



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 13, 2026 – 11:20 PM JST

PDB ID : 8IRI / pdb_00008iri
Title : XFEL structure of cyanobacterial photosystem II following two flashes (2F)
with a 5-millisecond delay
Authors : Li, H.; Suga, M.; Shen, J.R.
Deposited on : 2023-03-17
Resolution : 2.25 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

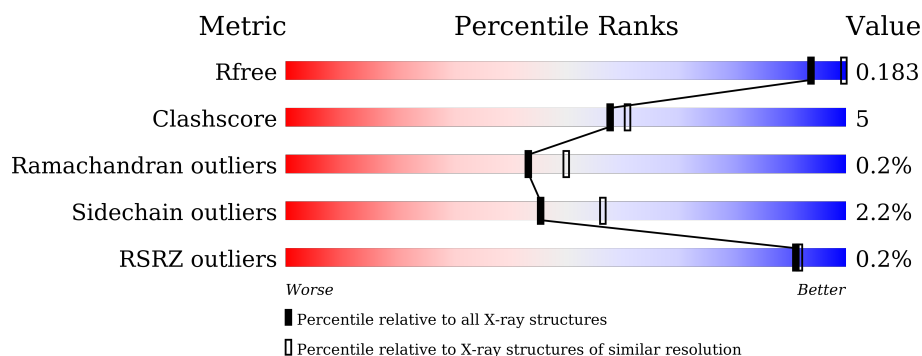
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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.



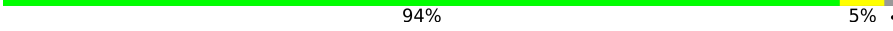
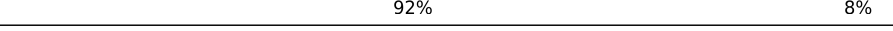
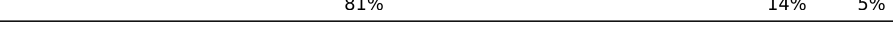
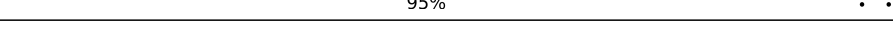
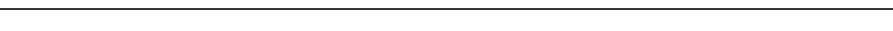
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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

Mol	Chain	Length	Quality of chain
1	A	344	92% ...
1	a	344	88% 9% •
2	B	505	93% 7%
2	b	505	92% 7% •
3	C	455	91% 8% •
3	c	455	92% 8%

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Mol	Chain	Length	Quality of chain
4	D	342	
4	d	342	
5	E	84	
5	e	84	
6	F	44	
6	f	44	
7	H	65	
7	h	65	
8	I	38	
8	i	38	
9	J	39	
9	j	39	
10	K	37	
10	k	37	
11	L	37	
11	l	37	
12	M	36	
12	m	36	
13	O	244	
13	o	244	
14	T	32	
14	t	32	
15	U	104	
15	u	104	
16	V	137	

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Mol	Chain	Length	Quality of chain
16	v	137	 91% 9%
17	X	40	 88% 8% 5%
17	x	40	 88% 8% 5%
18	Y	30	 87% 10% •
18	y	30	 70% 27% •
19	Z	62	 85% 13% •
19	z	62	 81% 19%
20	R	34	 6% 76% 21% •

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
27	GOL	D	403	-	-	X	-
27	GOL	a	419	-	-	X	-
41	HEC	V	201	X	-	-	-
41	HEC	v	201	X	-	-	-

2 Entry composition [i](#)

There are 42 unique types of molecules in this entry. The entry contains 62604 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Photosystem II protein D1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	334	Total	C	N	O	S	0	222	0
			4338	2836	717	760	25			
1	a	334	Total	C	N	O	S	0	221	0
			4330	2830	716	759	25			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	279	PRO	ARG	conflict	UNP P51765
a	279	PRO	ARG	conflict	UNP P51765

- Molecule 2 is a protein called Photosystem II CP47 reaction center protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	504	Total	C	N	O	S	0	20	0
			4146	2721	692	720	13			
2	b	504	Total	C	N	O	S	0	19	0
			4134	2718	687	716	13			

- Molecule 3 is a protein called Photosystem II CP43 reaction center protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	451	Total	C	N	O	S	0	97	0
			4260	2788	713	741	18			
3	c	455	Total	C	N	O	S	0	100	0
			4308	2821	719	750	18			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	19	ASN	-	expression tag	UNP D0VWR7
C	20	SER	-	expression tag	UNP D0VWR7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	21	ILE	-	expression tag	UNP D0VWR7
C	22	PHE	-	expression tag	UNP D0VWR7
c	19	ASN	-	expression tag	UNP D0VWR7
c	20	SER	-	expression tag	UNP D0VWR7
c	21	ILE	-	expression tag	UNP D0VWR7
c	22	PHE	-	expression tag	UNP D0VWR7

- Molecule 4 is a protein called Photosystem II D2 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	342	Total	C	N	O	S	0	114	0
			3620	2387	596	622	15			
4	d	341	Total	C	N	O	S	0	116	0
			3628	2391	599	623	15			

- Molecule 5 is a protein called Cytochrome b559 subunit alpha.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	81	Total	C	N	O	0	0	0
			662	432	107	123			
5	e	79	Total	C	N	O	0	2	0
			670	439	110	121			

- Molecule 6 is a protein called Cytochrome b559 subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	34	Total	C	N	O	S	0	0	0
			275	187	45	42	1			
6	f	31	Total	C	N	O	S	0	1	0
			261	179	43	38	1			

- Molecule 7 is a protein called Photosystem II reaction center protein H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	64	Total	C	N	O	S	0	0	0
			506	339	81	84	2			
7	h	64	Total	C	N	O	S	0	1	0
			517	345	85	85	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	38	Total	C	N	O	S	0	0	0
			314	211	48	54	1			
8	i	38	Total	C	N	O	S	0	0	0
			314	211	48	54	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	38	Total	C	N	O	S	0	0	0
			272	182	42	47	1			
9	j	39	Total	C	N	O	S	0	0	0
			277	185	43	48	1			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	K	37	Total	C	N	O	0	0	0
			293	204	43	46			
10	k	37	Total	C	N	O	0	0	0
			293	204	43	46			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	33	LEU	PHE	conflict	UNP P19054
K	39	TRP	VAL	conflict	UNP P19054
k	33	LEU	PHE	conflict	UNP P19054
k	39	TRP	VAL	conflict	UNP P19054

- Molecule 11 is a protein called Photosystem II reaction center protein L.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	L	36	Total	C	N	O	0	2	0
			311	207	49	55			
11	l	36	Total	C	N	O	0	2	0
			311	207	49	55			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	M	33	Total	C	N	O	S	0	1	0
			268	179	39	49	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	m	34	Total	C	N	O	S	0	2	0
			286	190	43	52	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	8	LEU	PHE	conflict	UNP P12312
m	8	LEU	PHE	conflict	UNP P12312

- Molecule 13 is a protein called Photosystem II manganese-stabilizing polypeptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	O	243	Total	C	N	O	S	0	10	0
			1958	1221	335	398	4			
13	o	243	Total	C	N	O	S	0	8	0
			1933	1207	330	392	4			

- Molecule 14 is a protein called Photosystem II reaction center protein T.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	T	30	Total	C	N	O	S	0	6	0
			311	213	48	48	2			
14	t	30	Total	C	N	O	S	0	5	0
			302	208	47	45	2			

- Molecule 15 is a protein called Photosystem II 12 kDa extrinsic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	U	96	Total	C	N	O		0	4	0
			800	508	133	159				
15	u	97	Total	C	N	O		0	4	0
			807	513	134	160				

- Molecule 16 is a protein called Cytochrome c-550.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	V	137	Total	C	N	O	S	0	6	0
			1120	711	185	220	4			
16	v	137	Total	C	N	O	S	0	6	0
			1117	712	185	216	4			

- Molecule 17 is a protein called Photosystem II reaction center protein X.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	X	38	Total	C	N	O	0	1	0
			289	194	46	49			
17	x	38	Total	C	N	O	0	0	0
			281	188	45	48			

- Molecule 18 is a protein called Photosystem II reaction center protein Ycf12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	Y	29	Total	C	N	O	S	0	0	0
			215	142	37	33	3			
18	y	29	Total	C	N	O	S	0	0	0
			215	142	37	33	3			

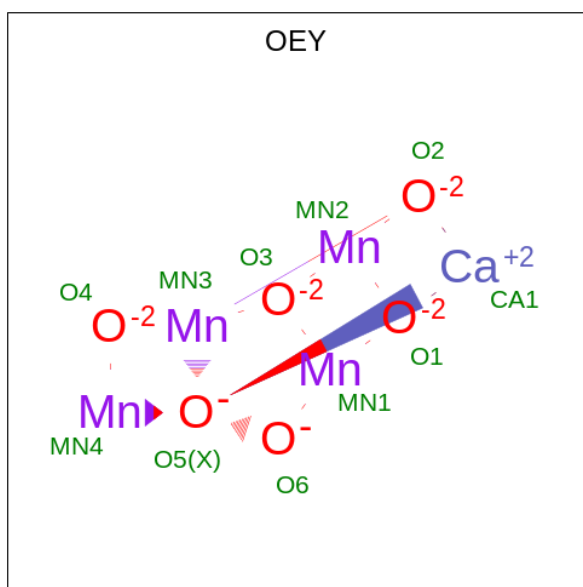
- Molecule 19 is a protein called Photosystem II reaction center protein Z.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	Z	62	Total	C	N	O	S	0	0	0
			479	328	72	77	2			
19	z	62	Total	C	N	O	S	0	0	0
			479	328	72	77	2			

- Molecule 20 is a protein called Photosystem II protein Y.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	R	34	Total	C	N	O	0	0	0
			273	186	47	40			

- Molecule 21 is CA-MN4-O6 CLUSTER (CCD ID: OEY) (formula: CaMn_4O_6) (labeled as "Ligand of Interest" by depositor).

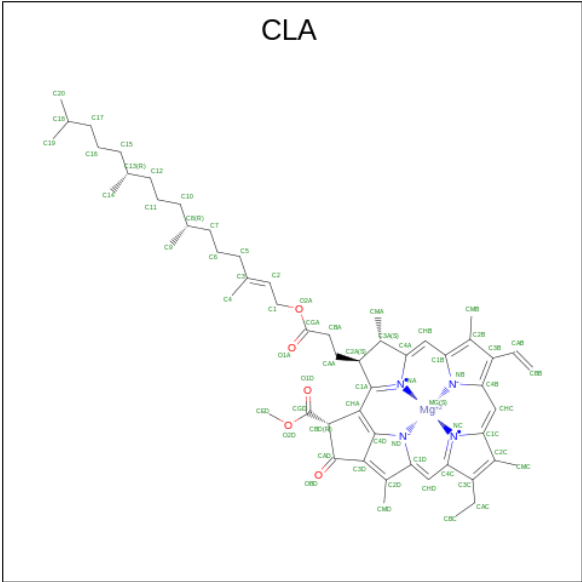


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
21	A	1	Total	Ca	Mn	O	0	1
			11	1	4	6		
21	a	1	Total	Ca	Mn	O	0	1
			11	1	4	6		

- Molecule 22 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	2	Total	Cl	0	2
			4	4		
22	a	2	Total	Cl	0	2
			4	4		

- Molecule 23 is CHLOROPHYLL A (CCD ID: CLA) (formula: C₅₅H₇₂MgN₄O₅) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
23	A	1	Total	C	Mg	N	O	0	1
			130	110	2	8	10		
23	A	1	Total	C	Mg	N	O	0	1
			130	110	2	8	10		
23	A	1	Total	C	Mg	N	O	0	1
			130	110	2	8	10		
23	A	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	B	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	C	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	D	1	Total	C	Mg	N	O	0	1
			130	110	2	8	10		
23	D	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

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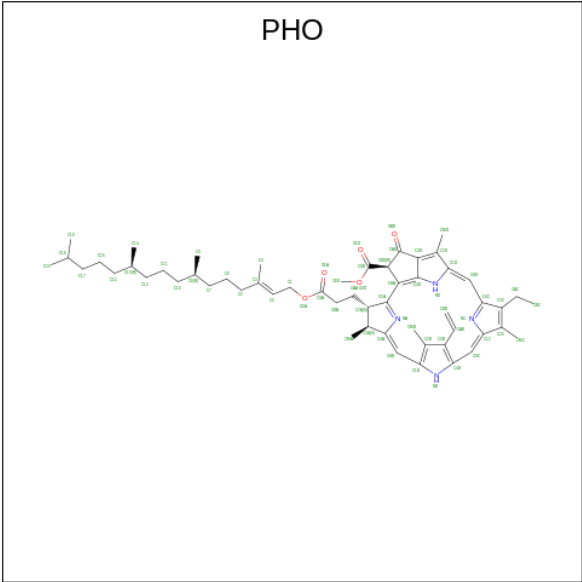
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
23	a	1	Total	C	Mg	N	O	0	1
			130	110	2	8	10		
23	a	1	Total	C	Mg	N	O	0	1
			130	110	2	8	10		
23	a	1	Total	C	Mg	N	O	0	1
			130	110	2	8	10		
23	a	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	b	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

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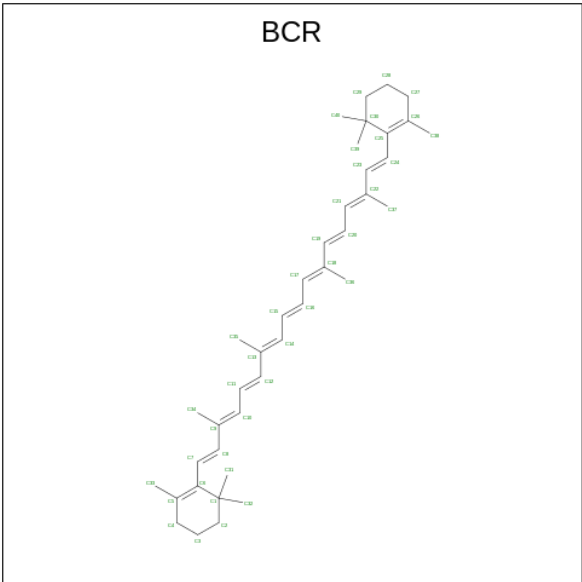
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	c	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		
23	d	1	Total	C	Mg	N	O	0	1
			130	110	2	8	10		
23	d	1	Total	C	Mg	N	O	0	0
			65	55	1	4	5		

- Molecule 24 is PHEOPHYTIN A (CCD ID: PHO) (formula: $C_{55}H_{74}N_4O_5$).



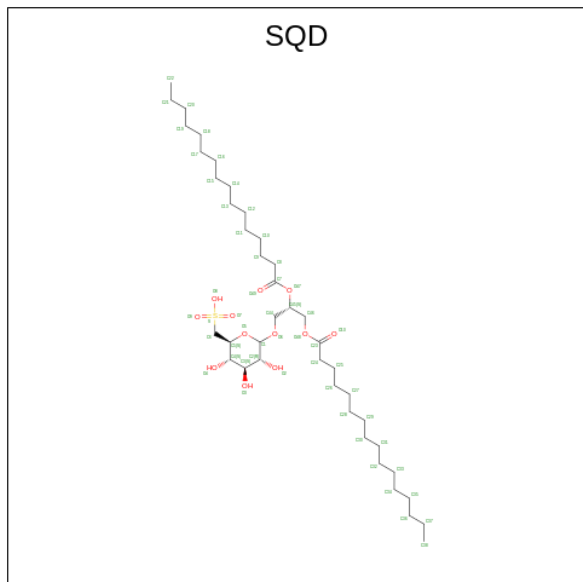
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
24	A	1	Total	C	N	O	0	1
			128	110	8	10		
24	A	1	Total	C	N	O	0	1
			128	110	8	10		
24	a	1	Total	C	N	O	0	1
			128	110	8	10		
24	a	1	Total	C	N	O	0	1
			128	110	8	10		

- Molecule 25 is BETA-CAROTENE (CCD ID: BCR) (formula: C₄₀H₅₆).



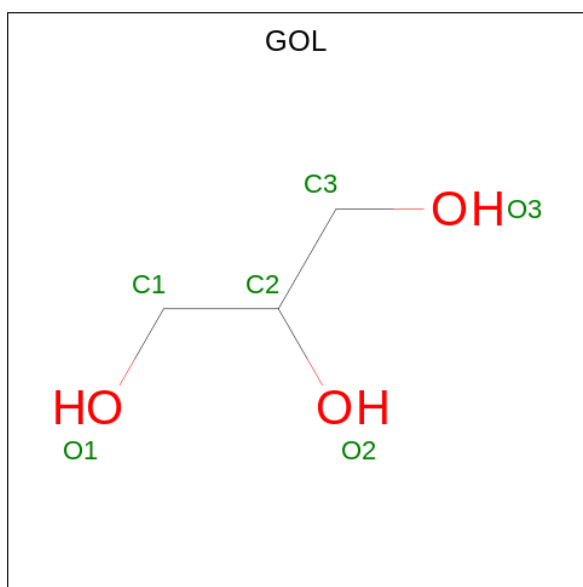
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
25	A	1	Total C 40 40	0	0
25	B	1	Total C 40 40	0	0
25	B	1	Total C 40 40	0	0
25	B	1	Total C 40 40	0	0
25	C	1	Total C 40 40	0	0
25	C	1	Total C 40 40	0	0
25	D	1	Total C 40 40	0	0
25	H	1	Total C 40 40	0	0
25	K	1	Total C 40 40	0	0
25	K	1	Total C 40 40	0	0
25	T	1	Total C 40 40	0	0
25	a	1	Total C 40 40	0	0
25	b	1	Total C 40 40	0	0
25	b	1	Total C 40 40	0	0
25	b	1	Total C 40 40	0	0
25	c	1	Total C 40 40	0	0
25	c	1	Total C 40 40	0	0
25	d	1	Total C 40 40	0	0
25	h	1	Total C 40 40	0	0
25	k	1	Total C 40 40	0	0
25	t	1	Total C 40 40	0	0
25	y	1	Total C 40 40	0	0

- Molecule 26 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				ZeroOcc	AltConf
26	A	1	Total	C	O	S	0	1
			108	82	24	2		
26	A	1	Total	C	O	S	0	0
			54	41	12	1		
26	B	1	Total	C	O	S	0	0
			54	41	12	1		
26	X	1	Total	C	O	S	0	0
			43	30	12	1		
26	a	1	Total	C	O	S	0	1
			108	82	24	2		
26	a	1	Total	C	O	S	0	0
			54	41	12	1		
26	b	1	Total	C	O	S	0	0
			54	41	12	1		
26	f	1	Total	C	O	S	0	0
			43	30	12	1		

- Molecule 27 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



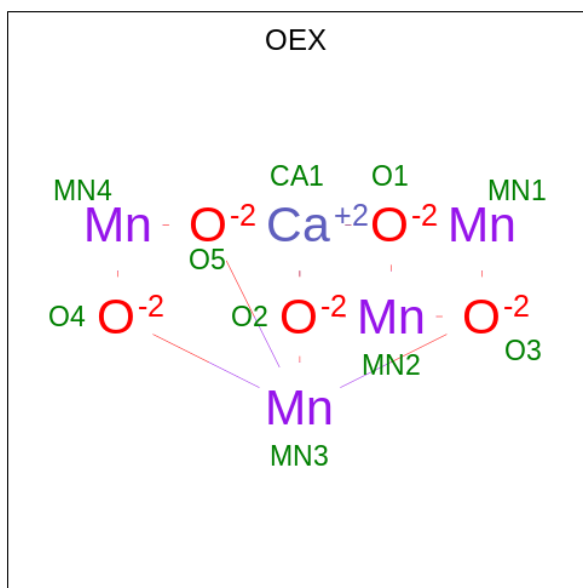
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
27	A	1	Total	C	O	0	0
			6	3	3		
27	B	1	Total	C	O	0	0
			6	3	3		
27	B	1	Total	C	O	0	0
			6	3	3		
27	B	1	Total	C	O	0	0
			6	3	3		
27	C	1	Total	C	O	0	1
			12	6	6		
27	D	1	Total	C	O	0	0
			6	3	3		
27	D	1	Total	C	O	0	0
			6	3	3		
27	O	1	Total	C	O	0	0
			6	3	3		
27	O	1	Total	C	O	0	0
			6	3	3		
27	V	1	Total	C	O	0	1
			12	6	6		
27	a	1	Total	C	O	0	0
			6	3	3		
27	a	1	Total	C	O	0	0
			6	3	3		
27	b	1	Total	C	O	0	0
			6	3	3		
27	b	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
27	c	1	Total	C	O	0	1
			12	6	6		
27	c	1	Total	C	O	0	0
			6	3	3		
27	d	1	Total	C	O	0	0
			6	3	3		
27	l	1	Total	C	O	0	1
			12	6	6		
27	o	1	Total	C	O	0	0
			6	3	3		
27	o	1	Total	C	O	0	0
			6	3	3		
27	v	1	Total	C	O	0	1
			12	6	6		

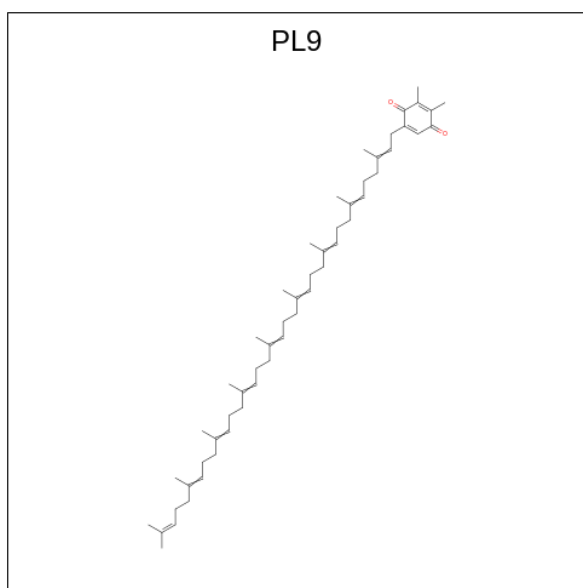
- Molecule 28 is CA-MN4-O5 CLUSTER (CCD ID: OEX) (formula: CaMn_4O_5) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
28	A	1	Total	Ca	Mn	O	0	1
			10	1	4	5		
28	a	1	Total	Ca	Mn	O	0	1
			10	1	4	5		

- Molecule 29 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: $\text{C}_{53}\text{H}_{80}\text{O}_2$)

(labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
29	A	1	Total	C	O	0	1
			110	106	4		
29	D	1	Total	C	O	0	1
			110	106	4		
29	a	1	Total	C	O	0	1
			110	106	4		
29	d	1	Total	C	O	0	1
			110	106	4		

- Molecule 30 is UNKNOWN LIGAND (CCD ID: UNL) (formula:).

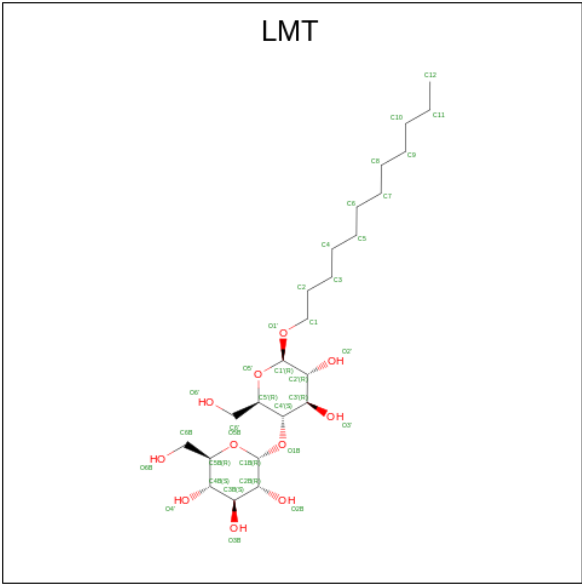
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
30	A	1	Total	C	O	0	0
			28	23	5		
30	B	1	Total	C	O	0	0
			33	28	5		
30	D	2	Total	C	O	0	0
			57	51	6		
30	I	1	Total	C	O	0	0
			40	35	5		
30	J	1	Total	C		0	0
			10	10			
30	K	1	Total	C	O	0	1
			68	58	10		
30	X	1	Total	C	O	0	0
			18	16	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
30	a	1	Total	C	O	0	0
			30	25	5		
30	b	1	Total	C	O	0	0
			33	28	5		
30	c	1	Total	C	O	0	1
			64	54	10		
30	d	2	Total	C	O	0	0
			53	47	6		
30	i	1	Total	C	O	0	0
			40	35	5		
30	j	1	Total	C		0	0
			10	10			
30	l	1	Total	C		0	0
			10	10			
30	m	1	Total	C		0	0
			10	10			
30	x	1	Total	C	O	0	0
			18	16	2		

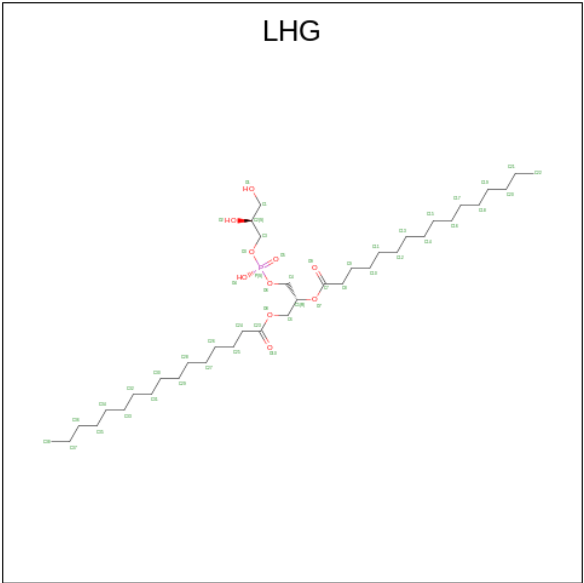
- Molecule 31 is DODECYL-BETA-D-MALTOSE (CCD ID: LMT) (formula: C₂₄H₄₆O₁₁).



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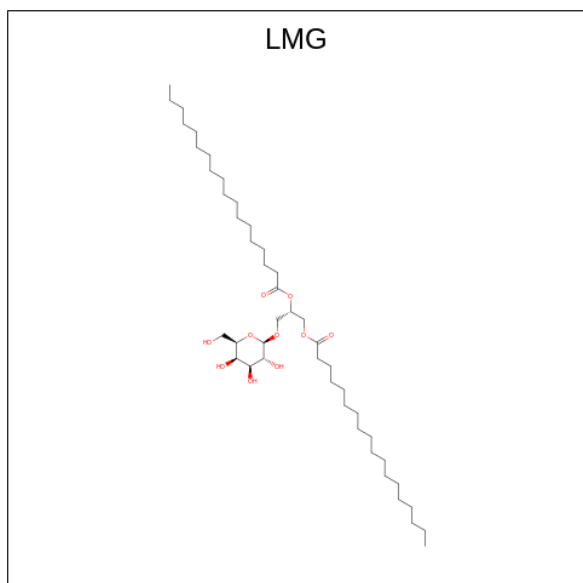
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
31	B	1	Total	C	O	0	0
			35	24	11		
31	B	1	Total	C	O	0	0
			35	24	11		
31	B	1	Total	C	O	0	0
			25	19	6		
31	F	1	Total	C	O	0	0
			35	24	11		
31	M	1	Total	C	O	0	0
			35	24	11		
31	M	1	Total	C	O	0	0
			35	24	11		
31	b	1	Total	C	O	0	0
			25	19	6		
31	b	1	Total	C	O	0	0
			25	19	6		
31	c	1	Total	C	O	0	0
			35	24	11		
31	e	1	Total	C	O	0	0
			35	24	11		
31	m	1	Total	C	O	0	0
			35	24	11		
31	t	1	Total	C	O	0	0
			26	19	7		

- Molecule 32 is 1,2-DIPALMITOYL-PHOSPHATIDYL-GLYCEROLE (CCD ID: LHG) (formula: C₃₈H₇₅O₁₀P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
32	A	1	Total	C	O	P	0	1
			98	76	20	2		
32	D	1	Total	C	O	P	0	1
			98	76	20	2		
32	D	1	Total	C	O	P	0	1
			98	76	20	2		
32	E	1	Total	C	O	P	0	1
			84	62	20	2		
32	L	1	Total	C	O	P	0	1
			98	76	20	2		
32	a	1	Total	C	O	P	0	1
			84	62	20	2		
32	b	1	Total	C	O	P	0	1
			98	76	20	2		
32	d	1	Total	C	O	P	0	1
			98	76	20	2		
32	d	1	Total	C	O	P	0	1
			98	76	20	2		
32	d	1	Total	C	O	P	0	1
			98	76	20	2		

- Molecule 33 is 1,2-DISTEAROYL-MONOGALACTOSYL-DIGLYCERIDE (CCD ID: LMG) (formula: $C_{45}H_{86}O_{10}$).



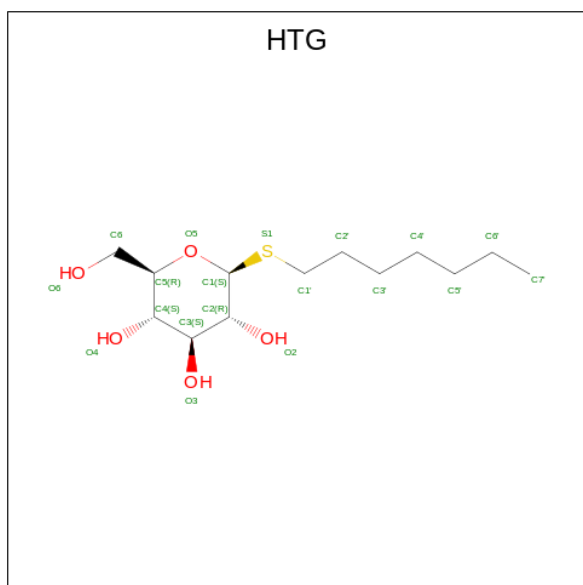
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
33	B	1	Total	C	O	0	0
			51	41	10		

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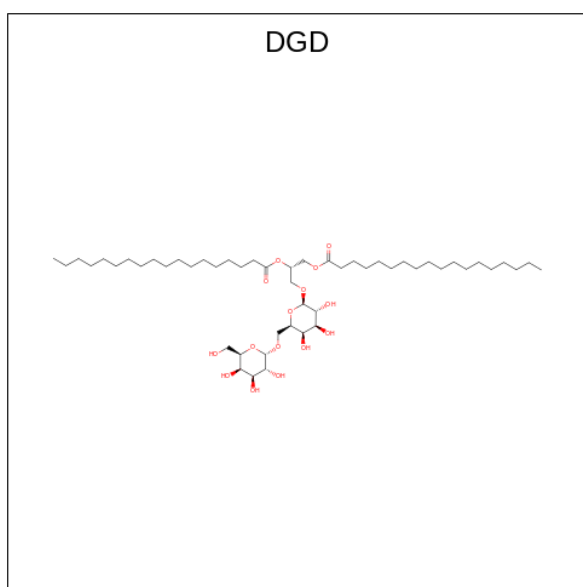
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
33	C	1	Total	C	O	0	0
			51	41	10		
33	C	1	Total	C	O	0	0
			51	41	10		
33	C	1	Total	C	O	0	0
			51	41	10		
33	D	1	Total	C	O	0	0
			51	41	10		
33	a	1	Total	C	O	0	0
			51	41	10		
33	c	1	Total	C	O	0	0
			51	41	10		
33	c	1	Total	C	O	0	0
			51	41	10		
33	d	1	Total	C	O	0	0
			51	41	10		
33	m	1	Total	C	O	0	0
			51	41	10		
33	Z	1	Total	C	O	0	0
			37	27	10		
33	z	1	Total	C	O	0	0
			39	29	10		

- Molecule 34 is heptyl 1-thio-beta-D-glucopyranoside (CCD ID: HTG) (formula: C₁₃H₂₆O₅S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
34	B	1	Total C O S 19 13 5 1	0	0
34	B	1	Total C O S 19 13 5 1	0	0
34	B	1	Total C O S 19 13 5 1	0	0
34	C	1	Total C O S 19 13 5 1	0	0
34	D	1	Total C O S 16 10 5 1	0	0
34	V	1	Total C O 11 6 5	0	0
34	b	1	Total C O S 19 13 5 1	0	0
34	b	1	Total C O S 19 13 5 1	0	0
34	b	1	Total C O S 19 13 5 1	0	0
34	c	1	Total C O S 19 13 5 1	0	0
34	d	1	Total C O S 16 10 5 1	0	0

- Molecule 35 is DIGALACTOSYL DIACYL GLYCEROL (DGDG) (CCD ID: DGD) (formula: $C_{51}H_{96}O_{15}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
35	C	1	Total C O 124 94 30	0	1
35	C	1	Total C O 124 94 30	0	1
35	C	1	Total C O 62 47 15	0	0
35	H	1	Total C O 62 47 15	0	0
35	c	1	Total C O 124 94 30	0	1
35	c	1	Total C O 124 94 30	0	1
35	c	1	Total C O 62 47 15	0	0
35	h	1	Total C O 62 47 15	0	0

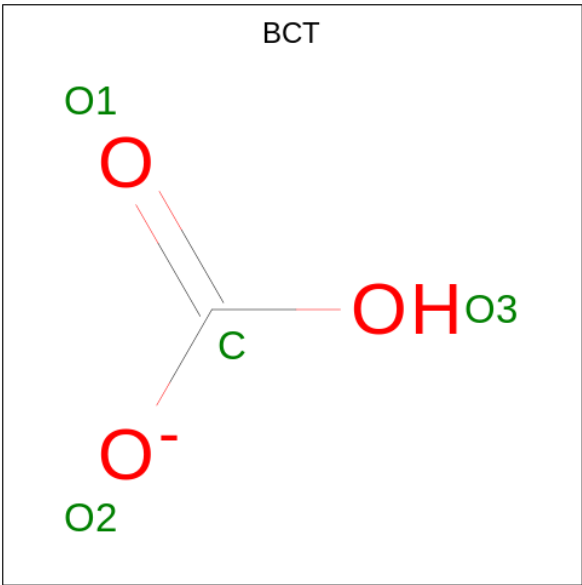
- Molecule 36 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
36	C	1	Total Ca 1 1	0	0
36	F	1	Total Ca 1 1	0	0
36	O	1	Total Ca 1 1	0	0
36	c	2	Total Ca 2 2	0	0
36	f	1	Total Ca 1 1	0	0
36	o	1	Total Ca 1 1	0	0

- Molecule 37 is FE (II) ION (CCD ID: FE2) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

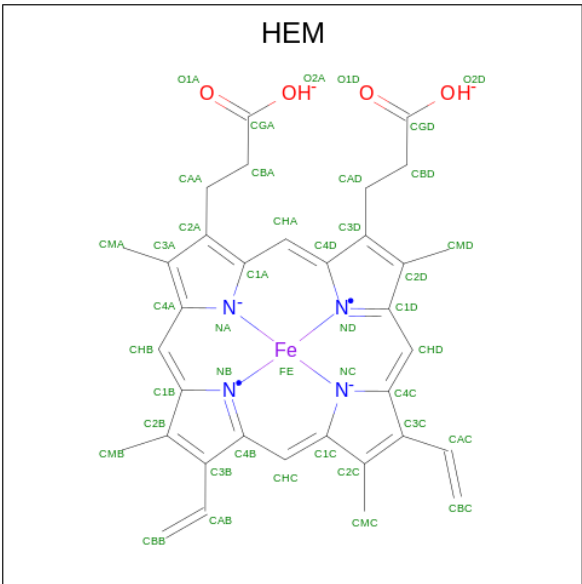
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
37	D	1	Total Fe 2 2	0	1
37	a	1	Total Fe 2 2	0	1

- Molecule 38 is BICARBONATE ION (CCD ID: BCT) (formula: CHO₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
38	D	1	Total	C	O	0	1
			8	2	6		
38	d	1	Total	C	O	0	1
			8	2	6		

- Molecule 39 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
39	F	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

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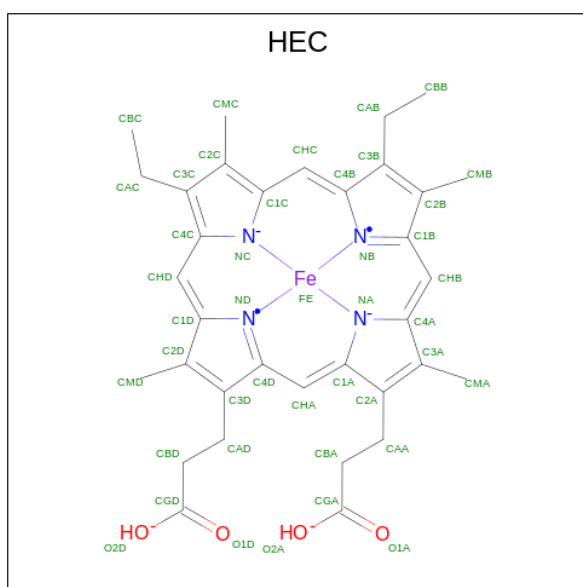
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
39	f	1	Total	C	Fe	N	O	
			43	34	1	4	4	0

- Molecule 40 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
40	J	1	Total	Mg	0	0
			1	1		
40	j	1	Total	Mg	0	0
			1	1		

- Molecule 41 is HEME C (CCD ID: HEC) (formula: C₃₄H₃₆FeN₄O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
41	V	1	Total	C	Fe	N	O	
			43	34	1	4	4	0
41	v	1	Total	C	Fe	N	O	
			43	34	1	4	4	0

- Molecule 42 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
42	A	137	Total	O	0	83
			218	218		
42	B	196	Total	O	0	3
			199	199		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
42	C	170	Total O 207 207	0	38
42	D	122	Total O 157 157	0	35
42	E	17	Total O 17 17	0	0
42	F	5	Total O 5 5	0	0
42	H	18	Total O 18 18	0	0
42	I	4	Total O 4 4	0	0
42	J	7	Total O 7 7	0	0
42	K	6	Total O 6 6	0	0
42	L	8	Total O 9 9	0	1
42	M	5	Total O 5 5	0	0
42	O	102	Total O 106 106	0	4
42	T	11	Total O 14 14	0	3
42	U	46	Total O 49 49	0	3
42	V	78	Total O 80 80	0	2
42	X	8	Total O 8 8	0	0
42	a	130	Total O 208 208	0	79
42	b	200	Total O 203 203	0	3
42	c	159	Total O 192 192	0	33
42	d	120	Total O 154 154	0	34
42	e	8	Total O 8 8	0	0
42	f	3	Total O 3 3	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
42	h	17	Total 17	O 17	0	0
42	i	2	Total 2	O 2	0	0
42	j	2	Total 2	O 2	0	0
42	k	3	Total 3	O 3	0	0
42	l	7	Total 8	O 8	0	1
42	m	13	Total 13	O 13	0	0
42	o	98	Total 102	O 102	0	4
42	t	8	Total 11	O 11	0	3
42	u	49	Total 50	O 50	0	1
42	v	58	Total 61	O 61	0	3
42	x	6	Total 6	O 6	0	0
42	y	2	Total 2	O 2	0	0

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Photosystem II protein D1

Chain A:  92%



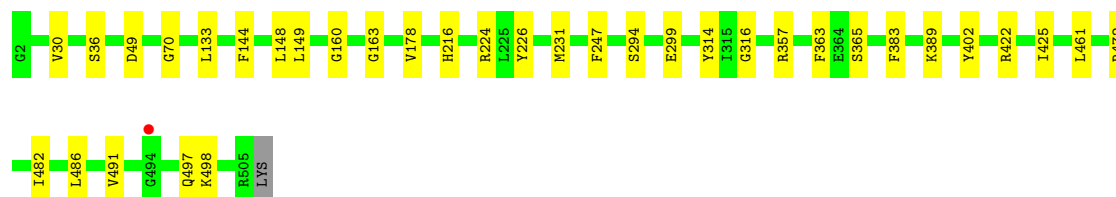
- Molecule 1: Photosystem II protein D1

Chain a:  88% 9%



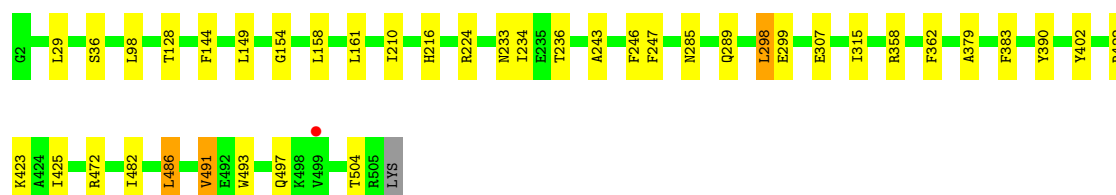
- Molecule 2: Photosystem II CP47 reaction center protein

Chain B:  93% 7%

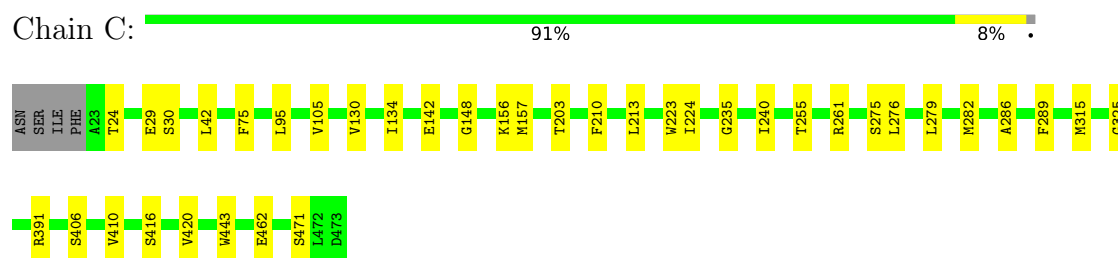


- Molecule 2: Photosystem II CP47 reaction center protein

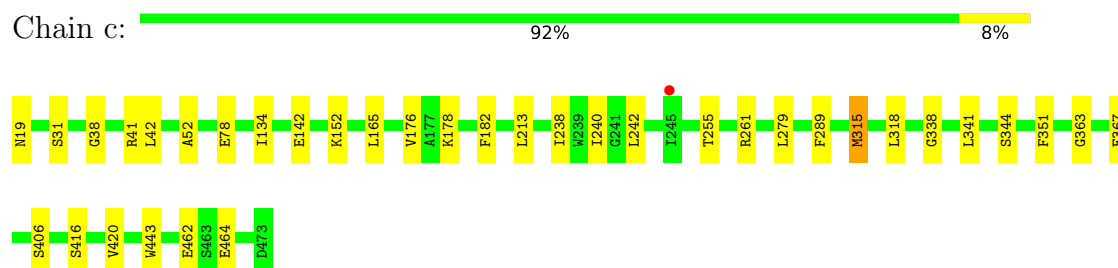
Chain b:  92% 7%



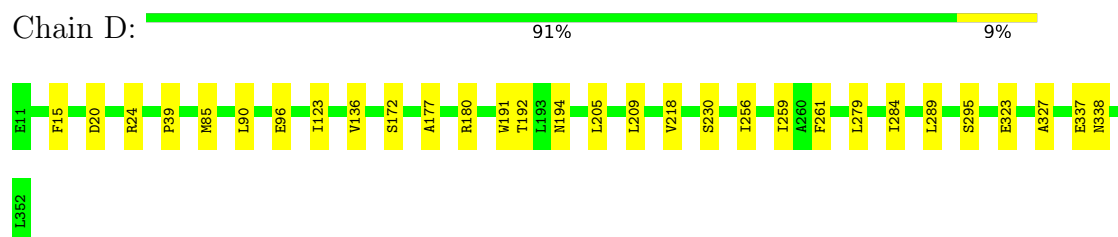
- Molecule 3: Photosystem II CP43 reaction center protein



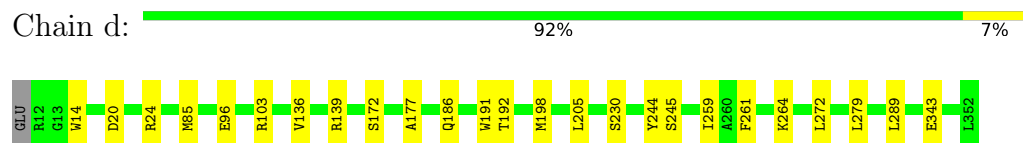
- Molecule 3: Photosystem II CP43 reaction center protein



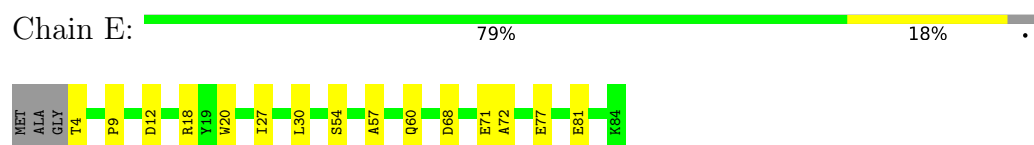
- Molecule 4: Photosystem II D2 protein



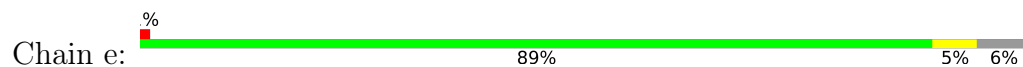
- Molecule 4: Photosystem II D2 protein



- Molecule 5: Cytochrome b559 subunit alpha



- Molecule 5: Cytochrome b559 subunit alpha





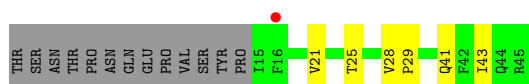
- Molecule 6: Cytochrome b559 subunit beta

Chain F: 66% 11% 23%



- Molecule 6: Cytochrome b559 subunit beta

Chain f: 2% 57% 14% 30%



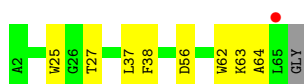
- Molecule 7: Photosystem II reaction center protein H

Chain H: 2% 94% 5%



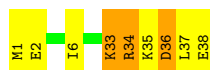
- Molecule 7: Photosystem II reaction center protein H

Chain h: 2% 86% 12%



- Molecule 8: Photosystem II reaction center protein I

Chain I: 76% 16% 8%



- Molecule 8: Photosystem II reaction center protein I

Chain i: 87% 13%



- Molecule 9: Photosystem II reaction center protein J

Chain J: 82% 13% 5%



- Molecule 9: Photosystem II reaction center protein J

Chain j: 92% 8%



- Molecule 10: Photosystem II reaction center protein K

Chain K: 78% 19%



- Molecule 10: Photosystem II reaction center protein K

Chain k: 81% 14% 5%



- Molecule 11: Photosystem II reaction center protein L

Chain L: 95%



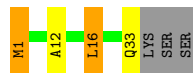
- Molecule 11: Photosystem II reaction center protein L

Chain l: 89% 8%



- Molecule 12: Photosystem II reaction center protein M

Chain M: 81% 6% 6% 8%



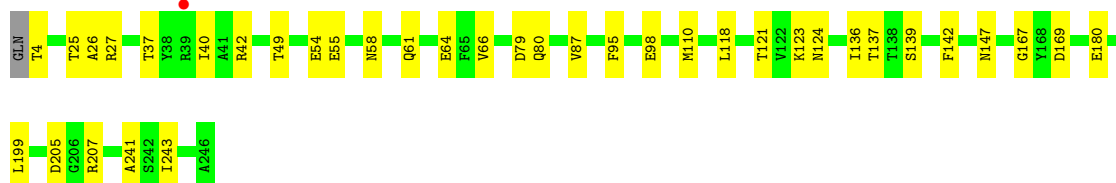
- Molecule 12: Photosystem II reaction center protein M

Chain m: 81% 11% 6%



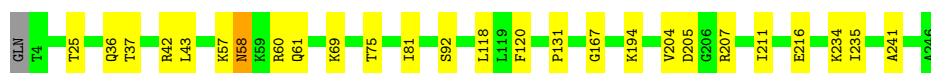
- Molecule 13: Photosystem II manganese-stabilizing polypeptide

Chain O: 84% 15%



- Molecule 13: Photosystem II manganese-stabilizing polypeptide

Chain o: 89% 10%



- Molecule 14: Photosystem II reaction center protein T

Chain T: 81% 12% 6%



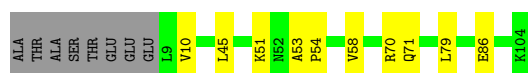
- Molecule 14: Photosystem II reaction center protein T

Chain t: 78% 16% 6%



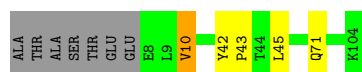
- Molecule 15: Photosystem II 12 kDa extrinsic protein

Chain U: 83% 10% 8%

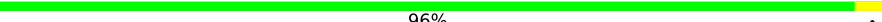


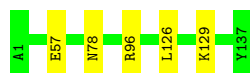
- Molecule 15: Photosystem II 12 kDa extrinsic protein

Chain u: 88% 7% 5%



- Molecule 16: Cytochrome c-550

Chain V:  96% .



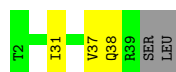
- Molecule 16: Cytochrome c-550

Chain v:  91% 9%



- Molecule 17: Photosystem II reaction center protein X

Chain X:  88% 8% 5%



- Molecule 17: Photosystem II reaction center protein X

Chain x:  88% 8% 5%



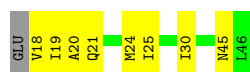
- Molecule 18: Photosystem II reaction center protein Ycf12

Chain Y:  87% 10% .



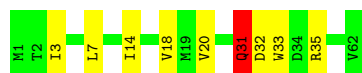
- Molecule 18: Photosystem II reaction center protein Ycf12

Chain y:  70% 27% .

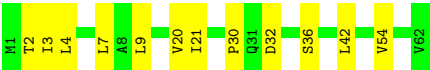
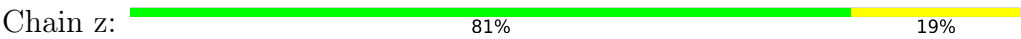


- Molecule 19: Photosystem II reaction center protein Z

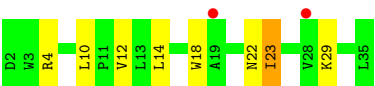
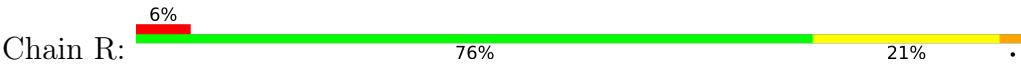
Chain Z:  85% 13% .



- Molecule 19: Photosystem II reaction center protein Z



● Molecule 20: Photosystem II protein Y



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	125.77Å 231.76Å 288.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.25 19.99 – 2.25	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.99-2.25) 99.8 (19.99-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.66 (at 2.26Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.142 , 0.181 0.144 , 0.183	Depositor DCC
R_{free} test set	19914 reflections (2.44%)	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.465	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 73.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	62604	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, LMT, HTG, CL, LMG, BCR, PL9, GOL, FE2, CLA, FME, DGD, OEX, PHO, BCT, LHG, CA, UNL, SQD, OEY, MG, HEC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.27	0/4478	0.42	1/6098 (0.0%)
1	a	0.26	0/4470	0.40	0/6087
2	B	0.37	0/4293	0.51	0/5851
2	b	0.34	0/4285	0.49	0/5841
3	C	0.29	0/4404	0.43	0/5997
3	c	0.28	0/4459	0.43	0/6071
4	D	0.35	0/3741	0.47	0/5095
4	d	0.31	0/3749	0.44	0/5106
5	E	0.34	0/681	0.51	0/928
5	e	0.30	0/690	0.49	0/939
6	F	0.33	0/284	0.50	0/387
6	f	0.31	0/269	0.45	0/365
7	H	0.33	0/519	0.51	0/708
7	h	0.30	0/530	0.49	0/722
8	I	0.32	0/311	0.47	0/419
8	i	0.32	0/311	0.47	0/419
9	J	0.32	0/278	0.38	0/376
9	j	0.34	0/283	0.47	0/383
10	K	0.30	0/303	0.46	0/416
10	k	0.33	0/303	0.50	0/416
11	L	0.38	0/318	0.48	0/433
11	l	0.38	0/318	0.46	0/433
12	M	0.40	0/261	0.51	0/357
12	m	0.35	0/279	0.50	0/380
13	O	0.35	0/1991	0.51	0/2698
13	o	0.34	0/1966	0.52	0/2665
14	T	0.34	0/310	0.43	0/419
14	t	0.32	0/301	0.41	0/406
15	U	0.37	0/811	0.55	0/1095
15	u	0.37	0/818	0.52	0/1105
16	V	0.37	0/1142	0.51	0/1545

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	v	0.31	0/1139	0.47	0/1542
17	X	0.23	0/292	0.35	0/395
17	x	0.25	0/284	0.40	0/384
18	Y	0.26	0/216	0.43	0/289
18	y	0.24	0/216	0.40	0/289
19	Z	0.22	0/490	0.38	0/669
19	z	0.22	0/490	0.41	0/669
20	R	0.25	0/279	0.34	0/383
All	All	0.31	0/50562	0.46	1/68780 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	131	TRP	CA-CB-CG	-5.18	103.75	113.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4338	0	4142	16	0
1	a	4330	0	4132	32	0
2	B	4146	0	3983	26	0
2	b	4134	0	3976	36	0
3	C	4260	0	4123	23	0
3	c	4308	0	4172	27	0
4	D	3620	0	3484	34	0
4	d	3628	0	3490	21	0
5	E	662	0	648	10	0
5	e	670	0	655	3	0
6	F	275	0	282	4	0
6	f	261	0	269	6	0
7	H	506	0	529	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	h	517	0	541	7	0
8	I	314	0	328	6	0
8	i	314	0	328	2	0
9	J	272	0	279	6	0
9	j	277	0	284	2	0
10	K	293	0	305	4	0
10	k	293	0	305	8	0
11	L	311	0	320	1	0
11	l	311	0	320	3	0
12	M	268	0	285	4	0
12	m	286	0	305	7	0
13	O	1958	0	1920	17	0
13	o	1933	0	1900	13	0
14	T	311	0	318	1	0
14	t	302	0	311	4	0
15	U	800	0	796	5	0
15	u	807	0	805	3	0
16	V	1120	0	1122	3	0
16	v	1117	0	1131	8	0
17	X	289	0	322	3	0
17	x	281	0	312	3	0
18	Y	215	0	246	2	0
18	y	215	0	246	6	0
19	Z	479	0	516	5	0
19	z	479	0	516	2	0
20	R	273	0	305	4	0
21	A	11	0	0	1	0
21	a	11	0	0	1	0
22	A	4	0	0	0	0
22	a	4	0	0	0	0
23	A	455	0	504	13	0
23	B	1040	0	1152	23	0
23	C	845	0	936	34	0
23	D	195	0	216	8	0
23	a	455	0	504	20	0
23	b	1040	0	1152	23	0
23	c	845	0	936	33	0
23	d	195	0	216	8	0
24	A	256	0	296	5	0
24	a	256	0	296	3	0
25	A	40	0	56	1	0
25	B	120	0	168	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	C	80	0	112	2	0
25	D	40	0	56	0	0
25	H	40	0	56	2	0
25	K	80	0	112	1	0
25	T	40	0	56	5	0
25	a	40	0	56	1	0
25	b	120	0	168	9	0
25	c	80	0	112	5	0
25	d	40	0	56	3	0
25	h	40	0	56	4	0
25	k	40	0	56	1	0
25	t	40	0	56	4	0
25	y	40	0	56	2	0
26	A	162	0	234	3	0
26	B	54	0	78	2	0
26	X	43	0	53	3	0
26	a	162	0	232	7	0
26	b	54	0	78	2	0
26	f	43	0	53	0	0
27	A	6	0	8	0	0
27	B	18	0	24	3	0
27	C	12	0	16	0	0
27	D	12	0	14	7	0
27	O	12	0	16	2	0
27	V	12	0	16	0	0
27	a	12	0	16	6	0
27	b	12	0	16	4	0
27	c	18	0	24	0	0
27	d	6	0	7	0	0
27	l	12	0	16	1	0
27	o	12	0	16	0	0
27	v	12	0	16	3	0
28	A	10	0	0	0	0
28	a	10	0	0	0	0
29	A	110	0	160	19	0
29	D	110	0	160	1	0
29	a	110	0	160	8	0
29	d	110	0	160	0	0
30	A	28	0	0	0	0
30	B	33	0	0	0	0
30	D	57	0	0	0	0
30	I	40	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	J	10	0	0	0	0
30	K	68	0	0	0	0
30	X	18	0	0	0	0
30	a	30	0	0	0	0
30	b	33	0	0	0	0
30	c	64	0	0	0	0
30	d	53	0	0	0	0
30	i	40	0	0	0	0
30	j	10	0	0	0	0
30	l	10	0	0	0	0
30	m	10	0	0	0	0
30	x	18	0	0	0	0
31	A	70	0	92	1	0
31	B	95	0	127	3	0
31	F	35	0	46	0	0
31	M	70	0	92	1	0
31	b	50	0	70	2	0
31	c	35	0	46	1	0
31	e	35	0	46	1	0
31	m	35	0	46	0	0
31	t	26	0	34	2	0
32	A	98	0	148	2	0
32	D	196	0	296	10	0
32	E	84	0	114	5	0
32	L	98	0	148	0	0
32	a	84	0	114	9	0
32	b	98	0	148	0	0
32	d	294	0	444	24	0
33	B	51	0	72	1	0
33	C	153	0	216	3	0
33	D	51	0	72	0	0
33	Z	37	0	44	1	0
33	a	51	0	72	1	0
33	c	102	0	144	1	0
33	d	51	0	72	3	0
33	m	51	0	72	0	0
33	z	39	0	48	2	0
34	B	57	0	78	3	0
34	C	19	0	26	0	0
34	D	16	0	17	1	0
34	V	11	0	10	0	0
34	b	57	0	78	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
34	c	19	0	26	1	0
34	d	16	0	17	1	0
35	C	310	0	410	4	0
35	H	62	0	82	1	0
35	c	310	0	410	8	0
35	h	62	0	82	0	0
36	C	1	0	0	0	0
36	F	1	0	0	0	0
36	O	1	0	0	0	0
36	c	2	0	0	0	0
36	f	1	0	0	0	0
36	o	1	0	0	0	0
37	D	2	0	0	0	0
37	a	2	0	0	0	0
38	D	8	0	0	0	0
38	d	8	0	0	0	0
39	F	43	0	30	2	0
39	f	43	0	30	0	0
40	J	1	0	0	0	0
40	j	1	0	0	0	0
41	V	43	0	30	0	0
41	v	43	0	30	0	0
42	A	218	0	0	1	0
42	B	199	0	0	1	0
42	C	207	0	0	0	0
42	D	157	0	0	3	0
42	E	17	0	0	0	0
42	F	5	0	0	0	0
42	H	18	0	0	0	0
42	I	4	0	0	0	0
42	J	7	0	0	1	0
42	K	6	0	0	0	0
42	L	9	0	0	0	0
42	M	5	0	0	0	0
42	O	106	0	0	0	0
42	T	14	0	0	0	0
42	U	49	0	0	0	0
42	V	80	0	0	0	0
42	X	8	0	0	0	0
42	a	208	0	0	2	0
42	b	203	0	0	1	0
42	c	192	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	d	154	0	0	1	0
42	e	8	0	0	0	0
42	f	3	0	0	0	0
42	h	17	0	0	0	0
42	i	2	0	0	0	0
42	j	2	0	0	0	0
42	k	3	0	0	1	0
42	l	8	0	0	0	0
42	m	13	0	0	0	0
42	o	102	0	0	0	0
42	t	11	0	0	1	0
42	u	50	0	0	1	0
42	v	61	0	0	0	0
42	x	6	0	0	0	0
42	y	2	0	0	0	0
All	All	62604	0	61443	553	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 5.

The worst 5 of 553 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)
27:D:403:GOL:H11	12:M:1:FME:HG2	1.45	0.97
1:a:250[B]:ALA:HA	2:b:491[B]:VAL:HG11	1.50	0.94
1:a:250[A]:ALA:HA	2:b:491[A]:VAL:HG11	1.51	0.93
21:a:401[B]:OEY:O6	21:a:401[B]:OEY:O5	1.90	0.89
21:A:401[B]:OEY:O6	21:A:401[B]:OEY:O5	1.91	0.88

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	553/344 (161%)	544 (98%)	7 (1%)	2 (0%)	30	31
1	a	552/344 (160%)	545 (99%)	5 (1%)	2 (0%)	30	31
2	B	522/505 (103%)	515 (99%)	7 (1%)	0	100	100
2	b	521/505 (103%)	511 (98%)	10 (2%)	0	100	100
3	C	546/455 (120%)	539 (99%)	6 (1%)	1 (0%)	43	50
3	c	553/455 (122%)	542 (98%)	10 (2%)	1 (0%)	43	50
4	D	453/342 (132%)	438 (97%)	15 (3%)	0	100	100
4	d	454/342 (133%)	444 (98%)	10 (2%)	0	100	100
5	E	79/84 (94%)	78 (99%)	1 (1%)	0	100	100
5	e	79/84 (94%)	79 (100%)	0	0	100	100
6	F	32/44 (73%)	32 (100%)	0	0	100	100
6	f	30/44 (68%)	30 (100%)	0	0	100	100
7	H	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
7	h	63/65 (97%)	59 (94%)	3 (5%)	1 (2%)	7	4
8	I	36/38 (95%)	33 (92%)	2 (6%)	1 (3%)	4	2
8	i	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
9	J	36/39 (92%)	36 (100%)	0	0	100	100
9	j	37/39 (95%)	36 (97%)	1 (3%)	0	100	100
10	K	35/37 (95%)	35 (100%)	0	0	100	100
10	k	35/37 (95%)	34 (97%)	1 (3%)	0	100	100
11	L	36/37 (97%)	36 (100%)	0	0	100	100
11	l	36/37 (97%)	36 (100%)	0	0	100	100
12	M	32/36 (89%)	32 (100%)	0	0	100	100
12	m	34/36 (94%)	34 (100%)	0	0	100	100
13	O	251/244 (103%)	242 (96%)	8 (3%)	1 (0%)	30	31
13	o	249/244 (102%)	243 (98%)	6 (2%)	0	100	100
14	T	33/32 (103%)	33 (100%)	0	0	100	100
14	t	32/32 (100%)	32 (100%)	0	0	100	100
15	U	97/104 (93%)	93 (96%)	4 (4%)	0	100	100
15	u	98/104 (94%)	93 (95%)	5 (5%)	0	100	100
16	V	140/137 (102%)	136 (97%)	4 (3%)	0	100	100
16	v	140/137 (102%)	134 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	X	37/40 (92%)	37 (100%)	0	0	100	100
17	x	36/40 (90%)	36 (100%)	0	0	100	100
18	Y	27/30 (90%)	26 (96%)	1 (4%)	0	100	100
18	y	27/30 (90%)	27 (100%)	0	0	100	100
19	Z	60/62 (97%)	58 (97%)	1 (2%)	1 (2%)	7	3
19	z	60/62 (97%)	59 (98%)	0	1 (2%)	7	3
20	R	32/34 (94%)	31 (97%)	1 (3%)	0	100	100
All	All	6171/5384 (115%)	6040 (98%)	120 (2%)	11 (0%)	43	50

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
8	I	36	ASP
3	C	416	SER
3	c	416	SER
19	Z	31	GLN
19	z	30	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	444/279 (159%)	440 (99%)	4 (1%)	70	79
1	a	443/279 (159%)	442 (100%)	1 (0%)	87	92
2	B	421/403 (104%)	418 (99%)	3 (1%)	76	82
2	b	420/403 (104%)	410 (98%)	10 (2%)	43	54
3	C	430/356 (121%)	419 (97%)	11 (3%)	40	50
3	c	436/356 (122%)	429 (98%)	7 (2%)	55	66
4	D	368/277 (133%)	365 (99%)	3 (1%)	73	80
4	d	369/277 (133%)	363 (98%)	6 (2%)	55	66
5	E	72/73 (99%)	69 (96%)	3 (4%)	26	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	e	72/73 (99%)	70 (97%)	2 (3%)	38	48
6	F	28/38 (74%)	28 (100%)	0	100	100
6	f	26/38 (68%)	26 (100%)	0	100	100
7	H	54/54 (100%)	52 (96%)	2 (4%)	30	37
7	h	55/54 (102%)	55 (100%)	0	100	100
8	I	34/34 (100%)	32 (94%)	2 (6%)	18	18
8	i	34/34 (100%)	33 (97%)	1 (3%)	37	47
9	J	26/27 (96%)	25 (96%)	1 (4%)	29	36
9	j	26/27 (96%)	25 (96%)	1 (4%)	29	36
10	K	30/30 (100%)	26 (87%)	4 (13%)	4	2
10	k	30/30 (100%)	27 (90%)	3 (10%)	7	5
11	L	36/35 (103%)	36 (100%)	0	100	100
11	l	36/35 (103%)	36 (100%)	0	100	100
12	M	30/32 (94%)	28 (93%)	2 (7%)	15	14
12	m	32/32 (100%)	30 (94%)	2 (6%)	16	16
13	O	216/207 (104%)	208 (96%)	8 (4%)	30	37
13	o	213/207 (103%)	206 (97%)	7 (3%)	33	42
14	T	32/28 (114%)	28 (88%)	4 (12%)	4	3
14	t	31/28 (111%)	31 (100%)	0	100	100
15	U	86/89 (97%)	84 (98%)	2 (2%)	44	55
15	u	87/89 (98%)	85 (98%)	2 (2%)	44	55
16	V	123/117 (105%)	123 (100%)	0	100	100
16	v	123/117 (105%)	120 (98%)	3 (2%)	43	54
17	X	32/33 (97%)	32 (100%)	0	100	100
17	x	31/33 (94%)	31 (100%)	0	100	100
18	Y	22/23 (96%)	22 (100%)	0	100	100
18	y	22/23 (96%)	18 (82%)	4 (18%)	2	0
19	Z	52/52 (100%)	49 (94%)	3 (6%)	18	19
19	z	52/52 (100%)	45 (86%)	7 (14%)	4	2
20	R	29/29 (100%)	26 (90%)	3 (10%)	7	5
All	All	5103/4403 (116%)	4992 (98%)	111 (2%)	45	56

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	b	486[B]	LEU
19	z	42	LEU
4	d	272[A]	LEU
19	z	21	ILE
19	Z	20	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
3	c	19	ASN
3	c	415	ASN
16	v	86	GLN
13	o	58	ASN
15	u	78	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
14	FME	T	1	14	8,9,10	0.59	0	7,9,11	1.43	1 (14%)
8	FME	I	1	8	8,9,10	0.62	0	7,9,11	1.38	2 (28%)
12	FME	m	1	12	8,9,10	0.49	0	7,9,11	1.45	2 (28%)
12	FME	M	1	12	8,9,10	0.71	0	7,9,11	1.23	1 (14%)
14	FME	t	1	14	8,9,10	0.67	0	7,9,11	1.80	2 (28%)
8	FME	i	1	8	8,9,10	0.68	0	7,9,11	1.23	1 (14%)

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
14	FME	T	1	14	-	2/7/9/11	-
8	FME	I	1	8	-	0/7/9/11	-
12	FME	m	1	12	-	1/7/9/11	-
12	FME	M	1	12	-	1/7/9/11	-
14	FME	t	1	14	-	1/7/9/11	-
8	FME	i	1	8	-	1/7/9/11	-

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	t	1	FME	O-C-CA	-2.74	117.60	124.78
14	t	1	FME	CA-N-CN	-2.68	118.70	122.82
14	T	1	FME	CG-CB-CA	2.32	119.38	112.95
12	M	1	FME	O-C-CA	-2.29	118.77	124.78
8	I	1	FME	CA-N-CN	-2.26	119.34	122.82

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	M	1	FME	O1-CN-N-CA
8	i	1	FME	O-C-CA-CB
14	t	1	FME	O1-CN-N-CA
14	T	1	FME	N-CA-CB-CG
14	T	1	FME	C-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	m	1	FME	3	0
12	M	1	FME	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 274 ligands modelled in this entry, 21 are monoatomic and 20 are unknown - leaving 233 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$
34	HTG	C	522	-	19,19,19	0.89	1 (5%)	23,24,24	1.39	1 (4%)
23	CLA	c	509	3	69,73,73	2.11	20 (28%)	83,113,113	2.79	26 (31%)
35	DGD	c	517[B]	-	63,63,67	0.86	2 (3%)	77,77,81	1.09	4 (5%)
25	BCR	K	103	-	41,41,41	1.00	1 (2%)	56,56,56	1.77	12 (21%)
23	CLA	c	511	3	69,73,73	2.04	20 (28%)	83,113,113	2.78	33 (39%)
25	BCR	D	406	-	41,41,41	1.10	1 (2%)	56,56,56	1.83	16 (28%)
26	SQD	X	101	-	42,43,54	1.20	4 (9%)	51,54,65	2.16	13 (25%)
23	CLA	B	601	42	69,73,73	2.08	21 (30%)	83,113,113	2.86	28 (33%)
33	LMG	c	520	-	51,51,55	0.91	2 (3%)	59,59,63	1.11	5 (8%)
33	LMG	d	411	40	51,51,55	0.92	2 (3%)	59,59,63	1.19	6 (10%)
28	OEX	a	413[A]	42,1,3	0,14,14	-	-	-	-	-
28	OEX	A	413[A]	42,1,3	0,14,14	-	-	-	-	-
23	CLA	A	404[B]	1	69,73,73	2.06	19 (27%)	83,113,113	2.87	33 (39%)
23	CLA	B	614	2	69,73,73	2.02	19 (27%)	83,113,113	3.02	34 (40%)
26	SQD	a	412	-	53,54,54	1.08	4 (7%)	62,65,65	1.19	9 (14%)
27	GOL	V	203[B]	-	5,5,5	1.05	0	5,5,5	0.95	0
34	HTG	b	622	-	19,19,19	1.20	2 (10%)	23,24,24	1.92	7 (30%)
38	BCT	d	401[B]	37	2,3,3	0.65	0	2,3,3	0.88	0
23	CLA	b	613	2	69,73,73	2.00	19 (27%)	83,113,113	2.76	29 (34%)
31	LMT	A	417	-	36,36,36	0.96	2 (5%)	47,47,47	1.07	3 (6%)
25	BCR	B	619	-	41,41,41	1.09	1 (2%)	56,56,56	1.29	5 (8%)
32	LHG	D	408[B]	-	48,48,48	0.90	2 (4%)	51,54,54	1.00	4 (7%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	SQD	A	412	-	53,54,54	1.05	3 (5%)	62,65,65	1.28	6 (9%)
31	LMT	c	501	-	36,36,36	0.98	0	47,47,47	1.05	2 (4%)
33	LMG	a	417	-	51,51,55	0.91	2 (3%)	59,59,63	1.25	6 (10%)
23	CLA	B	611	2	69,73,73	2.60	20 (28%)	83,113,113	4.11	32 (38%)
23	CLA	A	404[A]	1	69,73,73	2.00	20 (28%)	83,113,113	2.87	30 (36%)
34	HTG	b	623	-	19,19,19	1.06	1 (5%)	23,24,24	1.84	2 (8%)
32	LHG	L	101[A]	-	48,48,48	0.88	2 (4%)	51,54,54	1.15	4 (7%)
35	DGD	h	102	-	63,63,67	0.88	3 (4%)	77,77,81	1.10	8 (10%)
39	HEM	F	102	5,6	50,50,50	1.53	8 (16%)	66,82,82	1.93	15 (22%)
31	LMT	A	419	-	36,36,36	1.03	2 (5%)	47,47,47	1.16	4 (8%)
23	CLA	C	512	3	69,73,73	2.03	21 (30%)	83,113,113	2.76	29 (34%)
32	LHG	D	408[A]	-	48,48,48	0.87	2 (4%)	51,54,54	1.01	3 (5%)
23	CLA	B	604	2	69,73,73	2.04	22 (31%)	83,113,113	2.66	28 (33%)
32	LHG	E	101[A]	-	41,41,48	1.08	2 (4%)	44,47,54	1.10	3 (6%)
31	LMT	B	628	-	36,36,36	1.17	3 (8%)	47,47,47	1.32	5 (10%)
23	CLA	B	610	42	69,73,73	2.01	19 (27%)	83,113,113	2.89	34 (40%)
27	GOL	c	526[B]	-	5,5,5	0.96	0	5,5,5	0.96	0
27	GOL	B	627	-	5,5,5	0.94	0	5,5,5	0.99	0
32	LHG	d	406[B]	-	48,48,48	0.91	2 (4%)	51,54,54	1.06	4 (7%)
33	LMG	c	521	-	51,51,55	1.00	2 (3%)	59,59,63	1.36	6 (10%)
32	LHG	a	420[A]	-	41,41,48	1.06	2 (4%)	44,47,54	0.92	2 (4%)
29	PL9	d	405[A]	-	55,55,55	0.70	1 (1%)	68,69,69	1.63	18 (26%)
31	LMT	e	101	-	36,36,36	1.01	2 (5%)	47,47,47	1.00	1 (2%)
35	DGD	C	518[B]	-	63,63,67	0.89	3 (4%)	77,77,81	0.99	4 (5%)
33	LMG	z	101	-	39,39,55	1.08	2 (5%)	47,47,63	1.05	2 (4%)
21	OXY	A	401[B]	42,1,3	0,16,16	-	-	-	-	-
31	LMT	M	101	-	36,36,36	1.13	4 (11%)	47,47,47	1.23	5 (10%)
23	CLA	B	613	2	69,73,73	2.00	19 (27%)	83,113,113	2.82	31 (37%)
25	BCR	T	101	-	41,41,41	0.95	1 (2%)	56,56,56	1.69	14 (25%)
23	CLA	C	502	3	69,73,73	1.98	19 (27%)	83,113,113	2.83	32 (38%)
25	BCR	A	409	-	41,41,41	1.02	1 (2%)	56,56,56	1.38	7 (12%)
24	PHO	a	408[A]	-	58,69,69	2.74	13 (22%)	56,99,99	2.81	14 (25%)
23	CLA	D	404[A]	4	69,73,73	2.00	20 (28%)	83,113,113	2.86	32 (38%)
34	HTG	B	623	-	19,19,19	0.83	1 (5%)	23,24,24	1.44	2 (8%)
23	CLA	d	402[B]	4	69,73,73	2.02	20 (28%)	83,113,113	2.83	28 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
23	CLA	b	612	2	69,73,73	2.00	21 (30%)	83,113,113	2.74	33 (39%)
23	CLA	c	513	3	69,73,73	2.08	19 (27%)	83,113,113	2.84	33 (39%)
27	GOL	b	624	-	5,5,5	1.24	1 (20%)	5,5,5	0.73	0
24	PHO	A	407[B]	-	58,69,69	2.73	13 (22%)	56,99,99	2.72	13 (23%)
38	BCT	D	402[B]	37	2,3,3	0.67	0	2,3,3	0.91	0
27	GOL	o	303	-	5,5,5	1.11	1 (20%)	5,5,5	1.06	0
41	HEC	v	201	16	50,50,50	1.78	7 (14%)	68,82,82	1.54	13 (19%)
25	BCR	b	617	-	41,41,41	1.06	1 (2%)	56,56,56	1.45	5 (8%)
32	LHG	d	413[B]	-	48,48,48	0.91	2 (4%)	51,54,54	1.11	5 (9%)
23	CLA	b	604	2	69,73,73	2.05	20 (28%)	83,113,113	2.77	26 (31%)
32	LHG	D	409[B]	-	48,48,48	0.93	2 (4%)	51,54,54	1.02	3 (5%)
23	CLA	c	505	42	69,73,73	2.04	21 (30%)	83,113,113	2.77	29 (34%)
34	HTG	B	622	-	19,19,19	1.12	2 (10%)	23,24,24	1.69	5 (21%)
23	CLA	d	402[A]	4	69,73,73	1.95	20 (28%)	83,113,113	2.76	32 (38%)
34	HTG	c	522	-	19,19,19	0.94	1 (5%)	23,24,24	1.52	2 (8%)
29	PL9	a	414[B]	-	55,55,55	0.64	2 (3%)	68,69,69	1.95	21 (30%)
23	CLA	A	405[B]	42	69,73,73	2.06	18 (26%)	83,113,113	2.83	34 (40%)
31	LMT	F	101	-	36,36,36	1.06	1 (2%)	47,47,47	1.05	3 (6%)
25	BCR	C	515	-	41,41,41	1.00	1 (2%)	56,56,56	1.42	6 (10%)
26	SQD	b	620	-	53,54,54	1.04	3 (5%)	62,65,65	1.72	13 (20%)
35	DGD	c	517[A]	-	63,63,67	0.85	2 (3%)	77,77,81	1.10	7 (9%)
32	LHG	d	413[A]	-	48,48,48	0.89	2 (4%)	51,54,54	1.11	4 (7%)
35	DGD	c	519	-	63,63,67	0.85	4 (6%)	77,77,81	1.06	4 (5%)
32	LHG	A	418[B]	-	48,48,48	0.90	2 (4%)	51,54,54	1.16	5 (9%)
25	BCR	t	102	-	41,41,41	1.04	1 (2%)	56,56,56	1.50	8 (14%)
23	CLA	a	406[B]	42	69,73,73	2.00	16 (23%)	83,113,113	2.85	30 (36%)
23	CLA	b	607	42	69,73,73	1.92	20 (28%)	83,113,113	2.79	30 (36%)
32	LHG	d	407[B]	-	48,48,48	0.91	2 (4%)	51,54,54	0.96	3 (5%)
23	CLA	b	603	2	69,73,73	1.96	18 (26%)	83,113,113	2.90	31 (37%)
27	GOL	D	403	-	5,5,5	1.50	2 (40%)	5,5,5	0.98	1 (20%)
23	CLA	B	605	2	69,73,73	2.07	19 (27%)	83,113,113	2.97	30 (36%)
23	CLA	c	514	3	69,73,73	2.11	21 (30%)	83,113,113	2.89	31 (37%)
31	LMT	B	630	-	36,36,36	1.02	3 (8%)	47,47,47	1.15	4 (8%)
31	LMT	b	621	-	25,25,36	0.97	1 (4%)	30,30,47	1.19	2 (6%)
23	CLA	C	503	3	69,73,73	2.05	19 (27%)	83,113,113	2.70	30 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	GOL	a	419	-	5,5,5	1.21	1 (20%)	5,5,5	0.98	0
41	HEC	V	201	16	50,50,50	1.75	7 (14%)	68,82,82	1.50	11 (16%)
27	GOL	V	203[A]	-	5,5,5	1.34	0	5,5,5	0.80	0
23	CLA	c	503	3	69,73,73	1.93	17 (24%)	83,113,113	2.72	28 (33%)
23	CLA	a	406[A]	42	69,73,73	2.04	17 (24%)	83,113,113	2.86	32 (38%)
32	LHG	d	407[A]	-	48,48,48	0.92	2 (4%)	51,54,54	1.01	3 (5%)
23	CLA	a	405[B]	1	69,73,73	2.05	20 (28%)	83,113,113	2.89	34 (40%)
23	CLA	a	407[B]	42	69,73,73	2.05	19 (27%)	83,113,113	2.85	31 (37%)
38	BCT	d	401[A]	37	2,3,3	0.59	0	2,3,3	1.49	0
25	BCR	c	516	-	41,41,41	0.99	1 (2%)	56,56,56	1.36	10 (17%)
23	CLA	b	611	2	69,73,73	1.92	19 (27%)	83,113,113	2.92	29 (34%)
33	LMG	C	521	-	51,51,55	1.09	3 (5%)	59,59,63	1.37	6 (10%)
25	BCR	y	101	-	41,41,41	1.01	1 (2%)	56,56,56	1.48	9 (16%)
25	BCR	a	410	-	41,41,41	1.08	1 (2%)	56,56,56	1.34	8 (14%)
35	DGD	C	519	-	63,63,67	0.86	3 (4%)	77,77,81	1.04	5 (6%)
35	DGD	H	102	-	63,63,67	0.89	4 (6%)	77,77,81	1.01	7 (9%)
34	HTG	d	410	-	16,16,19	0.91	1 (6%)	20,21,24	1.54	1 (5%)
23	CLA	C	509	3	69,73,73	2.06	20 (28%)	83,113,113	2.77	27 (32%)
34	HTG	D	412	-	16,16,19	1.02	1 (6%)	20,21,24	1.56	1 (5%)
31	LMT	B	631	-	25,25,36	0.89	2 (8%)	30,30,47	1.20	3 (10%)
23	CLA	c	510	3	69,73,73	2.04	20 (28%)	83,113,113	2.79	32 (38%)
34	HTG	V	202	-	11,11,19	0.32	0	15,15,24	1.31	1 (6%)
27	GOL	c	526[A]	-	5,5,5	1.00	0	5,5,5	0.98	0
23	CLA	A	406[B]	42	69,73,73	2.10	19 (27%)	83,113,113	2.87	32 (38%)
32	LHG	d	406[A]	-	48,48,48	0.87	2 (4%)	51,54,54	1.04	4 (7%)
27	GOL	o	302	-	5,5,5	1.04	0	5,5,5	0.99	0
23	CLA	B	615	2	69,73,73	2.06	20 (28%)	83,113,113	2.90	30 (36%)
35	DGD	C	518[A]	-	63,63,67	0.90	3 (4%)	77,77,81	1.03	5 (6%)
23	CLA	B	603	2	69,73,73	2.00	20 (28%)	83,113,113	2.94	31 (37%)
23	CLA	c	512	3	69,73,73	2.06	20 (28%)	83,113,113	2.84	30 (36%)
24	PHO	A	416[B]	-	58,69,69	2.79	15 (25%)	56,99,99	2.91	17 (30%)
26	SQD	B	620	-	53,54,54	1.07	3 (5%)	62,65,65	1.83	13 (20%)
26	SQD	A	410[B]	-	53,54,54	0.94	3 (5%)	62,65,65	1.67	11 (17%)
31	LMT	m	103	-	36,36,36	1.03	3 (8%)	47,47,47	1.10	3 (6%)
23	CLA	c	502	3	69,73,73	2.01	21 (30%)	83,113,113	2.86	30 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	GOL	d	412	-	5,5,5	1.30	1 (20%)	5,5,5	1.00	0
23	CLA	b	601	42	69,73,73	2.08	20 (28%)	83,113,113	2.80	27 (32%)
33	LMG	m	101	-	51,51,55	0.87	2 (3%)	59,59,63	1.37	6 (10%)
23	CLA	b	610	42	69,73,73	2.06	20 (28%)	83,113,113	2.95	33 (39%)
23	CLA	b	602	2	69,73,73	2.06	18 (26%)	83,113,113	2.99	34 (40%)
25	BCR	K	102	-	41,41,41	1.03	1 (2%)	56,56,56	1.49	12 (21%)
26	SQD	f	102	-	42,43,54	1.23	3 (7%)	51,54,65	1.48	10 (19%)
21	OEY	a	401[B]	42,1,3	0,16,16	-	-	-	-	-
27	GOL	c	527	-	5,5,5	1.13	0	5,5,5	0.92	0
33	LMG	D	413	40	51,51,55	0.83	3 (5%)	59,59,63	1.07	4 (6%)
34	HTG	B	625	-	19,19,19	1.13	2 (10%)	23,24,24	1.45	4 (17%)
24	PHO	A	407[A]	-	58,69,69	2.66	12 (20%)	56,99,99	2.81	14 (25%)
38	BCT	D	402[A]	37	2,3,3	0.64	0	2,3,3	1.30	0
33	LMG	C	501	-	51,51,55	0.92	2 (3%)	59,59,63	1.55	6 (10%)
23	CLA	A	408	1	69,73,73	2.01	21 (30%)	83,113,113	2.96	37 (44%)
27	GOL	l	102[B]	-	5,5,5	0.94	0	5,5,5	0.96	0
32	LHG	D	409[A]	-	48,48,48	0.93	2 (4%)	51,54,54	1.02	3 (5%)
35	DGD	c	518[B]	-	63,63,67	0.88	2 (3%)	77,77,81	0.94	4 (5%)
23	CLA	C	508	42	69,73,73	1.96	20 (28%)	83,113,113	2.87	29 (34%)
29	PL9	a	414[A]	-	55,55,55	0.65	2 (3%)	68,69,69	2.01	22 (32%)
23	CLA	A	405[A]	42	69,73,73	2.02	18 (26%)	83,113,113	2.85	33 (39%)
25	BCR	B	618	-	41,41,41	0.97	1 (2%)	56,56,56	1.42	9 (16%)
29	PL9	D	407[B]	-	55,55,55	0.64	2 (3%)	68,69,69	1.56	14 (20%)
35	DGD	C	517[B]	-	63,63,67	0.83	2 (3%)	77,77,81	1.06	6 (7%)
25	BCR	C	516	-	41,41,41	1.01	1 (2%)	56,56,56	1.27	6 (10%)
23	CLA	c	508	42	69,73,73	2.01	19 (27%)	83,113,113	2.87	30 (36%)
23	CLA	b	609	2	69,73,73	2.03	19 (27%)	83,113,113	2.76	32 (38%)
23	CLA	C	511	3	69,73,73	2.03	20 (28%)	83,113,113	2.95	31 (37%)
23	CLA	B	607	42	69,73,73	2.02	19 (27%)	83,113,113	2.83	30 (36%)
32	LHG	A	418[A]	-	48,48,48	0.87	2 (4%)	51,54,54	1.27	6 (11%)
23	CLA	b	614	2	69,73,73	2.01	20 (28%)	83,113,113	2.98	32 (38%)
33	LMG	B	621	-	51,51,55	0.90	2 (3%)	59,59,63	1.29	5 (8%)
27	GOL	b	628	-	5,5,5	0.52	0	5,5,5	1.43	1 (20%)
24	PHO	a	416[B]	-	58,69,69	2.79	13 (22%)	56,99,99	2.85	15 (26%)
23	CLA	B	612	2	69,73,73	2.06	19 (27%)	83,113,113	2.78	30 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
25	BCR	d	404	-	41,41,41	1.12	2 (4%)	56,56,56	1.96	20 (35%)
32	LHG	b	629[B]	-	48,48,48	0.90	2 (4%)	51,54,54	1.04	4 (7%)
25	BCR	b	619	-	41,41,41	1.07	1 (2%)	56,56,56	1.45	10 (17%)
26	SQD	a	411[B]	-	53,54,54	0.94	3 (5%)	62,65,65	1.64	11 (17%)
27	GOL	O	303	-	5,5,5	0.91	0	5,5,5	1.09	1 (20%)
27	GOL	a	418	-	5,5,5	1.15	0	5,5,5	1.00	0
23	CLA	C	510	3	69,73,73	2.02	20 (28%)	83,113,113	2.82	30 (36%)
23	CLA	a	405[A]	1	69,73,73	1.99	20 (28%)	83,113,113	2.87	33 (39%)
23	CLA	a	407[A]	42	69,73,73	1.98	19 (27%)	83,113,113	2.83	30 (36%)
23	CLA	b	608	2	69,73,73	2.00	20 (28%)	83,113,113	2.88	33 (39%)
25	BCR	c	515	-	41,41,41	1.00	1 (2%)	56,56,56	1.61	15 (26%)
23	CLA	d	403	4	69,73,73	2.04	19 (27%)	83,113,113	2.89	31 (37%)
31	LMT	b	627	-	25,25,36	0.87	0	30,30,47	1.12	2 (6%)
23	CLA	b	616	2	69,73,73	2.01	19 (27%)	83,113,113	2.93	31 (37%)
26	SQD	a	411[A]	-	53,54,54	0.96	3 (5%)	62,65,65	1.83	13 (20%)
27	GOL	C	523[B]	-	5,5,5	1.06	0	5,5,5	0.86	0
27	GOL	O	302	-	5,5,5	0.99	0	5,5,5	0.86	0
25	BCR	k	101	-	41,41,41	1.06	1 (2%)	56,56,56	1.47	10 (17%)
33	LMG	C	520	-	51,51,55	0.94	2 (3%)	59,59,63	1.09	3 (5%)
23	CLA	B	608	2	69,73,73	1.88	19 (27%)	83,113,113	2.83	34 (40%)
33	LMG	Z	101	-	37,37,55	1.01	2 (5%)	45,45,63	1.43	7 (15%)
23	CLA	a	409	1	69,73,73	1.93	19 (27%)	83,113,113	3.00	33 (39%)
23	CLA	c	506	3	69,73,73	2.01	18 (26%)	83,113,113	2.79	28 (33%)
31	LMT	t	101	-	26,26,36	0.92	2 (7%)	31,31,47	1.27	2 (6%)
23	CLA	C	507	3	69,73,73	2.05	21 (30%)	83,113,113	2.87	32 (38%)
25	BCR	H	101	-	41,41,41	1.02	1 (2%)	56,56,56	1.42	9 (16%)
27	GOL	C	523[A]	-	5,5,5	1.11	0	5,5,5	0.88	0
27	GOL	B	624	-	5,5,5	0.79	0	5,5,5	1.12	1 (20%)
23	CLA	c	507	3	69,73,73	2.02	21 (30%)	83,113,113	2.85	30 (36%)
23	CLA	c	504	3	69,73,73	2.05	19 (27%)	83,113,113	2.87	28 (33%)
23	CLA	A	406[A]	42	69,73,73	2.04	19 (27%)	83,113,113	2.85	32 (38%)
27	GOL	B	629	-	5,5,5	0.98	0	5,5,5	1.02	0
32	LHG	L	101[B]	-	48,48,48	0.92	2 (4%)	51,54,54	1.12	4 (7%)
25	BCR	B	617	-	41,41,41	1.13	1 (2%)	56,56,56	1.24	7 (12%)
23	CLA	C	506	3	69,73,73	2.02	19 (27%)	83,113,113	2.87	29 (34%)
39	HEM	f	101	5,6	50,50,50	1.47	6 (12%)	66,82,82	1.76	14 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
27	GOL	v	202[B]	-	5,5,5	1.03	0	5,5,5	0.94	0
23	CLA	C	514	3	69,73,73	2.05	19 (27%)	83,113,113	2.82	31 (37%)
27	GOL	A	411	-	5,5,5	1.04	0	5,5,5	0.89	0
24	PHO	A	416[A]	-	58,69,69	2.79	15 (25%)	56,99,99	2.85	15 (26%)
32	LHG	E	101[B]	-	41,41,48	1.06	2 (4%)	44,47,54	1.11	4 (9%)
26	SQD	A	410[A]	-	53,54,54	0.93	3 (5%)	62,65,65	1.88	10 (16%)
25	BCR	b	618	-	41,41,41	1.01	1 (2%)	56,56,56	1.25	7 (12%)
23	CLA	b	605	2	69,73,73	1.96	19 (27%)	83,113,113	3.04	28 (33%)
25	BCR	h	101	-	41,41,41	1.02	1 (2%)	56,56,56	1.38	10 (17%)
27	GOL	D	414	-	5,5,5	1.41	1 (20%)	5,5,5	0.85	0
27	GOL	v	202[A]	-	5,5,5	1.20	0	5,5,5	0.82	0
23	CLA	B	606	2	69,73,73	1.95	21 (30%)	83,113,113	2.91	33 (39%)
32	LHG	a	420[B]	-	41,41,48	1.04	2 (4%)	44,47,54	0.93	2 (4%)
23	CLA	B	616	2	69,73,73	2.00	21 (30%)	83,113,113	2.83	27 (32%)
29	PL9	d	405[B]	-	55,55,55	0.67	1 (1%)	68,69,69	1.64	19 (27%)
23	CLA	D	405	4	69,73,73	2.11	18 (26%)	83,113,113	2.76	32 (38%)
23	CLA	C	505	42	69,73,73	1.98	19 (27%)	83,113,113	2.80	28 (33%)
27	GOL	l	102[A]	-	5,5,5	0.93	0	5,5,5	0.98	0
34	HTG	b	625	-	19,19,19	1.01	2 (10%)	23,24,24	1.46	3 (13%)
35	DGD	c	518[A]	-	63,63,67	0.85	3 (4%)	77,77,81	0.97	3 (3%)
29	PL9	D	407[A]	-	55,55,55	0.63	1 (1%)	68,69,69	1.61	17 (25%)
35	DGD	C	517[A]	-	63,63,67	0.83	2 (3%)	77,77,81	1.20	8 (10%)
29	PL9	A	414[B]	-	55,55,55	0.64	1 (1%)	68,69,69	1.95	23 (33%)
24	PHO	a	408[B]	-	58,69,69	2.70	12 (20%)	56,99,99	2.73	17 (30%)
23	CLA	D	404[B]	4	69,73,73	2.05	20 (28%)	83,113,113	2.84	28 (33%)
23	CLA	C	504	3	69,73,73	1.98	19 (27%)	83,113,113	2.89	28 (33%)
23	CLA	B	609	2	69,73,73	2.05	17 (24%)	83,113,113	2.79	30 (36%)
23	CLA	b	606	2	69,73,73	2.03	19 (27%)	83,113,113	2.91	30 (36%)
31	LMT	M	102	-	36,36,36	1.06	3 (8%)	47,47,47	1.06	3 (6%)
29	PL9	A	414[A]	-	55,55,55	0.69	2 (3%)	68,69,69	2.01	24 (35%)
23	CLA	C	513	3	69,73,73	2.07	19 (27%)	83,113,113	2.85	32 (38%)
24	PHO	a	416[A]	-	58,69,69	2.77	13 (22%)	56,99,99	2.94	17 (30%)
23	CLA	B	602	2	69,73,73	2.03	20 (28%)	83,113,113	2.88	28 (33%)
23	CLA	b	615	2	69,73,73	1.98	18 (26%)	83,113,113	2.77	32 (38%)
32	LHG	b	629[A]	-	48,48,48	0.83	2 (4%)	51,54,54	1.04	4 (7%)

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
34	HTG	C	522	-	-	1/10/30/30	0/1/1/1
23	CLA	c	509	3	-	5/39/115/115	-
35	DGD	c	517[B]	-	-	16/51/91/95	0/2/2/2
25	BCR	K	103	-	-	2/29/63/63	0/2/2/2
23	CLA	c	511	3	-	12/39/115/115	-
25	BCR	D	406	-	-	4/29/63/63	0/2/2/2
26	SQD	X	101	-	-	13/38/58/69	0/1/1/1
23	CLA	B	601	42	-	13/39/115/115	-
33	LMG	c	520	-	-	13/46/66/70	0/1/1/1
33	LMG	d	411	40	-	10/46/66/70	0/1/1/1
23	CLA	A	404[B]	1	-	6/39/115/115	-
23	CLA	B	614	2	-	14/39/115/115	-
26	SQD	a	412	-	-	15/49/69/69	0/1/1/1
27	GOL	V	203[B]	-	-	3/4/4/4	-
34	HTG	b	622	-	-	4/10/30/30	0/1/1/1
23	CLA	b	613	2	-	7/39/115/115	-
31	LMT	A	417	-	-	8/21/61/61	0/2/2/2
25	BCR	B	619	-	-	0/29/63/63	0/2/2/2
32	LHG	D	408[B]	-	-	16/53/53/53	-
26	SQD	A	412	-	-	13/49/69/69	0/1/1/1
31	LMT	c	501	-	-	10/21/61/61	0/2/2/2
33	LMG	a	417	-	-	12/46/66/70	0/1/1/1
23	CLA	B	611	2	-	2/39/115/115	-
23	CLA	A	404[A]	1	-	3/39/115/115	-
34	HTG	b	623	-	-	4/10/30/30	0/1/1/1
32	LHG	L	101[A]	-	-	20/53/53/53	-
35	DGD	h	102	-	-	14/51/91/95	0/2/2/2
39	HEM	F	102	5,6	-	4/14/54/54	-
31	LMT	A	419	-	-	16/21/61/61	0/2/2/2
23	CLA	C	512	3	-	4/39/115/115	-
32	LHG	D	408[A]	-	-	17/53/53/53	-
23	CLA	B	604	2	-	3/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	LHG	E	101[A]	-	-	22/46/46/53	-
31	LMT	B	628	-	-	12/21/61/61	0/2/2/2
23	CLA	B	610	42	-	10/39/115/115	-
27	GOL	c	526[B]	-	-	0/4/4/4	-
27	GOL	B	627	-	-	2/4/4/4	-
32	LHG	d	406[B]	-	-	16/53/53/53	-
33	LMG	c	521	-	-	11/46/66/70	0/1/1/1
32	LHG	a	420[A]	-	-	16/46/46/53	-
29	PL9	d	405[A]	-	-	7/53/73/73	0/1/1/1
31	LMT	e	101	-	-	15/21/61/61	0/2/2/2
35	DGD	C	518[B]	-	-	13/51/91/95	0/2/2/2
33	LMG	z	101	-	-	9/34/54/70	0/1/1/1
31	LMT	M	101	-	-	5/21/61/61	0/2/2/2
23	CLA	B	613	2	-	8/39/115/115	-
25	BCR	T	101	-	-	1/29/63/63	0/2/2/2
23	CLA	C	502	3	-	3/39/115/115	-
25	BCR	A	409	-	-	0/29/63/63	0/2/2/2
24	PHO	a	408[A]	-	-	6/37/103/103	0/5/6/6
23	CLA	D	404[A]	4	-	2/39/115/115	-
34	HTG	B	623	-	-	2/10/30/30	0/1/1/1
23	CLA	d	402[B]	4	-	4/39/115/115	-
23	CLA	b	612	2	-	1/39/115/115	-
23	CLA	c	513	3	-	12/39/115/115	-
27	GOL	b	624	-	-	2/4/4/4	-
24	PHO	A	407[B]	-	-	2/37/103/103	0/5/6/6
27	GOL	o	303	-	-	2/4/4/4	-
41	HEC	v	201	16	1/1/3/7	5/14/54/54	-
25	BCR	b	617	-	-	2/29/63/63	0/2/2/2
32	LHG	d	413[B]	-	-	14/53/53/53	-
23	CLA	b	604	2	-	11/39/115/115	-
32	LHG	D	409[B]	-	-	14/53/53/53	-
23	CLA	c	505	42	-	7/39/115/115	-
34	HTG	B	622	-	-	3/10/30/30	0/1/1/1
23	CLA	d	402[A]	4	-	4/39/115/115	-
34	HTG	c	522	-	-	2/10/30/30	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
29	PL9	a	414[B]	-	-	14/53/73/73	0/1/1/1
23	CLA	A	405[B]	42	-	5/39/115/115	-
31	LMT	F	101	-	-	8/21/61/61	0/2/2/2
25	BCR	C	515	-	-	0/29/63/63	0/2/2/2
26	SQD	b	620	-	-	18/49/69/69	0/1/1/1
35	DGD	c	517[A]	-	-	18/51/91/95	0/2/2/2
32	LHG	d	413[A]	-	-	17/53/53/53	-
35	DGD	c	519	-	-	7/51/91/95	0/2/2/2
32	LHG	A	418[B]	-	-	14/53/53/53	-
25	BCR	t	102	-	-	1/29/63/63	0/2/2/2
23	CLA	a	406[B]	42	-	7/39/115/115	-
23	CLA	b	607	42	-	2/39/115/115	-
32	LHG	d	407[B]	-	-	10/53/53/53	-
23	CLA	b	603	2	-	5/39/115/115	-
27	GOL	D	403	-	-	2/4/4/4	-
23	CLA	B	605	2	-	5/39/115/115	-
23	CLA	c	514	3	-	12/39/115/115	-
31	LMT	B	630	-	-	10/21/61/61	0/2/2/2
31	LMT	b	621	-	-	9/17/37/61	0/1/1/2
23	CLA	C	503	3	-	10/39/115/115	-
27	GOL	a	419	-	-	2/4/4/4	-
41	HEC	V	201	16	1/1/3/7	6/14/54/54	-
27	GOL	V	203[A]	-	-	2/4/4/4	-
23	CLA	c	503	3	-	7/39/115/115	-
23	CLA	a	406[A]	42	-	8/39/115/115	-
32	LHG	d	407[A]	-	-	13/53/53/53	-
23	CLA	a	405[B]	1	-	5/39/115/115	-
23	CLA	a	407[B]	42	-	7/39/115/115	-
25	BCR	c	516	-	-	1/29/63/63	0/2/2/2
23	CLA	b	611	2	-	2/39/115/115	-
33	LMG	C	521	-	-	14/46/66/70	0/1/1/1
25	BCR	y	101	-	-	5/29/63/63	0/2/2/2
25	BCR	a	410	-	-	2/29/63/63	0/2/2/2
35	DGD	C	519	-	-	20/51/91/95	0/2/2/2
35	DGD	H	102	-	-	11/51/91/95	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
34	HTG	d	410	-	-	1/7/27/30	0/1/1/1
23	CLA	C	509	3	-	5/39/115/115	-
34	HTG	D	412	-	-	3/7/27/30	0/1/1/1
31	LMT	B	631	-	-	11/17/37/61	0/1/1/2
23	CLA	c	510	3	-	13/39/115/115	-
34	HTG	V	202	-	-	0/2/19/30	0/1/1/1
27	GOL	c	526[A]	-	-	0/4/4/4	-
23	CLA	A	406[B]	42	-	4/39/115/115	-
32	LHG	d	406[A]	-	-	13/53/53/53	-
27	GOL	o	302	-	-	2/4/4/4	-
23	CLA	B	615	2	-	8/39/115/115	-
35	DGD	C	518[A]	-	-	13/51/91/95	0/2/2/2
23	CLA	B	603	2	-	6/39/115/115	-
23	CLA	c	512	3	-	8/39/115/115	-
24	PHO	A	416[B]	-	-	1/37/103/103	0/5/6/6
26	SQD	B	620	-	-	13/49/69/69	0/1/1/1
26	SQD	A	410[B]	-	-	10/49/69/69	0/1/1/1
31	LMT	m	103	-	-	6/21/61/61	0/2/2/2
23	CLA	c	502	3	-	6/39/115/115	-
27	GOL	d	412	-	-	4/4/4/4	-
23	CLA	b	601	42	-	20/39/115/115	-
33	LMG	m	101	-	-	12/46/66/70	0/1/1/1
23	CLA	b	610	42	-	9/39/115/115	-
23	CLA	b	602	2	-	5/39/115/115	-
25	BCR	K	102	-	-	2/29/63/63	0/2/2/2
26	SQD	f	102	-	-	12/38/58/69	0/1/1/1
27	GOL	c	527	-	-	3/4/4/4	-
33	LMG	D	413	40	-	8/46/66/70	0/1/1/1
34	HTG	B	625	-	-	4/10/30/30	0/1/1/1
24	PHO	A	407[A]	-	-	3/37/103/103	0/5/6/6
33	LMG	C	501	-	-	11/46/66/70	0/1/1/1
23	CLA	A	408	1	-	9/39/115/115	-
27	GOL	l	102[B]	-	-	2/4/4/4	-
32	LHG	D	409[A]	-	-	14/53/53/53	-
35	DGD	c	518[B]	-	-	16/51/91/95	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
23	CLA	C	508	42	-	11/39/115/115	-
29	PL9	a	414[A]	-	-	14/53/73/73	0/1/1/1
23	CLA	A	405[A]	42	-	3/39/115/115	-
25	BCR	B	618	-	-	0/29/63/63	0/2/2/2
29	PL9	D	407[B]	-	-	9/53/73/73	0/1/1/1
35	DGD	C	517[B]	-	-	14/51/91/95	0/2/2/2
25	BCR	C	516	-	-	0/29/63/63	0/2/2/2
23	CLA	c	508	42	-	10/39/115/115	-
23	CLA	b	609	2	-	5/39/115/115	-
23	CLA	C	511	3	-	13/39/115/115	-
23	CLA	B	607	42	-	2/39/115/115	-
32	LHG	A	418[A]	-	-	14/53/53/53	-
23	CLA	b	614	2	-	15/39/115/115	-
33	LMG	B	621	-	-	14/46/66/70	0/1/1/1
27	GOL	b	628	-	-	0/4/4/4	-
24	PHO	a	416[B]	-	-	1/37/103/103	0/5/6/6
23	CLA	B	612	2	-	7/39/115/115	-
25	BCR	d	404	-	-	5/29/63/63	0/2/2/2
32	LHG	b	629[B]	-	-	17/53/53/53	-
25	BCR	b	619	-	-	5/29/63/63	0/2/2/2
26	SQD	a	411[B]	-	-	8/49/69/69	0/1/1/1
27	GOL	O	303	-	-	2/4/4/4	-
27	GOL	a	418	-	-	2/4/4/4	-
23	CLA	C	510	3	-	5/39/115/115	-
23	CLA	a	405[A]	1	-	4/39/115/115	-
23	CLA	a	407[A]	42	-	8/39/115/115	-
23	CLA	b	608	2	-	7/39/115/115	-
25	BCR	c	515	-	-	1/29/63/63	0/2/2/2
23	CLA	d	403	4	-	8/39/115/115	-
31	LMT	b	627	-	-	11/17/37/61	0/1/1/2
23	CLA	b	616	2	-	9/39/115/115	-
26	SQD	a	411[A]	-	-	9/49/69/69	0/1/1/1
27	GOL	C	523[B]	-	-	0/4/4/4	-
27	GOL	O	302	-	-	2/4/4/4	-
25	BCR	k	101	-	-	0/29/63/63	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
33	LMG	C	520	-	-	10/46/66/70	0/1/1/1
23	CLA	B	608	2	-	3/39/115/115	-
33	LMG	Z	101	-	-	10/31/51/70	0/1/1/1
23	CLA	a	409	1	-	9/39/115/115	-
23	CLA	c	506	3	-	7/39/115/115	-
31	LMT	t	101	-	-	7/17/38/61	0/1/1/2
23	CLA	C	507	3	-	12/39/115/115	-
25	BCR	H	101	-	-	2/29/63/63	0/2/2/2
27	GOL	C	523[A]	-	-	0/4/4/4	-
27	GOL	B	624	-	-	4/4/4/4	-
23	CLA	c	507	3	-	7/39/115/115	-
23	CLA	c	504	3	-	2/39/115/115	-
23	CLA	A	406[A]	42	-	5/39/115/115	-
27	GOL	B	629	-	-	4/4/4/4	-
32	LHG	L	101[B]	-	-	17/53/53/53	-
25	BCR	B	617	-	-	1/29/63/63	0/2/2/2
23	CLA	C	506	3	-	7/39/115/115	-
39	HEM	f	101	5,6	-	6/14/54/54	-
27	GOL	v	202[B]	-	-	2/4/4/4	-
23	CLA	C	514	3	-	7/39/115/115	-
27	GOL	A	411	-	-	2/4/4/4	-
24	PHO	A	416[A]	-	-	1/37/103/103	0/5/6/6
32	LHG	E	101[B]	-	-	20/46/46/53	-
26	SQD	A	410[A]	-	-	12/49/69/69	0/1/1/1
25	BCR	b	618	-	-	0/29/63/63	0/2/2/2
23	CLA	b	605	2	-	7/39/115/115	-
25	BCR	h	101	-	-	2/29/63/63	0/2/2/2
27	GOL	D	414	-	-	3/4/4/4	-
27	GOL	v	202[A]	-	-	2/4/4/4	-
23	CLA	B	606	2	-	7/39/115/115	-
32	LHG	a	420[B]	-	-	16/46/46/53	-
23	CLA	B	616	2	-	7/39/115/115	-
29	PL9	d	405[B]	-	-	7/53/73/73	0/1/1/1
23	CLA	D	405	4	-	13/39/115/115	-
23	CLA	C	505	42	-	6/39/115/115	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
27	GOL	l	102[A]	-	-	1/4/4/4	-
34	HTG	b	625	-	-	3/10/30/30	0/1/1/1
35	DGD	c	518[A]	-	-	16/51/91/95	0/2/2/2
29	PL9	D	407[A]	-	-	6/53/73/73	0/1/1/1
35	DGD	C	517[A]	-	-	14/51/91/95	0/2/2/2
29	PL9	A	414[B]	-	-	12/53/73/73	0/1/1/1
24	PHO	a	408[B]	-	-	6/37/103/103	0/5/6/6
23	CLA	D	404[B]	4	-	2/39/115/115	-
23	CLA	C	504	3	-	1/39/115/115	-
23	CLA	B	609	2	-	1/39/115/115	-
23	CLA	b	606	2	-	15/39/115/115	-
31	LMT	M	102	-	-	8/21/61/61	0/2/2/2
29	PL9	A	414[A]	-	-	15/53/73/73	0/1/1/1
23	CLA	C	513	3	-	13/39/115/115	-
24	PHO	a	416[A]	-	-	1/37/103/103	0/5/6/6
23	CLA	B	602	2	-	11/39/115/115	-
23	CLA	b	615	2	-	8/39/115/115	-
32	LHG	b	629[A]	-	-	14/53/53/53	-

The worst 5 of 1865 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	a	408[A]	PHO	C1B-C2B	9.21	1.49	1.39
24	A	407[B]	PHO	C1B-C2B	9.19	1.49	1.39
24	a	416[B]	PHO	C1D-C2D	9.12	1.49	1.39
24	A	407[B]	PHO	C1D-C2D	8.95	1.49	1.39
24	A	407[A]	PHO	C1D-C2D	8.89	1.49	1.39

The worst 5 of 3326 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	B	611	CLA	C2B-C1B-NB	17.56	122.00	110.23
23	B	611	CLA	C3B-C2B-C1B	-14.21	90.00	107.16
24	A	407[A]	PHO	C2D-C1D-ND	11.89	117.73	109.53
23	B	611	CLA	C1D-ND-C4D	-11.62	98.08	106.33
24	A	407[B]	PHO	C2D-C1D-ND	11.49	117.46	109.53

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
41	V	201	HEC	NA
41	v	201	HEC	NA

5 of 1674 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
23	A	404[B]	CLA	C2B-C3B-CAB-CBB
23	A	404[B]	CLA	C4B-C3B-CAB-CBB
23	A	408	CLA	C2-C3-C5-C6
23	A	408	CLA	C4-C3-C5-C6
23	B	602	CLA	C6-C7-C8-C9

There are no ring outliers.

