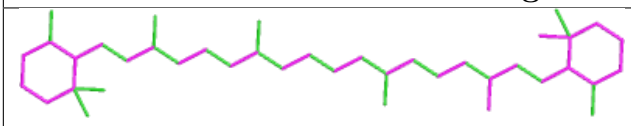


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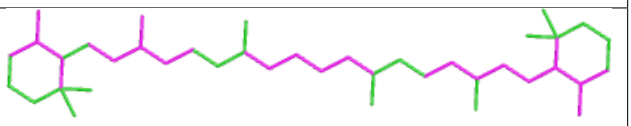


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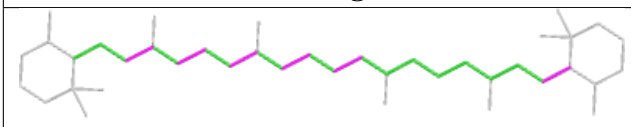
Ligand BCR X 201



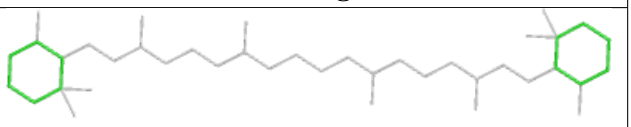
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Bond angles

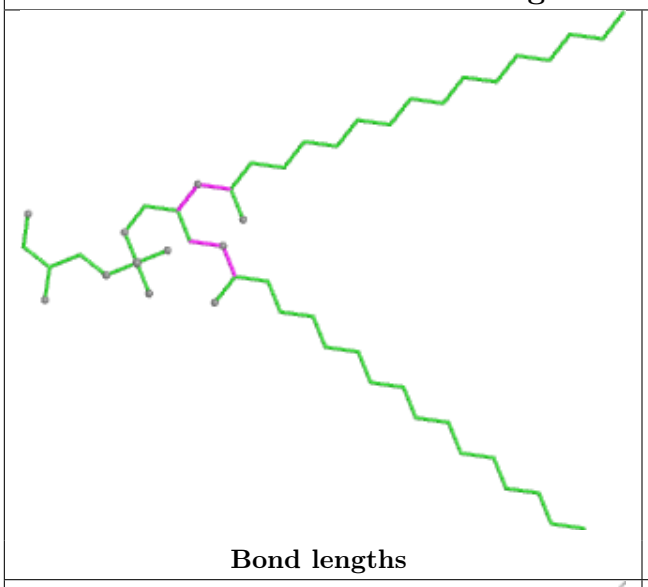


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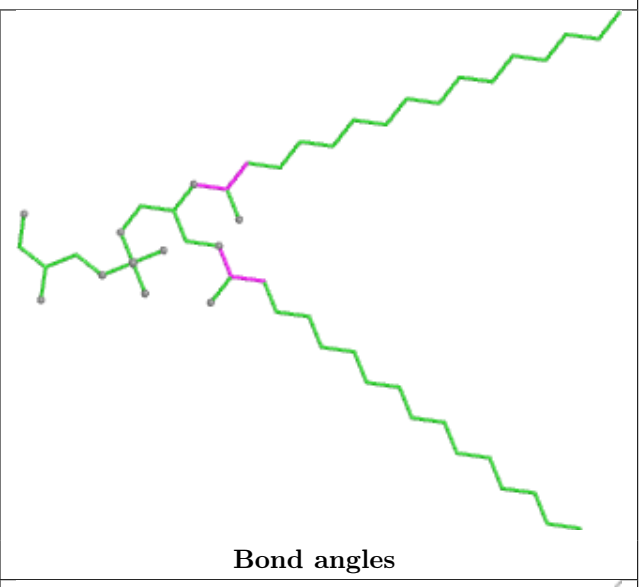


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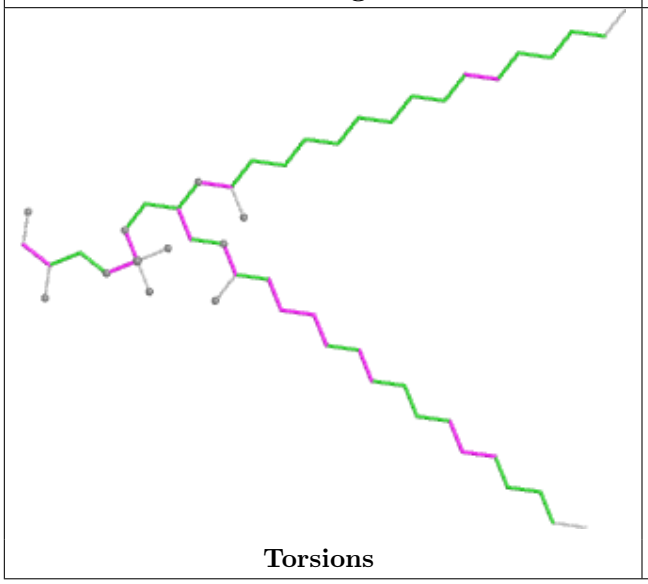
Ligand LHG 3 310



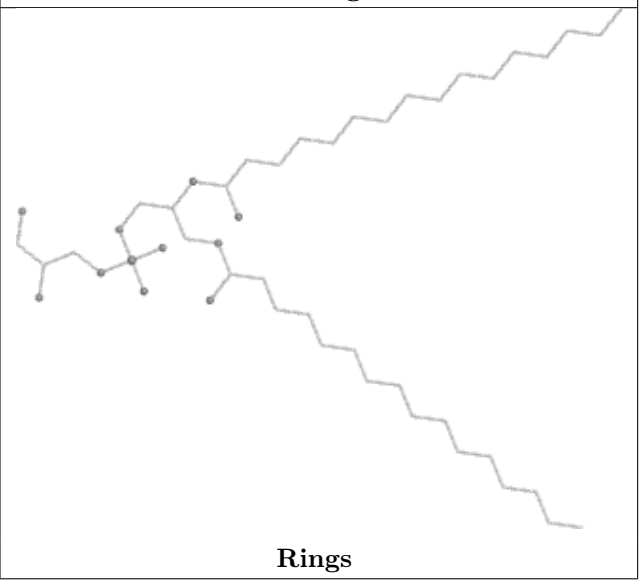
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Bond angles

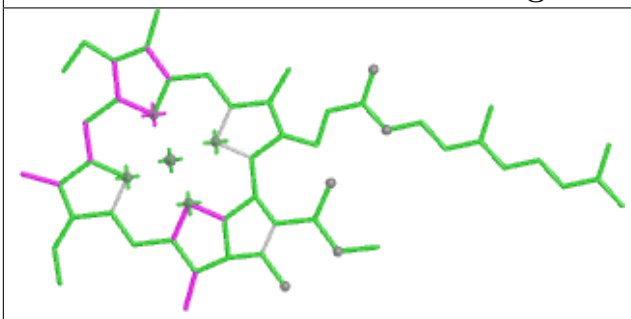


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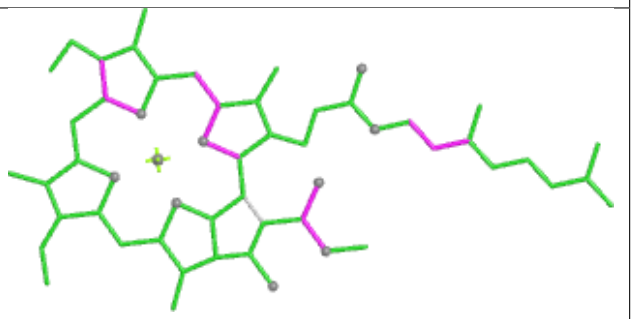


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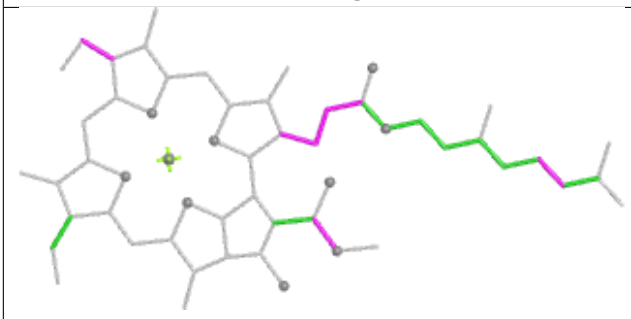
Ligand CLA S 305



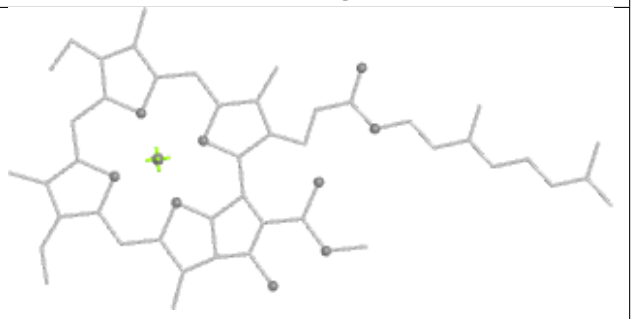
Bond lengths



Bond angles

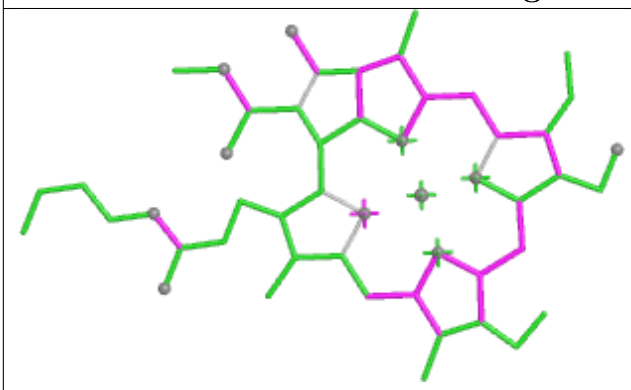


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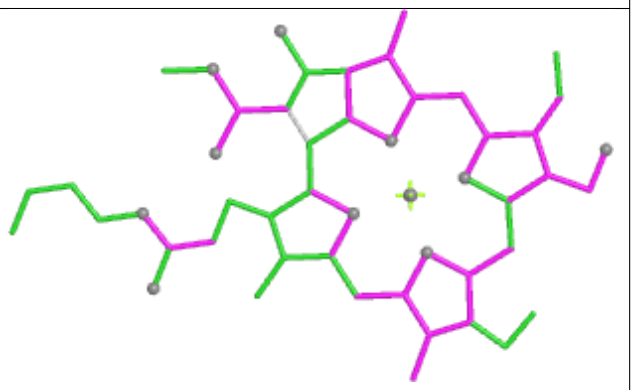


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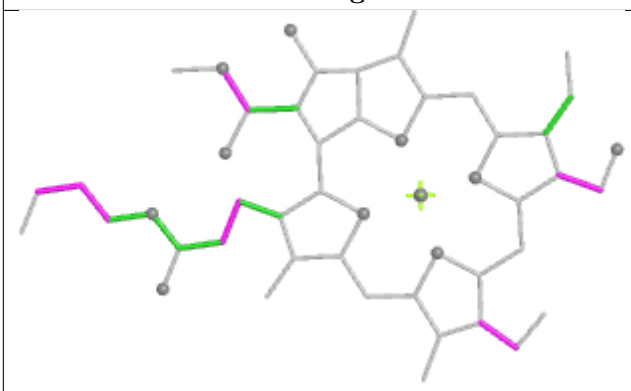
Ligand CHL V 315



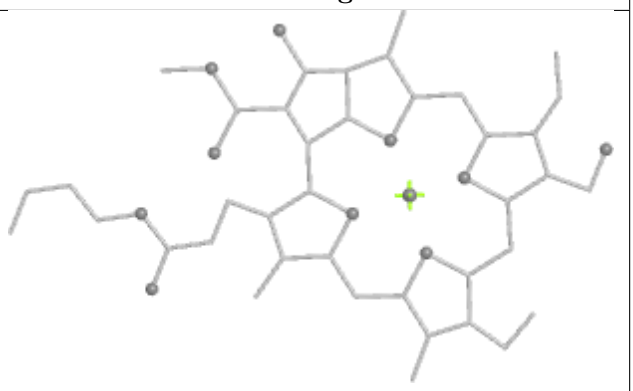
Bond lengths



Bond angles

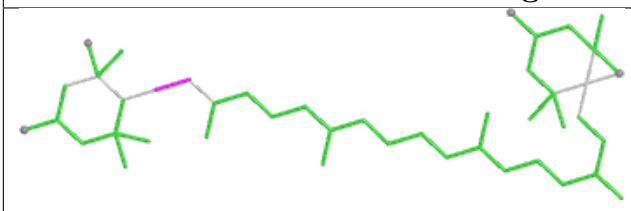


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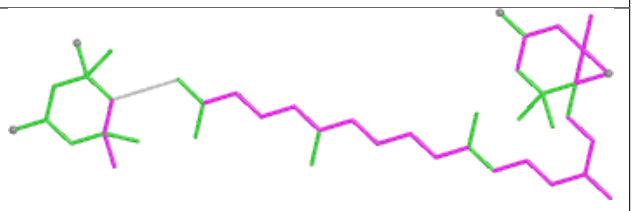


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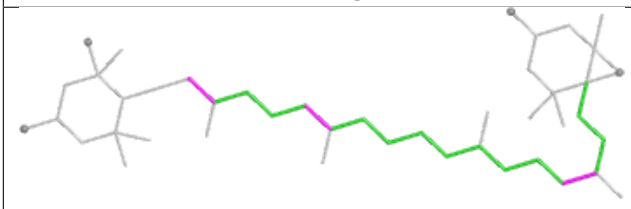
Ligand NEX V 319



Bond lengths



Bond angles

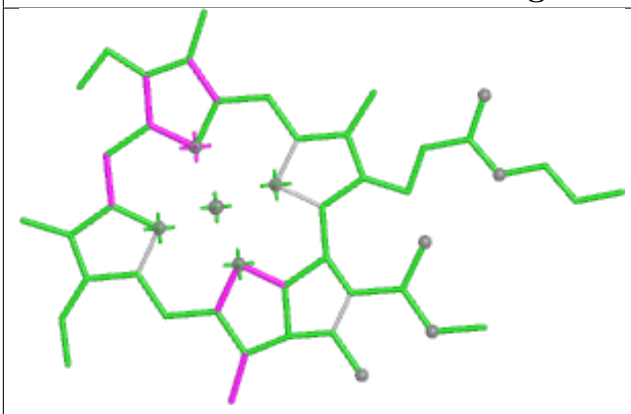


Torsions

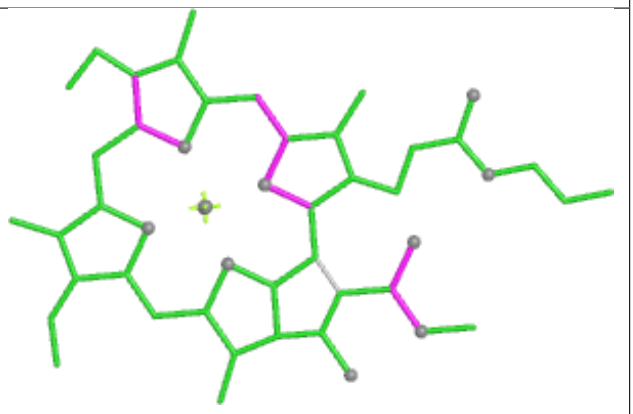


Rings

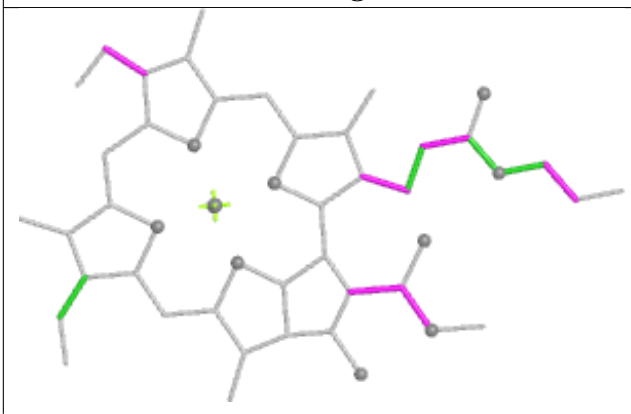
Ligand CLA v 308



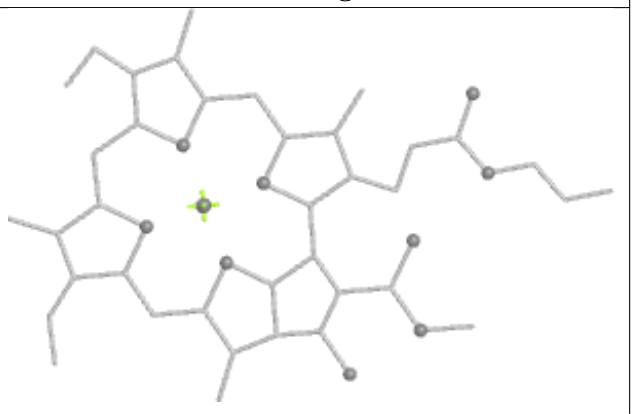
Bond lengths



Bond angles

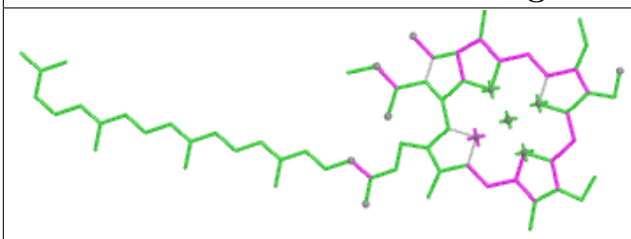


Torsions

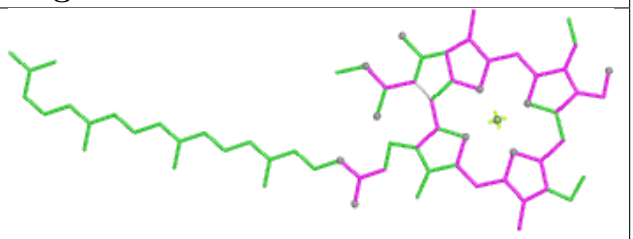


Rings

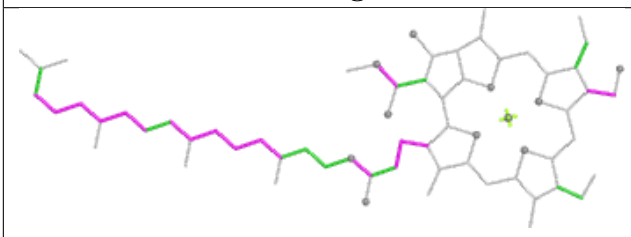
Ligand CHL g 315



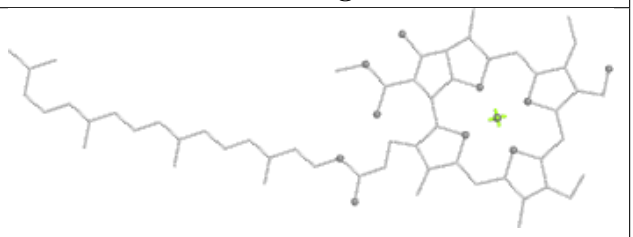
Bond lengths



Bond angles

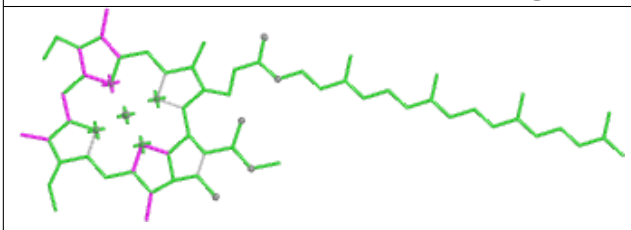


Torsions

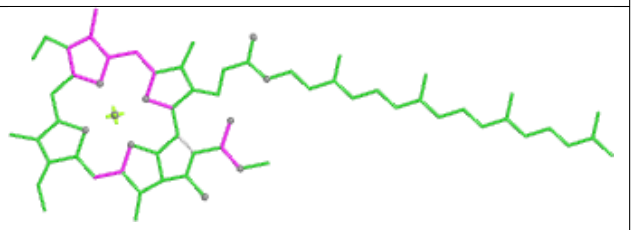


Rings

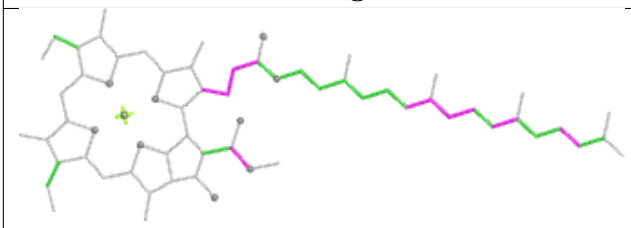
Ligand CLA 3 301



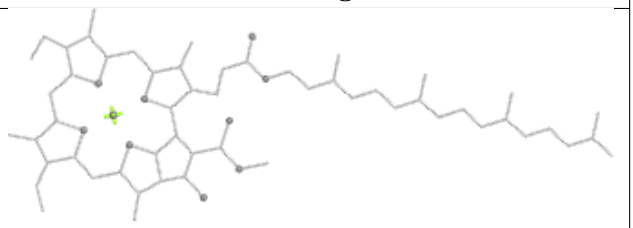
Bond lengths



Bond angles

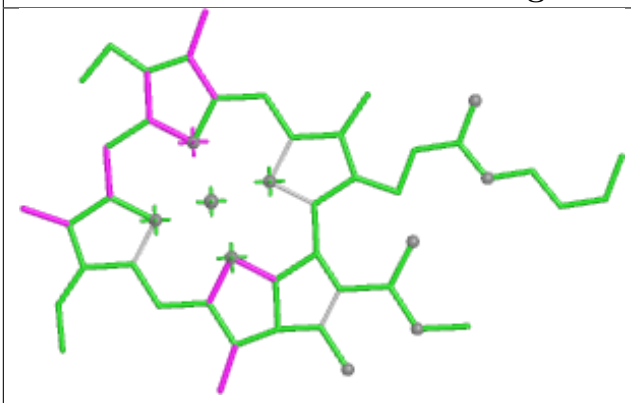


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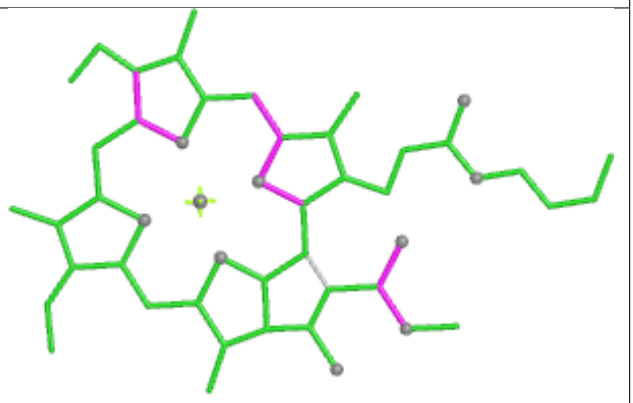


Rings

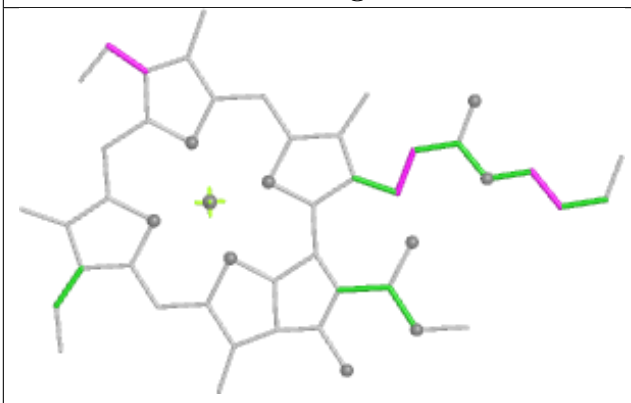
Ligand CLA S 309



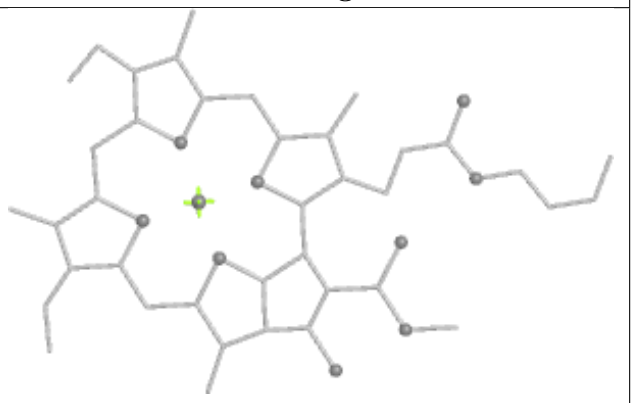
Bond lengths



Bond angles

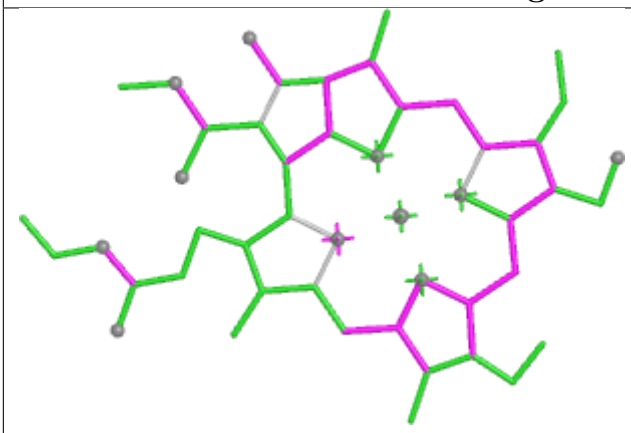


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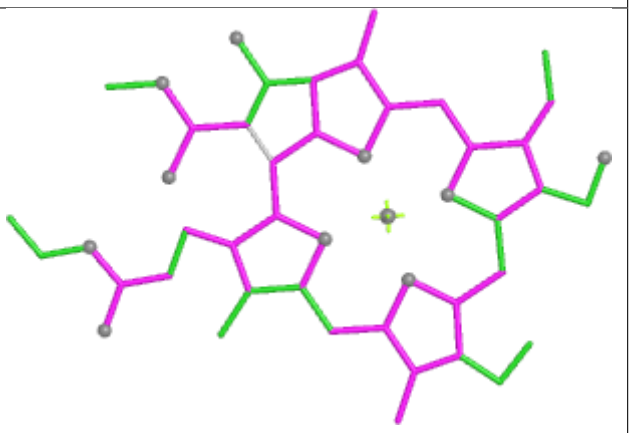


Rings

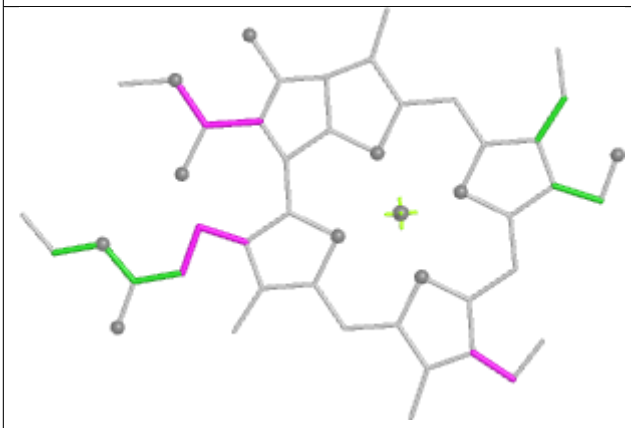
Ligand CHL 3 312



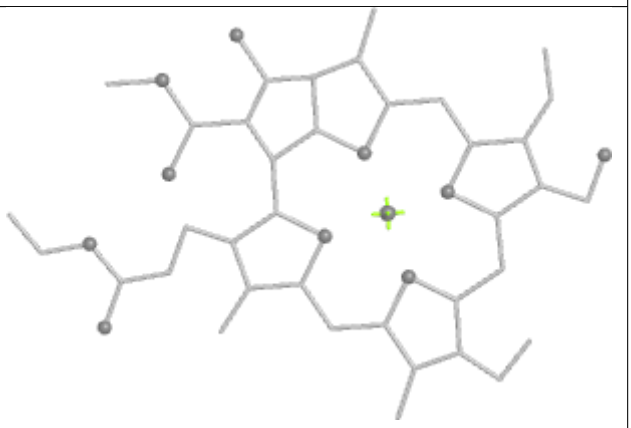
Bond lengths



Bond angles

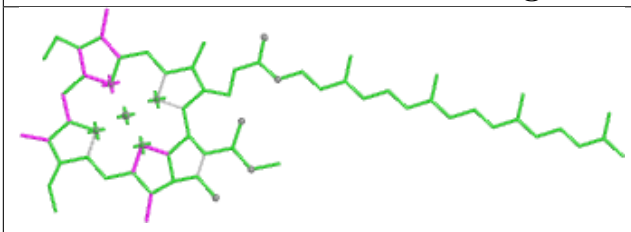


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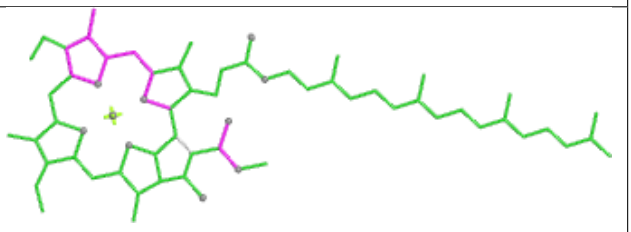


Rings

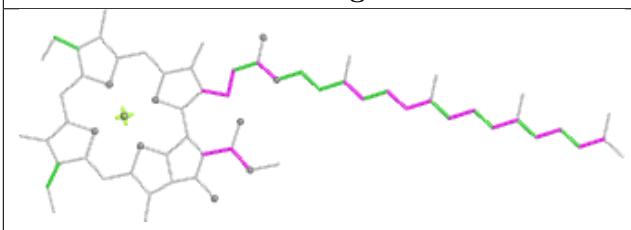
Ligand CLA G 301



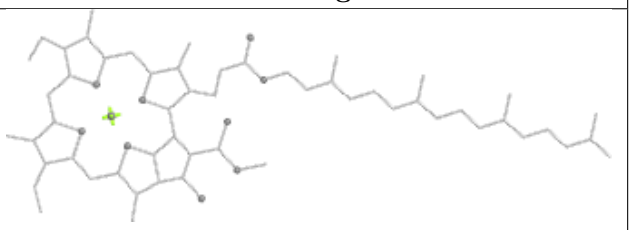
Bond lengths



Bond angles

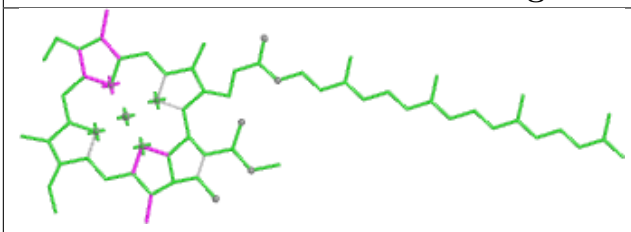


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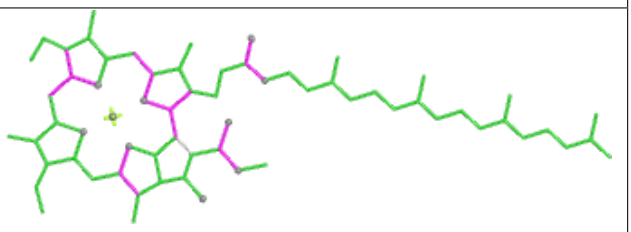


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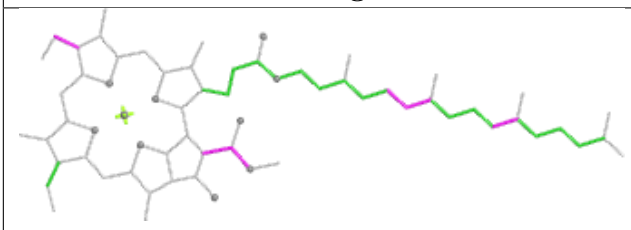
Ligand CLA b 616



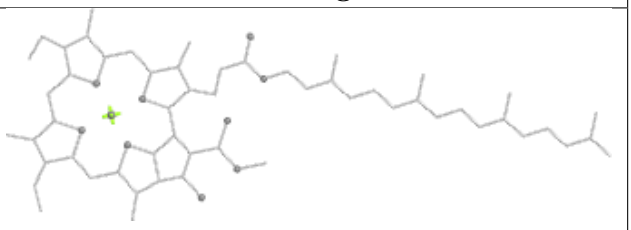
Bond lengths



Bond angles



Torsions

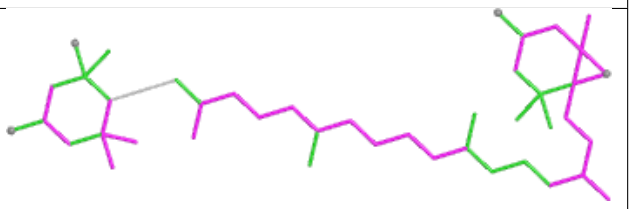


Rings

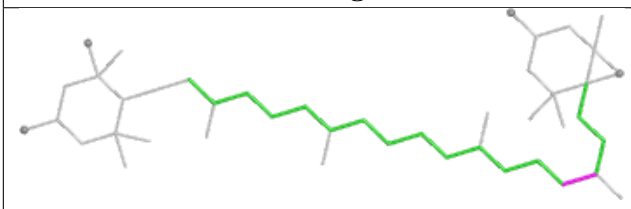
Ligand NEX u 320



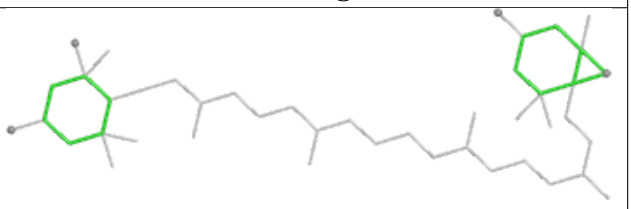
Bond lengths



Bond angles

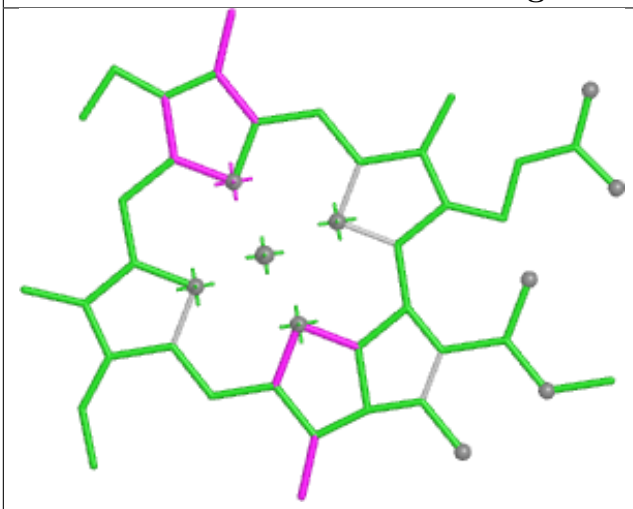


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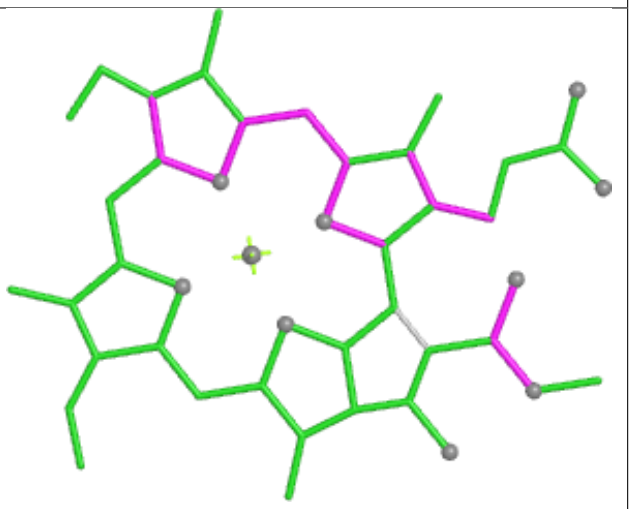


Rings

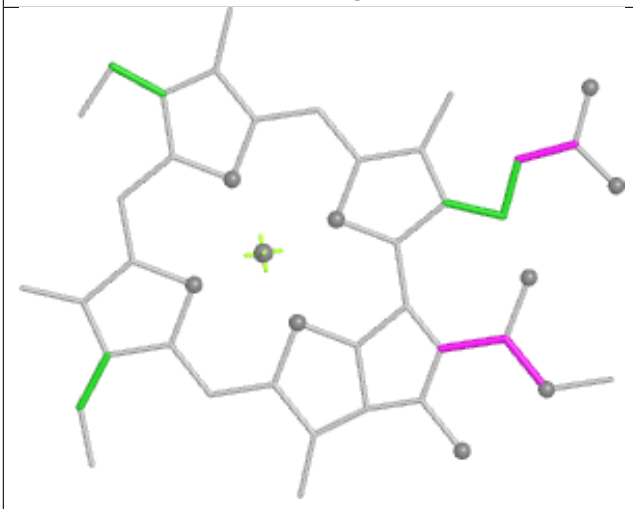
Ligand CLA S 302



Bond lengths



Bond angles

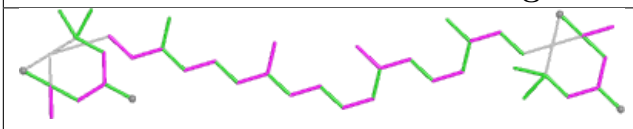


Torsions

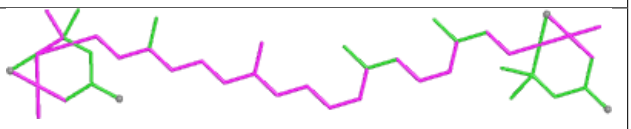


Rings

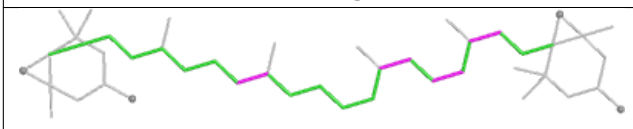
Ligand XAT U 311



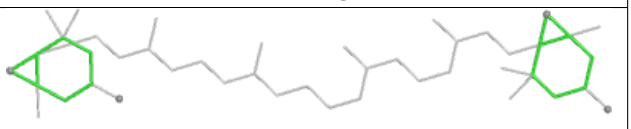
Bond lengths



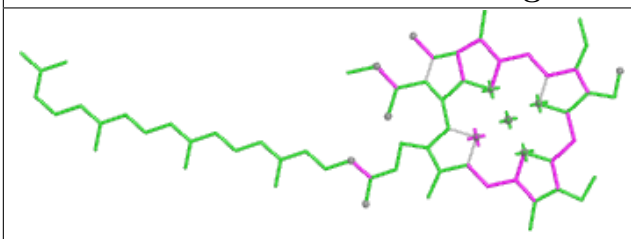
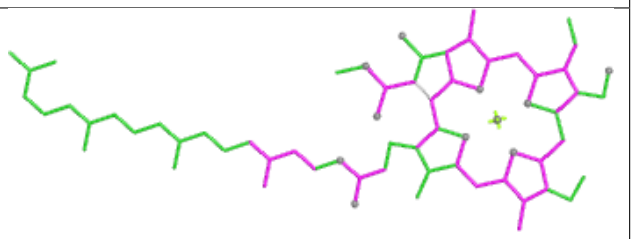
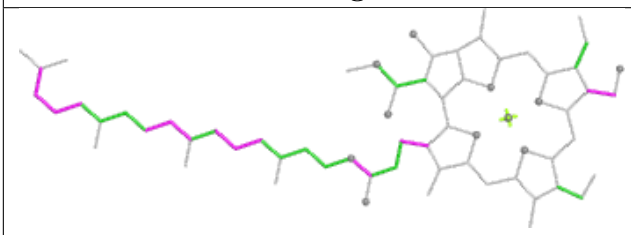
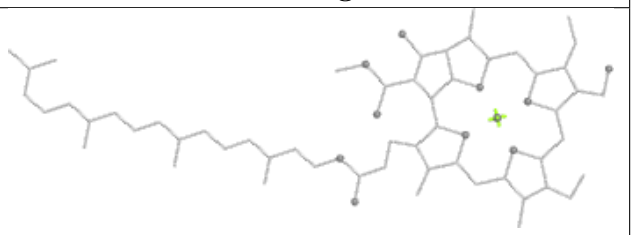
Bond angles

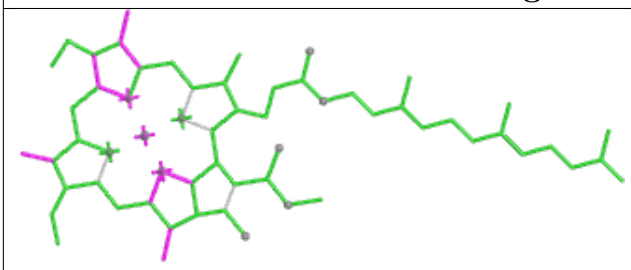
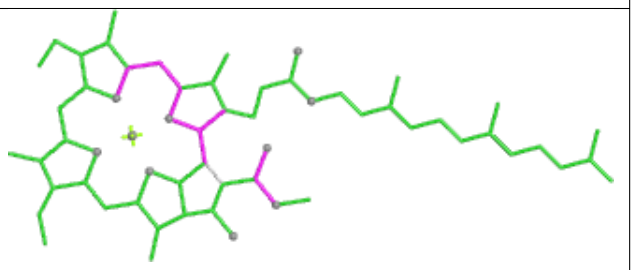
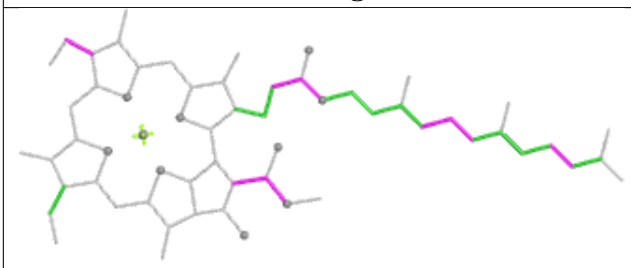
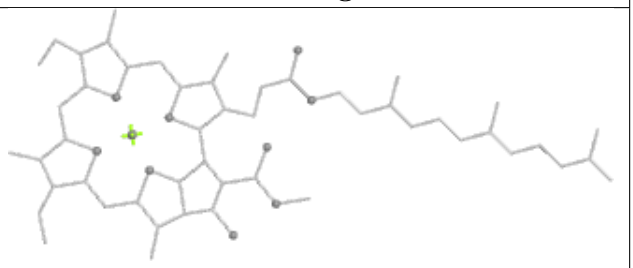


Torsions

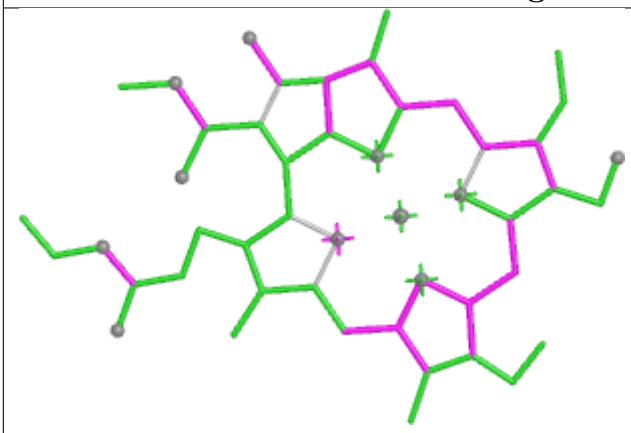


Rings

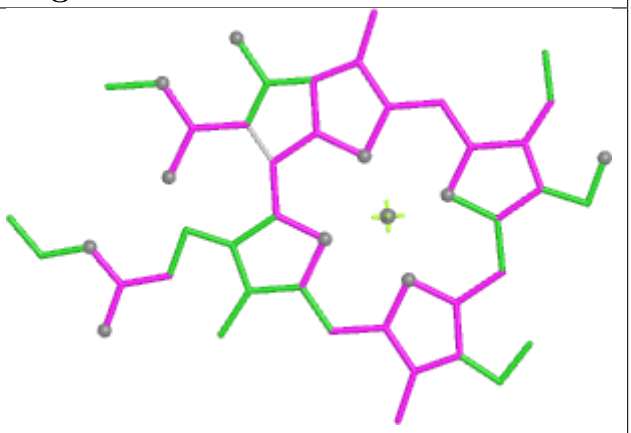
Ligand CHL V 317	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA U 306	
 Bond lengths	 Bond angles
 Torsions	 Rings

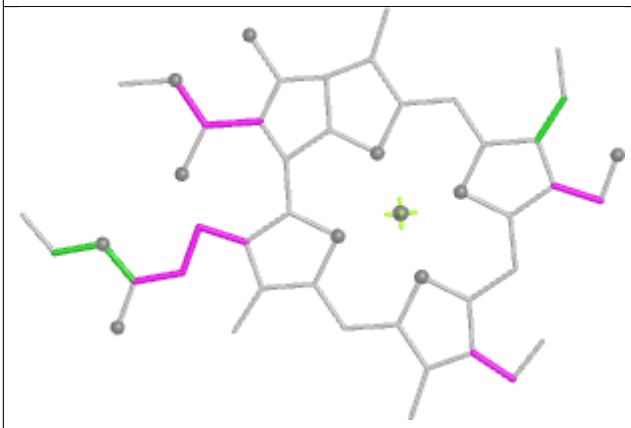
Ligand CHL g 312



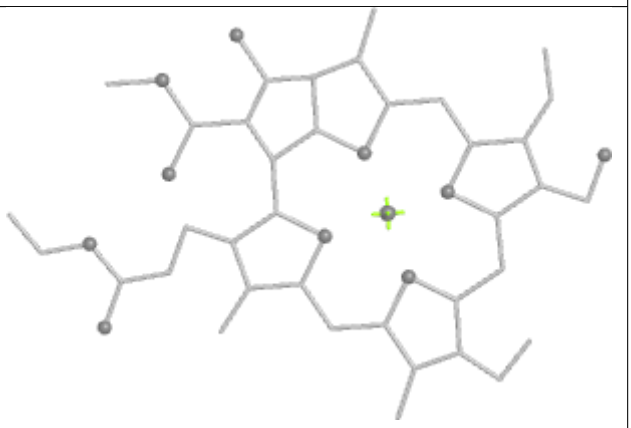
Bond lengths



Bond angles

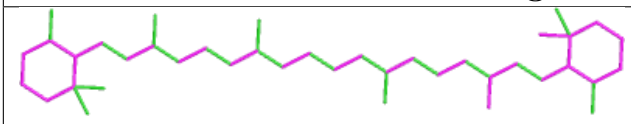


Torsions

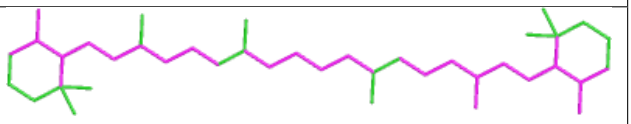


Rings

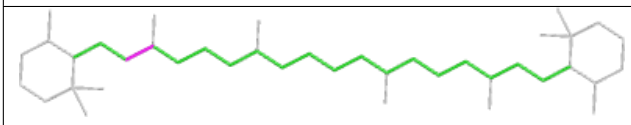
Ligand BCR a 409



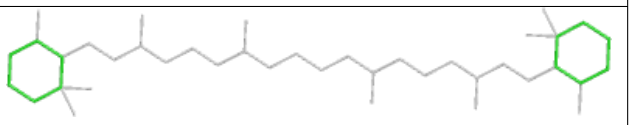
Bond lengths



Bond angles

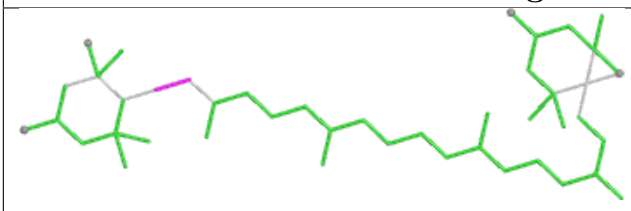


Torsions

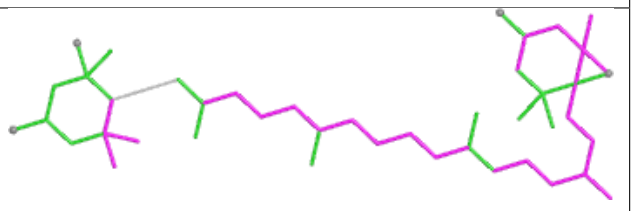


Rings

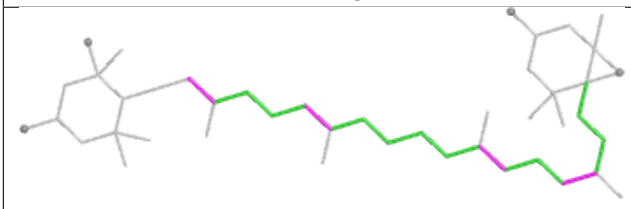
Ligand NEX 5 319



Bond lengths



Bond angles

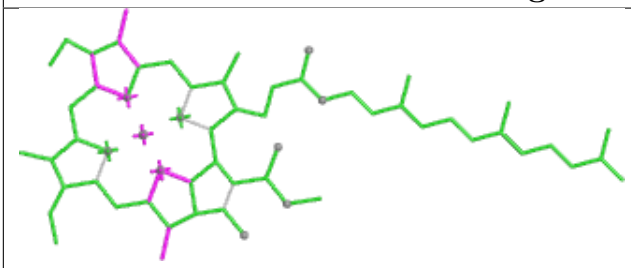


Torsions

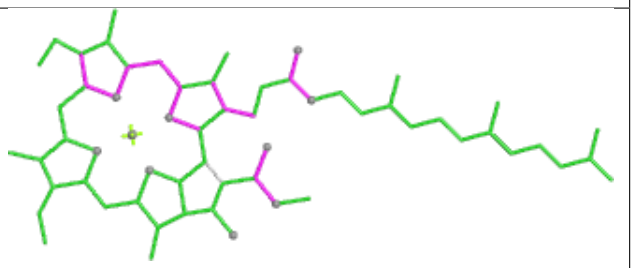


Rings

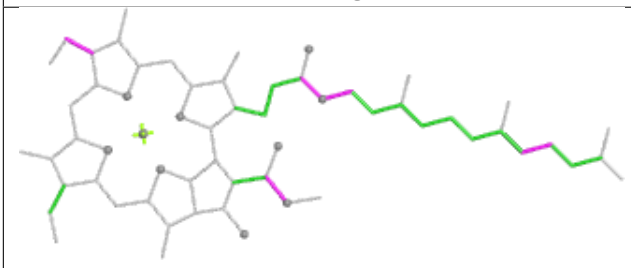
Ligand CLA 4 305



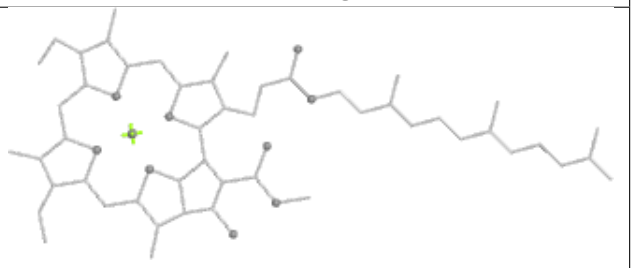
Bond lengths



Bond angles

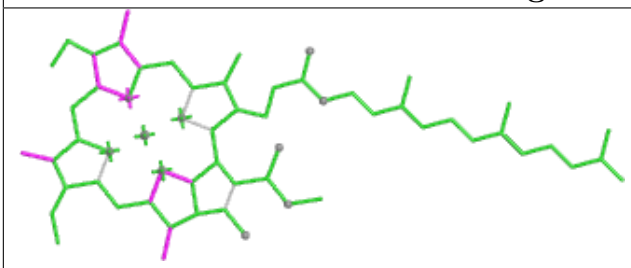


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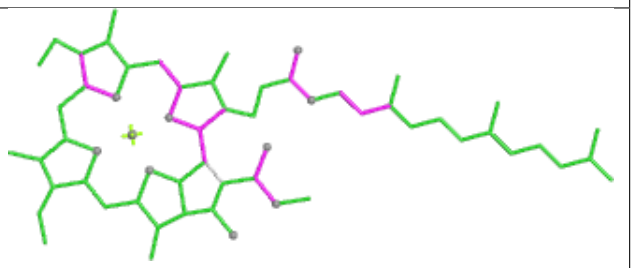


Rings

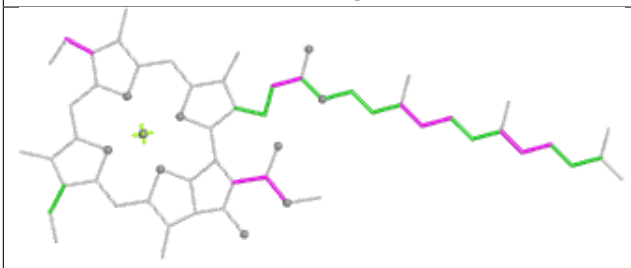
Ligand CLA v 306



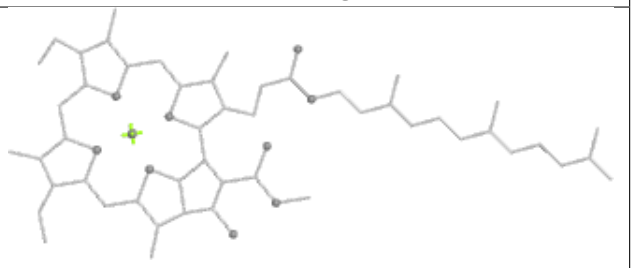
Bond lengths



Bond angles

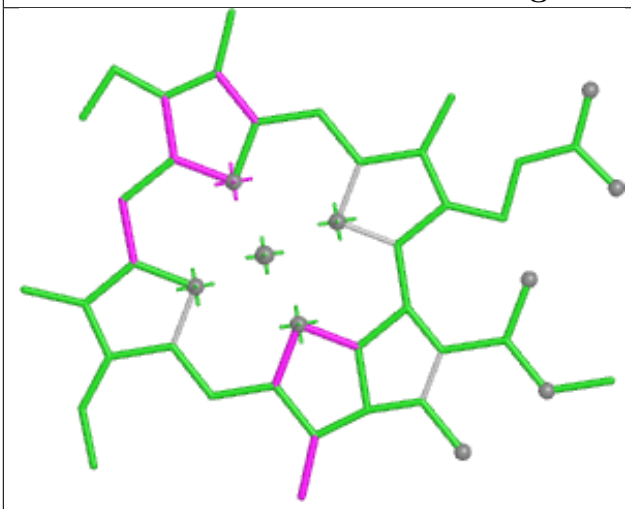


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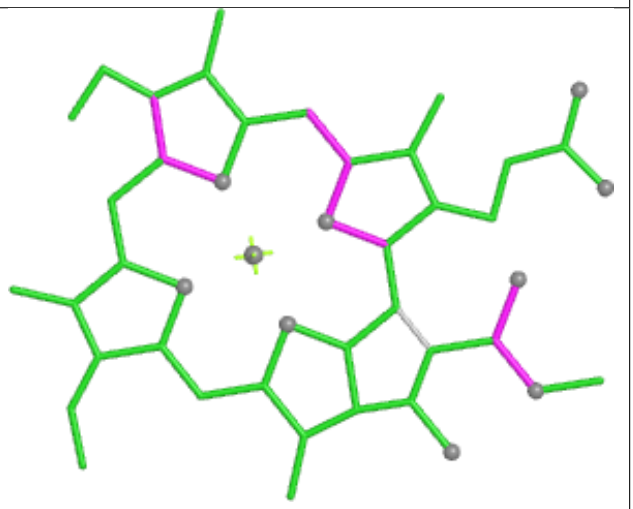


Rings

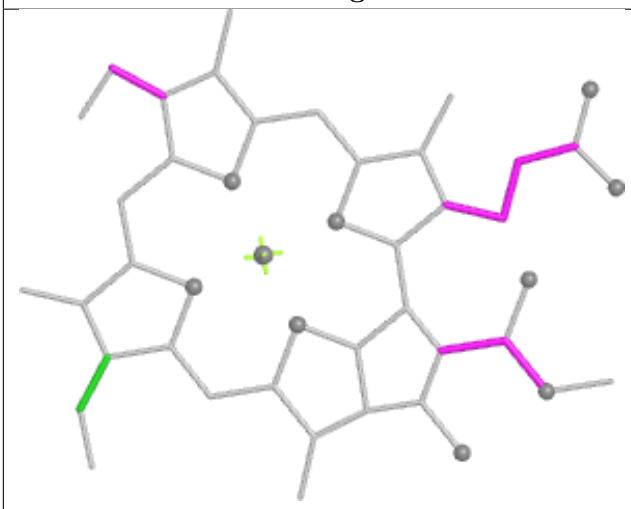
Ligand CLA s 304



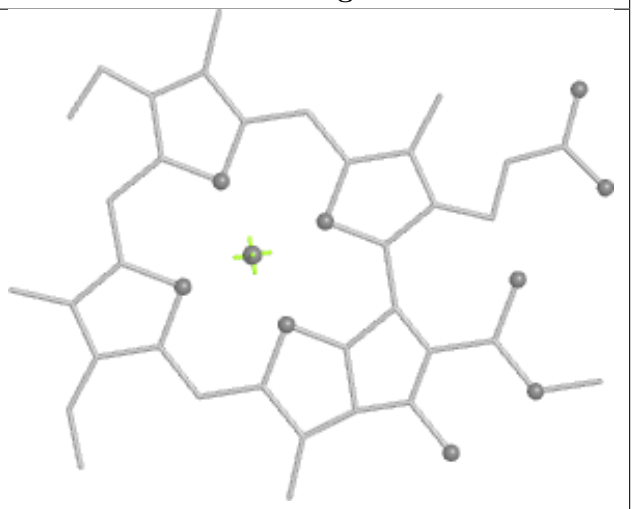
Bond lengths



Bond angles

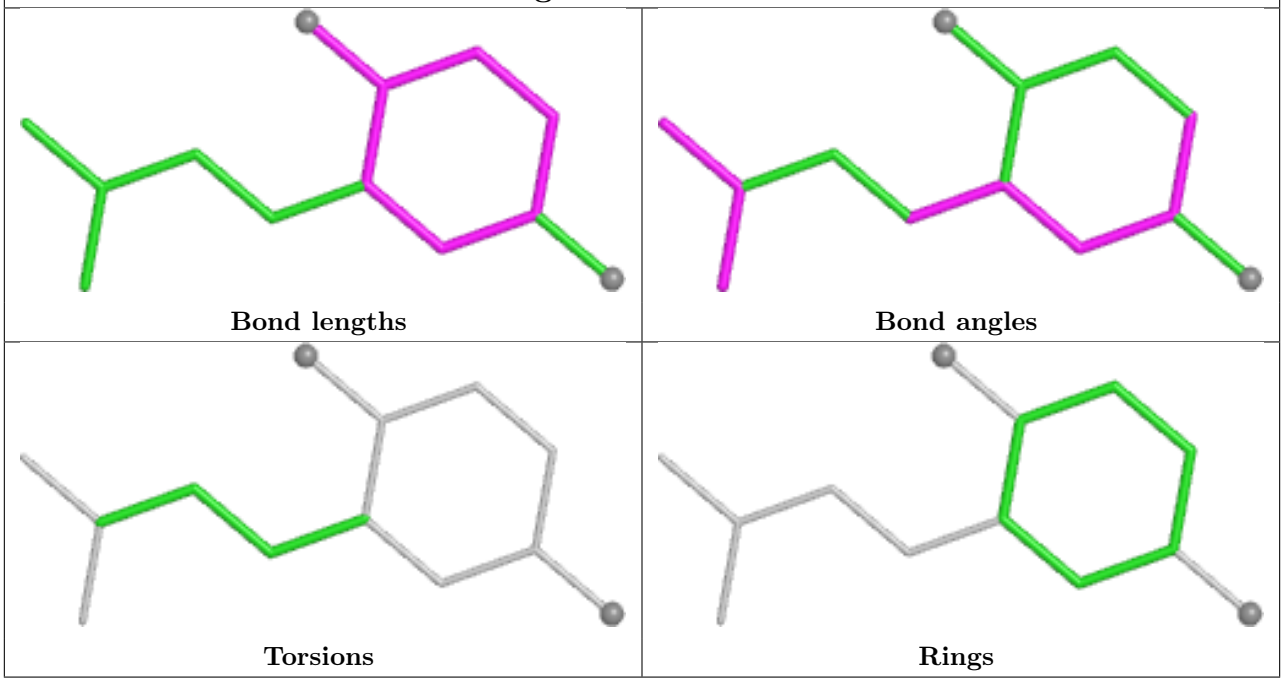


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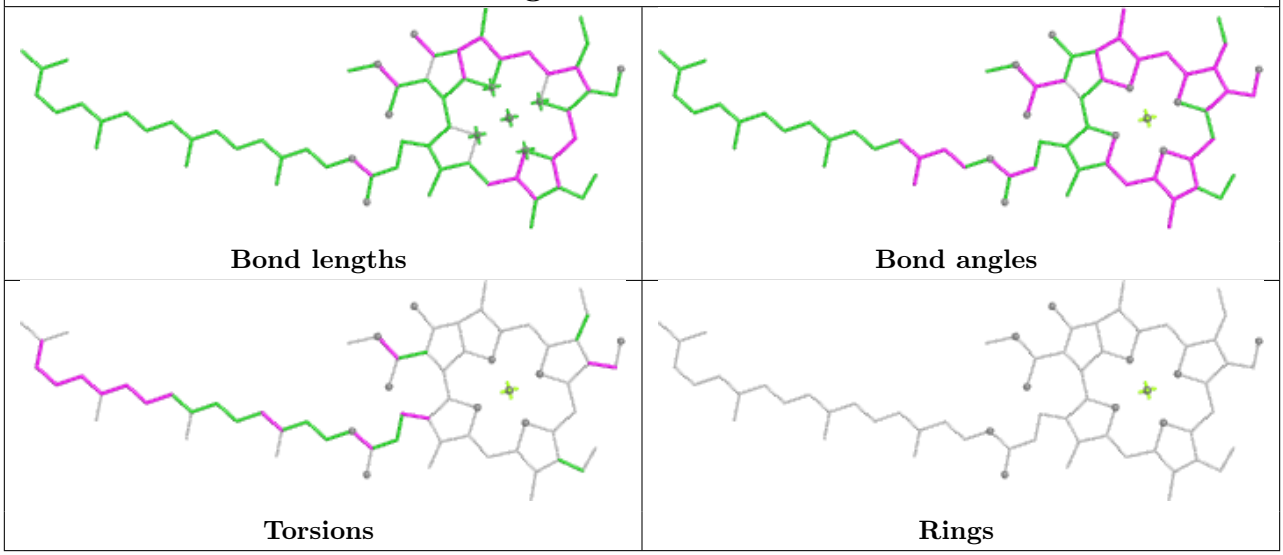


Rings

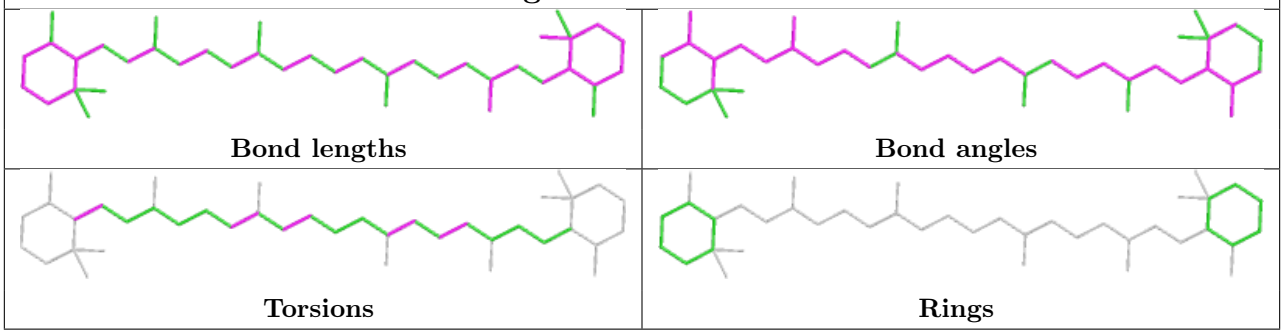
Ligand PL9 a 411



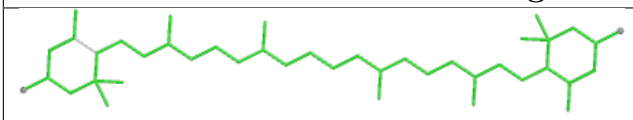
Ligand CHL R 315



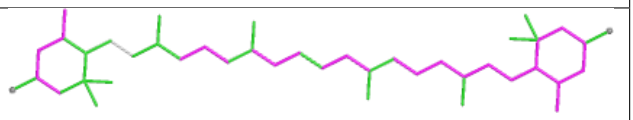
Ligand BCR C 516



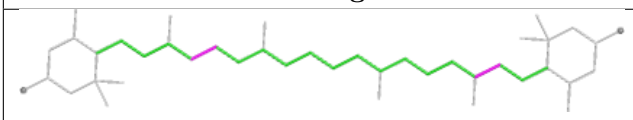
Ligand LUT n 310



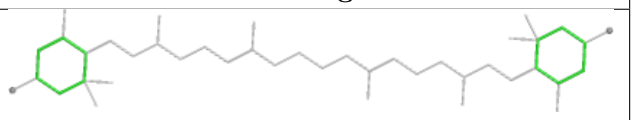
Bond lengths



Bond angles

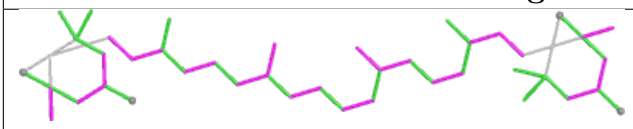


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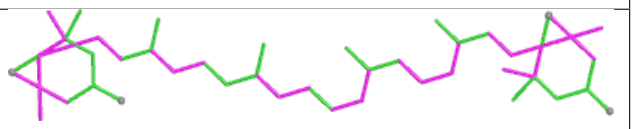


Rings

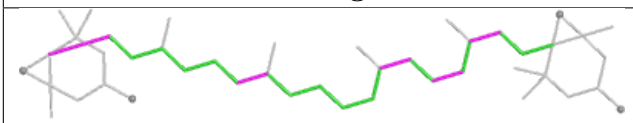
Ligand XAT 6 310



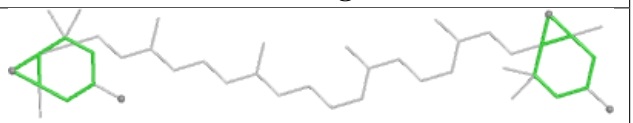
Bond lengths



Bond angles

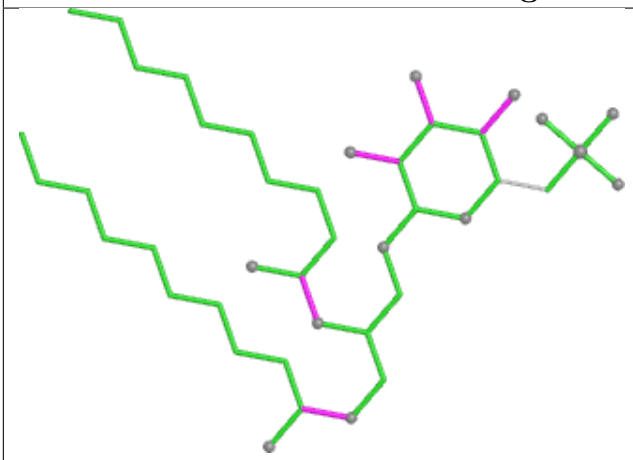


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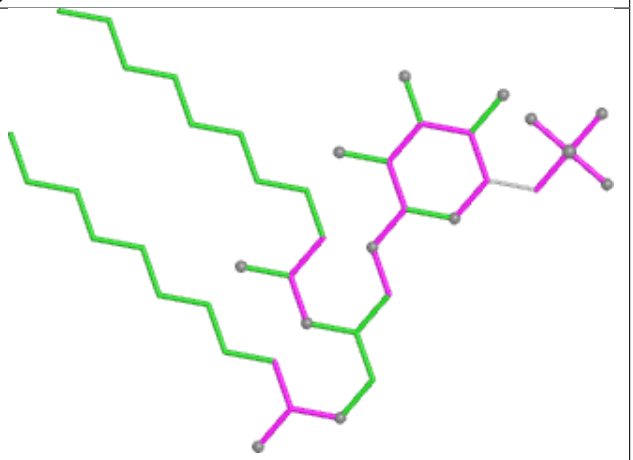


Rings

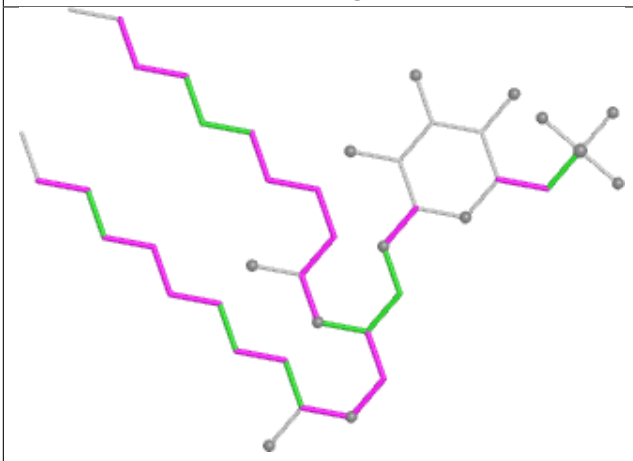
Ligand SQD M 101



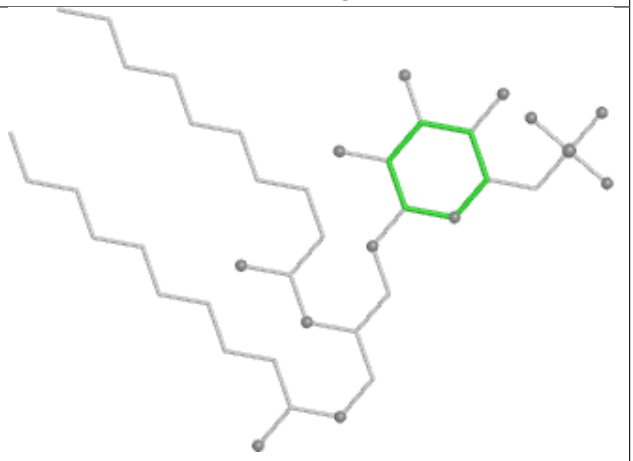
Bond lengths



Bond angles

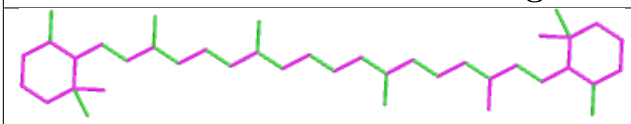


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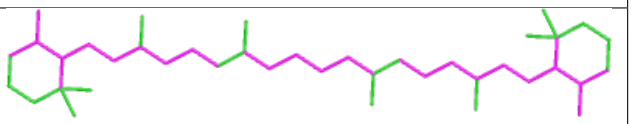


Rings

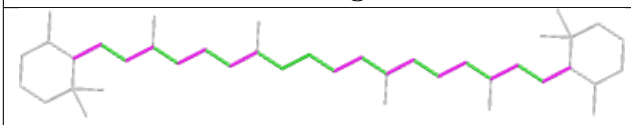
Ligand BCR k 101



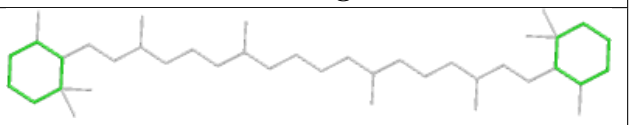
Bond lengths



Bond angles

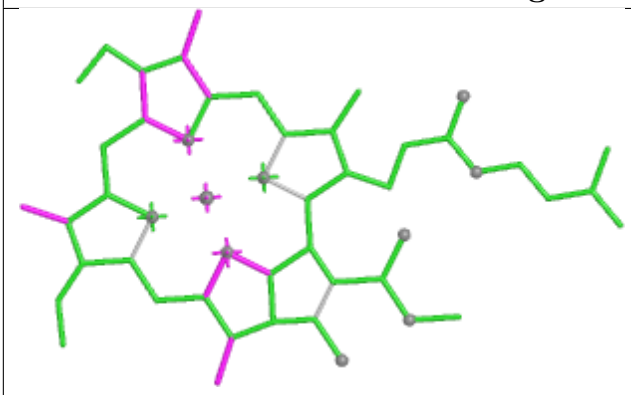


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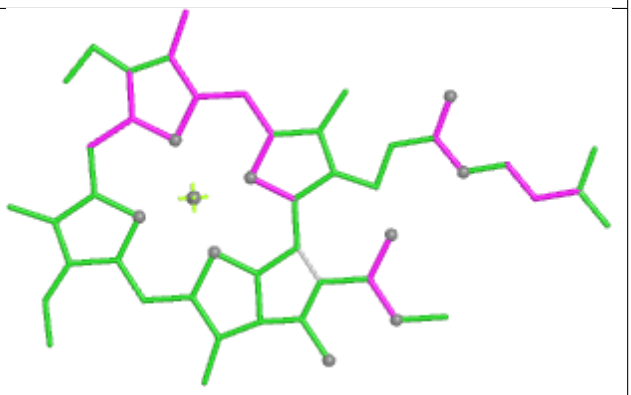


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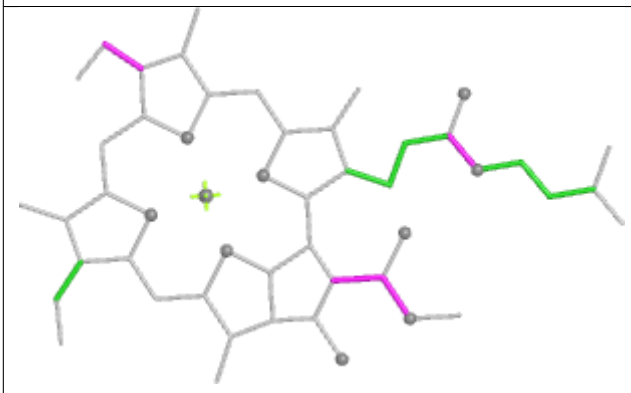
Ligand CLA 1 303



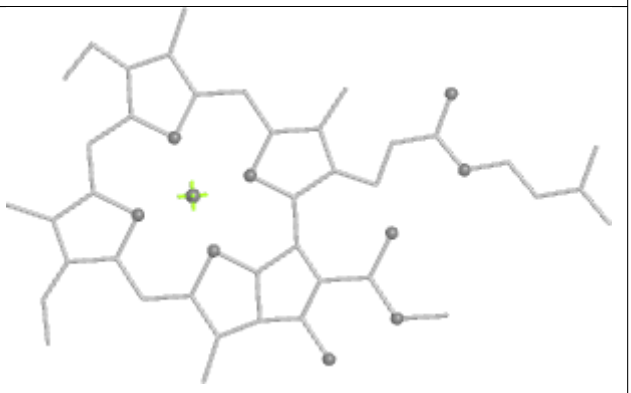
Bond lengths



Bond angles

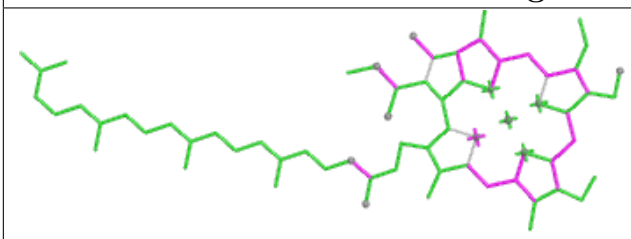


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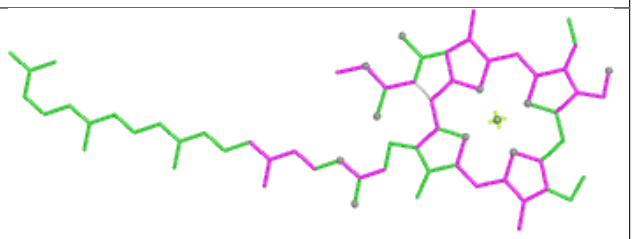


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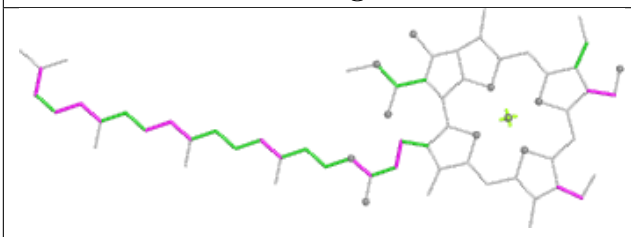
Ligand CHL v 316



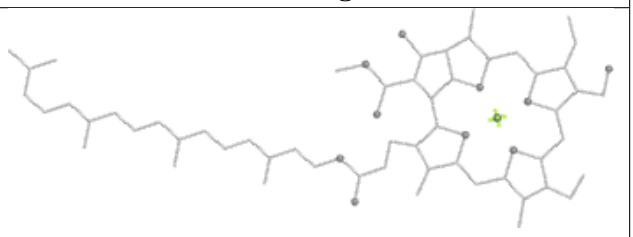
Bond lengths



Bond angles

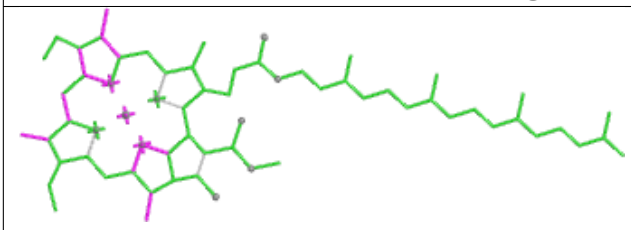


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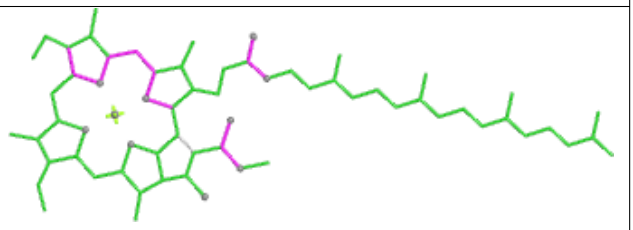


Rings

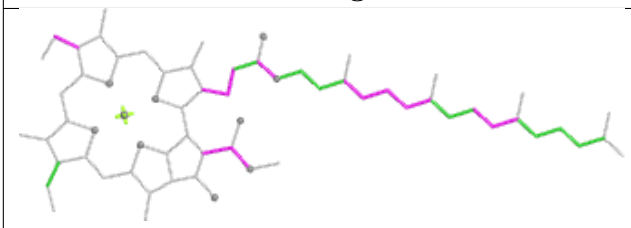
Ligand CLA C 505



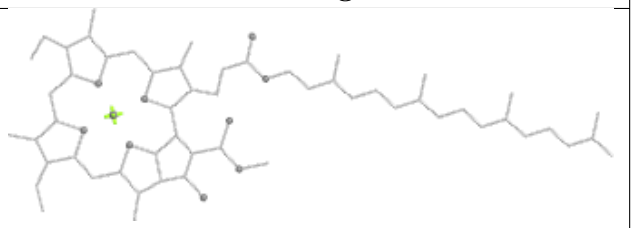
Bond lengths



Bond angles

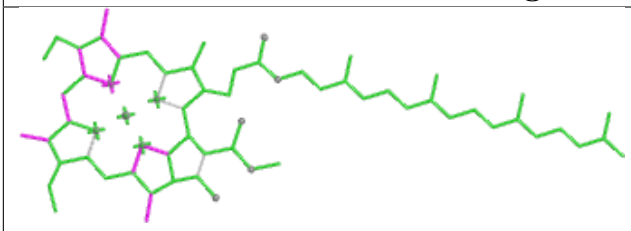


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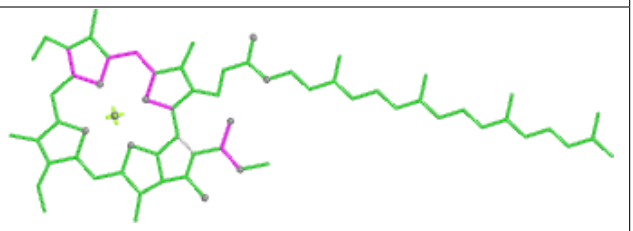


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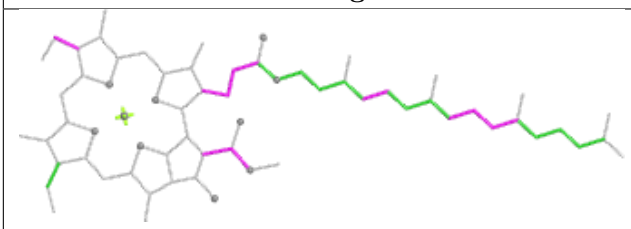
Ligand CLA V 301