169 monomers are involved in 333 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	c	509	CLA	6	0
35	c	517[B]	DGD	1	0
25	K	103	BCR	1	0
23	c	511	CLA	1	0
26	X	101	SQD	3	0
23	B	601	CLA	2	0
33	d	411	LMG	3	0
23	A	404[B]	CLA	3	0
23	B	614	CLA	3	0
26	a	412	SQD	1	0
34	b	622	HTG	2	0
25	B	619	BCR	1	0
32	D	408[B]	LHG	2	0
31	c	501	LMT	1	0
33	a	417	LMG	1	0
23	A	404[A]	CLA	2	0
39	F	102	HEM	2	0
31	A	419	LMT	1	0
23	C	512	CLA	1	0
32	D	408[A]	LHG	2	0
23	B	604	CLA	1	0
32	E	101[A]	LHG	3	0
31	B	628	LMT	1	0
27	B	627	GOL	1	0
32	d	406[B]	LHG	2	0
33	c	521	LMG	1	0
32	a	420[A]	LHG	5	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
31	e	101	LMT	1	0
33	z	101	LMG	2	0
21	A	401[B]	OEY	1	0
31	M	101	LMT	1	0
23	B	613	CLA	4	0
25	T	101	BCR	5	0
23	C	502	CLA	4	0
25	A	409	BCR	1	0
23	D	404[A]	CLA	3	0
34	B	623	HTG	1	0
23	d	402[B]	CLA	5	0
23	c	513	CLA	4	0
27	b	624	GOL	1	0
24	A	407[B]	PHO	1	0
23	b	604	CLA	2	0
32	D	409[B]	LHG	3	0
23	c	505	CLA	2	0
34	B	622	HTG	1	0
23	d	402[A]	CLA	1	0
34	c	522	HTG	1	0
29	a	414[B]	PL9	4	0
23	A	405[B]	CLA	5	0
25	C	515	BCR	1	0
26	b	620	SQD	2	0
35	c	517[A]	DGD	1	0
35	c	519	DGD	2	0
32	A	418[B]	LHG	1	0
25	t	102	BCR	4	0
23	a	406[B]	CLA	3	0
23	b	607	CLA	1	0
32	d	407[B]	LHG	9	0
27	D	403	GOL	4	0
23	B	605	CLA	3	0
23	c	514	CLA	2	0
31	B	630	LMT	1	0
31	b	621	LMT	2	0
23	C	503	CLA	3	0
27	a	419	GOL	4	0
23	c	503	CLA	1	0
23	a	406[A]	CLA	3	0
32	d	407[A]	LHG	11	0
23	a	405[B]	CLA	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	a	407[B]	CLA	4	0
25	c	516	BCR	2	0
23	b	611	CLA	1	0
33	C	521	LMG	3	0
25	y	101	BCR	2	0
25	a	410	BCR	1	0
35	C	519	DGD	1	0
35	H	102	DGD	1	0
34	d	410	HTG	1	0
23	C	509	CLA	4	0
34	D	412	HTG	1	0
31	B	631	LMT	1	0
23	c	510	CLA	1	0
23	A	406[B]	CLA	1	0
32	d	406[A]	LHG	2	0
23	B	615	CLA	4	0
35	C	518[A]	DGD	1	0
23	c	512	CLA	7	0
24	A	416[B]	PHO	2	0
26	B	620	SQD	2	0
26	A	410[B]	SQD	2	0
23	c	502	CLA	2	0
23	b	601	CLA	1	0
23	b	610	CLA	1	0
23	b	602	CLA	1	0
21	a	401[B]	OEY	1	0
34	B	625	HTG	1	0
24	A	407[A]	PHO	1	0
23	A	408	CLA	2	0
32	D	409[A]	LHG	3	0
35	c	518[B]	DGD	2	0
23	C	508	CLA	2	0
29	a	414[A]	PL9	4	0
23	A	405[A]	CLA	1	0
25	B	618	BCR	3	0
35	C	517[B]	DGD	1	0
25	C	516	BCR	1	0
23	c	508	CLA	2	0
23	b	609	CLA	4	0
23	C	511	CLA	4	0
32	A	418[A]	LHG	1	0
23	b	614	CLA	3	0

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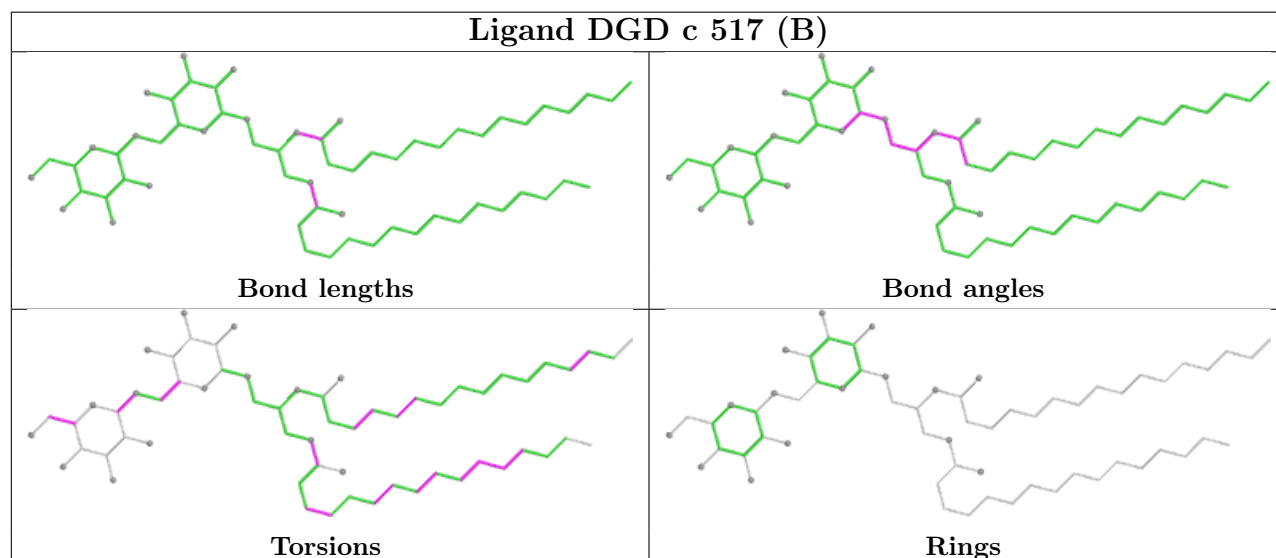
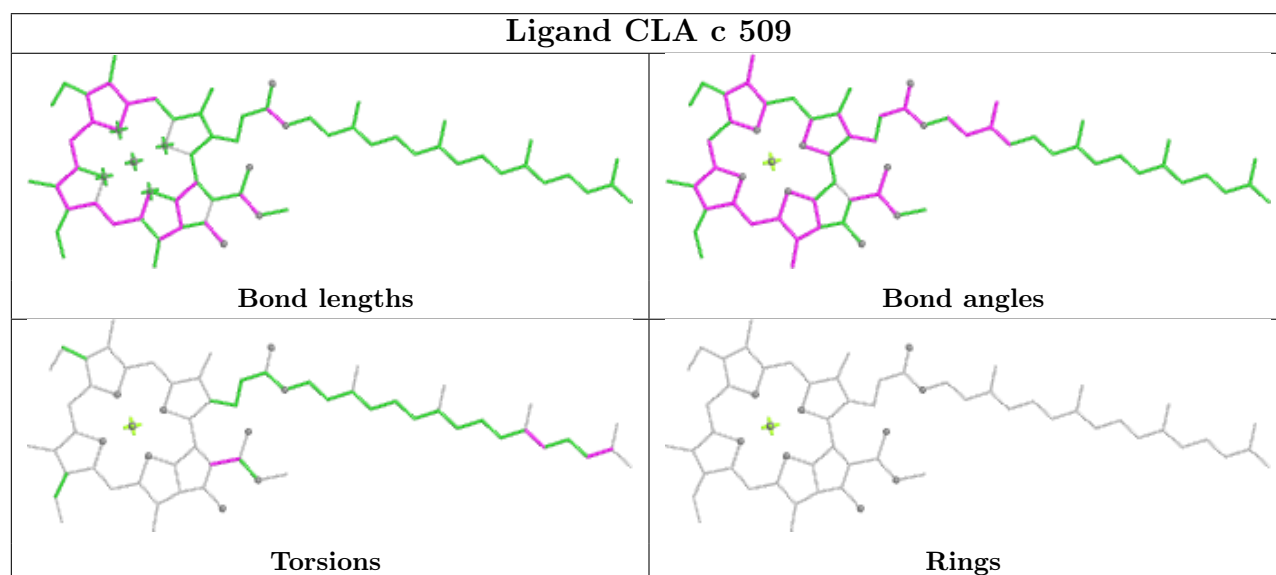
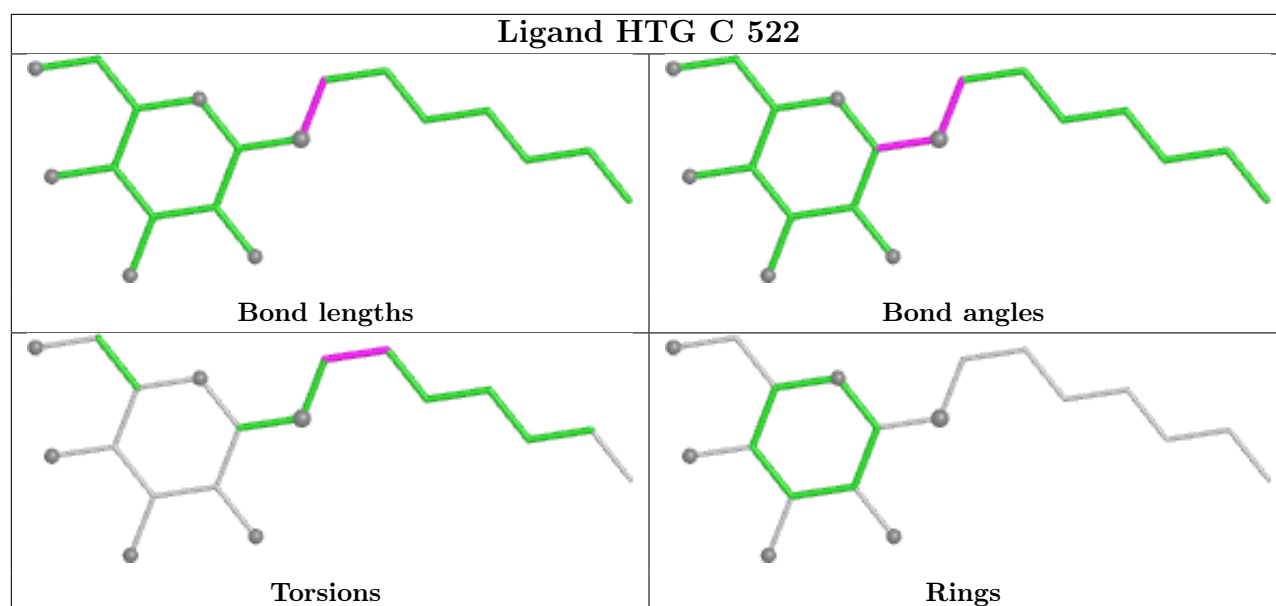
Mol	Chain	Res	Type	Clashes	Symm-Clashes
33	B	621	LMG	1	0
27	b	628	GOL	3	0
24	a	416[B]	PHO	1	0
25	d	404	BCR	3	0
25	b	619	BCR	5	0
26	a	411[B]	SQD	3	0
27	O	303	GOL	1	0
27	a	418	GOL	2	0
23	C	510	CLA	5	0
23	a	405[A]	CLA	2	0
23	a	407[A]	CLA	2	0
25	c	515	BCR	3	0
23	d	403	CLA	2	0
23	b	616	CLA	3	0
26	a	411[A]	SQD	3	0
27	O	302	GOL	1	0
25	k	101	BCR	1	0
33	Z	101	LMG	1	0
23	a	409	CLA	4	0
23	c	506	CLA	6	0
31	t	101	LMT	2	0
23	C	507	CLA	5	0
25	H	101	BCR	2	0
27	B	624	GOL	2	0
23	c	507	CLA	4	0
23	c	504	CLA	3	0
23	A	406[A]	CLA	1	0
25	B	617	BCR	1	0
23	C	506	CLA	4	0
27	v	202[B]	GOL	2	0
23	C	514	CLA	2	0
24	A	416[A]	PHO	1	0
32	E	101[B]	LHG	2	0
26	A	410[A]	SQD	1	0
25	b	618	BCR	4	0
23	b	605	CLA	5	0
25	h	101	BCR	4	0
27	D	414	GOL	3	0
27	v	202[A]	GOL	1	0
23	B	606	CLA	2	0
32	a	420[B]	LHG	4	0
23	B	616	CLA	3	0

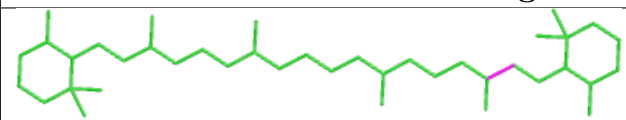
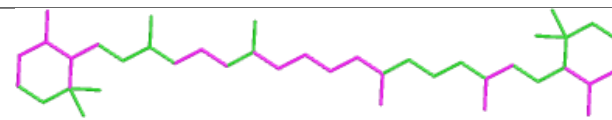
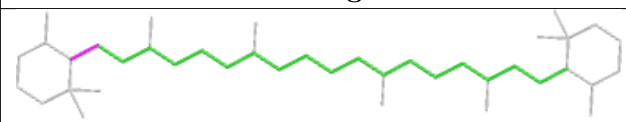
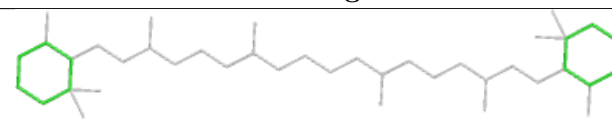
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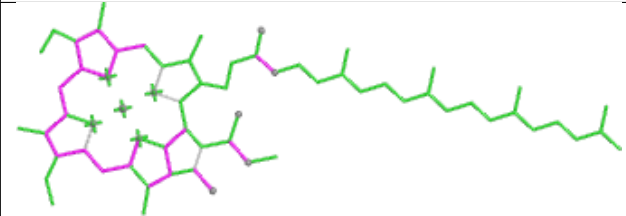
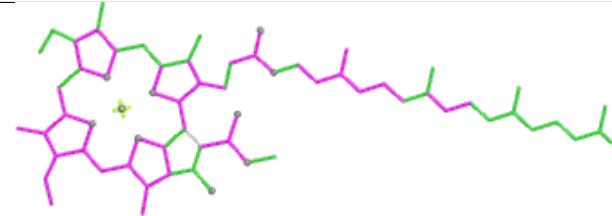
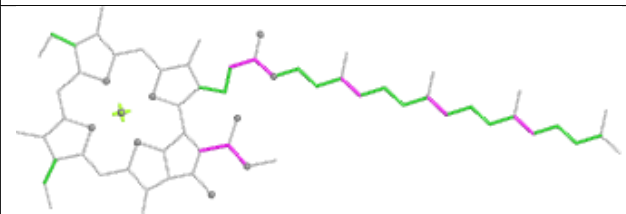
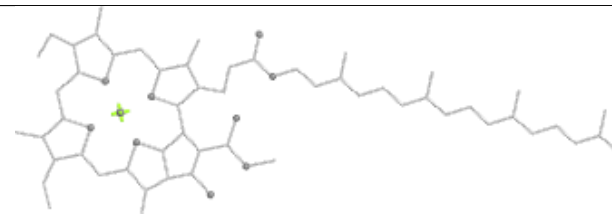
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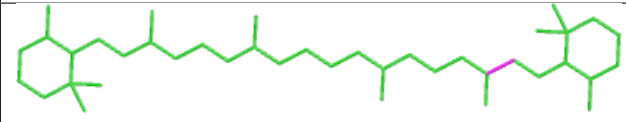
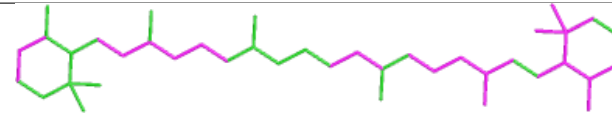
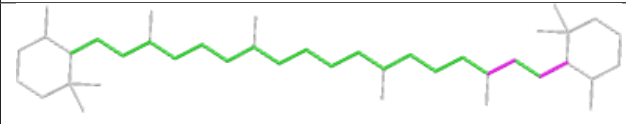
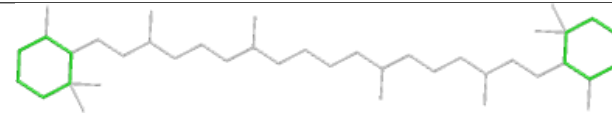
Mol	Chain	Res	Type	Clashes	Symm-Clashes
23	C	505	CLA	1	0
27	l	102[A]	GOL	1	0
35	c	518[A]	DGD	2	0
29	D	407[A]	PL9	1	0
35	C	517[A]	DGD	1	0
29	A	414[B]	PL9	8	0
24	a	408[B]	PHO	1	0
23	D	404[B]	CLA	5	0
23	C	504	CLA	4	0
23	B	609	CLA	2	0
23	b	606	CLA	1	0
29	A	414[A]	PL9	11	0
23	C	513	CLA	2	0
24	a	416[A]	PHO	1	0
23	B	602	CLA	2	0
23	b	615	CLA	1	0

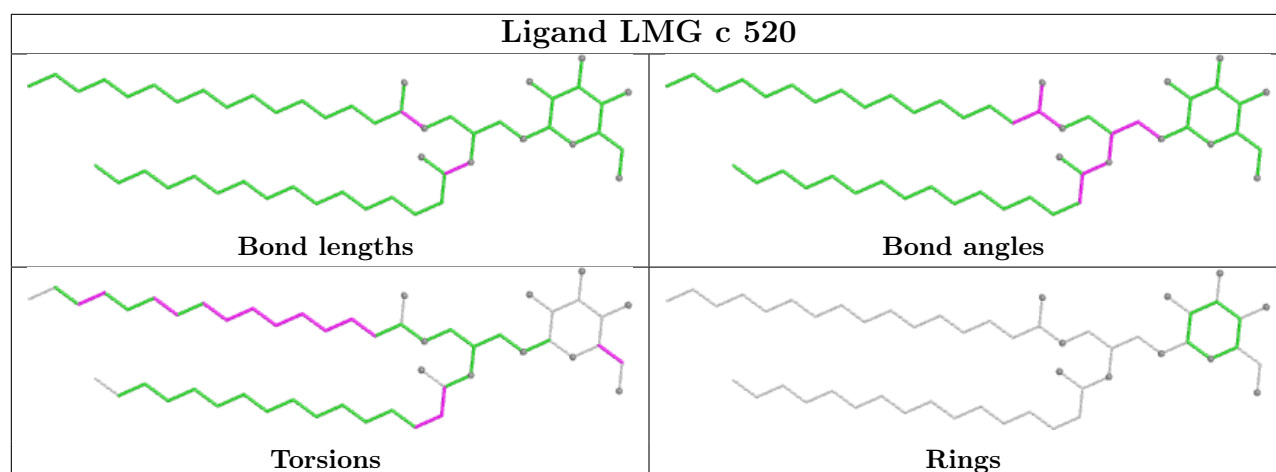
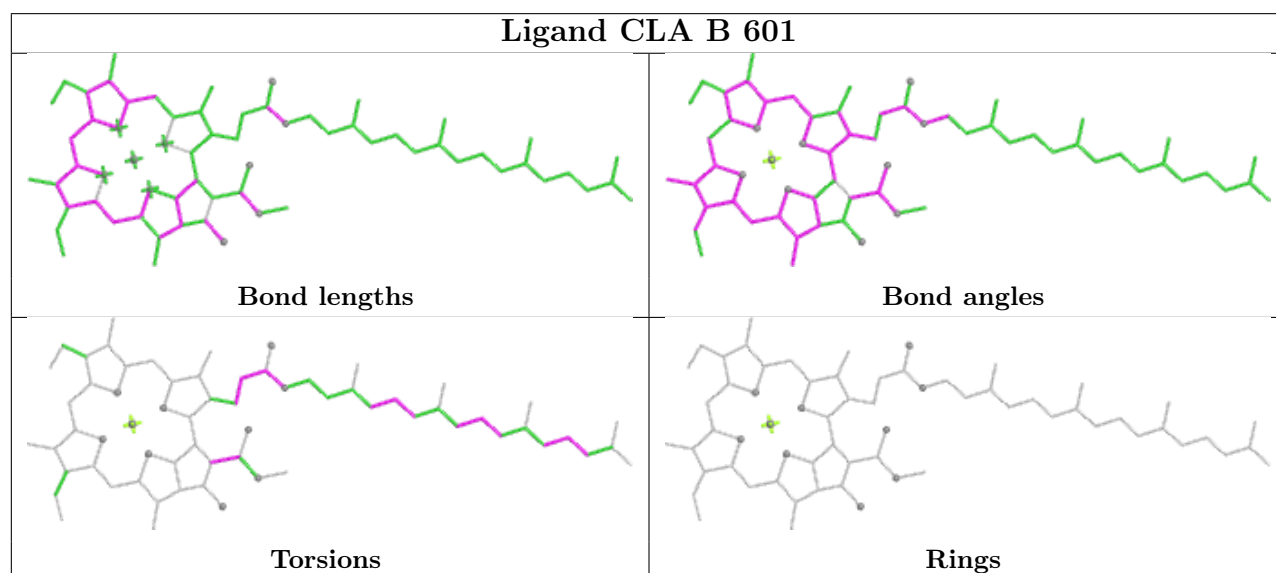
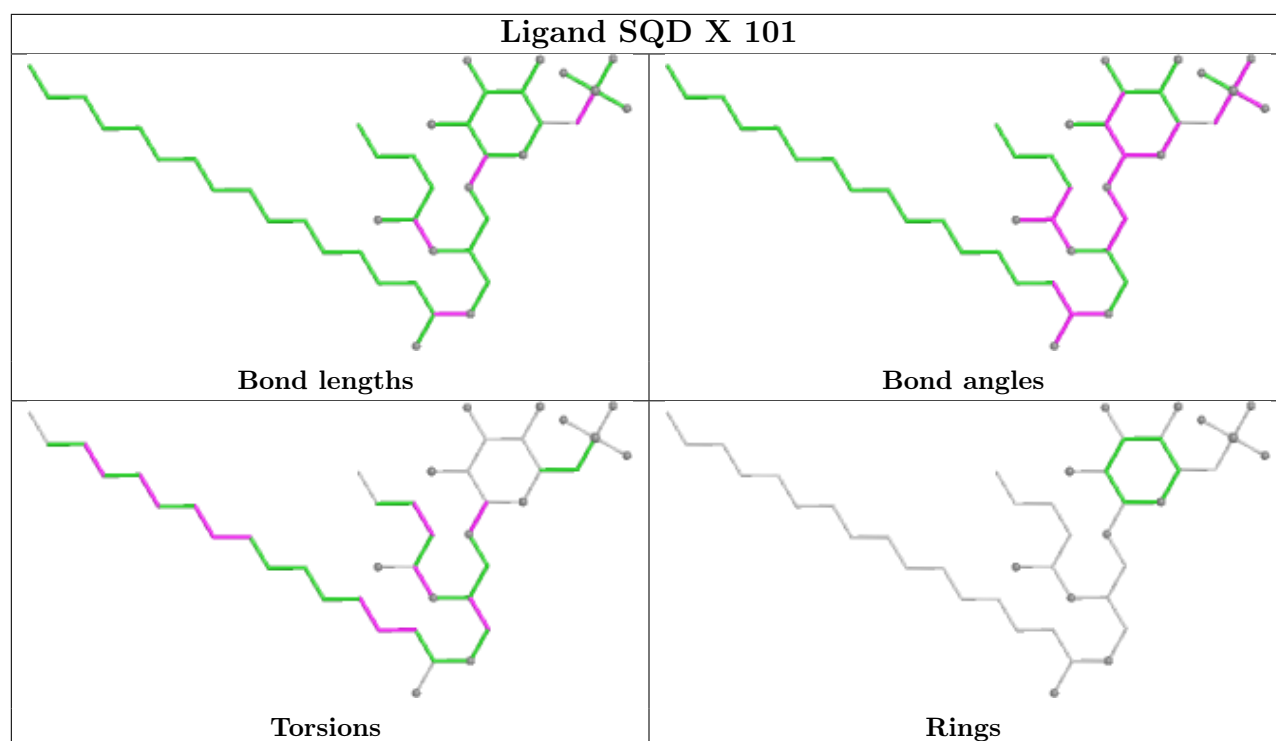
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

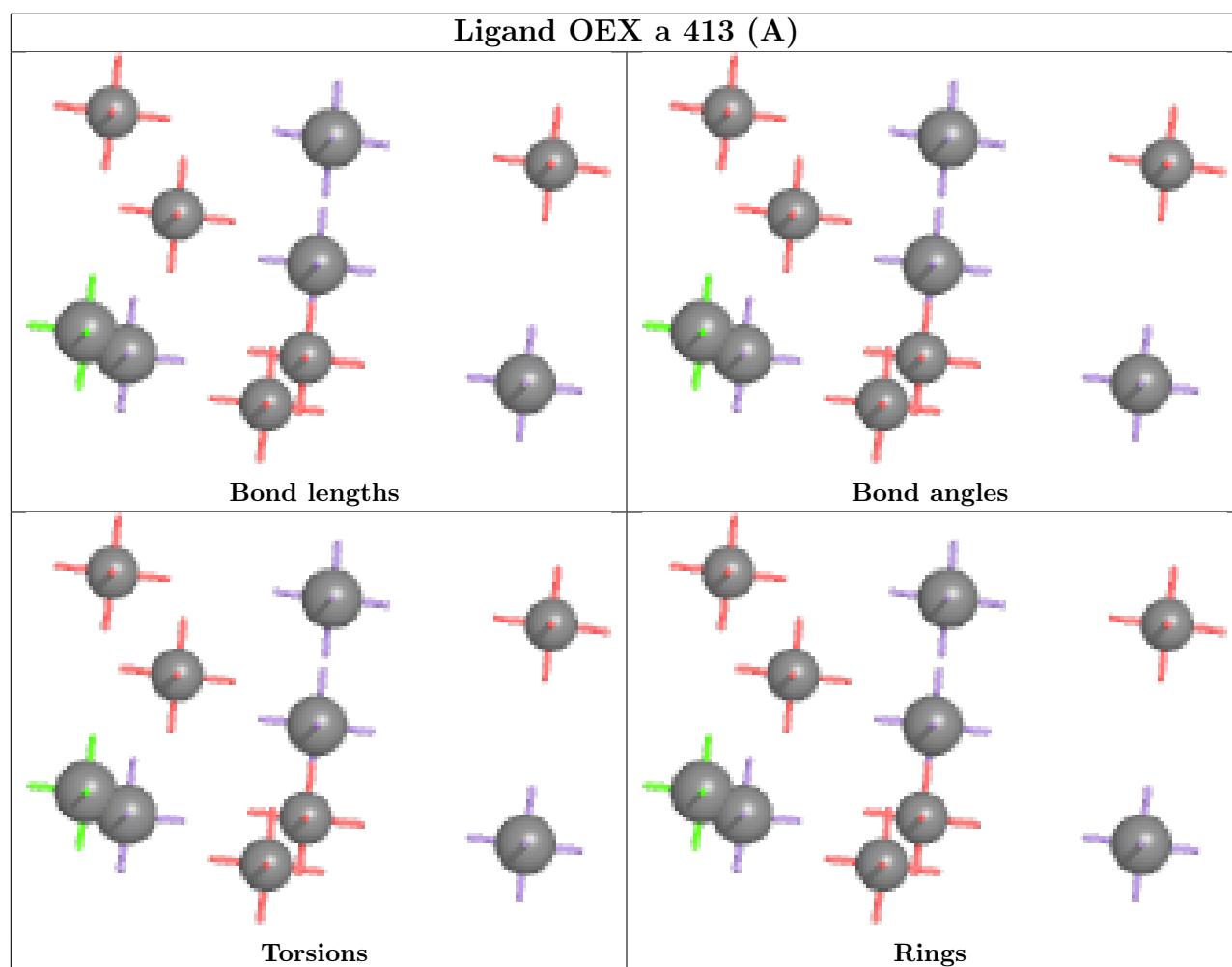
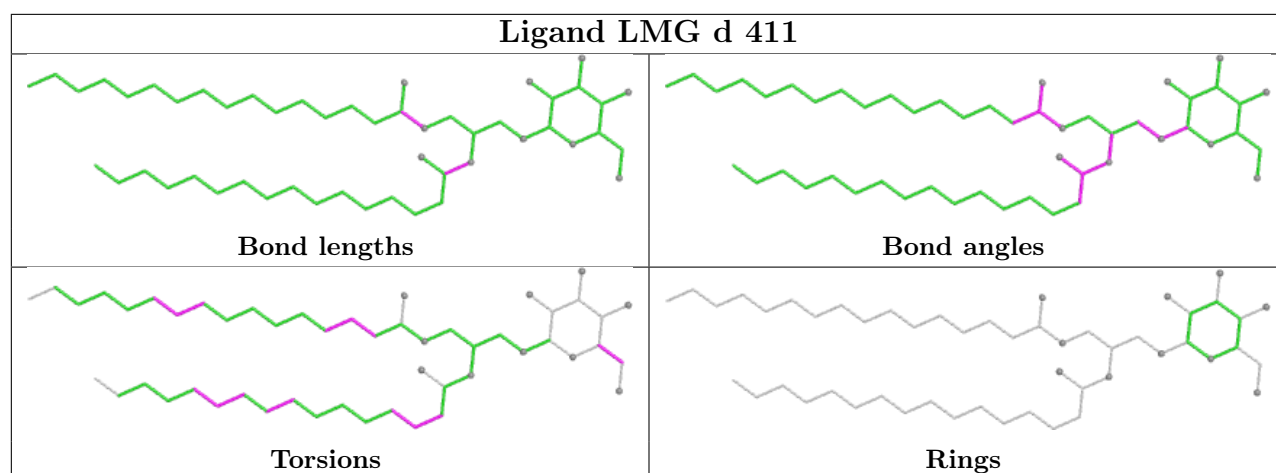


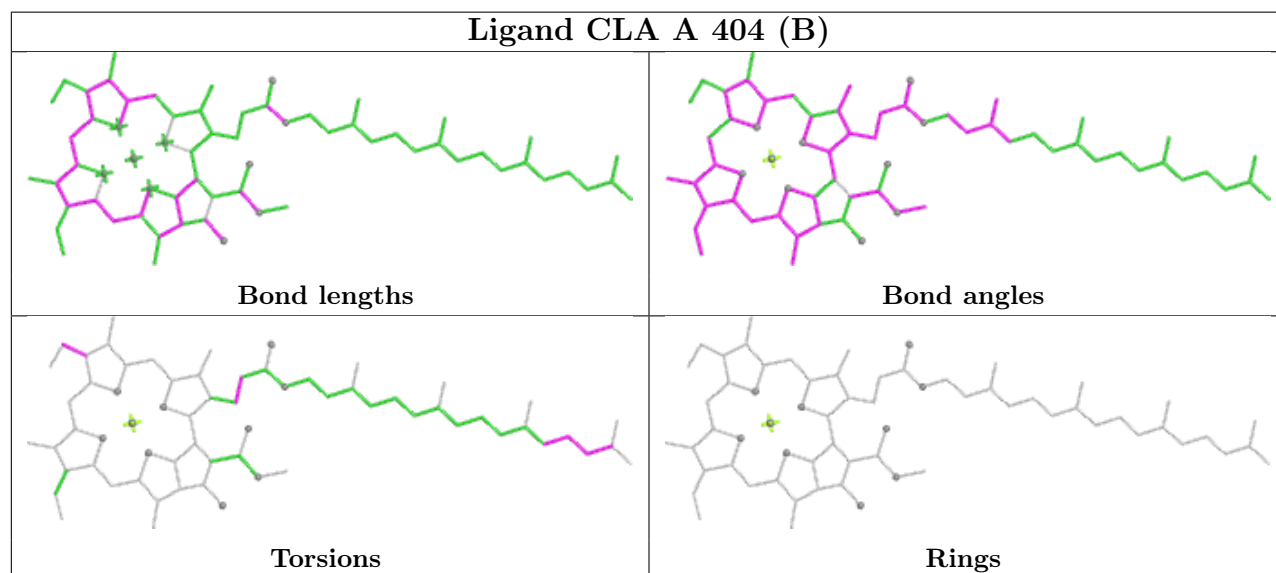
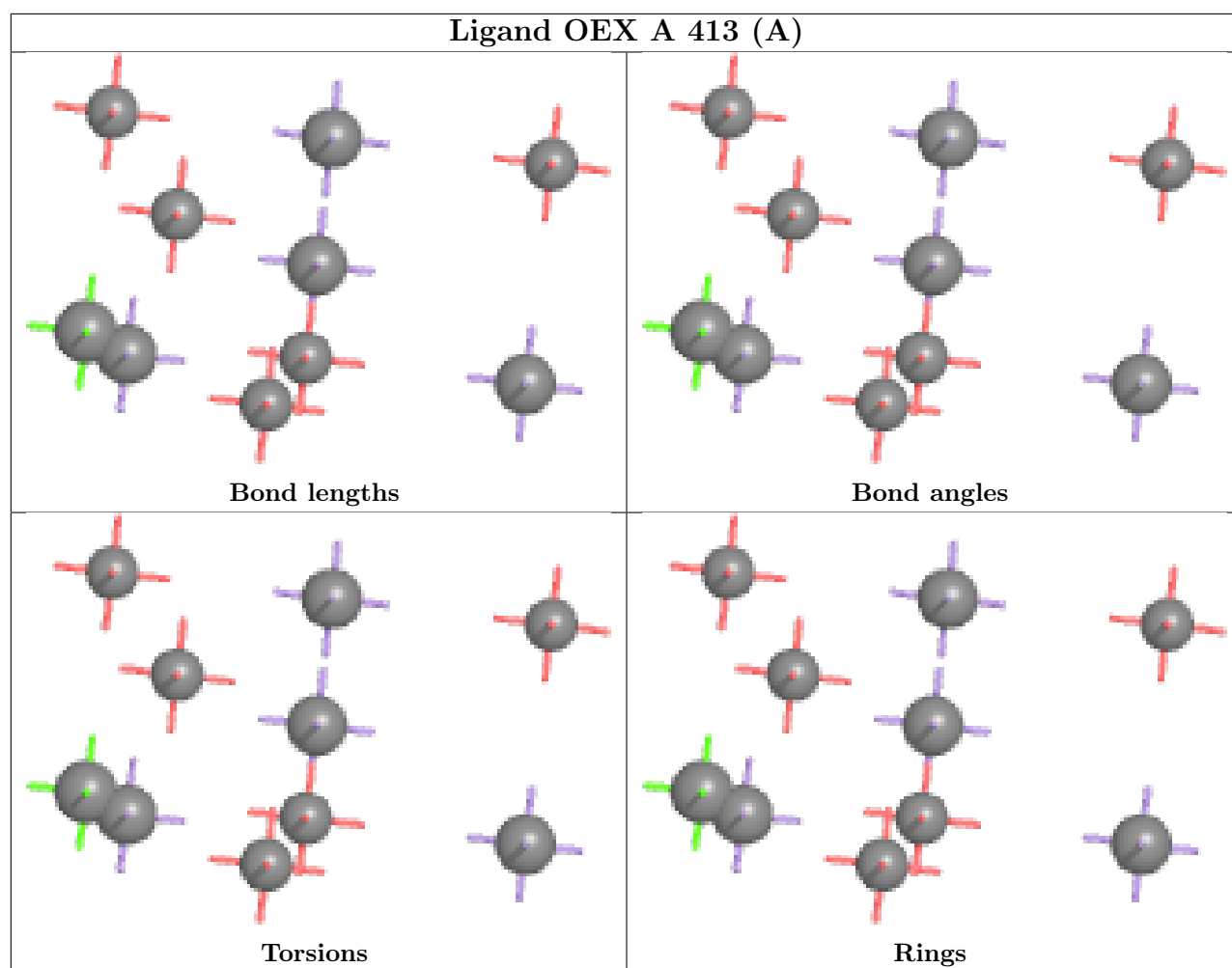
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Bond lengths	Bond angles
	
Torsions	Rings

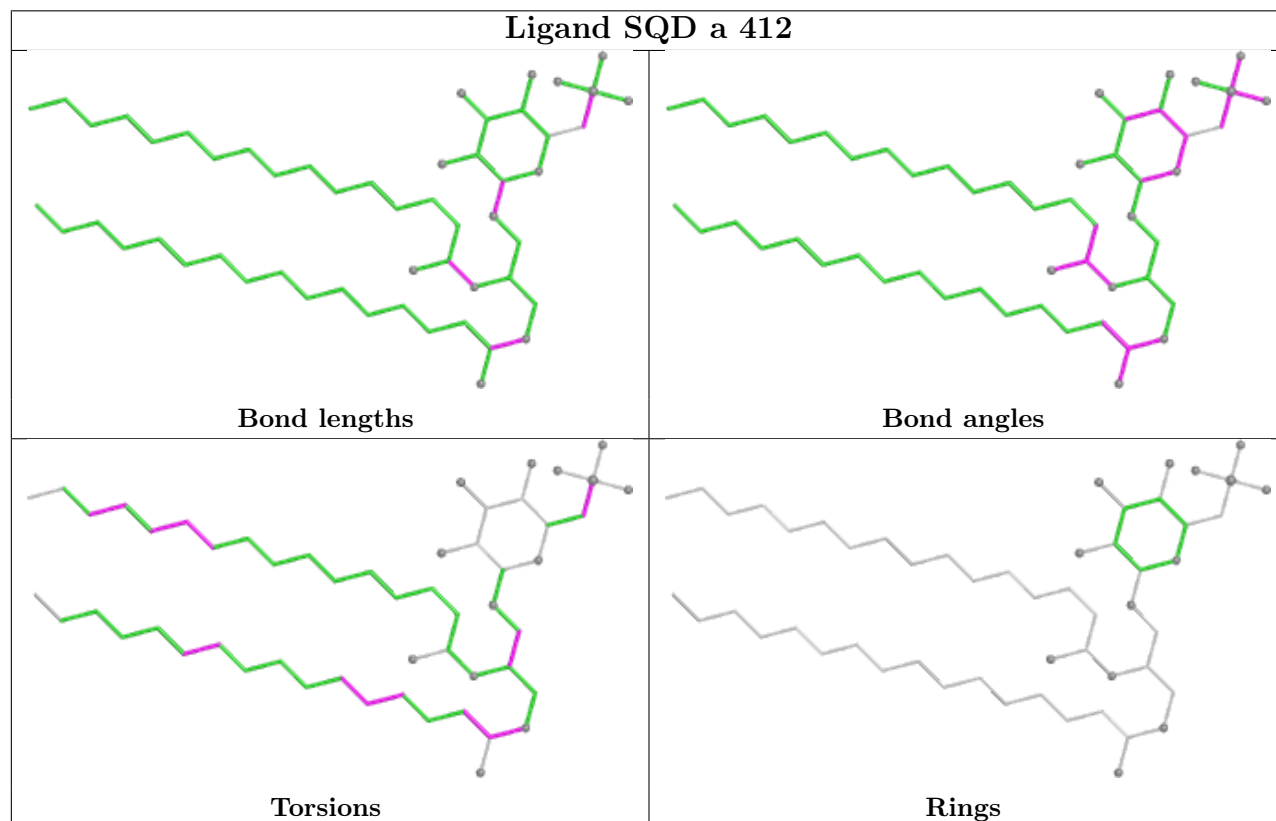
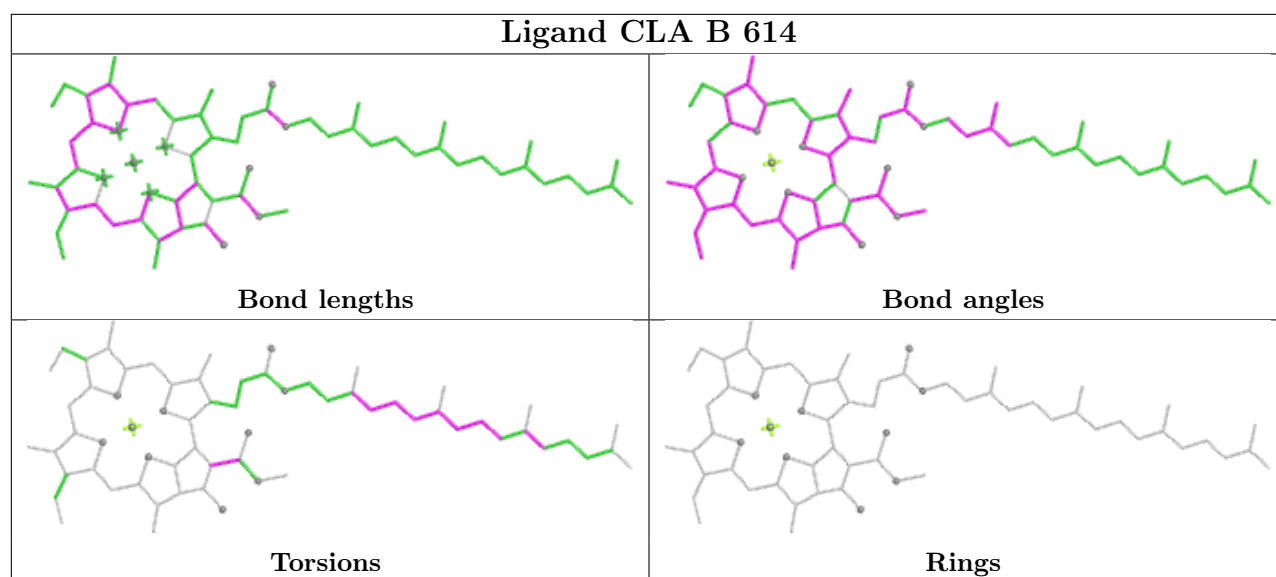
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Bond lengths	Bond angles
	
Torsions	Rings

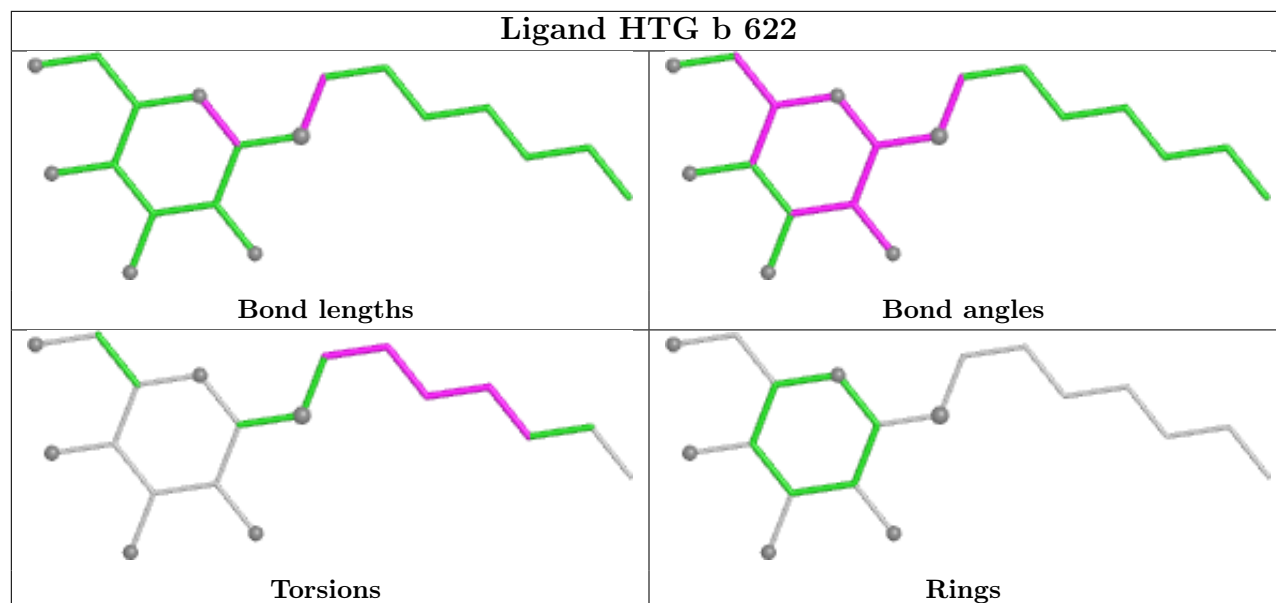
Ligand BCR D 406	
	
Bond lengths	Bond angles
	
Torsions	Rings

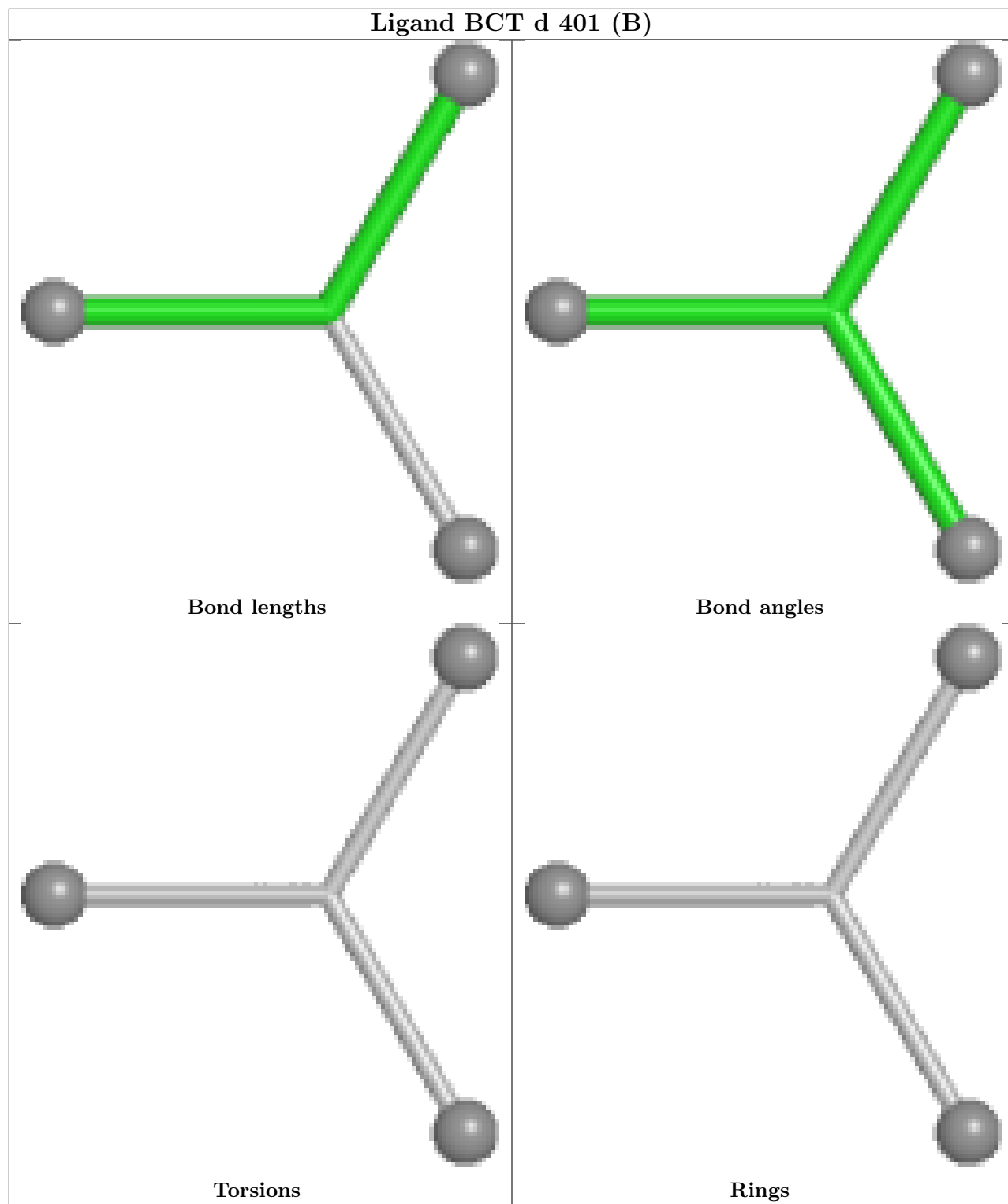


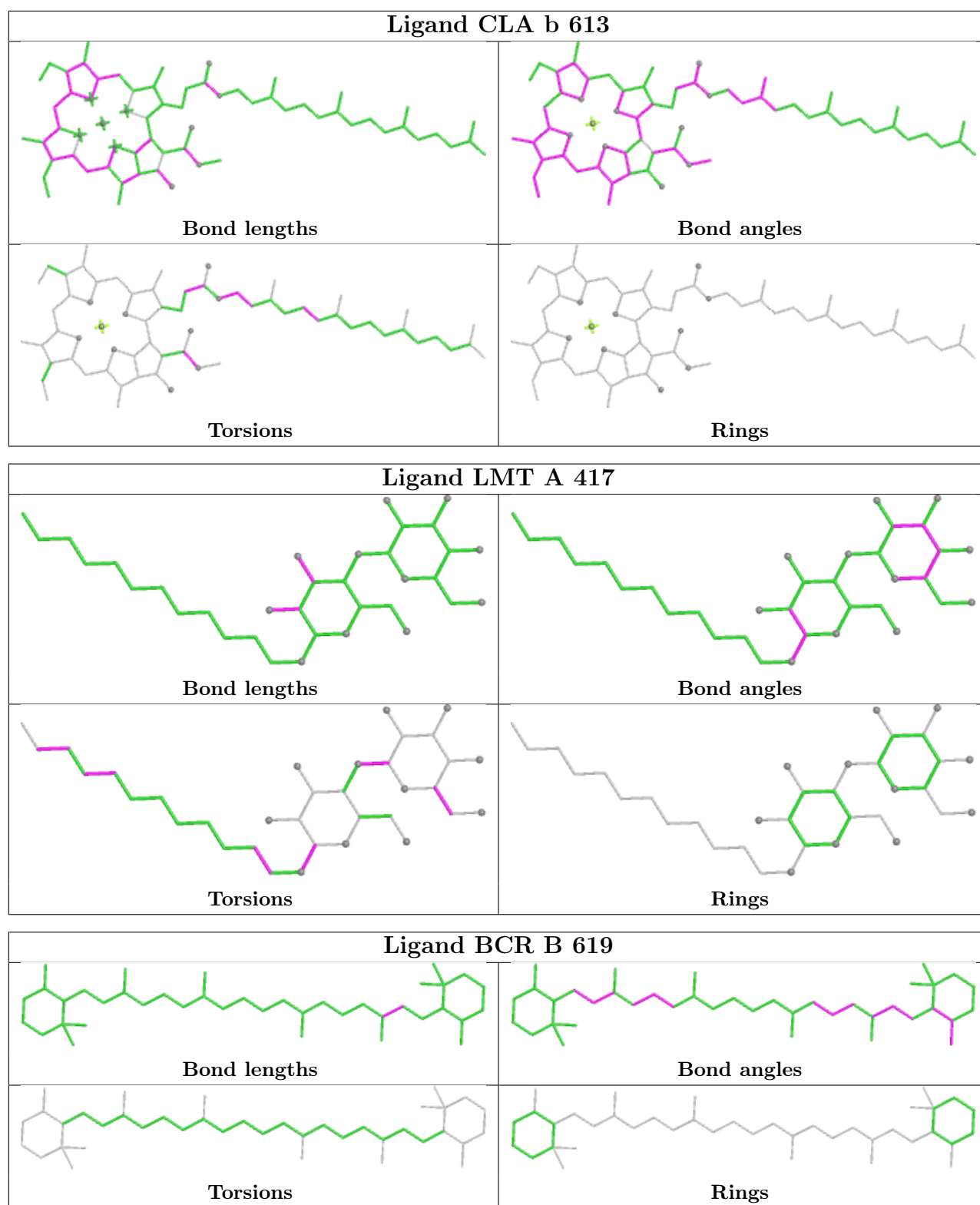


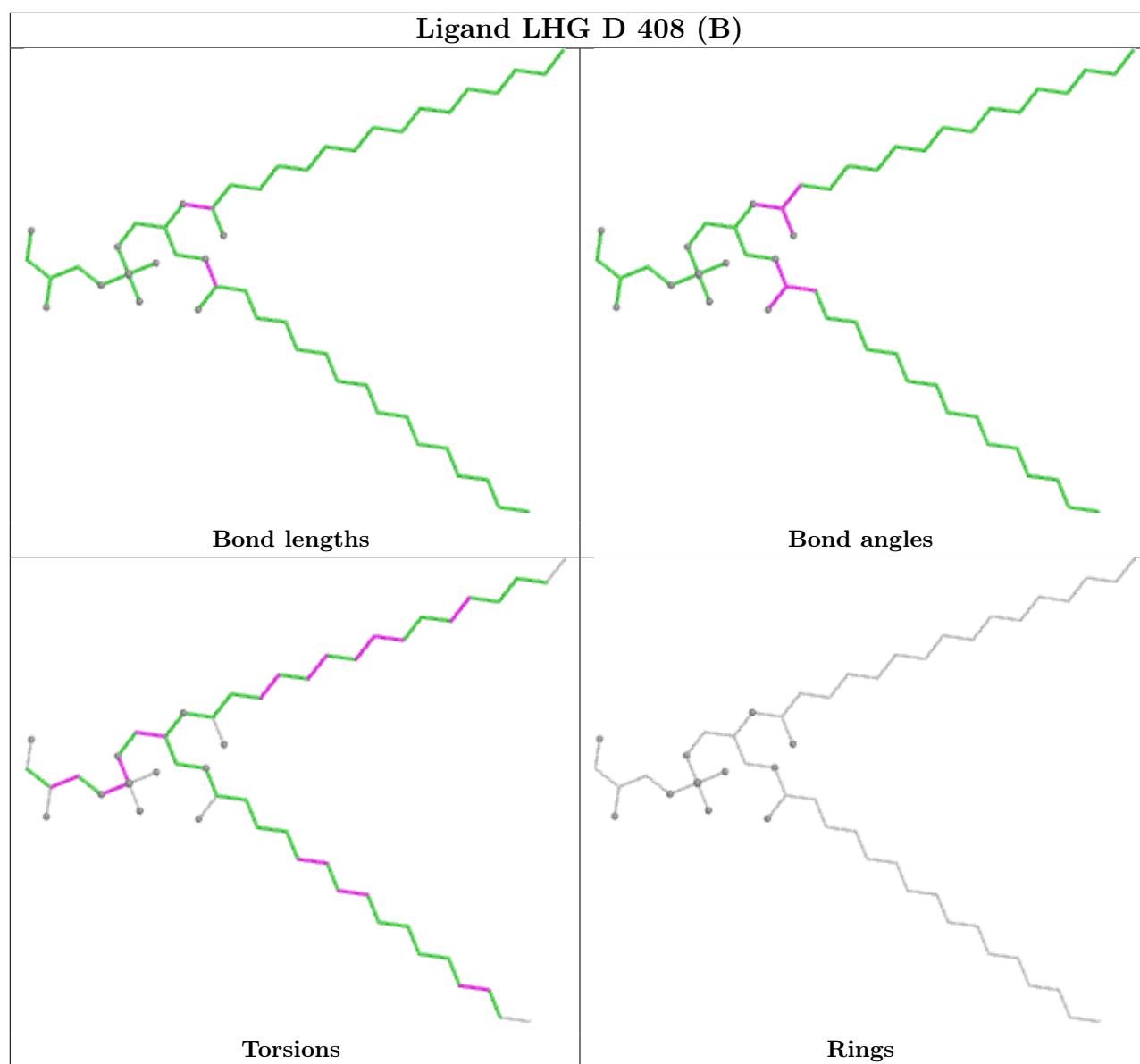


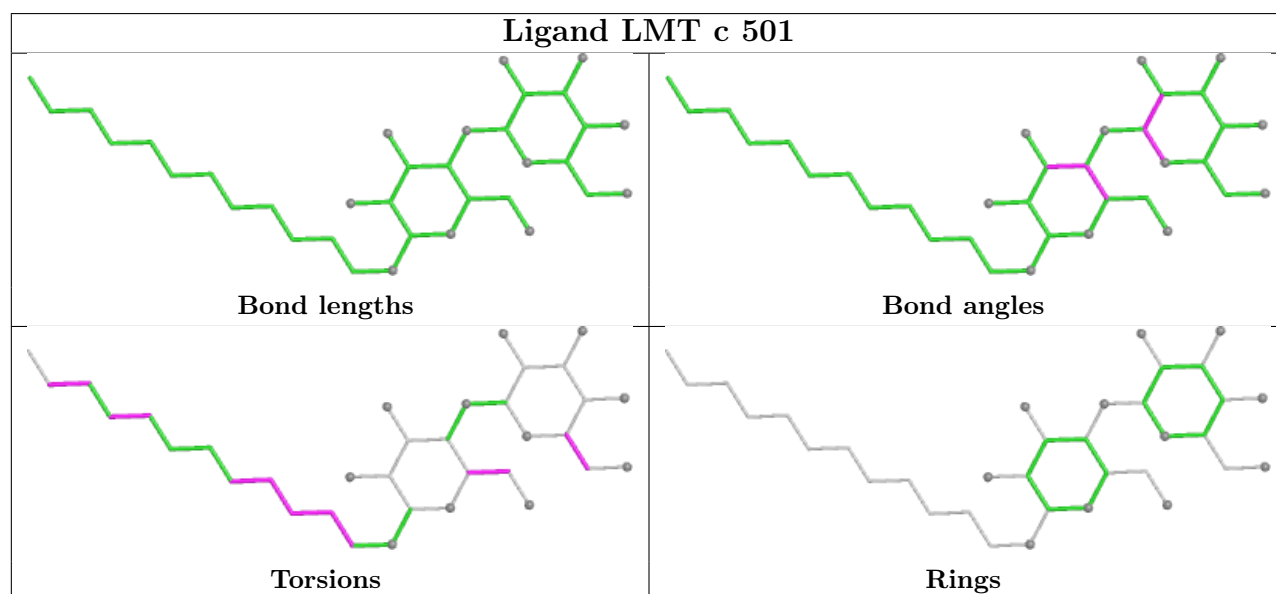
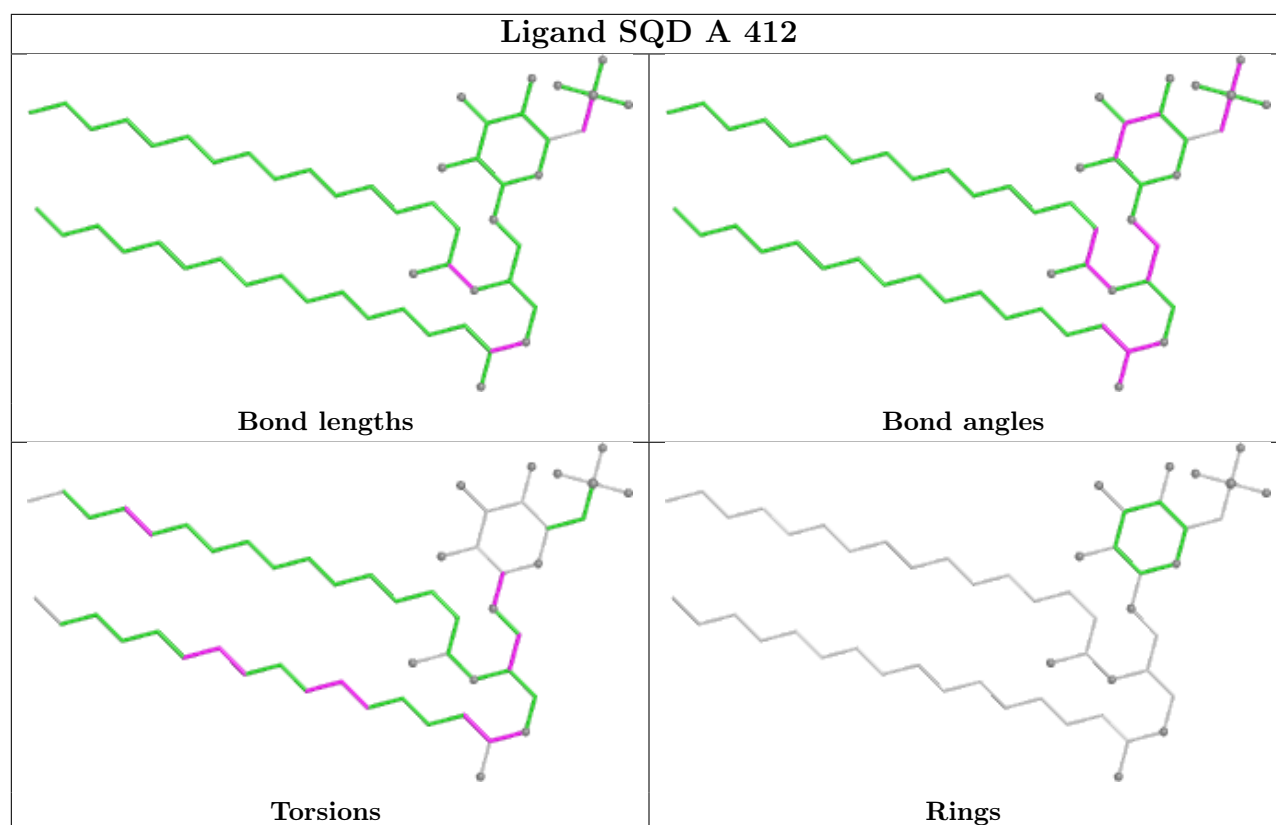


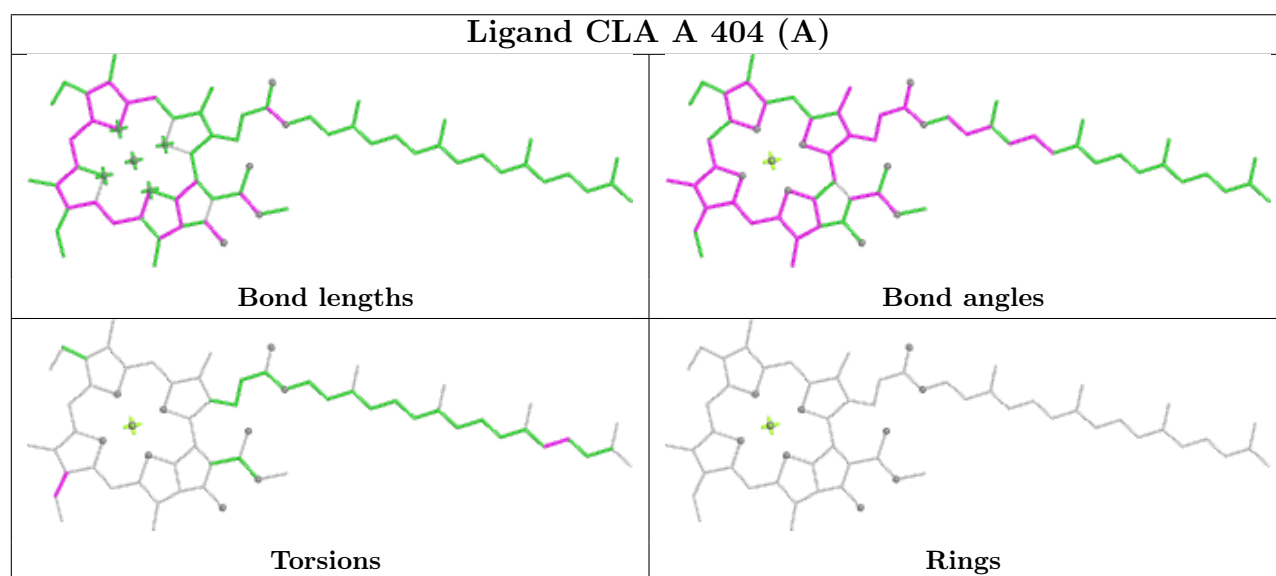
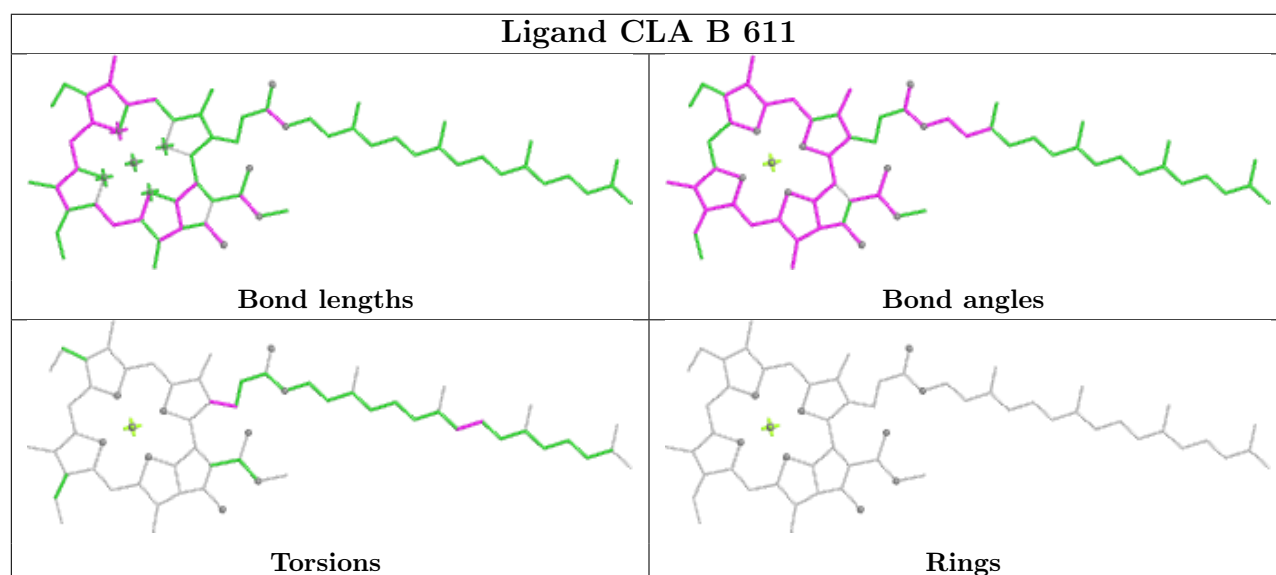
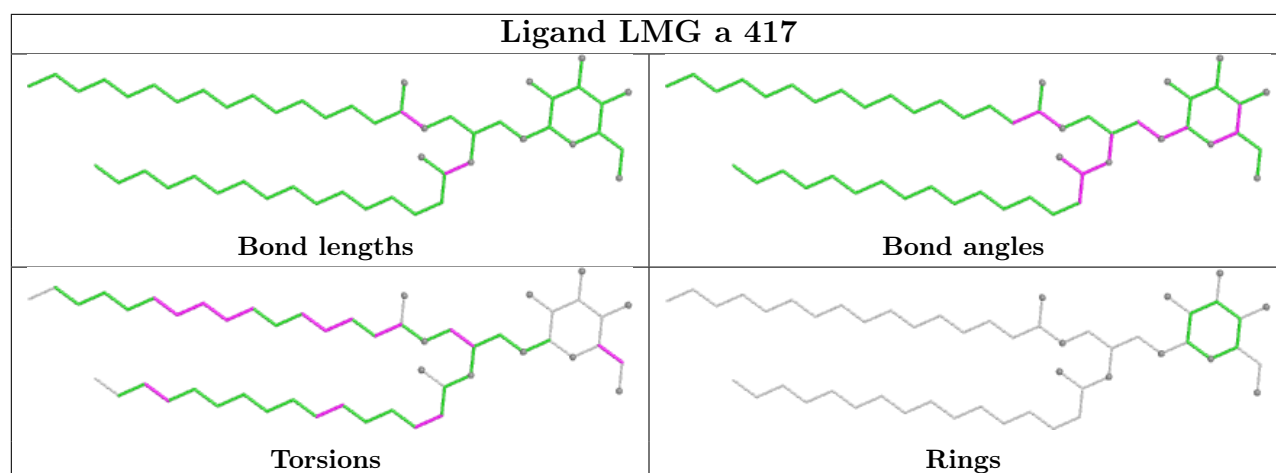


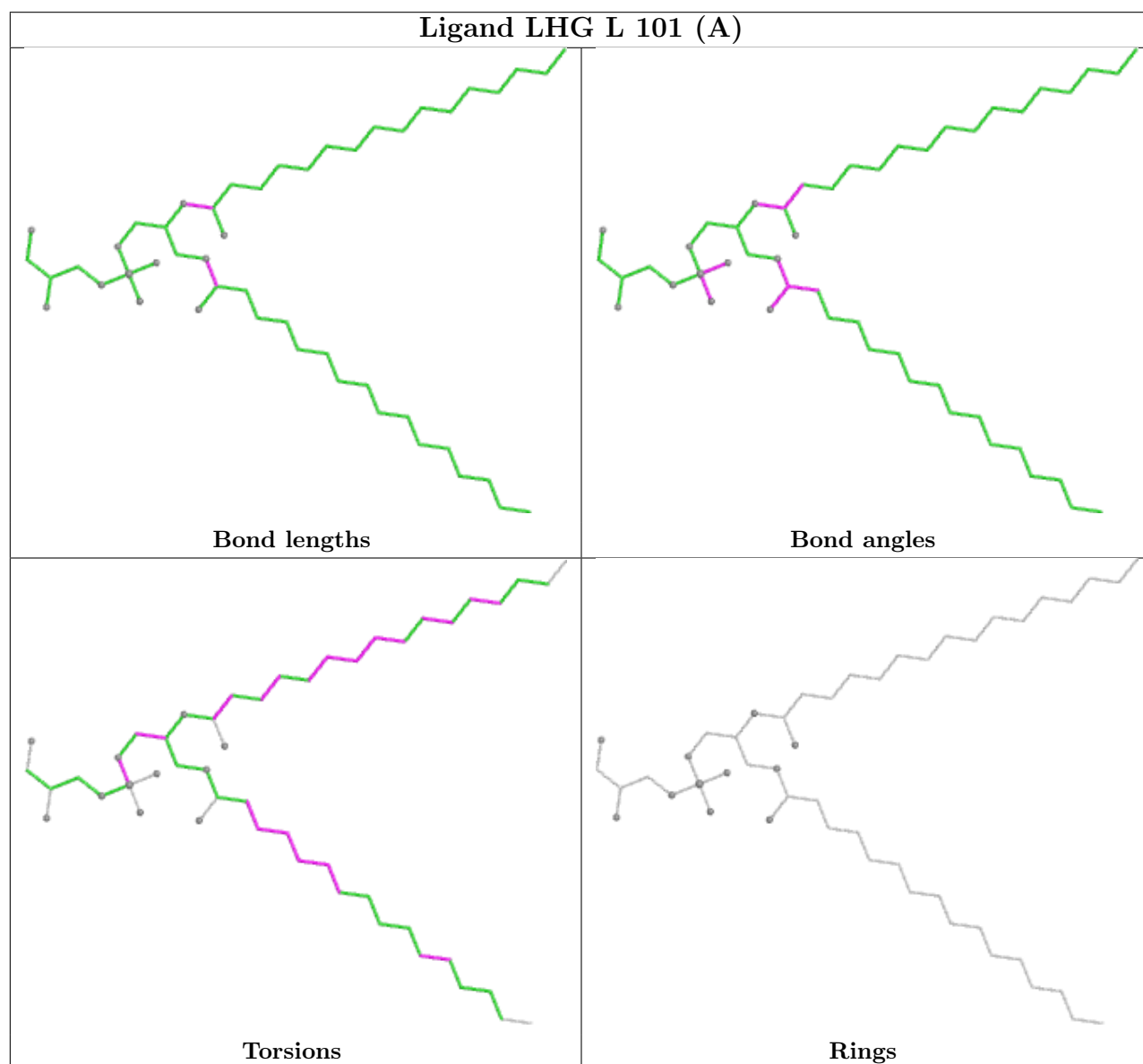
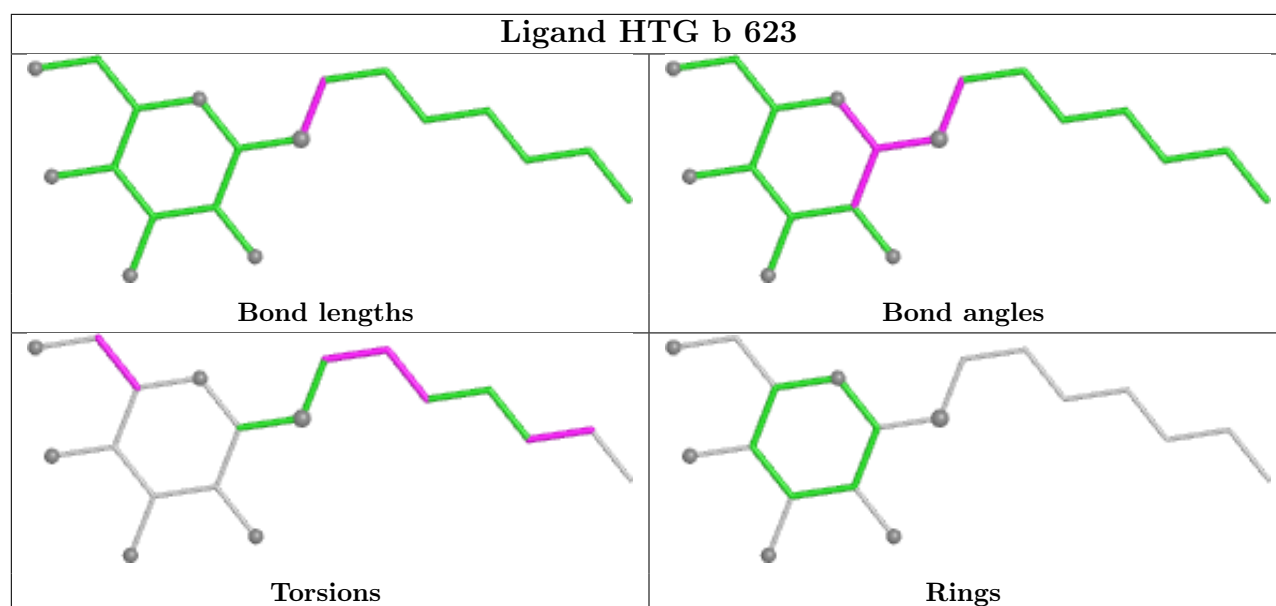


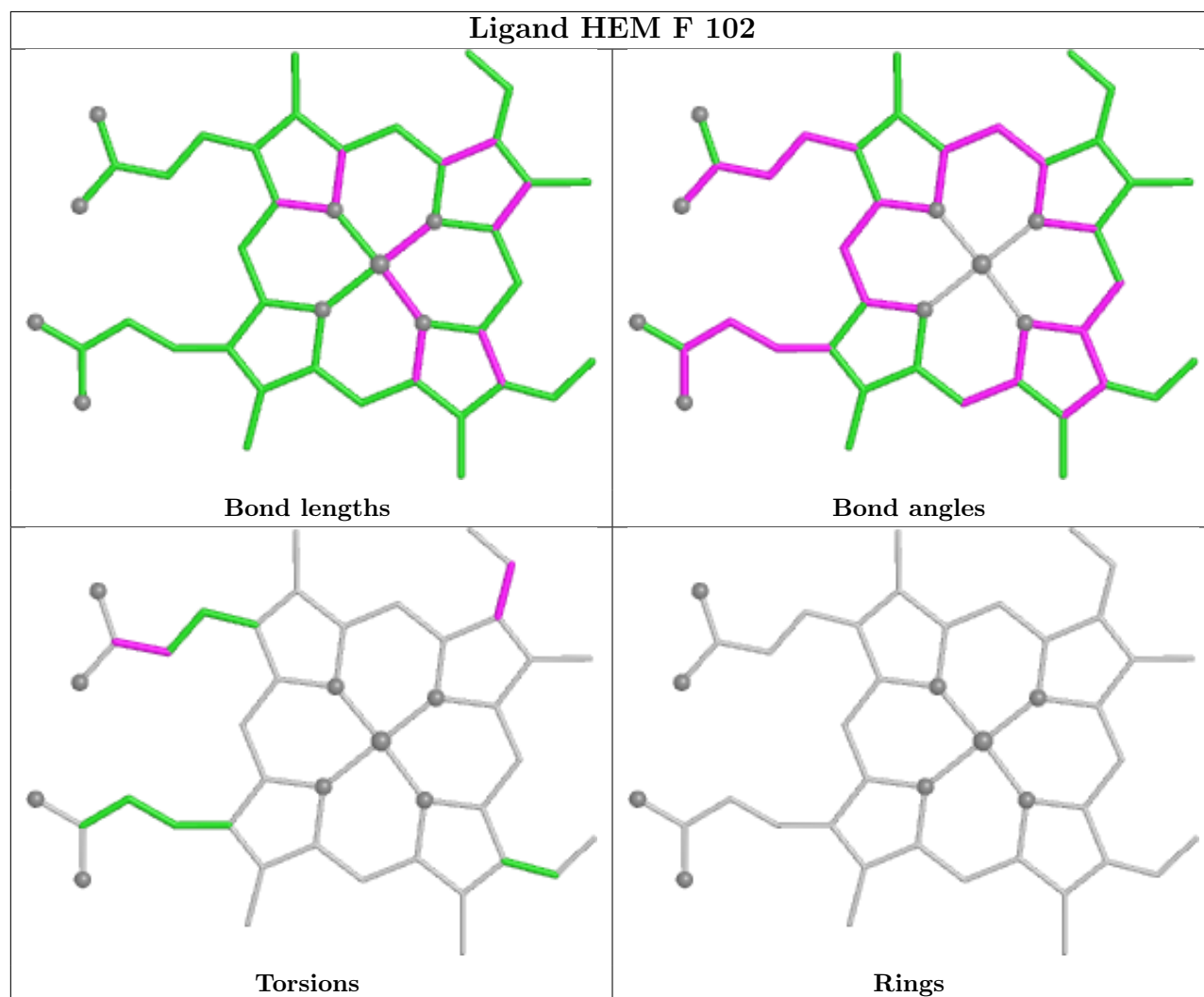
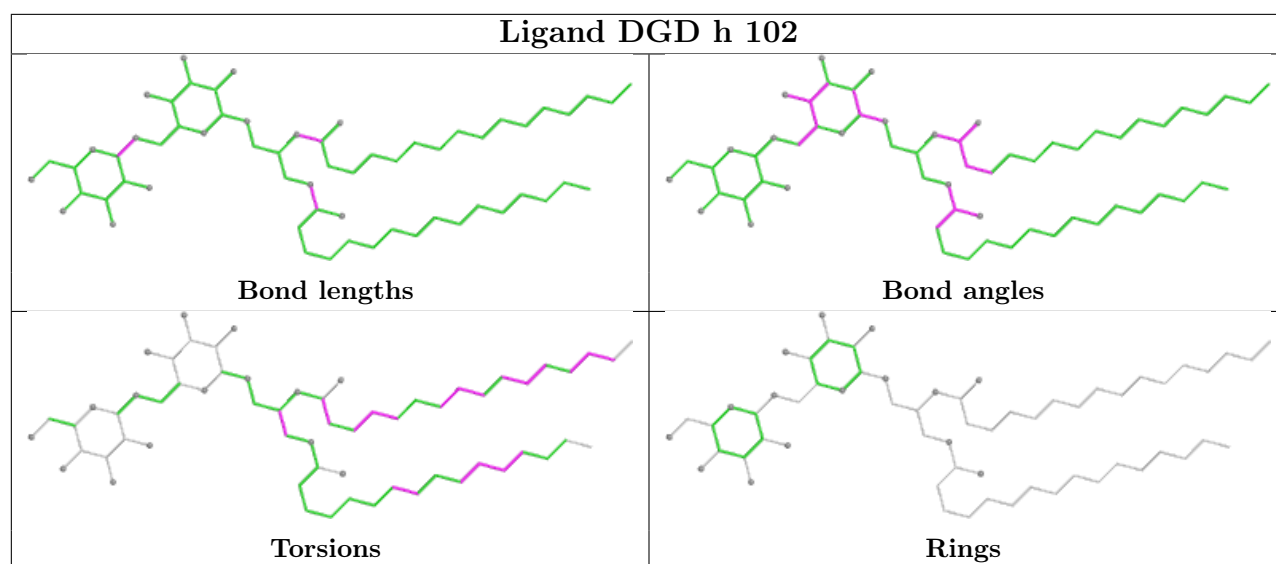


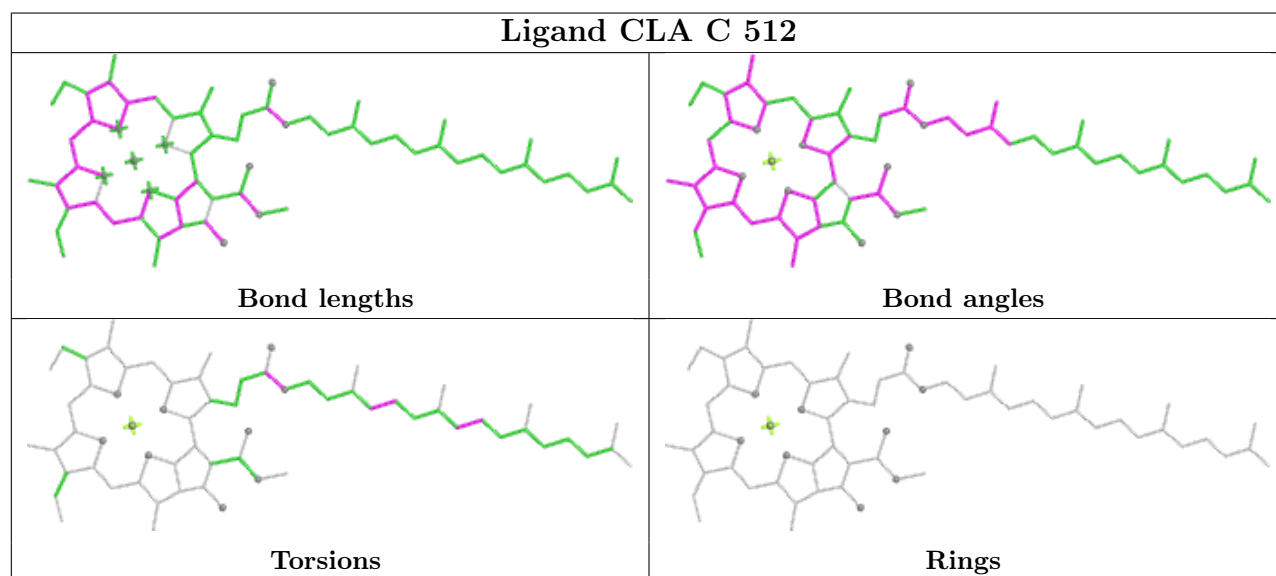
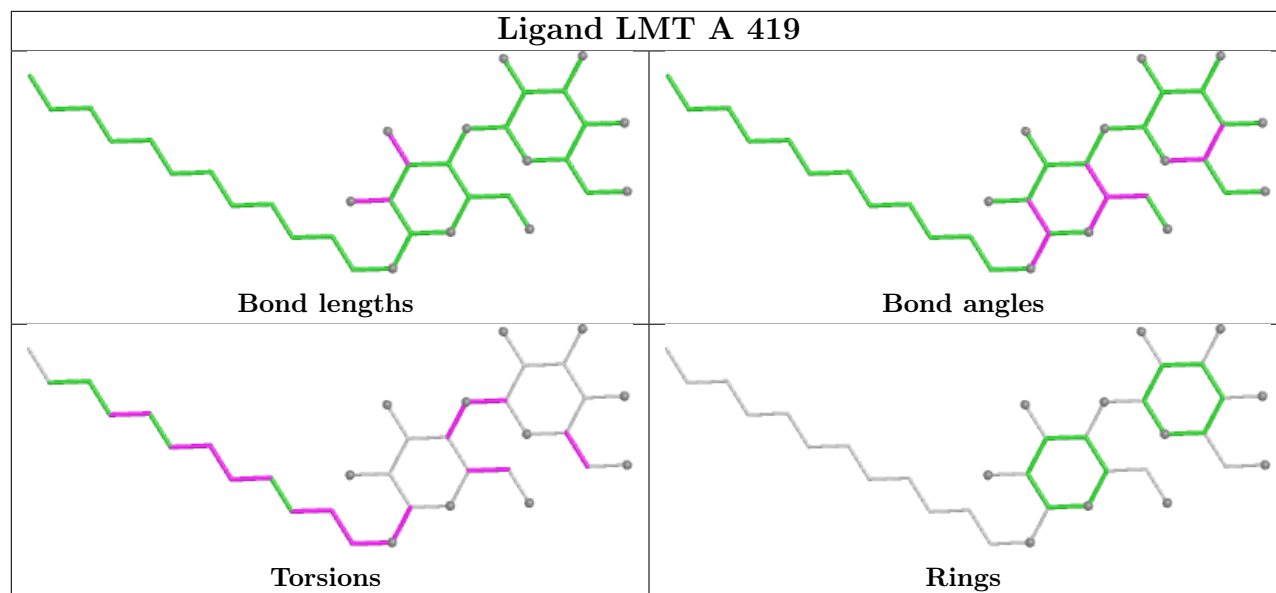




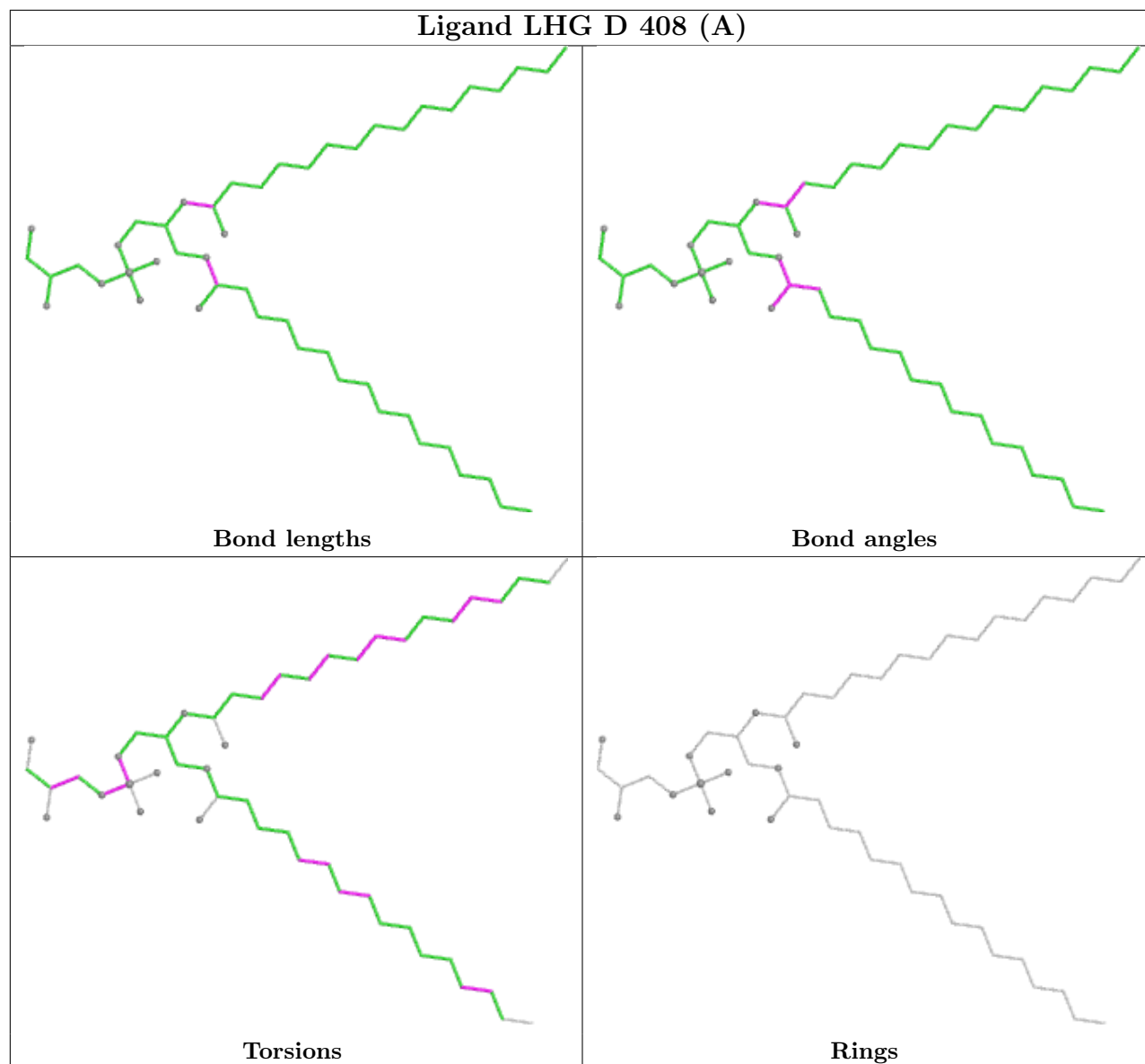




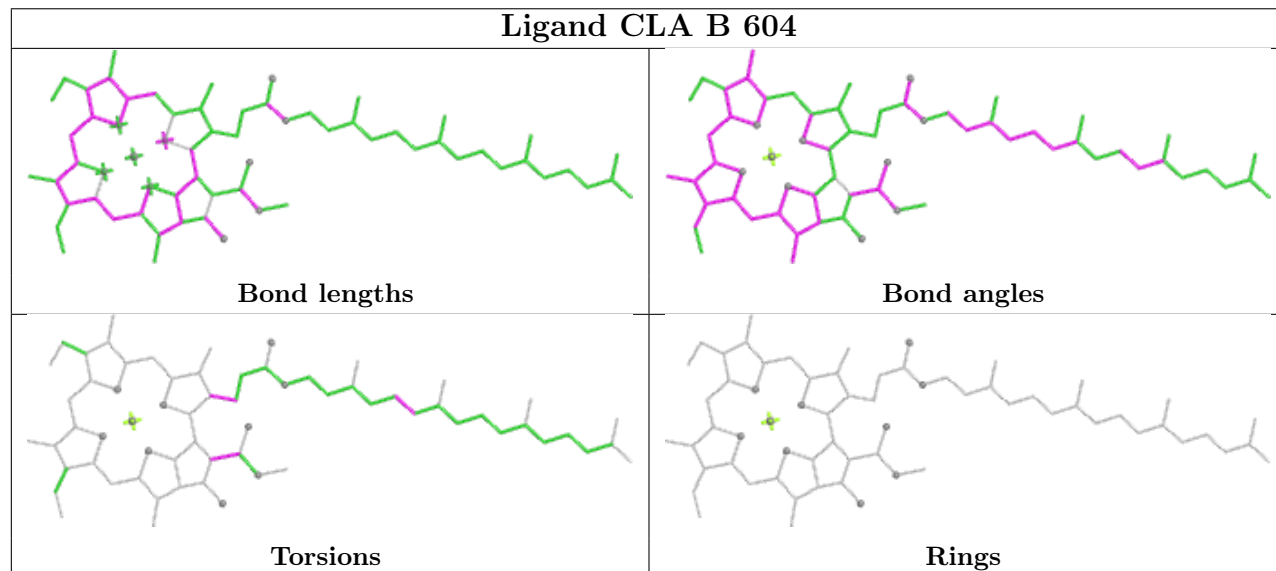




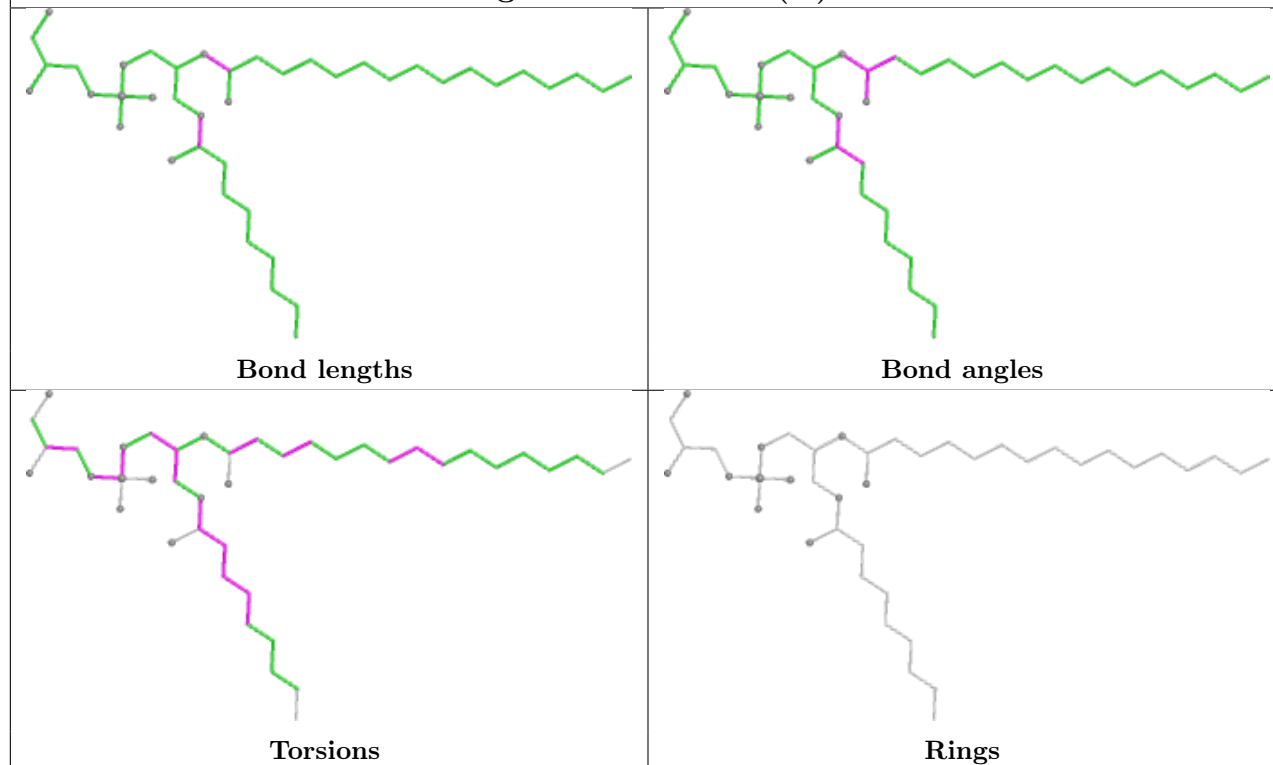
Ligand LHG D 408 (A)



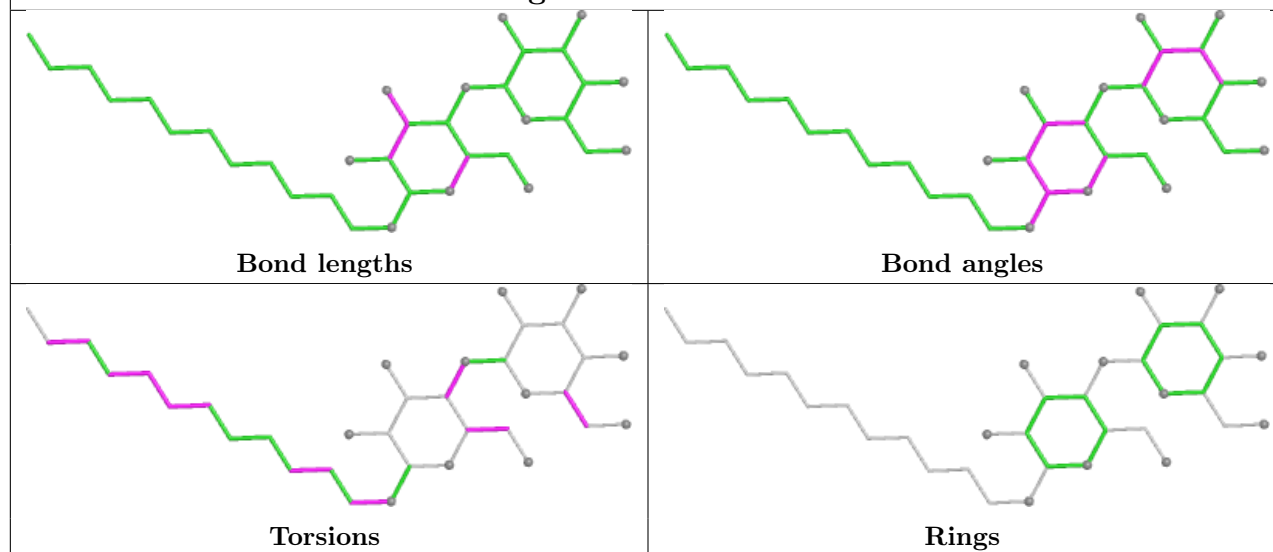
Ligand CLA B 604

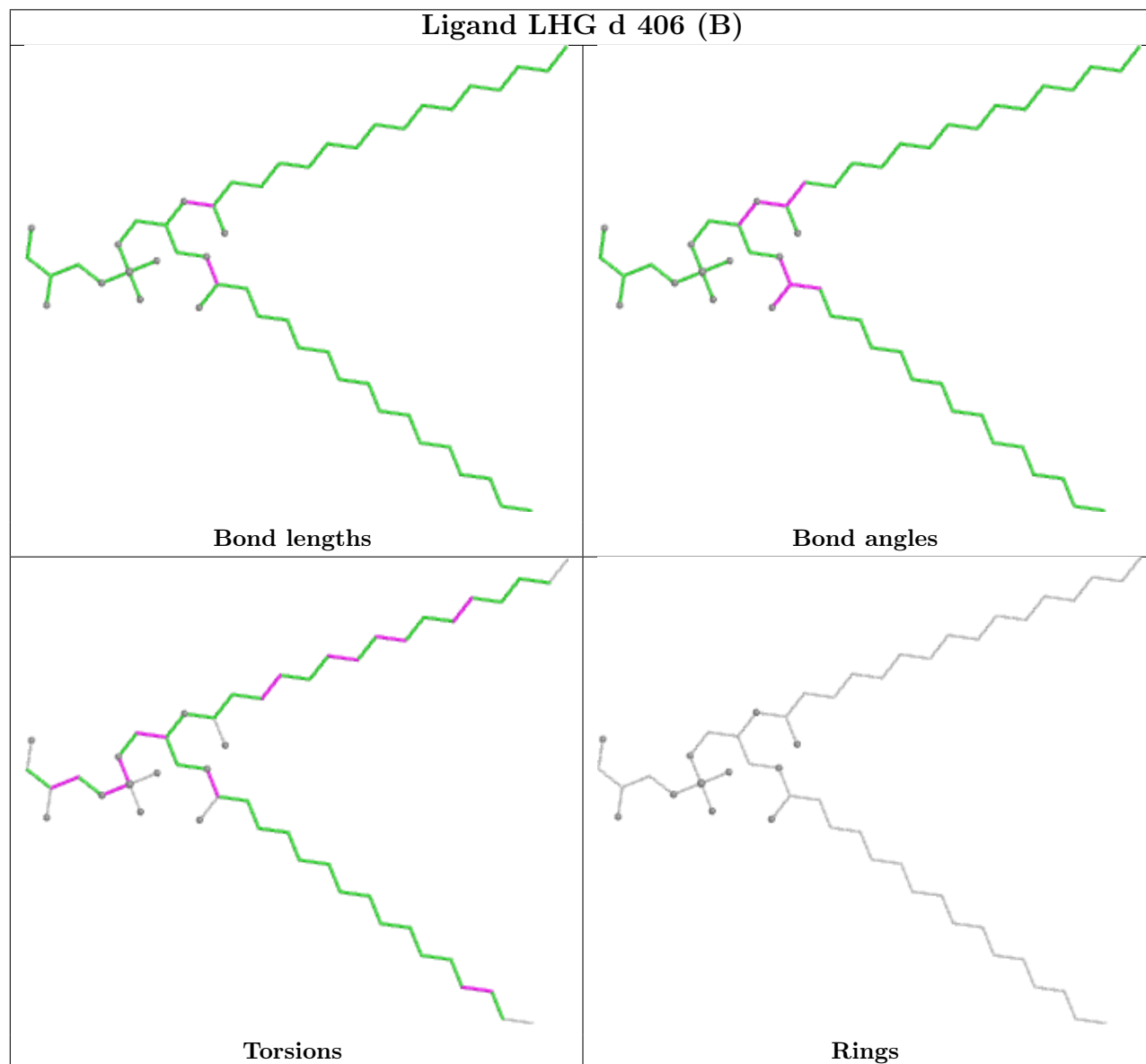
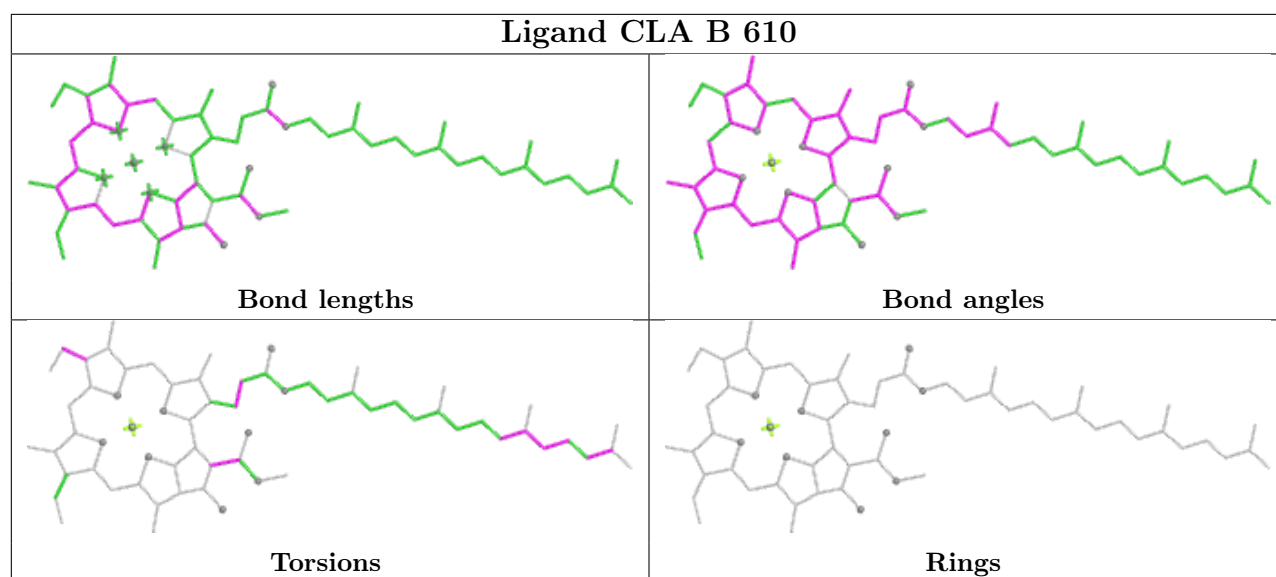


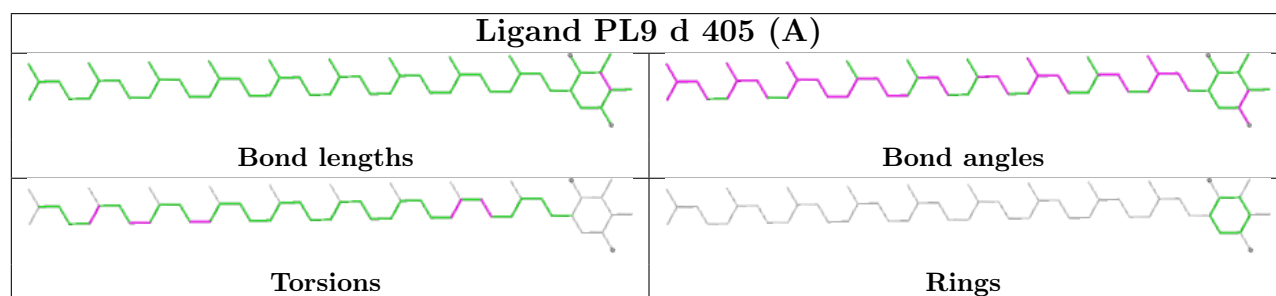
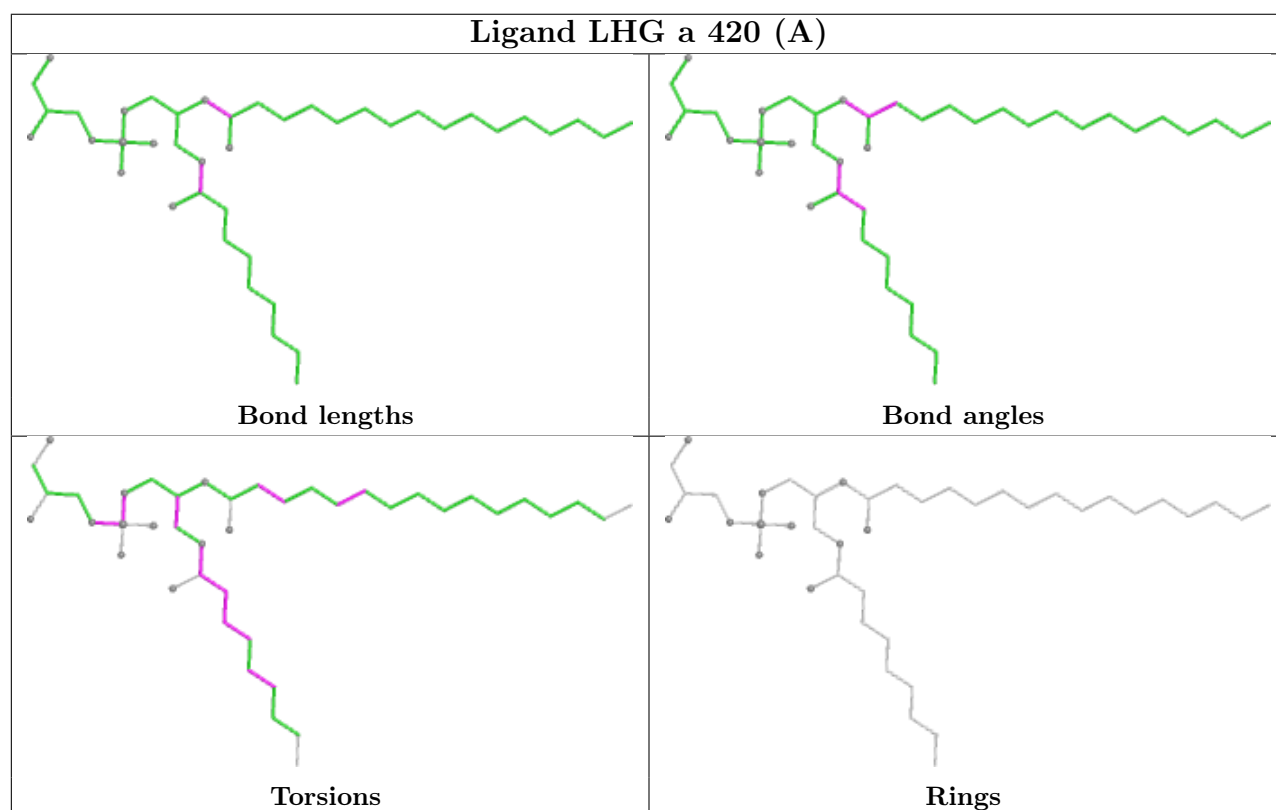
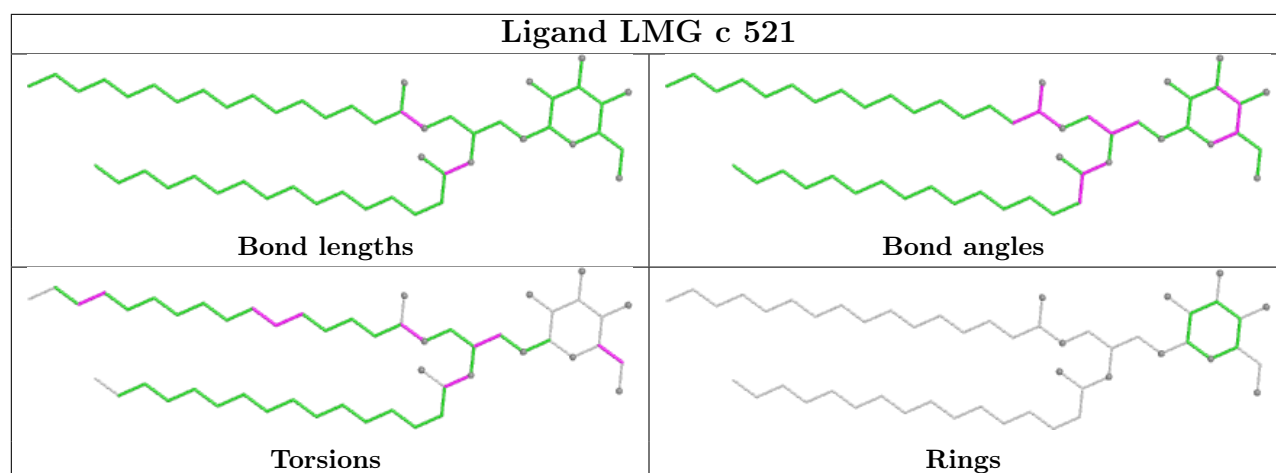
Ligand LHG E 101 (A)

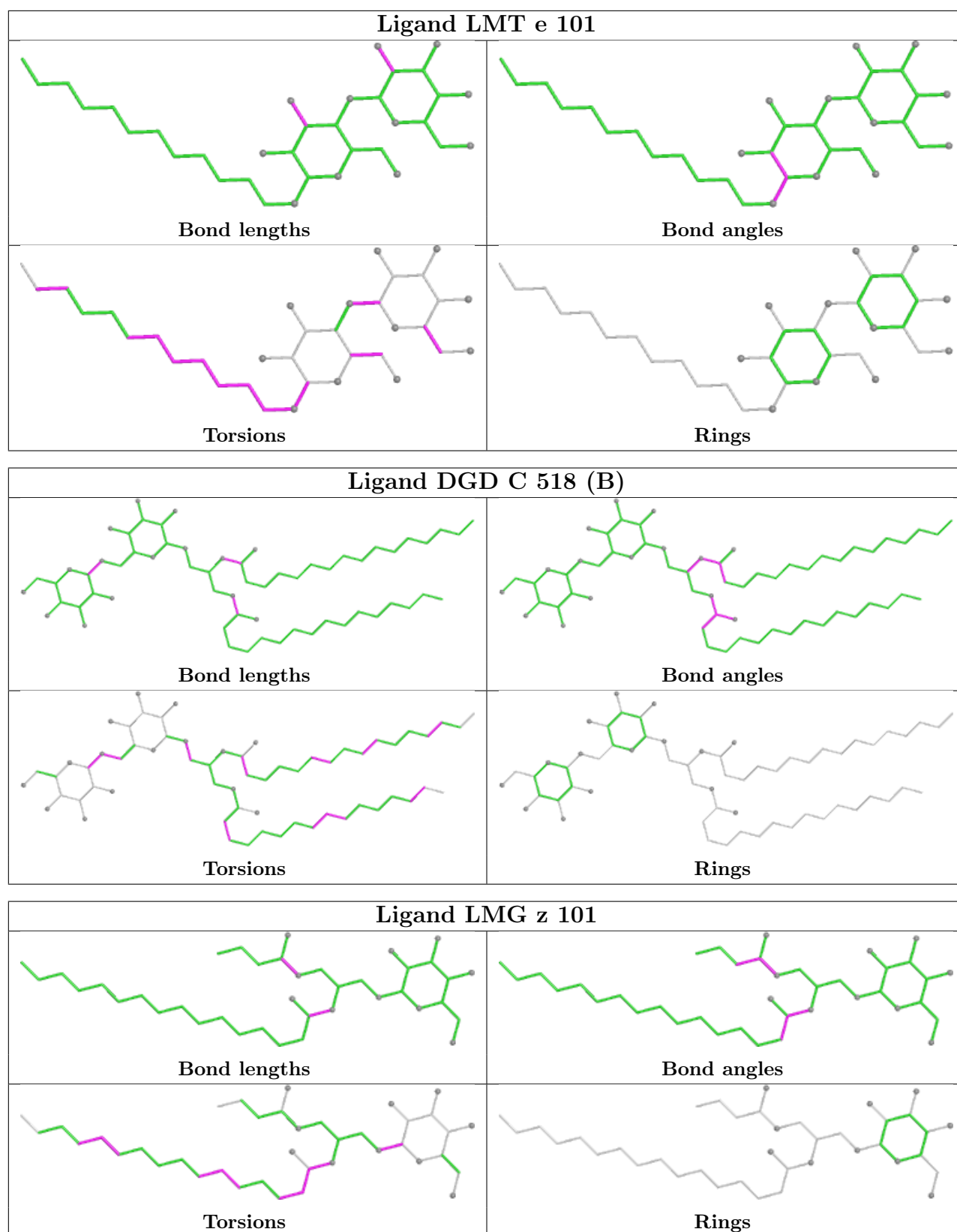


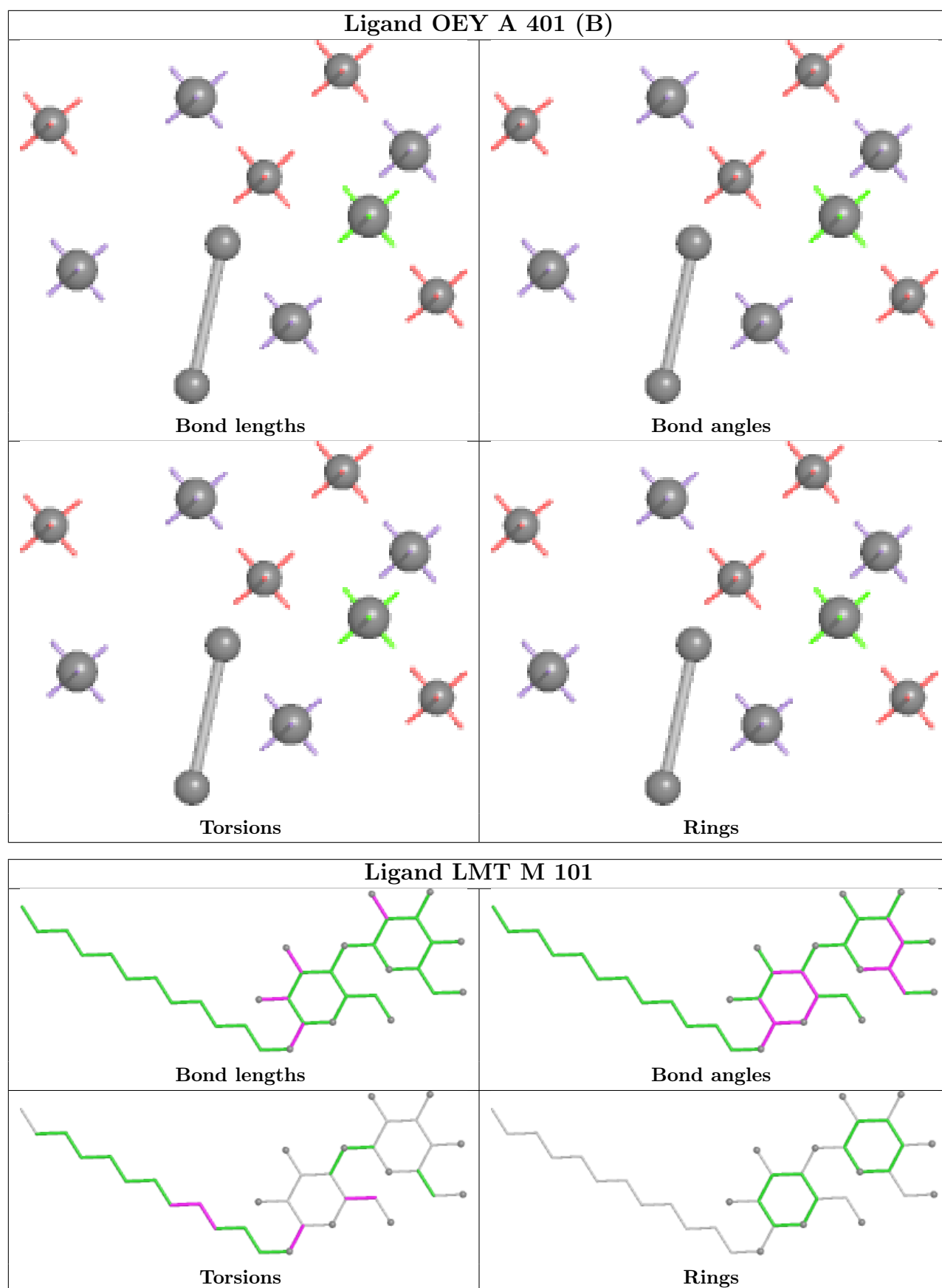
Ligand LMT B 628

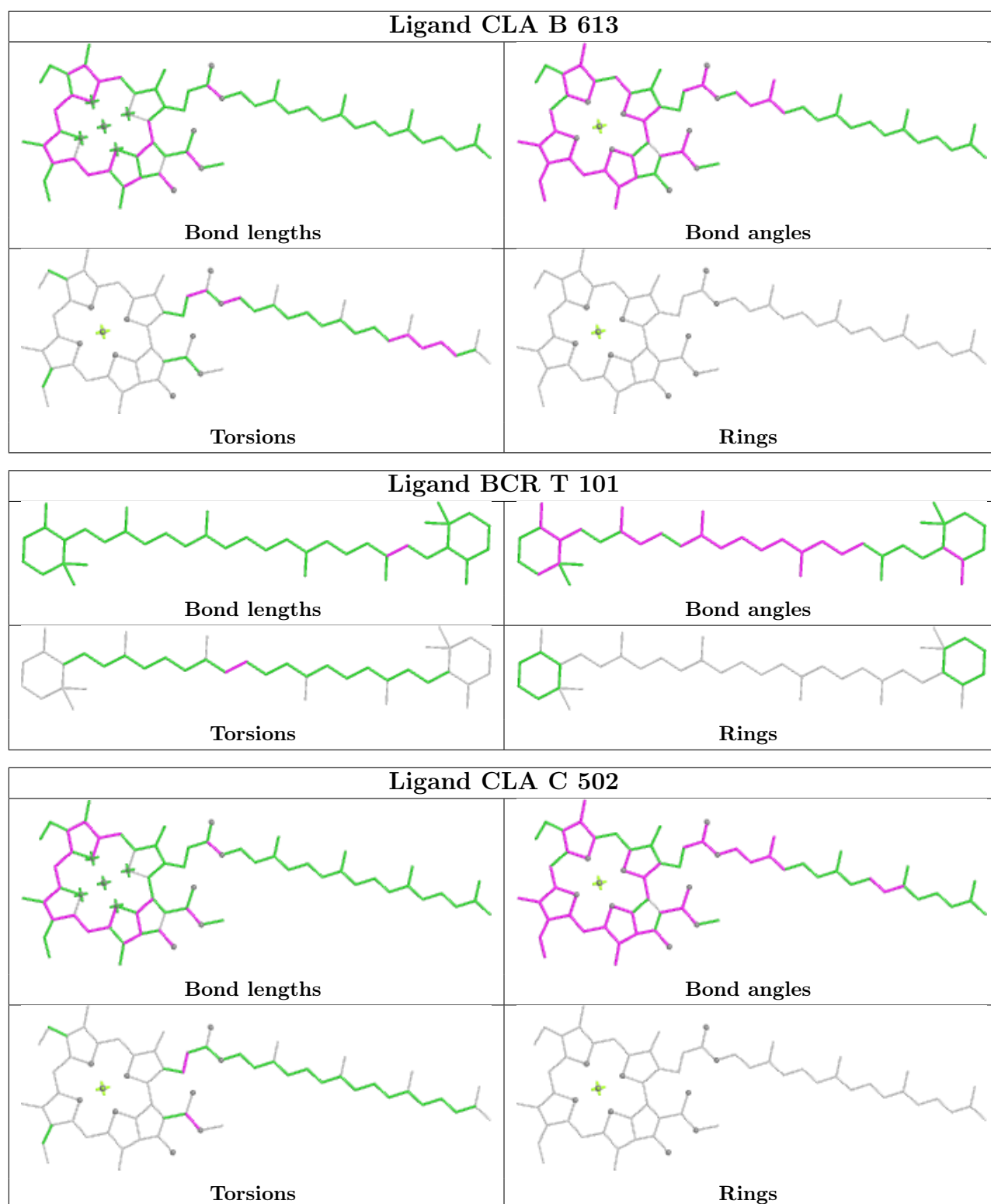


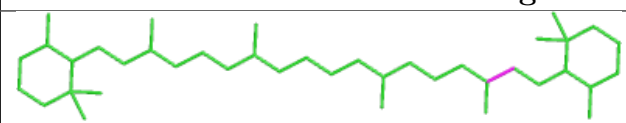
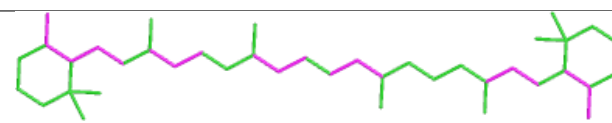
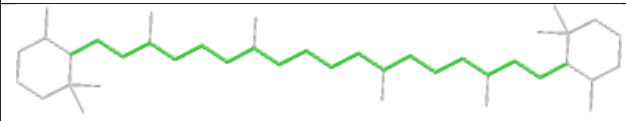
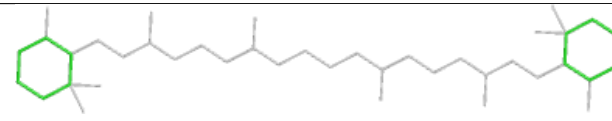


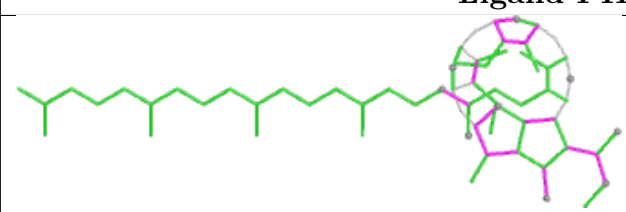
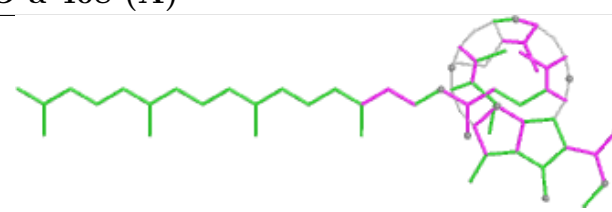
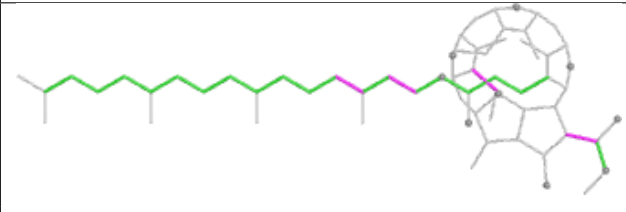
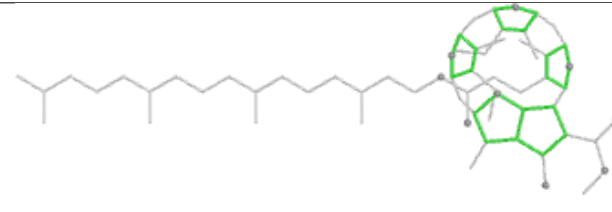


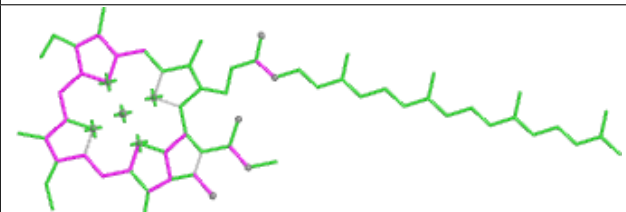
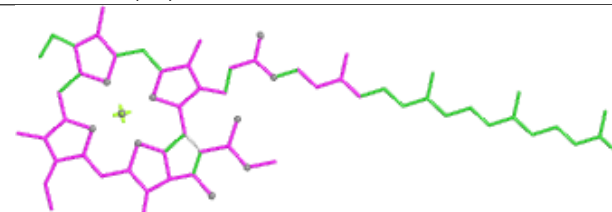
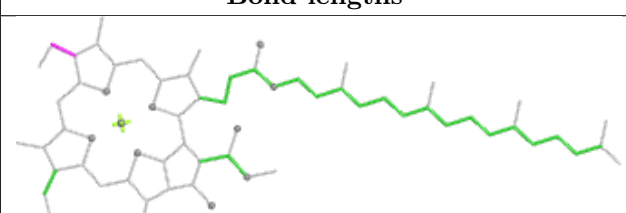
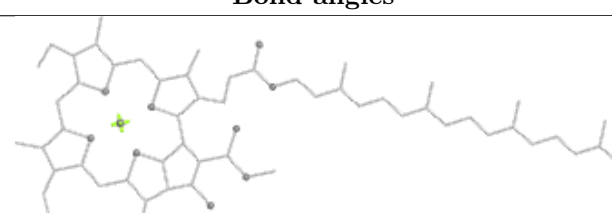


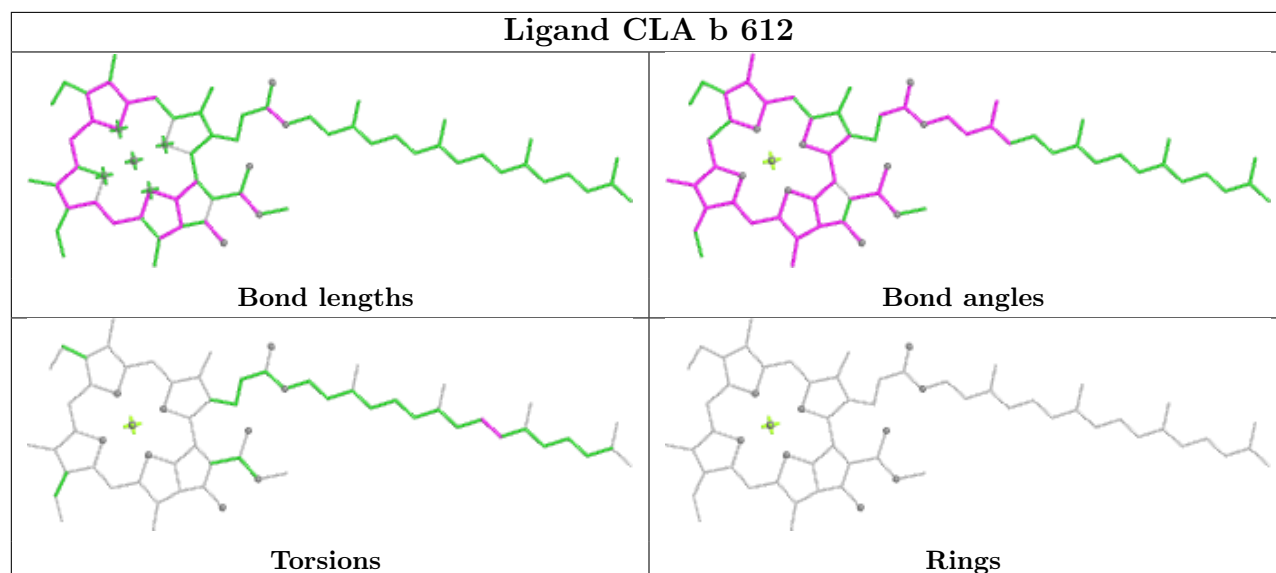
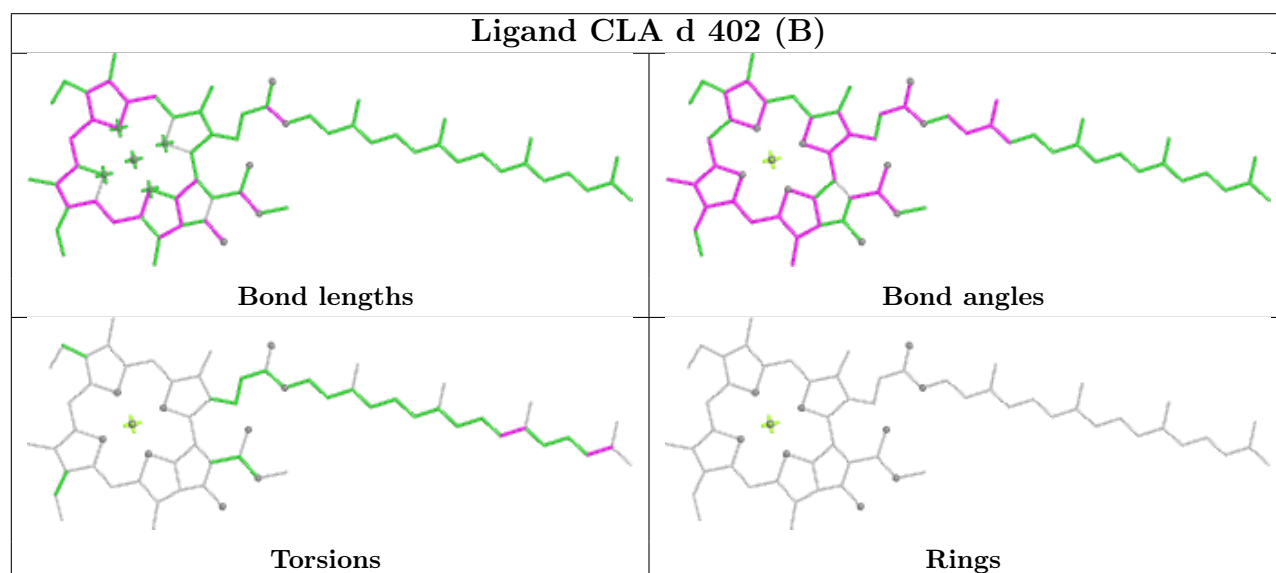
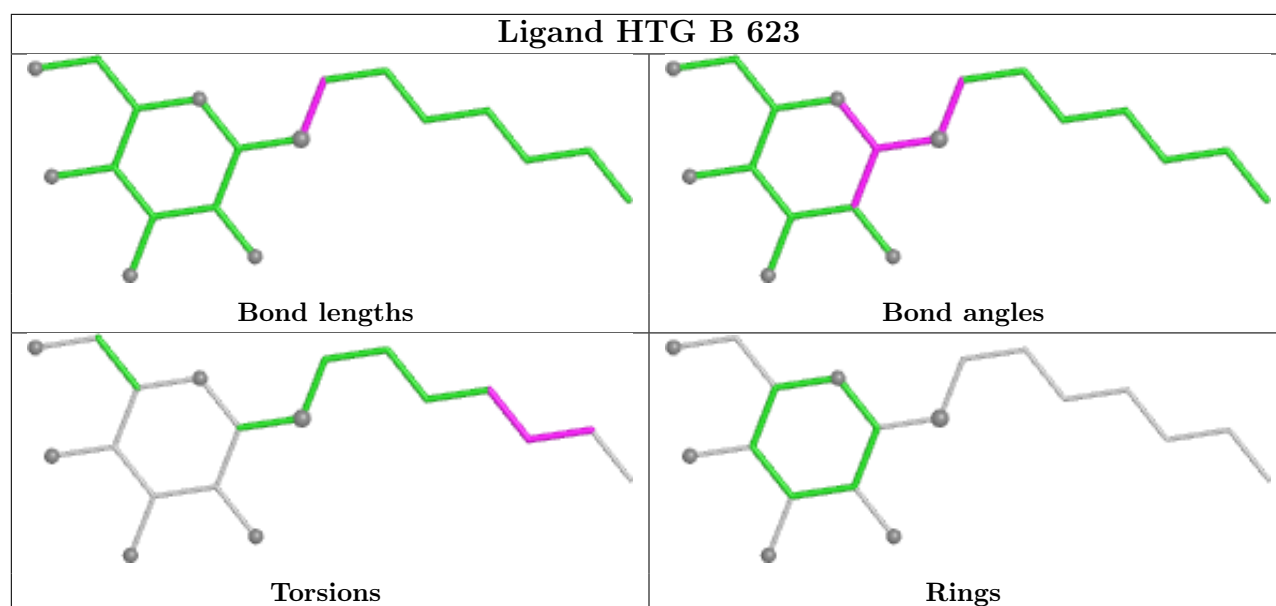


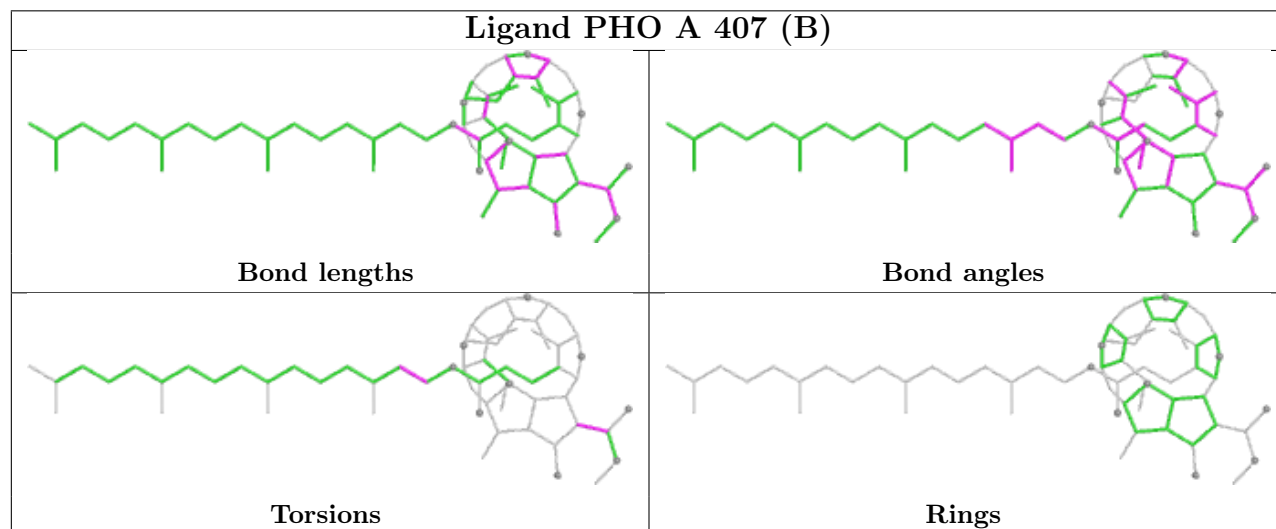
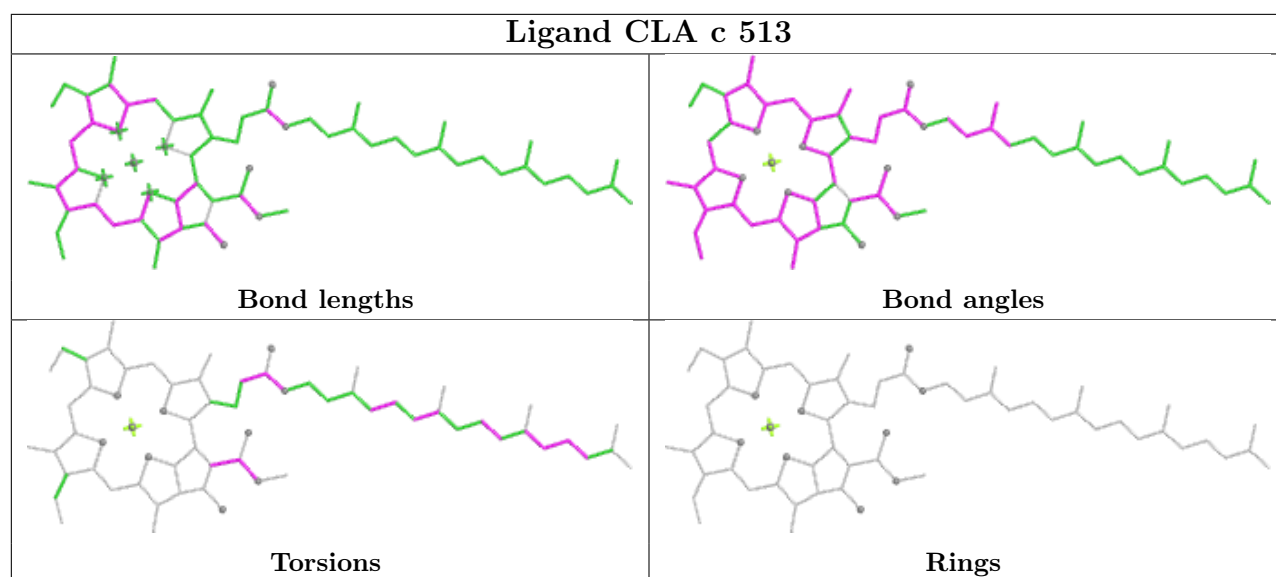