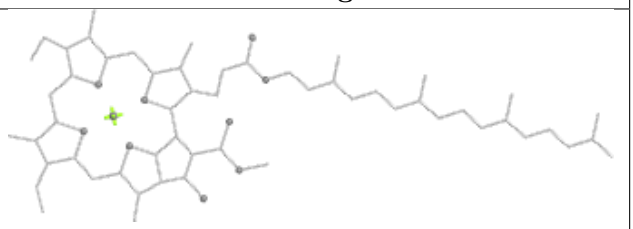
Bond lengths



Bond angles

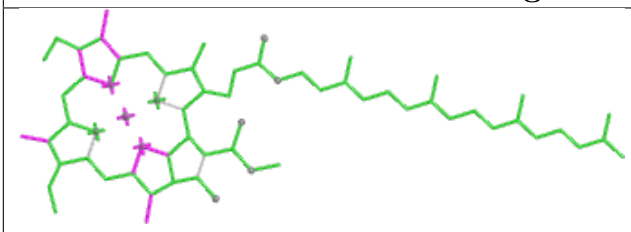


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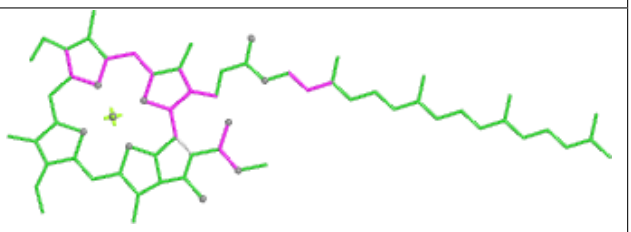


Rings

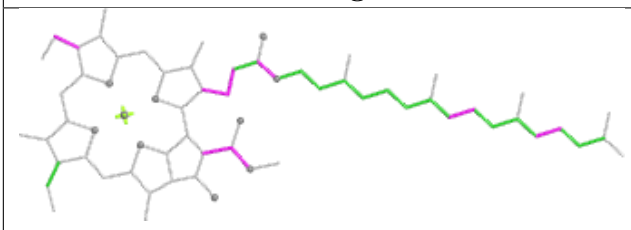
Ligand CLA A 405



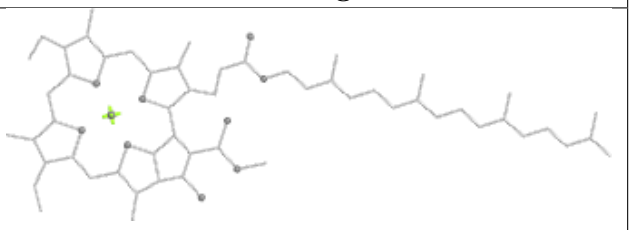
Bond lengths



Bond angles

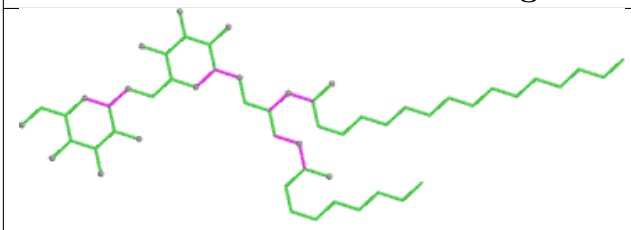


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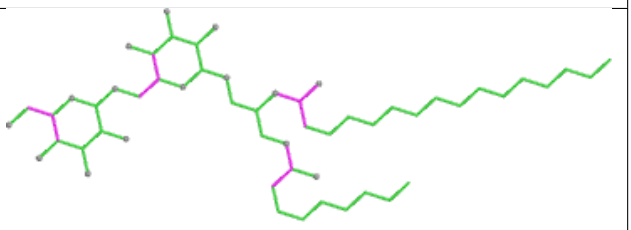


Rings

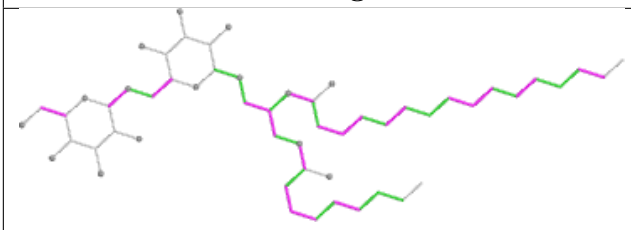
Ligand DGD C 519



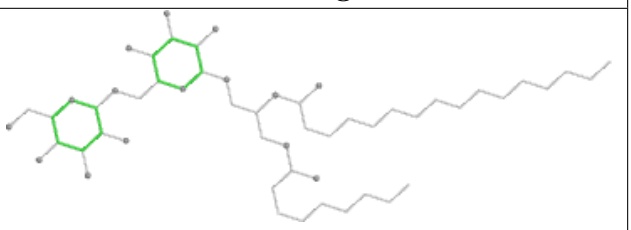
Bond lengths



Bond angles

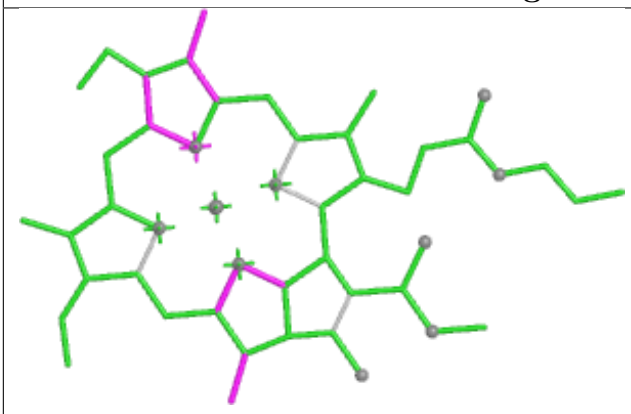


Torsions

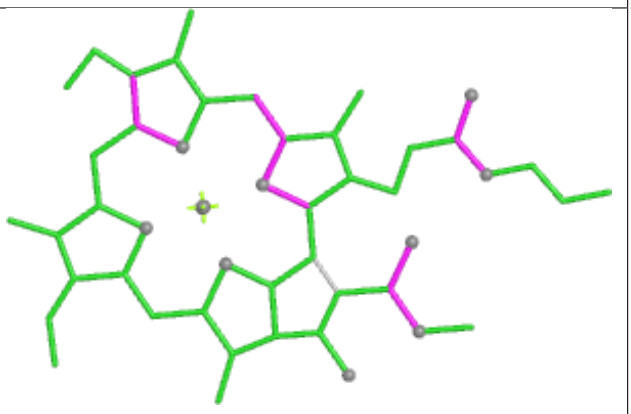


Rings

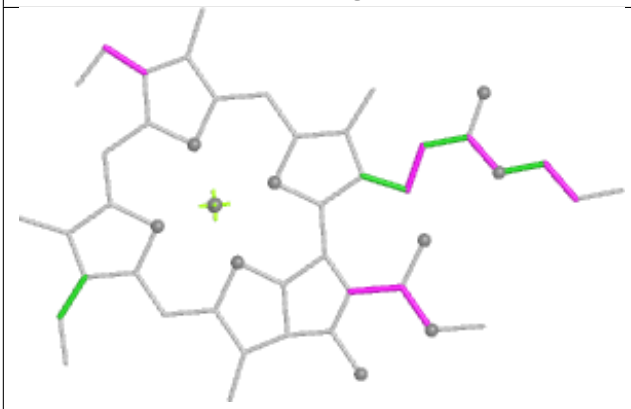
Ligand CLA U 308



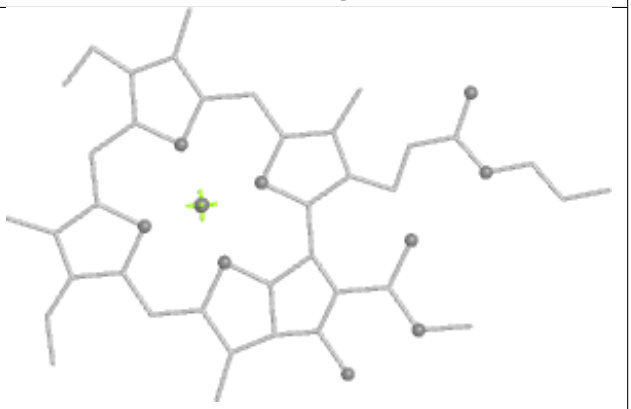
Bond lengths



Bond angles

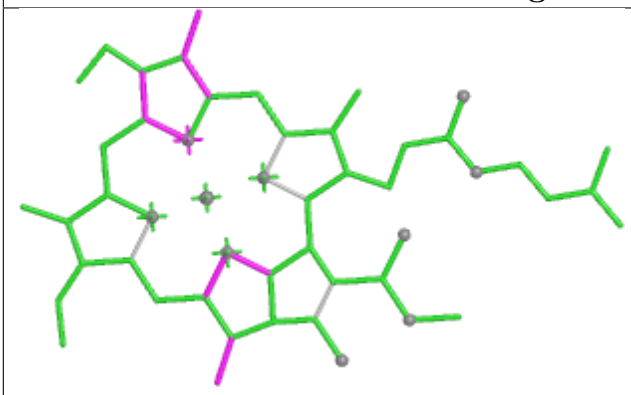


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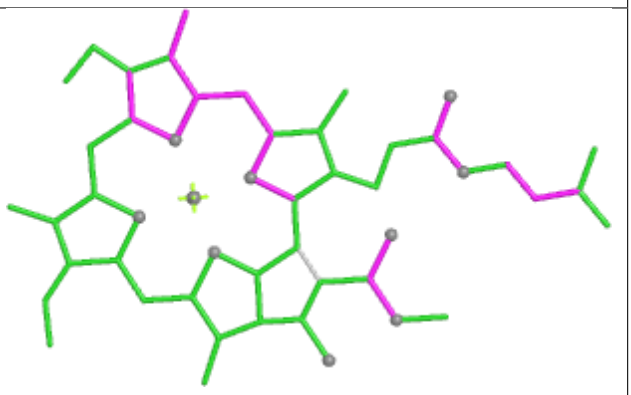


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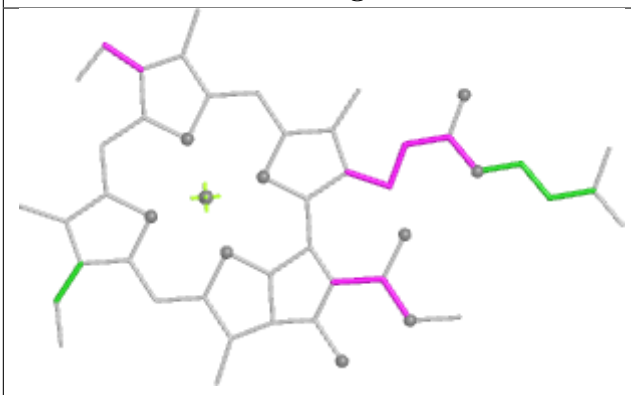
Ligand CLA 3 303



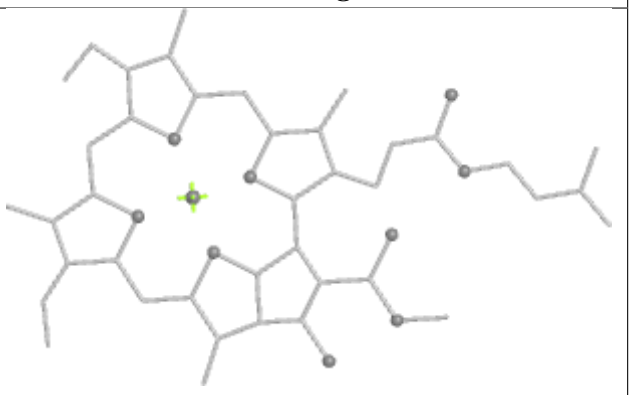
Bond lengths



Bond angles

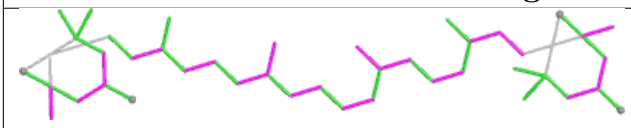


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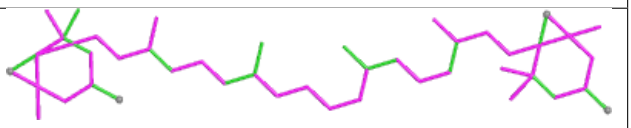


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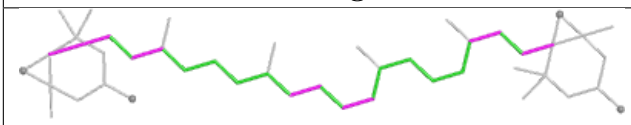
Ligand XAT R 313



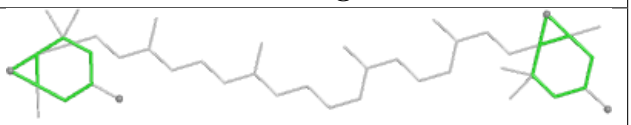
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Bond angles

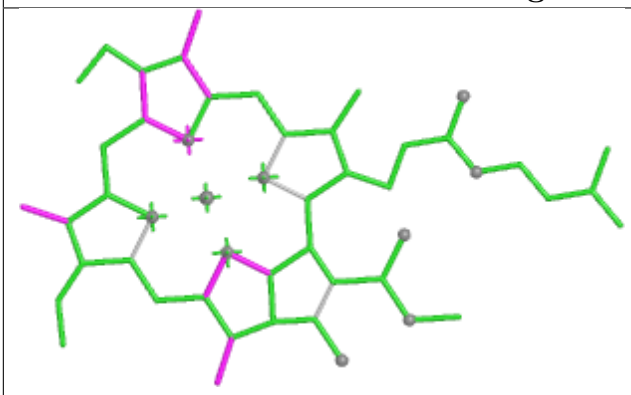


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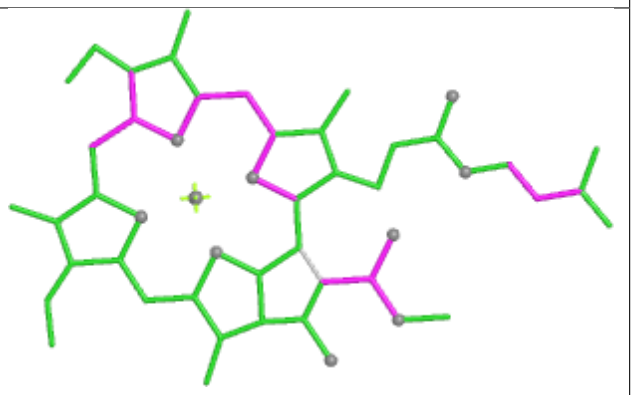


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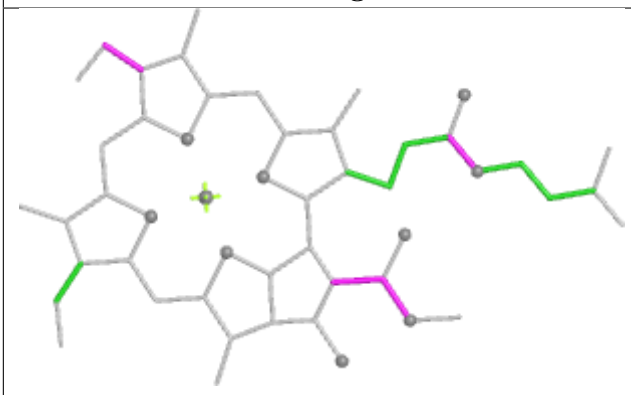
Ligand CLA u 303



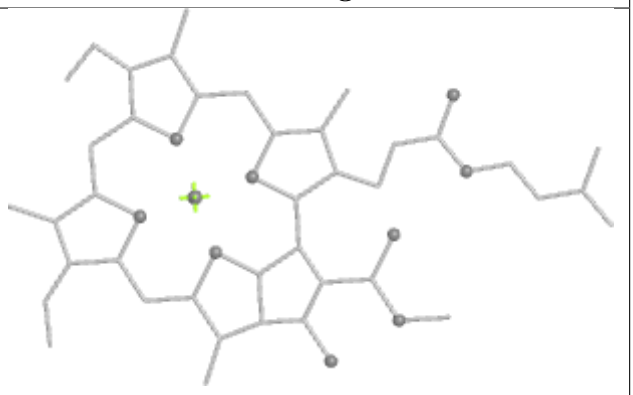
Bond lengths



Bond angles

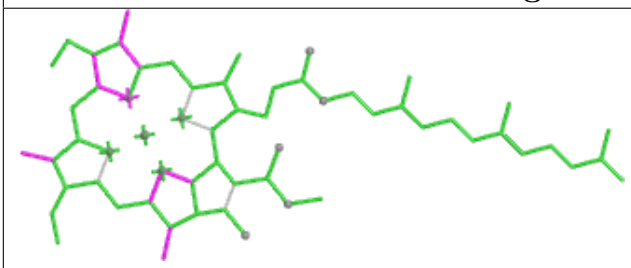


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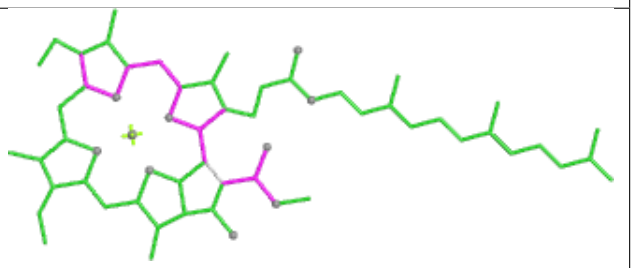


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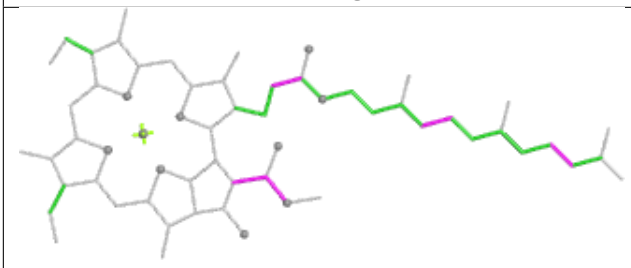
Ligand CLA V 306



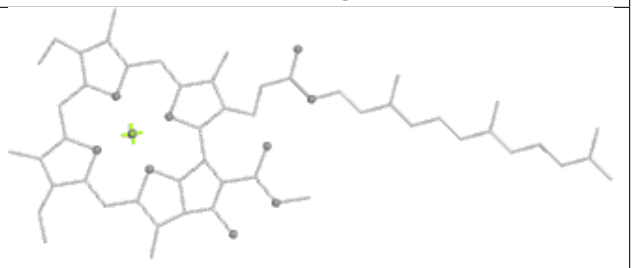
Bond lengths



Bond angles

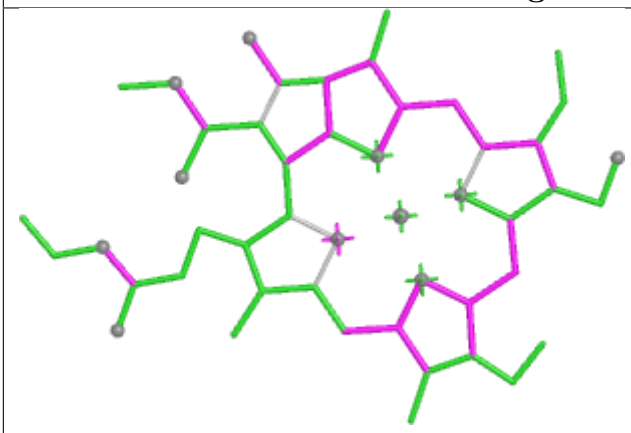


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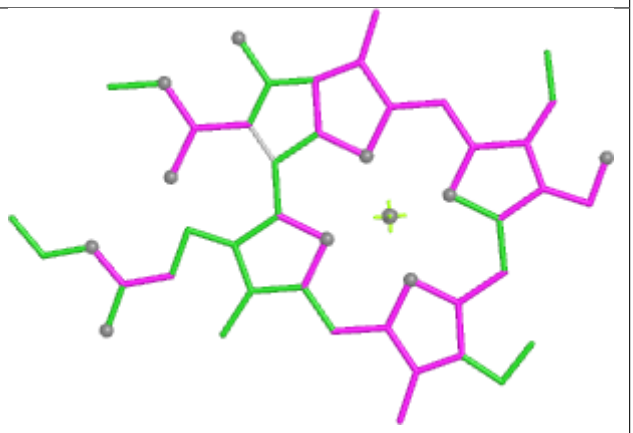


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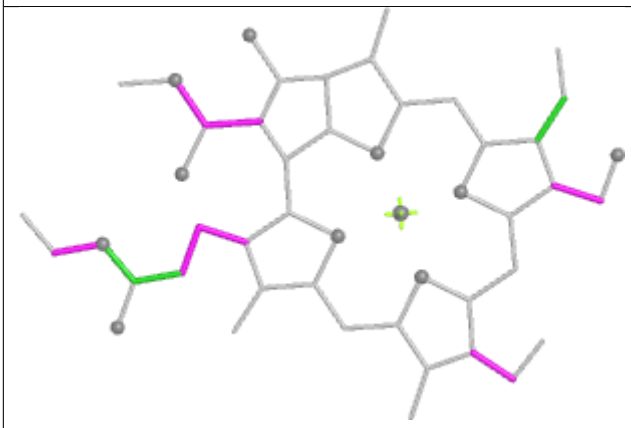
Ligand CHL 5 314



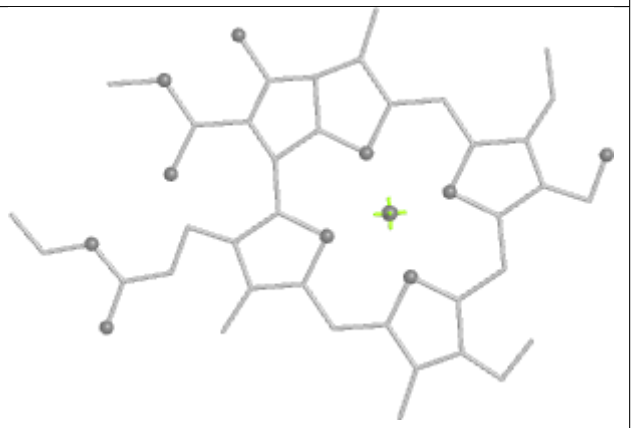
Bond lengths



Bond angles

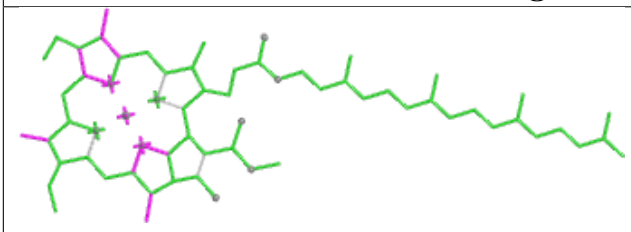


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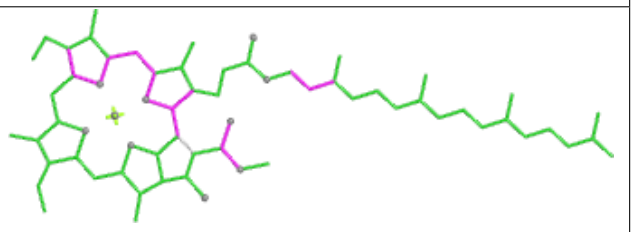


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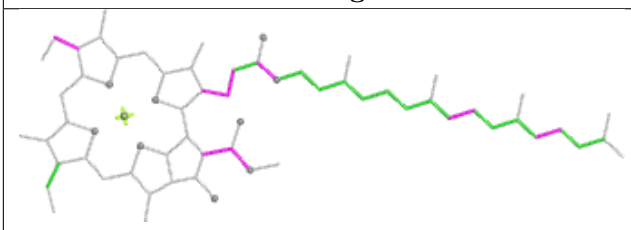
Ligand CLA a 405



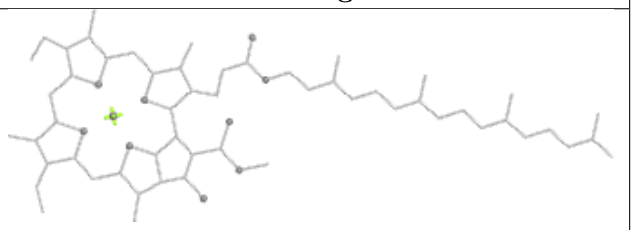
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Bond angles

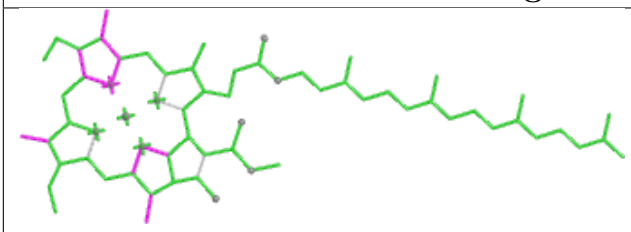


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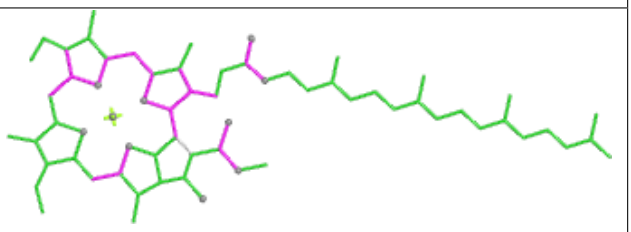


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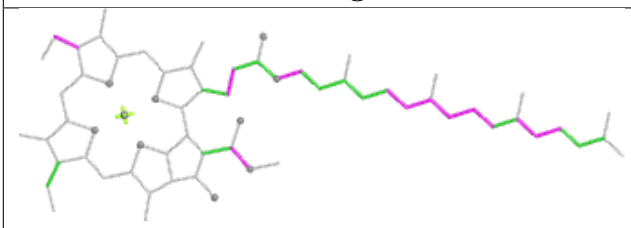
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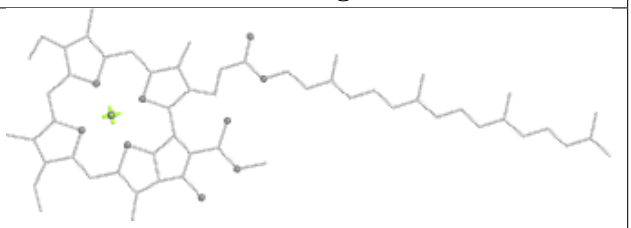
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Bond angles

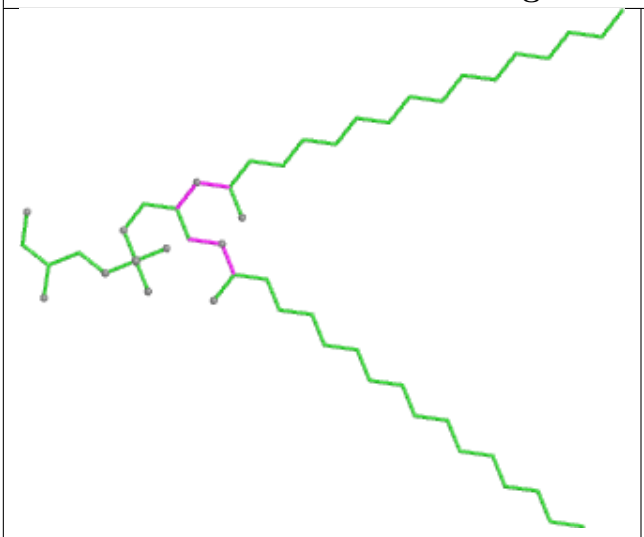


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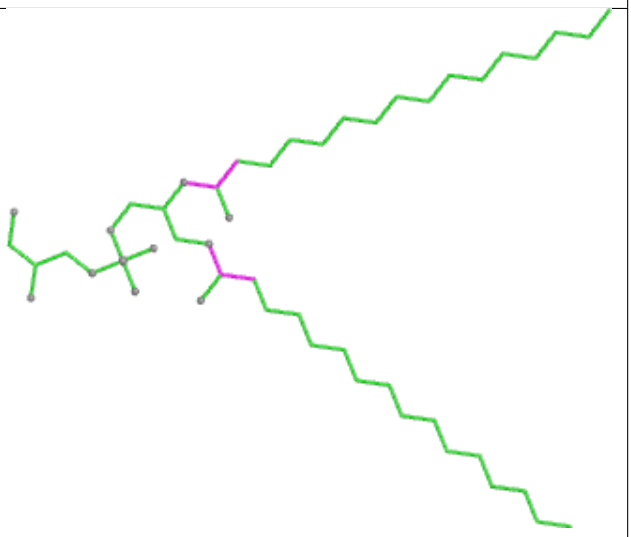


Rings

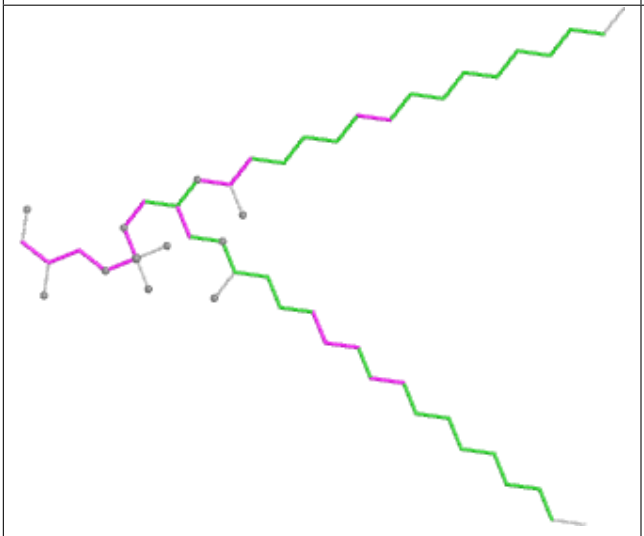
Ligand LHG B 623



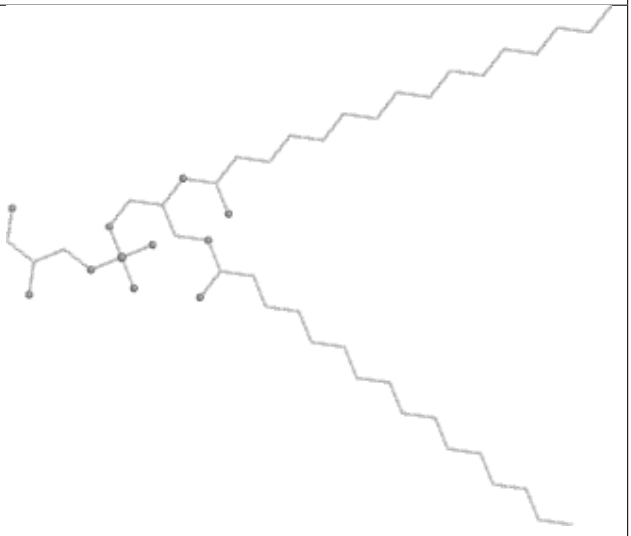
Bond lengths



Bond angles

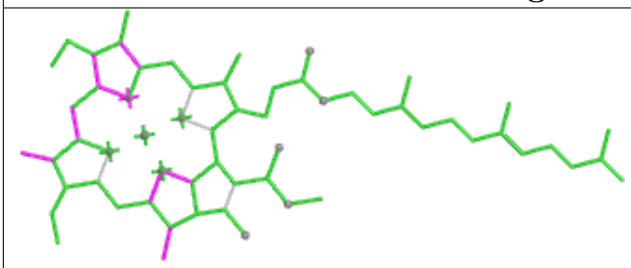


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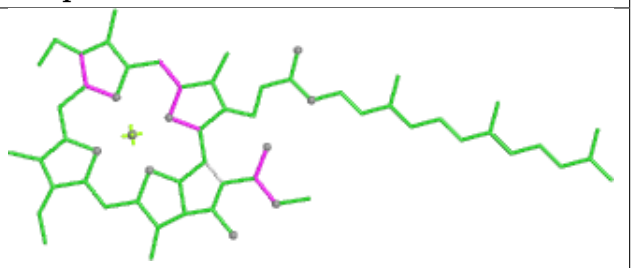


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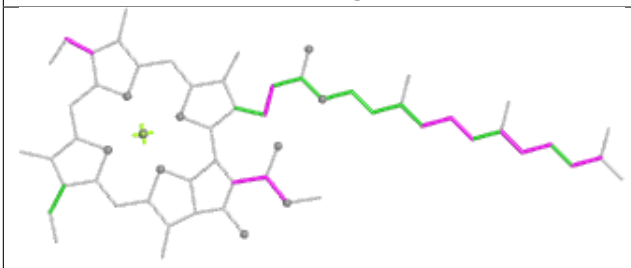
Ligand CLA q 305



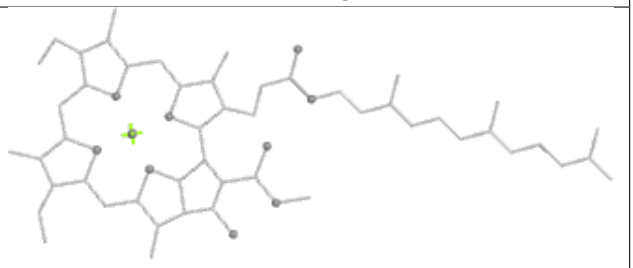
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Bond angles

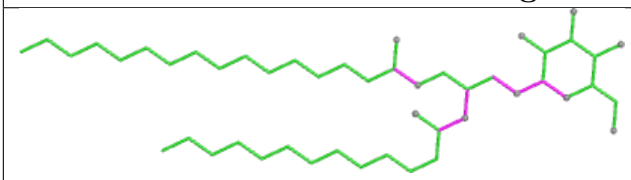


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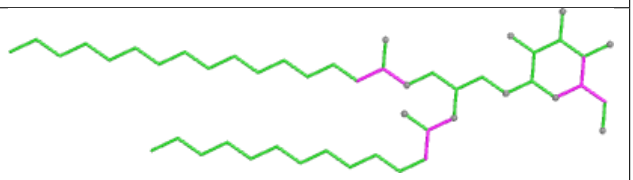


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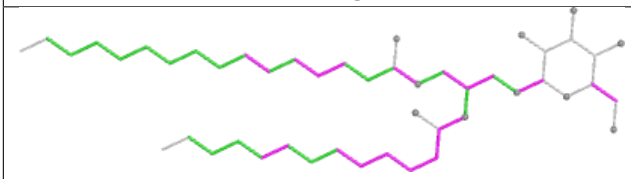
Ligand LMG w 201



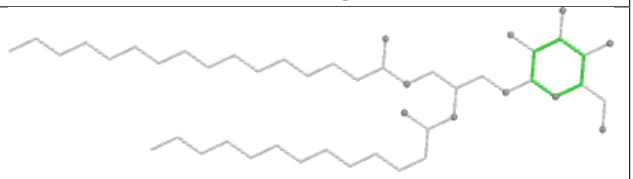
Bond lengths



Bond angles

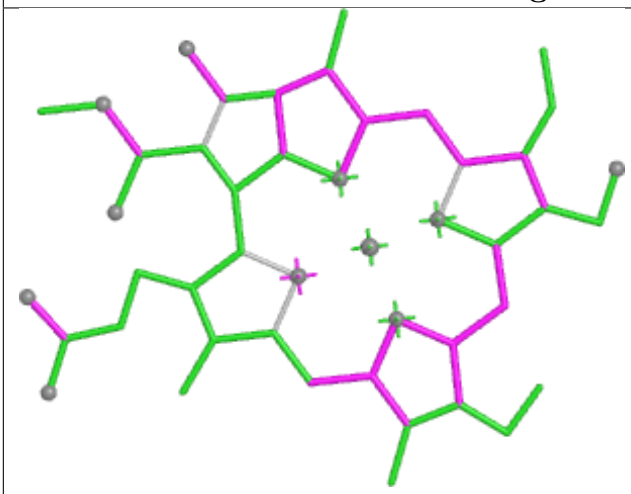


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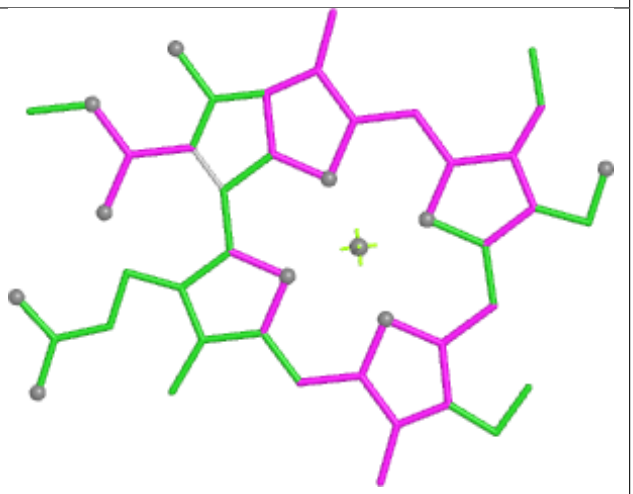


Rings

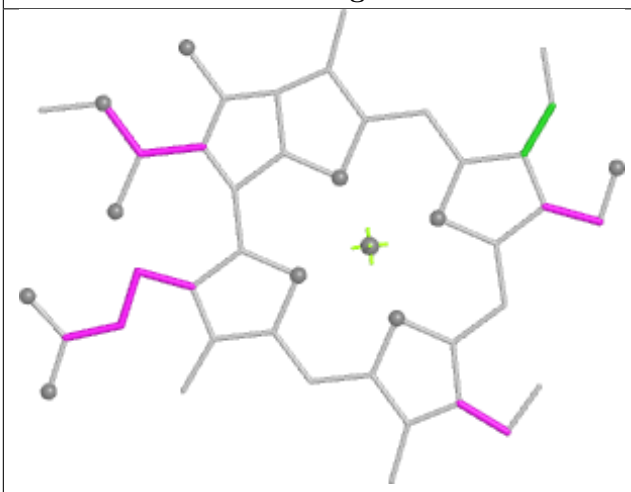
Ligand CHL s 316



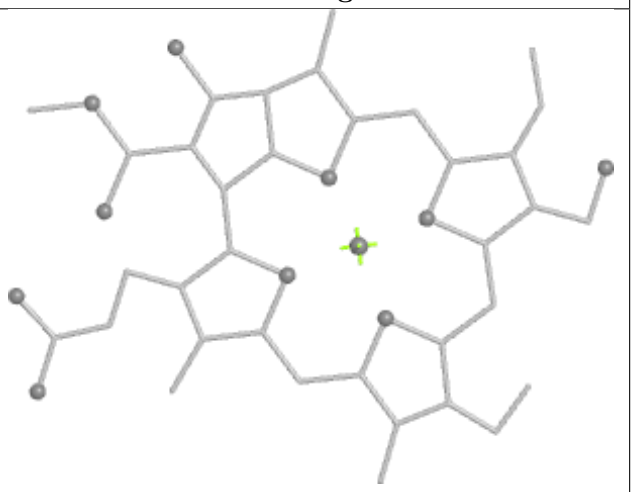
Bond lengths



Bond angles

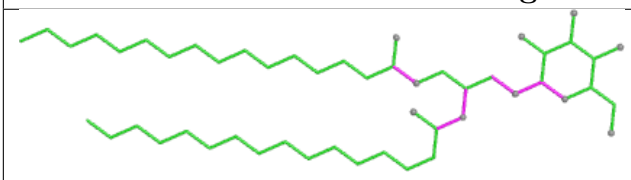


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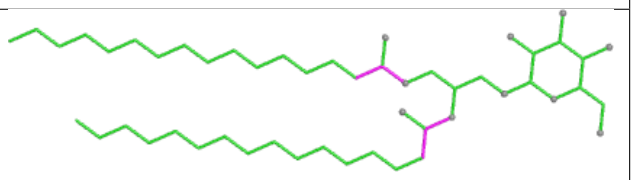


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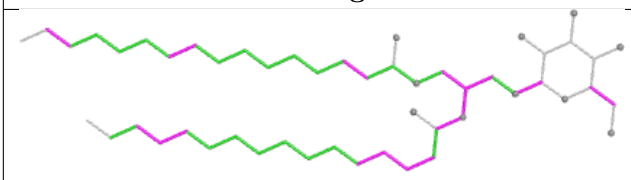
Ligand LMG C 521



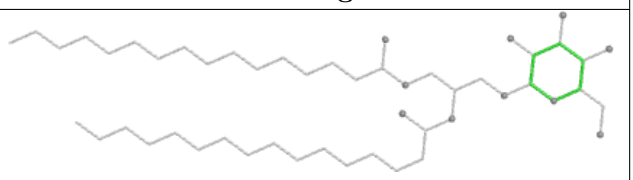
Bond lengths



Bond angles

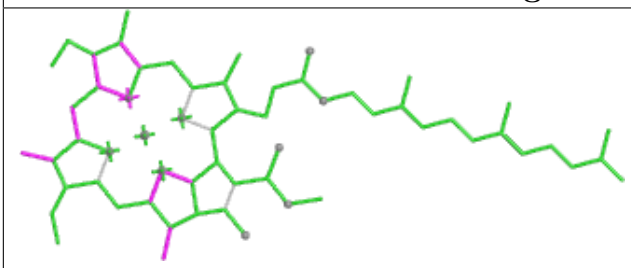


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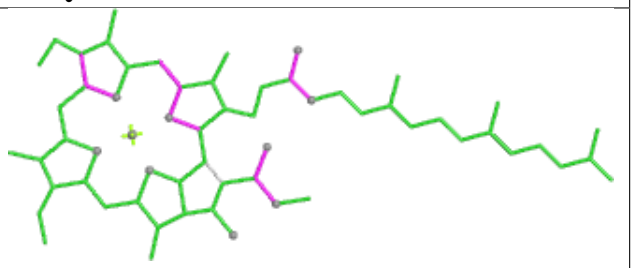


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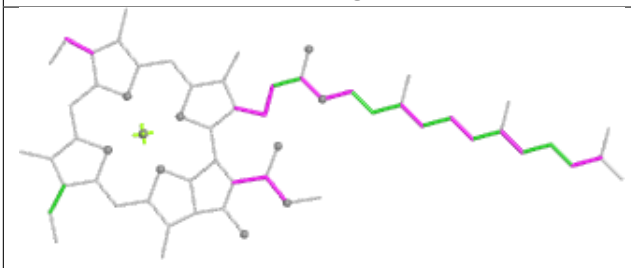
Ligand CLA Q 305



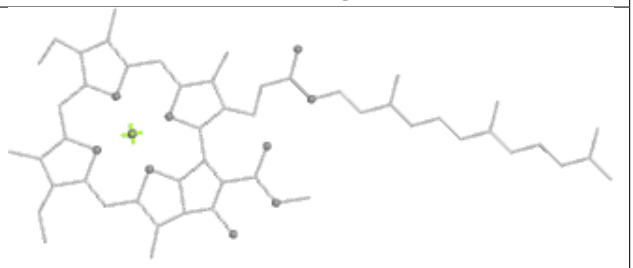
Bond lengths



Bond angles

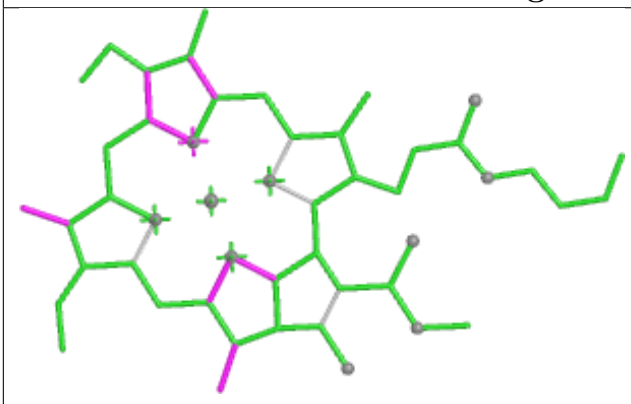


Torsions

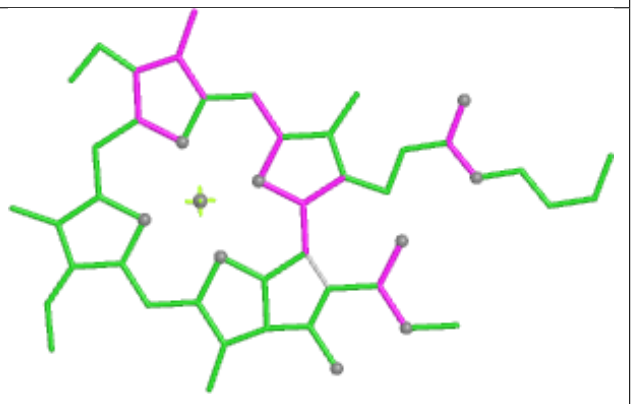


Rings

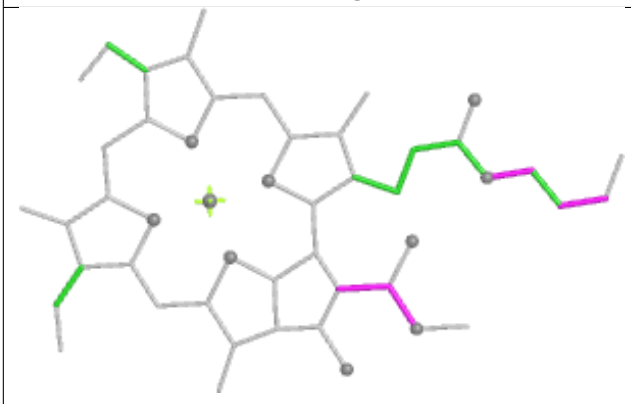
Ligand CLA S 307



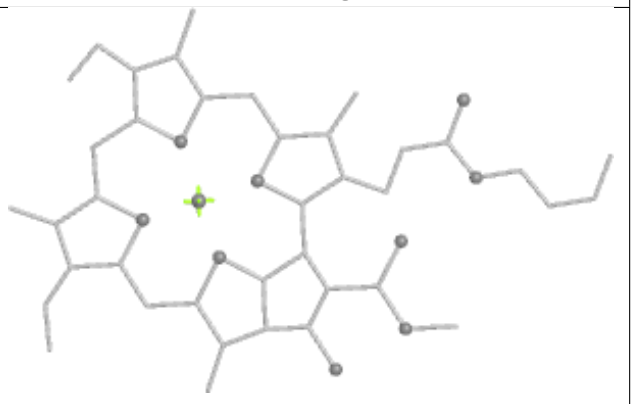
Bond lengths



Bond angles

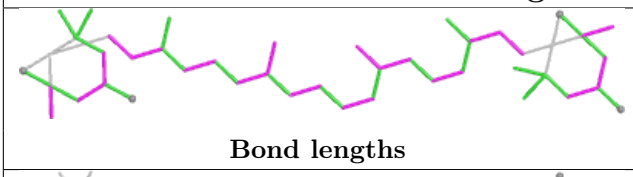


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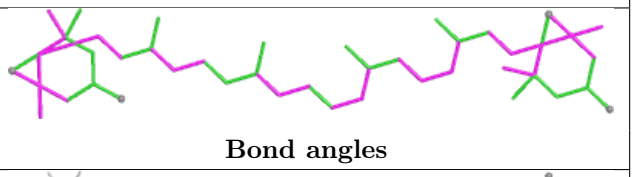


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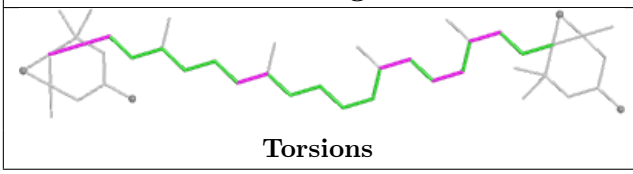
Ligand XAT 3 309



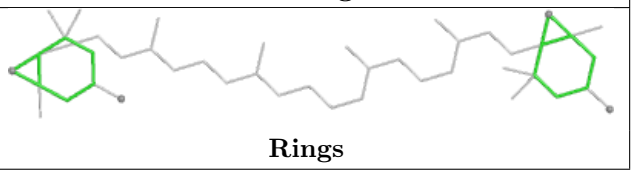
Bond lengths



Bond angles

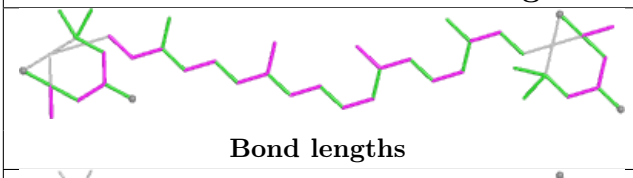


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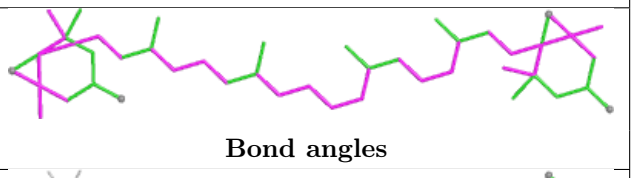


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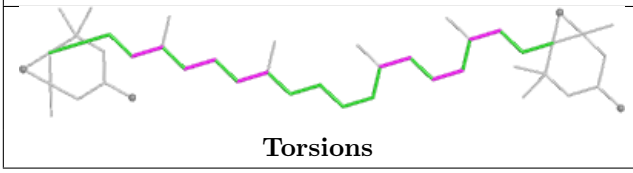
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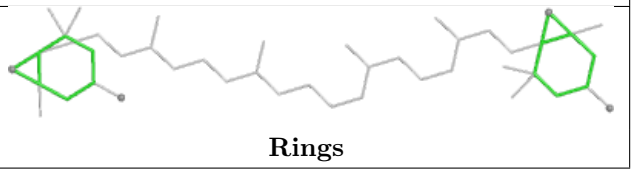
Bond lengths



Bond angles

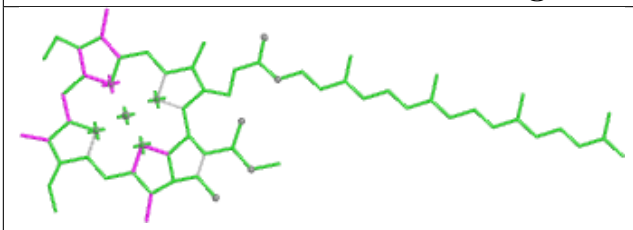


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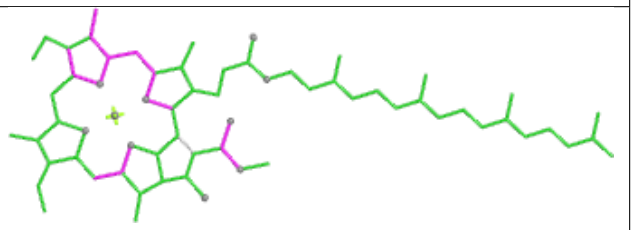


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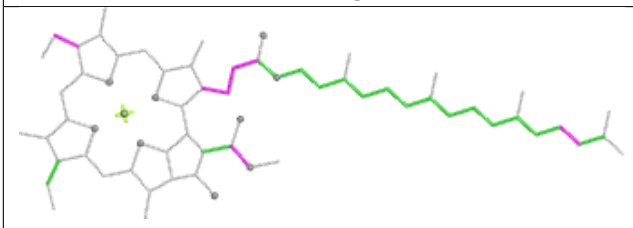
Ligand CLA 1 301



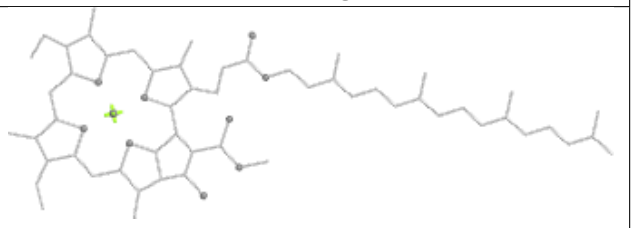
Bond lengths



Bond angles

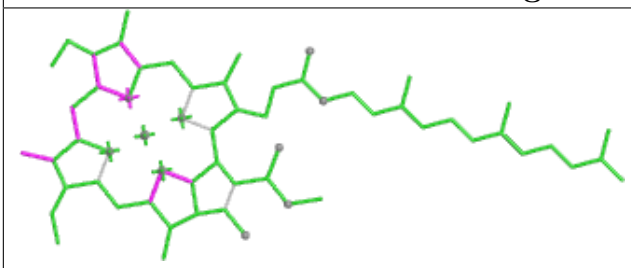


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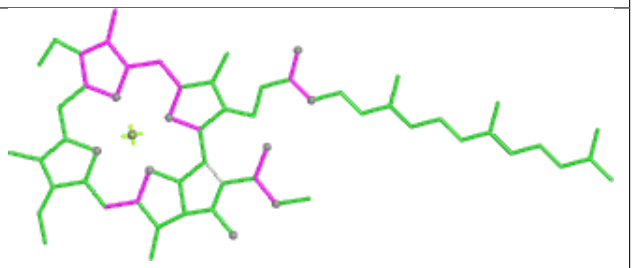


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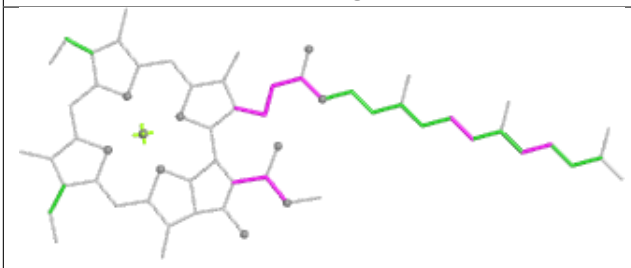
Ligand CLA V 304



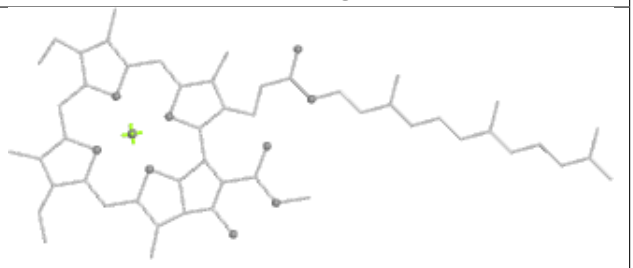
Bond lengths



Bond angles

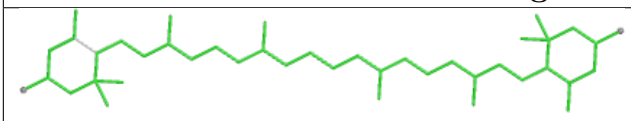


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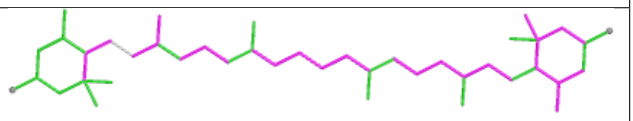


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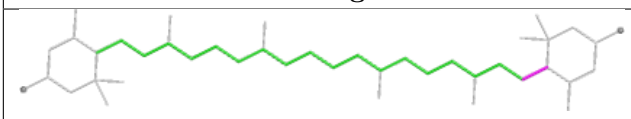
Ligand LUT s 310



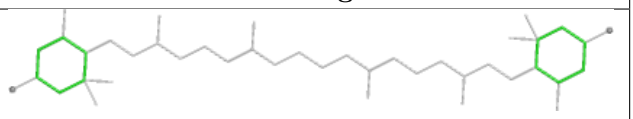
Bond lengths



Bond angles

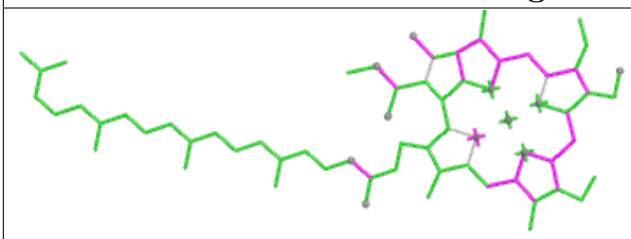


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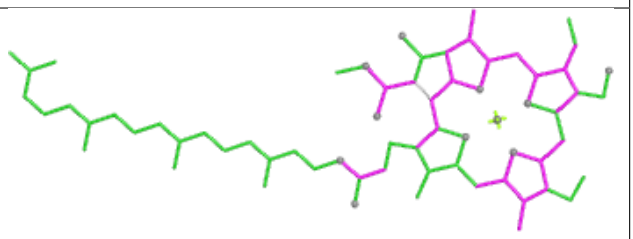


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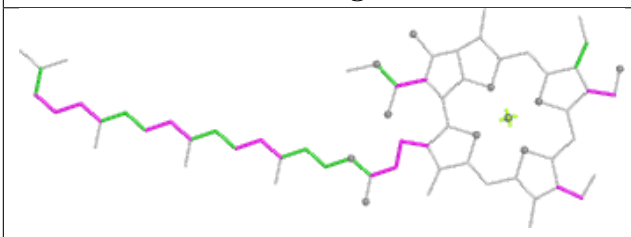
Ligand CHL 5 316



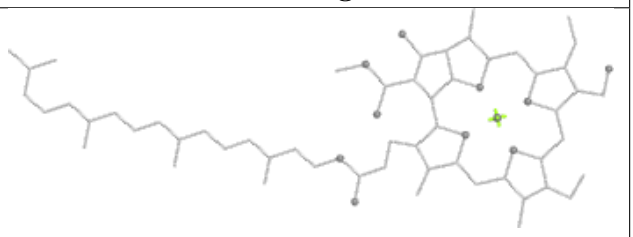
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Bond angles

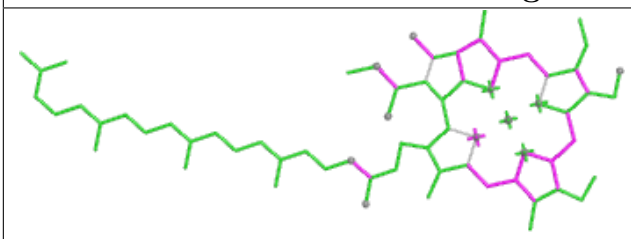


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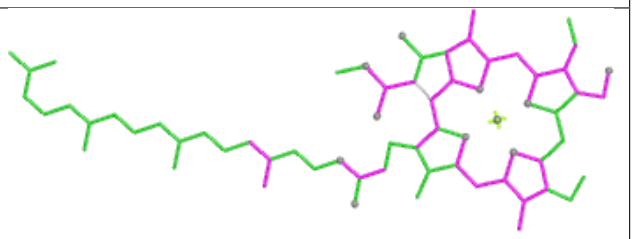


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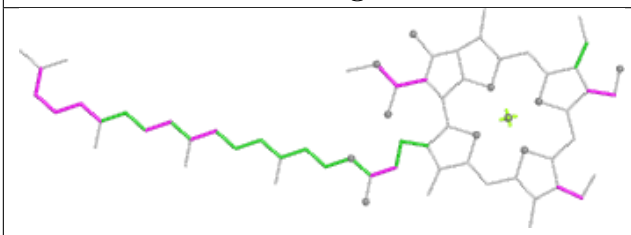
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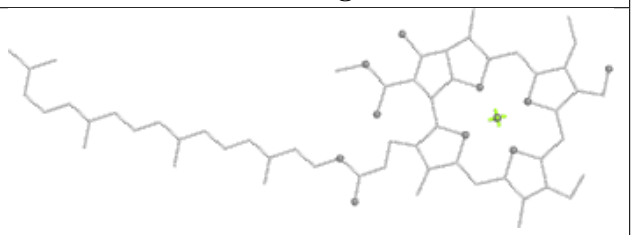
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Bond angles

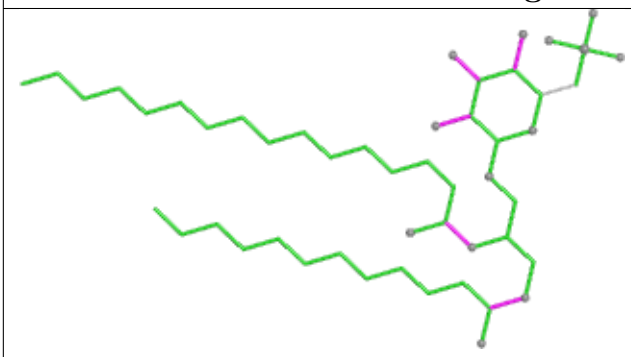


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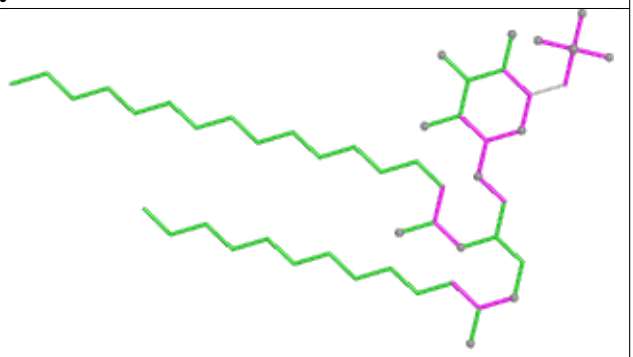


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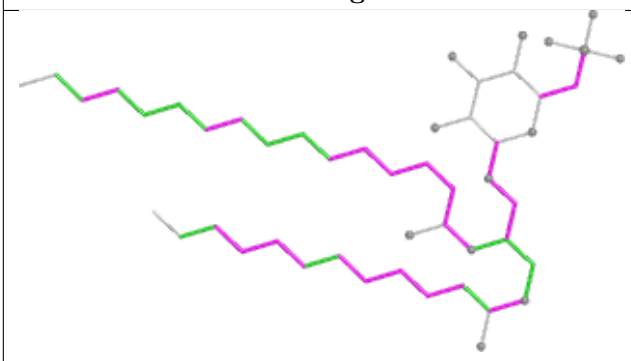
Ligand SQD C 501



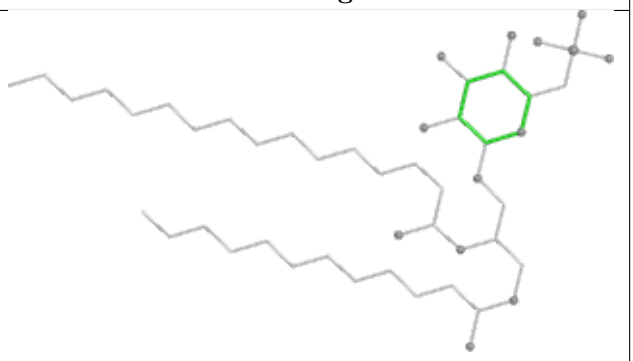
Bond lengths



Bond angles

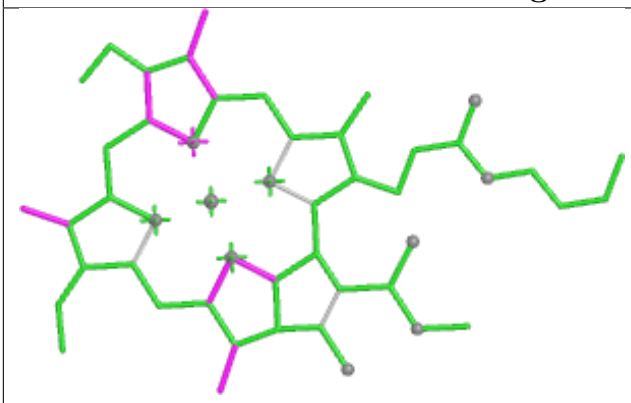


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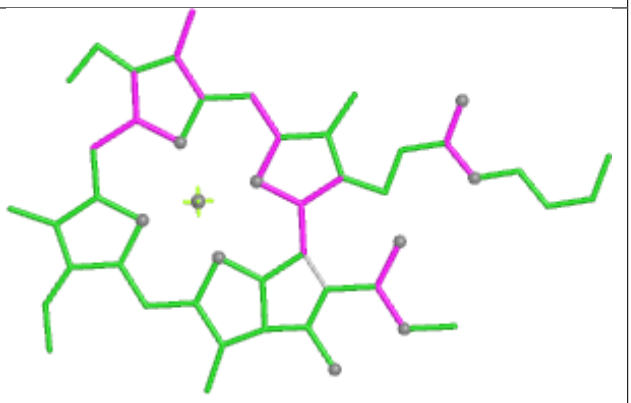


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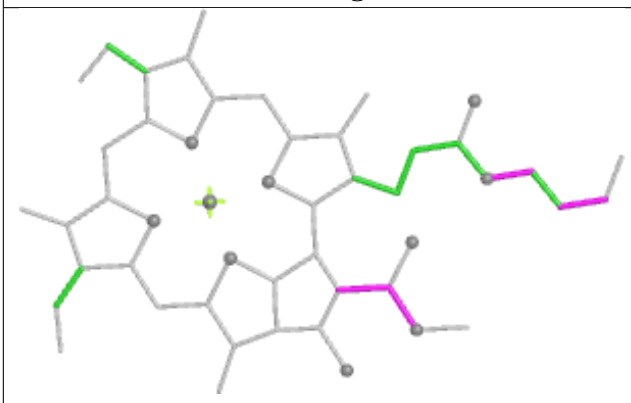
Ligand CLA s 307



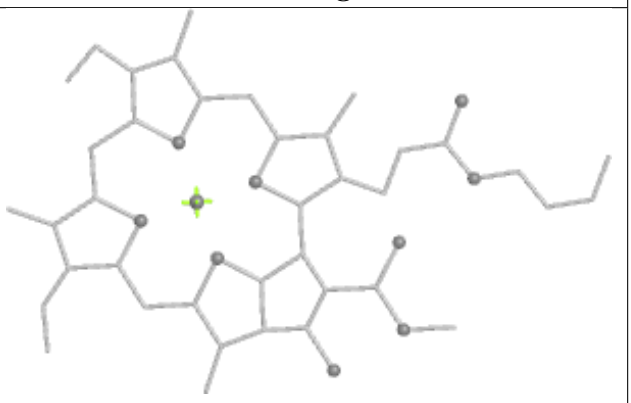
Bond lengths



Bond angles

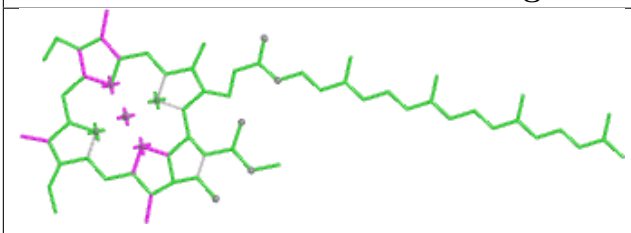


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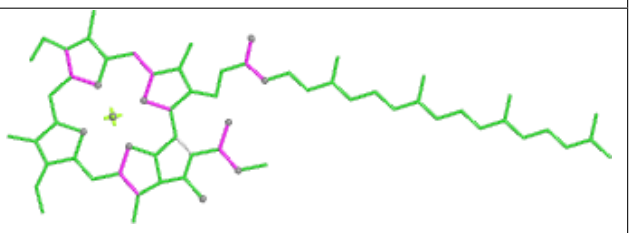


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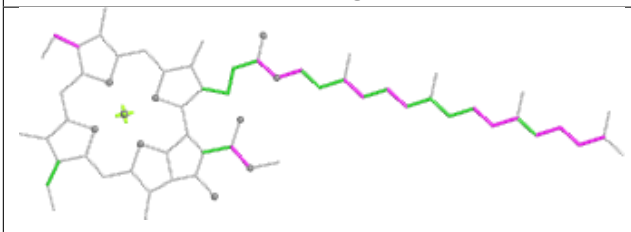
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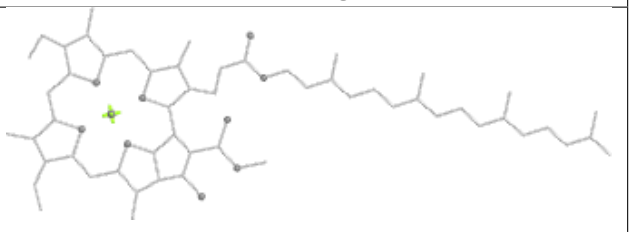
Bond lengths



Bond angles

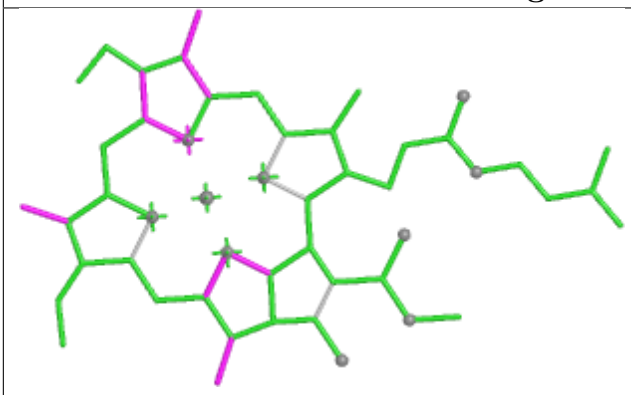


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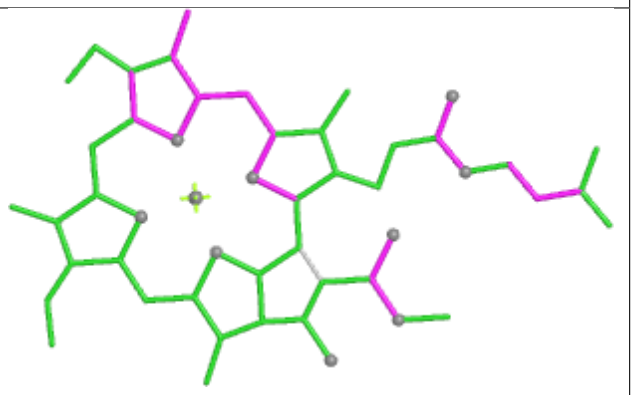


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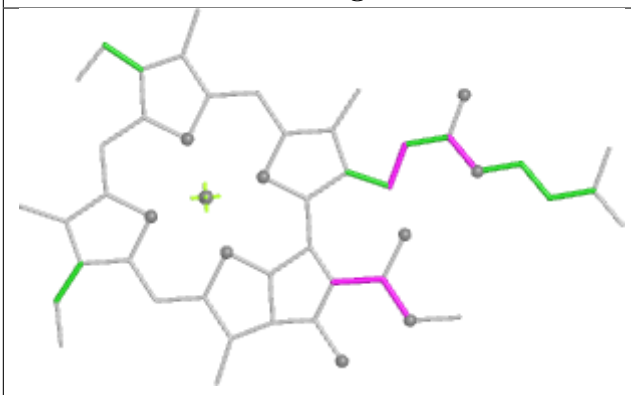
Ligand CLA S 303



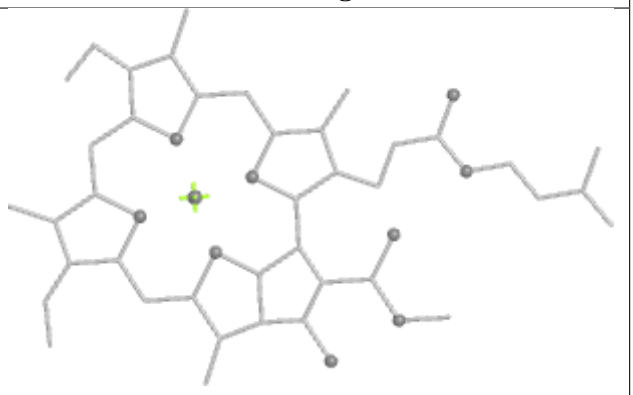
Bond lengths



Bond angles

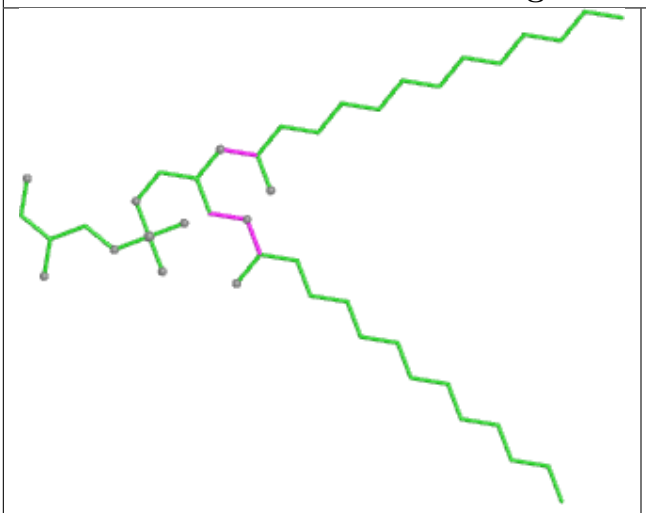


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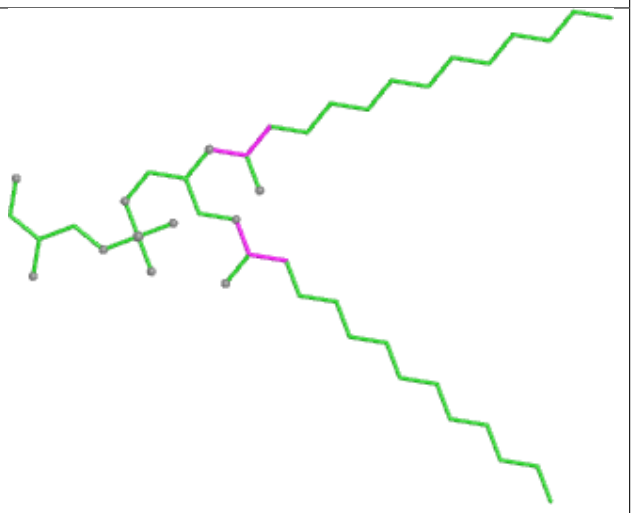


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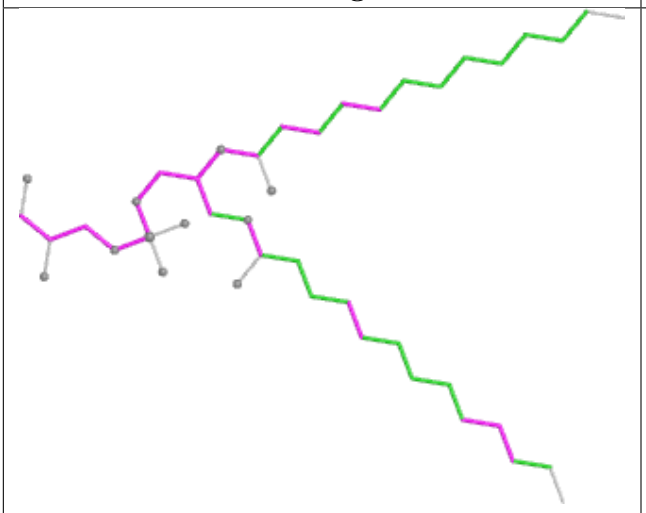
Ligand LHG a 415



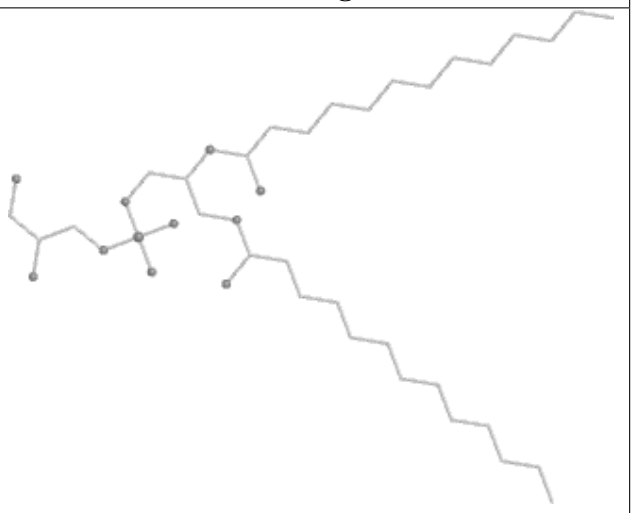
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Bond angles

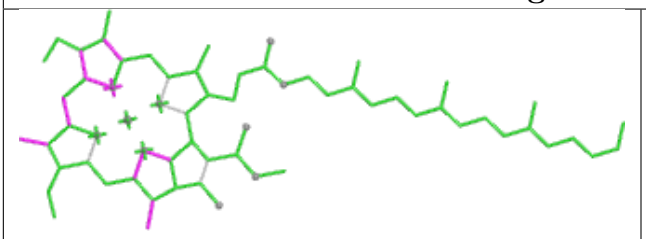


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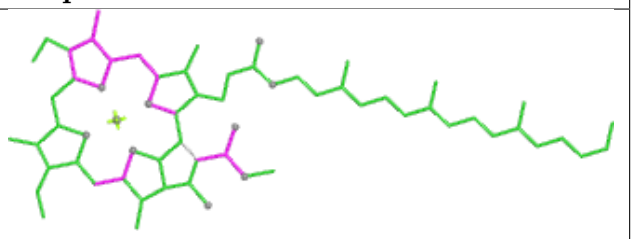


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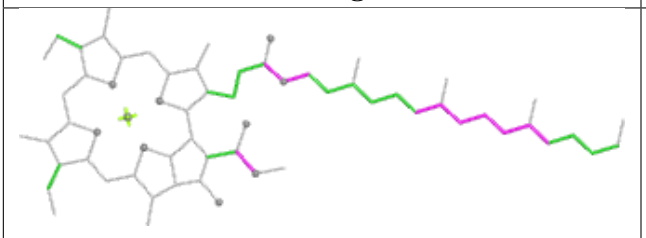
Ligand CLA q 304



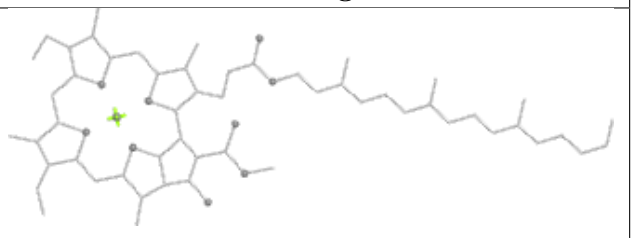
Bond lengths



Bond angles

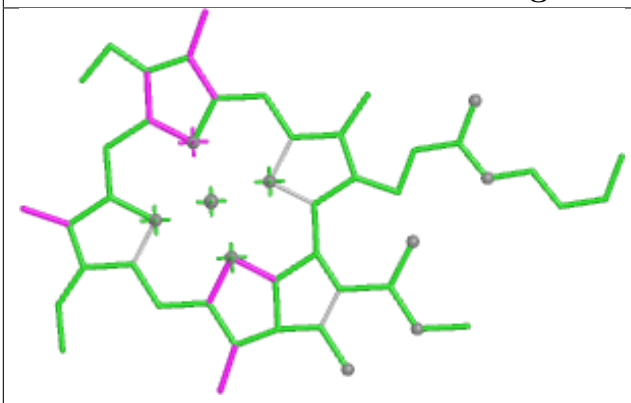


Torsions

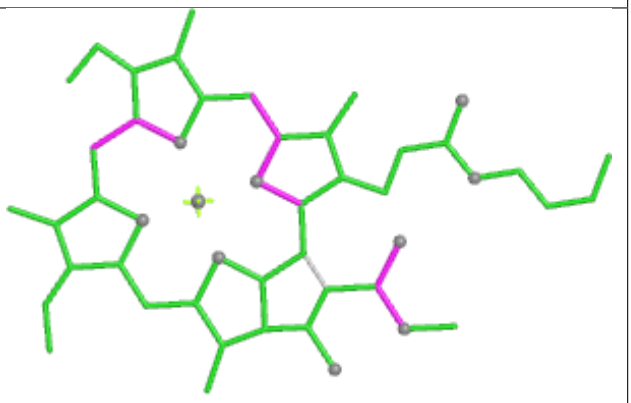


Rings

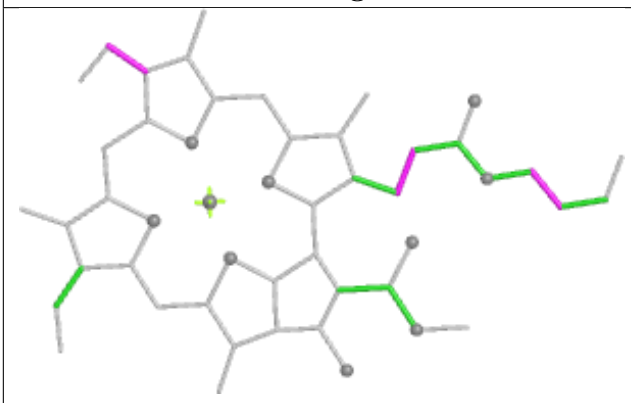
Ligand CLA s 309



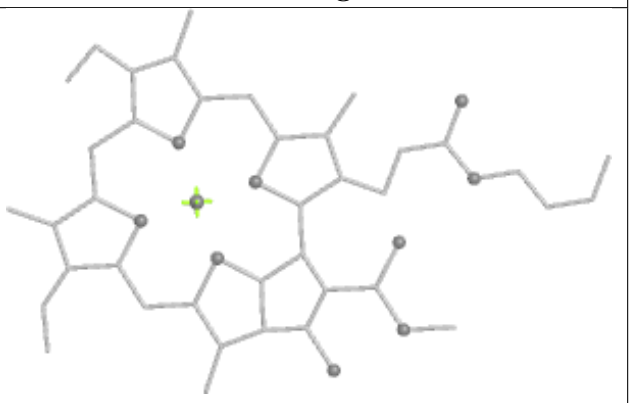
Bond lengths



Bond angles

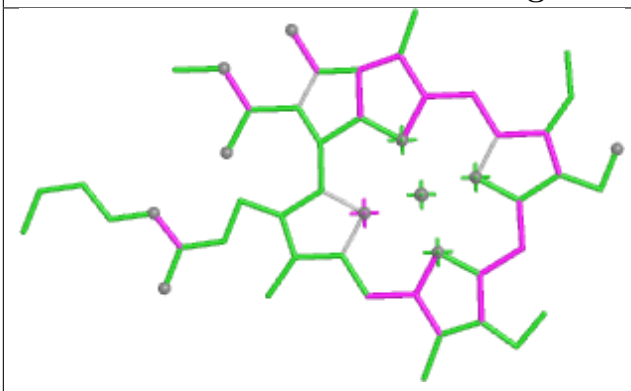


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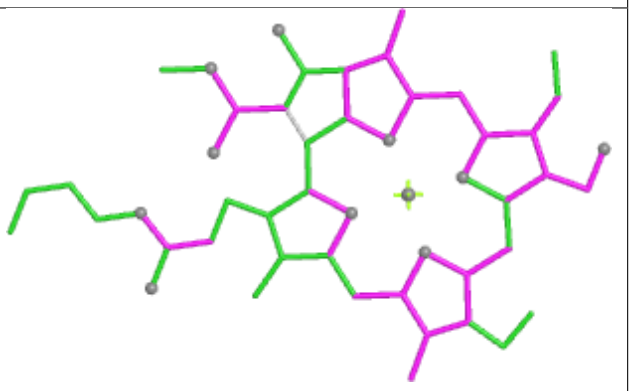