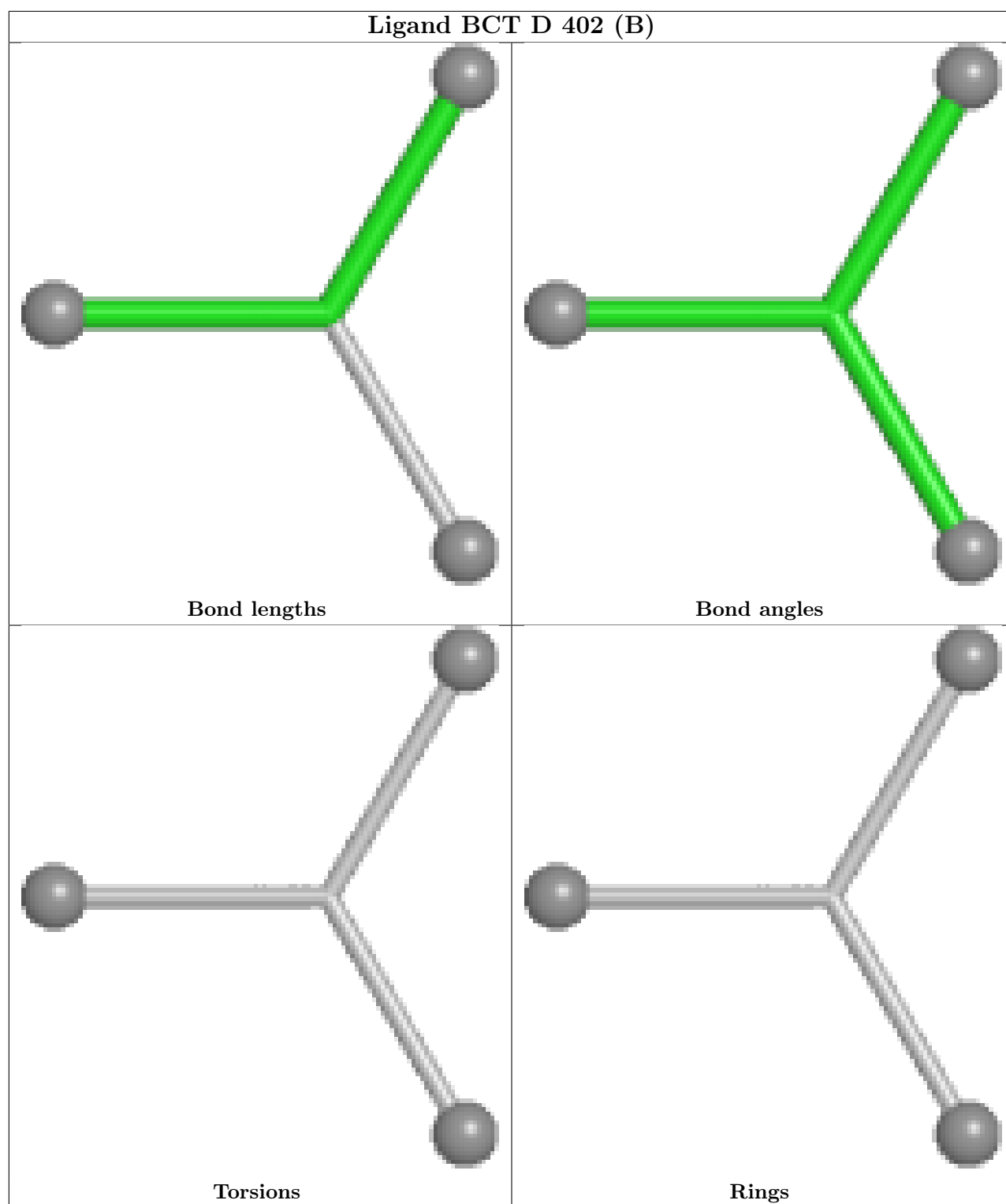
Ligand BCR A 409	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PHO a 408 (A)	
	
Bond lengths	Bond angles
	
Torsions	Rings

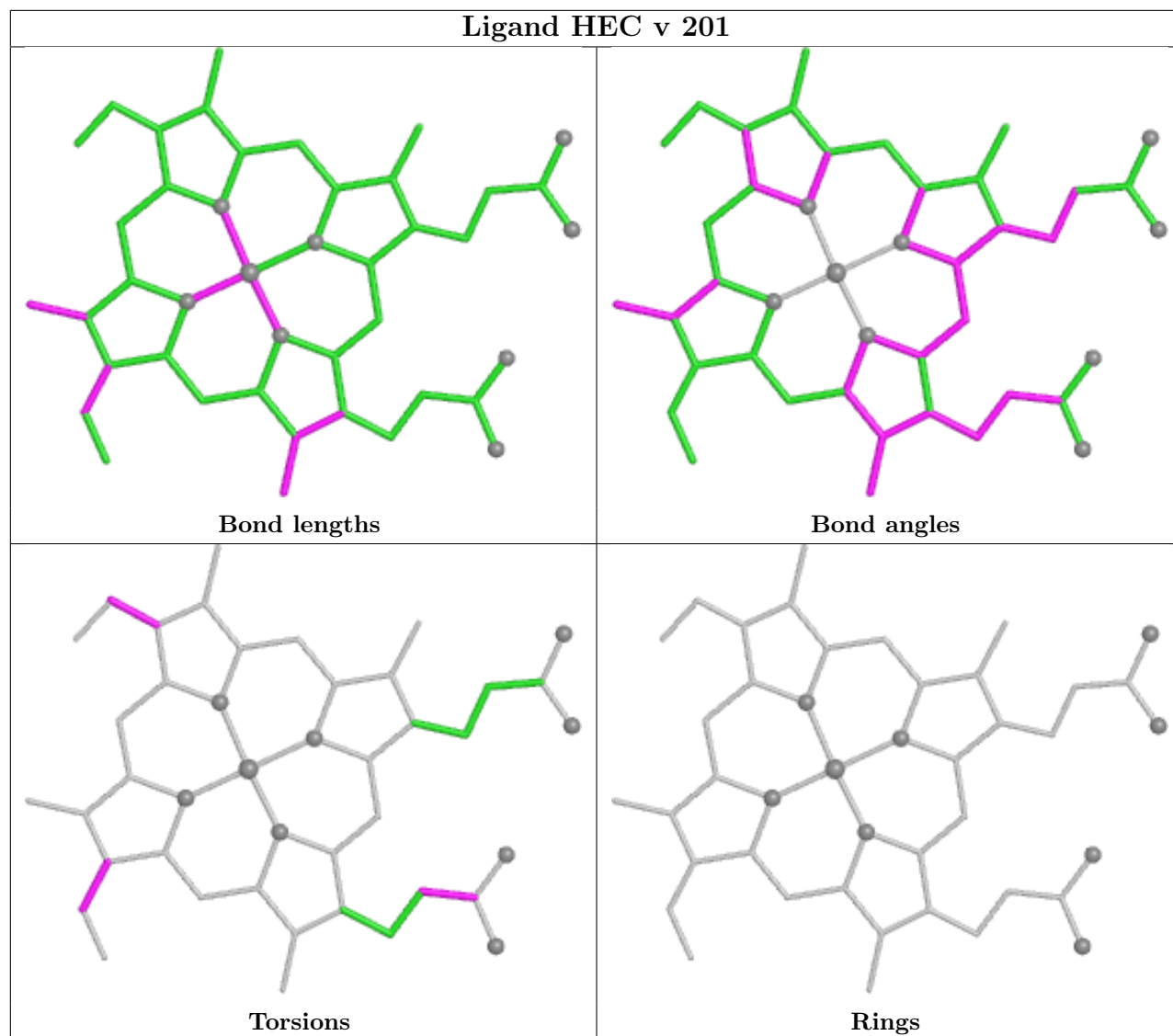
Ligand CLA D 404 (A)	
	
Bond lengths	Bond angles
	
Torsions	Rings



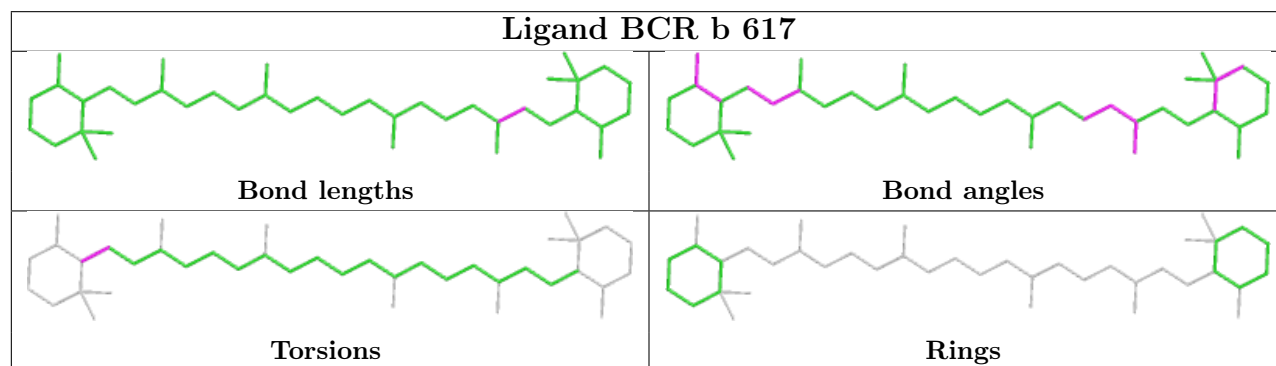




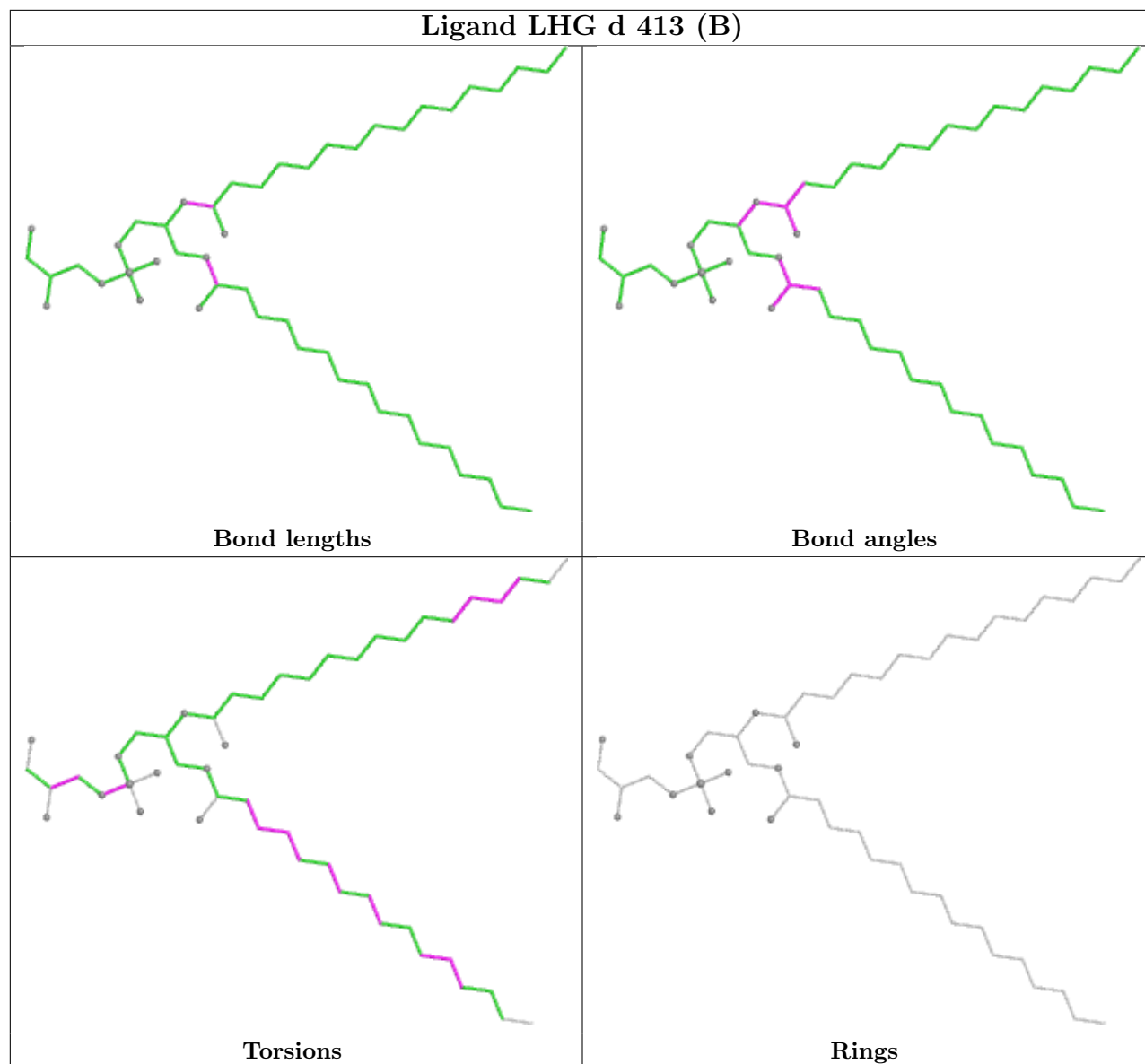
Ligand HEC v 201



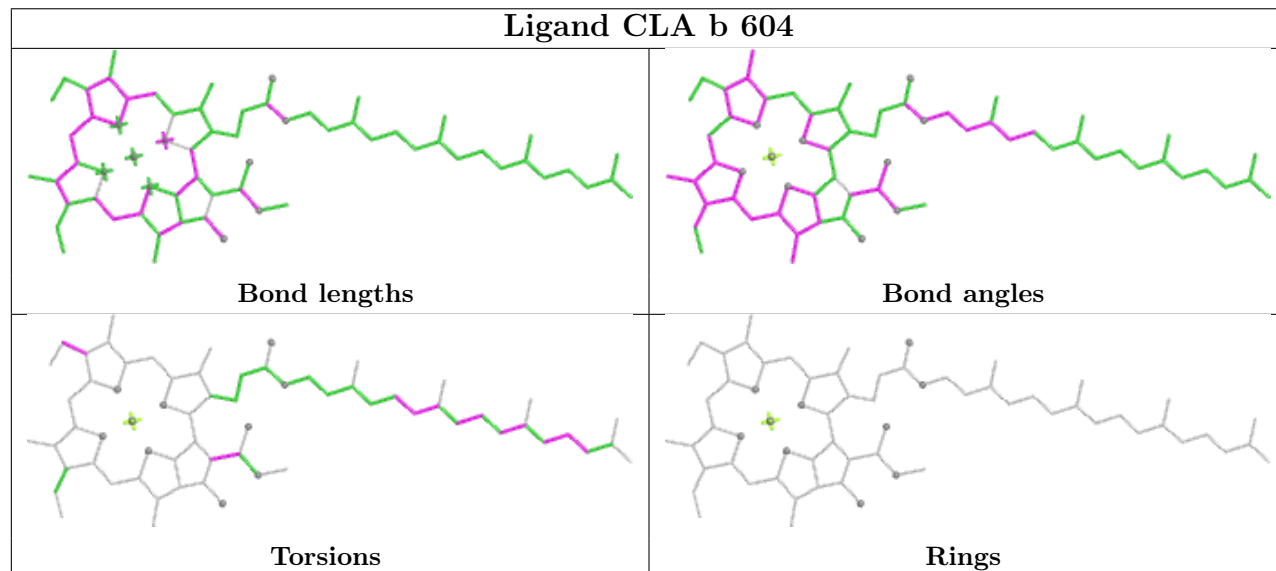
Ligand BCR b 617



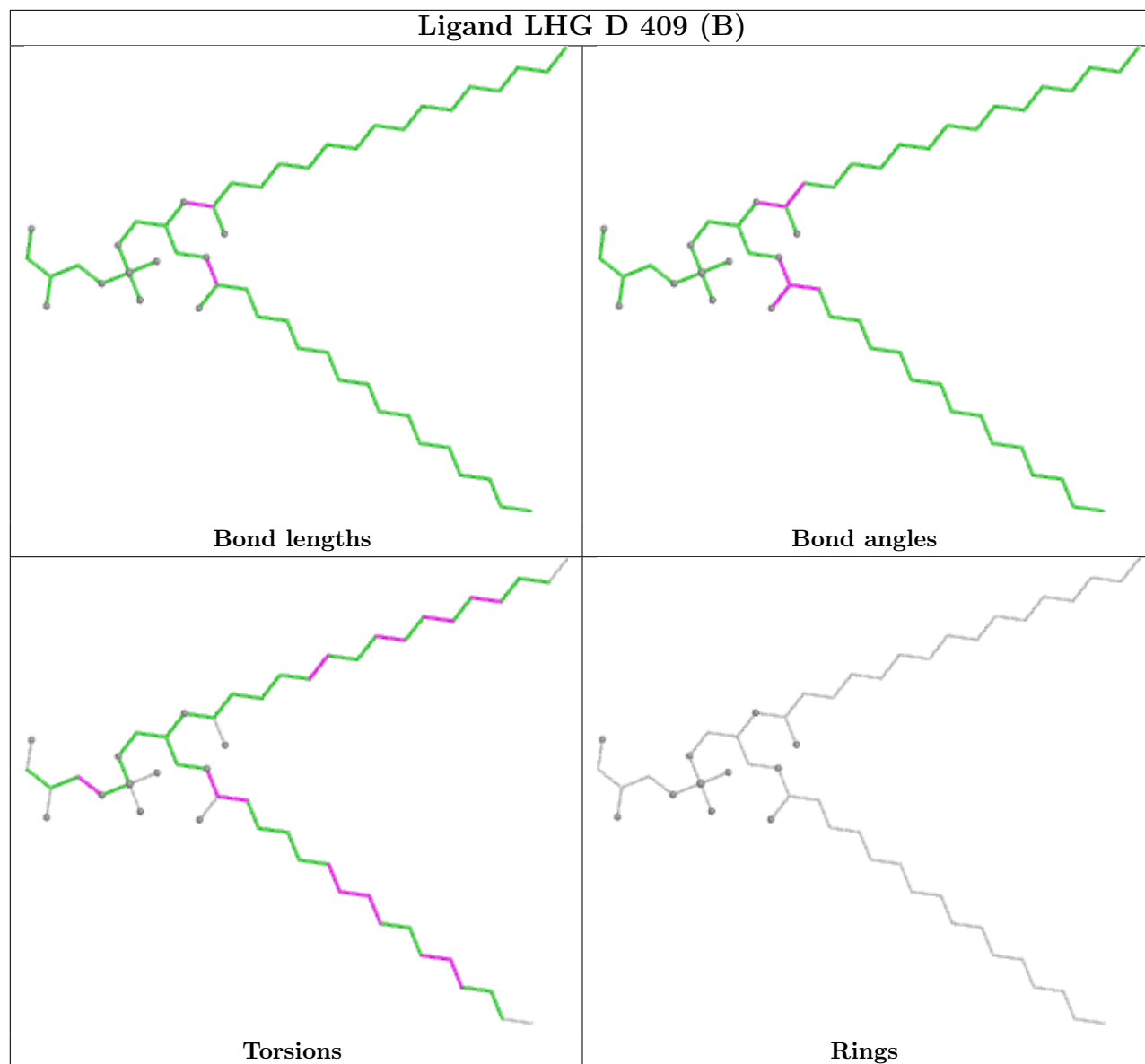
Ligand LHG d 413 (B)



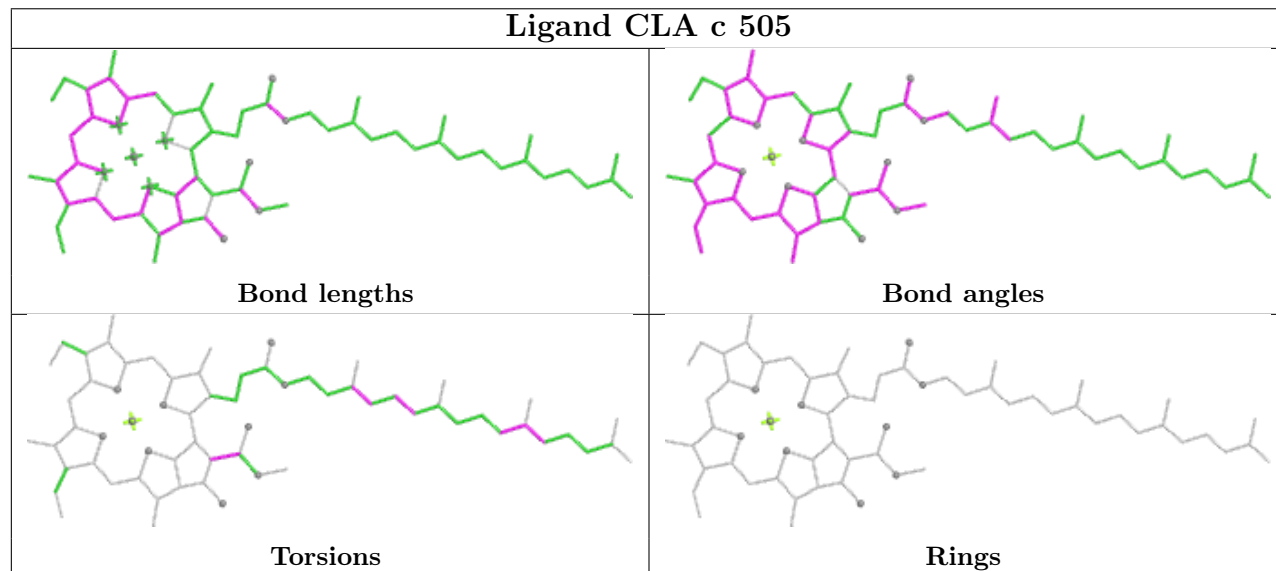
Ligand CLA b 604

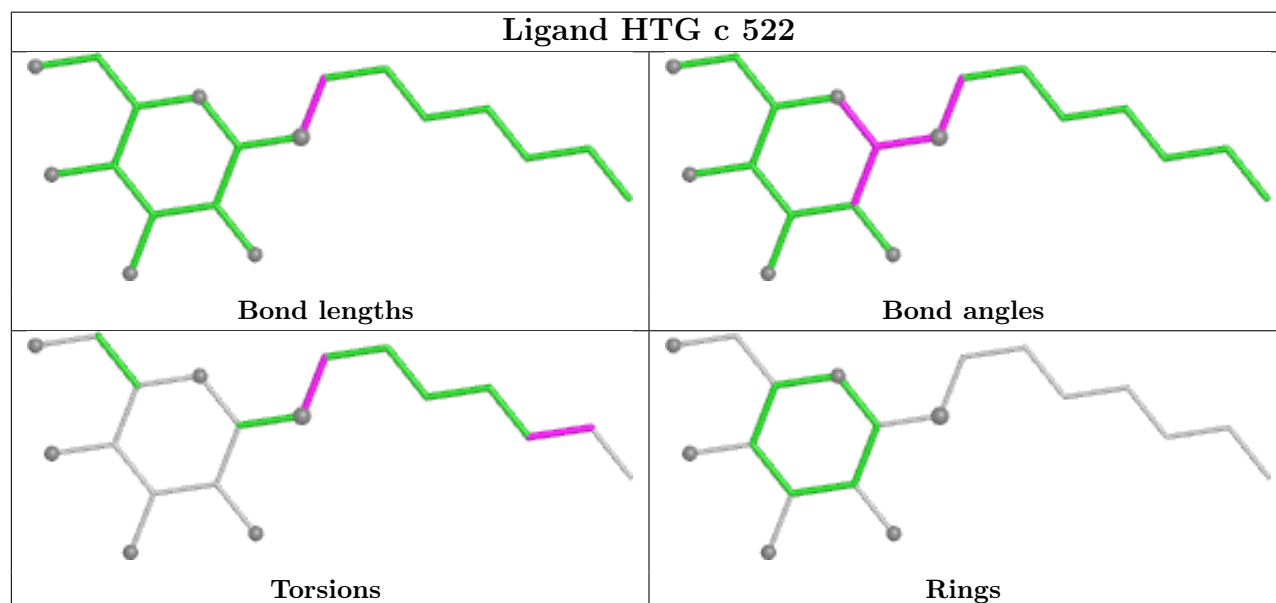
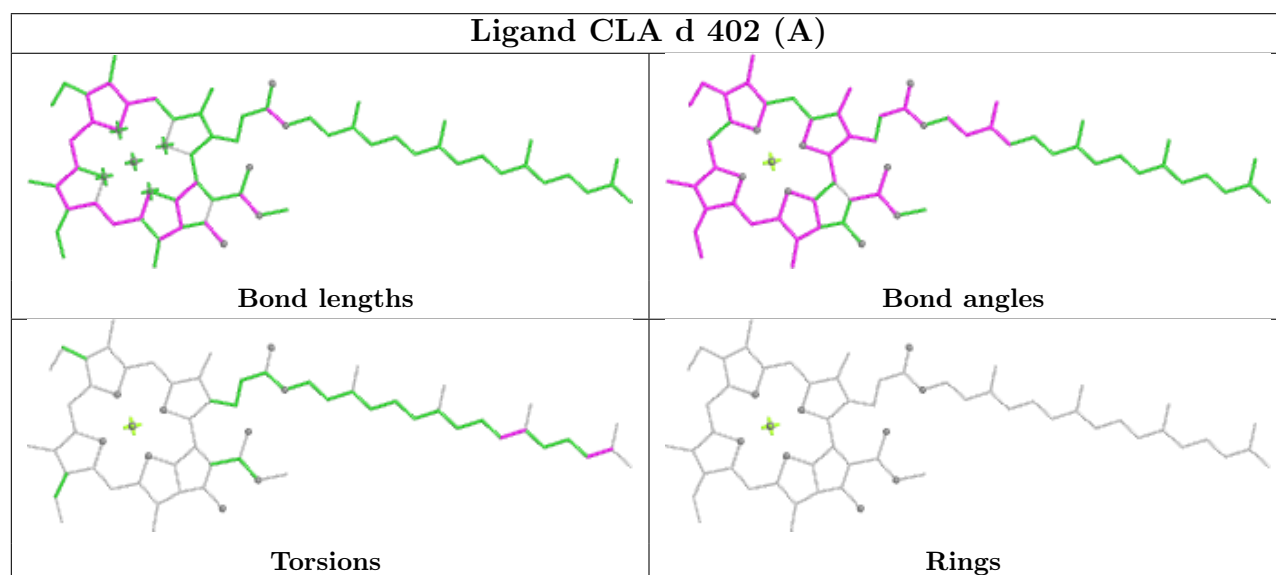
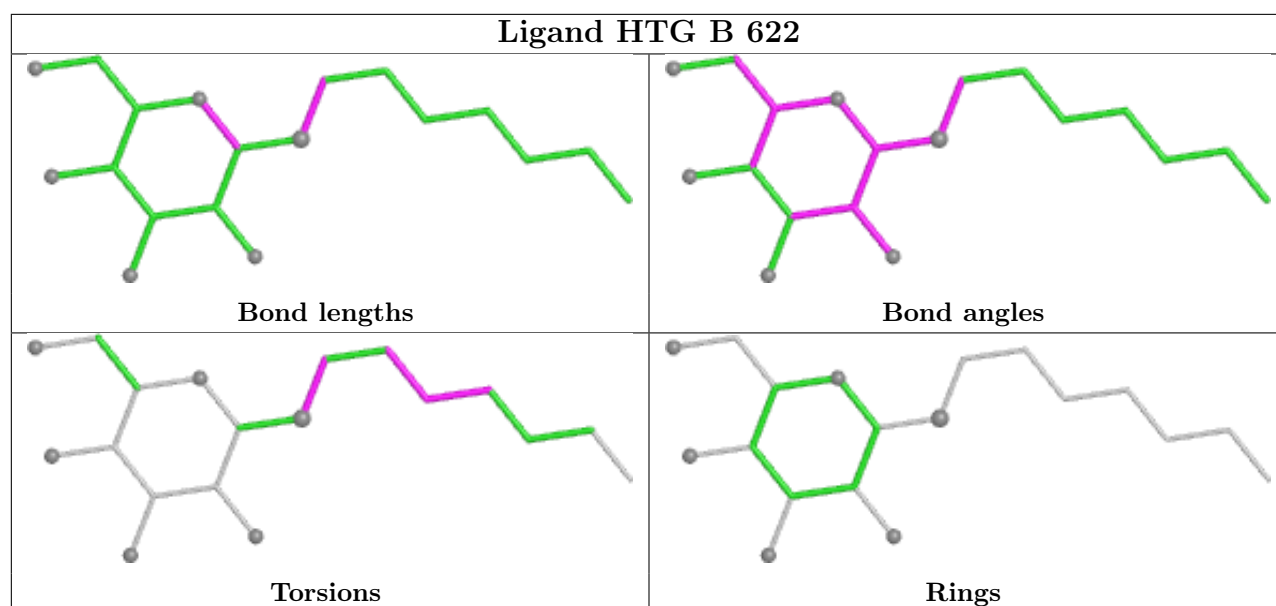


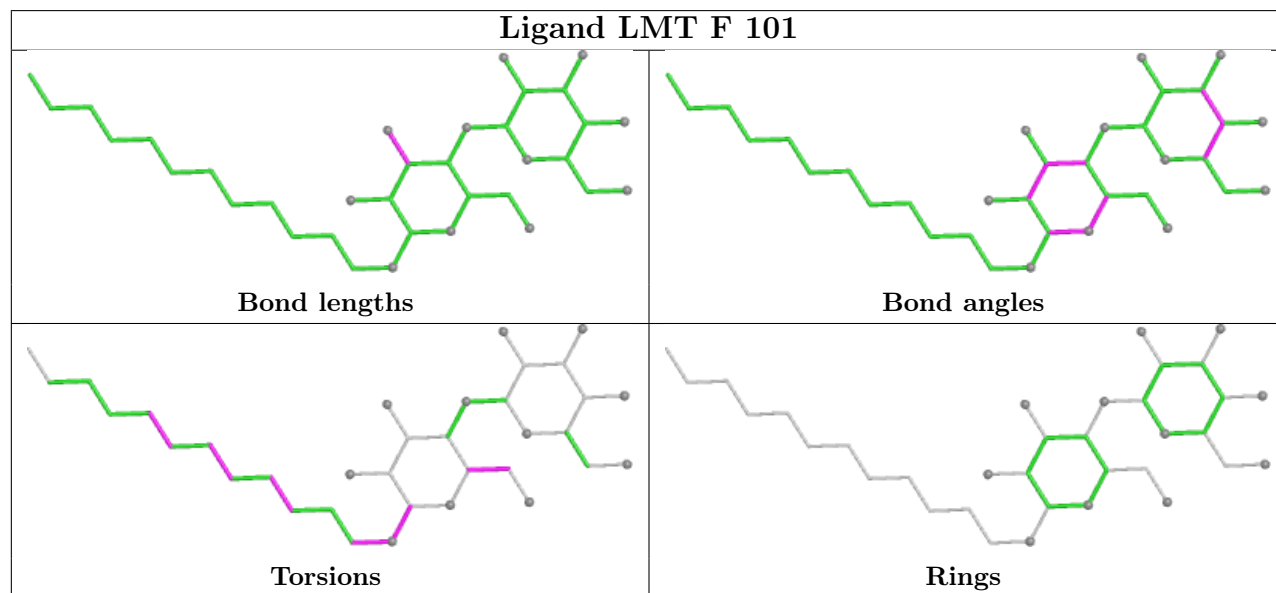
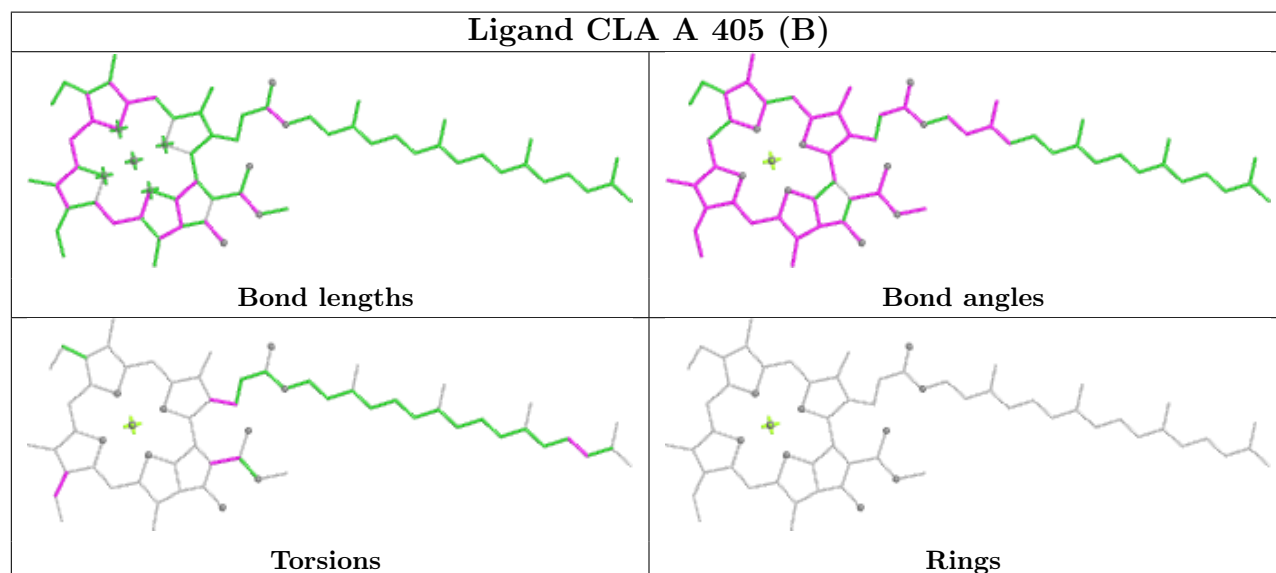
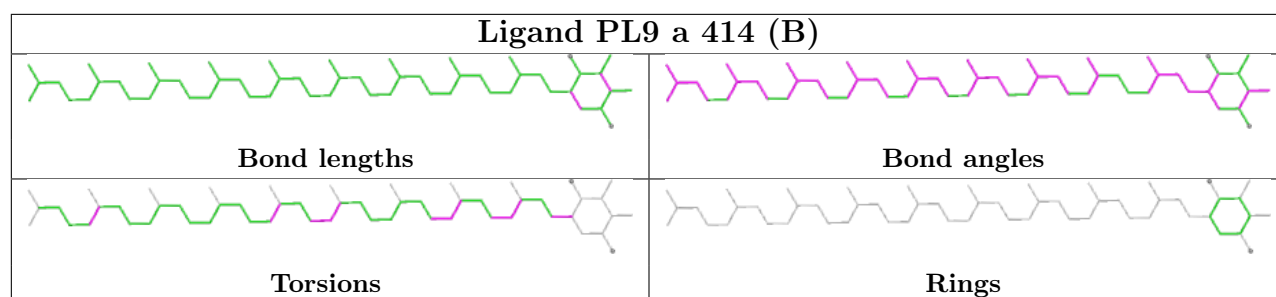
Ligand LHG D 409 (B)

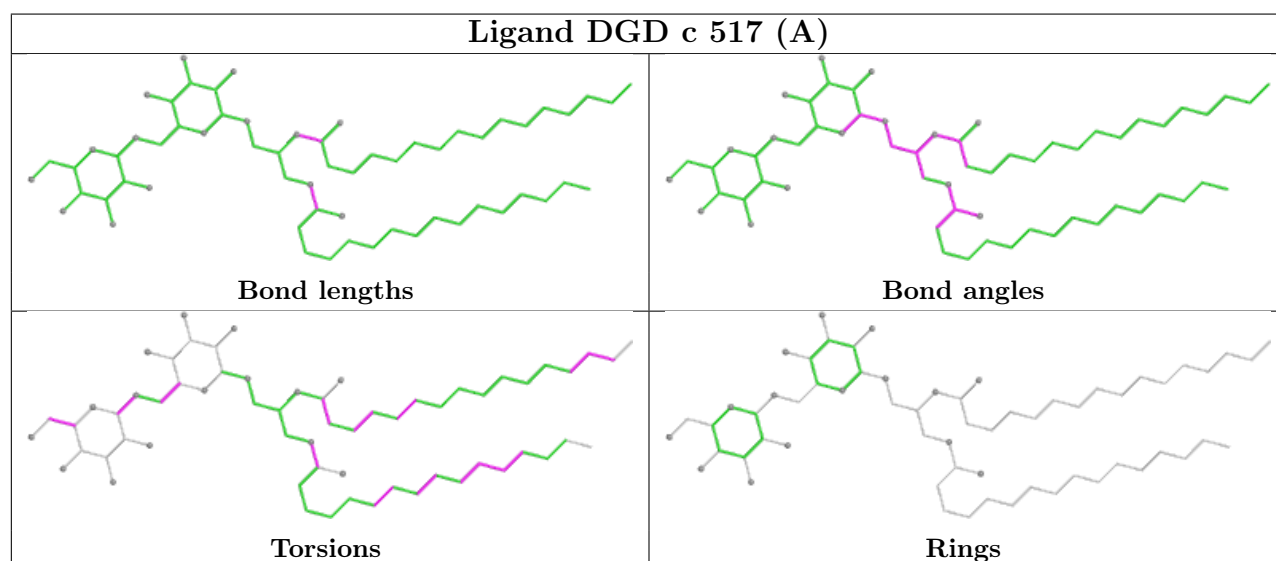
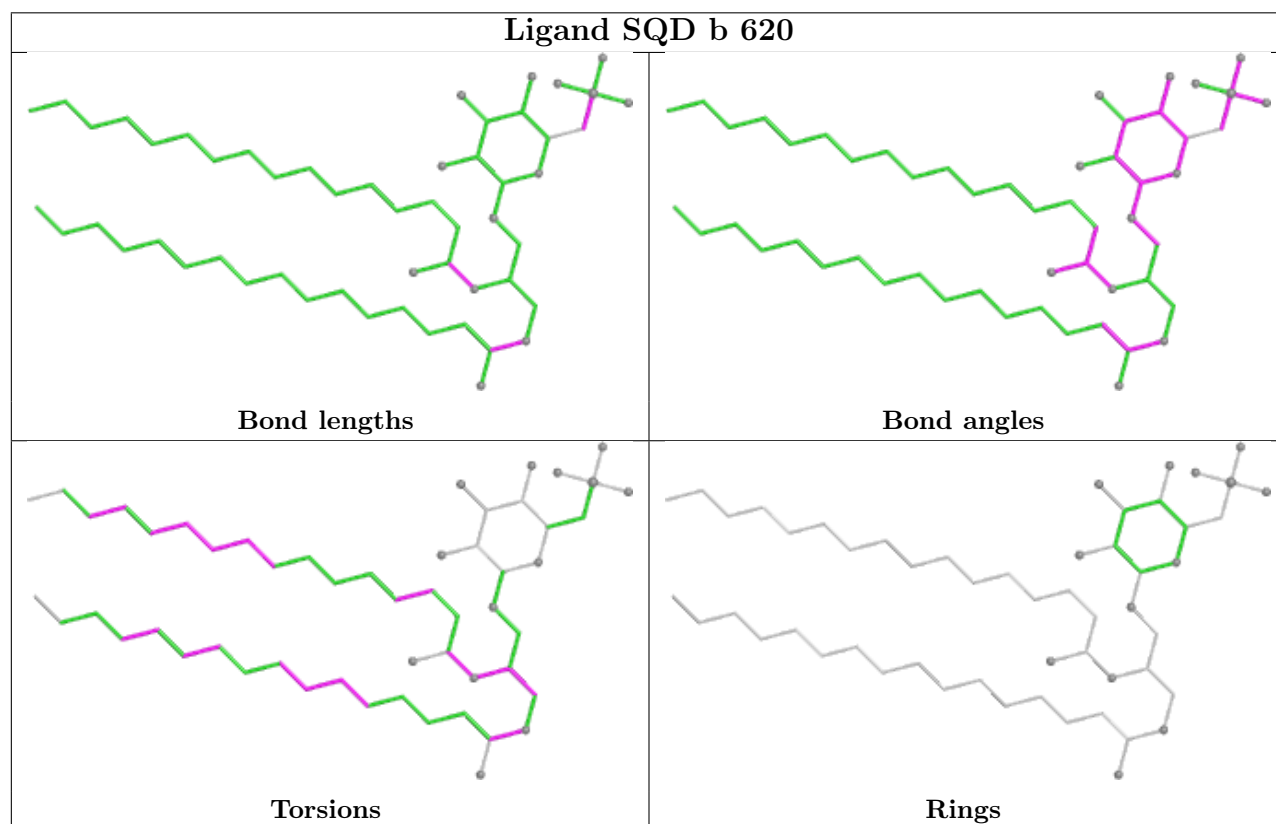
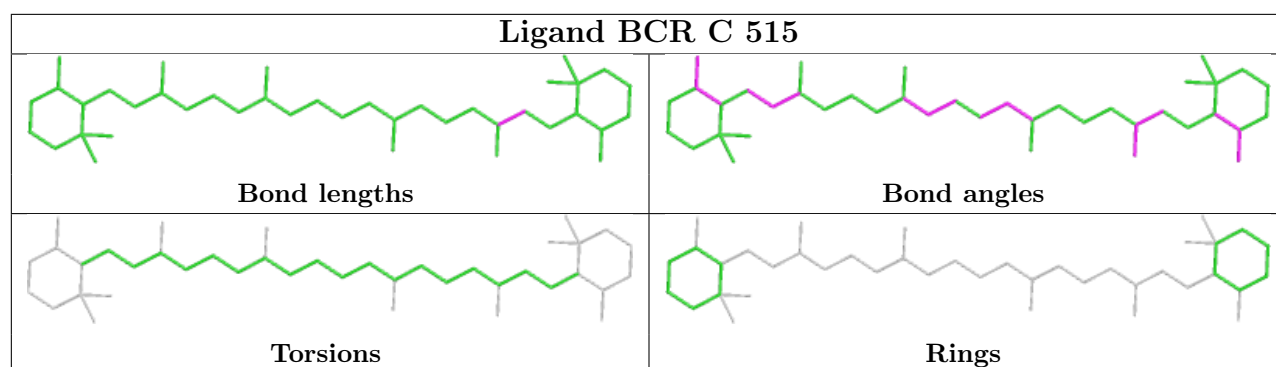


Ligand CLA c 505

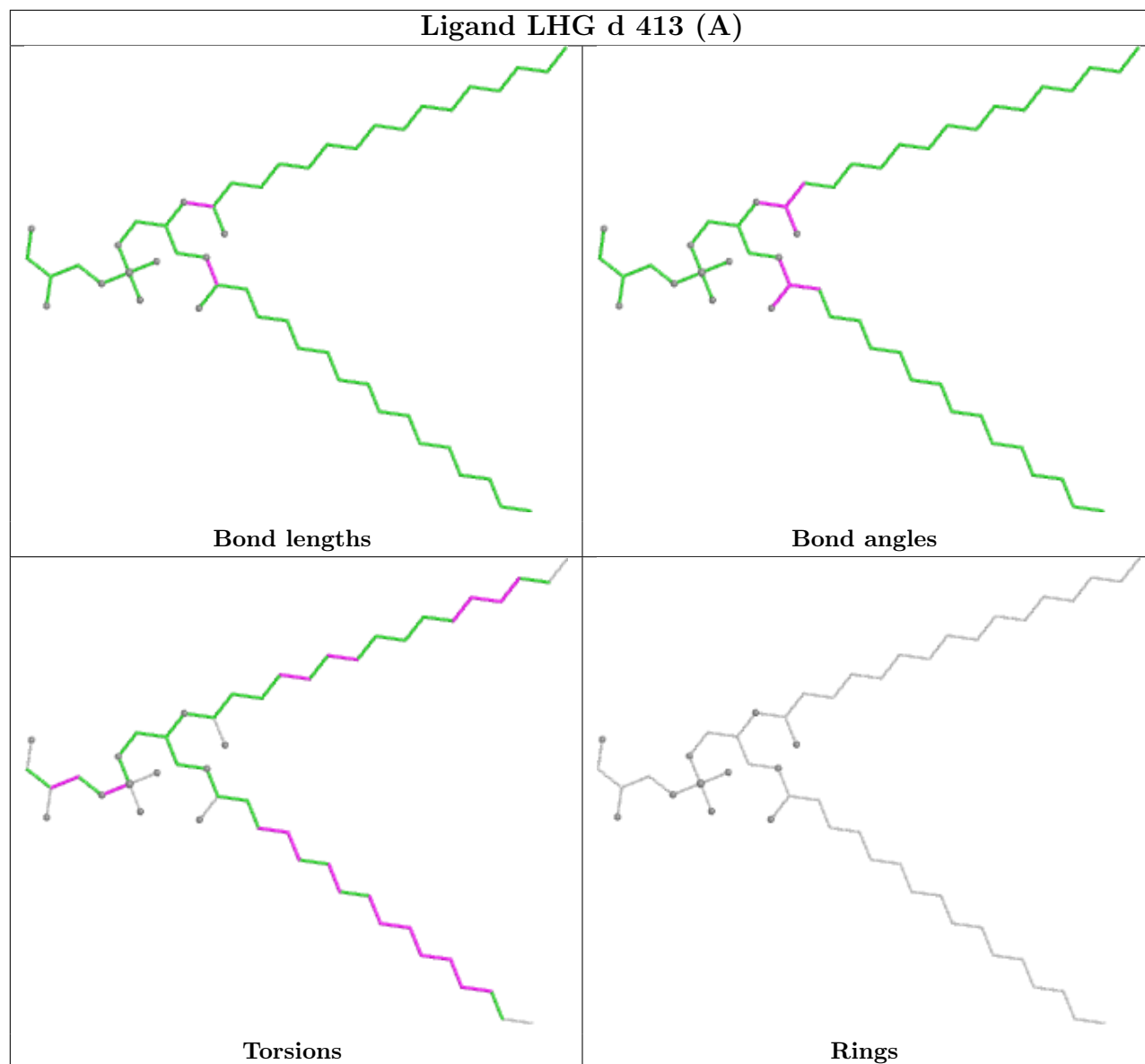




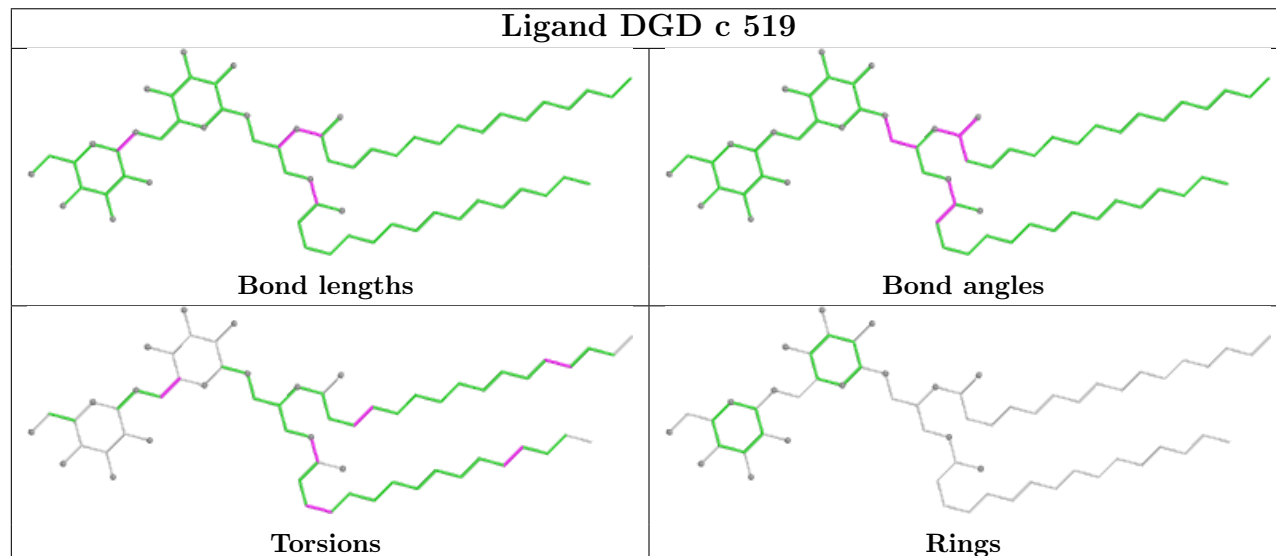




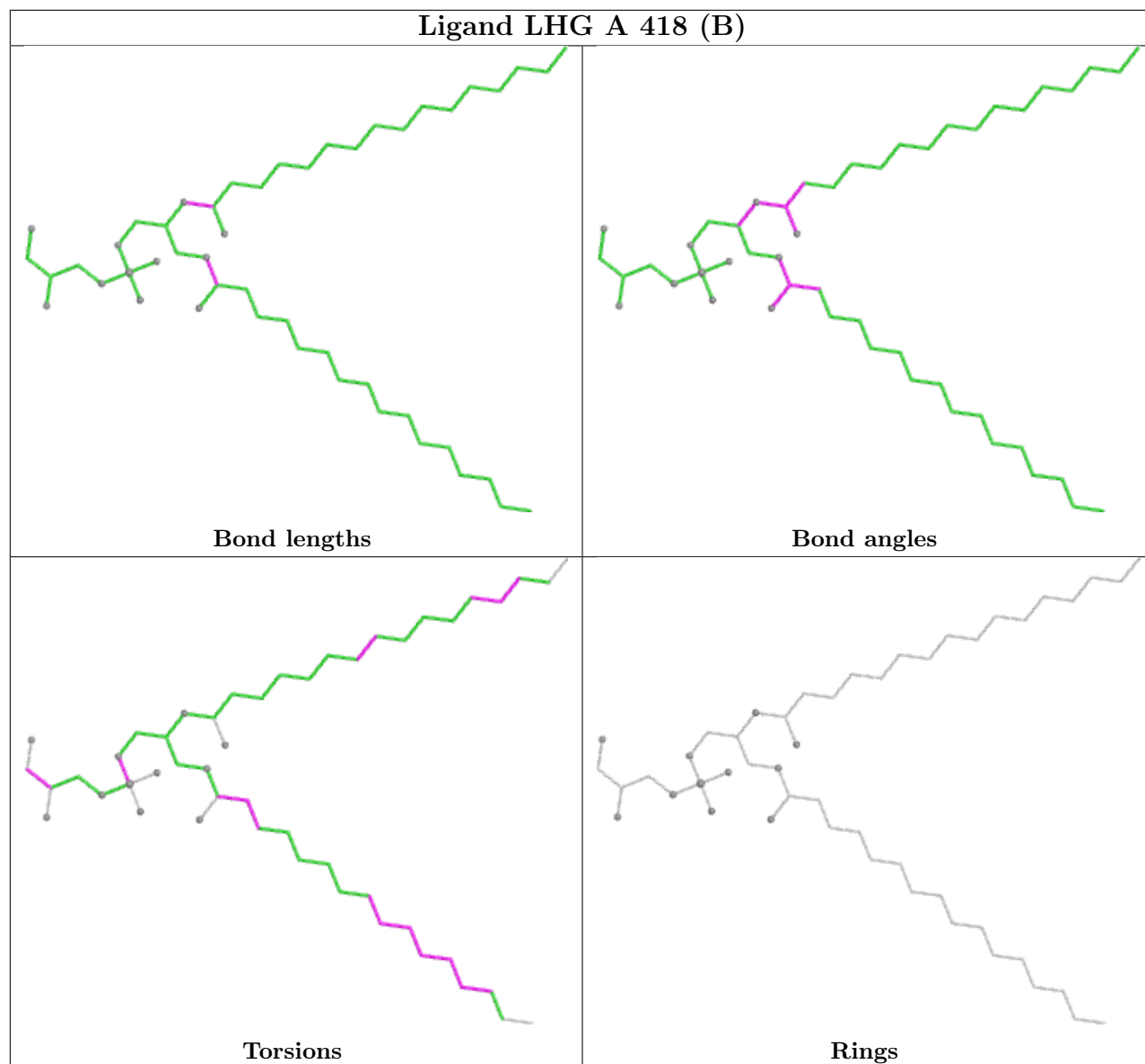
Ligand LHG d 413 (A)



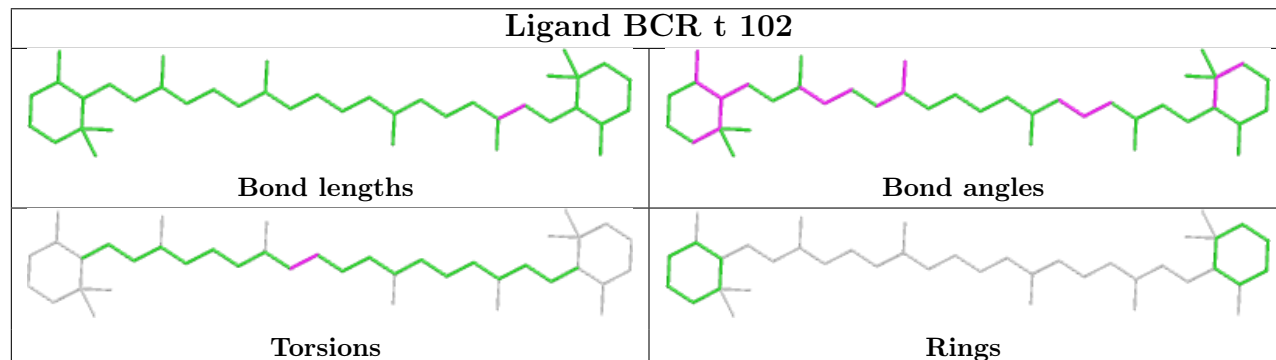
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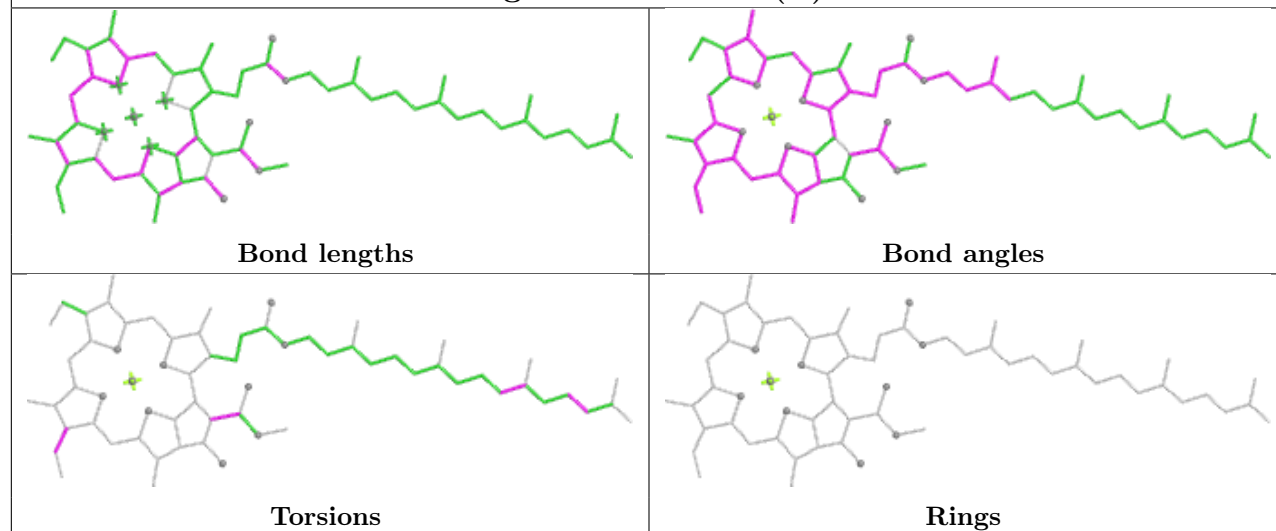
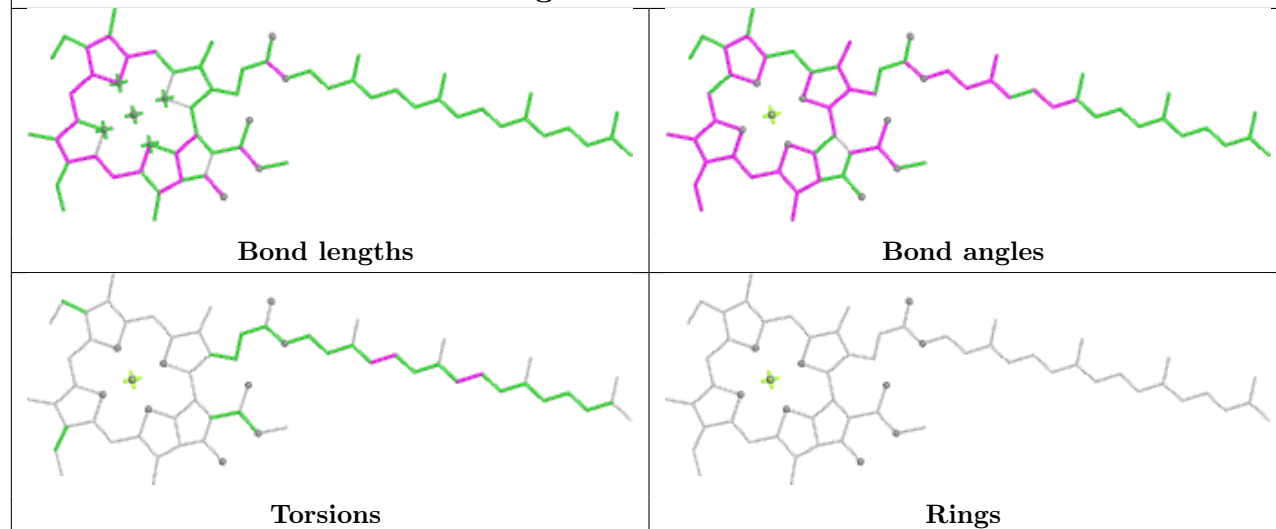


Ligand LHG A 418 (B)

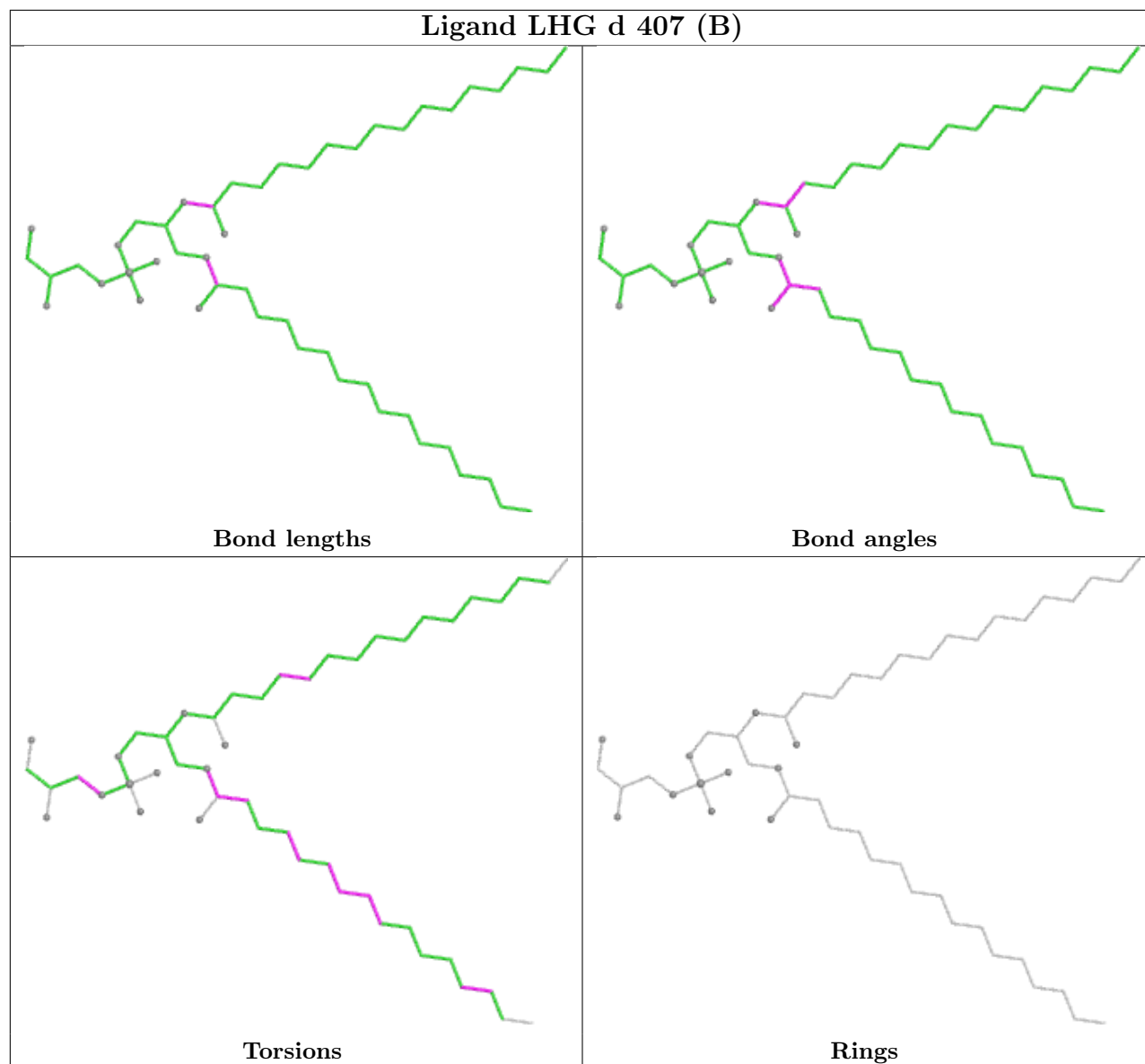


Ligand BCR t 102

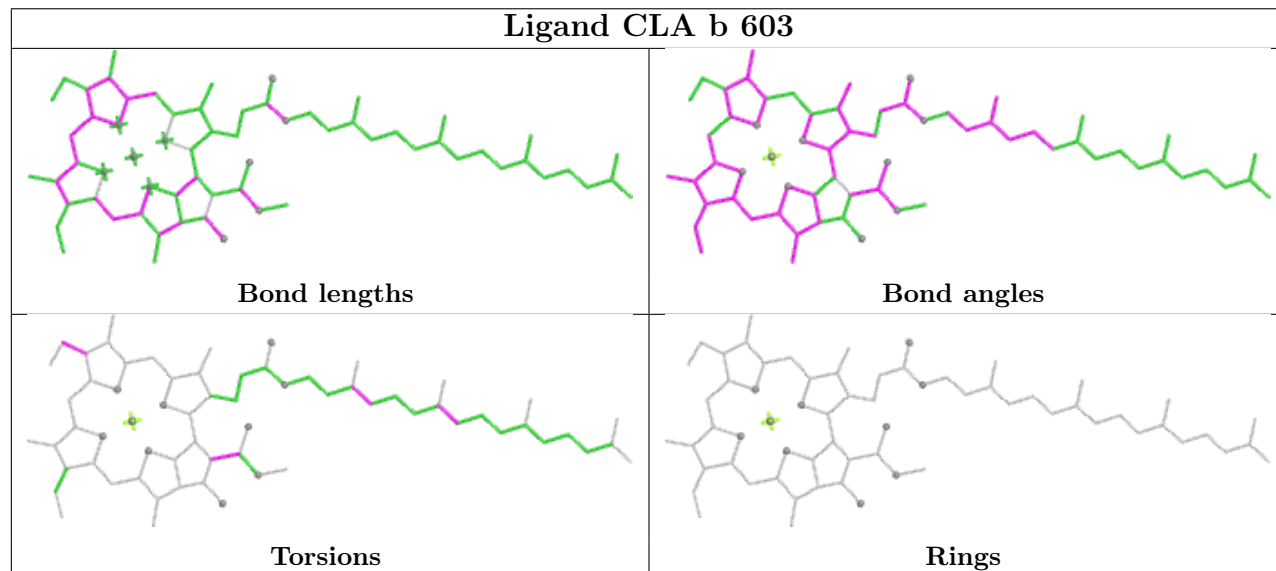


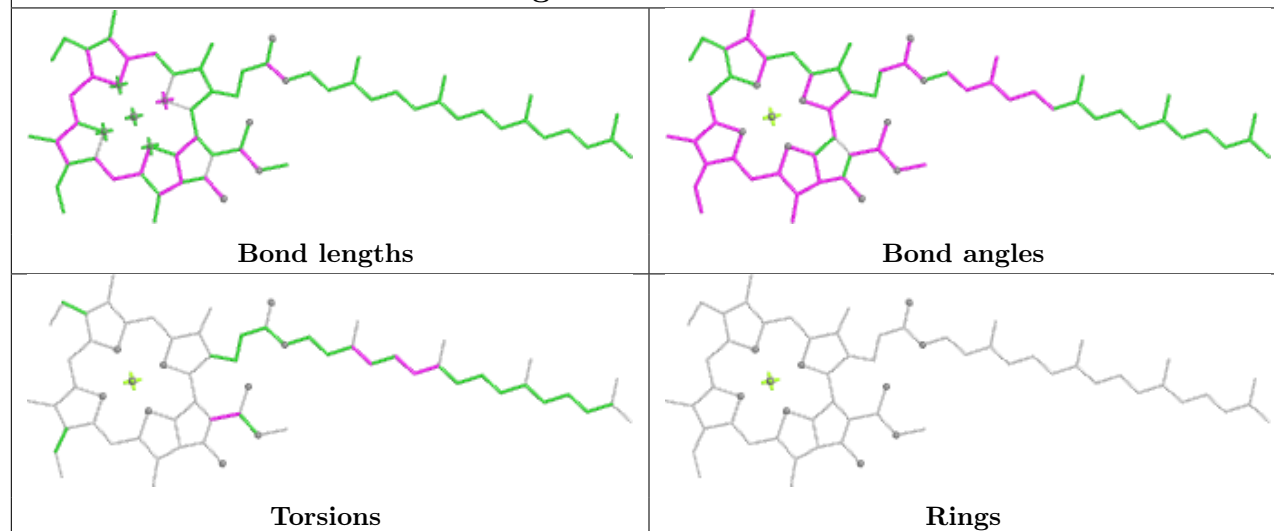
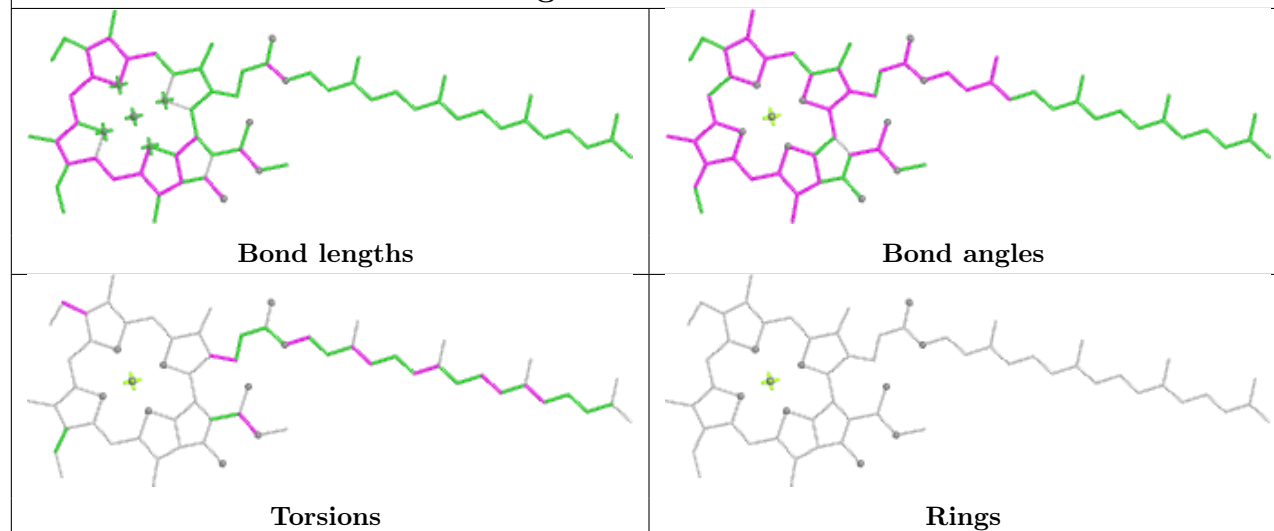
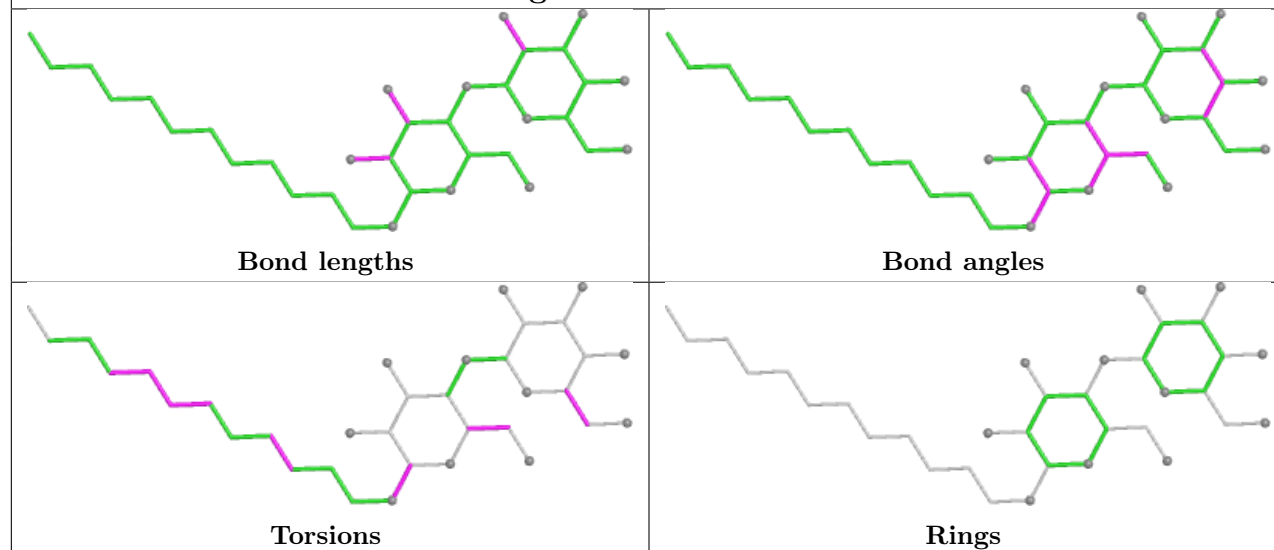
Ligand CLA a 406 (B)**Ligand CLA b 607**

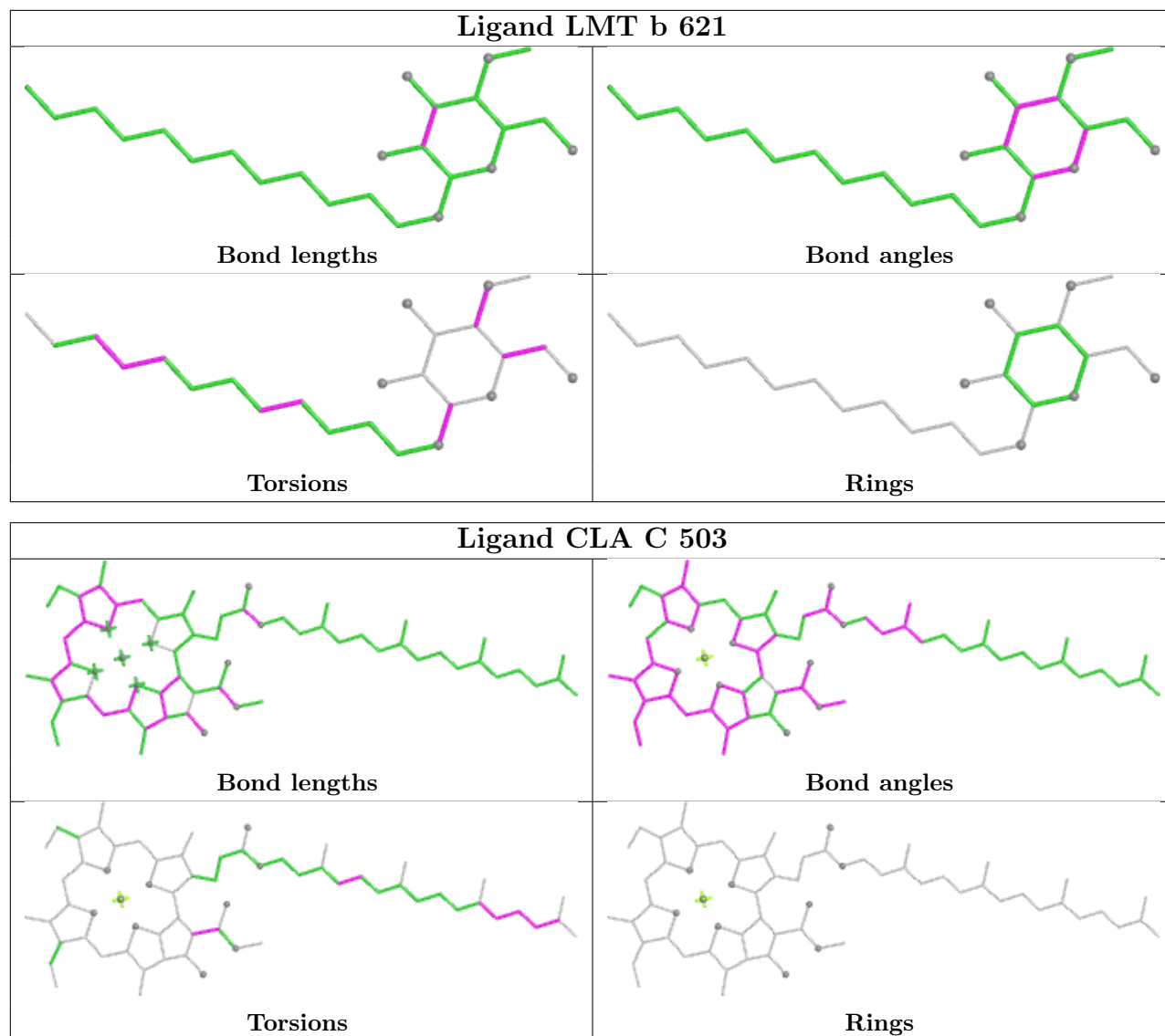
Ligand LHG d 407 (B)



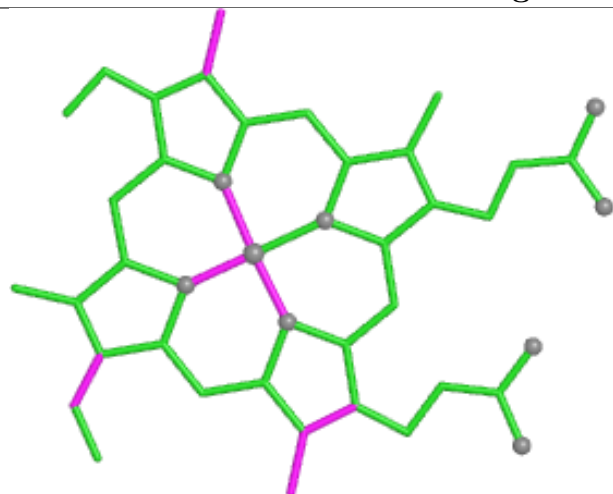
Ligand CLA b 603



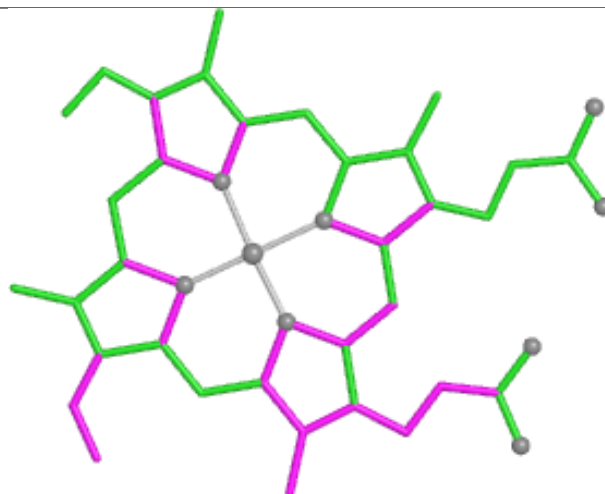
Ligand CLA B 605**Ligand CLA c 514****Ligand LMT B 630**



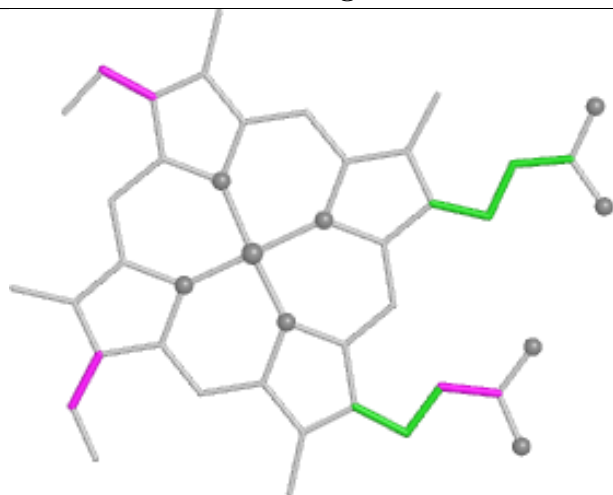
Ligand HEC V 201



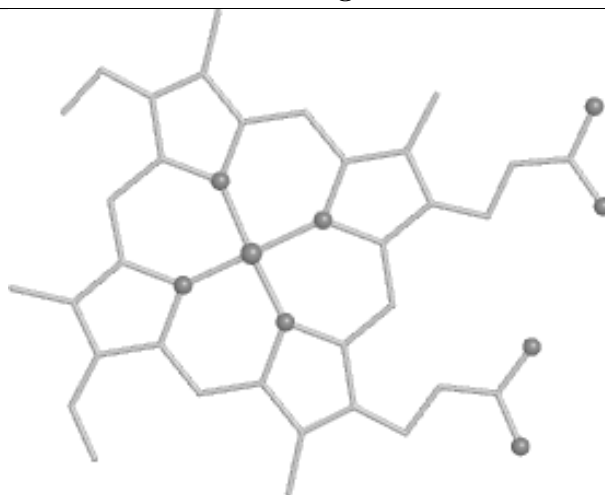
Bond lengths



Bond angles

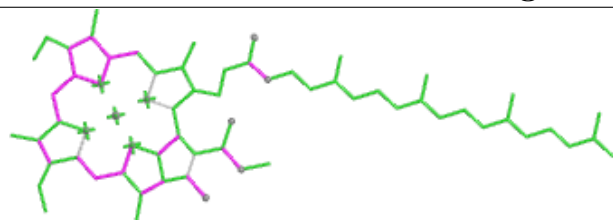


Torsions

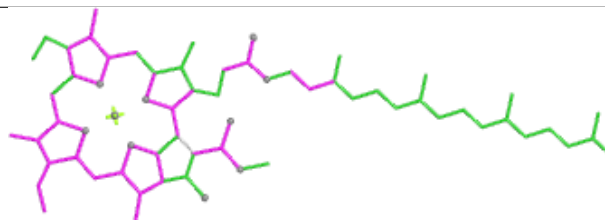


Rings

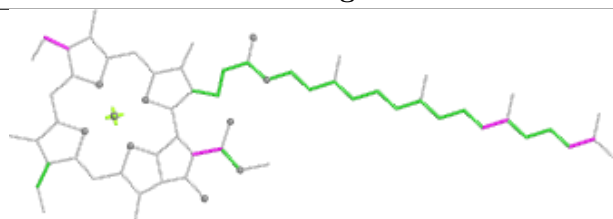
Ligand CLA c 503



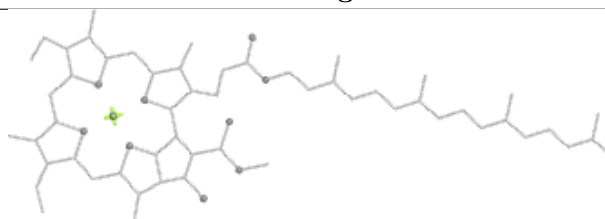
Bond lengths



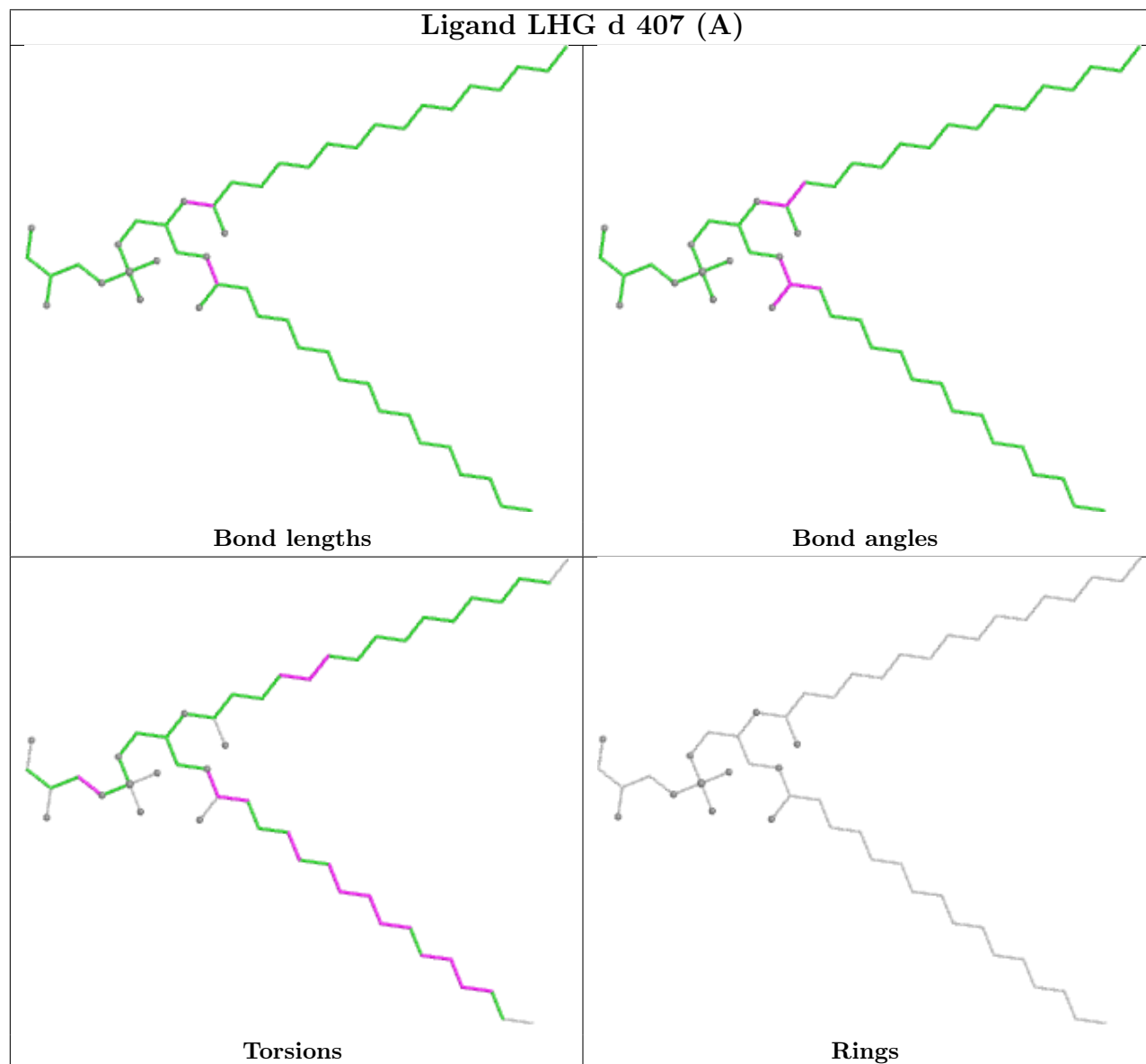
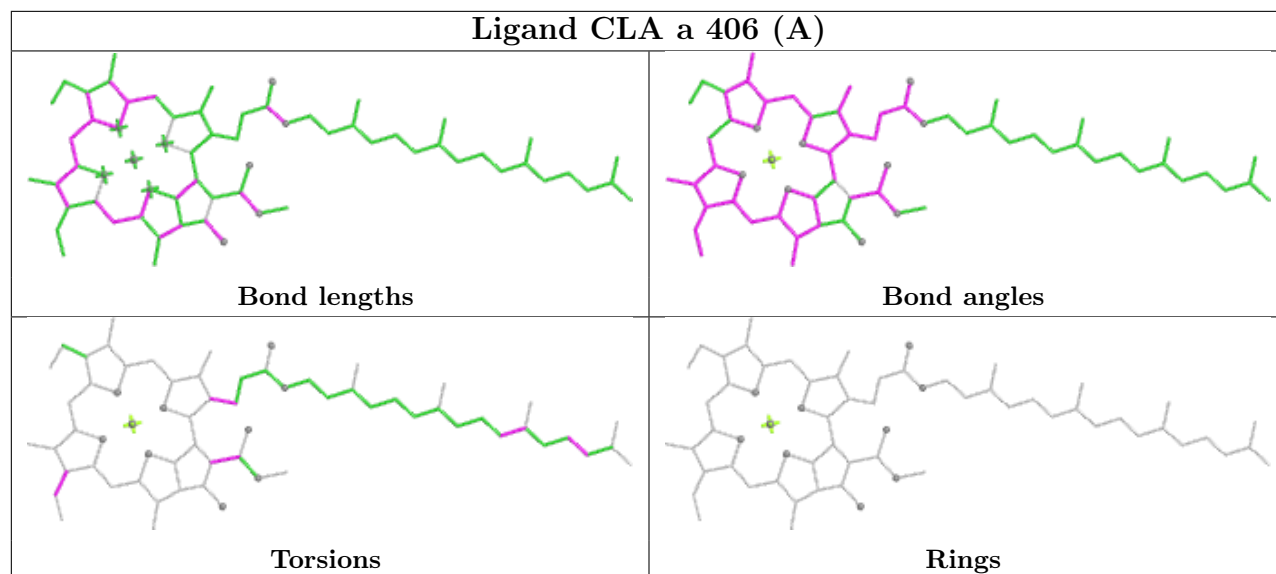
Bond angles

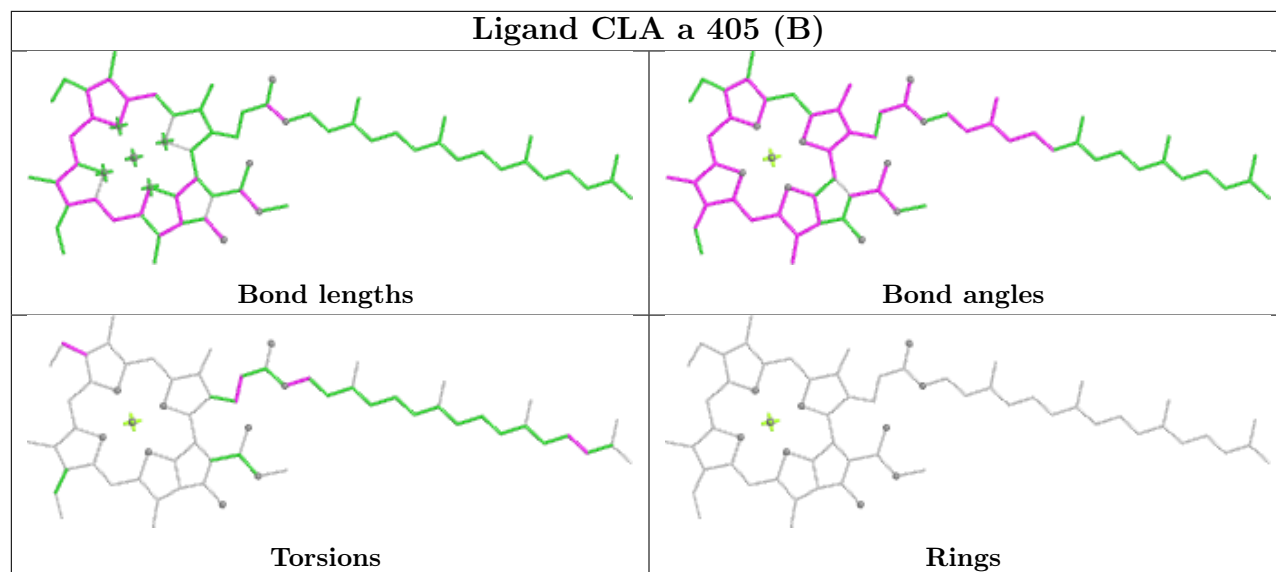
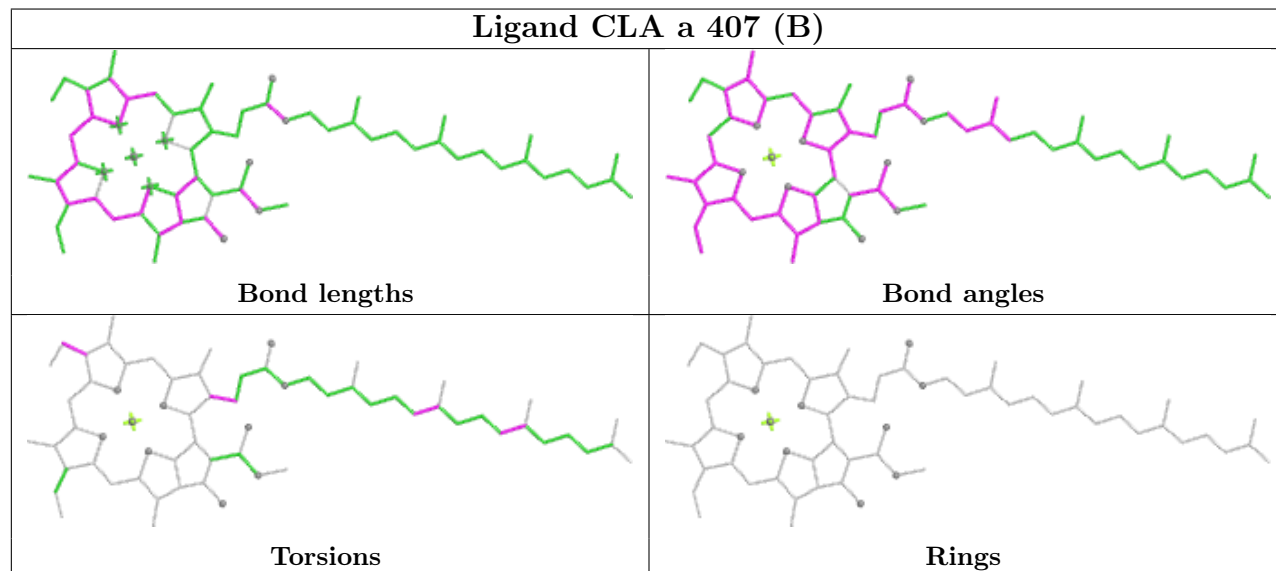


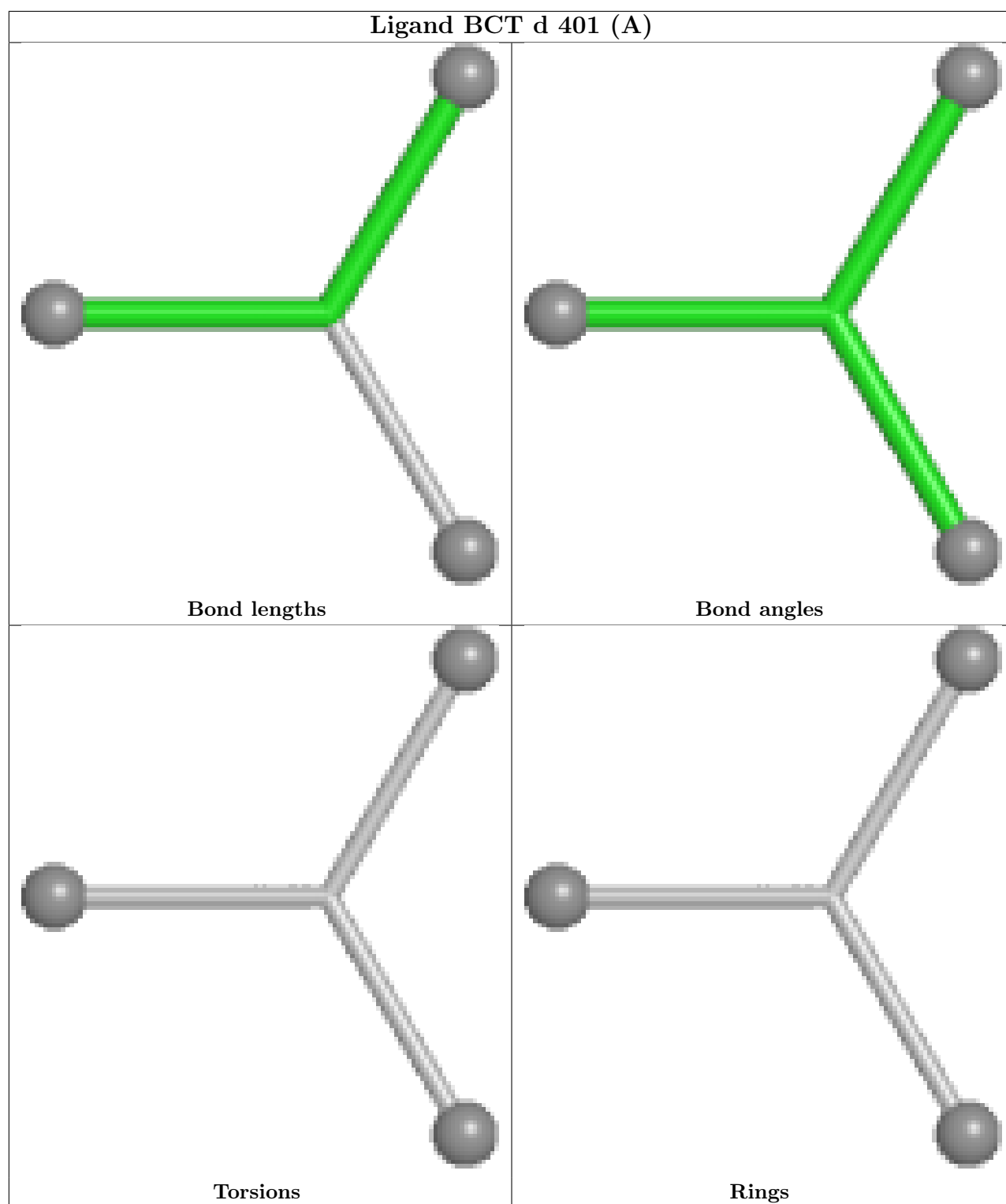
Torsions

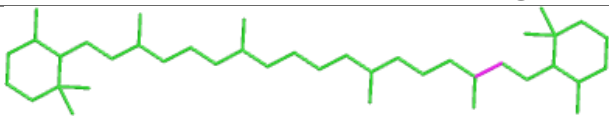
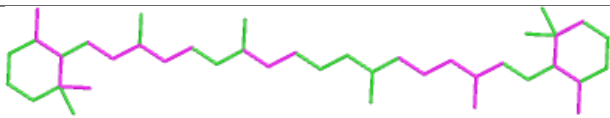
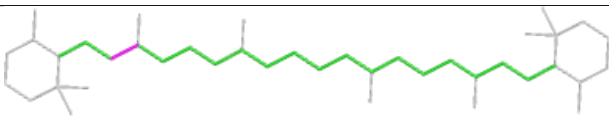
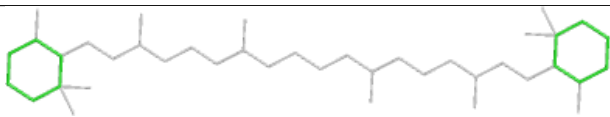


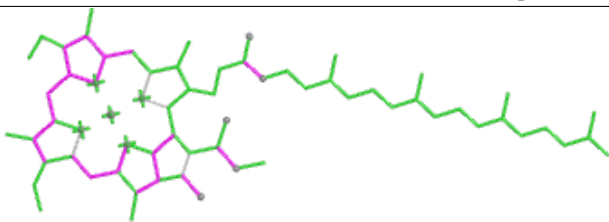
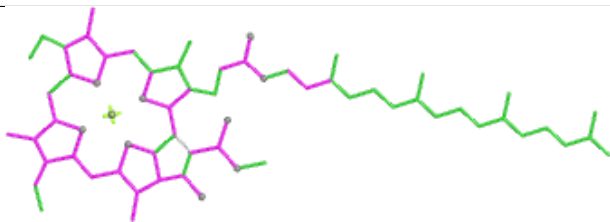
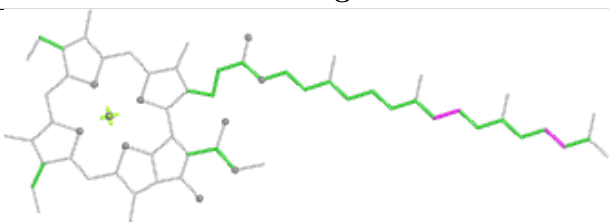
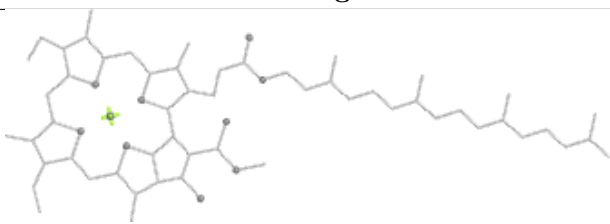
Rings

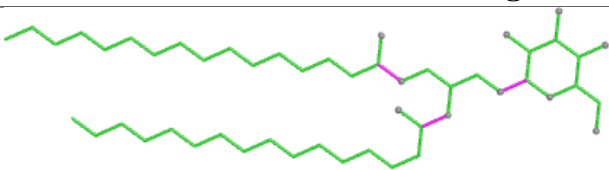
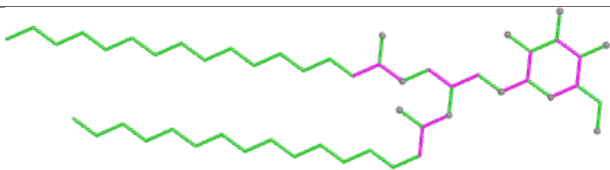
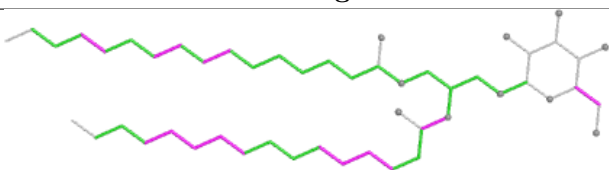
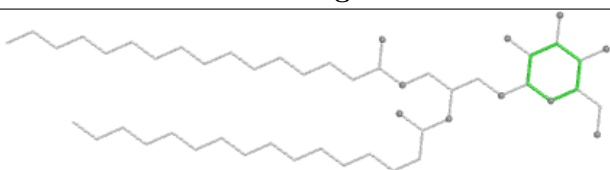


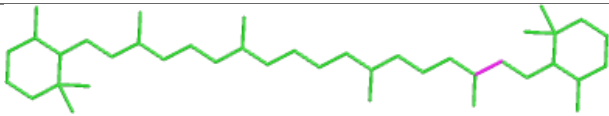
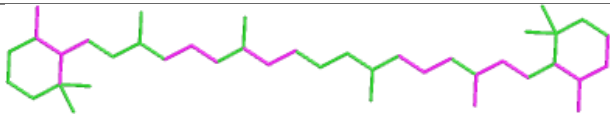
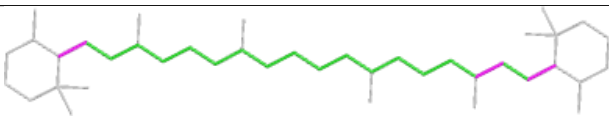
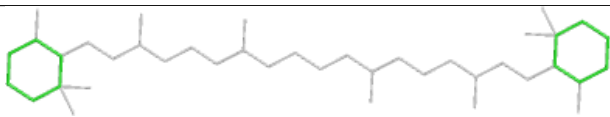
Ligand CLA a 405 (B)**Ligand CLA a 407 (B)**

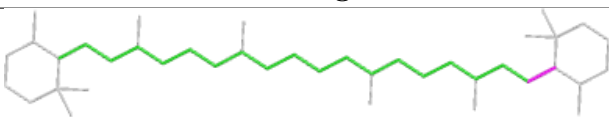
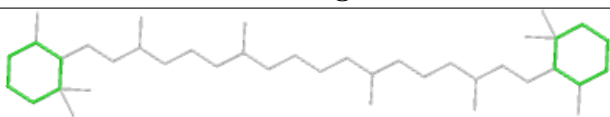


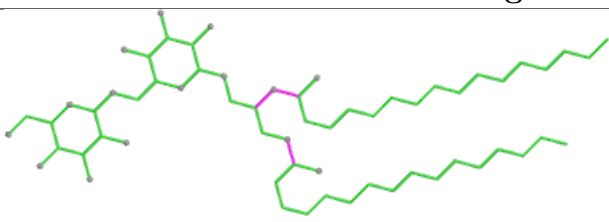
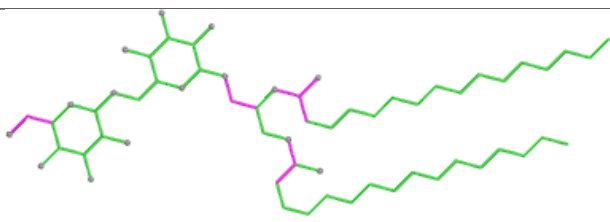
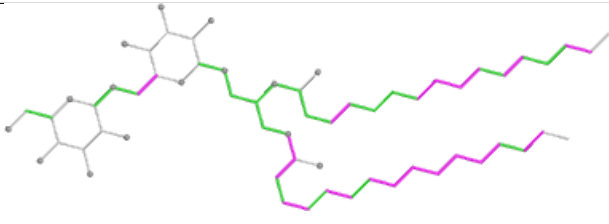
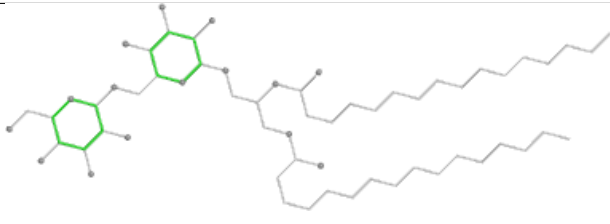
Ligand BCR c 516	
	
Bond lengths	Bond angles
	
Torsions	Rings

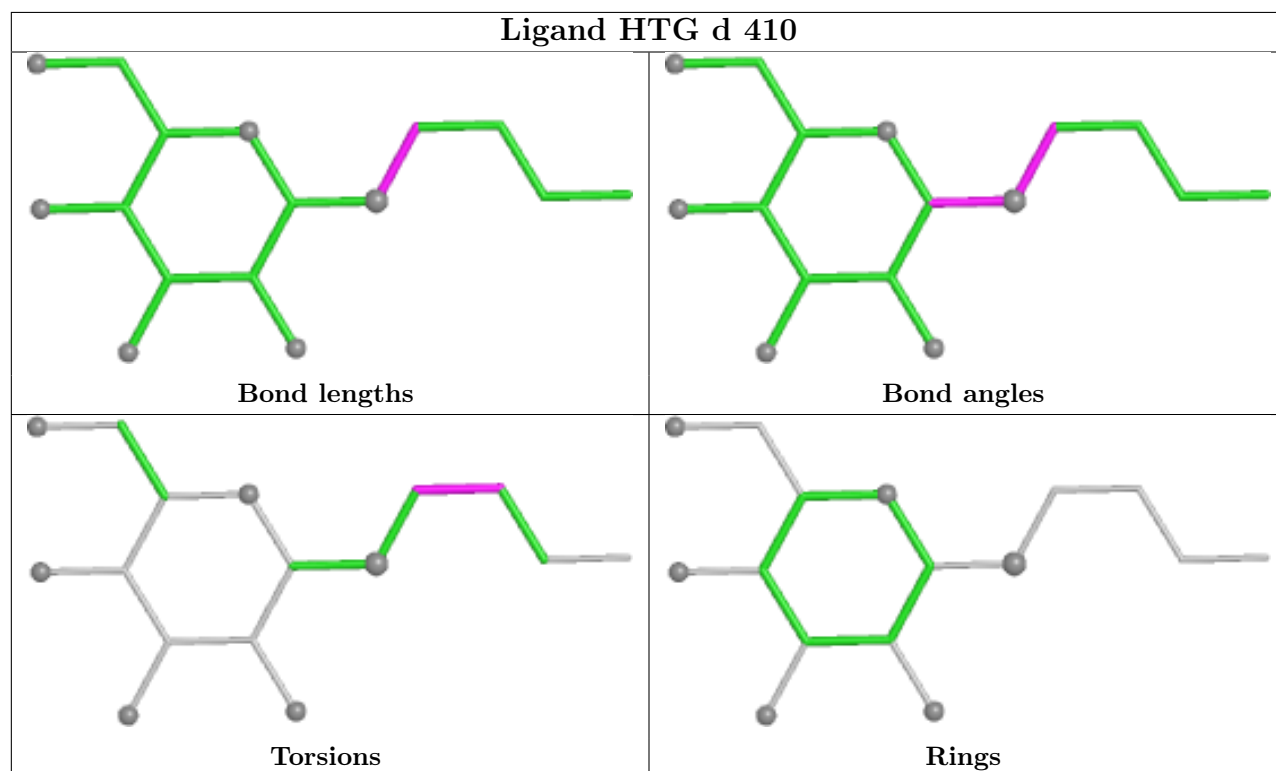
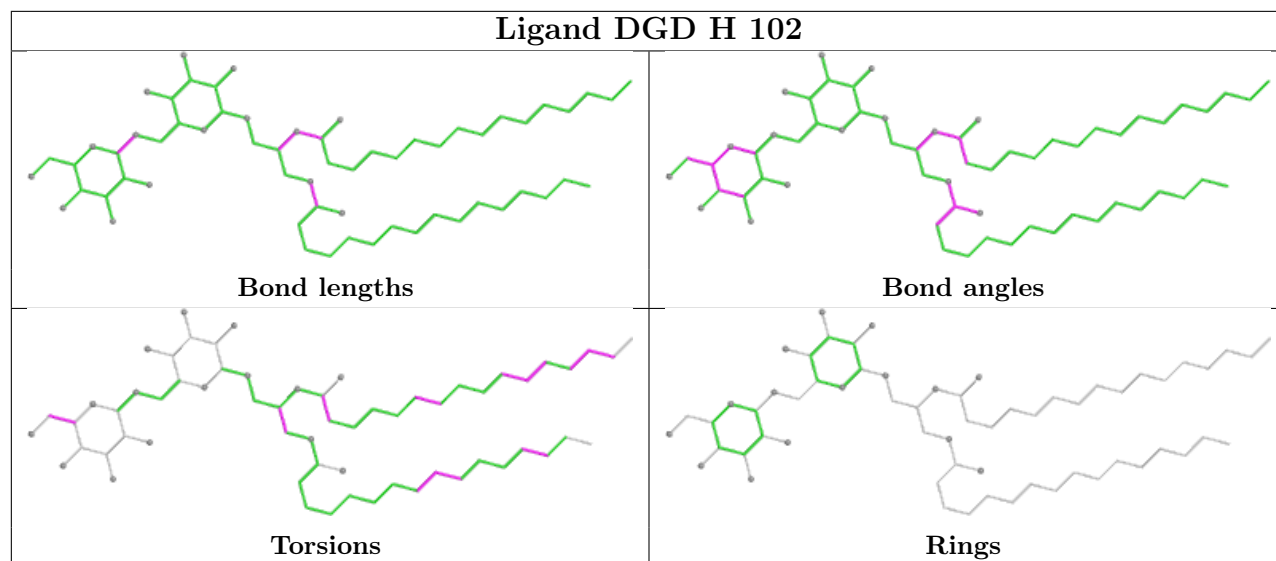
Ligand CLA b 611	
	
Bond lengths	Bond angles
	
Torsions	Rings

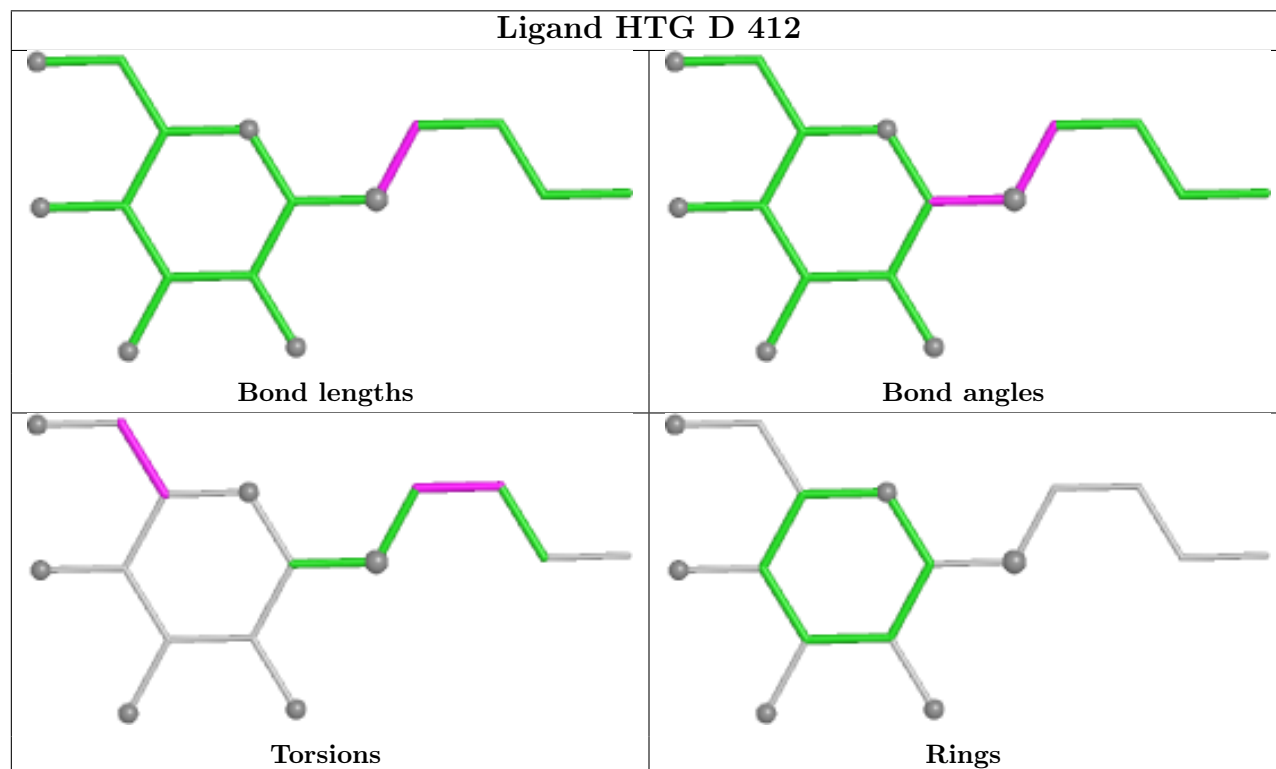
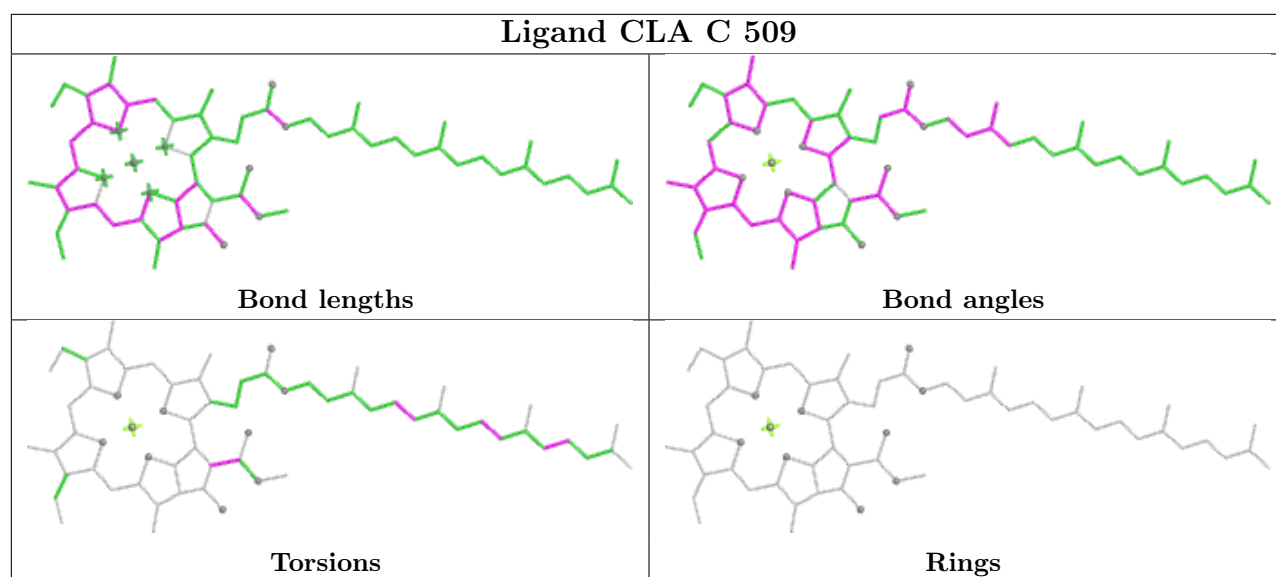
Ligand LMG C 521	
	
Bond lengths	Bond angles
	
Torsions	Rings

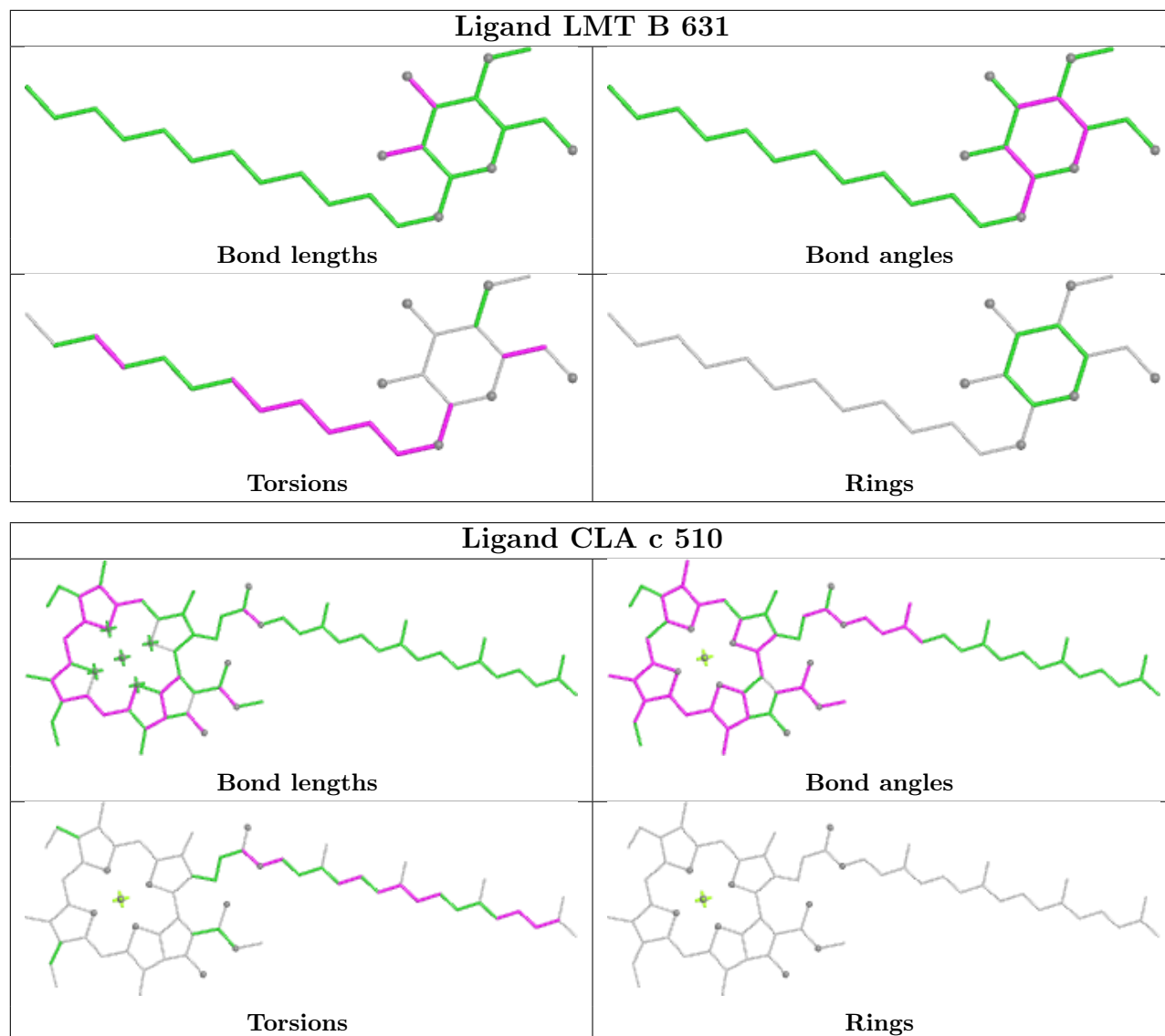
Ligand BCR y 101	
	
Bond lengths	Bond angles
	
Torsions	Rings

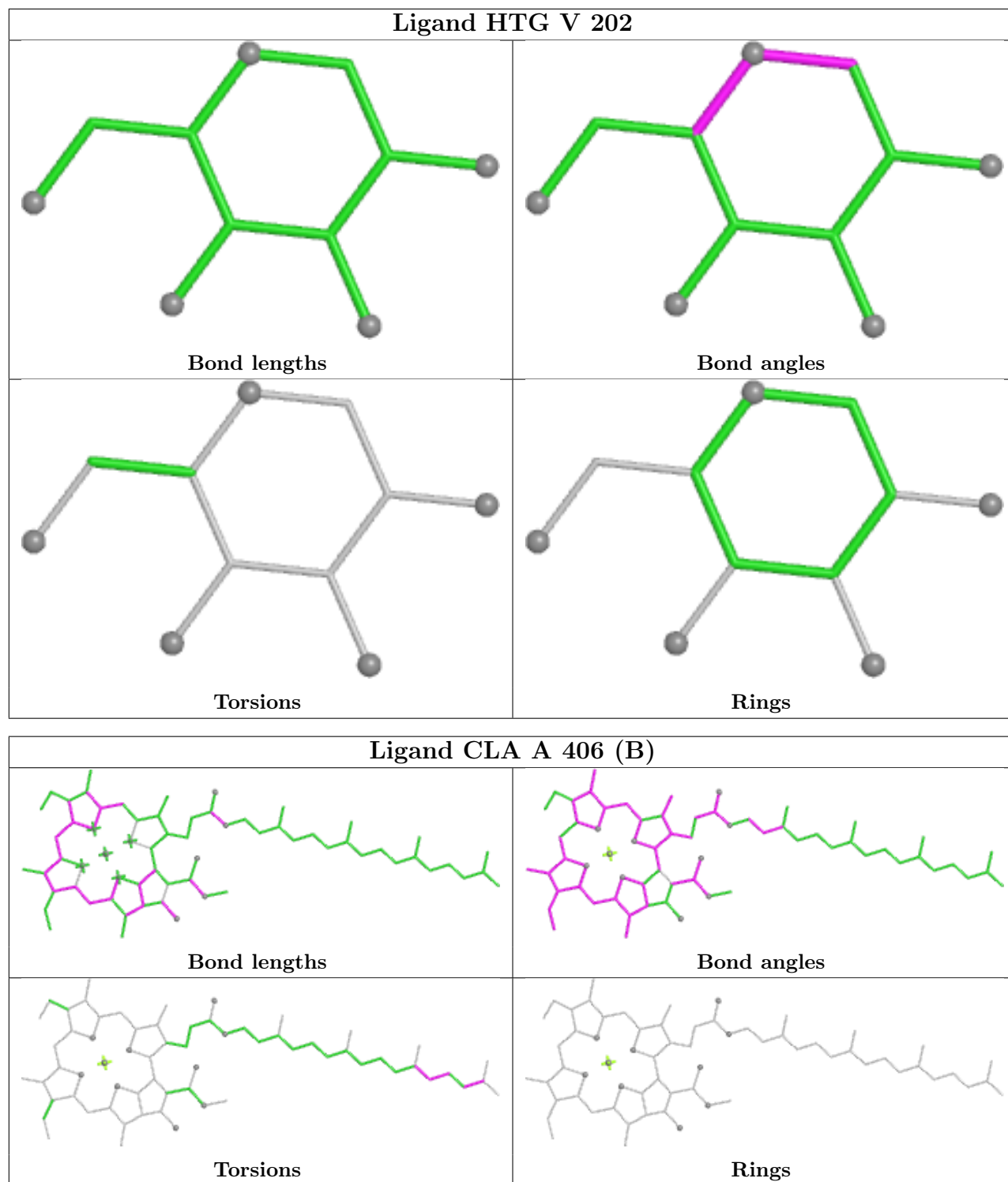
Ligand BCR a 410	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand DGD C 519	
	
Bond lengths	Bond angles
	
Torsions	Rings

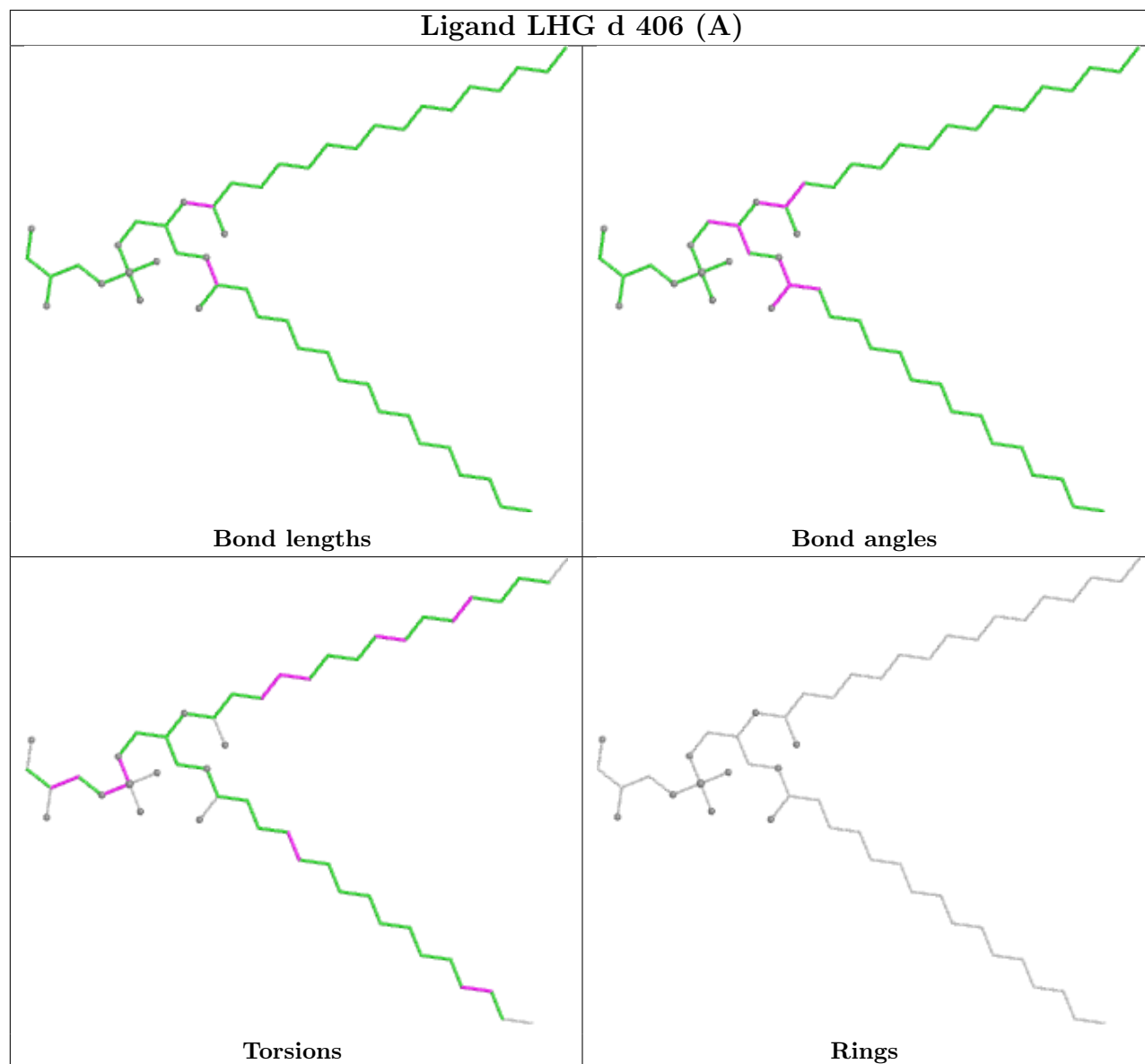




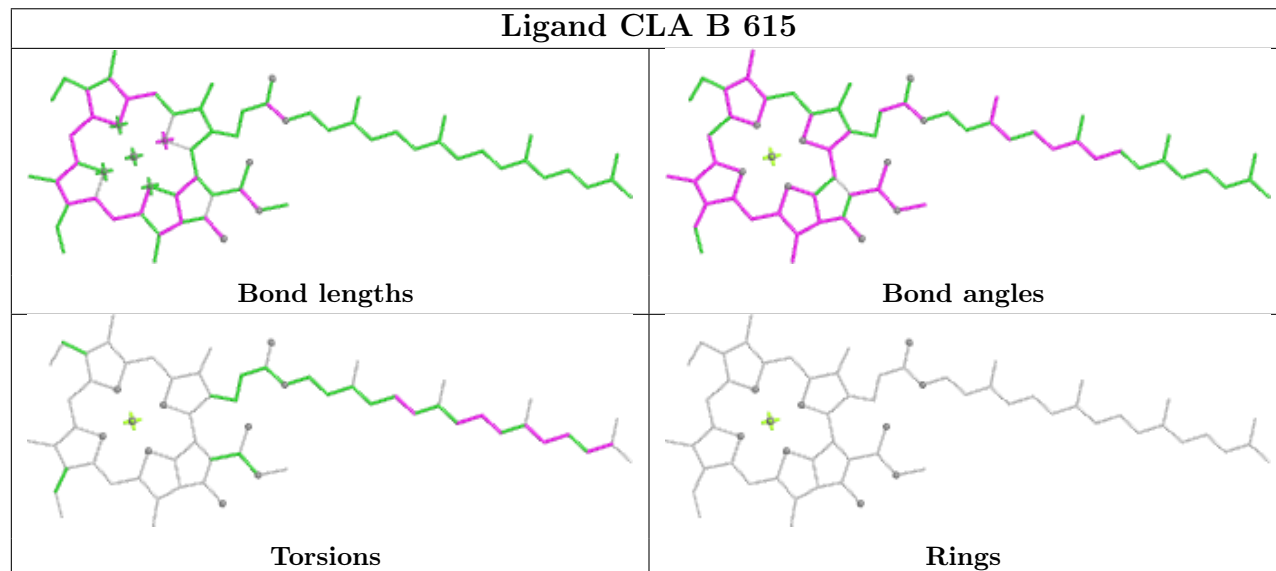


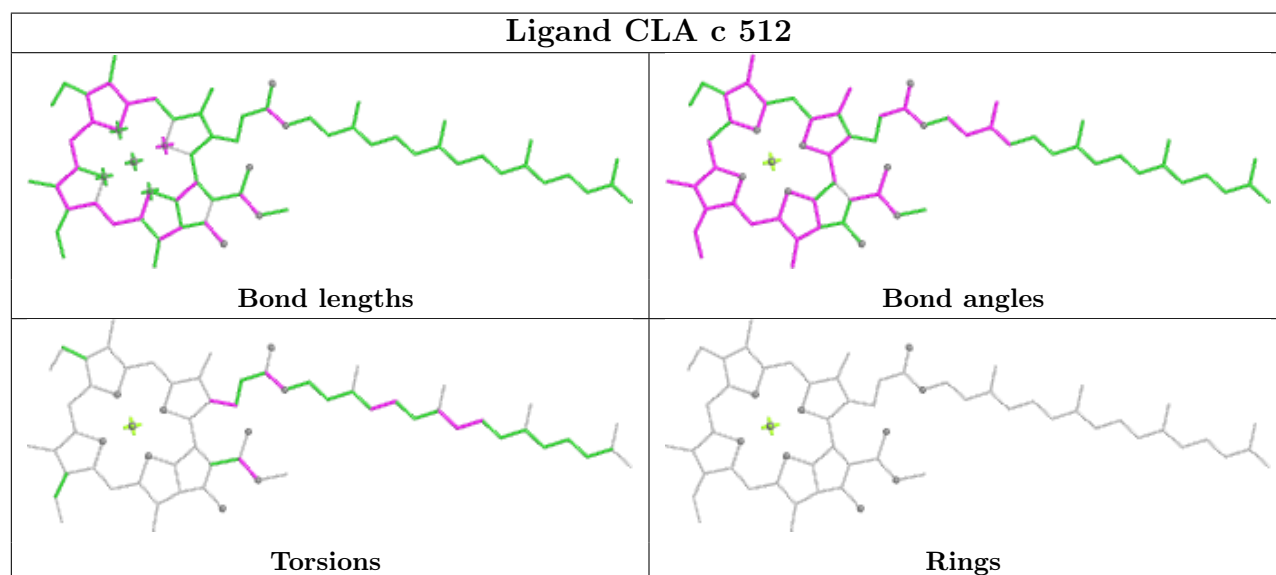
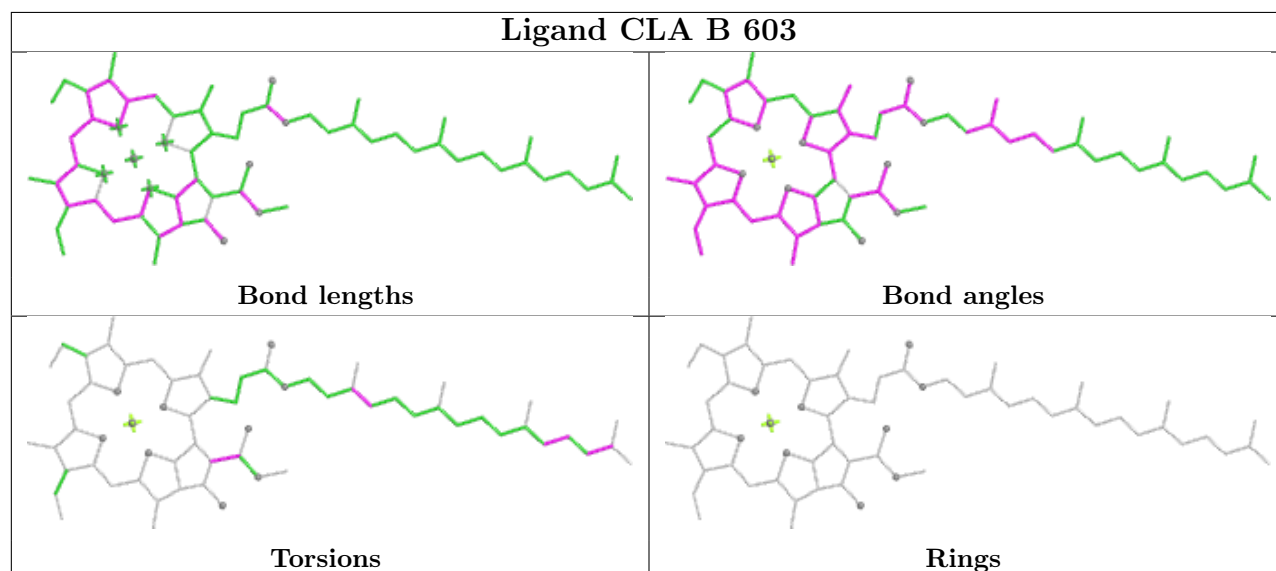
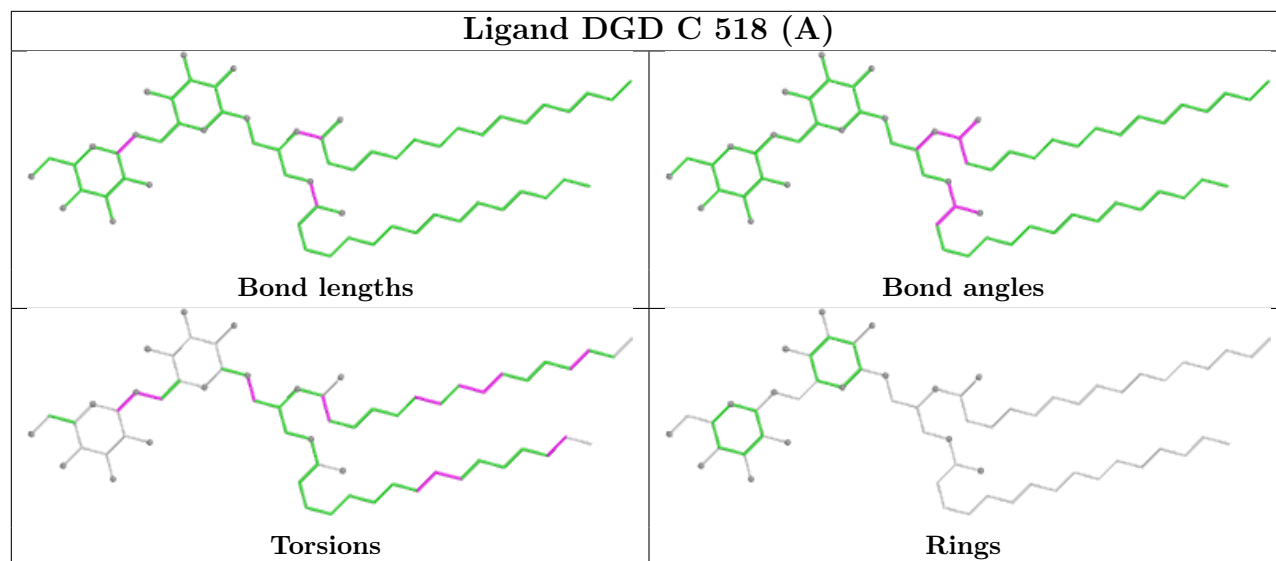


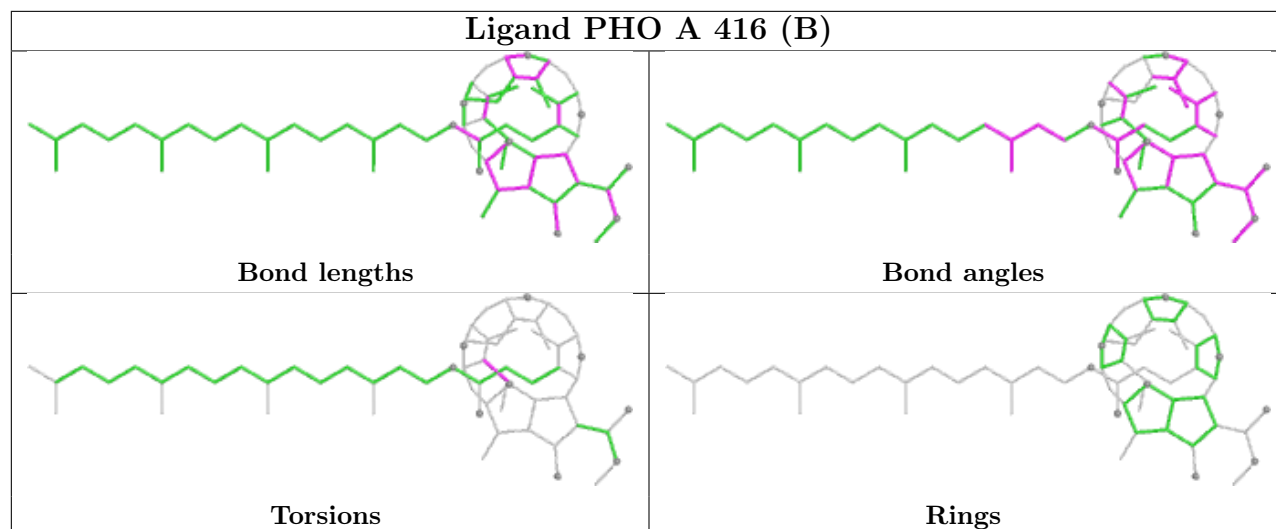
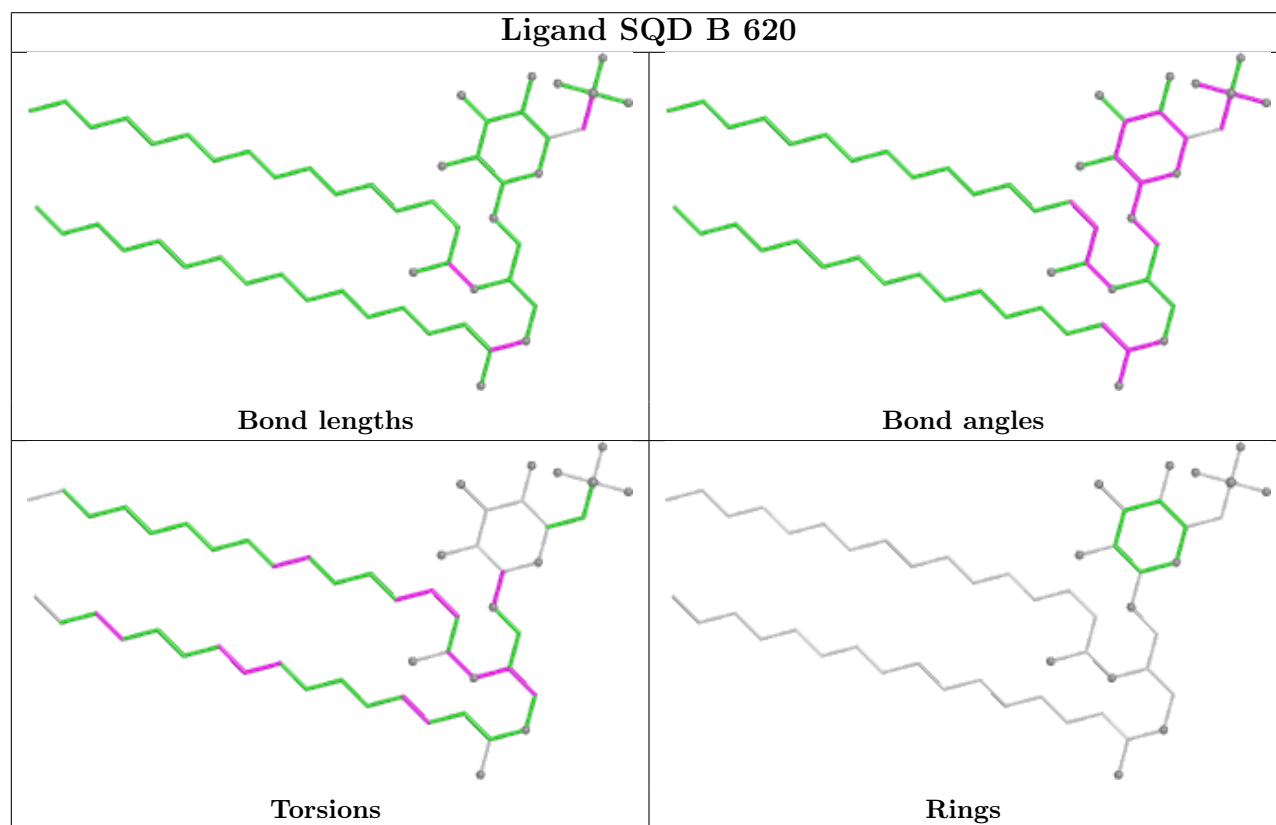
Ligand LHG d 406 (A)

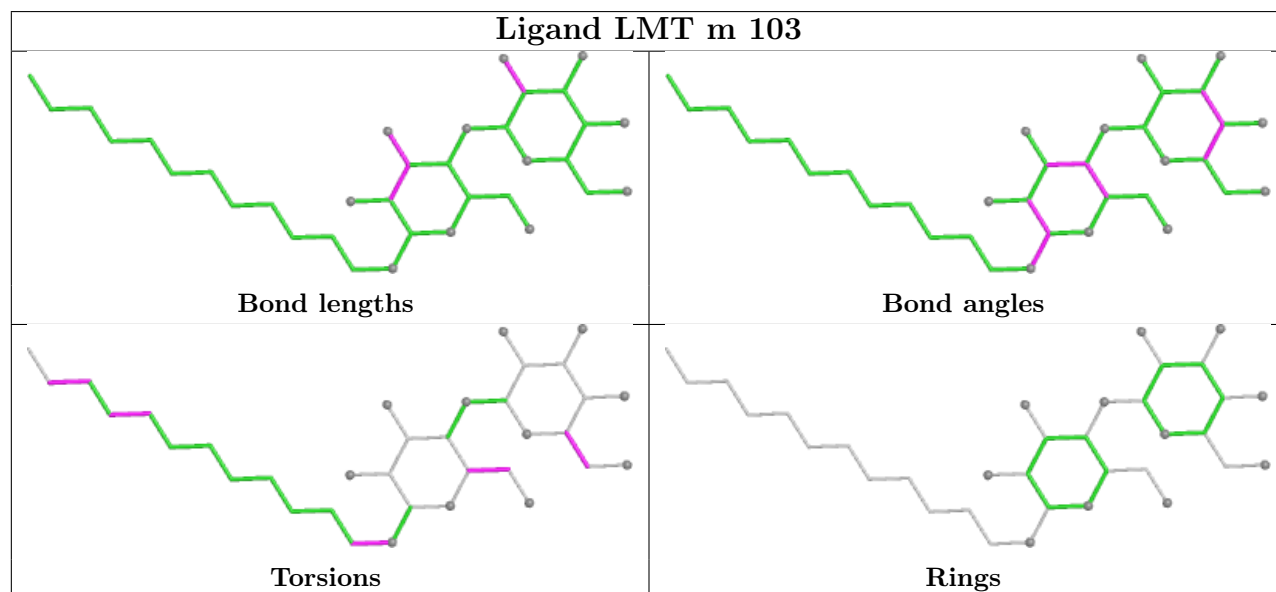
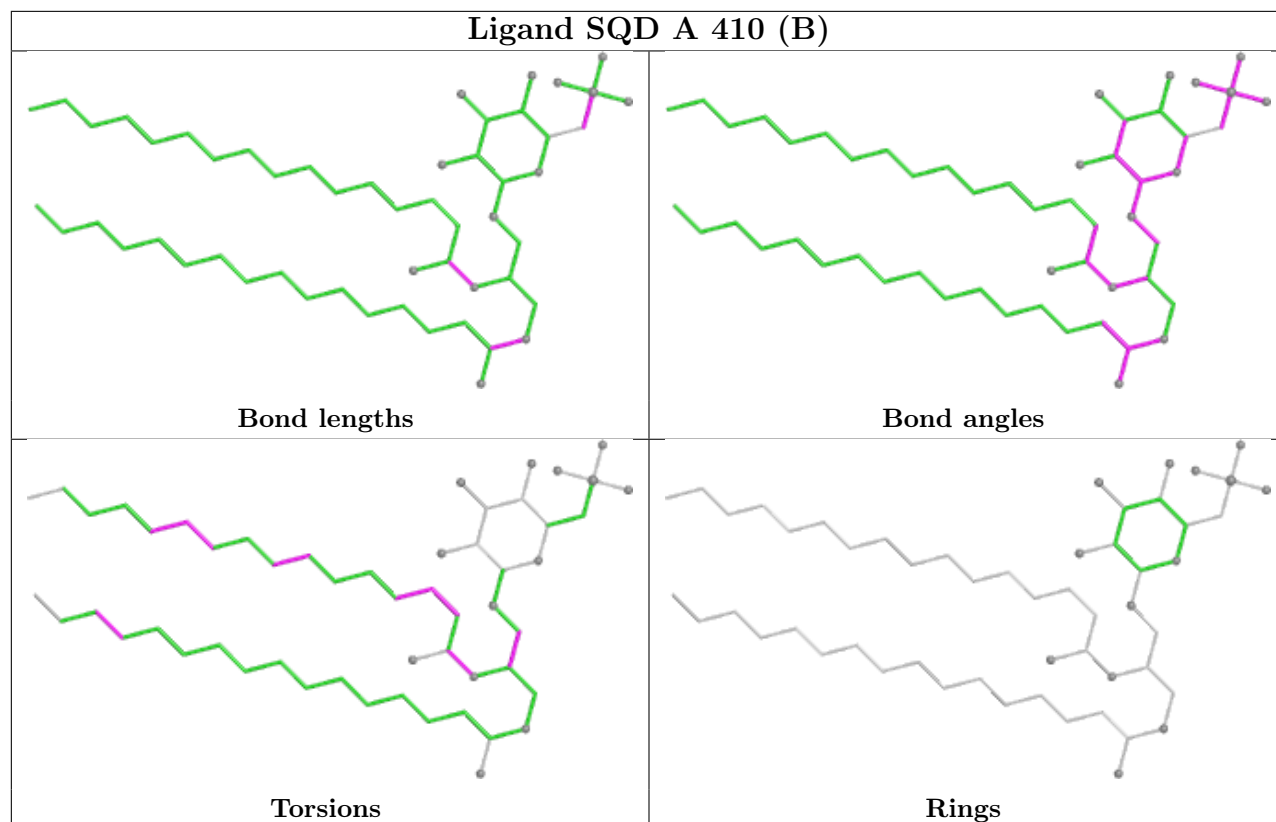


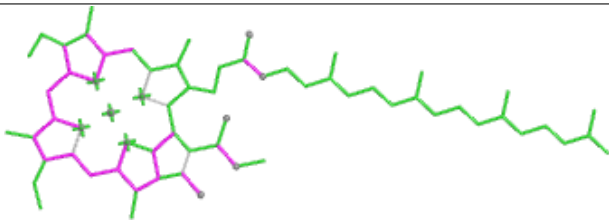
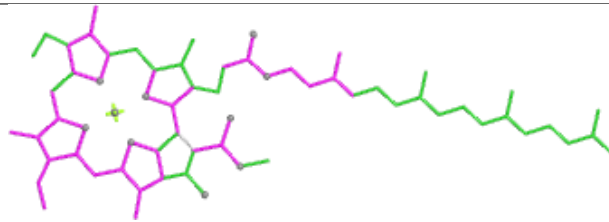
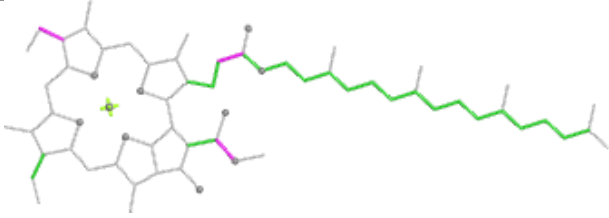
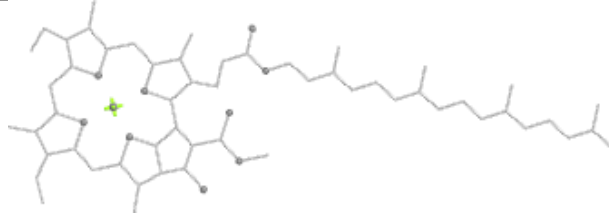
Ligand CLA B 615

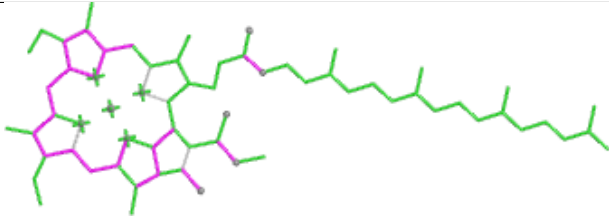
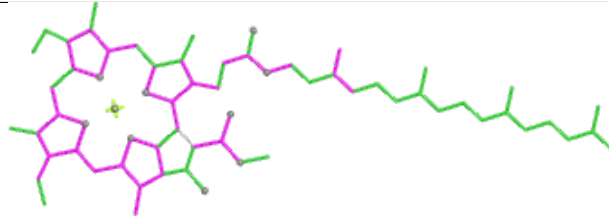
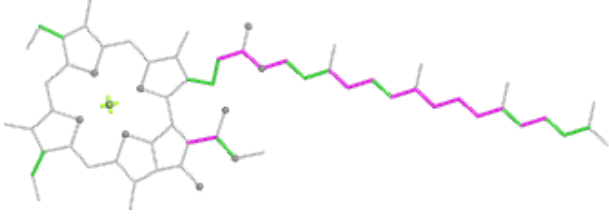
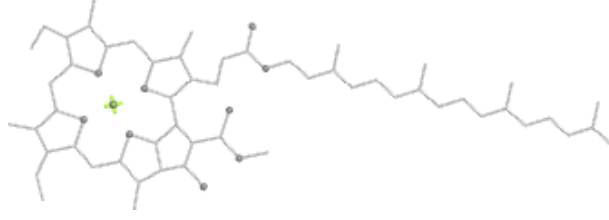


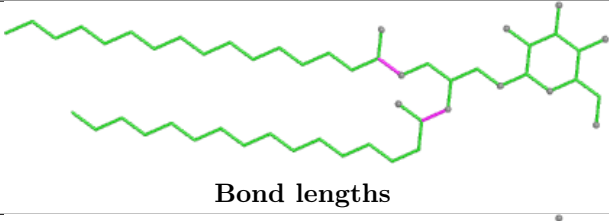
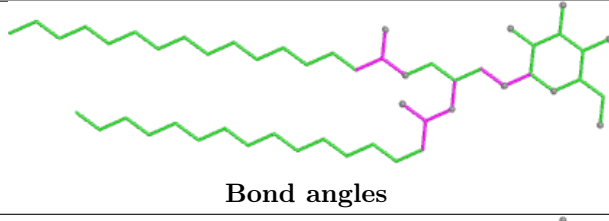
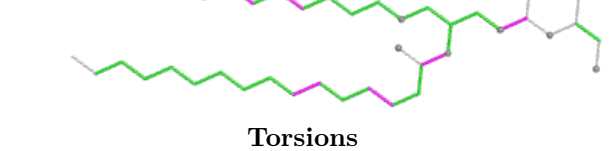


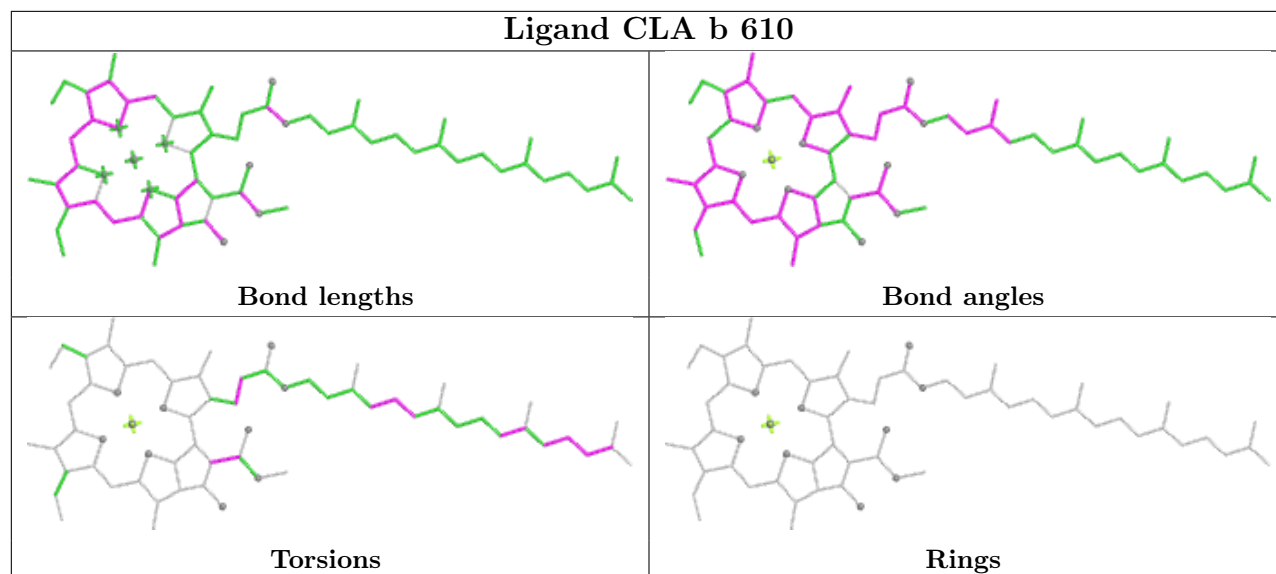
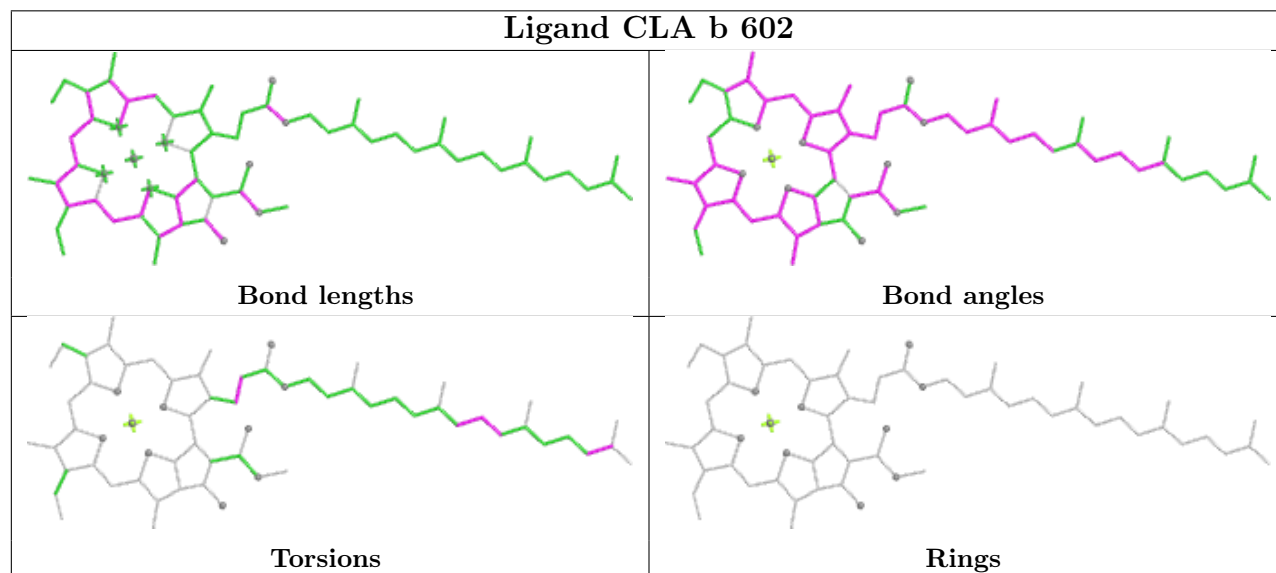
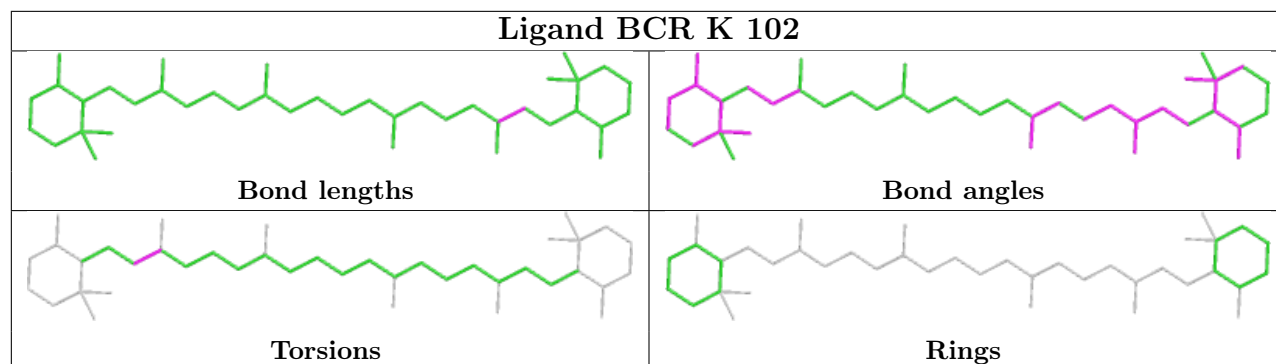
Ligand PHO A 416 (B)**Ligand SQD B 620**

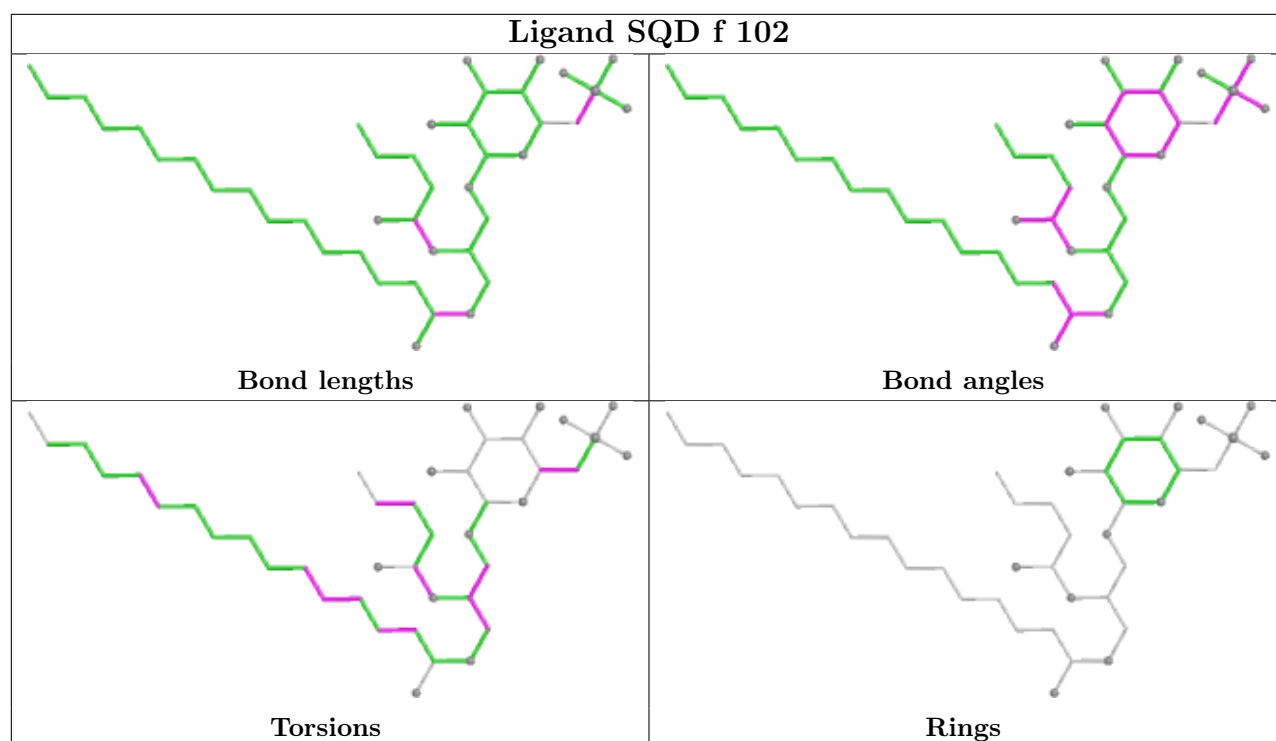


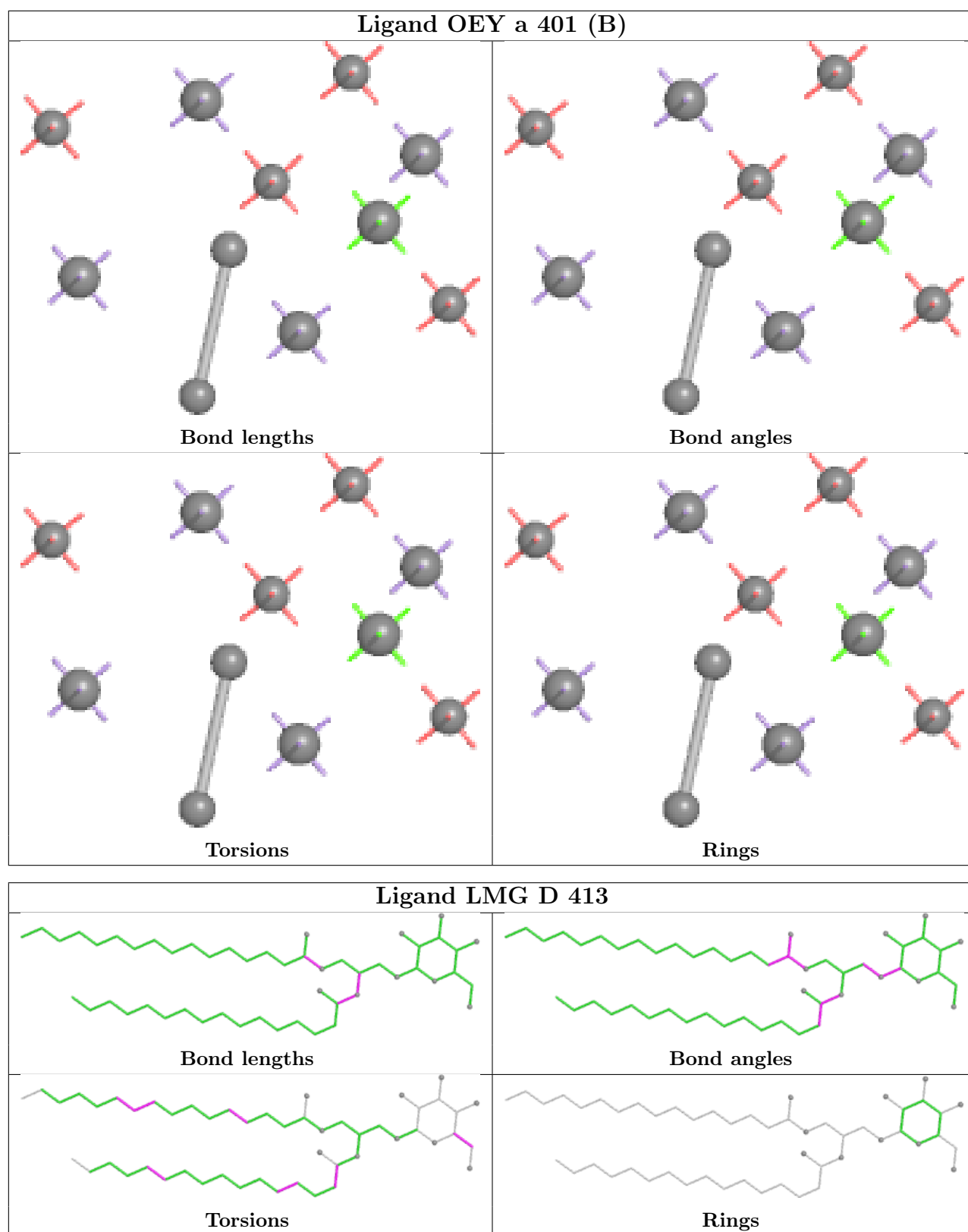
Ligand CLA c 502	
	
Bond lengths	Bond angles
	
Torsions	Rings

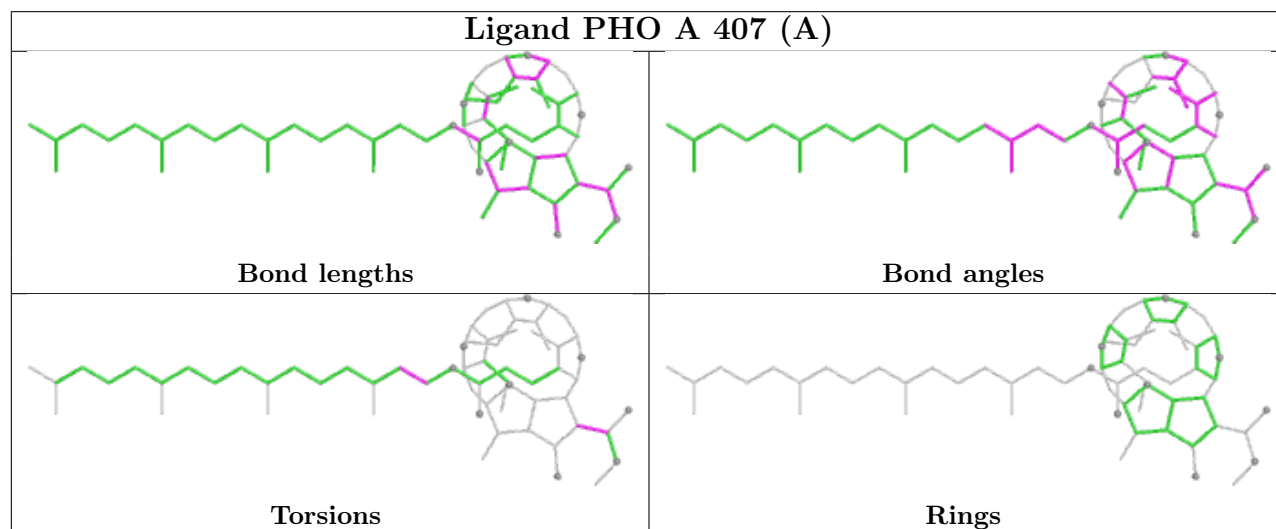
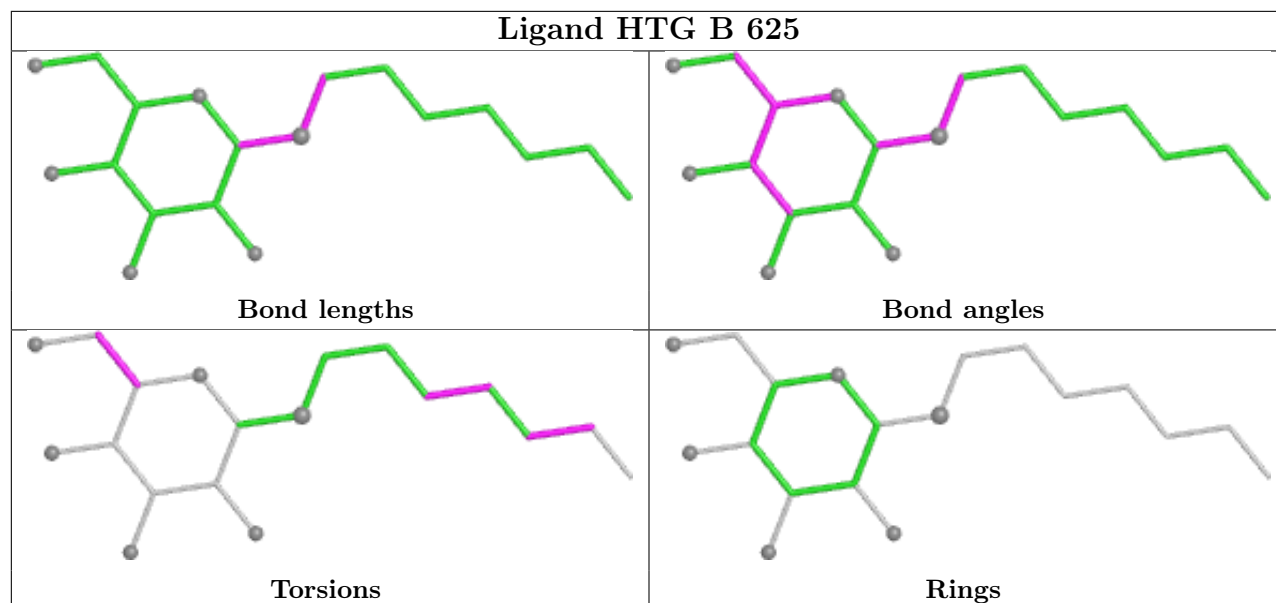
Ligand CLA b 601	
	
Bond lengths	Bond angles
	
Torsions	Rings

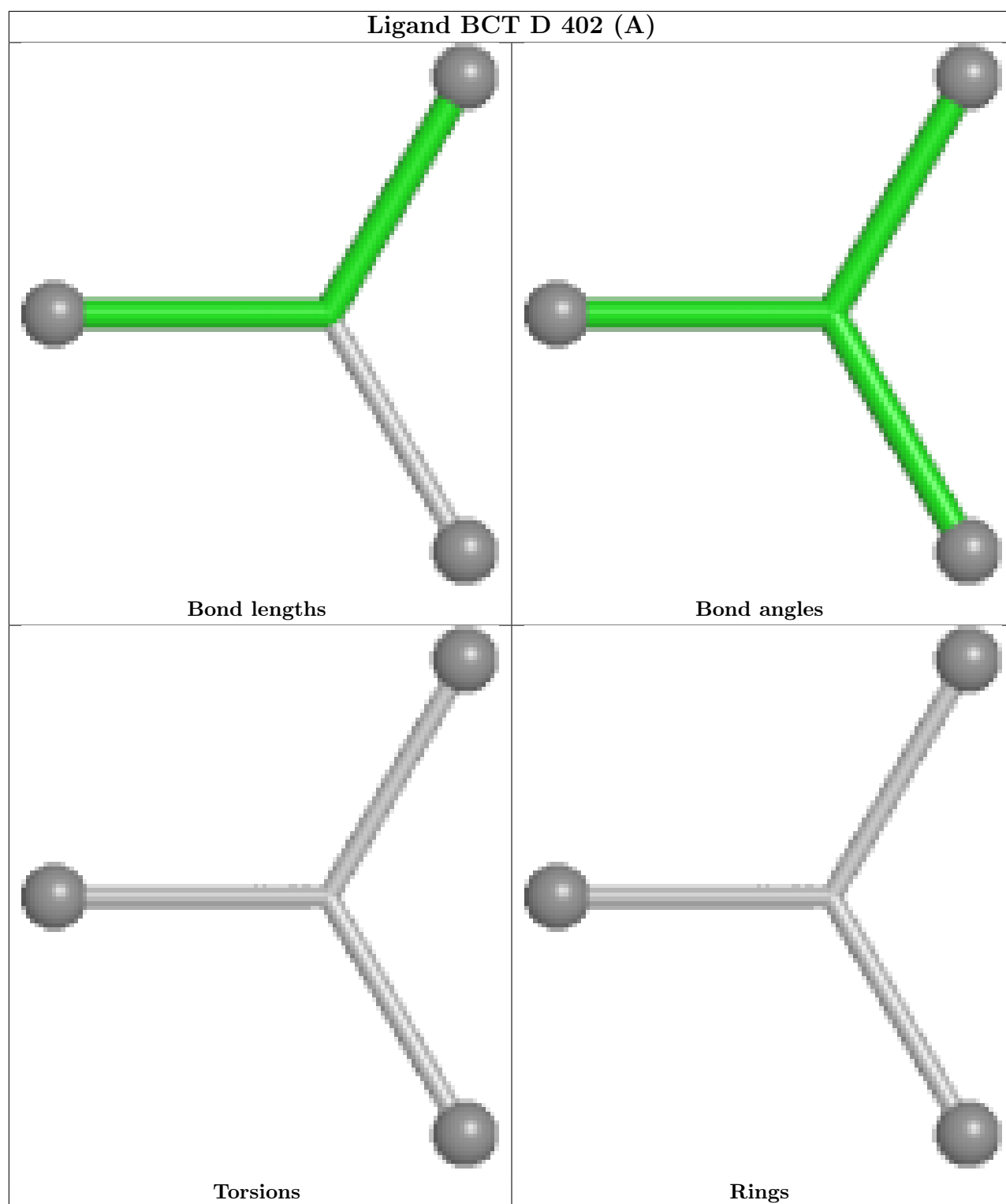
Ligand LMG m 101	
	
Bond lengths	Bond angles
	
Torsions	Rings

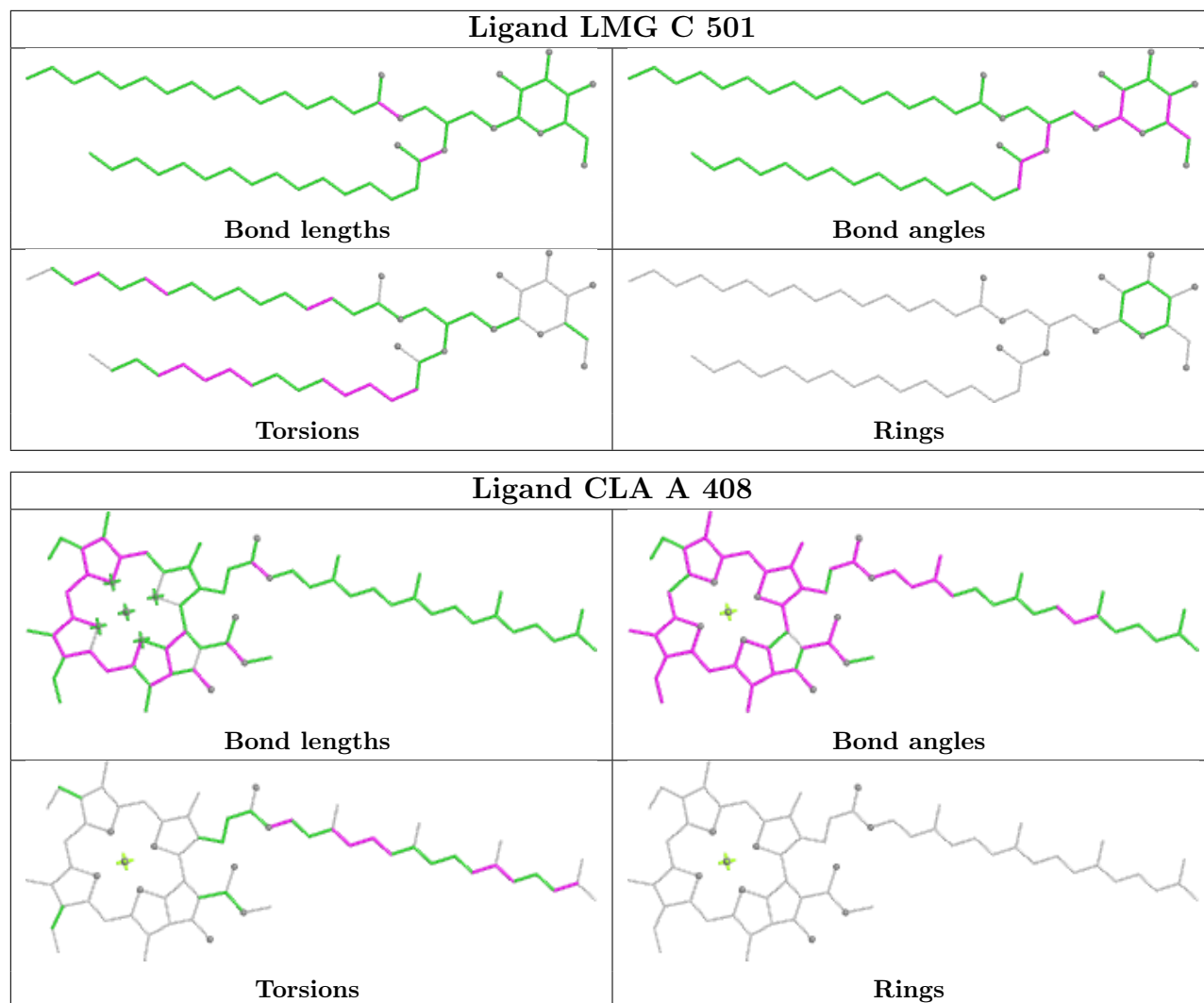
Ligand CLA b 610**Ligand CLA b 602****Ligand BCR K 102**

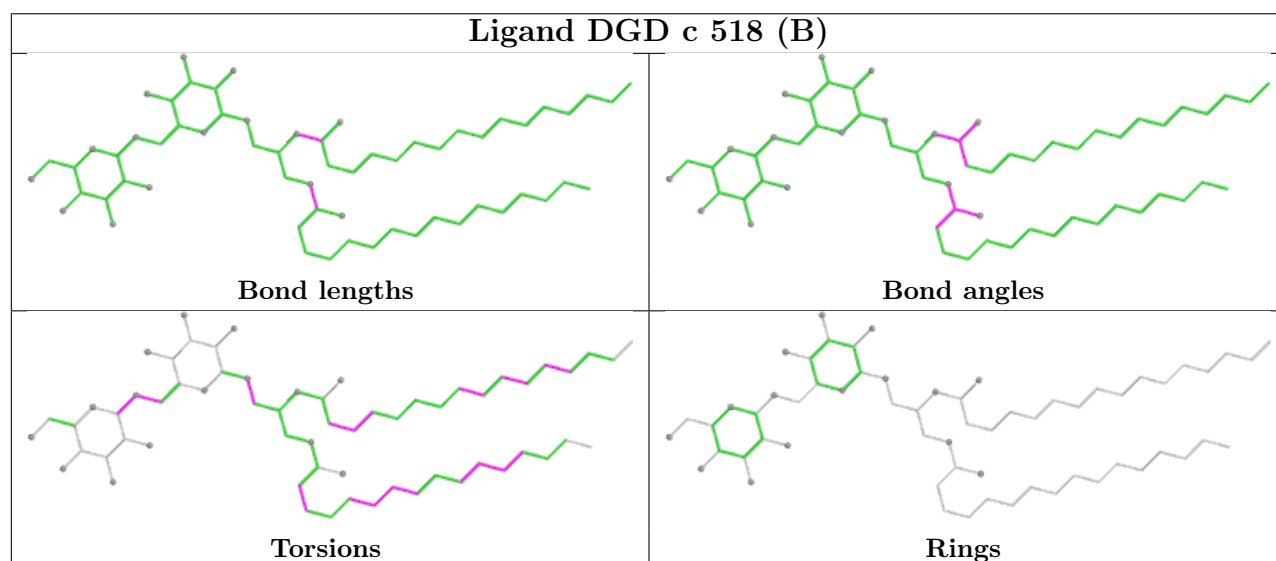
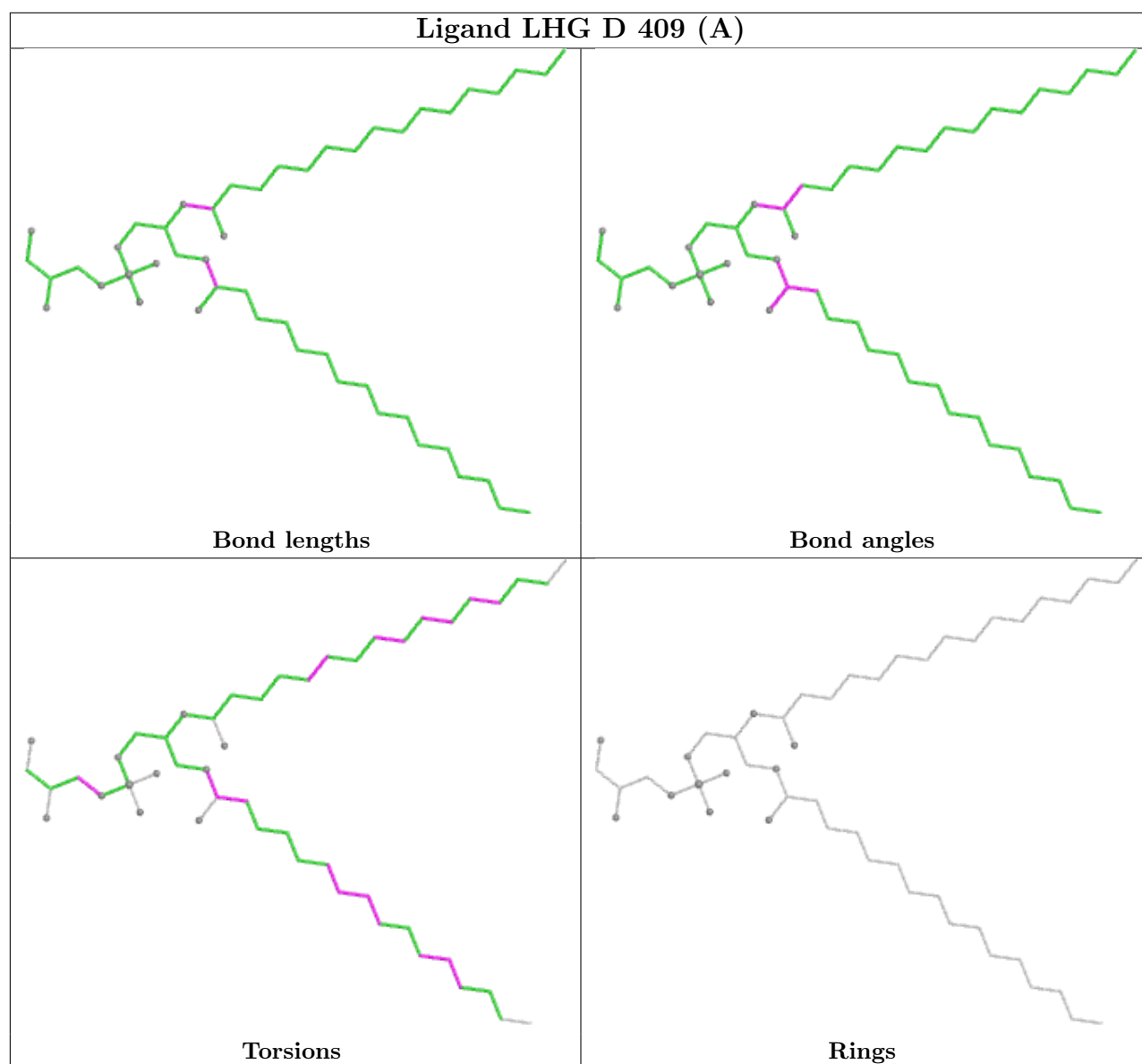


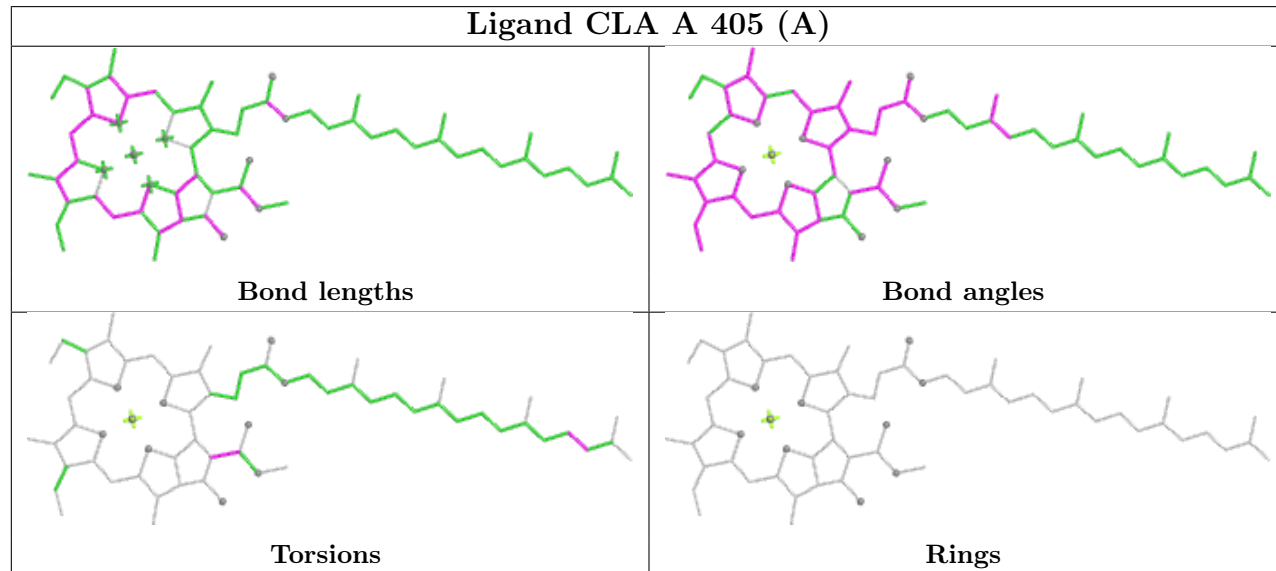
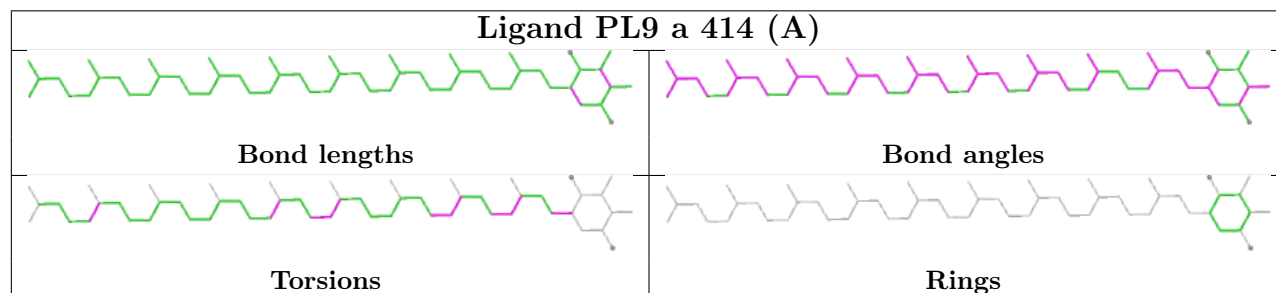
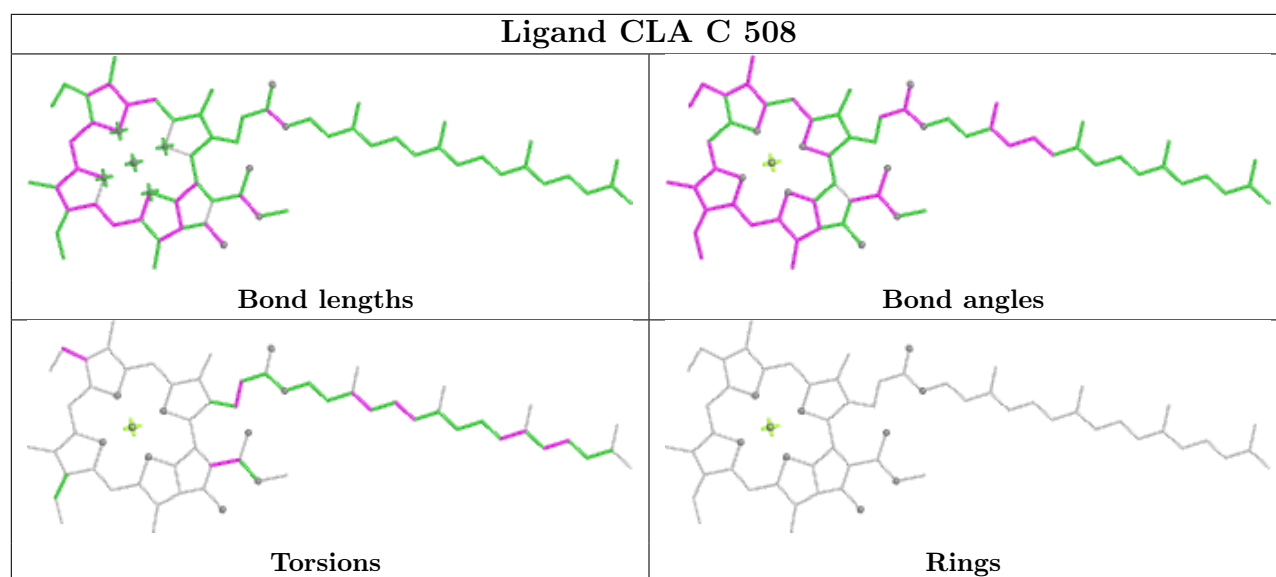


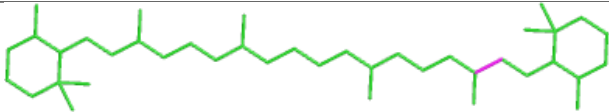
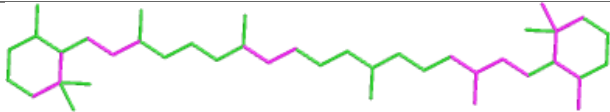
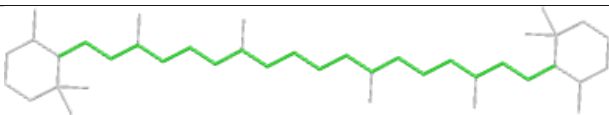
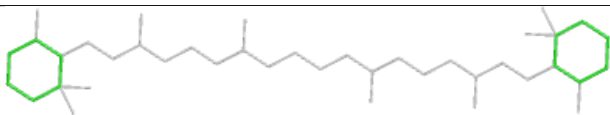




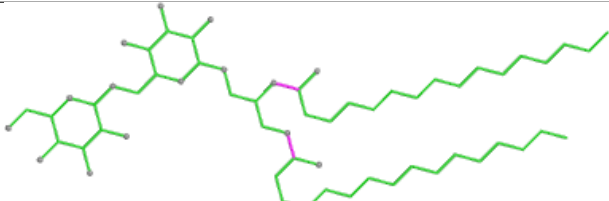
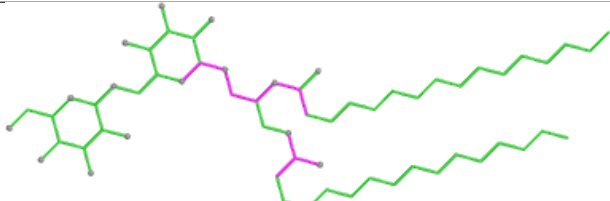
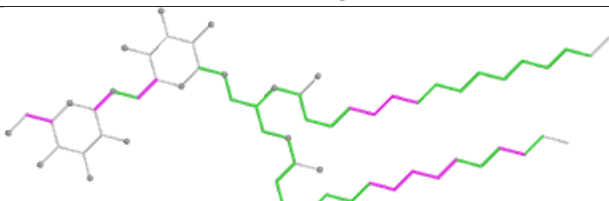
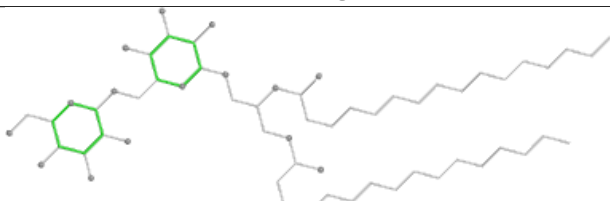


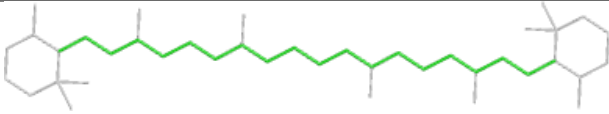
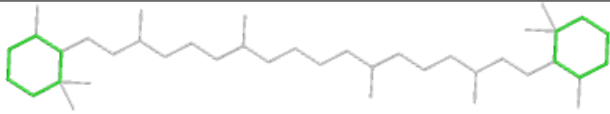


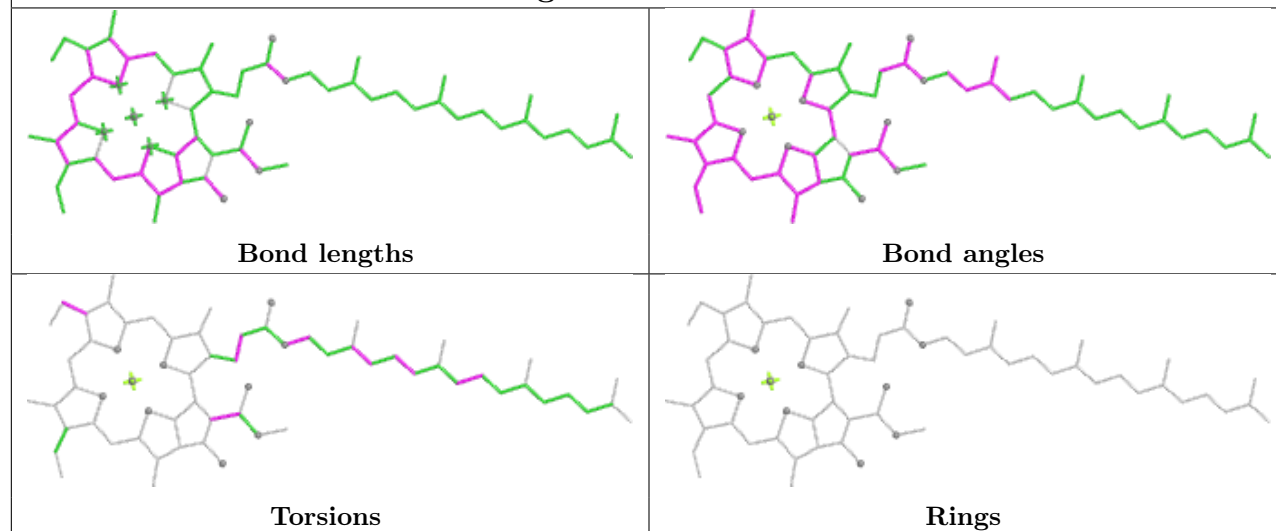
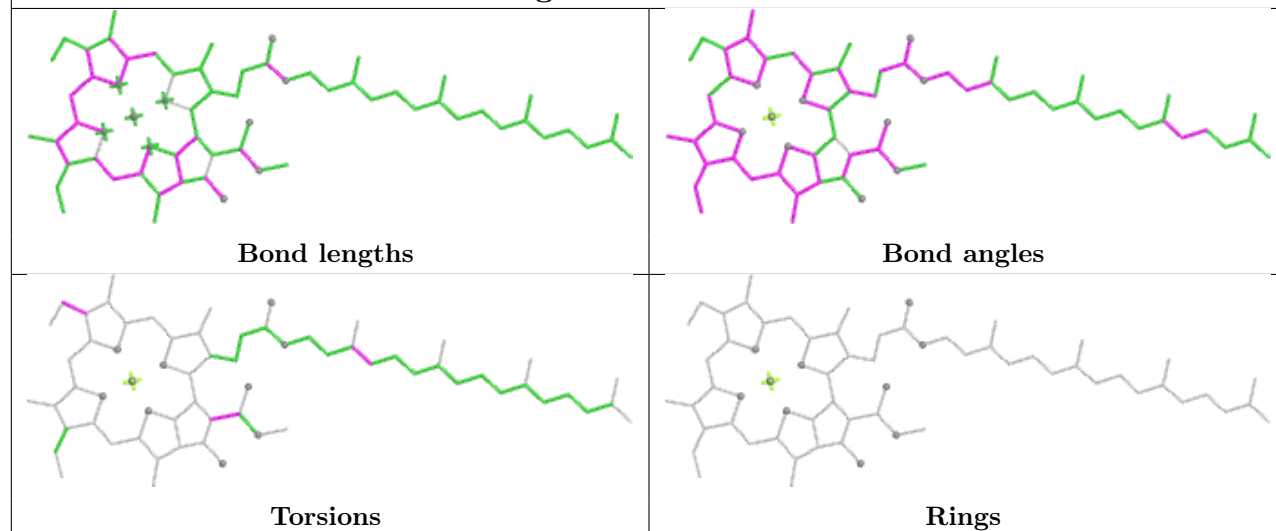
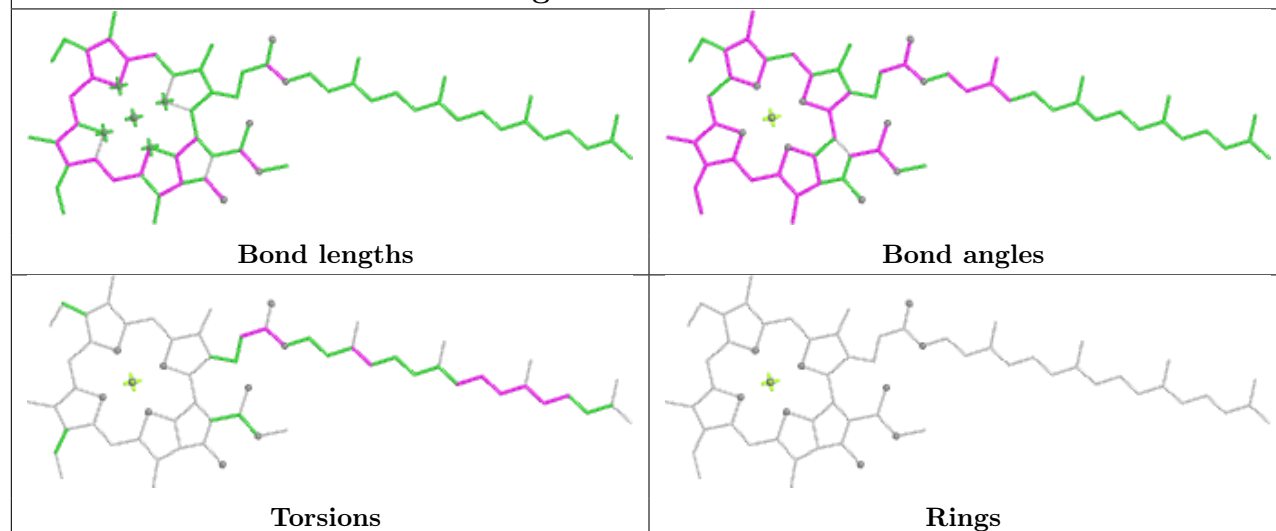


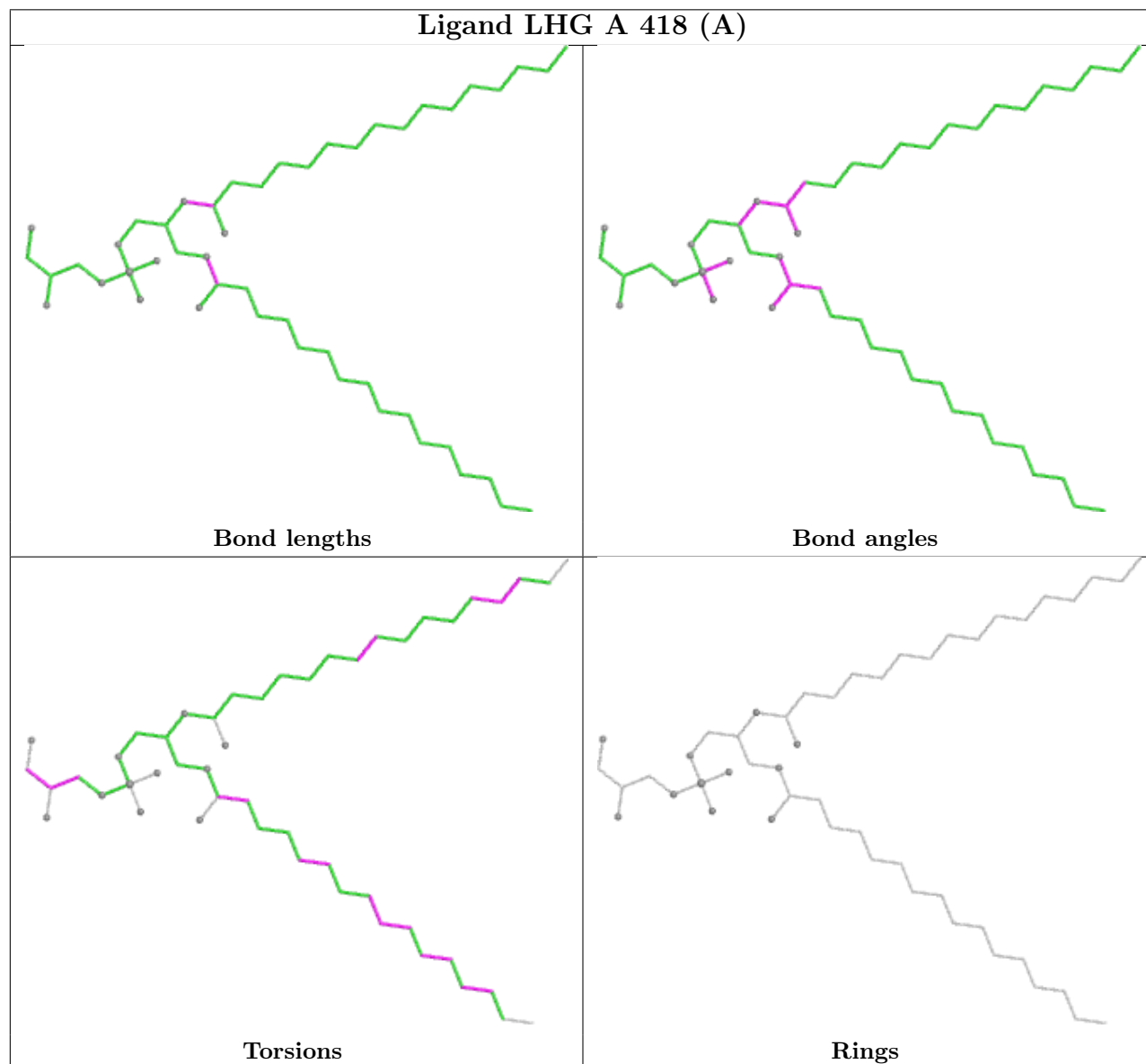
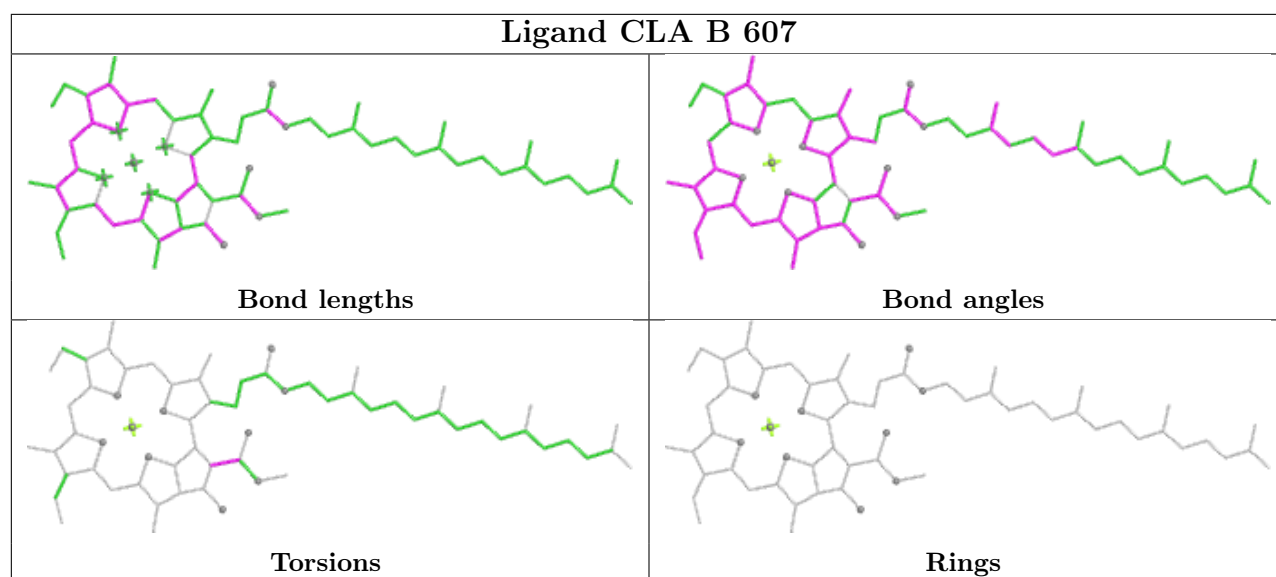
Ligand BCR B 618	
	
Bond lengths	Bond angles
	
Torsions	Rings

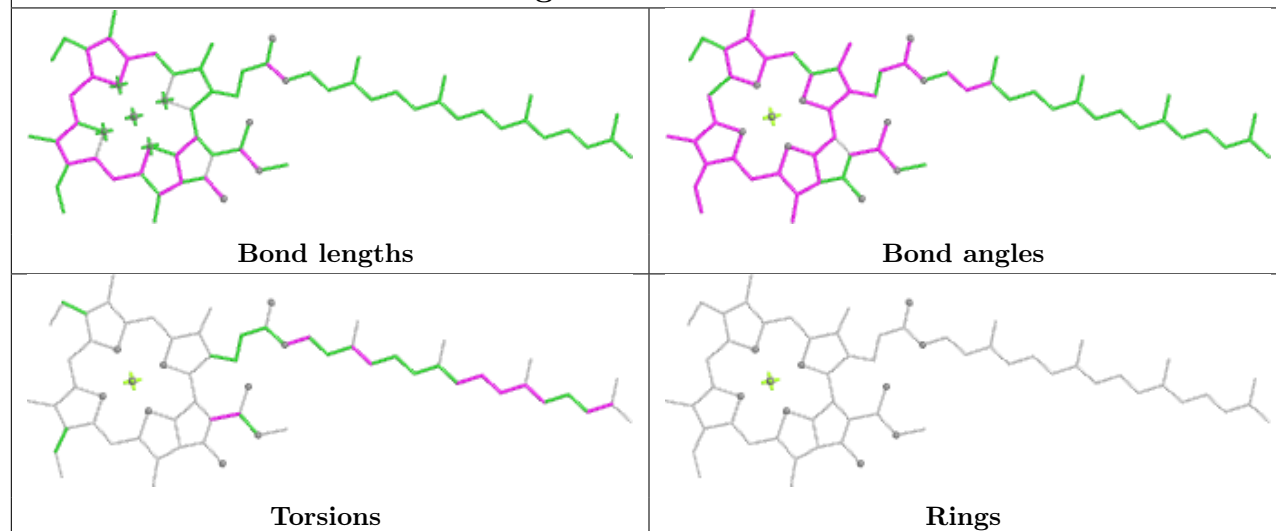
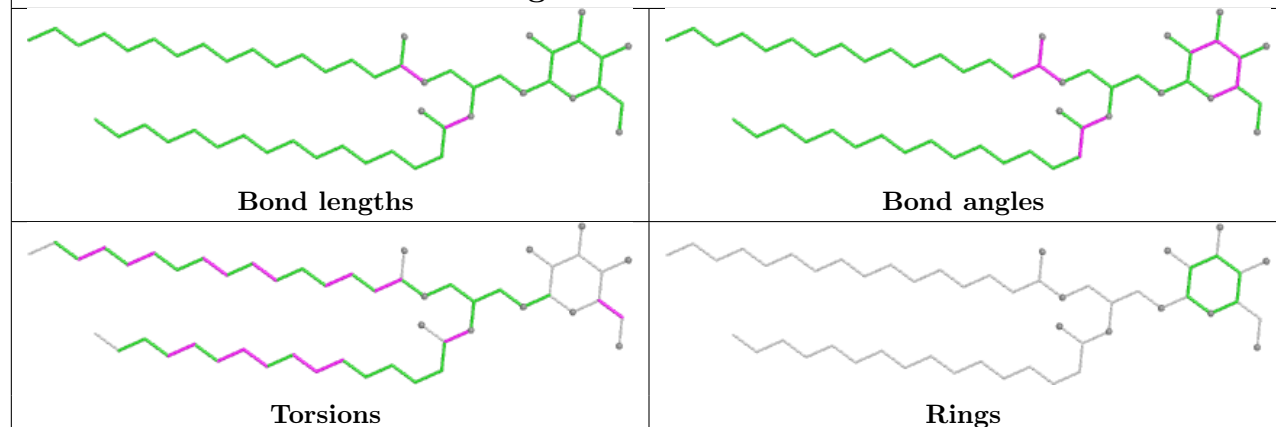
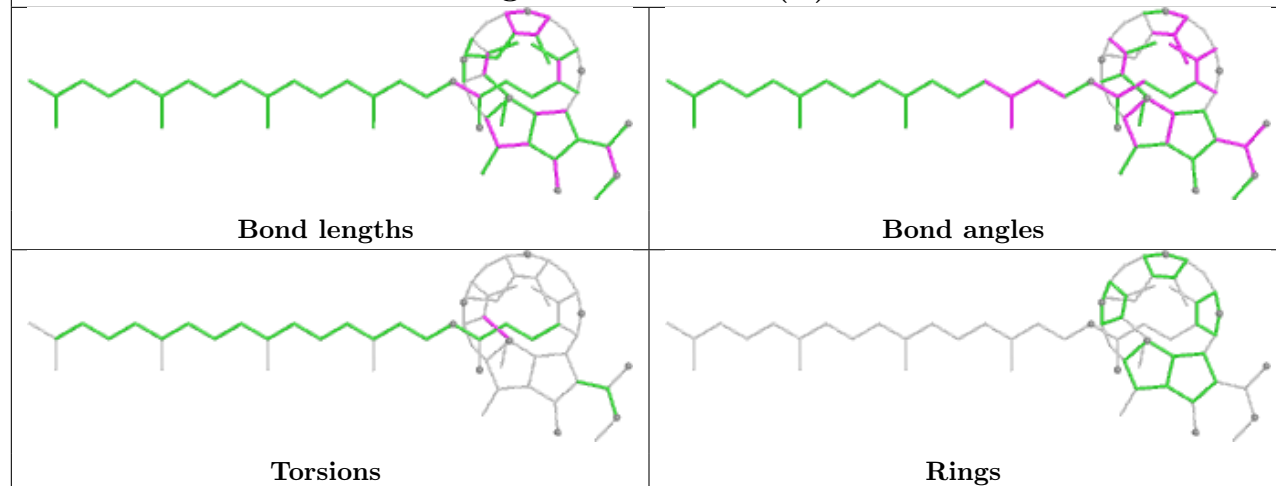
Ligand PL9 D 407 (B)	
	
Bond lengths	Bond angles
	
Torsions	Rings

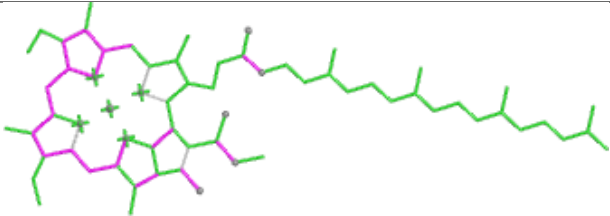
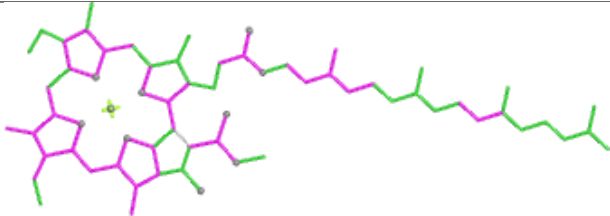
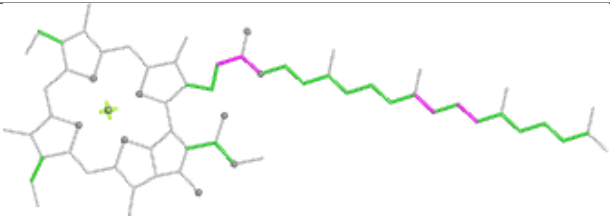
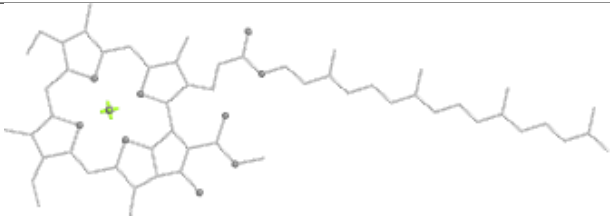
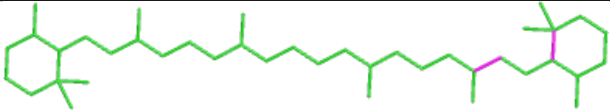
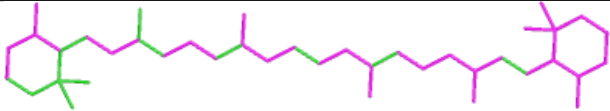
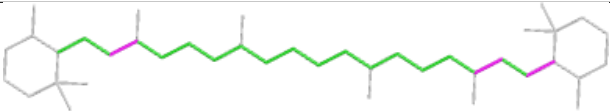
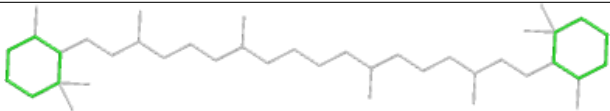
Ligand DGD C 517 (B)	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand BCR C 516	
	
Bond lengths	Bond angles
	
Torsions	Rings

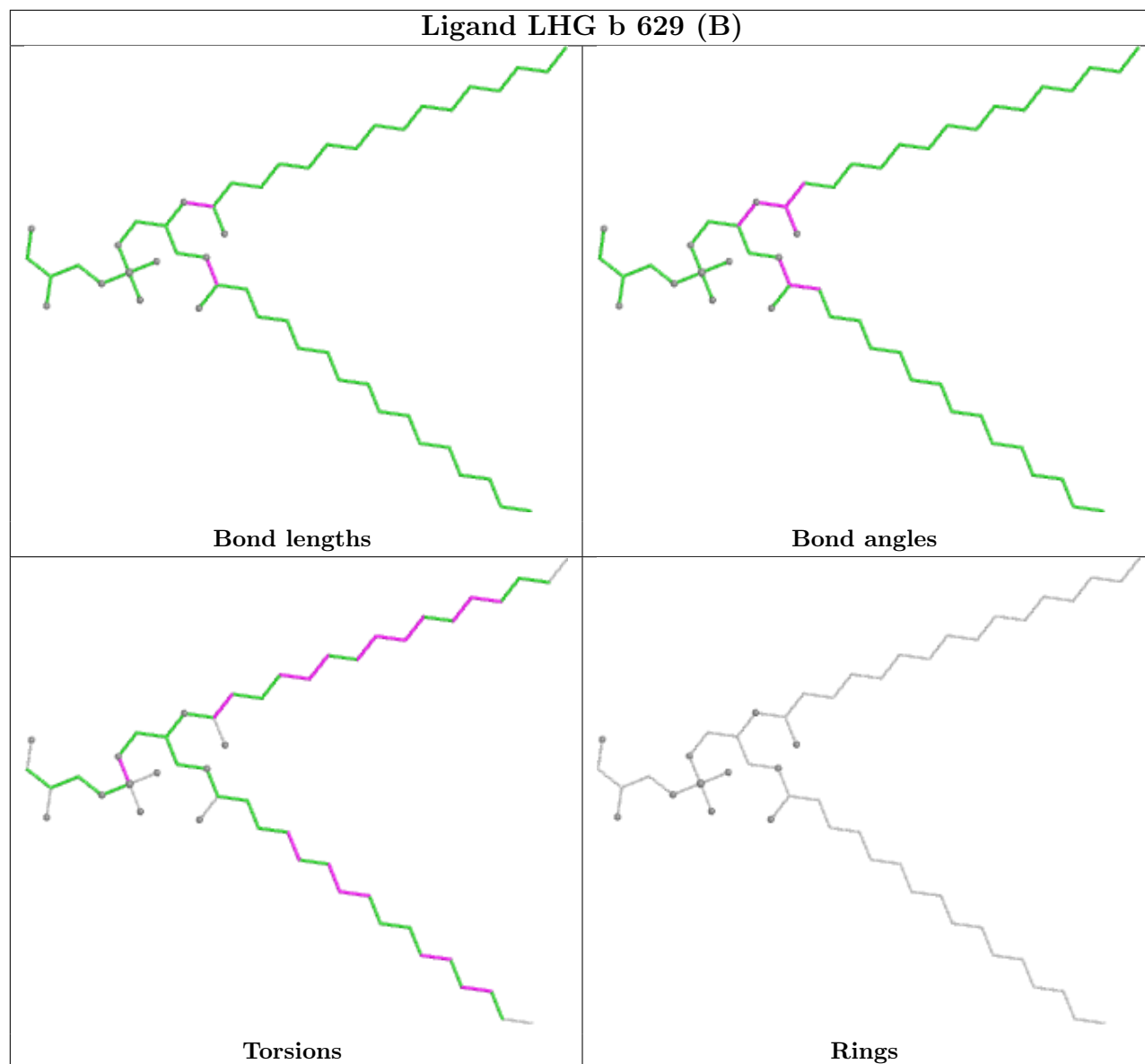
Ligand CLA c 508**Ligand CLA b 609****Ligand CLA C 511**



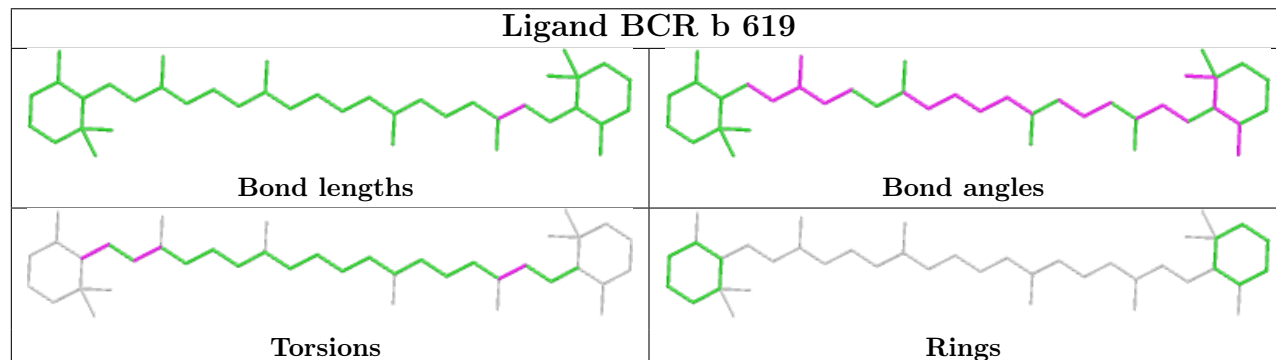
Ligand CLA b 614**Ligand LMG B 621****Ligand PHO a 416 (B)**

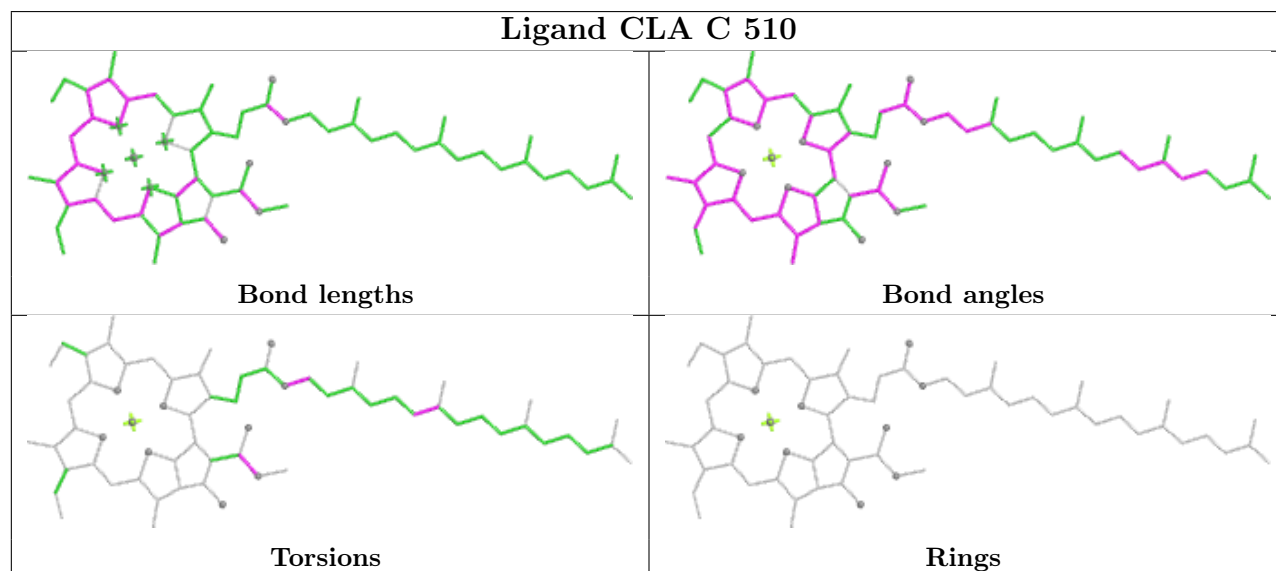
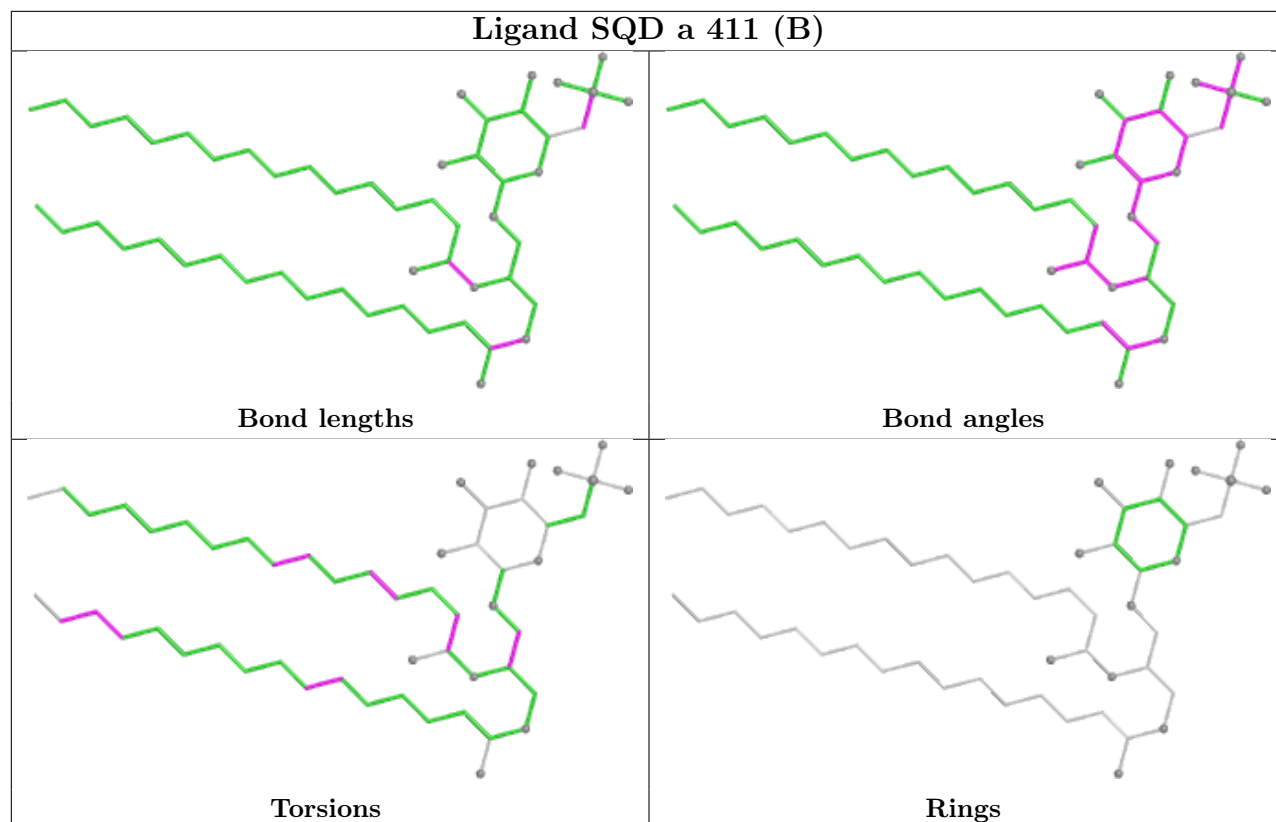
Ligand CLA B 612	
 Bond lengths	 Bond angles
 Torsions	 Rings
Ligand BCR d 404	
 Bond lengths	 Bond angles
 Torsions	 Rings

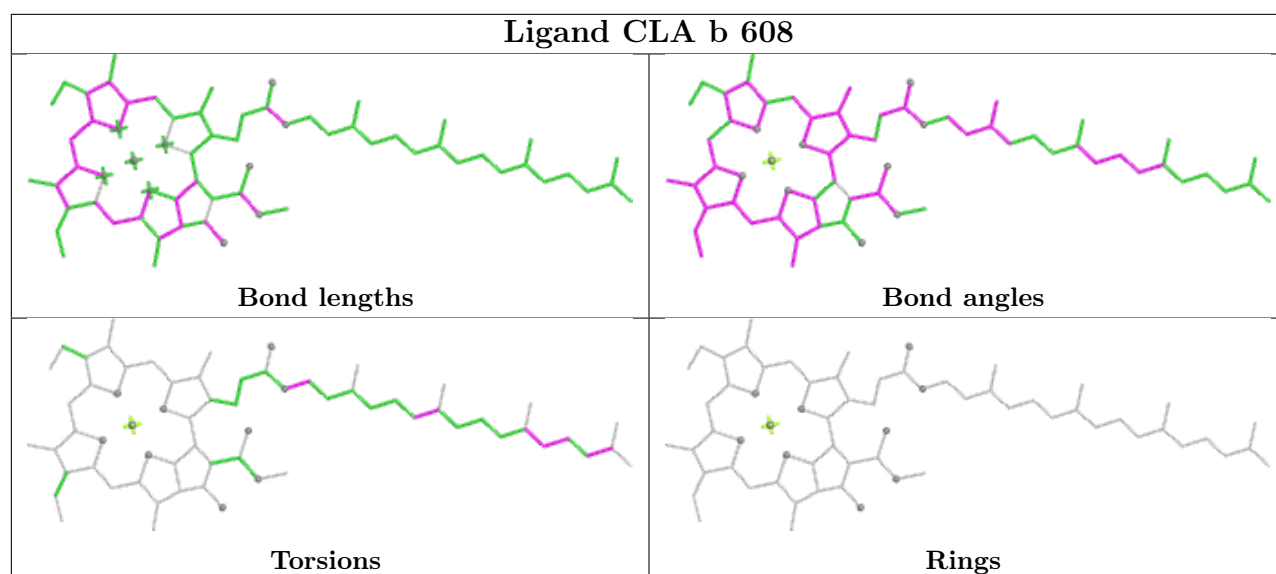
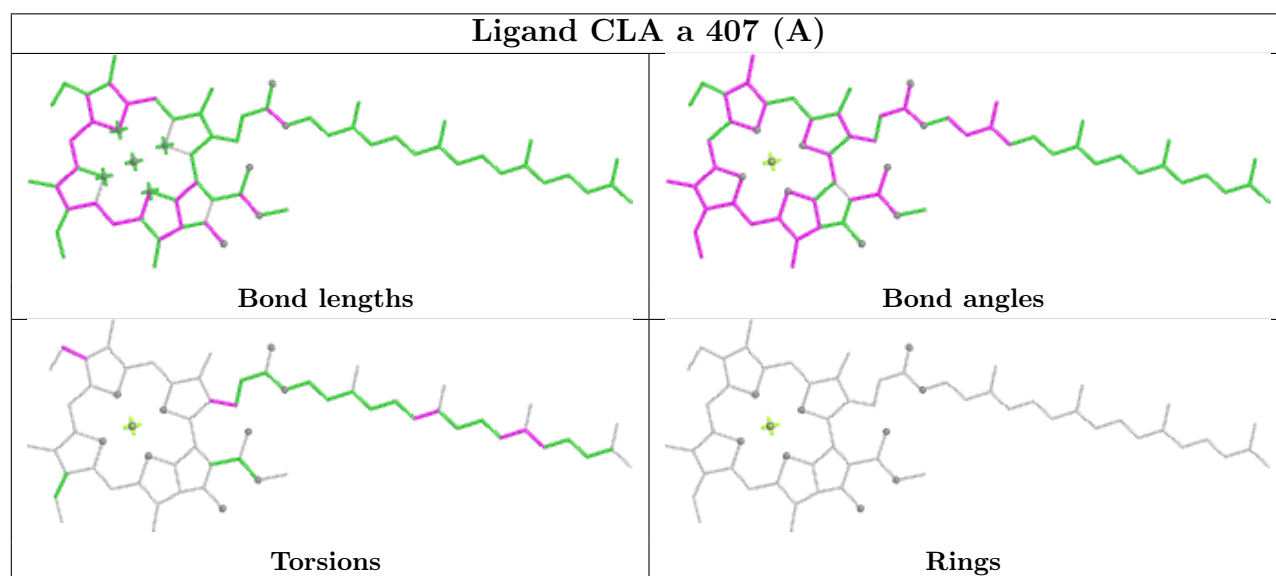
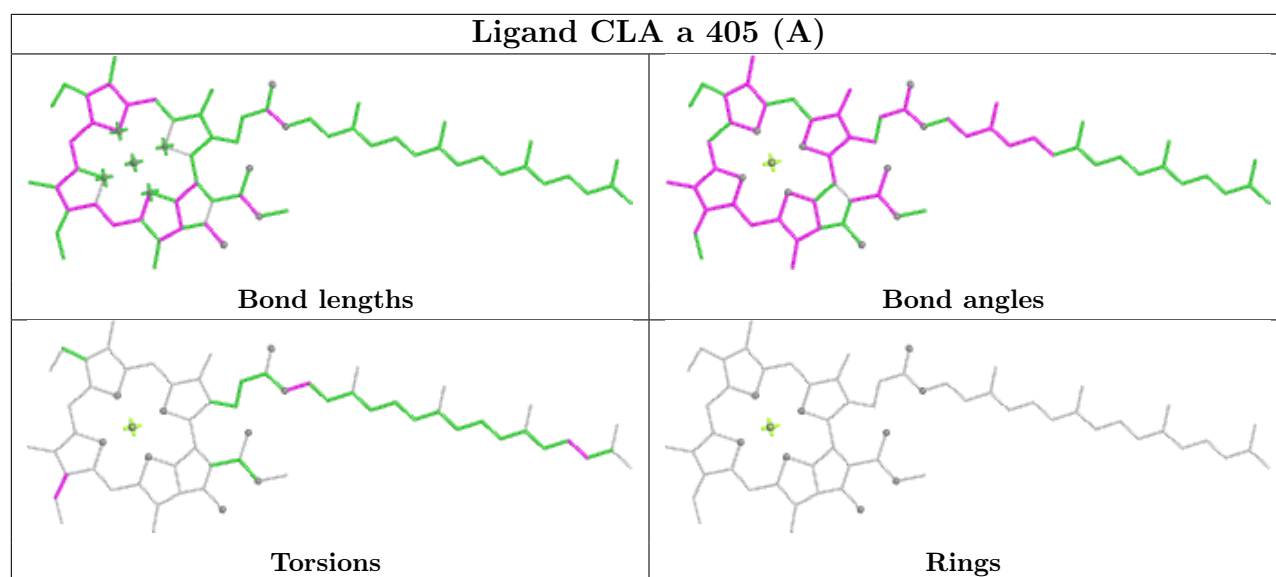
Ligand LHG b 629 (B)

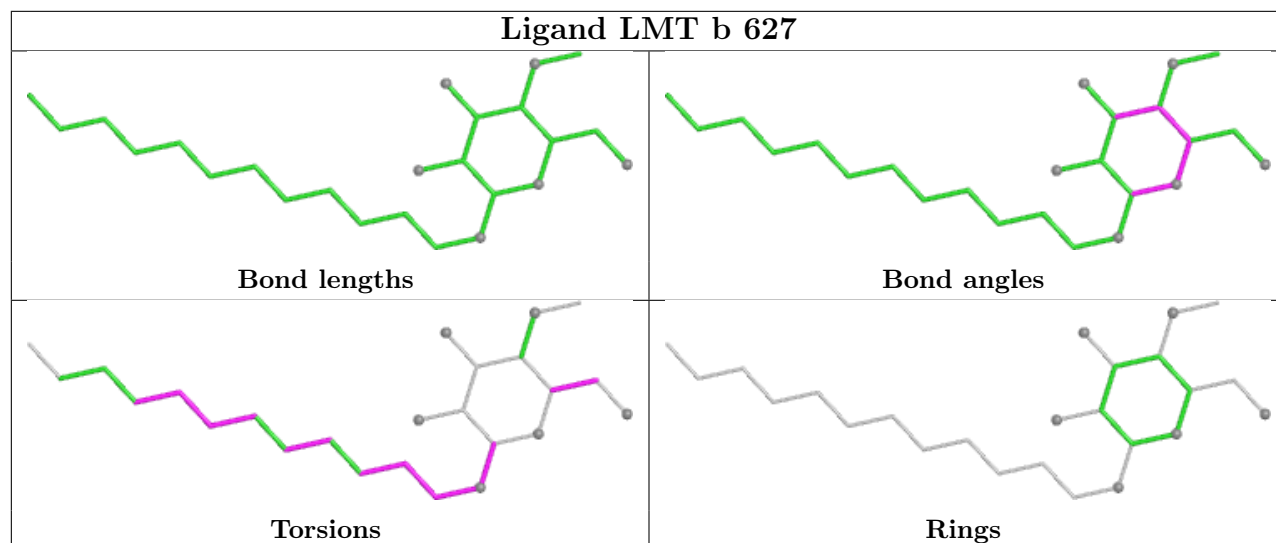
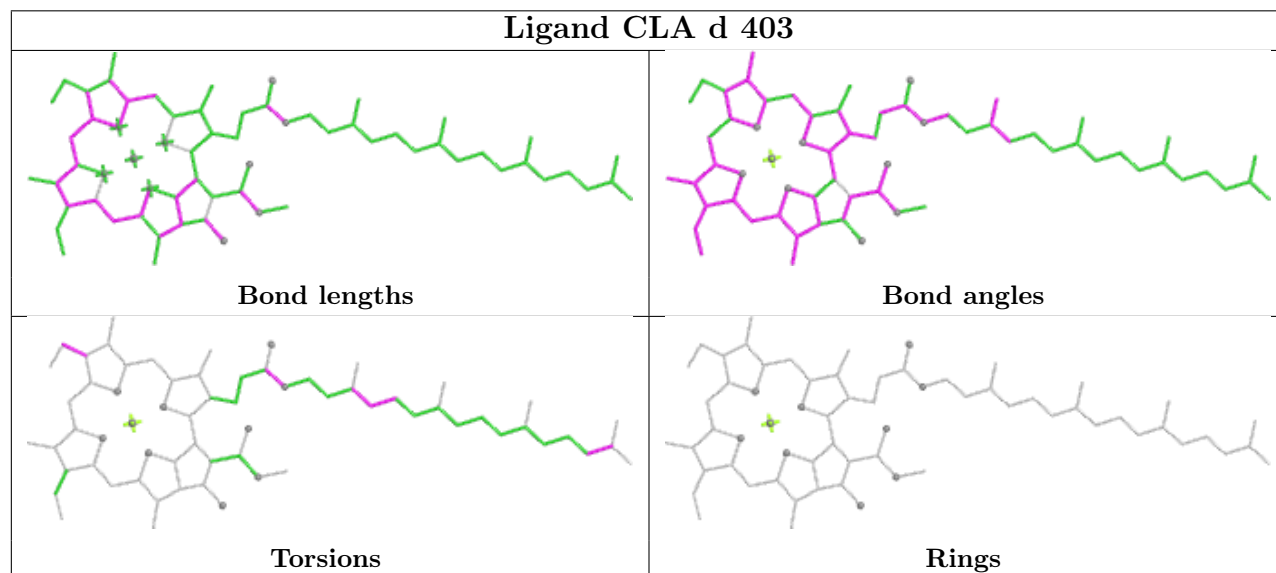
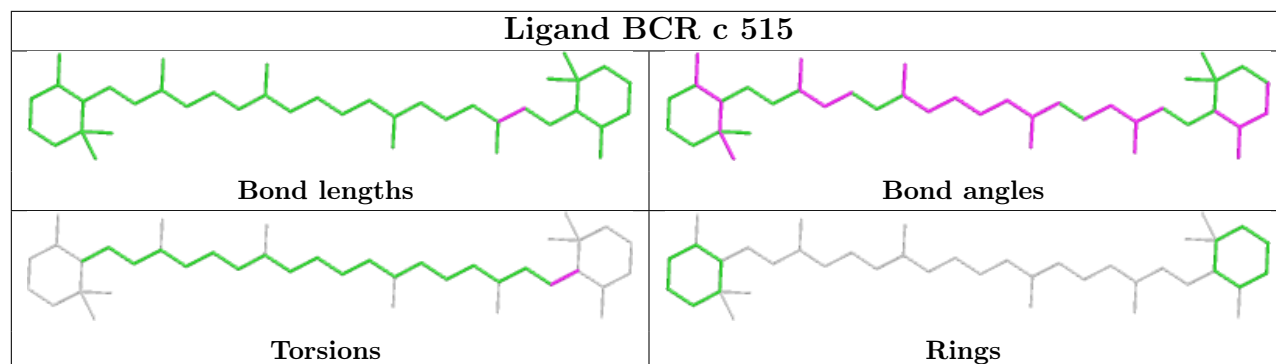


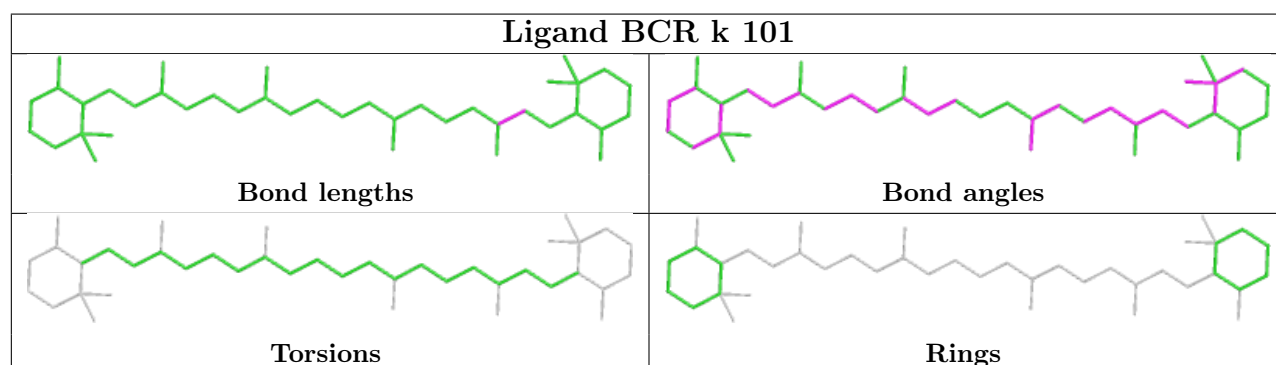
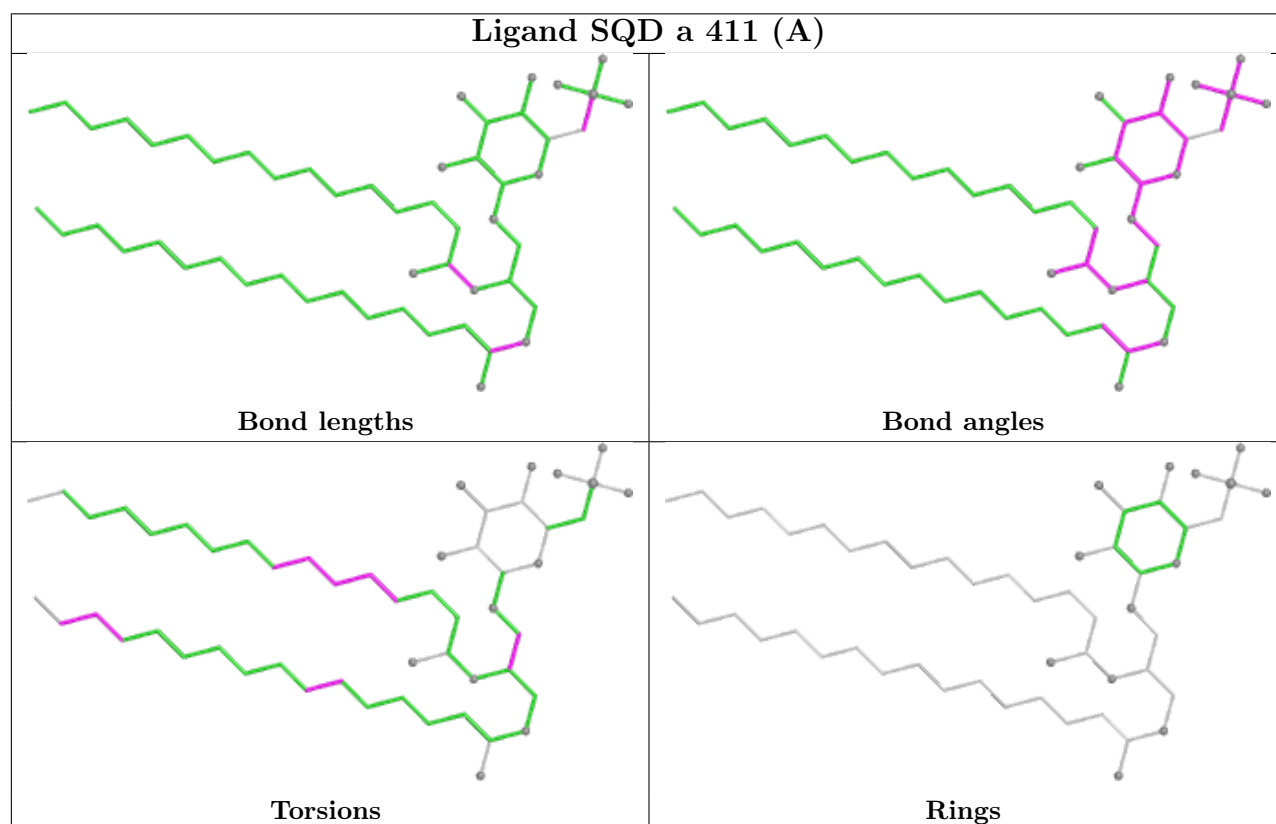
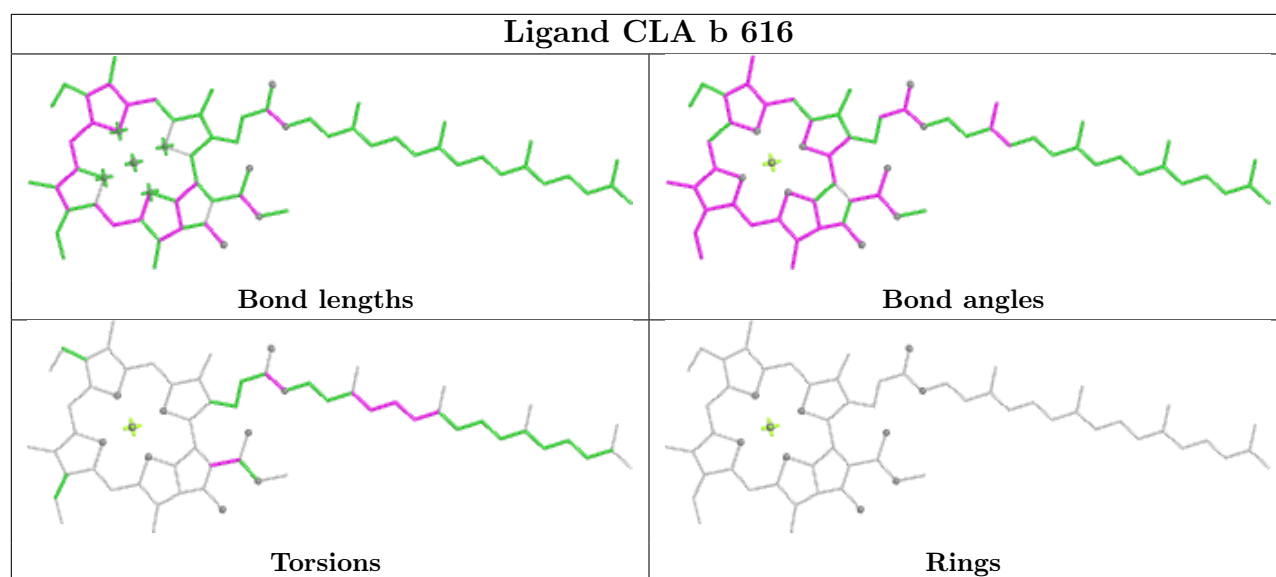
Ligand BCR b 619