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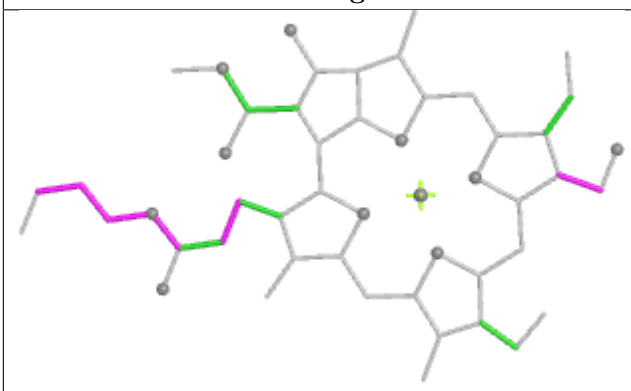
Ligand CHL v 315



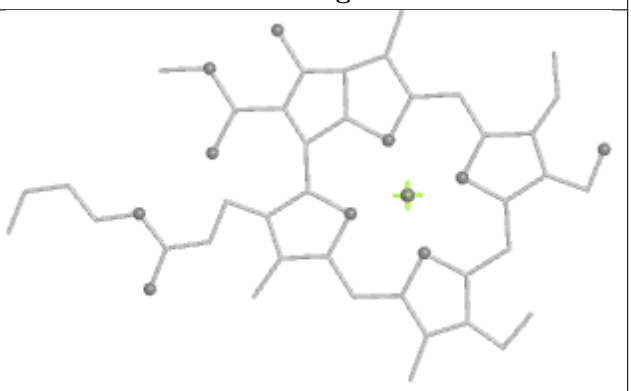
Bond lengths



Bond angles

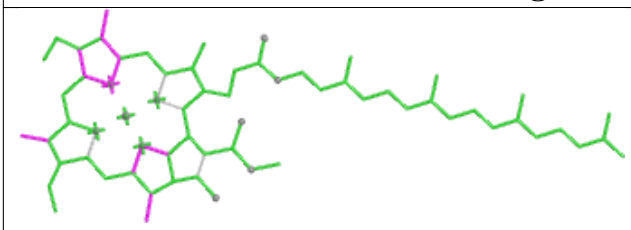


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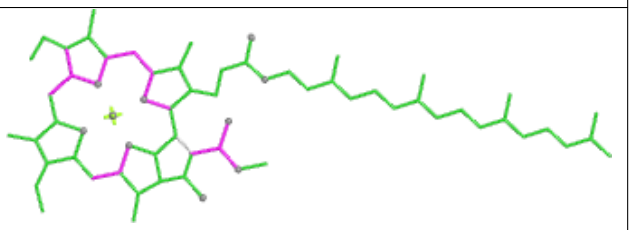


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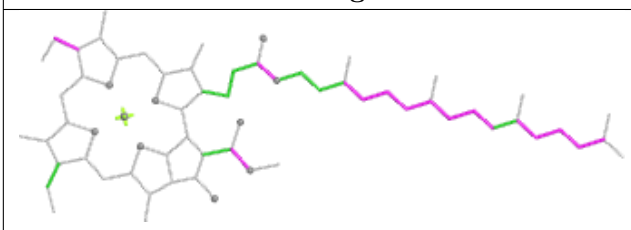
Ligand CLA c 507



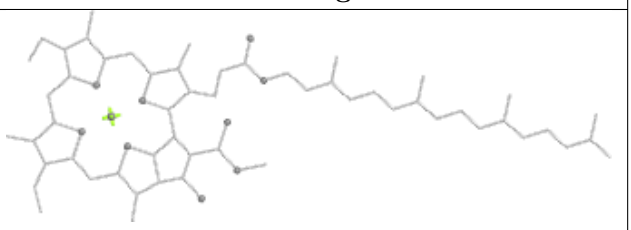
Bond lengths



Bond angles

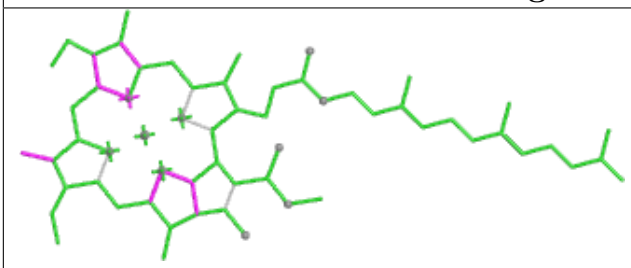


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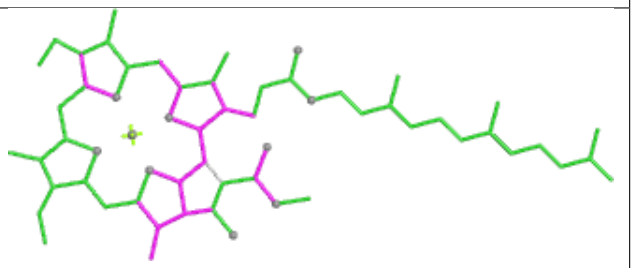


Rings

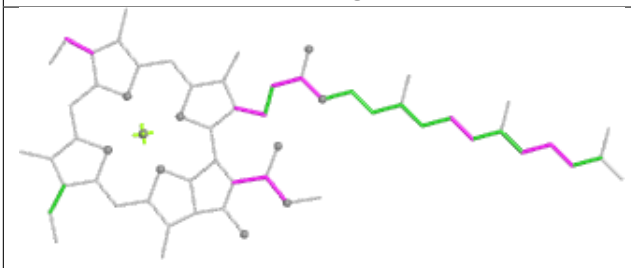
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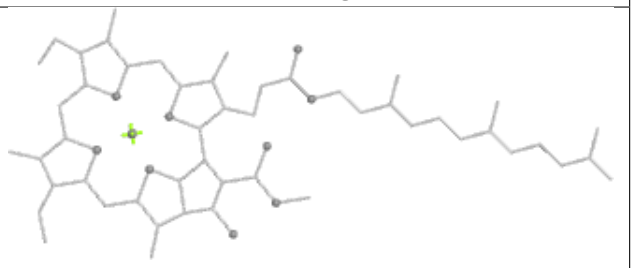
Bond lengths



Bond angles

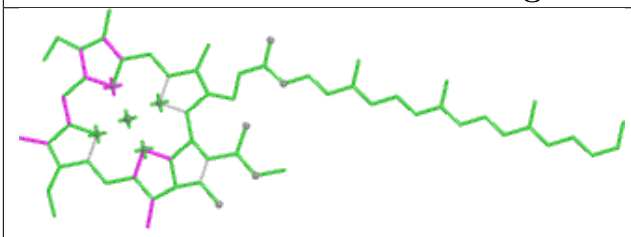


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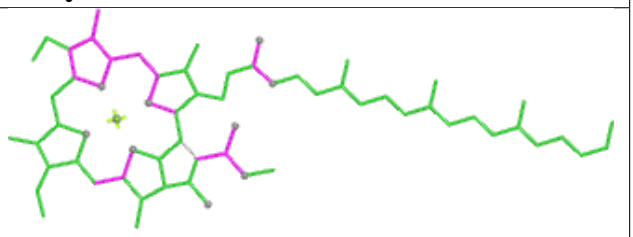


Rings

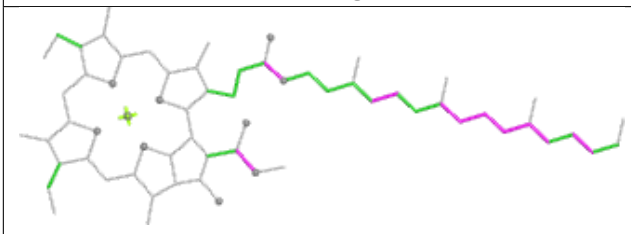
Ligand CLA Q 304



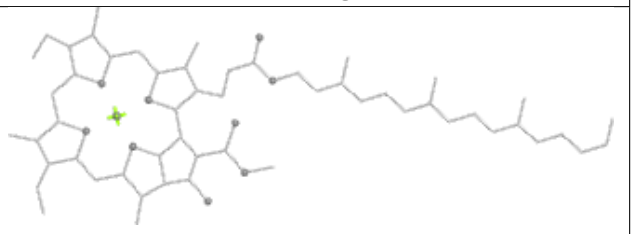
Bond lengths



Bond angles

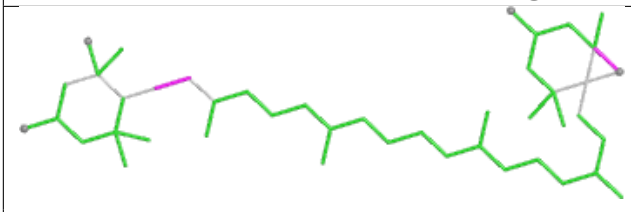


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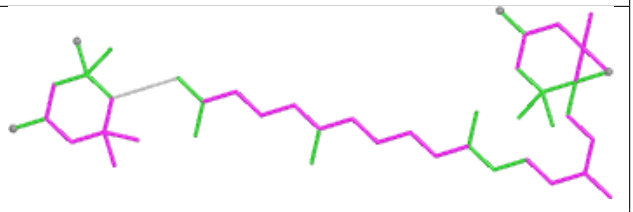


Rings

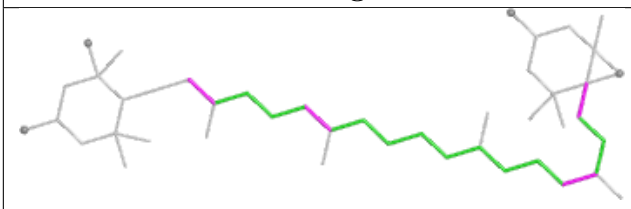
Ligand NEX n 319



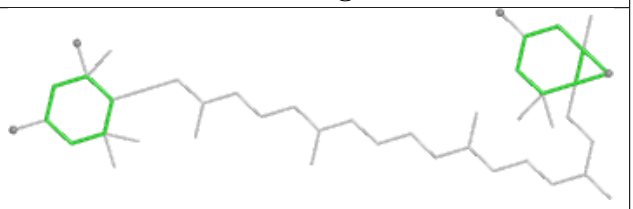
Bond lengths



Bond angles

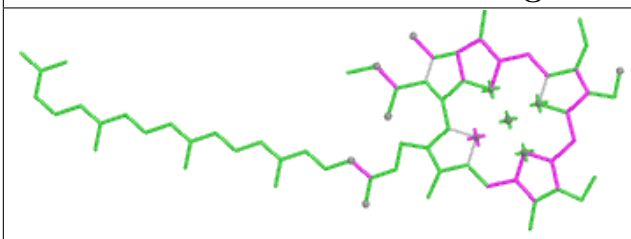


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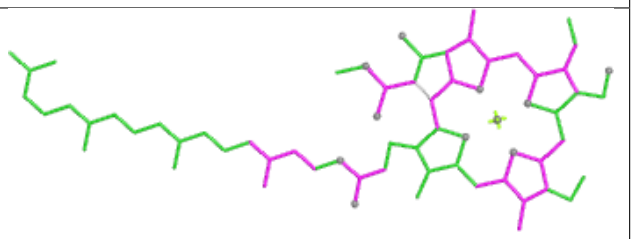


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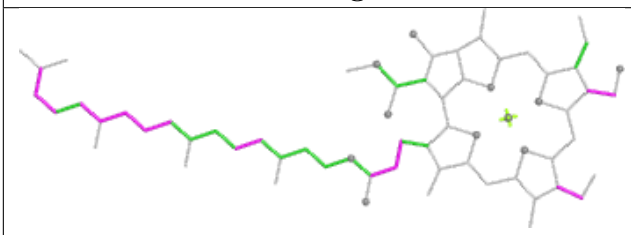
Ligand CHL P 314



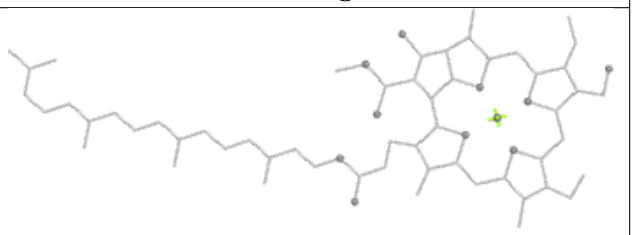
Bond lengths



Bond angles

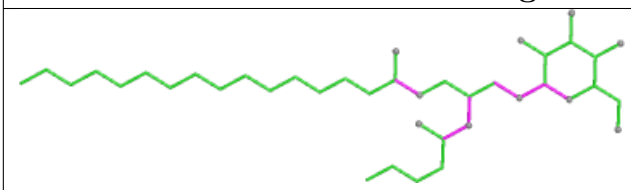


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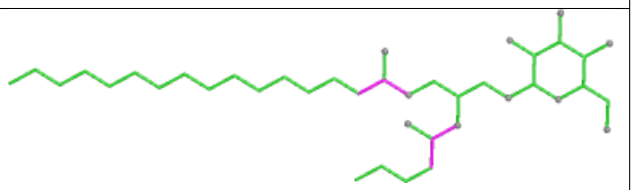


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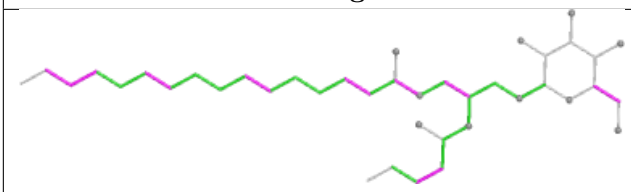
Ligand LMG A 411



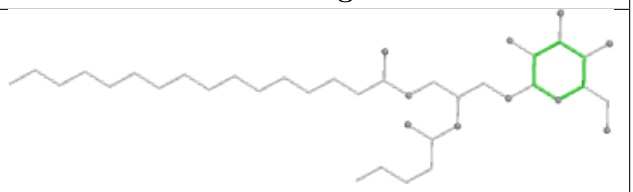
Bond lengths



Bond angles

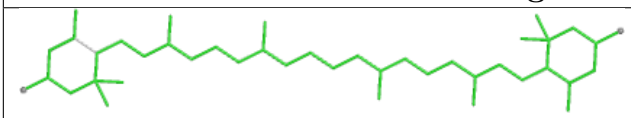


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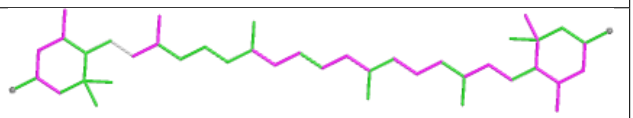


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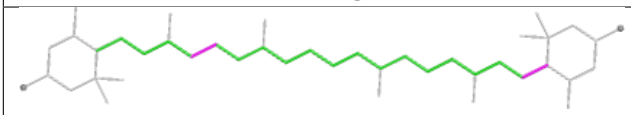
Ligand LUT u 310



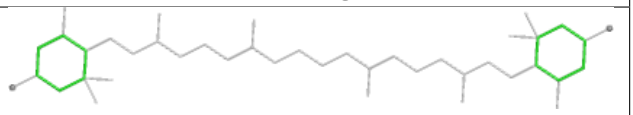
Bond lengths



Bond angles

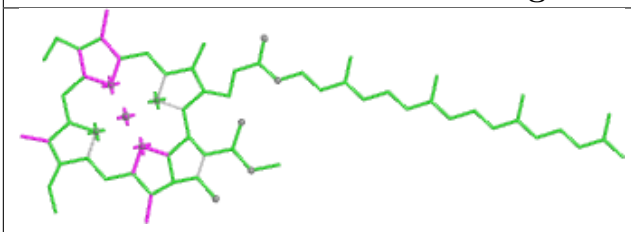


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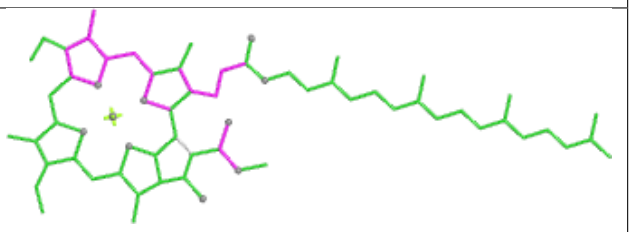


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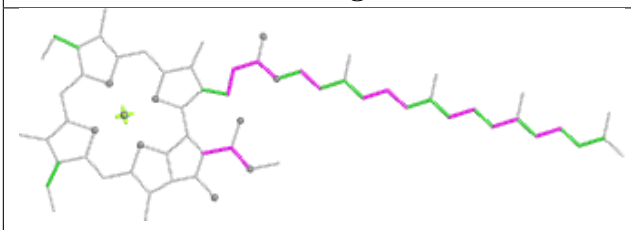
Ligand CLA a 404



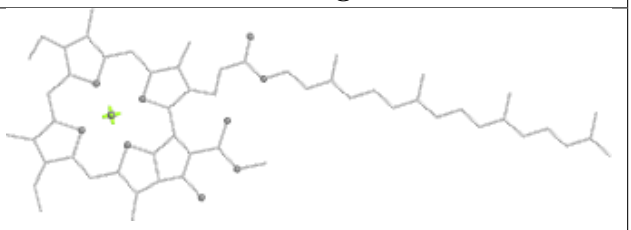
Bond lengths



Bond angles

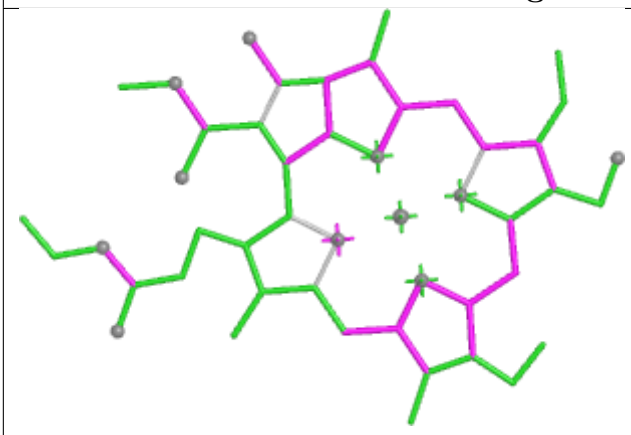


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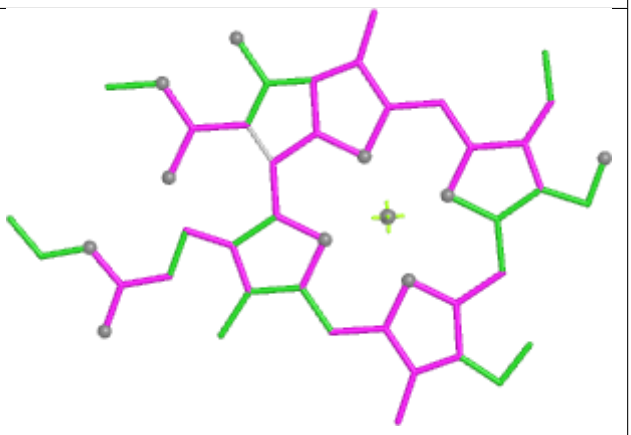


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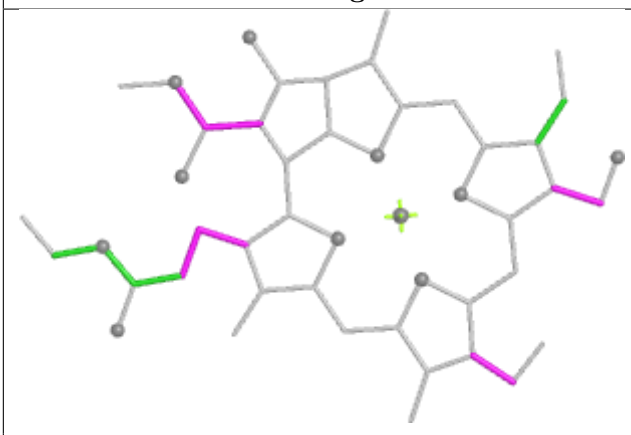
Ligand CHL n 314



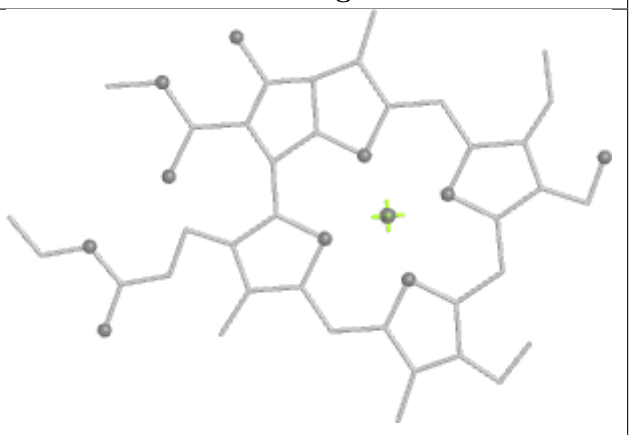
Bond lengths



Bond angles

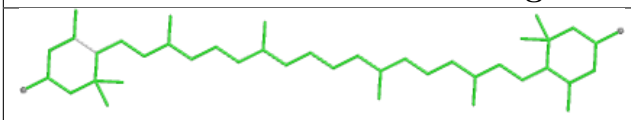


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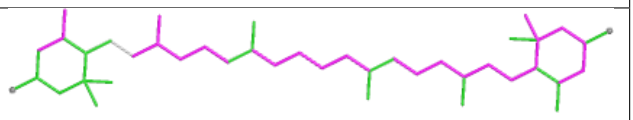


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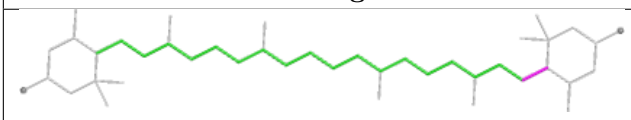
Ligand LUT P 310



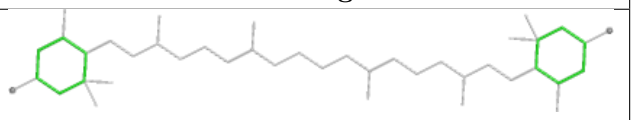
Bond lengths



Bond angles

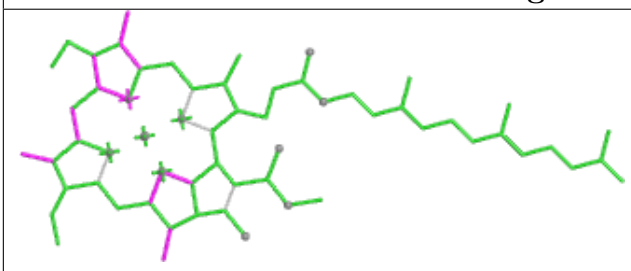


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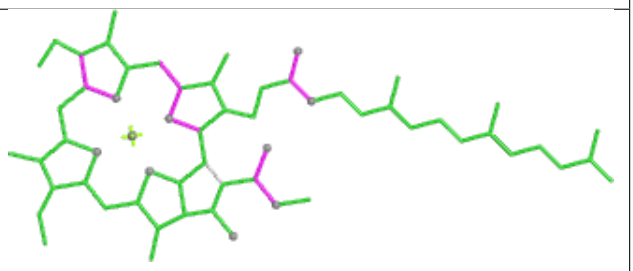


Rings

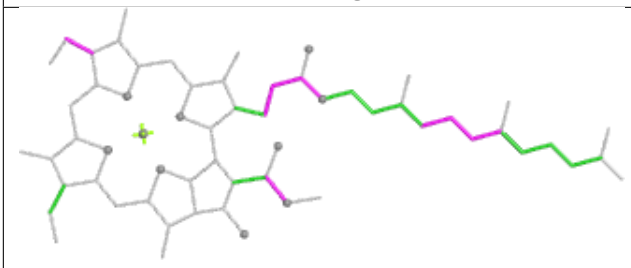
Ligand CLA n 307



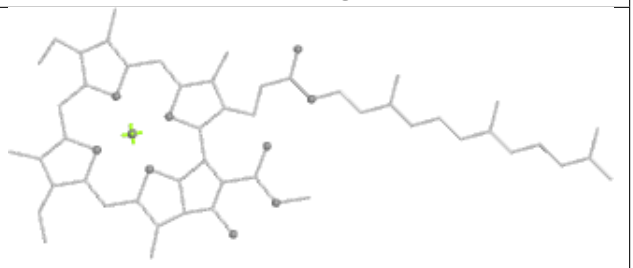
Bond lengths



Bond angles

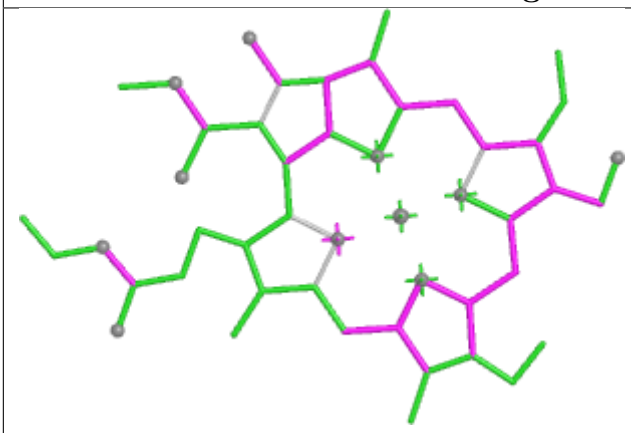


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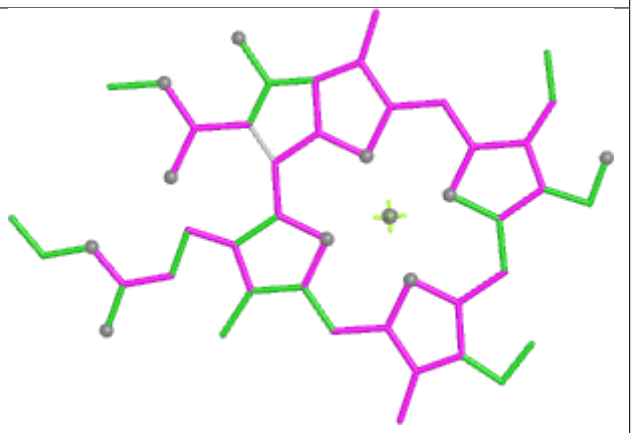


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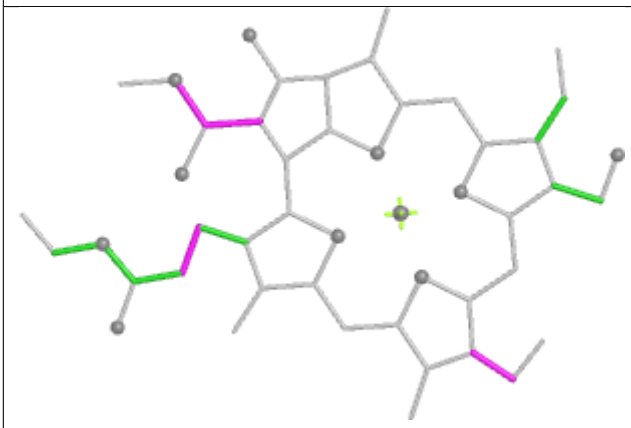
Ligand CHL G 312



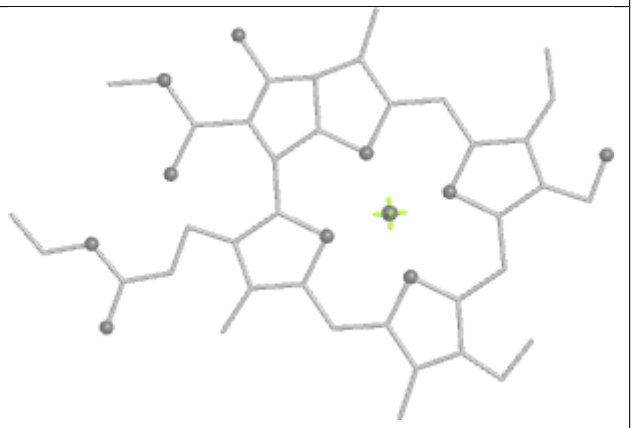
Bond lengths



Bond angles

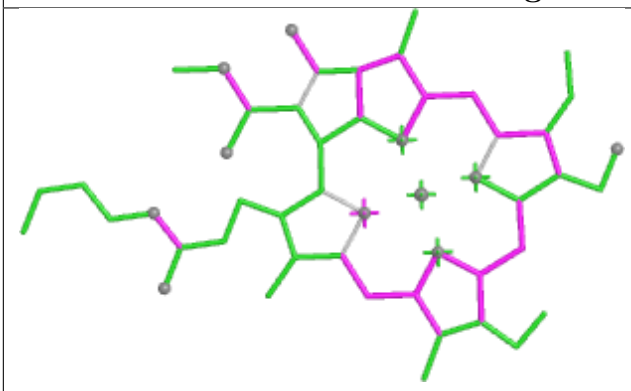


Torsions

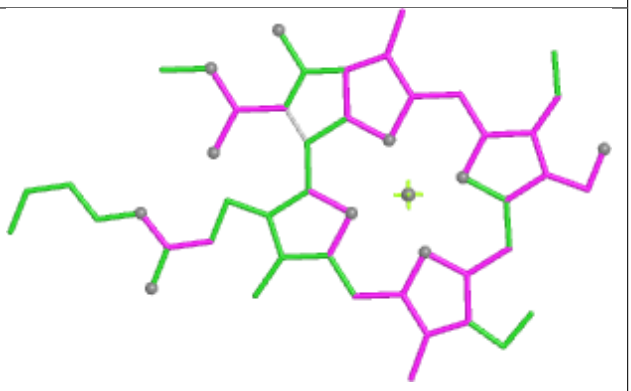


Rings

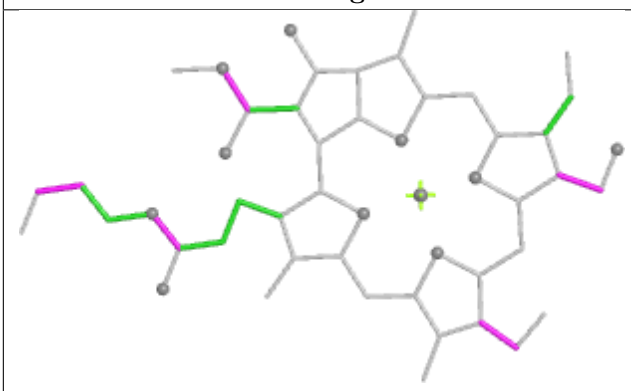
Ligand CHL P 316



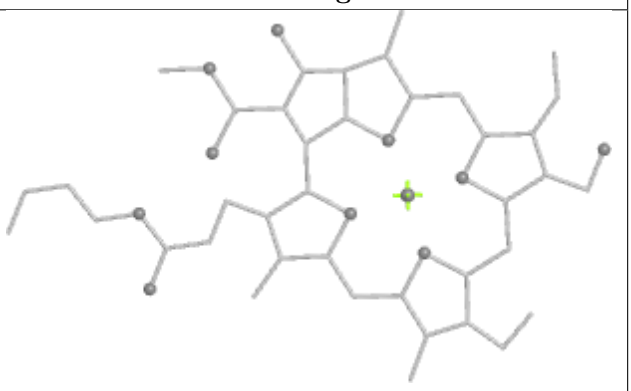
Bond lengths



Bond angles

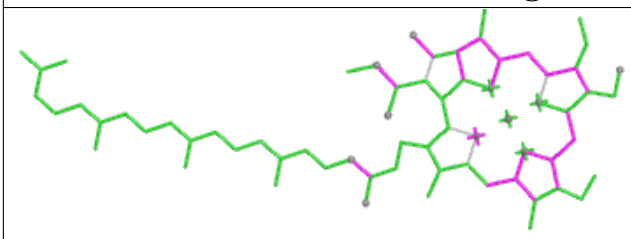


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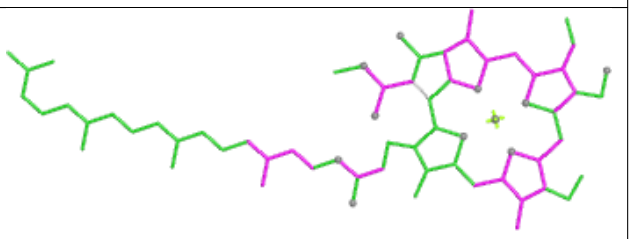


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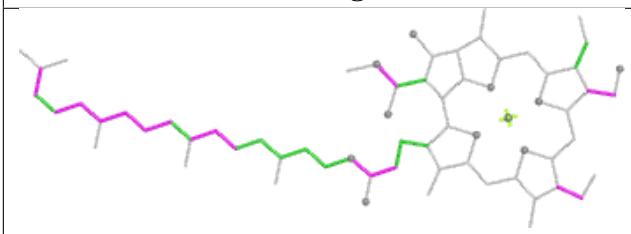
Ligand CHL V 313



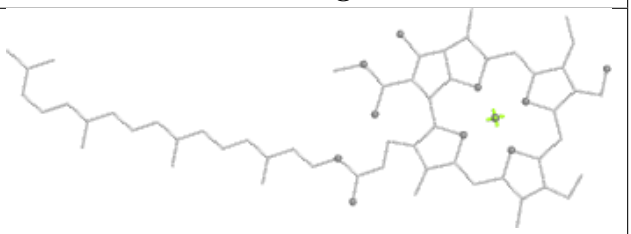
Bond lengths



Bond angles

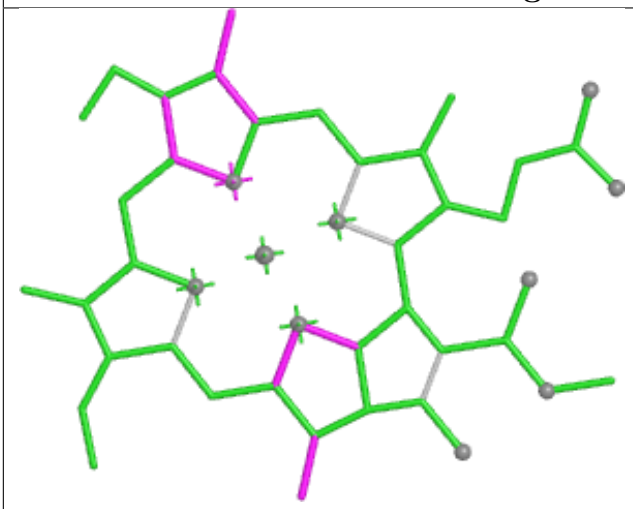


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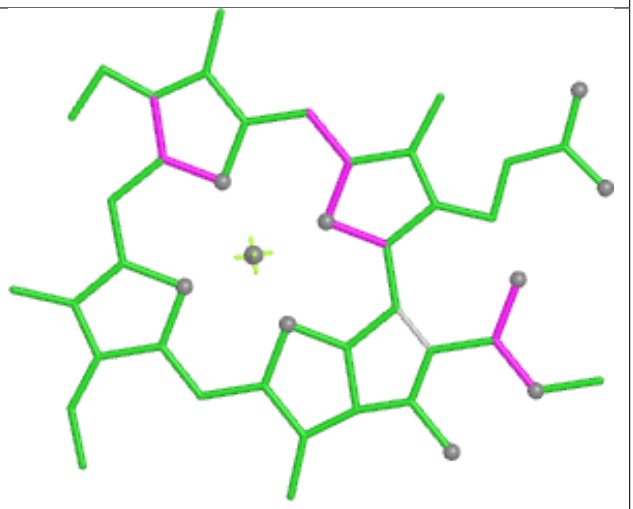


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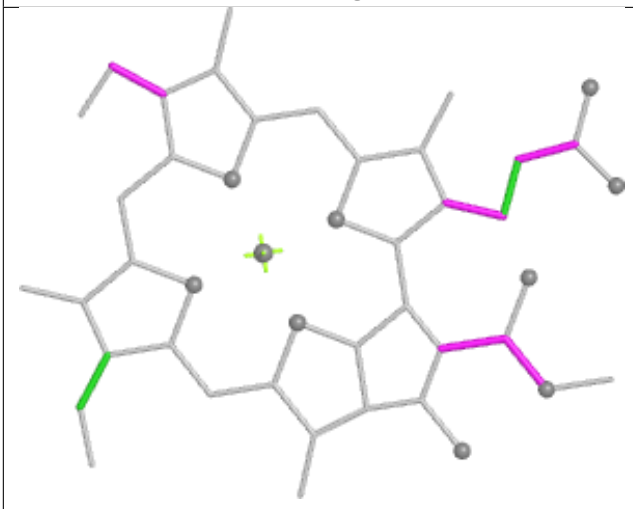
Ligand CLA R 311



Bond lengths



Bond angles

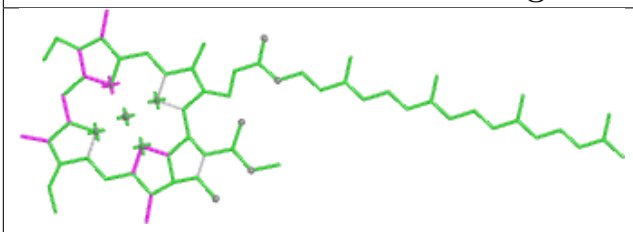


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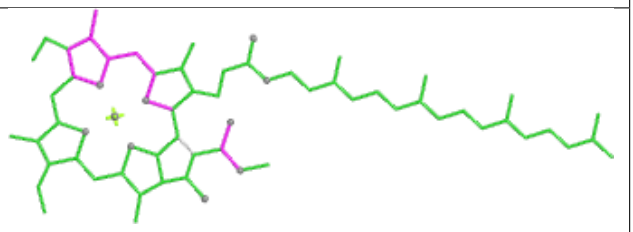


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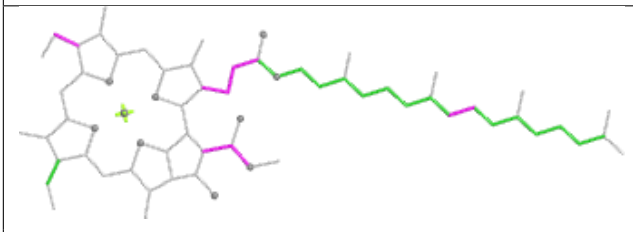
Ligand CLA u 301



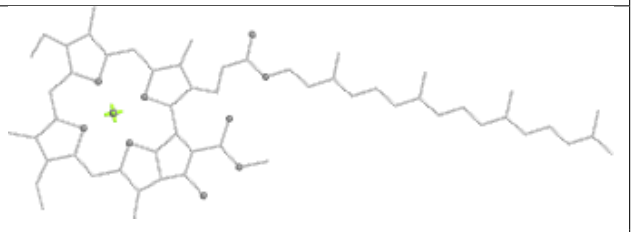
Bond lengths



Bond angles

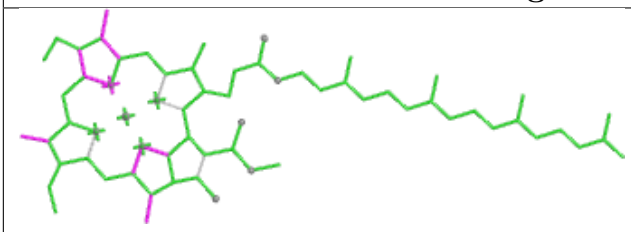


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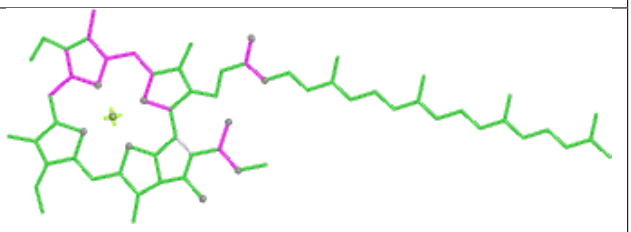


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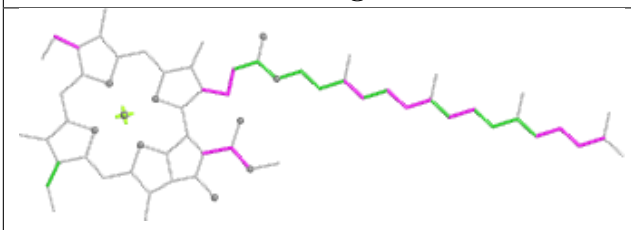
Ligand CLA b 604



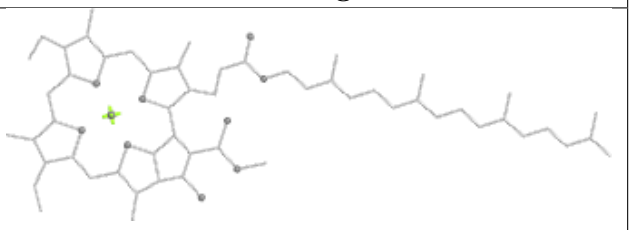
Bond lengths



Bond angles

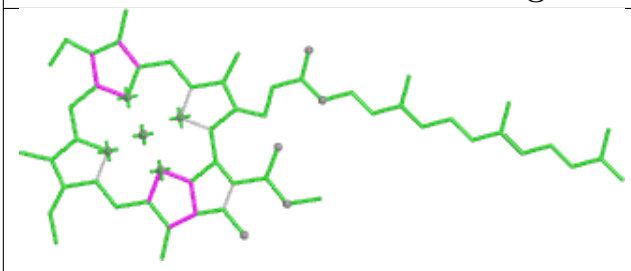


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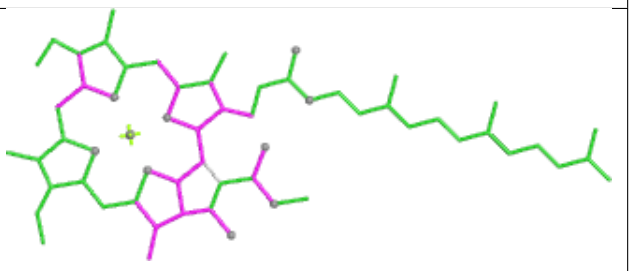


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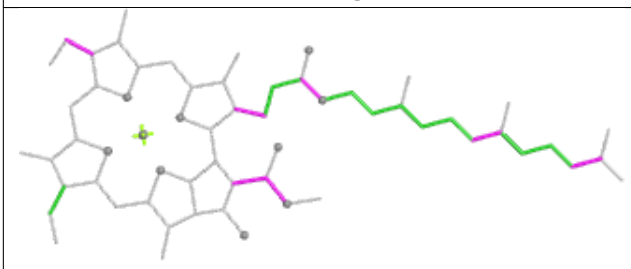
Ligand CLA n 305



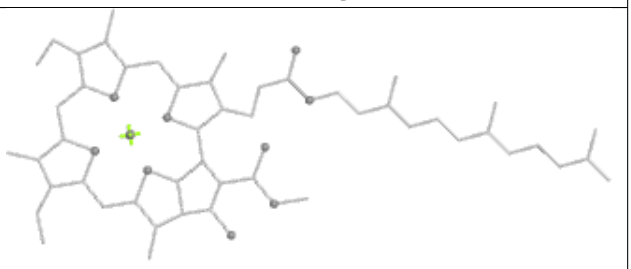
Bond lengths



Bond angles

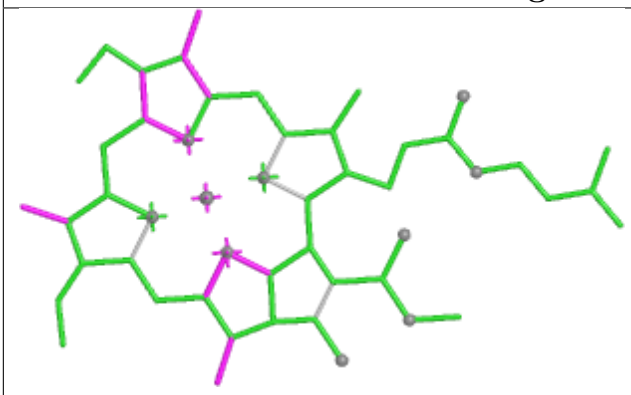


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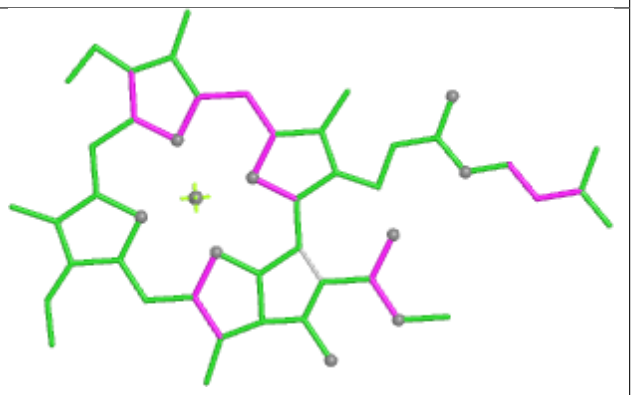


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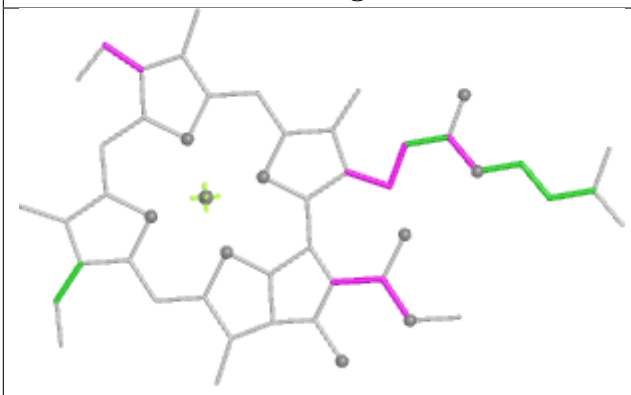
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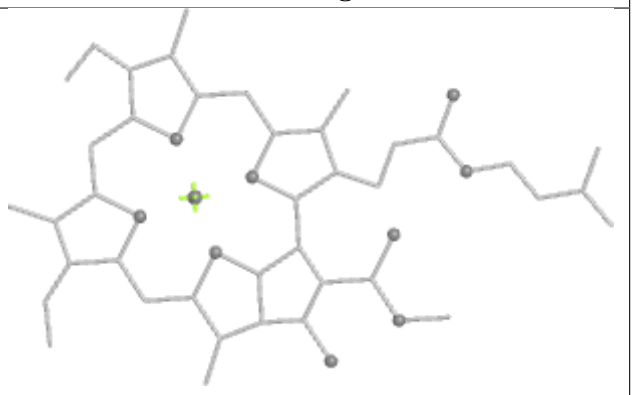
Bond lengths



Bond angles

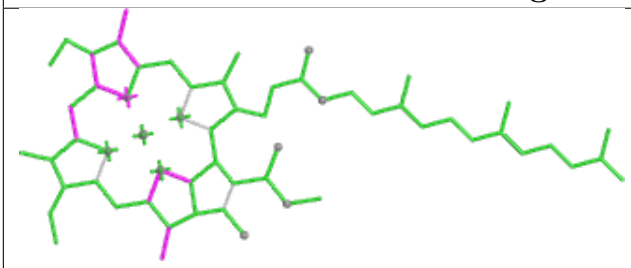


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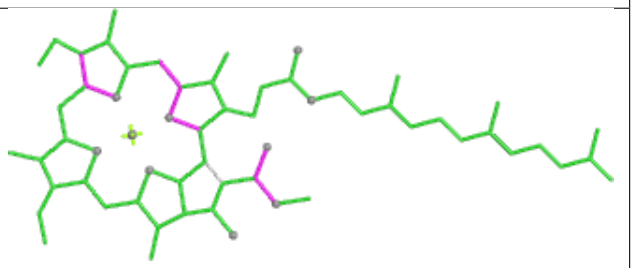


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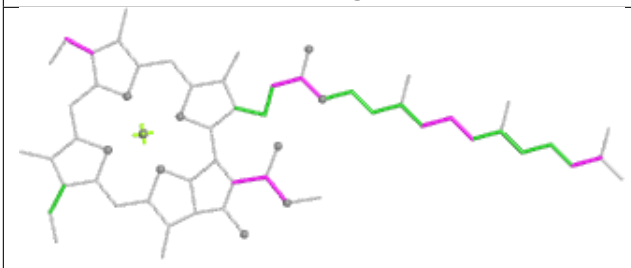
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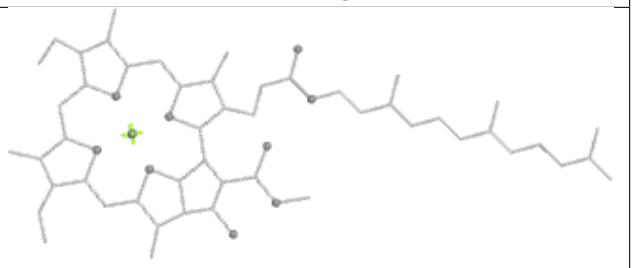
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Bond angles

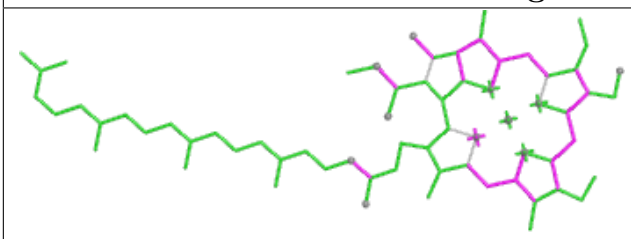


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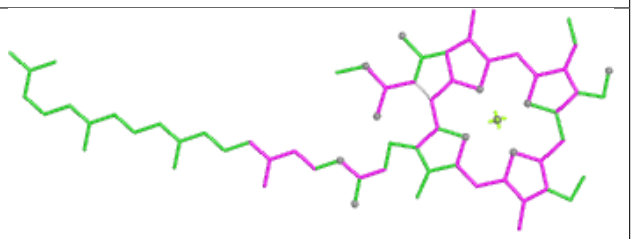


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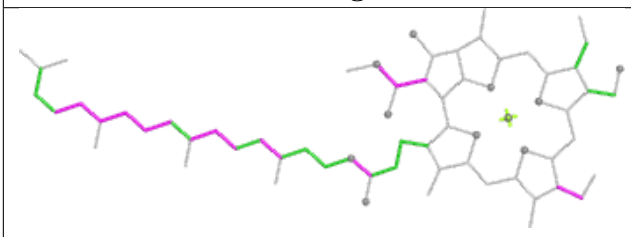
Ligand CHL 6 312



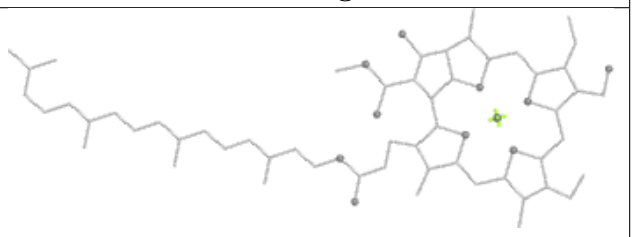
Bond lengths



Bond angles

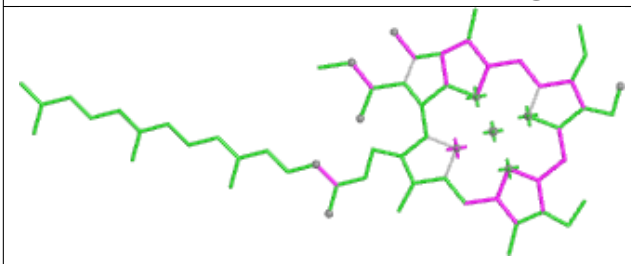


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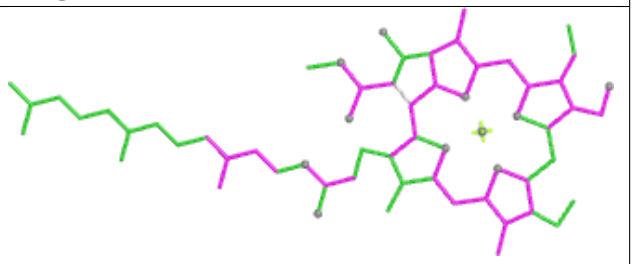


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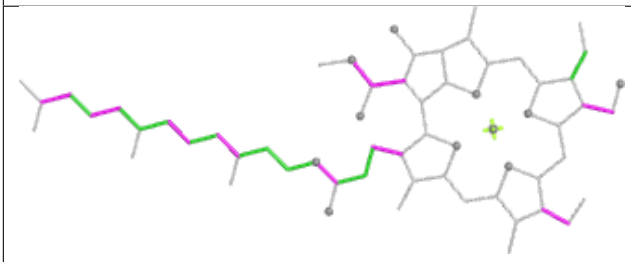
Ligand CHL g 316



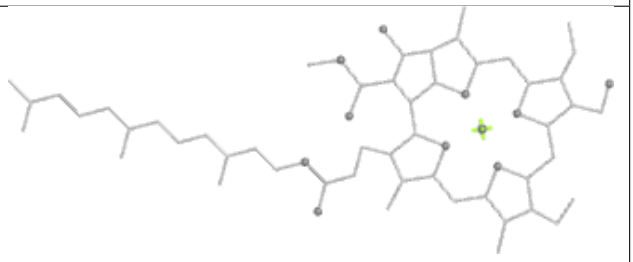
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Bond angles

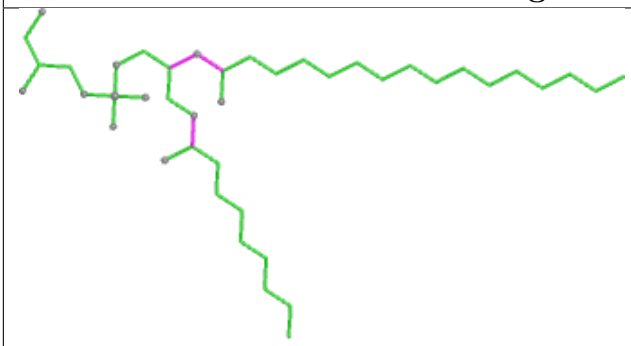


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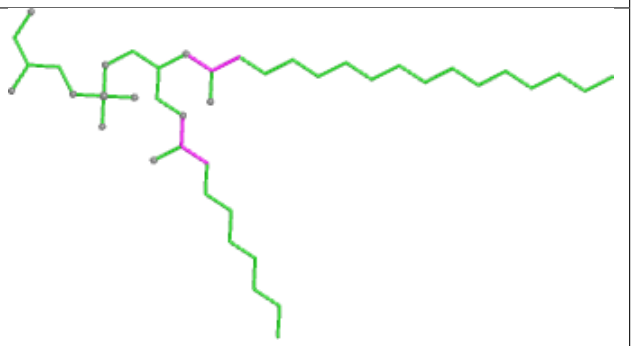


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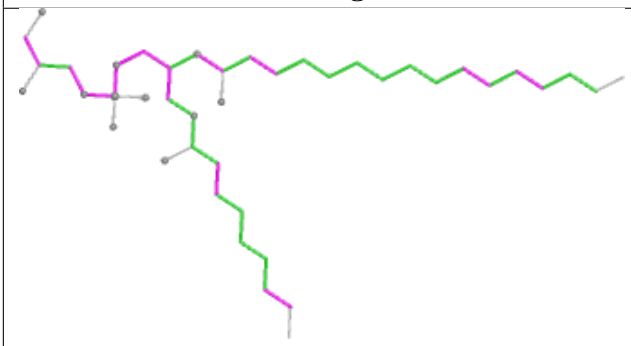
Ligand LHG r 613



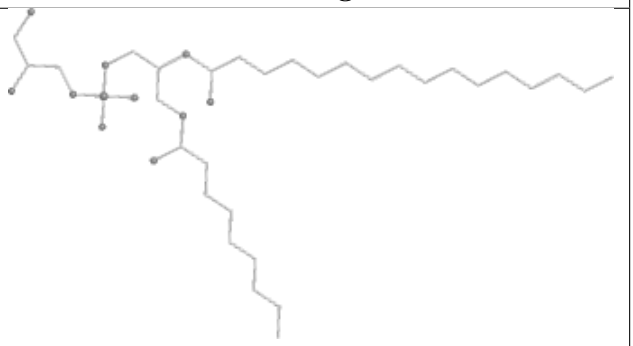
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Bond angles

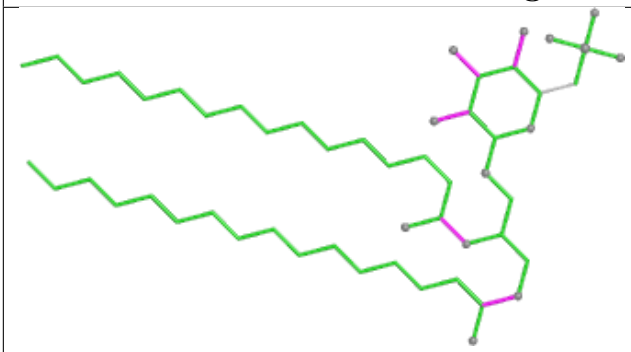


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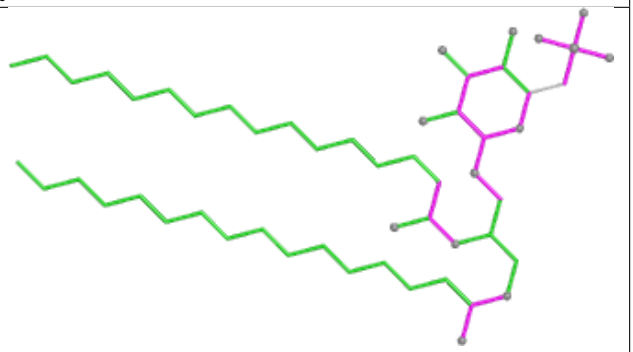


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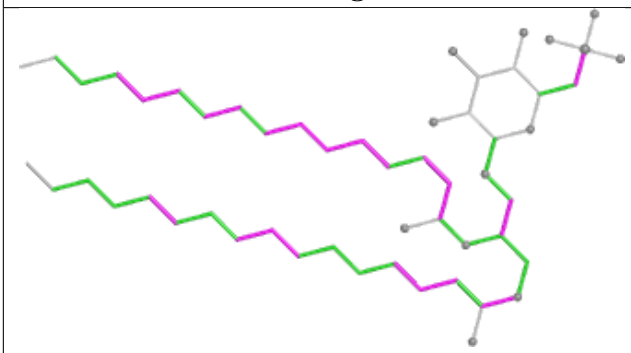
Ligand SQD A 412



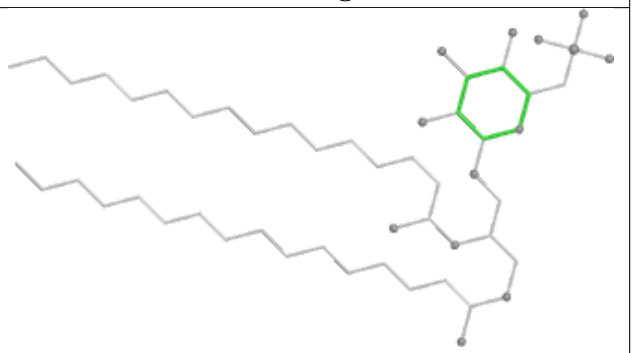
Bond lengths



Bond angles

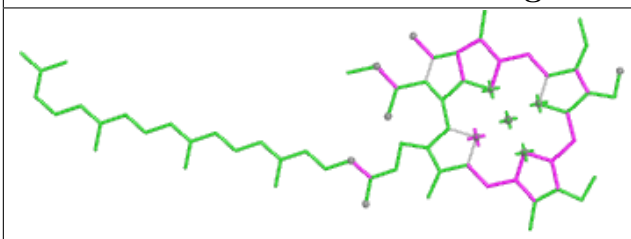


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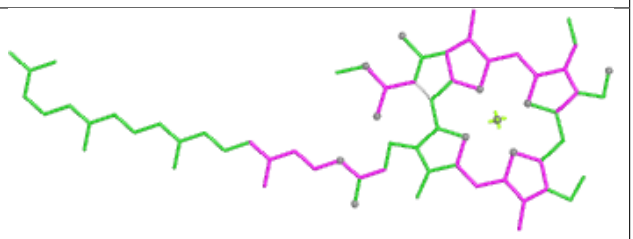


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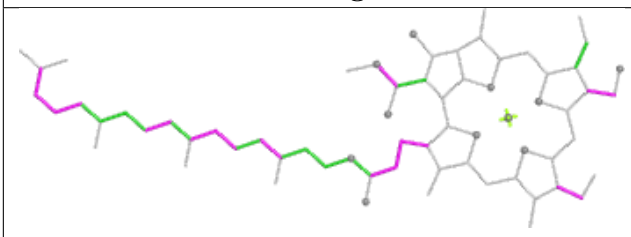
Ligand CHL P 318



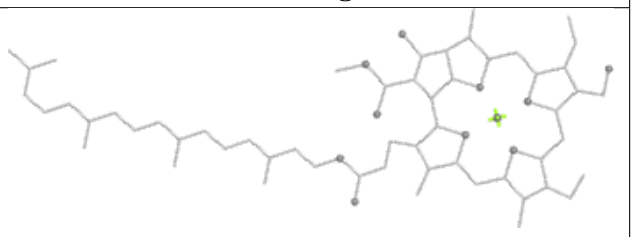
Bond lengths



Bond angles

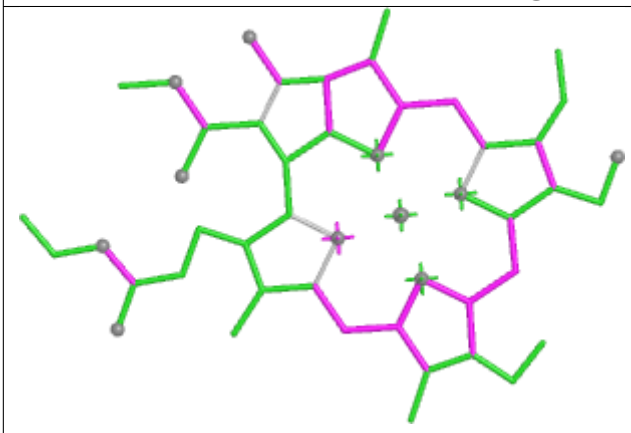


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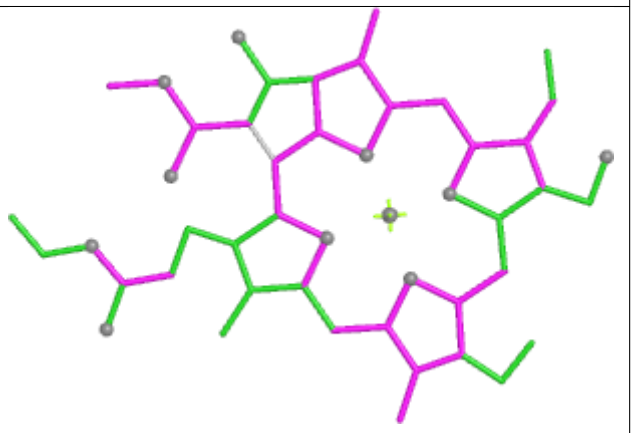


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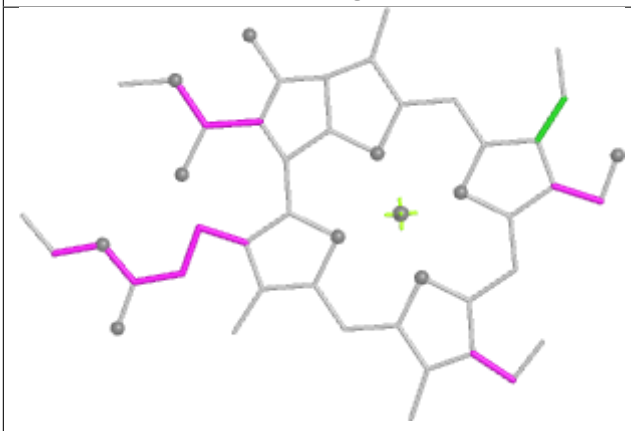
Ligand CHL 1 314



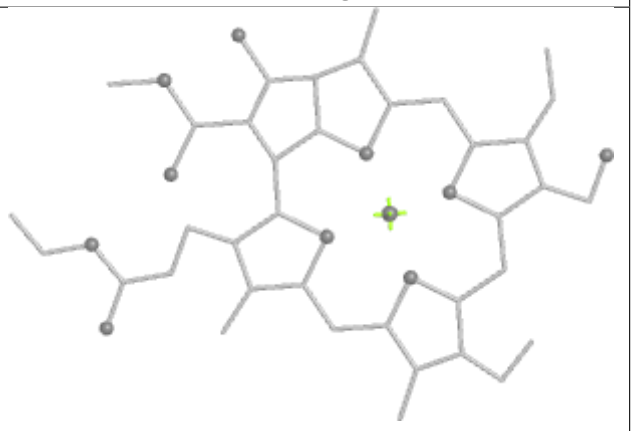
Bond lengths



Bond angles

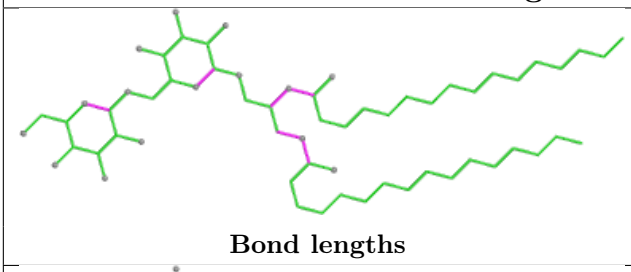


Torsions

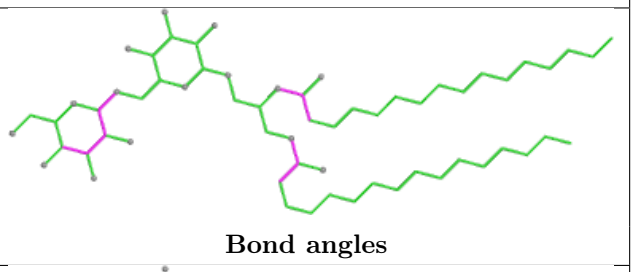


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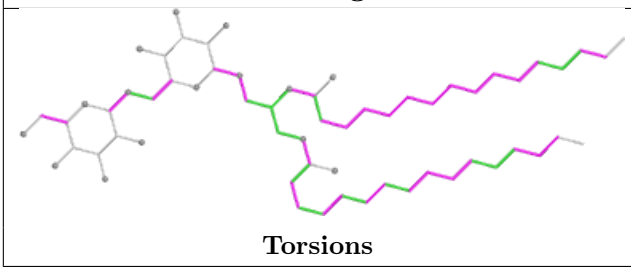
Ligand DGD c 518



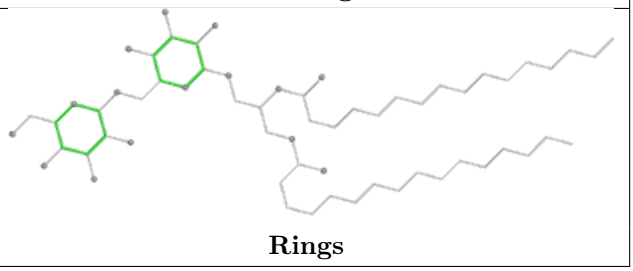
Bond lengths



Bond angles

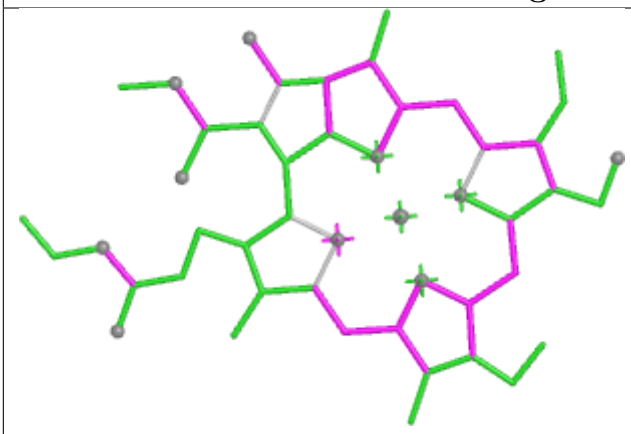


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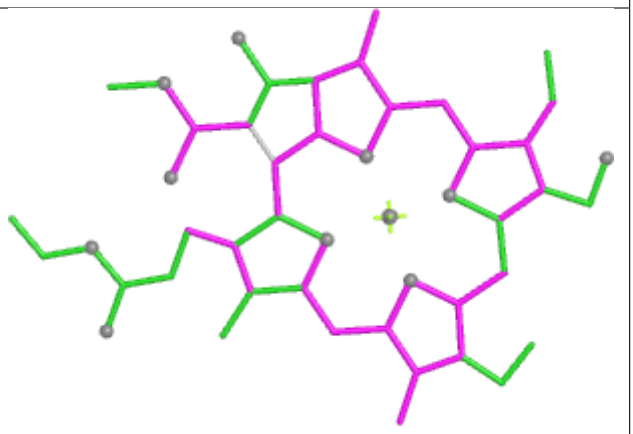


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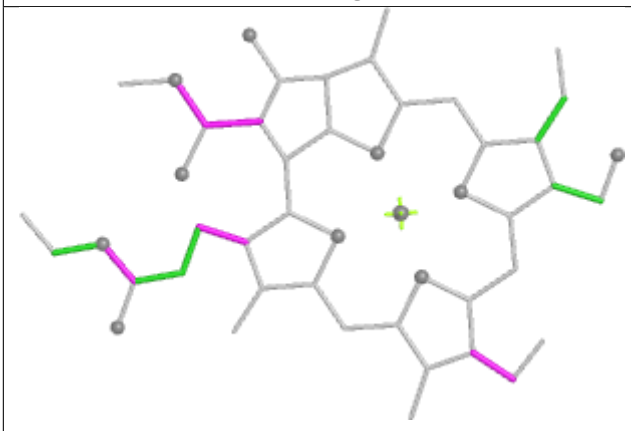
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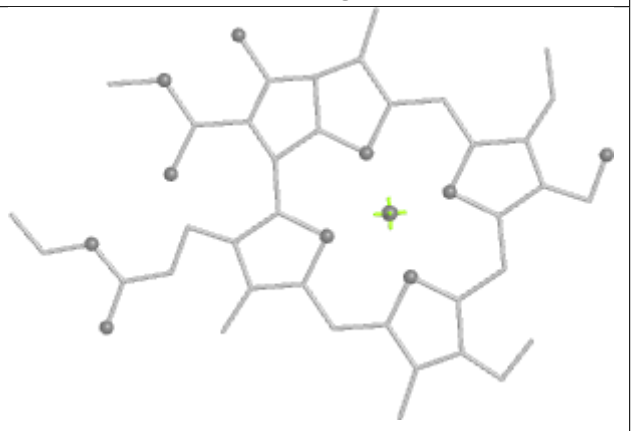
Bond lengths



Bond angles

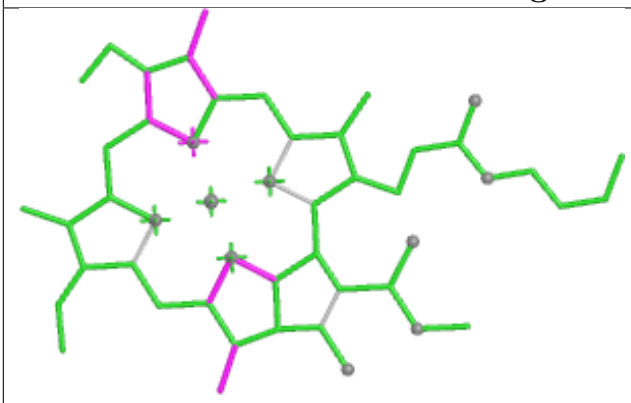


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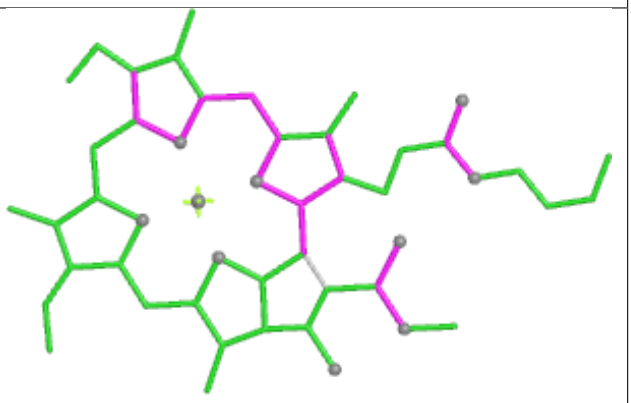


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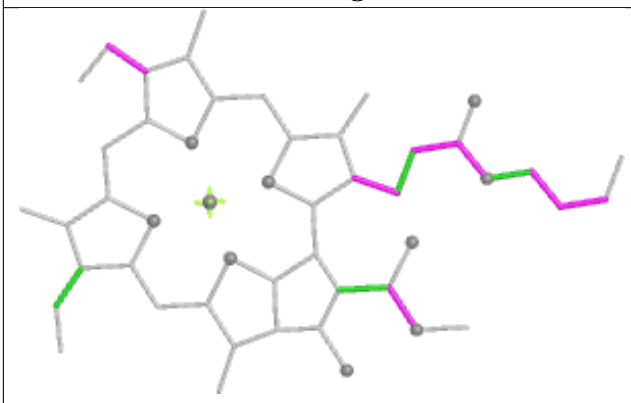
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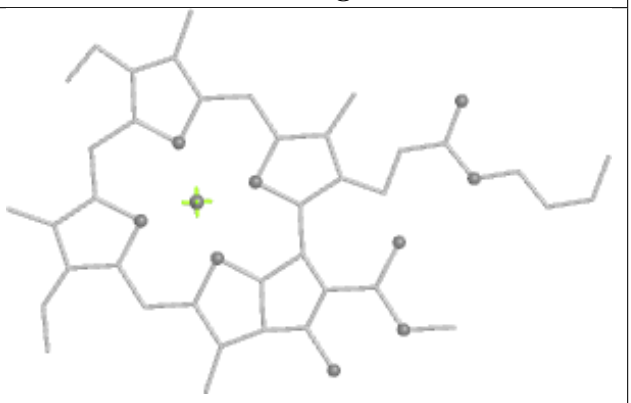
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Bond angles

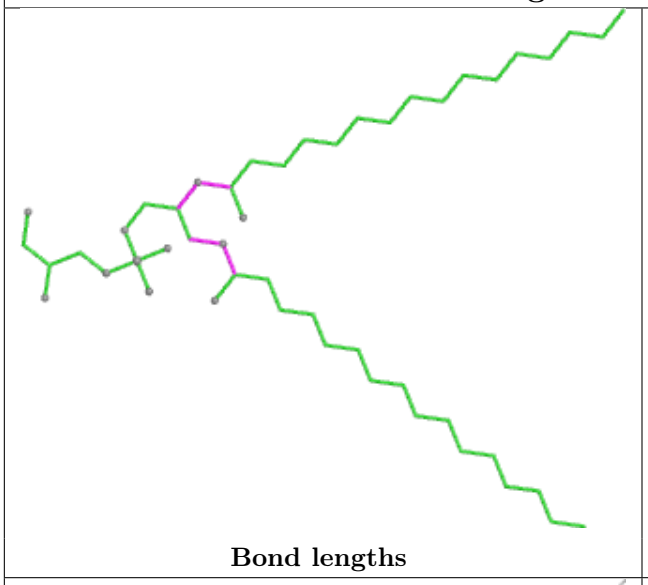


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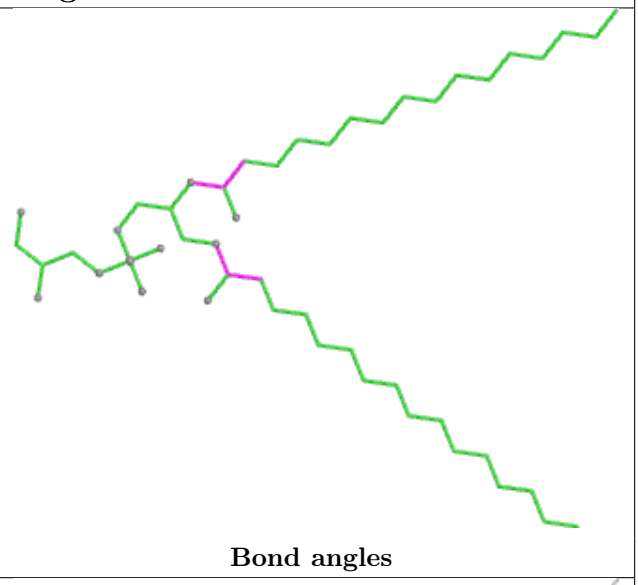


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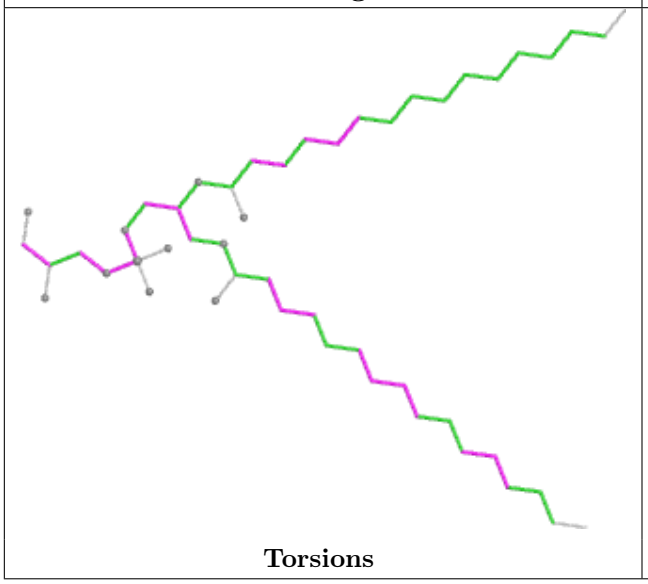
Ligand LHG g 310



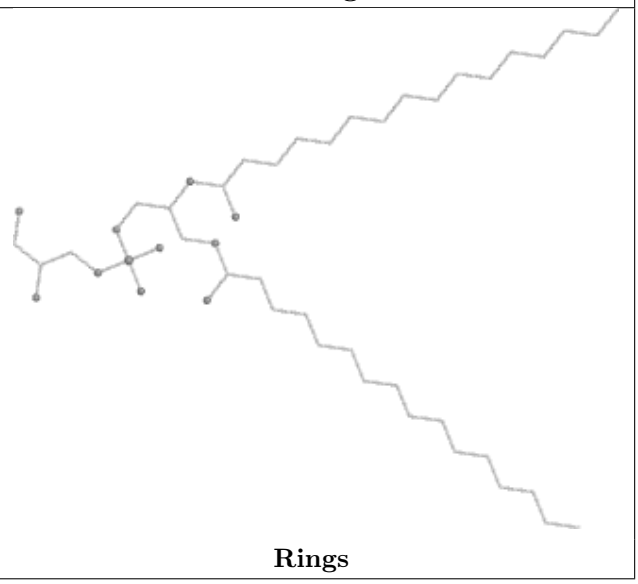
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Bond angles

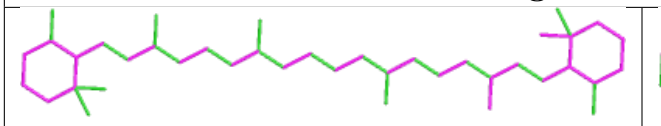


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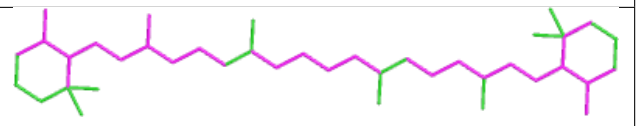


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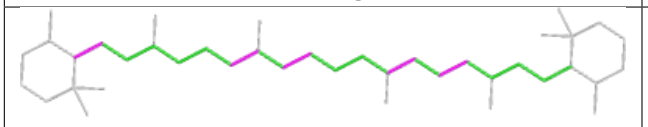
Ligand BCR z 101



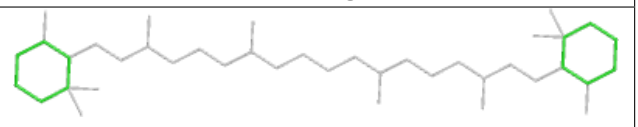
Bond lengths



Bond angles

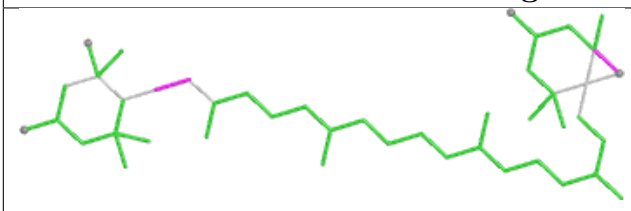


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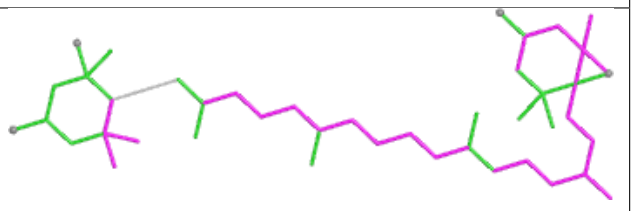


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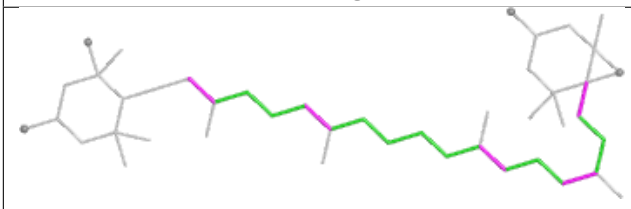
Ligand NEX N 318



Bond lengths



Bond angles

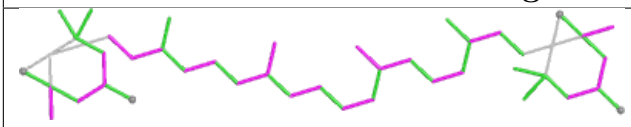


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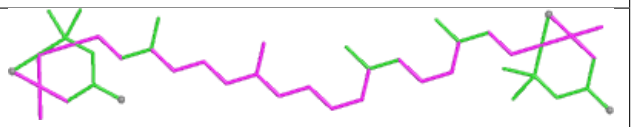


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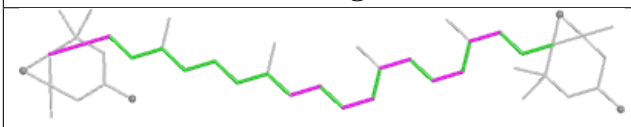
Ligand XAT N 311



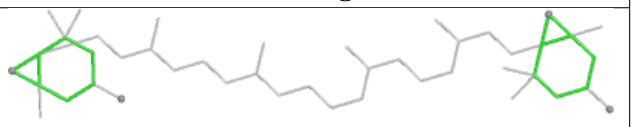
Bond lengths



Bond angles

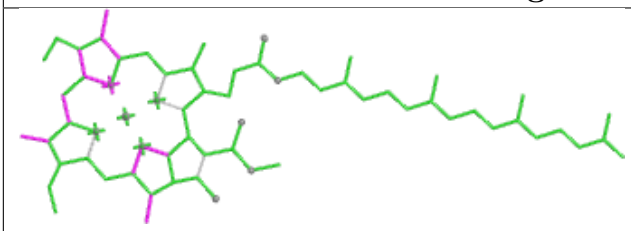


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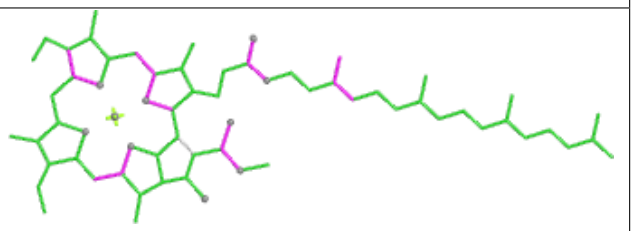


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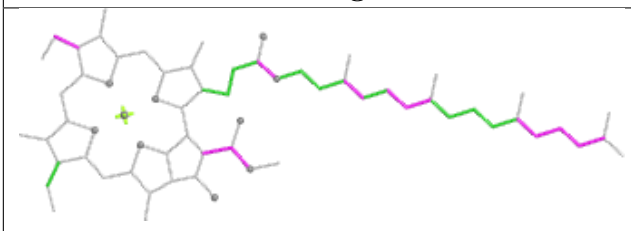
Ligand CLA b 610



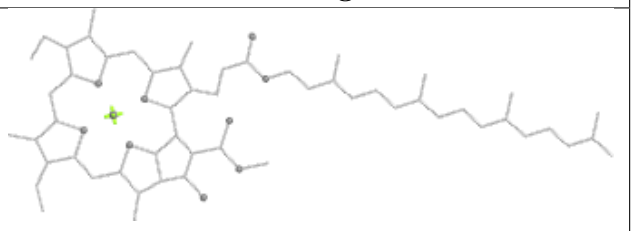
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Bond angles

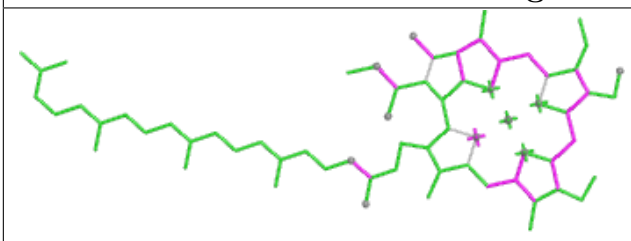


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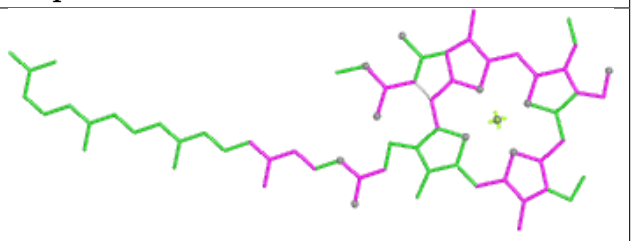


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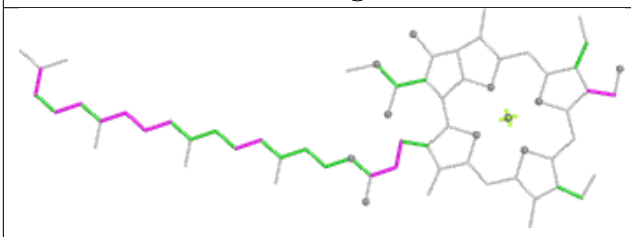
Ligand CHL p 314



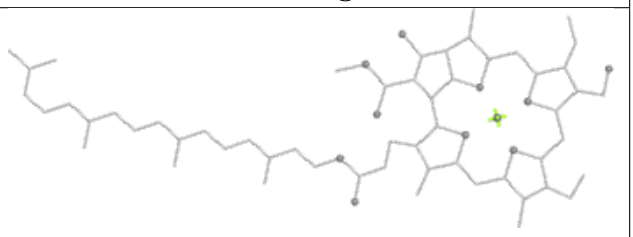
Bond lengths



Bond angles

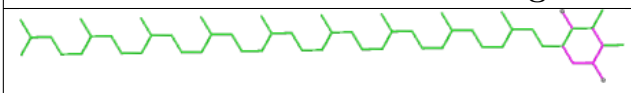


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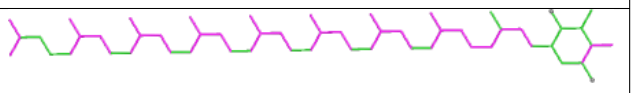


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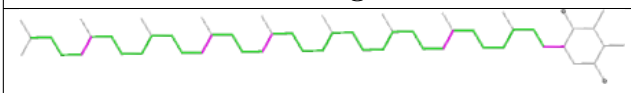
Ligand PL9 D 405



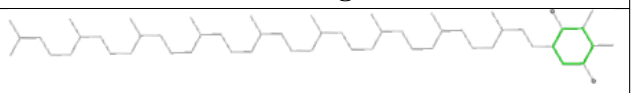
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Bond angles

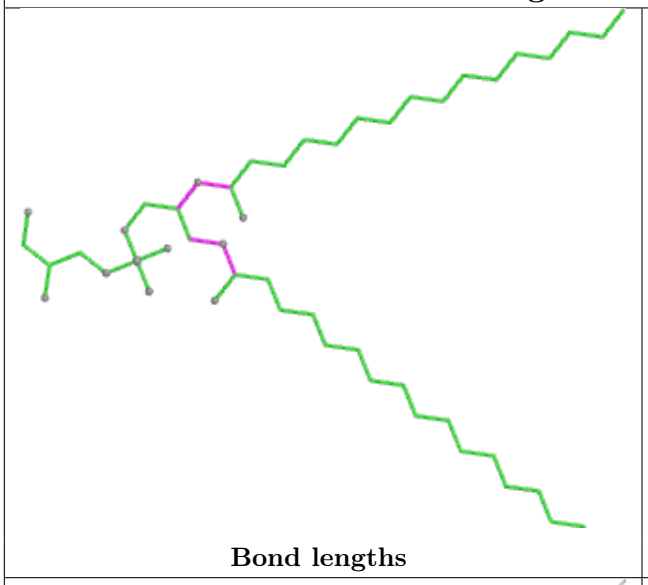


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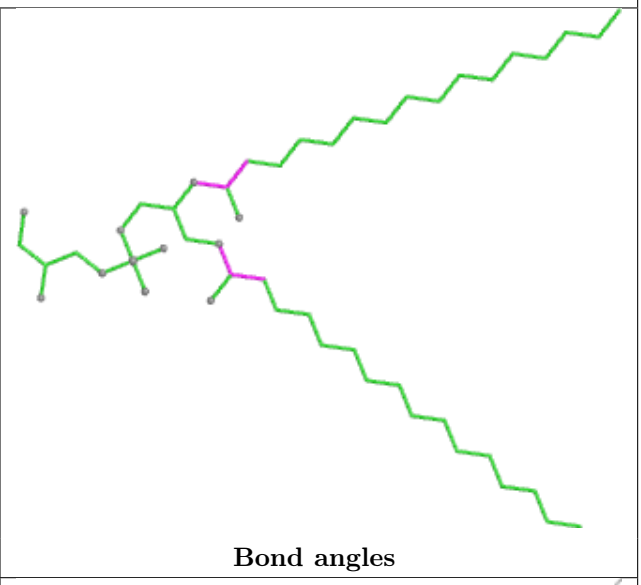


Rings

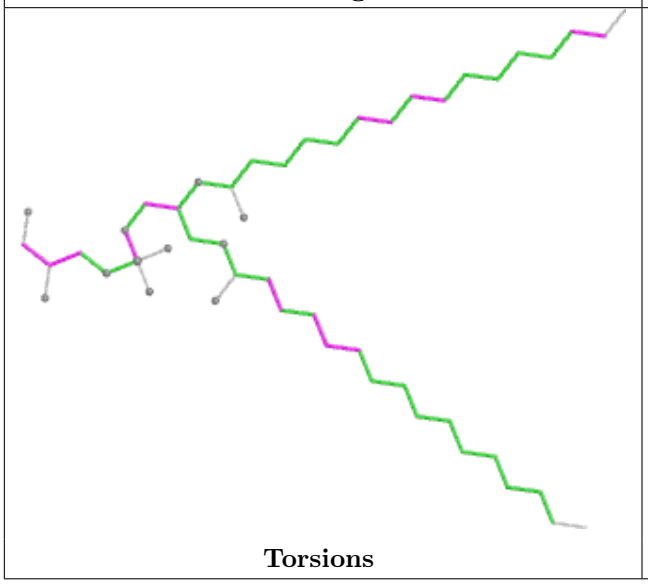
Ligand LHG 1 312



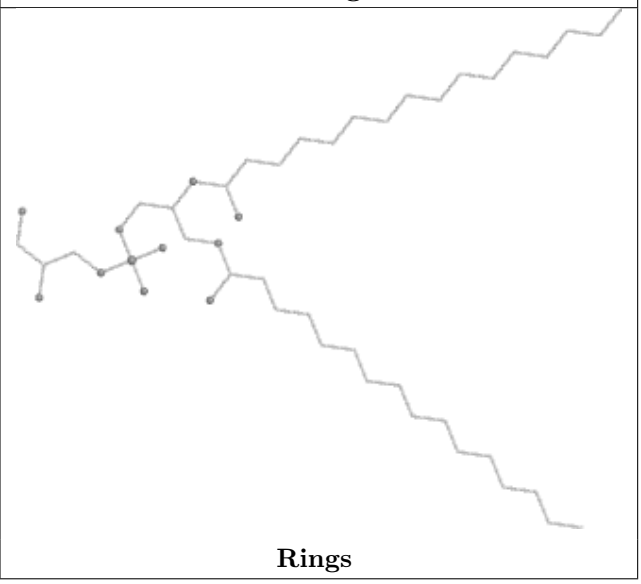
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Bond angles

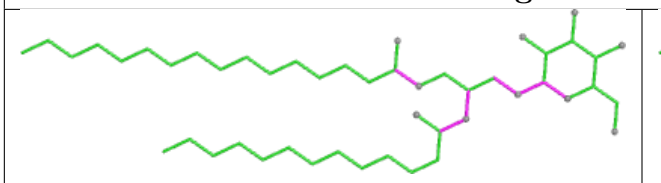


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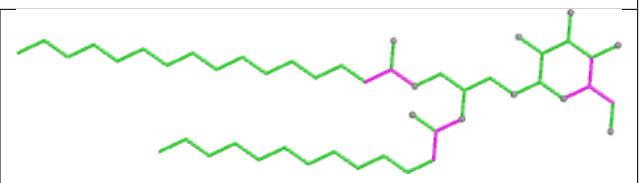


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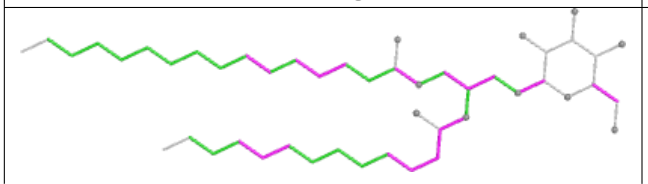
Ligand LMG W 201



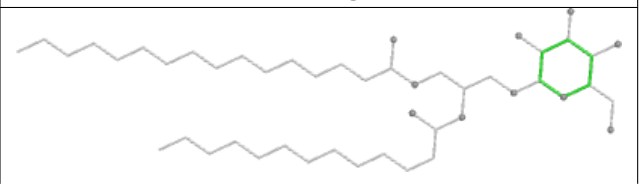
Bond lengths



Bond angles

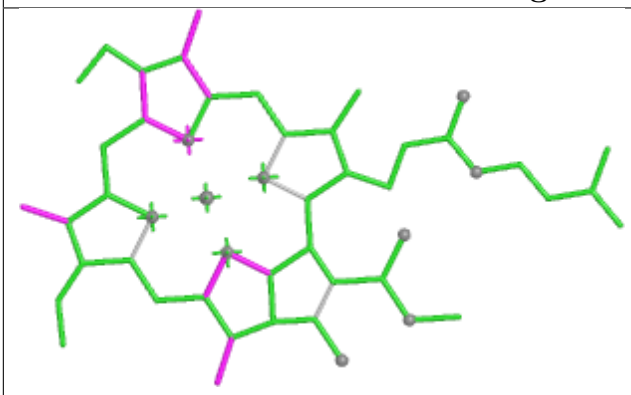


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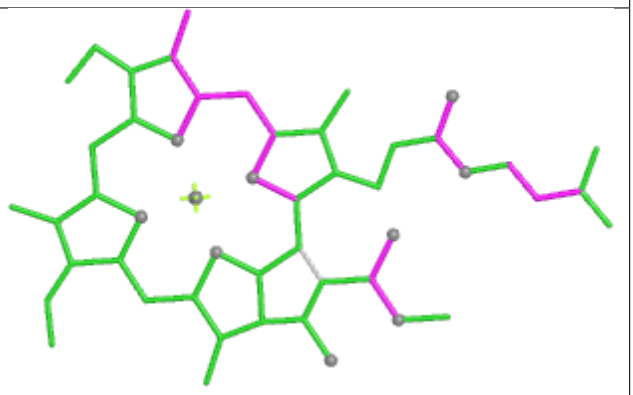


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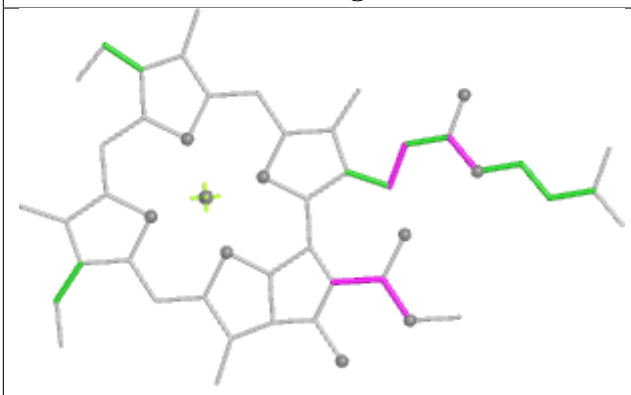
Ligand CLA s 303



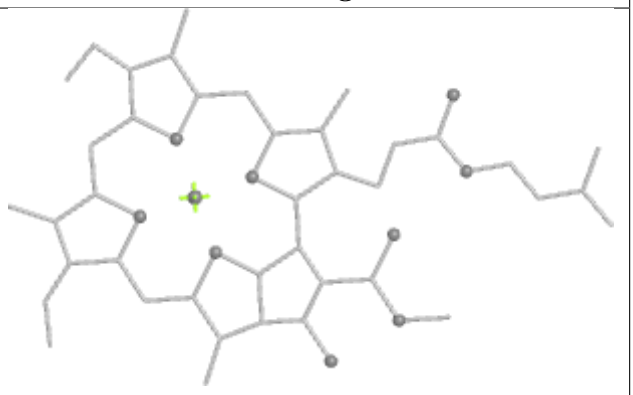
Bond lengths



Bond angles

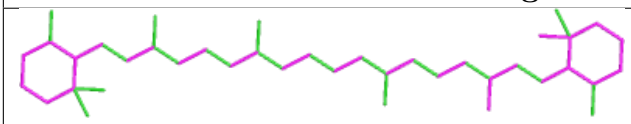


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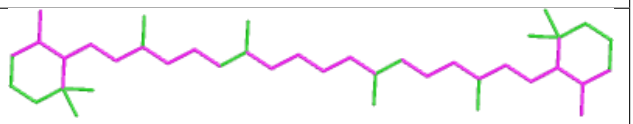


Rings

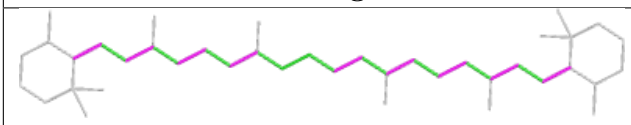
Ligand BCR K 101



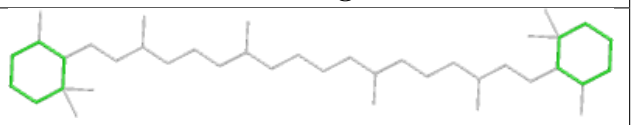
Bond lengths



Bond angles

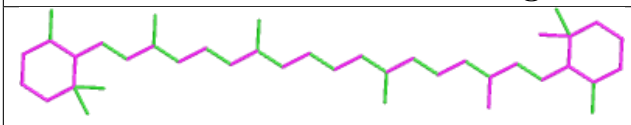


Torsions

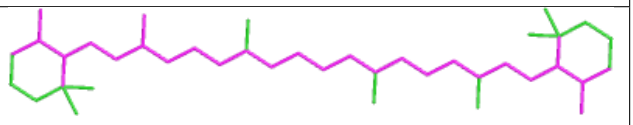


Rings

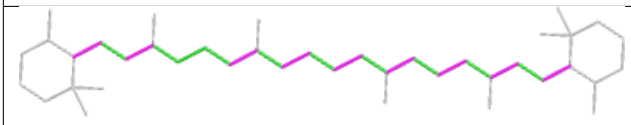
Ligand BCR B 619



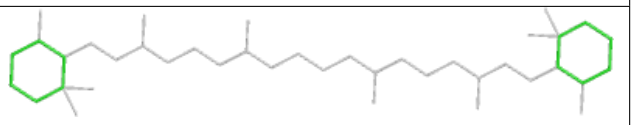
Bond lengths



Bond angles

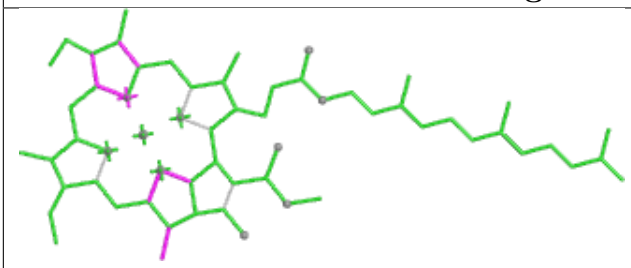


Torsions

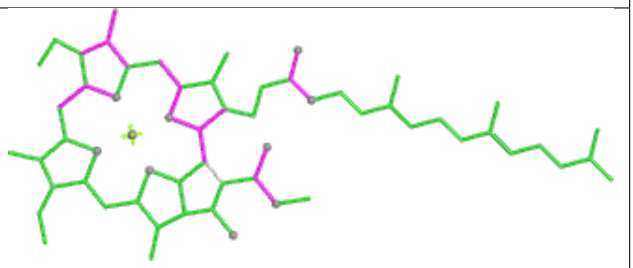


Rings

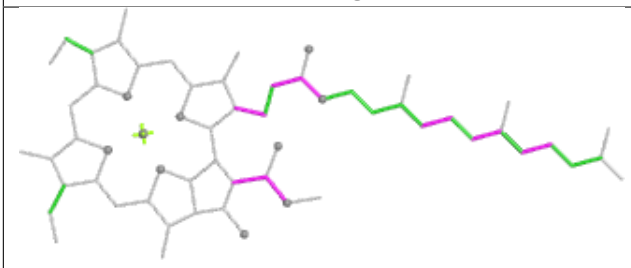
Ligand CLA P 307



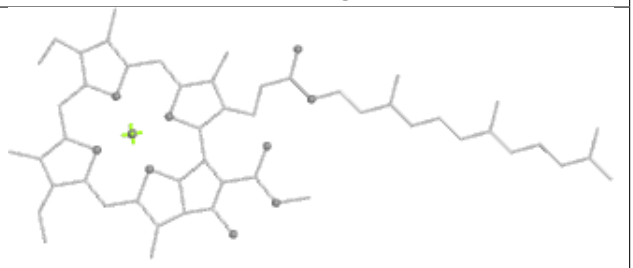
Bond lengths



Bond angles

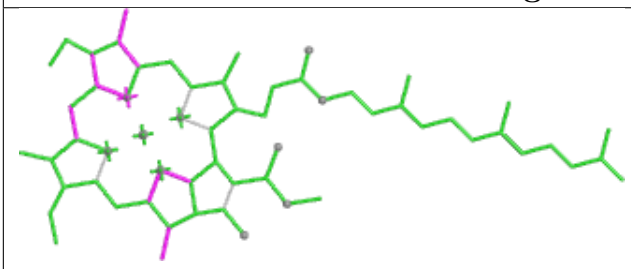


Torsions

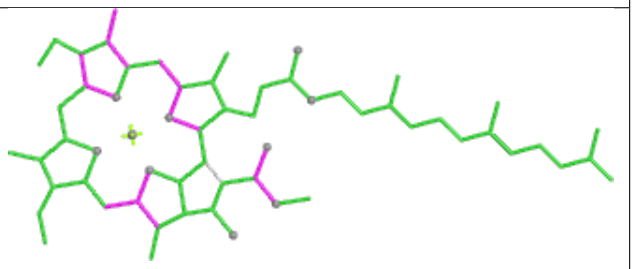


Rings

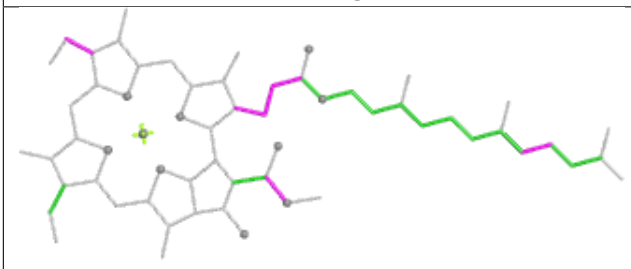
Ligand CLA R 303



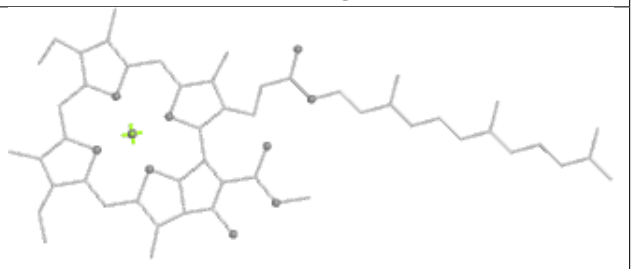
Bond lengths



Bond angles

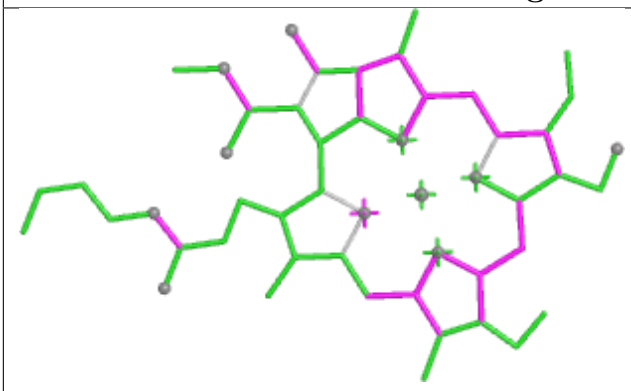


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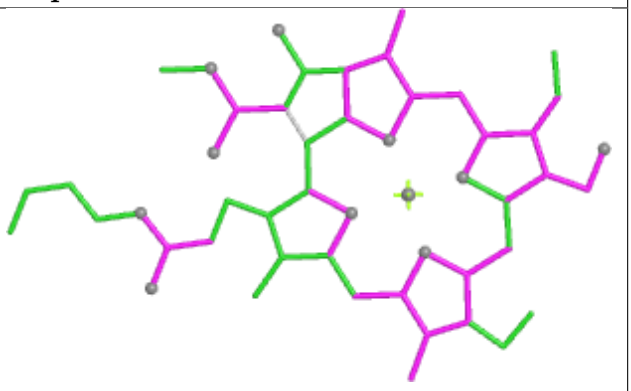


Rings

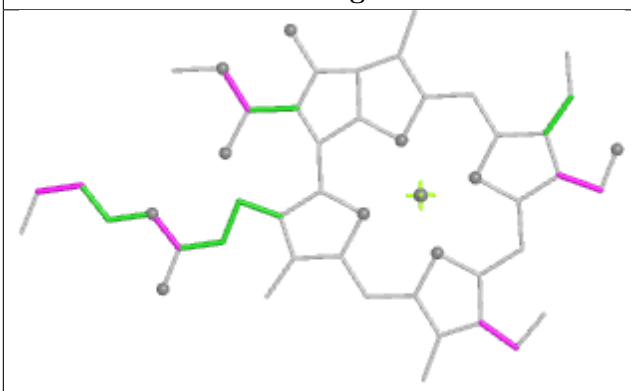
Ligand CHL p 316



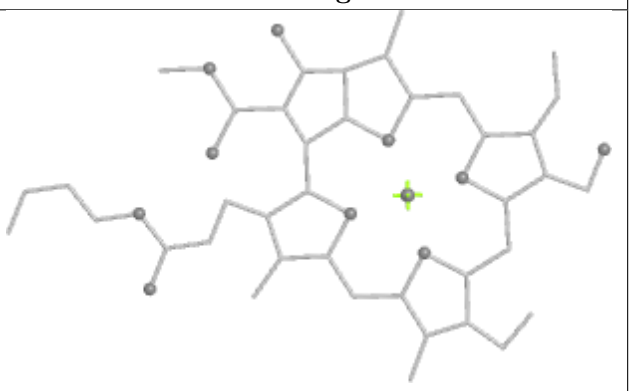
Bond lengths



Bond angles

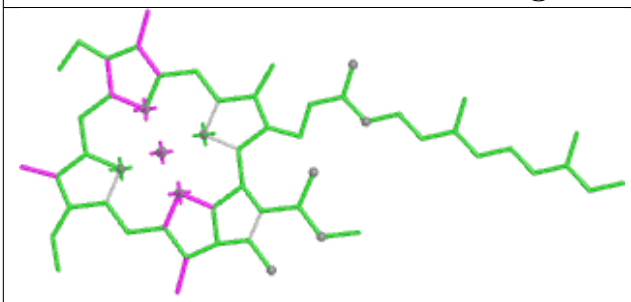


Torsions

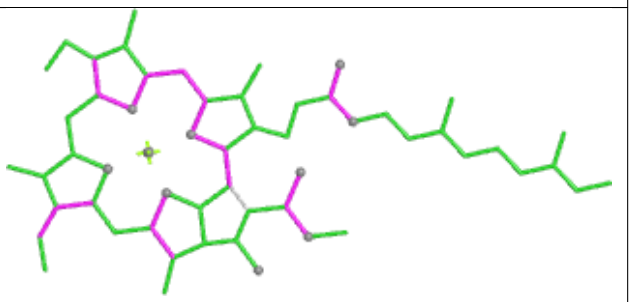


Rings

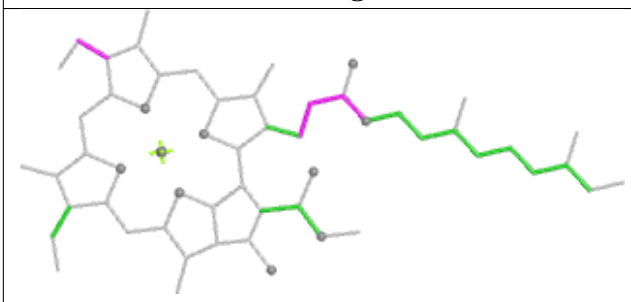
Ligand CLA s 306



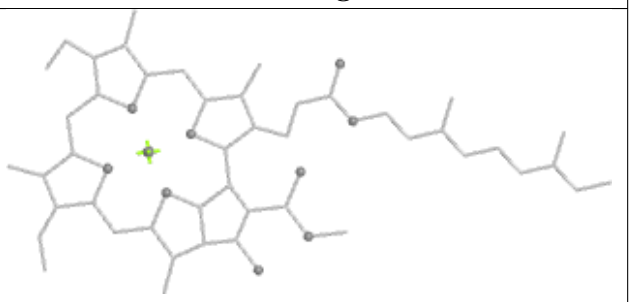
Bond lengths



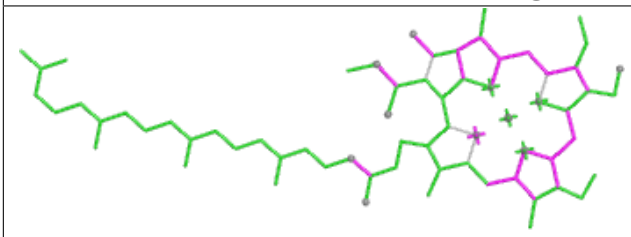
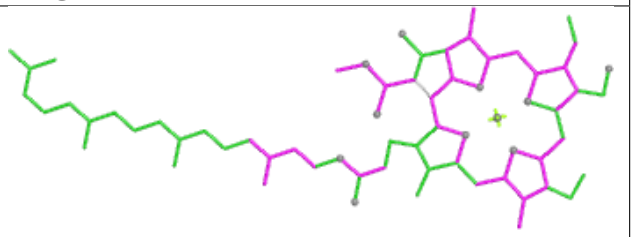
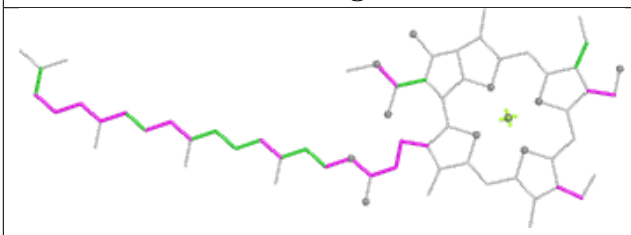
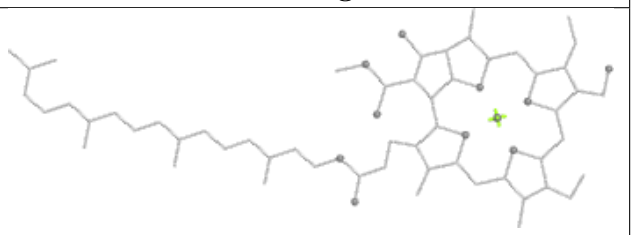
Bond angles

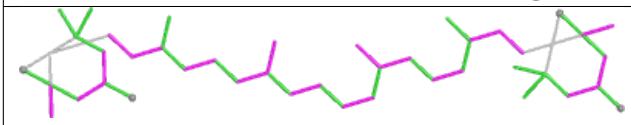
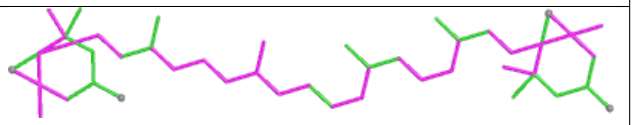
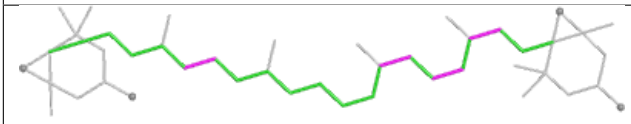
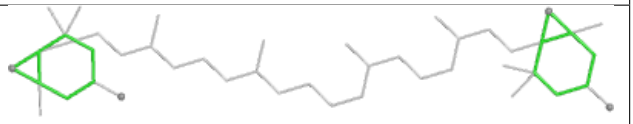


Torsions

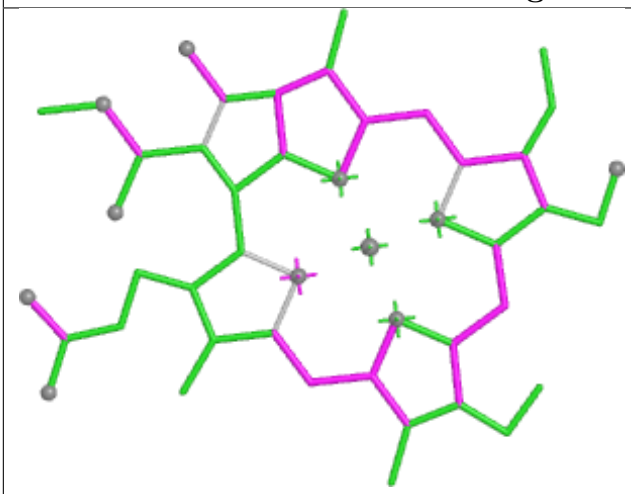


Rings

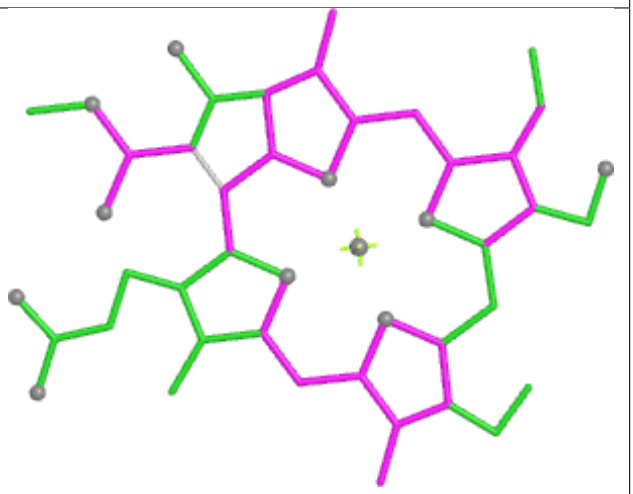
Ligand CHL g 314	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand XAT 5 311	
 Bond lengths	 Bond angles
 Torsions	 Rings

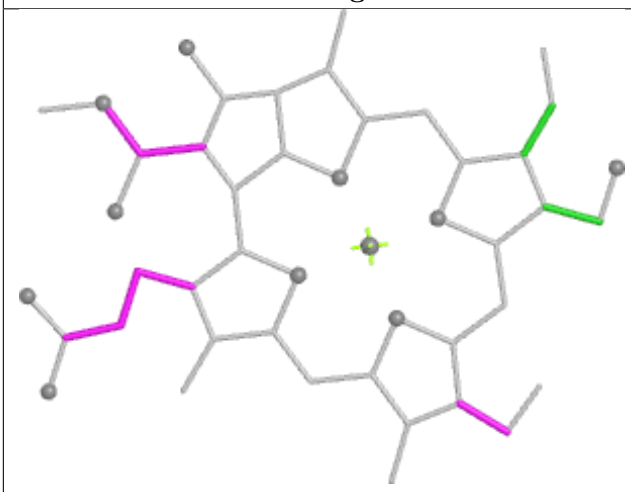
Ligand CHL S 314



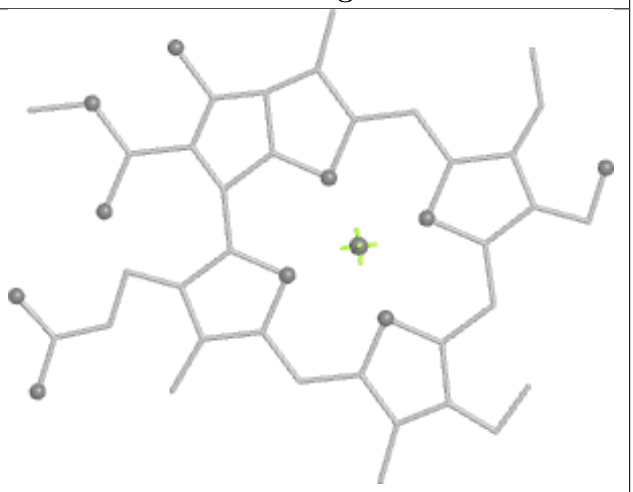
Bond lengths



Bond angles

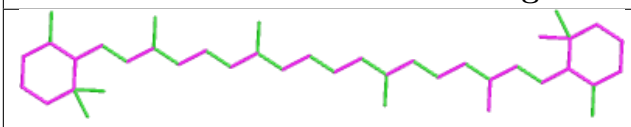


Torsions

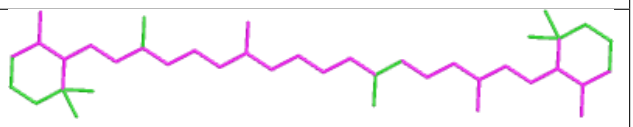


Rings

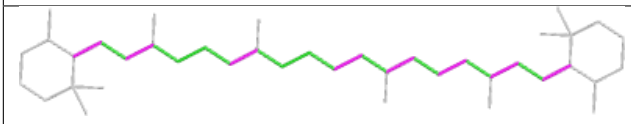
Ligand BCR D 404



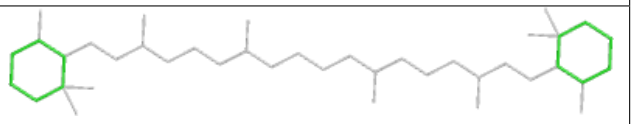
Bond lengths



Bond angles

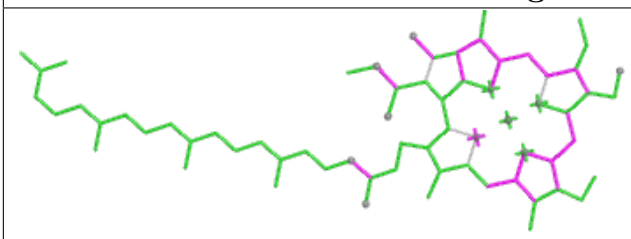


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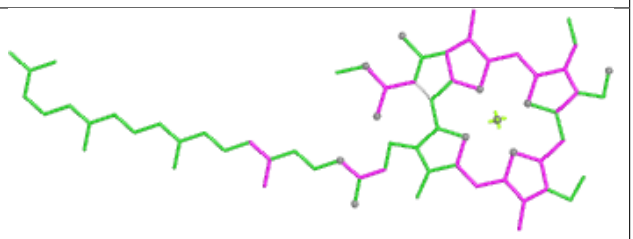


Rings

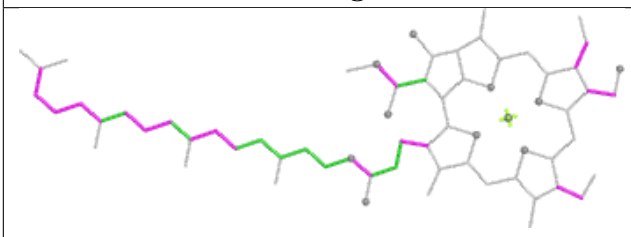
Ligand CHL v 318



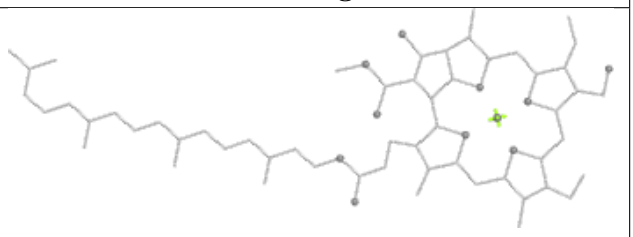
Bond lengths



Bond angles

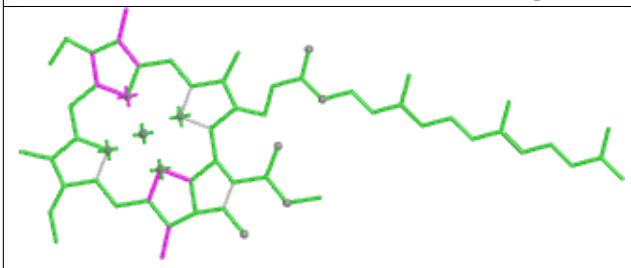


Torsions

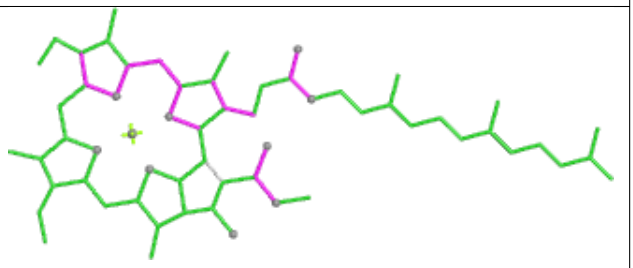


Rings

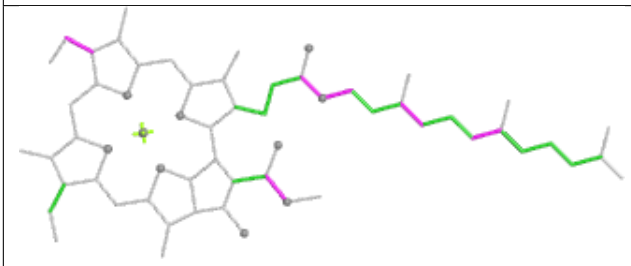
Ligand CLA 1 305



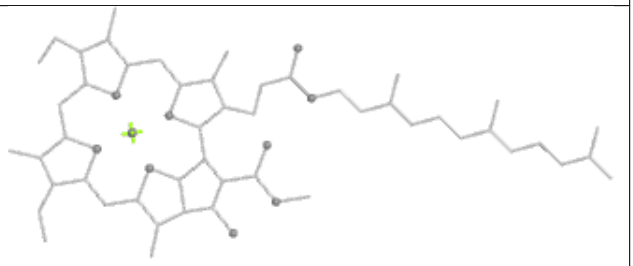
Bond lengths



Bond angles



Torsions



Rings

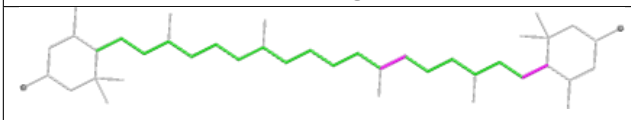
Ligand LUT U 309



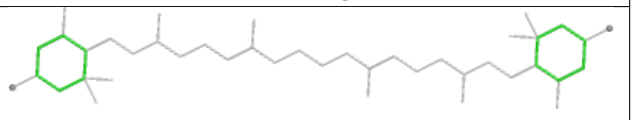
Bond lengths



Bond angles

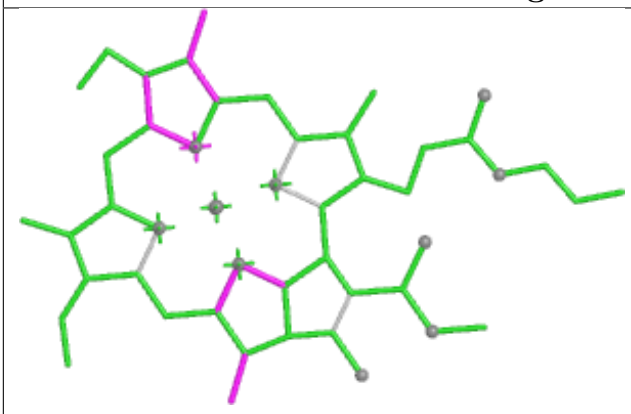


Torsions

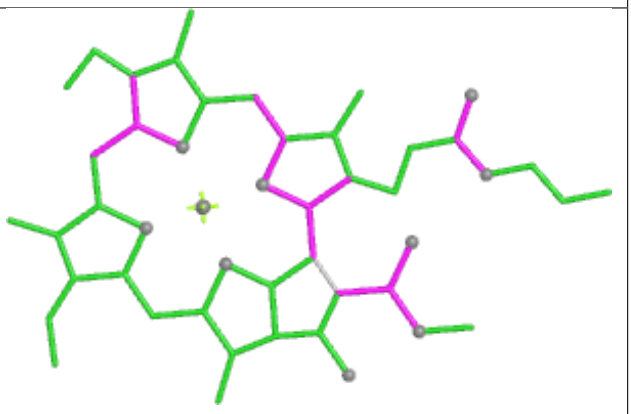


Rings

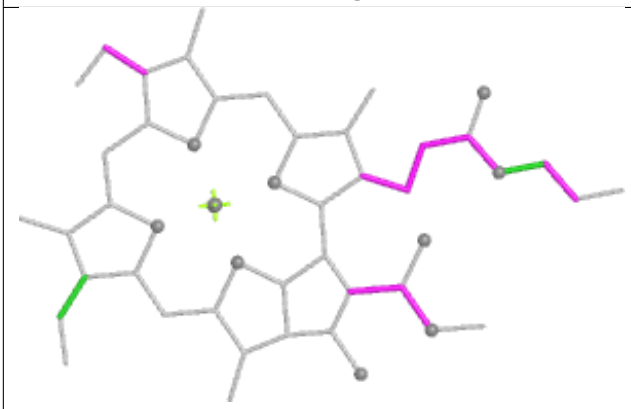
Ligand CLA n 308



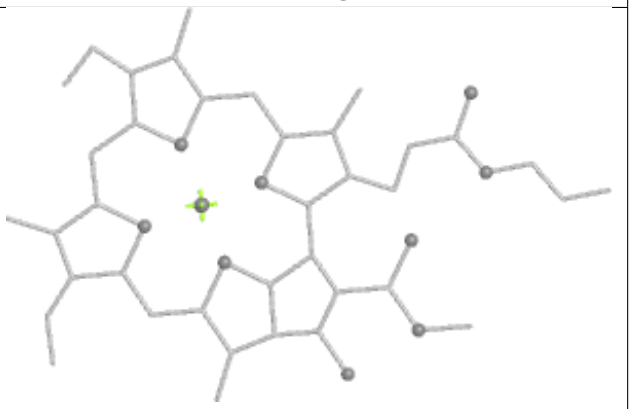
Bond lengths



Bond angles

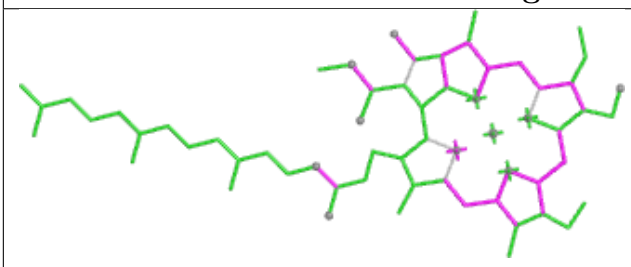


Torsions

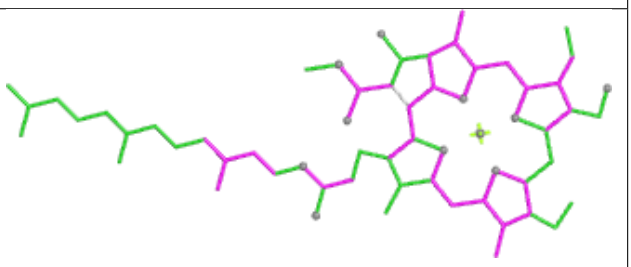


Rings

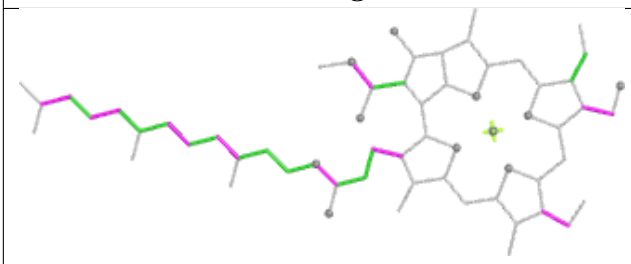
Ligand CHL G 316



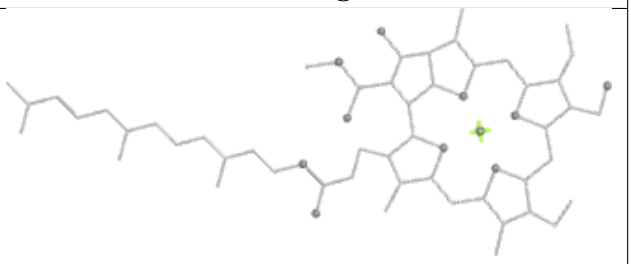
Bond lengths



Bond angles

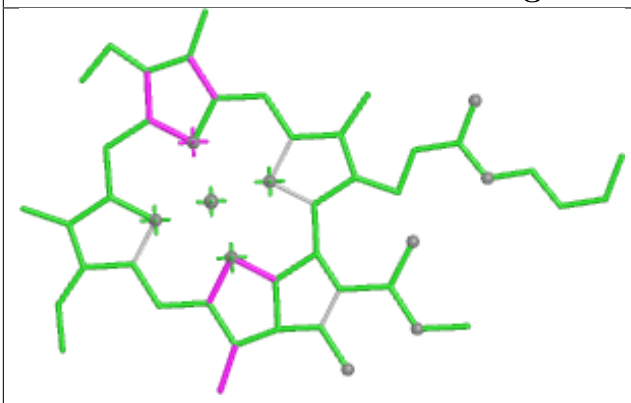


Torsions

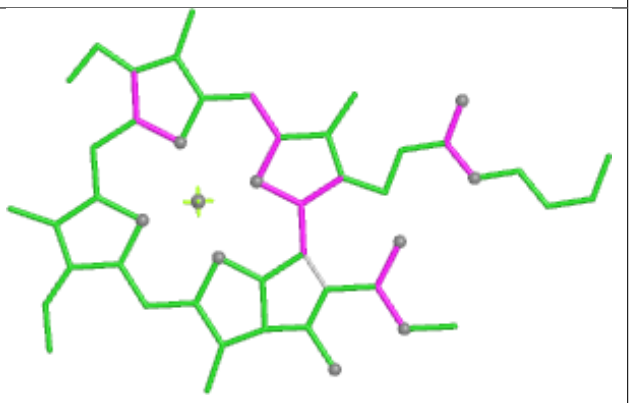


Rings

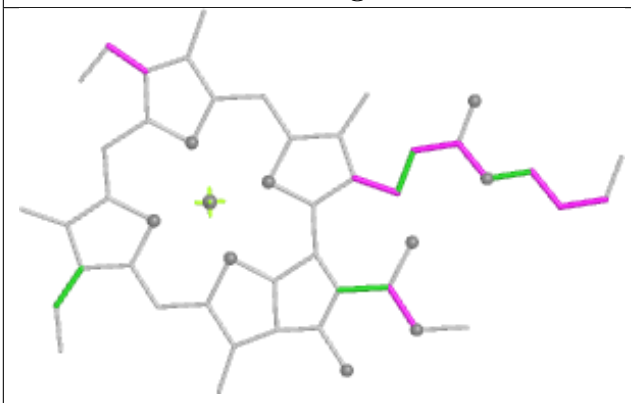
Ligand CLA R 308



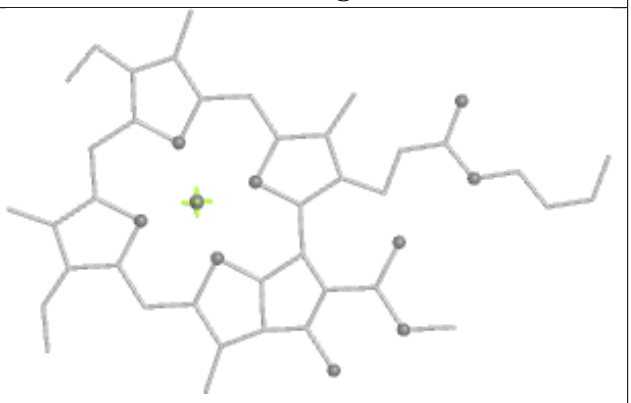
Bond lengths



Bond angles

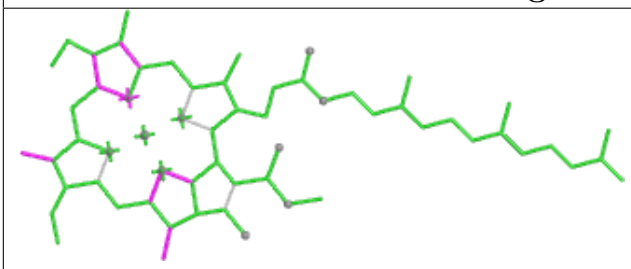


Torsions

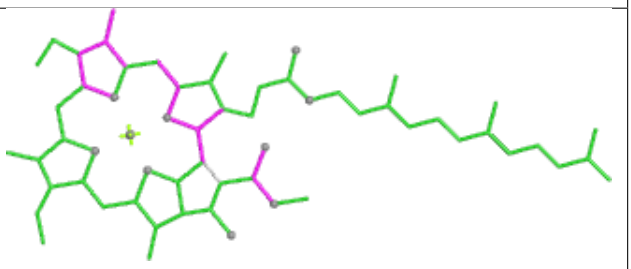


Rings

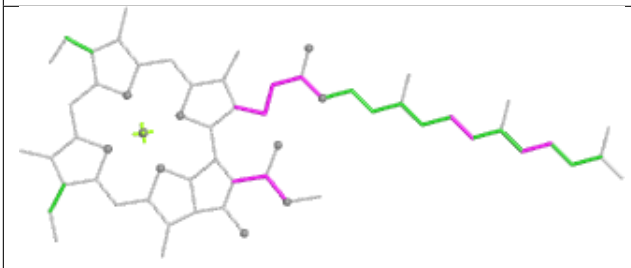
Ligand CLA 5 306



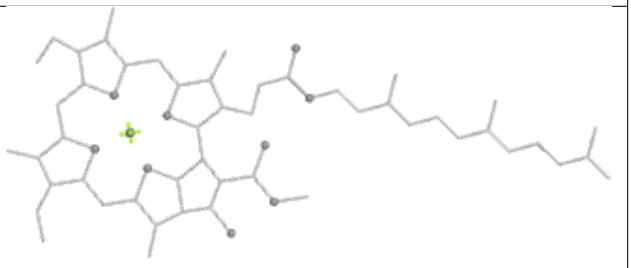
Bond lengths



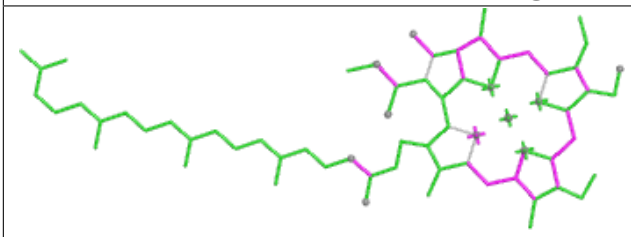
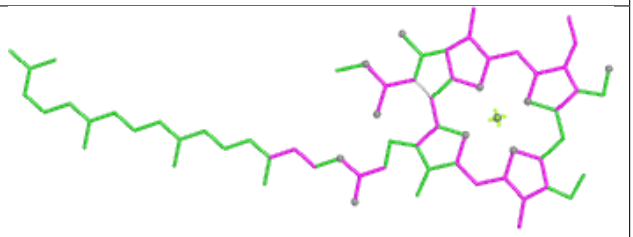
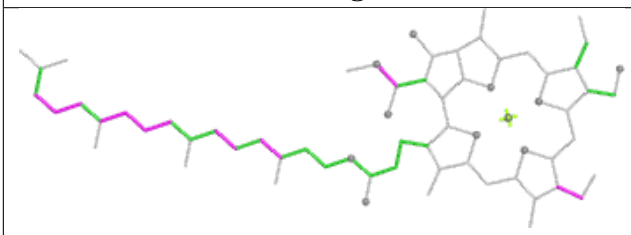
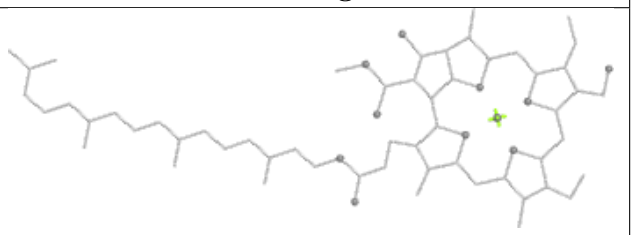
Bond angles

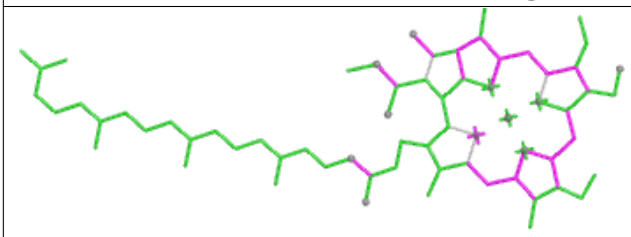
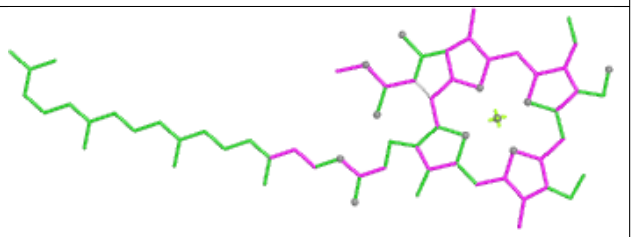
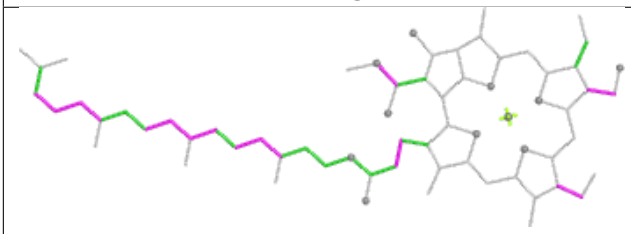
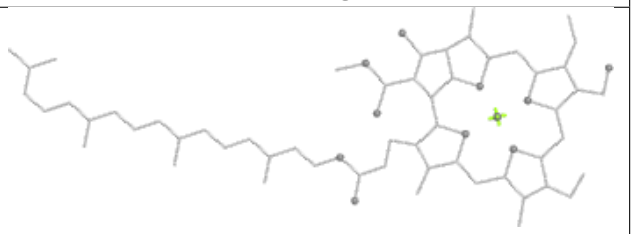


Torsions

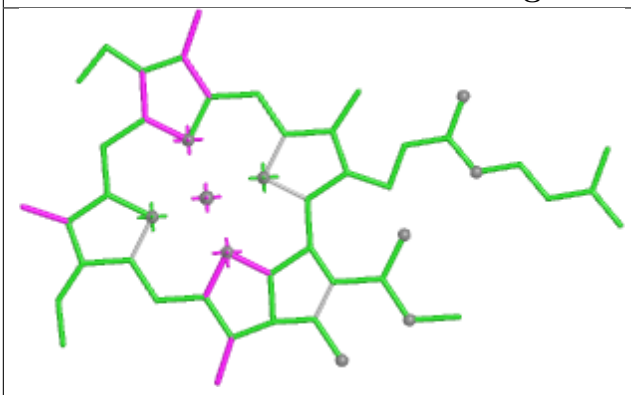


Rings

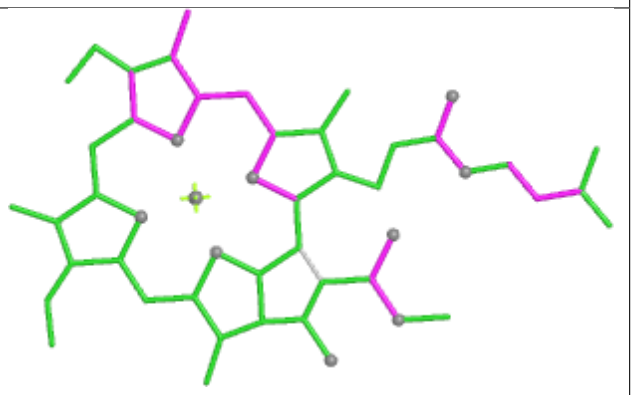
Ligand CHL 2 317	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CHL G 314	
 Bond lengths	 Bond angles
 Torsions	 Rings

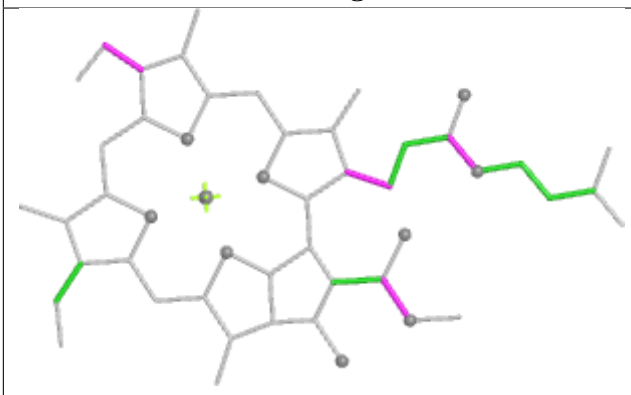
Ligand CLA V 303



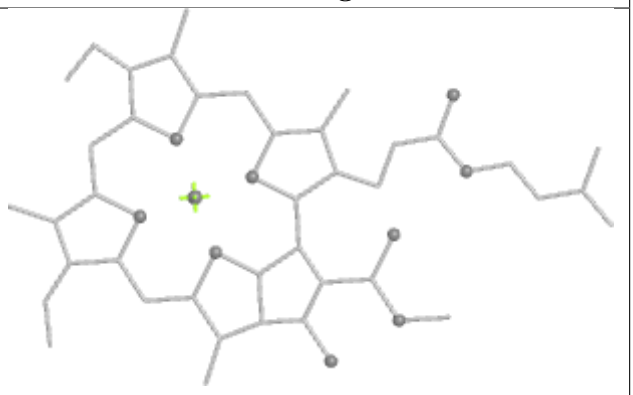
Bond lengths



Bond angles

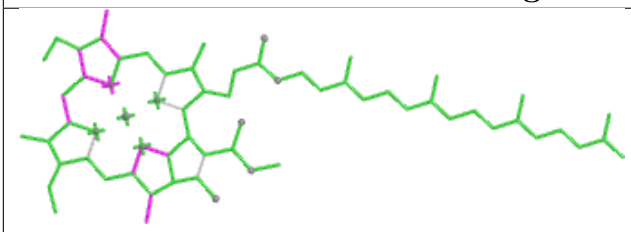


Torsions

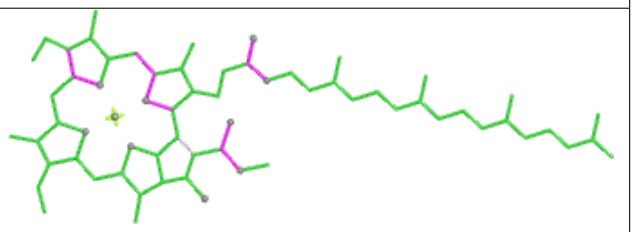


Rings

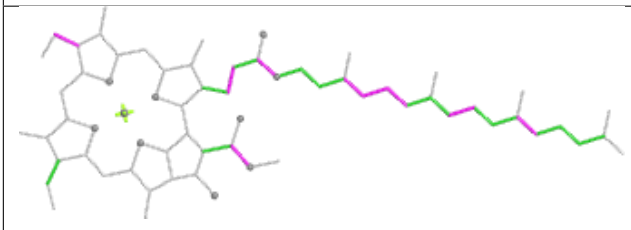
Ligand CLA G 307



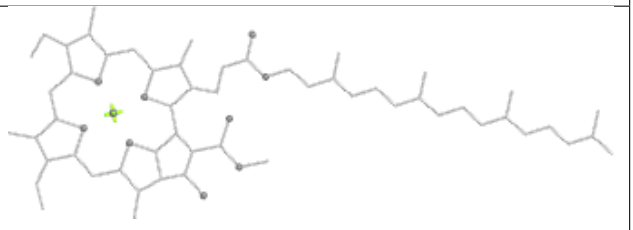
Bond lengths



Bond angles

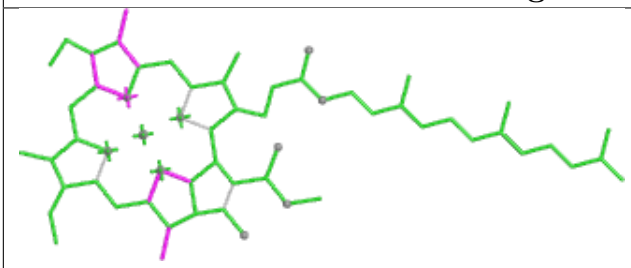


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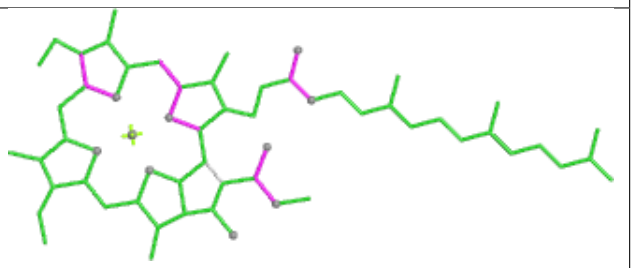


Rings

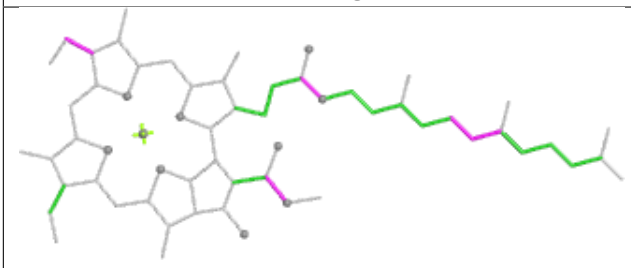
Ligand CLA v 305



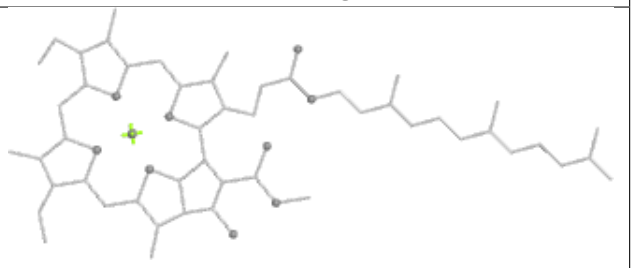
Bond lengths



Bond angles

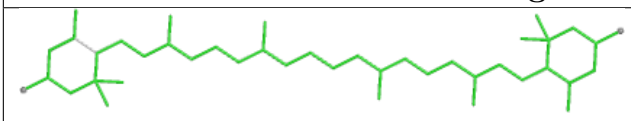


Torsions

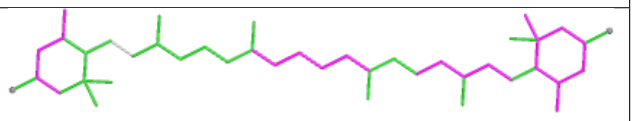


Rings

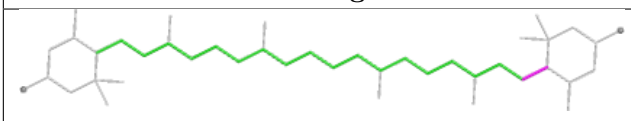
Ligand LUT 5 310



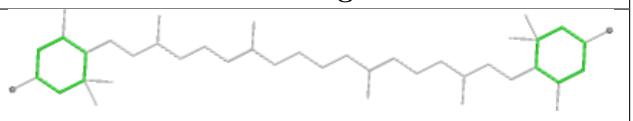
Bond lengths



Bond angles

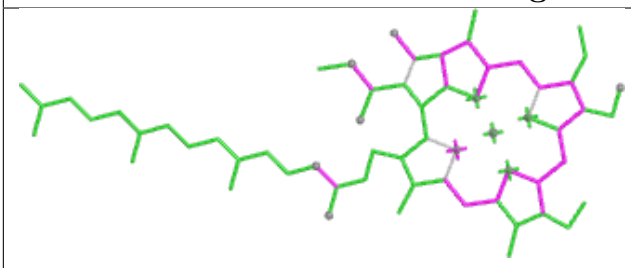


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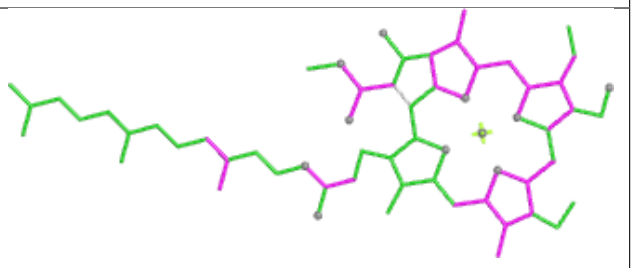


Rings

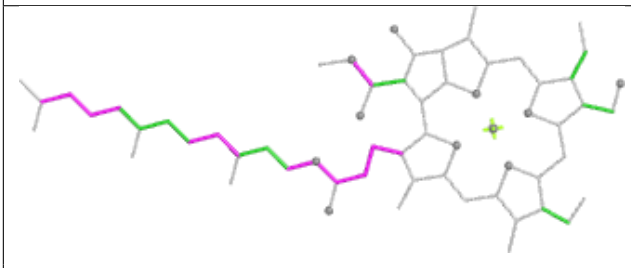
Ligand CHL r 616



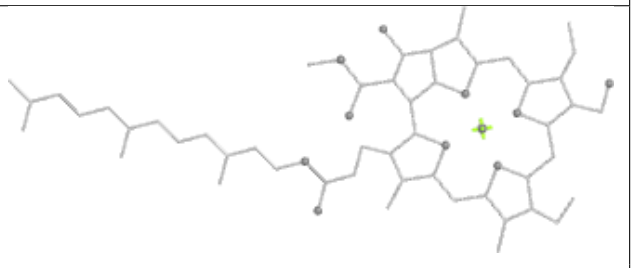
Bond lengths



Bond angles

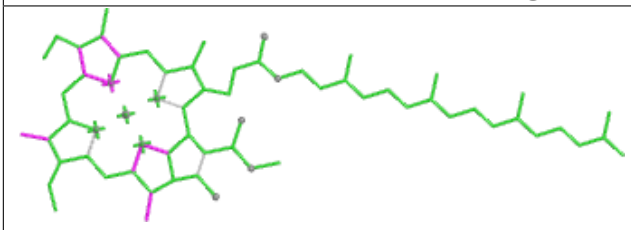


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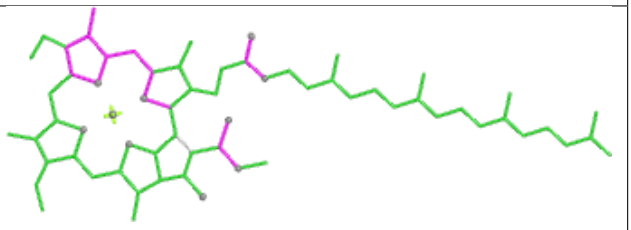


Rings

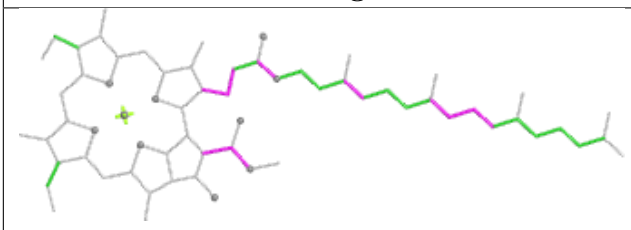
Ligand CLA B 608



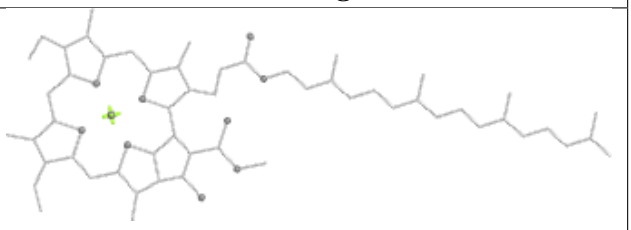
Bond lengths



Bond angles

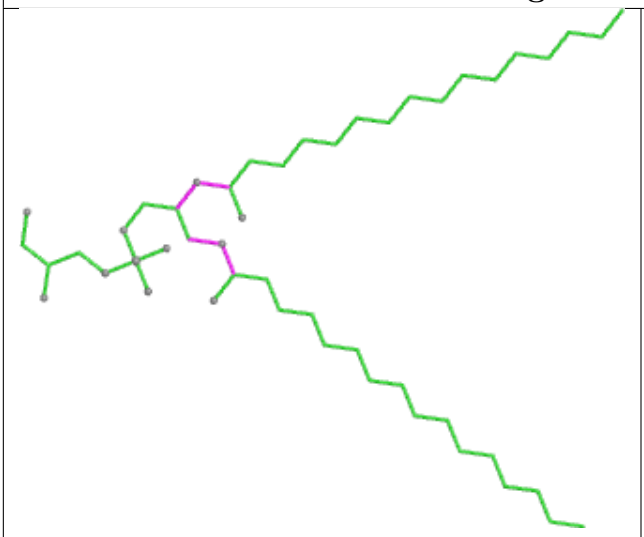


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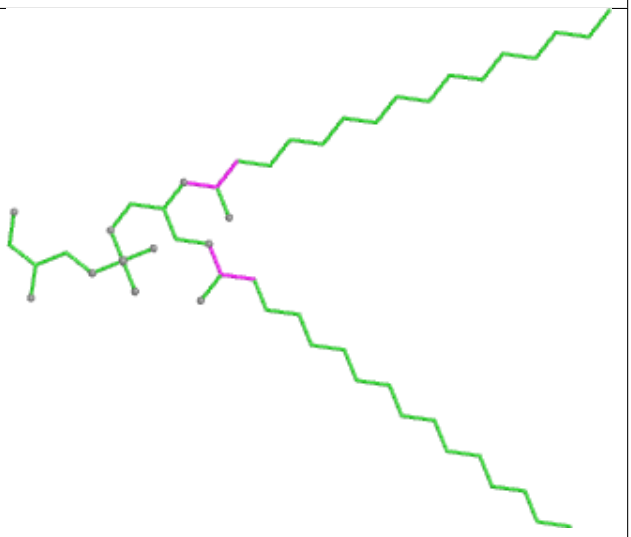


Rings

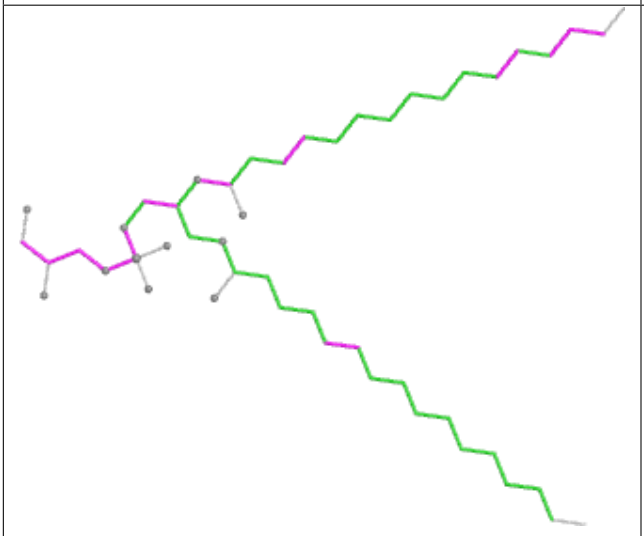
Ligand LHG c 523



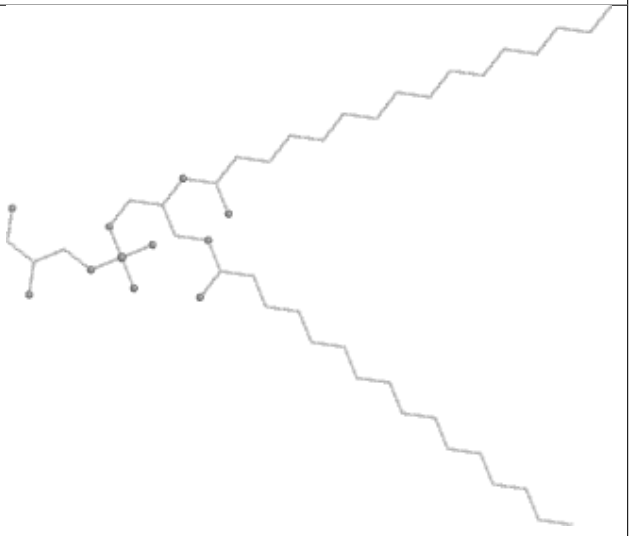
Bond lengths



Bond angles

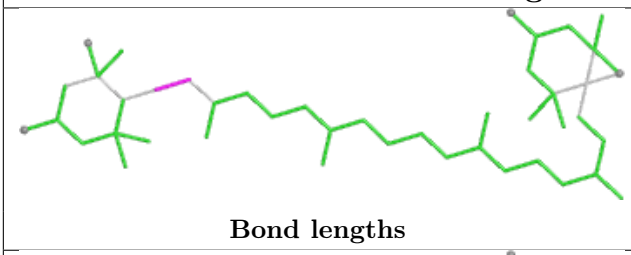


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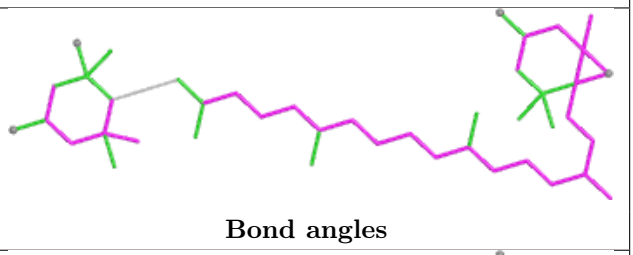


Rings

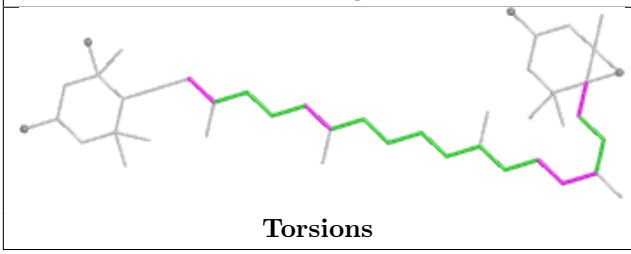
Ligand NEX u 319



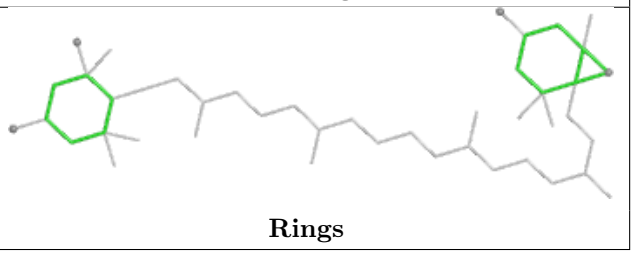
Bond lengths



Bond angles

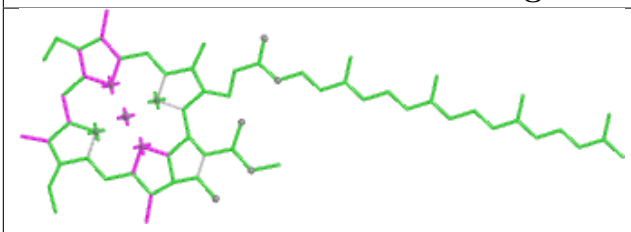


Torsions

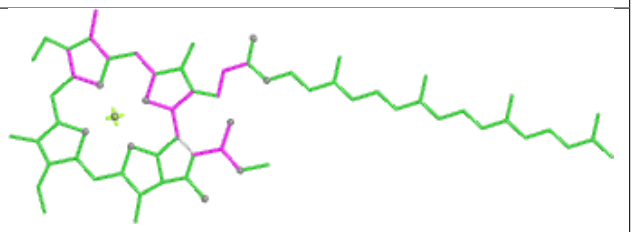


Rings

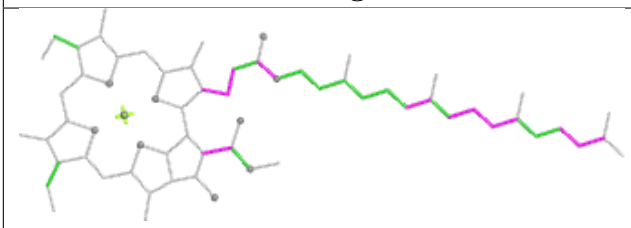
Ligand CLA B 613



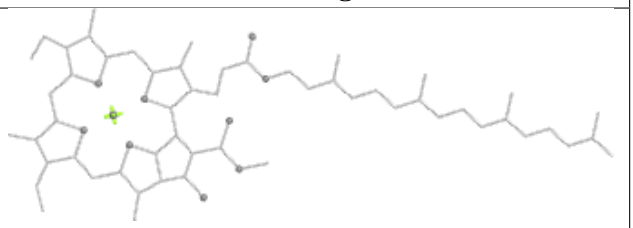
Bond lengths



Bond angles

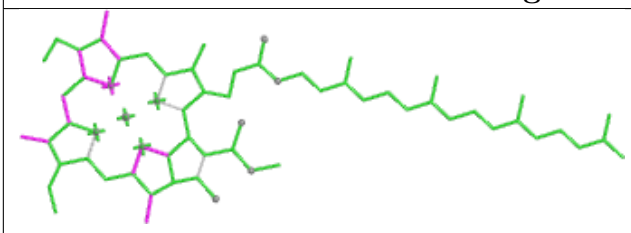


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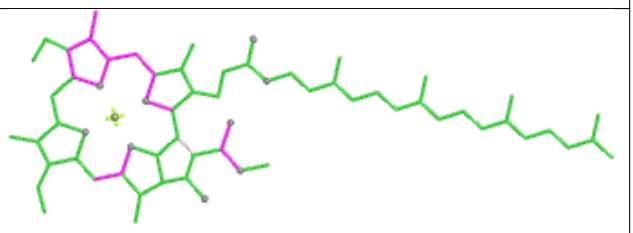