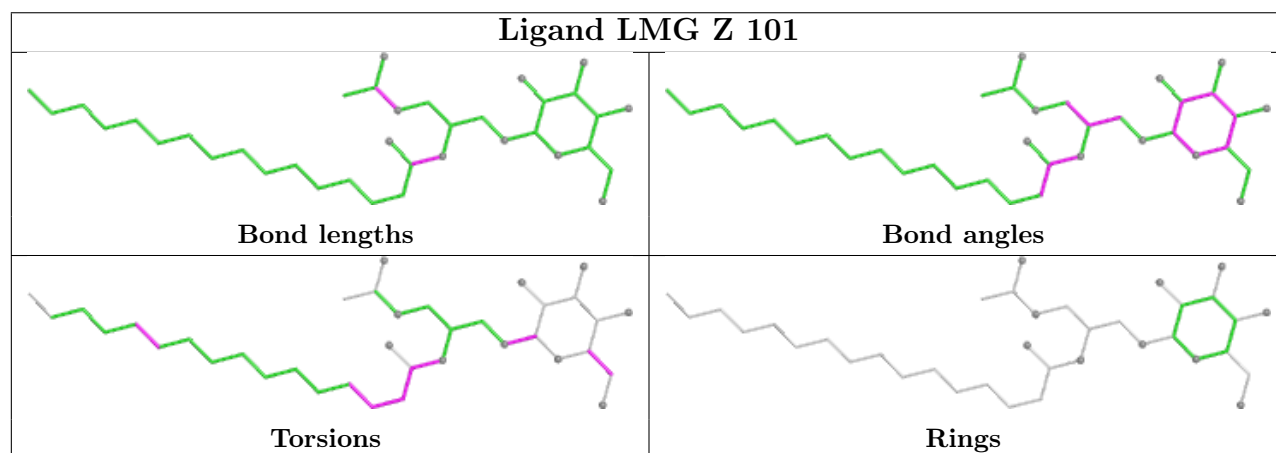
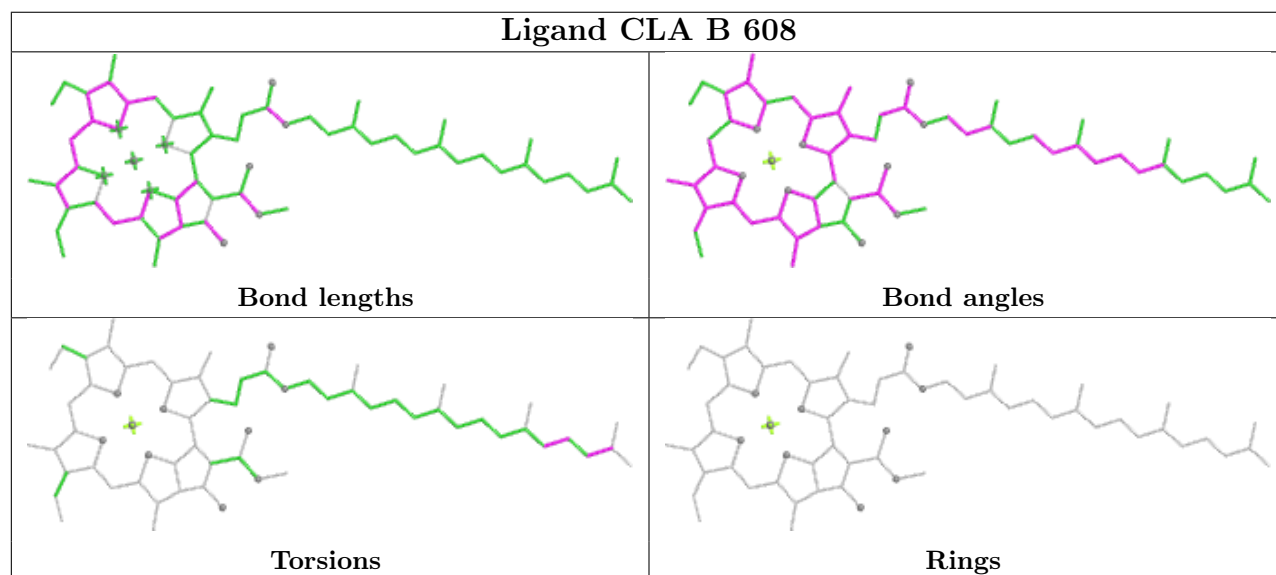
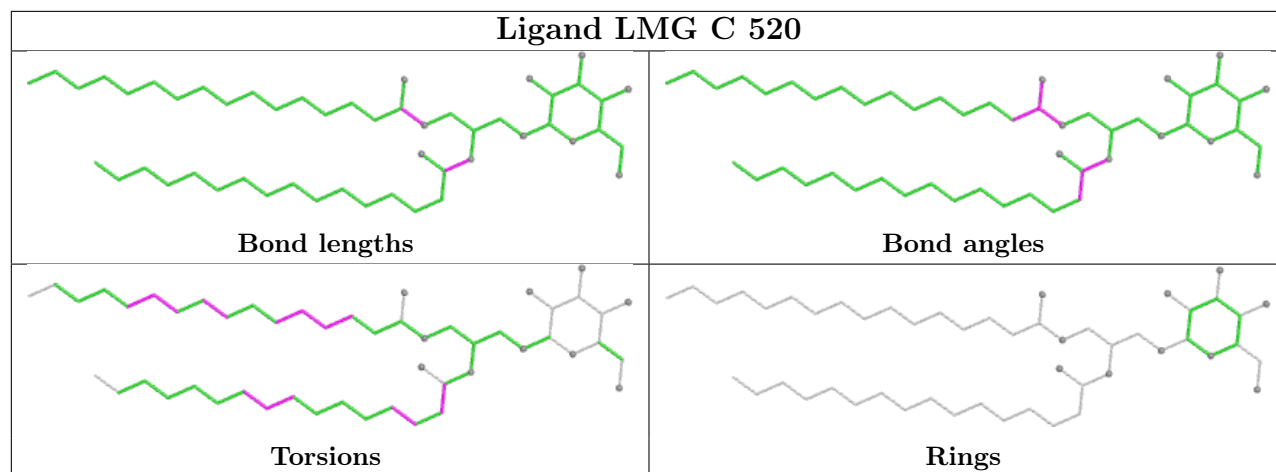




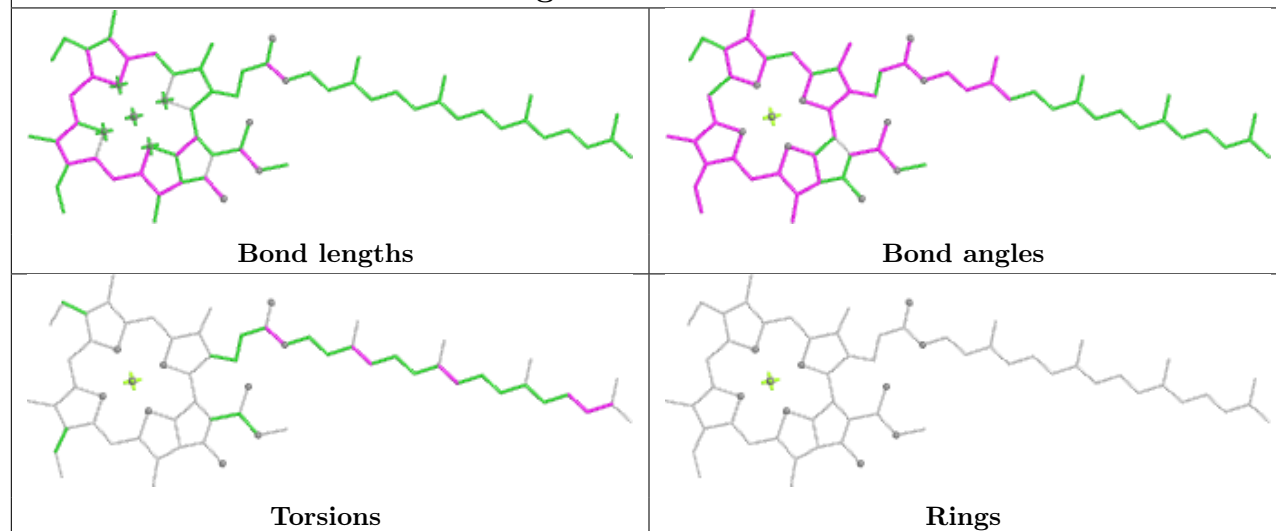




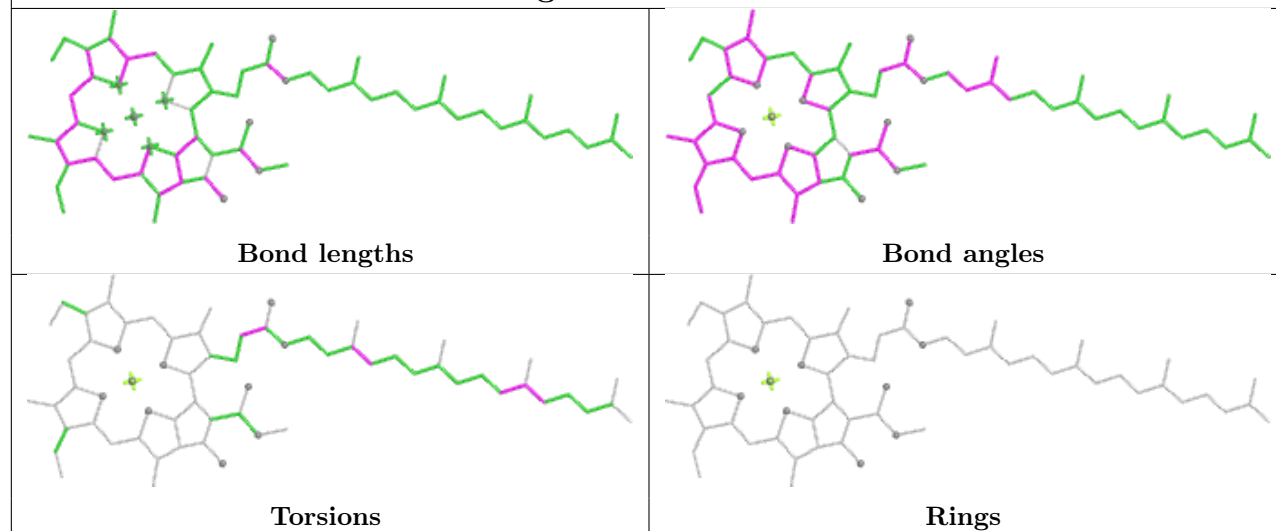




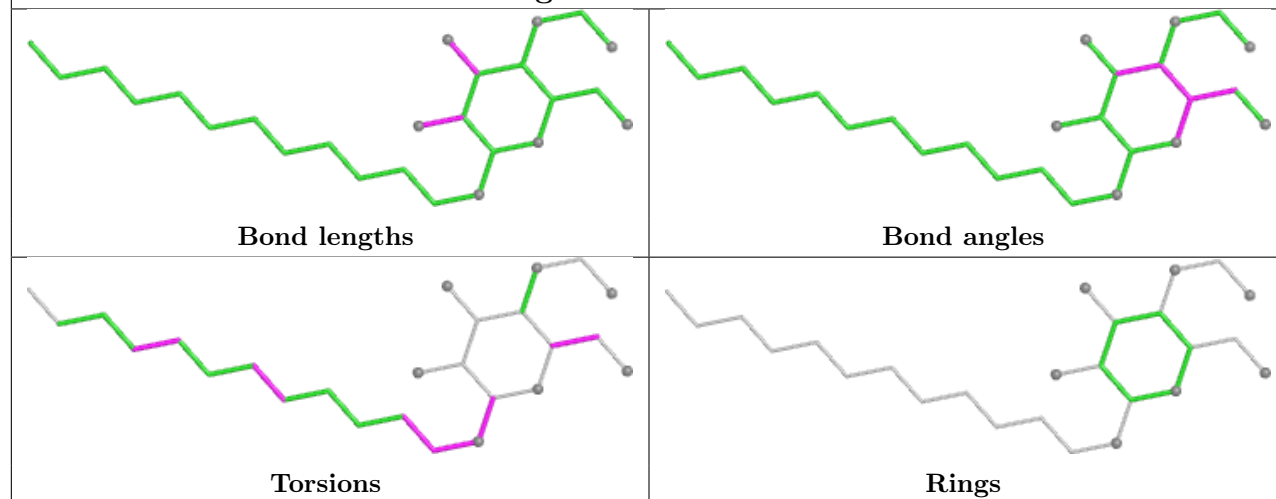
Ligand CLA a 409

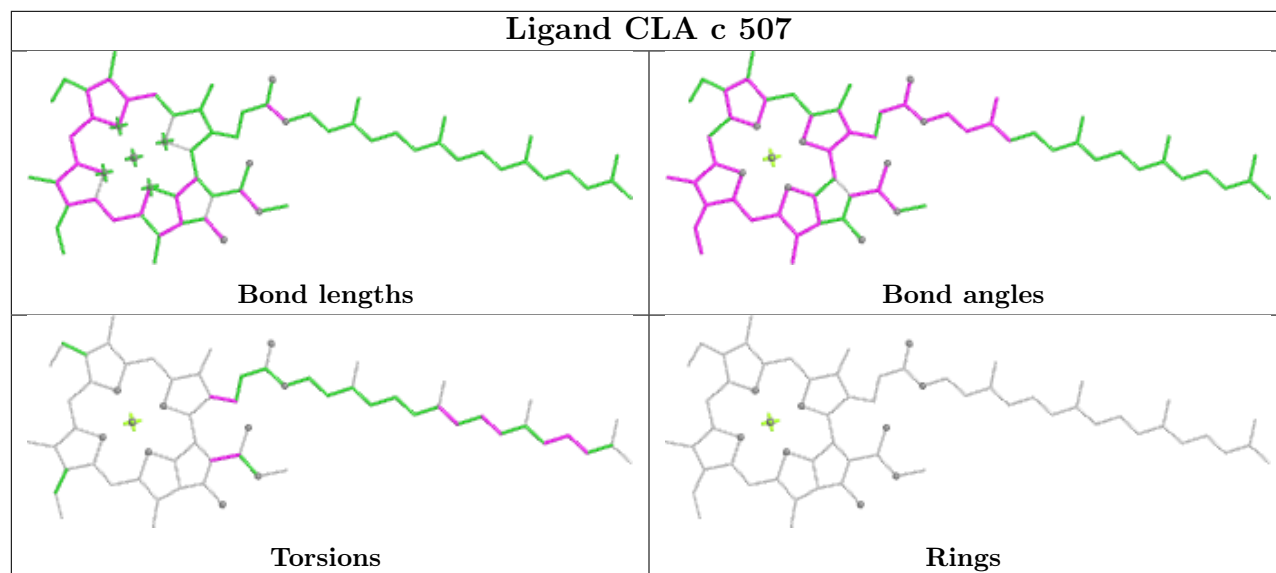
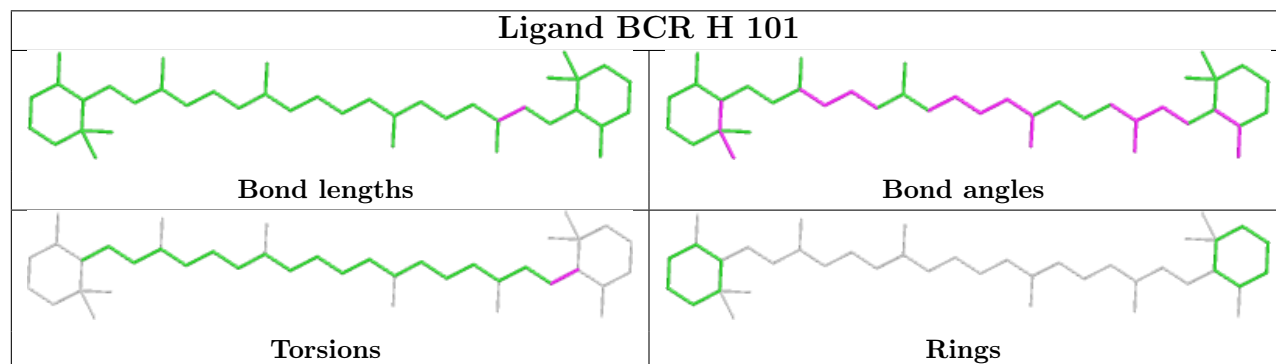
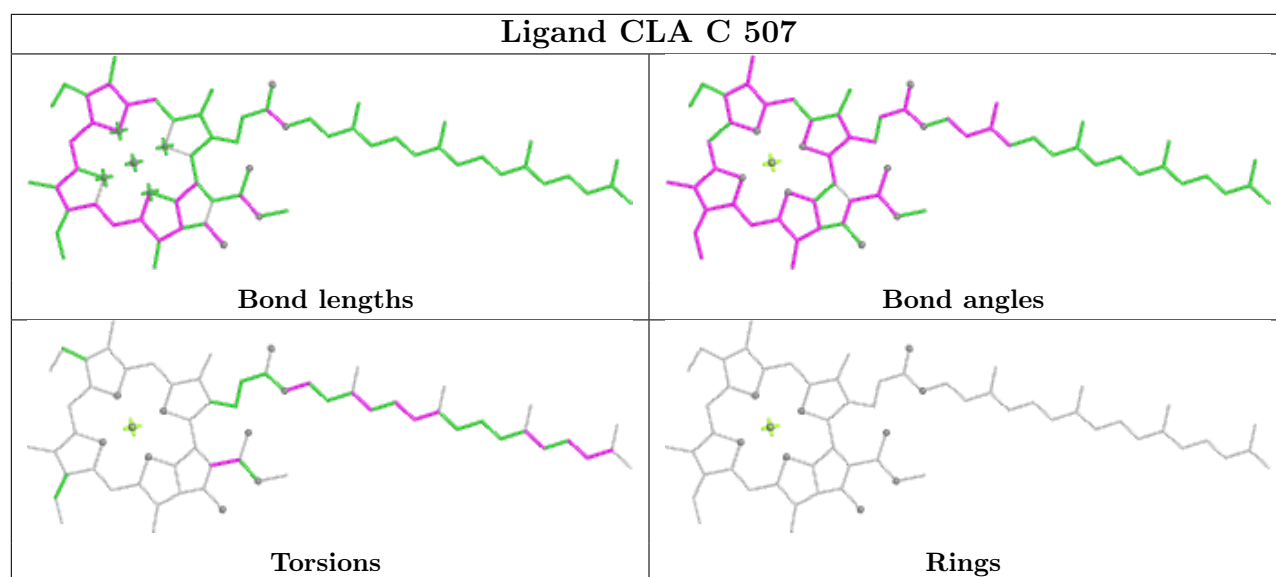


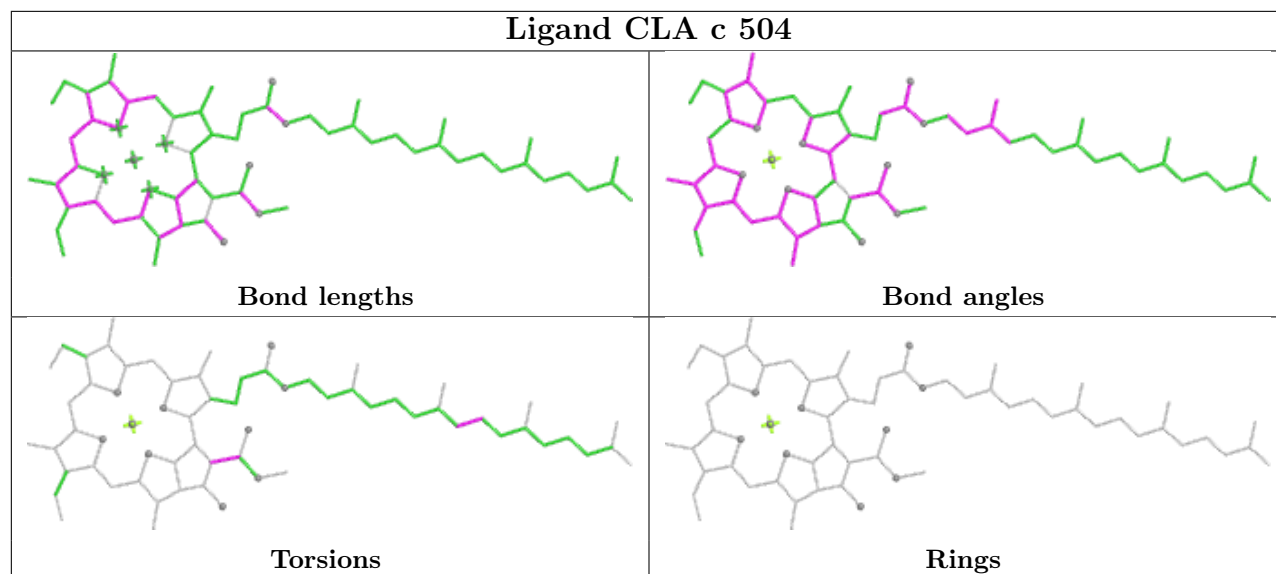
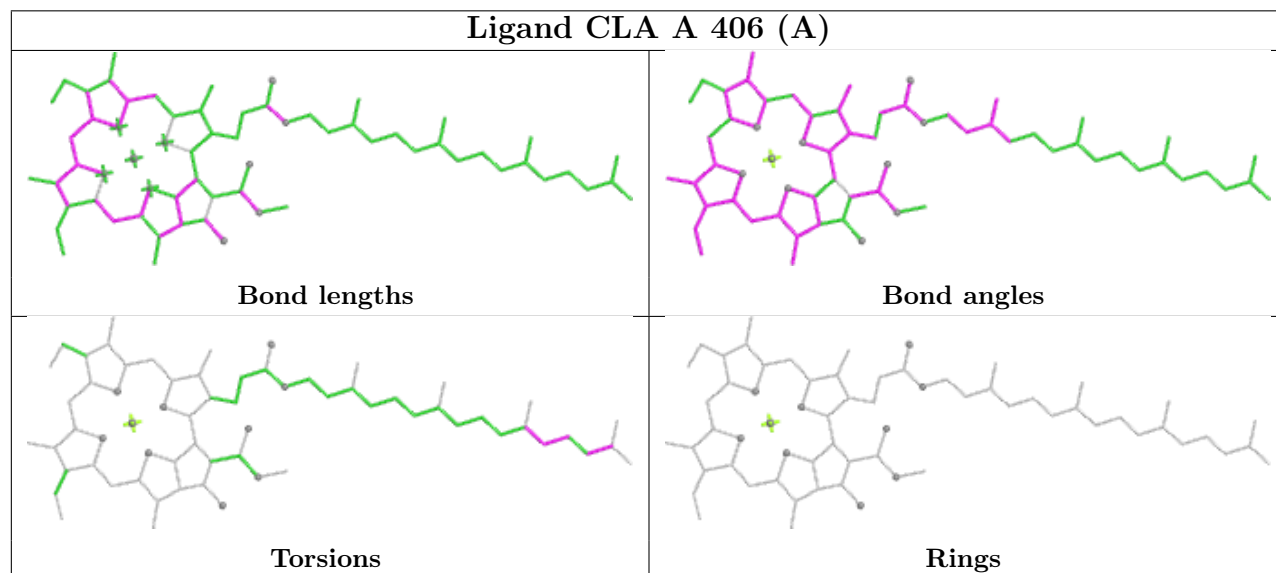
Ligand CLA c 506



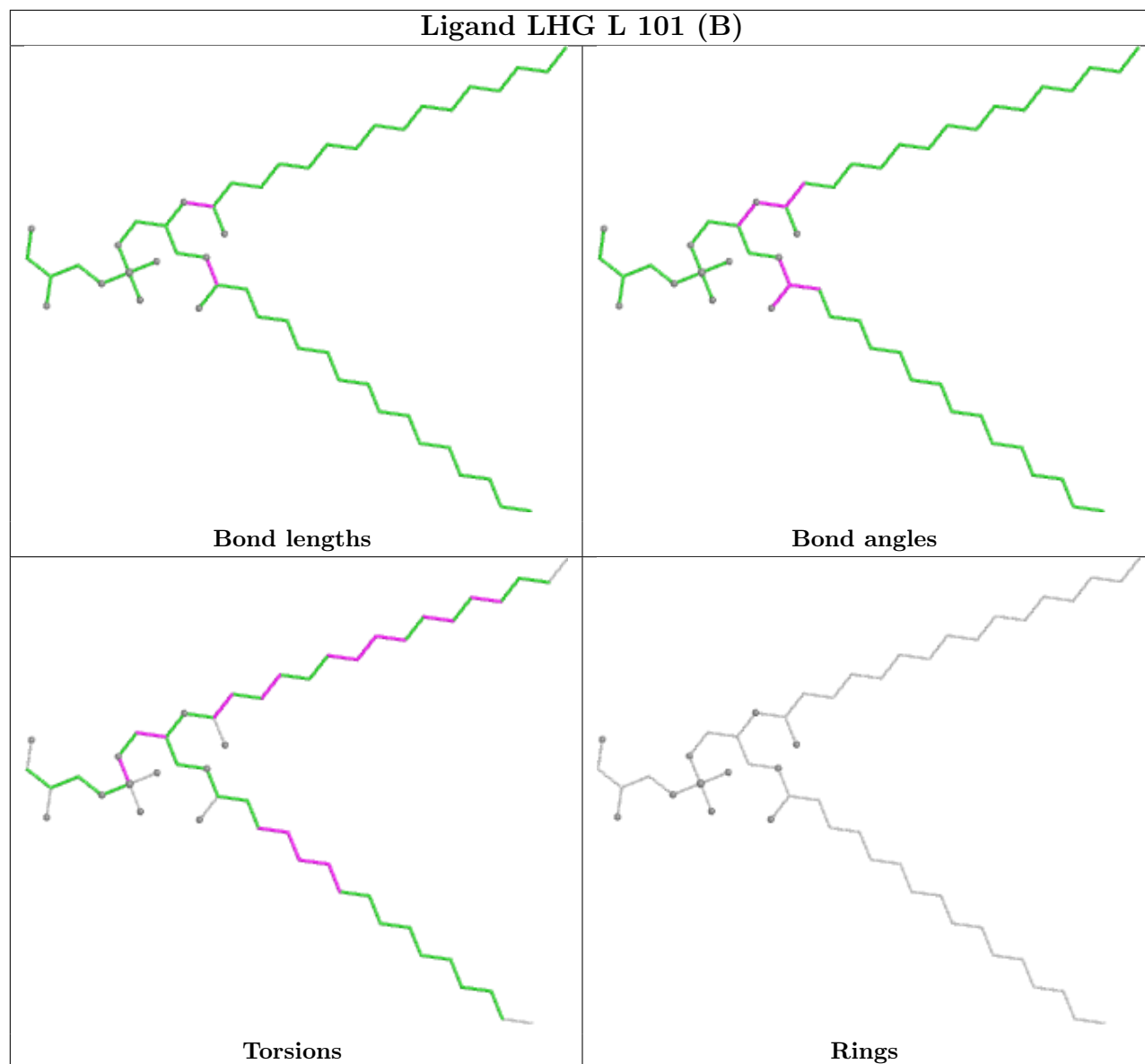
Ligand LMT t 101



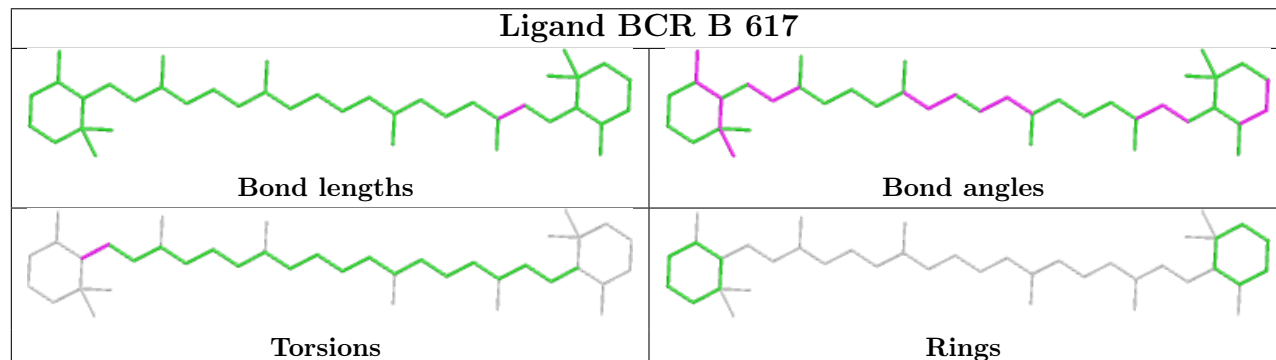


Ligand CLA c 504**Ligand CLA A 406 (A)**

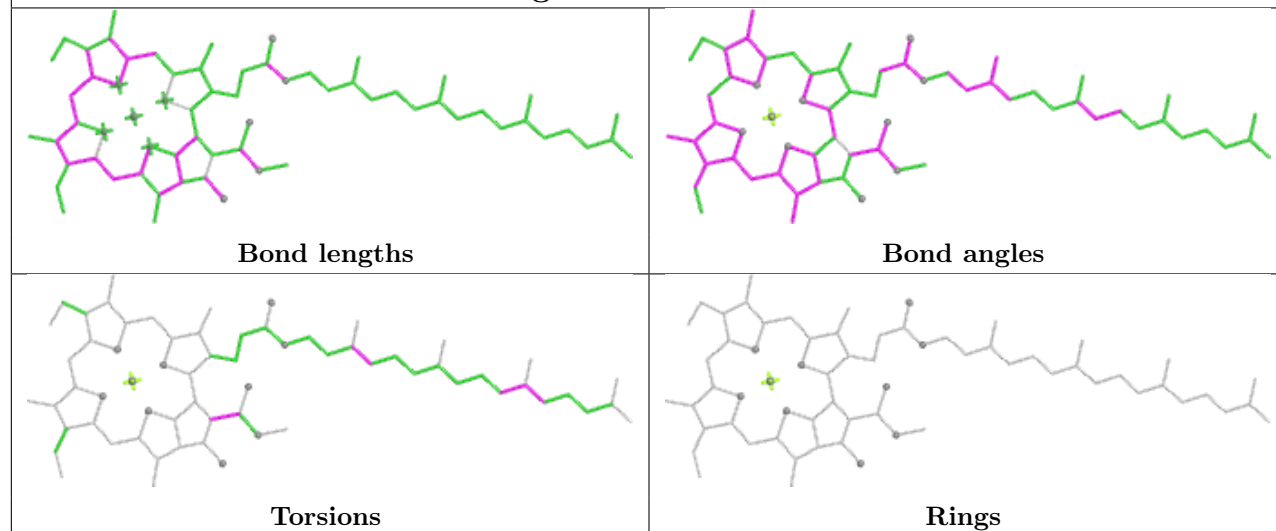
Ligand LHG L 101 (B)



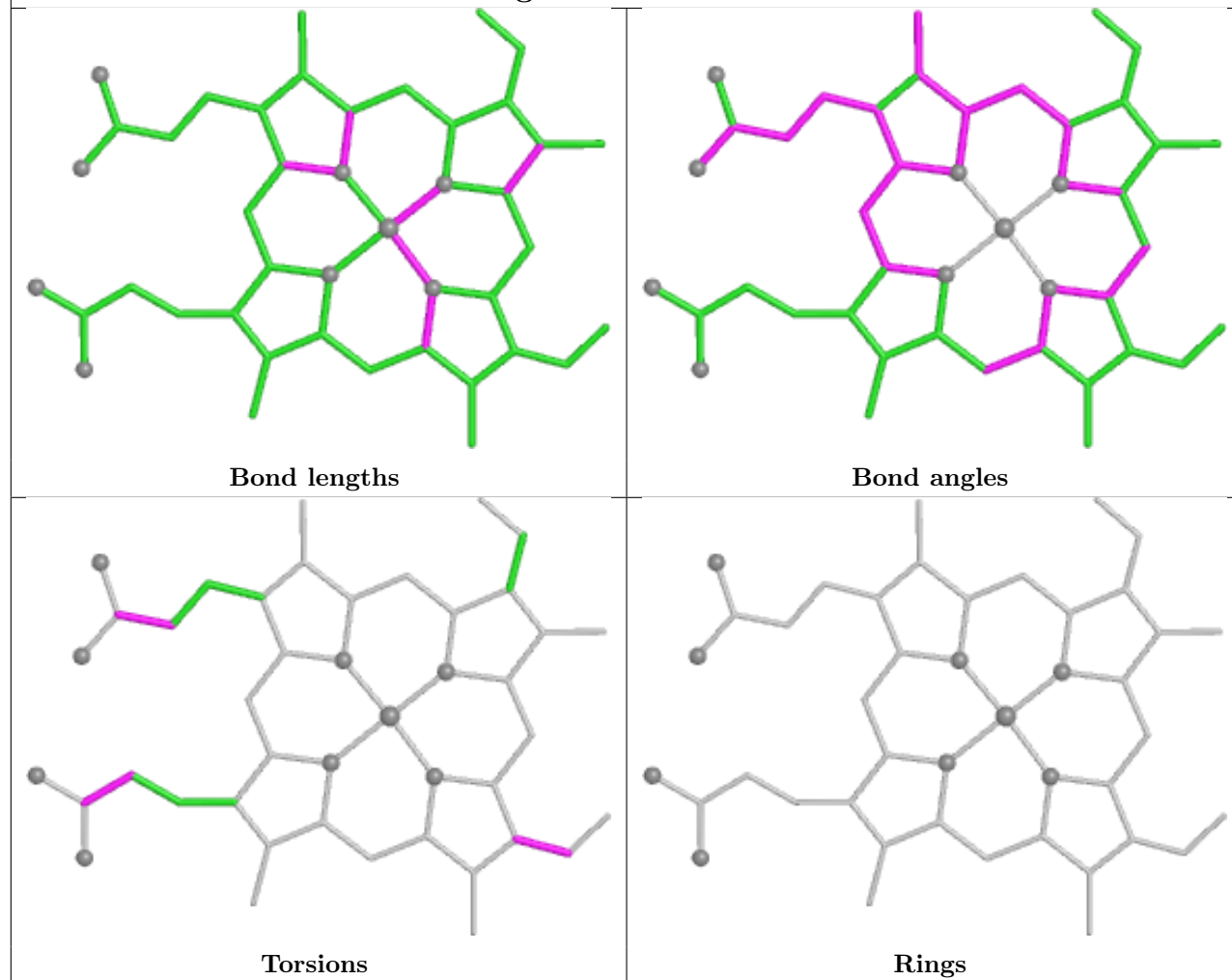
Ligand BCR B 617

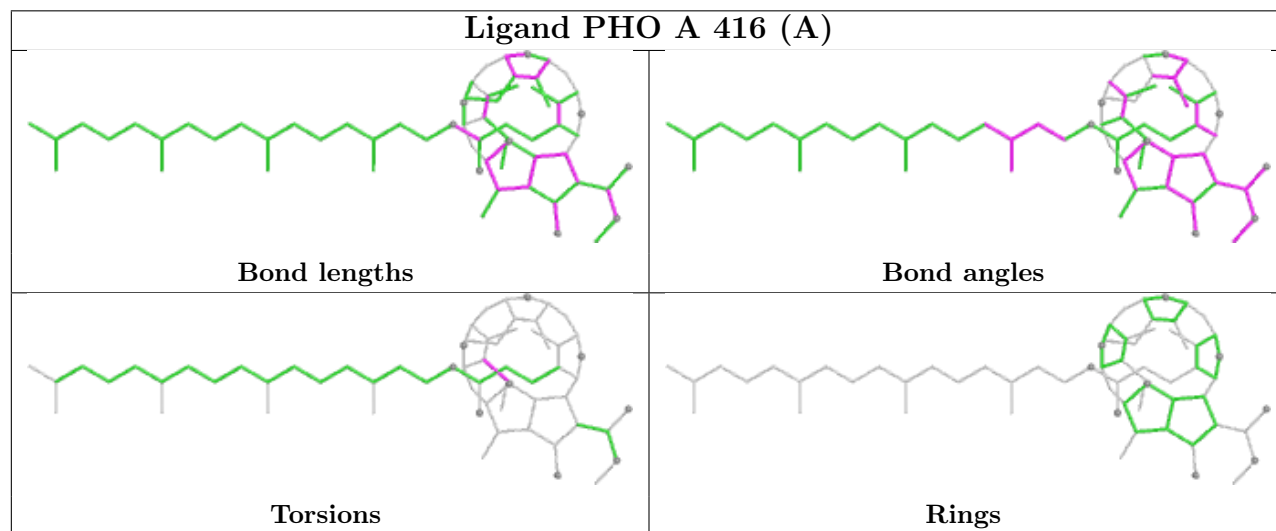
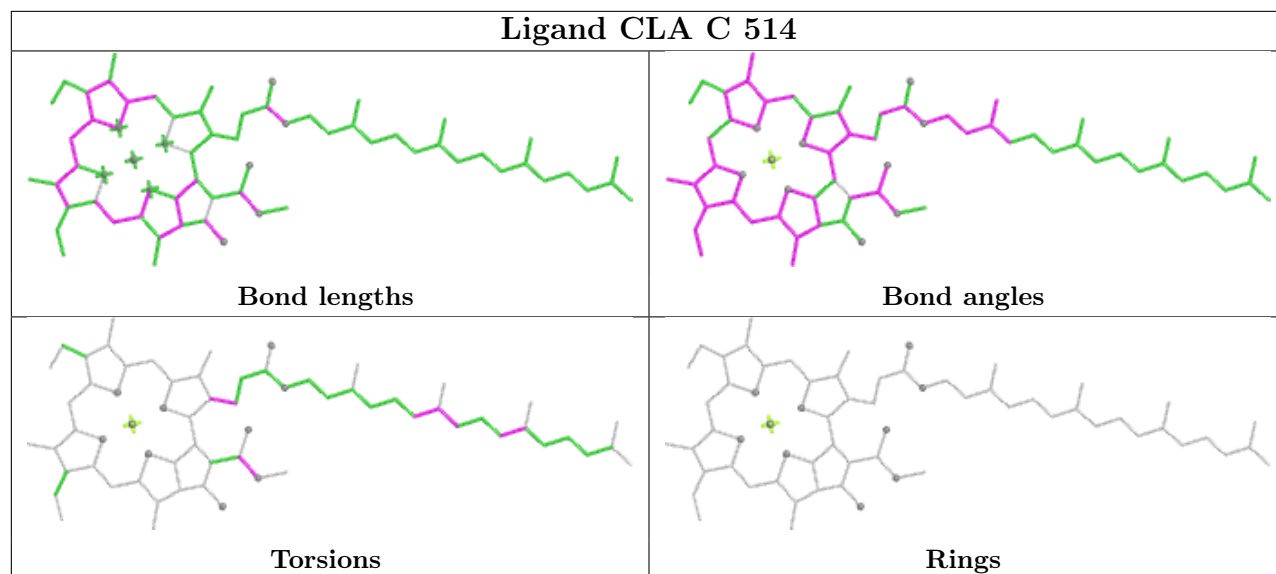


Ligand CLA C 506

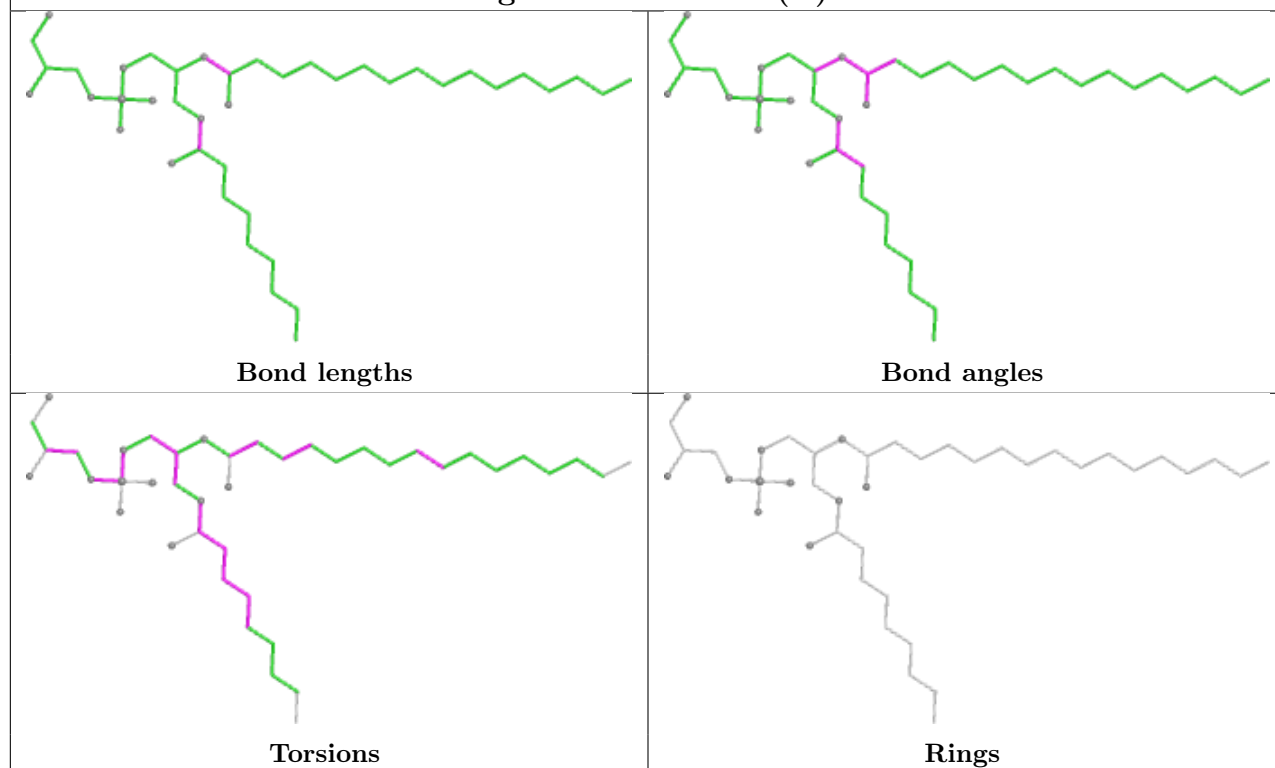


Ligand HEM f 101

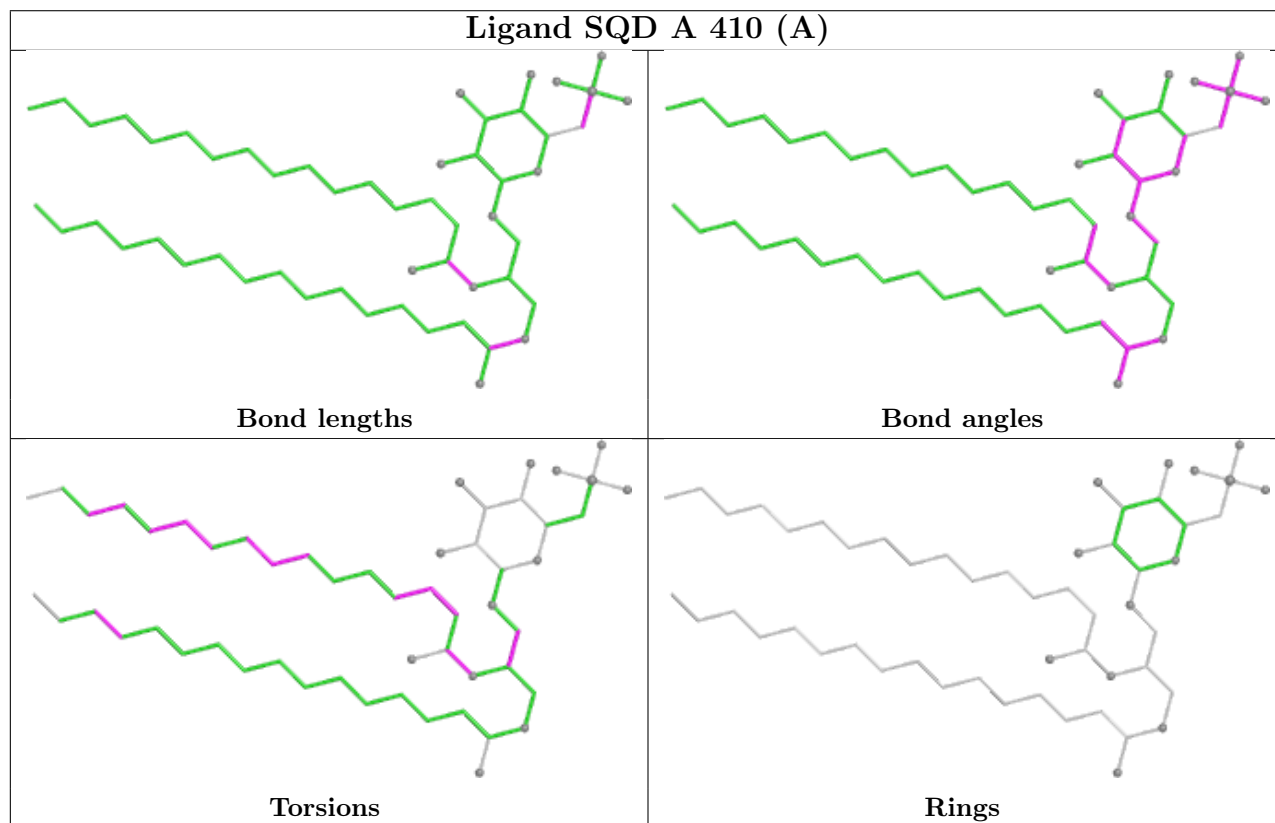




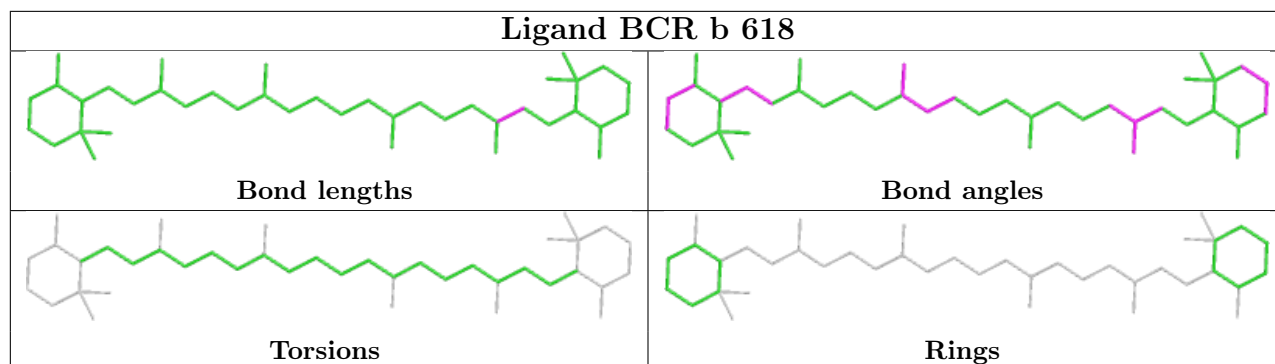
Ligand LHG E 101 (B)



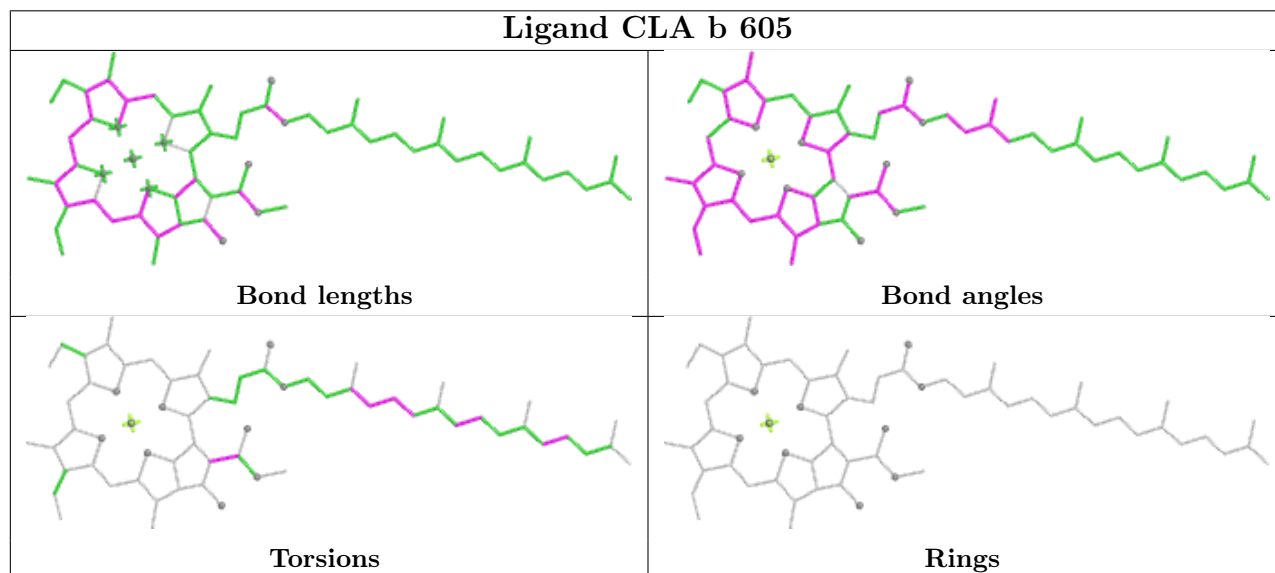
Ligand SQD A 410 (A)



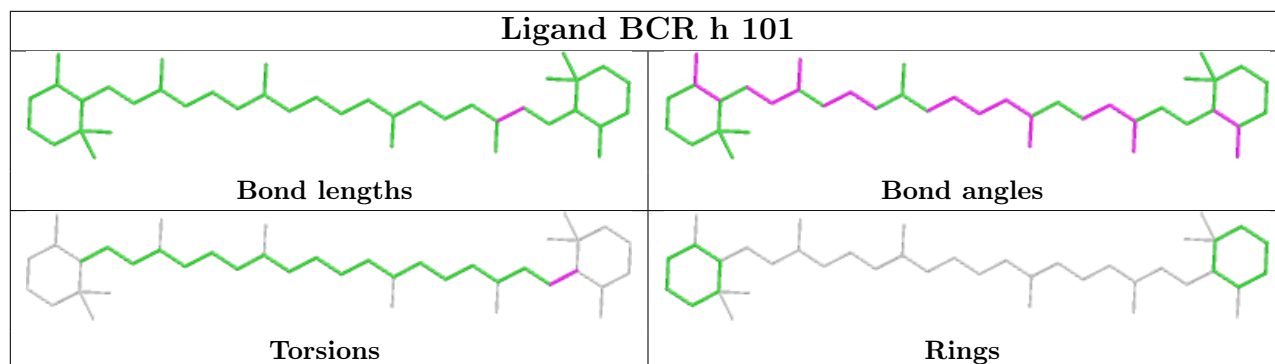
Ligand BCR b 618

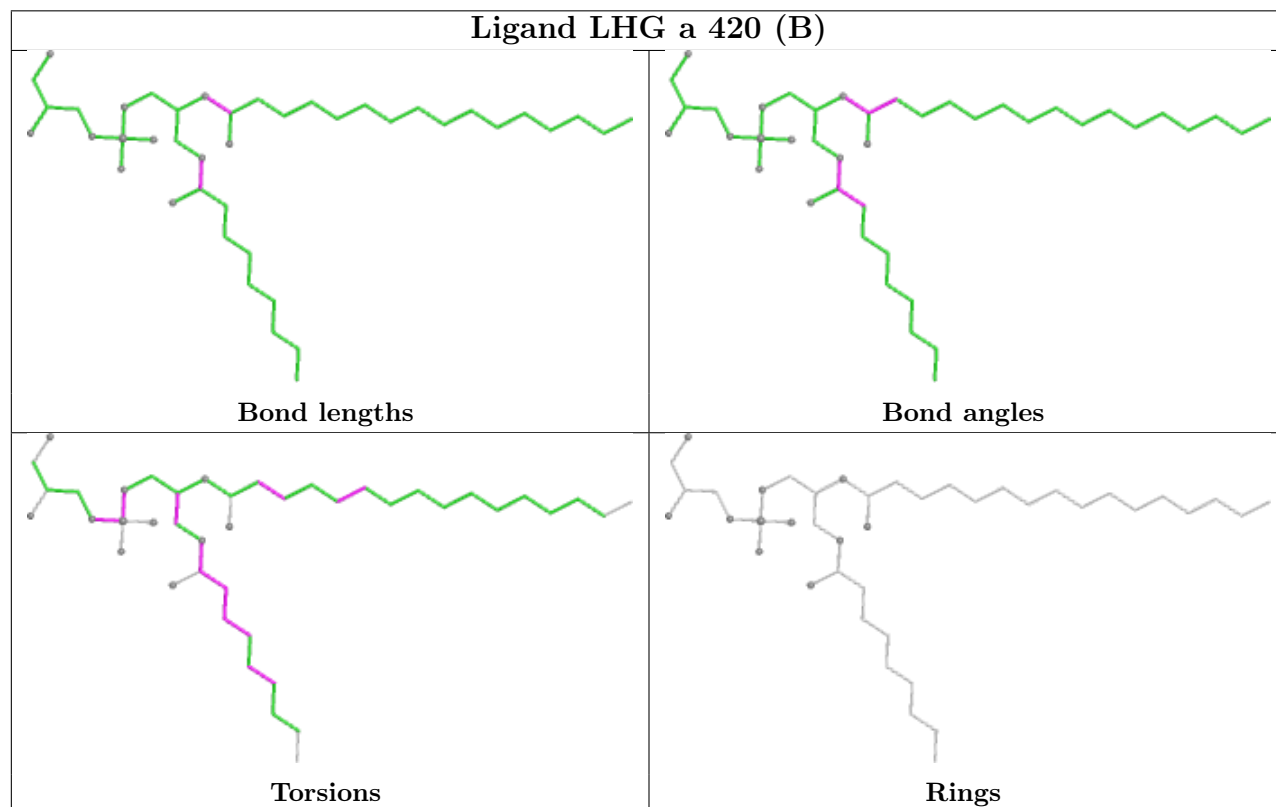
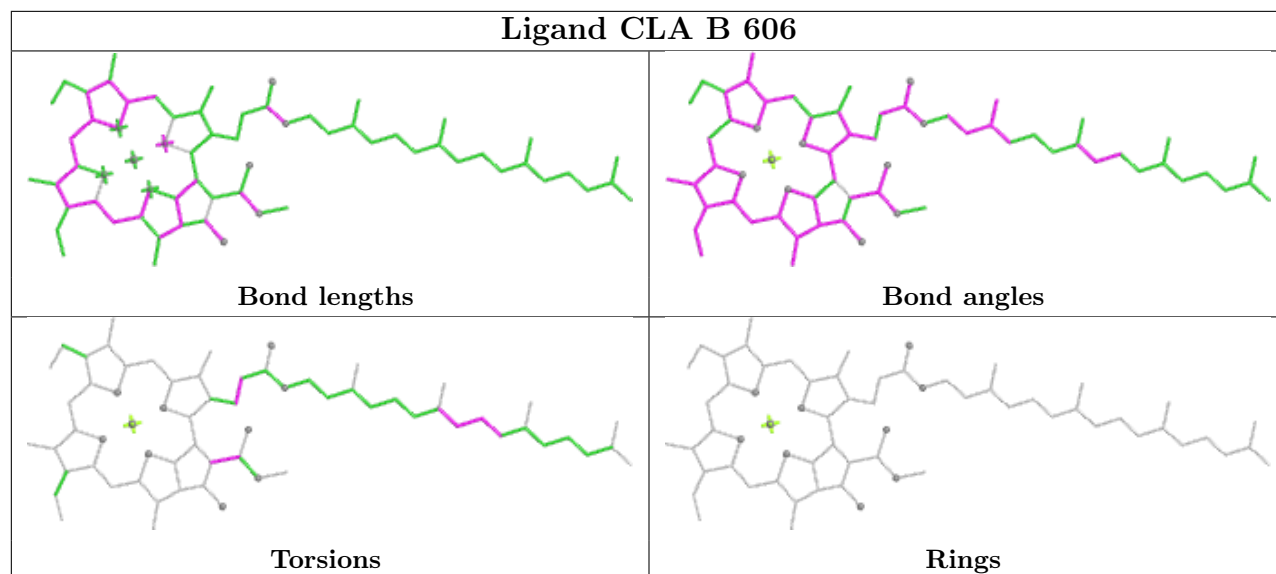


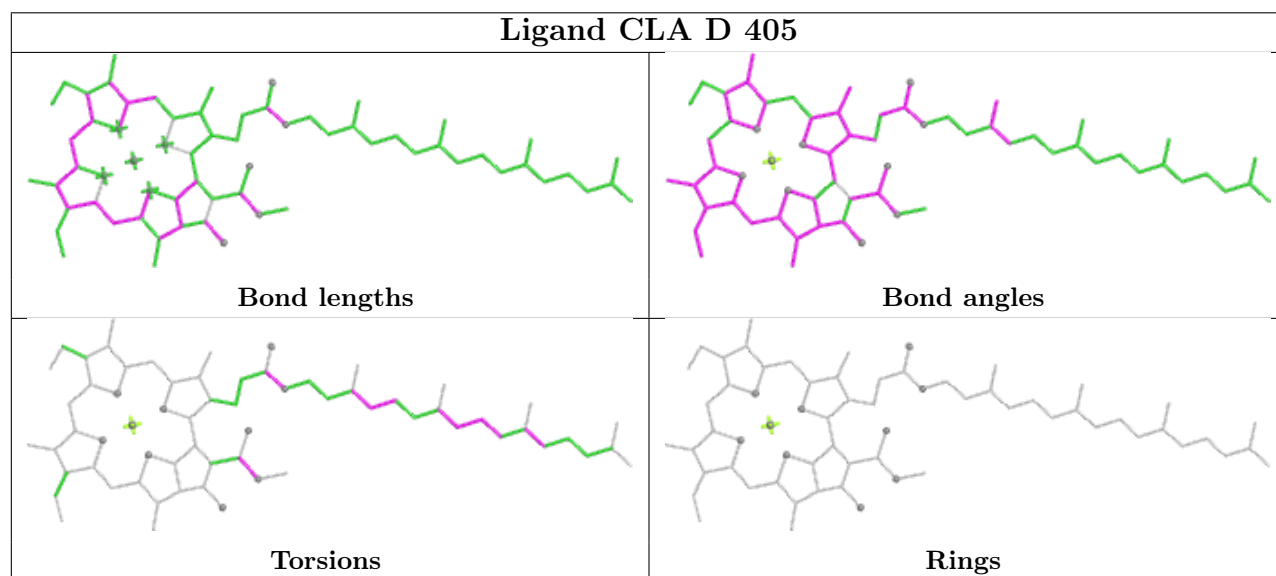
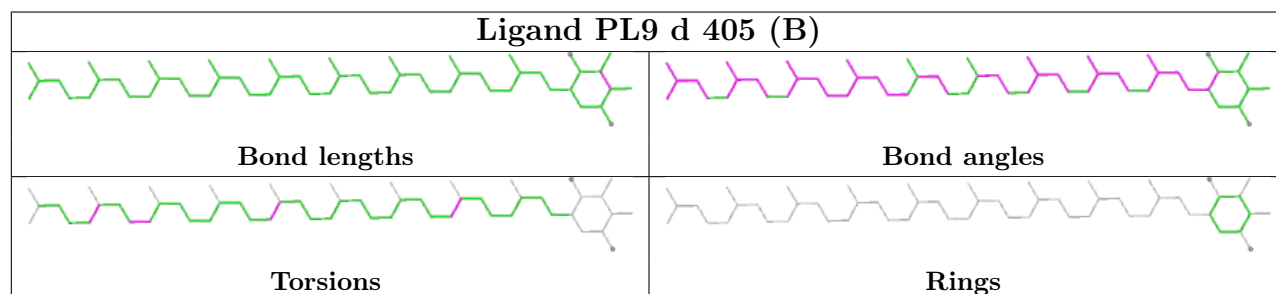
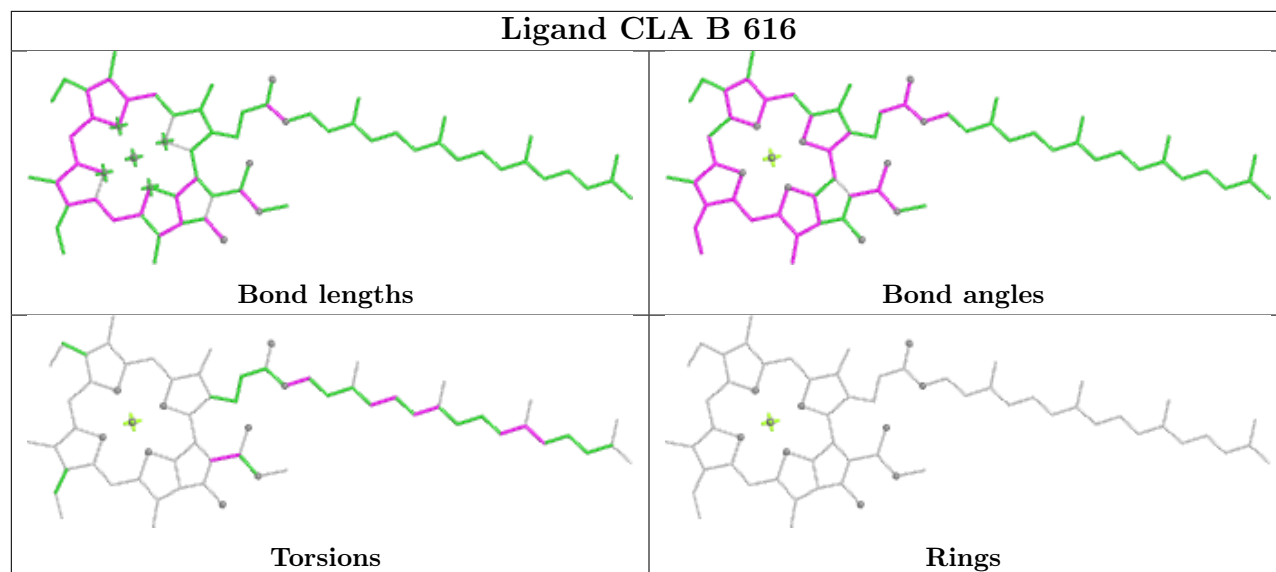
Ligand CLA b 605

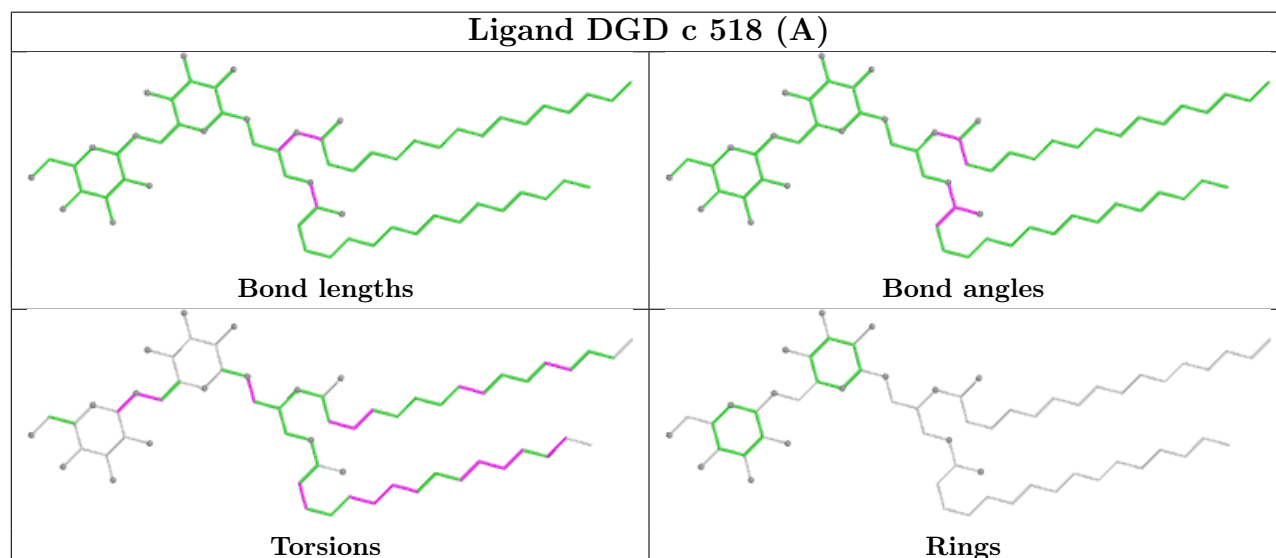
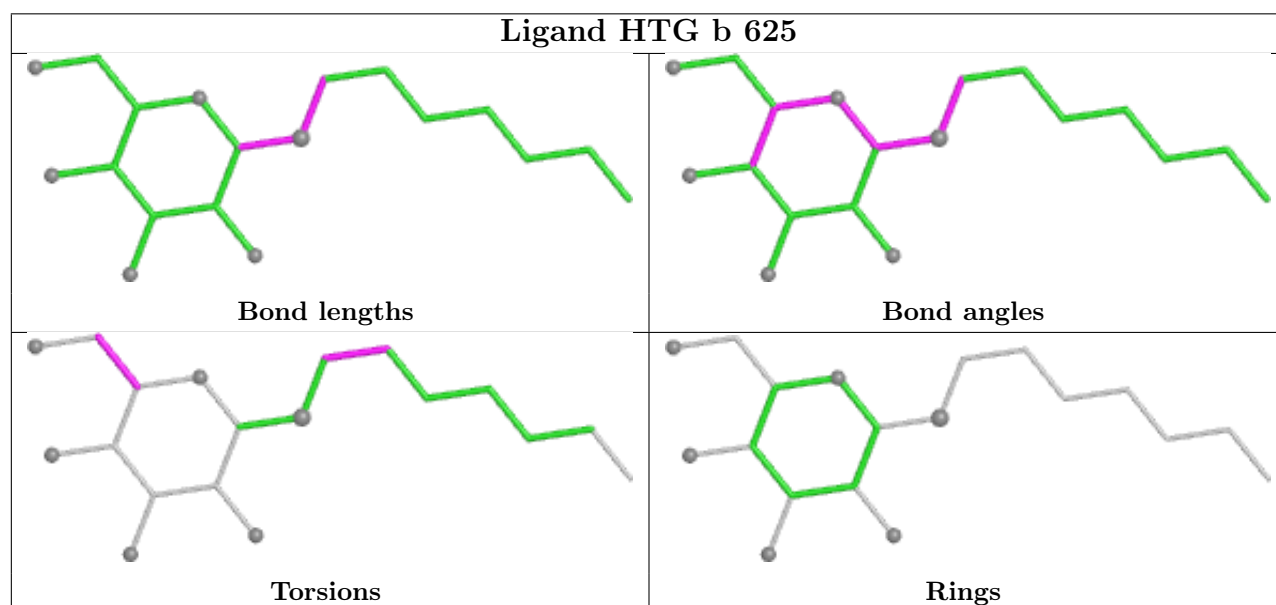
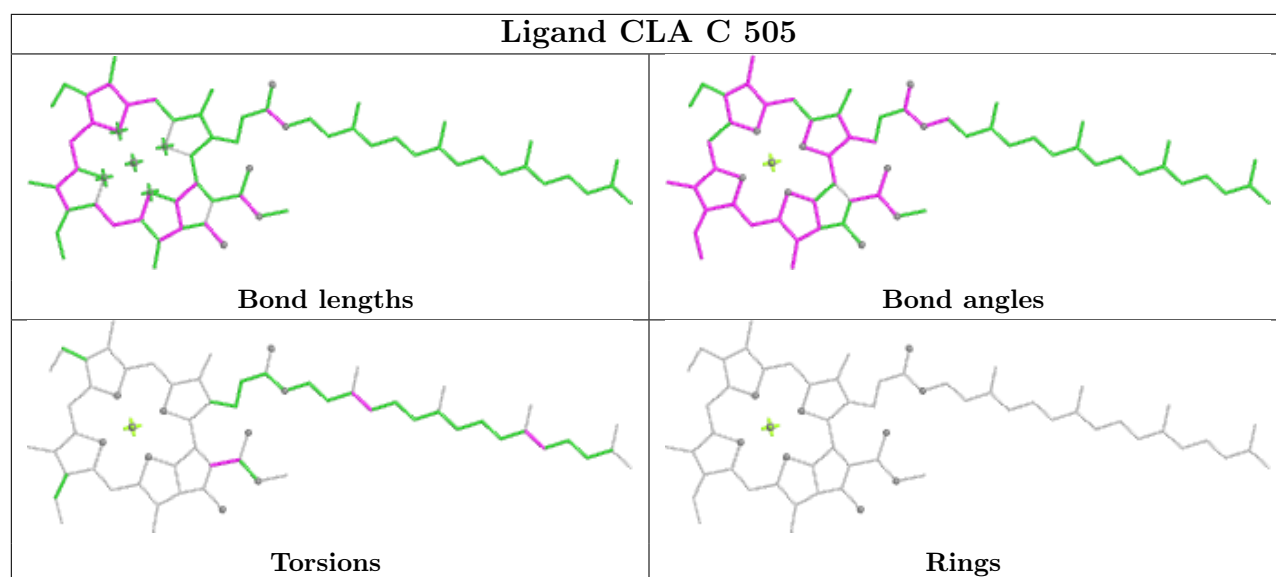


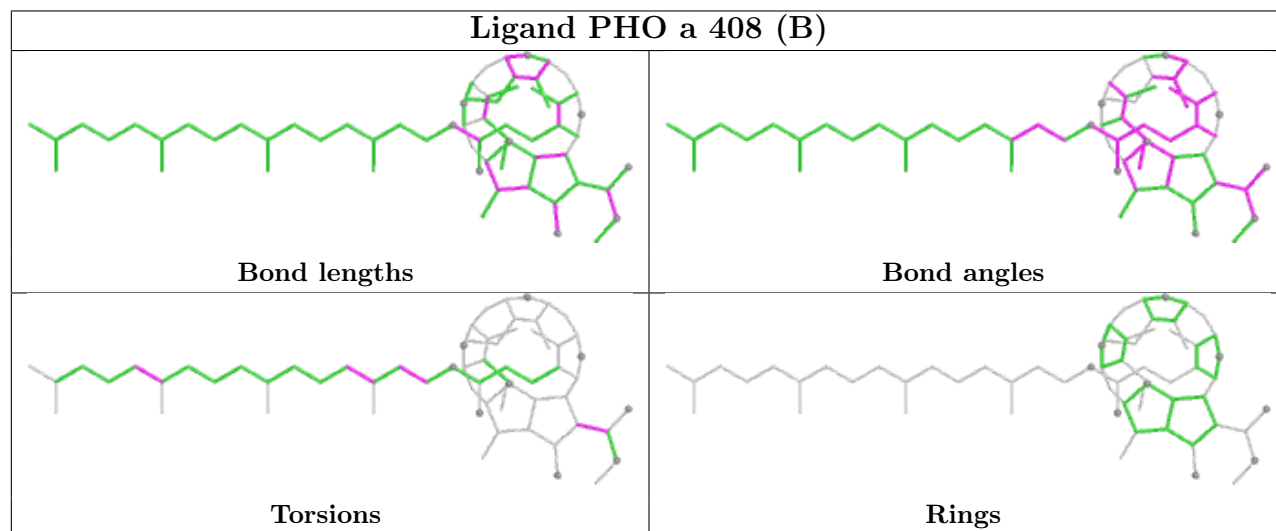
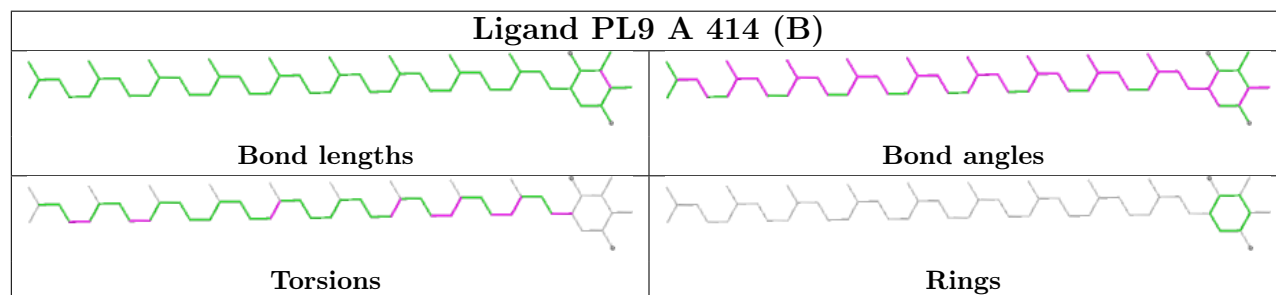
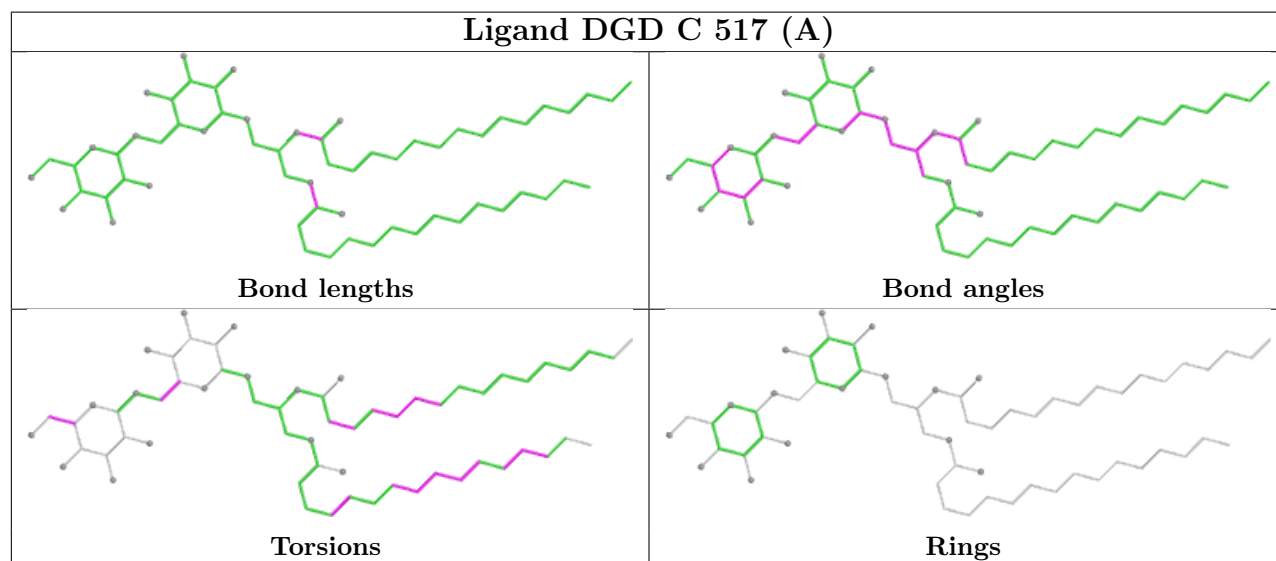
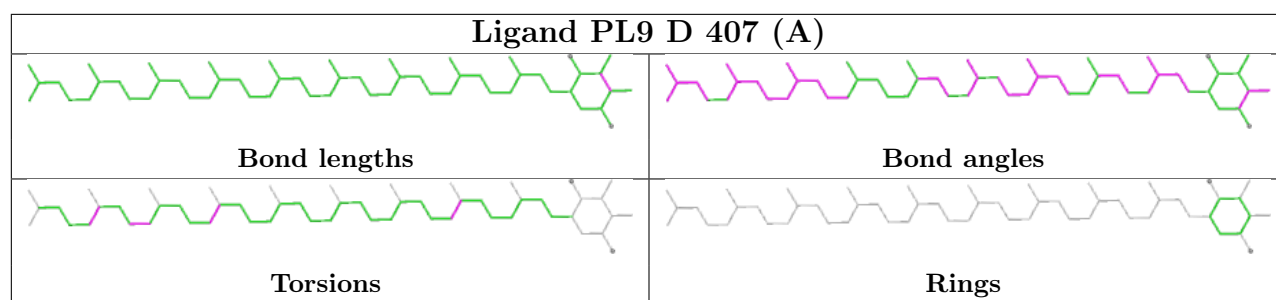
Ligand BCR h 101

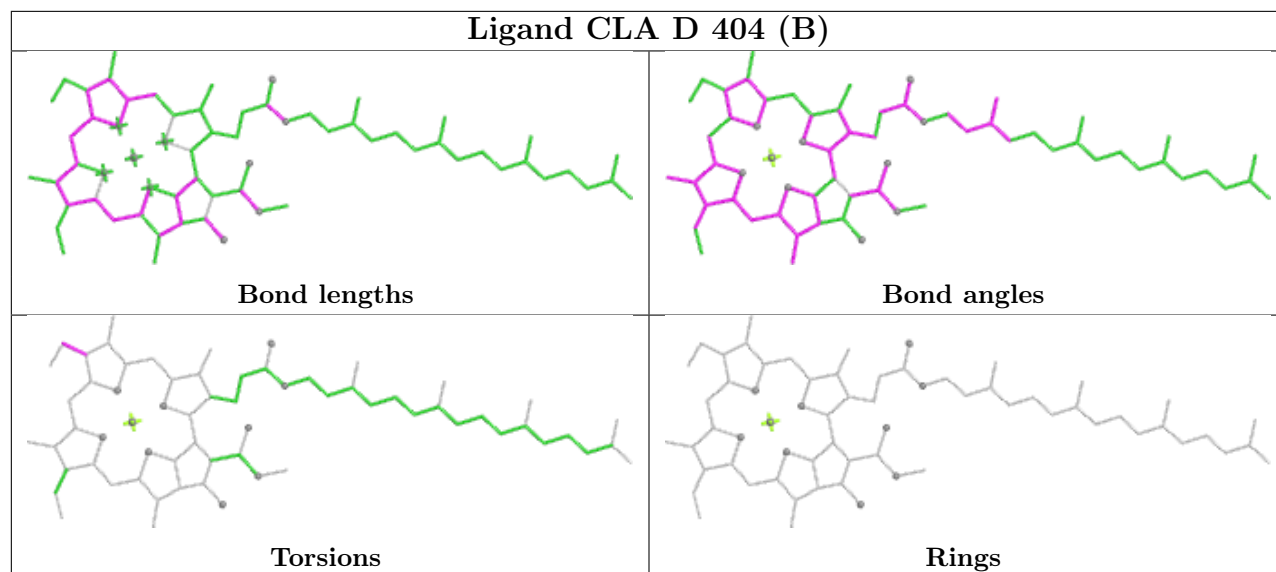
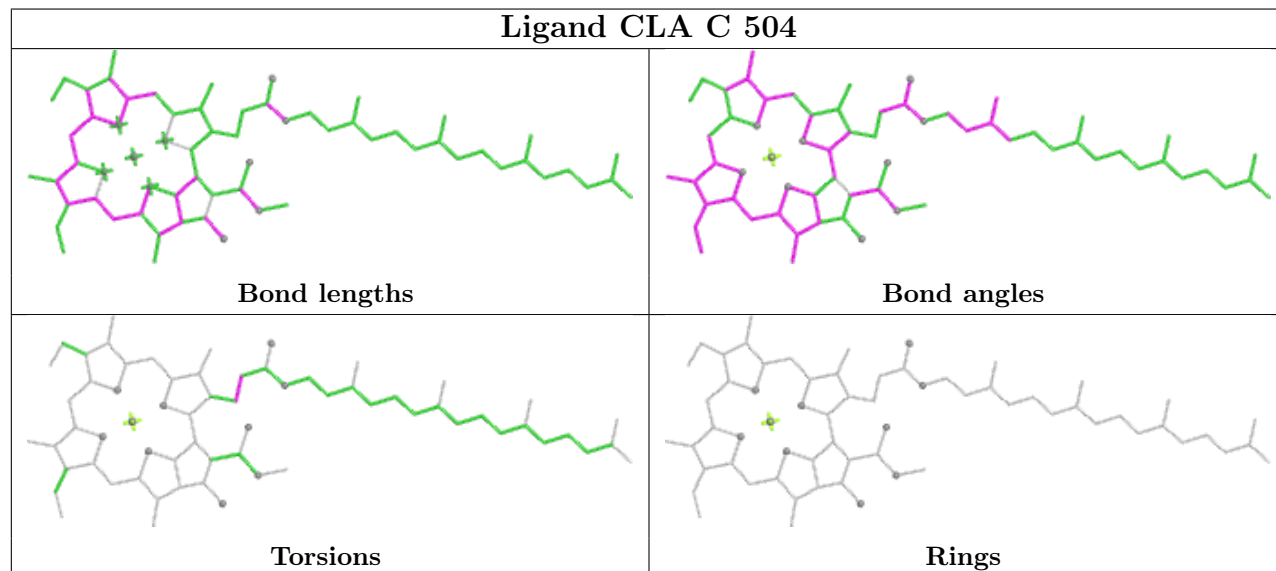
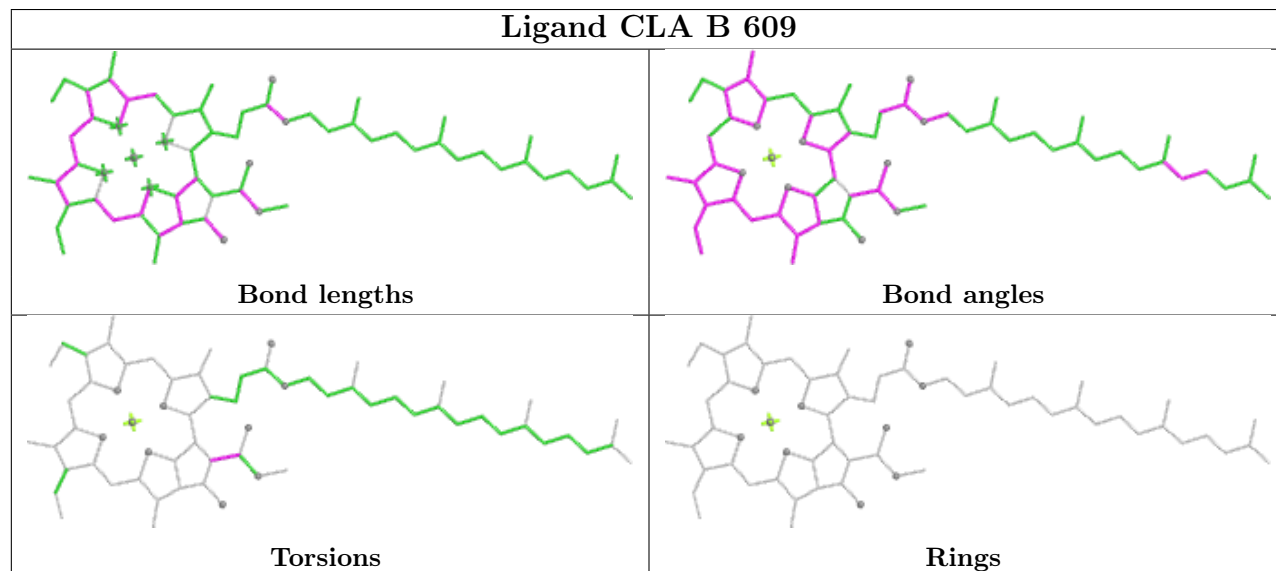


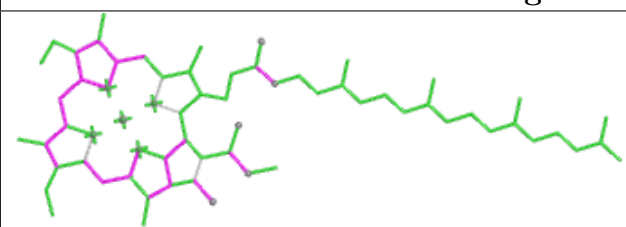
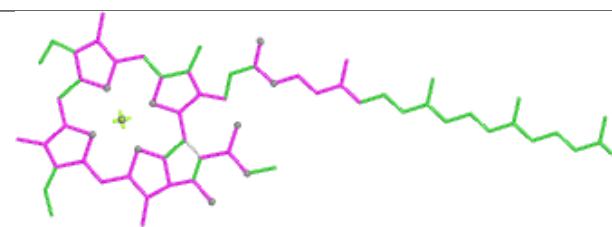
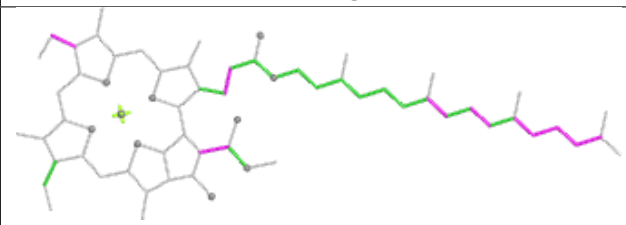
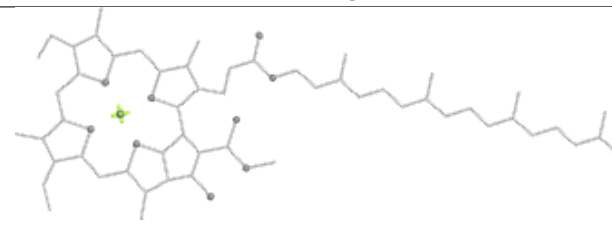


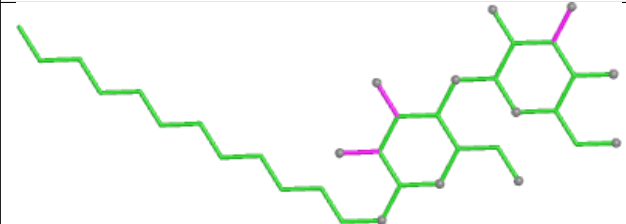
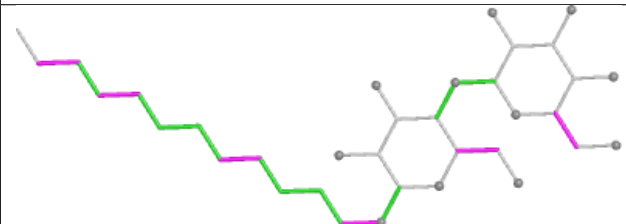
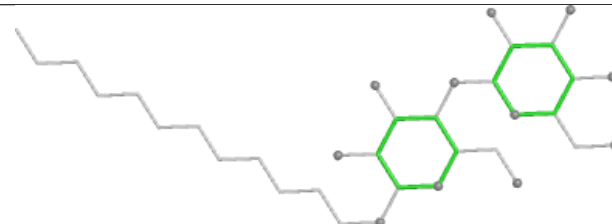


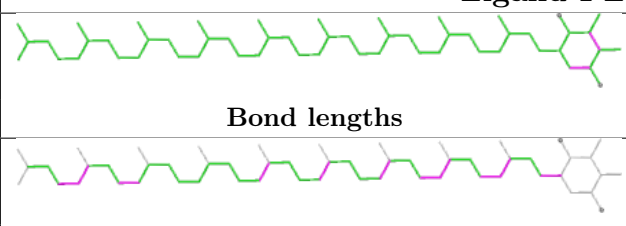
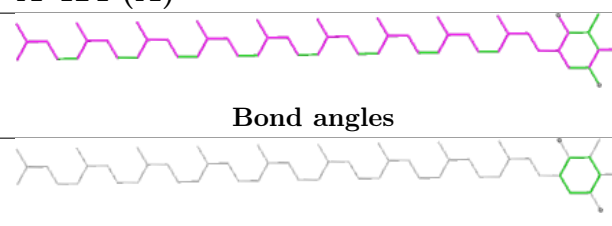
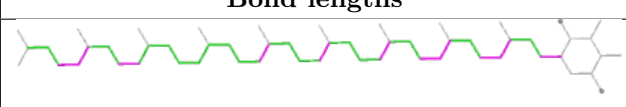
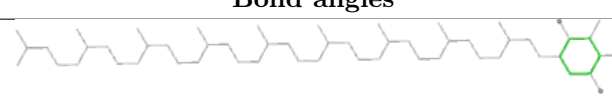


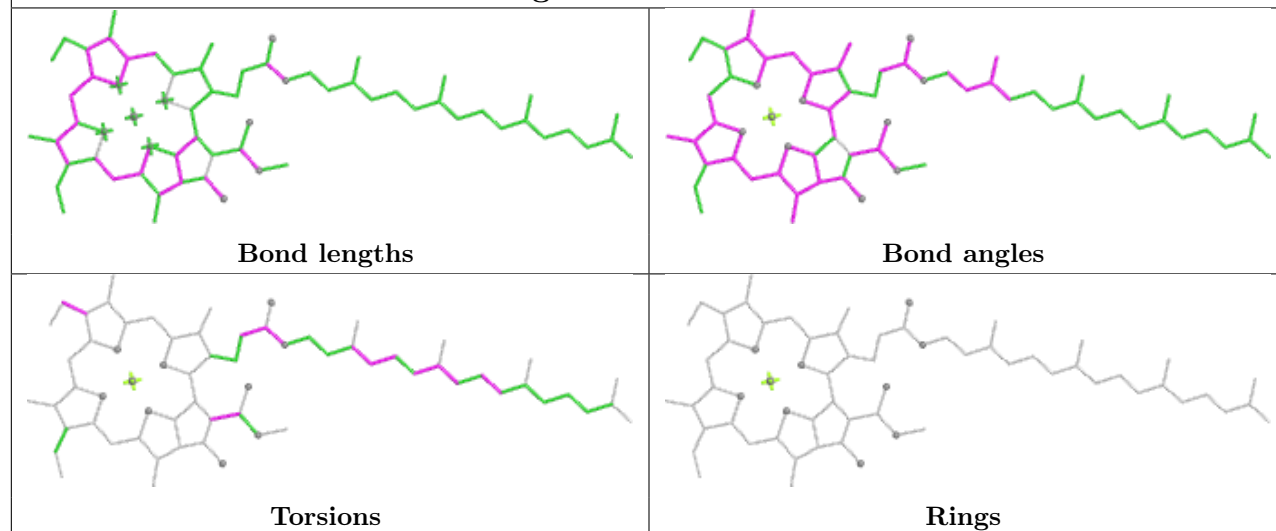
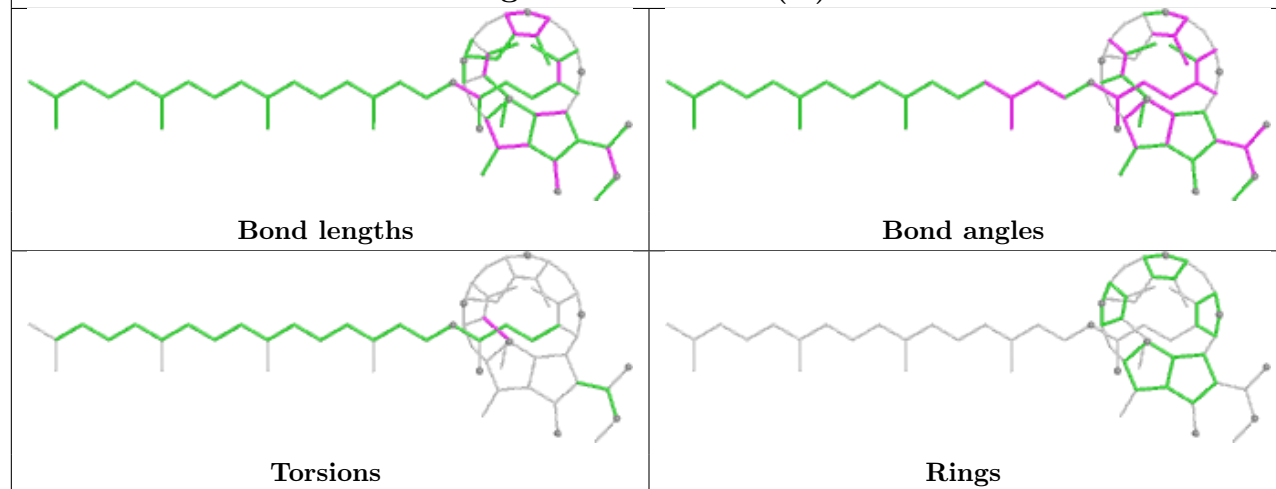
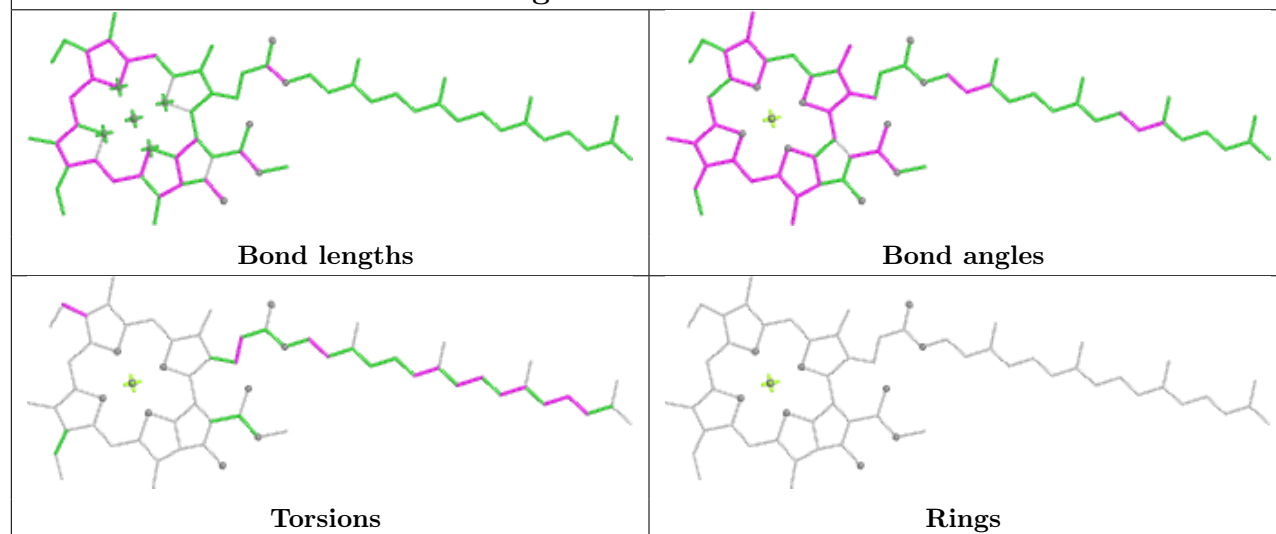


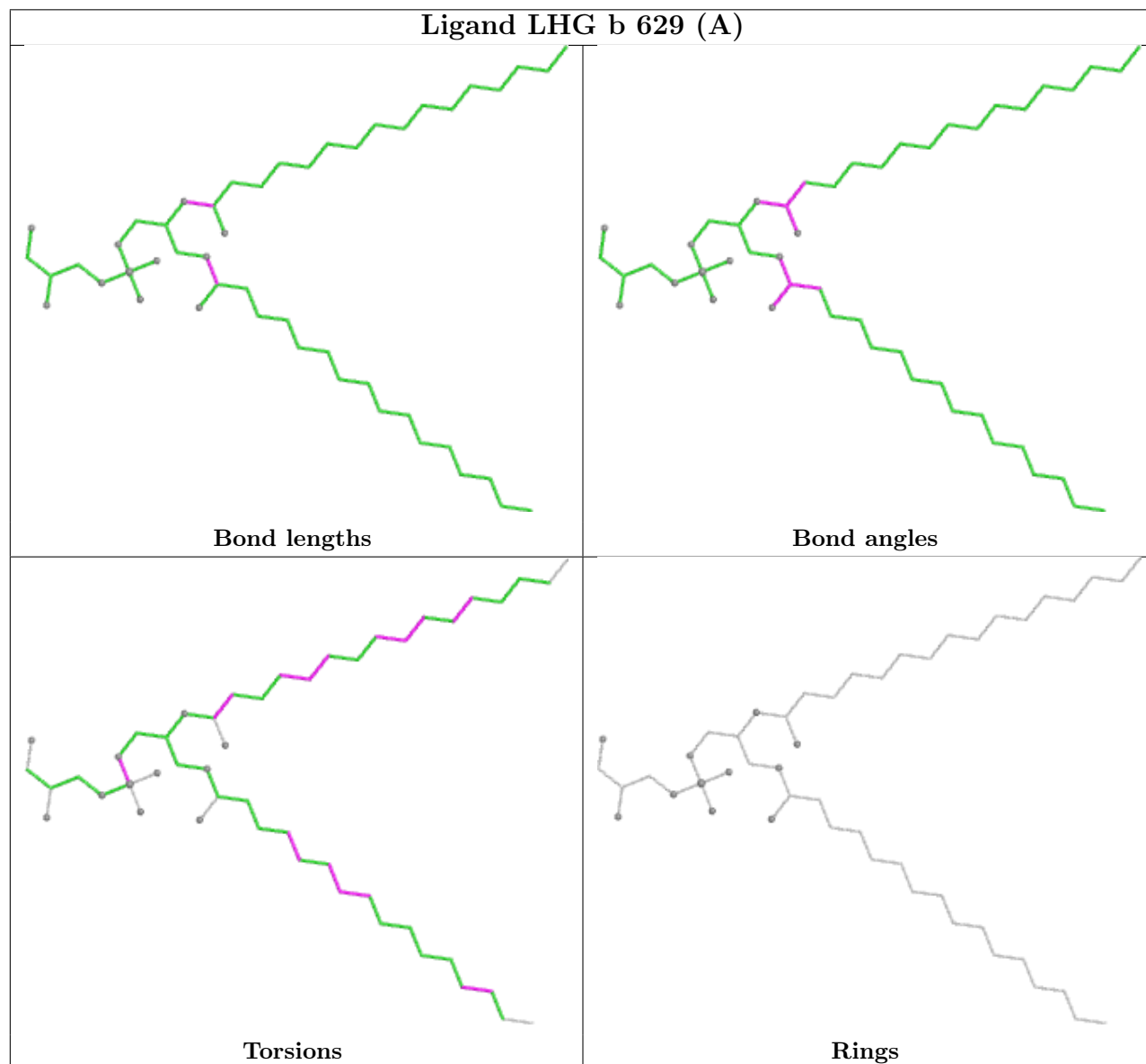
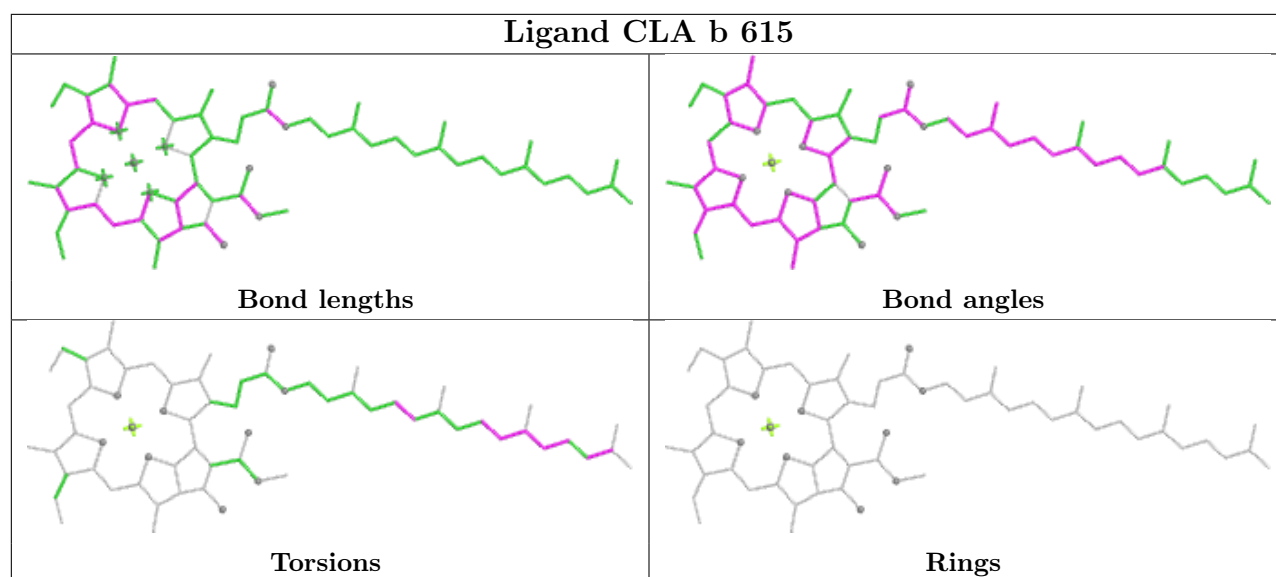
Ligand CLA D 404 (B)**Ligand CLA C 504****Ligand CLA B 609**

Ligand CLA b 606	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand LMT M 102	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand PL9 A 414 (A)	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLA C 513**Ligand PHO a 416 (A)****Ligand CLA B 602**



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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	334/344 (97%)	-0.67	1 (0%) 90 90	19, 25, 60, 122	222 (66%)
1	a	334/344 (97%)	-0.61	1 (0%) 90 90	19, 28, 63, 131	221 (66%)
2	B	504/505 (99%)	-0.56	1 (0%) 91 92	22, 52, 81, 113	20 (3%)
2	b	504/505 (99%)	-0.46	1 (0%) 91 92	23, 56, 96, 158	19 (3%)
3	C	451/455 (99%)	-0.56	0 100 100	21, 58, 81, 134	97 (21%)
3	c	455/455 (100%)	-0.49	1 (0%) 91 92	24, 65, 86, 121	100 (21%)
4	D	342/342 (100%)	-0.70	0 100 100	19, 43, 63, 128	114 (33%)
4	d	341/342 (99%)	-0.66	0 100 100	20, 49, 74, 126	116 (34%)
5	E	81/84 (96%)	-0.33	0 100 100	51, 68, 98, 147	0
5	e	79/84 (94%)	-0.31	1 (1%) 75 76	32, 76, 122, 142	2 (2%)
6	F	34/44 (77%)	-0.58	0 100 100	53, 61, 89, 111	0
6	f	31/44 (70%)	-0.29	1 (3%) 50 50	54, 67, 95, 134	1 (3%)
7	H	64/65 (98%)	-0.34	1 (1%) 70 71	52, 61, 85, 107	0
7	h	64/65 (98%)	-0.30	1 (1%) 70 71	38, 71, 93, 105	1 (1%)
8	I	37/38 (97%)	-0.17	0 100 100	55, 63, 119, 145	0
8	i	37/38 (97%)	-0.32	0 100 100	53, 63, 113, 130	0
9	J	38/39 (97%)	-0.38	0 100 100	50, 66, 116, 159	0
9	j	39/39 (100%)	-0.23	0 100 100	56, 76, 128, 155	0
10	K	37/37 (100%)	-0.69	0 100 100	56, 66, 84, 102	0
10	k	37/37 (100%)	-0.45	0 100 100	64, 74, 95, 111	0
11	L	36/37 (97%)	-0.65	0 100 100	21, 43, 113, 128	2 (5%)
11	l	36/37 (97%)	-0.56	0 100 100	23, 45, 100, 117	2 (5%)
12	M	32/36 (88%)	-0.64	0 100 100	25, 47, 75, 125	1 (3%)
12	m	33/36 (91%)	-0.57	0 100 100	23, 46, 69, 139	2 (6%)

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
13	O	243/244 (99%)	-0.51	1 (0%) 88 89	20, 64, 116, 165	10 (4%)
13	o	243/244 (99%)	-0.45	0 100 100	22, 67, 121, 155	8 (3%)
14	T	29/32 (90%)	-0.68	0 100 100	25, 46, 53, 63	6 (20%)
14	t	29/32 (90%)	-0.66	0 100 100	26, 46, 59, 71	5 (17%)
15	U	96/104 (92%)	-0.64	0 100 100	24, 56, 88, 101	4 (4%)
15	u	97/104 (93%)	-0.66	0 100 100	28, 60, 82, 119	4 (4%)
16	V	137/137 (100%)	-0.71	0 100 100	22, 55, 78, 102	6 (4%)
16	v	137/137 (100%)	-0.55	0 100 100	26, 69, 101, 131	6 (4%)
17	X	38/40 (95%)	-0.22	0 100 100	33, 72, 92, 112	1 (2%)
17	x	38/40 (95%)	-0.03	0 100 100	66, 78, 124, 154	0
18	Y	29/30 (96%)	-0.15	0 100 100	66, 82, 115, 121	0
18	y	29/30 (96%)	-0.18	0 100 100	75, 88, 107, 113	0
19	Z	62/62 (100%)	-0.28	0 100 100	65, 79, 131, 149	0
19	z	62/62 (100%)	0.10	0 100 100	80, 92, 137, 164	0
20	R	34/34 (100%)	0.60	2 (5%) 28 26	89, 113, 135, 148	0
All	All	5283/5384 (98%)	-0.52	12 (0%) 91 92	19, 56, 100, 165	970 (18%)

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
7	H	65	LEU	3.9
5	e	79[A]	PHE	3.4
6	f	16[A]	PHE	2.9
2	b	499	VAL	2.8
1	a	11	ALA	2.6

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
14	FME	T	1	10/11	0.95	0.08	44,52,66,69	0
8	FME	I	1	10/11	0.96	0.07	58,70,80,82	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
14	FME	t	1	10/11	0.96	0.07	41,47,64,74	0
12	FME	m	1	10/11	0.97	0.07	48,62,89,111	0
8	FME	i	1	10/11	0.97	0.07	51,70,75,80	0
12	FME	M	1	10/11	0.98	0.06	47,58,93,94	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
30	UNL	m	102	10/-	0.69	0.20	68,74,92,95	0
31	LMT	F	101	35/35	0.69	0.15	99,125,174,181	0
27	GOL	a	418	6/6	0.70	0.14	74,91,102,106	0
30	UNL	a	415	30/-	0.70	0.12	82,107,135,143	0
30	UNL	A	415	28/-	0.71	0.13	75,106,122,143	0
30	UNL	j	101	10/-	0.71	0.18	74,84,94,103	0
30	UNL	K	101[A]	34/-	0.71	0.14	76,100,114,120	34
30	UNL	K	101[B]	34/-	0.71	0.14	75,100,114,120	34
30	UNL	J	101	10/-	0.72	0.23	62,77,82,84	0
31	LMT	e	101	35/35	0.72	0.14	101,141,173,185	0
34	HTG	C	522	19/19	0.72	0.13	100,120,131,134	0
31	LMT	A	417	35/35	0.74	0.13	63,110,133,143	0
31	LMT	c	501	35/35	0.74	0.13	96,127,142,156	0
31	LMT	A	419	35/35	0.74	0.12	84,125,147,154	0
32	LHG	a	420[A]	42/49	0.74	0.13	86,128,146,160	42
32	LHG	a	420[B]	42/49	0.74	0.13	86,128,146,161	42
31	LMT	B	630	35/35	0.74	0.13	64,112,141,149	0
27	GOL	o	302	6/6	0.75	0.18	79,96,106,107	0
26	SQD	f	102	43/54	0.75	0.13	98,125,174,183	0
30	UNL	I	101	40/-	0.75	0.15	70,98,154,158	0
30	UNL	c	525[B]	32/-	0.77	0.14	85,105,118,125	32
30	UNL	c	525[A]	32/-	0.77	0.14	85,105,118,124	32
36	CA	F	103	1/1	0.77	0.23	123,123,123,123	0
30	UNL	l	101	10/-	0.78	0.15	65,71,90,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
27	GOL	B	627	6/6	0.79	0.14	68,83,98,114	0
27	GOL	A	411	6/6	0.79	0.15	62,73,77,86	0
30	UNL	D	411	40/-	0.80	0.13	62,92,143,144	0
31	LMT	b	621	25/35	0.80	0.12	80,108,155,168	0
30	UNL	b	626	33/-	0.80	0.12	66,92,150,160	0
30	UNL	i	101	40/-	0.80	0.13	69,101,149,158	0
36	CA	f	103	1/1	0.80	0.14	118,118,118,118	0
34	HTG	B	623	19/19	0.81	0.14	61,90,112,112	0
30	UNL	d	409	36/-	0.81	0.11	68,91,127,139	0
34	HTG	D	412	16/19	0.81	0.12	86,106,131,142	0
27	GOL	d	412	6/6	0.81	0.21	50,69,79,87	0
33	LMG	C	521	51/55	0.81	0.11	59,109,155,182	0
27	GOL	b	624	6/6	0.82	0.17	85,90,98,109	0
27	GOL	o	303	6/6	0.82	0.13	76,84,95,96	0
29	PL9	a	414[B]	55/55	0.83	0.14	73,95,109,111	55
29	PL9	a	414[A]	55/55	0.83	0.14	74,95,109,111	55
34	HTG	b	623	19/19	0.83	0.11	77,129,156,158	0
34	HTG	c	522	19/19	0.83	0.09	99,118,138,139	0
31	LMT	M	102	35/35	0.83	0.10	70,116,169,173	0
31	LMT	t	101	26/35	0.83	0.12	68,101,143,157	0
29	PL9	A	414[B]	55/55	0.84	0.13	59,83,98,106	55
27	GOL	O	302	6/6	0.84	0.10	81,88,98,99	0
27	GOL	v	202[A]	6/6	0.84	0.12	65,79,82,84	6
34	HTG	V	202	11/19	0.84	0.09	75,108,122,129	0
27	GOL	v	202[B]	6/6	0.84	0.12	65,79,82,84	6
31	LMT	B	631	25/35	0.84	0.12	56,79,145,158	0
34	HTG	d	410	16/19	0.84	0.11	84,118,135,151	0
30	UNL	B	626	33/-	0.84	0.13	49,100,140,150	0
29	PL9	A	414[A]	55/55	0.84	0.13	59,83,98,106	55
27	GOL	l	102[A]	6/6	0.85	0.15	61,90,91,96	6
27	GOL	l	102[B]	6/6	0.85	0.15	61,90,91,96	6
27	GOL	O	303	6/6	0.85	0.12	73,86,96,96	0
26	SQD	a	412	54/54	0.85	0.10	66,94,138,154	0
31	LMT	B	628	35/35	0.85	0.10	64,104,142,147	0
31	LMT	m	103	35/35	0.86	0.11	59,91,105,123	0
34	HTG	b	622	19/19	0.86	0.11	55,79,115,117	0
33	LMG	c	521	51/55	0.86	0.10	74,127,151,183	0
33	LMG	Z	101	37/55	0.86	0.13	73,119,150,165	0
31	LMT	b	627	25/35	0.86	0.12	49,93,146,152	0
27	GOL	c	527	6/6	0.86	0.17	96,104,109,110	0
26	SQD	A	412	54/54	0.86	0.10	61,84,127,151	0
26	SQD	b	620	54/54	0.87	0.10	60,93,127,136	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
31	LMT	M	101	35/35	0.88	0.10	59,95,122,132	0
33	LMG	z	101	39/55	0.88	0.10	70,121,149,162	0
26	SQD	B	620	54/54	0.88	0.10	61,88,137,149	0
23	CLA	b	601	65/65	0.89	0.09	60,85,120,153	0
32	LHG	E	101[A]	42/49	0.89	0.10	71,96,110,120	42
32	LHG	E	101[B]	42/49	0.89	0.10	71,96,110,120	42
34	HTG	B	622	19/19	0.89	0.11	60,85,119,121	0
27	GOL	B	629	6/6	0.89	0.11	71,76,90,96	0
27	GOL	D	414	6/6	0.89	0.15	46,63,67,82	0
26	SQD	X	101	43/54	0.89	0.11	71,104,131,133	0
27	GOL	c	526[B]	6/6	0.90	0.09	65,69,74,75	6
27	GOL	D	403	6/6	0.90	0.23	47,76,78,81	0
33	LMG	C	501	51/55	0.90	0.09	70,86,112,128	0
27	GOL	C	523[A]	6/6	0.90	0.10	56,60,64,69	6
27	GOL	C	523[B]	6/6	0.90	0.10	56,60,65,69	6
27	GOL	c	526[A]	6/6	0.90	0.09	65,69,74,75	6
27	GOL	V	203[B]	6/6	0.91	0.12	57,65,72,73	6
23	CLA	c	514	65/65	0.91	0.10	69,94,124,151	0
27	GOL	a	419	6/6	0.91	0.23	51,78,82,88	0
23	CLA	B	601	65/65	0.91	0.09	56,76,108,146	0
27	GOL	V	203[A]	6/6	0.91	0.12	57,64,72,73	6
30	UNL	D	410	17/-	0.91	0.09	56,71,101,118	0
33	LMG	a	417	51/55	0.92	0.08	67,93,108,115	0
33	LMG	c	520	51/55	0.92	0.09	61,88,133,163	0
25	BCR	T	101	40/40	0.92	0.07	40,57,73,80	0
33	LMG	m	101	51/55	0.92	0.08	50,72,94,107	0
27	GOL	B	624	6/6	0.92	0.11	63,69,80,88	0
33	LMG	B	621	51/55	0.92	0.08	48,68,90,106	0
30	UNL	d	408	17/-	0.92	0.10	64,78,111,121	0
25	BCR	d	404	40/40	0.92	0.08	50,64,99,110	0
34	HTG	B	625	19/19	0.92	0.08	65,76,101,101	0
33	LMG	d	411	51/55	0.93	0.09	52,74,116,144	0
26	SQD	A	410[A]	54/54	0.93	0.09	54,78,112,115	54
33	LMG	C	520	51/55	0.93	0.08	53,83,109,128	0
26	SQD	A	410[B]	54/54	0.93	0.09	54,78,112,115	54
33	LMG	D	413	51/55	0.93	0.09	47,67,117,134	0
23	CLA	C	514	65/65	0.93	0.08	59,85,113,121	0
35	DGD	C	518[A]	62/66	0.93	0.08	47,64,107,111	62
35	DGD	C	518[B]	62/66	0.93	0.08	47,63,107,111	62
32	LHG	A	418[A]	49/49	0.93	0.09	48,60,79,83	49
32	LHG	A	418[B]	49/49	0.93	0.09	48,60,80,83	49
36	CA	o	301	1/1	0.93	0.07	108,108,108,108	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	BCR	K	103	40/40	0.94	0.08	54,63,84,87	0
29	PL9	D	407[A]	55/55	0.94	0.07	37,47,57,68	55
29	PL9	D	407[B]	55/55	0.94	0.07	37,47,57,68	55
23	CLA	C	505	65/65	0.94	0.08	41,56,107,134	0
25	BCR	c	515	40/40	0.94	0.08	65,78,91,96	0
23	CLA	C	507	65/65	0.94	0.08	52,70,118,141	0
25	BCR	k	101	40/40	0.94	0.09	58,73,86,88	0
32	LHG	D	409[A]	49/49	0.94	0.09	47,60,109,113	49
32	LHG	D	409[B]	49/49	0.94	0.09	47,60,109,113	49
25	BCR	t	102	40/40	0.94	0.06	42,62,75,83	0
23	CLA	b	616	65/65	0.94	0.08	48,63,121,133	0
23	CLA	c	513	65/65	0.94	0.09	60,79,121,133	0
23	CLA	C	513	65/65	0.94	0.09	58,74,116,126	0
32	LHG	d	407[A]	49/49	0.94	0.09	52,62,108,122	49
32	LHG	d	407[B]	49/49	0.94	0.09	52,62,108,122	49
34	HTG	b	625	19/19	0.94	0.07	61,78,94,103	0
32	LHG	d	413[A]	49/49	0.94	0.08	49,64,78,85	49
32	LHG	d	413[B]	49/49	0.94	0.08	48,64,79,85	49
25	BCR	D	406	40/40	0.94	0.08	43,57,102,106	0
25	BCR	H	101	40/40	0.94	0.08	48,65,85,89	0
35	DGD	c	518[A]	62/66	0.94	0.07	53,68,114,129	62
35	DGD	c	518[B]	62/66	0.94	0.07	54,68,114,129	62
35	DGD	c	519	62/66	0.94	0.07	49,61,101,125	0
26	SQD	a	411[A]	54/54	0.94	0.09	59,78,111,118	54
26	SQD	a	411[B]	54/54	0.94	0.09	59,78,111,118	54
25	BCR	K	102	40/40	0.94	0.09	56,64,76,79	0
23	CLA	B	614	65/65	0.95	0.07	36,47,102,121	0
23	CLA	d	403	65/65	0.95	0.09	50,66,117,142	0
25	BCR	A	409	40/40	0.95	0.06	37,51,65,67	0
25	BCR	B	618	40/40	0.95	0.06	39,55,70,78	0
25	BCR	B	619	40/40	0.95	0.07	46,58,93,96	0
25	BCR	C	515	40/40	0.95	0.08	54,73,89,94	0
23	CLA	B	616	65/65	0.95	0.09	41,57,131,139	0
23	CLA	D	405	65/65	0.95	0.08	46,59,121,138	0
23	CLA	a	407[A]	65/65	0.95	0.07	39,52,118,132	65
23	CLA	a	407[B]	65/65	0.95	0.07	39,52,118,132	65
23	CLA	a	409	65/65	0.95	0.10	43,56,138,157	0
29	PL9	d	405[A]	55/55	0.95	0.07	36,49,60,73	55
29	PL9	d	405[B]	55/55	0.95	0.07	36,49,60,73	55
25	BCR	a	410	40/40	0.95	0.06	42,53,63,67	0
25	BCR	b	619	40/40	0.95	0.07	46,63,86,89	0
23	CLA	A	408	65/65	0.95	0.08	37,49,126,140	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
25	BCR	c	516	40/40	0.95	0.07	56,64,78,81	0
23	CLA	b	606	65/65	0.95	0.07	44,59,112,127	0
25	BCR	h	101	40/40	0.95	0.09	59,72,94,97	0
23	CLA	b	614	65/65	0.95	0.07	40,50,98,117	0
23	CLA	B	606	65/65	0.95	0.08	44,57,111,135	0
30	UNL	X	102	18/-	0.95	0.10	55,71,104,104	0
25	BCR	y	101	40/40	0.95	0.07	56,70,83,96	0
27	GOL	b	628	6/6	0.95	0.08	72,79,85,88	0
23	CLA	c	505	65/65	0.95	0.07	47,63,102,132	0
35	DGD	C	519	62/66	0.95	0.07	42,59,95,109	0
35	DGD	H	102	62/66	0.95	0.08	43,61,76,93	0
35	DGD	c	517[A]	62/66	0.95	0.07	46,63,97,105	62
35	DGD	c	517[B]	62/66	0.95	0.07	46,63,97,105	62
32	LHG	b	629[A]	49/49	0.95	0.08	47,56,75,91	49
32	LHG	b	629[B]	49/49	0.95	0.08	47,56,75,92	49
23	CLA	c	507	65/65	0.95	0.08	46,70,118,131	0
35	DGD	h	102	62/66	0.95	0.07	52,64,77,86	0
23	CLA	c	508	65/65	0.95	0.08	49,67,83,90	0
23	CLA	c	509	65/65	0.95	0.07	42,62,124,152	0
23	CLA	C	509	65/65	0.95	0.07	45,54,113,140	0
38	BCT	d	401[A]	4/4	0.95	0.06	53,54,63,71	4
38	BCT	d	401[B]	4/4	0.95	0.06	53,53,63,70	4
23	CLA	b	609	65/65	0.96	0.07	49,64,77,92	0
23	CLA	b	612	65/65	0.96	0.07	41,53,69,76	0
23	CLA	A	404[B]	65/65	0.96	0.06	34,41,59,67	65
23	CLA	C	506	65/65	0.96	0.07	49,59,87,103	0
23	CLA	c	502	65/65	0.96	0.07	51,67,81,95	0
30	UNL	x	101	18/-	0.96	0.10	64,80,124,134	0
23	CLA	c	504	65/65	0.96	0.07	52,70,82,98	0
23	CLA	B	602	65/65	0.96	0.07	43,55,72,95	0
23	CLA	c	506	65/65	0.96	0.07	49,64,90,97	0
23	CLA	C	508	65/65	0.96	0.08	50,61,84,92	0
23	CLA	B	603	65/65	0.96	0.07	42,52,71,81	0
23	CLA	C	512	65/65	0.96	0.07	49,62,80,89	0
23	CLA	c	512	65/65	0.96	0.07	53,68,86,97	0
23	CLA	A	406[A]	65/65	0.96	0.06	37,45,105,116	65
23	CLA	B	607	65/65	0.96	0.06	36,44,74,81	0
23	CLA	B	609	65/65	0.96	0.06	46,58,72,81	0
24	PHO	A	416[A]	64/64	0.96	0.06	37,48,53,60	64
24	PHO	A	416[B]	64/64	0.96	0.06	37,47,53,60	64
24	PHO	a	416[A]	64/64	0.96	0.06	44,55,61,65	64
24	PHO	a	416[B]	64/64	0.96	0.06	44,55,61,65	64

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	CLA	a	405[A]	65/65	0.96	0.06	34,44,60,74	65
25	BCR	B	617	40/40	0.96	0.05	38,50,61,65	0
32	LHG	D	408[A]	49/49	0.96	0.07	43,53,64,73	49
35	DGD	C	517[A]	62/66	0.96	0.06	46,57,97,102	62
35	DGD	C	517[B]	62/66	0.96	0.06	46,57,97,102	62
32	LHG	D	408[B]	49/49	0.96	0.07	43,53,64,73	49
23	CLA	a	405[B]	65/65	0.96	0.06	36,44,63,74	65
23	CLA	B	611	65/65	0.96	0.06	33,42,64,68	0
23	CLA	A	406[B]	65/65	0.96	0.06	37,45,105,116	65
25	BCR	C	516	40/40	0.96	0.06	52,64,80,85	0
23	CLA	A	404[A]	65/65	0.96	0.06	34,41,59,67	65
23	CLA	C	502	65/65	0.96	0.07	48,60,71,76	0
23	CLA	b	602	65/65	0.96	0.07	48,61,80,91	0
23	CLA	b	604	65/65	0.96	0.07	40,52,102,119	0
32	LHG	d	406[A]	49/49	0.96	0.07	44,55,68,76	49
32	LHG	d	406[B]	49/49	0.96	0.07	44,55,68,76	49
23	CLA	C	504	65/65	0.96	0.06	47,61,72,85	0
23	CLA	b	607	65/65	0.96	0.06	37,47,79,93	0
25	BCR	b	617	40/40	0.96	0.06	43,54,60,67	0
25	BCR	b	618	40/40	0.96	0.05	43,55,77,84	0
23	CLA	b	615	65/65	0.97	0.06	47,61,82,92	0
23	CLA	C	503	65/65	0.97	0.06	41,54,72,86	0
23	CLA	B	604	65/65	0.97	0.06	37,45,117,138	0
23	CLA	c	503	65/65	0.97	0.06	41,57,81,96	0
23	CLA	B	610	65/65	0.97	0.07	39,52,67,79	0
23	CLA	a	406[A]	65/65	0.97	0.05	35,42,61,70	65
23	CLA	a	406[B]	65/65	0.97	0.05	35,43,61,70	65
23	CLA	B	605	65/65	0.97	0.06	39,48,62,78	0
23	CLA	B	612	65/65	0.97	0.06	31,47,58,74	0
23	CLA	B	613	65/65	0.97	0.06	35,44,93,108	0
23	CLA	c	510	65/65	0.97	0.07	42,60,84,98	0
23	CLA	c	511	65/65	0.97	0.06	47,61,80,91	0
32	LHG	L	101[A]	49/49	0.97	0.06	45,54,69,88	49
32	LHG	L	101[B]	49/49	0.97	0.06	45,54,69,89	49
23	CLA	A	405[A]	65/65	0.97	0.06	33,41,58,69	65
23	CLA	C	510	65/65	0.97	0.07	48,58,80,86	0
23	CLA	b	603	65/65	0.97	0.06	46,55,82,93	0
23	CLA	C	511	65/65	0.97	0.06	46,57,76,81	0
24	PHO	A	407[A]	64/64	0.97	0.05	33,44,51,54	64
24	PHO	A	407[B]	64/64	0.97	0.05	33,44,51,54	64
23	CLA	b	605	65/65	0.97	0.07	36,49,74,76	0
23	CLA	B	615	65/65	0.97	0.06	44,54,76,83	0