Rings

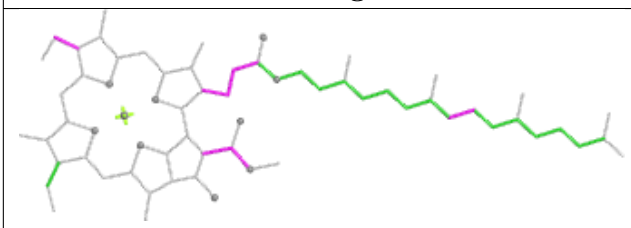
Ligand CLA U 301



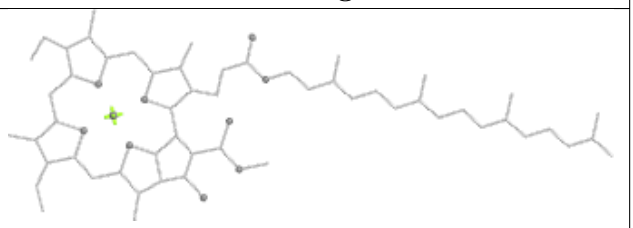
Bond lengths



Bond angles

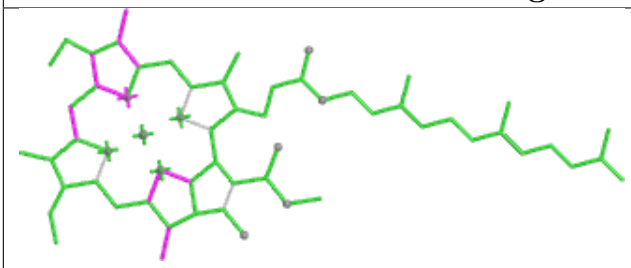


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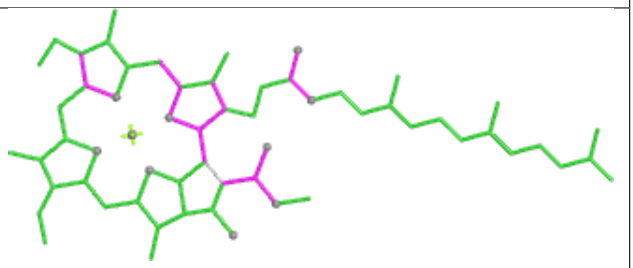


Rings

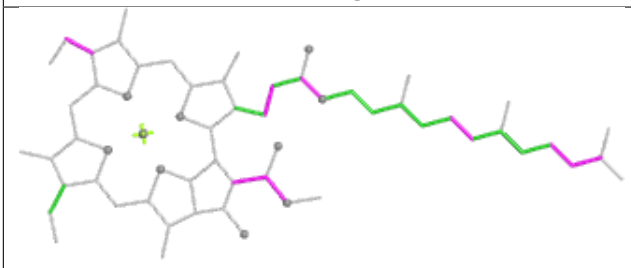
Ligand CLA 3 305



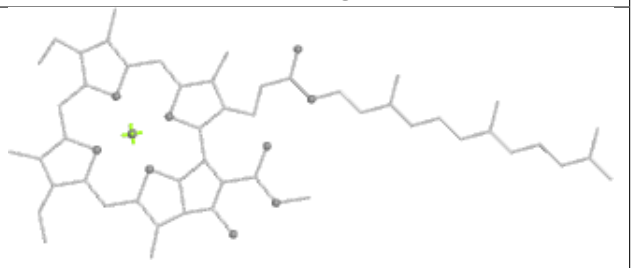
Bond lengths



Bond angles

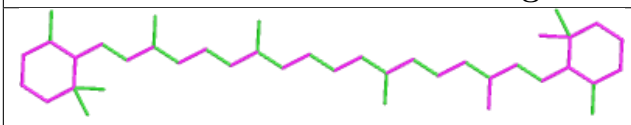


Torsions

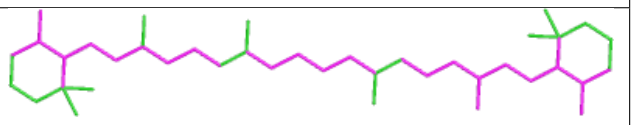


Rings

Ligand BCR A 409



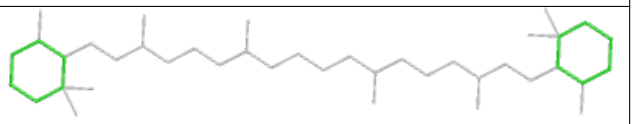
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Bond angles

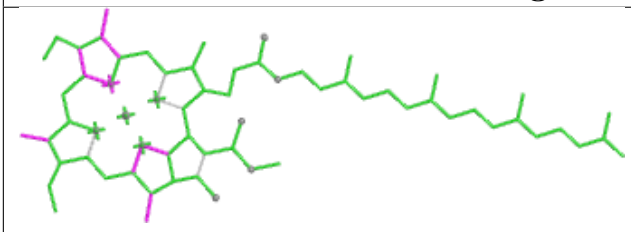


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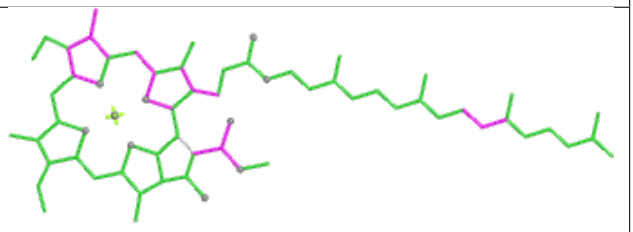


Rings

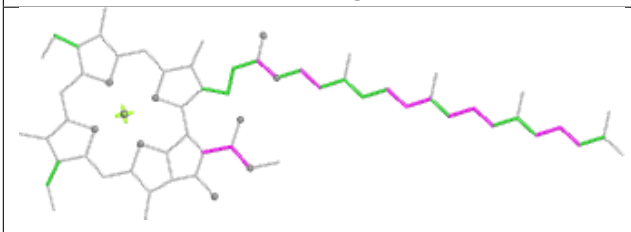
Ligand CLA c 510



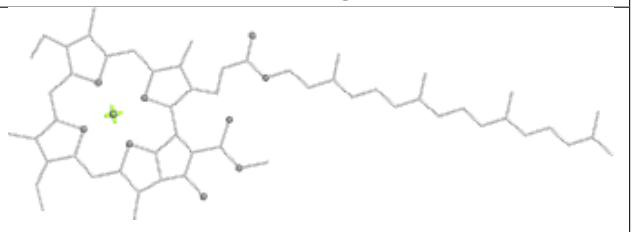
Bond lengths



Bond angles

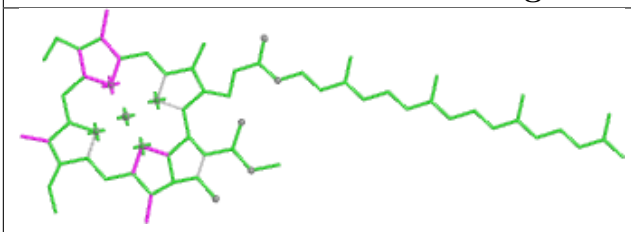


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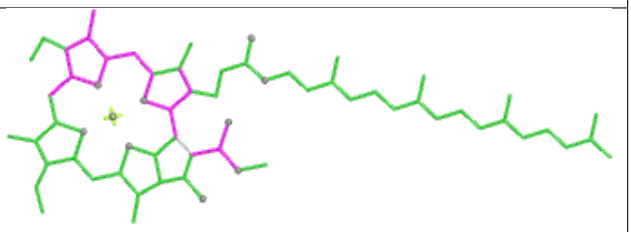


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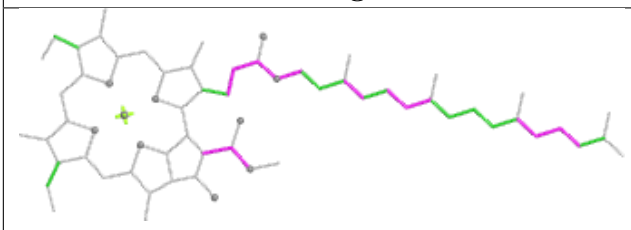
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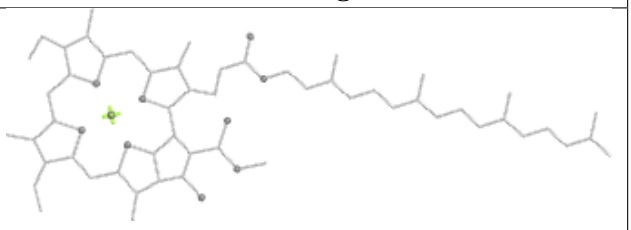
Bond lengths



Bond angles

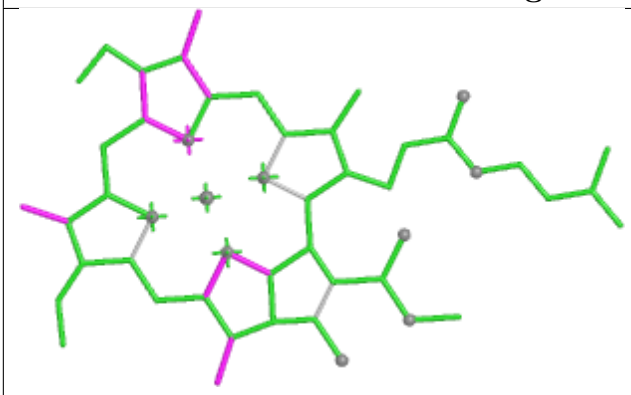


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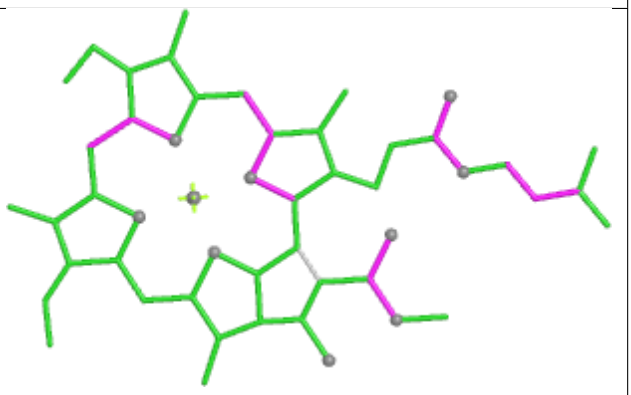


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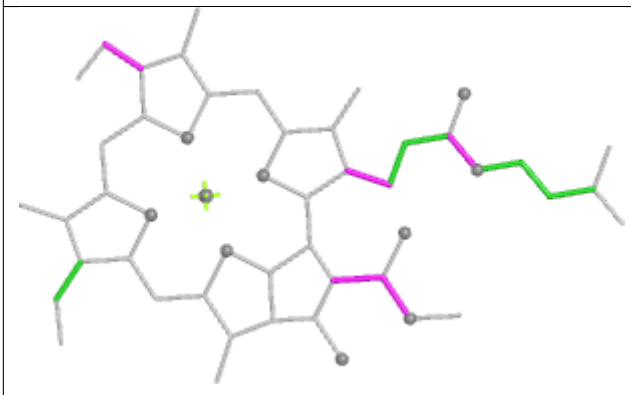
Ligand CLA P 304



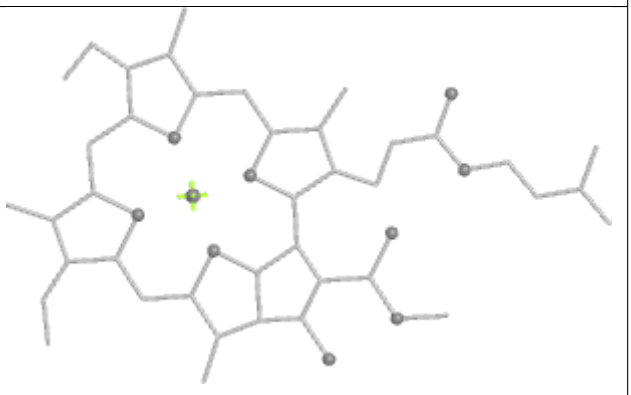
Bond lengths



Bond angles

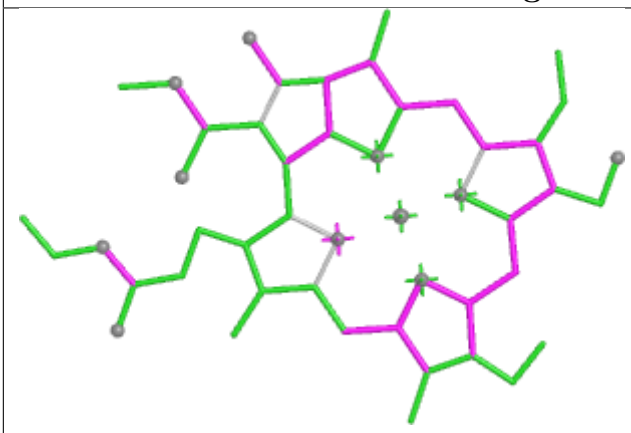


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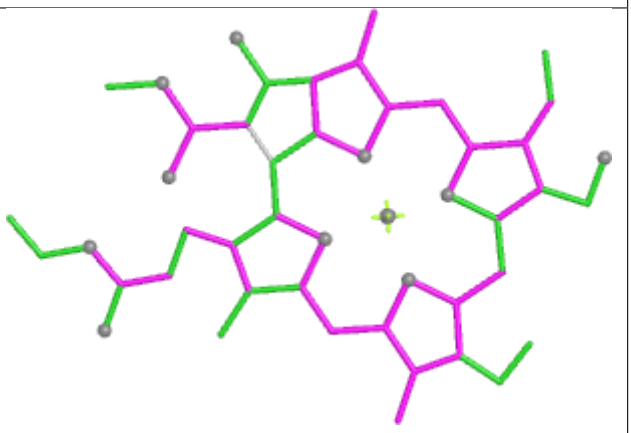


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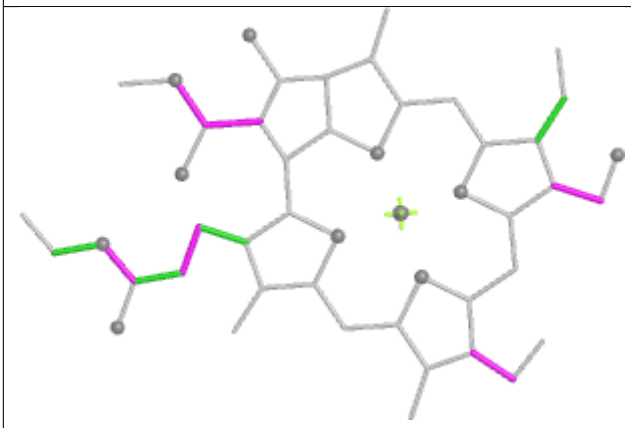
Ligand CHL V 314



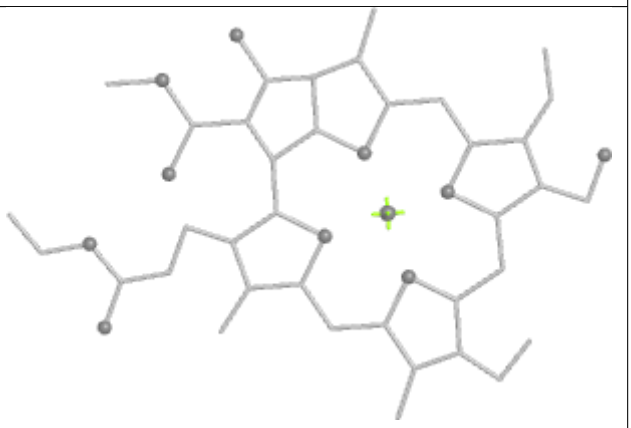
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Bond angles

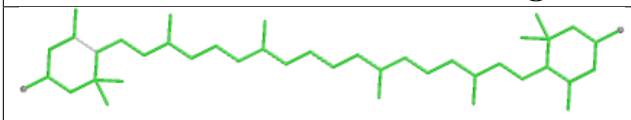


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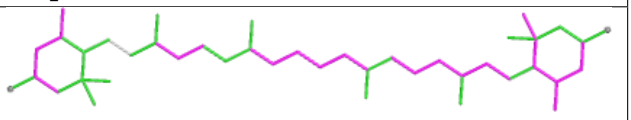


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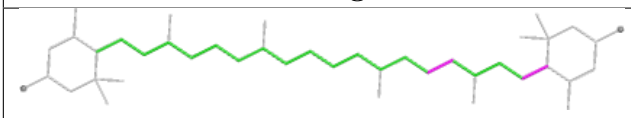
Ligand LUT p 311



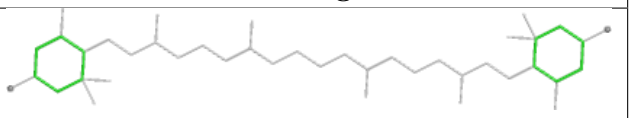
Bond lengths



Bond angles

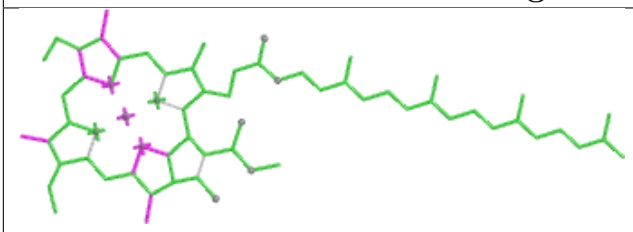


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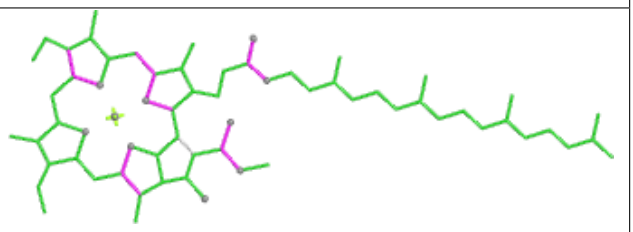


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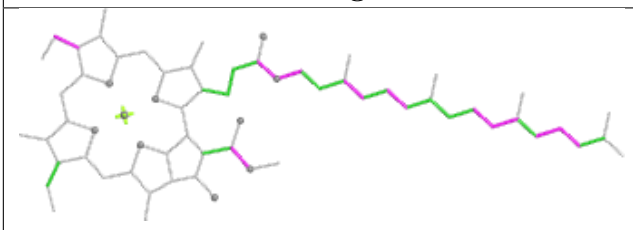
Ligand CLA d 402



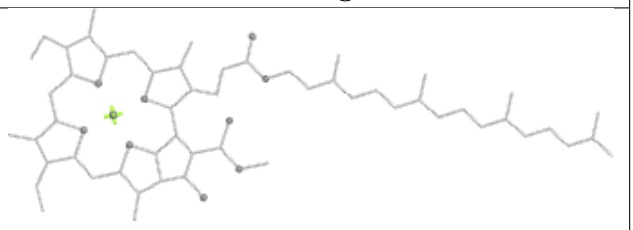
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Bond angles

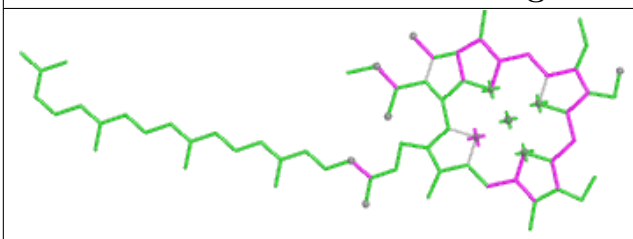


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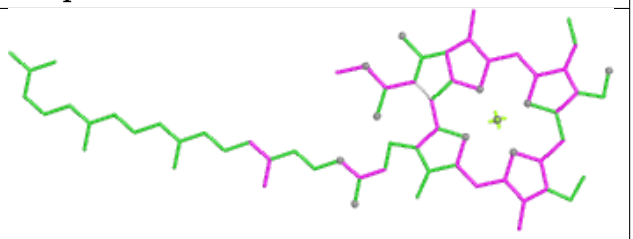


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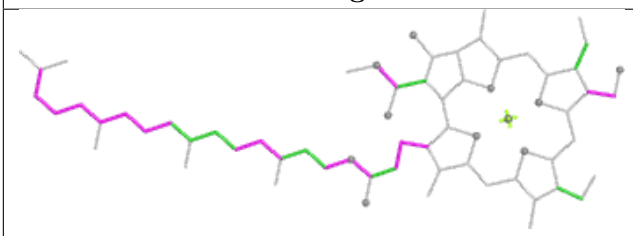
Ligand CHL q 314



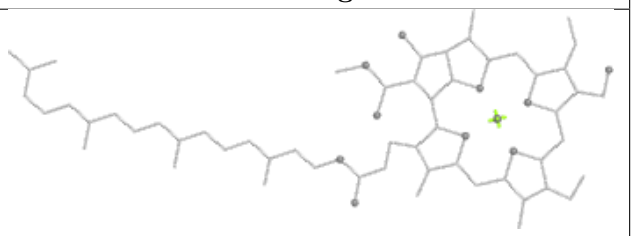
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Bond angles

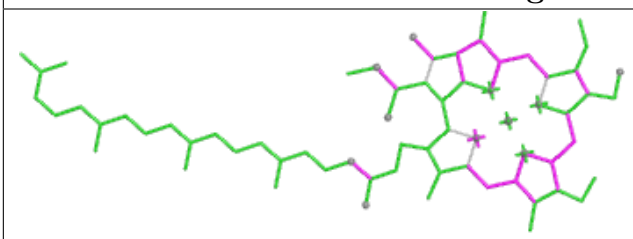


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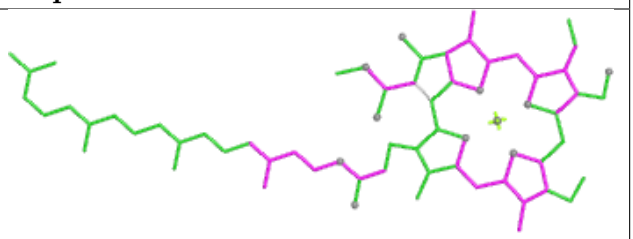


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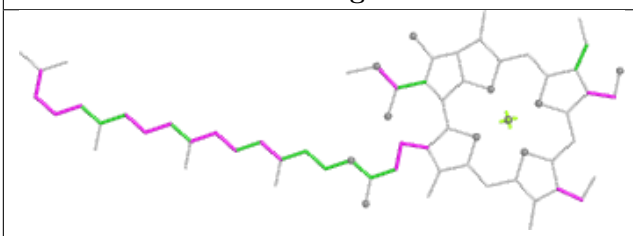
Ligand CHL p 318



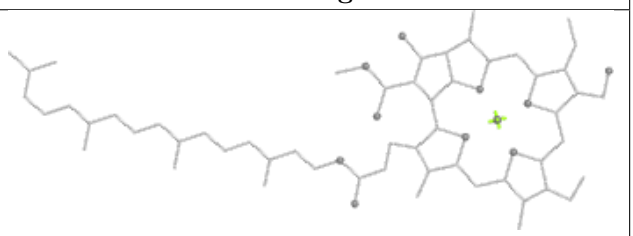
Bond lengths



Bond angles

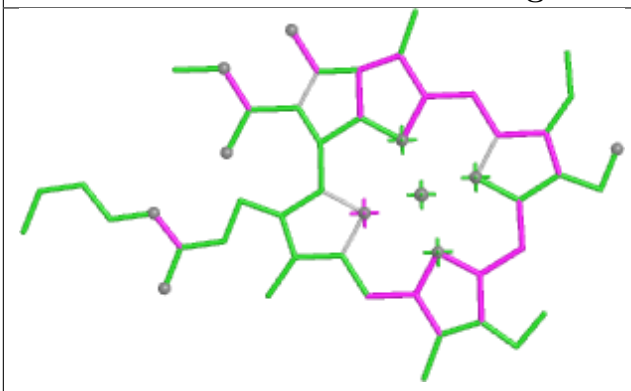


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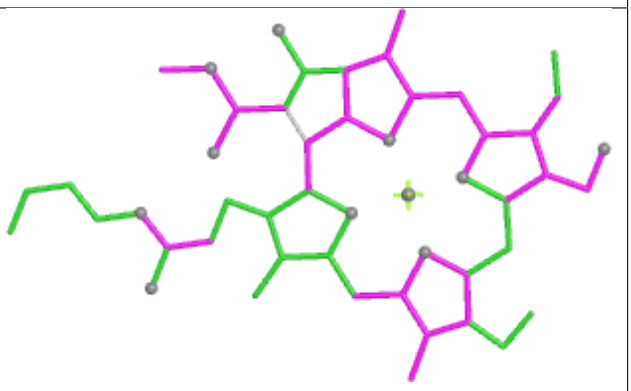


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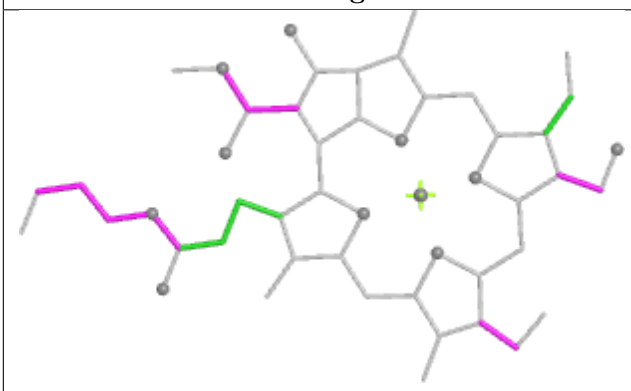
Ligand CHL n 315



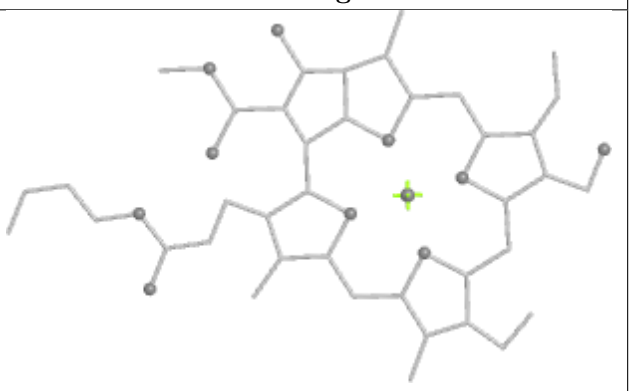
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Bond angles

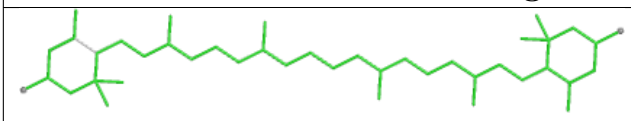


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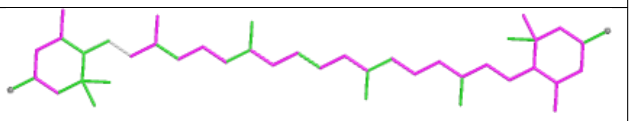


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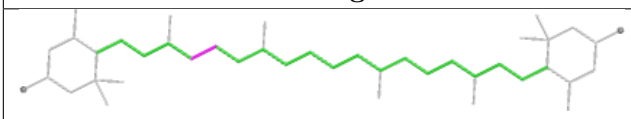
Ligand LUT N 310



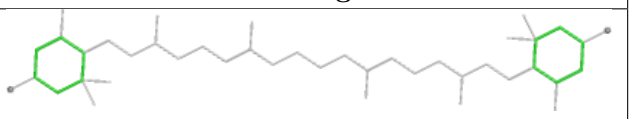
Bond lengths



Bond angles

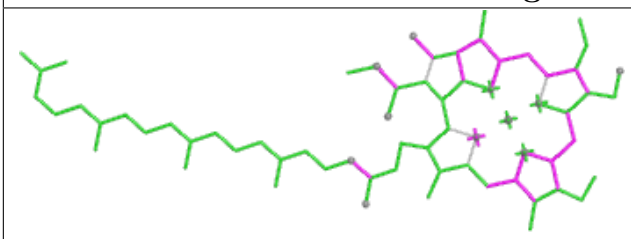


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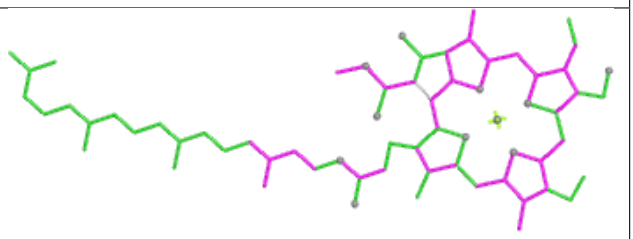


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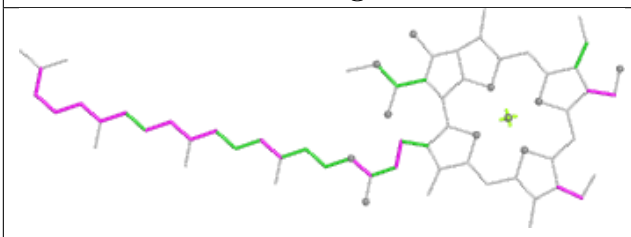
Ligand CHL V 316



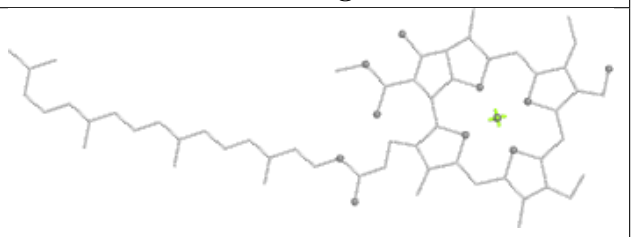
Bond lengths



Bond angles

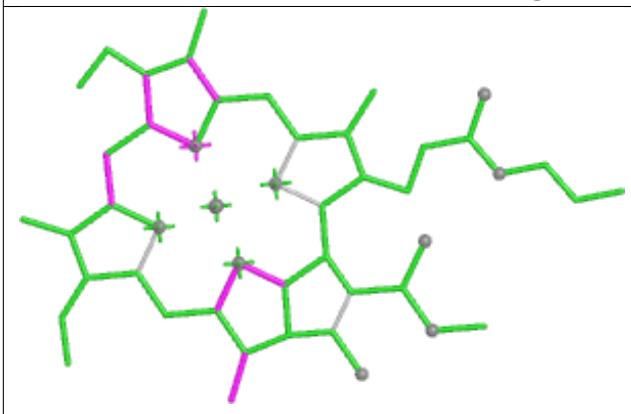


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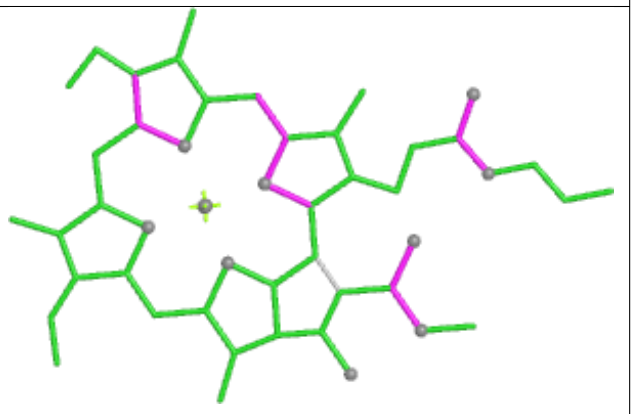


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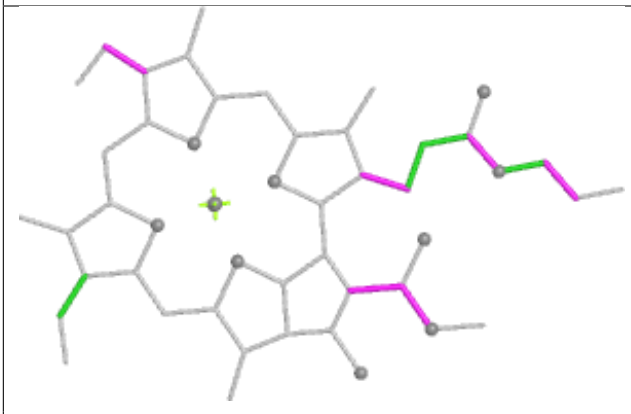
Ligand CLA 6 309



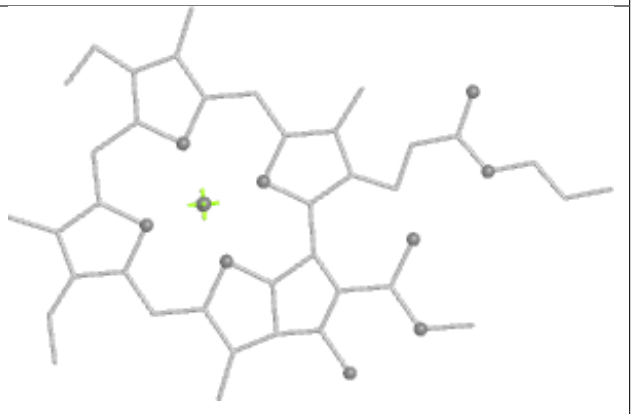
Bond lengths



Bond angles

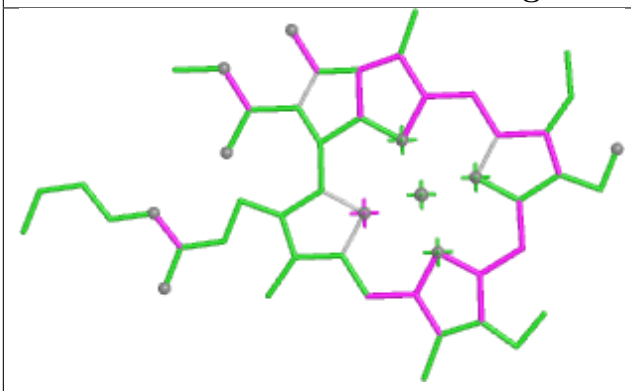


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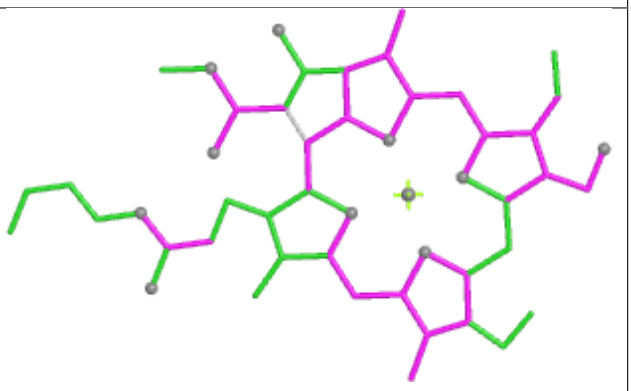


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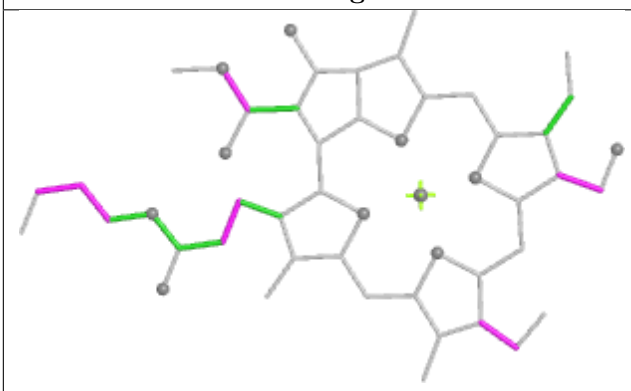
Ligand CHL N 315



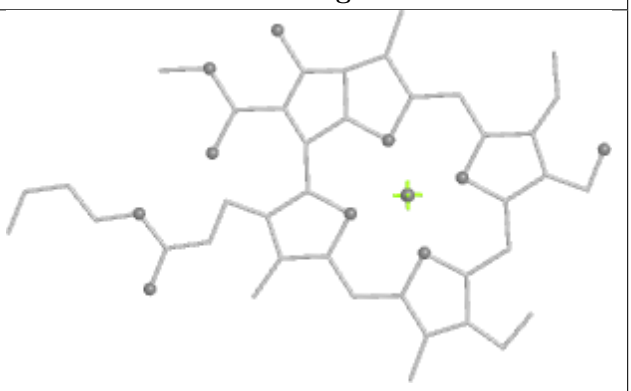
Bond lengths



Bond angles

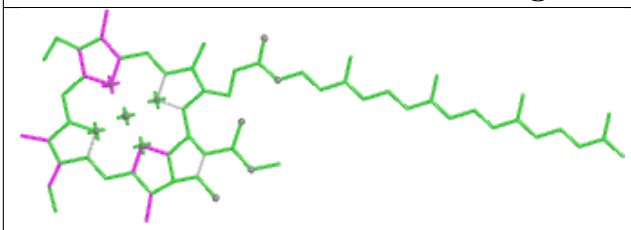


Torsions

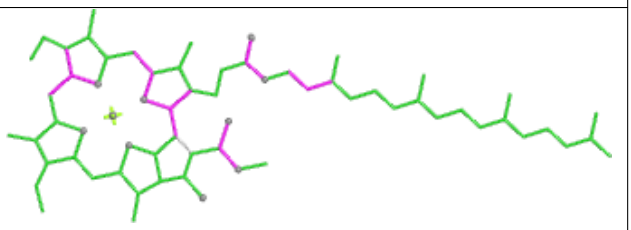


Rings

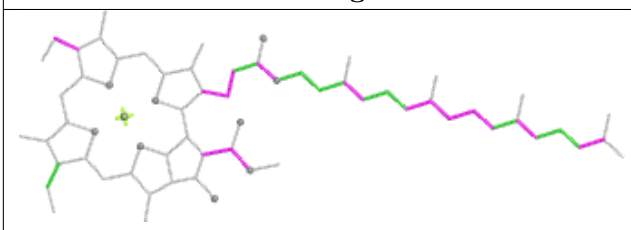
Ligand CLA c 503



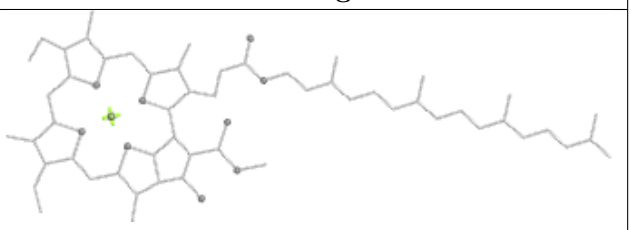
Bond lengths



Bond angles

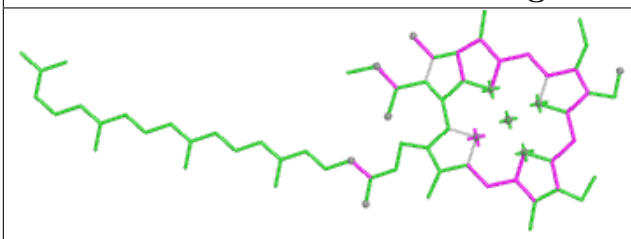


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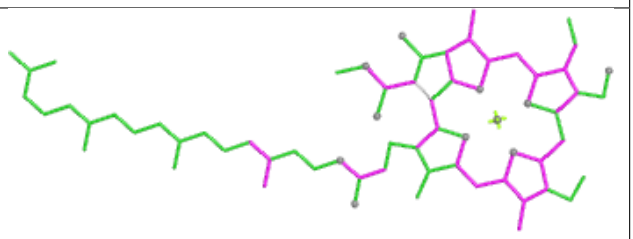


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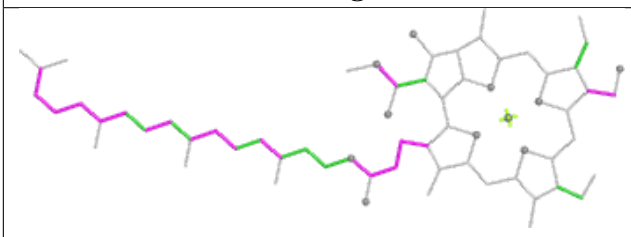
Ligand CHL 6 316



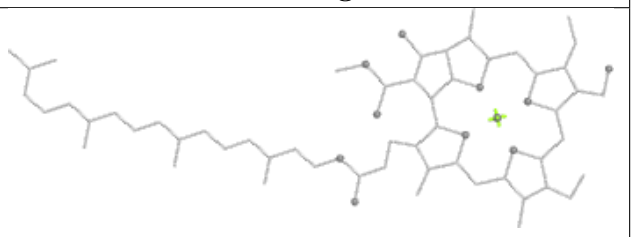
Bond lengths



Bond angles

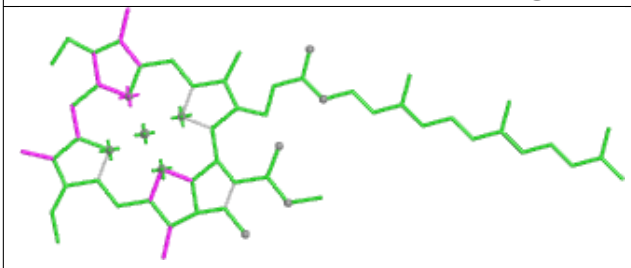


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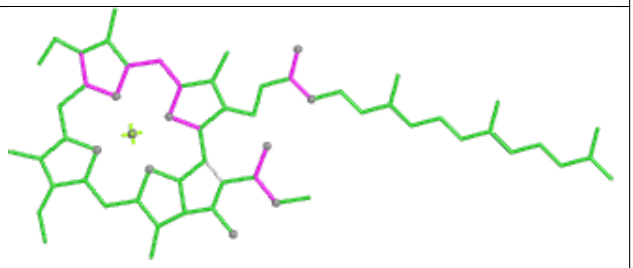


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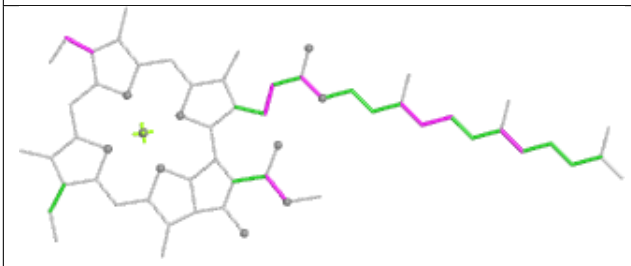
Ligand CLA 5 307



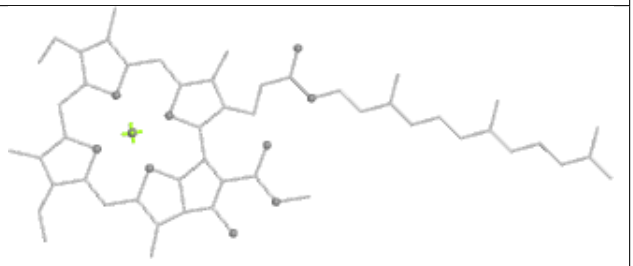
Bond lengths



Bond angles

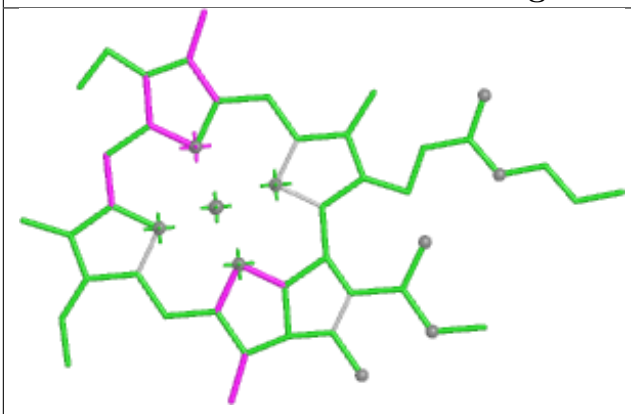


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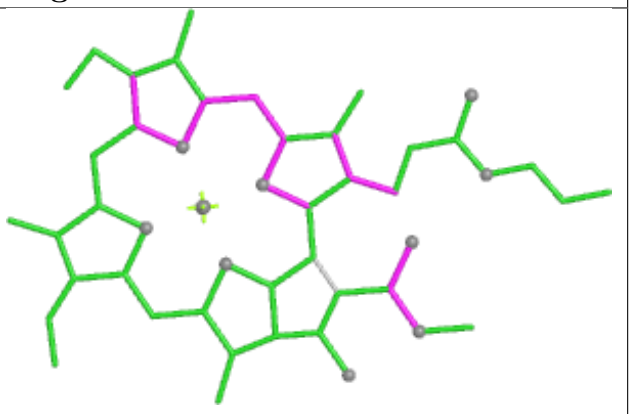


Rings

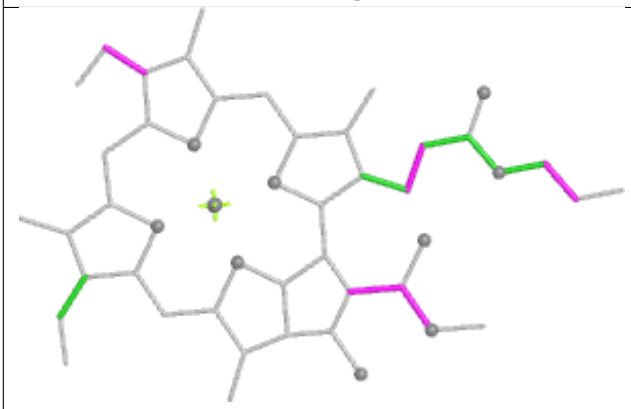
Ligand CLA g 308



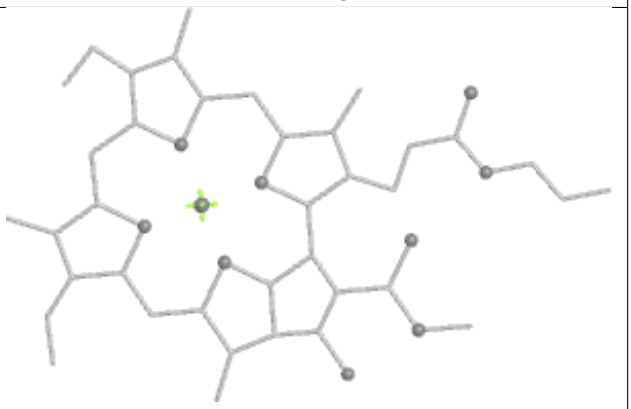
Bond lengths



Bond angles

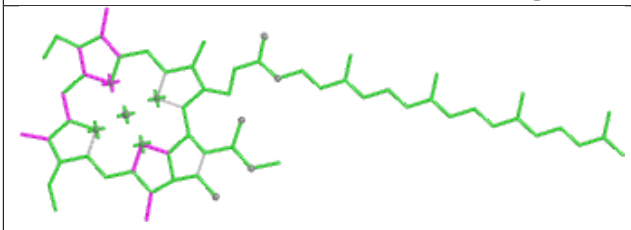


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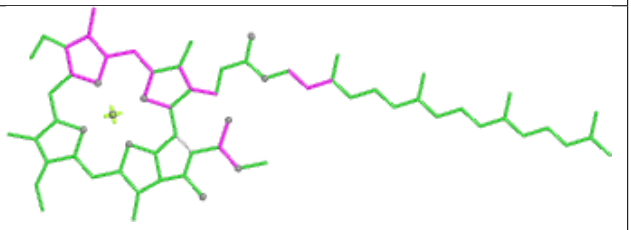


Rings

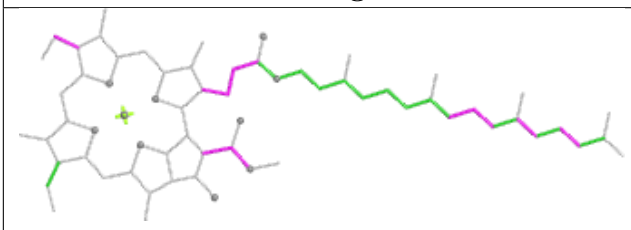
Ligand CLA 2 301



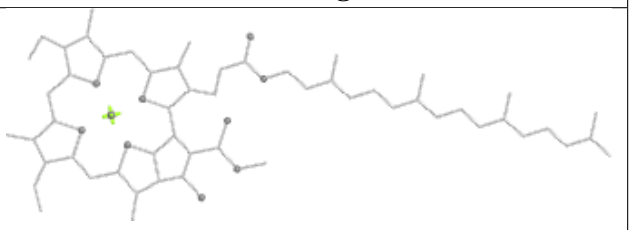
Bond lengths



Bond angles

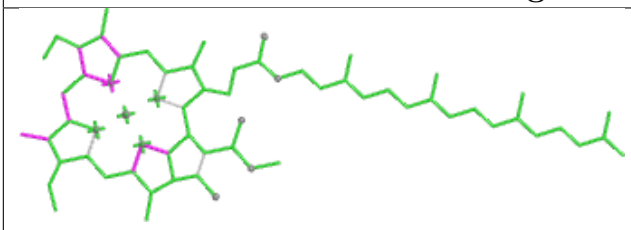


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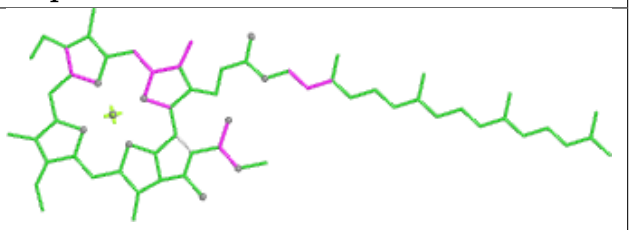


Rings

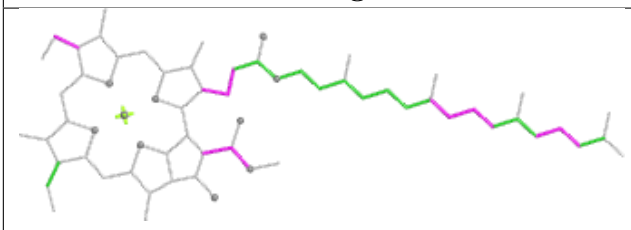
Ligand CLA p 305



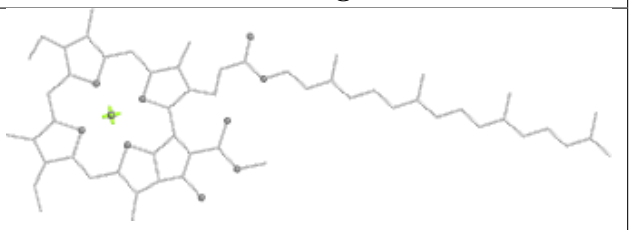
Bond lengths



Bond angles

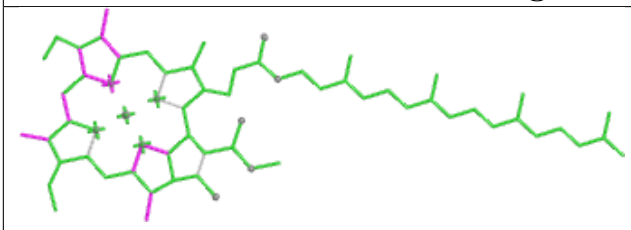


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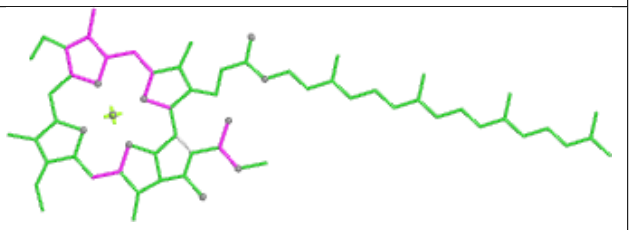


Rings

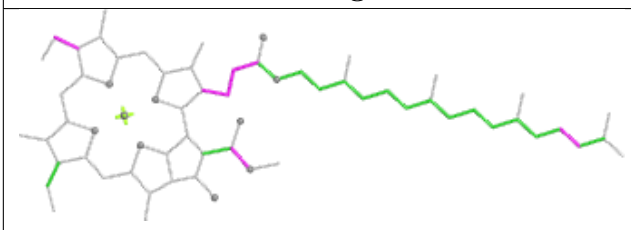
Ligand CLA 4 301



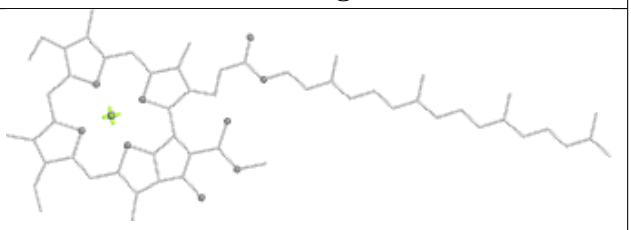
Bond lengths



Bond angles

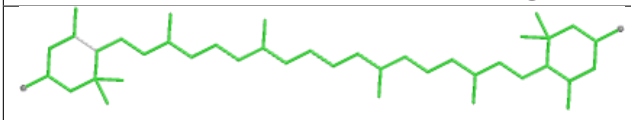


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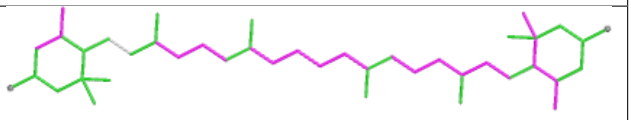


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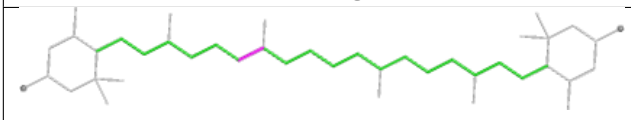
Ligand LUT N 309



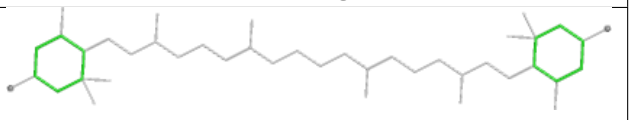
Bond lengths



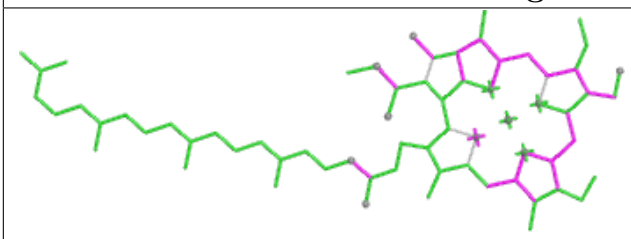
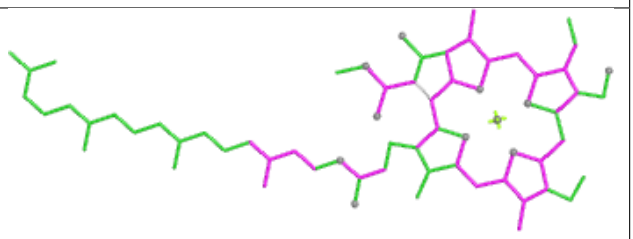
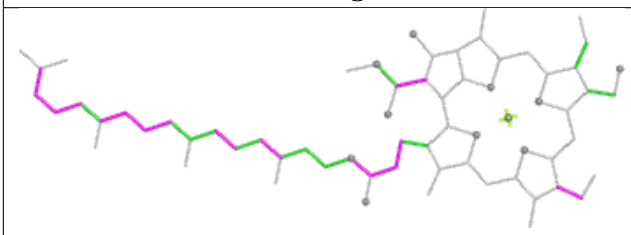
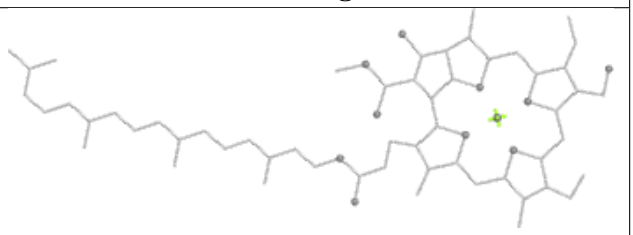
Bond angles

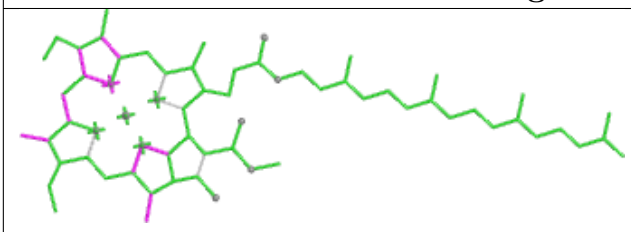
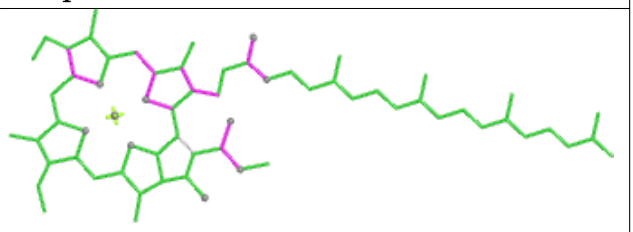
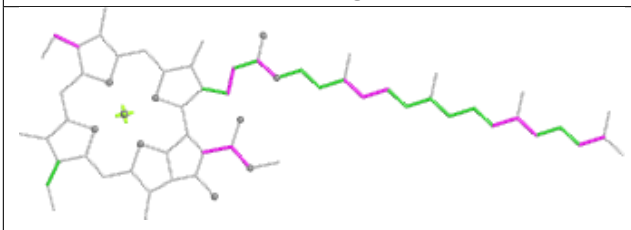
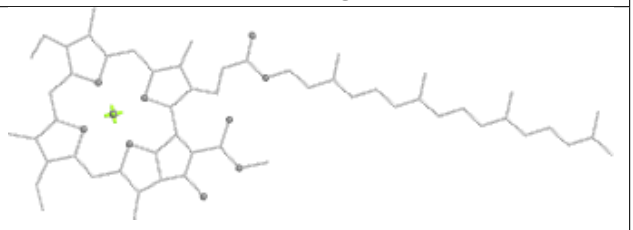


Torsions

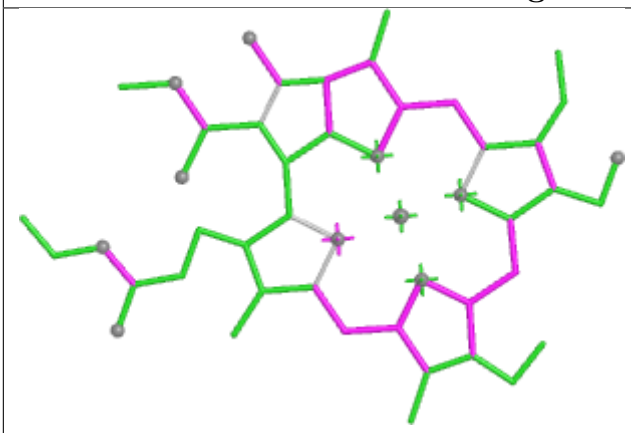


Rings

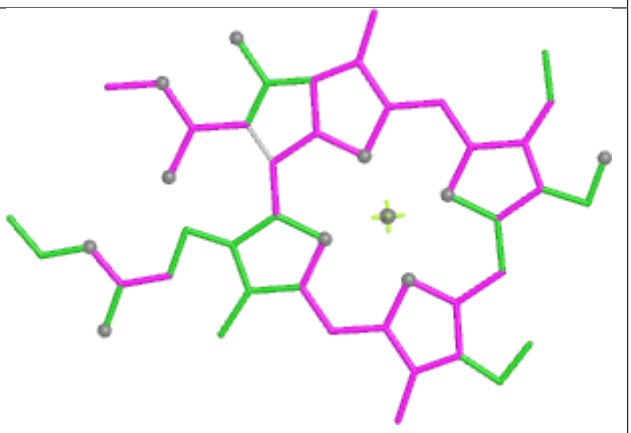
Ligand CHL u 313	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA q 307	
	
Bond lengths	Bond angles
	
Torsions	Rings

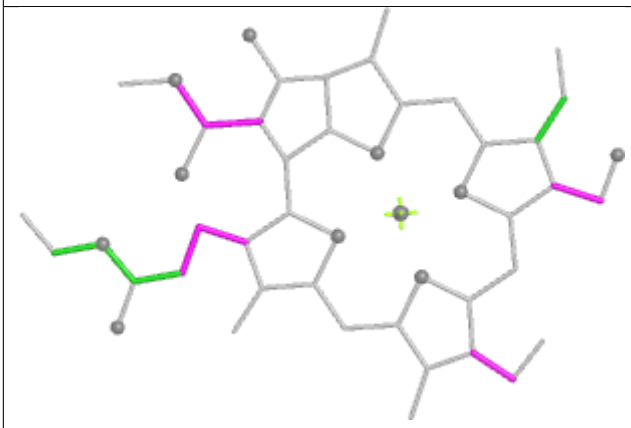
Ligand CHL 4 314



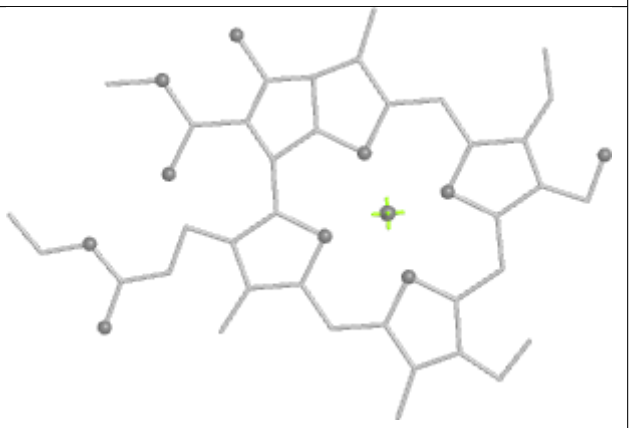
Bond lengths



Bond angles

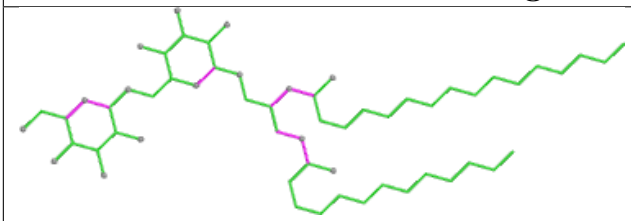


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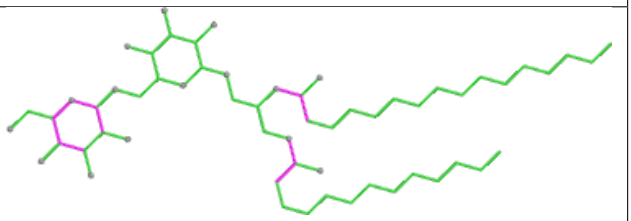


Rings

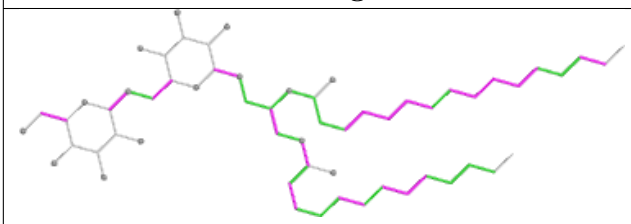
Ligand DGD a 416



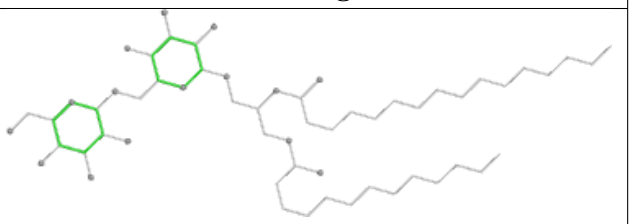
Bond lengths



Bond angles

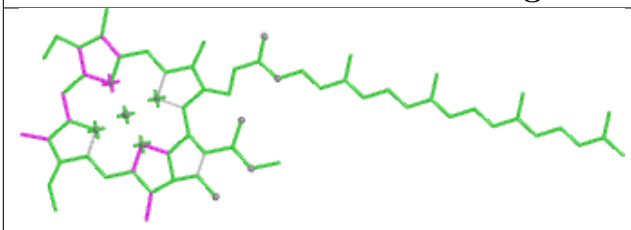


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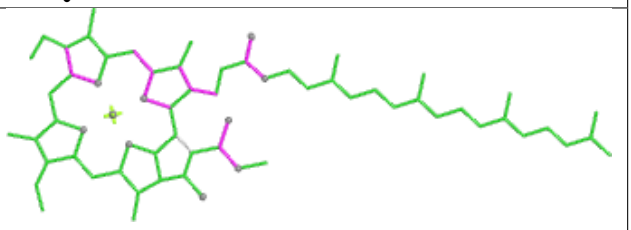


Rings

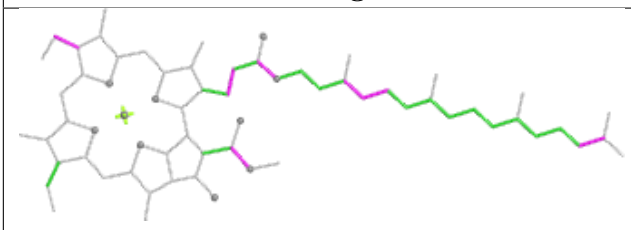
Ligand CLA Q 307



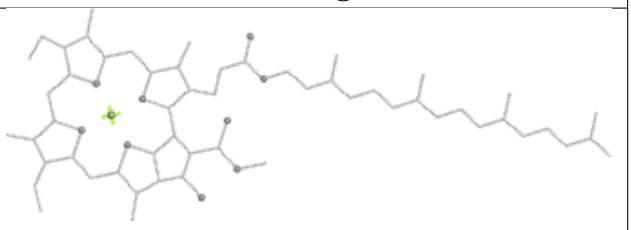
Bond lengths



Bond angles

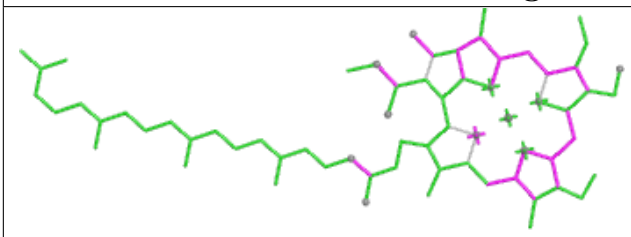


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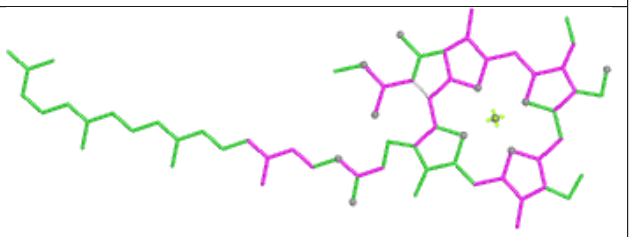


Rings

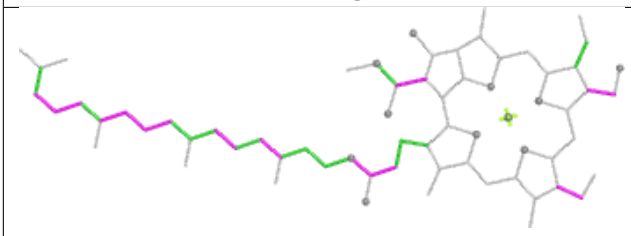
Ligand CHL U 313



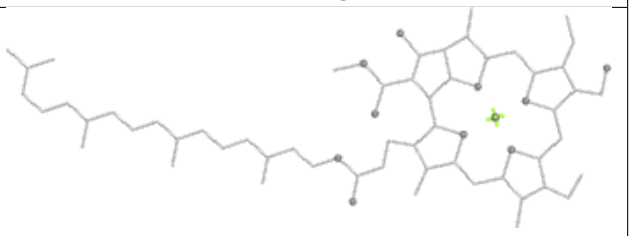
Bond lengths



Bond angles

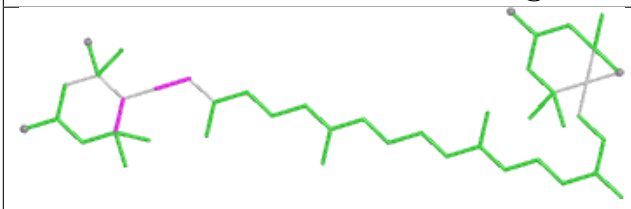


Torsions

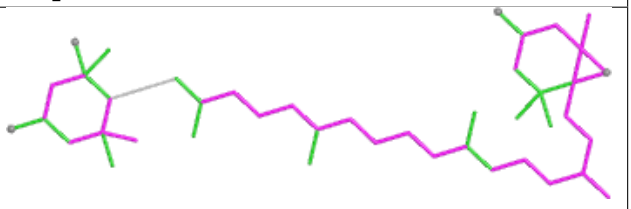


Rings

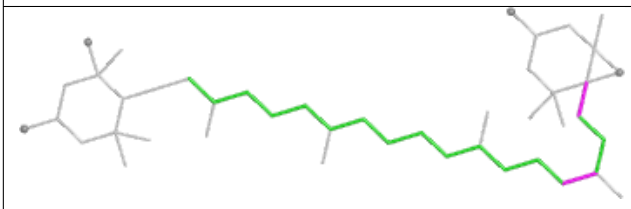
Ligand NEX p 301



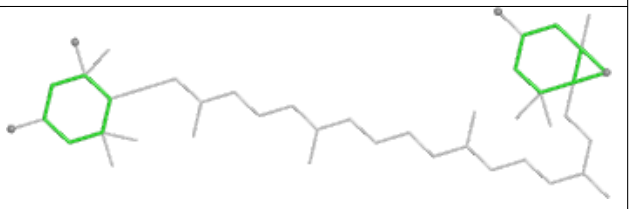
Bond lengths



Bond angles

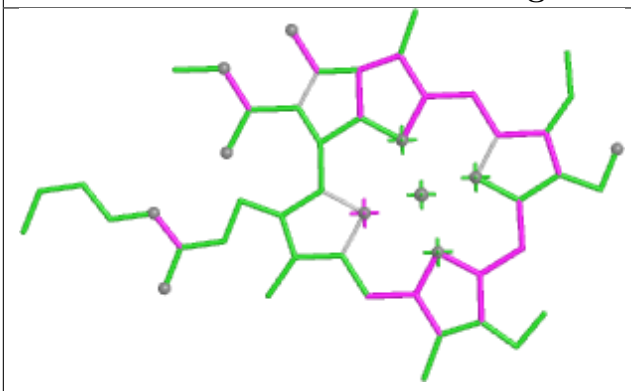


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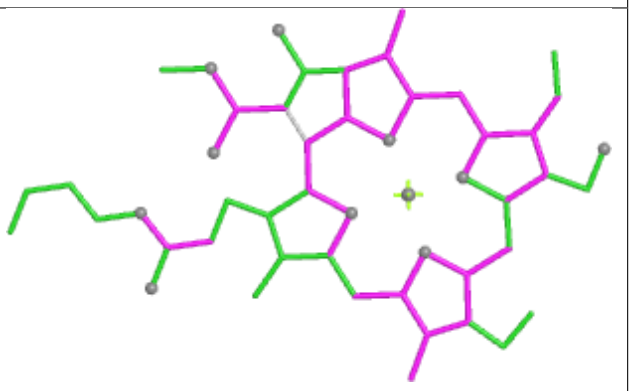


Rings

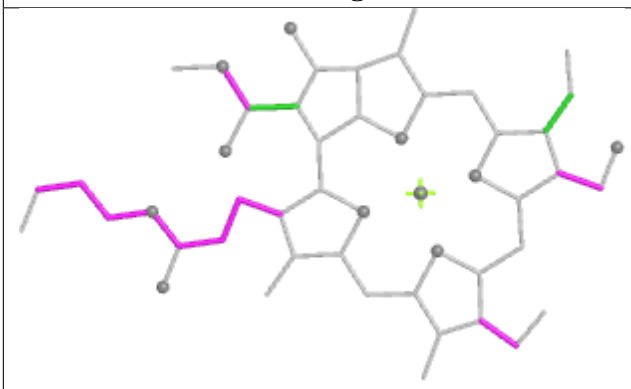
Ligand CHL 3 313



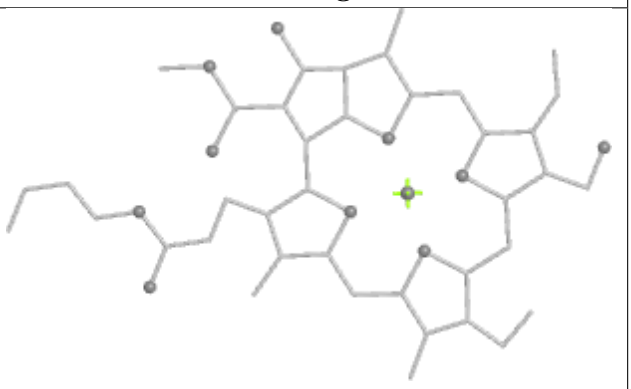
Bond lengths



Bond angles

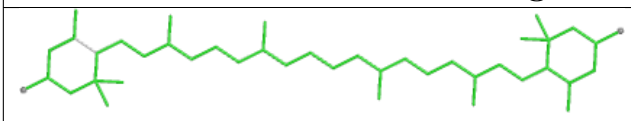


Torsions

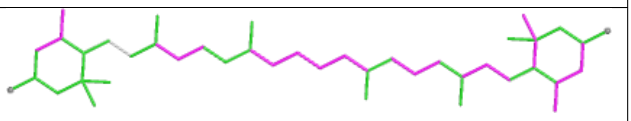


Rings

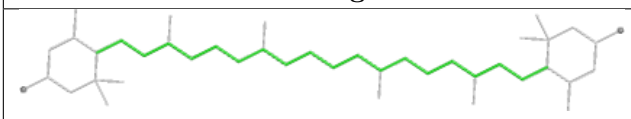
Ligand LUT v 310



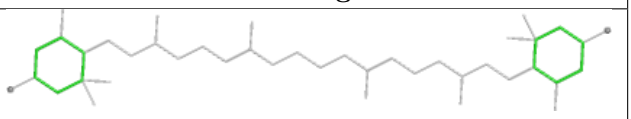
Bond lengths



Bond angles

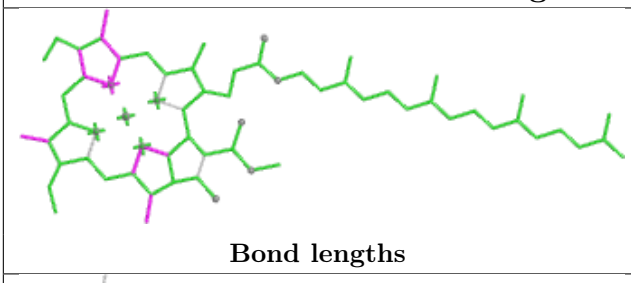


Torsions

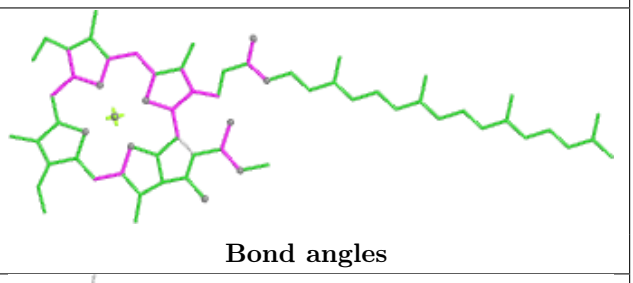


Rings

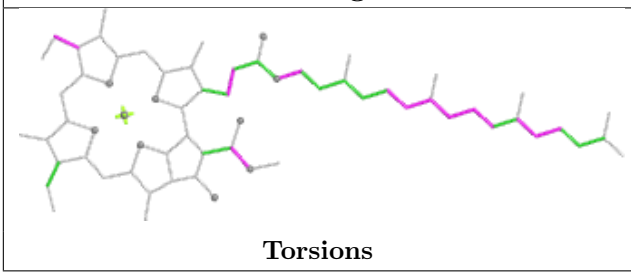
Ligand CLA c 508



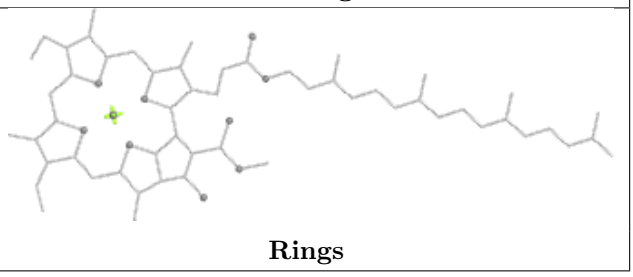
Bond lengths



Bond angles

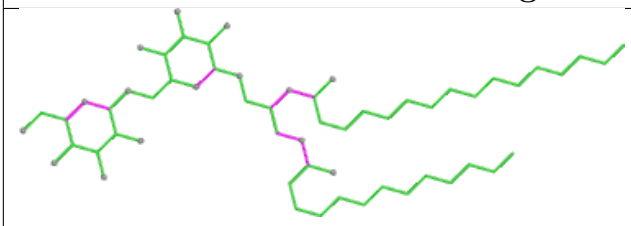


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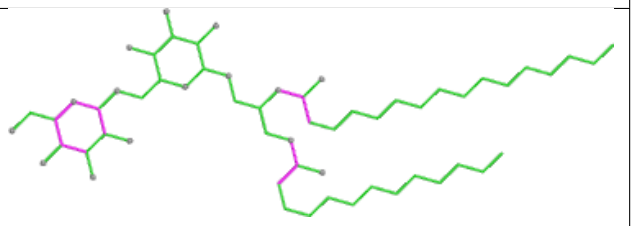


Rings

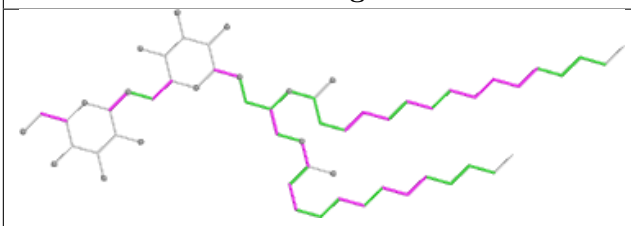
Ligand DGD A 414



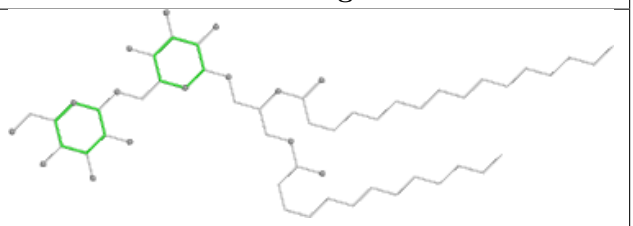
Bond lengths



Bond angles

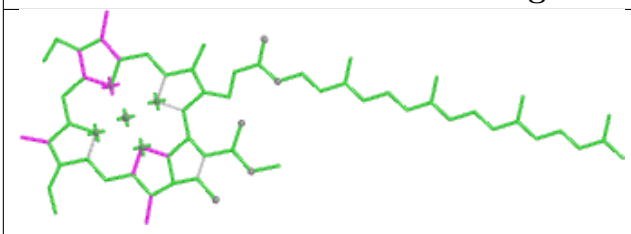


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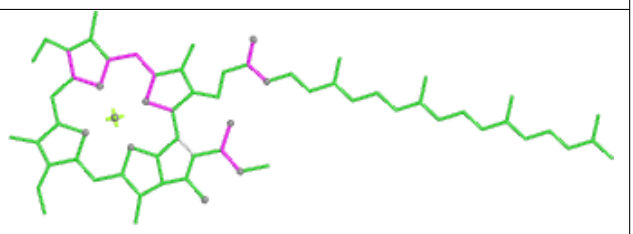