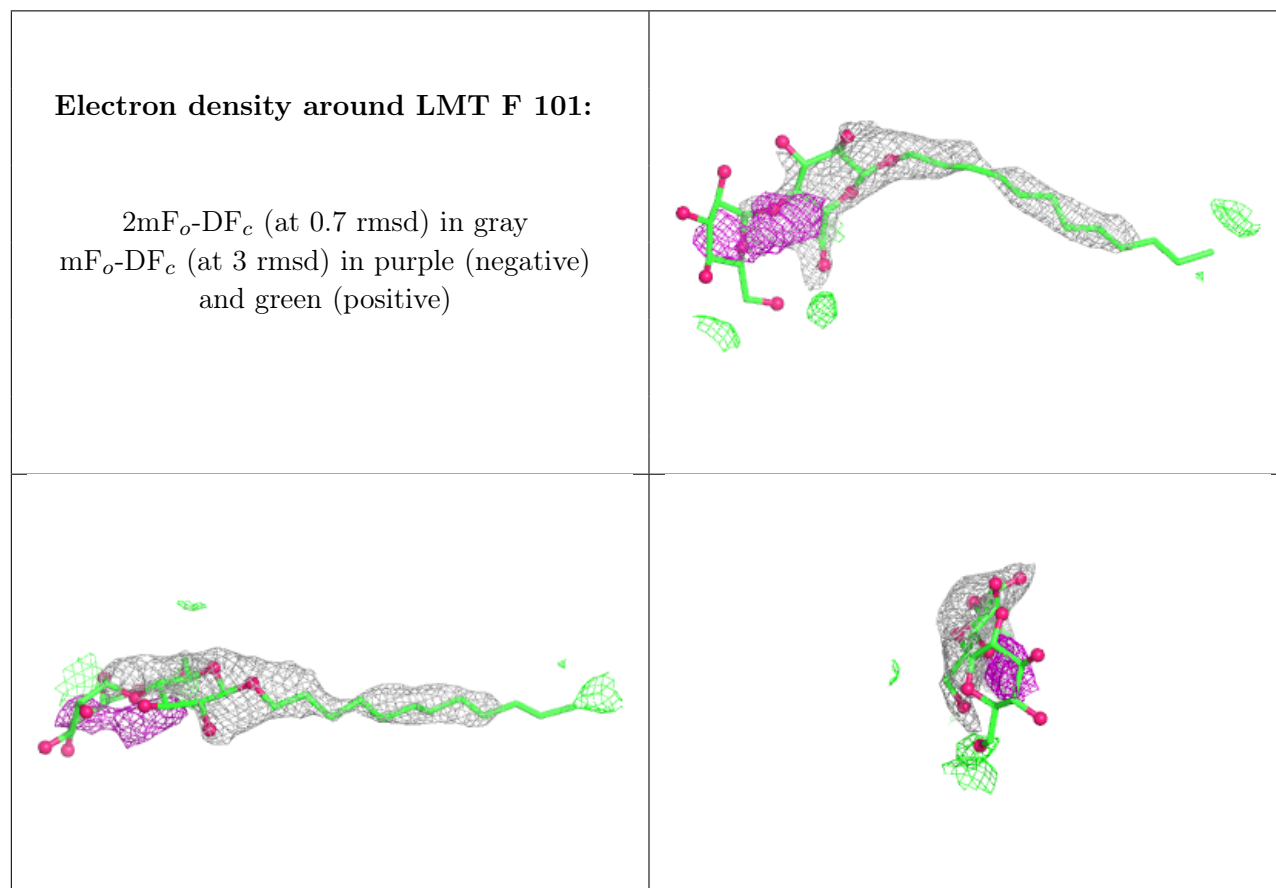
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	PHO	a	408[A]	64/64	0.97	0.04	38,47,53,58	64
24	PHO	a	408[B]	64/64	0.97	0.04	38,47,52,58	64
23	CLA	A	405[B]	65/65	0.97	0.06	33,41,58,69	65
23	CLA	b	608	65/65	0.97	0.06	40,54,84,96	0
23	CLA	B	608	65/65	0.97	0.05	37,48,67,73	0
36	CA	C	524	1/1	0.97	0.05	77,77,77,77	0
23	CLA	b	610	65/65	0.97	0.07	48,57,67,72	0
36	CA	O	301	1/1	0.97	0.04	104,104,104,104	0
36	CA	c	523	1/1	0.97	0.07	76,76,76,76	0
23	CLA	b	611	65/65	0.97	0.06	38,48,70,75	0
23	CLA	D	404[A]	65/65	0.97	0.06	34,42,64,74	65
38	BCT	D	402[A]	4/4	0.97	0.06	50,52,56,67	4
38	BCT	D	402[B]	4/4	0.97	0.06	50,52,56,68	4
23	CLA	b	613	65/65	0.97	0.05	40,48,85,98	0
23	CLA	D	404[B]	65/65	0.97	0.06	34,42,64,75	65
22	CL	a	404[B]	1/1	0.98	0.06	52,52,52,52	1
22	CL	a	403[A]	1/1	0.98	0.06	47,47,47,47	1
22	CL	a	403[B]	1/1	0.98	0.06	47,47,47,47	1
22	CL	a	404[A]	1/1	0.98	0.06	52,52,52,52	1
23	CLA	d	402[A]	65/65	0.98	0.05	38,45,69,85	65
23	CLA	d	402[B]	65/65	0.98	0.05	38,45,69,85	65
39	HEM	F	102	43/43	0.98	0.06	54,70,82,90	0
39	HEM	f	101	43/43	0.98	0.08	65,85,116,138	0
41	HEC	V	201	43/43	0.98	0.07	38,50,58,66	0
41	HEC	v	201	43/43	0.98	0.07	48,62,68,75	0
21	OEY	A	401[B]	11/11	0.99	0.03	37,44,47,47	11
22	CL	A	402[A]	1/1	0.99	0.06	41,41,41,41	1
22	CL	A	402[B]	1/1	0.99	0.06	41,41,41,41	1
36	CA	c	524	1/1	0.99	0.04	76,76,76,76	0
28	OEX	A	413[A]	10/10	0.99	0.03	37,43,47,48	10
40	MG	J	102	1/1	0.99	0.03	56,56,56,56	0
40	MG	j	102	1/1	0.99	0.03	63,63,63,63	0
22	CL	A	403[A]	1/1	0.99	0.04	45,45,45,45	1
22	CL	A	403[B]	1/1	0.99	0.04	45,45,45,45	1
37	FE2	a	402[A]	1/1	1.00	0.01	52,52,52,52	1
37	FE2	a	402[B]	1/1	1.00	0.01	52,52,52,52	1
21	OEY	a	401[B]	11/11	1.00	0.02	45,48,52,55	11
28	OEX	a	413[A]	10/10	1.00	0.02	47,48,51,52	10
37	FE2	D	401[A]	1/1	1.00	0.02	48,48,48,48	1
37	FE2	D	401[B]	1/1	1.00	0.02	48,48,48,48	1

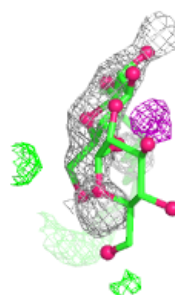
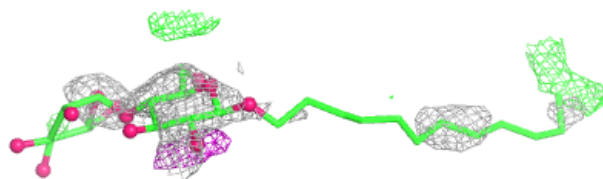
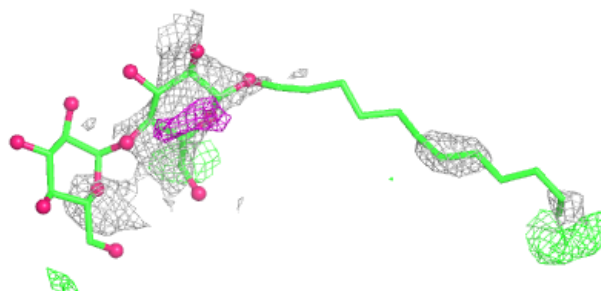
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers

as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

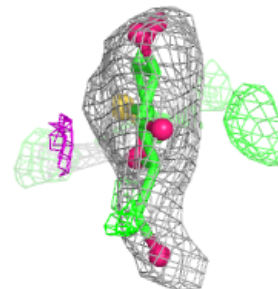
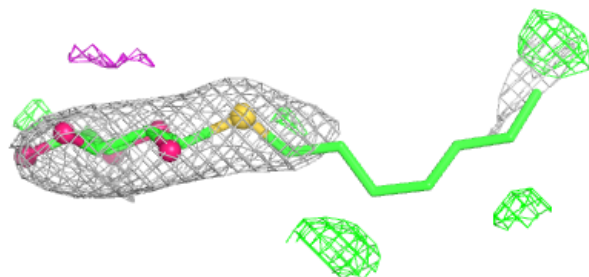
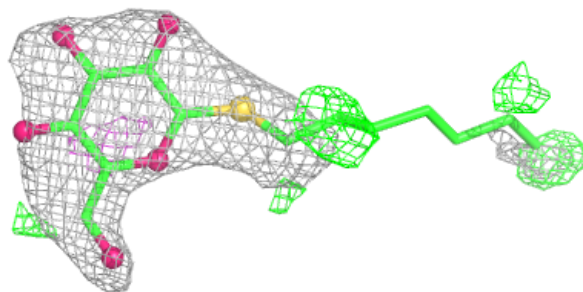


Electron density around LMT e 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

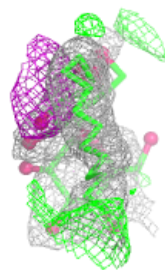
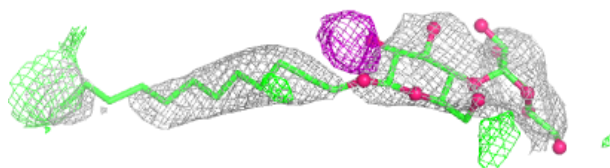
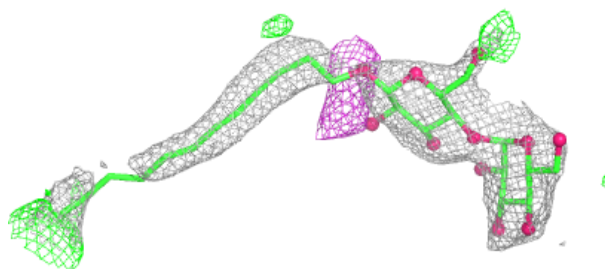
**Electron density around HTG C 522:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

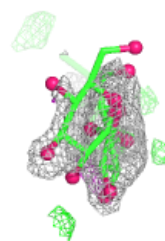
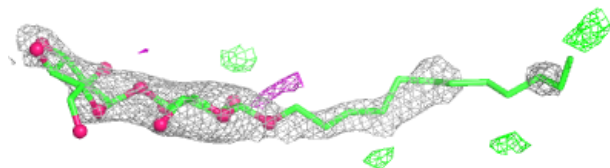
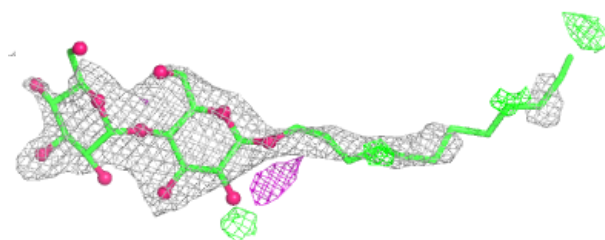


Electron density around LMT A 417:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

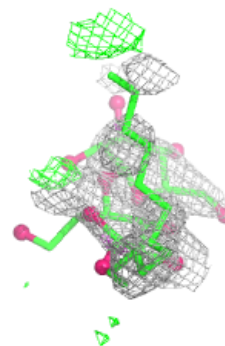
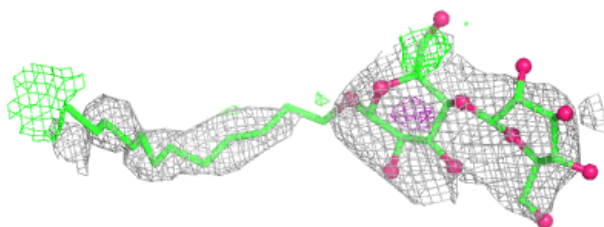
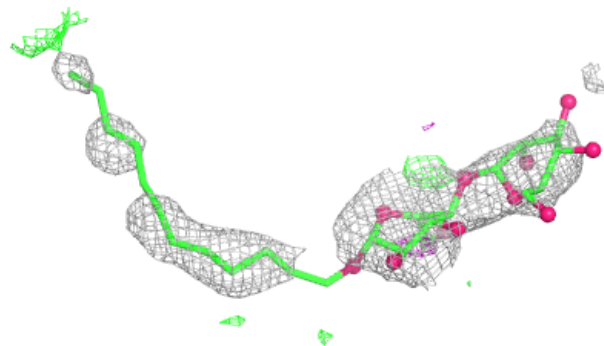
**Electron density around LMT c 501:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

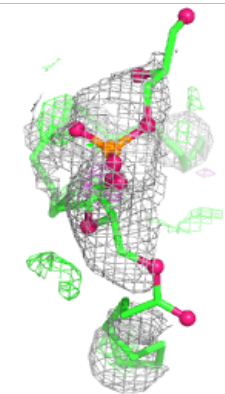
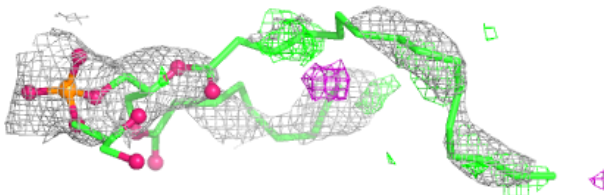
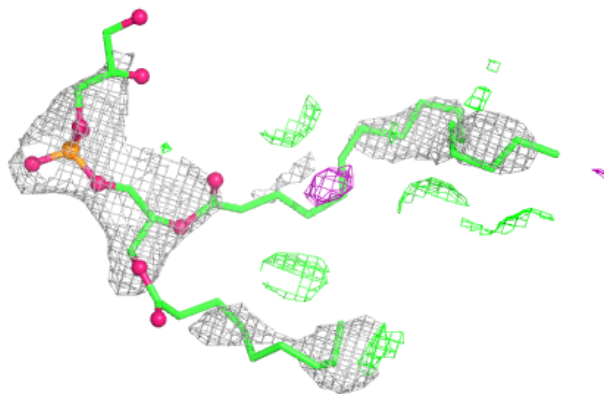


Electron density around LMT A 419:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

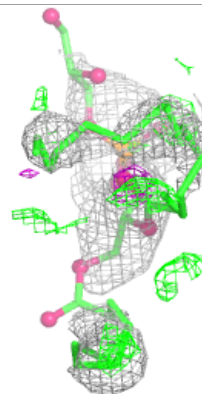
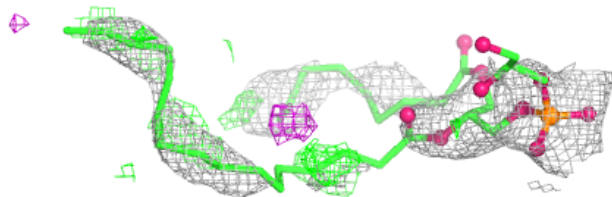
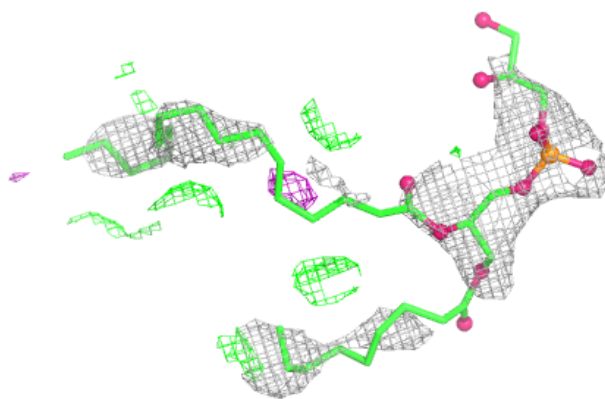
**Electron density around LHG a 420 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

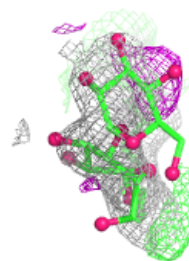
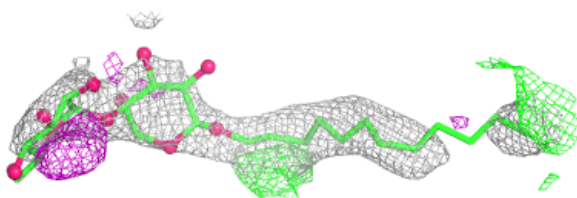
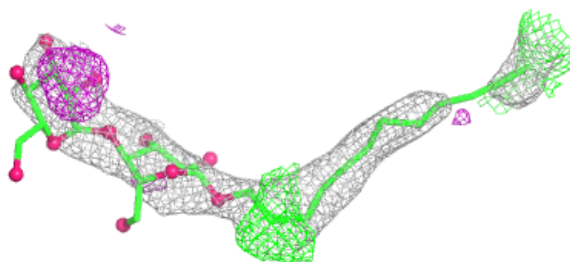


Electron density around LHG a 420 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

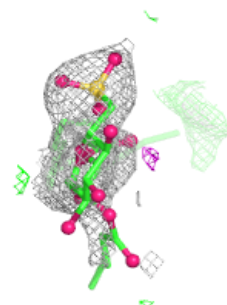
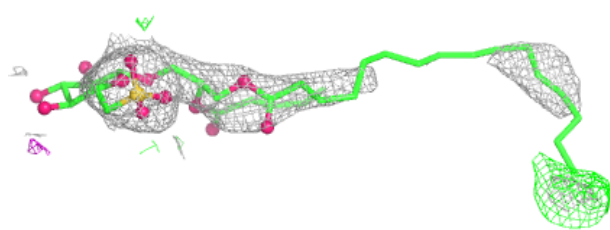
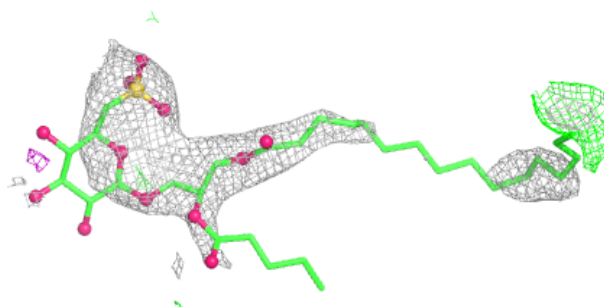
**Electron density around LMT B 630:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

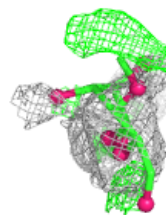
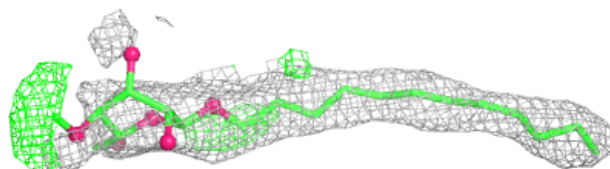
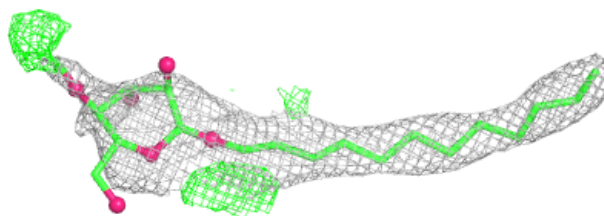


Electron density around SQD f 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

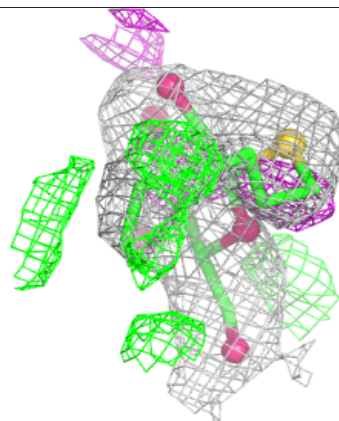
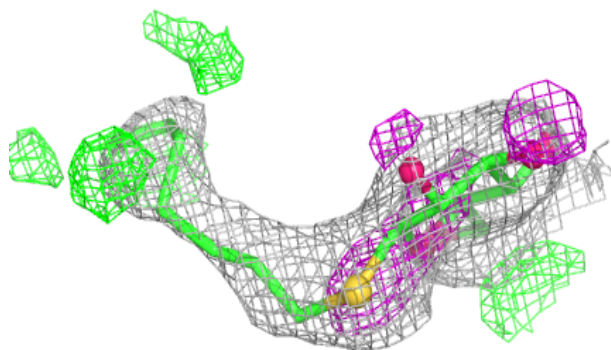
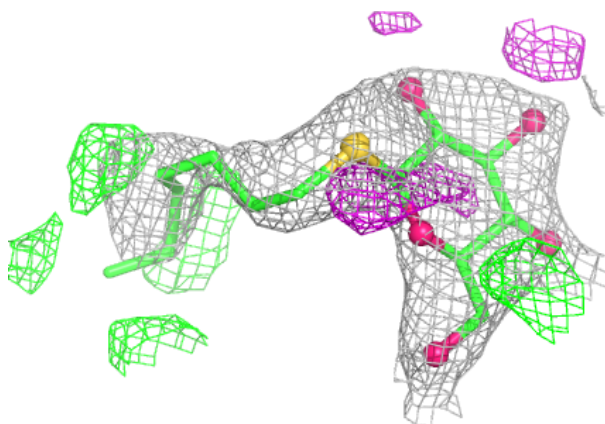
**Electron density around LMT b 621:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

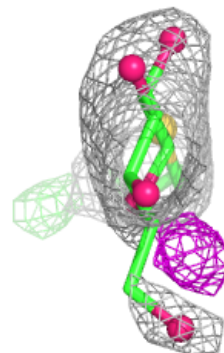
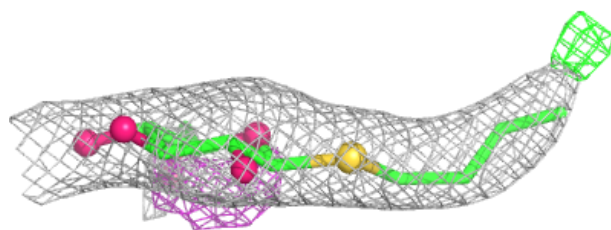
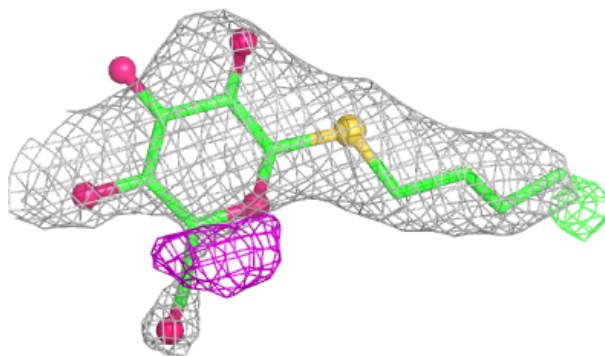


Electron density around HTG B 623:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

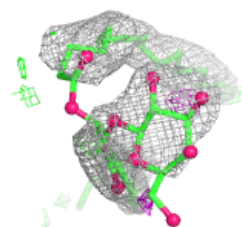
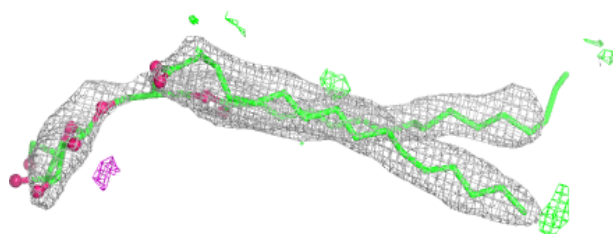
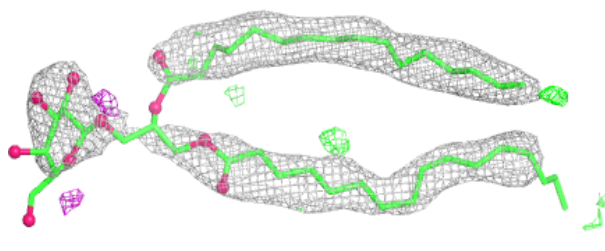
**Electron density around HTG D 412:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

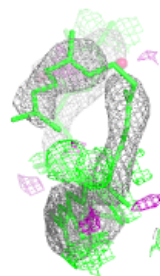
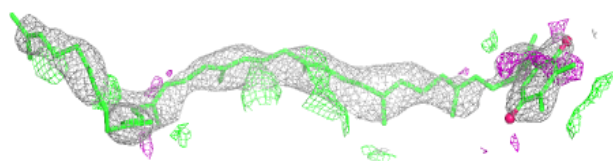
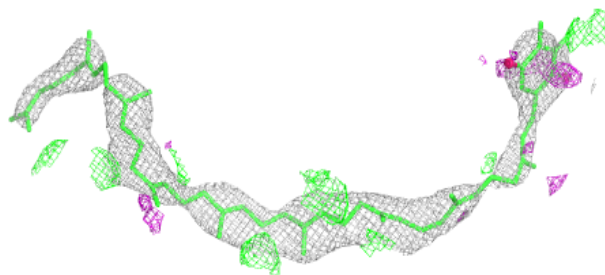


Electron density around LMG C 521:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

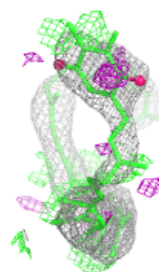
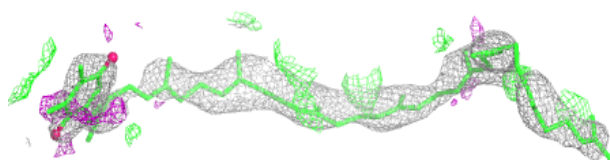
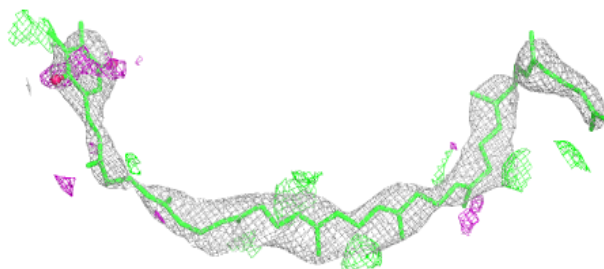
**Electron density around PL9 a 414 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

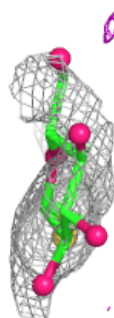
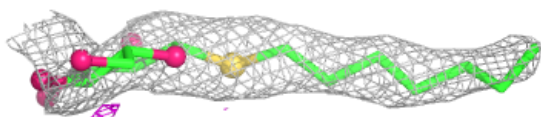
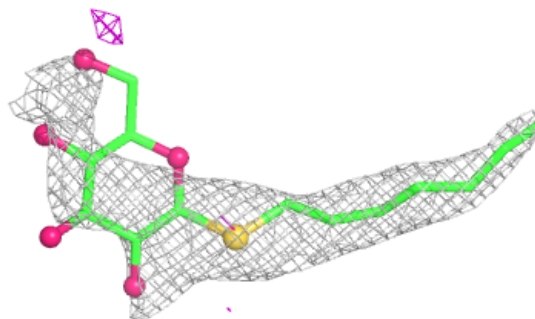


Electron density around PL9 a 414 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

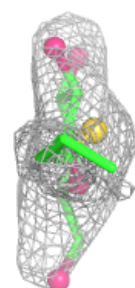
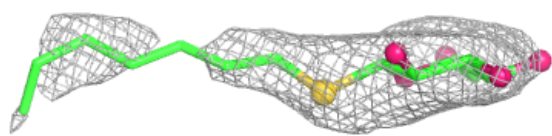
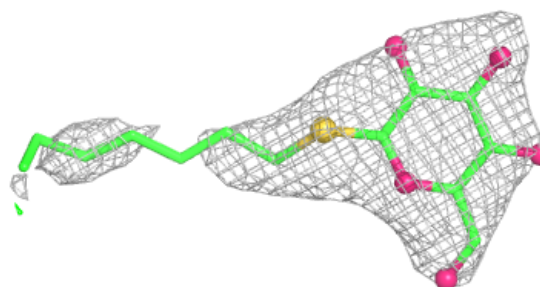
**Electron density around HTG b 623:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

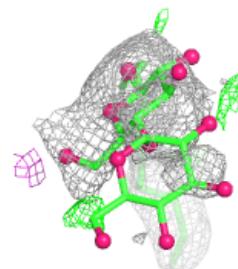
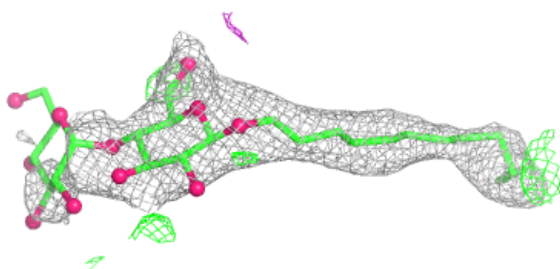
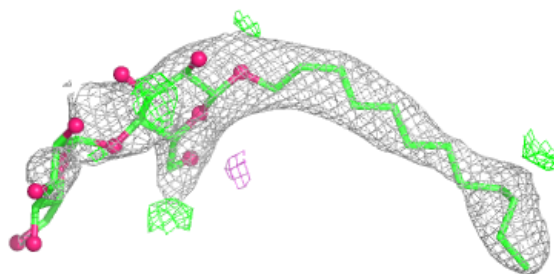


Electron density around HTG c 522:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

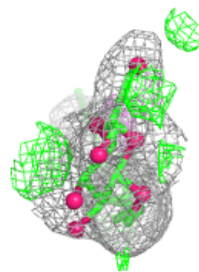
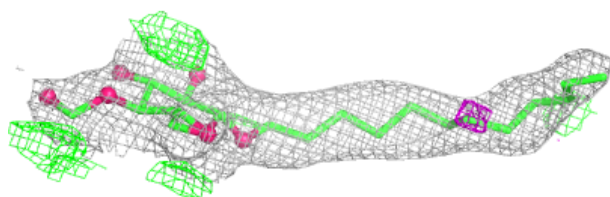
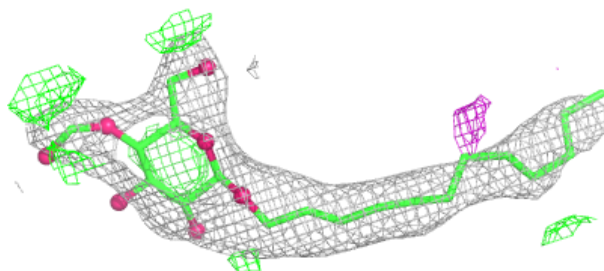
**Electron density around LMT M 102:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

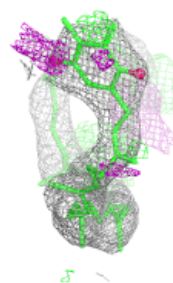
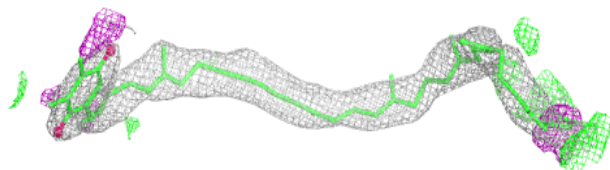
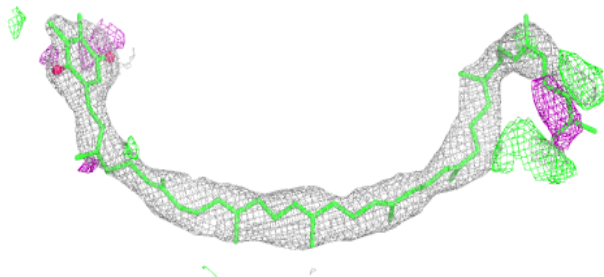


Electron density around LMT t 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

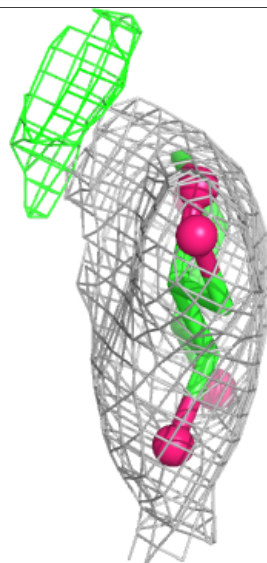
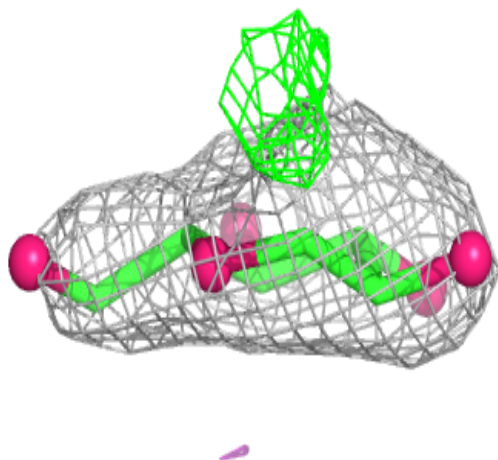
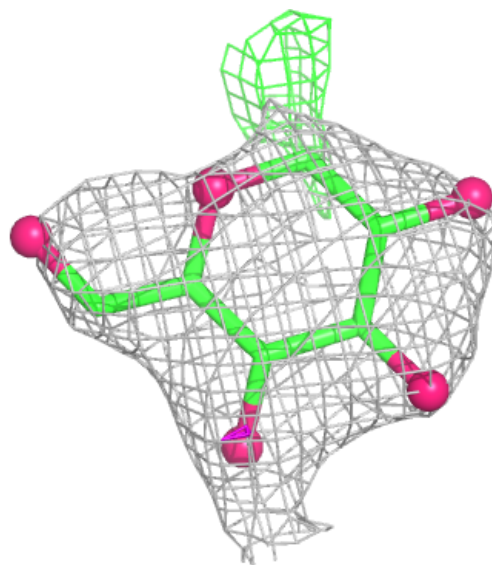
**Electron density around PL9 A 414 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



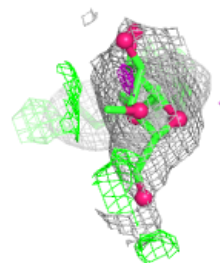
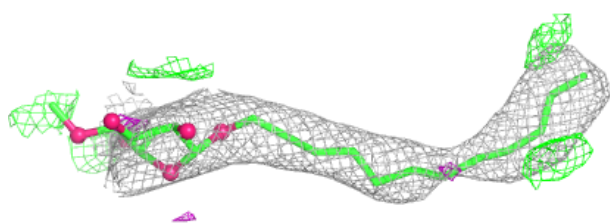
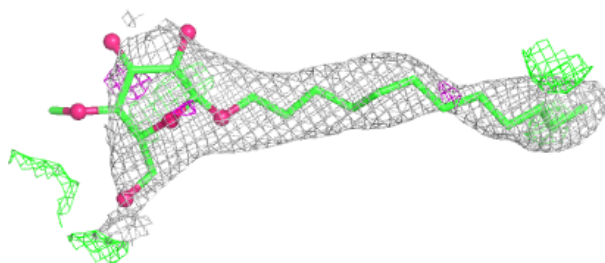
Electron density around HTG V 202:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

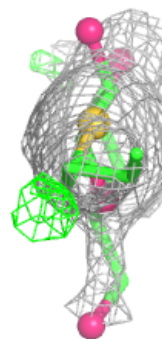
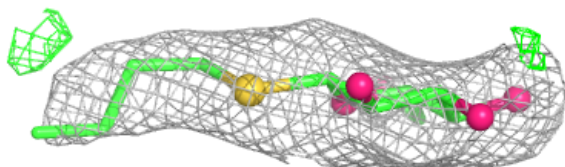
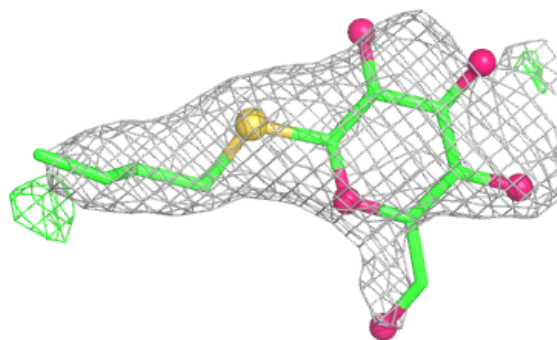


Electron density around LMT B 631:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

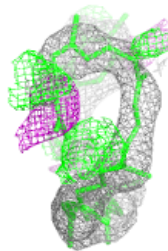
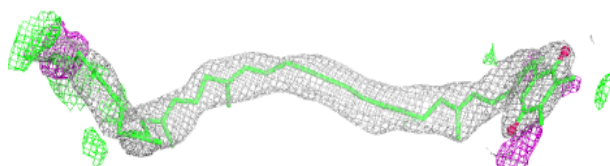
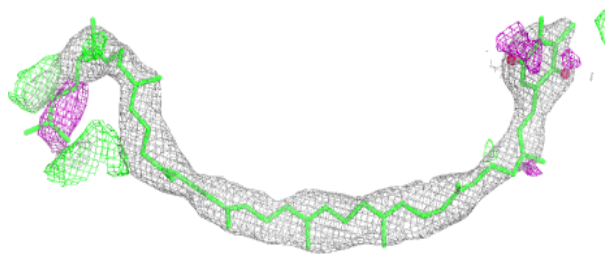
**Electron density around HTG d 410:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

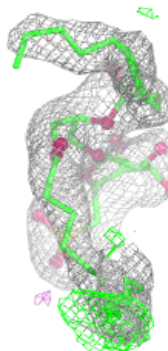
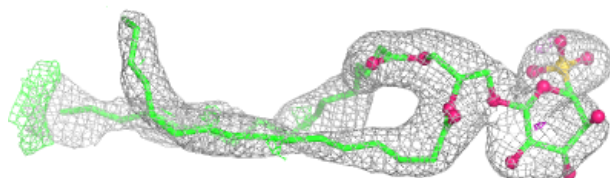
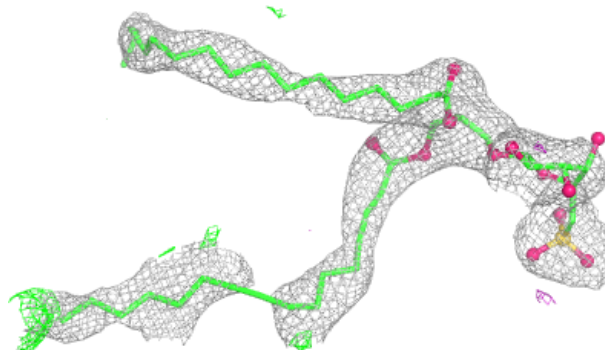


Electron density around PL9 A 414 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

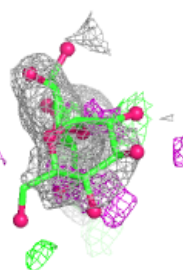
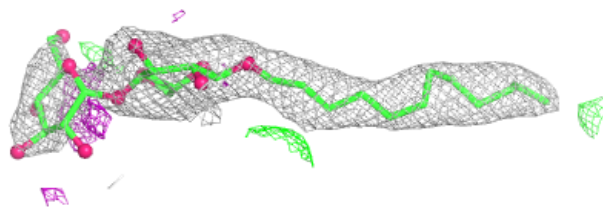
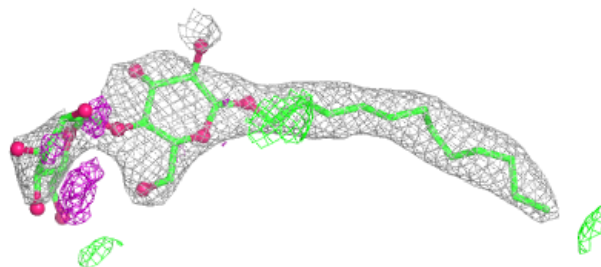
**Electron density around SQD a 412:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

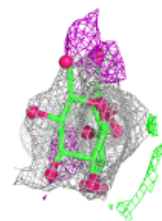
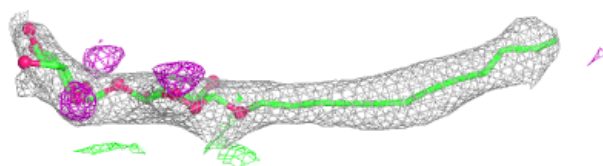
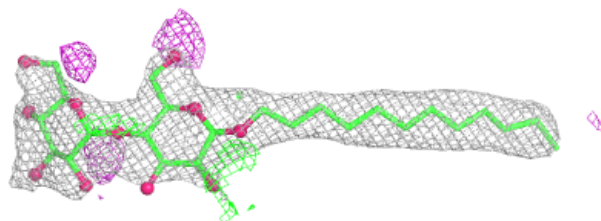


Electron density around LMT B 628:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

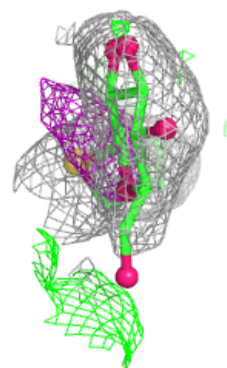
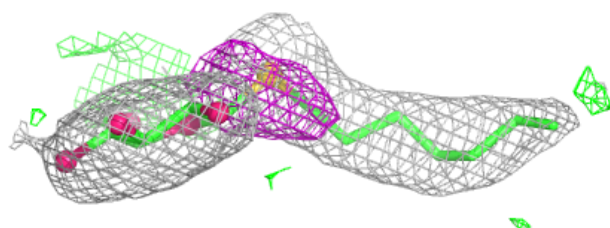
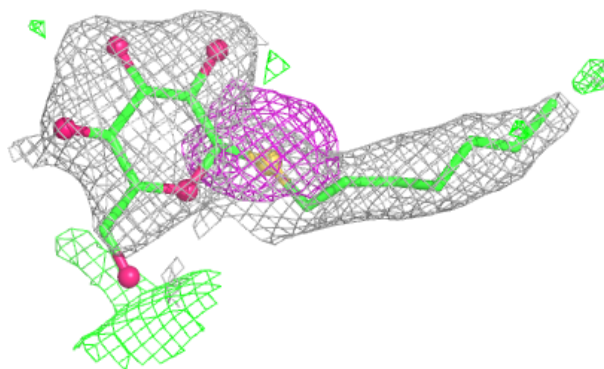
**Electron density around LMT m 103:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

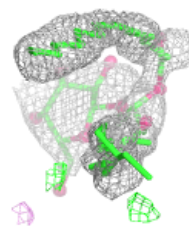
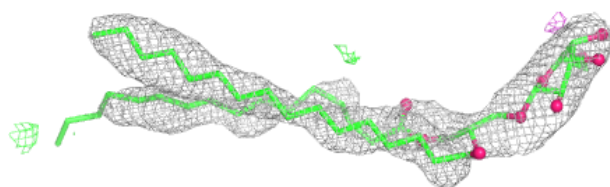
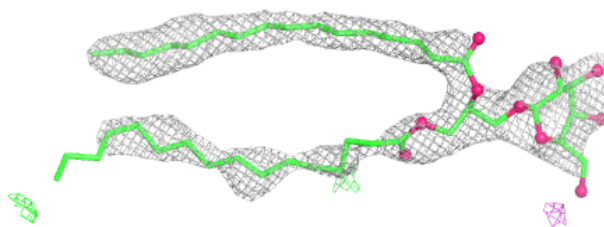


Electron density around HTG b 622:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

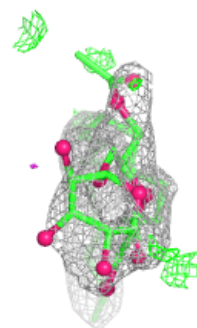
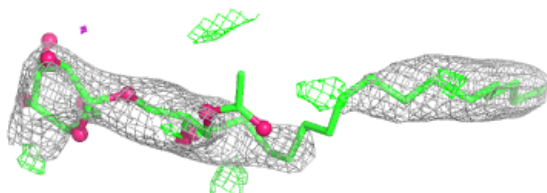
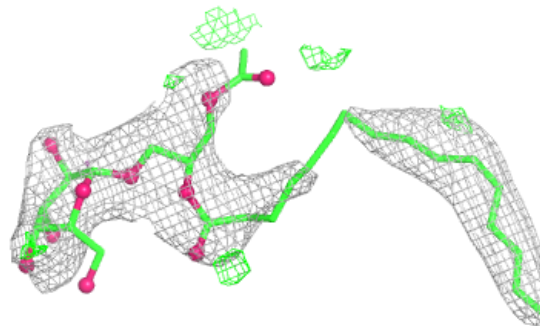
**Electron density around LMG c 521:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

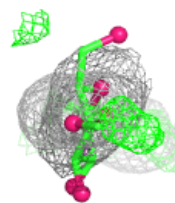
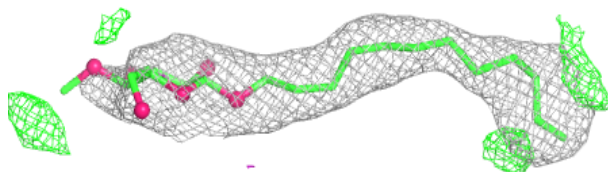
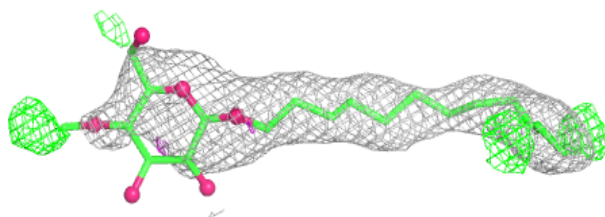


Electron density around LMG Z 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

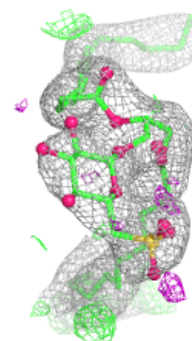
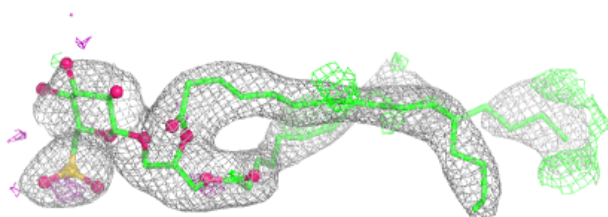
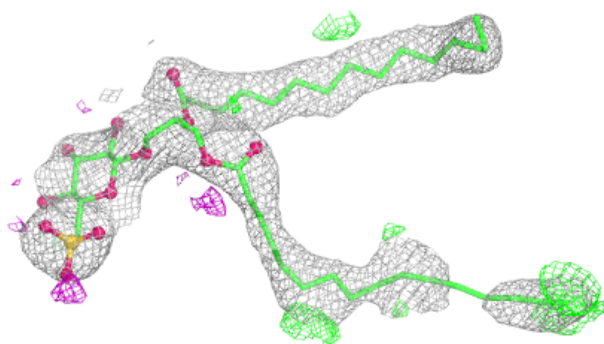
**Electron density around LMT b 627:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

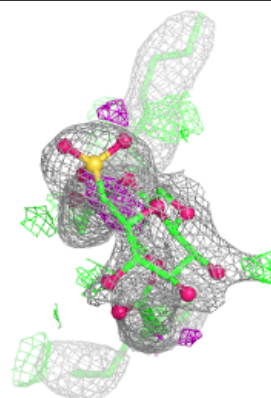
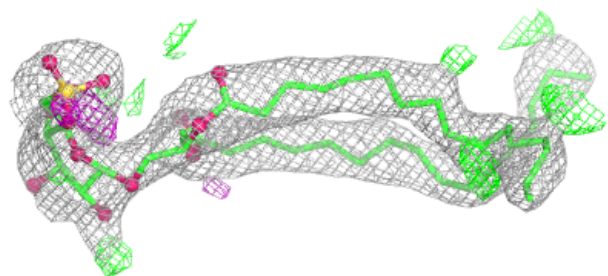
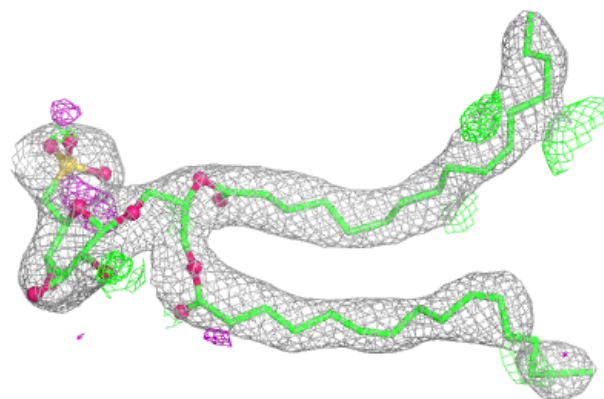


Electron density around SQD A 412:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

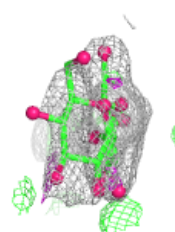
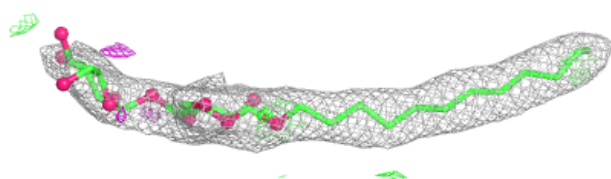
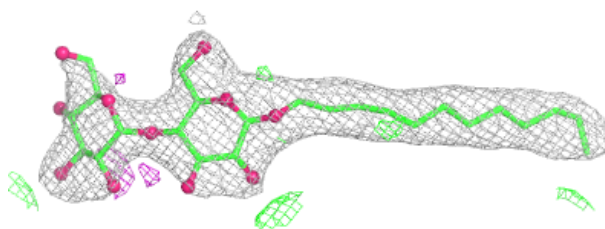
**Electron density around SQD b 620:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

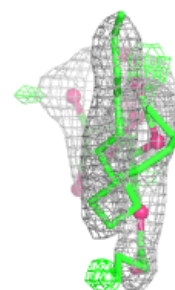
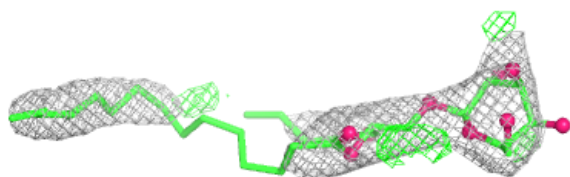
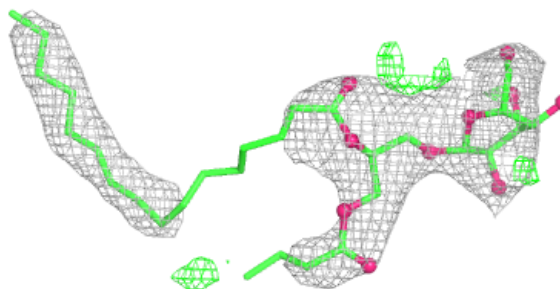


Electron density around LMT M 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

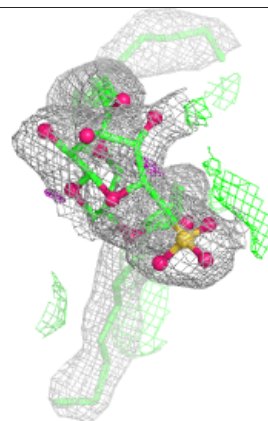
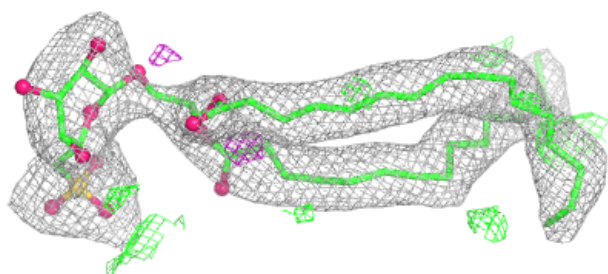
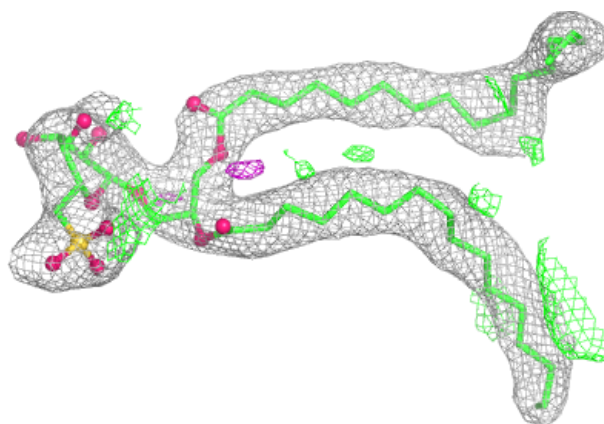
**Electron density around LMG z 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



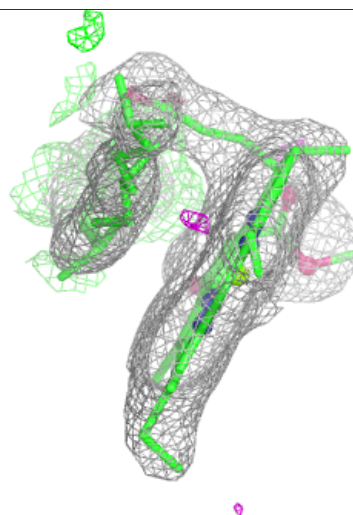
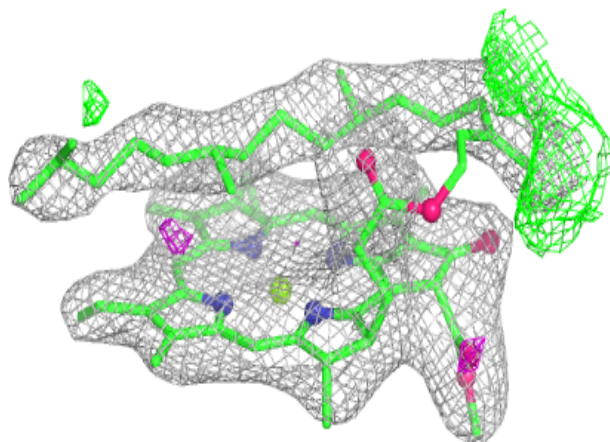
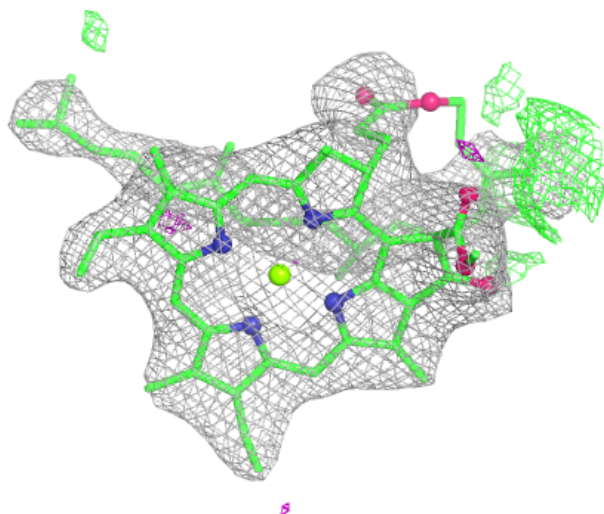
Electron density around SQD B 620:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



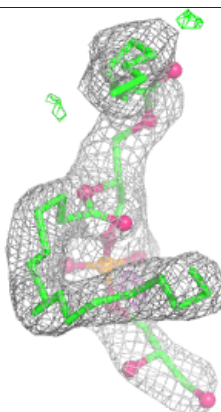
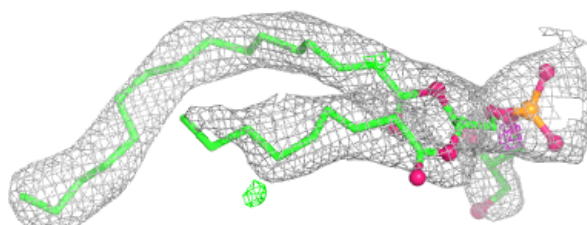
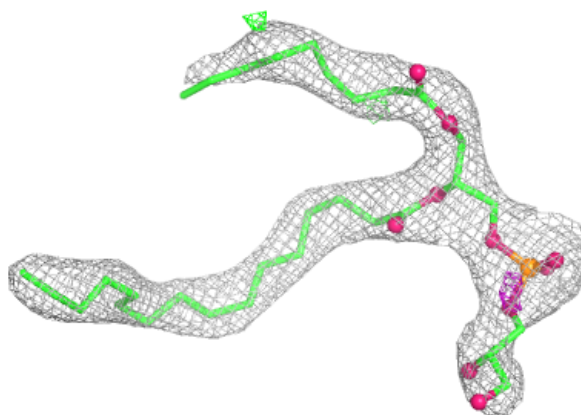
Electron density around CLA b 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

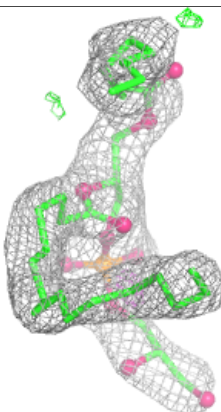
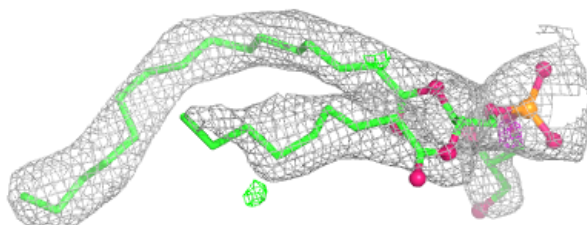
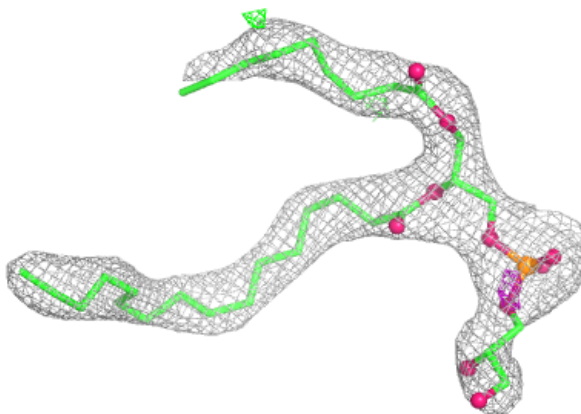


Electron density around LHG E 101 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

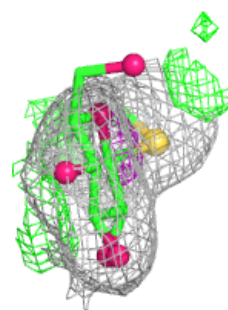
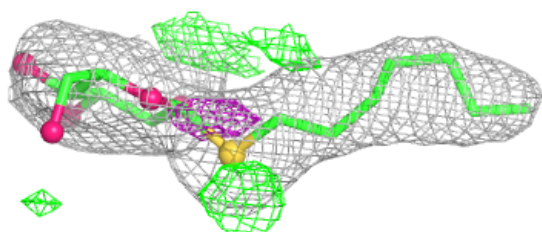
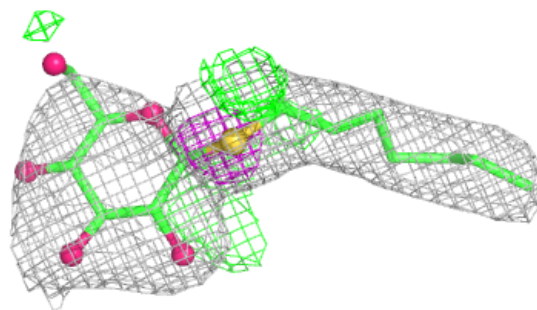
**Electron density around LHG E 101 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

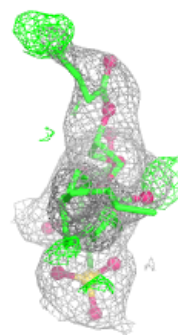
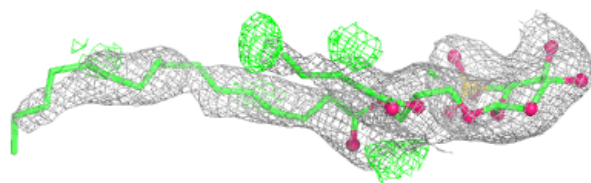
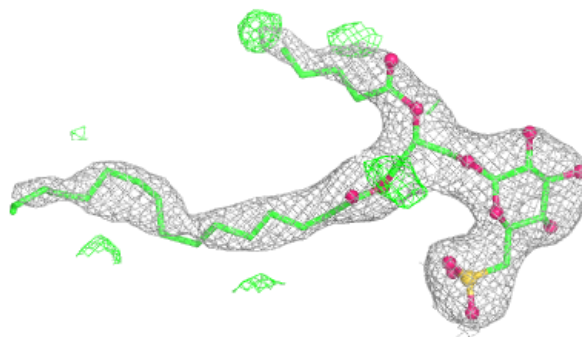


Electron density around HTG B 622:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

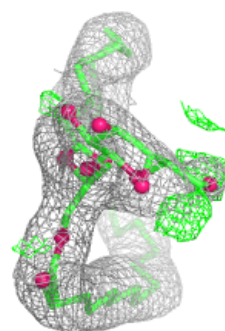
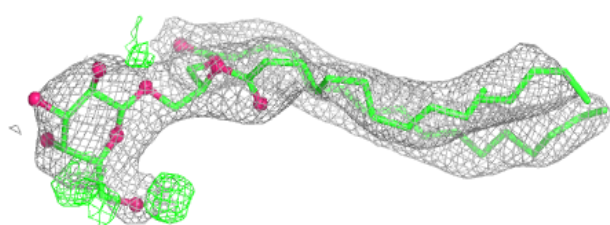
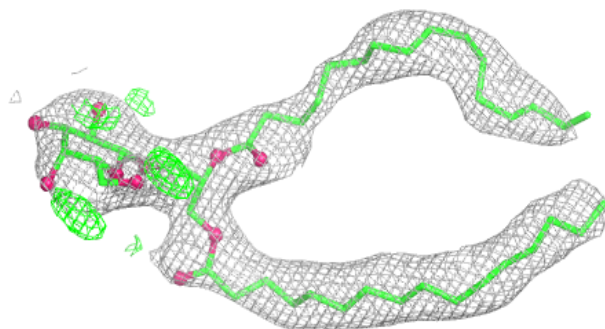
**Electron density around SQD X 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

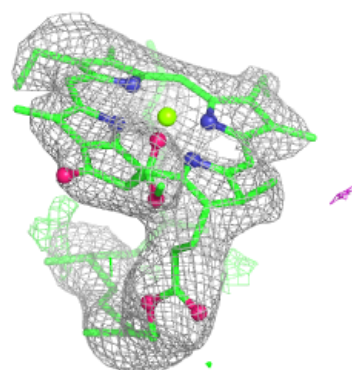
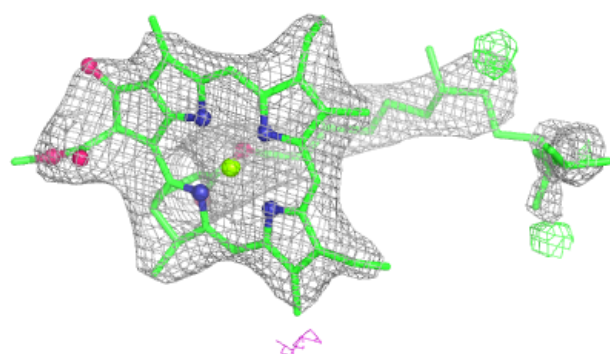
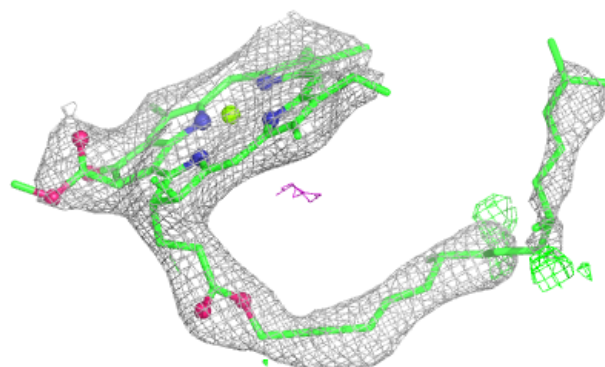


Electron density around LMG C 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

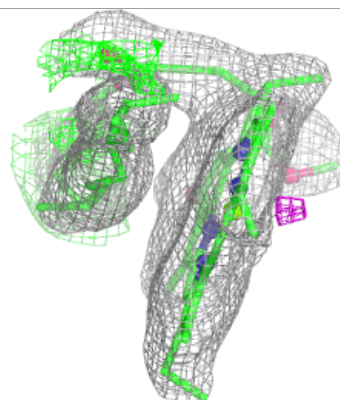
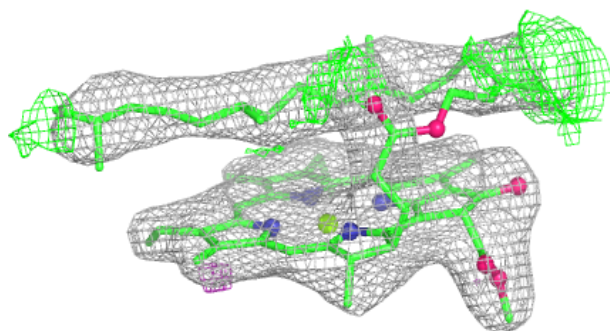
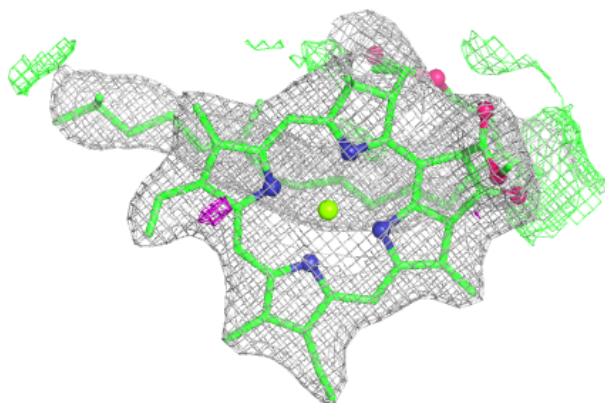
**Electron density around CLA c 514:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

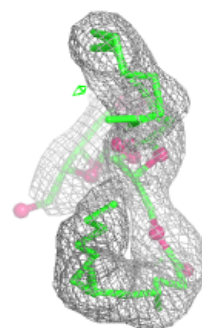
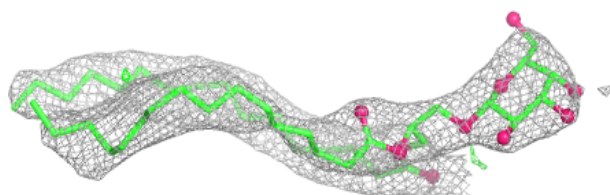
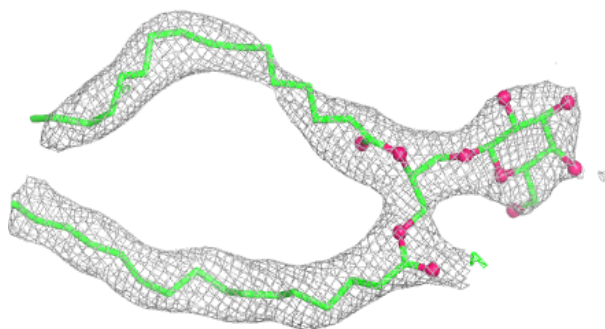


Electron density around CLA B 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

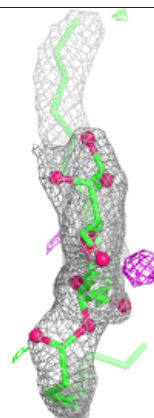
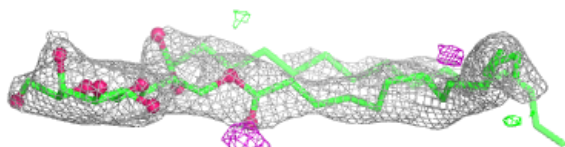
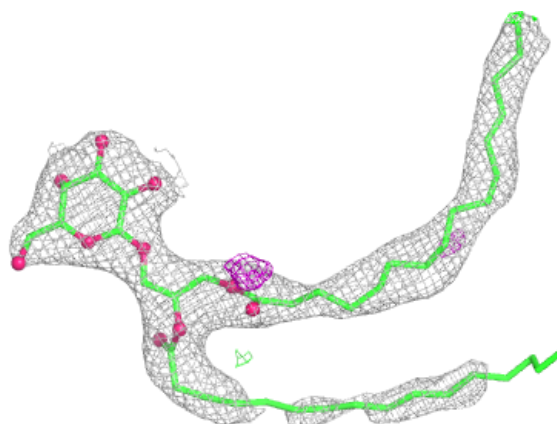
**Electron density around LMG a 417:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

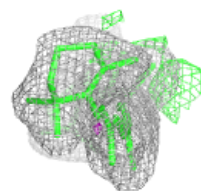
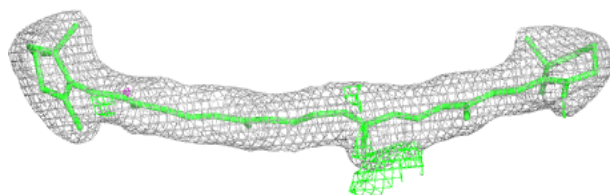
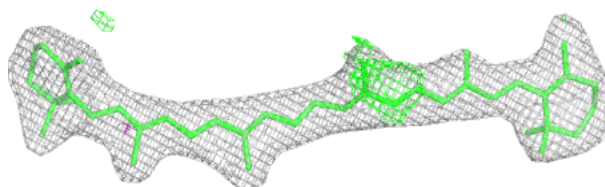


Electron density around LMG c 520:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

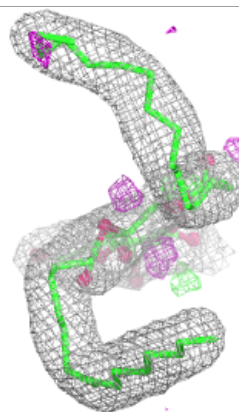
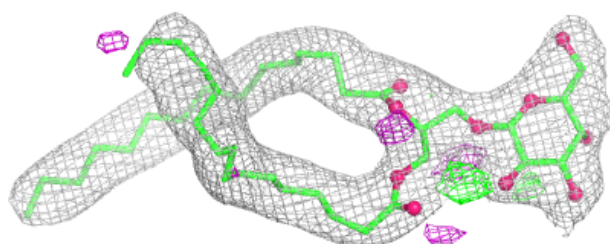
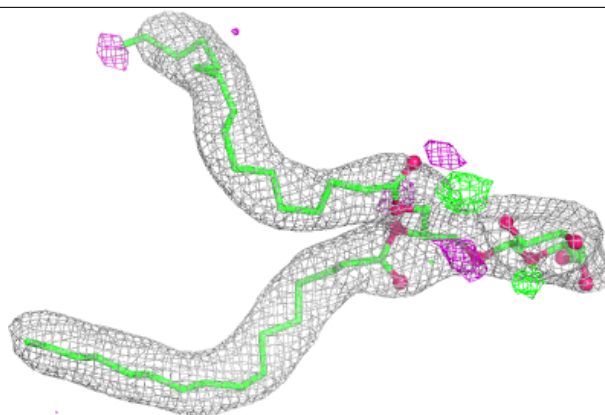
**Electron density around BCR T 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

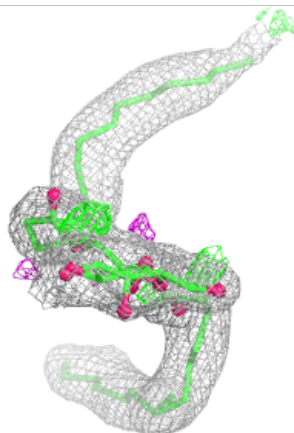
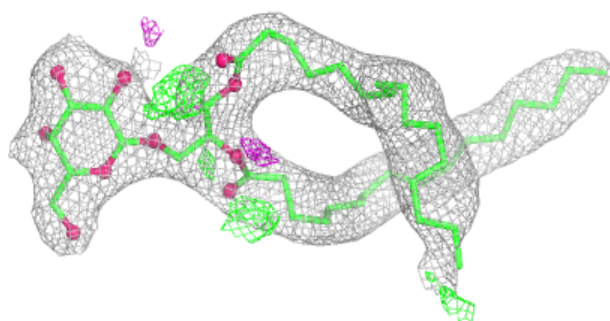
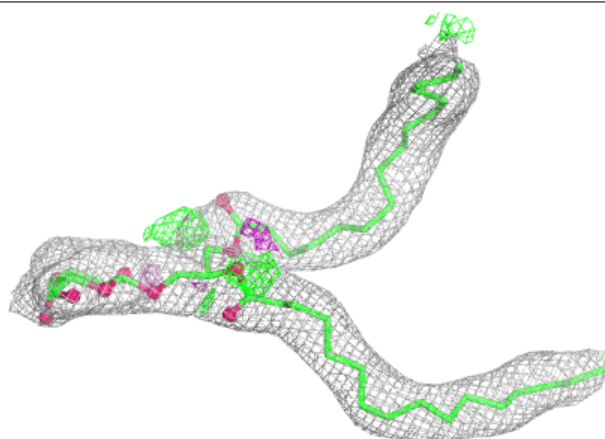


Electron density around LMG m 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

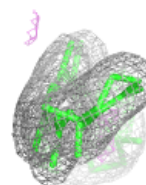
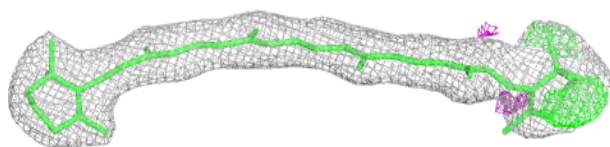
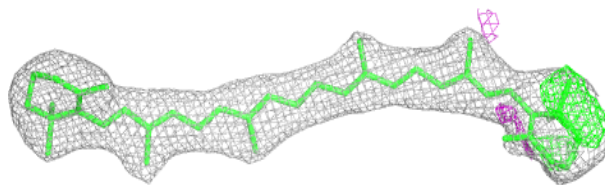
**Electron density around LMG B 621:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

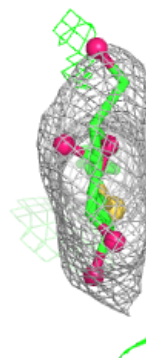
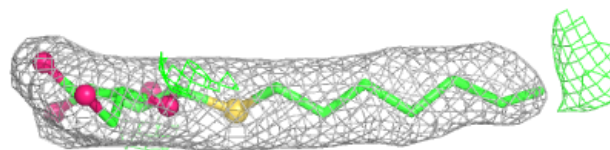
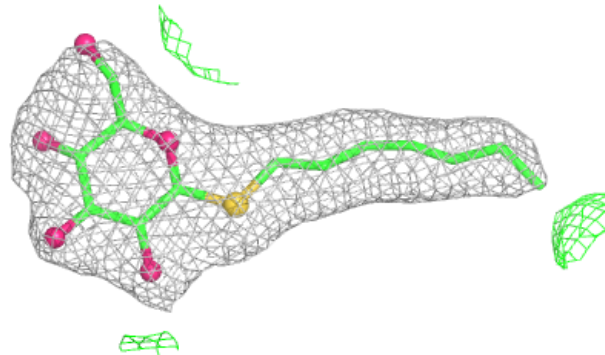


Electron density around BCR d 404:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

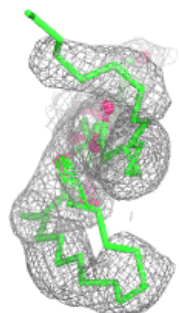
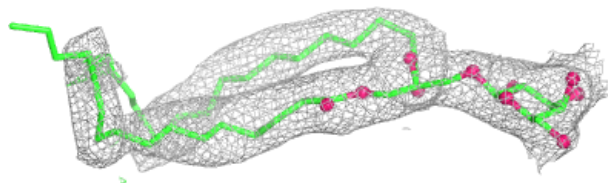
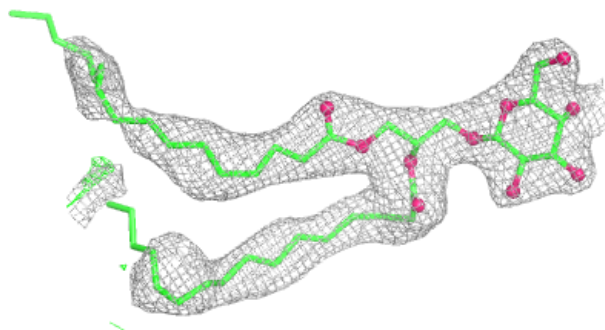
**Electron density around HTG B 625:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



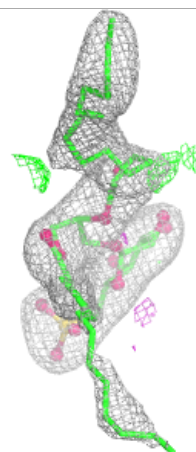
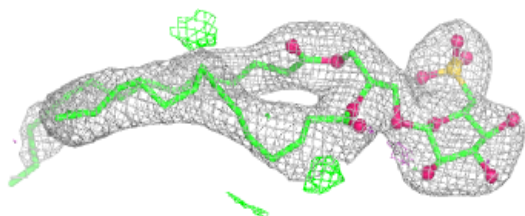
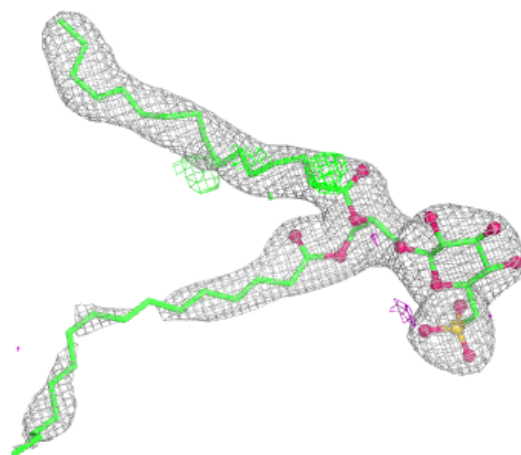
Electron density around LMG d 411:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



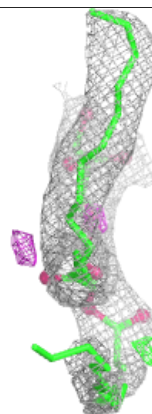
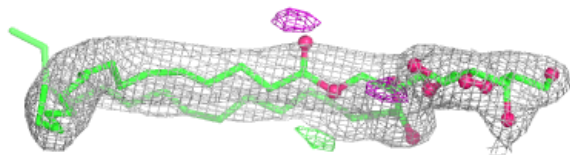
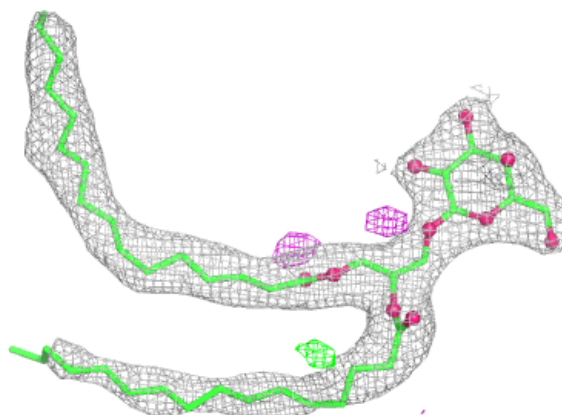
Electron density around SQD A 410 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



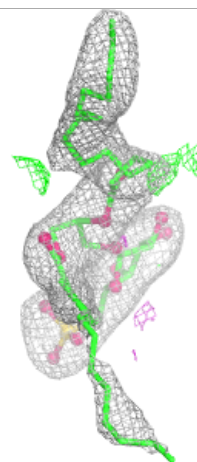
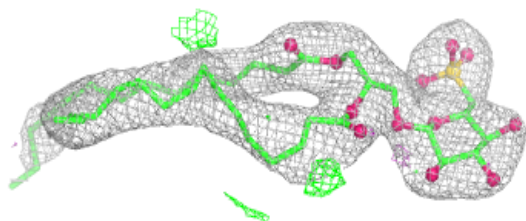
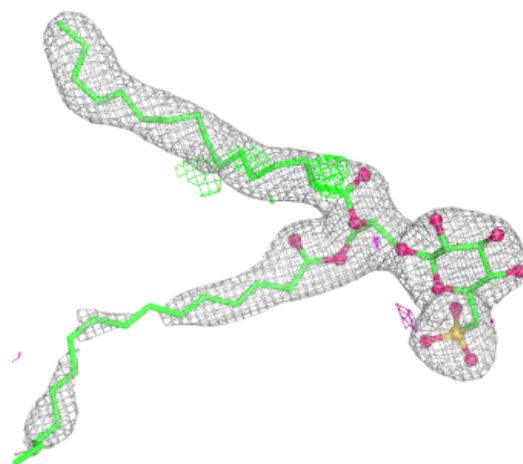
Electron density around LMG C 520:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



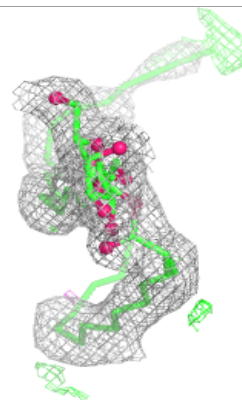
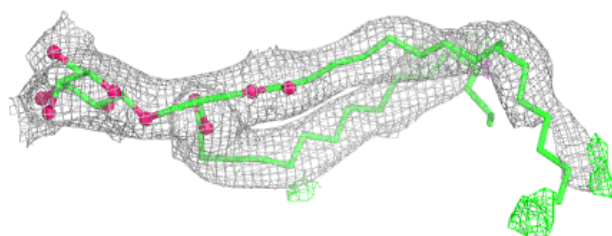
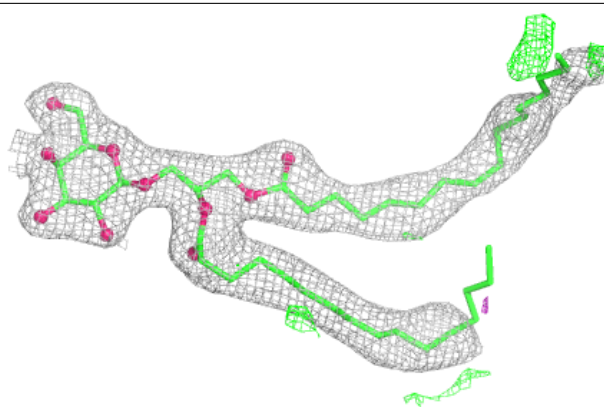
Electron density around SQD A 410 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

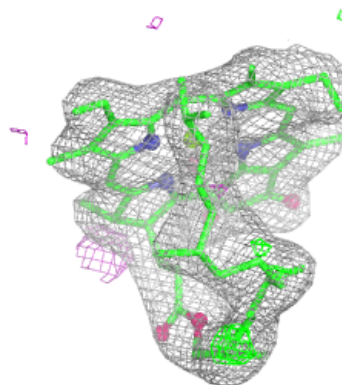
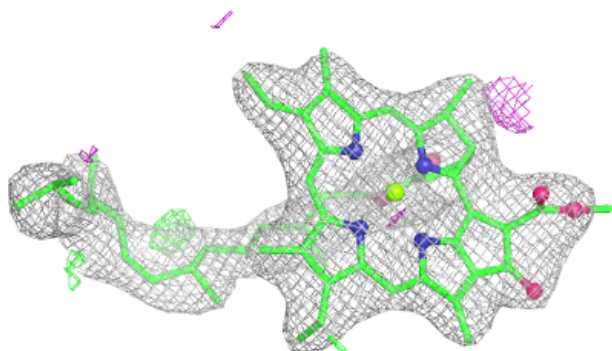
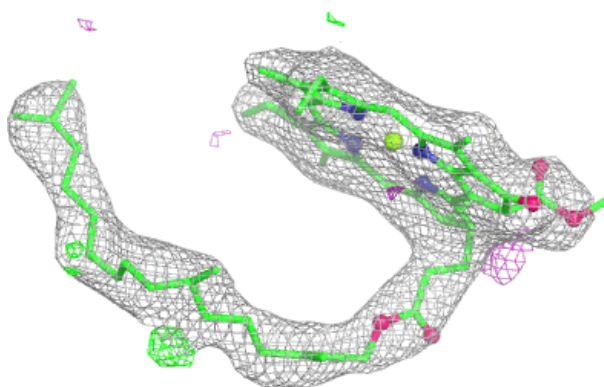


Electron density around LMG D 413:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

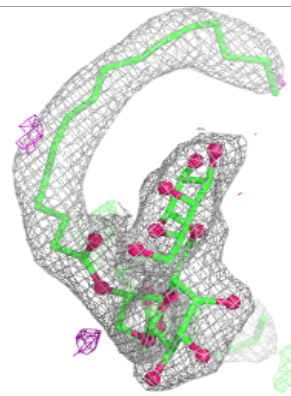
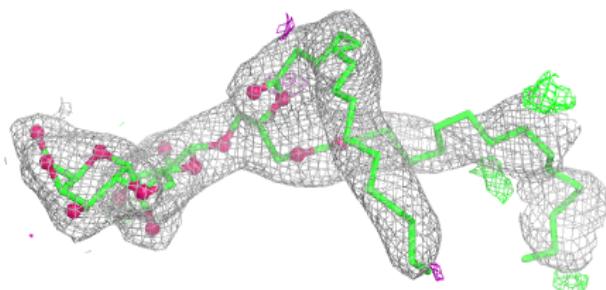
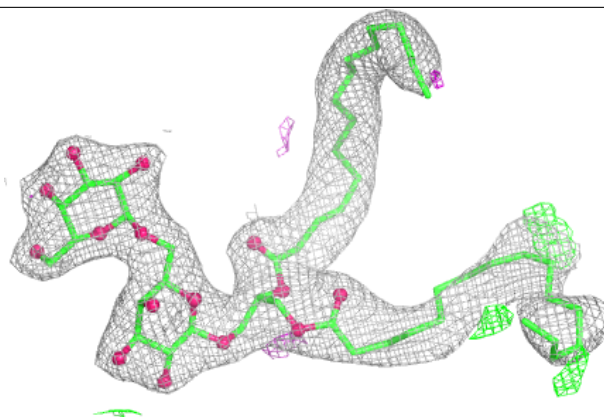
**Electron density around CLA C 514:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

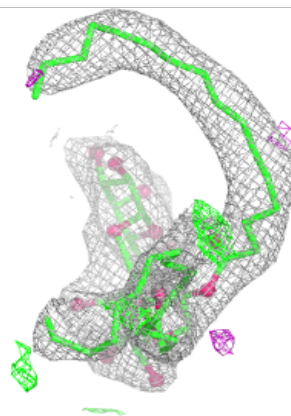
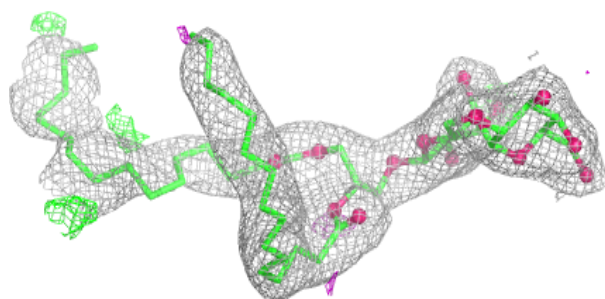
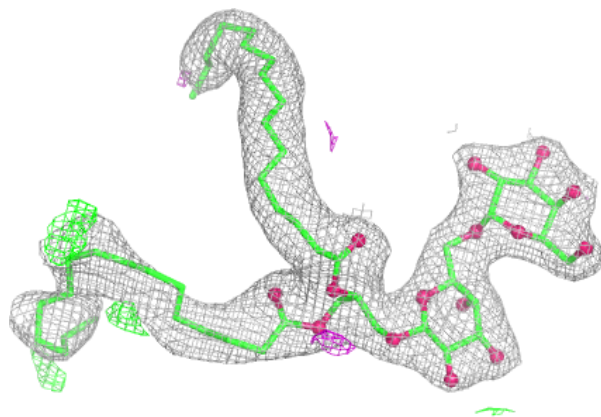


Electron density around DGD C 518 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

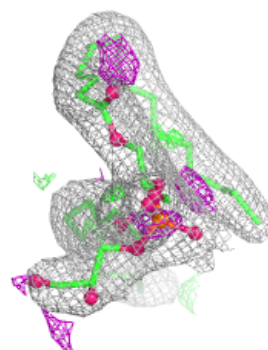
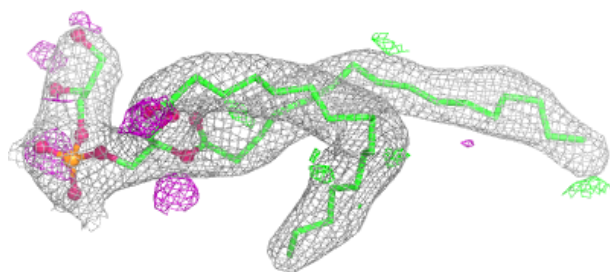
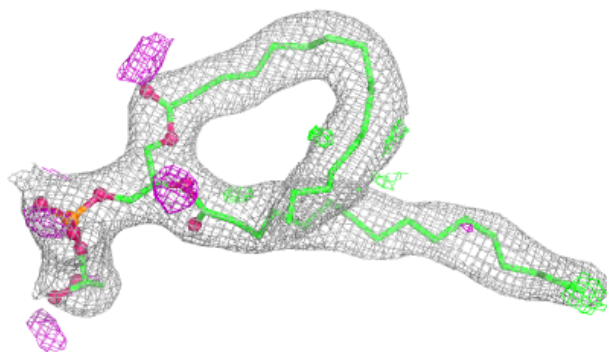
**Electron density around DGD C 518 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

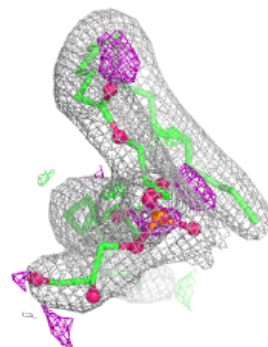
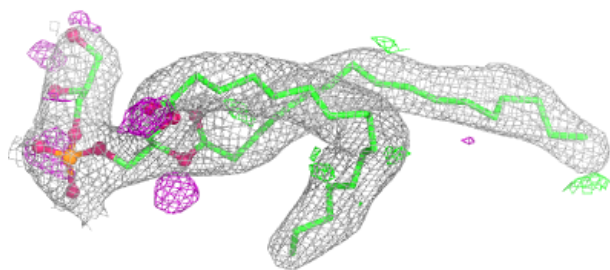
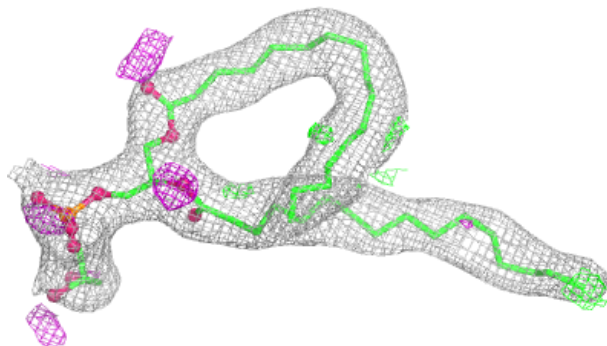


Electron density around LHG A 418 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

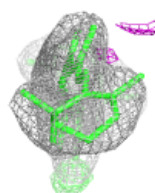
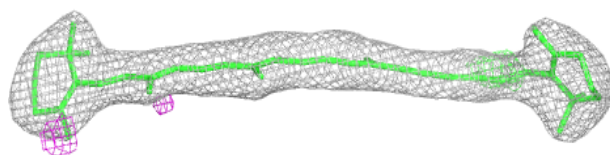
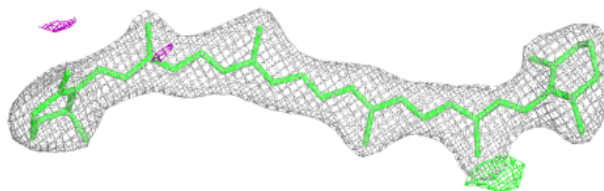
**Electron density around LHG A 418 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

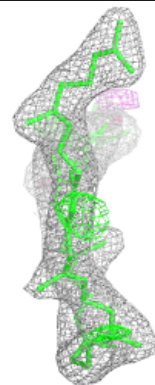
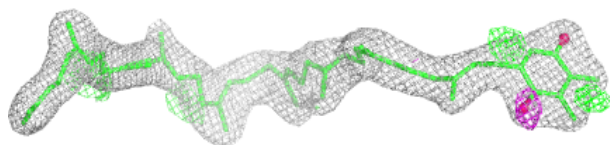
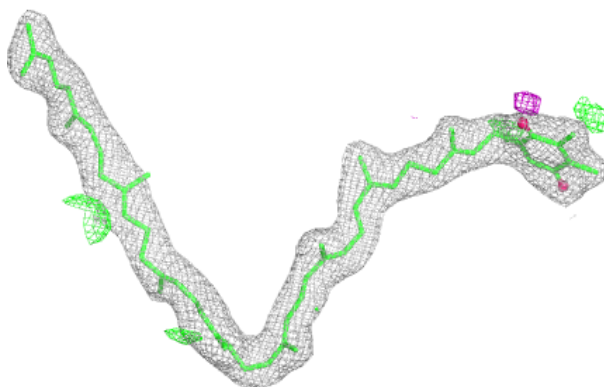


Electron density around BCR K 103:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

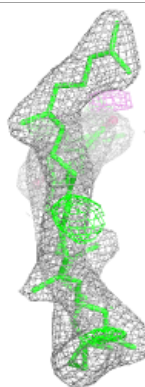
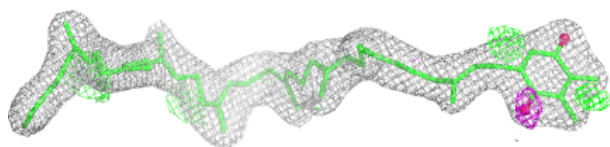
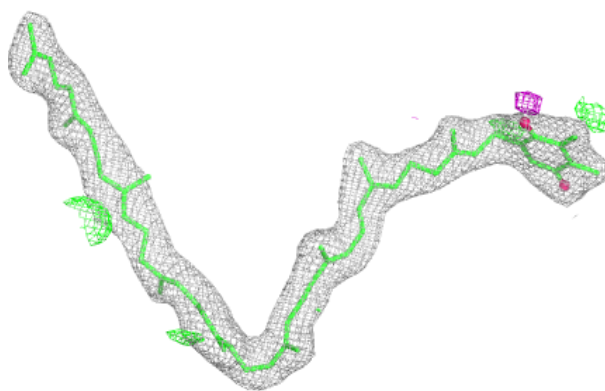
**Electron density around PL9 D 407 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

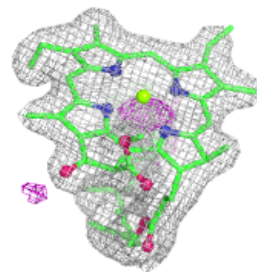
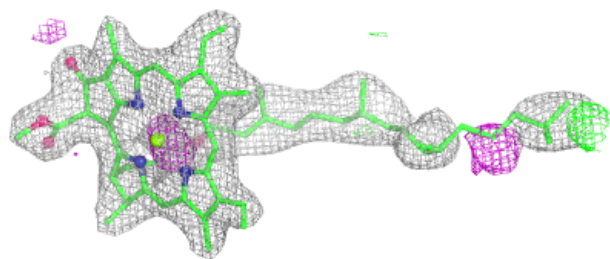
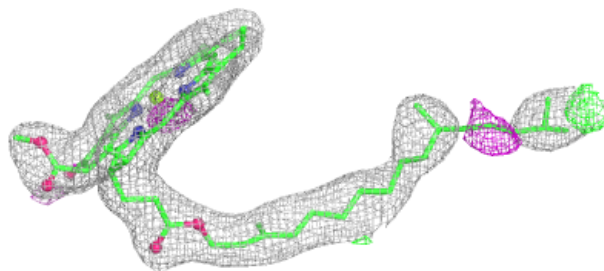


Electron density around PL9 D 407 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

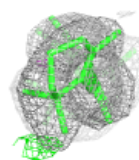
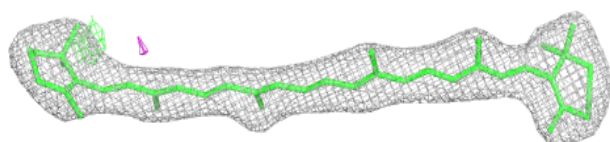
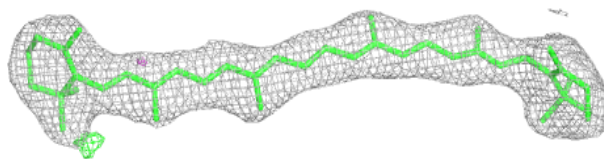
**Electron density around CLA C 505:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

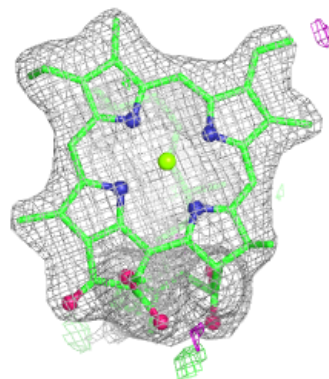
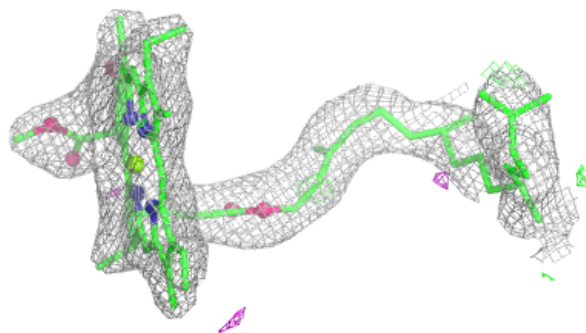
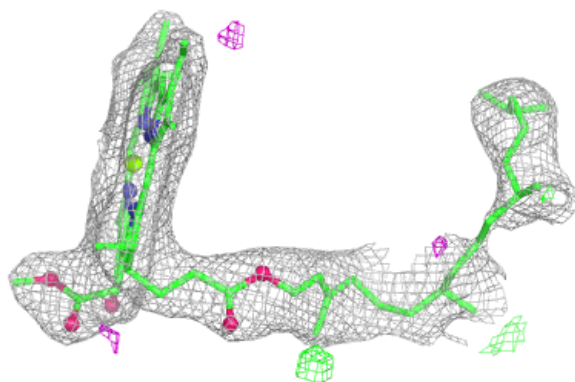


Electron density around BCR c 515:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

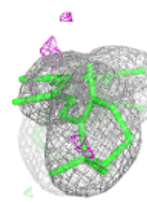
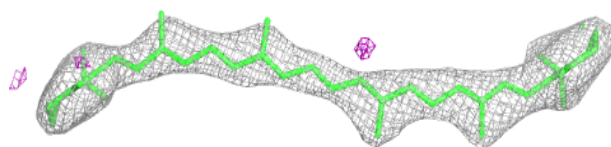
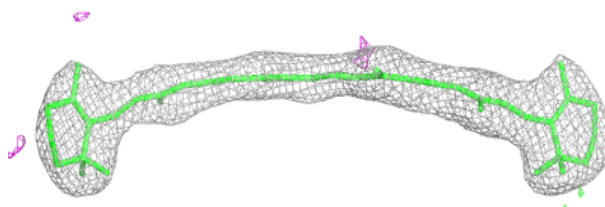
**Electron density around CLA C 507:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

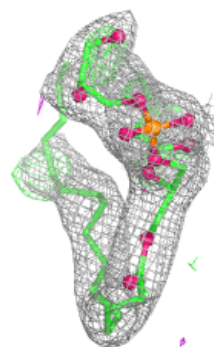
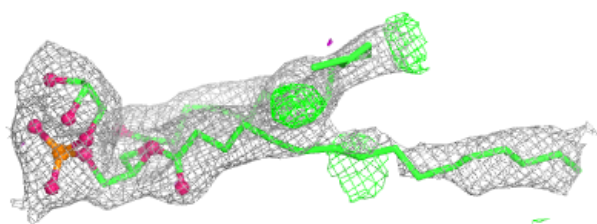
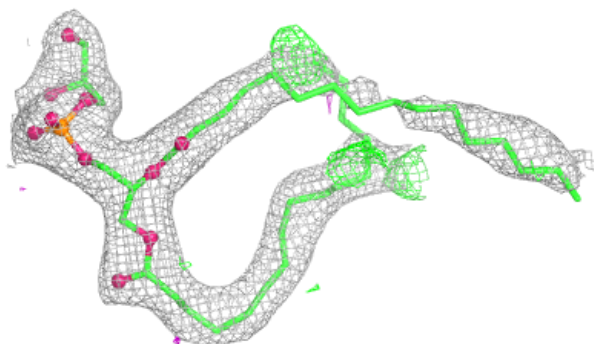


Electron density around BCR k 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

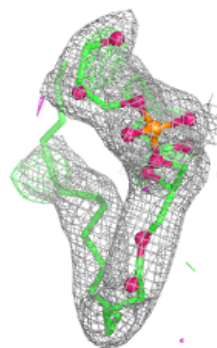
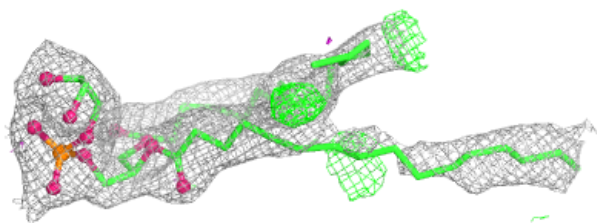
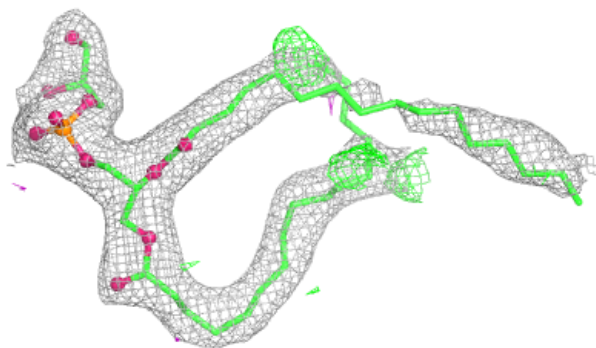
**Electron density around LHG D 409 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

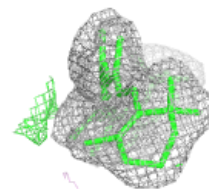
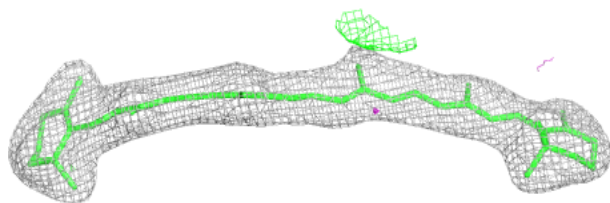
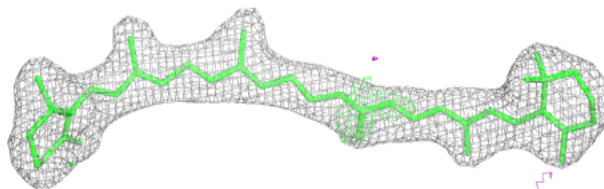


Electron density around LHG D 409 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

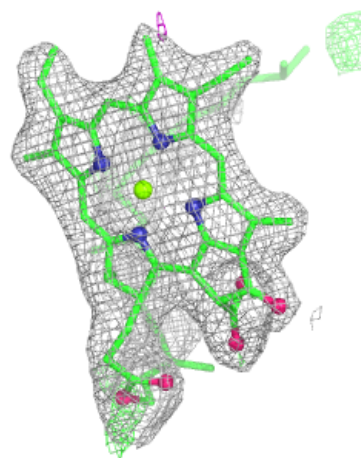
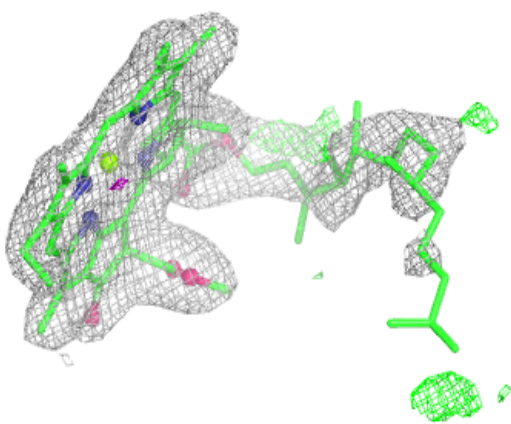
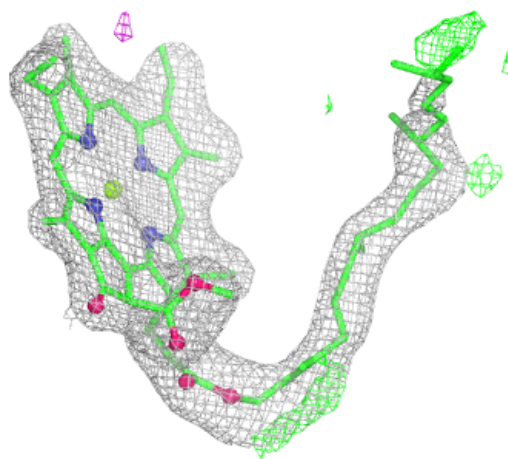
**Electron density around BCR t 102:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



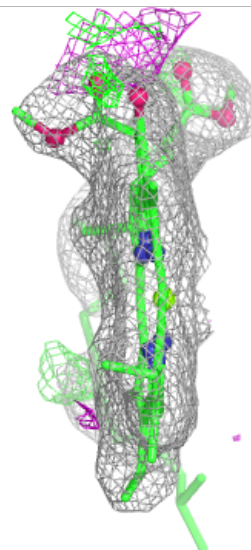
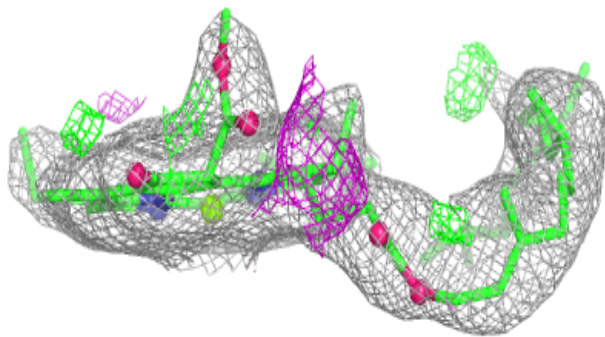
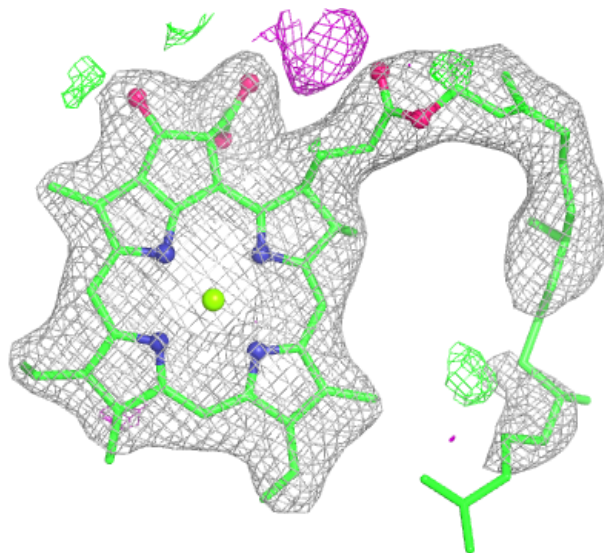
Electron density around CLA b 616:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



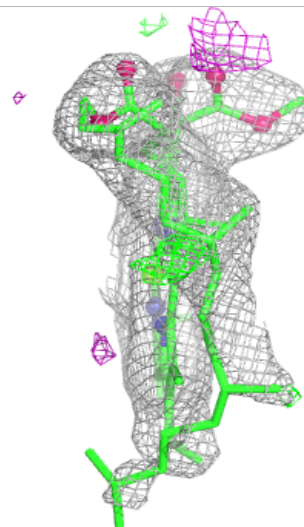
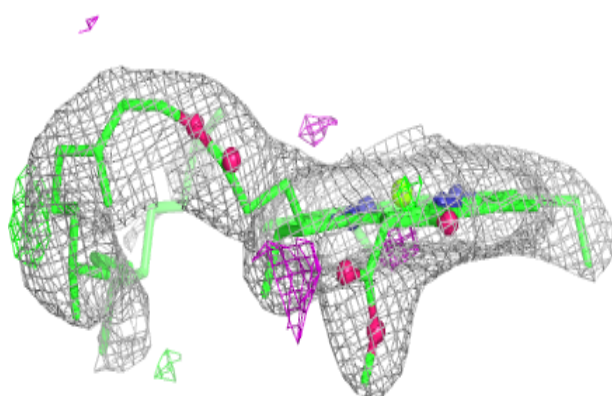
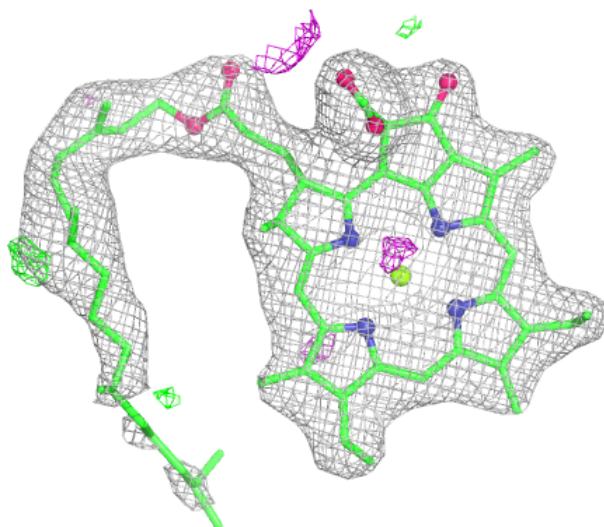
Electron density around CLA c 513:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



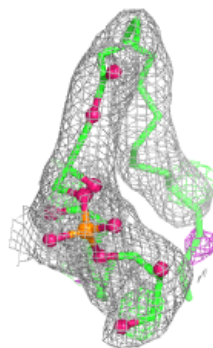
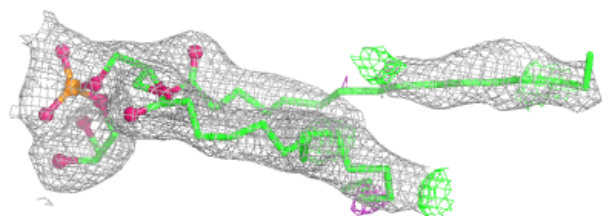
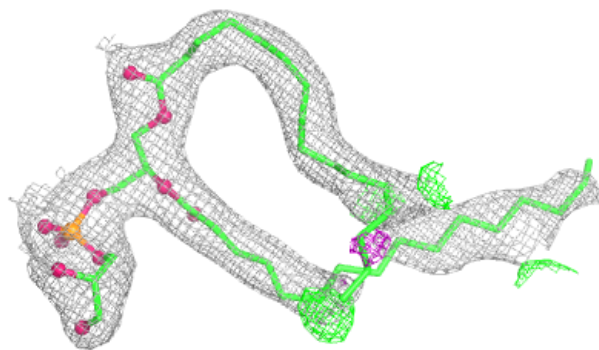
Electron density around CLA C 513:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

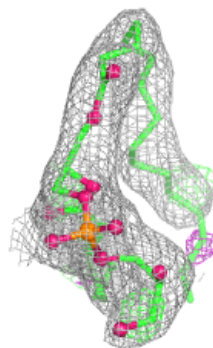
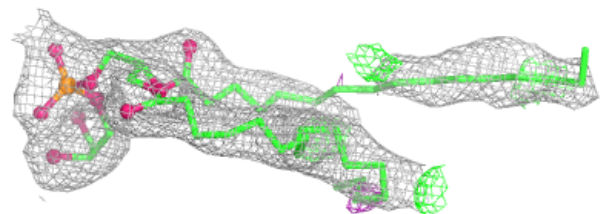
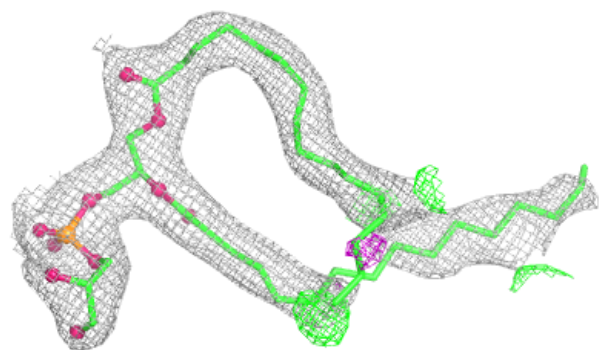


Electron density around LHG d 407 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

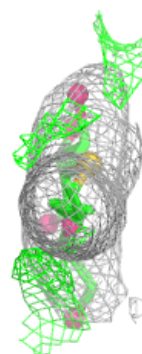
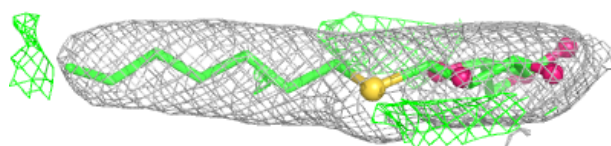
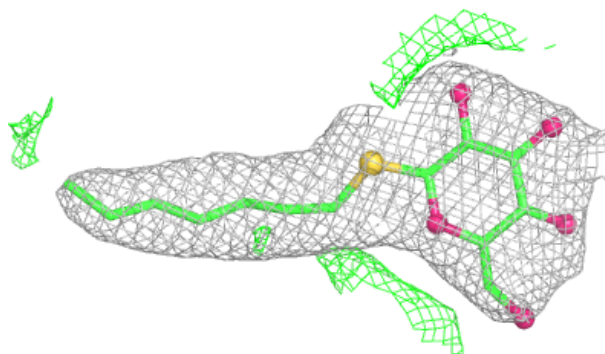
**Electron density around LHG d 407 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

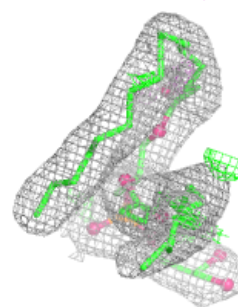
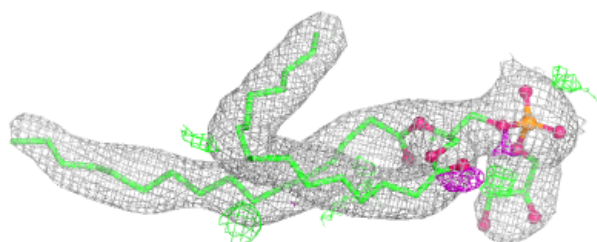
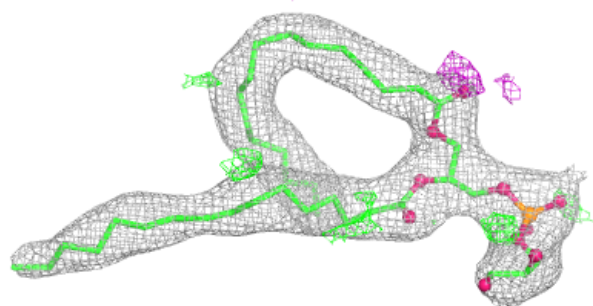


Electron density around HTG b 625:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

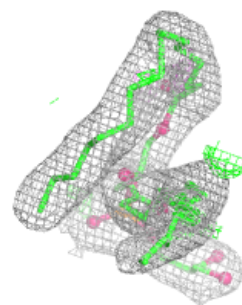
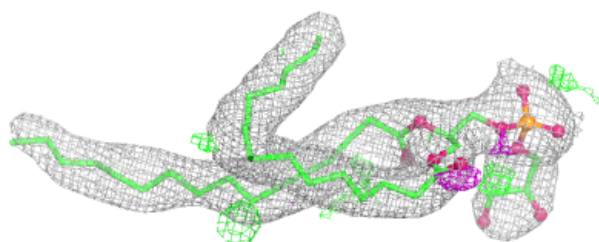
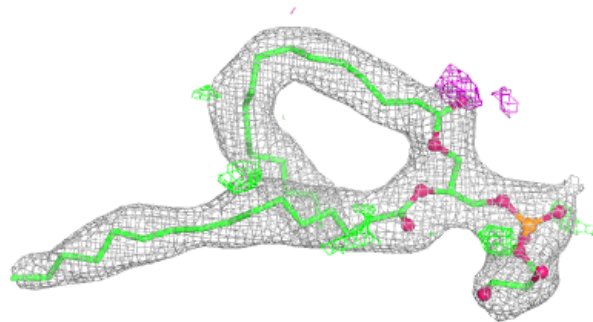
**Electron density around LHG d 413 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

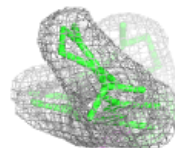
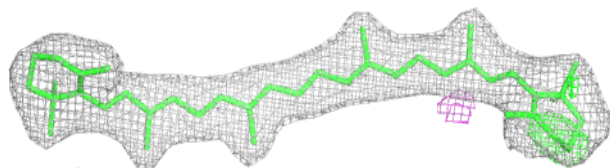
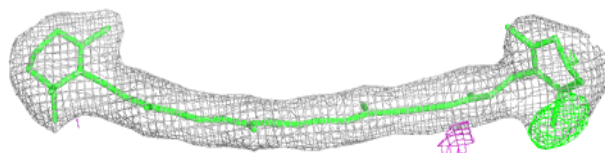


Electron density around LHG d 413 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

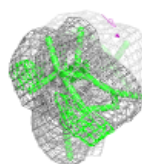
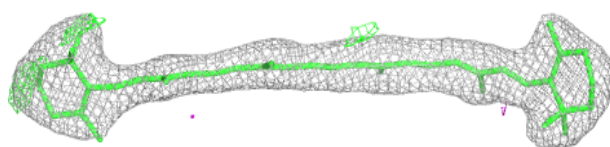
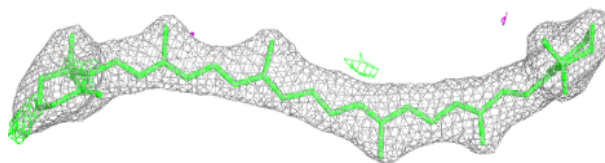
**Electron density around BCR D 406:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

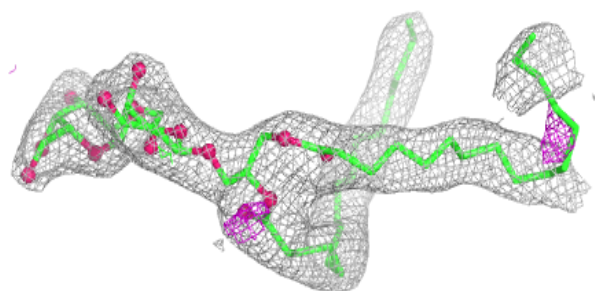
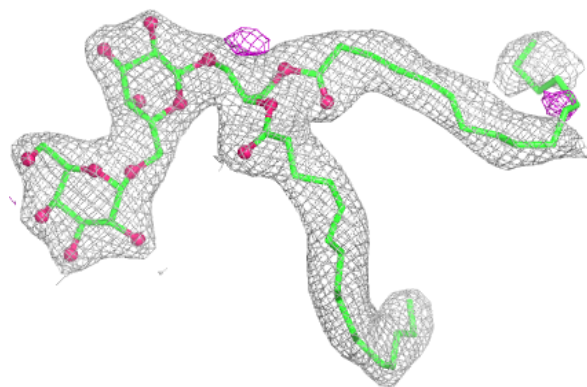


Electron density around BCR H 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

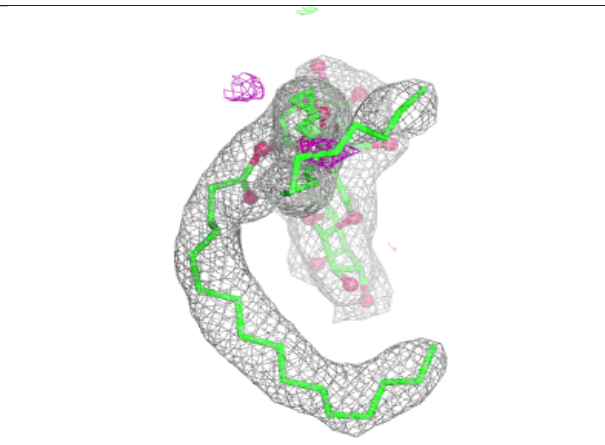
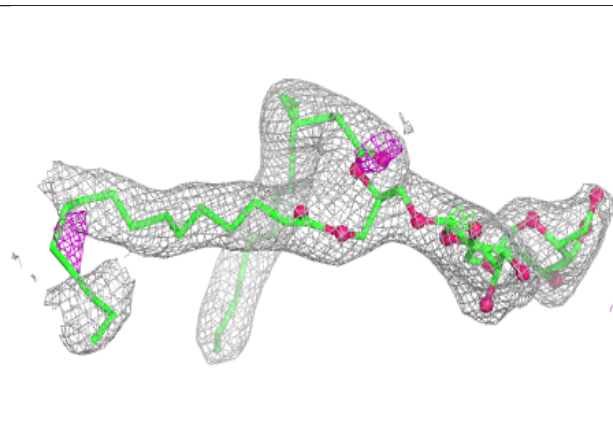
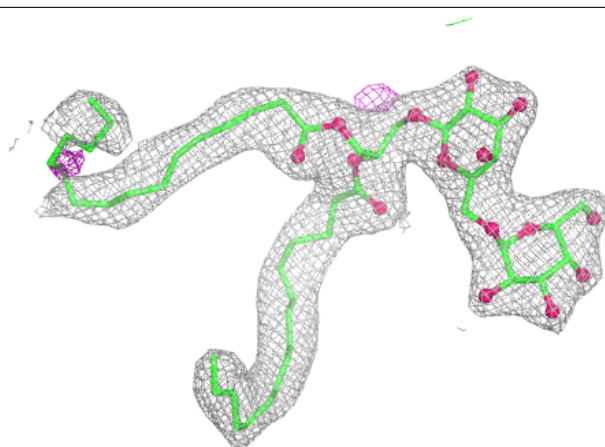
**Electron density around DGD c 518 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

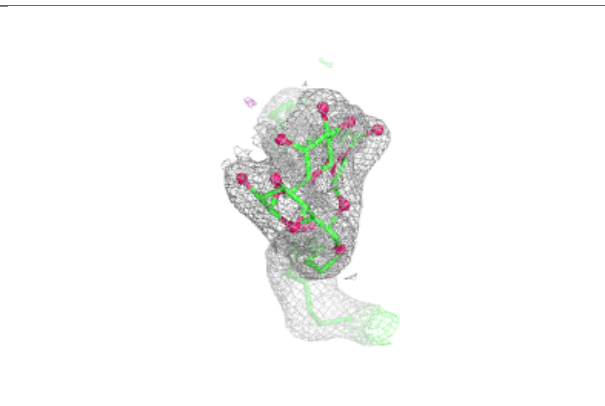
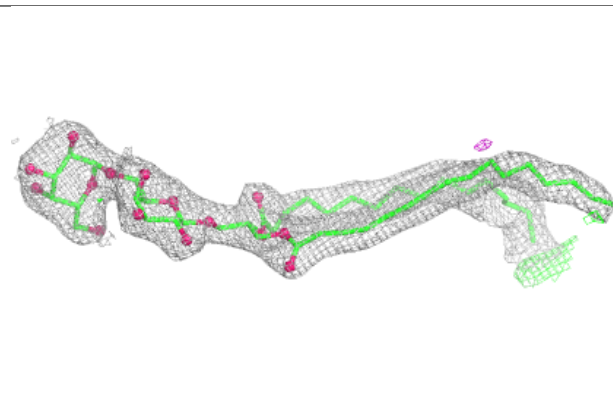
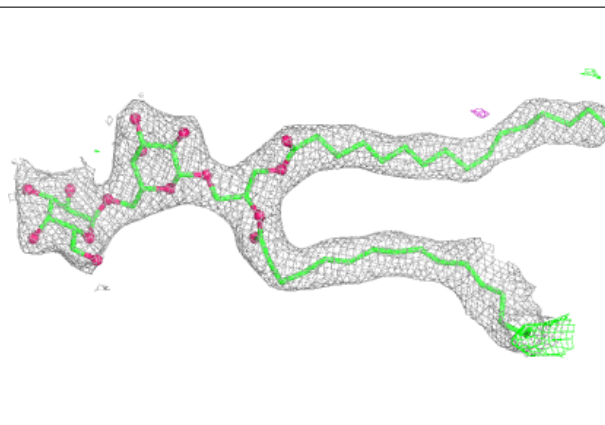


Electron density around DGD c 518 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

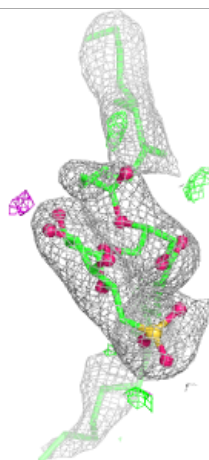
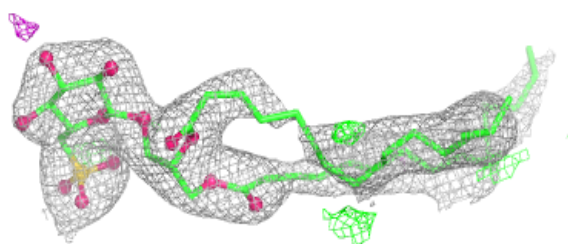
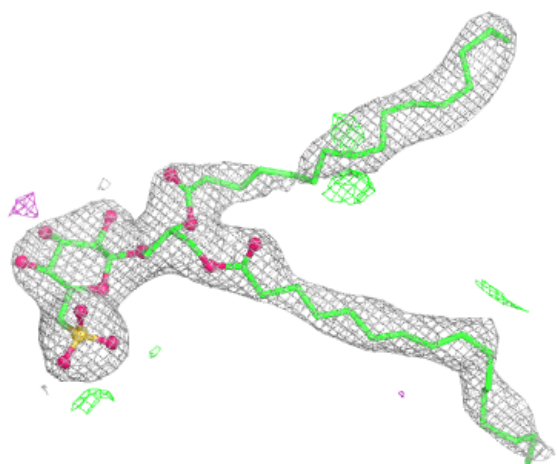
**Electron density around DGD c 519:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



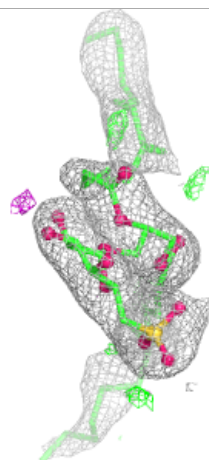
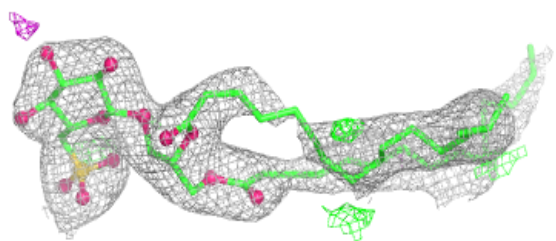
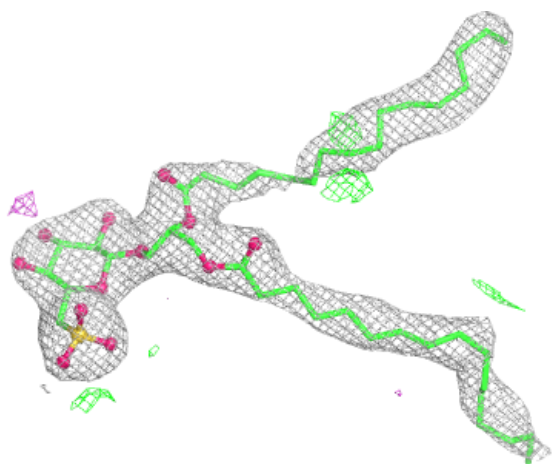
Electron density around SQD a 411 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



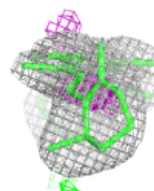
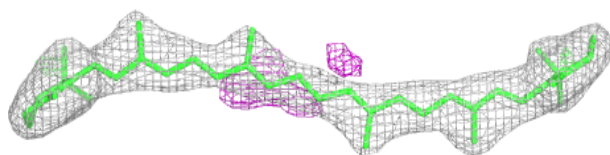
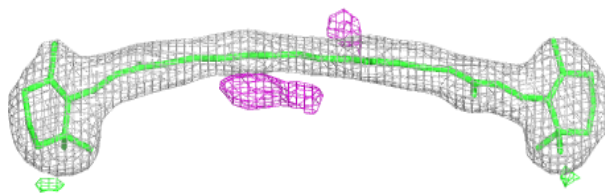
Electron density around SQD a 411 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

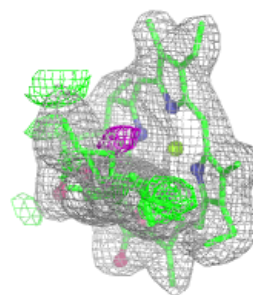
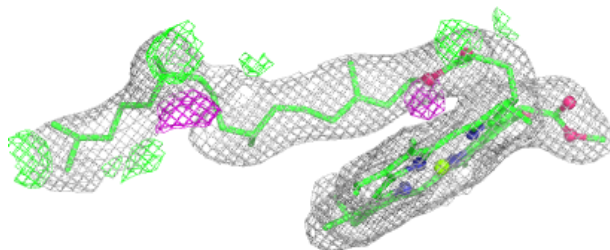
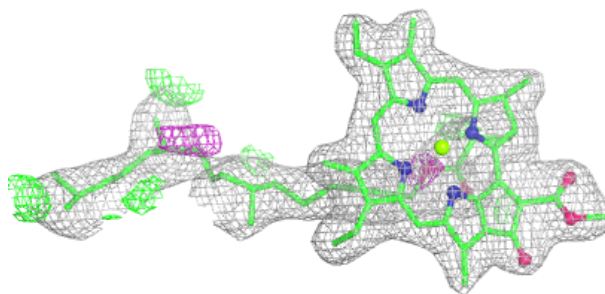


Electron density around BCR K 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

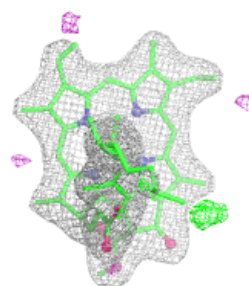
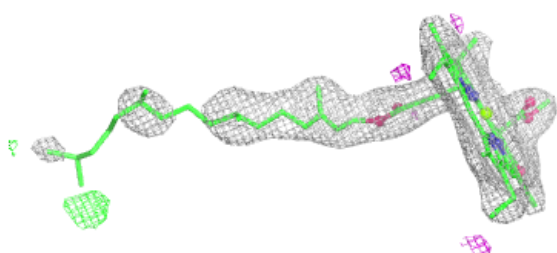
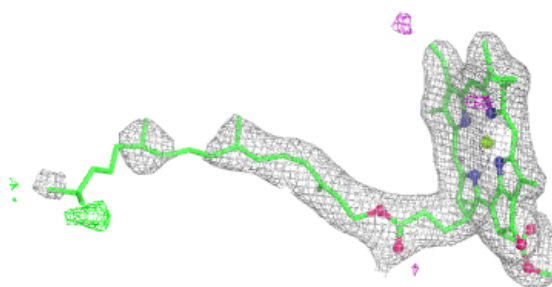
**Electron density around CLA B 614:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

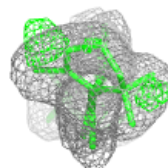
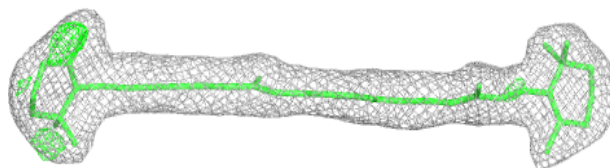
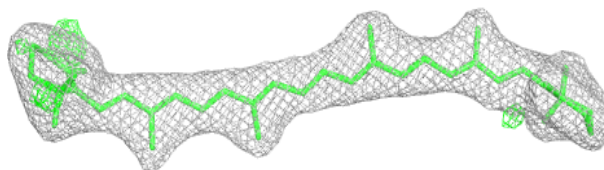


Electron density around CLA d 403:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

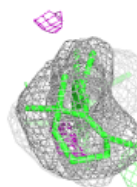
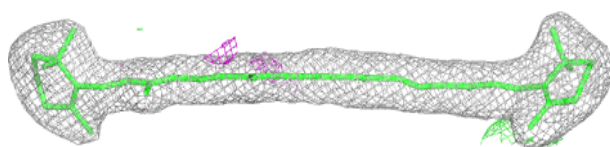
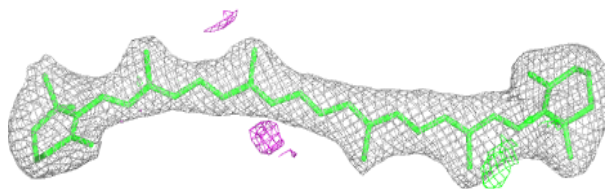
**Electron density around BCR A 409:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

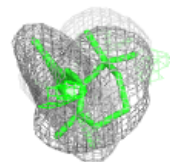
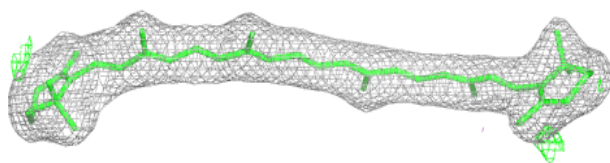
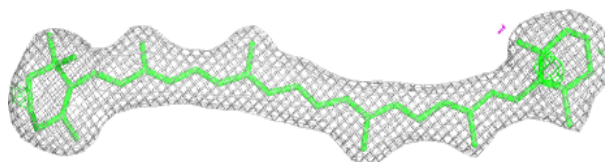


Electron density around BCR B 618:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

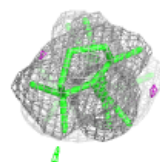
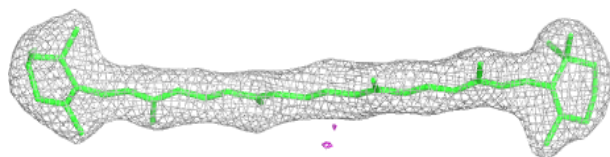
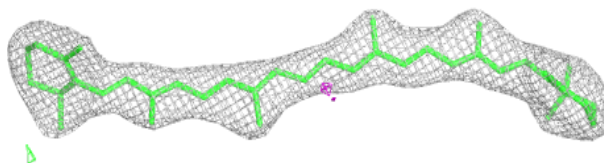
**Electron density around BCR B 619:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



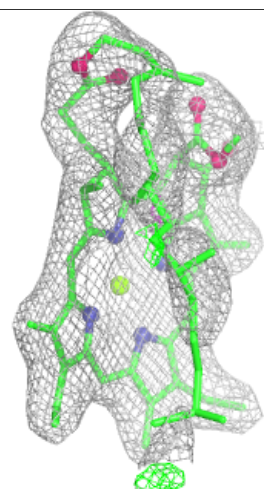
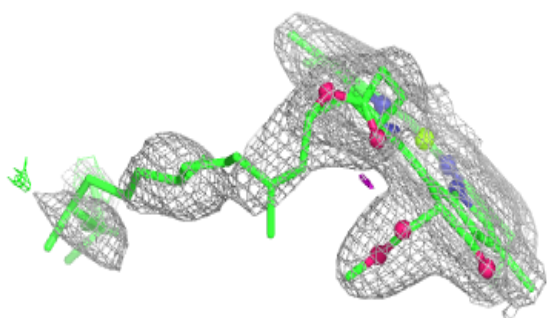
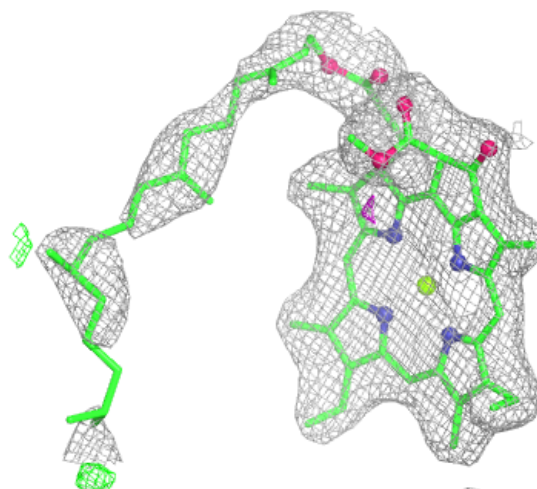
Electron density around BCR C 515:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



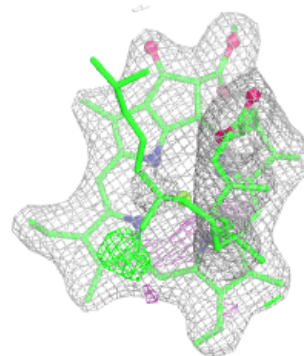
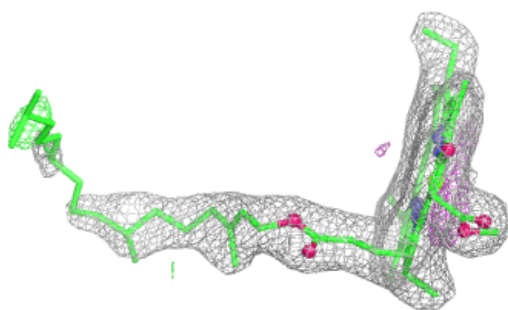
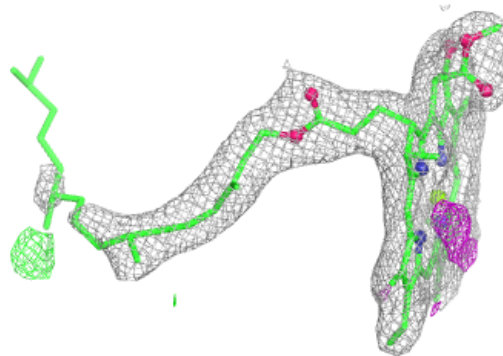
Electron density around CLA B 616:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

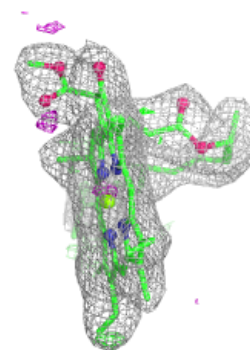
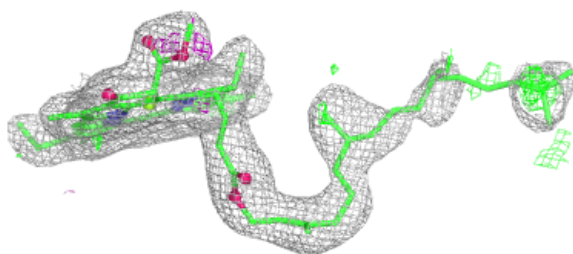
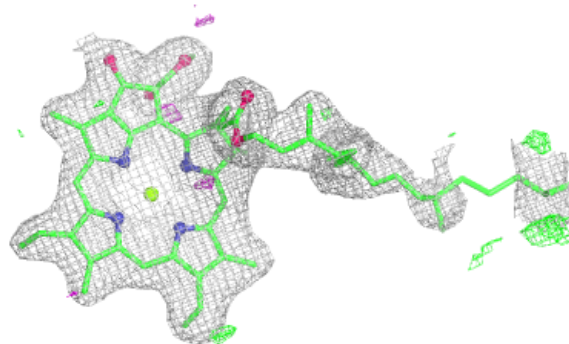


Electron density around CLA D 405:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

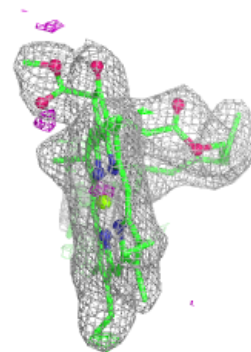
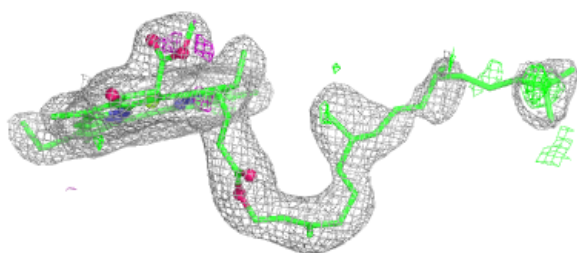
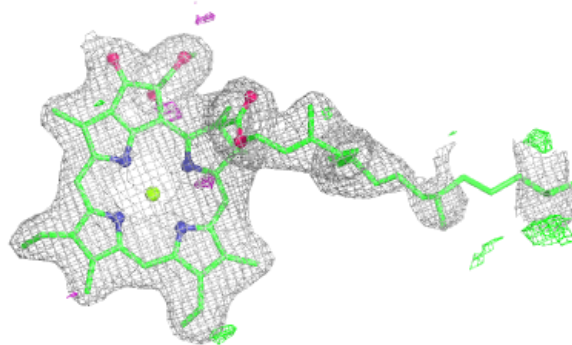
**Electron density around CLA a 407 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

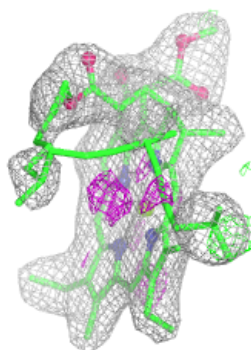
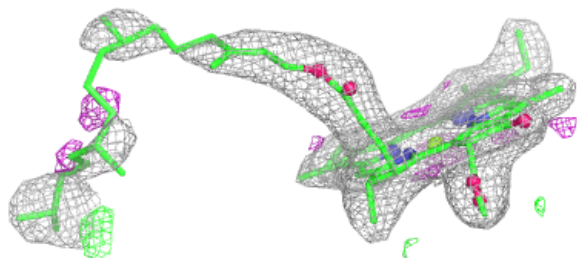
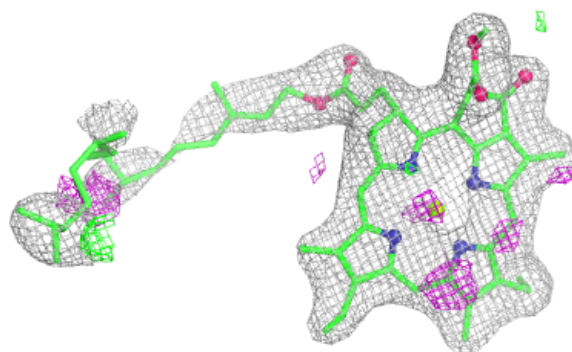


Electron density around CLA a 407 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

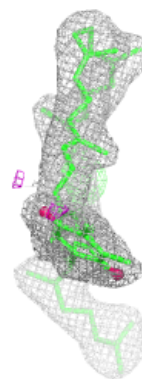
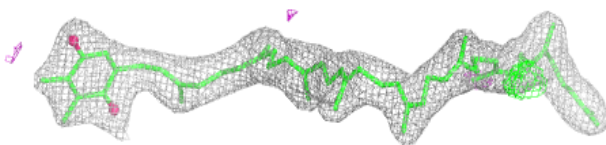
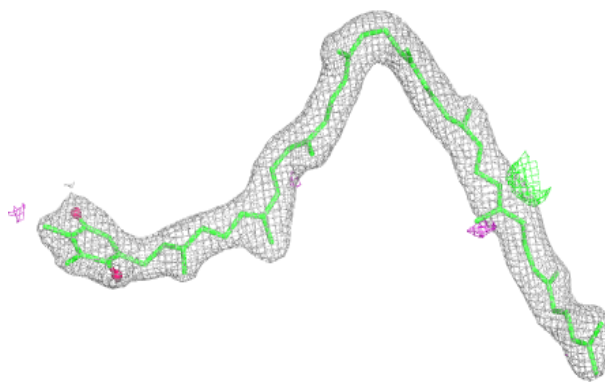
**Electron density around CLA a 409:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

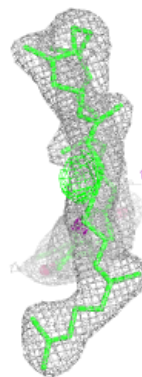
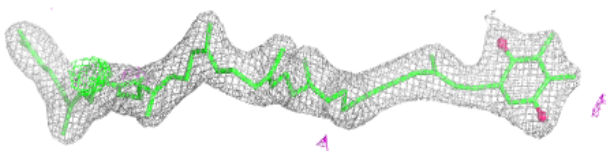
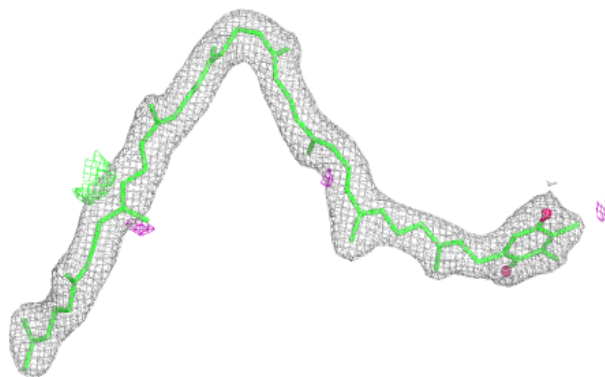


Electron density around PL9 d 405 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

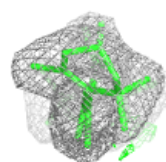
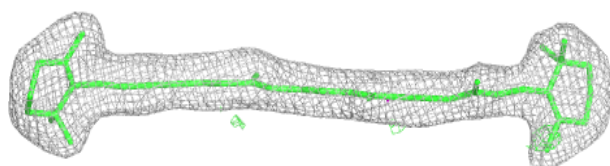
**Electron density around PL9 d 405 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

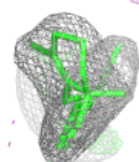
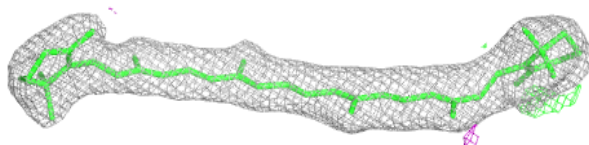
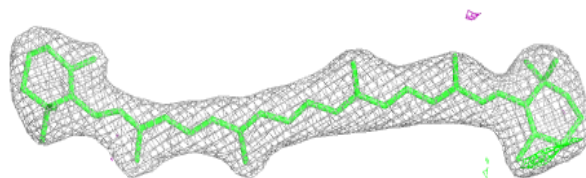


Electron density around BCR a 410:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

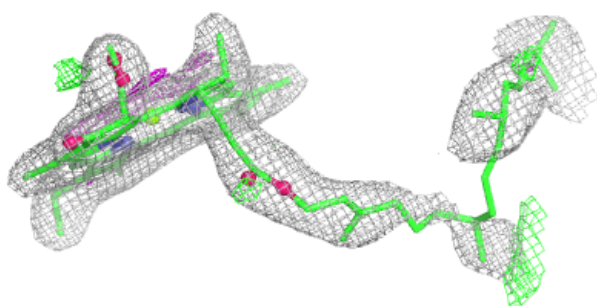
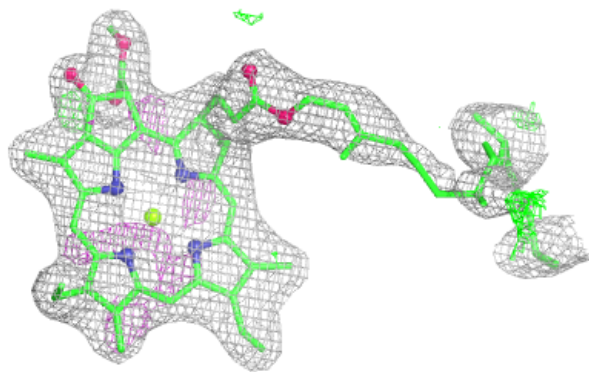
**Electron density around BCR b 619:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

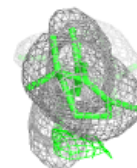
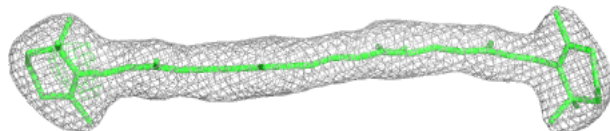
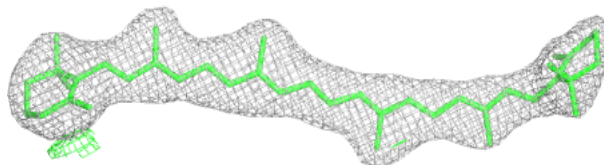


Electron density around CLA A 408:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

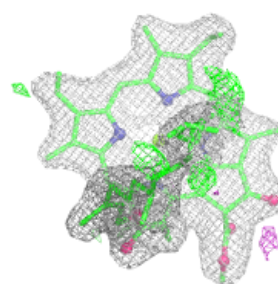
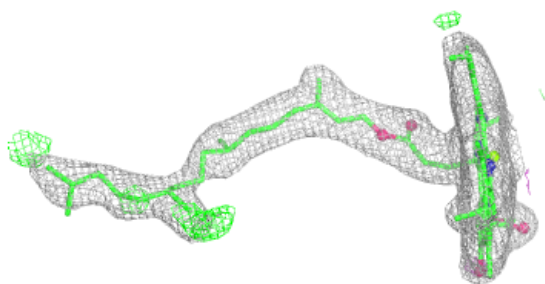
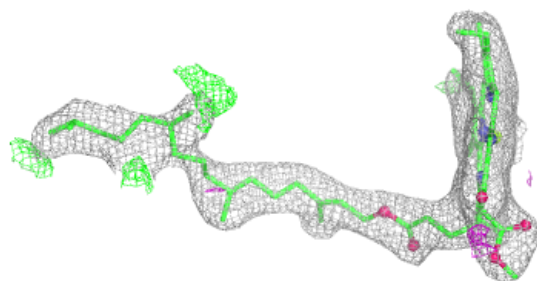
**Electron density around BCR c 516:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

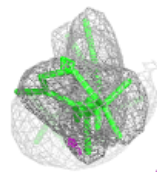
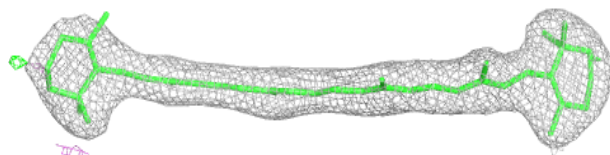
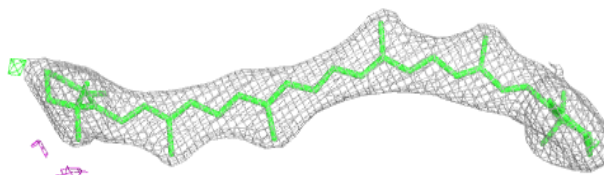


Electron density around CLA b 606:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

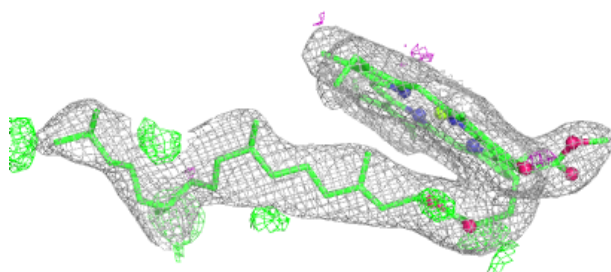
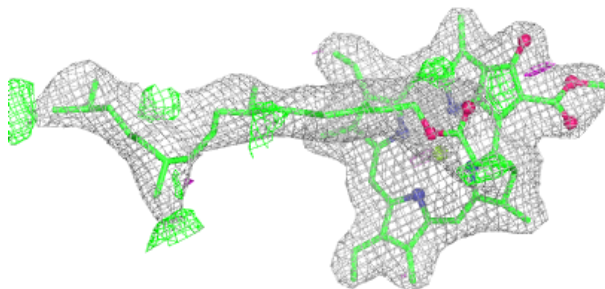
**Electron density around BCR h 101:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

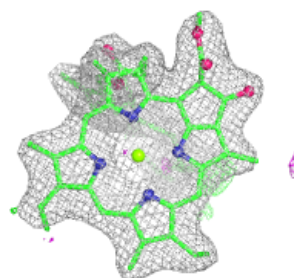
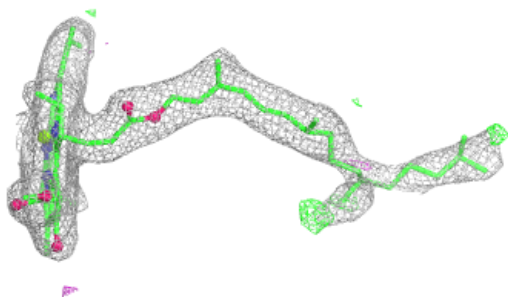
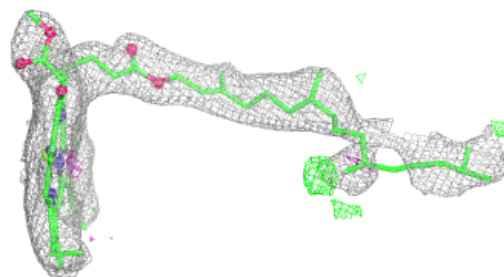


Electron density around CLA b 614:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

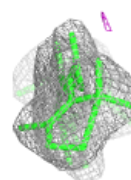
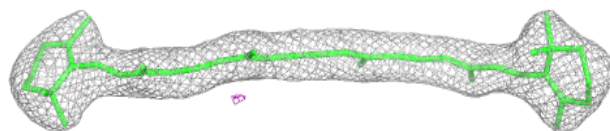
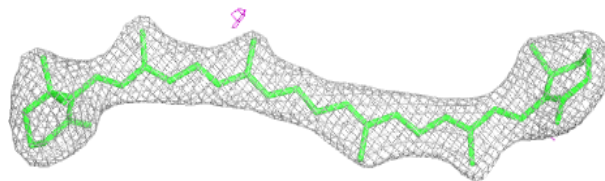
**Electron density around CLA B 606:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

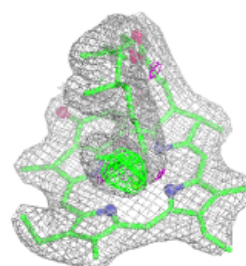
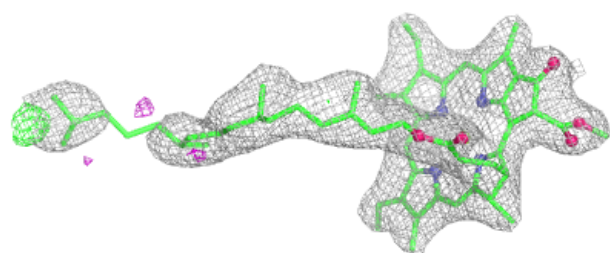
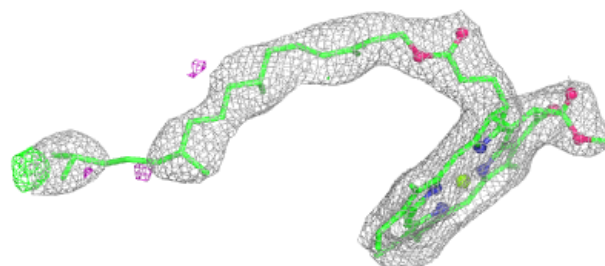


Electron density around BCR y 101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

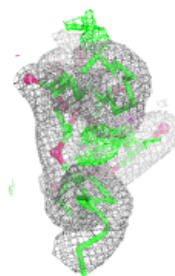
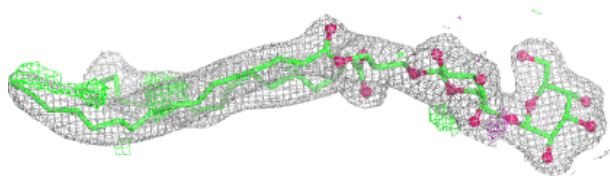
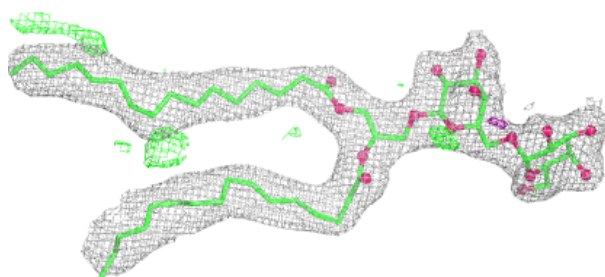
**Electron density around CLA c 505:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

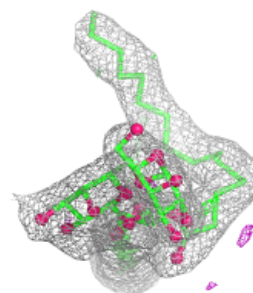
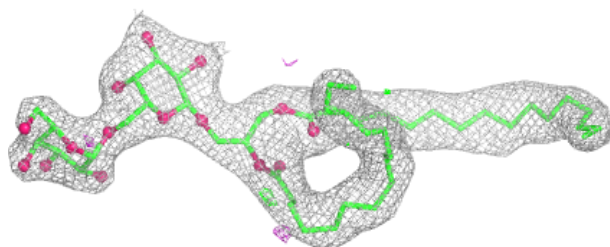
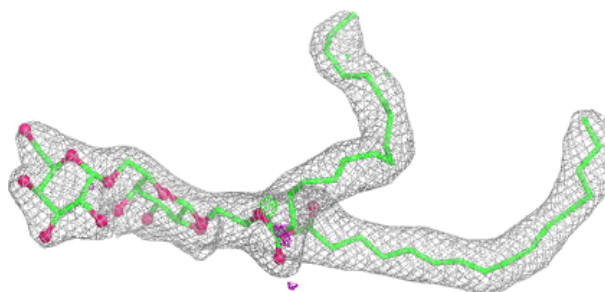


Electron density around DGD C 519:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

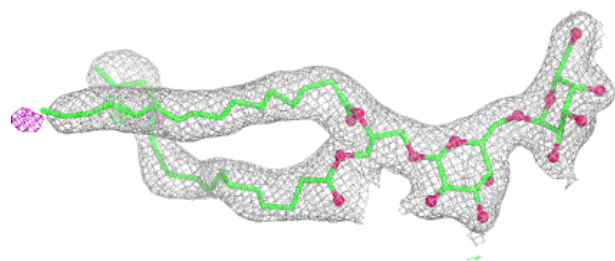
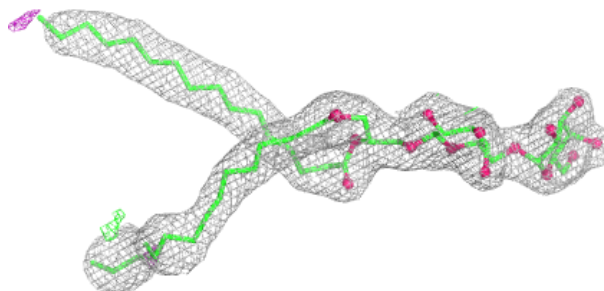
**Electron density around DGD H 102:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

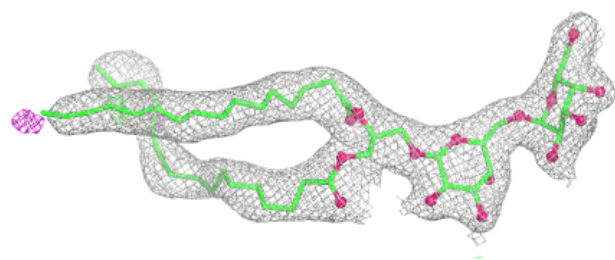
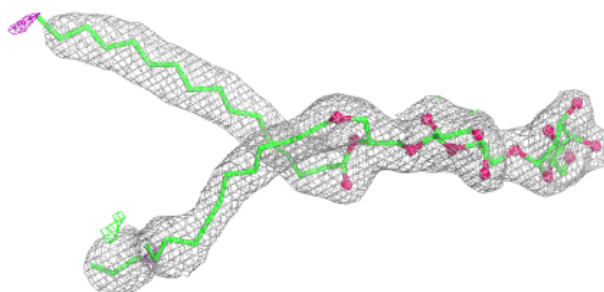


Electron density around DGD c 517 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

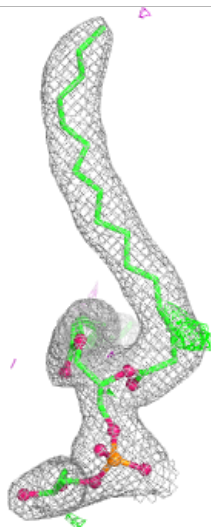
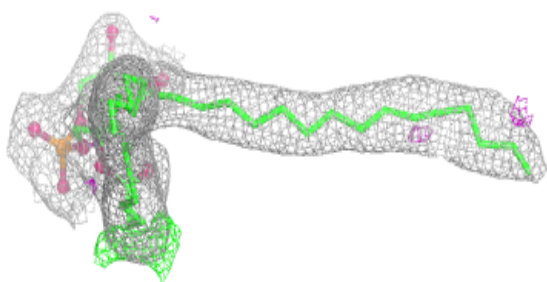
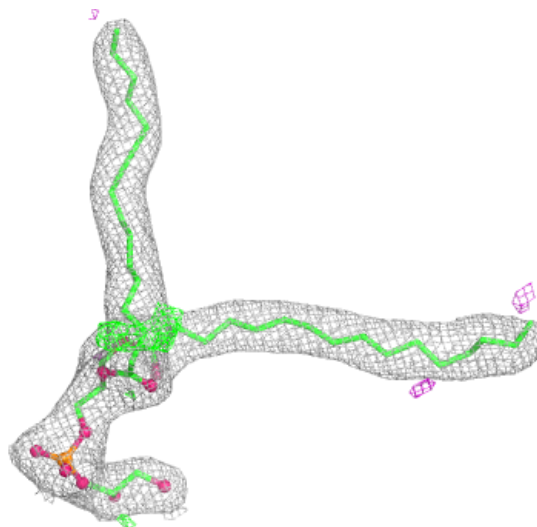
**Electron density around DGD c 517 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



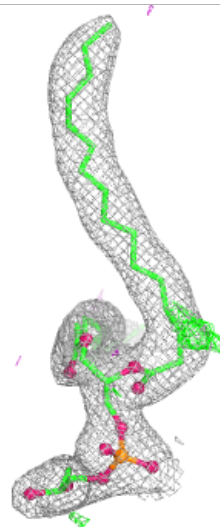
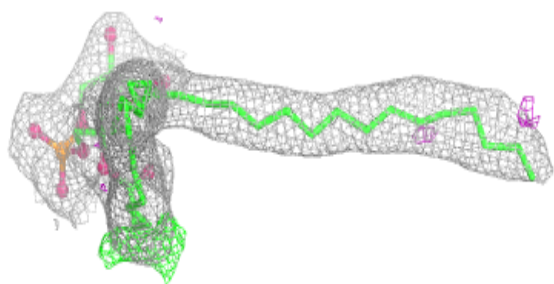
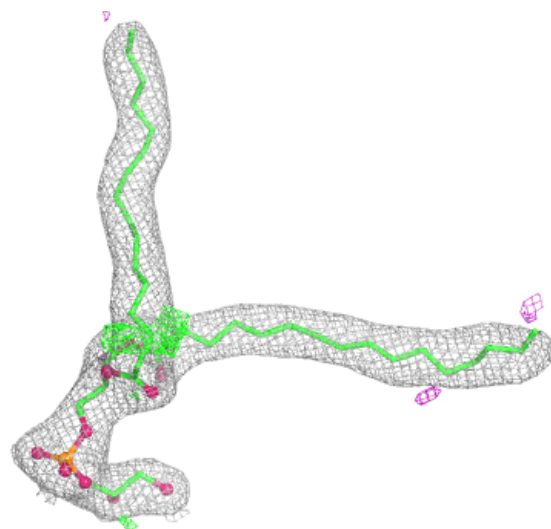
Electron density around LHG b 629 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



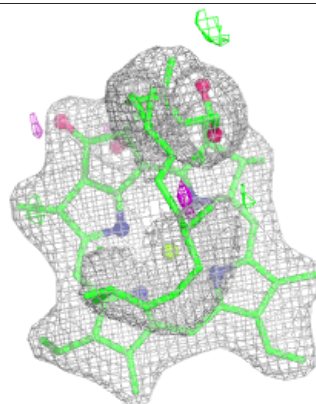
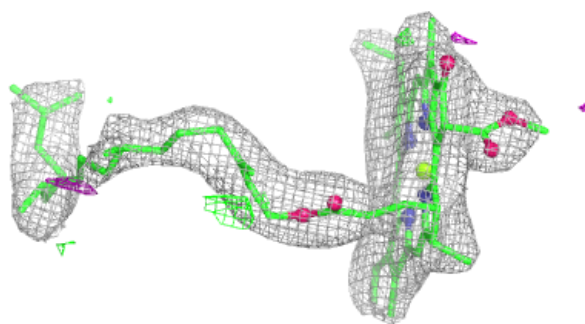
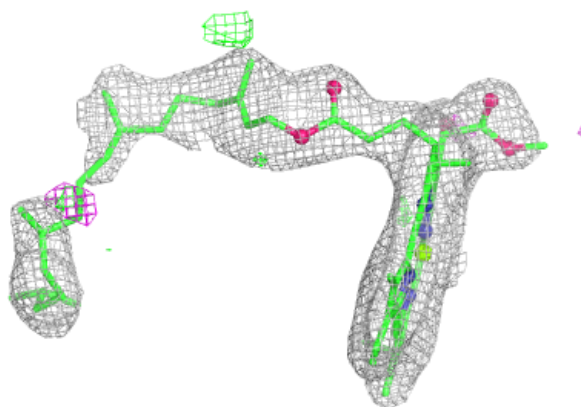
Electron density around LHG b 629 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

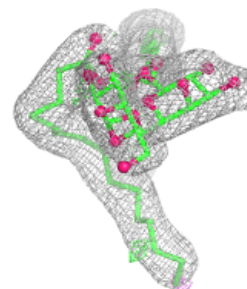
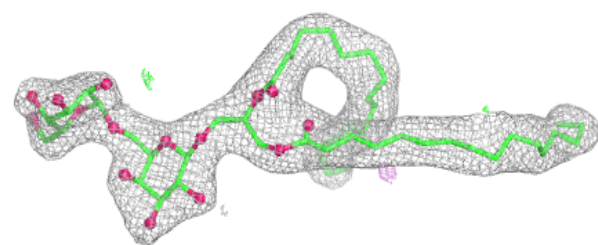
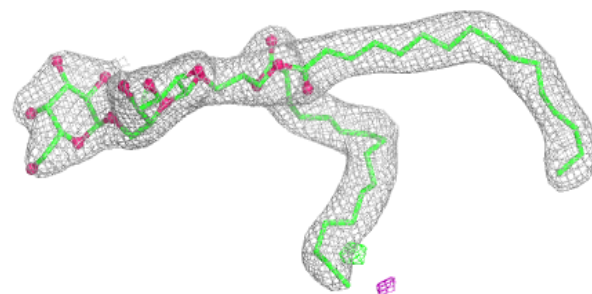


Electron density around CLA c 507:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

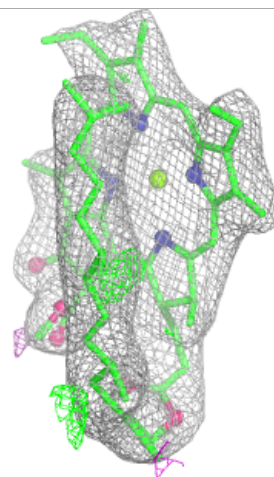
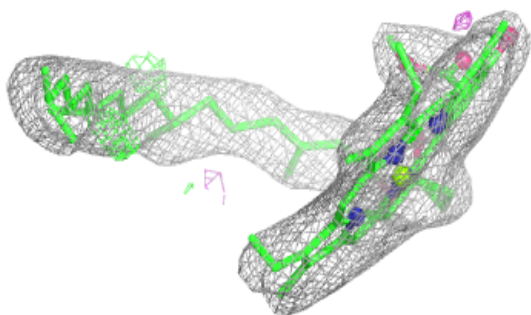
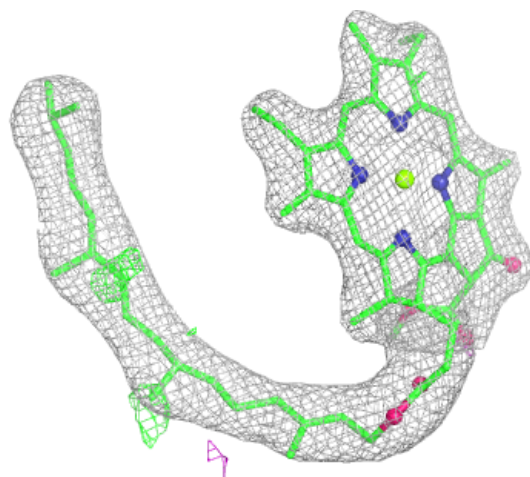
**Electron density around DGD h 102:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



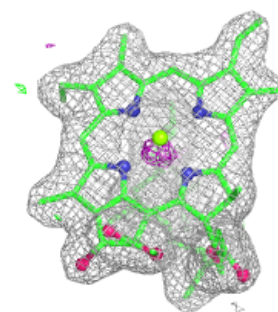
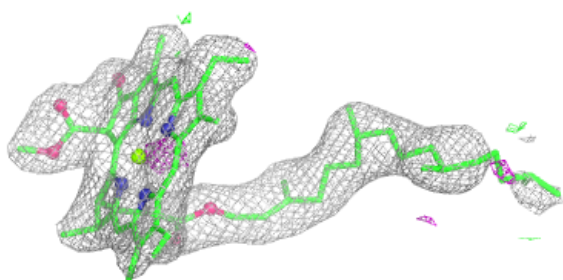
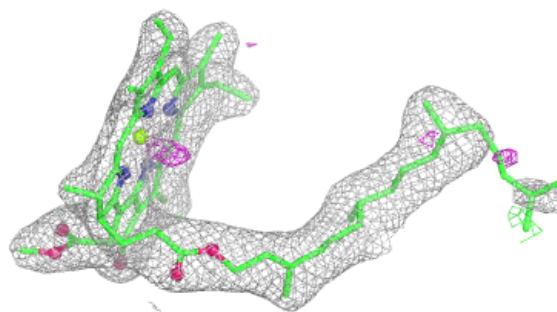
Electron density around CLA c 508:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

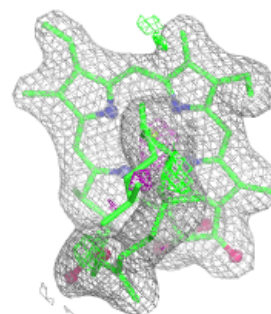
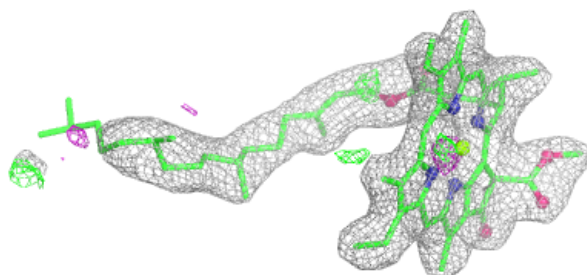
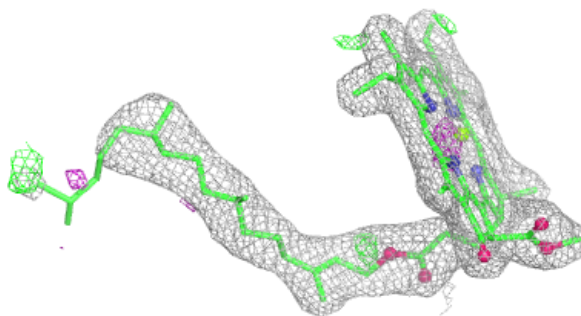


Electron density around CLA c 509:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

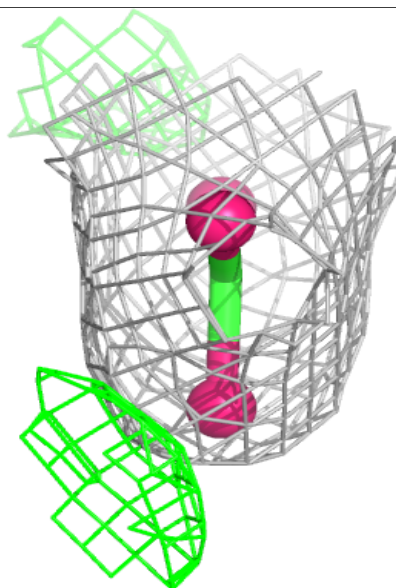
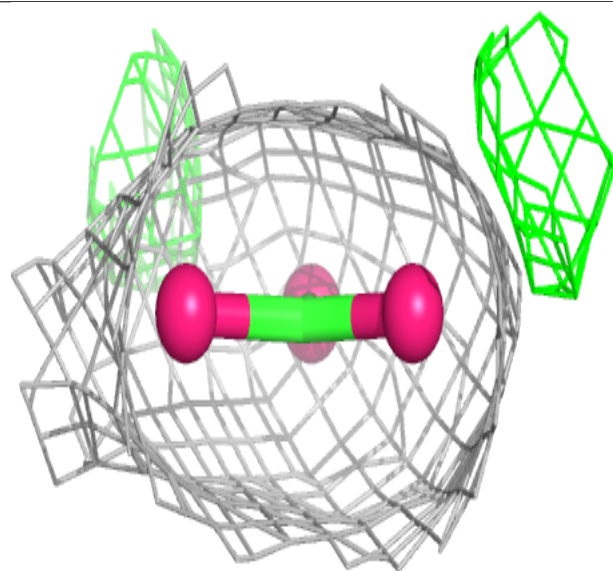
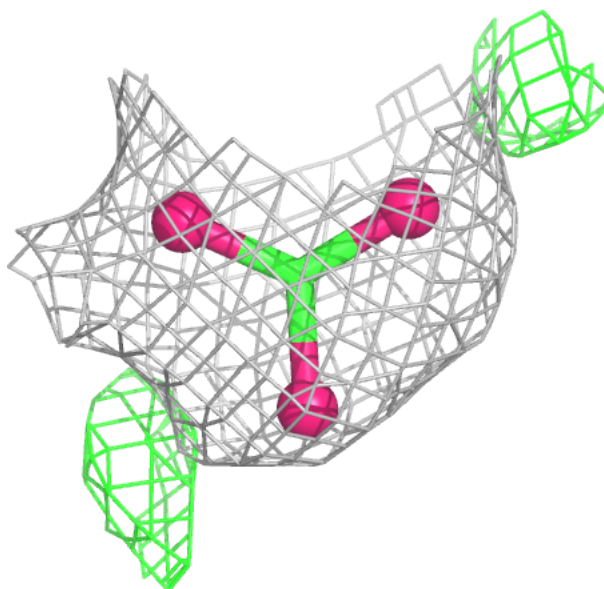
**Electron density around CLA C 509:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



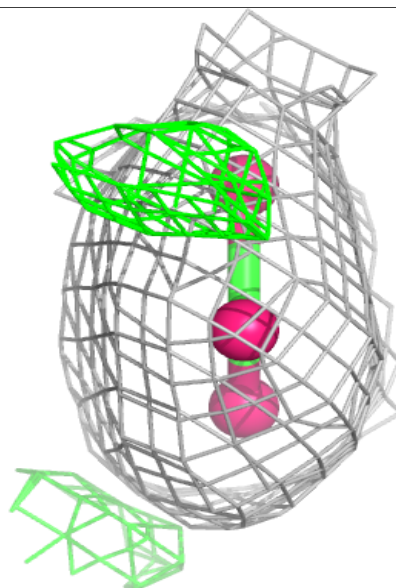
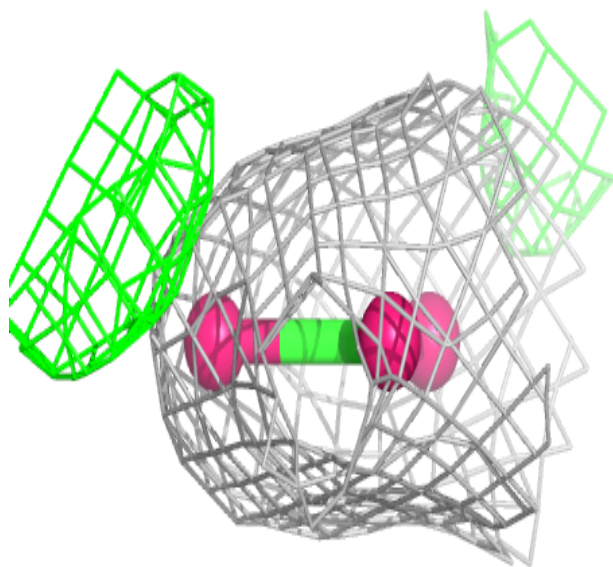
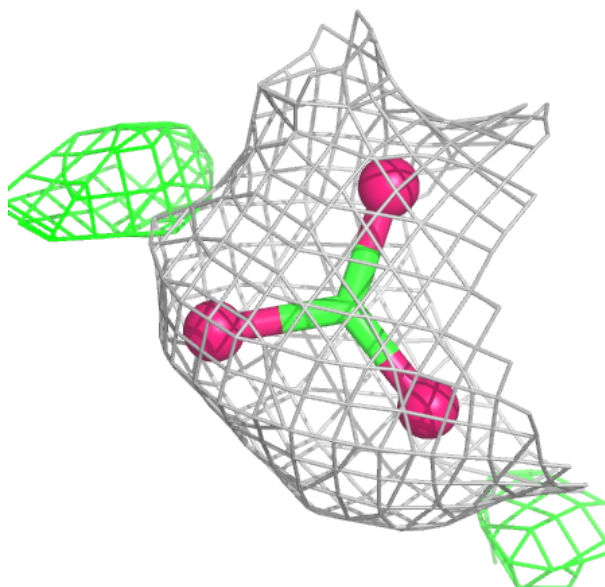
Electron density around BCT d 401 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



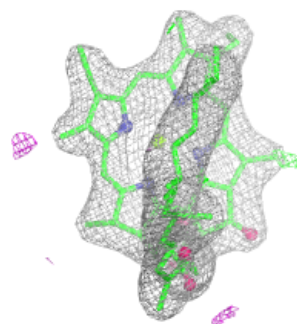
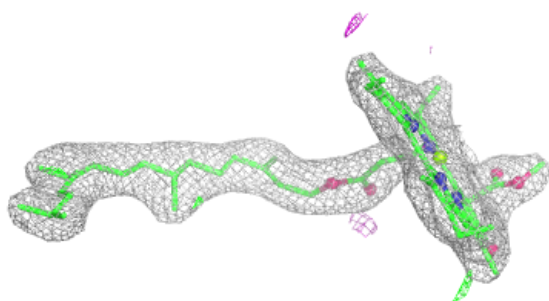
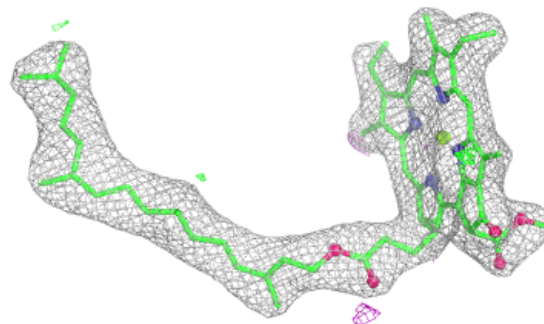
Electron density around BCT d 401 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

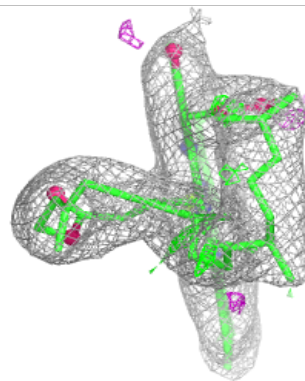
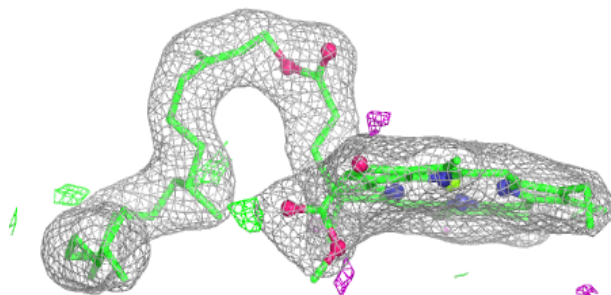
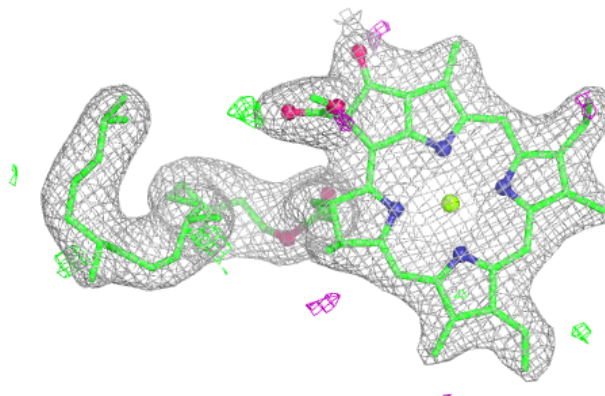


Electron density around CLA b 609:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

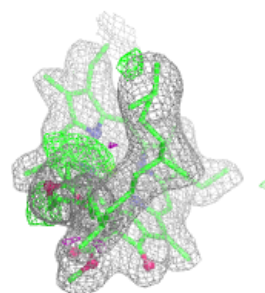
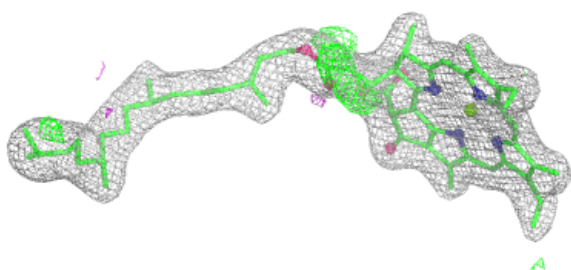
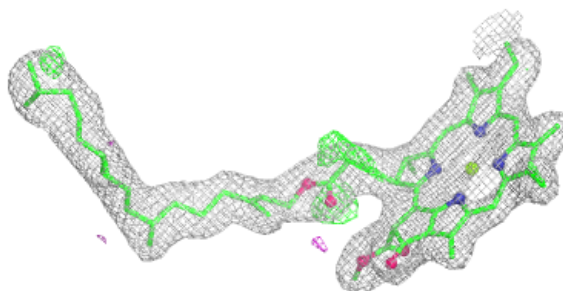
**Electron density around CLA b 612:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

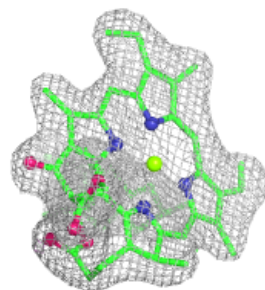
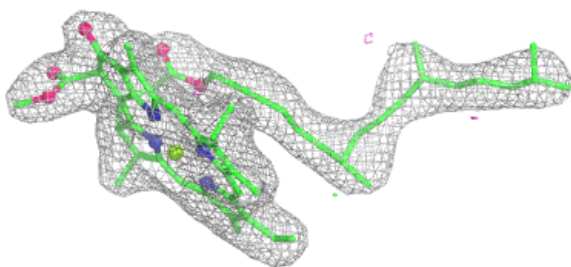
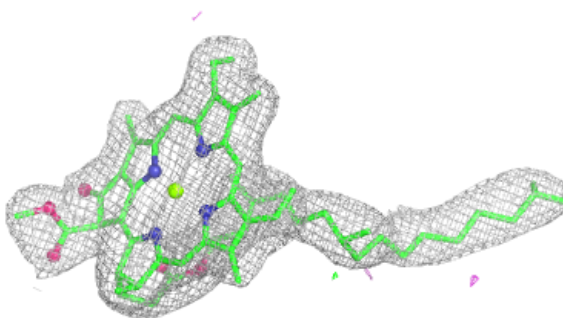


Electron density around CLA A 404 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

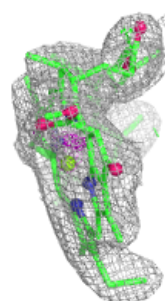
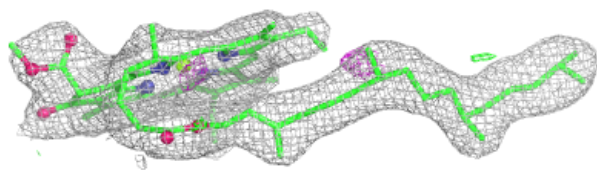
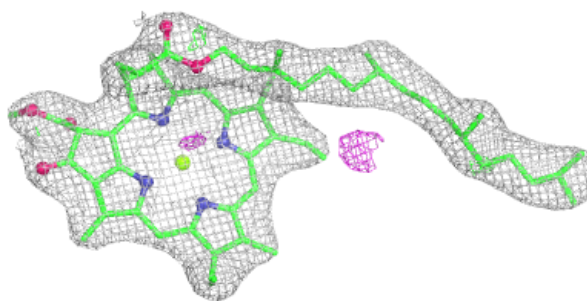
**Electron density around CLA C 506:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



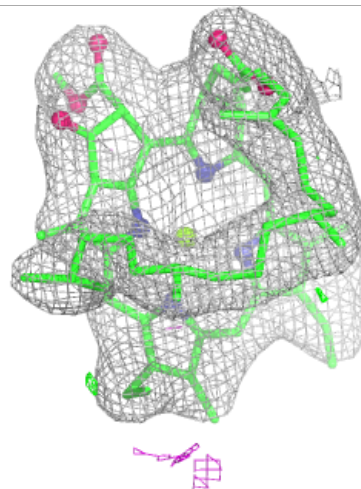
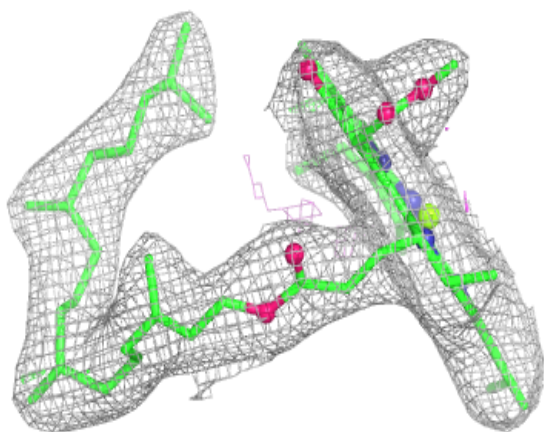
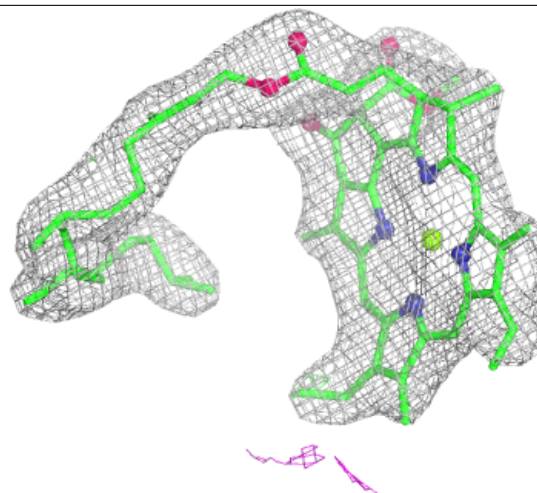
Electron density around CLA c 502:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



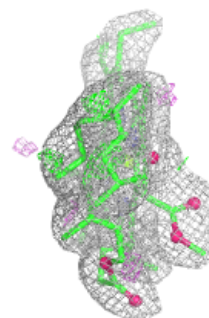
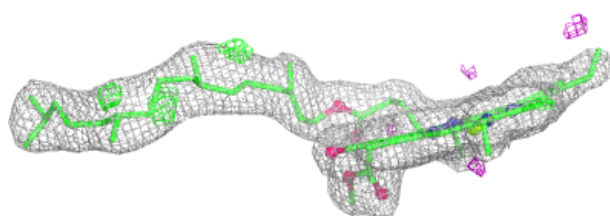
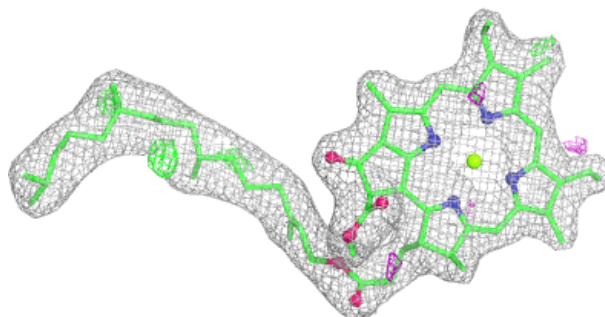
Electron density around CLA c 504:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

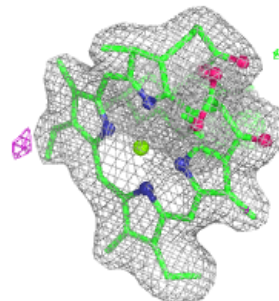
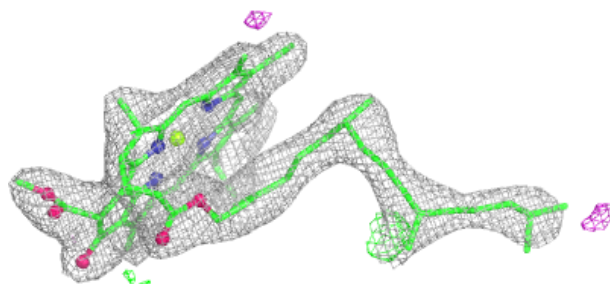
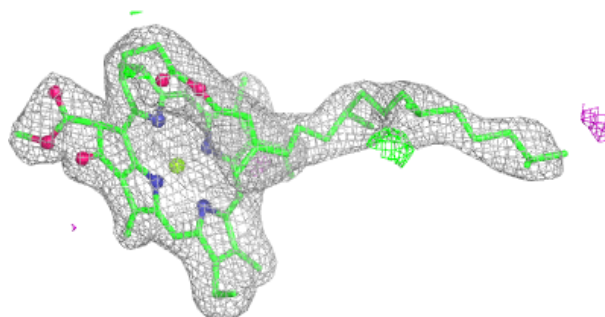


Electron density around CLA B 602:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

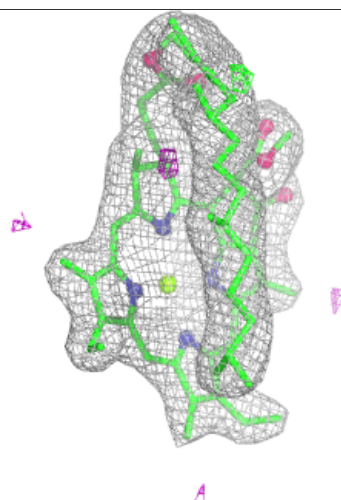
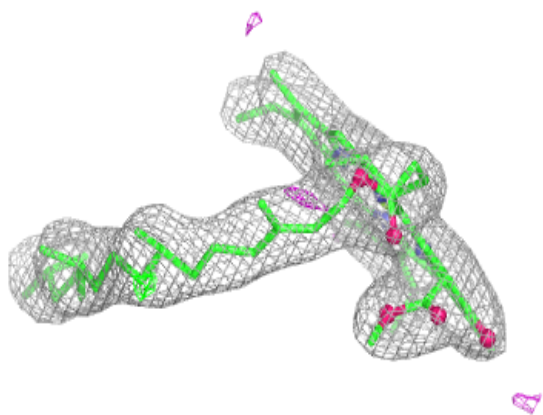
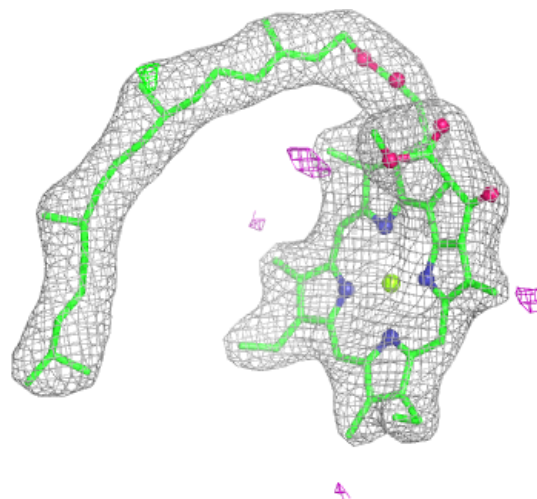
**Electron density around CLA c 506:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



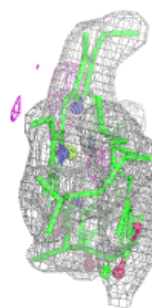
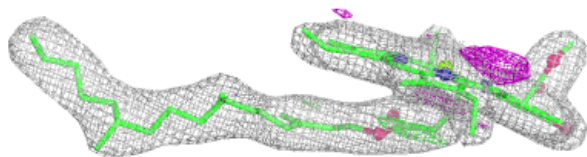
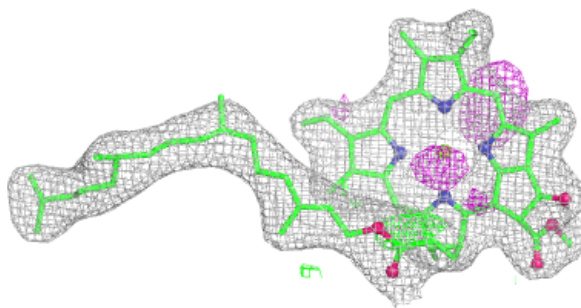
Electron density around CLA C 508:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

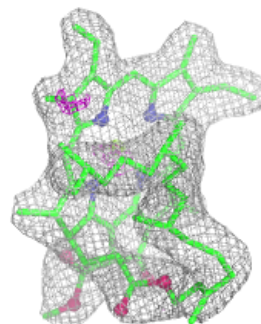
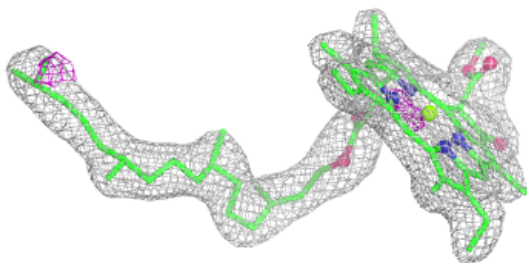
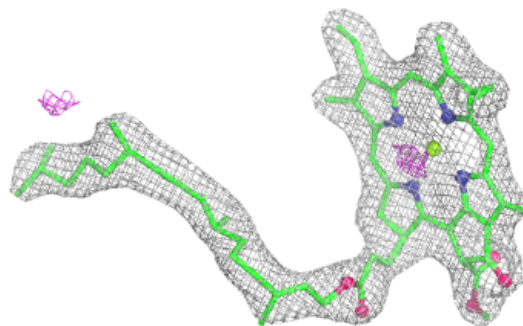


Electron density around CLA B 603:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

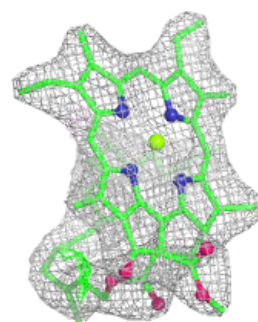
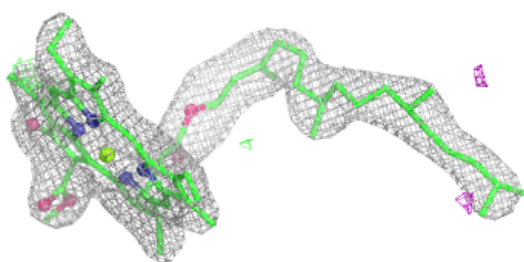
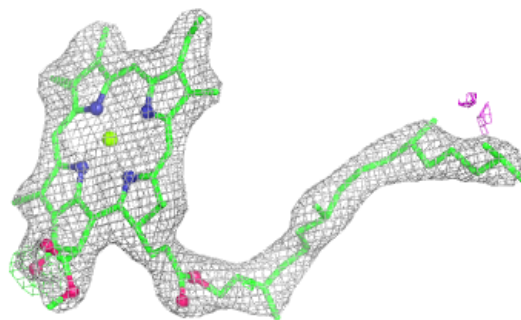
**Electron density around CLA C 512:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

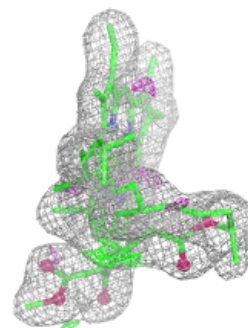
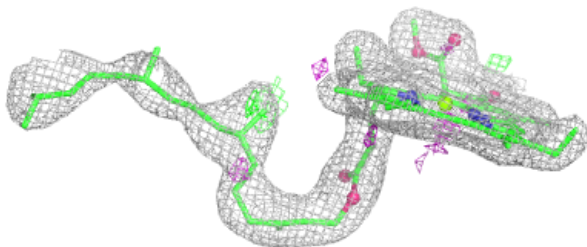
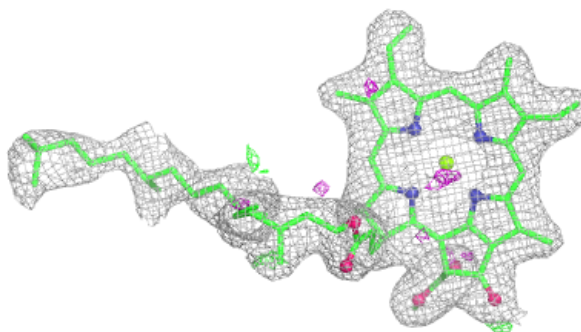


Electron density around CLA c 512:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

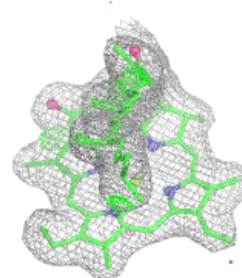
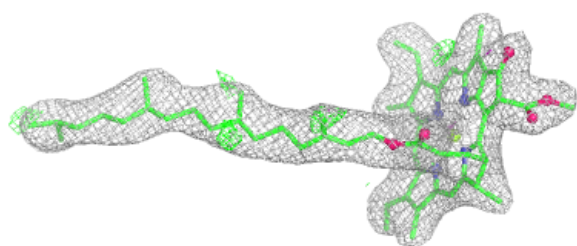
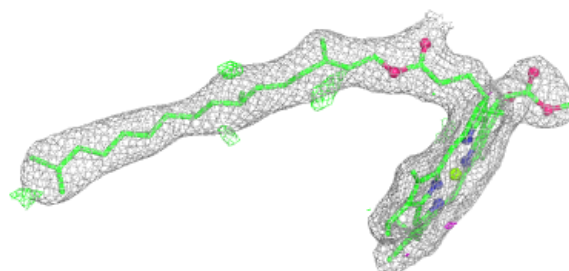
**Electron density around CLA A 406 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

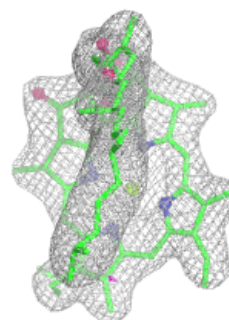
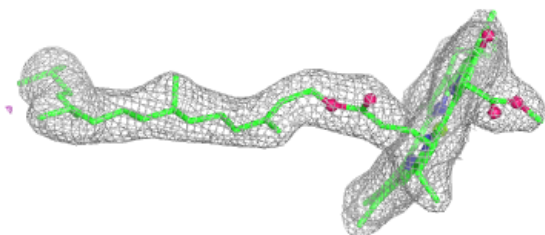
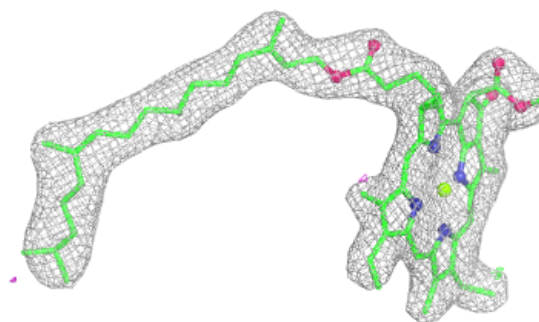


Electron density around CLA B 607:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

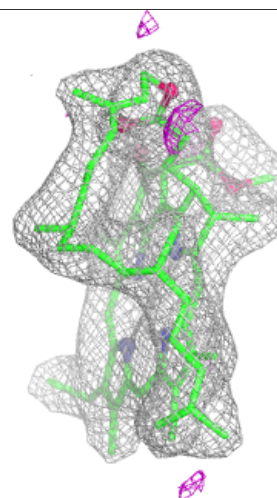
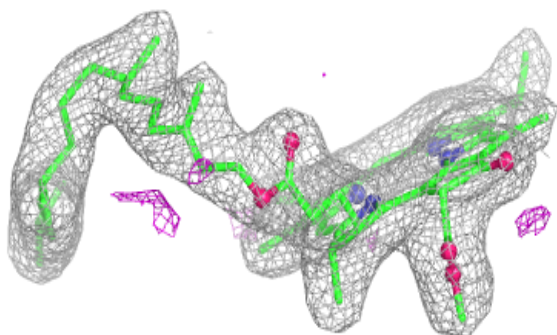
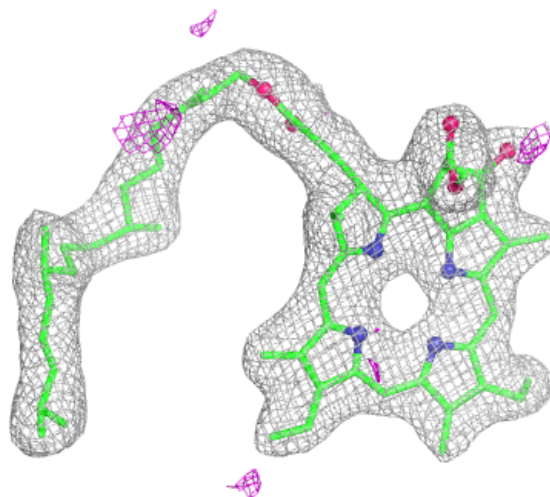
**Electron density around CLA B 609:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



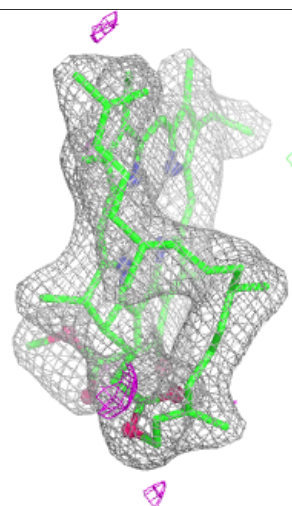
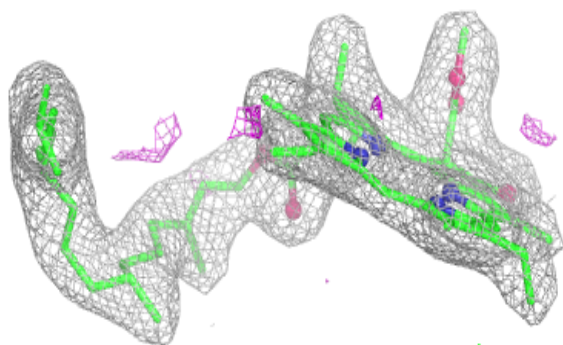
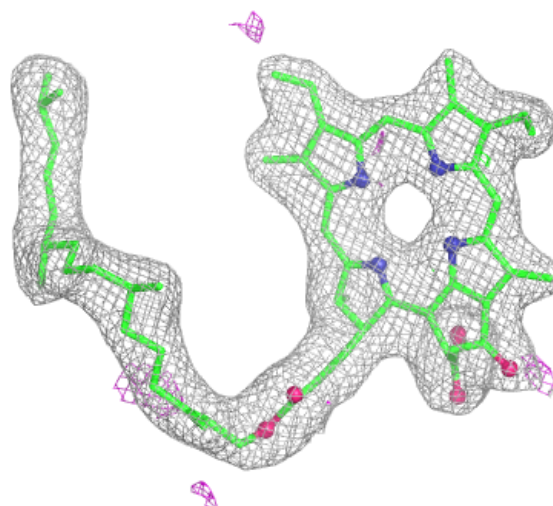
Electron density around PHO A 416 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



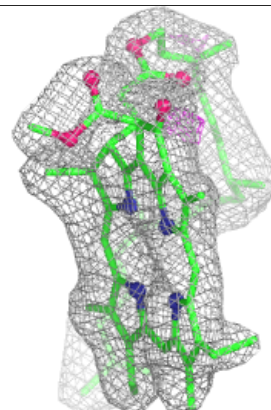
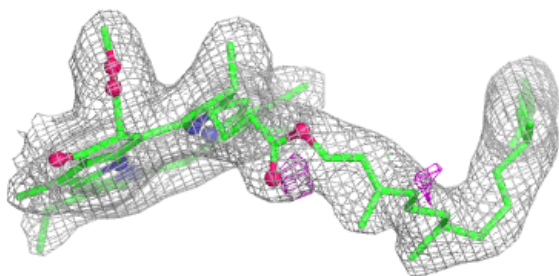
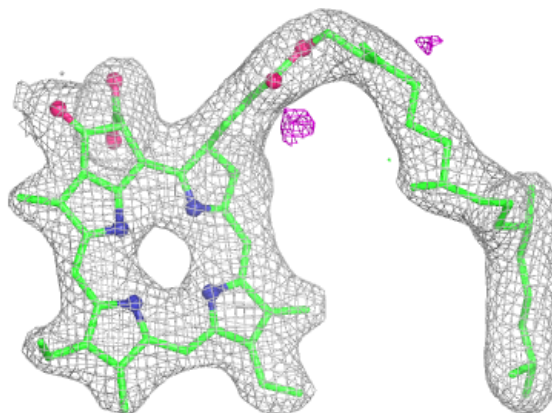
Electron density around PHO A 416 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

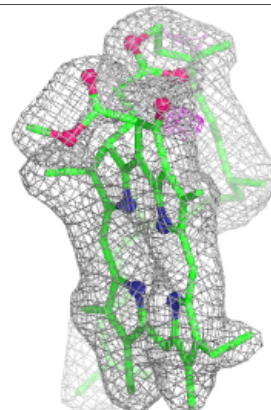
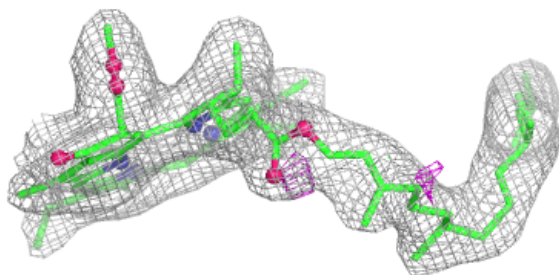
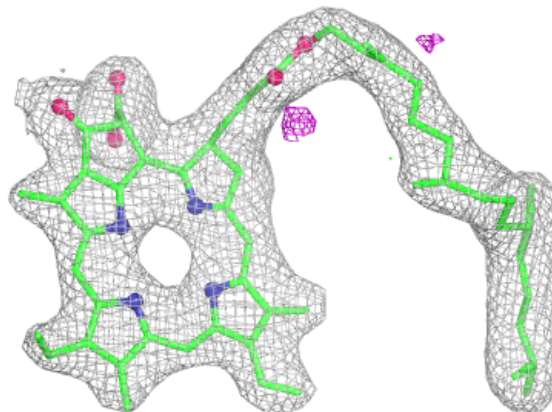


Electron density around PHO a 416 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

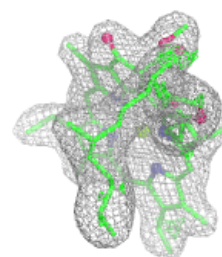
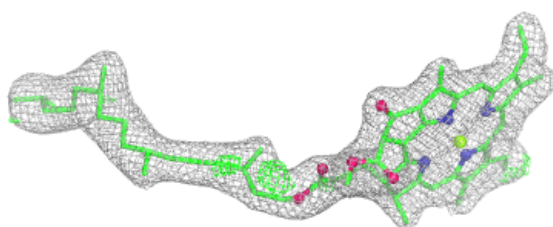
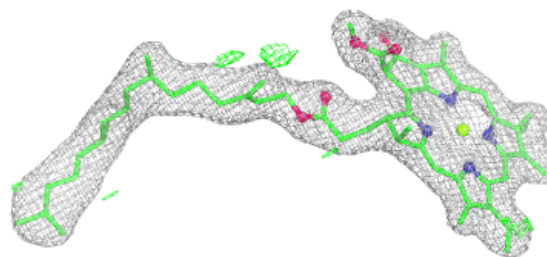
**Electron density around PHO a 416 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

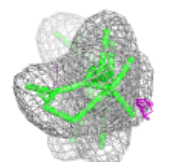
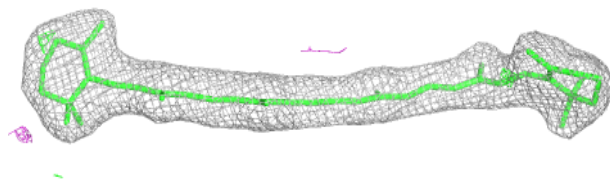
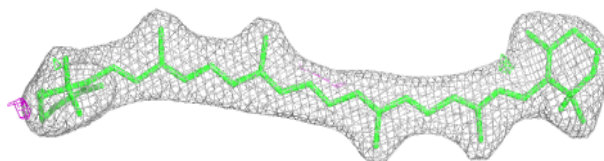


Electron density around CLA a 405 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

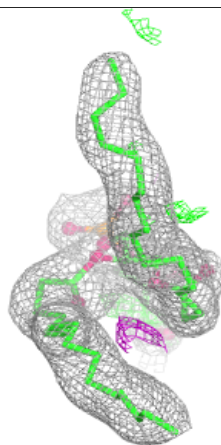
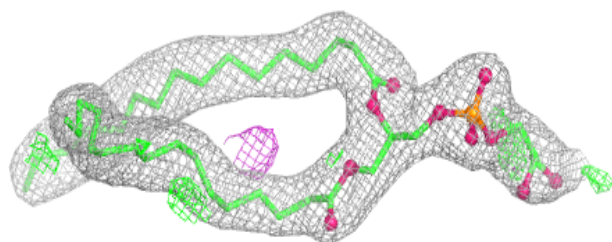
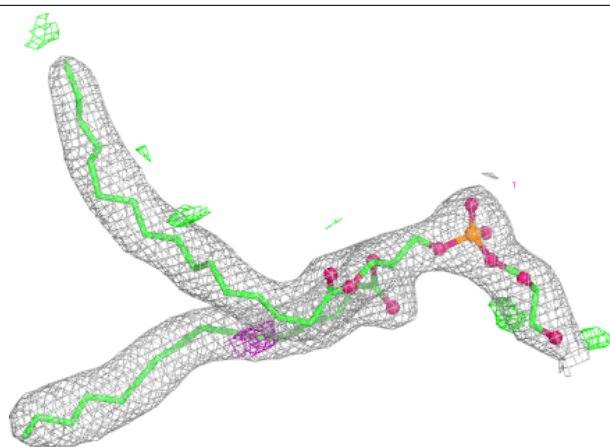
**Electron density around BCR B 617:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

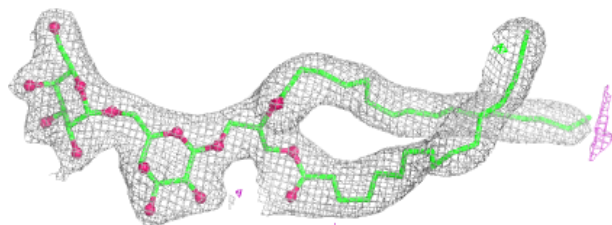
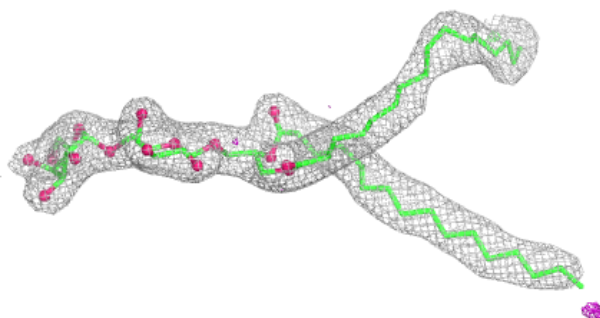


Electron density around LHG D 408 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

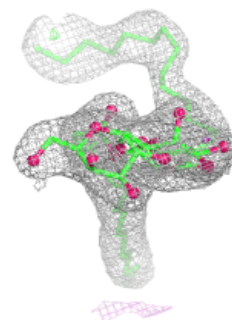
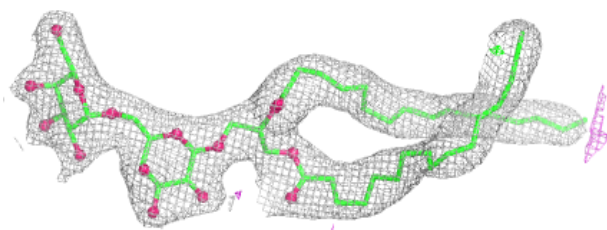
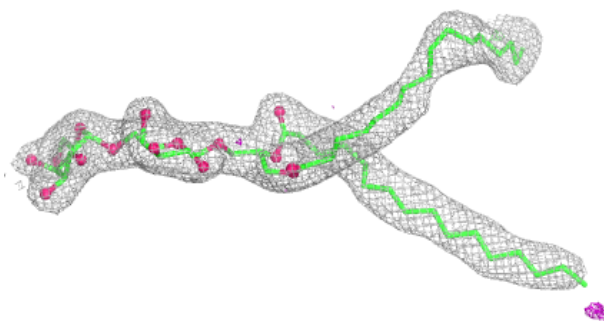
**Electron density around DGD C 517 (A):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

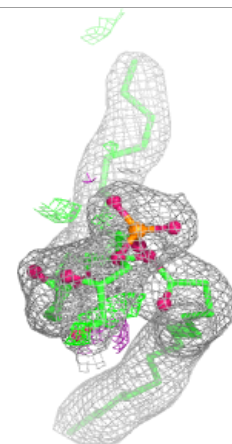
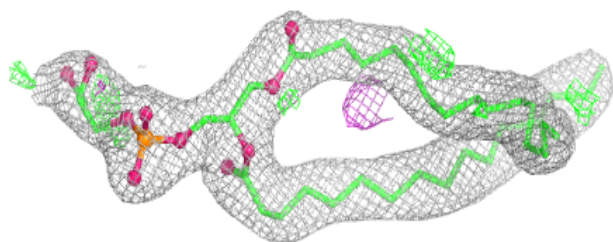
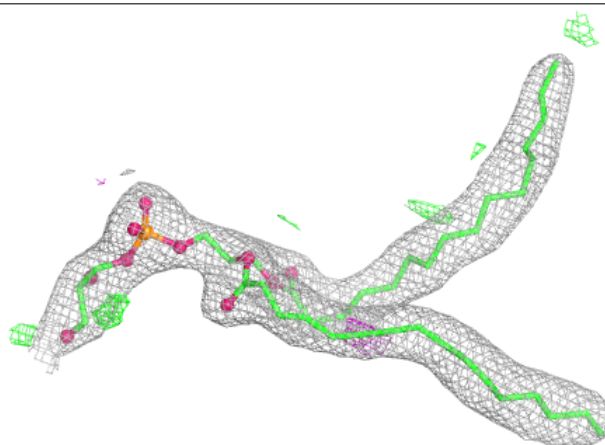


Electron density around DGD C 517 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

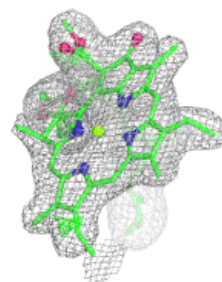
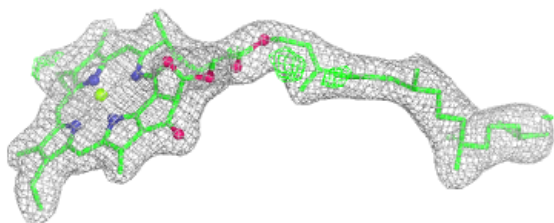
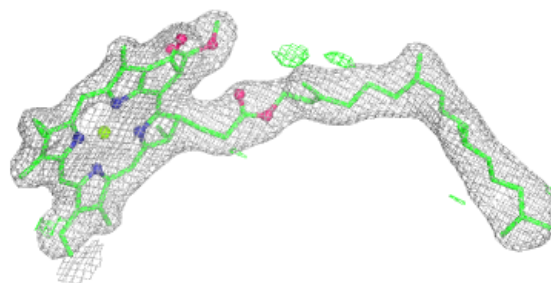
**Electron density around LHG D 408 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



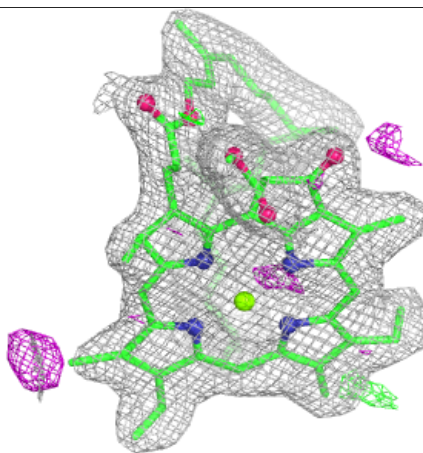
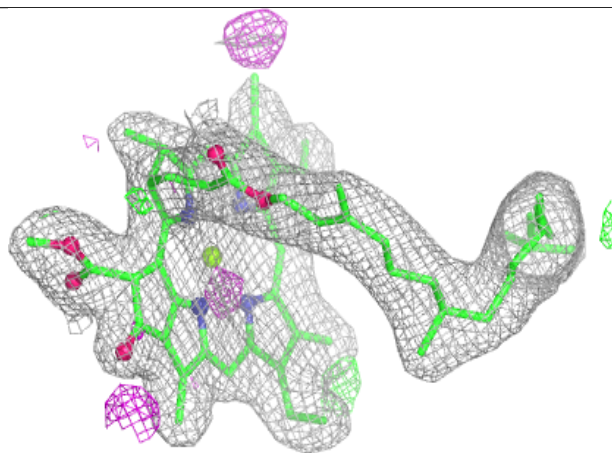
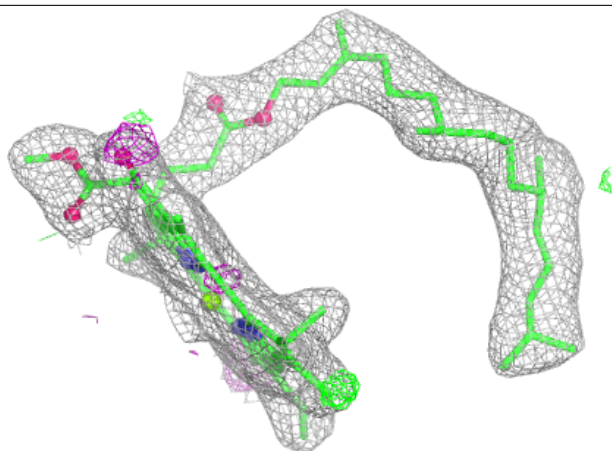
Electron density around CLA a 405 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



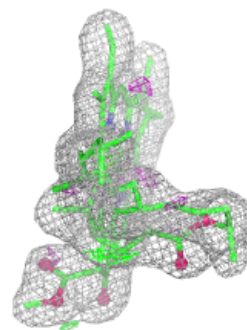
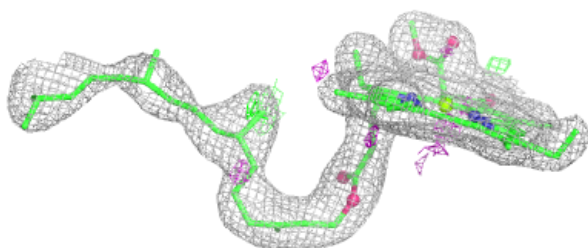
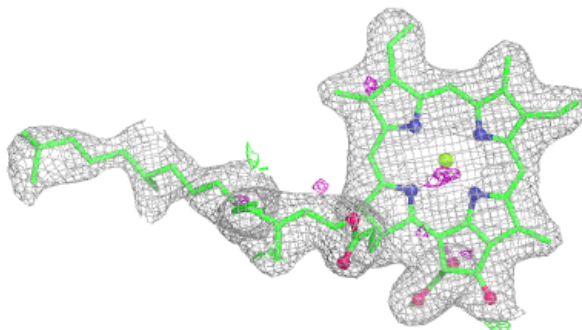
Electron density around CLA B 611:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

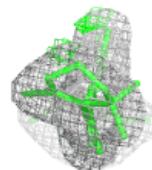
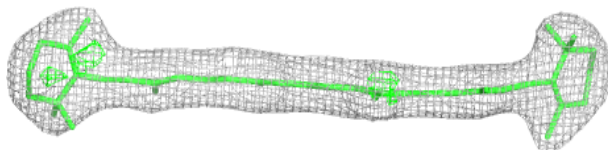
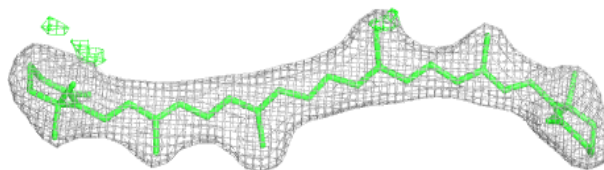


Electron density around CLA A 406 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

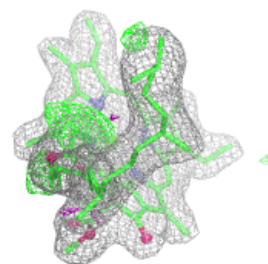
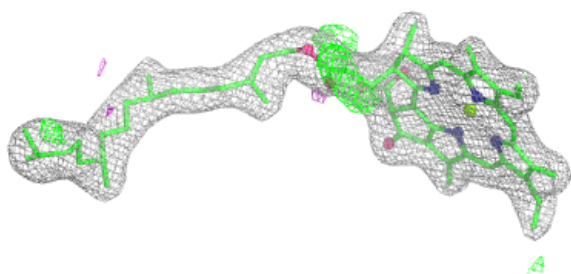
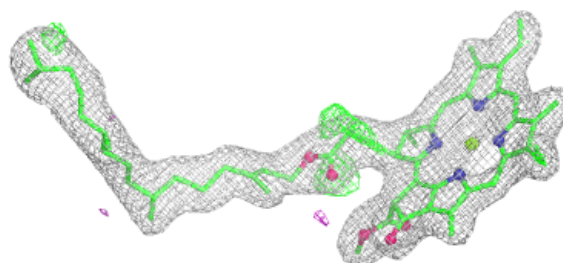
**Electron density around BCR C 516:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

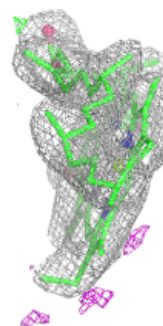
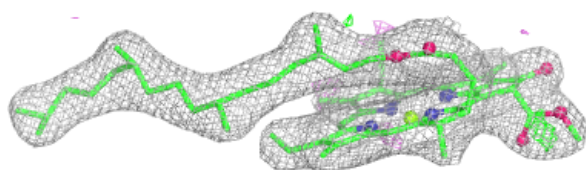
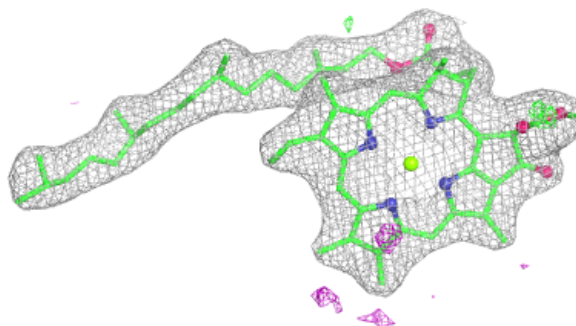


Electron density around CLA A 404 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

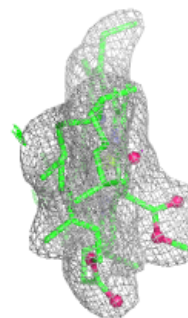
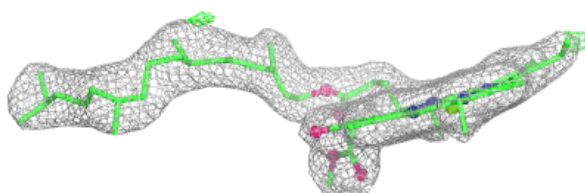
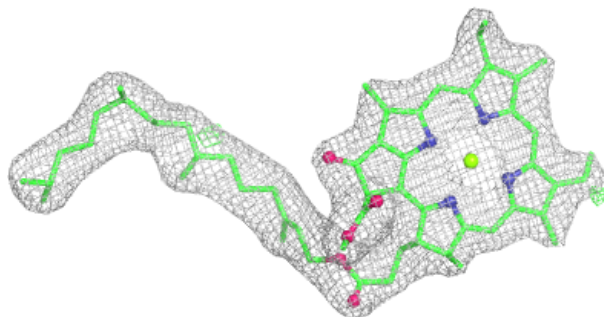
**Electron density around CLA C 502:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

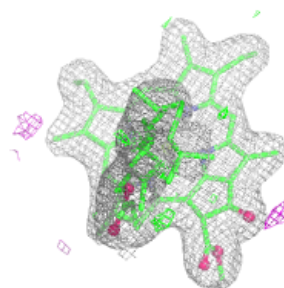
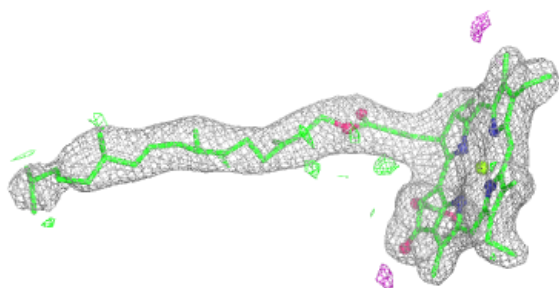
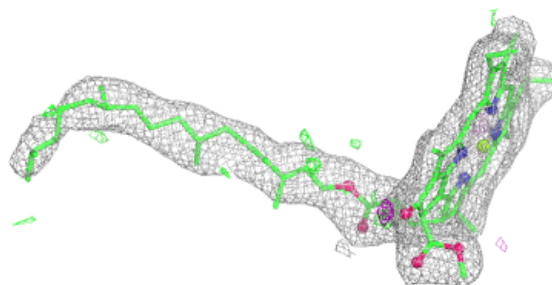


Electron density around CLA b 602:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

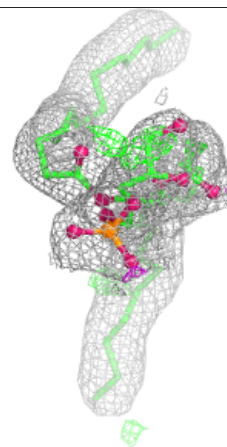
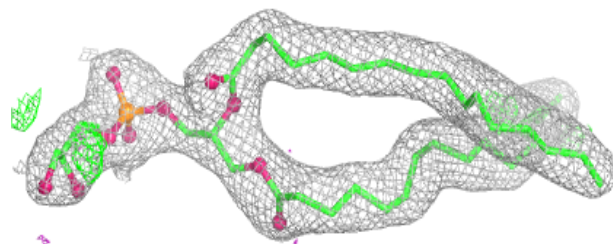
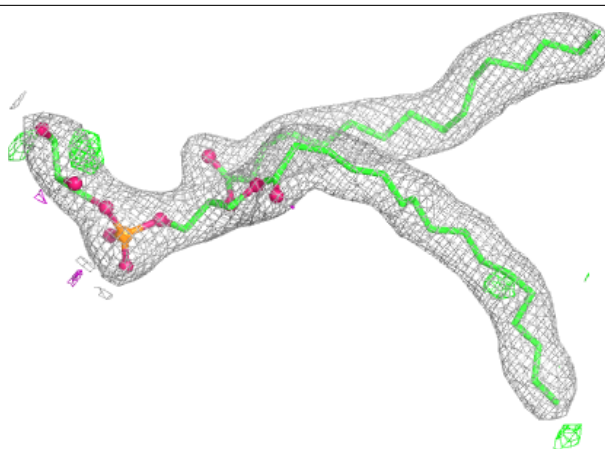
**Electron density around CLA b 604:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



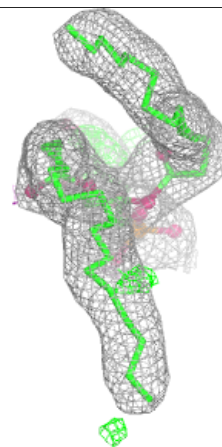
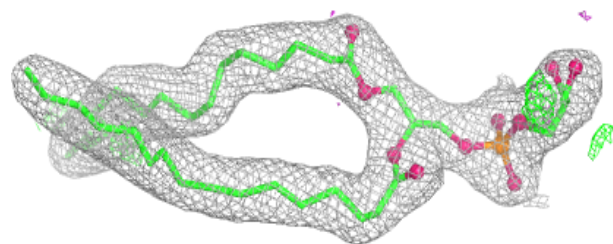
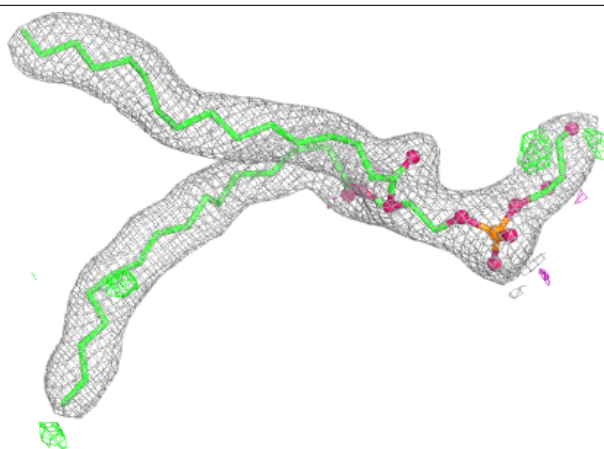
Electron density around LHG d 406 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



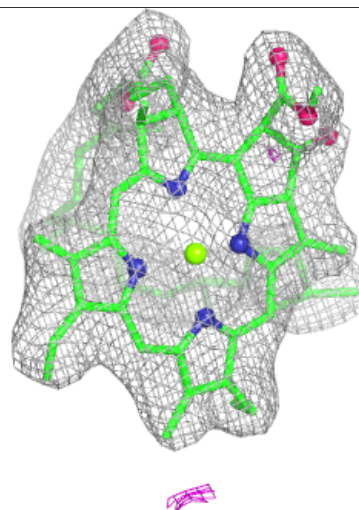
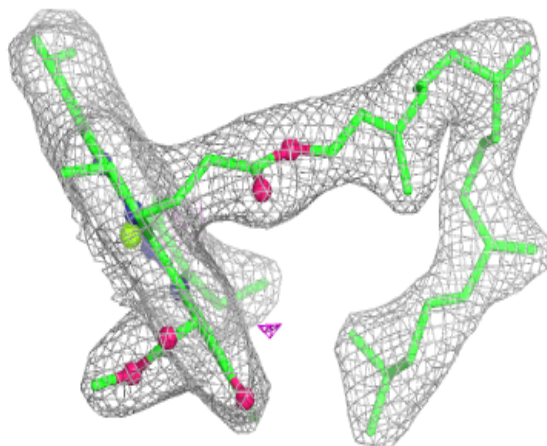
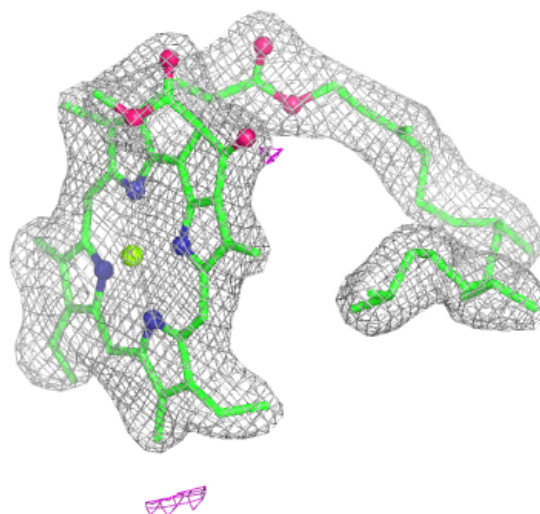
Electron density around LHG d 406 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



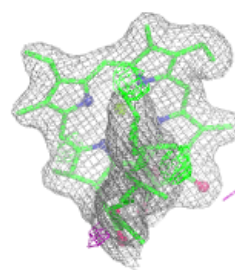
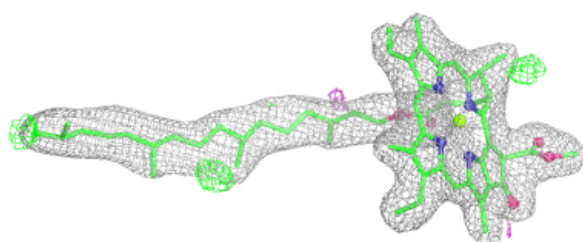
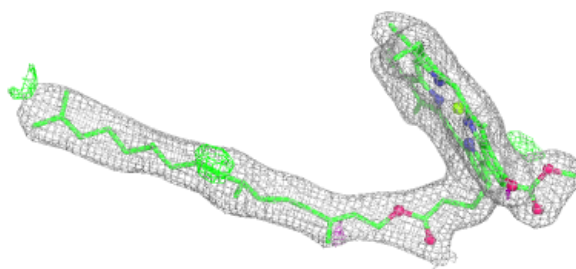
Electron density around CLA C 504:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

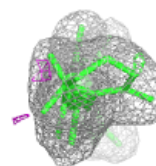
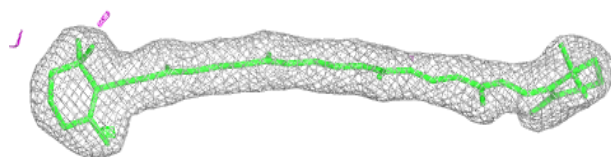
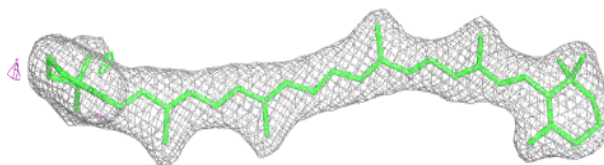


Electron density around CLA b 607:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

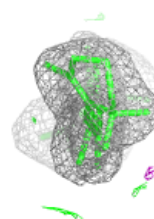
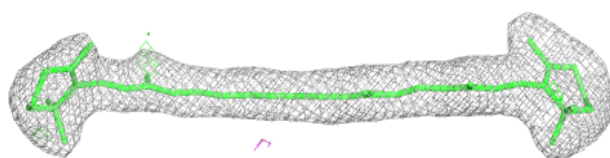
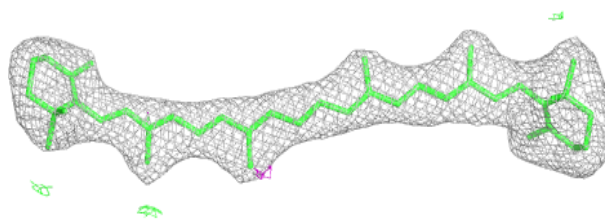
**Electron density around BCR b 617:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



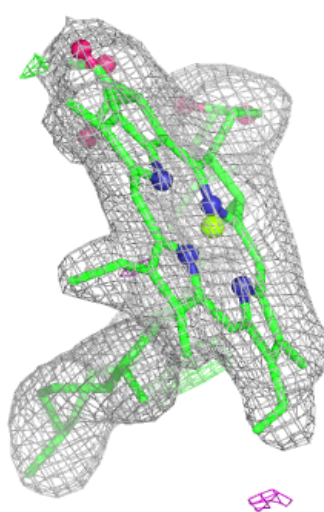
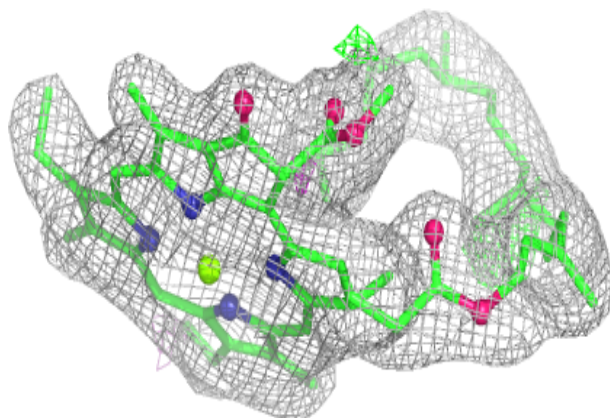
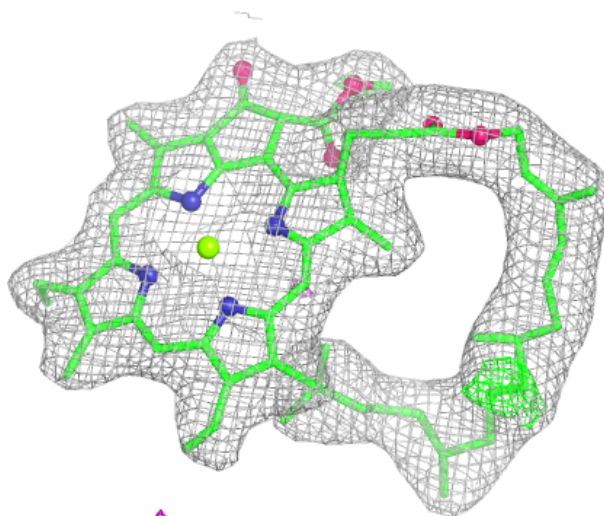
Electron density around BCR b 618:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



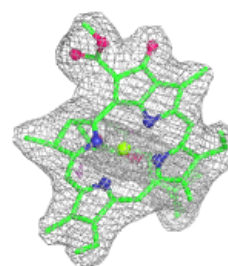
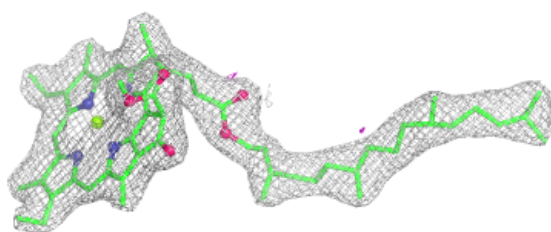
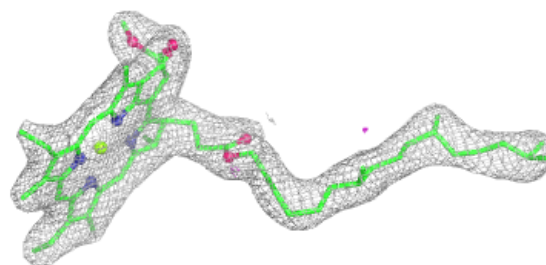
Electron density around CLA b 615:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

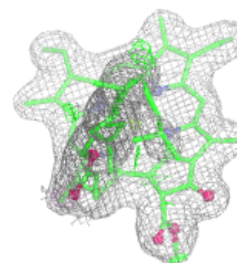
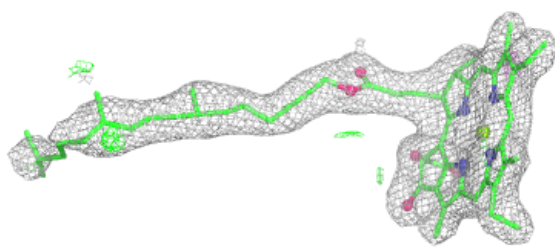
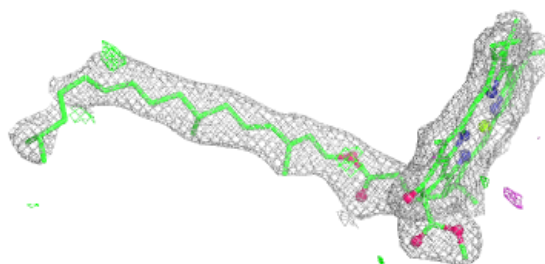


Electron density around CLA C 503:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

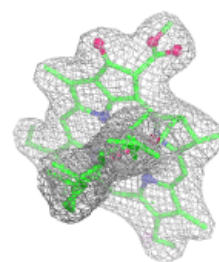
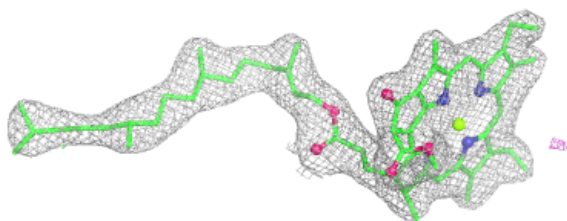
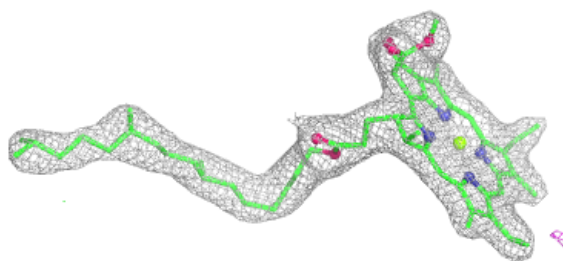
**Electron density around CLA B 604:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



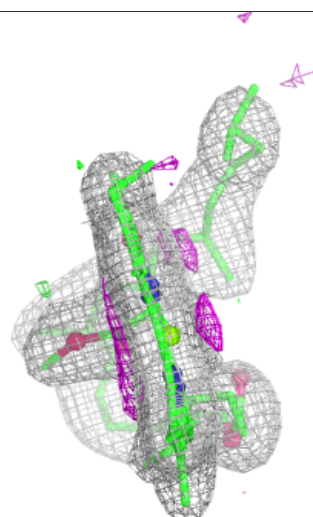
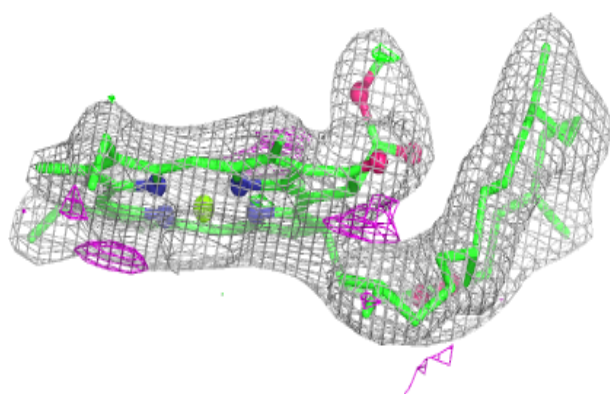
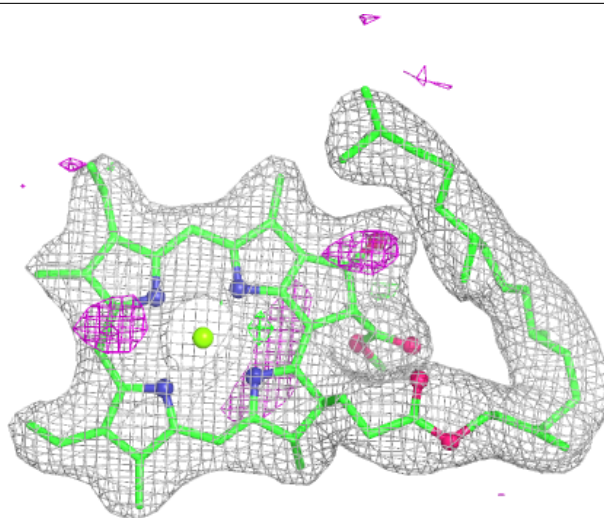
Electron density around CLA c 503:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