Rings

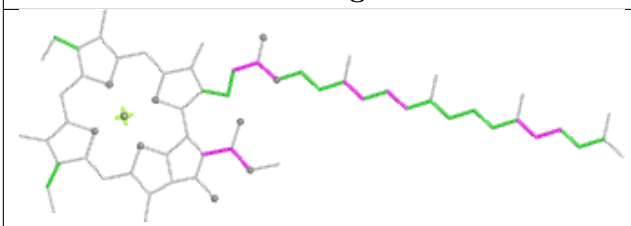
Ligand CLA 4 302



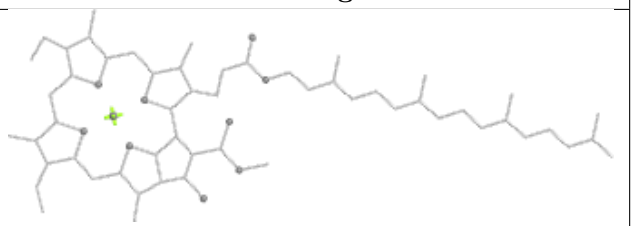
Bond lengths



Bond angles

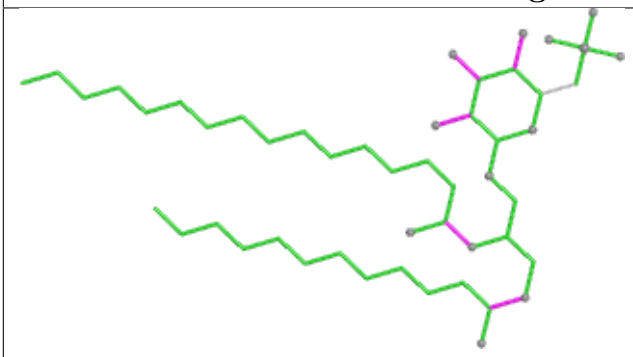


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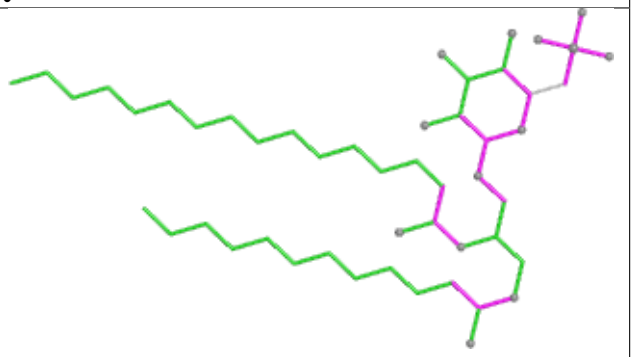


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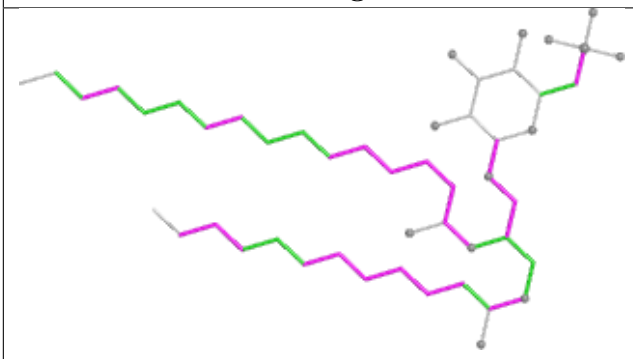
Ligand SQD a 410



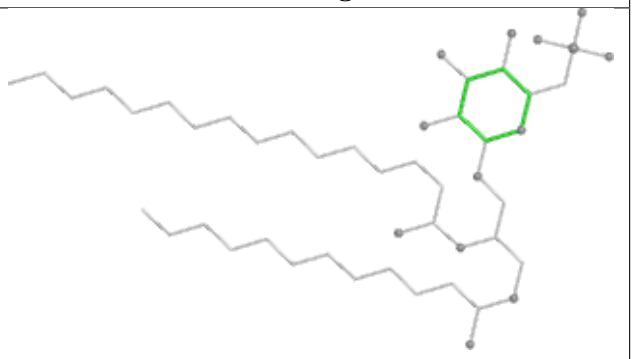
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Bond angles

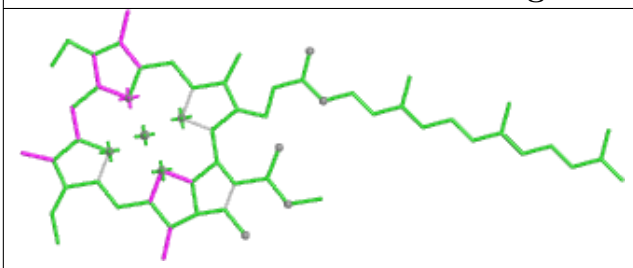


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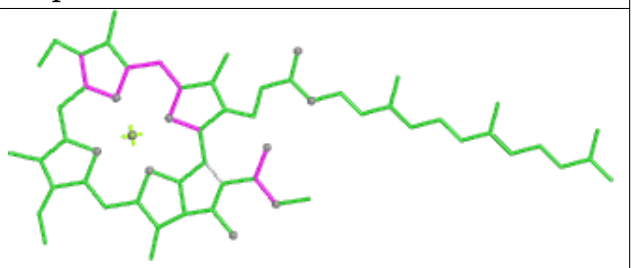


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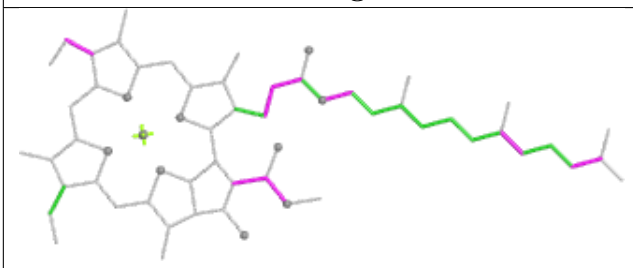
Ligand CLA p 308



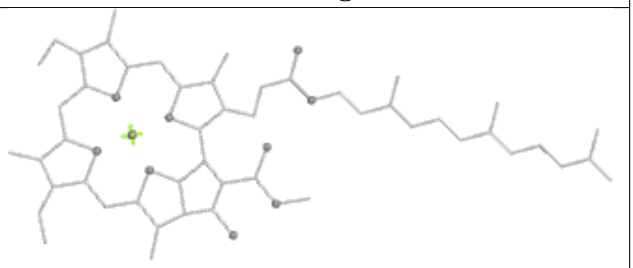
Bond lengths



Bond angles

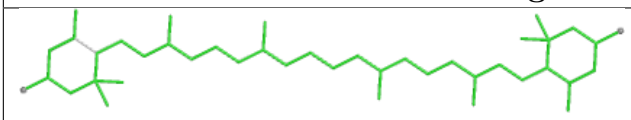


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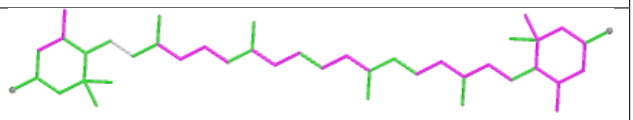


Rings

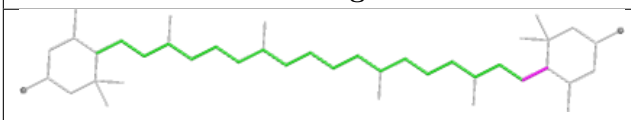
Ligand LUT v 309



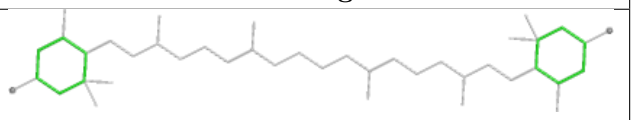
Bond lengths



Bond angles

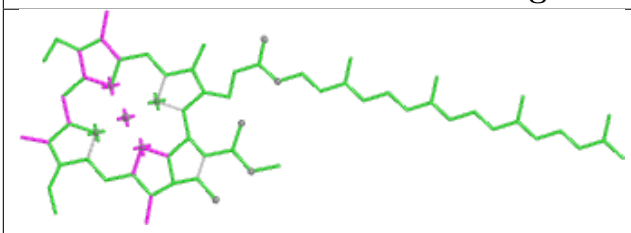


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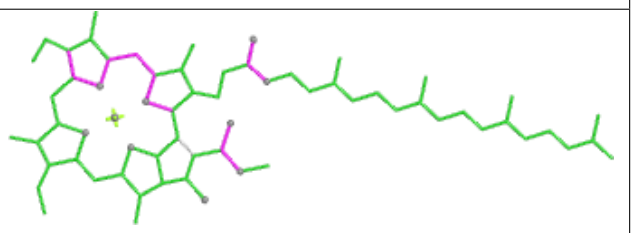


Rings

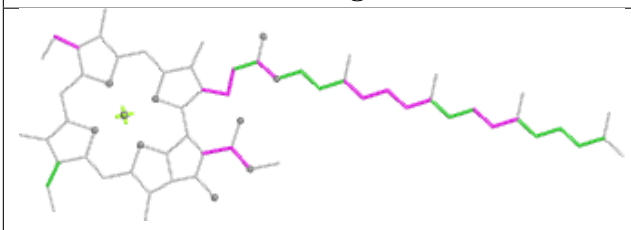
Ligand CLA c 504



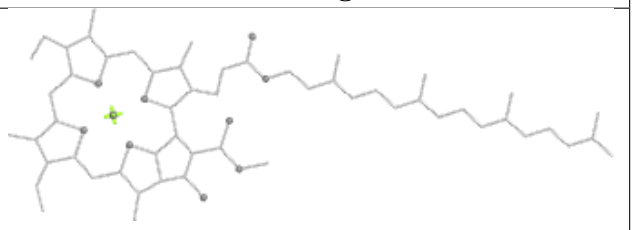
Bond lengths



Bond angles

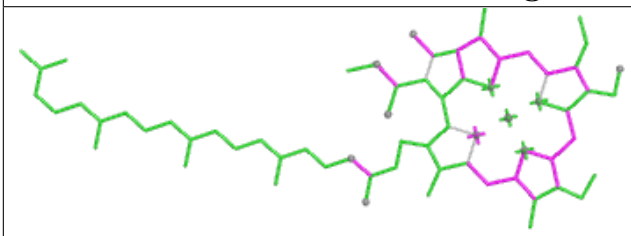


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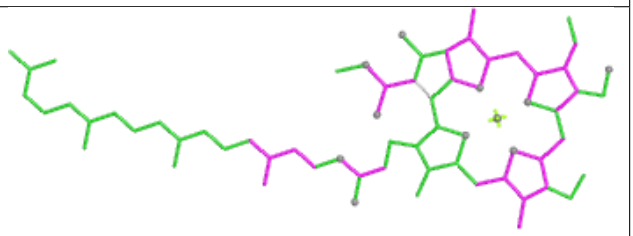


Rings

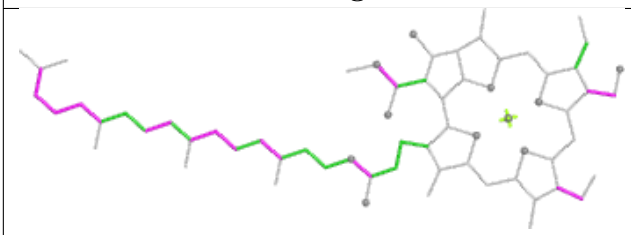
Ligand CHL V 318



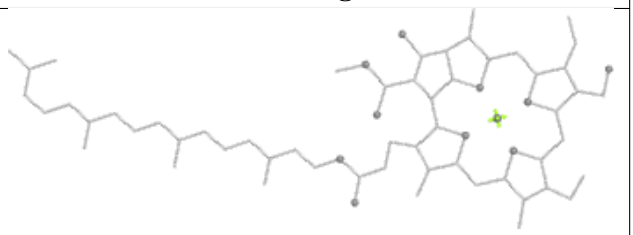
Bond lengths



Bond angles

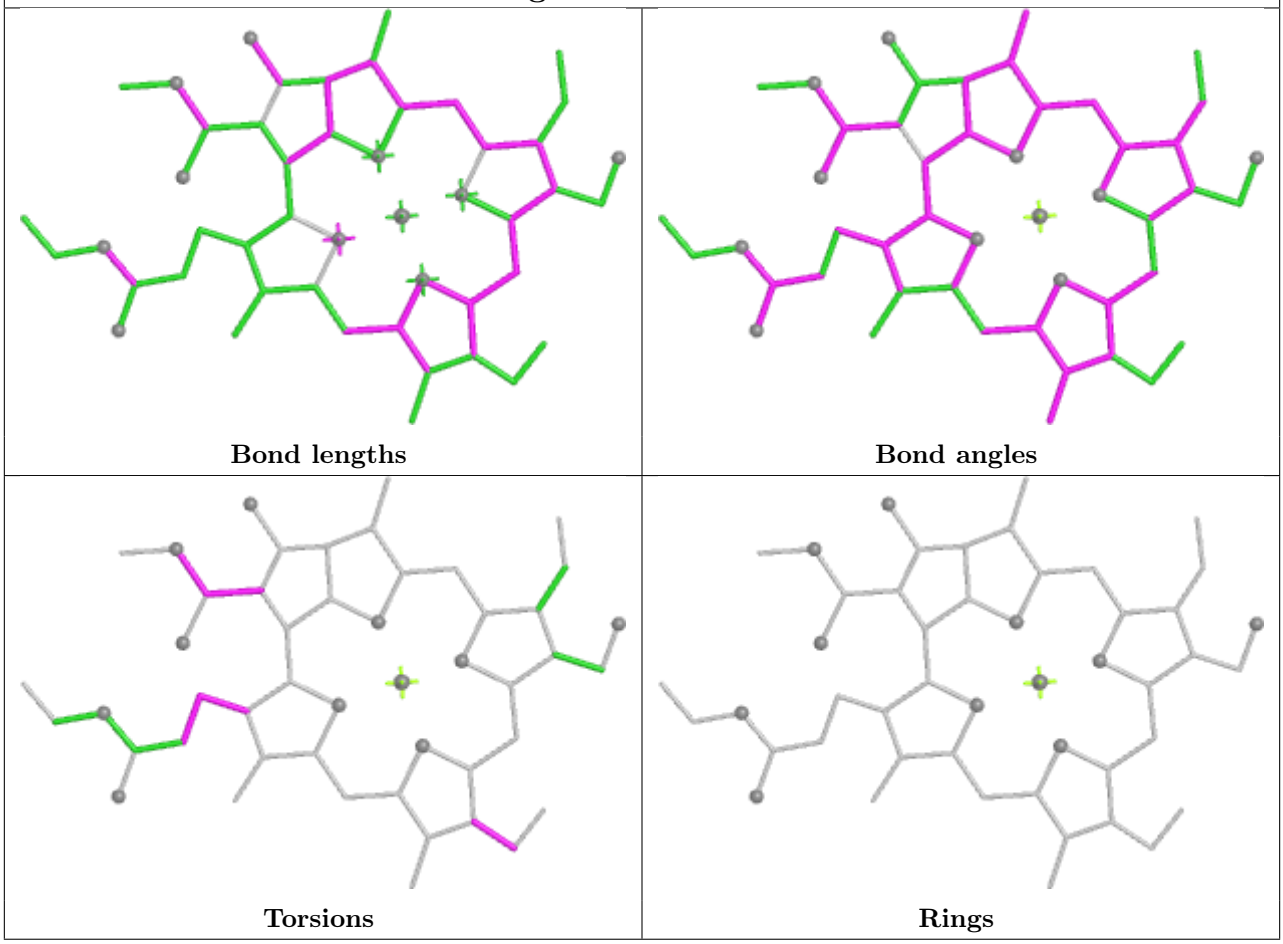


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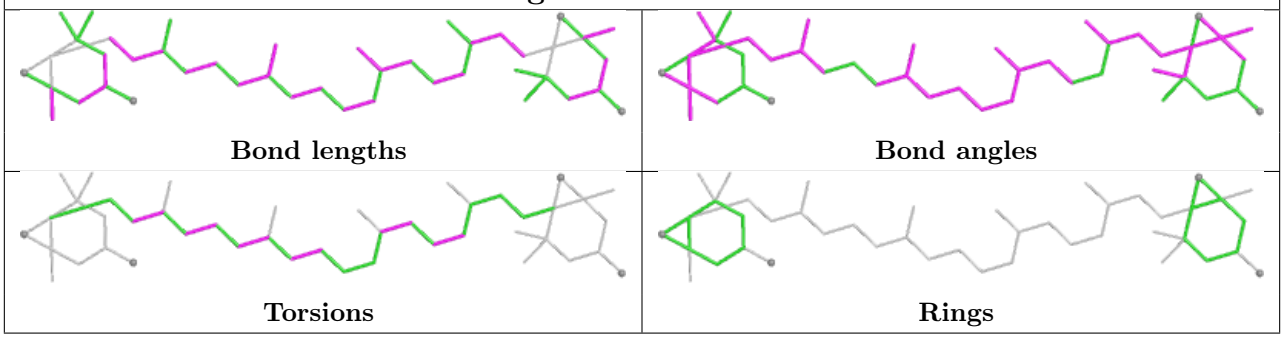


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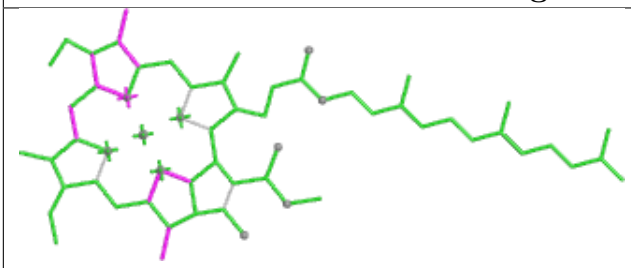
Ligand CHL 6 313



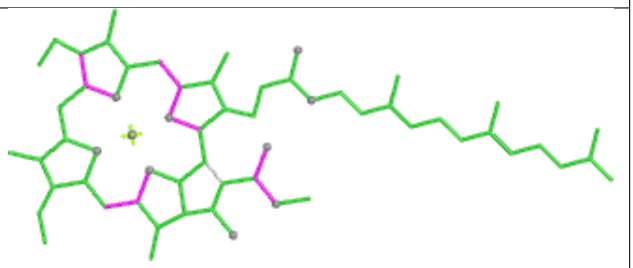
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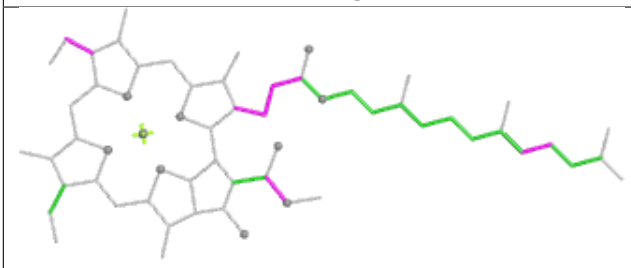
Ligand CLA r 602



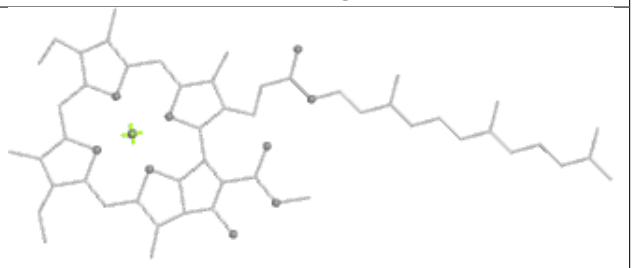
Bond lengths



Bond angles

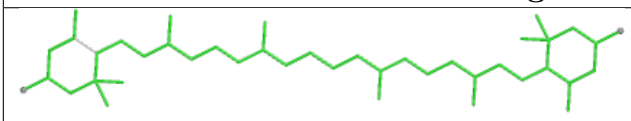


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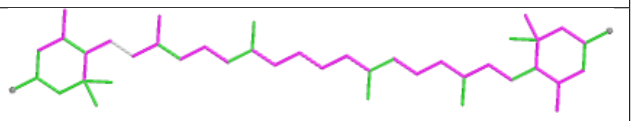


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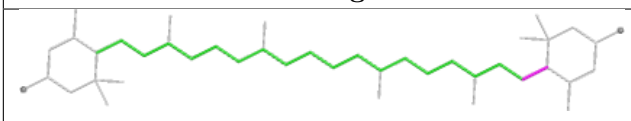
Ligand LUT S 310



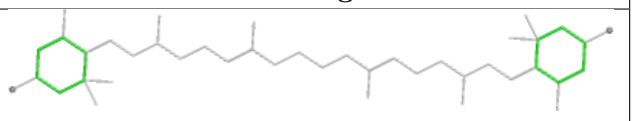
Bond lengths



Bond angles

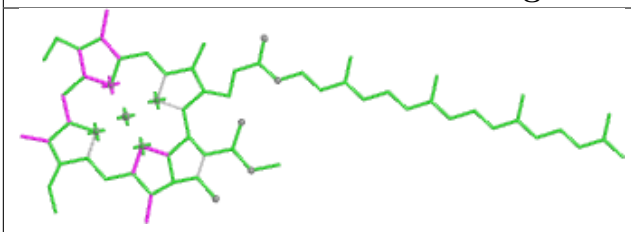


Torsions

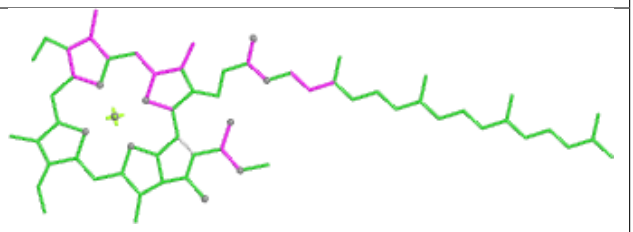


Rings

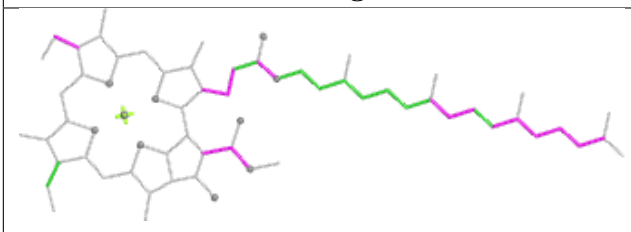
Ligand CLA N 304



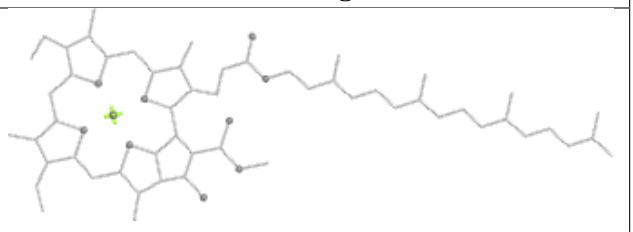
Bond lengths



Bond angles

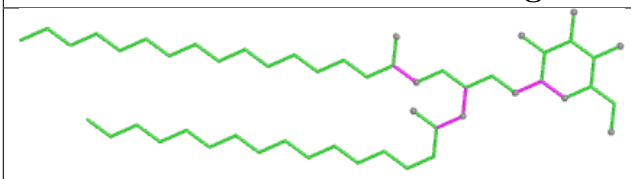


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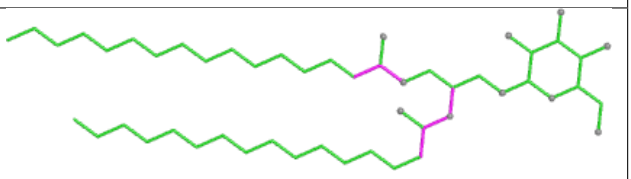


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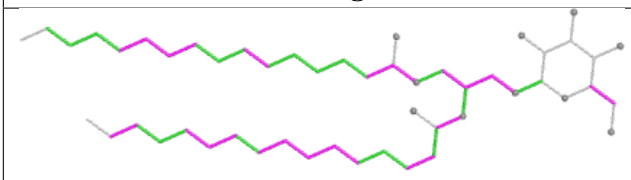
Ligand LMG c 501



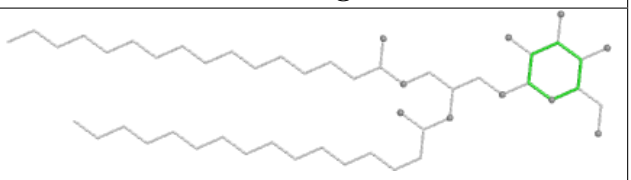
Bond lengths



Bond angles

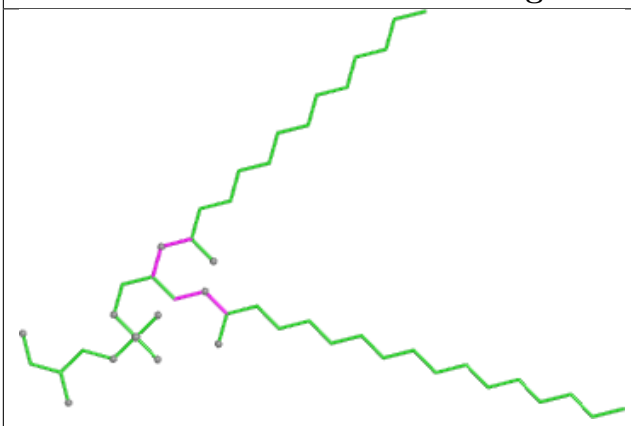


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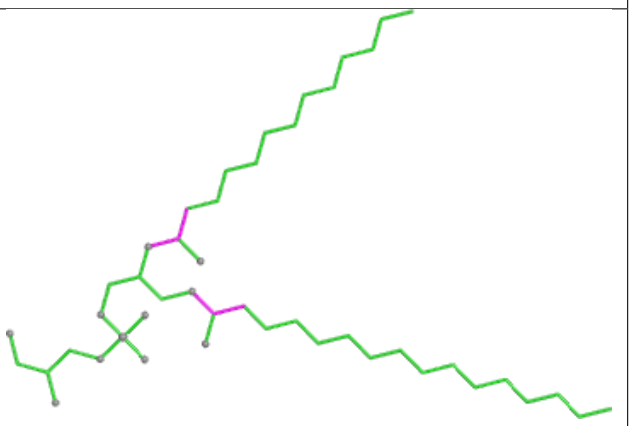


Rings

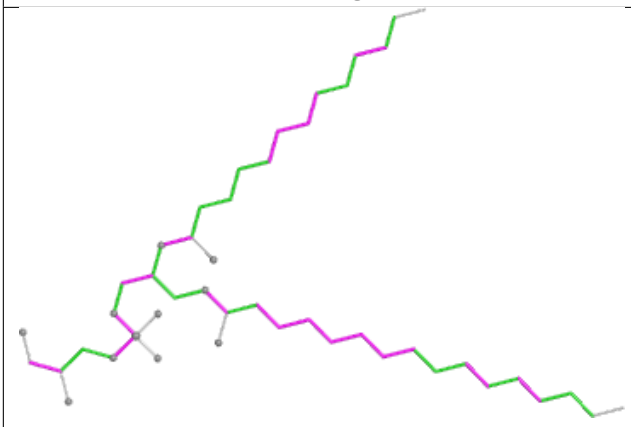
Ligand LHG d 405



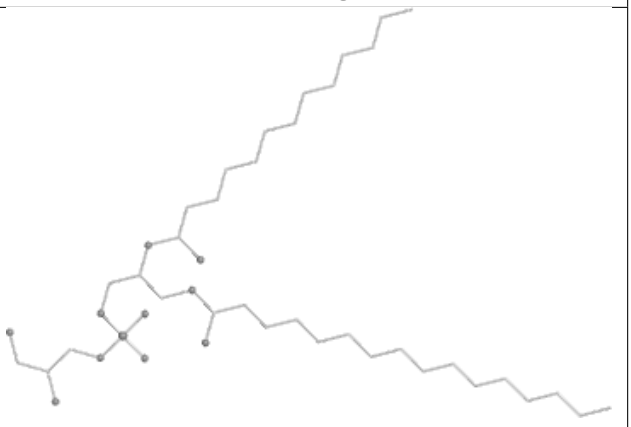
Bond lengths



Bond angles

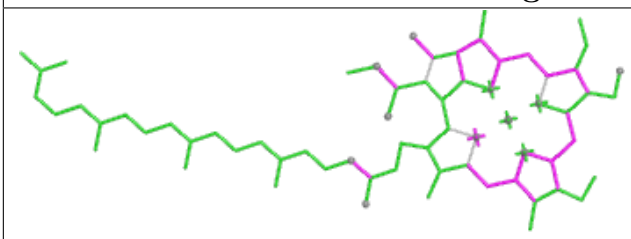


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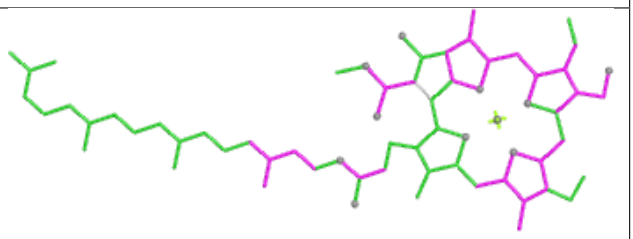


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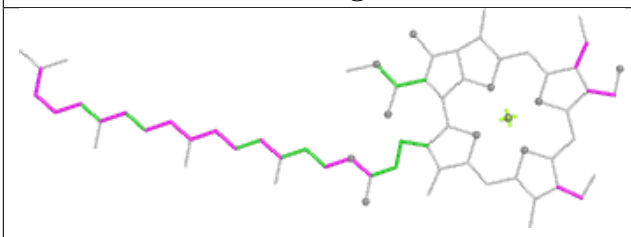
Ligand CHL N 317



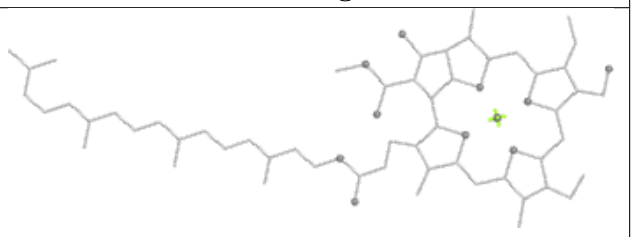
Bond lengths



Bond angles

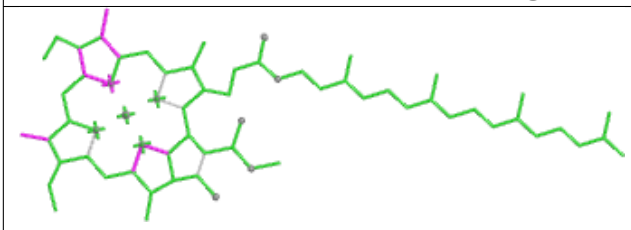


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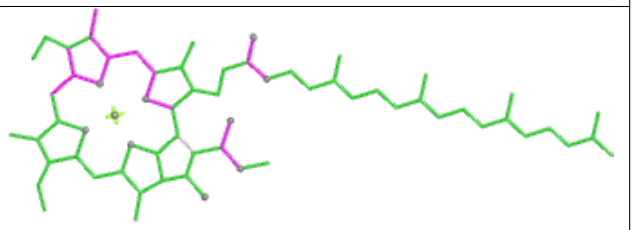


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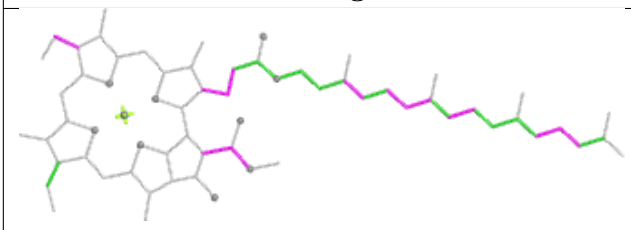
Ligand CLA B 604



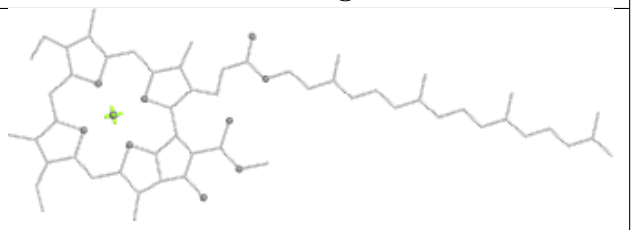
Bond lengths



Bond angles

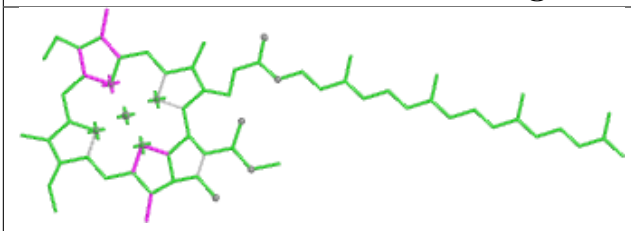


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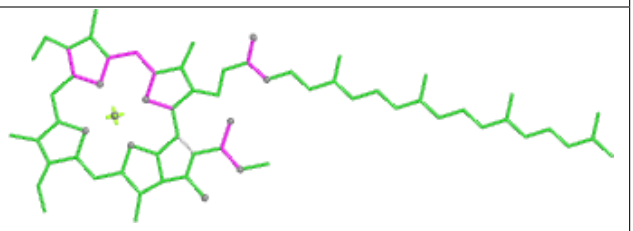


Rings

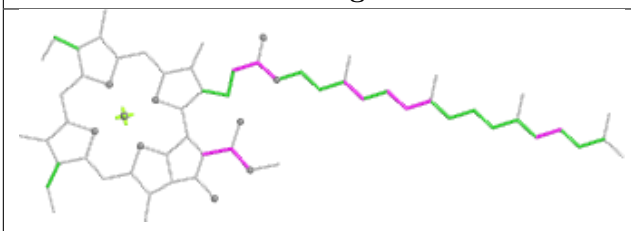
Ligand CLA 1 302



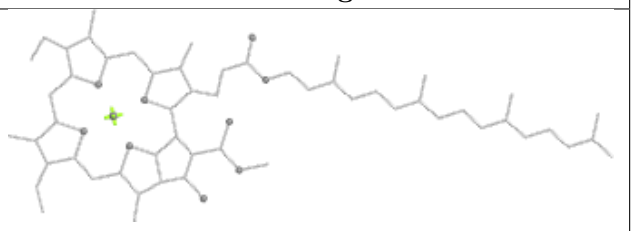
Bond lengths



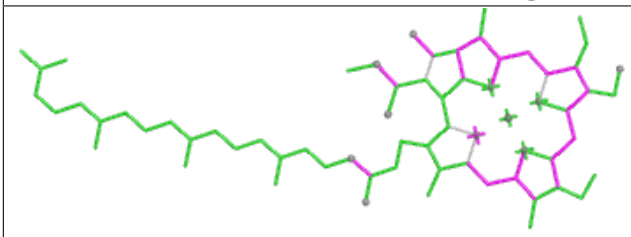
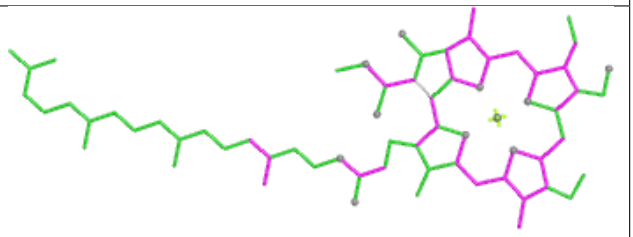
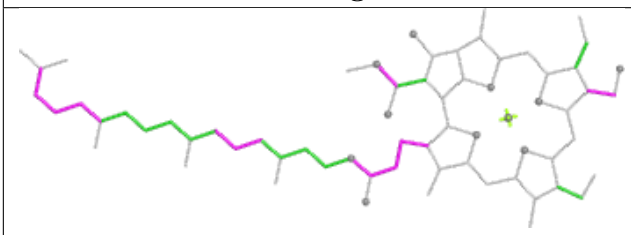
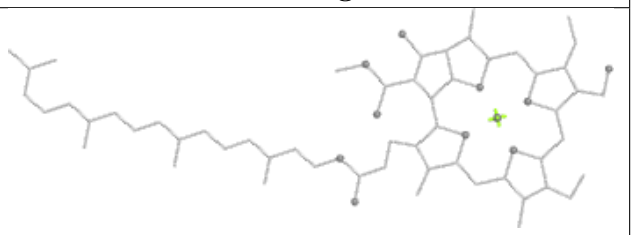
Bond angles

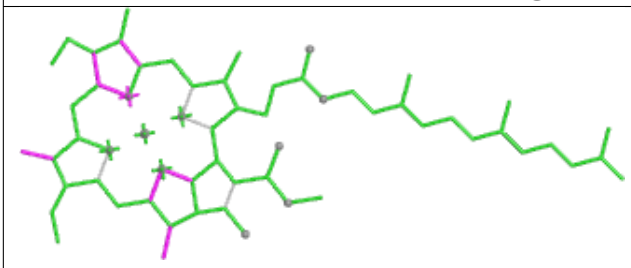
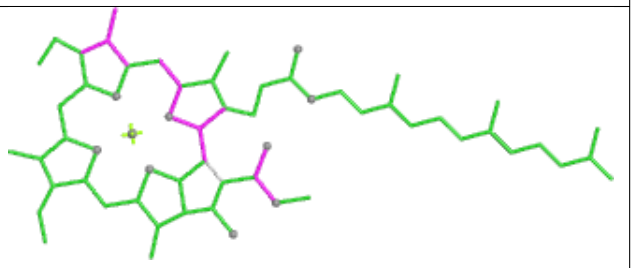
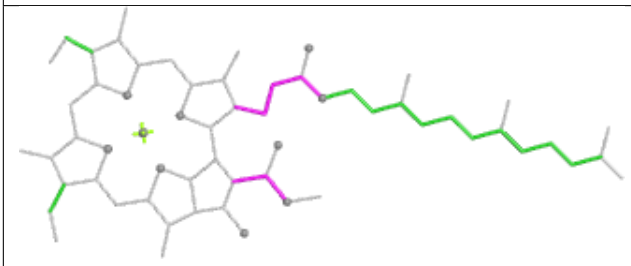
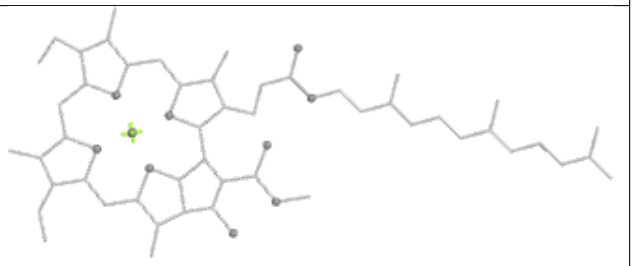


Torsions

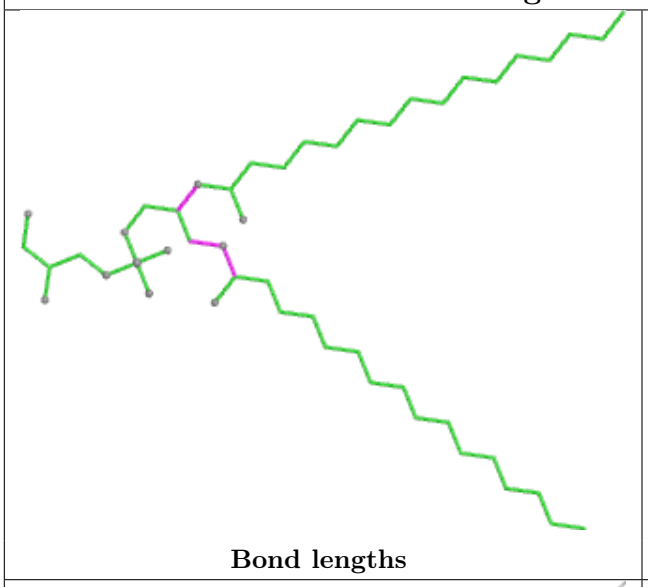


Rings

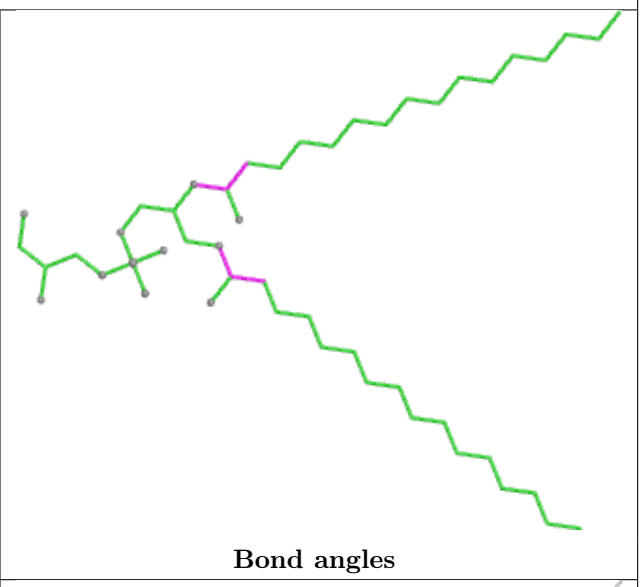
Ligand CHL G 315	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA 2 306	
	
Bond lengths	Bond angles
	
Torsions	Rings

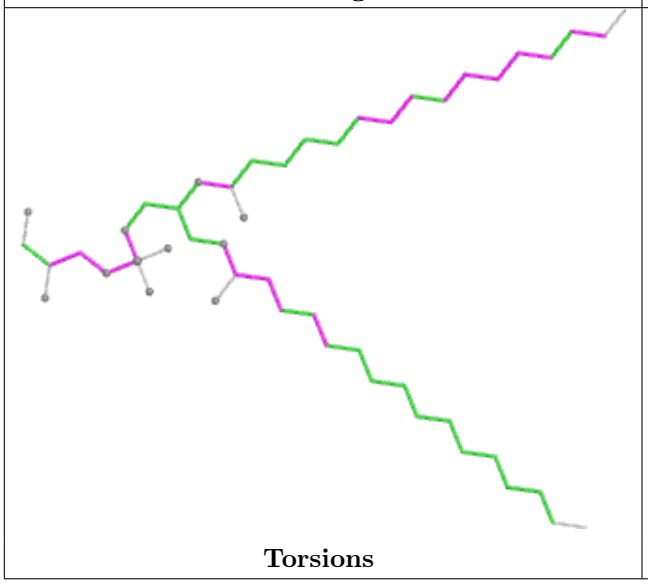
Ligand LHG C 523



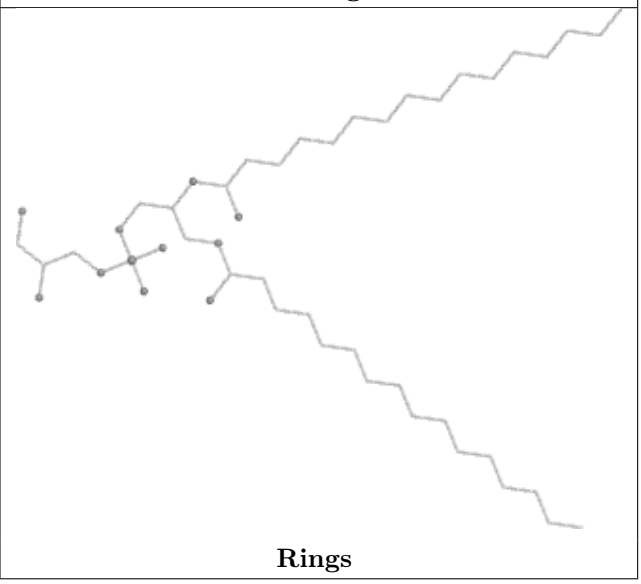
Bond lengths



Bond angles

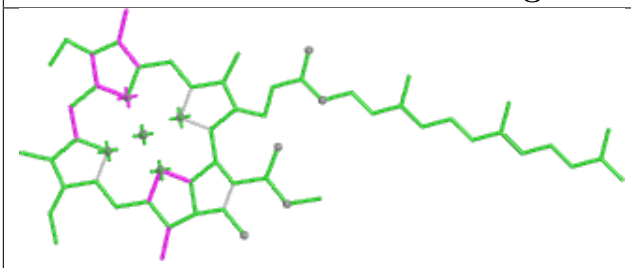


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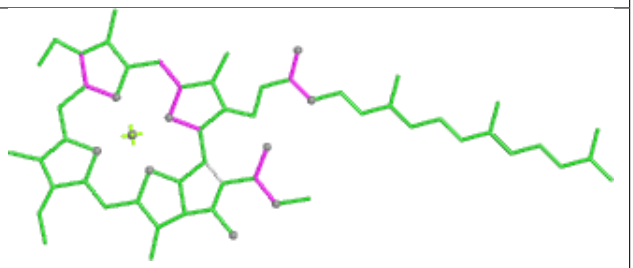


Rings

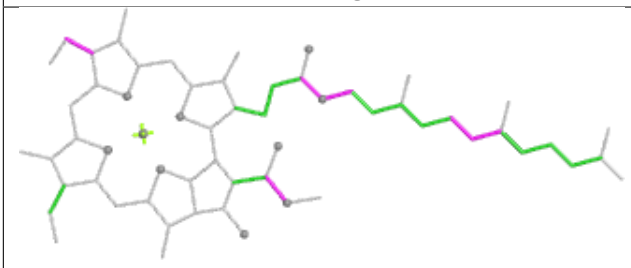
Ligand CLA V 305



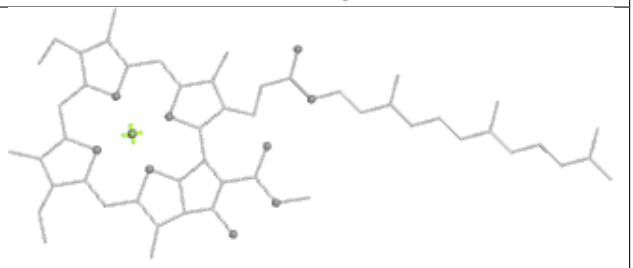
Bond lengths



Bond angles

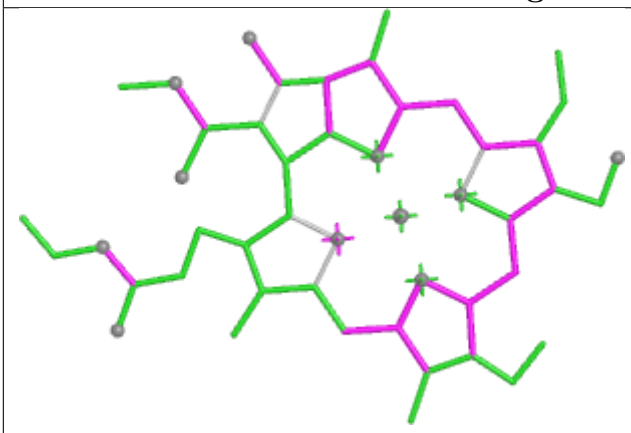


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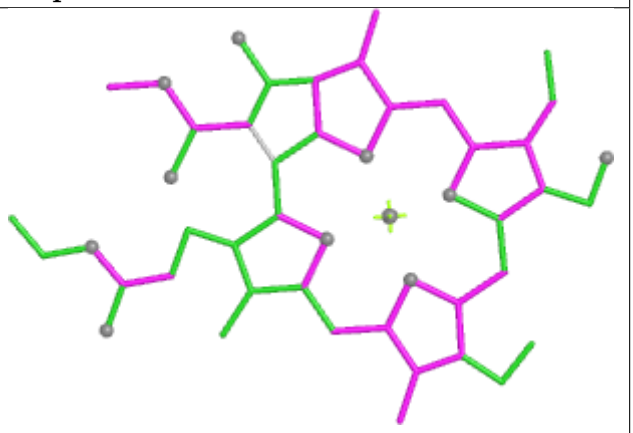


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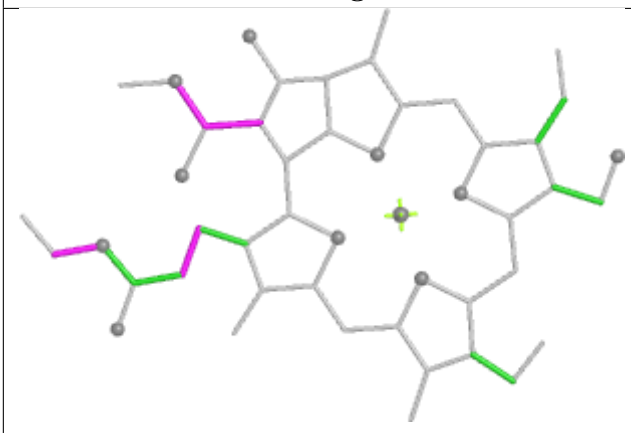
Ligand CHL p 315



Bond lengths



Bond angles

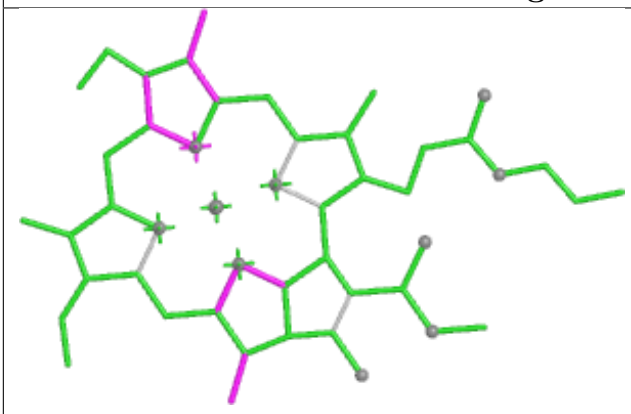


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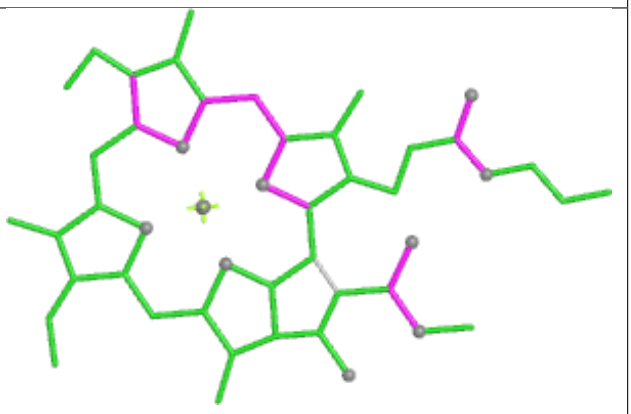


Rings

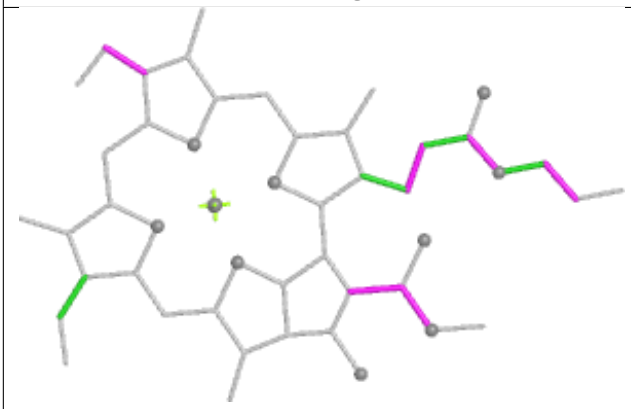
Ligand CLA u 308



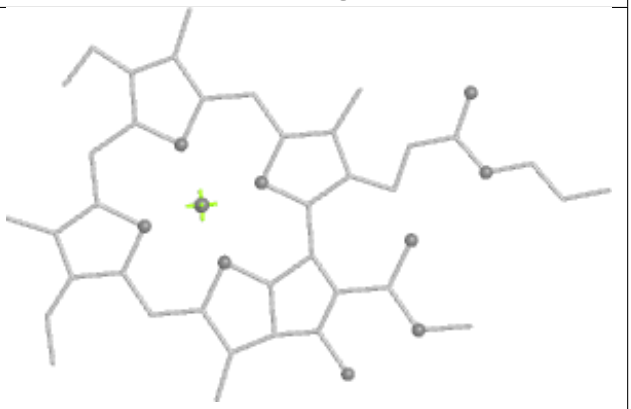
Bond lengths



Bond angles

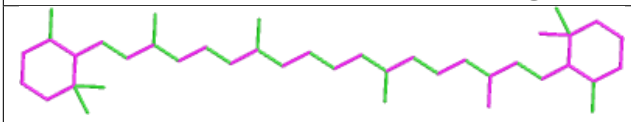


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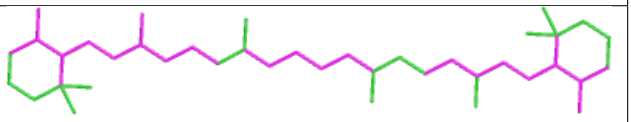


Rings

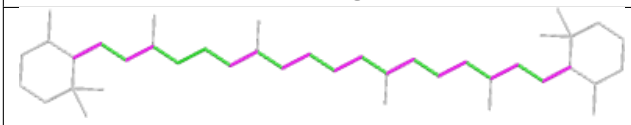
Ligand BCR b 619



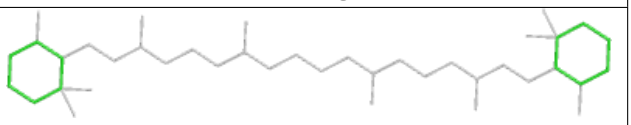
Bond lengths



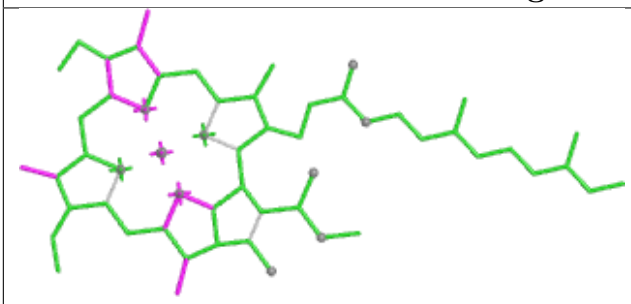
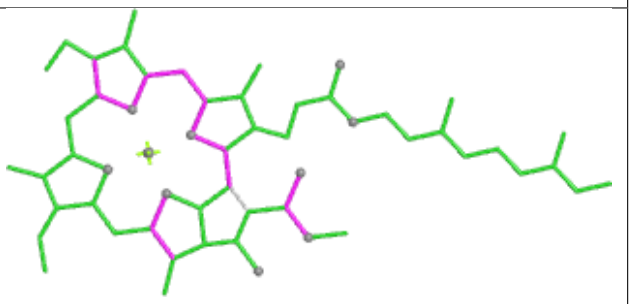
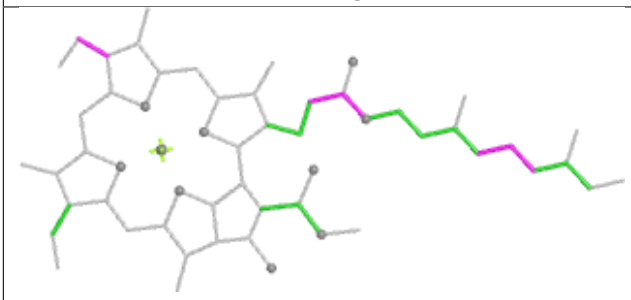
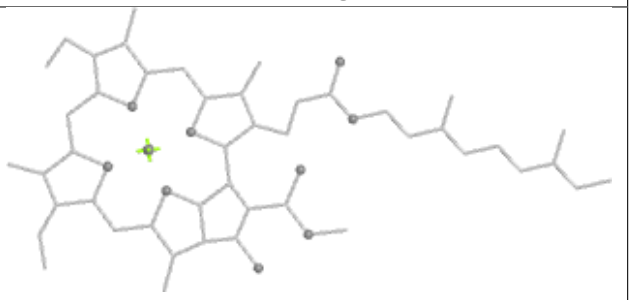
Bond angles

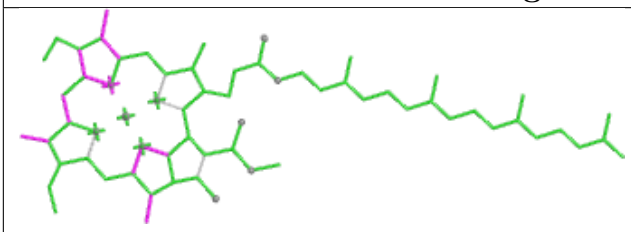
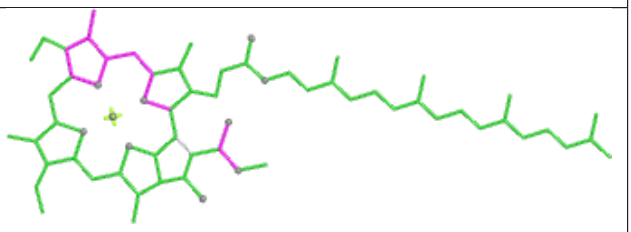
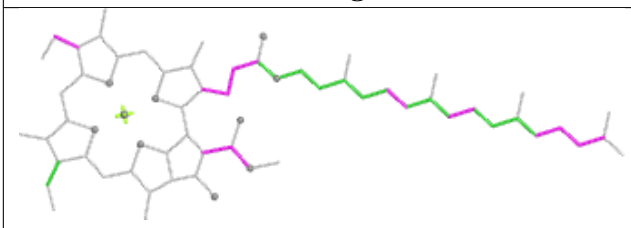
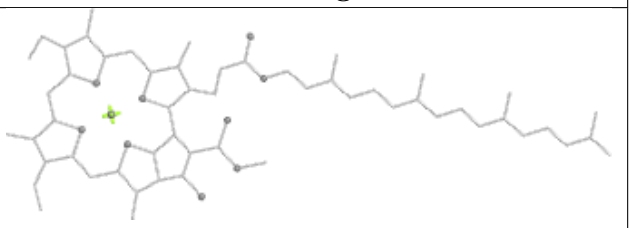


Torsions

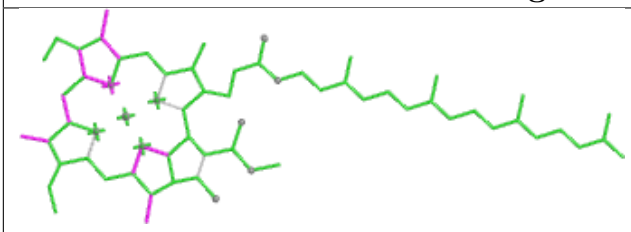


Rings

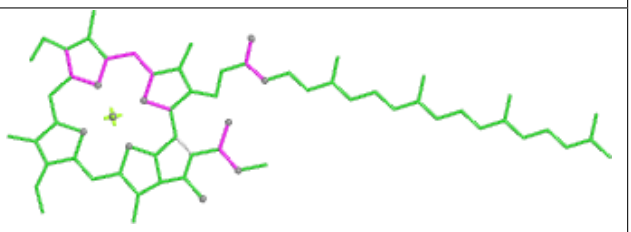
Ligand CLA S 306	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA N 301	
	
Bond lengths	Bond angles
	
Torsions	Rings

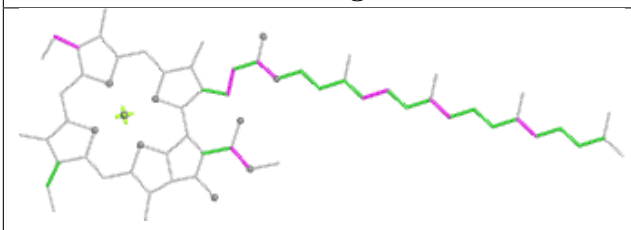
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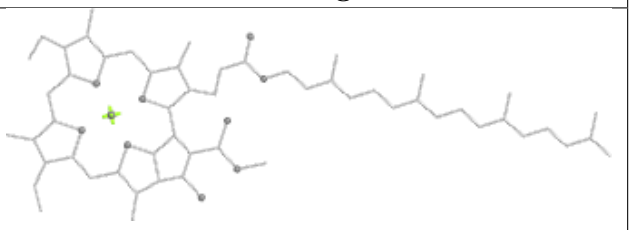
Bond lengths



Bond angles

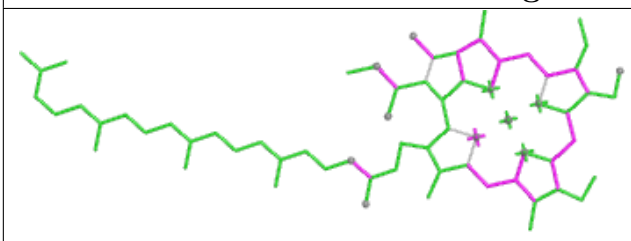


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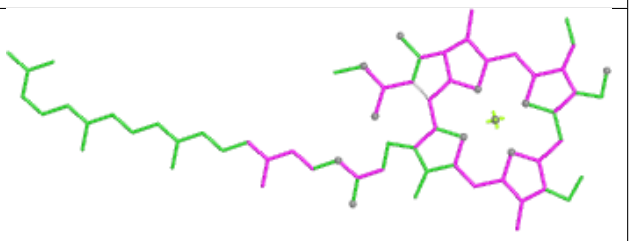


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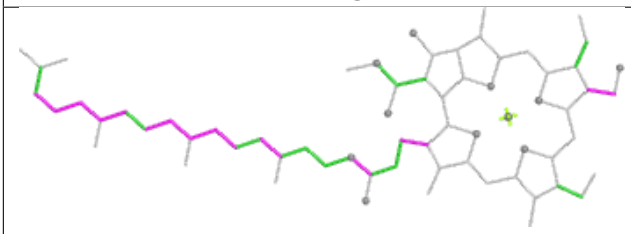
Ligand CHL G 311



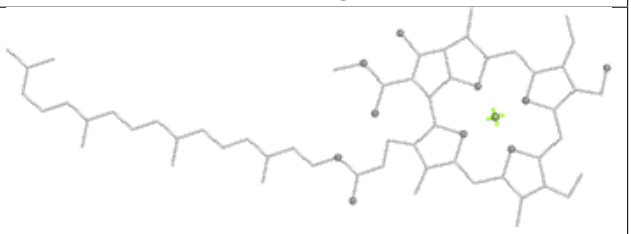
Bond lengths



Bond angles

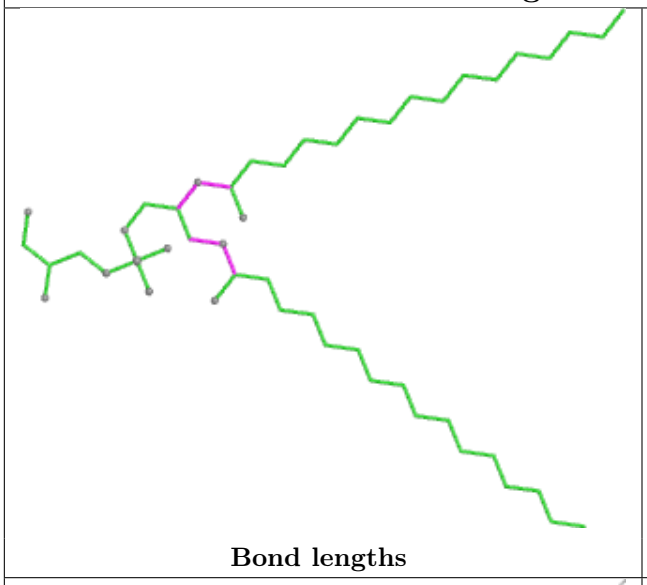


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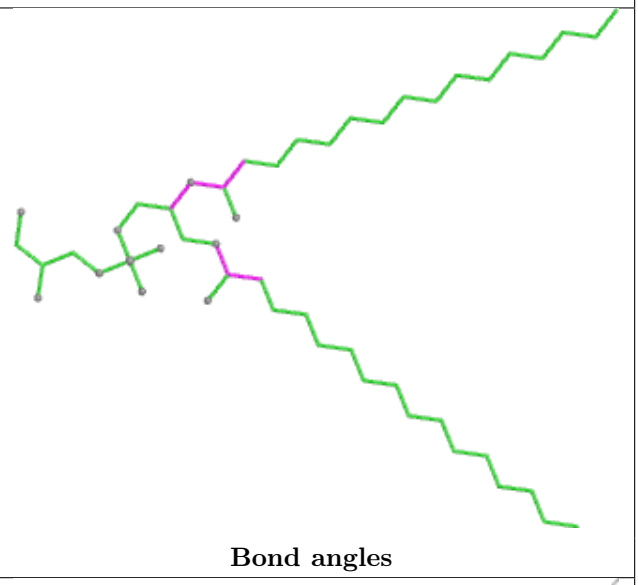


Rings

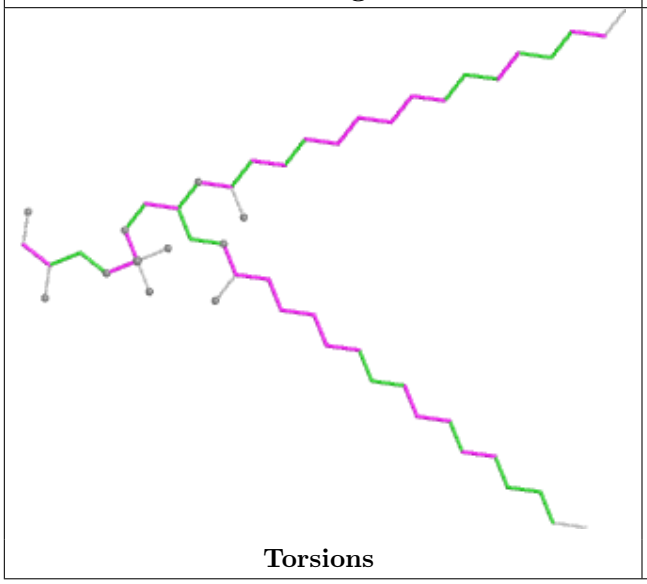
Ligand LHG U 312



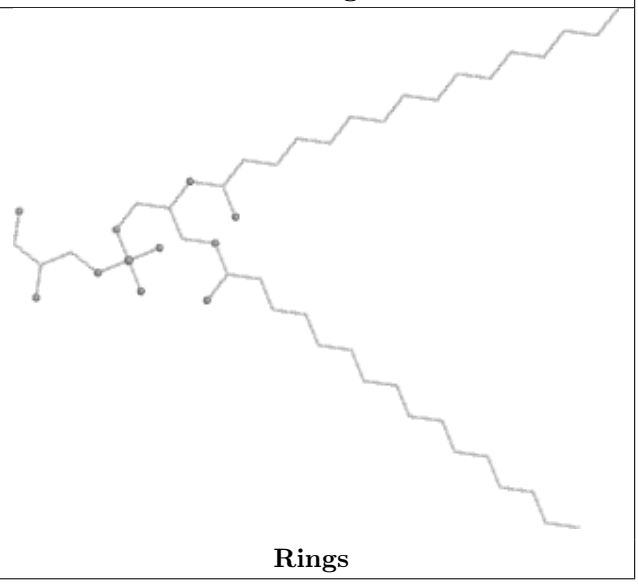
Bond lengths



Bond angles

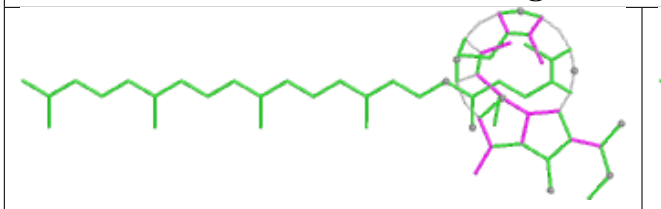


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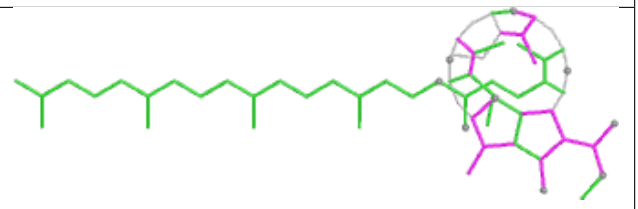


Rings

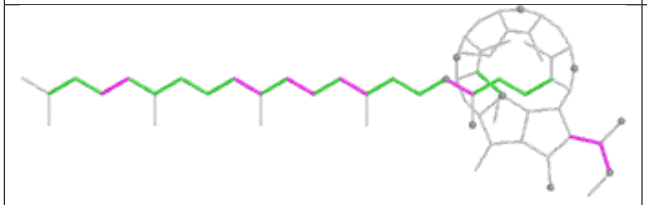
Ligand PHO a 407



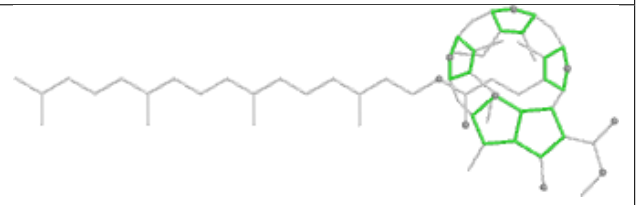
Bond lengths



Bond angles

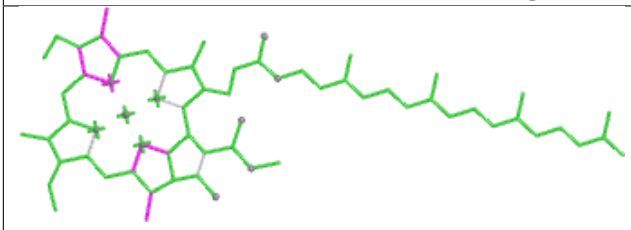


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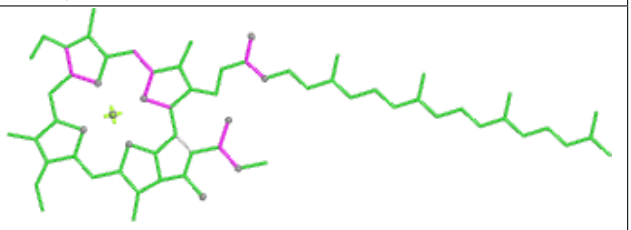


Rings

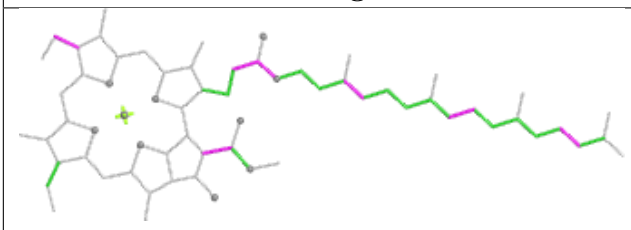
Ligand CLA Q 302



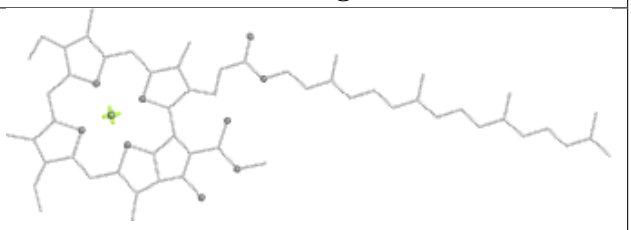
Bond lengths



Bond angles

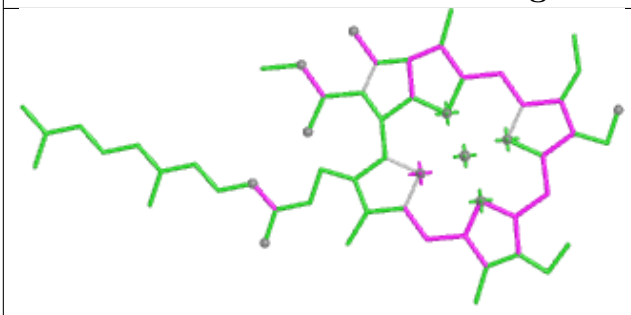


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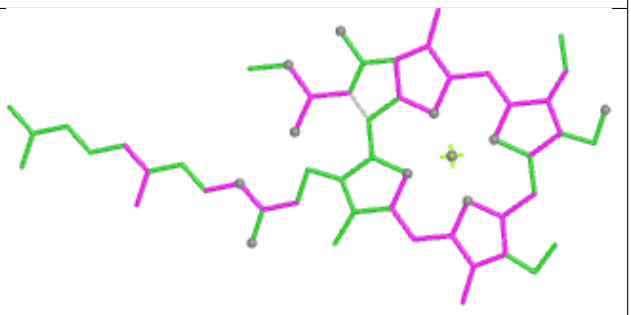


Rings

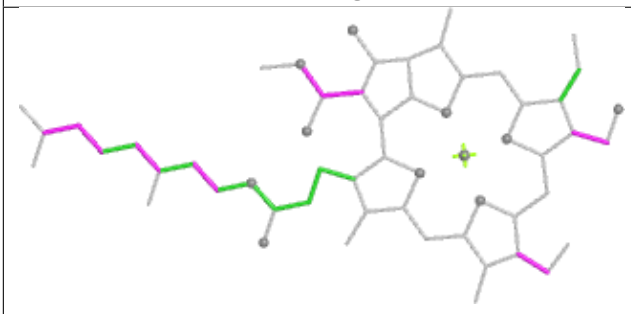
Ligand CHL r 615



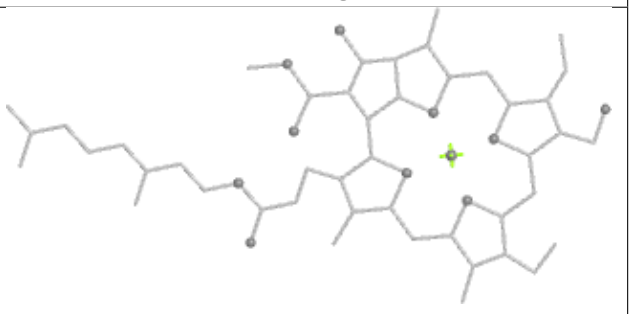
Bond lengths



Bond angles

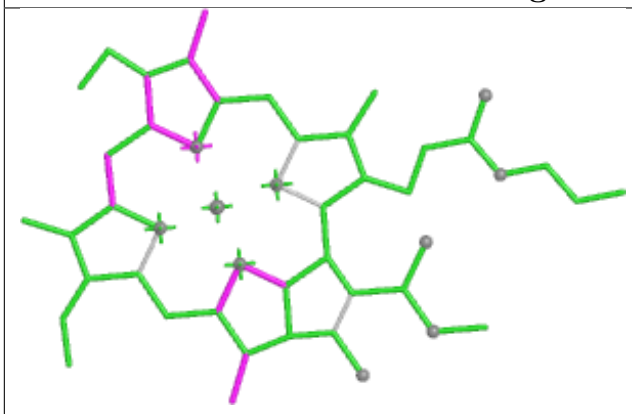


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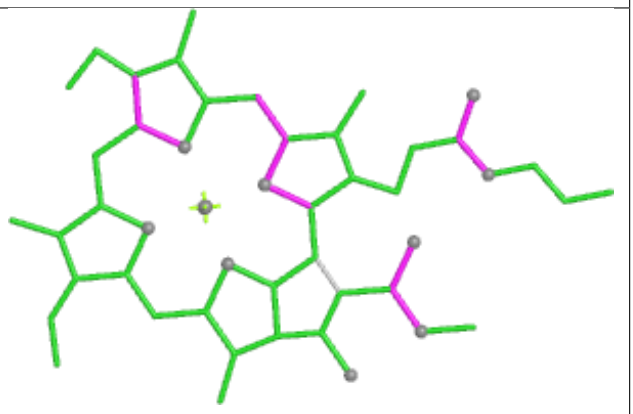


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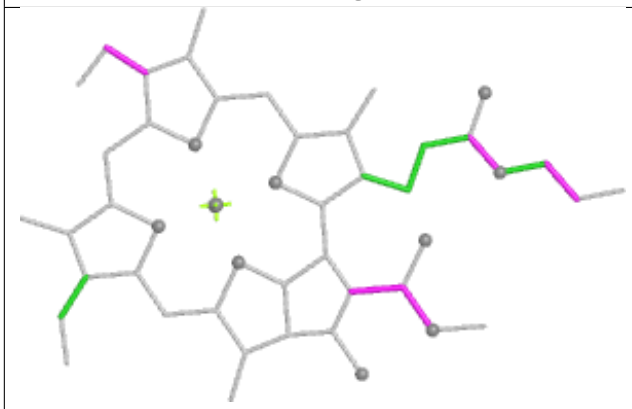
Ligand CLA 2 308



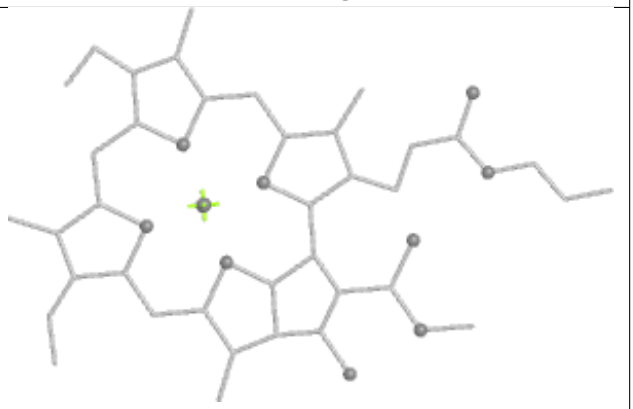
Bond lengths



Bond angles

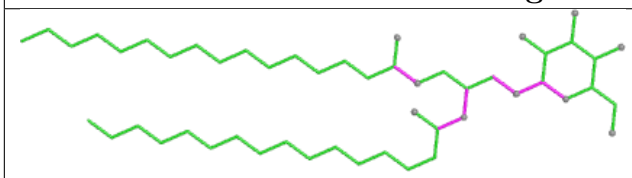


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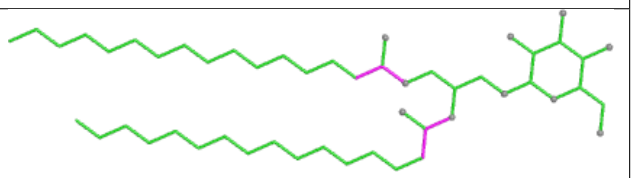


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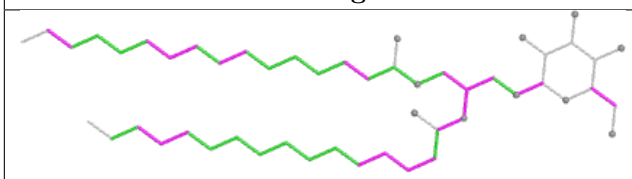
Ligand LMG c 520



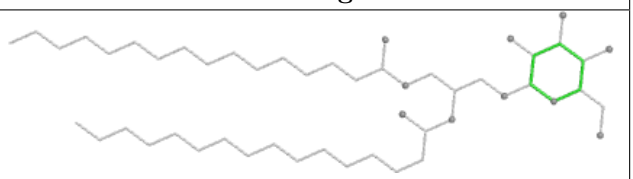
Bond lengths



Bond angles

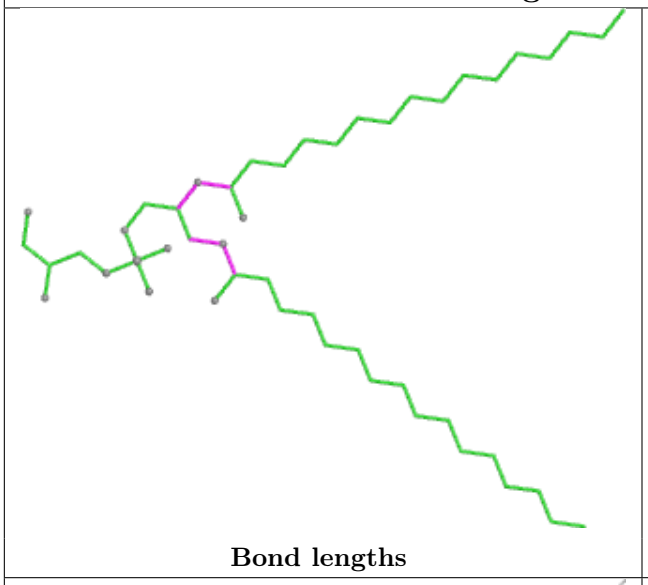


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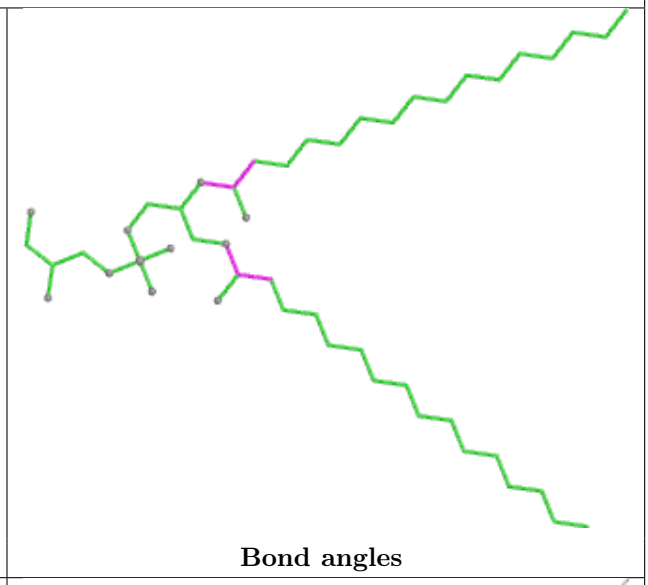