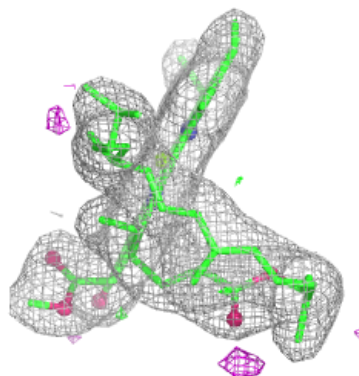
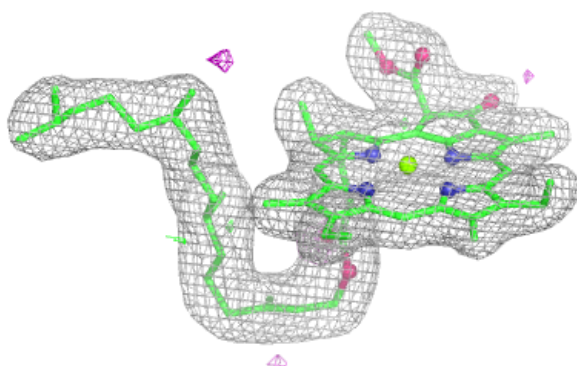
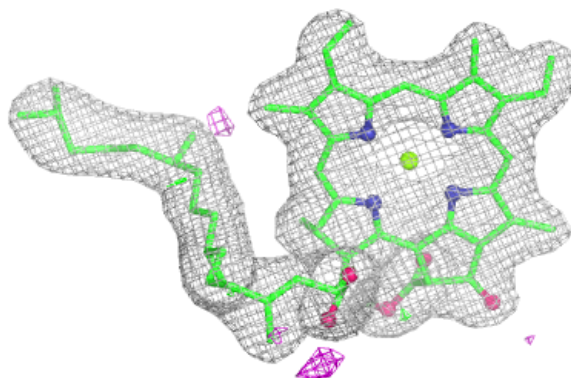
Electron density around CLA B 610:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

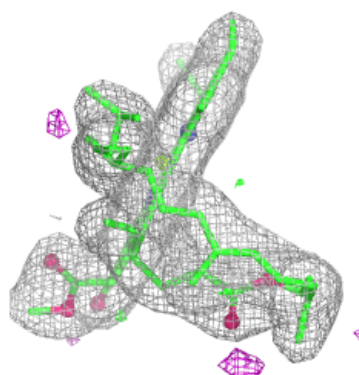
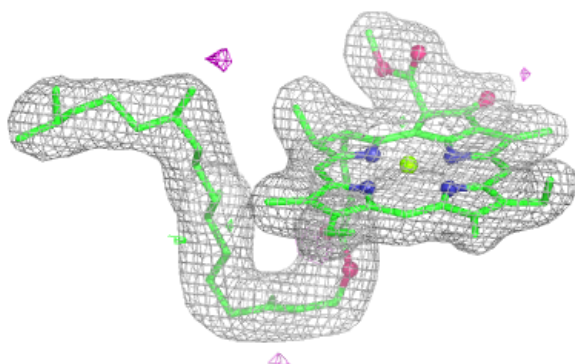
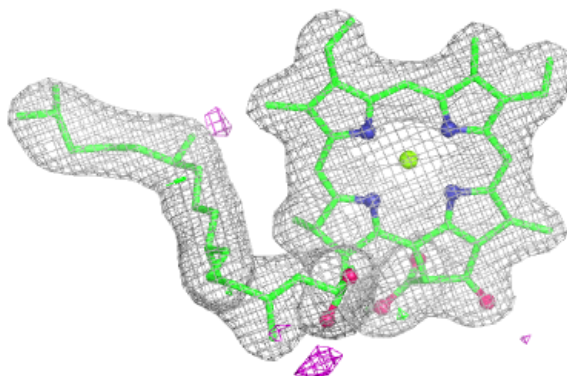


Electron density around CLA a 406 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

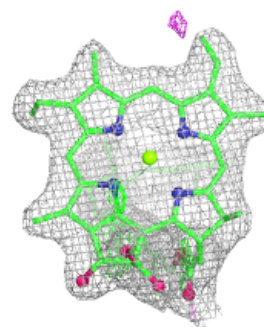
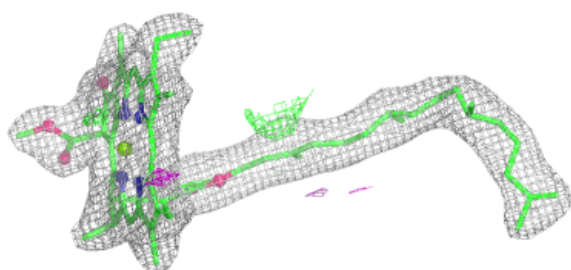
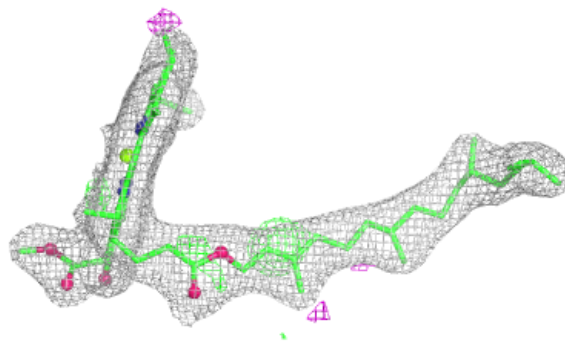
**Electron density around CLA a 406 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

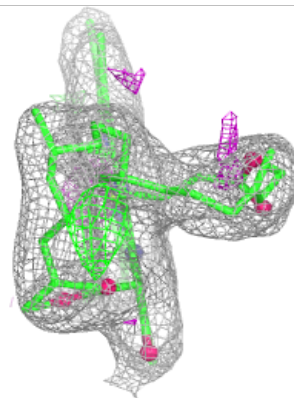
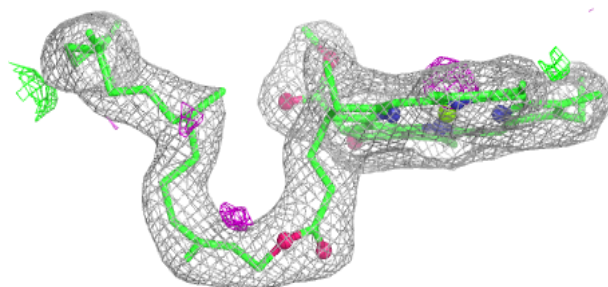
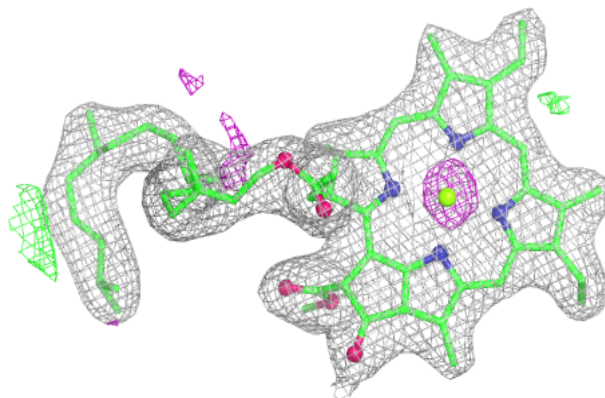


Electron density around CLA B 605:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

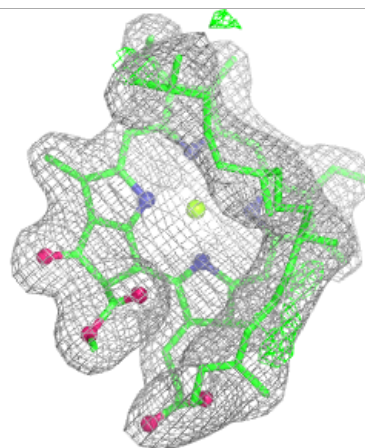
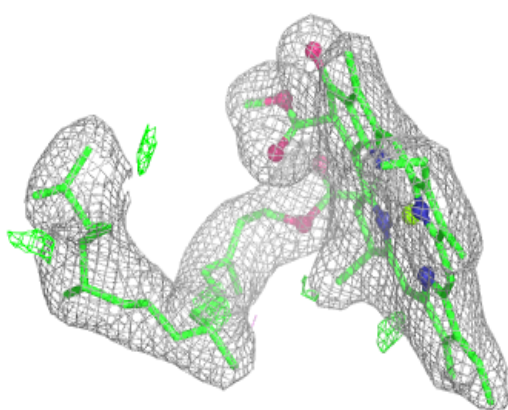
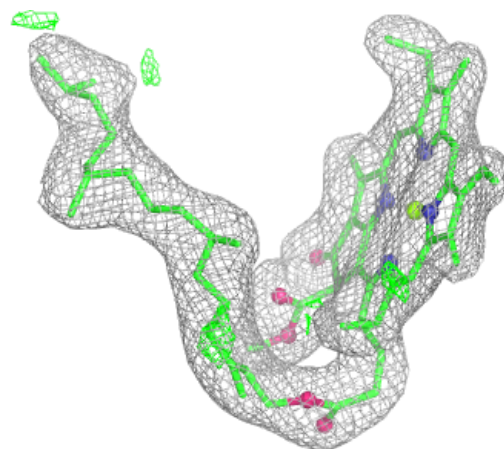
**Electron density around CLA B 612:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



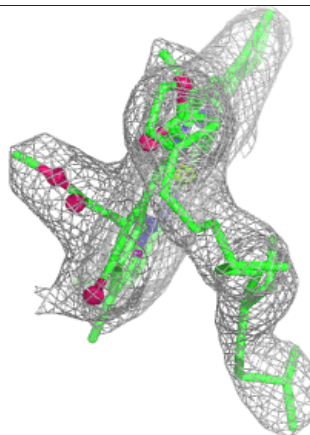
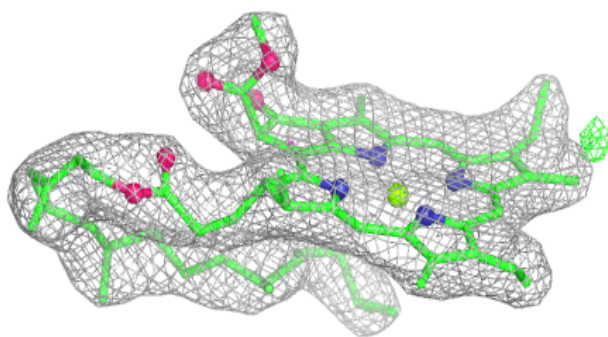
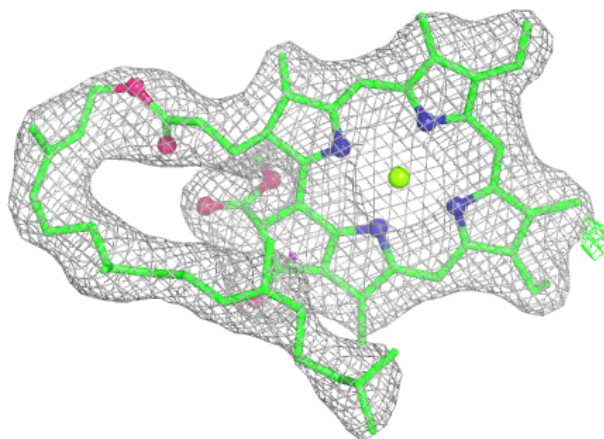
Electron density around CLA B 613:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



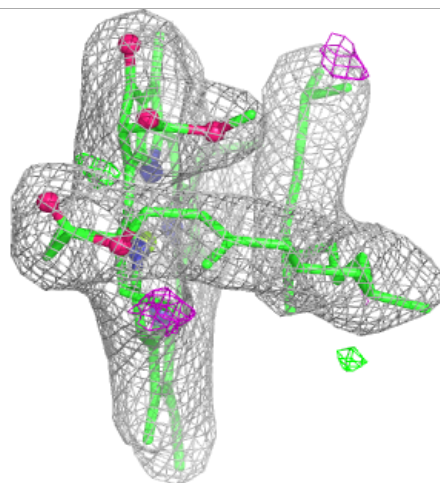
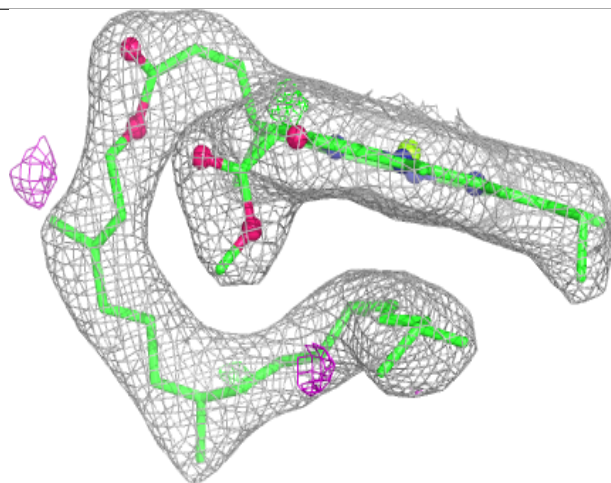
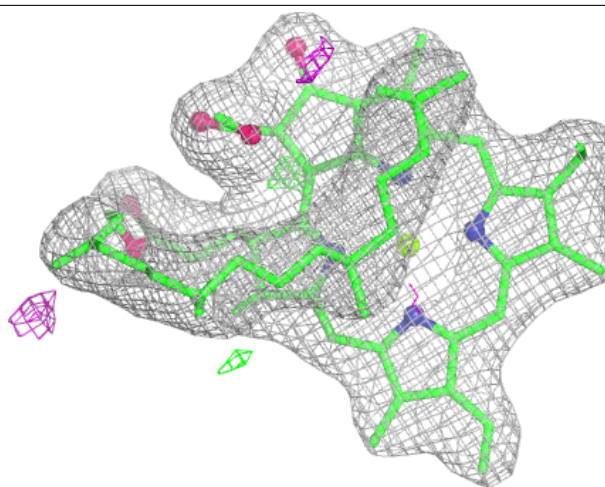
Electron density around CLA c 510:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



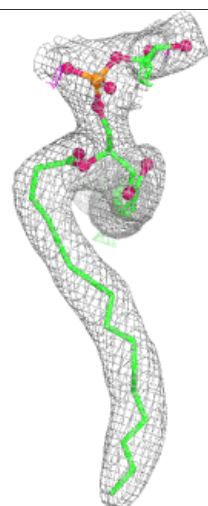
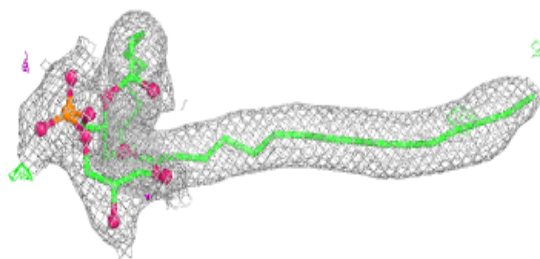
Electron density around CLA c 511:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



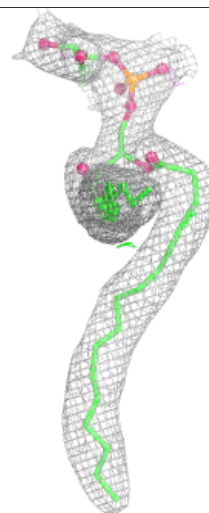
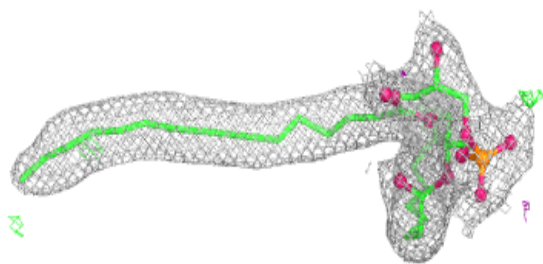
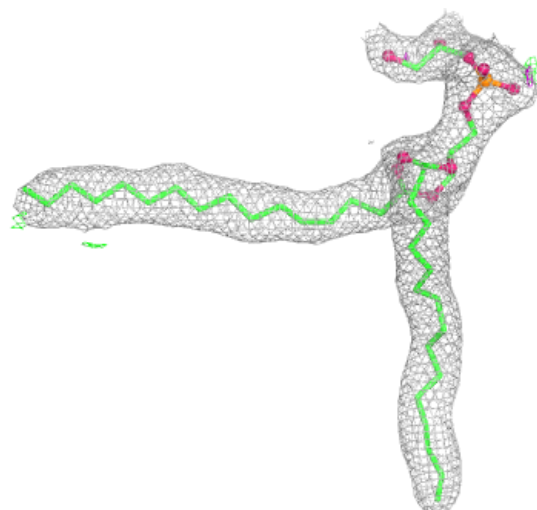
Electron density around LHG L 101 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



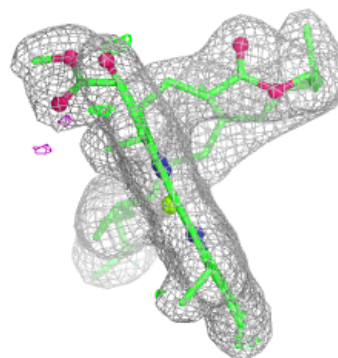
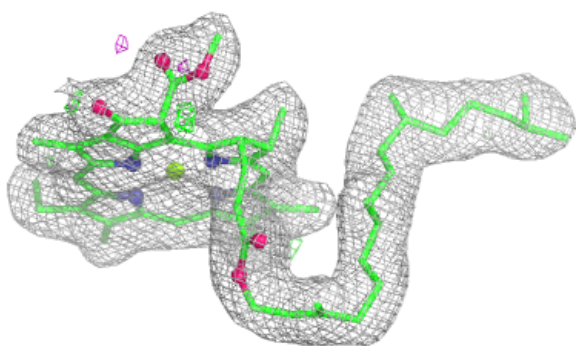
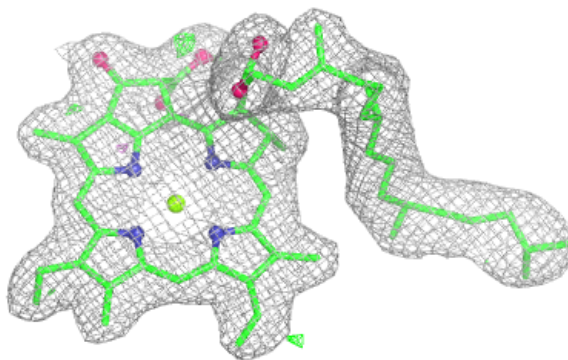
Electron density around LHG L 101 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



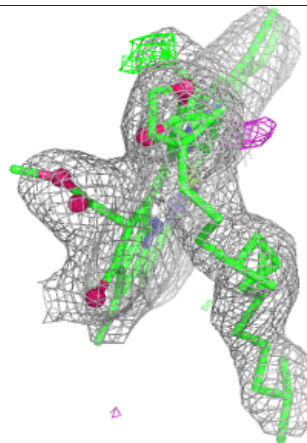
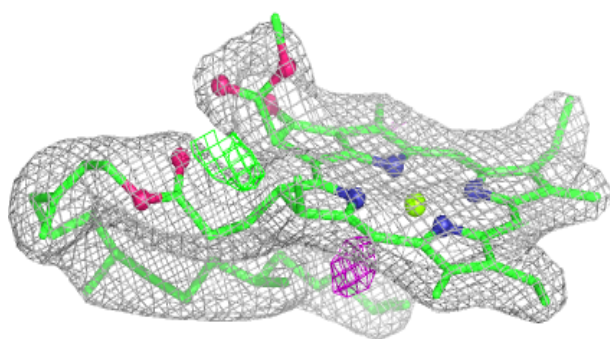
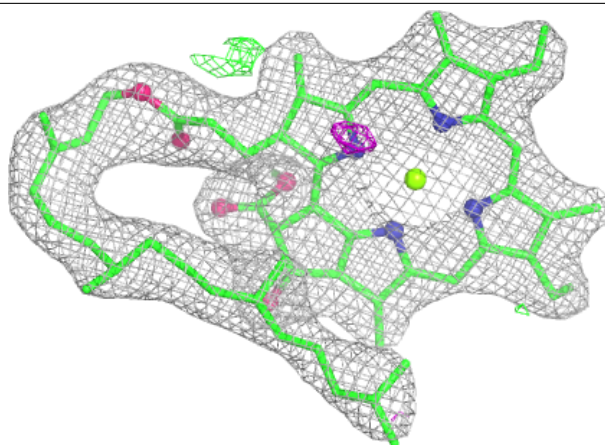
Electron density around CLA A 405 (A):

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



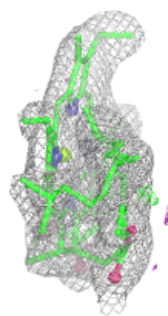
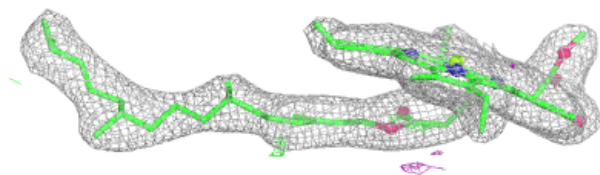
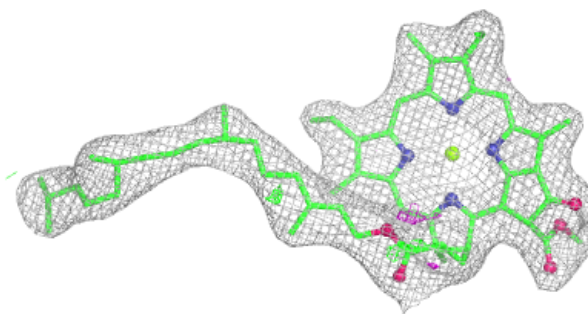
Electron density around CLA C 510:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



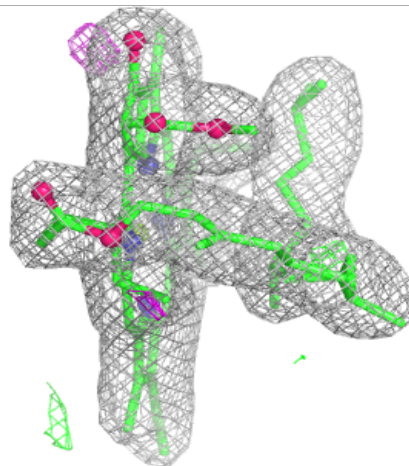
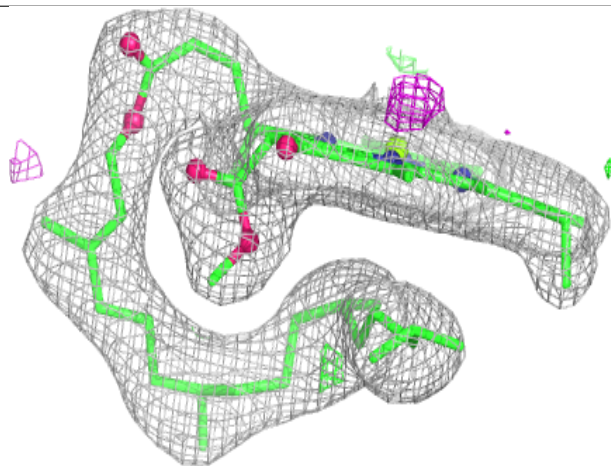
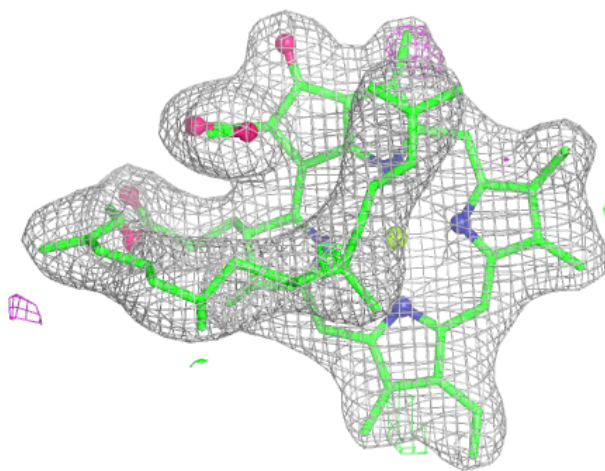
Electron density around CLA b 603:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



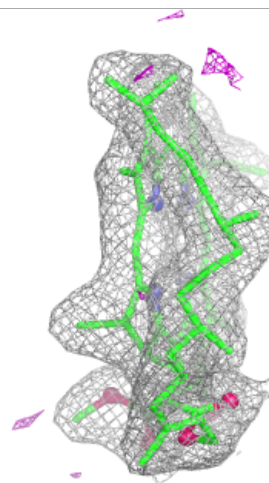
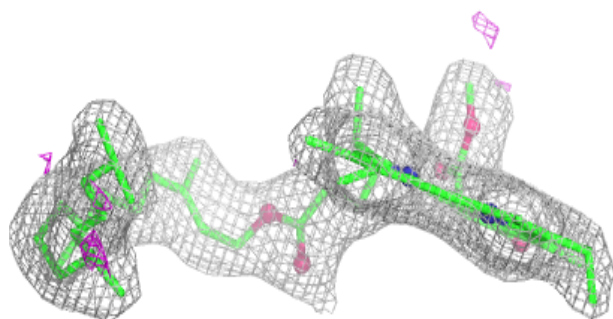
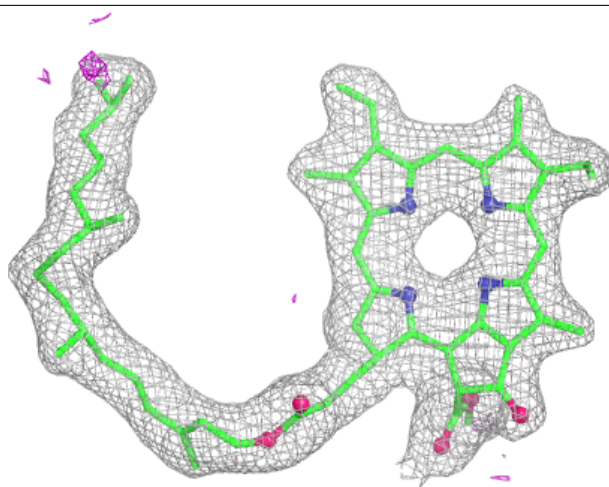
Electron density around CLA C 511:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



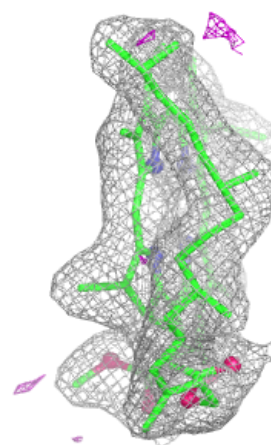
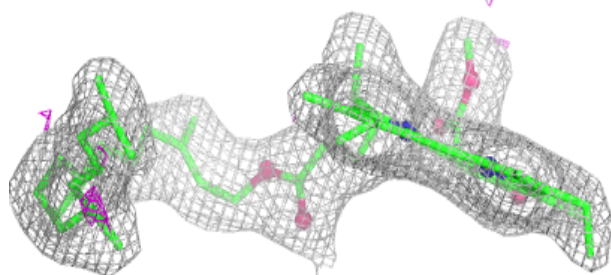
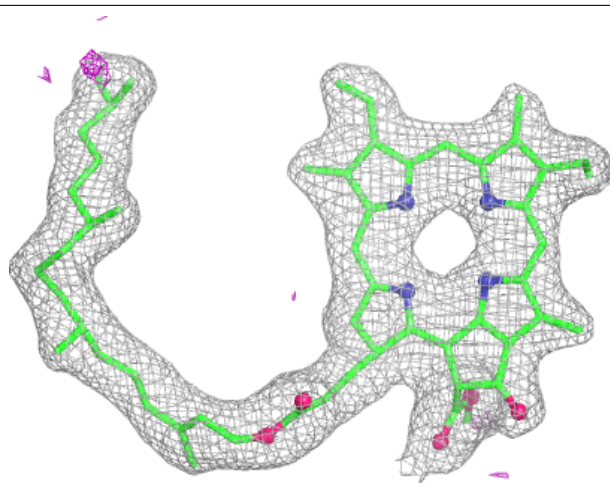
Electron density around PHO A 407 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



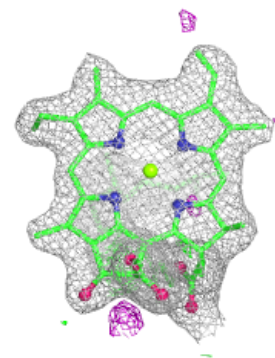
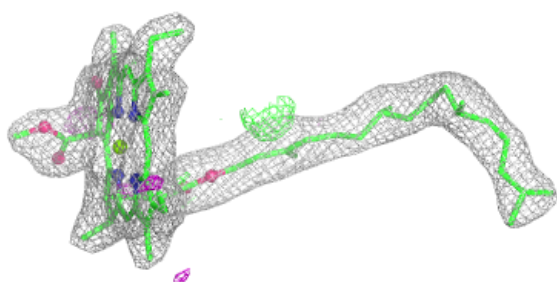
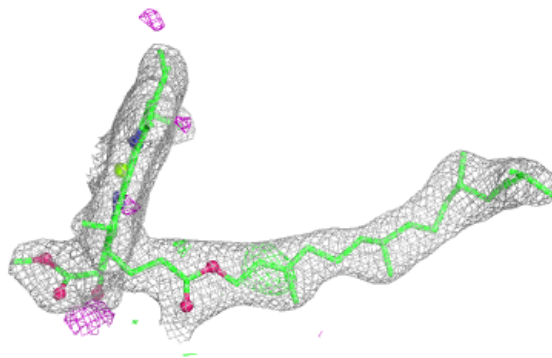
Electron density around PHO A 407 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



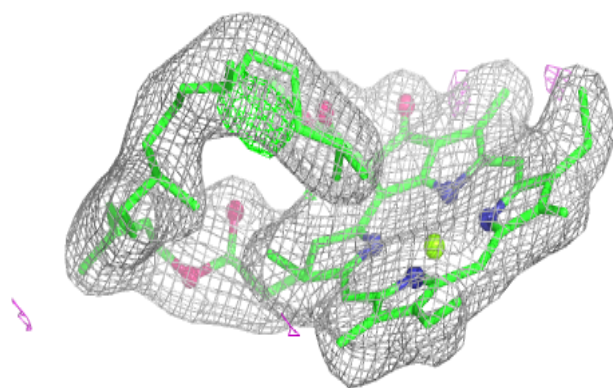
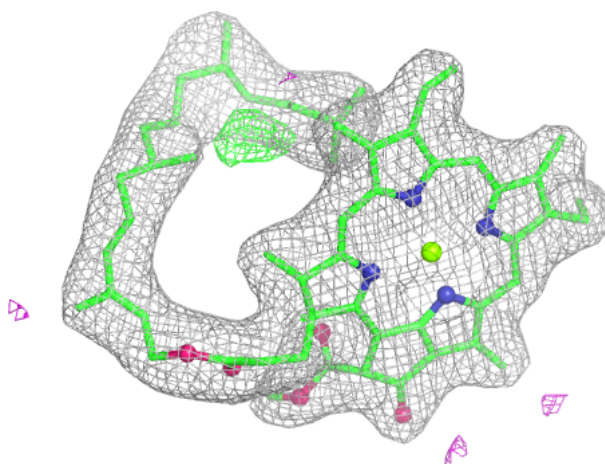
Electron density around CLA b 605:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



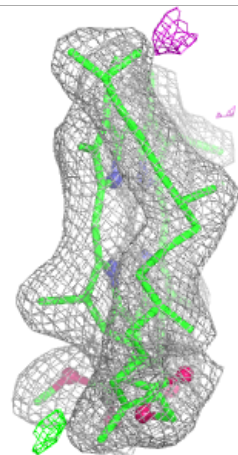
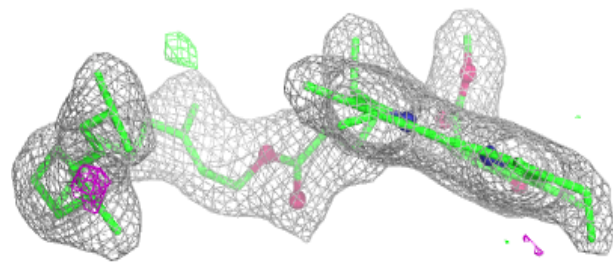
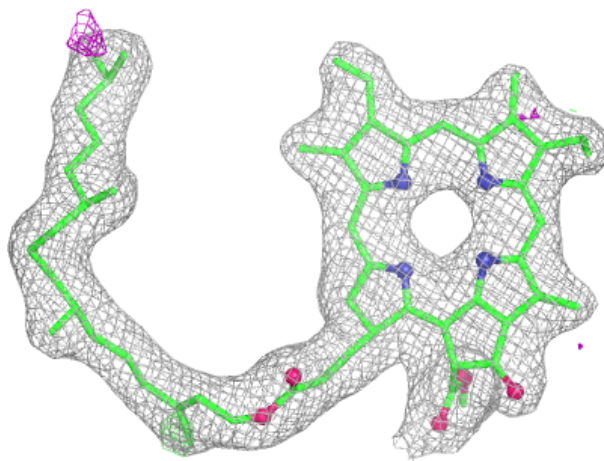
Electron density around CLA B 615:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



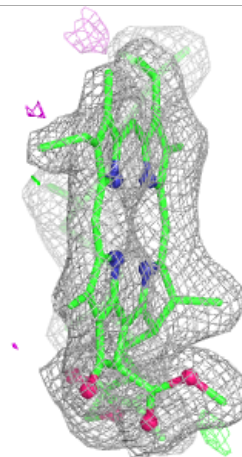
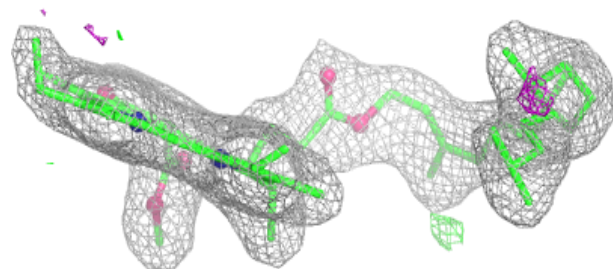
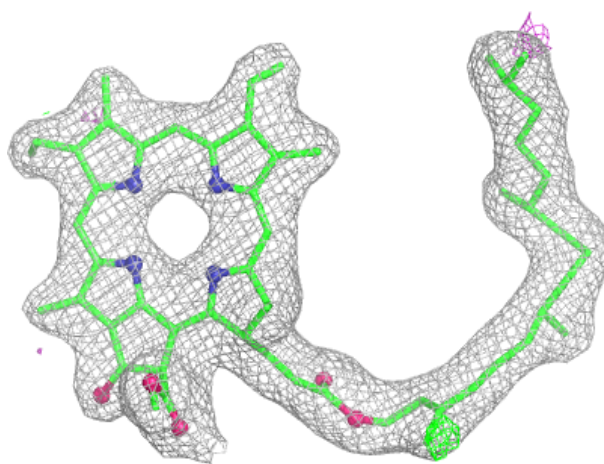
Electron density around PHO a 408 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



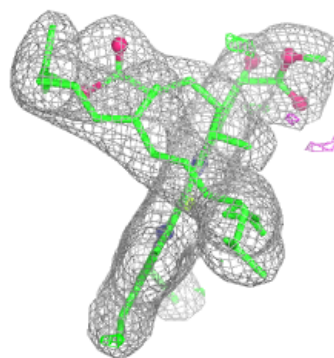
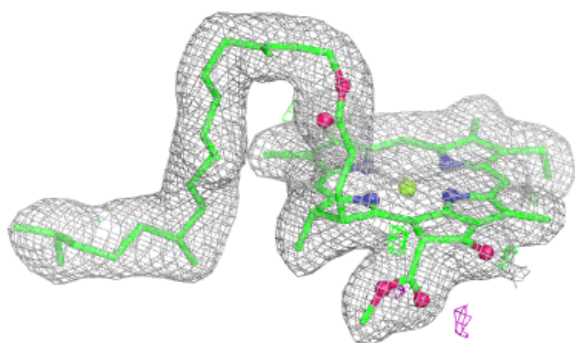
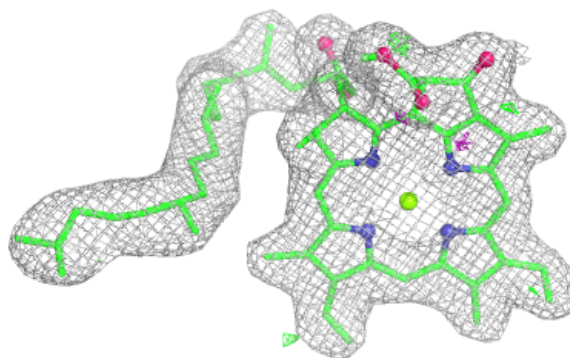
Electron density around PHO a 408 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

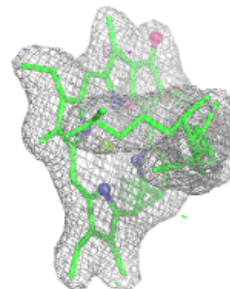
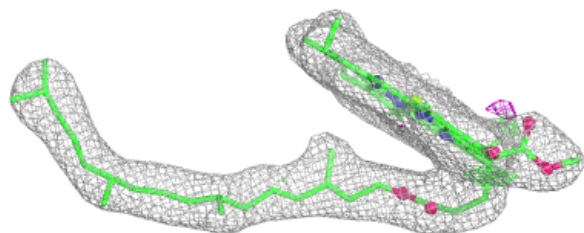
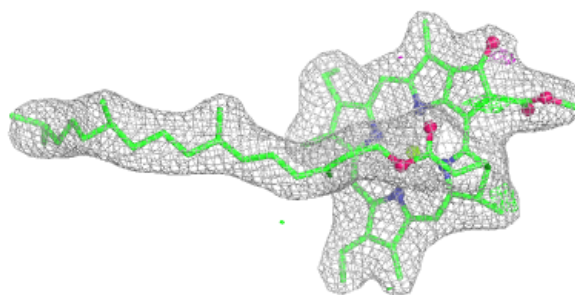


Electron density around CLA A 405 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

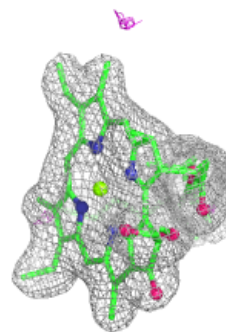
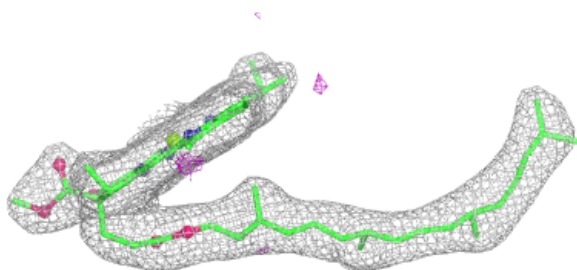
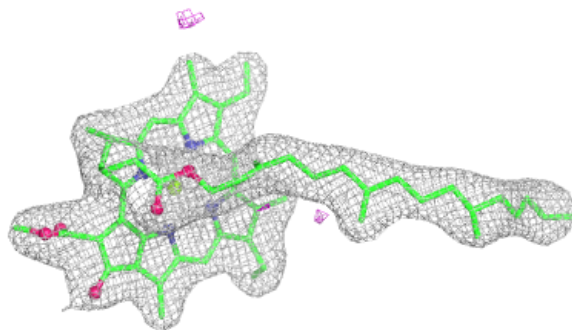
**Electron density around CLA b 608:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



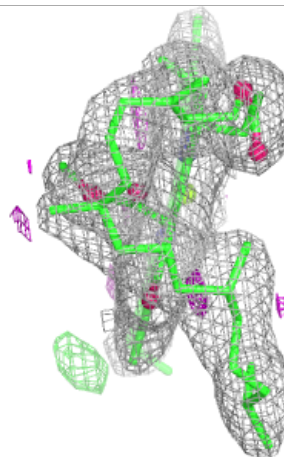
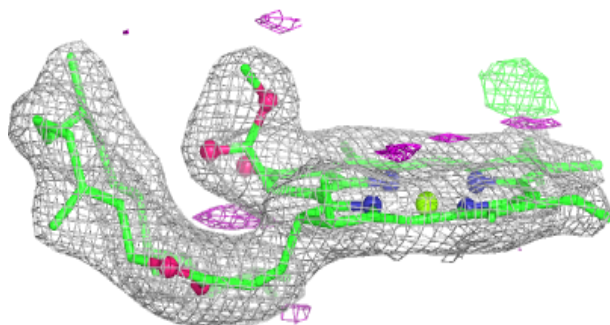
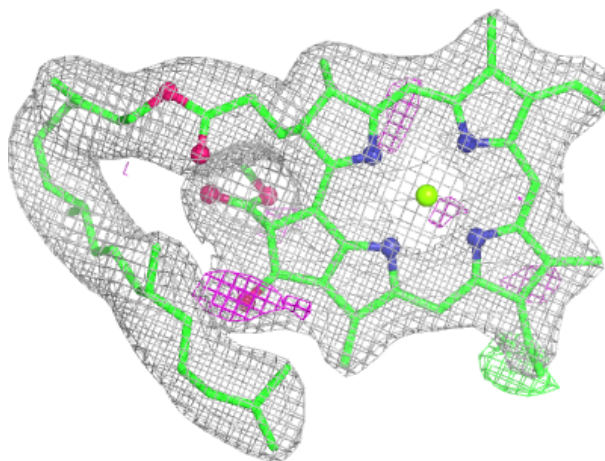
Electron density around CLA B 608:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



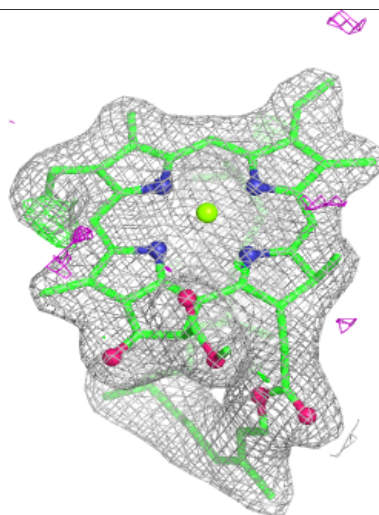
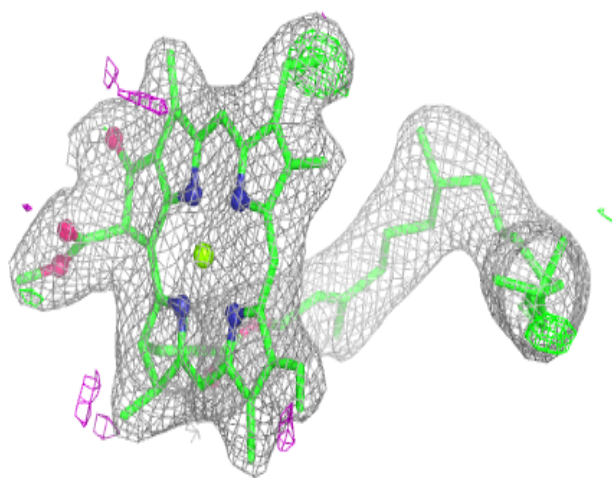
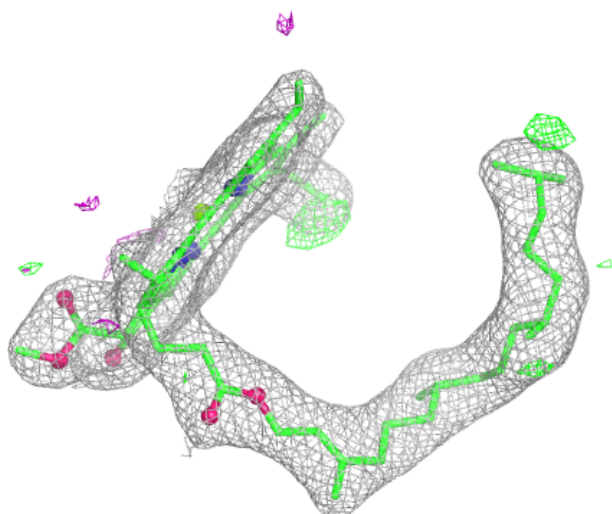
Electron density around CLA b 610:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



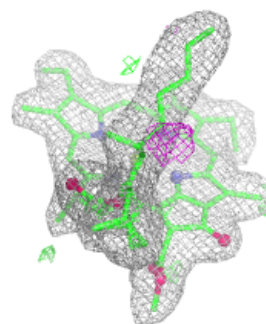
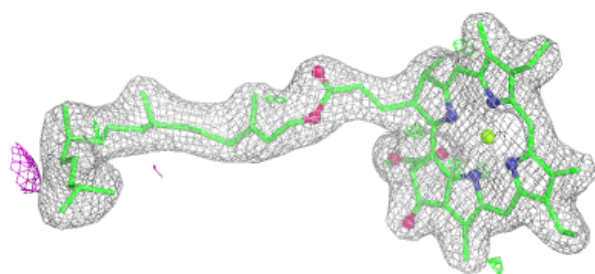
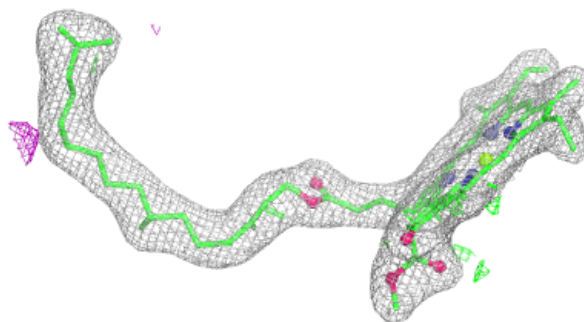
Electron density around CLA b 611:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



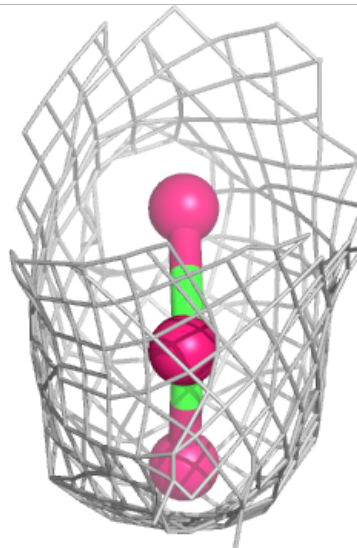
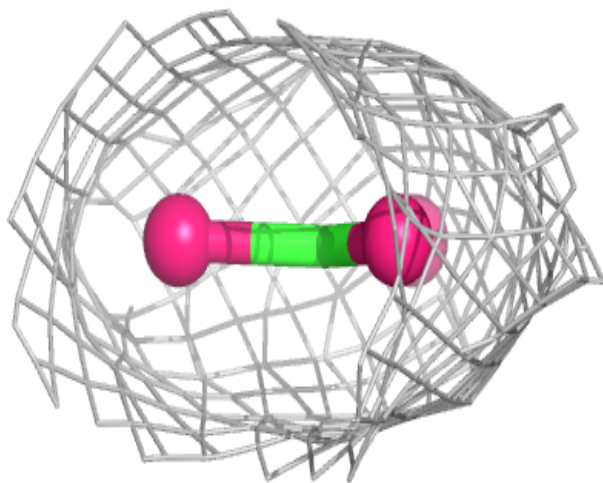
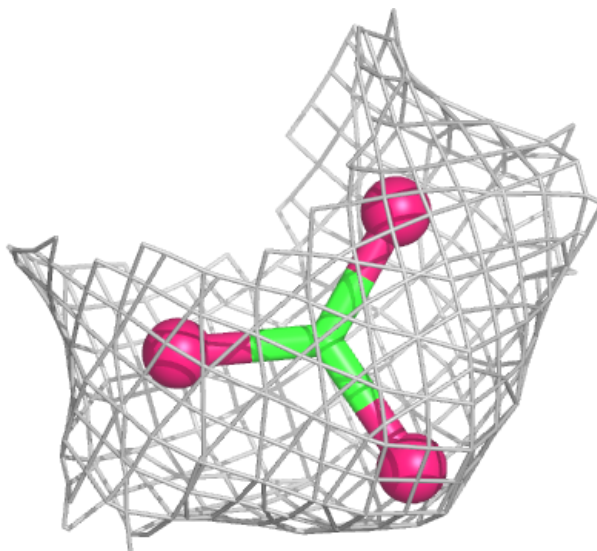
Electron density around CLA D 404 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



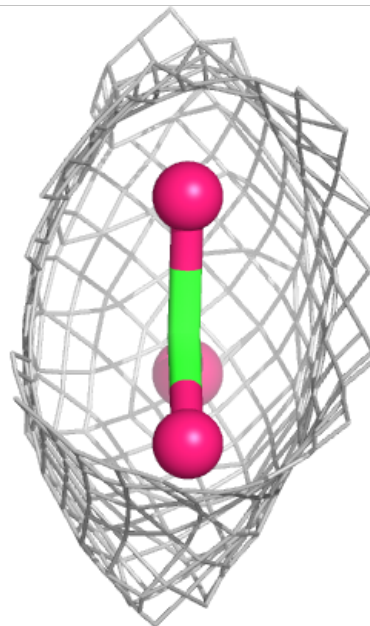
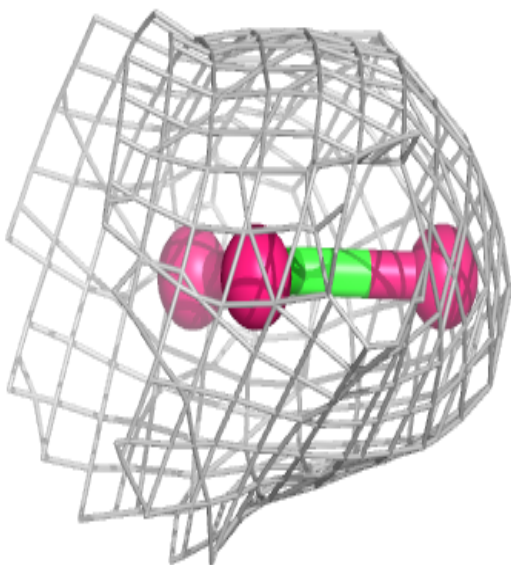
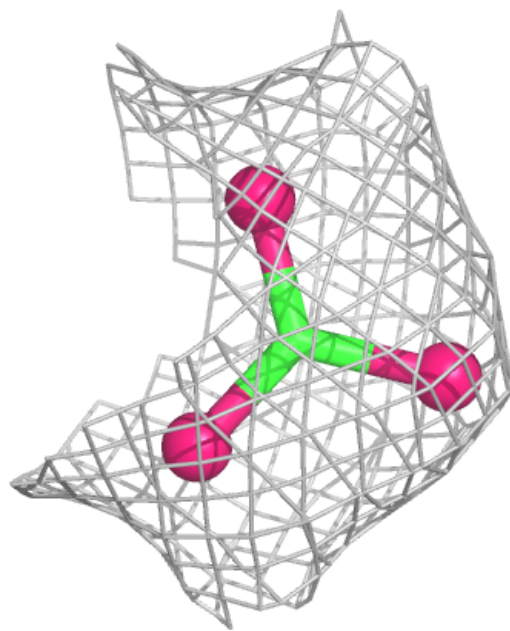
Electron density around BCT D 402 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



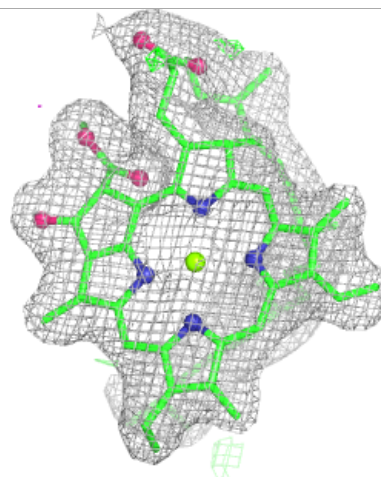
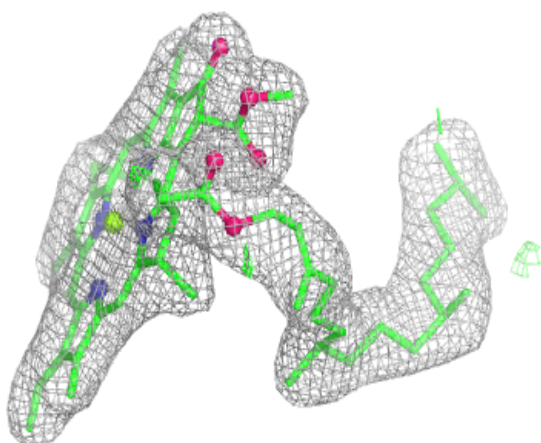
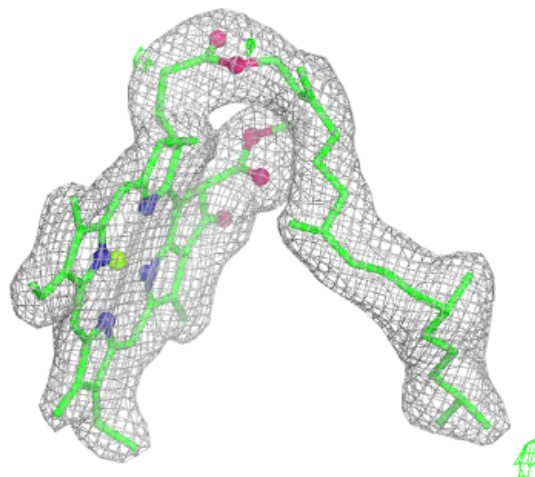
Electron density around BCT D 402 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



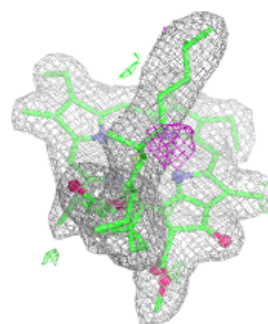
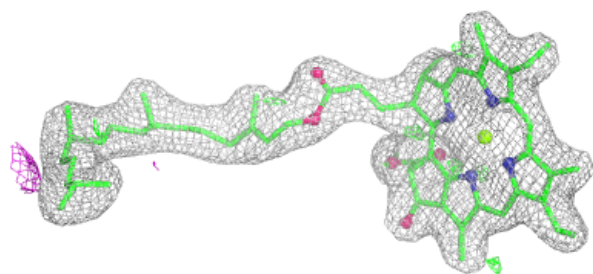
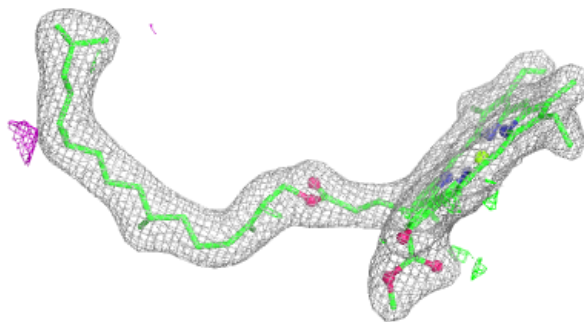
Electron density around CLA b 613:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



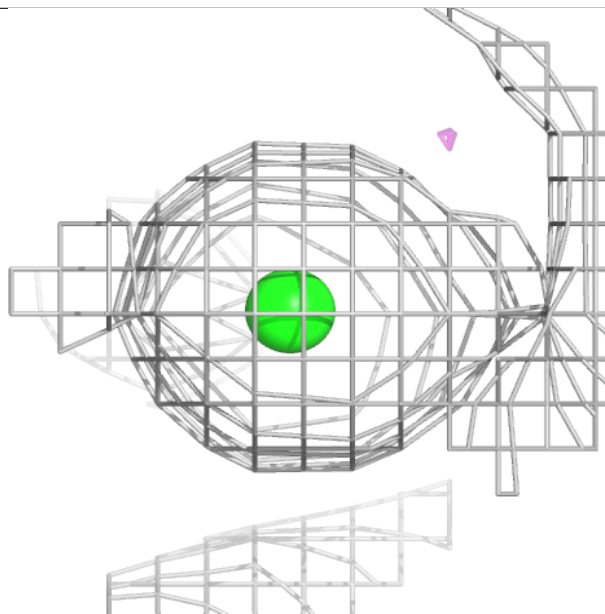
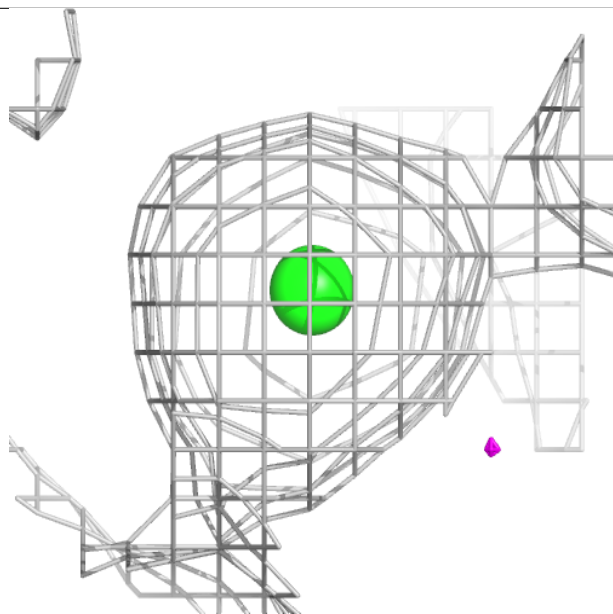
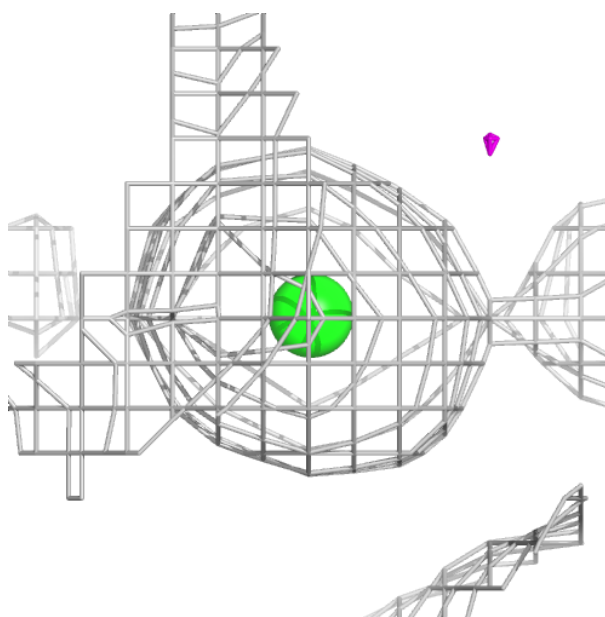
Electron density around CLA D 404 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



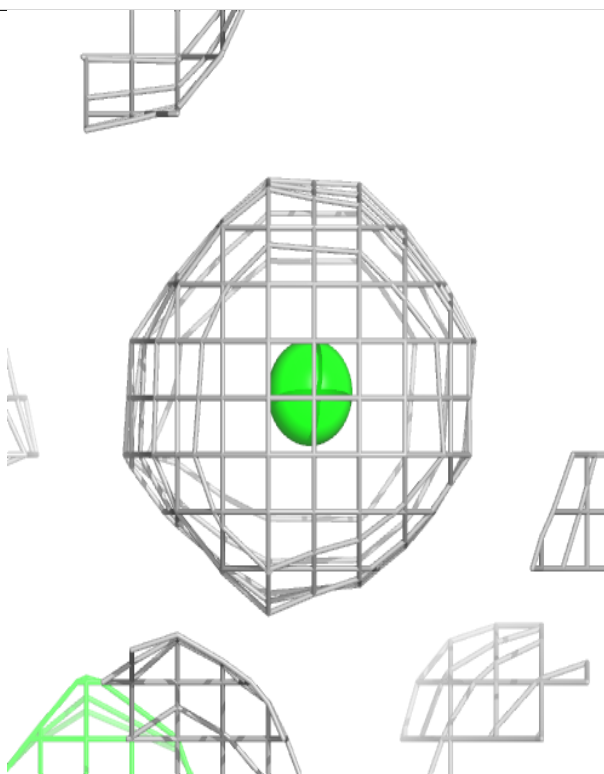
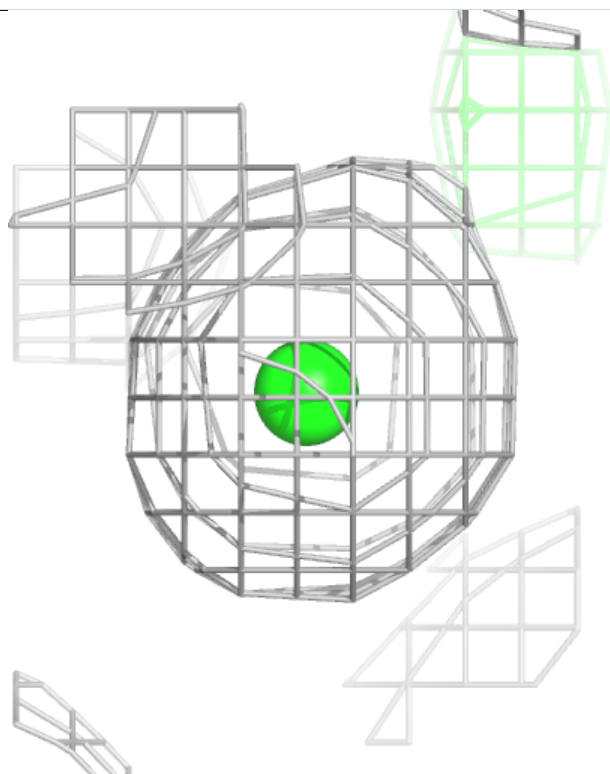
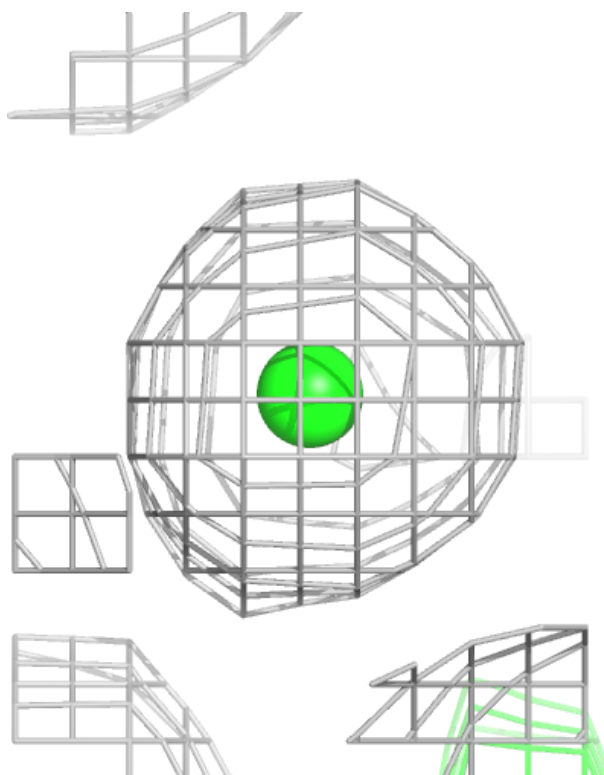
Electron density around CL a 404 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



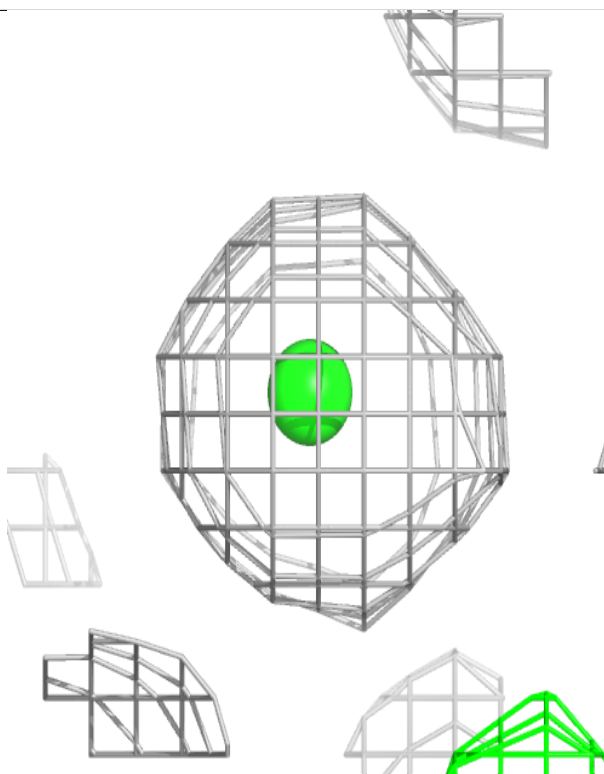
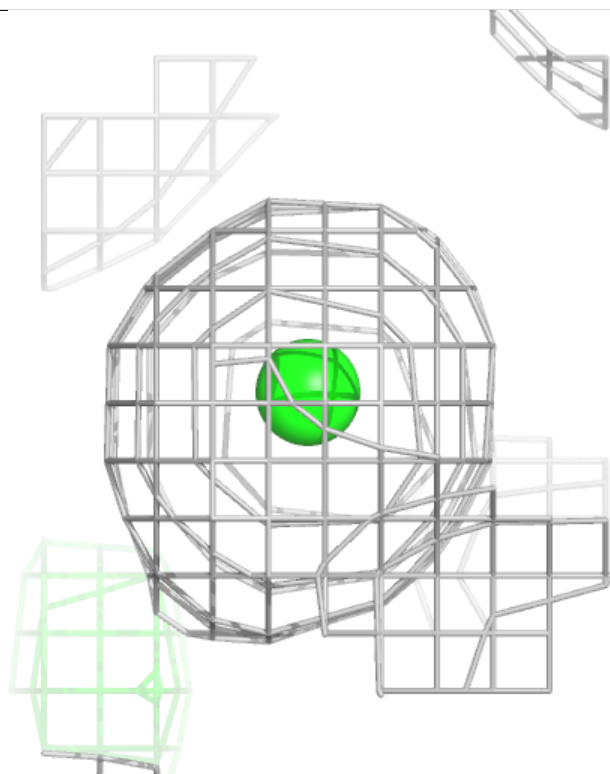
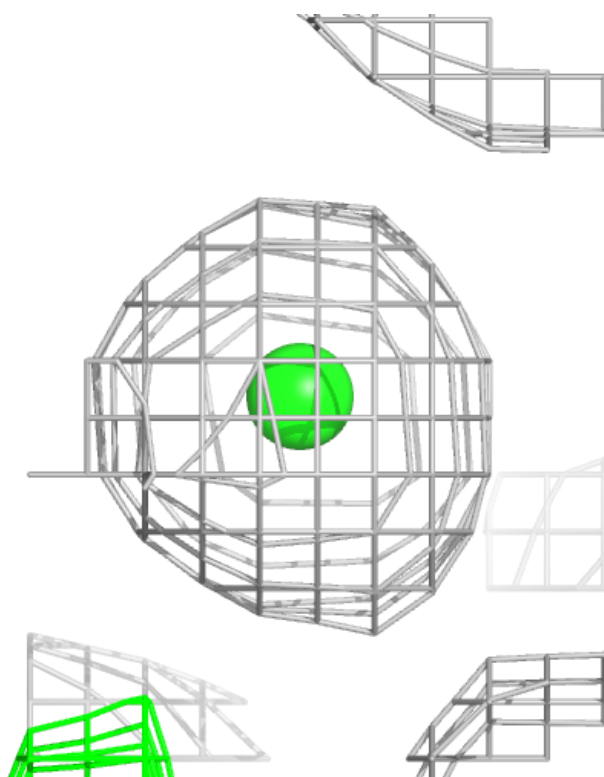
Electron density around CL a 403 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



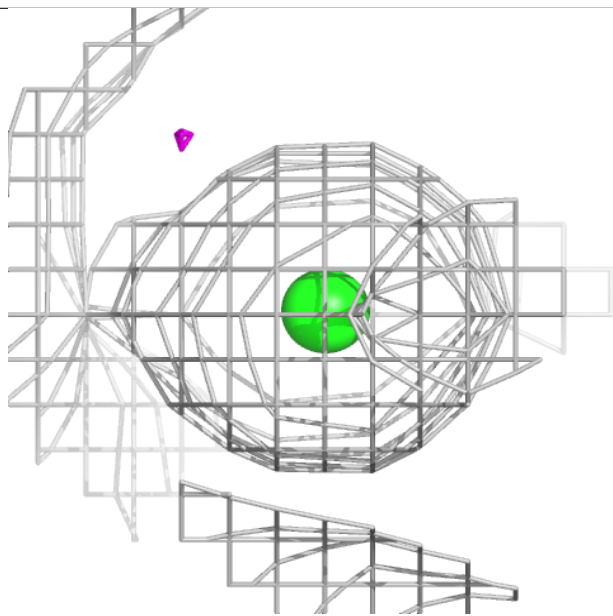
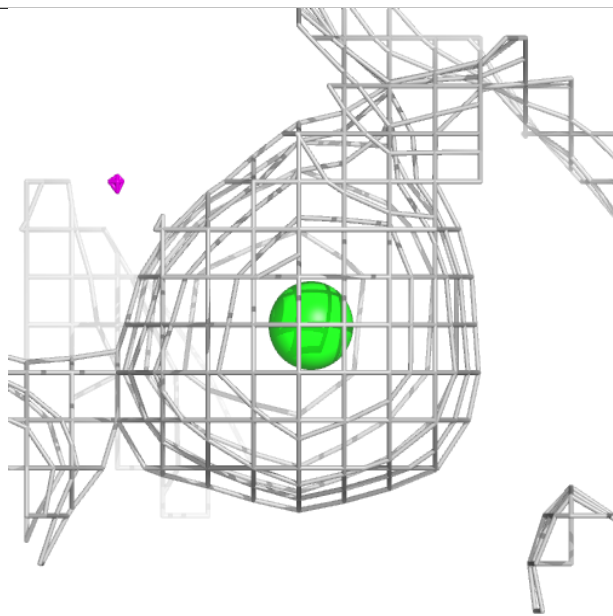
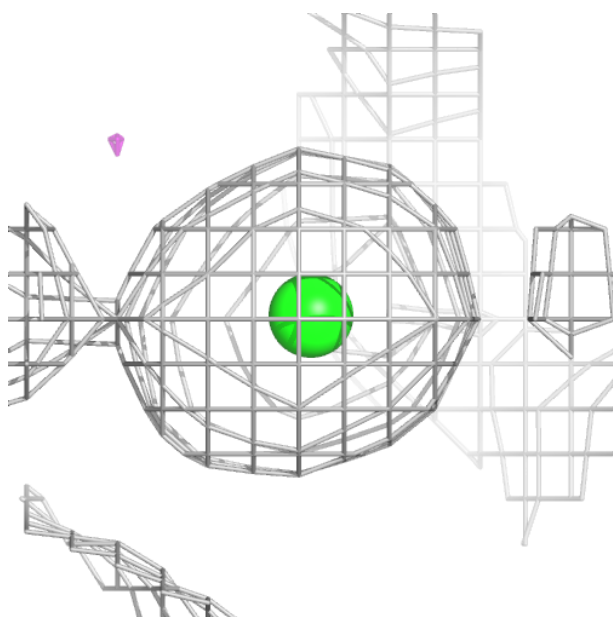
Electron density around CL a 403 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



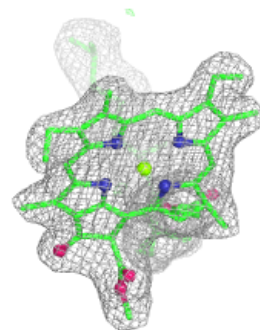
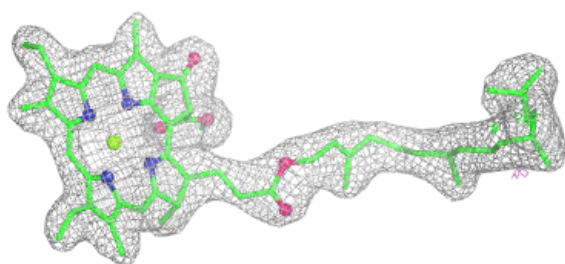
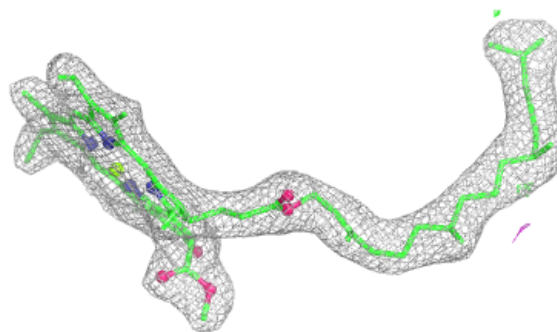
Electron density around CL a 404 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

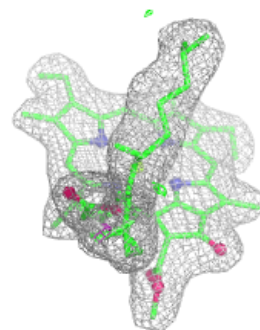
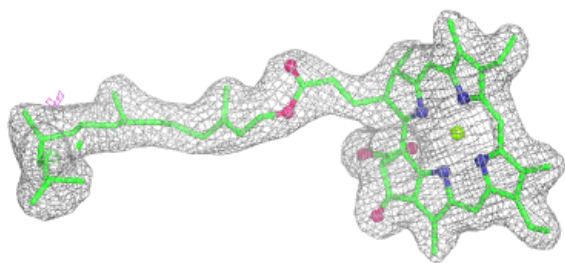
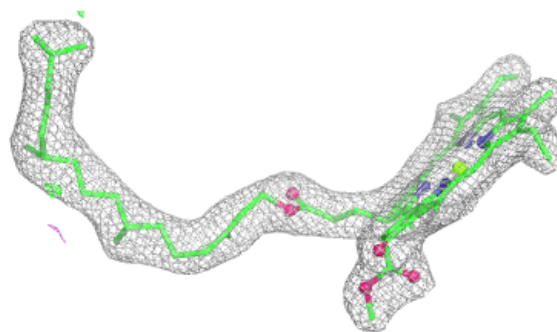


Electron density around CLA d 402 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

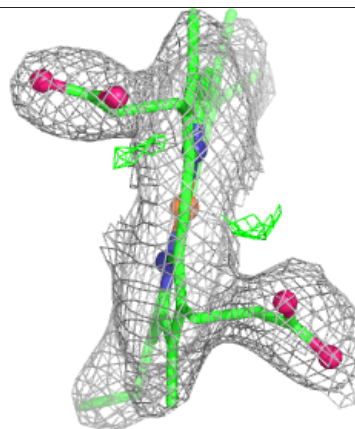
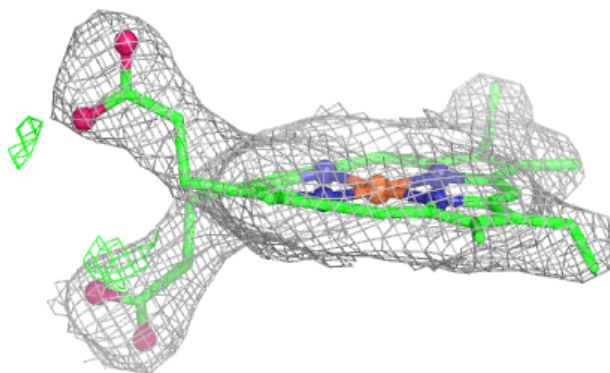
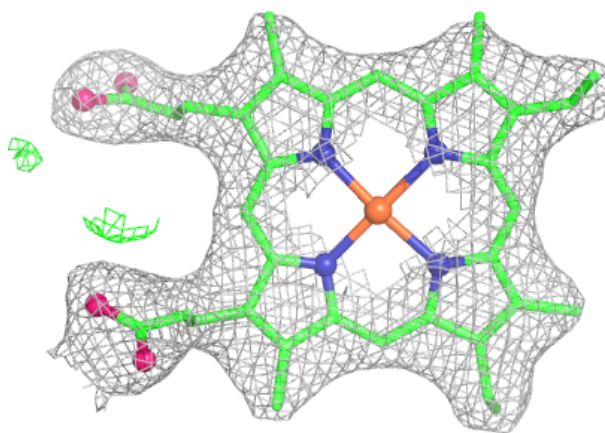
**Electron density around CLA d 402 (B):**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



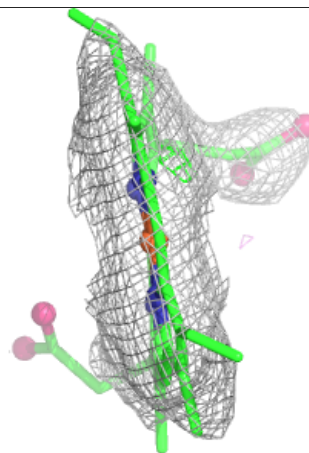
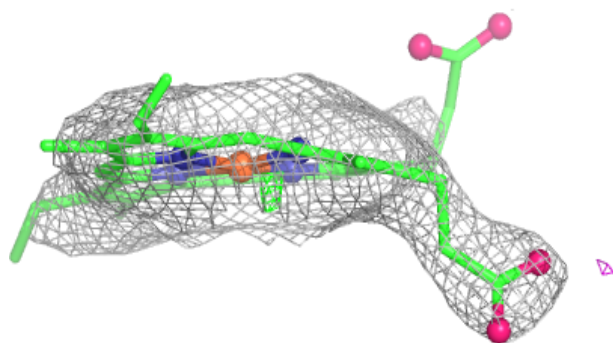
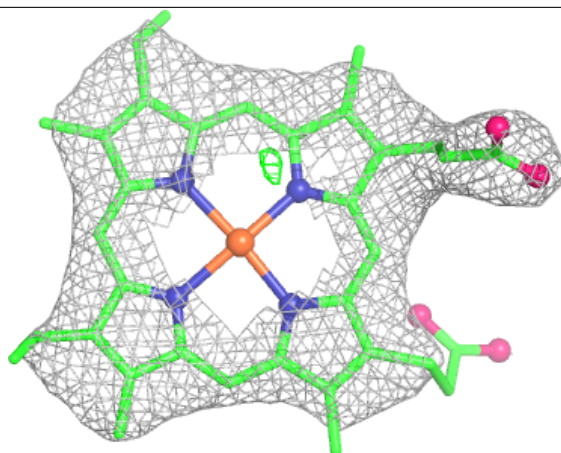
Electron density around HEM F 102:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



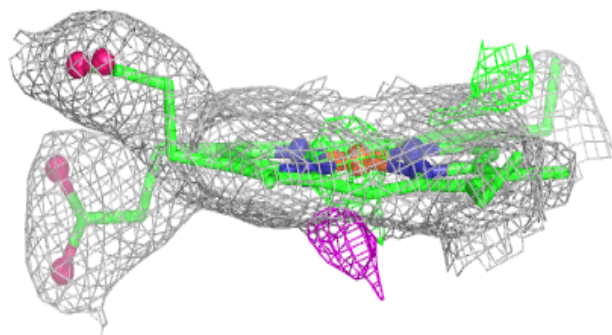
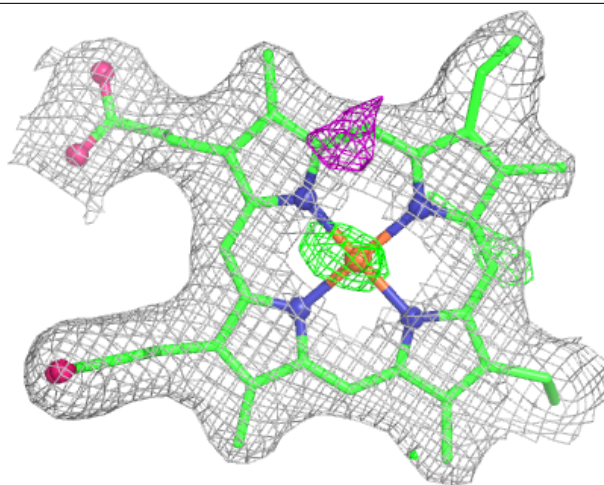
Electron density around HEM f 101:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



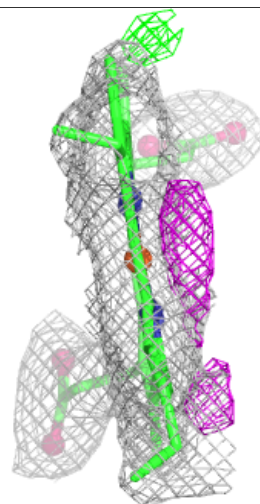
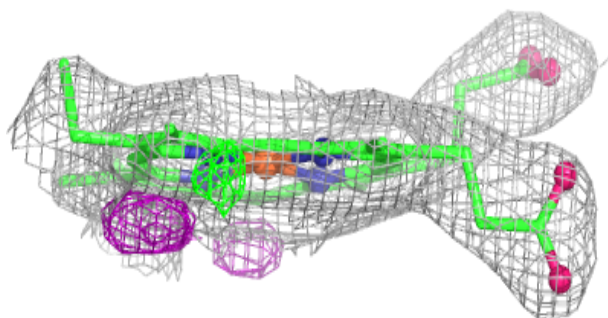
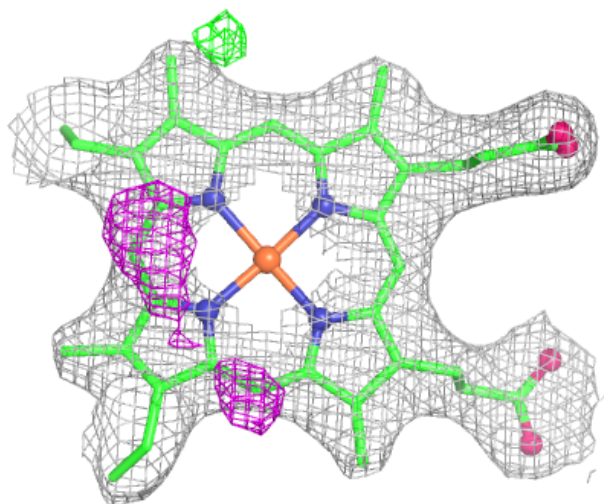
Electron density around HEC V 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



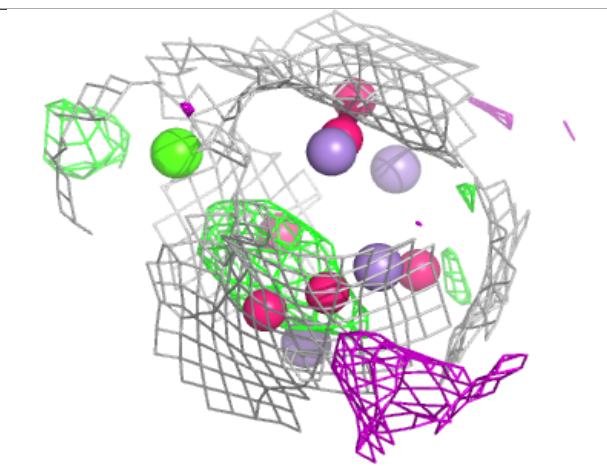
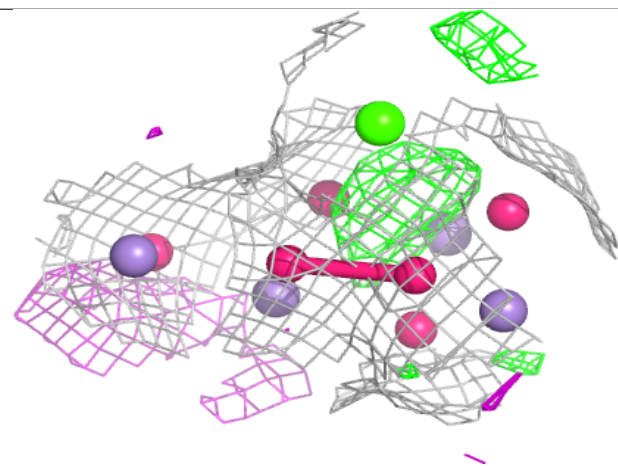
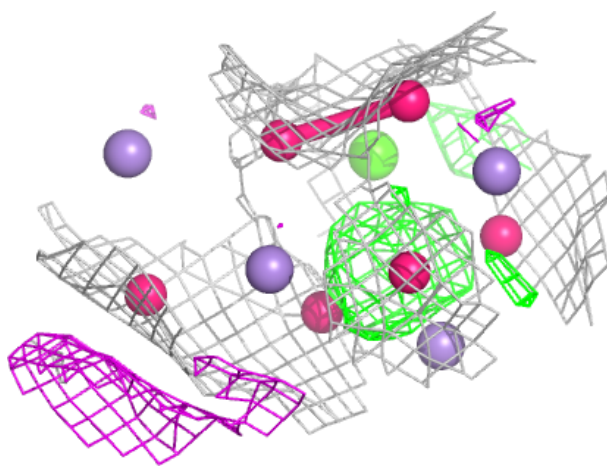
Electron density around HEC v 201:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



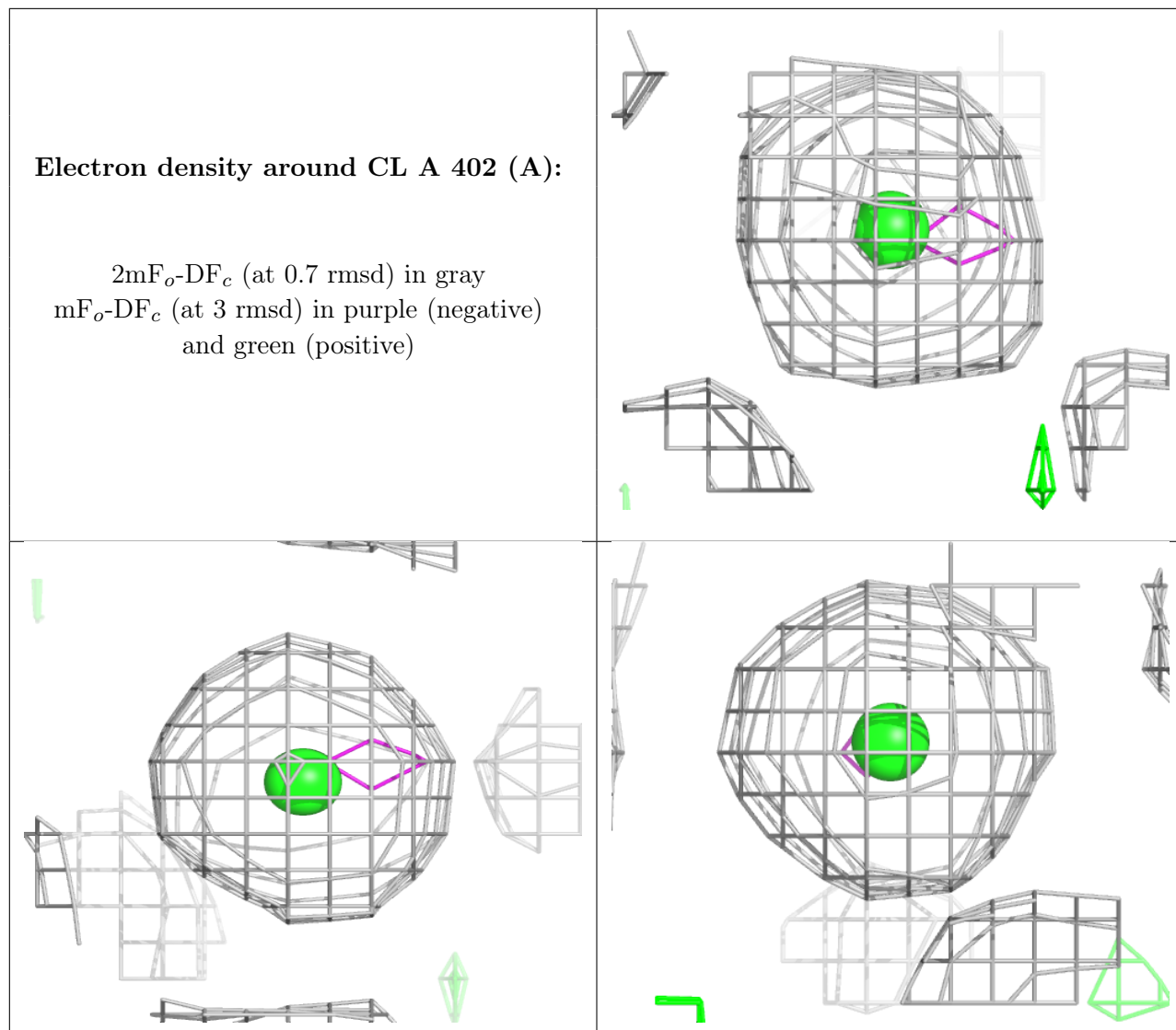
Electron density around OEY A 401 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



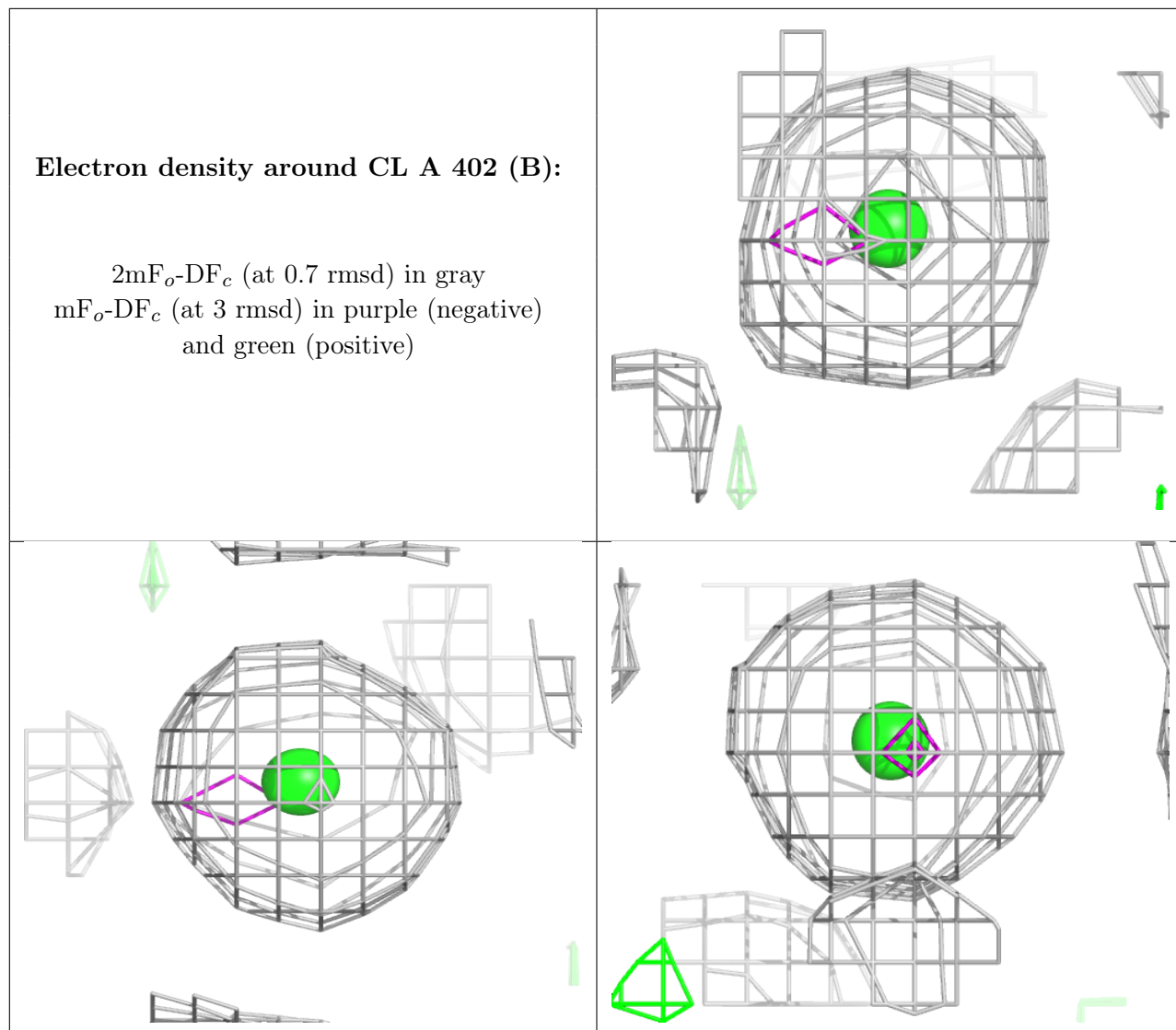
Electron density around CL A 402 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



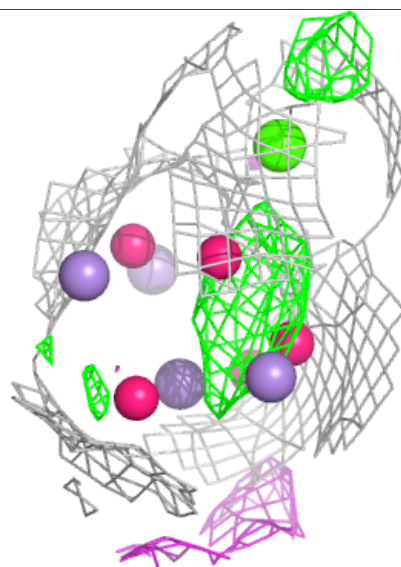
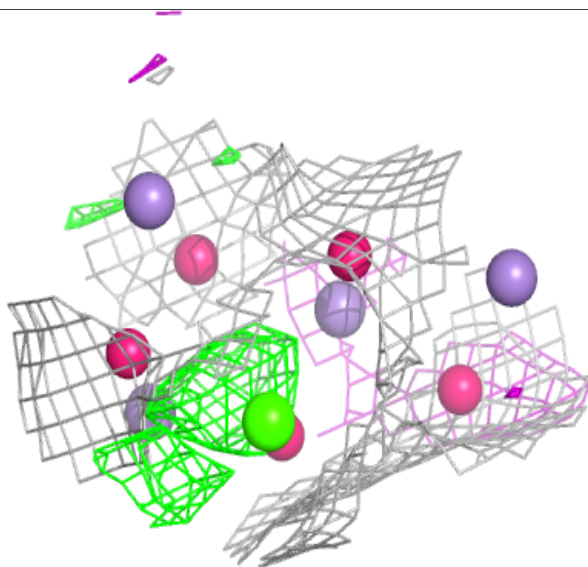
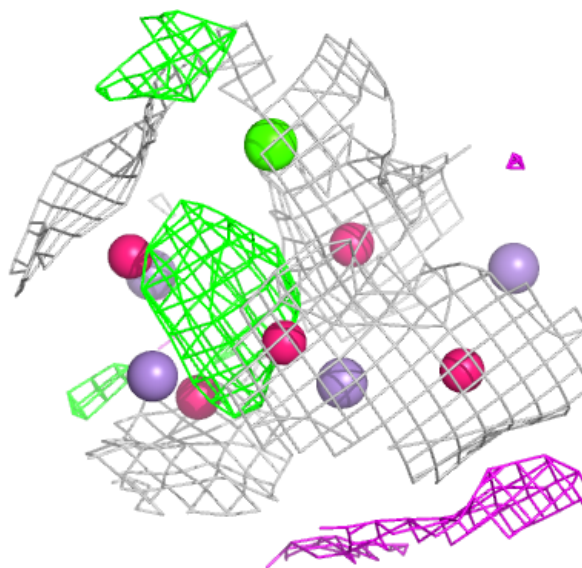
Electron density around CL A 402 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



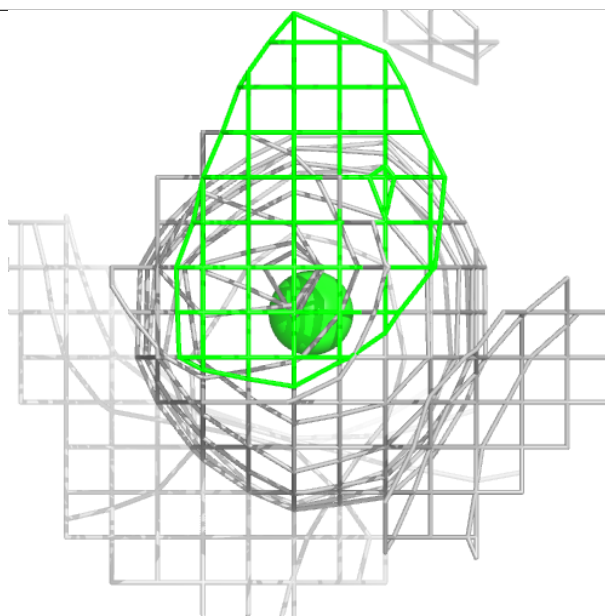
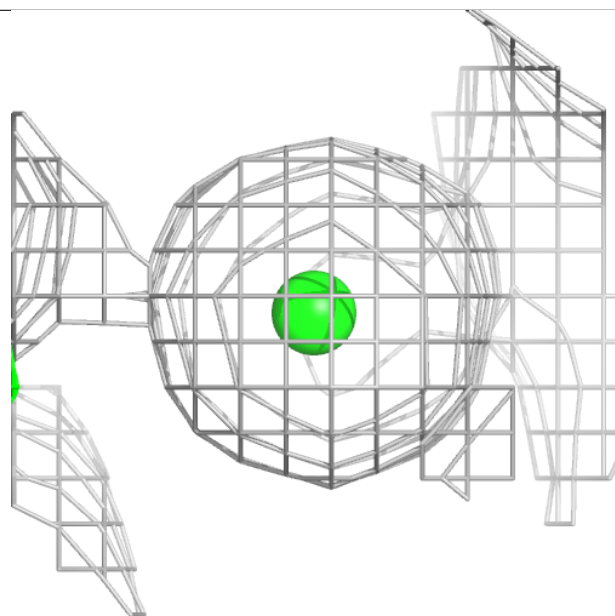
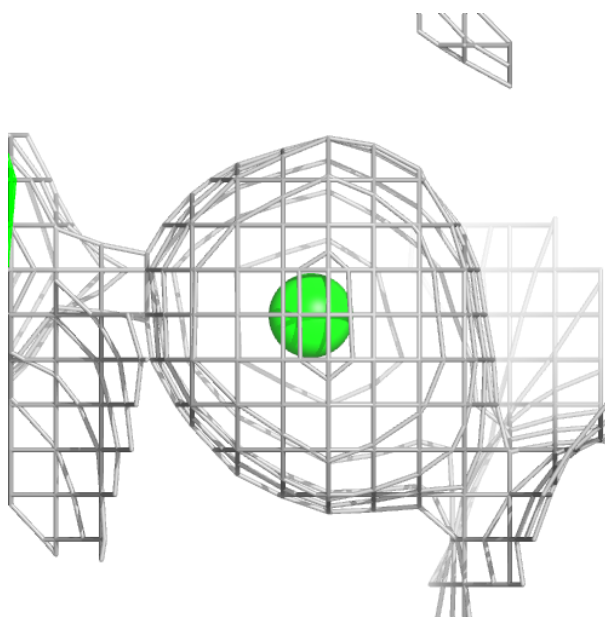
Electron density around OEX A 413 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



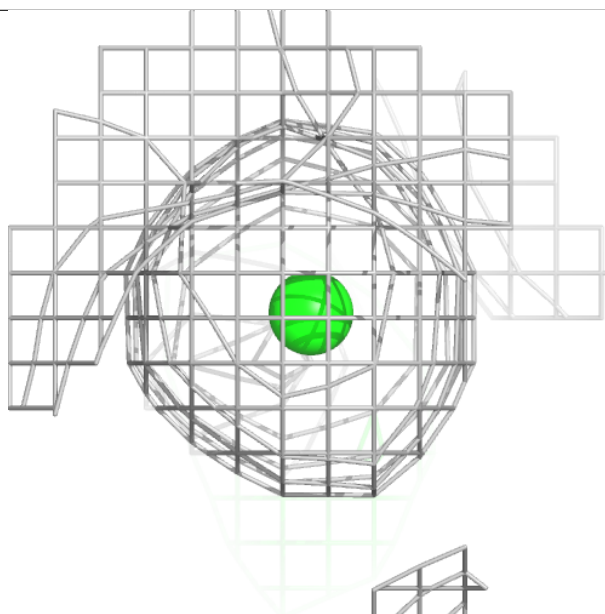
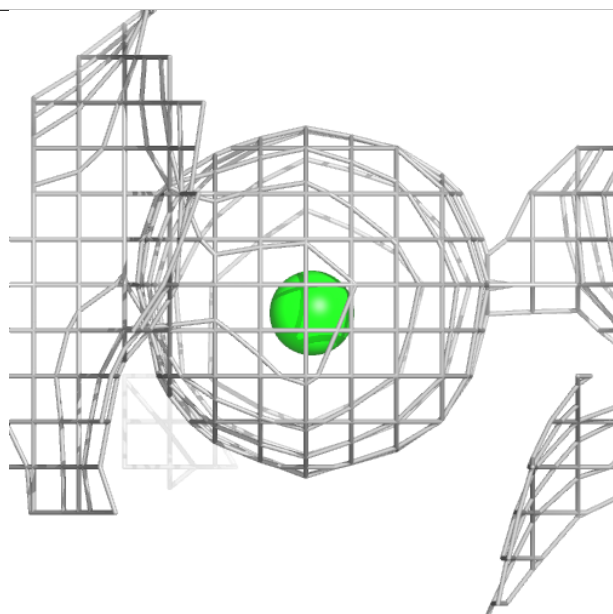
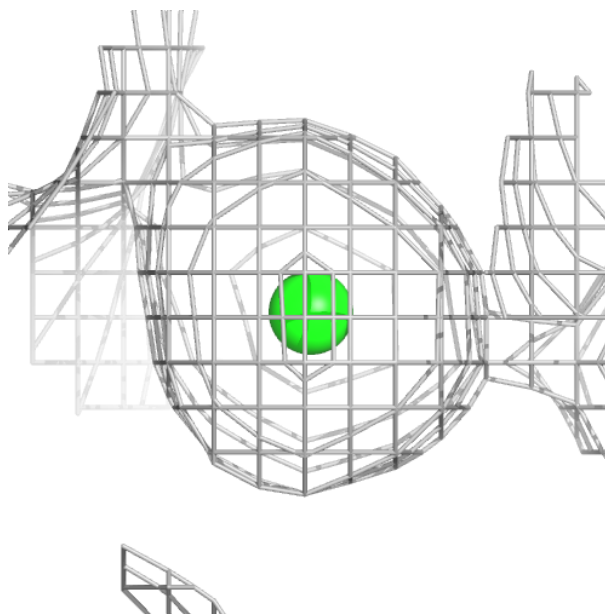
Electron density around CL A 403 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



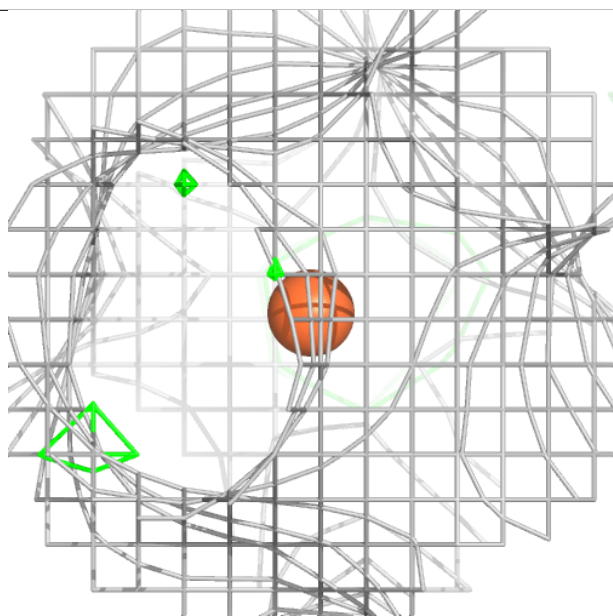
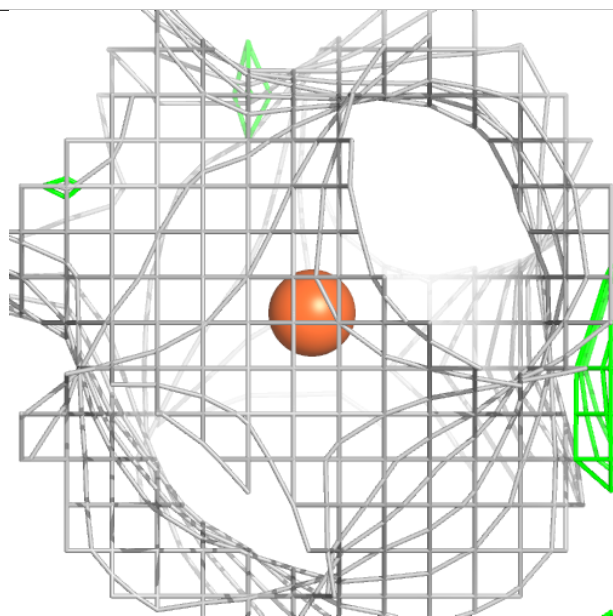
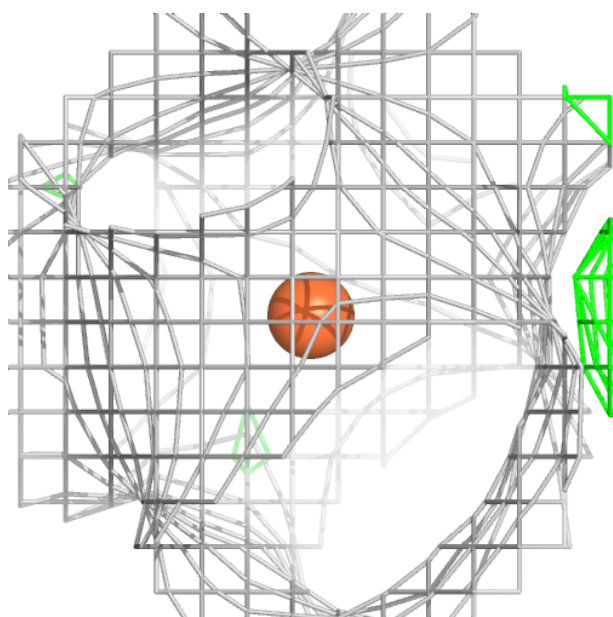
Electron density around CL A 403 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



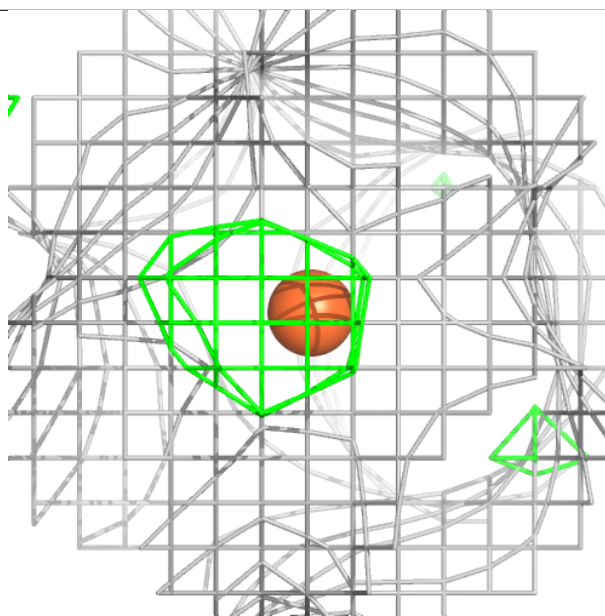
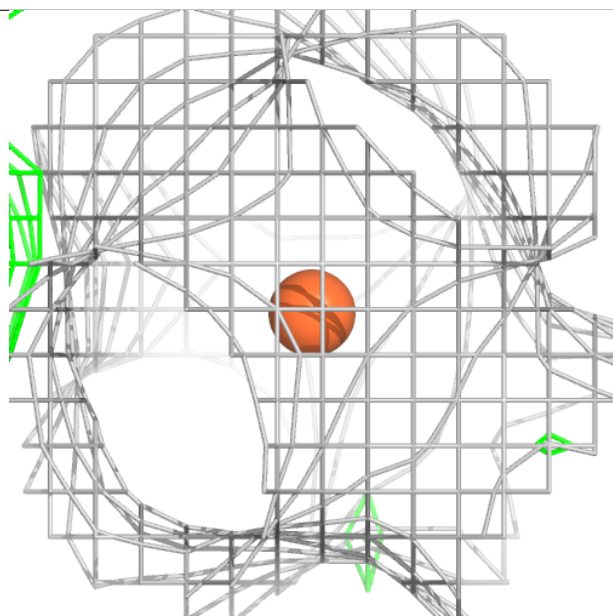
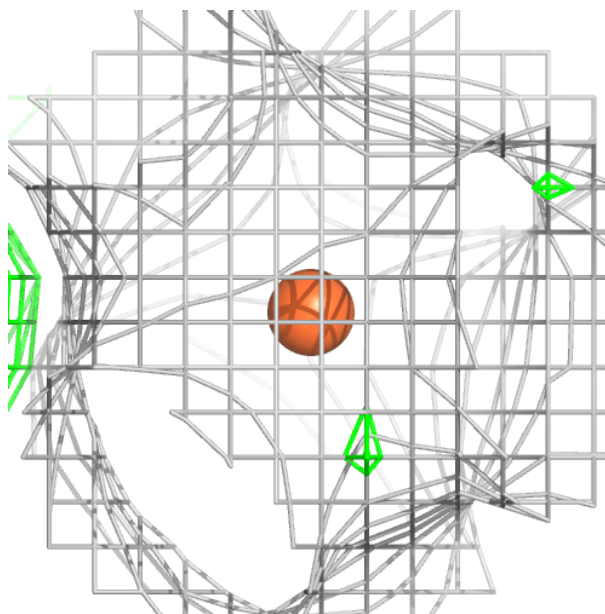
Electron density around FE2 a 402 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



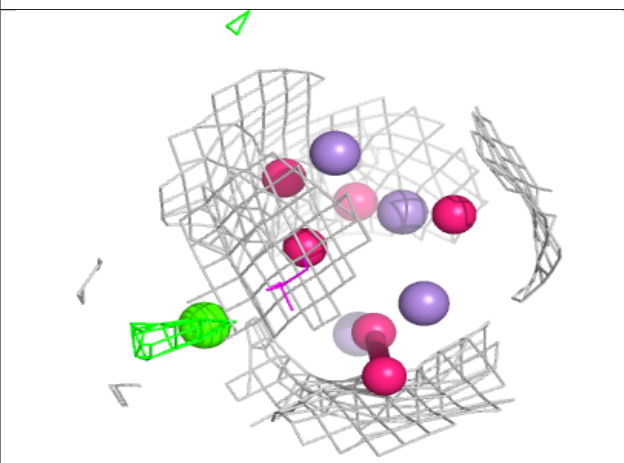
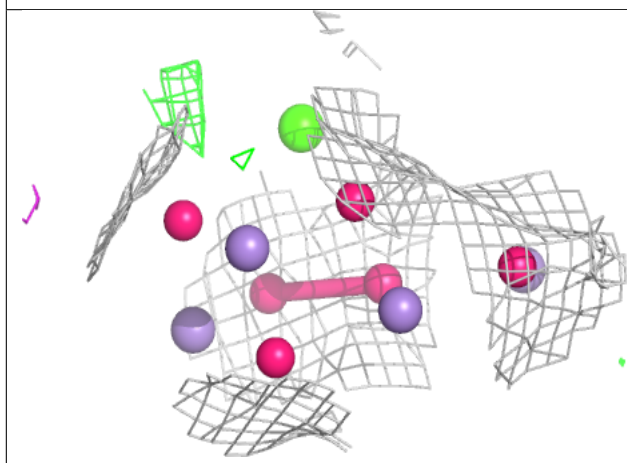
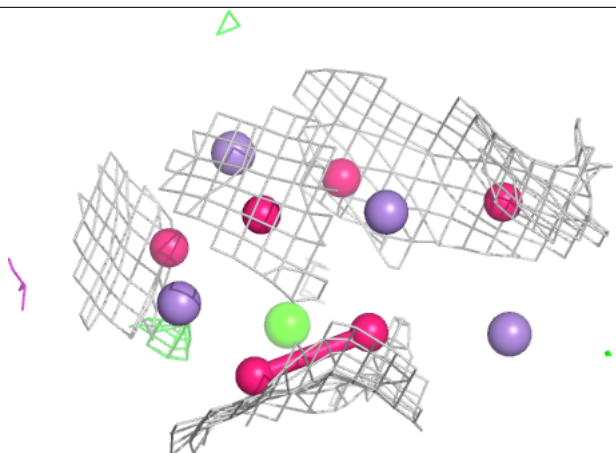
Electron density around FE2 a 402 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



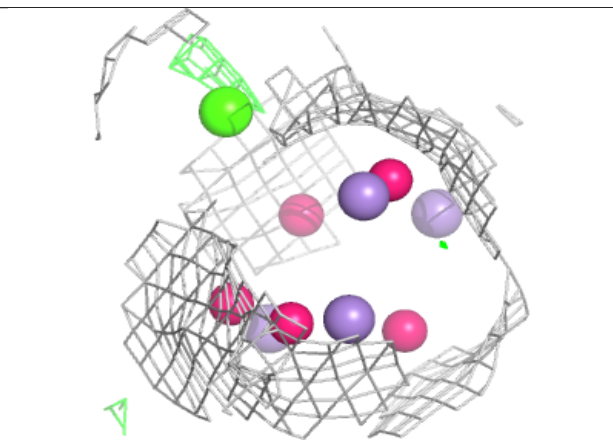
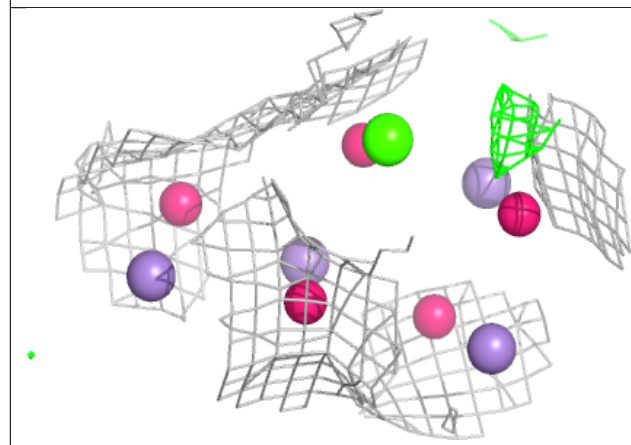
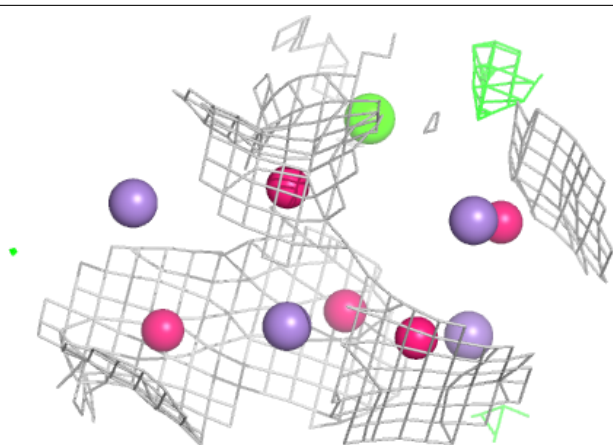
Electron density around OEY a 401 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



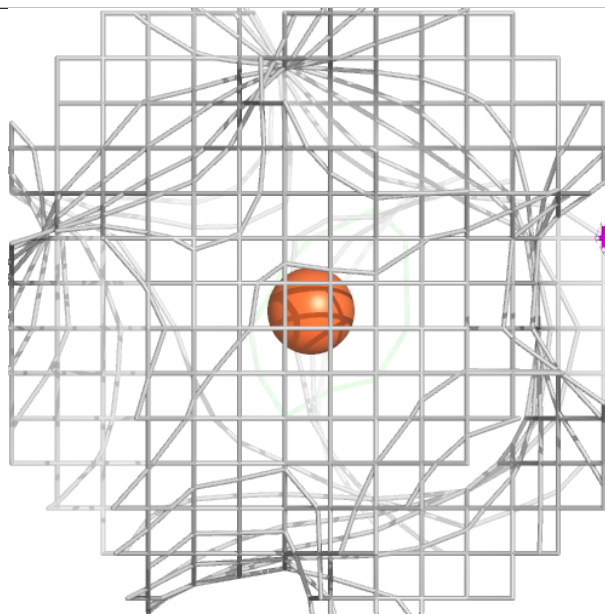
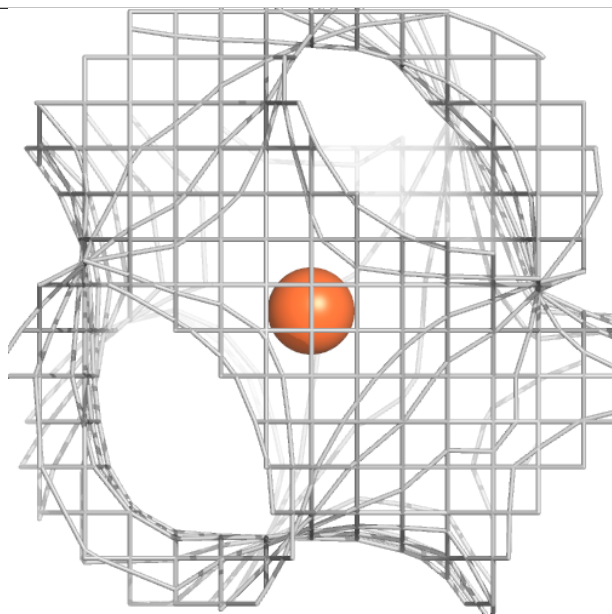
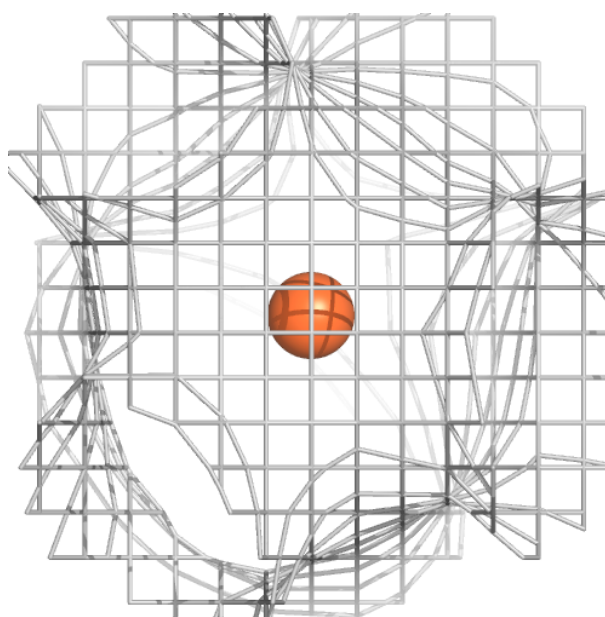
Electron density around OEX a 413 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



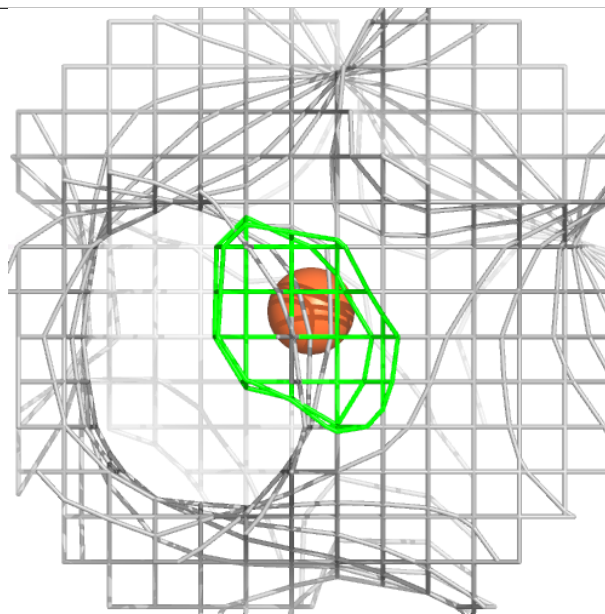
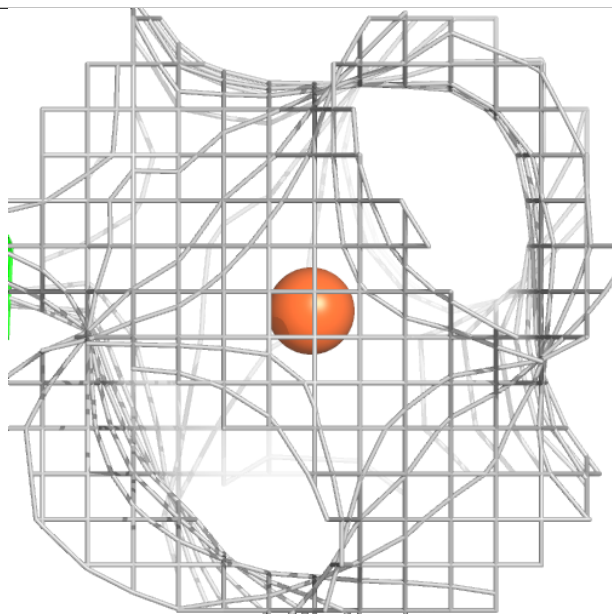
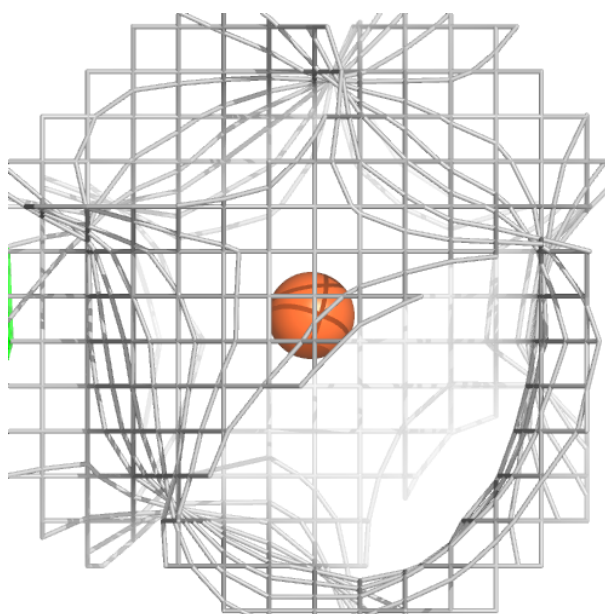
Electron density around FE2 D 401 (A):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FE2 D 401 (B):

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.