Rings

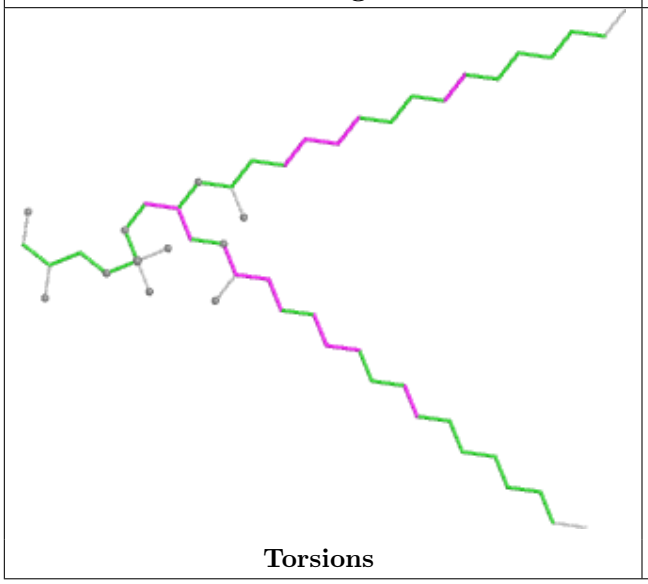
Ligand LHG N 312



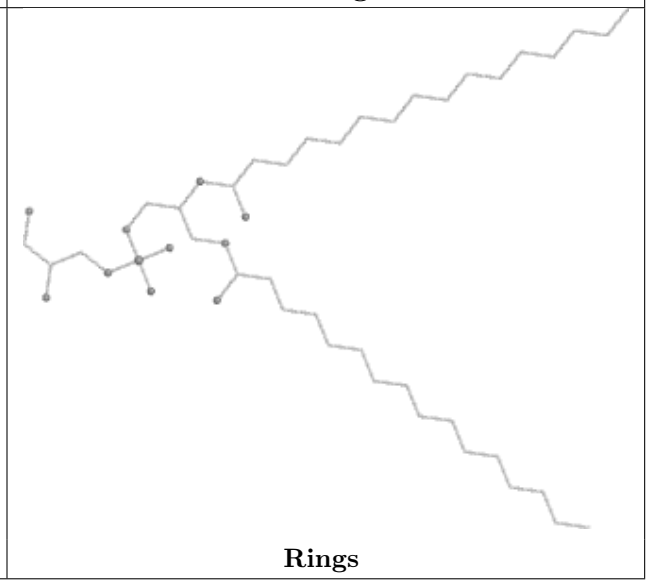
Bond lengths



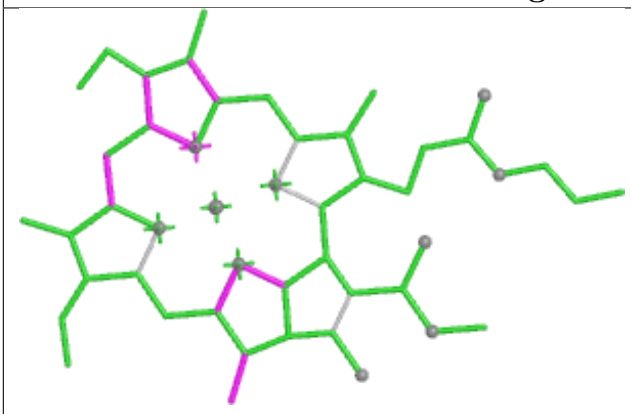
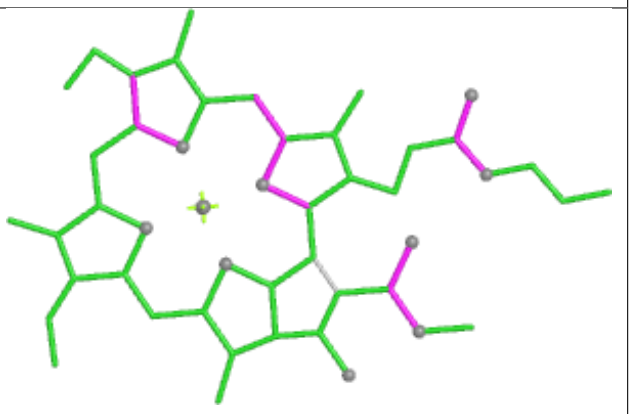
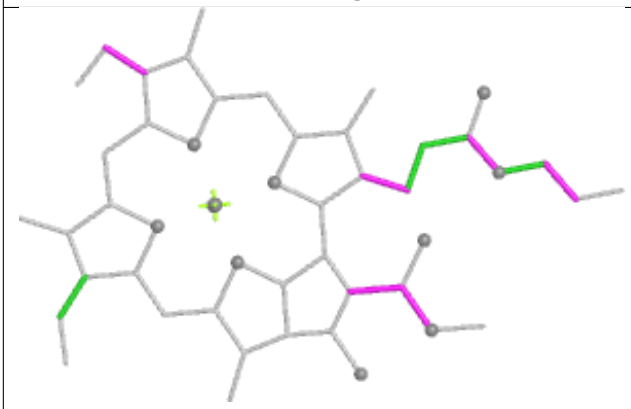
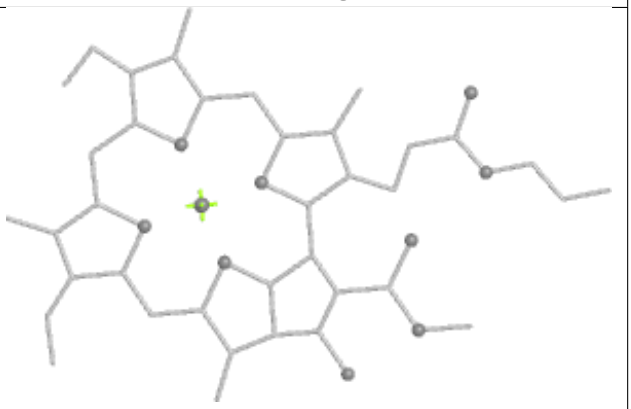
Bond angles

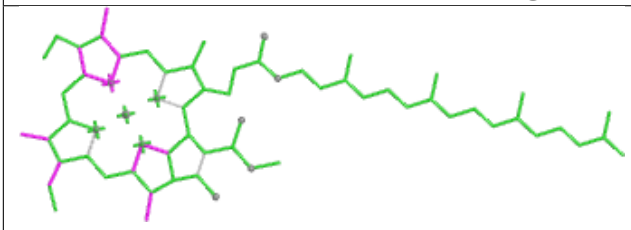
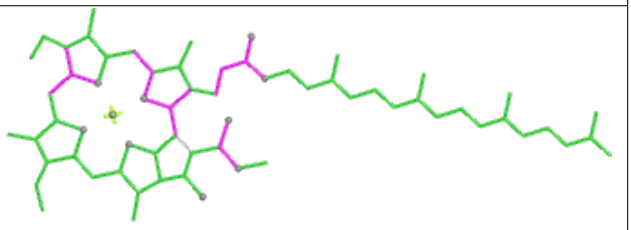
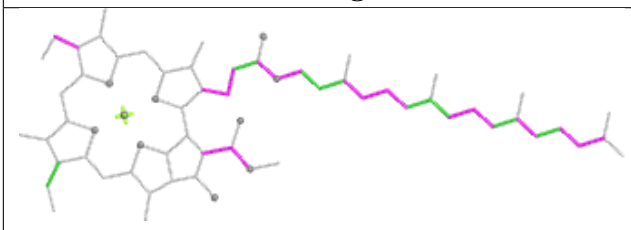
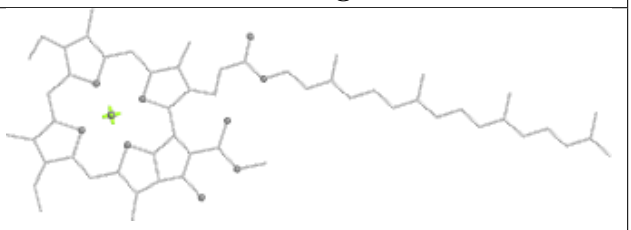


Torsions

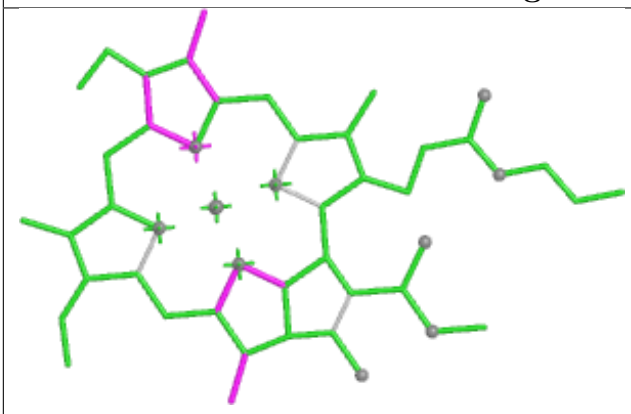


Rings

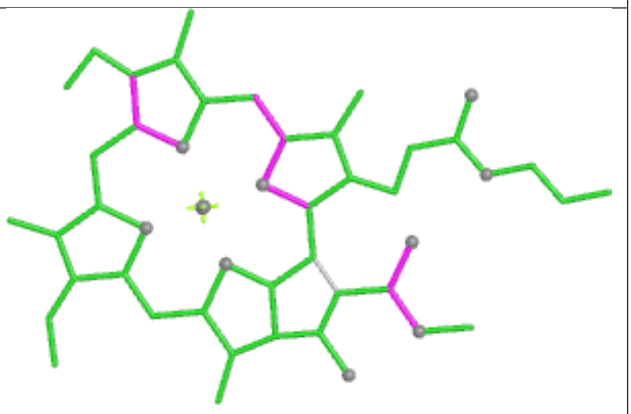
Ligand CLA 3 308	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA C 504	
	
Bond lengths	Bond angles
	
Torsions	Rings

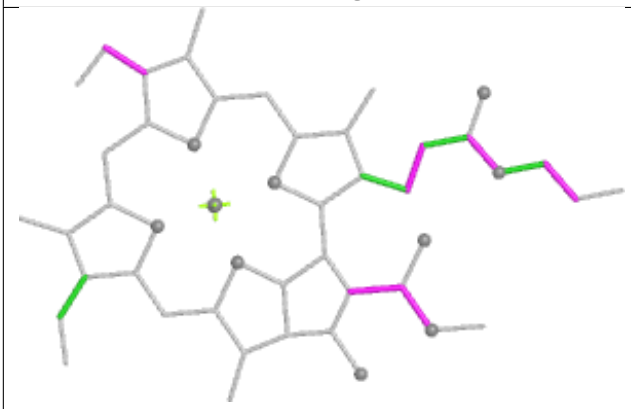
Ligand CLA V 308



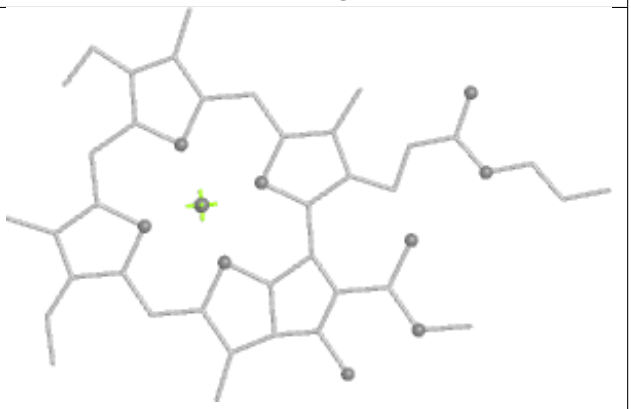
Bond lengths



Bond angles

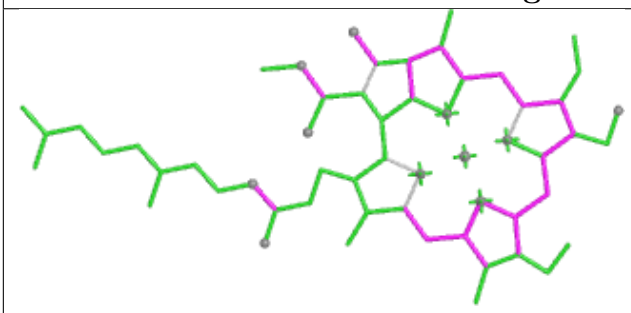


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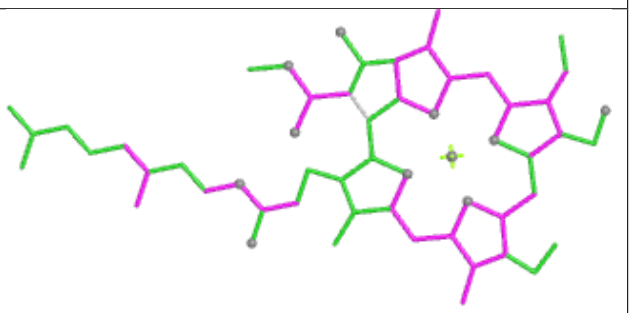


Rings

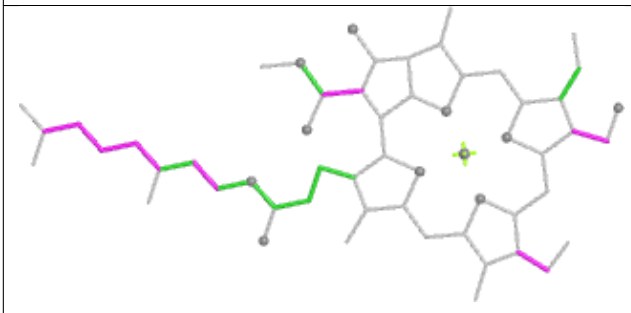
Ligand CHL R 316



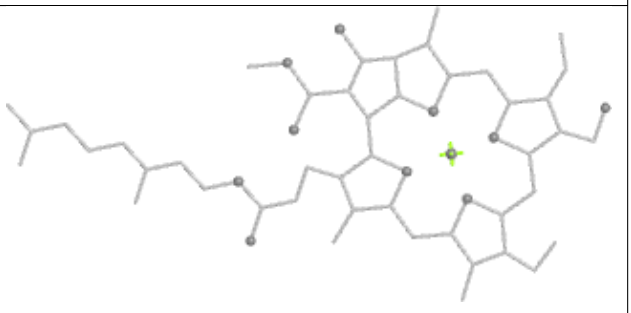
Bond lengths



Bond angles

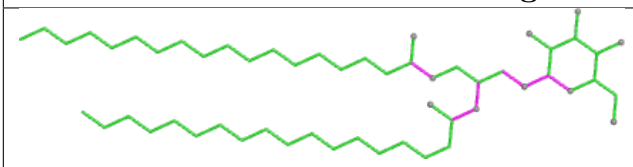


Torsions

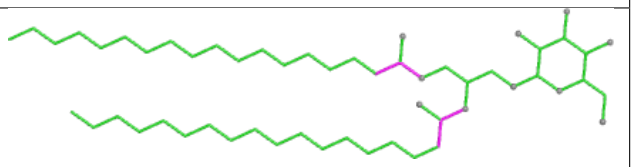


Rings

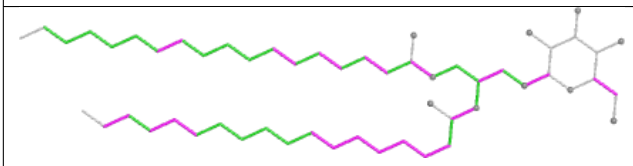
Ligand LMG B 624



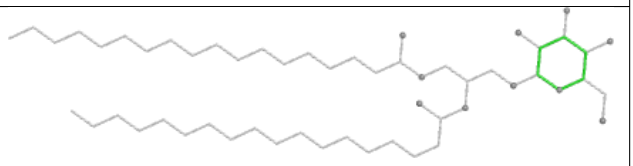
Bond lengths



Bond angles

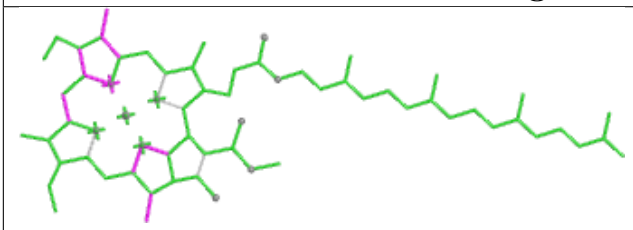


Torsions

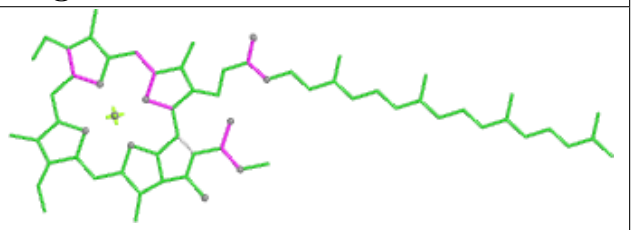


Rings

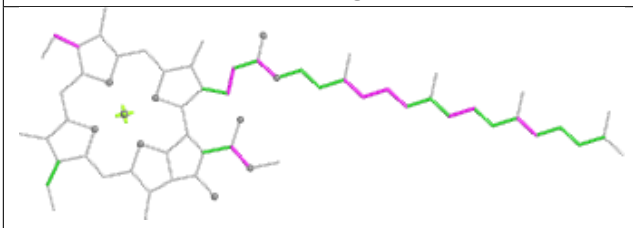
Ligand CLA g 307



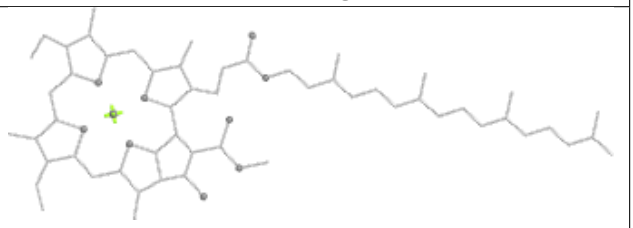
Bond lengths



Bond angles

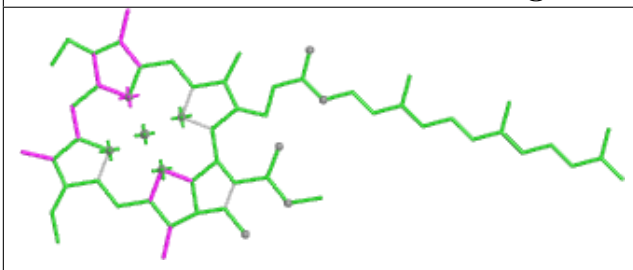


Torsions

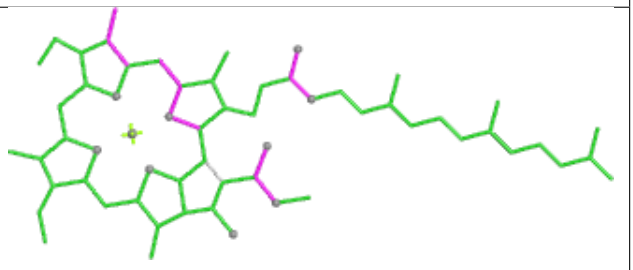


Rings

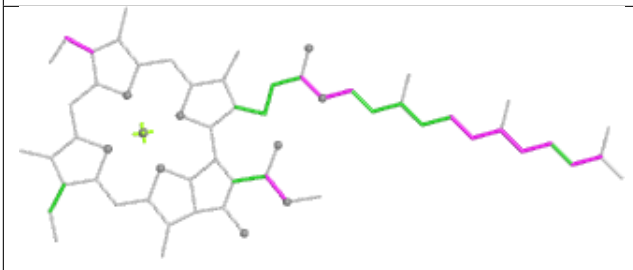
Ligand CLA u 305



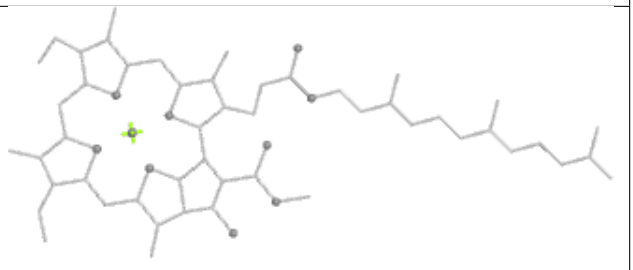
Bond lengths



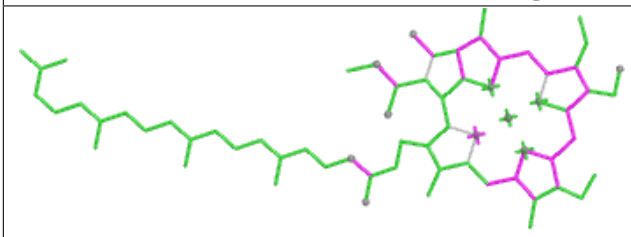
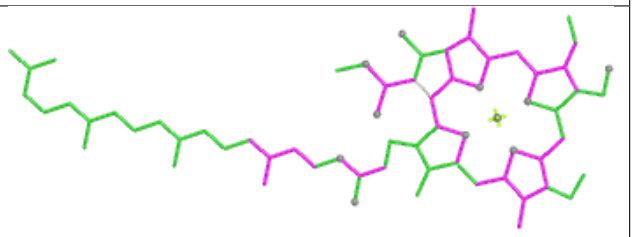
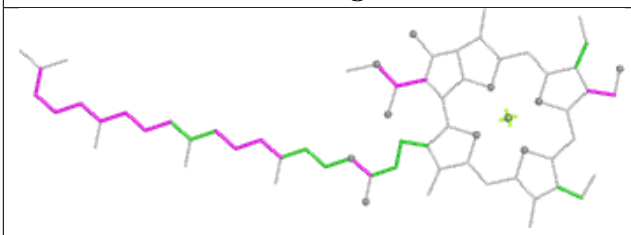
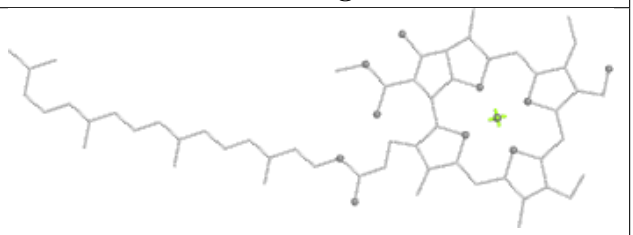
Bond angles

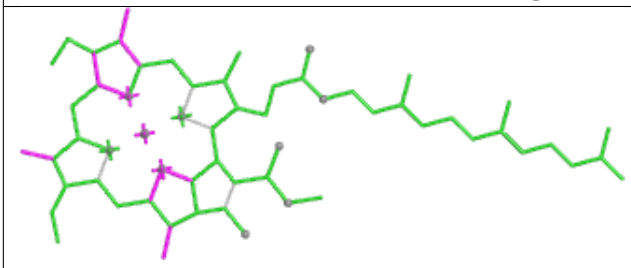
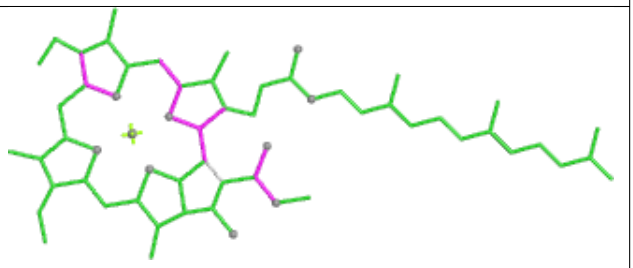
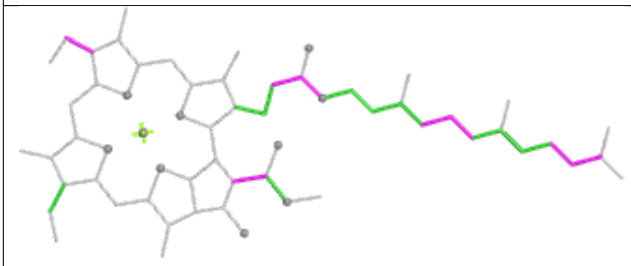
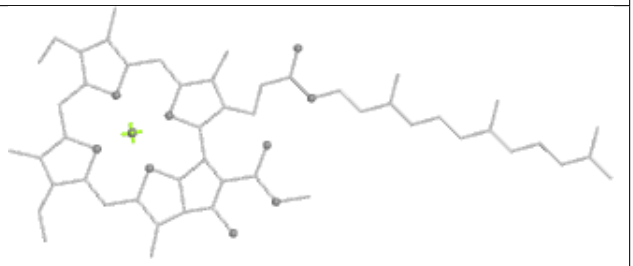


Torsions

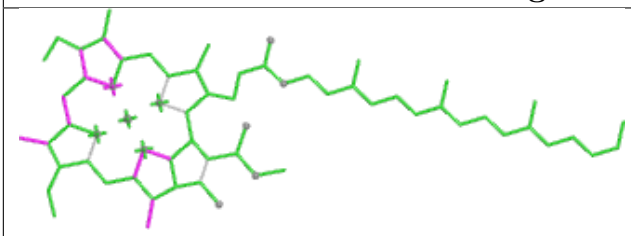


Rings

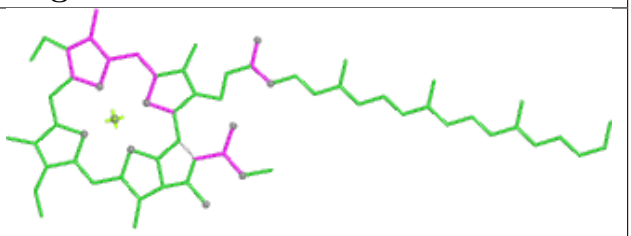
Ligand CHL 5 313	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA u 306	
 Bond lengths	 Bond angles
 Torsions	 Rings

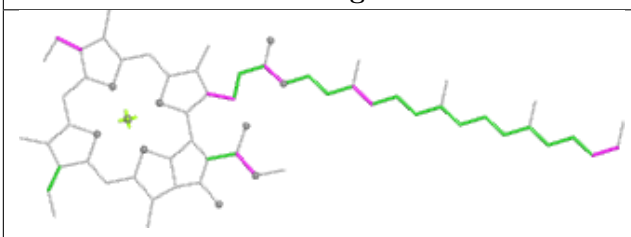
Ligand CLA g 304



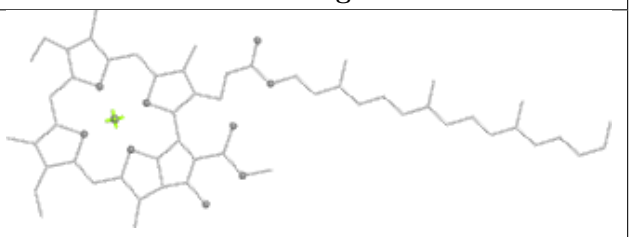
Bond lengths



Bond angles

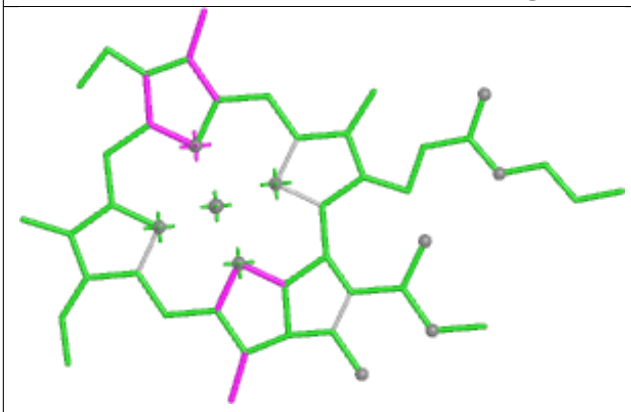


Torsions

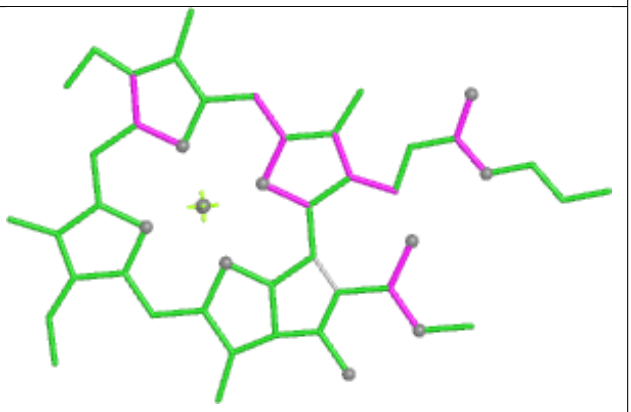


Rings

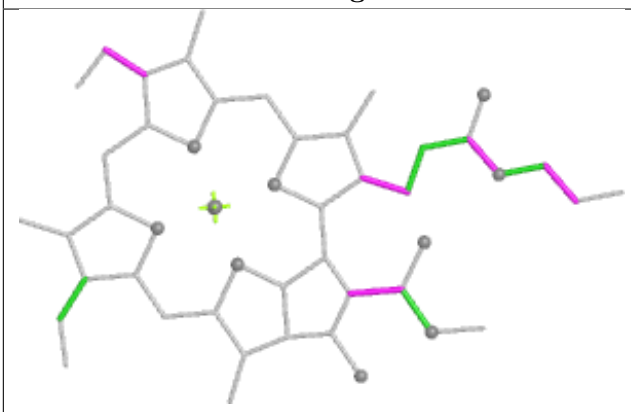
Ligand CLA R 305



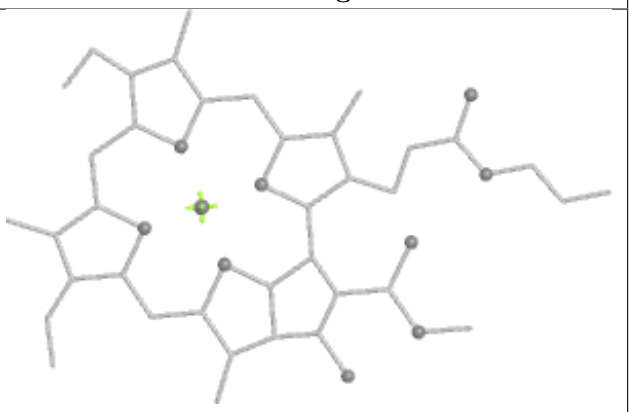
Bond lengths



Bond angles

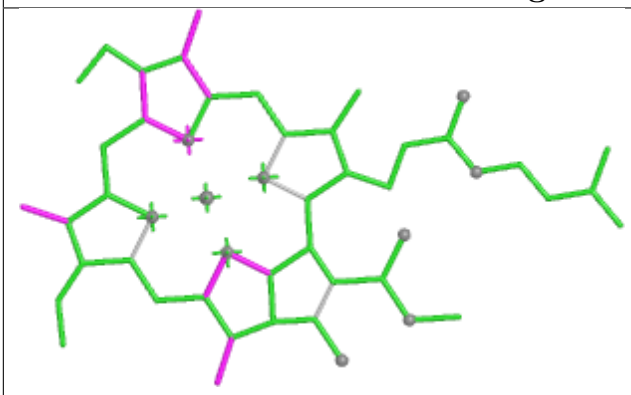


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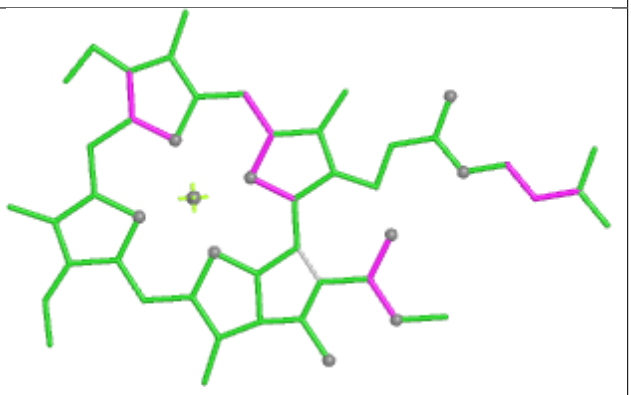


Rings

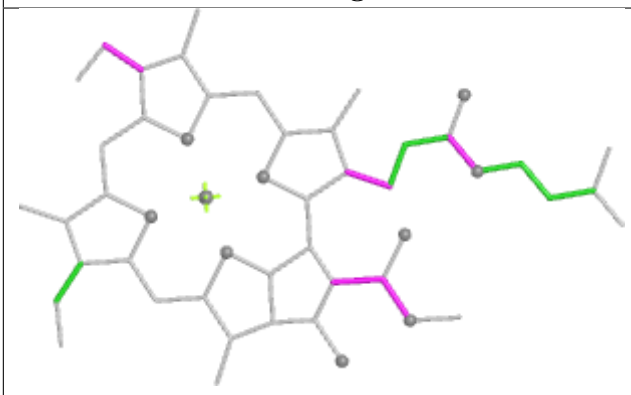
Ligand CLA 2 303



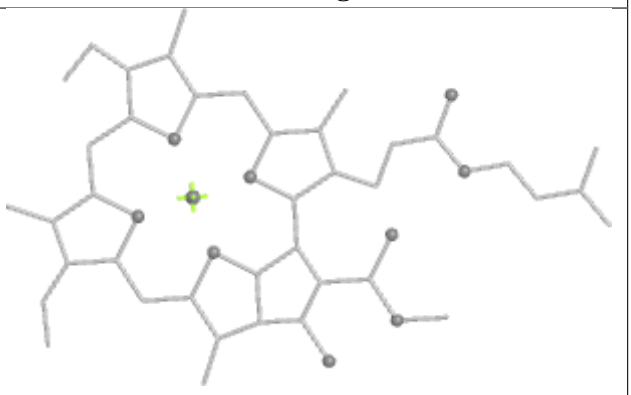
Bond lengths



Bond angles

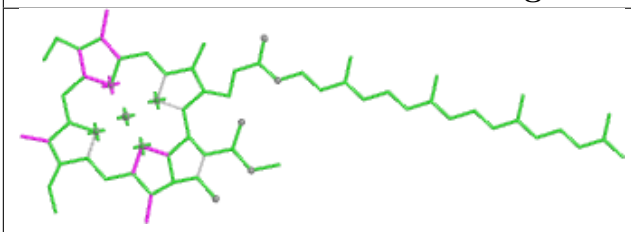


Torsions

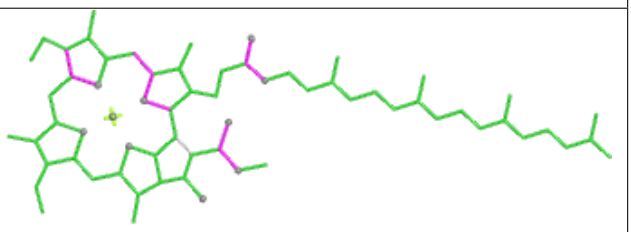


Rings

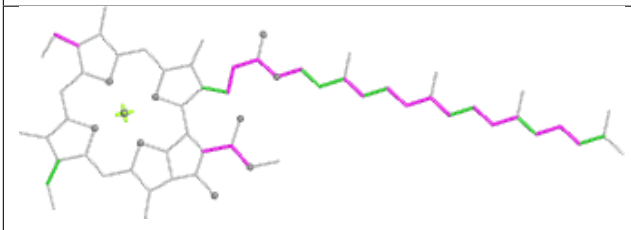
Ligand CLA C 512



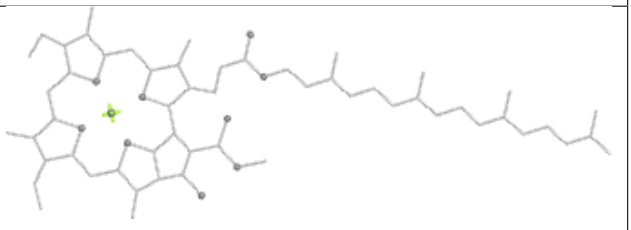
Bond lengths



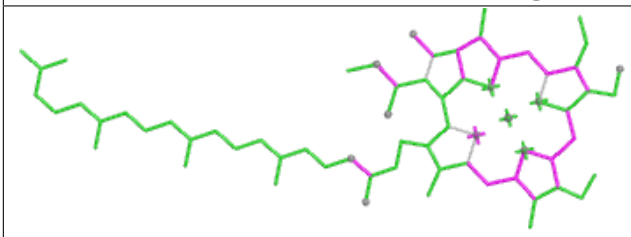
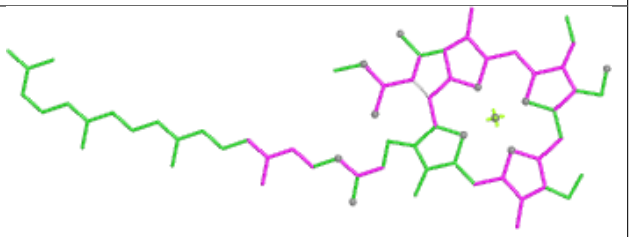
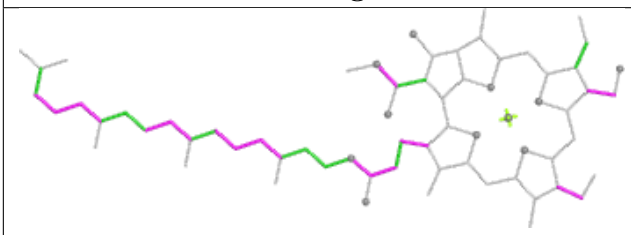
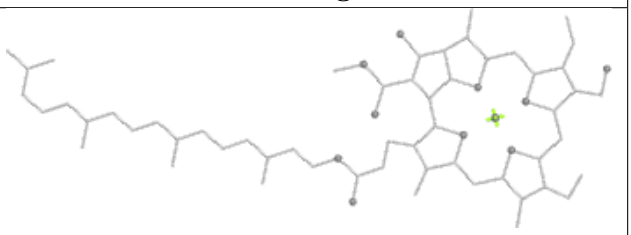
Bond angles

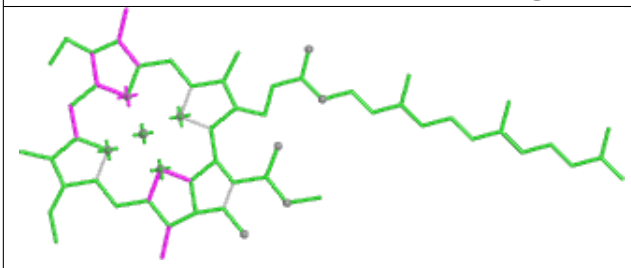
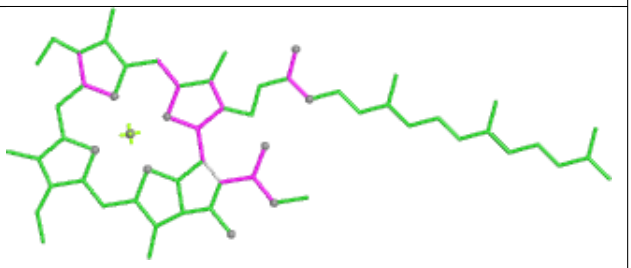
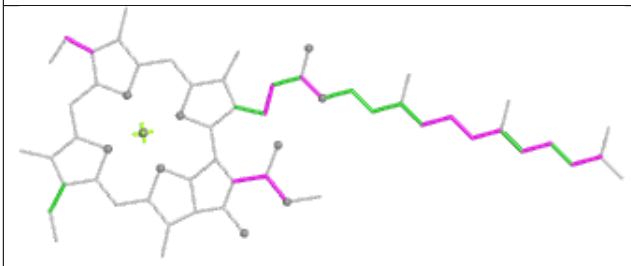
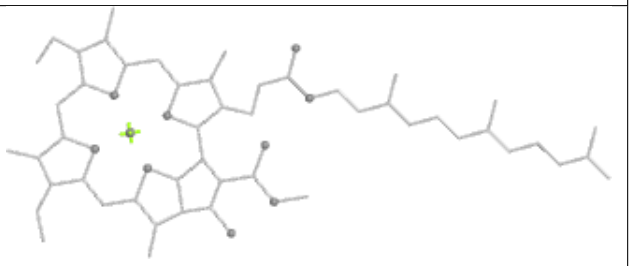


Torsions

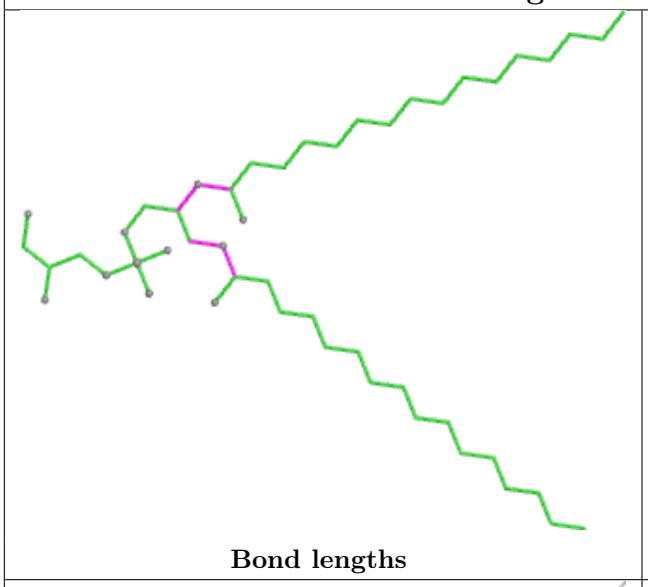


Rings

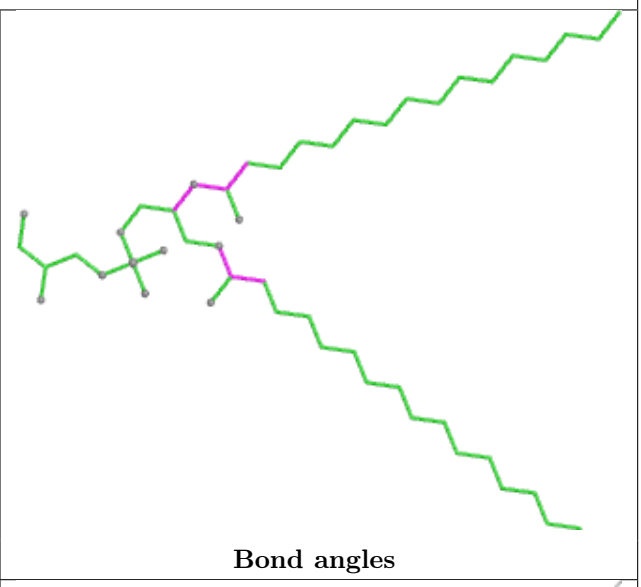
Ligand CHL 1 316	
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand CLA 6 306	
 Bond lengths	 Bond angles
 Torsions	 Rings

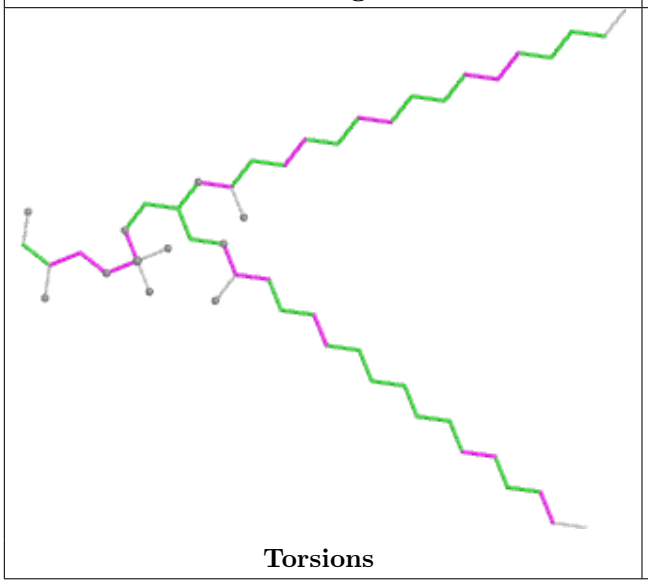
Ligand LHG S 312



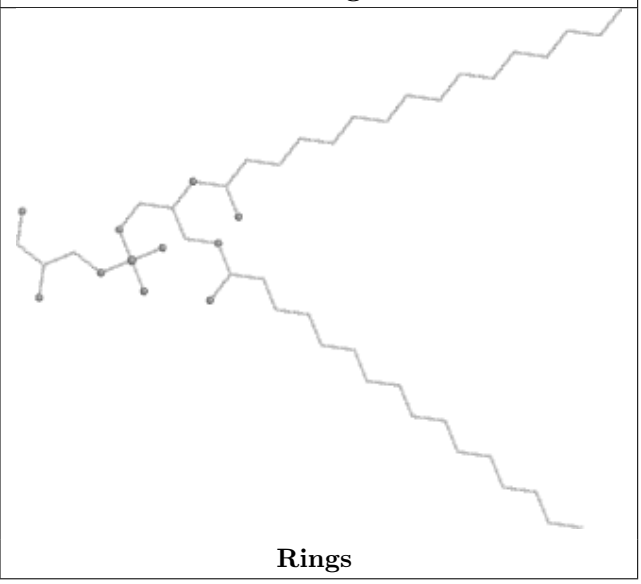
Bond lengths



Bond angles

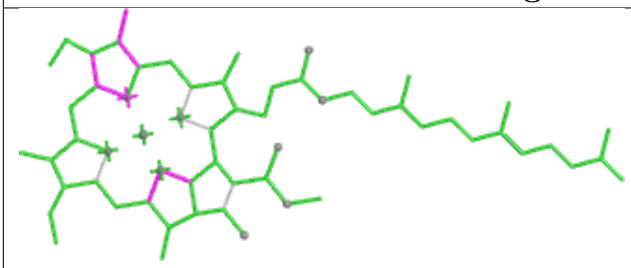


Torsions

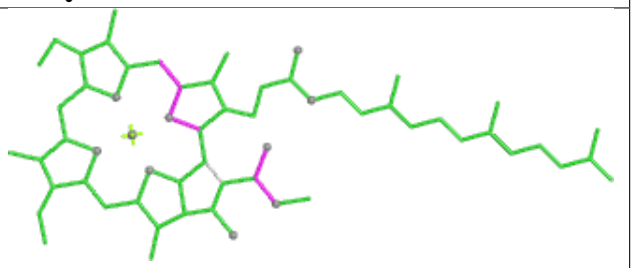


Rings

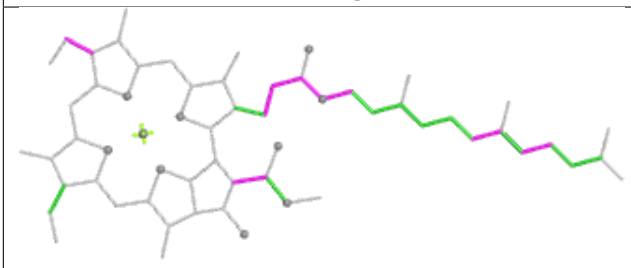
Ligand CLA Q 306



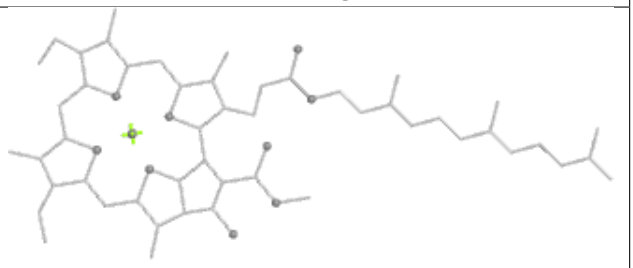
Bond lengths



Bond angles

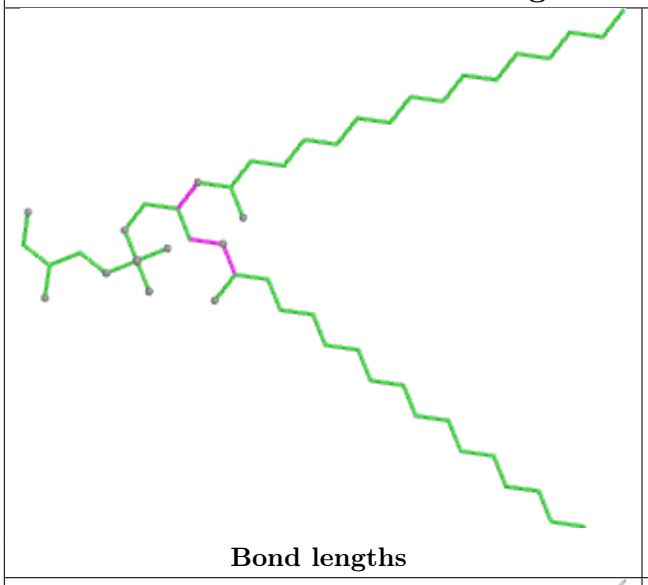


Torsions

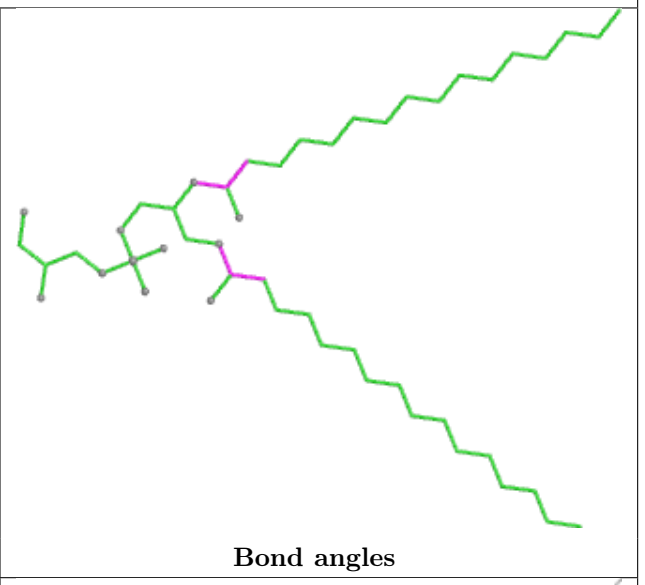


Rings

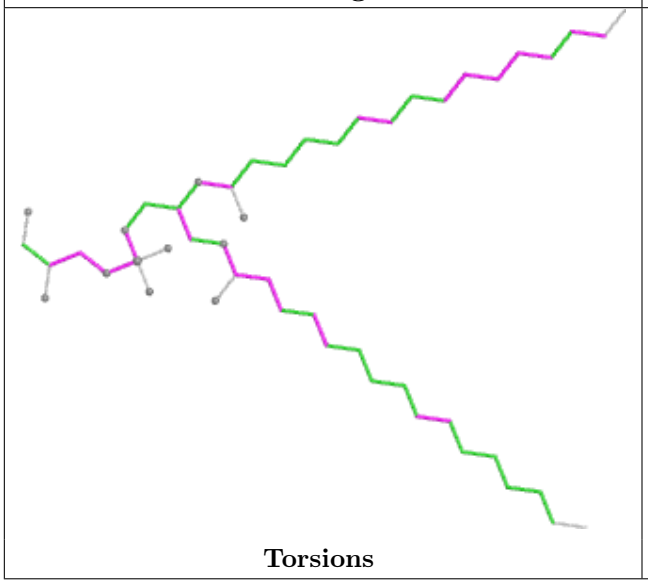
Ligand LHG c 522



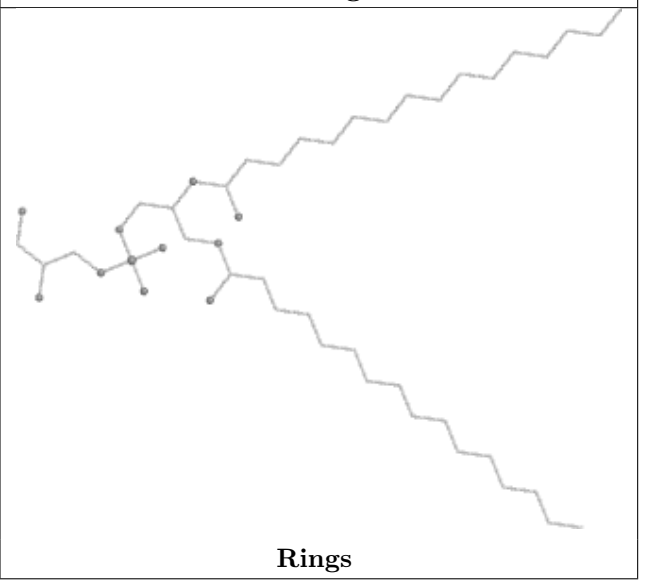
Bond lengths



Bond angles

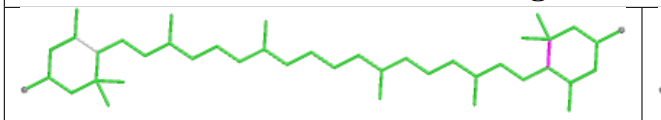


Torsions

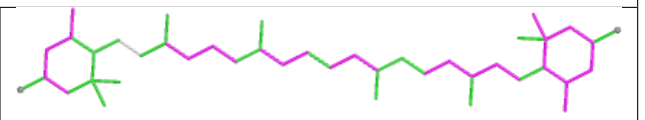


Rings

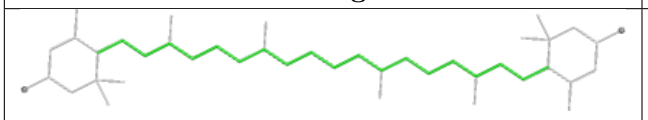
Ligand LUT 4 310



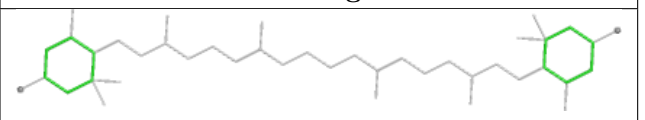
Bond lengths



Bond angles

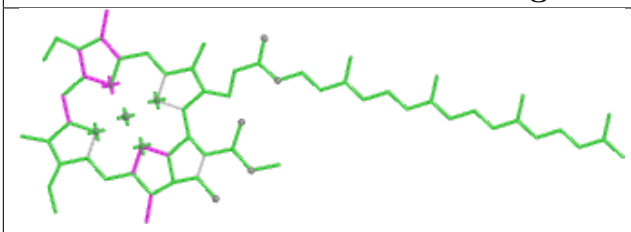


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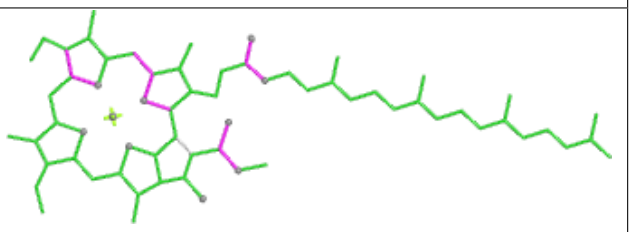


Rings

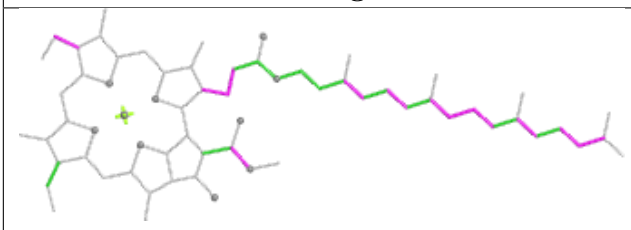
Ligand CLA r 606



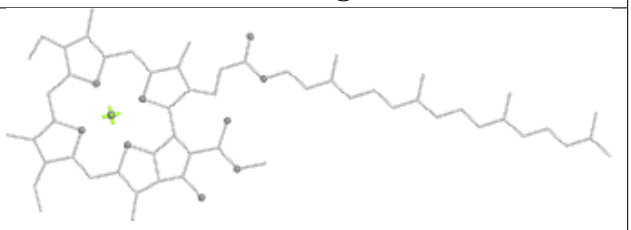
Bond lengths



Bond angles

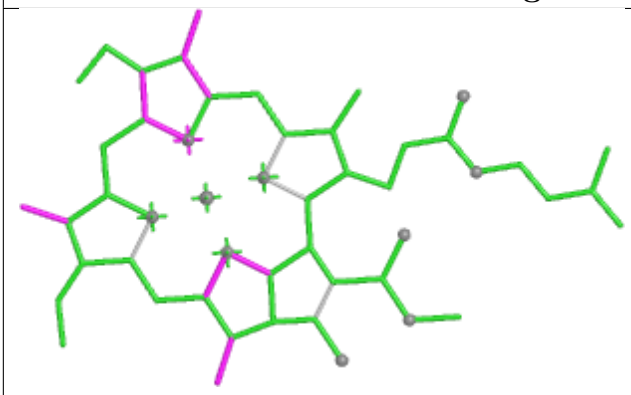


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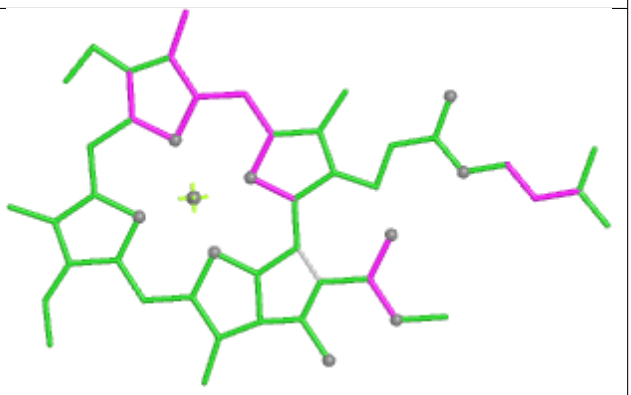


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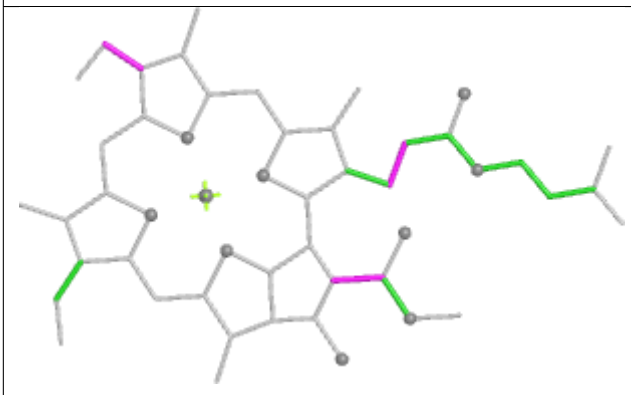
Ligand CLA N 303



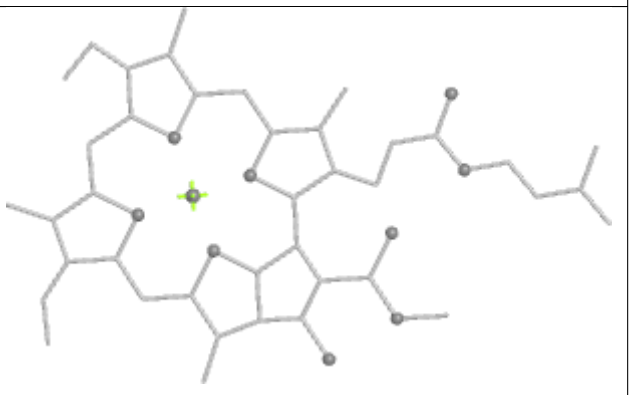
Bond lengths



Bond angles

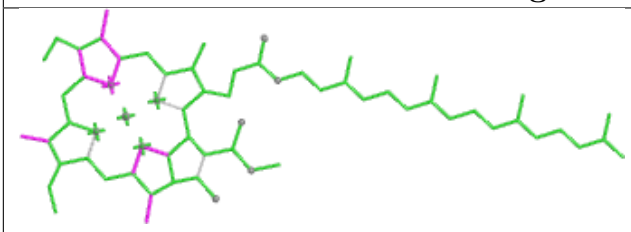


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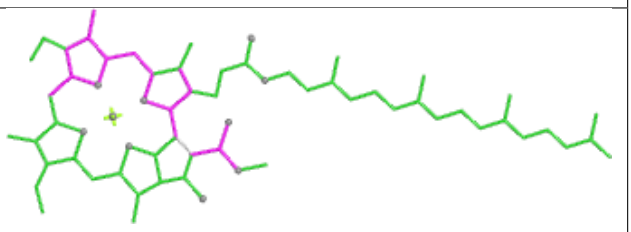


Rings

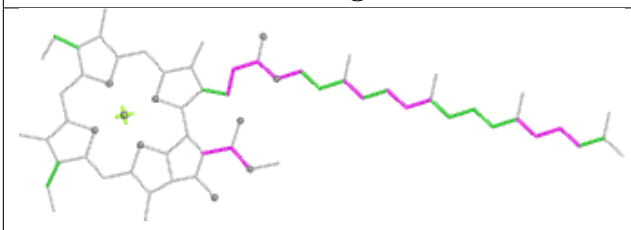
Ligand CLA c 506



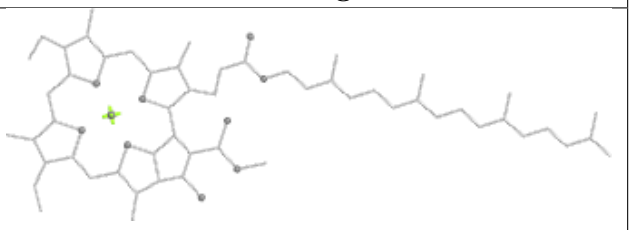
Bond lengths



Bond angles

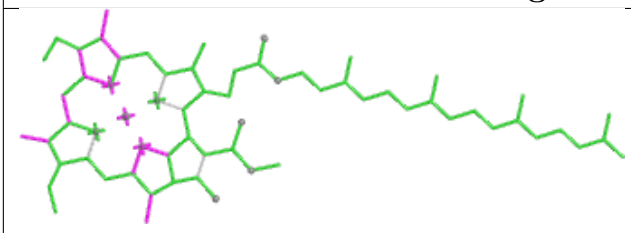


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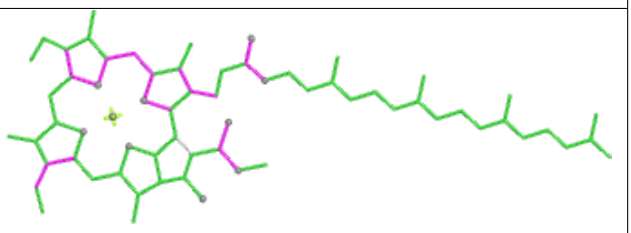


Rings

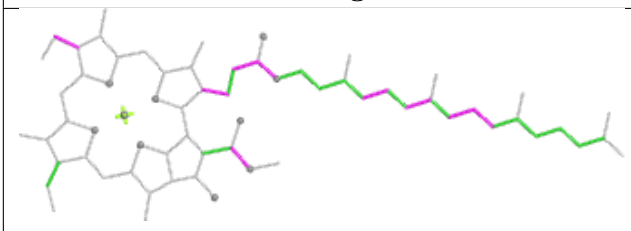
Ligand CLA 1 307



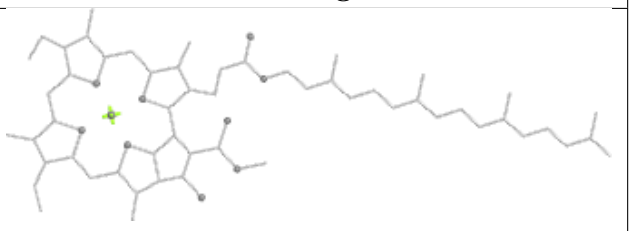
Bond lengths



Bond angles

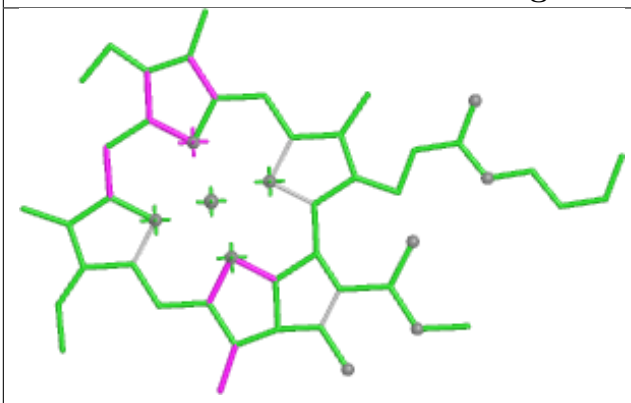


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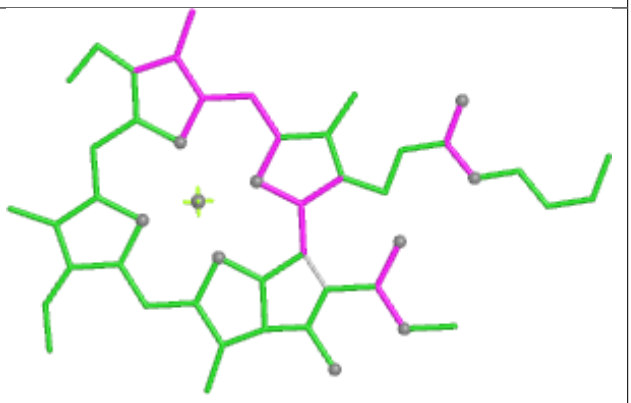


Rings

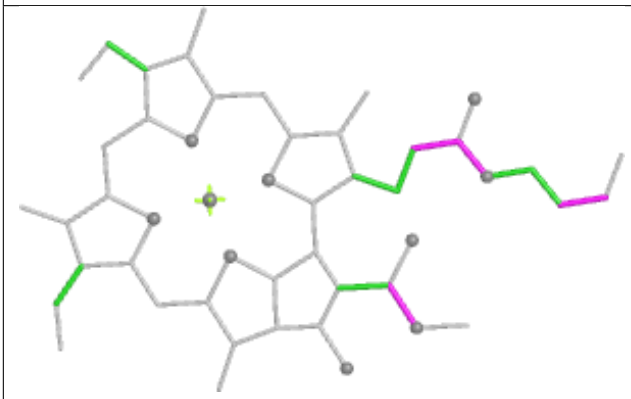
Ligand CLA r 608



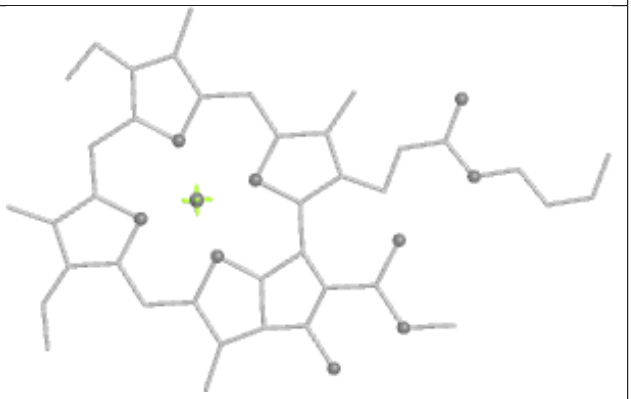
Bond lengths



Bond angles

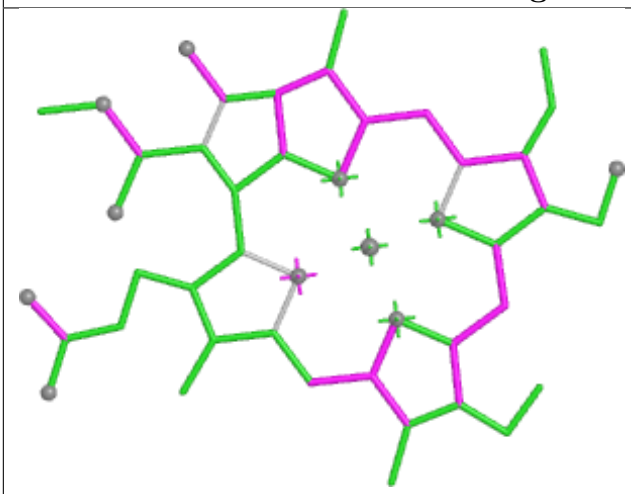


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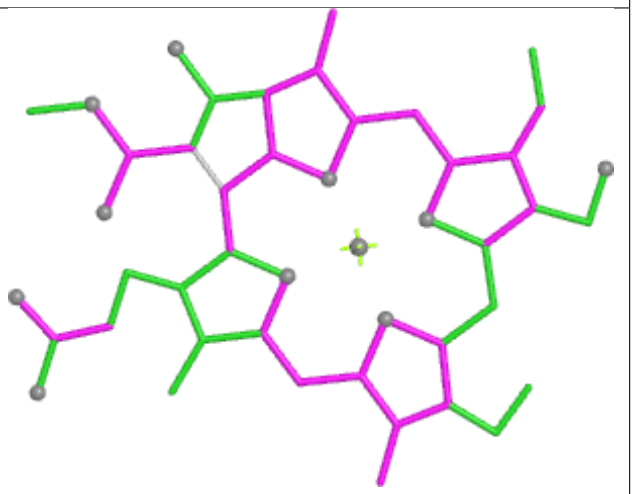


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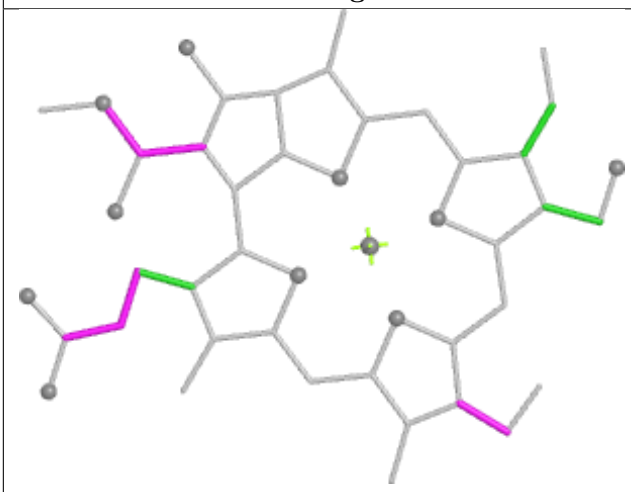
Ligand CHL s 314



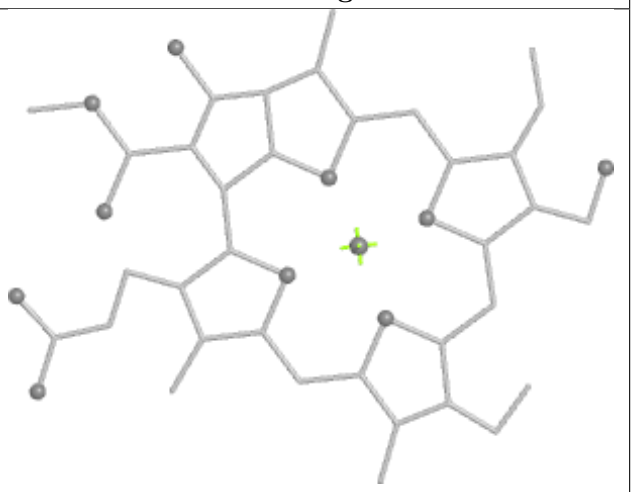
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Bond angles

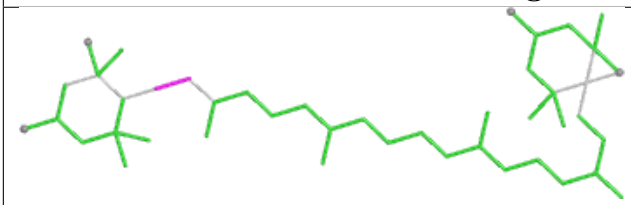


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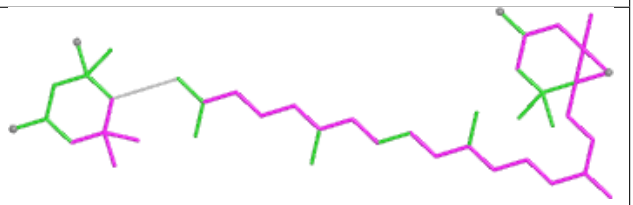


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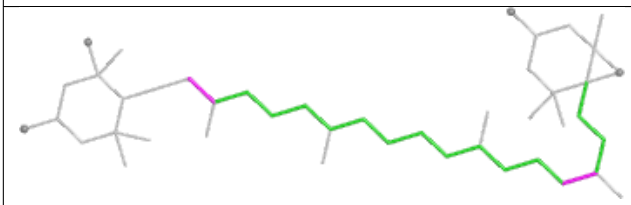
Ligand NEX S 317



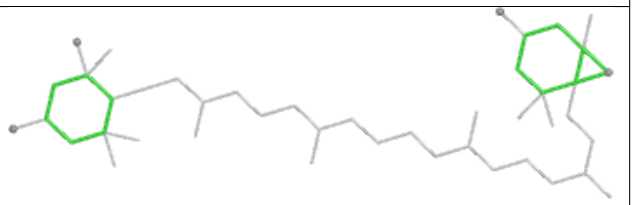
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Bond angles

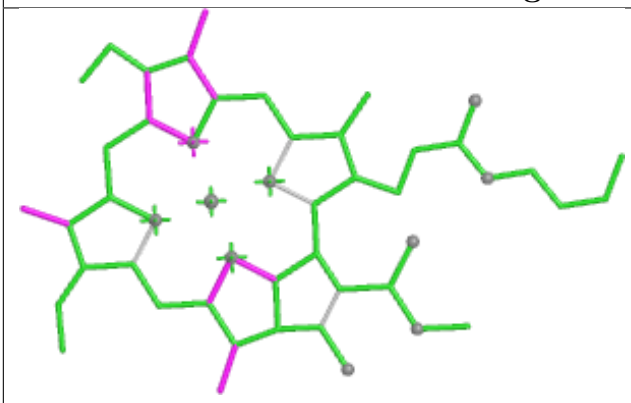


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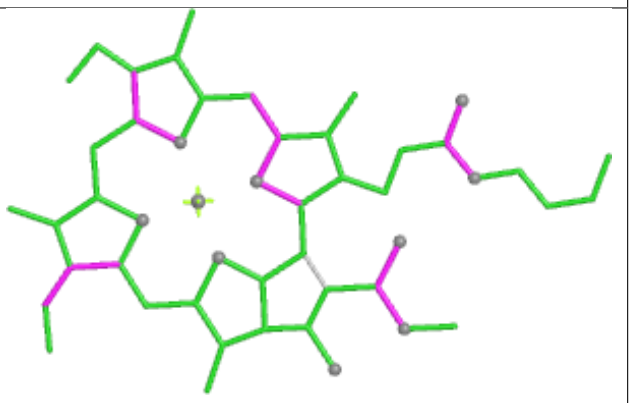


Rings

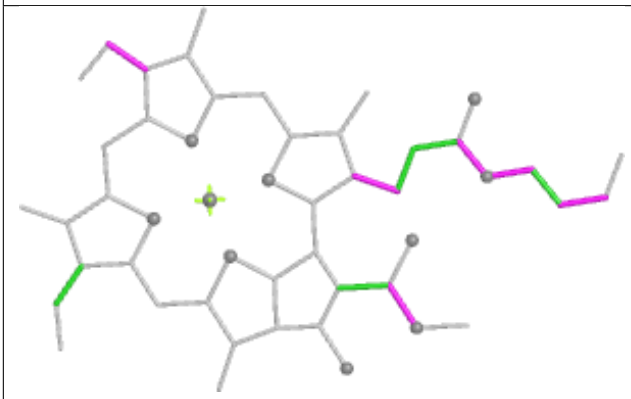
Ligand CLA R 302



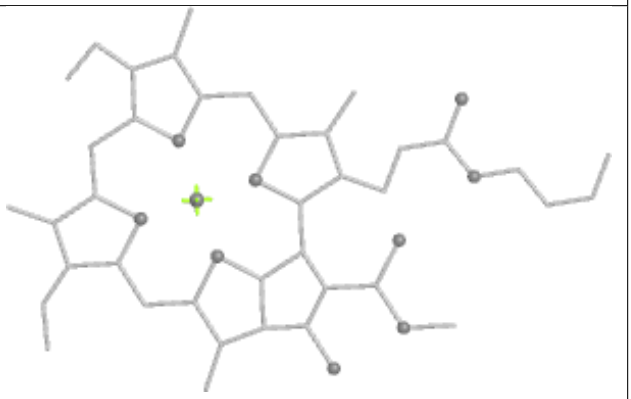
Bond lengths



Bond angles

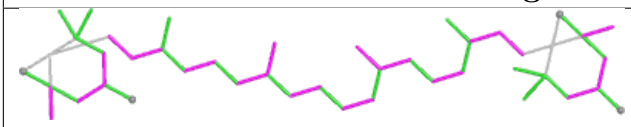


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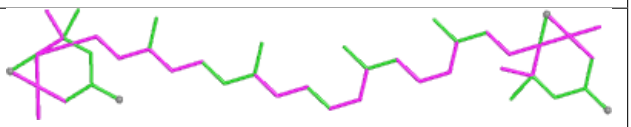


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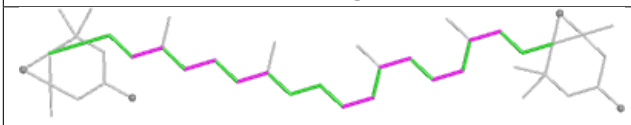
Ligand XAT V 311



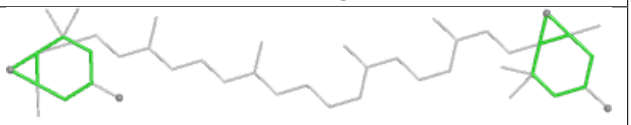
Bond lengths



Bond angles

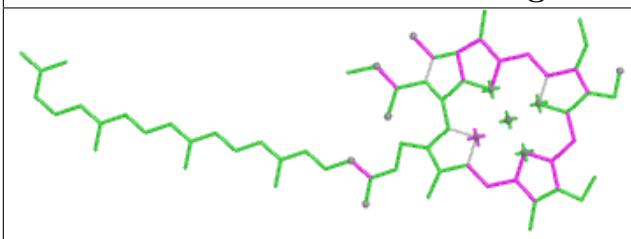


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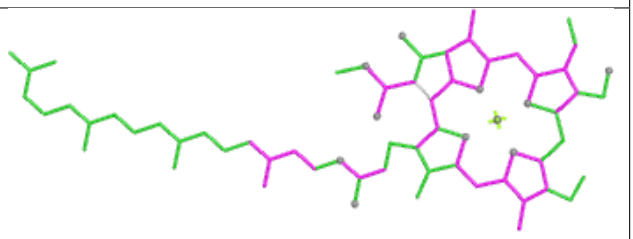


Rings

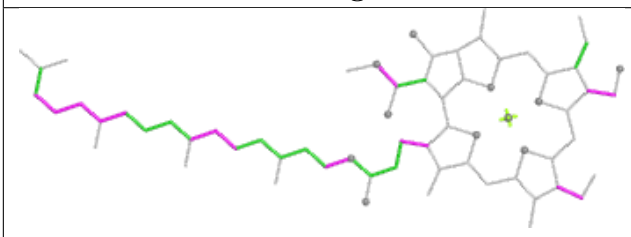
Ligand CHL 1 318



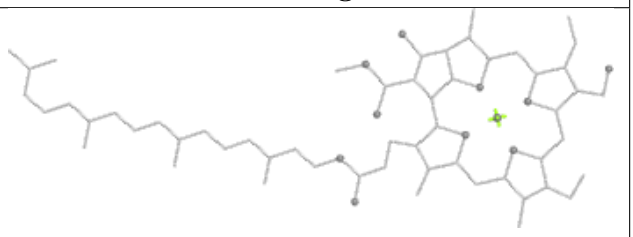
Bond lengths



Bond angles

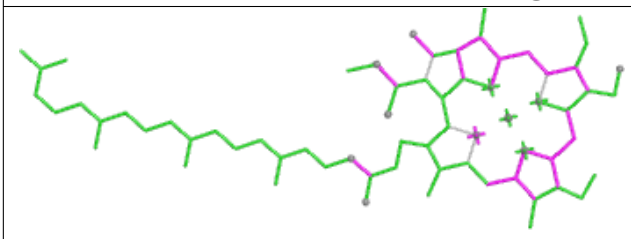


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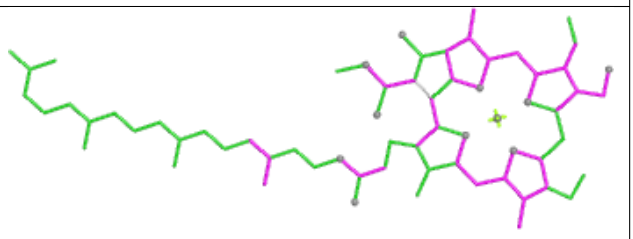


Rings

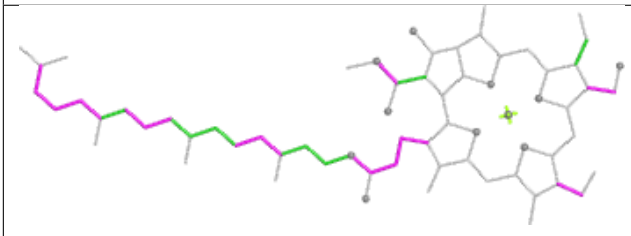
Ligand CHL 3 315



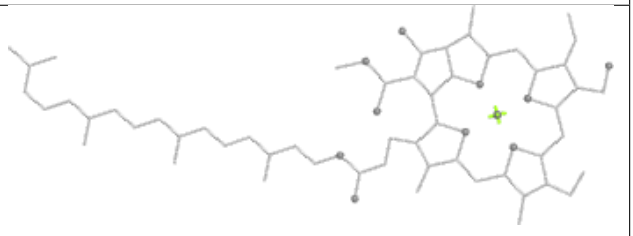
Bond lengths



Bond angles

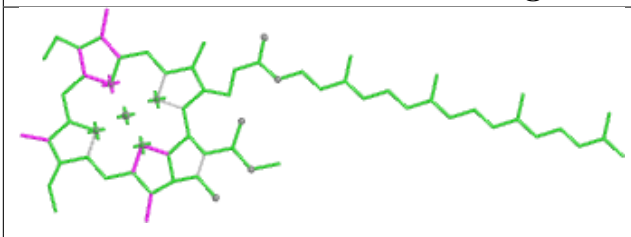


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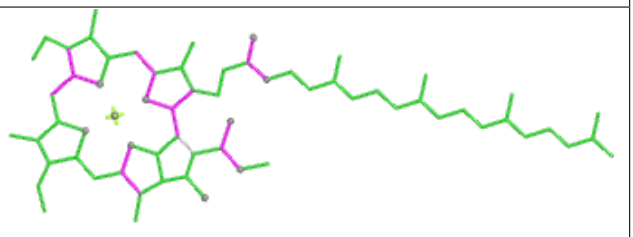


Rings

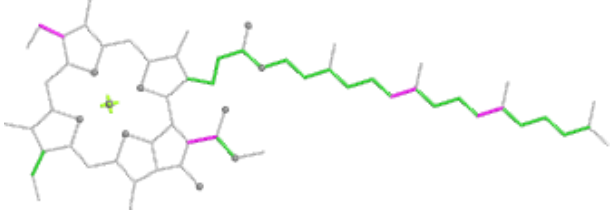
Ligand CLA B 616



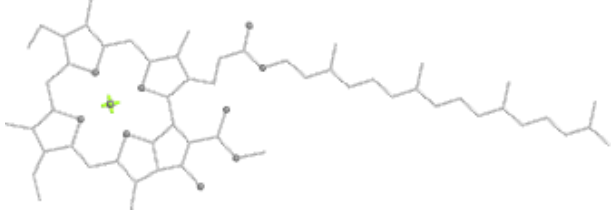
Bond lengths



Bond angles

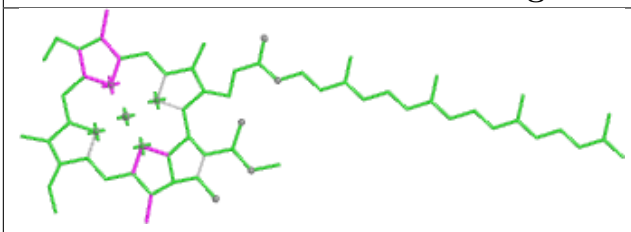


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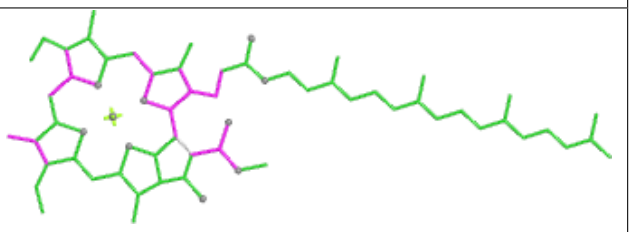


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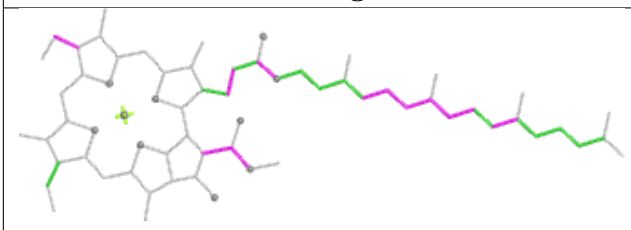
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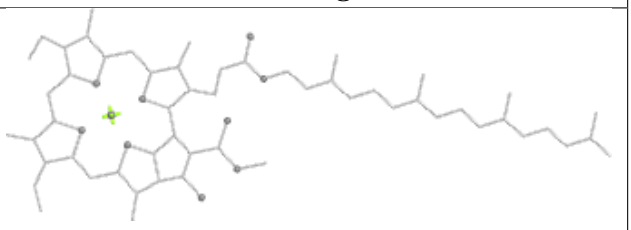
Bond lengths



Bond angles

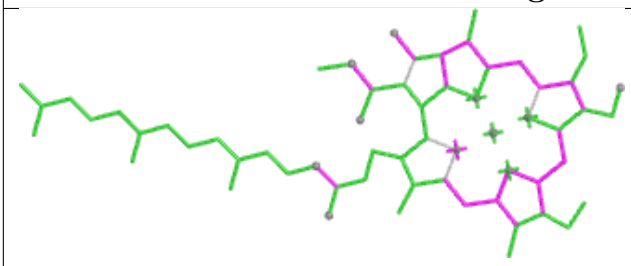


Torsions

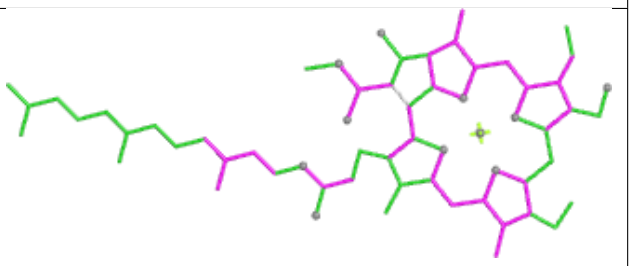


Rings

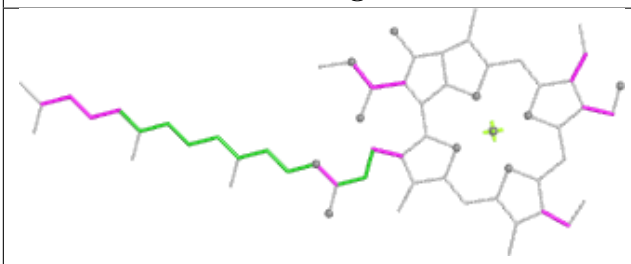
Ligand CHL 3 316



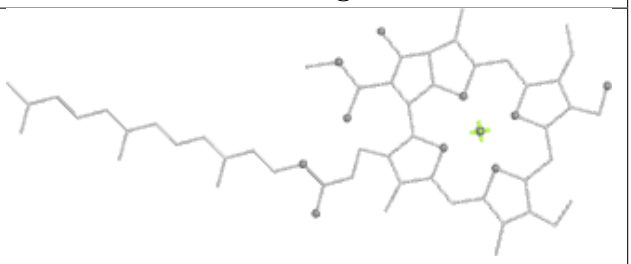
Bond lengths



Bond angles

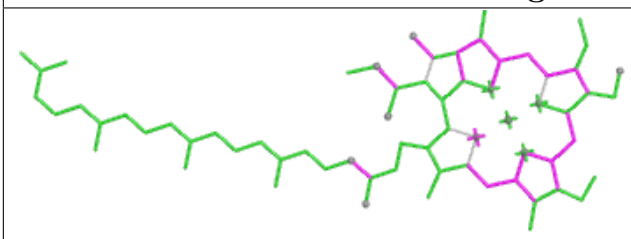


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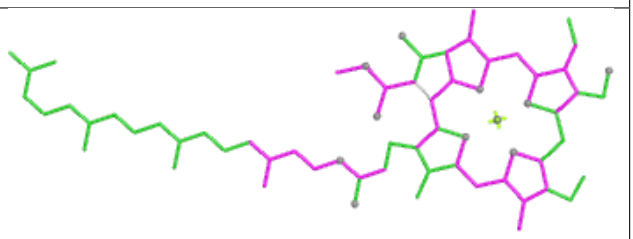


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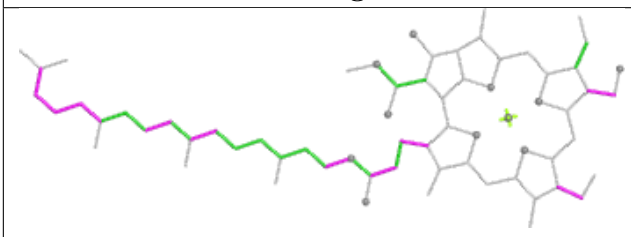
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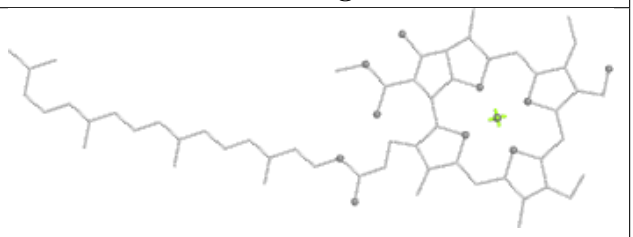
Bond lengths



Bond angles

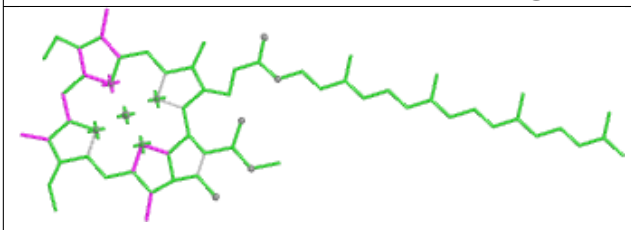


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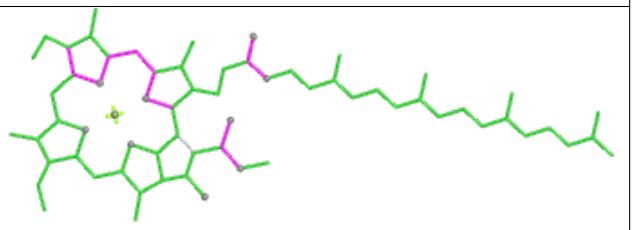


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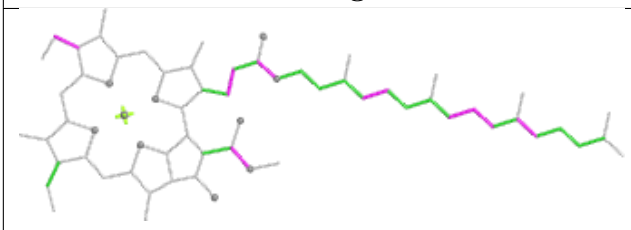
Ligand CLA v 307



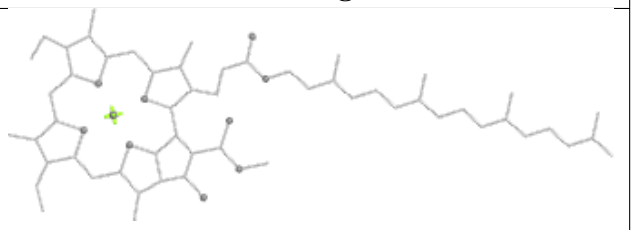
Bond lengths



Bond angles

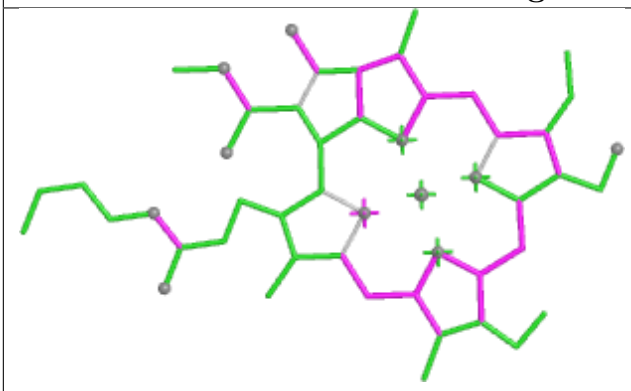


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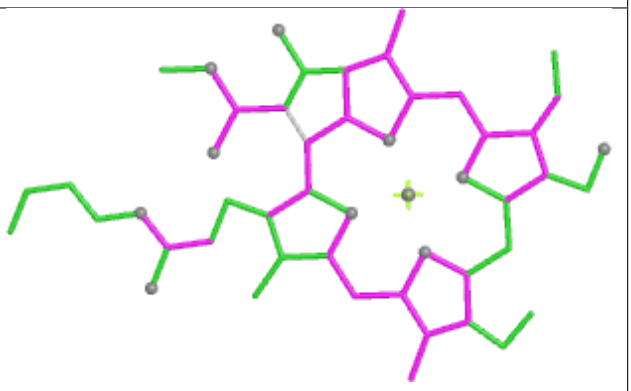


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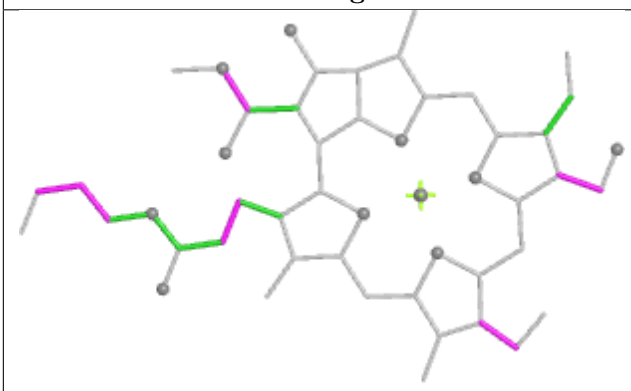
Ligand CHL 5 315



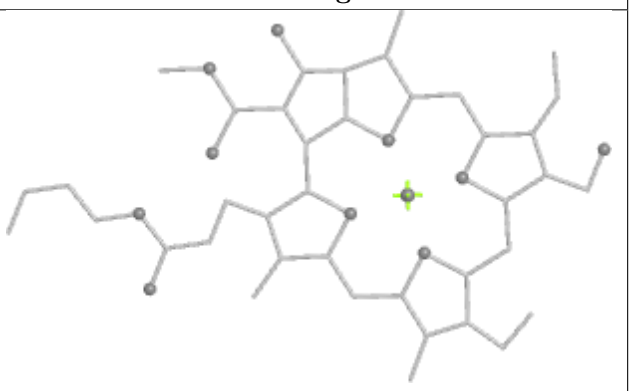
Bond lengths



Bond angles

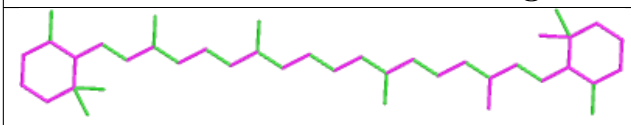


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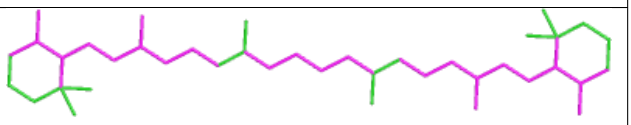


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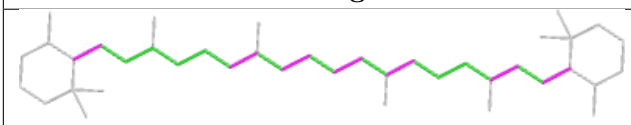
Ligand BCR B 620



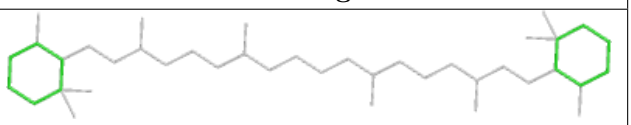
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Bond angles

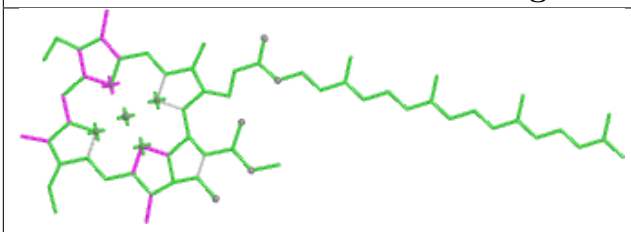


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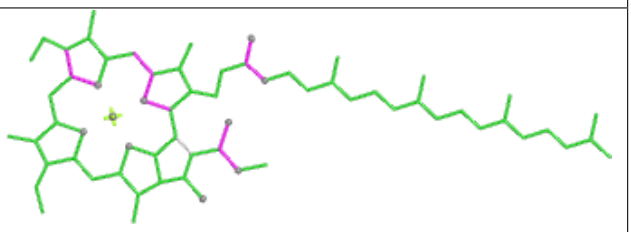


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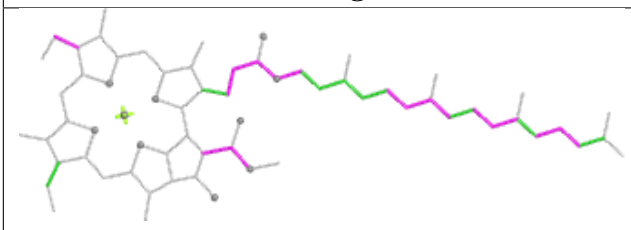
Ligand CLA c 511



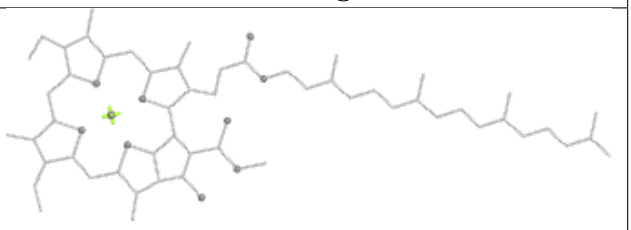
Bond lengths



Bond angles

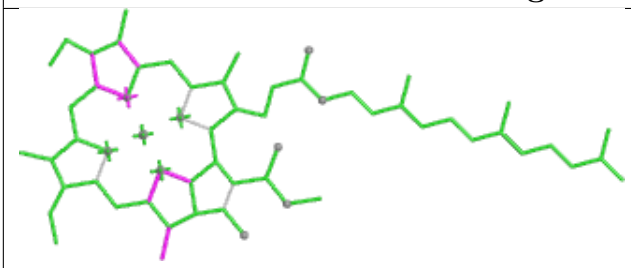


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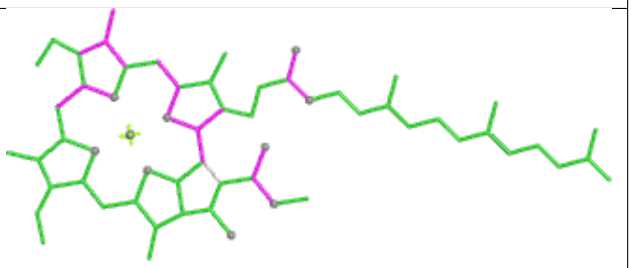


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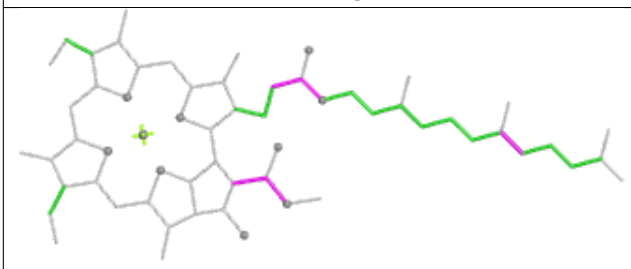
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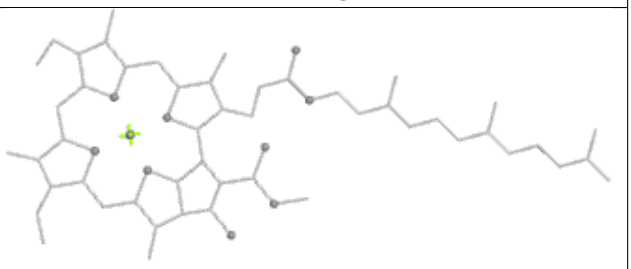
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Bond angles

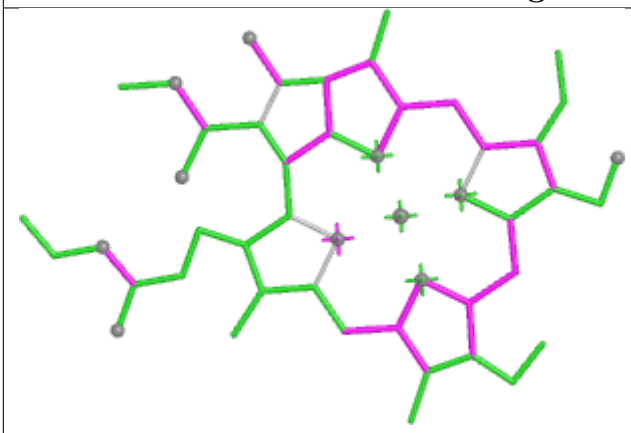


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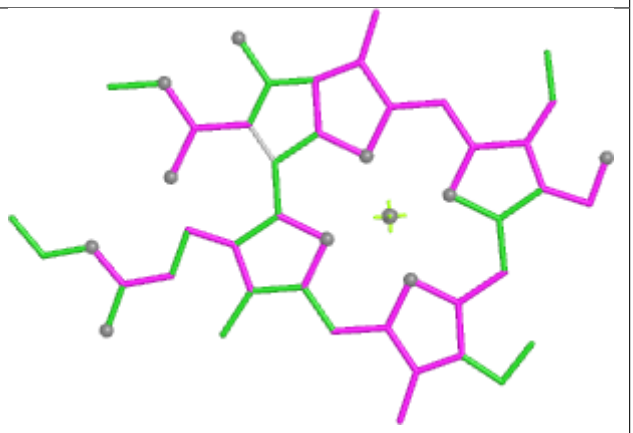


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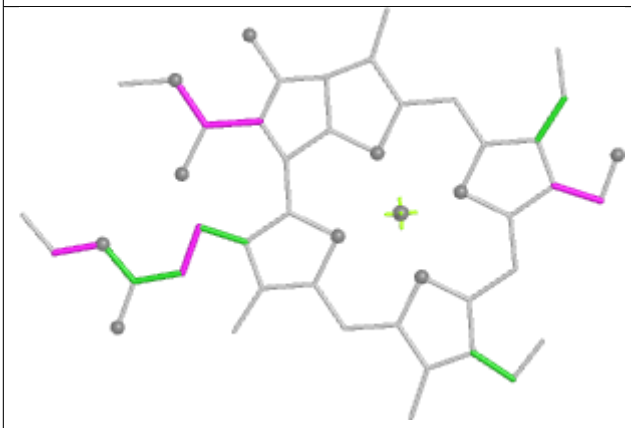
Ligand CHL 2 314



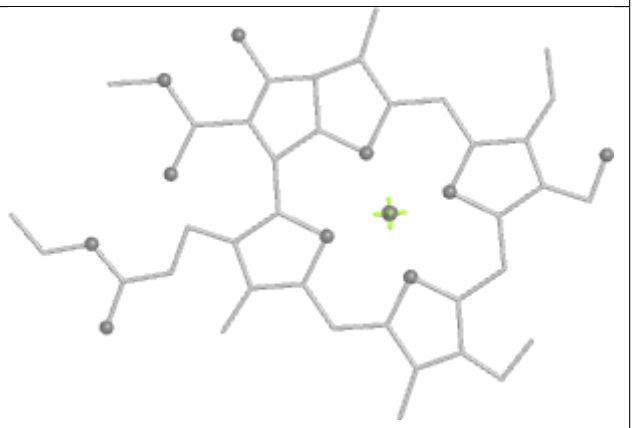
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Bond angles

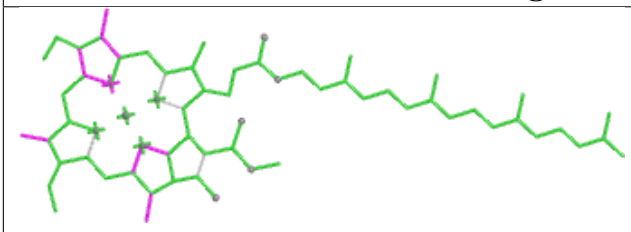


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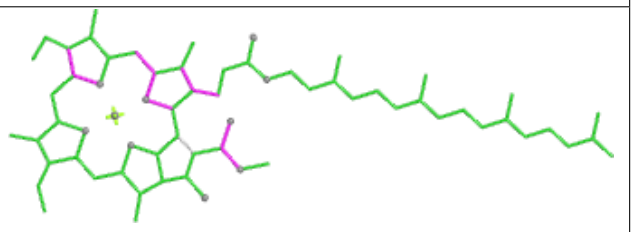


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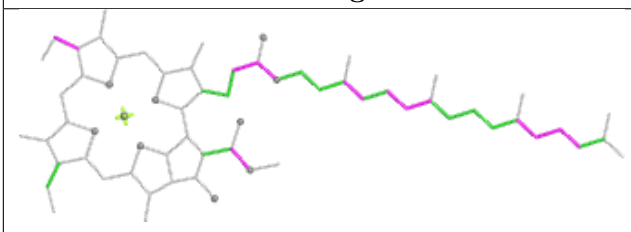
Ligand CLA u 302



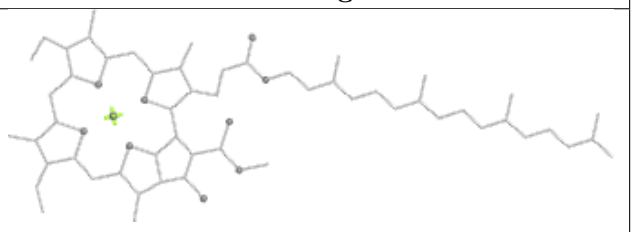
Bond lengths



Bond angles

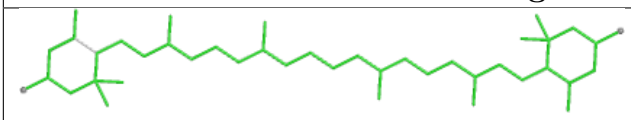


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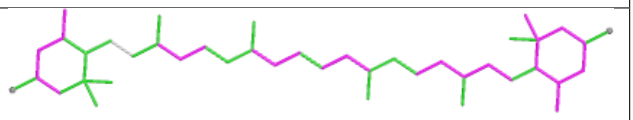


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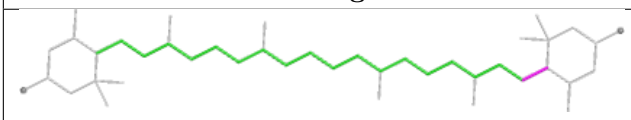
Ligand LUT 2 310



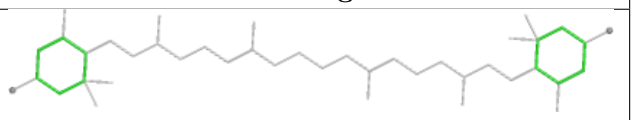
Bond lengths



Bond angles

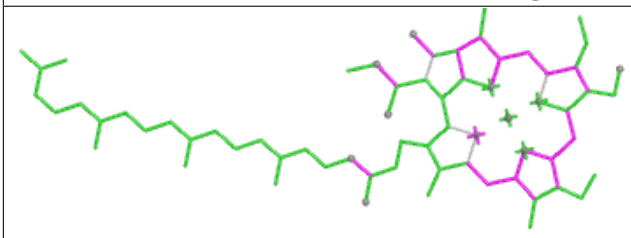


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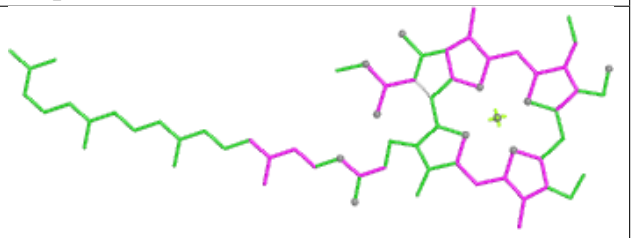


Rings

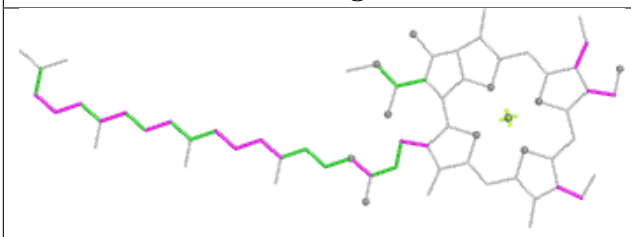
Ligand CHL p 319



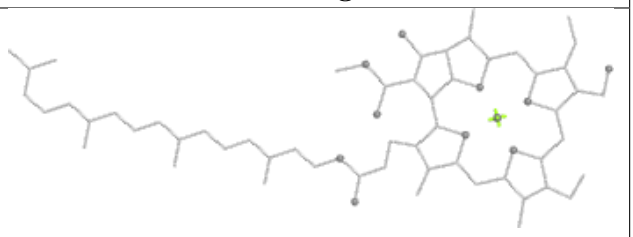
Bond lengths



Bond angles

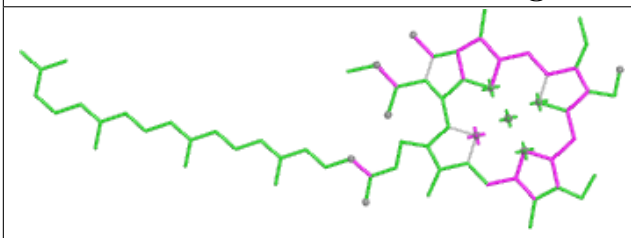


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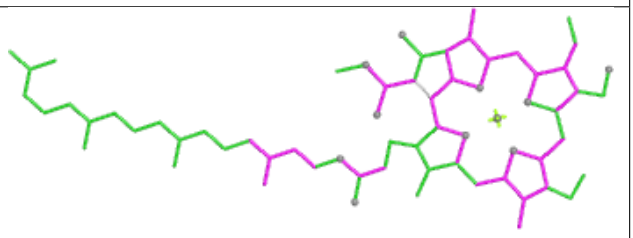


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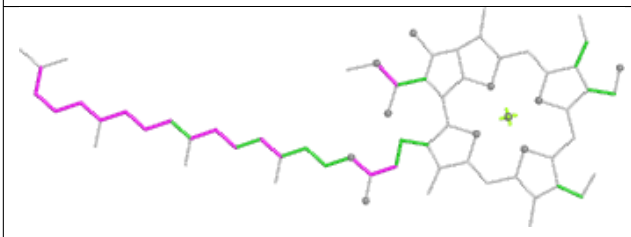
Ligand CHL 2 313



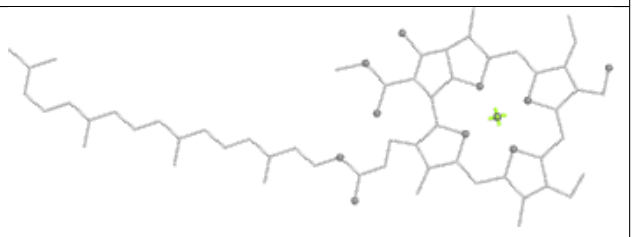
Bond lengths



Bond angles

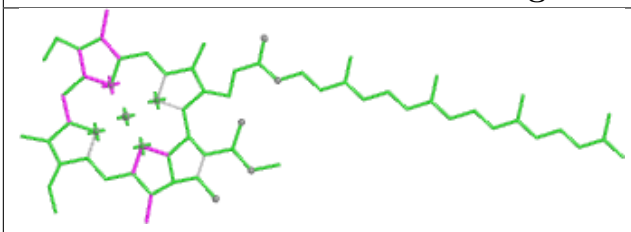


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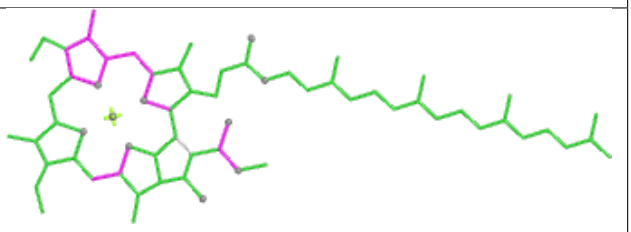


Rings

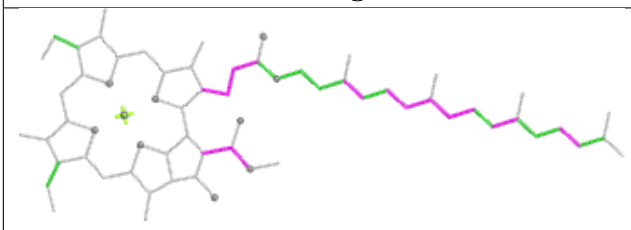
Ligand CLA 6 302



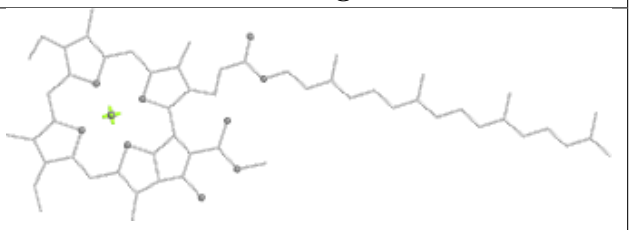
Bond lengths



Bond angles

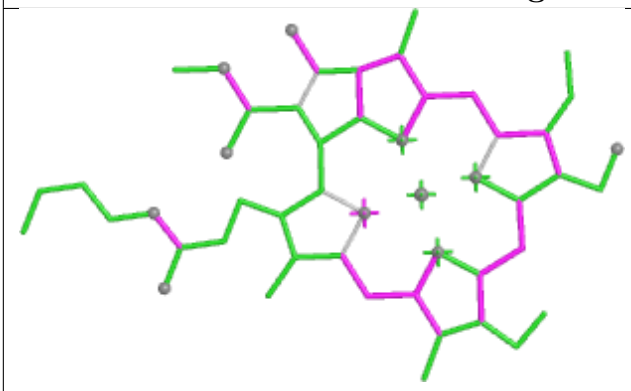


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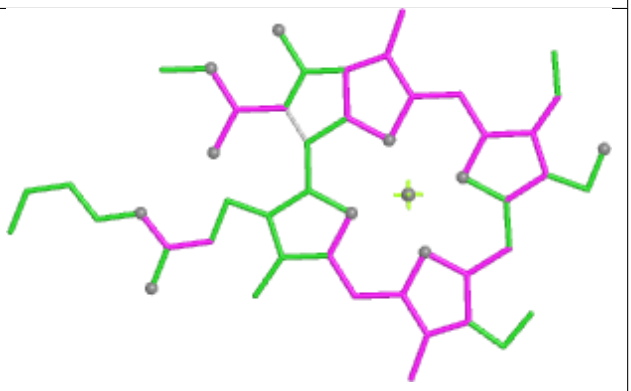


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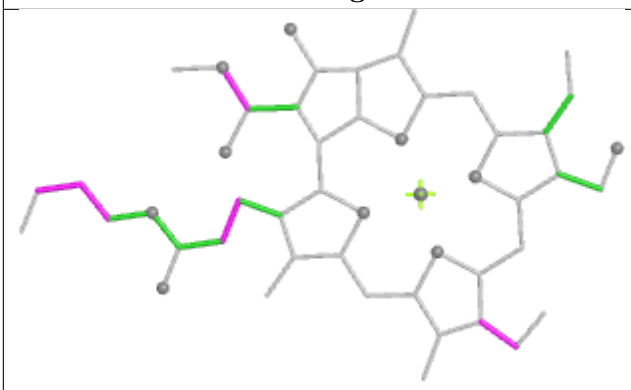
Ligand CHL 2 315



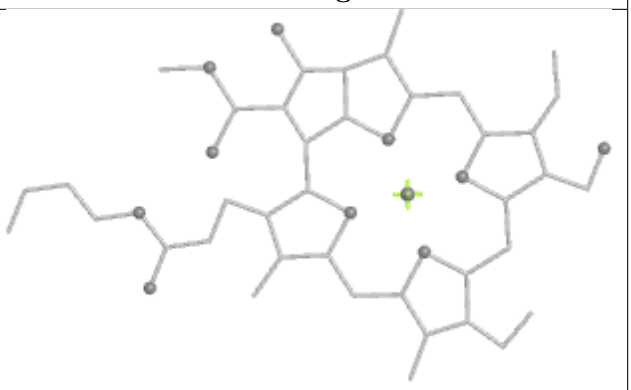
Bond lengths



Bond angles

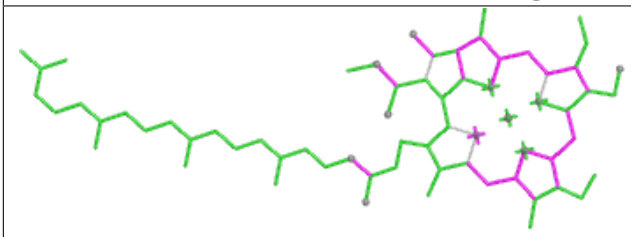


Torsions

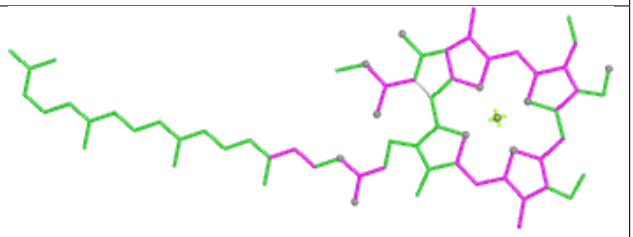


Rings

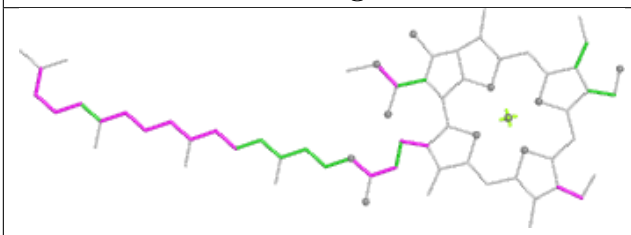
Ligand CHL 4 313



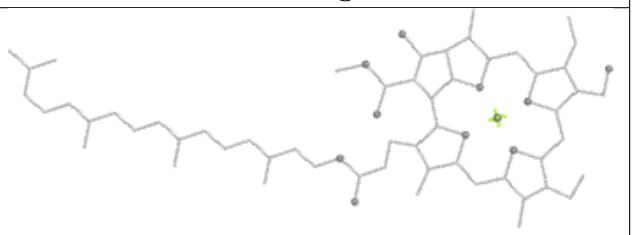
Bond lengths



Bond angles

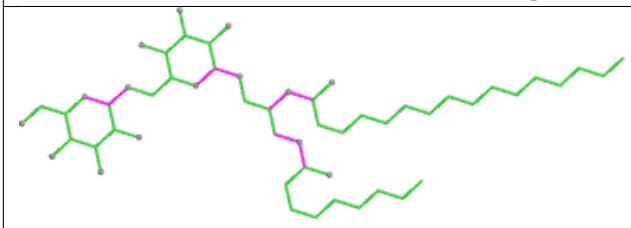


Torsions

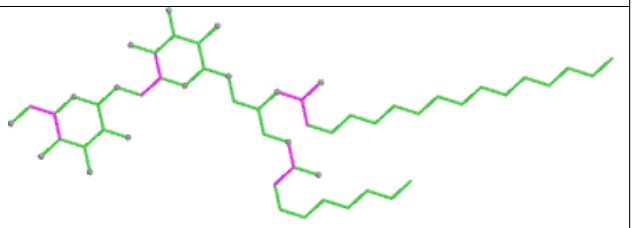


Rings

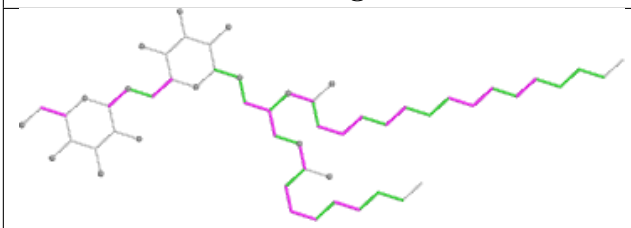
Ligand DGD c 517



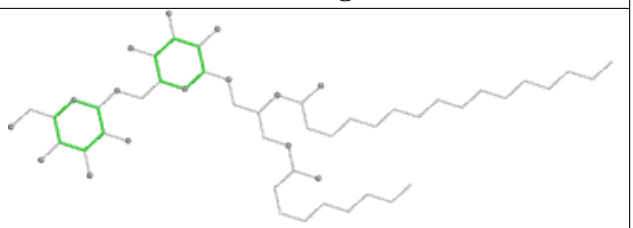
Bond lengths



Bond angles

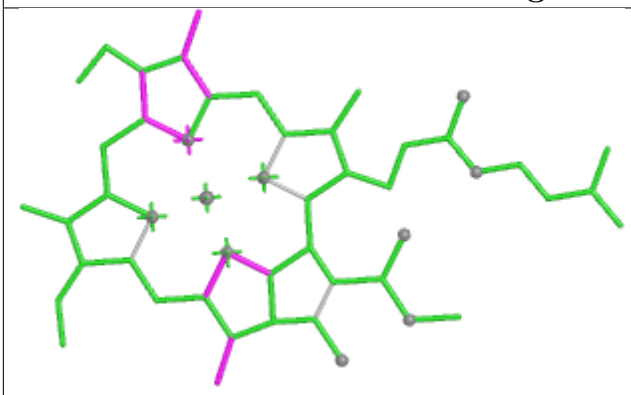


Torsions

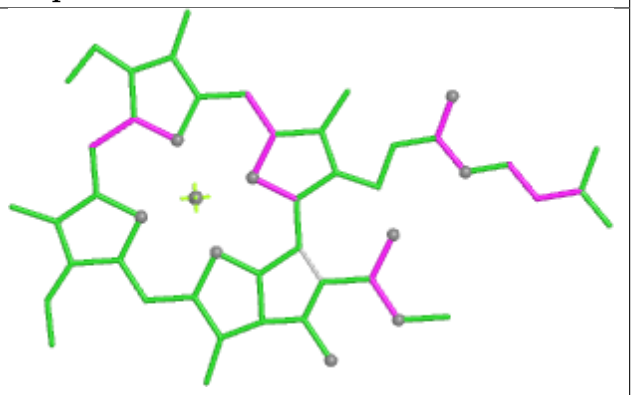


Rings

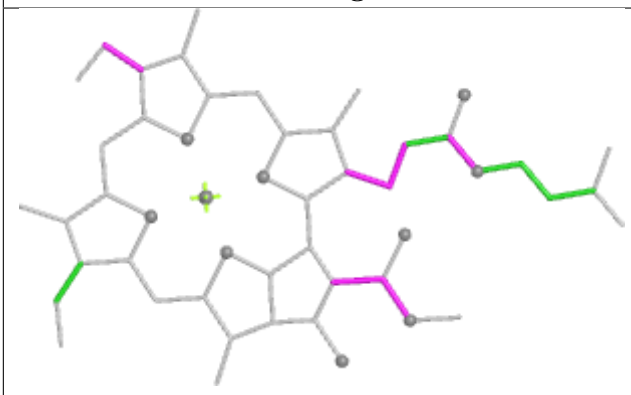
Ligand CLA p 304



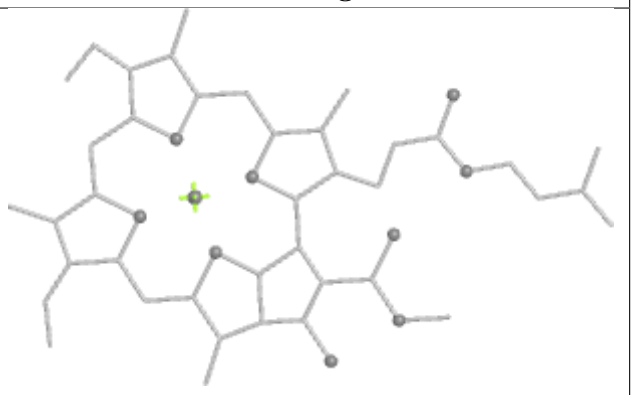
Bond lengths



Bond angles

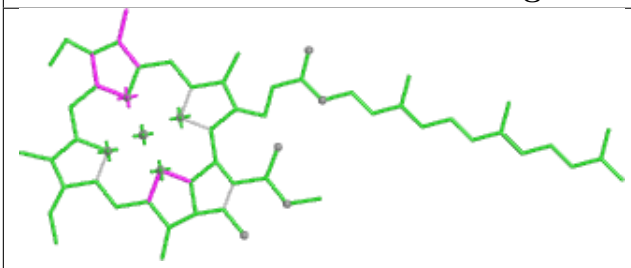


Torsions

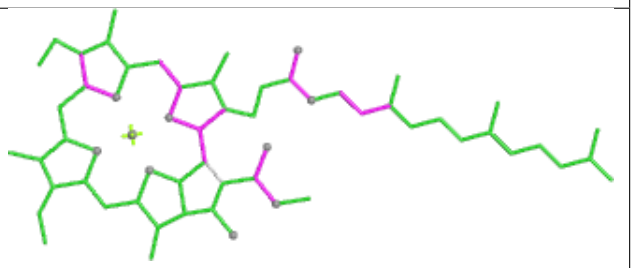


Rings

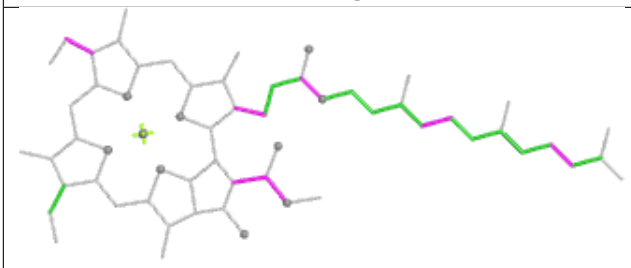
Ligand CLA R 310



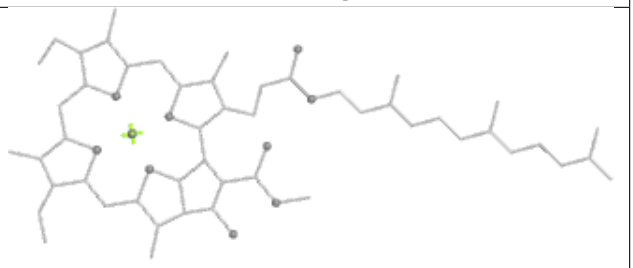
Bond lengths



Bond angles

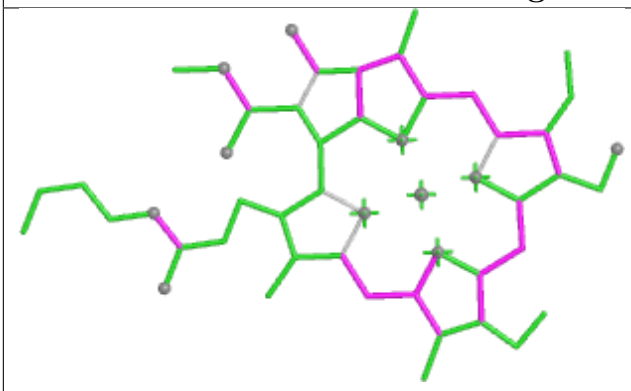


Torsions

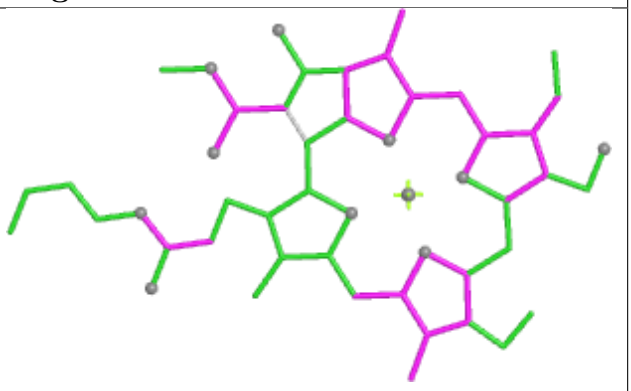


Rings

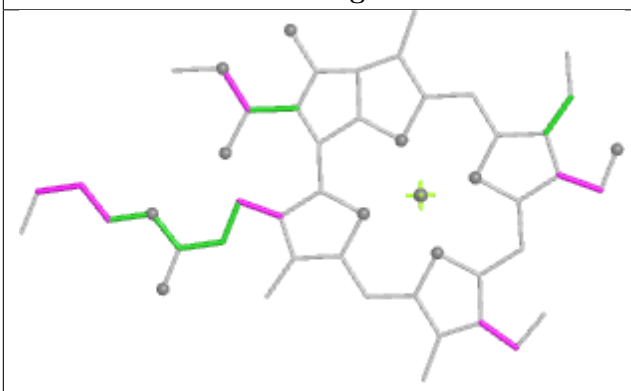
Ligand CHL g 313



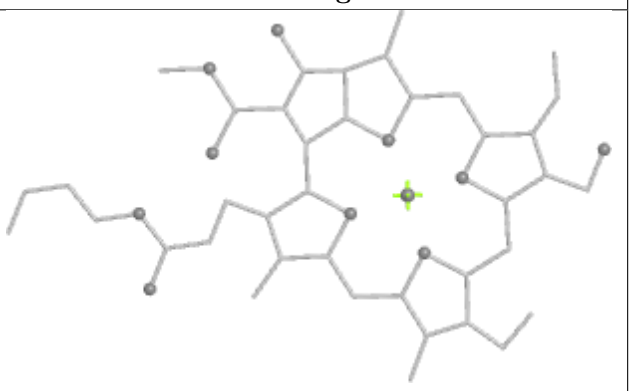
Bond lengths



Bond angles

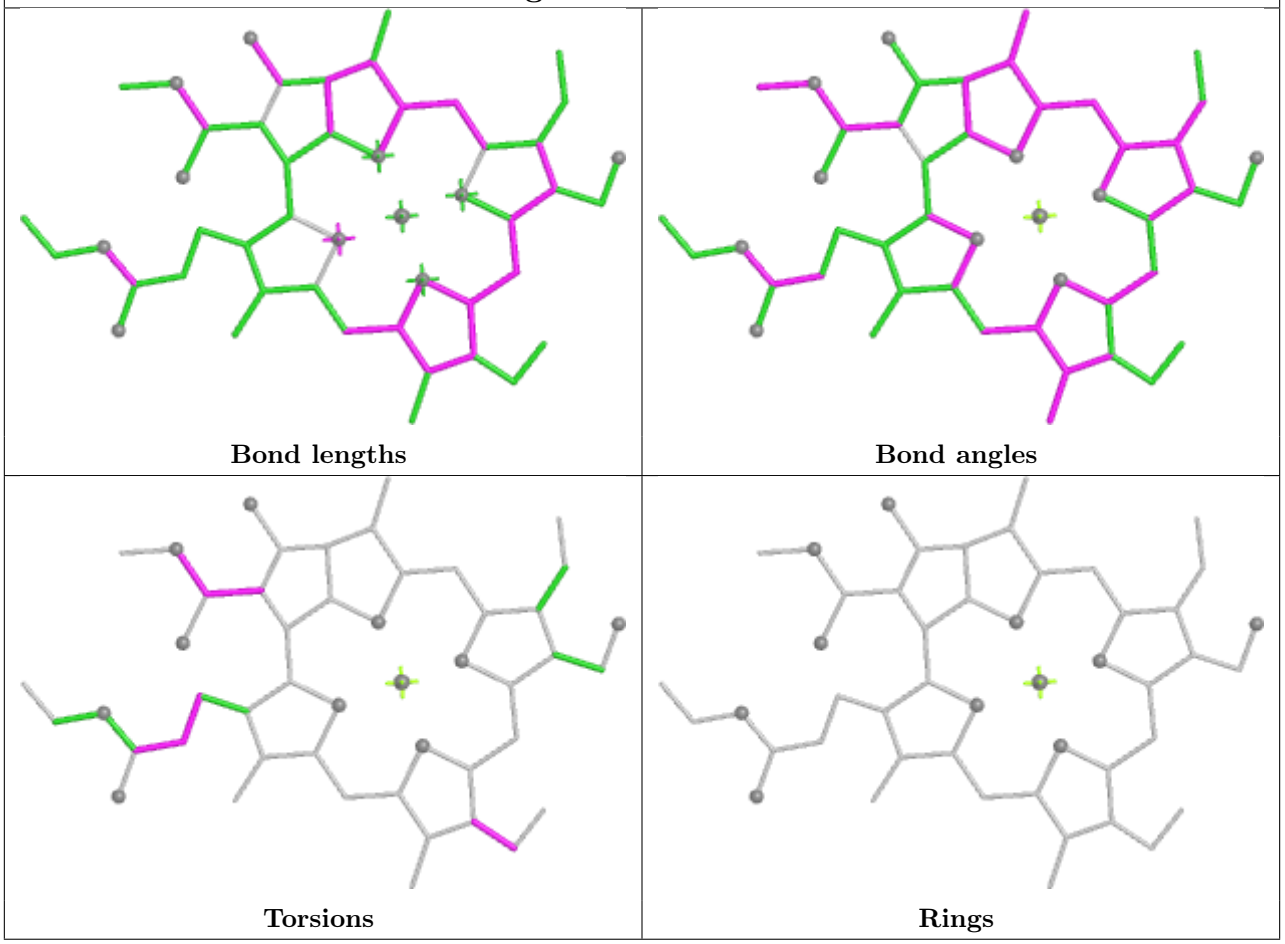


Torsions

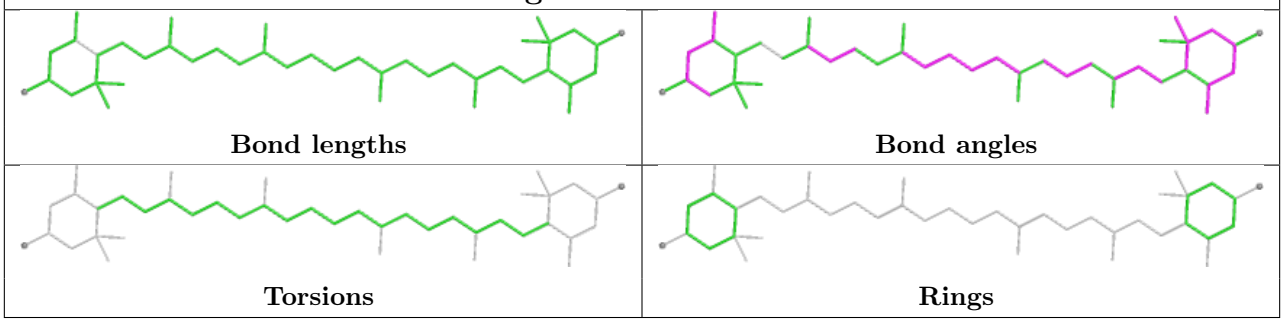


Rings

Ligand CHL P 315



Ligand LUT V 310



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.

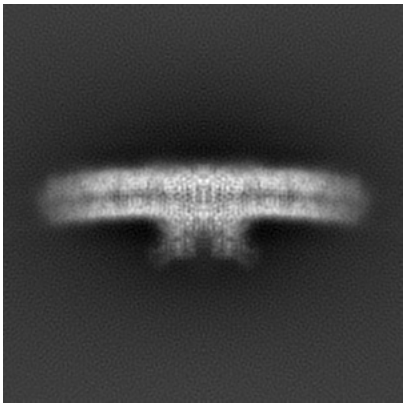
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-9957. These allow visual inspection of the internal detail of the map and identification of artifacts.

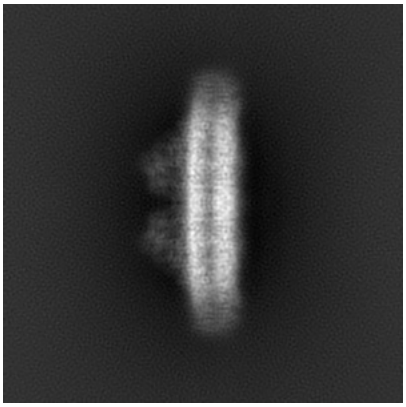
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

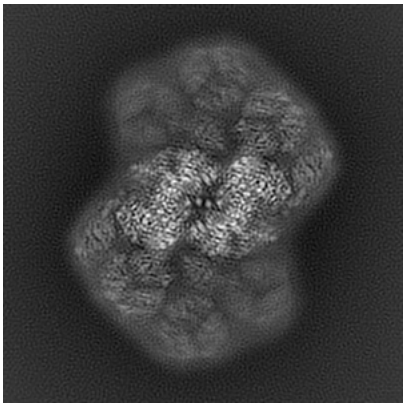
6.1.1 Primary map



X



Y

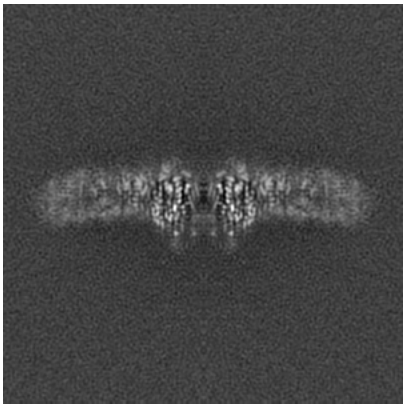


Z

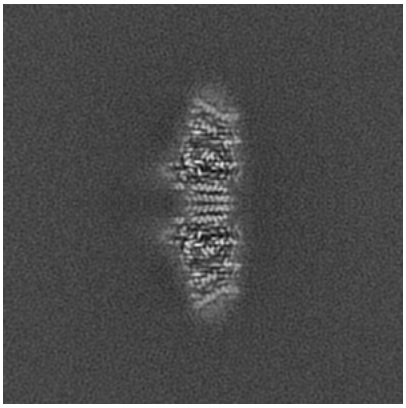
The images above show the map projected in three orthogonal directions.

6.2 Central slices

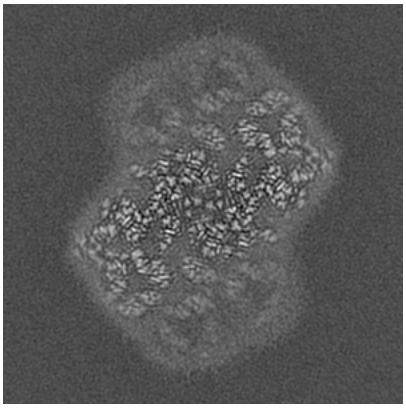
6.2.1 Primary map



X Index: 150



Y Index: 150

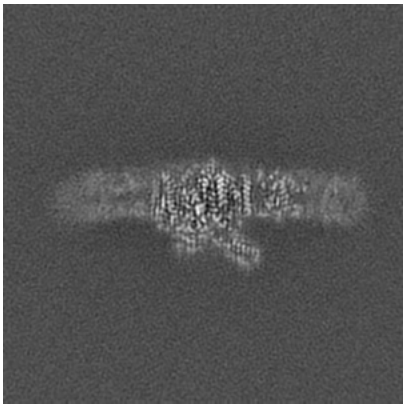


Z Index: 150

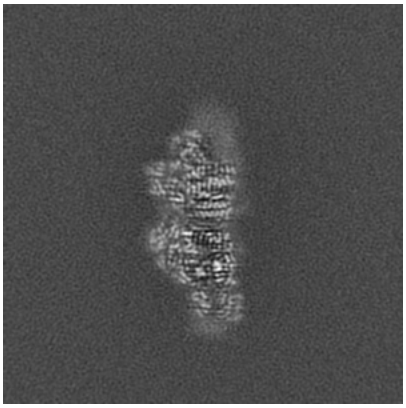
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

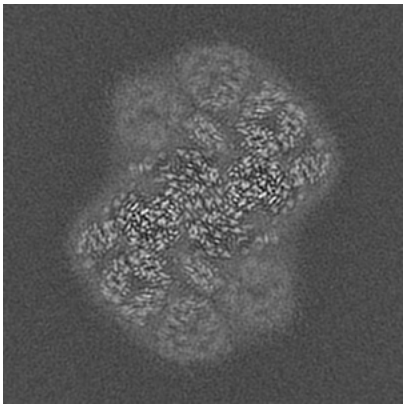
6.3.1 Primary map



X Index: 180



Y Index: 131

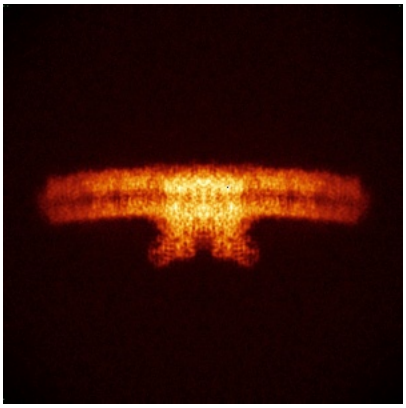


Z Index: 164

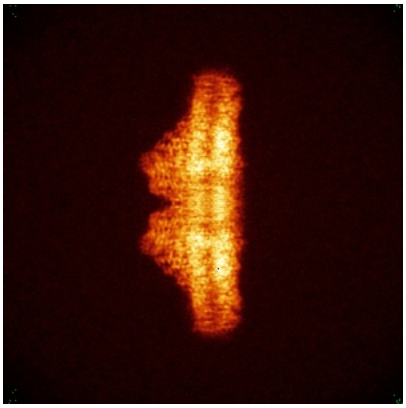
The images above show the largest variance slices of the map in three orthogonal directions.

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

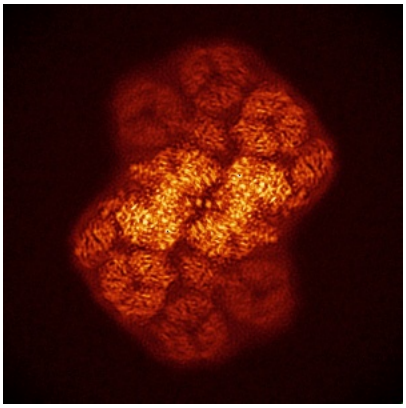
6.4.1 Primary map



X



Y



Z

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 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

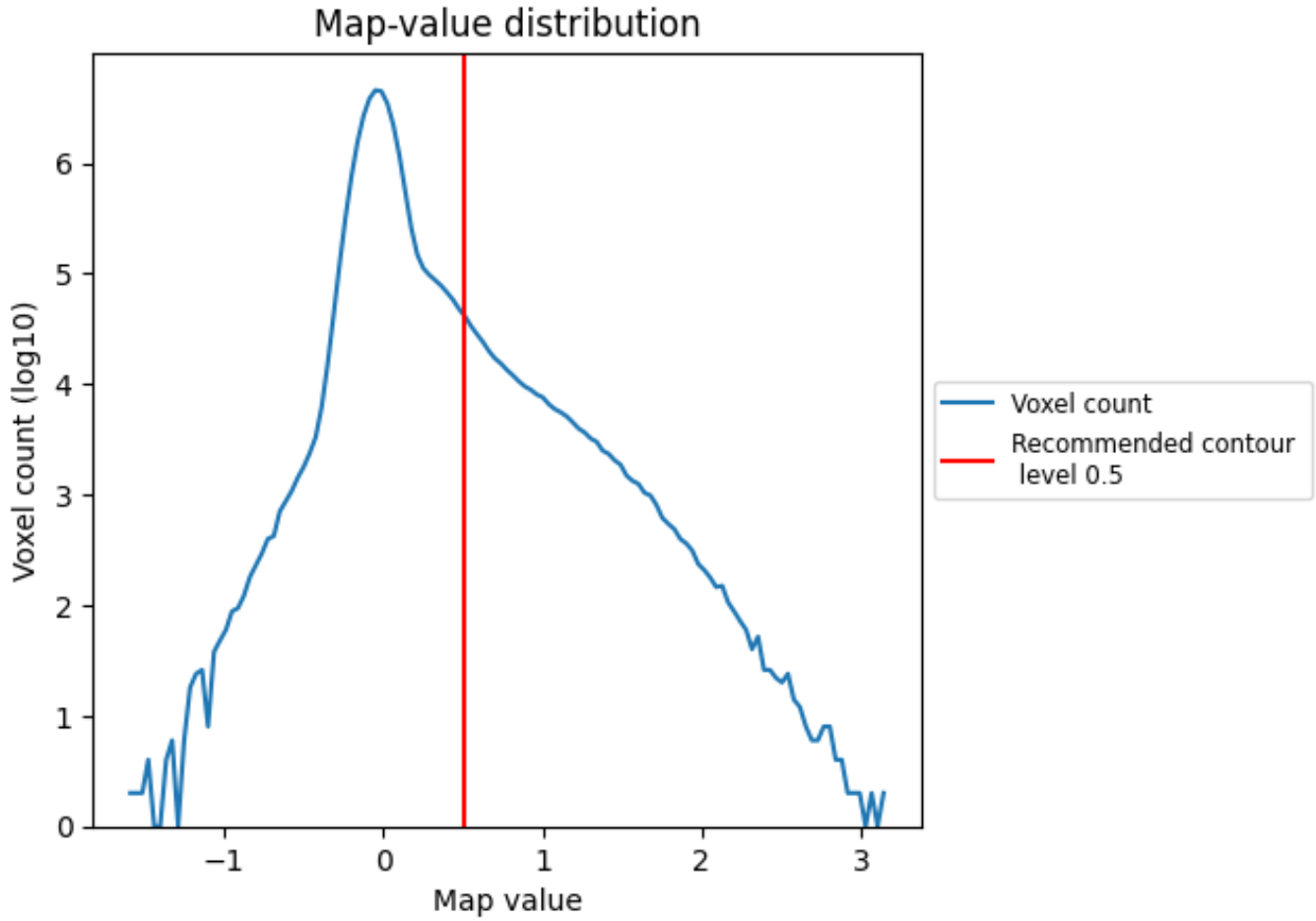
6.6 Mask visualisation (i)

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

7 Map analysis

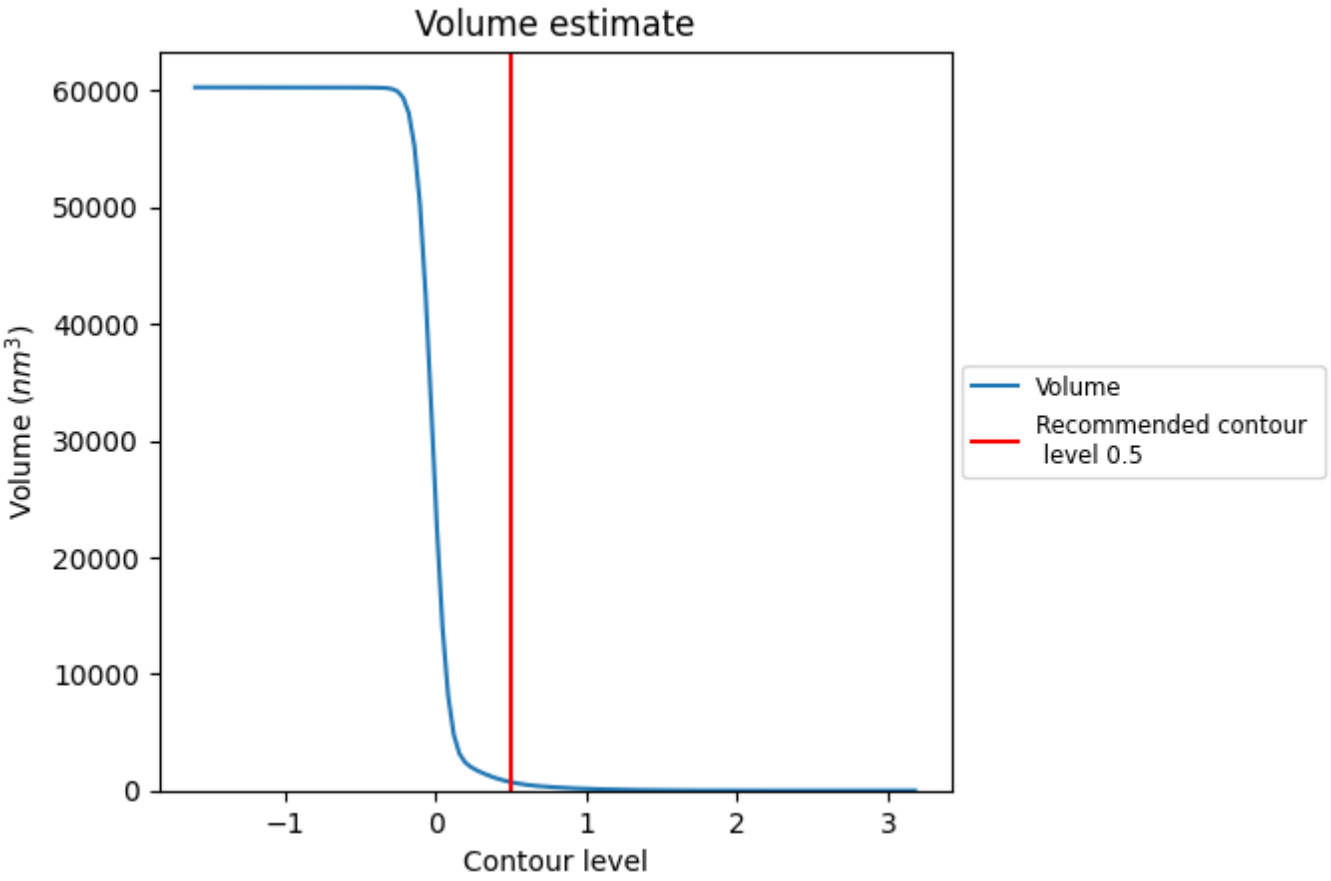
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

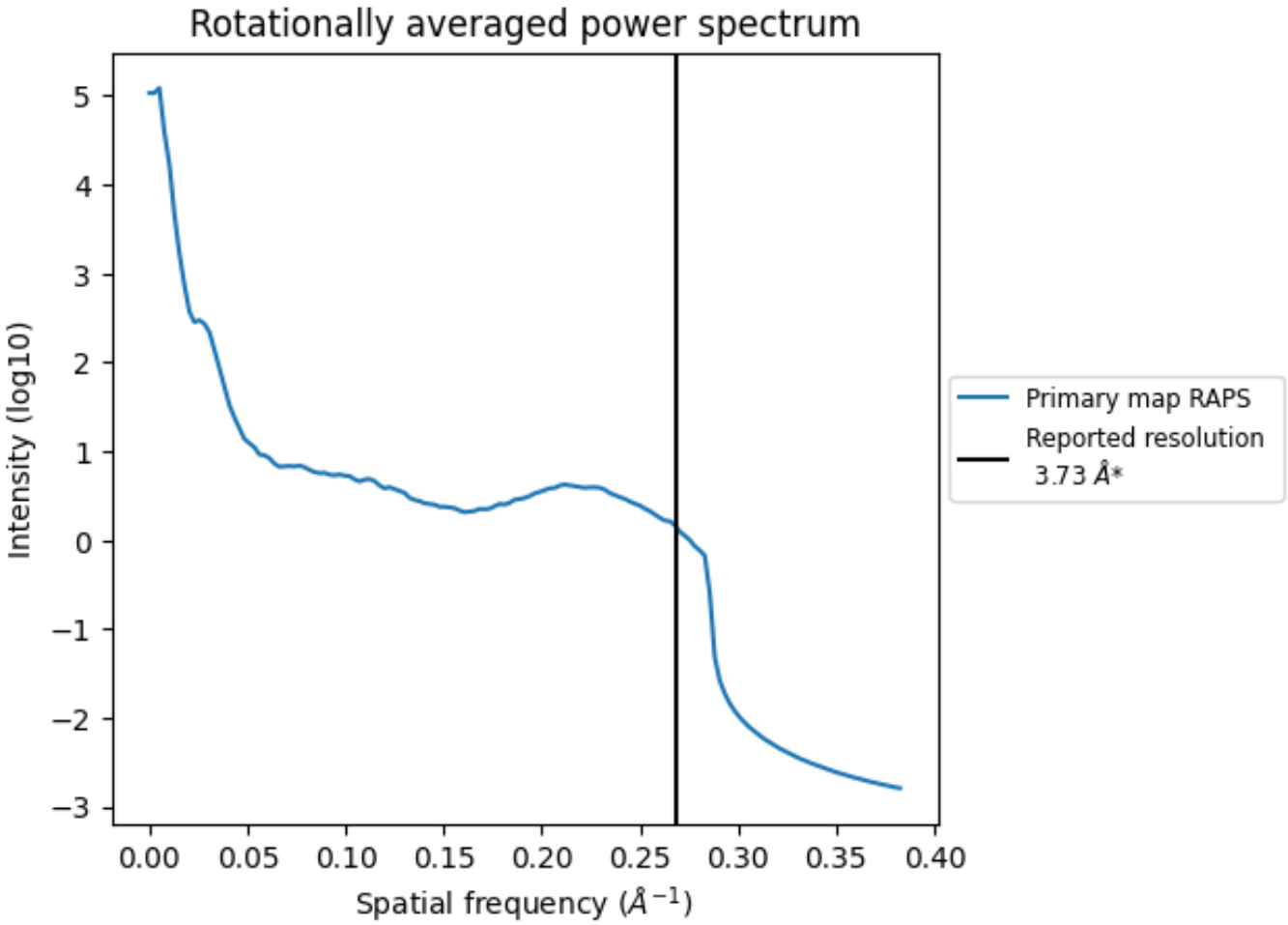
7.2 Volume estimate



The volume at the recommended contour level is 727 nm^3; this corresponds to an approximate mass of 657 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 0.268 Å^{-1}

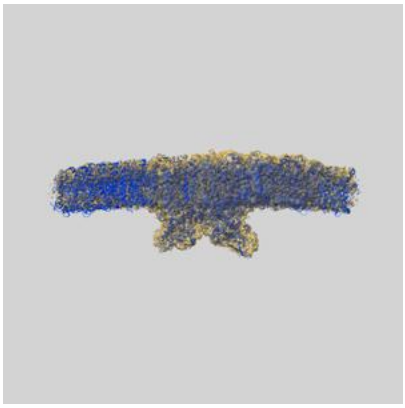
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

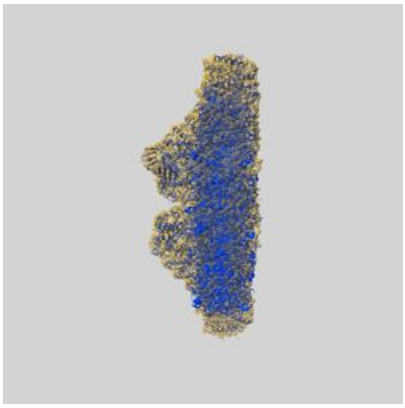
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-9957 and PDB model 6KAF. Per-residue inclusion information can be found in section 3 on page 45.

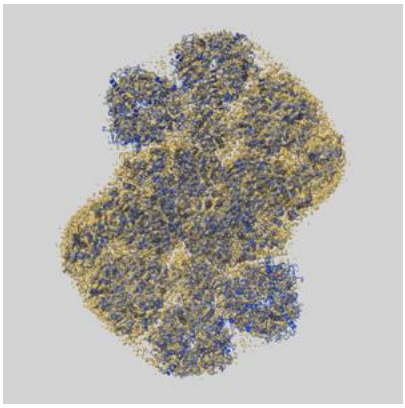
9.1 Map-model overlay



X



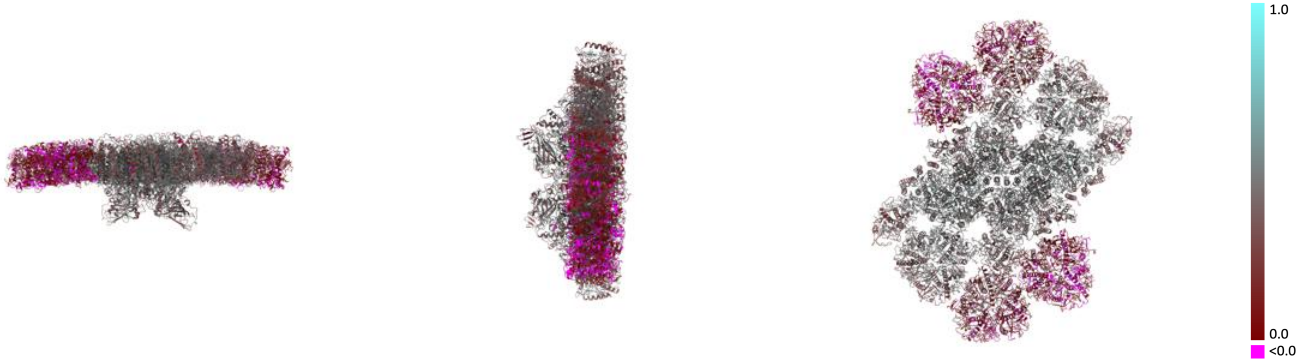
Y



Z

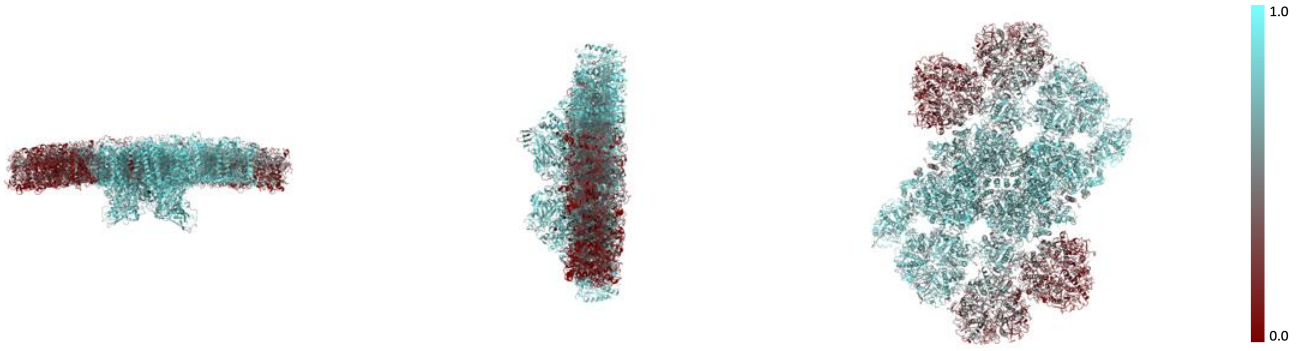
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



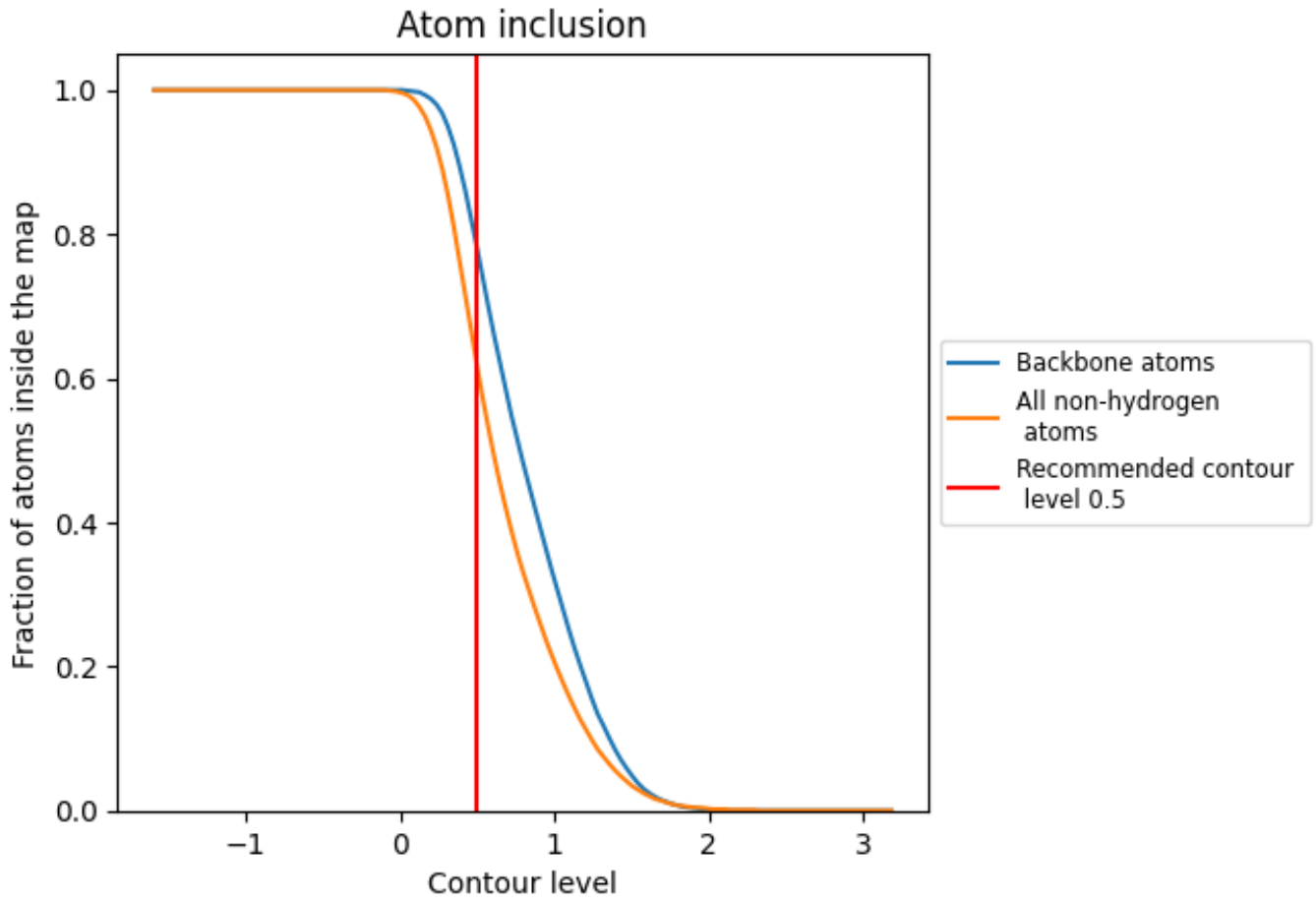
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.5).

9.4 Atom inclusion (i)



At the recommended contour level, 78% of all backbone atoms, 62% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6150	0.3260
1	0.4690	0.2180
2	0.2680	0.1130
3	0.2680	0.1030
4	0.4800	0.2330
5	0.2690	0.1100
6	0.2770	0.1120
A	0.8490	0.4710
B	0.7780	0.4420
C	0.8260	0.4680
D	0.8310	0.4580
E	0.7560	0.3920
F	0.7560	0.3190
G	0.7130	0.3870
H	0.8090	0.4290
I	0.9010	0.4840
J	0.4170	0.2730
K	0.8150	0.4280
L	0.7390	0.4530
M	0.7010	0.4110
N	0.7720	0.4060
O	0.7120	0.3810
P	0.2560	0.0890
Q	0.1050	0.0300
R	0.6320	0.3760
S	0.7690	0.3680
T	0.6880	0.4350
U	0.7830	0.4490
V	0.2130	0.0700
W	0.7840	0.4360
X	0.6850	0.3900
Y	0.6120	0.3520
Z	0.7730	0.3730
a	0.8460	0.4710
b	0.7770	0.4400



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
c	0.8220	0.4660
d	0.8320	0.4570
e	0.7540	0.3870
f	0.7600	0.3190
g	0.7080	0.3760
h	0.8160	0.4260
i	0.9010	0.4870
j	0.4120	0.2370
k	0.8150	0.4320
l	0.7360	0.4490
m	0.7010	0.4070
n	0.7640	0.3960
o	0.7120	0.3830
p	0.2400	0.0800
q	0.1080	0.0270
r	0.6390	0.3800
s	0.7680	0.3660
t	0.6880	0.4350
u	0.7850	0.4490
v	0.2150	0.0810
w	0.7790	0.4330
x	0.6850	0.3930
y	0.6120	0.3550
z	0.7630	0.3830